

Table S2 The putative TFBSs in the lnc2300 promoter

TFs	Matrix ID	Score	Relative score	Start	End	Strand	Predicted sequence
SPI1	MA0080.2	11.542796	1.00000001	462	468	-	AGGAAGT
	MA0080.1	8.578765	0.994463805	938	943	+	GGGAAG
	MA0080.1	8.578765	0.994463805	1175	1180	+	GGGAAG
	MA0080.1	8.578765	0.994463805	1353	1358	-	GGGAAG
	MA0080.1	8.184016	0.977897674	463	468	-	AGGAAG
	MA0080.1	8.184016	0.977897674	1780	1785	-	AGGAAG
	MA0080.1	8.184016	0.977897674	1966	1971	-	AGGAAG
	MA0080.1	7.727144	0.95872444	316	321	+	GGGAAC
	MA0080.1	7.727144	0.95872444	1680	1685	-	GGGAAC
	MA0080.1	7.332395	0.94215831	1506	1511	-	AGGAAC
	MA0080.2	9.198412	0.921884202	1965	1971	-	AGGAAGC
	MA0080.2	8.762131	0.90734714	178	184	+	AAGAAGT
	MA0080.1	6.483284	0.906524284	286	291	-	TGGAAG
	MA0080.1	6.483284	0.906524284	724	729	+	TGGAAG
	MA0080.2	8.637205	0.903184569	1505	1511	-	AGGAAC
NKX2-5	MA0063.3	12.903166	1.000000011	509	515	-	CACTCAA
	MA0063.2	12.767332	0.971073835	507	517	-	ATCACTCAAGT
	MA0063.1	7.8374496	0.940424333	332	338	-	TCAATTG
	MA0063.1	7.7384925	0.936440237	372	378	+	ATAATAG
	MA0063.1	7.5166273	0.927507755	331	337	+	ACAATTG
	MA0063.1	7.4187694	0.92356791	31	37	-	ATAATTT
	MA0063.1	7.3795266	0.921987964	506	512	-	TCAAGTG
	MA0063.3	8.7301035	0.900061788	828	834	+	CACTAAA
SOX5	MA0087.1	10.898025	1.000000008	329	335	-	ATTGTTT
	MA0087.1	9.766585	0.957837008	88	94	-	ATTGTTC
	MA0087.3	11.457525	0.936340359	89	96	+	AACAATGC
	MA0087.3	11.071726	0.926384189	1383	1390	+	GACAATGG
GATA2	MA0036.1	6.6514316	1.000000007	43	47	+	GGATA
	MA0036.1	6.6514316	1.000000007	872	876	-	GGATA
	MA0036.4	12.923377	0.99999999	355	361	-	CTTATCT
	MA0036.1	6.2320204	0.975650738	117	121	+	AGATA
	MA0036.1	6.2320204	0.975650738	355	359	+	AGATA
	MA0036.1	6.2320204	0.975650738	388	392	+	AGATA
	MA0036.1	6.2320204	0.975650738	410	414	+	AGATA
	MA0036.1	6.2320204	0.975650738	806	810	-	AGATA
	MA0036.1	6.2320204	0.975650738	974	978	-	AGATA
	MA0036.1	6.2320204	0.975650738	1072	1076	-	AGATA
	MA0036.1	5.9783006	0.960920821	50	54	-	GGATG
	MA0036.1	5.9783006	0.960920821	167	171	+	GGATG
	MA0036.1	5.9783006	0.960920821	660	664	-	GGATG
	MA0036.3	12.395524	0.95768839	353	363	-	ATCTTATCTAG
	MA0036.1	5.778177	0.949302466	102	106	-	TGATA
	MA0036.1	5.55889	0.93657158	148	152	+	AGATG
	MA0036.1	5.55889	0.93657158	449	453	+	AGATG
	MA0036.1	5.55889	0.93657158	766	770	+	AGATG
	MA0036.1	5.55889	0.93657158	846	850	+	AGATG
	MA0036.1	5.55889	0.93657158	885	889	+	AGATG
	MA0036.1	5.55889	0.93657158	1252	1256	+	AGATG
	MA0036.4	9.837546	0.931655849	117	123	-	GTTATCT
	MA0036.3	11.0408535	0.929886553	115	125	-	TCGTTATCTTT
	MA0036.4	9.46815	0.923474562	410	416	-	ATTATCT
	MA0036.1	5.105046	0.91022328	311	315	+	TGATG
	MA0036.1	5.105046	0.91022328	837	841	-	TGATG
	MA0036.1	5.105046	0.91022328	1078	1082	+	TGATG
	MA0036.2	11.410582	0.907166062	115	128	-	CAATCGTTATCTTT
	MA0036.3	9.61292	0.90058114	408	418	-	AGATTATCTCT

GATA3	MA0037.5	14.198255	1.000000006	355	362	-	TCTTATCT
	MA0037.3	12.12428	1.000000003	355	362	+	AGATAAGA
	MA0037.1	8.388122	0.999999995	973	978	-	AGATAG
	MA0037.2	14.680983	0.999999994	355	362	+	AGATAAGA
	MA0037.3	11.087017	0.976147682	117	124	+	AGATAACG
	MA0037.1	7.4223614	0.959484907	138	143	+	AGATTG
	MA0037.4	13.552274	0.958060577	353	364	-	GATCTTATCTAG
	MA0037.1	7.1894307	0.949713117	117	122	+	AGATAA
	MA0037.1	7.1894307	0.949713117	355	360	+	AGATAA
	MA0037.1	7.1894307	0.949713117	410	415	+	AGATAA
	MA0037.1	6.666897	0.927792038	123	128	+	CGATTG
	MA0037.3	8.93766	0.926722266	410	417	+	AGATAATC
	MA0037.1	6.422963	0.917558655	388	393	+	AGATAT
	MA0037.1	6.422963	0.917558655	1071	1076	-	AGATAT
	MA0037.1	6.2236705	0.90919803	413	418	-	AGATTA
	MA0037.1	6.1273165	0.905155835	101	106	-	TGATAT
GATA1	MA0100.4	11.632136	0.99999999	1153	1158	-	CAACTG
	MA0035.1	7.1048713	0.99999999	167	172	+	GGATGG
	MA0035.1	7.1048713	0.99999999	659	664	-	GGATGG
	MA0100.3	12.625234	0.996821062	1151	1160	-	AGCAACTGCC
	MA0035.1	6.9222393	0.990063527	1252	1257	+	AGATGG
	MA0035.5	11.376707	0.969364926	355	361	-	CTTATCT
	MA0035.1	6.503564	0.967284639	449	454	+	AGATGC
	MA0035.2	11.57598	0.945244696	115	125	+	AAAGATAACGA
	MA0035.1	6.066477	0.943504029	973	978	-	AGATAG
	MA0035.4	11.989657	0.940933378	353	363	-	ATCTTATCTAG
	MA0035.1	5.8304334	0.930661605	871	876	-	GGATAC
	MA0035.1	5.7952647	0.928748184	920	925	-	GGATTG
	MA0035.1	5.7837687	0.928122717	766	771	+	AGATGT
	MA0035.1	5.7837687	0.928122717	846	851	+	AGATGT
	MA0035.1	5.7837687	0.928122717	885	890	+	AGATGT
	MA0035.1	5.706837	0.923937103	123	128	+	CGATTG
	MA0035.1	5.6478014	0.920725142	805	810	-	AGATAC
	MA0035.1	5.6126328	0.91881172	138	143	+	AGATTG
	MA0035.3	10.869412	0.916756473	353	363	-	ATCTTATCTAG
	MA0035.1	5.57462	0.916743547	1078	1083	+	TGATGT
	MA0035.2	10.017137	0.916712347	353	363	+	CTAGATAAGAT
	MA0035.1	5.497942	0.912571735	49	54	-	GGATGA
	MA0035.3	10.244559	0.908194927	115	125	-	TCGTTATCTTT
	MA0035.1	5.3765893	0.905969296	791	796	-	GGATTC
	MA0035.5	8.688167	0.904497598	412	418	+	ATAATCT
	MA0035.1	5.31531	0.902635271	148	153	+	AGATGA
CREB1	MA0018.5	14.634522	1	1078	1085	+	TGATGTCA
	MA0018.4	13.748613	0.943552697	1075	1087	+	CTCTGATGTCAGC
	MA0018.3	11.962328	0.907457718	1076	1087	+	TCTGATGTCAGC
	MA0018.3	11.962328	0.907457718	1076	1087	-	GCTGACATCAGA
	MA0018.2	9.00289	0.906041171	1078	1085	-	TGACATCA
ETS1	MA0098.1	7.7971845	0.99999999	637	642	-	TTTCCG
	MA0098.1	7.632889	0.992421538	419	424	+	TTTCCT
	MA0098.1	7.632889	0.992421538	776	781	-	TTTCCT
	MA0098.1	7.632889	0.992421538	1232	1237	+	TTTCCT
	MA0098.1	7.632889	0.992421538	1236	1241	+	CTTCCT
	MA0098.1	7.632889	0.992421538	1422	1427	+	CTTCCT
	MA0098.1	7.632889	0.992421538	1442	1447	+	TTTCCT
	MA0098.1	7.229176	0.973799495	42	47	-	TATCCT
	MA0098.1	7.229176	0.973799495	50	55	+	CATCCT
	MA0098.1	7.229176	0.973799495	872	877	+	TATCCT
	MA0098.1	6.2997546	0.930928106	180	185	-	CTTCCA
	MA0098.1	5.9774914	0.916063081	156	161	-	ATTTCCT
	MA0098.1	5.9774914	0.916063081	549	554	-	ATTTCCT
	MA0098.1	5.9774914	0.916063081	690	695	-	ATTTCCT
	MA0098.1	5.9774914	0.916063081	710	715	-	ATTTCCT
	MA0098.1	5.9774914	0.916063081	962	967	+	GTTTCCT
	MA0098.1	5.896042	0.912306063	166	171	-	CATCCA
	MA0098.1	5.896042	0.912306063	660	665	+	CATCCA
	MA0098.1	5.777124	0.906820739	394	399	-	CTTCCC
	MA0098.1	5.777124	0.906820739	631	636	-	CTTCCC

	MA0098.1	5.777124	0.906820739	733	738	-	TTTCCC
	MA0098.1	5.777124	0.906820739	809	814	+	CTTCCC
	MA0098.1	5.777124	0.906820739	1209	1214	+	TTTCCC
	MA0098.1	5.777124	0.906820739	1447	1452	+	TTTCCC
SRY	MA0087.1	10.898025	1.000000008	329	335	-	ATTGTTT
	MA0084.2	10.434652	0.999999995	329	335	+	AAACAAT
	MA0078.1	11.260087	0.987081021	1383	1391	-	CCCATTGTC
	MA0087.1	9.766585	0.957837008	88	94	-	ATTGTTC
	MA0084.2	9.146702	0.952822615	641	647	+	AAACAAA
	MA0084.2	9.146702	0.952822615	1059	1065	-	AAACAAA
	MA0084.2	9.146702	0.952822615	1191	1197	+	AAACAAA
	MA0084.1	9.953469	0.942802375	327	335	+	TGAAACAAT
	MA0077.2	10.364841	0.939941124	330	337	-	CAATTGTT
	MA0087.3	11.457525	0.936340359	89	96	+	AACAATGC
	MA0084.1	9.754481	0.936140356	639	647	+	GAAAACAAA
	MA0084.1	9.754481	0.936140356	1189	1197	+	GAAAACAAA
	MA0077.1	10.670611	0.933323677	329	337	-	CAATTGTTT
	MA0077.1	10.6386175	0.93240523	88	96	-	GCATTGTTC
	MA0084.2	8.51782	0.929786809	88	94	+	GAACAAT
	MA0084.1	9.533368	0.928737594	1059	1067	-	CTAAACAAA
	MA0077.2	9.990993	0.928605825	89	96	-	GCATTGTT
	MA0087.3	11.071726	0.926384189	1383	1390	+	GACAATGG
	MA0077.1	10.379702	0.924972542	1382	1390	-	CCATTGTCC
	MA0077.2	9.732078	0.920755385	1383	1390	-	CCATTGTC
	MA0084.1	8.904487	0.907682952	86	94	+	ATGAACAAT
	MA0078.3	11.993277	0.901685168	1381	1390	+	TGGACAATGG
MYB	MA0100.4	11.632136	0.99999999	1153	1158	-	CAACTG
	MA0100.1	11.373983	0.997551642	1151	1158	+	GGCAGTTG
	MA0100.3	12.625234	0.996821062	1151	1160	-	AGCAACTGCC
	MA1523.2	10.636069	0.970129348	509	515	-	CACTCAA
	MA0100.2	12.833582	0.959175509	1150	1159	-	GCAACTGCCT
	MA1523.2	9.211503	0.929450882	538	544	-	CACTCAT
	MA0100.2	10.937767	0.927946689	736	745	+	AAAAGTACA
	MA0100.1	8.97511	0.923128967	1097	1104	-	TGCGGTTG
	MA0100.2	10.114325	0.914382529	1081	1090	-	TCAGCTGACA
	MA1523.2	8.336504	0.904465299	1031	1037	+	AACTCAC
YY1	MA0095.1	8.38313	0.999999988	168	173	-	GCCATC
	MA0095.1	8.38313	0.999999988	1253	1258	-	GCCATC
	MA0095.1	7.219338	0.940561022	568	573	+	GCCATG
	MA0095.1	7.219338	0.940561022	995	1000	+	GCCATA
	MA0095.1	7.0274825	0.930762288	454	459	-	ACCATG
PAX2	MA0067.1	9.065812	0.999999986	893	900	-	AGTCACGC
	MA0067.1	7.3921394	0.934276949	540	547	-	GGTCACTC
	MA0067.1	6.8099236	0.911414061	364	371	-	AATCACTG
	MA0067.1	6.8099236	0.911414061	528	535	+	AATCACTG
	MA0067.1	6.8099236	0.911414061	1200	1207	-	AATCACTC
PRRX2	MA0075.1	9.124368	0.999999981	32	36	+	AATTA
	MA0075.1	9.124368	0.999999981	261	265	+	AATTA
	MA0075.1	9.124368	0.999999981	381	385	-	AATTA
	MA0075.1	9.124368	0.999999981	706	710	+	AATTA
	MA0075.1	9.124368	0.999999981	783	787	+	AATTA
	MA0075.1	9.124368	0.999999981	1118	1122	+	AATTA
	MA0075.1	9.124368	0.999999981	1337	1341	-	AATTA
	MA0075.1	9.124368	0.999999981	1366	1370	-	AATTA
	MA0075.2	10.399081	0.991999128	1336	1343	-	CCAATTAG
	MA0075.4	11.320504	0.975355285	1337	1343	-	CCAATTA
	MA0075.2	9.756483	0.971438387	1365	1372	-	TCAATTAG
	MA0075.3	11.467791	0.969917775	1336	1343	-	CCAATTAG
	MA0075.4	9.534265	0.939315185	1366	1372	-	TCAATTA
	MA0075.3	9.681482	0.93450812	1365	1372	-	TCAATTAG
	MA0075.3	8.98222	0.920646768	1365	1372	+	CTAATTGA
	MA0075.4	8.539251	0.919239281	1336	1342	+	CTAATTG
	MA0075.4	8.539251	0.919239281	1365	1371	+	CTAATTG
	MA0075.3	8.6861725	0.914778279	1336	1343	+	CTAATTGG
	MA0075.2	7.8776283	0.911322054	1116	1123	+	CAAATTAC

	MA0075.2	7.647078	0.903945306	301	308	+	CCAATAAA
MZF1	MA0056.1	9.085277	0.999999979	1014	1019	-	TGGGGA
	MA0056.1	8.252144	0.96198674	629	634	+	GGGGGA
	MA0056.1	8.252144	0.96198674	1412	1417	+	GGGGGA
	MA0056.3	10.311743	0.906646299	1012	1019	+	AGTCCCCA
EN1	MA0027.2	11.660858	0.994960629	1336	1343	-	CCAATTAG
	MA0027.3	10.230499	0.994552924	1337	1342	-	CAATTA
	MA0027.3	10.230499	0.994552924	1366	1371	-	CAATTA
	MA0132.3	9.726224	0.980607887	1337	1342	-	CAATTA
	MA0132.3	9.726224	0.980607887	1366	1371	-	CAATTA
	MA0132.2	10.716987	0.978883095	1336	1343	-	CCAATTAG
	MA0027.2	10.520355	0.970178579	1365	1372	-	TCAATTAG
	MA0132.3	8.654493	0.957792088	177	182	-	CCATTA
	MA0132.2	9.590623	0.956351331	1365	1372	-	TCAATTAG
	MA0027.3	7.91491	0.940162372	46	51	+	TAATCA
	MA0027.3	7.91491	0.940162372	367	372	-	TAATCA
	MA0132.2	8.51888	0.934912199	176	183	-	TCCATTAG
	MA0132.3	6.735349	0.916935918	31	36	+	AAATTA
	MA0132.3	6.735349	0.916935918	260	265	+	AAATTA
	MA0132.3	6.735349	0.916935918	705	710	+	AAATTA
	MA0132.3	6.735349	0.916935918	782	787	+	AAATTA
	MA0132.3	6.735349	0.916935918	1117	1122	+	AAATTA
	MA0027.3	6.7217226	0.912135766	31	36	+	AAATTA
	MA0027.3	6.7217226	0.912135766	260	265	+	AAATTA
	MA0027.3	6.7217226	0.912135766	705	710	+	AAATTA
	MA0027.3	6.7217226	0.912135766	782	787	+	AAATTA
	MA0027.3	6.7217226	0.912135766	1117	1122	+	AAATTA
	MA0132.2	7.1597347	0.907723879	704	711	+	AAAATTAG
	MA0132.3	6.078618	0.902954937	46	51	-	TGATTA
	MA0132.3	6.078618	0.902954937	367	372	+	TGATTA
	MA0027.2	7.3312216	0.900881721	1116	1123	+	CAAATTAC
FOXLI	MA0033.2	10.119886	0.960696958	203	209	-	ATAAATA
	MA0033.2	8.451631	0.930146495	849	855	-	ACAAACA
	MA0033.1	7.034594	0.923844532	344	351	-	ACTACATA
	MA0033.1	6.888278	0.917213179	100	107	-	ATGATATA
	MA0033.1	6.553537	0.902042003	114	121	+	TAAAGATA
SOX17	MA0078.1	11.260087	0.987081021	1383	1391	-	CCCATTGTC
	MA0078.3	11.993277	0.901685168	1381	1390	+	TGGACAATGG
TBP	MA0108.3	8.372203	0.917686417	1126	1132	+	TTTAAAA
	MA0108.3	8.058816	0.909523312	204	210	-	CATAAAT
	MA0108.3	8.058816	0.909523312	614	620	-	CATAAAT
ZEB1	MA0103.1	8.660517	0.976125124	173	178	+	CACCTA
GFI1	MA0038.1	11.56924	0.969600297	526	535	+	GAAATCACTG
	MA0038.1	10.560506	0.939297178	1200	1209	-	AAAATCACTC
	MA0483.1	12.454052	0.928917719	527	537	+	AAATCACTGGA
	MA0483.2	11.718515	0.926241205	527	536	+	AAATCACTGG
	MA0038.3	10.153501	0.901830456	1198	1208	-	AAATCACTCCT
CEBPA	MA0102.5	15.600994	0.970913473	1047	1056	-	ATTGCACAAC
	MA0102.2	10.29983	0.966777739	1048	1056	+	TTGTGCAAT
	MA0102.3	13.740437	0.962601079	1046	1056	-	ATTGCACAACG
	MA0102.2	9.902968	0.952481916	1110	1118	-	TTGCACAAT
	MA0102.4	15.404368	0.942533224	1045	1058	-	AAATTGCACAACGT
	MA0102.5	13.700067	0.93741654	1110	1119	-	TTTGCACAAT
	MA0102.1	10.487324	0.934129029	1048	1059	+	TTGTGCAATTTT
	MA0102.2	9.255406	0.92915534	1047	1055	-	TTGCACAAC
	MA0102.1	10.208203	0.92548997	1044	1055	-	TTGCACAACGTG
	MA0019.2	11.391544	0.924367509	587	596	+	ATGAAATACC
	MA0102.4	14.17384	0.922129818	1108	1121	-	AATTGCACAATTT
	MA0102.1	9.870134	0.915026396	1107	1118	-	TTGCACAATTTG
FOXC1	MA0032.1	6.7231374	0.958132958	931	938	-	GGCCAGTA
	MA0032.1	6.6642437	0.954838593	816	823	-	TCTAAGTA
	MA0032.2	11.275734	0.922751349	1186	1196	+	AAAGAAAACAA

	MA0032.2	10.786831	0.915412416	92	102	+	AATGCCAATAT
	MA0032.1	5.9157825	0.91297155	673	680	+	CTAGAGTA
	MA0032.1	5.834169	0.908406294	906	913	-	GGTGGGTA
	MA0032.1	5.816247	0.907403786	866	873	+	TGGCAGTA
	MA0032.1	5.7231374	0.902195468	425	432	+	GGACCGTA
TEAD1	MA0090.2	11.441157	0.957857108	548	557	-	TGCATTCTTA
	MA0090.2	9.748321	0.922977643	689	698	-	TGAATTCCTT
	MA0090.2	9.194282	0.911562139	709	718	-	CTCATTCCTA
	MA0090.4	11.410822	0.90778265	533	541	-	TCATTCCAG
IRF1	MA0050.3	18.187761	0.947593313	1020	1034	+	AATAAACTGAACT
	MA0050.4	15.947445	0.946739741	1022	1032	+	TAAAACTGAAA
	MA0050.1	13.873308	0.92405857	1023	1034	+	AAAACTGAACT
SOX9	MA0077.2	10.364841	0.939941124	330	337	-	CAATTGTT
	MA0077.1	10.670611	0.933323677	329	337	-	CAATTGTTT
	MA0077.1	10.6386175	0.93240523	88	96	-	GCATTGTTC
	MA0077.2	9.990993	0.928605825	89	96	-	GCATTGTT
	MA0077.1	10.379702	0.924972542	1382	1390	-	CCATTGTCC
	MA0077.2	9.732078	0.920755385	1383	1390	-	CCATTGTC
FOXD3	MA0041.1	11.603629	0.901065698	1054	1065	+	AATTTTTGTTT
TFAP2A	MA0810.1	12.270277	0.943402843	1406	1417	-	TCCCCCAAGCCA
	MA0810.2	11.340706	0.941463587	1407	1417	-	TCCCCCAAGCC
	MA0003.1	8.377142	0.934256504	1145	1153	-	GCCTCCAGC
	MA0003.3	10.436339	0.918857372	1144	1154	-	TGCCTCCAGCT
	MA0810.2	9.5613575	0.912899714	1391	1401	-	CACCCCCAGCC
ARNT	MA0006.2	8.844031	1.000000014	893	897	+	GCGTG
	MA0259.2	9.08275	1.00000001	285	289	+	ACGTG
	MA0259.2	9.08275	1.00000001	902	906	-	ACGTG
	MA0259.2	9.08275	1.00000001	1044	1048	-	ACGTG
	MA0006.1	9.602817	0.999999989	892	897	+	TGCGTG
	MA1106.2	11.279793	0.999999988	901	906	-	ACGTGC
	MA0259.1	11.075476	0.996313886	901	908	-	GTACGTGC
	MA1106.1	12.386301	0.983766922	899	908	-	GTACGTGCAG
	MA0259.2	7.42617	0.936361795	893	897	+	GCGTG
	MA0004.1	8.609213	0.930502841	284	289	+	AACGTG
	MA0004.1	8.609213	0.930502841	1044	1049	-	AACGTG
	MA1106.2	8.139631	0.917227289	1043	1048	-	ACGTGA
	MA1106.1	9.529688	0.916505469	901	910	+	GCACGTACCC
	MA1106.2	8.066213	0.91529202	903	908	+	ACGTAC
	MA0259.1	8.037127	0.905672503	891	898	+	GTGCGTGA
HLF	MA2325.1	12.937772	0.961836449	900	908	+	TGCACGTAC
	MA0043.4	12.862008	0.948101704	278	286	+	TTATACAAC
	MA0043.2	11.271339	0.927165245	276	287	+	TATTATACAACG
	MA0043.3	12.865879	0.923612022	275	288	+	GTATTATACAACGT
	MA0043.2	10.614634	0.916865596	276	287	-	CGTTGTATAATA
	MA0043.4	10.941155	0.91641025	1048	1056	+	TTGTGCAAT
USF1	MA0093.2	10.650306	0.913100208	144	154	-	ATCATCTGACC
NR2F1	MA0017.2	12.052353	0.912310803	1316	1328	-	CTGGGGTCAGCAG
	MA0017.3	11.095114	0.910129227	1316	1327	-	TGGGGTCAGCAG
MAX	MA0801.1	11.161443	0.945202033	285	292	+	ACGTGTGA
	MA0058.2	11.642768	0.938494117	553	562	+	ATGCACATGC
	MA0058.4	7.3973193	0.910888846	556	561	+	CACATG
	MA0058.4	6.9119	0.900830475	556	561	-	CATGTG
NFIL3	MA0025.3	10.926346	0.910160697	1048	1056	+	TTGTGCAAT
PAX5	MA0014.4	11.449593	0.933217158	893	900	+	GCGTGACT
	MA0014.3	11.859799	0.909554209	891	902	+	GTGCGTGACTGC
ZNF354C	MA0130.1	6.9157825	0.912462499	907	912	+	ACCCAC

	MA0130.1	6.7231374	0.904030665	1399	1404	-	CCCCAC
NKX3-1	MA0124.1	11.580482	1.000000013	815	821	+	ATACTTA
	MA0124.1	9.80297	0.936114631	235	241	+	TTACTTA
MEIS1	MA0498.3	9.351322	1.000000007	741	745	+	TGACA
	MA0498.3	9.351322	1.000000007	1081	1085	-	TGACA
	MA0498.2	9.947893	0.991412464	740	746	+	CTGACAG
	MA0498.2	8.963122	0.970557878	1080	1086	-	CTGACAT
	MA0498.3	6.21157	0.929896798	926	930	+	AGACA
	MA1640.2	11.826582	0.919134721	202	210	+	TTATTTATG
	MA0498.1	12.762214	0.907263105	734	748	-	TTCTGTCAGTTTCC
	MA0498.3	5.056073	0.904097305	290	294	+	TGACT
	MA0498.3	5.056073	0.904097305	314	318	+	TGACT
	MA0498.3	5.056073	0.904097305	436	440	-	TGACT
	MA0498.3	5.056073	0.904097305	862	866	+	TGACT
	MA0498.3	5.056073	0.904097305	896	900	+	TGACT
	MA0498.2	5.823239	0.904064263	925	931	+	CAGACAT
	MA0774.1	8.975588	0.900114101	740	747	+	CTGACAGA
NFIC	MA0161.1	9.697425	1.000000005	94	99	-	TTGGCA
	MA0161.1	8.52041	0.960577536	189	194	+	TTGGCT
	MA0161.1	8.52041	0.960577536	1312	1317	+	TTGGCT
	MA0161.1	8.395941	0.956408629	865	870	+	CTGGCA
	MA0161.1	7.969342	0.942120312	1340	1345	+	TTGGCC
	MA0161.1	7.586748	0.929305861	20	25	+	TTGGAA
	MA0161.1	7.2189264	0.916986192	1354	1359	-	CTGGCT
	MA0161.1	7.2189264	0.916986192	1405	1410	+	CTGGCT
SOX2	MA0143.5	12.655396	1.000000002	1384	1390	+	ACAATGG
	MA1152.2	10.763686	0.992981672	1384	1390	-	CCATTGT
	MA1152.1	12.656869	0.98229582	1190	1199	-	CTTTGTTTT
	MA0143.3	12.854551	0.980282321	1383	1390	-	CCATTGTC
	MA1152.2	10.252575	0.98004721	1193	1199	-	CTTTTGT
	MA1152.2	10.252575	0.98004721	1269	1275	+	CTTTTGT
	MA1152.1	11.62548	0.959136417	640	649	-	TTTTTGTTTT
	MA1152.2	9.221187	0.953946332	643	649	-	TTTTTGT
	MA1152.2	9.221187	0.953946332	1057	1063	+	TTTTTGT
	MA1152.2	8.943854	0.946928008	856	862	+	TCTTTGT
	MA1152.2	8.943854	0.946928008	1161	1167	+	TCTTTGT
	MA1152.2	8.904757	0.945938578	90	96	-	GCATTGT
	MA1152.1	10.888298	0.942583319	1057	1066	+	TTTTTGTTTA
	MA0143.4	11.644117	0.939559738	1382	1392	+	GGACAATGGGG
	MA1152.1	10.705774	0.938484827	1269	1278	+	CTTTTGTGTT
	MA1152.1	10.332454	0.930102073	1381	1390	-	CCATTGTCCA
	MA1152.2	8.177122	0.927524662	331	337	-	CAATTGT
	MA0143.5	9.551398	0.926911619	90	96	+	ACAATGC
	MA1152.1	9.903961	0.920480457	1161	1170	+	TCTTTGTTCA
	MA1152.1	9.864862	0.919602511	87	96	-	GCATTGTTCA
	MA1152.2	7.736913	0.916384493	372	378	-	CTATTAT
	MA1152.1	9.49879	0.911382507	328	337	-	CAATTGTTTC
	MA0143.4	10.160259	0.907619734	88	98	+	GAACAATGCCA
NFATC2	MA0152.1	9.490151	0.931047145	418	424	+	TTTTCCT
	MA0152.1	9.490151	0.931047145	776	782	-	TTTTCCT
	MA0152.1	9.490151	0.931047145	1231	1237	+	TTTTCCT
	MA0152.1	9.490151	0.931047145	1441	1447	+	TTTTCCT
	MA0152.1	9.186889	0.91986211	733	739	-	TTTTCCC
	MA0152.1	9.186889	0.91986211	1208	1214	+	TTTTCCC
	MA0152.3	10.455441	0.906004792	1442	1449	-	AAAGGAAA
SOX10	MA0442.3	11.610084	1	857	862	-	ACAAAG
	MA0442.3	11.610084	1	1162	1167	-	ACAAAG
	MA0442.1	8.909793	0.999999997	857	862	+	CTTGT
	MA0442.1	8.909793	0.999999997	1162	1167	+	CTTGT
	MA0442.1	8.625231	0.987366854	90	95	-	CATTGT
	MA0442.1	8.625231	0.987366854	1384	1389	-	CATTGT
	MA0442.2	13.344964	0.980032022	1160	1170	-	TGAACAAAGAA
	MA0442.2	11.764093	0.946113929	855	865	-	GTCACAAAGAA
	MA0442.1	7.093567	0.919368595	282	287	-	CGTTGT

	MA0442.1	7.093567	0.919368595	1046	1051	+	CGTTGT
NOBOX	MA0125.2	9.791516	0.999999995	1337	1342	+	TAATTG
	MA0125.2	9.791516	0.999999995	1366	1371	+	TAATTG
	MA0125.1	11.012397	0.988437709	1337	1344	+	TAATTGGC
	MA0125.2	7.1938314	0.900529453	177	182	+	TAATGG
PDX1	MA0132.1	9.569862	0.999999988	706	711	-	CTAATT
	MA0132.1	9.569862	0.999999988	1336	1341	+	CTAATT
	MA0132.1	9.569862	0.999999988	1365	1370	+	CTAATT
	MA0132.3	9.726224	0.980607887	1337	1342	-	CAATTA
	MA0132.3	9.726224	0.980607887	1366	1371	-	CAATTA
	MA0132.2	10.716987	0.978883095	1336	1343	-	CCAATTAG
	MA0132.1	8.729877	0.965432864	176	181	+	CTAATG
	MA0132.3	8.654493	0.957792088	177	182	-	CCATTA
	MA0132.2	9.590623	0.956351331	1365	1372	-	TCAATTAG
	MA0132.2	8.51888	0.934912199	176	183	-	TCCATTAG
	MA0132.1	7.8961897	0.931124879	261	266	-	GTAATT
	MA0132.1	7.8961897	0.931124879	380	385	+	GTAATT
	MA0132.1	7.8961897	0.931124879	783	788	-	GTAATT
	MA0132.1	7.8961897	0.931124879	1118	1123	-	GTAATT
	MA0132.3	6.735349	0.916935918	31	36	+	AAATTA
	MA0132.3	6.735349	0.916935918	260	265	+	AAATTA
	MA0132.3	6.735349	0.916935918	705	710	+	AAATTA
	MA0132.3	6.735349	0.916935918	782	787	+	AAATTA
	MA0132.3	6.735349	0.916935918	1117	1122	+	AAATTA
	MA0132.2	7.1597347	0.907723879	704	711	+	AAAATTAG
	MA0132.3	6.078618	0.902954937	46	51	-	TGATTA
	MA0132.3	6.078618	0.902954937	367	372	+	TGATTA
KLF1	MA0493.2	14.058395	0.989221481	1396	1404	+	GGGGTGGGG
	MA0493.3	13.478703	0.988640421	1397	1404	+	GGGTGGGG
	MA0493.2	12.644633	0.963870111	1413	1421	+	GGGGAGGGG
	MA0493.3	12.065764	0.961947585	7	14	-	GGGAGGGG
	MA0493.3	12.065764	0.961947585	1414	1421	+	GGGAGGGG
	MA0493.2	12.056301	0.953320226	7	15	-	AGGGAGGGG
	MA0741.1	14.709045	0.951393384	1395	1405	-	GCCCCACCCCC
	MA0740.2	12.637965	0.949901903	1413	1421	+	GGGGAGGGG
	MA0740.2	12.568541	0.948742454	1396	1404	+	GGGGTGGGG
	MA0741.1	14.413998	0.946570192	1412	1422	-	GCCCCCTCCCCC
	MA0742.2	12.27413	0.931315085	1413	1421	+	GGGGAGGGG
	MA0493.1	12.105816	0.916262052	1396	1406	-	AGCCCCACCCC
HOXA5	MA0158.1	9.440825	0.985374461	261	268	-	CAGTAATT
	MA0158.1	9.025553	0.970748931	1118	1125	-	CGGTAATT
	MA0158.1	8.662787	0.957972664	613	620	-	CATAAATT
	MA0158.2	9.958706	0.955313279	1336	1343	-	CCAATTAG
	MA0158.2	8.918438	0.935973603	1365	1372	-	TCAATTAG
	MA0158.2	8.044875	0.919733151	584	591	+	GTCATGAA
	MA0158.2	7.9850907	0.918621696	176	183	-	TCCATTAG
	MA0158.2	7.516502	0.909910136	584	591	-	TTCATGAC
	MA0158.1	7.2169533	0.90705169	1363	1370	+	AGCTAATT
ZFX	MA0146.3	14.002719	0.979707905	1303	1312	+	GGCGAGGCCT
	MA0146.3	12.610323	0.951922262	1307	1316	-	GCCAAGGCCT
	MA0146.1	13.316816	0.924796927	1306	1319	-	GCAGCCAAGGCCTC
	MA0146.2	13.317081	0.924676033	1306	1319	-	GCAGCCAAGGCCTC
	MA0146.2	12.498447	0.910426816	1300	1313	+	GGTGGCGAGGCCTT
	MA0146.1	12.482402	0.910264983	1300	1313	+	GGTGGCGAGGCCTT
CEBPB	MA0466.1	14.696246	0.973987474	1047	1057	-	AATTGCACAAC
	MA0466.2	13.023246	0.961180639	1047	1056	-	ATTGCACAAC
	MA0466.2	11.805978	0.944699116	1047	1056	+	GTTGTGCAAT
	MA0466.2	9.648945	0.915493397	1110	1119	-	TTTGCAAT
	MA0466.2	9.57752	0.914526326	277	286	+	ATTATACAAC
	MA0466.4	10.268873	0.905484971	1047	1056	+	GTTGTGCAAT
	MA0466.4	10.189109	0.904553506	1047	1056	-	ATTGCACAAC
NFYB	MA0502.3	10.75325	0.907021653	1337	1345	+	TAATTGGCC

GATA4	MA0482.3	12.683303	0.961537649	355	362	-	TCTTATCT
	MA0482.1	10.375805	0.920965911	114	124	-	CGTTATCTTTA
FOXO3	MA0157.1	10.798385	0.954864362	769	776	-	TGAAAACA
	MA0157.1	10.205409	0.934945143	638	645	+	GGAAAACA
	MA0157.1	9.639356	0.915930294	1275	1282	-	GCTAAACA
	MA0157.3	10.834027	0.912667918	1187	1198	+	AAGAAAACAAAA
	MA0157.4	9.145695	0.905764123	639	645	+	GAAAACA
	MA0157.4	9.145695	0.905764123	769	775	-	GAAAACA
	MA0157.4	9.145695	0.905764123	1189	1195	+	GAAAACA
E2F6	MA0471.1	12.886842	0.951151205	936	946	-	AGGAGGGAGGC
GFI1B	MA0483.1	12.454052	0.928917719	527	537	+	AAATCACTGGA
	MA0483.2	11.718515	0.926241205	527	536	+	AAATCACTGG
MAFB	MA0117.2	13.915601	0.948821402	307	318	+	AAAATGATGACT
	MA0117.3	13.344545	0.946422229	307	317	+	AAAATGATGAC
	MA0117.1	7.904832	0.930945084	1080	1087	-	GCTGACAT
	MA0117.1	7.4820466	0.912635779	1318	1325	+	GCTGACCC
HOXC9	MA0485.2	12.761919	0.947208386	613	622	-	GTCATAAATT
	MA0485.3	12.384145	0.946310632	204	212	-	GTCATAAAT
	MA0485.3	12.384145	0.946310632	614	622	-	GTCATAAAT
	MA0485.2	12.131913	0.93886429	203	212	-	GTCATAAATA
	MA0485.1	12.518416	0.897571012	201	213	-	GGTCATAAATAAG
	MA0485.1	12.469821	0.896822755	611	623	-	GGTCATAAATTG
	MA0485.2	6.006022	0.857730078	584	593	+	GTCATGAAAT
	MA0485.1	9.887497	0.857060957	95	107	+	GCCAATATATCAT
	MA0485.3	5.637074	0.855426979	584	592	+	GTCATGAAA
	MA0485.1	7.5493307	0.821058623	1202	1214	-	GGGAAAAAATCAC
	MA0485.2	3.166124	0.820117122	25	34	+	ATAGTTAAAT
	MA0485.3	2.7972946	0.817174895	25	33	+	ATAGTTAA
	MA0485.3	2.3626244	0.811319848	857	865	-	GTCACAAAG
	MA0485.2	2.1025412	0.806030525	856	865	-	GTCACAAAGA
EBF1	MA0154.2	12.057421	0.944901505	986	996	+	GTCTCCTGGGC
	MA0154.1	11.508322	0.936568651	11	20	-	ACCTAAGGGA
STAT3	MA0144.2	12.058914	0.9436431	771	781	-	TTTCCTGAAAA
	MA0144.3	10.844938	0.94269125	772	780	-	TTTCCTGAAA
	MA0144.2	9.918375	0.917711422	771	781	+	TTTTCAGGAAA
	MA0144.2	9.722867	0.91534293	772	782	+	TTTCAGGAAAA
	MA0144.3	8.7044	0.914961738	772	780	+	TTTCAGGAA
	MA0144.3	8.508892	0.912429038	773	781	+	TTTCAGGAAA
	MA0144.1	11.805372	0.90504811	419	428	-	GTCCAGGAAA
ERG	MA1480.1	12.998129	0.958579318	410	419	+	AGATAATCTT
	MA0474.1	12.783721	0.941835626	1233	1243	-	GCAGGAAGGAA
	MA0475.1	11.845376	0.919576743	1233	1243	-	GCAGGAAGGAA
	MA1480.1	10.741141	0.914320258	409	418	-	AGATTATCTC
FOXA1	MA0148.1	12.990497	0.941848609	1185	1195	-	TGTTTTCTTTG
	MA0148.2	12.953144	0.941398611	1185	1195	-	TGTTTTCTTTG
	MA0148.2	11.479643	0.916121882	849	859	+	TGTTTGTCTT
	MA0148.1	11.455882	0.915194766	849	859	+	TGTTTGTCTT
MAFK	MA0496.1	14.257393	0.934228497	307	321	-	CCTAGTCATCATTTT
MYC	MA0058.2	11.642768	0.938494117	553	562	+	ATGCACATGC
	MA0058.4	7.3973193	0.910888846	556	561	+	CACATG
	MA0058.4	6.9119	0.900830475	556	561	-	CATGTG
EGR1	MA0162.2	14.175795	0.931990918	1392	1405	-	GCCCCACCCCCAGC
FOXP1	MA0481.1	15.822579	0.930511314	1184	1198	+	GCAAAGAAAACAAAA
CDX2	MA0465.1	11.803736	0.930367867	204	214	-	GGGTCATAAAT
	MA0465.1	11.623594	0.927659183	299	309	+	CTCCAATAAAA
	MA0465.3	11.089703	0.9232193	301	308	+	CCAATAAA

	MA0465.1	10.474386	0.910379195	614	624	-	TGGTCATAAAT
	MA0465.2	12.041732	0.906869771	299	310	+	CTCCAATAAAAA
MAFF	MA0495.4	14.961285	0.936440867	307	317	-	GTCATCATTTT
	MA0495.3	16.800354	0.929829514	304	319	-	TAGTCATCATTTTTAT
	MA0495.1	16.578255	0.925764249	305	322	-	GCCTAGTCATCATTTTTA
ELF5	MA0136.1	9.171918	0.920971172	1440	1448	+	TTTTTCCTT
	MA0136.1	8.865436	0.910954871	960	968	+	CAGTTCCTT
	MA0136.2	10.384761	0.907437512	1234	1244	-	AGCAGGAAGGA
	MA0136.3	11.656597	0.906797662	1233	1244	-	AGCAGGAAGGAA
	MA0136.1	8.635659	0.903445435	179	187	-	AACTTCCAT
FOXO1	MA0480.1	11.737359	0.920884516	1188	1198	-	TTTTGTTTTCT
	MA0480.1	11.311565	0.914386875	638	648	-	TTTTGTTTTCC
	MA0480.3	9.10647	0.902817741	769	775	-	GAAAACA
	MA0480.3	9.10647	0.902817741	1189	1195	+	GAAAACA
	MA0480.2	9.898741	0.901589206	1187	1197	+	AAGAAAACAAA
FLI1	MA0475.1	11.845376	0.919576743	1233	1243	-	GCAGGAAGGAA
INSM1	MA0155.1	12.91783	0.914965545	654	665	-	TGGATGGGGGCA
STAT1	MA0137.4	9.411399	0.910129759	1423	1431	-	CTCTAGGAA
	MA0137.4	9.324966	0.908866851	729	737	+	CTCTGGGAA
	MA0517.2	13.966054	0.9070936	1022	1034	-	AGTTTCAGTTTA
BCL6	MA0463.1	14.200922	0.908349166	1422	1435	+	CTCCTAGAGAGGC
NFE2L2	MA0150.1	12.705859	0.917514755	313	323	+	ATGACTAGGCA
	MA0150.3	13.6701	0.907614445	313	323	+	ATGACTAGGCA
JUN	MA0089.1	8.812264	0.999999981	584	589	-	CATGAC
	MA0089.1	8.691545	0.994771697	312	317	+	GATGAC
	MA0089.1	8.072033	0.96794114	207	212	+	TATGAC
	MA0089.1	8.072033	0.96794114	617	622	+	TATGAC
	MA0099.2	8.680231	0.927590055	290	296	+	TGACTGA
	MA0150.1	12.705859	0.917514755	313	323	+	ATGACTAGGCA
	MA0089.1	6.8111424	0.913332972	48	53	-	GATGAT
	MA0089.1	6.8111424	0.913332972	149	154	+	GATGAT
	MA0089.1	6.8111424	0.913332972	835	840	-	GATGAT
	MA0150.3	13.6701	0.907614445	313	323	+	ATGACTAGGCA
DUX4	MA0468.1	8.930404	0.902909756	138	148	-	TGACCCAATCT
NR4A2	MA0160.1	9.426869	0.922285154	542	549	-	TAGGTCAC
	MA0160.1	8.851206	0.90205841	513	520	-	GAGATCAC
MSX1	MA0666.1	11.730837	1.000000011	1336	1343	-	CCAATTAG
	MA0666.3	11.099844	1.000000004	1337	1342	-	CAATTA
	MA0666.3	11.099844	1.000000004	1366	1371	-	CAATTA
	MA0666.2	11.902181	0.988559602	1336	1343	-	CCAATTAG
	MA0666.1	10.353911	0.965898799	1365	1372	-	TCAATTAG
	MA0666.2	10.402785	0.959368945	1365	1372	-	TCAATTAG
	MA0666.3	6.7295413	0.909875569	31	36	+	AAATTA
	MA0666.3	6.7295413	0.909875569	260	265	+	AAATTA
	MA0666.3	6.7295413	0.909875569	705	710	+	AAATTA
	MA0666.3	6.7295413	0.909875569	782	787	+	AAATTA
	MA0666.3	6.7295413	0.909875569	1117	1122	+	AAATTA
	MA0666.3	6.262217	0.900238403	332	337	+	CAATTG
	MA0666.3	6.262217	0.900238403	332	337	-	CAATTG
NFIX	MA0671.2	10.156875	1.000000001	94	99	+	TGCCAA
	MA0671.1	9.693084	0.973705777	92	100	+	AATGCCAAT
	MA0671.2	8.787377	0.966408118	865	870	-	TGCCAG
	MA0671.2	8.618273	0.962260215	189	194	-	AGCCAA
	MA0671.2	8.618273	0.962260215	1312	1317	-	AGCCAA
	MA0671.1	8.58657	0.947655615	188	196	-	TTAGCCAAG
	MA0671.1	8.438839	0.944177655	1311	1319	-	GCAGCCAAG
	MA0671.2	7.691987	0.939539695	1340	1345	-	GGCCAA

	MA0671.1	7.9733977	0.933219981	864	872	-	ACTGCCAGT
	MA0671.1	7.887681	0.931201991	1352	1360	+	GGAGCCAGG
	MA0671.1	7.829471	0.929831581	1339	1347	-	GGGGCCAAT
	MA0671.2	7.2487755	0.928668323	1354	1359	+	AGCCAG
	MA0671.2	7.2487755	0.928668323	1405	1410	-	AGCCAG
	MA0671.1	7.4180307	0.920145225	1404	1412	-	CAAGCCAGC
	MA0671.1	7.031992	0.911056887	168	176	-	GGTGCCATC
	MA0671.2	6.4891257	0.910035155	20	25	-	TTCCAA
	MA0671.1	6.9139194	0.908277159	565	573	+	AGTGCCATG
	MA0671.2	6.4089537	0.908068645	169	174	-	TGCCAT
	MA0671.2	6.4089537	0.908068645	567	572	+	TGCCAT
	MA0671.2	6.32249	0.905947815	933	938	-	GGCCAG
	MA0671.2	6.32249	0.905947815	1359	1364	+	GGCCAG
SHOX	MA0630.2	9.702315	1.000000005	1337	1342	+	TAATTG
	MA0630.2	9.702315	1.000000005	1366	1371	+	TAATTG
	MA0720.2	10.458221	0.999522231	1337	1342	-	CAATTA
	MA0720.2	10.458221	0.999522231	1366	1371	-	CAATTA
	MA0720.1	11.690396	0.998531686	1336	1343	-	CCAATTAG
	MA0630.1	10.549183	0.99225475	1336	1343	+	CTAATTGG
	MA0720.1	11.013979	0.983357556	1365	1372	-	TCAATTAG
	MA0630.1	10.224366	0.981787948	1365	1372	+	CTAATTGA
	MA0630.2	7.841405	0.934642812	31	36	-	TAATTT
	MA0630.2	7.841405	0.934642812	260	265	-	TAATTT
	MA0630.2	7.841405	0.934642812	705	710	-	TAATTT
	MA0630.2	7.841405	0.934642812	782	787	-	TAATTT
	MA0630.2	7.841405	0.934642812	1117	1122	-	TAATTT
	MA0720.2	7.2980523	0.92313338	31	36	+	AAATTA
	MA0720.2	7.2980523	0.92313338	260	265	+	AAATTA
	MA0720.2	7.2980523	0.92313338	705	710	+	AAATTA
	MA0720.2	7.2980523	0.92313338	782	787	+	AAATTA
	MA0720.2	7.2980523	0.92313338	1117	1122	+	AAATTA
	MA0630.1	7.825834	0.904498315	1116	1123	-	GTAATTTG
	MA0720.1	7.4696827	0.903848047	1116	1123	+	CAAATTAC
EN2	MA0642.3	11.328404	1.000000004	1337	1343	-	CCAATTA
	MA0642.2	11.258872	0.98874207	1337	1344	-	GCCAATTA
	MA0642.1	11.809399	0.98130048	1335	1344	-	GCCAATTAGG
	MA0642.1	11.704382	0.979024702	1364	1373	-	CTCAATTAGC
	MA0642.2	10.220748	0.963054872	1366	1373	-	CTCAATTA
	MA0642.3	9.832412	0.962779361	1366	1372	-	TCAATTA
	MA0642.2	8.699914	0.925423567	212	219	+	CCCTATTA
	MA0642.3	8.3031645	0.924731335	213	219	+	CCTATTA
	MA0642.2	8.530815	0.921239409	1335	1342	+	CCTAATTG
	MA0642.3	8.136895	0.920594516	1336	1342	+	CTAATTG
	MA0642.3	8.136895	0.920594516	1365	1371	+	CTAATTG
	MA0642.2	8.075836	0.909981473	1364	1371	+	GCTAATTG
	MA0642.3	7.697307	0.909657464	177	183	-	TCCATTA
	MA0642.3	7.4706264	0.904017594	332	338	-	TCAATTG
HOXA13	MA0650.4	14.464836	1.000000004	301	308	+	CCAATAAA
	MA0650.1	15.2930975	0.999999998	301	310	+	CCAATAAAAA
	MA0650.3	15.155865	0.983421225	299	310	+	CTCCAATAAAAA
	MA0650.4	11.028828	0.929692464	1018	1025	+	CAAATAAA
	MA0650.2	12.346479	0.913847702	300	310	+	TCCAATAAAAA
	MA0650.3	11.395445	0.911096719	1016	1027	+	CCCAAATAAAAC
EHF	MA0598.1	13.8272	1.000000003	1235	1242	+	CCTTCCTG
NFIA	MA0670.2	11.978753	1.000000001	94	99	+	TGCCAA
	MA0670.1	11.691462	0.972173585	92	101	+	AATGCCAATA
TWIST2	MA0633.3	11.917516	1	1084	1089	+	CAGCTG
	MA0633.3	11.917516	1	1084	1089	-	CAGCTG
	MA0633.2	9.788133	0.948622401	1082	1091	-	CTCAGCTGAC
	MA0633.2	9.781447	0.94851405	1082	1091	+	GTGAGCTGAG
BARHL2	MA0635.2	10.168015	0.999999998	1124	1129	-	TAAACG
	MA0635.2	9.441398	0.984692452	105	110	-	TAAATG
	MA0635.1	11.059476	0.972467881	1122	1131	-	TTTAAACGGT
	MA0635.1	10.1777935	0.956055171	103	112	-	GGTAAATGAT

	MA0635.2	7.77637	0.949615526	1337	1342	+	TAATTG
	MA0635.2	7.77637	0.949615526	1366	1371	+	TAATTG
	MA0635.2	7.159774	0.936625772	1061	1066	-	TAAACA
	MA0635.2	7.159774	0.936625772	1275	1280	-	TAAACA
	MA0635.1	8.717442	0.928870401	1335	1344	+	CCTAATTGGC
	MA0635.2	6.433157	0.921318226	203	208	-	TAAATA
	MA0635.2	6.2042427	0.916495718	30	35	+	TAAATT
	MA0635.2	6.2042427	0.916495718	613	618	-	TAAATT
	MA0635.1	7.999004	0.915496527	28	37	+	GTAAATTAT
	MA0635.2	5.912434	0.910348223	624	629	+	AAAACG
	MA0635.1	7.4121876	0.904572813	1364	1373	+	GCTAATTGAG
	MA0635.2	5.494746	0.901548845	46	51	+	TAATCA
	MA0635.2	5.494746	0.901548845	367	372	-	TAATCA
TCF12	MA0521.3	11.687652	0.999999997	1084	1089	+	CAGCTG
	MA0521.3	11.687652	0.999999997	1084	1089	-	CAGCTG
	MA0521.2	9.835372	0.911610584	1081	1092	+	TGTCAGCTGAGC
	MA0521.2	9.834828	0.911599275	1081	1092	-	GCTCAGCTGACA
SOX3	MA0514.3	12.670143	0.999999994	1384	1390	+	ACAATGG
	MA0514.1	14.263844	0.976755792	1190	1199	-	CTTTTGT TTT
	MA0514.2	12.783486	0.976432725	1382	1392	+	GGACAATGGGG
	MA0514.2	11.463735	0.947033394	88	98	+	GAACAATGCCA
	MA0514.3	10.413392	0.946251588	90	96	+	ACAATGC
	MA0514.1	12.178224	0.945887874	1269	1278	+	CTTTTGTGTT
	MA0514.1	11.7445965	0.939470039	640	649	-	TTTTTGT TTT
	MA0514.1	11.741842	0.939429275	1213	1222	+	CCTTCTTCT
	MA0514.1	9.676996	0.908868819	1225	1234	+	TCTTCTTTT
NFATC3	MA0625.3	9.505253	0.984349483	637	642	+	CGGAAA
	MA0625.2	9.957303	0.960794223	636	644	+	GCGGAAAAC
	MA0625.2	9.742697	0.955794591	571	579	+	ATGGAACAA
	MA0625.3	8.246608	0.952311193	572	577	+	TGGAAC
	MA0625.3	7.7125983	0.938718203	21	26	+	TGGAAT
	MA0625.3	7.7125983	0.938718203	534	539	+	TGGAAT
	MA0625.2	8.695174	0.931390706	1207	1215	-	AGGGAAAAA
	MA0625.3	7.3205676	0.928739224	393	398	+	TGGGAA
	MA0625.3	7.3205676	0.928739224	732	737	+	TGGGAA
	MA0625.3	7.3205676	0.928739224	810	815	-	TGGGAA
	MA0625.3	7.3205676	0.928739224	1448	1453	-	TGGGAA
	MA0625.3	7.198099	0.925621839	733	738	+	GGGAAA
	MA0625.3	7.198099	0.925621839	1209	1214	-	GGGAAA
	MA0625.3	7.198099	0.925621839	1447	1452	-	GGGAAA
	MA0625.1	10.397401	0.923160616	635	644	-	GTTTCCGCT
	MA0625.1	10.250588	0.919430606	1440	1449	+	TTTTTCCTT
	MA0625.2	8.088652	0.917260693	1440	1448	-	AAGGAAAAA
	MA0625.2	7.828875	0.911208739	1446	1454	-	ATGGGAAAG
	MA0625.2	7.81941	0.91098823	392	400	+	ATGGGAAGA
	MA0625.2	7.81941	0.91098823	808	816	-	ATGGGAAGA
	MA0625.3	6.590789	0.910163007	419	424	-	AGGAAA
	MA0625.3	6.590789	0.910163007	776	781	+	AGGAAA
	MA0625.3	6.590789	0.910163007	1232	1237	-	AGGAAA
	MA0625.3	6.590789	0.910163007	1442	1447	-	AGGAAA
	MA0625.3	6.549654	0.909115937	180	185	+	TGGAAG
	MA0625.2	7.5977526	0.905824333	731	739	+	CTGGGAAAA
	MA0625.1	9.575281	0.902273322	1207	1216	+	TTTTCCCTT
NFATC1	MA0624.1	10.068329	0.936830235	635	644	-	GTTTCCGCT
	MA0624.1	9.486612	0.920250609	1440	1449	+	TTTTTCCTT
	MA0624.1	8.829435	0.90152027	570	579	-	TTGTTCCATG
KLF5	MA0599.1	15.429108	0.999532735	1396	1405	-	GCCCCACCCC
	MA0599.1	14.852804	0.992201348	1413	1422	-	GCCCCTCCCC
	MA0599.1	12.518292	0.962503091	6	15	+	CCCCCTCCCT
ISX	MA0654.2	10.699699	0.998157853	1337	1342	-	CAATTA
	MA0654.2	10.699699	0.998157853	1366	1371	-	CAATTA
	MA0654.1	11.868463	0.995525149	1336	1343	-	CCAATTAG
	MA0654.1	11.149993	0.980032615	1365	1372	-	TCAATTAG
NKX2-8	MA0673.2	11.807779	0.994195054	505	512	+	GCACTTGA

	MA0673.1	12.082113	0.989012973	505	513	+	GCACCTTGAG
	MA0673.2	7.2168984	0.908064827	949	956	+	CCTCTTCA
	MA0673.1	7.4907346	0.905990479	949	957	+	CCTCTTCAG
LIN54	MA0619.2	10.044813	0.957328743	1125	1131	-	TTTAAAC
	MA0619.2	9.076773	0.936842421	1126	1132	+	TTTAAAA
	MA0619.1	9.600581	0.927965561	1124	1132	-	TTTTAAACG
	MA0619.1	8.841201	0.912909081	1125	1133	+	GTTTAAAAAC
MIXL1	MA0662.2	9.504297	0.988367348	1337	1342	-	CAATTA
	MA0662.2	9.504297	0.988367348	1366	1371	-	CAATTA
	MA0662.1	10.338596	0.974282098	1364	1373	-	CTCAATTAGC
	MA0662.1	10.088807	0.967781317	1335	1344	-	GCCAATTAGG
	MA0662.2	7.3797574	0.927028309	31	36	+	AAATTA
	MA0662.2	7.3797574	0.927028309	260	265	+	AAATTA
	MA0662.2	7.3797574	0.927028309	705	710	+	AAATTA
	MA0662.2	7.3797574	0.927028309	782	787	+	AAATTA
	MA0662.2	7.3797574	0.927028309	1117	1122	+	AAATTA
	MA0662.2	7.2568274	0.923479112	46	51	+	TAATCA
	MA0662.2	7.2568274	0.923479112	367	372	-	TAATCA
	MA0662.2	7.036899	0.917129413	46	51	-	TGATTA
	MA0662.2	7.036899	0.917129413	367	372	+	TGATTA
	MA0662.2	6.703166	0.907493978	31	36	-	TAATTT
	MA0662.2	6.703166	0.907493978	260	265	-	TAATTT
	MA0662.2	6.703166	0.907493978	705	710	-	TAATTT
	MA0662.2	6.703166	0.907493978	782	787	-	TAATTT
	MA0662.2	6.703166	0.907493978	1117	1122	-	TAATTT
	MA0662.1	7.6303344	0.9037994	1115	1124	+	GCAAATTACC
ESX1	MA0894.2	10.835335	0.999999991	1337	1342	+	TAATTG
	MA0894.2	10.835335	0.999999991	1366	1371	+	TAATTG
	MA0644.2	11.659747	0.987759197	1336	1343	-	CCAATTAG
	MA0644.3	11.289511	0.987545172	1337	1343	-	CCAATTA
	MA0894.1	12.255182	0.977067619	1335	1344	+	CCTAATTGGC
	MA0644.2	11.022582	0.976054974	1365	1372	-	TCAATTAG
	MA0644.3	10.652354	0.975636302	1366	1372	-	TCAATTA
	MA0644.1	10.545884	0.962684303	1364	1373	-	CTCAATTAGC
	MA0644.1	10.369008	0.958137129	1335	1344	-	GCCAATTAGG
	MA0894.1	11.259271	0.957934188	1364	1373	+	GCTAATTGAG
	MA0644.3	7.6797767	0.920076886	1116	1122	+	CAAATTA
	MA0644.2	7.9681273	0.919947033	1336	1343	+	CTAATTGG
	MA0644.3	7.5980644	0.918549631	1336	1342	+	CTAATTG
	MA0644.3	7.5980644	0.918549631	1365	1371	+	CTAATTG
	MA0644.2	7.6847534	0.914741677	1116	1123	+	CAAATTAC
	MA0644.2	7.6230264	0.9136078	1365	1372	+	CTAATTGA
	MA0644.1	8.556956	0.911552449	1115	1124	+	GCAAATTACC
	MA0644.3	7.04262	0.908168016	30	36	+	TAAATTA
	MA0644.3	6.9016523	0.905533235	705	711	-	CTAATTT
	MA0894.2	6.556195	0.905494209	31	36	-	TAATTT
	MA0894.2	6.556195	0.905494209	260	265	-	TAATTT
	MA0894.2	6.556195	0.905494209	705	710	-	TAATTT
	MA0894.2	6.556195	0.905494209	782	787	-	TAATTT
	MA0894.2	6.556195	0.905494209	1117	1122	-	TAATTT
	MA0894.2	6.5042405	0.904346788	1053	1058	-	AAATTG
	MA0894.2	6.5042405	0.904346788	1108	1113	+	AAATTG
ALX3	MA0634.2	9.511346	0.986953539	1337	1342	-	CAATTA
	MA0634.2	9.511346	0.986953539	1366	1371	-	CAATTA
	MA0634.1	10.369786	0.946990381	1364	1373	-	CTCAATTAGC
	MA0634.2	7.459559	0.92308098	31	36	+	AAATTA
	MA0634.2	7.459559	0.92308098	260	265	+	AAATTA
	MA0634.2	7.459559	0.92308098	705	710	+	AAATTA
	MA0634.2	7.459559	0.92308098	782	787	+	AAATTA
	MA0634.2	7.459559	0.92308098	1117	1122	+	AAATTA
	MA0634.1	9.195242	0.915826493	1335	1344	-	GCCAATTAGG
	MA0634.2	6.949612	0.907206228	31	36	-	TAATTT
	MA0634.2	6.949612	0.907206228	260	265	-	TAATTT
	MA0634.2	6.949612	0.907206228	705	710	-	TAATTT
	MA0634.2	6.949612	0.907206228	782	787	-	TAATTT
	MA0634.2	6.949612	0.907206228	1117	1122	-	TAATTT
	MA0634.2	6.8104954	0.902875494	46	51	-	TGATTA

	MA0634.2	6.8104954	0.902875494	367	372	+	TGATTA
NKX6-2	MA0675.2	8.946917	0.984819618	1337	1342	-	CAATTA
	MA0675.2	8.946917	0.984819618	1366	1371	-	CAATTA
	MA0675.2	8.366475	0.967261456	177	182	-	CCATTA
	MA0675.2	7.327737	0.93583997	55	60	-	TTATTA
	MA0675.2	6.8259006	0.920659589	214	219	+	CTATTA
	MA0675.2	6.8259006	0.920659589	373	378	-	CTATTA
	MA0675.1	7.8125153	0.915705456	1336	1343	-	CCAATTAG
	MA0675.2	6.527517	0.91163358	55	60	+	TAATAA
	MA0675.2	6.385369	0.90733365	46	51	+	TAATCA
	MA0675.2	6.385369	0.90733365	367	372	-	TAATCA
	MA0675.1	7.451829	0.905778213	301	308	+	CCAATAAA
	MA0675.2	6.2442346	0.903064386	31	36	+	AAATTA
	MA0675.2	6.2442346	0.903064386	260	265	+	AAATTA
	MA0675.2	6.2442346	0.903064386	705	710	+	AAATTA
	MA0675.2	6.2442346	0.903064386	782	787	+	AAATTA
	MA0675.2	6.2442346	0.903064386	1117	1122	+	AAATTA
DUX	MA0611.1	8.709149	0.909975729	45	52	+	ATAATCAT
	MA0468.1	8.930404	0.902909756	138	148	-	TGACCCAATCT
HOXA9	MA0594.3	9.363868	0.974183173	120	126	-	ATCGTTA
	MA0594.3	8.968411	0.963751522	206	212	-	GTCATAA
	MA0594.3	8.968411	0.963751522	616	622	-	GTCATAA
	MA0594.2	9.737098	0.95296235	203	212	-	GTCATAAATA
	MA0594.2	9.725086	0.952674794	613	622	-	GTCATAAATT
	MA0594.2	9.315738	0.942875005	117	126	-	ATCGTTATCT
	MA0594.3	8.141107	0.941928238	427	433	+	ACCGTAA
	MA0594.2	8.007415	0.911553795	427	436	+	ACCGTAACTA
	MA0594.1	12.167036	0.906953189	202	212	-	GTCATAAATAA
EMX1	MA0612.2	10.989156	0.96934424	1336	1343	-	CCAATTAG
	MA0612.3	9.558468	0.967240885	1337	1342	-	CAATTA
	MA0612.3	9.558468	0.967240885	1366	1371	-	CAATTA
	MA0612.2	10.052071	0.952194722	1365	1372	-	TCAATTAG
	MA0612.1	10.156557	0.948492875	1335	1344	+	CCTAATTGGC
	MA0612.3	6.6334095	0.910035048	177	182	-	CCATTA
	MA0612.1	8.493362	0.901761055	1115	1124	+	GCAAATTACC
LBX1	MA0618.2	10.637409	0.968436414	1337	1343	+	TAATTGG
	MA0618.2	10.592086	0.967429838	431	437	+	TAACTAG
	MA0618.2	10.592086	0.967429838	443	449	-	TAACTAG
	MA0618.1	10.088422	0.938419359	430	437	+	GTAAC TAG
	MA0618.1	9.744656	0.931079189	1336	1343	+	CTAATTGG
	MA0618.1	9.699332	0.930111435	443	450	-	CTAACTAG
	MA0618.2	8.3320465	0.917237174	213	219	-	TAATAGG
	MA0618.1	8.897671	0.912994187	1365	1372	-	TCAATTAG
	MA0618.2	7.983834	0.909503802	1336	1342	-	CAATTAG
	MA0618.2	7.983834	0.909503802	1365	1371	-	CAATTAG
FOXJ2	MA0614.1	9.55606	0.919364283	639	646	+	GAAAACAA
	MA0614.1	9.55606	0.919364283	1189	1196	+	GAAAACAA
	MA0614.1	9.187719	0.911954634	202	209	-	ATAAATAA
SP2	MA0516.3	13.044691	0.95043338	1413	1421	+	GGGGAGGGG
	MA0516.1	15.029106	0.927993092	1391	1405	-	GCCCCACCC CAGCC
	MA0516.3	10.780567	0.911691827	7	15	-	AGGGAGGGG
	MA0516.1	13.680994	0.909698231	1408	1422	-	GCCCCTCCCCCAAGC
TCFL5	MA0632.2	11.607631	0.941888843	889	898	-	TCACGCACAC
	MA0632.3	9.3809185	0.938096201	891	898	-	TCACGCAC
	MA0632.3	6.7769394	0.900937083	901	908	+	GCACGTAC
FOXP2	MA0593.1	12.786722	0.940797259	1187	1197	+	AAGAAAACAAA
	MA0593.2	11.250482	0.937726637	1188	1196	+	AGAAAACAA
	MA0593.2	10.030412	0.91562071	638	646	+	GGAAAACAA
HOXC11	MA0651.1	12.808722	0.939614645	613	623	-	GGTCATAAATT

	MA0651.1	12.74218	0.938538675	203	213	-	GGTCATAAAATA
SOX6	MA0515.1	11.699764	0.93750718	1381	1390	-	CCATTGTCCA
	MA0515.1	11.319688	0.930263446	1190	1199	-	CTTTGTTTTT
	MA0515.1	10.454399	0.913772233	87	96	-	GCATTGTTCA
	MA0515.1	10.065938	0.906368699	640	649	-	TTTTTGTTTT
	MA0515.1	9.763407	0.900602869	1161	1170	+	TCTTGTTCA
GSC	MA0498.3	9.351322	1.000000007	741	745	+	TGACA
	MA0498.3	9.351322	1.000000007	1081	1085	-	TGACA
	MA0498.2	9.947893	0.991412464	740	746	+	CTGACAG
	MA0498.2	8.963122	0.970557878	1080	1086	-	CTGACAT
	MA0648.2	8.547501	0.936736682	413	418	+	TAATCT
	MA0891.2	8.175392	0.935802956	413	418	+	TAATCT
	MA0498.3	6.21157	0.929896798	926	930	+	AGACA
	MA0648.2	8.076256	0.924549158	381	386	+	TAATTC
	MA0891.2	7.4198046	0.913429816	275	280	-	TAATAC
	MA0891.2	7.114401	0.904386734	381	386	+	TAATTC
	MA0498.3	5.056073	0.904097305	290	294	+	TGACT
	MA0498.3	5.056073	0.904097305	314	318	+	TGACT
	MA0498.3	5.056073	0.904097305	436	440	-	TGACT
	MA0498.3	5.056073	0.904097305	862	866	+	TGACT
	MA0498.3	5.056073	0.904097305	896	900	+	TGACT
	MA0498.2	5.823239	0.904064263	925	931	+	CAGACAT
	MA0891.2	7.094253	0.903790153	43	48	-	TTATCC
	MA0648.2	7.1890044	0.901602704	275	280	-	TAATAC
MEOX1	MA0661.2	8.950097	0.936520995	1337	1343	-	CCAATTA
	MA0661.2	8.695665	0.930837032	1336	1342	+	CTAATTG
	MA0661.2	8.695665	0.930837032	1365	1371	+	CTAATTG
	MA0661.1	9.146161	0.914053511	1364	1373	+	GCTAATTGAG
	MA0661.1	8.676534	0.904377607	1335	1344	+	CCTAATTGGC
	MA0661.2	7.343514	0.900630196	366	372	+	GTGATTA
LHX6	MA0658.2	9.343269	0.925276036	1336	1343	-	CCAATTAG
	MA0658.2	9.288949	0.92427164	1336	1343	+	CTAATTGG
	MA0658.2	8.563713	0.910861856	1365	1372	+	CTAATTGA
	MA0658.1	9.33915	0.908516955	1335	1344	+	CCTAATTGGC
	MA0658.1	9.221741	0.906509154	1335	1344	-	GCCAATTAGG
	MA0658.2	8.268394	0.905401345	1365	1372	-	TCAATTAG
	MA0658.2	8.11642	0.902591297	443	450	-	CTAACTAG
DBP	MA0466.1	14.696246	0.973987474	1047	1057	-	AATTGCACAAC
	MA0466.2	13.023246	0.961180639	1047	1056	-	ATTGCACAAC
	MA0466.2	11.805978	0.944699116	1047	1056	+	GTTGTGCAAT
	MA1540.1	11.410727	0.92935266	1172	1182	+	CCCAAGGTTAC
	MA0019.2	11.391544	0.924367509	587	596	+	ATGAAATACC
	MA0639.2	9.870932	0.916685981	277	286	+	ATTATACAAC
	MA0466.2	9.648945	0.915493397	1110	1119	-	TTGCACAAT
	MA0466.2	9.57752	0.914526326	277	286	+	ATTATACAAC
	MA0639.2	9.503061	0.911758066	277	286	-	GTTGTATAAT
	MA0639.1	9.984427	0.911396553	276	287	-	CGTTGTATAATA
	MA0639.1	9.968258	0.911184532	276	287	+	TATTATACAACG
	MA0466.4	10.268873	0.905484971	1047	1056	+	GTTGTGCAAT
	MA0466.4	10.189109	0.904553506	1047	1056	-	ATTGCACAAC
PITX1	MA0682.3	7.4620743	0.916130243	413	418	+	TAATCT
TCF7L2	MA0523.2	9.600416	0.911710368	1075	1083	-	ACATCAGAG
TCF3	MA0092.2	11.194442	0.964049496	921	929	-	GTCTGGATT
	MA0092.1	11.151863	0.952147077	921	930	-	TGTCTGGATT
	MA0092.2	10.667699	0.948017539	792	800	-	ATCTGGATT
	MA0148.1	12.990497	0.941848609	1185	1195	-	TGTTTTCTTTG
	MA0148.2	12.953144	0.941398611	1185	1195	-	TGTTTTCTTTG
	MA0092.1	9.982523	0.917695361	792	801	-	AATCTGGATT
	MA0148.2	11.479643	0.916121882	849	859	+	TGTTTGTCTT
	MA0148.1	11.455882	0.915194766	849	859	+	TGTTTGTCTT
RXRA	MA0512.1	9.419818	0.900012865	1318	1328	-	CTGGGGTCAGC

MSX3	MA0709.2	11.105006	1.000000011	1337	1342	-	CAATTA
	MA0709.2	11.105006	1.000000011	1366	1371	-	CAATTA
	MA0709.1	12.037398	0.998862142	1336	1343	-	CCAATTAG
	MA0709.1	10.683251	0.968583761	1365	1372	-	TCAATTAG
	MA0709.2	6.987123	0.902833755	31	36	+	AAATTA
	MA0709.2	6.987123	0.902833755	260	265	+	AAATTA
	MA0709.2	6.987123	0.902833755	705	710	+	AAATTA
	MA0709.2	6.987123	0.902833755	782	787	+	AAATTA
	MA0709.2	6.987123	0.902833755	1117	1122	+	AAATTA
GATA5	MA0766.1	11.294104	1.000000003	355	362	+	AGATAAGA
	MA0766.3	12.402841	0.999436207	117	124	+	AGATAACG
	MA0766.3	12.251338	0.996898405	355	362	+	AGATAAGA
	MA0766.1	10.456418	0.978698036	117	124	+	AGATAACG
	MA0766.2	12.171033	0.977003485	116	125	+	AAGATAACGA
	MA0766.2	11.21564	0.961610351	354	363	+	TAGATAAGAT
	MA0766.1	8.259515	0.922831777	410	417	+	AGATAATC
	MA0766.1	8.232599	0.922147327	388	395	+	AGATATGG
	MA0766.1	8.232599	0.922147327	1069	1076	-	AGATATGG
	MA0766.3	7.439047	0.916288284	410	417	+	AGATAATC
	MA0766.1	7.8862853	0.913340719	803	810	-	AGATACGA
RAX	MA0718.2	10.4872	0.999999997	1337	1342	-	CAATTA
	MA0718.2	10.4872	0.999999997	1366	1371	-	CAATTA
	MA0717.2	9.771953	0.999999995	1337	1342	-	CAATTA
	MA0717.2	9.771953	0.999999995	1366	1371	-	CAATTA
	MA0654.2	10.699699	0.998157853	1337	1342	-	CAATTA
	MA0654.2	10.699699	0.998157853	1366	1371	-	CAATTA
	MA0717.1	10.817973	0.996592774	1336	1343	-	CCAATTAG
	MA0654.1	11.868463	0.995525149	1336	1343	-	CCAATTAG
	MA0717.1	10.252437	0.980127922	1365	1372	-	TCAATTAG
	MA0654.1	11.149993	0.980032615	1365	1372	-	TCAATTAG
	MA0718.1	11.3258705	0.962923719	1335	1344	-	GCCAATTAGG
	MA0718.1	10.678769	0.948646938	1364	1373	-	CTCAATTAGC
	MA0718.2	7.974167	0.936332134	31	36	+	AAATTA
	MA0718.2	7.974167	0.936332134	260	265	+	AAATTA
	MA0718.2	7.974167	0.936332134	705	710	+	AAATTA
	MA0718.2	7.974167	0.936332134	782	787	+	AAATTA
	MA0718.2	7.974167	0.936332134	1117	1122	+	AAATTA
	MA0848.1	8.825259	0.923128392	639	645	+	GAAAACA
	MA0848.1	8.825259	0.923128392	769	775	-	GAAAACA
	MA0848.1	8.825259	0.923128392	1189	1195	+	GAAAACA
	MA0717.2	7.3243523	0.92235854	31	36	+	AAATTA
	MA0717.2	7.3243523	0.92235854	260	265	+	AAATTA
	MA0717.2	7.3243523	0.92235854	705	710	+	AAATTA
	MA0717.2	7.3243523	0.92235854	782	787	+	AAATTA
	MA0717.2	7.3243523	0.92235854	1117	1122	+	AAATTA
	MA0848.1	8.571896	0.91811942	203	209	-	ATAAATA
	MA0717.1	7.6505632	0.9043778	1116	1123	+	CAAATTAC
	MA0718.1	8.649853	0.903883636	1115	1124	+	GCAAATTACC
	MA0717.2	6.6415567	0.90069927	46	51	-	TGATTA
	MA0717.2	6.6415567	0.90069927	367	372	+	TGATTA
	MA1524.1	8.815706	0.900492327	329	340	-	GGTCAATTGTTT
LBX2	MA0699.2	9.861742	0.999999997	1337	1342	-	CAATTA
	MA0699.2	9.861742	0.999999997	1366	1371	-	CAATTA
	MA0699.1	11.507837	0.989009125	1335	1344	-	GCCAATTAGG
	MA0699.1	10.747043	0.968101765	1364	1373	-	CTCAATTAGC
	MA0699.2	6.76798	0.902764217	177	182	-	CCATTA
LHX2	MA0700.3	11.454965	0.999999995	1337	1342	-	CAATTA
	MA0700.3	11.454965	0.999999995	1366	1371	-	CAATTA
	MA0700.1	11.593066	0.958110175	1335	1344	-	GCCAATTAGG
	MA0700.1	10.9656515	0.947523608	1364	1373	+	GCTAATTGAG
	MA0700.1	10.585644	0.941111616	1335	1344	+	CCTAATTGGC
	MA0700.2	11.179093	0.931523793	1335	1345	-	GGCCAATTAGG
	MA0700.1	9.035998	0.914963957	1364	1373	-	CTCAATTAGC
	MA0700.3	7.731684	0.909459564	214	219	+	CTATTA
	MA0700.3	7.731684	0.909459564	373	378	-	CTATTA
ZIC3	MA0697.3	13.1827965	0.999999993	1239	1245	-	CAGCAGG

	MA0697.2	13.970605	0.927365048	1235	1247	-	AGCAGCAGGAAGG
SHOX2	MA0720.2	10.458221	0.999522231	1337	1342	-	CAATTA
	MA0720.2	10.458221	0.999522231	1366	1371	-	CAATTA
	MA0720.1	11.690396	0.998531686	1336	1343	-	CCAATTAG
	MA0720.1	11.013979	0.983357556	1365	1372	-	TCAATTAG
	MA0720.2	7.2980523	0.92313338	31	36	+	AAATTA
	MA0720.2	7.2980523	0.92313338	260	265	+	AAATTA
	MA0720.2	7.2980523	0.92313338	705	710	+	AAATTA
	MA0720.2	7.2980523	0.92313338	782	787	+	AAATTA
	MA0720.2	7.2980523	0.92313338	1117	1122	+	AAATTA
	MA0720.1	7.4696827	0.903848047	1116	1123	+	CAAATTAC
LHX9	MA0701.1	10.83605	0.997932743	1336	1343	-	CCAATTAG
	MA0701.3	11.625071	0.982498491	1337	1343	-	CCAATTA
	MA0701.1	10.146802	0.979079421	1365	1372	-	TCAATTAG
	MA0701.2	11.978704	0.978994916	1336	1343	-	CCAATTAG
	MA0701.3	9.326906	0.938859757	1366	1372	-	TCAATTA
	MA0701.2	9.680447	0.936503127	1365	1372	-	TCAATTAG
	MA0701.2	8.886565	0.921825295	1365	1372	+	CTAATTGA
	MA0701.3	8.318939	0.919719958	1336	1342	+	CTAATTG
	MA0701.3	8.318939	0.919719958	1365	1371	+	CTAATTG
	MA0701.2	8.672183	0.917861648	1336	1343	+	CTAATTGG
	MA0701.1	7.8161263	0.91532737	176	183	-	TCCATTAG
	MA0701.1	7.3087754	0.901449565	704	711	+	AAAATTAG
MNX1	MA0707.2	10.852637	0.996226512	366	373	+	GTGATTAT
	MA0707.3	9.722625	0.996024242	46	51	-	TGATTA
	MA0707.3	9.722625	0.996024242	367	372	+	TGATTA
	MA0707.3	9.49008	0.991646942	1337	1342	-	CAATTA
	MA0707.3	9.49008	0.991646942	1366	1371	-	CAATTA
	MA0707.2	10.36355	0.987488964	45	52	-	ATGATTAT
	MA0707.2	9.62735	0.974336736	1336	1343	-	CCAATTAG
	MA0707.2	8.79501	0.959466967	1365	1372	-	TCAATTAG
	MA0707.3	6.93994	0.943644479	177	182	-	CCATTA
	MA0707.3	6.8044157	0.941093443	46	51	+	TAATCA
	MA0707.3	6.8044157	0.941093443	367	372	-	TAATCA
	MA0707.3	6.593203	0.93711769	151	156	+	TGATCA
	MA0707.3	6.593203	0.93711769	151	156	-	TGATCA
	MA0707.2	7.444891	0.93534708	45	52	+	ATAATCAT
	MA0707.2	7.353446	0.933713415	150	157	-	CTGATCAT
	MA0707.2	6.6102624	0.92043643	150	157	+	ATGATCAG
	MA0707.1	9.169538	0.919289446	300	309	+	TCCAATAAAA
	MA0707.2	6.4242005	0.917112432	366	373	-	ATAATCAC
	MA0707.1	8.979518	0.914934681	1335	1344	-	GCCAATTAGG
	MA0707.2	6.2445807	0.913903522	176	183	-	TCCATTAG
	MA0707.3	5.1980557	0.910856187	311	316	+	TGATGA
	MA0707.3	5.1980557	0.910856187	836	841	-	TGATGA
PRRX1	MA0716.2	10.034261	0.994420743	1337	1342	-	CAATTA
	MA0716.2	10.034261	0.994420743	1366	1371	-	CAATTA
	MA0716.1	10.723544	0.979743879	1336	1343	-	CCAATTAG
	MA0716.1	10.216182	0.966457124	1365	1372	-	TCAATTAG
	MA0716.2	7.8248343	0.932547238	31	36	+	AAATTA
	MA0716.2	7.8248343	0.932547238	260	265	+	AAATTA
	MA0716.2	7.8248343	0.932547238	705	710	+	AAATTA
	MA0716.2	7.8248343	0.932547238	782	787	+	AAATTA
	MA0716.2	7.8248343	0.932547238	1117	1122	+	AAATTA
	MA0716.1	7.9418364	0.906896793	1116	1123	+	CAAATTAC
	MA0716.2	6.880379	0.906098405	46	51	+	TAATCA
	MA0716.2	6.880379	0.906098405	367	372	-	TAATCA
	MA0716.2	6.769745	0.903000165	381	386	-	GAATTA
MSX2	MA0708.3	11.05564	0.999999998	1337	1342	-	CAATTA
	MA0708.3	11.05564	0.999999998	1366	1371	-	CAATTA
	MA0708.1	12.197154	0.990345166	1336	1343	-	CCAATTAG
	MA0708.2	11.830209	0.989620013	1336	1343	-	CCAATTAG
	MA0708.2	10.299102	0.960299737	1365	1372	-	TCAATTAG
	MA0708.1	10.013457	0.940085053	1365	1372	-	TCAATTAG
	MA0708.3	6.487643	0.907632652	46	51	+	TAATCA
	MA0708.3	6.487643	0.907632652	367	372	-	TAATCA

	MA0708.3	6.4622974	0.907120156	332	337	+	CAATTG
	MA0708.3	6.4622974	0.907120156	332	337	-	CAATTG
	MA0708.3	6.330817	0.904461555	31	36	+	AAATTA
	MA0708.3	6.330817	0.904461555	260	265	+	AAATTA
	MA0708.3	6.330817	0.904461555	705	710	+	AAATTA
	MA0708.3	6.330817	0.904461555	782	787	+	AAATTA
	MA0708.3	6.330817	0.904461555	1117	1122	+	AAATTA
TEAD3	MA0808.1	12.272152	0.982377192	549	556	-	GCATTCCT
	MA0808.1	9.958173	0.946555195	534	541	-	TCATTCCA
	MA0808.1	9.385312	0.937686915	690	697	-	GAATTCCT
	MA0808.1	9.309375	0.936511354	710	717	-	TCATTCCT
	MA0808.1	8.693201	0.926972558	557	564	+	ACATGCCT
VAX2	MA0723.3	9.070431	0.989189574	1337	1342	-	CAATTA
	MA0723.3	9.070431	0.989189574	1366	1371	-	CAATTA
	MA0723.2	9.806666	0.988146146	1336	1343	-	CCAATTAG
	MA0723.2	9.498714	0.98125308	1365	1372	-	TCAATTAG
	MA0723.3	7.812914	0.959238663	177	182	-	CCATTA
	MA0723.2	8.241086	0.953102854	176	183	-	TCCATTAG
	MA0723.2	8.002291	0.947757761	54	61	-	GTTATTAG
	MA0723.3	7.1906877	0.944418789	55	60	-	TTATTA
	MA0723.3	6.7368016	0.933608358	214	219	+	CTATTA
	MA0723.3	6.7368016	0.933608358	373	378	-	CTATTA
	MA0723.3	6.6786103	0.932222386	203	208	+	TATTTA
	MA0723.3	6.384157	0.925209248	31	36	+	AAATTA
	MA0723.3	6.384157	0.925209248	260	265	+	AAATTA
	MA0723.3	6.384157	0.925209248	705	710	+	AAATTA
	MA0723.3	6.384157	0.925209248	782	787	+	AAATTA
	MA0723.3	6.384157	0.925209248	1117	1122	+	AAATTA
	MA0723.1	8.707651	0.924265965	1336	1343	+	CTAATTGG
	MA0723.2	6.91938	0.923518347	213	220	+	CCTATTAC
	MA0723.1	8.6268835	0.922130815	1365	1372	+	CTAATTGA
	MA0723.3	6.2445865	0.921885022	55	60	+	TAATAA
	MA0723.3	6.2247243	0.921411955	105	110	+	CATTTA
	MA0723.2	6.7332187	0.919351386	1116	1123	-	GTAATTTG
	MA0723.3	6.1033244	0.918520513	585	590	+	TCATGA
	MA0723.3	6.1033244	0.918520513	585	590	-	TCATGA
	MA0723.2	6.637557	0.917210136	584	591	+	GTCATGAA
	MA0723.2	6.566027	0.915609041	1116	1123	+	CAAATTAC
	MA0723.3	5.9221864	0.914206257	31	36	-	TAATTT
	MA0723.3	5.9221864	0.914206257	260	265	-	TAATTT
	MA0723.3	5.9221864	0.914206257	705	710	-	TAATTT
	MA0723.3	5.9221864	0.914206257	782	787	-	TAATTT
	MA0723.3	5.9221864	0.914206257	1117	1122	-	TAATTT
	MA0723.1	8.276412	0.91286585	1336	1343	-	CCAATTAG
	MA0723.2	6.426841	0.912493552	54	61	+	CTAATAAC
	MA0723.1	8.260582	0.912447371	1116	1123	+	CAAATTAC
	MA0723.3	5.7907004	0.911074591	302	307	+	CAATAA
	MA0723.1	8.189892	0.910578626	54	61	+	CTAATAAC
	MA0723.3	5.757783	0.910290578	46	51	-	TGATTA
	MA0723.3	5.757783	0.910290578	367	372	+	TGATTA
	MA0723.2	6.248932	0.908511314	301	308	+	CCAATAAA
	MA0723.1	8.0076685	0.905761423	1365	1372	-	TCAATTAG
	MA0723.2	6.099179	0.905159304	104	111	+	TCATTTAC
	MA0723.2	6.0814266	0.904761947	704	711	+	AAAATTAG
	MA0723.3	5.4683003	0.903395826	1053	1058	+	CAATTT
	MA0723.3	5.4683003	0.903395826	1108	1113	-	CAATTT
	MA0723.2	5.9779363	0.902445462	584	591	-	TTCATGAC
	MA0723.3	5.421094	0.902271487	114	119	-	TCTTTA
VAX1	MA0722.2	8.770528	0.942577167	1336	1342	+	CTAATTG
	MA0722.2	8.770528	0.942577167	1365	1371	+	CTAATTG
	MA0722.2	8.357032	0.930482943	1337	1343	-	CCAATTA
	MA0722.2	8.195556	0.925759974	1366	1372	-	TCAATTA
	MA0722.1	8.353809	0.917248513	1116	1123	+	CAAATTAC
	MA0722.1	8.351835	0.917192474	1365	1372	+	CTAATTGA
	MA0722.1	8.286723	0.915344141	1336	1343	+	CTAATTGG
	MA0722.2	7.819134	0.914750133	1116	1122	+	CAAATTA
	MA0722.2	7.657657	0.910027137	30	36	+	TAAATTA
	MA0722.1	7.9491053	0.905760208	54	61	+	CTAATAAC

	MA0722.1	7.873134	0.903603621	1336	1343	-	CCAATTAG
	MA0722.2	7.4146056	0.902918194	54	60	+	CTAATAA
	MA0722.2	7.3509865	0.901057416	176	182	+	CTAATGG
	MA0722.1	7.782022	0.901017228	30	37	+	TAAATTAT
RAX2	MA0717.2	9.771953	0.999999995	1337	1342	-	CAATTA
	MA0717.2	9.771953	0.999999995	1366	1371	-	CAATTA
	MA0717.1	10.817973	0.996592774	1336	1343	-	CCAATTAG
	MA0717.1	10.252437	0.980127922	1365	1372	-	TCAATTAG
	MA0717.2	7.3243523	0.92235854	31	36	+	AAATTA
	MA0717.2	7.3243523	0.92235854	260	265	+	AAATTA
	MA0717.2	7.3243523	0.92235854	705	710	+	AAATTA
	MA0717.2	7.3243523	0.92235854	782	787	+	AAATTA
	MA0717.2	7.3243523	0.92235854	1117	1122	+	AAATTA
	MA0717.1	7.6505632	0.9043778	1116	1123	+	CAAATTAC
	MA0717.2	6.6415567	0.90069927	46	51	-	TGATTA
	MA0717.2	6.6415567	0.90069927	367	372	+	TGATTA
ETV4	MA0764.2	13.387904	0.979225743	1234	1243	-	GCAGGAAGGA
	MA0764.2	9.406507	0.909344804	1420	1429	-	CTAGGAAGCC
RHOXF1	MA0719.2	8.480559	0.978166059	1088	1093	+	TGAGCC
	MA0719.2	7.580493	0.960268293	43	48	-	TTATCC
	MA0719.1	8.0777025	0.959980111	1087	1094	+	CTGAGCCT
	MA0719.2	7.329758	0.955282447	413	418	+	TAATCT
	MA0719.2	7.285044	0.954393312	360	365	-	TGATCT
	MA0719.2	7.285044	0.954393312	514	519	+	TGATCT
	MA0719.1	7.460941	0.948092213	42	49	-	ATTATCCT
	MA0719.1	7.2102995	0.943261175	412	419	+	ATAATCTT
	MA0719.1	7.071726	0.940590209	513	520	+	GTGATCTC
	MA0719.2	6.54683	0.939713971	1433	1438	-	AGAGCC
	MA0719.2	6.527193	0.939323489	191	196	-	TTAGCC
	MA0719.1	6.9898205	0.939011507	190	197	-	TTAGCCA
	MA0719.1	6.8820925	0.936935082	359	366	-	CTGATCTT
	MA0719.2	6.2317443	0.933448507	1142	1147	+	TGAGCT
	MA0719.1	6.14385	0.922705674	1432	1439	-	CAGAGCCT
	MA0719.1	5.9066763	0.918134224	409	416	-	ATTATCTC
	MA0719.1	5.824692	0.916553997	1141	1148	+	CTGAGCTG
	MA0719.2	5.331678	0.915550742	117	122	-	TTATCT
	MA0719.2	5.331678	0.915550742	355	360	-	TTATCT
	MA0719.2	5.331678	0.915550742	410	415	-	TTATCT
	MA0719.2	5.142278	0.91178454	791	796	+	GAATCC
	MA0719.1	5.524543	0.910768715	354	361	-	CTTATCTA
	MA0719.1	5.334661	0.907108799	790	797	+	CGAATCCA
SP4	MA0685.2	14.535458	0.977230601	1413	1421	+	GGGGAGGGG
	MA0685.2	12.457943	0.942643962	7	15	-	AGGGAGGGG
LHX8	MA0705.1	10.450842	0.974639138	1336	1343	-	CCAATTAG
	MA0705.1	10.402068	0.973717839	1336	1343	+	CTAATTGG
	MA0705.2	8.746646	0.97329113	46	51	+	TAATCA
	MA0705.2	8.746646	0.97329113	367	372	-	TAATCA
	MA0705.2	8.685693	0.972020683	1337	1342	-	CAATTA
	MA0705.2	8.685693	0.972020683	1366	1371	-	CAATTA
	MA0705.2	8.636932	0.971004369	1337	1342	+	TAATTG
	MA0705.2	8.636932	0.971004369	1366	1371	+	TAATTG
	MA0705.2	8.431224	0.966716785	46	51	-	TGATTA
	MA0705.2	8.431224	0.966716785	367	372	+	TGATTA
	MA0705.1	9.751127	0.961422068	1365	1372	+	CTAATTGA
	MA0705.1	9.241301	0.951791836	1365	1372	-	TCAATTAG
	MA0705.2	7.2945485	0.94302505	332	337	+	CAATTG
	MA0705.2	7.2945485	0.94302505	332	337	-	CAATTG
	MA0705.2	7.1497927	0.940007902	151	156	+	TGATCA
	MA0705.2	7.1497927	0.940007902	151	156	-	TGATCA
	MA0705.2	6.013118	0.916316177	123	128	-	CAATCG
	MA0705.1	7.216328	0.91354167	366	373	-	ATAATCAC
	MA0705.2	5.6976957	0.909741832	123	128	+	CGATTG
	MA0705.1	6.587411	0.901661909	150	157	-	CTGATCAT
	MA0705.1	6.5072503	0.900147737	150	157	+	ATGATCAG

NOTO	MA0710.2	10.219405	0.970181259	1116	1122	+	CAAATTA
	MA0710.2	9.398601	0.954762985	1337	1343	-	CCAATTA
	MA0710.1	10.560234	0.954476473	1115	1124	+	GCAAATTACC
	MA0710.2	9.308239	0.953065602	30	36	+	TAAATTA
	MA0710.1	10.23964	0.9488071	1335	1344	-	GCCAATTAGG
	MA0710.1	9.6156645	0.93777273	1364	1373	-	CTCAATTAGC
	MA0710.2	8.487434	0.937647329	1366	1372	-	TCAATTA
	MA0710.1	9.579867	0.937139695	1335	1344	+	CCTAATTGGC
	MA0710.2	8.451789	0.936977752	1336	1342	+	CTAATTG
	MA0710.2	8.451789	0.936977752	1365	1371	+	CTAATTG
	MA0710.2	8.342421	0.93492334	705	711	-	CTAATTT
	MA0710.1	9.167516	0.92984768	1364	1373	+	GCTAATTGAG
	MA0710.2	7.2341094	0.914104445	177	183	-	TCCATTA
	MA0710.1	8.043502	0.909970649	703	712	-	CCTAATTTTC
	MA0710.2	6.864364	0.907159025	1107	1113	+	CAAATTG
	MA0710.2	6.7549953	0.905104604	611	617	+	CAAATTT
HIC2	MA0738.2	8.623369	0.9692024	93	98	+	ATGCCA
	MA0738.2	8.43513	0.964427302	170	175	-	GTGCCA
	MA0738.2	8.43513	0.964427302	566	571	+	GTGCCA
	MA0738.2	7.069202	0.929777534	653	658	+	TTGCCC
	MA0738.1	8.739875	0.923200556	905	913	+	GTACCCACC
	MA0738.2	6.5766997	0.917284133	592	597	+	ATACCC
	MA0738.2	6.5766997	0.917284133	680	685	+	ATACCC
	MA0738.2	6.4001355	0.912805194	553	558	+	ATGCAC
	MA0738.2	6.3884606	0.912509035	2	7	+	GTACCC
	MA0738.2	6.3884606	0.912509035	905	910	+	GTACCC
	MA0738.1	8.196731	0.911108313	167	175	-	GTGCCATCC
	MA0738.1	8.145921	0.909977113	93	101	+	ATGCCAATA
	MA0738.2	5.9528704	0.901459331	866	871	-	CTGCCA
	MA0738.2	5.927818	0.900823818	1013	1018	+	GTCCCC
KLF14	MA0740.2	12.637965	0.949901903	1413	1421	+	GGGGAGGGG
	MA0740.2	12.568541	0.948742454	1396	1404	+	GGGGTGGGG
TEAD4	MA0809.1	10.7410965	0.949552926	548	557	-	TGCATTCTA
	MA0809.1	9.99498	0.933588105	689	698	-	TGAATTCCCT
	MA0809.3	10.392411	0.912763971	534	541	-	TCATTCCA
	MA0809.1	8.862682	0.909360088	195	204	+	AAAAATCTTA
	MA0809.2	11.216544	0.90351041	532	543	-	ACTATTCCAGT
VENTX	MA0724.1	9.900938	0.93053012	1336	1344	-	GCCAATTAG
	MA0724.1	9.114359	0.917466736	176	184	-	TTCCATTAG
OTX2	MA0712.1	9.556845	0.942933403	412	419	+	ATAATCTT
VSX1	MA0725.1	9.735873	0.942602588	1336	1343	+	CTAATTGG
	MA0725.2	9.6278	0.942583846	1336	1342	+	CTAATTG
	MA0725.2	9.6278	0.942583846	1365	1371	+	CTAATTG
	MA0725.1	9.644828	0.940044064	1336	1343	-	CCAATTAG
	MA0725.2	9.536764	0.939988219	1337	1343	-	CCAATTA
	MA0725.1	9.262497	0.929299939	1365	1372	+	CTAATTGA
	MA0725.1	8.924696	0.919807178	1365	1372	-	TCAATTAG
	MA0725.2	8.816666	0.919456671	1366	1372	-	TCAATTA
	MA0725.2	8.776861	0.918321761	1116	1122	+	CAAATTA
	MA0725.1	8.843978	0.917538869	1116	1123	+	CAAATTAC
	MA0725.1	8.501366	0.907910903	704	711	-	CTAATTTT
	MA0725.2	8.364826	0.906573762	705	711	-	CTAATTT
YY2	MA0748.3	9.9029665	0.926587878	1254	1260	+	ATGGCGC
	MA0748.2	11.227893	0.904673755	1252	1262	+	AGATGGCGCCT
UNCX	MA0721.2	9.571919	0.991627226	1337	1342	-	CAATTA
	MA0721.2	9.571919	0.991627226	1366	1371	-	CAATTA
	MA0721.1	10.285656	0.980682046	1336	1343	-	CCAATTAG
	MA0721.1	10.231745	0.979095376	1365	1372	-	TCAATTAG
	MA0721.2	7.506708	0.925087304	31	36	+	AAATTA
	MA0721.2	7.506708	0.925087304	260	265	+	AAATTA
	MA0721.2	7.506708	0.925087304	705	710	+	AAATTA
	MA0721.2	7.506708	0.925087304	782	787	+	AAATTA

	MA0721.2	7.506708	0.925087304	1117	1122	+	AAATTA
	MA0721.1	7.801084	0.907558211	1116	1123	+	CAAATTAC
	MA0721.2	6.8353806	0.903457514	46	51	-	TGATTA
	MA0721.2	6.8353806	0.903457514	367	372	+	TGATTA
TCF7	MA0523.2	9.600416	0.911710368	1075	1083	-	ACATCAGAG
RUNX3	MA0684.1	12.30559	0.937213174	1097	1106	+	CAACCGCAAG
	MA0684.3	10.536069	0.92292023	1098	1105	+	AACCGCAA
TBX5	MA0807.1	9.687961	0.918159728	285	292	+	ACGTGTGA
MEOX2	MA0706.2	7.9936666	0.919484509	366	372	+	GTGATTA
	MA0706.2	7.9882064	0.919336484	1337	1343	-	CCAATTA
	MA0706.2	7.688643	0.911215508	1336	1342	+	CTAATTG
	MA0706.2	7.688643	0.911215508	1365	1371	+	CTAATTG
	MA0706.2	7.576616	0.908178521	311	317	-	GTCATCA
	MA0706.1	8.603174	0.906385043	365	374	+	AGTGATTATA
	MA0706.1	8.496315	0.903713385	1364	1373	+	GCTAATTGAG
	MA0706.2	7.2989264	0.900650534	584	590	+	GTCATGA
POU3F3	MA0788.1	13.521916	0.903412752	1110	1122	+	ATTGTGCAAATTA
MEIS2	MA1640.2	11.826582	0.919134721	202	210	+	TTATTTATG
	MA0774.1	8.975588	0.900114101	740	747	+	CTGACAGA
BARX1	MA0875.2	10.247913	1.00000001	1337	1342	-	CAATTA
	MA0875.2	10.247913	1.00000001	1366	1371	-	CAATTA
	MA0875.1	10.848159	0.993504843	1336	1343	-	CCAATTAG
	MA0875.2	9.50878	0.982661387	177	182	-	CCATTA
	MA0875.1	9.811555	0.970537741	1365	1372	-	TCAATTAG
	MA0875.1	9.072399	0.95416093	176	183	-	TCCATTAG
	MA0875.2	7.3802185	0.932729541	46	51	-	TGATTA
	MA0875.2	7.3802185	0.932729541	367	372	+	TGATTA
	MA0875.2	7.169925	0.927796475	31	36	+	AAATTA
	MA0875.2	7.169925	0.927796475	260	265	+	AAATTA
	MA0875.2	7.169925	0.927796475	705	710	+	AAATTA
	MA0875.2	7.169925	0.927796475	782	787	+	AAATTA
	MA0875.2	7.169925	0.927796475	1117	1122	+	AAATTA
	MA0875.1	7.809416	0.926178144	704	711	+	AAAATTAG
	MA0875.1	7.12083	0.910921768	366	373	+	GTGATTAT
	MA0875.1	7.0196214	0.908679378	259	266	+	AAAATTAC
	MA0875.1	7.0196214	0.908679378	781	788	+	AAAATTAC
	MA0875.1	6.980217	0.90780633	1116	1123	+	CAAATTAC
	MA0875.1	6.8670807	0.905299671	45	52	-	ATGATTAT
DLX1	MA0879.3	10.33489	1.000000008	1337	1342	-	CAATTA
	MA0879.3	10.33489	1.000000008	1366	1371	-	CAATTA
	MA0879.2	10.652619	0.993093977	1336	1343	-	CCAATTAG
	MA0879.2	9.65974	0.971278232	1365	1372	-	TCAATTAG
	MA0879.1	9.596272	0.946796049	703	712	-	CCTAATTTTC
	MA0879.3	7.9927025	0.946728519	177	182	-	CCATTA
	MA0879.1	9.3902855	0.941583344	1115	1124	+	GCAAATTACC
	MA0879.1	9.335752	0.940203307	1364	1373	-	CTCAATTAGC
	MA0879.1	9.065275	0.933358634	1335	1344	-	GCCAATTAGG
	MA0879.1	8.996578	0.931620189	258	267	+	CAAAATTACT
	MA0879.3	7.0353084	0.924953233	1053	1058	+	CAATTT
	MA0879.3	7.0353084	0.924953233	1108	1113	-	CAATTT
	MA0879.1	8.693003	0.923937908	703	712	+	GAAAATTAGG
	MA0879.3	6.8565392	0.92088725	214	219	+	CTATTA
	MA0879.3	6.8565392	0.92088725	373	378	-	CTATTA
	MA0879.2	7.365346	0.920865314	213	220	+	CCTATTAC
	MA0879.1	8.557914	0.920519348	780	789	+	AAAAATTACA
	MA0879.2	7.3409595	0.920329491	1052	1059	+	GCAATTTT
	MA0879.2	7.317272	0.919809027	176	183	-	TCCATTAG
	MA0879.3	6.7576547	0.918638187	46	51	-	TGATTA
	MA0879.3	6.7576547	0.918638187	367	372	+	TGATTA
	MA0879.2	7.063452	0.914232031	366	373	+	GTGATTAT
	MA0879.2	7.0083003	0.913020232	1116	1123	+	CAAATTAC
	MA0879.3	6.500196	0.912782462	31	36	+	AAATTA
	MA0879.3	6.500196	0.912782462	260	265	+	AAATTA

	MA0879.3	6.500196	0.912782462	705	710	+	AAATTA
	MA0879.3	6.500196	0.912782462	782	787	+	AAATTA
	MA0879.3	6.500196	0.912782462	1117	1122	+	AAATTA
	MA0879.1	8.199461	0.911448343	1106	1115	-	CACAATTTGC
	MA0879.2	6.7161713	0.906601511	1107	1114	-	ACAATTTG
	MA0879.3	6.194687	0.905833863	46	51	+	TAATCA
	MA0879.3	6.194687	0.905833863	367	372	-	TAATCA
	MA0879.3	6.138973	0.904566693	31	36	-	TAATTT
	MA0879.3	6.138973	0.904566693	260	265	-	TAATTT
	MA0879.3	6.138973	0.904566693	705	710	-	TAATTT
	MA0879.3	6.138973	0.904566693	782	787	-	TAATTT
	MA0879.3	6.138973	0.904566693	1117	1122	-	TAATTT
	MA0879.2	6.578533	0.903577298	1116	1123	-	GTAATTTG
	MA0879.1	7.8760858	0.903265011	1115	1124	-	GGTAATTTGC
	MA0879.2	6.4445333	0.900633026	259	266	-	GTAATTTT
	MA0879.2	6.4445333	0.900633026	781	788	-	GTAATTTT
	MA0879.3	5.960204	0.90050071	55	60	-	TTATTA
BSX	MA0876.2	9.806499	1.000000006	1337	1342	-	CAATTA
	MA0876.2	9.806499	1.000000006	1366	1371	-	CAATTA
	MA0876.1	10.760591	0.995707179	1336	1343	-	CCAATTAG
	MA0876.2	9.110977	0.983646172	177	182	-	CCATTA
	MA0876.2	8.158208	0.961243653	46	51	-	TGATTA
	MA0876.2	8.158208	0.961243653	367	372	+	TGATTA
	MA0876.1	9.02606	0.957496881	1365	1372	-	TCAATTAG
	MA0876.1	8.330511	0.942174501	176	183	-	TCCATTAG
	MA0876.2	6.8286734	0.929982232	31	36	+	AAATTA
	MA0876.2	6.8286734	0.929982232	260	265	+	AAATTA
	MA0876.2	6.8286734	0.929982232	705	710	+	AAATTA
	MA0876.2	6.8286734	0.929982232	782	787	+	AAATTA
	MA0876.2	6.8286734	0.929982232	1117	1122	+	AAATTA
	MA0876.1	7.7538977	0.929472175	1116	1123	+	CAAATTAC
	MA0876.2	6.7999477	0.929306804	1006	1011	+	CAGTTA
	MA0876.1	7.430615	0.92235052	366	373	+	GTGATTAT
	MA0876.1	6.9758635	0.912332714	443	450	+	CTAGTTAG
	MA0876.1	6.94721	0.911701497	430	437	-	CTAGTTAC
	MA0876.2	6.0219326	0.91101329	26	31	+	TAGTTA
	MA0876.2	6.0219326	0.91101329	431	436	-	TAGTTA
	MA0876.2	6.0219326	0.91101329	444	449	+	TAGTTA
	MA0876.2	5.9583983	0.909519405	413	418	-	AGATTA
	MA0876.1	6.778934	0.907994518	45	52	-	ATGATTAT
GBX2	MA0890.2	10.859208	1.000000006	1337	1342	-	CAATTA
	MA0890.2	10.859208	1.000000006	1366	1371	-	CAATTA
	MA0890.1	12.408764	0.986127407	1335	1344	-	GCCAATTAGG
	MA0890.1	10.953615	0.957790589	1364	1373	-	CTCAATTAGC
	MA0890.2	6.4677234	0.905009359	31	36	+	AAATTA
	MA0890.2	6.4677234	0.905009359	260	265	+	AAATTA
	MA0890.2	6.4677234	0.905009359	705	710	+	AAATTA
	MA0890.2	6.4677234	0.905009359	782	787	+	AAATTA
	MA0890.2	6.4677234	0.905009359	1117	1122	+	AAATTA
HOXD13	MA0909.4	13.295949	1.000000005	302	308	+	CAATAAA
	MA0909.1	15.334002	1	301	310	+	CCAATAAAAA
	MA0909.3	14.214013	0.994675758	300	309	+	TCCAATAAAAA
	MA0909.1	10.685784	0.914253421	1018	1027	+	CAAATAAAAC
	MA0909.2	11.864332	0.911433576	300	310	+	TCCAATAAAAA
	MA0909.2	11.401459	0.904210898	1017	1027	+	CCAATAAAAC
SOX11	MA0869.3	14.6586485	1.000000005	1162	1169	-	GAACAAAG
	MA0869.2	14.648126	0.962939752	1160	1171	-	TTGAACAAAGAA
	MA0869.3	10.933443	0.922968631	88	95	+	GAACAATG
	MA0869.3	10.485261	0.913700932	1214	1221	-	GAAGAAAG
	MA0869.2	11.764905	0.91046764	1212	1223	-	CAGAAGAAAGGG
DLX4	MA0881.2	10.143238	1.000000004	1337	1342	-	CAATTA
	MA0881.2	10.143238	1.000000004	1366	1371	-	CAATTA
	MA0881.1	10.12883	0.981202078	1336	1343	-	CCAATTAG
	MA0881.1	9.023999	0.951059536	1365	1372	-	TCAATTAG
	MA0881.2	7.1609955	0.914390776	177	182	-	CCATTA
	MA0881.1	7.627723	0.912965638	1116	1123	+	CAAATTAC

	MA0881.2	6.9538074	0.908443166	31	36	+	AAATTA
	MA0881.2	6.9538074	0.908443166	260	265	+	AAATTA
	MA0881.2	6.9538074	0.908443166	705	710	+	AAATTA
	MA0881.2	6.9538074	0.908443166	782	787	+	AAATTA
	MA0881.2	6.9538074	0.908443166	1117	1122	+	AAATTA
	MA0881.2	6.757577	0.902810112	1053	1058	+	CAATTT
	MA0881.2	6.757577	0.902810112	1108	1113	-	CAATTT
SOX8	MA0868.3	11.973391	0.999999998	89	95	+	AACAATG
	MA0868.2	12.243904	0.947974644	87	96	+	TGAACAATGC
	MA0868.3	9.352271	0.936340214	330	336	+	AACAATT
	MA0868.3	9.283063	0.934659338	1162	1168	-	AACAAAG
	MA0868.3	9.231514	0.933407356	1383	1389	+	GACAATG
	MA0868.3	8.856182	0.924291577	642	648	+	AACAAAA
	MA0868.3	8.856182	0.924291577	1058	1064	-	AACAAAA
	MA0868.3	8.856182	0.924291577	1192	1198	+	AACAAAA
	MA0868.2	10.597861	0.912479967	1381	1390	+	TGGACAATGG
	MA0868.2	10.253596	0.905056361	1190	1199	+	AAAACAAAAG
DLX6	MA0882.2	10.2504015	0.999999997	1337	1342	-	CAATTA
	MA0882.2	10.2504015	0.999999997	1366	1371	-	CAATTA
	MA0882.1	10.279752	0.979716527	1336	1343	-	CCAATTAG
	MA0882.1	9.148209	0.950376117	1365	1372	-	TCAATTAG
	MA0882.1	7.8181386	0.915887993	1116	1123	+	CAAATTAC
	MA0882.2	7.047838	0.912509035	177	182	-	CCATTA
	MA0882.2	7.007751	0.911413891	31	36	+	AAATTA
	MA0882.2	7.007751	0.911413891	260	265	+	AAATTA
	MA0882.2	7.007751	0.911413891	705	710	+	AAATTA
	MA0882.2	7.007751	0.911413891	782	787	+	AAATTA
	MA0882.2	7.007751	0.911413891	1117	1122	+	AAATTA
	MA0882.1	7.321525	0.903011026	213	220	+	CCTATTAC
	MA0882.1	7.209328	0.90010181	259	266	+	AAAATTAC
	MA0882.1	7.209328	0.90010181	781	788	+	AAAATTAC
MXI1	MA1108.3	11.675601	0.999999996	556	561	+	CACATG
	MA1108.2	11.888484	0.986180706	554	563	+	TGCACATGCC
BARHL1	MA0877.3	13.38544	0.999999995	1122	1129	+	ACCGTTTA
	MA0877.4	11.240475	0.999999999	1124	1129	+	CGTTTA
	MA0877.1	10.238417	0.975302027	1335	1344	+	CCTAATTGGC
	MA0877.2	9.616413	0.968893496	1123	1130	-	TTAAACGG
	MA0877.1	9.386726	0.952857981	1364	1373	+	GCTAATTGAG
	MA0877.2	8.712993	0.948418331	104	111	-	GTAAATGA
	MA0877.4	9.013484	0.948336913	105	110	+	CATTTA
	MA0877.2	8.608823	0.946057421	1336	1343	+	CTAATTGG
	MA0877.2	8.114429	0.934852466	1365	1372	+	CTAATTGA
	MA0877.3	9.998585	0.928922071	103	110	+	ATCATTTA
	MA0877.1	8.455889	0.928328215	103	112	-	GGTAAATGAT
	MA0877.2	7.6065254	0.923341304	1060	1067	-	CTAAACAA
	MA0877.2	7.5187173	0.921351217	1274	1281	-	CTAAACAC
	MA0877.1	7.539829	0.904187876	1122	1131	-	TTTAAACGGT
HESX1	MA0894.2	10.835335	0.999999991	1337	1342	+	TAATTG
	MA0894.2	10.835335	0.999999991	1366	1371	+	TAATTG
	MA0894.1	12.255182	0.977067619	1335	1344	+	CCTAATTGGC
	MA0894.1	11.259271	0.957934188	1364	1373	+	GCTAATTGAG
	MA0894.2	6.556195	0.905494209	31	36	-	TAATTT
	MA0894.2	6.556195	0.905494209	260	265	-	TAATTT
	MA0894.2	6.556195	0.905494209	705	710	-	TAATTT
	MA0894.2	6.556195	0.905494209	782	787	-	TAATTT
	MA0894.2	6.556195	0.905494209	1117	1122	-	TAATTT
	MA0894.2	6.5042405	0.904346788	1053	1058	-	AAATTG
	MA0894.2	6.5042405	0.904346788	1108	1113	+	AAATTG
HIF1A	MA0259.2	9.08275	1.000000001	285	289	+	ACGTG
	MA0259.2	9.08275	1.000000001	902	906	-	ACGTG
	MA0259.2	9.08275	1.000000001	1044	1048	-	ACGTG
	MA1106.2	11.279793	0.999999988	901	906	-	ACGTGC
	MA0259.1	11.075476	0.996313886	901	908	-	GTACGTGC
	MA1106.1	12.386301	0.983766922	899	908	-	GTACGTGCAG
	MA0259.2	7.42617	0.936361795	893	897	+	GCGTG

	MA1106.2	8.139631	0.917227289	1043	1048	-	ACGTGA
	MA1106.1	9.529688	0.916505469	901	910	+	GCACGTACCC
	MA1106.2	8.066213	0.91529202	903	908	+	ACGTAC
	MA0259.1	8.037127	0.905672503	891	898	+	GTGCGTGA
GBX1	MA0889.2	11.894336	0.999487004	1337	1343	-	CCAATTA
	MA0889.1	12.596521	0.974286337	1335	1344	-	GCCAATTAGG
	MA0889.2	9.898091	0.961018884	1366	1372	-	TCAATTA
	MA0889.1	11.481763	0.954883592	1364	1373	-	CTCAATTAGC
SOX4	MA0867.3	12.535857	0.986075966	1161	1168	-	AACAAAGA
	MA0867.2	13.67031	0.985322151	1160	1169	-	GAACAAAGAA
	MA0867.3	10.9526415	0.955944911	89	96	+	AACAATGC
	MA0867.2	12.020701	0.955801716	1382	1391	+	GGACAATGGG
	MA0867.3	10.835926	0.953723635	1192	1199	+	AACAAAG
	MA0867.3	10.797151	0.952985678	1383	1390	+	GACAATGG
	MA0867.2	11.787768	0.951633282	88	97	+	GAACAATGCC
	MA0867.2	11.256661	0.942128902	1191	1200	+	AAACAAAAGG
	MA0867.3	10.104298	0.93979961	642	649	+	AACAAAAA
	MA0867.3	10.104298	0.93979961	1057	1064	-	AACAAAAA
	MA0867.3	10.008083	0.937968503	856	863	-	CACAAAGA
	MA0867.2	10.4364605	0.927451064	641	650	+	AAACAAAAAA
	MA0867.2	10.4364605	0.927451064	1056	1065	-	AAACAAAAAA
	MA0867.2	9.863356	0.917195114	855	864	-	TCACAAAGAA
	MA0867.3	8.308152	0.905616173	1269	1276	-	CACAAAAG
HMBX1	MA0895.2	11.676908	0.999999993	26	32	+	TAGTTAA
	MA0895.2	11.031503	0.984257165	430	436	-	TAGTTAC
	MA0895.1	12.752018	0.975183851	429	438	-	ACTAGTTACG
	MA0895.2	9.225882	0.940214134	444	450	+	TAGTTAG
	MA0895.1	10.155465	0.920804715	24	33	+	AATAGTTAAA
	MA0895.1	10.101812	0.919681075	442	451	+	ACTAGTTAGA
HOXB3	MA0903.2	9.070827	0.982886415	1337	1342	-	CAATTA
	MA0903.2	9.070827	0.982886415	1366	1371	-	CAATTA
	MA0903.2	8.463723	0.967297044	177	182	-	CCATTA
	MA0903.1	9.834767	0.962843888	1335	1344	-	GCCAATTAGG
	MA0903.2	7.573166	0.944429064	31	36	+	AAATTA
	MA0903.2	7.573166	0.944429064	260	265	+	AAATTA
	MA0903.2	7.573166	0.944429064	705	710	+	AAATTA
	MA0903.2	7.573166	0.944429064	782	787	+	AAATTA
	MA0903.2	7.573166	0.944429064	1117	1122	+	AAATTA
	MA0903.1	9.029067	0.944080676	1364	1373	-	CTCAATTAGC
	MA0903.1	8.109695	0.922670277	175	184	-	TTCCATTAGG
	MA0903.2	6.5649276	0.918539236	46	51	-	TGATTA
	MA0903.2	6.5649276	0.918539236	367	372	+	TGATTA
	MA0903.2	6.309099	0.911970003	55	60	-	TTATTA
	MA0903.1	7.6444902	0.911836542	703	712	+	GAAAATTAGG
	MA0903.1	7.607476	0.910974557	1115	1124	+	GCAAATTACC
	MA0903.2	6.088313	0.906300596	381	386	-	GAATTA
HOXB2	MA0902.3	9.710864	0.989957392	1337	1342	-	CAATTA
	MA0902.3	9.710864	0.989957392	1366	1371	-	CAATTA
	MA0902.2	10.738756	0.981037606	1336	1343	-	CCAATTAG
	MA0902.3	8.656557	0.968411143	177	182	-	CCATTA
	MA0902.2	9.804248	0.963459998	1365	1372	-	TCAATTAG
	MA0902.1	9.174839	0.949310648	1335	1344	-	GCCAATTAGG
	MA0902.2	8.749867	0.94362766	176	183	-	TCCATTAG
	MA0902.3	7.296538	0.940617233	585	590	+	TCATGA
	MA0902.3	7.296538	0.940617233	585	590	-	TCATGA
	MA0902.1	8.643091	0.935497237	1364	1373	-	CTCAATTAGC
	MA0902.2	7.650479	0.922948741	584	591	+	GTCATGAA
	MA0902.1	8.007185	0.918978065	1115	1124	+	GCAAATTACC
	MA0902.1	7.8242645	0.914226272	703	712	+	GAAAATTAGG
	MA0902.2	6.864219	0.908159612	584	591	-	TTCATGAC
	MA0902.1	7.279856	0.900083974	175	184	-	TTCCATTAGG
GSX1	MA0892.2	8.538975	0.978455027	1337	1342	-	CAATTA
	MA0892.2	8.538975	0.978455027	1366	1371	-	CAATTA
	MA0892.2	7.5967455	0.949143874	177	182	-	CCATTA
	MA0892.2	7.146712	0.93514409	55	60	-	TTATTA

	MA0892.1	8.681717	0.929334224	1364	1373	-	CTCAATTAGC
	MA0892.1	8.523296	0.925031959	1335	1344	-	GCCAATTAGG
	MA0892.2	6.754124	0.922931354	31	36	+	AAATTA
	MA0892.2	6.754124	0.922931354	260	265	+	AAATTA
	MA0892.2	6.754124	0.922931354	705	710	+	AAATTA
	MA0892.2	6.754124	0.922931354	782	787	+	AAATTA
	MA0892.2	6.754124	0.922931354	1117	1122	+	AAATTA
	MA0892.2	6.454132	0.913599109	214	219	+	CTATTA
	MA0892.2	6.454132	0.913599109	373	378	-	CTATTA
	MA0892.2	6.0595775	0.901325185	26	31	+	TAGTTA
	MA0892.2	6.0595775	0.901325185	431	436	-	TAGTTA
	MA0892.2	6.0595775	0.901325185	444	449	+	TAGTTA
ISL2	MA0914.2	9.203034	0.975676359	1337	1342	-	CAATTA
	MA0914.2	9.203034	0.975676359	1366	1371	-	CAATTA
	MA0914.1	9.298632	0.929412034	1336	1343	-	CCAATTAG
	MA0914.2	7.589724	0.928329967	236	241	+	TACTTA
	MA0914.2	7.589724	0.928329967	816	821	+	TACTTA
	MA0914.2	7.1637387	0.915828424	1053	1058	+	CAATTT
	MA0914.2	7.1637387	0.915828424	1108	1113	-	CAATTT
	MA0914.2	7.0968113	0.913864281	510	515	-	CACTCA
	MA0914.2	7.0968113	0.913864281	539	544	-	CACTCA
GSX2	MA0893.2	10.243515	0.97660649	1336	1343	-	CCAATTAG
	MA0893.3	9.4622555	0.975634776	1337	1343	-	CCAATTA
	MA0893.2	8.882973	0.949785716	1336	1343	+	CTAATTGG
	MA0893.3	8.101597	0.947698685	1336	1342	+	CTAATTG
	MA0893.3	8.101597	0.947698685	1365	1371	+	CTAATTG
	MA0893.2	8.48986	0.942036161	1365	1372	+	CTAATTGA
	MA0893.2	8.388988	0.94004764	443	450	+	CTAGTTAG
	MA0893.3	7.6075344	0.937554941	431	437	-	CTAGTTA
	MA0893.3	7.6075344	0.937554941	443	449	+	CTAGTTA
	MA0893.3	7.1298	0.927746429	1116	1122	+	CAAATTA
	MA0893.3	6.852374	0.922050518	1385	1391	-	CCCATTG
	MA0893.1	8.608589	0.917045184	1335	1344	-	GCCAATTAGG
	MA0893.1	8.343844	0.909721343	1364	1373	-	CTCAATTAGC
	MA0893.3	6.1485014	0.907599096	25	31	+	ATAGTTA
	MA0893.3	6.036425	0.905298025	366	372	+	GTGATTA
	MA0893.2	6.5369887	0.903538639	25	32	+	ATAGTTAA
	MA0893.2	6.452472	0.90187254	704	711	+	AAAATTAG
	MA0893.3	5.830983	0.901080034	120	126	-	ATCGTTA
EVX2	MA0888.2	8.886423	0.972000767	46	51	-	TGATTA
	MA0888.2	8.886423	0.972000767	367	372	+	TGATTA
	MA0888.2	8.192437	0.955072379	1337	1342	-	CAATTA
	MA0888.2	8.192437	0.955072379	1366	1371	-	CAATTA
	MA0888.1	9.68198	0.943430873	1335	1344	-	GCCAATTAGG
	MA0888.1	9.633261	0.942380169	44	53	-	GATGATTATC
	MA0888.2	7.187567	0.930560602	177	182	-	CCATTA
	MA0888.2	7.0464573	0.927118509	31	36	+	AAATTA
	MA0888.2	7.0464573	0.927118509	260	265	+	AAATTA
	MA0888.2	7.0464573	0.927118509	705	710	+	AAATTA
	MA0888.2	7.0464573	0.927118509	782	787	+	AAATTA
	MA0888.2	7.0464573	0.927118509	1117	1122	+	AAATTA
	MA0888.1	8.481646	0.917543923	1115	1124	+	GCAAATTACC
	MA0888.1	8.243535	0.912408725	703	712	+	GAAAATTAGG
	MA0888.1	8.241042	0.912354962	365	374	+	AGTGATTATA
	MA0888.2	6.3549433	0.910250418	1337	1342	+	TAATTG
	MA0888.2	6.3549433	0.910250418	1366	1371	+	TAATTG
	MA0888.2	6.3510227	0.910154784	55	60	-	TTATTA
	MA0888.1	8.006631	0.907299544	1364	1373	-	CTCAATTAGC
	MA0888.1	7.8585124	0.904105155	1335	1344	+	CCTAATTGGC
EVX1	MA0887.2	8.897519	0.972622619	46	51	-	TGATTA
	MA0887.2	8.897519	0.972622619	367	372	+	TGATTA
	MA0887.2	8.194568	0.954105175	1337	1342	-	CAATTA
	MA0887.2	8.194568	0.954105175	1366	1371	-	CAATTA
	MA0887.1	10.157064	0.953723716	44	53	-	GATGATTATC
	MA0887.1	9.625632	0.941630453	1335	1344	-	GCCAATTAGG
	MA0887.2	7.23817	0.928911346	31	36	+	AAATTA
	MA0887.2	7.23817	0.928911346	260	265	+	AAATTA

	MA0887.2	7.23817	0.928911346	705	710	+	AAATTA
	MA0887.2	7.23817	0.928911346	782	787	+	AAATTA
	MA0887.2	7.23817	0.928911346	1117	1122	+	AAATTA
	MA0887.1	9.0519495	0.928575735	1115	1124	+	GCAAATTACC
	MA0887.2	7.051072	0.923982731	177	182	-	CCATTA
	MA0887.1	8.664416	0.919757035	365	374	+	AGTGATTATA
	MA0887.1	8.378595	0.913252896	703	712	+	GAAAATTAGG
	MA0887.2	6.5751905	0.911446857	55	60	-	TTATTA
	MA0887.2	6.5340424	0.910362914	1337	1342	+	TAATTG
	MA0887.2	6.5340424	0.910362914	1366	1371	+	TAATTG
	MA0887.1	7.950255	0.903505587	1335	1344	+	CCTAATTGGC
	MA0887.2	6.1988816	0.901533969	413	418	-	AGATTA
	MA0887.1	7.832769	0.900832077	1364	1373	-	CTCAATTAGC
HOXC10	MA0905.1	12.883218	0.968667148	613	622	-	GTCATAAAATT
	MA0905.2	12.445726	0.967947593	204	212	-	GTCATAAAAT
	MA0905.2	12.445726	0.967947593	614	622	-	GTCATAAAAT
	MA0905.1	12.741014	0.966264612	203	212	-	GTCATAAAATA
	MA0905.1	9.320727	0.908479001	25	34	+	ATAGTTAAAT
	MA0905.2	8.8840065	0.906384501	25	33	+	ATAGTTAAA
HOXB5	MA0904.3	8.150803	0.947107576	1337	1342	+	TAATTG
	MA0904.3	8.150803	0.947107576	1366	1371	+	TAATTG
	MA0904.2	9.260042	0.946362798	1336	1343	+	CTAATTGG
	MA0904.3	8.081908	0.945596933	1337	1342	-	CAATTA
	MA0904.3	8.081908	0.945596933	1366	1371	-	CAATTA
	MA0904.2	9.191114	0.944984962	1336	1343	-	CCAATTAG
	MA0904.3	7.485859	0.9325274	585	590	+	TCATGA
	MA0904.3	7.485859	0.9325274	585	590	-	TCATGA
	MA0904.3	6.632622	0.913818526	177	182	+	TAATGG
	MA0904.3	6.522933	0.911413388	177	182	-	CCATTA
	MA0904.2	7.313174	0.907445735	1365	1372	-	TCAATTAG
	MA0904.2	7.1438503	0.904061032	1365	1372	+	CTAATTGA
CDX1	MA0878.1	11.735905	0.966591043	301	309	+	CCAATAAAAA
	MA0878.1	11.16137	0.954898338	204	212	-	GTCATAAAAT
	MA0878.1	11.16137	0.954898338	614	622	-	GTCATAAAAT
	MA0878.3	13.113477	0.945259768	204	213	-	GGTCATAAAAT
	MA0878.3	13.113477	0.945259768	614	623	-	GGTCATAAAAT
	MA0878.2	12.737754	0.934443141	613	623	-	GGTCATAAAATT
	MA0878.2	11.649473	0.920692349	203	213	-	GGTCATAAAATA
EMX2	MA0886.2	9.288127	0.963870042	1337	1342	-	CAATTA
	MA0886.2	9.288127	0.963870042	1366	1371	-	CAATTA
	MA0886.1	11.310085	0.961529087	1335	1344	-	GCCAATTAGG
	MA0886.1	10.262179	0.943807759	1364	1373	-	CTCAATTAGC
	MA0886.2	6.384897	0.909229298	177	182	-	CCATTA
	MA0886.2	6.34861	0.908546347	55	60	-	TTATTA
	MA0886.2	6.1440234	0.90469589	31	36	+	AAATTA
	MA0886.2	6.1440234	0.90469589	260	265	+	AAATTA
	MA0886.2	6.1440234	0.90469589	705	710	+	AAATTA
	MA0886.2	6.1440234	0.90469589	782	787	+	AAATTA
	MA0886.2	6.1440234	0.90469589	1117	1122	+	AAATTA
FOXP3	MA0850.1	8.679832	0.934068008	478	484	-	GTTAACA
	MA0850.1	8.679832	0.934068008	479	485	+	GTTAACA
	MA0850.1	8.504095	0.929646506	849	855	-	ACAAACA
	MA0850.1	8.424592	0.927646232	81	87	-	ATAAGCA
	MA0850.1	8.13462	0.920350612	639	645	+	GAAAACA
	MA0850.1	8.13462	0.920350612	769	775	-	GAAAACA
	MA0850.1	8.13462	0.920350612	1189	1195	+	GAAAACA
	MA0850.1	8.122638	0.920049149	203	209	-	ATAAATA
	MA0850.1	7.337394	0.900292648	1102	1108	+	GCAAGCA
TCF4	MA0523.2	9.600416	0.911710368	1075	1083	-	ACATCAGAG
OLIG2	MA1997.2	11.89495	0.999999995	1084	1089	+	CAGCTG
	MA1997.2	11.89495	0.999999995	1084	1089	-	CAGCTG
	MA1997.1	9.339884	0.938730321	1082	1091	+	GTCAGCTGAG

	MA1997.1	9.339884	0.938730321	1082	1091	-	CTCAGCTGAC
HMGA1	MA2124.1	14.249774	0.999999995	304	311	-	ATTTTAT
NKX2 4	MA2003.2	11.12148	0.970272858	505	512	+	GCACTTGA
	MA2003.2	9.702452	0.937111344	949	956	+	CCTCTTCA
	MA2003.1	10.396266	0.934154968	505	514	+	GCACTTGAGT
	MA2003.1	10.060812	0.926843079	949	958	+	CCTCTTCAGA
HAND1	MA2123.1	13.776314	0.968782557	1376	1384	-	TCCAGACCC
	MA0092.2	11.194442	0.964049496	921	929	-	GTCTGGATT
	MA0092.1	11.151863	0.952147077	921	930	-	TGTCTGGATT
	MA0092.2	10.667699	0.948017539	792	800	-	ATCTGGATT
	MA0092.1	9.982523	0.917695361	792	801	-	AATCTGGATT
	MA2123.1	10.796737	0.900040879	923	931	+	TCCAGACAT
PGR	MA2327.1	10.684256	0.959901708	282	290	+	ACAACGTGT
	MA2327.1	10.684166	0.959899641	282	290	-	ACACGTTGT
EPAS1	MA2325.1	12.937772	0.961836449	900	908	+	TGCACGTAC
KLF7	MA1959.1	12.758263	0.958905932	1396	1404	+	GGGGTGGGG
	MA1959.2	12.07793	0.956821181	1397	1404	+	GGGTGGGG
	MA1959.1	11.035913	0.926570556	1413	1421	+	GGGGAGGGG
	MA1959.2	10.352867	0.922747206	7	14	-	GGGAGGGG
	MA1959.2	10.352867	0.922747206	1414	1421	+	GGGAGGGG
	MA1959.1	10.44251	0.915429995	7	15	-	AGGGAGGGG
TRPS1	MA1970.2	14.16564	1.000000008	355	362	-	TCTTATCT
	MA1970.1	13.4526205	0.948611515	353	364	-	GATCTTATCTAG
HOXB1	MA0901.3	16.231506	1	301	309	+	CCAATAAAA
	MA0901.1	16.123085	0.999372394	301	310	+	CCAATAAAAA
	MA2093.1	9.182493	0.950750711	1336	1342	+	CTAATTG
	MA2093.1	9.182493	0.950750711	1365	1371	+	CTAATTG
	MA2093.1	9.036439	0.947887951	366	372	+	GTGATTA
	MA0901.2	15.624405	0.943112947	299	312	+	CTCCAATAAAAAATG
	MA2093.1	8.5774	0.938890488	1337	1343	-	CCAATTA
	MA0901.3	12.299014	0.929947879	1018	1026	+	CAAATAAAA
	MA0901.1	11.737168	0.924866708	1018	1027	+	CAAATAAAAC
	MA2093.1	6.692627	0.901947686	584	590	+	GTCATGA
	MA2093.1	6.6444654	0.901003689	311	317	-	GTCATCA
	MA2093.1	6.6040936	0.900212373	380	386	+	GTAATTC
ZNF677	MA2101.1	14.946027	0.920648577	356	367	+	GATAAGATCAGT
PATZ1	MA1961.2	16.733126	0.986610864	1412	1422	+	GGGGGAGGGGC
	MA1961.2	15.57757	0.968665627	1395	1405	+	GGGGGTGGGGC
	MA1961.1	15.450415	0.955600072	1411	1422	+	TGGGGGAGGGGC
	MA1961.1	14.290629	0.938205261	1394	1405	+	TGGGGGTGGGGC
	MA1961.2	11.910597	0.911719259	6	16	-	AAGGGAGGGGG
PPARA	MA2338.1	8.679139	0.900160209	543	549	-	TAGGTCA
SOX13	MA1120.2	12.543894	1.000000012	1384	1390	+	ACAATGG
	MA1120.1	12.516054	0.968160923	1382	1392	+	GGACAATGGGG
	MA1120.1	11.718465	0.94945182	88	98	+	GAACAATGCCA
	MA1120.2	10.529084	0.949163574	90	96	+	ACAATGC
NR1H4	MA1110.3	11.616224	1.000000001	543	548	-	AGGTCA
	MA1110.2	11.331104	0.970801812	541	550	-	CTAGGTCACT
	MA1110.3	7.3638916	0.907763255	1176	1181	+	AGGTTA
	MA1110.3	7.0168915	0.900236524	108	113	-	AGGTAA
	MA1110.3	7.0168915	0.900236524	497	502	+	AGGTAA
	MA1110.3	7.0168915	0.900236524	946	951	-	AGGTAA
	MA1110.2	7.8647475	0.900025987	944	953	-	AGAGGTAAGG
NR2C2	MA1536.2	9.631251	1.000000008	543	548	-	AGGTCA
	MA1536.2	9.3469095	0.994630394	143	148	+	GGGTCA
	MA1536.2	9.3469095	0.994630394	209	214	-	GGGTCA

	MA1536.2	9.3469095	0.994630394	1320	1325	-	GGGTCA
	MA1536.1	9.902337	0.994045147	208	215	-	AGGGTCAT
	MA1536.1	9.472591	0.986197067	1319	1326	-	GGGGTCAG
	MA1536.1	8.966593	0.976956445	542	549	-	TAGGTCAC
	MA1536.1	8.316644	0.965086977	142	149	+	TGGGTCAG
	MA1536.2	7.5605807	0.960896713	1176	1181	+	AGGTTA
	MA1536.1	8.009972	0.959486485	1175	1182	+	AAGGTTAC
	MA1536.2	6.0773344	0.932886551	17	22	+	AGGTTG
	MA1536.1	6.4121013	0.930305936	698	705	+	AGGGTGAA
	MA1536.1	6.405777	0.930190441	653	660	-	GGGGGCAA
	MA1536.2	5.873294	0.929033376	699	704	+	GGGTGA
	MA1536.2	5.871795	0.929005074	1080	1085	+	ATGTCA
	MA1536.2	5.825279	0.92812665	654	659	-	GGGGCA
	MA1536.2	5.7929926	0.927516937	1169	1174	-	GGGTTG
	MA1536.1	5.996769	0.922721075	1079	1086	+	GATGTCAG
	MA1536.1	5.2178626	0.90849657	1168	1175	-	TGGGTTGA
	MA1536.1	5.0468006	0.905372611	16	23	+	TAGGTTGG
	MA1536.1	4.8806195	0.902337787	1298	1305	+	GGGGTGGC
	MA1536.2	4.3900476	0.901023214	909	914	-	GGGTGG
	MA1536.2	4.3900476	0.901023214	1299	1304	+	GGGTGG
	MA1536.2	4.3900476	0.901023214	1397	1402	+	GGGTGG
HOXB4	MA1499.2	8.712382	0.958489181	177	182	-	CCATTA
	MA1499.2	8.123389	0.946832478	1337	1342	-	CAATTA
	MA1499.2	8.123389	0.946832478	1366	1371	-	CAATTA
	MA1499.1	7.895544	0.921265474	176	183	-	TCCATTAG
	MA1499.1	7.7292156	0.918196576	1336	1343	-	CCAATTAG
	MA1499.1	7.306641	0.910399723	1365	1372	-	TCAATTAG
	MA1499.1	7.0393767	0.905468473	584	591	+	GTCATGAA
	MA1499.2	5.86405	0.902118119	585	590	+	TCATGA
	MA1499.2	5.86405	0.902118119	585	590	-	TCATGA
	MA1499.2	5.8344455	0.901532221	120	125	-	TCGTTA
RBPJ	MA1116.2	11.679968	1.000000004	393	398	+	TGGGAA
	MA1116.2	11.679968	1.000000004	732	737	+	TGGGAA
	MA1116.2	11.679968	1.000000004	810	815	-	TGGGAA
	MA1116.2	11.679968	1.000000004	1448	1453	-	TGGGAA
	MA1116.1	12.447275	0.983692995	730	739	+	TCTGGGAAAA
	MA1116.1	11.308458	0.959888766	391	400	+	TATGGGAAGA
	MA1116.1	11.308458	0.959888766	808	817	-	TATGGGAAGA
	MA1116.1	11.150779	0.956592853	1446	1455	-	AATGGGAAAG
DMRTA2	MA1478.2	9.78683	1.000000002	1178	1183	+	GTTACA
	MA1478.2	8.240225	0.958835077	499	504	+	GTAACA
	MA1478.2	7.810694	0.947402556	328	333	+	GAAACA
	MA1478.2	7.354816	0.935268758	267	272	-	GCAACA
	MA1478.2	7.354816	0.935268758	402	407	+	GCAACA
	MA1478.2	7.354816	0.935268758	651	656	-	GCAACA
	MA1478.2	6.696569	0.917748651	870	875	-	GATACT
	MA1478.2	6.3431354	0.908341551	288	293	-	GTCACA
	MA1478.2	6.3431354	0.908341551	860	865	-	GTCACA
	MA1478.2	6.2406907	0.905614852	222	227	+	GCTACT
	MA1478.2	6.2406907	0.905614852	473	478	+	GCTACT
NR2C1	MA1535.2	10.547004	1	543	548	-	AGGTCA
	MA1535.2	10.514188	0.999328297	143	148	+	GGGTCA
	MA1535.2	10.514188	0.999328297	209	214	-	GGGTCA
	MA1535.2	10.514188	0.999328297	1320	1325	-	GGGTCA
	MA1535.1	11.038952	0.98399701	1319	1327	-	TGGGGTCAG
	MA1535.1	10.862177	0.980592753	208	216	-	TAGGGTCAT
	MA1535.1	9.804973	0.960233568	542	550	-	CTAGGTCAC
	MA1535.1	8.973975	0.944230576	141	149	+	TTGGGTCAG
	MA1535.2	5.713468	0.90106329	699	704	+	GGGTGA
ZNF384	MA1125.2	10.433926	0.930169832	779	786	+	AAAAAATT
	MA1125.2	10.433926	0.930169832	1054	1061	-	AAAAAATT
	MA1125.2	10.203767	0.926340428	1204	1211	-	AAAAAATC
	MA1125.2	9.757992	0.918923581	645	652	+	AAAAAATG
	MA1125.1	11.343631	0.915405795	1054	1065	-	AAACAAAAAATT
	MA1125.1	10.667697	0.905060261	641	652	+	AAACAAAAAATG

OSR1	MA1542.2	14.26839	0.999999999	473	480	+	GCTACTGT
	MA1542.1	14.009699	0.977453191	472	481	+	GGCTACTGTT
HOXD4	MA1507.2	8.934631	0.967169131	177	182	-	CCATTA
	MA1507.2	8.664992	0.961314551	1337	1342	-	CAATTA
	MA1507.2	8.664992	0.961314551	1366	1371	-	CAATTA
	MA1507.1	8.82271	0.94848904	1336	1343	-	CCAATTAG
	MA1507.1	8.1474085	0.93468527	176	183	-	TCCATTAG
	MA1507.1	7.877748	0.929173168	1365	1372	-	TCAATTAG
	MA1507.2	6.2852845	0.909644767	120	125	-	TCGTTA
	MA1507.1	6.853699	0.908240692	25	32	+	ATAGTTAA
	MA1507.2	6.14549	0.90660946	1337	1342	+	TAATTG
	MA1507.2	6.14549	0.90660946	1366	1371	+	TAATTG
	MA1507.2	6.015646	0.903790198	26	31	+	TAGTTA
	MA1507.2	6.015646	0.903790198	431	436	-	TAGTTA
	MA1507.2	6.015646	0.903790198	444	449	+	TAGTTA
HOXA7	MA1498.3	9.2600355	0.999999995	1337	1342	-	CAATTA
	MA1498.3	9.2600355	0.999999995	1366	1371	-	CAATTA
	MA1498.3	8.968124	0.99136076	177	182	-	CCATTA
	MA1498.2	9.131606	0.959879914	1336	1343	-	CCAATTAG
	MA1498.1	9.267731	0.950277453	1336	1343	-	CCAATTAG
	MA1498.1	8.807328	0.940068219	1365	1372	-	TCAATTAG
	MA1498.3	7.0794215	0.935463789	31	36	+	AAATTA
	MA1498.3	7.0794215	0.935463789	260	265	+	AAATTA
	MA1498.3	7.0794215	0.935463789	705	710	+	AAATTA
	MA1498.3	7.0794215	0.935463789	782	787	+	AAATTA
	MA1498.3	7.0794215	0.935463789	1117	1122	+	AAATTA
	MA1498.1	8.466968	0.932520862	176	183	-	TCCATTAG
	MA1498.3	6.846176	0.928560792	214	219	+	CTATTA
	MA1498.3	6.846176	0.928560792	373	378	-	CTATTA
	MA1498.2	7.9671426	0.928334825	1365	1372	-	TCAATTAG
	MA1498.2	7.6752048	0.920426286	176	183	-	TCCATTAG
	MA1498.3	6.268025	0.911450159	302	307	+	CAATAA
	MA1498.1	7.501277	0.911107073	584	591	+	GTCATGAA
	MA1498.2	7.3072114	0.910457418	1116	1123	+	CAAATTAC
	MA1498.3	6.156664	0.908154382	55	60	-	TTATTA
	MA1498.2	7.091228	0.90460647	301	308	+	CCAATAAA
	MA1498.2	7.073824	0.904134997	213	220	+	CCTATTAC
	MA1498.3	5.9734697	0.902732672	1053	1058	+	CAATTT
	MA1498.3	5.9734697	0.902732672	1108	1113	-	CAATTT
HOXC4	MA1504.2	9.001886	0.970383955	177	182	-	CCATTA
	MA1504.2	8.490466	0.960192173	1337	1342	-	CAATTA
	MA1504.2	8.490466	0.960192173	1366	1371	-	CAATTA
	MA1504.1	8.623311	0.950871401	176	183	-	TCCATTAG
	MA1504.1	8.569432	0.949837315	1336	1343	-	CCAATTAG
	MA1504.1	8.11186	0.941055214	1365	1372	-	TCAATTAG
	MA1504.2	6.6339993	0.923195779	120	125	-	TCGTTA
	MA1504.2	6.6063604	0.92264498	1337	1342	+	TAATTG
	MA1504.2	6.6063604	0.92264498	1366	1371	+	TAATTG
	MA1504.1	6.7767544	0.915430755	25	32	+	ATAGTTAA
	MA1504.1	6.7178445	0.914300107	1365	1372	+	CTAATTGA
	MA1504.1	6.685015	0.91367002	1336	1343	+	CTAATTGG
	MA1504.2	6.1225786	0.913003988	26	31	+	TAGTTA
	MA1504.2	6.1225786	0.913003988	431	436	-	TAGTTA
	MA1504.2	6.1225786	0.913003988	444	449	+	TAGTTA
	MA1504.1	6.49527	0.910028269	119	126	-	ATCGTTAT
	MA1504.1	6.201063	0.904381612	443	450	+	CTAGTTAG
	MA1504.2	5.6316576	0.903220723	1385	1390	-	CCATTG
MAZ	MA1522.2	15.0898905	0.999999994	7	14	+	CCCCTCCC
	MA1522.2	15.0898905	0.999999994	1414	1421	-	CCCCTCCC
	MA1522.1	15.964675	0.987163078	5	15	+	CCCCCTCCCT
	MA1961.2	16.733126	0.986610864	1412	1422	+	GGGGGAGGGGC
	MA1522.1	15.787535	0.984582661	1413	1423	-	AGCCCCTCCCC
	MA1961.2	15.57757	0.968665627	1395	1405	+	GGGGGTGGGGC
	MA1961.1	15.450415	0.955600072	1411	1422	+	TGGGGGAGGGGC
	MA1961.1	14.290629	0.938205261	1394	1405	+	TGGGGGTGGGGC
	MA1961.2	11.910597	0.911719259	6	16	-	AAGGGAGGGGG

HOXA4	MA1496.2	8.604326	0.955442061	120	126	-	ATCGTTA
	MA1496.2	7.807783	0.938896906	25	31	+	ATAGTTA
	MA1496.2	7.6945996	0.936545949	366	372	+	GTGATTA
	MA1496.1	7.9511437	0.934224369	119	126	-	ATCGTTAT
	MA1496.1	7.8595033	0.932366573	25	32	+	ATAGTTAA
	MA1496.2	7.3722677	0.929850729	46	52	-	ATGATTA
	MA1496.2	7.0234017	0.922604365	311	317	-	GTCATCA
	MA1496.2	7.0078435	0.922281201	584	590	+	GTCATGA
	MA1496.1	7.31938	0.921416831	1336	1343	-	CCAATTAG
	MA1496.2	6.8737154	0.9194952	1337	1343	-	CCAATTA
	MA1496.1	7.05894	0.91613702	584	591	+	GTCATGAA
	MA1496.2	6.7010703	0.915909154	835	841	+	ATCATCA
	MA1496.1	7.040776	0.915768784	366	373	+	GTGATTAT
	MA1496.1	6.827953	0.911454297	443	450	+	CTAGTTAG
	MA1496.1	6.7521434	0.909917436	835	842	+	ATCATCAA
	MA1496.2	6.3823657	0.909289278	431	437	-	CTAGTTA
	MA1496.2	6.3823657	0.909289278	443	449	+	CTAGTTA
	MA1496.1	6.71841	0.909233571	45	52	-	ATGATTAT
	MA1496.1	6.369519	0.902160625	310	317	-	GTCATCAT
	MA1496.1	6.3349514	0.901459843	430	437	-	CTAGTTAC
	MA1496.2	6.0011845	0.901371687	380	386	+	GTAATTC
DRGX	MA1481.2	10.018127	0.98798106	1337	1342	-	CAATTA
	MA1481.2	10.018127	0.98798106	1366	1371	-	CAATTA
	MA1481.1	10.921629	0.984427717	1336	1343	-	CCAATTAG
	MA1481.1	10.632135	0.978647838	1365	1372	-	TCAATTAG
	MA1481.1	8.699124	0.940054342	1116	1123	+	CAAATTAC
	MA1481.2	7.7319374	0.939109333	46	51	-	TGATTA
	MA1481.2	7.7319374	0.939109333	367	372	+	TGATTA
	MA1481.2	7.6186604	0.936687819	381	386	-	GAATTA
	MA1481.2	7.5776806	0.935811795	31	36	+	AAATTA
	MA1481.2	7.5776806	0.935811795	260	265	+	AAATTA
	MA1481.2	7.5776806	0.935811795	705	710	+	AAATTA
	MA1481.2	7.5776806	0.935811795	782	787	+	AAATTA
	MA1481.2	7.5776806	0.935811795	1117	1122	+	AAATTA
	MA1481.1	7.831557	0.922732939	30	37	+	TAAATTAT
	MA1481.1	7.5777955	0.917666473	1336	1343	+	CTAATTGG
	MA1481.2	6.674046	0.916494862	1337	1342	+	TAATTG
	MA1481.2	6.674046	0.916494862	1366	1371	+	TAATTG
	MA1481.2	6.439658	0.911484368	46	51	+	TAATCA
	MA1481.2	6.439658	0.911484368	367	372	-	TAATCA
	MA1481.1	7.2229667	0.910582144	1365	1372	+	CTAATTGA
	MA1481.2	6.1118073	0.904475924	332	337	+	CAATTG
	MA1481.2	6.1118073	0.904475924	332	337	-	CAATTG
DLX5	MA1476.1	11.192919	0.982327946	1336	1343	-	CCAATTAG
	MA1476.1	10.297271	0.965897841	1365	1372	-	TCAATTAG
	MA1476.3	10.310078	0.909488347	1365	1372	-	TCAATTAG
	MA1476.3	10.27427	0.908698519	1336	1343	-	CCAATTAG
SOX15	MA1152.2	10.763686	0.992981672	1384	1390	-	CCATTGT
	MA1152.1	12.656869	0.98229582	1190	1199	-	CTTTGTTTT
	MA1152.2	10.252575	0.98004721	1193	1199	-	CTTTTGT
	MA1152.2	10.252575	0.98004721	1269	1275	+	CTTTTGT
	MA1152.1	11.62548	0.959136417	640	649	-	TTTTTGTTTT
	MA1152.2	9.221187	0.953946332	643	649	-	TTTTTGT
	MA1152.2	9.221187	0.953946332	1057	1063	+	TTTTTGT
	MA1152.2	8.943854	0.946928008	856	862	+	TCTTTGT
	MA1152.2	8.943854	0.946928008	1161	1167	+	TCTTTGT
	MA1152.2	8.904757	0.945938578	90	96	-	GCATTGT
	MA1152.1	10.888298	0.942583319	1057	1066	+	TTTTTGTTTA
	MA1152.1	10.705774	0.938484827	1269	1278	+	CTTTTGTTT
	MA1152.1	10.332454	0.930102073	1381	1390	-	CCATTGTCCA
	MA1152.2	8.177122	0.927524662	331	337	-	CAATTGT
	MA1152.1	9.903961	0.920480457	1161	1170	+	TCTTTGTTCA
	MA1152.1	9.864862	0.919602511	87	96	-	GCATTGTTCA
	MA1152.2	7.736913	0.916384493	372	378	-	CTATTAT
	MA1152.1	9.49879	0.911382507	328	337	-	CAATTGTTTC

MSANTD3	MA1523.2	10.636069	0.970129348	509	515	-	CACTCAA
	MA1523.2	9.211503	0.929450882	538	544	-	CACTCAT
	MA1523.2	8.336504	0.904465299	1031	1037	+	AACTCAC
HOXA1	MA0650.4	14.464836	1.000000004	301	308	+	CCAATAAAA
	MA0650.1	15.2930975	0.999999998	301	310	+	CCAATAAAAA
	MA0650.3	15.155865	0.983421225	299	310	+	CTCCAATAAAAA
	MA1495.2	8.064399	0.955433873	1337	1342	+	TAATTG
	MA1495.2	8.064399	0.955433873	1366	1371	+	TAATTG
	MA1495.2	8.037088	0.954884488	1337	1342	-	CAATTA
	MA1495.2	8.037088	0.954884488	1366	1371	-	CAATTA
	MA1495.2	7.8020525	0.950156425	46	51	+	TAATCA
	MA1495.2	7.8020525	0.950156425	367	372	-	TAATCA
	MA1495.2	7.7288384	0.948683626	46	51	-	TGATTA
	MA1495.2	7.7288384	0.948683626	367	372	+	TGATTA
	MA1495.1	8.609723	0.946704571	1336	1343	+	CTAATTGG
	MA1495.1	8.582402	0.946182509	1336	1343	-	CCAATTAG
	MA0899.2	11.151802	0.946179821	301	309	+	CCAATAAAAA
	MA0911.1	13.350228	0.941917115	612	623	-	GGTCATAAAATT
	MA0899.1	11.741887	0.939690986	203	213	-	GGTCATAAATA
	MA0911.2	11.3792095	0.937812261	204	212	-	GTCATAAAAT
	MA0911.2	11.3792095	0.937812261	614	622	-	GTCATAAAAT
	MA0899.2	10.710716	0.936527543	204	212	-	GTCATAAAAT
	MA0899.2	10.710716	0.936527543	614	622	-	GTCATAAAAT
	MA1495.1	7.8357596	0.93191526	1365	1372	-	TCAATTAG
	MA0899.1	11.334548	0.931222475	300	310	+	TCCAATAAAAA
	MA1495.1	7.7440886	0.930163562	366	373	-	ATAATCAC
	MA0650.4	11.028828	0.929692464	1018	1025	+	CAAATAAAA
	MA1495.2	6.762832	0.929251113	585	590	+	TCATGA
	MA1495.2	6.762832	0.929251113	585	590	-	TCATGA
	MA1495.1	7.6941767	0.929209817	1365	1372	+	CTAATTGA
	MA0899.1	11.186589	0.928146438	613	623	-	GGTCATAAATT
	MA1495.1	7.613684	0.927671723	366	373	+	GTGATTAT
	MA1495.2	6.3656745	0.921261754	177	182	+	TAATGG
	MA1495.2	6.218827	0.918307714	177	182	-	CCATTA
	MA0911.1	11.861265	0.915449778	202	213	-	GGTCATAAATAA
	MA1495.2	6.030114	0.914511507	311	316	+	TGATGA
	MA1495.2	6.030114	0.914511507	836	841	-	TGATGA
	MA0650.2	12.346479	0.913847702	300	310	+	TCCAATAAAAA
	MA1495.1	6.8878746	0.913802562	584	591	-	TTCATGAC
	MA1495.2	5.9837914	0.913579662	311	316	-	TCATCA
	MA1495.2	5.9837914	0.913579662	836	841	+	TCATCA
	MA0650.3	11.395445	0.911096719	1016	1027	+	CCCAAATAAAAC
	MA1495.2	5.821669	0.910318355	332	337	+	CAATTG
	MA1495.2	5.821669	0.910318355	332	337	-	CAATTG
	MA1495.1	6.6392846	0.90905237	584	591	+	GTCATGAA
	MA1495.1	6.510463	0.906590782	45	52	+	ATAATCAT
	MA1495.1	6.4372177	0.905191167	45	52	-	ATGATTAT
	MA0899.2	9.261475	0.904813797	827	835	+	GCACTAAAA
KLF10	MA1511.2	13.912693	0.96123547	1396	1404	+	GGGGTGGGG
	MA1511.1	14.24193	0.95397343	1395	1405	-	GCCCCACCCCC
	MA1511.2	12.249779	0.933626659	1413	1421	+	GGGGAGGGG
KLF2	MA1515.2	11.473531	0.960568414	1397	1404	-	CCCCACCC
	MA1515.1	11.778905	0.939110238	1396	1406	-	AGCCCCACCCC
	MA1515.2	9.940823	0.926902144	1395	1402	-	CCACCCCC
	MA1515.1	10.376302	0.911552109	1394	1404	-	CCCCACCCCCA
	MA1515.2	8.862616	0.903219092	907	914	+	ACCCACCC
CDX4	MA1473.2	12.287764	0.956616526	204	212	-	GTCATAAAAT
	MA1473.2	12.287764	0.956616526	614	622	-	GTCATAAAAT
	MA1473.1	13.238352	0.945483251	613	623	-	GGTCATAAATT
	MA1473.2	11.076282	0.94016611	301	309	+	CCAATAAAA
	MA1473.1	12.24583	0.93279196	203	213	-	GGTCATAAATA
	MA1473.1	9.834116	0.901953601	300	310	+	TCCAATAAAAA
BARX2	MA1471.2	10.557536	0.943118923	779	787	+	AAAAAATTA
	MA1471.2	9.651192	0.928029379	833	841	+	AAATCATCA
	MA1471.1	10.307261	0.917221323	831	842	+	TAAATCATCAA
	MA1471.2	8.948644	0.9163328	413	421	-	AAAAGATTA

	MA1471.2	8.776172	0.913461348	101	109	+	ATATCATTT
	MA1471.1	9.586363	0.905889153	777	788	+	GGAAAAAATTAC
	MA1471.1	9.279505	0.901065496	99	110	+	ATATATCATTTA
HOXC8	MA1505.2	8.785466	0.978487927	1337	1342	-	CAATTA
	MA1505.2	8.785466	0.978487927	1366	1371	-	CAATTA
	MA1505.2	8.711174	0.976922904	1337	1342	+	TAATTG
	MA1505.2	8.711174	0.976922904	1366	1371	+	TAATTG
	MA1505.2	7.6899886	0.955410833	332	337	+	CAATTG
	MA1505.2	7.6899886	0.955410833	332	337	-	CAATTG
	MA1505.2	7.0299196	0.941505962	177	182	-	CCATTA
	MA1505.2	6.917952	0.939147278	177	182	+	TAATGG
	MA1505.1	8.108955	0.938308863	1365	1372	+	CTAATTGA
	MA1505.1	8.083136	0.937795517	1365	1372	-	TCAATTAG
	MA1505.2	6.604315	0.932540263	55	60	-	TTATTA
	MA1505.2	6.572556	0.93187124	55	60	+	TAATAA
	MA1505.1	7.5676374	0.927546445	1336	1343	-	CCAATTAG
	MA1505.1	7.4933324	0.926069121	1336	1343	+	CTAATTGG
	MA1505.2	6.2578835	0.925242417	585	590	+	TCATGA
	MA1505.2	6.2578835	0.925242417	585	590	-	TCATGA
	MA1505.1	7.271047	0.921649672	331	338	+	ACAATTGA
	MA1505.1	7.1838202	0.919915438	331	338	-	TCAATTGT
	MA1505.2	5.934442	0.918428868	1385	1390	-	CCATTG
	MA1505.2	5.8967667	0.917635207	1385	1390	+	CAATGG
	MA1505.1	6.9295063	0.914859199	584	591	-	TTCATGAC
	MA1505.1	6.9036684	0.914345493	584	591	+	GTCATGAA
	MA1505.2	5.583129	0.911028182	214	219	+	CTATTA
	MA1505.2	5.583129	0.911028182	373	378	-	CTATTA
	MA1505.1	6.728238	0.910857609	54	61	+	CTAATAAC
	MA1505.2	5.55137	0.910359158	302	307	+	CAATAA
	MA1505.2	5.508837	0.909463169	302	307	-	TTATTG
	MA1505.1	6.6340604	0.908985179	54	61	-	GTTATTAG
	MA1505.2	5.4770784	0.908794145	214	219	-	TAATAG
	MA1505.2	5.4770784	0.908794145	373	378	+	TAATAG
	MA1505.1	6.3272953	0.902886113	176	183	-	TCCATTAG
	MA1505.1	6.315428	0.902650164	176	183	+	CTAATGGA
HOXB6	MA1500.2	8.373145	0.95058405	1337	1343	+	TAATTGG
	MA1500.2	7.9542727	0.941560386	366	372	-	TAATCAC
	MA1500.1	8.361792	0.939603526	1336	1343	+	CTAATTGG
	MA1500.2	7.859305	0.939514518	1366	1372	+	TAATTGA
	MA1500.1	7.848196	0.928842431	1365	1372	+	CTAATTGA
	MA1500.2	7.2806983	0.927049739	177	183	+	TAATGGA
	MA1500.1	7.450869	0.920517451	584	591	-	TTCATGAC
	MA1500.2	6.8727045	0.91826043	584	590	-	TCATGAC
	MA1500.1	7.269636	0.916720174	176	183	+	CTAATGGA
	MA1500.2	6.7966104	0.916621152	55	61	+	TAATAAC
	MA1500.1	7.2598486	0.916515101	205	212	+	TTTATGAC
	MA1500.1	7.2598486	0.916515101	615	622	+	TTTATGAC
	MA1500.2	6.68156	0.914142652	206	212	+	TTATGAC
	MA1500.2	6.68156	0.914142652	616	622	+	TTATGAC
	MA1500.1	7.090589	0.912968695	366	373	-	ATAATCAC
	MA1500.1	6.7860785	0.906588447	54	61	+	CTAATAAC
	MA1500.2	6.093018	0.901463838	46	52	+	TAATCAT
ATOH1	MA1467.3	9.381754	0.918333937	147	153	+	CAGATGA
SMAD4	MA1153.1	12.656732	0.988061978	923	930	-	TGTCTGGA
	MA1153.2	11.698889	0.987441268	924	930	-	TGTCTGG
	MA1153.2	9.63255	0.940430138	492	498	+	AGTCTAG
	MA1153.1	9.927388	0.928776464	1377	1384	+	GGTCTGGA
	MA1153.2	8.9712	0.925383802	1377	1383	+	GGTCTGG
	MA1153.1	8.678599	0.901650861	492	499	+	AGTCTAGG
NFATC4	MA1525.2	11.375256	0.940305321	635	644	+	AGCGGAAAAC
	MA1525.3	10.488596	0.938651829	636	644	+	GCGGAAAAC
	MA1525.1	10.728073	0.932913986	635	644	+	AGCGGAAAAC
	MA1525.3	9.932273	0.928857668	571	579	+	ATGGAACAA
	MA1525.1	10.466478	0.927949281	570	579	+	CATGGAACAA
	MA1525.2	9.603456	0.909955481	570	579	+	CATGGAACAA

LHX1	MA1518.1	9.449363	0.978894162	1336	1343	-	CCAATTAG
	MA1518.1	8.957214	0.964198667	1365	1372	-	TCAATTAG
	MA1518.1	7.347741	0.916139978	176	183	-	TCCATTAG
	MA1518.1	7.0550137	0.907399168	366	373	-	ATAATCAC
	MA1518.1	6.9895496	0.90544442	213	220	+	CCTATTAC
	MA1518.1	6.841208	0.901014955	366	373	+	GTGATTAT
TEAD2	MA1121.2	10.254896	0.93141433	550	556	-	GCATTCC
KLF11	MA1512.1	12.91729	0.93249525	1395	1405	-	GCCCCACCCCC
	MA1512.2	12.14513	0.930886024	1395	1404	-	CCCCACCCCC
FOXE1	MA1487.3	14.270725	0.929934214	1185	1196	+	CAAAGAAAACAA
	MA1487.2	15.028853	0.927392219	1184	1197	+	GCAAAGAAAACAAA
ARGFX	MA1463.2	10.704452	0.937407817	1365	1372	+	CTAATTGA
	MA1463.2	9.981001	0.924264962	1336	1343	+	CTAATTGG
	MA1463.2	9.590322	0.91716753	1336	1343	-	CCAATTAG
	MA1463.1	10.000957	0.905426645	1364	1373	+	GCTAATTGAG
ISL1	MA1608.2	12.6508465	1.000000009	176	182	-	CCATTAG
	MA1608.1	12.695923	0.975641576	174	184	-	TTCCATTAGGT
	MA1608.2	9.207418	0.915812541	1336	1342	-	CAATTAG
	MA1608.2	9.207418	0.915812541	1365	1371	-	CAATTAG
HAND2	MA1638.2	11.754366	1.000000004	147	152	+	CAGATG
	MA1638.1	9.988663	0.940573975	145	154	+	GTCAGATGAT
ZNF148	MA1653.2	17.688288	1	1412	1421	-	CCCCTCCCCC
	MA1653.1	16.89862	0.965648646	1412	1423	-	AGCCCCTCCCCC
	MA1653.1	13.784458	0.912936909	5	16	+	CCCCCTCCCTT
	MA1653.2	12.544679	0.907687918	7	16	+	CCCCTCCCTT
NFYC	MA1644.2	9.252333	0.909795537	123	129	-	CCAATCG
	MA1644.2	8.93829	0.902113281	919	925	+	CCAATCC
BHLHE22	MA1635.2	11.923375	0.999999995	1084	1089	+	CAGCTG
	MA1635.2	11.923375	0.999999995	1084	1089	-	CAGCTG
	MA1635.1	9.035366	0.920052915	1082	1091	+	GTCAGCTGAG
	MA1635.1	9.034346	0.920035881	1082	1091	-	CTCAGCTGAC
VEZF1	MA1578.2	11.409431	0.999999991	5	10	+	CCCCC
	MA1578.2	11.409431	0.999999991	595	600	+	CCCCC
	MA1578.2	8.948279	0.94012605	655	660	+	GCCCC
	MA1578.1	10.538091	0.924154	5	14	+	CCCCCTCCC
	MA1578.2	8.071317	0.918791647	4	9	+	ACCCCC
	MA1578.2	8.071317	0.918791647	594	599	+	ACCCCC
	MA1578.2	8.071317	0.918791647	1395	1400	-	ACCCCC
ZNF417	MA1727.2	13.558303	0.999999991	1255	1261	-	GGCGCCA
	MA1727.2	9.650839	0.917814829	170	176	-	GGTGCCA
ZNF281	MA1630.3	18.5403	0.999999988	1412	1421	+	GGGGGAGGGG
	MA1630.2	17.43709	0.969961144	1412	1423	+	GGGGGAGGGGCT
	MA1630.3	15.731853	0.957679732	1395	1404	+	GGGGGTGGGG
	MA1630.1	14.768269	0.932981347	1409	1419	+	CTTGGGGGAGG
	MA1630.2	14.629247	0.929836091	1395	1406	+	GGGGGTGGGGCT
SOX18	MA1563.2	11.609652	0.999042692	89	96	+	AACAATGC
	MA1563.2	11.2802725	0.991838333	330	337	+	AACAATTG
	MA1563.1	10.017501	0.987865102	89	96	+	AACAATGC
	MA1563.1	9.5690155	0.976508021	1383	1390	+	GACAATGG
	MA1563.2	9.948971	0.962719374	1383	1390	+	GACAATGG
	MA1563.1	8.116838	0.939734266	453	460	-	GACCATGC
	MA1563.2	7.7348633	0.914291205	59	66	+	AACACTAG
	MA1563.1	6.813227	0.906722669	1282	1289	+	CACACTGA
TLX2	MA1577.1	11.876933	0.998657285	1336	1343	-	CCAATTAG
	MA1577.2	10.668618	0.998551592	1337	1342	-	CAATTA
	MA1577.2	10.668618	0.998551592	1366	1371	-	CAATTA
	MA1577.1	11.765475	0.996332709	1365	1372	-	TCAATTAG

	MA1577.2	8.24627	0.944049417	31	36	+	AAATTA
	MA1577.2	8.24627	0.944049417	260	265	+	AAATTA
	MA1577.2	8.24627	0.944049417	705	710	+	AAATTA
	MA1577.2	8.24627	0.944049417	782	787	+	AAATTA
	MA1577.2	8.24627	0.944049417	1117	1122	+	AAATTA
	MA1577.2	7.8853903	0.935929717	381	386	-	GAATTA
	MA1577.1	8.107734	0.920046468	704	711	+	AAAATTAG
	MA1577.1	8.091787	0.919713889	1116	1123	+	CAAATTAC
	MA1577.1	7.35953	0.904441852	30	37	+	TAAATTAT
FOXN1	MA1684.1	9.694712	0.992300042	632	637	+	GGAAGC
	MA1684.1	9.694712	0.992300042	1421	1426	-	GGAAGC
	MA1684.1	8.8971615	0.975416811	398	403	+	AGAAGC
	MA1684.1	8.8971615	0.975416811	1158	1163	-	AGAAGC
	MA1684.1	8.629464	0.969749963	1287	1292	+	TGAAGC
PLAGL1	MA1615.2	12.177682	0.946804506	1341	1348	-	AGGGGCCA
TBX3	MA1566.1	9.877375	0.936520882	284	293	+	AACGTGTGAC
BATF	MA0462.1	12.299273	0.943455753	535	545	+	GGAATGAGTGA
STAT2	MA1623.2	13.891287	0.927808485	1023	1032	+	AAAAGTAAA
	MA1623.1	14.416338	0.911289284	1022	1034	+	TAAAAGTAAACT
	MA0517.2	13.966054	0.9070936	1022	1034	-	AGTTTCAGTTTA
FOXF1	MA1606.2	9.486112	0.927117349	1061	1067	-	CTAAACA
	MA1606.2	9.486112	0.927117349	1275	1281	-	CTAAACA
	MA1606.1	10.218521	0.901943521	1059	1069	-	GACTAAACAAA
OSR2	MA1646.2	11.1296835	0.926924955	473	480	-	ACAGTAGC
	MA1646.1	11.281508	0.910443333	471	482	-	TAACAGTAGCCC
ZNF768	MA1731.2	11.604219	0.926239938	1249	1257	-	CCATCTCTG
TBX6	MA0801.1	11.161443	0.945202033	285	292	+	ACGTGTGA
	MA1567.1	10.351264	0.925635929	284	293	+	AACGTGTGAC
WT1	MA1627.2	13.031456	0.920401101	1410	1419	-	CCTCCCCCAA
	MA1627.1	14.619978	0.913933083	1408	1421	-	CCCCTCCCCAAGC
PRDM4	MA1647.3	13.118398	0.914111469	324	334	+	ACTTGAAACAA
SOHLH2	MA1560.2	10.153858	0.912821766	901	908	-	GTACGTGC
SP9	MA1564.2	11.233106	0.912587776	1395	1404	-	CCCCACCCCC
	MA1564.2	10.965765	0.907471043	1412	1421	-	CCCCTCCCCC
PLAGL2	MA1548.2	9.650321	0.907964916	1341	1348	+	TGCCCCCT
ZSCAN21	MA2336.1	12.47509	1.000000012	825	831	+	AAGCACT
	MA2336.1	10.043045	0.931925324	503	509	+	CAGCACT
	MA2336.1	9.185758	0.907929233	349	355	-	TAGCACT
NR1H2	MA1996.2	11.594622	1.000000001	543	548	-	AGGTCA
	MA1996.1	10.575065	0.937629851	541	551	-	CCTAGGTCCT
NKX2-1	MA1994.2	13.200172	1.000000001	506	512	+	CACTTGA
	MA1994.1	12.92352	0.937319804	504	516	+	AGCACTTGAGTGA
BCL11A	MA2324.1	9.805109	0.92238618	143	149	-	CTGACCC
	MA2324.1	9.805109	0.92238618	1319	1325	+	CTGACCC
IKZF2	MA2326.1	11.805336	1.000000006	1236	1241	-	AGGAAG
	MA2326.1	11.805336	1.000000006	1422	1427	-	AGGAAG
SP5	MA1965.2	11.8823395	1.000000006	9	14	+	CCTCCC
	MA1965.2	11.8823395	1.000000006	937	942	+	CCTCCC
	MA1965.2	11.8823395	1.000000006	1092	1097	+	CCTCCC
	MA1965.2	11.8823395	1.000000006	1414	1419	-	CCTCCC

	MA1965.1	14.648793	1.000000004	1412	1421	-	CCCCTCCCCC
	MA1965.1	13.131495	0.975212988	7	16	+	CCCCTCCCTT
	MA1965.1	11.843978	0.954179728	935	944	+	GGCCTCCCTC
	MA1965.1	9.854973	0.921686763	1090	1099	+	AGCCTCCCAA
SMAD2	MA1964.2	11.578806	1.000000003	924	929	+	CCAGAC
	MA1964.2	11.578806	1.000000003	1378	1383	-	CCAGAC
	MA1964.1	11.348495	0.96122121	922	931	+	ATCCAGACAT
	MA1964.1	10.809946	0.950082966	1376	1385	-	GTCCAGACCC
NR1H3	MA2337.1	11.061011	0.999999999	543	548	-	AGGTCA
SATB1	MA1963.2	13.514758	0.999999998	54	60	+	CTAATAA
	MA1963.1	14.212443	0.951535226	51	63	+	ATCCTAATAACAC