

DNA methylation patterns in naïve CD4+ T cells identify epigenetic susceptibility loci for malar rash and discoid rash in systemic lupus erythematosus

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ABSTRACT

Objective: Systemic lupus erythematosus (SLE) is a complex autoimmune disease characterised by heterogeneous clinical manifestations, autoantibody production and epigenetic dysregulation in T cells. We sought to investigate the epigenetic contribution to the development of cutaneous manifestations in SLE.

Methods: We performed genome-wide DNA methylation analyses in patients with SLE stratified by a history of malar rash, discoid rash or neither cutaneous manifestation, and age, sex and ethnicity matched healthy controls. We characterised differentially methylated regions (DMRs) in naïve CD4+ T cells unique to each disease subset, and assessed functional relationships between DMRs using bioinformatic approaches.

Results: We identified 36 and 37 unique DMRs that contribute to the epigenetic susceptibility to malar rash and discoid rash, respectively. These DMRs were primarily localised to genes mediating cell proliferation and apoptosis. Hypomethylation of *MIR886* and *TRIM69*, and hypermethylation of *RNF39* were specific to patients with SLE with a history of malar rash. Hypomethylation of the cytoskeleton-related gene *RHOJ* was specific to patients with SLE with a history of discoid rash. In addition, discoid rash-specific hypomethylated DMRs were found in genes involved in antigen-processing and presentation such as *TAP1* and *PSMB8*. Network analyses showed that DMRs in patients with SLE with but not without a history of cutaneous manifestations are associated with TAP-dependent processing and major histocompatibility-class I antigen cross-presentation ($p=3.66\times10^{-18}$ in malar rash, and 3.67×10^{-13} in discoid rash).

Conclusions: We characterised DNA methylation changes in naïve CD4+ T cells specific to malar rash and discoid rash in patients with SLE. These data suggest unique epigenetic susceptibility loci that predispose to or are associated with the development of cutaneous manifestations in SLE.

KEY MESSAGES

- We identified epigenetic susceptibility loci for cutaneous involvement in SLE using DNA methylation profiles in naïve CD4+ T cells.
- Differentially methylated regions localized to genes mediating cell proliferation and apoptosis contribute to the epigenetic susceptibility to cutaneous involvement in SLE.
- Cutaneous involvement in SLE is characterized by differential DNA methylation in genes involved in TAP-dependent processing and MHC-I antigen cross-presentation.
- Novel targets that can help to better understand cutaneous manifestations in SLE have been identified.

INTRODUCTION

Systemic lupus erythematosus (SLE) is a complex autoimmune disease characterised by autoantibody production and heterogeneous clinical manifestations. The aetiology of SLE remains incompletely understood, however there is increasing evidence for a role of DNA methylation changes in the pathogenesis of SLE.¹ DNA methylation is a lineage-specific epigenetic mechanism with an integral role in the immune system. This DNA modification, which typically refers to the methylation of the 5' cytosine carbon of cytosine-guanine (CG) dinucleotides, is often a transcriptionally repressive mark able to alter gene accessibility and chromatin structure.² Through this effect, DNA methylation is capable of mediating cell differentiation and immune function.³ Indeed, differentiation of naïve CD4+ T cells to T_H1, T_H2 and T_H17 effector subsets is imparted by demethylation of IFN γ , IL-4/IL-5/IL-13 and IL-17A/IL-17F genes, respectively.³

Importantly, aberrancies in DNA methylation can cause significant dysregulation of the immune system and have been associated with several autoimmune conditions including SLE.^{1 2 4-18} We previously reported evidence linking type I interferon hyper-responsiveness in patients with SLE to transcriptional poising induced by DNA hypomethylation in naïve CD4+ T cells.¹

In this study, we explore DNA methylation changes in naïve CD4+ T cells in patients with SLE with a history of malar rash or discoid rash to identify patterns of epigenetic susceptibility that are specific to patients with a history of these cutaneous manifestations. We identified differentially methylated (DM) sites unique to either cutaneous manifestation in SLE. In addition, we associate manifestation-specific differentially methylated regions (DMRs) to pathways related to environmental stress response, apoptosis and proliferation, and antigen processing and presentation.

MATERIALS AND METHODS

Patient and control demographic information

This study included three independent groups of patients with SLE and healthy matched controls. Each group consisted of eight patients with SLE with a history of malar rash, discoid rash or neither, and eight age (± 5 years), sex and ethnicity matched healthy controls (see online supplementary table S1). All patients fulfilled the American College of Rheumatology classification criteria for SLE.¹⁹ The American College of Rheumatology classification criteria for SLE met in each patient, and disease activity scores and criteria measured using the SLE Disease Activity Index and background medications at the time of enrolment in this study are shown in online supplementary tables S2 and S3. Patients and healthy controls included in this study signed an informed consent, and were recruited from the University of Michigan, Oklahoma Medical Research Foundation and the Henry Ford Health System.

Naïve CD4+ T cell DNA extraction

From each study participant, 80 mL of whole blood was collected then subjected to Ficoll-gradient centrifugation (GE Healthcare Bio-Sciences AB, Uppsala, Sweden) to isolate peripheral blood mononuclear cells. Naïve CD4+ T cells were then isolated from peripheral blood mononuclear cells by negative selection magnetic bead cell separation (indirect labelling) using the Naïve CD4+ T Cell Isolation kit II (Miltenyi Biotec, Cambridge, Massachusetts, USA). The purity of the isolated naïve CD4+ T cells was confirmed $>95\%$ using fluorochrome-conjugated antibodies targeting CD4 and CD45RA. DNA was then extracted using the DNeasy Blood and Tissue Kit (Qiagen, Valencia, California, USA) and bisulfite converted using the EZ DNA Methylation Kit (Zymo Research, Irvine, California, USA) for subsequent DNA methylation analysis.

DNA methylation studies

Genome-wide DNA methylation analysis was performed using the Infinium HumanMethylation450K BeadChip array (Illumina, San Diego, California, USA). DNA methylation levels were assessed at 485 577 methylation sites throughout the human genome, across 96% of UCSC cytosine-phosphate-guanine island (CpG islands) and 99% of RefSeq genes with an average of 17 sites per gene covering enhancers, promoter regions, 5' untranslated region (UTRs), 3'UTRs and gene bodies.

Statistical and bioinformatic analyses

Genome-wide DNA methylation analyses were performed using GenomeStudio methylation module V1.9.0 (Illumina) as described previously.¹ Probe signal intensities were derived from raw image intensities then normalised using non-CG probes. Background subtraction was then performed based on unhybridised negative-control probe intensities. The normalised, background-subtracted signal intensities were used to calculate β values that represent DNA methylation levels on a scale of 0 to 1. Differential DNA methylation was calculated between patients with SLE and their respective matched controls within the malar rash, discoid rash or neither cutaneous involvement group using the GenomeStudio Illumina custom model described previously.¹ Probes with a single nucleotide polymorphism (SNP) within 10 bp of the 3' probe end and probes with a detection p value ≥ 0.05 were excluded from the analysis. Differentially methylated sites were then filtered to include CG sites with a methylation difference ($|\Delta\beta|$) ≥ 0.10 between patients and controls, and a differential methylation score ($|DiffScore|$) > 22 , which corresponds to a p value ≤ 0.01 after correction for multiple testing using a Benjamini and Hochberg false discovery rate of 5%. Hypomethylated regions (hypo-DMR) and hypermethylated regions (hyper-DMR) were identified as clusters of at least two respective hypomethylation or hypermethylation sites < 500 bp of each other using the clusterMaker function and Bump Hunter package for the R statistical programming language.²⁰ Regions were then filtered to exclude all hypo-DMR or hyper-DMR overlapping between different cutaneous manifestation groups to identify DMRs unique to each group. Network analyses were performed using GeneMANIA software with networks of gene-gene interactions based on attributes, coexpression, colocalisation, genetic interactions, pathways, physical interactions, predicted interactions and shared protein domains.^{21 22} Network analysis results are presented as false discovery rate corrected p values.

RESULTS

Global DNA methylation patterns in cutaneous SLE

Genome-wide DNA methylation profiles of peripheral blood naïve CD4+ T cells were created for SLE with a history of malar rash, discoid rash and neither cutaneous involvement by comparing DNA methylation levels at 485 577 sites between patients and matched healthy

controls. We identified 615 DM sites in the malar group, 466 DM sites in the discoid group and 613 DM sites in the SLE group with neither cutaneous involvement. The majority of DM sites identified in each group were manifestation-specific, and present only in one group but not the remaining two groups (figure 1). Common to all groups, however, was a consistent hypomethylation in interferon-regulated genes (see online supplementary table S4). DNA methylation changes unique to malar rash, discoid rash or the SLE group with neither cutaneous involvement were subjected to further analysis to identify DNA methylation changes that predispose to specific cutaneous manifestations in SLE.

The greatest methylation differences unique to malar rash were found in *GNAS* ($\Delta\beta=-0.27$) encoding the G-protein α -stimulatory subunit and an intergenic locus at 7p22.2 ($\Delta\beta=0.33$) (table 1, online supplementary table S4). In patients with discoid rash, the greatest unique methylation differences were found in *KNDC1* ($\Delta\beta=-0.21$) which has a potential role in p53-mediated cell cycle arrest, an intergenic locus at 3q29 ($\Delta\beta=0.26$), and *HLA-DRB6* ($\Delta\beta=0.26$) (table 1, online supplementary table S4).²³ The greatest unique methylation differences in patients with SLE with no cutaneous involvement are found in *NFYA* ($\Delta\beta=-0.28$) encoding a subunit of the NF-Y transcription factor and in *EXOC7* ($\Delta\beta=0.33$) which encodes a component of the exocyst complex which is involved in exocytosis and membrane remodelling (table 1, online supplementary table S4).

SLE manifestation-specific DMR analysis

Next, we identified genomic regions with extensive DNA methylation differences in patients with SLE with malar

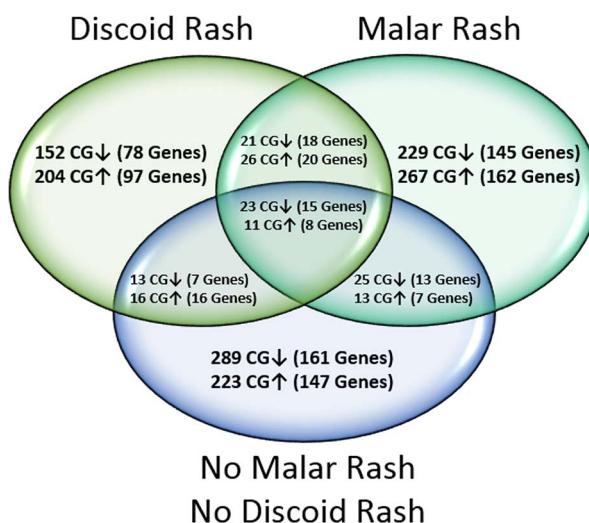


Figure 1 Venn diagram depicting the distribution of differentially methylated (DM) CG sites ($|\Delta\beta| \geq 0.10$) and associated genes between patients with systemic lupus erythematosus with a history of malar rash, discoid rash or neither cutaneous involvement, compared with healthy matched controls. Hypermethylated and hypomethylated CG sites are shown with ↑ and ↓ arrows, respectively.

rash, discoid rash or no cutaneous involvement compared with their respective controls. For each SLE group studied, unique DMRs were defined as genomic ranges of at least two CG sites within a 500 bp window that are uniquely hypomethylated or hypermethylated in each patient group subset compared with healthy controls, but not in the two remaining SLE groups. Our data for malar rash SLE showed 14 hypomethylated regions (hypo-DMRs) and 22 hypermethylated regions (hyper-DMRs) (table 2). The most extensive region contains 13 hypermethylated sites (mean $\Delta\beta=0.15$) in *LY6G5C*, a leucocyte antigen-6 gene of the major histocompatibility (MHC) class III genomic region. In patients with discoid rash, we show 17 hypo-DMRs and 20 hyper-DMRs with the most extensive DMR containing a cluster of 11 hypermethylated sites (mean $\Delta\beta=0.16$) within *RNF39* (*HZF*), a gene of the MHC class I genomic region encoding haematopoietic zinc finger protein (table 2).

Common to both cutaneous rashes are DMRs in an intergenic region in 7p22.3 and in *PRIC285* which encodes a transcriptional coactivator of peroxisome proliferator-activated receptor (PPAR) α and PPAR γ (see online supplementary table S5).^{24 25} In patients with SLE with no cutaneous involvement, we identified 28 hypo-DMRs and 16 hyper-DMRs with the most extensive region containing 15 hypomethylated sites (mean $\Delta\beta=-0.15$) within *TNXB*, a gene of the MHC class III genomic region encoding tenascin XB extracellular matrix glycoprotein (table 2). In all three patient subset groups, we identified a shared hypo-DMR in *IFI44L* (malar rash mean $\Delta\beta=-0.20$, discoid rash mean $\Delta\beta=-0.16$ and neither cutaneous involvement mean $\Delta\beta=-0.15$) and *GSTT1* (malar rash mean $\Delta\beta=-0.14$, discoid rash mean $\Delta\beta=-0.15$ and neither cutaneous involvement mean $\Delta\beta=-0.15$) (see online supplementary table S5). In addition, we identified a shared hyper-DMR in *GSTTP1* (malar rash mean $\Delta\beta=0.16$, discoid rash mean $\Delta\beta=0.15$ and neither cutaneous involvement mean $\Delta\beta=0.16$).

Gene network analysis of manifestation-specific DMRs

We then performed gene network analyses to assess relationships between the manifestation-specific DMR genes. Results for malar rash and discoid rash hypo-DMR analyses showed enrichment in genes functioning in antigen peptide transporter (TAP)-dependent antigen processing and presentation of exogenous peptides via MHC class I ($p=3.66 \times 10^{-18}$ in malar and $p=3.67 \times 10^{-13}$ in discoid) (figure 2, table 3, online supplementary table S6). This pathway was not significantly enriched in genes with unique hypo-DMR in patients with neither cutaneous involvement ($p>0.05$) (figure 2, online supplementary table S6). Network analyses were also performed for hyper-DMR genes, yet no functions were enriched in either discoid rash or neither cutaneous involvement groups. However, malar hyper-DMR genes were highly enriched in functions associated with type I interferon

Table 1 Differential methylation analysis results showing the 10 most hypomethylated and hypermethylated CG sites ($|Δβ| ≥ 0.10$) specific to (A) malar rash, (B) discoid rash or (C) neither cutaneous involvement in patients with systemic lupus erythematosus

CG site ID	Mean β case	Mean β control	Δβ	DiffScore	Location (HG19)	Gene name	Gene-relative location	CGI-relative location	Enhancer
<i>(A) Malar rash</i>									
Hypomethylation									
cg09885502	0.37	0.63	-0.27	-242.35	Chr20: 57463991	GNAS	TSS200, Body, 3'UTR	Island	FALSE
cg10090844	0.27	0.51	-0.24	-200.61	Chr12: 132167226			N_Shelf	TRUE
cg01821018	0.60	0.84	-0.24	-272.08	Chr1: 59043280	TACSTD2	TSS200	Island	TRUE
cg02891314	0.49	0.71	-0.22	-171.35	Chr5: 179741120	GFPT2	Body	Island	FALSE
cg23221052	0.45	0.67	-0.22	-158.78	Chr5: 179740743	GFPT2	Body	Island	FALSE
cg04863005	0.53	0.74	-0.21	-158.15	Chr1: 59043208	TACSTD2	TSS200	Island	TRUE
cg13944838	0.52	0.73	-0.20	-144.11	Chr5: 179740914	GFPT2	Body	Island	FALSE
cg26220594	0.28	0.48	-0.20	-129.25	Chr1: 19110978			S_Shore	TRUE
cg24853868	0.39	0.59	-0.19	-112.67	Chr1: 146555624			N_Shore	FALSE
cg01694488	0.78	0.96	-0.18	-328.93	Chr4: 1580172			Island	FALSE
Hypermethylation									
cg19214707	0.65	0.32	0.33	341.10	Chr7: 3157722				TRUE
cg15591384	0.75	0.49	0.26	341.10	Chr6: 32525960	HLA-DRB6	Body		FALSE
cg17178900	0.54	0.28	0.26	341.10	Chr1: 205818956	PM20D1	Body	Island	TRUE
cg22355889	0.33	0.08	0.25	341.10	Chr11: 107461585	LOC643923, ELMOD1	TSS1500, TSS1500	N_Shore	FALSE
cg26354017	0.50	0.26	0.24	341.10	Chr1: 205819088	PM20D1	1stExon	Island	TRUE
cg14159672	0.50	0.26	0.24	341.10	Chr1: 205819179	PM20D1	1stExon	Island	TRUE
cg11224582	0.39	0.15	0.24	341.10	Chr12: 4919138	KCNA6	5'UTR, 1stExon	Island	FALSE
cg19870512	0.33	0.10	0.24	341.10	Chr12: 4919081	KCNA6	5'UTR, 1stExon	Island	FALSE
cg07167872	0.48	0.24	0.24	341.10	Chr1: 205819463	PM20D1	TSS200	S_Shore	FALSE
cg10671668	0.32	0.09	0.23	341.10	Chr12: 4919230	KCNA6	1stExon	Island	FALSE
<i>(B) Discoid rash</i>									
Hypomethylation									
cg24668570	0.09	0.30	-0.21	-254.37	Chr10: 134973778	KNDC1	TSS200	Island	FALSE
cg18480627	0.42	0.63	-0.21	-137.10	Chr2: 130795582	LOC440905	Body	Island	FALSE
cg24088508	0.26	0.47	-0.21	-146.58	Chr1: 38156462	C1orf109	TSS1500	N_Shore	FALSE
cg19214707	0.31	0.52	-0.21	-133.32	Chr7: 3157722				TRUE
cg26762873	0.68	0.88	-0.20	-228.93	Chr11: 5879799	OR52E8	TSS1500		FALSE
cg01797371	0.18	0.36	-0.19	-139.72	Chr3: 195578240				FALSE
cg20917491	0.15	0.34	-0.19	-149.47	Chr3: 195578259				FALSE
cg08103988	0.49	0.67	-0.19	-109.96	Chr17: 6558365			Island	FALSE
cg07157030	0.45	0.63	-0.18	-95.79	Chr14: 63671356	RHOJ	5'UTR, 1stExon		TRUE
cg05779406	0.37	0.54	-0.18	-90.21	Chr7: 1198841	ZFAND2A	5'UTR	N_Shore	FALSE

Continued

Table 1 Continued

CG site ID	Mean β case	Mean β control	$\Delta\beta$	DiffScore	Location (HG19)	Gene name	Gene-relative location	CGI-relative location	Enhancer
Hypermethylation									
cg01079515	0.94	0.68	0.26	341.63	Chr3: 195576629				FALSE
cg00103771	0.67	0.41	0.26	341.63	Chr6: 32525805	HLA-DRB6	Body		FALSE
cg23350716	0.72	0.47	0.25	341.63	Chr1: 147956744	PPIAL4B, PPIAL4A	TSS1500, TSS1500		FALSE
cg05357209	0.42	0.17	0.25	341.63	Chr7: 872208	UNC84A	5'UTR, Body		TRUE
cg06550200	0.92	0.69	0.23	341.63	Chr5: 1325588	CLPTM1L	Body		FALSE
cg08477687	0.57	0.35	0.22	341.63	Chr1: 566570	MIR1977	TSS1500		FALSE
cg01694488	0.95	0.73	0.22	341.63	Chr4: 1580172			Island	FALSE
cg02239258	0.58	0.36	0.22	341.63	Chr8: 8241752			N_Shore	FALSE
cg12303247	0.88	0.67	0.21	341.63	Chr1: 155853542	SYT11	3'UTR		TRUE
cg03213289	0.52	0.32	0.19	114.27	Chr20: 61660250			Island	FALSE
(C) No cutaneous involvement									
Hypomethylation									
cg04346459	0.71	0.99	-0.28	-338.22	Chr6: 41068666	NFYA, LOC221442	3'UTR, TSS200	Island	TRUE
cg25110423	0.70	0.96	-0.26	-338.22	Chr6: 41068646	NFYA, LOC221442	3'UTR, TSS200	Island	TRUE
cg26893861	0.26	0.49	-0.22	-167.87	Chr17: 41843967	DUSP3	3'UTR		FALSE
cg19418458	0.42	0.64	-0.22	-154.86	Chr7: 158789849			Island	FALSE
cg10890302	0.28	0.49	-0.21	-142.85	Chr6: 32064246	TNXB	Body	Island	FALSE
cg14911689	0.33	0.54	-0.21	-135.21	Chr12: 739980	NINJ2	Body		FALSE
cg22531183	0.03	0.24	-0.20	-302.51	Chr19: 50554451	FLJ26850	Body	Island	FALSE
cg01079515	0.73	0.93	-0.20	-312.22	Chr3: 195576629				FALSE
cg01992382	0.24	0.44	-0.20	-140.47	Chr6: 32064212	TNXB	Body	Island	FALSE
cg05357209	0.15	0.34	-0.20	-175.62	Chr7: 872208	UNC84A	5'UTR, Body		TRUE
Hypermethylation									
cg26287080	0.85	0.52	0.33	340.66	Chr17: 74086286	EXOC7	Body		FALSE
cg08479752	0.67	0.37	0.30	340.66	Chr19: 54567279	VSTM1	TSS200		FALSE
cg16066505	0.84	0.55	0.29	340.66	Chr2: 171316530	MYO3B	Body		FALSE
cg25225073	0.30	0.06	0.24	340.66	Chr14: 90528983	KCNK13	Body	S_Shore	FALSE
cg18025438	0.63	0.39	0.24	340.66	Chr1: 228756789			Island	FALSE
cg16154810	0.41	0.18	0.23	340.66	Chr22: 47135258	CERK	TSS1500		FALSE
cg13830619	0.93	0.71	0.22	340.66	Chr12: 9555480				FALSE
cg17783317	0.53	0.31	0.22	340.66	Chr19: 54567123	VSTM1	1stExon, 5'UTR		FALSE
cg24247231	0.52	0.31	0.21	340.66	Chr15: 67904302	MAP2K5	Body		TRUE
cg07784793	0.91	0.70	0.20	340.66	Chr5: 33794720	ADAMTS12	Body		TRUE

Table 2 Unique differentially methylated regions (DMRs) in naïve CD4+ T cells from patients with systemic lupus erythematosus with a history of (A) malar rash, (B) discoid rash or (C) neither cutaneous involvement

DMR gene	DMR location	# DM sites in DMR	Mean β case	Mean β control	Mean Δβ
<i>(A) Malar rash</i>					
Hypo-DMR					
<i>MIR886</i>	Chr5: 135416331–135416412	6	0.33	0.44	-0.12
<i>TACSTD2</i>	Chr1: 59043199–59043280	4	0.51	0.70	-0.19
<i>CTBP1, C4orf42</i>	Chr4: 1243980–1244024	4	0.64	0.76	-0.12
<i>GFPT2</i>	Chr5: 179740743–179741120	3	0.49	0.70	-0.21
<i>C1orf86, LOC100128003</i>	Chr1: 2121039–2121349	2	0.38	0.51	-0.13
(Intergenic)	Chr5: 1857306–1857477	2	0.54	0.68	-0.14
<i>HLAH, HLAG, HLAJ, HCG4B</i>	Chr6: 29895175–29895187	2	0.25	0.35	-0.10
(Intergenic)	Chr6: 156983263–156983315	2	0.76	0.86	-0.11
<i>SVOP1</i>	Chr7: 138349158–138349443	2	0.44	0.55	-0.10
<i>TRIM69</i>	Chr15: 45028083–45028098	2	0.56	0.66	-0.10
<i>JPH3</i>	Chr16: 87682036–87682142	2	0.67	0.79	-0.12
<i>LOC728392</i>	Chr17: 5403337–5403516	2	0.53	0.63	-0.10
<i>RUNX1</i>	Chr21: 36258423–36258497	2	0.28	0.39	-0.11
<i>RUNX1</i>	Chr21: 36259067–36259383	2	0.29	0.41	-0.11
Hyper-DMR					
<i>LY6G5C</i>	Chr6: 31650735–31651151	13	0.69	0.54	0.15
<i>PM20D1</i>	Chr1: 205818956–205819492	7	0.46	0.24	0.22
<i>HTR2A</i>	Chr13: 47472138–47472349	5	0.62	0.47	0.16
(Intergenic)	Chr3: 196705629–196705898	4	0.51	0.38	0.13
<i>KCNA6</i>	Chr12: 4918848–4919230	4	0.33	0.10	0.23
(Intergenic)	Chr5: 154026371–154026448	3	0.45	0.33	0.12
<i>MUC5B</i>	Chr11: 1283875–1283970	3	0.23	0.10	0.13
<i>NINJ2</i>	Chr12: 739980–740338	3	0.51	0.32	0.19
<i>CRIP2</i>	Chr14: 105945022–105945685	3	0.62	0.49	0.13
<i>HOOK2</i>	Chr19: 12876846–12877000	3	0.48	0.33	0.15
<i>THADA</i>	Chr2: 43398171–43398339	2	0.50	0.36	0.14
<i>HDAC4</i>	Chr2: 240142694–240142806	2	0.67	0.54	0.13
(Intergenic)	Chr8: 43132451–43132507	2	0.52	0.41	0.11
(Intergenic)	Chr11: 128694184–128694303	2	0.55	0.44	0.11
<i>PLEKHG6</i>	Chr12: 6419570–6419575	2	0.40	0.29	0.11
(Intergenic)	Chr12: 11700321–11700489	2	0.90	0.78	0.13
<i>SLC38A4</i>	Chr12: 47219737–47219793	2	0.46	0.34	0.12
(Intergenic)	Chr13: 23309892–23309930	2	0.66	0.53	0.13
<i>LIG4</i>	Chr13: 108867111–108867154	2	0.50	0.38	0.12
<i>DEF8</i>	Chr16: 90016020–90016061	2	0.73	0.57	0.16
<i>DHX58</i>	Chr17: 40259724–40259828	2	0.33	0.21	0.12
<i>LASS4</i>	Chr19: 8273505–8273693	2	0.57	0.46	0.11
<i>(B) Discoid rash</i>					
Hypo-DMR					
(Intergenic)	Chr3: 195578040–195578280	5	0.12	0.28	-0.16
<i>TAP1</i>	Chr6: 32819911–32820214	4	0.34	0.45	-0.11
<i>RFPL2</i>	Chr22: 32599511–32599648	4	0.40	0.52	-0.12
<i>PRDM9</i>	Chr5: 23507573–23507617	3	0.69	0.80	-0.11
<i>RPH3AL</i>	Chr17: 154420–154671	3	0.38	0.49	-0.11
<i>C1orf109</i>	Chr1: 38156462–38156652	2	0.28	0.45	-0.17
<i>SPINK9</i>	Chr5: 147699718–147699892	2	0.48	0.59	-0.11
<i>LY6G5C</i>	Chr6: 31651020–31651029	2	0.62	0.74	-0.12
<i>PSMB8</i>	Chr6: 32810706–32810833	2	0.50	0.63	-0.13
<i>RHOJ</i>	Chr14: 63671356–63671737	2	0.43	0.60	-0.17
<i>BAIAP3</i>	Chr16: 1393584–1393797	2	0.56	0.68	-0.12
(Intergenic)	Chr16: 53407722–53407808	2	0.50	0.64	-0.13
(Intergenic)	Chr17: 6558365–6558440	2	0.50	0.67	-0.16
(Intergenic)	Chr17: 37024020–37024042	2	0.29	0.42	-0.13

Continued

Table 2 Continued

DMR gene	DMR location	# DM sites in DMR	Mean β case	Mean β control	Mean $\Delta\beta$
<i>TBC1D16</i>	Chr17: 77997833–77997997	2	0.83	0.95	-0.11
<i>SBNO2</i>	Chr19: 1155030–1155184	2	0.81	0.94	-0.13
<i>C21orf81</i>	Chr21: 15352608–15352983	2	0.35	0.48	-0.13
Hyper-DMR					
<i>RNF39</i>	Chr6: 30039142–30039524	11	0.47	0.30	0.16
(Intergenic)	Chr7: 158789849–158790115	3	0.55	0.42	0.14
(Intergenic)	Chr10: 43846281–43846539	3	0.35	0.22	0.13
<i>MIPEPP3</i>	Chr13: 21900426–21900810	3	0.60	0.48	0.12
<i>ZNF714</i>	Chr19: 21264896–21265421	3	0.39	0.26	0.14
<i>C1orf65</i>	Chr1: 223566761–223567173	2	0.39	0.29	0.10
<i>MYT1L</i>	Chr2: 1801628–1802045	2	0.70	0.59	0.11
<i>TMEM175</i>	Chr4: 940644–940893	2	0.63	0.52	0.11
(Intergenic)	Chr5: 74350132–74350214	2	0.38	0.27	0.11
<i>GFPT2</i>	Chr5: 179740743–179740914	2	0.60	0.47	0.13
<i>TRIM31</i>	Chr6: 30079265–30079280	2	0.63	0.51	0.12
(Intergenic)	Chr6: 167559851–167559913	2	0.59	0.45	0.14
<i>RADIL</i>	Chr7: 4848683–4848814	2	0.24	0.10	0.13
(Intergenic)	Chr8: 58055876–58056113	2	0.50	0.38	0.12
<i>FGFR2</i>	Chr10: 123355268–123355576	2	0.47	0.37	0.10
<i>RAD51B</i>	Chr14: 69095570–69095679	2	0.43	0.32	0.11
(Intergenic)	Chr15: 66947568–66947617	2	0.37	0.26	0.12
<i>SMAD3</i>	Chr15: 67356838–67356942	2	0.69	0.59	0.11
<i>SPIB</i>	Chr19: 50931432–50931515	2	0.32	0.20	0.12
(Intergenic)	Chr20: 61659980–61660250	2	0.58	0.41	0.17
(C) No cutaneous involvement					
Hypo-DMR					
<i>TNXB</i>	Chr6: 32063607–32064582	15	0.34	0.49	-0.15
<i>NFYA, LOC221442</i>	Chr6: 41068646–41068752	5	0.76	0.96	-0.21
<i>MUC4</i>	Chr3: 195489306–195489909	4	0.63	0.77	-0.13
(Intergenic)	Chr7: 158789723–158790115	4	0.43	0.59	-0.16
<i>RAD51B</i>	Chr14: 69095057–69095679	4	0.31	0.44	-0.12
(Intergenic)	Chr1: 75590912–75591353	3	0.34	0.46	-0.12
(Intergenic)	Chr6: 28447087–28447115	3	0.30	0.42	-0.12
<i>NINJ2</i>	Chr12: 739980–740338	3	0.38	0.57	-0.20
<i>KCNA6</i>	Chr12: 4919081–4919230	3	0.25	0.38	-0.13
<i>LMTK3</i>	Chr19: 49000743–49000998	3	0.65	0.76	-0.12
<i>LMTK3</i>	Chr19: 49001890–49002477	3	0.59	0.71	-0.12
<i>MYT1L</i>	Chr2: 1817263–1817409	2	0.58	0.70	-0.11
(Intergenic)	Chr4: 1550089–1550194	2	0.66	0.77	-0.12
(Intergenic)	Chr4: 6010075–6010164	2	0.46	0.56	-0.11
<i>RGS14</i>	Chr5: 176797920–176797999	2	0.46	0.57	-0.12
<i>RNF39</i>	Chr6: 30039202–30039442	2	0.32	0.45	-0.13
<i>VARS2</i>	Chr6: 30882641–30882708	2	0.44	0.57	-0.13
<i>TAP2</i>	Chr6: 32805548–32805570	2	0.55	0.67	-0.12
<i>HOXA5</i>	Chr7: 27183375–27183694	2	0.68	0.79	-0.11
<i>PTPRN2</i>	Chr7: 158046166–158046222	2	0.68	0.85	-0.17
(Intergenic)	Chr8: 1321333–1321375	2	0.40	0.53	-0.12
(Intergenic)	Chr10: 130726624–130726701	2	0.68	0.80	-0.12
<i>TRIM5</i>	Chr11: 5960015–5960081	2	0.69	0.80	-0.11
<i>STAT3</i>	Chr17: 40489584–40489785	2	0.27	0.40	-0.13
<i>FLJ26850</i>	Chr19: 50554451–50554510	2	0.06	0.22	-0.16
<i>NLRP2</i>	Chr19: 55477653–55477810	2	0.51	0.62	-0.11
<i>HLCS</i>	Chr21: 38362725–38362727	2	0.57	0.71	-0.14
<i>C21orf56</i>	Chr21: 47604166–47604291	2	0.24	0.38	-0.14
Hyper-DMR					
<i>NAPRT1</i>	Chr8: 144659831–144660772	5	0.37	0.23	0.14
<i>GSTM5</i>	Chr1: 110254662–110254709	3	0.47	0.35	0.12

Continued

Table 2 Continued

DMR gene	DMR location	# DM sites in DMR	Mean β case	Mean β control	Mean $\Delta\beta$
(Intergenic)	Chr10: 1939618–1939683	3	0.67	0.51	0.16
<i>CD101</i>	Chr1: 117544206–117544416	2	0.19	0.08	0.11
(Intergenic)	Chr2: 731298–731519	2	0.80	0.67	0.13
(Intergenic)	Chr2: 173539262–173539542	2	0.50	0.40	0.11
<i>PRDM9</i>	Chr5: 23507594–23507617	2	0.74	0.64	0.11
<i>FLOT1</i>	Chr6: 30706647–30706654	2	0.68	0.57	0.11
<i>C11orf21, TSPAN32</i>	Chr11: 2322507–2322517	2	0.21	0.10	0.12
(Intergenic)	Chr12: 19557334–19557343	2	0.25	0.13	0.11
<i>RARG</i>	Chr12: 53612551–53612734	2	0.53	0.41	0.12
<i>VSTM1</i>	Chr19: 54567123–54567279	2	0.60	0.34	0.26
<i>SPATC1L</i>	Chr21: 47581042–47581405	2	0.61	0.50	0.11
<i>CERK</i>	Chr22: 47135171–47135258	2	0.32	0.13	0.19
<i>BCOR</i>	ChrX: 39956534–39956558	2	0.31	0.19	0.12
<i>BCOR</i>	ChrX: 39958040–39958196	2	0.34	0.20	0.14

response ($p=1.11\times10^{-21}$) (see online supplementary figure S1, online supplementary table S7). It should be noted, however, that these hypermethylated interferon-related DMR genes are more specifically enriched in

negative regulation of type I interferon production ($p=4.83\times10^{-4}$) and are different from the interferon-regulated genes that constitute the interferon signature known to be hypomethylated in SLE. Indeed, SLE

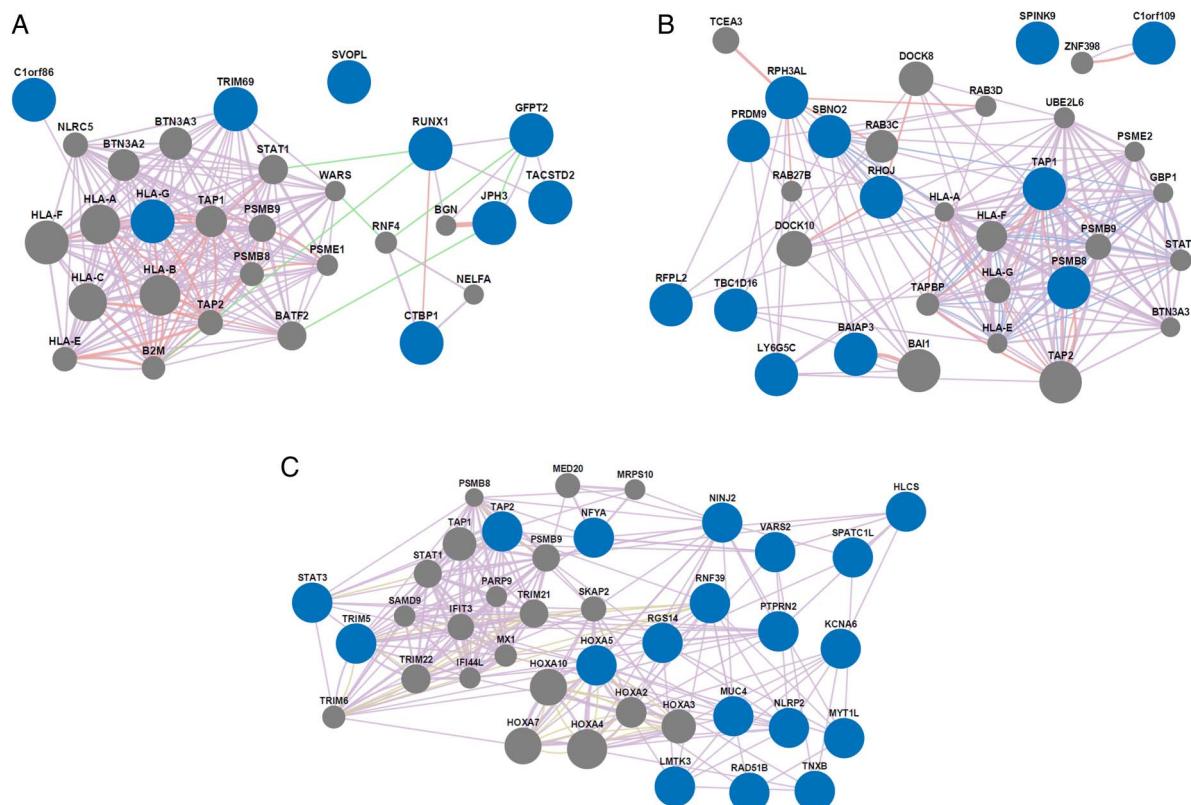


Figure 2 Network analysis results showing relationships among genes with hypomethylated regions (hypo-DMRs) specific to patients with systemic lupus erythematosus with a history of (A) malar rash, (B) discoid rash or (C) neither cutaneous involvement. Manifestation-specific hypo-DMR genes and network-associated genes are represented by blue and grey nodes, respectively. The lines connecting the nodes depict gene-gene relationships based on coexpression (purple), colocalisation (blue), genetic interactions (green), physical interactions (pink), and shared protein domains (yellow). Line thickness is relative to the strength of the gene-gene relationship. All network analyses were performed using GeneMANIA software. DMR, differentially methylated region.

Table 3 Network analysis results are shown for genes with unique hypomethylated regions (hypo-DMRs) in naïve CD4+ T cells from patients with systemic lupus erythematosus (SLE) with a history of malar rash, discoid rash or neither cutaneous involvement

Enriched function	p Value
Malar rash	
Antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent	3.66E-18
Antigen processing and presentation of exogenous peptide antigen via MHC class I	3.66E-18
Antigen processing and presentation of peptide antigen via MHC class I	2.65E-17
Peptide antigen binding	1.87E-15
Antigen processing and presentation of exogenous peptide antigen	1.91E-14
Discoid rash	
Antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent	3.67E-13
Antigen processing and presentation of exogenous peptide antigen via MHC class I	3.67E-13
Antigen processing and presentation of peptide antigen via MHC class I	1.73E-12
Peptide antigen binding	2.57E-12
Antigen processing and presentation	1.07E-10
No cutaneous involvement	
Protein trimerisation	1.60E-03
Type I interferon signalling pathway	5.85E-02
Cellular response to type I interferon	5.85E-02
Response to type I interferon	5.85E-02
Antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent	5.85E-02

For each SLE manifestation group, results are shown for the five most significantly enriched functions. All network analyses were performed using GeneMANIA software.

DMR, differentially methylated regions; MHC, major histocompatibility.

interferon-signature genes were consistently hypomethylated in all three SLE groups in this study (see online supplementary table S4).

DISCUSSION

DNA methylation is a stable and heritable epigenetic modification that has a considerable effect on naïve CD4+ T cell differentiation and immune function. Aberrancies in DNA methylation are found in several autoimmune diseases including SLE.^{15–26} Furthermore, robust demethylation of interferon-regulated genes in naïve CD4+ T cells in SLE has been associated with a hyper-responsive type I interferon signature in patients with SLE.¹ Not surprisingly, demethylation of these same interferon-regulated genes was common to all SLE groups with malar, discoid or neither cutaneous manifestation (see online supplementary table S4). In this study, we further investigate the important link between naïve CD4+ T cells and SLE pathogenesis in a clinical manifestation-specific manner with an in-depth analysis of aberrant DNA methylation in naïve CD4+ T cells from patients with SLE with a history of malar rash or discoid rash. This is accomplished with a case-control study design involving independent genome-wide DNA methylation analyses for SLE with a history of malar rash, discoid rash or neither cutaneous involvement. In each analysis, patients with SLE in each of the manifestation groups were compared with healthy controls carefully matched for age, sex and ethnicity on a one-by-one basis. We then excluded DM sites that were common

between the manifestation groups to characterise DNA methylation changes that are unique to only malar rash or discoid rash.

Our global DNA methylation profiles showed distinguishable manifestation-specific differences between each SLE group with 80.7% unique DM sites (229 hypomethylated and 267 hypermethylated CGs) for malar rash, and 76.4% unique DM sites (152 hypomethylated and 204 hypermethylated CGs) for discoid rash. In addition, we identified 14 hypo-DMRs and 22 hyper-DMRs unique to malar rash and 17 hypo-DMRs and 20 hyper-DMRs unique to discoid rash. Interestingly, several DMRs in either cutaneous manifestation are associated with genes mediating cell proliferation and apoptosis pathways. In patients with a history of malar rash, the most extensive malar rash DMR consists of six hypomethylated CG sites (mean $\Delta\beta=-0.12$) in the promoter region of precursor microRNA *MIR886* (*VTRNA2-1*).²⁷ Hypomethylation of the *VTRNA2-1* promoter has been shown to downregulate the interferon-inducible phosphorylated RNA-dependent protein kinase which in turn regulates eIF2 α and Nuclear Factor kappa B (NF- κ B) signalling pathways pivotal to determining cell survival or apoptosis.^{28–30} We also found a hypo-DMR in *TRIM69* (two hypomethylated CG sites, mean $\Delta\beta=-0.10$) whose overexpression has been shown to induce apoptosis in murine models. In patients with a history of discoid rash, we report a DMR in the DNA damage response genes *RHOJ* (2 hypomethylated CG sites, mean $\Delta\beta=-0.17$) and *HZF* (11 hypermethylated CG sites, mean $\Delta\beta=0.16$) which are also involved in cell survival/



apoptosis pathway commitment. Indeed, the haematoopoietic zinc finger encoded by *HZF* is a key cofactor of p53 tumour suppressor and serves as a critical switch promoting cell-cycle arrest over the alternative apoptosis pathway.^{31–32} Taken together, both cutaneous manifestations are associated with unique DMRs in genes that influence environmental stress response pathways and cell fate decisions. It is unclear what role these DMRs have in cutaneous manifestations in SLE. However, they may provide insight into the impaired apoptotic cell clearance found in the epidermis of patients with cutaneous lupus erythematosus and in germinal centres of patients with SLE.^{33–34}

Our DMR analyses also revealed a relationship between SLE cutaneous manifestations and antigen processing and presentation. In particular, SLE with discoid rash is associated with hypo-DMR in *PSMB8* (two hypomethylated sites, mean $\Delta\beta=-0.13$), encoding a subunit of the immunoproteasome involved in processing peptides for MHC-I loading. A hypo-DMR was also found in *TAP1* (four hypomethylated sites, mean $\Delta\beta=-0.11$) which encodes a key subunit of the transporter associated with antigen processing complex, TAP. In monocytes and dendritic cells, the TAP complex transports phagosome-processed exogenous peptides to the endoplasmic reticulum to bind and present on MHC-I in a process known as cross-presentation.³⁵ Interestingly, our network analyses of unique hypo-DMR in each cutaneous patient subset group showed enrichment in genes functioning in the TAP-dependent antigen processing and presentation of exogenous peptide antigen via MHC-I (malar rash $p=3.66\times10^{-18}$, discoid rash $p=3.67\times10^{-13}$). MHC-I cross-presentation is commonly used by antigen-presenting cells, and it is unclear what role it may have in CD4+ T cells in SLE. One possibility is that these changes represent epigenetic susceptibility loci that can manifest in other cell types that might be more directly involved in antigen cross presentation. The other possibility is that cross-presentation genes and pathways are aberrantly active in CD4+ T cells in a subset of patients with SLE and might play a different role in the pathogenesis of SLE that is independent of their classical known role in antigen cross-presentation. It is also worth noting that T cells have been previously shown to present antigens on MHC class I and MHC class II,³⁶ and whether this is involved in the pathogenesis of cutaneous SLE remains to be further examined.

In this study, we performed an extensive investigation of naïve CD4+ T cell DNA methylation changes associated with malar rash and discoid rash in SLE. In either of the cutaneous manifestations, we characterised aberrant DNA methylation profiles and identified DMRs in multiple genes that impact environmental stress response and cell fate. In addition, hypo-DMRs of malar rash and discoid rash are enriched in genes involved in the pathway for TAP-dependent exogenous antigen processing and MHC-I cross-presentation. Importantly, we revealed several novel targets of aberrant DNA

methylation in naïve CD4+ T cells that might aid in our understanding of SLE and its cutaneous manifestations. Future studies and replication efforts with a larger sample size to detect smaller DNA methylation changes between patients and controls, and to examine other cell subsets relevant to SLE might uncover additional epigenetic susceptibility loci for cutaneous SLE manifestations.

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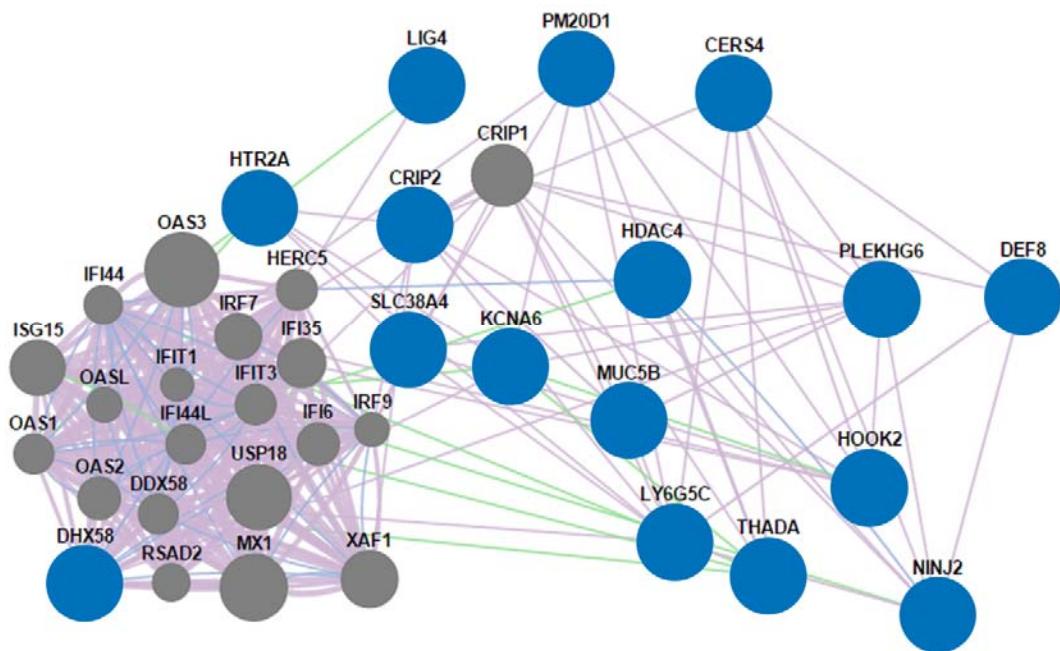
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Supplementary Figure 1: Network analysis results showing relationships amongst genes with hypermethylated regions (hyper-DMRs) specific to SLE patients with a history of malar rash. Manifestation-specific hyper-DMR genes and network-associated genes are represented by blue and grey nodes, respectively. The lines connecting the nodes depict gene-gene relationships based on co-expression (purple), co-localization (blue), and genetic interactions (green). Line thickness is relative to the strength of the gene-gene relationship. The network analysis was performed using GeneMANIA software.



Supplementary Table 1: Demographics of SLE patients with either malar rash, discoid rash, or neither cutaneous involvement and healthy controls matched by age, sex, and ethnicity.

Patients				Controls			
Sample ID	Sex	Ethnicity	Age	Sample ID	Sex	Ethnicity	Age
Malar Rash							
M1	Female	EA	22	C1	Female	EA	22
M2	Female	EA	33	C2	Female	EA	35
M3	Female	EA	36	C3	Female	EA	35
M4	Female	AA	38	C4	Female	AA	38
M5	Female	EA	49	C5	Female	EA	47
M6	Female	EA	56	C6	Female	EA	60
M7	Female	AA	60	C7	Female	AA	62
M8	Female	EA	66	C8	Female	EA	63
Discoid Rash							
D1	Female	EA	58	C9	Female	EA	53
D2	Female	EA	56	C10	Female	EA	57
D3	Female	AA	56	C11	Female	AA	56
D4	Female	EA	47	C12	Female	EA	43
D5	Female	AA	54	C13	Female	AA	58
D6	Female	AA	25	C14	Female	AA	26
D7	Female	EA	56	C15	Female	EA	60
D8	Female	AA	62	C16	Female	AA	57
No Cutaneous Involvement							
N1	Female	AA	23	C17	Female	AA	20
N2	Female	EA	34	C18	Female	EA	30
N3	Female	EA	36	C19	Female	EA	41
N4	Female	AA	42	C20	Female	AA	41
N5	Female	AA	50	C21	Female	AA	52
N6	Female	EA	54	C22	Female	EA	50
N7	Female	AA	57	C23	Female	AA	57
N8	Female	EA	64	C24	Female	EA	66

AA=African-American; EA=European-American.

Supplementary Table 2: American College of Rheumatology classification criteria for SLE in patients with either malar rash, discoid rash, or neither cutaneous manifestation.

Sample ID	Age	Ethnicity	Malar Rash	Discoid Rash	Photo-sensitivity	Oral Ulcers	Arthritis	Serositis	Renal Disorder	Neurologic Disorder	Hematologic Disorder	Immunologic Disorder	ANA Presence
Malar Rash													
M1	22	EA	X		X		X	X				X	X
M2	33	EA	X		X	X	X		X			X	X
M3	36	EA	X			X					X	X	X
M4	38	AA	X		X		X				X	X	X
M5	49	EA	X		X		X		X		X	X	X
M6	56	EA	X		X		X				X	X	X
M7	60	AA	X		X	X	X				X		X
M8	66	EA	X				X	X				X	
Discoid Rash													
D1	58	EA		X		X	X			X		X	X
D2	56	EA		X	X		X		X			X	X
D3	56	AA		X	X							X	X
D4	47	EA		X	X	X						X	X
D5	54	AA		X					X	X	X	X	X
D6	25	AA		X	X	X	X	X		X		X	X
D7	56	EA		X				X	X		X	X	X
D8	62	AA		X	X	X	X			X			X
No Cutaneous Involvement													
N1	23	AA							X	X		X	X
N2	34	EA								X		X	X
N3	36	EA					X				X	X	X
N4	42	AA					X	X	X			X	X
N5	50	AA				X	X				X	X	X
N6	54	EA			X		X				X		X
N7	57	AA			X		X				X		X
N8	64	EA			X			X				X	X

AA=African-American; EA=European-American.

Supplementary Table 3: SLEDAI scores and criteria, and background medications at the time of enrolment of the SLE patients included in this study.

Sample ID	Age	Ethnicity	SLEDAI Score	SLEDAI Criteria at the Time of Blood Draw	Medications
Malar Rash					
M1	22	EA	10	New rash, mucosal ulcers, pleurisy, low complement, increased DNA binding	-
M2	33	EA	6	Proteinuria, low complement	Prednisone, Azathioprine, Etanercept
M3	36	EA	4	Low complement, increased DNA binding	Hydroxychloroquine
M4	38	AA	0	-	Prednisone, Hydroxychloroquine, Methotrexate
M5	49	EA	3	Low complement, thrombocytopenia	Prednisone, Mycophenolate mofetil
M6	56	EA	0	-	Hydroxychloroquine, has been prescribed Cyclophosphamide
M7	60	AA	8	Arthritis, new rash, low complement	Prednisone
M8	66	EA	2	Increased DNA binding	-
Discoid Rash					
D1	58	EA	0	-	Hydroxychloroquine
D2	56	EA	4	Low complement, increased DNA binding	Prednisone, Hydroxychloroquine, Mycophenolate mofetil
D3	56	AA	2	Increased DNA binding	Hydroxychloroquine
D4	47	EA	0	-	Prednisone, Mycophenolate mofetil
D5	54	AA	4	Proteinuria	Hydroxychloroquine, Mycophenolate mofetil, has been prescribed Cyclophosphamide
D6	25	AA	13	Arthritis, new rash, alopecia, low complement, increased DNA binding, leukopenia	Hydroxychloroquine
D7	56	EA	0	-	Prednisone
D8	62	AA	2	Alopecia	Prednisone, Hydroxychloroquine
No Cutaneous Involvement					
N1	23	AA	0	-	Prednisone, Hydroxychloroquine, Mycophenolate mofetil
N2	34	EA	2	Low complement	Hydroxychloroquine
N3	36	EA	0	-	Hydroxychloroquine
N4	42	AA	4	Low complement, increased DNA binding	Hydroxychloroquine, Azathioprine
N5	50	AA	4	Arthritis	Hydroxychloroquine, Mycophenolate mofetil
N6	54	EA	10	Arthritis, hematuria, increased DNA binding	Prednisone, has been prescribed Cyclophosphamide
N7	57	AA	2	Alopecia	Hydroxychloroquine
N8	64	EA	2	Increased DNA binding	Hydroxychloroquine

AA=African-American; EA=European-American.

Supplementary Table 4: Differentially methylated CG sites in naïve CD4+ T cells from SLE patients with **A.** malar rash, **B.** discoid rash, or **C.** neither cutaneous involvement compared to respective healthy matched controls.

A.

Malar Rash

CG Site ID	Mean β Case	Mean β Control	Δβ	DiffScore	Location (HG19)	Gene Name	Gene-Relative Location	CGI-Relative Location	Enhancer
Hypomethylation									
cg21549285	0.31	0.66	-0.35	-338.82	Chr21: 42799141	<i>MX1, MX1</i>	5'UTR, 5'UTR	S_Shore	FALSE
cg14392283	0.61	0.91	-0.30	-338.82	Chr8: 144103587	<i>LY6E, LY6E</i>	3'UTR, 3'UTR	N_Shelf	FALSE
cg15065340	0.40	0.68	-0.28	-289.58	Chr3: 195632915	<i>TNK2</i>	5'UTR	N_Shelf	FALSE
cg11404906	0.56	0.84	-0.27	-338.82	Chr6: 32551749	<i>HLA-DRB1</i>	Body	N_Shore	FALSE
cg06981309	0.40	0.66	-0.27	-246.35	Chr3: 146260954	<i>PLSCR1</i>	5'UTR	N_Shore	FALSE
cg09885502	0.37	0.63	-0.27	-242.35	Chr20: 57463991	<i>GNAS, GNAS, GNAS, GNAS</i>	3'UTR, TSS200, 3'UTR, Body	Island	FALSE
cg01028142	0.59	0.85	-0.26	-338.82	Chr2: 7004578	<i>CMPK2</i>	Body	N_Shore	FALSE
cg08122652	0.50	0.76	-0.26	-265.15	Chr3: 122281939	<i>PARP9, PARP9, DTX3L, PARP9, PARP9, PARP9, PARP9</i>	5'UTR, 5'UTR, TSS1500, 5'UTR, 5'UTR, 5'UTR, 5'UTR	N_Shore	FALSE
cg03607951	0.47	0.72	-0.25	-221.63	Chr1: 79085586	<i>IFI44L</i>	TSS1500		FALSE
cg10090844	0.27	0.51	-0.24	-200.61	Chr12: 132167226			N_Shelf	TRUE
cg17384323	0.47	0.71	-0.24	-201.84	Chr4: 169242366			S_Shelf	FALSE
cg01821018	0.60	0.84	-0.24	-272.08	Chr1: 59043280	<i>TACSTD2</i>	TSS200	Island	TRUE
cg05696877	0.30	0.54	-0.23	-182.16	Chr1: 79088769	<i>IFI44L</i>	5'UTR		FALSE
cg14286514	0.36	0.58	-0.23	-167.02	Chr9: 32525315	<i>DDX58</i>	Body	N_Shore	TRUE
cg14212360	0.57	0.80	-0.23	-220.29	Chr4: 89302999	<i>HERC6, HERC6</i>	Body, Body	S_Shelf	FALSE
cg05552874	0.56	0.79	-0.22	-204.94	Chr10: 91153143	<i>IFIT1</i>	Body		FALSE
cg02891314	0.49	0.71	-0.22	-171.35	Chr5: 179741120	<i>GFPT2</i>	Body	Island	FALSE
cg23221052	0.45	0.67	-0.22	-158.78	Chr5: 179740743	<i>GFPT2</i>	Body	Island	FALSE
cg22862003	0.46	0.68	-0.22	-156.59	Chr21: 42797588	<i>MX1, MX1</i>	TSS1500, 5'UTR	N_Shore	FALSE
cg04863005	0.53	0.74	-0.21	-158.15	Chr1: 59043208	<i>TACSTD2</i>	TSS200	Island	TRUE
cg00274965	0.32	0.53	-0.20	-130.08	Chr21: 34405681			Island	FALSE
cg13944838	0.52	0.73	-0.20	-144.11	Chr5: 179740914	<i>GFPT2</i>	Body	Island	FALSE
cg26220594	0.28	0.48	-0.20	-129.25	Chr1: 19110978			S_Shore	TRUE
cg18686270	0.61	0.80	-0.19	-163.85	Chr3: 146258875	<i>PLSCR1</i>	5'UTR	N_Shelf	FALSE
cg24853868	0.39	0.59	-0.19	-112.67	Chr1: 146555624			N_Shore	FALSE
cg00855901	0.24	0.43	-0.19	-118.22	Chr1: 79085765	<i>IFI44L</i>	TSS1500		FALSE
cg01694488	0.78	0.96	-0.18	-328.93	Chr4: 1580172			Island	FALSE
cg16523850	0.42	0.60	-0.18	-95.04	Chr6: 54156824				TRUE
cg16301894	0.53	0.71	-0.18	-105.55	Chr4: 129389744				TRUE
cg23549331	0.36	0.54	-0.18	-89.64	Chr8: 6189008				TRUE

cg12051710	0.25	0.43	-0.17	-97.68	Chr12: 2989070	<i>C12orf32</i> , <i>C12orf32</i> , <i>C12orf32</i>	Body, Body, Body	S_Shelf	FALSE
cg16080552	0.48	0.66	-0.17	-89.43	Chr1: 59043199	<i>TACSTD2</i>	TSS200	Island	TRUE
cg01238044	0.19	0.36	-0.17	-106.32	Chr22: 24384105	<i>GSTT1</i>	Body	N_Shore	FALSE
cg17980508	0.43	0.60	-0.17	-79.50	Chr1: 79085713	<i>IFI44L</i>	TSS1500		FALSE
cg13200575	0.47	0.63	-0.16	-78.42	Chr17: 38096571				FALSE
cg06188083	0.20	0.37	-0.16	-96.21	Chr10: 91093005	<i>IFIT3</i> , <i>IFIT3</i>	Body, Body		TRUE
cg27107893	0.74	0.90	-0.16	-169.86	Chr5: 142776274	<i>NR3C1</i> , <i>NR3C1</i> , <i>NR3C1</i> , <i>NR3C1</i> , <i>NR3C1</i> , <i>NR3C1</i> , <i>NR3C1</i>	Body, Body, Body, Body, Body, Body, Body		TRUE
cg07833467	0.39	0.54	-0.16	-68.81	Chr22: 50986511	<i>KLHDC7B</i> , <i>KLHDC7B</i>	5'UTR, 1stExon	Island	FALSE
cg05073382	0.70	0.86	-0.16	-135.21	Chr8: 2045798	<i>MYOM2</i>	Body	N_Shore	FALSE
cg16699148	0.42	0.58	-0.16	-67.46	Chr1: 59043255	<i>TACSTD2</i>	TSS200	Island	TRUE
cg16824113	0.54	0.69	-0.16	-76.54	Chr12: 132166485				TRUE
cg15708909	0.64	0.80	-0.15	-101.71	Chr6: 32487314	<i>HLA-DRB5</i>	Body	N_Shelf	FALSE
cg00639218	0.24	0.40	-0.15	-78.00	ChrY: 14096487			N_Shelf	FALSE
cg08822075	0.57	0.72	-0.15	-78.80	Chr7: 26193607	<i>NFE2L3</i>	Body	S_Shore	TRUE
cg04234412	0.26	0.41	-0.15	-73.77	Chr22: 24373322	<i>LOC391322</i>	Body	Island	FALSE
cg20053110	0.64	0.79	-0.15	-97.71	Chr6: 37617864	<i>MDGA1</i>	Body	Island	TRUE
cg21159568	0.60	0.75	-0.15	-83.46	Chr7: 2445331	<i>CHST12</i>	5'UTR	S_Shore	FALSE
cg12397463	0.63	0.78	-0.15	-91.02	Chr6: 33128825			N_Shore	FALSE
cg13218423	0.47	0.62	-0.15	-63.95	Chr11: 89735737	<i>TRIM53</i>	TSS200		FALSE
cg09768983	0.53	0.68	-0.15	-67.57	Chr4: 183935060				FALSE
cg25303761	0.32	0.47	-0.15	-62.62	Chr1: 31256028				TRUE
cg22992730	0.47	0.62	-0.15	-60.80	Chr19: 4784940			N_Shore	FALSE
cg09976051	0.47	0.62	-0.15	-60.65	Chr4: 178362394	<i>AGA</i>	Body	N_Shore	FALSE
cg18792536	0.30	0.45	-0.15	-63.09	Chr7: 76145562	<i>UPK3B</i> , <i>UPK3B</i>	3'UTR, 3'UTR	Island	FALSE
cg12110437	0.16	0.31	-0.15	-90.48	Chr8: 144098888	<i>LY6E</i> , <i>LY6E</i> , <i>LOC100133669</i>	TSS1500, TSS1500, Body	N_Shore	FALSE
cg21656205	0.37	0.51	-0.15	-58.86	Chr20: 43439688	<i>RIMS4</i>	TSS1500	S_Shore	FALSE
cg20790798	0.52	0.67	-0.15	-63.62	Chr5: 1857306			Island	FALSE
cg10213302	0.48	0.63	-0.15	-59.33	ChrY: 2802975	<i>ZFY</i> , <i>ZFY</i> , <i>ZFY</i>	TSS1500, TSS200, TSS1500	Island	FALSE
cg21699330	0.36	0.51	-0.14	-56.52	Chr7: 26193032	<i>NFE2L3</i>	Body	S_Shore	FALSE
cg16399632	0.67	0.81	-0.14	-93.05	Chr4: 1244006	<i>CTBP1</i> , <i>CTBP1</i> , <i>C4orf42</i>	TSS1500, TSS1500, TSS200	Island	FALSE
cg26479374	0.70	0.84	-0.14	-103.85	Chr4: 1243980	<i>CTBP1</i> , <i>CTBP1</i> , <i>C4orf42</i>	TSS1500, TSS1500, TSS200	Island	FALSE
cg20062691	0.53	0.67	-0.14	-59.86	Chr1: 949392	<i>ISG15</i>	Body	Island	TRUE
cg20971158	0.50	0.64	-0.14	-55.90	Chr11: 35159382	<i>CD44</i> , <i>CD44</i> , <i>CD44</i> , <i>CD44</i> , <i>CD44</i>	TSS1500, TSS1500, TSS1500, TSS1500, TSS1500	N_Shore	FALSE
cg18085176	0.50	0.64	-0.14	-55.51	Chr4: 7939940	<i>AFAP1</i> , <i>AFAP1</i>	5'UTR, 5'UTR	N_Shore	FALSE
cg18451016	0.50	0.64	-0.14	-55.93	Chr1: 38461880			Island	FALSE

cg27192248	0.28	0.42	-0.14	-58.61	Chr15: 65285669		S_Shelf	FALSE
cg24100841	0.60	0.74	-0.14	-68.21	Chr6: 29649024			FALSE
cg23264429	0.52	0.66	-0.14	-56.65	Chr10: 90642003	<i>STAMBPL1</i>	5'UTR	S_Shore
cg21593149	0.65	0.79	-0.14	-81.49	Chr4: 1300163	<i>MAEA, MAEA</i>	Body, Body	N_Shelf
cg24796644	0.65	0.79	-0.14	-78.34	Chr6: 37617956	<i>MDGA1</i>	Body	Island
cg14951497	0.26	0.40	-0.14	-59.69	Chr2: 191875807	<i>STAT1, STAT1</i>	5'UTR, 5'UTR	N_Shelf
cg06343673	0.63	0.77	-0.14	-72.14	Chr17: 78778232	<i>RPTOR, RPTOR</i>	Body, Body	S_Shelf
cg26227225	0.34	0.48	-0.14	-51.08	Chr1: 2121039	<i>C1orf86, LOC100128003, C1orf86</i>	Body, Body, 3'UTR	Island
cg27207756	0.29	0.42	-0.14	-54.56	Chr4: 1607291			FALSE
cg02334775	0.49	0.62	-0.14	-50.98	Chr15: 89182676	<i>ISG20</i>	Body	FALSE
cg06889571	0.75	0.88	-0.14	-122.45	Chr10: 1416791	<i>ADARB2</i>	Body	S_Shore
cg08926253	0.60	0.74	-0.14	-62.38	Chr11: 614761	<i>IRF7, IRF7, IRF7</i>	Body, Body, Body	Island
cg23942717	0.73	0.87	-0.14	-107.63	Chr7: 56437746			S_Shore
cg15085883	0.47	0.60	-0.14	-48.22	Chr12: 68848994			TRUE
cg00676801	0.22	0.36	-0.13	-60.46	Chr2: 191876673	<i>STAT1, STAT1</i>	5'UTR, 5'UTR	N_Shore
cg08511818	0.37	0.50	-0.13	-46.91	Chr20: 30104637	<i>HM13, HM13, HM13, HM13</i>	Body, Body, Body, Body	S_Shore
cg10690152	0.05	0.18	-0.13	-140.32	Chr6: 31698089	<i>DDAH2</i>	TSS200	Island
cg14964336	0.13	0.26	-0.13	-86.70	Chr4: 1523275			Island
cg11222703	0.55	0.68	-0.13	-52.63	Chr4: 190983569			N_Shelf
cg26328633	0.34	0.48	-0.13	-47.27	Chr5: 135416394	<i>MIR886</i>	TSS200	Island
cg18071071	0.16	0.29	-0.13	-75.83	Chr4: 1558451			S_Shore
cg23066280	0.50	0.64	-0.13	-48.34	Chr7: 158032496	<i>PTPRN2, PTPRN2, PTPRN2</i>	Body, Body, Body	FALSE
cg17251423	0.57	0.71	-0.13	-54.78	Chr5: 139088815			Island
cg15935070	0.55	0.68	-0.13	-52.04	Chr6: 29944146	<i>HCG9</i>	Body	N_Shore
cg26764761	0.64	0.77	-0.13	-66.39	Chr16: 87682142	<i>JPH3</i>	Body	S_Shelf
cg18367631	0.55	0.68	-0.13	-51.34	Chr7: 653309	<i>PRKAR1B, PRKAR1B, PRKAR1B, PRKAR1B, PRKAR1B, PRKAR1B</i>	Body, Body, Body, Body, Body, Body	FALSE
cg21359950	0.52	0.65	-0.13	-47.41	Chr12: 94083470	<i>CRADD</i>	Body	TRUE
cg15287443	0.56	0.69	-0.13	-50.85	Chr3: 147121229	<i>ZIC4, ZIC4, ZIC4</i>	Body, 5'UTR, Body	TRUE
cg26207766	0.47	0.60	-0.13	-43.31	Chr2: 242763794			N_Shelf
cg04554929	0.19	0.32	-0.13	-62.68	Chr8: 105342491			Island
cg21079003	0.53	0.66	-0.13	-46.69	Chr15: 93615146	<i>RGMA, RGMA, RGMA, RGMA, RGMA</i>	Body, Body, Body, Body, Body	N_Shore
cg01948202	0.10	0.23	-0.13	-93.53	Chr3: 122400474	<i>PARP14</i>	Body	S_Shore
cg05600581	0.33	0.46	-0.13	-43.97	ChrX: 134232907	<i>NCRNA00087</i>	TSS200	Island
cg13458803	0.44	0.57	-0.13	-42.00	Chr3: 119276917	<i>CD80</i>	5'UTR	FALSE
cg25340688	0.32	0.45	-0.13	-44.36	Chr5: 135416398	<i>MIR886</i>	TSS200	Island
cg20167074	0.61	0.74	-0.13	-55.45	Chr1: 151967023	<i>S100A10</i>	TSS1500	S_Shore

cg18025438	0.40	0.53	-0.13	-41.41	Chr1: 228756789			Island	FALSE
cg21351392	0.66	0.79	-0.13	-65.52	Chr6: 161607487	<i>AGPAT4</i>	Body		TRUE
cg16486109	0.38	0.50	-0.13	-41.47	Chr11: 613632	<i>IRF7, IRF7, IRF7</i>	Body, Body, Body	N_Shore	FALSE
cg07111834	0.54	0.67	-0.13	-46.54	Chr1: 114402309	<i>PTPN22, PTPN22</i>	Body, Body		TRUE
cg01079652	0.71	0.84	-0.13	-84.51	Chr1: 79118191	<i>IFI44</i>	Body		FALSE
cg18749349	0.61	0.74	-0.13	-54.88	Chr11: 16431523	<i>SOX6, SOX6</i>	5'UTR, TSS1500		FALSE
cg00168785	0.29	0.42	-0.13	-45.26	Chr2: 160142643	<i>WDSUB1, WDSUB1, WDSUB1</i>	5'UTR, 5'UTR, 5'UTR	Island	FALSE
cg07971089	0.33	0.46	-0.13	-42.56	Chr8: 144629702			N_Shelf	FALSE
cg12510708	0.66	0.79	-0.13	-64.72	Chr7: 26193805	<i>NFE2L3</i>	Body	S_Shore	TRUE
cg01175610	0.21	0.33	-0.13	-55.52	Chr12: 12224246	<i>BCL2L14, BCL2L14, BCL2L14</i>	5'UTR, TSS200, TSS200		TRUE
cg14344620	0.64	0.76	-0.13	-57.89	Chr2: 3418831	<i>TTC15</i>	Body		FALSE
cg11168104	0.57	0.69	-0.13	-46.56	Chr5: 1857477			Island	FALSE
cg08124030	0.71	0.84	-0.13	-79.71	Chr3: 149095283	<i>TM4SF1</i>	1stExon		FALSE
cg10599438	0.32	0.45	-0.12	-40.84	Chr19: 844589	<i>PRTN3</i>	Body	N_Shore	FALSE
cg07480608	0.22	0.34	-0.12	-51.62	Chr3: 15352493	<i>SH3BP5, SH3BP5</i>	Body, 5'UTR		TRUE
cg25606201	0.40	0.52	-0.12	-37.80	Chr5: 180614858			N_Shore	FALSE
cg15798862	0.38	0.50	-0.12	-37.96	Chr7: 76129360	<i>DTX2, DTX2, DTX2, DTX2</i>	Body, Body, Body, Body	N_Shore	FALSE
cg15041044	0.76	0.88	-0.12	-102.79	Chr7: 23019795	<i>FAM126A</i>	Body		TRUE
cg13420273	0.73	0.85	-0.12	-82.41	Chr7: 18810212	<i>HDAC9, HDAC9, HDAC9, HDAC9</i>	Body, Body, Body, Body		TRUE
cg24113243	0.62	0.74	-0.12	-50.91	Chr12: 132882028	<i>GALNT9</i>	Body	Island	FALSE
cg00256231	0.17	0.29	-0.12	-59.86	Chr17: 77916733	<i>TBC1D16</i>	Body	Island	TRUE
cg20529645	0.42	0.55	-0.12	-36.39	Chr4: 5886898	<i>CRMP1, CRMP1</i>	Body, Body	N_Shelf	FALSE
cg02253142	0.63	0.75	-0.12	-51.06	Chr15: 52048211	<i>TMOD2, TMOD2</i>	5'UTR, 5'UTR	S_Shelf	FALSE
cg11186706	0.74	0.86	-0.12	-83.61	Chr14: 54815745				TRUE
cg17322044	0.67	0.79	-0.12	-60.32	Chr12: 125140105				TRUE
cg08477687	0.36	0.48	-0.12	-36.30	Chr1: 566570	<i>MIR1977</i>	TSS1500		FALSE
cg23280506	0.40	0.52	-0.12	-35.61	Chr17: 14201938			Island	FALSE
cg16985233	0.65	0.77	-0.12	-54.17	Chr15: 43806249			S_Shelf	FALSE
cg03513464	0.55	0.67	-0.12	-39.88	Chr1: 58898672				TRUE
cg04122858	0.79	0.91	-0.12	-118.35	Chr3: 46799010			S_Shore	FALSE
cg24550026	0.37	0.49	-0.12	-35.33	Chr1: 114430031	<i>BCL2L15, BCL2L15</i>	1stExon, 5'UTR		FALSE
cg03142697	0.28	0.40	-0.12	-39.68	Chr21: 36258497	<i>RUNX1, RUNX1, RUNX1</i>	Body, Body, Body	N_Shore	FALSE
cg05276469	0.20	0.32	-0.12	-50.58	Chr17: 16570473			Island	FALSE
cg07629776	0.40	0.52	-0.12	-34.26	Chr10: 13972210	<i>FRMD4A</i>	Body		TRUE
cg13144059	0.83	0.95	-0.12	-168.18	Chr2: 201245077	<i>SPATS2L, SPATS2L, SPATS2L, SPATS2L</i>	5'UTR, 5'UTR, 5'UTR, 5'UTR		TRUE
cg25753473	0.14	0.26	-0.12	-64.23	Chr6: 170532835			S_Shelf	FALSE
cg19046167	0.78	0.90	-0.12	-107.68	Chr17: 80928561	<i>B3GNTL1</i>	Body	N_Shore	FALSE
cg01911981	0.84	0.96	-0.12	-190.45	Chr8: 39380341	<i>ADAM3A, ADAM3A, ADAM3A</i>	Body, Body, Body	Island	FALSE

cg24341059	0.78	0.90	-0.12	-103.37	Chr8: 121604940	<i>SNTB1</i>	Body		TRUE
cg11652636	0.08	0.19	-0.12	-92.05	Chr2: 55450823	<i>C2orf63, C2orf63</i>	5'UTR, 5'UTR	Island	FALSE
cg00124993	0.31	0.43	-0.12	-36.67	Chr5: 135416412	<i>MIR886</i>	TSS200	Island	FALSE
cg15115365	0.53	0.65	-0.12	-36.70	Chr5: 88384656				TRUE
cg03995300	0.43	0.55	-0.12	-33.49	Chr17: 5019989	<i>ZNF232</i>	5'UTR	S_Shore	FALSE
cg01636599	0.27	0.39	-0.12	-39.91	Chr19: 639386	<i>FGF22</i>	TSS1500	Island	TRUE
cg16717578	0.73	0.85	-0.12	-76.98	Chr19: 867030			Island	FALSE
cg13909895	0.31	0.43	-0.12	-36.10	Chr22: 51066142	<i>ARSA, ARSA, ARSA, ARSA, ARSA</i>	1stExon, Body, Body, Body, 5'UTR	Island	FALSE
cg14939821	0.44	0.56	-0.12	-33.16	Chr10: 128947230	<i>DOCK1, FAM196A</i>	Body, Body		TRUE
cg03168497	0.26	0.38	-0.12	-40.07	Chr17: 48586147	<i>MYCBPAP</i>	Body	Island	FALSE
cg11478607	0.12	0.23	-0.12	-69.68	Chr22: 24384400	<i>GSTT1</i>	TSS200	Island	FALSE
cg25120325	0.75	0.86	-0.12	-80.26	Chr10: 118380370	<i>PNLIPRP2</i>	TSS200		FALSE
cg04602696	0.57	0.68	-0.12	-37.87	Chr16: 88846723	<i>FAM38A</i>	Body	S_Shore	TRUE
cg25034424	0.69	0.81	-0.12	-59.53	Chr4: 1513089			N_Shore	FALSE
cg03829194	0.71	0.83	-0.12	-65.77	Chr16: 875571			Island	TRUE
cg16853860	0.45	0.57	-0.12	-32.21	Chr6: 32823116	<i>PSMB9, PSMB9, TAP1</i>	Body, Body, TSS1500	S_Shore	FALSE
cg04974804	0.69	0.80	-0.12	-57.37	Chr1: 23521815	<i>HTR1D</i>	TSS1500		FALSE
cg02978505	0.39	0.51	-0.12	-31.93	Chr16: 85292322				TRUE
cg02869559	0.32	0.44	-0.12	-33.96	Chr21: 36259067	<i>RUNX1, RUNX1, RUNX1</i>	Body, Body, Body	Island	FALSE
cg06236987	0.79	0.90	-0.12	-103.21	Chr6: 114225023	<i>FLJ34503</i>	TSS1500		TRUE
cg20481287	0.53	0.64	-0.12	-34.35	Chr12: 12224457	<i>BCL2L14, BCL2L14, BCL2L14, BCL2L14</i>	5'UTR, 5'UTR, 1stExon, 5'UTR, 1stExon		TRUE
cg16379462	0.77	0.88	-0.12	-88.82	Chr14: 55119082	<i>SAMD4A, SAMD4A</i>	Body, Body		TRUE
cg02148547	0.60	0.72	-0.12	-40.36	Chr14: 21457502	<i>METT11D1, METT11D1</i>	TSS1500, TSS1500	N_Shore	FALSE
cg06536614	0.34	0.45	-0.12	-32.91	Chr5: 135416381	<i>MIR886</i>	TSS200	Island	FALSE
cg02830749	0.70	0.82	-0.11	-59.50	Chr4: 154451068	<i>KIAA0922, KIAA0922</i>	Body, Body		TRUE
cg12463578	0.49	0.60	-0.11	-31.99	Chr6: 29644756	<i>ZFP57</i>	1stExon		FALSE
cg04742550	0.43	0.54	-0.11	-30.80	Chr16: 31366429	<i>ITGAX</i>	TSS200		FALSE
cg08534443	0.51	0.62	-0.11	-32.44	Chr12: 133022550			N_Shore	FALSE
cg00169792	0.30	0.41	-0.11	-34.10	Chr20: 50418554	<i>SALL4</i>	Body	Island	FALSE
cg25849281	0.30	0.42	-0.11	-33.71	Chr1: 8937077	<i>ENO1</i>	5'UTR	N_Shore	FALSE
cg05337761	0.42	0.53	-0.11	-30.11	Chr1: 2121349	<i>C1orf86, LOC100128003, C1orf86</i>	Body, Body, Body	Island	FALSE
cg25737313	0.43	0.55	-0.11	-29.74	Chr19: 12899557			N_Shore	FALSE
cg13569486	0.49	0.60	-0.11	-30.47	Chr11: 8290738			S_Shore	TRUE
cg08787039	0.54	0.65	-0.11	-32.48	Chr1: 182921857	<i>C1orf14</i>	Body	Island	FALSE
cg26876834	0.72	0.83	-0.11	-61.32	Chr16: 2013573	<i>SNHG9, SNORA64, SNORA10, RPS2</i>	TSS1500, TSS1500, TSS1500, Body	N_Shore	FALSE
cg06385583	0.20	0.31	-0.11	-42.72	Chr2: 12596843				TRUE

cg18108683	0.77	0.88	-0.11	-81.44	Chr7: 102477205	<i>FBXL13, FBXL13</i>	Body, Body		TRUE
cg04380118	0.48	0.59	-0.11	-29.42	Chr1: 45670624	<i>ZSWIM5</i>	Body	N_Shore	FALSE
cg09704168	0.29	0.40	-0.11	-32.71	Chr17: 32751554				TRUE
cg27102141	0.65	0.76	-0.11	-43.78	Chr10: 131843798			Island	FALSE
cg24522654	0.66	0.77	-0.11	-44.14	Chr12: 19535154				TRUE
cg16366262	0.50	0.61	-0.11	-29.34	Chr1: 1118157	<i>TTLL10, TTLL10</i>	Body, Body	S_Shelf	FALSE
cg15309053	0.41	0.52	-0.11	-28.06	Chr8: 964076			S_Shore	FALSE
cg11834066	0.65	0.76	-0.11	-42.74	ChrX: 145701413			Island	FALSE
cg19751990	0.76	0.87	-0.11	-74.33	Chr11: 5800287	<i>OR52N5</i>	TSS1500		FALSE
cg11979743	0.02	0.13	-0.11	-130.60	Chr20: 814510	<i>FAM110A, FAM110A</i>	1stExon, 5'UTR	Island	FALSE
cg27366964	0.54	0.65	-0.11	-31.17	Chr10: 77946906	<i>C10orf11</i>	Body		TRUE
cg01088404	0.54	0.65	-0.11	-30.90	Chr12: 48214523	<i>HDAC7, HDAC7</i>	TSS1500, TSS1500	S_Shore	FALSE
cg17165241	0.60	0.71	-0.11	-36.12	Chr11: 400385	<i>PKP3</i>	Body	Island	FALSE
cg19637330	0.34	0.45	-0.11	-29.30	Chr1: 19110922			Island	TRUE
cg24506221	0.13	0.24	-0.11	-58.62	Chr1: 110230401	<i>GSTM1, GSTM1</i>	TSS200, TSS200	Island	FALSE
cg01664727	0.27	0.38	-0.11	-33.08	Chr21: 36258423	<i>RUNX1, RUNX1, RUNX1</i>	Body, Body, Body	N_Shore	FALSE
cg00599163	0.66	0.77	-0.11	-43.60	Chr2: 162100495			N_Shore	FALSE
cg12765123	0.51	0.62	-0.11	-29.09	Chr10: 132100019				FALSE
cg08381620	0.42	0.53	-0.11	-27.21	Chr13: 24062873				TRUE
cg16363586	0.22	0.33	-0.11	-38.50	Chr19: 17516329	<i>BST2</i>	1stExon		TRUE
cg15498134	0.68	0.79	-0.11	-46.75	Chr1: 25246854	<i>RUNX3, RUNX3</i>	Body, Body		TRUE
cg01406381	0.38	0.49	-0.11	-27.38	Chr19: 47288263	<i>SLC1A5, SLC1A5, SLC1A5</i>	TSS200, Body, 5'UTR	N_Shelf	FALSE
cg07777042	0.73	0.84	-0.11	-61.26	Chr8: 144702879			S_Shelf	FALSE
cg26896946	0.35	0.46	-0.11	-27.87	Chr5: 135416405	<i>MIR886</i>	TSS200	Island	FALSE
cg05282260	0.77	0.88	-0.11	-78.90	Chr6: 156983263				FALSE
cg09033563	0.13	0.24	-0.11	-55.63	Chr22: 24373618	<i>LOC391322</i>	Body	Island	FALSE
cg22094750	0.04	0.15	-0.11	-104.98	Chr1: 1851056	<i>TMEM52</i>	TSS1500	Island	FALSE
cg06952519	0.78	0.89	-0.11	-83.64	Chr17: 2057234	<i>SMG6, SMG6</i>	Body, Body		FALSE
cg12015615	0.60	0.71	-0.11	-34.11	Chr7: 55540725	<i>VOPP1</i>	Body		FALSE
cg03834411	0.70	0.81	-0.11	-49.83	Chr16: 87682036	<i>JPH3</i>	Body	S_Shelf	FALSE
cg17790273	0.45	0.56	-0.11	-26.63	Chr17: 49040709	<i>SPAG9, SPAG9</i>	3'UTR, 3'UTR		TRUE
cg05931119	0.65	0.76	-0.11	-40.03	Chr6: 168569742				FALSE
cg06603074	0.30	0.41	-0.11	-29.66	Chr18: 60192893	<i>ZCCHC2</i>	Body	N_Shore	FALSE
cg10407894	0.71	0.82	-0.11	-54.33	Chr7: 148517345	<i>EZH2, EZH2</i>	Body, Body		TRUE
cg23071186	0.41	0.52	-0.11	-26.35	Chr19: 6669849	<i>TNFSF14, TNFSF14</i>	Body, Body		FALSE
cg02018277	0.04	0.15	-0.11	-98.25	Chr15: 65116255	<i>PIF1</i>	Body	Island	FALSE
cg22549408	0.63	0.74	-0.11	-37.35	Chr18: 57566300	<i>PMAIP1</i>	TSS1500	N_Shore	FALSE
cg00538591	0.61	0.72	-0.11	-34.43	Chr16: 89008994	<i>CBFA2T3, CBFA2T3</i>	TSS1500, Body	S_Shore	FALSE
cg25232942	0.10	0.21	-0.11	-63.93	Chr19: 50194519	<i>CPT1C, CPT1C, CPT1C, CPT1C</i>	1stExon, 1stExon, 5'UTR, 5'UTR	Island	FALSE

cg27366766	0.12	0.22	-0.11	-59.08	Chr17: 56565286	<i>HSF5</i>	1stExon	Island	FALSE
cg07252200	0.55	0.66	-0.11	-29.57	Chr10: 125751941			Island	FALSE
cg18735015	0.36	0.47	-0.11	-26.80	Chr10: 105428506	<i>SH3PXD2A</i>	Body	Island	TRUE
cg08284263	0.36	0.46	-0.11	-26.81	Chr10: 92958627				TRUE
cg23085143	0.42	0.53	-0.11	-25.52	Chr7: 138349443	<i>SVOPL, SVOPL</i>	Body, TSS1500	Island	FALSE
cg13076785	0.76	0.86	-0.11	-67.49	Chr6: 32520916	<i>HLA-DRB6</i>	Body		FALSE
cg18678645	0.29	0.40	-0.11	-29.16	Chr5: 135416331	<i>MIR886</i>	TSS200	Island	FALSE
cg10510935	0.33	0.44	-0.11	-27.22	Chr1: 4059661				FALSE
cg09438522	0.29	0.40	-0.11	-29.05	Chr3: 15000765	<i>NR2C2</i>	5'UTR		TRUE
cg03809847	0.20	0.31	-0.11	-38.10	Chr17: 79093482	<i>AATK</i>	Body	Island	TRUE
cg00994804	0.27	0.37	-0.11	-30.82	Chr21: 36259383	<i>RUNX1, RUNX1, RUNX1</i>	1stExon, 1stExon, Body	Island	TRUE
cg23024343	0.73	0.83	-0.11	-54.92	Chr7: 107201750	<i>COG5, COG5, COG5</i>	Body, Body, Body	N_Shelf	FALSE
cg16341836	0.44	0.55	-0.11	-24.92	Chr10: 90641389	<i>STAMBPL1</i>	5'UTR	S_Shore	FALSE
cg26312951	0.15	0.25	-0.11	-47.95	Chr21: 42797847	<i>MX1, MX1</i>	TSS200, 5'UTR	N_Shore	TRUE
cg18125510	0.15	0.25	-0.11	-47.46	Chr14: 100841768	<i>WARS, WDR25, WARS, WARS, WDR25, WARS, WARS</i>	1stExon, TSS1500, 5'UTR, 5'UTR, TSS1500, 1stExon, 5'UTR, 5'UTR	N_Shore	FALSE
cg12623145	0.29	0.40	-0.11	-28.44	Chr2: 97778927	<i>ANKRD36</i>	TSS1500	Island	FALSE
cg11025609	0.68	0.79	-0.11	-42.81	Chr12: 110727072	<i>ATP2A2, ATP2A2, ATP2A2</i>	Body, Body, Body		TRUE
cg12800105	0.67	0.78	-0.11	-41.20	Chr12: 121972412	<i>KDM2B, KDM2B</i>	Body, Body	N_Shelf	FALSE
cg05487134	0.19	0.30	-0.11	-37.98	Chr17: 40489569	<i>STAT3, STAT3, STAT3</i>	Body, Body, Body		FALSE
cg17573270	0.58	0.68	-0.11	-29.15	Chr22: 42950376	<i>SERHL2</i>	Body	S_Shore	FALSE
cg06401414	0.58	0.68	-0.11	-29.33	Chr8: 141599436	<i>EIF2C2, EIF2C2</i>	Body, Body		FALSE
cg12362118	0.29	0.40	-0.10	-28.00	Chr3: 148995174				FALSE
cg12253071	0.65	0.75	-0.10	-36.28	Chr4: 19740944				TRUE
cg08562672	0.35	0.46	-0.10	-25.24	Chr19: 21860753			N_Shore	FALSE
cg19735514	0.65	0.75	-0.10	-36.47	Chr1: 161762739	<i>ATF6</i>	Body		FALSE
cg20737388	0.47	0.57	-0.10	-24.30	Chr11: 73668626	<i>DNAJB13</i>	Body		FALSE
cg27633287	0.65	0.76	-0.10	-36.97	Chr12: 130766243				FALSE
cg02402208	0.27	0.38	-0.10	-28.87	ChrY: 9384707			N_Shore	FALSE
cg26724018	0.18	0.29	-0.10	-39.25	Chr11: 5716255	<i>TRIM22</i>	5'UTR		FALSE
cg13593090	0.51	0.61	-0.10	-25.11	Chr19: 9546723	<i>ZNF266, ZNF266</i>	TSS1500, TSS1500	S_Shore	FALSE
cg20376189	0.77	0.87	-0.10	-66.64	Chr6: 7317168			S_Shelf	FALSE
cg06546677	0.67	0.78	-0.10	-39.50	Chr8: 145537504	<i>HSF1</i>	Body		TRUE
cg21058822	0.75	0.86	-0.10	-60.28	Chr8: 30002223	<i>MBOAT4</i>	TSS200		FALSE
cg13210558	0.72	0.82	-0.10	-49.13	Chr9: 138369918			N_Shore	FALSE
cg08010094	0.54	0.65	-0.10	-25.88	Chr2: 139539001	<i>NXPH2</i>	TSS1500	S_Shore	FALSE
cg13753488	0.34	0.44	-0.10	-24.71	Chr9: 136001623	<i>RALGDS</i>	Body		TRUE
cg10927178	0.25	0.35	-0.10	-29.76	Chr20: 56883965	<i>RAB22A, PPP4R1L</i>	TSS1500, Body	N_Shore	FALSE
cg17329648	0.69	0.79	-0.10	-41.32	Chr2: 73297389	<i>SFXN5</i>	Body	N_Shore	FALSE

cg09084320	0.70	0.80	-0.10	-43.12	Chr10: 33553435	<i>NRP1, NRP1, NRP1</i>	Body, Body, Body		TRUE
cg15954353	0.75	0.85	-0.10	-57.95	Chr17: 5403337	<i>LOC728392</i>	3'UTR	Island	FALSE
cg14628108	0.77	0.87	-0.10	-64.60	Chr12: 106631875	<i>CKAP4</i>	3'UTR	N_Shore	TRUE
cg00355656	0.61	0.72	-0.10	-30.72	Chr1: 229692519	<i>ABCB10</i>	Body	N_Shore	FALSE
cg22107533	0.49	0.59	-0.10	-23.62	Chr15: 45028083	<i>TRIM69, TRIM69</i>	TSS1500, TSS1500		TRUE
cg06679494	0.34	0.45	-0.10	-24.09	Chr17: 6921295	<i>MIR497, MIR195</i>	Body, TSS1500	S_Shelf	FALSE
cg00269725	0.74	0.84	-0.10	-54.55	Chr6: 156983315				FALSE
cg05439368	0.62	0.72	-0.10	-31.06	Chr15: 45028098	<i>TRIM69, TRIM69</i>	TSS1500, TSS1500		TRUE
cg10184328	0.46	0.57	-0.10	-22.94	Chr7: 138349158	<i>SVOPL, SVOPL</i>	Body, TSS200	Island	FALSE
cg00479463	0.55	0.65	-0.10	-25.71	Chr19: 33726786			Island	FALSE
cg01771247	0.67	0.77	-0.10	-37.21	Chr16: 61846623	<i>CDH8</i>	Body		TRUE
cg05883128	0.13	0.23	-0.10	-49.16	Chr4: 169239131	<i>DDX60</i>	5'UTR	N_Shore	FALSE
cg23835219	0.57	0.67	-0.10	-26.62	Chr4: 1244017	<i>CTBP1, CTBP1, C4orf42</i>	TSS1500, TSS1500, TSS200	Island	FALSE
cg04515608	0.65	0.75	-0.10	-34.24	Chr11: 48129067	<i>PTPRJ, PTPRJ</i>	Body, Body		TRUE
cg09315878	0.71	0.81	-0.10	-43.74	Chr1: 1152580	<i>SDF4, SDF4</i>	3'UTR, 3'UTR	Island	FALSE
cg25897951	0.62	0.72	-0.10	-30.76	Chr4: 1244024	<i>CTBP1, CTBP1, C4orf42</i>	TSS1500, TSS1500, TSS200	Island	FALSE
cg22544881	0.59	0.70	-0.10	-28.14	Chr7: 130712346	<i>FLJ43663, FLJ43663</i>	Body, Body		TRUE
cg05992904	0.75	0.85	-0.10	-56.45	Chr22: 48892994	<i>FAM19A5</i>	Body	N_Shelf	FALSE
cg04138046	0.70	0.80	-0.10	-42.09	Chr5: 112608004	<i>MCC, MCC</i>	Body, Body		TRUE
cg17502213	0.71	0.81	-0.10	-44.56	Chr1: 58704335	<i>DAB1</i>	5'UTR		TRUE
cg23084506	0.46	0.56	-0.10	-22.46	Chr1: 13111908	<i>PRAMEF5</i>	Body		FALSE
cg05850997	0.73	0.83	-0.10	-50.42	Chr4: 89207307	<i>PPM1K</i>	TSS1500	S_Shore	FALSE
cg16092135	0.53	0.63	-0.10	-24.27	Chr2: 307058			Island	FALSE
cg24115681	0.66	0.76	-0.10	-35.34	Chr7: 114566161	<i>MDFIC, MDFIC</i>	Body, Body	S_Shelf	FALSE
cg15411272	0.25	0.36	-0.10	-28.38	Chr6: 29895187			S_Shore	FALSE
cg00343839	0.31	0.41	-0.10	-24.58	Chr17: 5403516	<i>LOC728392, LOC728392</i>	1stExon, 3'UTR	Island	FALSE
cg09318375	0.10	0.20	-0.10	-56.28	Chr1: 67218090	<i>TCTEX1D1</i>	TSS200	Island	TRUE
cg21169490	0.48	0.58	-0.10	-22.37	Chr6: 73135072				TRUE
cg07600533	0.79	0.89	-0.10	-75.85	Chr22: 50986031	<i>KLHDC7B</i>	TSS1500	Island	FALSE
cg24680439	0.52	0.62	-0.10	-23.47	Chr10: 134778467			N_Shore	FALSE
cg12494529	0.71	0.81	-0.10	-44.43	Chr10: 1082432	<i>C10orf110, C10orf110, C10orf110, C10orf110</i>	Body, Body, Body, Body		TRUE
cg08575688	0.69	0.80	-0.10	-40.20	Chr2: 228678500	<i>CCL20, CCL20</i>	TSS200, TSS200		FALSE
cg24794857	0.20	0.30	-0.10	-33.99	Chr4: 187113578	<i>CYP4V2</i>	Body	S_Shore	FALSE
cg09987201	0.06	0.16	-0.10	-77.84	Chr9: 130549116	<i>CDK9</i>	Body	Island	FALSE
cg06357908	0.49	0.59	-0.10	-22.37	Chr1: 192548609	<i>RGS1</i>	3'UTR		FALSE
cg07621803	0.63	0.73	-0.10	-30.28	Chr18: 76674796			Island	FALSE
cg12115302	0.58	0.68	-0.10	-26.37	Chr12: 30323676			S_Shore	FALSE
cg04242525	0.79	0.89	-0.10	-74.96	Chr8: 144236576				FALSE

cg20128323	0.51	0.62	-0.10	-23.07	Chr6: 9503813				TRUE
cg05617801	0.71	0.82	-0.10	-44.32	Chr2: 108008839				FALSE
cg05656688	0.69	0.79	-0.10	-39.13	Chr1: 25254088	RUNX3, RUNX3	Body, Body	N_Shore	TRUE
cg01624173	0.32	0.42	-0.10	-23.73	Chr14: 75981868				TRUE
cg06508867	0.31	0.41	-0.10	-23.95	Chr16: 87814178			S_Shore	FALSE
cg06904356	0.53	0.63	-0.10	-23.35	Chr5: 1849983			N_Shore	FALSE
cg23681866	0.25	0.35	-0.10	-27.67	Chr6: 29895175			S_Shore	FALSE
cg02531227	0.51	0.61	-0.10	-22.59	Chr12: 129460621	GLT1D1	Body		FALSE
Hypermethylation									
cg05176970	0.75	0.35	0.40	341.10	Chr17: 724273	NXN	Body		FALSE
cg00256329	0.71	0.37	0.34	341.10	Chr17: 724374	NXN	Body		FALSE
cg19214707	0.65	0.32	0.33	341.10	Chr7: 3157722				TRUE
cg18402987	0.36	0.04	0.32	341.10	Chr7: 1209562				FALSE
cg03188948	0.50	0.19	0.31	341.10	Chr7: 1209495				FALSE
cg15262954	0.40	0.09	0.30	341.10	Chr20: 62198872	PRIC285, PRIC285	Body, 1stExon	Island	FALSE
cg15591384	0.75	0.49	0.26	341.10	Chr6: 32525960	HLA-DRB6	Body		FALSE
cg17178900	0.54	0.28	0.26	341.10	Chr1: 205818956	PM20D1	Body	Island	TRUE
cg22355889	0.33	0.08	0.25	341.10	Chr11: 107461585	ELMOD1, LOC643923, ELMOD1	TSS1500, TSS1500, TSS1500	N_Shore	FALSE
cg26354017	0.50	0.26	0.24	341.10	Chr1: 205819088	PM20D1	1stExon	Island	TRUE
cg14159672	0.50	0.26	0.24	341.10	Chr1: 205819179	PM20D1	1stExon	Island	TRUE
cg11224582	0.39	0.15	0.24	341.10	Chr12: 4919138	KCNA6, KCNA6	5'UTR, 1stExon	Island	FALSE
cg19870512	0.33	0.10	0.24	341.10	Chr12: 4919081	KCNA6, KCNA6	5'UTR, 1stExon	Island	FALSE
cg07167872	0.48	0.24	0.24	341.10	Chr1: 205819463	PM20D1	TSS200	S_Shore	FALSE
cg10671668	0.32	0.09	0.23	341.10	Chr12: 4919230	KCNA6	1stExon	Island	FALSE
cg24118521	0.67	0.45	0.22	341.10	Chr13: 47472330	HTR2A, HTR2A	TSS1500, TSS1500		FALSE
cg24503407	0.48	0.26	0.22	341.10	Chr1: 205819492	PM20D1	TSS1500	S_Shore	FALSE
cg19362774	0.87	0.66	0.21	341.10	Chr8: 6664522			S_Shore	FALSE
cg26858704	0.28	0.07	0.21	341.10	Chr12: 4918848	KCNA6, KCNA6	5'UTR, 1stExon	Island	FALSE
cg18803147	0.63	0.42	0.21	341.10	Chr5: 2743124			S_Shore	FALSE
cg14911689	0.48	0.27	0.20	341.10	Chr12: 739980	NINJ2	Body		FALSE
cg08624648	0.75	0.54	0.20	341.10	Chr6: 31651029			Island	FALSE
cg26654770	0.49	0.29	0.20	126.71	Chr12: 740100	NINJ2	Body		FALSE
cg18264486	0.71	0.52	0.19	126.71	Chr6: 31650916			Island	FALSE
cg25407410	0.77	0.58	0.19	341.10	Chr6: 143891975	LOC285740	TSS1500		FALSE
cg11965913	0.36	0.17	0.19	341.10	Chr1: 205819406	PM20D1	TSS200	S_Shore	FALSE
cg12119625	0.51	0.32	0.19	108.12	Chr19: 54106789	LOC284379	TSS200		FALSE
cg14893161	0.40	0.21	0.19	126.71	Chr1: 205819251	PM20D1, PM20D1	5'UTR, 1stExon	S_Shore	TRUE
cg00101728	0.64	0.46	0.18	103.94	Chr6: 2953027	SERPINB6	Body		TRUE
cg05380919	0.81	0.63	0.18	341.10	Chr22: 24376252	GSTT1	3'UTR	S_Shelf	FALSE
cg11738485	0.53	0.35	0.18	94.77	Chr19: 12877000	HOOK2, HOOK2	Body, Body	Island	FALSE
cg01500431	0.83	0.66	0.18	341.10	Chr22: 24388327	GSTTP2	Body	S_Shelf	FALSE

cg13679164	0.76	0.58	0.18	120.85	Chr6: 161258479				FALSE
cg01201512	0.58	0.40	0.18	92.49	Chr12: 740338	<i>NINJ2</i>	Body		TRUE
cg15242686	0.63	0.45	0.18	94.31	Chr22: 24348715	<i>GSTTP1</i>	TSS1500		FALSE
cg10604476	0.35	0.18	0.18	123.79	Chr19: 10403908	<i>ICAM5</i>	Body	Island	FALSE
cg23881368	0.61	0.43	0.18	90.87	Chr13: 47472343	<i>HTR2A, HTR2A</i>	TSS1500, TSS1500		FALSE
cg01243072	0.54	0.37	0.18	89.99	Chr2: 43398171			Island	FALSE
cg09584650	0.46	0.29	0.17	93.56	Chr8: 2002012	<i>MYOM2</i>	Body	N_Shore	FALSE
cg01560476	0.49	0.31	0.17	86.56	Chr16: 24743405	<i>TNRC6A</i>	Body	S_Shore	FALSE
cg23708337	0.26	0.09	0.17	341.10	Chr7: 1209742				FALSE
cg09727148	0.46	0.29	0.17	87.48	Chr21: 43560719	<i>UMODL1,</i> <i>UMODL1</i>	3'UTR, 3'UTR		FALSE
cg05185784	0.66	0.49	0.17	86.16	Chr16: 90016020	<i>DEF8, DEF8</i>	5'UTR, Body	Island	FALSE
cg01517680	0.72	0.55	0.17	93.15	Chr16: 49499006			Island	TRUE
cg14580085	0.62	0.45	0.17	80.09	Chr2: 239553406				TRUE
cg02389040	0.76	0.59	0.17	103.50	Chr6: 31650786			Island	FALSE
cg22240348	0.26	0.10	0.17	341.10	Chr21: 46975805			Island	FALSE
cg05082466	0.71	0.54	0.17	90.73	Chr6: 2953123	<i>SERPINB6</i>	Body		TRUE
cg08917117	0.37	0.21	0.16	99.14	Chr10: 115059021				TRUE
cg18105134	0.76	0.60	0.16	100.95	Chr13: 113819100	<i>PROZ</i>	Body		FALSE
cg00440797	0.26	0.10	0.16	341.10	Chr6: 32493873	<i>HLA-DRB5</i>	Body	S_Shelf	FALSE
cg01889448	0.86	0.70	0.16	341.10	Chr6: 32635871	<i>HLA-DQB1</i>	TSS1500	S_Shelf	FALSE
cg18200810	0.50	0.34	0.16	72.98	Chr13: 47472200	<i>HTR2A, HTR2A</i>	TSS1500, TSS1500		FALSE
cg06417478	0.47	0.31	0.16	70.85	Chr19: 12876846	<i>HOOK2, HOOK2</i>	Body, Body	N_Shore	FALSE
cg12064134	0.81	0.65	0.16	106.18	Chr16: 90016061	<i>DEF8, DEF8</i>	5'UTR, Body	Island	FALSE
cg00492070	0.62	0.46	0.16	68.49	Chr3: 107810716	<i>CD47, CD47, CD47</i>	TSS1500, TSS1500, TSS1500	S_Shore	FALSE
cg02285791	0.55	0.40	0.15	66.17	Chr6: 27550747				FALSE
cg16781264	0.33	0.18	0.15	93.66	Chr2: 101087575	<i>NMS</i>	Body		FALSE
cg27084028	0.39	0.24	0.15	77.80	Chr7: 6836436	<i>RSPH10B,</i> <i>RSPH10B2</i>	Body, Body		FALSE
cg20435535	0.71	0.55	0.15	75.82	Chr6: 31651151			Island	FALSE
cg10528576	0.63	0.47	0.15	66.07	Chr14: 101192913	<i>DLK1</i>	TSS1500	Island	FALSE
cg02304584	0.69	0.53	0.15	71.23	Chr6: 31650790			Island	FALSE
cg05857999	0.66	0.51	0.15	68.44	Chr6: 31650760			Island	FALSE
cg01274643	0.23	0.08	0.15	341.10	Chr11: 1283946				TRUE
cg06460587	0.74	0.59	0.15	79.45	Chr6: 31650930			Island	FALSE
cg01246520	0.28	0.13	0.15	106.99	Chr17: 17644344	<i>RAI1</i>	5'UTR		TRUE
cg11141652	0.58	0.43	0.15	62.14	Chr22: 24348549	<i>GSTTP1</i>	TSS1500		FALSE
cg17593958	0.30	0.15	0.15	94.68	Chr20: 62199034	<i>PRIC285, PRIC285,</i> <i>PRIC285</i>	5'UTR, Body, 1stExon	N_Shore	FALSE
cg16761754	0.44	0.29	0.15	63.91	Chr14: 105127242			S_Shore	FALSE
cg01252526	0.49	0.34	0.15	60.04	Chr16: 711033	<i>WDR90</i>	Body	N_Shore	TRUE
cg18576957	0.74	0.59	0.15	74.60	Chr6: 31651020			Island	FALSE

cg14641829	0.88	0.73	0.15	341.10	Chr9: 33270634	<i>SUGT1P1, CHMP5</i>	Body, Body		FALSE
cg07403350	0.64	0.49	0.15	59.75	Chr13: 108867111	<i>LIG4, LIG4, LIG4, LIG4</i>	5'UTR, 1stExon, 5'UTR, 5'UTR	Island	FALSE
cg05795849	0.50	0.36	0.15	57.48	Chr3: 4794082	<i>ITPR1, ITPR1, ITPR1, EGOT</i>	Body, Body, Body, TSS1500		TRUE
cg00813378	0.46	0.31	0.15	60.19	Chr1: 1475209	<i>C1orf70</i>	Body	Island	FALSE
cg08083251	0.69	0.54	0.14	63.82	Chr13: 23309930				FALSE
cg19980771	0.46	0.31	0.14	58.77	Chr6: 110798022	<i>SLC22A16</i>	TSS200	Island	FALSE
cg17518825	0.80	0.65	0.14	86.46	Chr2: 46523461	<i>EPAS1</i>	TSS1500	N_Shore	FALSE
cg25417675	0.76	0.62	0.14	76.52	Chr6: 31651059			Island	FALSE
cg27279301	0.65	0.50	0.14	57.27	Chr14: 105945287	<i>CRIP2</i>	Body	Island	FALSE
cg14279856	0.52	0.38	0.14	53.72	Chr6: 30851086	<i>DDR1, DDR1</i>	TSS1500, TSS1500	N_Shore	TRUE
cg22318514	0.54	0.40	0.14	52.87	Chr6: 31650850			Island	FALSE
cg15529432	0.54	0.40	0.14	52.70	Chr5: 16615750	<i>FAM134B</i>	Body	N_Shore	FALSE
cg27128560	0.73	0.59	0.14	65.51	Chr10: 105815443	<i>COL17A1</i>	Body		TRUE
cg11146691	0.56	0.42	0.14	51.77	Chr12: 47219737	<i>SLC38A4, SLC38A4, SLC38A4, SLC38A4</i>	1stExon, 5'UTR, 1stExon, 5'UTR		FALSE
cg18232235	0.89	0.75	0.14	341.10	Chr12: 11700321				FALSE
cg12367833	0.86	0.72	0.14	111.23	Chr4: 42764094				TRUE
cg04227007	0.74	0.61	0.14	66.91	Chr19: 37760583	<i>LOC284412</i>	TSS1500	N_Shore	FALSE
cg03393996	0.33	0.19	0.14	70.02	Chr4: 1580377			Island	FALSE
cg10430963	0.66	0.52	0.14	54.05	Chr17: 37124558	<i>FBXO47</i>	TSS1500		FALSE
cg18156486	0.57	0.43	0.14	49.40	Chr11: 2884295			Island	FALSE
cg01299579	0.29	0.15	0.14	82.11	Chr2: 10830716	<i>NOL10</i>	TSS1500	S_Shore	FALSE
cg07618780	0.57	0.43	0.14	48.84	Chr2: 240142806	<i>HDAC4</i>	Body		FALSE
cg05547895	0.50	0.36	0.14	48.79	Chr3: 196705855				FALSE
cg21434132	0.40	0.26	0.13	54.70	Chr3: 196705742				FALSE
cg16922644	0.71	0.58	0.13	56.99	Chr10: 45146765				TRUE
cg20558320	0.47	0.34	0.13	47.85	Chr2: 235210313				TRUE
cg13390570	0.32	0.19	0.13	67.57	Chr5: 1255616	<i>TERT, TERT</i>	Body, Body	N_Shore	FALSE
cg27182070	0.51	0.37	0.13	45.82	Chr1: 28218282	<i>RPA2</i>	3'UTR		FALSE
cg21078654	0.48	0.35	0.13	46.48	Chr15: 52130305	<i>TMOD3</i>	5'UTR		TRUE
cg15363314	0.22	0.08	0.13	108.37	Chr11: 1283970				TRUE
cg10920224	0.58	0.45	0.13	45.64	Chr14: 103367591	<i>TRAF3, TRAF3, TRAF3</i>	Body, Body, Body		FALSE
cg00739471	0.43	0.30	0.13	48.95	Chr14: 69415588	<i>ACTN1, ACTN1, ACTN1</i>	Body, Body, Body		FALSE
cg08133631	0.56	0.42	0.13	44.11	Chr1: 26527909	<i>CATSPER4</i>	Body		TRUE
cg04329125	0.50	0.37	0.13	44.31	Chr14: 105945022	<i>CRIP2</i>	Body	Island	FALSE
cg24456340	0.52	0.39	0.13	42.97	Chr17: 47286483	<i>ABI3, ABI3, GNGT2</i>	TSS1500, TSS1500, 5'UTR		FALSE
cg14316629	0.49	0.36	0.13	43.45	Chr6: 168436353	<i>KIF25, KIF25</i>	Body, Body	S_Shore	TRUE
cg07455790	0.86	0.73	0.13	95.92	Chr6: 31650735			Island	FALSE
cg07371521	0.45	0.32	0.13	45.34	Chr5: 154026371			N_Shore	TRUE
cg04097388	0.80	0.67	0.13	69.62	Chr2: 236671717	<i>AGAP1, AGAP1</i>	Body, Body	N_Shore	FALSE

cg27425314	0.40	0.28	0.13	46.83	Chr1: 26797619	<i>DHDDS, HMGN2, DHDDS</i>	3'UTR, TSS1500, 3'UTR	N_Shore	TRUE
cg00058449	0.49	0.36	0.13	40.92	Chr6: 31867956	<i>ZBTB12</i>	Body	Island	FALSE
cg13661648	0.71	0.58	0.13	49.46	Chr6: 33035284	<i>HLA-DPA1</i>	3'UTR		FALSE
cg26751588	0.78	0.65	0.13	61.24	Chr17: 14109671	<i>COX10</i>	Body	N_Shore	FALSE
cg03259126	0.88	0.76	0.13	104.07	Chr7: 56029683			N_Shelf	FALSE
cg09971646	0.66	0.54	0.13	43.37	Chr14: 101194145	<i>DLK1</i>	Body	S_Shore	FALSE
cg04118910	0.58	0.46	0.13	39.31	Chr13: 114875170	<i>RASA3</i>	Body	N_Shore	FALSE
cg18522231	0.45	0.32	0.13	41.31	Chr3: 196705629				FALSE
cg27216937	0.67	0.55	0.12	43.39	Chr11: 6425978	<i>APBB1, APBB1</i>	Body, Body		TRUE
cg03441844	0.46	0.33	0.12	39.85	Chr1: 161368947			Island	FALSE
cg24544490	0.33	0.20	0.12	53.71	Chr1: 155290961	<i>RUSC1, RUSC1, C1orf104</i>	5'UTR, 5'UTR, Body	Island	FALSE
cg09253696	0.32	0.20	0.12	53.99	Chr17: 73873529	<i>TRIM47</i>	Body	Island	TRUE
cg02341556	0.37	0.24	0.12	46.88	Chr11: 118781978	<i>BCL9L</i>	TSS1500	S_Shore	FALSE
cg02355304	0.59	0.47	0.12	38.03	Chr7: 5536984	<i>MIR589, FBXL18</i>	TSS1500, Body	N_Shelf	FALSE
cg27665146	0.44	0.31	0.12	40.03	Chr15: 51369926	<i>TNFAIP8L3</i>	Body		TRUE
cg10424681	0.61	0.49	0.12	38.45	Chr6: 4079350	<i>C6orf201, C6orf146, C6orf146</i>	TSS200, 5'UTR, 1stExon	Island	TRUE
cg17052675	0.71	0.58	0.12	45.59	Chr2: 3827356				TRUE
cg26922780	0.39	0.26	0.12	43.91	Chr16: 88769443	<i>RNF166</i>	Body	N_Shelf	FALSE
cg07115206	0.66	0.54	0.12	40.99	Chr16: 6425686	<i>A2BP1, A2BP1</i>	5'UTR, 5'UTR		TRUE
cg15556709	0.61	0.49	0.12	37.82	Chr7: 43739176	<i>C7orf44</i>	5'UTR		TRUE
cg06223736	0.77	0.65	0.12	55.93	Chr2: 240142694	<i>HDAC4</i>	Body		FALSE
cg04248271	0.35	0.23	0.12	47.47	Chr5: 158524404	<i>EBF1</i>	Body	Island	TRUE
cg27119456	0.34	0.22	0.12	48.19	Chr10: 42863173	<i>LOC441666</i>	Body	Island	FALSE
cg13286582	0.43	0.31	0.12	38.03	Chr2: 37883934	<i>CDC42EP3</i>	5'UTR		TRUE
cg13682187	0.50	0.38	0.12	35.23	Chr1: 196946512	<i>CFHR5</i>	TSS200		FALSE
cg19383211	0.62	0.50	0.12	36.20	Chr6: 32527588	<i>HLA-DRB6</i>	Body		FALSE
cg02228675	0.39	0.27	0.12	40.83	Chr17: 40259724	<i>DHX58</i>	Body	Island	TRUE
cg26429520	0.25	0.13	0.12	67.09	Chr11: 1283875				TRUE
cg11236515	0.32	0.20	0.12	49.28	Chr2: 74213762			S_Shore	FALSE
cg12108912	0.76	0.64	0.12	49.43	Chr2: 120435949	<i>TMEM177, TMEM177, TMEM177</i>	TSS1500, TSS1500, TSS1500	N_Shore	FALSE
cg10428938	0.40	0.28	0.12	39.53	Chr7: 98990837	<i>ARPC1B</i>	Body	Island	TRUE
cg13298116	0.41	0.30	0.12	37.89	Chr11: 62369859	<i>EML3, MTA2</i>	3'UTR, TSS1500	Island	FALSE
cg13374304	0.81	0.69	0.12	62.46	Chr7: 63016648			N_Shore	FALSE
cg17681079	0.59	0.47	0.12	34.17	Chr7: 27556963				TRUE
cg00253658	0.56	0.45	0.12	33.65	Chr16: 54210496				FALSE
cg26893861	0.38	0.27	0.12	39.88	Chr17: 41843967	<i>DUSP3</i>	3'UTR		FALSE
cg06022607	0.67	0.56	0.12	38.49	Chr12: 133412002			N_Shore	FALSE
cg12548638	0.57	0.45	0.12	33.40	Chr1: 38226812	<i>EPHA10, EPHA10</i>	3'UTR, Body	N_Shore	FALSE
cg03898365	0.64	0.53	0.12	35.99	Chr11: 6897491	<i>OR10A4</i>	TSS1500		FALSE

cg26843498	0.54	0.42	0.12	32.96	Chr19: 2361574		S_Shore	FALSE	
cg08754654	0.41	0.29	0.12	37.13	Chr5: 154026448		N_Shore	TRUE	
cg20557159	0.57	0.45	0.12	32.95	Chr17: 75445261	SEPT9, SEPT9, SEPT9, SEPT9, SEPT9, SEPT9	Body, Body, Body, Body, TSS1500, Body	N_Shelf	FALSE
cg05185038	0.70	0.59	0.12	40.44	Chr14: 105945685	CRIP2	Body	Island	FALSE
cg04657146	0.43	0.32	0.12	35.29	Chr19: 12876947	HOOK2, HOOK2	Body, Body	Island	FALSE
cg23691894	0.67	0.55	0.12	37.17	Chr10: 111765904	ADD3, ADD3	1stExon, 5'UTR	N_Shore	FALSE
cg08109568	0.80	0.68	0.12	55.91	Chr15: 31115862				FALSE
cg00638631	0.91	0.79	0.12	108.58	Chr21: 39039777	KCNJ6	Body	Island	FALSE
cg15205435	0.30	0.19	0.12	49.15	Chr1: 6187920	CHD5	Body	Island	TRUE
cg03816370	0.67	0.55	0.12	36.58	Chr2: 190616071	OSGEPL1	Body		FALSE
cg08017858	0.17	0.06	0.12	101.53	Chr11: 74022642	P4HA3	1stExon	Island	TRUE
cg08280368	0.24	0.12	0.12	65.33	Chr14: 71110536	TTC9	Body	S_Shore	FALSE
cg16777618	0.56	0.45	0.12	31.75	Chr11: 128694184			Island	FALSE
cg05662444	0.48	0.37	0.12	32.00	Chr5: 154026397			N_Shore	TRUE
cg04246864	0.80	0.69	0.12	56.39	Chr16: 33357426			Island	FALSE
cg25019722	0.46	0.34	0.12	32.68	Chr6: 37503610			Island	TRUE
cg04255230	0.45	0.33	0.11	32.76	Chr2: 74727010	LBX2	Body	Island	FALSE
cg25071634	0.41	0.30	0.11	34.61	ChrY: 9172441	TTY20	TSS200	N_Shore	FALSE
cg12770425	0.69	0.57	0.11	36.94	Chr6: 33585071			N_Shelf	FALSE
cg26371957	0.72	0.60	0.11	40.03	Chr12: 739280	NINJ2	Body		FALSE
cg18848287	0.37	0.26	0.11	37.73	Chr7: 5111641	LOC389458	TSS200	Island	FALSE
cg09553982	0.63	0.51	0.11	32.56	Chr10: 77875676	C10orf11	Body	S_Shelf	FALSE
cg24573207	0.50	0.39	0.11	30.70	Chr3: 75661206				FALSE
cg23774988	0.28	0.16	0.11	52.00	Chr11: 128419199	ETS1	Body	Island	FALSE
cg07502661	0.46	0.35	0.11	31.65	Chr2: 43398339			S_Shore	FALSE
cg09119854	0.63	0.51	0.11	32.33	Chr17: 63550766	AXIN2	Body		TRUE
cg26450717	0.49	0.38	0.11	30.65	Chr6: 31650835			Island	FALSE
cg21139150	0.45	0.33	0.11	32.12	Chr21: 46976175			Island	FALSE
cg01744331	0.98	0.86	0.11	341.10	Chr11: 2722358	KCNQ1OT1, KCNQ1, KCNQ1	TSS1500, Body, Body	S_Shore	FALSE
cg07639376	0.39	0.28	0.11	35.11	Chr16: 1584516	IFT140, TMEM204	Body, 1stExon	Island	TRUE
cg01139861	0.29	0.18	0.11	47.76	Chr7: 50343298	IKZF1	TSS1500	Island	FALSE
cg02965712	0.52	0.41	0.11	29.59	Chr1: 77746028			N_Shore	FALSE
cg27271937	0.43	0.32	0.11	32.11	Chr12: 6419570	PLEKHG6, PLEKHG6	TSS1500, TSS200	N_Shore	FALSE
cg04192168	0.29	0.18	0.11	48.07	Chr15: 64806741	ZNF609	Body		TRUE
cg04880091	0.56	0.45	0.11	29.65	Chr8: 43132451			Island	FALSE
cg06202470	0.92	0.80	0.11	112.28	Chr12: 11700489				FALSE
cg05825244	0.54	0.43	0.11	29.45	Chr20: 2730488	EBF4	Body	Island	FALSE
cg27102737	0.77	0.66	0.11	46.87	Chr8: 59468814	SDCBP, SDCBP, SDCBP, SDCBP, SDCBP	5'UTR, 5'UTR, 5'UTR, 5'UTR, 5'UTR	S_Shelf	FALSE
cg00547480	0.49	0.38	0.11	29.68	Chr10: 103875961	LDB1, LDB1	Body, TSS1500	N_Shelf	FALSE

cg00647820	0.27	0.16	0.11	51.90	Chr17: 40259828	<i>DHX58</i>	Body	Island	TRUE
cg20824294	0.61	0.50	0.11	30.38	Chr3: 142316082	<i>PLS1</i>	5'UTR	S_Shore	FALSE
cg10169515	0.74	0.63	0.11	41.02	Chr12: 123707536	<i>MPHOSPH9</i>	TSS1500		FALSE
cg14675881	0.43	0.32	0.11	31.41	Chr2: 43396331			N_Shore	TRUE
cg16553589	0.72	0.61	0.11	38.32	Chr5: 122766566				FALSE
cg12583076	0.39	0.28	0.11	33.63	Chr12: 65082713	<i>RASSF3</i>	Body		TRUE
cg20386487	0.31	0.20	0.11	42.64	Chr15: 96898045			Island	FALSE
cg26280976	0.46	0.34	0.11	30.09	Chr14: 69660603			S_Shore	FALSE
cg18470780	0.36	0.25	0.11	35.90	Chr14: 59064969				TRUE
cg13153942	0.78	0.67	0.11	46.58	ChrX: 12924247	<i>TLR8, LOC349408</i>	TSS1500, Body		FALSE
cg01863042	0.63	0.52	0.11	30.63	Chr13: 23309892				FALSE
cg02322400	0.36	0.25	0.11	36.37	Chr11: 95980186	<i>MAML2</i>	Body		TRUE
cg01297670	0.57	0.46	0.11	28.71	Chr6: 31651070			Island	FALSE
cg22063654	0.42	0.31	0.11	31.30	Chr8: 72758701			S_Shelf	FALSE
cg02396126	0.89	0.78	0.11	88.34	Chr13: 42536640	<i>KIAA0564, KIAA0564</i>	TSS1500, TSS1500	S_Shore	FALSE
cg01950479	0.71	0.60	0.11	35.85	Chr22: 23528162	<i>BCR, BCR</i>	Body, Body	S_Shelf	FALSE
cg04730355	0.22	0.11	0.11	65.53	Chr14: 51134070	<i>SAV1</i>	Body	N_Shore	FALSE
cg14216940	0.31	0.20	0.11	41.74	Chr7: 50343131	<i>IKZF1</i>	TSS1500	Island	FALSE
cg06307913	0.39	0.28	0.11	32.63	Chr4: 81118794	<i>PRDM8, PRDM8, PRDM8</i>	5'UTR, 1stExon, 5'UTR	N_Shore	FALSE
cg19093370	0.83	0.72	0.11	59.10	Chr17: 17110180	<i>PLD6</i>	TSS1500	Island	TRUE
cg07778180	0.68	0.56	0.11	32.52	Chr17: 34641309	<i>CCL4L1, CCL4L2</i>	Body, Body		FALSE
cg15201545	0.25	0.13	0.11	55.83	Chr4: 675137	<i>MYL5</i>	Body	Island	FALSE
cg24895155	0.48	0.37	0.11	27.93	Chr8: 127837199				TRUE
cg05506829	0.67	0.56	0.11	31.44	Chr13: 47472349	<i>HTR2A, HTR2A</i>	TSS1500, TSS1500		FALSE
cg12883014	0.39	0.28	0.11	31.86	Chr12: 104855500	<i>CHST11</i>	Body	S_Shelf	FALSE
cg13713218	0.77	0.66	0.11	43.17	Chr9: 100000033	<i>KIAA1529</i>	TSS1500	N_Shore	FALSE
cg06020661	0.66	0.55	0.11	31.01	Chr13: 47472138	<i>HTR2A, HTR2A</i>	TSS1500, TSS1500		FALSE
cg13924996	0.49	0.38	0.11	27.30	Chr11: 67053829	<i>ADRBK1</i>	3'UTR	S_Shore	FALSE
cg13117948	0.55	0.44	0.11	26.94	Chr4: 16086051	<i>PROM1, PROM1</i>	TSS1500, TSS1500	S_Shore	FALSE
cg04553307	0.87	0.76	0.11	71.36	Chr7: 922775	<i>C7orf20</i>	Body		FALSE
cg13405775	0.55	0.44	0.11	26.82	Chr22: 32599648	<i>RFPL2, RFPL2, RFPL2</i>	TSS200, 5'UTR, TSS1500		FALSE
cg13320138	0.37	0.26	0.11	32.71	Chr12: 6419575	<i>PLEKHG6, PLEKHG6</i>	TSS1500, TSS200	N_Shore	FALSE
cg14884931	0.84	0.73	0.11	59.27	Chr22: 42323359	<i>TNFRSF13C</i>	TSS1500	S_Shore	FALSE
cg06307939	0.87	0.76	0.11	72.16	Chr19: 12984645	<i>MAST1</i>	Body	Island	FALSE
cg07690882	0.54	0.43	0.11	26.64	Chr11: 128694303			Island	FALSE
cg14929208	0.40	0.29	0.11	30.32	Chr3: 156273297	<i>SSR3</i>	TSS1500	S_Shore	FALSE
cg26917640	0.62	0.51	0.11	28.07	Chr15: 67204380				FALSE
cg10928544	0.72	0.62	0.11	35.65	Chr14: 91862864	<i>CCDC88C</i>	Body		FALSE
cg12636607	0.45	0.34	0.11	27.88	Chr6: 112154581	<i>FYN</i>	5'UTR		TRUE

cg13064658	0.24	0.13	0.11	54.41	Chr1: 212003989	<i>LPGAT1, LPGAT1</i>	5'UTR, 1stExon	Island	FALSE
cg26256630	0.51	0.40	0.11	26.21	Chr6: 30070738	<i>TRIM31</i>	3'UTR	N_Shore	FALSE
cg24404329	0.60	0.49	0.11	26.99	Chr7: 115849899	<i>TES</i>	TSS1500	N_Shore	FALSE
cg17551891	0.60	0.49	0.11	26.88	Chr7: 1960795	<i>MAD1L1, MAD1L1, MAD1L1</i>	Body, Body, Body		FALSE
cg08006309	0.29	0.19	0.11	41.61	Chr16: 1587810	<i>IFT140, TMEM204</i>	Body, Body	Island	FALSE
cg15506703	0.68	0.57	0.11	31.11	Chr2: 242844601			Island	TRUE
cg08846011	0.89	0.79	0.11	85.66	Chr1: 117318133				FALSE
cg05837990	0.71	0.60	0.11	33.67	Chr7: 105596483				FALSE
cg14981532	0.23	0.12	0.11	56.99	Chr1: 17215477			Island	TRUE
cg12440927	0.78	0.68	0.11	43.60	Chr7: 157791721	<i>PTPRN2, PTPRN2, PTPRN2</i>	Body, Body, Body		TRUE
cg26582789	0.51	0.41	0.11	25.73	ChrX: 19531688	<i>MAP3K15</i>	Body	N_Shore	FALSE
cg11488033	0.70	0.59	0.11	32.00	Chr3: 196705898				FALSE
cg22968622	0.19	0.08	0.11	71.50	Chr17: 43663579			Island	FALSE
cg19584649	0.41	0.30	0.11	28.72	Chr7: 158607898	<i>ESYT2</i>	Body		TRUE
cg27527630	0.32	0.22	0.11	36.25	Chr7: 29923538	<i>WIPF3</i>	Body	N_Shore	FALSE
cg27663938	0.33	0.22	0.11	35.27	Chr12: 103696381	<i>C12orf42, C12orf42</i>	Body, Body	Island	FALSE
cg03277819	0.29	0.18	0.11	40.92	Chr12: 772529	<i>NINJ2</i>	1stExon		TRUE
cg21877680	0.49	0.38	0.11	25.56	Chr8: 43132507			S_Shore	FALSE
cg23187316	0.50	0.39	0.11	25.30	Chr7: 1099788	<i>C7orf50, C7orf50, C7orf50</i>	Body, Body, Body	S_Shore	TRUE
cg16474696	0.48	0.37	0.11	25.59	Chr19: 13875014	<i>MRI1, MRI1</i>	TSS1500, TSS1500	N_Shore	FALSE
cg13765957	0.60	0.50	0.11	26.03	ChrY: 21208621	<i>TTTY14</i>	Body		FALSE
cg06686742	0.80	0.69	0.11	44.82	Chr19: 8273505	<i>LASS4</i>	TSS1500	N_Shore	FALSE
cg13670957	0.80	0.69	0.11	44.93	Chr19: 18329801	<i>PDE4C, PDE4C, PDE4C</i>	Body, Body, Body	N_Shore	FALSE
cg10636447	0.47	0.36	0.11	25.57	Chr20: 826023	<i>FAM110A, FAM110A, FAM110A</i>	Body, Body, 1stExon	Island	FALSE
cg14632729	0.28	0.18	0.11	41.19	Chr7: 105755441			S_Shelf	FALSE
cg27519958	0.44	0.33	0.11	26.43	Chr1: 161735129	<i>ATF6</i>	TSS1500		FALSE
cg23876832	0.34	0.23	0.11	33.55	Chr11: 62092739				TRUE
cg02385173	0.63	0.53	0.11	26.64	Chr11: 76571534	<i>ACER3</i>	TSS1500	N_Shore	FALSE
cg22996170	0.55	0.45	0.11	24.65	Chr19: 12895529			S_Shore	TRUE
cg15896696	0.57	0.46	0.11	24.64	Chr7: 2059921	<i>MAD1L1, MAD1L1, MAD1L1</i>	Body, Body, Body	Island	FALSE
cg01249544	0.34	0.24	0.11	32.41	Chr10: 69372655	<i>CTNNA3, CTNNA3</i>	Body, Body		TRUE
cg06777732	0.41	0.31	0.11	27.00	Chr12: 131118426				TRUE
cg06106484	0.58	0.47	0.10	24.63	Chr8: 32985289				TRUE
cg13546858	0.57	0.46	0.10	24.45	Chr1: 869346	<i>SAMD11</i>	Body	Island	FALSE
cg04838988	0.22	0.11	0.10	56.38	Chr8: 70984437	<i>PRDM14</i>	TSS1500	Island	FALSE
cg18919209	0.39	0.29	0.10	27.96	Chr11: 96012039	<i>MAML2</i>	Body		TRUE
cg17501823	0.35	0.25	0.10	31.13	Chr12: 47219793	<i>SLC38A4, SLC38A4</i>	TSS200, TSS200		FALSE
cg00088688	0.65	0.55	0.10	26.97	Chr6: 167560504				TRUE
cg25061701	0.53	0.43	0.10	23.99	Chr17: 62608856	<i>SMURF2</i>	Body		TRUE

cg24413781	0.34	0.23	0.10	32.44	Chr19: 8273693	<i>LASS4</i>	TSS1500	Island	FALSE
cg06180910	0.79	0.69	0.10	43.07	Chr22: 24382663	<i>GSTT1</i>	Body	N_Shore	FALSE
cg15837308	0.55	0.45	0.10	24.04	Chr6: 32427751				FALSE
cg21156386	0.54	0.44	0.10	23.92	Chr11: 692983	<i>DEAF1</i>	Body	N_Shore	FALSE
cg09913449	0.76	0.65	0.10	36.69	Chr8: 42400586	<i>C8orf40, C8orf40, C8orf40, C8orf40</i>	5'UTR, 5'UTR, 5'UTR, 5'UTR	S_Shelf	FALSE
cg19318393	0.63	0.52	0.10	25.54	Chr1: 223936508	<i>CAPN2, CAPN2</i>	Body, Body	Island	TRUE
cg00330518	0.52	0.42	0.10	23.67	Chr1: 2228160	<i>SKI</i>	Body		FALSE
cg03227037	0.40	0.30	0.10	26.76	Chr20: 62212228			S_Shelf	FALSE
cg25345738	0.51	0.40	0.10	23.50	Chr12: 108078835	<i>PWP1</i>	TSS1500	N_Shore	FALSE
cg13912224	0.76	0.66	0.10	36.32	Chr6: 52172083			Island	FALSE
cg04349084	0.19	0.09	0.10	64.30	Chr8: 23602677				TRUE
cg08926642	0.85	0.75	0.10	58.42	Chr1: 7887455	<i>PER3</i>	Body	Island	FALSE
cg01890417	0.49	0.39	0.10	23.63	Chr1: 91488275	<i>ZNF644, ZNF644, ZNF644</i>	TSS1500, TSS1500, TSS1500	S_Shore	FALSE
cg02580986	0.56	0.46	0.10	23.40	ChrX: 105421602	<i>MUM1L1</i>	5'UTR		TRUE
cg10555744	0.36	0.25	0.10	29.37	Chr1: 25946258	<i>MAN1C1</i>	Body	S_Shelf	TRUE
cg15436354	0.49	0.39	0.10	23.29	Chr19: 8117875	<i>CCL25</i>	TSS200	S_Shelf	TRUE
cg26853458	0.52	0.42	0.10	23.06	Chr17: 9805074	<i>RCVRN</i>	Body	N_Shelf	FALSE
cg19536401	0.55	0.44	0.10	23.03	Chr19: 6504797			S_Shelf	FALSE
cg26485825	0.32	0.22	0.10	32.89	Chr18: 21452895	<i>LAMA3, LAMA3, LAMA3, LAMA3</i>	TSS200, TSS200, Body, Body		FALSE
cg00017826	0.33	0.23	0.10	31.47	Chr2: 30644955				TRUE
cg05388281	0.30	0.20	0.10	34.74	Chr4: 125504	<i>ZNF718</i>	Body	S_Shore	FALSE
cg14588003	0.48	0.37	0.10	23.32	Chr15: 93361889				TRUE
cg23829949	0.44	0.33	0.10	24.37	Chr1: 244214679	<i>ZNF238, ZNF238</i>	1stExon, 5'UTR	S_Shore	FALSE
cg27316811	0.53	0.42	0.10	22.73	Chr16: 1576146	<i>IFT140</i>	Body	S_Shore	FALSE
cg25481160	0.52	0.42	0.10	22.69	Chr3: 71111489	<i>FOXP1</i>	Body	N_Shelf	FALSE
cg24769830	0.60	0.49	0.10	23.47	Chr3: 108041508	<i>HHLA2</i>	5'UTR		FALSE
cg00821186	0.89	0.79	0.10	74.33	Chr1: 248790981	<i>OR2T11</i>	TSS1500		FALSE
cg07116010	0.18	0.08	0.10	67.12	Chr9: 35646325			N_Shore	FALSE
cg22485298	0.42	0.32	0.10	24.68	Chr6: 30853333	<i>DDR1, DDR1</i>	5'UTR, 5'UTR	S_Shore	FALSE
cg25810247	0.37	0.26	0.10	27.98	Chr13: 108867154	<i>LIG4, LIG4, LIG4</i>	5'UTR, TSS200, 5'UTR	Island	FALSE
cg08787988	0.56	0.46	0.10	22.68	Chr2: 27713044	<i>IFT172</i>	TSS1500	S_Shore	FALSE
cg18422587	0.20	0.10	0.10	59.61	Chr7: 3134670				FALSE
cg24127061	0.29	0.19	0.10	35.95	Chr11: 65839402	<i>PACS1</i>	Body	S_Shore	FALSE
cg01366941	0.24	0.14	0.10	44.99	Chr16: 12172962	<i>SNX29</i>	Body		FALSE
cg24549702	0.62	0.51	0.10	23.72	Chr2: 235364440				FALSE
cg23743554	0.61	0.51	0.10	23.62	Chr11: 65321226	<i>LTBP3, LTBP3, LTBP3</i>	Body, Body, Body	Island	FALSE
cg20737812	0.49	0.39	0.10	22.60	Chr15: 86336631	<i>KLHL25</i>	5'UTR	N_Shore	FALSE
cg23525438	0.28	0.18	0.10	37.34	Chr6: 17016226				FALSE

cg05195017	0.43	0.33	0.10	23.87	Chr2: 242758725	<i>NEU4, NEU4, NEU4, NEU4, NEU4</i>	3'UTR, 3'UTR, 3'UTR, 3'UTR, 3'UTR	N_Shore	FALSE
cg11251470	0.54	0.43	0.10	22.12	Chr7: 30008931	<i>SCRN1, SSCRN1, SSCRN1, SSCRN1</i>	5'UTR, Body, 5'UTR, 5'UTR		TRUE
cg19950606	0.42	0.32	0.10	24.40	Chr17: 76121276	<i>TMC6, TMC6</i>	Body, Body		FALSE
cg11779113	0.17	0.07	0.10	73.76	Chr20: 62199156	<i>PRIC285, PRIC285</i>	Body, TSS200	N_Shore	FALSE
cg17624673	0.58	0.48	0.10	22.54	Chr5: 140596187	<i>PCDHB13, PCDHB13</i>	3'UTR, 1stExon	S_Shore	FALSE
cg01565314	0.77	0.67	0.10	35.76	Chr19: 45737610	<i>EXOC3L2</i>	TSS200	Island	FALSE
cg11900509	0.69	0.59	0.10	27.26	Chr10: 81946545	<i>ANXA11, ANXA11, ANXA11</i>	5'UTR, 5'UTR, 5'UTR		TRUE
cg21171339	0.45	0.35	0.10	23.13	Chr9: 79791169	<i>VPS13A, VPS13A, VPS13A, VPS13A</i>	TSS1500, TSS1500, TSS1500, TSS1500	N_Shore	FALSE
cg20594982	0.88	0.78	0.10	65.63	Chr1: 976707	<i>AGRN</i>	Body	Island	FALSE
cg20970205	0.41	0.31	0.10	24.33	Chr17: 77766040			Island	FALSE
cg07420362	0.59	0.49	0.10	22.33	Chr11: 3647419	<i>TRPC2</i>	TSS1500		FALSE
cg20245116	0.84	0.74	0.10	51.70	Chr1: 55522013	<i>PCSK9</i>	Body		FALSE
cg05313153	0.44	0.34	0.10	22.65	Chr8: 119122430	<i>EXT1</i>	1stExon	N_Shore	FALSE

B.

Discoid Rash									
CG Site ID	Mean β Case	Mean β Control	Δβ	DiffScore	Location (HG19)	Gene Name	Gene-Relative Location	CGI-Relative Location	Enhancer
Hypomethylation									
cg11404906	0.42	0.76	-0.34	-338.91	Chr6: 32551749	<i>HLA-DRB1</i>	Body	N_Shore	FALSE
cg21549285	0.38	0.63	-0.25	-215.39	Chr21: 42799141	<i>MX1, MX1</i>	5'UTR, 5'UTR	S_Shore	FALSE
cg14392283	0.64	0.90	-0.25	-338.91	Chr8: 144103587	<i>LY6E, LY6E</i>	3'UTR, 3'UTR	N_Shelf	FALSE
						<i>PARP9, PARP9,</i>	5'UTR, 5'UTR,		
cg08122652	0.53	0.75	-0.22	-188.13	Chr3: 122281939	<i>DTX3L, PARP9,</i>	TSS1500, 5'UTR,	N_Shore	FALSE
						<i>PARP9, PARP9,</i>	5'UTR, 5'UTR,		
cg24668570	0.09	0.30	-0.21	-254.37	Chr10: 134973778	<i>KNDC1</i>	5'UTR	Island	FALSE
cg23066280	0.42	0.64	-0.21	-144.59	Chr7: 158032496	<i>PTPRN2, PTPRN2,</i>	TSS200		
						<i>PTPRN2</i>	Body, Body, Body		
cg18480627	0.42	0.63	-0.21	-137.10	Chr2: 130795582	<i>LOC440905</i>	Body	Island	FALSE
cg24088508	0.26	0.47	-0.21	-146.58	Chr1: 38156462	<i>C1orf109</i>	TSS1500	N_Shore	FALSE
cg19214707	0.31	0.52	-0.21	-133.32	Chr7: 3157722				TRUE
cg03607951	0.47	0.68	-0.20	-136.47	Chr1: 79085586	<i>IFI44L</i>	TSS1500		FALSE
cg05696877	0.27	0.48	-0.20	-133.32	Chr1: 79088769	<i>IFI44L</i>	5'UTR		FALSE
cg26762873	0.68	0.88	-0.20	-228.93	Chr11: 5879799	<i>OR52E8</i>	TSS1500		FALSE
cg05552874	0.57	0.76	-0.19	-132.81	Chr10: 91153143	<i>IFIT1</i>	Body		FALSE
cg01797371	0.18	0.36	-0.19	-139.72	Chr3: 195578240				FALSE
cg20917491	0.15	0.34	-0.19	-149.47	Chr3: 195578259				FALSE
cg08103988	0.49	0.67	-0.19	-109.96	Chr17: 6558365			Island	FALSE
cg06981309	0.44	0.62	-0.18	-95.19	Chr3: 146260954	<i>PLSCR1</i>	5'UTR	N_Shore	FALSE
cg07157030	0.45	0.63	-0.18	-95.79	Chr14: 63671356	<i>RHOJ, RHOJ</i>	5'UTR, 1stExon		TRUE
cg01028142	0.67	0.85	-0.18	-160.34	Chr2: 7004578	<i>CMPK2</i>	Body	N_Shore	FALSE
cg05779406	0.37	0.54	-0.18	-90.21	Chr7: 1198841	<i>ZFAND2A</i>	5'UTR	N_Shore	FALSE
cg17384323	0.54	0.71	-0.17	-93.18	Chr4: 169242366			S_Shelf	FALSE
cg18771300	0.42	0.58	-0.16	-73.27	Chr14: 63671737	<i>RHOJ</i>	1stExon		TRUE
cg04554929	0.22	0.38	-0.16	-90.54	Chr8: 105342491			Island	FALSE
cg11478607	0.03	0.18	-0.16	-216.49	Chr22: 24384400	<i>GSTT1</i>	TSS200	Island	FALSE
cg22862003	0.54	0.70	-0.16	-80.16	Chr21: 42797588	<i>MX1, MX1</i>	TSS1500, 5'UTR	N_Shore	FALSE
cg23804921	0.36	0.52	-0.16	-69.85	Chr15: 30861172			N_Shelf	FALSE
cg00555438	0.12	0.28	-0.16	-122.81	Chr3: 195578280				FALSE
cg24858233	0.10	0.26	-0.16	-130.18	Chr3: 195578055				FALSE
cg14687298	0.24	0.39	-0.15	-78.39	Chr12: 31272119				FALSE
cg03299990	0.34	0.50	-0.15	-64.48	Chr20: 17557570			N_Shore	FALSE
cg04234412	0.21	0.36	-0.15	-81.66	Chr22: 24373322	<i>LOC391322</i>	Body	Island	FALSE
cg06188083	0.22	0.37	-0.15	-79.72	Chr10: 91093005	<i>IFIT3, IFIT3</i>	Body, Body		TRUE
cg14951497	0.27	0.42	-0.15	-70.16	Chr2: 191875807	<i>STAT1, STAT1</i>	5'UTR, 5'UTR	N_Shelf	FALSE
cg01394167	0.45	0.60	-0.15	-62.69	Chr4: 9479622				FALSE
cg24898914	0.56	0.71	-0.15	-71.77	Chr6: 32810706	<i>PSMB8, PSMB8</i>	Body, Body	N_Shore	FALSE
cg14212360	0.62	0.77	-0.15	-82.94	Chr4: 89302999	<i>HERC6, HERC6</i>	Body, Body	S_Shelf	FALSE
cg02380802	0.40	0.55	-0.15	-58.79	Chr16: 53407808			S_Shore	FALSE
cg15708909	0.55	0.70	-0.15	-67.07	Chr6: 32487314	<i>HLA-DRB5</i>	Body	N_Shelf	FALSE
cg10384133	0.43	0.58	-0.15	-57.61	Chr9: 45733081			N_Shore	FALSE
cg00855901	0.27	0.41	-0.15	-65.47	Chr1: 79085765	<i>IFI44L</i>	TSS1500		FALSE
cg10819238	0.77	0.92	-0.15	-176.55	Chr19: 1155184	<i>SBNO2</i>	5'UTR	Island	TRUE
cg23733394	0.38	0.53	-0.15	-56.94	Chr1: 839752			Island	FALSE
cg21358336	0.52	0.66	-0.14	-59.58	Chr17: 6558440			Island	FALSE
cg14926196	0.39	0.53	-0.14	-54.74	Chr6: 37616482	<i>MDGA1</i>	Body	Island	FALSE
cg00676801	0.24	0.39	-0.14	-65.71	Chr2: 191876673	<i>STAT1, STAT1</i>	5'UTR, 5'UTR	N_Shore	FALSE
cg06917450	0.30	0.44	-0.14	-56.40	Chr1: 38156652	<i>C1orf109</i>	TSS1500	N_Shore	FALSE
						<i>SETDB1, SETDB1,</i>	TSS1500,		
cg15448220	0.63	0.77	-0.14	-73.50	Chr1: 150897856	<i>SETDB1</i>	TSS1500,	N_Shore	FALSE
							TSS1500		
cg21656205	0.43	0.57	-0.14	-51.42	Chr20: 43439688	<i>RIMS4</i>	TSS1500	S_Shore	FALSE
cg03913456	0.20	0.34	-0.14	-70.33	Chr2: 97000924	<i>NCAPH</i>	TSS1500	N_Shore	FALSE
cg13405775	0.42	0.56	-0.14	-50.75	Chr22: 32599648	<i>RFPL2, RFPL2,</i>	TSS200, 5'UTR,		FALSE
cg25100880	0.60	0.74	-0.14	-63.16	Chr11: 5878019	<i>RFPL2</i>	TSS1500		FALSE
cg26983430	0.11	0.25	-0.14	-95.61	ChrY: 24549675	<i>OR52E8</i>	1stExon		FALSE
						<i>RBMY1J, RBMY1J,</i>	5'UTR, 1stExon,	Island	FALSE

					<i>RBMY1F</i>	5'UTR		
cg08624648	0.60	0.73	-0.14	-62.04	Chr6: 31651029		Island	FALSE
cg08937107	0.57	0.70	-0.14	-57.47	Chr16: 3136857		N_Shelf	FALSE
cg08159663	0.42	0.55	-0.14	-47.05	Chr16: 57022486	<i>NLRC5</i>	N_Shore	TRUE
cg24247231	0.48	0.61	-0.13	-48.47	Chr15: 67904302	<i>MAP2K5, MAP2K5</i>	Body, Body	TRUE
cg10044179	0.39	0.53	-0.13	-46.86	Chr21: 15352983	<i>C21orf81</i>	TSS1500	S_Shore
cg01238044	0.12	0.26	-0.13	-88.87	Chr22: 24384105	<i>GSTT1</i>	Body	N_Shore
cg17980508	0.46	0.59	-0.13	-47.10	Chr1: 79085713	<i>IFI44L</i>	TSS1500	FALSE
cg14554813	0.64	0.77	-0.13	-68.78	Chr9: 69092015	<i>PGM5P2</i>	Body	FALSE
cg03671052	0.24	0.38	-0.13	-56.62	Chr5: 180086260			FALSE
cg16920502	0.56	0.69	-0.13	-54.24	Chr8: 133141439	<i>KCNQ3</i>	3'UTR	N_Shore
cg09592244	0.30	0.43	-0.13	-49.37	Chr17: 37024020		N_Shore	FALSE
cg25125450	0.64	0.77	-0.13	-65.54	Chr22: 32601274	<i>RFPL2</i>	TSS1500	FALSE
cg18686270	0.67	0.80	-0.13	-72.63	Chr3: 146258875	<i>PLSCR1</i>	5'UTR	N_Shelf
cg17052675	0.59	0.72	-0.13	-53.28	Chr2: 3827356			TRUE
cg03278514	0.42	0.54	-0.13	-41.69	Chr15: 70779346			TRUE
cg06161600	0.44	0.57	-0.13	-41.91	Chr16: 1393797	<i>BAIAP3</i>	Body	Island
cg08750459	0.43	0.56	-0.13	-41.38	Chr17: 6558815		N_Shore	FALSE
cg17393016	0.51	0.64	-0.13	-43.04	Chr17: 79283390	<i>C17orf55</i>	TSS1500	N_Shore
cg04335523	0.68	0.81	-0.13	-71.87	Chr10: 53790078	<i>PRKG1, PRKG1</i>	Body, Body	TRUE
cg00274965	0.40	0.52	-0.13	-39.36	Chr21: 34405681			Island
cg06442240	0.65	0.78	-0.13	-60.02	Chr16: 19129228	<i>ITPRIPL2, ITPRIPL2, ITPRIPL2</i>	1stExon, Body, 3'UTR	S_Shore
cg14582100	0.45	0.58	-0.13	-38.96	Chr15: 45693742	<i>SPATA5L1, SPATA5L1</i>	TSS1500, TSS1500	N_Shore
cg14126601	0.45	0.57	-0.12	-38.23	Chr2: 37384708	<i>EIF2AK2, EIF2AK2</i>	TSS1500, TSS1500	S_Shore
cg08284263	0.40	0.52	-0.12	-37.96	Chr10: 92958627			TRUE
cg06623899	0.82	0.94	-0.12	-165.71	Chr8: 142161840	<i>DENND3</i>	Body	FALSE
cg09232555	0.56	0.68	-0.12	-44.05	Chr8: 11619866			FALSE
cg01124132	0.41	0.53	-0.12	-37.38	Chr22: 32599511	<i>RFPL2, RFPL2, RFPL2</i>	TSS200, 5'UTR, TSS1500	FALSE
cg00807871	0.30	0.43	-0.12	-41.06	Chr6: 37617124	<i>MDGA1</i>	Body	Island
cg22886393	0.86	0.98	-0.12	-239.39	Chr10: 8006646	<i>TAF3</i>	Body	FALSE
cg00566515	0.31	0.43	-0.12	-39.53	Chr21: 15352608	<i>C21orf81</i>	Body	Island
cg27295118	0.25	0.37	-0.12	-45.01	Chr14: 22902226			FALSE
cg03453431	0.19	0.31	-0.12	-53.27	Chr7: 157225567			TRUE
cg04506728	0.61	0.73	-0.12	-47.16	Chr16: 53407722			Island
cg04387835	0.58	0.70	-0.12	-43.62	Chr17: 4649076	<i>ZMYND15, ZMYND15</i>	Body, Body	FALSE
cg07839457	0.14	0.26	-0.12	-65.78	Chr16: 57023022	<i>NLRC5</i>	TSS1500	N_Shore
cg06715136	0.73	0.85	-0.12	-77.75	Chr7: 158046025	<i>PTPRN2, PTPRN2, PTPRN2</i>	Body, Body, Body	FALSE
cg06614118	0.73	0.85	-0.12	-78.52	Chr5: 180414906	<i>BTNL3</i>	TSS1500	FALSE
cg19637330	0.47	0.59	-0.12	-34.92	Chr1: 19110922		Island	TRUE
cg17251423	0.59	0.71	-0.12	-42.92	Chr5: 139088815		Island	FALSE
cg11940040	0.32	0.44	-0.12	-36.77	Chr17: 154420	<i>RPH3AL</i>	Body	S_Shore
cg02181920	0.49	0.61	-0.12	-35.04	Chr6: 32820029	<i>TAP1</i>	Body	N_Shore
cg01754423	0.37	0.49	-0.12	-34.13	Chr16: 51465744			TRUE
cg01842774	0.84	0.96	-0.12	-176.89	Chr14: 106806179			FALSE
cg08808788	0.65	0.76	-0.12	-50.32	Chr6: 168780797			FALSE
cg20826740	0.29	0.41	-0.12	-37.63	Chr17: 37024042			N_Shore
cg08859406	0.31	0.43	-0.12	-35.77	Chr5: 147699718			FALSE
cg09848508	0.67	0.79	-0.12	-54.81	Chr16: 1393584	<i>BAIAP3</i>	Body	Island
cg21159568	0.61	0.73	-0.12	-43.82	Chr7: 2445331	<i>CHST12</i>	5'UTR	S_Shore
cg21649277	0.05	0.17	-0.12	-104.77	Chr19: 18117794	<i>ARRDC2, ARRDC2</i>	Body, TSS1500	N_Shore
cg03086067	0.58	0.70	-0.12	-38.57	Chr10: 82368399	<i>SH2D4B, SH2D4B</i>	Body, Body	FALSE
cg17573270	0.53	0.64	-0.12	-34.18	Chr22: 42950376	<i>SERHL2</i>	Body	S_Shore
cg20053110	0.47	0.58	-0.12	-31.74	Chr6: 37617864	<i>MDGA1</i>	Body	Island
cg23024343	0.61	0.73	-0.12	-42.14	Chr7: 107201750	<i>COG5, COG5, COG5</i>	Body, Body, Body	N_Shelf
cg02025737	0.66	0.78	-0.12	-50.49	Chr15: 33384751			TRUE
cg26383138	0.59	0.70	-0.12	-38.63	Chr2: 2119533	<i>MYT1L</i>	5'UTR	FALSE
cg11445109	0.10	0.22	-0.12	-74.12	Chr10: 135343248	<i>CYP2E1</i>	Body	S_Shore
cg13012494	0.14	0.26	-0.12	-58.37	Chr21: 47604986	<i>C21orf56, C21orf56</i>	TSS1500, TSS1500	S_Shelf

cg26706759	0.71	0.83	-0.12	-62.51	Chr5: 169011746	CCDC99	5'UTR	S_Shore	FALSE
cg07011961	0.71	0.82	-0.11	-60.88	Chr5: 23507594	PRDM9	TSS200		FALSE
cg02452435	0.31	0.43	-0.11	-33.42	Chr17: 71188192	COG1	TSS1500	N_Shore	FALSE
cg10440639	0.38	0.49	-0.11	-30.78	Chr17: 154499	RPH3AL	Body	N_Shelf	TRUE
cg16186435	0.44	0.55	-0.11	-30.34	Chr6: 32810833	PSMB8, PSMB8	Body, Body	N_Shore	FALSE
cg03263543	0.64	0.75	-0.11	-44.20	Chr2: 236673440	AGAP1, AGAP1	Body, Body	Island	FALSE
							TSS1500, Body,		
cg25288140	0.70	0.82	-0.11	-58.41	Chr17: 41278341	BRCA1, NBR2, BRCA1, BRCA1, BRCA1, BRCA1	TSS1500, TSS1500, TSS1500, TSS1500	Island	FALSE
cg06047990	0.05	0.16	-0.11	-105.00	Chr3: 195578040				FALSE
cg23264429	0.55	0.66	-0.11	-33.92	Chr10: 90642003	STAMBPL1	5'UTR	S_Shore	FALSE
cg25532627	0.86	0.98	-0.11	-209.20	Chr17: 77997833	TBC1D16	5'UTR	Island	FALSE
cg16853860	0.53	0.65	-0.11	-32.65	Chr6: 32823116	PSMB9, PSMB9, TAP1	Body, Body, TSS1500	S_Shore	FALSE
cg06376949	0.41	0.52	-0.11	-29.38	Chr10: 91173811	IFIT5	TSS1500	N_Shore	FALSE
cg08080396	0.51	0.63	-0.11	-31.22	Chr3: 11102832				FALSE
cg21494379	0.58	0.69	-0.11	-35.26	Chr5: 88275243				TRUE
cg05896524	0.22	0.33	-0.11	-39.67	Chr21: 47604654	C21orf56, C21orf56	TSS1500, TSS1500	S_Shore	FALSE
cg14172108	0.59	0.70	-0.11	-35.58	Chr21: 34405553			N_Shore	FALSE
cg12510708	0.70	0.82	-0.11	-55.96	Chr7: 26193805	NFE2L3	Body	S_Shore	TRUE
cg23927970	0.77	0.89	-0.11	-85.62	Chr11: 504933	RNHL1, RNHL1, RNHL1, RNHL1, RNHL1, RNHL1, RNHL1, RNHL1	5'UTR, 5'UTR, 5'UTR, 5'UTR, 5'UTR, 5'UTR, 5'UTR, 5'UTR	N_Shore	FALSE
cg26234900	0.25	0.36	-0.11	-36.20	Chr6: 32820214	TAP1	Body	N_Shore	FALSE
cg00225902	0.41	0.52	-0.11	-28.11	Chr3: 66444122	LRIG1	Body		TRUE
cg06168204	0.41	0.52	-0.11	-28.10	Chr6: 27570548				FALSE
cg24704287	0.59	0.70	-0.11	-34.65	Chr19: 13951481			N_Shore	FALSE
cg08356262	0.62	0.73	-0.11	-38.64	Chr5: 75838704	IQGAP2	Body		TRUE
cg24617313	0.37	0.48	-0.11	-28.30	Chr20: 57427146	GNAS, GNAS, GNAS, GNASAS	TSS1500, 3'UTR, TSS1500	N_Shore	TRUE
cg16341836	0.46	0.57	-0.11	-27.68	Chr10: 90641389	STAMBPL1	5'UTR	S_Shore	FALSE
cg24506221	0.11	0.22	-0.11	-65.11	Chr1: 110230401	GSTM1, GSTM1	TSS200, TSS200	Island	FALSE
cg17626301	0.21	0.32	-0.11	-39.22	Chr6: 32820201	TAP1	Body	N_Shore	FALSE
cg19650706	0.49	0.60	-0.11	-28.25	Chr5: 140594406	PCDHB13	1stExon	N_Shore	FALSE
cg25087499	0.64	0.75	-0.11	-39.86	Chr5: 177592761			Island	FALSE
cg23246911	0.44	0.55	-0.11	-27.14	Chr17: 154671	RPH3AL	Body	N_Shelf	TRUE
cg20045320	0.21	0.32	-0.11	-39.34	Chr11: 319555			S_Shore	FALSE
cg07244098	0.50	0.61	-0.11	-28.15	Chr11: 4415203	TRIM21	TSS1500		FALSE
cg24749559	0.23	0.34	-0.11	-36.12	Chr5: 141616065				FALSE
cg12494166	0.81	0.92	-0.11	-104.71	Chr4: 31998088				FALSE
cg07059402	0.42	0.53	-0.11	-26.50	Chr22: 38244781	MIR659, EIF3L	TSS1500, TSS1500	N_Shore	FALSE
cg06459104	0.42	0.52	-0.11	-26.51	Chr18: 5456880	EPB41L3	Body		TRUE
cg26724018	0.22	0.33	-0.11	-37.70	Chr11: 5716255	TRIM22	5'UTR		FALSE
cg24508426	0.31	0.42	-0.11	-29.48	Chr10: 124578209			Island	FALSE
cg02167713	0.38	0.49	-0.11	-26.80	Chr17: 79630115			N_Shelf	FALSE
cg13916469	0.60	0.71	-0.11	-33.83	Chr9: 95834820	SUSD3	Body		TRUE
cg04623458	0.77	0.87	-0.11	-74.46	Chr16: 871165			N_Shelf	FALSE
cg26702039	0.62	0.73	-0.11	-36.66	Chr16: 66170991				TRUE
cg07833467	0.46	0.56	-0.11	-26.21	Chr22: 50986511	KLHDC7B, KLHDC7B	5'UTR, 1stExon	Island	FALSE
cg26551200	0.84	0.95	-0.11	-144.32	Chr7: 2681369	TTYH3	Body		FALSE
cg20282814	0.49	0.60	-0.11	-26.71	Chr1: 43423072	SLC2A1	Body	N_Shore	FALSE
cg13937627	0.14	0.25	-0.11	-51.11	ChrX: 153236838	TMEM187, HCFC1	TSS1500, TSS200	Island	FALSE
cg21048763	0.80	0.91	-0.11	-99.30	Chr17: 77997997	TBC1D16	5'UTR	S_Shore	FALSE
cg111819121	0.79	0.89	-0.11	-85.18	Chr21: 37664031	DOPEY2	Body	N_Shelf	FALSE
cg04610450	0.77	0.88	-0.11	-77.69	Chr19: 18280601	PIK3R2	3'UTR	S_Shore	FALSE
cg04206742	0.29	0.40	-0.11	-29.51	Chr13: 95248882	TGDS	TSS1500	S_Shore	FALSE
cg17051704	0.11	0.21	-0.11	-62.45	Chr15: 29424197	FAM189A1	Body		FALSE
cg12427303	0.34	0.45	-0.11	-26.73	Chr22: 32599613	RFPL2, RFPL2, RFPL2	TSS200, 5'UTR, TSS1500		FALSE

cg10854819	0.74	0.85	-0.11	-60.92	Chr15: 31515852				TRUE
cg20811988	0.26	0.36	-0.11	-31.91	Chr20: 29611924	<i>FRG1B</i>	Body	Island	FALSE
cg20169823	0.19	0.30	-0.11	-40.08	Chr12: 116354837			Island	TRUE
cg05856321	0.36	0.47	-0.11	-25.49	Chr17: 1133546			Island	FALSE
cg19985056	0.09	0.19	-0.11	-70.05	Chr5: 56595244				FALSE
cg13368983	0.39	0.50	-0.11	-24.89	Chr2: 201995729	<i>CFLAR, CFLAR, CFLAR</i>	Body, Body, Body		FALSE
cg21265404	0.54	0.64	-0.11	-27.33	Chr9: 90531866	<i>FAM75C1</i>	TSS1500		FALSE
cg25472530	0.60	0.71	-0.11	-32.31	Chr5: 23507617	<i>PRDM9</i>	TSS200		FALSE
cg16273546	0.59	0.69	-0.11	-30.70	Chr10: 123070392				TRUE
cg00481159	0.72	0.83	-0.11	-53.48	Chr12: 96353086	<i>AMDHD1</i>	Body	S_Shelf	FALSE
cg12906381	0.44	0.55	-0.11	-24.27	Chr22: 32599516	<i>RFPL2, RFPL2, RFPL2</i>	TSS200, 5'UTR, TSS1500		FALSE
cg00034336	0.63	0.73	-0.11	-34.16	Chr2: 8684126				TRUE
cg19649900	0.85	0.95	-0.11	-138.39	Chr19: 1155030	<i>SBNO2</i>	5'UTR	Island	TRUE
cg00601042	0.28	0.39	-0.11	-28.59	Chr12: 132900274	<i>GALNT9</i>	Body	Island	FALSE
cg14020285	0.50	0.61	-0.11	-25.22	Chr2: 119401665				TRUE
cg12675714	0.07	0.18	-0.11	-75.48	Chr4: 159592618	<i>C4orf46, ETFDH</i>	Body, TSS1500	Island	FALSE
cg02334775	0.49	0.59	-0.11	-24.67	Chr15: 89182676	<i>ISG20</i>	Body		FALSE
cg01673307	0.39	0.49	-0.10	-23.98	Chr6: 32819911	<i>TAP1</i>	Body	N_Shore	FALSE
cg01219135	0.44	0.55	-0.10	-23.57	Chr7: 158766336			Island	FALSE
cg11572942	0.75	0.85	-0.10	-58.72	Chr1: 1656592	<i>CDK11A, CDK11B, CDK11B, CDK11A, CDK11B, CDK11B, CDK11B</i>	TSS1500, TSS1500, TSS1500, TSS1500, TSS1500, TSS1500, TSS1500, TSS1500	S_Shore	FALSE
cg18576957	0.64	0.74	-0.10	-34.32	Chr6: 31651020			Island	FALSE
cg04700648	0.81	0.91	-0.10	-93.37	Chr19: 52888958	<i>ZNF880</i>	3'UTR		FALSE
cg23400446	0.13	0.23	-0.10	-51.94	Chr10: 135342560	<i>CYP2E1</i>	Body	Island	FALSE
cg17190781	0.76	0.86	-0.10	-62.73	Chr6: 40387783	<i>LRFN2</i>	Body		TRUE
cg19651115	0.44	0.55	-0.10	-23.17	Chr12: 11700343				FALSE
cg27313577	0.75	0.86	-0.10	-59.81	Chr7: 157260021			N_Shore	FALSE
cg13022905	0.65	0.75	-0.10	-34.42	Chr5: 147699892				FALSE
cg05915866	0.41	0.51	-0.10	-22.40	Chr16: 73090838	<i>ZFHX3</i>	5'UTR	N_Shore	FALSE
cg04742550	0.50	0.61	-0.10	-23.45	Chr16: 31366429	<i>ITGAX</i>	TSS200		FALSE
cg07405182	0.67	0.77	-0.10	-36.66	Chr1: 40598455			N_Shore	TRUE
cg01948202	0.14	0.25	-0.10	-44.30	Chr3: 122400474	<i>PARP14</i>	Body	S_Shore	FALSE
cg12789884	0.60	0.70	-0.10	-27.75	Chr3: 175554437				TRUE
cg20971158	0.55	0.65	-0.10	-24.43	Chr11: 35159382	<i>CD44, CD44, CD44, CD44, CD44</i>	TSS1500, TSS1500, TSS1500, TSS1500, TSS1500	N_Shore	FALSE
cg01973676	0.70	0.80	-0.10	-42.56	Chr7: 101596404	<i>CUX1, CUX1, CUX1</i>	Body, Body, Body		TRUE
cg17888390	0.20	0.30	-0.10	-33.73	Chr10: 101282816			Island	FALSE
cg24104616	0.78	0.89	-0.10	-71.24	Chr6: 28969099	<i>ZNF311</i>	Body		FALSE
cg01741372	0.69	0.79	-0.10	-38.76	Chr11: 783889				TRUE
cg13732083	0.14	0.24	-0.10	-44.38	Chr21: 47605072	<i>C21orf56, C21orf56</i>	TSS1500, TSS1500	S_Shelf	FALSE
cg13298116	0.33	0.43	-0.10	-23.31	Chr11: 62369859	<i>EML3, MTA2</i>	3'UTR, TSS1500	Island	FALSE
cg19909865	0.12	0.22	-0.10	-50.04	Chr4: 134074421	<i>PCDH10</i>	Body	S_Shore	TRUE
cg04031093	0.57	0.67	-0.10	-25.13	Chr1: 233027124				TRUE
cg27473997	0.72	0.82	-0.10	-44.91	Chr4: 9355351	<i>USP17</i>	TSS200		FALSE
cg00916680	0.54	0.64	-0.10	-23.62	ChrX: 152529487			N_Shore	FALSE
cg01961752	0.23	0.33	-0.10	-30.00	Chr1: 1109012	<i>TTLL10</i>	TSS1500	N_Shore	TRUE
cg09166973	0.76	0.86	-0.10	-57.64	Chr5: 23507573	<i>PRDM9</i>	TSS200		FALSE
cg01190666	0.59	0.69	-0.10	-26.78	Chr20: 62204908	<i>PRIC285</i>	5'UTR	N_Shore	FALSE
cg13051013	0.75	0.85	-0.10	-55.32	Chr1: 149684418				FALSE
cg13979884	0.73	0.83	-0.10	-47.00	Chr9: 74061171			N_Shore	FALSE
Hypermethylation									
cg05380919	0.89	0.62	0.27	341.63	Chr22: 24376252	<i>GSTT1</i>	3'UTR	S_Shelf	FALSE
cg15262954	0.39	0.12	0.27	341.63	Chr20: 62198872	<i>PRIC285, PRIC285</i>	Body, 1stExon	Island	FALSE

cg01079515	0.94	0.68	0.26	341.63	Chr3: 195576629				FALSE
cg00103771	0.67	0.41	0.26	341.63	Chr6: 32525805	HLA-DRB6	Body		FALSE
cg23350716	0.72	0.47	0.25	341.63	Chr1: 147956744	PPIAL4B, PPIAL4A	TSS1500, TSS1500		FALSE
cg05357209	0.42	0.17	0.25	341.63	Chr7: 872208	UNC84A, UNC84A	5'UTR, Body		TRUE
cg06550200	0.92	0.69	0.23	341.63	Chr5: 1325588	CLPTM1L	Body		FALSE
cg00440797	0.31	0.09	0.22	341.63	Chr6: 32493873	HLA-DRB5	Body	S_Shelf	FALSE
cg08477687	0.57	0.35	0.22	341.63	Chr1: 566570	MIR1977	TSS1500		FALSE
cg01694488	0.95	0.73	0.22	341.63	Chr4: 1580172			Island	FALSE
cg01500431	0.91	0.69	0.22	341.63	Chr22: 24388327	GSTTP2	Body	S_Shelf	FALSE
cg02239258	0.58	0.36	0.22	341.63	Chr8: 8241752			N_Shore	FALSE
cg12303247	0.88	0.67	0.21	341.63	Chr1: 155853542	SYT11	3'UTR		TRUE
cg03188948	0.40	0.19	0.21	341.63	Chr7: 1209495				FALSE
cg03213289	0.52	0.32	0.19	114.27	Chr20: 61660250			Island	FALSE
cg06301252	0.90	0.71	0.19	341.63	Chr7: 157504143	PTPRN2, PTPRN2, PTPRN2	Body, Body, Body	Island	FALSE
cg00638631	0.90	0.72	0.19	341.63	Chr21: 39039777	KCNJ6	Body	Island	FALSE
cg13185413	0.43	0.25	0.18	109.95	Chr6: 30039202	RNF39, RNF39	Body, Body	Island	FALSE
cg12633154	0.56	0.38	0.18	95.16	Chr6: 30039435	RNF39, RNF39	Body, Body	Island	FALSE
cg00947782	0.36	0.18	0.18	123.86	Chr6: 30039142	RNF39, RNF39	Body, Body	Island	FALSE
cg10568066	0.59	0.42	0.18	92.38	Chr6: 30039442	RNF39, RNF39	Body, Body	Island	FALSE
cg20021790	0.45	0.28	0.17	94.32	Chr17: 181288	RPH3AL	5'UTR	N_Shelf	TRUE
cg10930308	0.43	0.26	0.17	94.18	Chr6: 30039476	RNF39, RNF39	Body, Body	Island	FALSE
cg20866694	0.37	0.20	0.17	108.72	Chr6: 27181670				FALSE
cg09279736	0.51	0.34	0.17	84.57	Chr6: 30039403	RNF39, RNF39	Body, Body	Island	FALSE
cg03847896	0.55	0.38	0.17	80.83	Chr1: 112154295				TRUE
cg06675417	0.79	0.62	0.17	113.88	Chr18: 7729443			Island	FALSE
cg03343571	0.44	0.28	0.17	87.26	Chr6: 30039175	RNF39, RNF39	Body, Body	Island	FALSE
cg19418458	0.56	0.40	0.16	75.44	Chr7: 158789849			Island	FALSE
cg09885502	0.51	0.35	0.16	74.06	Chr20: 57463991	GNAS, GNAS, GNAS, GNAS	3'UTR, TSS200, 3'UTR, Body	Island	FALSE
cg01717482	0.78	0.62	0.16	102.34	Chr3: 75657183				FALSE
cg06249604	0.30	0.14	0.16	114.27	Chr6: 30039206	RNF39, RNF39	Body, Body	Island	FALSE
cg11141652	0.74	0.58	0.16	89.39	Chr22: 24348549	GSTTP1	TSS1500		FALSE
cg14279361	0.59	0.44	0.16	69.00	Chr19: 6721955	C3	TSS1500		FALSE
cg26970113	0.89	0.74	0.16	341.63	Chr5: 133710892	UBE2B	Body	S_Shelf	FALSE
cg02524205	0.64	0.48	0.16	69.75	Chr6: 167559851				FALSE
cg13401893	0.57	0.41	0.15	66.02	Chr6: 30039432	RNF39, RNF39	Body, Body	Island	FALSE
cg06758191	0.87	0.72	0.15	341.63	Chr4: 7812988	AFAP1, AFAP1	Body, Body		FALSE
cg04097388	0.81	0.66	0.15	106.29	Chr2: 236671717	AGAP1, AGAP1	Body, Body	N_Shore	FALSE
cg06343673	0.73	0.58	0.15	78.99	Chr17: 78778232	RPTOR, RPTOR	Body, Body	S_Shelf	FALSE
cg10920224	0.57	0.42	0.15	63.03	Chr14: 103367591	TRAF3, TRAF3, TRAF3	Body, Body, Body		FALSE
cg00035636	0.53	0.38	0.15	62.62	Chr13: 21900591			Island	FALSE
cg11202023	0.77	0.62	0.15	86.03	Chr4: 73437692			S_Shelf	FALSE
cg26280976	0.41	0.26	0.15	71.31	Chr14: 69660603			S_Shore	FALSE
cg10599438	0.41	0.26	0.15	69.95	Chr19: 844589	PRTN3	Body	N_Shore	FALSE
cg17624673	0.67	0.52	0.15	66.74	Chr5: 140596187	PCDHB13, PCDHB13	3'UTR, 1stExon	S_Shore	FALSE
cg11775292	0.40	0.26	0.15	67.89	Chr15: 33487631			S_Shore	TRUE
cg01252526	0.51	0.37	0.15	58.75	Chr16: 711033	WDR90	Body	N_Shore	TRUE
cg15242686	0.70	0.55	0.15	66.54	Chr22: 24348715	GSTTP1	TSS1500		FALSE
cg17014757	0.49	0.34	0.15	58.65	Chr1: 203156097	CHI3L1	TSS200		TRUE
cg08045932	0.64	0.50	0.14	59.75	Chr20: 61659980			N_Shore	FALSE
cg26642960	0.79	0.64	0.14	85.82	Chr19: 54747789	LILRA6	TSS1500		FALSE
cg15948536	0.44	0.29	0.14	60.69	Chr4: 169770092	PALLD, PALLD, PALLD, PALLD	5'UTR, Body, Body, Body		TRUE
cg17416644	0.67	0.53	0.14	61.00	Chr11: 1474841	BRSK2	Body	S_Shelf	FALSE
cg02996355	0.48	0.34	0.14	56.55	Chr14: 81879375				FALSE
cg19537719	0.49	0.35	0.14	55.13	Chr8: 41583498	ANK1, ANK1, ANK1, ANK1, ANK1	Body, Body, Body, Body, Body	Island	FALSE
cg12310025	0.54	0.39	0.14	53.46	Chr6: 25882481			Island	FALSE
cg14017402	0.40	0.26	0.14	62.11	Chr2: 86225602				TRUE
cg15690347	0.40	0.26	0.14	61.52	Chr19: 50931515	SPIB	Body	Island	FALSE
cg09352518	0.38	0.24	0.14	63.50	Chr19: 21265421	ZNF714	5'UTR	Island	FALSE

cg09584650	0.49	0.35	0.14	52.33	Chr8: 2002012	<i>MYOM2</i>	Body	N_Shore	FALSE
cg02188185	0.57	0.44	0.14	50.92	Chr6: 30039524	<i>RNF39, RNF39</i>	Body, Body	S_Shore	FALSE
cg23221052	0.57	0.43	0.14	50.45	Chr5: 179740743	<i>GFPT2</i>	Body	Island	FALSE
cg02174092	0.36	0.22	0.14	65.09	Chr10: 43846539			Island	FALSE
cg17751872	0.47	0.34	0.14	50.86	Chr19: 21264982	<i>ZNF714, ZNF714</i>	5'UTR, 1stExon	N_Shore	FALSE
cg07512361	0.75	0.61	0.14	65.51	Chr7: 101944430	<i>SH2B2</i>	Body	Island	FALSE
cg27171569	0.70	0.57	0.13	56.38	Chr16: 83987465	<i>OSGIN1, OSGIN1, OSGIN1</i>	5'UTR, Body, 5'UTR		TRUE
cg12709009	0.80	0.67	0.13	77.78	Chr6: 170557582				FALSE
cg16338365	0.55	0.41	0.13	46.18	Chr6: 167559913				FALSE
cg05867499	0.27	0.13	0.13	83.27	Chr7: 4848814	<i>RADIL</i>	Body	Island	FALSE
cg24441899	0.54	0.40	0.13	44.81	Chr7: 4244372	<i>SDK1, SDK1</i>	Body, Body		FALSE
cg10555744	0.37	0.24	0.13	56.16	Chr1: 25946258	<i>MAN1C1</i>	Body	S_Shore	TRUE
cg06423211	0.77	0.64	0.13	65.39	Chr19: 551401			Island	FALSE
cg02779037	0.20	0.07	0.13	115.46	Chr7: 4848683	<i>RADIL</i>	Body	Island	FALSE
cg10277872	0.78	0.65	0.13	67.71	Chr4: 4136918				FALSE
cg26893861	0.45	0.32	0.13	46.81	Chr17: 41843967	<i>DUSP3</i>	3'UTR		FALSE
cg04111992	0.57	0.44	0.13	43.32	Chr7: 158790115			S_Shore	FALSE
cg20381404	0.15	0.02	0.13	341.63	Chr5: 34008215	<i>AMACR, AMACR, AMACR</i>	5'UTR, 1stExon, 5'UTR, 1stExon, 5'UTR, 1stExon, 5'UTR, 1stExon, 5'UTR, 1stExon, 5'UTR	S_Shore	FALSE
cg13448197	0.33	0.20	0.13	60.33	Chr10: 43846281			Island	FALSE
cg01483656	0.32	0.19	0.13	62.84	Chr19: 21264896	<i>ZNF714</i>	TSS200	N_Shore	FALSE
cg26576544	0.48	0.35	0.13	43.59	Chr7: 38316654				FALSE
cg18451016	0.71	0.58	0.13	52.53	Chr1: 38461880			Island	FALSE
cg11236515	0.33	0.20	0.13	59.15	Chr2: 74213762			S_Shore	FALSE
cg21809927	0.61	0.48	0.13	42.90	Chr6: 30079265	<i>TRIM31</i>	Body		FALSE
cg16767506	0.28	0.15	0.13	71.94	Chr7: 142494244			N_Shore	TRUE
cg05552543	0.29	0.16	0.13	67.34	Chr16: 75322715				TRUE
cg08858441	0.43	0.31	0.13	44.38	Chr1: 569427				FALSE
cg15942979	0.21	0.08	0.13	103.74	Chr8: 22497061	<i>BIN3</i>	Body		FALSE
cg12086421	0.87	0.74	0.13	95.11	Chr6: 68535378				FALSE
cg13318129	0.34	0.21	0.13	54.83	Chr22: 45737514	<i>FAM118A, FAM118A</i>	3'UTR, 3'UTR		FALSE
cg17593958	0.30	0.18	0.13	60.45	Chr20: 62199034	<i>PRIC285, PRIC285, PRIC285</i>	5'UTR, Body, 1stExon	N_Shore	FALSE
cg19052272	0.80	0.67	0.13	65.18	Chr2: 3704530	<i>ALLC</i>	TSS1500		FALSE
cg18930910	0.36	0.24	0.13	49.11	Chr6: 30039151	<i>RNF39, RNF39</i>	Body, Body	Island	FALSE
cg18805164	0.75	0.62	0.13	54.08	Chr19: 36265700	<i>SNX26</i>	TSS1500	N_Shore	FALSE
cg10686758	0.38	0.26	0.13	46.73	Chr17: 39279735	<i>KRTAP4-12, KRTAP4-12</i>	3'UTR, 1stExon		FALSE
cg04349084	0.29	0.17	0.12	62.63	Chr8: 23602677				TRUE
cg24838063	0.82	0.70	0.12	71.75	Chr12: 130822603	<i>PIWIL1</i>	TSS200	Island	FALSE
cg07390013	0.81	0.68	0.12	67.71	Chr1: 230838294	<i>AGT</i>	3'UTR		FALSE
cg17920646	0.51	0.39	0.12	37.85	Chr8: 216578			Island	FALSE
cg00758881	0.34	0.22	0.12	50.90	Chr16: 58534681	<i>NDRG4, NDRG4, NDRG4</i>	Body, Body, Body	N_Shore	FALSE
cg09640425	0.53	0.41	0.12	37.17	Chr7: 158790006			Island	FALSE
cg18402987	0.20	0.08	0.12	97.75	Chr7: 1209562				FALSE
cg17542795	0.73	0.61	0.12	48.81	Chr4: 178518017				TRUE
cg04255230	0.45	0.32	0.12	39.22	Chr2: 74727010	<i>LBX2</i>	Body	Island	FALSE
cg26099834	0.41	0.29	0.12	41.06	Chr15: 66947568			Island	FALSE
cg09425279	0.54	0.42	0.12	36.04	Chr16: 31188401			N_Shelf	FALSE
cg11062466	0.46	0.34	0.12	37.52	Chr8: 58055876			N_Shore	FALSE
cg27387030	0.44	0.32	0.12	38.23	Chr1: 203320541	<i>FMOD</i>	TSS1500		FALSE
cg02385173	0.66	0.54	0.12	39.41	Chr11: 76571534	<i>ACER3</i>	TSS1500	N_Shore	FALSE
cg13944838	0.63	0.51	0.12	37.52	Chr5: 179740914	<i>GFPT2</i>	Body	Island	FALSE
cg08779649	0.61	0.49	0.12	36.56	Chr13: 50194554				FALSE
cg18816397	0.56	0.44	0.12	34.96	Chr6: 32489555	<i>HLA-DRB5</i>	Body	N_Shore	FALSE
cg15145296	0.31	0.19	0.12	52.85	Chr3: 125709740			S_Shore	FALSE
cg14522718	0.19	0.07	0.12	98.71	Chr9: 130868874	<i>SLC25A25, SLC25A25, SLC25A25,</i>	Body, Body, Body, Body		FALSE

	SLC25A25						
	ACTN1, ACTN1, ACTN1			Body, Body, Body			
cg00739471	0.33	0.21	0.12	47.75	Chr14: 69415588		
cg20290983	0.21	0.09	0.12	83.12	Chr6: 43655470	MRPS18A	1stExon
cg19035788	0.43	0.31	0.12	36.68	Chr2: 242881634		S_Shelf
cg19453686	0.45	0.33	0.12	35.18	Chr14: 92334271	TC2N	TSS1500
cg08474748	0.44	0.32	0.12	35.58	Chr5: 74350214		Island
cg05600342	0.27	0.15	0.12	59.39	Chr11: 250989	PSMD13, PSMD13	Body, Body
cg13469425	0.79	0.67	0.12	54.98	Chr4: 48175353	TEC	Body
cg06180910	0.85	0.73	0.12	74.57	Chr22: 24382663	GSTT1	Body
cg08071329	0.93	0.81	0.12	126.76	Chr6: 170555857		N_Shore
cg11949518	0.44	0.32	0.12	35.17	Chr17: 78912765	RPTOR, RPTOR	Body, Body
cg21873524	0.43	0.31	0.12	35.60	Chr4: 190942744		Island
cg15529432	0.51	0.40	0.12	32.40	Chr5: 16615750	FAM134B	Body
cg14047540	0.86	0.74	0.12	77.48	Chr11: 133829660		S_Shelf
cg19595760	0.29	0.17	0.12	53.86	Chr1: 25948511	MAN1C1	S_Shelf
cg01050736	0.79	0.67	0.12	53.73	Chr6: 32710583	HLA-DQA2	Body
cg21724239	0.54	0.42	0.12	31.56	Chr8: 58056113		Island
cg13390570	0.28	0.16	0.12	54.03	Chr5: 1255616	TERT, TERT	Body, Body
cg07970799	0.21	0.10	0.11	74.92	Chr6: 6614719	LOC285780, LY86	Body, Body
cg12420107	0.42	0.31	0.11	33.11	Chr5: 140090300	VTRNA1-1	TSS1500
cg02486855	0.73	0.62	0.11	40.72	Chr15: 67356942	SMAD3	TSS1500
cg23939001	0.66	0.54	0.11	33.64	Chr4: 940644	TMEM175	5'UTR
cg16192197	0.26	0.14	0.11	56.75	Chr6: 112301106		Island
cg23917638	0.42	0.31	0.11	32.95	Chr1: 567501	MIR1977	TSS1500
cg21167269	0.41	0.30	0.11	33.73	Chr9: 98981500		Island
cg12196389	0.88	0.76	0.11	82.79	Chr10: 35504007		Island
cg01768001	0.34	0.22	0.11	40.63	Chr1: 24831147	RCAN3	5'UTR
cg12893697	0.36	0.25	0.11	37.02	Chr11: 970389	AP2A2	Body
cg03396347	0.67	0.56	0.11	33.66	Chr1: 1875803		Island
cg13719246	0.87	0.76	0.11	76.52	Chr8: 7639801		Island
cg23159337	0.55	0.44	0.11	28.41	Chr3: 193272778	ATP13A4	TSS200
					SEPT9, SEPT9,	Body, Body,	
cg20557159	0.56	0.45	0.11	28.33	Chr17: 75445261	SEPT9, SEPT9,	N_Shelf
					SEPT9, SEPT9	Body, Body,	FALSE
cg10598596	0.61	0.50	0.11	29.52	Chr19: 51517212	KLK10, KLK10,	3'UTR, 3'UTR,
					KLK10	3'UTR	N_Shelf
cg04682580	0.65	0.54	0.11	31.65	Chr1: 53016396	ZCCHC11,	5'UTR, 5'UTR,
					ZCCHC11,	5'UTR	N_Shore
cg12044599	0.31	0.20	0.11	42.35	Chr11: 67206308	CORO1B,	Body, Body,
					CORO1B,	TSS1500	S_Shelf
cg05262463	0.24	0.12	0.11	60.01	Chr19: 50056081	PTPRCAP	
cg27366766	0.29	0.18	0.11	45.12	Chr17: 56565286	HSF5	1stExon
cg27182070	0.52	0.41	0.11	27.73	Chr1: 28218282	RPA2	3'UTR
cg18566515	0.40	0.29	0.11	31.84	Chr10: 123356236	FGFR2, FGFR2,	5'UTR, 5'UTR,
cg06287775	0.38	0.27	0.11	33.47	Chr7: 4784174	FGFR2, FGFR2,	5'UTR, 5'UTR,
cg21177396	0.54	0.43	0.11	27.33	Chr9: 126888124	FGFR2, FGFR2	5'UTR, TSS200
cg02493602	0.65	0.54	0.11	30.17	Chr11: 86383696	ME3, ME3, ME3	TSS1500, TSS200,
						TSS1500	S_Shore
cg15009294	0.37	0.26	0.11	33.24	Chr1: 214813712	CENPF	Body
cg08154612	0.42	0.31	0.11	29.53	Chr17: 7037098		TRUE
cg09086987	0.44	0.33	0.11	28.47	Chr3: 18470432	SATB1	FALSE
cg06159404	0.36	0.25	0.11	34.21	Chr10: 43846376		FALSE
cg02090762	0.21	0.10	0.11	65.28	Chr17: 79503859	FSCN2, FSCN2	Island
cg12131419	0.46	0.35	0.11	27.64	Chr15: 49353073		Island
cg10411590	0.71	0.60	0.11	34.14	Chr13: 21900810		TRUE
cg08477332	0.35	0.24	0.11	35.20	Chr1: 153590243	S100A14	S_Shore
cg03227037	0.43	0.32	0.11	28.90	Chr20: 62212228		FALSE
cg05460226	0.29	0.18	0.11	42.86	Chr17: 8804279	PIK3R5, PIK3R5	S_Shelf
					ANXA2, ANXA2,	Body, Body	TRUE
cg27554954	0.72	0.61	0.11	35.17	Chr15: 60691595	ANXA2, ANXA2,	TSS1500,
					ANXA2, ANXA2	TSS1500,	TSS1500,
						TSS1500,	S_Shore
						TSS1500,	TRUE

						TSS1500		
cg05406088	0.33	0.22	0.11	36.81	Chr15: 66947617		S_Shore	TRUE
cg24885723	0.35	0.24	0.11	35.06	Chr1: 9030439	CA6	Body	FALSE
cg00106345	0.53	0.42	0.11	26.22	Chr7: 27138396		S_Shore	FALSE
cg21565496	0.38	0.27	0.11	31.86	Chr13: 40762150			FALSE
cg18489755	0.56	0.45	0.11	26.21	Chr3: 183533873	MAP6D1	3'UTR	FALSE
cg26485825	0.32	0.21	0.11	37.65	Chr18: 21452895	LAMA3, LAMA3, LAMA3, LAMA3	TSS200, TSS200, Body, Body	FALSE
cg22633036	0.36	0.25	0.11	33.58	Chr10: 123355576	FGFR2, FGFR2, FGFR2, FGFR2	5'UTR, 5'UTR, 5'UTR, 5'UTR	N_Shore
cg01322142	0.30	0.19	0.11	40.73	Chr4: 786718	CPLX1	Body	S_Shore
cg06872548	0.30	0.19	0.11	41.06	Chr17: 78716983	RPTOR, RPTOR	Body, Body	N_Shelf
cg19348272	0.80	0.70	0.11	49.06	Chr7: 77044158	PION	Body	N_Shore
cg20814179	0.60	0.49	0.11	26.73	Chr4: 940893	TMEM175	5'UTR	Island
cg13684379	0.88	0.77	0.11	76.13	Chr10: 1511173	ADARB2	Body	FALSE
cg04632378	0.56	0.45	0.11	25.90	Chr13: 21900426			Island
cg16620160	0.78	0.68	0.11	44.59	Chr5: 174825074			FALSE
cg23104954	0.27	0.17	0.11	45.58	Chr13: 50701501			FALSE
cg20070768	0.59	0.49	0.11	26.55	Chr15: 74285128	STOML1	TSS1500	S_Shore
cg10973622	0.69	0.59	0.11	31.96	Chr2: 86423274	IMMT, IMMT, IMMT	TSS1500, TSS1500, TSS1500	S_Shore
cg02299497	0.43	0.32	0.11	27.48	Chr14: 69095570			TRUE
cg14270590	0.42	0.31	0.11	27.91	Chr14: 105499706			N_Shore
cg26094651	0.71	0.61	0.11	33.32	Chr2: 1802045	MYT1L	Body	Island
cg08310519	0.91	0.81	0.11	98.57	Chr11: 86305199	ME3, ME3, ME3	Body, Body, Body	TRUE
cg21862353	0.68	0.58	0.11	30.54	Chr2: 1801628	MYT1L	Body	Island
cg12178432	0.44	0.34	0.11	26.77	Chr1: 26049105	MAN1C1	Body	FALSE
cg24755459	0.21	0.10	0.11	64.42	Chr14: 101908865			Island
cg18110333	0.51	0.40	0.11	25.06	Chr6: 292329	DUSP22, DUSP22	1stExon, 5'UTR	Island
cg27134251	0.73	0.62	0.11	34.30	Chr8: 1365049			N_Shore
cg04658243	0.57	0.47	0.11	25.17	Chr17: 78865755	RPTOR, RPTOR	Body, Body	S_Shore
cg03961283	0.41	0.30	0.11	28.01	Chr1: 223566761	C1orf65, C1orf65	5'UTR, 1stExon	Island
cg02722613	0.20	0.10	0.11	64.72	Chr4: 25162898	SEPSECS, SEPSECS, SEPSECS	TSS1500, TSS1500, TSS1500	S_Shore
cg14216940	0.37	0.26	0.11	30.94	Chr7: 50343131	IKZF1	TSS1500	Island
cg22052514	0.38	0.27	0.11	29.91	Chr8: 142401722			Island
cg19204924	0.65	0.54	0.11	27.32	Chr19: 20576478	ZNF826	3'UTR	FALSE
cg06476926	0.58	0.47	0.11	24.69	Chr17: 80867707	TBCD	Body	N_Shelf
cg04116354	0.35	0.24	0.11	32.37	Chr1: 26003643	MAN1C1	Body	TRUE
cg11227278	0.31	0.20	0.11	36.74	Chr2: 23749277	KLHL29	5'UTR	Island
cg22668906	0.39	0.28	0.11	28.68	Chr11: 128180077			TRUE
cg15052335	0.70	0.59	0.11	30.40	Chr18: 3011810	LPIN2, LPIN2	5'UTR, 1stExon	N_Shore
cg04548204	0.44	0.33	0.11	25.79	Chr12: 9162872	KLRG1	3'UTR	FALSE
cg08222513	0.65	0.55	0.11	27.14	Chr6: 30079280	TRIM31	Body	FALSE
cg23731272	0.66	0.55	0.11	27.43	Chr15: 67356838	SMAD3	TSS1500	N_Shore
cg00693583	0.87	0.76	0.11	66.52	Chr4: 25160982	SEPSECS, SEPSECS, SEPSECS	Body, Body, Body	N_Shore
cg03906434	0.35	0.25	0.10	30.91	Chr7: 27231819			Island
cg17346246	0.34	0.24	0.10	31.99	Chr12: 123214864	GPR81	1stExon 5'UTR, 5'UTR,	FALSE
cg25700686	0.45	0.35	0.10	24.57	Chr8: 72268832	EYA1, EYA1, EYA1, EYA1, EYA1, EYA1, EYA1	1stExon, 1stExon, 1stExon, 5'UTR, 5'UTR	TRUE
cg02398342	0.73	0.62	0.10	32.37	Chr17: 80708632	TBCD, FN3K	TSS1500, 3'UTR	N_Shore
cg04597393	0.26	0.15	0.10	44.62	Chr8: 142276533			FALSE
cg13578160	0.45	0.35	0.10	24.62	Chr7: 72813978			FALSE
cg19383211	0.72	0.62	0.10	32.29	Chr6: 32527588	HLA-DRB6	Body	FALSE
cg27064063	0.17	0.07	0.10	74.56	Chr6: 117869287	DCBLD1	Body	Island
cg18766900	0.65	0.55	0.10	26.23	Chr10: 11574616	USP6NL, USP6NL	Body, TSS1500	FALSE
cg19001909	0.24	0.14	0.10	47.76	Chr17: 26205940	C17orf108	3'UTR	FALSE
cg27257987	0.84	0.74	0.10	54.60	Chr19: 43709360	PSG4, PSG4	Body, Body	FALSE
cg24044478	0.78	0.67	0.10	39.45	Chr8: 145035191	PLEC1, PLEC1	Body, Body	FALSE

cg27216937	0.64	0.53	0.10	25.17	Chr11: 6425978	<i>APBB1, APBB1</i>	Body, Body		TRUE	
cg01154505	0.34	0.23	0.10	31.52	Chr2: 112940409	<i>FBLN7, FBLN7</i>	Body, Body	S_Shore	TRUE	
cg13260278	0.31	0.21	0.10	33.97	Chr10: 121265587	<i>RGS10, RGS10</i>	Body, Body		FALSE	
cg10528576	0.64	0.54	0.10	25.17	Chr14: 101192913	<i>DLK1</i>	TSS1500	Island	FALSE	
cg13318241	0.41	0.31	0.10	25.47	Chr6: 3455537	<i>SLC22A23</i>	Body	N_Shore	TRUE	
cg06221963	0.70	0.60	0.10	29.32	Chr1: 154839813	<i>KCNN3</i>	Body		FALSE	
cg10730425	0.80	0.70	0.10	44.04	Chr19: 1035093	<i>CNN2, CNN2</i>	Body, Body	Island	FALSE	
cg15007959	0.24	0.13	0.10	48.46	Chr19: 50931432	<i>SPIB</i>	Body	Island	FALSE	
cg21123519	0.42	0.32	0.10	24.78	Chr14: 69095679			S_Shore	TRUE	
cg01788113	0.47	0.37	0.10	23.10	Chr3: 46759472	<i>PRSS50</i>	TSS200	Island	FALSE	
cg12000995	0.79	0.69	0.10	41.16	Chr2: 27665139	<i>KRTCAP3, KRTCAP3</i>	TSS200, TSS200	Island	FALSE	
cg06307913	0.36	0.26	0.10	28.26	Chr4: 81118794	<i>PRDM8, PRDM8, PRDM8</i>	5'UTR, 1stExon, 5'UTR	N_Shore	FALSE	
cg00376816	0.27	0.17	0.10	39.80	Chr19: 39332571	<i>HNRNPL, HNRNPL</i>	Body, Body		FALSE	
cg13963793	0.38	0.28	0.10	26.50	Chr1: 223567173	<i>C1orf65</i>	1stExon	Island	TRUE	
cg00119778	0.23	0.13	0.10	48.01	Chr6: 32466447				FALSE	
cg20581490	0.71	0.61	0.10	29.52	Chr18: 12775841			N_Shore	FALSE	
cg09891288	0.80	0.70	0.10	42.39	Chr17: 78863674	<i>RPTOR, RPTOR</i>	Body, Body	Island	FALSE	
cg25407410	0.84	0.74	0.10	53.05	Chr6: 143891975	<i>LOC285740</i>	TSS1500		FALSE	
cg11370814	0.27	0.17	0.10	40.02	Chr2: 242927418			N_Shore	FALSE	
cg15950273	0.58	0.48	0.10	22.31	Chr14: 103367306	<i>TRAF3, TRAF3, TRAF3</i>	Body, Body, Body		FALSE	
cg11480019	0.23	0.13	0.10	48.16	Chr10: 75936982	<i>ADK, ADK</i>	Body, Body	S_Shore	FALSE	
cg10911276	0.84	0.74	0.10	51.97	Chr4: 4142417			N_Shelf	FALSE	
cg11677105	0.37	0.27	0.10	26.66	Chr22: 42078707	<i>NHP2L1, NHP2L1</i>	Body, TSS200	S_Shore	FALSE	
cg06791446	0.59	0.49	0.10	22.12	Chr10: 123355268	<i>FGFR2, FGFR2, FGFR2, FGFR2, FGFR2</i>	5'UTR, 5'UTR, 5'UTR, 5'UTR, 5'UTR	TSS1500, 5'UTR, 5'UTR	N_Shore	FALSE
cg00356916	0.61	0.51	0.10	22.77	Chr1: 116256618	<i>CASQ2</i>	Body		TRUE	
cg17446339	0.36	0.26	0.10	27.54	Chr11: 20385254	<i>HTATIP2, HTATIP2, HTATIP2, HTATIP2, HTATIP2, HTATIP2</i>	TSS200, 1stExon, TSS1500, 1stExon, 5'UTR, 5'UTR, TSS200	Island	FALSE	
cg06712767	0.64	0.54	0.10	23.65	Chr12: 131118561				TRUE	
cg06226386	0.25	0.15	0.10	42.35	Chr8: 22500449	<i>FLJ14107, BIN3</i>	TSS1500, Body		FALSE	
cg18405330	0.30	0.20	0.10	34.26	Chr6: 164171960				FALSE	
cg24659858	0.39	0.28	0.10	25.39	Chr13: 24270321			S_Shore	TRUE	
cg21111256	0.34	0.23	0.10	29.33	Chr19: 41386507	<i>CYP2A7, CYP2A7</i>	Body, Body	Island	FALSE	
cg17804342	0.77	0.67	0.10	35.10	Chr10: 121271663	<i>RGS10, RGS10</i>	Body, Body		FALSE	
cg11559192	0.83	0.73	0.10	49.64	Chr12: 25357592	<i>LYRM5</i>	3'UTR		FALSE	
cg16704958	0.23	0.12	0.10	48.66	Chr21: 38630728	<i>DSCR3</i>	Body	S_Shore	TRUE	
cg01466164	0.41	0.31	0.10	23.63	Chr8: 2481226			S_Shore	FALSE	
cg14279856	0.45	0.34	0.10	22.26	Chr6: 30851086	<i>DDR1, DDR1</i>	TSS1500, TSS1500	N_Shore	TRUE	
cg18681853	0.25	0.15	0.10	42.69	Chr2: 224889133	<i>SERPINE2, SERPINE2, SERPINE2, SERPINE2</i>	5'UTR, Body, 5'UTR, 5'UTR		TRUE	
cg13692134	0.32	0.22	0.10	29.91	Chr5: 74350132			Island	FALSE	

C.

No Molar or Discoid Rash

CG Site ID	Mean β Case	Mean β Control	Δβ	DiffScore	Location (HG19)	Gene Name	Gene-Relative Location	CGI-Relative Location	Enhancer
Hypomethylation									
cg21549285	0.36	0.65	-0.29	-301.97	Chr21: 42799141	<i>MX1, MX1</i> <i>NFYA, NFYA,</i> <i>LOC221442</i>	5'UTR, 5'UTR 3'UTR, 3'UTR, TSS200	S_Shore	FALSE
cg04346459	0.71	0.99	-0.28	-338.22	Chr6: 41068666	<i>NFYA, NFYA,</i> <i>LOC221442</i>	3'UTR, 3'UTR, TSS200	Island	TRUE
cg25110423	0.70	0.96	-0.26	-338.22	Chr6: 41068646	<i>NFYA, NFYA,</i> <i>LOC221442</i>	3'UTR, 3'UTR, TSS200	Island	TRUE
cg14392283	0.63	0.89	-0.26	-338.22	Chr8: 144103587	<i>LY6E, LY6E</i>	3'UTR, 3'UTR	N_Shelf	FALSE
cg15065340	0.49	0.72	-0.22	-174.57	Chr3: 195632915	<i>TNK2</i>	5'UTR	N_Shelf	FALSE
cg26893861	0.26	0.49	-0.22	-167.87	Chr17: 41843967	<i>DUSP3</i>	3'UTR		FALSE
cg19418458	0.42	0.64	-0.22	-154.86	Chr7: 158789849			Island	FALSE
cg23066280	0.43	0.64	-0.21	-147.50	Chr7: 158032496	<i>PTPRN2, PTPRN2,</i> <i>PTPRN2</i>	Body, Body, Body		FALSE
cg10890302	0.28	0.49	-0.21	-142.85	Chr6: 32064246	<i>TNXB</i>	Body	Island	FALSE
cg06715136	0.67	0.88	-0.21	-255.48	Chr7: 158046025	<i>PTPRN2, PTPRN2,</i> <i>PTPRN2</i>	Body, Body, Body		FALSE
cg14911689	0.33	0.54	-0.21	-135.21	Chr12: 739980	<i>NINJ2</i>	Body		FALSE
cg22531183	0.03	0.24	-0.20	-302.51	Chr19: 50554451	<i>FLJ26850</i>	Body	Island	FALSE
cg05696877	0.29	0.49	-0.20	-135.33	Chr1: 79088769	<i>IFI44L</i>	5'UTR		FALSE
cg01079515	0.73	0.93	-0.20	-312.22	Chr3: 195576629				FALSE
cg08122652	0.58	0.78	-0.20	-164.14	Chr3: 122281939	<i>PARP9, PARP9,</i> <i>DTX3L, PARP9,</i> <i>PARP9, PARP9,</i> <i>PARP9</i>	5'UTR, 5'UTR, TSS1500, 5'UTR, 5'UTR, 5'UTR, 5'UTR	N_Shore	FALSE
cg01992382	0.24	0.44	-0.20	-140.47	Chr6: 32064212	<i>TNXB</i>	Body	Island	FALSE
cg05357209	0.15	0.34	-0.20	-175.62	Chr7: 872208	<i>UNC84A, UNC84A</i>	5'UTR, Body		TRUE
cg26058907	0.52	0.71	-0.19	-130.32	ChrY: 22917942	<i>RPS4Y2</i>	TSS200		FALSE
cg14003022	0.42	0.61	-0.19	-115.72	Chr4: 3043019			Island	FALSE
cg00525277	0.37	0.56	-0.19	-113.90	Chr6: 32064239	<i>TNXB</i>	Body	Island	FALSE
cg00872984	0.38	0.57	-0.19	-112.22	Chr6: 32063991	<i>TNXB</i>	Body	Island	FALSE
cg26654770	0.35	0.54	-0.19	-112.28	Chr12: 740100	<i>NINJ2</i>	Body		FALSE
cg07524919	0.42	0.61	-0.19	-108.05	Chr6: 32063901	<i>TNXB</i>	Body	Island	FALSE
cg16834823	0.30	0.49	-0.19	-111.44	Chr6: 32064218	<i>TNXB</i>	Body	Island	FALSE
cg01201512	0.46	0.65	-0.19	-109.83	Chr12: 740338	<i>NINJ2</i>	Body		TRUE
cg06118351	0.66	0.84	-0.19	-175.88	Chr16: 4788808	<i>C16orf71</i>	Body	N_Shore	FALSE
cg14212360	0.58	0.76	-0.18	-131.39	Chr4: 89302999	<i>HERC6, HERC6</i>	Body, Body	S_Shelf	FALSE
cg22862003	0.53	0.72	-0.18	-115.18	Chr21: 42797588	<i>MX1, MX1</i> <i>NFYA, NFYA,</i> <i>LOC221442</i>	TSS1500, 5'UTR 3'UTR, 3'UTR, TSS200	N_Shore	FALSE
cg03644281	0.81	0.99	-0.18	-338.22	Chr6: 41068752			Island	TRUE
cg11478607	0.09	0.27	-0.18	-187.48	Chr22: 24384400	<i>GSTT1</i>	TSS200	Island	FALSE
cg09640425	0.40	0.59	-0.18	-96.88	Chr7: 158790006			Island	FALSE
cg14126601	0.44	0.61	-0.18	-92.12	Chr2: 37384708	<i>EIF2AK2, EIF2AK2</i>	TSS1500, TSS1500	S_Shore	FALSE
cg06188083	0.19	0.36	-0.17	-117.25	Chr10: 91093005	<i>IFIT3, IFIT3</i>	Body, Body		TRUE
cg02770061	0.64	0.81	-0.17	-126.84	Chr7: 158046166	<i>PTPRN2, PTPRN2,</i> <i>PTPRN2</i>	Body, Body, Body		FALSE
cg01624173	0.35	0.52	-0.17	-83.77	Chr14: 75981868				TRUE
cg03607951	0.53	0.70	-0.17	-91.33	Chr1: 79085586	<i>IFI44L</i>	TSS1500		FALSE
cg18838701	0.31	0.47	-0.17	-83.54	Chr19: 55668612	<i>TNNI3</i>	Body	S_Shore	FALSE
cg24419602	0.74	0.91	-0.17	-202.91	Chr19: 5510310			S_Shelf	FALSE
cg00274965	0.40	0.57	-0.17	-78.54	Chr21: 34405681			Island	FALSE
cg07777042	0.69	0.86	-0.17	-150.25	Chr8: 144702879			S_Shelf	FALSE
cg26287152	0.63	0.79	-0.16	-112.49	Chr17: 77923675	<i>TBC1D16</i>	Body	N_Shore	TRUE
cg06981309	0.46	0.63	-0.16	-78.24	Chr3: 146260954	<i>PLSCR1</i>	5'UTR	N_Shore	FALSE
cg10815657	0.76	0.92	-0.16	-215.62	Chr19: 289902	<i>PPAP2C, PPAP2C,</i> <i>PPAP2C</i>	Body, Body, 5'UTR	N_Shore	TRUE
cg19495714	0.56	0.72	-0.16	-89.02	Chr14: 105218551	<i>SIVA1, SIVA1</i>	TSS1500, TSS1500	Island	FALSE
cg05834845	0.61	0.77	-0.16	-102.34	Chr3: 195489306	<i>MUC4, MUC4,</i> <i>MUC4</i>	Body, Body, Body	Island	FALSE
cg06400119	0.72	0.89	-0.16	-168.78	Chr7: 158046222	<i>PTPRN2, PTPRN2,</i> <i>PTPRN2</i>	Body, Body, Body		FALSE
cg05401945	0.34	0.50	-0.16	-75.30	Chr3: 56590734	<i>CCDC66, CCDC66,</i> <i>CCDC66</i>	TSS1500, TSS1500,	N_Shore	FALSE

							TSS1500		
							1stExon, Body,		
							Body, Body,		
							5'UTR		
cg13909895	0.35	0.51	-0.16	-74.55	Chr22: 51066142	ARSA, ARSA, ARSA, ARSA, ARSA	1stExon, Body, Body, Body, 5'UTR	Island	FALSE
cg22000984	0.26	0.42	-0.16	-83.94	Chr5: 150226278	IRGM, IRGM NFYA, NFYA, LOC221442	1stExon, 5'UTR 3'UTR, 3'UTR, TSS200		FALSE
cg09580153	0.83	0.99	-0.16	-338.22	Chr6: 41068724	ADAP1 PTPRN2, PTPRN2, PTPRN2	Body	Island	TRUE
cg19665696	0.26	0.41	-0.16	-82.06	Chr7: 949154			Island	FALSE
cg19590115	0.66	0.82	-0.16	-115.67	Chr7: 157632890		Body, Body, Body	S_Shore	FALSE
cg04431054	0.29	0.45	-0.16	-76.26	Chr5: 126853024	PRRC1 C22orf34	TSS1500 Body	N_Shore	FALSE
cg20744362	0.66	0.82	-0.16	-116.94	Chr22: 50050164				FALSE
cg14951497	0.27	0.43	-0.16	-78.21	Chr2: 191875807	STAT1, STAT1	5'UTR, 5'UTR	N_Shelf	FALSE
cg13185413	0.24	0.40	-0.16	-82.25	Chr6: 30039202	RNF39, RNF39	Body, Body	Island	FALSE
cg17384323	0.55	0.70	-0.16	-78.22	Chr4: 169242366			S_Shelf	FALSE
cg03393996	0.17	0.32	-0.15	-96.90	Chr4: 1580377			Island	FALSE
cg14286514	0.42	0.57	-0.15	-65.75	Chr9: 32525315	DDX58 VARS2, VARS2, VARS2	Body Body, 5'UTR, Body	N_Shore	TRUE
cg15848685	0.34	0.50	-0.15	-65.54	Chr6: 30882641			S_Shore	TRUE
cg12694372	0.23	0.38	-0.15	-79.07	Chr6: 32064582	TNXB	Body	Island	FALSE
cg01097406	0.38	0.53	-0.15	-63.67	Chr16: 89675127				FALSE
cg12016809	0.23	0.38	-0.15	-78.64	Chr21: 47604291	C21orf56, C21orf56, C21orf56, C21orf56	5'UTR, 5'UTR, 1stExon, 1stExon	S_Shore	FALSE
cg02299497	0.30	0.46	-0.15	-67.57	Chr14: 69095570			S_Shore	TRUE
cg25443613	0.17	0.32	-0.15	-92.92	ChrY: 2709605	RPS4Y1	TSS200		FALSE
cg24336839	0.05	0.20	-0.15	-163.25	Chr22: 24384397	GSTT1 EIF4G1, EIF4G1, SNORD66, EIF4G1, EIF4G1, EIF4G1	TSS200 Body, Body, TSS200, Body, Body, Body	Island	FALSE
cg14531026	0.73	0.88	-0.15	-137.01	Chr3: 184043286			N_Shore	FALSE
cg21159568	0.59	0.74	-0.15	-74.98	Chr7: 2445331	CHST12	5'UTR	S_Shore	FALSE
cg14573478	0.27	0.41	-0.15	-66.87	Chr3: 140730858				TRUE
cg09350919	0.25	0.40	-0.15	-68.07	ChrY: 9365070	TSPY3, TSPY4	TSS1500, Body	N_Shore	FALSE
cg00855901	0.30	0.44	-0.15	-62.15	Chr1: 79085765	IFI4L	TSS1500		FALSE
cg15254640	0.06	0.20	-0.15	-151.39	Chr22: 24384393	GSTT1 RPL23A, SNORD4A	TSS200 Body, TSS1500	Island	FALSE
cg16565409	0.47	0.62	-0.15	-58.40	Chr17: 27048223			S_Shore	FALSE
cg02163885	0.57	0.71	-0.14	-67.24	Chr6: 27729346				FALSE
cg14089503	0.56	0.71	-0.14	-66.50	Chr8: 37755555	RAB11FIP1, RAB11FIP1	Body, Body	N_Shore	FALSE
cg20088245	0.39	0.54	-0.14	-55.37	Chr8: 1321375			Island	FALSE
cg19870512	0.23	0.37	-0.14	-68.75	Chr12: 4919081	KCNA6, KCNA6	5'UTR, 1stExon	Island	FALSE
cg12319143	0.57	0.71	-0.14	-66.62	Chr10: 134726771			N_Shelf	FALSE
cg25932599	0.22	0.37	-0.14	-70.16	Chr4: 1005201	FGFRL1, FGFRL1, FGFRL1	TSS1500, TSS1500, TSS1500	Island	FALSE
cg27192248	0.31	0.46	-0.14	-58.02	Chr15: 65285669			S_Shelf	FALSE
cg20398880	0.73	0.88	-0.14	-127.11	Chr6: 41068722	NFYA, NFYA, LOC221442	3'UTR, 3'UTR, TSS200	Island	TRUE
cg05552874	0.64	0.79	-0.14	-81.81	Chr10: 91153143	IFIT1	Body		FALSE
cg14926196	0.40	0.55	-0.14	-53.84	Chr6: 37616482	MDGA1	Body	Island	FALSE
cg14785464	0.52	0.66	-0.14	-58.33	Chr21: 38362725	HLCS	TSS200	Island	FALSE
cg01028142	0.72	0.86	-0.14	-115.11	Chr2: 7004578	CMPK2	Body	N_Shore	FALSE
cg23804921	0.44	0.58	-0.14	-52.55	Chr15: 30861172			N_Shelf	FALSE
cg17980508	0.49	0.63	-0.14	-54.27	Chr1: 79085713	IFI4L	TSS1500		FALSE
cg01996567	0.37	0.51	-0.14	-52.33	Chr7: 149484880	SSPO	Body	N_Shelf	FALSE
cg00843105	0.06	0.20	-0.14	-135.54	Chr19: 44645597	ZNF234, ZNF234	TSS200, TSS200	Island	FALSE
cg11224582	0.29	0.43	-0.14	-56.24	Chr12: 4919138	KCNA6, KCNA6	5'UTR, 1stExon	Island	FALSE
cg01238044	0.20	0.34	-0.14	-70.74	Chr22: 24384105	GSTT1	Body	N_Shore	FALSE
cg25849281	0.43	0.57	-0.14	-51.37	Chr1: 8937077	ENO1	5'UTR	N_Shore	FALSE
cg19106932	0.22	0.36	-0.14	-66.89	Chr17: 61926700			Island	FALSE
cg03482458	0.13	0.27	-0.14	-92.49	Chr22: 46692211	CN5H6.4, GTSE1	Body, TSS1500	Island	FALSE
cg13012494	0.20	0.34	-0.14	-68.92	Chr21: 47604986	C21orf56, C21orf56	TSS1500, TSS1500	S_Shelf	FALSE

cg12110437	0.21	0.35	-0.14	-67.89	Chr8: 144098888	<i>LY6E, LY6E, LOC100133669</i>	TSS1500, TSS1500, Body	N_Shore	FALSE
cg08133631	0.51	0.64	-0.14	-53.64	Chr1: 26527909	<i>CATSPER4</i>	Body		TRUE
cg05896524	0.29	0.43	-0.14	-55.21	Chr21: 47604654	<i>C21orf56, C21orf56</i>	TSS1500, TSS1500	S_Shore	FALSE
cg01175610	0.24	0.38	-0.14	-61.03	Chr12: 12224246	<i>BCL2L14, BCL2L14, BCL2L14</i>	5'UTR, TSS200, TSS200		TRUE
cg06167719	0.62	0.76	-0.14	-69.63	Chr21: 38362727	<i>HLCS</i>	TSS200	Island	FALSE
cg18955367	0.58	0.72	-0.14	-61.35	Chr19: 49002338	<i>LMTK3</i>	Body	Island	FALSE
cg18085787	0.28	0.42	-0.14	-55.44	ChrY: 14646665			N_Shelf	FALSE
cg12397463	0.66	0.80	-0.14	-81.11	Chr6: 33128825			N_Shore	FALSE
cg10909185	0.25	0.39	-0.14	-58.77	Chr11: 75139736	<i>KLHL35</i>	Body	Island	FALSE
cg08742575	0.24	0.38	-0.14	-58.93	Chr21: 47604166	<i>C21orf56, C21orf56</i>	5'UTR, 5'UTR	S_Shore	FALSE
cg05487134	0.23	0.37	-0.13	-59.65	Chr17: 40489569	<i>STAT3, STAT3, STAT3</i>	Body, Body, Body		FALSE
cg03206401	0.51	0.65	-0.13	-50.60	Chr2: 130956119	<i>TUBA3E</i>	TSS200	Island	FALSE
cg00676801	0.25	0.38	-0.13	-56.80	Chr2: 191876673	<i>STAT1, STAT1</i>	5'UTR, 5'UTR	N_Shore	FALSE
cg06614118	0.78	0.92	-0.13	-148.68	Chr5: 180414906	<i>BTNL3</i>	TSS1500		FALSE
cg13516209	0.46	0.59	-0.13	-46.30	Chr6: 29855302	<i>HLA-H</i>	TSS200	Island	FALSE
cg01677628	0.52	0.66	-0.13	-49.80	Chr11: 8361190				FALSE
cg24238852	0.07	0.20	-0.13	-117.22	Chr22: 24384340	<i>GSTT1</i>	TSS200	Island	FALSE
cg04234412	0.30	0.44	-0.13	-49.32	Chr22: 24373322	<i>LOC391322</i>	Body	Island	FALSE
cg00576139	0.38	0.51	-0.13	-45.54	ChrY: 6312218	<i>LOC100101115, TTTY21</i>	Body, Body		FALSE
cg12622242	0.46	0.59	-0.13	-45.87	Chr8: 19203257	<i>SH2D4A</i>	Body		TRUE
cg08596608	0.22	0.36	-0.13	-58.52	ChrY: 14533505			Island	FALSE
cg26536949	0.59	0.72	-0.13	-56.24	Chr17: 57053			Island	TRUE
cg00737841	0.68	0.81	-0.13	-79.15	Chr10: 130726624				FALSE
cg07971089	0.40	0.54	-0.13	-44.48	Chr8: 144629702			N_Shelf	FALSE
cg13732083	0.22	0.35	-0.13	-58.24	Chr21: 47605072	<i>C21orf56, C21orf56</i>	TSS1500, TSS1500	S_Shelf	FALSE
cg23613051	0.29	0.42	-0.13	-49.08	Chr4: 2820428	<i>SH3BP2, SH3BP2, SH3BP2, SH3BP2</i>	Body, Body, 5'UTR, TSS200	Island	FALSE
cg01066472	0.36	0.49	-0.13	-44.48	Chr1: 75591029			Island	FALSE
cg01022117	0.73	0.86	-0.13	-98.59	Chr1: 201258280	<i>PKP1, PKP1</i>	Body, Body		TRUE
cg06046490	0.24	0.38	-0.13	-53.70	Chr11: 320940	<i>IFITM3</i>	TSS200	S_Shore	FALSE
cg24124284	0.59	0.72	-0.13	-54.33	Chr11: 18476081	<i>LDHAL6A, LDHAL6A</i>	TSS1500, TSS1500	N_Shore	FALSE
cg25606201	0.46	0.59	-0.13	-43.38	Chr5: 180614858			N_Shore	FALSE
cg05852568	0.45	0.58	-0.13	-42.91	Chr2: 95537405	<i>TEKT4</i>	1stExon	Island	FALSE
cg16677019	0.19	0.32	-0.13	-62.77	Chr17: 44847268	<i>WNT3</i>	Body	Island	FALSE
cg11222703	0.49	0.62	-0.13	-44.03	Chr4: 190983569			N_Shelf	FALSE
cg24312520	0.23	0.36	-0.13	-53.27	Chr17: 40489584	<i>STAT3, STAT3, STAT3</i>	Body, Body, Body		FALSE
cg11685843	0.59	0.71	-0.13	-52.12	Chr4: 176349171				FALSE
cg13626582	0.52	0.65	-0.13	-45.00	Chr15: 57592083	<i>LOC283663</i>	TSS1500		FALSE
cg14586373	0.46	0.58	-0.13	-41.92	Chr22: 37447398	<i>KCTD17</i>	TSS1500	N_Shore	FALSE
cg26968378	0.30	0.43	-0.13	-45.52	Chr6: 28447087				FALSE
cg17052170	0.65	0.77	-0.13	-62.10	Chr8: 144099482	<i>LY6E, LY6E, LOC100133669</i>	TSS1500, Body	Island	FALSE
cg01828798	0.35	0.48	-0.13	-42.33	ChrY: 8571457	<i>TTTY19</i>	TSS1500		FALSE
cg16031515	0.28	0.40	-0.13	-47.01	Chr1: 205743344	<i>RAB7L1, RAB7L1, RAB7L1, RAB7L1</i>	Body, Body, Body, 5'UTR	N_Shore	FALSE
cg14931215	0.50	0.63	-0.13	-42.29	ChrY: 21867702	<i>KDM5D, KDM5D, KDM5D</i>	3'UTR, 3'UTR, 3'UTR		FALSE
cg17437770	0.35	0.48	-0.13	-41.24	Chr10: 43250800			Island	FALSE
cg08284263	0.39	0.52	-0.13	-40.20	Chr10: 92958627				TRUE
cg25319279	0.65	0.78	-0.13	-61.67	Chr11: 5960081				FALSE
cg09125754	0.65	0.77	-0.13	-60.95	Chr2: 130886714	<i>POTEF, POTEF</i>	1stExon, 5'UTR		FALSE
cg16006841	0.44	0.57	-0.13	-39.42	Chr5: 176797999	<i>RGS14</i>	Body	S_Shelf	FALSE
cg08433110	0.77	0.89	-0.13	-112.66	Chr6: 1684468	<i>GMDS</i>	Body		FALSE
cg03062944	0.70	0.82	-0.13	-73.06	Chr10: 6183455			N_Shelf	FALSE
cg14133106	0.38	0.51	-0.13	-39.23	ChrY: 14652924			S_Shelf	FALSE
cg02090762	0.10	0.23	-0.13	-85.57	Chr17: 79503859	<i>FSCN2, FSCN2</i>	Body, Body	Island	TRUE
cg13469590	0.23	0.36	-0.13	-49.71	Chr9: 19229767			N_Shore	FALSE

cg13752114	0.71	0.84	-0.12	-78.36	Chr3: 195489708	<i>MUC4, MUC4, MUC4</i>	Body, Body, Body	Island	FALSE
cg01819759	0.10	0.23	-0.12	-84.76	Chr13: 79234251	<i>RNF219</i>	TSS1500	S_Shore	FALSE
cg18286997	0.56	0.69	-0.12	-44.72	Chr1: 121448638			N_Shelf	FALSE
cg09611599	0.40	0.53	-0.12	-37.85	Chr11: 20382497			Island	FALSE
cg02784823	0.63	0.75	-0.12	-53.51	Chr19: 49000897	<i>LMTK3</i>	Body	N_Shore	FALSE
cg02219949	0.65	0.77	-0.12	-56.71	Chr17: 45927392	<i>SP6</i>	5'UTR	S_Shore	FALSE
cg20167074	0.62	0.74	-0.12	-51.09	Chr1: 151967023	<i>S100A10</i>	TSS1500	S_Shore	FALSE
cg04111992	0.50	0.62	-0.12	-39.06	Chr7: 158790115			S_Shore	FALSE
cg17833746	0.31	0.44	-0.12	-40.06	Chr17: 40489785	<i>STAT3, STAT3, STAT3</i>	Body, Body, Body		FALSE
cg15059639	0.61	0.74	-0.12	-49.92	Chr2: 171220061	<i>MYO3B, MYO3B, MYO3B</i>	Body, Body, Body		FALSE
cg05180887	0.57	0.69	-0.12	-43.84	Chr2: 1817263	<i>MYT1L</i>	Body		FALSE
cg08822897	0.31	0.43	-0.12	-39.59	Chr11: 64258103			N_Shore	FALSE
cg26280727	0.67	0.79	-0.12	-60.99	Chr19: 49000998	<i>LMTK3</i>	Body	Island	FALSE
cg16580985	0.78	0.90	-0.12	-111.78	Chr4: 1550194			Island	FALSE
cg07138768	0.71	0.83	-0.12	-71.32	Chr7: 917805	<i>C7orf20, MAD1L1, MAD1L1, MAD1L1</i>	Body, Body, Body	Island	FALSE
cg18650626	0.85	0.97	-0.12	-208.33	Chr7: 1914073			Island	FALSE
cg21827317	0.33	0.45	-0.12	-38.21	Chr3: 136751795			S_Shore	FALSE
cg03604322	0.46	0.58	-0.12	-36.42	Chr22: 32439052	<i>SLC5A1, SLC5A1</i>	5'UTR, 1stExon	Island	FALSE
cg10016788	0.38	0.50	-0.12	-36.24	Chr19: 55599029	<i>EPS8L1, EPS8L1</i>	3'UTR, 3'UTR	S_Shore	TRUE
cg22730047	0.24	0.36	-0.12	-46.32	Chr1: 161410551			Island	FALSE
cg08750459	0.53	0.65	-0.12	-39.27	Chr17: 6558815			N_Shore	FALSE
cg21132536	0.66	0.79	-0.12	-57.95	Chr20: 33465180	<i>ACSS2, ACSS2, ACSS2</i>	Body, Body, Body	S_Shore	FALSE
cg08570243	0.14	0.26	-0.12	-67.60	Chr2: 110969853	<i>NCRNA00116</i>	Body	Island	FALSE
cg15085883	0.53	0.65	-0.12	-39.25	Chr12: 68848994			N_Shore	TRUE
cg08985785	0.55	0.67	-0.12	-40.52	Chr6: 39196340	<i>KCNK5</i>	Body	N_Shore	FALSE
cg16474696	0.39	0.51	-0.12	-35.36	Chr19: 13875014	<i>MRI1, MRI1</i>	TSS1500, TSS1500	N_Shore	FALSE
cg19980771	0.23	0.35	-0.12	-46.09	Chr6: 110798022	<i>SLC22A16</i>	TSS200	Island	FALSE
cg09584650	0.49	0.61	-0.12	-36.60	Chr8: 2002012	<i>MYOM2</i>	Body	N_Shore	FALSE
cg00325531	0.28	0.40	-0.12	-40.72	Chr1: 75591353			Island	FALSE
cg26783481	0.77	0.89	-0.12	-101.56	Chr5: 93125895	<i>FAM172A, FAM172A, FAM172A, FAM172A</i>	Body, Body, Body, Body		TRUE
cg15546638	0.48	0.60	-0.12	-35.96	Chr15: 93277793				FALSE
cg12850892	0.47	0.59	-0.12	-35.72	Chr11: 75945585			N_Shore	FALSE
cg07341007	0.62	0.74	-0.12	-48.23	Chr3: 195489909	<i>MUC4, MUC4, MUC4</i>	Body, Body, Body	Island	FALSE
cg08516507	0.17	0.29	-0.12	-56.68	Chr6: 32064206	<i>TNXB</i>	Body	Island	FALSE
cg01116956	0.70	0.82	-0.12	-64.97	Chr2: 4048824			N_Shore	FALSE
cg03438552	0.59	0.71	-0.12	-42.34	Chr6: 32805548	<i>TAP2, TAP2</i>	Body, Body	N_Shore	FALSE
cg04887076	0.49	0.61	-0.12	-35.00	Chr19: 55477653	<i>NLRP2</i>	TSS200		FALSE
cg14213105	0.59	0.71	-0.12	-42.66	Chr9: 126980322				TRUE
cg16194588	0.61	0.73	-0.12	-44.72	Chr19: 49002477	<i>LMTK3</i>	Body	Island	FALSE
cg18918831	0.59	0.71	-0.12	-42.22	Chr3: 195489782	<i>MUC4, MUC4, MUC4</i>	Body, Body, Body	Island	FALSE
cg27387193	0.46	0.57	-0.12	-33.65	Chr6: 32064032	<i>TNXB</i>	Body	Island	FALSE
cg21903646	0.25	0.37	-0.12	-41.06	Chr6: 28447115				FALSE
cg11704005	0.40	0.52	-0.12	-33.27	Chr1: 19002948	<i>PAX7, PAX7, PAX7</i>	Body, Body, Body		TRUE
cg19901940	0.37	0.48	-0.12	-33.82	Chr14: 22689870				FALSE
cg12813394	0.33	0.44	-0.12	-35.25	Chr14: 69095057			Island	FALSE
cg12584458	0.34	0.46	-0.12	-34.20	Chr6: 28447107				FALSE
cg08998192	0.51	0.63	-0.12	-34.78	Chr6: 32805570	<i>TAP2, TAP2</i>	Body, Body	N_Shore	FALSE
cg13565129	0.56	0.68	-0.12	-38.29	Chr6: 28601419			N_Shore	FALSE
cg04850017	0.55	0.67	-0.12	-37.03	Chr11: 63683019	<i>RCOR2</i>	Body	N_Shore	FALSE
cg06862049	0.58	0.70	-0.12	-39.56	Chr19: 49001890	<i>LMTK3</i>	Body	Island	FALSE
cg13916469	0.62	0.74	-0.12	-45.04	Chr9: 95834820	<i>SUSD3</i>	Body		TRUE
cg20528787	0.46	0.58	-0.12	-32.74	Chr7: 158032352	<i>PTPRN2, PTPRN2, PTPRN2</i>	Body, Body, Body		FALSE
cg09826364	0.39	0.51	-0.12	-32.24	Chr7: 158789723			Island	FALSE
cg21123519	0.30	0.42	-0.12	-35.60	Chr14: 69095679			S_Shore	TRUE

cg25323841	0.59	0.71	-0.12	-40.04	Chr6: 108444506			S_Shelf	FALSE
cg10152449	0.65	0.77	-0.12	-48.23	Chr7: 2444534	CHST12	5'UTR	S_Shore	FALSE
cg19317226	0.67	0.79	-0.12	-52.18	Chr10: 130726701				FALSE
cg18756179	0.09	0.21	-0.11	-77.22	Chr19: 50554510	FLJ26850	Body	S_Shore	FALSE
cg07026904	0.55	0.67	-0.11	-35.34	Chr11: 114832606			S_Shore	FALSE
cg08889243	0.78	0.89	-0.11	-95.56	Chr1: 57892830	DAB1	5'UTR	S_Shelf	FALSE
cg18052511	0.44	0.55	-0.11	-30.81	Chr3: 46410222	CCR5, CCR5	TSS1500, TSS1500		FALSE
cg00600477	0.52	0.63	-0.11	-33.02	Chr8: 144715010			N_Shelf	FALSE
cg17542795	0.70	0.81	-0.11	-57.96	Chr4: 178518017				TRUE
cg09359103	0.46	0.57	-0.11	-30.95	Chr1: 154839909	KCNN3	Body		FALSE
cg12119625	0.43	0.54	-0.11	-30.48	Chr19: 54106789	LOC284379	TSS200		FALSE
cg04819497	0.67	0.78	-0.11	-49.33	Chr11: 58598444				FALSE
cg07684519	0.47	0.59	-0.11	-31.09	Chr12: 29303184			S_Shore	FALSE
cg25582488	0.31	0.43	-0.11	-33.17	Chr14: 69095171			Island	FALSE
cg06237805	0.32	0.44	-0.11	-32.71	ChrY: 8147958			Island	FALSE
cg17566325	0.28	0.39	-0.11	-35.32	Chr12: 133022423			N_Shore	FALSE
cg09253696	0.17	0.28	-0.11	-50.80	Chr17: 73873529	TRIM47	Body		TRUE
cg20737388	0.54	0.66	-0.11	-33.37	Chr11: 73668626	DNAJB13	Body		FALSE
cg05067427	0.58	0.69	-0.11	-36.01	Chr16: 54227914			N_Shore	TRUE
cg01574481	0.45	0.56	-0.11	-29.82	Chr14: 24641852	REC8, REC8	Body, Body	Island	TRUE
cg15931850	0.54	0.65	-0.11	-32.66	Chr4: 1550089				FALSE
cg10646950	0.30	0.41	-0.11	-32.85	ChrY: 20748782	HSFY1, TTTY9B, HSFY2, HSFY2, TTTY9A, HSFY1	Body, Body, Body, Body, Body, Body		FALSE
cg02061626	0.84	0.96	-0.11	-161.00	Chr2: 233274167	ALPPL2	Body	Island	FALSE
cg12584960	0.55	0.66	-0.11	-33.08	Chr13: 114965839			Island	TRUE
cg04863892	0.65	0.76	-0.11	-44.10	Chr7: 27183375	HOXA5	TSS200	Island	FALSE
cg03533500	0.20	0.31	-0.11	-43.79	ChrY: 21668420			S_Shelf	FALSE
cg22757362	0.45	0.57	-0.11	-29.22	Chr10: 43721445	RASGEF1A	5'UTR	N_Shelf	FALSE
cg08265926	0.62	0.73	-0.11	-39.05	Chr16: 81039227	CENPN, CENPN, CENPN, C16orf61	TSS1500, TSS1500, TSS1500, 5'UTR	N_Shore	FALSE
cg10365886	0.64	0.75	-0.11	-41.58	Chr6: 32063874	TNXB	Body	Island	FALSE
cg00495303	0.67	0.78	-0.11	-47.19	Chr18: 3771110	DLGAP1, DLGAP1	Body, Body	N_Shore	FALSE
cg10881225	0.60	0.71	-0.11	-36.33	Chr2: 9984929	TAF1B	Body	S_Shore	FALSE
cg02964324	0.55	0.66	-0.11	-32.38	Chr7: 43291318	HECW1	Body	S_Shelf	FALSE
cg25307665	0.70	0.81	-0.11	-54.31	Chr7: 27183694	HOXA5	TSS1500	Island	FALSE
cg24882324	0.10	0.21	-0.11	-69.80	Chr6: 32064508	TNXB	Body	Island	FALSE
cg16958594	0.54	0.65	-0.11	-31.52	Chr6: 30882708	VARS2, VARS2, VARS2	Body, 5'UTR, Body	S_Shore	TRUE
cg22462983	0.08	0.19	-0.11	-79.52	Chr6: 133561756	EYA4, EYA4, EYA4	TSS1500, TSS1500	N_Shore	FALSE
cg11693285	0.26	0.37	-0.11	-34.69	Chr10: 131927345			Island	TRUE
cg13773741	0.74	0.85	-0.11	-67.26	Chr17: 9967499	GAS7	Body		FALSE
cg01337207	0.52	0.63	-0.11	-30.09	Chr6: 32063835	TNXB	Body	Island	FALSE
cg01496720	0.41	0.52	-0.11	-27.97	Chr10: 3825398	KLF6, KLF6, KLF6, KLF6	Body, Body, Body, Body	N_Shore	FALSE
cg03556669	0.19	0.30	-0.11	-43.12	Chr6: 32064497	TNXB	Body	Island	FALSE
cg13457410	0.66	0.77	-0.11	-43.88	Chr1: 9762510	PIK3CD	5'UTR		FALSE
cg23118561	0.76	0.87	-0.11	-72.62	Chr13: 51565237				TRUE
cg18113731	0.51	0.62	-0.11	-28.96	ChrY: 16636984	NLGN4Y, NLGN4Y, NLGN4Y	Body, 5'UTR, Body	Island	FALSE
cg02160608	0.72	0.83	-0.11	-58.35	Chr2: 113956634	PSD4, LOC440839	Body, Body	Island	FALSE
cg05263479	0.18	0.29	-0.11	-44.73	Chr7: 47092529			Island	FALSE
cg27436995	0.47	0.58	-0.11	-27.52	Chr16: 743998	FBXL16	3'UTR	Island	FALSE
cg17430262	0.36	0.47	-0.11	-27.98	ChrY: 14649051			Island	FALSE
cg10612560	0.59	0.70	-0.11	-33.41	Chr17: 8019912	ALOXE3, ALOXE3	Body, Body	N_Shelf	FALSE
cg08291996	0.17	0.28	-0.11	-46.59	Chr19: 58791159	ZNF8	Body	S_Shore	FALSE
cg22973012	0.74	0.85	-0.11	-63.43	Chr6: 168760457				FALSE
cg06060754	0.47	0.58	-0.11	-27.37	Chr5: 176797920	RGS14	Body	S_Shelf	FALSE
cg17076635	0.12	0.22	-0.11	-60.26	Chr8: 144484205				TRUE
cg09757644	0.68	0.79	-0.11	-45.53	Chr6: 447497				FALSE
cg25970575	0.49	0.60	-0.11	-27.52	Chr4: 6010164			S_Shore	TRUE
cg05250380	0.82	0.93	-0.11	-117.61	Chr9: 140735359			N_Shore	FALSE

cg02482603	0.40	0.51	-0.11	-26.66	Chr1: 174843754	<i>RABGAP1L</i> , <i>RABGAP1L</i>	TSS1500, Body	Body	FALSE	
cg08288016	0.70	0.81	-0.11	-49.78	Chr4: 187590536	<i>FAT1</i>	TSS1500, Body	Body	TRUE	
cg16274205	0.40	0.51	-0.11	-26.60	Chr3: 94243571				TRUE	
cg27505492	0.22	0.33	-0.11	-36.09	Chr12: 133187045				TRUE	
cg00412772	0.55	0.66	-0.11	-29.53	Chr19: 38794845	<i>YIF1B</i> , <i>YIF1B</i> , <i>C19orf33</i> , <i>YIF1B</i> , <i>YIF1B</i> , <i>YIF1B</i> , <i>YIF1B</i> , <i>YIF1B</i> , <i>C19orf33</i>	3'UTR, 3'UTR, 1stExon, 3'UTR, 3'UTR, 3'UTR, 3'UTR, 3'UTR, 5'UTR	3'UTR, 3'UTR, 1stExon, 3'UTR, 3'UTR, 3'UTR, 3'UTR, 3'UTR, 5'UTR	Island	TRUE
cg13799081	0.57	0.68	-0.11	-30.71	Chr10: 112410313	<i>RBM20</i>	TSS1500, Body	Body	TRUE	
cg20092122	0.07	0.18	-0.11	-76.58	Chr19: 17517221	<i>BST2</i>	TSS1500	TSS1500	TRUE	
cg02251754	0.50	0.61	-0.11	-27.01	Chr1: 28572299				FALSE	
cg16288318	0.58	0.68	-0.11	-30.86	Chr13: 112986927				FALSE	
cg19650706	0.59	0.70	-0.11	-32.01	Chr5: 140594406	<i>PCDHB13</i>	1stExon	N_Shore	FALSE	
cg13661648	0.50	0.61	-0.11	-26.98	Chr6: 33035284	<i>HLA-DPA1</i>	3'UTR	N_Shore	FALSE	
cg00044354	0.36	0.47	-0.11	-26.33	Chr1: 67389884	<i>MIER1</i> , <i>WDR78</i> , <i>MIER1</i> , <i>MIER1</i> , <i>MIER1</i> , <i>WDR78</i> , <i>MIER1</i> , <i>MIER1</i>	TSS1500, Body, TSS1500, TSS1500, TSS1500, TSS1500, TSS1500, Body, TSS1500, TSS1500	TSS1500, Body, TSS1500, TSS1500, TSS1500, TSS1500, TSS1500, Body, TSS1500, TSS1500	N_Shore	FALSE
cg02916272	0.45	0.56	-0.11	-25.62	Chr11: 1769443	<i>HCCA2</i> , <i>LOC402778</i>	TSS200, Body	Body, TSS200	Island	FALSE
cg22094750	0.05	0.15	-0.11	-95.17	Chr1: 1851056	<i>TMEM52</i>	TSS1500	TSS1500	Island	FALSE
cg15971518	0.67	0.78	-0.11	-41.84	Chr11: 57159174	<i>PRG2</i>	TSS1500	TSS1500		FALSE
cg06201514	0.59	0.70	-0.11	-31.70	Chr2: 1817409	<i>MYT1L</i>	Body	Body		FALSE
cg07330481	0.68	0.78	-0.11	-42.51	Chr17: 37322330	<i>ARL5C</i> , <i>ARL5C</i>	1stExon	1stExon, 5'UTR	S_Shore	TRUE
cg25436886	0.24	0.35	-0.11	-32.78	Chr3: 127056972				Island	FALSE
cg16824113	0.50	0.60	-0.11	-25.88	Chr12: 132166485					TRUE
cg00791851	0.40	0.50	-0.11	-24.99	Chr1: 76518896					TRUE
cg02698668	0.46	0.57	-0.11	-24.99	Chr19: 44261472				S_Shelf	FALSE
cg13593090	0.47	0.58	-0.11	-25.19	Chr19: 9546723	<i>ZNF266</i> , <i>ZNF266</i>	TSS1500, TSS1500	TSS1500, TSS1500	S_Shore	FALSE
cg24040502	0.52	0.63	-0.11	-26.61	Chr19: 55477810	<i>NLRP2</i> , <i>NLRP2</i> , <i>BCL2L14</i> , <i>BCL2L14</i> , <i>BCL2L14</i> , <i>BCL2L14</i>	5'UTR, 1stExon	5'UTR, 1stExon		FALSE
cg20481287	0.56	0.66	-0.11	-28.26	Chr12: 12224457	<i>BCL2L14</i> , <i>BCL2L14</i>	1stExon, 5'UTR, 1stExon	1stExon, 5'UTR, 1stExon		TRUE
cg07676361	0.45	0.56	-0.11	-24.70	Chr16: 80966860				S_Shore	FALSE
cg26056498	0.45	0.55	-0.11	-24.57	Chr8: 1030319					FALSE
cg25099892	0.43	0.53	-0.11	-24.43	Chr13: 113313905	<i>C13orf35</i>	5'UTR	5'UTR		FALSE
cg15788369	0.53	0.63	-0.11	-26.66	Chr19: 15833777				Island	FALSE
cg12048965	0.32	0.43	-0.10	-26.39	Chr10: 3848384					TRUE
cg15015639	0.51	0.61	-0.10	-25.62	Chr2: 220282977	<i>DES</i>	TSS200	TSS200	N_Shore	TRUE
cg25987564	0.42	0.53	-0.10	-24.17	Chr4: 6010075				Island	FALSE
cg14005211	0.36	0.46	-0.10	-25.13	Chr2: 171676925	<i>GAD1</i> , <i>GAD1</i>	Body, Body	Body, Body	Island	FALSE
cg20045320	0.24	0.34	-0.10	-32.45	Chr11: 319555				S_Shore	FALSE
cg26535992	0.49	0.60	-0.10	-24.80	Chr6: 166671495				S_Shelf	FALSE
cg17842918	0.48	0.59	-0.10	-24.63	Chr13: 113540400	<i>ATP11A</i> , <i>ATP11A</i>	3'UTR, 3'UTR	3'UTR, 3'UTR	Island	TRUE
cg20583945	0.26	0.36	-0.10	-30.23	Chr8: 144636462	<i>GSDMD</i>	5'UTR	5'UTR	S_Shore	FALSE
cg24516106	0.60	0.70	-0.10	-30.42	Chr2: 72079413				Island	FALSE
cg03128011	0.42	0.52	-0.10	-23.77	Chr8: 1321333				Island	FALSE
cg25396728	0.36	0.46	-0.10	-24.67	Chr12: 248500	<i>IQSEC3</i> , <i>IQSEC3</i>	Body, Body	Body, Body	Island	TRUE
cg02002345	0.10	0.20	-0.10	-62.50	ChrY: 6777855	<i>TBL1Y</i> , <i>TBL1Y</i> , <i>TBL1Y</i>	TSS1500, TSS1500, TSS1500	TSS1500, TSS1500, TSS1500	N_Shore	FALSE
cg12526471	0.61	0.72	-0.10	-31.31	Chr11: 113929188	<i>ZBTB16</i>	TSS1500	TSS1500	N_Shore	FALSE
cg23141851	0.57	0.67	-0.10	-27.68	Chr3: 14615941				Island	FALSE
cg01219135	0.51	0.62	-0.10	-25.06	Chr7: 158766336				Island	FALSE
cg02002217	0.67	0.78	-0.10	-39.34	Chr13: 24520348					FALSE
cg20474581	0.44	0.55	-0.10	-23.48	ChrY: 14812997	<i>USP9Y</i>	TSS200	TSS200		FALSE
cg01428095	0.49	0.59	-0.10	-24.09	Chr1: 228134229	<i>WNT9A</i>	Body	Body	N_Shore	FALSE
cg10568066	0.40	0.50	-0.10	-23.50	Chr6: 30039442	<i>RNF39</i> , <i>RNF39</i>	Body, Body	Body, Body	Island	FALSE

cg21871091	0.64	0.74	-0.10	-34.10	Chr21: 38349937	<i>HLCS</i>	5'UTR	N_Shelf	TRUE
cg22771759	0.23	0.33	-0.10	-32.34	Chr13: 24902376		TSS1500,	Island	FALSE
cg03031988	0.77	0.88	-0.10	-67.82	Chr6: 31510729	<i>BAT1, BAT1</i>	TSS1500, TSS1500	S_Shore	FALSE
cg06904356	0.57	0.67	-0.10	-27.09	Chr5: 1849983			N_Shore	FALSE
cg02649063	0.55	0.65	-0.10	-25.90	Chr16: 55794731	<i>CES4</i>	Body	Island	FALSE
cg06065495	0.16	0.26	-0.10	-42.12	ChrY: 21666309	<i>BCORL2</i>	TSS1500	S_Shore	FALSE
cg15196197	0.10	0.20	-0.10	-60.37	Chr6: 32064573	<i>TNXB</i>	Body	Island	FALSE
cg26695758	0.72	0.83	-0.10	-49.67	Chr6: 32063607	<i>TNXB</i>	Body	Island	FALSE
cg08475194	0.06	0.16	-0.10	-77.70	Chr5: 111755481	<i>FLJ11235, EPB41L4A</i>	Body, TSS1500	Island	FALSE
cg13968390	0.67	0.77	-0.10	-37.08	Chr2: 108904812	<i>SULT1C2, SULT1C2</i>	TSS1500, TSS1500		TRUE
cg17651935	0.52	0.62	-0.10	-24.22	ChrY: 14078666			S_Shore	FALSE
cg08364137	0.10	0.21	-0.10	-57.46	Chr7: 156400990			S_Shore	FALSE
cg08895590	0.53	0.64	-0.10	-24.82	Chr1: 91227319			TRUE	
cg03486986	0.30	0.40	-0.10	-25.92	Chr13: 112986285			S_Shore	TRUE
cg09315878	0.72	0.82	-0.10	-46.96	Chr1: 1152580	<i>SDF4, SDF4</i>	3'UTR, 3'UTR	Island	FALSE
cg10671668	0.23	0.33	-0.10	-30.99	Chr12: 4919230	<i>KCNA6</i>	1stExon	Island	FALSE
cg16582517	0.38	0.49	-0.10	-22.81	Chr3: 5025885	<i>BHLHE40</i>	3'UTR	S_Shore	FALSE
cg13686059	0.79	0.90	-0.10	-77.46	Chr2: 11101549			S_Shore	FALSE
cg09115713	0.76	0.86	-0.10	-59.30	Chr16: 88832476	<i>FAM38A</i>	Body		FALSE
cg21119074	0.61	0.72	-0.10	-29.79	Chr6: 20211654	<i>MBOAT1</i>	Body	N_Shore	FALSE
cg19460095	0.26	0.36	-0.10	-28.16	Chr11: 34672025	<i>EHF</i>	Body		FALSE
cg00290607	0.51	0.61	-0.10	-23.50	Chr11: 67383545			Island	TRUE
cg20724680	0.64	0.74	-0.10	-32.38	Chr19: 49000743	<i>LMTK3</i>	Body	Island	FALSE
cg21052687	0.54	0.64	-0.10	-24.53	Chr11: 55561545	<i>OR5D14</i>	TSS1500		FALSE
cg10557773	0.32	0.42	-0.10	-24.37	ChrY: 2801877	<i>ZFY</i>	TSS1500	N_Shore	FALSE
cg25737313	0.45	0.55	-0.10	-22.23	Chr19: 12899557			N_Shore	FALSE
cg26974214	0.16	0.26	-0.10	-41.30	Chr10: 91151885	<i>IFIT1</i>	TSS1500		FALSE
cg08900409	0.61	0.71	-0.10	-28.73	Chr19: 18475669	<i>PGPEP1</i>	3'UTR		TRUE
cg10510935	0.45	0.55	-0.10	-22.10	Chr1: 4059661				FALSE
cg14741691	0.54	0.64	-0.10	-24.30	Chr19: 40855329	<i>PLD3, PLD3, C19orf47</i>	5'UTR, 5'UTR, TSS1500	S_Shore	FALSE
cg15473346	0.30	0.40	-0.10	-25.11	Chr1: 165798420	<i>UCK2</i>	Body	S_Shore	FALSE
cg23099319	0.53	0.63	-0.10	-23.70	Chr10: 1517224	<i>ADARB2</i>	Body	Island	TRUE
cg06351537	0.75	0.85	-0.10	-55.17	Chr22: 49798750			Island	FALSE
cg02297043	0.37	0.47	-0.10	-22.25	Chr1: 75590912			Island	FALSE
cg12154045	0.56	0.66	-0.10	-24.90	Chr19: 14655556	<i>APC2</i>	Body	Island	FALSE
cg16761754	0.32	0.42	-0.10	-23.75	Chr14: 105127242			S_Shore	FALSE
cg07021523	0.78	0.88	-0.10	-67.28	Chr1: 16810670	<i>CROCL2</i>	Body	Island	FALSE
cg17723710	0.49	0.59	-0.10	-22.27	Chr5: 34621927				TRUE
cg20857253	0.56	0.66	-0.10	-24.80	Chr21: 33957290	<i>TCP10L</i>	5'UTR		FALSE
cg05234568	0.72	0.82	-0.10	-45.76	Chr11: 5960015				FALSE
cg11955878	0.32	0.42	-0.10	-23.65	Chr4: 165898967	<i>TRIM61</i>	TSS200		FALSE
cg13978347	0.71	0.81	-0.10	-42.66	Chr9: 120140243	<i>ASTN2, ASTN2, ASTN2</i>	Body, Body, Body		FALSE
cg22716280	0.64	0.74	-0.10	-31.46	Chr10: 134727319			N_Shelf	FALSE
cg08879910	0.07	0.17	-0.10	-67.34	Chr6: 29974319	<i>HLA-J, NCRNA00171</i>	Body, Body	Island	TRUE
cg04789475	0.66	0.76	-0.10	-33.13	Chr4: 186960991				FALSE
Hypermethylation									
cg09885502	0.57	0.16	0.41	340.66	Chr20: 57463991	<i>GNAS, GNAS, GNAS, GNAS</i>	3'UTR, TSS200, 3'UTR, Body	Island	FALSE
cg05176970	0.79	0.41	0.37	340.66	Chr17: 724273	<i>NXN</i>	Body		FALSE
cg00256329	0.77	0.41	0.36	340.66	Chr17: 724374	<i>NXN</i>	Body		FALSE
cg26287080	0.85	0.52	0.33	340.66	Chr17: 74086286	<i>EXOC7, EXOC7, EXOC7, EXOC7, EXOC7, EXOC7</i>	Body, Body, Body, Body, Body, Body		FALSE
cg08479752	0.67	0.37	0.30	340.66	Chr19: 54567279	<i>VSTM1</i>	TSS200		FALSE
cg16066505	0.84	0.55	0.29	340.66	Chr2: 171316530	<i>MYO3B, MYO3B, MYO3B</i>	Body, Body, Body		FALSE
cg25225073	0.30	0.06	0.24	340.66	Chr14: 90528983	<i>KCNK13</i>	Body	S_Shore	FALSE
cg18025438	0.63	0.39	0.24	340.66	Chr1: 228756789			Island	FALSE
cg16154810	0.41	0.18	0.23	340.66	Chr22: 47135258	<i>CERK</i>	TSS1500		FALSE
cg13830619	0.93	0.71	0.22	340.66	Chr12: 9555480				FALSE

cg17783317	0.53	0.31	0.22	340.66	Chr19: 54567123	VSTM1, VSTM1	1stExon, 5'UTR	FALSE
cg24247231	0.52	0.31	0.21	340.66	Chr15: 67904302	MAP2K5, MAP2K5	Body, Body	TRUE
cg07784793	0.91	0.70	0.20	340.66	Chr5: 33794720	ADAMTS12	Body	TRUE
cg21139150	0.54	0.34	0.20	123.60	Chr21: 46976175			Island FALSE
cg01500431	0.88	0.68	0.20	340.66	Chr22: 24388327	GSTTP2	Body	S_Shelf FALSE
cg03086067	0.66	0.47	0.19	118.36	Chr10: 82368399	SH2D4B, SH2D4B	Body, Body	FALSE
cg16316162	0.28	0.09	0.19	340.66	Chr8: 144660157	NAPRT1	Body	Island FALSE
cg24265076	0.72	0.54	0.19	120.70	Chr10: 1939618			FALSE
cg05617307	0.43	0.26	0.18	103.00	Chr10: 121413182	BAG3	Body	S_Shore FALSE
cg20811988	0.43	0.25	0.18	103.09	Chr20: 29611924	FRG1B	Body	Island FALSE
cg06301252	0.83	0.65	0.18	340.66	Chr7: 157504143	PTPRN2, PTPRN2, PTPRN2	Body, Body, Body	Island FALSE
cg09191173	0.47	0.30	0.18	94.97	Chr11: 108090159	NPAT	Body	N_Shelf FALSE
cg18391209	0.54	0.36	0.17	88.48	Chr1: 223747670	CAPN8	Body	S_Shelf FALSE
cg12327866	0.65	0.48	0.17	88.63	Chr10: 1939663			FALSE
cg27182070	0.58	0.41	0.17	84.03	Chr1: 28218282	RPA2	3'UTR	FALSE
cg11141652	0.57	0.40	0.17	79.82	Chr22: 24348549	GSTTP1	TSS1500	FALSE
cg22240348	0.27	0.10	0.17	340.66	Chr21: 46975805			Island FALSE
cg05380919	0.82	0.65	0.17	126.50	Chr22: 24376252	GSTT1	3'UTR	S_Shelf FALSE
cg02691506	0.43	0.27	0.16	84.76	Chr3: 8685827	C3orf32	5'UTR	FALSE
cg24647015	0.55	0.38	0.16	74.51	Chr11: 114191367			TRUE
cg02398342	0.76	0.60	0.16	98.43	Chr17: 80708632	TBCD, FN3K	TSS1500, 3'UTR	N_Shore FALSE
cg02167713	0.44	0.28	0.16	80.30	Chr17: 79630115			N_Shelf FALSE
cg15039826	0.31	0.15	0.16	110.75	ChrX: 39958196	BCOR, BCOR, BCOR, BCOR	TSS1500, 5'UTR, TSS1500, 5'UTR	Island FALSE
cg10555744	0.38	0.22	0.16	85.26	Chr1: 25946258	MAN1C1	Body	S_Shore TRUE
cg27433982	0.41	0.26	0.16	77.71	ChrY: 2802985	ZFY, ZFY, ZFY	TSS1500, TSS200, TSS1500	Island FALSE
cg16662477	0.26	0.11	0.15	126.50	Chr17: 33401430	RFFL	5'UTR	TRUE
cg26046487	0.43	0.28	0.15	73.20	ChrY: 20736147	HSFY1, HSFY2, HSFY2, HSFY1	Body, Body, Body, Body	FALSE
cg15242686	0.55	0.39	0.15	64.32	Chr22: 24348715	GSTTP1	TSS1500	FALSE
cg06180910	0.87	0.71	0.15	340.66	Chr22: 24382663	GSTT1	Body	N_Shore FALSE
cg17099656	0.23	0.08	0.15	340.66	Chr22: 47135171	CERK	TSS1500	FALSE
cg08835041	0.80	0.65	0.15	95.94	Chr19: 37461278			N_Shelf FALSE
cg17524265	0.44	0.29	0.15	67.37	Chr8: 144659883	NAPRT1	Body	Island FALSE
cg01053087	0.23	0.08	0.15	340.66	Chr8: 637909	ERICH1	Body	Island FALSE
cg02032872	0.90	0.75	0.15	340.66	Chr19: 44260537	C19orf61	TSS1500	S_Shore FALSE
cg13116946	0.87	0.72	0.15	126.50	Chr22: 38479732	SLC16A8	TSS1500	S_Shore FALSE
cg22681495	0.83	0.69	0.15	102.92	Chr15: 86058755	AKAP13, AKAP13	Body, Body	TRUE
cg01479768	0.80	0.65	0.15	88.58	Chr2: 731298			N_Shore FALSE
cg06343673	0.78	0.63	0.14	81.99	Chr17: 78778232	RPTOR, RPTOR	Body, Body	S_Shelf FALSE
cg18679504	0.37	0.22	0.14	70.50	ChrX: 40439984	ATP6AP2	TSS1500	Island FALSE
cg09107344	0.36	0.22	0.14	70.51	Chr12: 53612734	RARG, RARG	Body, Body	N_Shore FALSE
cg02025737	0.82	0.67	0.14	92.53	Chr15: 3384751			TRUE
cg25593510	0.54	0.40	0.14	53.19	Chr1: 110254662	GSTM5	TSS1500	FALSE
cg05095590	0.26	0.12	0.14	101.00	Chr7: 2139259	MAD1L1, MAD1L1, MAD1L1	Body, Body, Body	FALSE
cg20916523	0.24	0.10	0.14	109.67	Chr3: 10184584	VHL, VHL	Body, Body	S_Shore FALSE
cg09381666	0.59	0.45	0.14	52.32	Chr16: 88757816			FALSE
cg15171154	0.65	0.51	0.14	54.85	Chr3: 30722557	TGFBR2, TGFBR2	Body, Body	TRUE
cg07598341	0.67	0.53	0.14	55.49	Chr1: 44344466	ST3GAL3, ST3GAL3, ST3GAL3, ST3GAL3, ST3GAL3, ST3GAL3, ST3GAL3	Body, Body, Body, Body, Body, Body, Body, Body, Body, Body, Body, Body	TRUE
cg02836135	0.30	0.17	0.14	77.47	Chr6: 108052093	SCML4	Body	TRUE
cg23971987	0.62	0.49	0.14	51.60	Chr4: 11652505			TRUE
cg05026884	0.44	0.30	0.14	53.43	ChrX: 40032180	BCOR, BCOR	5'UTR, 5'UTR	Island FALSE
cg26720010	0.32	0.18	0.14	71.52	Chr7: 45147131	TBRG4, SNORA5B, TBRG4, TBRG4	Body, TSS1500, Body, Body	N_Shelf FALSE

cg08017634	0.47	0.35	0.12	37.32	Chr8: 144659831	NAPRT1	Body	Island	FALSE
cg23352942	0.53	0.41	0.12	35.88	Chr3: 46931381	PTH1R	Body	N_Shelf	FALSE
cg07234876	0.76	0.64	0.12	52.92	Chr8: 600039			Island	FALSE
cg06937882	0.81	0.69	0.12	65.56	Chr20: 24974362	C20orf3	TSS1500	S_Shore	FALSE
cg25835179	0.43	0.31	0.12	38.50	Chr11: 67418291	ACY3	TSS200		FALSE
cg02771260	0.61	0.49	0.12	36.56	Chr11: 59836817	MS4A3, MS4A3, MS4A3	Body, Body, Body		FALSE
cg23496314	0.37	0.25	0.12	44.13	ChrX: 39956534	BCOR, BCOR, BCOR, BCOR BCOR, BCOR	5'UTR, 5'UTR, 1stExon, 5'UTR, 1stExon, 5'UTR	Island	FALSE
cg25393323	0.15	0.03	0.12	340.66	Chr15: 42565830	GANC, TMEM87A, TMEM87A	TSS1500, TSS200, TSS200	N_Shore	FALSE
cg26921093	0.29	0.17	0.12	58.26	Chr17: 63534688	AXIN2	Body	S_Shore	FALSE
cg05002314	0.97	0.85	0.12	340.66	Chr20: 54978854	CSTF1, CSTF1, CSTF1	3'UTR, 3'UTR, 3'UTR	S_Shore	FALSE
cg10430963	0.67	0.55	0.12	39.79	Chr17: 37124558	FBXO47	TSS1500		FALSE
cg02824443	0.60	0.48	0.12	35.63	Chr7: 108093448	NRCAM, NRCAM	5'UTR, 5'UTR	N_Shore	FALSE
cg08945443	0.39	0.27	0.12	41.10	Chr10: 75193254	ZMYND17	5'UTR		FALSE
cg07493435	0.48	0.36	0.12	35.17	Chr7: 128556140			Island	FALSE
cg02498120	0.69	0.57	0.12	41.34	Chr21: 15095903			Island	FALSE
cg25189608	0.70	0.58	0.12	42.39	Chr11: 96117844	CCDC82	Body		FALSE
cg04192168	0.27	0.15	0.12	60.23	Chr15: 64806741	ZNF609	Body		TRUE
cg22772691	0.36	0.24	0.12	43.50	Chr5: 1104195	SLC12A7	Body	S_Shelf	FALSE
cg26597838	0.54	0.43	0.12	33.91	Chr10: 835615			N_Shelf	TRUE
cg03092399	0.73	0.61	0.12	45.32	Chr11: 108149307	ATM	Body		TRUE
cg26476930	0.81	0.69	0.12	61.73	Chr2: 731519			N_Shore	FALSE
cg13286116	0.67	0.55	0.12	37.80	Chr11: 13302098	ARNTL, ARNTL, ARNTL	5'UTR, 5'UTR, 5'UTR	S_Shore	FALSE
cg15241074	0.29	0.18	0.12	52.81	Chr2: 12860614	TRIB2, TRIB2	Body, Body	S_Shore	FALSE
cg00208274	0.52	0.41	0.12	32.96	Chr7: 4779342	FOXK1	Body		FALSE
cg06892679	0.59	0.47	0.12	32.96	Chr14: 68008964	PLEKHH1	Body		FALSE
cg00859178	0.76	0.64	0.12	47.55	Chr1: 162467208	UHMK1	TSS1500	N_Shore	FALSE
cg14287022	0.27	0.15	0.12	57.88	Chr12: 19557343				FALSE
cg07110949	0.35	0.24	0.12	41.53	Chr4: 1309878	MAEA, MAEA	Body, Body	S_Shore	FALSE
cg26003388	0.55	0.44	0.12	31.95	Chr17: 76129533	TMC8, TMC6	Body, TSS1500	S_Shore	FALSE
cg24004368	0.62	0.51	0.12	33.72	Chr6: 30706647	FLOT1	Body	N_Shelf	FALSE
cg12277366	0.40	0.28	0.12	36.93	Chr8: 54931229	TCEA1, TCEA1	Body, Body	N_Shelf	FALSE
cg26764761	0.85	0.73	0.12	70.78	Chr16: 87682142	JPH3	Body	S_Shelf	FALSE
cg10296062	0.56	0.44	0.12	31.67	Chr11: 64528569	PYGM, PYGM	TSS1500, TSS1500		FALSE
cg18470780	0.39	0.28	0.12	36.72	Chr14: 59064969				TRUE
cg18808929	0.48	0.37	0.12	31.88	Chr8: 61825469			S_Shelf	TRUE
cg26280976	0.42	0.30	0.11	34.50	Chr14: 69660603			S_Shore	FALSE
cg19528654	0.36	0.24	0.11	39.45	Chr11: 67251154	AIP	Body	S_Shore	TRUE
cg15469871	0.39	0.27	0.11	36.61	Chr10: 27541418	LOC387646	TSS200	Island	FALSE
cg11900328	0.34	0.22	0.11	42.01	Chr8: 2263331				FALSE
cg03450844	0.77	0.65	0.11	46.95	Chr7: 150416671	GIMAP1	Body	N_Shore	FALSE
cg09417038	0.56	0.45	0.11	30.62	Chr21: 47716443	C21orf57	Body	N_Shore	FALSE
cg10008347	0.36	0.25	0.11	38.36	ChrX: 39958040	BCOR, BCOR, BCOR, BCOR	TSS1500, 5'UTR, TSS1500, 5'UTR	Island	FALSE
cg20803293	0.34	0.23	0.11	40.64	Chr1: 110254709	GSTM5	TSS200		FALSE
cg26702039	0.81	0.69	0.11	55.36	Chr16: 66170991				TRUE
cg25472530	0.68	0.57	0.11	35.67	Chr5: 23507617	PRDM9	TSS200		FALSE
cg24139837	0.29	0.18	0.11	48.98	ChrX: 3730151			N_Shelf	FALSE
cg04850148	0.67	0.56	0.11	34.10	Chr17: 34539744	CCL4L2, CCL4L1	Body, Body		FALSE
cg24370881	0.58	0.47	0.11	29.17	Chr4: 10112059	WDR1, WDR1	Body, Body		TRUE
cg05914034	0.51	0.40	0.11	28.78	Chr7: 5528179	FBXL18	Body	Island	FALSE
cg14124261	0.31	0.20	0.11	42.84	Chr9: 116262291	RGS3, RGS3, RGS3	TSS1500, Body, Body		FALSE
cg04691264	0.47	0.36	0.11	29.11	Chr10: 29697905	LOC387647	TSS1500	N_Shore	FALSE
cg06211550	0.35	0.23	0.11	37.39	Chr16: 3230726			N_Shelf	FALSE
cg10265387	0.30	0.19	0.11	44.04	ChrX: 20009123	LOC729609	TSS1500	Island	FALSE
cg11861406	0.89	0.78	0.11	85.32	Chr13: 21749154	SKA3, SKA3, MRP63	Body, Body, TSS1500	N_Shore	FALSE
cg156667493	0.36	0.25	0.11	35.38	Chr5: 55404179	ANKRD55, ANKRD55	Body, Body		TRUE

cg15935877	0.28	0.17	0.11	47.39	ChrY: 9303715	<i>TSPY1</i> , <i>TSPY4</i>	TSS1500, Body	Island	FALSE
cg13282195	0.46	0.35	0.11	28.96	Chr8: 144660772	<i>NAPRT1</i> <i>ACACA</i> , <i>ACACA</i> ,	TSS1500 Body, Body,	S_Shore	FALSE
cg17939040	0.47	0.36	0.11	28.58	Chr17: 35503956	<i>ACACA</i> , <i>ACACA</i> , <i>ACACA</i>	Body, Body, Body		TRUE
cg22068400	0.50	0.39	0.11	28.01	Chr2: 90016264				FALSE
cg13390570	0.27	0.16	0.11	49.76	Chr5: 1255616	<i>TERT</i> , <i>TERT</i>	Body, Body	N_Shore	FALSE
cg02125365	0.33	0.22	0.11	38.43	Chr5: 78813058			S_Shelf	FALSE
cg12417549	0.36	0.25	0.11	34.88	Chr4: 70697416				TRUE
cg04548204	0.48	0.37	0.11	27.99	Chr12: 9162872	<i>KLRG1</i>	3'UTR		FALSE
cg24168538	0.83	0.72	0.11	58.09	Chr4: 35527016				TRUE
cg07165260	0.39	0.28	0.11	31.44	Chr16: 85062881	<i>KIAA0513</i>	5'UTR	S_Shore	TRUE
cg09508730	0.50	0.39	0.11	27.02	Chr6: 27706275				FALSE
cg05509777	0.19	0.08	0.11	73.25	Chr11: 2322517	<i>C11orf21</i> , <i>TSPAN32</i> , <i>C11orf21</i>	Body, TSS1500, Body		FALSE
cg02713832	0.17	0.07	0.11	83.30	Chr11: 60772559	<i>CD6</i>	Body	N_Shelf	FALSE
cg15454820	0.31	0.20	0.11	39.80	Chr10: 96990858				FALSE
cg05600342	0.26	0.16	0.11	48.07	Chr11: 250989	<i>PSMD13</i> , <i>PSMD13</i>	Body, Body		TRUE
cg09926364	0.43	0.32	0.11	28.32	Chr14: 73137242	<i>DPF3</i>	3'UTR		FALSE
cg20894640	0.23	0.12	0.11	57.70	Chr12: 19557334				FALSE
cg02640489	0.35	0.25	0.11	33.46	Chr2: 219153935	<i>PNKD</i> , <i>TMBIM1</i>	Body, 5'UTR	N_Shelf	FALSE
cg24508426	0.38	0.27	0.11	31.19	Chr10: 124578209			Island	FALSE
cg11766577	0.64	0.53	0.11	28.17	Chr21: 47581405	<i>C21orf56</i> , <i>C21orf56</i>	Body, Body	Island	FALSE
cg24885723	0.39	0.28	0.11	30.54	Chr1: 9030439	<i>CA6</i>	Body		FALSE
cg22668906	0.41	0.30	0.11	28.99	Chr11: 128180077				TRUE
cg08537890	0.50	0.39	0.11	25.96	Chr12: 31272865				FALSE
cg22968622	0.14	0.03	0.11	111.73	Chr17: 43663579			Island	FALSE
cg05200811	0.58	0.47	0.11	26.06	Chr21: 47581042			Island	FALSE
cg20557159	0.56	0.45	0.11	25.39	Chr17: 75445261	<i>SEPT9</i> , <i>SEPT9</i> , <i>SEPT9</i> , <i>SEPT9</i> , <i>SEPT9</i> , <i>SEPT9</i>	Body, Body, Body, Body, Body, Body	N_Shelf	FALSE
cg01768001	0.34	0.23	0.11	33.98	Chr1: 24831147	<i>RCAN3</i>	5'UTR	S_Shore	FALSE
cg15493018	0.87	0.76	0.11	67.94	Chr1: 108710337	<i>SLC25A24</i> , <i>SLC25A24</i>	Body, Body		FALSE
cg17346246	0.28	0.18	0.11	41.70	Chr12: 123214864	<i>GPR81</i>	1stExon		FALSE
cg00101728	0.64	0.53	0.11	27.32	Chr6: 2953027	<i>SERPINB6</i>	Body		TRUE
cg23733394	0.43	0.33	0.11	27.06	Chr1: 8397952			Island	FALSE
cg15009294	0.39	0.28	0.11	29.57	Chr1: 214813712	<i>CENPF</i>	Body		TRUE
cg22715764	0.48	0.38	0.11	25.36	Chr1: 10556294	<i>PEX14</i>	Body		FALSE
cg00568384	0.67	0.56	0.11	28.90	Chr2: 173539262				TRUE
cg23088126	0.32	0.21	0.11	35.91	Chr1: 207078912	<i>FAIM3</i> , <i>FAIM3</i> , <i>FAIM3</i>	Body, Body, Body	N_Shelf	TRUE
cg06828418	0.74	0.64	0.11	35.81	Chr6: 30706654	<i>FLOT1</i>	Body	N_Shelf	FALSE
cg07544796	0.37	0.26	0.11	30.74	Chr6: 36817048				TRUE
cg22761176	0.33	0.23	0.11	33.76	Chr2: 173539542				TRUE
cg00141688	0.76	0.66	0.10	37.70	Chr2: 10517352	<i>HPCAL1</i> , <i>HPCAL1</i>	5'UTR, 5'UTR		FALSE
cg20208600	0.34	0.24	0.10	32.43	Chr11: 61159687	<i>TMEM216</i>	TSS200	N_Shore	FALSE
cg04681579	0.83	0.72	0.10	52.27	Chr7: 75027559	<i>TRIM73</i> , <i>TRIM74</i>	5'UTR, 5'UTR	S_Shelf	FALSE
cg12149986	0.93	0.82	0.10	105.58	Chr19: 50059027	<i>NOSIP</i>	Body	Island	FALSE
cg02402882	0.36	0.26	0.10	30.40	Chr5: 56620429				TRUE
cg21238284	0.66	0.56	0.10	27.66	Chr8: 127889295				TRUE
cg13937905	0.70	0.60	0.10	30.56	Chr12: 53612551	<i>RARG</i> , <i>RARG</i>	Body, Body	N_Shore	FALSE
cg15506890	0.79	0.69	0.10	42.19	Chr2: 3487001				TRUE
cg16906964	0.71	0.60	0.10	30.71	Chr1: 4660171				FALSE
cg25709050	0.43	0.32	0.10	25.96	Chr17: 29817279	<i>RAB11FIP4</i>	Body	S_Shore	TRUE
cg12421110	0.57	0.47	0.10	24.14	Chr13: 42035731	<i>C13orf15</i>	Body	S_Shelf	FALSE
cg11909526	0.50	0.39	0.10	24.01	Chr17: 33519851	<i>AMAC1</i> , <i>AMAC1</i>	3'UTR, 1stExon		FALSE
cg12419766	0.80	0.69	0.10	43.73	Chr7: 157620445	<i>PTPRN2</i> , <i>PTPRN2</i> , <i>PTPRN2</i>	Body, Body, Body	S_Shore	FALSE
cg03209332	0.26	0.15	0.10	44.95	Chr12: 132670372			N_Shelf	FALSE
cg15973818	0.54	0.44	0.10	23.59	Chr8: 53623995	<i>RB1CC1</i> , <i>RB1CC1</i>	5'UTR, 5'UTR	N_Shelf	FALSE
cg01560476	0.50	0.39	0.10	23.70	Chr16: 24743405	<i>TNRC6A</i>	Body	S_Shore	FALSE
cg14789911	0.72	0.62	0.10	31.46	Chr21: 47582049	<i>C21orf56</i> , <i>C21orf56</i>	Body, Body	Island	FALSE

cg25130381	0.42	0.31	0.10	26.01	Chr1: 27440721	<i>SLC9A1</i>	Body		FALSE
cg12850078	0.13	0.03	0.10	106.79	Chr15: 89922071	<i>LOC254559</i>	Body	Island	TRUE
cg09027133	0.35	0.25	0.10	30.28	Chr1: 25945042	<i>MAN1C1</i>	Body	S_Shore	FALSE
cg01567509	0.34	0.24	0.10	31.15	Chr1: 15104223	<i>KIAA1026</i> , <i>KIAA1026</i>	Body, Body		FALSE
cg19863426	0.30	0.20	0.10	36.01	Chr10: 124138853	<i>PLEKHA1</i>	5'UTR	S_Shelf	FALSE
cg13600149	0.16	0.06	0.10	79.42	Chr9: 98079129	<i>FANCC</i>	5'UTR	N_Shore	FALSE
cg09035699	0.37	0.26	0.10	29.02	Chr5: 131310461	<i>ACSL6</i> , <i>ACSL6</i>	Body, Body		TRUE
cg08113187	0.40	0.30	0.10	26.63	Chr16: 87469329	<i>ZCCHC14</i>	Body		FALSE
cg01540386	0.30	0.20	0.10	36.10	ChrX: 39873535			Island	FALSE
cg04284196	0.33	0.23	0.10	31.89	Chr14: 22975248				FALSE
cg16969872	0.56	0.46	0.10	23.46	Chr13: 79968324	<i>RBM26</i>	Body		FALSE
cg22211507	0.57	0.46	0.10	23.46	Chr3: 108564871	<i>TRAT1</i>	Body		FALSE
							TSS1500,		
cg27554954	0.80	0.69	0.10	42.44	Chr15: 60691595	<i>ANXA2</i> , <i>ANXA2</i> , <i>ANXA2</i> , <i>ANXA2</i>	TSS1500, TSS1500, TSS1500, TSS1500	S_Shore	TRUE
cg06329392	0.29	0.18	0.10	38.19	Chr13: 40762435				TRUE
cg08560373	0.38	0.27	0.10	28.12	Chr15: 25123381	<i>SNRPN</i> , <i>SNRPN</i> , <i>SNRPN</i> , <i>SNRPN</i>	5'UTR, 5'UTR, 5'UTR, 5'UTR	Island	FALSE
cg01052065	0.22	0.11	0.10	54.54	ChrX: 110339654	<i>PAK3</i> , <i>PAK3</i> , <i>PAK3</i>	5'UTR, 5'UTR, 5'UTR	Island	FALSE
cg05376982	0.52	0.41	0.10	23.13	Chr1: 110254692	<i>GSTM5</i>	TSS200		FALSE
cg01890417	0.46	0.35	0.10	23.85	Chr1: 91488275	<i>ZNF644</i> , <i>ZNF644</i> , <i>ZNF644</i>	TSS1500, TSS1500, TSS1500	S_Shore	FALSE
cg20306694	0.34	0.24	0.10	30.54	Chr12: 51718251	<i>BIN2</i>	TSS1500		FALSE
cg06758191	0.92	0.82	0.10	95.94	Chr4: 7812988	<i>AFAP1</i> , <i>AFAP1</i>	Body, Body		FALSE
cg21436572	0.73	0.63	0.10	31.88	Chr8: 70623422	<i>SLCO5A1</i> , <i>SLCO5A1</i> , <i>SLCO5A1</i>	Body, Body, Body		FALSE
cg15576492	0.23	0.13	0.10	48.31	Chr1: 1015447			N_Shore	TRUE
cg02540440	0.58	0.48	0.10	23.17	ChrX: 39866758			Island	FALSE
cg23737407	0.17	0.07	0.10	70.89	ChrX: 40029094	<i>BCOR</i> , <i>BCOR</i>	5'UTR, 5'UTR	Island	FALSE
cg02952635	0.86	0.75	0.10	57.81	Chr2: 178741216	<i>PDE11A</i> , <i>PDE11A</i> , <i>PDE11A</i> , <i>PDE11A</i>	Body, 5'UTR, Body, Body		FALSE
						<i>PCDHA2</i> , <i>PCDHA1</i> , <i>PCDHA1</i> , <i>PCDHA6</i> , <i>PCDHA6</i>	Body, Body, Body, TSS200,		
cg16987900	0.30	0.20	0.10	34.42	Chr5: 140207609	<i>PCDHA5</i> , <i>PCDHA6</i> , <i>PCDHA3</i> , <i>PCDHA4</i> ,	Body, TSS200, Body, Body,	N_Shore	FALSE
						<i>PCDHA6</i>	TSS200		
cg18753928	0.40	0.30	0.10	25.37	Chr3: 113234510	<i>CCDC52</i>	TSS1500	S_Shore	FALSE
cg20589243	0.39	0.29	0.10	25.91	ChrX: 109246229	<i>TMEM164</i> , <i>TMEM164</i>	TSS200, 5'UTR	Island	FALSE
cg22061832	0.29	0.19	0.10	35.80	Chr2: 173293627	<i>ITGA6</i> , <i>ITGA6</i>	Body, Body	S_Shore	TRUE
cg04618171	0.44	0.34	0.10	23.68	Chr2: 10470465	<i>HPCAL1</i> , <i>HPCAL1</i>	5'UTR, 5'UTR		TRUE
cg08964643	0.75	0.65	0.10	33.20	Chr7: 63560420			Island	FALSE
						<i>DNMT3A</i> , <i>DNMT3A</i>			
cg15302376	0.26	0.16	0.10	41.37	Chr2: 25560263	<i>DNMT3A</i> , <i>DNMT3A</i>	5'UTR, 5'UTR	N_Shelf	FALSE
cg07011961	0.80	0.70	0.10	42.66	Chr5: 23507594	<i>PRDM9</i>	TSS200		FALSE
cg12044599	0.30	0.19	0.10	34.86	Chr11: 67206308	<i>CORO1B</i> , <i>CORO1B</i> , <i>PTPRCAP</i>	Body, Body, TSS1500	S_Shelf	FALSE
cg07643762	0.29	0.19	0.10	36.03	Chr4: 75174080	<i>EPGN</i>	TSS200		FALSE
cg14699257	0.28	0.18	0.10	37.23	ChrX: 47092993	<i>USP11</i>	Body	Island	FALSE
cg11619648	0.85	0.75	0.10	54.77	Chr3: 44515242	<i>ZNF445</i>	5'UTR	N_Shelf	FALSE
cg00804354	0.35	0.25	0.10	28.62	Chr1: 249111407	<i>SH3BP5L</i>	Body		FALSE
cg26118221	0.67	0.57	0.10	25.83	Chr4: 8262589				FALSE
cg14780427	0.61	0.51	0.10	23.14	Chr17: 78754372	<i>RPTOR</i> , <i>RPTOR</i>	Body, Body		TRUE
cg08639389	0.33	0.22	0.10	30.77	Chr4: 26995889	<i>STIM2</i> , <i>STIM2</i> , <i>STIM2</i>	Body, Body, Body		TRUE
cg00876757	0.65	0.55	0.10	24.58	Chr16: 33483591			S_Shore	FALSE
cg18015035	0.45	0.35	0.10	22.88	ChrX: 19002577	<i>PHKA2</i>	TSS200	Island	FALSE
cg21191275	0.36	0.26	0.10	27.72	Chr9: 135907982	<i>GTF3C5</i> , <i>GTF3C5</i>	Body, Body	S_Shore	FALSE
cg13568659	0.40	0.30	0.10	24.80	Chr6: 159438801				FALSE

cg02188048	0.34	0.24	0.10	28.85	ChrX: 39871543			Island	TRUE
cg23486701	0.27	0.17	0.10	38.55	Chr2: 54789491	<i>SPTBN1, SPTBN1</i>	Body, Body	S_Shelf	FALSE
cg11909467	0.28	0.18	0.10	35.96	Chr8: 132912348			N_Shelf	FALSE
cg20197861	0.31	0.21	0.10	31.74	ChrX: 39964229	<i>BCOR, BCOR</i>	5'UTR, 5'UTR	Island	FALSE
cg23953831	0.18	0.08	0.10	62.38	Chr1: 117544416	<i>CD101, CD101</i>	5'UTR, 1stExon		FALSE
cg07129803	0.76	0.66	0.10	33.98	Chr16: 88370583				FALSE
cg10288578	0.88	0.78	0.10	65.53	Chr2: 16816994	<i>FAM49A</i>	5'UTR		TRUE

Supplementary Table 5: Shared differentially methylated regions (DMRs) in naïve CD4+ T cells from patients with a history of **A.** malar rash and discoid rash, or **B.** malar rash, discoid rash, and neither cutaneous involvement.

A.

Shared DMRs Between Malar Rash and Discoid Rash

DMR Gene	DMR Location	Malar Rash				Discoid Rash				No Cutaneous Involvement					
		# DM Sites in DMR	Mean β Case	Mean β Control	Mean Δβ	DMR Location	# DM Sites in DMR	Mean β Case	Mean β Control	Mean Δβ	DMR Location	# DM Sites in DMR	Mean β Case	Mean β Control	Mean Δβ
Hyper-DMR															
(Intergenic)	Chr7: 1209495-1209562	3	0.37	0.11	0.27	Chr7: 1209495-1209742	2	0.30	0.14	0.16	NA	NA	0.18	0.24	-0.06
<i>PRIC285</i>	Chr20: 62198872-62199034	3	0.29	0.10	0.18	Chr20: 62198872-62199156	2	0.35	0.15	0.20	NA	NA	0.24	0.16	0.07

B.

Shared DMRs Between Cutaneous and No Cutaneous Involvement

DMR Gene	DMR Location	Malar Rash				Discoid Rash				No Cutaneous Involvement					
		# DM Sites in DMR	Mean β Case	Mean β Control	Mean Δβ	DMR Location	# DM Sites in DMR	Mean β Case	Mean β Control	Mean Δβ	DMR Location	# DM Sites in DMR	Mean β Case	Mean β Control	Mean Δβ
Hypo-DMR															
<i>IFI44L</i>	Chr1: 79085586-79085765	3	0.38	0.58	-0.20	Chr1: 79085586-79085765	3	0.40	0.56	-0.16	Chr1: 79085586-79085765	3	0.44	0.59	-0.15
<i>GSTT1</i>	Chr22: 24384105-24384400	2	0.16	0.30	-0.14	Chr22: 24384105-24384400	2	0.07	0.22	-0.15	Chr22: 24384105-24384400	5	0.09	0.24	-0.15
Hyper-DMR															
<i>GSTTP1</i>	Chr22: 24348549-24348715	2	0.61	0.44	0.16	Chr22: 24348549-24348715	2	0.72	0.57	0.15	Chr22: 24348549-24348715	2	0.56	0.40	0.16

Supplementary Table 6: Network analysis results are depicted for genes with unique hypomethylated regions (hypo-DMRs) in naïve CD4+ T cells from SLE patients with a history of **A.** malar rash, **B.** discoid rash, or **C.** neither cutaneous involvement. All network analyses were performed using GeneMANIA software.

A.

Enriched Function	P Value
Antigen processing and presentation of exogenous peptide antigen via MHC class I	3.66E-18
Antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent	3.66E-18
Antigen processing and presentation of peptide antigen via MHC class I	2.65E-17
Peptide antigen binding	1.87E-15
Antigen processing and presentation of exogenous peptide antigen	1.91E-14
Antigen processing and presentation of exogenous antigen	2.29E-14
Antigen processing and presentation of peptide antigen	3.21E-14
Antigen processing and presentation	2.97E-13
Interferon-gamma-mediated signaling pathway	1.77E-12
Cellular response to type I interferon	1.77E-12
Type I interferon signaling pathway	1.77E-12
Response to type I interferon	1.85E-12
Phagocytic vesicle membrane	1.90E-12
Antigen processing and presentation of endogenous antigen	1.90E-12
Cellular response to interferon-gamma	7.37E-12
Antigen binding	2.27E-11
ER to Golgi transport vesicle membrane	2.29E-11
Response to interferon-gamma	2.86E-11
ER to Golgi transport vesicle	4.95E-11
Early endosome membrane	4.95E-11
Transport vesicle membrane	5.94E-10
Transport vesicle	6.73E-10
Integral component of endoplasmic reticulum membrane	7.68E-10
Intrinsic component of endoplasmic reticulum membrane	8.03E-10
Luminal side of membrane	1.32E-09
Peptide binding	1.32E-09
Integral component of luminal side of endoplasmic reticulum membrane	1.32E-09
Luminal side of endoplasmic reticulum membrane	1.32E-09
Amide binding	1.46E-09
Phagocytic vesicle	1.46E-09
T cell mediated immunity	2.41E-08
Lymphocyte mediated immunity	4.44E-08
Endocytic vesicle membrane	4.64E-08
Integral component of organelle membrane	6.05E-08
Coated vesicle membrane	6.31E-08
Intrinsic component of organelle membrane	9.05E-08
Regulation of leukocyte mediated cytotoxicity	2.65E-07
Leukocyte mediated immunity	2.67E-07
Early endosome	3.63E-07
Regulation of cell killing	4.23E-07
Positive regulation of lymphocyte mediated immunity	5.75E-07

Positive regulation of leukocyte mediated immunity	7.67E-07
Positive regulation of T cell mediated cytotoxicity	1.82E-06
Endosome membrane	2.19E-06
Coated vesicle	2.23E-06
Endocytic vesicle	2.46E-06
Adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	2.59E-06
Leukocyte mediated cytotoxicity	2.74E-06
Endosomal part	2.74E-06
Regulation of T cell mediated cytotoxicity	3.71E-06
Cell killing	5.37E-06
Regulation of lymphocyte mediated immunity	5.37E-06
T cell mediated cytotoxicity	8.61E-06
Positive regulation of leukocyte mediated cytotoxicity	8.61E-06
Positive regulation of cell killing	1.25E-05
Cytoplasmic vesicle membrane	1.37E-05
Positive regulation of immune effector process	1.39E-05
Adaptive immune response	1.44E-05
Regulation of leukocyte mediated immunity	1.57E-05
Vesicle membrane	1.57E-05
Positive regulation of T cell mediated immunity	1.89E-05
Positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	3.90E-05
Side of membrane	3.93E-05
Regulation of T cell mediated immunity	4.91E-05
Golgi membrane	5.20E-05
Positive regulation of adaptive immune response	5.39E-05
Regulation of immune effector process	7.60E-05
MHC class I protein binding	3.11E-04
Regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	4.60E-04
Regulation of adaptive immune response	7.63E-04
MHC protein binding	9.27E-04
Dendritic cell differentiation	1.23E-03
Proteasome complex	1.60E-02
Regulation of cellular amino acid metabolic process	2.20E-02
Protein polyubiquitination	2.42E-02
Tolerance induction	2.47E-02
RNA polymerase II core promoter sequence-specific DNA binding	2.98E-02
DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest	3.17E-02
Signal transduction involved in DNA integrity checkpoint	3.17E-02
Signal transduction involved in mitotic G1 DNA damage checkpoint	3.17E-02
Signal transduction involved in mitotic cell cycle checkpoint	3.17E-02
Signal transduction involved in DNA damage checkpoint	3.17E-02
Signal transduction involved in mitotic DNA damage checkpoint	3.17E-02
Negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle	3.17E-02
Signal transduction involved in mitotic DNA integrity checkpoint	3.17E-02
Regulation of cellular amine metabolic process	3.17E-02
Intracellular signal transduction involved in G1 DNA damage checkpoint	3.17E-02
Signal transduction involved in cell cycle checkpoint	3.27E-02
Negative regulation of ubiquitin-protein ligase activity	3.48E-02
Negative regulation of ligase activity	3.48E-02
Positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle	3.58E-02
Defense response to other organism	3.58E-02
Mitotic G1 DNA damage checkpoint	3.77E-02
Mitotic G1/S transition checkpoint	3.77E-02
G1 DNA damage checkpoint	3.88E-02
Regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle	4.32E-02

Detection of bacterium	4.49E-02
Anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process	4.98E-02
Positive regulation of cell cycle arrest	4.98E-02
Detection of other organism	4.98E-02
Positive regulation of ubiquitin-protein ligase activity	5.06E-02
Mitotic DNA damage checkpoint	5.06E-02
Mitotic DNA integrity checkpoint	5.50E-02
Positive regulation of ligase activity	5.50E-02
Proteasome core complex	6.03E-02
Negative regulation of G1/S transition of mitotic cell cycle	6.11E-02
Proteasome-mediated ubiquitin-dependent protein catabolic process	6.11E-02
Leukocyte differentiation	6.16E-02
Detection of external biotic stimulus	6.49E-02
Negative regulation of protein ubiquitination	6.95E-02
Regulation of ubiquitin-protein ligase activity	7.10E-02
Regulation of ligase activity	7.56E-02
Proteasomal protein catabolic process	7.56E-02
Regulation of cell cycle arrest	7.56E-02
Detection of biotic stimulus	8.14E-02
Regulation of interferon-gamma-mediated signaling pathway	8.14E-02
Modulation by virus of host morphology or physiology	8.14E-02
Regulation of response to interferon-gamma	8.84E-02
DNA damage response, signal transduction by p53 class mediator	9.23E-02
Regulation of leukocyte differentiation	9.23E-02
Negative regulation of cell morphogenesis involved in differentiation	9.39E-02
Regulation of G1/S transition of mitotic cell cycle	9.58E-02
Negative regulation of cell differentiation	9.99E-02

B.**Discoid Rash**

Enriched Function	P Value
Antigen processing and presentation of exogenous peptide antigen via MHC class I	3.67E-13
Antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent	3.67E-13
Antigen processing and presentation of peptide antigen via MHC class I	1.73E-12
Peptide antigen binding	2.57E-12
Antigen processing and presentation	1.07E-10
Antigen processing and presentation of exogenous peptide antigen	2.94E-10
Antigen processing and presentation of exogenous antigen	3.40E-10
Antigen processing and presentation of peptide antigen	4.47E-10
Antigen binding	1.17E-08
Intrinsic component of endoplasmic reticulum membrane	2.97E-07
Integral component of endoplasmic reticulum membrane	2.97E-07
Peptide binding	4.51E-07
Amide binding	5.11E-07
Luminal side of membrane	8.53E-07
Integral component of luminal side of endoplasmic reticulum membrane	8.53E-07
Luminal side of endoplasmic reticulum membrane	8.53E-07
Antigen processing and presentation of endogenous antigen	1.47E-06
Interferon-gamma-mediated signaling pathway	2.08E-06
Cellular response to type I interferon	2.08E-06
Type I interferon signaling pathway	2.08E-06
Response to type I interferon	2.15E-06
MHC class I protein binding	5.38E-06
Cellular response to interferon-gamma	5.57E-06
Integral component of organelle membrane	7.79E-06
Intrinsic component of organelle membrane	1.11E-05
Response to interferon-gamma	1.34E-05
MHC protein binding	2.11E-05
Phagocytic vesicle membrane	3.06E-05
Regulation of leukocyte mediated cytotoxicity	8.22E-05
Regulation of cell killing	1.18E-04
ER to Golgi transport vesicle membrane	1.18E-04
Positive regulation of lymphocyte mediated immunity	1.48E-04
ER to Golgi transport vesicle	1.73E-04
Positive regulation of leukocyte mediated immunity	1.73E-04
Early endosome membrane	1.73E-04
Transport vesicle	2.14E-04
Lymphocyte mediated immunity	2.32E-04
T cell mediated immunity	3.72E-04
Leukocyte mediated cytotoxicity	4.77E-04
Transport vesicle membrane	6.02E-04
Positive regulation of T cell mediated cytotoxicity	6.99E-04
Cell killing	7.70E-04
Regulation of lymphocyte mediated immunity	7.70E-04
Leukocyte mediated immunity	7.73E-04
Phagocytic vesicle	1.06E-03
Regulation of T cell mediated cytotoxicity	1.16E-03
Positive regulation of immune effector process	1.61E-03
Regulation of leukocyte mediated immunity	1.78E-03
T cell mediated cytotoxicity	2.08E-03
Positive regulation of leukocyte mediated cytotoxicity	2.08E-03
Side of membrane	2.47E-03
Positive regulation of cell killing	2.66E-03
Endosome membrane	3.10E-03
Coated vesicle	3.13E-03

Positive regulation of T cell mediated immunity	3.66E-03
Endosomal part	3.66E-03
Positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	5.99E-03
Endocytic vesicle membrane	5.99E-03
Adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	6.57E-03
Regulation of T cell mediated immunity	6.89E-03
Coated vesicle membrane	6.89E-03
Positive regulation of adaptive immune response	7.43E-03
ATPase activity, coupled to transmembrane movement of substances	1.27E-02
Hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances	1.27E-02
P-P-bond-hydrolysis-driven transmembrane transporter activity	1.33E-02
Primary active transmembrane transporter activity	1.33E-02
ATPase activity, coupled to movement of substances	1.72E-02
Early endosome	1.73E-02
Adaptive immune response	1.97E-02
Proteasome complex	2.25E-02
Golgi membrane	2.75E-02
Regulation of cellular amino acid metabolic process	3.05E-02
Regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	3.17E-02
DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest	4.37E-02
Regulation of adaptive immune response	4.37E-02
Signal transduction involved in DNA integrity checkpoint	4.37E-02
Signal transduction involved in mitotic G1 DNA damage checkpoint	4.37E-02
Signal transduction involved in mitotic cell cycle checkpoint	4.37E-02
Signal transduction involved in DNA damage checkpoint	4.37E-02
Endocytic vesicle	4.37E-02
Signal transduction involved in mitotic DNA damage checkpoint	4.37E-02
Negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle	4.37E-02
Signal transduction involved in mitotic DNA integrity checkpoint	4.37E-02
Regulation of cellular amine metabolic process	4.37E-02
Intracellular signal transduction involved in G1 DNA damage checkpoint	4.37E-02
Signal transduction involved in cell cycle checkpoint	4.46E-02
Positive regulation of cell cycle process	4.46E-02
Negative regulation of ubiquitin-protein ligase activity	4.74E-02
Negative regulation of ligase activity	4.74E-02
Positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle	4.84E-02
Regulation of immune effector process	4.84E-02
Mitotic G1 DNA damage checkpoint	5.13E-02
Mitotic G1/S transition checkpoint	5.13E-02
G1 DNA damage checkpoint	5.28E-02
Regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle	5.87E-02
Anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process	6.90E-02
Positive regulation of cell cycle arrest	6.90E-02
Positive regulation of ubiquitin-protein ligase activity	7.01E-02
Mitotic DNA damage checkpoint	7.01E-02
Proteasome core complex	7.58E-02
Mitotic DNA integrity checkpoint	7.58E-02
Positive regulation of ligase activity	7.58E-02
Negative regulation of G1/S transition of mitotic cell cycle	8.52E-02
<u>Negative regulation of protein ubiquitination</u>	<u>9.87E-02</u>

C.**No Malar or Discoid Rash**

Enriched Function	P Value
Protein trimerization	1.60E-03
Type I interferon signaling pathway	5.85E-02
Cellular response to type I interferon	5.85E-02
Response to type I interferon	5.85E-02
Antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent	5.85E-02
Antigen processing and presentation of exogenous peptide antigen via MHC class I	5.85E-02
Antigen processing and presentation of peptide antigen via MHC class I	1.05E-01
Antigen processing and presentation of endogenous antigen	4.27E-01
Antigen processing and presentation of exogenous peptide antigen	4.58E-01
MHC class I protein binding	4.58E-01

Supplementary Table 7: Network analysis results for genes with unique hypermethylated regions (hyper-DMRs) in naïve CD4+ T cells from SLE patients with a history of malar rash. The network analysis was performed using GeneMANIA software.

Malar Rash	Enriched Function	P Value
	Response to type I interferon	1.11E-21
	Cellular response to type I interferon	1.11E-21
	Type I interferon signaling pathway	1.11E-21
	Response to virus	3.20E-17
	Defense response to virus	3.53E-11
	Regulation of multiorganism process	3.80E-10
	Negative regulation of viral genome replication	1.40E-09
	Defense response to other organism	2.95E-09
	Negative regulation of multiorganism process	3.22E-09
	Regulation of viral genome replication	8.85E-09
	Viral genome replication	4.24E-08
	Negative regulation of viral process	4.35E-08
	Regulation of viral process	1.66E-07
	Regulation of symbiosis, encompassing mutualism through parasitism	2.45E-07
	Doublestranded RNA binding	2.69E-07
	Interferongammamediated signaling pathway	5.07E-06
	Cellular response to interferongamma	1.60E-05
	Response to interferongamma	4.08E-05
	Regulation of defense response to virus	1.41E-04
	Negative regulation of type I interferon production	4.83E-04
	Regulation of response to biotic stimulus	4.83E-04
	Regulation of immune effector process	8.98E-04
	Cytoplasmic pattern recognition receptor signaling pathway in response to virus	9.60E-04
	Regulation of type I interferon production	9.60E-04
	Type I interferon production	9.60E-04
	Cellular response to virus	9.60E-04
	Zinc ion binding	2.31E-03
	Adenyllyltransferase activity	3.28E-03
	Regulation of defense response to virus by host	7.80E-03
	Transition metal ion binding	1.11E-02
	Negative regulation of cytokine production	3.17E-02
	Cytoplasmic pattern recognition receptor signaling pathway	3.38E-02
	Regulation of innate immune response	4.85E-02
	Establishment of viral latency	8.55E-02
	Positive regulation of interferonalpha production	9.86E-02
	Viral latency	9.86E-02