

Supplementary data

Allele-specific gene expression patterns in primary leukemic cells reveal regulation of gene expression by CpG site methylation

Lili Milani , Anders Lundmark , Jessica Nordlund , Anna Kiialainen , Trond Flaegstad ,
Gudmundur Jonmundsson , Jukka Kanerva , Kjeld Schmiegelow , Kevin L. Gunderson ,
Gudmar Lönnérholm and Ann-Christine Syvänen

Contents

Supplementary Figure 1

Supplementary Figure 2

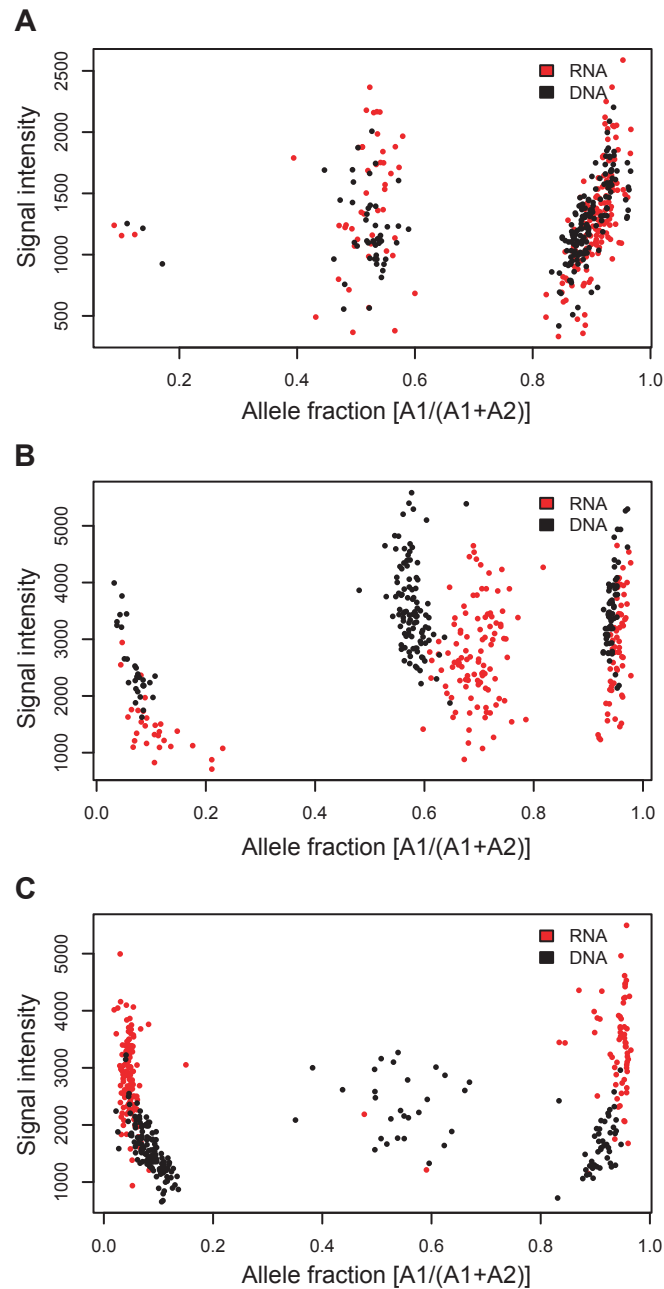
Supplementary Figure 3

Supplementary Figure 4

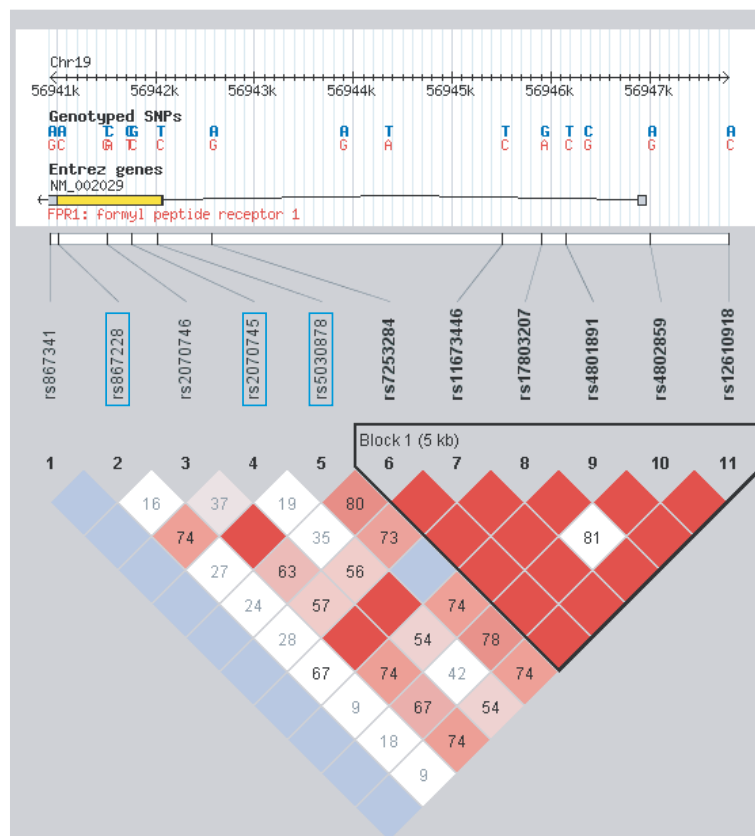
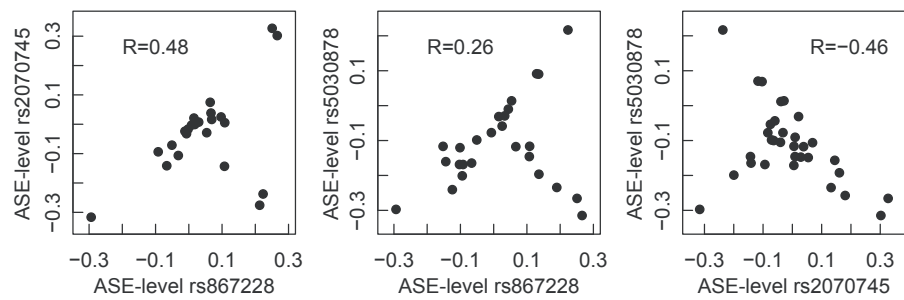
Supplementary Table 1

Supplementary Table 2

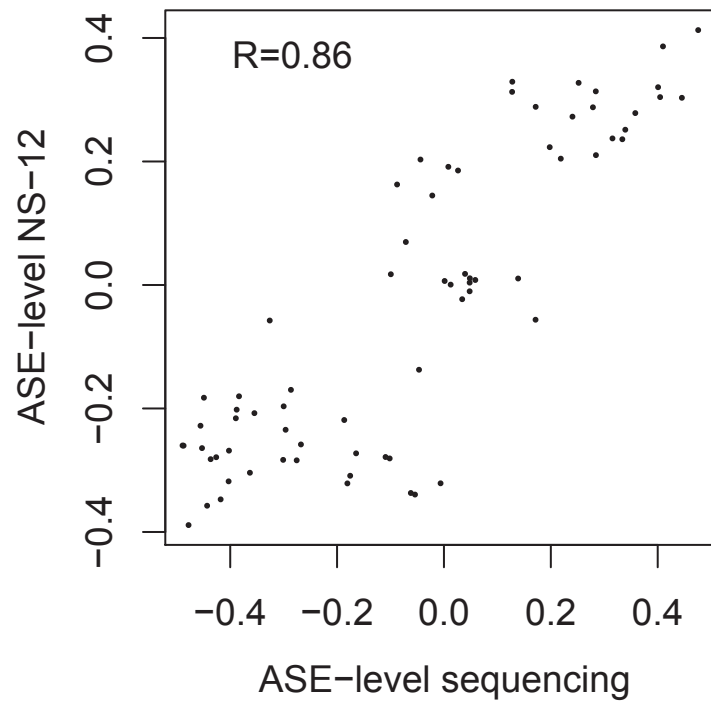
Supplementary Table 3



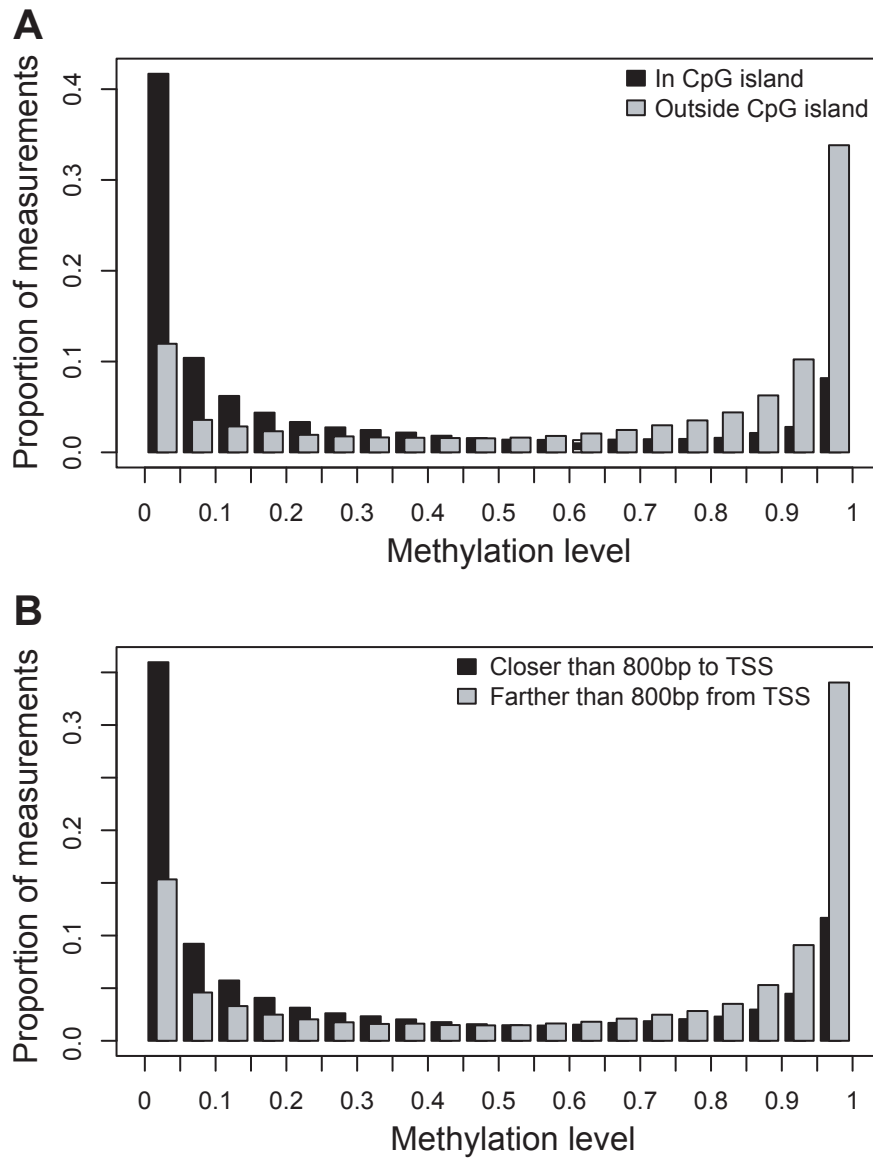
Supplementary Figure 1. Scatter plots obtained by genotyping three SNPs in 197 DNA (black dots) and RNA (red dots) samples. The sum of the fluorescence signal intensities ($A1+A2$) are plotted on the y axis and the allele fractions $[A1/(A1+A2)]$ calculated from the signal intensities are plotted on the x axis. **(A)** Equal expression of the two alleles of the SNP rs2098386 in the *CEBPZ* gene. Variations in the signal intensities between samples has a minor if any effect on the allele fractions. **(B)** Allele-specific expression of the SNP rs7190823 in the *FANCA* gene in 32 of the samples with informative heterozygous SNPs. **(C)** Monoallelic expression of the SNP rs3088074 in the *ATRX* gene in 19 of the samples with informative heterozygous SNPs.



Supplementary Figure 2. Inverse pair-wise correlation between SNP in the same exon of *FPR1* for a subset of samples with ASE. The three top panels show the pair-wise correlation between the ASE-levels determined with three SNPs in the *FPR1* gene. The lower panel shows the linkage disequilibrium (LD) pattern of the *FPR1* gene according to the data from the Human Haplotype Mapping project (<http://www.hapmap.org>). The SNPs that showed inverse correlations between ASE-levels in a subset of the samples located in a region of low LD, outside the major LD-block of the *FPR1* gene are high-lighted by blue boxes.



Supplementary Figure 3. Correlation between ASE-levels determined by genotyping using the NS-12 BeadChips and using Sanger sequencing of one SNPs per gene in 9 genes. The ASE-levels from the NS-12 BeadChips are shown on the vertical axis, and the ASE-levels obtained by sequencing are shown on the horizontal axis.



Supplementary Figure 4. Distribution of methylation levels between CpG sites located within or outside CpG islands (**A**) and between CpG sites located within or outside a 800 bp DNA region surrounding a transcription start site (TSS) (**B**). The methylation levels (Beta-values) for the CpG sites are shown on the horizontal axis and the vertical bars show the proportion of CpG measurements in each bin of methylation level. The graphs show that CpG sites outside CpG islands and further than 800 bp from the transcription start site have higher levels of methylation than CpG sites in CpG islands and within 800 bp from the TSS.

Supplementary Table 1. Pathway analysis of genes displaying ASE.

KEGG pathway	Gene symbol	Obs ^a	Exp ^b	Obs/Exp ^c	P-value ^d
Cell Communication	<i>TNXB, GJA9, DSC3, LAMC1, KRT1, ITGA6, COL6A2</i>	7	1.27	5.52	1.65E-05
ECM-receptor interaction	<i>TNXB, SDC2, LAMC1, ITGA6, COL6A2, HSPG2, CD44, GP6</i>	8	1.90	4.21	1.02E-04
beta-Alanine metabolism	<i>DPYD, ALDH1B1, ABAT</i>	3	0.48	6.31	4.14E-03
Antigen processing and presentation	<i>TAP2, CTSB, LGMN, HLA-DQB1, HLA-DQA1, HLA-DPB1, HLA-DOB, HLA-DOA, HLA-A</i>	9	3.64	2.47	5.87E-03
Cell adhesion molecules (CAMs)	<i>NRXN3, SDC2, ITGA6, HLA-DQA1, HLA-DPB1, HLA-DOB, HLA-DOA, PECAM1, HLA-DQB1, HLA-A</i>	10	4.28	2.34	5.89E-03
Type I diabetes mellitus	<i>PTPRN2, HLA-DQB1, HLA-DQA1, HLA-DPB1, HLA-DOB, HLA-DOA, HLA-A</i>	7	2.53	2.76	7.38E-03

a) Observed number of genes with ASE in the KEGG pathway.

b) Expected number of genes with ASE in the KEGG pathway (total number of genes in the KEGG pathway for the reference set multiplied by the total number of genes in the test set and divided by the total number of genes in the reference set).

c) Ratio of enrichment for the KEGG pathway (Observed/Expected).

d) P-value indicating the significance of enrichment, calculated using a hypergeometric test.

Supplementary Table 2. Complete list of genes with ASE.

Gene ^a	SNP rs-number	Location in Chr gene	Het (N) ^b	ASE (%) ^c	Abs mean ASE level ^d	ASE range ^e
<i>ABAT</i>	rs1731017	16 coding	79	10%	0.15	[0.14;-0.21]
<i>ACACB</i>	rs2075260	12 coding	45	36%	0.23	[0.35;-0.33]
<i>ACCS</i>	rs3107275	11 coding	87	48%	0.30	[0.49;-0.43]
<i>ACY3</i>	rs948445	11 coding	66	12%	0.22	[0.22;-0.39]
<i>AGER</i>	rs1035798	6 intron	85	12%	0.16	[0.18;-0.12]
<i>AIF1</i>	rs2857697	6 flanking	94	16%	0.21	[0.49;0.11]
<i>ALDH1B1</i>	rs2073478	9 coding	83	16%	0.21	[0.34;-0.45]
<i>AMICA1</i>	rs17121881	11 coding	96	10%	0.17	[0.17;-0.26]
<i>AMICA1</i>	rs2298831	11 coding	55	22%	0.16	[-0.11;-0.23]
<i>ANPEP</i>	rs25651	15 coding	69	13%	0.18	[0.19;-0.31]
<i>ANPEP</i>	rs25653	15 coding	101	12%	0.23	[0.29;-0.42]
<i>APOBEC3H</i>	rs139297	22 coding	88	23%	0.18	[0.15;-0.27]
<i>APOBEC3H</i>	rs139302	22 coding	88	25%	0.18	[0.13;-0.29]
<i>APOL2</i>	rs2010499	22 5'UTR	92	23%	0.18	[0.17;-0.24]
<i>APOL4</i>	rs2227168	22 coding	84	30%	0.28	[0.34;-0.44]
<i>ARHGEF3</i>	rs3772219	3 coding	71	13%	0.19	[0.29;0.11]
<i>ARL11</i>	rs3803185	13 coding	85	27%	0.17	[0.24;0.13]
<i>ARSA</i>	rs2071421	22 coding	45	56%	0.31	[0.4;-0.39]
<i>AS3MT</i>	rs11191439	10 coding	38	39%	0.22	[0.34;0.11]
<i>ASPRV1</i>	rs3796097	2 coding	100	10%	0.14	[0.22;0.11]
<i>ATF5</i>	rs283526	19 coding	93	16%	0.19	[-0.1;-0.37]
<i>ATG10</i>	rs1864182	5 coding	81	14%	0.15	[-0.11;-0.19]
<i>ATMIN</i>	rs2278022	16 coding	34	74%	0.20	[-0.14;-0.27]
<i>ATP10A</i>	rs3816800	15 coding	91	22%	0.21	[-0.13;-0.36]
<i>ATP5SL</i>	rs1043413	19 coding	88	9%	0.15	[0.21;0.12]
<i>ATP6V1C2</i>	rs1198849	2 coding	88	57%	0.19	[0.27;0.13]
<i>ATP7A</i>	rs2227291	X coding	23	65%	0.30	[0.46;-0.23]
<i>ATRX</i>	rs3088074	X coding	27	96%	0.37	[0.46;-0.5]
<i>B3GNTL1</i>	rs7225887	17 coding	66	12%	0.19	[0.2;-0.36]
<i>BAG3</i>	rs2234962	10 coding	64	25%	0.23	[0.38;-0.23]
<i>BAT4</i>	rs7029	6 3'UTR	75	25%	0.15	[0.21;0.11]
<i>BAT4</i>	rs805262	6 flanking	95	13%	0.15	[0.17;0.1]
<i>BBS4</i>	rs2277598	15 coding	101	8%	0.15	[0.18;0.13]
<i>BCR</i>	rs2071436	22 intron*	74	41%	0.21	[-0.12;-0.34]
<i>BDH2</i>	rs1054707	4 coding	51	59%	0.20	[-0.11;-0.44]
<i>BMP4</i>	rs17563	14 coding	93	25%	0.29	[0.36;-0.55]
<i>BPI</i>	rs5743509	20 coding	19	58%	0.26	[-0.15;-0.36]
<i>BSPRY</i>	rs3088235	9 coding	71	23%	0.20	[0.3;0.12]
<i>BTN1A1</i>	rs4343916	6 flanking*	86	23%	0.21	[0.32;-0.37]
<i>BTN3A3</i>	rs3846848	6 coding	53	51%	0.16	[0.2;0.12]
<i>C10orf33</i>	rs2147896	10 coding	94	59%	0.25	[0.4;-0.43]
<i>C15orf23</i>	rs7169404	15 coding	47	36%	0.16	[0.21;0.13]
<i>C15orf42</i>	rs3743372	15 coding	88	11%	0.14	[0.2;0.1]
<i>C18orf51</i>	rs2278154	18 coding	98	23%	0.26	[0.48;-0.44]
<i>C19orf15</i>	rs2302182	19 5'UTR	49	33%	0.17	[0.27;0.11]
<i>C1GALT1C1</i>	rs17261572	X coding	21	81%	0.28	[0.21;-0.53]
<i>C1R</i>	rs1801046	12 coding	74	18%	0.19	[0.25;-0.31]
<i>C1RL</i>	rs3742089	12 coding	86	9%	0.16	[0.27;0.11]
<i>C2orf24</i>	rs17655123	2 coding	46	20%	0.15	[-0.13;-0.2]
<i>C2orf3</i>	rs6722682	2 coding	68	15%	0.21	[0.27;-0.47]
<i>C2orf63</i>	rs14026	2 coding	86	9%	0.16	[0.14;-0.22]
<i>C4orf33</i>	rs337277	4 coding	70	16%	0.15	[0.2;0.11]
<i>C4orf42</i>	rs2279281	4 3'UTR	102	15%	0.15	[-0.11;-0.19]
<i>C5orf35</i>	rs2257505	5 coding	76	46%	0.25	[-0.17;-0.43]
<i>C5orf35</i>	rs40497	5 coding	78	18%	0.26	[-0.17;-0.4]
<i>TMEM217</i>	rs1150790	6 3'UTR	70	13%	0.18	[0.16;-0.3]
<i>C6orf145</i>	rs226959	6 coding	94	21%	0.23	[0.32;-0.41]
<i>TTC39B</i>	rs1407977	9 coding	75	13%	0.17	[0.23;0.1]
<i>CAMKK2</i>	rs3817190	12 coding	93	14%	0.16	[0.23;-0.21]
<i>CAPG</i>	rs2229668	2 coding	47	19%	0.19	[-0.13;-0.26]
<i>CAPSL</i>	rs1445898	5 coding	92	15%	0.17	[0.25;-0.18]
<i>CCDC125</i>	rs10471774	5 coding	102	15%	0.22	[0.32;-0.28]
<i>CCDC15</i>	rs4936966	11 3'UTR	63	35%	0.22	[0.34;0.14]

CCL25	rs1129763	19	coding	44	27%	0.23	[0.3;-0.19]
CCL25	rs2032887	19	coding	71	23%	0.24	[0.26;-0.48]
CCL25	rs2303164	19	coding	89	21%	0.24	[0.24;-0.4]
CD248	rs3741367	11	coding	91	11%	0.16	[0.24;0.11]
CD300LF	rs2034310	17	coding	59	22%	0.23	[0.2;-0.37]
CD44	rs1467558	11	coding	52	38%	0.19	[0.2;-0.28]
CD44	rs9666607	11	coding	89	9%	0.19	[0.27;-0.27]
CD68	rs9901673	17	coding	54	28%	0.22	[-0.16;-0.34]
CDC123	rs1051055	10	3'UTR	77	10%	0.13	[0.17;0.1]
CDH11	rs35195	16	coding	97	20%	0.30	[0.41;-0.53]
CDH11	rs35213	16	coding	63	13%	0.20	[0.23;-0.24]
CDH11	rs4424934	16	coding	33	24%	0.21	[0.31;-0.31]
CEACAM21	rs2302188	19	coding	80	29%	0.22	[-0.14;-0.4]
CEACAM21	rs714106	19	coding	80	33%	0.22	[0.45;0.1]
CELSR1	rs9615351	22	coding	60	18%	0.26	[0.29;-0.38]
AGAP1	rs2034648	2	coding	101	23%	0.25	[0.35;-0.54]
CETP	rs5882	16	coding	91	11%	0.16	[0.22;0.12]
CHAF1A	rs9352	19	coding	96	10%	0.15	[0.18;0.11]
CHD1L	rs11588753	1	coding	35	46%	0.16	[0.23;-0.19]
CHID1	rs6682	11	coding	86	9%	0.13	[-0.1;-0.16]
CHST12	rs10226762	7	flanking*	77	12%	0.16	[0.22;0.12]
CHST13	rs1056522	3	coding	81	26%	0.26	[0.24;-0.42]
CLEC10A	rs90951	17	coding	84	21%	0.19	[0.31;0.1]
CLEC4A	rs2024301	12	coding	75	13%	0.17	[-0.12;-0.22]
CLGN	rs12513290	4	coding	41	22%	0.28	[0.41;-0.32]
CLTCL1	rs1633399	22	coding	27	70%	0.24	[-0.1;-0.33]
CLTCL1	rs712952	22	coding	27	67%	0.23	[0.4;0.13]
CLTCL1	rs807459	22	coding	26	50%	0.23	[-0.12;-0.36]
CNDP2	rs2278161	18	coding	62	52%	0.19	[0.26;0.14]
CNTROB	rs11650083	17	coding	104	81%	0.23	[-0.12;-0.39]
COBL	rs2240089	7	coding	64	13%	0.23	[0.29;-0.32]
COBL	rs2240090	7	coding	87	18%	0.21	[0.32;-0.3]
COL27A1	rs2241671	9	coding	94	18%	0.20	[0.33;-0.46]
COL6A2	rs1042917	21	coding	81	20%	0.21	[0.32;-0.23]
COQ6	rs8500	14	coding	97	11%	0.15	[0.2;0.12]
CPAMD8	rs1054533	19	coding	95	11%	0.24	[0.37;0.13]
CPN2	rs3732477	3	coding	79	20%	0.28	[0.38;-0.2]
CPNE1	rs6579255	20	coding	55	45%	0.25	[0.31;0.19]
CPNE7	rs455527	16	coding	29	41%	0.23	[0.33;-0.17]
CPT1B	rs131758	22	5'UTR	94	19%	0.20	[-0.12;-0.34]
CPT1B	rs470117	22	coding	99	15%	0.20	[0.32;0.09]
CPT1B	rs8142477	22	coding	45	36%	0.21	[0.31;-0.23]
CPVL	rs1052200	7	coding	49	24%	0.21	[0.28;-0.46]
CPVL	rs7313	7	coding	84	24%	0.19	[0.33;-0.21]
CR1	rs3737002	1	coding	77	10%	0.17	[0.29;0.13]
CSGALNACT1	rs4244454	8	intron*	57	26%	0.18	[0.2;-0.34]
CSGALNACT1	rs7017776	8	coding	52	35%	0.22	[0.34;-0.31]
CTSB	rs12338	8	coding	99	26%	0.14	[0.14;-0.23]
CYBRD1	rs10455	2	coding	90	10%	0.18	[0.31;0.12]
DAPL1	rs9869	2	coding	108	8%	0.22	[0.32;0.14]
DDR1	rs9295924	6	flanking*	54	85%	0.30	[0.46;0.13]
DEPDC6	rs4871827	8	coding	85	16%	0.14	[0.21;-0.13]
DFNB31	rs2274158	9	coding	66	14%	0.17	[0.24;-0.14]
DLAT	rs627441	11	coding	90	42%	0.16	[0.37;-0.18]
DLGAP2	rs2301963	8	coding	91	16%	0.26	[0.48;-0.36]
SYNM	rs2292288	15	coding	95	16%	0.28	[0.4;-0.39]
DNAJC15	rs11617079	13	coding	66	65%	0.29	[0.45;0.13]
DNLZ	rs3812553	9	3'UTR	22	64%	0.19	[0.25;0.12]
DPEP1	rs1126464	16	coding	77	12%	0.19	[0.32;-0.31]
DPM2	rs7997	9	coding	51	84%	0.24	[0.31;0.17]
DPYD	rs1801265	1	coding	75	13%	0.25	[0.33;-0.36]
DSC3	rs276937	18	coding	99	9%	0.32	[0.45;0.17]
DUSP1	rs11538659	5	flanking*	38	29%	0.24	[0.31;-0.37]
DUSP6	rs770087	12	coding	46	26%	0.17	[0.22;0.12]
ECM1	rs13294	1	coding	100	10%	0.18	[0.29;0.14]
EFCAB4A	rs7126805	11	coding	75	17%	0.23	[0.29;-0.31]
EHBP1L1	rs3741380	11	coding	103	9%	0.14	[0.16;0.1]
ELA3A	rs760923	1	flanking*	62	13%	0.17	[-0.13;-0.32]

EPS15	rs17567	1	coding	77	79%	0.21	[-0.15;-0.29]
ERAP1	rs17482078	5	coding	61	13%	0.17	[-0.11;-0.22]
ERAP1	rs2287987	5	coding	58	24%	0.16	[0.21;-0.2]
ERAP1	rs27044	5	coding	85	19%	0.17	[-0.11;-0.23]
ERAP1	rs30187	5	coding	91	18%	0.17	[0.25;0.11]
EVC	rs2302075	4	coding	65	29%	0.24	[0.45;-0.29]
EVPL	rs7342883	17	coding	22	55%	0.24	[0.33;-0.41]
EYA4	rs9493627	6	coding	86	13%	0.18	[0.21;-0.28]
FAAH	rs324420	1	coding	69	28%	0.24	[0.34;-0.32]
FAM118A	rs6007594	22	coding	76	34%	0.24	[-0.14;-0.46]
FAM24B	rs1891110	10	coding	96	49%	0.33	[0.47;-0.48]
FAM48A	rs9469	13	coding	102	25%	0.15	[0.21;0.1]
FAM83A	rs7813708	8	coding	62	26%	0.19	[0.31;0.12]
FANCA	rs7190823	16	coding	104	33%	0.15	[0.2;0.12]
FAT	rs11939575	4	coding	60	12%	0.38	[0.46;-0.47]
FAT	rs328418	4	coding	105	12%	0.35	[0.39;-0.52]
FAT	rs3733413	4	coding	95	12%	0.30	[0.38;-0.52]
FAT	rs3733414	4	coding	81	11%	0.32	[0.46;-0.48]
FBLN2	rs9843344	3	coding	80	13%	0.29	[0.24;-0.54]
FGL2	rs2075761	7	coding	46	48%	0.24	[0.34;0.13]
FLJ10769'	rs11551105	13	3'UTR	38	55%	0.28	[0.32;-0.5]
FLJ10769'	rs7394	13	3'UTR	68	26%	0.23	[0.24;-0.42]
FLRT3	rs6079391	20	coding	89	9%	0.26	[0.29;-0.39]
FLVCR1	rs1047881	1	flanking*	115	80%	0.22	[0.3;0.14]
FPR1	rs2070745	19	coding	87	15%	0.21	[0.33;-0.32]
FPR1	rs5030878	19	coding	59	47%	0.19	[0.22;-0.31]
FPR1	rs867228	19	coding	61	18%	0.19	[0.27;-0.29]
FSIP1	rs937961	15	coding	42	19%	0.18	[0.33;0.11]
FUCA2	rs3762001	6	coding	60	15%	0.19	[0.27;-0.28]
FUCA2	rs3762002	6	coding	59	15%	0.19	[0.31;-0.31]
FUT8	rs1953416	14	intron*	88	9%	0.15	[0.17;0.13]
FXYD2	rs529623	11	coding	87	63%	0.33	[0.51;-0.3]
FZD6	rs3808553	8	coding	83	16%	0.26	[0.26;-0.47]
GATM	rs1288775	15	coding	90	47%	0.28	[0.5;-0.24]
GBE1	rs2229519	3	coding	93	16%	0.19	[0.44;0.11]
GBP3	rs10493821	1	coding	79	39%	0.22	[-0.12;-0.42]
GEFT'	rs1564374	12	coding	77	10%	0.21	[0.38;0.11]
GGT5	rs2275984	22	coding	75	25%	0.24	[0.43;-0.3]
GIMAP2	rs2075078	7	coding	67	13%	0.13	[0.17;0.1]
GIPC3	rs2108389	19	flanking*	103	12%	0.22	[0.23;-0.33]
GIPC3	rs8105780	19	flanking*	90	21%	0.22	[0.39;-0.27]
GJA10	rs12127091	1	3'UTR	88	51%	0.20	[0.31;0.12]
GLI3	rs846266	7	coding	96	33%	0.25	[0.31;-0.48]
GLI3	rs929387	7	coding	87	26%	0.27	[0.35;-0.55]
GNL3	rs1108842	3	5'UTR	100	9%	0.17	[-0.15;-0.19]
GP6	rs1613662	19	coding	43	23%	0.22	[0.33;-0.39]
GP6	rs2304167	19	coding	52	38%	0.19	[0.35;-0.3]
GPR109B	rs1798192	12	coding	90	14%	0.20	[0.12;-0.32]
GPR35	rs3749172	2	coding	95	9%	0.19	[0.33;-0.18]
GPR56	rs1801257	16	coding	96	16%	0.18	[-0.13;-0.24]
GSTM3	rs7483	1	coding	77	60%	0.26	[0.4;-0.3]
GSTZ1	rs7972	14	coding	45	18%	0.16	[0.2;0.14]
GTPBP10	rs42664	7	coding	98	34%	0.17	[0.28;0.12]
HCG27	rs9263870	6	coding	38	24%	0.23	[-0.12;-0.43]
HEBP1	rs1291361	12	flanking*	84	35%	0.19	[0.35;-0.43]
HEBP1	rs1291362	12	flanking*	81	17%	0.21	[0.37;-0.28]
HELB	rs4430553	12	coding	88	10%	0.15	[-0.13;-0.19]
HIBCH	rs1058180	2	coding	62	16%	0.14	[0.22;0.11]
HIST1H2BD	rs2183947	6	intron	83	13%	0.21	[0.26;-0.45]
HLA-A	rs2735097	6	flanking	94	29%	0.18	[0.23;-0.25]
HLA-A	rs7745413	6	flanking	62	26%	0.20	[-0.13;-0.27]
HLA-DOA	rs6920606	6	flanking	91	41%	0.18	[0.3;0.13]
HLA-DOB	rs11244	6	3'UTR	75	13%	0.16	[0.19;-0.18]
HLA-DPB1	rs9277554	6	flanking	86	48%	0.18	[0.35;0.12]
HLA-DQA1	rs6906021	6	flanking*	93	61%	0.27	[0.44;0.13]
HLA-DQA1	rs6927022	6	flanking*	83	20%	0.23	[0.34;-0.29]
HLA-DQA1	rs7744001	6	flanking*	73	62%	0.27	[-0.13;-0.55]
HMGNA4	rs9461267	6	flanking*	89	18%	0.20	[0.36;-0.37]

HSPG2	rs2254357	1	coding	93	13%	0.21	[-0.11;-0.34]
HYLS1	rs667782	11	coding	86	15%	0.16	[0.23;-0.25]
IER3	rs8512	6	3'UTR	62	15%	0.16	[0.15;-0.23]
IFI44L	rs273259	1	coding	80	55%	0.22	[-0.14;-0.42]
IGF2BP3	rs274018	7	intron*	82	12%	0.28	[0.3;-0.53]
IGSF3	rs6703791	1	coding	49	16%	0.19	[0.34;-0.23]
IHPK2	rs3172494	3	3'UTR	44	20%	0.19	[-0.15;-0.25]
IL12RB1	rs401502	19	coding	69	12%	0.18	[-0.12;-0.22]
IL17RC	rs708567	3	coding	103	11%	0.18	[0.21;-0.39]
IL17RE	rs455863	3	coding	103	22%	0.25	[0.43;-0.32]
INADL	rs1056513	1	coding	105	11%	0.25	[0.45;-0.3]
IQCE	rs3735109	7	coding	105	8%	0.13	[0.15;0.12]
IRAK1	rs1059703	X	coding	21	90%	0.37	[0.41;-0.52]
ITGA6	rs11895564	2	coding	81	12%	0.17	[0.19;-0.29]
ITIH3	rs3617	3	coding	100	12%	0.18	[0.24;-0.26]
ITIH4	rs13072536	3	coding	66	56%	0.19	[0.29;0.14]
ITIH4	rs4687657	3	coding	79	10%	0.17	[0.26;-0.16]
ITM2C	rs2289235	2	coding	99	33%	0.25	[0.33;-0.4]
JAG1	rs1051421	20	coding	72	15%	0.18	[0.34;-0.21]
JMY'	rs13182512	5	coding	90	13%	0.24	[0.37;-0.4]
KCNMB3	rs1170672	3	coding	48	38%	0.26	[0.31;-0.48]
KIAA0564	rs3742262	13	coding	93	10%	0.18	[0.31;-0.25]
KIAA0564	rs9562362	13	coding	92	9%	0.20	[0.22;-0.33]
KIAA1274	rs2275060	10	coding	63	17%	0.16	[0.26;-0.16]
KIAA1462	rs2185724	10	coding	83	18%	0.23	[0.37;0.13]
KIAA1683	rs1469023	19	coding	102	11%	0.15	[0.2;0.11]
KIAA1683	rs2277922	19	coding	88	15%	0.16	[0.21;0.13]
KIAA1683	rs8110972	19	coding	98	13%	0.15	[0.19;0.11]
KIAA1683	rs999814	19	intron*	84	10%	0.14	[-0.12;-0.18]
KIAA1804'	rs3795374	1	coding	65	31%	0.20	[0.27;0.12]
KIF14	rs12120084	1	coding	82	12%	0.14	[-0.1;-0.2]
KIF7	rs12900805	15	coding	102	12%	0.26	[0.4;-0.33]
KLHDC4	rs2303771	16	coding	100	32%	0.16	[0.15;-0.2]
KLHDC7B	rs131779	22	coding	80	10%	0.21	[0.22;-0.41]
KLHL33	rs1953225	14	coding	53	17%	0.19	[0.18;-0.33]
KLRK1	rs2255336	12	coding	58	31%	0.25	[0.35;-0.3]
KRT1	rs14024	12	coding	88	26%	0.21	[0.44;-0.18]
L3MBTL3	rs9388768	6	coding	81	10%	0.29	[0.48;-0.36]
LAMC1	rs20563	1	coding	88	13%	0.26	[0.44;-0.39]
LASS4	rs17160348	19	coding	45	20%	0.19	[0.33;-0.32]
LCN10	rs9886752	9	coding	50	26%	0.25	[0.17;-0.39]
LDLRAD2	rs3736360	1	coding	61	13%	0.25	[0.36;-0.32]
LGALS8	rs2273863	1	coding	13	92%	0.30	[-0.23;-0.34]
LGMN	rs2236264	14	coding	62	21%	0.19	[0.25;-0.31]
LIG4	rs1805388	13	coding	56	14%	0.28	[0.4;0.16]
LIPC	rs6083	15	coding	94	13%	0.19	[0.28;-0.27]
LLGL2	rs1671036	17	coding	99	19%	0.16	[0.25;0.12]
LOC170082'	rs5935650	X	coding	41	71%	0.29	[0.35;-0.54]
LOC26010'	rs842823	2	5'UTR	82	17%	0.25	[0.38;-0.44]
LOC553158'	rs6007344	22	coding	57	14%	0.21	[0.23;-0.36]
LOC93349'	rs7590429	2	coding	96	8%	0.16	[0.2;0.12]
LOC96610'	rs1985918	22	flanking*	44	41%	0.21	[0.38;-0.29]
LOXHD1	rs1377016	18	coding	96	16%	0.26	[0.41;-0.38]
LOXHD1	rs1893566	18	coding	54	17%	0.24	[0.35;-0.39]
LPCAT2	rs837550	16	coding	90	16%	0.37	[0.46;-0.53]
LRRC25	rs6512265	19	coding	89	18%	0.19	[0.31;-0.2]
MAGEF1	rs9872799	3	coding	64	17%	0.16	[0.23;0.1]
MAP7D3	rs2273221	X	coding	33	94%	0.40	[0.33;-0.54]
MAPKAPK5	rs3742000	12	flanking	56	32%	0.18	[0.25;0.11]
MED16	rs13090	19	coding	72	24%	0.17	[0.23;0.11]
MERTK	rs2230517	2	coding	18	44%	0.27	[0.35;0.17]
MERTK	rs3811635	2	coding	86	20%	0.25	[0.43;-0.31]
MFGES	rs1878326	15	coding	94	11%	0.24	[0.46;-0.24]
MICA	rs1131896	6	coding	51	35%	0.15	[0.21;0.11]
MICB	rs2844498	6	intron	91	14%	0.16	[0.25;0.12]
MMP14	rs1042704	14	coding	65	15%	0.21	[0.3;-0.37]
MRPL18	rs2273821	6	coding	73	29%	0.15	[-0.12;-0.2]
MS4A14	rs3825020	11	coding	86	24%	0.19	[0.34;0.12]

<i>MTHFSD</i>	rs3751800	16	coding	42	21%	0.15	[0.19;0.12]
<i>MTL5</i>	rs12365708	11	coding	52	71%	0.22	[-0.12;-0.36]
<i>MUC4</i>	rs2688513	3	coding	60	28%	0.29	[-0.11;-0.41]
<i>MYBPC2</i>	rs25665	19	coding	57	28%	0.18	[0.25;0.13]
<i>MYH11</i>	rs16967494	16	coding	86	12%	0.19	[-0.15;-0.23]
<i>MYO10</i>	rs11750538	5	coding	79	30%	0.27	[0.38;-0.5]
<i>MYO18B</i>	rs133885	22	coding	91	37%	0.32	[0.5;-0.43]
<i>MYO18B</i>	rs2236005	22	coding	57	42%	0.29	[0.41;-0.52]
<i>MYO3A</i>	rs1999240	10	coding	89	11%	0.32	[0.34;-0.49]
<i>MYOM1</i>	rs1071600	18	coding	46	20%	0.17	[0.3;0.11]
<i>MYOM2</i>	rs968381	8	coding	63	25%	0.24	[0.32;-0.31]
<i>NCR1</i>	rs2278428	19	coding	34	24%	0.22	[0.31;-0.33]
<i>NFATC4</i>	rs7149586	14	coding	91	20%	0.28	[0.39;-0.45]
<i>NID2</i>	rs2101919	14	coding	68	37%	0.28	[0.45;0.15]
<i>NID2</i>	rs3742536	14	coding	64	34%	0.22	[0.39;-0.43]
<i>NKAIN4</i>	rs1129659	20	coding	89	36%	0.35	[0.47;-0.2]
<i>NKAIN4</i>	rs872808	20	coding	89	35%	0.33	[0.43;-0.18]
<i>NOTCH3</i>	rs1044009	19	coding	65	17%	0.24	[0.26;-0.45]
<i>NRP1</i>	rs2070296	10	coding	63	25%	0.18	[0.28;-0.18]
<i>NRXN3</i>	rs11626446	14	coding	74	12%	0.30	[0.46;-0.36]
<i>NSUN7</i>	rs4861066	4	3'UTR	69	10%	0.18	[0.23;0.16]
<i>NT5C3L</i>	rs1046403	17	coding	74	16%	0.20	[0.18;-0.42]
<i>NT5E</i>	rs3812138	6	coding	75	31%	0.16	[0.29;0.12]
<i>NUP210</i>	rs3732671	3	coding	91	9%	0.13	[0.15;0.1]
<i>OAS1</i>	rs1051042	12	coding	78	91%	0.25	[-0.17;-0.38]
<i>OAS1</i>	rs3177979	12	coding	81	93%	0.36	[-0.22;-0.51]
<i>OAS1</i>	rs3741981	12	coding	90	22%	0.15	[0.24;-0.22]
<i>P2RX7</i>	rs1718119	12	coding	84	35%	0.17	[0.34;0.11]
<i>P2RY11</i>	rs3745601	19	coding	34	35%	0.16	[0.25;-0.22]
<i>PANX1</i>	rs1138800	11	coding	83	18%	0.17	[-0.1;-0.24]
<i>PAX8</i>	rs6734610	2	intron*	102	40%	0.31	[0.42;-0.51]
<i>PCLO</i>	rs10954696	7	coding	95	9%	0.22	[0.3;-0.3]
<i>PCLO</i>	rs2877	7	coding	74	14%	0.28	[0.37;-0.38]
<i>PDE4A</i>	rs1051738	19	coding	61	36%	0.19	[0.3;-0.31]
<i>PDE4DIP</i>	rs1628172	1	coding	75	76%	0.25	[0.46;-0.14]
<i>PDLIM5</i>	rs7690296	4	coding	109	7%	0.21	[0.35;-0.37]
<i>PDXDC2</i>	rs929843	16	coding	75	16%	0.16	[0.21;-0.27]
<i>PECAM1</i>	rs1131012	17	coding	98	30%	0.18	[0.28;0.11]
<i>PER3</i>	rs10462021	1	coding	52	29%	0.28	[0.38;-0.42]
<i>PGM1</i>	rs11208257	1	coding	64	17%	0.26	[0.28;-0.52]
<i>PHACTR1</i>	rs454563	6	flanking*	49	31%	0.19	[0.29;-0.14]
<i>PI16</i>	rs1405069	6	coding	96	28%	0.23	[-0.14;-0.41]
<i>PIH1D1</i>	rs7462	19	coding	84	10%	0.13	[0.14;0.12]
<i>PKLR</i>	rs1052176	1	coding	69	22%	0.21	[-0.13;-0.37]
<i>PLD2</i>	rs3764897	17	coding	50	26%	0.19	[0.32;-0.12]
<i>PLEKHG2</i>	rs10407035	19	coding	41	27%	0.17	[0.26;0.13]
<i>PLEKHG4</i>	rs3868142	16	coding	48	17%	0.18	[0.25;-0.26]
<i>PLEKHG4B</i>	rs11949577	5	coding	40	20%	0.39	[0.26;-0.5]
<i>PLXDC2</i>	rs2778979	10	coding	46	26%	0.24	[0.34;-0.37]
<i>POLG2</i>	rs1427463	17	coding	33	30%	0.18	[-0.14;-0.23]
<i>POMZP3</i>	rs1134609	7	coding	97	24%	0.18	[0.18;-0.31]
<i>PON2</i>	rs7493	7	coding	73	22%	0.30	[0.38;-0.47]
<i>POU5F1</i>	rs3130931	6	intron*	85	19%	0.21	[0.33;0.14]
<i>PPIL3</i>	rs7562391	2	coding	42	29%	0.16	[0.22;0.13]
<i>PPP1R15A</i>	rs556052	19	coding	85	12%	0.15	[0.18;0.11]
<i>PPP1R15A</i>	rs557806	19	coding	48	23%	0.17	[-0.14;-0.23]
<i>PPP4R1L</i>	rs3746405	20	coding	90	29%	0.19	[0.3;-0.33]
<i>PRDM9</i>	rs1501940	5	flanking*	86	19%	0.44	[0.44;-0.53]
<i>PROCR</i>	rs867186	20	coding	31	26%	0.17	[0.21;0.13]
<i>PTK2B</i>	rs751019	8	coding	96	13%	0.13	[0.16;0.11]
<i>PTPRN2</i>	rs3800855	7	coding	53	15%	0.20	[0.28;-0.2]
<i>R3HCC1</i>	rs2272761	8	coding	93	27%	0.15	[-0.12;-0.2]
<i>RAI14</i>	rs1048944	5	coding	96	10%	0.20	[0.28;-0.22]
<i>RAI14</i>	rs17521570	5	coding	38	34%	0.19	[0.29;-0.44]
<i>RARS</i>	rs2305734	5	coding	60	17%	0.15	[0.2;0.12]
<i>RASAL1</i>	rs1284879	12	coding	64	23%	0.25	[0.35;-0.4]
<i>REG4</i>	rs1052972	1	3'UTR	94	14%	0.22	[-0.12;-0.38]
<i>RELL2</i>	rs11742646	5	coding	63	17%	0.20	[0.18;-0.28]

RELL2	rs14251	5	coding	94	14%	0.22	[0.34;-0.28]
RNASE3	rs3748340	14	flanking*	73	18%	0.19	[0.23;-0.29]
RNASET2	rs3777722	6	intron*	42	26%	0.22	[0.35;-0.22]
RNF168	rs3796129	3	coding	83	33%	0.23	[0.31;-0.28]
RNFT2	rs903775	12	intron*	75	13%	0.25	[0.23;-0.4]
ROR1	rs7527017	1	coding	89	10%	0.29	[0.35;-0.45]
RPS6KL1	rs7156590	14	coding	84	21%	0.20	[0.3;-0.34]
RTP4	rs3821812	3	coding	91	9%	0.14	[0.19;0.12]
RYR3	rs6495228	15	coding	54	15%	0.25	[0.29;-0.3]
SDC2	rs1042381	8	coding	60	13%	0.27	[-0.15;-0.46]
SDCBP2	rs1048621	20	coding	76	16%	0.15	[0.18;-0.16]
SEC14L4	rs17738527	22	coding	68	22%	0.16	[0.25;0.12]
SEC31B	rs2295774	10	coding	67	25%	0.16	[0.26;0.11]
SERPINB6	rs2236277	6	coding	79	15%	0.18	[0.3;-0.24]
SERPINF1	rs1136287	17	coding	100	38%	0.17	[0.27;0.11]
SERPINF2	rs1057335	17	coding	63	16%	0.20	[0.25;-0.28]
SH3PXD2A	rs3740472	10	coding	36	44%	0.28	[0.45;-0.42]
SHANK3	rs9616915	22	coding	99	18%	0.20	[0.43;0.11]
SHROOM3	rs344141	4	coding	105	22%	0.22	[0.3;-0.37]
SHROOM3	rs3733242	4	coding	85	14%	0.24	[0.4;-0.27]
SIRPG	rs6034239	20	coding	98	14%	0.16	[0.2;-0.33]
SLC12A7	rs3810854	5	3'UTR	92	13%	0.19	[0.25;-0.15]
SLC12A7	rs4526148	5	coding	93	38%	0.17	[0.24;0.12]
SLC14A1	rs1058396	18	coding	107	11%	0.16	[0.25;-0.14]
SLC15A2	rs2257212	3	coding	95	35%	0.20	[0.28;0.13]
SLC22A18	rs1048047	11	coding	98	8%	0.22	[0.24;-0.34]
SLC22A18	rs1129782	11	coding	65	40%	0.19	[0.37;0.12]
SLC22A20	rs514076	11	coding	69	19%	0.23	[0.2;-0.39]
SLC22A4	rs272893	5	coding	91	20%	0.16	[0.23;0.12]
SLC25A43	rs3810755	X	coding	42	93%	0.38	[0.46;-0.45]
SLC2A9	rs2280205	4	coding	88	30%	0.26	[0.38;-0.45]
SLC7A3	rs6525447	X	coding	14	79%	0.37	[0.36;-0.54]
SLC7A8	rs7157021	14	coding	90	23%	0.23	[0.38;-0.23]
SLC9A3R2	rs11876	16	3'UTR	57	40%	0.19	[0.34;0.11]
SLCO5A1	rs3750266	8	coding	100	16%	0.24	[0.4;-0.35]
SLFN11	rs12453150	17	coding	86	12%	0.28	[0.47;-0.4]
SP2	rs2229358	17	coding	93	9%	0.14	[0.16;0.13]
SPATA20	rs8076632	17	coding	86	74%	0.26	[-0.12;-0.47]
SPATA20	rs9913430	17	coding	72	74%	0.26	[0.31;-0.49]
SPATA6	rs1056042	1	coding	83	16%	0.27	[0.36;-0.36]
SPCS1	rs6617	3	5'UTR	99	8%	0.13	[0.16;0.11]
SPON2	rs11247975	4	coding	79	11%	0.20	[0.28;-0.28]
SPON2	rs2279279	4	coding	79	15%	0.19	[0.27;-0.37]
SPON2	rs6836335	4	coding	33	33%	0.19	[0.29;-0.29]
SPTA1	rs3737515	1	coding	78	13%	0.16	[0.21;0.09]
ST3GAL3	rs37458	1	coding	83	25%	0.14	[0.17;0.12]
STK33	rs3751096	11	coding	62	32%	0.25	[0.27;-0.58]
STK33	rs7947230	11	flanking*	53	26%	0.17	[0.25;-0.21]
STRN3	rs2273171	14	coding	105	10%	0.17	[0.22;-0.25]
STXBP5	rs9390459	6	coding	93	10%	0.33	[0.41;-0.46]
SYTL3	rs901363	6	coding	70	11%	0.19	[-0.13;-0.26]
TACC2	rs2295873	10	coding	37	32%	0.31	[0.35;-0.43]
TACC2	rs2295879	10	coding	75	13%	0.27	[0.33;-0.49]
TAGLN3	rs8070	3	3'UTR	71	15%	0.27	[0.34;-0.24]
TAP2	rs4148876	6	coding	35	26%	0.16	[0.2;0.14]
TAP2	rs4576294	6	coding	36	42%	0.17	[0.22;0.14]
TBC1D25	rs2293948	X	coding	27	85%	0.31	[0.37;-0.41]
TBC1D4	rs1062087	13	coding	48	19%	0.18	[0.24;-0.25]
TBC1D8	rs1062062	2	coding	43	23%	0.19	[0.26;0.14]
TCF7L1	rs11547160	2	coding	18	44%	0.22	[0.33;-0.22]
TCL1A	rs10146784	14	flanking*	76	20%	0.21	[0.38;-0.21]
TCL1B	rs1064017	14	coding	95	31%	0.26	[0.46;-0.35]
TCP11L2	rs4964460	12	coding	66	12%	0.16	[0.21;0.13]
TEX261	rs2302561	2	coding	80	20%	0.14	[0.17;0.1]
THG1L	rs2270812	5	coding	86	10%	0.13	[0.15;0.11]
THSD7A	rs2285744	7	coding	92	12%	0.25	[0.34;-0.44]
THSD7A	rs47	7	coding	72	17%	0.21	[0.37;-0.3]
THUMPD3	rs1129174	3	coding	64	52%	0.16	[0.2;0.13]

TMEM176B	rs2072443	7	coding	104	38%	0.24	[0.27;-0.41]
TMEM176B	rs3173833	7	coding	92	28%	0.22	[0.3;-0.3]
TMEM187	rs7350355	X	coding	26	88%	0.34	[0.39;-0.46]
TMEM2	rs25688	9	coding	26	38%	0.18	[0.21;-0.16]
TMEM2	rs25695	9	coding	30	50%	0.21	[0.35;-0.21]
TMEM43	rs4685076	3	coding	73	11%	0.15	[-0.11;-0.2]
TMEM8	rs11248931	16	coding	92	23%	0.16	[0.21;0.12]
TMEM99	rs10558	17	coding	50	16%	0.22	[0.12;-0.36]
TMTC4	rs946837	13	coding	75	19%	0.14	[0.17;0.12]
TNFRSF10A	rs6557634	8	coding	98	16%	0.21	[0.28;-0.33]
TNFRSF11A	rs1805034	18	coding	95	23%	0.22	[0.41;-0.18]
TNIK	rs17857452	3	coding	22	45%	0.19	[0.25;0.14]
TNXB	rs4713498	6	coding	29	62%	0.25	[0.37;0.16]
TPO	rs1042589	2	3'UTR	92	13%	0.19	[0.22;-0.34]
TRAP1	rs13926	16	coding	95	23%	0.15	[-0.1;-0.21]
TRIM10	rs2022065	6	3'UTR	92	9%	0.15	[0.17;-0.17]
TRIM45	rs1289658	1	coding	95	42%	0.17	[-0.1;-0.26]
TSPAN16	rs420703	19	intron*	72	38%	0.36	[0.15;-0.47]
TSP0	rs6971	22	coding	82	12%	0.19	[0.28;-0.22]
TSPYL1	rs3749894	6	coding	61	15%	0.16	[-0.12;-0.18]
TTL13	rs2063743	15	coding	83	12%	0.17	[-0.14;-0.21]
UBA1	rs11558783	X	coding	17	47%	0.20	[0.26;-0.23]
UMODL1	rs220159	21	coding	95	17%	0.22	[0.18;-0.3]
UMODL1	rs3819142	21	coding	66	17%	0.19	[0.25;-0.22]
UQCRFS1	rs8100724	19	coding	32	28%	0.15	[0.17;0.12]
USP36	rs1057040	17	coding	95	8%	0.15	[-0.1;-0.21]
USP36	rs3088040	17	coding	103	30%	0.15	[0.21;0.1]
USP8	rs11638390	15	coding	48	17%	0.16	[0.19;-0.18]
VANGL1	rs4839469	1	coding	45	22%	0.19	[0.33;-0.3]
VARS2	rs1264303	6	5'UTR	97	16%	0.19	[-0.12;-0.34]
VARS2	rs2252863	6	coding	95	12%	0.16	[0.22;0.13]
VPREB1	rs2073447	22	flanking*	79	46%	0.26	[0.51;-0.49]
VWA2	rs597371	10	coding	94	11%	0.20	[0.41;-0.24]
WDR35	rs1191778	2	coding	100	15%	0.30	[0.5;-0.34]
WDR4	rs2248490	21	coding	84	18%	0.19	[0.34;0.12]
WDR41	rs33204	5	coding	88	10%	0.19	[0.24;-0.32]
WDR52	rs2291905	3	coding	70	19%	0.16	[-0.13;-0.21]
WDR60	rs2788478	7	coding	88	23%	0.17	[0.25;0.1]
WDSUB1	rs7591849	2	coding	102	10%	0.18	[0.25;0.1]
WFS1	rs1801212	4	coding	77	23%	0.20	[0.36;-0.45]
WFS1	rs734312	4	coding	82	28%	0.20	[0.32;-0.51]
WSB1	rs9303634	17	coding	85	14%	0.20	[-0.12;-0.29]
WWOX	rs2288033	16	coding	84	11%	0.18	[0.28;0.12]
XIAP	rs5956583	X	coding	22	86%	0.36	[0.46;-0.41]
XRR1	rs4944960	11	coding	84	82%	0.20	[-0.11;-0.3]
ZACN	rs2257020	17	coding	92	9%	0.13	[0.17;0.12]
ZC3HAV1	rs3735007	7	coding	104	14%	0.17	[0.24;0.13]
ZFP28	rs10409531	19	coding	89	16%	0.20	[0.27;-0.21]
ZMAT1	rs17282855	X	coding	12	100%	0.34	[0.49;-0.35]
ZNF274	rs7256349	19	coding	78	21%	0.24	[0.4;-0.35]
ZNF286A	rs3760299	17	coding	92	9%	0.28	[-0.14;-0.39]
ZNF311	rs6456880	6	coding	100	8%	0.26	[-0.12;-0.38]
ZNF415	rs1133327	19	coding	96	19%	0.24	[0.34;-0.4]
ZNF419	rs2074071	19	intron*	83	36%	0.20	[0.35;0.13]
ZNF434	rs27241	16	5'UTR	76	12%	0.16	[0.16;-0.22]
ZNF443	rs7256321	19	coding	77	10%	0.16	[0.27;0.12]
ZNF462	rs10217192	9	coding	41	37%	0.37	[0.51;-0.51]
ZNF462	rs3814538	9	coding	87	15%	0.28	[0.4;-0.46]
ZNF462	rs3814541	9	coding	44	23%	0.31	[0.34;-0.51]
ZNF502	rs7640654	3	coding	94	29%	0.35	[0.32;-0.44]
ZNF554	rs867168	19	coding	62	15%	0.18	[0.21;0.12]
ZNF597	rs2270493	16	coding	16	69%	0.31	[0.32;-0.4]
ZNF624	rs8065506	17	coding	86	10%	0.17	[0.28;0.11]
ZNF641	rs2732481	12	coding	89	12%	0.15	[0.18;0.13]
ZNF667	rs3760849	19	coding	100	12%	0.35	[0.42;-0.43]
ZNF75A	rs17611866	16	coding	80	18%	0.24	[0.35;-0.32]
ZNF768	rs10871453	16	coding	94	9%	0.15	[-0.12;-0.18]

a) Gene symbol according to HUGO Gene Nomenclature Committee (<http://www.genenames.org/>).

Symbols marked with an apostrophe (') are genes for which HGNC symbol were not available.

b) Number of samples with heterozygous genotypes for the SNP analyzed.

c) Proportion of heterozygous samples with allele-specific expression.

d) Absolute value of mean ASE across individuals with ASE, calculated as the difference in allele fraction between RNA and DNA.

e) Range of ASE across the samples, + indicates over-expression of allele 1 and - indicates over-expression of allele 2.

*) SNPs in flanking or intronic regions of annotated genes but within coding regions of reported GenBank mRNA transcripts or expressed sequence tags.

Supplementary Table 3. Differences in ASE levels between CpG sites with low/high or intermediate methylation.

Gene Symbol ^a	CpG site ^b	N ^c Low/High	Median ASE ^d Low/High	N ^e Intermediate	Median ASE ^f Intermediate	p-value ^g	Permuted p-value ^h
<i>FAM24B</i>	cg17560056	49	0.09	32	0.37	4.9E-08	2.0E-04
<i>DNAJC15</i>	cg26288331	42	0.17	20	0.35	5.7E-07	2.0E-04
<i>ZNF75A</i>	cg13161844	66	0.03	10	0.25	3.0E-06	2.0E-04
<i>ZNF75A</i>	cg05506643	67	0.03	9	0.24	4.2E-06	2.0E-04
<i>TSPO</i>	cg06758027	68	0.03	7	0.18	5.4E-05	8.0E-04
<i>ZNF75A</i>	cg04907193	68	0.03	8	0.25	8.9E-05	2.0E-04
<i>ZNF274</i>	cg16113200	57	0.03	11	0.15	1.1E-04	2.0E-04
<i>ZNF667</i>	cg05412820	58	0.03	8	0.37	1.6E-04	2.0E-04
<i>FLJ10769</i>	cg11955762	50	0.07	30	0.20	3.0E-04	1.2E-03
<i>CLEC10A</i>	cg21550483	39	0.05	34	0.11	3.3E-04	6.8E-03
<i>FAT</i>	cg17448665	38	0.08	11	0.47	3.4E-04	2.0E-04
<i>BMP4</i>	cg26240298	65	0.08	12	0.29	3.5E-04	2.0E-04
<i>FAM24B</i>	cg04189241	56	0.15	25	0.37	3.9E-04	6.0E-04
<i>ZNF667</i>	cg18243335	61	0.03	5	0.37	4.5E-04	3.0E-03
<i>MYOM2</i>	cg05245209	47	0.09	3	0.31	5.6E-04	4.4E-03
<i>RASAL1</i>	cg12961697	48	0.06	4	0.35	5.7E-04	3.6E-03
<i>KIAA1683</i>	cg18019887	27	0.06	91	0.09	1.0E-03	3.0E-03
<i>AGAP1</i>	cg18731507	55	0.08	9	0.23	1.4E-03	5.2E-03
<i>CPT1B</i>	cg21596097	81	0.08	46	0.11	1.5E-03	1.9E-02
<i>FZD6</i>	cg24442586	68	0.07	7	0.27	1.6E-03	2.0E-04
<i>PDLIM5</i>	cg27478071	92	0.04	9	0.08	1.7E-03	1.0E-02
<i>MYO10</i>	cg26840270	35	0.08	10	0.27	2.0E-03	6.8E-03
<i>ACY3</i>	cg11096993	46	0.05	5	0.17	2.0E-03	2.8E-03
<i>WFS1</i>	cg06569272	87	0.08	6	0.38	2.1E-03	2.0E-04
<i>HEBP1</i>	cg04588079	77	0.11	3	0.37	2.3E-03	4.0E-04
<i>MYO3A</i>	cg20746559	13	0.09	7	0.34	2.3E-03	1.1E-02
<i>HEBP1</i>	cg00810659	44	0.09	36	0.15	2.7E-03	1.4E-03
<i>WFS1</i>	cg22794485	85	0.08	8	0.18	2.8E-03	1.0E-03
<i>PDLIM5</i>	cg07319098	88	0.04	13	0.08	2.8E-03	2.8E-03
<i>TSPO</i>	cg13392232	70	0.04	5	0.14	2.8E-03	2.0E-02
<i>C5orf35</i>	cg12654349	104	0.08	3	0.35	3.0E-03	2.0E-04
<i>CCDC125</i>	cg24338643	84	0.04	12	0.14	3.1E-03	4.0E-04
<i>ZNF667</i>	cg21290245	60	0.03	6	0.35	3.4E-03	2.2E-03
<i>ZNF415</i>	cg16250649	47	0.08	3	0.31	3.4E-03	9.6E-03
<i>FAAH</i>	cg11293517	49	0.07	20	0.14	3.6E-03	1.3E-02
<i>IRAK1</i>	cg02258409	9	0.32	9	0.42	3.9E-03	3.1E-02
<i>C5orf35</i>	cg12311346	103	0.08	4	0.31	4.2E-03	6.0E-04
<i>CCDC15</i>	cg03298804	49	0.12	4	0.23	4.4E-03	2.2E-02
<i>HEBP1</i>	cg06058092	20	0.08	60	0.13	4.6E-03	2.4E-03
<i>AGAP1</i>	cg13253797	52	0.08	12	0.22	4.8E-03	1.2E-03
<i>TSPO</i>	cg20491652	72	0.04	3	0.20	4.9E-03	1.3E-02
<i>FZD6</i>	cg02160804	69	0.07	6	0.21	5.4E-03	4.8E-03
<i>PCLO</i>	cg27190496	56	0.08	3	0.32	6.2E-03	9.8E-03
<i>RELL2</i>	cg01208614	85	0.05	15	0.13	6.2E-03	6.8E-03
<i>PKLR</i>	cg15708776	41	0.04	27	0.09	6.4E-03	3.4E-03
<i>HIBCH</i>	cg25152524	43	0.08	13	0.11	6.6E-03	5.4E-03
<i>HSPG2</i>	cg01079163	111	0.08	4	0.27	7.1E-03	2.8E-03
<i>MYOM2</i>	cg25102683	36	0.08	14	0.21	7.4E-03	3.0E-03
<i>CHST13</i>	cg02122884	13	0.12	16	0.24	7.6E-03	2.5E-02
<i>TCL1B</i>	cg01313424	66	0.09	14	0.23	7.7E-03	1.0E-02
<i>TNFRSF11A</i>	cg23129163	49	0.09	3	0.25	9.2E-03	3.9E-02
<i>MAGEF1</i>	cg01730653	50	0.07	7	0.13	9.5E-03	1.5E-02
<i>HIST1H2BD</i>	cg26882456	6	0.03	72	0.05	9.8E-03	3.6E-02
<i>COL27A1</i>	cg06687010	76	0.08	9	0.15	1.0E-02	4.0E-03
<i>FAAH</i>	cg06388115	54	0.08	15	0.17	1.0E-02	7.0E-03
<i>COL27A1</i>	cg06032189	61	0.08	24	0.12	1.1E-02	8.4E-03
<i>CDH11</i>	cg12376435	55	0.06	25	0.15	1.2E-02	1.1E-02
<i>ZNF462</i>	cg27601046	77	0.08	4	0.35	1.2E-02	1.6E-02
<i>DSC3</i>	cg16172586	15	0.06	3	0.37	1.3E-02	7.3E-02
<i>SLC25A43</i>	cg05895666	33	0.39	6	0.43	1.4E-02	2.3E-02
<i>MYO3A</i>	cg04049425	17	0.11	3	0.39	1.4E-02	6.4E-02
<i>ITIH3</i>	cg00121349	34	0.04	19	0.09	1.4E-02	5.2E-02
<i>PON2</i>	cg21661083	47	0.05	15	0.12	1.4E-02	8.8E-03
<i>BAG3</i>	cg02064719	34	0.06	16	0.14	1.5E-02	1.2E-02
<i>FUCA2</i>	cg03699528	45	0.06	15	0.13	1.7E-02	1.3E-02
<i>PCLO</i>	cg04266902	44	0.07	15	0.14	1.7E-02	1.6E-02
<i>RNF165/LOXHD1</i>	cg12675333	43	0.06	19	0.14	2.0E-02	1.3E-02

ST3GAL3	cg00655391	42	0.11	32	0.12	2.0E-02	3.3E-02
ZNF667	cg08903932	62	0.03	4	0.37	2.1E-02	2.8E-03
FAM83A	cg21208244	26	0.10	19	0.15	2.3E-02	3.3E-02
C1GALT1C1	cg23503504	15	0.16	4	0.49	2.4E-02	8.8E-03
FXYD2	cg08702326	47	0.23	24	0.34	2.5E-02	1.7E-02
DNAJC15	cg11124584	40	0.17	22	0.25	2.6E-02	3.4E-02
APOL2	cg14592586	83	0.07	4	0.16	2.6E-02	4.4E-02
IRAK1	cg15882145	4	0.31	14	0.40	3.1E-02	3.3E-02
IL17RC	cg22546786	79	0.05	18	0.09	3.2E-02	5.6E-03
FGL2	cg08241295	33	0.15	4	0.29	3.3E-02	2.2E-02
CTSB	cg19641538	87	0.10	6	0.13	3.3E-02	6.8E-02
MGC17403	cg19561671	28	0.23	11	0.33	3.4E-02	9.0E-03
KIF14	cg26506603	52	0.08	24	0.10	3.4E-02	1.2E-02
CHST12	cg24076242	53	0.07	17	0.09	3.5E-02	6.2E-02
LIG4	cg20641113	41	0.04	5	0.11	3.6E-02	7.1E-02
IHPK2	cg12782431	14	0.09	30	0.13	3.6E-02	3.5E-02
ZNF286A	cg06534877	82	0.03	3	0.06	3.6E-02	1.5E-01
WDSUB1	cg05434245	88	0.06	5	0.07	3.6E-02	3.3E-01
C18orf51	cg15700173	66	0.07	8	0.15	3.7E-02	6.9E-02
OAS1	cg01655955	18	0.24	82	0.34	3.8E-02	1.1E-02
FAT	cg20367067	40	0.09	9	0.33	3.8E-02	1.5E-02
CPT1B	cg19726898	72	0.08	55	0.10	3.8E-02	4.0E-02
FLVCR1	cg10965032	5	0.16	105	0.21	3.9E-02	6.5E-02
C1RL	cg27377871	77	0.06	4	0.09	4.0E-02	1.2E-01
FBLN2	cg27355986	34	0.06	3	0.17	4.0E-02	9.8E-02
GSTZ1	cg03738767	26	0.09	16	0.12	4.5E-02	4.8E-02
LIPC	cg04382594	61	0.06	28	0.08	4.7E-02	5.2E-02
DNAJC15	cg14729962	22	0.15	40	0.24	4.8E-02	1.4E-02
PECAM1	cg00707339	68	0.11	20	0.12	4.9E-02	1.7E-01
CHST13	cg24901725	13	0.14	16	0.24	5.0E-02	6.3E-02
ACY3	cg23130075	43	0.05	8	0.09	5.0E-02	4.6E-02
CCL25	cg02118161	37	0.06	73	0.10	5.1E-02	1.7E-02
LRRC25	cg26719568	77	0.07	9	0.11	5.2E-02	8.3E-02
MYOM2	cg13428978	37	0.08	13	0.19	5.4E-02	1.1E-02
THSD7A	cg07431898	44	0.07	15	0.11	5.4E-02	1.4E-01
DLGAP2	cg18790916	51	0.07	6	0.14	5.5E-02	9.6E-02
ZNF641	cg05470698	54	0.07	32	0.09	5.5E-02	6.2E-02
IL17RE/IL17RC	cg23266308	53	0.07	45	0.10	5.7E-02	1.5E-01
APOBEC3H	cg06912503	67	0.10	14	0.15	5.7E-02	4.9E-02
C20orf58	cg24813333	26	0.33	11	0.41	5.8E-02	3.0E-02
SPATA6	cg11915739	36	0.09	9	0.13	5.8E-02	1.5E-01
ZFP28	cg10589635	73	0.09	3	0.21	6.1E-02	1.5E-02
ATP6V1C2	cg13950936	55	0.14	29	0.15	6.3E-02	2.2E-01
MAGEF1	cg13428746	51	0.06	6	0.12	6.4E-02	2.5E-02
AGAP1	cg06885440	54	0.08	10	0.21	6.6E-02	8.8E-03
NOTCH3	cg17944161	28	0.07	10	0.13	6.7E-02	6.7E-02
SLC14A1	cg00377772	62	0.04	39	0.06	6.7E-02	6.3E-02
ZNF462	cg06617749	46	0.07	35	0.13	6.8E-02	7.9E-02
ROR1	cg01680459	27	0.09	7	0.10	6.9E-02	2.9E-01
CR1	cg24793169	35	0.07	35	0.08	7.0E-02	1.4E-01
FAAH	cg21019707	62	0.09	7	0.10	7.2E-02	3.6E-01
DFNB31	cg10529000	57	0.08	3	0.14	7.2E-02	8.3E-02
MYO3A	cg01870539	16	0.11	4	0.38	7.4E-02	2.9E-02
AGER	cg18427292	55	0.03	24	0.04	7.7E-02	3.4E-01
BPI	cg16654530	14	0.19	3	0.31	7.8E-02	9.0E-02
AMICA1	cg15885703	45	0.04	60	0.05	8.0E-02	1.0E-01
KIAA1462	cg19833317	32	0.07	26	0.09	8.1E-02	1.3E-01
UMODL1	cg19997214	83	0.06	28	0.10	8.2E-02	4.8E-02
CLGN	cg25905485	13	0.06	10	0.15	8.3E-02	9.3E-02
RPS6KL1	cg24246262	53	0.08	17	0.14	8.3E-02	7.4E-03
SDC2	cg12968080	26	0.05	23	0.07	8.6E-02	2.5E-01
SLC15A2	cg18636558	32	0.12	51	0.12	8.8E-02	4.1E-01
CHID1	cg25695122	37	0.07	42	0.08	9.2E-02	5.9E-02
CCDC15	cg20250779	22	0.11	31	0.13	9.3E-02	1.7E-01
RARS	cg12479407	47	0.09	3	0.12	9.4E-02	2.1E-01
SERPINF1	cg25940393	79	0.11	16	0.13	9.7E-02	2.0E-01
TNIK	cg23577468	14	0.16	3	0.18	9.9E-02	2.1E-01
VWA2	cg06106025	24	0.08	7	0.13	9.9E-02	4.7E-02
BMP4	cg16288394	64	0.08	13	0.17	9.9E-02	2.0E-02
MYO3A	cg10623726	11	0.11	9	0.27	1.0E-01	9.5E-02
TNIK	cg19141375	13	0.15	4	0.18	1.0E-01	2.2E-01
RNF168	cg14402252	69	0.06	4	0.12	1.0E-01	4.1E-01
LIG4	cg25810247	39	0.04	7	0.16	1.0E-01	1.1E-02

CD68	cg13749033	39	0.09	14	0.11	1.0E-01	2.1E-01
NT5E	cg07827942	61	0.11	7	0.13	1.1E-01	1.9E-01
SDCBP2	cg25461681	60	0.06	12	0.09	1.1E-01	8.0E-02
CDH11	cg08299181	68	0.06	12	0.15	1.1E-01	6.8E-02
ANPEP	cg14754216	69	0.07	47	0.09	1.1E-01	2.6E-01
SYTL3	cg05707981	35	0.06	33	0.07	1.1E-01	1.3E-01
RNASET2	cg20990980	9	0.06	22	0.10	1.1E-01	2.5E-01
IL17RC	cg25223364	45	0.05	52	0.06	1.1E-01	2.9E-01
PDLIM5	cg06223640	83	0.04	18	0.07	1.1E-01	3.2E-03
ABAT	cg06095849	62	0.04	12	0.07	1.1E-01	1.2E-01
C4orf33	cg26185305	43	0.08	25	0.10	1.1E-01	9.5E-02
CCL25	cg10555876	79	0.09	31	0.08	1.1E-01	5.3E-01
FLRT3	cg14606305	33	0.05	5	0.11	1.2E-01	2.0E-01
RASAL1	cg02522523	49	0.07	3	0.14	1.2E-01	1.9E-01
C6orf128	cg04331102	49	0.03	20	0.05	1.2E-01	7.1E-02
TNIK	cg16556888	14	0.16	3	0.19	1.2E-01	1.4E-01
PTK2B	cg00377497	80	0.07	10	0.10	1.2E-01	1.4E-01
SPON2	cg02229888	75	0.09	4	0.12	1.2E-01	2.2E-01
GTPBP10	cg15224703	29	0.12	45	0.13	1.3E-01	2.4E-01
VANGL1	cg15161861	27	0.09	15	0.12	1.3E-01	1.5E-01
RARS	cg24309730	42	0.09	8	0.11	1.3E-01	2.6E-01
FANCA	cg04590923	17	0.12	83	0.12	1.3E-01	2.8E-01
NCR1	cg10500120	22	0.07	8	0.13	1.3E-01	1.0E-01
THSD7A	cg14937472	56	0.09	3	0.22	1.3E-01	1.0E-01
APOBEC3H	cg08999478	65	0.10	16	0.13	1.3E-01	1.9E-01
C20orf58	cg23700015	31	0.34	6	0.41	1.3E-01	8.9E-02
ASPRV1	cg21685387	32	0.08	61	0.08	1.4E-01	1.9E-01
LGALS8	cg03796549	8	0.28	4	0.32	1.4E-01	1.2E-01
MYBPC2	cg20838358	30	0.13	4	0.16	1.4E-01	1.8E-01
EYA4	cg24842760	22	0.05	10	0.12	1.4E-01	1.3E-01
HYLS1	cg25041439	68	0.08	13	0.11	1.4E-01	2.1E-02
FAM83A	cg00188472	34	0.12	11	0.15	1.4E-01	1.2E-01
DLGAP2	cg16107931	52	0.07	5	0.11	1.5E-01	3.0E-01
RYR3	cg22827842	13	0.09	17	0.13	1.5E-01	1.9E-01
C2orf3	cg23648175	53	0.07	11	0.08	1.5E-01	2.3E-01
VANGL1	cg15095884	29	0.09	13	0.11	1.5E-01	2.3E-01
HLA-DPB1	cg08405587	30	0.13	47	0.15	1.5E-01	7.6E-02
TRIM10	cg18678389	18	0.03	57	0.05	1.5E-01	1.4E-01
TCL1B	cg07248169	63	0.09	17	0.14	1.5E-01	6.7E-02
ZNF641	cg15014046	75	0.08	11	0.09	1.5E-01	2.0E-01
LAMC1	cg15985297	48	0.03	23	0.05	1.5E-01	8.3E-02
SP2	cg02691091	19	0.09	70	0.09	1.6E-01	4.0E-01
SLC7A8	cg21846671	43	0.06	33	0.09	1.6E-01	1.5E-01
GSTM3	cg06738278	37	0.23	27	0.22	1.6E-01	6.1E-01
NUP210	cg13856317	54	0.06	35	0.07	1.6E-01	3.0E-01
NOTCH3	cg21042385	13	0.06	25	0.10	1.6E-01	6.1E-02
ATRX	cg03275820	15	0.34	11	0.38	1.7E-01	8.8E-02
CAPSL	cg10547011	42	0.07	43	0.08	1.7E-01	1.6E-01
ITIH4	cg18045355	60	0.14	18	0.16	1.7E-01	1.9E-01
ZACN	cg24005618	78	0.08	8	0.10	1.7E-01	1.8E-01
GIPC3	cg24285215	84	0.09	5	0.13	1.7E-01	1.7E-01
MFGE8	cg27011042	86	0.05	4	0.11	1.7E-01	3.8E-02
KLHDC7B	cg13787913	57	0.04	15	0.06	1.7E-01	1.4E-01
GPR35	cg06489818	70	0.04	17	0.04	1.7E-01	4.4E-01
C10orf33	cg20092615	20	0.17	71	0.20	1.8E-01	2.5E-01
PLEKHG4B	cg04494967	24	0.07	5	0.39	1.8E-01	1.2E-02
POMZP3	cg23194690	84	0.09	7	0.15	1.8E-01	3.0E-02
RNF168	cg02647990	68	0.06	5	0.17	1.8E-01	2.3E-01
STK33	cg18933494	35	0.15	4	0.19	1.8E-01	2.4E-01
CCL25	cg27576353	90	0.09	20	0.08	1.8E-01	5.3E-01
LOC553158	cg26348418	24	0.06	14	0.11	1.8E-01	1.1E-01
CLEC4A	cg20624280	47	0.07	13	0.10	1.8E-01	1.3E-01
FAT	cg06830038	14	0.12	35	0.10	1.9E-01	6.2E-01
TNFRSF10A	cg23890101	92	0.05	3	0.06	1.9E-01	4.7E-01
RNASE3	cg03067851	28	0.08	11	0.12	1.9E-01	2.4E-01
JAG1	cg21881707	62	0.07	6	0.10	1.9E-01	1.4E-01
PON2	cg12948586	13	0.02	49	0.07	1.9E-01	3.2E-02
HSPG2	cg20336312	110	0.08	5	0.18	2.0E-01	2.3E-02
CPNE7	cg05915887	17	0.14	6	0.22	2.0E-01	1.3E-01
SEC14L4	cg16312095	29	0.09	28	0.12	2.0E-01	1.1E-01
PLEKHG2	cg04713300	6	0.09	32	0.11	2.0E-01	1.4E-01
RNFT2	cg07099426	66	0.05	5	0.07	2.0E-01	3.5E-01
PDE4A	cg24240619	50	0.09	7	0.13	2.0E-01	2.1E-01

STXBP5	cg11039846	73	0.04	10	0.05	2.0E-01	3.6E-01
BIRC4	cg03239193	4	0.34	15	0.37	2.1E-01	2.4E-01
HSPG2	cg26954156	3	0.05	45	0.07	2.1E-01	3.1E-01
CD44	cg04957921	5	0.07	96	0.08	2.1E-01	3.4E-01
ZACN	cg15727348	57	0.08	29	0.09	2.1E-01	2.6E-01
ZNF502	cg12111944	17	0.33	16	0.35	2.1E-01	3.0E-01
IL12RB1	cg22629524	63	0.06	3	0.09	2.1E-01	3.6E-01
FAT	cg18894054	42	0.11	7	0.13	2.1E-01	4.0E-01
MRPL18	cg21696319	14	0.10	54	0.12	2.1E-01	1.1E-01
CDC123	cg26451923	57	0.07	18	0.09	2.2E-01	8.6E-02
KIAA1804	cg16230059	20	0.17	7	0.19	2.2E-01	3.1E-01
IRAK1	cg04195926	9	0.32	9	0.38	2.2E-01	2.1E-01
COL6A2	cg19250192	55	0.07	21	0.08	2.2E-01	3.3E-01
SLC7A3	cg03171119	5	0.20	9	0.34	2.2E-01	9.8E-02
CD300LF	cg17827225	32	0.07	21	0.10	2.2E-01	2.8E-01
CETP	cg26916607	75	0.07	8	0.09	2.2E-01	2.0E-01
TACC2	cg25533387	25	0.19	7	0.23	2.2E-01	3.5E-01
ROR1	cg08497122	29	0.10	5	0.09	2.2E-01	5.5E-01
TCL1B	cg22847276	63	0.09	17	0.14	2.3E-01	8.9E-02
MGC17403	cg24075232	22	0.23	17	0.24	2.3E-01	3.5E-01
FLVCR1	cg22759408	101	0.21	9	0.22	2.3E-01	2.0E-01
ST3GAL3	cg24888535	43	0.11	31	0.12	2.3E-01	9.5E-02
TCL1A	cg04400661	42	0.09	14	0.09	2.3E-01	4.4E-01
FXYD2	cg07533223	65	0.26	6	0.32	2.3E-01	2.5E-01
CD300LF	cg21640749	21	0.07	32	0.08	2.3E-01	2.6E-01
SERPINB6	cg08010278	47	0.07	26	0.07	2.3E-01	4.1E-01
SLC9A3R2	cg21365157	48	0.13	3	0.17	2.4E-01	2.3E-01
TTC39B	cg19453915	61	0.07	7	0.10	2.4E-01	2.4E-01
TMEM176B	cg22989073	67	0.12	45	0.11	2.4E-01	6.3E-01
MAP7D3	cg14466529	26	0.42	5	0.45	2.4E-01	2.3E-01
NUP210	cg08210481	38	0.06	51	0.07	2.4E-01	2.6E-01
EVC	cg20761282	14	0.17	18	0.17	2.4E-01	4.7E-01
PTPRN2	cg17399037	13	0.05	22	0.09	2.4E-01	6.4E-02
LASS4	cg17510709	24	0.10	19	0.11	2.4E-01	3.9E-01
CLTCL1	cg20875638	9	0.22	17	0.25	2.5E-01	3.4E-01
WDR4	cg02135171	51	0.10	13	0.11	2.5E-01	3.8E-01
ZC3HAV1	cg01107185	52	0.09	49	0.09	2.5E-01	3.8E-01
PLEKHG4	cg13493306	28	0.08	3	0.12	2.5E-01	2.5E-01
MYH11	cg04839981	28	0.13	3	0.17	2.5E-01	2.4E-01
FXYD2	cg15906566	41	0.25	30	0.31	2.5E-01	1.5E-01
RELL2	cg21945772	31	0.05	69	0.06	2.5E-01	2.0E-01
DPM2	cg19245301	44	0.23	6	0.24	2.6E-01	2.2E-01
ACCS	cg13600474	27	0.19	37	0.19	2.6E-01	5.0E-01
R3HCC1	cg15185144	62	0.13	26	0.13	2.6E-01	4.6E-01
ZNF462	cg26858328	60	0.08	21	0.10	2.6E-01	4.0E-01
NUP210	cg21967672	70	0.06	19	0.07	2.6E-01	1.6E-01
GLI3	cg04131524	79	0.09	29	0.09	2.6E-01	3.5E-01
C20orf58	cg08737732	30	0.36	7	0.40	2.7E-01	3.3E-01
ACCS	cg21898949	53	0.19	11	0.19	2.7E-01	5.0E-01
PCLO	cg23914438	55	0.09	4	0.14	2.7E-01	2.0E-01
APOL4	cg21412084	9	0.12	58	0.10	2.7E-01	6.4E-01
SPON2	cg25002788	28	0.09	51	0.10	2.7E-01	2.7E-01
SPATA20	cg20067719	86	0.24	12	0.28	2.8E-01	1.8E-01
GTPBP10	cg14542865	70	0.13	4	0.14	2.8E-01	3.7E-01
FSIP1	cg10613822	17	0.08	19	0.11	2.9E-01	3.8E-01
ZNF502	cg24962159	13	0.35	20	0.35	2.9E-01	4.5E-01
ZNF274	cg00647741	58	0.04	10	0.07	2.9E-01	2.7E-01
TMEM187	cg02177827	17	0.33	4	0.33	2.9E-01	5.3E-01
WDR35	cg19023968	48	0.07	12	0.09	2.9E-01	2.7E-01
STXBP5	cg26370329	71	0.04	12	0.04	2.9E-01	4.6E-01
TRIM10	cg21126020	15	0.03	60	0.05	2.9E-01	2.1E-01
FPR1	cg26410849	123	0.07	7	0.06	2.9E-01	5.8E-01
HSPG2	cg13586701	42	0.07	6	0.09	3.0E-01	3.4E-01
SLC7A8	cg26660414	71	0.08	5	0.08	3.0E-01	5.3E-01
ELA3A	cg25997939	39	0.06	18	0.06	3.0E-01	4.8E-01
BBS4	cg11658652	47	0.04	52	0.04	3.0E-01	2.6E-01
AYTL1	cg22393926	75	0.04	6	0.15	3.0E-01	4.3E-02
EVC	cg00875039	23	0.17	9	0.18	3.1E-01	2.4E-01
SLC12A7	cg24769613	108	0.11	8	0.14	3.1E-01	1.9E-01
CELSR1	cg17519107	27	0.08	4	0.17	3.1E-01	1.3E-01
CPNE7	cg26222018	20	0.16	3	0.16	3.2E-01	4.8E-01
MED16	cg05645620	54	0.10	15	0.11	3.2E-01	3.0E-01
ATP6V1C2	cg22645358	29	0.14	55	0.15	3.2E-01	5.0E-01

HELB	cg14519793	69	0.07	9	0.08	3.2E-01	3.5E-01
KCNMB3	cg25384231	19	0.11	26	0.16	3.2E-01	2.7E-01
GNL3	cg22545108	75	0.07	16	0.07	3.2E-01	3.5E-01
ROR1	cg00152515	28	0.10	6	0.08	3.2E-01	6.1E-01
IRAK1	cg20010847	14	0.35	4	0.41	3.2E-01	2.6E-01
RP11-125A7.3	cg26492720	66	0.07	15	0.06	3.2E-01	5.9E-01
BSPRY	cg16047932	60	0.08	4	0.10	3.3E-01	4.1E-01
UMODL1	cg21935742	59	0.06	52	0.07	3.3E-01	2.6E-01
TSPYL1	cg03926674	49	0.05	10	0.07	3.3E-01	3.3E-01
BPI	cg18041810	10	0.20	7	0.22	3.3E-01	4.3E-01
CPN2	cg06493646	3	0.06	32	0.09	3.4E-01	4.0E-01
AMICA1	cg06379088	16	0.05	89	0.05	3.4E-01	5.4E-01
PLD2	cg19467033	44	0.11	4	0.17	3.4E-01	7.0E-02
DPEP1	cg14674527	64	0.06	6	0.07	3.4E-01	3.0E-01
PAX8	cg23718339	49	0.25	9	0.24	3.4E-01	5.9E-01
MED16	cg03085259	37	0.11	32	0.11	3.5E-01	4.2E-01
P2RX7	cg08688169	76	0.13	7	0.13	3.5E-01	5.3E-01
ZNF554	cg00705295	38	0.08	21	0.07	3.5E-01	5.8E-01
ARSA	cg05039563	39	0.24	4	0.23	3.5E-01	3.9E-01
RNASE3	cg19386892	3	0.06	36	0.10	3.5E-01	3.1E-01
PKLR	cg00764632	58	0.05	10	0.09	3.5E-01	1.3E-01
DPEP1	cg15906884	49	0.06	21	0.06	3.6E-01	3.6E-01
DLGAP2	cg06254659	54	0.08	3	0.07	3.7E-01	5.4E-01
MTL5	cg21698794	37	0.21	5	0.23	3.7E-01	2.1E-01
CARD9	cg22225031	15	0.18	5	0.20	3.7E-01	3.0E-01
C20orf58	cg13459349	28	0.34	9	0.39	3.7E-01	2.8E-01
BSPRY	cg10886696	48	0.09	16	0.07	3.7E-01	7.3E-01
BPI	cg00527986	9	0.19	8	0.21	3.7E-01	4.3E-01
OAS1	cg12660834	23	0.30	77	0.33	3.7E-01	2.1E-01
EYA4	cg24766857	20	0.05	12	0.09	3.7E-01	2.7E-01
ZACN	cg03971142	73	0.08	13	0.09	3.7E-01	3.9E-01
GIPC3	cg25936595	28	0.08	61	0.09	3.8E-01	3.5E-01
ATP10A	cg18939241	57	0.10	17	0.10	3.8E-01	4.6E-01
C15orf23	cg01057767	30	0.11	16	0.12	3.8E-01	4.4E-01
UQCRRFS1	cg22013735	18	0.11	13	0.11	3.8E-01	3.8E-01
ANPEP	cg17347750	113	0.08	3	0.11	3.8E-01	3.2E-01
UBA1	cg25059428	5	0.09	10	0.16	3.8E-01	2.5E-01
MYOM2	cg20215519	46	0.10	4	0.17	3.8E-01	2.1E-01
FAM118A	cg24477255	49	0.12	23	0.13	3.9E-01	4.0E-01
TSPO	cg22098071	21	0.03	54	0.04	3.9E-01	3.7E-01
INADL	cg00319915	71	0.04	22	0.06	3.9E-01	3.3E-01
PDE4A	cg17157663	52	0.10	5	0.11	3.9E-01	4.5E-01
FLJ10769	cg19124628	27	0.09	53	0.11	4.0E-01	2.5E-01
ECM1	cg01408870	91	0.06	7	0.05	4.0E-01	6.5E-01
LIPC	cg22298191	51	0.07	38	0.07	4.0E-01	3.0E-01
PANX1	cg25680561	63	0.09	14	0.09	4.0E-01	1.9E-01
FXVD2	cg24632799	61	0.26	10	0.32	4.0E-01	2.3E-01
IRAK1	cg26847013	4	0.35	14	0.36	4.0E-01	3.7E-01
PGM1	cg18759728	26	0.05	35	0.07	4.0E-01	1.3E-01
RTP4	cg15728214	80	0.06	5	0.08	4.0E-01	2.9E-01
DEPDC6	cg06374952	53	0.07	16	0.07	4.0E-01	5.0E-01
PDE4A	cg08033699	18	0.09	39	0.10	4.0E-01	4.3E-01
C6orf47/BAT4	cg05829931	110	0.11	9	0.10	4.0E-01	6.5E-01
KCNMB3	cg10735539	16	0.16	29	0.15	4.0E-01	5.7E-01
RNF165/LOXHD1	cg24345817	34	0.07	28	0.07	4.0E-01	4.6E-01
SLC25A43	cg04860026	30	0.41	9	0.41	4.0E-01	3.9E-01
LLGL2	cg26902889	84	0.10	3	0.09	4.0E-01	6.2E-01
CNTROB	cg24080808	86	0.22	12	0.23	4.1E-01	4.1E-01
ANPEP	cg13288243	48	0.08	68	0.09	4.1E-01	4.3E-01
CETP	cg21292272	30	0.07	53	0.09	4.1E-01	2.8E-01
BCR	cg08146988	53	0.13	18	0.13	4.1E-01	4.2E-01
SIRPG	cg00625330	70	0.08	16	0.07	4.1E-01	7.2E-01
LLGL2	cg02970545	83	0.10	4	0.11	4.2E-01	3.3E-01
ZNF597	cg14961581	5	0.30	8	0.31	4.2E-01	3.2E-01
C6orf47/BAT4	cg23509266	72	0.10	47	0.11	4.2E-01	1.3E-01
ITM2C	cg25775379	49	0.09	43	0.11	4.2E-01	3.3E-01
TTC39B	cg14376943	61	0.07	7	0.07	4.2E-01	5.9E-01
GIPC3	cg12807712	44	0.08	45	0.09	4.2E-01	2.3E-01
TTC39B	cg21191737	51	0.07	17	0.10	4.2E-01	1.2E-01
MYOM1	cg21479732	30	0.07	13	0.08	4.2E-01	4.5E-01
CPNE7	cg16514932	19	0.15	4	0.16	4.2E-01	5.3E-01
CETP	cg19503728	73	0.08	10	0.09	4.3E-01	4.1E-01
MERTK	cg21108990	68	0.13	3	0.17	4.3E-01	2.5E-01

UMODL1	cg27193677	96	0.07	15	0.06	4.3E-01	5.8E-01
CELSR1	cg09764624	26	0.08	5	0.10	4.3E-01	3.7E-01
IRAK1	cg04925494	7	0.32	11	0.38	4.3E-01	2.0E-01
LLGL2	cg19845902	37	0.10	50	0.10	4.3E-01	6.1E-01
TSPO	cg07513548	64	0.04	11	0.03	4.3E-01	6.4E-01
CPNE7	cg16418620	17	0.16	6	0.18	4.3E-01	4.5E-01
PLXDC2	cg05184383	36	0.06	6	0.15	4.4E-01	1.1E-01
EFCAB4A	cg08002036	17	0.11	25	0.12	4.4E-01	5.1E-01
KLHDC7B	cg21186585	55	0.04	17	0.05	4.4E-01	3.5E-01
ACACB	cg00546992	8	0.07	33	0.07	4.4E-01	4.2E-01
POU5F1	cg09904051	58	0.09	11	0.12	4.4E-01	1.6E-01
TRIM45	cg15366769	72	0.14	8	0.14	4.5E-01	3.9E-01
SLC25A43	cg23030765	19	0.41	20	0.41	4.5E-01	3.5E-01
ST3GAL3	cg09343842	52	0.11	22	0.11	4.5E-01	6.4E-01
SPON2	cg17398669	71	0.09	8	0.08	4.5E-01	6.5E-01
ATP5SL	cg10804268	9	0.09	76	0.10	4.5E-01	1.9E-01
CEACAM21	cg25528786	51	0.08	23	0.09	4.5E-01	3.5E-01
LCN10	cg09123770	28	0.08	10	0.11	4.5E-01	1.6E-01
WDSUB1	cg11307605	69	0.06	24	0.06	4.6E-01	5.7E-01
TMEM187	cg01479014	14	0.33	7	0.33	4.6E-01	5.5E-01
SEC14L4	cg16354157	23	0.10	34	0.11	4.6E-01	2.6E-01
C2orf3	cg23725986	40	0.08	24	0.07	4.6E-01	7.1E-01
COBL	cg24806859	62	0.07	28	0.09	4.6E-01	4.0E-01
SLC2A9	cg23630970	70	0.07	7	0.06	4.6E-01	6.7E-01
AMICA1	cg25377028	82	0.05	23	0.04	4.6E-01	8.5E-01
CHST12	cg09949988	66	0.08	4	0.09	4.6E-01	3.3E-01
DPEP1	cg13915117	58	0.06	12	0.05	4.7E-01	7.6E-01
C4orf42	cg11974036	97	0.08	3	0.08	4.7E-01	4.9E-01
PI16	cg14847849	38	0.08	38	0.09	4.7E-01	4.6E-01
AGAP1	cg05160451	42	0.09	22	0.08	4.7E-01	5.8E-01
DEPDC6	cg02919712	10	0.08	59	0.07	4.7E-01	6.8E-01
PLEKHG4B	cg03621279	10	0.07	19	0.07	4.7E-01	5.0E-01
APOBEC3H	cg18696237	71	0.11	10	0.10	4.7E-01	7.0E-01
GIPC3	cg22091742	76	0.09	13	0.06	4.7E-01	9.0E-01
APOL4	cg10246125	38	0.10	29	0.11	4.8E-01	4.7E-01
SLCO5A1	cg11025169	67	0.08	14	0.08	4.8E-01	4.3E-01
B3GNTL1	cg01837360	44	0.05	18	0.05	4.8E-01	4.9E-01
CCDC125	cg00958878	87	0.05	9	0.05	4.8E-01	4.8E-01
CAPG	cg04881903	31	0.07	10	0.07	4.8E-01	4.8E-01
GEFT	cg09262898	45	0.05	24	0.06	4.8E-01	3.0E-01
TMEM187	cg02681355	15	0.35	6	0.31	4.8E-01	7.1E-01
PPP4R1L	cg14877936	67	0.10	18	0.09	4.8E-01	7.8E-01
COL6A2	cg09142839	44	0.07	32	0.07	4.9E-01	5.1E-01
RNFT2	cg03109701	43	0.05	28	0.05	4.9E-01	5.8E-01
LRRC25	cg05370447	80	0.07	6	0.07	4.9E-01	4.4E-01
MGC17403	cg17743930	35	0.24	4	0.22	4.9E-01	5.9E-01
LCN10	cg05909349	28	0.08	10	0.08	4.9E-01	5.2E-01
BDH2	cg22393468	13	0.15	36	0.17	5.0E-01	2.6E-01
DPYD	cg17731695	28	0.07	34	0.06	5.0E-01	5.2E-01
C15orf23	cg14916983	43	0.11	3	0.14	5.0E-01	2.6E-01
PRDM9	cg00482432	5	0.48	11	0.44	5.0E-01	7.1E-01
MYOM1	cg24234169	38	0.08	5	0.04	5.1E-01	8.0E-01
KIAA1462	cg17040848	44	0.08	14	0.08	5.1E-01	5.3E-01
MFGE8	cg01062556	65	0.05	25	0.04	5.1E-01	7.2E-01
ITIH4	cg09629355	35	0.16	43	0.14	5.1E-01	7.8E-01
MMP14	cg26214703	21	0.05	40	0.04	5.2E-01	6.9E-01
MMP14	cg01508380	50	0.05	11	0.04	5.2E-01	6.6E-01
RYR3	cg27532581	23	0.10	7	0.11	5.2E-01	4.4E-01
FUCA2	cg22488492	49	0.08	11	0.06	5.2E-01	7.6E-01
PDE4A	cg22803653	43	0.10	14	0.09	5.3E-01	6.0E-01
DFNB31	cg18528364	38	0.08	22	0.08	5.3E-01	5.3E-01
SERPINF1	cg09128350	67	0.11	28	0.12	5.3E-01	2.7E-01
LASS4	cg09497409	35	0.10	8	0.10	5.3E-01	4.9E-01
ZNF75A	cg05121237	64	0.03	12	0.04	5.4E-01	3.5E-01
GLI3	cg13773900	75	0.09	33	0.09	5.4E-01	7.0E-01
SPATA6	cg10552195	35	0.10	10	0.07	5.4E-01	8.9E-01
GNL3	cg01256146	88	0.07	3	0.05	5.4E-01	6.5E-01
C19orf15	cg23043473	34	0.12	14	0.12	5.4E-01	6.4E-01
ATP7A	cg07101723	15	0.31	3	0.23	5.4E-01	6.4E-01
COBL	cg24011258	41	0.07	49	0.10	5.4E-01	2.6E-01
BBS4	cg00679167	92	0.04	7	0.04	5.5E-01	5.8E-01
RELL2	cg17982929	72	0.06	28	0.06	5.5E-01	3.8E-01
SDCBP2	cg09723970	23	0.07	49	0.06	5.5E-01	5.8E-01

ITIH4	cg07463115	71	0.15	7	0.13	5.5E-01	7.3E-01
ITM2C	cg19833427	41	0.10	51	0.10	5.5E-01	5.4E-01
ATP6V1C2	cg14810315	80	0.14	4	0.14	5.5E-01	5.9E-01
RYR3	cg16195243	20	0.10	10	0.11	5.6E-01	4.5E-01
PTK2B	cg15033589	33	0.08	57	0.07	5.6E-01	5.8E-01
GPR56	cg20850743	65	0.07	21	0.06	5.6E-01	6.8E-01
ZNF286A	cg14568193	74	0.03	11	0.03	5.7E-01	5.4E-01
ATP10A	cg06932470	71	0.10	3	0.10	5.7E-01	5.2E-01
ZACN	cg20940332	37	0.09	49	0.08	5.7E-01	7.2E-01
FAM48A	cg01881091	95	0.11	3	0.10	5.7E-01	6.5E-01
MUC4	cg10593292	14	0.25	8	0.21	5.7E-01	5.9E-01
ZNF624	cg08160916	31	0.07	52	0.06	5.7E-01	8.1E-01
CPN2	cg02174862	31	0.08	4	0.09	5.7E-01	6.5E-01
STK33	cg02345567	39	0.09	7	0.09	5.7E-01	5.5E-01
ZNF443	cg02455778	57	0.07	5	0.06	5.7E-01	5.6E-01
OAS1	cg17819200	46	0.33	54	0.32	5.7E-01	7.2E-01
GBE1	cg25965079	76	0.09	5	0.06	5.7E-01	7.2E-01
CSGALNACT1	cg24423468	38	0.10	25	0.07	5.7E-01	8.6E-01
SPATA20	cg01878658	94	0.25	4	0.23	5.7E-01	6.0E-01
PPP4R1L	cg14067017	74	0.10	11	0.10	5.8E-01	6.0E-01
PLXDC2	cg16458319	30	0.06	12	0.06	5.8E-01	5.4E-01
FBLN2	cg26339114	12	0.08	25	0.07	5.8E-01	6.1E-01
SPON2	cg18159636	73	0.09	6	0.10	5.8E-01	4.4E-01
C1GALT1C1	cg17814586	13	0.20	6	0.20	5.8E-01	5.6E-01
KIAA1683	cg24782497	101	0.08	17	0.07	5.8E-01	7.2E-01
KIAA1462	cg04068932	47	0.08	11	0.07	5.9E-01	6.1E-01
KRT1	cg08687200	62	0.12	9	0.10	5.9E-01	6.2E-01
SLC9A3R2	cg08759448	13	0.15	38	0.13	5.9E-01	7.4E-01
SERPINF2	cg26661174	27	0.06	28	0.06	5.9E-01	4.8E-01
LASS4	cg19691474	31	0.11	12	0.09	5.9E-01	7.9E-01
CD300LF	cg20043431	28	0.07	25	0.08	5.9E-01	4.5E-01
HSPG2	cg07379331	98	0.09	17	0.07	6.0E-01	7.3E-01
ZNF415	cg21229740	18	0.09	32	0.07	6.0E-01	7.2E-01
ZFP28	cg04911596	47	0.09	29	0.09	6.0E-01	5.0E-01
SPON2	cg01508291	75	0.09	4	0.08	6.0E-01	5.7E-01
KLHDC4	cg01087540	54	0.11	43	0.11	6.0E-01	4.7E-01
ZNF311	cg21668475	40	0.06	5	0.06	6.0E-01	5.6E-01
REG4	cg15742572	33	0.12	15	0.13	6.0E-01	3.5E-01
ZMAT1	cg15880010	7	0.35	4	0.34	6.1E-01	6.6E-01
TSPAN16	cg19216194	28	0.24	23	0.16	6.1E-01	7.2E-01
CPAMD8	cg13074817	63	0.04	3	0.02	6.1E-01	8.2E-01
IER3	cg04940526	29	0.06	31	0.04	6.1E-01	7.4E-01
TSPAN16	cg22139730	48	0.16	3	0.35	6.1E-01	2.9E-01
CAPSL	cg01119090	72	0.08	13	0.05	6.1E-01	8.4E-01
C4orf33	cg12432461	48	0.09	20	0.09	6.1E-01	5.8E-01
KLHDC4	cg23648292	73	0.11	24	0.10	6.1E-01	5.6E-01
SLC7A3	cg22553994	11	0.34	3	0.34	6.2E-01	6.0E-01
CDH11	cg03357333	72	0.08	8	0.06	6.2E-01	6.7E-01
FAM24B	cg13832514	60	0.21	21	0.17	6.2E-01	7.3E-01
C10orf33	cg11678810	67	0.20	24	0.20	6.2E-01	4.0E-01
TBC1D8	cg12707631	34	0.04	6	0.04	6.2E-01	5.7E-01
SH3PXD2A	cg02647192	26	0.14	9	0.10	6.2E-01	6.4E-01
PECAM1	cg12476586	54	0.12	34	0.12	6.3E-01	5.1E-01
ATP6V1C2	cg13382186	53	0.15	31	0.13	6.4E-01	8.6E-01
AGER	cg23179210	74	0.04	5	0.02	6.4E-01	7.3E-01
ZNF502	cg15328382	22	0.35	11	0.32	6.4E-01	6.9E-01
SLC22A18	cg25427871	92	0.08	22	0.08	6.4E-01	5.3E-01
LGMN	cg14939219	20	0.10	40	0.07	6.4E-01	8.8E-01
IL17RC	cg23183100	53	0.06	44	0.05	6.4E-01	6.2E-01
MUC4	cg12514913	14	0.21	8	0.21	6.4E-01	5.4E-01
C4orf42	cg08201860	40	0.08	60	0.08	6.4E-01	5.4E-01
SLC7A3	cg12912090	7	0.34	7	0.34	6.4E-01	6.2E-01
L3MBTL3	cg02678104	51	0.05	23	0.04	6.5E-01	6.8E-01
ATP6V1C2	cg05448951	76	0.14	8	0.15	6.5E-01	4.6E-01
C2orf63	cg04689018	58	0.06	25	0.04	6.5E-01	8.4E-01
LGALS8	cg26796108	8	0.30	4	0.29	6.6E-01	7.2E-01
PTPRN2	cg14654980	32	0.07	3	0.07	6.6E-01	5.2E-01
PROCR	cg20981611	23	0.12	8	0.11	6.6E-01	6.7E-01
MYH11	cg10842842	23	0.14	8	0.13	6.6E-01	6.3E-01
SIRPG	cg09582890	55	0.08	31	0.08	6.6E-01	5.1E-01
PDE4DIP	cg06482143	57	0.23	14	0.22	6.7E-01	5.8E-01
FAM24B	cg25217124	75	0.21	6	0.16	6.7E-01	7.0E-01
FAM83A	cg24527132	41	0.13	4	0.10	6.7E-01	6.9E-01

CR1	cg13444707	15	0.08	55	0.07	6.7E-01	7.2E-01
TCL1B	cg09811014	56	0.10	24	0.11	6.8E-01	4.1E-01
EVC	cg22548764	21	0.17	11	0.17	6.8E-01	6.1E-01
TPO	cg23136645	62	0.06	4	0.06	6.8E-01	4.8E-01
POU5F1	cg22588377	64	0.09	5	0.07	6.8E-01	8.4E-01
B3GNTL1	cg07062613	26	0.05	36	0.05	6.8E-01	4.8E-01
ZNF434	cg12379911	10	0.06	51	0.05	6.8E-01	6.0E-01
IQCE	cg07204806	67	0.06	34	0.06	6.9E-01	8.1E-01
C15orf42	cg14638314	72	0.07	11	0.07	6.9E-01	5.5E-01
GPR56	cg22509326	3	0.07	83	0.06	6.9E-01	6.4E-01
CARD9	cg05490015	3	0.18	17	0.18	6.9E-01	4.9E-01
PAX8	cg02500031	54	0.24	4	0.23	6.9E-01	5.5E-01
FAM48A	cg15272137	80	0.11	18	0.10	7.0E-01	7.0E-01
NRP1	cg21970360	46	0.08	3	0.04	7.0E-01	8.3E-01
TNXB	cg26503834	19	0.23	3	0.22	7.1E-01	6.2E-01
SP2	cg22310262	63	0.09	26	0.08	7.1E-01	9.1E-01
ARHGEF3	cg17537252	62	0.05	7	0.05	7.1E-01	6.4E-01
TMEM2	cg24186972	20	0.17	9	0.17	7.2E-01	5.4E-01
IHPK2	cg07497072	19	0.11	25	0.12	7.2E-01	5.0E-01
PON2	cg07666065	58	0.07	4	0.04	7.2E-01	7.7E-01
TTLL13	cg21655969	54	0.08	25	0.05	7.2E-01	8.9E-01
ITIH3	cg25865553	23	0.05	30	0.04	7.2E-01	6.4E-01
KLHDC7B	cg24822876	52	0.05	20	0.03	7.2E-01	8.1E-01
ZNF415	cg03019139	6	0.17	44	0.09	7.3E-01	8.9E-01
STXBP5	cg06501295	63	0.04	20	0.04	7.3E-01	7.3E-01
CD44	cg08356130	67	0.09	34	0.07	7.3E-01	9.4E-01
UBA1	cg15887717	8	0.18	7	0.13	7.3E-01	7.1E-01
SLC22A18	cg22589403	46	0.08	68	0.08	7.4E-01	4.3E-01
FUCA2	cg22590165	51	0.08	9	0.06	7.4E-01	6.8E-01
MAP7D3	cg17932342	4	0.43	27	0.43	7.4E-01	5.6E-01
COL27A1	cg00511096	82	0.09	3	0.04	7.4E-01	9.0E-01
JAG1	cg05419505	65	0.07	3	0.08	7.4E-01	4.7E-01
VWA2	cg10407585	12	0.09	19	0.08	7.5E-01	5.5E-01
IGSF3	cg13654571	25	0.10	10	0.07	7.5E-01	7.4E-01
SPON2	cg01546047	64	0.09	15	0.08	7.5E-01	6.5E-01
CTSB	cg19160505	68	0.11	25	0.09	7.5E-01	8.0E-01
FLVCR1	cg24260529	104	0.21	6	0.17	7.5E-01	9.3E-01
ELA3A	cg10204734	41	0.06	16	0.04	7.6E-01	8.3E-01
ZNF624	cg06981520	61	0.07	22	0.06	7.6E-01	6.5E-01
P2RY11	cg06110313	31	0.12	3	0.06	7.6E-01	9.2E-01
CARD9	cg09377623	7	0.18	13	0.18	7.6E-01	5.1E-01
STK33	cg27123313	8	0.20	31	0.15	7.6E-01	8.2E-01
BPI	cg08073914	8	0.23	9	0.19	7.6E-01	8.2E-01
VAR2S1	cg00548595	70	0.11	25	0.11	7.6E-01	5.8E-01
ZNF311	cg03878764	34	0.06	11	0.06	7.6E-01	5.5E-01
TNXB	cg25307089	13	0.22	9	0.23	7.6E-01	5.1E-01
WDR35	cg05412990	40	0.07	20	0.07	7.7E-01	5.8E-01
CHST12	cg26118380	25	0.08	45	0.08	7.7E-01	6.0E-01
UBA1	cg21058097	7	0.19	8	0.15	7.7E-01	7.7E-01
GEFT	cg25614200	33	0.07	36	0.05	7.7E-01	8.1E-01
KIAA1804	cg09524235	23	0.19	4	0.14	7.8E-01	8.9E-01
SLC22A18	cg11213910	66	0.09	48	0.07	7.8E-01	8.7E-01
BCR	cg01574123	54	0.13	17	0.10	7.8E-01	7.5E-01
KCNMB3	cg23400754	42	0.16	3	0.05	7.8E-01	8.9E-01
BIRC4	cg08398784	8	0.36	11	0.37	7.8E-01	4.1E-01
CLTCL1	cg09703637	23	0.25	3	0.17	7.8E-01	8.3E-01
MS4A14	cg27663936	68	0.11	8	0.10	7.8E-01	7.5E-01
GPR35	cg06129789	63	0.04	24	0.04	7.8E-01	5.2E-01
ARL11	cg12467823	65	0.11	14	0.07	7.8E-01	8.1E-01
ZNF597	cg08624109	5	0.32	8	0.29	7.8E-01	8.7E-01
C6orf145	cg09761256	20	0.10	50	0.09	7.8E-01	7.4E-01
APOL2	cg23240967	33	0.08	54	0.07	7.9E-01	6.9E-01
SLC7A8	cg15043674	44	0.09	32	0.07	7.9E-01	8.0E-01
PGM1	cg22624827	36	0.07	25	0.05	7.9E-01	9.1E-01
RP11-125A7.3	cg23268170	10	0.09	71	0.06	8.0E-01	9.4E-01
PI16	cg01210642	34	0.11	42	0.07	8.0E-01	8.5E-01
C6orf47/BAT4	cg00388208	56	0.11	63	0.10	8.0E-01	8.6E-01
ARHGEF3	cg19274856	65	0.05	4	0.04	8.1E-01	6.8E-01
HLA-DOB	cg01530082	53	0.06	17	0.05	8.1E-01	6.9E-01
CPVL	cg09696143	97	0.08	8	0.07	8.1E-01	6.1E-01
PTPRN2	cg06699987	23	0.08	12	0.06	8.1E-01	8.0E-01
CSGALNACT1	cg17690518	60	0.09	3	0.04	8.1E-01	8.6E-01
PDE4DIP	cg05074392	27	0.24	44	0.22	8.1E-01	8.5E-01

WDR60	cg05932259	79	0.10	9	0.09	8.1E-01	7.4E-01
EYA4	cg22887581	16	0.08	16	0.04	8.2E-01	7.5E-01
ATP7A	cg15696442	10	0.32	8	0.20	8.2E-01	9.2E-01
PTPRN2	cg02661557	21	0.08	14	0.06	8.2E-01	8.0E-01
RNASET2	cg12885596	26	0.10	5	0.06	8.2E-01	7.8E-01
COBL	cg06011684	71	0.09	19	0.08	8.2E-01	5.4E-01
SPON2	cg15742471	50	0.10	29	0.08	8.2E-01	7.6E-01
CARD9	cg23973065	6	0.19	14	0.17	8.2E-01	7.9E-01
ZC3HAV1	cg10039938	84	0.09	17	0.08	8.2E-01	8.8E-01
CPAMD8	cg03925226	42	0.04	24	0.03	8.3E-01	8.4E-01
THSD7A	cg05269979	40	0.09	19	0.09	8.3E-01	4.8E-01
PIH1D1	cg27631287	75	0.09	3	0.08	8.3E-01	7.0E-01
DNAJC15	cg11679069	56	0.22	6	0.15	8.3E-01	8.4E-01
ACCS	cg16503256	21	0.21	43	0.16	8.4E-01	8.4E-01
C6orf128	cg25776458	61	0.03	8	0.02	8.4E-01	8.4E-01
ZNF419	cg18821165	41	0.15	29	0.12	8.4E-01	9.0E-01
INADL	cg02381358	78	0.05	15	0.04	8.4E-01	7.3E-01
GPR56	cg05774389	83	0.07	3	0.06	8.4E-01	6.9E-01
SEC14L4	cg25909582	7	0.12	50	0.10	8.4E-01	7.0E-01
C6orf47/BAT4	cg16718500	64	0.11	55	0.10	8.5E-01	8.3E-01
GGT5	cg06962072	34	0.09	25	0.09	8.5E-01	7.2E-01
NID2	cg19718310	85	0.12	3	0.05	8.5E-01	8.9E-01
C6orf47/BAT4	cg25734790	77	0.11	42	0.11	8.5E-01	6.2E-01
JAG1	cg10749266	61	0.08	7	0.05	8.5E-01	7.7E-01
ARSA	cg06622939	6	0.34	37	0.19	8.5E-01	9.2E-01
IQCE	cg03365627	65	0.06	36	0.06	8.5E-01	3.5E-01
EFCAB4A	cg05957751	33	0.13	9	0.09	8.6E-01	8.2E-01
GIMAP2	cg04784491	52	0.09	10	0.07	8.6E-01	7.0E-01
INADL	cg08054679	70	0.05	23	0.04	8.6E-01	8.2E-01
EPS15	cg17466355	68	0.20	4	0.15	8.6E-01	9.9E-01
R3HCC1	cg27160970	65	0.13	23	0.12	8.6E-01	8.4E-01
SEC31B	cg20831708	55	0.12	10	0.11	8.6E-01	9.0E-01
CLEC10A	cg13318344	41	0.09	32	0.08	8.6E-01	5.8E-01
RPS6KL1	cg20668012	32	0.09	38	0.08	8.7E-01	8.5E-01
SLCO5A1	cg05894061	34	0.08	47	0.06	8.7E-01	8.5E-01
NID2	cg22881914	84	0.12	4	0.06	8.7E-01	8.6E-01
SYTL3	cg12691330	37	0.07	31	0.06	8.7E-01	8.7E-01
MAP7D3	cg04830168	16	0.44	15	0.43	8.7E-01	5.6E-01
CLEC4A	cg12401842	49	0.08	11	0.07	8.7E-01	6.2E-01
CLEC4A	cg17477618	49	0.09	11	0.06	8.7E-01	9.5E-01
POU5F1	cg09142415	59	0.09	10	0.07	8.7E-01	8.6E-01
TNXB	cg19108771	10	0.25	12	0.22	8.7E-01	8.4E-01
SH3PXD2A	cg04241721	29	0.15	6	0.07	8.7E-01	8.3E-01
RNF165/LOXHD1	cg06284290	25	0.08	37	0.07	8.8E-01	7.9E-01
PPP4R1L	cg05882622	32	0.12	53	0.10	8.8E-01	8.5E-01
ARSA	cg11003051	30	0.28	13	0.10	8.8E-01	8.7E-01
CD300LF	cg26366833	47	0.09	6	0.07	8.8E-01	8.0E-01
CNDP2	cg05664348	55	0.16	7	0.14	8.8E-01	8.0E-01
JAG1	cg00155795	65	0.08	3	0.05	8.8E-01	6.9E-01
FAM24B	cg03283421	10	0.31	71	0.20	8.8E-01	8.2E-01
MMP14	cg06782489	56	0.05	5	0.02	8.9E-01	9.3E-01
NCR1	cg17804112	8	0.16	22	0.07	8.9E-01	9.7E-01
BBS4	cg17045424	85	0.04	14	0.03	8.9E-01	7.6E-01
BCR	cg24953055	45	0.14	26	0.09	8.9E-01	9.5E-01
FUCA2	cg23490921	31	0.11	29	0.06	8.9E-01	9.4E-01
PAX8	cg23136554	4	0.34	54	0.24	8.9E-01	8.8E-01
IL17RC	cg07705835	53	0.05	44	0.05	8.9E-01	5.6E-01
TMEM176B	cg05076206	66	0.13	46	0.10	8.9E-01	8.8E-01
KCNMB3	cg02006743	36	0.16	9	0.07	8.9E-01	8.3E-01
GP6	cg05215830	42	0.14	6	0.10	9.0E-01	8.7E-01
CETP	cg13854752	71	0.09	12	0.04	9.1E-01	9.7E-01
SLCO5A1	cg00627249	77	0.08	4	0.02	9.1E-01	9.9E-01
CPAMD8	cg19476835	22	0.04	44	0.03	9.1E-01	7.3E-01
CCL25	cg19597449	76	0.09	34	0.06	9.1E-01	9.1E-01
EPS15	cg14407667	58	0.20	14	0.17	9.1E-01	9.3E-01
VAR52	cg18873361	80	0.11	15	0.09	9.1E-01	7.7E-01
ECM1	cg17628903	78	0.06	20	0.05	9.1E-01	8.4E-01
PECAM1	cg17583448	37	0.13	51	0.11	9.1E-01	9.8E-01
INADL	cg24178332	66	0.05	27	0.04	9.1E-01	7.1E-01
MS4A14	cg21996029	58	0.11	18	0.11	9.1E-01	6.1E-01
ABAT	cg16396393	68	0.05	6	0.03	9.2E-01	8.4E-01
STXBP5	cg19916519	76	0.05	7	0.02	9.2E-01	9.4E-01
LRRRC25	cg10618882	83	0.07	3	0.05	9.2E-01	7.8E-01

<i>STRN3</i>	cg22076453	30	0.06	64	0.05	9.2E-01	8.7E-01
<i>TTC39B</i>	cg17659508	55	0.08	13	0.05	9.3E-01	9.6E-01
<i>DNAJC15</i>	cg12504148	50	0.23	12	0.13	9.3E-01	9.9E-01
<i>SEC31B</i>	cg24467927	44	0.13	21	0.11	9.3E-01	9.3E-01
<i>RASAL1</i>	cg21448723	30	0.10	22	0.06	9.3E-01	9.7E-01
<i>ZNF419</i>	cg18762588	67	0.14	3	0.07	9.3E-01	9.4E-01
<i>SLC9A3R2</i>	cg14589894	29	0.15	22	0.12	9.4E-01	9.4E-01
<i>GSTM3</i>	cg13349502	58	0.24	6	0.17	9.4E-01	7.9E-01
<i>HLA-DPB1</i>	cg12365667	71	0.14	6	0.10	9.4E-01	9.6E-01
<i>WDR35</i>	cg23811268	30	0.08	30	0.05	9.4E-01	9.0E-01
<i>KRT1</i>	cg10538533	68	0.13	3	0.04	9.4E-01	9.6E-01
<i>CTSB</i>	cg23246268	57	0.11	36	0.10	9.4E-01	6.0E-01
<i>TTLL13</i>	cg20146755	73	0.08	6	0.01	9.5E-01	9.9E-01
<i>SPON2</i>	cg14669409	69	0.09	10	0.04	9.5E-01	9.9E-01
<i>EVPL</i>	cg19500385	16	0.20	4	0.07	9.5E-01	8.8E-01
<i>RNASET2</i>	cg16426562	3	0.21	28	0.07	9.5E-01	9.2E-01
<i>GGT5</i>	cg21681908	19	0.16	40	0.08	9.5E-01	9.9E-01
<i>TRIM45</i>	cg01595724	50	0.14	30	0.12	9.6E-01	9.9E-01
<i>ITIH4</i>	cg18923046	61	0.16	17	0.12	9.6E-01	9.5E-01
<i>BIRC4</i>	cg12656984	6	0.42	13	0.35	9.6E-01	1.0E+00
<i>HLA-DPB1</i>	cg00750366	71	0.14	6	0.10	9.6E-01	9.4E-01
<i>CPVL</i>	cg17154981	87	0.09	18	0.06	9.6E-01	9.1E-01
<i>VARS2</i>	cg10783063	20	0.12	75	0.10	9.7E-01	9.4E-01
<i>ATP7A</i>	cg19434674	6	0.34	12	0.22	9.7E-01	9.6E-01
<i>ARHGEF3</i>	cg25098034	19	0.07	50	0.05	9.7E-01	9.3E-01
<i>SIRPG</i>	cg00498144	35	0.09	51	0.06	9.7E-01	9.1E-01
<i>ITIH3</i>	cg02617595	28	0.09	25	0.03	9.7E-01	9.9E-01
<i>KIAA1804</i>	cg09115440	18	0.20	9	0.15	9.7E-01	9.4E-01
<i>NID2</i>	cg25490128	83	0.12	5	0.05	9.8E-01	9.6E-01
<i>FPR1</i>	cg15811427	72	0.09	58	0.06	9.8E-01	9.5E-01
<i>IRAK1</i>	cg24732640	4	0.44	14	0.32	9.8E-01	9.4E-01
<i>AIF1</i>	cg14694191	77	0.09	10	0.04	9.9E-01	9.9E-01
<i>KIAA1683</i>	cg16354428	73	0.09	45	0.07	9.9E-01	1.0E+00
<i>KLRK1</i>	cg19792694	43	0.10	5	0.02	9.9E-01	9.7E-01
<i>MYO18B</i>	cg25022405	78	0.21	7	0.08	1.0E+00	9.3E-01
<i>CYBRD1</i>	cg06748421	65	0.06	19	0.02	1.0E+00	1.0E+00
<i>C2orf63</i>	cg10275183	40	0.08	43	0.03	1.0E+00	1.0E+00

a) Gene symbol according to HUGO Gene Nomenclature Committee (<http://www.genenames.org/>).

b) CpG site ID assigned by Illumina.

c) Number of individuals with ASE and low or high methylation levels (Beta-value <0.25 or >0.75).

d) Median ASE level for individuals with low or high methylation levels (Beta-value <0.25 or >0.75).

e) Number of individuals with ASE and intermediate methylation levels (Beta-value between 0.25-0.75).

f) Median ASE level for individuals with intermediate methylation levels (Beta-value between 0.25-0.75).

g) P-value for the difference in ASE level between the groups of samples with intermediate and low or high methylation levels calculated using a one-sided Mann-Whitney test.

h) P-value computed by permuting the methylation groups and re-calculating the median ASE levels 5000 times.