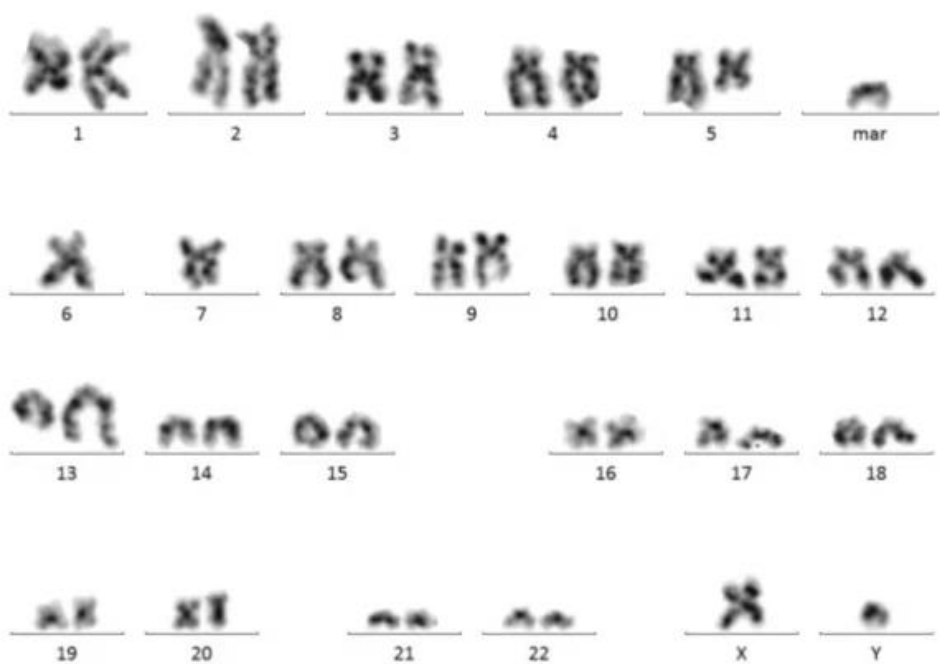
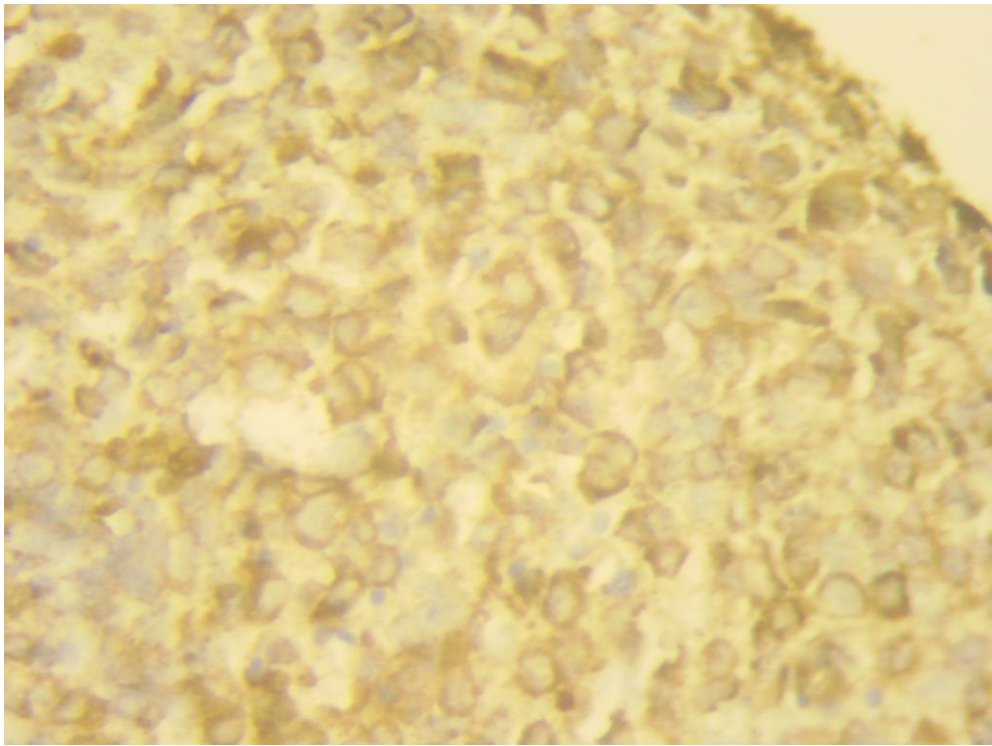


Supplementary Figure 1

A

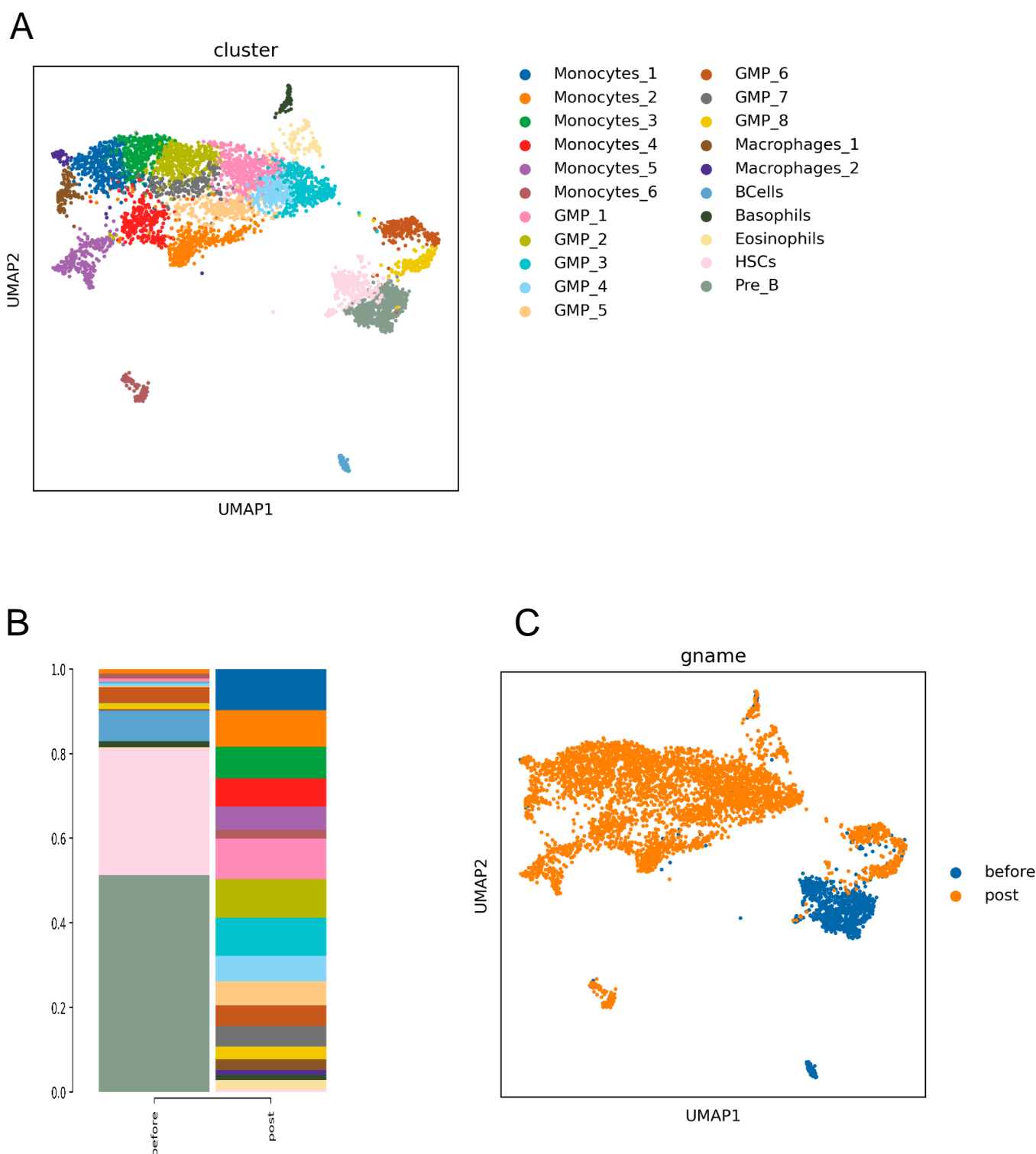


B



Post,MPO stained bone marrow

Supplementary Figure 1: clinical diagnosis of the patient.  
A. Complex karyotypes before CAR-T infusion. ISCN2020: 45,XY, ?der (5;6)(p10;p10), add (9)(p22), der(13)t(5;13)(q13;34),+mar, inc[cp8]/46,XY[12]  
B. Bone marrow biopsy stain demonstrated MPO positivity after CAR-T infusion.



Supplementary Figure 2: ScRNA-seq analysis of the patient underwent lineage switch post CAR-T treatment.

A. UMAP plots of BM cells from before and post CAR-T treatment. Each cell type (as indicated) was shown in different color. R package harmony was used to correct batch effects and constructed one UMAP based on all cell.

B. The ratio of different cell types before and post CAR-T treatment.

C. UMAP plots of BM cells from before and post CAR-T treatment. Each cell type (as indicated) was shown in different color.

A



C



D



Supplementary Figure 3: The cell communications before and post CAR-T treatment.

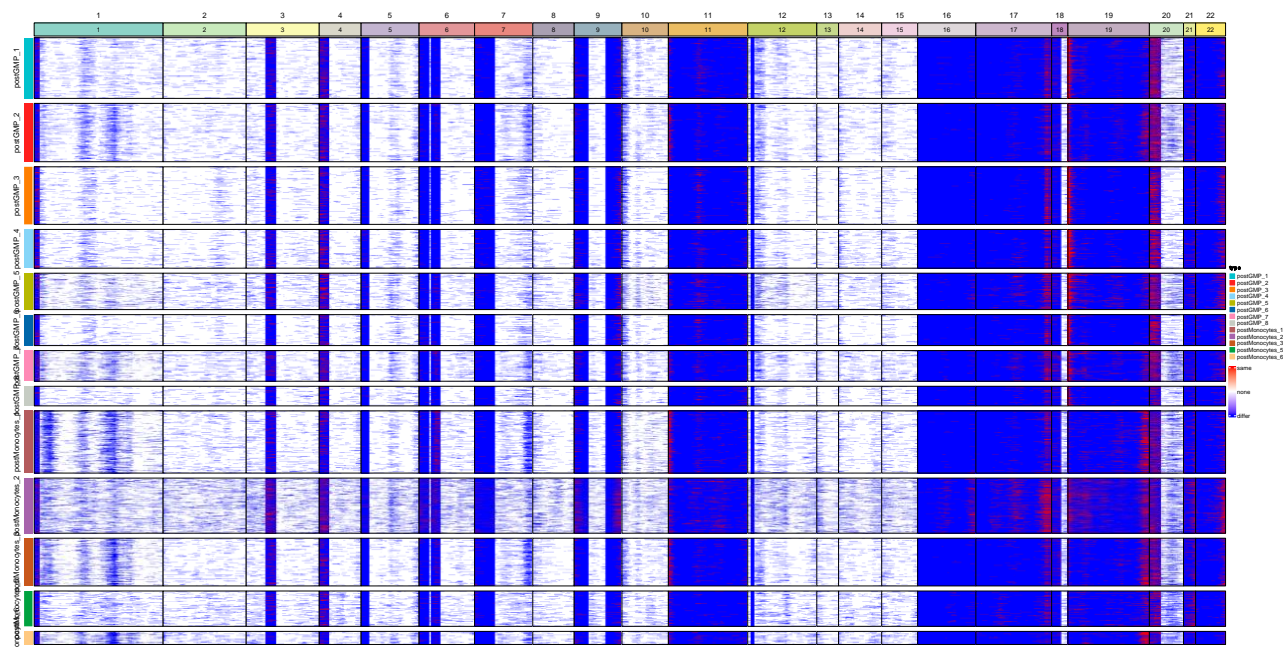
A-B. Circos plot of intercellular communication among HSCs, GMP, B cells, Pre-B cells, Monocytes, and TandNK from before (A) and post (B) CAR-T treatment. The outer ring displays color-coded cell types, and the inner ring represents the involved ligand (red)-receptor (blue) interacting pairs. Color transparency of the line is negatively correlated with the number of interaction pairs.

C-D. Overview of rank 30 ligand–receptor interactions between Monocytes and other cell types in before (C) and post (D) CAR-T treatment. The left panel represents Monocytes as receptor, and the right panel represents Monocytes as ligand. P values are indicated by circle size, with the scale to the right (permutation test). The means of the average expression levels of interacting molecule 1 in cluster 1 and interacting molecule 2 in cluster 2 are indicated by color.



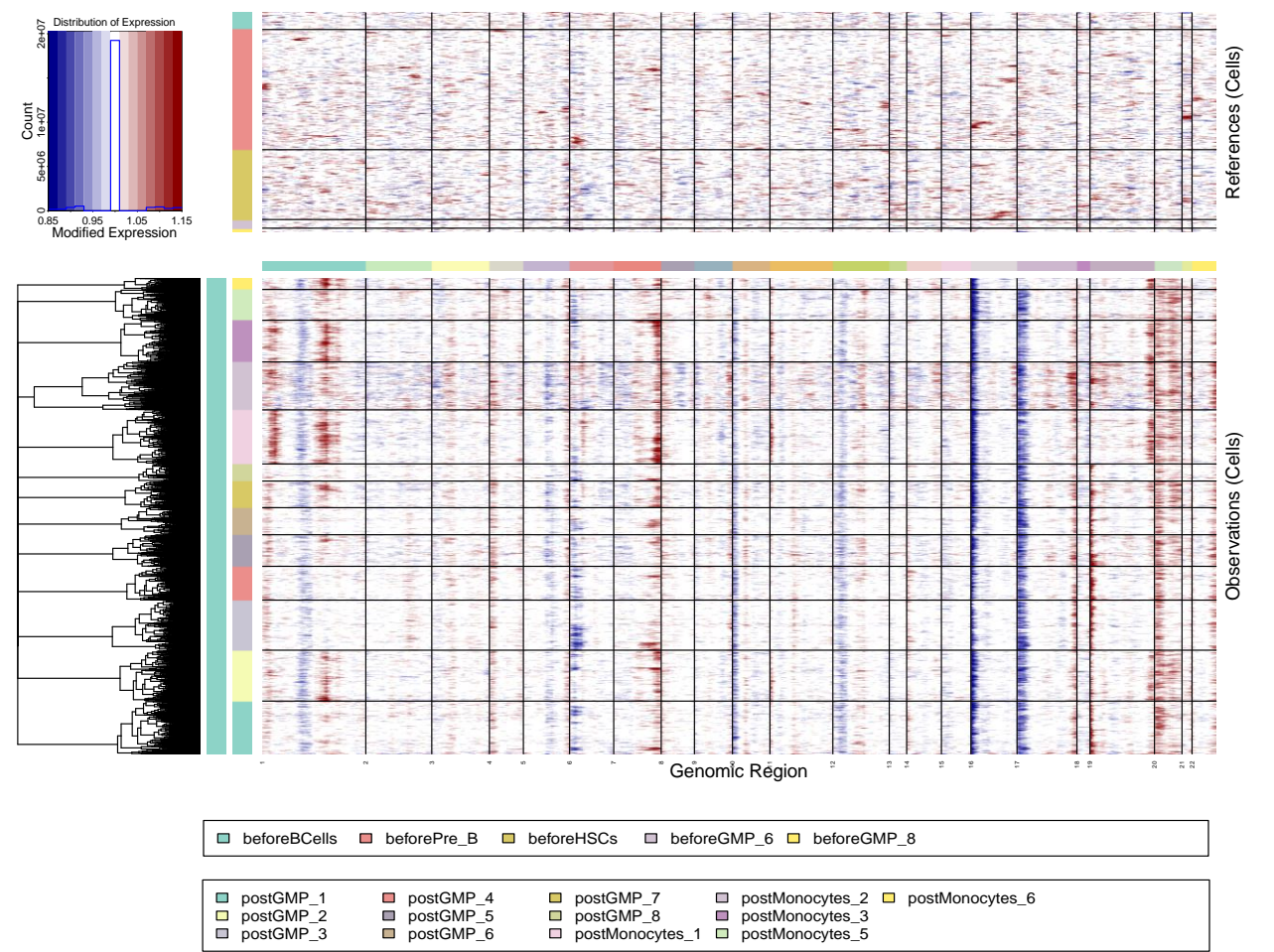
Supplementary Figure 4:

A



B

inferCNV



Supplementary Figure 4: The combination analysis of ScRNA-seq and WES of the patient underwent lineage switch after CAR-T treatment.

A. Colored plot showing the comparisons in the detected mutations between single-cell analyses and matched bulk tumor analyses. Red and blue colors indicate cells showing the same or different variants compared to the bulk tumor, respectively. White blocks indicate no reads covering the mutation region. Each row indicates a single cell and shows the cell type with different color.

B. Representative heatmap displaying the large-scale copy number variations (CNVs) identified in different cell types with scRNA-seq data. Top panel shows that no significant large-scale CNVs were identified in reference normal cells(T cells and NK), whereas chromosomal-scale deletions (blue) and gains (red) were observed for several chromosomes in different cell subtypes of tumor cells (second panel). The heatmap was created by inferCNV.