



**S1 Fig. Results for synthetic data.** We ran CDSeq, CIBERSORT, csSAM, DeconRNAseq, UNDO, deconf, ssKL, and DSA on our synthetic mixtures. We set  $\alpha = 5, \beta = 0.5, N = 700$  for CDSeq, and used default settings for all other methods. (A). Correlations between estimated sample-specific proportion (SSP) of cell types with true SSP; (B). Correlations between estimated cell-type-specific GEPs (csGEPs) with true csGEPs; (C). RMSEs of SSP estimations; (D). RMSE of csGEPs estimations. Notice that we do not show the result for UNDO in (A) and (B) because UNDO only estimates the proportions of tumor and non-tumor cell types.