

Table SI. Top 24 genes with the most significant methylation changes.

Chromosome	Gene symbol	EnsembleID	Raw β -value ^a	
			MDS-L	MDS-L-DAC
Chr5	MIR143	ENSG00000208035	0.70	0.12
Chr11	OR8K5	ENSG00000181752	0.62	0.08
Chr11	OR52M1	ENSG00000197790	0.62	0.06
Chr22	APOBEC3B	ENSG00000179750	0.53	0.20
Chr5	PPP2R2B-IT1	ENSG00000249553	0.47	0.14
Chr5	PCDHB8	ENSG00000120322	0.50	0.16
Chr11	MMP10	ENSG00000166670	0.42	0.04
Chr12	HCAR3	ENSG00000255398	0.43	0.03
Chr3	TRAT1	ENSG00000163519	0.75	0.28
Chr11	OR5AP2	ENSG00000172464	0.76	0.28
Chr9	IL33	ENSG00000137033	0.72	0.26
Chr21	KRTAP11-1	ENSG00000182591	0.65	0.23
Chr1	S100A8	ENSG00000143546	0.78	0.42
Chr11	MS4A3	ENSG00000149516	0.81	0.32
Chr4	IGJ	ENSG00000132465	0.82	0.37
Chr4	ADH1B	ENSG00000196616	0.95	0.12
Chr1	FCGR3B	ENSG00000162747	0.89	0.53
Chr3	HTR3C	ENSG00000178084	0.91	0.50
Chr17	KRT17	ENSG00000128422	0.83	0.48
Chr17	GAST	ENSG00000184502	0.86	0.50
Chr22	RFPL1	ENSG00000128250	0.87	0.47
Chr6	MAS1	ENSG00000130368	0.95	0.57
Chr19	CEACAM3	ENSG00000170956	0.92	0.55
Chr9	FBP2	ENSG00000130957	0.92	0.57

^a β -value represents the proportion of DNA methylation with the DNA methylation level ranging from 0.0 (completely unmethylated) to 1.0 (fully methylated). MDS, myelodysplastic syndromes; MDS-L, MDS cell line; DAC, decitabine; Chr, chromosome.

Table SII. Top 35 promoter sites with the most significant methylation changes.

Chromosome	Gene symbol	Ensemble ID	Raw β -value ^a	
			MDS-L	MDS-L-DAC
Chr4	DDK2	ENSG00000155011	0.85	0.02
Chr7	CLEC5A	ENSG00000258227	0.98	0.12
Chr3	CSTA	ENSG00000121552	0.69	0.25
Chr11	MS4A3	ENSG00000149516	0.71	0.27
Chr15	SNORD115-10	ENSG00000201943	0.68	0.29
Chr2	IGKV1OR2-108	ENSG00000231292	0.68	0.34
Chr2	RASGRP3	ENSG00000152689	0.74	0.32
Chr12	FAM60A	ENSG00000139146	0.74	0.31
Chr12	SLC48A1	ENSG00000211584	0.77	0.25
Chr18	SERPINB3	ENSG00000057149	0.78	0.27
Chr7	ZAN	ENSG00000146839	0.75	0.40
Chr1	S100A8	ENSG00000143546	0.78	0.40
Chr21	KRTAP22-1	ENSG00000186924	0.81	0.44
Chr6	OR2H1	ENSG00000204688	0.92	0.56
Chr5	TSSK1B	ENSG00000212122	0.91	0.54
Chr14	TRAJ53	ENSG00000211837	0.90	0.56
Chr14	TRAJ54	ENSG00000211836	0.90	0.56
Chr5	EDIL3	ENSG00000164176	0.90	0.56
Chr1	FCGR3A	ENSG00000203747	0.89	0.53
Chr11	OR1S2	ENSG00000197887	0.90	0.53
Chr10	C10orf85	ENSG00000177234	0.96	0.56
Chr14	BMP4	ENSG00000125378	0.97	0.59
Chr2	IL36RN	ENSG00000136695	0.99	0.37
Chr11	NAV2-AS2	ENSG00000254453	0.65	0.12
Chr11	OR8K5	ENSG00000181752	0.62	0.08
Chr11	OR52M1	ENSG00000197790	0.62	0.06
Chr10	LIPN	ENSG00000204020	0.65	0.02
Chr10	MIR603	ENSG00000207930	0.65	0.03
Chr6	TMEM151B-SPATS1	ENSG00000272442	0.52	0.08
Chr7	SSPO	ENSG00000197558	0.58	0.23
Chr21	IFNGR2	ENSG00000159128	0.62	0.21
Chr11	CYB5R2	ENSG00000166394	0.43	0.04
Chr12	HCAR3	ENSG00000255398	0.43	0.03
Chr14	SNORD113-3	ENSG00000201700	0.44	0.02
Chr14	OR11H6	ENSG00000176219	0.43	0.01

^a β -value represents the proportion of DNA methylation with the DNA methylation level ranging from 0.0 (completely unmethylated) to 1.0 (fully methylated). MDS, myelodysplastic syndromes; MDS-L, MDS cell line; DAC, decitabine; Chr, chromosome.