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Supplemental information

Prioritizing exhausted T cell marker

genes highlights immune subtypes in pan-cancer

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Supplemental Figures

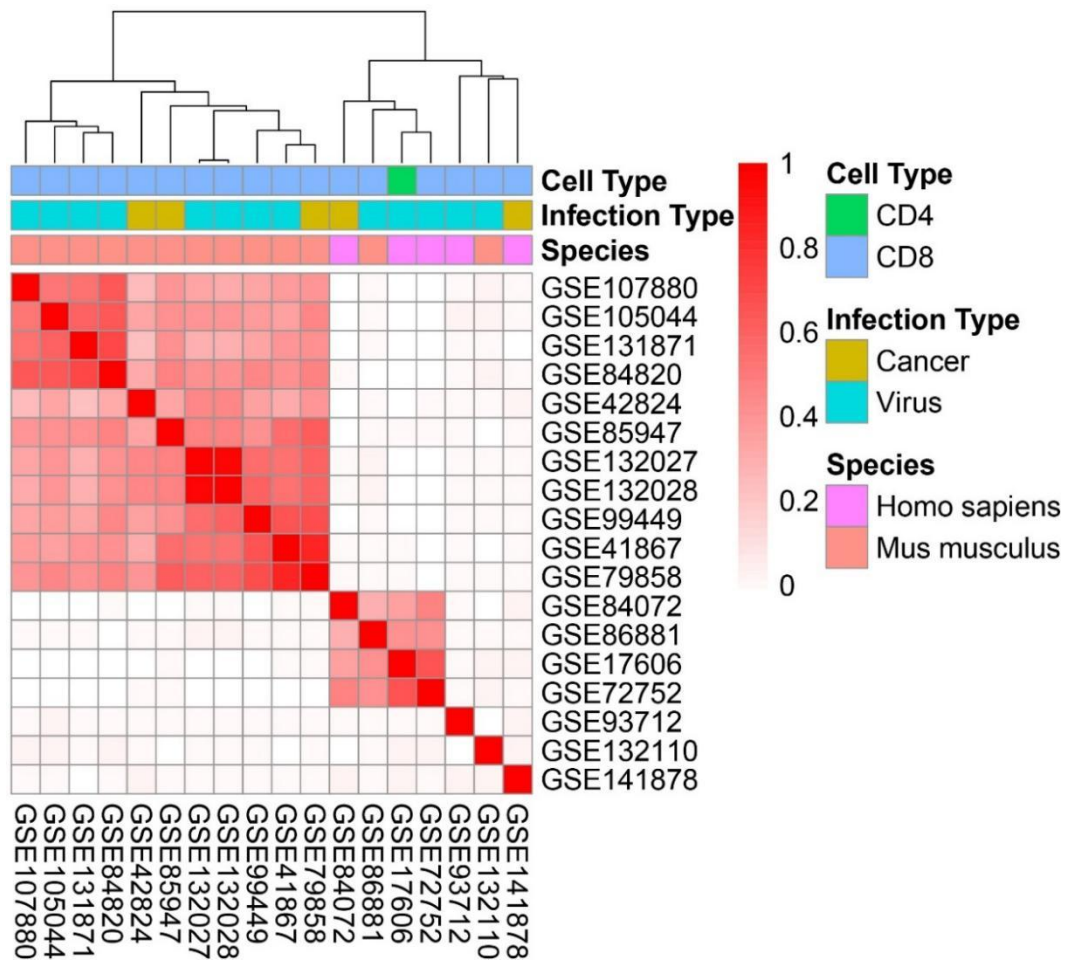


Figure S1. The correlation of exhaustion-related expression profiles based on candidate genes. The color shows the Pearson correlation coefficient. Related to Figure 2.

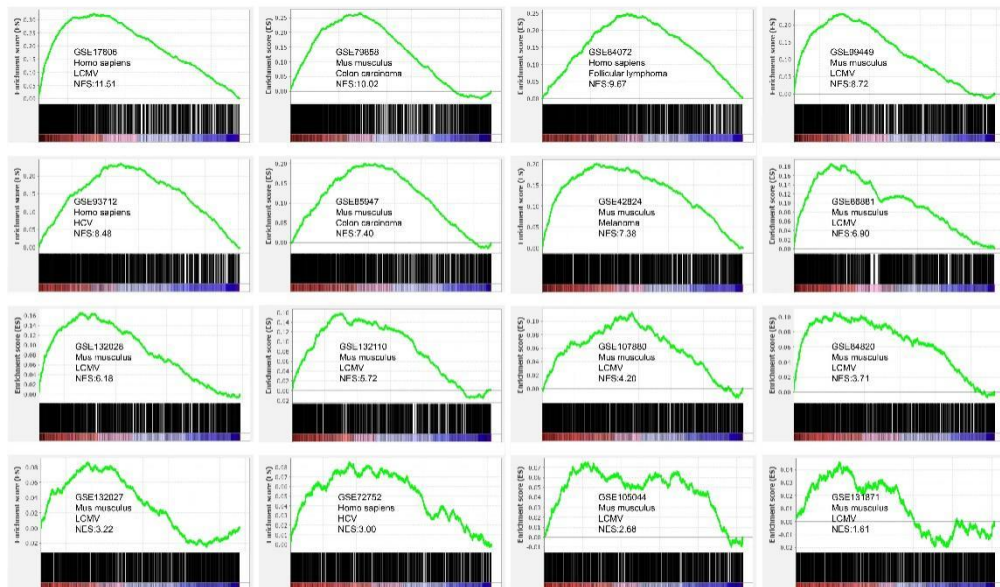


Figure S2. The GSEA enrichment results of candidate genes in different expression profiles. Related to Figure 2.

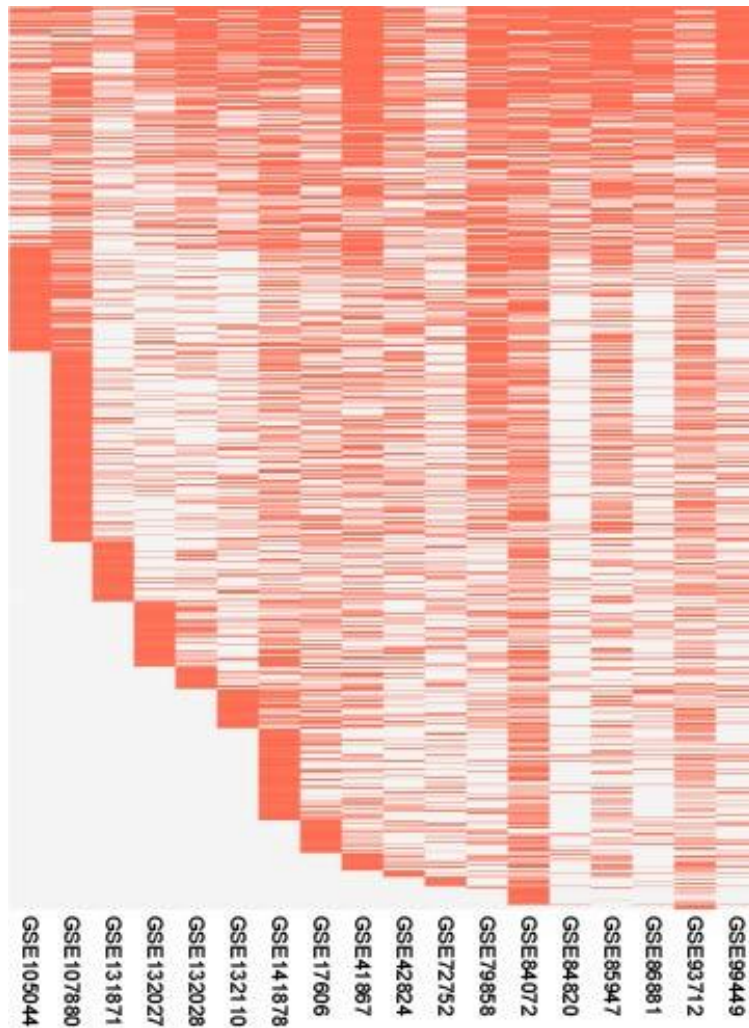


Figure S3. The leading edge results of candidate genes in different expression profiles. The x-axis shows the candidate genes, and the y-axis shows the exhaustion-related expression profiles. The red color represents the candidate gene as the leading edge gene in expression profile. Related to Figure 2.

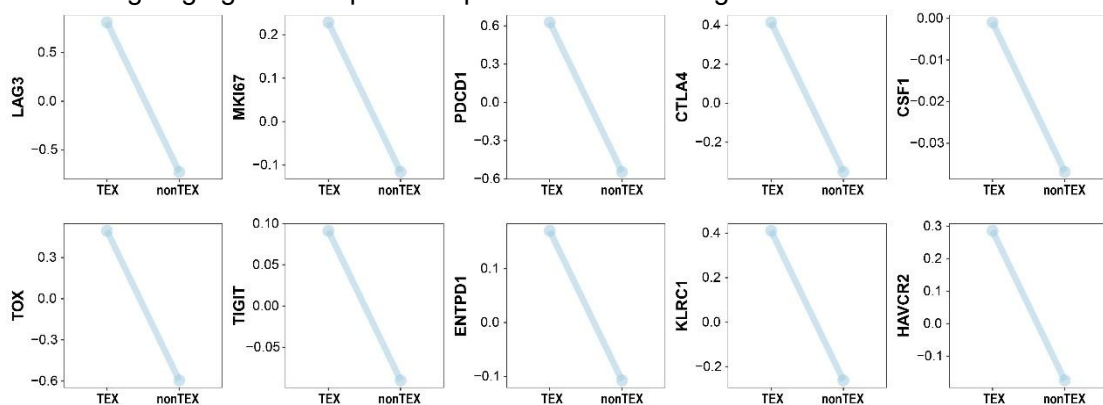


Figure S4. The expression levels of marker genes between TEX and nonTEX samples in mouse single-cell expression profile. The x-axis shows the different cell types, and the y-axis shows the expression levels. Related to Figure 6.