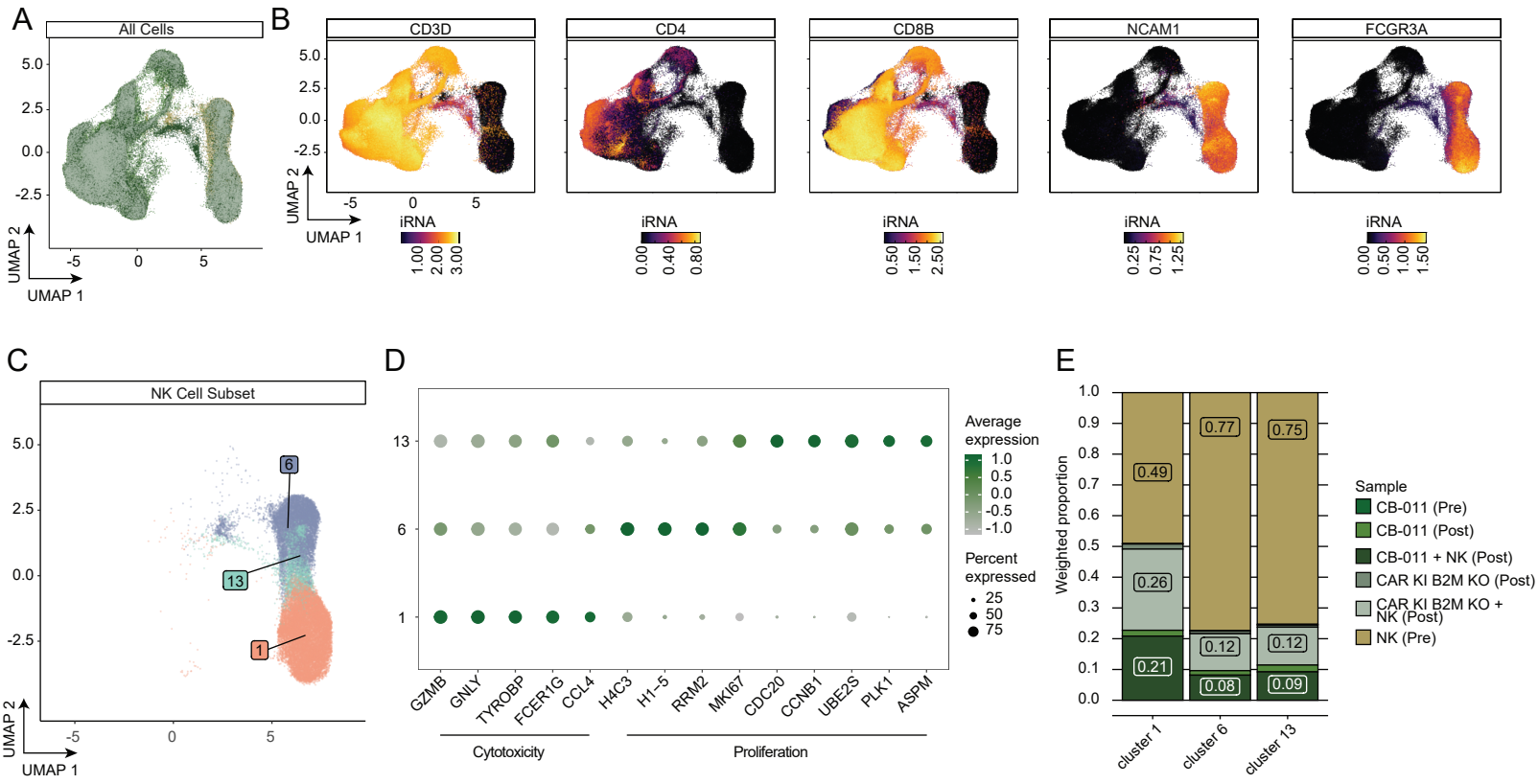
Figure S8. CB-011 immune-cloaking armoring strategy reduced NK cell proliferation and CAR+ T cell stress signatures.



(A) UMAP plot of scRNA-Seq analysis of all cells from an *in vivo* study of CB-011 or CAR KI B2M KO cells with NK cells. CB-011 (CB-011 IP) or CAR KI B2M KO cells were injected with (CB-011 + NK *in vivo*, CAR KI B2M KO + NK *in vivo*) or without (CB-011 only *in vivo*, B2M KO only *in vivo*) NK cells (NK IP), and NK T cells were harvested from spleens 4 days later. (B) UMAP plots colored by expression of the indicated genes. Dimensional reduction of all cells in the dataset broadly separated cells into CD4/8 T cells, NK T cells, and NK cells. (C) UMAP plots colored by subset on NK cells and colored by unbiased clustering identities. Unbiased clustering of cells identified 3 major populations of NK cells. (D) Dot heatmap visualization of the top 5 marker genes for each of the indicated NK cell clusters. The size of the dots represents the proportion of cells in the indicated cluster which expressed the indicated gene. The color of the dots indicates the scaled log-normalized RNA expression of the indicated gene. Cluster 1 represents activated/cytotoxic NK cell signatures, and Cluster 6 represents proliferative NK cells. (E) Bar plots demonstrating the weighted proportion (corrected for the total number of cells from that sample in the dataset, see Methods) of each sample type in the indicated NK cell clusters. All clusters showed an enrichment for CAR KI B2M KO *in vivo* condition relative to CB-011.

B2M, beta-2 microglobulin; CAR, chimeric antigen receptor; CD, cluster of differentiation; iRNA, MAGIC imputed RNA expression; IP, intraperitoneal; KI, knock-in; KO, knockout; NK, natural killer; scRNA-Seq, single-cell RNA sequencing; UMAP, uniform manifold projection.