Supporting Information

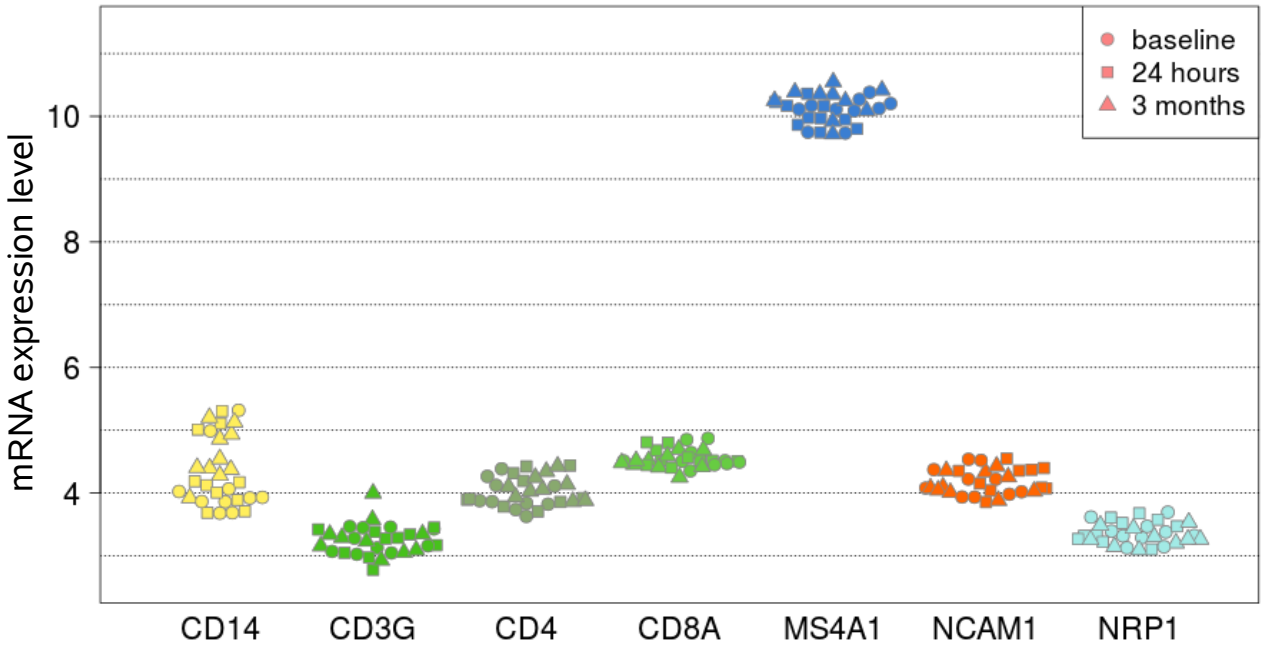

Figure S1: Purity of the isolated B cells. We visualized the measured transcript levels of seven selected genes, which are relatively specifically expressed in different blood cell types, namely CD14 (monocytes), CD3G (T cells), CD4 (T helper cells), CD8A (cytotoxic T cells), MS4A1 (B cells), NCAM1 (natural killer cells) and NRP1 (dendritic cells). The processed probe set signals for each gene are in log2 scale. MS4A1 was expressed at high levels (range, 9.72-10.55) in all 30 samples of CD19+ cells, whereas the other genes were expressed at low levels (≤5.32).

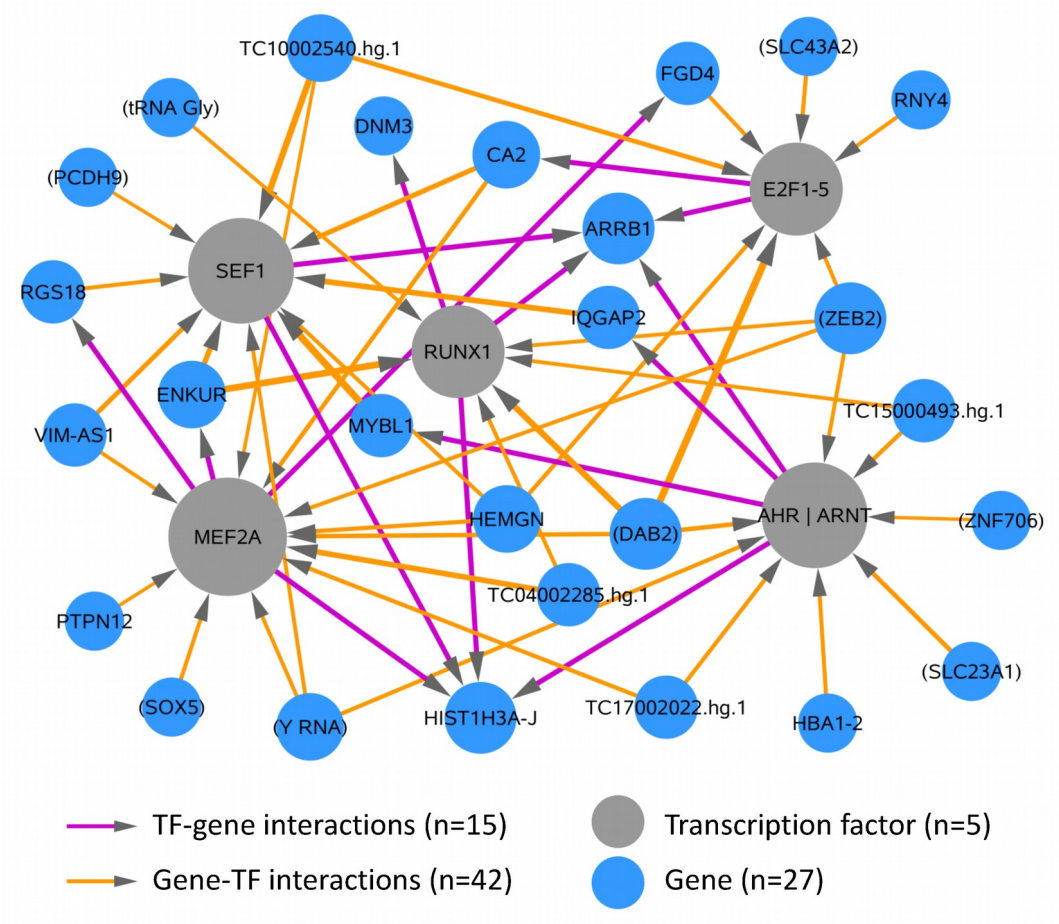

Figure S2: Network of fingolimod-responsive genes in B cells. The gene regulatory network was reconstructed by applying the TILAR algorithm (http://www.leibniz-hki.de/en/tilar.html) on the list of genes, which were differentially expressed in CD19+ B cells during fingolimod therapy (Table 2). TILAR infers a network of interactions between genes and transcription factors (TF) based on gene expression data and predicted TF binding sites (TFBS). The size of the nodes corresponds to their degree of connectivity. TILAR = TFBS-integrating least angle regression.