Supplementary Material for "Cancer-Associated Fibroblasts and Metabolic Reprogramming Predict Pathologic Response to Neoadjuvant PD-1 Blockade in Resected Non-Small Cell Lung Cancer"

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Supplementary Figures

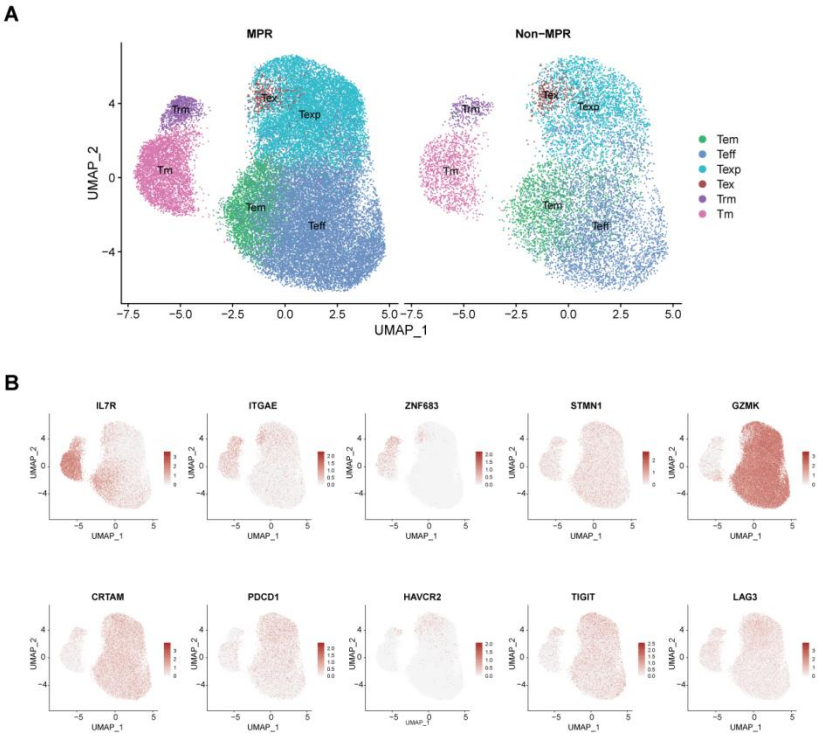

Figure S1. Identification of different clusters of CD8$^+$ T cells.

(A) UMAP plot of CD8$^+$ T cells colored by clusters in MPR and non-MPR patients.

(B) UMAP plots showing the expression levels of certain signature genes in the clusters from A.

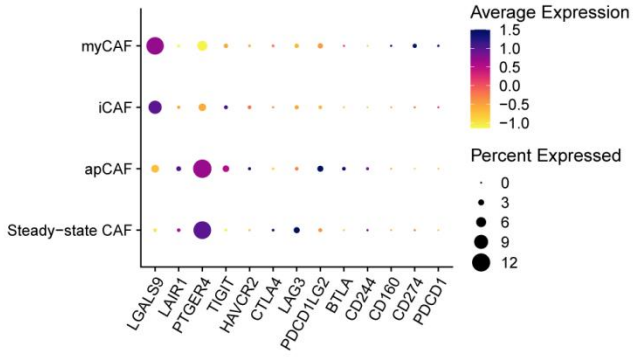

Figure S2. The expression levels of immune checkpoint-related genes in different subtypes of CAFs.

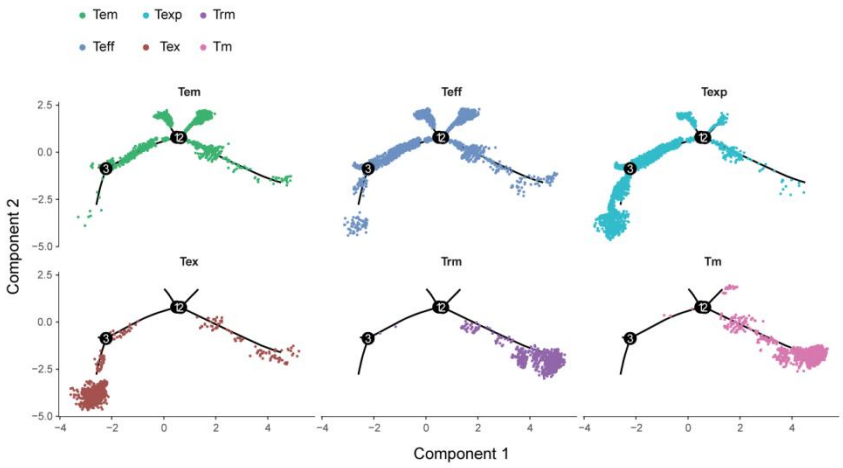

Figure S3. The developmental trajectory of CD8$^+$ T cells inferred by Monocle 2.

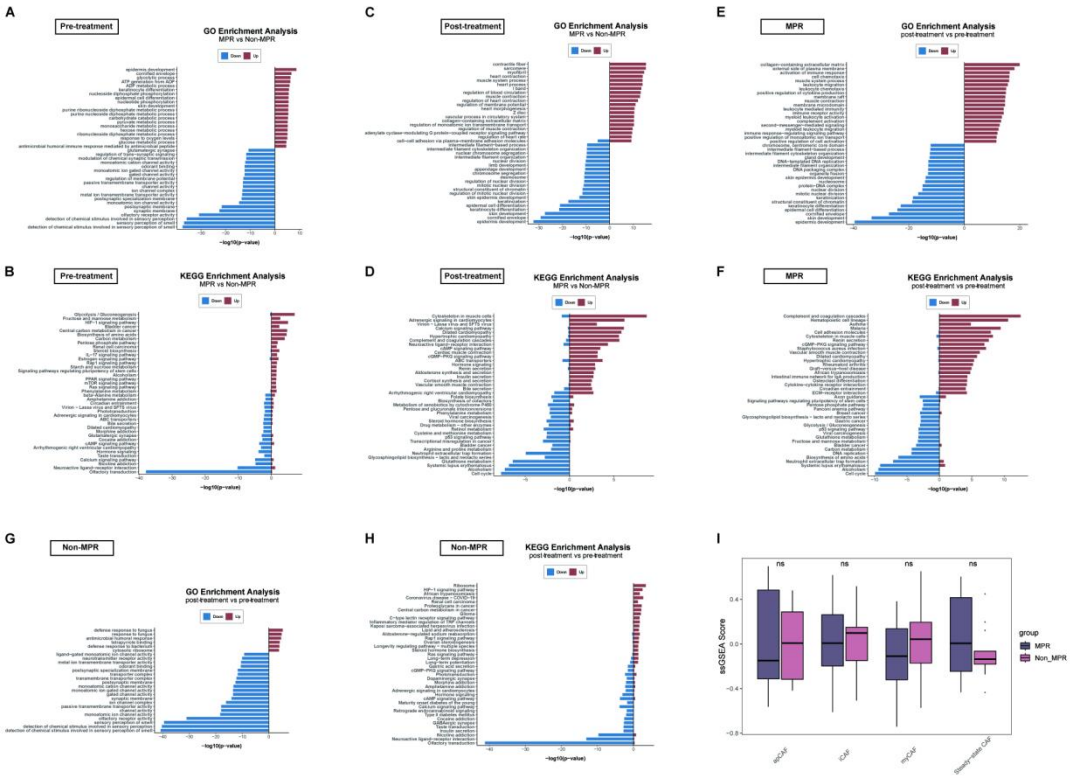

Figure S4. Pathway alterations and CAF subtype enrichment in response to neoadjuvant immunotherapy.

(A, C, E, G) GO enrichment analysis of DEGs in Figure 5A-D.

(B, D, F, H) KEGG enrichment analysis of DEGs in Figure 5A-D.

(I) Enrichment of each CAF subtype in MPR and non-MPR patients from pre-treatment biopsies determined by ssGSEA.

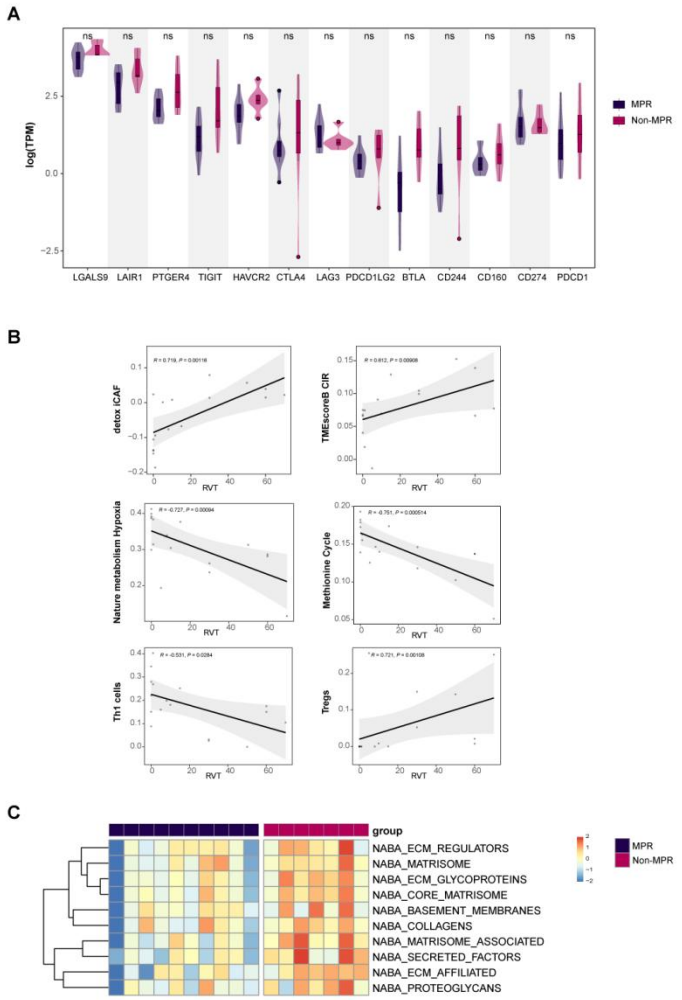

Figure S5. ECM signatures are associated with treatment resistance.

(A) Changes in checkpoint genes of MPR and non-MPR patients from pre-treatment biopsies.

(B) Estimating the correlation between the indicated signature and residual viable tumor in SYSUCC cohort. The corresponding Pearson correlation values are shown.

(C) Gene set enrichment analysis of ECM genes in MPR and non-MPR patients from pre-treatment biopsies.

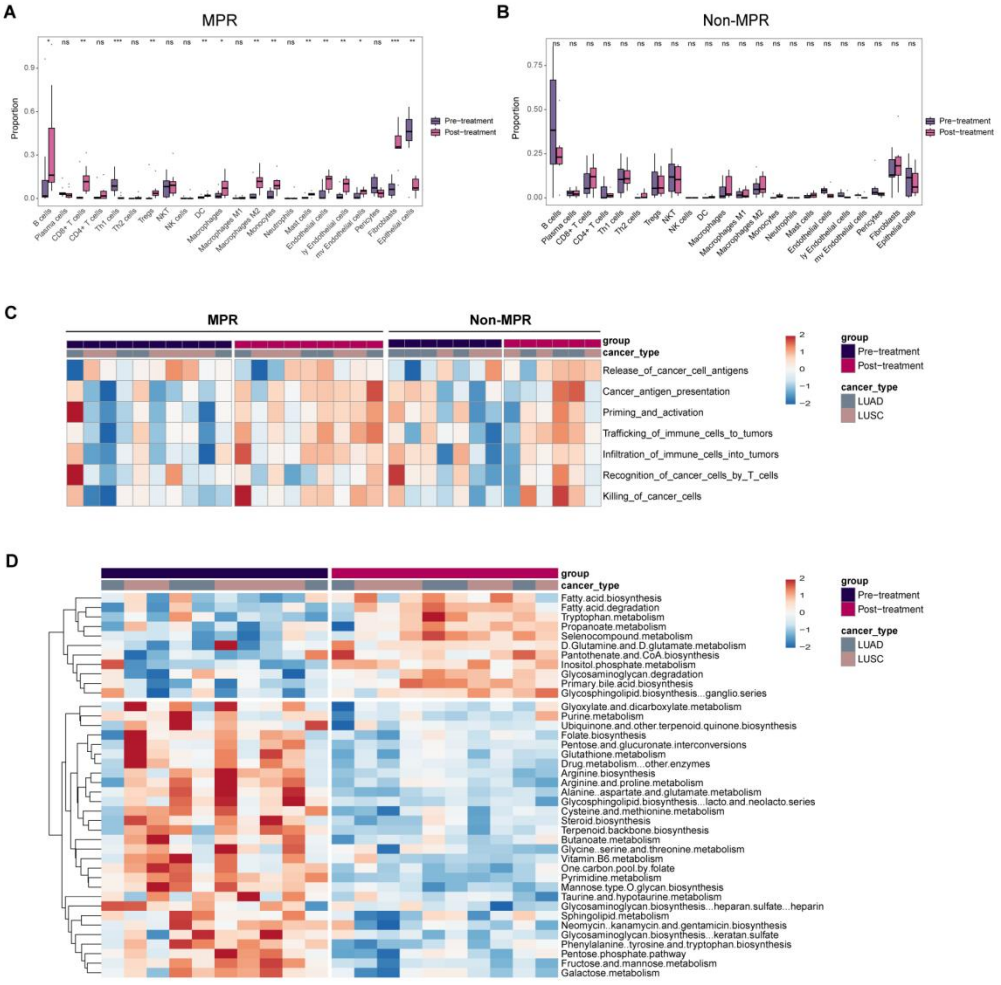

Figure S6. Anti-tumor immunity and metabolic reprogramming in MPR group.

(A) Change in immune cell populations of MPR patients from pre- to post-treatment.

(B) Change in immune cell populations of non-MPR patients from pre- to post-treatment.

(C) Heatmap for the results of TIP analysis.

(D) Metabolic pathway activities of MPR patients from pre- to post-treatment.