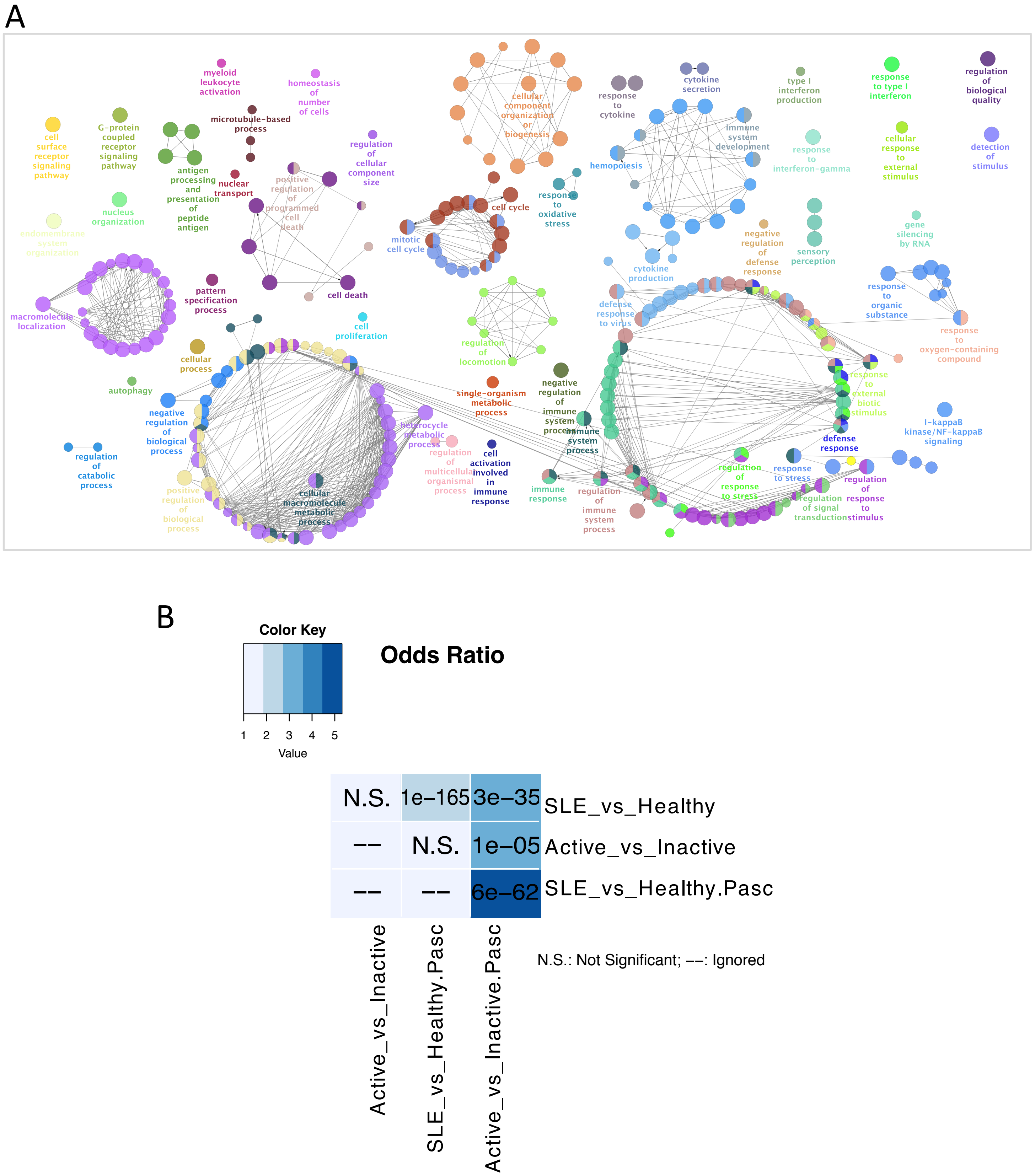
Supplementary Figure 3



	Active_vs_Inactive	SLE_vs_Healthy.Pasc	Active_vs_Inactive.Pasc
SLE_vs_Healthy	N.S.	1e−165	3e−35
Active_vs_Inactive	--	N.S.	1e−05
SLE_vs_Healthy.Pasc	--	--	6e−62

Figure S3. Mechanistic map of the biological regulation in SLE and comparison of differentially expressed genes with external data.

(A)For all DEGs, functionally-grouped networks of enriched GO term categories were generated. Each node represents a GO term and the size of each node represents the enrichment significance. The connection between nodes is based on Cohen's kappa statistic (≥0.4) which depends on the gene sharing between nodes. For each network, only the most significant node is labelled. (B) Comparison of differentially expressed genes with data from a paediatric SLE study (Banchereau, …, Pascual; Cell 2016). Fisher's exact p-values of overlap are plotted in accordance with the odds rations denoted as heatmap.