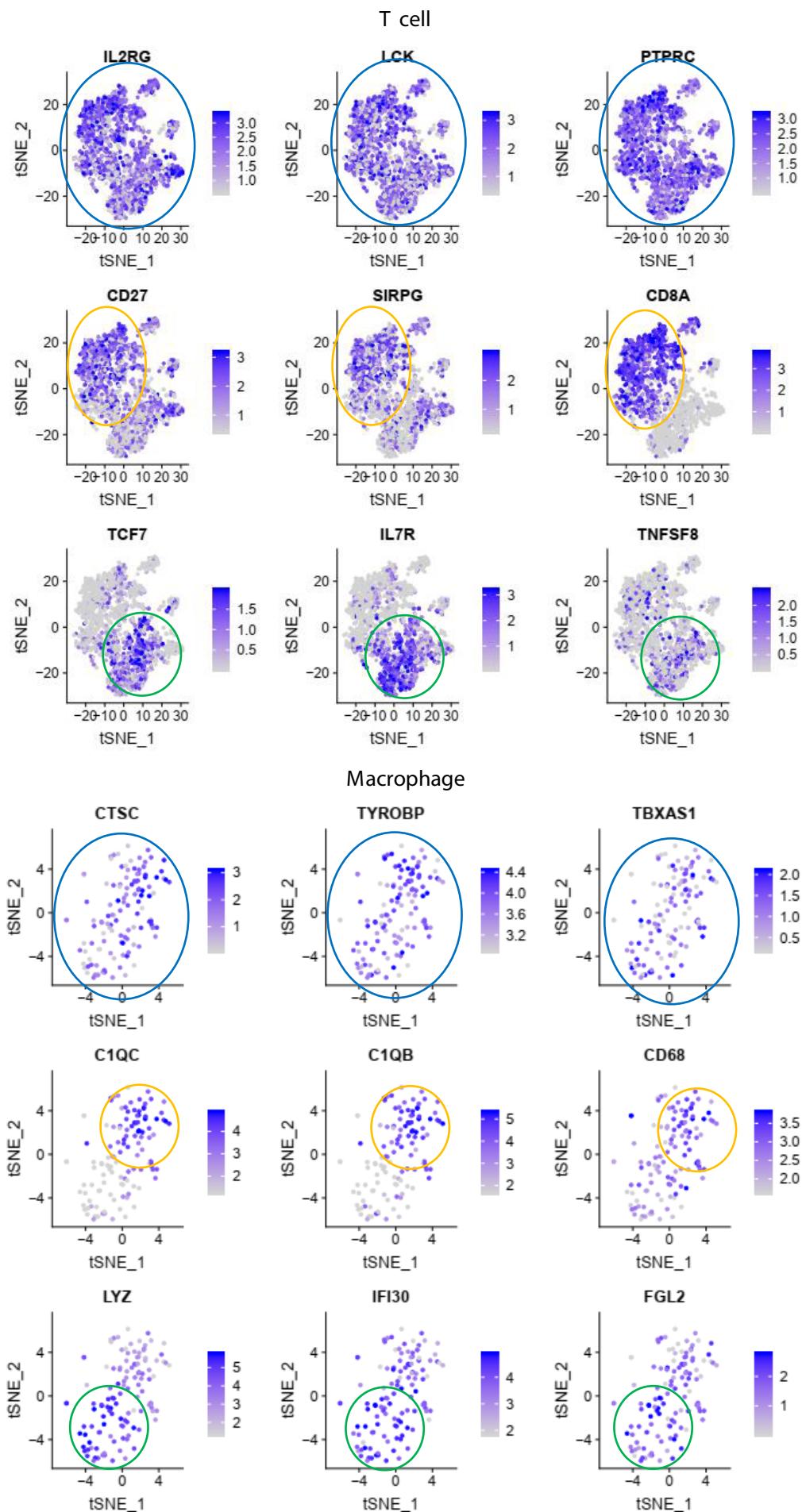
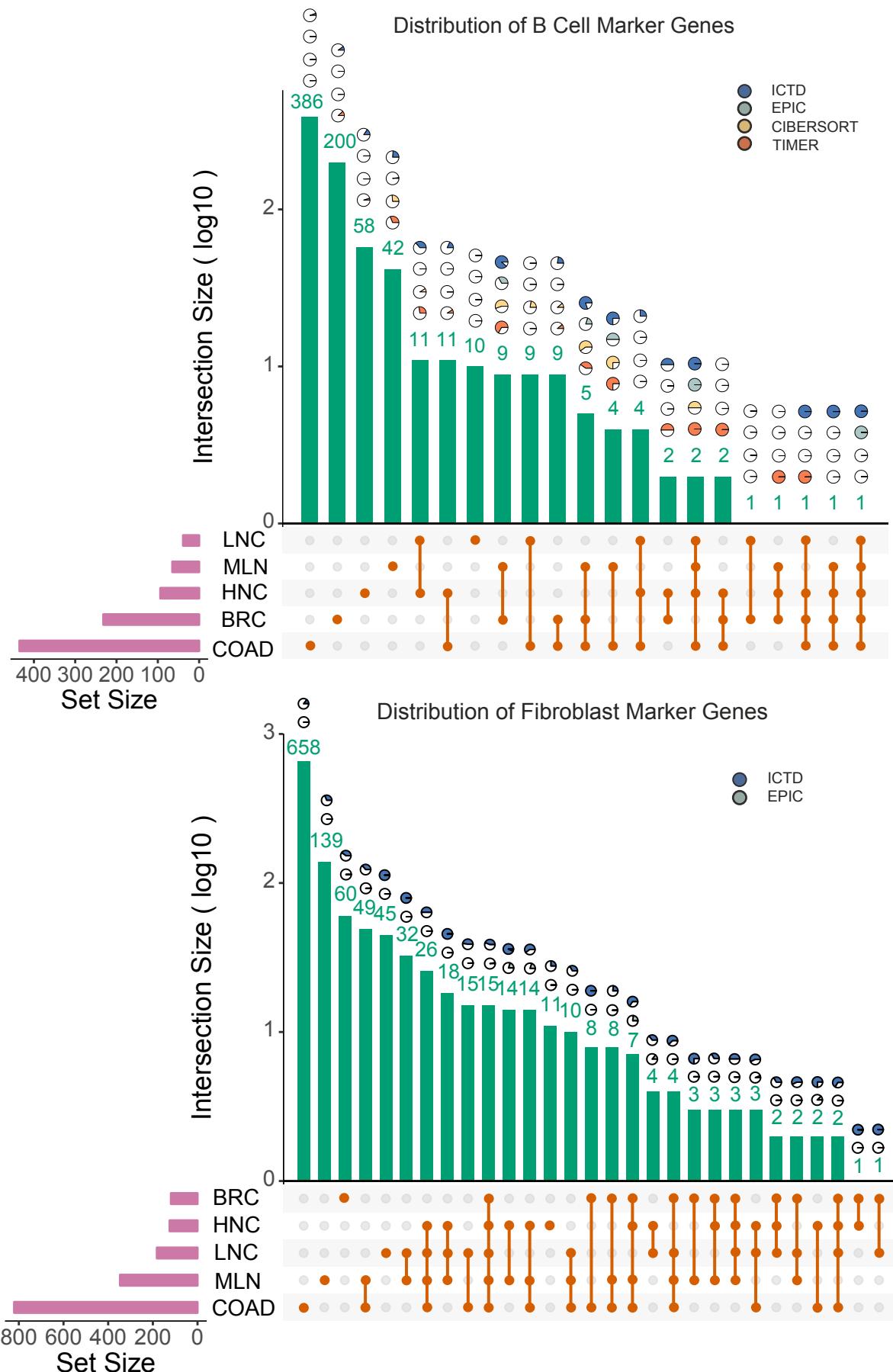


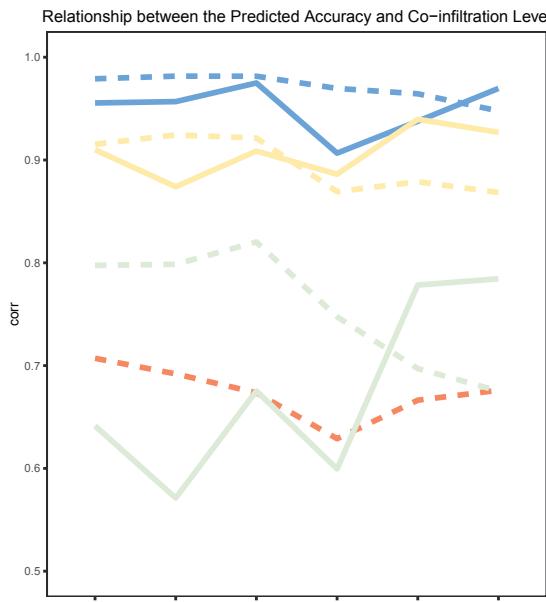
Supplementary Figure S1. Heatmap of ICTD identified marker genes on the SC data set. ICTD owns the capability of identifying the marker genes data specifically, each rank-1 module corresponds to one cell type or sub-cell type.



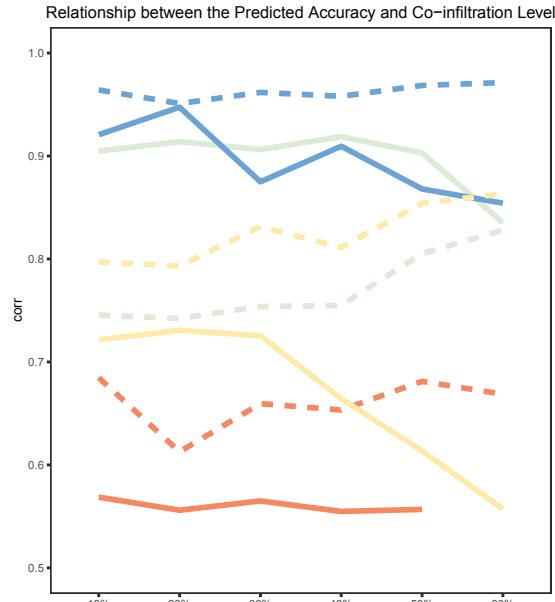
Supplementary Figure S2. tSNE plots of T, myeloid sub-cell types. General cell type marker genes show expression on overall cells, and sub-cell type marker genes show significant expression on sub-cell type clusters in tSNE.



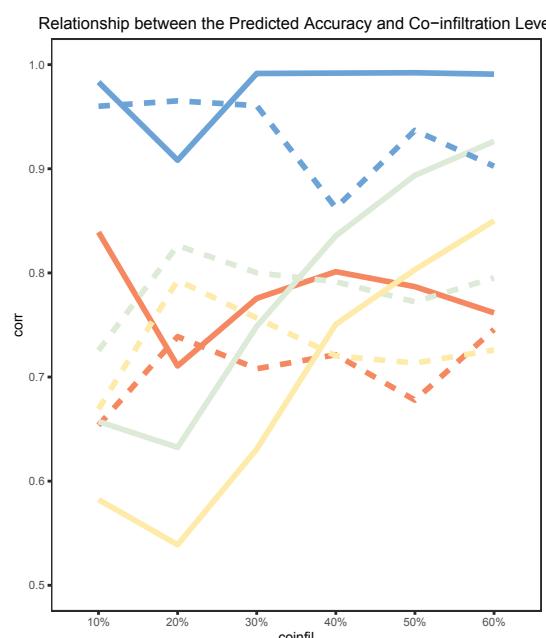
Supplementary Figure S3. tSNE plots of T, myeloid sub-cell types. General cell type marker genes show expression on overall cells, and sub-cell type marker genes show significant expression on sub-cell type clusters in tSNE.



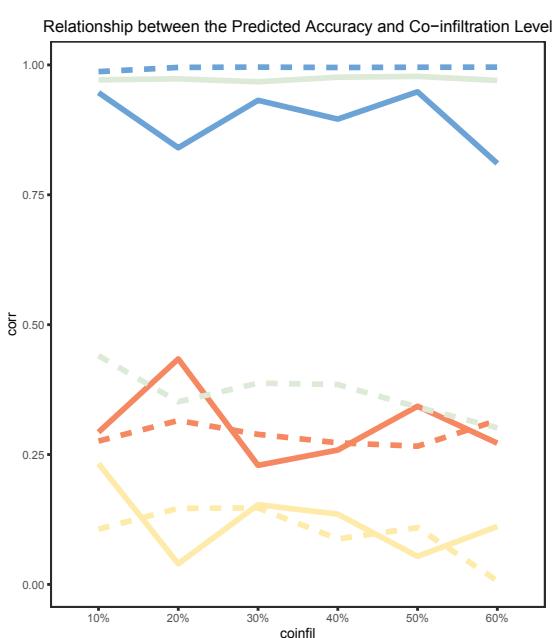
GSE75688



GSE81861

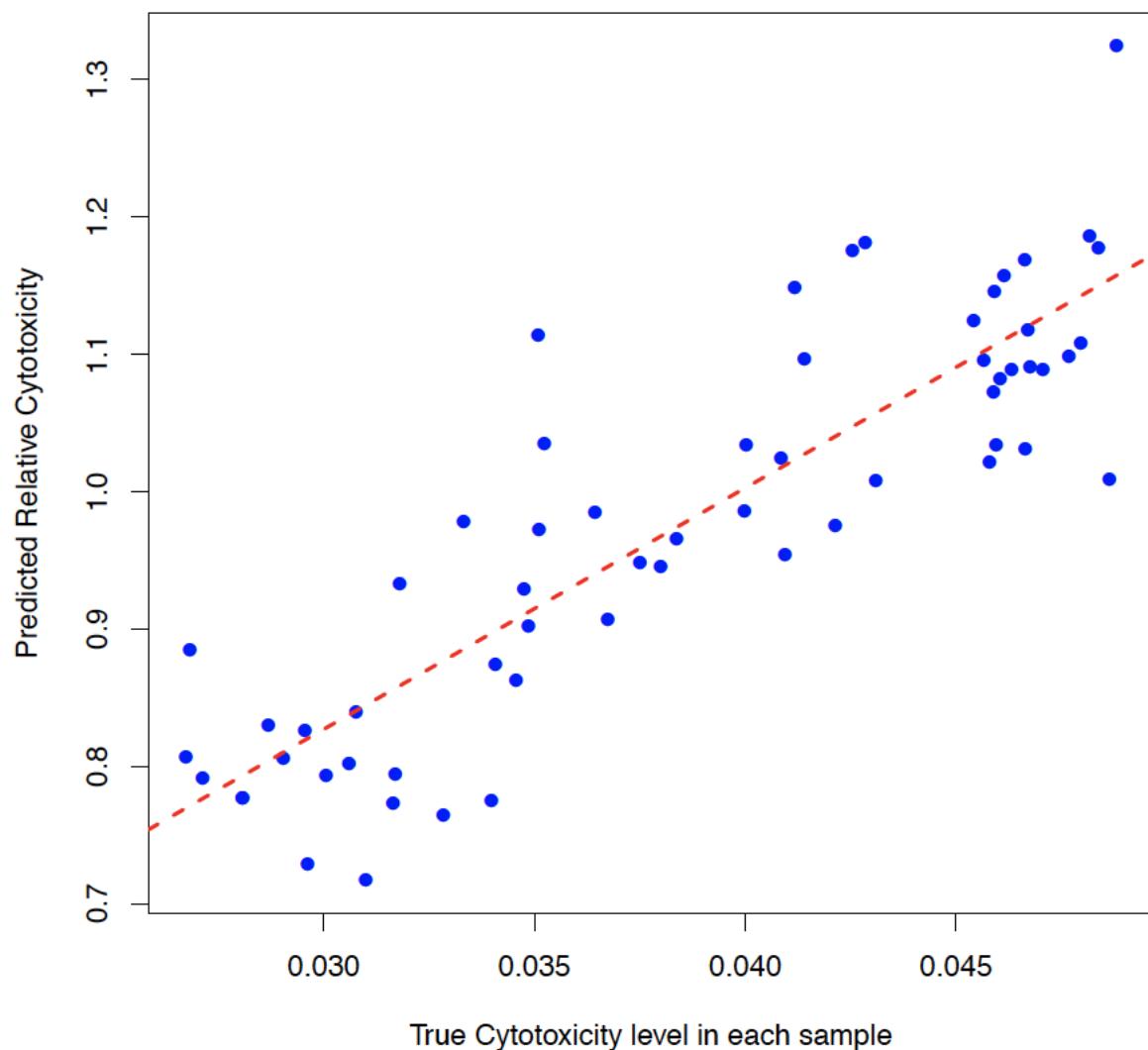


GSE103322

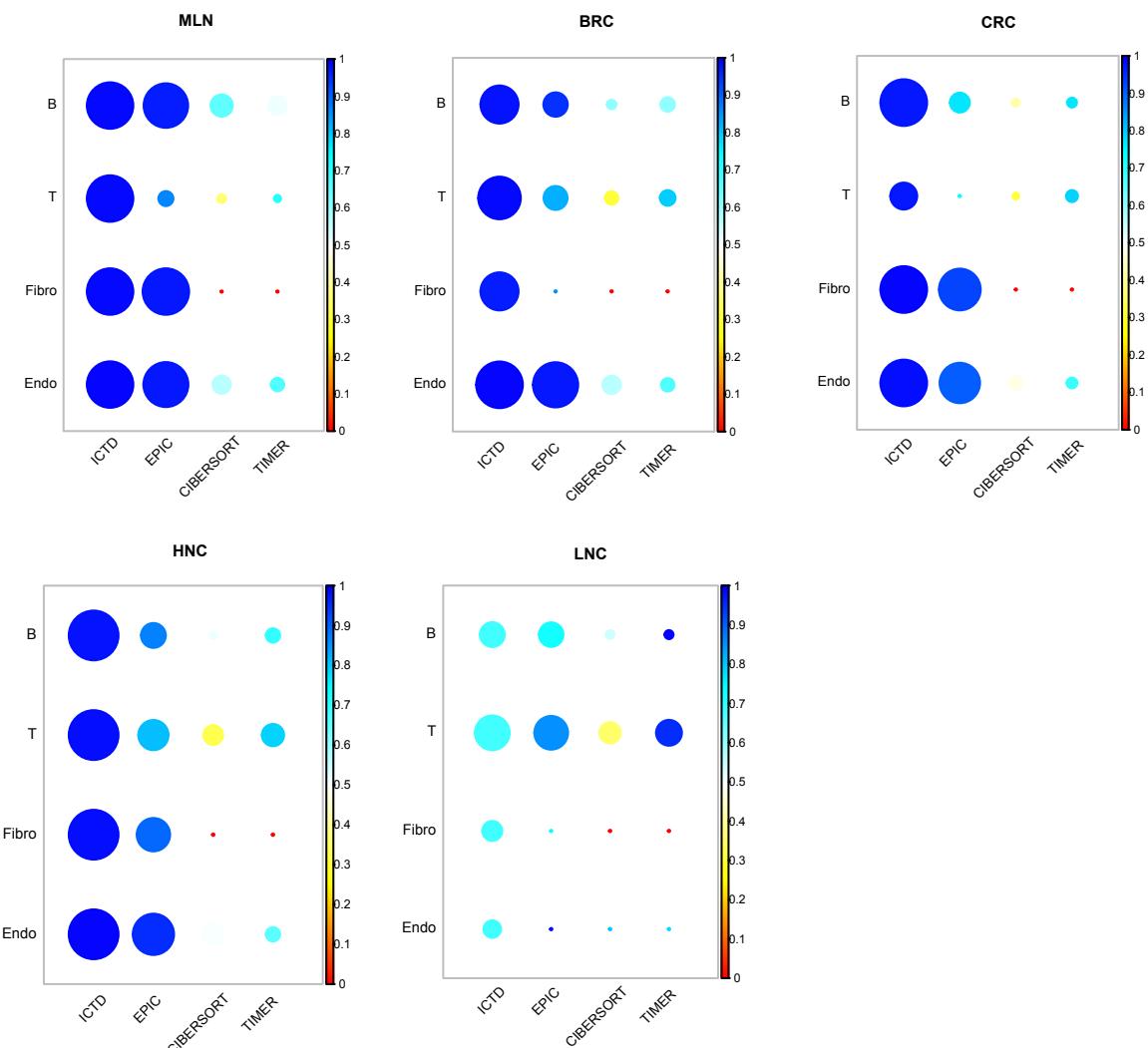


lung SC

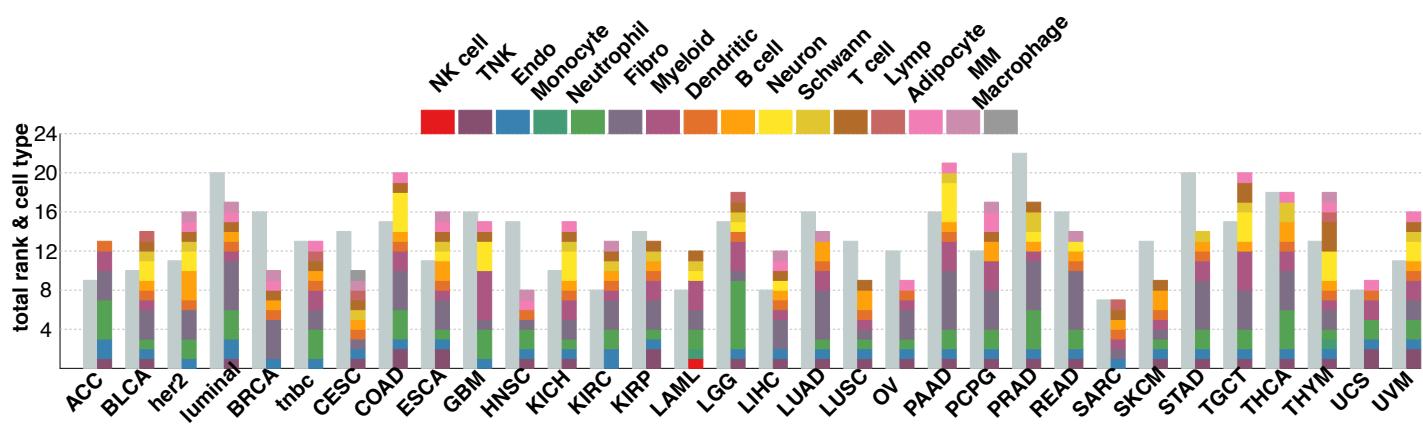
Supplementary Figure S4. Relationship of the predicted accuracy and the simulated co-infiltration level.
Several experiments were executed for each method and mean value shows as plot. As co-infiltration level increased, the performance of other deconvolution methods was harmed due to heavy co-linearity.



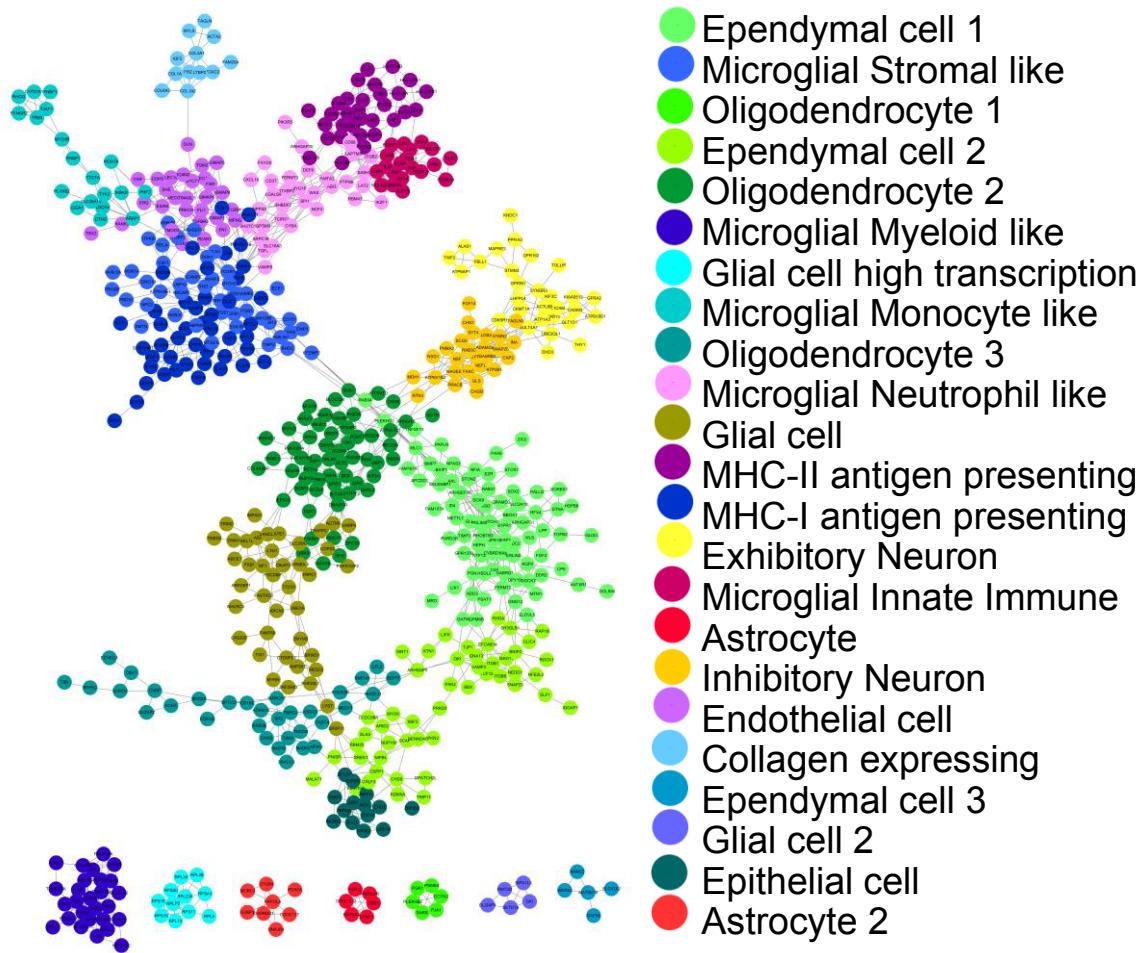
Supplementary Figure S5. Correlation between the true and predicted cytotoxicity level per unit T cell.



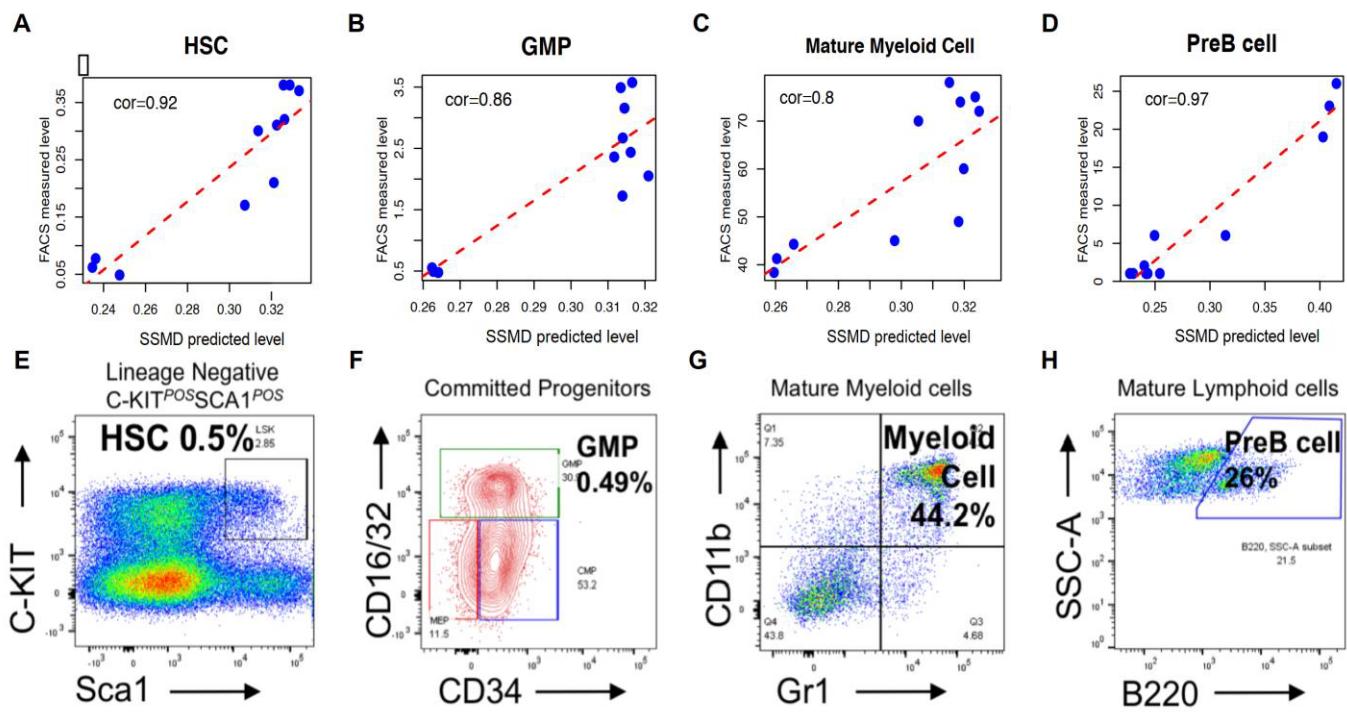
Supplementary Figure S6. Accuracy of cell type specific markers. The circle size represents the ratio of cell type signature genes used in each method as the true cell type specific markers, while the color represents the explanation score.



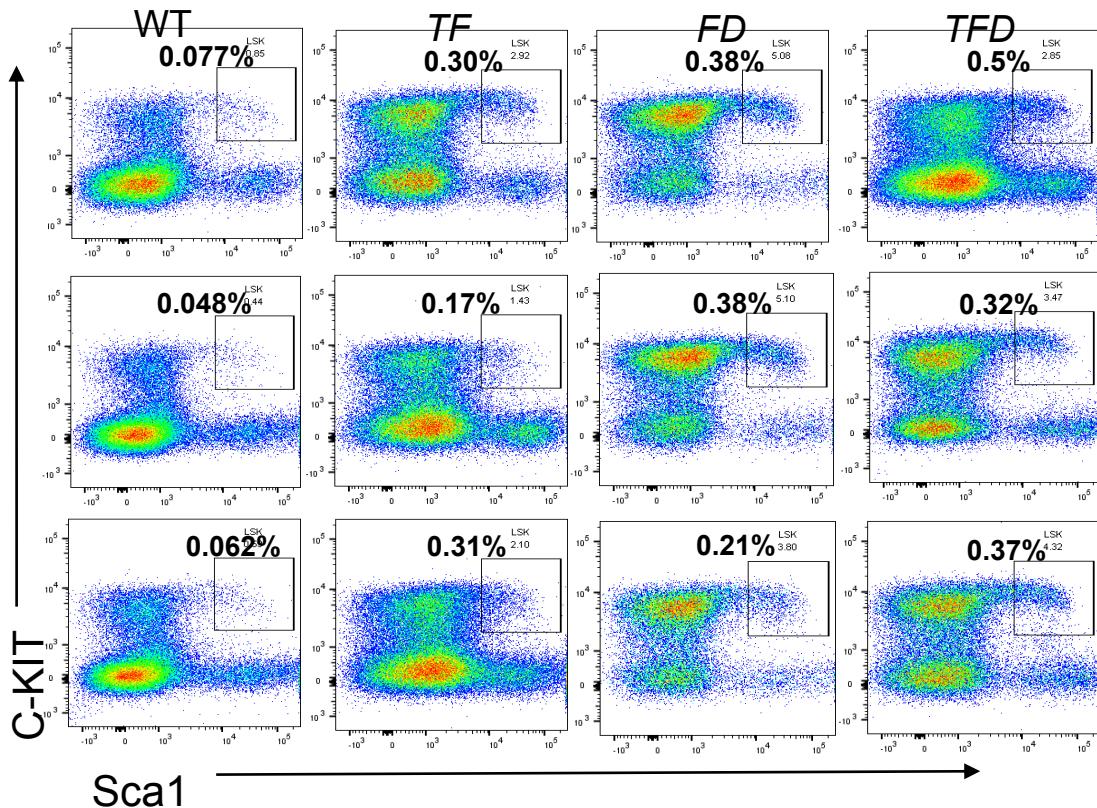
Supplementary Figure S7. Consistency of the number of ICTD identified cell types and the matrix rank of the expression profile of the markers of identified cell types in selected TCGA data.



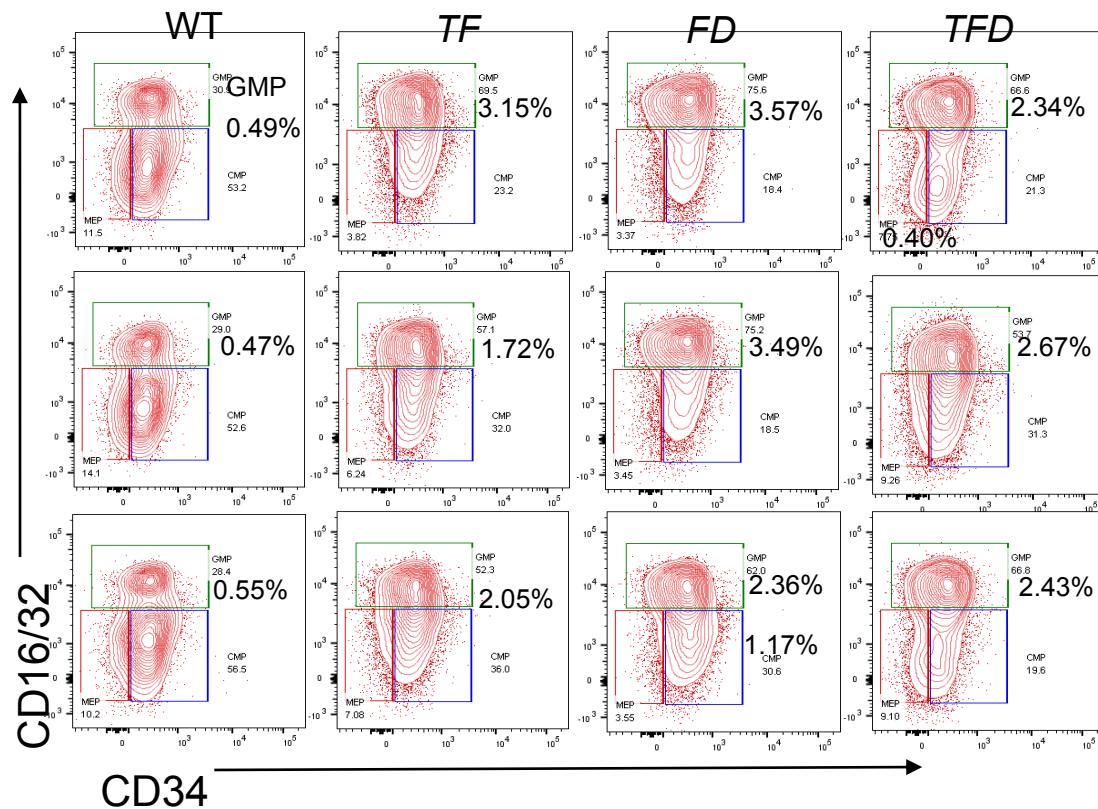
Supplementary Figure S8. Network of the marker genes of the commonly identified cell (sub) types in the human brain environment.



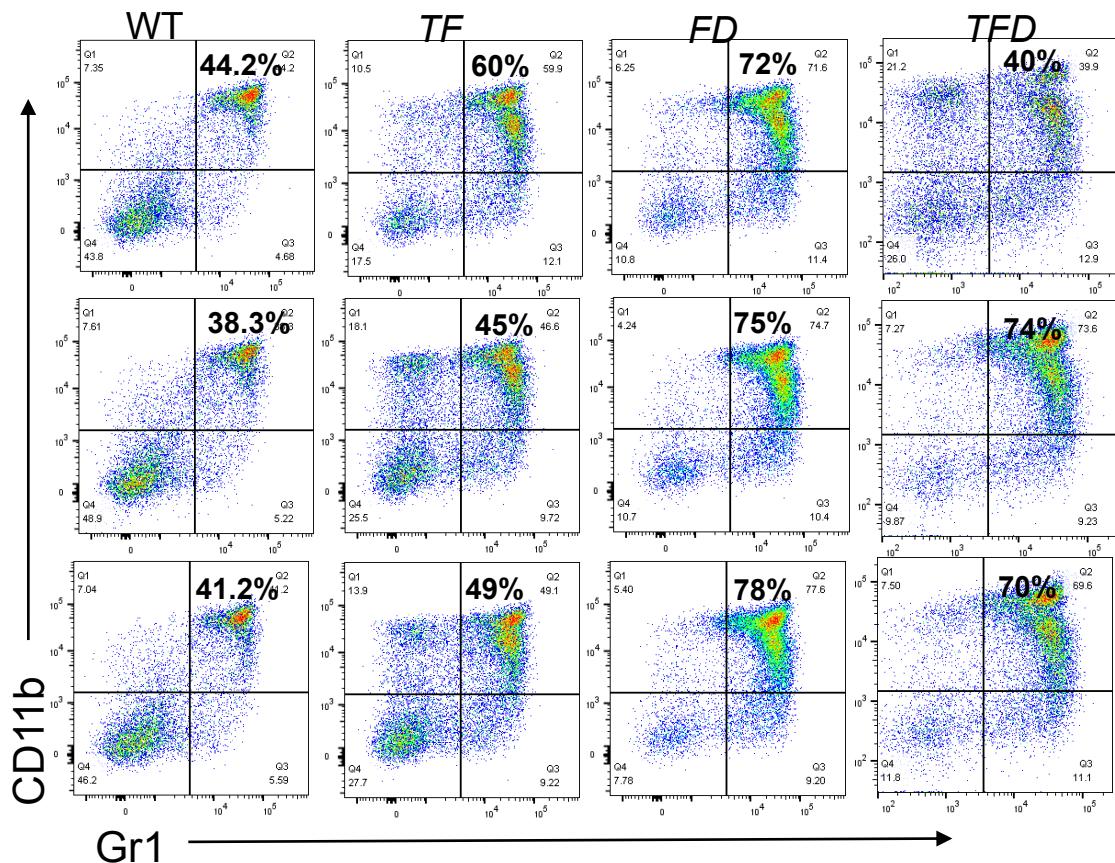
I. Hematopoietic Stem Cell (LSK cell)



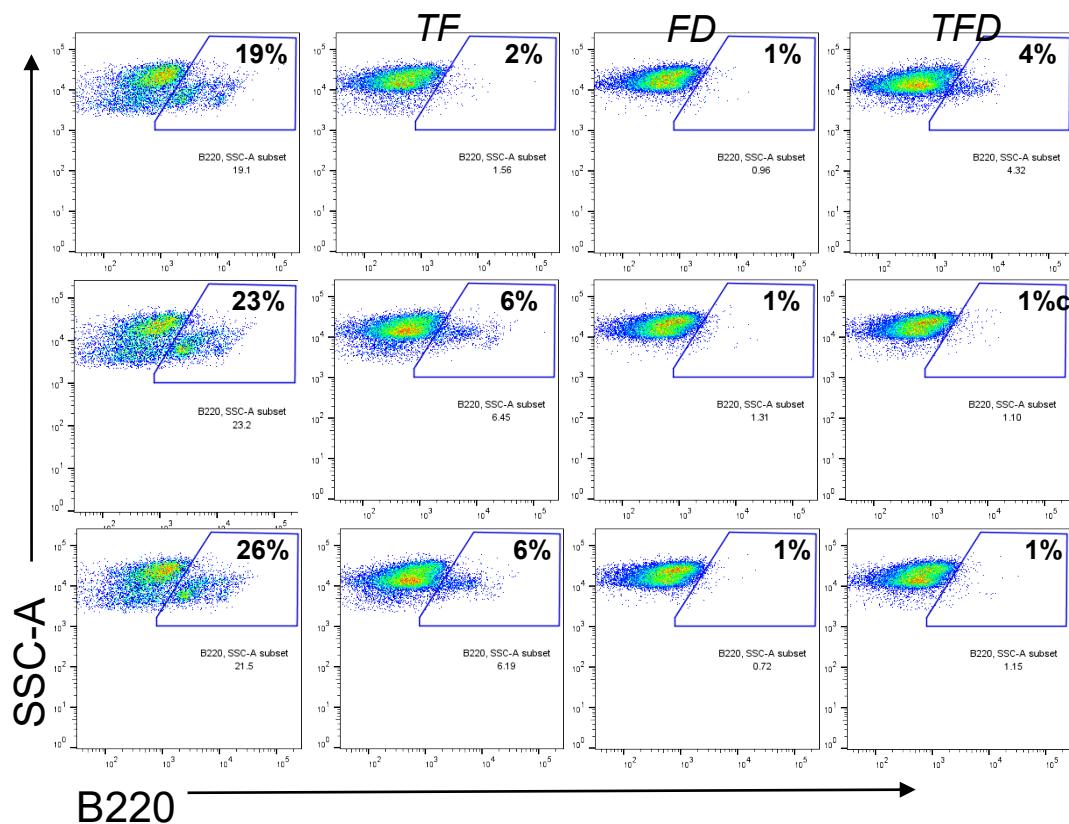
J. General Myeloid Progenitor (GMP) cells



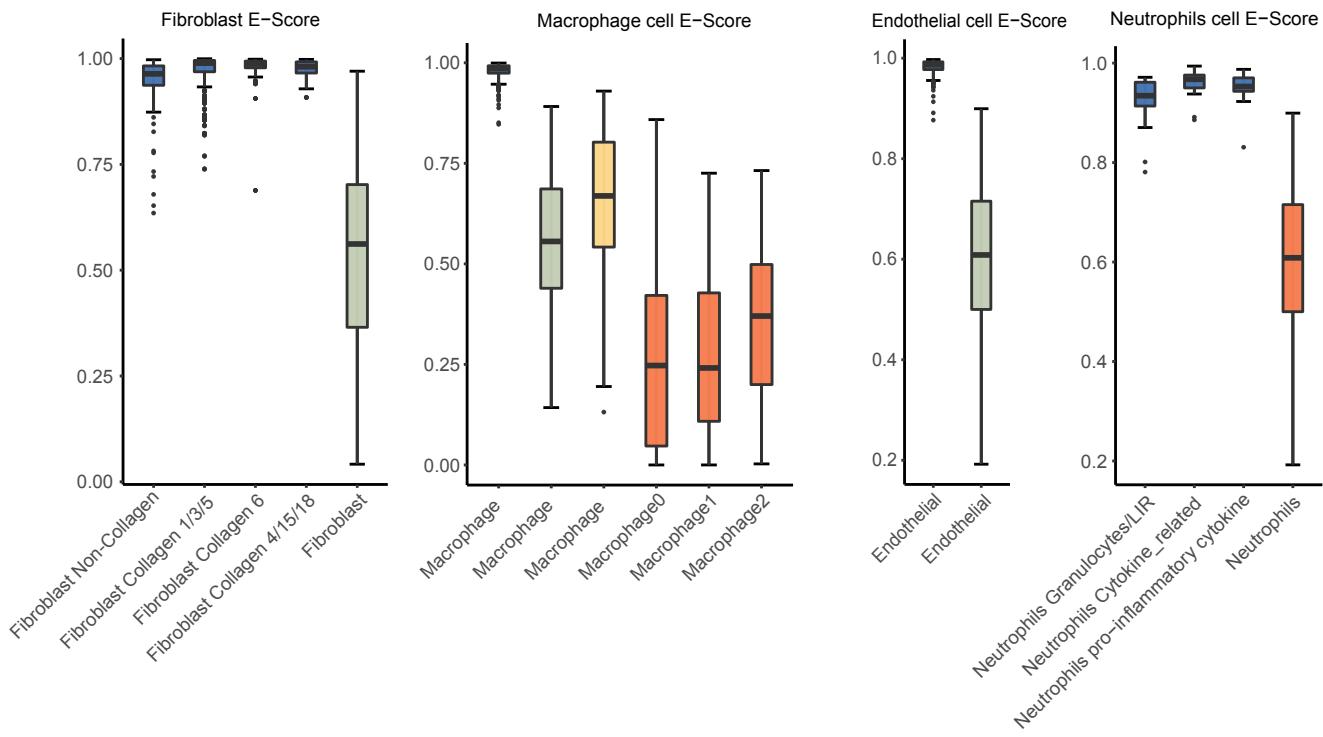
K. Mature Myeloid cells



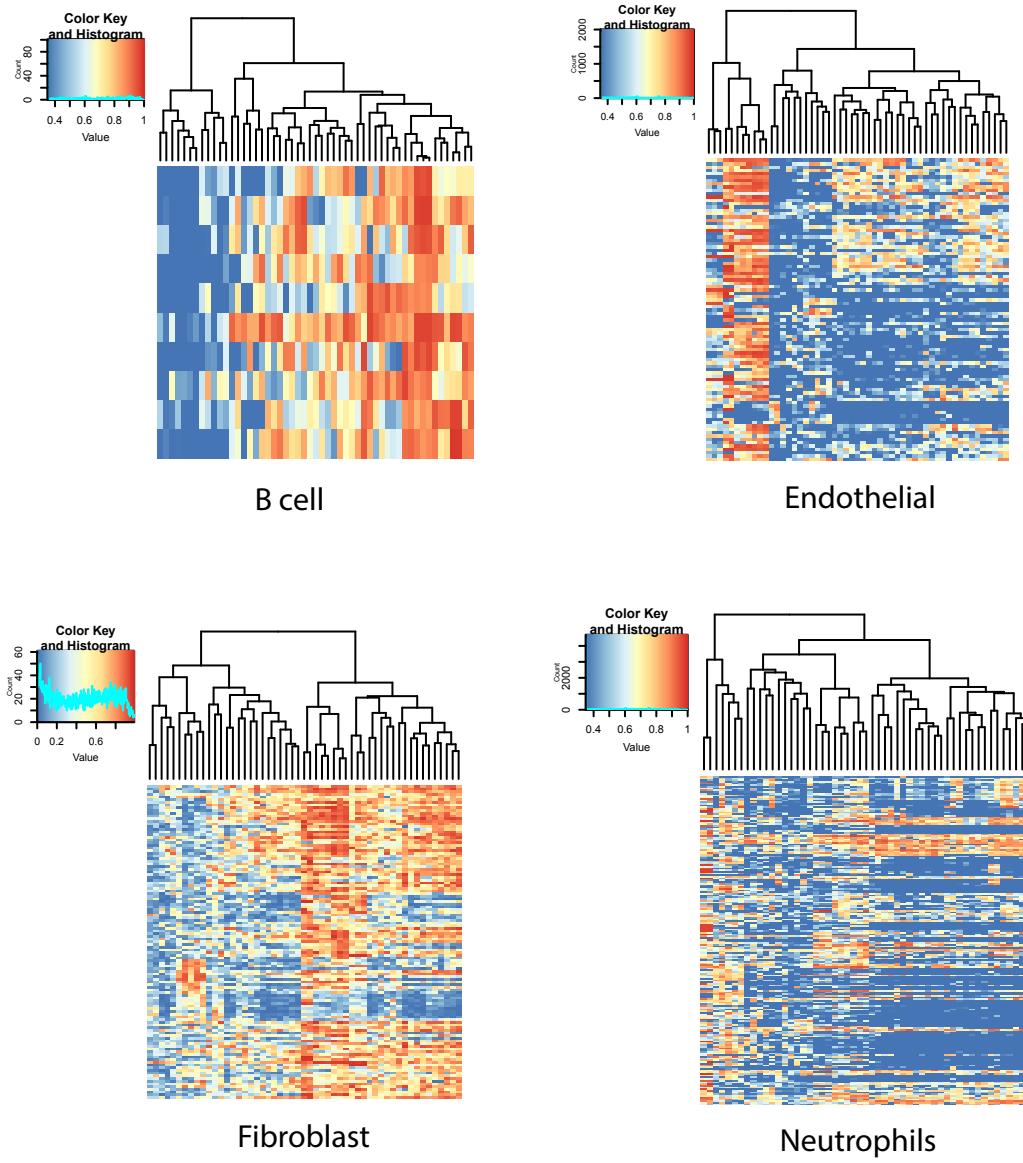
L. Pre-B Cells



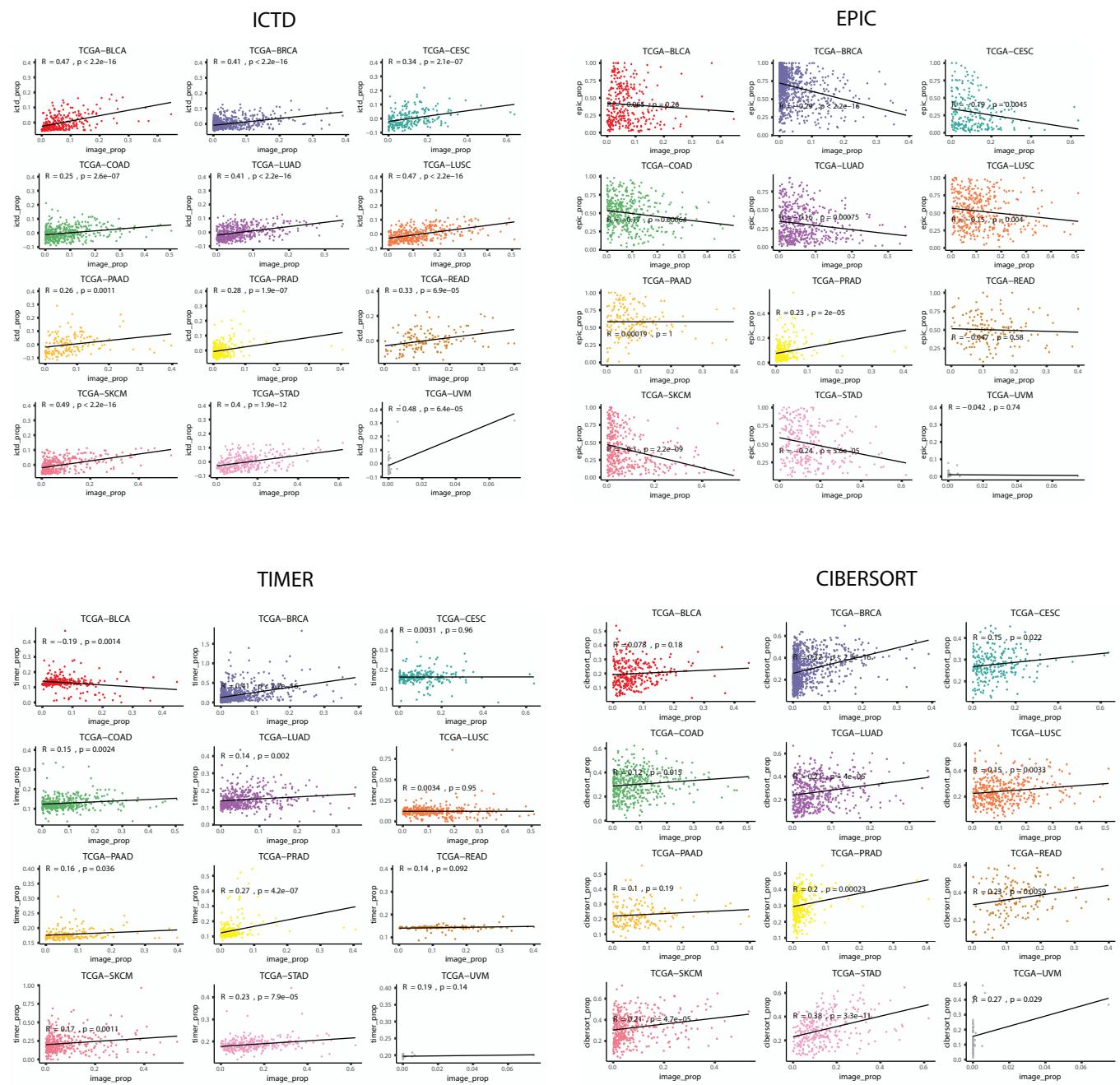
Supplementary Figure S9. FACS analysis. (A-D) Correlation between ICTD predicted (x-axis) and FACS identified (y-axis) cell proportions of HSC, GMP, mature myeloid cell and pre-B cell. **(E-H)** marker proteins utilized to identify the four cell types by using FACS. **(I-L)** FACS of LSK cells, GMP cells, mature myeloid cells, and pre-B cells.



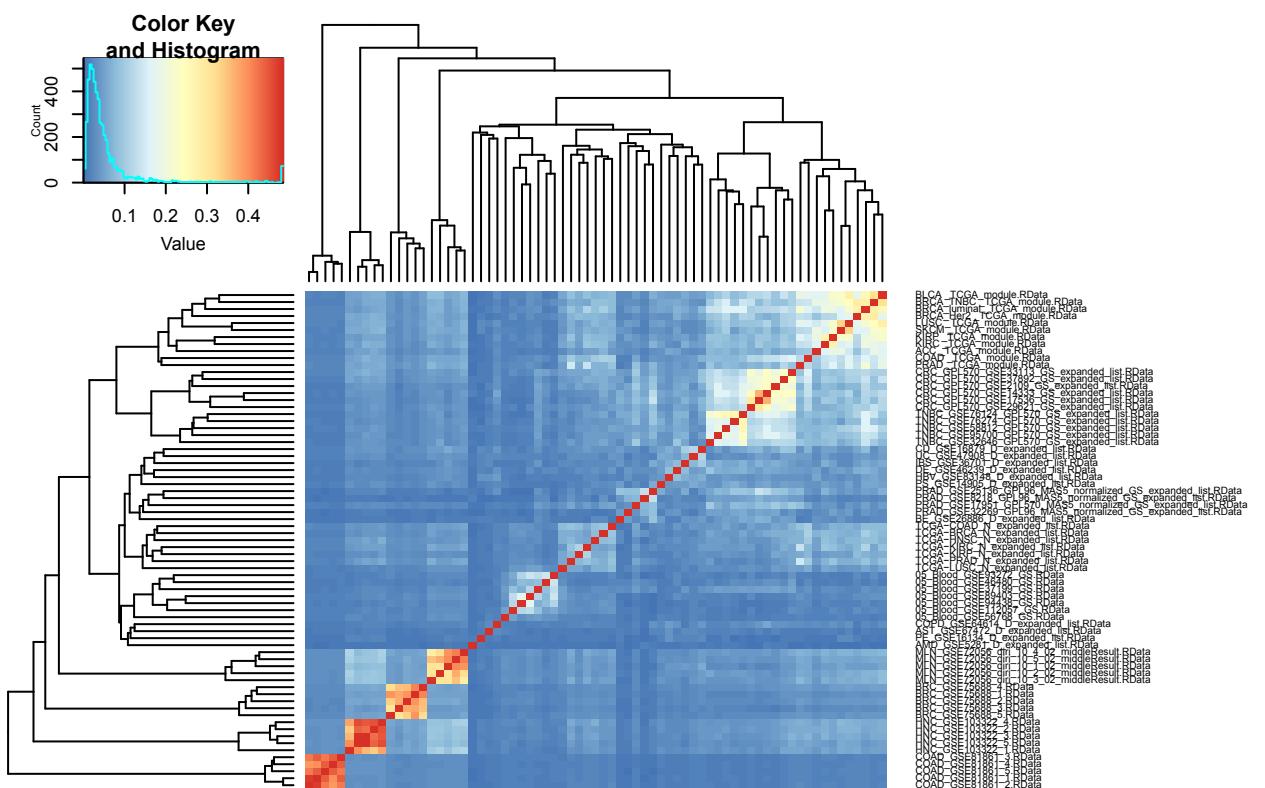
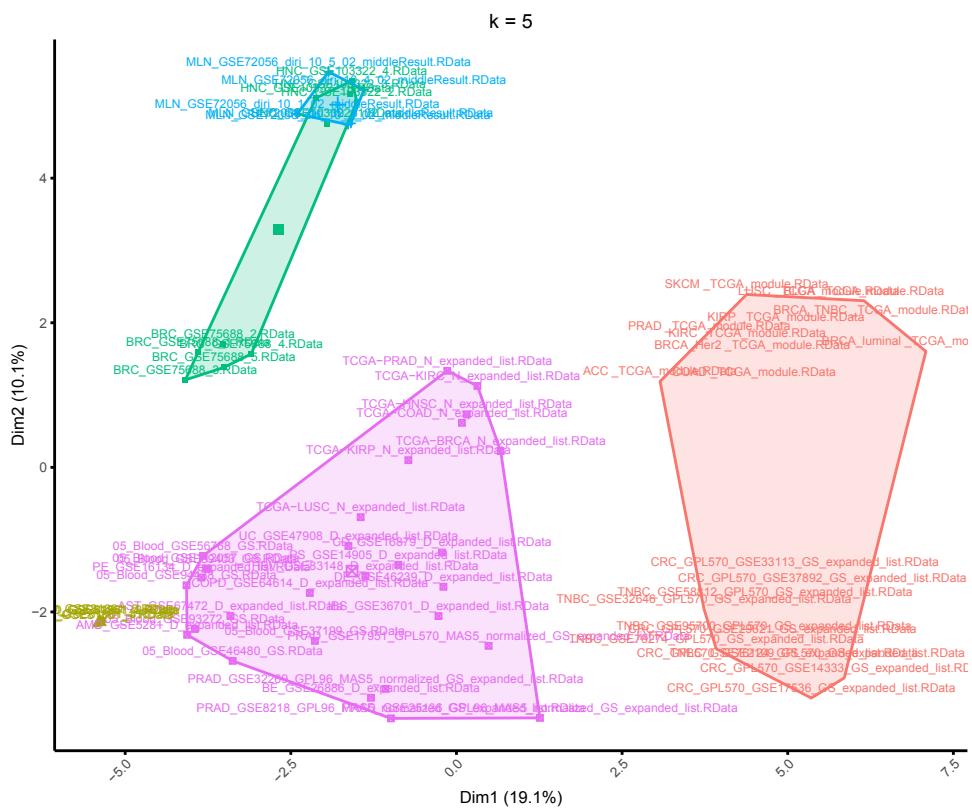
Supplementary Figure S11. E-score of the fibroblast, macrophage, endothelial and neutrophils cell marker genes identified by ICTD and used by EPIC, TIMER and CIBERSORT in TCGA data.



Supplementary Figure S12. Variation of B cell, endothelial, fibroblast and neutrophils markers in identified CNBI data.



Supplementary Figure S13. Correlation between omics data predicted cell proportions and image data predicted cell proportions for ICTD and other methods.



Supplementary Figure S14. Consistency of overall identified immune and stromal (sub) cell types and marker genes identified in the CNBI data.