SUPPLEMENTARY INFORMATION

RNA isolation from Peyer's patch lymphocytes and mononuclear phagocytes to determine gene expression profiles using nanostring technology

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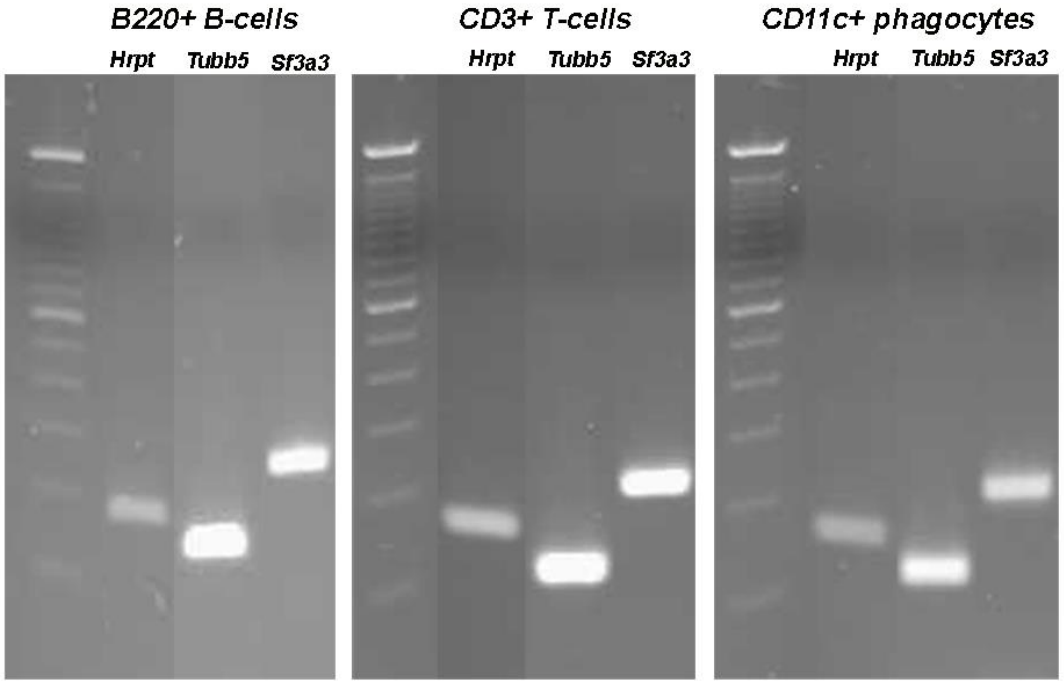

Figure S1. Specific gene targets in all cell types are tested by RT-PCR. Three housekeeping genes from the immune profiling codesets Hprt, Tubb5 and Sf3a3 were amplified in B-cells, T-cells and CD11c$^+$ phagocytes to ensure amplification efficiency and specificity. The primer sequences that were used to detect Hprt (forward) 5'AAGCTTGCTGGTGAAAAGGA3' (reverse) 5'TTGCGCTCATCTTAGGCTTT3'. For Tubb 5 we used (forward) 5'GGGAGGTGATAAGCGATGAA3'and (reverse) 5'CCCAGGTTCTAGATCCACCA3'. For Sf3a3 we used (forward) 5'GCCAAAAATCCCAAGTCAAA3' and (reverse) 5'GCAGGTTCTTGGGGTTGTAA3'.

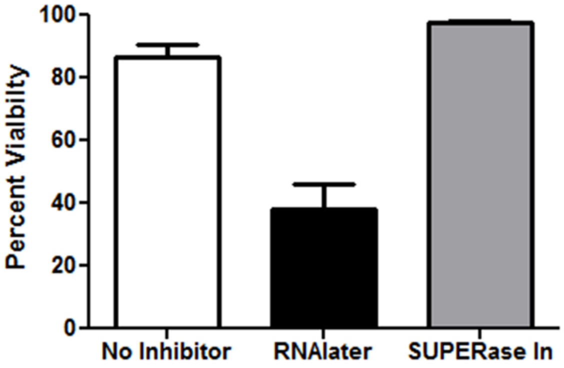

Figure S2. Percent viability of PP single cell suspensions. Viability of single cell suspensions from PPs was measured using trypan blue exclusion; percent viability was determined using the Countess Cell Counter.

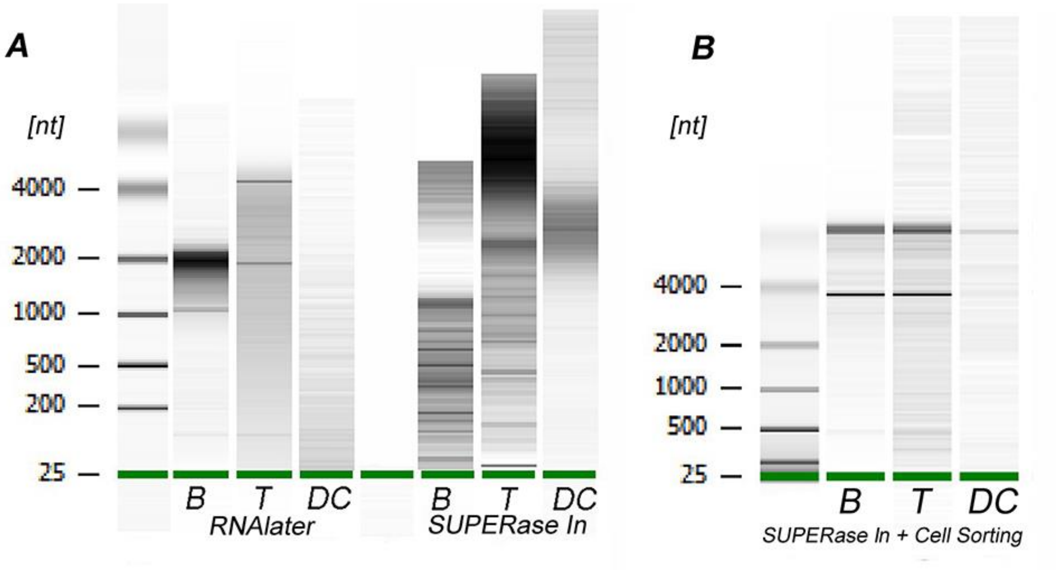

Figure S3. Stabilization of PP RNA is important for nanostring-based methods. A. Isolation of PP RNA from B-cells, T-cells and CD11c$^+$ phagocytes required optimization using popular RNA stabilization reagents such as RNAlater (lanes 2-4), SUPERase In (lanes 6-8). RNAlater yielded low quantity and quality of RNA. **B.** Combination of SUPERase In and on column DNA digestion with DNAse I (lanes 2-4). Treatment with SUPERase In and on column DNA digestion with DNAse I yielded defined bands.

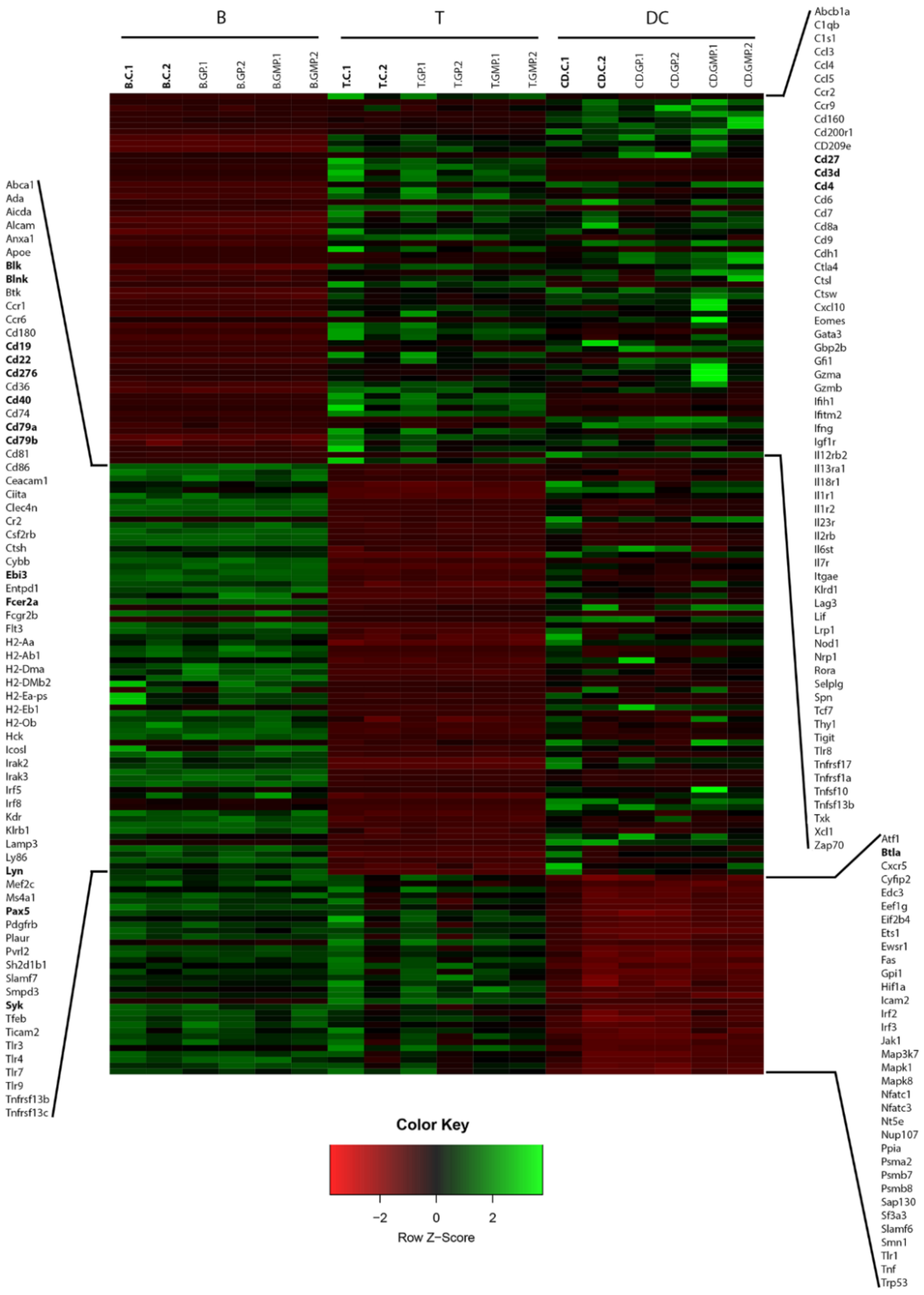

Figure S4. Heatmap compares gene expression profiles of downregulated genes in B-cells, T-cells and DCs. Z-scores in this heatmap show that a set of genes are downregulated specifically per cell type. Red indicates downregulation, while green indicates upregulation. Genes highlighted in bold show specificity per cell type. C denotes control, and GP and GMPs indicate treatment with particles. Data is presented in duplicate.