



Supplementary Figure S3. The heatmap of the normalized expression levels of the representative marker genes across major cell types identified by scRNA-seq. Marker genes were selected based on differential expression analysis using the Wilcoxon rank sum test. The heatmap displays cell type-specific expression profiles for key genes associated with monocytes, dendritic cells (DCs), CD4+ T cells, CD8+ T cells, natural killer (NK) cells, cycling cells, B cells, and platelets. Color intensity indicates normalized expression values scaled from 0 to 1.