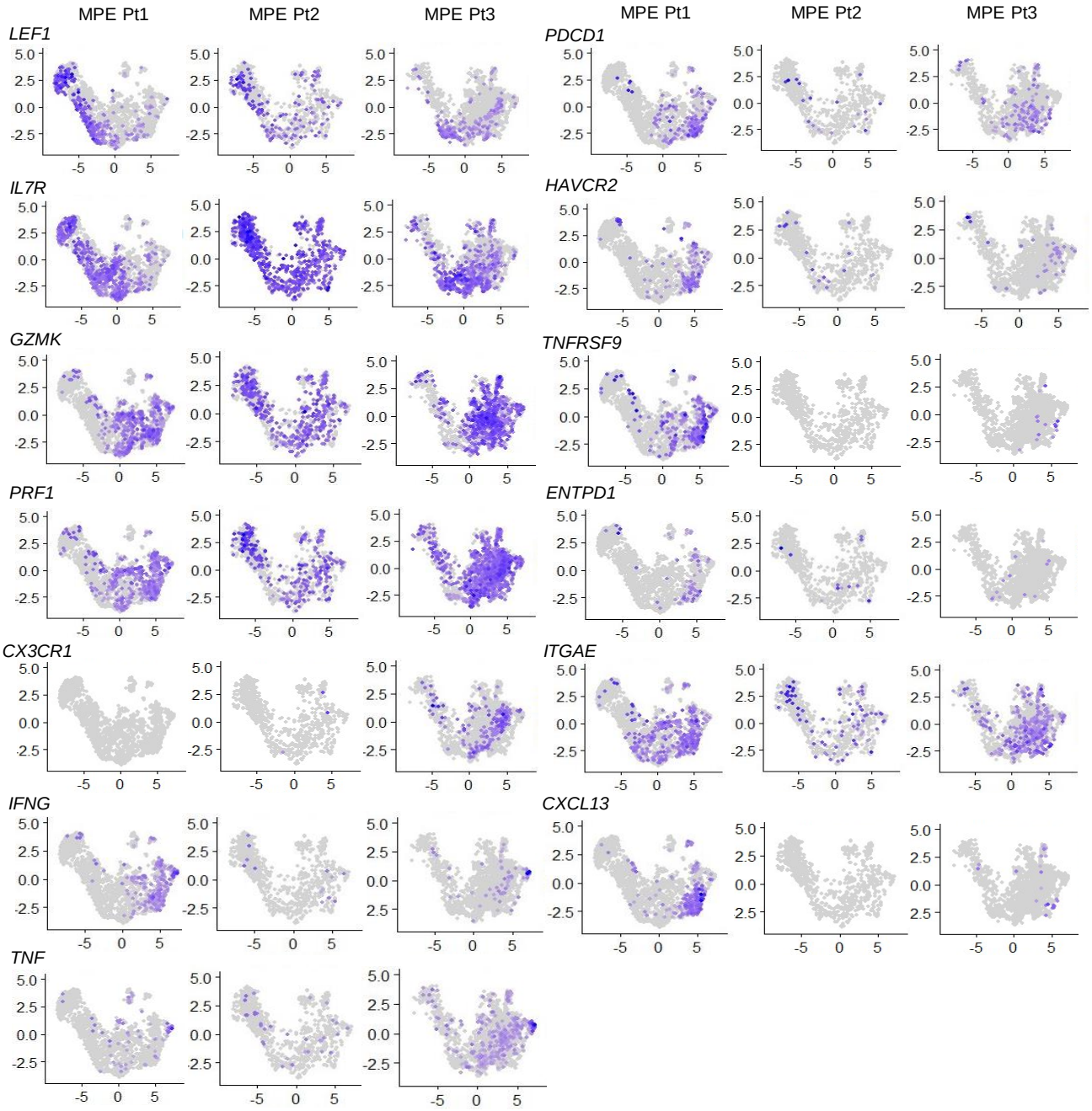
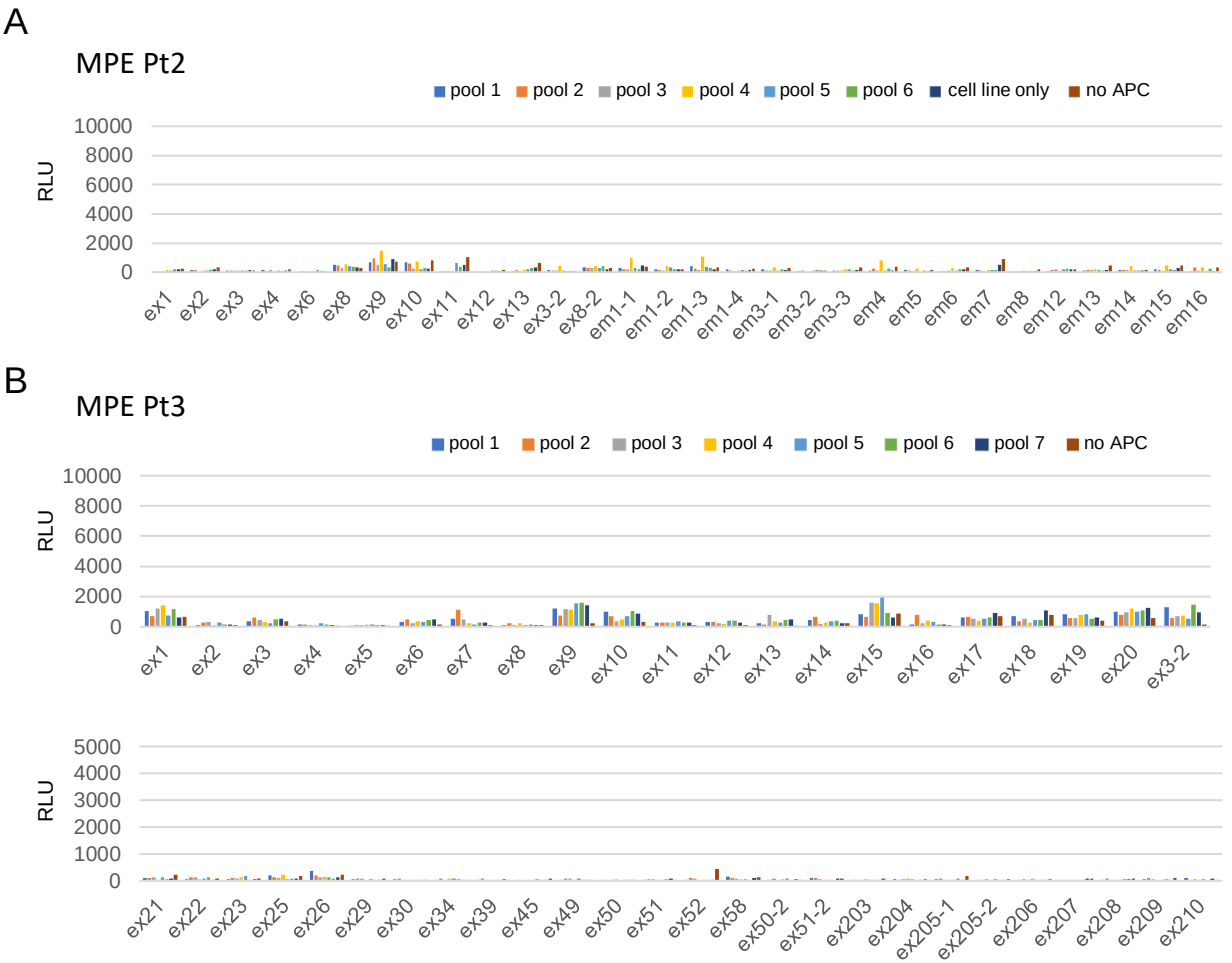
Supplementary Fig. S1



Supplementary Fig. S1. UMAPs of the distribution of representative marker genes.
Gene expression of *LEF1*, *IL7R*, *GZMK*, *PRF1*, *CX3CR1*, *IFNG*, *TNF*, *PDCD1*, *HAVCR2*, *TNFRSF9*, *ENTPD1*, *ITGAE*, and *CXCL13* detected in hierarchical clustering (Figure 1E) in each patient.

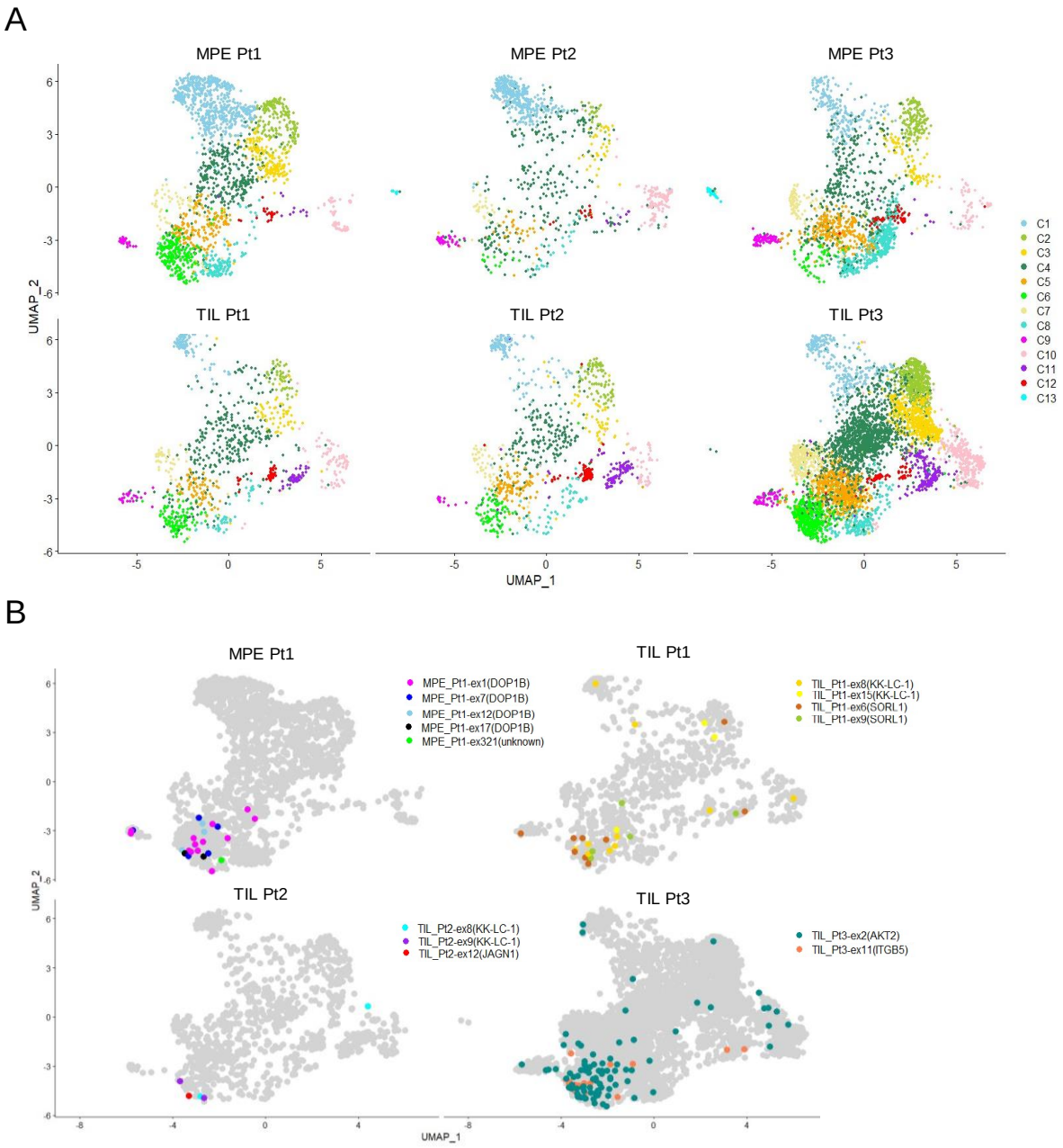
Supplementary Fig. S2



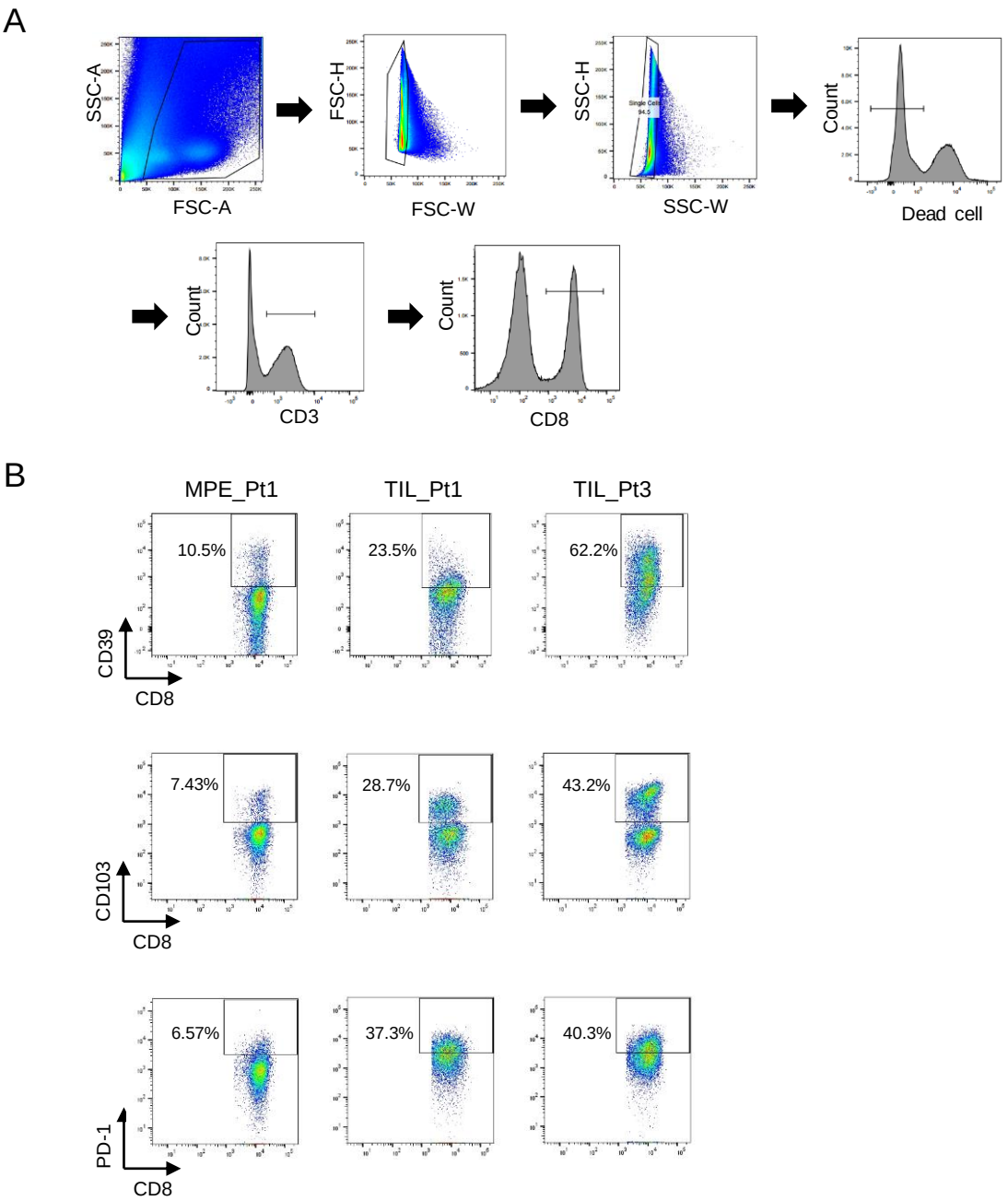
Supplementary Fig. S2. Screening of tumor neoantigens recognized by TCR-transduced CD8-J2 cells in MPE Pt2 and MPE Pt3.

A, The specificity of 30 TCRs against 47 predicted neoantigen peptides was tested for screening in MPE Pt2 (Supplementary Table S2 and S5). All TCR clonotypes in clusters C4-C7 were selected. TCR's TAP fragment/luciferase-transduced CD8-J2 (TCR's TAP/luc-CD8-J2) cells were cocultured with autologous B-APC or tumor cells with pooled antigenic peptides (7-9 peptides/pool). Activation of TCR signaling was assessed by luciferase reporter assay driven by NFAT-response element. **B**, 47 TCRs from the exhausted cluster C5 but overlapped with many other clusters like C4 having a T cell clonotype (n = 283) with high clonality were tested against 38 predicted neoantigen peptides in MPE Pt3 (Supplementary Table S3 and S6).

Supplementary Fig. S3

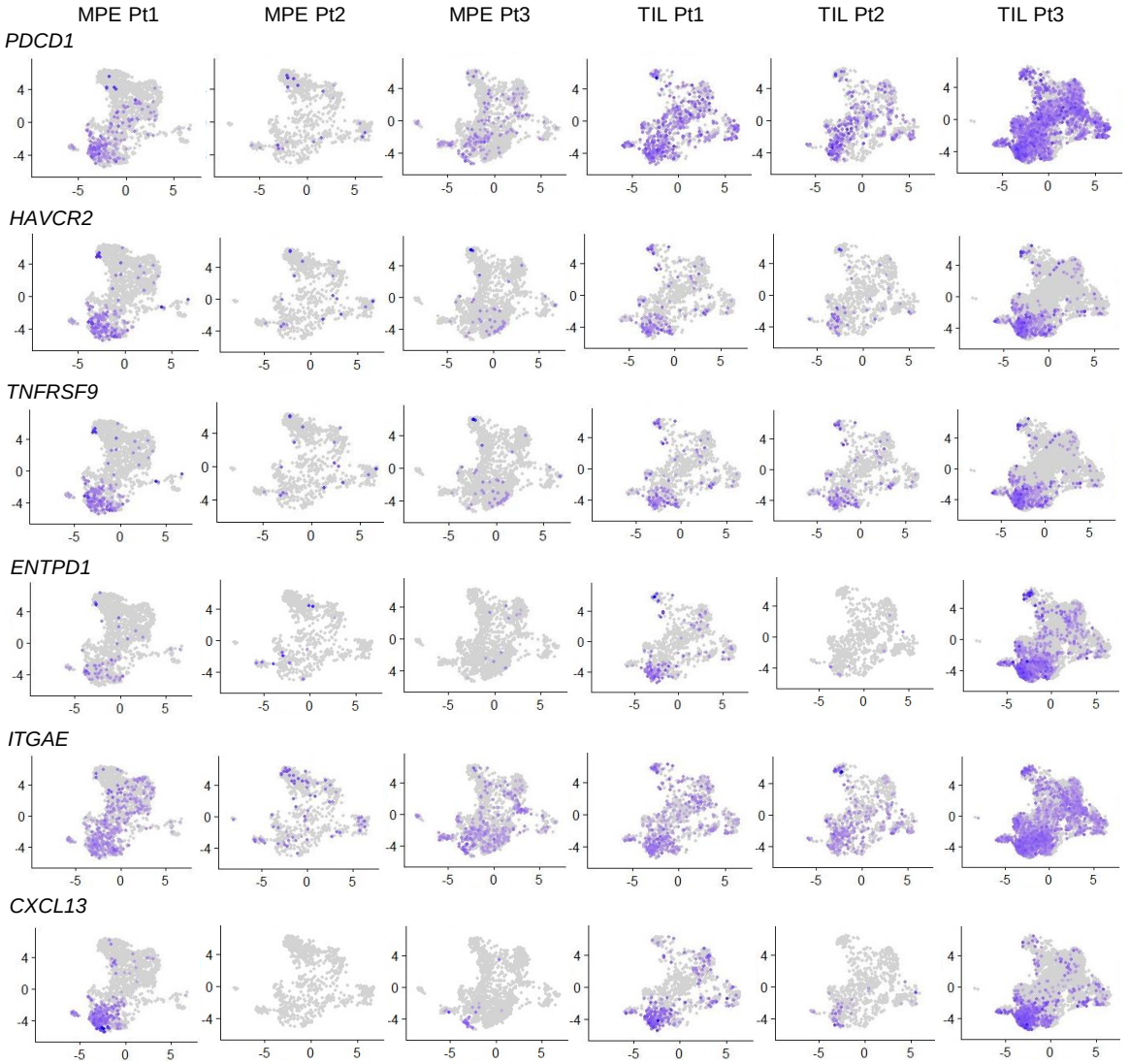


Supplementary Fig. S3. Combined analyses of tumor-specific T cells from both MPE and TILs. **A**. The uniform manifold approximation and projection (UMAP) of the expression profiles of single CD8$^+$ T cells in each patient (3 MPE and 3 TIL) after combination (Fig. 4A). **B**. Tumor-specific T cells in MPE (MPE Pt1) and TILs (TIL Pt1, TIL Pt2, and TIL Pt3) are projected onto UMAPs. The number of T cells in the 10 clusters of each patient.



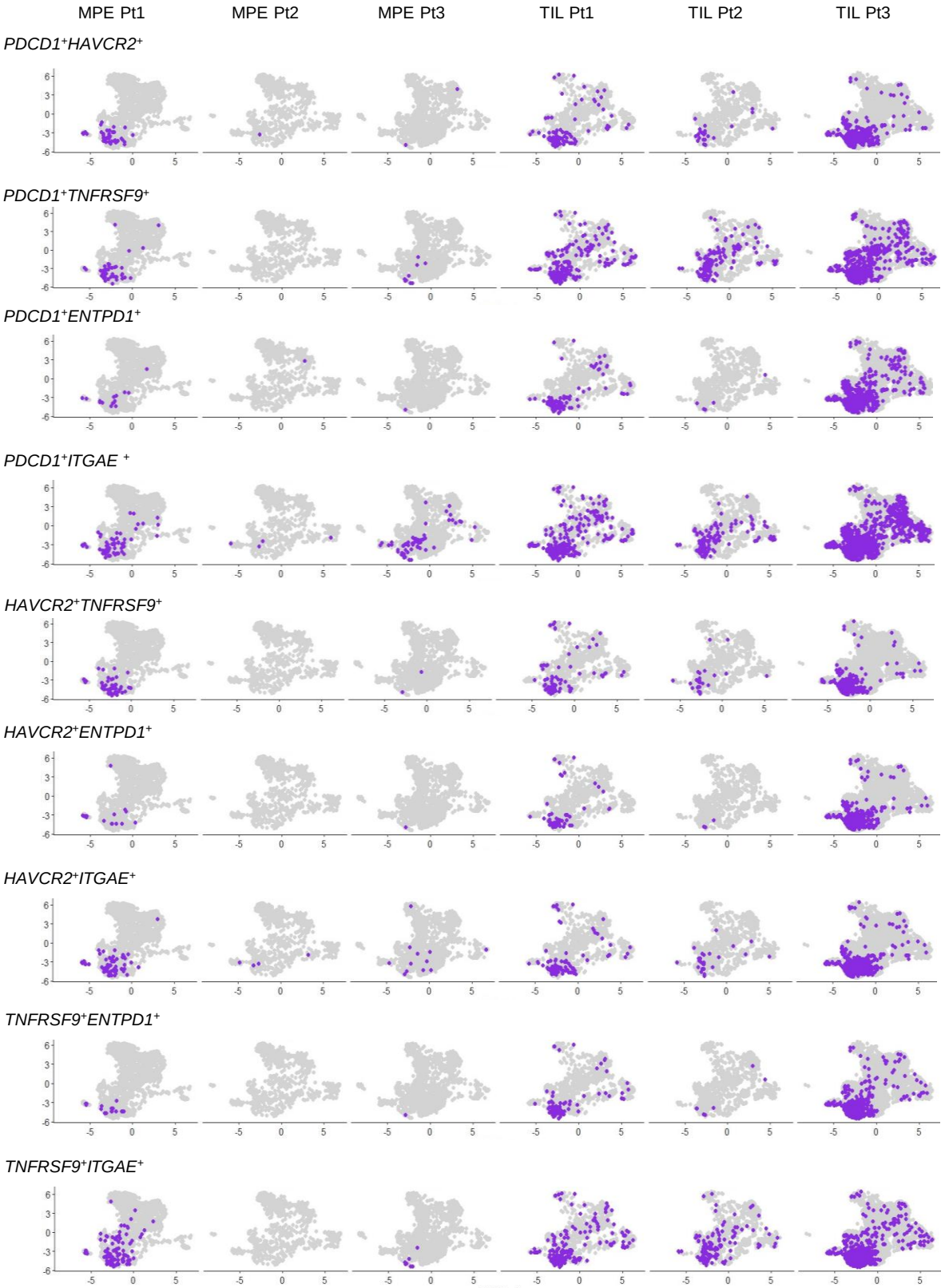
Supplementary Fig. S4. Flow cytometry analysis.
The gating strategy is shown including initial gates (FSC singlet, SSC singlet and live cells) followed by $CD3^+$ and $CD8^+$ cells (A). $CD8^+$ T cells were further gated by the expression of surface markers CD39, CD103, and PD-1 (antibodies used in this analysis are shown in **Supplementary Table S1**) in MPE (MPE_Pt1) and TILs (TIL_Pt1 and TIL_Pt3) (B).

Supplementary Fig. S5

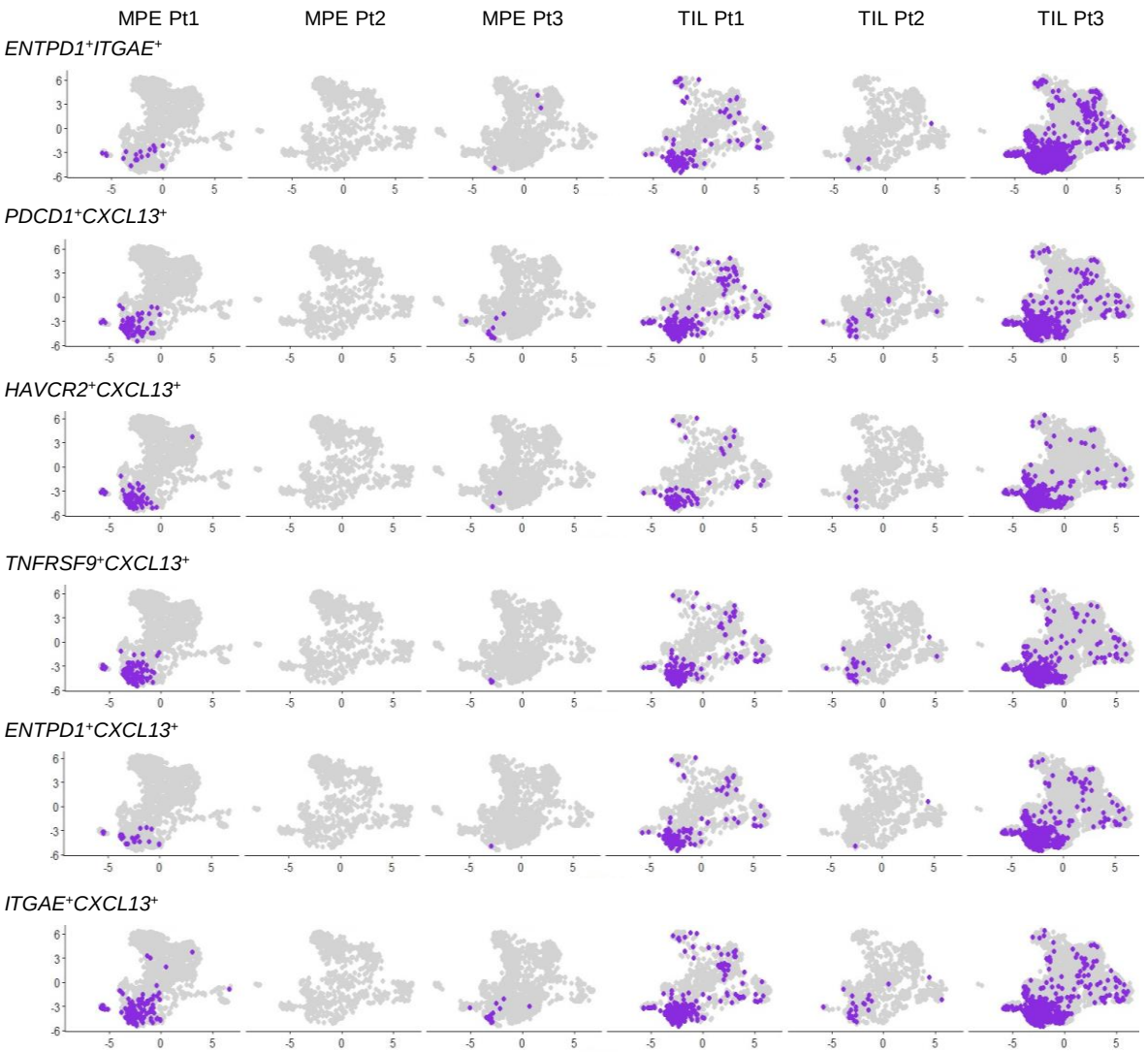


Supplementary Fig. S5. UMAPs of the distribution of representative marker genes.
Gene expression of *PDCD1*, *HAVCR2*, *TNFRSF9*, *ENTPD1*, *ITGAE*, and *CXCL13* in six patient.

Supplementary Fig. S6



Supplementary Fig. S6 (continued)



Supplementary Fig. S6. UMAPs of the distribution of representative marker genes. Gene expression of the combinations of *PDCD1*, *HAVCR2*, *TNFRSF9*, *ENTPD1*, *ITGAE*, and *CXCL13* in six patient. RNA expression, >0.5 (both genes)

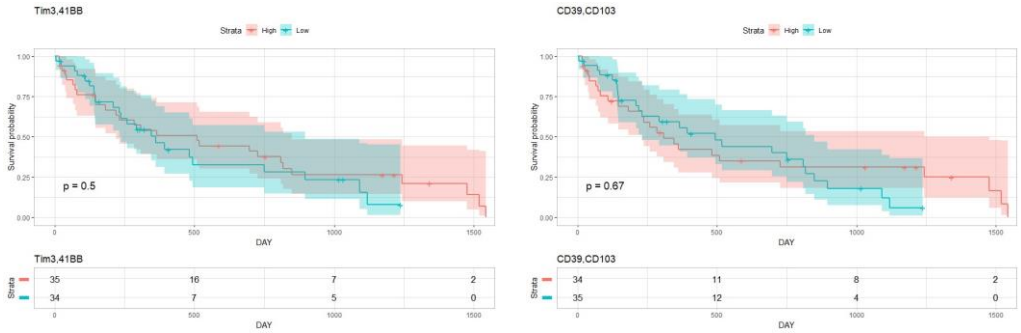
Supplementary Fig. S7

A

All

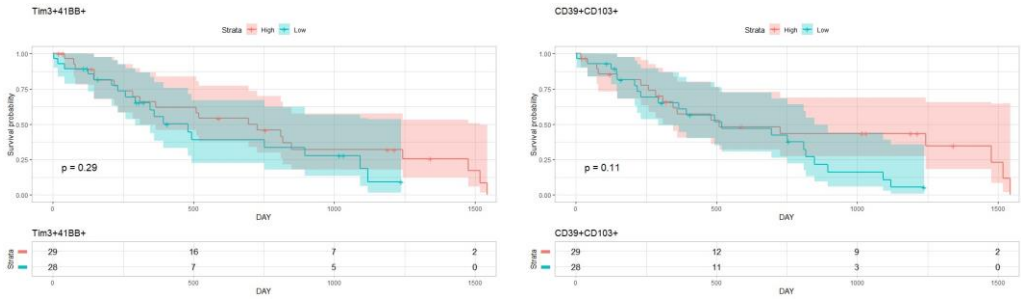
TIM3/4-1BB

CD39/CD103



B

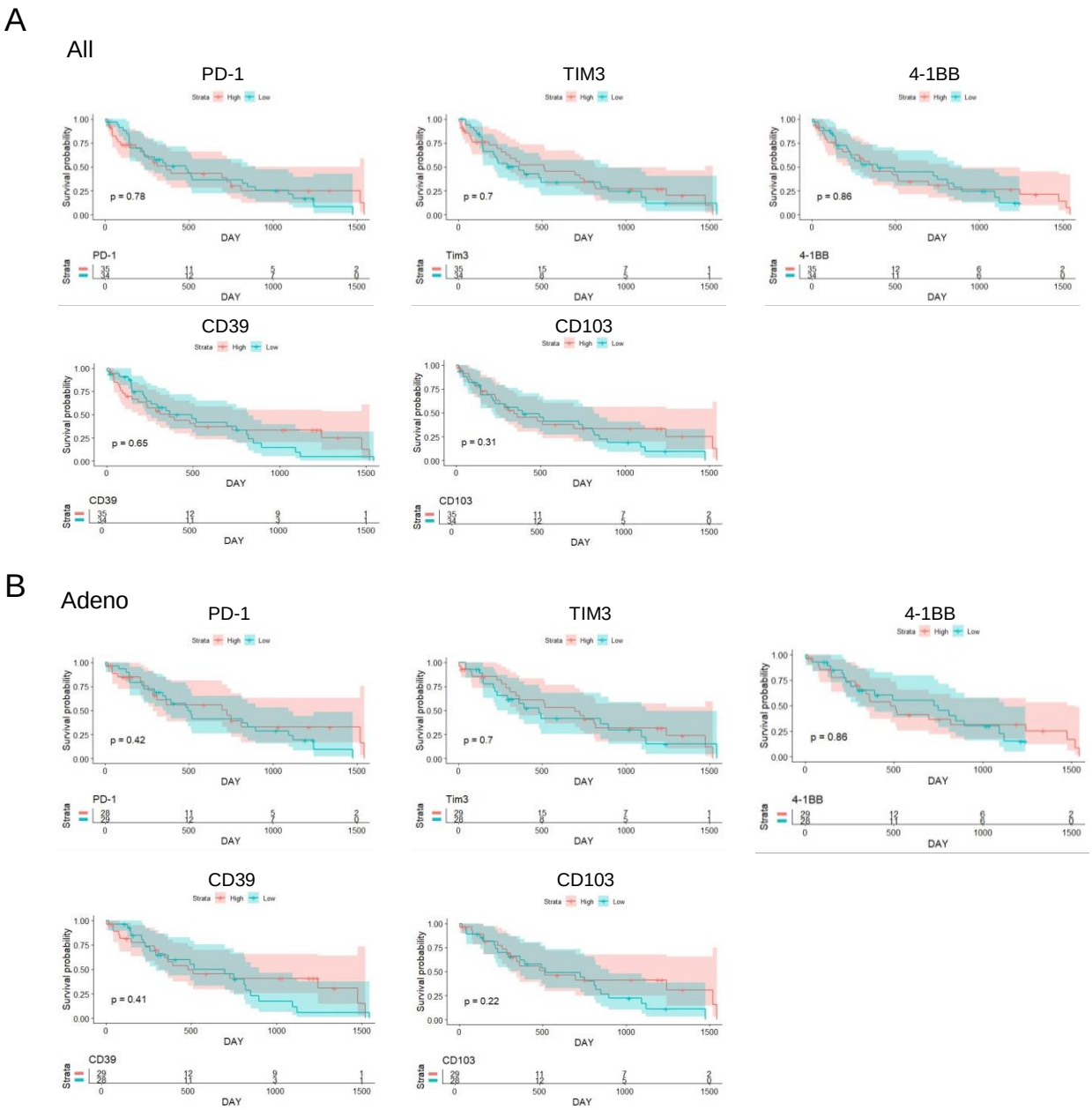
Adeno



Supplementary Fig. S7. Survival analysis based on the expression of exhausted T cell-related markers.

Kaplan-Meier survival curve dividing patients into two groups by the median values of the expression TIM3/4-1BB and CD39/CD103 in all patients (n = 69) (A) and adenocarcinoma patients (n = 57) (B).

Supplementary Fig. S8



Supplementary Fig. S8. Survival analysis based on the expression of exhausted T cell-related markers.

Kaplan-Meier survival curve dividing patients into two groups by the median values of the expression PD-1, 4-1BB, TIM3, CD39, CD103, and CXCL13 in all patients (*n* = 69) (A) and adenocarcinoma patients (*n* = 57) (B).