Supplementary Figure 5

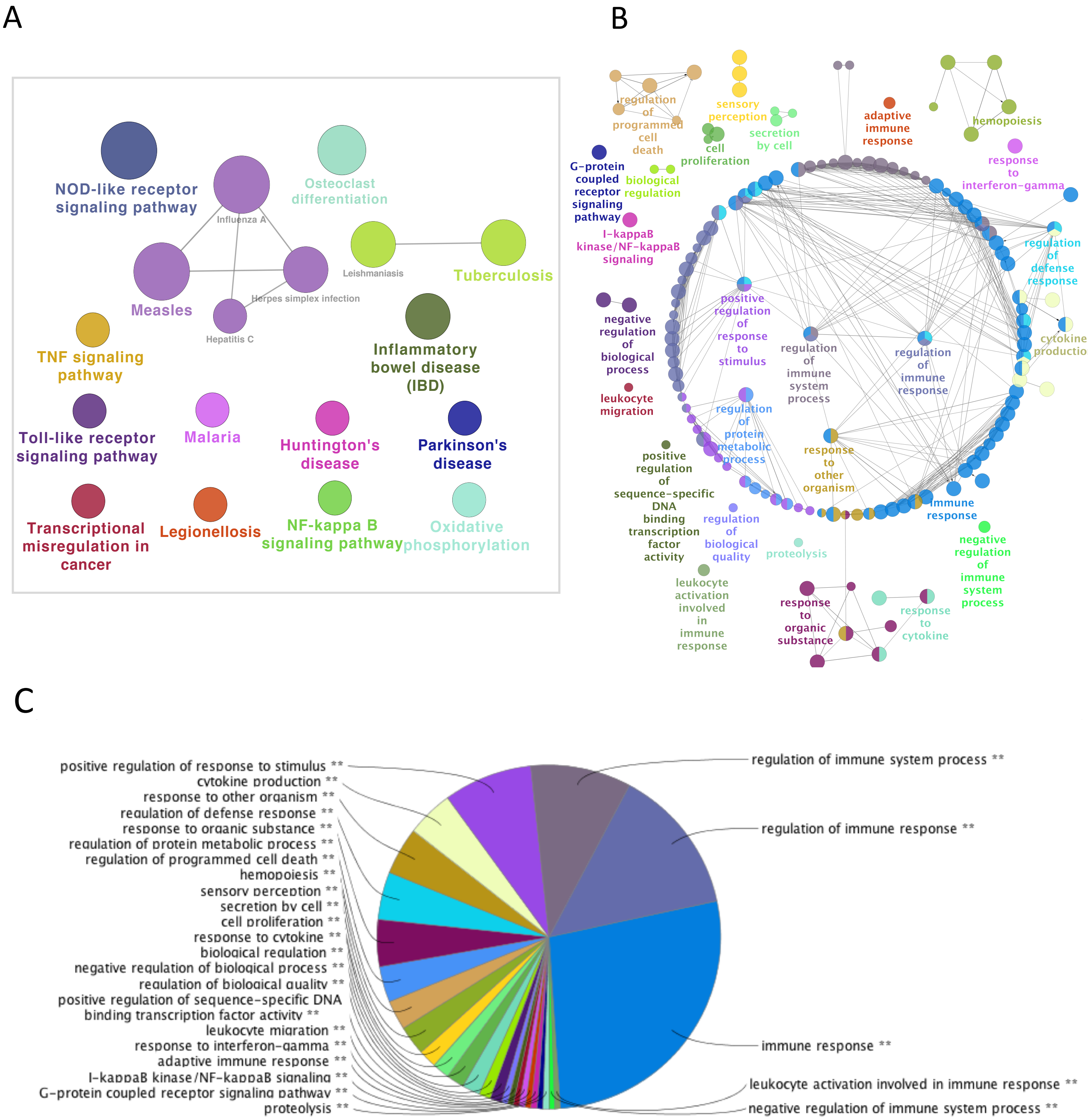

Figure S5 . Enriched pathways and Mechanistic map of the biological regulation of the *susceptibility* SLE signature.
(A) Pathway enrichment of the 2726 DEGs (5% FDR) defining the *susceptibility* disease signature. Each circle represents a significantly enriched pathway; the size of the circle represents the degree of enrichment. Enrichment p-values were calculated by a two-sided hypergeometric test and corrected for multiple testing with Benjamini-Hochberg. The threshold for corrected p-values was 0.05 (5% FDR) **(B)** 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) that depends on the gene-sharing between nodes. For each network, only the most significant node is labelled .**(C)** Pie chart representation of the mechanistic map. More than half of the networks are related to immune system, responses and regulation.