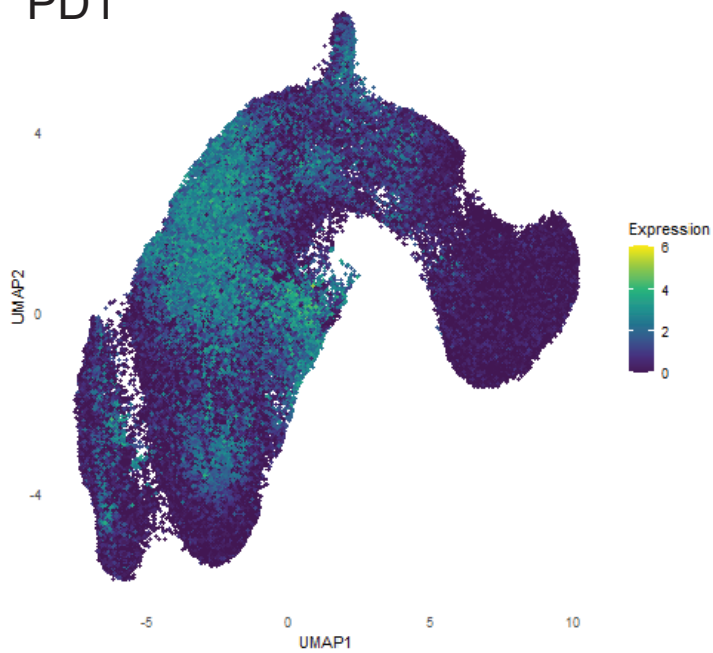
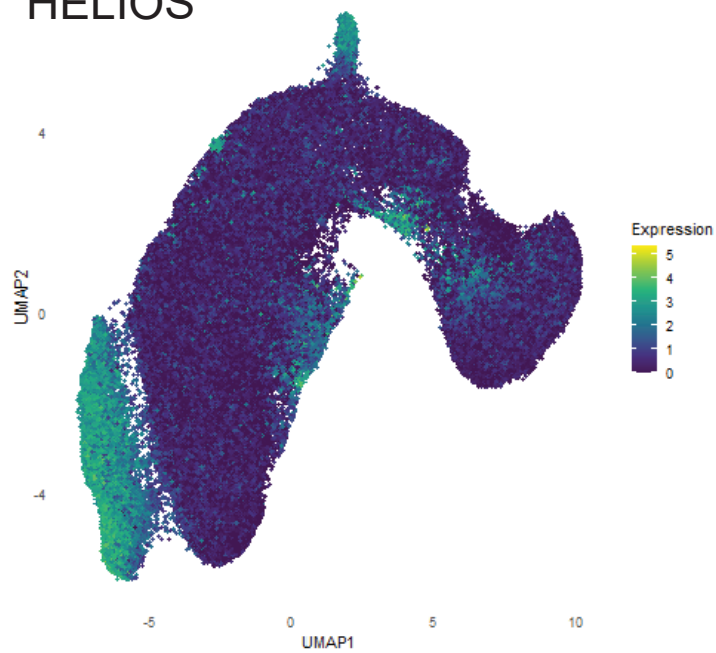


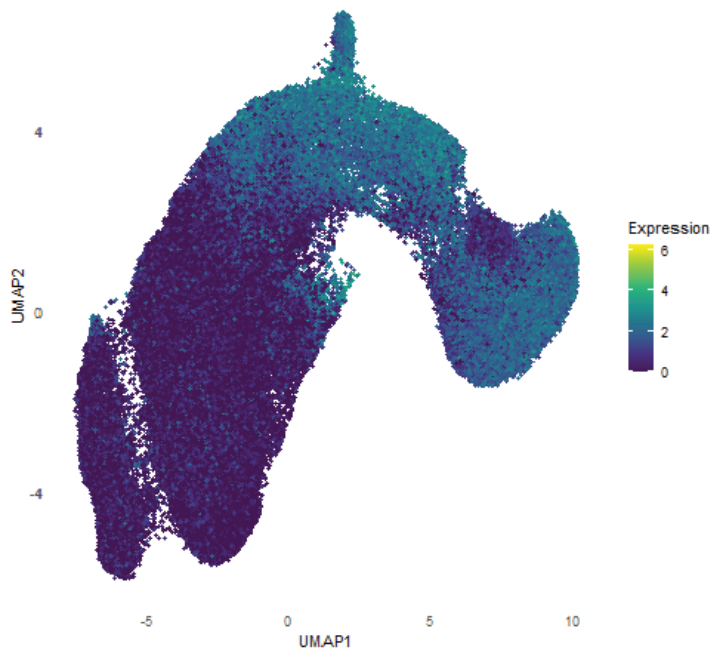
PD1



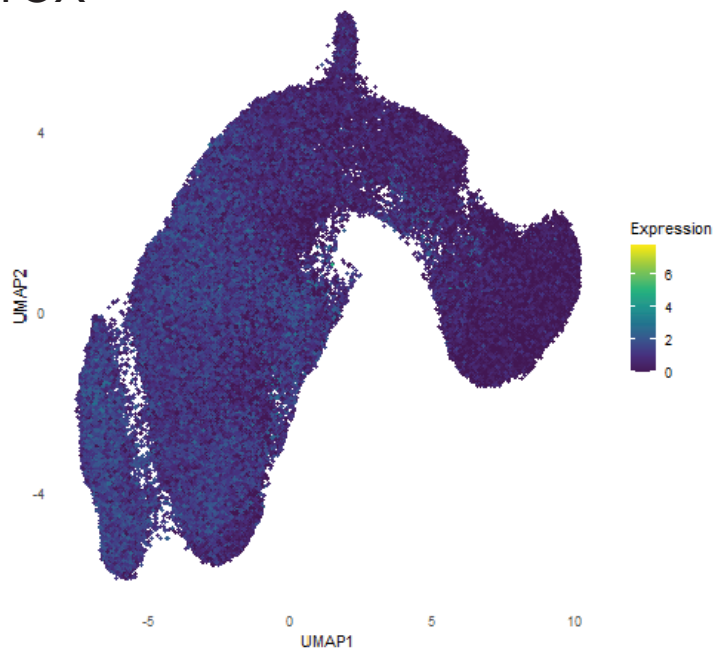
HELIOS



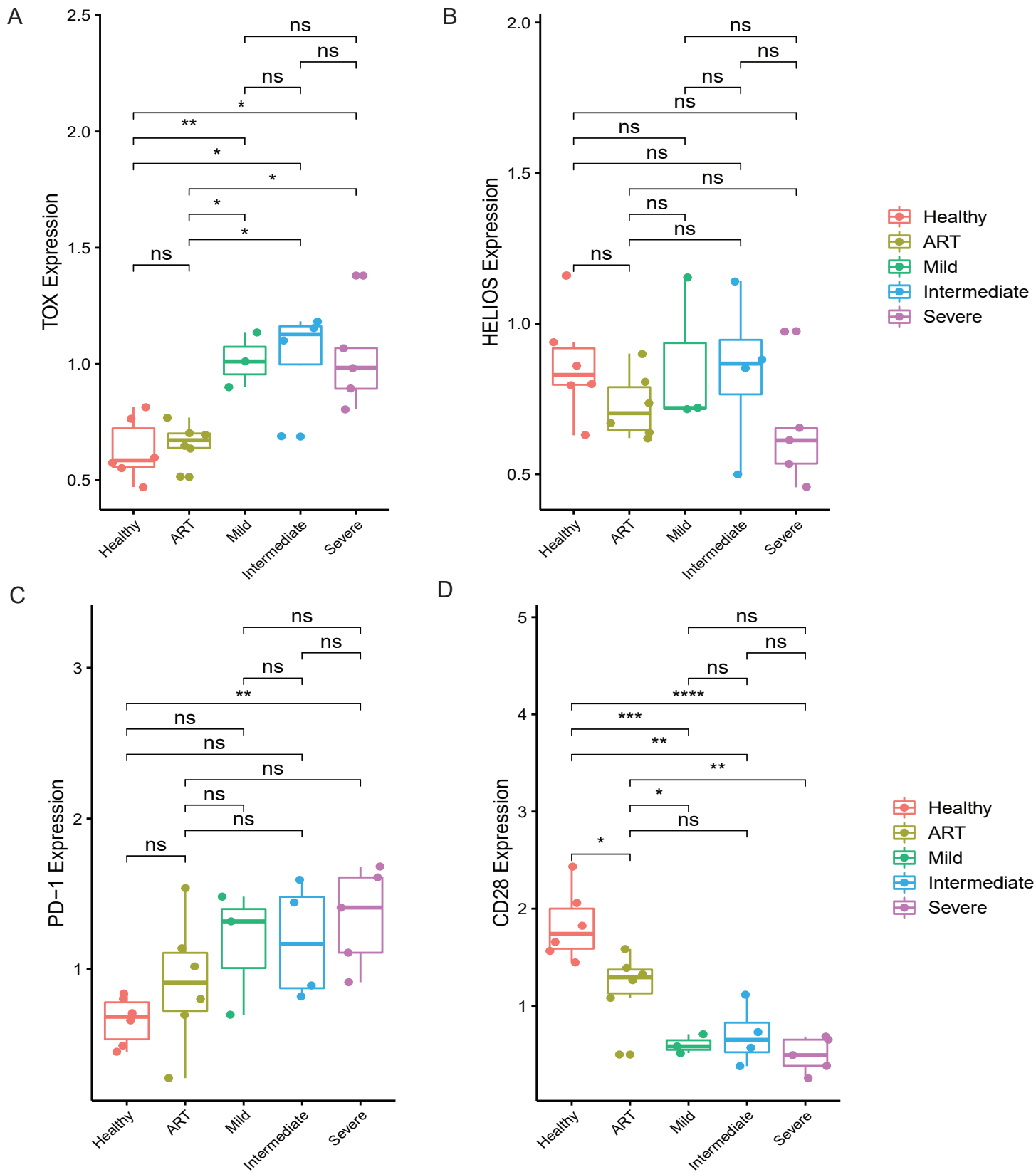
CD28



TOX

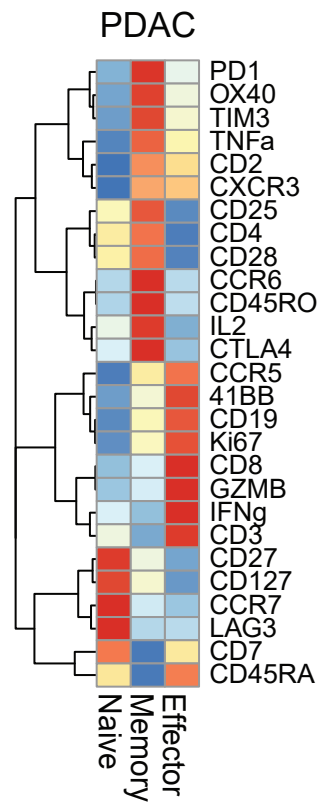


Supplemental Figure 1. UMAP overlaid with expression of exhaustion markers PD-1, HELIOS, TOX and activation marker CD28.

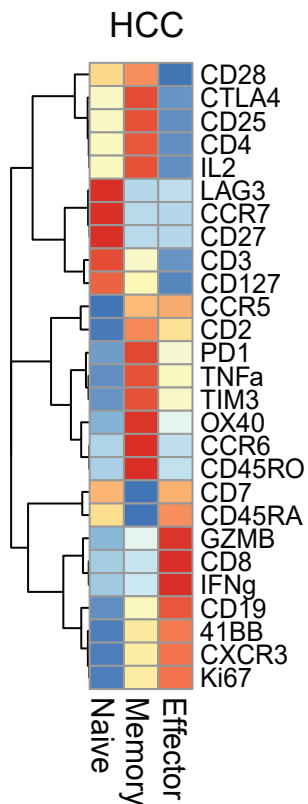


Supplemental Figure 2. Comparison of single marker expression across patients. Exhaustion markers TOX (A), HELIOS (B), PD-1 (C), and activation marker CD28 (D) average expression by patient. Statistical significance was determined by group mean comparison t-tests. Statistically significant P values are shown as follows: * $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$.

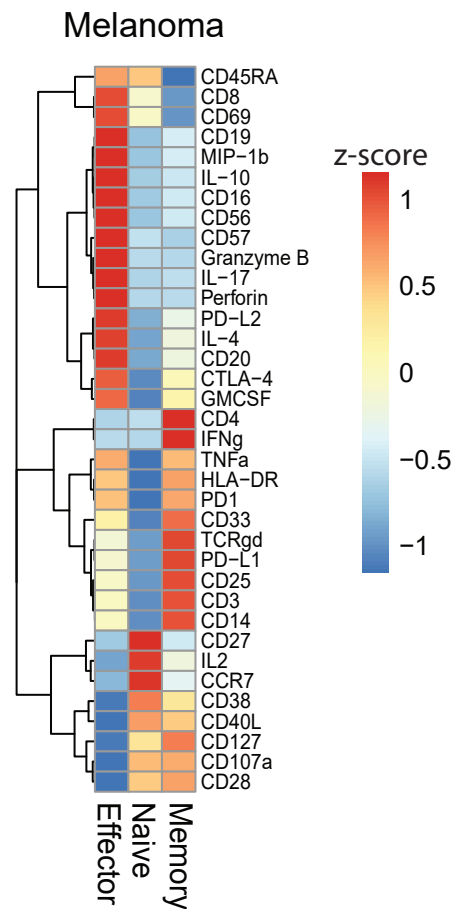
A



B

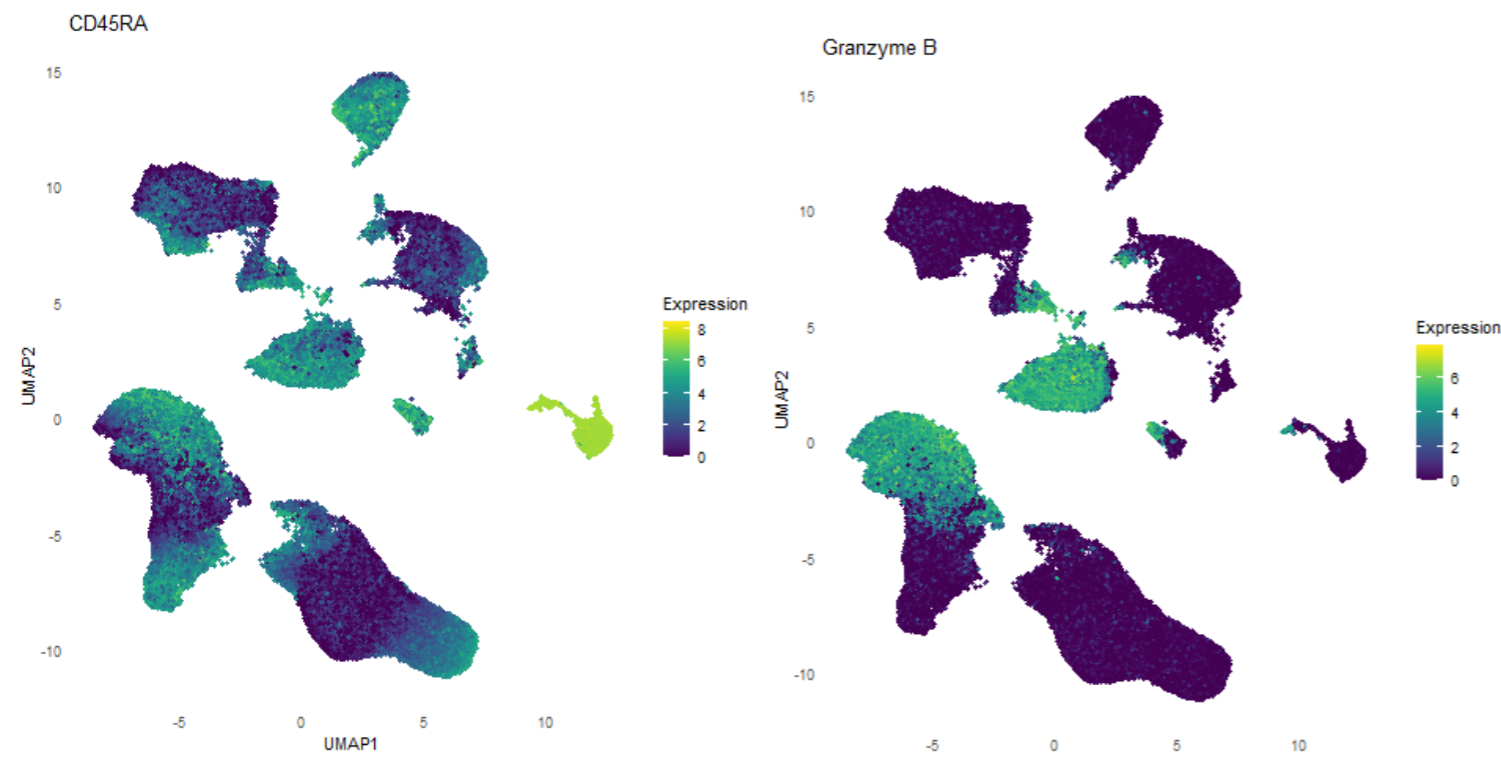
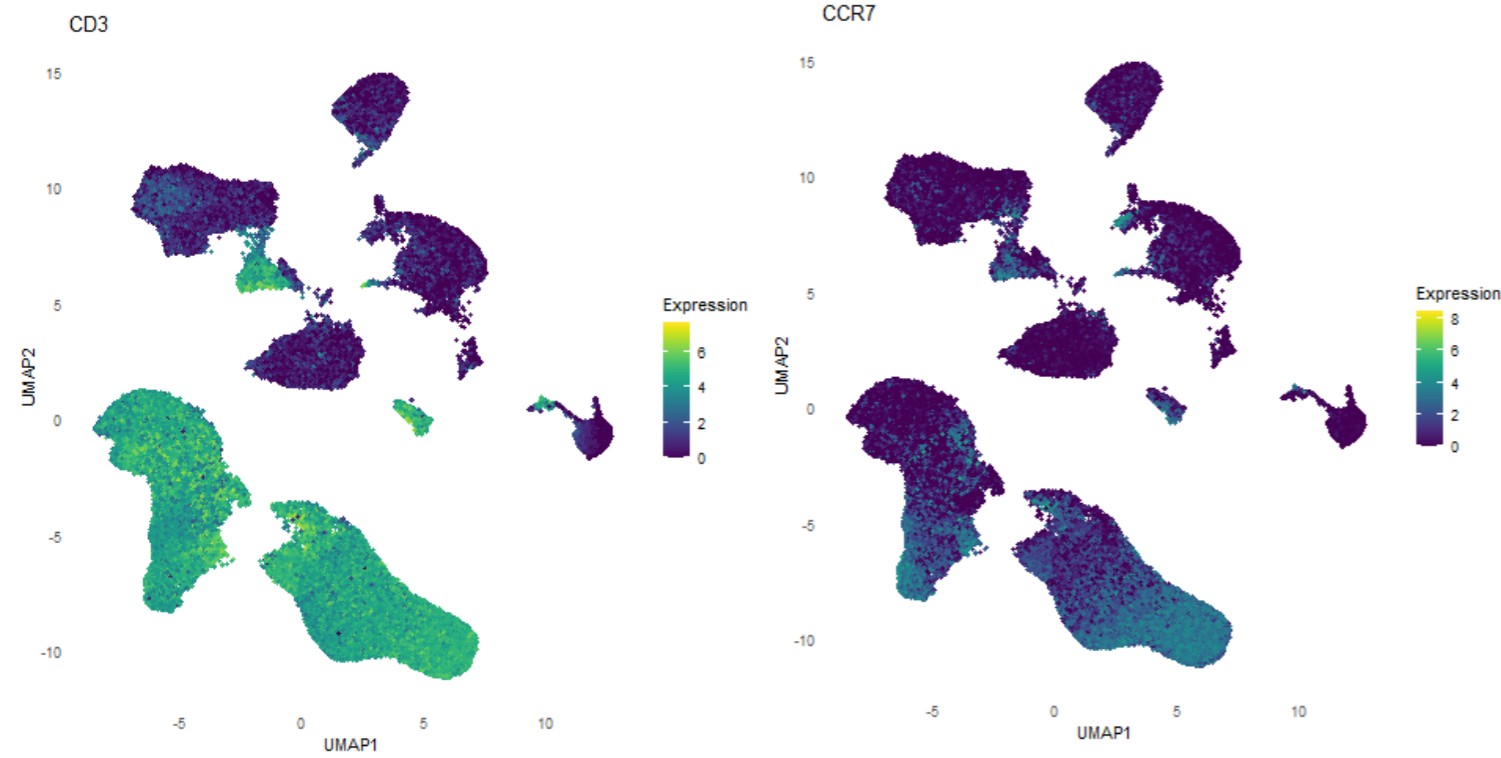


C

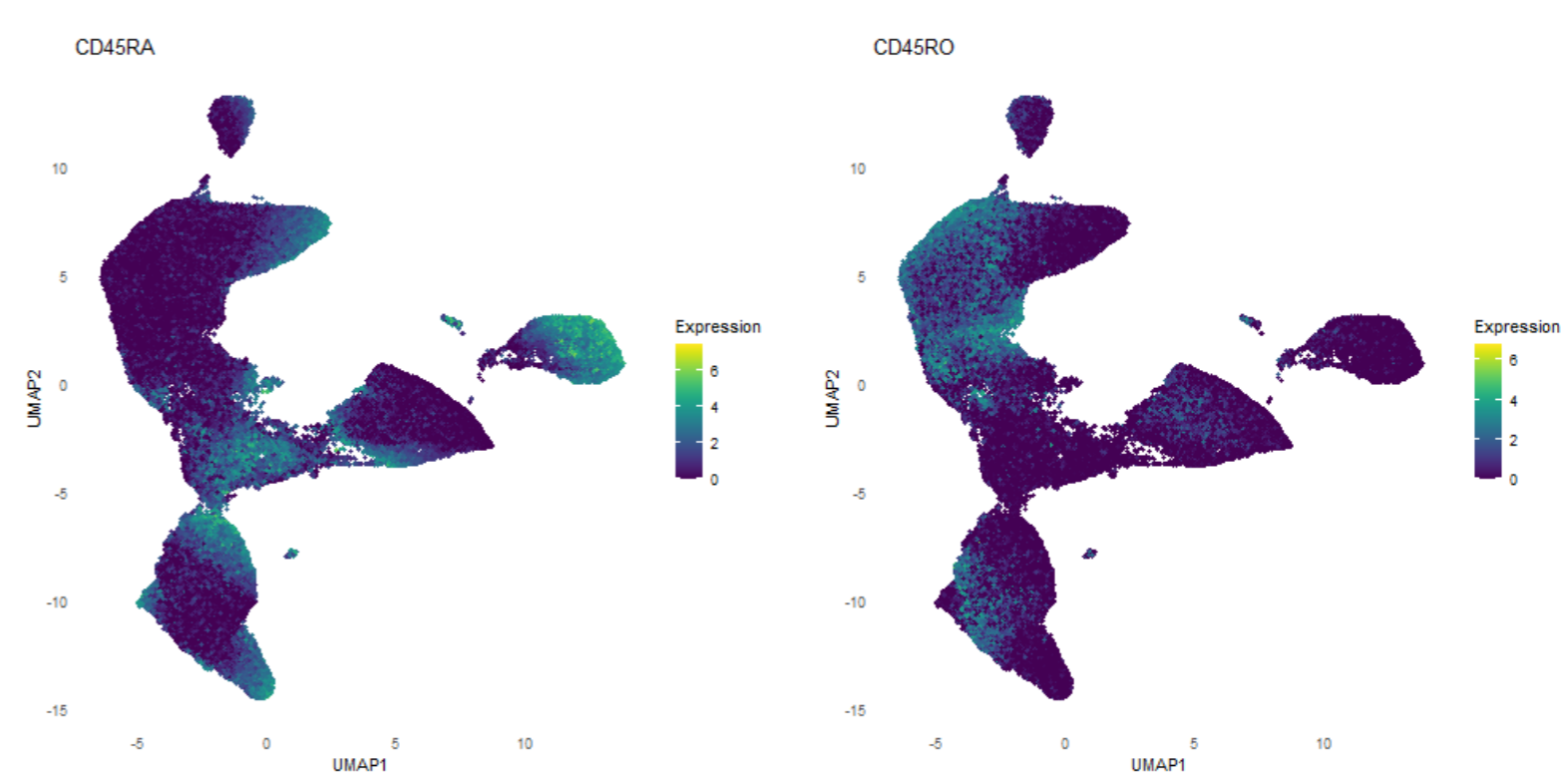
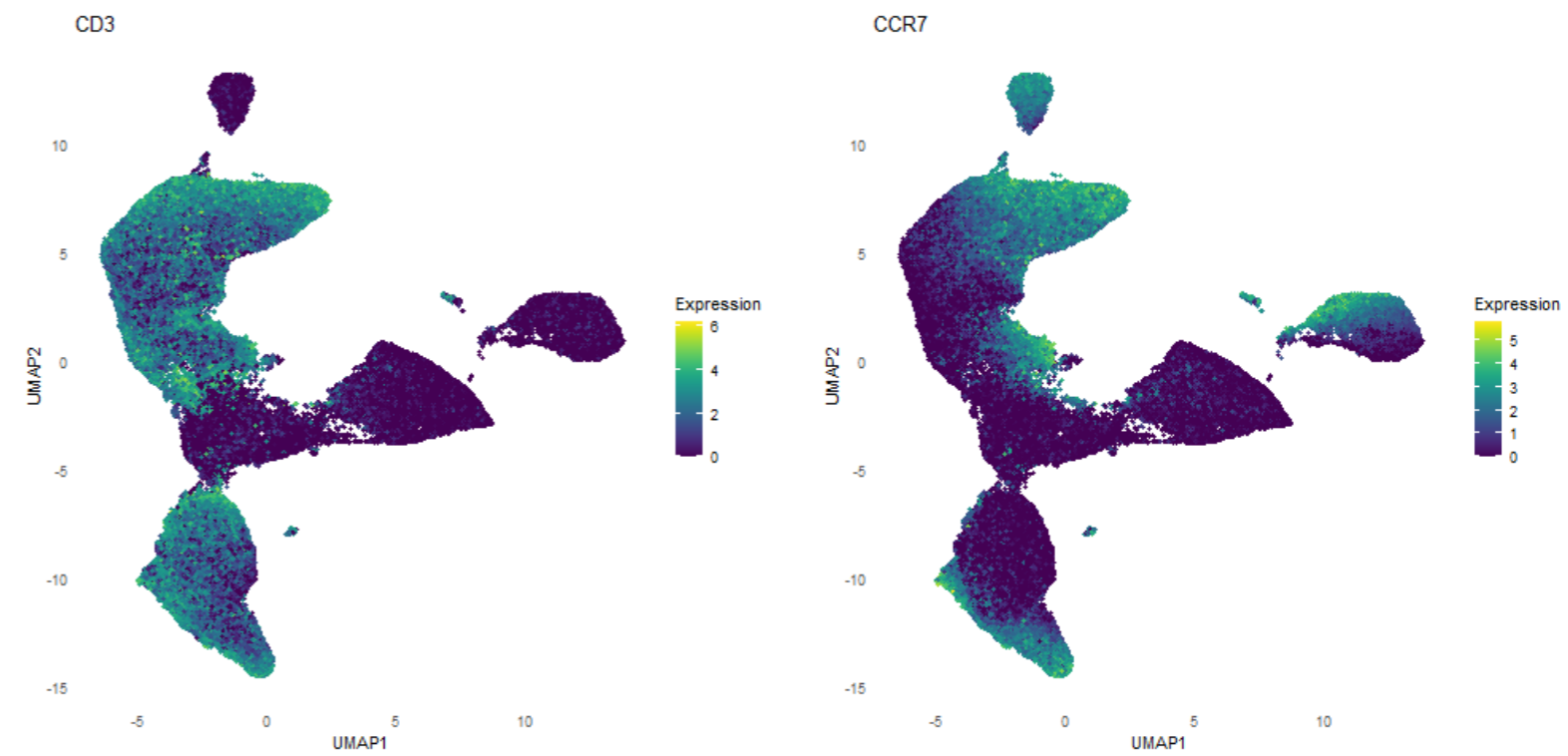


Supplemental Figure 3. Comparison of learned T cell NMF patterns in PDAC (A), HCC (B) and Melanoma (C) CyTOF datasets.

A



B



Supplemental Figure 4. UMAPs overlaid with expression of representative markers in Melanoma Hodi dataset (A) and HCC dataset (B).



Generate Raw CyTOF Data

Assess sample quality (Ir191, Beads, event length)

Randomization

CD45 channel debarcoding

Bead normalization and removal

Gating for live singlet cells

Aggregate patient protein expression matrices

Arcsine transformation & metadata incorporation

*Downstream Machine Learning:
Trajectory inference, CoGAPS, projectR*

Supplemental Figure 5. Schematic of computational preprocessing and workflow.