Fig. S3

A Principal Component Analysis

PC1 vs PC2

PC1 vs PC3

Species
● MM
▲ NM-R

Organ
■ Spleen
■ lsSpleen
■ ssSpleen

B Venn Diagram of all deregulated genes

C Peripheral BC1/BC2 Gene Signature

Spleen Lymphoid Gene Signature

D Peripheral Granulocyte Gene Signature

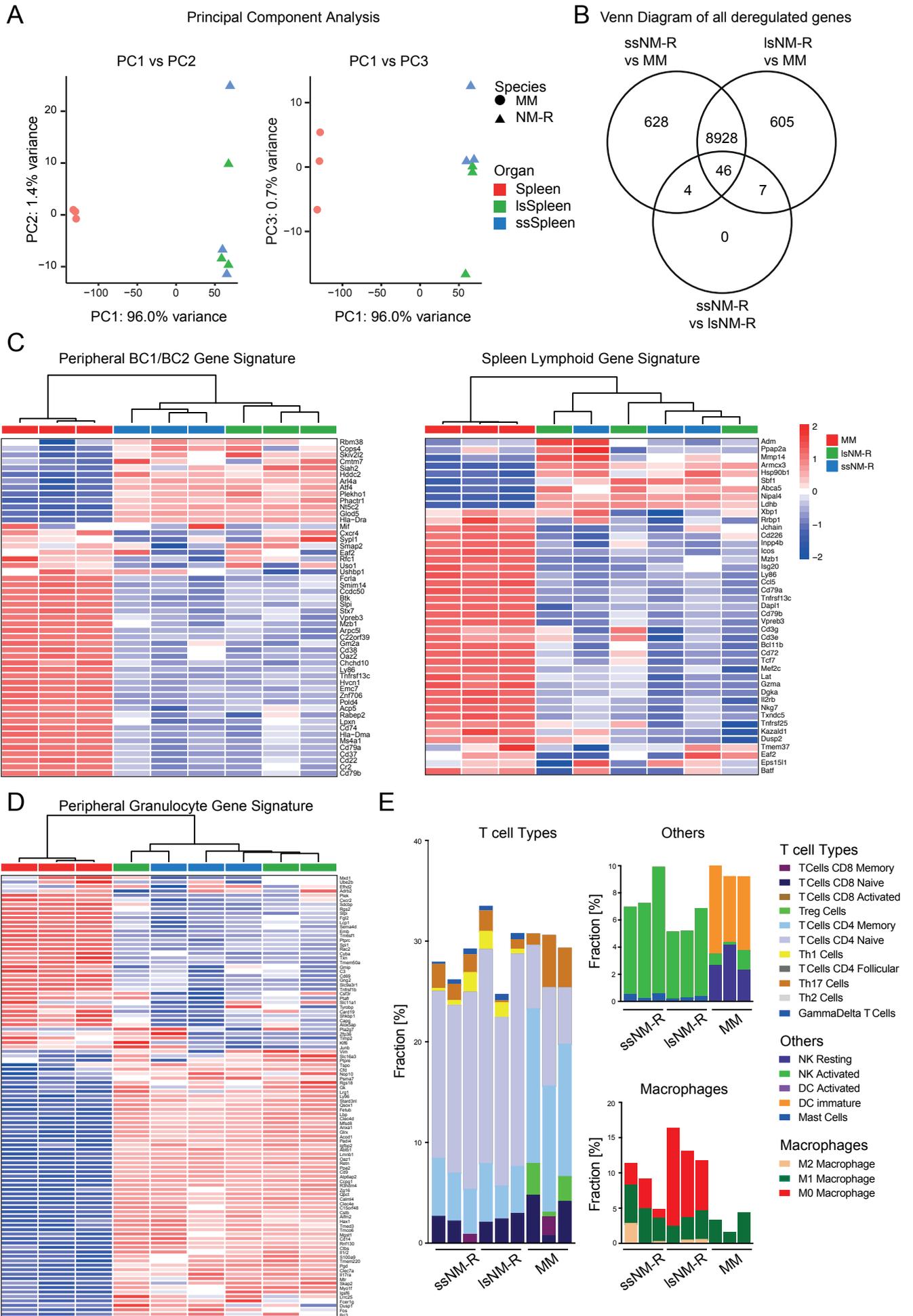**E** T cell Types   Others

Macrophages

Fig. S3: Transcriptomic analysis of NM-R and mouse spleen.

(**A**) Principal component analysis (PCA) based on the top 3000 most variably expressed genes. Principal component (PC): 1 versus 2 (left panel) and 1 versus 3 (right panel) are displayed. (**B**) Venn diagram of differentially regulated genes in the spleen of ssNM-R, lsNM-R compared to mouse or to each other. (**C**) Heatmap of peripheral BC1/BC2 gene sets associated with B cells from [1] (left panel) and of lymphoid gene sets from [2] (right panel) for the spleen of mouse, ssNM-R and lsNM-R. (**D**) Heatmap of peripheral granulocyte genes from [1] for the spleen of mouse, ssNM-R and lsNM-R. **(E)** CIBERSORT prediction of fraction of T cell types, macrophage types (M1, M2 and M0) and other cell types (DC: dendritic cells, mast cells and NK: natural killer cells) found in the spleen of ssNM-R, lsNM-R in comparison to mouse. n = 3 per group. Data is based on RNAseq and bars represent fraction in %. MM: mouse (*Mus musculus*).