



**Supplementary Figure S3**  
**Functional regional distribution.** Heat maps of the functional regional distribution of differentially methylated CpG sites (DMCs) in the association analysis of patients with SLE compared to patients with pSS. The plots show the functional genomic distribution of all associated DMCs (n=2,244; left panel), of the DMCs with increased methylation in SLE compared to pSS (n=242; middle panel) and of the DMCs with decreased methylation in SLE compared to pSS (n=2,002; right panel) annotated **(A)** in relation to the CpG island context, **(B)** in relation to exonic and intronic genomic regions, **(C)** in relation to functional gene regions and **(D)** in relation to genomic overlap with chromatin states in reference CD3<sup>+</sup> T cells and CD19<sup>+</sup> B cells. 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 differ compared with the distribution of all probes on the HM450k array (post-QC probe set) ( $\chi^2$ -test p<0.0035).

Abbreviations: TSS1500, 1500 bp upstream of transcription start site (TSS); TSS200, 200 bp upstream of TSS; ncRNA, non-coding RNA; NA, probe not annotated to a defined gene property or region; n.a., not applicable