



### Supplemental Figure 1. Heatmap illustration of differentially expressed genes

Spinal cords from Oligo2-Cre RiboTag EAE mice at disease onset and naïve control mice were homogenized, and mRNA was isolated via immunoprecipitation with anti-HA antibodies targeting ribosomes. The purified mRNAs underwent RNA-Seq using an Illumina NovaSeq sequencer, and the resulting data were analyzed. The heatmap depicts differentially expressed genes categorized as follows:

A) Cytokine receptors and Toll-like receptors (TLRs).

B) Chemokine and chemokine receptors.

C) IFN- $\beta$  response genes.

D) IFN- $\gamma$  response genes. Within the GO biological process category (Panel A-D).

E) Venn diagram of IFN- $\gamma$  and IFN- $\beta$  response genes.  $n = 4/\text{group}$ . Related to Figure 2.