



### Supplementary Figure 1: Single-cell RNA/TCR sequencing (scRNA/TCR-seq) quality assessment.

**A** Gating strategy of identifying single live CD45<sup>+</sup>CD19<sup>-</sup>CD3<sup>+</sup>CD56<sup>-</sup> cells from cryopreserved peripheral mononuclear blood cells for scRNA/TCR-seq.

**B** Representative flow cytometric plots showing the frequency of CD45<sup>+</sup>CD19<sup>-</sup>CD3<sup>+</sup>CD56<sup>-</sup> cells after flow-sort.

**C** Scatterplots depicting total features, counts, doublet scores, mitochondrial content and ribosomal content across all cells prior to filtering. Filtering thresholds applied are shown.

**D** Elbow plot of PCA (top 50 components). PC selection for downstream analysis was limited to those components accounting for at least 0.1 % of total variation (n = 44).

**E** UMAP representations of all-post filtered, normalized cells showing cellular distributions of total unique counts, mitochondrial scores, ribosomal scores, G2M/S phase scores and doublet scores.

**F** UMAP plot identifying doublets by hashtag oligos (HTO).