Supplementary Figure 2

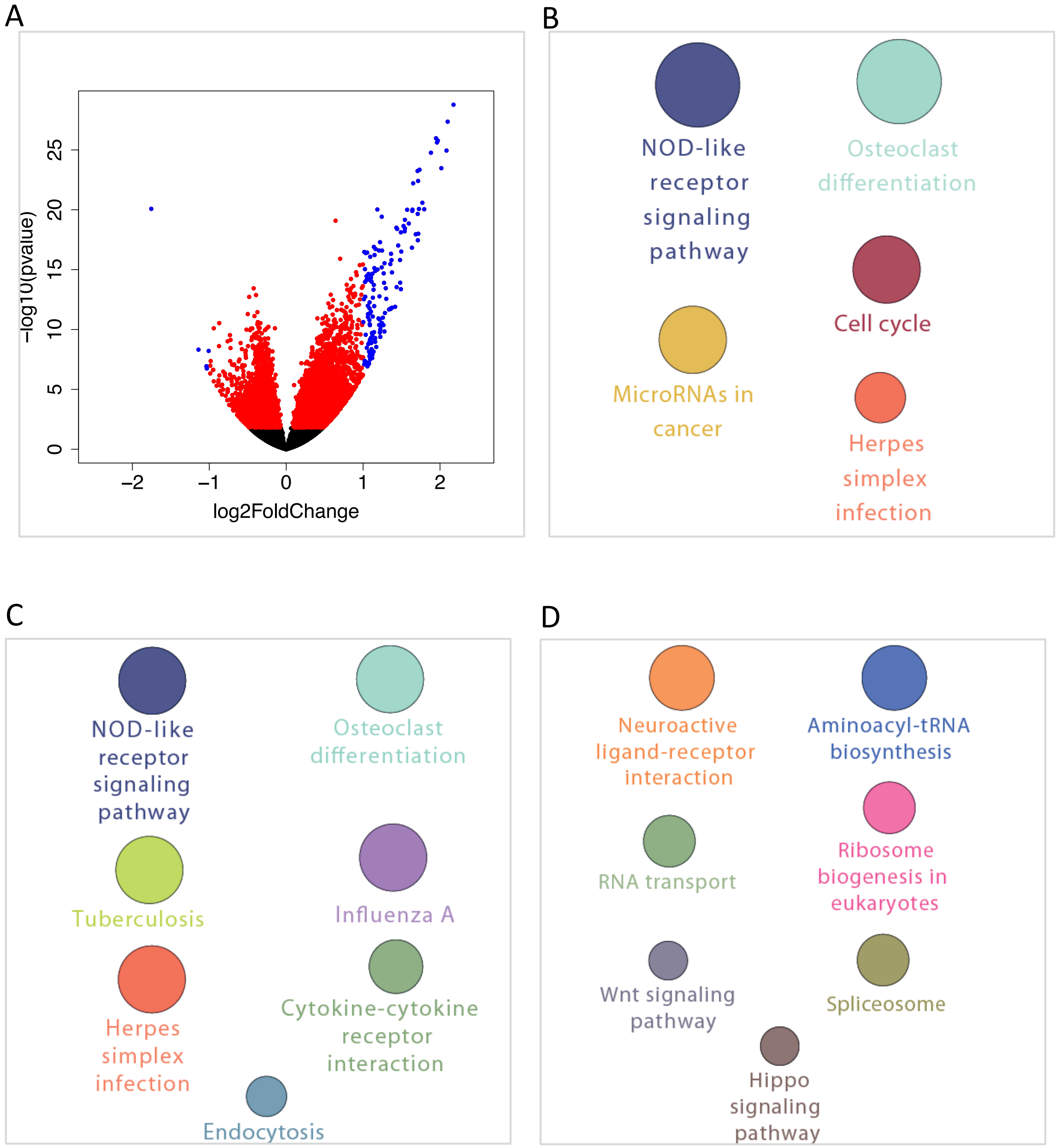

Figure S2. Differential gene expression and pathway analyses in the peripheral blood of SLE patients compared to healthy individuals

(A) Volcano plot of DEGs between SLE and healthy individuals. The *x*-axis indicates the log2-fold change (SLE over healthy) while the *y*-axis indicates the –log10 of the Benjamini-Hochberg–adjusted p-value. Black dots indicate genes that do not pass the 5% FDR threshold of statistical significance, red dots indicate genes that do pass the 5% FDR threshold of statistical significance, and blue dots indicate genes that pass the significance threshold and have log2-fold change >1. Up-regulated genes (n=3977) outnumber down-regulated (n=2753) genes in SLE versus healthy individuals and demonstrate higher statistical significance. **(B)** Pathway enrichment analysis with all DEGs. Each circle represents a significantly enriched pathway. The size of the circle represents higher enrichment of the specific pathway. The enrichment p-values were calculated by a two-sided hypergeometric test and corrected for multiple testing with Bonferroni. The threshold for Bonferroni corrected p-values was set to 0.05. **(C)** Pathway enrichment analysis for the up-regulated DEGs in SLE. **(D)** Pathway enrichment analysis for the down-regulated DEGs in SLE.