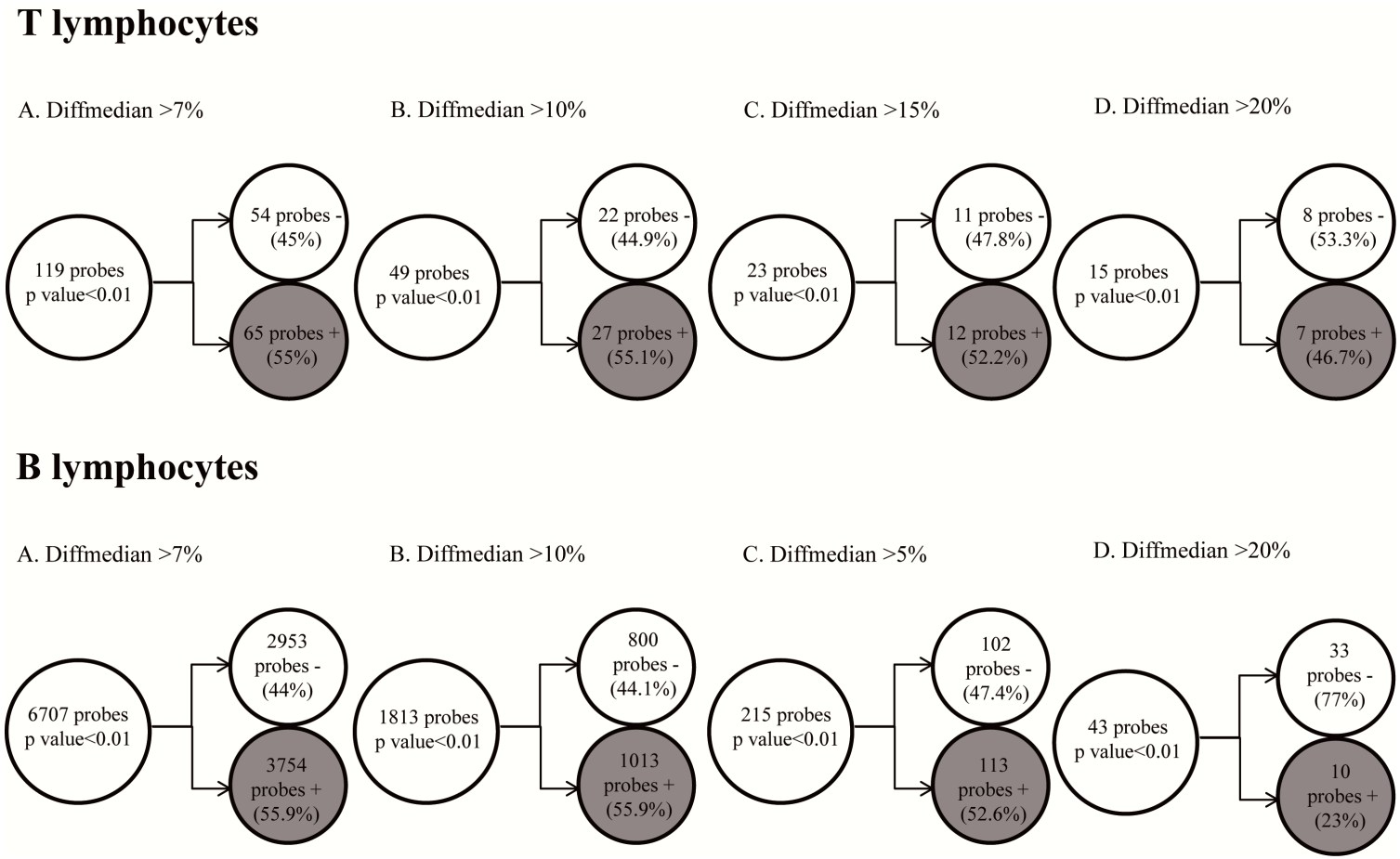
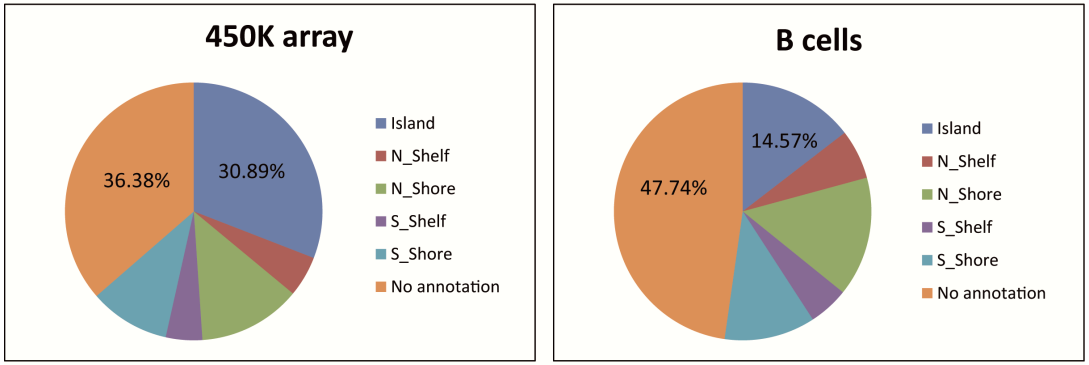
Supplementary figure S1. Numbers of probes with a median methylation difference of at least 7%, 10%, 15% or 20% and p<0.01 in purified T or B lymphocyte from pSS patients compared to controls. Hypermethylated probes are denoted with '+'; hypomethylated probes with '-'.

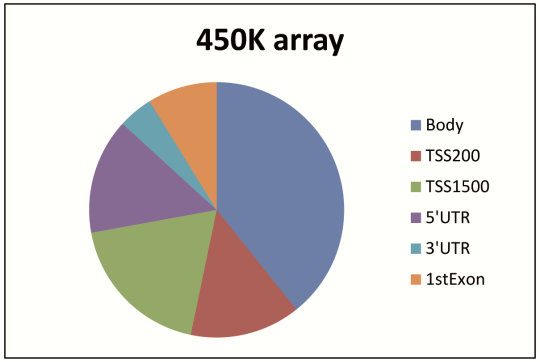


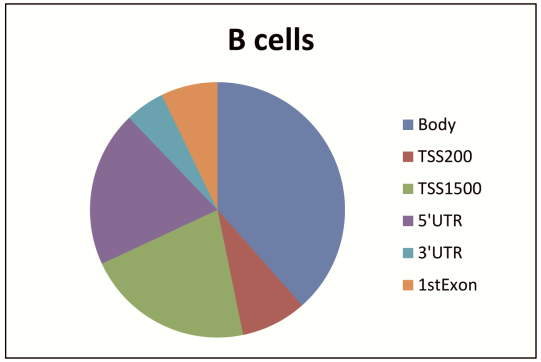
Supplementary figure S2. The distribution of differentially methylated probes found in B lymphocytes in relation to the UCSC annotated CpG islands (A) and the distribution of differentially methylated probes found in B lymphocytes (B) in function of their position in the gene compared to the all probes present on the 450K array.

A.

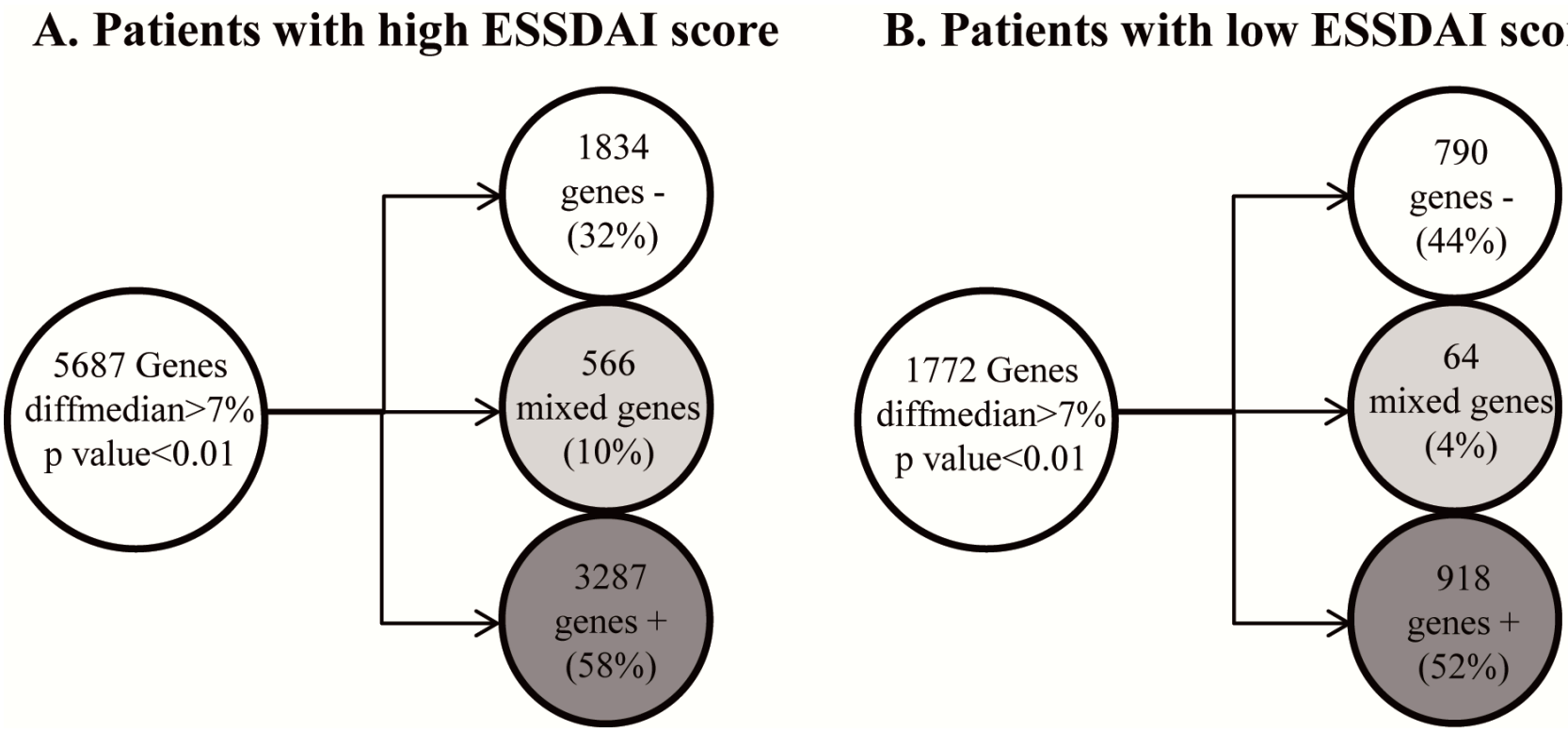


B.





Supplementary figure S3. Association of DNA methylation differences with ESSDAI score in B lymphocytes from pSS patients. Genes with at least one CpG site showing at least a 7% median methylation difference and a $p<0.01$ in B lymphocytes from pSS patients with high ESSDAI score (A) and low ESSDAI score (B) compared to the control cohort, respectively;



Supplementary figure S4. Association of DNA methylation differences with autoantibody producing activity in B lymphocytes from pSS patients. Genes with at least one CpG site showing at least a 7% median methylation difference and a p<0.01 found in B lymphocytes from pSS patients with anti-SSA+ and anti-SSB+ (A), anti-SSA+ and anti-SSB- (B) and patients with anti-SSA- (C) compared to the control cohort, respectively.