



Figure 1. Gene expression profile of lamina propria (LP) plasma cells (PC) compared with bone marrow (BM) and splenic (SPL) B220 negative PCs. PC subsets were sorted from BM, SPL and LP samples collected from wild type C57Bl/6 mice. Data represents the mean expression of three individual mice. (A) 3658 genes were determined to be differentially expressed between B220 negative PCs from BM, SPL and LP which clustered into 2 major and 2 minor groups. (B) Cluster 1 consisted of 1296 genes expressed more highly LP PCs than BM and SPL PCs. This group displayed enrichment of gene ontology (GO) terms including inflammation and apoptosis. The top five by enrichment score are shown. (C) Cluster 2 consisted of 2289 genes more highly expressed in SPL and BM PCs than in LP PCs. This cluster was enriched for GO terms including protein and RNA processing. The top five results are shown. Cluster 3 consisted of 36 genes expressed preferentially in SPL samples. (D) Cluster 4 consisted of 37 genes that were enriched GO terms including host defense to bacteria. GSEA comparing LP PCs against both SPL and BM PCs was performed and network topology analysis (not shown) displayed major networks centered on cytokine signaling (E) enriched in LP PCs and centered on mRNA processing (F) enriched in BM and SPL.