

Supplementary Materials

Supplementary Figure S1. Data quality control. (A-B) Threshold screening of gene expression and mitochondrial gene content of CD8⁺ T cells from healthy donors (A) and tuberculosis patients (B). (C) The fitting degree of correlation between CD8⁺ T cells in two states was reflected by a PCA scatter plot. (D-E) Threshold screening of gene expression and mitochondrial gene content of CD4⁺ T cells in healthy donors (D) and tuberculosis patients (E). (F) The fitting degree of correlation between CD4⁺ T cells in two states was reflected by a PCA scatter plot.

Supplementary Figure S2. Single sample data processing. (A-B) The t-SNE projection of HC (A) and TB (B) of CD8⁺ T cells. Each dot corresponds to a single cell, coloured according to cell subsets. (C-D) The heatmaps showing the top marker genes across each CD8⁺ T-cell clusters of HC (C) and TB (D). (E-F) The t-SNE projection of HC (E) and TB (F) of CD4⁺ T cell. Each dot corresponds to a single cell, coloured according to cell subsets. (G-H) The heatmaps showing the top marker genes across each CD4⁺ T-cell clusters of HC (G) and TB (H).

Supplementary Figure S3. Single-cell transcriptomic clustering for CD4⁺ and CD8⁺ T cells. (A–B) The t-SNE plots showing the original CD8⁺ (A) and CD4⁺ (B) T-cell clusters. Each dot represents a single cell, and the clusters were labelled with individual colours. (C–D) The heatmaps showing the top 10 marker genes across each CD8⁺ (C) and CD4⁺ (D) T-cell clusters. (E-F) Dot plot of subset marker expression levels across each CD8⁺ (E) and CD4⁺ (F) T-cell subset. The dot sizes represent the expression percentage of selected cell markers in each T-cell subset, and the dot colours represent the average expression levels of selected markers.

Supplementary Figure S4. Cell cycle analysis. (A) UMAP projection of cell cycle of CD8⁺ T cell subsets. (B) Stacked bar chart showing the proportion of each subgroup of CD8⁺ T cells in each cell cycle. (C) UMAP projection of CD8⁺ T cell subsets in each cell cycle. (D) UMAP projection of cell cycle of CD4⁺ T cell subsets. (E) Stacked bar chart showing the proportion of each subgroup of CD4⁺ T cells in each cell cycle. (F) UMAP projection of CD4⁺ T cell subsets in each cell cycle.

Supplementary Figure S5. Dissection of CD4⁺ exhausted T cells. UMAP projection diagram (left) showing the distribution of CD4⁺ exhausted T-cell sub-clusters. Each dot represents a single cell coloured according to the cell clustering information. T-SNE diagrams (right) showing CD4⁺ exhausted T-cell sub-clusters across the tuberculosis and healthy donor groups.

Supplementary Table S1. Summary of scRNA-Seq QC.

Supplementary Table S2. Characteristics of participating HCs and of individuals with TB infection.

Supplementary Table S3. Unique genes of depleted subgroups.







