

## Appendix

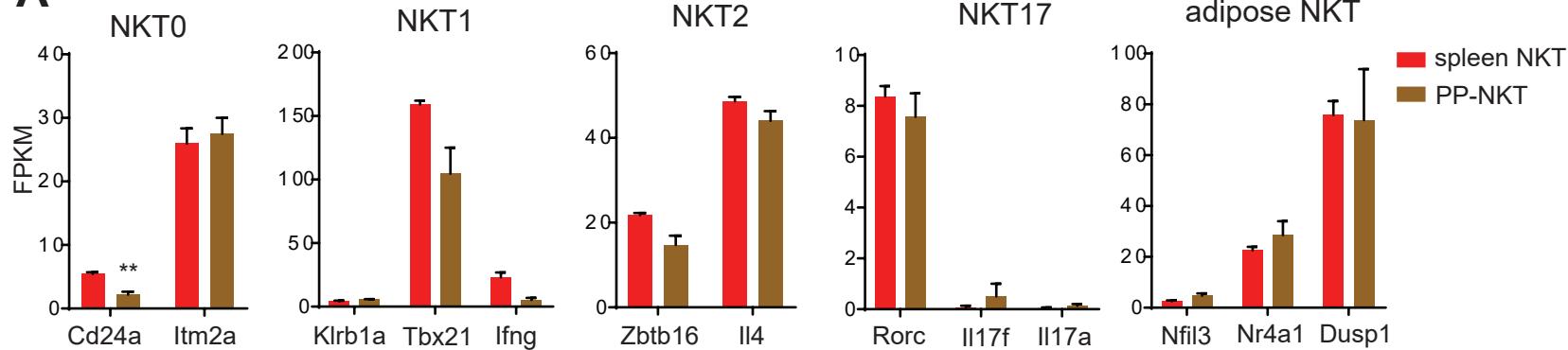
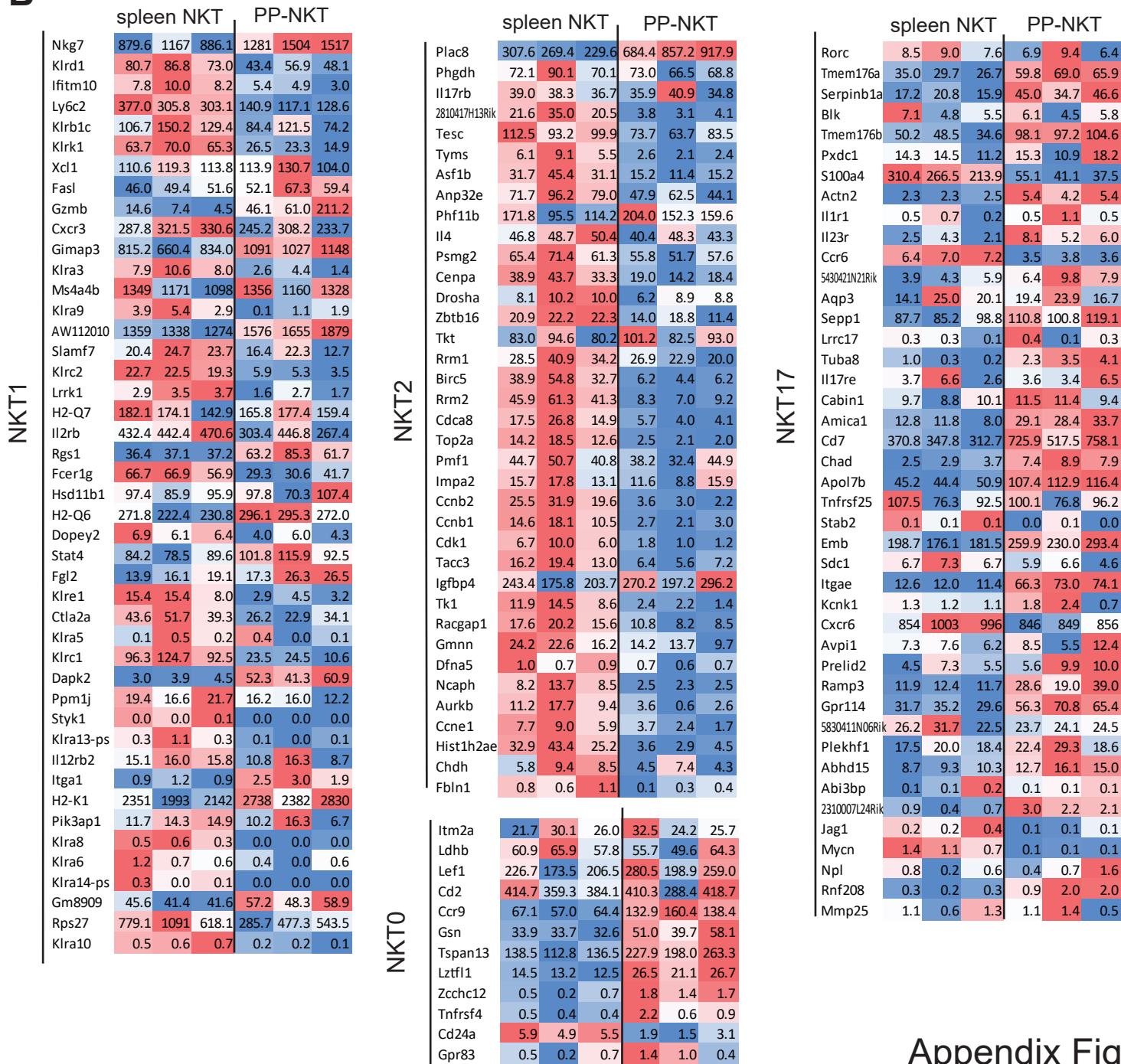
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**Figure S1. PP-NKT are not enriched for gene signatures consistent with NKT0, NKT1, NKT2, NKT17, or adipose NKT cells.** (A) Expression levels of signature genes associated with the indicated NKT subsets. FPKM values are from bulk RNAseq of sorted spleen or PP-NKT populations from V $\alpha$ 14 TN mice. Values are means of 3 biological replicates; error bars are SEM. (B) Heatmap showing expression of gene sets associated with NKT0, NKT1, NKT2, or NKT17 cells as reported in (Engel, Seumois et al., 2016).

### Reference:

Engel I, Seumois G, Chavez L, Samaniego-Castruita D, White B, Chawla A, Mock D, Vijayanand P, Kronenberg M (2016) Innate-like functions of natural killer T cell subsets result from highly divergent gene programs. *Nat Immunol* 17: 728-39

**A****B**

Appendix Figure S1