Supplementary Figure to Jernås et al. ” Differential expression of T-cell genes in blood and bone marrow between ITP and controls” 
(Thromb Haemost 2013; 109.1)

Suppl. Figure 1: Differentially expressed blood-derived and bone marrow-derived T-cell genes between ITP patients and controls. In the DNA microarray analysis we identified 1554 differently expressed genes in T-cells from blood and 976 in the bone marrow (Q<0.05; PLIER) between chronic ITP patients and healthy controls. From these data we performed functional enrichment analysis base on GO classifications (GO Biological process, enrichment \( P<10^{-5} \)) and constructed a heat map. The enrichment P-values are shown in red for up-regulated gene ontology terms and blue for down-regulated gene ontology terms in patients compared with controls. The number in brackets indicates the number of genes within a biological process.