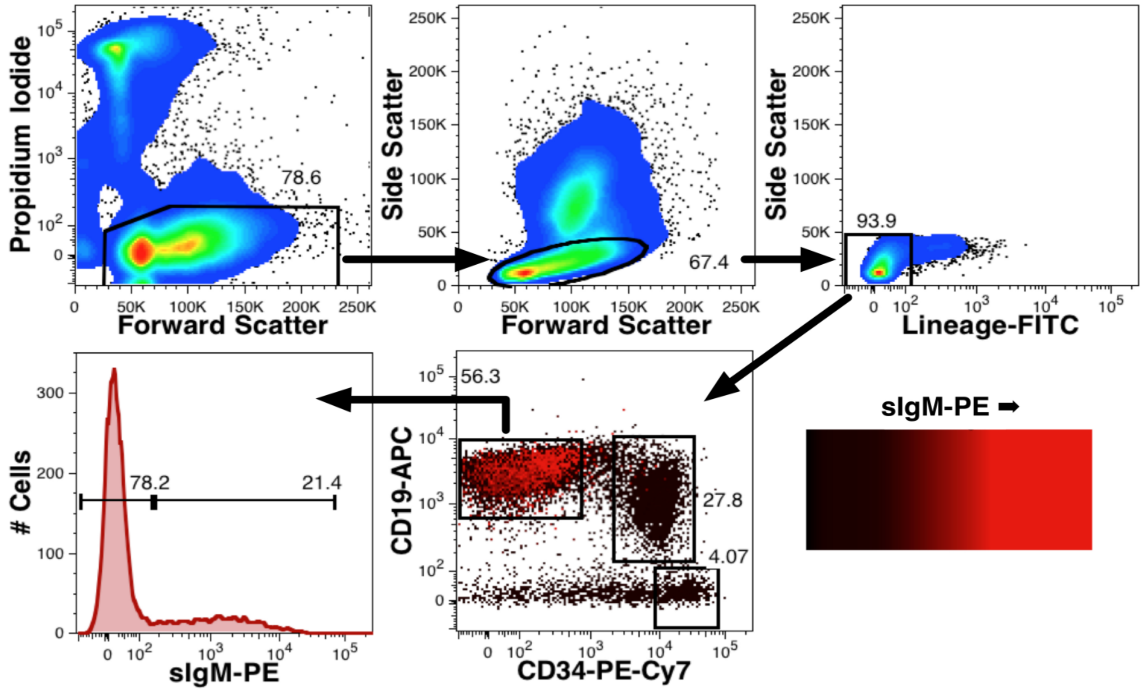
Supplementary Methods and Data

1. Isolation of fetal B-cells and their progenitors.

Four stages of B-cell precursors were isolated through flow cytometry sorting (Supplementary Figure 1). The gating strategy used to sort FBM cells employed a PI$^-$ live cell gate, a light-scatter gate that encompassed lymphoid and progenitor cells followed by a gate to eliminate any lineage$^+$ cells that have not removed by the immunomagnetic bead depletion. CD34^{++}CD19$^-$ early progenitors (S1) and CD19$^+$CD34$^+$ B-cell progenitors (S2) were gated as shown in the dot plot. Additionally, CD19$^+$CD34$^-$ B-cells (S3/4) were gated and sorted based on sIgM expression (red color in dot plot) using the gates shown in the histogram. Numbers refer to the percentage of events found in the corresponding gates. Light-density FBM cells were prepared using Lymphoprep (Axis-Shield PoC, Oslo, Norway). Light-density FBM cells were suspended in cold (4°C) blocking buffer consisting of phosphate-buffered saline (PBS) supplemented with 0.01% NaN_3 (Sigma Chemical Company; St. Louis, MO) and 5% normal mouse serum. FBM was depleted of a number of mature cell populations using BioMag goat anti-mouse IgG immunomagnetic beads (Qiagen Inc., Valencia, CA). Mature lineage$^+$ cells were labeled for depletion using saturating amounts of monoclonal antibodies (mAbs) conjugated with fluorescein isothiocyanate: CD3 (clone UCHT1, BioLegend, San Diego, CA), CD14 (clone Tük4, Invitrogen, Carlsbad, CA), CD56 (clone C5.9, Exalpha Biologicals Inc., Boston, MA) and CD235a (clone CLB-ery-1, Invitrogen). The depleted cells were then stained overnight in blocking buffer with anti-human IgM-phycoerythrin (PE) (clone G20-127, BD Biosciences, Franklin Lakes, NJ), CD19-allophycocyanin (APC) (clone HIB19, BioLegend) and CD34-PE-cyanine 7 (PE-Cy7) (clone 581, BioLegend). Cells were washed, suspended in PBS with 0.01% NaN_3 and 2 µg/ml propidium iodide (PI; Invitrogen) and filtered through a 40 µm cell strainer (BD Biosciences). Fluorescence-activated cell sorting was performed with a FACSAria cell sorter (BD Bioscience). All cell populations were isolated based on their lack of PI staining (live cells), low to moderate forward-light scatter, low side-light scatter, and lack of lineage antigen expression (FITC$^-$).



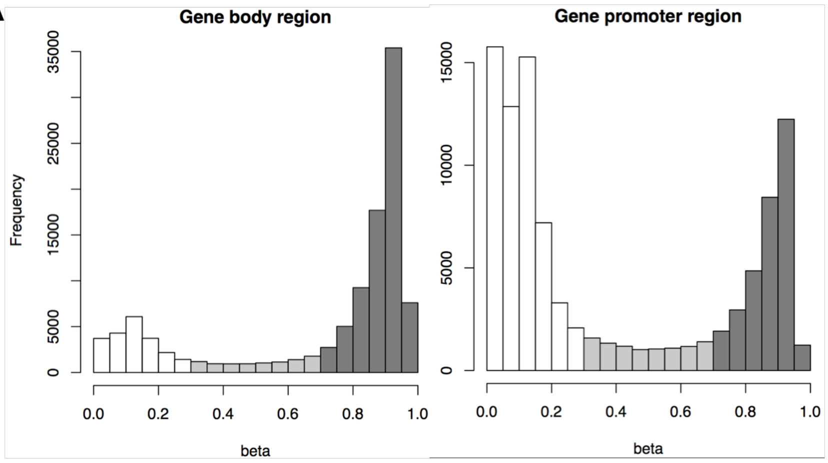
Supplementary Figure 1. Isolation of fetal B-cells and their progenitors. The gating strategy used to sort FBM cells employed a PI$^-$ live cell gate, a light-scatter gate that encompassed lymphoid and progenitor cells followed by a gate to eliminate any lineage$^+$ cells that have not removed by the immunomagnetic bead depletion. CD34^{++}CD19$^-$ early progenitors and CD19$^+$CD34$^+$ B-cell progenitors were gated as shown in the dot plot. Additionally, CD19$^+$CD34$^-$ B-cells were gated and sorted based on sIgM expression (red color in dot plot) using the gates shown in the histogram. Numbers refer to the percentage of events found in the corresponding gates.

2. Characteristics of DNA methylation patterns of lymphoid progenitors

Association of DNA methylation with promoters and CpG islands

The common lymphoid progenitors (S1) serve as the baseline DNA methylation levels before the cells are committed to any lineages. At S1, similar to a previous report, we observed lower methylation levels near the promoter region compared to the body of a gene (Supplementary Figure 2A). The correlation between body and promoter methylation is low in S1 cells with the spearman correlation coefficient equaling 0.17. If we designate $\beta \leq 0.3$, $0.3 < \beta \leq 0.7$ and $\beta > 0.7$ to be hypo-methylated, semi-methylated and hyper-methylated respectively, CpG sites close to the promoter regions of genes in lymphoid progenitors were mostly hypomethylated (57% of loci), whereas 71% of those located in the body regions of genes were hypermethylated (Supplementary Figure 2). Loci within CpG islands (CGI) had the highest percentage of hypomethylated loci (73%), followed by CGI shores (within 2 kb distance from the nearest CGI; 36%) and CGI shelves (within 2 kb distance from the shore; 6%), establishing a methylation gradient that has its lowest point centering on CGIs and increases outwards. Interestingly, while CGIs were in general depleted of methylation, we found that CGIs located in the body region were more methylated and more variable than CGIs sites lying within promoters (Supplementary Figures 2A and B).

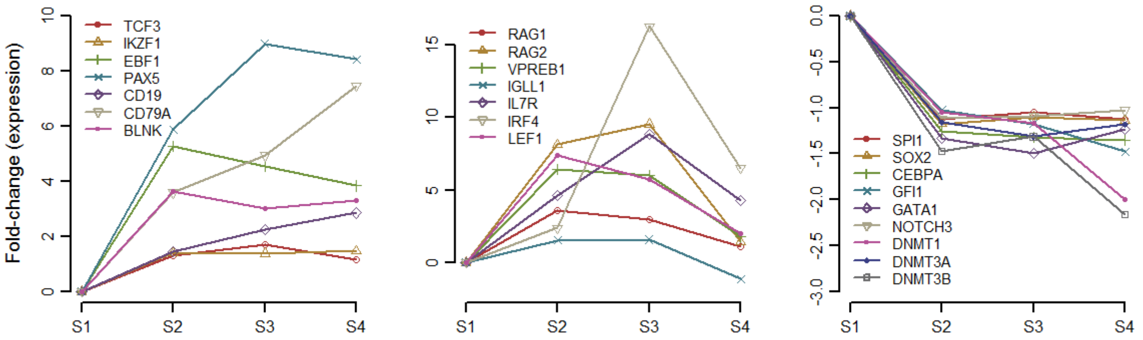
A



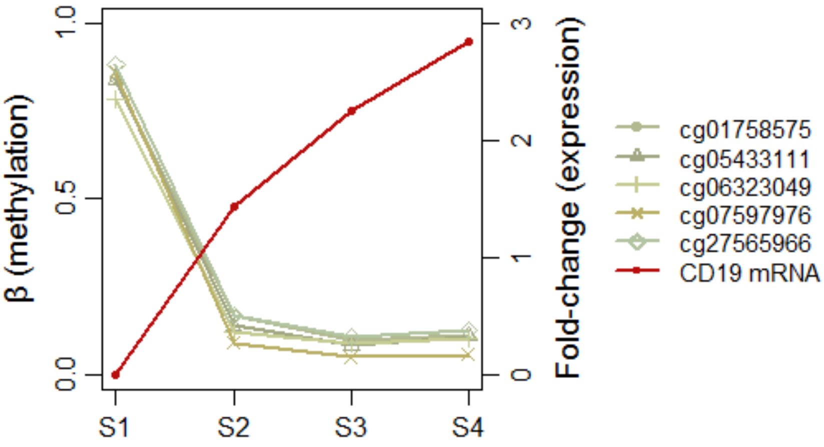
B

Median (MAD) of methylation beta values in S1 (lymphoid progenitor) cells						
		CGI	Shore	Shelf	non-Island	All
Promoter Region	TSS1500	0.10 (0.07)	0.44 (0.47)	0.88 (0.07)	0.87 (0.09)	0.37 (0.46)
	TSS200	0.07 (0.06)	0.27 (0.10)	0.65 (0.16)	0.81 (0.19)	0.11(0.10)
	5' UTR	0.12 (0.09)	0.40 (0.44)	0.88 (0.07)	0.87 (0.25)	0.65 (0.43)
	1st Exon	0.12 (0.10)	0.58 (0.52)	0.89 (0.07)	0.90 (0.06)	0.16 (0.18)
Body Region	Body	0.28 (0.36)	0.85 (0.15)	0.90 (0.06)	0.90 (0.06)	0.88 (0.10)
	3' UTR	0.75 (0.33)	0.89 (0.07)	0.90 (0.06)	0.89 (0.06)	0.89 (0.07)
intergenic		0.17 (0.18)	0.76 (0.27)	0.88 (0.07)	0.87 (0.09)	0.83 (0.15)
All		0.13 (0.12)	0.68 (0.39)	0.89 (0.07)	0.88 (0.09)	0.76 (0.28)

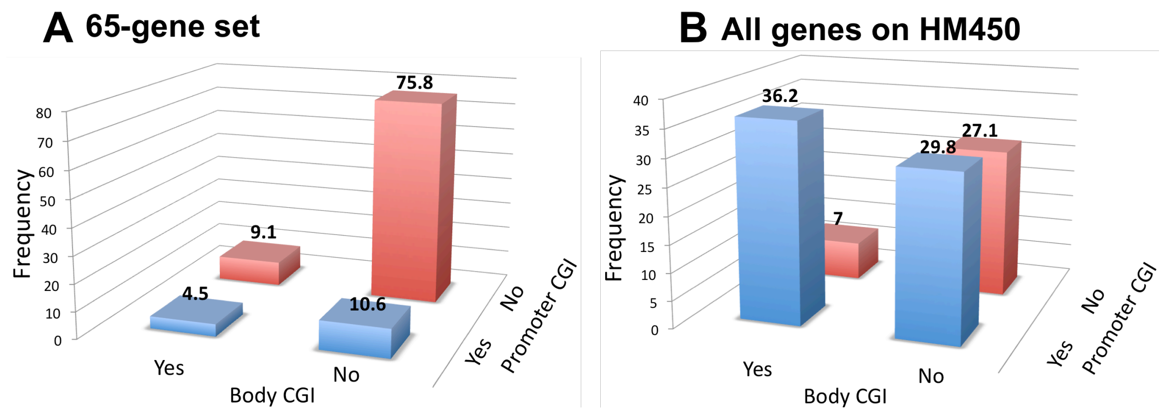
Supplementary Figure 2. Baseline DNA methylation levels at S1. (A) Histograms of gene body and promoter methylation levels (in beta values) at the initial stage (S1). Bars are colored based on methylation levels: hypomethylated (beta ≤ 0.3) in white, semi-methylated (0.3< beta ≤0.7) in light gray and hyper-methylated (beta > 0.7) in dark gray. (B) Median methylation (beta) values of CpG sites with respect to annotation categories. Median absolute deviations (MADs) are provided in parenthese. Cells are shaded according to the same beta cutoffs as in (A).



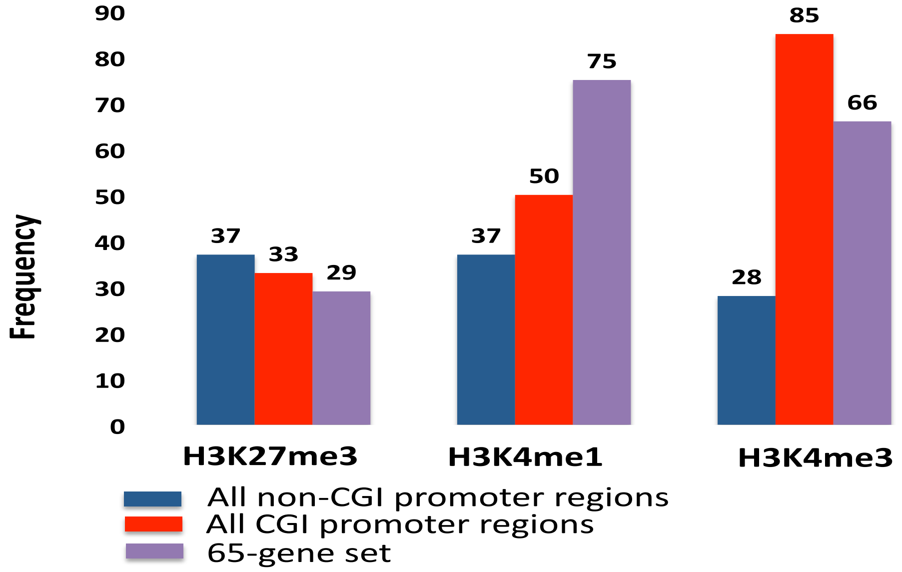
Supplementary Figure 3. The putative B-cell related genes, *TCF3*, *IKZF1*, *EBF1*, *PAX5*, *CD19*, *CD79A* and *BLNK*, were up-regulated during stage progression, while *RAG1*, *RAG2*, *VPREB1* and *IGLL1* were down-regulated again after activation. The non-B lineage genes such as *GFI1*, *GATA1* and *NOTCH3* were down regulated as well as DNA methyltransferases, *DNMT1*, *DNMT3A* and *DNMT3B*.



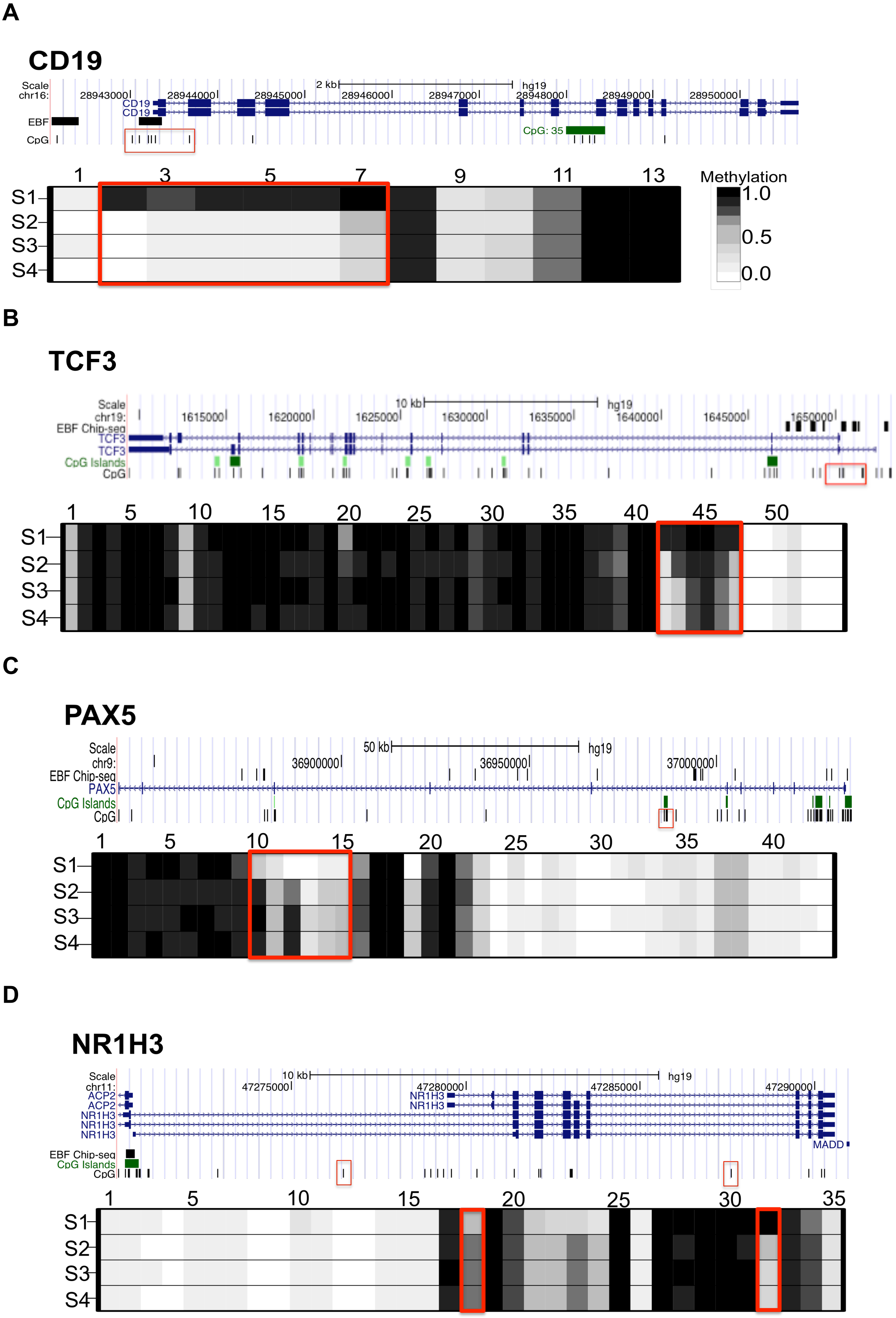
Supplementary Figure 4. Exemplary CpGs showing delayed or lagged expression changes. CpGs near CD19 gene are substantially demethylated from S1 to S2 but also shows substantial expression changes in later stages.



Supplementary Figure 5. (A) Methylation and gene expression changes of this 65-gene set are listed in Supplementary Table 1. Examining the CpG dinucleotide density of these 65 genes, we found that a surprisingly high percentage (75.8%) do not contain any CGI regions in their entire genic region, furthermore, 86.4% had no CGI at their promoter region. **(B)** This is in sharp contrast to the fact that only 7% of the transcripts on HM450 contain no overlapping CGIs in their genic region and 34.1% have non-CGI promoters.



Supplementary Figure 6. To characterize the chromatin structure associated with the 65 genes that are listed in Supplementary Table 1, we examined the histone modification ChIP-seq data of the lymphostoid cell line GM12878 from the ENCODE project. A large majority, 75% and 66%, of these 65 genes have their non-CGI promoter regions marked with active histone modifications H3K4me1 and H3K4me3, respectively. Only 37% and 28% of all the non-CGI promoter regions on HM450 are marked with these two active histone modifications. The percentages are notably higher, at 50% and 85%, for CGI promoter regions.


A
CD19
Scale
chr16:
28943000
28944000
28945000
2 kb
28946000
28947000
hg19
28948000
28949000
28950000
CD19
CD19
EBF
CpG
CpG: 35
1
3
5
7
9
11
13
S1
S2
S3
S4
Methylation
1.0
0.5
0.0
B
TCF3
Scale
chr19:
1615000
1620000
10 kb
1625000
1630000
1635000
hg19
1640000
1645000
1650000
EBF Chip-seq
TCF3
TCF3
CpG Islands
CpG
1
5
10
15
20
25
30
35
40
45
50
S1
S2
S3
S4
C
PAX5
Scale
chr9:
EBF Chip-seq
PAX5
CpG Islands
CpG
36900000
50 kb
36950000
hg19
37000000
1
5
10
15
20
25
30
35
40
S1
S2
S3
S4
D
NR1H3
Scale
chr11:
ACP2
ACP2
NR1H3
NR1H3
NR1H3
EBF Chip-seq
CpG Islands
CpG
47275000
10 kb
47280000
NR1H3
NR1H3
47285000
hg19
47290000
MADD
1
5
10
15
20
25
30
35
S1
S2
S3
S4

Supplementary Figure 7. Exemplary genes of differential methylation during B cell development. Upper panel shows genome browser annotation tracks for the specific gene. The first track is the RefSeq transcript. The second track indicates EBF binding sites based on the ChIP-Seq binding data from ENCODE. The third track displays CGIs and the fourth track marks the CpG sites on the HM450 array. The lower panel illustrates stage-specific methylation levels of these CpG sites. Red rectangles for both panels highlight DMRs. (A) CD19: its expression level was up-regulated (see Supplementary Figure 1). It showed demethylation of CpG sites in the transcription start site (TSS). (B) *TCF3* (E2A): the upstream TSS encoding isoform E12 was hypomethylated at S1 and its methylation level remained unchanged during B cell development whereas regions around the second TSS encoding isoform E47 underwent demethylation during stage progression.

Supplementary Table 1. AME analysis transcription factor binding sites within DMRs during different stage progression (P-values): DNA methylation changes during B-cell development (Seung-Tae Lee, et al).

TF Motif	***de novo* DMR (S1-S2)**	**de-DMR (S1-S2)**	**de-DMR (S2-S3)**	**de-DMR (S3-S4)**
V$EBF_Q6	1	3.2×10^{-37}	1	1
V$OLF1_01	1	1.4×10^{-20}	0.13	1
V$ETS_Q4	1.8×10^{-14}	1.3×10^{-12}	0.99	1
V$ETS_Q6	3.6×10^{-10}	7.3×10^{-12}	1	1
V$ETS1_B	9.3×10^{-7}	2.2×10^{-11}	1	1
V$ETS2_Q6	3.9×10^{-6}	3.6×10^{-10}	0.54	1
V$ESE1_Q3	0.25	4.1×10^{-9}	1	1
V$E47_01	1	6.1×10^{-8}	1	7×10^{-4}
V$CETS1P54_03	0.01	1.4×10^{-7}	1	1
V$CETS1P54_01	2.7×10^{-5}	4.6×10^{-7}	1	1
V$GADP_01	2.2×10^{-5}	8.8×10^{-7}	1	1
V$CETS168_Q6	2.3×10^{-8}	1.5×10^{-6}	1	1
V$E12_Q6	1	2.8×10^{-6}	0.59	0.42
V$E47_02	1	1.9×10^{-5}	0.91	0.23
V$MOVOB_01	1	1.9×10^{-5}	1	1
V$ETS2_B	9.3×10^{-5}	6.9×10^{-5}	1	1
V$MEF2_02	1	8.6×10^{-5}	0.99	1
V$OCT1_Q5_01	1	1.4×10^{-4}	1	1
V$PU1_Q6	4.1×10^{-11}	1.9×10^{-4}	1	1
V$FLI1_Q6	1.1×10^{-4}	6.2×10^{-4}	1	1
V$RSRFC4_01	1	6.7×10^{-4}	0.1	1
V$OCT1_01	1	6.7×10^{-4}	0.93	1
V$PU1_Q4	1.1×10^{-14}	6.5×10^{-3}	0.99	1
V$ELF1_Q6	1.1×10^{-10}	0.026	1	1
V$SPI1_01	1.9×10^{-7}	0.14	1	1
V$SPIB_01	3×10^{-7}	1	0.94	1

Supplementary Table 2. Pathway enrichment analysis for differentially expressed genes in different stages (-log*P* values): Gene expression changes during B-cell development (Seung-Tae Lee, et al).

Pathway	**Up-DEG (S1-S2)**	**Down-DEG (S1-S2)**	**Up-DEG (S2-S3)**	**Down-DEG (S2-S3)**	**Up-DEG (S3-S4)**	**Down-DEG (S1-S2)**
Cyclins and Cell Cycle Regulation	3.07	0	0	0.249	0.309	8.96
Role of BRCA1 in DNA Damage Response	3.64	0	0	0	0	22.8
Mitotic Roles of Polo-Like Kinase	4.68	0	0	0	0	10
Cell Cycle: G2/M DNA Damage Checkpoint Regulation	5.34	0	0.0468	0	0	8.55
Antigen Presentation Pathway	7.09	0	0	0	1.74	0
Protein Ubiquitination Pathway	6.19	0	0	0.446	0	1.35
Estrogen Receptor Signaling	4.82	0	0	0	0	0
Glucocorticoid Receptor Signaling	4.82	0.795	0.169	0.444	0	0
Protein Kinase A Signaling	4.66	0.449	0.452	1.45	0.228	0.213
IL-3 Signaling	4.45	1.24	0.227	0.894	0.639	0.175
HGF Signaling	4.39	1.11	0.154	1.61	0.445	0.259
CCR3 Signaling in Eosinophils	3.87	0.56	0.107	1.44	0.648	0.542
Cdc42 Signaling	3.79	0	0	0.179	0.648	0
fMLP Signaling in Neutrophils	3.79	0.576	0.413	1.5	1.57	0.379
RAN Signaling	3.75	0	0	0	0	1.48
IL-8 Signaling	3.74	2.93	0.0956	2.13	2.72	0
Androgen Signaling	3.67	0.409	0	1.17	0.202	0
ERK/MAPK Signaling	3.67	0.36	0	1.41	0	0
GM-CSF Signaling	3.67	0.567	2.3	0	0.694	0
CXCR4 Signaling	3.62	1.37	0.342	2.39	1.04	0
Type I Diabetes Mellitus Signaling	3.42	0.576	0	1.78	0.664	0
T Cell Receptor Signaling	3.26	0.928	1.84	1.37	0.752	0.0197
Calcium-induced T Lymphocyte Apoptosis	3.19	0.567	0.276	1.44	1.19	0.0899
CREB Signaling in Neurons	3.19	0.406	0.169	1.23	0.381	0
PKCθ Signaling in T Lymphocytes	3.16	0.757	0.517	0.79	2.63	0
Telomerase Signaling	3.14	0	0.151	0.632	0.443	0
Assembly of RNA Polymerase II Complex	3.12	0	0	0	0	0
Antiproliferative Role of TOB in T Cell Signaling	3.08	0	0.107	0	0	2.24
Phospholipase C Signaling	3	1.15	2.71	2.39	1.96	0
Prolactin Signaling	3	0.705	0	1.61	0.133	0
α-Adrenergic Signaling	3	0.38	0.0737	1.44	0.51	0.193
Role of NFAT in Regulation of the Immune Response	4.82	1.07	1.39	1.69	4.5	0
IL-4 Signaling	3.68	0.138	0.452	0	3.13	0
iCOS-iCOSL Signaling in T Helper Cells	3.19	0.283	1.64	1.53	3.51	0
CD28 Signaling in T Helper Cells	3.13	0.756	2.54	0.785	3.9	0.0412
Primary Immunodeficiency Signaling	3.36	0	3.35	0.377	1.38	0.402
B Cell Development	5.72	0.35	3.43	0.231	4.5	0.171
B Cell Receptor Signaling	6.33	0.395	4.67	0.362	2.66	0
PI3K Signaling in B Lymphocytes	3.96	0.576	5.58	1.28	3.51	0
Role of JAK1, JAK2 and TYK2 in Interferon Signaling	0.129	0	3.43	0	0.309	0
Cholecystokinin/Gastrin-mediated Signaling	2.11	1.11	0.147	3.19	0.714	0
T Helper Cell Differentiation	0.556	0.512	0.247	1.37	3.13	0
Dendritic Cell Maturation	1.96	0.967	0	0.733	4.16	0
TREM1 Signaling	0.237	2.75	0	1.17	3.62	0
p53 Signaling	2.41	0.519	0.168	0.219	0.243	3.52
Role of CHK Proteins in Cell Cycle Checkpoint Control	1.96	0	0	0	0	11.7
Cell Cycle: G1/S Checkpoint Regulation	1.93	0	0	0.698	0.405	6.95
ATM Signaling	1.72	0	0	0	0	10.3
Purine Metabolism	1.3	0.281	0	0.596	0	4.9
Pyrimidine Metabolism	1.22	0.56	0	0.236	0	5.85
DNA Double-Strand Break Repair by Homologous Recombination	0.776	0	0	0	0	3.81
Mismatch Repair in Eukaryotes	0.664	0	0	0	0	10.1
Aryl Hydrocarbon Receptor Signaling	0.525	0.574	0	1.78	0	4.28

Lysine Degradation	0.502	0.843	0	0	0	4.03
Cell Cycle Control of Chromosomal Replication	0.29	0	0	0.27	0	13.4

Supplemental Table 3a. Statistics of the 224 genes that had concurrent methylation and expression changes from S1 to S2.

								Methylation							Expression		
GeneSymbol	**GeneTitle**	**ChrLoc**	**Methylation. S2vsS1**	**Expression. S2vsS1**	**IlmnID**	**UCSC_RefGene_Group**	**UCSC_CpG_Islands_Name**	**Relation_to_UCSC_CpG_Island**	**Mean.S1**	**Mean.S2**	**Mean.S3**	**Mean.S4**	**ProbeSetID**	**Mean.S 1**	**Mean.S 2**	**Mean.S 3**	**Mean.S 4**
GTDC1	glycosyltransfe	chr2:14441979	-0.52	0.82	cg25812095	5'UTR;5'UTR			0.87	0.35	0.14	0.11	8055606	7.61	8.42	8.60	8.49
TERF1	telomeric repea	chr8:74083661	-0.62	1.16	cg18250453	Body;Body	chr8:73920858	S_Shelf	0.94	0.32	0.17	0.15	8146914	8.37	9.53	10.27	9.65
RGS10	regulator of G-	chr10:1212489	0.22	-0.84	cg20345915	5'UTR;Body;1stExon			0.57	0.79	0.8	0.79	7936673	8.47	7.64	7.29	7.47
LYN	v-yes-1 Yamag	chr8:56954926	-0.20	-0.90	cg24856456	3'UTR;3'UTR			0.58	0.39	0.32	0.31	8146500	8.80	7.90	10.22	11.02
SLC35F2	solute carrier f	chr11:1071669	0.36	-0.68	cg03851835	Body			0.31	0.66	0.68	0.65	7951485	7.50	6.82	6.55	6.89
BLNK	B-cell linker	chr10:9794098	-0.43	2.06	cg18448570	TSS200;TSS200			0.61	0.19	0.17	0.18	7935270	8.81	10.87	10.41	10.69
PRTN3	proteinase 3	chr19:791965-	-0.47	-0.95	cg24347562	TSS1500	chr19:843468-	N_Shelf	0.73	0.26	0.25	0.24	8024048	9.14	8.20	7.99	8.14
HMHB1	histocompatibi	chr5:14317191	-0.51	1.41	cg02228160	Body			0.67	0.15	0.11	0.1	8108900	8.07	9.47	9.30	9.21
TOP1MT	topoisomerase	chr8:14446256	0.38	-1.31	cg17117981	Body			0.49	0.87	0.9	0.85	8153390	9.06	7.75	8.00	8.17
EBF1	early B-cell fac	chr5:15805800	0.22	2.54	cg18816534	Body			0.31	0.53	0.42	0.37	8115543	9.30	11.84	11.49	11.30
IKZF2	IKAROS family	chr2:21357900	0.30	1.54	cg14227558	Body;Body			0.46	0.76	0.79	0.8	8058670	7.73	9.27	10.74	10.30
SHOC2	soc-2 suppress	chr10:1126692	-0.33	1.02	cg08253072	5'UTR	chr10:1126783	S_Shore	0.54	0.2	0.19	0.18	7930470	9.91	10.93	11.24	11.35
PCCA	propionyl Coen	chr13:9953933	0.23	-1.11	cg25084760	Body;Body			0.33	0.56	0.57	0.55	7969835	7.23	6.12	6.76	6.27
PTRF	polymerase I a	chr17:3780799	0.25	-0.59	cg27196880	Body	chr17:4057374	N_Shelf	0.56	0.8	0.78	0.8	8015635	6.93	6.34	6.41	6.47
EDEM1	ER degradation	chr3:5204358-	-0.36	1.25	cg16505233	Body			0.48	0.11	0.13	0.09	8077458	8.02	9.27	8.82	8.83
IL1B	interleukin 1, b	chr2:11330379	0.29	-0.92	cg01290568	5'UTR			0.21	0.5	0.51	0.47	8054722	8.19	7.27	6.35	5.98
TESC	tescalcin	chr12:1159611	-0.38	-0.67	cg14224600	Body;Body;Bo	chr12:1174768	S_Shore	0.8	0.42	0.44	0.4	7966749	8.50	7.83	7.03	7.03
ETV6	ets variant 6	chr12:1169405	-0.31	-0.85	cg06516865	Body			0.37	0.07	0.07	0.05	7953981	9.44	8.59	8.13	8.29
CTCF	CCCTC-binding	chr16:6615396	-0.42	0.78	cg04545079	5'UTR	chr16:6759586	S_Shelf	0.91	0.49	0.4	0.38	7996593	9.62	10.41	10.43	9.93
ADAM28	ADAM metallop	chr8:24207525	0.28	-2.36	cg17969683	TSS200;TSS200			0.15	0.43	0.48	0.47	8145293	8.57	6.21	5.97	6.33
RAB11FIP1	RAB11 family i	chr8:37835628	-0.68	-0.74	cg22881435	Body;TSS1500;Body			0.87	0.19	0.12	0.11	8150225	8.18	7.45	7.77	8.37
TBC1D1	TBC1 (tre-2/US	chr4:37569103	-0.54	0.88	cg10274108	Body			0.64	0.11	0.13	0.09	8094574	8.83	9.71	10.34	10.52
RNF220	ring finger prot	chr1:44643453	0.26	-0.67	cg01804134	Body			0.55	0.81	0.82	0.81	7900979	9.26	8.58	8.29	8.43
QRSL1	glutaminyl-tRN	chr6:10718414	-0.46	2.10	cg18067520	3'UTR			0.63	0.17	0.12	0.09	8121300	8.24	10.34	10.60	10.40
POU2AF1	POU class 2 as	chr11:1107281	-0.64	1.23	cg10694914	TSS1500			0.75	0.11	0.09	0.07	7951596	8.31	9.55	9.87	9.67
CD84	CD84 molecule	chr1:15877751	-0.39	-1.05	cg27304328	Body			0.94	0.55	0.17	0.1	7921637	7.73	6.68	7.85	8.09
LITAF	lipopolysacchar	chr16:1154935	-0.74	0.90	cg08767044	5'UTR;5'UTR;B	chr16:1168000	N_Shore	0.85	0.11	0.09	0.07	7999468	7.99	8.89	9.01	8.72
RAPGEF1	Rap guanine nu	chr9:13354144	-0.40	2.08	cg13655250	Body;Body			0.65	0.24	0.22	0.17	8164692	5.44	7.53	7.64	7.15
PARP1	poly (ADP-ribo	chr1:22461501	-0.59	0.62	cg18590995	Body			0.93	0.33	0.11	0.08	7924733	9.47	10.10	10.25	10.13
TYROBP	TYRO protein t	chr19:4108714	0.26	-0.73	cg21495704	TSS200;TSS200			0.41	0.67	0.74	0.7	8036224	9.66	8.93	8.66	8.97
SLC8A1	solute carrier f	chr2:40192790	-0.37	1.41	cg08780166	Body;Body;Body;Body			0.91	0.54	0.45	0.44	8051762	6.32	7.73	7.20	6.45
ZCCHC7	zinc finger, CCH	chr9:37110469	-0.25	1.21	cg14060402	Body			0.79	0.54	0.16	0.25	8155234	9.13	10.33	10.33	10.42
GCNT2	glucosaminyl (	chr6:10636575	0.26	-0.70	cg14112601	TSS1500			0.27	0.53	0.56	0.56	8116835	6.26	5.57	5.15	5.66
LCN6	lipocalin 6	chr9:13875829	-0.65	0.98	cg17935703	TSS200	chr9:1396406	S_Shelf	0.81	0.16	0.15	0.12	8165277	7.33	8.31	7.10	7.15
CD52	CD52 molecule	chr1:26516998	0.22	1.21	cg22517705	Body;TSS1500			0.44	0.66	0.31	0.16	7899160	10.19	11.40	11.87	12.46
CMTM7	CKLF-like MAR	chr3:32408167	-0.35	1.10	cg07116972	Body;Body			0.42	0.07	0.07	0.05	8078405	8.91	10.01	10.04	9.69
CDC42EP3	CDC42 effector	chr2:37724247	-0.29	-1.06	cg19275008	5'UTR			0.83	0.54	0.41	0.35	8051573	7.27	6.21	6.12	6.55
PXDN	peroxidasin ho	chr2:1614666-	-0.32	1.17	cg01271695	Body			0.4	0.09	0.11	0.07	8050007	8.02	9.19	8.25	7.88
KIT	v-kit Hardy-Zu	chr4:55218842	0.21	-2.19	cg17854066	Body;Body			0.38	0.59	0.59	0.58	8095110	9.89	7.70	6.29	5.81
TBC1D15	TBC1 domain f	chr12:7051980	-0.37	0.66	cg15437231	Body;Body;Body;Body			0.81	0.44	0.42	0.42	7957186	9.64	10.30	10.23	9.90
MYCN	v-myc myelocy	chr2:15998134	0.23	-0.72	cg19623054	Body	chr2:1607980	S_Shelf	0.61	0.85	0.88	0.87	8040419	7.98	7.26	7.01	7.01
FAM65B	family with sec	chr6:24912492	-0.23	0.72	cg24960799	5'UTR	chr6:24910626	N_Shore	0.57	0.34	0.15	0.13	8124280	8.00	8.72	9.48	9.84
DNTT	deoxynucleotid	chr10:9805407	-0.51	4.41	cg20728490	5'UTR;1stExon;1stExon;5'UTR			0.85	0.34	0.18	0.16	7929574	7.82	12.23	8.06	6.84
PSMB8	proteasome (p	chr6_cox_hap1	-0.49	1.39	cg11381564	3'UTR;3'UTR	chr6:3280628	S_Shore	0.6	0.11	0.06	0.04	8178855	7.84	9.22	9.27	9.14
FCER1G	Fc fragment of	chr1:15945169	0.28	-1.26	cg26394055	TSS200			0.12	0.4	0.45	0.43	7906720	7.92	6.66	5.54	5.97
FAM107B	family with sec	chr10:1460056	0.24	0.60	cg14152591	Body			0.33	0.58	0.58	0.58	7932160	9.35	9.95	10.18	10.15
MYO5C	myosin VC	chr15:5027181	-0.50	1.12	cg02703248	Body			0.92	0.41	0.24	0.15	7988876	7.62	8.73	5.95	6.04
CD72	CD72 molecule	chr9:35599976	-0.22	2.47	cg13409077	TSS200	chr9:3561698	S_Shore	0.34	0.12	0.14	0.12	8161004	7.38	9.85	10.97	11.49
MBNL2	muscleblind-lik	chr13:9667257	0.31	0.77	cg24714606	Body;Body			0.34	0.65	0.72	0.72	7969677	8.37	9.13	9.10	9.43
CD81	CD81 molecule	chr11:2355096	-0.68	0.80	cg02525637	Body	chr11:2406711	S_Shore	0.93	0.25	0.12	0.09	7937802	9.34	10.14	10.52	10.04
SH2D4B	SH2 domain co	chr10:8228763	-0.76	1.29	cg04421348	TSS1500;Body	chr10:8229550	S_Shelf	0.87	0.11	0.09	0.08	7928723	6.45	7.75	6.78	6.73
PLD1	phospholipase	chr3:17280088	-0.24	-1.43	cg07064537	5'UTR;5'UTR			0.93	0.7	0.56	0.56	8092134	7.07	5.64	5.37	5.60
MED12L	mediator comp	chr3:15228687	-0.54	-0.72	cg05094216	Body;5'UTR			0.71	0.18	0.16	0.15	8083360	6.70	5.99	6.03	5.88
GPR126	G protein-coup	chr6:14266468	-0.23	-0.65	cg27656786	Body;Body;Body;Body			0.45	0.22	0.26	0.24	8122365	6.41	5.76	5.67	5.81
TSSC1	tumor suppres	chr2:3171743-	-0.61	0.95	cg14950134	Body			0.94	0.33	0.13	0.11	8050060	7.67	8.62	8.40	7.97
HDC	histidine decar	chr15:4832143	-0.23	-1.55	cg26188685	Body			0.72	0.49	0.48	0.44	7988672	7.71	6.16	5.89	5.98
IL7R	interleukin 7 re	chr5:35892748	-0.25	2.53	cg04312209	1stExon			0.82	0.57	0.39	0.38	8104901	7.16	9.69	10.31	9.60
GRB10	growth factor r	chr7:50625259	-0.28	-0.64	cg01495332	5'UTR;Body;Body			0.92	0.64	0.48	0.47	8139656	7.58	6.94	6.61	6.75
VPREB1	pre-B lymphoc	chr22:2092920	-0.69	2.85	cg04776489	TSS1500			0.86	0.17	0.11	0.1	8071646	8.32	11.17	10.91	9.36
CSGALNACT1	chondroitin sul	chr8:19305952	-0.28	1.14	cg11365913	Body;Body;Bo	chr8:19319030	N_Shore	0.41	0.12	0.13	0.1	8149574	6.59	7.73	6.85	7.34
ALOX5AP	arachidonate 5	chr13:3020764	-0.29	0.96	cg08529529	1stExon			0.74	0.44	0.22	0.19	7968344	8.36	9.33	8.54	9.84
IGF2R	insulin-like gro	chr6:16031012	-0.25	0.63	cg16111231	Body			0.8	0.55	0.44	0.43	8123181	6.88	7.51	8.80	8.61
IGLL1	immunoglobuli	chr22:2224531	-0.41	0.69	cg19558972	1stExon;5'UTR;1stExon;5'UTR			0.53	0.11	0.11	0.1	8074909	10.15	10.84	10.80	9.97
PBX1	pre-B-cell leuk	chr1:16279549	0.24	-1.05	cg22802296	Body			0.5	0.74	0.76	0.71	7906954	8.12	7.07	6.99	7.08
NID2	nidogen 2 (ost	chr14:5154127	-0.61	1.69	cg05884192	Body			0.76	0.14	0.15	0.14	7979133	6.60	8.29	7.05	6.55
BACH2	BTB and CNC h	chr6:90692969	0.28	2.39	cg27644327	5'UTR;5'UTR			0.44	0.72	0.75	0.75	8128247	6.81	9.20	10.36	10.15
FBXW7	F-box and WD	chr4:15346186	-0.66	1.57	cg05052463	Body;Body;1stExon;5'UTR			0.79	0.13	0.11	0.1	8103206	8.07	9.63	8.11	8.18
BUB1	budding uninhi	chr2:11111188	-0.49	1.23	cg23198623	Body	chr2:1114353	N_Shelf	0.79	0.3	0.13	0.09	8054580	8.14	9.37	9.62	7.65
ARAP2	ArfGAP with RH	chr4:35744017	-0.20	1.17	cg22518157	Body			0.44	0.24	0.25	0.23	8099760	7.37	8.54	8.10	8.78
TTF1	transcription te	chr9:13424075	-0.23	1.14	cg02735762	5'UTR	chr9:1352820	N_Shore	0.35	0.12	0.1	0.09	8164729	6.56	7.70	7.73	6.97
PRPF4B	PRP4 pre-mRN	chr6:3966500-	-0.24	0.98	ch.6.115952F	Body			0.37	0.13	0.08	0.07	8116664	8.35	9.33	9.32	9.11
GALNT7	UDP-N-acetyl-a	chr4:17432650	-0.62	1.04	cg03238899	Body			0.9	0.28	0.24	0.21	8098328	9.37	10.41	10.08	9.85
ZNF423	zinc finger prot	chr16:4808202	-0.30	0.76	cg07089942	Body	chr16:4966957	N_Shelf	0.81	0.51	0.3	0.22	8001337	6.80	7.56	6.84	6.84
GCET2	germinal cente	chr3:11332237	-0.59	1.67	cg22256853	3'UTR;3'UTR			0.85	0.26	0.14	0.12	8089478	6.43	8.10	9.84	9.13
PLCB2	phospholipase	chr15:3836739	0.30	-1.11	cg02240622	TSS1500			0.54	0.84	0.88	0.88	7987475	8.46	7.35	6.94	7.51
NRM	nurim (nuclear	chr6_cox_hap1	-0.27	0.91	cg14646977	Body;TSS1500	chr6:3065439	S_Shore	0.9	0.63	0.47	0.35	8178399	8.40	9.31	9.20	8.52
LTA	lymphotoxin al	chr6_qbl_hap2	-0.71	0.83	cg17169196	TSS200;1stExon;5'UTR			0.78	0.07	0.1	0.07	8179258	7.71	8.53	7.56	8.00
GNG2	guanine nucleo	chr14:5138370	-0.23	1.07	cg08001559	TSS200			0.52	0.29	0.28	0.28	7974341	8.12	9.20	8.92	8.92
ZDHHC14	zinc finger, DH	chr6:15772254	-0.57	-0.59	cg03125341	Body;Body			0.69	0.12	0.09	0.06	8122982	7.70	7.11	7.04	7.24
PRKCB	protein kinase	chr16:2375482	0.20	0.94	cg09529437	Body;Body			0.23	0.43	0.46	0.44	7994131	9.55	10.49	10.96	11.00
KIAA0748	KIAA0748	chr12:5362806	0.37	-0.92	cg24536818	5'UTR;5'UTR			0.26	0.63	0.69	0.7	7963851	8.33	7.41	7.22	7.65
ARHGEF7	Rho guanine nu	chr13:1105656	-0.69	0.77	cg20847766	Body;5'UTR;5'UTR;Body;Body			0.84	0.15	0.14	0.12	7970111	9.14	9.91	9.94	9.92
GPR125	G protein-coup	chr4:21998097	-0.47	0.95	cg00178728	Body	chr4:22516856	N_Shore	0.8	0.33	0.15	0.14	8099612	7.92	8.87	7.94	6.70
CLEC2D	C-type lectin d	chr12:9713473	-0.73	2.07	cg12810837	TSS200;TSS200			0.89	0.16	0.11	0.1	7953878	8.07	10.15	10.83	10.47
ZHX2	zinc fingers an	chr8:12386308	-0.51	2.41	cg25115537	5'UTR			0.78	0.27	0.14	0.09	8148149	8.06	10.47	11.17	10.68
LILRA2	leukocyte imm	chr19:5977707	-0.66	0.94	cg14575739	Body;Body			0.88	0.22	0.19	0.18	8031207	7.87	8.81	8.10	8.09
IFT81	intraflagellar tr	chr12:1090465	-0.38	0.98	cg10236261	Body;Body;Body			0.52	0.14	0.17	0.12	7958620	6.66	7.64	7.94	7.03
MGEA5	meningioma ex	chr10:1035341	-0.62	0.90	cg02505177	Body;Body	chr10:1035773	N_Shelf	0.91	0.29	0.12	0.09	7935910	9.03	9.93	10.28	10.45
RNASEH2B	ribonuclease H	chr13:5038181	-0.61	0.79	cg10361659	TSS1500;TSS1	chr13:5148374	N_Shore	0.78	0.18	0.16	0.15	7969179	9.16	9.94	10.04	9.40
ENPP3	ectonucleotide	chr6:13200013	-0.21	-0.62	cg08678755	TSS1500			0.92	0.71	0.32	0.3	8122071	6.31	5.68	5.76	5.90
CABLES1	Cdk5 and Abl e	chr18:1896972	-0.39	-1.11	cg25221092	Body;Body;Body			0.64	0.25	0.18	0.17	8020495	7.32	6.21	6.16	6.71
GPR18	G protein-coup	chr13:9870497	-0.64	0.76	cg18967835	Body;Body;Body;Body;Body			0.87	0.23	0.23	0.23	7972548	8.57	9.33	10.35	10.38
SERINC5	serine incorpor	chr5:79442806	-0.58	0.97	cg02417427	Body			0.88	0.3	0.17	0.16	8112865	7.57	8.54	7.46	6.90
COTL1	coactosin-like	chr16:8315670	-0.21	-0.74	cg03892543	Body	chr16:8465096	N_Shore	0.42	0.22	0.14	0.12	8003171	9.21	8.46	8.48	8.87
TNF	tumor necrosis	chr6_cox_hap1	-0.62	0.98	cg21370522	TSS200			0.71	0.09	0.1	0.07	8177983	7.86	8.84	7.68	7.85
RUNX2	runt-related tra	chr6:45404032	-0.66	-1.37	cg08842021	Body;Body;Body			0.88	0.22	0.2	0.16	8120043	8.64	7.27	6.64	6.83
HIVEP2	human immuno	chr6:14311429	-0.47	2.02	cg20743720	5'UTR			0.78	0.31	0.21	0.21	8129953	6.75	8.77	8.43	8.22
PART1	prostate andro	chr5:59819516	-0.65	1.80	cg24893378	Body			0.79	0.14	0.14	0.11	8105495	5.29	7.08	8.05	8.22
CCND3	cyclin D3	chr6:42010649	-0.46	1.12	cg01143547	3'UTR;3'UTR;3'UTR;3'UTR			0.9	0.45	0.19	0.15	8126371	8.07	9.19	9.59	8.56
HADH	hydroxyacyl-Co	chr4:10913031	-0.22	0.79	cg01150799	3'UTR			0.4	0.18	0.19	0.18	8096753	8.69	9.48	9.45	8.23
FCRLA	Fc receptor-like	chr1:15994338	-0.20	0.99	cg05033369	TSS1500			0.9	0.7	0.28	0.09	7906786	6.59	7.58	10.20	11.12
ZNF124	zinc finger prot	chr1:24538581	0.28	1.38	cg02952913	TSS1500	chr1:2473348	S_Shore	0.32	0.6	0.61	0.6	7925691	7.96	9.34	8.66	8.51
CYP2C8	cytochrome P4	chr10:9678651	-0.24	-0.74	cg14717122	3'UTR			0.38	0.14	0.16	0.17	7935169	6.04	5.30	5.27	5.31
JAK1	Janus kinase 1	chr1:65071494	-0.33	1.01	cg12075498	5'UTR	chr1:6543145	N_Shelf	0.44	0.1	0.12	0.08	7916747	9.54	10.54	10.63	10.70
TCF7L2	transcription fa	chr10:1147002	0.31	0.94	cg03683087	Body;Body;Body;Body;Body;Body			0.19	0.5	0.54	0.52	7930537	8.98	9.92	7.44	7.32
DOCK1	dedicator of cy	chr10:1285840	-0.21	-0.96	cg11261261	Body			0.92	0.72	0.7	0.66	7931293	7.25	6.29	5.62	5.75
GMDS	GDP-mannose	chr6:1569040-	0.20	-0.77	cg09571972	Body			0.41	0.59	0.7	0.67	8123562	8.29	7.52	7.39	7.27
ANKRD50	ankyrin repeat	chr4:12580491	0.26	0.97	cg04525852	5'UTR;5'UTR	chr4:1256333	N_Shore	0.55	0.81	0.82	0.85	8102720	7.94	8.91	8.68	8.33
PDIA5	protein disulfid	chr3:12426859	-0.27	-0.79	cg27383859	Body;Body			0.92	0.65	0.28	0.15	8082133	7.85	7.06	7.76	7.59
FRYL	FRY-like	chr4:48314378	0.27	0.71	cg02886077	5'UTR	chr4:4878133	N_Shore	0.32	0.59	0.59	0.6	8100292	8.79	9.50	9.50	9.57
ABCA1	ATP-binding ca	chr9:10658310	-0.25	1.02	cg13559409	3'UTR			0.88	0.64	0.57	0.6	8162940	6.73	7.75	8.67	8.78
CMTM8	CKLF-like MAR	chr3:32255175	-0.24	1.70	cg24924051	Body			0.84	0.59	0.34	0.3	8078397	7.28	8.99	8.84	7.86

PAG1	phosphoprotei	chr8:8204260	-0.60	1.80	cg19004971	TSS1500	chr8:8202385	S_Shore	0.83	0.22	0.16	0.15	8151512	7.88	9.68	8.86	8.94
C11orf21	chromosome 1	chr11:227344	0.24	-0.77	cg19766471	Body;TSS1500;Body			0.26	0.5	0.56	0.55	7945734	7.70	6.93	6.99	7.18
CPM	carboxypeptid	chr12:675312	0.23	1.08	cg02266731	TSS1500			0.67	0.9	0.92	0.91	7964834	6.47	7.55	8.75	8.73
MSI2	musashi homo	chr17:526889	0.39	0.60	cg07377994	Body;Body			0.29	0.68	0.65	0.59	8008682	9.04	9.65	9.82	9.59
MS4A3	membrane-spa	chr11:595806	0.21	-2.27	cg03348161	TSS200;TSS200;TSS200			0.54	0.75	0.73	0.74	7940216	9.83	7.56	5.66	6.36
ARID5B	AT rich interac	chr10:633310	-0.26	1.54	cg13344587	Body			0.82	0.56	0.4	0.35	7927732	7.83	9.37	9.60	9.68
ZMIZ1	zinc finger, MI	chr10:804987	-0.45	0.59	cg10427868	5'UTR			0.58	0.13	0.13	0.11	7928558	8.46	9.05	8.32	7.85
IGF2BP3	insulin-like gro	chr7:2331635	0.29	0.97	cg17209188	Body			0.55	0.84	0.88	0.88	8138566	8.14	9.11	8.67	8.51
CD79A	CD79a molecu	chr19:470730	-0.43	1.90	cg19825589	TSS1500;TSS1500			0.45	0.02	0.05	0.02	8029136	8.15	10.05	10.46	11.05
IRF8	interferon regu	chr16:844902	-0.41	-1.34	cg27208925	Body			0.57	0.16	0.1	0.07	7997712	10.60	9.27	9.20	10.04
SNAPIN	SNAP-associat	chr1:1518977	-0.68	1.12	cg06942637	3'UTR	chr1:1536310	S_Shelf	0.82	0.14	0.18	0.16	7905598	7.88	9.00	9.11	8.86
PRKCE	protein kinase	chr2:4573254	-0.29	0.98	cg02073763	Body			0.58	0.29	0.09	0.07	8041763	7.63	8.61	9.02	8.75
RANBP9	RAN binding p	chr6:1372970	-0.54	0.81	cg08622666	Body			0.83	0.29	0.28	0.29	8123989	9.76	10.57	10.50	10.09
DUSP26	dual specificity	chr8:3356839	-0.38	0.60	cg00319774	5'UTR	chr8:3345691	N_Shore	0.45	0.07	0.09	0.06	8150197	7.38	7.98	7.52	7.47
PSD3	pleckstrin and	chr8:1843234	0.22	2.56	cg06399735	Body			0.62	0.84	0.85	0.86	8149555	6.92	9.48	8.16	7.74
RAG1	recombination	chr11:364935	-0.58	1.96	cg06288355	TSS200			0.73	0.14	0.17	0.12	7939398	7.26	9.23	8.83	7.47
TNNI2	troponin I type	chr11:181679	-0.26	-0.60	cg14975206	TSS1500;TSS200;5'UTR			0.37	0.11	0.11	0.08	7937728	8.29	7.69	7.71	7.85
ID3	inhibitor of DN	chr1:2375699	0.24	1.16	cg18150584	TSS1500	chr1:2388568	S_Shore	0.15	0.39	0.42	0.36	7913655	6.58	7.74	7.37	6.95
CEP192	centrosomal p	chr18:129984	-0.36	0.83	ch.18.310800	Body			0.54	0.18	0.12	0.11	8020267	8.62	9.45	9.54	8.81
STAT5A	signal transdu	chr17:376930	0.32	-0.68	cg05744184	3'UTR	chr17:404642	N_Shore	0.23	0.55	0.59	0.58	8007212	8.17	7.49	7.06	7.01
IL5RA	interleukin 5 r	chr3:3086421-	-0.27	-1.59	cg14749590	5'UTR;5'UTR;5'UTR;5'UTR;5'UTR;5'UTR			0.88	0.61	0.46	0.45	8085062	7.28	5.69	5.40	5.53
CAMK1D	calcium/calmo	chr10:124314	-0.45	0.73	cg26169081	Body;Body			0.82	0.37	0.35	0.29	7926223	8.23	8.96	9.03	9.10
ERLIN1	ER lipid raft as	chr10:101899	0.27	-0.80	cg26746309	Body;Body	chr10:101945	N_Shelf	0.16	0.43	0.47	0.46	7935692	10.33	9.53	9.17	8.57
GATA2	GATA binding	chr3:1296809	-0.27	-0.87	cg15038286	Body;Body;Body			0.8	0.53	0.57	0.52	8090469	8.03	7.16	7.03	7.11
LY86	lymphocyte an	chr6:6533340-	-0.56	1.12	cg13125224	TSS1500;Body			0.81	0.26	0.21	0.2	8116734	7.67	8.79	9.46	10.18
CUL3	cullin 3	chr2:2250431	0.23	0.94	cg25451702	Body			0.24	0.47	0.36	0.3	8059393	9.57	10.51	10.70	10.57
ZBTB16	zinc finger and	chr11:113435	0.48	-1.03	cg04226002	Body;Body	chr11:113953	N_Shore	0.33	0.81	0.83	0.82	7943984	8.10	7.07	6.94	7.13
KATNAL1	katanin p60 su	chr13:296747	0.23	1.31	cg02788021	TSS1500	chr13:308808	S_Shore	0.26	0.49	0.53	0.53	7970844	7.71	9.02	9.14	8.75
SLC9A9	solute carrier f	chr3:1444667	-0.54	1.02	cg03804400	Body			0.91	0.37	0.26	0.25	8091260	6.65	7.66	6.48	6.99
MBNL1	muscleblind-lik	chr3:1534685	0.36	0.83	cg09219813	TSS200;TSS200;5'UTR;TSS200;5'UTR;TSS2			0.43	0.79	0.82	0.81	8083429	10.48	11.30	11.42	11.36
C10orf28	chromosome 1	chr10:998844	-0.68	0.85	cg03302822	5'UTR			0.84	0.16	0.12	0.11	7929719	7.87	8.72	9.06	8.74
SLC12A6	solute carrier f	chr15:323094	-0.31	0.87	cg01053714	TSS1500	chr15:346295	S_Shore	0.85	0.54	0.38	0.33	7987192	8.67	9.55	9.54	9.40
PDGFC	platelet derive	chr4:1579022	-0.46	-1.86	cg18933943	Body			0.87	0.4	0.33	0.3	8103399	7.98	6.13	5.44	5.80
DAZAP2	DAZ associate	chr12:499188	0.21	0.79	cg24637417	3'UTR;3'UTR;3	chr12:516324	S_Shelf	0.62	0.83	0.84	0.83	7955464	9.76	10.56	10.71	10.83
MAP1LC3B	microtubule-as	chr16:859829	-0.21	1.02	ch.16.2068605	3'UTR	chr16:874413	N_Shelf	0.34	0.13	0.12	0.07	7997740	7.46	8.47	8.29	8.69
EFHA1	EF-hand doma	chr13:209648	0.20	0.59	cg22280671	Body			0.57	0.77	0.77	0.81	7970546	7.92	8.51	8.61	8.52
PRKAA1	protein kinase,	chr5:4079523	0.21	0.74	cg13345558	Body;Body	chr5:4079765	N_Shore	0.61	0.82	0.82	0.82	8111796	8.05	8.79	8.55	8.71
HLA-DMB	major histocon	chr6_qbl_hap2	0.42	0.61	cg10453850	Body			0.35	0.77	0.82	0.78	8180078	8.69	9.30	9.71	10.40
PHKB	phosphorylase	chr16:460527	-0.21	0.83	cg03720617	Body;Body			0.35	0.14	0.14	0.13	7995382	8.59	9.42	9.36	9.40
ARPP-21	cyclic AMP-reg	chr3:3565608	-0.51	2.97	cg17936572	5'UTR			0.71	0.21	0.15	0.15	8078497	6.34	9.30	9.46	8.39
RAB8B	RAB8B, memb	chr15:612687	0.33	0.94	cg07068735	Body			0.26	0.59	0.66	0.62	7984112	8.71	9.65	8.99	9.37
CD22	CD22 molecule	chr19:405119	-0.73	2.31	cg12126686	5'UTR			0.88	0.15	0.12	0.11	8027837	7.49	9.80	10.04	10.60
ALOX5	arachidonate 5	chr10:451896	-0.37	0.61	cg09832911	Body	chr10:459228	S_Shore	0.61	0.24	0.22	0.18	7927215	7.24	7.86	8.59	9.60
FAIM3	Fas apoptotic i	chr1:2051442	-0.22	1.65	cg22945467	TSS1500;TSS1500;TSS1500			0.38	0.16	0.17	0.15	7923917	7.30	8.94	9.49	10.58
PAK2	p21 protein (C	chr3:1979513	0.20	1.03	cg12930392	5'UTR			0.41	0.61	0.64	0.65	8084963	8.78	9.82	9.99	9.89
SAPS3	SAPS domain f	chr11:679847	-0.28	0.60	cg10133100	5'UTR;5'UTR;5'UTR;5'UTR;5'UTR;5'UTR			0.69	0.42	0.3	0.3	7942032	9.50	10.10	10.15	9.91
CORO2B	coronin, actin	chr15:666586	-0.74	0.87	cg19905757	Body			0.84	0.11	0.08	0.08	7984475	6.65	7.52	7.59	7.54
KIAA0182	KIAA0182	chr16:842025	-0.54	-0.82	cg02817932	Body;Body	chr16:856841	N_Shore	0.88	0.34	0.31	0.35	7997680	8.60	7.78	8.02	8.09
ZNF608	zinc finger pro	chr5:1240005	-0.42	0.96	cg26696655	Body			0.91	0.49	0.33	0.31	8113761	8.08	9.04	8.89	8.93
ARHGEF3	Rho guanine n	chr3:5673648	0.26	-0.97	cg11229273	Body			0.6	0.87	0.88	0.88	8088247	7.95	6.99	7.74	7.89
SNX29	sorting nexin 2	chr16:120801	-0.50	0.81	cg02910054	Body			0.66	0.16	0.15	0.13	7993281	7.88	8.69	8.64	8.95
EPSTI1	epithelial stron	chr13:423585	-0.24	-0.75	cg03753191	TSS1500;TSS1	chr13:435660	S_Shore	0.38	0.14	0.14	0.12	7971296	7.22	6.47	6.60	7.43
MGC29506	hypothetical p	chr5:1387510	-0.69	1.03	cg13500819	1stExon	chr5:1387277	N_Shelf	0.82	0.14	0.12	0.1	8114511	8.43	9.46	9.56	9.70
LSP1	lymphocyte-sp	chr11:183077	-0.68	-0.84	cg08687540	5'UTR;1stExon	chr11:189203	N_Shore	0.74	0.06	0.07	0.04	7937735	9.32	8.48	8.99	9.01
DTX1	deltex homolo	chr12:111979	-0.49	0.92	cg08447520	Body	chr12:113515	N_Shelf	0.93	0.43	0.17	0.1	7958931	7.64	8.56	9.26	9.62
TBXAS1	thromboxane	chr7:1391245	-0.36	-0.75	cg18568570	Body;Body;Body;Body;Body;Body			0.74	0.37	0.34	0.33	8136557	7.77	7.02	6.65	6.73
PAX5	paired box 5	chr9:3682327	0.64	2.66	cg14317609	Body	chr9:3698598	Island	0.07	0.7	0.85	0.85	8161211	7.90	10.57	11.07	11.07
ARIH1	ariadne homol	chr15:705537	-0.31	0.69	cg15188939	Body			0.86	0.55	0.25	0.28	7984641	9.03	9.72	9.64	9.43
LGALS1	lectin, galactos	chr22:364015	0.25	-0.90	cg07219769	TSS200	chr22:380730	N_Shore	0.44	0.69	0.75	0.68	8072876	9.66	8.76	8.51	8.63
BCL11A	B-cell CLL/lym	chr2:6053180	-0.23	0.59	cg00543073	Body;Body;Bo	chr2:6077659	N_Shelf	0.39	0.16	0.2	0.17	8052399	9.68	10.27	9.47	9.90
BTBD3	BTB (POZ) don	chr20:118194	0.35	0.91	cg20981848	Body;Body			0.39	0.73	0.77	0.72	8060988	7.75	8.67	8.96	8.16
ITPR1	inositol 1,4,5-t	chr3:4510136-	0.27	0.96	cg21407899	Body;Body;Body			0.31	0.58	0.58	0.57	8077376	8.31	9.27	8.18	8.97
ETS1	v-ets erythrobl	chr11:127833	-0.25	1.35	cg24065451	Body	chr11:128419	Island	0.92	0.67	0.69	0.65	7952601	8.40	9.75	10.77	10.94
AK5	adenylate kina	chr1:7752025	-0.39	1.30	cg10386431	Body;Body			0.58	0.18	0.17	0.18	7902452	6.10	7.40	6.27	5.60
CSF3R	colony stimula	chr1:3670423	0.28	-1.70	cg07285167	TSS1500;TSS1500;TSS1500;TSS1500			0.49	0.76	0.8	0.79	7914950	8.13	6.43	6.26	6.30
WASF2	WAS protein fa	chr1:2760331	-0.56	0.73	cg09588020	5'UTR			0.75	0.19	0.16	0.15	7914094	8.60	9.33	9.34	9.03
VAT1	vesicle amine	chr17:384201	0.24	-0.61	cg25070639	Body	chr17:411738	N_Shelf	0.47	0.71	0.71	0.71	8015759	8.11	7.50	7.72	7.68
OAS2	2'-5'-oligoaden	chr12:111900	-0.37	0.94	cg19371652	TSS1500;TSS1500;TSS1500			0.85	0.48	0.26	0.17	7958913	6.79	7.73	7.56	7.79
PPP3CC	protein phosph	chr8:2235454	-0.34	1.86	cg20910008	Body	chr8:2229811	S_Shelf	0.64	0.31	0.15	0.12	8145136	7.71	9.57	8.96	9.38
HK2	hexokinase 2	chr2:7491329	-0.25	-0.75	cg16626875	Body			0.92	0.67	0.55	0.57	8042942	8.48	7.73	7.39	7.60
GAPVD1	GTPase activat	chr9:1270639	-0.36	0.73	ch.9.2043201	Body			0.48	0.12	0.1	0.08	8157858	8.10	8.83	8.70	8.75
SEMA6A	sema domain,	chr5:1158071	-0.63	1.28	cg13364558	5'UTR	chr5:1159083	N_Shelf	0.8	0.16	0.15	0.14	8113666	6.97	8.25	6.28	6.28
APLP2	amyloid beta (	chr11:129445	-0.39	-1.22	cg23729763	Body;Body;Bo	chr11:129993	N_Shore	0.8	0.4	0.14	0.12	7945182	10.50	9.28	10.26	10.19
ADHFE1	alcohol dehydr	chr8:6750728	-0.35	-0.63	cg20040765	Body			0.54	0.2	0.18	0.15	8146687	5.81	5.18	5.26	5.32
HHIP	hedgehog inte	chr4:1457866	-0.54	0.81	cg10203922	TSS1500	chr4:1455662	N_Shore	0.65	0.11	0.11	0.07	8097628	6.67	7.48	6.90	6.77
C7orf23	chromosome 7	chr7:8666341	-0.33	1.98	cg06824394	Body	chr7:8684891	N_Shelf	0.53	0.2	0.1	0.09	8140730	7.56	9.54	9.95	10.02
FNDC3B	fibronectin typ	chr3:1732401	0.21	-1.77	cg14016236	5'UTR;5'UTR			0.26	0.47	0.48	0.49	8083901	8.56	6.78	6.50	6.66
KIAA1949	KIAA1949	chr6:3075211	-0.47	0.61	cg00010853	Body;1stExon	chr6:3065439	N_Shore	0.78	0.3	0.19	0.19	8124798	8.88	9.48	9.16	9.08
TMOD2	tropomodulin	chr15:498310	0.30	0.65	cg07772516	3'UTR;3'UTR			0.43	0.74	0.75	0.78	7983734	6.77	7.42	6.58	7.03
ERG	v-ets erythrobl	chr21:386610	-0.61	1.33	cg27471246	Body;Body;Body;Body			0.76	0.15	0.15	0.13	8070297	9.04	10.37	6.95	6.73
AKT3	v-akt murine t	chr1:2417181	-0.70	0.68	cg13396060	Body;Body			0.81	0.11	0.11	0.09	7925531	8.51	9.19	9.36	9.66
9-Sep	septin 9	chr17:727891	-0.55	0.69	cg00871371	5'UTR;Body;B	chr17:753686	S_Shore	0.64	0.09	0.1	0.08	8010161	8.59	9.28	8.87	8.71
PPM1A	protein phosph	chr14:597822	0.24	0.86	cg04964845	3'UTR;3'UTR			0.43	0.67	0.7	0.73	7974781	7.28	8.14	8.27	8.19
AUTS2	autism suscept	chr7:6870135	0.23	0.67	cg21557473	Body;Body;Body			0.32	0.56	0.62	0.62	8133233	7.72	8.39	8.14	7.76
ZSCAN16	zinc finger and	chr6:2820031	-0.41	0.98	cg22896917	Body			0.58	0.17	0.18	0.14	8117640	6.38	7.36	7.58	7.33
GNG7	guanine nucle	chr19:246221	-0.30	1.32	cg19653589	5'UTR	chr19:261393	S_Shore	0.44	0.14	0.14	0.13	8032509	8.52	9.83	9.78	9.46
TSPAN14	tetraspanin 14	chr10:822039	0.25	1.26	cg08560387	5'UTR;5'UTR			0.65	0.9	0.92	0.92	7928705	8.14	9.40	8.84	8.52
BEST3	bestrophin 3	chr12:683236	-0.21	1.80	cg07618900	TSS200			0.81	0.6	0.44	0.44	7964852	5.16	6.96	8.85	7.57
C3orf37	chromosome 3	chr3:1304803	-0.69	1.66	cg25821399	TSS1500;TSS1	chr3:1289973	N_Shore	0.82	0.13	0.1	0.09	8082504	8.28	9.95	10.18	10.12
PPP1CA	protein phosph	chr11:669222	-0.22	0.69	cg08114533	Body;Body;Bo	chr11:671686	N_Shore	0.41	0.18	0.21	0.17	7949765	9.82	10.51	10.82	10.13
PCDH9	protocadherin	chr13:657749	-0.37	1.52	cg10707081	Body;Body			0.58	0.21	0.18	0.14	7971922	5.76	7.29	8.70	8.91
P4HA2	prolyl 4-hydro	chr5:1315554	-0.30	1.70	cg11293275	Body;Body;Body;Body;Body			0.57	0.27	0.27	0.23	8113981	6.88	8.57	9.52	8.18
SLC44A2	solute carrier f	chr19:105741	0.30	1.33	cg06943912	Body	chr19:107130	S_Shelf	0.3	0.6	0.65	0.62	8025672	8.51	9.84	10.30	10.36
CD53	CD53 molecule	chr1:1112153	-0.60	0.69	cg10516886	TSS1500;5'UTR			0.73	0.14	0.13	0.12	7903893	10.15	10.84	10.81	11.34
C22orf9	chromosome 2	chr22:439667	0.20	-0.64	cg20026613	Body;TSS1500			0.64	0.83	0.89	0.84	8076690	8.66	8.02	7.85	7.98
AZU1	azurocidin 1	chr19:776097-	0.40	-1.07	cg10752406	TSS200			0.48	0.87	0.93	0.89	8024038	8.34	7.28	7.20	7.35
DPYSL2	dihydropyrimid	chr8:2649132	-0.76	0.84	cg19610383	Body			0.91	0.15	0.17	0.17	8145470	9.52	10.36	10.17	8.90
SPIN1	spindlin 1	chr9:9019311	-0.73	0.59	cg13554018	3'UTR			0.87	0.14	0.09	0.08	8156263	9.66	10.25	10.21	9.51
ZNF217	zinc finger pro	chr20:516170	0.27	0.72	cg20979153	TSS200	chr20:521980	S_Shore	0.55	0.83	0.84	0.82	8067113	8.61	9.33	9.45	9.45
LRIG1	leucine-rich re	chr3:6651183	-0.61	1.01	cg00225902	Body			0.73	0.13	0.17	0.1	8088642	7.04	8.06	7.63	7.20
SPTBN1	spectrin, beta,	chr2:5453695	-0.35	0.82	cg08449164	TSS1500;Body	chr2:5478502	N_Shore	0.74	0.4	0.3	0.25	8041995	9.84	10.66	11.26	10.62
HIF1A	hypoxia induci	chr14:612319	-0.51	1.03	cg23174662	Body;Body	chr14:621618	S_Shelf	0.72	0.21	0.17	0.16	7974851	8.87	9.90	9.76	9.46
BANK1	B-cell scaffold	chr4:1029309	-0.41	2.34	cg21997986	Body;Body;5'UTR			0.87	0.46	0.2	0.21	8096617	7.34	9.69	8.57	9.61
FYB	FYN binding pr	chr5:3914111	0.33	-1.33	cg27606341	1stExon;5'UTR;5'UTR;1stExon			0.42	0.75	0.78	0.76	8111739	8.00	6.67	5.84	6.18
RAG2	recombination	chr11:365700	0.48	3.22	cg21671607	5'UTR;TSS200			0.36	0.84	0.87	0.86	7947548	6.73	9.95	9.98	7.25
FMN1	formin 1	chr15:308461	-0.51	-0.60	cg25493948	Body			0.77	0.26	0.24	0.21	7987145	6.42	5.81	6.06	6.65
FBXL4	F-box and leuc	chr6:9942805	-0.68	1.56	cg12604490	Body			0.84	0.16	0.15	0.13	8128356	7.36	8.92	8.61	8.30
SKAP1	src kinase ass	chr17:435658	-0.50	-0.69	cg05106502	Body;Body	chr17:465073	N_Shore	0.69	0.2	0.22	0.21	8016414	6.08	5.39	5.66	5.98
PRKCQ	protein kinase	chr10:650911	-0.22	-0.65	cg01389728	5'UTR	chr10:662190	N_Shore	0.55	0.33	0.3	0.3	7931930	8.36	7.71	7.10	6.45
ACSL5	acyl-CoA synth	chr10:114123	-0.52	-0.81	cg16066219	TSS1500;1stExon;5'UTR;5'UTR			0.68	0.16	0.14	0.1	7930498	8.16	7.35	7.89	8.37
FAM49A	family with sec	chr2:1659420	-0.51	1.06	cg17981790	5'UTR			0.89	0.38	0.23	0.21	8050427	6.82	7.89	7.32	8.06
MS4A1	membrane-spa	chr11:599798	-0.69	2.44	cg06806711	1stExon;1stExon;5'UTR;5'UTR			0.81	0.12	0.1	0.08	7940287	7.12	9.56	9.67	11.77

Supplemental Table 3b. Statistics of the 60 genes that had concurrent methylation and expression changes from S2 to S3.

								Methylation						Expression			
GeneSymbol	**GeneTitle**	**ChrLoc**	**Methylation.S3vsS2**	**Expression.S3vsS2**	**IlmnID**	**UCSC_RefGene_Group**	**UCSC_CpG_Islands_Name**	**Relation_to_UCSC_CpG_Island**	**Mean.S1**	**Mean.S2**	**Mean.S3**	**Mean.S4**	**ProbeSetID**	**Mean.S1**	**Mean.S2**	**Mean.S3**	**Mean.S4**
CD84	CD84 molecule	chr1:15877751	-0.4	1.17	cg13188263	3'UTR			0.94	0.83	0.42	0.18	7921637	7.73	6.68	7.85	8.09
FAM65B	family with sec	chr6:24912492	-0.3	0.76	cg13708298	5'UTR			0.54	0.66	0.35	0.38	8124280	8.00	8.72	9.48	9.84
ALOX5AP	arachidonate 5	chr13:3020764	-0.22	-0.79	cg08529529	1stExon			0.74	0.44	0.22	0.19	7968344	8.36	9.33	8.54	9.84
IGF2R	insulin-like gro	chr6:16031012	-0.27	1.29	cg09555124	Body			0.85	0.68	0.41	0.23	8123181	6.88	7.51	8.80	8.61
ZNF423	zinc finger prot	chr16:4808202	-0.23	-0.72	cg03087880	Body	chr16:4966957	N_Shelf	0.92	0.65	0.43	0.45	8001337	6.80	7.56	6.84	6.84
GCET2	germinal cente	chr3:11332237	-0.45	1.75	cg12663553	TSS200;TSS200			0.81	0.68	0.23	0.21	8089478	6.43	8.10	9.84	9.13
LTA	lymphotoxin al	chr6_qbl_hap2	-0.24	-0.97	cg14441276	TSS1500;TSS200			0.88	0.41	0.18	0.12	8179258	7.71	8.53	7.56	8.00
BTG2	BTG family, me	chr1:20154124	-0.2	0.68	cg01798157	3'UTR	chr1:20327430	S_Shore	0.8	0.67	0.47	0.43	7908917	8.78	10.06	10.74	10.74
TCL6	T-cell leukemia	chr14:9518726	-0.24	1.71	cg07036035	Body			0.93	0.86	0.62	0.49	7976523	6.19	6.96	8.67	8.56
SERINC5	serine incorpor	chr5:79442806	-0.31	-1.08	cg14711743	Body			0.79	0.88	0.57	0.56	8112865	7.57	8.54	7.46	6.90
FCRLA	Fc receptor-like	chr1:15994338	-0.47	2.61	cg04888234	TSS1500			0.73	0.61	0.15	0.12	7906786	6.59	7.58	10.20	11.12
TCF7L2	transcription fa	chr10:1147002	-0.22	-2.47	cg03339956	Body;Body;Body;Body;Body;Body			0.72	0.64	0.41	0.39	7930537	8.98	9.92	7.44	7.32
PDIA5	protein disulfid	chr3:12426859	-0.36	0.70	cg27383859	Body;Body			0.92	0.65	0.28	0.15	8082133	7.85	7.06	7.76	7.59
ZMIZ1	zinc finger, MIZ	chr10:8049879	-0.21	-0.73	cg02145310	5'UTR			0.84	0.4	0.19	0.17	7928558	8.46	9.05	8.32	7.85
IKZF3	IKAROS family	chr17:3517471	-0.43	2.56	cg08441850	Body;Body;Body;Body;Body;Body			0.74	0.64	0.21	0.19	8014891	6.20	7.12	9.67	10.14
ARHGEF3	Rho guanine nu	chr3:56736486	-0.22	0.75	cg25799109	5'UTR;5'UTR			0.86	0.86	0.64	0.66	8088247	7.95	6.99	7.74	7.89
DTX1	deltex homolog	chr12:1119798	-0.27	0.70	cg08447520	Body	chr12:1135151	N_Shelf	0.93	0.43	0.17	0.1	7958931	7.64	8.56	9.26	9.62
PION	pigeon homolo	chr7:76796780	-0.25	0.73	cg19348272	Body	chr7:77044840	N_Shore	0.94	0.76	0.51	0.46	8140478	6.42	8.37	9.10	9.51
APLP2	amyloid beta (A	chr11:1294450	-0.31	0.99	cg25354657	Body;Body;Bod	chr11:1299935	N_Shelf	0.83	0.49	0.19	0.15	7945182	10.50	9.28	10.26	10.19
PPFIBP1	PTPRF interacti	chr12:2756831	-0.27	-0.92	cg20095669	5'UTR;5'UTR			0.92	0.86	0.6	0.61	7954559	7.56	8.76	7.84	7.34
MPEG1	macrophage ex	chr11:5873471	-0.26	2.04	cg26340740	1stExon;5'UTR			0.56	0.63	0.36	0.19	7948364	8.36	7.09	9.13	9.63
BAALC	brain and acute	chr8:10422209	-0.26	-0.82	cg01706991	Body;Body			0.92	0.88	0.63	0.61	8147756	8.25	7.18	6.36	6.56
SPTBN1	spectrin, beta,	chr2:54536958	-0.39	0.60	cg10854528	Body;Body	chr2:54856098	N_Shore	0.93	0.89	0.5	0.31	8041995	9.84	10.66	11.26	10.62
BANK1	B-cell scaffold	chr4:10293091	-0.26	-1.11	cg21997986	Body;Body;5'UTR			0.87	0.46	0.2	0.21	8096617	7.34	9.69	8.57	9.61
GRN	granulin	chr17:3977801	-0.38	0.76	cg23570245	5'UTR			0.76	0.81	0.43	0.23	8007620	8.70	7.91	8.67	9.07
TCL1A	T-cell leukemia	chr14:9524605	-0.22	3.27	cg14127336	1stExon;1stExo	chr14:9618025	Island	0.87	0.8	0.57	0.4	7981183	6.52	8.42	11.69	11.97
LDB2	LIM domain bin	chr4:16112262	-0.26	-0.71	cg07691684	Body;Body			0.9	0.88	0.62	0.58	8099524	7.56	7.50	6.79	6.88
FGD2	FYVE, RhoGEF	chr6:37081400	-0.23	0.83	cg23185774	TSS1500			0.93	0.55	0.32	0.29	8119132	7.45	7.08	7.91	8.70
MTSS1	metastasis sup	chr8:12563221	-0.31	1.76	cg15235922	Body			0.93	0.5	0.19	0.1	8152764	7.66	7.45	9.21	10.44
PTPRJ	protein tyrosin	chr11:4795868	-0.59	1.05	cg14997711	Body;Body			0.81	0.73	0.14	0.09	7939839	7.52	7.45	8.50	10.27
RHOBTB1	Rho-related BT	chr10:6229920	-0.3	0.85	cg09207077	Body;Body	chr10:6270330	S_Shelf	0.93	0.84	0.54	0.33	7933821	7.16	6.70	7.54	7.35
TNFRSF1A	tumor necrosis	chr12:6308184	-0.24	-1.55	cg10589094	TSS1500			0.9	0.67	0.43	0.48	7960518	9.20	8.71	7.17	7.01
FOXP1	forkhead box P	chr3:71087426	-0.22	0.60	cg19776833	Body			0.95	0.92	0.7	0.44	8088776	9.00	9.26	9.86	9.92
VAV3	vav 3 guanine	chr1:10791530	-0.53	-1.14	cg12047260	Body			0.87	0.86	0.32	0.25	7918157	9.36	9.84	8.70	9.32
CD55	CD55 molecule	chr1:20556147	-0.27	0.75	cg23633330	Body;Body			0.69	0.68	0.41	0.23	7909332	9.02	9.40	10.15	10.76
CDC25B	cell division cy	chr20:3724386	-0.44	1.22	cg02737268	Body;Body;Bod	chr20:3776198	S_Shelf	0.94	0.74	0.29	0.07	8060675	7.60	8.10	9.32	9.13
SORL1	sortilin-related	chr11:1208281	-0.38	-1.49	cg05921138	Body			0.84	0.86	0.47	0.24	7944667	8.95	8.68	7.18	6.83
JARID2	jumonji, AT ric	chr6:15354468	-0.28	0.61	cg26797722	Body			0.91	0.81	0.53	0.51	8116998	8.94	8.53	9.14	9.14
HEY2	hairy/enhancer	chr6:12611050	-0.24	1.05	cg22124590	3'UTR	chr6:12608033	S_Shore	0.81	0.57	0.34	0.31	8121850	6.44	6.30	7.35	7.16
RHOH	ras homolog ge	chr4:39874965	-0.4	1.40	cg26163153	TSS1500			0.9	0.86	0.46	0.36	8094743	8.71	9.16	10.56	10.17
FCRL1	Fc receptor-like	chr1:15603095	-0.22	2.01	cg08933467	Body;Body;Body			0.83	0.61	0.39	0.19	7921319	7.04	7.60	9.61	11.16
SYK	spleen tyrosine	chr9:92603890	-0.38	0.85	cg14054883	Body;Body;Body;Body			0.89	0.89	0.51	0.48	8156321	8.92	9.46	10.31	10.30
ROR1	receptor tyrosi	chr1:64012278	-0.26	1.86	cg06743782	Body;Body			0.85	0.87	0.61	0.63	7901969	6.79	7.15	9.00	8.16
CD180	CD180 molecul	chr5:66513872	-0.2	1.61	cg19919989	1stExon			0.87	0.7	0.5	0.47	8112428	7.67	7.57	9.18	10.46
TGFBR2	transforming g	chr3:30622998	-0.35	0.75	cg05450916	Body;Body			0.85	0.74	0.39	0.34	8078350	8.21	8.62	9.37	9.73
COBL	cordon-bleu ho	chr7:51051404	-0.33	-0.60	cg10765387	Body			0.83	0.52	0.2	0.18	8139680	6.59	7.06	6.46	7.00
NSMCE1	non-SMC elem	chr16:2714381	-0.25	0.91	cg02115302	Body			0.93	0.88	0.63	0.46	8000413	8.92	8.86	9.77	9.42
LCP2	lymphocyte cyt	chr5:16960766	-0.23	-1.61	cg02676052	TSS1500			0.94	0.82	0.6	0.58	8115734	9.42	9.18	7.57	7.70
TNFRSF17	tumor necrosis	chr16:1196646	-0.42	3.60	cg16177830	1stExon;5'UTR			0.83	0.76	0.33	0.14	7993267	4.93	5.19	8.80	7.52
GALNT2	UDP-N-acetyl-a	chr1:22826957	-0.2	-0.59	cg17930505	Body			0.77	0.46	0.26	0.24	7910427	8.78	9.19	8.60	8.20
AEBP1	AE binding pro	chr7:44110485	-0.22	0.93	cg01399219	Body			0.5	0.55	0.33	0.24	8132557	8.86	8.92	9.85	10.00
GAS7	growth arrest-s	chr17:9754651	-0.34	0.98	cg02605292	Body;Body			0.89	0.64	0.3	0.22	8012605	7.56	7.56	8.54	7.71
SPIB	Spi-B transcrip	chr19:5561402	-0.21	1.18	cg26522743	TSS1500			0.51	0.48	0.27	0.15	8030671	7.30	7.28	8.45	8.95
PIK3C2B	phosphoinositi	chr1:20265837	-0.27	0.70	cg26064794	Body			0.27	0.38	0.11	0.08	7923662	7.33	7.73	8.43	9.16
CARD11	caspase recruit	chr7:2912302-	-0.59	0.82	cg17768768	Body	chr7:2946236-	S_Shore	0.95	0.72	0.13	0.03	8137874	7.93	7.57	8.39	9.24
BLK	B lymphoid tyr	chr8:11388919	-0.35	0.62	cg10147394	TSS1500			0.9	0.52	0.16	0.14	8144625	6.84	7.21	7.83	8.15
IGF1R	insulin-like gro	chr15:9701028	-0.32	-0.64	cg03795574	Body			0.79	0.57	0.26	0.22	7986359	8.40	8.40	7.75	7.42
DGKD	diacylglycerol k	chr2:23392789	-0.33	0.69	cg25107522	Body;Body			0.89	0.68	0.35	0.34	8049317	7.50	7.96	8.65	9.17
CD19	CD19 molecule	chr16:2885076	-0.27	0.66	cg14102807	Body			0.92	0.56	0.3	0.25	7994487	7.54	8.06	8.72	9.07
ZFP106	zinc finger prot	chr15:4049231	-0.22	0.72	cg03402235	1stExon			0.92	0.81	0.59	0.34	7987892	8.42	8.72	9.44	9.64

Supplemental Table 3c. Statistics of the 7 genes that had concurrent methylation and expression changes from S3 to S4.

								Methylation							Expression		
GeneSymbol	**GeneTitle**	**ChrLoc**	**Methylation .S4vsS3**	**Expression .S4vsS3**	**IlmnID**	**UCSC_RefGene_Group**	**UCSC_CpG_Islands_Name**	**Relation_to_UCSC_CpG_Island**	**Mean.S1**	**Mean.S2**	**Mean.S3**	**Mean.S4**	**ProbeSetID**	**Mean.S1**	**Mean.S2**	**Mean.S3**	**Mean.S4**
BTLA	B and T lymph	chr3:1136674	-0.34	2.32	cg24157392	Body;Body			0.79	0.86	0.67	0.33	8089519	7.29	6.60	7.73	10.04
MCOLN2	mucolipin 2	chr1:8516385	-0.22	1.34	cg02621376	Body	chr1:8546258	N_Shore	0.81	0.84	0.5	0.27	7917283	6.64	5.88	6.26	7.61
ADARB1	adenosine dea	chr21:453189	-0.2	0.89	cg19810954	5'UTR;5'UTR;5	chr21:464941	S_Shore	0.54	0.77	0.71	0.52	8069178	7.31	6.83	9.17	10.05
CARD11	caspase recrui	chr7:2912302-	-0.23	0.85	cg16586807	Body	chr7:2946236-	S_Shore	0.96	0.85	0.37	0.14	8137874	7.93	7.57	8.39	9.24
CTPS	CTP synthase	chr1:4121759	-0.26	-0.68	cg06083001	3'UTR			0.82	0.86	0.78	0.52	7900510	9.53	9.91	9.88	9.20
CLEC4C	C-type lectin d	chr12:777327	-0.22	0.82	cg22194129	5'UTR;5'UTR			0.85	0.86	0.61	0.38	7960832	6.74	6.20	6.35	7.17
GLO1	glyoxalase I	chr6:3875163	-0.28	-0.79	cg26053840	3'UTR			0.89	0.91	0.7	0.42	8126135	9.28	9.83	10.26	9.47

Supplemental Table 4: Genes in which expression changes were delayed from methylation changes

CpG	chrom	position	Gene	Methylation change	Expression change
cg00226923	chr6	36972027	*FGD2*	de-DMR from S1 to S2	Upregulated DEG from S2 to S3
cg01468567	chr19	49843922	*TEAD2*	de-DMR from S1 to S2	Upregulated DEG from S2 to S3
cg01758575	chr16	28943288	*CD19*	de-DMR from S1 to S2	Upregulated DEG from S2 to S3
cg01801603	chr8	123795433	*ZHX2*	de-DMR from S1 to S2	Upregulated DEG from S2 to S3
cg01883759	chr7	28220576	*JAZF1*	de-DMR from S1 to S2	Upregulated DEG from S2 to S3
cg02368508	chr16	12060182	*TNFRSF17*	de-DMR from S1 to S2	Upregulated DEG from S2 to S3
cg02585724	chr15	81116461	*KIAA1199*	de-DMR from S1 to S2	Upregulated DEG from S2 to S3
cg02903589	chr6	18215340	*KDM1B*	de-DMR from S1 to S2	Upregulated DEG from S2 to S3
cg03220363	chr8	134115661	*TG*	de-DMR from S1 to S2	Upregulated DEG from S2 to S3
cg04499011	chr6	36972127	*FGD2*	de-DMR from S1 to S2	Upregulated DEG from S2 to S3
cg04515608	chr11	48129067	*PTPRJ*	de-DMR from S1 to S2	Upregulated DEG from S2 to S3
cg04728789	chr22	38711154	*CSNK1E*	de-DMR from S1 to S2	Upregulated DEG from S2 to S3
cg04856396	chr17	3589140	*P2RX5*	de-DMR from S1 to S2	Upregulated DEG from S2 to S3
cg05234415	chr19	38743744	*PPP1R14A*	de-DMR from S1 to S2	Upregulated DEG from S2 to S3
cg05433111	chr16	28943232	*CD19*	de-DMR from S1 to S2	Upregulated DEG from S2 to S3
cg06323049	chr16	28943094	*CD19*	de-DMR from S1 to S2	Upregulated DEG from S2 to S3
cg06510261	chr3	111852227	*GCET2*	de-DMR from S1 to S2	Upregulated DEG from S2 to S3
cg07597976	chr16	28943019	*CD19*	de-DMR from S1 to S2	Upregulated DEG from S2 to S3
cg07613391	chr3	30708746	*TGFBR2*	de-DMR from S1 to S2	Upregulated DEG from S2 to S3
cg07618900	chr12	70093350	*BEST3*	de-DMR from S1 to S2	Upregulated DEG from S2 to S3
cg08449164	chr2	54784402	*SPTBN1*	de-DMR from S1 to S2	Upregulated DEG from S2 to S3
cg08818610	chr6	24910720	*FAM65B*	de-DMR from S1 to S2	Upregulated DEG from S2 to S3
cg09299082	chr17	45286354	*MYL4*	de-DMR from S1 to S2	Upregulated DEG from S2 to S3
cg09832911	chr10	45923678	*ALOX5*	de-DMR from S1 to S2	Upregulated DEG from S2 to S3
cg10274108	chr4	38082931	*TBC1D1*	de-DMR from S1 to S2	Upregulated DEG from S2 to S3
cg10397389	chr4	100738011	*DAPP1*	de-DMR from S1 to S2	Upregulated DEG from S2 to S3
cg10517535	chr17	9929698	*GAS7*	de-DMR from S1 to S2	Upregulated DEG from S2 to S3
cg10707081	chr13	67721697	*PCDH9*	de-DMR from S1 to S2	Upregulated DEG from S2 to S3
cg11293275	chr5	131543977	*P4HA2*	de-DMR from S1 to S2	Upregulated DEG from S2 to S3
cg12810837	chr12	9822287	*CLEC2D*	de-DMR from S1 to S2	Upregulated DEG from S2 to S3
cg13409077	chr9	35618528	*CD72*	de-DMR from S1 to S2	Upregulated DEG from S2 to S3
cg13559409	chr9	107545269	*ABCA1*	de-DMR from S1 to S2	Upregulated DEG from S2 to S3
cg14973892	chr13	46944143	*KIAA0226L*	de-DMR from S1 to S2	Upregulated DEG from S2 to S3
cg15706621	chr2	54861447	*SPTBN1*	de-DMR from S1 to S2	Upregulated DEG from S2 to S3
cg16111231	chr6	160399700	*IGF2R*	de-DMR from S1 to S2	Upregulated DEG from S2 to S3
cg16495448	chr7	3019260	*CARD11*	de-DMR from S1 to S2	Upregulated DEG from S2 to S3
cg18967835	chr13	99907350	*GPR18*	de-DMR from S1 to S2	Upregulated DEG from S2 to S3
cg21195376	chr1	204449827	*PIK3C2B*	de-DMR from S1 to S2	Upregulated DEG from S2 to S3
cg21614638	chr4	100737821	*DAPP1*	de-DMR from S1 to S2	Upregulated DEG from S2 to S3
cg22256853	chr3	111840865	*GCET2*	de-DMR from S1 to S2	Upregulated DEG from S2 to S3
cg22826986	chr8	11351507	*BLK*	de-DMR from S1 to S2	Upregulated DEG from S2 to S3
cg22888848	chr2	222320536	*EPHA4*	de-DMR from S1 to S2	Upregulated DEG from S2 to S3
cg24856456	chr8	56923352	*LYN*	de-DMR from S1 to S2	Upregulated DEG from S2 to S3
cg24960799	chr6	24908812	*FAM65B*	de-DMR from S1 to S2	Upregulated DEG from S2 to S3
cg25115537	chr8	123801352	*ZHX2*	de-DMR from S1 to S2	Upregulated DEG from S2 to S3
cg25821783	chr17	63746944	*CEP112*	de-DMR from S1 to S2	Upregulated DEG from S2 to S3
cg26291600	chr10	45923705	*ALOX5*	de-DMR from S1 to S2	Upregulated DEG from S2 to S3
cg27565966	chr16	28943198	*CD19*	de-DMR from S1 to S2	Upregulated DEG from S2 to S3
cg00129811	chr6	116726398	*DSE*	de-DMR from S1 to S2	Upregulated DEG from S3 to S4
cg00226923	chr6	36972027	*FGD2*	de-DMR from S1 to S2	Upregulated DEG from S3 to S4
cg01468567	chr19	49843922	*TEAD2*	de-DMR from S1 to S2	Upregulated DEG from S3 to S4
cg02212836	chr6	6589075	*LY86*	de-DMR from S1 to S2	Upregulated DEG from S3 to S4
cg03220363	chr8	134115661	*TG*	de-DMR from S1 to S2	Upregulated DEG from S3 to S4
cg03349397	chr6	6588693	*LY86*	de-DMR from S1 to S2	Upregulated DEG from S3 to S4

cg03753191	chr13	43566902	*EPSTI1*	de-DMR from S1 to S2	Upregulated DEG from S3 to S4
cg04499011	chr6	36972127	*FGD2*	de-DMR from S1 to S2	Upregulated DEG from S3 to S4
cg04515608	chr11	48129067	*PTPRJ*	de-DMR from S1 to S2	Upregulated DEG from S3 to S4
cg04599946	chr16	85936480	*IRF8*	de-DMR from S1 to S2	Upregulated DEG from S3 to S4
cg04856396	chr17	3589140	*P2RX5*	de-DMR from S1 to S2	Upregulated DEG from S3 to S4
cg05021589	chr6	6588931	*LY86*	de-DMR from S1 to S2	Upregulated DEG from S3 to S4
cg05033369	chr1	161676469	*FCRLA*	de-DMR from S1 to S2	Upregulated DEG from S3 to S4
cg05257202	chr13	99934873	*UBAC2*	de-DMR from S1 to S2	Upregulated DEG from S3 to S4
cg06806711	chr11	60223291	*MS4A1*	de-DMR from S1 to S2	Upregulated DEG from S3 to S4
cg06829760	chr2	16845412	*FAM49A*	de-DMR from S1 to S2	Upregulated DEG from S3 to S4
cg07623567	chr6	32909523	*HLA-DMB*	de-DMR from S1 to S2	Upregulated DEG from S3 to S4
cg07978738	chr10	116298339	*ABLIM1*	de-DMR from S1 to S2	Upregulated DEG from S3 to S4
cg08174715	chr19	43012255	*CEACAM1*	de-DMR from S1 to S2	Upregulated DEG from S3 to S4
cg08529529	chr13	31309799	*ALOX5AP*	de-DMR from S1 to S2	Upregulated DEG from S3 to S4
cg08933467	chr1	157776690	*FCRL1*	de-DMR from S1 to S2	Upregulated DEG from S3 to S4
cg09100014	chr16	85937496	*IRF8*	de-DMR from S1 to S2	Upregulated DEG from S3 to S4
cg09832911	chr10	45923678	*ALOX5*	de-DMR from S1 to S2	Upregulated DEG from S3 to S4
cg09970481	chr19	42379744	*CD79A*	de-DMR from S1 to S2	Upregulated DEG from S3 to S4
cg10466421	chr21	27010696	*JAM2*	de-DMR from S1 to S2	Upregulated DEG from S3 to S4
cg10853416	chr11	60145275	*MS4A7*	de-DMR from S1 to S2	Upregulated DEG from S3 to S4
cg13066703	chr1	211526705	*TRAF5*	de-DMR from S1 to S2	Upregulated DEG from S3 to S4
cg13125224	chr6	6587445	*LY86*	de-DMR from S1 to S2	Upregulated DEG from S3 to S4
cg13765961	chr11	60223238	*MS4A1*	de-DMR from S1 to S2	Upregulated DEG from S3 to S4
cg15235922	chr8	125678187	*MTSS1*	de-DMR from S1 to S2	Upregulated DEG from S3 to S4
cg15474337	chr19	50848247	*NAPSB*	de-DMR from S1 to S2	Upregulated DEG from S3 to S4
cg15975769	chr3	19521725	*KCNH8*	de-DMR from S1 to S2	Upregulated DEG from S3 to S4
cg16495448	chr7	3019260	*CARD11*	de-DMR from S1 to S2	Upregulated DEG from S3 to S4
cg16705546	chr16	85936666	*IRF8*	de-DMR from S1 to S2	Upregulated DEG from S3 to S4
cg17100176	chr1	207096358	*FAIM3*	de-DMR from S1 to S2	Upregulated DEG from S3 to S4
cg17768768	chr7	2948123	*CARD11*	de-DMR from S1 to S2	Upregulated DEG from S3 to S4
cg17981790	chr2	16807234	*FAM49A*	de-DMR from S1 to S2	Upregulated DEG from S3 to S4
cg18865207	chr1	160765919	*LY9*	de-DMR from S1 to S2	Upregulated DEG from S3 to S4
cg18920397	chr1	160765805	*LY9*	de-DMR from S1 to S2	Upregulated DEG from S3 to S4
cg19190593	chr6	6588737	*LY86*	de-DMR from S1 to S2	Upregulated DEG from S3 to S4
cg19583076	chr19	42381099	*CD79A*	de-DMR from S1 to S2	Upregulated DEG from S3 to S4
cg19825589	chr19	42379710	*CD79A*	de-DMR from S1 to S2	Upregulated DEG from S3 to S4
cg20419542	chr6	116726587	*DSE*	de-DMR from S1 to S2	Upregulated DEG from S3 to S4
cg21195376	chr1	204449827	*PIK3C2B*	de-DMR from S1 to S2	Upregulated DEG from S3 to S4
cg21470947	chr6	32909493	*HLA-DMB*	de-DMR from S1 to S2	Upregulated DEG from S3 to S4
cg21997986	chr4	102745414	*BANK1*	de-DMR from S1 to S2	Upregulated DEG from S3 to S4
cg22518157	chr4	36210723	*ARAP2*	de-DMR from S1 to S2	Upregulated DEG from S3 to S4
cg22610434	chr1	158259914	*CD1C*	de-DMR from S1 to S2	Upregulated DEG from S3 to S4
cg22888848	chr2	222320536	*EPHA4*	de-DMR from S1 to S2	Upregulated DEG from S3 to S4
cg22945467	chr1	207096833	*FAIM3*	de-DMR from S1 to S2	Upregulated DEG from S3 to S4
cg23185774	chr6	36972163	*FGD2*	de-DMR from S1 to S2	Upregulated DEG from S3 to S4
cg23730277	chr4	102734752	*BANK1*	de-DMR from S1 to S2	Upregulated DEG from S3 to S4
cg24703661	chr19	42381258	*CD79A*	de-DMR from S1 to S2	Upregulated DEG from S3 to S4
cg24856456	chr8	56923352	*LYN*	de-DMR from S1 to S2	Upregulated DEG from S3 to S4
cg26291600	chr10	45923705	*ALOX5*	de-DMR from S1 to S2	Upregulated DEG from S3 to S4
cg27208925	chr16	85937106	*IRF8*	de-DMR from S1 to S2	Upregulated DEG from S3 to S4
cg01005605	chr2	60757902	*BCL11A*	*de novo* DMR from S1 to S2	Downregulated DEG from S2 to S3
cg01290568	chr2	113593859	*IL1B*	*de novo* DMR from S1 to S2	Downregulated DEG from S2 to S3
cg02816367	chr6	112081490	*FYN*	*de novo* DMR from S1 to S2	Downregulated DEG from S2 to S3
cg03348161	chr11	59824089	*MS4A3*	*de novo* DMR from S1 to S2	Downregulated DEG from S2 to S3
cg04086531	chr16	49732376	*ZNF423*	*de novo* DMR from S1 to S2	Downregulated DEG from S2 to S3
cg05517541	chr6	112115209	*FYN*	*de novo* DMR from S1 to S2	Downregulated DEG from S2 to S3
cg06192883	chr15	52554171	*MYO5C*	*de novo* DMR from S1 to S2	Downregulated DEG from S2 to S3

cg06399735	chr8	18836280	*PSD3*	*de novo* DMR from S1 to S2	Downregulated DEG from S2 to S3
cg06650246	chr1	206897270	*MAPKAPK2*	*de novo* DMR from S1 to S2	Downregulated DEG from S2 to S3
cg06688763	chr7	92238207	*CDK6*	*de novo* DMR from S1 to S2	Downregulated DEG from S2 to S3
cg07091220	chr4	146752115	*ZNF827*	*de novo* DMR from S1 to S2	Downregulated DEG from S2 to S3
cg07772516	chr15	52107742	*TMOD2*	*de novo* DMR from S1 to S2	Downregulated DEG from S2 to S3
cg08601457	chr6	112115117	*FYN*	*de novo* DMR from S1 to S2	Downregulated DEG from S2 to S3
cg09080522	chr22	44568387	*PARVG*	*de novo* DMR from S1 to S2	Downregulated DEG from S2 to S3
cg09472600	chr1	183537770	*NCF2*	*de novo* DMR from S1 to S2	Downregulated DEG from S2 to S3
cg09824900	chr15	99227735	*IGF1R*	*de novo* DMR from S1 to S2	Downregulated DEG from S2 to S3
cg11091914	chr8	105598224	*LRP12*	*de novo* DMR from S1 to S2	Downregulated DEG from S2 to S3
cg11303988	chr8	19266685	*CSGALNACT1*	*de novo* DMR from S1 to S2	Downregulated DEG from S2 to S3
cg12554857	chr4	95264019	*HPGDS*	*de novo* DMR from S1 to S2	Downregulated DEG from S2 to S3
cg13359998	chr1	230241764	*GALNT2*	*de novo* DMR from S1 to S2	Downregulated DEG from S2 to S3
cg15836722	chr2	113593785	*IL1B*	*de novo* DMR from S1 to S2	Downregulated DEG from S2 to S3
cg17753789	chr10	81026766	*ZMIZ1*	*de novo* DMR from S1 to S2	Downregulated DEG from S2 to S3
cg17854066	chr4	55575932	*KIT*	*de novo* DMR from S1 to S2	Downregulated DEG from S2 to S3
cg20744163	chr10	80999841	*ZMIZ1*	*de novo* DMR from S1 to S2	Downregulated DEG from S2 to S3
cg20909017	chr12	54805345	*ITGA5*	*de novo* DMR from S1 to S2	Downregulated DEG from S2 to S3
cg22328837	chr6	45422120	*RUNX2*	*de novo* DMR from S1 to S2	Downregulated DEG from S2 to S3
cg23261343	chr6	45413792	*RUNX2*	*de novo* DMR from S1 to S2	Downregulated DEG from S2 to S3
cg24168002	chr2	169588344	*CERS6*	*de novo* DMR from S1 to S2	Downregulated DEG from S2 to S3
cg24211388	chr6	31582837	*AIF1*	*de novo* DMR from S1 to S2	Downregulated DEG from S2 to S3
cg24590708	chr15	52554357	*MYO5C*	*de novo* DMR from S1 to S2	Downregulated DEG from S2 to S3
cg26280911	chr5	133891771	*PHF15*	*de novo* DMR from S1 to S2	Downregulated DEG from S2 to S3
cg26394055	chr1	161184921	*FCER1G*	*de novo* DMR from S1 to S2	Downregulated DEG from S2 to S3
cg26929700	chr16	49732567	*ZNF423*	*de novo* DMR from S1 to S2	Downregulated DEG from S2 to S3
cg27606341	chr5	39219632	*FYB*	*de novo* DMR from S1 to S2	Downregulated DEG from S2 to S3
cg02225720	chr17	3623472	*ITGAE*	*de novo* DMR from S1 to S2	Downregulated DEG from S3 to S4
cg04739200	chr6	135517046	*MYB*	*de novo* DMR from S1 to S2	Downregulated DEG from S3 to S4
cg05568549	chr6	41907198	*CCND3*	*de novo* DMR from S1 to S2	Downregulated DEG from S3 to S4
cg06688763	chr7	92238207	*CDK6*	*de novo* DMR from S1 to S2	Downregulated DEG from S3 to S4
cg10785340	chr5	134715577	*H2AFY*	*de novo* DMR from S1 to S2	Downregulated DEG from S3 to S4
cg15153141	chr5	81470056	*ATG10*	*de novo* DMR from S1 to S2	Downregulated DEG from S3 to S4
cg20981848	chr20	11899258	*BTBD3*	*de novo* DMR from S1 to S2	Downregulated DEG from S3 to S4
cg26288715	chr6	135506834	*MYB*	*de novo* DMR from S1 to S2	Downregulated DEG from S3 to S4
cg27434890	chr6	135517041	*MYB*	*de novo* DMR from S1 to S2	Downregulated DEG from S3 to S4

Supplementary Table 5. Methylation and expression changes of the 65 genes exhibiting methylation changes in CpG sites located in non-CGI region and in promoters with accompanied inversedly correlated expression changes.

IlmnID	**Chr**	**Pos**	**RefSeq**	**gene**	**Δmethylation**	**ΔExpression**	**Stage**
cg12126686	19	35821634	NM_001771	CD22	-0.732	2.190	S2vsS1
cg12810837	12	9822287	NM_001004419	CLEC2D	-0.731	1.839	S2vsS1
cg17169196	6	31540026	NM_000595	LTA	-0.718	0.666	S2vsS1
cg20847766	13	111840490	NM_003899	ARHGEF7	-0.701	0.618	S2vsS1
cg04776489	22	22597965	NM_007128	VPREB1	-0.693	2.835	S2vsS1
cg06806711	11	60223291	NM_152866	MS4A1	-0.690	2.348	S2vsS1
cg03302822	10	99928067	NM_014472	C10orf28	-0.685	0.851	S2vsS1
cg23324787	11	36619694	NM_000536	C11orf74	-0.648	3.237	S2vsS1
cg21923959	11	111250566	NM_006235	POU2AF1	-0.639	1.281	S2vsS1
cg21370522	6	31543219	NM_000594	TNF	-0.619	0.872	S2vsS1
cg06288355	11	36589379	NM_000448	RAG1	-0.582	1.988	S2vsS1
cg09588020	1	27755803	NM_006990	WASF2	-0.563	0.661	S2vsS1
cg13125224	6	6587445	NM_004271	LY86	-0.558	1.148	S2vsS1
cg20894963	12	9885564	NM_172004	CLECL1	-0.527	1.325	S3vsS2
cg25812095	2	144998514	NM_001006636	GTDC1	-0.522	0.861	S2vsS1
cg25115537	8	123801352	NM_014943	ZHX2	-0.514	2.459	S2vsS1
cg17981790	2	16807234	NM_030797	FAM49A	-0.508	1.046	S2vsS1
cg17936572	3	35706114	NM_016300	ARPP-21	-0.508	3.013	S2vsS1
cg20728490	10	98064175	NM_004088	DNTT	-0.505	4.374	S2vsS1
cg10678215	5	143191565	NM_021182	HMHB1	-0.498	1.540	S2vsS1
cg04888234	1	161675579	NM_032738	FCRLA	-0.466	2.649	S3vsS2
cg06510261	3	111852227	NM_001008756	GCET2	-0.463	1.492	S2vsS1
cg12663553	3	111852312	NM_001008756	GCET2	-0.451	1.974	S3vsS2
cg20743720	6	143257108	NM_006734	HIVEP2	-0.451	1.942	S2vsS1
cg19825589	19	42379710	NM_001783	CD79A	-0.430	1.983	S2vsS1
cg18448570	10	98031337	NM_013314	BLNK	-0.426	1.906	S2vsS1
cg16177830	16	12059019	NM_001192	TNFRSF17	-0.425	3.689	S3vsS2
cg08719515	5	115857138	NM_020796	SEMA6A	-0.418	1.456	S2vsS1

cg19558972	22	23922378	NM_020070	IGLL1	-0.415	0.658	S2vsS1
cg26163153	4	40197912	NM_004310	RHOH	-0.400	1.400	S3vsS2
cg23570245	17	42426011	NM_002087	GRN	-0.381	0.832	S3vsS2
cg19371652	12	113415883	NM_002535	OAS2	-0.368	0.923	S2vsS1
cg10147394	8	11350297	NM_001715	BLK	-0.355	0.596	S3vsS2
cg13708298	6	24900051	NM_014722	FAM65B	-0.301	0.675	S3vsS2
cg08529529	13	31309799	NM_001629	ALOX5AP	-0.293	0.741	S2vsS1
cg26340740	11	58980377	NM_001039396	MPEG1	-0.264	2.202	S3vsS2
cg03112433	7	90338555	NM_012395	CDK14	-0.261	0.907	S3vsS2
cg14168009	7	3082006	NM_032415	CARD11	-0.254	0.731	S3vsS2
cg04312209	5	35857130	NM_002185	IL7R	-0.248	2.550	S2vsS1
cg13782919	9	93588842	NM_003177	SYK	-0.243	0.809	S3vsS2
cg22194129	12	7901661	NM_130441	CLEC4C	-0.234	0.799	S4vsS2
cg08001559	14	52326905	NM_053064	GNG2	-0.230	1.147	S2vsS1
cg23185774	6	36972163	NM_173558	FGD2	-0.226	0.797	S3vsS2
cg25799109	3	57102900	NM_001128615	ARHGEF3	-0.223	0.821	S3vsS2
cg03402235	15	42749336	NM_022473	ZFP106	-0.223	0.610	S3vsS2
cg22945467	1	207096833	NM_005449	FAIM3	-0.222	1.773	S2vsS1
cg07618900	12	70093350	NM_032735	BEST3	-0.210	1.961	S2vsS1
cg26522743	19	50921745	NM_003121	SPIB	-0.207	1.223	S3vsS2
cg05033369	1	161676469	NM_032738	FCRLA	-0.198	1.149	S2vsS1
cg19919989	5	66492464	NM_005582	CD180	-0.195	1.642	S3vsS2
cg19705564	14	105389886	NM_138790	PLD4	-0.195	0.671	S3vsS2
cg12554857	4	95264019	NM_014485	HPGDS	0.209	-3.854	S2vsS1
cg03348161	11	59824089	NM_006138	MS4A3	0.210	-2.589	S2vsS1
cg19766471	11	2322802	NM_139022	C11orf21	0.244	-0.645	S2vsS1
cg24474182	3	151047307	NM_176894	MED12L	0.261	-0.583	S2vsS1
cg21495704	19	36399346	NM_003332	TYROBP	0.262	-0.725	S2vsS1
cg14112601	6	10520874	NM_145649	GCNT2	0.264	-0.934	S2vsS1
cg26394055	1	161184921	NM_004106	FCER1G	0.277	-1.669	S2vsS1
cg17969683	8	24151514	NM_014265	ADAM28	0.278	-2.571	S2vsS1
cg07285167	1	36948981	NM_156039	CSF3R	0.278	-1.904	S2vsS1
cg01290568	2	113593859	NM_000576	IL1B	0.291	-1.080	S2vsS1

cg02240622	15	40601467	NM_004573	PLCB2	0.301	-1.228	S2vsS1
cg27606341	5	39219632	NM_001465	FYB	0.330	-1.676	S2vsS1
cg24536818	12	55371892	NM_001098815	KIAA0748	0.366	-1.149	S2vsS1
cg10752406	19	827776	NM_001700	AZU1	0.398	-1.102	S2vsS1