

**Table S2. Gene set enrichment analysis (GSEA).** GSEA was performed in which the genes with differential expression were sorted on the basis of gene function using Ingenuity Pathway Analysis software. The top 5 canonical pathways identified by the program are shown. The ratio shows the number of differentially expressed genes as a proportion of the total number of genes in that pathway.

<b>Pathway name</b>	<b>p-value</b>	<b>Ratio</b>
PI3K Signaling in B Lymphocytes	2.70E-07	8/146 (0.055)
B Cell Development	2.70E-05	4/37 (0.108)
Altered T Cell and B Cell Signaling in Rheumatoid Arthritis	6.07E-05	5/92 (0.054)
B Cell receptor Signalling	7.33E-05	6/157 (0.038)
Primary Immunodeficiency Signaling	1.26E-04	4/63 (0.063)