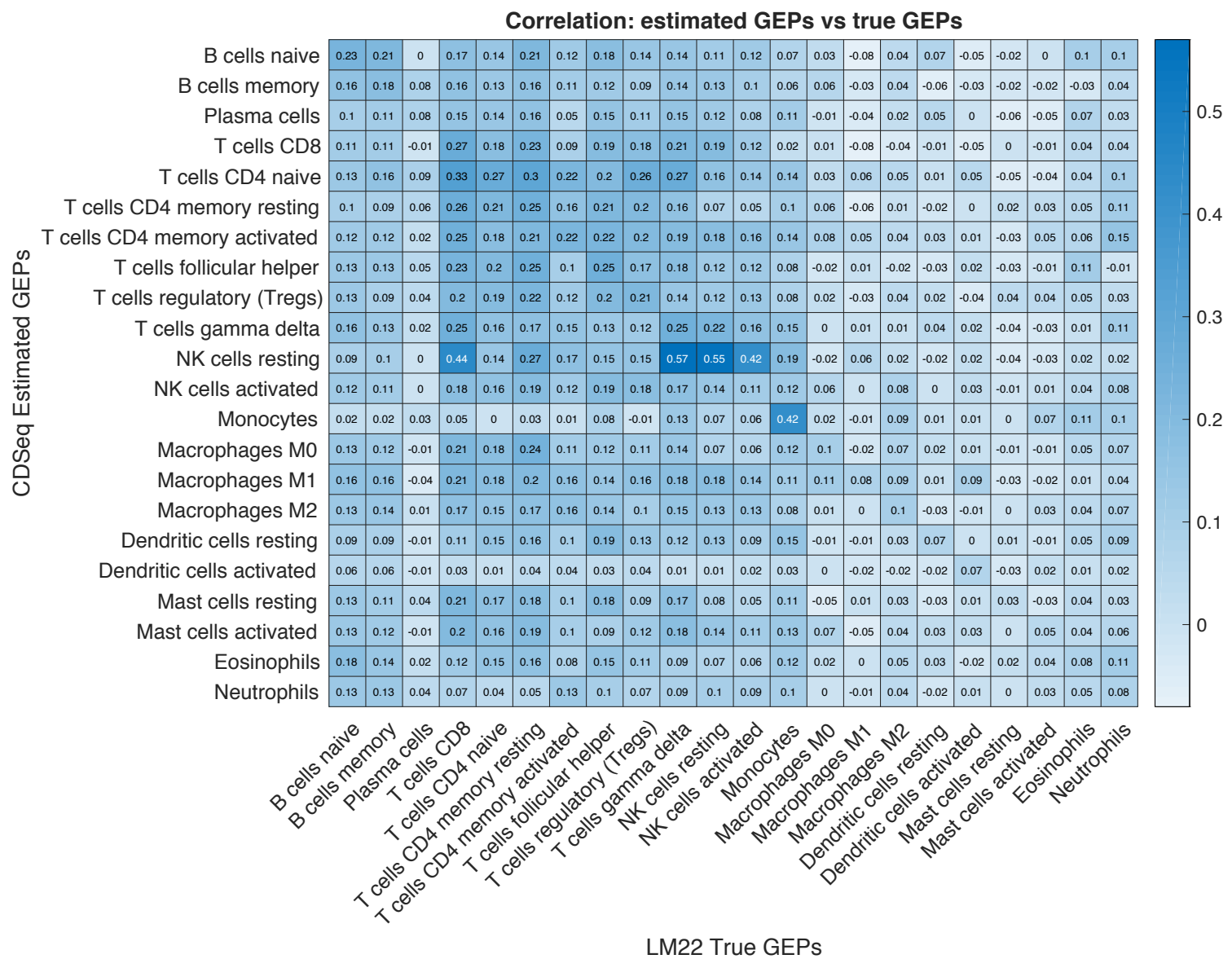
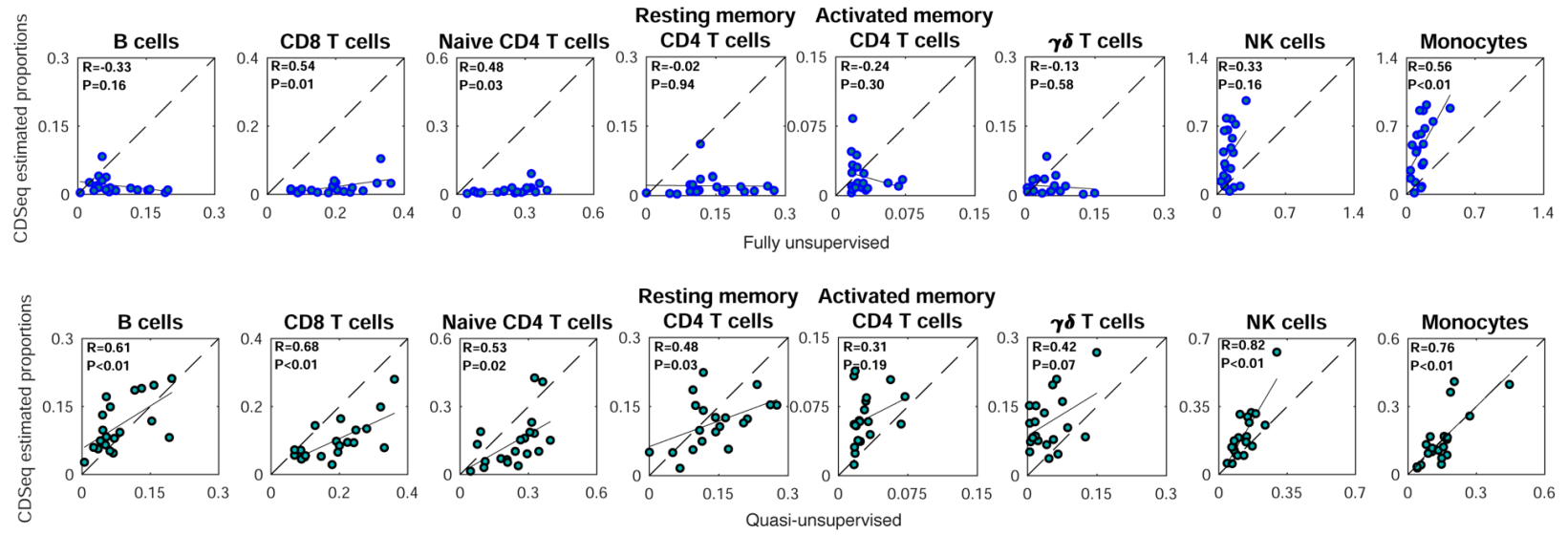


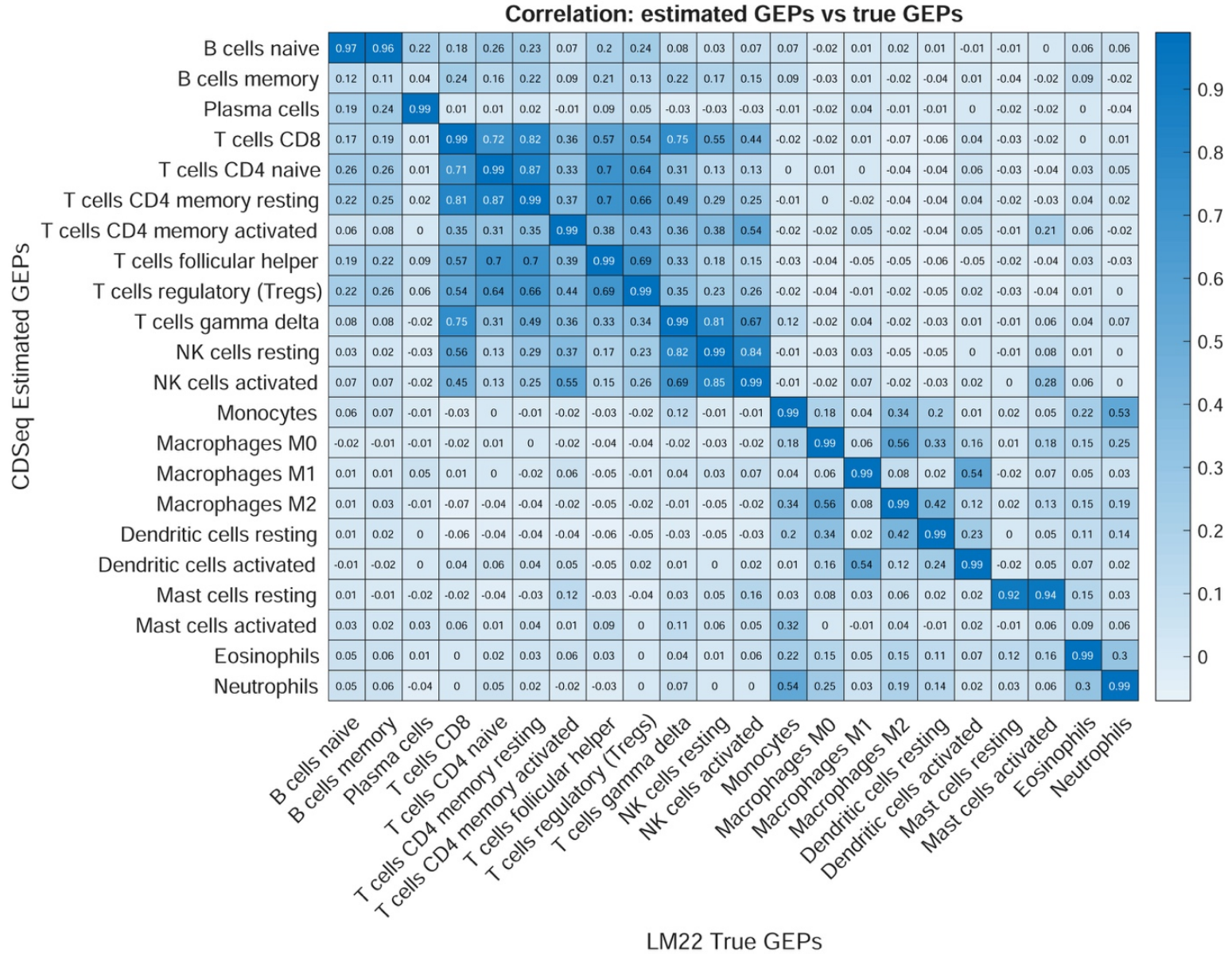
CDSeq on deep deconvolution

A



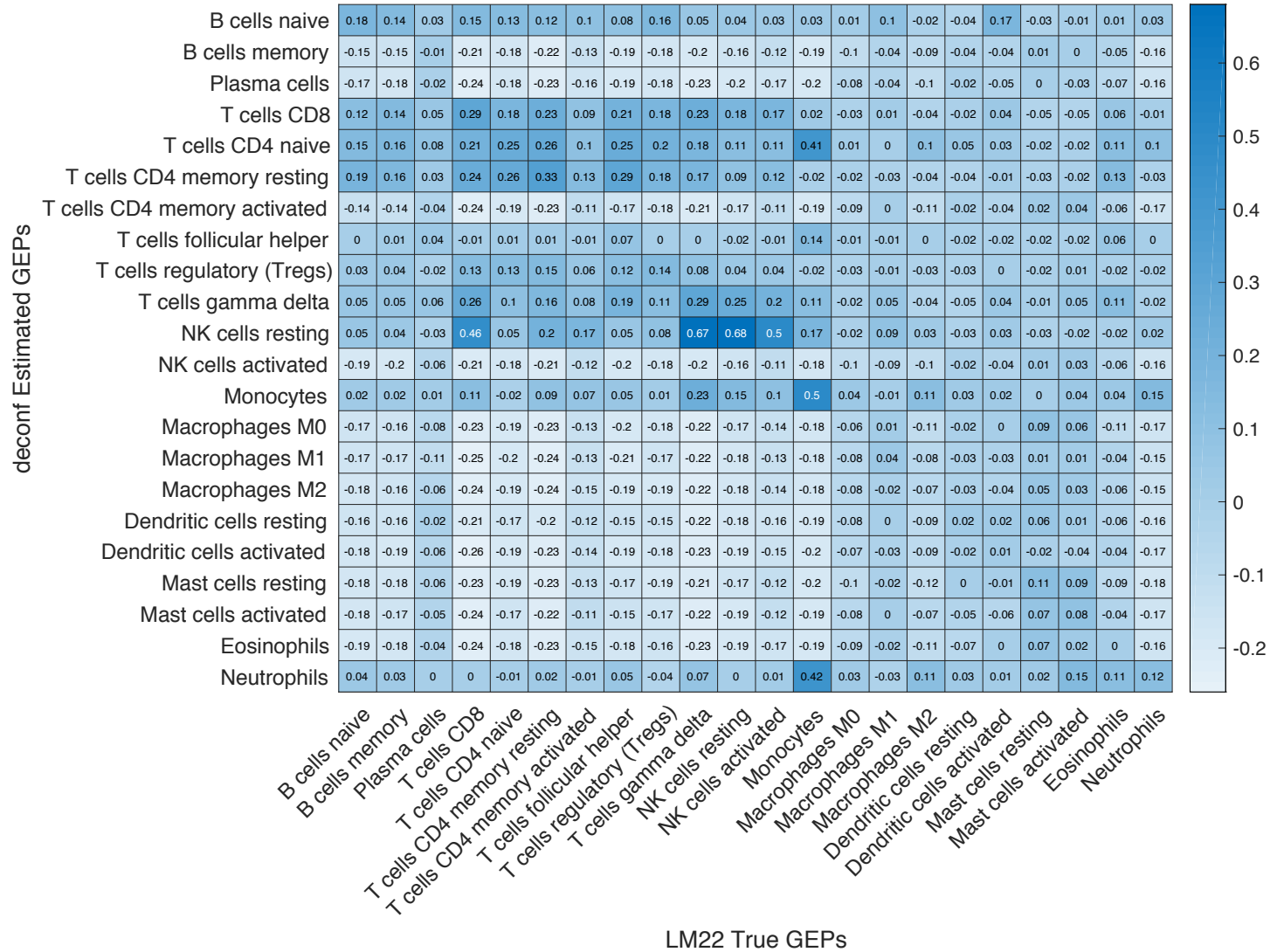
B

C



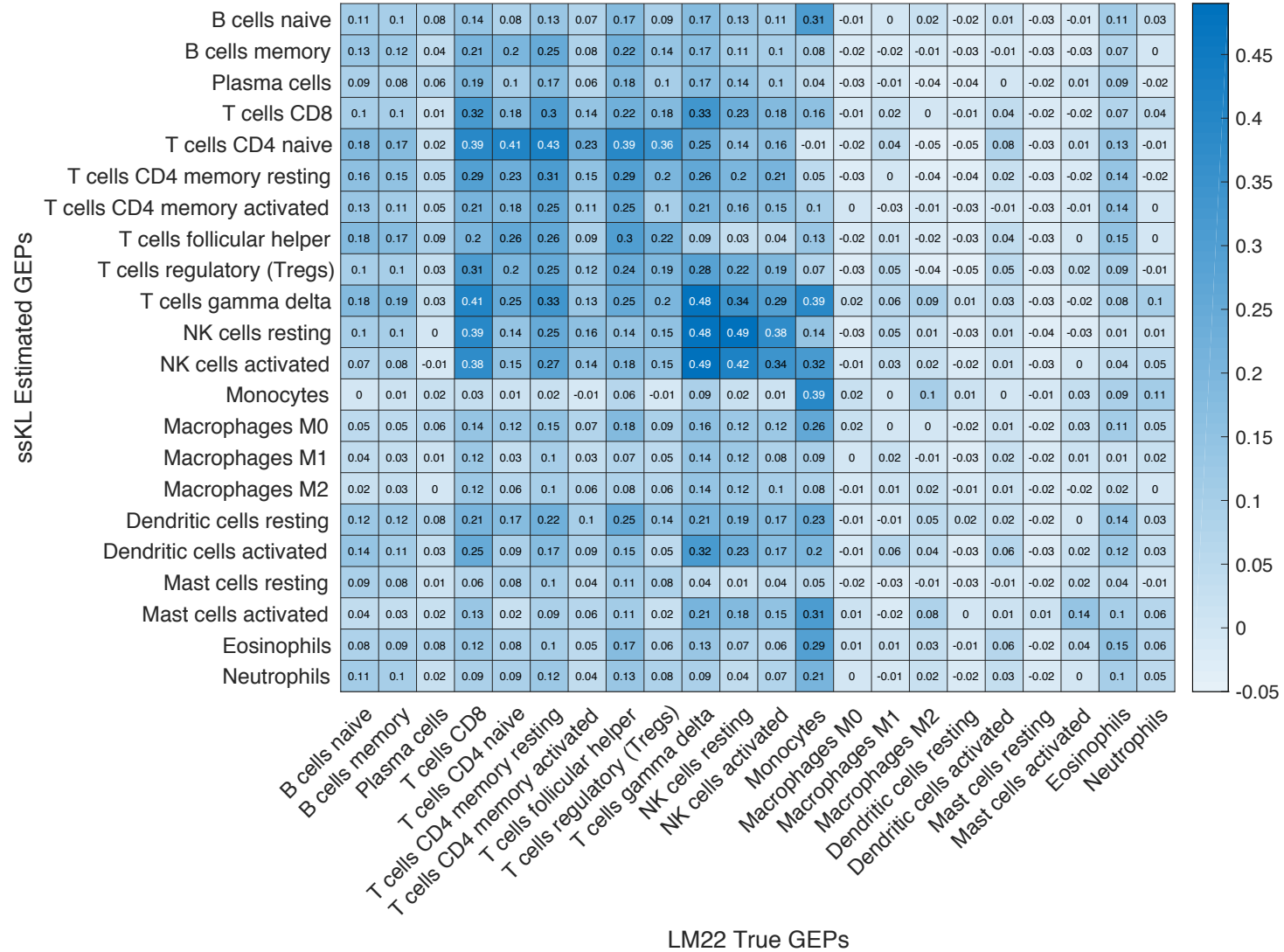
D

Correlation: estimated GEPs vs true GEPs



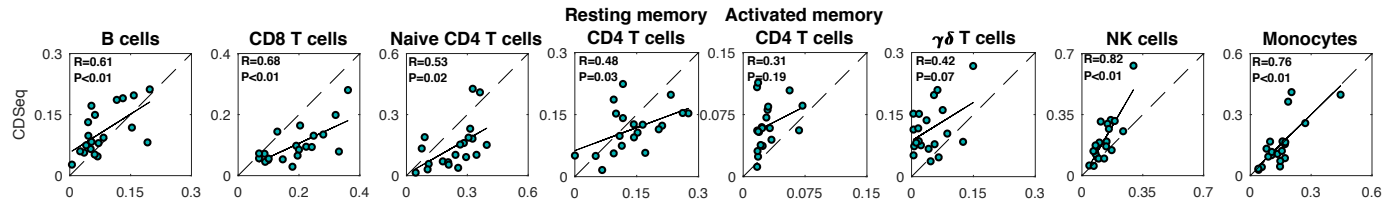
E

Correlation: estimated GEPs vs true GEPs

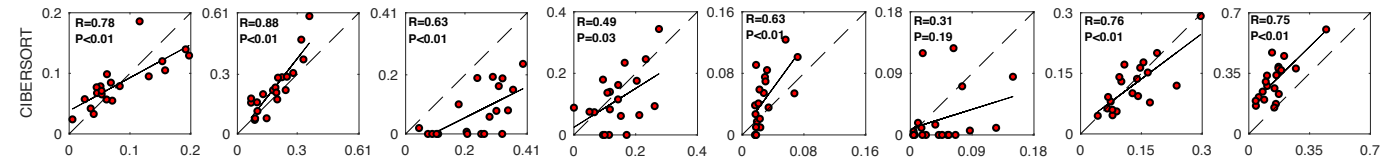


LM22 True GEPs

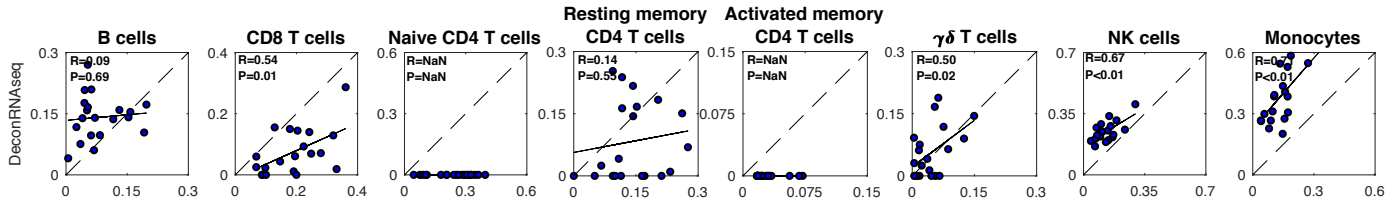
F



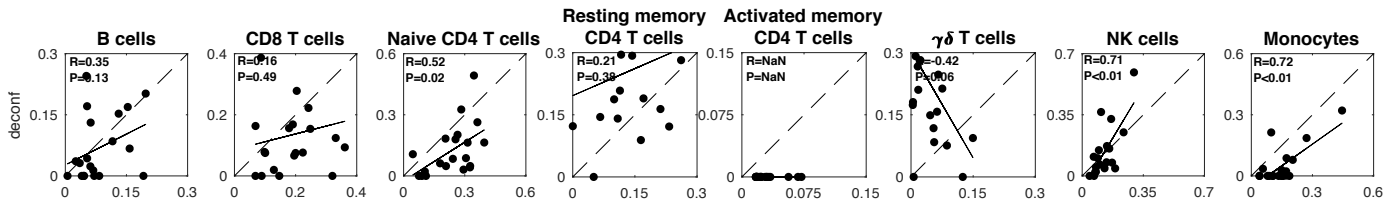
G



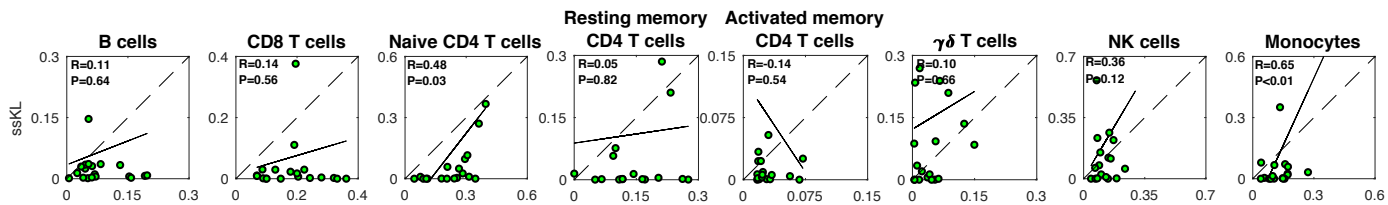
H



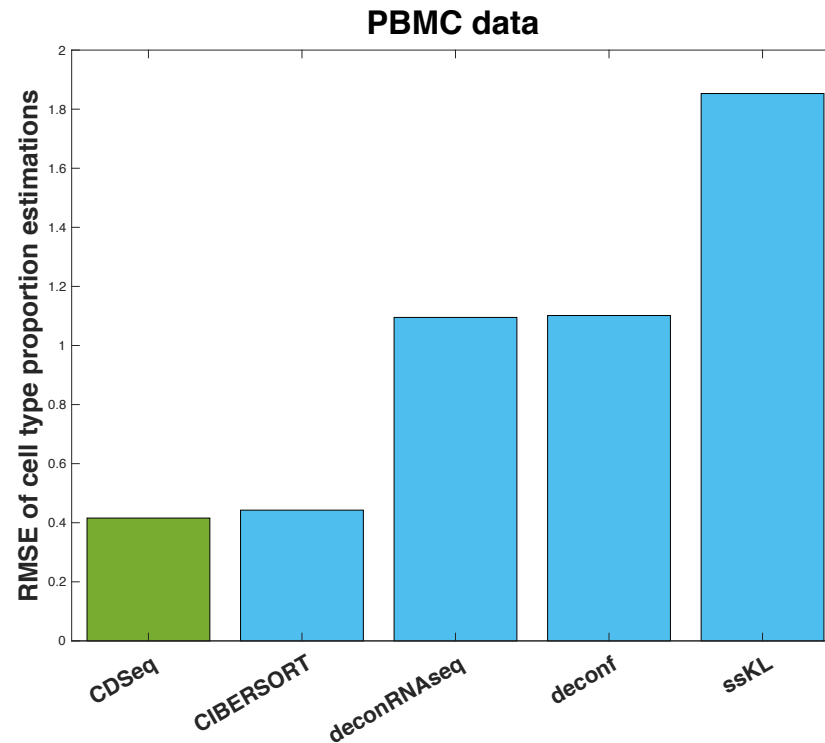
I



J



K



S8 Fig. Performance comparison on deep deconvolution. We applied CDSeq, CIBERSORT, DeconRNAseq, deconf, ssKL on PBMC data set. We set the number of cell types to be 22, $\alpha=50$, $\beta=20$ for CDSeq and used default settings for other methods. R is the correlation coefficient; and P is the p-value for testing the null hypothesis of no correlation: (A) Heat map of correlations between CDSeq-estimated cell-type-specific GEPs and LM22 GEPs; and, (B) CDSeq-estimated cell-type proportions compared to flow cytometry estimates, where the upper panel (blue dots) is the result of fully unsupervised mode and the lower panel (green dots) is the result of quasi-unsupervised mode. The black line is the linear regression line; We show correlations between estimated cell-type-specific GEPs and LM22 GEPs by different methods: (C) CDSeq with quasi-unsupervised learning (heatmap of correlations of true GEPs is given in **S5 Fig.**); (D) deconf; (E) ssKL; We show estimated SSP versus flow-cytometry measurements by different methods: (F) CDSeq with quasi-unsupervised learning; (G) CIBERSORT; (H) DeconRNAseq; (I) deconf; (J) ssKL; (K) RMSEs of cell type proportion estimations.