Supplementary Results

Table 1. High- and lower-confidence imprinted gene candidates.

Ensembl ID	Band	Pred.†		Ensembl ID	Band	Pred.†		Ensembl ID	Band	Pred.†	
173447	1p36.33	S	M	143921 (*ABCG8*)	2p21	E,S	M	159674 (*SPON2*)	4p16.3	E,S	P
184235	1p36.33	S	M	138083 (*SIX3*)	2p21	S	P	163945 (*NP_065945.1*)	4p16.3	E,S	M
131591 (*NM_017891*)	1p36.33	S	M	055813 (*Q96PX6*)	2p16.1	E,S	P	174141 (*Q15270*)	4p16.3	S	P
182839	1p36.33	E	M	115507 (*OTX1*)	2p15	E,S	M	068078 (*FGFR3*)	4p16.3	S	M
184163 (*Q5EBL5*)	1p36.33	E,S	M	116035 (*VAX2*)	2p13.3	E,S	M	163956 (*LRPAP1*)	4p16.3	S	M
131584 (*CENTB5*)	1p36.33	S	M	178455	2p13.2	S	P	183190	4p13	E	M
127054 (*NM_017871*)	1p36.33	S	M	003137 (*C26A*)	2p13.2	S	P	182739 (*GRINL1B*)	4q13.2	S	P
169962 (*TAS1R3*)	1p36.33	S	M	144040 (*SFXN5*)	2p13.2	S	P	153851 (*Q9NYI9*)	4q13.2	E,S	P
107404 (*DVL1*)	1p36.33	E,S	M	135637 (*MRPL53*)	2p13.1	S	M	153852 (*Q9NYJ6*)	4q13.2	E,S	P
162576 (*NM_032348*)	1p36.33	S	M	115325 (*DOK1*)	2p13.1	S	M	180769 (*Q8N507*)	4q21.23	S	M
160075 (*NM_014188*)	1p36.33	S	M	116119 (*KV2A*)	2p11.2	S	P	138821 (*NM_022154*)	4q24	S	P
178821 (*TMEM52*)	1p36.33	E,S	P	115085 (*ZAP70*)	2q11.2	S	P	168743 (*NP_001028219.1*)	4q24	E	P
157916 (*RER1*)	1p36.33	S	P	135951 (*TSGA10*)	2q11.2	E	P	164093 (*PITX2*)	4q25	S	P
157911 (*PEX10*)	1p36.32	E,S	M	071082 (*RPL31*)	2q11.2	S	P	177826	4q28.1	S	P
157881 (*PANK4*)	1p36.32	S	M	169636	2q12.3	E,S	P	170153 (*Q9ULK6*)	4q31.21	S	M
169797	1p36.32	S	M	183998 (*RPL22*)	2q13	E	P	180519	4q31.21	S	P
157870 (*NM_152371*)	1p36.32	S	M	015568 (*RANBP2L1*)	2q13	S	P	151615 (*POU4F2*)	4q31.22	S	M
177121 (*Q8N6L5*)	1p36.32	E,S	P	184764 (*RPL22*)	2q13	E,S	P	172799	4q31.3	S	M
142611 (*PRDM16*)	1p36.32	E,S	P	184538 (*RANBP2L1*)	2q13	S	P	145431 (*PDGFC*)	4q32.1	E	P
162591 (*EGFL3*)	1p36.32	S	P	153094 (*BCL2L11*)	2q13	S	P	038295 (*TLL1*)	4q32.3	S	P
182956	1p36.32	S	M	125618 (*PAX8*)	2q13	S	M	056050 (*NM_017867*)	4q33	S	M
116213 (*WDR8*)	1p36.32	E,S	M	183300	2q14.3	S	P	168322 (*NM_030970*)	4q34.3	S	P
183509 (*Q8IYL3*)	1p36.32	S	M	136720 (*HS6ST1*)	2q14.3	S	P	177310 (*NM_153008*)	4q35.1	E	M
131697 (*Q9UFQ2*)	1p36.31	S	M	169822 (*NM_030970*)	2q14.3	S	P	186158	4q35.2	E,S	M
130940 (*NM_017766*)	1p36.22	S	M	136698 (*NM_032545*)	2q21.1	S	M	186147 (*DUX2*)	4q35.2	E,S	P
117154 (*NM_032880*)	1p36.13	S	P	179843 (*RAB6C*)	2q21.1	S	M	066230 (*SLC9A3*)	5p15.33	S	M
179002 (*TAS1R2*)	1p36.13	S	P	183840 (*GPR39*)	2q21.2	E	M	185486	5p15.33	S	M
179163 (*FUCA1*)	1p36.11	E,S	P	136539 (*NM_014880*)	2q24.2	S	P	125063 (*NM_017808*)	5p15.33	S	M
142698 (*NM_032884*)	1p35.1	E	P	174470 (*Q96M44*)	2q24.2	S	M	112877 (*NM_018140*)	5p15.33	S	M
126070 (*EIF2C3*)	1p34.3	E	M	128714 (*HOXD13*)	2q31.1	S	M	145506 (*NKD2*)	5p15.33	S	M
185668 (*POU3F1*)	1p34.3	S	P	128713 (*HOXD11*)	2q31.1	S	M	113504 (*SLC12A7*)	5p15.33	S	M
183682 (*BMP8*)	1p34.3	E,S	P	128709 (*HOXD9*)	2q31.1	S	M	174358	5p15.33	S	M
173935 (*NM_182518*)	1p34.2	E,S	M	170166 (*HOXD4*)	2q31.1	E	M	153395 (*Q8NF37*)	5p15.33	S	M
178973 (*NM_024547*)	1p34.2	E,S	M	171567 (*TIGD1*)	2q37.1	E,S	P	113430 (*IRX4*)	5p15.33	S	M
117410 (*ATP6V0B*)	1p34.1	S	M	157985 (*CENTG2*)	2q37.2	E	M	170561 (*IRX2*)	5p15.33	S	P
118473 (*SGIP1*)	1p31.2	E	P	144485 (*HES6*)	2q37.3	S	M	170549 (*IRX1*)	5p15.33	S	M
132489 (*NM_020948*)	1p31.2	E	P	132326 (*PER2*)	2q37.3	S	M	145536 (*ADAMTS16*)	5p15.32	E,S	M
117069 (*SI7E*)	1p31.1	E	P	186540 (*Q9Y419*)	2q37.3	E,S	M	164236 (*XP_293937.5*)	5p15.2	E	P
137944 (*NM_019610*)	1p22.2	E,S	M	178580 (*Q8WXC7*)	2q37.3	S	P	133357 (*NM_030970*)	5p15.2	E	P
162676 (*GFI1*)	1p22.1	E,S	P	172428 (*MYEOV2*)	2q37.3	E,S	P	145526 (*CDH18*)	5p14.3	E,S	P
182166	1p21.2	S	P	178602 (*NM_148961*)	2q37.3	S	P	132404	5p14.1	S	P
186371 (*NDUFA4*)	1p13.3	E,S	P	063660 (*GPC1*)	2q37.3	S	M	113492 (*AGXT2*)	5p13.2	E	P
121931 (*NM_018372*)	1p13.3	S	P	142327 (*RNPEPL1*)	2q37.3	S	M	168621 (*GDNF*)	5p13.2	S	P
116455 (*ME50*)	1p13.2	S	P	115687 (*PASK*)	2q37.3	E	M	016082 (*ISL1*)	5q11.2	S	P
179735 (*Q8NE92*)	1q21.1	S	P	132170 (*PPARG*)	3p25.2	S	P	164258 (*NDUFS4*)	5q11.2	S	P
184458 (*Q86YZ3*)	1q21.3	S	P	131374 (*TBC1D5*)	3p24.3	E	M	164283 (*ESM1*)	5q11.2	S	P
169474 (*SPRR1A*)	1q21.3	S	M	060971 (*ACAA1*)	3p22.3	S	P	152929 (*Q9BXE3*)	5q12.1	S	M
160691 (*SHC1*)	1q22	S	M	010282 (*KB73*)	3p22.1	S	P	145645 (*Q9P193*)	5q12.1	S	P
143620 (*EFNA4*)	1q22	S	M	178055 (*NM_182702*)	3p21.31	S	M	171540 (*OTP*)	5q14.1	S	M
160856 (*NM_052939*)	1q23.1	S	P	068028 (*RASSF1*)	3p21.31	S	M	131730 (*CKMT2*)	5q14.1	S	M
132704 (*FCRL2*)	1q23.1	E	M	145050 (*ARMET*)	3p21.31	S	P	131732 (*NM_032280*)	5q14.1	S	M
132703 (*APCS*)	1q23.2	S	P	114841 (*NM_015512*)	3p21.1	S	M	153922 (*CHD1*)	5q15	E	M
173110 (*HSPA6*)	1q23.3	E,S	M	010322 (*NISCH*)	3p21.1	S	M	174132 (*Q8TBP5*)	5q21.1	E,S	P
143152 (*Q9C074*)	1q24.1	S	M	168268 (*NM_022908*)	3p21.1	S	M	181751 (*NM_033211*)	5q21.1	S	M
117501 (*NM_025063*)	1q24.3	S	P	144741 (*NM_173471*)	3p14.1	S	P	176857	5q21.3	E	M
116147 (*TNR*)	1q25.1	S	P	183185 (*Q9UIV9*)	3q12.1	S	P	080709 (*KCNN2*)	5q22.3	S	M
116703 (*PDC*)	1q31.1	S	P	184804	3q13.12	E	M	113396 (*SLC27A6*)	5q23.3	S	M
118194 (*TNNT2*)	1q32.1	S	P	185565 (*LSAMP*)	3q13.31	S	M	164400 (*CSF2*)	5q23.3	E,S	M
152104 (*PTPN14*)	1q32.3	E,S	M	144908 (*FTHFD*)	3q21.3	E,S	M	069011 (*PITX1*)	5q31.1	S	P
152120 (*Q9NQI3*)	1q41	S	P	114626 (*ABTB1*)	3q21.3	S	P	174313	5q31.1	E	P
117791 (*NM_017898*)	1q41	S	P	179348 (*GATA2*)	3q21.3	S	M	081818 (*PCDHB4*)	5q31.3	S	M
185495 (*Q9H5Q3*)	1q42.11	S	M	004399 (*PLXND1*)	3q22.1	S	P	177895 (*PCDHB16*)	5q31.3	S	P
173419 (*Q8IVP0*)	1q42.12	S	P	174640 (*SLC21A2*)	3q22.1	S	P	120327 (*PCDHB14*)	5q31.3	E	P
081692 (*NM_023007*)	1q42.13	S	P	144872	3q22.2	S	P	081853 (*PCDHGC5*)	5q31.3	S	M
124860 (*OBSCN*)	1q42.13	E,S	P	181882	3q22.3	E,S	P	113580 (*NR3C1*)	5q31.3	E	P
181203 (*HIST3H2BB*)	1q42.13	E,S	M	168875 (*SOX14*)	3q22.3	S	M	169302	5q32	S	P
168159 (*Q5TA31*)	1q42.13	E	M	114120 (*NM_018155*)	3q23	S	M	113667 (*Y555*)	5q32	E	M
182887	1q42.13	E	P	175685 (*Q9BZ57*)	3q24	S	P	145888 (*GLRA1*)	5q33.1	E	P
162946 (*DISC1*)	1q42.2	S	M	174963 (*ZIC4*)	3q24	S	M	182344	5q35.2	S	M
179397 (*NM_173807*)	1q44	S	M	152977 (*ZIC1*)	3q24	E,S	M	185548	5q35.3	S	M
177356 (*Q8NGX0*)	1q44	E,S	P	175726	3q25.1	S	M	178392	5q35.3	S	M
035115 (*NM_015677*)	2p25.3	S	M	174948 (*Q86SP6*)	3q25.2	S	M	185784 (*Q8TAJ0*)	5q35.3	E	M
172554 (*SNTG2*)	2p25.3	S	P	151967 (*SCHIP1*)	3q25.32	S	P	168903 (*BTNL3*)	5q35.3	S	P
186170 (*TMSL2*)	2p25.3	S	M	181501	3q26.33	E	M	137273 (*FOXF2*)	6p25.3	S	P
182551 (*NM_018269*)	2p25.2	S	P	163882 (*POLR2H*)	3q27.1	S	M	184250 (*Q86WA7*)	6p25.2	S	M
134321 (*NM_080657*)	2p25.2	S	P	114315 (*HES1*)	3q29	E,S	P	145945 (*FAM50B*)	6p25.2	E,S	M
115738 (*ID2*)	2p25.1	E	M	169020 (*ATP5I*)	4p16.3	S	M	124785 (*NRN1*)	6p25.1	S	M
138061 (*CYP1B1*)	2p22.2	E,S	P	145214 (*DGKQ*)	4p16.3	S	M	137203 (*TFAP2A*)	6p24.3	S	M
152154 (*NM_152390*)	2p22.1	S	P	127418 (*FGFRL1*)	4p16.3	E,S	M	176078 (*Q8NAN4*)	6p24.3	S	M
152518 (*ZFP36L2*)	2p21	E,S	M	176836	4p16.3	S	P	185694	6p22.1	E	P

181573 (*Q96MM2*)	6p22.1	S	P	120896 (*VINE*)	8p21.3	S	M	180740 (*Q9H6Z8*)	10q23.31	E,S	P
112498 (*PPP1R11*)	6p22.1	S	M	179388 (*EGR3*)	8p21.3	S	M	095585 (*BLNK*)	10q24.1	S	P
161877 (*C6orf10*)	6p21.32	S	M	172733 (*PURG*)	8p12	E,S	P	148820 (*LDB1*)	10q24.32	E,S	M
168426 (*BTNL2*)	6p21.32	E,S	M	167912 (*Q96QE0*)	8q12.1	E,S	M	166275 (*NM_144591*)	10q24.32	S	P
168383 (*HLA-DPB1*)	6p21.32	E	P	183226	8q12.3	E	P	176584	10q26.13	S	M
161896 (*IHPK3*)	6p21.31	S	M	185942 (*FAM77D*)	8q12.3	E,S	P	119965 (*C10orf88*)	10q26.13	E	M
156582	6p21.2	S	M	165084 (*NM_052958*)	8q13.2	E	M	108001 (*EBF3*)	10q26.3	S	M
137252 (*HCRTR2*)	6p12.1	S	P	184234 (*NM_172239*)	8q21.2	S	M	165752 (*NM_173575*)	10q26.3	S	P
146151 (*HMGCLL1*)	6p12.1	S	P	180694 (*Q8N3G6*)	8q21.3	S	P	171813 (*Q96F43*)	10q26.3	S	P
179713 (*Q8N480*)	6q14.1	S	P	156486 (*KCNS2*)	8q22.2	S	P	180066 (*C10orf91*)	10q26.3	E,S	M
135324 (*C6orf117*)	6q14.2	E,S	P	164796 (*CSMD3*)	8q23.3	S	M	148826 (*NKX6-2*)	10q26.3	E,S	M
135315 (*C6orf84*)	6q14.2	S	P	104406 (*NM_032205*)	8q24.22	E	P	171811 (*C10orf93*)	10q26.3	E,S	M
184486 (*POU3F4*)	6q16.1	S	M	169427 (*KCNK9*)	8q24.3	E,S	M	151646 (*GPR123*)	10q26.3	S	M
183075	6q21	S	P	184489 (*PTP4A3*)	8q24.3	S	P	171798 (*Q8TEE5*)	10q26.3	S	M
153989 (*C6orf68*)	6q22.1	S	P	181790 (*BAI1*)	8q24.3	S	M	165824 (*NM_152643*)	10q26.3	S	M
146350 (*C6orf170*)	6q22.31	E	P	180838 (*Q8NAM3*)	8q24.3	E	M	171794 (*UTF1*)	10q26.3	S	P
184362 (*Q9BZ63*)	6q22.31	S	P	167656 (*LY6D*)	8q24.3	E,S	P	151650 (*VENTX2*)	10q26.3	E,S	M
175211 (*Q9BXE6*)	6q23.2	S	P	179142 (*CYP11B2*)	8q24.3	S	M	178592 (*Q8N377*)	10q26.3	E,S	M
135521 (*C6orf93*)	6q24.2	S	M	182851 (*NM_178172*)	8q24.3	E	P	148832 (*PAOX*)	10q26.3	E,S	M
118508 (*RAB32*)	6q24.3	S	P	158106 (*RHPN1*)	8q24.3	S	M	186730 (*DUX4*)	10q26.3	S	P
112499 (*SLC22A2*)	6q25.3	E,S	P	181528	8q24.3	S	M	184243	10q26.3	S	P
146477 (*SLC22A3*)	6q25.3	S	P	179950 (*NM_078480*)	8q24.3	S	P	179882 (*DUX2*)	10q26.3	S	P
060762 (*BRP44L*)	6q27	E,S	P	185189 (*NM_178564*)	8q24.3	S	M	177947 (*ODF3*)	11p15.5	S	M
153471 (*TCP10*)	6q27	S	P	186574 (*Q8ND02*)	8q24.3	S	M	174885 (*PYA5*)	11p15.5	S	M
186340 (*THBS2*)	6q27	S	P	178719 (*GRINA*)	8q24.3	E	P	185885 (*IFITM1*)	11p15.5	E,S	M
164493 (*Q96N37*)	6q27	S	P	167701 (*GPT*)	8q24.3	E,S	M	182272 (*B4GALNT4*)	11p15.5	E,S	M
170767 (*C6orf208*)	6q27	E	M	160959 (*Y014*)	8q24.3	S	P	184363 (*PKP3*)	11p15.5	E,S	M
177706 (*FAM20C*)	7p22.3	S	P	177742 (*NM_178535*)	8q24.3	E	M	176828 (*Q8N9U2*)	11p15.5	E,S	M
184773 (*Q96GH9*)	7p22.3	E	M	120215 (*MLANA*)	9p24.1	S	M	177700 (*POLR2L*)	11p15.5	S	M
122691 (*TWIST2*)	7p21.1	S	M	186758 (*Q8N7I0*)	9p21.1	E,S	M	184956 (*MUC6*)	11p15.5	S	M
105855 (*ITGB8*)	7p21.1	E	M	174994 (*Q96M55*)	9p12	S	P	183116	11p15.5	S	M
105996 (*HOXA2*)	7p15.2	E,S	M	170152	9p11.2	S	M	184545 (*DUSP8*)	11p15.5	S	P
105997 (*HOXA3*)	7p15.2	E,S	M	154537 (*Q8NCQ8*)	9p11.2	S	M	130598 (*TNNI2*)	11p15.5	S	P
164519 (*Q96MZ3*)	7p15.2	S	M	178784 (*Q96F02*)	9q12	S	P	184682	11p15.5	E,S	M
106001 (*HOXA4*)	7p15.2	E,S	M	184879	9q13	S	M	183680 (*Q8N2L8*)	11p15.5	S	P
106004 (*HOXA5*)	7p15.2	E,S	M	182368 (*Q8NCQ8*)	9q13	S	M	181963 (*Q8NGK3*)	11p15.4	S	P
106006 (*HOXA6*)	7p15.2	S	M	170215 (*Q8NCQ8*)	9q13	S	M	180785 (*NM_152430*)	11p15.4	S	M
005073 (*HOXA11*)	7p15.2	E,S	M	170217	9q13	S	M	176904 (*Q8NH63*)	11p15.4	S	P
106038 (*EVX1*)	7p15.2	E,S	P	107282 (*APBA1*)	9q21.11	E,S	P	180974 (*Q8NGH9*)	11p15.4	S	P
106483 (*SFRP4*)	7p14.1	S	P	155621 (*NM_182505*)	9q21.12	E,S	P	051009 (*NM_032127*)	11p15.4	S	M
106571 (*GLI3*)	7p14.1	E,S	M	186788 (*NP_001001670*)	9q21.32	E,S	M	166337 (*TAF10*)	11p15.4	S	P
164543 (*STK17A*)	7p13	E	P	177992 (*NM_178828*)	9q22.1	S	P	170748 (*NM_014469*)	11p15.4	S	P
058404 (*CAMK2B*)	7p13	S	P	186359 (*Q8NDS1*)	9q22.1	S	P	170688 (*OR5E1P*)	11p15.4	E	P
164742 (*ADCY1*)	7p13	S	M	130222 (*GADD45G*)	9q22.2	S	P	129152 (*MYOD1*)	11p15.1	S	M
185292	7p13	S	M	169027 (*NM_030970*)	9q22.31	S	P	184193 (*Q8N7V1*)	11p14.3	E,S	M
179869 (*NM_152701*)	7p12.3	S	P	131662 (*PHF2*)	9q22.31	S	P	129151 (*BBOX1*)	11p14.2	E	P
042813 (*ZPBP*)	7p12.2	S	P	119523 (*NM_033087*)	9q22.33	S	P	007372 (*PAX6*)	11p13	S	M
185037	7q11.21	E,S	M	177945 (*NM_016158*)	9q33.3	E,S	P	183242 (*WIT1*)	11p13	S	M
185947 (*Q8IVV5*)	7q11.21	E,S	P	136944 (*LMX1B*)	9q33.3	E,S	M	182565	11p11.12	S	P
135211 (*C7orf35*)	7q11.23	E,S	P	123454 (*DBH*)	9q34.2	S	M	185927	11q11	S	P
187391 (*MAGI2*)	7q21.11	E,S	M	186459	9q34.3	S	P	186660 (*ZFP91*)	11q12.1	S	P
185191	7q21.12	S	P	160345 (*NM_144654*)	9q34.3	E,S	P	172289 (*Q8NGI7*)	11q12.1	S	P
182348 (*NM_181646*)	7q21.13	S	P	148411 (*NM_144653*)	9q34.3	S	M	134824 (*FADS2*)	11q12.2	S	M
105810 (*CDK6*)	7q21.2	S	M	160360 (*Q9UFS8*)	9q34.3	S	M	174903 (*RAB1B*)	11q13.2	E,S	M
006377 (*DLX6*)	7q21.3	S	P	148400 (*NOTCH1*)	9q34.3	S	M	174851 (*YIF1*)	11q13.2	S	M
121716 (*PILRB*)	7q22.1	S	M	172889 (*EGFL7*)	9q34.3	E,S	P	173621 (*NM_024036*)	11q13.2	S	P
128594 (*NM_022143*)	7q32.1	S	P	169692 (*AGPAT2*)	9q34.3	S	M	172932	11q13.2	S	P
106028 (*SSBP1*)	7q34	S	M	054148 (*PHPT1*)	9q34.3	E,S	M	162105 (*SHANK2*)	11q13.3	S	M
181551	7q34	S	P	184709	9q34.3	S	M	175534 (*Q8TB74*)	11q13.4	S	M
184412	7q34	S	P	185863	9q34.3	S	M	137474 (*MYO7A*)	11q13.5	S	P
133624 (*NM_024910*)	7q36.1	S	P	176248 (*NM_013366*)	9q34.3	S	M	168959 (*GRM5*)	11q14.2	S	P
164889 (*SLC4A2*)	7q36.1	E,S	M	176058 (*NM_173691*)	9q34.3	S	M	182359 (*KBTBD3*)	11q22.3	E,S	P
164896 (*FASTK*)	7q36.1	E,S	M	182569 (*NM_053045*)	9q34.3	S	M	150750 (*C11orf53*)	11q23.1	E	M
164690 (*SHH*)	7q36.3	S	P	186909	10p15.3	E,S	P	184824 (*C1QTNF5*)	11q23.3	S	M
187177	7q36.3	E	M	151632 (*AKR1C2*)	10p15.1	S	P	154146 (*NRGN*)	11q24.2	S	P
146909 (*C7orf3*)	7q36.3	E	P	178462 (*NM_024803*)	10p15.1	S	M	182657	11q24.3	E,S	M
130675 (*HLXB9*)	7q36.3	S	M	178372 (*CLSP*)	10p15.1	S	P	120462 (*Q9P195*)	11q24.3	S	M
178158 (*Q8N7D3*)	7q36.3	S	M	176730 (*Q8N218*)	10p15.1	E	M	182667 (*NTRI*)	11q25	E,S	P
155093 (*PTPRN2*)	7q36.3	S	M	107485 (*GATA3*)	10p14	E,S	P	170257 (*NM_030970*)	11q25	S	P
180204 (*NM_181648*)	8p23.3	E,S	P	182077 (*NP_001030014.1*)	10p12.1	E	M	080854 (*Q9UPX0*)	11q25	S	M
104284 (*DLGAP2*)	8p23.3	E,S	P	099250 (*NRP1*)	10p11.22	E	P	151503 (*Y056*)	11q25	S	M
036448 (*MYOM2*)	8p23.3	S	M	175395 (*ZNF25*)	10p11.21	E	M	149328 (*NM_138342*)	11q25	S	M
186550	8p23.1	E	M	165511 (*NM_145022*)	10q11.21	S	M	109956 (*B3GAT1*)	11q25	S	M
186553	8p23.1	E	M	165406 (*MARCH8*)	10q11.21	E	P	139194 (*RBP5*)	12p13.31	E,S	P
186555	8p23.1	E	P	148611 (*SYT15*)	10q11.22	S	M	150045 (*KLRF1*)	12p13.31	S	P
186558	8p23.1	E	P	165606	10q11.23	S	M	121374 (*KLRC3*)	12p13.2	S	P
186560	8p23.1	E	M	107671 (*NM_018245*)	10q11.23	S	M	171681 (*ATF7IP*)	12p13.1	S	M
186647	8p23.1	E	M	165443 (*NM_032439*)	10q21.1	S	M	111404 (*NM_024730*)	12p12.3	S	P
185161 (*Q8N9I4*)	8p23.1	E,S	P	148575 (*NM_178505*)	10q21.2	S	M	172572 (*PDE3A*)	12p12.2	S	M
158815 (*FGF17*)	8p21.3	S	M	182771 (*GRID1*)	10q23.2	E	M	111700 (*SLC21A8*)	12p12.2	S	P
168487 (*BMP1*)	8p21.3	S	P	138135 (*CH25H*)	10q23.31	S	P	069431 (*ABCC9*)	12p12.1	E,S	M

013573 (*DDX11*)	12p11.21	S	M
177627 (*NM_152319*)	12q13.11	E	P
123364 (*HOXC13*)	12q13.13	S	M
123388 (*HOXC11*)	12q13.13	S	M
180818 (*HOXC10*)	12q13.13	S	M
180806 (*HOXC9*)	12q13.13	E,S	M
186426 (*HOXC4*)	12q13.13	E,S	M
170338 (*HOXC6*)	12q13.13	S	M
172789 (*HOXC5*)	12q13.13	E	M
174604 (*Q9BXE6*)	12q13.2	S	P
135502 (*SLC26A10*)	12q13.3	E,S	M
135446 (*CDK4*)	12q14.1	E,S	M
079081 (*SRGAP1*)	12q14.2	S	M
173401 (*NM_152779*)	12q21.1	E	M
165891 (*Q96AV8*)	12q21.2	E,S	M
111046 (*MYF6*)	12q21.31	S	P
151572 (*NM_178826*)	12q23.1	S	P
089116 (*LHX5*)	12q24.13	S	M
175727 (*NM_014938*)	12q24.31	S	P
184967 (*NM_024078*)	12q24.33	S	M
112787 (*Q9HCM7*)	12q24.33	E,S	M
139495 (*NM_153023*)	13q12.12	S	P
169840 (*GSH1*)	13q12.2	S	M
102760 (*NM_014059*)	13q14.11	S	M
152207 (*CYSLTR2*)	13q14.2	S	P
171945 (*NM_030970*)	13q14.3	S	P
178215 (*Q8N7V5*)	13q21.1	E,S	M
178205 (*Q8N7V5*)	13q21.1	S	M
178200 (*Q8N7V5*)	13q21.1	S	P
177527 (*Q8N7F4*)	13q21.31	E,S	P
185498	13q21.32	E,S	P
152192 (*POU4F1*)	13q31.1	S	M
171650 (*PTMA*)	13q31.1	S	P
184052	13q31.1	E	P
165300 (*Y918*)	13q31.2	S	P
139800 (*ZIC5*)	13q32.3	S	M
102466 (*FGF14*)	13q33.1	E	M
185950 (*IRS2*)	13q34	S	M
153481 (*NM_018210*)	13q34	S	M
126218 (*F10*)	13q34	S	M
186009 (*ATP4B*)	13q34	S	M
184497 (*FAM70B*)	13q34	E,S	M
185989 (*RASA3*)	13q34	S	M
176294 (*OR4N2*)	14q11.2	E	P
136367 (*ZFHX2*)	14q11.2	S	M
176165 (*FOXG1C*)	14q12	E,S	P
136352 (*TITF1*)	14q13.3	S	M
186215 (*Q86SZ3*)	14q13.3	S	P
136327 (*NKX2-8*)	14q13.3	S	P
151338 (*MIPOL1*)	14q13.3	E	M
151748 (*SAV1*)	14q22.1	E	M
073712 (*PLEKHC1*)	14q22.1	E,S	P
125378 (*BMP4*)	14q22.2	S	M
184302 (*SIX6*)	14q23.1	S	P
177126 (*C14orf141*)	14q24.3	S	P
183992	14q31.1	E,S	M
140093 (*SERPINA10*)	14q32.13	E	P
036530 (*CYP46A1*)	14q32.2	S	P
140107 (*Q86U14*)	14q32.2	E	M
185469 (*RTL1*)	14q32.31	E,S	M
066735 (*KIF26A*)	14q32.33	E	M
184601 (*Q8N912*)	14q32.33	S	M
130235 (*NM_032714*)	14q32.33	S	M
184916 (*JAG2*)	14q32.33	S	M
184552 (*Q8NAF8*)	14q32.33	S	M
182351 (*CRIP1*)	14q32.33	S	M
177199 (*IGHA2*)	14q32.33	S	M
177154 (*IGHE*)	14q32.33	S	P
177145 (*IGHG1*)	14q32.33	S	M
126309 (*HV1A*)	14q32.33	S	P
126290 (*HV2A*)	14q32.33	E,S	P
151802 (*Q9P168*)	15q13.1	E,S	P
103832 (*O60374*)	15q13.2	E	P
134146 (*NM_080650*)	15q14	S	P
179315	15q14	S	P
184263	15q21.2	S	P
169856 (*ONECUT1*)	15q21.3	S	M
069667 (*RORA*)	15q22.2	S	M
138622 (*HCN4*)	15q24.1	S	M
186690	15q24.3	S	P
140557 (*SIAT8B*)	15q26.1	S	P
183643 (*C15orf32*)	15q26.1	E	M
184254 (*ALDH1A3*)	15q26.3	S	M
140479 (*PACE4*)	15q26.3	S	M
103326 (*SOLH*)	16p13.3	S	M
127585 (*NM_153350*)	16p13.3	S	M
127586 (*CHTF18*)	16p13.3	S	M
005513 (*SOX8*)	16p13.3	E,S	P
172268 (*Q96S05*)	16p13.3	E,S	P
172257 (*Q96S03*)	16p13.3	S	P
184471	16p13.3	S	M
073761 (*CACNA1H*)	16p13.3	S	M
140650 (*PMM2*)	16p13.2	S	P
182375	16p11.2	S	P
185836	16p11.2	S	P
102924 (*CBLN1*)	16q12.1	S	M
103449 (*SALL1*)	16q12.1	E,S	M
183022	16q12.2	S	M
103005 (*C16orf57*)	16q13	E,S	M
102890 (*ELMO3*)	16q22.1	S	P
102977 (*ACD*)	16q22.1	E,S	M
103056 (*SMPD3*)	16q22.1	S	M
103241 (*FOXF1*)	16q24.1	E,S	M
179588 (*ZFPM1*)	16q24.2	S	M
051523 (*CYBA*)	16q24.2	S	M
183788 (*Q8N206*)	16q24.3	E,S	M
183518	17p13.3	E,S	M
183688 (*NM_182705*)	17p13.3	S	M
167874 (*TMEM88*)	17p13.1	E,S	M
109061 (*MYH1*)	17p13.1	S	P
108448 (*TRIM16*)	17p12	E	M
160516 (*RPS28*)	17p11.2	S	M
181977 (*PYY2*)	17q11.2	E,S	P
184142 (*TIAF1*)	17q11.2	E	M
108587 (*GOSR1*)	17q11.2	S	P
172716 (*NM_152270*)	17q12	S	M
171532 (*NEUROD2*)	17q12	S	P
173917 (*HOXB2*)	17q21.32	E,S	M
120093 (*HOXB3*)	17q21.32	E,S	M
182742 (*HOXB4*)	17q21.32	S	M
108511 (*HOXB6*)	17q21.32	S	M
120068 (*HOXB8*)	17q21.32	S	M
141378 (*YCE7*)	17q23.2	E,S	M
121068 (*TBX2*)	17q23.2	S	M
187013 (*C17orf82*)	17q23.2	E	M
136492 (*BRIP1*)	17q23.2	S	P
125398 (*SOX9*)	17q24.3	S	P
161547 (*SFRS2*)	17q25.1	E	M
167281	17q25.3	S	P
141570 (*CBX8*)	17q25.3	S	M
141582 (*CBX4*)	17q25.3	S	M
175901 (*Q8NBT7*)	17q25.3	S	M
181428 (*Q8N8L1*)	17q25.3	E,S	P
181409 (*AATK*)	17q25.3	S	M
187207	17q25.3	S	M
186765 (*FSCN2*)	17q25.3	S	P
184703 (*SIRT7*)	17q25.3	S	M
184715 (*NM_032711*)	17q25.3	S	M
169750 (*RAC3*)	17q25.3	S	P
169727 (*GPS1*)	17q25.3	S	M
154655 (*NM_173464*)	18p11.31	S	P
067900 (*ROCK1*)	18q11.1	S	M
141448 (*GATA6*)	18q11.2	E	M
141441 (*FAM59A*)	18q12.1	E,S	P
101746 (*NOL4*)	18q12.1	S	M
101489 (*BRUNOL4*)	18q12.2	E,S	M
152217 (*SETBP1*)	18q12.3	E	P
183677 (*ELA2*)	18q21.1	S	M
141644 (*MBD1*)	18q21.1	S	M
041353 (*RAB27B*)	18q21.2	E	P
141668 (*NM_182511*)	18q22.3	S	P
141665 (*NM_152676*)	18q22.3	S	P
101544 (*NM_014913*)	18q23	S	M
178184 (*PARD6G*)	18q23	S	P
141934 (*PPAP2C*)	19p13.3	E,S	M
118050 (*NM_017914*)	19p13.3	S	M
180866 (*Q8NB05*)	19p13.2	E,S	P
105655 (*NM_016368*)	19p13.11	S	M
172684 (*Q8NE65*)	19p13.11	E,S	P
172666	19p13.11	E,S	P
187135	19q12	S	M
121297 (*TSH3*)	19q12	E,S	P
130876 (*SLC7A10*)	19q13.11	S	M
124302 (*CHST8*)	19q13.11	E,S	M
105698 (*USF2*)	19q13.12	S	M
126266 (*GPR40*)	19q13.12	S	M
105663 (*TRX2*)	19q13.12	E	M
180458 (*Q8N3U1*)	19q13.13	E,S	P
105737 (*GRIK5*)	19q13.2	S	M
159904 (*ZNF225*)	19q13.31	E,S	P
167383 (*ZNF229*)	19q13.31	E,S	M
176499 (*Q9Y4U5*)	19q13.33	E	M
175856 (*Q8NB48*)	19q13.41	E	M
186818 (*LILRB4*)	19q13.42	E,S	M
105132 (*ZN550*)	19q13.43	E,S	M
130724 (*CHMP2A*)	19q13.43	E,S	M
099326 (*ZNF42*)	19q13.43	E,S	M
175487 (*Q9BPX8*)	19q13.43	S	P
178591 (*DEFB125*)	20p13	S	M
088782 (*DEFB127*)	20p13	S	P
125906 (*Q9H4I0*)	20p13	E	P
125861 (*GFRA4*)	20p13	S	P
101230 (*C20orf82*)	20p12.1	E,S	P
172264 (*C20orf133*)	20p12.1	S	M
125798 (*FOXA2*)	20p11.21	S	M
125810 (*C1QR1*)	20p11.21	S	M
125831 (*CST11*)	20p11.21	S	M
154930 (*ACAS2L*)	20p11.21	E	P
183029 (*Q8NCY9*)	20q11.21	S	P
026559 (*KCNG1*)	20q13.13	S	P
124222 (*STX16*)	20q13.32	E	P
179242 (*CDH4*)	20q13.33	S	M
101180 (*HRH3*)	20q13.33	S	M
130702 (*LAMA5*)	20q13.33	S	M
174407 (*C20orf166*)	20q13.33	S	M
101188 (*NTSR1*)	20q13.33	S	M
101189 (*C20orf20*)	20q13.33	E,S	M
060491 (*OGFR*)	20q13.33	S	M
092758 (*COL9A3*)	20q13.33	E,S	M
101204 (*CHRNA4*)	20q13.33	E	M
075043 (*KCNQ2*)	20q13.33	S	M
130589 (*P285*)	20q13.33	E	M
125520 (*SLC2A4RG*)	20q13.33	S	M
171700 (*RGS19*)	20q13.33	S	M
171695 (*Q8TD35*)	20q13.33	S	P
181872	20q13.33	S	P
175302 (*Q9NSI9*)	21q11.2	S	P
184856 (*C21orf74*)	21q21.1	E	P
186930 (*KRTAP6-2*)	21q22.11	S	P
185569 (*OLIG2*)	21q22.11	S	M
159263 (*SIM2*)	21q22.13	E,S	P
183067 (*Q9NSI5*)	21q22.2	E	P
141956 (*PRDM15*)	21q22.3	S	M
014442 (*ADARB1*)	21q22.3	E	M
182586 (*C21orf89*)	21q22.3	E	P
186866 (*C21orf80*)	21q22.3	S	P
187153	21q22.3	S	M
142156 (*COL6A1*)	21q22.3	S	M
160294 (*MCM3AP*)	21q22.3	E	M
160305 (*DIP2*)	21q22.3	S	M
160307 (*S100B*)	21q22.3	E	P
160310 (*HRMT1L1*)	21q22.3	E	P
183628 (*DGCR6*)	22q11.21	E,S	P
100075 (*SLC25A1*)	22q11.21	S	M
183099	22q11.21	E,S	M
100208 (*IGLC1*)	22q11.22	S	P
186746	22q11.22	E	M
178803 (*Q8NAW6*)	22q11.23	S	P
100104 (*SRR1*)	22q12.1	E	M
169184 (*MN1*)	22q12.1	S	P
184390 (*Q6ICM0*)	22q12.2	E,S	P
166897 (*Q96PY3*)	22q13.1	S	P
184687 (*Q8ND38*)	22q13.31	E,S	P
075275 (*CELSR1*)	22q13.31	E	M
182858 (*NM_024105*)	22q13.33	S	M
128159 (*TUBGCP6*)	22q13.33	S	M
185386 (*MAPK12*)	22q13.33	S	M
100239 (*K685*)	22q13.33	S	P
025770 (*NM_014551*)	22q13.33	S	M
182786	22q13.33	S	P

Genes predicted to be imprinted by both the linear and RBF kernel classifiers learned by Equbits are denoted by E, and those predicted by both the linear and RBF kernel classifiers learned by SMLR by S. Genes predicted to be imprinted by both programs are denoted by E,S and represent the 'high-confidence' set presented in Table 1 of the article. Genes predicted to be expressed from the maternal or paternal allele are denoted by M or P, respectively. To enhance legibility, the common prefix "ENSG00000" has been dropped from the Ensembl ID.

Table 2. Chromosomal bands with high frequencies of genes proved or predicted with high confidence to be imprinted.

Band	Freq. (# known)	P	Novel candidates
11p15.5	10/82 (5)	$< 3 \times 10^{-16}$	*PKP3*, an oncogene involved in lung cancer (Furukawa et al., 2005), located distal to the *IGF2/H19* cluster.
1p36.32	5/24 (1)	$< 3 \times 10^{-16}$	*PRDM16*, whose orthologue was also predicted to be imprinted in mouse (Luedi et al., 2005), and is associated with leukemia (Du et al., 2005).
7p15.2	6/26 (0)	$< 3 \times 10^{-16}$	Several loci are involved in development and are susceptible to epigenetic regulation.
10q26.3	6/44 (0)	9×10^{-16}	*NKX6-2*, which was also predicted to be imprinted in the mouse (Luedi et al., 2005), is preferentially expressed in the brain (Lee et al., 2001). *NKX6-2*, along with five neighboring candidate genes, was predicted to show maternal expression. This region on 10q26 is near the marker D10S217, which has been found to be maternally linked to male sexual orientation (Mustanski et al., 2005). A germline differentially methylated region was found in this region (Strichman-Almashanu et al., 2002), lending further support to the prediction of imprinted genes within the immediate vicinity of this region.
14q32.31	2/5 (1)	1×10^{-11}	*RTL1*, imprinted in the mouse (Seitz et al., 2003) and sheep (Charlier et al., 2001).
15q12	2/6 (2)	7×10^{-10}	
7q21.3	4/35 (4)	2×10^{-8}	

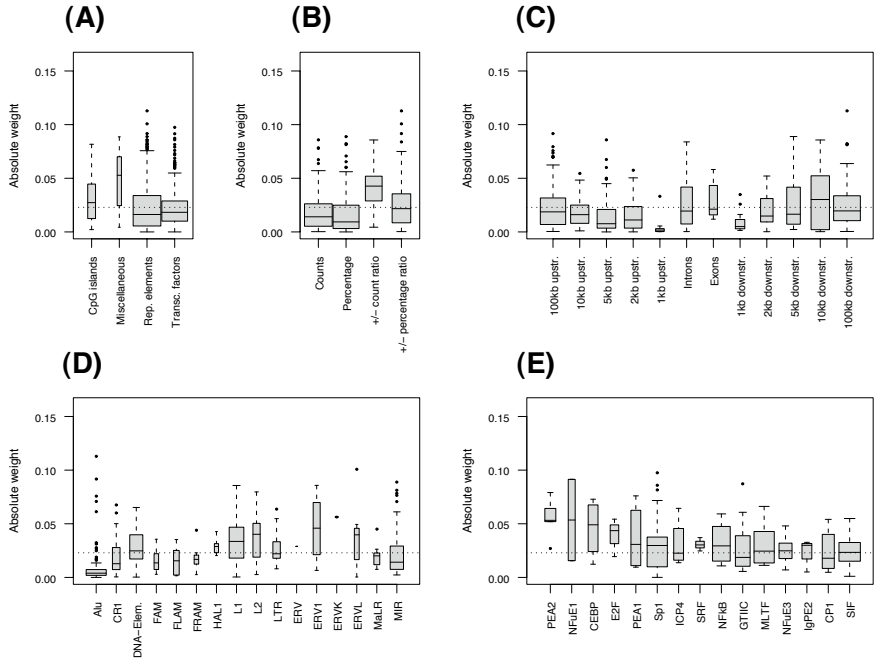
P-values derived from a χ^2-test with 1 degree of freedom.

Table 3. High-confidence imprinted gene candidates predicted in human and mouse.

Gene	Band	Expression		Description
		Human	Mouse	
GFI1	1p22	P	M	Oncogenic growth factor (Gilks et al., 1993), also involved in development (Moroy, 2005).
PRDM16, MEL1	1p36	P	P	Myeloid leukemia gene (Du et al., 2005).
Q96PX6	2p16	P	P	
MAGI2, ACVRIP1, AIP1	7q21	M	M	Specifically expressed in human brain and interacts specifically with atrophin-1 (Wood et al., 1998). A mutation in atrophin-1 causes dentatorubral and pallidoluysian atrophy (DRPLA), a progressive neurodegenerative disorder (Li et al., 1993; Koide et al., 1994; Nagafuchi et al., 1994). *MAGI2* is also involved in zebrafish development (Wright et al., 2004)
LY6D	8q24	P	M	Expressed in head and neck squamous carcinoma (Kato et al., 1998; Brakenhoff et al., 1999)
KCNK9	8q24	M	M	K^+ channel protein involved in neuron apoptosis and cell tumorigenesis (Patel and Lazdunski, 2004).
NKX6-2	10q26	M	M	Shows tissue-specific regulation with highest expression in the brain (Lee et al., 2001) and is located near marker D10S217 that Mustanski et al. (2005) found was maternally linked to male sexual orientation.
ENSG00000184682	11p15	M	M	Contained within an intron of *LSP1*, both in human and in mouse.
FOXG1C	14q12	P	P	Shows haploinsufficiency in a patient with severe mental retardation, brain malformations and microcephaly (Shoichet et al., 2005). Mouse orthologue is essential for normal development of the telencephalon (Xuan et al., 1995).
NM_024598	16q13	M	M	

Genes predicted to be expressed from the maternal or paternal allele are denoted by M or P, respectively. For brevity, we did not include genes previously known to be imprinted.

Equbits



SMLR

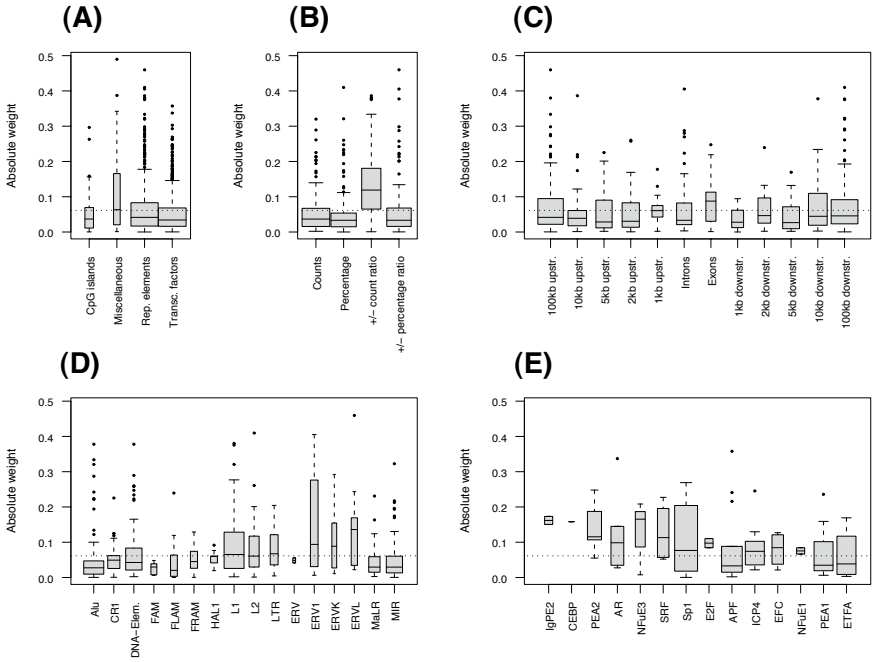


Figure 1. Distributions of the weights of features characteristic of imprinted genes, as determined by two feature selection methods, those of Equbits and SMLR. Absolute weights are shown as box plots, the dotted line represents the overall mean of all selected features. (*A*) Distribution of feature type. (*B*) Distribution of different ways of quantifying repetitive elements. Ratios of $\pm$ counts carried the greatest weight ($P < 6 \times 10^{-11}$). (*C*) Distribution of different repetitive element locations. The 1 kb downstream window was of least importance ($P < 1 \times 10^{-3}$). (*D*) Distribution of different families of repetitive elements. Alus carried the lowest weight ($P < 4 \times 10^{-3}$), whereas endogenous retroviruses were of greatest importance ($P < 3 \times 10^{-3}$). (*E*) Distribution of counts of the highest scoring transcription factor binding sites.

Table 4. Relevant features for prediction of imprinting by Equbits classifiers.

		Mean (Standard deviation)				
Feature	Weight	All Genes		Imprinted		P
downstream 10:100 SINE_Alu± [2]	−16.96	4.11	(61.50)	1.68	(0.81)	4.76×10^{-9}
downstream 10:100 AluS± [2]	11.28	16.89	(162.70)	161.12	(557.13)	5.70×10^{-2}
upstream 60:0 LTR_ERVL± [2]	10.08	11.31	(21.28)	34.03	(55.48)	7.28×10^{-3}
upstream 9:8 Sp1 [1]	−9.75	0.34	(1.09)	0.15	(0.53)	1.64×10^{-2}
upstream 100:10 AluJ± [2]	9.16	61.09	(228.98)	193.30	(372.53)	1.63×10^{-2}
upstream 5:4 NFuE1 [1]	9.14	0.04	(0.21)	0.13	(0.33)	6.88×10^{-2}
downstream 0:5 MIR3 [2]	8.89	0.33	(0.99)	0.45	(1.34)	2.91×10^{-1}
upstream 100:downstream 100 CCACGTGG within THE1B/B-int elements [3]	8.86	0.13	(0.33)	0.30	(0.46)	1.31×10^{-2}
upstream 8:7 GTIIC [1]	8.73	0.34	(0.61)	0.53	(0.78)	7.02×10^{-2}
upstream 3:2 Sp1 [1]	8.59	0.36	(1.13)	0.93	(1.40)	8.41×10^{-3}
upstream 5:0 LTR_ERV1 [1]	8.58	0.36	(1.07)	0.58	(2.11)	2.68×10^{-1}
downstream 5:10 L1ME± [1]	−8.57	0.01	(0.99)	−0.28	(1.18)	6.79×10^{-2}
intron LTR_ERV1± [2]	8.39	173.80	(743.12)	617.58	(1711.93)	5.68×10^{-2}
upstream 100:downstream 100 CCACGTGG within THE1B/B-int elements [1]	8.27	0.15	(0.43)	0.43	(0.78)	1.70×10^{-2}
downstream 10:100 L1M4 [2]	8.22	0.70	(1.11)	1.45	(1.77)	5.85×10^{-3}
intron CpGi [2]	8.17	44.47	(86.92)	102.33	(186.25)	2.98×10^{-2}
upstream 10:9 Sp1 [1]	−8.15	0.34	(1.11)	0.30	(0.61)	3.46×10^{-1}
downstream 10:100 L1P [2]	−8.14	0.31	(1.06)	0.14	(0.58)	3.61×10^{-2}
downstream 10:100 SINE_MIR± [1]	−8.13	0.11	(2.25)	−0.41	(2.31)	8.33×10^{-2}
upstream 50:0 L2± [1]	7.97	0.29	(2.90)	1.05	(4.42)	1.47×10^{-1}
upstream 100:10 L1ME± [1]	−7.94	0.29	(4.79)	−1.72	(3.94)	1.42×10^{-3}
upstream 2:1 PEA2 [1]	7.91	0.02	(0.15)	0.05	(0.22)	2.18×10^{-1}
upstream 5:4 AP1 [1] × downstream 0:100 MLT1C phase change [2]	−7.89	0.77	(2.32)	0.03	(0.16)	0
downstream 0:5 MIR3 [1]	7.84	0.14	(0.41)	0.18	(0.50)	3.43×10^{-1}
downstream 5:10 L1PB [1]	7.79	0.04	(0.29)	0.13	(0.56)	1.75×10^{-1}
upstream 100:10 DNA_Tip100 [1] × upstream 6:5 GTIIC [3]	−7.77	0.18	(0.72)	0.00	(0.00)	0
downstream 0:5 MIR3± [1]	7.65	0.01	(0.41)	0.10	(0.44)	1.01×10^{-1}
upstream 4:3 PEA1 [1]	7.6	0.10	(0.32)	0.13	(0.40)	3.50×10^{-1}
upstream 100:10 AluJ± [1]	7.57	0.27	(2.37)	1.17	(2.83)	2.73×10^{-2}
intron LTR_ERV1± [1]	−7.53	−0.49	(2.02)	−1.75	(4.90)	5.78×10^{-2}
downstream 5:10 L1MC± [2]	7.5	71.64	(271.78)	129.05	(386.82)	1.80×10^{-1}
upstream 100:10 L1MA± [1]	7.36	0.07	(2.70)	1.13	(3.64)	3.81×10^{-2}
upstream 6:5 SIF [3] × upstream 2:0 BPVE2 [3]	−7.31	0.13	(0.33)	0.00	(0.00)	0
upstream 9:8 CEBP [1]	7.29	0.04	(0.20)	0.10	(0.38)	1.64×10^{-1}
downstream 40:100 LTR_ERV1± [1]	7.26	0.59	(2.87)	1.95	(6.14)	8.60×10^{-2}
exon 0.225:0.41 nucleosome potential [2]	−7.22	0.67	(0.92)	−0.10	(1.06)	2.65×10^{-5}
upstream 3:2 Sp1 [3]	7.17	0.21	(0.41)	0.43	(0.50)	5.46×10^{-3}
downstream 5:10 Alu [2]	7.08	0.01	(0.06)	0.01	(0.09)	3.05×10^{-1}
upstream 100:10 MIR3± [1]	7.07	0.14	(1.84)	0.51	(1.74)	9.53×10^{-2}
upstream 3:2 BPVE2 [1] × upstream 1:0 Pit1 [3]	−7.06	0.14	(0.44)	0.00	(0.00)	0
upstream 30:20 CpGi [2,10]	7.02	0.13	(0.28)	0.17	(0.35)	2.47×10^{-1}
upstream 100:10 LTR_ERV1± [2]	−6.98	459.12	(1253.59)	183.25	(433.61)	1.56×10^{-4}
upstream 100:10 L1MC± [1]	6.96	0.24	(4.23)	1.23	(5.64)	1.40×10^{-1}
upstream 8:7 EFC [1]	6.87	0.00	(0.04)	0.03	(0.16)	1.82×10^{-1}
upstream 8:7 GT2B [1] × upstream 9:8 Sp1 [3]	−6.86	0.11	(0.44)	0.00	(0.00)	0
upstream 9:8 Sp1 [3] × upstream 8:7 GT2B [3]	−6.82	0.08	(0.27)	0.00	(0.00)	0
downstream 5:10 LINE_L2± [2]	6.8	106.50	(243.27)	116.37	(272.10)	4.11×10^{-1}
upstream distance to closest recomb. hotspot	−6.79	315.02	(1369.12)	122.40	(94.52)	0
upstream 100:10 L1M4± [2] × upstream 1:0 MLTF [3]	−6.78	229.05	(605.18)	25.45	(91.09)	0
upstream 8:7 SIF [3] × upstream 5:0 ETFA [3]	−6.76	0.06	(0.24)	0.00	(0.00)	0
upstream 5:0 LINE_CR1± [2]	6.75	12.41	(69.05)	38.48	(121.07)	9.33×10^{-2}
intron L1M2 [1]	−6.73	0.05	(0.37)	0.00	(0.00)	0
upstream 5:4 AP1 [3] × downstream 0:100 MLT1C phase change [2]	−6.71	0.34	(0.85)	0.03	(0.16)	5.55×10^{-16}
upstream 9:8 MLTF [3]	6.62	0.57	(0.50)	0.70	(0.46)	4.03×10^{-2}
upstream 5:4 AP1 [1] × downstream 0:100 MLT1C phase change [2]	−6.59	0.23	(0.69)	0.01	(0.08)	0
upstream 6:5 SIF [1] × upstream 2:0 BPVE2 [3]	−6.57	0.16	(0.50)	0.00	(0.00)	0
upstream 0.83:0.61 nucleosome potential [1]	−6.55	182.33	(154.05)	102.79	(169.84)	2.87×10^{-3}
downstream 5:10 L1MC [2]	6.54	0.78	(2.85)	1.29	(3.87)	2.06×10^{-1}
downstream 5:10 DNA_MER2_type± [2]	6.52	46.30	(230.76)	190.05	(602.01)	7.20×10^{-2}
downstream 5:10 CpGi [1] × upstream 10:9 NFuE5 [3]	−6.51	0.12	(0.44)	0.00	(0.00)	0
upstream 7:6 NFuE5 [3]	6.47	0.28	(0.45)	0.35	(0.48)	1.73×10^{-1}
upstream 8:7 SIF [1] × upstream 8:7 BPVE2 [3]	−6.45	0.10	(0.37)	0.00	(0.00)	0
upstream 8:7 ICP4 [1]	−6.44	0.05	(0.24)	0.03	(0.16)	1.58×10^{-1}
upstream 4:3 PEA2 [1]	6.43	0.02	(0.13)	0.10	(0.30)	4.92×10^{-2}
upstream 100:10 DNA_Tip100 [1] × upstream 3:2 Pit1 [3]	−6.42	0.29	(0.89)	0.00	(0.00)	0
downstream 0:100 MLT1A0 phase change [1]	6.37	0.40	(0.86)	0.83	(1.03)	7.45×10^{-3}
upstream 1:0 BPVE2 [1] × upstream 10:9 NFuE5 [3]	−6.32	0.12	(0.40)	0.00	(0.00)	0
upstream 9:8 MLTF [1]	6.31	0.91	(1.13)	1.23	(1.10)	4.28×10^{-2}
upstream 7:6 NFuE4 [1]	6.29	0.04	(0.21)	0.05	(0.22)	3.85×10^{-1}
upstream 100:10 DNA_Tip100± [2]	−6.24	90.37	(251.03)	69.05	(309.29)	3.35×10^{-1}
upstream 9:8 CEBP [3]	6.22	0.04	(0.19)	0.08	(0.27)	1.99×10^{-1}
upstream 2:0 Oct1 [3]	6.18	0.61	(0.49)	0.73	(0.45)	5.29×10^{-2}
upstream 10:9 GT2B [1] × upstream 3:2 Pit1 [3]	−6.17	0.17	(0.49)	0.00	(0.00)	0
downstream 5:10 AluY± [2]	6.12	80.80	(155.01)	145.40	(217.27)	3.55×10^{-2}
downstream 10:100 MIR± [1]	−6.11	0.12	(2.35)	−0.23	(2.46)	1.84×10^{-1}
upstream 2:0 CpGi [1] × upstream 9:8 E4F1 [3]	−6.08	0.07	(0.26)	0.00	(0.00)	0
upstream 8:7 GTIIC [3]	6.07	0.28	(0.45)	0.38	(0.49)	1.05×10^{-1}

downstream 10:100 FLAM$\pm^{2}$ × upstream 10:9 ATF^{1}	−6.06	34.06	(129.03)	0.22	(0.62)	0
upstream 40:30 CpGi^{1,10}	6.05	0.36	(0.85)	0.45	(1.30)	3.28×10^{-1}
downstream 5:10 DNA_MER2_type^{2}	6.03	0.50	(2.39)	1.90	(6.02)	7.69×10^{-2}
upstream 6:5 ATF^{3}	6.01	0.36	(0.48)	0.48	(0.51)	7.39×10^{-2}
upstream 5:0 LINE_CR1^{2}	6	0.26	(1.42)	0.77	(2.42)	9.71×10^{-2}
upstream 9:8 Sp1^{3} × upstream 1:0 ICSBP^{3}	−5.95	0.14	(0.35)	0.00	(0.00)	0
upstream 7:6 NFkB^{3}	5.92	0.08	(0.27)	0.15	(0.36)	1.14×10^{-1}
upstream 100:10 HAL1$\pm^{2}$ × upstream 9:8 TFIID^{3}	−5.86	141.37	(392.44)	13.28	(47.90)	0
upstream 2:0 MIR^{2} × upstream 8:7 GT2B^{3}	−5.85	0.79	(2.90)	0.00	(0.00)	0
downstream 10:100 DNA^{1} × upstream 10:9 PU1^{3}	−5.83	0.23	(0.66)	0.00	(0.00)	0
exon LINE_L2$\pm^{1}$	5.82	0.00	(0.23)	0.05	(0.22)	8.77×10^{-2}
upstream 100:10 DNA_Tip100^{1} × upstream 8:7 ICSBP^{3}	−5.79	0.53	(1.14)	0.08	(0.27)	1.61×10^{-13}
upstream 100:10 DNA_Tip100^{2} × upstream 8:7 ICSBP^{3}	−5.78	0.09	(0.27)	0.01	(0.04)	0
upstream 2:0 L1M2$\pm^{1}$	5.74	0.00	(0.10)	0.03	(0.16)	1.82×10^{-1}
upstream 100:10 L1P^{1}	−5.71	0.42	(0.96)	0.28	(0.55)	6.08×10^{-2}
downstream 5:10 LTR_ERVK$\pm^{1}$	−5.7	0.00	(0.26)	−0.15	(0.95)	1.64×10^{-1}
downstream 0:1 CpGi^{1}	−5.68	0.04	(0.19)	0.03	(0.16)	2.86×10^{-1}
upstream 100:10 HAL1^{1} × upstream 8:7 GT2B^{1}	−5.66	0.49	(1.88)	0.03	(0.16)	0
downstream 10:100 MIR3$\pm^{2}$ × upstream 4:3 GATA1^{1}	−5.65	48.09	(147.61)	1.72	(9.34)	0
downstream 5:10 LTR_ERVK^{1}	5.64	0.03	(0.27)	0.15	(0.95)	2.23×10^{-1}
downstream 10:100 L1MB^{2}	5.61	1.24	(1.54)	1.67	(2.02)	9.54×10^{-2}
upstream 2:0 MIR^{1} × upstream 8:7 GT2B^{3}	−5.58	0.12	(0.45)	0.00	(0.00)	0
upstream 100:10 DNA$\pm^{2}$	5.57	45.51	(150.10)	99.38	(312.29)	1.44×10^{-1}
downstream 10:100 LTR_ERVK^{2}	5.55	0.38	(1.24)	0.83	(1.89)	7.35×10^{-2}
upstream 9:8 Sp1^{3} × upstream 10:0 CpGi^{1,11}	−5.53	0.66	(1.70)	0.08	(0.27)	0
upstream 2:1 SIF^{3}	5.49	0.24	(0.43)	0.28	(0.45)	3.22×10^{-1}
downstream 0:100 LTR phase change^{2,99}	5.48	0.29	(0.28)	0.40	(0.27)	1.09×10^{-2}
upstream 100:10 DNA_Tip100^{1} × upstream 8:7 ICSBP^{1}	−5.47	1.00	(2.50)	0.10	(0.38)	0
upstream 5:0 CpGi^{1} × upstream 9:8 E4F1^{3}	−5.46	0.09	(0.32)	0.00	(0.00)	0
upstream 10:5 L1MC^{2}	−5.45	0.77	(2.82)	0.57	(2.26)	2.83×10^{-1}
upstream 4:3 E2F^{1}	−5.43	0.01	(0.11)	0.00	(0.00)	0
upstream 2:0 SINE_MIR^{2} × upstream 8:7 GT2B^{3}	−5.42	0.93	(3.19)	0.00	(0.00)	0
upstream 1:0 CP1^{3}	−5.41	0.07	(0.25)	0.03	(0.16)	5.73×10^{-2}
downstream 0:5 DNA_Tip100^{2}	−5.4	0.10	(1.02)	0.00	(0.00)	0
downstream 10:100 L1MC^{1} × downstream 0:100 MLT1C phase change^{2}	−5.39	1.96	(5.89)	0.13	(0.40)	0
downstream 5:10 CpGi2^{1}	5.37	2.26	(2.27)	2.93	(2.55)	5.61×10^{-2}
intron CpGi^{3}	5.36	0.08	(0.27)	0.28	(0.45)	5.48×10^{-3}
intron CpGi^{1}	5.35	0.47	(1.10)	1.05	(1.52)	1.10×10^{-2}
downstream 0:2 AluY^{1} × upstream 10:9 MLTF^{3}	−5.33	0.07	(0.30)	0.00	(0.00)	0
upstream 9:8 PEA2^{1}	−5.32	0.02	(0.14)	0.03	(0.16)	4.06×10^{-1}
upstream 350:350 downstream recomb^{1}	5.28	4.84	(2.75)	6.15	(2.18)	2.96×10^{-4}
downstream 5:10 DNA_MER1_type^{1} × upstream 3:2 Pit1^{3}	−5.27	0.15	(0.53)	0.00	(0.00)	0
upstream 10:5 LTR_MaLR$\pm^{2}$ × upstream 6:5 APF^{3}	−5.26	94.23	(233.79)	3.92	(23.86)	0
upstream 9:8 ATF^{3} × upstream 5:4 NFuE5^{3}	−5.25	0.11	(0.31)	0.00	(0.00)	0
upstream 100:10 L1PB^{2}	5.24	0.49	(1.48)	0.69	(1.89)	2.64×10^{-1}
downstream 5:10 L1MD$\pm^{1}$	5.23	0.00	(0.47)	0.00	(0.45)	5.00×10^{-1}
downstream 0:2 MIR^{2}	5.21	1.73	(3.99)	1.80	(4.79)	4.63×10^{-1}
upstream 5:0 PEA2^{3}	5.2	0.12	(0.32)	0.25	(0.44)	3.12×10^{-2}
upstream 9:8 Sp1^{1} × upstream 1:0 ICSBP^{3}	−5.19	0.24	(0.93)	0.00	(0.00)	0
downstream 5:10 LINE_L2^{2}	5.18	1.52	(3.00)	1.65	(3.31)	3.99×10^{-1}
upstream 100:10 L1MB$\pm^{2}$ × upstream 5:4 ATF^{3}	−5.17	188.41	(642.54)	6.87	(40.74)	0
intron DNA$\pm^{1}$	−5.16	0.00	(0.50)	−0.15	(0.58)	5.62×10^{-2}
intron MIR3^{2} × upstream 4:3 TFIID^{1}	−5.15	16.59	(66.36)	1.43	(6.31)	0
downstream 10:100 MIR3$\pm^{2}$ × upstream 4:3 GATA1^{3}	−5.12	33.26	(88.69)	1.62	(9.32)	0
upstream 2:0 LINE_L2^{1} × upstream 5:4 GATA1^{3}	−5.11	0.14	(0.48)	0.00	(0.00)	0
upstream 9:8 NFkB^{1}	5.08	0.08	(0.29)	0.13	(0.40)	2.45×10^{-1}
upstream 10:9 NFuE5^{3} × upstream 1:0 BPVE2^{3}	−5.07	0.10	(0.30)	0.00	(0.00)	0
downstream 10:100 L1M4$\pm^{1}$	5.06	0.05	(2.87)	0.79	(3.97)	1.26×10^{-1}
I^{5} × downstream 10:100 DNA_Mariner^{1}	−5.05	0.17	(0.57)	0.00	(0.00)	0
upstream 2:0 LINE_L2^{2}	5.04	2.88	(7.56)	3.35	(10.80)	3.93×10^{-1}
downstream 5:10 CpGi^{1} × upstream 10:9 NFuE5^{1}	−5.03	0.15	(0.63)	0.00	(0.00)	0
downstream 10:100 FLAM$\pm^{2}$ × upstream 10:9 ATF^{3}	−5.02	25.49	(84.33)	0.22	(0.62)	0
upstream 5:0 LINE_CR1$\pm^{1}$	−5.01	0.01	(0.36)	−0.10	(0.50)	9.50×10^{-2}
upstream 7:6 NFkB^{1}	4.98	0.08	(0.29)	0.15	(0.36)	1.27×10^{-1}
upstream 5:0 L1M2$\pm^{1}$	4.97	0.00	(0.16)	0.03	(0.16)	1.94×10^{-1}
downstream 10:100 LTR_ERV1^{2}	−4.96	2.65	(3.61)	2.50	(3.07)	3.82×10^{-1}
downstream 10:100 DNA_Mariner^{1} × upstream 3:2 MLTF^{3}	−4.95	0.23	(0.64)	0.00	(0.00)	0
downstream 50:90 LTR_ERVL$\pm^{1}$	4.94	0.43	(1.55)	1.19	(2.30)	2.34×10^{-2}
upstream 90:20 MIR$\pm^{1}$	4.93	0.21	(2.27)	0.85	(2.69)	7.48×10^{-2}
upstream 5:0 LINE_CR1^{1}	4.92	0.07	(0.36)	0.20	(0.46)	5.03×10^{-2}
upstream 6:5 PEA1^{3}	4.91	0.10	(0.29)	0.18	(0.38)	1.01×10^{-1}
upstream 2:1 Oct1^{3}	4.9	0.42	(0.49)	0.50	(0.51)	1.62×10^{-1}
upstream 8:7 E4F1^{1}	4.89	0.20	(0.49)	0.45	(1.45)	1.49×10^{-1}
downstream 10:100 DNA^{2}	−4.88	0.06	(0.17)	0.02	(0.05)	2.98×10^{-6}
downstream 10:100 L1MC^{1} × downstream 0:100 MLT1C phase change^{2}	−4.86	0.59	(1.67)	0.06	(0.20)	0
downstream 10:100 DNA$\pm^{1}$	4.85	0.02	(0.80)	0.10	(0.50)	1.56×10^{-1}
upstream 4:3 E4F1^{3}	4.84	0.18	(0.38)	0.20	(0.41)	3.77×10^{-1}
upstream 10:5 LTR_ERV1$\pm^{1}$	4.83	0.01	(1.05)	0.13	(1.02)	2.47×10^{-1}
upstream 2:0 LINE_L2$\pm^{1}$	4.82	0.03	(0.68)	0.23	(0.58)	2.01×10^{-2}
downstream 5:10 MIR^{1}	−4.81	0.77	(1.14)	0.40	(0.50)	2.14×10^{-5}
upstream 3:2 NFuE3^{1}	4.8	0.08	(0.29)	0.15	(0.43)	1.49×10^{-1}

downstream 0:2 SINE_MIR^{2}	4.78	2.06	(4.34)	2.02	(4.90)	4.80×10^{-1}
exon DNA_MER2_type^{2}	4.76	0.18	(2.98)	2.21	(10.17)	1.09×10^{-1}
upstream 1:0 NFkB^{3}	4.75	0.11	(0.31)	0.08	(0.27)	2.33×10^{-1}
I^{5} × upstream 2:1 BPVE2^{3}	−4.74	0.16	(0.37)	0.00	(0.00)	0
upstream 2:0 DNA_MER1_type^{1} × upstream 6:5 AP1^{3}	−4.73	0.11	(0.40)	0.00	(0.00)	0
upstream 2:0 LTR_ERV1±^{2}	4.72	34.74	(150.24)	60.40	(234.23)	2.49×10^{-1}
upstream 5:4 SIF^{3} × upstream 4:3 PU1^{3}	−4.71	0.12	(0.32)	0.00	(0.00)	0
downstream 5:10 DNA_MER2_type±^{1}	−4.7	0.00	(0.56)	−0.18	(0.78)	8.61×10^{-2}
downstream 5:10 L1PA^{2}	−4.68	2.70	(10.90)	2.43	(10.47)	4.37×10^{-1}
upstream 9:8 SIF^{3} × m3_m11	−4.67	0.09	(0.29)	0.00	(0.00)	0
upstream 2:0 CpGi^{2}	4.66	152.21	(161.47)	222.15	(212.49)	2.33×10^{-2}
downstream 10:100 DNA_MER1_type^{2} × upstream 10:5 LTR_MaLR±^{2}	−4.63	128.89	(371.35)	6.60	(32.09)	0
downstream 5:10 L1PA±^{2}	−4.62	231.39	(1001.15)	179.41	(978.02)	3.71×10^{-1}
upstream 100:10 HAL1^{1} × upstream 8:7 GT2B^{3}	−4.61	0.37	(1.26)	0.03	(0.16)	0
downstream 0:5 LTR_ERV1^{1}	−4.59	0.28	(0.92)	0.10	(0.38)	3.00×10^{-3}
downstream 10:100 Other^{2}	−4.57	0.19	(0.60)	0.06	(0.27)	1.37×10^{-3}
upstream 6:5 NF1^{3}	4.56	0.12	(0.33)	0.18	(0.38)	2.00×10^{-1}
downstream 0:1 CpGi^{2}	−4.55	47.19	(117.94)	54.10	(122.05)	3.63×10^{-1}
downstream 10:100 FLAM±^{2} × upstream 100:10 MIR3±^{2}	−4.53	5099.30	(18824.72)	54.26	(133.79)	0
upstream 2:1 MLTF^{1}	4.52	0.96	(1.06)	1.10	(1.22)	2.34×10^{-1}
upstream 100:10 L1M1±^{1}	−4.51	0.04	(0.87)	−0.23	(0.97)	4.79×10^{-2}
upstream 5:0 LTR_MaLR±^{2}	−4.5	87.69	(215.92)	64.15	(132.75)	1.38×10^{-1}
upstream 10:5 LTR_MaLR±^{2} × upstream 100:10 LINE_L2^{2}	−4.49	315.39	(889.70)	25.95	(109.14)	0
downstream 10:100 L1MB^{1}	4.48	3.62	(3.92)	4.08	(3.86)	2.31×10^{-1}
downstream 10:100 L1PB±^{1}	−4.47	0.01	(1.37)	0.03	(1.05)	4.63×10^{-1}
upstream 80:70 CpGi^{1,10}	−4.46	0.34	(0.81)	0.23	(0.62)	1.21×10^{-1}
upstream 10:0 ETFA^{1} × upstream 10:9 E4F1^{3}	−4.45	0.14	(0.48)	0.00	(0.00)	0
upstream 5:0 LINE_L2±^{1}	4.44	0.05	(1.24)	0.30	(1.32)	1.23×10^{-1}
upstream 3:2 APF^{1} × downstream 0:100 MLT1C phase change^{2}	−4.43	1.01	(2.96)	0.05	(0.22)	0
upstream 10:5 LTR_MaLR^{2} × upstream 10:9 COUP^{3}	−4.42	1.26	(2.92)	0.12	(0.57)	7.77×10^{-16}
upstream 3:2 Oct1^{3} × downstream 0:100 MLT1C phase change^{2}	−4.41	0.05	(0.18)	0.00	(0.00)	0
downstream 0:5 FRAM±^{1}	−4.4	0.00	(0.23)	−0.05	(0.22)	8.06×10^{-2}
downstream 10:100 CpGi^{3} × upstream 100:10 L1MB±^{2}	−4.39	286.48	(761.12)	22.01	(95.07)	0
downstream 10:100 DNA_Mariner^{1} × upstream 10:0 ETFA^{3}	−4.38	0.17	(0.55)	0.00	(0.00)	0
downstream 35:68 L2±^{1}	4.37	0.52	(2.58)	0.98	(2.07)	8.56×10^{-2}
upstream 7:6 E2F^{1}	4.36	0.01	(0.10)	0.05	(0.22)	1.35×10^{-1}
upstream 5:4 NFuE5^{1} × upstream 9:8 ATF^{3}	−4.35	0.13	(0.43)	0.00	(0.00)	0
upstream 10:0 NFkB^{1}	4.34	0.85	(0.98)	1.08	(1.02)	9.27×10^{-2}
exon L1^{2}	4.33	0.03	(1.56)	0.17	(1.09)	2.13×10^{-1}
upstream 10:9 E4F1^{3} × upstream 3:2 MLTF^{3}	−4.32	0.10	(0.30)	0.00	(0.00)	0
upstream 6:5 MLTF^{3}	4.31	0.57	(0.50)	0.63	(0.49)	2.44×10^{-1}
upstream 5:0 CpGi^{1} × upstream 9:8 E4F1^{1}	−4.3	0.11	(0.43)	0.00	(0.00)	0
upstream 8:7 BPVE2^{3} × upstream 8:7 SIF^{3}	−4.29	0.09	(0.28)	0.00	(0.00)	0
upstream 8:7 MLTF^{1}	4.28	0.90	(1.08)	1.20	(1.86)	1.60×10^{-1}
downstream 10:100 HAL1±^{1}	−4.27	−0.03	(1.92)	−0.44	(2.23)	1.29×10^{-1}
downstream 5:10 MIR^{2}	−4.26	1.02	(1.55)	0.58	(0.76)	4.61×10^{-4}
upstream 6:5 ATF^{1}	4.25	0.49	(0.78)	0.63	(0.81)	1.43×10^{-1}
upstream 2:0 LINE_L2^{1} × upstream 5:4 GATA1^{1}	−4.24	0.20	(0.75)	0.00	(0.00)	0
upstream 100:10 DNA_Mariner^{1}	−4.23	0.41	(0.83)	0.23	(0.58)	2.43×10^{-2}
upstream 2:0 DNA_MER1_type^{1} × upstream 10:9 AP1^{3}	−4.22	0.11	(0.40)	0.00	(0.00)	0
upstream 100:60 LTR_ERVL±^{1}	−4.21	0.41	(1.56)	−0.11	(3.58)	1.84×10^{-1}
downstream 10:100 L1M1^{2}	−4.2	0.12	(0.64)	0.18	(0.66)	2.84×10^{-1}
upstream 5:0 LINE_L2±^{2}	4.19	112.34	(241.50)	164.27	(305.43)	1.48×10^{-1}
intron DNA_Tip100^{1}	−4.18	0.19	(0.76)	0.10	(0.38)	7.26×10^{-2}
downstream 0:5 LTR_ERV1^{2}	−4.17	2.52	(10.32)	0.41	(1.91)	1.65×10^{-8}
upstream 9:8 GATA1^{3} × downstream 0:100 MLT1C phase change^{2}	−4.15	0.06	(0.18)	0.00	(0.00)	0
upstream 6:5 APF^{3} × upstream 5:4 E4F1^{3}	−4.14	0.15	(0.35)	0.00	(0.00)	0
upstream 10:9 NFuE5^{1} × upstream 10:0 NFuE3^{3}	−4.13	0.17	(0.48)	0.00	(0.00)	0
upstream 10:9 E4F1^{1} × upstream 9:8 PU1^{3}	−4.12	0.12	(0.38)	0.00	(0.00)	0
downstream 5:10 L1PB^{2}	4.11	0.35	(3.49)	1.46	(6.49)	1.45×10^{-1}
upstream 10:5 SINE_MIR±^{2} × upstream 7:6 BPVE2^{3}	−4.1	23.93	(74.12)	0.02	(0.14)	0
intron DNA_Tip100±^{1}	−4.09	0.00	(0.59)	0.00	(0.39)	4.73×10^{-1}
upstream 10:5 LTR_ERVL±^{1}	4.08	0.00	(0.66)	0.18	(0.75)	7.32×10^{-2}
upstream 100:10 HAL1±^{2} × upstream 9:8 TFIID^{1}	−4.07	264.58	(860.20)	17.11	(63.06)	0
upstream 10:9 E4F1^{1} × upstream 10:0 ETFA^{3}	−4.06	0.11	(0.38)	0.00	(0.00)	0
upstream 2:0 DNA_MER1_type±^{2}	−4.05	19.25	(74.01)	2.20	(13.91)	1.34×10^{-9}
upstream 10:9 NFuE5^{1} × upstream 1:0 BPVE2^{3}	−4.04	0.12	(0.42)	0.00	(0.00)	0
upstream 100:10 L1MB^{1}	4.03	3.70	(3.98)	4.38	(4.80)	1.93×10^{-1}
upstream 100:10 LTR_ERV1^{1} × upstream 10:0 NFuE4^{3}	−4.02	2.12	(5.53)	0.18	(0.50)	0
upstream 7:6 CP1^{1}	4.01	0.05	(0.26)	0.08	(0.27)	2.84×10^{-1}
upstream 100:10 L1MD±^{1}	−4	0.04	(2.40)	−0.06	(2.73)	4.09×10^{-1}
upstream 2:1 AP2^{1}	3.99	0.42	(0.82)	0.90	(1.46)	2.38×10^{-2}
downstream 10:100 DNA_Tc2±^{1}	−3.98	−0.01	(0.63)	−0.03	(0.66)	4.34×10^{-1}
downstream 10:100 DNA_MER2_type±^{1}	3.97	0.11	(2.47)	0.58	(1.90)	6.53×10^{-2}
upstream 9:8 ATF^{1} × upstream 5:4 NFuE5^{1}	−3.96	0.19	(0.74)	0.00	(0.00)	0
upstream 6:5 GT2B^{1}	3.95	0.44	(0.77)	0.70	(0.94)	4.81×10^{-2}
downstream 10:100 DNA_Mariner^{1} × upstream 1:0 ATF^{1}	−3.94	0.35	(1.23)	0.00	(0.00)	0
upstream 100:10 DNA^{2}	3.93	0.06	(0.17)	0.10	(0.31)	2.08×10^{-1}
upstream 10:9 E4F1^{3} × upstream 3:2 GATA1^{3}	−3.92	0.08	(0.27)	0.00	(0.00)	0
upstream 10:5 LTR_MaLR±^{2} × upstream 3:2 AP1^{3}	−3.9	91.79	(229.88)	0.15	(0.65)	0
upstream 4:3 NFuE5^{3} × upstream 4:3 Pit1^{3}	−3.89	0.10	(0.30)	0.00	(0.00)	0

upstream 10:9 GT2B^{1} × upstream 1:0 MLTF^{1}	−3.88	0.58	(1.54)	0.08	(0.27)	5.88×10^{-15}
downstream 10:100 DNA_Mariner^{1} × upstream 1:0 TFIID^{3}	−3.87	0.21	(0.62)	0.00	(0.00)	0
downstream 0:2 LTR_ERVL^{1}	−3.86	0.06	(0.37)	0.00	(0.00)	0
exon LINE_L2^{1}	3.85	0.04	(0.24)	0.05	(0.22)	3.73×10^{-1}
upstream 1:0 NFuE3^{1}	−3.84	0.05	(0.24)	0.03	(0.16)	1.31×10^{-1}
upstream 10:9 GTIIC^{3} × upstream 4:3 BPVE2^{3}	−3.83	0.10	(0.30)	0.00	(0.00)	0
upstream 7:6 COUP^{3} × upstream 2:1 E4TF1^{3}	−3.82	0.06	(0.25)	0.00	(0.00)	0
upstream 10:5 DNA_MER2_type±^{2}	−3.81	32.24	(145.71)	13.18	(70.83)	5.09×10^{-2}
upstream 5:4 GATA1^{3} × downstream 0:100 MLT1C phase change^{2}	−3.8	0.19	(0.65)	0.00	(0.00)	0
upstream 2:1 BPVE2^{3} × upstream 5:0 ETFA^{3}	−3.79	0.11	(0.31)	0.00	(0.00)	0
upstream 2:0 LINE_L2^{1} × upstream 7:6 Pit1^{3}	−3.78	0.13	(0.46)	0.00	(0.00)	0
upstream 2:1 TFIID^{3} × downstream 0:100 MLT1C phase change^{2}	−3.77	0.24	(0.73)	0.00	(0.00)	0
upstream 7:6 Sp1^{3}	3.76	0.20	(0.40)	0.35	(0.48)	2.81×10^{-2}
downstream 5:10 L1PB±^{1}	−3.75	0.00	(0.28)	−0.03	(0.58)	3.95×10^{-1}
upstream 7:6 GTIIC^{3} × upstream 5:0 CP1^{3}	−3.73	0.06	(0.24)	0.00	(0.00)	0
upstream 2:0 DNA_MER1_type^{1}	−3.72	0.13	(0.44)	0.03	(0.16)	7.19×10^{-5}
upstream 2:1 SRF^{1}	−3.71	0.02	(0.13)	0.00	(0.00)	0
upstream 4:3 Pit1^{3} × downstream 0:100 MLT1C phase change^{2}	−3.7	0.18	(0.63)	0.00	(0.00)	0
upstream 2:0 E4TF1^{1}	3.69	0.21	(0.48)	0.13	(0.46)	1.32×10^{-1}
upstream 9:8 NFuE5^{1} × upstream 6:5 Oct1^{3}	−3.68	0.14	(0.42)	0.00	(0.00)	0
upstream 10:0 CpGi^{1,11}	3.67	2.32	(2.09)	2.48	(1.97)	3.14×10^{-1}
downstream 0:2 SINE_MIR^{1}	3.66	0.32	(0.66)	0.25	(0.59)	2.16×10^{-1}
upstream 7:6 SIF^{3}	3.65	0.22	(0.41)	0.30	(0.46)	1.31×10^{-1}
upstream 5:4 E4F1^{1} × upstream 6:5 APF^{3}	−3.63	0.17	(0.50)	0.00	(0.00)	0
upstream 7:6 AP1^{3} × upstream 2:1 E4TF1^{3}	−3.62	0.06	(0.25)	0.00	(0.00)	0
upstream 5:4 NFuE5^{3} × upstream 4:3 Pit1^{3}	−3.61	0.11	(0.31)	0.00	(0.00)	0
downstream 10:100 L1PA^{1}	−3.6	2.76	(3.56)	3.03	(3.09)	2.95×10^{-1}
upstream 4:3 CEBP^{3}	3.59	0.04	(0.19)	0.10	(0.30)	9.64×10^{-2}
upstream 5:0 L1M^{2}	3.58	0.01	(0.21)	0.06	(0.36)	1.96×10^{-1}
upstream 10:5 MIR3^{1}	−3.57	0.14	(0.41)	0.08	(0.27)	6.80×10^{-2}
downstream 0:5 FAM^{1}	−3.56	0.01	(0.13)	0.00	(0.00)	0
downstream 5:10 L1MD±^{2}	−3.55	26.33	(197.25)	24.09	(152.26)	4.64×10^{-1}
upstream 3:2 Pit1^{1} × upstream 7:6 BPVE2^{3}	−3.54	0.25	(0.77)	0.00	(0.00)	0
downstream 0:2 FLAM±^{1}	3.53	0.00	(0.22)	0.03	(0.16)	2.08×10^{-1}
upstream 2:0 SINE_MIR±^{2} × upstream 8:7 GT2B^{3}	−3.52	13.67	(50.16)	0.00	(0.00)	0
upstream 2:0 DNA_MER1_type^{1} × upstream 8:7 ICSBP^{3}	−3.51	0.10	(0.39)	0.00	(0.00)	0
upstream 6:5 ETFA^{3}	3.5	0.06	(0.23)	0.10	(0.30)	1.85×10^{-1}
downstream 0:1 L1M±^{1}	−3.49	0.00	(0.02)	−0.03	(0.16)	1.66×10^{-1}
downstream 0:1 CpGi^{1}	−3.48	0.22	(0.47)	0.25	(0.49)	3.67×10^{-1}
downstream 0:100 MLT1C phase change^{2}	−3.47	0.12	(0.25)	0.06	(0.20)	3.07×10^{-2}
upstream 10:0 GTIIC^{3} × upstream 10:0 Oct1^{3}	3.46	0.92	(0.26)	1.00	(0.00)	0
upstream 9:8 Sp1^{3}	−3.45	0.20	(0.40)	0.10	(0.30)	2.67×10^{-2}
upstream 3:2 AP1^{1} × downstream 0:100 MLT1C phase change^{2}	−3.44	0.78	(2.91)	0.03	(0.16)	0
upstream 10:5 LINE_L1^{2}	−3.43	5.05	(8.09)	5.06	(8.30)	4.97×10^{-1}
upstream 10:5 AluJ±^{2} × upstream 10:0 CP1^{3}	−3.42	44.66	(129.92)	2.10	(13.28)	0
upstream 100:10 L1P±^{2}	−3.41	230.89	(832.85)	61.10	(160.04)	3.76×10^{-8}
upstream 90:80 CpGi^{1,10}	−3.4	0.35	(0.83)	0.28	(0.64)	2.33×10^{-1}
upstream 6:5 AP2^{3} × upstream 3:2 Pit1^{3}	−3.39	0.09	(0.28)	0.00	(0.00)	0
upstream 100:10 L1MB±^{1}	−3.38	0.14	(3.76)	−0.51	(3.60)	1.35×10^{-1}
downstream 10:100 LTR_ERV1^{1}	−3.37	6.24	(7.74)	6.30	(7.51)	4.80×10^{-1}
downstream 10:100 FRAM±^{2} × upstream 8:7 SIF^{3}	−3.36	18.57	(67.07)	0.07	(0.36)	0
upstream 4:3 ETFA^{1}	3.35	0.06	(0.24)	0.10	(0.30)	1.96×10^{-1}
upstream 6:5 PU1^{1}	3.34	0.89	(1.05)	1.10	(1.19)	1.34×10^{-1}
downstream 0:5 L1MC±^{2}	−3.33	53.61	(230.70)	98.35	(454.18)	2.71×10^{-1}
upstream 1:0 L1MA^{1}	−3.32	0.01	(0.12)	0.00	(0.00)	0
upstream 4:3 NFuE5^{3} × upstream 2:1 Pit1^{3}	−3.31	0.10	(0.30)	0.00	(0.00)	0
upstream 2:1 NFIII^{1} × upstream 10:9 E4F1^{3}	−3.3	0.36	(1.09)	0.00	(0.00)	0
ditan10kup	−3.29	23.10	(54.47)	15.50	(23.28)	2.46×10^{-2}
upstream 2:0 NFkB^{3}	3.28	0.18	(0.38)	0.13	(0.33)	1.64×10^{-1}
upstream 10:0 IgPE2^{1}	3.27	0.20	(0.46)	0.25	(0.49)	2.73×10^{-1}
upstream 9:8 GATA1^{3} × upstream 2:0 NFkB^{3}	−3.26	0.08	(0.27)	0.00	(0.00)	0
upstream 9:8 NFuE5^{1} × upstream 6:5 Oct1^{1}	−3.25	0.18	(0.64)	0.00	(0.00)	0
downstream 5:10 AluY^{1}	3.24	0.37	(0.69)	0.50	(0.75)	1.44×10^{-1}
upstream 4:3 PU1^{1}	3.23	0.88	(1.04)	1.13	(1.20)	1.09×10^{-1}
upstream 10:5 LTR_MaLR±^{2} × upstream 1:0 MLTF^{3}	−3.22	68.32	(203.70)	0.08	(0.51)	0
upstream 2:1 E4TF1^{3} × upstream 10:0 NFuE5^{3}	−3.21	0.07	(0.25)	0.00	(0.00)	0
upstream 10:5 L1M3^{1}	3.2	0.01	(0.14)	0.08	(0.47)	1.96×10^{-1}
upstream 10:9 E4F1^{3} × upstream 3:2 TFIID^{3}	−3.19	0.11	(0.31)	0.00	(0.00)	0
upstream 100:10 MIR±^{1}	3.18	0.10	(2.33)	0.31	(3.55)	3.63×10^{-1}
upstream 9:8 GATA1^{1}	3.17	0.68	(0.89)	0.78	(1.07)	2.88×10^{-1}
upstream 10:9 SIF^{1}	−3.16	0.27	(0.65)	0.28	(0.55)	4.59×10^{-1}
upstream 100:10 HAL1±^{2}	−3.15	221.71	(473.89)	119.00	(233.60)	4.63×10^{-3}
upstream 100:10 LTR_ERVL^{2}	3.14	1.06	(1.45)	1.89	(2.96)	4.46×10^{-2}
upstream 2:0 LINE_L2^{1} × upstream 6:5 Oct1^{3}	−3.13	0.13	(0.47)	0.00	(0.00)	0
upstream 9:8 APF^{1}	−3.12	2.42	(1.99)	1.65	(1.48)	1.18×10^{-3}
downstream 0:2 AluY±^{1}	−3.11	0.01	(0.37)	−0.08	(0.27)	3.23×10^{-2}
upstream 10:5 DNA_AcHobo^{2}	3.1	0.06	(0.51)	0.22	(1.24)	2.09×10^{-1}
upstream 3:2 SIF^{3} × upstream 5:0 NFkB^{3}	−3.09	0.08	(0.27)	0.00	(0.00)	0
upstream 100:10 MIR3±^{2}	−3.08	71.24	(118.59)	35.53	(72.54)	1.95×10^{-3}
downstream 5:10 L1MB±^{2}	−3.07	60.96	(281.86)	84.80	(423.47)	3.64×10^{-1}
upstream 10:0 IgPE2^{3}	3.06	0.18	(0.38)	0.23	(0.42)	2.59×10^{-1}

downstream 10:100 LINE_CR1^{1} × upstream 3:2 Pit1^{3}	−3.05	0.58	(1.31)	0.10	(0.30)	1.47×10^{-12}
upstream 2:0 NFkB^{1} × upstream 5:4 TFIID^{3}	−3.04	0.12	(0.37)	0.00	(0.00)	0
upstream 1:0 SRF^{1}	−3.03	0.01	(0.12)	0.00	(0.00)	0
upstream 10:5 LINE_L1^{1} × downstream 0:100 MLT1C phase change^{2}	−3.02	0.61	(2.34)	0.00	(0.00)	0
upstream 5:0 CpGi^{2}	3.01	91.87	(92.76)	126.55	(121.01)	4.07×10^{-2}
upstream 4:3 SIF^{1}	−3	0.27	(0.68)	0.13	(0.33)	5.44×10^{-3}
upstream 100:10 LINE_CR1±^{1}	−2.99	0.07	(1.61)	−0.11	(1.11)	1.52×10^{-1}
downstream 0:2 L1MB±^{1}	−2.98	0.00	(0.26)	−0.05	(0.22)	8.95×10^{-2}
downstream 5:10 DNA_AcHobo±^{1}	2.97	0.00	(0.22)	0.03	(0.16)	1.73×10^{-1}
downstream 0:2 LINE_L2^{1} × upstream 8:7 ICSBP^{1}	−2.96	0.32	(1.07)	0.00	(0.00)	0
upstream 9:8 SIF^{1} × upstream 1:0 ATF^{3}	−2.95	0.15	(0.49)	0.00	(0.00)	0
upstream 8:7 NFkB^{3}	−2.94	0.07	(0.26)	0.05	(0.22)	2.54×10^{-1}
upstream 4:3 IgPE2^{1}	2.93	0.02	(0.14)	0.03	(0.16)	4.22×10^{-1}
Motif$^{9}_{7}$	−2.92	0.00	(0.17)	−0.05	(0.22)	7.52×10^{-2}
upstream 2:0 ETFA^{3} × downstream 0:100 MIR phase change^{2}	−2.91	0.06	(0.16)	0.00	(0.00)	0
upstream 9:8 NFuE5^{1}	−2.9	0.34	(0.63)	0.25	(0.54)	1.49×10^{-1}
downstream 10:100 LTR_ERV^{1}	−2.89	0.03	(0.24)	0.03	(0.16)	3.57×10^{-1}
upstream 6:5 AP2^{1}	2.88	0.38	(0.79)	0.65	(1.00)	5.07×10^{-2}
upstream 5:4 TFIID^{1} × upstream 2:0 NFkB^{3}	−2.87	0.20	(0.72)	0.00	(0.00)	0
downstream 10:100 FRAM±^{2} × upstream 5:0 GATA1^{1}	−2.86	235.74	(440.52)	35.12	(90.45)	0
downstream 10:100 LINE_CR1^{2} × upstream 100:10 MIR3^{1}	−2.85	0.77	(1.91)	0.06	(0.19)	0
upstream 4:3 BPVE2^{3} × downstream 0:100 MLT1C phase change^{2}	−2.84	0.04	(0.16)	0.00	(0.00)	0
upstream 60:50 CpGi^{1,10}	2.83	0.35	(0.80)	0.53	(1.13)	1.71×10^{-1}
downstream 5:10 MIR3^{1}	2.82	0.14	(0.41)	0.20	(0.41)	1.88×10^{-1}
upstream 5:0 L1PA±^{1}	2.81	0.01	(0.35)	0.05	(0.22)	1.12×10^{-1}
upstream 100:10 LTR_ERV1^{2}	2.8	2.85	(3.93)	3.68	(6.61)	2.19×10^{-1}
upstream 10:9 NFuE5^{1} × upstream 10:9 Oct1^{1}	−2.79	0.17	(2.41)	0.00	(0.00)	0
upstream 10:5 DNA_MER1_type^{2} × upstream 5:4 Pit1^{3}	−2.78	0.28	(1.09)	0.00	(0.00)	0
downstream 10:100 AluJ±^{1}	2.77	−0.08	(2.42)	0.05	(2.65)	3.78×10^{-1}
downstream 10:100 LINE_CR1^{1} × upstream 9:8 TFIID^{3}	−2.76	0.84	(1.50)	0.10	(0.30)	0
upstream 2:0 SINE_MIR^{2} × upstream 10:9 BPVE2^{3}	−2.75	1.03	(3.37)	0.00	(0.00)	0
upstream 9:8 TFIID^{3} × upstream 2:0 ICP4^{3}	−2.74	0.08	(0.27)	0.00	(0.00)	0
upstream 2:1 BPVE2^{1} × upstream 6:5 Pit1^{3}	−2.73	0.21	(0.52)	0.00	(0.00)	0
exon CpGi^{2}	2.72	161.59	(186.01)	272.77	(250.19)	4.22×10^{-3}
upstream 100:10 FAM^{2} × upstream 6:5 Pit1^{3}	−2.71	0.02	(0.06)	0.00	(0.00)	0
downstream 5:10 AluS^{2} × upstream 1:0 MLTF^{3}	−2.7	3.47	(5.11)	0.34	(0.92)	0
upstream 2:0 PEA2^{1}	2.69	0.07	(0.28)	0.08	(0.27)	4.77×10^{-1}
upstream 3:2 ICP4^{3}	2.68	0.05	(0.22)	0.03	(0.16)	1.59×10^{-1}
upstream 100:10 SINE_MIR±^{1}	2.67	0.10	(2.22)	0.33	(3.43)	3.36×10^{-1}
upstream 10:5 FAM±^{1}	−2.66	0.00	(0.13)	−0.03	(0.16)	1.61×10^{-1}
upstream 10:5 L1PB^{2}	−2.65	0.15	(1.51)	0.00	(0.00)	0
upstream 5:0 LTR_ERV1±^{2} × upstream 4:3 TFIID^{3}	−2.64	58.25	(241.18)	1.42	(8.07)	0
upstream 100:10 CpGi^{1} × upstream 100:10 AluS^{2}	−2.63	37.02	(53.50)	12.01	(11.29)	0
downstream 0:5 SINE_MIR^{1}	2.62	0.86	(1.21)	0.65	(0.83)	6.03×10^{-2}
upstream 2:0 Sp1^{3}	2.61	0.62	(0.49)	0.73	(0.45)	7.79×10^{-2}
upstream 8:7 AP1^{3} × upstream 7:6 NF1^{3}	−2.6	0.10	(0.29)	0.00	(0.00)	0
upstream 8:7 GT2B^{1} × upstream 5:4 NFuE5^{3}	−2.59	0.13	(0.45)	0.00	(0.00)	0
downstream 0:1 LINE_CR1^{2}	2.58	0.19	(2.17)	0.47	(2.97)	2.78×10^{-1}
downstream 0:5 AluS^{1} × upstream 3:2 TFIID^{1}	−2.57	1.83	(3.74)	0.28	(0.82)	4.77×10^{-15}
upstream 100:10 AluJ^{2} × upstream 10:9 NFuE5^{3}	−2.56	1.11	(2.27)	0.12	(0.37)	0
upstream 2:0 NFuE3^{3}	−2.55	0.11	(0.31)	0.10	(0.30)	4.15×10^{-1}
upstream 10:5 DNA_MER1_type^{1} × upstream 5:4 Pit1^{1}	−2.54	0.26	(1.08)	0.00	(0.00)	0
upstream 1:0 PU1^{1}	−2.53	1.00	(1.09)	0.73	(0.85)	2.39×10^{-2}
downstream 0:5 FLAM±^{1}	−2.52	0.01	(0.38)	−0.08	(0.35)	7.23×10^{-2}
upstream 100:10 CpGi^{1} × upstream 100:10 SINE_Alu^{2}	−2.51	60.28	(85.57)	22.82	(21.91)	1.48×10^{-13}
upstream 10:5 Alu^{1}	−2.5	0.02	(0.16)	0.00	(0.00)	0
downstream 10:100 CpGi^{3} × upstream 2:0 PEA1^{1}	−2.49	0.08	(0.32)	0.00	(0.00)	0
upstream 2:0 NFuE3^{1}	−2.48	0.12	(0.38)	0.10	(0.30)	3.18×10^{-1}
upstream 8:7 SRF^{1}	2.47	0.01	(0.12)	0.03	(0.16)	3.27×10^{-1}
upstream 7:6 APF^{3}	2.46	0.83	(0.37)	0.88	(0.33)	2.22×10^{-1}
upstream 1:0 MLTF^{1}	−2.45	1.23	(1.32)	0.63	(0.90)	6.82×10^{-5}
upstream 10:0 CpGi^{1,10}	2.44	0.38	(0.86)	0.63	(0.95)	5.63×10^{-2}
downstream 10:100 DNA_Mariner^{1} × upstream 9:8 Pit1^{1}	−2.43	0.33	(1.34)	0.00	(0.00)	0
downstream 0:5 LTR_MaLR^{1} × upstream 2:0 BPVE2^{1}	−2.42	0.37	(1.23)	0.00	(0.00)	0
upstream 100:10 DNA_Tc2^{2}	2.41	0.04	(0.13)	0.11	(0.43)	1.47×10^{-1}
upstream 100:10 AluJ^{2} × upstream 10:9 E4F1^{1}	−2.4	0.72	(2.14)	0.04	(0.14)	0
upstream 7:6 NF1^{1} × upstream 7:6 AP1^{3}	−2.39	0.11	(0.36)	0.00	(0.00)	0
upstream 100:10 CpGi^{2} × upstream 100:10 AluS^{2}	−2.38	601.34	(769.54)	185.70	(151.99)	0
upstream 5:4 E4F1^{3} × upstream 1:0 MLTF^{3}	−2.37	0.12	(0.32)	0.00	(0.00)	0
upstream 4:3 TFIID^{3} × downstream 0:100 MLT1C phase change^{2}	−2.36	0.25	(0.72)	0.00	(0.00)	0
downstream 10:100 LINE_CR1^{2} × upstream 100:10 DNA_MER1_type^{1}	−2.35	1.70	(3.44)	0.31	(0.63)	0
upstream 10:5 LTR_MaLR±^{2} × upstream 1:0 MLTF^{1}	−2.34	129.34	(473.41)	0.08	(0.51)	0
upstream 4:3 AP1^{1} × upstream 5:4 E4F1^{3}	−2.33	0.33	(0.91)	0.00	(0.00)	0
upstream 9:8 ICSBP^{1}	2.32	1.50	(1.21)	1.35	(1.05)	1.89×10^{-1}
upstream 2:0 ETFA^{1} × upstream 10:9 MLTF^{3}	−2.31	0.10	(0.34)	0.00	(0.00)	0
upstream 10:5 L1PA^{1}	−2.3	0.12	(0.45)	0.13	(0.46)	4.87×10^{-1}
upstream 10:5 FRAM±^{2}	2.29	8.63	(36.14)	7.60	(33.59)	4.25×10^{-1}
upstream 100:10 DNA_Tc2±^{1}	−2.28	0.00	(0.63)	0.07	(0.77)	2.86×10^{-1}
upstream 1:0 NFuE5^{3}	2.27	0.20	(0.40)	0.15	(0.36)	1.96×10^{-1}
upstream 2:0 MIR^{2} × upstream 10:9 BPVE2^{3}	−2.26	0.88	(3.06)	0.00	(0.00)	0

upstream 100:10 MIR3±[2] × upstream 1:0 MLTF[1]	−2.25	87.83	(235.51)	11.73	(37.57)	3.33×10^{-16}
upstream 100:10 DNA_MER1_type[2]	2.24	1.12	(0.84)	1.23	(0.97)	2.45×10^{-1}
downstream 10:100 FAM[1] × upstream 4:3 TFIID[1]	−2.23	0.30	(1.03)	0.00	(0.00)	0
upstream 10:5 LTR_MaLR±[2] × upstream 2:0 BPVE2[3]	−2.22	62.93	(194.19)	0.00	(0.00)	0
downstream 10:100 LINE_CR1[2] × upstream 100:10 SINE_MIR[2]	−2.21	0.60	(1.19)	0.07	(0.17)	0
upstream 2:0 DNA_MER1_type[1] × upstream 5:0 Pit1[1]	−2.2	0.45	(2.01)	0.00	(0.00)	0
downstream 0:2 LINE_CR1[2]	2.19	0.20	(1.82)	0.83	(5.23)	2.31×10^{-1}
downstream 10:100 LINE_CR1[2] × upstream 9:8 APF[3]	−2.18	0.20	(0.34)	0.04	(0.10)	2.76×10^{-13}
downstream 10:100 LINE_CR1[2] × downstream 5:10 SINE_MIR[1]	−2.17	0.26	(0.72)	0.03	(0.07)	0
intron L1P[1]	−2.16	0.13	(0.61)	0.03	(0.16)	1.61×10^{-4}
upstream 8:7 GT2B[3] × upstream 2:0 NFkB[3]	−2.15	0.06	(0.24)	0.00	(0.00)	0
upstream 5:0 L1MA±[2]	−2.14	30.55	(188.23)	0.00	(0.00)	0
downstream 0:5 DNA_MER2_type±[2]	−2.13	40.07	(209.05)	7.73	(48.86)	1.02×10^{-4}
exon LTR_ERV1[1]	−2.12	0.01	(0.16)	0.00	(0.00)	0
upstream 5:0 AluY[2] × upstream 9:8 Pit1[3]	−2.11	0.75	(2.43)	0.00	(0.00)	0
downstream 10:100 FRAM±[2] × upstream 5:0 TFIID[1]	−2.1	411.51	(770.95)	93.55	(208.60)	4.38×10^{-12}
intron LINE_L1±[1]	−2.09	−1.28	(3.60)	−1.64	(3.66)	2.68×10^{-1}
downstream 0:5 AluJ[1] × upstream 4:3 GTIIC[3]	−2.08	0.17	(0.59)	0.00	(0.00)	0
downstream 10:100 LTR_MaLR[1]	−2.07	8.71	(7.00)	7.75	(5.15)	1.26×10^{-1}
downstream 0:2 MIR[1] × upstream 1:0 ATF[3]	−2.06	0.14	(0.45)	0.00	(0.00)	0
upstream 5:0 DNA_AcHobo[1]	2.05	0.04	(0.24)	0.03	(0.16)	3.17×10^{-1}
upstream 100:10 Other[1] × upstream 100:0 MIR phase change[2]	−2.04	0.07	(0.23)	0.00	(0.00)	0
intron MIR±[2] × upstream 6:5 APF[3]	−2.03	36.15	(112.42)	0.72	(1.16)	0
upstream 100:10 Other[1] × upstream 5:4 ICSBP[3]	−2.02	0.14	(0.48)	0.00	(0.00)	0
downstream 0:2 DNA[2]	−2.01	0.06	(1.08)	0.00	(0.00)	0
upstream 2:1 BPVE2[1] × upstream 4:3 ATF[3]	−2	0.18	(0.49)	0.00	(0.00)	0
upstream 7:6 NF1[1] × upstream 2:0 ATF[3]	−1.99	0.09	(0.33)	0.00	(0.00)	0
upstream 5:0 DNA_MER2_type[2]	−1.98	0.60	(2.74)	0.36	(2.27)	2.56×10^{-1}
upstream 4:3 Pit1[1]	−1.97	0.70	(1.20)	0.50	(0.88)	7.67×10^{-2}
downstream 10:100 L1M3±[1]	1.96	0.00	(0.71)	0.13	(1.22)	2.66×10^{-1}
upstream 2:0 NFuE4[1] × upstream 5:0 GATA1[3]	−1.95	0.07	(0.28)	0.00	(0.00)	0
upstream 5:0 E2F[1]	−1.94	0.09	(0.31)	0.10	(0.30)	4.17×10^{-1}
downstream 0:2 SINE_MIR[1] × upstream 1:0 ATF[3]	−1.93	0.17	(0.51)	0.00	(0.00)	0
upstream 8:7 SIF[3]	−1.92	0.21	(0.41)	0.13	(0.33)	5.63×10^{-2}
upstream 5:4 PEA1[1] × upstream 3:2 APF[3]	−1.91	0.09	(0.31)	0.00	(0.00)	0
downstream 10:100 AluY[2] × downstream 0:2 LINE_L2[1]	−1.9	0.39	(1.33)	0.01	(0.05)	0
downstream 10:100 Alu±[1]	1.89	0.02	(0.58)	0.00	(0.55)	4.10×10^{-1}
upstream 5:0 AluY[2] × upstream 6:5 PU1[3]	−1.88	1.03	(2.86)	0.00	(0.00)	0
upstream 100:10 FRAM[1]	1.87	1.09	(1.29)	0.88	(1.28)	1.56×10^{-1}
downstream 0:2 SINE_MIR[2] × upstream 1:0 ATF[3]	−1.86	1.08	(3.30)	0.00	(0.00)	0
upstream 3:2 TFIID[1]	−1.85	1.14	(1.29)	0.85	(1.12)	5.99×10^{-2}
upstream 10:9 ICP4[3]	1.84	0.05	(0.21)	0.08	(0.27)	2.70×10^{-1}
upstream 5:0 L1PA[1]	1.83	0.09	(0.37)	0.10	(0.44)	4.59×10^{-1}
downstream 10:100 L1MC[2]	−1.82	1.41	(1.55)	1.43	(1.64)	4.69×10^{-1}
upstream 9:8 TFIID[3] × upstream 8:7 Sp1[3]	−1.81	0.10	(0.30)	0.00	(0.00)	0
intron L1PB[1]	1.8	0.26	(1.11)	0.45	(2.25)	2.98×10^{-1}
upstream 10:5 SINE_MIR[2] × upstream 5:0 AluS[1]	−1.79	2.08	(4.66)	0.23	(0.63)	0
upstream 5:0 AluS[2] × upstream 2:0 AP2[3]	−1.78	5.68	(9.31)	1.28	(2.82)	2.27×10^{-12}
exon L1ME[2]	1.77	0.23	(3.77)	3.17	(20.06)	1.83×10^{-1}
upstream 10:5 FAM[2]	1.76	0.02	(0.20)	0.03	(0.22)	3.89×10^{-1}
upstream 1:0 AP1[1] × upstream 10:9 NFuE5[3]	−1.75	0.40	(0.94)	0.03	(0.16)	0
upstream 10:5 SINE_MIR±[2]	1.74	63.22	(108.32)	53.71	(117.12)	3.08×10^{-1}
upstream 4:3 AP2[3]	1.73	0.26	(0.44)	0.38	(0.49)	8.00×10^{-2}
upstream 100:10 AluJ[2] × upstream 70:60 CpGi[1,11]	−1.72	7.82	(11.89)	2.40	(3.04)	3.97×10^{-14}
upstream 100:10 AluY±[1]	−1.71	0.29	(2.38)	0.09	(1.98)	2.70×10^{-1}
downstream 10:100 LINE_CR1[1] × upstream 10:5 AluS±[2]	−1.7	249.42	(708.04)	23.28	(81.55)	0
upstream 2:0 BPVE2[1] × upstream 5:0 NFuE5[1]	−1.69	1.57	(2.87)	0.28	(0.55)	0
upstream 5:0 DNA_Tc2[1]	1.68	0.01	(0.13)	0.05	(0.32)	2.13×10^{-1}
upstream 2:0 ETFA[3] × downstream 0:100 MIR phase change[1]	−1.67	1.16	(3.68)	0.00	(0.00)	0
upstream 3:2 BPVE2[1]	1.66	0.48	(0.71)	0.58	(0.84)	2.54×10^{-1}
downstream 0:5 DNA_Mariner±[1]	1.65	0.00	(0.18)	0.00	(0.23)	4.81×10^{-1}
upstream 100:10 DNA_T2_type±[2]	−1.64	12.81	(88.09)	0.00	(0.00)	0
downstream 0:1 L1ME[1]	1.63	0.03	(0.21)	0.08	(0.35)	2.27×10^{-1}
upstream 100:10 DNA_Tip100[2]	−1.62	0.12	(0.30)	0.10	(0.35)	3.51×10^{-1}
upstream 5:0 Pit1[1] × downstream 0:100 MLT1C phase change[2]	−1.61	0.43	(1.24)	0.04	(0.17)	0
upstream 10:5 AluJ[2] × upstream 2:0 BPVE2[3]	−1.6	1.27	(2.41)	0.02	(0.13)	0
exon SINE_Alu±[1]	−1.59	0.00	(0.43)	−0.05	(0.22)	7.73×10^{-2}
upstream 2:0 L1M2[1]	−1.58	0.01	(0.11)	0.03	(0.16)	2.52×10^{-1}
intron DNA_MER2_type[2]	−1.57	40.83	(121.55)	36.63	(89.65)	3.86×10^{-1}
upstream 5:0 NFuE1[3]	1.56	0.20	(0.40)	0.25	(0.44)	2.55×10^{-1}
downstream 10:100 FLAM[2]	1.55	0.34	(0.32)	0.22	(0.23)	1.57×10^{-3}
upstream 5:0 L1ME[1] × upstream 10:0 NF1[1]	−1.54	0.38	(1.64)	0.00	(0.00)	0
upstream 5:0 AluY[1] × upstream 100:0 MIR phase change[2]	−1.53	0.14	(0.29)	0.01	(0.07)	7.22×10^{-15}
upstream 5:4 APF[3]	1.52	0.84	(0.37)	0.80	(0.41)	2.95×10^{-1}
upstream 10:5 LTR_MaLR[1] × upstream 2:0 BPVE2[3]	−1.51	0.31	(0.84)	0.00	(0.00)	0
intron MIR±[2] × upstream 5:0 AP2[3]	−1.5	33.71	(108.04)	0.77	(1.32)	0
upstream 2:1 COUP[3] × upstream 2:0 NFuE4[3]	−1.49	0.07	(0.25)	0.00	(0.00)	0
intron MIR±[2] × upstream 7:6 NFIII[3]	−1.48	34.33	(109.61)	0.78	(1.20)	0
downstream 0:5 AluJ[2] × upstream 5:4 SIF[3]	−1.47	0.88	(3.00)	0.00	(0.00)	0
upstream 2:0 AluS[2] × upstream 1:0 Pit1[3]	−1.46	2.32	(7.10)	0.00	(0.00)	0

upstream 6:5 NFuE3[1]	1.45	0.08	(0.29)	0.13	(0.33)	1.87×10^{-1}
downstream 0:5 SINE_Alu[1] × upstream 5:4 SIF[3]	−1.44	0.78	(2.14)	0.05	(0.22)	0
upstream 5:0 AluY[1] × upstream 2:0 PU1[3]	−1.43	0.28	(0.61)	0.03	(0.16)	8.00×10^{-13}
downstream 0:2 SINE_MIR±[1]	−1.42	0.00	(0.64)	0.00	(0.51)	4.88×10^{-1}
upstream 10:5 L1MD[1]	−1.41	0.08	(0.48)	0.00	(0.00)	0
intron MIR±[2] × upstream 9.04:8.99 nucleosome potential [sd]	−1.4	17.79	(52.21)	1.61	(8.15)	7.77×10^{-16}
upstream 100:10 AluS[2] × upstream 10:9 NFuE5[3]	−1.39	3.02	(6.15)	0.41	(1.13)	0
upstream 100:10 AluS[1] × upstream 100:10 MIR3±[2]	−1.38	2450.40	(5083.01)	449.61	(1068.36)	7.55×10^{-15}
downstream 0:1 AluS[2] × upstream 4:3 PU1[3]	−1.37	3.83	(11.21)	0.00	(0.00)	0
upstream 5:0 CpGi[1] × upstream 2:0 AluJ[1]	−1.36	0.12	(0.48)	0.00	(0.00)	0
upstream 2:0 AluJ[2] × upstream 10:9 PU1[3]	−1.35	1.57	(4.94)	0.00	(0.00)	0
exon MIR3[2]	−1.34	0.20	(1.75)	0.00	(0.00)	0
downstream 0:5 AluJ±[2] × upstream 10:0 NFuE4[3]	−1.33	36.43	(116.04)	0.00	(0.00)	0
downstream 10:100 CpGi[1]	1.32	21.32	(16.93)	22.00	(14.76)	3.87×10^{-1}
downstream 10:100 DNA_Mariner[1] × upstream 100:10 LTR_ERV1[1]	−1.31	2.71	(8.90)	0.00	(0.00)	0
downstream 0:5 AluJ[2] × upstream 7:6 GTIIC[1]	−1.3	1.01	(3.61)	0.00	(0.00)	0
upstream 9:8 COUP[1]	1.29	1.97	(1.44)	1.90	(1.68)	3.94×10^{-1}
upstream 10:5 L1MD[2]	−1.28	0.28	(1.95)	0.00	(0.00)	0
upstream 10:9 NFuE5[1] × upstream 1:0 Oct1[3]	−1.27	0.11	(0.39)	0.00	(0.00)	0
upstream 2:1 NFkB[1]	−1.26	0.09	(0.30)	0.05	(0.22)	1.54×10^{-1}
upstream 100:10 MIR[1] × upstream 100:10 SINE_Alu[2]	−1.25	220.09	(225.99)	78.31	(77.03)	1.77×10^{-14}
upstream 10:5 AluS[2] × upstream 2:1 BPVE2[3]	−1.24	2.29	(4.66)	0.15	(0.93)	0
upstream 5:0 CEBP[3]	1.23	0.16	(0.37)	0.20	(0.41)	2.63×10^{-1}
downstream 10:100 LINE_CR1[2] × upstream 10:0 AP1[1]	−1.22	4.29	(6.65)	0.96	(1.61)	3.33×10^{-16}
upstream 100:10 AluS[1] × upstream 3:2 COUP[3]	−1.21	30.04	(26.21)	12.90	(11.02)	2.74×10^{-12}
upstream 10:9 NFuE5[1]	−1.2	0.34	(0.64)	0.20	(0.56)	6.81×10^{-2}
exon LTR_ERV1[2]	−1.19	0.44	(5.96)	0.00	(0.00)	0
upstream 10:5 AluS[1] × upstream 2:1 BPVE2[3]	−1.18	0.83	(1.71)	0.05	(0.32)	0
downstream 5:10 L1M3[2]	−1.17	0.03	(0.68)	0.00	(0.00)	2.10×10^{-12}
downstream 0:2 AluS[1] × upstream 1:0 BPVE2[1]	−1.16	0.27	(0.84)	0.00	(0.00)	0
upstream 2:0 L1MC[1]	1.15	0.07	(0.34)	0.08	(0.35)	4.45×10^{-1}
downstream 0:1 SINE_MIR[1] × upstream 3:2 AP1[1]	−1.14	0.29	(1.00)	0.00	(0.00)	0
upstream 10:5 SINE_MIR[2] × upstream 2:0 AluS[2]	−1.13	9.05	(25.90)	0.00	(0.00)	0
downstream 0:1 SINE_Alu[2] × upstream 7:6 GTIIC[1]	−1.12	3.58	(13.55)	0.00	(0.00)	0
upstream 1:0 SINE_Alu[1] × upstream 7:6 Oct1[3]	−1.11	0.16	(0.47)	0.00	(0.00)	0
upstream 5:0 SINE_Alu[2] × upstream 8:7 GT2B[1]	−1.1	7.19	(17.39)	1.40	(3.55)	5.11×10^{-13}
downstream 0:5 L1MB[2]	−1.09	0.94	(4.69)	0.45	(1.79)	4.94×10^{-2}
upstream 100:0 CpGi[2,10]	−1.08	0.18	(0.15)	0.17	(0.12)	3.12×10^{-1}
upstream 100:10 SINE_MIR[1] × upstream 100:0 Alu phase change[1]	−1.07	447.93	(440.90)	157.03	(154.06)	8.10×10^{-15}
downstream 10:100 LINE_CR1[2] × upstream 5:0 AluS[1]	−1.06	0.39	(0.90)	0.04	(0.13)	0
upstream 2:0 AluS[2] × upstream 5:0 ETFA[3]	−1.05	2.19	(7.07)	0.00	(0.00)	0
downstream 10:100 AluY[1] × upstream 100:10 AluS[1]	−1.04	291.62	(389.69)	97.25	(119.91)	7.77×10^{-13}
downstream 10:100 LINE_CR1[2] × upstream 3:2 TFIID[1]	−1.03	0.27	(0.68)	0.01	(0.05)	0
upstream 5:0 AluS[2] × m3upIndicator	−1.02	6.98	(10.28)	1.40	(3.52)	1.48×10^{-12}
upstream 6:5 GATA1[1]	−1.01	0.68	(0.88)	0.58	(0.78)	2.13×10^{-1}
upstream 100:10 L1M3±[2]	−1	50.39	(302.85)	96.83	(305.95)	1.75×10^{-1}
upstream 7:6 Sp1[1]	−0.99	0.35	(1.14)	0.50	(0.96)	1.66×10^{-1}
upstream 5:0 SINE_Alu[2] × upstream 5:0 BPVE2[1]	0.98	43.86	(59.14)	12.93	(19.79)	2.28×10^{-12}
upstream 3:2 Pit1[1] × upstream 10:9 NFuE5[3]	−0.97	0.17	(0.63)	0.00	(0.00)	0
upstream 4:3 AR[1]	−0.96	12.17	(4.69)	10.98	(4.59)	5.66×10^{-2}
upstream 2:0 AluS[2] × upstream 10:9 COUP[1]	−0.95	17.48	(33.29)	0.30	(1.91)	0
downstream 10:100 LINE_CR1[2] × upstream 5:0 SINE_Alu[2]	−0.94	3.49	(7.39)	0.29	(0.78)	0
upstream 5:0 SINE_Alu[1] × upstream 5:0 AP1[1]	0.93	33.65	(40.19)	10.73	(15.01)	4.43×10^{-12}
upstream 2:0 AluS±[2] × m11intronIndicator	−0.92	76.80	(162.84)	4.68	(29.57)	0
downstream 10:100 AluJ[2]	0.91	3.43	(2.48)	2.20	(1.31)	3.56×10^{-7}
downstream 5:10 L1MA[2]	−0.9	0.85	(4.96)	0.58	(2.57)	2.61×10^{-1}
upstream 8:7 BPVE2[1] × upstream 2:0 E4TF1[3]	−0.89	0.09	(0.36)	0.00	(0.00)	0
upstream 1:0 NFIII[3]	0.88	0.70	(0.46)	0.65	(0.48)	2.43×10^{-1}
upstream 10:5 GC[2] × upstream 100:10 AluS[1]	−0.87	1585.80	(1238.67)	795.33	(490.41)	9.69×10^{-13}
upstream 100:10 AluS[2] × upstream 3:2 AP1[3]	−0.86	8.16	(7.16)	2.97	(3.15)	5.57×10^{-13}
upstream 5:0 LINE_L1[2]	−0.85	7.68	(13.27)	5.61	(10.69)	1.17×10^{-1}
upstream 9:8 CP1[1]	−0.84	0.05	(0.25)	0.00	(0.00)	0
upstream 10:5 L1MA±[1]	−0.83	0.00	(0.49)	−0.05	(0.45)	2.34×10^{-1}
downstream 10:100 AluS±[1]	−0.82	−0.08	(2.12)	0.46	(2.72)	1.10×10^{-1}
downstream 10:100 SINE_Alu[2] × upstream 10:0 AP1[1]	0.81	290.85	(240.38)	144.13	(86.25)	1.96×10^{-13}
upstream 10:5 FLAM[1]	0.8	0.17	(0.44)	0.10	(0.30)	8.06×10^{-2}
upstream 5:0 AluS[1] × upstream 9:8 COUP[3]	0.79	1.64	(1.98)	0.50	(0.75)	4.92×10^{-12}
downstream 10:100 AluJ[2] × downstream 5:10 SINE_Alu[2]	0.78	38.62	(53.95)	12.50	(15.75)	3.94×10^{-13}
upstream 5:0 SINE_Alu[2] × upstream 2:0 Sp1[3]	0.77	11.27	(15.08)	3.61	(5.46)	4.35×10^{-11}
downstream 0:5 AluS[1] × upstream 2:1 BPVE2[3]	−0.76	0.67	(1.46)	0.05	(0.22)	0
upstream 100:0 MIR phase change[2]	−0.75	0.41	(0.16)	0.37	(0.26)	1.74×10^{-1}
upstream 2:0 SINE_Alu[2] × upstream 2:1 AP2[1]	−0.74	4.12	(13.16)	0.00	(0.00)	0
downstream 0:1 MIR[1] × upstream 1:0 AP1[3]	−0.73	0.09	(0.33)	0.00	(0.00)	0
upstream 5:0 AluS[1] × upstream 8:7 SIF[3]	−0.72	0.53	(1.46)	0.03	(0.16)	0
upstream 10:5 SINE_MIR[1] × upstream 2:0 SINE_Alu[2]	−0.71	11.65	(29.39)	0.66	(2.91)	0
upstream 5:0 NFuE3[1]	0.7	0.36	(0.64)	0.43	(0.59)	2.40×10^{-1}
upstream 5:0 SINE_Alu[2] × upstream 9:8 COUP[3]	0.69	14.50	(15.32)	4.48	(5.56)	3.46×10^{-14}
intron MIR±[2] × upstream 90:80 CpGi[1,11]	−0.68	81.39	(319.80)	1.38	(3.50)	0
downstream 0:5 AluJ[1] × upstream 50:40 CpGi[1,11]	−0.67	1.58	(3.89)	0.20	(0.65)	1.11×10^{-16}
upstream 5:0 DNA_MER1_type±[2]	−0.66	48.94	(128.50)	31.56	(80.74)	9.38×10^{-2}

upstream 100:10 SINE_Alu[1] × upstream 2:1 BPVE2[1]	−0.65	31.40	(59.03)	2.78	(8.41)	0
downstream 5:10 AluS[1] × upstream 100:10 SINE_Alu[1]	−0.64	151.46	(229.53)	24.95	(33.88)	0
upstream 9:8 AP1[3]	0.63	0.84	(0.37)	0.80	(0.41)	2.92×10^{-1}
upstream 5:0 SINE_Alu[2] × upstream 10:0 COUP[1]	0.62	353.25	(372.57)	115.04	(152.24)	2.27×10^{-12}
upstream 1:0 AluS±[2] × upstream 2:1 NFIII[1]	−0.61	102.61	(315.31)	0.00	(0.00)	0
downstream 5:10 AluS[1] × downstream 0:1 AluS±[2]	−0.6	180.97	(537.94)	0.00	(0.00)	0
downstream 10:100 AluS[2] × upstream 5:0 AluY[2]	−0.59	24.05	(57.00)	2.15	(7.83)	0
upstream 10:5 AluJ[2] × upstream 10:5 MIR±[2]	−0.58	118.71	(369.97)	8.33	(51.58)	0
downstream 0:1 MIR[1] × upstream 2:0 AP1[1]	−0.57	0.41	(1.49)	0.00	(0.00)	0
downstream 10:100 MIR3±[2] × upstream 2:0 SINE_Alu[2]	−0.56	939.36	(2652.77)	66.28	(285.18)	0
upstream 100:10 AluS[1] × upstream 6:5 ICSBP[3]	−0.55	27.43	(26.55)	11.55	(10.88)	1.55×10^{-11}
upstream 10:5 CpGi[1] × upstream 5:0 AluS[2]	0.54	36.71	(59.08)	7.97	(12.59)	0
upstream 5:0 SINE_Alu[2] × upstream 100:0 L2 phase change[1]	0.53	82.44	(101.53)	25.81	(35.89)	1.75×10^{-12}
downstream 10:100 FRAM[1] × upstream 2:0 AluJ±[2]	−0.52	73.35	(256.02)	0.00	(0.00)	0
upstream 1:0 IgPE2[1]	−0.51	0.02	(0.15)	0.00	(0.00)	0
downstream 5:10 AluS[2] × downstream 0:1 AluS[2]	−0.5	55.81	(160.17)	0.00	(0.00)	0
downstream 0:5 FLAM±[2] × upstream 2:0 ICSBP[1]	−0.49	43.41	(149.18)	0.14	(0.89)	0
upstream 8:7 CP1[3]	0.48	0.04	(0.20)	0.03	(0.16)	2.51×10^{-1}
upstream 1:0 AluS±[2] × upstream 6:5 COUP[3]	−0.47	46.39	(113.64)	0.00	(0.00)	0
intron SINE_MIR±[2] × upstream 90:80 CpGi[1,11]	−0.46	77.89	(320.76)	1.47	(3.81)	0
downstream 0:5 AluS[2] × upstream 2:1 BPVE2[1]	−0.45	4.77	(11.64)	0.31	(1.35)	0
downstream 0:1 SINE_Alu±[1]	0.44	0.04	(0.82)	0.00	(0.55)	3.43×10^{-1}
upstream 5:0 CpGi[2] × upstream 1:0 SINE_Alu±[2]	−0.43	7072.20	(19530.74)	465.95	(2091.10)	0
downstream 5:10 AluS[2] × upstream 2:1 AR[1]	−0.42	57.25	(66.33)	18.73	(26.75)	2.23×10^{-11}
upstream 100:10 SINE_Alu[2] × upstream 2:1 BPVE2[3]	−0.41	6.19	(10.16)	0.75	(2.32)	0
downstream 5:10 AluS[2] × upstream 2:0 AluJ[2]	−0.4	20.65	(63.27)	0.00	(0.00)	0
upstream 2:0 SINE_Alu[2] × upstream 10:9 GT2B[1]	−0.39	5.98	(17.47)	0.26	(1.62)	0
downstream 10:100 FLAM[1] × downstream 5:10 AluS[2]	−0.38	19.73	(33.22)	3.74	(7.76)	3.33×10^{-16}
upstream 5:0 AluY[2] × upstream 2:0 BPVE2[1]	−0.37	2.02	(5.93)	0.14	(0.91)	2.22×10^{-16}
upstream 2:0 FAM[1]	−0.36	0.00	(0.06)	0.00	(0.00)	0
downstream 5:10 SINE_Alu[2] × upstream 10:5 SINE_Alu[1]	0.35	41.12	(65.94)	10.41	(15.68)	2.00×10^{-15}
upstream 100:10 AluJ[2] × upstream 7:6 AP1[1]	−0.34	7.16	(8.55)	2.49	(3.04)	3.46×10^{-12}
upstream 2:0 SINE_Alu[1] × upstream 2:0 BPVE2[1]	0.33	1.16	(2.44)	0.18	(0.50)	1.55×10^{-15}
upstream 10:5 L1MB[2]	0.32	0.68	(2.83)	0.60	(1.84)	3.90×10^{-1}
downstream 10:100 FLAM[2] × downstream 5:10 AluS[2]	−0.31	2.38	(4.01)	0.47	(0.97)	1.55×10^{-15}
upstream 100:10 AluS[1] × upstream 5:0 BPVE2[1]	−0.3	87.38	(100.91)	30.50	(29.91)	6.00×10^{-15}
downstream 10:100 FAM[1]	−0.29	0.26	(0.56)	0.13	(0.33)	8.12×10^{-3}
downstream 5:10 SINE_Alu[2] × upstream 2:0 SINE_Alu[2]	0.28	152.03	(285.85)	21.61	(74.28)	6.67×10^{-14}
upstream 100:10 AluS[2] × upstream 2:0 AluJ[1]	−0.27	3.39	(9.25)	0.19	(0.73)	0
upstream 2:0 ATF[1] × upstream 2:0 E4TF1[3]	−0.26	0.30	(0.91)	0.03	(0.16)	5.10×10^{-14}
upstream 1:0 AluS[1] × upstream 2:0 Sp1[3]	−0.25	0.14	(0.41)	0.00	(0.00)	0
upstream 100:10 AluS[1] × upstream 3:2 COUP[1]	−0.24	72.30	(84.53)	30.48	(26.66)	1.99×10^{-12}
downstream 0:2 DNA_MER2_type[1]	−0.23	0.05	(0.29)	0.03	(0.16)	1.75×10^{-1}
upstream 5:0 SINE_Alu[1] × upstream 4:3 TFIID[3]	−0.22	2.12	(2.97)	0.60	(1.08)	4.59×10^{-11}
upstream 2:0 AluS[2] × upstream 8:7 SIF[3]	−0.21	2.32	(7.64)	0.00	(0.00)	0
downstream 5:10 AluS[2] × upstream 10:5 SINE_Alu[1]	−0.2	25.68	(43.78)	3.78	(6.36)	0
upstream 5:0 AluS[1] × upstream 10:9 NFuE5[3]	−0.19	0.61	(1.49)	0.05	(0.22)	0
downstream 5:10 LTR_ERVL[1]	−0.18	0.21	(0.69)	0.18	(0.50)	3.42×10^{-1}
downstream 5:10 FLAM[1]	0.17	0.15	(0.41)	0.08	(0.27)	3.67×10^{-2}
upstream 2:0 DNA_AcHobo[2]	−0.16	0.11	(1.32)	0.00	(0.00)	0
downstream 10:100 AluJ[2] × upstream 5:0 AluS[2]	0.15	45.82	(68.17)	8.98	(17.67)	2.22×10^{-16}
downstream 0:1 L1MB[2]	0.14	0.48	(5.11)	0.22	(1.36)	1.16×10^{-1}
downstream 10:100 AluY[1] × upstream 5:0 SINE_Alu[1]	0.13	28.15	(43.61)	5.80	(9.77)	0
downstream 0:2 SINE_Alu[1] × upstream 2:1 BPVE2[1]	−0.12	0.56	(1.50)	0.03	(0.16)	0
downstream 0:2 L1MB[1]	−0.11	0.04	(0.26)	0.05	(0.22)	3.94×10^{-1}
downstream 10:100 LINE_CR1[2] × upstream 100:10 AluS[1]	0.1	7.26	(13.49)	1.45	(3.33)	7.67×10^{-14}
downstream 5:10 AluS[1] × upstream 1:0 AluS[2]	−0.09	15.56	(49.12)	0.00	(0.00)	0
upstream 100:10 L1MB[1] × upstream 5:0 AluY[1]	−0.08	1.46	(4.19)	0.15	(0.58)	0
upstream 1:0 AluS[2] × upstream 10:0 NFuE5[1]	−0.07	24.38	(66.70)	1.18	(7.46)	0
downstream 5:10 AluS[2] × upstream 1:0 AluS[1]	−0.06	1.66	(5.16)	0.00	(0.00)	0
downstream 5:10 SINE_Alu[1] × upstream 1:0 SINE_Alu[2]	0.05	42.54	(106.75)	3.85	(16.09)	0
downstream 10:100 LTR_ERVL±[2]	0.04	292.21	(693.57)	450.10	(1064.61)	1.80×10^{-1}
intron DNA_Tc2±[2]	0.03	14.45	(81.71)	6.91	(30.34)	6.53×10^{-2}
downstream 0:2 Other[2]	−0.02	0.62	(6.75)	0.00	(0.00)	0
upstream 2:0 SINE_Alu[2] × upstream 5:0 Sp1[3]	−0.01	10.60	(15.55)	2.05	(5.41)	1.71×10^{-12}
upstream 5:0 SINE_Alu[2] × upstream 2:1 COUP[1]	0.01	35.57	(48.80)	11.25	(14.45)	2.53×10^{-13}

Unit is kilobases and it refers to the beginning of the first or the end of the last exon, respectively. Corresponding table for SMLR available upon request.
For example, "downstream 10:100" refers to the 90 kb window from 10 kb to 100 kb downstream of the last exon.

[1] Number of this feature within the sequence window.

±[1] denotes the ratio of repeated elements in + versus − orientation with respect to the gene. It is the negative inverse if there are more elements in − orientation than in +.

[2] Percentage.

±[2] Ratio of the percentage of the sequence window covered by repeated elements in ± orientation.

[3] Indicator for presence of this feature within the sequence window.

[4] Indicator for presence of upstream CTCF consensus-binding site.

[5] Indicator for presence of TGTTTGCAG consensus site.

[6] The phase change happened at one of the following LTR elements: MLT1A0, MLT1B, MSTA, MSTB1, MLT1D, MLT2B4, or MLT1G1.

[7] Indicator for presence of CpG island overlapping the last exon.

[8] Indicator for presence of CpG island overlapping the first exon.

[9] Orientation of motif relative to gene.

[10] Methylation prone.

[11] Methylation resistant.

× indicates pairwise interaction between two variables.

Table 5. Relevant features for prediction of parental preference by Equbits classifier.

		Mean (Standard deviation)				
Feature	Weight	Maternally expressed		Paternally expressed		P
downstream 10:100 AluJ$\pm^1$ $\times$ upstream 1:0 ATF^3	19.57	-0.71	(1.15)	1.06	(1.46)	8.49×10^{-5}
downstream 10:100 CpGi^3 $\times$ upstream 3:2 Oct1^3	-18.86	0.47	(0.51)	0	(0)	3.97×10^{-4}
downstream 10:100 CpGi^1 $\times$ upstream 10:0 GATA1^3	-17.94	4.68	(3.37)	0.85	(0.99)	5.19×10^{-5}
upstream 7:6 APF^3 $\times$ upstream 5:4 BPVE2^3	-17.75	0.47	(0.51)	0	(0)	3.97×10^{-4}
upstream 4:3 E4F1^3	-16.86	0.37	(0.50)	0.05	(0.22)	8.41×10^{-3}
downstream 50:90 LTR_ERVL$\pm^1$	16.49	0.21	(0.54)	2.08	(2.97)	5.93×10^{-3}
upstream 10:9 MLTF^3 $\times$ upstream 7:6 AP1^3	-16.42	0.68	(0.48)	0.10	(0.31)	4.42×10^{-5}
upstream 4:3 E4F1^1	-15.92	0.42	(0.61)	0.05	(0.22)	9.90×10^{-3}
downstream 10:100 AluS$\pm^2$	-15.45	337.17	(781.15)	1.84	(1.10)	3.88×10^{-2}
upstream 10:5 AluY^1	-14.9	0.47	(0.61)	0.10	(0.31)	1.21×10^{-2}
upstream 100:90 CpGi^{2,10}	-14.88	0.18	(0.35)	0.03	(0.11)	3.47×10^{-2}
upstream 10:5 AluY^2	-14.69	1.43	(1.86)	0.31	(0.95)	1.31×10^{-2}
downstream 10:100 CpGi^1	-14.57	4.68	(3.37)	1.30	(1.45)	2.36×10^{-4}
downstream 10:100 SINE_MIR$\pm^1$	14	-1.31	(1.80)	0.38	(2.51)	1.02×10^{-2}
downstream 10:100 LTR_ERVL$\pm^1$	13.99	-0.22	(2.05)	1.65	(2.90)	1.29×10^{-2}
downstream 10:100 MIR$\pm^2$	13.86	2.28	(3.47)	70.32	(153.20)	3.08×10^{-2}
upstream 6:5 GTIIC^1	13.79	0.21	(0.42)	0.60	(0.68)	1.90×10^{-2}
downstream 10:100 MIR3$\pm^2$	-13.7	67.91	(99.59)	12.00	(29.01)	1.42×10^{-2}
upstream 7:6 CP1^1	-13.32	0.16	(0.37)	0	(0)	4.14×10^{-2}
upstream 100:10 L1^2	13.27	0.07	(0.21)	0.73	(1.28)	1.73×10^{-2}
upstream 2:0 AluS$\pm^1$	-13.02	0.11	(0.32)	-0.25	(0.55)	9.23×10^{-3}
exon 0.225:0.41 nucleosome potential^2	12.99	-0.42	(1.24)	0.26	(0.81)	2.62×10^{-2}
upstream 100:10 L1M^2	12.83	0	(0)	0.03	(0.08)	6.64×10^{-2}
upstream 100:10 L1M^1	12.73	0	(0)	0.15	(0.37)	4.14×10^{-2}
downstream 10:100 LINE_L1^2 $\times$ upstream 5:4 APF^1	12.66	17.90	(22.58)	61.57	(37.34)	5.10×10^{-5}
upstream 9:8 NFuE4^1	12.63	0	(0)	0.10	(0.31)	8.13×10^{-2}
upstream 100:10 LTR_ERV1$\pm^1$	-12.58	0.49	(1.74)	-1.07	(2.53)	1.54×10^{-2}
upstream 100:10 L1M4^2	12.3	0.32	(0.66)	1.52	(1.76)	4.67×10^{-3}
upstream 6:5 GTIIC^3	12.29	0.21	(0.42)	0.50	(0.51)	3.05×10^{-2}
downstream 10:100 LINE_CR1^2	12.21	0.03	(0.05)	0.11	(0.17)	3.29×10^{-2}

Unit is kilobases and it refers to the beginning of the first or the end of the last exon, respectively.
For example, "downstream 10:100" refers to the 90 kb window from 10 kb to 100 kb downstream of the last exon.
^{1} Number of this feature within the sequence window.
$\pm^1$ denotes the ratio of repeated elements in $+$ versus $-$ orientation with respect to the gene. It is the negative inverse if there are more elements in $-$ orientation than in $+$.
^{2} Percentage of the sequence window covered by this feature.
$\pm^2$ Ratio of the percentage of the sequence window covered by repeated elements in $\pm$ orientation.
^{3} Indicator for presence of this feature within the sequence window.
^{10} Methylation prone.
$\times$ indicates pairwise interaction between two variables.

Table 6. Genes proved or predicted with high confidence to be imprinted map to loci linked to various human conditions.

Condition	Band	Locus	Coordinate	Allele	Linkage/Reference
Alcoholism					
	2p14	TSC0053926	66.5	*p*	Linkage to alcoholism (LOD=1.52) (Liu et al., 2005).
		OTX1	63.2	M	Involved in brain development (Boyl et al., 2001).
	12q24	D12S1045	128.8	*m*	Linkage to alcoholism (LOD=3.17; MOD=3.68) (Liu et al., 2005; Strauch et al., 2005).
		Q9HCM7	131.6	M	
	21q22	D21S1440	38.1	*m*	Linkage to alcoholism (MOD=3.86) (Strauch et al., 2005).
		SIM2	37.0	P	Involved in brain development (Goshu et al., 2004).
Alzheimer's					
	10q23	D10S583	94.4		Linkage to Alzheimer's disease (LOD=3.3) (Bertram et al., 2000; Ait-Ghezala et al., 2002).
		Q9H6Z8	92.4	P	
	10q24	D10S1710	102.8		Linkage to Alzheimer's disease (LOD=0.9) (Bertram et al., 2000).
		LDB1	103.8	M	
	12p13	D12S1623	6.8		Linkage to Alzheimer's disease (LOD=3.15) (Mayeux et al., 2002).
		RBP5	7.2	P	
	12p11	D12S1042	27.5		Linkage to Alzheimer's disease (LOD=1.43) (Mayeux et al., 2002).
		ABCC9	21.9	M	
	12q13	D12S398-D12S1632	51.5-54.7		Linkage to Alzheimer's disease (LOD=1.40) (Scott et al., 2000).
		HOXC9	52.7	M	
		HOXC4	52.7	M	
Asthma/Atopy					
	3q21	D3S3606	128.7	*m*	Linkage to allergic sensitization (Z_{all}=4.31) (Lee et al., 2000*b*).
		FTHFD	128.3	M	Mice deficient in this gene show decreased hepatic folate levels (Champion et al., 1994).
	14q24	D14S74	77.7	*p*	Suggestive linkage to atopy and indications for imprinting (MOD=2.88) (Strauch et al., 2001).
		ENSG00000183992	80.7	M	
Autism					
	1q25	D1S1677-D1S1589	156-172.5		Linkage to autism (Bartlett et al., 2005).
		HSPA6	159.8	M	
	7q32	D7S530-D7S640	128.9-132.3	*m*	Linkage to autism (MLS=2.31) (Lamb et al., 2005).
		CPA4	129.7	**M**	Known human imprinted gene (Kayashima et al., 2003).
		MEST	129.9	**P**	Known human imprinted gene (Kobayashi et al., 1997).
	9q34	D9S158-D9S905	136.3-137.2		Linkage to autism (MLS=1.67) (Lamb et al., 2005).
		PHPT1	137.0	M	
		EGFL7	136.8	P	
	10p14	D10S189	6.8		Linkage to autism (MLS=1.15) and schizophrenia (LOD=3.60) (Lamb et al., 2005; DeLisi et al., 2002).
		GATA3	8.1	P	Regulates the development of serotoninergic neurons (van Doorninck et al., 1999). In 30% of autistic people the most frequent dysfunction is the increase of serotonine (Baghdadli et al., 2002). Haploinsufficiency for *GATA3* was observed in a patient with autism and severe mental retardation (Verri et al., 2004).
	17q11	D17S1800	26.7		Linkage to autism-spectrum disorders (MLS=2.83) (Yonan et al., 2003).
	17q11	D17S1871,D17S1824	21.9,23.7	*p*	Suggestive linkage to ASD and indications for imprinting (Bartlett et al., 2005).
		PYY2	23.6	P	

Bipolar disorder					
	1q41	D1S549	217.7	*m*	Linkage to bipolar disorder (MLS=1.43) (McInnis et al., 2003).
		PTPN14	212.6	M	
	2q36	D2S396-D2S206	230.4-233.4	*m*	Linkage to bipolar disorder (HLOD=2.20) (Cichon et al., 2001).
		TIGD1	233.1	P	
	8q24	D8S256	134.5		Linkage to bipolar disorder (NPL=3.13) (McInnis et al., 2003).
		KCNK9	140.7	**M**†	K^+ channel protein involved in neuron apoptosis and cell tumorigenesis (Patel and Lazdunski, 2004).
	14q32	D14S65-D14S78	96.7-99.5	*p*	Linkage to bipolar disorder (HLOD=2.47) (Cichon et al., 2001).
		DLK1	100.3	**P**	Known human imprinted gene (Wylie et al., 2000; Kobayashi et al., 2000).
		MEG3	100.4	**M**	Known human imprinted gene (Miyoshi et al., 2000).
		RTL1	100.4	M	Imprinted in mouse (Seitz et al., 2003) and sheep (Charlier et al., 2001).
Fetal malformation					
	14q12	D14S608	27.9		Paternal UPD results in fetal malformations (Kurosawa et al., 2002).
		FOXG1C	28.3	P†	Shows haploinsufficiency in a patient with severe mental retardation, brain malformations and microcephaly (Shoichet et al., 2005). Mouse orthologue is essential for normal development of the telencephalon (Xuan et al., 1995).
Male homosexuality					
	10q26	D10S217	129.4	*m*	Linkage to male sexual orientation (MLOD=1.81) (Mustanski et al., 2005).
		C10orf91	134.1	M	
		NKX6-2	134.4	M†	Predominantly expressed in the brain (Lee et al., 2001).
		C10orf93	134.6	M	
		VENTX2	134.9	M	
		Q8N377	135.0	M	
		PAOX	135.1	M	
Obesity/Diabetes					
	2q37	D2S2987	242.5		Linkage to type 2 diabetes (LOD=3.19) (Einarsdottir et al., 2006).
	2q37	GATA23A02-GATA178G09M	235.7-237.7	*m*	Linkage to body mass index (BMI) and percentage of fat mass (LOD=2.23/3.34) (Guo et al., 2006).
		Q9Y419	239.4	M	
		MYEOV2	240.7	P	
	3q24	AAT071	151.5	*m*	Linkage to BMI (LOD=1.97) (Guo et al., 2006).
		ZIC1	148.6	M	
	19q13	Mfd232	55.6	*m*	Linkage to BMI (LOD=1.81) (Guo et al., 2006).
		LILRB4	59.9	M	
Schizophrenia					
	1q42	D1S2709	228.3		Linkage to schizophrenia (LOD=2.71) (Ekelund et al., 2001).
		OBSCN	224.7	P	
		HIST3H2BB	225	M	
	8p11	D8S532	40.9		Linkage to schizophrenia (LOD=3.06) (Stefansson et al., 2002).
		PURG	31	P	
	9q21	D9S922	80		Linkage to schizophrenia (LOD=1.95) (Hovatta et al., 1999).
		NP_001001670	81.8	M	
	22q11	*PRODH2-DGCR6*	17.3		Linkage to schizophrenia (Liu et al., 2002).
		DGCR6	17.3	P	Expressed in the developing and adult mouse brain (Maynard et al., 2003).

The table lists loci that have previously been linked to various human conditions, and high-confidence imprinted gene candidates that map into or within 10 mb (or less) of that locus. If a locus has been observed to have a parent-of-origin effect, this is denoted by a lowercase *m* or *p*, for maternal or paternal effects, respectively. Genes predicted to be expressed from the maternal or paternal allele are denoted by M or P, respectively. Genes also predicted to be imprinted in the mouse are marked by †. Alleles that have been proved to be exclusively expressed are printed in bold face.

Supplementary Methods

We used a number of criteria to prioritize our 156 predictions for experimental validation: large posterior probabilities of being imprinted (in the case of SMLR), large signed hyperplane distances (in the case of SVM), potential involvement in an important condition (such as a cancer or one of the conditions listed in Table 2), and location in a chromosome not known to contain imprinted genes (many imprinted genes have to date been identified by searching near known imprinted genes, so finding some on a completely different chromosome would be compelling; also this would ensure we would not see confounding effects related to known imprinted genes nearby). We further decided that we wanted one candidate to have an orthologue predicted to be imprinted in the mouse but the other not, to emphasize that the two sets of predictions do not overlap significantly and that novel human imprinted genes can be discovered even without relying on any conservation of imprinting status between human and mouse. This resulted in a high-priority list of five genes. We then quickly screened the conceptuses we had available to determine for each gene, whether a sufficient number possessed an informative genotype that would permit us to experimentally detect monoallelic expression. After this, we narrowed our list to *DLGAP2* and *KCNK9*, and these were the only two genes for which we undertook a detailed validation of imprinting status.

DLGAP2 (Disks large-associated protein 2), also known as *DAP-2*, is annotated to have four splice variants (UCSC Genome Website, May 2004 assembly (Karolchik et al., 2003)). The four splice variants chr8.27.24, chr8.27.25, chr8.27.26, and chr8.27.27, are referred to as *DLGAP2*-24, -25, -26, and -27, respectively. Variants *DLGAP2*-24 and *DLGAP2*-27 lack exon 7 compared to isoforms *DLGAP2*-25 and *DLGAP2*-26. Conversely, isoforms *DLGAP2*-24 and *DLGAP2*-25 share common exons in the $3'$ end, which are absent from *DLGAP2*-26 and *DLGAP2*-27 and vice-versa. Thus, we were able to distinguish the four transcripts as follows (see Supplementary Fig. 2 for a schematic). Isoforms *DLGAP2*-24 and *DLGAP2*-25 were reverse transcribed using primer DLGAP2-RT1 (square), while DLGAP2-RT2 (diamond)

was used to reverse transcribe *DLGAP2*-26 and *DLGAP2*-27. cDNA from *DLGAP2*-24 and *DLGAP2*-27 was specifically amplified using reverse primer DLGAP2-M1R (upward triangle), while DLGAP2-M2R (downward triangle) was used to amplify *DLGAP2*-25 and *DLGAP2*-26. DLGAP2-M1F (circle) was used as a common forward primer to amplify cDNA. When amplifying cDNA, the primers bridged two long introns, ruling out any potential influence of undigested genomic DNA. Genomic DNA was amplified and sequenced using DLGAP2-1F and DLGAP2-1R.

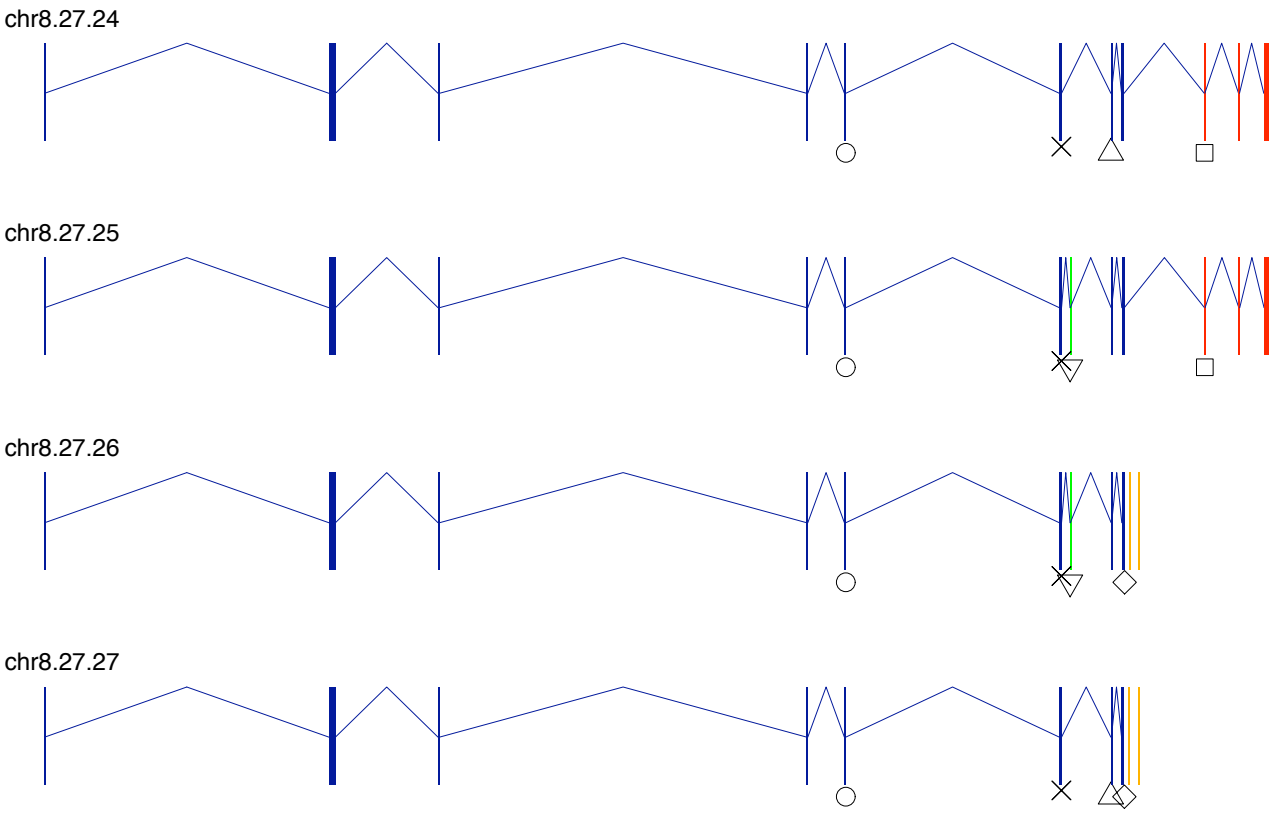


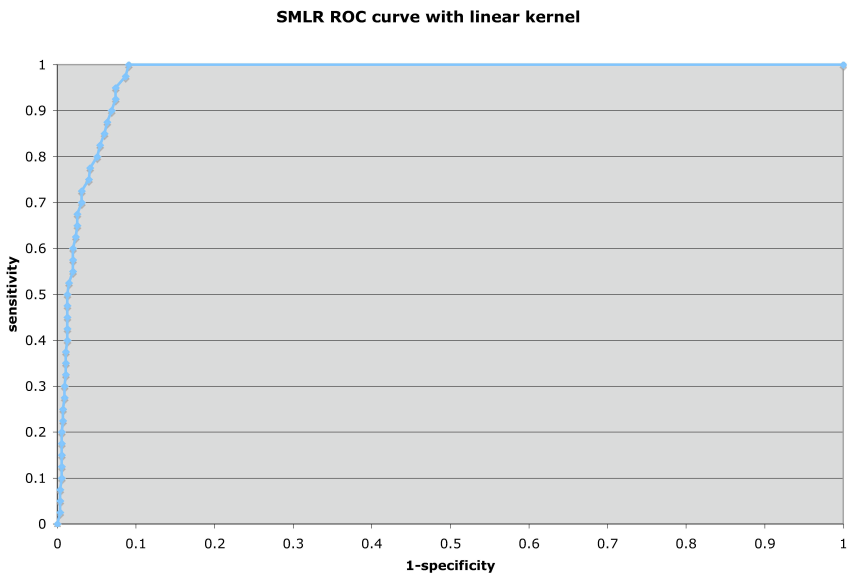
Figure 2. Schematic representation of the four *DLGAP2* isoforms studied. Vertical lines represent exons. Exons colored in dark blue are shared in common among all isoforms, red exons are unique to *DLGAP2*-24 and *DLGAP2*-25, the green exon is unique to *DLGAP2*-25 and *DLGAP2*-26, and the orange exons are unique to *DLGAP2*-26 and *DLGAP2*-27. The primers used for reverse transcription, DLGAP2-RT1 and DLGAP2-RT2, are represented as a square and a diamond, respectively. The PCR primers DLGAP2-M1R, DLGAP2-M2R, and DLGAP2-M1F are depicted as an upward triangle, a downward triangle, and a circle, respectively. The cross symbolizes the polymorphic sites.

KCNK9 (potassium channel, subfamily K, member 9), also known as *TASK-3*, is annotated to have one isoform. We used primers KCNK9-1F and -1R for the amplification of genomic DNA. cDNA was amplified using KCNK9-M1F and -M1R, which bridge an 84kb intron.

Table 7. Primers used for expression analysis of *DLGAP2* and *KCNK9*.

Name	Sequence 5′ -. . . -3′	Position
DLGAP2-1F	TAGGCTAGACGTCCAGGAACA	1603779-1603799
DLGAP2-1R	TATTGGCAGGACTGAGTGGAG	1604304-1604284
DLGAP2-RT1	ACATGAGAAGCTGGGCACTC	2585-2604†
DLGAP2-RT2	CGTCACCTCCATCGACTTCT	2651-2670‡
DLGAP2-M1F	CAGCTACCTTCGAGCCATTC	1605-1624†
DLGAP2-M1R	GGCCGTTTCCACCTGAATC	2048-2066†
DLGAP2-M2R	TGATGCTCTGGGAATTCAG	2059-2077‡
KCNK9-1F	CAAGGCCTTCTGCATGTTCT	53849487-53849468
KCNK9-1R	GTGAATGACCATGCTGTTGC	53848983-53849002
KCNK9-M1F	TCCTTCTACTTTGCGATCACG	53933168-53933148
KCNK9-M1R	CATGGTCAAGAACCTGAGGAC	53849058-53849078

Positions for *DLGAP2* primers refer to GI37552484, chr8.27.24 (†), and chr8.27.26 (‡). Positions for *KCNK9* primers are given for GI51467074.



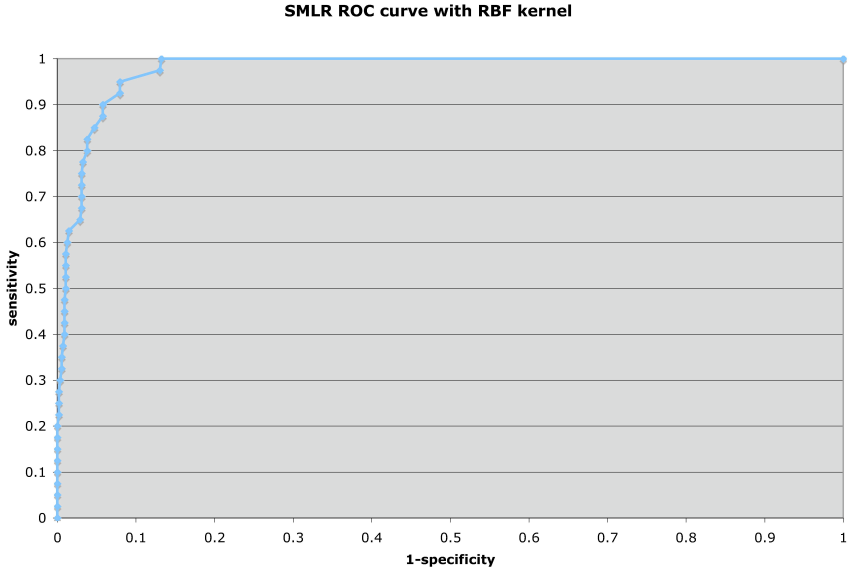


Figure 3. A receiver operator characteristic (ROC) curve illustrating the relationship between sensitivity and specificity for the SMLR classifier under the two different kernel functions, linear and RBF.

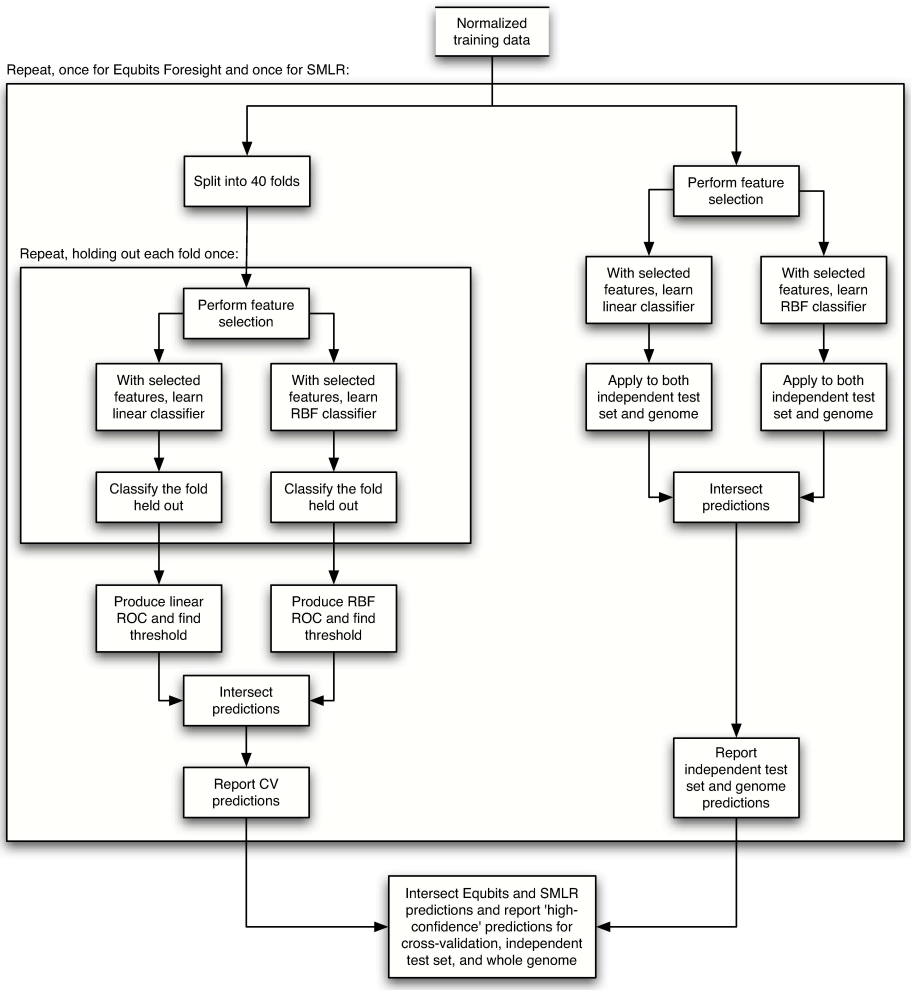


Figure 4. Flow-chart illustrating schematically the processes of cross-validation, training, testing, and prediction under two different kernels and employing both the Equbits and SMLR classifier learning strategies.

Table 8. Independent negative test genes.

Gene	Band	Expression	Reference
Stochastic monoallelic expression			
IL2	4q27	X	Monoallelically expressed (Hollander et al., 1998).
IL4	5q23	X	Monoallelically expressed (Bix and Locksley, 1998).
IL5	5q23	X	Monoallelically expressed (Kelly and Locksley, 2000).
IL13	5q23	X	Monoallelically expressed (Kelly and Locksley, 2000).
OR2A1	7q35	X	Monoallelically expressed (Singh et al., 2003).
TLR4	9q33	X	Monoallelically expressed (Pereira et al., 2003).
SFTPD	10q22	X	Heterogeneous allele-specific expression in extrapulmonary tissues (Lin and Floros, 2002).
KLRC1	12p13	X	Monoallelically expressed (Vance et al., 2002).
KLRA1	12p13	X	Monoallelically expressed (Tanamachi et al., 2001; Byun et al., 2003).
NUBP2	16p13	X	Monoallelically expressed (Sano et al., 2001).
IGFALS	16p13	X	Monoallelically expressed (Sano et al., 2001).
JSAP1	16p13	X	Monoallelically expressed (Sano et al., 2001).
OR7A17	19p13	X	Monoallelically expressed (Singh et al., 2003).
Presumed biallelic expression			
CD2	1p13	X	Synchronously replicated (Mostoslavsky et al., 2001).
APOB	2p24	X	Synchronously replicated (Kitsberg et al., 1993).
GPD2	2q24	X	No evidence of imprinting (Piras et al., 2000).
IGFBP5	2q35	X	No evidence of imprinting (Piras et al., 2000).
RPL23	2q36	X	Biallelically expressed (Greally et al., 1998).
Gt(ROSA)26asSor	3p25	X	Biallelically expressed (Singh et al., 2003).
MSX1	4p16	X	No evidence of imprinting (Blin-Wakkach et al., 2001).
GHR	5p12	X	Biallelically expressed (Buettner et al., 2004).
OSMR	5p13	X	Biallelically expressed (Buettner et al., 2004).
PRLR	5p13	X	Biallelically expressed (Buettner et al., 2004).
IL7R	5p13	X	Biallelically expressed (Buettner et al., 2004).
NPR3	5p13	X	Biallelically expressed (Buettner et al., 2004).
SEMA5A	5p15	X	Biallelically expressed (Buettner et al., 2004).
CDH10	5p14	X	Biallelically expressed (Buettner et al., 2004).
GABRA6	5q34	X	Biallelically expressed (Takahashi and Ko, 1993).
SLC22A1	6q25	X	Biallelically expressed (Schweifer et al., 1997).
SOD2	6q25	X	Biallelically expressed in mouse (Barlow et al., 1991).
TCP1	6q25	X	Biallelically expressed in mouse (Barlow et al., 1991).
MAS1	6q25	X	Biallelically expressed in mouse (Schweifer et al., 1997; Lyle et al., 2000).
PLG	6q26	X	Biallelically expressed in mouse (Barlow et al., 1991).
COL1A2	7q21	X	Biallelically expressed (Mizuno et al., 2002).
ACTB	7p22	X	Biallelically expressed (Zhang et al., 1994).
ACHE	7q22	X	Synchronously replicated (Kitsberg et al., 1993).
UBE2H	7q32	X	Biallelically expressed (Yamada et al., 2003).
MKRN1	7q34	X	No evidence of imprinting (Walter and Paulsen, 2003).
SDC2	8q22	X	Biallelically expressed (Buettner et al., 2004).
FZD6	8q22	X	Biallelically expressed (Buettner et al., 2004).
NOV	8q24	X	Biallelically expressed (Buettner et al., 2004).
MYC	8q24	X	Synchronously replicated (Chess et al., 1994).
DOCK8	9p24	X	Biallelically expressed (Lerer et al., 2005).
TYRL	11p11	X	Synchronously replicated (Singh et al., 2003).
PAX6	11p13	X	Biallelically expressed (van Raamsdonk and Tilghman, 2000).
GAS2	11p14	X	No evidence of imprinting (Piras et al., 2000).
STIM1	11p15	X	Biallelically expressed (Overall et al., 1998).
TPH1	11p15	X	Biallelically expressed (Buettner et al., 2004).
CARS	11p15	X	Biallelically expressed (Clark et al., 2002).
RNH	11p15	X	Biallelically expressed (Rachmilewitz et al., 1993).
TH	11p15	X	Biallelically expressed (Reik and Walter, 2001).
ASCL2	11p15	X	Imprinted in mouse but not in human (Monk et al., 2006).
CTSD	11p15	X	Biallelically expressed in human hydatidiform mole, mature teratoma, and normal placenta (Rachmilewitz et al., 1993).

RRM1	11p15	X	No evidence of imprinting (Byrne and Smith, 1993).
DUSP8	11p15	X	Biallelically expressed (Goldberg et al., 2003).
NAP1L4	11p15	X	Biallelic expression in multiple murine fetal and adult tissues (Hu et al., 1996; Paulsen et al., 1998; Umlauf et al., 2004), not imprinted in the human (Monk et al., 2006).
PYGM	11q13	X	Synchronously replicated (Kitsberg et al., 1993).
CD3D	11q23	X	Synchronously replicated (Kitsberg et al., 1993).
GAPD	12p13	X	Biallelically expressed (Paulsen et al., 1998).
CD4	12p13	X	Biallelically expressed (Williamson et al., 1995).
DCN	12q21	X	Imprinted in mouse but not in human (Monk et al., 2006).
RB1	13q14	X	Synchronously replicated (Amiel et al., 1999).
YY1	14q32	X	Biallelically expressed (Yevtodiyenko et al., 2002).
WARS	14q32	X	Biallelically expressed (Yevtodiyenko et al., 2002).
PPP2R5C	14q32	X	Biallelically expressed (Tierling et al., 2006).
DNCHC1	14q32	X	Biallelically expressed (Tierling et al., 2006).
HERC2	15q11	X	Biallelically expressed (Chai et al., 2003).
NDNL2	15q13	X	Biallelically expressed (Chibuk et al., 2001).
DUOX1	15q21	X	No evidence of imprinting (Sandell et al., 2003).
SLC28A2	15q21	X	No evidence of imprinting (Sandell et al., 2003).
DUOX2	15q21	X	No evidence of imprinting (Sandell et al., 2003).
SLC30A4	15q21	X	No evidence of imprinting (Sandell et al., 2003).
GATM	15q21	X	Imprinted in mouse but not in human (Monk et al., 2006).
TP53	17p13	X	Synchronously replicated (Kitsberg et al., 1993).
RPL19	17q12	X	Biallelically expressed (Piras et al., 2000).
ERBB2	17q12	X	Synchronously replicated (Amiel et al., 1999).
APLP1	19q13	X	Biallelically expressed (Buettner et al., 2004).
MAG	19q13	X	Biallelically expressed (Buettner et al., 2004).
SCN1B	19q13	X	Biallelically expressed (Buettner et al., 2004).
GRIK5	19q13	X	Biallelically expressed (Buettner et al., 2004).
APOE	19q13	X	Biallelically expressed (Buettner et al., 2004).
KCNA7	19q13	X	Biallelically expressed (Buettner et al., 2004).
SYT3	19q13	X	Biallelically expressed (Buettner et al., 2004).
GRIN2D	19q13	X	Biallelically expressed (Buettner et al., 2004).
HRC	19q13	X	Biallelically expressed (Buettner et al., 2004).
KCNC3	19q13	X	Biallelically expressed (Buettner et al., 2004).
RRAS	19q13	X	Synchronously replicated (Kitsberg et al., 1993).
E2F1	20q11	X	Biallelically expressed (Williamson et al., 1995).
BC10, BLCAP	20q11	X	Biallelically expressed (Evans et al., 2001; John et al., 2001).
PLCG1	20q12	X	Biallelically expressed (Williamson et al., 1995).
PPGB	20q13	X	Biallelically expressed (Williamson et al., 1994).
TNFRSF5	20q13	X	Biallelically expressed (Williamson et al., 1995).
KCNB1	20q13	X	Biallelically expressed (Williamson et al., 1995).
CYP24A1	20q13	X	Biallelically expressed (Williamson et al., 1995).
EDN3	20q13	X	Biallelically expressed (Williamson et al., 1995).
PCK1	20q13	X	Biallelically expressed (Williamson et al., 1995).
NTSR1	20q13	X	Biallelically expressed (Williamson et al., 1995).
BMP7	20q13	X	No evidence of imprinting (Marker et al., 1995).
CDH4	20q13	X	Synchronously replicated (Williamson et al., 1995).
RUNX1	21q22	X	Synchronously replicated (Dotan et al., 2000).
PFKL	21q22	X	Synchronously replicated (Kitsberg et al., 1993).

Expression can be one of the following: P (Imprinted and paternally expressed), M (Imprinted and maternally expressed), or X (Not imprinted). All 101 genes were correctly predicted not to be imprinted by the combined classifier. The experimental results cited here may relate to either mouse or human.

Table 9. Training genes of known imprint status.

Gene	Band	Expression	Reference
Imprinted			
ARHI	1p31	P	Yu et al. (1999); Luo et al. (2001)
TP73	1p36	M	Kaghad et al. (1997); Mai et al. (1998); Cai et al. (2000)
HYMAI	6q24	P	Arima et al. (2000)
PLAGL1	6q24	P	Kamiya et al. (2000)
GRB10	7p12	I	Blagitko et al. (2000); Yoshihashi et al. (2000)
DLX5	7q21	M	Okita et al. (2003)
PPP1R9A	7q21	M	Nakabayashi et al. (2004)
SGCE	7q21	P	Zimprich et al. (2001)
PEG10	7q21	P	Ono et al. (2001)
CPA4	7q32	M	Kayashima et al. (2003)
MEST	7q32	P	Kobayashi et al. (1997)
WT1	11p13	P	Dallosso et al. (2004)
IGF2	11p15	P	Ogawa et al. (1993*a*); Ohlsson et al. (1993); Rainier et al. (1993)
OSBPL5	11p15	M	Higashimoto et al. (2002)
SLC22A1L	11p15	M	Dao et al. (1998); Cooper et al. (1998*a*)
CDKN1C	11p15	M	Matsuoka et al. (1996); Chung et al. (1996); Taniguchi et al. (1997)
ZNF215	11p15	M	Alders et al. (2000)
KCNQ1DN	11p15	M	Xin et al. (2000)
PHLDA2	11p15	M	Qian et al. (1997)
SLC22A1LS	11p15	M	Cooper et al. (1998*b*); Bajaj et al. (2004)
KCNQ1	11p15	M	Lee et al. (1997)
H19	11p15	M	Zhang and Tycko (1992); Rachmilewitz et al. (1992); Rainier et al. (1993)
IGF2AS	11p15	P	Okutsu et al. (2000)
INS	11p15	P	Moore et al. (2001)
SMPD1	11p15	M	Simonaro et al. (2006)
MEG3	14q32	M	Miyoshi et al. (2000)
DLK1	14q32	P	Wylie et al. (2000); Kobayashi et al. (2000)
SNURF	15q11	P	Gray et al. (1999)
MKRN3	15q11	P	Driscoll et al. (1992); Glenn et al. (1993, 1997); Jong et al. (1999)
NDN	15q11	P	MacDonald and Wevrick (1997); Jay et al. (1997)
MAGEL2	15q11	P	Boccaccio et al. (1999); Lee et al. (2000*a*)
IPW	15q11	P	Wevrick et al. (1994)
UBE3A	15q12	M	Rougeulle et al. (1997); Vu and Hoffman (1997)
ATP10A	15q12	M	Meguro et al. (2001); Herzing et al. (2001)
TCEB3C	18q21	M	Strichman-Almashanu et al. (2001)
ZIM2	19q13	P	Murphy et al. (2001); Van den Veyver et al. (2001)
NNAT	20q11	P	Evans et al. (2001)
NESP55	20q13	M	Hayward et al. (1998)
L3MBTL	20q13	P	Li et al. (2004)
GNAS1	20q13	P	Liu et al. (2000)
Non-imprinted			
NGFB	1p13	X	P. Luedi (unpublished)
CDKN2C	1p32	X	Cost et al. (1997)
COMMD1	2p15	X	Nabetani et al. (1997)
CDKN1A	6p21	X	Cost et al. (1997)
SERPINB6	6p25	X	P. P. Luedi (unpublished)
IGF2R	6q25	X	Kalscheuer et al. (1993); Ogawa et al. (1993*b*); Killian et al. (2001)
EGFR	7p11	X	Wakeling et al. (1998)
COBL	7p12	X	Hitchins et al. (2002)
DDC	7p12	X	Hitchins et al. (2002)
IGFBP3	7p13	X	Eggermann et al. (1999); Wakeling et al. (2000)
IGFBP1	7p13	X	Eggermann et al. (1999); Wakeling et al. (2000)
CPA1	7q32	X	Bentley et al. (2003)
HSPC216	7q32	X	Yamada et al. (2003)
NRF1	7q32	X	Yamada et al. (2003)

TSGA14	7q32	X	Yamada et al. (2002)
KIAA0265	7q32	X	Yamada et al. (2003)
Flj14803	7q32	X	Yamada et al. (2003)
CPA2	7q32	X	Bentley et al. (2003)
UBE2H	7q32	X	Yamada et al. (2003)
CNTNAP2	7q36	X	P. P. Luedi (unpublished)
EN2	7q36	X	P. P. Luedi (unpublished)
C9ORF39	9p22	X	P. P. Luedi (unpublished)
NOR1/NR4A3	9q22	X	P. P. Luedi (unpublished)
SAMD6	9q22	X	K. S. Kucera (unpublished)
C10orf9	10p11	X	P. P. Luedi (unpublished)
SFMBT2	10p14	X	P. P. Luedi (unpublished)
C10ORF28	10q24	X	P. P. Luedi (unpublished)
PHEMX	11p15	X	Paulsen et al. (2000); Monk et al. (2006)
DRD4	11p15	X	Cichon et al. (1996)
MUCDHL	11p15	X	Goldberg et al. (2003)
MRPL23	11p15	X	Ishihara et al. (1998); Paulsen et al. (2000)
CD81	11p15	X	Maecker et al. (1998); Gabriel et al. (1998); Monk et al. (2006)
TNNT3	11p15	X	Yuan et al. (1996)
HRAS	11p15	X	Goldberg et al. (2003)
TSSC4	11p15	X	Paulsen et al. (2000)
C11ORF2	11q13	X	Zhu et al. (2000)
NEU3	11q13	X	P. P. Luedi (unpublished)
CDKN1B	12p13	X	Cost et al. (1997)
NOVA1	14q12	X	K. S. Kucera, P. P. Luedi (unpublished)
CYFIP1	15q11	X	Chai et al. (2003)
NIPA2	15q11	X	Chai et al. (2003)
TUBGCP5	15q11	X	Chai et al. (2003)
NIPA1	15q11	X	Chai et al. (2003)
C15ORF2	15q11	X	Farber et al. (2000)
OCA2	15q12	X	Chai et al. (2003)
GABRB3	15q12	X	Chai et al. (2003)
GABRG3	15q12	X	Chai et al. (2003)
CABLES	18q11	X	P. P. Luedi (unpublished)
IMPACT	18q11	X	Morison et al. (2001)
JAG1	20p12	X	P. P. Luedi (unpublished)
TH1L	20q13	X	Bonthron et al. (2000)
CTSZ	20q13	X	Bonthron et al. (2000)

Expression can be one of the following: P (Imprinted and paternally expressed), M (Imprinted and maternally expressed), or X (Not imprinted). The *GRB10* locus encodes oppositely imprinted transcripts and was excluded from the maternal/paternal model (denoted by I). The experimental results cited here may relate to either mouse or human.

Table 10. Randomly chosen control genes.

Ensembl ID	Band		Ensembl ID	Band		Ensembl ID	Band		Ensembl ID	Band	
065183 (*WDR3*)	1p12	i	053900 (*NM_013367*)	4p15	t	184879	9q13	i	183000	15q26	i
092621 (*PHGDH*)	1p12	f	159788 (*RGS12*)	4p16	t	165059 (*PRKACG*)	9q21	f	183208	15q26	t
134245 (*WNT2B*)	1p13	t	177631 (*NM_182524*)	4p16	t	135045 (*NM_017998*)	9q21	f	184508 (*Q8N4P3*)	15q26	f
134253 (*TRIM45*)	1p13	t	130997 (*NM_181808*)	4p16	f	106782 (*CHAC*)	9q21	f	185442 (*Q8NBH7*)	15q26	f
007341 (*ST7L*)	1p13	t	178988 (*NM_152301*)	4p16	t	135049 (*AGTPBP1*)	9q21	t	185594 (*NM_173499*)	15q26	f, i
116793 (*PHTF1*)	1p13	f	179010 (*NM_033296*)	4p16	i	186632	9q21	f	185907 (*NM_018621*)	15q26	f
122481 (*RWDD3*)	1p21	t	159692 (*CTBP1*)	4p16	f, t	186747 (*Q8N493*)	9q21	f	186092	15q26	t
173146 (*Q96CI4*)	1p21	t	087269 (*C4orf9*)	4p16	t	136936 (*XPA*)	9q22	f	180096 (*SEPT1*)	16p11	t
117600 (*NM_014839*)	1p21	t	170891 (*C17*)	4p16	f	106809 (*OGN*)	9q22	f	175995 (*NM_175901*)	16p11	t
162688 (*AGL*)	1p21	f, i	184855	4p16	t	021374 (*IARS*)	9q22	t	179755 (*NM_153227*)	16p11	f
142951	1p21	f	109184 (*NM_015115*)	4q11	i	158122	9q22	i	179965 (*NM_016643*)	16p11	t
069702 (*TGFBR3*)	1p22	i	179378 (*NM_006692*)	4q13	i	185544	9q22	t	149925 (*ALDOA*)	16p11	f
122417 (*Q9ULJ1*)	1p22	t	124882 (*EREG*)	4q13	f	106692 (*FCMD*)	9q31	f	169861	16p11	t
097096 (*Q8NDB8*)	1p22	i	087128 (*DES1*)	4q13	i	186943 (*Q8NGS7*)	9q31	t	181601	16p11	f
171488 (*NM_032270*)	1p22	t	124875 (*CXCL6*)	4q13	t	187003 (*ACTL7A*)	9q31	f	183604 (*Q9H2H6*)	16p11	i
117174 (*NM_017953*)	1p22	f	135222 (*CSN2*)	4q13	f	136868 (*SLC31A1*)	9q32	i	184110 (*EIF3S8*)	16p11	t
153898 (*MCOLN2*)	1p22	f	081051 (*AFP*)	4q13	i	173238 (*Q9P1E1*)	9q32	t	175758 (*Y220*)	16p12	t
162624 (*Q9BYB7*)	1p31	t	079557 (*AFM*)	4q13	i	173242	9q32	f	169344 (*UMOD*)	16p12	i
178965 (*Q8ND41*)	1p31	f	186942 (*Q9BQR7*)	4q13	i	136856 (*SLC2A8*)	9q33	t	047578 (*Q8N803*)	16p12	i
079739 (*PGM1*)	1p31	i	173130 (*Q9P1E1*)	4q21	t	119446 (*NM_033117*)	9q33	t	179038 (*NM_145237*)	16p12	f
117114 (*LPHN2*)	1p31	t	138670 (*NM_152545*)	4q21	t	136950 (*NM_030978*)	9q33	i	103275 (*UBE2I*)	16p13	i, t
116641 (*DOC7*)	1p31	t	138759 (*FRAS1*)	4q21	i	136861 (*CDK5RAP2*)	9q33	i	103197 (*TSC2*)	16p13	i
162433 (*AK3*)	1p31	f	138769 (*CDKL2*)	4q21	t	160446 (*ZDHHC12*)	9q34	f	095917 (*TPSD1*)	16p13	f
185483 (*ROR1*)	1p31	t	118785 (*SPP1*)	4q22	t	165699 (*TSC1*)	9q34	t	162009 (*SSTR5*)	16p13	i
162402 (*USP24*)	1p32	t	174421 (*Q9P1E1*)	4q22	t	119363 (*SPTAN1*)	9q34	f	162065 (*Q9ULP9*)	16p13	t
134744 (*Q12764*)	1p32	i	163644 (*NM_152542*)	4q22	i	160271 (*RALGDS*)	9q34	f	171559 (*Q96EU1*)	16p13	i
162398 (*NM_152607*)	1p32	i	138641 (*HERC3*)	4q22	t	107290 (*NM_015046*)	9q34	t	069651 (*NPIP*)	16p13	f
121310 (*NM_018281*)	1p32	i	052592 (*DMP1*)	4q22	i	125484 (*GTF3C4*)	9q34	t	161998 (*NM_145294*)	16p13	t
058804 (*NM_018087*)	1p32	i	164035 (*NM_016242*)	4q24	f	136877 (*FPGS*)	9q34	t	153060 (*NM_144674*)	16p13	f
162384 (*NM_017887*)	1p32	i	179078	4q24	i	169583 (*CLIC3*)	9q34	f	161995 (*NM_053284*)	16p13	i
181150	1p32	i	109534 (*NOLA1*)	4q25	t	148408 (*CACNA1B*)	9q34	t	168101 (*NM_032349*)	16p13	i
186857 (*Q9HBS7*)	1p32	f	174720 (*NM_016648*)	4q25	f	160323 (*ADAMTS13*)	9q34	t	059122 (*NM_032296*)	16p13	i
142973 (*CYP4B1*)	1p33	i	145384 (*FABP2*)	4q26	t	159247	9q34	t	033011 (*NM_019109*)	16p13	i
186160 (*NM_178134*)	1p33	i	170917 (*NUDT6*)	4q27	i	177185	9q34	f	100726 (*NM_016111*)	16p13	t
054116 (*TRAPPC3*)	1p34	f	138686 (*BBS7*)	4q27	i	186350 (*RXRA*)	9q34	f	072864 (*NDE1*)	16p13	f, t
132773 (*TOE1*)	1p34	f	164057	4q28	t	187195 (*NM_030898*)	9q34	f	102858 (*MGRN1*)	16p13	f
126091 (*SIAT6*)	1p34	i	109424 (*UCP1*)	4q31	i	136737 (*ZNF25*)	10p11	f	103313 (*MEFV*)	16p13	t
131238 (*PPT1*)	1p34	t	153130 (*SCOC*)	4q31	f	173776 (*Q96HT2*)	10p11	f	103222 (*ABCC1*)	16p13	t
179178 (*NM_144626*)	1p34	t	137460 (*Q9C0D6*)	4q31	f	177353 (*O75029*)	10p11	f	103229 (*ABAT*)	16p13	i
117400 (*MPL*)	1p34	i	151623 (*NR3C2*)	4q31	t	177291 (*NM_153368*)	10p11	f	166737	16p13	i
127129 (*EDN2*)	1p34	t	137463 (*NM_032623*)	4q31	t	183621 (*NM_182755*)	10p11	f	184629 (*Q8NCX2*)	16p13	f
171812 (*COL8A2*)	1p34	f, t	180484 (*NM_024914*)	4q31	f	151025 (*Q9ULT3*)	10p12	f	069329 (*VPS35*)	16q11	t
117407 (*ARTN*)	1p34	i	109452 (*INPP4B*)	4q31	i	095739 (*NMA*)	10p12	i	129635 (*Q9P1B8*)	16q11	t
185421	1p34	f	164142	4q31	f	150051 (*NM_173576*)	10p12	i	103460 (*TNRC9*)	16q12	t
186444 (*TMSL1*)	1p34	f	151005 (*NM_032136*)	4q32	f	182649	10p12	f	103494 (*Q9Y2K8*)	16q12	t
186973	1p34	f	171557 (*FGG*)	4q32	f	152465 (*NMT2*)	10p13	i	166152 (*NM_144602*)	16q12	f
084628 (*TCBA1*)	1p35	f	164117 (*FBXO8*)	4q34	i	134465 (*Q8TE30*)	10p15	f	129636 (*NM_030790*)	16q12	i
175089 (*Q9BXE6*)	1p35	f	185075 (*Q9H399*)	4q34	t	180525 (*Q8N8Z3*)	10p15	i	171208 (*NETO2*)	16q12	f, t
168528 (*NM_178865*)	1p35	f	173320 (*Q9P2F5*)	4q35	t	134453 (*NM_032905*)	10p15	f	169715 (*MT1E*)	16q12	f
134668 (*NM_144569*)	1p35	i	180712 (*NM_173796*)	4q35	i	165568 (*NM_031436*)	10p15	i	102978 (*POLR2C*)	16q13	f, i
121774 (*KHDRBS1*)	1p35	t	164303 (*NM_153343*)	4q35	i	134460 (*IL2RA*)	10p15	t	070729 (*CNGB1*)	16q13	i
183615 (*YSEC*)	1p35	f, t	109771 (*NM_018409*)	4q35	t	172619 (*Y514*)	10q11	i	187185 (*Q86VG7*)	16q13	f
125945 (*ZNF436*)	1p36	f	168556 (*ING1L*)	4q35	f	177457 (*NM_173524*)	10q11	t	103043 (*TAX1BP2*)	16q22	f
133226 (*SRRM1*)	1p36	i	151726 (*FACL6*)	4q35	f, t	165388 (*NM_153034*)	10q11	t	140824 (*TAT*)	16q22	i
173413 (*Q9BXE6*)	1p36	t	075705 (*DUX2*)	4q35	t	170324 (*NM_152428*)	10q11	i	157405 (*Q96JG3*)	16q22	f
179589 (*Q8NA34*)	1p36	t	182552 (*NM_152682*)	4q35	t	152728 (*NM_147156*)	10q11	f	159708 (*NM_018296*)	16q22	i
008130 (*PPNK*)	1p36	f	186158	4q35	i	148582	10q11	f	090857 (*NM_017990*)	16q22	f
177799 (*O4F3*)	1p36	t	172239 (*NM_182789*)	5p12	t	122952 (*ZWINT*)	10q21	t	038358 (*NM_014329*)	16q22	i
175262 (*NM_173507*)	1p36	t	178846 (*NM_175921*)	5p13	f	108064 (*TCF6L1*)	10q21	i	168625 (*HYDIN*)	16q22	f
175087 (*NM_152835*)	1p36	t	113361 (*CDH6*)	5p13	f	170312 (*CDC2*)	10q21	i	090863 (*GLG1*)	16q22	i
160072 (*NM_031921*)	1p36	f	113460 (*BRIX*)	5p13	i	079332 (*SARA1*)	10q22	t	135723 (*FHOD1*)	16q22	i
117701 (*NM_022078*)	1p36	t	182564	5p13	t	107719 (*Q9ULE6*)	10q22	f	103089 (*FAXDC1*)	16q22	f
127054 (*NM_017871*)	1p36	f	182977 (*Q9P1I1*)	5p13	t	122861 (*PLAU*)	10q22	t	103018 (*CYM5*)	16q22	i
177000 (*MTHFR*)	1p36	t	153416 (*ZDHHC11*)	5p15	t	178365 (*NUDT13*)	10q22	f	141076 (*CIRH1A*)	16q22	i
008125 (*MMP23A*)	1p36	t	142319 (*SLC6A3*)	5p15	i	166220 (*NM_152710*)	10q22	i	062038 (*CDH3*)	16q22	i
158748 (*HTR6*)	1p36	i	133398 (*Q9BTT4*)	5p15	i	122359 (*ANXA11*)	10q22	f	067955 (*CBFB*)	16q22	t
162426 (*DNB5*)	1p36	f	164363 (*NM_182632*)	5p15	i	182180 (*DNAJC9*)	10q22	t	166454 (*Y431*)	16q23	i
117682 (*DHDDS*)	1p36	f	173545 (*NM_033414*)	5p15	i	182523	10q22	t	166455 (*NM_152337*)	16q23	t
162438 (*CTRC*)	1p36	i	125063 (*NM_017808*)	5p15	f	180850 (*NM_178512*)	10q23	i	153815 (*NM_030629*)	16q23	i, t
169504 (*CLIC4*)	1p36	f	176788 (*BASP1*)	5p15	i	152778 (*IFT5*)	10q23	i	140905 (*GCSH*)	16q23	t
171735 (*CAMTA1*)	1p36	f	184204	5p15	f	165678 (*GHITM*)	10q23	t	168589 (*DNCL2B*)	16q23	f
053371 (*AKR7A2*)	1p36	t	164512 (*NM_024669*)	5q11	f	138180 (*C10orf3*)	10q23	i	166522	16q23	f
158803	1p36	f	153914 (*SFRS12*)	5q12	f	148835 (*TAF5*)	10q24	i	131149 (*Y182*)	16q24	t
186410	1p36	i	113598 (*NM_019072*)	5q12	i	095637 (*SORBS1*)	10q24	i	140950 (*Q9HCG3*)	16q24	f
160670 (*S100A6*)	1q21	f	164253 (*NM_018268*)	5q13	i	156398 (*SFXN2*)	10q24	f	131153 (*NM_016095*)	16q24	i
177954 (*RPS27*)	1q21	i	132835 (*NM_013303*)	5q13	t	107816 (*Q8N1I9*)	10q24	f	124391 (*IL17C*)	16q24	f
143545 (*RAB13*)	1q21	i	113161 (*HMGCR*)	5q13	f	171160 (*NM_178832*)	10q24	f	178773 (*CPNE7*)	16q24	f
163155 (*Q96S90*)	1q21	t	181104 (*F2R*)	5q13	f	075826 (*NM_015490*)	10q24	t	182376 (*NM_182605*)	16q24	f
178527 (*Q8N9C2*)	1q21	t	164300 (*NM_178276*)	5q14	f	065613 (*NM_014720*)	10q24	f	183967	16q24	f
143615 (*O14634*)	1q21	i	164299 (*NM_032567*)	5q14	i	148820 (*LDB1*)	10q24	i	133030 (*NM_015134*)	17p11	t
160741 (*NM_181715*)	1q21	t	174715	5q14	f	138136 (*LBX1*)	10q24	t	072210 (*ALDH3A2*)	17p11	f
143415 (*NM_020239*)	1q21	t	176819	5q14	t	120053 (*GOT1*)	10q24	t	154050	17p11	t
143621 (*ILF2*)	1q21	t	183772 (*CMYA5*)	5q14	f	107831 (*FGF8*)	10q24	t	184185 (*KCNJ12*)	17p11	f
131781 (*FMO5*)	1q21	t	133302 (*NM_032290*)	5q15	f	171311 (*CSL4*)	10q24	i	141028 (*Q96T59*)	17p12	i
143369 (*ECM1*)	1q21	t	185261 (*NM_173665*)	5q15	i	165851	10q24	f	108445 (*O95611*)	17p12	i
132043	1q21	i	169736 (*Q9NS32*)	5q21	f	151553 (*Q9HCH2*)	10q25	f	175091	17p12	f

163122	1q21	i	184213 (*NM_173488*)	5q21	f	151884	10q25	i	154914 (*USP43*)	17p13	f
183558 (*HIST1H2AH*)	1q21	t	134982 (*APC*)	5q22	i	151893 (*NM_153810*)	10q26	f	132388 (*UBE2G1*)	17p13	t
183598 (*NM_021059*)	1q21	i	125341 (*SLC22A5*)	5q23	f	154490 (*NM_145235*)	10q26	t	161955 (*TNFSF13*)	17p13	t
187170 (*SPRL4A*)	1q21	t	180831 (*Q8N933*)	5q23	t	107902 (*NM_022126*)	10q26	t	181856 (*SLC2A4*)	17p13	t
187173 (*NM_178428*)	1q21	i	164406 (*LEA2*)	5q23	f	119979 (*NM_018472*)	10q26	f	141504 (*SAT2*)	17p13	i
187223 (*SPRL1A*)	1q21	f	138829 (*FBN2*)	5q23	t	174755 (*ACADSB*)	10q26	i	161929 (*Q96MD0*)	17p13	t
187428 (*NM_178353*)	1q21	i	182549	5q23	f, i, t	176584	10q26	f	007168 (*PAFAH1B1*)	17p13	t
160753 (*RUSC1*)	1q22	i	073905 (*VDAC1*)	5q31	t	186730 (*DUX4*)	10q26	f	129235 (*NM_032731*)	17p13	i
163239 (*NM_182499*)	1q22	i	152700 (*SARA2*)	5q31	t	176567 (*Q8NH49*)	11p11	f	132376 (*NM_016532*)	17p13	i
160752 (*FDPS*)	1q22	i	053108 (*Q8TBU0*)	5q31	t	165905 (*NM_152312*)	11p11	t	141503 (*M4K6*)	17p13	f
160716 (*CHRNB2*)	1q22	f	078795 (*PKD2L2*)	5q31	f	110492 (*MDK*)	11p11	t	161958 (*FGF11*)	17p13	i
143595 (*AQP10*)	1q22	i	113212 (*PCDHB7*)	5q31	f	180210 (*F2*)	11p11	i	178999 (*AURKB*)	17p13	i
132704 (*SPAP1*)	1q23	f	113070 (*DTR*)	5q31	i	175104 (*TRAF6*)	11p12	i	182335 (*Q8TE90*)	17p13	t
162729 (*IGSF8*)	1q23	i	173250 (*Q8TDV0*)	5q32	f	110422 (*HIPK3*)	11p13	t	184166 (*OR1D2*)	17p13	t
158481 (*CD1C*)	1q23	f	185777	5q32	f	186688 (*NM_181807*)	11p13	i	185530 (*NM_030970*)	17p13	f
158485 (*CD1B*)	1q23	f	155846 (*NM_133263*)	5q33	t	121621 (*NM_031217*)	11p14	t	185561	17p13	f
186950 (*Q96M18*)	1q23	f, i, t	086570 (*FAT2*)	5q33	i	187398 (*Q86TE4*)	11p14	t	187071 (*GPS2*)	17p13	f
120370 (*NM_152281*)	1q24	t	055163 (*CYFIP2*)	5q33	t	134339 (*SAA2*)	11p15	f	076604 (*TRAF4*)	17q11	i
000457 (*NM_020423*)	1q24	f	181884	5q33	i	133818 (*RRAS2*)	11p15	i	141316 (*SPACA3*)	17q11	f
178454 (*NM_018578*)	1q24	t	183111	5q33	i	151117 (*NM_153347*)	11p15	t	160551 (*Q9P2I6*)	17q11	f
143167 (*GPA33*)	1q24	t	113327 (*GABRG2*)	5q34	i	166800 (*NM_144972*)	11p15	f	173012 (*Q8TCQ8*)	17q11	i
094975 (*C1orf9*)	1q24	t	145864 (*GABRB2*)	5q34	t	166788 (*NM_138421*)	11p15	i	141298 (*NM_033389*)	17q11	f
162666 (*Y040*)	1q25	i	113328 (*CCNG1*)	5q34	t	179826 (*NM_054031*)	11p15	f	087095 (*NM_016231*)	17q11	t
116147 (*TNR*)	1q25	i	118322 (*ATP10B*)	5q34	i	151116 (*NM_018314*)	11p15	i	108651 (*HC66*)	17q11	i
117586 (*TNFSF4*)	1q25	f	178187 (*ZNF454*)	5q35	t	129158 (*NM_012139*)	11p15	t	108278 (*TRIP3*)	17q12	f
172762 (*Q9P1E1*)	1q25	t	170089 (*THOC3*)	5q35	i	129152 (*MYOD1*)	11p15	f	172660 (*TAF15*)	17q12	t
135870 (*Q8IVE6*)	1q25	f	131183 (*SLC34A1*)	5q35	t	181939 (*Q8NGM1*)	11q11	t	174111 (*SOC6*)	17q12	f
162779 (*NM_182766*)	1q25	f, t	181538 (*Q8N0T8*)	5q35	f	184741 (*Q8NH20*)	11q11	i, t	132142 (*ACACA*)	17q12	i
162787 (*NM_181572*)	1q25	f	145912 (*NOLA2*)	5q35	t	186117 (*Q8NGL2*)	11q11	f	108270 (*AATF*)	17q12	i
135862 (*LAMC1*)	1q25	i	170074 (*NM_173663*)	5q35	t	149150 (*SLC43A1*)	11q12	i	178655	17q12	i
183831	1q25	i	168246 (*NM_152277*)	5q35	f	172685 (*Q96PG2*)	11q12	i	108379 (*WNT3*)	17q21	i
143355 (*LHX9*)	1q31	f	146067 (*NM_019057*)	5q35	t	176495 (*Q8NGI8*)	11q12	f	131462 (*TUBG1*)	17q21	f
122185 (*RPS27*)	1q32	t	040275 (*NM_017785*)	5q35	i	109991 (*P2RX3*)	11q12	t	073861 (*TBX21*)	17q21	t
174307 (*PHLDA3*)	1q32	t	064747 (*NM_015043*)	5q35	t	162222 (*NM_173810*)	11q12	t	167941 (*SOST*)	17q21	t
174514 (*NM_181644*)	1q32	i	169045 (*HNRPH1*)	5q35	i	149532 (*NM_024811*)	11q12	i	131096 (*PYY*)	17q21	i
162757 (*NM_152485*)	1q32	t	131459 (*GFPT2*)	5q35	f	162194 (*NM_024099*)	11q12	t	108819 (*PPP1R9B*)	17q21	i
158715 (*NM_033102*)	1q32	t	160867 (*FGFR4*)	5q35	t	166930 (*MS4A5*)	11q12	i	141696 (*NO55*)	17q21	f
117153 (*NM_021633*)	1q32	i	113732 (*ATP6V0E*)	5q35	i	149516 (*MS4A3*)	11q12	f	167914 (*NM_178171*)	17q21	i
077152 (*NM_014176*)	1q32	f	183718 (*TRIM52*)	5q35	t	134825 (*C11orf10*)	11q12	i	167105 (*NM_153229*)	17q21	i
117691 (*NM_013349*)	1q32	t	184550 (*Q9H7L9*)	5q35	f	173101 (*SIPA1*)	11q13	f	167159 (*NM_152466*)	17q21	f
117650 (*NEK2*)	1q32	i	184714	5q35	i	173959 (*RBM14*)	11q13	f	108825 (*NM_025267*)	17q21	f
118193 (*KIF14*)	1q32	t	185005 (*NM_022471*)	5q35	t	175514 (*Q8TDT2*)	11q13	i	108800 (*NM_014897*)	17q21	f
162891 (*IL20*)	1q32	f	112210 (*RAB23*)	6p11	f	179263 (*Q8NH65*)	11q13	t	159224 (*GIP*)	17q21	f
162809 (*Q9NQI1*)	1q41	t	112200 (*ZNF451*)	6p12	t	166439 (*Q8NCN4*)	11q13	f	178743	17q21	t
162814 (*NM_138796*)	1q41	f	065308 (*TRAM2*)	6p12	i	021300 (*PLEKHB1*)	11q13	t	180386	17q21	i
154309 (*NM_032890*)	1q41	i	112077 (*RHAG*)	6p12	t	171631 (*P2RY6*)	11q13	i	182076 (*NBR2*)	17q21	t
186063 (*NM_022831*)	1q41	i	174201 (*Q9P1E1*)	6p12	t	175591 (*P2RY2*)	11q13	i	183978 (*NM_014019*)	17q21	i
135763 (*Y133*)	1q42	t	168116 (*Q9HCI6*)	6p12	f	178795 (*NM_182833*)	11q13	t	184502 (*GAS*)	17q21	f
116918 (*TSNAX*)	1q42	t	124743 (*Q9H511*)	6p12	i	173914 (*NM_031492*)	11q13	f	185845 (*Q8N0T2*)	17q21	i
116957 (*TBCE*)	1q42	f	096087 (*GSTA2*)	6p12	f	172732 (*NM_025128*)	11q13	f	186916	17q21	i
116991 (*Q8NA38*)	1q42	f	146233 (*CYP39A1*)	6p12	i	132749 (*MTL5*)	11q13	t	178012 (*PECAM1*)	17q23	i
162913 (*Q8N372*)	1q42	t	112715 (*VEGF*)	6p21	i	168056 (*LTBP3*)	11q13	f	153951 (*O4D2*)	17q23	t
162885 (*NM_152490*)	1q42	i	137394 (*TRIM10*)	6p21	f	172638 (*EFEMP2*)	11q13	i	136490 (*NM_030576*)	17q23	i
081692 (*NM_023007*)	1q42	i	175802 (*Q9UGE0*)	6p21	f	175602 (*DIPA*)	11q13	f	108375 (*NM_017763*)	17q23	t
168148 (*HIST3H3*)	1q42	t	168471 (*Q9H3W0*)	6p21	t	175315 (*CST6*)	11q13	i	087995 (*METTL2*)	17q23	t
152904 (*GGPS1*)	1q42	f	178214 (*Q96QB7*)	6p21	t	175334 (*BANF1*)	11q13	t	187013 (*Q86X59*)	17q23	i
143669 (*CHS1*)	1q42	t	168379 (*Q8WM95*)	6p21	f	176245	11q13	t	141331 (*HELZ*)	17q24	t
173576	1q42	f	172764 (*Q8TDV1*)	6p21	t	184154 (*NM_145309*)	11q13	t	108878 (*CACNG1*)	17q24	i
185495 (*Q9H5Q3*)	1q42	f	180911 (*Q8N925*)	6p21	i	186642 (*PDE2A*)	11q13	f	182481 (*KPNA2*)	17q24	t
116984 (*MTR*)	1q43	i	176415 (*Q8N1I6*)	6p21	f	187040	11q13	t	132481 (*TRIM47*)	17q25	i
117009 (*KMO*)	1q43	i	172738 (*NM_145316*)	6p21	t	118369 (*USP35*)	11q14	i	178932 (*Q8N811*)	17q25	f
143700	1q43	f, i	096080 (*MRPS18A*)	6p21	i	137509 (*PRCP*)	11q14	t	178789 (*NM_174892*)	17q25	t
182097 (*Q96CB2*)	1q43	t	111971 (*LY6G5C*)	6p21	i	172946 (*Q9P1E1*)	11q21	t	173818 (*NM_173627*)	17q25	f
185346 (*Q96B84*)	1q43	t	096158 (*LTB*)	6p21	f	150312	11q21	t	167302 (*NM_144679*)	17q25	t
179510 (*Q9H5F0*)	1q44	t	112095 (*HLA-DOA*)	6p21	t	137693 (*YAP1*)	11q22	f	125457 (*NM_020679*)	17q25	t
162727 (*Q96R29*)	1q44	f	137333 (*DHX16*)	6p21	t	110723 (*SL2B*)	11q22	f	141580 (*NM_019613*)	17q25	i
177564 (*Q8TC70*)	1q44	t	112195 (*C6orf76*)	6p21	t	166253 (*Q96LP0*)	11q22	i	109065 (*NM_015654*)	17q25	i
177535 (*Q8NGW7*)	1q44	f	007816 (*C6orf11*)	6p21	i	137692 (*NM_032299*)	11q22	i	125445 (*MRPS7*)	17q25	t
171163 (*NM_017865*)	1q44	f, i	168426 (*BTNL2*)	6p21	f	118113 (*MMP8*)	11q22	t	166685 (*COG1*)	17q25	i
162711 (*CIAS1*)	1q44	t	064999 (*ANKS1*)	6p21	i	166648 (*DNCH2*)	11q22	f	141527 (*CARD14*)	17q25	t
185420 (*SMYD3*)	1q44	f	124655 (*AIF1*)	6p21	f	176610	11q22	i	167281	17q25	f
187117 (*Q8NG85*)	1q44	i	137406	6p21	i	187069	11q22	i	184703 (*SIRT7*)	17q25	f
178486 (*Q8N1I5*)	2p11	i	161912	6p21	f, t	036672 (*USP2*)	11q23	i	185262 (*NM_182565*)	17q25	i
068654 (*POLR1A*)	2p11	i	173580	6p21	t	173524 (*Q9BXE6*)	11q23	t	185298	17q25	t
173758 (*KV2F*)	2p11	f	184729 (*NM_018540*)	6p21	t	160613 (*PCSK7*)	11q23	t	175319 (*Q14179*)	18p11	t
153586 (*IGKV4-1*)	2p11	t	137403 (*HLA-F*)	6p22	t	154114 (*NM_152715*)	11q23	i	176014 (*NM_032525*)	18p11	t
172116 (*CD8B1*)	2p11	i	178458 (*HIST1H3A*)	6p22	t	095110 (*NM_152315*)	11q23	t	132199 (*NM_017512*)	18p11	t
183281 (*PLGL*)	2p11	t	146047 (*HIST1H2BA*)	6p22	f	137747 (*NM_032046*)	11q23	t	168461	18p11	t
184943 (*NM_052871*)	2p11	i	161777 (*HCG9*)	6p22	i	110367 (*DDX6*)	11q23	i	183206	18p11	f
186854 (*Q86V40*)	2p11	i	112293 (*GPLD1*)	6p22	t	167283 (*ATP5L*)	11q23	f	141447 (*OSBPL1A*)	18q11	f, t
115353 (*TACR1*)	2p12	i	137414 (*FAM8A1*)	6p22	i	110244 (*APOA4*)	11q23	i	158201 (*ABHD3*)	18q11	i
163219 (*Y053*)	2p13	i	112242 (*E2F3*)	6p22	i, t	182581 (*Q9BXE6*)	11q23	f	134779 (*NM_015476*)	18q12	i
173027 (*WBP1*)	2p13	i	168405 (*CMAH*)	6p22	i	023171 (*Q9ULL9*)	11q24	t	141434 (*MEP1B*)	18q12	i
143977 (*SNRPG*)	2p13	f	124508 (*BTN2A2*)	6p22	t	170953 (*Q8NGG6*)	11q24	f, t	134765 (*DSC1*)	18q12	t
075292 (*NM_014497*)	2p13	f, t	183679 (*HIST1H4J*)	6p22	f	176952 (*Q8N6I7*)	11q24	t	186412	18q12	f, t
135638 (*EMX1*)	2p13	i	185193 (*Q9BXE2*)	6p22	f	165526 (*NM_032795*)	11q24	t	186496 (*ZNF396*)	18q12	f
144048 (*DUSP11*)	2p13	f	185694	6p22	i	149552 (*NM_024556*)	11q24	f	081916 (*SERPINB8*)	18q21	i
114956 (*DGUOK*)	2p13	i	112149 (*CD83*)	6p23	f	110013 (*NM_018978*)	11q24	t	179981 (*SDCCAG33*)	18q22	t
115980 (*ANXA4*)	2p13	i	181590 (*Q8NC12*)	6p24	t	120457 (*KCNJ5*)	11q24	t	186411	18q23	i
138072 (*Q9NTE1*)	2p14	t	124827 (*GCM2*)	6p24	i	151704 (*KCNJ1*)	11q24	i	168892 (*ZNF253*)	19p13	f, t
011523 (*NM_015147*)	2p14	i	184431	6p24	i	109832 (*DDX25*)	11q24	t	132010 (*ZNF20*)	19p13	i
143995 (*MEIS1*)	2p14	t	185689	6p25	f	183483 (*Q8IZY5*)	11q24	f	150732 (*YE73*)	19p13	f
014641 (*MDH1*)	2p15	f	112280 (*COL9A1*)	6q13	t	185688 (*Q8NH79*)	11q24	i	125735 (*TNFSF14*)	19p13	i

152518 (*ZFP36L2*)	2p21	i	175596 (*Q9P1E1*)	6q14	t	187072	11q24	i	181143 (*Q9H8T7*)	19p13	t
152527 (*Q8IVE3*)	2p21	f	085382 (*HACE1*)	6q16	f	175724 (*NM_152711*)	11q25	t	132001 (*Q9H0M5*)	19p13	f, i
138095 (*LRPPRC*)	2p21	t	132429 (*POPDC3*)	6q21	i	177340 (*NM_024799*)	12p11	f	141933 (*Q96GE2*)	19p13	t
172877 (*Q9BXE6*)	2p22	t	177214 (*NM_173559*)	6q21	t	123106 (*NM_018318*)	12p11	t	129933 (*Q8N7K4*)	19p13	i
055332 (*PRKR*)	2p22	t	123510 (*BXDC1*)	6q21	t	110888 (*C1QDC1*)	12p11	f	099817 (*POLR2E*)	19p13	i
138068	2p22	i	146374 (*THSD2*)	6q22	t	151490 (*PTPRO*)	12p12	f	130313 (*PGLS*)	19p13	f
084733 (*RAB10*)	2p23	t	111817 (*SART2*)	6q22	i	067182 (*TNFRSF1A*)	12p13	f	104883 (*PEX11G*)	19p13	f
163795 (*NM_144631*)	2p23	f	152894 (*PTPRK*)	6q22	i	121314 (*TAS2R8*)	12p13	i	176995 (*OR7C1*)	19p13	f
119777 (*NM_017727*)	2p23	t	111912 (*NCOA7*)	6q22	f	121379 (*TAS2R14*)	12p13	i	099308 (*O60307*)	19p13	t
138028 (*CGREF1*)	2p23	f	146376 (*ARHGAP18*)	6q22	f	013588 (*RAI3*)	12p13	f	175217 (*NM_138774*)	19p13	i
186453 (*Q96NH8*)	2p23	i	146411 (*SLC2A12*)	6q23	f	126838 (*PZP*)	12p13	t	167807 (*NM_080665*)	19p13	i
068697 (*LAPTM4A*)	2p24	f	154269 (*ENPP3*)	6q23	i	173342 (*PRB1*)	12p13	f	130307 (*NM_031941*)	19p13	f
171863 (*RPS7*)	2p25	f	146386 (*Q9P0A1*)	6q24	t	173391 (*OLR1*)	12p13	f	129951 (*NM_024888*)	19p13	i
130508 (*Q92626*)	2p25	i	135577 (*NMBR*)	6q24	f	172322 (*NM_138337*)	12p13	f	132000 (*NM_024825*)	19p13	f
174685 (*NM_153011*)	2p25	i	111962 (*UST*)	6q25	t	111671 (*NM_032641*)	12p13	i	079313 (*NM_020695*)	19p13	t
175652	2p25	f	130338 (*TULP4*)	6q25	f	171792 (*NM_031465*)	12p13	f	125912 (*NM_020170*)	19p13	t
182717	2p25	f	122335 (*SERAC1*)	6q25	f	126740 (*NM_007273*)	12p13	f	130813 (*NM_018381*)	19p13	f
084090 (*STARD7*)	2q11	t	180821 (*RBM16*)	6q25	t	121373 (*KLRC4*)	12p13	i	167487 (*NM_018316*)	19p13	i
163126 (*NM_144994*)	2q11	f	120253 (*NUP43*)	6q25	i	111218 (*HRMT1L3*)	12p13	t	171466 (*NM_017656*)	19p13	f
163699 (*NM_025024*)	2q11	i	049618 (*NM_175863*)	6q25	f	111664 (*GNB3*)	12p13	f	105229 (*NM_015897*)	19p13	i
158435 (*NM_017546*)	2q11	i	120276	6q25	t	118972 (*FGF23*)	12p13	i	127666 (*NM_014261*)	19p13	f
115446 (*NM_014044*)	2q11	i	174218	6q25	f	111652 (*COPS7A*)	12p13	t	064489 (*MEF2B*)	19p13	i
071073 (*MGAT4A*)	2q11	t	185068 (*Q9BST5*)	6q25	i	180574	12p13	t	099617 (*EFNA2*)	19p13	t
168677 (*HMGN1*)	2q11	t	185345 (*PARK2*)	6q26	t	151229 (*SLC2A13*)	12q12	t	123146 (*CD97*)	19p13	f
144191 (*CNGA3*)	2q11	f	153471 (*TCP10*)	6q27	i	151233 (*Q8IXV1*)	12q12	f	161082 (*BRUNOL5*)	19p13	f
115669 (*SULT1C1*)	2q12	t	120436 (*GPR31*)	6q27	t	186518 (*Q96SJ6*)	12q12	t	115268	19p13	f
170417 (*NM_144632*)	2q12	f, t	146731 (*CCT6A*)	7p11	t	166888 (*STAT6*)	12q13	i	183617 (*MRPL54*)	19p13	i
176120 (*NM_032658*)	2q12	i	154997	7p11	t	172602 (*RHO6*)	12q13	i	185113 (*NM_032281*)	19p13	f
015568 (*RANBP2L1*)	2q13	i	180594 (*Q96C79*)	7p13	f	076067 (*RBMS2*)	12q13	t	185293	19p13	t
179757 (*Q9P1E1*)	2q13	i	106628 (*POLD2*)	7p13	t	167566 (*Q9HCH0*)	12q13	i	187365 (*NM_175910*)	19p13	t
175772 (*NM_152518*)	2q13	i	015676 (*NM_015332*)	7p13	i	179962 (*Q8NGE6*)	12q13	t	159905 (*ZNF234*)	19q13	t
153214 (*NM_032824*)	2q13	t	106624 (*AEBP1*)	7p13	f	139645 (*Q8NB46*)	12q13	i	018607 (*ZNF221*)	19q13	i
136688 (*IL1F9*)	2q13	f	010270 (*STARD3NL*)	7p14	t	139540 (*NM_173596*)	12q13	i	159882 (*ZNF155*)	19q13	t
136696 (*IL1F8*)	2q13	i	164542 (*Q8NCT3*)	7p14	i	139579 (*NM_024068*)	12q13	f	063244 (*U2AF*)	19q13	i
184764 (*RPL22*)	2q13	i	181211 (*Q8NA17*)	7p14	t	139625 (*MAP3K12*)	12q13	i	063176 (*SPHK2*)	19q13	t
074054 (*CLASP1*)	2q14	t	173862 (*NM_017937*)	7p14	i	170477 (*KRT4*)	12q13	f	160296 (*SIGLECL1*)	19q13	t
176119 (*Q96N27*)	2q21	i	122641 (*INHBA*)	7p14	t	135472 (*FAIM2*)	12q13	t	168995 (*SIGLEC7*)	19q13	i
173302 (*Q8TDV2*)	2q21	f	106105 (*GARS*)	7p14	f	139631 (*CSAD*)	12q13	i	161681 (*SHANK1*)	19q13	t
136698 (*NM_032545*)	2q21	i	187258 (*Q86SP4*)	7p14	f	177981 (*ASB8*)	12q13	i	180281 (*Q8N843*)	19q13	i
178206 (*NM_032248*)	2q21	f	176514 (*Q9UDC8*)	7p15	f	167580 (*AQP2*)	12q13	i	179873 (*PYA6*)	19q13	f
076003 (*MCM6*)	2q21	i	174487 (*Q9BXE6*)	7p15	f, t	135409 (*AMHR2*)	12q13	f	104960 (*PTOV1*)	19q13	f
182316	2q21	i	105928 (*DFNA5*)	7p15	f	185389 (*NM_018507*)	12q13	f	011485 (*PPP5C*)	19q13	f
115919 (*KYNU*)	2q22	t	153790 (*C7orf31*)	7p15	f	185971	12q13	i	105568 (*PPP2R1A*)	19q13	t
169432 (*SCN9A*)	2q24	i	105889	7p15	t	186897 (*Q86Z23*)	12q13	f	087074 (*PPP1R15A*)	19q13	f
144285 (*SCN1A*)	2q24	i	186179	7p15	i	177221 (*Q8WYW9*)	12q14	t	105223 (*PLD3*)	19q13	t
174470 (*Q96M44*)	2q24	i	186797	7p15	t	155974 (*GRIP1*)	12q14	t	104967 (*NOVA2*)	19q13	f
169507 (*NM_173512*)	2q24	f	106443 (*PHF14*)	7p21	t	111537 (*IFNG*)	12q15	f	179932 (*NM_178511*)	19q13	f
172292	2q24	f	146530 (*NM_182545*)	7p21	t	166225 (*FRS2*)	12q15	f	176472 (*NM_174945*)	19q13	i
155657 (*TTN*)	2q31	i	173467 (*NM_176813*)	7p21	i	111596 (*CNOT2*)	12q15	t	161652 (*NM_152358*)	19q13	f, t
172845 (*SP3*)	2q31	i	106541 (*AGR2*)	7p21	f	185393 (*Q9BTS6*)	12q15	t	104892 (*NM_145275*)	19q13	i
163364 (*Q96D13*)	2q31	f	146587 (*NM_021163*)	7p22	i	185563	12q15	f	142544 (*NM_145232*)	19q13	i
175892 (*Q8NAT4*)	2q31	i	164818 (*NM_017802*)	7p22	t	165899 (*NM_173591*)	12q21	f	105479 (*NM_144577*)	19q13	t
128655 (*PDE11A*)	2q31	f	106263 (*EIF3S9*)	7p22	f	139330 (*KERA*)	12q21	i	160410 (*NM_138392*)	19q13	i
163492 (*NM_173648*)	2q31	t	169549	7p22	f	139292 (*GPR49*)	12q21	f	126249 (*NM_032346*)	19q13	f
163093 (*NM_152384*)	2q31	f	174959	7p22	i	083782 (*DSPG3*)	12q21	i	104865 (*NM_018111*)	19q13	i
144306 (*NM_024583*)	2q31	i	175987	7p22	i	180318 (*CART1*)	12q21	f	076650 (*NM_018025*)	19q13	t
115806 (*GORASP2*)	2q31	f	179800	7p22	f	182127	12q21	t	160505 (*NAL4*)	19q13	t
079150 (*FKBP7*)	2q31	f	187127 (*POL1*)	7p22	t	187111	12q21	f	174562 (*KLKF*)	19q13	i
018510 (*AGPS*)	2q31	t	009950 (*WBSCR14*)	7q11	i	028203 (*VEZA*)	12q22	f, i	167749 (*KLK4*)	19q13	t
115942 (*ORC2L*)	2q33	t	135174 (*Q9Y4L9*)	7q11	t	139343 (*SNRPF*)	12q23	i	105063 (*KB15*)	19q13	f
155754 (*NM_152525*)	2q33	i	133380 (*NM_153363*)	7q11	f	136051 (*Q9NV91*)	12q23	f	167644 (*IMUP*)	19q13	t
155729 (*NM_152387*)	2q33	i	177585	7q11	i	166629 (*Q96L24*)	12q23	f	160007 (*GRLF1*)	19q13	i
178420 (*NM_030804*)	2q33	f	184569	7q11	i	151136 (*NM_152322*)	12q23	i	126262 (*GPR43*)	19q13	t
115520 (*NM_025147*)	2q33	i	146745 (*NM_032763*)	7q21	t	111670 (*NM_024312*)	12q23	i	105220 (*GPI*)	19q13	i
155760 (*FZD7*)	2q33	f	105781 (*GRM3*)	7q21	t	139420 (*NM_007076*)	12q23	f	123859 (*FPRL2*)	19q13	t
155755 (*ALS2CR4*)	2q33	t	157240 (*FZD1*)	7q21	i	174600 (*CMKLR1*)	12q23	i	104884 (*ERCC2*)	19q13	f
186680	2q33	i	127962	7q21	i	139352 (*ASCL1*)	12q23	f	142025 (*DMRTC2*)	19q13	f
168582 (*CRYGA*)	2q34	i	166526 (*ZNF3*)	7q22	t	120868 (*APAF1*)	12q23	f	105205 (*CLC*)	19q13	i
135912 (*Y173*)	2q35	f	169899 (*Q96MA9*)	7q22	f	183395 (*PMCH*)	12q23	i	170956 (*CEACAM3*)	19q13	i
127831 (*VIL1*)	2q35	t	167011 (*Q8N8M0*)	7q22	t	185046 (*NM_020140*)	12q23	t	142273 (*CBLC*)	19q13	t
135913 (*USP37*)	2q35	f	078319 (*PMS2L1*)	7q22	t	139370 (*SLC15A4*)	12q24	t	008364 (*AP2A1*)	19q13	t
163526 (*TUBA4*)	2q35	i	146834 (*NM_019606*)	7q22	f	061936 (*SFRS8*)	12q24	t	142513 (*ACPT*)	19q13	t
115592 (*PRKAG3*)	2q35	t	021461 (*CYP3A43*)	7q22	t	089232 (*SCA2*)	12q24	t	176898	19q13	f
115655 (*NM_024085*)	2q35	i	173685	7q22	t	139697 (*SBNO1*)	12q24	f, i	179930	19q13	t
163497 (*NM_017521*)	2q35	t	184414 (*IRS3L*)	7q22	f	178043 (*Q9HA69*)	12q24	f	182582 (*Q96GE3*)	19q13	f
066216 (*TNRC15*)	2q37	i	185055	7q22	t	180645 (*Q9BUH0*)	12q24	t	186888	19q13	f
176946 (*THA4*)	2q37	i, t	128519 (*TAS2R16*)	7q31	f, i	177213 (*Q96LP1*)	12q24	i	187092 (*Q8N0S4*)	19q13	i
173100 (*Q9P0V4*)	2q37	i	135272 (*Q9P1T7*)	7q31	f	139767 (*Q96JH4*)	12q24	i	187116 (*NM_181879*)	19q13	i
144488 (*Q8IVU2*)	2q37	i	106034 (*NM_024913*)	7q31	t	089159 (*PXN*)	12q24	t	187356	19q13	f
066248 (*NGEF*)	2q37	i	106041 (*FAM3C*)	7q31	i	177192 (*PUS1*)	12q24	f	177587 (*Q96MG3*)	20p11	t
115488 (*NEU2*)	2q37	i	180324 (*CAPZA2*)	7q31	f	089250 (*NOS1*)	12q24	i	179447 (*Q8N7Z9*)	20p11	t
135916 (*ITM2C*)	2q37	i	146809 (*ASB15*)	7q31	t	130921 (*NM_152269*)	12q24	t	132661 (*NXT1*)	20p11	i, t
135930 (*EIF4EL3*)	2q37	i	128578 (*Q9ULQ0*)	7q32	t	111412 (*NM_024738*)	12q24	t	101004 (*NM_025176*)	20p11	i
163286 (*ALPPL2*)	2q37	i	064419 (*NM_012470*)	7q32	i	135090 (*NM_016281*)	12q24	t	173404 (*INSM1*)	20p11	t
182177	2q37	f	105875 (*Q96AE5*)	7q33	t	135148 (*NM_006700*)	12q24	i	101435 (*CST9L*)	20p11	i
182202	2q37	f	122786 (*CALD1*)	7q33	f	122965 (*K682*)	12q24	t	125815 (*CST8*)	20p11	i
184945 (*Q8IXF9*)	2q37	t	127364 (*TAS2R4*)	7q34	t	158104 (*HPD*)	12q24	i	077984 (*CST7*)	20p11	i
186235	2q37	t	171082 (*Q8N3Z8*)	7q34	f	135108 (*FBXO21*)	12q24	i	125872 (*C20orf75*)	20p12	f
064835 (*POU1F1*)	3p11	t	184412	7q34	f	111249 (*CUTL2*)	12q24	f	101247 (*C20orf7*)	20p12	i
179021 (*NM_173824*)	3p11	f	122063 (*XRCC2*)	7q36	t	111707	12q24	f, t	172296 (*C20orf38*)	20p12	f
179799 (*Q8NHB5*)	3p12	f	106615 (*RHEB*)	7q36	f	184967 (*NM_024078*)	12q24	f	089177 (*C20orf23*)	20p12	f
170837 (*GPR27*)	3p13	t	181652 (*NM_173681*)	7q36	f	132950 (*ZNF237*)	13q12	t	089123 (*C20orf13*)	20p12	f
157467 (*O15083*)	3p14	f	133574 (*NM_018326*)	7q36	i	023957 (*TUBA2*)	13q12	i	132623 (*ANKRD5*)	20p12	i

177664 (*DNAH12*)	3p14	i	126870 (*NM_018051*)	7q36	t	139514 (*SLC7A1*)	13q12	t	149497 (*Q9BYW8*)	20p13	i
168374 (*ARF4*)	3p14	f	106560 (*NM_015660*)	7q36	t	150459 (*SAP18*)	13q12	t	171864 (*PRND*)	20p13	i
163638 (*ADAMTS9*)	3p14	f	127360 (*IAN4L1*)	7q36	i	180776 (*Q8N2S7*)	13q12	i	125787 (*GNRH2*)	20p13	t
163825 (*TMEM7*)	3p21	t	106648 (*GALNT15*)	7q36	t	121390 (*PSPC1*)	13q12	f, t	125903 (*DEFB129*)	20p13	t
162244 (*RPL29*)	3p21	t	105993 (*DNAJB6*)	7q36	i	122038 (*POLR1D*)	13q12	t	125843 (*C20orf29*)	20p13	f, t
168237 (*NM_145262*)	3p21	t	164885 (*CDK5*)	7q36	i	150456 (*NM_174928*)	13q12	f	149451 (*ADAM33*)	20p13	t
163817 (*NM_020208*)	3p21	i	170279 (*C7orf33*)	7q36	t	102699 (*ADPRTL1*)	13q12	t	183994 (*Q9Y2V8*)	20p13	f
145029 (*NICN1*)	3p21	t	168172 (*NM_032410*)	8p11	i	073910 (*NM_023037*)	13q13	i	101400 (*SNTA1*)	20q11	t
160808 (*MYL3*)	3p21	i	104371 (*DKK4*)	8p11	f	133101 (*CCNA1*)	13q13	t	125991 (*SDBCAG84*)	20q11	i
180929 (*GPR62*)	3p21	i	185900 (*NM_032237*)	8p11	i	179630 (*U124*)	13q14	i	088303 (*Q9NQF5*)	20q11	i
088538 (*DOCK3*)	3p21	i	181329 (*O95724*)	8p12	i	180331 (*Q8IX95*)	13q14	t	101464 (*CDC91L1*)	20q11	f
121797 (*CCRL2*)	3p21	f	133872 (*NM_016127*)	8p12	i	083635 (*NUFIP1*)	13q14	i	149611 (*C20orf93*)	20q11	t
121807 (*CCR2*)	3p21	f	184844	8p12	f	171945 (*NM_030970*)	13q14	f	167104 (*BPIL3*)	20q11	t
164062 (*APEH*)	3p21	i	147454 (*NM_016612*)	8p21	f	102837 (*NM_006418*)	13q14	i	182171	20q11	i
184345 (*Q8IXL9*)	3p21	i	147443 (*DOK2*)	8p21	i	150506 (*PCDH20*)	13q21	i	183566 (*NM_173859*)	20q11	t
186748 (*NM_018651*)	3p21	f	069206 (*ADAM7*)	8p21	t	118946 (*PCDH17*)	13q21	i	171940 (*ZNF217*)	20q13	t
163673 (*Q9C098*)	3p22	t	182406	8p21	f	005810 (*NM_015057*)	13q22	f	064205 (*WISP2*)	20q13	i
168026 (*NM_145755*)	3p22	i	184661 (*CDCA2*)	8p21	i	165621 (*GPR80*)	13q32	i	180305 (*WFDC10A*)	20q13	t
114853 (*NM_145166*)	3p22	f	181897 (*NM_018422*)	8p22	t	134900 (*TPP2*)	13q33	t	101150 (*TPD52L2*)	20q13	i
172936 (*MYD88*)	3p22	t	156011 (*NM_015310*)	8p22	i	139780	13q33	f	101448 (*SPINLW1*)	20q13	f
157036 (*ENDOGL1*)	3p22	t	154316 (*TDH*)	8p23	f	139832 (*RAB20*)	13q34	i	124216 (*SNAI1*)	20q13	f
185313 (*SCN10A*)	3p22	i	177405 (*Q8NAJ9*)	8p23	f	134905 (*NM_024537*)	13q34	t	174334 (*Q9H3Z8*)	20q13	t
187091 (*PLCD1*)	3p22	i	154359 (*NM_152271*)	8p23	f	139835 (*GRTP1*)	13q34	i	177410 (*Q8N5E3*)	20q13	f
170266 (*GLB1*)	3p23	t	147364 (*FBXO25*)	8p23	i	057593 (*F7*)	13q34	t	168734 (*PKIG*)	20q13	t
163513 (*TGFBR2*)	3p24	t	177023 (*DEFB104*)	8p23	f	130177 (*CDC16*)	13q34	f	132786 (*O43713*)	20q13	f
131374 (*TBC1D5*)	3p24	i	171060	8p23	t	102606 (*ARHGEF7*)	13q34	i	149657 (*NM_144703*)	20q13	t
185690 (*Q9NYD7*)	3p24	f	184608 (*C8orf12*)	8p23	f	129563 (*TVA2*)	14q11	t	124217 (*MOCS3*)	20q13	f
186032	3p24	i	186600 (*Q9UDD8*)	8p23	f	166056 (*TCA*)	14q11	i	101052 (*C20orf9*)	20q13	i
171148 (*TADA3L*)	3p25	i	082556 (*OPRK1*)	8q11	f	169488 (*Q8NH41*)	14q11	i	132823 (*C20orf111*)	20q13	f
157103 (*SLC6A1*)	3p25	f, i	047249 (*ATP6V1H*)	8q11	t	176281 (*Q8NGD3*)	14q11	i	130706 (*ADRM1*)	20q13	i
171135 (*NM_032492*)	3p25	t	157556 (*Q8NHT1*)	8q13	f	136315 (*Q12762*)	14q11	t	184402 (*SSI8L1*)	20q13	i
154743 (*NM_025265*)	3p25	t	165093 (*BTF3L2*)	8q13	i, t	100813 (*ACINUS*)	14q11	f	155282	21q11	f
088726 (*NM_018306*)	3p25	f	121039 (*RDH10*)	8q21	i	182545	14q11	i	185272 (*RBM11*)	21q11	i
163703 (*CRELD1*)	3p25	i	176731 (*Q8N0T1*)	8q21	f	185271	14q11	f	156253 (*C21orf6*)	21q21	f
131375 (*CAPN7*)	3p25	f	176206 (*NM_030970*)	8q21	i	092108 (*C14orf163*)	14q12	t	182598	21q21	f
178700 (*NM_176815*)	3q11	f	155099 (*NM_018710*)	8q21	f	176127 (*C14orf128*)	14q12	t	160305 (*DIP2*)	21q22	f
178694 (*NM_022072*)	3q11	t	176623 (*NM_016033*)	8q21	i	129518 (*C14orf11*)	14q13	f	159055 (*C21orf45*)	21q22	i
178660	3q11	i	156170 (*NM_152416*)	8q22	i	185941	14q13	i	182871 (*COL18A1*)	21q22	i
181065 (*Q9P161*)	3q13	f	104324 (*NM_016134*)	8q22	t	092208 (*SIP1*)	14q21	f	184724 (*KRTAP6-1*)	21q22	t
163428 (*Q96CX6*)	3q13	i	164949 (*GEM*)	8q22	f	165506 (*C14orf104*)	14q21	i	184809 (*C21orf88*)	21q22	i
144848 (*NM_022488*)	3q13	f	155097 (*ATP6V1C1*)	8q22	f	182090 (*C14orf25*)	14q21	i	184836 (*C21orf86*)	21q22	f
121570 (*NM_018189*)	3q13	t	147666	8q22	t	131959 (*Q9H373*)	14q22	f	184900 (*SMT3H1*)	21q22	t
091972 (*MOX2*)	3q13	f	147667	8q22	t	131969 (*C14orf29*)	14q22	f	185225 (*C21orf32*)	21q22	t
082701 (*GSK3B*)	3q13	f	183299	8q22	f	126778 (*SIX1*)	14q23	f	185397 (*C21orf51*)	21q22	t
121594 (*CD80*)	3q13	i	147654 (*EBAG9*)	8q23	i	126821 (*SGPP1*)	14q23	t	185706 (*Q8TCY0*)	21q22	i
144811	3q13	f	104415 (*WISP1*)	8q24	t	100612 (*NM_016029*)	14q23	f	187026 (*KRTAP21-2*)	21q22	t
182491	3q13	f	147804 (*SLC39A4*)	8q24	i	179008 (*C14orf39*)	14q23	t	128218 (*VPREB3*)	22q11	i
058262 (*S612*)	3q21	i	161016 (*RPL8*)	8q24	t	184902	14q23	f	138842 (*Q9BWW2*)	22q11	f
114544 (*NM_017836*)	3q21	i	170616 (*Q9BRH9*)	8q24	i	140044 (*NM_130469*)	14q24	t	133525 (*Q99919*)	22q11	t
065534 (*MYLK*)	3q21	i	180838 (*Q8NAM3*)	8q24	i	133997 (*MED6*)	14q24	t	099958 (*Q96Q80*)	22q11	f
173702 (*MUC13*)	3q21	t	132297 (*OC90*)	8q24	f	139985 (*ADAM21*)	14q24	f	178026 (*Q8N0S9*)	22q11	i, t
184621 (*Q9HDC0*)	3q21	i	167702 (*NM_145754*)	8q24	f	072110 (*ACTN1*)	14q24	t	100034 (*PPM1F*)	22q11	i
163785 (*RYK*)	3q22	t	153310 (*NM_016623*)	8q24	t	187073 (*Q86TS2*)	14q24	i	100023 (*PPIL2*)	22q11	t
170883 (*Q9BXE5*)	3q22	t	147724 (*NM_015912*)	8q24	f	165417 (*GTF2A1*)	14q31	f	161149 (*NM_145042*)	22q11	f
163770 (*Q86XG3*)	3q22	f	147684 (*NDUFB9*)	8q24	i	042088 (*TDP1*)	14q32	i	177663 (*IL17R*)	22q11	f
163864 (*NMNAT3*)	3q23	i	104419 (*NDRG1*)	8q24	f	140090 (*SLC24A4*)	14q32	f, t	100056 (*DGCR14*)	22q11	t
175110 (*MRPS22*)	3q23	f	172172 (*MRPL13*)	8q24	f	178069 (*Q8WYT3*)	14q32	t	159664	22q11	i
114124 (*GPRK7*)	3q23	i	179527 (*C8orf17*)	8q24	t	166428 (*NM_138790*)	14q32	t	172963	22q11	t
152977 (*ZIC1*)	3q24	i	177205	8q24	f	165943 (*MOAP1*)	14q32	t	172981	22q11	i
181467 (*RAP2B*)	3q25	t	185582	8q24	f	130076 (*IGHA1*)	14q32	f	183229	22q11	f
174928 (*NM_173657*)	3q25	t	035445 (*UNC13*)	9p13	t	165521	14q32	f	183307 (*CECR6*)	22q11	i
144974 (*NM_024621*)	3q25	f, i	165006 (*UBAP1*)	9p13	f	183940	14q32	i	183506 (*Q8WUK7*)	22q11	f, i
118855 (*NM_022736*)	3q25	f	107371 (*RR40*)	9p13	i	153684 (*Q8NDK0*)	15q13	i	183785 (*PEX26*)	22q11	t
163659 (*NM_015508*)	3q25	i	165012 (*Q96GJ8*)	9p13	t	169926 (*KLF13*)	15q13	t	184273	22q11	i
114771 (*AADAC*)	3q25	f	175768 (*Q8N4H5*)	9p13	f	179938	15q13	i	099995 (*SF3A1*)	22q12	i, t
169760 (*NLGN1*)	3q26	t	180810 (*NM_014113*)	9p13	i, t	175779 (*Q8NAA6*)	15q14	t	099985 (*OSM*)	22q12	f
136521 (*NDUFB5*)	3q26	i	137104 (*GALT*)	9p13	i	178351 (*Q8N345*)	15q14	f	100350 (*NM_024955*)	22q12	i
171109 (*MFN1*)	3q26	f, t	122735 (*DNAI1*)	9p13	f	159495 (*TGM7*)	15q15	f	100365 (*NCF4*)	22q12	t
176494	3q26	t	122705 (*CLTA*)	9p13	t	103932 (*NM_015540*)	15q15	i	100385 (*IL2RB*)	22q12	f
177694	3q26	f	164972 (*C9orf24*)	9p13	f	128928 (*IVD*)	15q15	t	100118 (*HMG1L10*)	22q12	f
073849 (*SIAT1*)	3q27	t	165269 (*AQP7*)	9p13	f	166947 (*EPB42*)	15q15	i	128284 (*APOL3*)	22q12	t
145012 (*LPP*)	3q27	t	159712	9p13	f	092529 (*CAPN3*)	15q15	t	175329	22q12	i
090539 (*CHRD*)	3q27	f	182355 (*NM_015667*)	9p13	i	179646 (*Q9UI57*)	15q21	f	182763 (*Q96EQ7*)	22q12	t
161204 (*ABCF3*)	3q27	t	120247 (*IFNA13*)	9p21	i	166262 (*NM_152647*)	15q21	i	183579 (*Q9ULT6*)	22q12	f
058705 (*IL1RAP*)	3q28	t	147885 (*IFNA13*)	9p21	f	140274	15q21	f	184117 (*NIPSNAP1*)	22q12	f
119231 (*SEN5*)	3q29	f	147889 (*CDKN2A*)	9p21	i	166466	15q21	i	184122 (*Q96NJ4*)	22q12	i
178413 (*Q8N266*)	3q29	i	186758 (*Q8N7I0*)	9p21	f	170236	15q21	i	184654 (*Q8N9L7*)	22q12	t
173950 (*NM_152531*)	3q29	i, t	186802 (*IFNA16*)	9p21	f, i	140416 (*TPM2*)	15q22	t	100426 (*ZBED4*)	22q13	f, t
163975 (*MFI2*)	3q29	f	147893	9p22	i	074621 (*SLC24A1*)	15q22	t	100106 (*TARA*)	22q13	f
075711 (*DLG1*)	3q29	i	155156	9p22	f	090470 (*PDCD7*)	15q22	i	100241 (*SBF1*)	22q13	t
170455 (*CNGA1*)	4p12	i	147852 (*VLDLR*)	9p24	f	140368 (*PSTPIP1*)	15q24	f	100413 (*RPC8*)	22q13	f
145246 (*ATP10D*)	4p12	f	080503 (*SMARCA2*)	9p24	t	140367 (*NM_173469*)	15q24	i	073150 (*PANX2*)	22q13	t
170462	4p12	t	120158 (*RCL1*)	9p24	t	173546 (*CSPG4*)	15q24	t	100266 (*PACSIN2*)	22q13	i
183380	4p12	f	170777 (*NM_033516*)	9p24	i	169553 (*Q8N824*)	15q25	i	176177 (*NM_152512*)	22q13	i, t
163281 (*NM_138335*)	4p13	f	107020 (*NM_018465*)	9p24	t	173867 (*MRPL46*)	15q25	t	100101 (*NM_024313*)	22q13	i
174123 (*TLR10*)	4p14	f	120210 (*INSL6*)	9p24	t	140607	15q25	i	128285 (*GPR24*)	22q13	i
154279 (*Q8WZ27*)	4p14	f	064218 (*DMRT3*)	9p24	f	184206	15q25	t	184472 (*YV02*)	22q13	f
121895 (*NM_024943*)	4p14	f	183276	9p24	i	140545 (*SPAG10*)	15q26	f	185022 (*MAFF*)	22q13	i
174343 (*CHRNA9*)	4p14	t	183354 (*Q8IVE5*)	9p24	f	140534 (*NM_152259*)	15q26	i			
175524 (*Q9UN81*)	4p15	i	178798 (*Q8NGA9*)	9q12	f	131873 (*CHSY1*)	15q26	t			
163142 (*Q8TE30*)	4p15	f	170215 (*Q8NCQ8*)	9q13	f	173607	15q26	f			

Genes used for the calculation of the pairwise interactions, feature selection, and model training are denoted by i, f, and t, respectively. To enhance legibility, the common prefix "ENSG00000" has been dropped from the Ensembl ID.

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