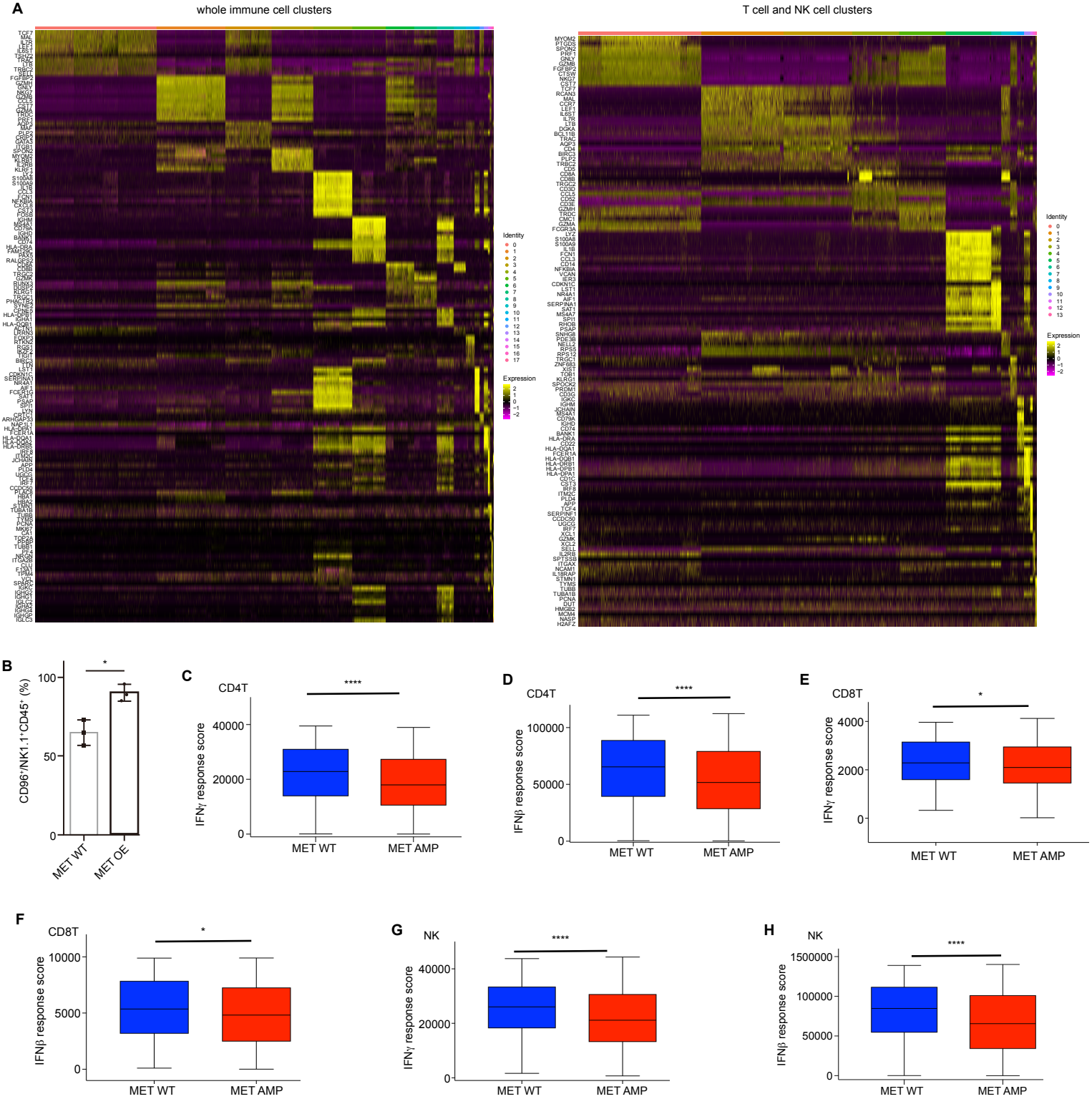
Supplementary Figure S3



Supplementary Figure S3. Single-cell RNA-seq reveals the distinctive functional composition of immune cells in MET amplification patients

A, Gene expression matrix from single-cell RNA-seq experiment characterizing expression of lineage-defining genes in whole 17 immune cell clusters and gene expression matrix from CD4, CD8 and NK clusters with single-cell RNA-seq experiment characterizing expression of cell marker genes.

B, CD96 NK cell populations from isolated tumor-infiltrating lymphocytes in MET OE (overexpression) tumor model (n = 3). samples by two-sided unpaired t-test; *$p < 0.05$.

C-H, Single-cell gene set enrichment scores of IFNγ **(C, E, G)** and IFNβ **(D, F, H)** response signature scores within individual immune subpopulations (CD4, CD8 and NK) from MET amplification and MET WT patients PBMCs. (Kolmogorov-Smirnov test; *$p < 0.05$; **$p < 0.01$; ***$p < 0.001$, and ****$p < 0.0001$).