Supplementary Table 1-Posterior class probability of each tissue type; relate to Fig. 1b and Extended Data Fig. 1

Tissue Types	Sample size	mean ± standard deviat	P(C1lT)	Classification
Liver	153	42.4434 ±10.9155	0	high
SI	76	45.9105±13.0085	0	high
Esophagus	271	40.6468±14.8043	0	high
Stomach	149	31.6402±12.3226	0	high
Colon	129	34.7311±13.6174	0	high
Salivary Gland	97	25.3163±7.5447	0	high
Prostate	169	34.1201±13.0331	0	high
Bladder	91	31.3717±8.8247	0	high
Breast	240	25.5097±9.3526	0	high
Lung	306	23.1637±5.9364	0	high
Ovary	106	30.9952±8.4593	0	high
Uterine/Cervix	28	29.5271±10.9981	0	high
Pancreas	80	8.8798±2.7321	0	low
Thyroid	98	6.7295±2.3581	0	low
Brain	84	5.4363±2.0664	0	low
Muscle	353	6.1393±2.2842	0	low
Kidney	186	8.0419±2.2623	0	low
Adrenal gland	99	6.0696±2.0218	0	low
Lymph nodes	104	6.5961±1.9084	0	low

Supplementary Table 2-siRNA transfection efficiency RT-PCR NAMPT; relate to Fig. 1c and Extended Data Fig. 3b,3c

	siNTC	siNAPRT	siNADSyn1	siNAMPT	siNMRK1	siNMRK2
NHA	-0.4558045	-0.4349248	-0.4749749	-2.0347422	-0.5057958	-0.6334649
IMR90	-0.6047295	-0.654733	-0.6348648	-2.1842848	-0.6349489	-0.7046446
RPE-1	-0.6349492	-0.6048482	-0.6347494	-2.1934749	-0.7247925	-0.7734723
MCF10a	-0.7746843	-0.8046842	-0.7746865	-2.7947424	-0.8049234	-0.7173746
HEK293T	-0.6347422	-0.6747925	-0.8174725	-2.9534375	-0.8247948	-0.6483042
LE:K_562	0.63599146	0.6680757	0.64432004	-2.5505082	0.6209333	0.63494742
LE:SR	2.20481452	2.16002408	2.19683347	-2.2404168	2.02507735	2.03534714
RE:A498	2.07381993	1.98444747	2.12074181	-2.0774003	2.14666917	2.036397
RE:RXF_393	0.61878671	0.55719865	0.62168552	-2.8664001	0.56865257	0.57516838
GBM:U87	0.62752725	0.67943875	0.62845076	-1.762254	0.59907102	0.73887996
GBM:U87vIII	1.40900865	1.44250005	1.36587869	-2.3926773	1.50268863	1.45542538
GBM:GBM39	1.46791664	1.50709084	1.46352271	-2.4053267	1.36767019	1.36990129
GBM:GBM6	1.39148552	1.39793457	1.36194885	-2.3889454	1.35937248	1.40819169
CNS:SF_539	-0.7977991	-0.843745	-0.7686007	-1.7661788	-0.7085772	-0.6444941
CNS:SNB_75	-0.2557219	-0.2679477	-0.2210624	-2.2738572	-0.3064026	-0.2483701
CNS:SNB_19	-0.9628197	-0.9414868	-0.9765771	-1.9443015	-0.8794605	-0.914271
CNS:U251	-0.7938484	-0.754974	-0.7960201	-1.6158485	-0.810848	-0.7254651
CNS:SF_268	-0.121718	-0.1783419	-0.0914275	-2.0499411	-0.0683235	-0.0191303
ME:MALME_3M	0.97674053	0.98170063	0.96913367	-1.8114963	0.9672448	0.83871437
ME:M14	1.0871972	1.11455474	1.05962851	-1.672551	1.01534713	1.05641093
ME:SK_MEL_5	0.55358985	0.58226845	0.54464198	-2.052337	0.51089791	0.66135161
ME:LOXIMVI	0.97177549	0.95425966	0.95244283	-2.0390909	0.94094306	0.86396628
ME:SK_MEL_2	-0.1701256	-0.1637077	-0.1960523	-2.2347031	-0.1311622	-0.1726729
ME:UACC_257	-0.340082	-0.3323973	-0.314714	-2.3836775	-0.3865795	-0.3191738
PR:PC3	-0.643241	-0.6794135	-0.6370285	-2.393901	-0.7217924	-0.6591123
PR:LNCAP	-0.8502926	-0.8156116	-0.8588217	-2.3939677	-0.8206317	-0.7884228
PR:DU_145	-0.1514957	-0.1691765	-0.1251735	-2.1503549	-0.1735278	-0.1950034
BR: T47D	-0.8815264	-0.8836121	-0.8388567	-1.7306316	-0.868459	-0.8531236
BR:Hs578T	-0.6675724	-0.668611	-0.6808932	-1.6330453	-0.6093108	-0.5538868
BR:BT_549	-0.2661794	-0.2878722	-0.3157215	-1.888788	-0.347807	-0.428644
BR:MDA_MB_231	1.45133944	1.3893533	1.45012876	-1.9792776	1.32705075	1.45520194
BR: MCF7	0.16368809	0.12778069	0.17678098	-1.6979112	0.2053545	0.16392628
LU:PC9	-0.6075814	-0.600563	-0.6024835	-1.846552	-0.6692576	-0.6231411
LU:H23	-0.7734006	-0.7352185	-0.7594192	-1.9336768	-0.7329954	-0.7054083
LU:H322M	-0.9620018	-0.9457566	-0.9739204	-1.9373235	-0.9631579	-0.9087864
LU:H522	-0.9280655	-0.9147196	-0.9449561	-1.8374488	-0.9117651	-0.8477807
LU:HOP62	-0.6156568	-0.5942034	-0.6268383	-1.7494009	-0.623547	-0.6687013
LU:HOP92	-0.5698488	-0.5694621	-0.5568734	-1.4048476	-0.6072761	-0.6817043
LU:H460	2.1613107	2.20797122	2.19189195	-2.0425954	2.14893147	2.11704239
LU:A549	1.72440875	1.74697874	1.60444321	-2.0484738	1.5688674	1.6686942
CO:HT29	-0.5650881	-0.5457533	-0.5767888	-1.8649424	-0.5232166	-0.6425976

CO:COLO205	-0.9589008	-0.9583822	-0.948189	-1.9384947	-0.9062361	-0.9475593
CO:HCC_2998	-0.1362587	-0.2263814	-0.1147658	-2.064094	-0.254303	-0.2050553
CO:HCT_15	-0.5958855	-0.6289725	-0.5809255	-2.4440647	-0.6869042	-0.5254821
CO:KM12	-0.912356	-0.9153208	-0.9058566	-1.8494407	-0.9016327	-0.910512
CO:HCT_116	0.93453595	0.87723703	0.94836765	-1.964945	0.84752271	0.98187403
CO:SW_620	0.88464415	1.03090678	0.73418895	-1.9094435	0.90886206	0.80444369
OV:OVCAR_4	-0.1749292	-0.1823512	-0.1138424	-1.8407811	-0.1945515	-0.1813339
OV:OVCAR_5	-0.7620032	-0.7442542	-0.7369903	-1.9155085	-0.729407	-0.800447
OV:OVCAR_8	-0.9239541	-0.9189447	-0.8876702	-2.0248611	-0.9052189	-0.7671865
OV:SK_OV_3	-0.9851683	-0.9783376	-0.9611346	-2.4804988	-0.9824663	-0.9480763
OV:NCI_ADR_RES	-0.9795395	-0.9848172	-0.9780469	-2.0484857	-0.9399218	-0.9188302
PAN:CAPAN1	-0.7808498	-0.7541838	-0.7960574	-2.0497777	-0.7594628	-0.8049712
PAN:CAPAN2	-0.8886812	-0.8638058	-0.903693	-1.9381852	-0.9135011	-0.8720525
ESO:KYSE510	-0.9968926	-0.9826601	-1.0041176	-1.9855422	-0.9236467	-0.8374733
ESO:KYSE140	-0.9016451	-0.9152873	-0.9036069	-1.494969	-0.9081747	-1.0163159
H&N:BHY	-0.9884911	-0.9781435	-0.9934418	-2.1383537	-0.9462933	-0.9689458
H&N:OE21	-0.8336696	-0.7919474	-0.8253667	-2.038686	-0.8283644	-0.8048477
CER:HELA	1.40470901	1.30664192	1.48090439	-2.3949982	1.48474323	1.30374643

Supplementary Table 2-siRNA transfection efficiency RT-PCR
NMRK1; relate to Fig. 1c and Extended Data Fig. 3b,3c

	siNTC	siNAPRT	siNADSyn1	siNAMPT	siNMRK1	siNMRK2
NHA	-0.4558045	-0.4349248	-0.4749749	-0.5057958	-2.4294948	-0.6334649
IMR90	-0.6047295	-0.654733	-0.6348648	-0.6349489	-2.6349489	-0.7046446
RPE-1	-0.6349492	-0.6048482	-0.6347494	-0.7247925	-2.7247925	-0.7734723
MCF10a	-0.7746843	-0.8046842	-0.7746865	-0.8049234	-2.8049234	-0.7173746
HEK293T	-0.6347422	-0.6747925	-0.8174725	-0.8247948	-2.2247948	-0.6483042
LE:K_562	-1.1945568	-1.2001521	-1.1891136	-1.1721062	-2.0294944	-1.0603941
LE:SR	1.07166057	1.07469323	1.11115401	1.00873614	-2.2494543	1.34057101
RE:A498	1.10293285	1.12630184	1.04254064	1.11984472	-2.3235541	1.04295581
RE:RXF_39	0.75582901	0.71034571	0.7230065	0.82033276	-2.0077989	0.79013399
GBM:U87	0.65753094	0.60323102	0.61886912	0.73858927	-1.8987677	0.74020879
GBM:U87vIII	0.65544376	0.5106342	0.80875794	0.63344619	-1.5724233	0.72487782
GBM:GBM3	0.88749948	0.88622209	0.86917587	0.89066597	-1.8987447	0.85298005
GBM:GBM6	0.61624793	0.69219232	0.52072645	0.62508125	-2.4209949	0.54833807
CNS:SF_53	2.34010201	2.31250947	2.3355797	2.32851511	-2.294396	2.33052357
CNS:SNB_7	2.40426011	2.37152616	2.38419369	2.41230205	-2.6311643	2.5887535
CNS:SNB_1	2.08679849	2.13147628	2.08562207	2.00423686	-2.2204189	2.03793848
CNS:U251	1.53241822	1.56102825	1.50470228	1.5030839	-1.8879621	1.64413687
CNS:SF_26	1.50765047	1.47253293	1.42580565	1.59717687	-2.8936736	1.48449114
ME:MALME_	0.49166097	0.59551174	0.48375852	0.38649229	-1.9513297	0.54917813
ME:M14	1.44700034	1.41453296	1.4260248	1.47359654	-1.5544229	1.39904908
ME:SK_MEL	0.37664425	0.36820931	0.29939655	0.45597893	-1.4880648	0.36937952
ME:LOXIMVI	-0.0517595	-0.0662184	-0.0654811	-0.0224752	-2.7877291	-0.0171815
ME:SK_MEL	-1.1601566	-1.1635007	-1.1526215	-1.142713	-2.1868803	-1.2106804
ME:UACC_2	-0.9113097	-0.9343867	-0.9042176	-0.8783223	-2.4412105	-0.8389033
PR:PC3	-0.409572	-0.4272466	-0.3507499	-0.4435674	-1.5858132	-0.354946
PR:LNCAP	-1.0463036	-1.0168479	-1.0109077	-1.0919285	-2.4412324	-1.0533967
PR:DU_145	1.63816135	1.56337263	1.76473843	1.55467422	-1.6157523	1.57819372
BR: T47D	0.89923147	0.94902102	0.87008186	0.8619873	-1.6412343	0.85534223
BR:Hs578T	-0.0615556	-0.0663826	-0.0378602	-0.0794796	-1.4022396	-0.0511217
BR:BT_549	-1.2793593	-1.2583288	-1.2731183	-1.2827777	-2.2204077	-1.4868286
BR:MDA_ME	-0.974448	-0.9429676	-0.9814622	-0.9806551	-2.2609297	-0.9626238
BR: MCF7	-0.1241974	-0.1330924	-0.1261547	-0.1109966	-2.4465458	-0.1340752
LU:PC9	-0.7667674	-0.796032	-0.7187216	-0.771609	-1.5840065	-0.7559466
LU:H23	-0.5164236	-0.5192893	-0.547967	-0.4720719	-1.8443592	-0.4733386
LU:H322M	-0.2783968	-0.2650206	-0.3308396	-0.233668	-1.6870204	-0.2388699
LU:H522	-0.3671142	-0.3941166	-0.3600115	-0.3403869	-1.9111612	0.37749189
LU:HOP62	0.31301452	0.30931081	0.30409503	0.3198663	-2.5019765	0.37099319
LU:HOP92	0.03435648	0.05169999	-0.0678172	0.11943918	-1.5369413	0.09773061
LU:H460	-0.0334391	-0.0294059	-0.0678179	-0.0021652	-1.4433807	-0.028608
LU:A549	-1.1375021	-1.1184192	-1.1520875	-1.120612	-2.7924199	-1.1482609
CO:HT29	-0.282985	-0.2762208	-0.2869644	-0.2804477	-1.4968917	-0.2588749

CO:COLO20	-0.143246	-0.0524529	-0.1092791	-0.2657127	-1.5101531	-0.1504873
CO:HCC_29	0.00675886	0.0221771	-0.0216966	0.01990928	-1.3912863	0.04110486
CO:HCT_15	0.00728045	0.08843162	-0.0366266	-0.0297828	-1.8473495	-0.0288766
CO:KM12	0.33054959	0.27227021	0.33026468	0.38298755	-2.3829006	0.31751012
CO:HCT_11	-0.4696192	-0.5266893	-0.4018698	-0.4720667	-2.0564863	-0.4494981
CO:SW_620	0.50452409	0.59658375	0.55540041	0.35161392	-2.3132689	0.34829614
OV:OVCAR_	0.02169996	-0.0146773	0.07731937	0.00158948	-1.3032422	0.03432724
OV:OVCAR_	-1.2931143	-1.2739532	-1.2901404	-1.2911079	-2.1122426	-1.1938069
OV:OVCAR_	-1.2900302	-1.281146	-1.2792307	-1.2856906	-2.3105818	-1.2995526
OV:SK_OV_	0.22795676	0.15452106	0.26090725	0.26395206	-2.3126608	0.35649184
OV:NCI_AD	-1.2621371	-1.2368418	-1.2872166	-1.2385463	-2.2214537	-1.3312232
PAN:CAPAN	-1.0873859	-1.0834557	-1.0819723	-1.076444	-2.4943593	1.19077321
PAN:CAPAN	-1.0600124	-1.0759626	-1.0175427	-1.0670701	-2.029574	-1.0603941
ESO:KYSE5	-0.9838042	-1.0086672	-0.9363923	-0.9883526	-2.2976245	-1.0340571
ESO:KYSE1	-0.9736149	-0.9270098	-1.0029396	-0.9724669	-2.3235146	-0.9295581
H&N:BHY	-0.9842283	-1.0087424	-0.9371097	-0.9888223	-2.0077944	-0.990134
H&N:OE21	-0.9690304	-0.9423974	-1.0109085	-0.9353124	-2.1898761	-0.9402088
CER:HELA	-0.8051434	-0.7987109	-0.7652808	-0.8367408	-2.0216966	-0.748943

Supplementary Table 2-siRNA transfection efficiency RT-PCR
NMRK2; relate to Fig. 1c and Extended Data Fig. 3b,3c

	siNTC	siNAPRT	siNADSyn1	siNAMPT	siNMRK1	siNMRK2
NHA	-0.4558045	-0.4349248	-0.4749749	-0.6334649	-0.5057958	-2.6334649
IMR90	-0.6047295	-0.654733	-0.6348648	-0.7046446	-0.6349489	-2.7046446
RPE-1	-0.6349492	-0.6048482	-0.6347494	-0.7734723	-0.7247925	-2.7734723
MCF10a	-0.7746843	-0.8046842	-0.7746865	-0.7173746	-0.8049234	-2.7173746
HEK293T	-0.6347422	-0.6747925	-0.8174725	-0.6483042	-0.8247948	-2.6483042
LE:K_562	0.27582585	0.2460022	0.31705501	0.27915277	0.3115377	-2.2092471
LE:SR	2.26548485	2.34266999	2.26370318	2.28498339	2.40052521	-2.3024833
RE:A498	-0.7938131	-0.8234846	-0.833933	-0.7542767	-0.7454069	-2.0349761
RE:RXF_393	-0.9970044	-1.1127052	-1.0643068	-0.8392577	-0.9748279	-2.2330041
GBM:U87	-0.8514183	-0.8060223	-1.0149958	-0.7694516	-0.9781812	-2.4808766
GBM:U87vIII	-0.8300377	-0.7910603	-0.9821124	-0.7519342	-0.7435898	-1.9455173
GBM:GBM39	-0.8263967	-0.8534405	-0.9409509	-0.7122084	-0.9440196	-1.971617
GBM:GBM6	-0.842861	-0.7930141	-0.9797786	-0.7939714	-0.9456694	-1.8326211
CNS:SF_539	1.17221263	1.23538527	1.16056025	1.16702944	1.1498746	-2.1534788
CNS:SNB_75	0.00588259	0.00918546	-0.0155262	0.02514367	-0.0744629	-1.8162731
CNS:SNB_19	1.2180474	1.16133235	1.27462856	1.28012364	1.02106988	-2.0328816
CNS:U251	0.16838005	0.16086569	0.15405702	0.20014913	0.17042022	-2.0707749
CNS:SF_268	1.08799705	1.0408446	1.19941864	1.07463871	1.36449787	-2.5103336
ME:MALME_	1.14638628	1.17117131	1.12763468	1.19163964	1.12663559	-1.9847639
ME:M14	1.24171582	1.2360749	1.3230273	1.2199222	1.27613073	-1.9660772
ME:SK_MEL_	1.22634232	1.17438636	1.34759643	1.2145288	1.26941099	-1.6564703
ME:LOXIMVI	2.52541333	2.43500748	2.1916682	2.37940389	2.94597791	-2.3026641
ME:SK_MEL_	2.50827883	2.51708576	2.59296096	2.52571118	2.38737345	-1.7121562
ME:UACC_2	0.72510926	0.60995223	0.75708444	0.85737515	0.84645338	-1.7130576
PR:PC3	-0.415933	-0.4111359	-0.4858312	-0.3665807	-0.4619854	-1.3715816
PR:LNCAP	-1.2076262	-1.111071	-1.1626716	-1.423011	-1.3478619	-2.9260799
PR:DU_145	-0.5157715	-0.601691	-0.5530898	-0.4015645	-0.6010723	-1.9121069
BR: T47D	1.03773319	1.19833917	1.24288301	1.18364609	1.28060167	-1.8804191
BR:Hs578T	0.4147869	0.4231719	0.4010109	0.43926865	0.4009015	-1.4563846
BR:BT_549	0.88762831	0.97118305	0.94640349	0.77074942	0.8572407	-1.6185817
BR:MDA_MB	-0.4217589	-0.2500404	-0.4366131	-0.6229829	-0.5479745	-1.5996789
BR: MCF7	1.36094672	1.3219236	1.60703035	1.20777232	1.39974776	-2.2895849
LU:PC9	-0.5851779	-0.5042223	-0.5969046	-0.6931388	-0.5636356	-1.6531488
LU:H23	-0.8492904	-0.9961864	-0.932562	-0.6317912	-0.8585676	-1.9544885
LU:H322M	-0.0164841	-0.0131122	-0.0264587	-0.0105173	-0.0260376	-1.5970171
LU:H522	-0.2512556	-0.2944595	-0.2225666	-0.2439393	-0.2267797	-1.7202459
LU:HOP62	-0.1539875	-0.14061	-0.1401155	-0.1913361	-0.1022882	-1.9139754
LU:HOP92	-0.1857659	-0.2341338	-0.1177239	-0.2113179	-0.170871	-1.9817617
LU:H460	0.69929764	0.55940909	0.73253351	0.85741959	0.57929036	-1.3422472
LU:A549	0.52559888	0.50564149	0.52377769	0.57511411	0.53659692	-0.6370902
CO:HT29	-0.1125582	-0.0963749	-0.1423018	-0.1047797	-0.1833661	-2.1409193

CO:COLO2	-0.0007435	-0.0453215	0.06187842	-0.0162034	0.05856819	-1.6238966
CO:HCC_29	0.11463016	0.16086387	0.0796609	0.10410746	-0.0396167	-1.3958949
CO:HCT_15	0.1828943	0.16086386	0.21156363	0.18627421	0.13187054	-1.2992819
CO:KM12	-0.5965413	-0.7216697	-0.5517345	-0.5284663	-0.6958219	-1.8302984
CO:HCT_11	0.12412117	0.12776276	0.13801147	0.11098081	0.1331039	-1.8144188
CO:SW_620	0.06835231	0.02348827	0.04674949	0.14607745	0.08489283	-2.0590123
OV:OVCAR_	-0.6839474	-0.7368013	-0.7082424	-0.6294666	-0.7284002	-1.7882182
OV:OVCAR_	-0.624852	-0.6617508	-0.6735084	-0.5600057	-0.705902	-1.7406884
OV:OVCAR_	-0.7141631	-0.8282422	-0.7329627	-0.5966199	-0.8021951	-1.7379129
OV:SK_OV_	-0.6734765	-0.7931383	-0.7022182	-0.5370337	-0.8922954	-1.9621354
OV:NCI_AD	-0.7904417	-0.8056336	-0.8338057	-0.7639275	-0.6475545	-1.6947242
PAN:CAPAN	-1.2665194	-1.1655584	-1.3116128	-1.3939157	-1.396773	-2.6326295
PAN:CAPAN	-1.1399122	-1.1502659	-1.1461906	-1.1748065	-1.4846294	-2.925383
ESO:KYSE5	-1.1163729	-1.0437203	-1.1296901	-1.2380199	-1.284749	-2.137353
ESO:KYSE1	-1.0510369	-0.9894255	-1.0641979	-1.1571028	-1.1047464	-2.3916393
H&N:BHY	-0.9906319	-0.9066031	-1.0146583	-1.1080539	-1.283632	-2.301683
H&N:OE21	-0.9228538	-0.7387034	-1.031271	-1.0623103	-1.0836352	-2.3102731
CER:HELA	-1.0544331	-0.9730115	-1.1523589	-1.0932235	-1.1362934	-2.1037352

Supplementary Table 2-siRNA transfection efficiency RT-PCR NAPRT; relate to Fig. 1c and Extended Data Fig. 3b,3c

	siNTC	siNAPRT	siNADSyn1	siNAMPT	siNMRK1	siNMRK2
NHA	-0.3554954	-2.3204243	-0.3884749	-0.3047464	-0.3064648	-0.2836352
IMR90	-0.634649	-1.9470343	-0.6353994	-0.6732468	-0.6248375	-0.7273636
RPE-1	-0.692439	-1.7944934	-0.7349034	-0.7049348	-0.7634749	-0.7243749
MCF10a	-0.728354	-2.4034306	-0.8440381	-0.7044284	-0.7346864	-0.7173746
HEK293T	-0.8479434	-2.2349892	-0.8043579	-0.8246443	-0.8736846	-0.8246472
LE:K_562	-0.6613338	-2.2714536	-0.6411901	-0.6590241	-0.6188316	-0.6260234
LE:SR	-0.9743029	-2.1531828	-0.9574625	-0.994335	-0.9534857	-0.9047498
RE:A498	-0.6421946	-2.543803	-0.6409233	-0.6196901	-0.6261493	-0.6287573
RE:RXF_393	-1.0531093	-2.2444592	-1.0463591	-1.0487517	-1.0312403	-1.0461064
GBM:U87	-1.0437879	-2.4647945	-1.01173	-1.0523426	-1.1419847	-1.1793947
GBM:U87vIII	-1.0534162	-2.8476795	-1.0440993	-1.0488348	-1.0375409	-1.0439368
GBM:GBM39	-1.0515405	-2.7390088	-1.045544	-1.0505063	-1.1267435	-1.0004655
GBM:GBM6	-1.0468787	-2.4342261	-1.0419241	-1.0450028	-1.018829	-1.0659601
CNS:SF_539	-1.0545145	-2.0844212	-1.0478364	-1.0518608	-1.0602849	-1.0761341
CNS:SNB_75	-0.9430524	-2.0939235	-0.9276661	-0.9447289	-0.9307092	-0.9383683
CNS:SNB_19	-1.0026913	-2.1970352	-1.0007578	-0.9915302	-1.1296866	-0.985848
CNS:U251	-1.0419515	-2.0474034	-1.0348596	-1.0378305	-1.244801	-1.1246163
CNS:SF_268	-1.0403758	-2.2420326	-1.0361574	-1.0353184	-1.0364577	-1.1398249
ME:MALME_3M	-1.0511134	-2.0374046	-1.0446381	-1.0463554	-1.033163	-1.0438126
ME:M14	-0.3074448	-2.6247322	-0.3033688	-0.3275276	-0.3726536	-0.2736448
ME:SK_MEL_5	-0.9398422	-2.4403754	-0.9525279	-0.917563	-0.9348879	-0.9568742
ME:LOXIMVI	-0.3795636	-2.5383676	-0.3826656	-0.3671737	-0.378832	-0.3784876
ME:SK_MEL_2	-0.8184022	-2.3936364	-0.7579058	-0.8177452	-0.8464261	-0.8278713
ME:UACC_257	0.5068416	-2.2630367	0.45009904	0.49337009	0.45615087	0.4985724
PR:PC3	1.13861078	-2.4038324	1.10923177	1.15969455	1.1416392	1.19042636
PR:LNCAP	-0.2348233	-2.4404841	-0.2527549	-0.2094044	0.25097586	-0.2974958
PR:DU_145	0.17271323	-2.084731	0.16267534	0.11153861	0.13642001	0.16523692
BR: T47D	-1.1149114	-2.2937044	-1.0703019	-1.2231689	-1.1766937	-1.013682
BR:Hs578T	0.86569225	-2.40483	0.85688045	0.83014226	0.85241514	0.87248632
BR:BT_549	0.30756557	-1.8336656	0.32058422	0.27653903	0.36282324	0.21094498
BR:MDA_MB_231	-1.044551	-2.304484	-1.0518111	-1.0161483	-1.0725377	-1.0750861
BR: MCF7	0.9037695	-2.0484345	0.9031826	0.8837465	0.9571398	0.8224597
LU:PC9	1.12992749	-2.4948868	1.12504779	1.09447551	1.18652642	1.09749847
LU:H23	1.79738785	-2.4949481	1.7763311	1.72884176	1.5936343	1.84789516
LU:H322M	1.10624341	-2.4634427	1.1152343	1.09136642	1.29781785	1.03710134
LU:H522	0.76455236	-2.3038475	0.75409129	0.75528486	0.75326824	0.74731476
LU:HOP62	0.56647015	-2.3984748	0.56871063	0.56263774	0.54075637	0.51101693
LU:HOP92	1.18525449	-2.0474649	1.16869783	1.19598972	1.12251159	1.14314882
LU:H460	-0.9855728	-1.9440948	-0.9959233	-0.9802954	-1.0554091	-0.9605376
LU:A549	-0.9824921	-2.0383052	-0.968858	-0.9943545	-0.9333264	-0.9263651
CO:HT29	2.1372623	-1.3837427	2.12023396	2.14777131	2.35723884	2.13970158

CO:COLO205	1.72403799	-2.0388052	1.79852054	1.68315486	1.61984732	1.63091645
CO:HCC_2998	1.45556765	-1.5244848	1.49319296	1.31925445	1.46688956	1.27651085
CO:HCT_15	1.29994454	-2.2754489	1.2478308	1.35247096	1.2395657	1.26106523
CO:KM12	1.11152129	-2.1494747	1.03598163	1.1663048	1.01641024	1.15685562
CO:HCT_116	-0.9247747	-1.3844067	-0.8972064	-0.9632147	-0.8594607	-0.9832151
CO:SW_620	-0.9185325	-1.8474047	-0.9330905	-0.9062695	-0.9485823	-0.9045924
OV:OVCAR_4	1.50486879	-2.4840375	1.54814772	1.4537543	1.37525252	1.51449186
OV:OVCAR_5	1.11278635	-2.0484311	1.05419996	1.19604219	1.17601404	1.18825835
OV:OVCAR_8	1.52009113	-1.6374742	1.53945847	1.51088535	1.36239078	1.48714811
OV:SK_OV_3	0.71071003	-2.3847469	0.68649176	0.75273076	0.70055205	0.74473271
OV:NCI_ADR_RE	0.93487732	-1.846473	0.99470635	0.87682652	0.91874326	0.80898584
PAN:CAPAN1	-0.0763381	-2.047495	-0.1388064	-0.0414523	-0.0619988	-0.0362472
PAN:CAPAN2	-0.2932627	-2.4949845	-0.2533002	-0.3165453	-0.2604067	-0.3259845
ESO:KYSE510	-0.0390024	-1.8647635	-0.0243066	-0.0999267	-0.029801	-0.0916362
ESO:KYSE140	-0.3005638	-2.3536485	-0.3029227	-0.2389146	-0.2937738	-0.3084236
H&N:BHY	-0.4091197	-2.2837474	-0.4168767	-0.3500374	-0.472933	-0.3248658
H&N:OE21	-0.0650097	-1.7366404	-0.0952425	-0.0509618	-0.0481937	-0.0482829
CER:HELA	-0.8845098	-1.9148456	-0.8447508	-0.8748511	-0.7937367	-0.8203737

Supplementary Table 2-siRNA transfection efficiency RT-PCR NADSYN1; relate to Fig. 1c and Extended Data Fig. 3b,3c

	siNTC	siNAPRT	siNADSyn1	siNAMPT	siNMRK1	siNMRK2
NHA	-0.6493845	-0.6747294	-2.428402	-0.6743729	-0.7249492	-0.7734648
IMR90	-0.7349248	-0.7447297	-2.140384	-0.7472837	-0.7947923	-0.7524682
RPE-1	-0.7446823	-0.8047924	-2.4038445	-0.7947975	-0.8249423	-0.7846823
MCF10a	-0.7847948	-0.8247924	-2.0942847	-0.8249284	-0.8047949	-0.8247974
HEK293T	-0.6742984	-0.7349248	-2.2348305	-0.6347949	-0.7048642	-0.8048742
LE:K_562	-0.68105	-0.6279646	-1.4999688	-0.6934593	-0.6423821	-0.6031397
LE:SR	-0.7937185	-0.7014483	-1.7349494	-0.8616593	-0.7044453	-0.7439842
RE:A498	-1.2895092	-1.2891537	-2.7336301	-1.2509609	-1.2049713	-1.1777448
RE:RXF_393	-0.6160305	-0.60835	-1.7303834	-0.5514105	-0.5976249	-0.638459
GBM:U87	-0.5773678	-0.558575	-1.7363088	-0.5741896	-0.6064033	-0.5869482
GBM:U87vIII	-0.7291209	-0.7552502	-1.6393711	-0.7128857	-0.6913178	-0.6740279
GBM:GBM39	-0.589425	-0.5447543	-1.9336672	-0.5975532	-0.51809	-0.569177
GBM:GBM6	-0.229855	-0.1925391	-2.3303731	-0.1887897	-0.1650087	-0.176083
CNS:SF_539	-1.1296879	-1.1213079	-2.2839327	-1.1352551	-1.1228809	-1.1940971
CNS:SNB_75	-0.9708905	-0.9883606	-2.0373704	-0.9894612	-0.9588643	-0.9144666
CNS:SNB_19	-1.2944479	-1.3014122	-2.7363623	-1.251284	-1.3568885	-1.1695754
CNS:U251	-0.975941	-0.9533949	-1.837376	-0.9894195	-0.9328112	-0.9606592
CNS:SF_268	-0.4428482	-0.4560436	-1.8363635	-0.4138317	-0.374583	-0.4122043
ME:MALME_3M	-1.2998966	-1.2892426	-2.3394284	-1.2469762	-1.3289721	-1.2827292
ME:M14	-0.4500063	-0.4807772	-1.3993736	-0.3749118	-0.4501989	-0.3236345
ME:SK_MEL_5	0.31034468	0.29962974	-2.0283731	0.30170549	0.25920769	0.35359161
ME:LOXIMVI	-0.4351241	-0.4284216	-1.393817	-0.4259395	-0.4339506	-0.4572041
ME:SK_MEL_2	-1.1649724	-1.1793745	-2.148451	-1.1456547	-1.1380632	-1.1389601
ME:UACC_257	0.33991668	0.3301446	-2.3003867	0.38524237	0.41960357	0.36126648
PR:PC3	0.15042226	0.18683497	-2.4848127	0.09783166	0.19433742	0.08392362
PR:LNCAP	0.27280557	0.39229422	-2.048422	0.13427701	0.39126261	0.16231346
PR:DU_145	-0.0336928	0.11649286	-2.0849436	-0.0830653	0.19277831	-0.0735675
BR: T47D	-0.7922976	-0.8103865	-2.030426	-0.7812969	-0.774764	-0.7635759
BR:Hs578T	0.57768478	0.56728759	-1.7383166	0.58207162	0.62766427	0.63234435
BR:BT_549	-0.9846019	-0.9820042	-2.3633994	-0.9894064	-1.0681066	-0.9397253
BR:MDA_MB_231	-0.780678	-0.7654679	-2.0790493	-0.7550518	-0.8266552	-0.8029105
BR: MCF7	0.02542598	0.02300801	-2.3383186	0.02109205	0.06960254	0.02775175
LU:PC9	0.36930703	0.36482935	-2.39398	0.37984573	0.39952969	0.35215941
LU:H23	0.35180752	0.39045078	-1.2739642	0.27994486	0.40869978	0.21714866
LU:H322M	-0.0151377	-0.0151779	-2.1732949	0.04244991	-0.0273554	0.0698618
LU:H522	-0.0992024	-0.083399	-2.3365199	-0.087751	-0.039845	-0.0881548
LU:HOP62	0.17365868	0.18017106	-2.2499456	0.12515932	0.22781539	0.17846319
LU:HOP92	-0.1935759	-0.2398237	-2.2743484	-0.1628853	-0.2746326	-0.1782663
LU:H460	-0.4222352	-0.4193044	-2.8373564	-0.4237015	-0.5000863	-0.4988212
LU:A549	-1.1428591	-1.1841592	-2.4944832	-1.1151895	-1.1277549	-1.1782758
CO:HT29	0.75270371	0.63210442	-1.8039948	0.72216203	0.58451685	0.6110269

CO:COLO205	0.29742159	0.18049329	-2.3241247	0.29177322	0.18112334	0.14889639
CO:HCC_2998	0.09876386	0.07501275	-2.2630404	0.05226615	0.02719939	0.01662047
CO:HCT_15	0.99558124	0.98096717	-1.8043909	0.98962088	0.96945795	0.94856886
CO:KM12	0.45759931	0.40357621	-2.0494926	0.44347465	-0.5770272	0.51285617
CO:HCT_116	-0.4347337	-0.4088132	-1.4858094	-0.4596069	-0.4230981	-0.4118909
CO:SW_620	0.19000931	0.13072571	-2.0003595	0.20058331	0.13866381	0.12301172
OV:OVCAR_4	0.31497877	0.39958939	-1.4928986	0.27994031	0.35666908	0.40664862
OV:OVCAR_5	0.31667024	0.29515781	-1.4500404	0.33438	0.27660093	0.35407825
OV:OVCAR_8	0.017774	0.03626744	-1.8340406	0.04574812	0.0373361	0.04337986
OV:SK_OV_3	0.03563862	-0.0200342	-1.8335674	0.10429922	-0.0109503	0.10014291
OV:NCI_ADR_RES	-0.0269538	-0.0350572	-1.9539335	-0.0393428	-0.034049	-0.0188926
PAN:CAPAN1	0.17049546	0.00052188	-1.4303335	0.10218671	-0.0004087	0.11281225
PAN:CAPAN2	0.61797015	0.60216357	-1.7020004	0.54040652	0.63795006	0.57589495
ESO:KYSE510	2.07335683	2.05881821	-1.1034253	2.50272332	2.91661384	2.87225469
ESO:KYSE140	2.50645459	2.60728217	-0.5679074	2.30105047	2.25722381	2.31269746
H&N:BHY	2.15793147	2.06634189	-0.9857567	2.35934292	2.04226207	2.3510209
H&N:OE21	2.51644661	2.54142205	-2.3342151	2.62364461	2.497503	2.49374
CER:HELA	-1.0799046	-1.0423625	-2.1949499	-1.0048776	-1.0194844	-1.0346465

Supplementary Table 3-Known motif discovery analysis of NAMPT enhancer using TRANSFAC relate to Figs. 3d, 3e and Extended Data Figs. 5d, 5e

Matrix	Factor name	Position (strand)	Core score	Matrix score	Sequence
A$CGD2	Cgd2	2 (+)	0.808	0.849	agacACATGcacat
V$OCT2_04	OCT_2	6 (+)	1	0.972	acATGCAcatg
V$DEC1_Q2	DEC_1	10 (-)	0.965	0.934	gcaCATGTgtg
V$TEAD4CEBPB_01	TEF-3:C/EBPbeta	12 (-)	0.686	0.733	acatgtgtgtttattgCGGCAc
V$MEQ_01	MEQ	14 (-)	1	1	aTGTGTgtt
V$GCM1CEBPB_01	GCMa:C/EBPbeta	14 (+)	1	0.78	atgtgtgtttaTTGCGgcac
V$XFD2_01	XFD-2	15 (-)	1	0.934	tgtgtgTTTATtgc
F$TEA1_01	Tea1p	16 (-)	0.776	0.754	gtgtgTTTATtgcggcacta
V$RUNX2_02	RUNX2	16 (-)	0.881	0.788	gtgtgtttattGCGGCac
P$AT1G53910_02	AT1G53910	16 (+)	1	0.788	gtgtgtttattGCGGCactat
V$FOXP1_06	FOXP1	17 (+)	1	0.996	tgTGTTTat
I$MIRR_01	mirr	19 (-)	1	1	TGTTT
V$FOXC1_06	Foxc1	19 (-)	1	1	TGTTTat
V$FOXM1_Q3_02	FOXM1	19 (+)	1	0.997	TGTTTattg
V$HOXD9_02	Hoxd9	19 (-)	1	0.95	tgTTTATtgc
V$CEBP_C	C/EBPalpha	19 (-)	1	0.916	tgtttATTGCggcactat
F$YBR239C_01	Ybr239c	19 (+)	0.796	0.766	tgtttatTGCGGcactattc
V$CDX1_03	CDX1	20 (-)	1	0.992	gTTTATtgc
V$CDX2_05	Cdx-2	20 (+)	1	0.957	gtttATTGCggc
V$CDX1_Q5	Cdx-1	21 (+)	1	1	TTTATt
I$CAD_01	cad	21 (+)	1	1	TTTATtg
I$CG4328_01	CG4328	21 (+)	1	1	tTTATTg
V$CEBPD_Q6	C/EBPdelta	23 (+)	1	0.957	tATTGCggcact
P$ERF11_01	ERF11	24 (-)	0.981	0.966	attgCGGCAc
P$RRTF1_02	RRTF1	25 (-)	0.815	0.805	ttgCGGCAct
P$AT1G68550_03	AT1G68550	25 (+)	0.946	0.946	ttgCGGCAc
P$ERF098_01	ERF098	26 (-)	1	0.897	tGCGGCac
P$HSFA4A_01	HSFA4A	32 (+)	1	1	aCTATT
P$GT1_Q6	GT-1	34 (-)	1	1	taTTCAC

V$SRY_12	SRY	38 (+)	1	0.99	cACAATag
V$SRY_10	SRY	39 (+)	0.602	0.746	acaatagCAAAGa
V$NFIA_02	NF-1A	53 (+)	0.894	0.91	TTGGAaccaacccac
P$TCP7_01	TCP7	53 (-)	0.854	0.822	ttggaaCCAAC
P$CBF3_02	CBF3	58 (+)	0.796	0.805	accaaCCCACatgt
V$ZNF777_02	ZNF777	61 (+)	0.557	0.717	aacccaCATGTccatcaat
P$ASR1_01	ASR-1	62 (+)	1	1	ACCCA
V$EGR3_Q3	egr-3	62 (-)	1	1	aCCCAC
V$DEC1_Q3	1-Dec	62 (+)	0.983	0.967	acccACATGtcc
V$DEC1_Q2	1-Dec	63 (+)	0.965	0.948	cccACATGtcc
V$CUX1TBX21_01	CDP:T-bet	63 (+)	0.969	0.825	cccacatgtccATCAAtg
V$PBX1_04	Pbx1	68 (+)	1	0.954	atgtccATCAAtgatag
V$CDPCR1_01	CDP	71 (-)	0.929	0.916	tccaTCAATg
V$CUX1HOXA13_01	CDP:HOXA13	74 (+)	0.876	0.764	aTCAATgatagactgga
V$CUX1_05	CDP	74 (+)	0.547	0.785	atcaatgatagaCTGGAt
I$OPTIX_01	Optix	79 (+)	1	1	TGATA
V$IPF1_07	ipf1	79 (+)	0.929	0.867	TGATAgact
F$FZF1_01	FZF1	79 (-)	1	1	tGATAG
V$TCF1_07	TCF1	82 (+)	1	0.992	tagactgGATTAaa
V$CRX_06	Crx	83 (+)	1	0.972	agactgGATTAa
V$DMBX1_02	DMBX1	86 (+)	1	0.995	ctgGATTAaa
V$GTF2IRD1_01	GTF2IRD1-isoform2	87 (+)	1	0.959	tgGATTAaa
I$GSC_01	Gsc	88 (-)	1	1	gGATTA
I$PTX1_01	Ptx1	88 (-)	1	1	gGATTAa
I$BCD_02	bcd	88 (-)	1	1	gGATTA
I$OC_01	oc	88 (-)	1	1	gGATTA
I$BCD_04	BCD	88 (-)	1	1	gGATTAa
V$CRX_Q4_01	CRX	89 (-)	1	1	GATTAa
V$LHX3_Q3	LHX3	90 (+)	1	1	ATTAAa
F$RAP1_01	RAP1	104 (-)	1	0.826	gcacatatACACCatggaat
V$NFAT2_02	NFAT2c1dimer	113 (+)	1	0.837	caccaTGGAAt
P$SPL1_01	SPL1	124 (+)	0.847	0.774	acTGTACagc
P$SPL1_01	SPL1	124 (-)	0.847	0.772	actGTACAgc

V$CDX2_01	Cdx-2	128 (+)	1	0.947	tacagccATAAAaatg
V$CDX2_05	Cdx-2	129 (-)	0.948	0.964	acaGCCATaaaa
I$ABDB_01	Abd-B	129 (-)	1	0.985	acagccATAAAaat
V$HOXA9_01	hoxa9	129 (+)	1	0.97	acagccATAAAaatgga
V$EVX2_05	EVX2	129 (-)	1	0.996	acagccATAAAa
V$EVX2_06	Evx2	129 (-)	1	0.995	acagccATAAAa
V$EVX2_07	EVX2	129 (-)	1	0.997	acagccATAAAaa
V$CDX2_06	Cdx-2	129 (-)	1	0.992	acagccATAAAa
V$EVX2_08	Evx2	129 (-)	1	0.997	acagccATAAAa
V$CDX2_04	Cdx-2	130 (+)	1	0.998	cagccATAAAa
V$CDX2_Q5	Cdx-2	131 (-)	1	0.941	agccATAAAaatgg
V$HOXA10_04	HOXA10	131 (+)	1	0.963	agccATAAAaa
V$HOXC11_04	HOXC11	131 (+)	1	0.995	agccATAAAaa
V$HOXD11_04	HOXD11	131 (+)	1	0.969	agccATAAAa
V$HOXA11_04	Hoxa11	131 (+)	1	0.998	agccATAAAaa
I$CAD_02	CAD	131 (+)	1	0.994	agccATAAAaa
V$HOXC9_04	HOXC9	131 (-)	1	0.993	agccATAAAa
V$CDX2_03	Cdx-2	132 (+)	1	0.989	gccATAAAa
V$HOXC10_03	HOXC10	132 (+)	1	0.996	gccATAAAaa
V$HOXC10_04	HOXC10	132 (+)	1	0.972	gccATAAAaa
V$HOXD9_01	Hoxd9	132 (+)	1	0.99	gccATAAAa
V$CUX1HOXB13_01	CDP:HOXB13	132 (+)	0.917	0.94	gccataaaaATGGAtg
V$HOXB13ONECUT2_01	HOXB13:OC-2	132 (+)	0.945	0.948	gccataaaaATGGAtg
V$CDPCR3_01	CDP	133 (-)	1	0.87	CCATAaaaatggatg
I$CAD_Q6	CAD	133 (-)	1	0.987	ccATAAAaat
I$ABDB_Q6	Abd-B	134 (+)	1	1	cATAAAa
V$YY1_Q4_01	YY1	134 (+)	1	0.987	cataaaAATGGatga
V$HOXA13_01	HOXA13	135 (+)	1	1	ATAAAa
V$SATB1_Q5_01	SATB1	135 (-)	1	1	ATAAAa
V$YY1_Q6_03	YY1	138 (-)	1	1	aaAATGG
I$PRD_03	Prd	139 (-)	0.969	0.911	aaaTGGATga
V$POU3F2_01	POU3F2	141 (+)	1	0.87	atggatgagTTCAT
V$PRDM16_04	MEL1	144 (+)	1	1	GATGAg

V$MEQCJUN_02	MEQ:c-Jun	144 (+)	0.716	0.836	gatgAGTTCat
V$VDR_02	VDR	146 (+)	1	1	tgaGTTCA
V$RXRA_06	RXRA	147 (-)	0.862	0.812	gaGTTCAtgtcctt
V$RXRA_06	RXRA	147 (+)	0.812	0.804	gagttcaTGTCCtt
V$SOX9_Q5	Sox-9	152 (-)	1	0.966	catgtccTTTGTaggga
V$SOX9_Q4	Sox-9	155 (-)	1	0.979	gtcCTTTGtag
V$SOX2_08	Sox-2	155 (+)	1	0.957	gtccTTTGTaggg
V$ZNF214_04	ZNF214	156 (+)	0.855	0.868	tcctttgtagggacaTGGATga
V$TCF1_Q5_01	TCF-1	157 (-)	1	0.988	cCTTTGtaggga
P$SPL15_01	SPL15	157 (+)	0.795	0.843	cctttGTAGGgaca
V$TCF1_Q5	TCF-1	158 (+)	1	1	CTTTGt
V$SOX10_Q6_01	Sox-10	158 (-)	1	1	cTTTGTa
V$SOX10_01	Sox-10	158 (+)	1	1	cTTTGT
P$SPL5_02	SPL5	158 (+)	0.8	0.853	ctttGTAGGgac
P$BHLH28_01	bHLH28	158 (+)	0.8	0.836	ctttGTAGGgac
P$SPL3_01	SPL3	161 (-)	0.8	0.839	tgTAGGGa
V$HELIOSA_01	Helios	161 (+)	1	0.986	tgtAGGGAcat
V$PIT1_Q6	Pit-1	163 (-)	1	0.888	tagggacatggATGAAgc
V$P54NRB_Q5	p54NRB	166 (+)	1	0.887	ggacatGGATGaagctggc
V$CUX1TBX21_01	CDP:T-bet	169 (-)	0.922	0.769	caTGGATgaagctggcaa
V$CUX1HOXA13_01	CDP:HOXA13	170 (+)	0.823	0.754	aTGGATgaagctggcaa
V$PBX_Q3	Pbx	184 (-)	0.868	0.917	caaccatCATTC
V$CMAF_01	c-Maf	188 (-)	1	0.943	catcattctCAGCAaacta
V$CMAF_04	c-MAF	189 (-)	1	0.935	atcattcTCAGCaaact
V$CMAF_Q5	c-MAF	191 (+)	1	0.993	cattcTCAGCa
V$MAFB_Q4_01	MAFB	195 (+)	1	1	cTCAGCa
P$C1_Q2	C1	200 (+)	1	0.983	caAACTAtccc
V$PRDM16_06	Prdm16	207 (+)	1	0.977	tCCCAGggac
V$MYOGNF1_01	myogenin	210 (-)	0.929	0.717	cagggacaaaatACCAAgcaccac
V$SOX17_Q2	Sox-17	213 (-)	1	1	gGACAA
V$ARID5A_04	ARID5A	214 (+)	0.889	0.879	gacaaaATACCaagcac
V$TEF3_Q3	TEF-3	216 (-)	1	0.92	caAAATAcc
V$AR_02	AR	220 (+)	1	0.913	ataccaagcaccacaTGTTCtcac

V$PR_01	PR	220 (+)	1	0.951	ataccaagcaccacaTGTTCtcac
V$GR_01	GR	220 (+)	1	0.969	ataccaagcaccacaTGTTCtcac
V$AR_03	AR	220 (+)	1	0.957	ataccaagcaccacaTGTTCtcac
V$PR_02	PR	220 (+)	1	0.967	ataccaagcaccacaTGTTCtcac
V$NR3C1_01	NR3C1	224 (-)	0.875	0.865	caaGCACCacatgttctc
V$AR_08	AR	225 (-)	0.806	0.848	aaGCACCacatgttctc
V$AR_09	AR	225 (-)	0.804	0.853	aaGCACCacatgttctc
V$NR3C1_03	NR3C1	225 (-)	0.764	0.852	aaGCACCacatgttctc
V$PR_03	PR	225 (-)	0.782	0.879	aaGCACCacatgttct
V$AR_08	AR	225 (+)	0.998	0.867	aagcaccacaTGTTCtc
V$AR_09	AR	225 (+)	0.981	0.897	aagcaccacaTGTTCtc
V$NR3C1_03	NR3C1	225 (+)	1	0.883	aagcaccacaTGTTCtc
V$AR_Q2	AR	226 (-)	0.899	0.878	AGCACcacatgttct
V$AR_01	AR	226 (-)	0.869	0.887	aGCACCacatgttct
V$AR_13	AR	226 (-)	0.683	0.861	aGCACCacatgttct
V$GR_02	GR	226 (-)	0.873	0.914	aGCACCacatgttct
V$NR3C1_10	GR	226 (+)	0.869	0.877	aGCACCacatgttct
V$GR_03	GR	226 (+)	0.843	0.9	aGCACCacatgttct
V$AR_01	AR	226 (+)	1	0.904	agcaccacaTGTTCt
V$AR_04	AR	226 (+)	1	0.913	agcaccacaTGTTCt
V$NR3C1_04	GR	226 (+)	1	0.91	agcaccacaTGTTC
V$AR_13	AR	226 (+)	1	0.859	agcaccacaTGTTCt
V$GR_02	GR	226 (+)	1	0.917	agcaccacaTGTTCt
V$AR_14	AR	226 (+)	1	0.942	agcaccacaTGTTCtca
V$NR3C1_10	GR	226 (-)	1	0.903	agcaccacaTGTTCt
V$GR_03	GR	226 (-)	1	0.866	agcaccacaTGTTCt
V$PR_03	PR	226 (+)	1	0.882	agcaccacaTGTTCtc
V$AR_16	AR	226 (+)	1	0.885	agcaccacaTGTTCtc
V$GRE_C	GR	226 (+)	1	0.904	agcaccacatGTTCTc
V$AR_Q2	AR	226 (+)	1	0.905	agcaccacatGTTCT
V$NR3C1_04	GR	227 (-)	0.774	0.86	GCACCacatgttct
V$AR_Q6_01	AR	227 (+)	1	0.985	gcaccacaTGTTCtc
V$AR_10	AR	227 (-)	1	0.936	gcaccacaTGTTCtc

V$AML1_01	AML1a	229 (-)	1	1	ACCACa
V$AML1_Q6	AML1	229 (-)	1	1	aCCACA
V$AML1_Q5	AML1	229 (-)	1	1	aCCACA
I$SN_02	Sn	229 (+)	0.953	0.958	accacATGTTctca
V$GR_Q6_02	GR	230 (+)	1	0.995	ccacaTGTTCtca
F$HSF_01	HSF	236 (-)	1	1	GTTCT
V$PAX8_B	Pax-8	236 (-)	0.919	0.881	gttctCACTCacaggtga
V$BRACH_03	Brachyury	239 (+)	0.938	0.898	ctcactcacaggTGAGAatt
V$CLOCK_02	CLOCK	243 (+)	0.932	0.926	ctcacAGGTGagaa
V$ZBTB44_01	Zbtb44	244 (-)	1	1	tCACAG
V$AREB6_01	AREB6	244 (-)	1	0.963	tcaCAGGTgagaa
V$AREB6_02	AREB6	244 (-)	1	0.993	tcacAGGTGaga
V$GATAD2A_01	GATAD2A	245 (-)	1	1	CACAGg
V$ZEB_01	ZEB	246 (-)	1	1	aCAGGTga
V$TEAD4TCF3_01	TEF-3:E2A	246 (+)	1	0.963	acAGGTGagaattga
V$TBET_04	T-bet	246 (+)	0.978	0.964	acagGTGAGaat
V$ZEB1_03	ZEB1	247 (+)	1	1	CAGGTga
V$PAX4_Q2	Pax-4	248 (-)	0.974	0.895	aGGTGAgaatt
V$MEIS1SOX2_01	meis1:Sox-2	251 (+)	0.765	0.82	TGAGAattgaacaatga
V$SOX21_04	Sox-21	254 (-)	1	0.971	gaattgaACAATgagaa
V$SRY_05	SRY	254 (+)	1	0.98	gaattgaACAATgagaa
V$SOX9_B1	Sox-9	256 (+)	1	0.967	attgaACAATgaga
V$SOX30_03	Sox-30	256 (+)	1	0.983	attgaACAATgagaac
V$SOX17_09	Sox-17	256 (+)	1	0.953	attgaACAAT
V$SOX_Q6	SOX	256 (-)	0.901	0.877	attgaaCAATGag
V$HBP1_04	HBP1	256 (-)	0.913	0.928	attgaacAATGAgaaca
I$CT_01	ct	257 (+)	1	1	tTGAAC
I$SOXN_01	SoxN	257 (+)	1	0.94	ttgaACAATga
V$VDR_01	VDR	258 (-)	1	0.818	TGAACaatgagaacac
V$SOX6_01	Sox-6	258 (-)	1	0.964	tgaACAATga
V$SOX17_Q2	Sox-17	259 (-)	1	1	gAACAA
F$ROX1_Q6	ROX1	260 (-)	1	0.981	aACAATgag
V$SOX10_Q6_01	Sox-10	260 (+)	1	1	aACAATg

V$SRY_12	SRY	260 (+)	1	0.994	aACAATga
V$PR_01	PR	261 (-)	1	0.921	acaatgaGAACAcatggacacagg
V$PR_02	PR	261 (-)	1	0.91	acaatgaGAACAcatggacacagg
V$GR_Q6	GR	265 (-)	1	0.983	tgaGAACAcatggacacag
V$GR_Q6_02	GR	265 (-)	1	0.996	tgaGAACAcatgg
F$HSF_01	HSF	267 (+)	1	1	AGAAC
N$LIN14_01	lin-14	268 (+)	1	1	GAACAc
V$MYC_07	c-Myc	268 (-)	0.941	0.935	gaaCACGTgga
V$FOXO1ELK3_02	FOXO1A:Net	276 (+)	0.796	0.84	ggaCACAGgaagag
V$ERFFOXO1_01	ERF:FOXO1A	276 (+)	1	0.902	ggacACAGGaagag
V$FOXO1ETV7_01	FOXO1A:ETV7	276 (+)	1	0.771	ggacACAGGaagaggaacctc
V$ELK1EOMES_03	Elk-1:TBR2	276 (+)	0.845	0.855	ggacaCAGGAaga
V$ELK1TBX21_02	Elk-1:T-bet	276 (+)	0.874	0.879	ggacaCAGGAagag
V$FOXO1ELK1_02	FOXO1A:Elk-1	276 (+)	1	0.881	ggacaCAGGAagag
V$ERFFOXI1_02	ERF:FOXI1	276 (+)	1	0.944	ggacacAGGAAgag
V$FOXJ2ELF1_01	FOXJ2:Elf-1	276 (+)	1	0.935	ggacacAGGAAgag
V$ETS1_09	Ets1	277 (-)	1	0.969	gacacAGGAAgagga
V$ETS1_11	c-Ets-1	277 (+)	1	0.96	gacacaGGAAGagg
V$FLI1_10	Fli-1	277 (+)	1	0.952	gacacaGGAAGagg
V$ERG_08	Erg	278 (+)	1	0.986	acacAGGAAgagg
V$ERG_09	Erg	278 (+)	1	0.99	acacAGGAAgagga
V$ETS1_10	c-Ets-1	278 (+)	1	0.956	acacaGGAAGagg
V$GATAD2A_01	GATAD2A	279 (-)	1	1	CACAGg
V$PEA3_03	PEA3	279 (+)	1	0.996	cacAGGAAgag
V$ETS2_Q4	c-Ets-2	279 (-)	1	0.993	cacaGGAAGag
V$ETS2_03	c-Ets-2	279 (+)	1	0.993	cacaGGAAGagga
V$ETS2_04	c-Ets-2	279 (+)	1	0.993	cacaGGAAGagga
V$ER71_Q2	ER71	280 (-)	1	1	aCAGGAag
V$ELK1_11	Elk-1	280 (+)	0.912	0.874	acAGGAAgagg
V$GABP_B	GABP	280 (+)	1	0.934	acaGGAAGagga
V$SAP1A_Q6	SAP-1a	280 (-)	1	1	acaGGAAG
V$FLI1_05	Fli-1	280 (+)	1	0.967	acaGGAAGagg
V$GABPBETA_01	GABPBETA	280 (-)	1	0.986	acaGGAAGagg

V$PET1_03	Pet-1	280 (+)	1	0.968	acaGGAAGag
V$PET1_04	Pet-1	280 (+)	1	0.968	acaGGAAGag
V$ELK1_Q4	Elk-1	281 (-)	1	1	cAGGAAg
V$ETS2_Q6	c-Ets-2	281 (-)	1	1	caGGAAG
V$ELF1_Q5	Elf-1	282 (+)	1	1	AGGAAg
V$SPI1_Q5	PU.1	282 (+)	1	1	AGGAAg
V$DREF_02	DREF	282 (-)	0.997	0.967	aggAAGAGgaac
V$ZNF35_04	ZNF35	283 (+)	1	1	gGAAGA
V$SPIB_Q3	Spi-B	287 (-)	1	1	gAGGAA
V$MUSCLEINI_B	Muscle	289 (+)	0.974	0.915	ggaacctcaCACACcggggcc
V$RUNX2_02	RUNX2	290 (+)	0.875	0.787	gaACCTCacacaccgggg
V$P53_01	p53	295 (+)	0.57	0.686	tcACACAccggggcctgtca
V$E2F3FOXO6_01	E2F-3:FOXO6	301 (-)	0.796	0.749	accggggCCTGTcatgg
P$HSF3_01	HSF3	302 (+)	1	1	cCGGGG
V$CPBP_Q6	CPBP	302 (-)	1	1	ccGGGGC
V$PLAG1_02	PLAG1	304 (-)	0.924	0.941	ggggcctgtcaTGGGG
I$ACHI_01	achi	309 (-)	1	1	cTGTCA
I$HTH_01	hth	309 (-)	1	1	cTGTCA
I$VIS_01	vis	309 (-)	1	1	cTGTCA
I$ACHI_02	achi	309 (-)	1	1	cTGTCA
I$VIS_02	vis	309 (-)	1	1	cTGTCA
V$ETF_Q6_01	ETF	314 (-)	0.965	0.954	atggGGTGGgg
V$GKLF_Q3_01	GKLF	314 (+)	0.992	0.988	atggggtGGGGGg
F$ADR1_01	Adr1p	315 (+)	1	1	tGGGGT
V$SREBP1_Q6	SREBP-1	315 (-)	1	1	tgGGGTG
V$MAZ_03	MAZ	315 (+)	0.943	0.881	tggGGTGGggggagggcgacgg
V$ZNF692_02	ZNF692	315 (-)	1	0.917	tgggGTGGGgggagg
V$PAX4_03	Pax-4	316 (-)	1	0.985	gGGGTGggggga
V$SP1_02	SP1	316 (+)	0.989	0.993	gGGGTGggggg
V$LKLF_Q3	LKLF	316 (+)	1	1	gGGGTGgggg
V$LKLF_Q6	LKLF	316 (-)	1	1	gGGGTGggg
V$DB1_02	DB1	316 (+)	1	0.907	ggggtggggGGAGGgcgacggg
V$SALL2_01	SALL2	317 (+)	1	1	GGGTGgg

V$KLF_Q3	KLF	317 (+)	1	1	GGGTGggg
V$MAZ_02	MAZ	317 (+)	0.952	0.871	gGGTGGggggagggcgacggga
V$KID3_01	Kid3	318 (-)	1	1	GGTGG
F$HMO1CA_01	HMO1	318 (-)	0.989	0.962	ggtGGGGGgag
V$CPBP_Q6	CPBP	319 (-)	1	1	gtGGGGG
V$ZFP740_05	Zfp740	319 (-)	1	0.923	gtgGGGGGag
P$ANAC042_01	ANAC042	319 (-)	0.925	0.8	gtgggggagggcgACGGGa
V$ETF_Q6_01	ETF	321 (-)	0.965	0.917	ggggGGAGGgc
V$WT1_Q6	WT1	322 (-)	1	1	gggGGAGGg
V$REST_13	REST	322 (-)	0.797	0.741	gggggAGGGCgacggga
V$MAZ_Q6	MAZ	323 (+)	1	1	gGGGAGgg
V$FKLF_Q5	FKLF	323 (+)	0.984	0.988	gGGGAGggcg
V$CKROX_Q2	CKROX	323 (-)	1	1	gggGAGGGc
P$RRTF1_02	RRTF1	328 (-)	0.866	0.824	gggCGACGgg
P$RAP26_03	RAP2-6	328 (-)	0.844	0.83	gggCGACGgg
P$RAP210_04	RAP2-10	328 (-)	0.814	0.794	gggCGACGgg
I$MAD_Q6	MAD	330 (+)	1	1	gCGACGgg
P$HSFA1E_01	HSFA1E	331 (-)	0.996	0.997	CGACGg
I$ARA_01	ara	339 (+)	1	1	TAACA
I$CAUP_01	caup	339 (+)	1	1	TAACA
F$YDR520C_01	Ydr520c	340 (+)	0.786	0.84	aacattAGGAGatacaccta
V$OCT1_Q6	1-Oct	356 (+)	0.909	0.926	cctaatGTAAAtgac
V$POU2F2_08	2-Oct	358 (-)	0.881	0.906	taATGTAaatgac
V$OCT_Q6	Octamer	359 (-)	0.963	0.966	aATGTAaatga
V$OCT1_Q5_01	1-Oct	359 (-)	0.986	0.988	aatGTAAAtga
V$MEIS1BHOXA9_02	MEIS1B:HOXA9	367 (+)	1	0.948	TGACAagttaatgc
V$MEIS1DLX2_01	meis1:Dlx-2	367 (+)	1	0.976	TGACAagttaatgc
V$HNF1B_Q6_01	HNF-1beta	372 (-)	1	0.91	aGTTAAtgcgtaca
V$IPF1_Q6	ipf1	374 (-)	1	1	tTAATG
P$SPL15_01	SPL15	376 (-)	1	0.848	aatgCGTACagcac
P$SPL4_01	SPL4	377 (-)	1	0.988	atgCGTACa
P$SPL5_02	SPL5	377 (-)	1	0.847	atgCGTACagca
P$BHLH28_01	bHLH28	377 (-)	1	0.864	atgCGTACagca

P$SPL3_01	SPL3	378 (+)	0.8	0.839	tGCGTAca
P$SPL1_01	SPL1	378 (+)	1	0.787	tgCGTACagc
P$SPL12_01	SPL12	378 (-)	1	0.971	tgCGTACa
P$SPL5_01	SPL5	378 (-)	1	0.963	tgCGTACag
P$SPL1_01	SPL1	378 (-)	0.847	0.805	tgcGTACAgc
V$THAP1_01	Thap1	379 (-)	1	0.746	gcgtacagcacaccaacATGGCa
V$YY1_07	YY1	382 (-)	1	0.868	tacagcacaccaacATGGCaca
P$CBF3_02	CBF3	386 (+)	0.796	0.806	gcacaCCAACatgg
P$AT1G77200_03	AT1G77200	388 (+)	0.797	0.821	acaCCAACatggca
V$YY1_Q6	YY1	392 (-)	1	0.997	caacATGGC
V$YY1_03	YY1	392 (-)	1	0.889	caacATGGCaca
V$YY1_12	YY1	392 (+)	1	0.95	caacATGGCaca
V$YY1_14	YY1	392 (+)	1	0.893	caacATGGCaca
P$MYB118_01	MYB118	412 (-)	1	0.817	tatGTAACaaacctgca
I$ARA_01	ara	416 (+)	1	1	TAACA
I$CAUP_01	caup	416 (+)	1	1	TAACA
P$ATMYB15_Q2	Myb-15	416 (+)	1	1	TAACAa
V$SOX4_Q5	Sox-4	417 (+)	1	1	AACAAa
P$MYB3R5_01	MYB3R5	419 (+)	0.827	0.798	caaacctgcACGTTg
P$MYB3R1_01	MYB3R1	420 (+)	0.858	0.813	aaacctgcACGTTgt
P$MYB3R4_01	MYB3R4	420 (+)	0.839	0.81	aaacctgcACGTTgt
V$SOX10_09	Sox-10	420 (+)	0.941	0.887	aaacctgcacGTTGTg
V$GABPA_08	GABP-alpha	421 (+)	0.865	0.858	AACCTgcac
V$HIF1A_Q6	HIF-1alpha	426 (+)	1	1	gCACGT
V$TRP53_02	Trp53	426 (+)	0.954	0.844	gCACGTtgtggtcatgt
V$HIF1A_04	HIF-1alpha	426 (-)	1	0.981	gCACGTtg
P$OCSBF1_01	OCSBF-1	427 (+)	1	1	CACGT
P$HMG1_01	HMG-1	430 (+)	1	0.963	GTTGTggtc
V$AML1_Q6	AML1	432 (+)	1	1	TGTGGt
V$AML1_Q5	AML1	432 (+)	1	1	TGTGGt
V$PEBP2B_Q6	PEBP2beta	432 (+)	1	1	TGTGGtc
V$AML1_01	AML1a	432 (+)	1	1	tGTGGT
V$NR4A2RXRA_01	NURR1:RXR-ALPHA	433 (-)	1	0.821	gtGGTCAtgtaccct

V$RXRA_06	RXRA	433 (+)	0.675	0.831	gtggtcaTGTACcc
V$PRDM16_01	PRDM16	434 (-)	0.632	0.817	tggtcaTGTACc
P$SRS7_01	SRS7	441 (+)	1	0.714	gtACCCTagaacttaaagtttaa
P$MYB1L_01	MYB1-like	442 (+)	1	1	taCCCTAgaa
F$HSF_01	HSF	448 (+)	1	1	AGAAC
V$LHX3_Q3	LHX3	459 (-)	1	1	tTTAAT
V$HOXD13_Q6	HOXD13	459 (+)	0.987	0.97	tttaATAATag
V$PMX1_Q6	PMX1	461 (+)	1	1	TAATAa
V$ZNF333_01	ZNF333	463 (+)	1	1	ATAAT
V$FREAC3_01	Freac-3	464 (+)	1	0.901	taataGTAAAaaaaaa
V$FOXA2_04	HNF3-beta	464 (+)	1	0.922	taataGTAAAaaaaaaa
V$FOXA2_05	FOXA2	464 (+)	1	0.924	taataGTAAAaaaaaaa
P$HSFA4A_01	HSFA4A	465 (-)	1	1	AATAGt
P$GT1_Q6_01	GT-1	468 (-)	1	0.991	agtaaaaAAAAA
V$FOXJ3_07	FOXJ3	469 (+)	0.968	0.975	gtAAAAAa
P$MADSA_Q2	MADS-A	471 (+)	0.8	0.872	aaaaaaAAAAAggaaa
P$AP1_01	AP1	474 (+)	1	0.956	aaAAAAAaggaaa
V$STAT1_11	STAT1	474 (-)	0.908	0.904	aaaaaaaaGGAAAaaaaag
I$DATI_01	dati	475 (+)	1	0.993	aAAAAAaggaaaaaaaa
V$IRF4_Q5_01	IRF4	475 (+)	1	0.999	aaaaaaAGGAAa
V$STAT1_11	STAT1	475 (-)	0.955	0.912	aaaaaaagGAAAAaaaaga
P$PBF_Q2	PBF	478 (+)	1	1	aAAAGG
P$PBF_Q2_01	PBF	478 (-)	1	1	aAAAGG
V$PRDM6_02	PRDM6	478 (+)	1	0.999	aaaagGAAAAaaa
V$NFAT1_Q6	NFATc2	482 (+)	1	1	GGAAAa
V$NFAT4_Q3	NFATc3	482 (+)	1	1	GGAAAa
V$NFAT1_Q4	NFATc2	482 (+)	1	1	GGAAAa
P$AT3G51080_01	AT3G51080	482 (+)	1	1	GGAAAaa
P$PBF_01	PBF	485 (+)	1	0.995	aaaAAAAGaga
V$STAT1_11	STAT1	486 (-)	0.955	0.918	aaaaaagaGAAAAtgacat
V$BCL11A_04	BCL-11A	488 (+)	0.871	0.892	aaaagAGAAAatgacat
N$BLMP1_01	blmp-1	488 (+)	1	0.999	aaaagaGAAAA
V$IRF4_11	IRF-4	488 (+)	0.98	0.873	aaaagagaAAATGacatc

V$IRF2_03	IRF-2	489 (+)	0.984	0.959	aaagaGAAAAtg
P$TGA2_04	TGA2	489 (-)	0.816	0.849	aaagagaaaatgaCATCAga
V$IRF7_Q3	IRF-7	490 (+)	1	1	AAGAGaa
P$TGA7_02	TGA7	493 (-)	0.826	0.864	agaaaatGACATcagac
V$FOS_09	C-FOS	494 (+)	0.877	0.895	gaaaaTGACAtcagact
P$TGA6_02	TGA6	494 (-)	0.821	0.843	gaaaatgaCATCAga
V$ATF1_03	Atf-1	495 (+)	0.797	0.849	aaaatGACATcagact
V$ATF1_03	Atf-1	495 (-)	0.797	0.848	aaaatgACATCagact
P$TGA5_02	TGA5	495 (-)	0.815	0.839	aaaatgaCATCAga
V$ATF3_Q6	ATF3	496 (+)	0.881	0.864	aaaTGACAtcagac
P$TGA7_02	TGA7	496 (+)	0.816	0.847	aaatgACATCagactca
V$ATF3_Q6	ATF3	496 (-)	0.877	0.87	aaatgaCATCAgac
V$NFE2L1_Q5	Nfe2l1	497 (-)	1	0.953	aATGACatcaga
V$JUNFRA2_02	C-JUN:FRA-2	497 (+)	0.874	0.901	aaTGACAtcag
P$TGA2_04	TGA2	497 (+)	0.82	0.852	aaTGACAtcagactcatatg
P$TGA5_02	TGA5	497 (+)	0.821	0.841	aaTGACAtcagact
P$TGA6_02	TGA6	497 (+)	0.824	0.843	aaTGACAtcagactc
V$CREB1_04	CREB1	497 (+)	0.881	0.928	aatGACATcaga
V$CREB1_04	CREB1	497 (-)	0.881	0.928	aatgACATCaga
V$JUNDFRA1_02	JUND:FRA-1	498 (+)	0.925	0.905	aTGACAtcag
V$MEQCJUN_02	MEQ:c-Jun	498 (-)	0.867	0.867	atGACATcaga
V$JUND_01	JunD	498 (+)	0.868	0.922	atgaCATCA
V$ATF2_02	ATF-2	498 (-)	1	0.978	atgaCATCAga
V$ATF2_03	ATF-2	498 (-)	1	0.978	atgaCATCAga
V$CREBP1CJUN_01	ATF2:c-Jun	499 (+)	0.848	0.891	tGACATca
V$NEUROD_01	NeuroD-2	509 (-)	1	0.954	ctcATATGtc
V$SPIB_Q3	Spi-B	524 (-)	1	1	gGAGAA
V$LEF1_04	LEF-1	524 (-)	1	0.912	ggagaaTCAAAgtatta
I$TCF_Q6	TCF	525 (+)	1	0.986	gagaaTCAAAgtatta
V$LEF1_Q4	LEF-1	525 (+)	1	0.996	gagaatCAAAGta
V$TCF7RELATED_Q4	TCF7RELATED	525 (+)	1	0.997	gagaatCAAAGt
V$BETACATENIN_Q6	Beta-catenin	526 (-)	1	0.977	agaatCAAAGtatta
V$LEF1_Q3	LEF-1	526 (+)	1	0.999	agaatCAAAGt

V$TCF4_Q5_02	TCF-4	527 (+)	1	0.998	gaatCAAAGt
V$TCF3_Q6_01	TCF3	527 (+)	1	0.979	gaatCAAAGt
V$LEF1_Q2_01	LEF-1	528 (+)	1	0.989	aatCAAAGta
V$BETACATENIN_Q3_01	beta-catenin	528 (-)	1	0.999	aatCAAAG
V$BETACATENIN_Q6_01	beta-catenin	528 (-)	1	1	aatCAAAG
V$LEF1_07	LEF-1	529 (-)	1	0.995	aTCAAAgtat
V$LEF1_Q2	TCF-7	530 (+)	1	1	tCAAAG
V$TCF3_Q6	TCF-3	530 (-)	1	1	tCAAAG
V$AP2GAMMA_Q5	AP-2	541 (-)	1	1	CAGGCaa
F$MOT3_01	MOT3	541 (+)	1	1	cAGGCA
P$EDT1_01	EDT1	549 (-)	0.965	0.962	gcATTTAata
V$LHX3_Q3	LHX3	552 (-)	1	1	tTTAAT
V$SALL3_03	Sall3	562 (-)	0.981	0.969	tccctgGTACCt
I$SD_01	sd	578 (+)	1	0.953	gaCATTCattaa
V$SOX8_04	Sox-8	579 (+)	1	0.973	acATTCAttaaatg
V$IPF1_05	ipf1	581 (+)	1	0.979	attcATTAAatg
I$DFD_02	Dfd	583 (-)	1	1	tCATTAa
I$SCR_01	Scr	583 (-)	1	1	tCATTAa
I$BTN_01	btn	583 (-)	1	1	tCATTAa
I$EMS_01	ems	583 (-)	1	1	tCATTAa
I$ANTP_01	Antp	583 (-)	1	1	tcATTAA
I$FTZ_02	ftz	583 (-)	1	1	tcATTAA
P$EDT1_01	EDT1	583 (-)	1	0.978	tcATTAAatg
V$IPF1_Q6	ipf1	584 (+)	1	1	CATTAa
V$MSX1_01	Msx-1	584 (+)	0.996	0.958	catTAAATg
V$LHX3_Q3	LHX3	585 (+)	1	1	ATTAAa
I$ZEN_Q6	Zen	586 (-)	1	1	ttaAATGT
V$FOXO1_06	FOXO1	586 (+)	0.858	0.79	ttaaatGTGTTtc
V$FOXO1HOXA10_01	FOXO1A:HOXA10	586 (-)	1	0.901	ttaaatgTGTTTtc
V$ELK1EVX1_01	Elk-1:EVX1	587 (-)	1	0.816	taaatgtgtTTTCCttc
V$MEQ_01	MEQ	590 (-)	1	0.976	aTGTGTttt
I$MIRR_01	mirr	593 (-)	1	1	TGTTT
V$FOXK1_11	FOXK1	593 (+)	1	0.986	TGTTTtcctt

V$TEAD4CEBPB_01	TEF-3:C/EBPbeta	594 (-)	0.783	0.729	gttttccttctctttcTGCAAc
V$NFAT1_Q6	NFATc2	595 (-)	1	1	tTTTCC
V$NFAT4_Q3	NFATc3	595 (-)	1	1	tTTTCC
V$NFAT1_Q4	NFATc2	595 (-)	1	1	tTTTCC
V$TAL1_01	Tal-1	596 (+)	0.996	0.97	tttccTTCTCttt
V$IRF7_Q3	IRF-7	601 (-)	1	1	ttCTCTT
V$MAFB_03	MAFB	603 (-)	0.953	0.942	ctctTTCTGcaacac
V$CEBP_Q2	C/EBP	604 (-)	0.987	0.975	tctttctGCAACac
P$BPC1_Q2	BPC1	605 (-)	1	1	cTTTCT
V$CEBPA_05	C/EBPalpha	605 (+)	1	0.928	ctttcTGCAAcac
V$SPIB_Q3	Spi-B	607 (+)	1	1	TTCTGc
V$MEQ_01	MEQ	613 (+)	1	0.995	aacACACAa
F$MIG1_03	Mig1p	616 (+)	0.853	0.813	acacaaatGCGGTgtg
I$TWI_03	Twi	623 (-)	0.846	0.905	tgCGGTGtgttg
V$FAC1_01	FAC1	626 (-)	1	0.961	ggtgtGTTGTggga
V$FOXJ1_04	FOXJ1	626 (-)	1	0.94	ggtgtGTTGTgggac
V$CEBPGELF1_01	C/EBPgamma:Elf-1	632 (+)	0.846	0.768	ttgtgggacacaGGAACt
P$TCP7_01	TCP7	634 (+)	1	0.853	GTGGGacacag
V$ERFFOXI1_02	ERF:FOXI1	637 (+)	1	0.932	ggacacAGGAActa
V$CETS1P54_02	c-Ets-1(p54)	639 (+)	0.993	0.983	acacAGGAActaa
V$GATAD2A_01	GATAD2A	640 (-)	1	1	CACAGg
V$ETS_B	c-Ets	640 (+)	1	0.924	cacAGGAActaact
F$YBR239C_02	Ybr239c	641 (+)	0.8	0.813	acAGGAAc
V$SPIB_02	Spi-B	641 (+)	0.986	0.975	acaGGAACta
V$ERFSREBF2_02	ERF:SREBP-2	641 (+)	0.85	0.787	acaggaactaACTTGac
P$WRKY18_Q2	WRKY18	649 (-)	1	1	taacTTGAC
V$CDP_Q6_01	CDP	650 (+)	0.993	0.988	aacttgaCAAATg
I$PRD_02	Prd	651 (+)	0.822	0.85	acTTGACaaatg
P$SPL15_01	SPL15	658 (+)	0.795	0.81	aaatgGTAAGgata
P$SPL5_02	SPL5	659 (+)	0.8	0.826	aatgGTAAGgat
P$BHLH28_01	bHLH28	659 (+)	0.8	0.822	aatgGTAAGgat
P$SPL3_01	SPL3	662 (-)	0.8	0.837	ggTAAGGa
V$HOXA13_01	HOXA13	669 (+)	1	1	ATAAAa

V$SATB1_Q5_01	SATB1	669 (-)	1	1	ATAAAa
V$HOXD13_Q6	HOXD13	670 (+)	1	0.994	taaaATAAAac
V$FOXL1_02	FOXL1	671 (+)	1	0.973	aaaataaAACAAaaaa
V$HOXA13_02	HOXA13	672 (+)	1	1	aaATAAAac
V$CDX1_Q5	Cdx-1	673 (-)	1	1	aATAAA
V$FOXP3_Q6	FOXP3	673 (+)	1	0.994	aataAAACAaaa
V$HOXA13_01	HOXA13	674 (+)	1	1	ATAAAa
V$SATB1_Q5_01	SATB1	674 (-)	1	1	ATAAAa
V$FOXC1_Q4	Foxc1	674 (-)	1	1	ataaAACAA
V$SRY_01	SRY	677 (+)	1	1	AAACAaa
I$MIRR_01	mirr	677 (+)	1	1	AAACA
V$FOXO1A_Q5	FOXO1A	677 (+)	1	1	AAACAa
V$SRY_Q6	SRY	677 (-)	1	1	aAACAA
V$SOX4_Q5	Sox-4	678 (+)	1	1	AACAAa
P$MYB3R1_01	MYB3R1	685 (-)	0.789	0.797	aaAAAGGtaatattt
P$MYB3R4_01	MYB3R4	685 (-)	0.792	0.795	aaAAAGGtaatattt
P$PBF_Q2	PBF	686 (+)	1	1	aAAAGG
P$PBF_Q2_01	PBF	686 (-)	1	1	aAAAGG
P$MYB3R5_01	MYB3R5	686 (-)	0.792	0.801	aAAAGGtaatatttg
V$XVENT1_01	Xvent-1	691 (+)	1	0.946	gtaatATTTGtgt
P$ATHSFA1D_01	ATHSFA1D	701 (-)	1	1	TGTAGt
V$HSF1_Q6_01	HSF1	705 (+)	1	0.979	gtagtTTCTGgcag
V$HSF1_Q5	HSF1	705 (-)	1	0.962	gtagtTTCTGgc
V$HSF1_Q5_01	HSF1	705 (+)	1	0.987	gtagtTTCTGgc
V$NF1B_Q6_01	NF-1B	708 (-)	1	0.998	gtttCTGGC
V$HSF4_Q3	HSF4	712 (-)	1	1	ctGGCAG
V$SMAD1_Q6	Smad1	719 (+)	1	0.987	agGCAGAcc
I$EVE_Q6	Eve	721 (-)	1	0.966	GCAGAccaga
V$GATA5_Q4	GATA-5	727 (-)	1	1	cAGATA
F$STP4_02	Stp4p	729 (+)	0.8	0.808	gaTAGAGct
V$FOXM1_Q3	FOXM1	738 (-)	0.985	0.907	aaaaCACTCta
I$MIRR_01	mirr	739 (+)	1	1	AAACA
V$CMAF_03	c-MAF	747 (+)	1	0.952	taagttGCTGAaaaagact

V$CMAF_04	c-MAF	748 (+)	1	0.937	aagttGCTGAaaaagac
V$CMAF_Q5	c-MAF	752 (-)	1	0.961	tGCTGAaaaag
V$MAFB_Q4_01	MAFB	752 (-)	1	1	tGCTGAa
V$NKX22_01	Nkx2-2	759 (-)	1	0.958	aaagACTTAa
V$HOXD12ELK1_01	HOXD12:Elk-1	764 (-)	0.79	0.764	cttaaaaaCTTCTgtta
V$ELK1HOXB13_01	Elk-1:HOXB13	764 (-)	0.777	0.768	cttaaaaacTTCTGtt
P$MYB24_01	MYB24	775 (+)	1	0.966	ctgTTAGGc
I$ARA_01	ara	776 (-)	1	1	TGTTA
I$CAUP_01	caup	776 (-)	1	1	TGTTA
V$REST_16	REST	787 (-)	0.914	0.812	gggtaCTGGCctagctgttgt
V$FOXJ1_04	FOXJ1	798 (-)	1	0.932	tagctGTTGTaacta
V$RFX4_04	RFX4	803 (-)	1	0.995	gttGTAACtaagaaa
I$LBE_01	lbe	807 (+)	1	1	TAACTa
F$YML081W_01	Yml081wp	811 (+)	0.911	0.84	taagaaagcCCCACatataat
V$PARP_Q4	PARP	812 (-)	1	1	aAGAAA
P$BPC1_Q2	BPC1	813 (+)	1	1	AGAAAg
V$CPBP_Q6	CPBP	818 (+)	1	1	GCCCCac
V$NANOG_Q3	Nanog	825 (+)	1	0.991	ataTAATGgt
V$BARX1_05	Barx1	826 (+)	0.957	0.951	tatAATGGttta
V$ZNF333_01	ZNF333	827 (+)	1	1	ATAAT
V$YY2	YY2	827 (-)	1	1	atAATGG
F$ADR1_Q6	Adr1p	843 (+)	0.988	0.938	atgGGAGTtt
V$RELA_05	RelA-p65	845 (-)	0.974	0.984	GGGAGttt
P$AZF3_01	AZF3	847 (+)	0.937	0.962	gAGTTTatttt
V$CDX_Q5	Cdx	850 (-)	1	0.904	TTTATttttctccatgta
V$CDX1_Q5	Cdx-1	850 (+)	1	1	TTTATt
V$MEF2C_Q4	MEF-2C	852 (+)	1	1	TATTTtt
V$SPIB_Q3	Spi-B	857 (+)	1	1	TTCTCc
F$MATALPHA2_01	MATalpha2p	861 (+)	1	0.976	cCATGTaata
V$PMX1_Q6	PMX1	866 (+)	1	1	TAATAa
V$PPARG_06	PPARGAMMA	867 (-)	0.98	0.955	aaTAACCcagaa
V$ELF1_02	ELF1	870 (+)	0.751	0.842	aacccAGAAGta
P$ASR1_01	ASR-1	871 (+)	1	1	ACCCA

V$FOXA1_02	HNF-3alpha	876 (+)	1	0.948	gaaGTAAAc
V$LYL1_01	Lyl-1	884 (-)	1	0.911	ctgttcaCAGCTga
V$LYL1_02	Lyl-1	884 (-)	1	0.911	ctgttcaCAGCTga
V$PAX2_01	Pax-2	884 (-)	0.97	0.86	ctgttcacagCTGACaagg
V$ZBTB44_01	Zbtb44	888 (-)	1	1	tCACAG
V$VMAF_01	v-Maf	889 (+)	1	0.883	cacaGCTGAcaaggcggct
V$MYOGENIN_Q6_01	myogenin	891 (+)	1	1	CAGCTg
V$MYOGENIN_Q6_01	myogenin	891 (-)	1	1	cAGCTG
P$AT1G53910_02	AT1G53910	891 (+)	1	0.84	cagctgacaagGCGGCtcgtc
V$E2F3TBX21_01	E2F-3:T-bet	892 (+)	0.927	0.844	agcTGACAaggcggct
P$BZIP42_01	bZIP42	892 (+)	0.623	0.775	agctgACAAGgc
P$BZIP43_01	bZIP43	892 (-)	0.624	0.785	agctgACAAGgc
V$E2F3EOMES_01	E2F-3:TBR2	892 (+)	0.794	0.764	agctgacaaGGCGGctcgtcttc
V$E2F1EOMES_02	E2F-1:TBR2	892 (+)	0.951	0.818	agctgacaaGGCGGctcgtcttc
V$E2F3EOMES_01	E2F-3:TBR2	892 (-)	0.786	0.735	agctgacaagGCGGCtcgtcttc
V$MAFB_01	MafB	893 (+)	1	1	GCTGAc
P$ERF7_02	ERF7	898 (-)	1	0.988	caagGCGGCt
P$ERF8_01	ERF8	898 (-)	0.972	0.967	caaggCGGCT
P$ERF096_01	ERF096	899 (-)	1	0.991	aagGCGGCtc
P$ERF11_01	ERF11	899 (-)	0.984	0.979	aaggCGGCTc
P$RRTF1_02	RRTF1	900 (-)	0.823	0.825	aggCGGCTcg
P$RAP26_03	RAP2-6	900 (-)	0.815	0.84	aggCGGCTcg
P$RAP210_04	RAP2-10	900 (-)	0.803	0.857	aggCGGCTcg
P$ERF069_01	ERF069	900 (-)	0.989	0.988	aggCGGCTc
P$AT1G68550_03	AT1G68550	900 (+)	0.949	0.952	aggCGGCTc
P$ERF1_Q2	ERF1	901 (+)	1	1	GGCGGctc
P$ERF098_01	ERF098	901 (-)	1	0.998	gGCGGCtc
P$BPC1_Q2	BPC1	911 (-)	1	1	cTTTCT
V$FOXO1ETV7_01	FOXO1A:ETV7	917 (+)	1	0.764	caacACAGGatttccatcttt
V$ERFSREBF2_02	ERF:SREBP-2	918 (-)	0.562	0.732	aaCACAGgatttccatc
V$GATAD2A_01	GATAD2A	920 (-)	1	1	CACAGg
V$ELK1ETV7_01	Elk-1:ETV7	920 (-)	0.669	0.772	cacaggatttcCATCTttgg
V$ERG_05	ERG	921 (-)	0.846	0.793	acAGGATttccatc

V$FLI1_04	FLI1	921 (-)	0.825	0.775	acAGGATttccatc
V$ELK1SPDEF_01	Elk-1:PDEF	921 (-)	0.946	0.832	acAGGATttccatctttg
V$OCT1_05	1-Oct	923 (+)	0.934	0.913	aggaTTTCCatctt
V$AP3_Q6_01	AP-3	925 (-)	1	1	gaTTTCCa
P$AGL15_02	AGL15	927 (-)	1	0.947	TTTCCatctttgg
P$AGL15_03	AGL15	927 (+)	1	0.931	TTTCCatctttggct
V$E2F3_05	E2F-3	932 (+)	0.758	0.723	atctttGGCTCcaacggg
V$E2F2_06	E2F2	932 (-)	0.881	0.759	atctttgGCTCCaacggg
V$E2F3_05	E2F-3	932 (-)	0.845	0.756	atctttgGCTCCaacggg
V$E2F4_03	E2F-4	935 (+)	0.803	0.831	ttTGGCTccaac
V$E2F1_04	E2F-1	935 (-)	0.793	0.843	tttGGCTCcaac
V$E2F4_02	E2F-4	935 (-)	0.8	0.778	tttGGCTCcaac
V$E2F4_03	E2F-4	935 (-)	0.798	0.849	tttggCTCCAac
V$VMYB_02	v-Myb	941 (+)	1	0.973	tccAACGGg
P$AT5G54070_01	AT5G54070	942 (+)	1	1	cCAACG
P$MYB3R1_01	MYB3R1	942 (-)	1	0.852	ccAACGGggttgctt
P$MYB3R4_01	MYB3R4	942 (-)	1	0.853	ccAACGGggttgctt
P$MYB3R5_01	MYB3R5	943 (-)	1	0.857	cAACGGggttgcttt
V$NR2C2_04	TR4	945 (-)	1	0.988	acGGGGT
V$MIF1_01	MIF-1	947 (-)	0.769	0.826	ggggttgctttGGATCct
V$MIF1_01	MIF-1	948 (+)	1	0.782	ggGTTGCtttggatcctg
V$RFX_Q6_01	RFX	948 (+)	1	0.971	ggGTTGCtttgga
V$RFX1_Q6	Rfx1	950 (+)	1	0.963	GTTGCtttggatcc
P$CBNAC_01	CBNAC	951 (+)	1	1	tTGCTT
V$BLIMP1_03	Blimp-1	951 (+)	1	0.858	ttgctTTGGAtc
V$ARID3A_02	ARID3A	962 (+)	1	0.963	cctgaTATCAtctag
I$OPTIX_01	Optix	964 (+)	1	1	TGATA
I$OPTIX_01	Optix	967 (-)	1	1	TATCA
V$OSR1_04	OSR1	970 (-)	1	0.97	catctagGTAGCggga
V$OSR2_04	OSR2	970 (-)	1	0.958	catctagGTAGCggga
V$E2F1_11	E2F-1	975 (+)	1	0.941	aggtaGCGGGaagg
F$STP4_02	Stp4p	976 (+)	1	0.942	ggTAGCGgg
V$E2F4_11	E2F-4	976 (+)	1	0.939	ggtaGCGGGaagg

V$E2F4_05	E2F-4	977 (-)	1	0.942	gtaGCGGGaagg
V$E2F1_09	E2F-1	977 (+)	1	0.946	gtaGCGGGaag
V$E2F3_07	E2F-3	977 (+)	1	0.939	gtaGCGGGaag
V$E2F4_09	E2F-4	978 (+)	1	0.96	taGCGGGaagg
V$STAT3_12	STAT3	978 (-)	0.983	0.922	tagcgGGAAGgggga
V$ELK1EVX1_01	Elk-1:EVX1	979 (+)	0.91	0.813	agcGGGAAggggataa
F$LEU3_02	Leu3p	980 (-)	0.915	0.9	GCGGGaaggg
V$E2F4_Q6	E2F-4	980 (+)	1	0.904	GCGGGaaggg
V$E2F1DP1_01	E2F-1:DP-1	980 (-)	1	0.96	gCGGGAag
V$GABP_B	GABP	980 (+)	1	0.925	gcgGGAAGgggg
V$PET1_03	Pet-1	980 (+)	1	0.988	gcgGGAAGgg
V$PET1_04	Pet-1	980 (+)	1	0.988	gcgGGAAGgg
V$DR3_Q4	VDR,	983 (-)	0.848	0.837	ggaagGGGGAtaaaggccagg
V$COUPTF_Q6	COUPTF	984 (-)	0.927	0.887	gaaggggataaaGGCCAgggga
V$CPBP_Q6	CPBP	985 (-)	1	1	aaGGGGG
V$PPARG_03	PPAR	985 (+)	1	0.869	aagggggatAAAGGcca
V$PPARARXRA_01	PPARALPHA:RXR-A	985 (+)	1	0.852	aagggggatAAAGGccag
V$PPARG_08	PPARgamma	985 (+)	1	0.925	aagggggatAAAGGcca
V$PPARA_03	PPARalpha	985 (+)	1	0.919	aagggggatAAAGGcca
V$PPARG_09	PPARgamma	985 (+)	1	0.924	aagggggatAAAGGcca
V$PPARA_04	PPARalpha	985 (+)	1	0.904	aagggggatAAAGGcca
V$PPARG_10	PPARgamma	985 (+)	1	0.915	aagggggatAAAGGcca
V$ESRRA_06	ESRRA	985 (+)	0.876	0.776	aagggggataAAGGCca
V$PPARGRXRA_03	PPARGAMMA:RXR-	986 (+)	1	0.871	agggggatAAAGGcc
V$PPARGRXRA_01	PPARgamma:RXR-a	987 (+)	1	0.919	gggggatAAAGGcca
V$RXRB_02	Rxrb	988 (+)	1	0.78	ggggatAAAGGcca
V$RXRA_13	RXR-ALPHA	988 (+)	1	0.822	ggggatAAAGGccag
V$NR2F1_06	COUP-TF1	988 (+)	0.935	0.927	ggggataaaGGCCAggg
V$PPARDR1_Q2	PPAR	989 (-)	0.854	0.868	gggataaAGGCCa
V$RXRA_16	RXRALPHA	992 (-)	0.984	0.966	ataaaGGCCAggg
V$ESRRA_07	ESRRA	994 (+)	0.889	0.769	aaaggccaggggAAGGGag
V$NURR1_Q3	NURR1	995 (-)	1	1	AAGGCca
V$REST_13	REST	997 (-)	0.797	0.74	ggccaGGGGAagggagg

V$DPF2_01	DPF2	997 (-)	1	0.925	ggccaggGGAAGggag
V$KAISO_Q2	Kaiso	998 (+)	0.938	0.929	gccaggGGAAGg
V$SPIB_Q3	Spi-B	1002 (-)	1	1	gGGGAA
V$IRF4_07	IRF-4	1003 (+)	1	0.97	gGGAAGgga
V$HOXD12ELK1_01	HOXD12:Elk-1	1005 (+)	0.82	0.767	gaagGGAGGatgtaaat
V$GKLF_Q4	GKLF	1007 (-)	1	1	agGGAGG
V$FOXO1SPDEF_01	FOXO1A:PDEF	1008 (+)	1	0.889	gggaGGATGtaaa
V$PEA3_Q6	PEA3	1011 (-)	1	1	aGGATGt
V$HMGIY_Q3	HMGIY	1014 (+)	1	0.942	atgtaAATTTctttt
V$PARP_Q4	PARP	1021 (+)	1	1	TTTCTt
F$GCN4_01	Gcn4p	1026 (+)	1	0.961	tttaaggacaTGACTcagaaatgac
V$BATF_07	B-ATF	1026 (+)	1	0.957	tttaaggacaTGACTcag
F$GCN4_02	Gcn4p	1029 (-)	1	0.963	aaggacatgACTCAgaaatga
V$TCF11MAFG_01	TCF11:MafG	1030 (+)	1	0.835	aggacATGACtcagaaatgaca
V$JUN_04	c-Jun	1030 (+)	1	0.986	aggacaTGACTcag
V$BATFJUN_01	c-Jun:B-ATF	1032 (+)	1	0.987	gacaTGACTca
V$AP1_01	AP-1	1033 (-)	1	0.961	acaTGACTcagaa
V$FOSL2_02	Fra-2	1033 (+)	1	0.988	acaTGACTcag
V$JUNB_01	JunB	1033 (+)	1	0.987	acaTGACTcag
V$JUNBFRA1_01	JUNB:FRA-1	1033 (+)	1	0.977	acaTGACTcagaa
V$JUNBFOS_01	JUNB:C-FOS	1033 (-)	1	0.976	acaTGACTcaga
V$JUNDFOS_01	JUND:C-FOS	1033 (-)	1	0.977	acaTGACTcagaa
V$JUNFRA1_01	C-JUN:FRA-1	1033 (+)	1	0.979	acaTGACTcagaa
V$FOS_10	c-Fos	1033 (-)	1	0.989	acaTGACTcag
V$AP1_01	AP-1	1033 (+)	0.968	0.959	acatgACTCAgaa
V$TRP53_02	Trp53	1033 (-)	0.726	0.795	acatgactcagAAATGa
V$NRF2_Q4	Nrf-2	1034 (-)	1	0.907	caTGACTcagaaa
V$FOS_06	c-Fos	1034 (-)	0.995	0.996	caTGACTcaga
V$NRF2_Q4_01	Nrf2	1034 (+)	1	0.92	caTGACTcagaaa
V$JUNBFOSB_01	JUNB:FOSB	1034 (+)	1	0.978	caTGACTcag
V$JUNBFRA2_01	JUNB:FRA-2	1034 (+)	1	0.975	caTGACTcag
V$FOSBJUND_01	FOSB:JUND	1034 (+)	1	0.945	caTGACTcaga
V$JUNDFRA1_01	JUND:FRA-1	1034 (+)	1	0.99	caTGACTcag

V$JUNDFRA2_01	JUND:FRA-2	1034 (+)	1	0.975	caTGACTcag
V$JUNFOSB_01	C-JUN:FOSB	1034 (+)	1	0.991	caTGACTcag
V$JUNFRA2_01	C-JUN:FRA-2	1034 (-)	1	0.983	caTGACTcagaa
V$FOSJUN_02	C-FOS:C-JUN	1034 (-)	1	0.974	caTGACTcag
V$JUNBJUN_01	JUNB:C-JUN	1034 (+)	1	0.98	caTGACTcag
V$FOS_08	C-FOS	1034 (-)	1	0.916	caTGACTcaga
V$FOSL1_03	Fra-1	1034 (+)	1	0.99	caTGACTcaga
V$FOSL1_05	Fra-1	1034 (-)	1	0.991	caTGACTcagaa
V$FRA2_04	Fra-2	1034 (-)	1	0.984	caTGACTcagaa
V$JUND_08	JunD	1034 (-)	1	0.989	caTGACTcaga
V$JUN_06	c-Jun	1034 (-)	1	0.985	caTGACTcaga
V$FOSL1_06	Fra-1	1034 (-)	1	0.991	caTGACTcagaa
V$FRA2_05	Fra-2	1034 (-)	1	0.989	caTGACTcaga
V$FOS_12	c-Fos	1034 (-)	1	0.982	caTGACTcagaa
V$JUND_04	JunD	1034 (-)	0.978	0.969	catgACTCAga
V$AP1_C	AP-1	1035 (-)	1	0.985	aTGACTcag
V$AP1_Q6_01	AP-1	1035 (+)	1	1	aTGACTcag
V$AP1_Q4_01	AP-1	1035 (-)	1	1	aTGACTca
V$MAF_Q6_01	MAF	1035 (-)	1	0.965	aTGACTcagaa
V$FRA1_Q5	Fra-1	1035 (-)	1	1	aTGACTca
V$NFE2_04	NF-E2	1035 (+)	1	1	aTGACTcag
V$FOS_02	c-Fos	1035 (+)	0.997	0.961	aTGACTcag
V$MAF_Q4	MAF	1035 (-)	1	0.958	aTGACTcaga
V$FRA2_01	FRA-2	1035 (+)	1	1	aTGACTca
V$JUNB_02	JUNB	1035 (+)	1	1	aTGACTca
V$JUND_06	JUND	1035 (-)	1	0.969	aTGACTcaga
V$FRA2_03	Fra-2	1035 (+)	1	0.994	aTGACTcagaa
V$JUNB_04	JunB	1035 (-)	1	0.99	aTGACTcagaa
V$NRF2_03	Nrf2	1035 (-)	1	0.886	aTGACTcagaaatg
V$JUNB_06	JunB	1035 (-)	1	0.997	aTGACTcag
V$JUND_09	JunD	1035 (-)	1	0.988	aTGACTcagaa
V$JUN_07	c-Jun	1035 (-)	1	0.993	aTGACTcaga
V$AP1_C	AP-1	1035 (+)	0.989	0.993	atgACTCAg

V$JUN_04	c-Jun	1035 (-)	0.99	0.954	atgACTCAgaaatg
V$NFE2_01	NF-E2	1035 (-)	0.884	0.929	atgacTCAGAa
V$AP1_02	AP1	1036 (+)	1	1	TGACTca
V$CJUN_Q6	C-Jun	1036 (+)	1	1	TGACTc
V$JUNB_Q6	JunB	1036 (+)	1	1	TGACTcag
V$CFOS_Q6	c-Fos	1036 (+)	1	1	TGACTcag
V$FRA1_Q6_01	Fra-1	1036 (+)	1	0.999	TGACTcag
V$TCF11MAFG_01	TCF11:MafG	1041 (+)	1	0.843	cagaaATGACacagctcattct
V$MAFG_Q3	MafG	1044 (+)	0.861	0.801	aaatgacACAGCtca
V$E2F3EOMES_01	E2F-3:TBR2	1044 (+)	0.673	0.768	aaatgacacAGCTCattctcaccc
V$E2F3EOMES_01	E2F-3:TBR2	1044 (-)	0.696	0.799	aaatgacacaGCTCAttctcaccc
V$NFE2L1_Q5	Nfe2l1	1045 (-)	1	0.977	aATGACacagct
V$NRF2_Q4	Nrf-2	1045 (-)	0.905	0.893	aaTGACAcagctc
V$NRF2_Q4_01	Nrf2	1045 (+)	0.925	0.912	aaTGACAcagctc
V$NFE2L2_01	NFE2L2	1046 (+)	1	0.947	ATGACacagct
V$MAF_Q4	MAF	1046 (-)	0.944	0.962	aTGACAcagc
V$NRF2_03	Nrf2	1046 (-)	0.846	0.855	aTGACAcagctcat
V$PPARG_02	PPARgamma:RXRal	1049 (+)	0.795	0.703	acacaGCTCAttctcacccagca
V$PPARG_02	PPARgamma:RXRal	1049 (-)	0.899	0.686	acacagctcattcTCACCcagca
V$ESR1_03	ESR1	1052 (-)	0.813	0.802	caGCTCAttctcaccca
V$E2F3TBX21_01	E2F-3:T-bet	1052 (-)	0.94	0.844	cagctcatTCTCAccc
V$PAX4_Q2	Pax-4	1057 (+)	0.974	0.88	cattcTCACCc
V$ZIC3_05	ZIC3	1062 (+)	1	0.967	tcaccCAGCAtgacc
V$TCF11_01	TCF11	1063 (-)	1	0.999	cacccagcATGAC
P$ASR1_01	ASR-1	1064 (+)	1	1	ACCCA
V$PAX5_07	Pasx-5	1067 (-)	0.918	0.887	cagcATGAC
V$PAX5_13	PAX5	1067 (+)	0.83	0.879	cagcATGACcaa
I$PRD_02	Prd	1069 (+)	0.872	0.844	gcATGACcaaat
I$PRD_03	Prd	1077 (+)	0.969	0.899	aaATCCAtgc
V$RHOX11_07	Rhox11	1084 (+)	0.991	0.992	tgCTGTAaa
I$CHES1L_02	CHES1L	1084 (+)	0.801	0.805	tgctgtaaaGATGCcaagaaaag
V$NF1A_Q6_01	NF-1A	1095 (+)	1	1	tGCCAAg
F$RIM101_01	Rim101p	1097 (+)	1	1	CCAAGaaa

V$PARP_Q4	PARP	1099 (-)	1	1	aAGAAA
V$NKX22_02	NKX2B	1104 (+)	1	0.905	aagtaCACTTgaactgg
V$NKX25_03	NKX25	1104 (+)	1	0.868	aagtaCACTTgaactg
V$NKX25_Q6	CSX	1107 (+)	1	0.984	taCACTTgaac
V$NKX28_01	NKX2-8	1108 (+)	1	0.993	aCACTTgaa
V$NKX25_01	Nkx2-5	1109 (-)	1	1	CACTTga
V$NKX2B_Q3	NKX2B	1109 (+)	1	1	CACTTga
I$CT_01	ct	1112 (+)	1	1	tTGAAC
F$YDR520C_01	Ydr520c	1116 (+)	0.786	0.765	actggcCAGAGaaattctca
V$NF1B_Q6_01	NF-1B	1120 (+)	1	0.998	GCCAGagaa
F$AMT1_Q2	AMT1	1133 (+)	1	1	TCAGCtaa
V$FOXP3_Q6	FOXP3	1136 (+)	1	0.991	gctaAAACAcag
I$MIRR_01	mirr	1140 (+)	1	1	AAACA
V$GATAD2A_01	GATAD2A	1143 (-)	1	1	CACAGg
V$PMX1_Q6	PMX1	1156 (-)	1	1	tTATTA
V$LHX3_Q3	LHX3	1158 (+)	1	1	ATTAAa
V$SMAD2_Q6	Smad2	1163 (+)	1	1	AGACAg
V$P54NRB_Q5	p54NRB	1170 (+)	1	0.875	gaatatGGATGttgctgga
V$FOXO1SPDEF_01	FOXO1A:PDEF	1172 (+)	1	0.901	atatGGATGttgc
V$ZNF777_02	ZNF777	1180 (-)	0.778	0.708	gttgctggACAGGtagcca
V$OSR1_04	OSR1	1185 (-)	1	0.972	tggacagGTAGCcatc
V$OSR2_04	OSR2	1185 (-)	1	0.949	tggacagGTAGCcatc
V$SMAD4_Q6	SMAD4	1187 (+)	1	0.914	gacaggtAGCCAtct
F$MOT3_01	MOT3	1189 (+)	1	1	cAGGTA
P$O2_04	O2	1193 (+)	0.934	0.872	taGCCATctcagc
P$BZIP42_01	bZIP42	1195 (-)	0.606	0.756	gcCATCTcagcc
P$BZIP43_01	bZIP43	1195 (+)	0.624	0.781	gcCATCTcagcc
V$AREB6_01	AREB6	1206 (+)	1	0.992	cacatACCTGtgt
F$MOT3_01	MOT3	1210 (-)	1	1	TACCTg
V$GATAD2A_01	GATAD2A	1212 (+)	1	1	cCTGTG
V$FAC1_01	FAC1	1212 (-)	0.956	0.944	cctgtGTTATgttt
V$IRX2_03	IRX2	1214 (-)	0.954	0.952	tgtgtTATGTtt
V$IRX5_03	IRX5	1214 (-)	0.984	0.97	tgtgtTATGTtt

I$ARA_01	ara	1216 (-)	1	1	TGTTA
I$CAUP_01	caup	1216 (-)	1	1	TGTTA
V$FOXP3_Q6	FOXP3	1218 (-)	1	0.996	ttaTGTTTtctc
V$FOXP1_05	FOXP1	1220 (+)	1	0.953	aTGTTTtctctag
I$MIRR_01	mirr	1221 (-)	1	1	TGTTT
V$FOXM1_05	foxm1	1221 (+)	1	0.933	TGTTTtctctag
V$ELK1HOXB13_01	Elk-1:HOXB13	1232 (-)	0.777	0.781	gtctaaaacTTCAGgc
V$FOXJ2_01	FOXJ2	1251 (+)	1	0.967	caaaaaacAAACAaaaca
V$HNF3_Q6_01	HNF3	1251 (-)	1	0.975	caaaaaacAAACAaaaca
V$FOXC1_Q4	Foxc1	1252 (-)	1	1	aaaaAACAA
V$FOXP1_05	FOXP1	1252 (-)	1	0.955	aaaaaacAAACAa
V$FOXO1_Q5	FOXO1	1253 (+)	1	1	aaAAACAaa
V$FOXO1A_Q3	FOXO1A	1253 (-)	1	1	aaAAACAa
V$HNF3ALPHA_Q6	HNF3alpha	1253 (-)	1	1	aaaaacAAACA
V$HNF3_Q6	HNF3	1253 (+)	1	0.99	aaaaacAAACAaa
V$HNF3B_01	HNF3beta	1254 (-)	1	0.955	aaaacAAACAaaaca
V$HFH3_01	HFH3	1254 (-)	1	0.984	aaaacAAACAaaa
V$FOX_Q2	FOX	1254 (-)	1	0.956	aaaacAAACAaaa
V$SRY_01	SRY	1255 (+)	1	1	AAACAaa
I$MIRR_01	mirr	1255 (+)	1	1	AAACA
V$FOXO1A_Q5	FOXO1A	1255 (+)	1	1	AAACAa
V$SRY_Q6	SRY	1255 (-)	1	1	aAACAA
V$FOXD3_01	FOXD3	1255 (-)	1	0.96	aaacaAACAAaa
V$SOX4_Q5	Sox-4	1256 (+)	1	1	AACAAa
V$HNF3G_Q4	HNF-3gamma	1256 (-)	1	1	aacAAACA
V$FOXM1_Q6	Foxm1	1257 (-)	1	1	acAAACAa
V$FOXL1_02	FOXL1	1258 (+)	1	0.963	caaacaaAACAAcaaa
V$SRY_01	SRY	1259 (+)	1	1	AAACAaa
I$MIRR_01	mirr	1259 (+)	1	1	AAACA
V$FOXO1A_Q5	FOXO1A	1259 (+)	1	1	AAACAa
V$SRY_Q6	SRY	1259 (-)	1	1	aAACAA
V$FOXL2_Q5	FOXL2	1259 (+)	1	0.96	aaaCAAAAcaa
V$FAC1_01	FAC1	1259 (+)	0.978	0.947	aaacAAAACaacaa

V$SOX4_Q5	Sox-4	1260 (+)	1	1	AACAAa
V$FOXK1_04	FOXK1	1260 (+)	1	0.952	aacaaaACAACaaag
V$FOXJ1_04	FOXJ1	1261 (+)	1	0.943	acaaaACAACaaagc
V$TCF3_01	TCF-3	1263 (-)	1	0.984	aaaacaaCAAAGc
I$MIRR_01	mirr	1264 (+)	1	1	AAACA
V$FOXO1A_Q5	FOXO1A	1264 (+)	1	1	AAACAa
V$SRY_Q6	SRY	1264 (-)	1	1	aAACAA
V$LEF1_Q4	LEF-1	1264 (+)	1	0.995	aaacaaCAAAGct
V$TCF7RELATED_Q4	TCF7RELATED	1264 (+)	1	0.991	aaacaaCAAAGc
V$TCF1_10	TCF-1	1264 (+)	1	0.967	aaacaaCAAAGctaac
V$BETACATENIN_Q6	Beta-catenin	1265 (-)	1	0.98	aacaaCAAAGctaac
V$SOX10_08	SOX10	1266 (+)	1	0.998	acaACAAAgct
V$BETACATENIN_Q3_01	beta-catenin	1267 (-)	1	0.996	caaCAAAG
V$BETACATENIN_Q6_01	beta-catenin	1267 (-)	1	0.986	caaCAAAG
V$SOX4_Q5	Sox-4	1268 (+)	1	1	AACAAa
V$SOX10_Q6_01	Sox-10	1268 (+)	1	1	aACAAAg
V$SOX10_01	Sox-10	1269 (-)	1	1	ACAAAg
V$TCF1_Q5	TCF-1	1269 (-)	1	1	aCAAAG
I$ARA_01	ara	1276 (+)	1	1	TAACA
I$CAUP_01	caup	1276 (+)	1	1	TAACA
V$HOXA10_Q5	HOXA10	1279 (-)	1	0.997	cATAAAct
P$AT4G12670_01	AT4G12670	1280 (+)	1	0.658	aTAAACtccaaaatataagcccaatt
F$ADR1_Q6	Adr1p	1282 (-)	0.988	0.958	aaACTCCaaa
P$TRP2_01	TRP2	1282 (+)	0.6	0.691	aaactccAAAATataagccc
P$HSFA2_01	HSFA2	1287 (+)	1	1	CCAAAa
V$FOXL2_Q2	FOXL2	1295 (+)	1	0.936	taagcccAATTT
V$TCF1_10	TCF-1	1302 (-)	0.972	0.946	aatttCTTTCttgtta
V$PARP_Q4	PARP	1304 (+)	1	1	TTTCTt
P$BPC1_Q2	BPC1	1307 (-)	1	1	cTTTCT
P$NAC078_01	NAC078	1307 (-)	1	0.861	cttTCTTGttattcaat
V$PARP_Q4	PARP	1308 (+)	1	1	TTTCTt
V$HOXC8_Q3	HOXC-8	1311 (-)	1	0.981	cttGTTATtc
P$NAC078_01	NAC078	1311 (+)	0.742	0.874	cttgttattCAATAaat

P$ATMYB15_Q2	Myb-15	1312 (-)	1	1	tTGTTA
V$SOX1_03	Sox-1	1312 (+)	1	0.943	ttgttATTCAataaat
I$ARA_01	ara	1313 (-)	1	1	TGTTA
I$CAUP_01	caup	1313 (-)	1	1	TGTTA
V$FOXJ2HOXB13_01	FOXJ2:HOXB13	1313 (-)	1	0.915	tgttattcaATAAAt
V$ZFP105_04	ZFP105	1314 (+)	1	0.947	gttatTCAATaaatatt
I$SGF3_Q6	SGF-3	1315 (+)	1	1	tTATTCa
N$CEH48_01	ceh-48	1317 (+)	0.985	0.979	atTCAATaa
V$OC2_Q3	OC-2	1319 (+)	1	1	TCAATa
V$CUX1HOXB13_01	CDP:HOXB13	1319 (+)	0.716	0.831	tcaataaatATTTAta
I$CG4328_01	CG4328	1320 (-)	1	1	cAATAAa
I$CAD_01	cad	1320 (-)	1	1	caATAAA
V$CDX1_Q5	Cdx-1	1321 (-)	1	1	aATAAA
V$CUX1HOXB13_01	CDP:HOXB13	1321 (-)	0.716	0.829	aaTAAATatttataga
V$POU2F2_03	POU2F2	1321 (+)	0.995	0.916	aataAATATttata
V$FOXC2_01	FOXC2	1321 (+)	1	0.932	aataAATATttata
V$FOXD2_01	FOXD2	1321 (+)	1	0.991	aataAATATttata
V$FOXD3_04	FOXD3	1321 (-)	1	0.957	aataAATATttata
V$POU2F2_03	POU2F2	1321 (-)	0.995	0.912	aataaATATTtata
V$FOXC2_01	FOXC2	1321 (-)	1	0.931	aataaATATTtata
V$FOXD2_01	FOXD2	1321 (-)	1	0.99	aataaATATTtata
V$FOXD3_04	FOXD3	1321 (+)	1	0.957	aataaATATTtata
V$SATB1_Q5_01	SATB1	1322 (-)	1	1	ATAAAt
V$MEF2C_Q4	MEF-2C	1322 (-)	1	1	atAAATA
V$POU2F3_04	POU2F3	1322 (+)	1	0.912	ataAATATttat
V$POU3F3_04	POU3F3	1322 (+)	1	0.985	ataAATATttat
V$POU2F3_04	POU2F3	1322 (-)	1	0.912	ataaATATTtat
V$POU3F3_04	POU3F3	1322 (-)	1	0.985	ataaATATTtat
V$MEF2C_Q4	MEF-2C	1327 (+)	1	1	TATTTat
V$CDXA_02	CdxA	1328 (+)	1	1	aTTTATa
V$SATB1_Q5_01	SATB1	1328 (+)	1	1	aTTTAT
V$CDX2_Q5_02	CDX-2	1329 (+)	1	1	TTTATa
I$VVL_01	vvl	1345 (+)	1	1	tATGCA

V$XVENT1_01	Xvent-1	1355 (+)	1	0.913	gcactATTTGaaa
P$HSFA4A_01	HSFA4A	1357 (+)	1	1	aCTATT
V$DMRT4_01	DMRT4	1359 (-)	0.94	0.944	tatttGAAACatt
I$MIRR_01	mirr	1365 (+)	1	1	AAACA
V$MAFF_08	MafF	1366 (-)	1	0.908	aacattgcagattCAGCA
V$MAFG_01	MAFG	1367 (-)	1	0.927	acattgcagatTCAGCagact
V$MAFF_09	MafF	1367 (-)	1	0.888	acattgcagatTCAGCagactg
V$MAFB_07	MafB	1369 (+)	0.859	0.92	attGCAGAttcagcaga
V$MAFB_07	MafB	1369 (-)	1	0.949	attgcagatTCAGCaga
V$MAFK_06	MAFK	1370 (+)	0.879	0.94	ttGCAGAttcagcag
V$MAFK_06	MAFK	1370 (-)	1	0.949	ttgcagatTCAGCag
V$CMAF_03	c-MAF	1370 (-)	1	0.956	ttgcagatTCAGCagactg
V$CMAF_04	c-MAF	1371 (-)	1	0.963	tgcagatTCAGCagact
F$RDS1_01	Rds1p	1372 (+)	0.643	0.737	gcagattCAGCAgactgcaa
F$RDS1_01	Rds1p	1372 (-)	0.643	0.735	gcagattcAGCAGactgcaa
V$CMAF_Q5	c-MAF	1373 (+)	1	0.965	cagatTCAGCa
V$MAFB_09	MafB	1373 (-)	1	0.984	cagatTCAGCa
V$MAFB_10	MafB	1373 (-)	1	0.984	cagatTCAGCa
V$MAFB_Q4_01	MAFB	1377 (+)	1	1	tTCAGCa
V$MAFA_Q4	MAFA	1378 (+)	1	1	TCAGCag
F$PDR3_02	PDR3	1378 (+)	0.8	0.75	TCAGCaga
F$PDR3_02	PDR3	1378 (-)	0.8	0.75	tcaGCAGA
V$SMAD5_Q5_01	SMAD5	1382 (+)	1	0.999	CAGACtgc
F$FLP1_01	Flp	1383 (-)	1	1	agACTGC
I$MIRR_01	mirr	1391 (+)	1	1	AAACA
F$YBR239C_01	Ybr239c	1397 (+)	0.792	0.759	atcagctTCCCGatcccaga
V$CETS168_Q6	c-Ets-1	1401 (-)	1	0.98	gCTTCCcg
V$STAT_Q6	STAT	1410 (-)	1	0.993	tccCAGAAagctg
P$BPC1_Q2	BPC1	1414 (+)	1	1	AGAAAg
V$OC2_Q3	OC-2	1426 (+)	1	1	TCAATa
V$HELIOSA_01	Helios	1428 (+)	1	0.987	aatAGGGAgag
I$TRL_02	GAGA	1432 (-)	1	0.935	ggGAGAGaag
V$FREAC3_01	Freac-3	1437 (+)	1	0.901	agaagGTAAAcaaatg

V$FOXA2_04	HNF3-beta	1437 (+)	1	0.989	agaagGTAAAcaaatga
V$FOXA2_05	FOXA2	1437 (+)	1	0.989	agaagGTAAAcaaatga
V$FREAC2_01	Freac-2	1437 (+)	1	0.986	agaaggTAAACaaatg
V$FREAC4_01	Freac-4	1437 (+)	1	0.888	agaaggTAAACaaatg
V$FOXK1_03	Foxk1	1437 (+)	1	0.986	agaaggtAAACAaatga
V$FOXL1_04	FOXL1	1437 (+)	1	0.964	agaaggtAAACAaatga
V$FOXP1_03	FOXP1	1437 (+)	1	0.989	agaaggtAAACAaat
V$FOXA1_08	HNF-3alpha	1437 (-)	1	0.966	agaaggtAAACAa
V$HNF3A_02	HNF-3alpha	1437 (-)	1	0.967	agaaggtAAACA
V$HNF3B_04	HNF-3beta	1437 (-)	1	0.954	agaaggtAAACA
V$FOXM1_05	foxm1	1437 (-)	1	0.946	agaaggtAAACA
V$ZNF394_04	ZNF394	1437 (+)	0.969	0.894	agaaggtaaacaaaTGAAAa
V$FOXA2_07	HNF-3beta	1438 (-)	1	0.959	gaaggtAAACA
V$HNF3B_03	HNF-3beta	1438 (-)	1	0.966	gaaggtAAACAa
V$HNF3G_02	HNF-3gamma	1438 (-)	1	0.963	gaaggtAAACAaa
V$FOXL2_01	foxl2	1438 (-)	1	0.98	gaaggtAAACA
V$XFD3_01	XFD-3	1439 (+)	1	0.933	aagGTAAAcaaatg
V$FOXA1_02	HNF-3alpha	1439 (+)	1	0.979	aagGTAAAc
F$NCU00019_01	FKH1	1439 (+)	1	0.999	aagGTAAAcaaa
V$HNF3A_03	HNF-3alpha	1439 (-)	1	0.982	aagGTAAAca
V$HNF3B_05	HNF-3beta	1439 (-)	1	0.973	aagGTAAAcaaat
V$FOXO1_02	FOXO1	1439 (-)	1	0.976	aaggtAAACAaatg
V$FOXJ1_03	FOXJ1	1439 (+)	1	0.997	aaggtAAACAaatgaa
I$SLP1_01	slp1	1439 (-)	1	0.992	aaggtAAACAa
V$FOXC2_03	FOXC2	1439 (+)	1	0.984	aaggtAAACAaa
V$FOXO3A_Q3	FOXO3A	1439 (+)	1	0.996	aaggtAAACAaat
I$CROC_02	Croc	1439 (+)	1	0.936	aaggtAAACAa
V$FOXA1_07	HNF-3alpha	1439 (+)	1	0.975	aaggtAAACA
V$FOXK1_11	FOXK1	1439 (-)	1	0.998	aaggtAAACA
V$FOXO4_02	FOXO4	1439 (-)	1	0.978	aaggtaAACAAatg
V$FOXO3_01	FOXO3	1439 (-)	1	0.984	aaggtaAACAAatg
V$HNF3A_01	HNF3A	1440 (+)	1	0.978	aggtAAACAa
V$FOXM1_Q3_02	FOXM1	1440 (-)	1	0.987	aggtAAACA

V$FOXK2_02	FOXK2	1440 (+)	1	0.998	aggtAAACAaa
V$FOXK1_12	FOXK1	1440 (-)	1	0.993	aggtAAACAaa
V$FOXO1_01	FOXO1	1441 (+)	1	0.99	ggtAAACAaa
V$FOXO3A_Q1	FOXO3A	1441 (+)	1	0.978	ggtAAACAaatg
V$FOXO3_02	FOXO3	1441 (+)	1	0.977	ggtAAACA
V$FOXO1_08	FOXO1A	1441 (-)	1	0.964	ggtAAACAaat
V$FOXO3_06	FOXO3a	1441 (-)	1	0.995	ggtAAACAaa
V$FOXI1_02	FOXI1	1442 (+)	1	1	GTAAAca
V$FOXG1_06	FOXG1	1442 (+)	1	1	gTAAACaa
V$FOXD2_02	FOXD2	1442 (+)	1	1	gtAAACA
V$FOXD3_05	FOXD3	1442 (+)	1	1	gtAAACA
V$FOXJ2_04	FOXJ2	1442 (+)	1	1	gtAAACAa
V$FOXJ3_07	FOXJ3	1442 (+)	1	1	gtAAACAa
V$FOXL1_05	FOXL1	1442 (+)	1	1	gtAAACA
V$FOXO1_05	FOXO1	1442 (+)	1	1	gtAAACAa
V$FOXO3_04	FOXO3	1442 (+)	1	1	gtAAACAa
V$FOXO4_04	FOXO4	1442 (+)	1	1	gtAAACA
V$FOXO6_02	FOXO6	1442 (+)	1	1	gtAAACA
V$FOXP3_03	FOXP3	1442 (+)	1	1	gtAAACA
V$FOXG1_05	Foxg1	1442 (+)	1	1	gtAAACA
V$FOXJ3_12	Foxj3	1442 (+)	1	1	gtAAACAa
V$FOXK1_07	Foxk1	1442 (+)	1	1	gtAAACA
V$FOXJ2_06	Foxj2	1442 (+)	1	1	gtAAACAa
N$FKH2_01	fkh-2	1442 (+)	1	1	gtAAACAa
V$FOXP1_06	FOXP1	1442 (-)	1	1	gtAAACAaa
V$FOXO1_10	FOXO1A	1442 (-)	1	0.989	gtAAACAaat
V$SRY_01	SRY	1444 (+)	1	1	AAACAaa
I$MIRR_01	mirr	1444 (+)	1	1	AAACA
V$FOXO1A_Q5	FOXO1A	1444 (+)	1	1	AAACAa
V$SRY_Q6	SRY	1444 (-)	1	1	aAACAA
V$SOX4_Q5	Sox-4	1445 (+)	1	1	AACAAa
V$FOXP3_Q6	FOXP3	1451 (+)	1	0.991	tgaaAAACAgaa
V$FOXO1ELF1_01	FOXO1A:Elf-1	1451 (+)	0.808	0.859	tgaaaaACAGAaac

V$STAT1_11	STAT1	1452 (-)	1	0.898	gaaaaacaGAAACaacagt
I$MIRR_01	mirr	1455 (+)	1	1	AAACA
V$IRF2_03	IRF-2	1455 (+)	0.996	0.956	aaacaGAAACaa
I$MIRR_01	mirr	1461 (+)	1	1	AAACA
V$FOXO1A_Q5	FOXO1A	1461 (+)	1	1	AAACAa
V$SRY_Q6	SRY	1461 (-)	1	1	aAACAA
F$NIT2_01	NIT2	1470 (-)	1	1	tAGATA
P$BHLH64_02	bHLH64	1475 (+)	1	1	ACCAGt
V$TCF1_10	TCF-1	1480 (+)	1	0.956	taagagCAAAGatgaa
V$EAR2_Q2	EAR2	1481 (-)	1	0.926	aagagCAAAGatga
V$OCT1_Q6	1-Oct	1487 (+)	0.893	0.92	aaagatGAAAAttaa
V$POU3F1_04	POU3F1	1488 (+)	1	0.903	aagATGAAaattaagg
V$OCT1_05	1-Oct	1488 (-)	0.934	0.911	aagatGAAAAttaa
V$POU2F2_08	2-Oct	1489 (-)	0.879	0.907	agATGAAaattaa
V$OCT_C	OCT-x	1489 (-)	0.884	0.888	agatGAAAAttaa
V$OCT_Q6	Octamer	1490 (-)	0.957	0.955	gATGAAaatta
I$FTZ_01	Ftz	1491 (+)	1	0.926	atgaaaATTAAg
V$PRRX2_03	Prrx2	1496 (+)	1	1	AATTA
V$DLX5_Q3	Dlx-5	1496 (+)	1	1	AATTAa
V$DRI1_01	DRI1	1496 (+)	1	1	aATTAA
V$TEAD4ELF1_01	TEF-3:Elf-1	1503 (+)	0.817	0.838	gcaatGGGGAaatg
V$SPI1_11	PU.1	1503 (+)	0.919	0.878	gcaatgggGAAATgagc
V$SPI1_12	PU.1	1503 (+)	0.937	0.889	gcaatgggGAAATgag
V$SOX18_Q5	Sox-18	1504 (+)	1	1	CAATGgg
V$IRF4_11	IRF-4	1504 (+)	0.98	0.864	caatggggAAATGagcga
V$CEBPD_Q6	C/EBPdelta	1505 (-)	0.986	0.962	aatgggGAAATg
V$CEBPG_Q6_01	C/EBPgamma	1505 (+)	1	0.977	aatgggGAAATg
V$SPIB_Q3	Spi-B	1508 (-)	1	1	gGGGAA
V$E2F3DRGX_01	E2F-3:Prrxl1	1511 (-)	0.807	0.785	gaaaTGAGCgac
V$ZNF777_02	ZNF777	1513 (-)	0.778	0.71	aatgagcgACTGGgtggct
V$GLI1_02	GLI	1521 (+)	1	0.874	actgGGTGGctc
P$ASR1_01	ASR-1	1523 (-)	1	1	TGGGT
V$KID3_01	Kid3	1525 (-)	1	1	GGTGG

V$GKLF_Q3	GKLF	1527 (-)	0.99	0.976	tggctCCTCCcttt
V$BTEB3_Q5	BTEB3	1529 (-)	1	0.97	gctCCTCCctttg
V$GKLF_Q4	GKLF	1532 (+)	1	1	CCTCCct
V$SOX18_Q5	Sox-18	1535 (-)	1	1	ccCTTTG
V$GLI1_Q3	GLI	1539 (-)	1	0.965	ttGGGTGgtta
V$GLI_Q3	GLI	1539 (+)	1	0.989	ttgGGTGGtt
P$ASR1_01	ASR-1	1540 (-)	1	1	TGGGT
V$GLI2_Q6	GLI2	1540 (+)	1	0.971	TGGGTggttag
V$ZIC3_01	Zic3	1540 (+)	1	0.945	tGGGTGgtt
V$ZIC1_01	Zic1	1540 (+)	1	0.904	tgGGTGGtt
N$TRA1_01	Tra-1	1540 (+)	0.998	0.998	tgGGTGGt
N$TRA1_02	Tra-1	1540 (+)	1	1	tggGTGGT
P$C1_Q2	C1	1540 (-)	0.996	0.982	tgggTGGTTag
V$KID3_01	Kid3	1542 (-)	1	1	GGTGG
V$ELK1_Q6	Elk-1	1551 (+)	1	1	GGAAGt
I$TLL_03	Tll	1552 (+)	0.631	0.809	gaagtcagcCAGGCa
V$MAFB_01	MafB	1555 (-)	1	1	gTCAGC
V$NF1C_02	NF1C	1558 (+)	1	1	aGCCAGg
F$MOT3_01	MOT3	1561 (+)	1	1	cAGGCA
V$ZNF35_04	ZNF35	1569 (+)	1	1	gGAAGA
V$E2F1_11	E2F-1	1570 (+)	1	0.94	gaagaGCGGGaagc
V$E2F4_11	E2F-4	1571 (+)	1	0.935	aagaGCGGGaagc
V$E2F4_05	E2F-4	1572 (-)	1	0.944	agaGCGGGaagc
V$E2F1_09	E2F-1	1572 (+)	1	0.968	agaGCGGGaag
V$E2F3_07	E2F-3	1572 (+)	1	0.945	agaGCGGGaag
V$E2F4_09	E2F-4	1573 (+)	1	0.963	gaGCGGGaagc
V$ETS2_03	c-Ets-2	1574 (+)	1	0.985	agcgGGAAGcaga
V$E2F4_Q6	E2F-4	1575 (+)	1	0.945	GCGGGaagca
V$E2F1DP1_01	E2F-1:DP-1	1575 (-)	1	0.96	gCGGGAag
V$KAISO_Q2	Kaiso	1575 (+)	0.986	0.936	gcgggaAGCAGa
V$CETS168_Q6	c-Ets-1	1576 (+)	1	0.98	cgGGAAGc
V$SPIB_Q3	Spi-B	1582 (-)	1	1	gCAGAA
V$TFIII_Q6_01	TFII-I	1583 (+)	0.979	0.979	cAGAAAgtgc

P$BPC1_Q2	BPC1	1584 (+)	1	1	AGAAAg
V$LTF_Q6	LTF	1585 (-)	1	0.992	gaaAGTGCc
F$MOT3_01	MOT3	1590 (-)	1	1	TGCCTg
V$HES1_02	Hes1	1594 (+)	0.96	0.957	tgCACGGgaa
V$DEC1_05	1-Dec	1594 (+)	0.843	0.861	tgcACGGGaa
V$RFX3SREBF2_01	rfx3:SREBP-2	1594 (-)	0.835	0.758	tgcaCGGGAagctgcaag
F$PHO4_03	Pho4p	1595 (+)	0.965	0.927	GCACGgg
V$CETS168_Q6	c-Ets-1	1598 (+)	1	0.98	cgGGAAGc
V$PPARA_01	PPARalpha:RXRalph	1603 (+)	1	0.806	agctgcaagggCAAAGgtcc
V$HSF4_Q3	HSF4	1605 (+)	1	1	CTGCAag
V$HDAC1_Q3	HDAC1	1606 (+)	1	0.981	tgCAAGGgc
V$PPARG_01	PPARgamma:RXRal	1606 (+)	0.792	0.821	tgcaaGGGCAaaggtcccgat
V$PPARG_03	PPAR	1606 (+)	1	0.896	tgcaagggcAAAGGtcc
V$PPARARXRA_01	PPARALPHA:RXR-A	1606 (+)	1	0.868	tgcaagggcAAAGGtccc
V$PPARG_08	PPARgamma	1606 (+)	1	0.873	tgcaagggcAAAGGtcc
V$PPARA_03	PPARalpha	1606 (+)	1	0.869	tgcaagggcAAAGGtcc
V$PPARG_09	PPARgamma	1606 (+)	1	0.876	tgcaagggcAAAGGtcc
V$PPARG_10	PPARgamma	1606 (+)	1	0.867	tgcaagggcAAAGGtcc
V$HNF4_01	HNF-4	1607 (+)	1	0.953	gcaagggCAAAGgtcccga
V$PPARGRXRA_03	PPARGAMMA:RXR-	1607 (+)	1	0.947	gcaagggcAAAGGtc
V$PPARGRXRA_01	PPARgamma:RXR-a	1608 (+)	1	0.909	caagggcAAAGGtcc
I$USP_02	CF1	1608 (+)	0.822	0.829	caagggcaaaGGTCC
V$HNF4_01_B	HNF4alpha1	1609 (+)	1	0.946	aagggCAAAGgtccc
V$EAR2_Q2	EAR2	1609 (-)	1	0.938	aagggCAAAGgtcc
V$HNF4A_06	HNF4A	1609 (+)	1	0.858	aagggCAAAGgtcc
V$RXRA_05	RXRA	1609 (+)	1	0.819	aagggCAAAGgtcc
V$RXRB_02	Rxrb	1609 (+)	1	0.801	aagggcAAAGGtcc
V$RXRA_13	RXR-ALPHA	1609 (+)	1	0.898	aagggcAAAGGtccc
V$NR2F1_02	COUP-TF1	1609 (+)	1	0.841	aagggcaaAGGTCcc
V$COUP_01	COUP-TF,	1609 (-)	0.857	0.912	aagggcaaaGGTCC
V$DR1_Q3	PPAR,	1610 (+)	1	0.938	agggCAAAGgtcc
V$HNF4DR1_Q3	HNF4	1610 (-)	1	0.914	agggCAAAGgtcc
V$HNF4A_03	HNF4A	1610 (+)	1	0.964	agggCAAAGgtcc

V$PPARDR1_Q2	PPAR	1610 (-)	1	0.952	agggcaaAGGTCc
V$COUPDR1_Q6	COUP	1610 (-)	1	0.935	agggcaaAGGTCc
V$HNF4ALPHA_Q6	HNF4alpha	1611 (-)	1	0.925	gggCAAAGgtccc
V$HNF4A_Q6_01	HNF-4alpha	1611 (+)	1	0.963	gggCAAAGgtcccga
V$MYBL1ELF1_01	A-Myb:Elf-1	1614 (-)	0.796	0.739	cAAAGGtcccgatg
V$RELA_05	RelA-p65	1616 (+)	1	0.923	aagGTCCC
F$YBR239C_02	Ybr239c	1619 (-)	0.8	0.811	gTCCCGat
F$LEU3_02	Leu3p	1622 (-)	0.884	0.932	CCGATgccgg
F$LEU3_02	Leu3p	1622 (+)	0.989	0.982	ccgatGCCGG
V$STAT3_03	STAT3	1624 (+)	1	0.955	gattccaGGGAAgatct
V$STAT3_11	STAT3	1625 (-)	1	0.956	atgccGGGAAg
V$STAT3_14	STAT3	1626 (-)	1	0.962	tgccgGGAAGat
V$ELK1HOXA3_01	Elk-1:HOXA3	1627 (+)	0.922	0.764	gcCGGGAagatcttggagggtttg
V$ZNF35_04	ZNF35	1631 (+)	1	1	gGAAGA
V$PRDM16_05	MEL1	1632 (+)	1	1	GAAGAt
V$SPZ1_01	Spz1	1638 (+)	1	0.967	cttGGAGGgtttgtg
V$TAXCREB_02	Tax/CREB	1642 (-)	0.6	0.743	gagggtttgTGACAc
P$ANAC094_01	ANAC094	1643 (-)	0.974	0.808	agggtttgtgacACGGAa
V$ZNF777_02	ZNF777	1647 (-)	0.832	0.709	tttgtgacACGGAagggct
F$YBR239C_02	Ybr239c	1654 (+)	1	0.933	caCGGAAg
V$TEL1_01	TEL1	1654 (+)	1	0.989	caCGGAAggg
V$TEL1_02	TEL1	1654 (+)	1	0.989	caCGGAAggg
V$ELK1ONECUT2_01	Elk-1:OC-2	1654 (+)	1	0.708	caCGGAAgggctggtgtg
V$GCM1ELF1_02	GCMa:Elf-1	1654 (+)	1	0.876	caCGGAAgggctggt
V$ELK1_11	Elk-1	1654 (+)	1	0.885	caCGGAAgggc
V$ELF5_03	Elf5	1654 (+)	1	0.98	cacGGAAGgg
V$GABPA_Q4	GABP-alpha	1656 (-)	1	1	cGGAAG
P$BZIP43_01	bZIP43	1662 (-)	0.588	0.762	ggctgGTGTGgc
V$TBX5_05	Tbx5	1663 (+)	1	0.951	gctGGTGTggctgga
V$AML2_Q3	AML2	1665 (-)	1	1	tggTGTGG
F$MET31_01	Met31p	1666 (+)	1	1	ggTGTGGc
V$MYF6_04	MYF6	1666 (-)	1	0.904	ggtgtGGCTGgattt
V$GEMIN3_01	GEMIN3	1681 (+)	0.998	0.941	agtGGGAGagggagaa

V$GKLF_Q3_01	GKLF	1681 (+)	0.989	0.991	agtgggaGAGGGa
I$TRL_02	GAGA	1684 (-)	1	0.911	ggGAGAGgga
V$NKX25_08	CSX	1684 (+)	1	0.996	ggGAGAGg
V$RXRA_04	RXR-ALPHA	1690 (+)	1	0.931	gggagAAGGTtataag
V$SPIB_Q3	Spi-B	1691 (-)	1	1	gGAGAA
V$PPARGRXRA_02	PPARGAMMA:RXR-	1694 (+)	0.97	0.892	gaaGGTTAtaaggggag
V$GCM1FOXO1_01	GCMa:FOXO1A	1697 (+)	1	0.822	ggttatAAGGGgag
I$TRL_02	GAGA	1706 (-)	1	0.935	ggGAGAGaag
F$HSF_02	HSF	1711 (+)	0.997	0.903	AGAAGagatcagaaa
V$LEF1_09	LEF-1	1715 (-)	0.985	0.962	gagatcaGAAAGgc
I$TLL_03	Tll	1715 (+)	0.84	0.791	gagatcagaAAGGCa
P$BPC1_Q2	BPC1	1721 (+)	1	1	AGAAAg
V$MYOGENIN_Q6	myogenin	1726 (+)	1	1	ggCAGCTg
V$OLIG2_02	OLIG2	1726 (+)	1	0.944	ggcAGCTGggagcaggcttg
V$ITF2_02	ITF-2	1726 (+)	1	1	ggcAGCTGgg
V$AP4_Q6_01	AP-4	1727 (-)	1	0.981	gCAGCTggg
V$LBP1_Q6	LBP-1	1727 (-)	1	1	gcAGCTG
V$MYOGENIN_Q6_01	myogenin	1728 (+)	1	1	CAGCTg
V$MYOGENIN_Q6_01	myogenin	1728 (-)	1	1	cAGCTG
V$KAISO_Q2	Kaiso	1730 (+)	0.986	0.97	gctgggAGCAGg
V$AR_02	AR	1759 (+)	1	0.968	tagccagggacagttTGTTCtctggc
V$PR_01	PR	1759 (+)	1	0.982	tagccagggacagttTGTTCtctggc
V$GR_01	GR	1759 (+)	1	0.992	tagccagggacagttTGTTCtctggc
V$AR_03	AR	1759 (+)	1	0.975	tagccagggacagttTGTTCtctggc
V$PR_02	PR	1759 (+)	1	0.984	tagccagggacagttTGTTCtctggc
V$NF1C_02	NF1C	1760 (+)	1	1	aGCCAGg
V$NR3C1_01	NR3C1	1763 (-)	1	0.92	cagGGACAgtttgttctc
V$AR_14	AR	1763 (-)	0.959	0.967	cagGGACAgtttgttct
V$GR_Q6	GR	1763 (+)	1	0.988	cagggacagttTGTTCtct
V$AR_08	AR	1764 (-)	0.976	0.937	agGGACAgtttgttctc
V$AR_09	AR	1764 (-)	0.968	0.936	agGGACAgtttgttctc
V$NR3C1_03	NR3C1	1764 (-)	0.985	0.962	agGGACAgtttgttctc
V$AR_10	AR	1764 (+)	0.977	0.968	agGGACAgtttgttc

V$PR_03	PR	1764 (-)	0.98	0.904	agGGACAgtttgttct
V$AR_16	AR	1764 (-)	0.995	0.934	agGGACAgtttgttct
V$MYB_10	c-Myb	1764 (+)	1	0.944	agggaCAGTTtg
V$NR3C1_01	NR3C1	1764 (+)	0.989	0.852	agggacagttTGTTCtct
V$AR_08	AR	1764 (+)	0.998	0.95	agggacagttTGTTCtc
V$AR_09	AR	1764 (+)	0.981	0.946	agggacagttTGTTCtc
V$NR3C1_03	NR3C1	1764 (+)	1	0.96	agggacagttTGTTCtc
V$AR_01	AR	1765 (-)	0.975	0.912	gGGACAgtttgttct
V$AR_04	AR	1765 (-)	0.982	0.888	gGGACAgtttgttct
V$AR_13	AR	1765 (-)	0.883	0.883	gGGACAgtttgttct
V$GR_02	GR	1765 (-)	0.99	0.948	gGGACAgtttgttct
V$NR3C1_10	GR	1765 (+)	0.998	0.993	gGGACAgtttgttct
V$GR_03	GR	1765 (+)	0.993	0.919	gGGACAgtttgttct
V$AR_01	AR	1765 (+)	1	0.978	gggacagttTGTTCt
V$AR_04	AR	1765 (+)	1	0.98	gggacagttTGTTCt
V$NR3C1_04	GR	1765 (+)	1	0.974	gggacagttTGTTC
V$AR_13	AR	1765 (+)	1	0.884	gggacagttTGTTCt
V$GR_02	GR	1765 (+)	1	0.978	gggacagttTGTTCt
V$AR_14	AR	1765 (+)	1	0.986	gggacagttTGTTCtct
V$NR3C1_10	GR	1765 (-)	1	0.937	gggacagttTGTTCt
V$GR_03	GR	1765 (-)	1	0.993	gggacagttTGTTCt
V$PR_03	PR	1765 (+)	1	0.958	gggacagttTGTTCtc
V$AR_16	AR	1765 (+)	1	0.983	gggacagttTGTTCtc
V$GRE_C	GR	1765 (+)	1	0.943	gggacagtttGTTCTc
V$AR_Q2	AR	1765 (+)	1	0.855	gggacagtttGTTCT
V$NR3C1_04	GR	1766 (-)	0.991	0.933	GGACAgtttgttct
V$AR_Q6_01	AR	1766 (+)	1	0.992	ggacagttTGTTCtc
V$AR_10	AR	1766 (-)	1	0.987	ggacagttTGTTCtc
V$GR_Q6_02	GR	1769 (+)	1	0.999	cagttTGTTCtct
V$SOX4_Q5	Sox-4	1772 (-)	1	1	tTTGTT
V$SOX17_Q2	Sox-17	1773 (+)	1	1	TTGTTc
F$HSF_01	HSF	1775 (-)	1	1	GTTCT
V$NF1B_Q6_01	NF-1B	1776 (-)	1	0.998	ttctCTGGC

F$YBR239C_01	Ybr239c	1782 (+)	0.787	0.767	ggcatttTCCAGcactgatt
V$NFAT3_Q3_01	NFATc4	1785 (-)	1	1	atTTTCCa
V$NFAT1_Q6	NFATc2	1786 (-)	1	1	tTTTCC
V$NFAT4_Q3	NFATc3	1786 (-)	1	1	tTTTCC
V$NFATC2_01	NFATc2	1786 (+)	1	1	tTTTCCa
V$NFAT1_Q4	NFATc2	1786 (-)	1	1	tTTTCC
V$SOX10_09	Sox-10	1794 (+)	1	0.9	cactgattgcATTGTa
V$LHX8_06	Lhx8	1797 (+)	1	1	TGATTg
V$BRN1_Q6	BRN1	1801 (-)	1	1	tGCATTg
V$SOX10_Q6_01	Sox-10	1803 (-)	1	1	cATTGTa
V$SOX12_04	Sox-12	1805 (+)	1	0.933	ttgtacACAAAgtagg
V$SOX10_Q6	Sox-10	1810 (-)	1	1	cACAAAg
V$SOX10_Q6_01	Sox-10	1810 (+)	1	1	cACAAAg
V$SOX10_01	Sox-10	1811 (-)	1	1	ACAAAg
V$TCF1_Q5	TCF-1	1811 (-)	1	1	aCAAAG
V$YB1_Q4	YB-1	1820 (+)	1	0.984	gcacCCAATga
V$ALPHACP1_01	alpha-CP1	1821 (+)	1	0.966	cacCCAATgag
P$ASR1_01	ASR-1	1822 (+)	1	1	ACCCA
V$PAX3_01	Pax-3	1825 (-)	0.774	0.797	caatgagtGATGA
V$FOSBJUND_01	FOSB:JUND	1826 (-)	0.929	0.943	aatgAGTGAtg
V$JUND_08	JunD	1826 (+)	0.825	0.873	aatgAGTGAtg
V$FOXM1_Q3	FOXM1	1827 (+)	0.985	0.907	atGAGATgGactga
V$IPF1_07	ipf1	1828 (+)	0.862	0.912	TGAGTgatg
V$PAX8_B	Pax-8	1828 (+)	0.886	0.878	tgagtgatGAATGaacaa
V$IPF1_07	ipf1	1832 (+)	0.924	0.877	TGATGaatg
V$SOX17_Q2	Sox-17	1840 (-)	1	1	gAACAA
I$BRCZ3_01	BR-C	1840 (+)	1	0.97	gaacaAACTAaaaga
V$SOX4_Q5	Sox-4	1841 (+)	1	1	AACAAa
V$CDX_Q5	Cdx	1841 (+)	1	0.913	aacaaactaaaagATAAA
V$GATA1_11	Gata1	1850 (-)	1	0.927	aaaGATAAaga
V$GATA3_Q4	GATA-3	1852 (+)	1	1	AGATAa
V$GATA4_Q5_01	GATA-4	1852 (+)	1	1	AGATAaa
V$TFAP2C_05	AP-2gamma	1857 (+)	0.93	0.95	aagACCTGaggctg

V$MYB_10	c-Myb	1863 (+)	0.967	0.963	tgaggCTGTTga
V$HNF3B_05	HNF-3beta	1866 (+)	0.932	0.938	ggctgTTGACact
V$TBX20_07	Tbx20	1866 (+)	1	0.906	ggctgtTGACActc
V$FOXO1_03	FOXO1	1869 (+)	1	1	TGTTGac
V$HNF3A_03	HNF-3alpha	1869 (+)	0.937	0.951	tgTTGACact
V$MEIS1DRGX_01	meis1:Prrxl1	1872 (+)	1	0.921	TGACActcatag
V$TCF1_10	TCF-1	1884 (-)	1	0.947	ctttcCTTTGctttac
V$LEF1_09	LEF-1	1887 (+)	1	0.959	tcCTTTGctttact
P$CBNAC_01	CBNAC	1891 (+)	1	1	tTGCTT
V$EFC_Q6	RFX1	1894 (+)	0.82	0.89	cTTTACttggcaaa
V$NFATC1_03	NFATc1	1894 (+)	0.883	0.764	ctttactTGGCAaa
V$NF1A_Q6_01	NF-1A	1899 (-)	1	1	cTTGGCa
V$HNF1_Q6	HNF-1	1905 (-)	1	0.9	aaagattaggATTAAcct
V$GTF2IRD1_01	GTF2IRD1-isoform2	1906 (+)	1	0.936	aaGATTAgg
V$PITX1_01	Pitx1	1907 (+)	1	0.934	agattaGGATTaacctc
V$CRX_02	Crx	1907 (+)	1	0.93	agattagGATTAacct
V$CRX_Q4_01	CRX	1908 (-)	1	1	GATTAg
V$PITX2_01	PITX2	1908 (+)	1	0.95	gattagGATTAacctct
V$HNF1B_Q6_01	HNF-1beta	1908 (+)	1	0.908	gattaggaTTAACc
V$DMBX1_02	DMBX1	1911 (+)	1	0.997	tagGATTAac
V$DPRX_01	DPRX	1911 (+)	1	0.997	tagGATTAac
V$OTX1_06	Otx1	1912 (-)	1	0.999	agGATTAa
V$PITX1_Q6	PITX1	1913 (-)	1	0.943	gGATTAacctc
I$GSC_01	Gsc	1913 (-)	1	1	gGATTA
I$PTX1_01	Ptx1	1913 (-)	1	1	gGATTAa
I$BCD_02	bcd	1913 (-)	1	1	gGATTA
I$OC_01	oc	1913 (-)	1	1	gGATTA
I$BCD_04	BCD	1913 (-)	1	1	gGATTAa
V$CRX_Q4_01	CRX	1914 (-)	1	1	GATTAa
V$PRDM16_04	MEL1	1926 (-)	1	1	cTCATC
V$TEF_08	TEF1	1928 (-)	0.923	0.915	catcctttgcATACC
V$OCT1_05	1-Oct	1929 (+)	1	0.905	atccTTTGCatacc
V$OCT1_Q6	1-Oct	1929 (-)	1	0.943	atccTTTGCatacct

V$OCT_C	OCT-x	1929 (+)	1	0.925	atccTTTGCatac
V$OCT_Q6	Octamer	1930 (+)	1	0.957	tccttTGCATa
V$OCT2_Q6	2-Oct	1930 (-)	1	0.947	tccttTGCATacct
V$OCT1_B	1-Oct	1931 (-)	1	0.953	ccttTGCATa
V$OCT2_04	2-Oct	1931 (-)	1	0.956	ccttTGCATac
V$POU2F2_05	Pou2f2	1932 (-)	1	0.911	ctttGCATA
I$VVL_01	vvl	1935 (-)	1	1	TGCATa
P$LBD23_01	LBD23	1935 (+)	0.986	0.799	tgcatacctCTCGCt
V$IRF4_04	IRF4	1938 (+)	1	0.91	ataccTCTCGctcag
V$IRF6_04	IRF6	1938 (+)	1	0.922	ataccTCTCGctcag
F$HSF_01	HSF	1951 (+)	1	1	AGAAC
V$EOMES_04	EOMES	1954 (-)	1	0.959	acctcaaCACCTcttt
V$TBX5_01	Tbx5	1956 (-)	1	0.972	ctcaACACCtct
V$TBX5_02	Tbx5	1958 (-)	1	0.975	caACACCtct
P$BPC1_Q2	BPC1	1966 (-)	1	1	cTTTCT
V$SPIB_Q3	Spi-B	1968 (+)	1	1	TTCTCc
V$ZNF35_04	ZNF35	1976 (+)	1	1	gCAAGA
V$SRY_12	SRY	1979 (-)	1	0.986	agATTGTt
V$CUX1TBX21_01	CDP:T-bet	1980 (-)	0.797	0.802	gaTTGTTcttagtgtcct
V$GR_Q6	GR	1981 (+)	0.989	0.956	attgttcttagTGTCCttg
V$SOX17_Q2	Sox-17	1982 (+)	1	1	TTGTTc
F$HSF_01	HSF	1984 (-)	1	1	GTTCT
V$AR_10	AR	1984 (-)	0.977	0.933	gttcttagTGTCCtt
V$DR3_Q4	VDR,	1990 (+)	0.775	0.835	agtgtccttggTAGCCcagtg
V$REVERBALPHA_03	Rev-ErbAalpha	1996 (-)	0.995	0.913	cttggtagCCCAGtgtccc
I$LAG1_01	Lag1	1997 (-)	1	1	ttGGTAG
V$PPARG_02	PPARgamma:RXRal	1998 (+)	0.627	0.692	tggtaGCCCAgtgtcccctggtt
F$STP4_02	Stp4p	1999 (+)	0.8	0.815	ggTAGCCca
V$THAP1_01	Thap1	2008 (-)	1	0.864	gtgtcccctggttaaaaATGGCct
V$ZXDL_02	ZXDL	2010 (-)	1	1	gTCCCCt
V$CTCF_06	CTCF	2010 (-)	1	0.887	gtcccCTGGT
V$YY1_07	YY1	2011 (-)	1	0.869	tcccctggttaaaaATGGCctt
V$AMEF2_Q6	aMEF-2	2015 (+)	1	0.917	ctggtTAAAAatggcctt

V$MMEF2_Q6	MEF-2A	2015 (+)	1	0.968	ctggtTAAAAatggcc
V$YY1_Q4_01	YY1	2018 (+)	1	0.99	gttaaaAATGGcctt
V$YY1_Q6	YY1	2021 (-)	1	0.994	aaaaATGGC
V$YY1_03	YY1	2021 (-)	1	0.875	aaaaATGGCctt
V$YY1_12	YY1	2021 (+)	1	0.935	aaaaATGGCctt
V$YY1_13	YY1	2021 (+)	1	0.97	aaaaATGGCctta
V$YY1_14	YY1	2021 (+)	1	0.883	aaaaATGGCctt
V$YY1_Q6_03	YY1	2022 (-)	1	1	aaAATGG
V$YY1_Q6_02	YY1	2022 (-)	1	0.983	aaaATGGCctt
V$TEAD4CEBPD_01	TEF-3:C/EBPdelta	2022 (+)	0.777	0.807	aaaatggccTTAGGgaaa
V$TFAP2A_10	TFAP2A	2024 (+)	0.912	0.932	aatggccttAGGGAa
V$AP2ALPHA_02	AP-2alphaA	2025 (+)	0.979	0.967	atGGCCTtagggaaa
V$NURR1_Q3	NURR1	2026 (+)	1	1	tgGCCTT
V$HELIOSA_01	Helios	2030 (+)	1	0.991	cttAGGGAaag
V$TEAD4CEBPD_01	TEF-3:C/EBPdelta	2035 (+)	1	0.87	ggaaagaatTTGCGgaaa
P$DEL2_02	DEL2	2035 (+)	0.825	0.729	ggaaagaattTGCGGaaaag
V$ETV2CEBPD_01	ER71:C/EBPdelta	2036 (+)	0.946	0.804	gaaaGAATTtgcggaaa
V$FLI1CEBPD_01	Fli-1:C/EBPdelta	2036 (+)	0.877	0.793	gaaaGAATTtgcggaaa
V$ERFCEBPD_01	ERF:C/EBPdelta	2036 (+)	1	0.83	gaaagaatTTGCGgaaa
V$FLI1CEBPB_01	Fli-1:C/EBPbeta	2036 (+)	1	0.782	gaaagaatTTGCGgaaa
V$ETV5CEBPD_01	Erm:C/EBPdelta	2036 (+)	1	0.789	gaaagaatTTGCGgaaa
V$POU2F1ELK1_01	POU2F1:Elk-1	2038 (-)	0.788	0.779	aagAATTTgcgga
F$YBR239C_01	Ybr239c	2038 (+)	0.796	0.82	aagaattTGCGGaaaagatg
F$PDR1_01	Pdr1p	2038 (+)	0.86	0.879	aagaattTGCGGaaaagatg
F$YBR239C_01	Ybr239c	2038 (-)	0.796	0.809	aagaatttGCGGAaaagatg
V$TEAD4FLI1_01	TEF-3:Fli-1	2039 (-)	0.883	0.816	agaATTTGcgga
V$E2F3DRGX_01	E2F-3:Prrxl1	2039 (-)	0.864	0.806	agaaTTTGCgga
V$ZNF236_02	ZNF236	2039 (+)	1	0.982	agaatTTGCGga
V$SFPI1_04	SFPI1	2040 (+)	0.953	0.934	gaatttgcGGAAAa
V$SP100_03	Sp100	2041 (-)	0.958	0.955	aatTTGCGgaaaag
P$AT4G27900_01	AT4G27900	2041 (+)	0.693	0.748	aattTGCGGaaaagatggctat
V$SP100_03	Sp100	2041 (+)	1	0.967	aatttgCGGAAaag
P$DEL1_02	DEL1	2041 (-)	0.805	0.739	aatttgCGGAAaagatggcta

V$YY1_07	YY1	2041 (-)	1	0.843	aatttgcggaaaagATGGCtat
V$E2F1_Q4	E2F-1	2042 (+)	0.919	0.941	aTTTGCgg
V$CEBPB_08	C/EBPBETA	2042 (+)	1	0.905	atTTGCGgaaa
V$CEBPB_03	CEBPB	2043 (-)	1	0.907	tTTGCGgaaa
V$CEBPD_01	CEBPD	2043 (-)	1	0.92	tTTGCGgaaa
V$CEBPE_02	CEBPE	2043 (-)	1	0.927	tTTGCGgaaa
V$CEBPA_04	C/EBPalpha	2043 (+)	1	0.905	tTTGCGgaaa
V$CEBPB_07	C/EBPbeta	2043 (+)	1	0.91	tTTGCGgaaa
V$TEAD4CEBPB_01	TEF-3:C/EBPbeta	2043 (+)	1	0.805	tTTGCGgaaaagatggctatct
F$PDR3_02	PDR3	2043 (-)	1	0.75	tttGCGGA
V$CEBPB_08	C/EBPBETA	2043 (-)	0.926	0.898	tttgCGGAAaa
F$YBR239C_02	Ybr239c	2045 (+)	1	0.935	tgCGGAAa
V$ELK1ONECUT2_01	Elk-1:OC-2	2045 (+)	1	0.788	tgCGGAAaagatggctat
V$YY1_02	YY1	2045 (-)	1	0.874	tgcggaaaagATGGCtatct
V$E2F1DP1_01	E2F-1:DP-1	2046 (-)	0.887	0.918	gCGGAAaa
V$E2F1DP2_01	E2F-1:DP-2	2046 (-)	0.902	0.937	gCGGAAaa
V$E2F4DP1_01	E2F-4:DP-1	2046 (-)	0.79	0.869	gCGGAAaa
V$E2F1DP1RB_01	Rb:E2F-1:DP-1	2046 (-)	0.79	0.863	gCGGAAaa
V$SPIB_Q3	Spi-B	2046 (-)	1	1	gCGGAA
V$E2F_02	E2F	2046 (-)	0.816	0.893	gcgGAAAA
V$NFAT1_Q6	NFATc2	2048 (+)	1	1	GGAAAa
V$NFAT4_Q3	NFATc3	2048 (+)	1	1	GGAAAa
V$NFAT1_Q4	NFATc2	2048 (+)	1	1	GGAAAa
V$YY1_Q4_01	YY1	2048 (+)	0.996	0.987	ggaaaaGATGGctat
V$YY1_Q6	YY1	2051 (-)	1	0.996	aaagATGGC
V$YY1_12	YY1	2051 (+)	1	0.939	aaagATGGCtat
V$YY1_13	YY1	2051 (+)	1	0.965	aaagATGGCtatc
V$YY1_14	YY1	2051 (+)	1	0.893	aaagATGGCtat
V$YY1_Q6_02	YY1	2052 (-)	1	0.986	aagATGGCtat
V$GATA2_01	GATA-2	2057 (-)	1	0.996	ggCTATCtga
V$GATA5_Q4	GATA-5	2060 (+)	1	1	TATCTg
V$SPIB_Q3	Spi-B	2065 (-)	1	1	gAAGAA
V$PRDM16_05	MEL1	2068 (+)	1	1	GAAGAt

V$FOS_09	C-FOS	2068 (+)	0.877	0.84	gaagaTGACCacatctc
V$ESR1_05	ER-alpha	2069 (+)	1	0.973	aagaTGACC
V$MEQCJUN_02	MEQ:c-Jun	2072 (-)	0.717	0.837	atGACCAcatc
V$PEBP2B_Q6	PEBP2beta	2074 (-)	1	1	gaCCACA
V$AML1_01	AML1a	2075 (-)	1	1	ACCACa
V$AML1_Q6	AML1	2075 (-)	1	1	aCCACA
V$AML1_Q5	AML1	2075 (-)	1	1	aCCACA
V$HLTF_Q4	HLTF	2078 (-)	1	0.939	acatctccTTTTTggct
P$PBF_Q2	PBF	2084 (-)	1	1	CCTTTt
P$PBF_Q2_01	PBF	2084 (+)	1	1	CCTTTt
P$HSFA2_01	HSFA2	2087 (-)	1	1	tTTTGG
V$SOX12_04	Sox-12	2089 (-)	1	0.921	ttggcTTTGTctattc
V$TCF1_Q5	TCF-1	2093 (+)	1	1	CTTTGt
V$SOX10_Q6	Sox-10	2093 (+)	1	1	cTTTGTc
V$SOX10_01	Sox-10	2093 (+)	1	1	cTTTGT
I$CT_01	ct	2106 (-)	1	1	GTTCAa
V$NFAT2_Q5_01	NFATc1	2124 (+)	1	0.999	tgatttTTTCCa
V$ZNF721_03	ZNF721	2125 (-)	1	1	gaTTTTTtcc
V$CIZ_01	CIZ	2125 (-)	1	1	gatTTTTTc
V$NFAT4_Q5	NFATc3	2127 (-)	1	1	tttTTTCCa
V$POU2F1_04	POU2F1	2127 (-)	0.997	0.935	tttttTCCATagggtt
V$POU2F1_05	POU2F1	2127 (-)	0.997	0.935	tttttTCCATagggtt
P$AT3G51080_01	AT3G51080	2128 (-)	1	1	ttTTTCC
V$NFAT_Q3	NFAT	2128 (-)	1	1	ttTTTCCat
V$NFATC1_04	NFATC1	2128 (+)	1	0.998	ttTTTCCata
V$NFATC3_01	NFATC3	2128 (+)	1	0.996	ttTTTCCata
V$NFAT1_Q6	NFATc2	2129 (-)	1	1	tTTTCC
V$NFAT4_Q3	NFATc3	2129 (-)	1	1	tTTTCC
V$NFATC2_01	NFATc2	2129 (+)	1	1	tTTTCCa
V$NFAT1_Q4	NFATc2	2129 (-)	1	1	tTTTCC
P$GATA8_01	GATA8	2146 (+)	1	0.999	caGATCTgg
V$ZNF644_01	ZNF644	2160 (+)	1	0.941	gcCTGCCactct
V$PBX2_01	PBX2	2161 (-)	0.932	0.925	cCTGCCactct

V$CTCF_08	CTCF	2162 (-)	1	0.889	cTGCCActcttgg
F$TBF1_01	Tbf1p	2169 (-)	1	0.988	tcttggtTAGGGttaagttt
P$MYB1L_01	MYB1-like	2173 (-)	1	0.999	ggtTAGGGtt
F$TBF1_04	Tbf1p	2175 (-)	1	1	tTAGGGtt
V$ZNF511_01	ZNF511	2188 (+)	1	0.942	tgaagaGGCAGtg
P$MYB118_01	MYB118	2197 (-)	1	0.847	agtGTAACagtggagtg
I$ARA_01	ara	2201 (+)	1	1	TAACA
I$CAUP_01	caup	2201 (+)	1	1	TAACA
V$NKX25_09	CSX	2205 (+)	1	0.995	agtgGAGTGg
V$TTF1_04	TTF-1	2206 (+)	1	0.978	gtgGAGTGgc
V$NKX22_05	NKX2B	2206 (+)	1	0.995	gtgGAGTGgca
V$PBX2_01	PBX2	2208 (+)	0.932	0.925	ggagtGGCAGg
V$ZNF644_01	ZNF644	2208 (-)	1	0.976	ggagtGGCAGga
F$MET28_01	MET28	2237 (+)	1	1	CTGTGg
V$RXRA_16	RXRALPHA	2237 (+)	0.984	0.97	ctgTGGCCtttag
V$NURR1_Q3	NURR1	2240 (+)	1	1	tgGCCTT
V$E2F1HES7_02	E2F-1:HES-7	2247 (-)	0.759	0.738	tagagccagactgCCCGAgta
V$SMAD5_Q5_01	SMAD5	2253 (+)	1	0.999	CAGACtgc
F$FLP1_01	Flp	2254 (-)	1	1	agACTGC
F$LEU3_02	Leu3p	2261 (-)	0.871	0.913	CCGAGtaagg
V$VMAF_01	v-Maf	2277 (-)	0.91	0.867	gccttcttggTCATCaatt
P$NAC078_01	NAC078	2282 (+)	0.709	0.8	cttggtcatCAATTtac
V$CDP_02	CDP	2283 (-)	0.93	0.91	ttggtcaTCAATtta
V$CLOX_01	Clox	2283 (-)	0.941	0.896	ttggtcaTCAATtta
V$CDPCR3HD_01	CDP	2286 (-)	0.996	0.964	gtcATCAAtt
I$PRD_03	Prd	2287 (+)	0.993	0.928	tcATCAAttt
V$CUX1_07	CDP	2287 (+)	0.97	0.936	tcaTCAATtt
I$ABDA_Q6	Abd-A	2289 (-)	1	0.994	atcaATTTAc
V$CUX1_05	CDP	2289 (+)	0.696	0.845	atcaatttacttATCTGt
V$FOXA1_02	HNF-3alpha	2293 (-)	1	0.954	aTTTACtta
V$GATA6_04	GATA-6	2293 (-)	1	0.972	atttacTTATCtgtgaa
V$GATA2_09	GATA2	2293 (+)	1	0.971	atttacTTATCtgt
V$GATA_C	GATA-X	2294 (-)	1	0.992	tttacTTATCt

V$GATA6_08	GATA-6	2294 (-)	1	0.953	tttacTTATCtgtg
V$GATA6_10	GATA-6	2294 (-)	1	0.969	tttacTTATCtgt
V$GATA1_Q6	GATA-1	2295 (-)	1	0.998	ttacTTATCtgtgaa
V$GATA6_09	GATA6	2295 (-)	1	0.961	ttacTTATCtgtg
V$GATA1_04	GATA-1	2295 (-)	1	0.988	ttactTATCTgtg
V$GATA1_11	Gata1	2296 (+)	1	0.986	tacTTATCtgt
V$GATA2_10	GATA-2	2296 (-)	1	0.987	tacTTATCtgt
V$GATA1_14	GATA-1	2296 (-)	1	0.992	tacTTATCtgt
V$GATA2_11	GATA-2	2296 (-)	1	0.99	tacTTATCtgt
V$SMARCC2_02	BAF170	2296 (+)	1	0.988	tacTTATCtgt
V$GATA1_16	GATA-1	2296 (-)	1	0.943	tacTTATCtgtgaaatggg
V$GATA2_14	GATA-2	2296 (-)	1	0.985	tactTATCTgt
V$GATA2_02	GATA-2	2297 (-)	1	0.986	acTTATCtgt
V$GATA3_07	GATA3	2297 (-)	1	0.996	acTTATCt
V$GATA1_10	GATA-1	2297 (+)	1	0.978	acTTATCtg
V$GATA4_03	GATA-4	2297 (+)	1	0.973	acTTATCtgtg
V$GATA3_11	GATA-3	2297 (-)	1	0.991	acTTATCt
V$GATA1_13	GATA-1	2297 (-)	1	0.934	acTTATCtgtgaaatgggc
V$GATA4_05	GATA-4	2297 (-)	1	0.974	acTTATCtgt
V$GATA6_11	GATA-6	2297 (-)	1	0.983	acTTATCtgt
V$GATA3_10	GATA3	2297 (-)	1	0.97	actTATCT
V$GATA_Q6	GATA	2298 (-)	1	1	cTTATCt
V$GATA6_Q5	GATA-6	2298 (-)	1	1	cTTATCt
V$GATA1_12	GATA-1	2298 (-)	1	1	cTTATCt
V$GATA3_12	GATA-3	2298 (+)	1	1	cTTATC
V$GATA3_Q4	GATA-3	2299 (-)	1	1	tTATCT
V$GATA5_Q4	GATA-5	2300 (+)	1	1	TATCTg
V$CEBPG_Q6	C/EBPgamma	2302 (-)	1	0.896	tctgtGAAATggg
V$ZBTB44_01	Zbtb44	2303 (+)	1	1	CTGTGa
V$SNAP190_02	SNAP190	2309 (-)	0.928	0.94	AATGGgca
P$AT4G27900_01	AT4G27900	2311 (-)	0.769	0.714	tgggcaaccataaTCGTTcatg
P$MYB3R5_01	MYB3R5	2315 (+)	0.821	0.785	caaccataaTCGTTc
P$MYB3R1_01	MYB3R1	2316 (+)	0.845	0.807	aaccataaTCGTTca

P$MYB3R4_01	MYB3R4	2316 (+)	0.83	0.802	aaccataaTCGTTca
V$CDP_01	CDP	2317 (+)	0.818	0.785	aCCATAatcgtt
V$CDPCR3_01	CDP	2318 (-)	1	0.843	CCATAatcgttcatg
V$ZNF333_01	ZNF333	2320 (+)	1	1	ATAAT
V$PAX2_01	Pax-2	2320 (-)	0.991	0.895	ataatcgttcATGACtgca
I$EVE_Q6	Eve	2328 (+)	0.982	0.926	tcatgACTGC
V$ARID5A_03	Arid5a	2336 (+)	1	0.989	gcAATATtgaaagc
V$OC2_Q3	OC-2	2340 (-)	1	1	tATTGA
V$TCF4_Q5	TCF-4	2348 (+)	1	0.992	gCTTTGaa
V$LEF1_Q2	TCF-7	2349 (-)	1	1	CTTTGa
V$TCF3_Q6	TCF-3	2349 (+)	1	1	CTTTGa
V$IRF8_Q6	IRF-8	2352 (-)	1	1	tGAAACt
V$ZNF835_02	ZNF835	2356 (+)	1	1	actAAGATt
P$MYB118_01	MYB118	2366 (-)	1	0.815	ttaGTAACtcacttgag
V$ERFSREBF2_02	ERF:SREBP-2	2366 (+)	0.85	0.751	ttagtaactcACTTGag
V$DEC_Q1	DEC	2371 (-)	1	0.936	aactcACTTGagg
V$NKX25_Q6	CSX	2373 (+)	1	0.992	ctCACTTgagg
V$NKX25_01	Nkx2-5	2375 (-)	1	1	CACTTga
V$NKX2B_Q3	NKX2B	2375 (+)	1	1	CACTTga
I$TIN_01	tin	2375 (-)	1	1	CACTTgag
V$TRP53_01	Trp53	2376 (-)	0.977	0.918	acttgaggcaacaCCTGT
V$EOMES_04	EOMES	2380 (-)	1	0.975	gaggcaaCACCTgtcc
V$RFX_Q6	RFX	2381 (-)	1	0.982	agGCAACac
V$TALLIKE_Q6	Tal	2382 (+)	1	0.981	ggcaaCACCTgt
V$E47_02	E47	2382 (-)	1	0.979	ggcaacACCTGtcctg
V$GRE_C	GR	2382 (+)	0.978	0.862	ggcaacacctGTCCTg
N$HLH2HLH14_01	hlh-2:hlh-14	2383 (+)	1	0.998	gcaacACCTGtcctga
V$TBX5_02	Tbx5	2384 (-)	1	0.975	caACACCtgt
V$MYOD_01	MyoD	2384 (-)	1	1	caacACCTGtcc
V$DEC1_Q3	1-Dec	2384 (+)	0.966	0.941	caacACCTGtcc
V$FIGLA_01	FIGLA	2385 (+)	1	0.997	aaCACCTgtc
V$ID4_01	ID4	2385 (+)	1	0.999	aaCACCTgtc
V$MESP1_01	MESP1	2385 (+)	1	1	aaCACCTgtc

V$ITF2_01	ITF-2	2385 (+)	1	0.999	aaCACCTgtc
V$SNAI2_01	slug	2386 (-)	1	1	acACCTGtc
V$E2A_Q6	E2A	2387 (+)	1	1	CACCTgtc
F$YDR520C_01	Ydr520c	2389 (+)	0.786	0.775	cctgtcCTGAGttaatctga
V$NR1H3RXRA_01	LXR-alpha:RXR-alph	2391 (+)	0.962	0.827	TGTCCtgagttaatctgaa
V$CRX_Q4_01	CRX	2400 (+)	1	1	tTAATC
V$PRX2_Q2	Prx2	2400 (-)	0.98	0.985	ttaaTCTGA
V$IRF8_Q6	IRF-8	2406 (-)	1	1	tGAAACt
P$REM16_01	REM16	2406 (+)	1	0.749	tgaaactgtttggaaGGAAAa
P$DEL2_02	DEL2	2407 (+)	0.611	0.792	gaaactgtttGGAAGgaaaa
I$MIRR_01	mirr	2412 (-)	1	1	TGTTT
P$DEL1_02	DEL1	2413 (-)	0.591	0.762	gtttggAAGGAaaacttgaca
V$NFAT1_Q6	NFATc2	2421 (+)	1	1	GGAAAa
V$NFAT4_Q3	NFATc3	2421 (+)	1	1	GGAAAa
V$NFAT1_Q4	NFATc2	2421 (+)	1	1	GGAAAa
V$TITF1_Q3	TTF1	2424 (-)	1	0.926	aaaCTTGAca
P$WRKY18_Q2	WRKY18	2424 (-)	1	1	aaacTTGAC
F$MATALPHA2_01	MATalpha2p	2427 (-)	1	0.984	cttgACATGa
P$O2_Q4	Opaque-2	2429 (-)	1	0.984	tgACATGaaac
F$STE12_Q4	Ste12p	2433 (+)	1	1	aTGAAAc
V$IRF8_Q6	IRF-8	2434 (-)	1	1	tGAAACt
V$NKX22_01	Nkx2-2	2437 (-)	1	0.968	aactACTTAt
I$EMS_02	Ems	2439 (+)	0.917	0.94	ctACTTAt
V$CUX1_04	Cux1	2440 (+)	0.987	0.94	tacttATAATcatta
V$CUX1_04	Cux1	2440 (-)	0.969	0.934	tacttATAATcatta
V$SATB1_Q3	SATB1	2444 (-)	1	0.956	tataatCATTAtttat
V$ZNF333_01	ZNF333	2445 (+)	1	1	ATAAT
V$PMX1_Q6	PMX1	2446 (+)	1	1	TAATCa
V$FOXM1_Q3	FOXM1	2446 (-)	0.906	0.937	taatCATTAtt
V$CUX1HOXB13_01	CDP:HOXB13	2447 (-)	0.71	0.824	aaTCATTatttattcc
I$DFD_03	Dfd	2447 (+)	1	0.986	aatCATTAtt
V$POU2F1GSC2_01	POU2F1:Gscl	2448 (+)	0.958	0.895	atCATTAtttattccattt
V$POU3F3_04	POU3F3	2448 (-)	0.999	0.979	atcaTTATTtat

V$POU6F1_01	POU6F1	2449 (+)	1	0.885	tcattaTTTAT
V$ZNF333_01	ZNF333	2451 (-)	1	1	ATTAT
V$MEF2C_Q4	MEF-2C	2453 (+)	1	1	TATTTat
V$SATB1_Q5_01	SATB1	2454 (+)	1	1	aTTTAT
V$CDX1_Q5	Cdx-1	2455 (+)	1	1	TTTATt
V$YY1_01	YY1	2456 (+)	1	0.984	ttatTCCATtttttaaa
P$MADSA_Q2	MADS-A	2458 (-)	1	0.967	attccATTTTttaaat
V$YY1_Q6_03	YY1	2461 (+)	1	1	CCATTtt
V$ARID5A_03	Arid5a	2465 (-)	1	0.986	tttttaaATATTag
V$FOXJ2_02	FOXJ2	2468 (-)	0.839	0.864	ttaaatATTAGtgc
V$HMGIY_Q3	HMGIY	2477 (+)	0.96	0.955	agtgcATTTTgtttg
V$BRN1_Q6	BRN1	2479 (-)	1	1	tGCATTt
I$TCF_Q6	TCF	2482 (-)	1	0.97	attttgTTTGAttagg
V$SOX4_Q5	Sox-4	2484 (-)	1	1	tTTGTT
V$SRY_01	SRY	2484 (-)	1	1	ttTGTTT
V$PBX1_03	Pbx-1	2484 (-)	1	0.972	tttgtTTGATta
V$SRY_Q6	SRY	2485 (+)	1	1	TTGTTt
V$FOXO1A_Q5	FOXO1A	2485 (-)	1	1	tTGTTT
I$MIRR_01	mirr	2486 (-)	1	1	TGTTT
V$PMX1_Q6	PMX1	2490 (-)	1	1	tGATTA
V$CRX_Q4_01	CRX	2491 (-)	1	1	GATTAg
V$SMAD3_05	Smad3	2494 (-)	0.99	0.956	tAGGAGacagtc
V$SMAD2_02	Smad2	2495 (-)	0.922	0.938	aggagacAGTCA
V$SMAD2_Q6	Smad2	2498 (+)	1	1	AGACAg
V$NFAT2_02	NFAT2c1dimer	2513 (-)	1	0.854	cTTCCAgggga
F$YDR520C_01	Ydr520c	2514 (+)	0.786	0.765	ttccagGGGAGttatataat
V$RELA_03	RelA-p65	2516 (+)	0.99	0.988	cCAGGGgagtt
V$ELK1TEF_01	Elk-1:TEF	2517 (+)	0.593	0.739	caGGGGAgttatataat
F$YAP1_01	yAP-1	2519 (+)	0.694	0.793	ggggagTTATAtaatttata
F$YAP1_01	yAP-1	2519 (-)	0.694	0.792	ggggagttaTATAAtttata
V$HLF_01	HLF	2524 (+)	0.892	0.908	GTTATataat
V$POU6F1_01	POU6F1	2527 (+)	1	0.894	atataaTTTAT
V$ZNF333_01	ZNF333	2529 (+)	1	1	ATAAT

V$PRRX2_03	Prrx2	2530 (-)	1	1	TAATT
V$CDXA_02	CdxA	2532 (+)	1	1	aTTTATa
V$SATB1_Q5_01	SATB1	2532 (+)	1	1	aTTTAT
V$CUX1_05	CDP	2532 (-)	0.748	0.787	aTTTATaatgtaatttat
V$CDX2_Q5_02	CDX-2	2533 (+)	1	1	TTTATa
F$MATALPHA2_Q4	MATalpha2p	2533 (+)	0.898	0.913	tttaTAATGtaatttat
F$MATALPHA2P_Q4	MATALPHA2P	2533 (-)	1	0.959	tttataATGTAatt
V$CUX1HOXA13_01	CDP:HOXA13	2533 (-)	0.702	0.828	tttataatgtaATTTAt
V$ZNF333_01	ZNF333	2536 (+)	1	1	ATAAT
V$UNCX_02	UNCX	2536 (+)	0.924	0.945	ataatgtAATTTa
V$HOXA9_Q5	Hoxa9	2538 (-)	1	0.958	aatgTAATTtat
V$PRRX2_03	Prrx2	2542 (-)	1	1	TAATT
V$HBP1_04	HBP1	2543 (-)	1	0.921	aatttatAATGGgccat
V$CDXA_02	CdxA	2544 (+)	1	1	aTTTATa
V$SATB1_Q5_01	SATB1	2544 (+)	1	1	aTTTAT
V$SATB1_Q3	SATB1	2544 (+)	1	0.931	atttaTAATGggccat
V$CDX2_Q5_02	CDX-2	2545 (+)	1	1	TTTATa
V$NANOG_Q3	Nanog	2546 (+)	1	0.99	ttaTAATGgg
V$ZNF333_01	ZNF333	2548 (+)	1	1	ATAAT
V$YY2	YY2	2548 (-)	1	1	atAATGG
P$PEND_01	PEND	2560 (-)	1	1	acTTCTTa
V$BLIMP1_03	Blimp-1	2586 (-)	1	0.891	atTCCAAaacac
V$FAC1_01	FAC1	2587 (+)	0.978	0.93	ttccAAAACactgg
P$HSFA2_01	HSFA2	2589 (+)	1	1	CCAAAa
I$MIRR_01	mirr	2592 (+)	1	1	AAACA
V$PPARG_08	PPARgamma	2609 (+)	1	0.862	aatttggatAAAGGact
V$PPARA_03	PPARalpha	2609 (+)	1	0.864	aatttggatAAAGGact
V$PPARG_10	PPARgamma	2609 (+)	1	0.856	aatttggatAAAGGact
V$ZNF445_02	ZNF445	2613 (+)	1	1	tggatAAAGGa
V$NR4A2RXRA_01	NURR1:RXR-ALPHA	2619 (+)	0.865	0.822	aaggactgTGAACca
V$ZBTB44_01	Zbtb44	2624 (+)	1	1	CTGTGa
V$RARA_07	RARA	2627 (-)	0.843	0.78	TGAACcattactgtcct
V$RARG_02	RARG	2627 (-)	0.824	0.819	tgaaccattacTGTCCtt

V$RARA_09	RARA	2627 (-)	0.852	0.78	tgaaccattacTGTCCt
V$THAP1_01	Thap1	2636 (-)	1	0.816	actgtccttcctaaaacATGGCag
V$YY1_07	YY1	2639 (-)	1	0.94	gtccttcctaaaacATGGCagc
V$ELF1_Q5	Elf-1	2642 (-)	1	1	cTTCCT
V$SPI1_Q5	PU.1	2642 (-)	1	1	cTTCCT
V$YY1_02	YY1	2643 (-)	1	0.867	ttcctaaaacATGGCagcta
I$MIRR_01	mirr	2649 (+)	1	1	AAACA
V$YY1_08	YY1	2649 (+)	1	1	AAACAtggc
V$YY1_Q6	YY1	2649 (-)	1	0.994	aaacATGGC
V$YY1_03	YY1	2649 (-)	1	0.872	aaacATGGCagc
V$YY1_12	YY1	2649 (+)	1	0.971	aaacATGGCagc
V$YY1_13	YY1	2649 (+)	1	0.97	aaacATGGCagct
V$YY1_14	YY1	2649 (+)	1	0.937	aaacATGGCagc
V$YY1_15	YY1	2649 (+)	1	0.95	aaacATGGCagc
V$YY1_Q6_02	YY1	2650 (-)	1	0.995	aacATGGCagc
V$REX1_05	REX-1	2650 (-)	1	0.949	aacATGGCagct
V$SOX8_04	Sox-8	2659 (-)	1	0.968	gctaaaaTGAATgt
P$O2_04	O2	2670 (-)	0.898	0.826	tgtgagCTGGCag
V$CMYB_01	c-Myb	2672 (+)	0.988	0.954	tgagctggcaGTTGTggt
V$MYB_03	MYB	2674 (-)	1	0.963	agctggCAGTTgtggt
V$MYB_Q3	c-MYB	2675 (+)	1	0.999	gctggCAGTTg
V$MYB_10	c-Myb	2675 (+)	1	0.993	gctggCAGTTgt
V$MYB_11	c-Myb	2675 (+)	1	0.983	gctggCAGTTgt
V$HSF4_Q3	HSF4	2676 (-)	1	1	ctGGCAG
V$MYB_Q4	c-Myb	2676 (+)	1	0.998	ctggCAGTTgtg
V$MYB_08	c-Myb	2676 (+)	1	0.986	ctggCAGTTgt
V$MYB_Q5_01	MYB	2677 (-)	1	1	tggCAGTTg
V$CMYB_Q5	c-Myb	2677 (-)	1	0.997	tggCAGTTgtg
V$MYB_07	c-Myb	2677 (-)	1	0.996	tggCAGTTgt
V$MYB_Q6	c-Myb	2678 (-)	1	0.995	ggCAGTTgtg
V$MYB_09	MYB	2678 (-)	1	1	ggCAGTTgtg
P$MYBAS1_01	MYBAS1	2678 (-)	0.999	0.999	ggcaGTTGTgg
V$AML_Q6	AML	2679 (+)	1	0.974	gcagtTGTGGttaat

V$AML2_01	AML2	2683 (-)	1	1	ttGTGGTt
V$AML3_Q6	AML3	2683 (-)	1	1	ttGTGGTt
V$AML1_Q6	AML1	2684 (+)	1	1	TGTGGt
V$AML1_Q5	AML1	2684 (+)	1	1	TGTGGt
V$PEBP2B_Q6	PEBP2beta	2684 (+)	1	1	TGTGGtt
V$AML1_01	AML1a	2684 (+)	1	1	tGTGGT
V$AML1_Q4	AML1	2684 (+)	1	1	tGTGGTt
V$AML_Q4	AML	2684 (+)	1	1	tGTGGTta
V$E2F3EOMES_01	E2F-3:TBR2	2684 (-)	0.765	0.74	tgtggttaatGTGCCagctcaaag
V$ISL1_Q3	islet1	2687 (+)	1	1	ggtTAATG
V$IPF1_Q6	ipf1	2689 (-)	1	1	tTAATG
P$O2_04	O2	2694 (+)	0.898	0.826	gtGCCAGctcaaa
V$EAR2_Q2	EAR2	2698 (-)	1	0.914	cagctCAAAGttaa
V$RXRA_05	RXRA	2698 (+)	1	0.781	cagctCAAAGttaa
V$LEF1_Q2	TCF-7	2702 (+)	1	1	tCAAAG
V$TCF3_Q6	TCF-3	2702 (-)	1	1	tCAAAG
V$MSX2_Q3	Msx-2	2709 (+)	0.905	0.941	TAAATggggagt
V$P300_01	p300	2712 (+)	1	0.978	atggGGAGTgagaa
V$MZF1_Q5	MZF-1	2713 (+)	1	1	tGGGGAg
V$E2F3TBX21_01	E2F-3:T-bet	2717 (+)	0.94	0.825	gagTGAGAaggtgtct
V$TFIII_Q6_01	TFII-I	2721 (+)	0.963	0.966	gAGAAGgtgt
V$SMAD3_03	Smad3	2723 (-)	1	0.987	gaaggtGTCTGgatgtc
V$SMAD_Q6	SMAD	2724 (-)	1	0.997	aaggTGTCT
F$RAP1_03	RAP1	2724 (-)	0.941	0.911	aaggtgtctGGATGt
V$SMAD4_Q6	SMAD4	2725 (-)	0.99	0.922	aggTGTCTggatgtc
V$SMAD4_05	SMAD4	2728 (+)	0.977	0.982	tGTCTGga
V$FOXO1SPDEF_01	FOXO1A:PDEF	2729 (+)	1	0.918	gtctGGATGtcat
I$CHES1L_02	CHES1L	2734 (-)	0.8	0.827	gatgtcatgGAGTCattctccaa
I$TLL_03	Tll	2734 (+)	0.794	0.841	gatgtcatgGAGTCa
V$FOS_09	C-FOS	2737 (-)	0.883	0.844	gtcatggAGTCAttctc
V$NFE2L1_Q5	Nfe2l1	2739 (+)	1	0.964	catggaGTCATt
F$GCN4_Q2	Gcn4p	2740 (+)	1	0.964	atggAGTCAtt
F$GCN4_C	Gcn4p	2742 (-)	1	0.99	ggAGTCAttc

V$CJUN_Q6	C-Jun	2743 (-)	1	1	gAGTCA
F$ADR1_Q6	Adr1p	2748 (-)	1	0.958	atTCTCCaaa
V$SPIB_Q3	Spi-B	2749 (+)	1	1	TTCTCc
V$BRN1_Q6	BRN1	2760 (-)	1	1	tGCATTt
P$MYB3R5_01	MYB3R5	2760 (+)	0.792	0.782	tgcatttcaCCCTTg
P$MYB3R1_01	MYB3R1	2761 (+)	0.789	0.792	gcatttcaCCCTTgt
P$MYB3R4_01	MYB3R4	2761 (+)	0.792	0.801	gcatttcaCCCTTgt
P$AT1G77200_03	AT1G77200	2768 (-)	0.797	0.831	acccttGTGGGtga
V$PAX8_B	Pax-8	2768 (+)	0.902	0.893	acccttgtGGGTGagatg
V$EGR3_Q3	egr-3	2774 (+)	1	1	GTGGGt
P$ASR1_01	ASR-1	2775 (-)	1	1	TGGGT
V$TEAD4HOXB13_01	TEF-3:HOXB13	2783 (+)	1	0.917	atggTAAAAtgtg
I$DMRT93B_01	dmrt93B	2801 (+)	1	0.996	aatGATACagt
I$OPTIX_01	Optix	2803 (+)	1	1	TGATA
I$SIX4_01	Six-4	2803 (+)	1	1	TGATAc
I$SO_01	so	2803 (+)	1	1	TGATAc
V$FOXO1ETV7_01	FOXO1A:ETV7	2806 (+)	0.627	0.795	tacaGTAGGaggattttccag
V$ETS1_03	ETS1	2810 (+)	0.861	0.725	gtaggaggatTTTCCagg
V$CREL_Q6	c-Rel	2814 (+)	1	0.961	gaggatTTTCCa
V$RELA_Q6	RelA-p65	2815 (+)	0.996	0.976	aGGATTttccag
I$DL_01	dl	2815 (+)	1	0.904	aggatTTTCCa
V$NFKB1_03	NF-kappaB1	2815 (+)	1	0.98	aggatTTTCCa
V$RELA_09	RelA-p65	2815 (+)	1	0.955	aggatTTTCCa
F$FACBCA_Q2	FACB	2817 (-)	0.911	0.91	gattTTCCAggcctcacaggagtgtt
F$FACBCA_Q2	FACB	2817 (+)	0.989	0.905	gattttccaggcctcacAGGAGtgtt
V$NFAT3_Q3_01	NFATc4	2818 (-)	1	1	atTTTCCa
V$NFAT1_Q6	NFATc2	2819 (-)	1	1	tTTTCC
V$NFAT4_Q3	NFATc3	2819 (-)	1	1	tTTTCC
V$NFATC2_01	NFATc2	2819 (+)	1	1	tTTTCCa
V$NFAT1_Q4	NFATc2	2819 (-)	1	1	tTTTCC
V$NFE4_Q5_01	NF-E4	2827 (-)	1	1	gCCTCAc
V$ZBTB44_01	Zbtb44	2830 (-)	1	1	tCACAG
V$GATAD2A_01	GATAD2A	2831 (-)	1	1	CACAGg

P$REM16_01	REM16	2836 (+)	0.782	0.739	gagtgttttttggggGGAGAt
V$RREB1_01	RREB-1	2837 (-)	1	0.875	agtgttttTTGGGg
P$DEL2_02	DEL2	2837 (+)	0.818	0.813	agtgttttttGGGGGgagat
I$MIRR_01	mirr	2839 (-)	1	1	TGTTT
F$YML081W_01	Yml081wp	2840 (-)	0.897	0.829	gttttttGGGGGgagatctta
V$ZBTB7B_03	Zbtb7b	2841 (-)	1	0.988	ttttttGGGGGgaga
V$E2F2_06	E2F2	2841 (+)	0.763	0.725	ttttttGGGGGgagatct
V$MSX2_Q3	Msx-2	2842 (+)	0.966	0.951	TTTTTgggggga
P$HSFA2_01	HSFA2	2843 (-)	1	1	tTTTGG
P$DEL1_02	DEL1	2843 (-)	0.796	0.794	ttttggGGGGAgatcttacgg
V$ETS1_03	ETS1	2847 (+)	0.807	0.736	ggggggagatCTTACggt
V$GATA3_03	GATA-3	2851 (+)	1	0.967	ggaGATCTta
P$SPL1_01	SPL1	2855 (+)	0.791	0.755	atCTTACggt
P$SPL1_01	SPL1	2855 (-)	0.791	0.755	atcTTACGgt

Extended Data Table 3-Known motif discovery analysis of NAMPT enhancer using GENOMATIX Software suite
relate to Figs. 3d, 3e and Extended Data Figs. 5d, 5e

Motif ID	Detailed Family Information	Alt Motif ID	Motif Information	Start	End	Anchor	Strand	Matrix sim	Matched Sequence
V$ARID	AT rich interactive domain factor	V$MRF2.01	Modulator recognition factor 2 (MRF2, ARID5B)	215	235	225	(+)	1	acaaAATAccaagcaccacat
V$ZF02	C2H2 zinc finger transcription factors 2	V$ZKSCAN3.01	Zinc finger with KRAB and SCAN domains 3	307	329	318	(-)	1	cctccCCCCaccccatgacaggc
V$MZF1	Myeloid zinc finger 1 factors	V$MZF1.03	Myeloid zinc finger protein MZF1	321	331	326	(+)	1	ggGGGGagggc
V$TCFF	TCF11 transcription factor	V$TCF11.01	TCF11/LCR-F1/Nrf1 homodimers	364	370	367	(-)	1	GTCAttt
V$TCFF	TCF11 transcription factor	V$TCF11.01	TCF11/LCR-F1/Nrf1 homodimers	496	502	499	(-)	1	GTCAttt
V$FKHD	Fork head domain factors	V$ILF1.01	Winged-helix transcription factor IL-2 enhancer binding fact	588	604	596	(-)	1	agaaggaaAACAcattt
V$RUSH	SWI/SNF related nucleophosphoproteins	V$SMARCA3.01	SWI/SNF related, matrix associated, actin dependent regul	655	665	660	(-)	1	taCCATttgtc
V$FKHD	Fork head domain factors	V$FOXP1_ES.01	Alternative splicing variant of FOXP1, activated in ESCs	671	687	679	(+)	1	aaaataaAACAaaaaaa
V$FKHD	Fork head domain factors	V$FOXP1_ES.01	Alternative splicing variant of FOXP1, activated in ESCs	733	749	741	(+)	1	gagctaaAACActctaa
V$TAIP	TGF-beta induced apoptosis proteins	V$CSRNP1.01	Cysteine-serine-rich nuclear protein 1 (AXUD1, AXIN1 up-	741	747	744	(-)	1	AGAGtgt
V$PLAG	Pleomorphic adenoma gene	V$PLAG1.02	Pleomorphic adenoma gene 1	985	1007	996	(+)	1	aaGGGGgataaaggccaggggaa
V$TCFF	TCF11 transcription factor	V$TCF11.01	TCF11/LCR-F1/Nrf1 homodimers	1044	1050	1047	(-)	1	GTCAttt
V$RUSH	SWI/SNF related nucleophosphoproteins	V$SMARCA3.02	SWI/SNF related, matrix associated, actin dependent regul	1101	1111	1106	(-)	1	gtgtACTTttc
V$NKXH	NKX homeodomain factors	V$NKX25.01	Homeo domain factor Nkx-2.5/Csx, tinman homolog, high a	1101	1119	1110	(-)	1	cagttcAAGTgtacttttc
V$FKHD	Fork head domain factors	V$FOXP1_ES.01	Alternative splicing variant of FOXP1, activated in ESCs	1134	1150	1142	(+)	1	cagctaaAACAcaggag
V$FKHD	Fork head domain factors	V$FOXP1_ES.01	Alternative splicing variant of FOXP1, activated in ESCs	1215	1231	1223	(-)	1	tagagaaAACAtaacac
V$FKHD	Fork head domain factors	V$FOXP1_ES.01	Alternative splicing variant of FOXP1, activated in ESCs	1249	1265	1257	(+)	1	ttcaaaaAACAaacaaa
V$FKHD	Fork head domain factors	V$FOXP1_ES.01	Alternative splicing variant of FOXP1, activated in ESCs	1258	1274	1266	(+)	1	caaacaaAACAacaaag
V$CABL	C-abl DNA binding sites	V$CABL.01	Multifunctional c-Abl src type tyrosine kinase	1263	1273	1268	(+)	1	aaAACAacaaa
V$FKHD	Fork head domain factors	V$FOXP1.02	Sites bound by FOXP1 and an alternative splicing variant F	1261	1277	1269	(+)	1	acaaaacAACAaagcta
V$FKHD	Fork head domain factors	V$FOXP1_ES.01	Alternative splicing variant of FOXP1, activated in ESCs	1385	1401	1393	(+)	1	actgcaaAACAgatcag
V$FKHD	Fork head domain factors	V$FOXP1_ES.01	Alternative splicing variant of FOXP1, activated in ESCs	1449	1465	1457	(+)	1	aatgaaaAACAgaaaca
V$BRAC	Brachyury gene, mesoderm developmenta	V$TBX20.01	T-box transcription factor TBX20	1946	1974	1960	(-)	1	aggagaaagAGGTgttgaggttctgagcg
V$TAIP	TGF-beta induced apoptosis proteins	V$CSRNP1.01	Cysteine-serine-rich nuclear protein 1 (AXUD1, AXIN1 up-	2165	2171	2168	(-)	1	AGAGtgg
V$NKXH	NKX homeodomain factors	V$NKX25.01	Homeo domain factor Nkx-2.5/Csx, tinman homolog, high a	2367	2385	2376	(-)	1	tgcctcAAGTgagttacta
V$FKHD	Fork head domain factors	V$FOXP1_ES.01	Alternative splicing variant of FOXP1, activated in ESCs	2586	2602	2594	(+)	1	attccaaAACActgggc
V$FKHD	Fork head domain factors	V$FOXP1_ES.01	Alternative splicing variant of FOXP1, activated in ESCs	2643	2659	2651	(+)	1	ttcctaaAACAtggcag
V$SMAD	Vertebrate SMAD family of transcription fa	V$SMAD3.01	Smad3 transcription factor involved in TGF-beta signaling	2726	2736	2731	(+)	1	ggtGTCTggat
V$FKHD	Fork head domain factors	V$FOXP1_ES.01	Alternative splicing variant of FOXP1, activated in ESCs	2833	2849	2841	(-)	1	cccaaaaAACActcctg
V$EVI1	EVI1-myleoid transforming protein	V$MEL1.02	MEL1 (MDS1/EVI1-like gene 1) DNA-binding domain 2	137	153	145	(+)	0.999	aaaaatgGATGagttca
V$EVI1	EVI1-myleoid transforming protein	V$MEL1.02	MEL1 (MDS1/EVI1-like gene 1) DNA-binding domain 2	1922	1938	1930	(-)	0.999	tgcaaagGATGagtaga
V$MYBL	Cellular and viral myb-like transcriptional r	V$CMYB.01	c-Myb, important in hematopoesis, cellular equivalent to avi	2674	2694	2684	(-)	0.998	cattaaccaCAACtgccagct
V$CABL	C-abl DNA binding sites	V$CABL.01	Multifunctional c-Abl src type tyrosine kinase	676	686	681	(+)	0.997	aaAACAaaaaa
V$ZFHX	Two-handed zinc finger homeodomain tra	V$DELTAEF1.02	Delta-crystallin enhancer binding factor, transcription factor	244	256	250	(-)	0.996	ttctcACCTgtga
V$BPTF	Bromodomain and PHD domain transcripti	V$FAC1.01	Fetal Alz-50 clone 1 (FAC1)	628	638	633	(-)	0.996	cccacAACAca
V$FKHD	Fork head domain factors	V$FOXP1.01	Forkhead box P1	1437	1453	1445	(+)	0.996	agaaggtAAACaaatga
V$NEUR	NeuroD, Beta2, HLH domain	V$OLIG2.01	Oligodendrocyte lineage transcription factor 2	1723	1737	1730	(-)	0.996	ctcccaGCTGccttt
V$MZF1	Myeloid zinc finger 1 factors	V$MZF1.01	Myeloid zinc finger protein MZF1	2847	2857	2852	(+)	0.996	ggGGGGagatc
V$MZF1	Myeloid zinc finger 1 factors	V$MZF1.02	Myeloid zinc finger protein MZF1	1506	1516	1511	(+)	0.995	atGGGGaaatg
V$SMAD	Vertebrate SMAD family of transcription fa	V$SMAD3.01	Smad3 transcription factor involved in TGF-beta signaling	2250	2260	2255	(-)	0.995	gcaGTCTggct
V$RU49	Zinc finger transcription factor RU49, zinc	V$RU49.01	Zinc finger transcription factor RU49 (zinc finger proliferatio	788	794	791	(-)	0.994	cAGTAcc
V$GREF	Glucocorticoid responsive and related ele	V$ARE.03	Androgene receptor binding site, IR3 sites	1763	1781	1772	(+)	0.994	cagggacagtttGTTCtct
V$ZF02	C2H2 zinc finger transcription factors 2	V$ZNF219.01	Kruppel-like zinc finger protein 219	309	331	320	(-)	0.993	gccctCCCCccaccccatgacag
V$ZTRE	Zinc transcriptional regulatory element	V$ZTRE.03	5' half site of ZTRE motif	314	330	322	(-)	0.993	ccCTCCccccaccccat
V$ZF02	C2H2 zinc finger transcription factors 2	V$ZBP89.01	Zinc finger transcription factor ZBP-89	312	334	323	(-)	0.993	gtcgccctCCCCccaccccatga
V$BTBF	BTB/POZ (broad complex, TramTrack, Br	V$KAISO.01	Transcription factor Kaiso, ZBTB33	2207	2221	2214	(-)	0.993	catcCTGCcactcca
V$BCDF	Bicoid-like homeodomain transcription fact	V$OTX2.01	Homeodomain transcription factor Otx2 (homolog of Droso	82	98	90	(-)	0.992	cttttTAATccagtcta
V$ETSF	Human and murine ETS1 factors	V$ETV1.02	Ets variant 1	275	295	285	(+)	0.992	tggacacaGGAAgaggaacct
V$EGRF	EGR/nerve growth factor induced protein	V$CKROX.01	Collagen krox protein (zinc finger protein 67 - zfp67)	318	336	327	(+)	0.992	ggtgggGGGAgggcgacgg
V$ZF11	C2H2 zinc finger transcription factors 11	V$ZBTB3.01	Zinc finger and BTB domain containing 3	1555	1565	1560	(+)	0.992	gtcaGCCAggc
V$MOKF	Mouse Krueppel like factor	V$MOK2.02	Ribonucleoprotein associated zinc finger protein MOK-2 (h	1612	1632	1622	(-)	0.992	cccggcatcgggaCCTTtgcc
V$ZF35	Zinc finger protein ZNF35	V$ZNF35.01	Human zinc finger protein ZNF35	1627	1639	1633	(+)	0.992	gccgggAAGAtct
V$HEAT	Heat shock factors	V$HSF2.02	Heat shock factor 2	1976	2000	1988	(-)	0.992	ccaaggacactaAGAAcaatcttgc
V$GATA	GATA binding factors	V$GATA.01	GATA binding factor	2295	2307	2301	(-)	0.992	cacaGATAagtaa
V$CDXF	Vertebrate caudal related homeodomain p	V$CDX2.03	Caudal type homeobox transcription factor 2	14	32	23	(+)	0.991	atgtgtgtTTATtgcggca
V$KLFS	Krueppel like transcription factors	V$KLF2.01	Krueppel-like factor 2 (lung) (LKLF)	312	330	321	(+)	0.991	tcatgGGGTggggggaggg
V$AP1F	AP1, Activating protein 1	V$JUNB.01	Transcription factor Jun-B	1033	1045	1039	(-)	0.991	ttctgaGTCAtgt
V$AP1R	MAF and AP1 related factors	V$MARE.02	Binding sites for homodimers of large Maf-proteins	1366	1390	1378	(+)	0.991	aacattgcagattcAGCAgactgca
V$LTSM	Localized tandem sequence motif	V$LTSM.03	LTSM elements with 8 bp spacer	1623	1637	1630	(-)	0.991	ATCTtcccggcatcg
V$MZF1	Myeloid zinc finger 1 factors	V$MZF1.02	Myeloid zinc finger protein MZF1	1703	1713	1708	(+)	0.991	aaGGGGagaga
V$SORY	SOX/SRY-sex/testis determining and relat	V$SOX6.01	SRY (sex determining region Y)-box 6	2081	2103	2092	(-)	0.991	aatagACAAagccaaaaaggaga
V$HAND	Twist subfamily of class B bHLH transcrip	V$SCX.01	Tendon-specific bHLH transcription factor scleraxis	392	412	402	(-)	0.99	aggtatacatgTGCCatgttg

V$MYOD	Myoblast determining factors	V$TCFE2A.03	Transcription factor E2a (E12/E47)	1723	1739	1731	(-)	0.99	tgctccCAGCtgccttt
V$CIZF	CAS interating zinc finger protein	V$NMP4.01	NMP4 (nuclear matrix protein 4) / CIZ (Cas-interacting zinc	2124	2134	2129	(-)	0.99	ggAAAAaatca
V$BEDF	BED subclass of zinc-finger proteins	V$ZBED4.02	Zinc finger, BED-type containing 4; polyG binding sites	315	329	322	(+)	0.989	tggggtgGGGGgagg
V$CDXF	Vertebrate caudal related homeodomain p	V$CDX2.03	Caudal type homeobox transcription factor 2	1315	1333	1324	(-)	0.989	ataaatatTTATtgaataa
V$ABDB	Abdominal-B type homeodomain transcrip	V$HOXB9.02	Homeobox B9	128	144	136	(+)	0.988	tacagccaTAAAaatgg
V$SORY	SOX/SRY-sex/testis determining and relat	V$SOX30.01	SRY-related HMG-box gene 30	256	278	267	(+)	0.988	attgaACAAtgagaacacatgga
V$XBBF	X-box binding factors	V$RFX4.02	Regulatory factor X, 4 (secondary DNA binding preference)	803	821	812	(-)	0.988	gggctttcttaGTTAcaac
V$AP1R	MAF and AP1 related factors	V$BACH2.02	BTB and CNC homology 1, basic leucine zipper transcriptio	1026	1050	1038	(-)	0.988	gtcatttcTGAGtcatgtccttaaa
V$YY1F	Activator/repressor binding to transcription	V$YY2.01	Transcription factor yin yang 2	128	150	139	(-)	0.987	actcatCCATttttatggctgta
V$RUSH	SWI/SNF related nucleophosphoproteins w	V$SMARCA3.02	SWI/SNF related, matrix associated, actin dependent regula	2556	2566	2561	(+)	0.987	ccatACTTctt
V$EGRF	EGR/nerve growth factor induced protein (	V$WT1.01	Wilms Tumor Suppressor	315	333	324	(+)	0.986	tggggTGGGgggagggcga
V$RUSH	SWI/SNF related nucleophosphoproteins w	V$SMARCA3.02	SWI/SNF related, matrix associated, actin dependent regula	2293	2303	2298	(+)	0.986	atttACTTatc
V$SATB	Special AT-rich sequence binding protein	V$SATB1.01	Special AT-rich sequence-binding protein 1, predominantly	2465	2479	2472	(-)	0.986	actAATAtttaaaaa
V$BZIP	Heterodimers between bZIP family membe	V$CEBPE_ATF4.01	Heterodimer of CEBP epsilon and ATF4	2377	2389	2383	(+)	0.985	cttgagGCAAcac
V$RUSH	SWI/SNF related nucleophosphoproteins w	V$SMARCA3.01	SWI/SNF related, matrix associated, actin dependent regula	2707	2717	2712	(-)	0.985	ccCCATttaac
V$ZFXY	Zfx and Zfy - transcription factors implicat	V$ZFX.01	X-linked zinc finger protein	2821	2831	2826	(-)	0.985	gaGGCCtggaa
V$ZTRE	Zinc transcriptional regulatory element	V$ZTRE.04	3' half site of ZTRE motif	322	338	330	(+)	0.984	gggGGAGggcgacggga
V$NF1F	Nuclear factor 1	V$NF1.03	Non-palindromic nuclear factor I binding sites	709	729	719	(-)	0.984	ctggtctgcctctGCCAgaaa
V$NF1F	Nuclear factor 1	V$NF1.03	Non-palindromic nuclear factor I binding sites	1083	1103	1093	(+)	0.984	atgctgtaaagatGCCAagaa
V$ZFHX	Two-handed zinc finger homeodomain tra	V$AREB6.01	AREB6 (Atp1a1 regulatory element binding factor 6)	1206	1218	1212	(+)	0.984	cacatACCTgtgt
V$ZFHX	Two-handed zinc finger homeodomain tra	V$AREB6.04	AREB6 (Atp1a1 regulatory element binding factor 6)	1361	1373	1367	(-)	0.984	gcaatGTTTcaaa
O$INRE	Core promoter initiator elements	O$DINR.01	Drosophila initiator motifs	1445	1455	1450	(-)	0.984	ttTCATttgtt
V$SPZ1	Testis-specific bHLH-Zip transcription fac	V$SPZ1.01	Spermatogenic Zip 1 transcription factor	1640	1650	1645	(+)	0.984	tGGAGggtttg
V$CDXF	Vertebrate caudal related homeodomain p	V$CDX1.01	Intestine specific homeodomain factor CDX-1	462	480	471	(-)	0.983	tttttttTTTActattatt
V$AP1F	AP1, Activating protein 1	V$BATF.01	Basic leucine zipper transcription factor, ATF-like	1033	1045	1039	(+)	0.983	acatgaCTCAgaa
V$HOMF	Homeodomain transcription factors	V$HHEX.01	Hematopoietically expressed homeobox, proline-rich home	1154	1172	1163	(-)	0.983	ttccctgtcttTAATaaga
V$BPTF	Bromodomain and PHD domain transcripti	V$FAC1.01	Fetal Alz-50 clone 1 (FAC1)	1263	1273	1268	(+)	0.983	aaaacAACAaa
V$HAML	Human acute myelogenous leukemia facto	V$AML2.01	RUNX3 (Runt-related transcription factor 3), AML2 (Acute r	2681	2695	2688	(+)	0.983	agtTGTGgttaatgt
V$ZF02	C2H2 zinc finger transcription factors 2	V$ZBTB7.01	Zinc finger and BTB domain containing 7, Proto-oncogene F	2835	2857	2846	(-)	0.983	gatctcCCCCcaaaaaacactcc
V$SORY	SOX/SRY-sex/testis determining and relat	V$SOX3.01	SRY-box containing gene 3	146	168	157	(-)	0.982	tccctaCAAAggacatgaactca
V$MYT1	MYT1 C2HC zinc finger protein	V$MYT1.02	MyT1 zinc finger transcription factor involved in primary ne	453	465	459	(+)	0.982	ttaAAGTttaata
O$PTBP	Plant TATA binding protein factor	O$PTATA.02	Plant TATA box	1324	1338	1331	(-)	0.982	agtcTATAaatattt
V$AP1R	MAF and AP1 related factors	V$NRL.02	Neural retinal basic leucine zipper factor (bZIP)	1370	1394	1382	(+)	0.982	ttgcagattcAGCAgactgcaaaac
V$SORY	SOX/SRY-sex/testis determining and relat	V$SOX6.01	SRY (sex determining region Y)-box 6	1806	1828	1817	(+)	0.982	tgtacACAAagtaggcacccaat
V$MYBL	Cellular and viral myb-like transcriptional r	V$CMYB.01	c-Myb, important in hematopoesis, cellular equivalent to avi	1862	1882	1872	(-)	0.982	tatgagtgtCAACagcctcag
V$HAND	Twist subfamily of class B bHLH transcrip	V$TAL1_E2A.01	Complex of Lmo2 bound to Tal-1, E2A proteins, and GATA-	2379	2399	2389	(-)	0.982	ctcaggaCAGGtgttgcctca
V$PAX3	PAX-3 binding sites	V$PAX3.03	Pax-3 paired domain protein	2734	2752	2743	(+)	0.982	gatgtCATGgagtcattct
V$XBBF	X-box binding factors	V$RFX5.01	Regulatory factor X, 5 (influences HLA class II expression)	1177	1195	1186	(-)	0.981	ctacctgtccAGCAacatc
V$AP4R	AP4 and related proteins	V$AP4.03	Activating enhancer binding protein 4	1722	1738	1730	(-)	0.981	gctcccaGCTGcctttc
V$ARID	AT rich interactive domain factor	V$ARID5A.01	AT rich interactive domain 5A (MRF1-like)	2334	2354	2344	(+)	0.981	ctgcaATATtgaaagctttga
V$CEBP	Ccaat/Enhancer Binding Protein	V$CEBPE.02	CCAAT/enhancer binding protein (C/EBP), epsilon	603	617	610	(+)	0.98	ctctttctGCAAcac
V$ETSF	Human and murine ETS1 factors	V$PDEF.01	Prostate-derived Ets factor	2209	2229	2219	(+)	0.979	gagtggcaGGATgggatggta
V$CEBP	Ccaat/Enhancer Binding Protein	V$CEBPB.02	CCAAT/enhancer binding protein beta	2299	2313	2306	(+)	0.979	ttatcTGTGaaatgg
V$ARID	AT rich interactive domain factor	V$ARID5A.01	AT rich interactive domain 5A (MRF1-like)	2327	2347	2337	(-)	0.979	tttcaATATtgcagtcatgaa
V$ARID	AT rich interactive domain factor	V$ARID5A.01	AT rich interactive domain 5A (MRF1-like)	2460	2480	2470	(-)	0.979	cactaATATttaaaaaatgga
V$PAX3	PAX-3 binding sites	V$PAX3.03	Pax-3 paired domain protein	308	326	317	(+)	0.978	cctgtCATGgggtgggggg
V$CIZF	CAS interating zinc finger protein	V$NMP4.01	NMP4 (nuclear matrix protein 4) / CIZ (Cas-interacting zinc	482	492	487	(+)	0.978	ggAAAAaaaag
V$FKHD	Fork head domain factors	V$HFH3.01	HNF-3/Fkh Homolog 3 (FOXI1, Freac-6)	1252	1268	1260	(+)	0.978	aaaaaacAAACaaaaca
V$SORY	SOX/SRY-sex/testis determining and relat	V$SOX6.01	SRY (sex determining region Y)-box 6	1264	1286	1275	(+)	0.978	aaacaACAAagctaacataaact
V$SAL2	Spalt-like transcription factor 2	V$SALL2.01	Zinc finger protein Spalt-2, sal-like 2, p150(sal2)	315	325	320	(+)	0.977	tgggGTGGggg
V$SORY	SOX/SRY-sex/testis determining and relat	V$SOX5.01	Sox-5	1968	1990	1979	(-)	0.977	taagaaCAATcttgcaaggagaa
V$ZF05	C2H2 zinc finger transcription factors 5	V$ZFP410.01	Zinc finger protein 410, APA-1	2215	2229	2222	(+)	0.977	caggatgGGATggta
V$LEFF	LEF1/TCF	V$LEF1.02	TCF/LEF-1, involved in the Wnt signal transduction pathwa	2344	2360	2352	(-)	0.977	ttagtttCAAAgctttc
V$ETSF	Human and murine ETS1 factors	V$ERG.02	v-ets erythroblastosis virus E26 oncogene homolog	474	494	484	(+)	0.976	aaaaaaaaGGAAaaaaaagag
V$NKXH	NKX homeodomain factors	V$NKX25.05	Homeodomain factor Nkx-2.5/Csx	1867	1885	1876	(-)	0.976	agctaTGAGtgtcaacagc
V$HOMF	Homeodomain transcription factors	V$HHEX.01	Hematopoietically expressed homeobox, proline-rich home	450	468	459	(+)	0.975	aacttaaagttTAATaata
V$ZFHX	Two-handed zinc finger homeodomain tra	V$AREB6.02	AREB6 (Atp1a1 regulatory element binding factor 6)	2383	2395	2389	(+)	0.975	gcaaCACCtgtcc
O$INRE	Core promoter initiator elements	O$DINR.01	Drosophila initiator motifs	2797	2807	2802	(-)	0.975	taTCATttgag
V$HIFF	Hypoxia inducible factor, bHLH/PAS prote	V$HRE.03	Hypoxia response elements, binding sites for HIF1alpha/AF	422	438	430	(-)	0.974	gaccacaACGTgcaggt
V$BCDF	Bicoid-like homeodomain transcription fact	V$CRX.01	Cone-rod homeobox-containing transcription factor / otx-lik	1907	1923	1915	(-)	0.974	gaggtTAATcctaatct
V$CABL	C-abl DNA binding sites	V$CABL.01	Multifunctional c-Abl src type tyrosine kinase	1254	1264	1259	(+)	0.973	aaAACAaacaa
V$YY1F	Activator/repressor binding to transcription	V$YY2.01	Transcription factor yin yang 2	2012	2034	2023	(-)	0.973	ctaaggCCATttttaaccagggg
V$NKXH	NKX homeodomain factors	V$NKX25.05	Homeodomain factor Nkx-2.5/Csx	233	251	242	(-)	0.972	acctgTGAGtgagaacatg
V$AP1R	MAF and AP1 related factors	V$NRL.02	Neural retinal basic leucine zipper factor (bZIP)	188	212	200	(+)	0.971	catcattctcAGCAaactatcccag
V$GREF	Glucocorticoid responsive and related ele	V$ARE.04	Androgene receptor binding site, IR3 sites	1763	1781	1772	(-)	0.971	agagaacaaactGTCCctg
V$BCDF	Bicoid-like homeodomain transcription fact	V$PTX1.01	Pituitary Homeobox 1 (Ptx1, Pitx-1)	2133	2149	2141	(-)	0.971	tctgCTAAaccctatgg
V$ZTRE	Zinc transcriptional regulatory element	V$ZTRE.03	5' half site of ZTRE motif	2705	2721	2713	(-)	0.971	caCTCCccatttaactt

V$HMTB	Human muscle-specific Mt binding site	V$MTBF.01	Muscle-specific Mt binding site	217	225	221	(-)	0.97	tggtATTTt
V$LEFF	LEF1/TCF	V$LEF1.02	TCF/LEF-1, involved in the Wnt signal transduction pathwa	524	540	532	(+)	0.97	ggagaatCAAAgtatta
V$LHXF	Lim homeodomain factors	V$LMX1A.02	LIM homeobox transcription factor 1, alpha	575	597	586	(-)	0.969	aaacacatTTAAtgaatgtctac
V$GATA	GATA binding factors	V$GATA1.06	Complex of Lmo2 bound to Tal-1, E2A proteins, and GATA-	725	737	731	(+)	0.969	accaGATAgagct
V$YY1F	Activator/repressor binding to transcriptior	V$YY2.01	Transcription factor yin yang 2	924	946	935	(+)	0.969	ggatttCCATctttggctccaac
V$ZICF	Members of ZIC-family, zinc finger protein	V$ZIC2.02	Zic family member 2 (odd-paired Drosophila homolog) (sec	1062	1076	1069	(+)	0.969	tcaccCAGCatgacc
V$YY1F	Activator/repressor binding to transcriptior	V$YY2.01	Transcription factor yin yang 2	1161	1183	1172	(-)	0.969	caacatCCATattccctgtcttt
V$BRNF	Brn POU domain factors	V$BRN2.03	Brn-2, POU-III protein class	1489	1507	1498	(-)	0.969	attgccttaATTTtcatct
V$NFKB	Nuclear factor kappa B/c-rel	V$NFKAPPAB65.01	NF-kappaB (p65)	2813	2827	2820	(+)	0.969	ggaggattTTCCagg
V$OCT1	Octamer binding protein	V$OCT2.02	Octamer-binding transcription factor-2, POU class 2 homed	5	19	12	(+)	0.968	cacaTGCAcatgtgt
V$MIZ1	Myc-interacting Zn finger protein 1	V$MIZ1.01	Myc-interacting Zn finger protein 1, zinc finger and BTB dor	1746	1756	1751	(-)	0.968	aaagcCCTCta
V$CDXF	Vertebrate caudal related homeodomain p	V$CDX2.03	Caudal type homeobox transcription factor 2	128	146	137	(-)	0.967	atccatttTTATggctgta
V$ETSF	Human and murine ETS1 factors	V$SPI1.02	SPI-1 proto-oncogene; hematopoietic transcription factor P	996	1016	1006	(+)	0.967	aggccaggGGAAgggaggatg
V$IRFF	Interferon regulatory factors	V$IRF4.01	Interferon regulatory factor (IRF)-related protein (NF-EM5,	1217	1241	1229	(-)	0.967	agttttagactagaGAAAacataac
V$GATA	GATA binding factors	V$GATA1.03	GATA-binding factor 1	1849	1861	1855	(+)	0.967	aaaaGATAaagac
V$YY1F	Activator/repressor binding to transcriptior	V$YY2.01	Transcription factor yin yang 2	2455	2477	2466	(+)	0.967	tttattCCATtttttaaatatta
V$ZF57	KRAB domain zinc finger protein 57	V$ZFP57.01	Krueppel-associated box-containing zinc-finger protein 57 (	23	35	29	(-)	0.966	tagTGCCgcaata
V$TALE	TALE homeodomain class recognizing TG	V$MEIS1.01	Binding site for monomeric Meis1 homeodomain protein	302	318	310	(+)	0.966	ccggggccTGTCatggg
V$NFAT	Nuclear factor of activated T-cells	V$NFAT.01	Nuclear factor of activated T-cells	476	494	485	(+)	0.966	aaaaaaGGAAaaaaaagag
V$ARID	AT rich interactive domain factor	V$ARID5A.01	AT rich interactive domain 5A (MRF1-like)	689	709	699	(+)	0.966	aggtaATATttgtgtagtagt
V$RUSH	SWI/SNF related nucleophosphoproteins v	V$SMARCA3.01	SWI/SNF related, matrix associated, actin dependent regula	859	869	864	(+)	0.966	ctCCATgtaat
V$BPTF	Bromodomain and PHD domain transcripti	V$FAC1.01	Fetal Alz-50 clone 1 (FAC1)	1214	1224	1219	(-)	0.966	aacatAACAca
V$BRAC	Brachyury gene, mesoderm development	V$EOMES.02	Eomesodermin, TBR-2 (secondary DNA binding preference	2372	2400	2386	(-)	0.966	actcaggacaGGTGttgcctcaagtgagt
V$HESF	Vertebrate homologues of enhancer of spl	V$DEC2.01	Basic helix-loop-helix protein known as Dec2, Sharp1 or BH	7	21	14	(+)	0.965	catgcaCATGtgtgt
V$RUSH	SWI/SNF related nucleophosphoproteins v	V$SMARCA3.01	SWI/SNF related, matrix associated, actin dependent regula	821	831	826	(+)	0.965	ccACATataat
V$MYBL	Cellular and viral myb-like transcriptional r	V$VMYB.02	v-Myb	934	954	944	(+)	0.965	ctttggctccAACGgggttgc
V$MYOD	Myoblast determining factors	V$E47.02	E47 homodimer	2382	2398	2390	(-)	0.965	tcaggacaGGTGttgcc
V$SATB	Special AT-rich sequence binding protein	V$SATB1.01	Special AT-rich sequence-binding protein 1, predominantly	462	476	469	(+)	0.964	aatAATAgtaaaaaa
V$SMAD	Vertebrate SMAD family of transcription fa	V$SMAD.01	Sma- and Mad-related proteins	719	729	724	(-)	0.964	ctgGTCTgcct
V$OCT1	Octamer binding protein	V$OCT1.02	Octamer-binding factor 1	1928	1942	1935	(-)	0.964	ggtATGCaaaggatg
V$EBOX	E-box binding factors	V$ATF6.01	Member of b-zip family, induced by ER damage/stress, bind	2161	2177	2169	(+)	0.964	cctgCCACtcttggtta
V$MYT1	MYT1 C2HC zinc finger protein	V$MYT1L.01	Myelin transcription factor 1-like, neuronal C2HC zinc finge	2343	2355	2349	(+)	0.964	tgaaAGCTttgaa
V$GREF	Glucocorticoid responsive and related ele	V$ARE.03	Androgene receptor binding site, IR3 sites	224	242	233	(+)	0.963	caagcaccacatGTTCtca
V$MEF3	MEF3 binding sites	V$SIX2.02	Sine oculis homeobox homolog 2	1395	1407	1401	(+)	0.963	agaTCAGcttccc
V$NDPK	Nucleoside diphosphate kinase	V$NM23.01	NME/NM23 nucleoside diphosphate kinase1 and 2	314	330	322	(+)	0.962	atGGGGtggggggaggg
O$INRE	Core promoter initiator elements	O$DINR.01	Drosophila initiator motifs	1041	1051	1046	(-)	0.962	tgTCATttctg
V$MYBL	Cellular and viral myb-like transcriptional r	V$CMYB.02	c-Myb, important in hematopoesis, cellular equivalent to avi	1763	1783	1773	(-)	0.962	ccagagaacAAACtgtccctg
V$NF1F	Nuclear factor 1	V$NF1.03	Non-palindromic nuclear factor I binding sites	1777	1797	1787	(-)	0.962	agtgctggaaaatGCCAgaga
V$AP2F	Activator protein 2	V$AP2.02	Activator protein 2 alpha	2025	2039	2032	(+)	0.962	atgGCCTtagggaaa
V$GATA	GATA binding factors	V$GATA1.06	Complex of Lmo2 bound to Tal-1, E2A proteins, and GATA-	2055	2067	2061	(-)	0.962	ttcaGATAgccat
V$CEBP	Ccaat/Enhancer Binding Protein	V$CEBPA.01	CCAAT/enhancer binding protein alpha	909	923	916	(-)	0.961	tgtgttgaGAAAgac
V$LTSM	Localized tandem sequence motif	V$LTSM.03	LTSM elements with 8 bp spacer	960	974	967	(+)	0.961	ATCCtgatatcatct
V$NFAT	Nuclear factor of activated T-cells	V$NFAT.01	Nuclear factor of activated T-cells	2122	2140	2131	(-)	0.961	ccctatGGAAaaaatcaga
V$HOXF	Paralog hox genes 1-8 from the four hox c	V$NANOG.01	Homeobox transcription factor Nanog	2661	2679	2670	(+)	0.961	taaaatgAATGtgagctgg
V$AP4R	AP4 and related proteins	V$AP4.03	Activating enhancer binding protein 4	885	901	893	(-)	0.96	cttgtcaGCTGtgaaca
V$LTFM	Lactotransferrin motif	V$LACTOFERRIN.01	Lactotransferrin and delta-lactoferrin, growth-inhibiting prote	1585	1593	1589	(-)	0.96	gGCACtttc
V$NF1F	Nuclear factor 1	V$NF1.03	Non-palindromic nuclear factor I binding sites	1897	1917	1907	(-)	0.96	aatcctaatctttGCCAagta
V$HOMF	Homeodomain transcription factors	V$BARX2.01	Barx2, homeobox transcription factor that preferentially bind	821	839	830	(+)	0.959	ccacataTAATggtttaaa
V$SORY	SOX/SRY-sex/testis determining and relat	V$SOX3.01	SRY-box containing gene 3	1441	1463	1452	(+)	0.959	ggtaaaCAAAtgaaaaacagaaa
V$BCDF	Bicoid-like homeodomain transcription fact	V$CRX.01	Cone-rod homeobox-containing transcription factor / otx-lik	1901	1917	1909	(-)	0.959	aatccTAATctttgcca
V$EVI1	EVI1-myleoid transforming protein	V$EVI1.07	Evi-1 zinc finger protein, carboxy-terminal zinc finger doma	2064	2080	2072	(+)	0.959	tgaagAAGAtgaccaca
V$ZTRE	Zinc transcriptional regulatory element	V$ZTRE.04	3' half site of ZTRE motif	2713	2729	2721	(+)	0.959	tggGGAGtgagaaggtg
V$STAT	Signal transducer and activator of transcri	V$STAT3.02	Signal transducer and activator of transcription 3	2817	2835	2826	(+)	0.959	gattTTCCaggcctcacag
V$MITF	Microphthalmia transcription factor	V$MIT.01	MIT (Microphthalmia transcription factor) and TFE3	227	241	234	(-)	0.958	gagaaCATGtggtgc
V$ZF07	C2H2 zinc finger transcription factors 7	V$ZNF263.01	Zinc finger protein 263, ZKSCAN12 (zinc finger protein with	320	334	327	(-)	0.958	gtcgccCTCCcccca
V$HOMF	Homeodomain transcription factors	V$BARX2.01	Barx2, homeobox transcription factor that preferentially bind	368	386	377	(+)	0.958	gacaagtTAATgcgtacag
V$EVI1	EVI1-myleoid transforming protein	V$EVI1.07	Evi-1 zinc finger protein, carboxy-terminal zinc finger doma	1483	1499	1491	(+)	0.958	gagcaAAGAtgaaaatt
V$HOMF	Homeodomain transcription factors	V$BARX2.01	Barx2, homeobox transcription factor that preferentially bind	2443	2461	2452	(-)	0.958	gaataaaTAATgattataa
V$BCDF	Bicoid-like homeodomain transcription fact	V$CRX.01	Cone-rod homeobox-containing transcription factor / otx-lik	2484	2500	2492	(-)	0.958	tctccTAATcaaacaaa
V$HOXF	Paralog hox genes 1-8 from the four hox c	V$NANOG.01	Homeobox transcription factor Nanog	369	387	378	(+)	0.957	acaagttAATGcgtacagc
V$HOMF	Homeodomain transcription factors	V$HHEX.01	Hematopoietically expressed homeobox, proline-rich home	543	561	552	(+)	0.957	ggcaaggcattTAATatag
V$NKXH	NKX homeodomain factors	V$NKX25.02	Homeo domain factor Nkx-2.5/Csx, tinman homolog low aff	1487	1505	1496	(-)	0.957	tgcctTAATtttcatcttt
V$NR2F	Nuclear receptor subfamily 2 factors	V$COUP.01	Chicken ovalbumin upstream promoter 1 (COUP-TFI) and	1604	1628	1616	(+)	0.957	gctgcaagggcaaAGGTcccgatgc
V$YY1F	Activator/repressor binding to transcriptior	V$YY1.02	Yin and Yang 1 repressor sites	855	877	866	(+)	0.956	ttttctCCATgtaataacccaga
V$PERO	Peroxisome proliferator-activated receptor	V$PPARG.02	Peroxisome proliferator-activated receptor gamma	1603	1625	1614	(+)	0.956	agctgcaagggcAAAGgtcccga
V$ARID	AT rich interactive domain factor	V$ARID5A.01	AT rich interactive domain 5A (MRF1-like)	682	702	692	(-)	0.955	cacaaATATtacctttttttt
V$CHRF	Cell cycle regulators: Cell cycle homology	V$CHR.01	Cell cycle gene homology region (CDE/CHR tandem eleme	1358	1370	1364	(+)	0.955	ctatTTGAaacat

V$CAAT	CCAAT binding factors	V$NFY.04	Nuclear factor Y (Y-box binding factor)	1820	1834	1827	(+)	0.955	gcacCCAAtgagtga
V$MYOD	Myoblast determining factors	V$MYOGENIN.03	Myogenic bHLH protein myogenin (myf4)	885	901	893	(+)	0.954	tgttcaCAGCtgacaag
V$AP1R	MAF and AP1 related factors	V$MAFA.01	Lens-specific Maf/MafA-sites	1364	1388	1376	(-)	0.954	cagtctgctgaatcTGCAatgtttc
V$STAT	Signal transducer and activator of transcri	V$STAT3.02	Signal transducer and activator of transcription 3	1620	1638	1629	(-)	0.954	gatcTTCCcGGAAcacggga
V$HAND	Twist subfamily of class B bHLH transcrip	V$TH1E47.01	Thing1/E47 heterodimer, TH1 bHLH member specific expre	2723	2743	2733	(-)	0.954	ccatgacatCCAGacaccttc
V$SORY	SOX/SRY-sex/testis determining and relat	V$SOX3.01	SRY-box containing gene 3	613	635	624	(+)	0.953	aacacaCAAAtgcggtgtgttgt
V$SORY	SOX/SRY-sex/testis determining and relat	V$HMGIY.01	HMGI(Y) high-mobility-group protein I (Y), architectural trar	2037	2059	2048	(+)	0.953	aaagAATTtgcggaaaagatggc
V$GATA	GATA binding factors	V$GATA3.02	GATA-binding factor 3	2850	2862	2856	(+)	0.953	gggAGATcttacg
V$HAML	Human acute myelogenous leukemia facto	V$AML2.01	RUNX3 (Runt-related transcription factor 3), AML2 (Acute r	429	443	436	(+)	0.952	cgtTGTGgtcatgta
V$HOMF	Homeodomain transcription factors	V$HHEX.01	Hematopoietically expressed homeobox, proline-rich home	581	599	590	(-)	0.952	gaaaacacattTAATgaat
V$STAT	Signal transducer and activator of transcri	V$STAT5B.01	Signal transducer and activator of transcription 5B	1405	1423	1414	(+)	0.952	cccgatcccAGAAagctgt
V$ZF07	C2H2 zinc finger transcription factors 7	V$ZNF263.02	Zinc finger protein 263, ZKSCAN12 (zinc finger protein with	1527	1541	1534	(+)	0.952	tggctcCTCCctttg
V$MYRF	Myelin regulatory factors	V$MYRF.01	Myelin regulatory factor	2692	2704	2698	(+)	0.952	atgtgCCAGctca
V$CLOX	CLOX and CLOX homology (CDP) factors	V$CDPCR3HD.01	Cut-like homeodomain protein (Cut Repeat III / homeodoma	62	84	73	(-)	0.951	ctatcattGATGgacatgtgggt
V$HOXF	Paralog hox genes 1-8 from the four hox c	V$NANOG.01	Homeobox transcription factor Nanog	572	590	581	(-)	0.951	tttaatgAATGtctactag
V$YY1F	Activator/repressor binding to transcriptior	V$YY1.02	Yin and Yang 1 repressor sites	647	669	658	(-)	0.951	tccttaCCATttgtcaagttagt
V$SF1F	Vertebrate steroidogenic factor	V$SF1.01	SF1 steroidogenic factor 1	1604	1618	1611	(+)	0.951	gctgCAAGggcaaag
V$CLOX	CLOX and CLOX homology (CDP) factors	V$CDPCR3HD.01	Cut-like homeodomain protein (Cut Repeat III / homeodoma	2277	2299	2288	(-)	0.951	agtaaattGATGaccaagaaggc
V$CHRF	Cell cycle regulators: Cell cycle homology	V$CHR.01	Cell cycle gene homology region (CDE/CHR tandem eleme	2578	2590	2584	(+)	0.951	aattTTGAattcc
V$FKHD	Fork head domain factors	V$FOXJ1.01	Forkhead box J1	14	30	22	(-)	0.95	ccgcaataAACAcacat
V$MYT1	MYT1 C2HC zinc finger protein	V$MYT1L.01	Myelin transcription factor 1-like, neuronal C2HC zinc finge	1414	1426	1420	(+)	0.95	agaaAGCTgtatt
V$GATA	GATA binding factors	V$GATA3.02	GATA-binding factor 3	1713	1725	1719	(+)	0.95	aagAGATcagaaa
V$ZF02	C2H2 zinc finger transcription factors 2	V$ZBP89.01	Zinc finger transcription factor ZBP-89	2838	2860	2849	(-)	0.95	taagatctCCCCccaaaaaacac
V$ARID	AT rich interactive domain factor	V$ARID5A.01	AT rich interactive domain 5A (MRF1-like)	1314	1334	1324	(-)	0.949	tataaATATttattgaataac
O$VTBP	Vertebrate TATA binding protein factor	O$VTATA.01	Cellular and viral TATA box elements	1321	1337	1329	(-)	0.949	gtctaTAAAtatttatt
V$ARID	AT rich interactive domain factor	V$ARID5A.01	AT rich interactive domain 5A (MRF1-like)	1321	1341	1331	(+)	0.949	aataaATATttatagactact
V$LEFF	LEF1/TCF	V$LEF1.02	TCF/LEF-1, involved in the Wnt signal transduction pathwa	2696	2712	2704	(+)	0.949	gccagctCAAAgttaaa
V$BRNF	Brn POU domain factors	V$TST1.01	POU-factor Tst-1/Oct-6	85	103	94	(+)	0.948	actggATTAaaaagatgtg
V$P53F	p53 tumor suppressor	V$P53.02	Tumor suppressor p53 (5' half site)	1028	1052	1040	(-)	0.948	gtgtcatttctgagtCATGtcctta
V$HAND	Twist subfamily of class B bHLH transcrip	V$TWIST.01	TWIST homolog of drosophila	223	243	233	(-)	0.947	gtgagaaCATGtggtgcttgg
V$SORY	SOX/SRY-sex/testis determining and relat	V$SOX3.01	SRY-box containing gene 3	651	673	662	(+)	0.947	acttgaCAAAtggtaaggataaa
V$GREF	Glucocorticoid responsive and related ele	V$ARE.02	Androgene receptor binding site, IR3 sites	1981	1999	1990	(+)	0.947	attgttcttagtGTCCttg
V$ETSF	Human and murine ETS1 factors	V$FLI1.03	Friend leukemia virus integration 1	975	995	985	(+)	0.946	aggtagcgGGAAgggggataa
V$BHLH	bHLH transcription factors expressed in m	V$MESP1_2.01	Mesoderm posterior 1 and 2	1443	1455	1449	(+)	0.946	taaaCAAAtgaaa
V$CEBP	Ccaat/Enhancer Binding Protein	V$CEBPB.01	CCAAT/enhancer binding protein beta	2584	2598	2591	(-)	0.946	agtgttttGGAAttc
V$MYT1	MYT1 C2HC zinc finger protein	V$MYT1L.01	Myelin transcription factor 1-like, neuronal C2HC zinc finge	197	209	203	(-)	0.945	ggatAGTTtgctg
V$KLFS	Krueppel like transcription factors	V$KLF6.01	Core promoter-binding protein (CPBP) with 3 Krueppel-type	317	335	326	(+)	0.945	gggtggGGGGagggcgacg
V$KLFS	Krueppel like transcription factors	V$BKLF.02	Kruppel-like factor 3 (basic)	319	337	328	(+)	0.945	gtggggGGAGggcgacggg
V$SATB	Special AT-rich sequence binding protein	V$SATB1.01	Special AT-rich sequence-binding protein 1, predominantly	459	473	466	(+)	0.945	tttAATAatagtaaa
V$PBXC	PBX - MEIS complexes	V$PBX3.01	Pre-B-cell leukemia homeobox 3	1511	1527	1519	(+)	0.945	gaaatgagCGACtgggt
V$AP2F	Activator protein 2	V$TCFAP2A.01	Transcription factor AP-2, alpha	2025	2039	2032	(-)	0.945	tttccctaAGGCcat
V$HAND	Twist subfamily of class B bHLH transcrip	V$TH1E47.01	Thing1/E47 heterodimer, TH1 bHLH member specific expre	2143	2163	2153	(-)	0.945	aggctgatgCCAGatctgcta
V$CDXF	Vertebrate caudal related homeodomain p	V$CDX1.01	Intestine specific homeodomain factor CDX-1	2639	2657	2648	(-)	0.945	gccatgtTTTAggaaggac
V$LTSM	Localized tandem sequence motif	V$LTSM.02	LTSM elements with 6 bp spacer	79	93	86	(-)	0.944	taatccagtcTATCa
V$AP2F	Activator protein 2	V$TCFAP2A.02	Transcription factor AP-2, alpha	1857	1871	1864	(+)	0.944	aagaCCTGaggctgt
V$ARID	AT rich interactive domain factor	V$ARID5A.01	AT rich interactive domain 5A (MRF1-like)	2467	2487	2477	(+)	0.944	tttaaATATtagtgcattttg
V$SORY	SOX/SRY-sex/testis determining and relat	V$SOX3.01	SRY-box containing gene 3	472	494	483	(+)	0.943	aaaaaaAAAAggaaaaaaaagag
V$HAML	Human acute myelogenous leukemia facto	V$AML2.01	RUNX3 (Runt-related transcription factor 3), AML2 (Acute r	2069	2083	2076	(-)	0.943	agaTGTGgtcatctt
V$YY1F	Activator/repressor binding to transcriptior	V$YY1.02	Yin and Yang 1 repressor sites	2640	2662	2651	(-)	0.943	tagctgCCATgttttaggaagga
O$VTBP	Vertebrate TATA binding protein factor	O$VTATA.02	Mammalian C-type LTR TATA box	131	147	139	(+)	0.942	agccaTAAAaatggatg
V$GATA	GATA binding factors	V$GATA1.04	GATA-binding factor 1	333	345	339	(+)	0.942	acggGATAacatt
V$XBBF	X-box binding factors	V$RFX5.01	Regulatory factor X, 5 (influences HLA class II expression)	747	765	756	(-)	0.942	agtctttttcAGCAactta
V$STAT	Signal transducer and activator of transcri	V$STAT5B.01	Signal transducer and activator of transcription 5B	1033	1051	1042	(+)	0.942	acatgactcAGAAatgaca
V$SIX3	Sine oculis homeobox homolog 3	V$SIX3.02	SIX3 / SIXdomain (SD) and Homeodomain (HD) transcriptic	1148	1168	1158	(-)	0.942	ctgtcttTAATaagagcactc
V$SORY	SOX/SRY-sex/testis determining and relat	V$HBP1.02	HMG box-containing protein 1	1830	1852	1841	(+)	0.942	agtgatgAATGaacaaactaaaa
V$SF1F	Vertebrate steroidogenic factor	V$FTF.02	Alpha (1)-fetoprotein transcription factor (FTF), liver recept	1989	2003	1996	(-)	0.942	ctaccAAGGacacta
V$MEF3	MEF3 binding sites	V$SIX2.02	Sine oculis homeobox homolog 2	2566	2578	2572	(-)	0.942	tttTCAGatttta
V$IRXF	Iroquois homeobox transcription factors	V$IRX5.01	Iroquois homeobox 5	398	410	404	(+)	0.941	ggcaCATGtatac
V$XBBF	X-box binding factors	V$RFX5.01	Regulatory factor X, 5 (influences HLA class II expression)	947	965	956	(-)	0.94	caggatccaaAGCAacccc
V$HOXF	Paralog hox genes 1-8 from the four hox c	V$NANOG.01	Homeobox transcription factor Nanog	2684	2702	2693	(+)	0.94	tgtggttAATGtgccagct
V$IRXF	Iroquois homeobox transcription factors	V$IRX5.01	Iroquois homeobox 5	397	409	403	(-)	0.939	tataCATGtgcca
V$BHLH	bHLH transcription factors expressed in m	V$MESP1_2.01	Mesoderm posterior 1 and 2	507	519	513	(+)	0.939	gactCATAtgtct
V$SORY	SOX/SRY-sex/testis determining and relat	V$HBP1.02	HMG box-containing protein 1	572	594	583	(-)	0.939	cacatttAATGaatgtctactag
V$E2FF	E2F-myc activator/cell cycle regulator	V$E2F6.01	E2F transcription factor 6	975	991	983	(+)	0.936	aggtaGCGGgaaggggg
V$SORY	SOX/SRY-sex/testis determining and relat	V$HMGIY.01	HMGI(Y) high-mobility-group protein I (Y), architectural trar	1004	1026	1015	(-)	0.936	aagaAATTtacatcctcccttcc
V$ETSF	Human and murine ETS1 factors	V$ERG.02	v-ets erythroblastosis virus E26 oncogene homolog	1877	1897	1887	(-)	0.936	aaagcaaaGGAAagctatgag
V$CEBP	Ccaat/Enhancer Binding Protein	V$CEBP.02	CCAAT/enhancer binding protein	1245	1259	1252	(-)	0.935	tgttttttGAAAgcc

V$EBOX	E-box binding factors	V$MYCMAX.02	c-Myc/Max heterodimer	226	242	234	(+)	0.934	agcacaaCACGtGctac
V$CDXF	Vertebrate caudal related homeodomain p	V$CDX2.03	Caudal type homeobox transcription factor 2	1322	1340	1331	(+)	0.934	ataaatatTTATagactac
V$NDPK	Nucleoside diphosphate kinase	V$NM23.01	NME/NM23 nucleoside diphosphate kinase1 and 2	321	337	329	(+)	0.933	ggGGGGagggcgacggg
V$LHXF	Lim homeodomain factors	V$LMX1A.02	LIM homeobox transcription factor 1, alpha	452	474	463	(+)	0.933	cttaaagtTTAAtaatagtaaaa
V$MEF2	MEF2, myocyte-specific enhancer binding	V$SL1.01	Member of the RSRF (related to serum response factor) pr	454	476	465	(-)	0.933	ttttttaCTATtattaaacttta
V$ETSF	Human and murine ETS1 factors	V$ERG.02	v-ets erythroblastosis virus E26 oncogene homolog	588	608	598	(-)	0.933	aaagagaaGGAAaacacattt
V$ETSF	Human and murine ETS1 factors	V$ERG.02	v-ets erythroblastosis virus E26 oncogene homolog	636	656	646	(+)	0.933	gggacacaGGAActaacttga
V$NEUR	NeuroD, Beta2, HLH domain	V$NEUROG.01	Neurogenin 1 and 3 (ngn1/3) binding sites	652	666	659	(-)	0.933	ttaCCATttgtcaag
V$LHXF	Lim homeodomain factors	V$LMX1A.02	LIM homeobox transcription factor 1, alpha	1148	1170	1159	(-)	0.933	ccctgtctTTAAtaagagcactc
V$HMTB	Human muscle-specific Mt binding site	V$MTBF.01	Muscle-specific Mt binding site	1470	1478	1474	(-)	0.933	tggtATCTa
V$ETSF	Human and murine ETS1 factors	V$FLI1.02	Friend leukemia virus integration 1	1592	1612	1602	(+)	0.933	cctgcacgGGAAgctgcaagg
V$GREF	Glucocorticoid responsive and related ele	V$ARE.02	Androgene receptor binding site, IR3 sites	446	464	455	(-)	0.932	attaaactttaaGTTCtag
V$NKXH	NKX homeodomain factors	V$NKX31.01	Prostate-specific homeodomain protein NKX3.1	2288	2306	2297	(-)	0.932	acagatAAGTaaattgatg
V$PARF	PAR/bZIP family	V$TEF.01	Thyrotrophic embryonic factor	2532	2548	2540	(+)	0.932	atttataatGTAAttta
V$NFAT	Nuclear factor of activated T-cells	V$NFAT5.02	Nuclear factor of activated T-cells 5	2810	2828	2819	(-)	0.932	gcctGGAAaatcctcctac
V$FAST	FAST-1 SMAD interacting proteins	V$FAST1.01	FAST-1 SMAD interacting protein	14	30	22	(+)	0.931	atgtgtgttTATTgcgg
V$LHXF	Lim homeodomain factors	V$LMX1A.02	LIM homeobox transcription factor 1, alpha	1487	1509	1498	(-)	0.931	ccattgccTTAAttttcatcttt
V$MYT1	MYT1 C2HC zinc finger protein	V$MYT1L.01	Myelin transcription factor 1-like, neuronal C2HC zinc finge	1766	1778	1772	(+)	0.931	ggacAGTTtgttc
V$MYT1	MYT1 C2HC zinc finger protein	V$MYT1L.01	Myelin transcription factor 1-like, neuronal C2HC zinc finge	1877	1889	1883	(-)	0.931	ggaaAGCTatgag
V$GATA	GATA binding factors	V$GATA2.01	GATA-binding factor 2	664	676	670	(+)	0.93	taagGATAaaata
V$SORY	SOX/SRY-sex/testis determining and relat	V$SRY.01	Sex-determining region Y gene product	674	696	685	(+)	0.93	ataaaACAAaaaaaaaggtaata
V$ESRR	Estrogen-related receptors	V$ESRRA.03	Estrogen-related receptor alpha	1988	2010	1999	(-)	0.93	cactgggctaccAAGGacactaa
V$NKXH	NKX homeodomain factors	V$NKX31.01	Prostate-specific homeodomain protein NKX3.1	2432	2450	2441	(-)	0.93	gattatAAGTagtttcatg
V$ETSF	Human and murine ETS1 factors	V$FLI1.03	Friend leukemia virus integration 1	2505	2525	2515	(-)	0.93	actcccctGGAAgggtctatg
O$VTBP	Vertebrate TATA binding protein factor	O$VTATA.01	Cellular and viral TATA box elements	2537	2553	2545	(-)	0.93	cattaTAAAttacatta
V$ABDB	Abdominal-B type homeodomain transcrip	V$HOXC13.01	Homeodomain transcription factor HOXC13	1314	1330	1322	(+)	0.929	gttattcaaTAAAtatt
V$E2FF	E2F-myc activator/cell cycle regulator	V$E2F6.01	E2F transcription factor 6	1570	1586	1578	(+)	0.929	gaagaGCGGgaagcaga
V$ETSF	Human and murine ETS1 factors	V$ELF1.01	E74-like factor 1	1649	1669	1659	(+)	0.929	tgtgacacGGAAgggctggtg
V$CHRF	Cell cycle regulators: Cell cycle homology	V$CHR.01	Cell cycle gene homology region (CDE/CHR tandem eleme	2183	2195	2189	(+)	0.929	aagtTTGAagagg
V$ETSF	Human and murine ETS1 factors	V$SPI1.04	SPI-1 proto-oncogene; hematopoietic transcription factor P	281	301	291	(+)	0.928	caggaagaGGAAcctcacaca
V$THAP	THAP domain containing protein	V$THAP1.01	THAP domain containing, apoptosis associated protein	537	547	542	(+)	0.928	attacaGGCAa
V$ABDB	Abdominal-B type homeodomain transcrip	V$HOXD10.01	Homeobox D10	667	683	675	(+)	0.928	ggataaaaTAAAacaaa
V$BRNF	Brn POU domain factors	V$BRN2.03	Brn-2, POU-III protein class	2284	2302	2293	(+)	0.928	tggtcatcaATTTacttat
V$NR2F	Nuclear receptor subfamily 2 factors	V$HNF4A.01	Hepatic nuclear factor 4alpha, DR1 sites	148	172	160	(-)	0.927	catgtccctaCAAAggacatgaact
V$MITF	Microphthalmia transcription factor	V$MIT.01	MIT (Microphthalmia transcription factor) and TFE3	396	410	403	(-)	0.927	gtataCATGtgccat
V$BHLH	bHLH transcription factors expressed in m	V$MESP1_2.01	Mesoderm posterior 1 and 2	508	520	514	(-)	0.927	tagaCATAtgagt
V$HEAT	Heat shock factors	V$HSF1.05	Heat shock factor 1	2589	2613	2601	(+)	0.927	ccaaaacactgggcttCAAGaattt
V$KLFS	Krueppel like transcription factors	V$KKLF.01	Kidney-enriched kruppel-like factor, KLF15	314	332	323	(+)	0.926	atggggtggGGGGagggcg
V$TALE	TALE homeodomain class recognizing TG	V$TGIF2LX.01	TGFB-induced factor homeobox 2-like, X-linked, dimeric bi	887	903	895	(+)	0.926	ttcacagctGACAaggc
V$CHRF	Cell cycle regulators: Cell cycle homology	V$CHR.01	Cell cycle gene homology region (CDE/CHR tandem eleme	1108	1120	1114	(+)	0.926	acacTTGAactgg
V$HNF6	Onecut homeodomain factor HNF6	V$HNF6.02	Liver enriched Cut - Homeodomain transcription factor HNI	67	83	75	(+)	0.925	catgtccatCAATgata
V$GREF	Glucocorticoid responsive and related ele	V$GRE.02	Glucocorticoid receptor, IR3 sites	224	242	233	(-)	0.925	tgaGAACatgtggtgcttg
V$NEUR	NeuroD, Beta2, HLH domain	V$NEUROG.01	Neurogenin 1 and 3 (ngn1/3) binding sites	266	280	273	(-)	0.925	tgtCCATgtgttctc
V$CREB	cAMP-responsive element binding proteins	V$CREB1.02	cAMP-responsive element binding protein 1	492	512	502	(-)	0.925	tgagtCTGAtgtcattttctc
V$NFAT	Nuclear factor of activated T-cells	V$NFAT5.02	Nuclear factor of activated T-cells 5	1777	1795	1786	(-)	0.925	tgctGGAAaatgccagaga
V$P53F	p53 tumor suppressor	V$P53.02	Tumor suppressor p53 (5' half site)	137	161	149	(+)	0.924	aaaaatggatgagttCATGtccttt
V$GATA	GATA binding factors	V$GATA3.02	GATA-binding factor 3	1486	1498	1492	(+)	0.924	caaAGATgaaaat
V$STEM	Motif composed of binding sites for pluripo	V$OCT3_4.02	POU domain, class 5, transcription factor 1	1929	1947	1938	(+)	0.924	atcctttGCATacctctcg
V$NF1F	Nuclear factor 1	V$NF1.04	Nuclear factor 1	50	70	60	(-)	0.923	catgtgggttggttCCAAgtc
V$HOXH	HOX - MEIS1 heterodimers	V$MEIS1B_HOXA9.01	Meis1b and Hoxa9 form heterodimeric binding complexes c	367	381	374	(+)	0.923	TGACaagttaatgcg
V$AP2F	Activator protein 2	V$AP2.02	Activator protein 2 alpha	1857	1871	1864	(-)	0.923	acaGCCTcaggtctt
V$MITF	Microphthalmia transcription factor	V$MIT.01	MIT (Microphthalmia transcription factor) and TFE3	1	15	8	(-)	0.922	atgtgCATGtgtctt
V$BHLH	bHLH transcription factors expressed in m	V$MESP1_2.01	Mesoderm posterior 1 and 2	615	627	621	(+)	0.922	cacaCAAAtgcgg
V$HOMF	Homeodomain transcription factors	V$HMX3.02	Hmx3/Nkx5-1 homeodomain transcription factor	548	566	557	(-)	0.921	agggactataTTAAatgcc
V$MYOD	Myoblast determining factors	V$MYOD.02	Myogenic regulatory factor MyoD (myf3)	886	902	894	(-)	0.921	ccttgtCAGCtgtgaac
V$P53F	p53 tumor suppressor	V$P53.03	Tumor suppressor p53 (3' half site)	61	85	73	(-)	0.92	tctatcattgatggaCATGtgggtt
V$IRXF	Iroquois homeobox transcription factors	V$IRX5.01	Iroquois homeobox 5	229	241	235	(+)	0.92	accaCATGttctc
V$LHXF	Lim homeodomain factors	V$ISL2.01	ISL LIM homeobox 2	574	596	585	(+)	0.92	agtagacattcATTAaatgtgtt
V$PERO	Peroxisome proliferator-activated receptor	V$PPARG.02	Peroxisome proliferator-activated receptor gamma	982	1004	993	(+)	0.92	gggaagggggatAAAGgccaggg
V$GLIF	GLI zinc finger family	V$ZIC2.01	Zinc finger transcription factor, Zic family member 2 (odd-pa	1534	1550	1542	(-)	0.92	ctaaccaCCCAaaggga
V$BRAC	Brachyury gene, mesoderm development	V$TBX20.02	T-box transcription factor TBX20	1857	1885	1871	(+)	0.92	aagacctgaggctgttGACActcatagct
V$HOMF	Homeodomain transcription factors	V$HMX3.02	Hmx3/Nkx5-1 homeodomain transcription factor	2703	2721	2712	(-)	0.92	cactccccatTTAActttg
V$IRXF	Iroquois homeobox transcription factors	V$IRX5.01	Iroquois homeobox 5	228	240	234	(-)	0.919	agaaCATGtggtg
V$PARF	PAR/bZIP family	V$VBP.01	PAR-type chicken vitellogenin promoter-binding protein	406	422	414	(+)	0.919	tatacctatGTAAcaaa
V$PARF	PAR/bZIP family	V$TEF.01	Thyrotrophic embryonic factor	2520	2536	2528	(+)	0.919	gggagttatATAAttta
V$GATA	GATA binding factors	V$GATA3.02	GATA-binding factor 3	2564	2576	2570	(-)	0.919	ttcAGATtttaag
V$NBRE	NGFI-B response elements, nur subfamily	V$NUR77.01	Nuclear hormone receptor NUR77 (NR4A1)	684	698	691	(+)	0.918	aaaaaagGTAAtatt

V$HNF1	Hepatic Nuclear Factor 1	V$HMBOX.01	Homeobox containing 1	2010	2026	2018	(+)	0.918	gtcccctgGTTAaaaat
V$HOXC	HOX - PBX complexes	V$HOXC9.02	Member of the vertebrate HOX - cluster of homeobox facto	2538	2554	2546	(+)	0.918	aatgtaaTTTAtaatgg
V$HAND	Twist subfamily of class B bHLH transcrip	V$PARAXIS.01	Paraxis (TCF15), member of the Twist subfamily of Class	224	244	234	(+)	0.917	caagcACCAcatgttctcact
V$FKHD	Fork head domain factors	V$HNF3B.03	Hepatic nuclear factor 3 beta (FOXA2)	464	480	472	(+)	0.917	taatagTAAAaaaaaaa
V$ZF02	C2H2 zinc finger transcription factors 2	V$ZNF219.01	Kruppel-like zinc finger protein 219	974	996	985	(-)	0.917	tttatCCCCcttcccgctaccta
V$NKX6	NK6 homeobox transcription factors	V$NKX61.01	NK6 homeobox 1	1491	1505	1498	(-)	0.917	tgccTTAAttttcat
V$NF1F	Nuclear factor 1	V$NFIB.01	Nuclear factor I/B	1546	1566	1556	(+)	0.917	gttagggaagtcaGCCAggca
V$ARID	AT rich interactive domain factor	V$JARID2.01	Jumonji, AT rich interactive domain 2 (JMJ)	1837	1857	1847	(-)	0.917	ttatctTTTAgtttgttcatt
V$HOXC	HOX - PBX complexes	V$HOXC9.02	Member of the vertebrate HOX - cluster of homeobox facto	2526	2542	2534	(+)	0.917	tatataaTTTAtaatgt
V$ZF03	C2H2 zinc finger transcription factors 3	V$ZNF217.01	Zinc finger protein 217	183	195	189	(-)	0.916	GAATgatggttgc
V$MYRF	Myelin regulatory factors	V$MYRF.01	Myelin regulatory factor	561	573	567	(-)	0.916	aggtaCCAGggac
V$FKHD	Fork head domain factors	V$XFD2.01	Xenopus fork head domain factor 2 (FoxI1a)	1322	1338	1330	(-)	0.916	agtctaTAAAtatttat
V$GFI1	Growth factor independence transcriptiona	V$GFI1.02	Growth factor independence 1	1790	1804	1797	(-)	0.916	tgcAATCagtgctgg
V$NFAT	Nuclear factor of activated T-cells	V$NFAT5.01	Nuclear factor of activated T-cells 5	2120	2138	2129	(-)	0.916	ctatGGAAaaaatcagaat
V$ABDB	Abdominal-B type homeodomain transcrip	V$HOXC9.01	Homeobox C9 / Hox-3beta	2282	2298	2290	(+)	0.916	cttggtcaTCAAtttac
O$VTBP	Vertebrate TATA binding protein factor	O$VTATA.01	Cellular and viral TATA box elements	2525	2541	2533	(-)	0.916	cattaTAAAttatataa
V$ABDB	Abdominal-B type homeodomain transcrip	V$HOXC13.01	Homeodomain transcription factor HOXC13	578	594	586	(+)	0.915	gacattcatTAAAtgtg
V$NKX6	NK6 homeobox transcription factors	V$NKX61.01	NK6 homeobox 1	1152	1166	1159	(-)	0.915	gtctTTAAtaagagc
V$ETSF	Human and murine ETS1 factors	V$SPI1.03	SPI-1 proto-oncogene; hematopoietic transcription factor P	1502	1522	1512	(+)	0.915	ggcaatggGGAAatgagcgac
V$HESF	Vertebrate homologues of enhancer of spl	V$HELT.01	Hey-like bHLH-transcriptional repressor	1592	1606	1599	(+)	0.915	cctgCACGggaagct
V$FKHD	Fork head domain factors	V$HNF3B.02	Hepatic nuclear factor 3beta (FOXA2)	2481	2497	2489	(-)	0.915	cctaatCAAAcaaaatg
V$BRNF	Brn POU domain factors	V$BRN3.01	Brn-3, POU-IV protein class	2524	2542	2533	(-)	0.915	acattataaATTAtataac
V$ZF02	C2H2 zinc finger transcription factors 2	V$ZBTB7.03	Zinc finger and BTB domain containing 7A, pokemon	314	336	325	(-)	0.914	ccgtcGCCCtccccccaccccat
V$HOXC	HOX - PBX complexes	V$HOXC9.02	Member of the vertebrate HOX - cluster of homeobox facto	2448	2464	2456	(+)	0.914	atcattaTTTAttccat
V$NKX6	NK6 homeobox transcription factors	V$NKX63.01	NK6 homeobox 3	579	593	586	(-)	0.913	acattTAATgaatgt
V$FKHL16	Fork head domain factors	V$FOXM1.01	Forkhead box protein M1	1864	1880	1872	(-)	0.913	AgaTgGAcT
V$NKX6	NK6 homeobox transcription factors	V$NKX61.01	NK6 homeobox 1	456	470	463	(+)	0.912	aagtTTAAtaatagt
V$CART	Cart-1 (cartilage homeoprotein 1)	V$PHOX2.01	Phox2a (ARIX) and Phox2b	508	528	518	(-)	0.912	tctccTAATagacatatgagt
V$P53F	p53 tumor suppressor	V$TP63.02	Tumor protein p63	637	661	649	(+)	0.912	ggacacaggaactaaCTTGacaaat
V$ZF07	C2H2 zinc finger transcription factors 7	V$ZNF263.02	Zinc finger protein 263, ZKSCAN12 (zinc finger protein with	1004	1018	1011	(-)	0.912	tacatcCTCCcttcc
V$GFI1	Growth factor independence transcriptiona	V$GFI1.02	Growth factor independence 1	1075	1089	1082	(+)	0.912	ccaAATCcatgctgt
V$GFI1	Growth factor independence transcriptiona	V$GFI1.02	Growth factor independence 1	2353	2367	2360	(-)	0.912	aaaAATCttagtttc
O$PTBP	Plant TATA binding protein factor	O$PTATA.02	Plant TATA box	2540	2554	2547	(-)	0.912	ccatTATAaattaca
V$LHXF	Lim homeodomain factors	V$LMX1B.01	LIM-homeodomain transcription factor	448	470	459	(+)	0.911	agaacttaaagttTAATaatagt
V$KLFS	Krueppel like transcription factors	V$EKLF.01	Erythroid krueppel like factor (EKLF)	2506	2524	2515	(-)	0.911	ctcccctggaaGGGTctat
V$BHLH	bHLH transcription factors expressed in m	V$MESP1_2.01	Mesoderm posterior 1 and 2	267	279	273	(+)	0.91	agaaCACAtggac
V$MEF2	MEF2, myocyte-specific enhancer binding	V$SL1.01	Member of the RSRF (related to serum response factor) pr	1320	1342	1331	(-)	0.91	aagtagtCTATaaatatttattg
V$HNF6	Onecut homeodomain factor HNF6	V$HNF6.02	Liver enriched Cut - Homeodomain transcription factor HN	2282	2298	2290	(+)	0.91	cttggtcatCAATttac
V$DLXF	Distal-less homeodomain transcription fac	V$DLX1.01	DLX-1, -2, and -5 binding sites	2521	2539	2530	(+)	0.91	ggagttatatAATTtataa
V$TEAF	TEA/ATTS DNA binding domain factors	V$TEAD.01	TEA domain-containing factors, transcriptional enhancer fa	1831	1843	1837	(-)	0.908	gttCATTcatcac
V$LEFF	LEF1/TCF	V$LEF1.01	TCF/LEF-1, involved in the Wnt signal transduction pathwa	1884	1900	1892	(-)	0.908	agtaaagCAAAggaaag
V$TALE	TALE homeodomain class recognizing TG	V$TGIF2LX.01	TGFB-induced factor homeobox 2-like, X-linked, dimeric bi	2383	2399	2391	(+)	0.908	gcaacacctGTCCtgag
V$TALE	TALE homeodomain class recognizing TG	V$TGIF2LX.01	TGFB-induced factor homeobox 2-like, X-linked, dimeric bi	2673	2689	2681	(-)	0.908	accacaactGCCAgctc
V$PEG3	Imprinted transcription factor PEG3	V$PEG3.01	Paternally expressed 3	780	794	787	(-)	0.907	cagtaccctaTGCCt
V$NF1F	Nuclear factor 1	V$NFIB.01	Nuclear factor I/B	985	1005	995	(+)	0.907	aagggggataaagGCCAgggg
V$ETSF	Human and murine ETS1 factors	V$SPI1.03	SPI-1 proto-oncogene; hematopoietic transcription factor P	1543	1563	1553	(+)	0.907	gtggttagGGAAgtcagccag
V$AP1F	AP1, Activating protein 1	V$AP1.02	Activator protein 1	1825	1837	1831	(+)	0.907	caatGAGTgatga
V$MYBL	Cellular and viral myb-like transcriptional r	V$CMYB.01	c-Myb, important in hematopoesis, cellular equivalent to avi	795	815	805	(-)	0.906	tcttagttaCAACagctaggc
V$ZF03	C2H2 zinc finger transcription factors 3	V$ZNF217.01	Zinc finger protein 217	26	38	32	(-)	0.905	GAATagtgccgca
V$IRFF	Interferon regulatory factors	V$ISRE.02	Interferon-stimulated response element	480	504	492	(+)	0.905	aaggaaaaaaaagaGAAAatgacat
V$PAX6	PAX-4/PAX-6 paired domain binding sites	V$PAX6.04	PAX6 paired domain binding site	2034	2052	2043	(-)	0.905	tttCCGCaaattctttccc
V$OCT1	Octamer binding protein	V$OCT1.05	Octamer-binding factor 1	2430	2444	2437	(+)	0.905	gaCATGaaactactt
V$EVI1	EVI1-myleoid transforming protein	V$EVI1.07	Evi-1 zinc finger protein, carboxy-terminal zinc finger doma	91	107	99	(+)	0.904	ttaaaAAGAtgtggcac
V$MYC	E-box binding factors	V$MYC.03	c-Myc	960	1019	967	(-)	0.904	tggcCACGTG
V$MAZF	Myc associated zinc fingers	V$MAZR.01	MYC-associated zinc finger protein related transcription fac	315	327	321	(+)	0.904	tggggtGGGGgga
V$PARF	PAR/bZIP family	V$VBP.01	PAR-type chicken vitellogenin promoter-binding protein	353	369	361	(+)	0.904	acacctaatGTAAatga
V$ZF03	C2H2 zinc finger transcription factors 3	V$ZNF217.01	Zinc finger protein 217	877	889	883	(-)	0.904	GAACagtttactt
V$DMRT	DM domain-containing transcription factor	V$DMRT4.01	Doublesex and mab-3 related transcription factor 4	1357	1377	1367	(+)	0.904	actatttgaAACAttgcagat
V$MYBL	Cellular and viral myb-like transcriptional r	V$CMYB.01	c-Myb, important in hematopoesis, cellular equivalent to avi	2100	2120	2110	(+)	0.904	tattctgttCAACagctccca
V$ABDB	Abdominal-B type homeodomain transcrip	V$HOXB9.01	Abd-B-like homeodomain protein Hoxb-9	2779	2795	2787	(+)	0.904	tgagatggTAAAatgtg
V$BRNF	Brn POU domain factors	V$TST1.01	POU-factor Tst-1/Oct-6	365	383	374	(-)	0.903	tacgcATTAacttgtcatt
V$DMRT	DM domain-containing transcription factor	V$DMRT3.01	Doublesex and mab-3 related transcription factor 3	406	426	416	(-)	0.903	caggtttgtTACAtaggtata
V$MYT1	MYT1 C2HC zinc finger protein	V$MYT1.02	MyT1 zinc finger transcription factor involved in primary ne	765	777	771	(-)	0.903	cagAAGTttttaa
V$NOLF	Neuron-specific olfactory factor	V$EBF1.01	Early B-cell factor 1	2507	2529	2518	(-)	0.903	tataacTCCCctggaagggtcta
O$PTBP	Plant TATA binding protein factor	O$PTATA.02	Plant TATA box	2528	2542	2535	(-)	0.903	acatTATAaattata
V$SORY	SOX/SRY-sex/testis determining and relat	V$SOX7.01	SRY-related HMG-box gene 7	34	56	45	(+)	0.902	tattcACAAtagcaaagacttgg
V$BRNF	Brn POU domain factors	V$TST1.01	POU-factor Tst-1/Oct-6	829	847	838	(+)	0.902	aatggTTTAaaaagatggg

O$VTBP	Vertebrate TATA binding protein factor	O$VTATA.01	Cellular and viral TATA box elements	2518	2534	2526	(-)	0.902	aattaTATAactcccct
V$PARF	PAR/bZIP family	V$VBP.01	PAR-type chicken vitellogenin promoter-binding protein	2521	2537	2529	(-)	0.902	ataaattatATAActcc
V$ABDB	Abdominal-B type homeodomain transcrip	V$HOXB9.01	Abd-B-like homeodomain protein Hoxb-9	2558	2574	2566	(+)	0.902	atacttctTAAAatctg
V$LEFF	LEF1/TCF	V$LEF1.04	TCF/LEF-1 (secondary DNA binding preference)	69	85	77	(+)	0.901	tgtccaTCAAtgataga
V$FAST	FAST-1 SMAD interacting proteins	V$FAST1.01	FAST-1 SMAD interacting protein	510	526	518	(+)	0.901	tcatatgtcTATTagga
V$GFI1	Growth factor independence transcription	V$GFI1.02	Growth factor independence 1	525	539	532	(+)	0.901	gagAATCaaagtatt
V$OCT1	Octamer binding protein	V$OCT1.04	Octamer-binding factor 1	922	936	929	(-)	0.901	aaGATGgaaatcctg
V$HMTB	Human muscle-specific Mt binding site	V$MTBF.01	Muscle-specific Mt binding site	1206	1214	1210	(-)	0.901	aggtATGTg
V$CEBP	Ccaat/Enhancer Binding Protein	V$CEBPG.01	CCAAT/enhancer binding protein (C/EBP), gamma	2040	2054	2047	(+)	0.901	gaatTTGCggaaaag
V$PAX5	PAX-2/5/8 binding sites	V$PAX8.01	PAX 2/5/8 binding site	2417	2445	2431	(+)	0.901	ggaaggaaaacTTGAcatgaaactactta
V$NR2F	Nuclear receptor subfamily 2 factors	V$HNF4A.03	Hepatic nuclear factor 4alpha homodimer, DR1 sites (speci	2614	2638	2626	(-)	0.901	agtaatggttcacaGTCCtttatcc
V$PLZF	C2H2 zinc finger protein PLZF	V$PLZF.01	Promyelocytic leukemia zink finger (TF with nine Krueppel-	451	465	458	(+)	0.9	actTAAAgtttaata
V$EVI1	EVI1-myleoid transforming protein	V$EVI1.07	Evi-1 zinc finger protein, carboxy-terminal zinc finger doma	835	851	843	(+)	0.9	ttaaaAAGAtgggagtt
V$GCMF	Chorion-specific transcription factors with	V$GCM1.03	Glial cells missing homolog 1 (secondary DNA binding pref	1698	1712	1705	(-)	0.9	ctctcCCCTtataac
V$BRAC	Brachyury gene, mesoderm developmenta	V$EOMES.02	Eomesodermin, TBR-2 (secondary DNA binding preferenc	2716	2744	2730	(+)	0.899	ggagtgagaaGGTGtctggatgtcatgga
V$IRXF	Iroquois homeobox transcription factors	V$IRX5.01	Iroquois homeobox 5	63	75	69	(+)	0.898	cccaCATGtccat
V$GLIF	GLI zinc finger family	V$GLIS3.01	GLIS family zinc finger 3, Gli-similar 3	314	330	322	(-)	0.898	ccctCCCCccaccccat
V$MYT1	MYT1 C2HC zinc finger protein	V$MYT1.01	MyT1 zinc finger transcription factor involved in primary ne	877	889	883	(-)	0.898	gaaCAGTttactt
V$FAST	FAST-1 SMAD interacting proteins	V$FAST1.01	FAST-1 SMAD interacting protein	2091	2107	2099	(+)	0.898	ggctttgtcTATTctgt
V$BRNF	Brn POU domain factors	V$BRN3.02	Brn-3, POU-IV protein class	2439	2457	2448	(+)	0.898	ctacttaTAATcattattt
V$KLFS	Krueppel like transcription factors	V$GKLF.01	Gut-enriched Krueppel-like factor	471	489	480	(+)	0.897	aaaaaaaaaAAGGaaaaaa
V$OCT1	Octamer binding protein	V$OCT1.04	Octamer-binding factor 1	1488	1502	1495	(+)	0.897	aaGATGaaaattaag
V$IRXF	Iroquois homeobox transcription factors	V$IRX5.01	Iroquois homeobox 5	8	20	14	(-)	0.896	cacaCATGtgcat
V$BNCF	Basonuclein rDNA transcription factor (Po	V$BNC.01	Basonuclin, cooperates with UBF1 in rDNA PolI transcriptio	209	227	218	(-)	0.896	cttggtatttTGTCcctgg
V$XBBF	X-box binding factors	V$RFX1.01	X-box binding protein RFX1	633	651	642	(+)	0.896	tgtgggacacaGGAActaa
V$NOLF	Neuron-specific olfactory factor	V$OLF1.02	Olfactory neuron-specific factor	2021	2043	2032	(-)	0.896	attcttTCCCtaaggccattttt
V$IRXF	Iroquois homeobox transcription factors	V$IRX5.01	Iroquois homeobox 5	62	74	68	(-)	0.895	tggaCATGtgggt
V$AP1R	MAF and AP1 related factors	V$BACH2.02	BTB and CNC homology 1, basic leucine zipper transcriptio	1037	1061	1049	(-)	0.895	gaatgagcTGTGtcatttctgagtc
V$MYT1	MYT1 C2HC zinc finger protein	V$MYT1.02	MyT1 zinc finger transcription factor involved in primary ne	1233	1245	1239	(-)	0.895	ctgAAGTtttaga
V$FKHD	Fork head domain factors	V$FOXJ1.01	Forkhead box J1	1802	1818	1810	(+)	0.895	gcattgtaCACAaagta
V$ARID	AT rich interactive domain factor	V$JARID2.01	Jumonji, AT rich interactive domain 2 (JMJ)	2478	2498	2488	(+)	0.895	gtgcatTTTGtttgattagga
V$PLZF	C2H2 zinc finger protein PLZF	V$PLZF.02	Promyelocytic leukemia zink finger (TF with nine Krueppel-	118	132	125	(-)	0.894	ctgTACAgtattcca
V$HAND	Twist subfamily of class B bHLH transcrip	V$PARAXIS.01	Paraxis (TCF15), member of the Twist subfamily of Class	264	284	274	(+)	0.894	atgagAACAcatggacacagg
V$IRFF	Interferon regulatory factors	V$IRF7.01	Interferon regulatory factor 7 (IRF-7)	1571	1595	1583	(+)	0.894	aagagcggGAAGcagaaagtgcctg
V$HAND	Twist subfamily of class B bHLH transcrip	V$PARAXIS.01	Paraxis (TCF15), member of the Twist subfamily of Class	2380	2400	2390	(+)	0.894	gaggcAACAcctgtcctgagt
V$SORY	SOX/SRY-sex/testis determining and relat	V$HBP1.01	HMG box-containing protein 1	2660	2682	2671	(+)	0.894	ctaaaatgAATGtgagctggcag
V$GREF	Glucocorticoid responsive and related ele	V$PRE.01	Progesterone receptor binding site, IR3 sites	265	283	274	(-)	0.893	ctgtgtccatgTGTTctca
V$KLFS	Krueppel like transcription factors	V$EKLF.01	Erythroid krueppel like factor (EKLF)	1633	1651	1642	(+)	0.893	aagatcttggaGGGTttgt
V$KLFS	Krueppel like transcription factors	V$EKLF.01	Erythroid krueppel like factor (EKLF)	2764	2782	2773	(-)	0.893	ctcacccacaaGGGTgaaa
V$OCT1	Octamer binding protein	V$OCT1.06	Octamer-binding factor 1	1011	1025	1018	(+)	0.892	aggatgtaAATTtct
V$HNF6	Onecut homeodomain factor HNF6	V$HNF6.02	Liver enriched Cut - Homeodomain transcription factor HN	1072	1088	1080	(+)	0.892	tgaccaaatCCATgctg
V$NKXH	NKX homeodomain factors	V$NKX31.01	Prostate-specific homeodomain protein NKX3.1	1330	1348	1339	(-)	0.892	catagtAAGTagtctataa
V$IRFF	Interferon regulatory factors	V$ISRE.02	Interferon-stimulated response element	1446	1470	1458	(+)	0.892	acaaatgaaaaacaGAAAcaacagt
V$SP1F	GC-Box factors SP1/GC	V$GC.01	GC box elements	1526	1542	1534	(-)	0.892	ccaaagGGAGgagccac
V$SORY	SOX/SRY-sex/testis determining and relat	V$HMGA.01	HMGA family of architectural transcription factors (HMGA1	1827	1849	1838	(+)	0.892	atgagtgatgAATGaacaaacta
V$STAT	Signal transducer and activator of transcri	V$STAT.01	Signal transducers and activators of transcription	2637	2655	2646	(-)	0.892	catgttttaGGAAggacag
V$IRXF	Iroquois homeobox transcription factors	V$IRX5.01	Iroquois homeobox 5	9	21	15	(+)	0.891	tgcaCATGtgtgt
V$HOXF	Paralog hox genes 1-8 from the four hox	V$HOXB8.01	Homeobox B8 / Hox-2delta	14	32	23	(-)	0.891	tgccgcaATAAacacacat
V$SP1F	GC-Box factors SP1/GC	V$SP1.01	Stimulating protein 1, ubiquitous zinc finger transcription fac	319	335	327	(+)	0.891	gtgggGGGAgggcgacg
V$BARB	Barbiturate-inducible element box from pr	V$BARBIE.01	Barbiturate-inducible element	835	849	842	(+)	0.891	ttaaAAAGatgggag
V$FKHD	Fork head domain factors	V$FOXO1.01	Forkhead box protein O1	880	896	888	(-)	0.891	cagctgtgAACAgttta
V$MYOD	Myoblast determining factors	V$MYOD.01	Myogenic regulatory factor MyoD (myf3)	2674	2690	2682	(+)	0.891	agctGGCAgttgtggtt
V$SP1F	GC-Box factors SP1/GC	V$GC.01	GC box elements	312	328	320	(+)	0.89	tcatggGGTGgggggag
V$EGRF	EGR/nerve growth factor induced protein	V$EGR1.04	EGR1, early growth response 1	313	331	322	(+)	0.89	catggggtgGGGGgagggc
V$NOLF	Neuron-specific olfactory factor	V$EBF1.01	Early B-cell factor 1	2005	2027	2016	(+)	0.89	ccagtgTCCCctggttaaaaatg
V$GREF	Glucocorticoid responsive and related ele	V$ARE.02	Androgene receptor binding site, IR3 sites	2851	2869	2860	(+)	0.89	ggagatcttacgGTGCtcc
V$PLAG	Pleomorphic adenoma gene	V$PLAG1.01	Pleomorphic adenoma gene (PLAG) 1, a developmentally r	302	324	313	(+)	0.889	ccGGGGcctgtcatggggtgggg
V$HOXC	HOX - PBX complexes	V$MEIS1.03	Meis homeobox 1	1671	1687	1679	(+)	0.889	ggctgGATTtagtggga
V$HNF1	Hepatic Nuclear Factor 1	V$HNF1.04	Hepatocyte nuclear factor 1 alpha (Tcf-1)	2391	2407	2399	(+)	0.889	tgtcctgaGTTAatctg
V$NKRF	Nuclear factor-kappaB repressing factor	V$NKRF.01	NFKB repressing factor (NRF)	1121	1131	1126	(-)	0.888	aatTTCTctgg
V$LEFF	LEF1/TCF	V$LEF1.01	TCF/LEF-1, involved in the Wnt signal transduction pathwa	1263	1279	1271	(+)	0.888	aaaacaaCAAAgctaac
V$SORY	SOX/SRY-sex/testis determining and relat	V$HMGA.01	HMGA family of architectural transcription factors (HMGA1	366	388	377	(+)	0.887	atgacaagttAATGcgtacagca
V$IRFF	Interferon regulatory factors	V$IRF2.02	Interferon regulatory factor 2	469	493	481	(+)	0.887	gtaaaaaaAAAAaggaaaaaaaaga
V$MYT1	MYT1 C2HC zinc finger protein	V$MYT1.02	MyT1 zinc finger transcription factor involved in primary ne	2420	2432	2426	(-)	0.887	gtcAAGTtttcct
O$VTBP	Vertebrate TATA binding protein factor	O$LTATA.01	Lentivirus LTR TATA box	2434	2450	2442	(-)	0.887	gatTATAagtagtttca
V$CART	Cart-1 (cartilage homeoprotein 1)	V$CART1.01	Cart-1 (cartilage homeoprotein 1)	2532	2552	2542	(+)	0.887	atttaTAATgtaatttataat
V$PLZF	C2H2 zinc finger protein PLZF	V$PLZF.02	Promyelocytic leukemia zink finger (TF with nine Krueppel-	2803	2817	2810	(+)	0.887	tgaTACAgtaggagg

V$AP1F	AP1, Activating protein 1	V$AP1.02	Activator protein 1	237	249	243	(-)	0.886	ctgtGAGTgagaa
V$CART	Cart-1 (cartilage homeoprotein 1)	V$PHOX2.01	Phox2a (ARIX) and Phox2b	2480	2500	2490	(-)	0.886	tctccTAATcaaacaaaatgc
V$NOLF	Neuron-specific olfactory factor	V$EBF1.01	Early B-cell factor 1	990	1012	1001	(-)	0.885	ctccctTCCCctggcctttatcc
O$VTBP	Vertebrate TATA binding protein factor	O$LTATA.01	Lentivirus LTR TATA box	1290	1306	1298	(+)	0.885	aaaTATAagcccaattt
V$HNF1	Hepatic Nuclear Factor 1	V$HNF1.03	Hepatic nuclear factor 1	1905	1921	1913	(-)	0.885	gGTTAatcctaatcttt
V$E2FF	E2F-myc activator/cell cycle regulator	V$E2F.02	E2F, involved in cell cycle regulation, interacts with Rb p10	2041	2057	2049	(+)	0.885	aatttgcggAAAAgatg
V$IRFF	Interferon regulatory factors	V$IRF7.01	Interferon regulatory factor 7 (IRF-7)	2573	2597	2585	(-)	0.885	gtgttttgGAATtcaaaatttttca
V$OCT1	Octamer binding protein	V$OCT1.02	Octamer-binding factor 1	2753	2767	2760	(-)	0.885	gaaATGCaagtttgg
V$GREF	Glucocorticoid responsive and related ele	V$GRE.03	Glucocorticoid receptor, IR3 sites	256	274	265	(-)	0.884	tgtgttctcatTGTTcaat
V$CART	Cart-1 (cartilage homeoprotein 1)	V$PHOX2.01	Phox2a (ARIX) and Phox2b	353	373	363	(+)	0.884	acaccTAATgtaaatgacaag
V$PARF	PAR/bZIP family	V$VBP.01	PAR-type chicken vitellogenin promoter-binding protein	797	813	805	(+)	0.884	ctagctgttGTAActaa
V$SRFF	Serum response element binding factor	V$SRF.02	Serum response factor	925	943	934	(-)	0.884	ggagcCAAAgatggaaatc
V$GATA	GATA binding factors	V$GATA1.07	GATA-binding factor 1	987	999	993	(+)	0.884	ggggGATAaaggc
V$NKX6	NK6 homeobox transcription factors	V$NKX63.01	NK6 homeobox 3	2445	2459	2452	(-)	0.884	ataaaTAATgattat
V$ETSF	Human and murine ETS1 factors	V$SPIB.01	Spi-B transcription factor (Spi-1/PU.1 related)	2450	2470	2460	(-)	0.884	taaaaaatGGAAtaaataatg
V$SRFF	Serum response element binding factor	V$SRF.04	Serum response factor	926	944	935	(+)	0.883	atttccatcTTTGgctcca
V$MYOD	Myoblast determining factors	V$MYOD.01	Myogenic regulatory factor MyoD (myf3)	1722	1738	1730	(+)	0.883	gaaaGGCAgctgggagc
V$NKXH	NKX homeodomain factors	V$NKX25.02	Homeo domain factor Nkx-2.5/Csx, tinman homolog low aff	2316	2334	2325	(+)	0.883	aaccaTAATcgttcatgac
V$BRNF	Brn POU domain factors	V$BRN2.01	Brn-2, POU-III protein class	2537	2555	2546	(-)	0.883	ccCATTataaattacatta
V$GCMF	Chorion-specific transcription factors with	V$GCM1.02	Glial cells missing homolog 1	58	72	65	(+)	0.882	accaaCCCAcatgtc
V$MYBL	Cellular and viral myb-like transcriptional r	V$VMYB.01	v-Myb	1446	1466	1456	(+)	0.882	acaaatgaaaAACAgaaacaa
V$MYBL	Cellular and viral myb-like transcriptional r	V$VMYB.01	v-Myb	1455	1475	1465	(+)	0.882	aaacagaaacAACAgtagata
V$GLIF	GLI zinc finger family	V$GLI3.02	GLI-Kruppel family member GLI3	1517	1533	1525	(-)	0.882	ggagCCACccagtcgct
V$MYT1	MYT1 C2HC zinc finger protein	V$MYT1.02	MyT1 zinc finger transcription factor involved in primary ne	2702	2714	2708	(+)	0.882	tcaAAGTtaaatg
V$BRNF	Brn POU domain factors	V$BRN2.02	Brn-2, POU-III protein class	140	158	149	(+)	0.881	aatggatgagtTCATgtcc
V$SORY	SOX/SRY-sex/testis determining and relat	V$HBP1.01	HMG box-containing protein 1	569	591	580	(-)	0.881	atttaatgAATGtctactaggta
V$ABDB	Abdominal-B type homeodomain transcrip	V$HOXB9.01	Abd-B-like homeodomain protein Hoxb-9	1021	1037	1029	(-)	0.881	catgtcctTAAAagaaa
V$HOXC	HOX - PBX complexes	V$HOXB4.02	Homeobox B4	1828	1844	1836	(+)	0.881	tgagTGATgaatgaaca
V$IRFF	Interferon regulatory factors	V$ISRE.02	Interferon-stimulated response element	1878	1902	1890	(-)	0.881	caagtaaagcaaagGAAAgctatga
V$MYT1	MYT1 C2HC zinc finger protein	V$MYT1.02	MyT1 zinc finger transcription factor involved in primary ne	2180	2192	2186	(+)	0.881	gttAAGTttgaag
V$ABDB	Abdominal-B type homeodomain transcrip	V$HOXB9.01	Abd-B-like homeodomain protein Hoxb-9	2639	2655	2647	(+)	0.881	gtccttccTAAAacatg
V$P53F	p53 tumor suppressor	V$TP63.01	Tumor protein p63	227	251	239	(-)	0.88	acctgtgagtgagaaCATGtggtgc
V$SP1F	GC-Box factors SP1/GC	V$TIEG.01	TGFbeta-inducible early gene (TIEG) / Early growth respor	620	636	628	(+)	0.879	aaatGCGGtgtgttgtg
V$ABDB	Abdominal-B type homeodomain transcrip	V$HOXC9.01	Homeobox C9 / Hox-3beta	2322	2338	2330	(-)	0.879	tgcagtcaTGAAcgatt
V$CREB	cAMP-responsive element binding proteins	V$E4BP4.01	E4BP4, bZIP domain, transcriptional repressor	2531	2551	2541	(+)	0.879	aatttataatGTAAtttataa
V$OCT1	Octamer binding protein	V$OCT2.01	Octamer-binding transcription factor-2, POU class 2 home	2606	2620	2613	(-)	0.879	tttATCCaaattctt
V$SORY	SOX/SRY-sex/testis determining and relat	V$HBP1.01	HMG box-containing protein 1	1046	1068	1057	(-)	0.878	tgggtgagAATGagctgtgtcat
Signal transducer and ac	V$STAT.01	Signal transducers and ac	1622	1640	1631	(+)	0.878	ccgatgccgGGAAgatctt	
V$STAT	Signal transducer and activator of transcri	V$STAT6.01	STAT6: signal transducer and activator of transcription 6	2509	2527	2518	(-)	0.878	taacTCCCctggaagggtc
V$LHXF	Lim homeodomain factors	V$LHX3.02	LIM-homeodomain transcription factor LHX3	2517	2539	2528	(+)	0.878	caggggagttataTAATttataa
V$OSRF	Odd-skipped related factors	V$OSR1.01	Odd-skipped related 1	2805	2817	2811	(+)	0.878	atacaGTAGgagg
V$BRAC	Brachyury gene, mesoderm developmenta	V$TBX21.01	T-box transcription factor TBX21, dimeric binding site	374	402	388	(-)	0.877	gtgccatgttGGTGtgctgtacgcattaa
V$EVI1	EVI1-myleoid transforming protein	V$EVI1.05	Ecotropic viral integration site 1 encoded factor, amino-term	722	738	730	(+)	0.877	cagaccaGATAgagcta
V$ETSF	Human and murine ETS1 factors	V$GABP.01	GABP: GA binding protein	1561	1581	1571	(+)	0.877	caggcattGGAAgagcgggaa
V$STAT	Signal transducer and activator of transcri	V$STAT.01	Signal transducers and activators of transcription	2039	2057	2048	(+)	0.877	agaatttgcGGAAaagatg
V$CLOX	CLOX and CLOX homology (CDP) factors	V$CLOX.01	Cut-like homeodomain protein	2284	2306	2295	(+)	0.877	tggtcATCAatttacttatctgt
V$CREB	cAMP-responsive element binding proteins	V$E4BP4.01	E4BP4, bZIP domain, transcriptional repressor	2518	2538	2528	(-)	0.877	tataaattatATAActcccct
V$AP1R	MAF and AP1 related factors	V$MAFB.01	MAFB/Kreisler basic region/leucine zipper transcription fact	745	769	757	(-)	0.876	tttaagtcttttTCAGcaacttaga
V$CART	Cart-1 (cartilage homeoprotein 1)	V$PROP1.02	Prophet of Pit 1, PROP paired-like homeobox 1, dimeric bin	2532	2552	2542	(-)	0.876	attataaattacATTAtaaat
V$EVI1	EVI1-myleoid transforming protein	V$EVI1.06	Ecotropic viral integration site 1 encoded factor, amino-term	366	382	374	(+)	0.875	atgacaAGTTaatgcgt
O$VTBP	Vertebrate TATA binding protein factor	O$ATATA.01	Avian C-type LTR TATA box	758	774	766	(-)	0.875	aagttttTAAGtctttt
V$OSRF	Odd-skipped related factors	V$OSR1.01	Odd-skipped related 1	1464	1476	1470	(+)	0.875	caacaGTAGatac
V$ZF10	C2H2 zinc finger transcription factors 10	V$PRDM14.01	PR domain zinc finger protein 14	1544	1558	1551	(+)	0.875	tggTTAGggaagtca
V$HOXC	HOX - PBX complexes	V$HOXB4.02	Homeobox B4	1824	1840	1832	(+)	0.875	ccaaTGAGtgatgaatg
V$EVI1	EVI1-myleoid transforming protein	V$EVI1.06	Ecotropic viral integration site 1 encoded factor, amino-term	1846	1862	1854	(+)	0.875	actaaaAGATaaagacc
V$AP1F	AP1, Activating protein 1	V$AP1.02	Activator protein 1	2367	2379	2373	(-)	0.875	aagtGAGTtacta
V$CREB	cAMP-responsive element binding proteins	V$E4BP4.01	E4BP4, bZIP domain, transcriptional repressor	2519	2539	2529	(+)	0.875	ggggagttatATAAtttataa
V$BZIP	Heterodimers between bZIP family membe	V$CEBPE_ATF4.02	Heterodimer of CEBP epsilon and ATF4	2535	2547	2541	(+)	0.875	tataatGTAAttt
V$NKXH	NKX homeodomain factors	V$NKX31.01	Prostate-specific homeodomain protein NKX3.1	754	772	763	(-)	0.874	gtttttAAGTctttttcag
V$ESRR	Estrogen-related receptors	V$ERR.01	Estrogen related receptor	1597	1619	1608	(+)	0.874	acgggaagctgcAAGGgcaaagg
V$ARID	AT rich interactive domain factor	V$ARID5A.01	AT rich interactive domain 5A (MRF1-like)	551	571	561	(+)	0.873	atttaATATagtccctggtac
V$HNF6	Onecut homeodomain factor HNF6	V$HNF6.01	Liver enriched Cut - Homeodomain transcription factor HN	1311	1327	1319	(+)	0.873	cttgttatTCAAtaaat
V$NFAT	Nuclear factor of activated T-cells	V$NFAT5.02	Nuclear factor of activated T-cells 5	1875	1893	1884	(-)	0.873	caaaGGAAagctatgagtg
V$NFAT	Nuclear factor of activated T-cells	V$NFAT5.02	Nuclear factor of activated T-cells 5	2417	2435	2426	(+)	0.873	ggaaGGAAaacttgacatg
V$HBOX	Homeobox transcription factors	V$GSH1.01	Homeobox transcription factor Gsh-1	2628	2646	2637	(-)	0.873	ggaaggacagTAATggttc
V$NBRE	NGFI-B response elements, nur subfamily	V$NBRE.01	Monomers of the nur subfamily of nuclear receptors (nur77	2236	2250	2243	(-)	0.872	tctaAAGGccacagc
V$CDXF	Vertebrate caudal related homeodomain p	V$CDX1.02	Caudal type homeo box 1	2282	2300	2291	(-)	0.872	aagtaaaTTGAtgaccaag

V$PAX6	PAX-4/PAX-6 paired domain binding sites	V$PAX6.02	PAX6 paired domain and homeodomain are required for bin	1780	1798	1789	(+)	0.871	ctggcattttCCAGcactg
V$CDXF	Vertebrate caudal related homeodomain p	V$CDX2.02	Caudal type homeobox transcription factor 2	2448	2466	2457	(+)	0.871	atcattatTTATtccattt
V$NKRF	Nuclear factor-kappaB repressing factor	V$NKRF.01	NFKB repressing factor (NRF)	2516	2526	2521	(-)	0.871	aacTCCCctgg
V$BRNF	Brn POU domain factors	V$BRN2.01	Brn-2, POU-III protein class	87	105	96	(+)	0.87	tgGATTaaaaagatgtggc
V$BRAC	Brachyury gene, mesoderm development	V$TBR1.01	T-box brain protein 1	239	267	253	(+)	0.87	ctcactcacagGTGAgaattgaacaatga
V$IRFF	Interferon regulatory factors	V$IRF2.02	Interferon regulatory factor 2	486	510	498	(+)	0.87	aaaaaagaGAAAtgacatcagact
V$IRXF	Iroquois homeobox transcription factors	V$IRX3.01	Iroquois homeobox 3	858	870	864	(+)	0.87	tctcCATGtaata
V$NBRE	NGFI-B response elements, nur subfamily	V$NBRE.01	Monomers of the nur subfamily of nuclear receptors (nur77	991	1005	998	(+)	0.87	gataAAGGccagggg
V$HNF1	Hepatic Nuclear Factor 1	V$HMBOX.01	Homeobox containing 1	1306	1322	1314	(+)	0.87	tctttcttGTTAttcaa
V$IKRS	Ikaros zinc finger family	V$IK3.01	Ikaros 3, potential regulator of lymphocyte differentiation	1626	1638	1632	(+)	0.87	tgccgGGAAgatc
V$SORY	SOX/SRY-sex/testis determining and relat	V$SOX5.01	Sox-5	1791	1813	1802	(-)	0.87	tgtgtaCAATgcaatcagtgctg
V$HAML	Human acute myelogenous leukemia facto	V$AML3.01	Runt-related transcription factor 2 / CBFA1 (core-binding fa	1539	1553	1546	(+)	0.869	ttggGTGGttaggga
V$EBOX	E-box binding factors	V$MAX.02	MYC associated factor X	225	241	233	(-)	0.868	gagaaCATGtggtgctt
V$IKRS	Ikaros zinc finger family	V$IK3.01	Ikaros 3, potential regulator of lymphocyte differentiation	1164	1176	1170	(+)	0.868	gacagGGAAtatg
V$NBRE	NGFI-B response elements, nur subfamily	V$NBRE.01	Monomers of the nur subfamily of nuclear receptors (nur77	1612	1626	1619	(+)	0.868	ggcaAAGGtcccgat
V$LEFF	LEF1/TCF	V$LEF1.01	TCF/LEF-1, involved in the Wnt signal transduction pathwa	1748	1764	1756	(-)	0.868	tggctagCAAAgccctc
V$LEFF	LEF1/TCF	V$LEF1.01	TCF/LEF-1, involved in the Wnt signal transduction pathwa	39	55	47	(+)	0.867	acaatagCAAAgacttg
V$PARF	PAR/bZIP family	V$TEF.01	Thyrotrophic embryonic factor	495	511	503	(-)	0.867	gagtctgatGTCAtttt
V$SIXF	Sine oculis (SIX) homeodomain factors	V$SIX1.01	Sine oculis homeobox homolog 1	961	975	968	(-)	0.867	tagatgaTATCagga
V$PARF	PAR/bZIP family	V$VBP.01	PAR-type chicken vitellogenin promoter-binding protein	1007	1023	1015	(+)	0.867	agggaggatGTAAattt
V$PARF	PAR/bZIP family	V$TEF.01	Thyrotrophic embryonic factor	1272	1288	1280	(-)	0.867	ggagtttatGTTAgctt
V$RREB	Ras-responsive element binding protein	V$RREB1.01	Ras-responsive element binding protein 1	2836	2850	2843	(-)	0.867	cCCCAaaaaacactc
V$PAX3	PAX-3 binding sites	V$PAX3.02	Pax-3 paired domain protein	2189	2207	2198	(-)	0.866	actgTTACactgcctcttc
V$CP2F	CP2-erythrocyte Factor related to drosopl	V$CP2.02	LBP-1c (leader-binding protein-1c), LSF (late SV40 factor),	2249	2267	2258	(-)	0.866	tACTCgggcagtctggctc
V$GREF	Glucocorticoid responsive and related ele	V$GRE.01	Glucocorticoid receptor, C2C2 zinc finger protein binds gluc	2380	2398	2389	(+)	0.866	gaggcaacacctGTCCtga
V$MEF2	MEF2, myocyte-specific enhancer binding	V$SL1.01	Member of the RSRF (related to serum response factor) pr	2432	2454	2443	(+)	0.866	catgaaaCTACttataatcatta
V$PAXH	PAX homeodomain binding sites	V$PAX6_HD.01	Paired box 6, homeodomain binding site	2525	2539	2532	(-)	0.866	ttataAATTatataa
V$BRN5	Brn-5 POU domain factors	V$BRN5.04	POU class 6 homeobox 1 (POU6F1)	1147	1169	1158	(+)	0.865	ggagtgctcttATTAaagacagg
V$STAF	Selenocysteine tRNA activating factor	V$STAF.02	Se-Cys tRNA gene transcription activating factor	2206	2236	2221	(-)	0.864	ccttcactaccatCCCAtcctgccactccac
V$AP1R	MAF and AP1 related factors	V$MAFB.01	MAFB/Kreisler basic region/leucine zipper transcription fact	2275	2299	2287	(+)	0.864	tagccttcttggTCATcaatttact
V$BRNF	Brn POU domain factors	V$BRN3.01	Brn-3, POU-IV protein class	2446	2464	2455	(+)	0.864	taatcattaTTTAttccat
V$HNF1	Hepatic Nuclear Factor 1	V$HNF1.04	Hepatocyte nuclear factor 1 alpha (Tcf-1)	2699	2715	2707	(+)	0.864	agctcaaaGTTAaatgg
V$CLOX	CLOX and CLOX homology (CDP) factors	V$CLOX.01	Cut-like homeodomain protein	129	151	140	(-)	0.863	aactcATCCatttttatggctgt
V$LEFF	LEF1/TCF	V$LEF1.01	TCF/LEF-1, involved in the Wnt signal transduction pathwa	153	169	161	(-)	0.863	gtccctaCAAAggacat
V$PERO	Peroxisome proliferator-activated receptor	V$PPARG.03	Peroxisome proliferator-activated receptor gamma, DR1 sit	151	173	162	(-)	0.863	ccatgtccctacAAAGgacatga
V$P53F	p53 tumor suppressor	V$TP63.01	Tumor protein p63	154	178	166	(+)	0.863	tgtcctttgtagggaCATGgatgaa
V$CART	Cart-1 (cartilage homeoprotein 1)	V$RHOX6.01	Reproductive homeobox 6, placenta specific homeobox 1	573	593	583	(-)	0.863	acattTAATgaatgtctacta
V$IRXF	Iroquois homeobox transcription factors	V$IRX6.01	Iroquois homeobox 6	857	869	863	(-)	0.863	attaCATGgagaa
V$HOXF	Paralog hox genes 1-8 from the four hox c	V$HOXB6.01	Homeobox B6 / Hox2-beta	861	879	870	(+)	0.863	ccatgtAATAacccagaag
V$IRFF	Interferon regulatory factors	V$ISRE.01	Interferon-stimulated response element	2393	2417	2405	(+)	0.863	tcctgagttaatctGAAActgtttg
V$PBXC	PBX - MEIS complexes	V$PBX1_MEIS1.02	Binding site for a Pbx1/Meis1 heterodimer	65	81	73	(-)	0.862	tcatTGATggacatgtg
V$CLOX	CLOX and CLOX homology (CDP) factors	V$CPHX.01	Cytoplasmic polyadenylated homeobox	954	976	965	(-)	0.862	ctAGATgatatcaggatccaaag
V$FAST	FAST-1 SMAD interacting proteins	V$FAST1.01	FAST-1 SMAD interacting protein	1833	1849	1841	(-)	0.862	tagtttgttCATTcatc
V$OCT1	Octamer binding protein	V$OCT1.03	Octamer-binding transcription factor-1, POU class 2 homeo	2446	2460	2453	(-)	0.862	aataaataATGAtta
V$BNCF	Basonuclein rDNA transcription factor (Po	V$BNC.01	Basonuclin, cooperates with UBF1 in rDNA PolI transcriptio	144	162	153	(+)	0.861	gatgagttcaTGTCctttg
V$XBBF	X-box binding factors	V$RFX3.02	Regulatory factor X, 3 (secondary DNA binding preference)	266	284	275	(+)	0.861	gagaacacatgGACAcagg
V$ZF05	C2H2 zinc finger transcription factors 5	V$ZFP410.01	Zinc finger protein 410, APA-1	310	324	317	(+)	0.861	tgtcatgGGGTgggg
V$CREB	cAMP-responsive element binding proteins	V$E4BP4.01	E4BP4, bZIP domain, transcriptional repressor	405	425	415	(+)	0.861	gtatacctatGTAAcaaacct
V$HNF6	Onecut homeodomain factor HNF6	V$HNF6.02	Liver enriched Cut - Homeodomain transcription factor HNF	1170	1186	1178	(-)	0.861	cagcaacatCCATattc
V$EVI1	EVI1-myleoid transforming protein	V$EVI1.02	Ecotropic viral integration site 1 encoded factor, amino-term	666	682	674	(+)	0.86	aggatAAAAtaaaacaa
V$SRFF	Serum response element binding factor	V$SRF.04	Serum response factor	2140	2158	2149	(-)	0.86	gatgccagaTCTGctaaac
V$PRDF	Positive regulatory domain I binding factor	V$PRDM1.02	PRDI (positive regulatory domain I element) binding factor 1	487	505	496	(+)	0.859	aaaaagaGAAAatgacatc
V$HBOX	Homeobox transcription factors	V$VAX2.01	Ventral anterior homeobox 2	577	595	586	(+)	0.859	agacattcATTAaatgtgt
V$FAST	FAST-1 SMAD interacting proteins	V$FAST1.02	Forkhead box H1 (Foxh1)	1010	1026	1018	(+)	0.859	gaggaTGTAaatttctt
V$OCT1	Octamer binding protein	V$POU3F3.01	POU class 3 homeobox 3 (POU3F3), OTF8	1931	1945	1938	(+)	0.859	cctttGCATacctct
V$HOXF	Paralog hox genes 1-8 from the four hox c	V$HOXC6.01	Homeobox C6 / Hox-3C	2537	2555	2546	(+)	0.859	taatgtAATTtataatggg
V$RXRF	RXR heterodimer binding sites	V$THRB.02	Thyroid hormone receptor, beta (ER5 - everted repeat, spa	150	174	162	(+)	0.858	ttcatgtcctttgtagGGACatgga
V$HNF1	Hepatic Nuclear Factor 1	V$HNF1.01	Hepatic nuclear factor 1	372	388	380	(+)	0.858	aGTTAatgcgtacagca
V$HOXF	Paralog hox genes 1-8 from the four hox c	V$HOXC8.01	Homeobox C8 / Hox-3alpha	858	876	867	(-)	0.858	ctgggttATTAcatggaga
V$ETSF	Human and murine ETS1 factors	V$SPDEF.01	SAM pointed domain containing ets transcription factor	951	971	961	(-)	0.858	tgatatcAGGAtccaaagcaa
V$BNCF	Basonuclein rDNA transcription factor (Po	V$BNC.01	Basonuclin, cooperates with UBF1 in rDNA PolI transcriptio	1182	1200	1191	(-)	0.858	gatggctaccTGTCcagca
V$OCT1	Octamer binding protein	V$OCT2.01	Octamer-binding transcription factor-2, POU class 2 homeo	357	371	364	(+)	0.857	ctaATGTaaatgaca
V$HOXF	Paralog hox genes 1-8 from the four hox c	V$HOXC4.01	Homeobox C4 / Hox-3epsilon	578	596	587	(+)	0.857	gacattCATTaaatgtgtt
V$AP1R	MAF and AP1 related factors	V$VMAF.01	v-Maf	885	909	897	(-)	0.857	cgagccgccttGTCAgctgtgaaca
V$LEFF	LEF1/TCF	V$LEF1.04	TCF/LEF-1 (secondary DNA binding preference)	2284	2300	2292	(+)	0.857	tggtcaTCAAtttactt
V$YY1F	Activator/repressor binding to transcription	V$YY1.03	Transcription factor yin yang 1	383	405	394	(-)	0.856	catgtgCCATgttggtgtgctgt
V$MYT1	MYT1 C2HC zinc finger protein	V$MYT1.01	MyT1 zinc finger transcription factor involved in primary ne	1101	1113	1107	(+)	0.856	gaaAAGTacactt

V$NKXH	NKX homeodomain factors	V$NKX31.01	Prostate-specific homeodomain protein NKX3.1	1318	1336	1327	(+)	0.856	ttcaatAAATatttataga
V$RXRF	RXR heterodimer binding sites	V$VDR_RXR.05	Bipartite binding site of VDR/RXR heterodimers, DR4 sites	1923	1947	1935	(-)	0.856	cgaGAGGtatgcaaaggatgagtag
V$HESF	Vertebrate homologues of enhancer of spl	V$DEC1.01	Basic helix-loop-helix protein known as Dec1, Stra13, Shar	2370	2384	2377	(-)	0.856	gcctCAAGtgagtta
V$FAST	FAST-1 SMAD interacting proteins	V$FAST1.03	Forkhead box H1 (Foxh1)	2472	2488	2480	(+)	0.856	atattagtgCATTttgt
V$LHXF	Lim homeodomain factors	V$LHX3.02	LIM-homeodomain transcription factor LHX3	2529	2551	2540	(+)	0.856	ataatttataatgTAATttataa
O$VTBP	Vertebrate TATA binding protein factor	O$MTATA.01	Muscle TATA box	826	842	834	(-)	0.855	cttttTAAAccattata
O$VTBP	Vertebrate TATA binding protein factor	O$MTATA.01	Muscle TATA box	831	847	839	(+)	0.855	tggttTAAAaagatggg
V$BRN5	Brn-5 POU domain factors	V$BRN5.04	POU class 6 homeobox 1 (POU6F1)	1047	1069	1058	(+)	0.855	tgacacagctcATTCtcacccag
V$NF1F	Nuclear factor 1	V$NF1.01	Nuclear factor 1	1083	1103	1093	(-)	0.855	ttcTTGGcatctttacagcat
V$AP1R	MAF and AP1 related factors	V$BACH1.01	BTB/POZ-bZIP transcription factor BACH1 forms heterodin	1820	1844	1832	(+)	0.855	gcacccaaTGAGtgatgaatgaaca
V$HOXF	Paralog hox genes 1-8 from the four hox c	V$HOXB8.01	Homeobox B8 / Hox-2delta	2448	2466	2457	(-)	0.855	aaatggaATAAataatgat
V$HBOX	Homeobox transcription factors	V$GSH1.01	Homeobox transcription factor Gsh-1	544	562	553	(+)	0.854	gcaaggcattTAATatagt
V$PAX3	PAX-3 binding sites	V$PAX3.02	Pax-3 paired domain protein	625	643	634	(-)	0.854	tgtgTCCCacaacacaccg
V$NR2F	Nuclear receptor subfamily 2 factors	V$HNF4.01	Hepatic nuclear factor 4, DR1 sites	983	1007	995	(+)	0.854	ggaaggggggaTAAAggccaggggaa
V$EREF	Estrogen response elements	V$ER.01	Estrogen receptor, IR3 sites	1051	1069	1060	(-)	0.854	ctggGTGAgaatgagctgt
V$PARF	PAR/bZIP family	V$TEF.01	Thyrotrophic embryonic factor	1079	1095	1087	(+)	0.854	atccatgctGTAAagat
V$NKRF	Nuclear factor-kappaB repressing factor	V$NKRF.01	NFKB repressing factor (NRF)	1127	1137	1132	(+)	0.854	aaaTTCTcagc
V$STAT	Signal transducer and activator of transcri	V$STAT6.01	STAT6: signal transducer and activator of transcription 6	438	456	447	(+)	0.853	catgTACCctagaacttaa
V$CP2F	CP2-erythrocyte Factor related to drosopl	V$CP2.02	LBP-1c (leader-binding protein-1c), LSF (late SV40 factor),	640	658	649	(+)	0.853	cACAGgaactaacttgaca
V$NKXH	NKX homeodomain factors	V$NKX31.01	Prostate-specific homeodomain protein NKX3.1	1319	1337	1328	(-)	0.853	gtctatAAATatttattga
V$HOXF	Paralog hox genes 1-8 from the four hox c	V$HOXD3.01	Homeobox D3 / Hox-4alpha	1490	1508	1499	(+)	0.853	gatgaaAATTaaggcaatg
V$YY1F	Activator/repressor binding to transcriptior	V$YY1.01	Yin and Yang 1 activator sites	2042	2064	2053	(-)	0.853	agatagCCATcttttccgcaaat
V$HNF6	Onecut homeodomain factor HNF6	V$OC2.01	CUT-homeodomain transcription factor Onecut-2	2118	2134	2126	(-)	0.853	ggaaaaAATCagaatgg
V$RXRF	RXR heterodimer binding sites	V$THRA.01	Thyroid hormone receptor, alpha (ER4 - everted repeat, sp	2254	2278	2266	(+)	0.853	agactgcccgagtaAGGTacctagc
V$CREB	cAMP-responsive element binding proteins	V$E4BP4.01	E4BP4, bZIP domain, transcriptional repressor	352	372	362	(+)	0.852	tacacctaatGTAAatgacaa
V$CREB	cAMP-responsive element binding proteins	V$CREB2.01	cAMP-responsive element binding protein 2	493	513	503	(+)	0.852	agaaaaTGACatcagactcat
V$ZF10	C2H2 zinc finger transcription factors 10	V$PRDM14.01	PR domain zinc finger protein 14	1985	1999	1992	(+)	0.852	ttcTTAGtgtccttg
V$HOXC	HOX - PBX complexes	V$HOXB4.02	Homeobox B4	75	91	83	(+)	0.851	tcaaTGATagactggat
V$HOXF	Paralog hox genes 1-8 from the four hox c	V$HOXC4.01	Homeobox C4 / Hox-3epsilon	575	593	584	(-)	0.851	acatttAATGaatgtctac
V$BRNF	Brn POU domain factors	V$BRN3.03	POU class 4 homeobox 3 (POU4F3), BRN3C	577	595	586	(-)	0.851	acacattTAATgaatgtct
V$OCT1	Octamer binding protein	V$OCT1.03	Octamer-binding transcription factor-1, POU class 2 homeo	580	594	587	(-)	0.851	cacatttaATGAatg
V$NR2F	Nuclear receptor subfamily 2 factors	V$HNF4A.03	Hepatic nuclear factor 4alpha homodimer, DR1 sites (speci	1996	2020	2008	(+)	0.851	cttggtagcccagtGTCCcctggtt
V$HOXF	Paralog hox genes 1-8 from the four hox c	V$HOXC6.01	Homeobox C6 / Hox-3C	2534	2552	2543	(-)	0.851	attataAATTacattataa
V$NR2F	Nuclear receptor subfamily 2 factors	V$HNF4.01	Hepatic nuclear factor 4, DR1 sites	2693	2717	2705	(+)	0.851	tgtgccagctCAAAgttaaatgggg
V$OCT1	Octamer binding protein	V$OCT1.03	Octamer-binding transcription factor-1, POU class 2 homeo	577	591	584	(+)	0.85	agacattcATTAaat
V$CART	Cart-1 (cartilage homeoprotein 1)	V$PROP1.01	Prophet of Pit 1, PROP paired-like homeobox 1	578	598	588	(+)	0.85	gacattCATTaaatgtgtttt
V$PAX6	PAX-4/PAX-6 paired domain binding sites	V$PAX6.04	PAX6 paired domain binding site	1497	1515	1506	(-)	0.85	attTCCCcattgccttaat
V$CP2F	CP2-erythrocyte Factor related to drosopl	V$CP2.02	LBP-1c (leader-binding protein-1c), LSF (late SV40 factor),	1755	1773	1764	(-)	0.85	aACTGtccctggctagcaa
V$ZF10	C2H2 zinc finger transcription factors 10	V$PRDM14.01	PR domain zinc finger protein 14	2243	2257	2250	(+)	0.85	cctTTAGagccagac
V$BRNF	Brn POU domain factors	V$BRN3.03	POU class 4 homeobox 3 (POU4F3), BRN3C	2443	2461	2452	(-)	0.85	gaataaaTAATgattataa
V$HNF1	Hepatic Nuclear Factor 1	V$HNF1.04	Hepatocyte nuclear factor 1 alpha (Tcf-1)	2680	2696	2688	(+)	0.85	cagttgtgGTTAatgtg
V$SIXF	Sine oculis (SIX) homeodomain factors	V$SIX1.01	Sine oculis homeobox homolog 1	2800	2814	2807	(-)	0.85	cctactgTATCattt
V$PERO	Peroxisome proliferator-activated receptor	V$PPARG.03	Peroxisome proliferator-activated receptor gamma, DR1 sit	675	697	686	(+)	0.849	taaaacaaaaaaAAAGgtaatat
V$E2FF	E2F-myc activator/cell cycle regulator	V$E2F.02	E2F, involved in cell cycle regulation, interacts with Rb p107	931	947	939	(-)	0.849	cgttggagcCAAAgatg
O$VTBP	Vertebrate TATA binding protein factor	O$MTATA.01	Muscle TATA box	1230	1246	1238	(+)	0.849	tagtcTAAAacttcagg
V$HOXF	Paralog hox genes 1-8 from the four hox c	V$HOXB3.01	Homeobox B3 / Hox 2-gamma	2444	2462	2453	(+)	0.849	tataaTCATtatttattcc
V$SP1F	GC-Box factors SP1/GC	V$TIEG.01	TGFbeta-inducible early gene (TIEG) / Early growth respor	2710	2726	2718	(+)	0.849	aaatGGGGagtgagaag
V$HOXC	HOX - PBX complexes	V$HOXB4.02	Homeobox B4	65	81	73	(-)	0.848	tcatTGATggacatgtg
V$IRFF	Interferon regulatory factors	V$ISRE.01	Interferon-stimulated response element	843	867	855	(-)	0.848	tacatggagaaaaaTAAActcccat
V$SIXF	Sine oculis (SIX) homeodomain factors	V$SIX1.01	Sine oculis homeobox homolog 1	960	974	967	(+)	0.848	atcctgaTATCatct
V$DICE	Downstream Immunoglobulin Control Elem	V$DICE.01	Downstream Immunoglobulin Control Element, interacting fa	1085	1099	1092	(-)	0.848	tggcATCTttacagc
V$HEAT	Heat shock factors	V$HSF1.01	Heat shock factor 1	1402	1426	1414	(+)	0.848	cttcccgatcccAGAAagctgtatt
V$HNF6	Onecut homeodomain factor HNF6	V$HNF6.01	Liver enriched Cut - Homeodomain transcription factor HNF	1418	1434	1426	(+)	0.848	agctgtatTCAAtaggg
V$TALE	TALE homeodomain class recognizing TG	V$MEIS1.02	Meis homeobox 1	173	189	181	(+)	0.847	gatgaagctGGCAacca
V$ETSF	Human and murine ETS1 factors	V$ETV6.01	Ets variant 6	867	887	877	(+)	0.847	aataacccAGAAgtaaactgt
V$FKHD	Fork head domain factors	V$FREAC2.01	Fork head related activator-2 (FOXF2)	1083	1099	1091	(+)	0.847	atgctgTAAAgatgcca
V$TEAF	TEA/ATTS DNA binding domain factors	V$TEF1.01	TEF-1 related muscle factor	1205	1217	1211	(+)	0.847	ccaCATAcctgtg
V$PERO	Peroxisome proliferator-activated receptor	V$PPARG.03	Peroxisome proliferator-activated receptor gamma, DR1 sit	1882	1904	1893	(-)	0.847	gccaagtaaagcAAAGgaaagct
V$PARF	PAR/bZIP family	V$HLF.01	Hepatic leukemia factor	2360	2376	2368	(+)	0.847	agatttttaGTAActca
V$LHXF	Lim homeodomain factors	V$ISL1.01	Pancreatic and intestinal lim-homeodomain factor	2540	2562	2551	(+)	0.847	tgtaatttaTAATgggccatact
V$HNF1	Hepatic Nuclear Factor 1	V$HNF1.04	Hepatocyte nuclear factor 1 alpha (Tcf-1)	365	381	373	(+)	0.846	aatgacaaGTTAatgcg
V$DMRT	DM domain-containing transcription factors	V$DMRT5.01	Doublesex and mab-3 related transcription factor 5	1451	1471	1461	(-)	0.846	tactgttGTTTctgtttttca
V$TALE	TALE homeodomain class recognizing TG	V$TGIF2LX.01	TGFB-induced factor homeobox 2-like, X-linked, dimeric bir	2227	2243	2235	(-)	0.846	gccacagccTTCActac
V$FKHD	Fork head domain factors	V$FHXB.01	Fork head homologous X binds DNA with a dual sequence	2314	2330	2322	(+)	0.846	gcaaccATAAtcgttca
V$HOMF	Homeodomain transcription factors	V$TLX1.01	T-cell leukemia homeobox 1	2315	2333	2324	(-)	0.846	tcatgaaCGATtatggttg
O$VTBP	Vertebrate TATA binding protein factor	O$MTATA.01	Muscle TATA box	2464	2480	2472	(+)	0.846	tttttTAAAtattagtg
V$HAML	Human acute myelogenous leukemia facto	V$AML3.01	Runt-related transcription factor 2 / CBFA1 (core-binding fa	57	71	64	(-)	0.845	acatGTGGgttggtt

V$RP58	RP58 (ZFP238) zinc finger protein	V$RP58.01	Zinc finger protein RP58 (ZNF238), associated preferentiall	228	240	234	(-)	0.845	agaaCATGtggtg
V$LHXF	Lim homeodomain factors	V$LHX3.02	LIM-homeodomain transcription factor LHX3	579	601	590	(-)	0.845	aggaaaacacattTAATgaatgt
V$CDXF	Vertebrate caudal related homeodomain p	V$CDX2.01	Cdx-2 mammalian caudal related intestinal transcr. factor	667	685	676	(-)	0.845	tttttgtTTTAttttatcc
V$NFKB	Nuclear factor kappa B/c-rel	V$NFKAPPAB.02	NF-kappaB	1780	1794	1787	(+)	0.845	ctGGCAttttccagc
V$LTSM	Localized tandem sequence motif	V$LTSM.03	LTSM elements with 8 bp spacer	2059	2073	2066	(-)	0.845	ATCTtcttcagatag
V$HBOX	Homeobox transcription factors	V$VAX1.01	Ventral anterior homeobox 1	576	594	585	(-)	0.844	cacatttAATGaatgtcta
V$MYT1	MYT1 C2HC zinc finger protein	V$MYT1.01	MyT1 zinc finger transcription factor involved in primary ne	1104	1116	1110	(-)	0.844	ttcAAGTgtactt
V$LHXF	Lim homeodomain factors	V$LHX6.01	LIM homeobox 6	1147	1169	1158	(+)	0.844	ggagtgctcTTATtaaagacagg
V$FAST	FAST-1 SMAD interacting proteins	V$FAST1.02	Forkhead box H1 (Foxh1)	57	73	65	(-)	0.843	ggacaTGTGggttggtt
V$ZF12	C2H2 zinc finger transcription factors 12	V$ZFP652.01	Zinc finger protein 652 (ZNF652)	2763	2777	2770	(-)	0.843	ccacaagggTGAAat
V$CART	Cart-1 (cartilage homeoprotein 1)	V$RHOX6.01	Reproductive homeobox 6, placenta specific homeobox 1	1146	1166	1156	(-)	0.842	gtcttTAATaagagcactcct
V$PARF	PAR/bZIP family	V$DBP.01	Albumin D-box binding protein	1213	1229	1221	(+)	0.842	ctgtgTTATgttttctc
V$RXRF	RXR heterodimer binding sites	V$RAR_RXR.01	Retinoic acid receptor / retinoid X receptor heterodimer, DR	1606	1630	1618	(+)	0.842	tgcaagggcaaAGGTcccgatgccg
V$BHLH	bHLH transcription factors expressed in m	V$BHLHA15.01	Muscle, intestine and stomach expression 1 (MIST1)	2131	2143	2137	(-)	0.842	aaacccTATGgaa
V$RXRF	RXR heterodimer binding sites	V$RARG.01	Retinoic acid receptor gamma, homodimer DR2 binding site	2236	2260	2248	(+)	0.842	gctgtggcctTTAGagccagactgc
V$ZF57	KRAB domain zinc finger protein 57	V$ZFP57.01	Krueppel-associated box-containing zinc-finger protein 57 (	23	35	29	(+)	0.841	tatTGCGgcacta
V$BHLH	bHLH transcription factors expressed in m	V$BHLHA15.01	Muscle, intestine and stomach expression 1 (MIST1)	227	239	233	(+)	0.841	gcaccaCATGttc
V$EBOX	E-box binding factors	V$MNT.01	MAX binding protein	421	437	429	(-)	0.841	accacAACGtgcaggtt
V$EVI1	EVI1-myleoid transforming protein	V$EVI1.02	Ecotropic viral integration site 1 encoded factor, amino-term	1213	1229	1221	(-)	0.841	gagaaAACAtaacacag
V$ZF05	C2H2 zinc finger transcription factors 5	V$ZFP410.01	Zinc finger protein 410, APA-1	1405	1419	1412	(-)	0.841	ctttctgGGATcggg
V$EVI1	EVI1-myleoid transforming protein	V$EVI1.02	Ecotropic viral integration site 1 encoded factor, amino-term	1434	1450	1442	(+)	0.841	gagagAAGGtaaacaaa
V$AP1R	MAF and AP1 related factors	V$MAFB.01	MAFB/Kreisler basic region/leucine zipper transcription fact	184	208	196	(+)	0.84	caaccatcattcTCAGcaaactatc
V$LTSM	Localized tandem sequence motif	V$LTSM.03	LTSM elements with 8 bp spacer	503	517	510	(+)	0.84	ATCAgactcatatgt
V$LEFF	LEF1/TCF	V$LEF1.04	TCF/LEF-1 (secondary DNA binding preference)	1313	1329	1321	(+)	0.84	tgttatTCAAtaaatat
V$HEAT	Heat shock factors	V$HSF1.04	Heat shock factor 1	1770	1794	1782	(+)	0.84	agtttgttctctggcattTTCCagc
V$HOXF	Paralog hox genes 1-8 from the four hox c	V$HOX1-3.01	Hox-1.3, vertebrate homeobox protein	2623	2641	2632	(-)	0.84	gacagTAATggttcacagt
V$RXRF	RXR heterodimer binding sites	V$THRB.02	Thyroid hormone receptor, beta (ER5 - everted repeat, spa	150	174	162	(-)	0.839	tccatgtccctacaaaGGACatgaa
V$BRNF	Brn POU domain factors	V$BRN3.03	POU class 4 homeobox 3 (POU4F3), BRN3C	1153	1171	1162	(+)	0.839	ctcttatTAAAgacaggga
V$SREB	Sterol regulatory element binding proteins	V$SREBP.02	Sterol regulatory element binding protein	316	330	323	(-)	0.838	cccTCCCcccacccc
V$HOMF	Homeodomain transcription factors	V$HMX1.01	H6 family homeobox 1 / NKX5-3	544	562	553	(-)	0.838	actatatTAAAtgccttgc
V$SORY	SOX/SRY-sex/testis determining and relat	V$HBP1.02	HMG box-containing protein 1	1314	1336	1325	(+)	0.838	gttattcAATAaatatttataga
V$BRN5	Brn-5 POU domain factors	V$POU6F2.01	Retina-derived POU-domain factor-1, dimeric binding site	1835	1857	1846	(+)	0.838	tgaatgaacaaACTAaaagataa
V$DMRT	DM domain-containing transcription factor	V$DMRT5.01	Doublesex and mab-3 related transcription factor 5	2191	2211	2201	(-)	0.838	ctccactGTTAcactgcctct
V$HNF1	Hepatic Nuclear Factor 1	V$HMBOX.01	Homeobox containing 1	802	818	810	(-)	0.837	ctttcttaGTTAcaaca
V$LHXF	Lim homeodomain factors	V$ISL1.01	Pancreatic and intestinal lim-homeodomain factor	857	879	868	(+)	0.837	ttctccatgTAATaacccagaag
V$HNF1	Hepatic Nuclear Factor 1	V$HNF1.01	Hepatic nuclear factor 1	1313	1329	1321	(+)	0.837	tGTTAttcaataaatat
V$PAX2	PAX-2 binding sites	V$PAX2.01	Zebrafish PAX2 paired domain protein	2004	2026	2015	(+)	0.837	cccagtgtcccctggttAAAAat
V$P53F	p53 tumor suppressor	V$TP63.01	Tumor protein p63	2426	2450	2438	(-)	0.837	gattataagtagtttCATGtcaagt
V$LHXF	Lim homeodomain factors	V$ISL1.01	Pancreatic and intestinal lim-homeodomain factor	366	388	377	(+)	0.836	atgacaagtTAATgcgtacagca
V$BRN5	Brn-5 POU domain factors	V$BRN5.03	Brn-5, POU-VI protein class (also known as emb and CNS-	567	589	578	(-)	0.836	tTAATgaatgtctactaggtacc
V$EVI1	EVI1-myleoid transforming protein	V$EVI1.06	Ecotropic viral integration site 1 encoded factor, amino-term	1302	1318	1310	(-)	0.836	ataacaAGAAagaaatt
V$LHXF	Lim homeodomain factors	V$ISL1.01	Pancreatic and intestinal lim-homeodomain factor	2623	2645	2634	(-)	0.836	gaaggacagTAATggttcacagt
V$LHXF	Lim homeodomain factors	V$ISL1.01	Pancreatic and intestinal lim-homeodomain factor	2681	2703	2692	(+)	0.836	agttgtggtTAATgtgccagctc
V$CLOX	CLOX and CLOX homology (CDP) factors	V$CLOX.01	Cut-like homeodomain protein	158	180	169	(-)	0.835	gcttcATCCatgtccctacaaag
V$CEBP	Ccaat/Enhancer Binding Protein	V$CEBPE.01	CCAAT/enhancer binding protein (C/EBP), epsilon	254	268	261	(-)	0.835	ctcattgtTCAAttc
V$NR2F	Nuclear receptor subfamily 2 factors	V$HNF4.01	Hepatic nuclear factor 4, DR1 sites	1476	1500	1488	(+)	0.835	ccagtaagagCAAAgatgaaaatta
V$CREB	cAMP-responsive element binding proteins	V$BATF3.01	Basic leucine zipper transcription factor, ATF-like 3	2066	2086	2076	(-)	0.835	aggaGATGtggtcatcttctt
V$PERO	Peroxisome proliferator-activated receptor	V$PPARG.03	Peroxisome proliferator-activated receptor gamma, DR1 sit	2237	2259	2248	(-)	0.835	cagtctggctctAAAGgccacag
V$CAAT	CCAAT binding factors	V$ACAAT.01	Avian C-type LTR CCAAT box	71	85	78	(+)	0.834	tccaTCAAtgataga
V$ABDB	Abdominal-B type homeodomain transcrip	V$HOXC9.01	Homeobox C9 / Hox-3beta	145	161	153	(-)	0.834	aaaggacaTGAActcat
V$CART	Cart-1 (cartilage homeoprotein 1)	V$XVENT2.01	Xenopus homeodomain factor Xvent-2; early BMP signaling	505	525	515	(+)	0.834	cagacTCATatgtctattagg
V$BRN5	Brn-5 POU domain factors	V$BRN5.04	POU class 6 homeobox 1 (POU6F1)	2440	2462	2451	(+)	0.834	tacttataatcATTAtttattcc
V$CEBP	Ccaat/Enhancer Binding Protein	V$CEBPE.01	CCAAT/enhancer binding protein (C/EBP), epsilon	253	267	260	(+)	0.833	agaattgaACAAtga
V$EVI1	EVI1-myleoid transforming protein	V$EVI1.02	Ecotropic viral integration site 1 encoded factor, amino-term	1708	1724	1716	(+)	0.833	gagagAAGAgatcagaa
V$SORY	SOX/SRY-sex/testis determining and relat	V$HBP1.02	HMG box-containing protein 1	70	92	81	(+)	0.832	gtccatcAATGatagactggatt
V$AP1R	MAF and AP1 related factors	V$MAFF.01	Transcription factor MafF	747	771	759	(+)	0.832	taagttGCTGaaaaagacttaaaaa
V$BRNF	Brn POU domain factors	V$BRN3.03	POU class 4 homeobox 3 (POU4F3), BRN3C	1150	1168	1159	(-)	0.832	ctgtcttTAATaagagcac
V$PRDF	Positive regulatory domain I binding factor	V$PRDM1.02	PRDI (positive regulatory domain I element) binding factor 1	1578	1596	1587	(+)	0.832	ggaagcaGAAAgtgcctgc
V$PRDF	Positive regulatory domain I binding factor	V$PRDM1.02	PRDI (positive regulatory domain I element) binding factor 1	2029	2047	2038	(+)	0.832	ccttaggGAAAgaatttgc
V$HZIP	Homeodomain-leucine zipper transcription	V$HOMEZ.01	Homeobox and leucine zipper encoding transcription factor	2318	2332	2325	(+)	0.832	ccataATCGttcatg
V$ABDB	Abdominal-B type homeodomain transcrip	V$HOXC10.01	Homeobox C10/ Hox-3iota	1154	1170	1162	(-)	0.831	ccctgtctTTAAtaaga
V$LHXF	Lim homeodomain factors	V$LHX3.02	LIM-homeodomain transcription factor LHX3	2388	2410	2399	(+)	0.83	acctgtcctgagtTAATctgaaa
V$HNF6	Onecut homeodomain factor HNF6	V$OC2.01	CUT-homeodomain transcription factor Onecut-2	2441	2457	2449	(+)	0.83	acttatAATCattattt
V$HOMF	Homeodomain transcription factors	V$HMX2.01	Hmx2/Nkx5-2 homeodomain transcription factor	2848	2866	2857	(+)	0.83	gggggagatCTTAcggtgc
V$HOXC	HOX - PBX complexes	V$HOX_PBX.01	HOX/PBX binding sites	180	196	188	(-)	0.829	agaaTGATggttgccag
V$PAX2	PAX-2 binding sites	V$PAX2.01	Zebrafish PAX2 paired domain protein	2391	2413	2402	(+)	0.829	tgtcctgagttaatctgAAACtg
V$ZBED	Zinc finger BED domain-containing protein	V$ZBED1.02	Zinc finger, BED-type containing 1	160	172	166	(+)	0.828	tTGTAgggacatg

V$LEFF	LEF1/TCF	V$LEF1.03	TCF/LEF-1	1479	1495	1487	(+)	0.828	gtaagaGCAAagatgaa
V$PAX7	Paired box 7	V$PAX7.01	Paired box 7 homeodomain-binding motif	2284	2298	2291	(-)	0.828	gtaaattGATGacca
V$BRAC	Brachyury gene, mesoderm developmenta	V$MGA.01	MAX gene associated, dimeric binding site	276	304	290	(+)	0.827	ggacacaggaagaggaacctcACACaccg
V$BHLH	bHLH transcription factors expressed in m	V$BHLHA15.01	Muscle, intestine and stomach expression 1 (MIST1)	654	666	660	(-)	0.827	ttaccaTTTGtca
V$FAST	FAST-1 SMAD interacting proteins	V$FAST1.02	Forkhead box H1 (Foxh1)	586	602	594	(+)	0.826	ttaaaTGTGttttcctt
V$ZF12	C2H2 zinc finger transcription factors 12	V$ZFP652.01	Zinc finger protein 652 (ZNF652)	826	840	833	(+)	0.826	tataatggtTTAAaa
V$PRDF	Positive regulatory domain I binding factor	V$BLIMP1.01	Transcriptional repressor B lymphocyte-induced maturatio	1959	1977	1968	(-)	0.826	gcaaggaGAAAgaggtgtt
V$BHLH	bHLH transcription factors expressed in m	V$BHLHA15.01	Muscle, intestine and stomach expression 1 (MIST1)	2130	2142	2136	(+)	0.826	tttccaTAGGgtt
V$MYBL	Cellular and viral myb-like transcriptional r	V$MYBL1.01	V-myb avian myeloblastosis viral oncogene homolog-like 1	2399	2419	2409	(+)	0.826	gttaatctgaaACTGtttgga
V$HOXF	Paralog hox genes 1-8 from the four hox c	V$HOX1-3.01	Hox-1.3, vertebrate homeobox protein	2441	2459	2450	(-)	0.826	ataaaTAATgattataagt
V$HUB1	HTLV-I U5 repressive element-binding pro	V$ZNF282.01	Zinc finger protein 282 (HTLV-I U5 repressive element-bind	912	926	919	(+)	0.825	TTTCtcaacacagga
V$OCT1	Octamer binding protein	V$OCT.01	Octamer binding site (OCT1/OCT2)	2125	2139	2132	(-)	0.825	cctATGGaaaaaatc
V$BHLH	bHLH transcription factors expressed in m	V$BHLHA15.01	Muscle, intestine and stomach expression 1 (MIST1)	228	240	234	(-)	0.824	agaacaTGTGgtg
V$STEM	Motif composed of binding sites for pluripo	V$OCT3_4.01	POU domain, class 5, transcription factor 1	352	370	361	(-)	0.824	gtcatttACATtaggtgta
V$GABF	GA-boxes	V$GAGA.01	GAGA-Box	1682	1706	1694	(+)	0.824	gtgggAGAGggagaaggttataagg
V$E2FF	E2F-myc activator/cell cycle regulator	V$RB_E2F1_DP1.01	RB/E2F-1/DP-1 heterotrimeric complex	2038	2054	2046	(-)	0.824	cttttCCGCaaattctt
V$DMRT	DM domain-containing transcription factor	V$DMRT5.01	Doublesex and mab-3 related transcription factor 5	2193	2213	2203	(+)	0.824	aggcagtGTAAcagtggagtg
V$PRDF	Positive regulatory domain I binding factor	V$BLIMP1.01	Transcriptional repressor B lymphocyte-induced maturatio	2337	2355	2346	(+)	0.824	caatattGAAAgctttgaa
V$HOXF	Paralog hox genes 1-8 from the four hox c	V$HOXA4.01	Homeobox A4	2525	2543	2534	(+)	0.824	ttatatAATTtataatgta
V$MYBL	Cellular and viral myb-like transcriptional r	V$MYBL1.01	V-myb avian myeloblastosis viral oncogene homolog-like 1	878	898	888	(-)	0.823	gtcagctgtgaACAGtttact
V$HOXH	HOX - MEIS1 heterodimers	V$MEIS1B_HOXA9.01	Meis1b and Hoxa9 form heterodimeric binding complexes c	1085	1099	1092	(-)	0.823	TGGCatctttacagc
V$OCT1	Octamer binding protein	V$OCT.01	Octamer binding site (OCT1/OCT2)	1447	1461	1454	(+)	0.823	caaATGAaaaacaga
O$VTBP	Vertebrate TATA binding protein factor	O$LTATA.01	Lentivirus LTR TATA box	1690	1706	1698	(-)	0.823	cctTATAaccttctccc
V$HOMF	Homeodomain transcription factors	V$HMX3.03	H6 homeodomain HMX3/Nkx5.1 transcription factor	2285	2303	2294	(-)	0.823	gataagtAAATtgatgacc
V$SORY	SOX/SRY-sex/testis determining and relat	V$SOX21.02	SRY (sex determining region Y)-box 21, dimeric binding site	734	756	745	(-)	0.822	cagCAACttagagtgttttagct
V$ETSF	Human and murine ETS1 factors	V$ETV6.01	Ets variant 6	1232	1252	1242	(-)	0.822	tgaaagccTGAAgttttagac
V$OCT1	Octamer binding protein	V$OCT1.06	Octamer-binding factor 1	2289	2303	2296	(-)	0.822	gataagtaAATTgat
V$NF1F	Nuclear factor 1	V$NF1.01	Nuclear factor 1	50	70	60	(+)	0.821	gacTTGGaaccaacccacatg
V$HOMF	Homeodomain transcription factors	V$HMX2.03	Hmx2/Nkx5-2 homeodomain transcription factor	580	598	589	(+)	0.821	cattcaTTAAatgtgtttt
V$RXRF	RXR heterodimer binding sites	V$RAR_RXR.01	Retinoic acid receptor / retinoid X receptor heterodimer, DR	985	1009	997	(+)	0.821	aagggggataaAGGCcaggggaagg
V$GATA	GATA binding factors	V$GATA3.03	GATA-binding protein 3	1904	1916	1910	(+)	0.821	cacaGATAAcaggat
V$DMRT	DM domain-containing transcription factor	V$DMRT4.01	Doublesex and mab-3 related transcription factor 4	2797	2817	2807	(+)	0.821	ctcaaatgaTACAgtaggagg
V$DMRT	DM domain-containing transcription factor	V$DMRT7.01	Doublesex and mab-3 related transcription factor 7	667	687	677	(-)	0.82	ttttTTTGttttattttatcc
V$HESF	Vertebrate homologues of enhancer of spl	V$BHLHB2.02	Basic helix-loop-helix domain containing, class B, 2 (second	1591	1605	1598	(-)	0.82	gcttccCGTGcaggc
V$TALE	TALE homeodomain class recognizing TG	V$MRG1.02	TALE homeobox protein Meis 2, dimeric binding site	884	900	892	(-)	0.819	ttgtCAGCtgtgaacag
V$MYBL	Cellular and viral myb-like transcriptional r	V$MYBL1.01	V-myb avian myeloblastosis viral oncogene homolog-like 1	2405	2425	2415	(-)	0.819	tttccttccaaACAGtttcag
V$MYBL	Cellular and viral myb-like transcriptional r	V$MYBL1.01	V-myb avian myeloblastosis viral oncogene homolog-like 1	872	892	882	(+)	0.818	cccagaagtaaACTGttcaca
V$CAAT	CCAAT binding factors	V$NFY.03	Nuclear factor Y (Y-box binding factor)	1793	1807	1800	(-)	0.818	caatGCAAtcagtgc
V$BRN5	Brn-5 POU domain factors	V$BRN5.01	Brn-5, POU-VI protein class (also known as emb and CNS	2522	2544	2533	(+)	0.818	gagttaTATAatttataatgtaa
V$BRN5	Brn-5 POU domain factors	V$BRN5.03	Brn-5, POU-VI protein class (also known as emb and CNS	363	385	374	(+)	0.817	tAAATgacaagttaatgcgtaca
V$HNF1	Hepatic Nuclear Factor 1	V$HNF1.03	Hepatic nuclear factor 1	2017	2033	2025	(+)	0.817	gGTTAaaaatggcctta
V$ZF12	C2H2 zinc finger transcription factors 12	V$ZFP652.01	Zinc finger protein 652 (ZNF652)	2172	2186	2179	(+)	0.816	tggttagggTTAAgt
V$MYOD	Myoblast determining factors	V$TCF21.01	Podocyte-expressed 1 (POD1)	2381	2397	2389	(+)	0.816	aggcaacaCCTGtcctg
V$FKHD	Fork head domain factors	V$FREAC4.01	Fork head related activator-4 (FOXD1)	399	415	407	(-)	0.815	cataggtaTACAtgtgc
V$CLOX	CLOX and CLOX homology (CDP) factors	V$CLOX.01	Cut-like homeodomain protein	2318	2340	2329	(+)	0.815	ccataATCGttcatgactgcaat
V$ATBF	AT-binding transcription factor	V$ATBF1.01	AT-binding transcription factor 1	2528	2544	2536	(-)	0.815	ttacattataAATTata
V$OCT1	Octamer binding protein	V$POU3F3.01	POU class 3 homeobox 3 (POU3F3), OTF8	1340	1354	1347	(-)	0.814	ctagtGCATagtaag
V$PRDF	Positive regulatory domain I binding factor	V$BLIMP1.01	Transcriptional repressor B lymphocyte-induced maturatio	1877	1895	1886	(-)	0.814	agcaaagGAAAgctatgag
V$BRN5	Brn-5 POU domain factors	V$BRN5.01	Brn-5, POU-VI protein class (also known as emb and CNS	2444	2466	2455	(-)	0.814	aaatggAATAaataatgattata
V$AIRE	Autoimmune regulatory element binding fa	V$AIRE.02	Autoimmune regulator	687	701	694	(+)	0.813	aaaggtaataTTTGt
V$ZF12	C2H2 zinc finger transcription factors 12	V$ZNF652.02	Zinc finger protein 652 (ZNF652)	1914	1928	1921	(-)	0.813	gagtagAGGTtaatc
V$PAX2	PAX-2 binding sites	V$PAX2.01	Zebrafish PAX2 paired domain protein	2485	2507	2496	(-)	0.813	atgactgtctcctaatcAAACaa
V$ZF12	C2H2 zinc finger transcription factors 12	V$ZFP652.01	Zinc finger protein 652 (ZNF652)	756	770	763	(+)	0.812	gaaaaagacTTAAaa
V$BRN5	Brn-5 POU domain factors	V$BRN5.01	Brn-5, POU-VI protein class (also known as emb and CNS	2444	2466	2455	(+)	0.812	tataatCATTatttattccattt
V$TALE	TALE homeodomain class recognizing TG	V$TGIF2.01	TGFB-induced factor homeobox 2, TALE homeobox TG-in	650	666	658	(-)	0.811	ttaccatttGTCAagtt
V$PAX2	PAX-2 binding sites	V$PAX2.01	Zebrafish PAX2 paired domain protein	722	744	733	(+)	0.811	cagaccagatagagctaAAACac
V$RREB	Ras-responsive element binding protein	V$RREB1.01	Ras-responsive element binding protein 1	1539	1553	1546	(-)	0.811	tCCCTaaccacccaa
V$HNF1	Hepatic Nuclear Factor 1	V$HNF1.01	Hepatic nuclear factor 1	2398	2414	2406	(+)	0.811	aGTTAatctgaaactgt
V$PIT1	GHF-1 pituitary specific pou domain trans	V$PIT1.02	POU domain, class 1, transcription factor 1 (POU1F1) / Pit	2446	2460	2453	(-)	0.811	aataaATAAtgatta
V$PIT1	GHF-1 pituitary specific pou domain trans	V$PIT1.02	POU domain, class 1, transcription factor 1 (POU1F1) / Pit	2447	2461	2454	(+)	0.811	aatcaTTATttattc
V$OVOL	OVO homolog-like transcription factors	V$OVOL1.01	Zinc finger transcription factor OVO homolog-like 1	2853	2867	2860	(-)	0.811	agcaccGTAAgatct
V$XBBF	X-box binding factors	V$RFX4.03	Regulatory factor X 4	947	965	956	(+)	0.81	gggGTTGctttggatcctg
V$DMRT	DM domain-containing transcription factor	V$DMRT1.01	Doublesex and mab-3 related transcription factor 1	1969	1989	1979	(+)	0.81	tctccttgcaagaTTGTtctt
V$DMRT	DM domain-containing transcription factor	V$DMRT3.01	Doublesex and mab-3 related transcription factor 3	797	817	807	(-)	0.808	tttcttagtTACAacagctag
V$BRNF	Brn POU domain factors	V$BRN3.01	Brn-3, POU-IV protein class	69	87	78	(+)	0.807	tgtccatcaATGAtagact
V$OVOL	OVO homolog-like transcription factors	V$OVOL1.01	Zinc finger transcription factor OVO homolog-like 1	823	837	830	(-)	0.807	taaaccATTAtatgt
V$BCL6	POZ domain zinc finger expressed in B-C	V$BCL6.03	B-cell CLL/lymphoma 6, member B (BCL6B)	1178	1194	1186	(+)	0.807	atgttgcTGGAcaggta

V$BRN5	Brn-5 POU domain factors	V$BRN5.01	Brn-5, POU-VI protein class (also known as emb and CNS	2522	2544	2533	(-)	0.807	ttacatTATAaattatataactc
V$PBXC	PBX - MEIS complexes	V$PBX1_MEIS1.03	Binding site for a Pbx1/Meis1 heterodimer	75	91	83	(+)	0.806	tcaatgatAGACtggat
V$HNF1	Hepatic Nuclear Factor 1	V$HNF1.03	Hepatic nuclear factor 1	458	474	466	(+)	0.806	gTTTAataatagtaaaa
V$SRFF	Serum response element binding factor	V$SRF.05	Serum response factor	2257	2275	2266	(+)	0.806	ctgcccgagtAAGGtacct
V$PDX1	Pancreatic and intestinal homeodomain tra	V$PDX1.01	Pdx1 (IDX1/IPF1) pancreatic and intestinal homeodomain T	2283	2301	2292	(-)	0.806	taagtaaatTGATgaccaa
V$PAX2	PAX-2 binding sites	V$PAX2.01	Zebrafish PAX2 paired domain protein	2407	2429	2418	(+)	0.806	gaaactgtttggaaggaAAACtt
O$VTBP	Vertebrate TATA binding protein factor	O$ATATA.01	Avian C-type LTR TATA box	804	820	812	(+)	0.805	ttgtaacTAAGaaagcc
V$CREB	cAMP-responsive element binding proteins	V$E4BP4.01	E4BP4, bZIP domain, transcriptional repressor	2288	2308	2298	(-)	0.805	tcacagataaGTAAattgatg
V$XBBF	X-box binding factors	V$MIF1.01	MIBP1 / RFX1 complex	2396	2414	2405	(+)	0.805	tgagttaatctGAAActgt
V$ZF16	C2H2 zinc finger transcription factors 16	V$PRDM15.01	PR/SET domain 15	2116	2130	2123	(-)	0.804	aaaatcagaatGGGA
V$CREB	cAMP-responsive element binding proteins	V$BATF3.01	Basic leucine zipper transcription factor, ATF-like 3	426	446	436	(+)	0.803	gcacGTTGtggtcatgtaccc
V$MYBL	Cellular and viral myb-like transcriptional r	V$MYBL2.01	v-myb myeloblastosis viral oncogene homolog (avian)-like	798	818	808	(+)	0.803	tagctgttgTAACtaagaaag
V$PAX7	Paired box 7	V$PAX7.01	Paired box 7 homeodomain-binding motif	826	840	833	(+)	0.803	tataatgGTTTaaaa
V$BRN5	Brn-5 POU domain factors	V$BRN5.02	Brn-5, POU-VI protein class (also known as emb and CNS	519	541	530	(-)	0.802	gtaatactttgATTCtcctaata
V$NR2F	Nuclear receptor subfamily 2 factors	V$TR2_TR4.01	DR1 binding sites for TR2 homodimers or TR2/TR4 hetero	1040	1064	1052	(+)	0.802	tcagaaatgacacaGCTCattctca
V$HOXH	HOX - MEIS1 heterodimers	V$MEIS1B_HOXA9.01	Meis1b and Hoxa9 form heterodimeric binding complexes c	171	185	178	(-)	0.801	TGCCagcttcatcca
V$SORY	SOX/SRY-sex/testis determining and relat	V$SOX9.03	SRY (sex determining region Y)-box 9 homodimer	1140	1162	1151	(+)	0.801	aaACACaggagtgctcttattaa
V$NR2F	Nuclear receptor subfamily 2 factors	V$TR2.01	Nuclear hormone receptor TR2, DR5 binding sites	2621	2645	2633	(-)	0.801	gaaggacagtaatgGTTCacagtcc
V$STAF	Selenocysteine tRNA activating factor	V$STAF.01	Se-Cys tRNA gene transcription activating factor	621	651	636	(-)	0.8	ttagttcctgtgtCCCAcaacacaccgcatt
V$FXRE	Farnesoid X - activated receptor response	V$FXRE.01	Farnesoid X - activated receptor (RXR/FXR dimer), IR1 site	786	798	792	(+)	0.8	AGGGtactggcct
V$FKHD	Fork head domain factors	V$FREAC4.01	Fork head related activator-4 (FOXD1)	874	890	882	(+)	0.8	cagaagtaAACTgttca
V$SORY	SOX/SRY-sex/testis determining and relat	V$SOX1.04	SRY (sex determining region Y)-box 1, dimeric binding sites	1312	1334	1323	(-)	0.8	tatAAATatttattgaataacaa
V$ATBF	AT-binding transcription factor	V$ATBF1.01	AT-binding transcription factor 1	2444	2460	2452	(+)	0.8	tataatcattATTTatt
V$SORY	SOX/SRY-sex/testis determining and relat	V$SOX1.04	SRY (sex determining region Y)-box 1, dimeric binding sites	1317	1339	1328	(+)	0.799	attCAATaaatatttatagacta
V$HOXH	HOX - MEIS1 heterodimers	V$MEIS1B_HOXA9.01	Meis1b and Hoxa9 form heterodimeric binding complexes c	2685	2699	2692	(-)	0.799	TGGCacattaaccac
V$PARF	PAR/bZIP family	V$TEF_HLF.01	Thyrotrophic embryonic factor / hepatic leukemia factor	1543	1559	1551	(-)	0.798	ctgacTTCCctaaccac
V$CREB	cAMP-responsive element binding proteins	V$BATF3.01	Basic leucine zipper transcription factor, ATF-like 3	1945	1965	1955	(-)	0.798	aggtGTTGaggttctgagcga
V$PAX2	PAX-2 binding sites	V$PAX2.01	Zebrafish PAX2 paired domain protein	831	853	842	(-)	0.796	taaactcccatctttttAAACca
V$PAX2	PAX-2 binding sites	V$PAX2.01	Zebrafish PAX2 paired domain protein	121	143	132	(+)	0.795	aatactgtacagccataAAAAtg
V$EVI1	EVI1-myleoid transforming protein	V$EVI1.03	Ecotropic viral integration site 1 encoded factor, amino-term	1272	1288	1280	(+)	0.795	aagctAACAtaaactcc
V$RXRF	RXR heterodimer binding sites	V$VDR_RXR.05	Bipartite binding site of VDR/RXR heterodimers, DR4 sites	1691	1715	1703	(+)	0.795	ggaGAAGgttataaggggagagaag
V$BRN5	Brn-5 POU domain factors	V$BRN5.03	Brn-5, POU-VI protein class (also known as emb and CNS	1824	1846	1835	(+)	0.795	cCAATgagtgatgaatgaacaaa
V$SORY	SOX/SRY-sex/testis determining and relat	V$SOX9.03	SRY (sex determining region Y)-box 9 homodimer	1874	1896	1885	(-)	0.795	aaGCAAaggaaagctatgagtgt
V$SNAP	snRNA-activating protein complex	V$PSE.02	Proximal sequence element (PSE) of RNA polymerase III-tr	2166	2184	2175	(-)	0.795	ttaacCCTAaccaagagtg
V$EVI1	EVI1-myleoid transforming protein	V$EVI1.03	Ecotropic viral integration site 1 encoded factor, amino-term	2289	2305	2297	(-)	0.795	cagatAAGTaaattgat
V$DMRT	DM domain-containing transcription factors	V$DMRT4.01	Doublesex and mab-3 related transcription factor 4	2685	2705	2695	(-)	0.795	ttgagctggCACAttaaccac
V$CLOX	CLOX and CLOX homology (CDP) factors	V$CUX1.01	Cut-like homeobox 1, dimeric binding site	69	91	80	(+)	0.794	tgtccatCAATgatagactggat
V$HOXC	HOX - PBX complexes	V$PBX_HOXA9.01	PBX - HOXA9 binding site	2641	2657	2649	(-)	0.794	gccaTGTTttaggaagg
V$SORY	SOX/SRY-sex/testis determining and relat	V$SOX1.04	SRY (sex determining region Y)-box 1, dimeric binding sites	2581	2603	2592	(+)	0.793	tttGAATtccaaaacactgggct
V$DMRT	DM domain-containing transcription factors	V$DMRT1.01	Doublesex and mab-3 related transcription factor 1	2778	2798	2788	(+)	0.793	gtgagatggtaaaATGTggct
V$PARF	PAR/bZIP family	V$TEF_HLF.01	Thyrotrophic embryonic factor / hepatic leukemia factor	455	471	463	(-)	0.792	tactaTTATtaaacttt
V$MOKF	Mouse Krueppel like factor	V$MOK2.01	Ribonucleoprotein associated zinc finger protein MOK-2 (m	744	764	754	(-)	0.792	gtctttttcagcaACTTagag
V$AIRE	Autoimmune regulatory element binding fa	V$AIRE.01	Autoimmune regulator	859	873	866	(-)	0.792	ggTTATtacatggag
V$NR2F	Nuclear receptor subfamily 2 factors	V$HPF1.01	HepG2-specific P450 2C factor-1, DR1 sites	1879	1903	1891	(-)	0.792	ccaagtaaagcAAAGgaaagctatg
V$HBOX	Homeobox transcription factors	V$EN1.01	Homeobox protein engrailed (en-1)	1106	1124	1115	(-)	0.791	ctggccagTTCAagtgtac
V$ZF14	C2H2 zinc finger transcription factors 14	V$ZNF232.01	Zinc finger protein 232 (ZSCAN11)	2705	2723	2714	(+)	0.791	aaGTTAaatggggagtgag
V$STAF	Selenocysteine tRNA activating factor	V$ZNF76_143.01	ZNF143 is the human ortholog of Xenopus Staf, ZNF76 is a	1718	1748	1733	(-)	0.79	ctacaagcctgctCCCAgctgcctttctgat
V$NFAT	Nuclear factor of activated T-cells	V$NFATC1.01	Nuclear factor of activated T-cells, cytoplasmic, calcineurin	1894	1912	1903	(+)	0.79	ctttacTTGGcaaagatta
V$XBBF	X-box binding factors	V$RFX2.01	Regulatory factor X 2	1989	2007	1998	(+)	0.79	tagtgtCCTTggtagccca
V$NFAT	Nuclear factor of activated T-cells	V$NFATC1.01	Nuclear factor of activated T-cells, cytoplasmic, calcineurin	106	124	115	(-)	0.788	tattccATGGtgtatatgt
V$ZBED	Zinc finger BED domain-containing protein	V$ZBED1.02	Zinc finger, BED-type containing 1	159	171	165	(-)	0.787	aTGTCcctacaaa
V$OCT1	Octamer binding protein	V$OCT.01	Octamer binding site (OCT1/OCT2)	1091	1105	1098	(+)	0.787	aagATGCcaagaaaa
V$GZF1	GDNF-inducible zinc finger gene 1	V$GZF1.01	GDNF-inducible zinc finger protein 1 (ZNF336)	1290	1302	1296	(-)	0.787	TGGGcttatattt
V$PARF	PAR/bZIP family	V$TEF_HLF.01	Thyrotrophic embryonic factor / hepatic leukemia factor	2582	2598	2590	(+)	0.787	ttgaaTTCCaaaacact
V$PAX2	PAX-2 binding sites	V$PAX2.01	Zebrafish PAX2 paired domain protein	740	762	751	(+)	0.786	aacactctaagttgctgAAAAag
V$PBXC	PBX - MEIS complexes	V$PBX1_MEIS1.02	Binding site for a Pbx1/Meis1 heterodimer	1178	1194	1186	(+)	0.786	atgtTGCTggacaggta
V$HEAT	Heat shock factors	V$HSF1.04	Heat shock factor 1	1581	1605	1593	(-)	0.786	gcttcccgtgcaggcactTTCTgct
V$BRN5	Brn-5 POU domain factors	V$POU6F2.01	Retina-derived POU-domain factor-1, dimeric binding site	2526	2548	2537	(-)	0.786	taaattacattATAAattatata
V$PAX9	PAX-9 binding sites	V$PAX9.01	Zebrafish PAX9 binding sites	235	255	245	(+)	0.785	tgttctcactcacaGGTGaga
V$PARF	PAR/bZIP family	V$TEF_HLF.01	Thyrotrophic embryonic factor / hepatic leukemia factor	2533	2549	2541	(-)	0.785	ataaaTTACattataaa
V$BRNF	Brn POU domain factors	V$BRN3.01	Brn-3, POU-IV protein class	133	151	142	(-)	0.784	aactcatccATTTttatgg
V$DUXF	Double homeobox factors	V$DUX4.01	Double homeobox protein 4	1795	1809	1802	(+)	0.784	actGATTgcattgta
V$EVI1	EVI1-myleoid transforming protein	V$EVI1.01	Ecotropic viral integration site 1 encoded factor, amino-term	2095	2111	2103	(-)	0.784	ttgaaCAGAatagacaa
V$PAX2	PAX-2 binding sites	V$PAX2.01	Zebrafish PAX2 paired domain protein	456	478	467	(-)	0.783	tttttttactattattAAACtt
V$HEAT	Heat shock factors	V$HSF1.03	Heat shock factor 1	1466	1490	1478	(+)	0.782	acagtagataccAGTAagagcaaag
V$PROX	Prospero-related homeobox	V$PROX1.01	Prospero homeobox protein 1, dimeric binding site	2722	2734	2728	(-)	0.782	ccaGACAccttct
O$VTBP	Vertebrate TATA binding protein factor	O$ATATA.01	Avian C-type LTR TATA box	2523	2539	2531	(+)	0.781	agttataTAATttataa

V$PROX	Prospero-related homeobox	V$PROX1.01	Prospero homeobox protein 1, dimeric binding site	897	909	903	(-)	0.78	cgaGCCGccttgt
V$DUXF	Double homeobox factors	V$DUX4.01	Double homeobox protein 4	2488	2502	2495	(+)	0.78	tttGATTaggagaca
V$BCL6	POZ domain zinc finger expressed in B-C	V$BCL6.02	POZ/zinc finger protein, transcriptional repressor, transloca	1244	1260	1252	(-)	0.779	ttgttttTTGAaagcct
V$MYT1	MYT1 C2HC zinc finger protein	V$MYT1.01	MyT1 zinc finger transcription factor involved in primary ne	1269	1281	1275	(+)	0.777	acaAAGCtaacat
V$HEAT	Heat shock factors	V$HSF1.02	Heat shock factor 1	701	725	713	(-)	0.776	tctgcctctgCCAGaaactactaca
V$ZTRE	Zinc transcriptional regulatory element	V$ZTRE.02	ZTRE motifs (2 bp spacer), ZNF658 binding site	2510	2526	2518	(-)	0.776	aaCTCCcctggaagggt
V$PBXC	PBX - MEIS complexes	V$PBX1_MEIS1.02	Binding site for a Pbx1/Meis1 heterodimer	177	193	185	(-)	0.775	atgaTGGTtgccagctt
V$MEF2	MEF2, myocyte-specific enhancer binding	V$MEF2.01	Myocyte-specific enhancer factor 2	2012	2034	2023	(+)	0.775	cccctggtTAAAaatggccttag
V$BRN5	Brn-5 POU domain factors	V$BRN5.02	Brn-5, POU-VI protein class (also known as emb and CNS	509	531	520	(+)	0.774	ctcatatgtctATTAggagaatc
V$HUB1	HTLV-I U5 repressive element-binding pro	V$ZNF282.01	Zinc finger protein 282 (HTLV-I U5 repressive element-bind	2038	2052	2045	(-)	0.774	TTTCcgcaaattctt
V$CLOX	CLOX and CLOX homology (CDP) factors	V$CUX2.01	Cut-like homeobox 2, dimeric binding site	74	96	85	(-)	0.773	ttttaatccagtctatcaTTGAt
V$SORY	SOX/SRY-sex/testis determining and relat	V$SOX9.06	SRY (sex-determining region Y) box 9, dimeric binding sites	492	514	503	(-)	0.773	tatgagtctgatGTCAttttctc
V$STAT	Signal transducer and activator of transcri	V$STAT1.01	Signal transducer and activator of transcription 1	974	992	983	(+)	0.773	taggtagcgGGAAggggga
V$ZF12	C2H2 zinc finger transcription factors 12	V$ZFP652.01	Zinc finger protein 652 (ZNF652)	329	343	336	(+)	0.772	ggcgacgggATAAca
V$SNAP	snRNA-activating protein complex	V$PSE.02	Proximal sequence element (PSE) of RNA polymerase III-tr	1018	1036	1027	(-)	0.772	atgtcCTTAaaagaaattt
V$EVI1	EVI1-myleoid transforming protein	V$EVI1.01	Ecotropic viral integration site 1 encoded factor, amino-term	1710	1726	1718	(+)	0.772	gagaaGAGAtcagaaag
V$ZF01	C2H2 zinc finger transcription factors 1	V$ZBRK1.01	Transcription factor with 8 central zinc fingers and an N-ter	2611	2635	2623	(-)	0.772	aatggttcACAGtcctttatccaaa
V$ZF14	C2H2 zinc finger transcription factors 14	V$ZNF232.01	Zinc finger protein 232 (ZSCAN11)	2784	2802	2793	(+)	0.772	tgGTAAaatgtggctcaaa
V$PAX6	PAX-4/PAX-6 paired domain binding sites	V$PAX6.03	Pax-6 paired domain binding site	1920	1938	1929	(+)	0.771	cctctACTCatcctttgca
V$RXRF	RXR heterodimer binding sites	V$LXRE.02	Highly conserved DR1 element selected by LXRbeta/RXR	2695	2719	2707	(+)	0.77	tgccaGCTCaaagttaaatggggag
V$HEAT	Heat shock factors	V$HSF1.03	Heat shock factor 1	2812	2836	2824	(-)	0.769	cctgtgaggcctGGAAaatcctcct
V$PAX6	PAX-4/PAX-6 paired domain binding sites	V$PAX6.01	Pax-6 paired domain binding site	369	387	378	(-)	0.768	gctgtACGCattaacttgt
V$AIRE	Autoimmune regulatory element binding fa	V$AIRE.02	Autoimmune regulator	2176	2190	2183	(+)	0.767	tagggttaagTTTGa
V$PRDM	PR (PRDI-BF1-RIZ1 homologous) domain	V$PRDM4.01	PR domain zinc finger protein 4 (PFM1)	2815	2843	2829	(+)	0.766	aggatTTTCcaggcctcacaggagtgttt
V$XBBF	X-box binding factors	V$MIF1.01	MIBP1 / RFX1 complex	2358	2376	2367	(+)	0.763	taagatttttaGTAActca
V$ZTRE	Zinc transcriptional regulatory element	V$ZTRE.01	ZTRE motifs (1 bp spacer), ZNF658 binding site	2512	2528	2520	(+)	0.763	ccttccagGGGAgttat
V$SORY	SOX/SRY-sex/testis determining and relat	V$SOX8.02	SRY (sex determining region Y)-box 8, dimeric binding sites	144	166	155	(+)	0.762	gatGAGTtcatgtcctttgtagg
V$BRN5	Brn-5 POU domain factors	V$BRN5.03	Brn-5, POU-VI protein class (also known as emb and CNS	663	685	674	(+)	0.762	gTAAGgataaaataaaacaaaaa
V$AP1R	MAF and AP1 related factors	V$MARE_ARE.01	Antioxidant response elements	1052	1076	1064	(-)	0.762	ggtcatgctggGTGAgaatgagctg
V$HEAT	Heat shock factors	V$HSF1.04	Heat shock factor 1	1597	1621	1609	(-)	0.762	gacctttgcccttgcagcTTCCcgt
V$HEAT	Heat shock factors	V$HSF1.04	Heat shock factor 1	1967	1991	1979	(+)	0.762	tttctccttgcaagattgTTCTtag
V$NR2F	Nuclear receptor subfamily 2 factors	V$HNF4.02	Hepatic nuclear factor 4, DR2 sites	2234	2258	2246	(-)	0.762	agtctggctctAAAGgccacagcct
V$STAF	Selenocysteine tRNA activating factor	V$ZNF76_143.01	ZNF143 is the human ortholog of Xenopus Staf, ZNF76 is a	2002	2032	2017	(-)	0.761	aaggccatttttaACCAggggacactgggct
V$PERO	Peroxisome proliferator-activated receptor	V$PPAR_RXR.01	PPAR/RXR heterodimers, DR1 sites	2692	2714	2703	(+)	0.76	atgtgccagctcaaAGTTaaatg
V$ZTRE	Zinc transcriptional regulatory element	V$ZTRE.02	ZTRE motifs (2 bp spacer), ZNF658 binding site	2766	2782	2774	(-)	0.759	ctCACCcacaagggtga
V$SNAP	snRNA-activating protein complex	V$PSE.02	Proximal sequence element (PSE) of RNA polymerase III-tr	2126	2144	2135	(-)	0.758	taaacCCTAtggaaaaaat
V$BRAC	Brachyury gene, mesoderm development	V$MGA.01	MAX gene associated, dimeric binding site	623	651	637	(-)	0.757	ttagttcctgtgtcccacaacACACcgca
V$MYT1	MYT1 C2HC zinc finger protein	V$MYT1.01	MyT1 zinc finger transcription factor involved in primary ne	2422	2434	2428	(+)	0.756	gaaAACTtgacat
V$E2FF	E2F-myc activator/cell cycle regulator	V$E2F.01	E2F, involved in cell cycle regulation, interacts with Rb p10	1783	1799	1791	(-)	0.755	tcagtgctgGAAAatgc
V$CART	Cart-1 (cartilage homeoprotein 1)	V$HESX1.01	HESX homeobox 1, dimeric binding site	1892	1912	1902	(+)	0.755	tgcttTACTtggcaaagatta
V$MYBL	Cellular and viral myb-like transcriptional r	V$MYBL2.01	v-myb myeloblastosis viral oncogene homolog (avian)-like	1267	1287	1277	(+)	0.752	caacaaagcTAACataaactc
V$PRDM	PR (PRDI-BF1-RIZ1 homologous) domain	V$PRDM5.01	PR domain containing 5	1694	1722	1708	(+)	0.751	gaaggttatAAGGgagagaagagatcag

Supplementary Table 4. siRNA sets used in this study relate to Figs. 1, 3; Extended Data Figs. 2, 3, 5, 9

Product Description	Catalog Number	CloneIds	ishRNA sequences	Reference
ON-TARGETplus Human NAPRT siRNA #1	L-016912-01-0005	L-016912-09	GCAACAACAUUGACGAGGA	Dharmacon
ON-TARGETplus Human NAPRT siRNA #2		L-016912-10	CUGGAAACAACACGAAUCA	Dharmacon
ON-TARGETplus Human NAPRT siRNA #3		L-016912-11	GGUAGAGCCCUGACUGGGA	Dharmacon
ON-TARGETplus Human NAPRT siRNA #4		L-016912-12	GGACAGUGGUGACCUGCUA	Dharmacon
Silencer® Select Human NAPRT siRNA #5		s195572	GAAUGAAGCUGACCGAGGAtt	Ambion-ThermoFischer Scientific
ON-TARGETplus Human NAMPT siRNA #1	L-004581-00-0005	J-004581-05	GGUAAGAAGUUUCCUGUUA	Dharmacon
ON-TARGETplus Human NAMPT siRNA #2		J-004581-06	CAAAUUGGAUUGAGACUAU	Dharmacon
ON-TARGETplus Human NAMPT siRNA #3		J-004581-07	UAACUUAGAUGGUCUGGAA	Dharmacon
ON-TARGETplus Human NAMPT siRNA #4		J-004581-08	CAAGCAAAGUUUAUUCCUA	Dharmacon
Silencer® Select Human NAMPT siRNA #5		s19725	CAAAUUGGAUUGAGACUAUtt	Ambion-ThermoFischer Scientific
ON-TARGETplus Human NADSYN1 siRNA #1	L-007723-01-0005	J-007723-09	GGAAAUAUGCGGCUACGGA	Dharmacon
ON-TARGETplus Human NADSYN1 siRNA #2		J-007723-10	CAUUAUUACGAGUCGGACA	Dharmacon
ON-TARGETplus Human NADSYN1 siRNA #3		J-007723-11	UCUGCAAACUCCUCGGCAU	Dharmacon
ON-TARGETplus Human NADSYN1 siRNA #4		J-007723-12	CUGACAAAGUGAAGCGGUU	Dharmacon
Silencer® Select Human NADSYN1siRNA #5		s30396	GGGUGGAUCUCGUGACUAUtt	Ambion-ThermoFischer Scientific
ON-TARGETplus Human NMRK1 siRNA #1	L-006722-01-0005	J-006722-09	CUCCAGACUCUCCGGGAUA	Dharmacon
ON-TARGETplus Human NMRK1 siRNA #2		J-006722-10	GGACUGUACCUUAGCAAGU	Dharmacon
ON-TARGETplus Human NMRK1 siRNA #3		J-006722-11	CUUUCUGAACAUAGCUCUA	Dharmacon
ON-TARGETplus Human NMRK1 siRNA #4		J-006722-12	CUUGACACUAUAUAUGGAAUA	Dharmacon
Silencer® Select Human NMRK1 siRNA #5		S29916	GACACUAUAUGGAAUAGAAtt	Ambion-ThermoFischer Scientific
ON-TARGETplus Human NMRK2 siRNA #1	L-006747-01-0005	J-006747-10	UGGUCUACCUGGACGGCAU	Dharmacon
ON-TARGETplus Human NMRK2 siRNA #2		J-006747-11	GGACAGCAUGUGAGCGUUU	Dharmacon
ON-TARGETplus Human NMRK2 siRNA #3		J-006747-12	GGGACGUGCUGGAGUCUCU	Dharmacon
ON-TARGETplus Human NMRK2 siRNA #4		J-006747-13	CAGAAGUAUAGGCAGGAGA	Dharmacon
Silencer® Select Human NMRK2 siRNA #5		S25996	ACUGCUGCGUGAUCCAUCAtt	Ambion-ThermoFischer Scientific
Silencer® Select Human STAT3 siRNA #1		S744	GGCUGGACAAUAUCAUUGAtt	Ambion-ThermoFischer Scientific
Silencer® Select Human STAT3 siRNA #2		S745	GCACCUUCCUGCUAAGAUUtt	Ambion-ThermoFischer Scientific
Human GATA3 siRNA #1			GCAGGGCAGUAUCAUGAAGCCUAA	Song H. JBC. 2009
Human GATA3 siRNA #2			GGCAUGAAGGAUGCCAAGAAGUUU	Song H. JBC. 2009
Human MAX siRNA			CAAAGACAGCUUUCACAGU	Babic. Cell Metabolism. 2013
Silencer® Select Human MYC siRNA		103828	GAGCUAAAACGGAGCUUUUtt	Ambion-ThermoFischer Scientific
Human FOXM1 siRNA			GGACCACUUUCCCUACUUU	Wu. Acta Pharmacologica Sinica. 2010
Silencer Select Human Negative Control #2		4390846		Ambion-ThermoFischer Scientific Babic. Cell Metabolism. 2013

Supplementary Table 4. shRNA sets used in this study relate to Fig. 4 Extended Data Figs. 4, 8, 9

Product Description	Catalog Number	CloneIds	shRNA sequences (target sequence)	Reference
shLuciferase-Control			CTTACGCTGAGTACTTCGA	Li. F. Cancer Cell. 2015
MISSION® pLKO.1-puro Non-Mammalian shRNA Control	SHC002		TRC1 and TRC1.5 pLKO.1-puro Non-Mammalian shRNA Control Plasmid DNA (SHC002), is a negative control containing a sequence that should not target any known mammalian genes, but will engage with RISC	
NAMPT MISSION shRNA #1	TRCN0000116177	NM_182790.1-1070s1c1	CCGGCCACCTTATCTTAGAGTTATTCTCGAGAATAACTCTAAGATAAGGTGGTTTTTG	
NAMPT MISSION shRNA #2	TRCN0000116180	NM_182790.1-579s1c1	CCGGGTAACTTAGATGGTCTGGAATCTCGAGATTCCAGACCATCTAAGTTACTTTTTG	
NAPRT1 MISSION shRNA #1	TRCN0000242730	NM_145201.4-94s21c1	CCGGCACCATGGCGTTGGGCTATTGCTCGAGCAATAGCCCAACGCCATGGTGTTTTTG	
NAPRT1 MISSION shRNA #2	TRCN0000242731	NM_145201.4-1192s21c1	CCGGTTCCCTGGGTGGCGTCTATAACTCGAGTTATAGACGCCACCCAGGGAATTTTTG	
NAPRT1 MISSION shRNA #3	TRCN0000242729	NM_145201.4-1069s21c1	CCGGGTCAGTCCTCATCGTAGTCAGCTCGAGCTGACTACGATGAGGACTGACTTTTTG	
NMRK1 MISSION shRNA #1	TRCN0000160349	NM_017881.1-382s1c1	CCGGCTTGAAGCACTTAACATGGAACTCGAGTTCCATGTTAAGTGCTTCAAGTTTTTTG	
NMRK1 MISSION shRNA #2	TRCN0000360129	NM_017881.2-782s21c1	CCGGGCAAGTATATGAAGATCTAATCTCGAGATTAGATCTTCATATACTTGCTTTTTG	
NMRK2 MISSION shRNA #1	TRCN0000359472	NM_170678.2-679s21c1	CCGGGGAGAAGTACCCGCAACTACACTCGAGTGTAGTTGCGGGTACTTCTCCTTTTTG	
NMRK2 MISSION shRNA #2	TRCN0000359397	NM_170678.2-645s21c1	CCGGTTCCTGACCGTCCCGTATGAACTCGAGTTCATACGGGACGGTCAGGAATTTTTG	
NADSYN1 MISSION shRNA #1	TRCN0000045508	NM_018161.4-1446s1c1	CCGGCCACCACATCAGTCTCAACATCTCGAGATGTTGAGACTGATGTGGTGGTTTTTG	
NADSYN1 MISSION shRNA #2	TRCN0000232702	NM_018161.4-276s21c1	CCGGCTACGGATGTTGGGATCATTACTCGAGTAATGATCCCAACATCCGTAGTTTTTG	

Supplementary Table 4. Inducible shRNA sets used in this study, relate to Figs. 1, 4 and Extended Data Figs. 6, 7

Product Description	Catalog Number	CloneIds	ishRNA sequences
SMARTvector Inducible Nontargeting mEF1a-TurboRFP shRNA	VSC11658	VSH11660	
SMARTvector Inducible Human NAPRT mEF1a - TurboRFP shRNA #1 (UTR)	V3SH11255-10EG93100	V3SH11252-226366844	TTTGAGATCACCTAAACAC
SMARTvector Inducible Human NAPRT mEF1a - TurboRFP shRNA #2		V3SH11252-225421625	GAGACCACTCCTCCACACG
SMARTvector Inducible Human NAPRT mEF1a - TurboRFP shRNA #3		V3SH11252-225577913	CCTGCGATCAAGCGAAGCC
SMARTvector Inducible Human NMRK1 mEF1a-TurboRFP shRNA #1 (UTR)	V3SH11255-10EG54981	V3SH11252-226740701	GAGCTCTGCTGTATCTATG
SMARTvector Inducible Human NMRK1 mEF1a-TurboRFP shRNA #2		V3SH11252-226475183	CTGATTCCAATGATAAATG
SMARTvector Inducible Human NMRK1 mEF1a-TurboRFP shRNA #3		V3SH11252-226699253	TCCGTCTTTATGCTGTCAC
SMARTvector Inducible Human NMRK2 mEF1a - TurboRFP shRNA #1	V3SH11255-10EG27231	V3SH11252-224727305	TGGGCACGGGCAAACTTCT
SMARTvector Inducible Human NMRK2 mEF1a - TurboRFP shRNA #2		V3SH11252-225138617	GCTGTAGAGCAGGAAGCCT
SMARTvector Inducible Human NMRK2 mEF1a - TurboRFP shRNA #3		V3SH11252-227090666	TTACAGAGGCGTCTTGGGG
SMARTvector Inducible Human NAMPT mEF1a - TurboRFP shRNA #1 (UTR)	V3SH11255-10EG10135	V3SH11252-229940249	GGAAAAGTGAGTGATTCGT
SMARTvector Inducible Human NAMPT mEF1a - TurboRFP shRNA #2		V3SH11252-226167755	CAAACCTCCACCAGAACCG
SMARTvector Inducible Human NAMPT mEF1a - TurboRFP shRNA #3		V3SH11252-226214912	TTCACCCCATATTTTCTCA
SMARTvector Inducible Human NADSYN1 mEF1a - TurboRFP shRNA #1	V3SH11255-08EG55191	V3SH11252-224734628	CTGAGTTTCCCATAGACCG
SMARTvector Inducible Human NADSYN1 mEF1a - TurboRFP shRNA #2		V3SH11252-224850260	GGCAGGTCCAAGGCTTATC
SMARTvector Inducible Human NADSYN1 mEF1a - TurboRFP shRNA #3		V3SH11252-225184913	CCGAGACCAGAGGCTCAAC

Supplementary Table 4. RT-PCR primer sets used in this study, relate to Fig. 3 and Extended Data Figs. 1, 5, 8

Description	Primer ID	5' --> 3'	3' --> 5'
TBP	TBP	GAGCTGTGATGTGAAGTTTCC	TCTGGGTTTGATCATTCTGTAG
B2M	B2M	ATGAGTATGCCTGCCGTGTGA	GGCATCTTCAAACCTCCATG
YWHAZ	YWHAZ	TGATCCCCAATGCTTCACAAG	GCCAAGTAACGGTAGTAATCTCC
RPL13A	RPL13A	GGACCGTGCGAGGTATGCT	ATGCCGTCAAACACCTTGAGA
NAMPT	NAMPT #1	AGTGGTGCCTGTGTACTTCT	TGCCTGTATCTGTGGTCAGC
NAMPT	NAMPT #2	AATGTTCTCTTCACGGTGGAAA	ACTGTGATTGGATACCAGGAC
NAMPT	NAMPT #3	ATCCTGTTCCAGGCTATTCTGT	CCCCATATTTTCTCACACGCAT
NMRK1	NMRK1 #1	TCCTCAGCACTTTCCTGGTC	CAGCCATTTCCTGCTGGATG
NMRK1	NMRK1 #2	TCATCCTGAGATATGACACTGCAA	GTGGCAAAACAACACTGGCT
NMRK1	NMRK1 #3	ACACTTTTGCTTTGCTAGTTCTTGT	TGGAACAAAATCTGAAGAGGACC
NMRK2	NMRK2 #1	ATGACCAACGGCGGCAAG	ATCCTGATGGATCACGCAGC
NMRK2	NMRK2 #2	TCTCTGGACATGGAGGCCA	AGCTGTAGAGCAGGAAGCCT
NMRK2	NMRK2 #3	CATGAAGTCCCGAGAGGAGC	GATTCCTGGGAGCGGTTCAG
NAPRT	NAPRT #1	GTGAGGTGAATGTCATTGG	GGCCACCAGCTTATAGAC
NAPRT	NAPRT #2	GCCAATGACATTCACCTCACT	AGGTCTTCCGAGCTGCT
NAPRT	NAPRT #3	TGGACATGCTGCAGTTAGCA	GCAGTAGTGGCTCCACCTG
NADSYN1	NADSYN1 #1	CGCATACTGACCACCTGCTA	CAATCTGCTGGGCCAACTCT
NADSYN1	NADSYN1 #2	CTCAACATCGATCCAGCCGT	CAAACAGAGGGCTCTTCCCC
NADSYN1	NADSYN1 #3	ACAAGATGACCACGCTCACA	ATGGTCGCAGATCAAACCTGT

Supplementary Table 4. qPCR primer sets used in this study, relate to Extended Data Fig. 1

Description	Primer ID	5' --> 3'	3' --> 5'
RPPH1	RPPH1 #1	CGG AGG GAA GCT CAT CAG TG	TGG CCC TAG TCT CAG ACC TT
HBB	HBB #1	CAG GTA CGG CTG TCA TCA CTT AGA	CAT GGT GTC TGT TTG AGG TTG CTA
NAMPT	NAMPT #1	AAGTGAATTTTGAGTCTGGGAAGA	ATCAGAGTTGGCAAGAGGAAGC
NAMPT	NAMPT #2	AGGCAGTTTGGAAGAGGTAGTG	TATGAGGCGTCCGGAATAGA
NAMPT	NAMPT #3	TTAAGTCACTGCTCGGTCGG	CCAGAGCTCCCAGACTGC
NMRK1	NMRK1 #1	ACAACTCACAAAGATGGCTTCA	GGCCCCTTGACACTATATGGAAT
NMRK1	NMRK1 #2	CAGGTCTGCAATGCCTTCACTTT	ATAGAACAGCTATGGAGGGGGC
NMRK1	NMRK1 #3	TGCTGTATCTATGCGCTCCC	ACTGTGGTACAATGACAGCCA
NMRK2	NMRK2 #1	GGCGCCAGGTTTTCTCAATG	GGACGACTTCCAAGGCAGC
NMRK2	NMRK2 #2	TTCCTTGACGCCACGAGAAC	TCAGCAGCCCCACACTTTTC
NMRK2	NMRK2 #3	CCATAGGACACAGAGAGCGG	TCCTGGCCAGAGAGCTCAGAT
NAPRT	NAPRT #1	GGT GCT TTG AAG GTG GAC AG	CAC GAA TGA AGC TGA CCG AG
NAPRT	NAPRT #2	TCC CAG GGT GAG GAT CAC TA	CTT CAG GGT GTA AGG AGG GG
NAPRT	NAPRT #3	CCCAGGTAGCTGTAGGTGGA	AGAGAAGCGGCTGCTAGAGA
NADSYN1	NADSYN1 #1	GCCCTGCTTTCCACATGACAG	CCAGCTCTGTCGCGGTTAATG
NADSYN1	NADSYN1 #2	ACATGACAGTGTCCCCAGAGG	TTCTCTTCAAAGCCCTTCCAGC
NADSYN1	NADSYN1 #3	TCTGATATCACAAAGCTTCGATCC	CAGGCTCACGAGACGATCAG

Supplementary Table 4. Primer sets used in this study, relate to Figs. 2, 3 and Extended Data Fig. 5

Primers for cloning NAMPT enhancer [backbone vector: pGL3-Basic (Promega)]

Description	Primer ID	5' --> 3'	3' --> 5'
NAMPT-Enhancer-4.6 Kb clone upstream	PGL3Enh-MLUI/XHOI4.6K	CG ACGCGT AGGATTATAAATCATGCTGCTATAAAGACACATGC	CG CTCGAG GTCATTACTTACCTGTTGGTTGCATGCCTCTTAAG
NAMPT-Enhancer-4.6 Kb clone downstream	PGL3Enh-XBAI/XBAI4.6K	CGTCTAGAAGGATTATAAATCATGCTGCTATAAAGACACATGC	CGTCTAGAGTCATTACTTACCTGTTGGTTGCATGCCTCTTAAG
NAMPT-Promotor	PGL3proFW-BGLII/HINDIII	GC AGATCT GTGAGCCGAGATCCAGCCACTGCACTCCAGCCTG	AAGCTT GCGGGGCGCGGCAGCGCGCTGCGCAGTGCGCGGA
NAMPT-Enhancer-4.6 Kb clone upstream-A	PGL3Enh-MLUI/XHOI-A	CG ACGCGT AGGATTATAAATCATGCTGCTATAAAGACACATGC	CTCGAGACCATTATATGTGGGGCTTTCTTAGTTACAACAGCTAGGCC
NAMPT-Enhancer-4.6 Kb clone upstream-B	PGL3Enh-MLUI/XHOI-B	CG ACGCGT GATGGGAGTTTATTTTTCTCCATGTAATAACCCAG	CTCGAGTAGTTTGTTCATTCATCACTCATTGGGTGCC
NAMPT-Enhancer-4.6 Kb clone upstream-C	PGL3Enh-MLUI/XHOI-C	CG ACGCGT GACCTGAGGCTGTTGACACTCATAGCTTTCC	CTCGAGGTATCATTTGAGCCACATTTTACCATCTCACCC
NAMPT-Enhancer-4.6 Kb clone upstream-D	PGL3Enh-MLUI/XHOI-D	CG ACGCGT AGTAGGAGGATTTTCCAGGCCTCACAGGAGTG	CTCGAGACTGGGGAGGTGAAACACTTCAACCATCC
NAMPT-Enhancer-4.6 Kb clone upstream-E	PGL3Enh-MLUI/XHOI-E	CG ACGCGT CTATCAGTGCACAGGCTGTGCCTGG	CG CTCGAG GTCATTACTTACCTGTTGGTTGCATGCCTCTTAAG

Supplementary Table 4. Primer sets used in this study, relate to Fig. 2

Primers used for site-directed mutagenesis [backbone vector: pGL3-Basic (Promega)]

Description	Primer ID	5' --> 3'	3' --> 5'	DNA coordinates (GRCh37/hg19)
NAMPT-Enh△A	BCDE	AGGATTATAAATCATGCTGCGCATAGGGTACTGGCCTAGCTGTTGTA	TACAACAGCTAGGCCAGTACCCTATGCGCAGCATGATTTATAATCCT	105856198-105856822
NAMPT-Enh△B	ACDE	GCATAGGGTACTGGCCTAGCTGTTGTACCTTTGCTTTACTTGGCAAAGATTAGG	CTGTGAGGCCTGGAAAATCCTCCTACTCCTAATCTTTGCCAAGTAAAGCAAAGG	105856850-105857928
NAMPT-Enh△C	ABDE	CCTTTGCTTTACTTGGCAAAGATTAGGAGTAGGAGGATTTTCCAGGCCTCACAG	CTGTGAGGCCTGGAAAATCCTCCTACTCCTAATCTTTGCCAAGTAAAGCAAAGG	105857929-105858849
NAMPT-Enh△D	ABCE	AGTAGGAGGATTTTCCAGGCCTCACAGCTATCAGTGCACAGGCTGTGCCTGG	CCAGGCACAGCCTGTGCACTGATAGCTGTGAGGCCTGGAAAATCCTCCTACT	105858850-105859749
NAMPT-Enh△E	ABCD	CTATCAGTGCACAGGCTGTGCCTGGGCTGTGTGTGCAGTTTGGGTAAGATC	GATCTTACCCAAACTGCACACACAGCCCAGGCACAGCCTGTGCACTGATAG	105859750-105860665

Supplementary Table 4. Primer sets used in this study, relate to Fig. 3

Primers used for CHIP-qPCR

Description	Primer ID	5' --> 3'	3' --> 5'	DNA coordinates (GRCh37/hg19)
NAMPT-Enhancer Negative Contr	Neg	ACTCCAGTCTCAAAGCCTCAT	ACCCAGAGACAGCATCTGTAA	105843605-105843795
NAMPT-Enhancer H3K27ac	p1	CAGCTCATTCTCACCCAGCA	ATGGCTACCTGTCCAGCAAC	105857093-105857240
NAMPT-Enhancer H3K27ac	p2	ACAGGTAGCCATCTCAGCCA	AGCTTTCTGGGATCGGGAAG	105857229-105857462

Supplementary Table 4. sgRNA primer sets used in this study, relate to Fig. 3 and Extended Data Fig. 5

CRISPRi sgRNA KRAB-dCas9 primer sequences (sgRNA sequence is underlined)

Description	Primer ID	DNA coordinates
Dummy_sgRNA	Target = none predicted	N/A
Dummy_sgRNA_F	CACCGATCGTTTCCGCTTAACGGCG	
Dummy_sgRNA_R	AAACCGCCGTTAAGCGGAAACGATC	
g1-sgRNA	Target = CTGCATTGGATGGTCCGTGT CGG	chr7:hg19
g1-sgRNA-F	CACCCTGCATTGGATGGTCCGTGT	105791320-105791342
g1-sgRNA-R	AAACACACGGACCATCCAATGCAG	
g2-sgRNA	Target = CATGTCCATCAATGATAGAC TGG	chr7:hg19
g2-sgRNA-F	CACCCATGTCCATCAATGATAGAC	105,856,108-105,856,127
g2-sgRNA-R	AAACGTCTATCATTGATGGACATG	
g3-sgRNA	Target = AGGATCCAAAGCAACCCCGT TGG	chr7:hg19
g3-sgRNA-F	CACCGAGGATCCAAAGCAACCCCGT	105856983-105857005
g3-sgRNA-R	AAACACGGGGTTGCTTTGGATCCTC	
g4-sgRNA	Target = TCCAAGATCTTCCCGGCATC GGG	chr7:hg19
g4-sgRNA-F	CACCGTCCAAGATCTTCCCGGCATC	105857662-105857684
g4-sgRNA-R	AAACGATGCCGGGAAGATCTTGGAC	

Supplementary Table 4. Primer sets used in this study, relate to Extended Data Figs. 7, 10

Primers for cloning NAMPT; NMRK1 and NAPRT cDNA [backbone vector: pLV cs2.0 N-Flag]

Description	Primer ID	5' --> 3'	3' --> 5'
nampt-FLAG	NAMPT-BamHI/XmaI	AGAGAATTCGGATCC ATGAATCCTGCGGCAGAAG	TGGCTCGAGCCCGGG CTAATGATGTGCTGCTTCCAG
nmrk1-FLAG	NMRK1-BamHI/XmaI	AGAGAATTCGGATCC ATGAAAACATTTATCATTGGAATCAGTGGTG	TGGCTCGAGCCCGGG TTATGCTGTCACTTGCAAACAC
naprt-FLAG	NAPRT-BamHI/XmaI	AGAGAATTCGGATCC ATGGCGGCGGAGCAGGAC	TGGCTCGAGCCCGGG TCAGGGGGACTGCCCCGCACACAG