



FIGURE S1

Fig. S1

Expression of cell type markers in CITE-seq and comparison of cell subset abundance between technical replicates and across different centers.

- A) Gene and protein expressions of canonical cell type markers for CITE-seq (related to Fig. 1F). Cells are colored by normalized expression.
- B) Reproducibility of technical replicates for scRNA-seq in terms of cell subset frequency. Linear regression line is shown in grey. Dots are colored by immune cell types and shaped by samples. R = Pearson correlation coefficient.
- C) Reproducibility of technical replicates for CyTOF. Dots are colored by immune cell types and shaped by samples. R = Pearson correlation coefficient.
- D) Reproducibility of technical replicates for CITE-seq. CITE-seq populations are determined by integrated RNA and ADT expressions. Dots are colored by immune cell types and shaped by samples. R = Pearson correlation coefficient.
- E) Overview of datasets used in cross-center comparisons. * denotes that BIDMC scRNA-seq data is from CITE-seq with cells analyzed using RNA signal alone.
- F) Immune cell population (CD45+) frequencies observed by scRNA-seq in three different centers. Boxplot is colored by center.
- G) Immune cell population (CD45+) frequencies observed by CyTOF in three different centers. Boxplot is colored by center.
- H) A heatmap showing Pearson correlation coefficient of expression profiles of B cell marker genes in B cells between populations detected from different centers using scRNA-seq. B cell markers include *CD79A*, *CD79B*, *MS4A1* and pre-B cell markers listed in the Supplementary Table S1B.