Figure 1: **Analysis of platform bias in deconvolution across multiple methods and matrices. (a)** Goodness of fit values across 1071 human PBMC samples as a function of microarray platform using the IRIS signature matrix. Goodness of fit is displayed as a stacked barplot with color indicating corresponding values starting from goodness of fit value of 0.5 or lower up to values of 0.9 and above. Barplots are grouped by the method of deconvolution used for the analysis. **(b)** Same as in **(a)** for LM22. **(c)** Same as in **(a)** for immunoStates.

Figure 2: **Effect of disease on deconvolution. (a)** ROC curves indicating the ability of IRIS, LM22, and immunoStates (denoted by line color) to distinguish blood-derived samples from tissue biopsies in healthy donors (1383 samples) using goodness of fit across all tested methods (denoted by line type). AUCs indicate mean AUC for an individual signature matrix across all methods **(b)** Same as in **(a)** but in disease samples (2684 samples).

Figure 3: **Deconvolution concordance by matrix and method.** Boxplots representing the distribution of pairwise correlation coefficients between estimated proportions for all matrices and deconvolution methods. Center lines correspond to the median value of each box and the lower and upper bounds of each box correspond to their first and the third quartiles, respectively. Comparisons were divided in (1) pairs with the same signature matrix but run with different methods, (2) pairs with different signature matrices but run using the same method, and (3) pairs where both matrix and method were different. Significance analysis was performed using the Wilcoxon’s paired rank sum test.

Figure 4: **Correlation with measured cell proportions across 402 human blood samples. (a)** Correlation between measured cell proportions and deconvolution estimates in five different human sample cohorts (denoted by different shapes) across different deconvolution methods (denoted by different colors) using IRIS, LM22, and immunoStates (x-axis). Correlation is measured by Pearson’s correlation coefficient. Center dot represents mean value for each violin plot. Error bars represent standard error of the mean. **(b)** Same as in **(a)** for RMSE between measured and estimated cell proportions. Significance analysis was performed using the Wilcoxon’s paired rank sum test.