Supplementary Figure 8

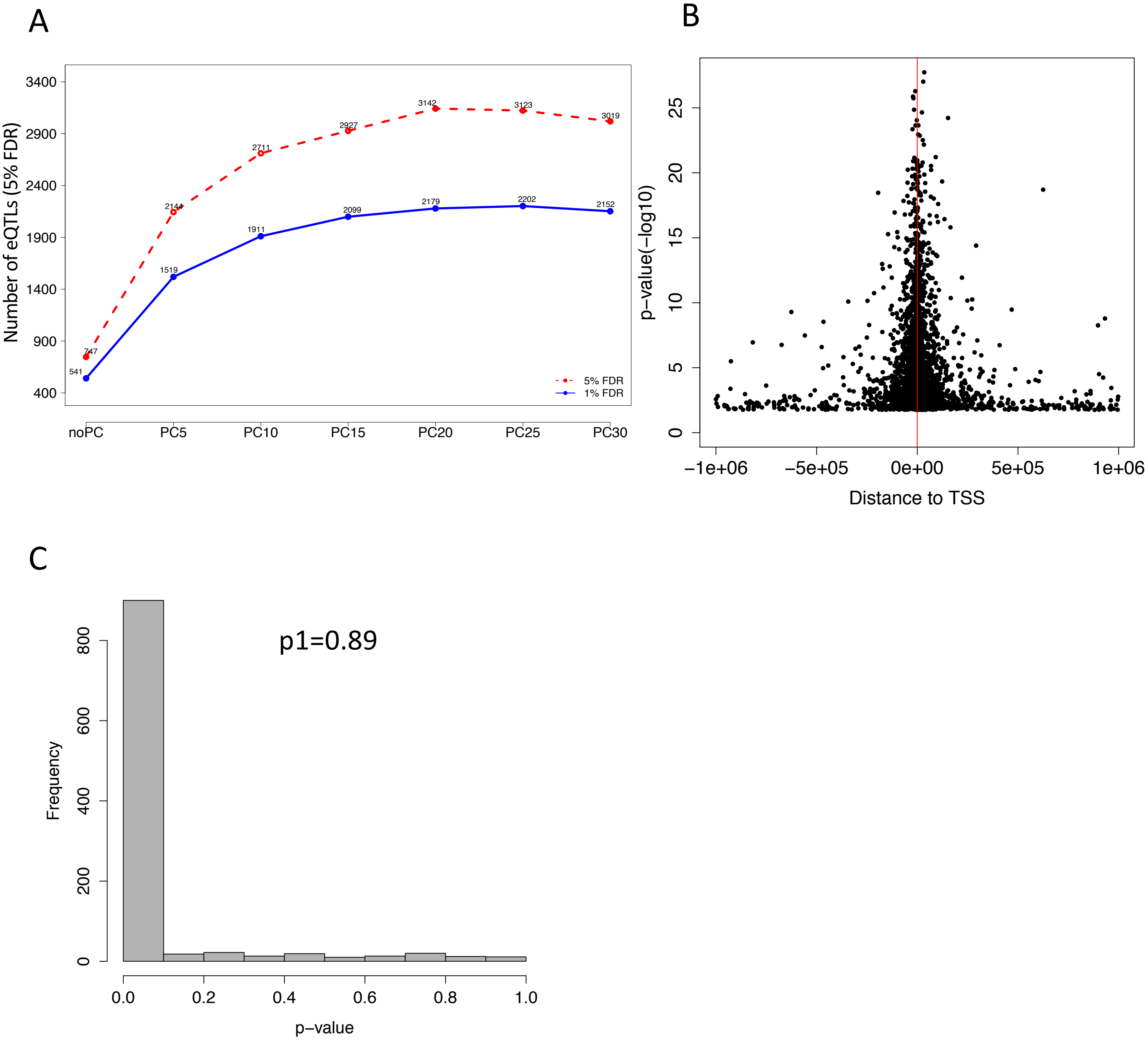

Figure S8. Expression-QTL analysis in SLE blood transcriptome

(A) Number of detected *cis*-eQTLs using 142 SLE individuals at 5% FDR (red dotted line) and at 1% FDR (blue line) without correction and by increasing number of principal components (PCs). The highest number of eQTLs (3142, 5% FDR) is detected by correcting for the first 20 PCs. **(B)** Distance of cis-eQTLs from the Transcriptional Start Site (TTS) of the genes. The significance of the associations is plotted on the *y*-axis (–log10 p-value). Highly significant eQTLs are clustered close to TSS. **(C)** Replication of significant eQTLs identified in our SLE dataset with the results from a blood RNA-seq study in healthy donors (n=384 samples).[41] The two sets of eQTLs replicated well (π1=0.89), suggesting the lack of SLE specificity.