

A

			All replicated DMCs	Replicated DMCs with decreased methylation	Replicated DMCs with increased methylation
Enhancer	H3K4me1	CD3+	1.26	1.13	1.65
		CD19+	1.36	1.32	1.45
Enhancer	H3K27ac	CD3+	1.05	0.75	1.96
		CD19+	0.96	0.84	1.30
Promoter	H3K4me3	CD3+	0.65	0.49	1.12
		CD19+	0.61	0.61	0.61
Transcribed Gene Body	H3K36me3	CD3+	1.46	1.42	1.56
		CD19+	1.53	1.40	1.93
Repressive	H3K27me3	CD3+	0.22	0.26	0.10
		CD19+	0.42	0.51	0.15
Heterochromatin	H3K9me3	CD3+	0.39	0.26	0.77
		CD19+	0.34	0.37	0.24
Open Chromatin	DHS	CD3+	0.90	0.71	1.47
		CD19+	0.84	0.82	0.89

B

CpG Island	0.16	0.16	0.14
Shore	0.98	1.08	0.69
Shelf	1.23	1.20	1.32
Open Sea	1.60	1.54	1.77

C

TSS1500	0.91	0.98	0.73
TSS200	0.47	0.5	0.37
5'UTR	1.02	1.02	1.02
First Exon	0.46	0.46	0.46
Gene Body	1.23	1.21	1.28
3'UTR	1.28	1.13	1.71
ncRNA	0.96	0.98	0.89
NA	1.00	0.99	1.01

Supplementary Figure S3 *Overlap of replicated differentially methylated CpG sites (DMCs, n=7,245) in the SLE case-control epigenome-wide association analysis (EWAS) with functional genomic regions.* Heat-map illustrating the functional genomic distribution of all associated autosomal DMCs (first panel), of the DMCs with decreased methylation in SLE (second panel) and of the DMCs with increased methylation in SLE (third panel) annotated a) in relation to chromatin states in CD19+ B cell and CD3+ T cell reference data sets, b) in relation to CpG island context and c) in relation to gene region. The color scale indicates fold-enrichment (red) or fold-depletion (blue) of DMCs in each functionally annotated region. Bold numbers represent annotations to which the DMCs significantly differed compared with the distribution of probes on the HM450k array (post-QC probe set) applying a Bonferroni corrected χ^2 -test p-value < 0.005.

DHS, DNase I hypersensitivity site; DMC, differentially methylated CpG site in the case-control analysis; NA, probe without annotation to any defined gene property; ncRNA, non-coding RNA; TSS1500, 1500 bp upstream of transcription start site (TSS); TSS200, 200 bp upstream of TSS; UTR, untranslated region.