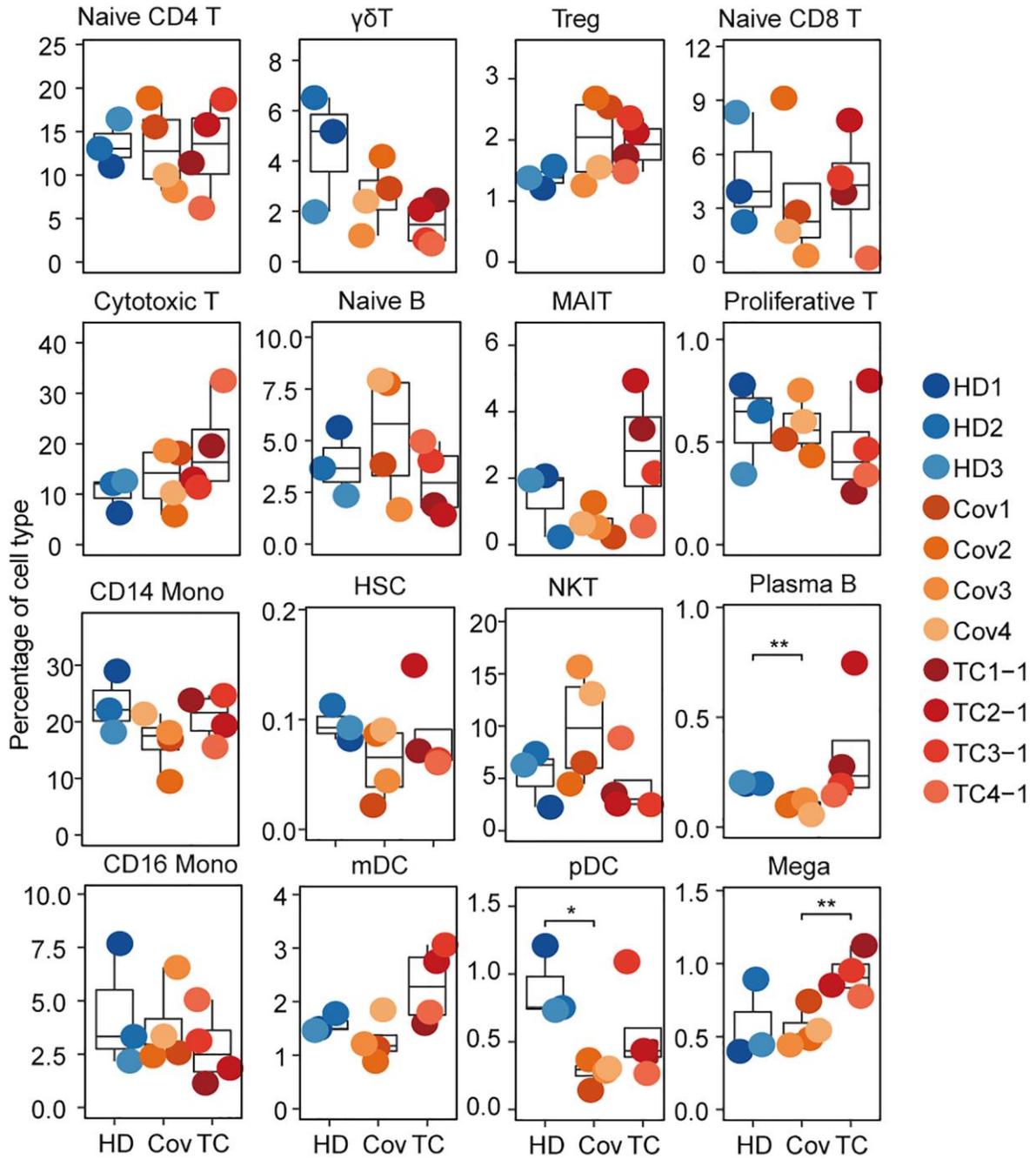
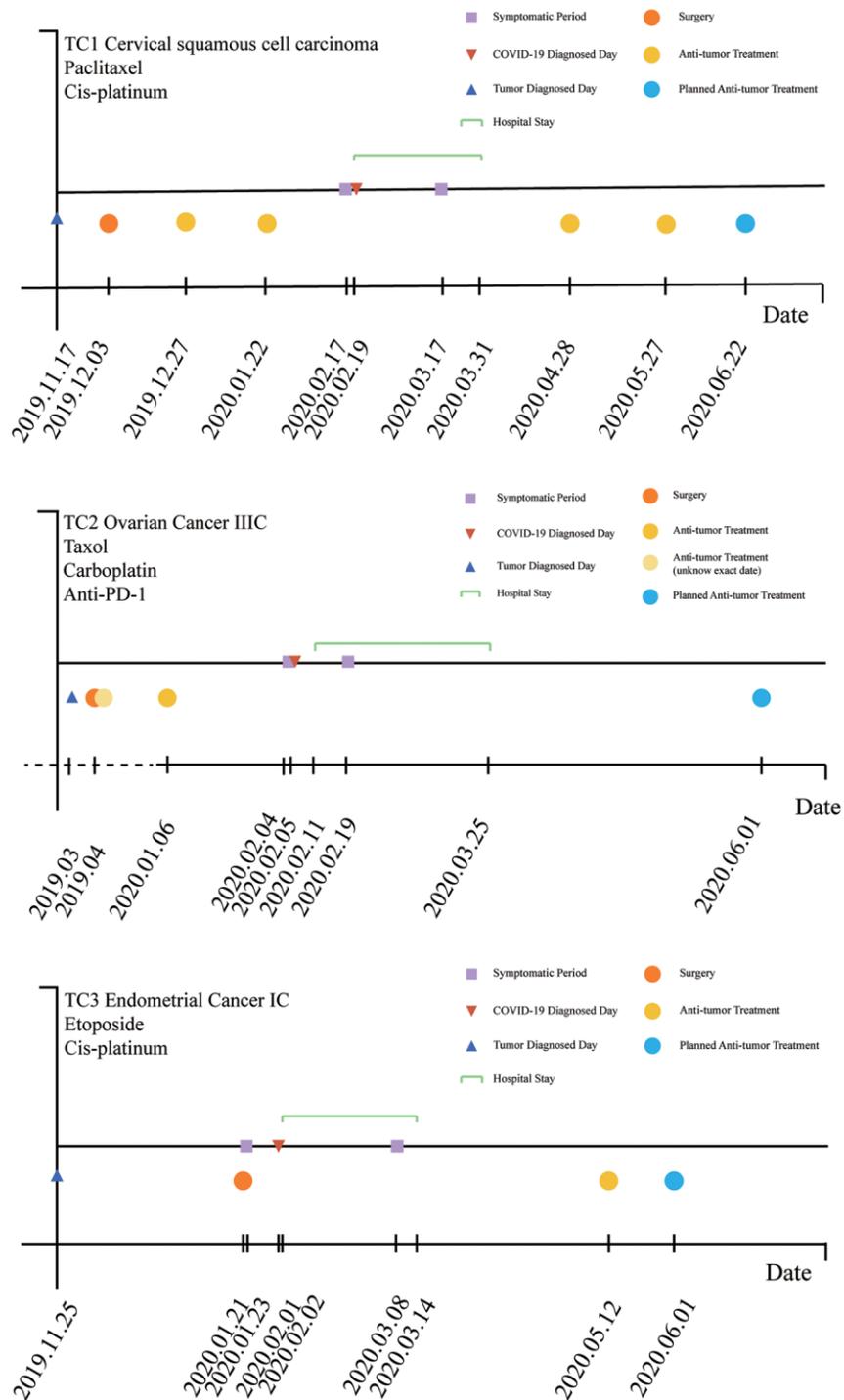


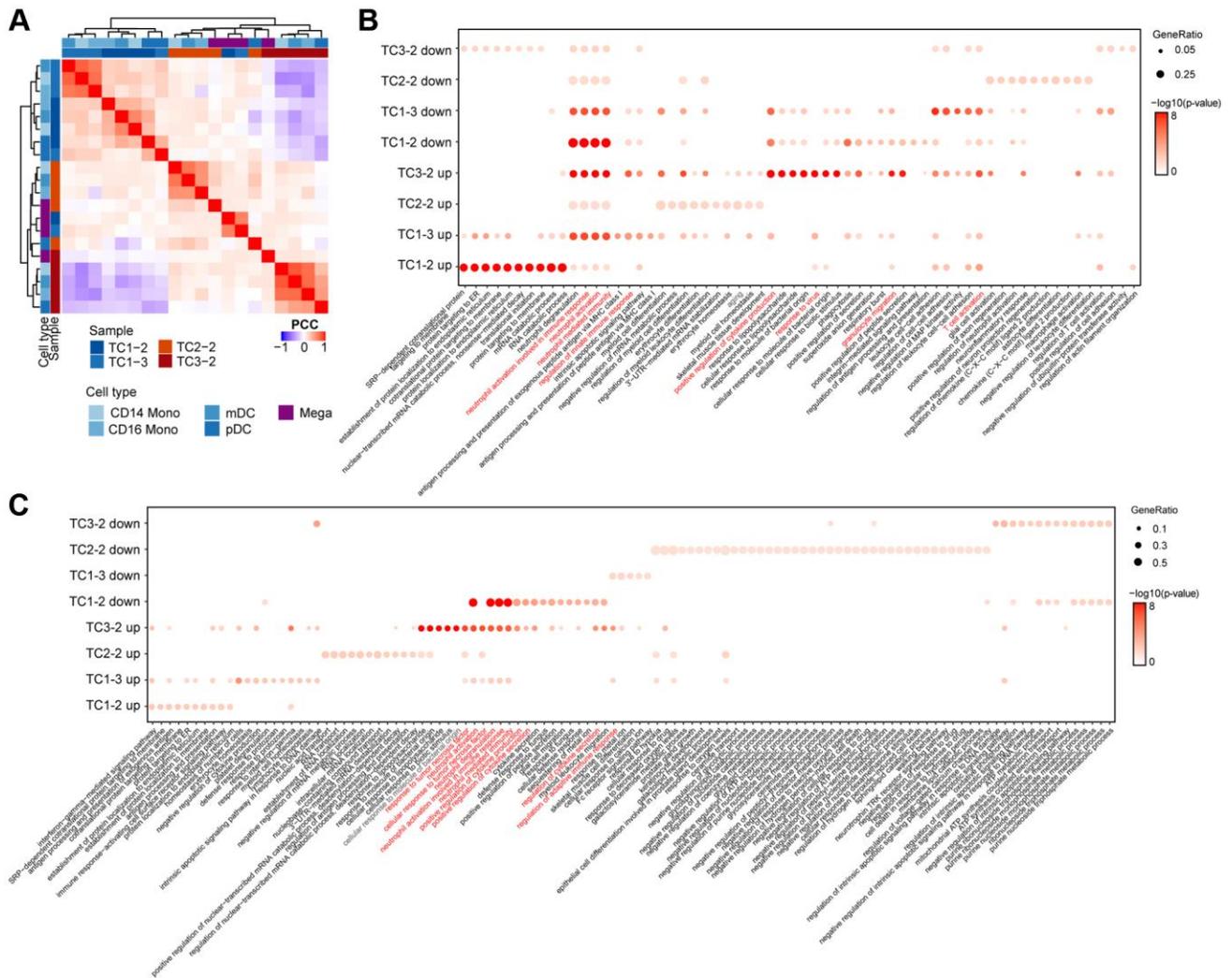
SUPPLEMENTARY FIGURES



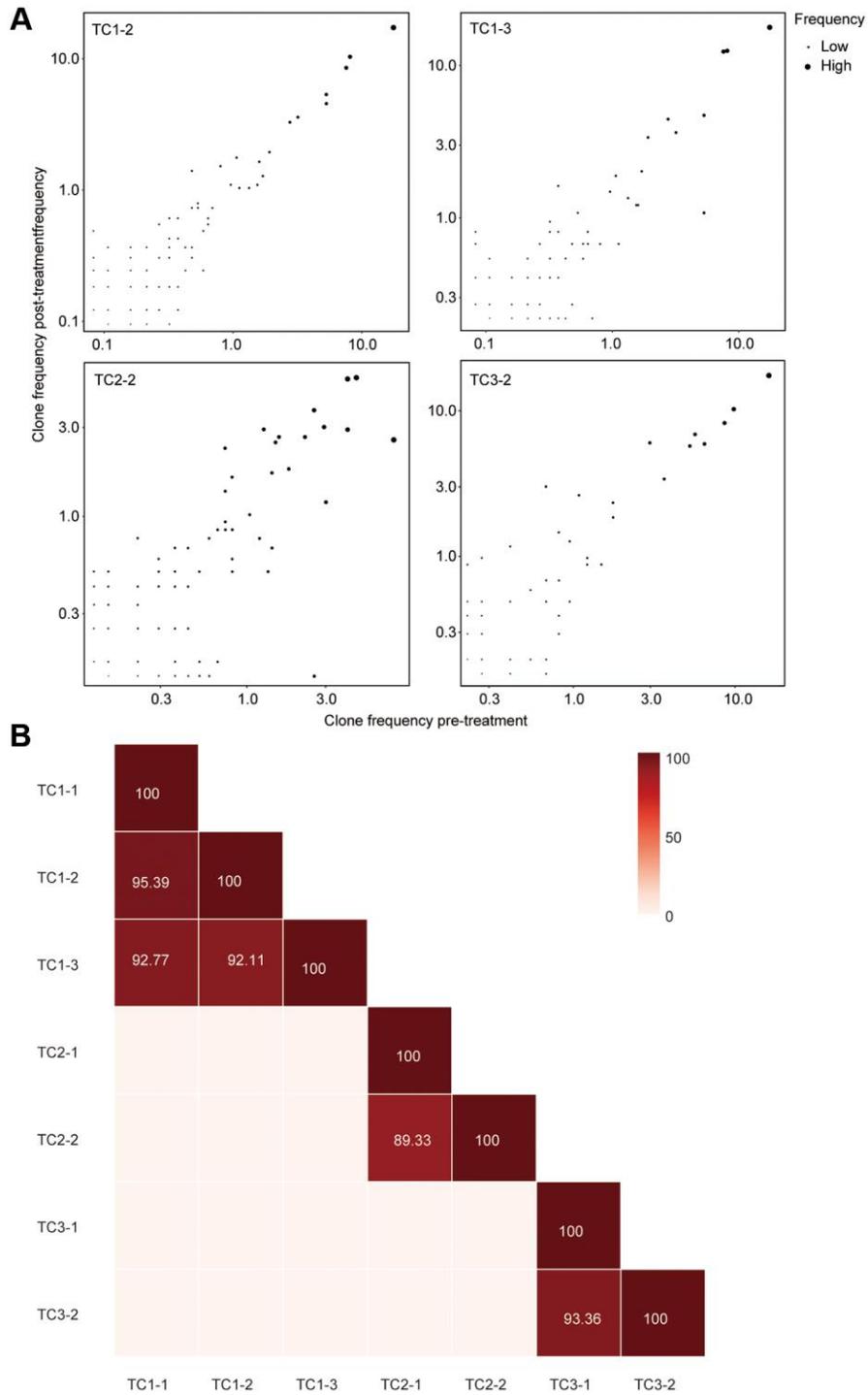
**Supplementary Figure 1. Box plots of proportion of each cell type in each group.** Samples are shown in different colors. Horizontal lines represent median values, with a maximum of 1.5× interquartile range. Significance was determined by Student’s *t*-test. \**p* < 0.05; \*\**p* < 0.01.



**Supplementary Figure 2. Flow chart of TC patients’ diagnosis and treatment during the epidemic of COVID-19.** Horizontal axis represent timeline. Medical events are represented by symbols in different shape & color. Diagnose and regents are annotated above.



**Supplementary Figure 3. Functional changes of myeloid cells pre- and post-treatment in COVID19 patients with tumor. (A)** Hierarchical clustering using the Pearson correlation coefficient (PCC) of a normalized transcriptome change between post- and pre-treatment in myeloid cells at cell type resolution. The color intensity indicates the PCC and the color bars above the heatmap indicate the cell type and disease group. **(B, C)** Enriched GO pathways of COVID-19 patients with tumor after treatment in Monocyte **(B)** and mDC **(C)** cells (top 4 columns: downregulated GO pathways after treatment, bottom 4 columns: upregulated GO pathways after treatment). The color intensity indicates the enrichment  $p$ -values and the point size indicates the ratio of gene enrichment in each pathway.



**Supplementary Figure 4. Clonal dynamics of T cells pre- and post-treatment in COVID19 patients with tumor.** (A) Scatterplots comparing TCR clone frequencies pre- and post-treatment in each sample after treatment. Shown are amplified clones ( $n > 1$ ). (B) The color intensity indicates the proportion of shared clones ( $n > 4$ ), which are labeled if they are over zero.