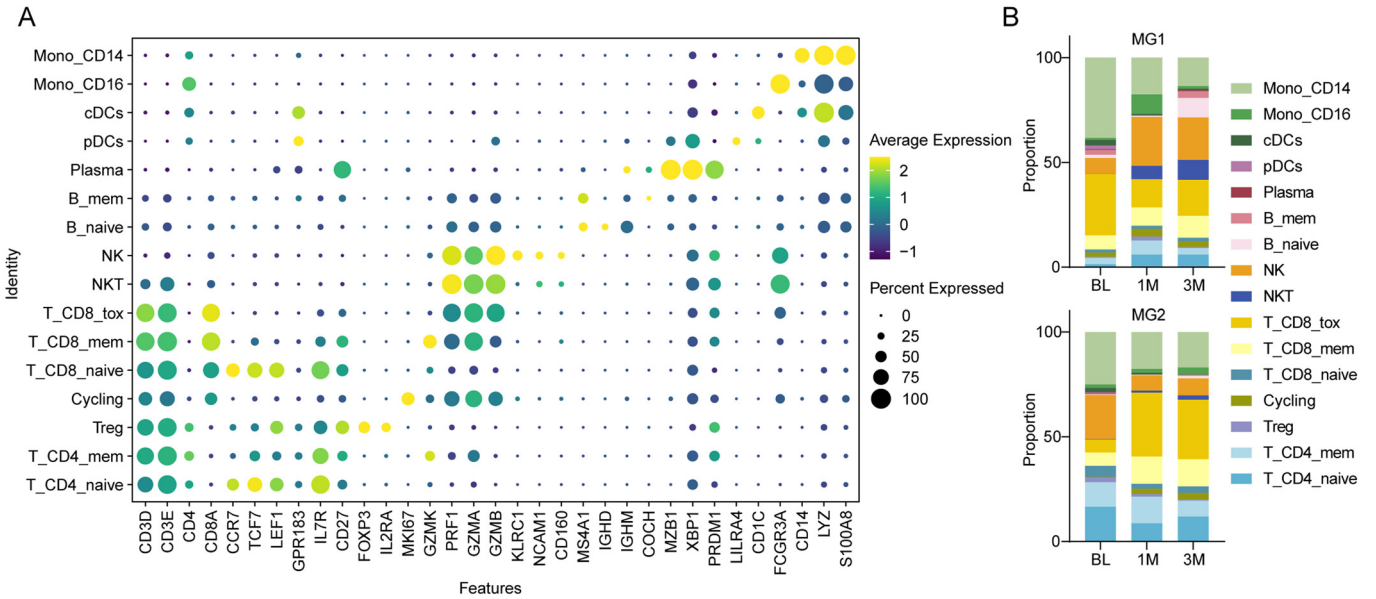


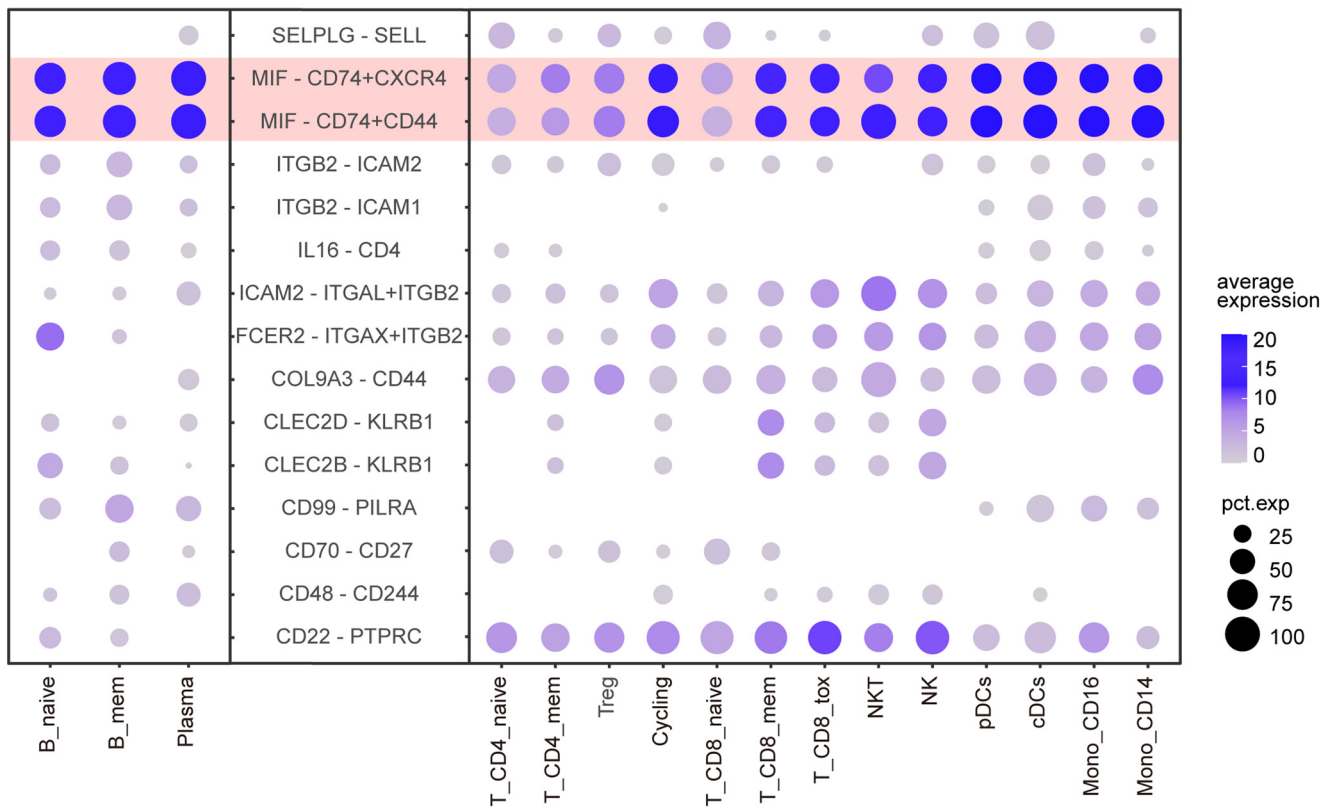
# Expanded View Figures



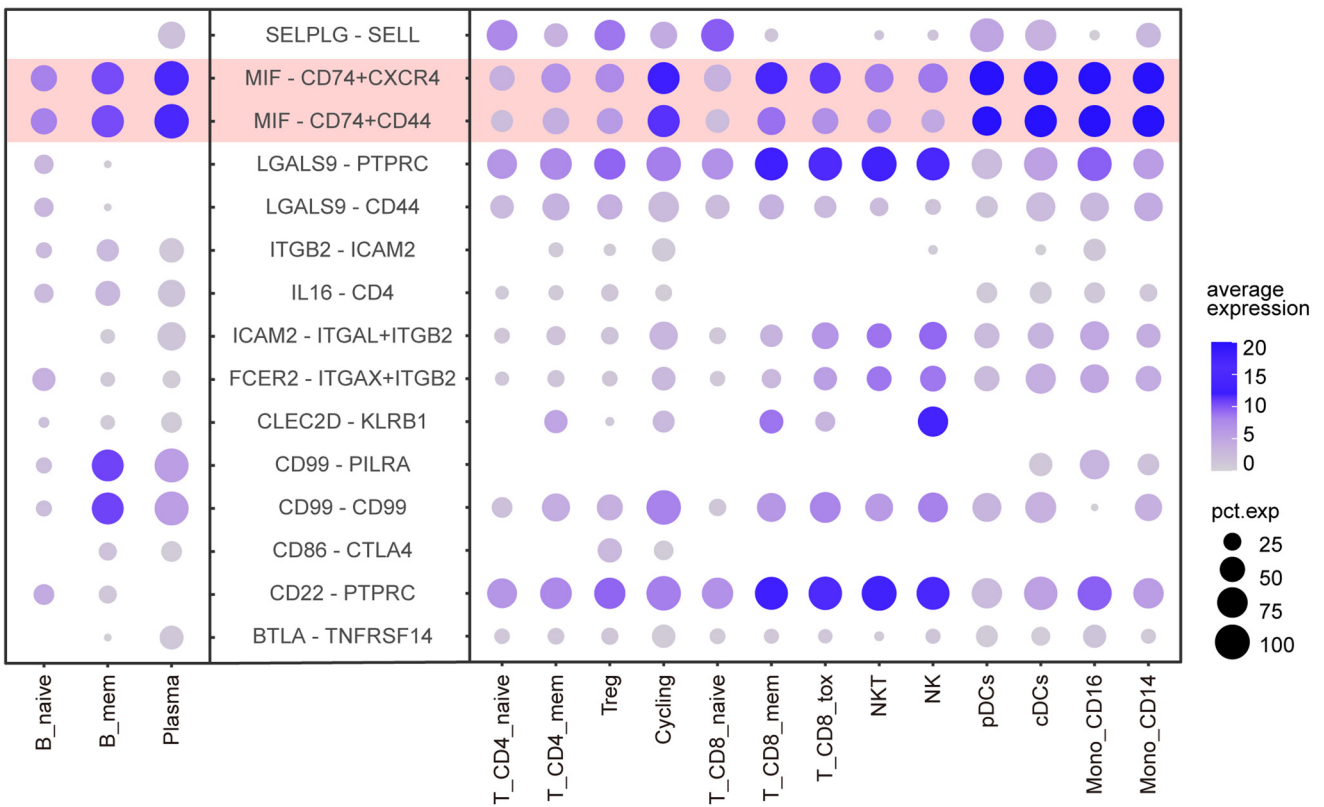
**Figure EV1. Additional single-cell transcriptional features of patients with myasthenia gravis treated with CAR-BCMA T-cell therapy.**

(A) Dot plot showing cell clusters denoted by gene expression of known markers. (B) Bar plots showing the frequency of cell subsets in individual patient at indicated time points.

A

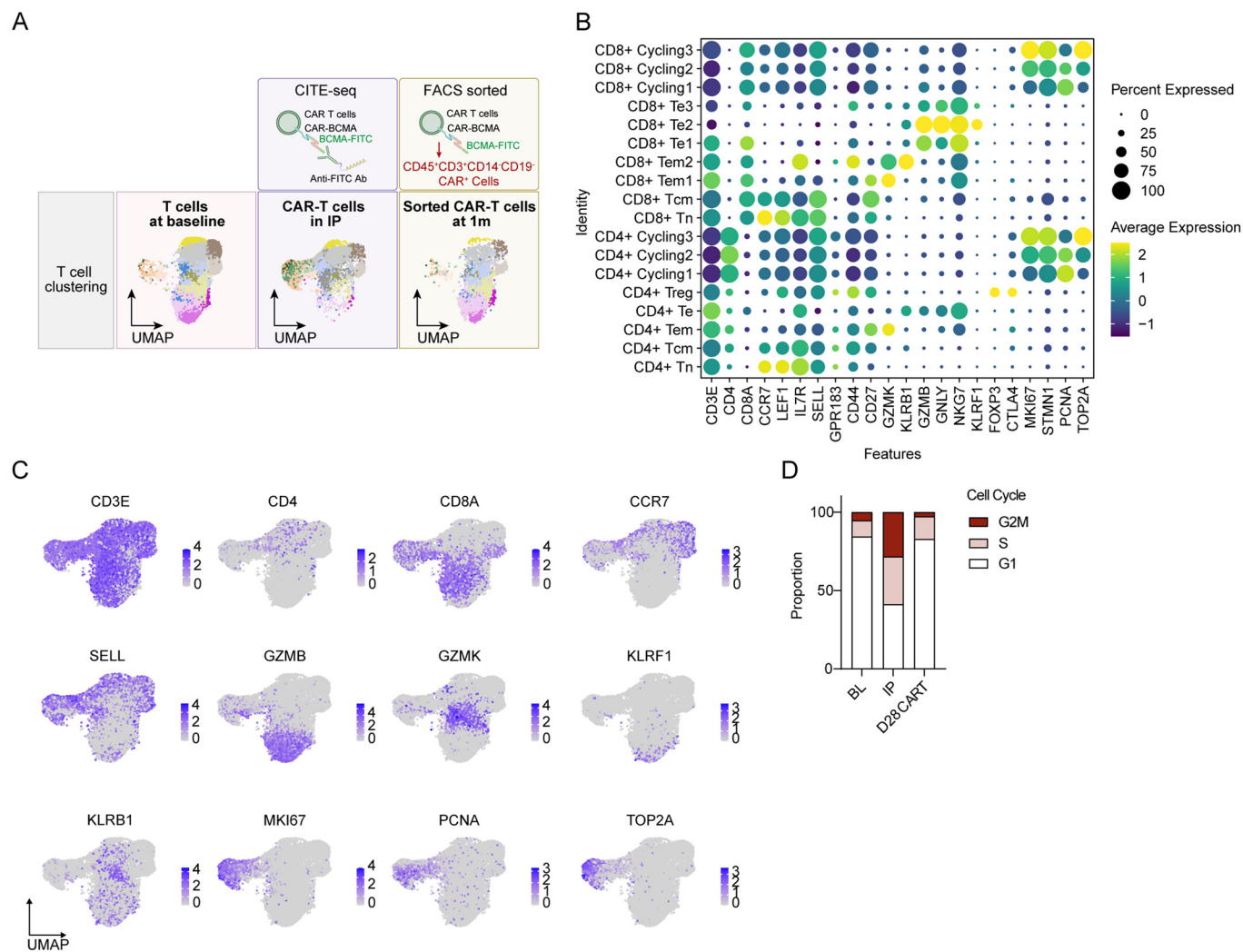


B



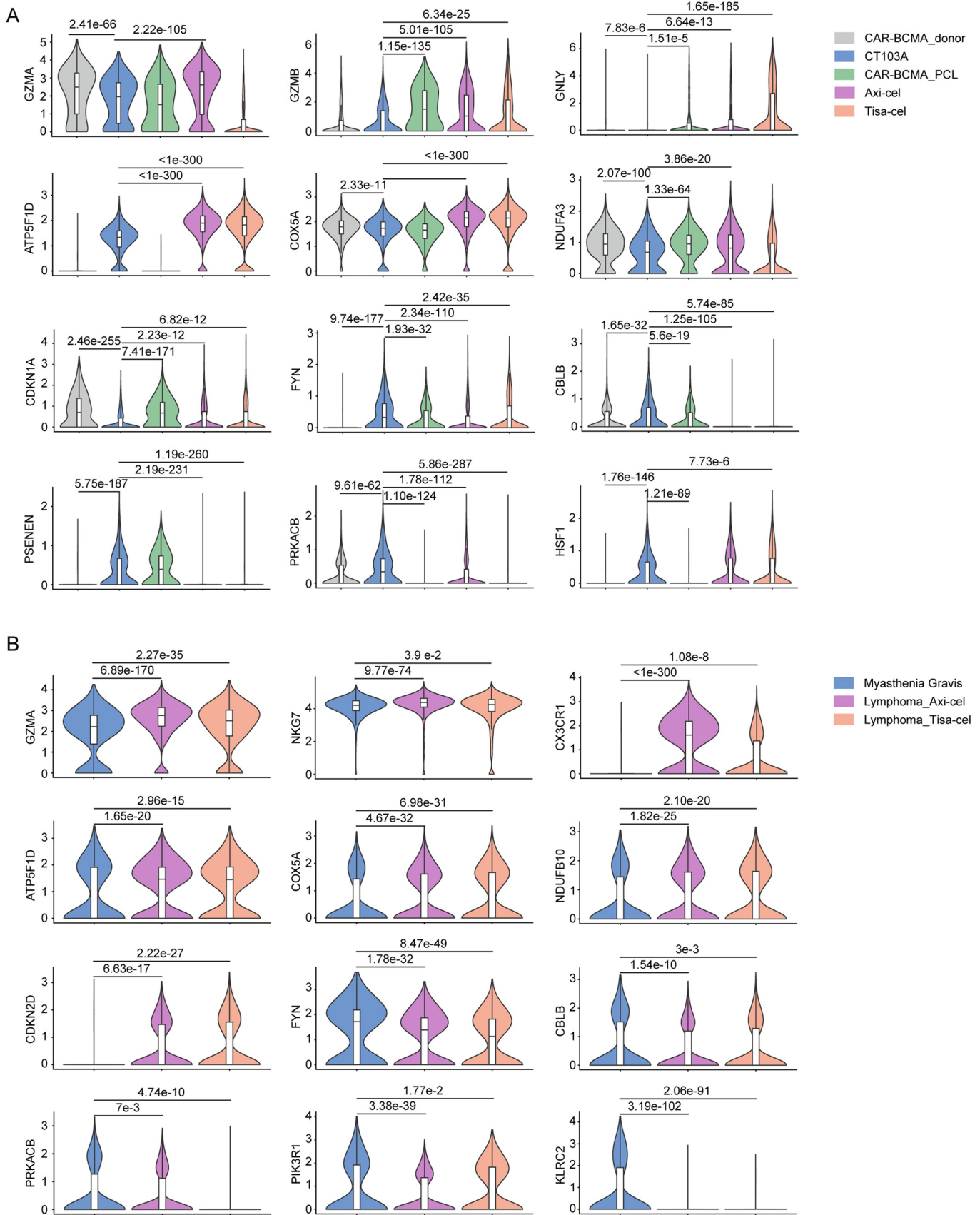
**Figure EV2. Additional ligand-receptor interaction analysis between immune cells.**

Gene expression dot plot of ligand-receptor expression. Left, expression in B-cell subsets; right, expression in other immune cell types. Shown are the Top15 interactions between B-cell subsets and other immune cell types with communication probabilities in (A) MG-1, (B) MG-2 at baseline.



**Figure EV3. Expression of canonical markers identifies behavior of CAR-T cells in patients with myasthenia gravis.**

(A) Schematic illustration of cellular indexing of transcriptomes and epitopes by sequencing (CITE-seq) strategy used to detect the CAR on the T-cell surface, and flow cytometry to sort CAR-T cells in vivo at 1 month post infusion (see “Methods” for details). UMAP plots of T cells colored by different cell cluster and clone size. (B) Dot plots showing gene expression of known markers for T-cell and CAR T-cell subclusters. (C) UMAP plots indicating RNA expression of *CD3E*, *CD4*, *CD8A*, *CCR7*, *SELL*, *GZMB*, *GZMK*, *KLRF1*, *KLRB1*, *TOP2A*, *MKI67*, and *PCNA*. (D) Bar plots showing the frequency of cells in S phase or G2/M phase by cell cycle scoring (see “Methods” for details).



◀ **Figure EV4. Expression of indicated genes identifies characteristics of CD8<sup>+</sup> Te cells (Baseline) and CD8<sup>+</sup> cycling CAR-T cells (IP) in patients with myasthenia gravis.**

(A) Violin plots illustrating indicated genes in Fig. 5B, and representing the distribution of expression across each product. CT103A,  $N = 4044$  cells; CAR-BCMA\_donor,  $N = 4739$  cells; CAR-BCMA\_PCL,  $N = 2111$  cells; Axi-cel,  $N = 11,392$  cells; Tisa-cel,  $N = 16,348$  cells. Boxes show median, Q1 and Q3 quartiles and whiskers up to 1.5 $\times$  interquartile range. Pairwise comparisons were performed using a two-sided Wilcoxon rank-sum test with a Bonferroni correction. (B) Violin plots illustrating indicated genes in Fig. 5C, and representing the distribution of expression across each cohort. Myasthenia Gravis,  $N = 2898$  cells; Lymphoma\_Axi-cel,  $N = 7123$  cells; Lymphoma\_Tisa-cel,  $N = 4857$  cells. Boxes show median, Q1 and Q3 quartiles and whiskers up to 1.5 $\times$  interquartile range. Pairwise comparisons were performed using a two-sided Wilcoxon rank-sum test with a Bonferroni correction.