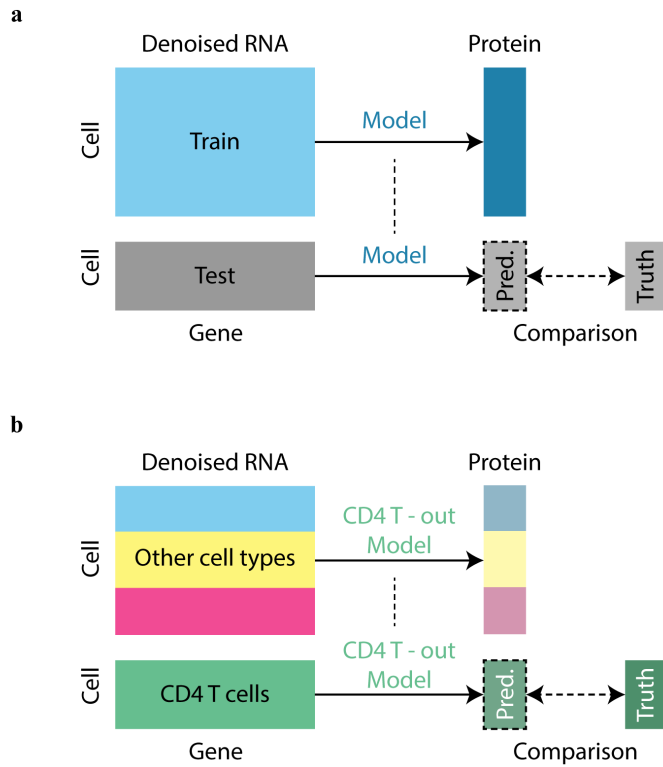


Supplementary Figure 1

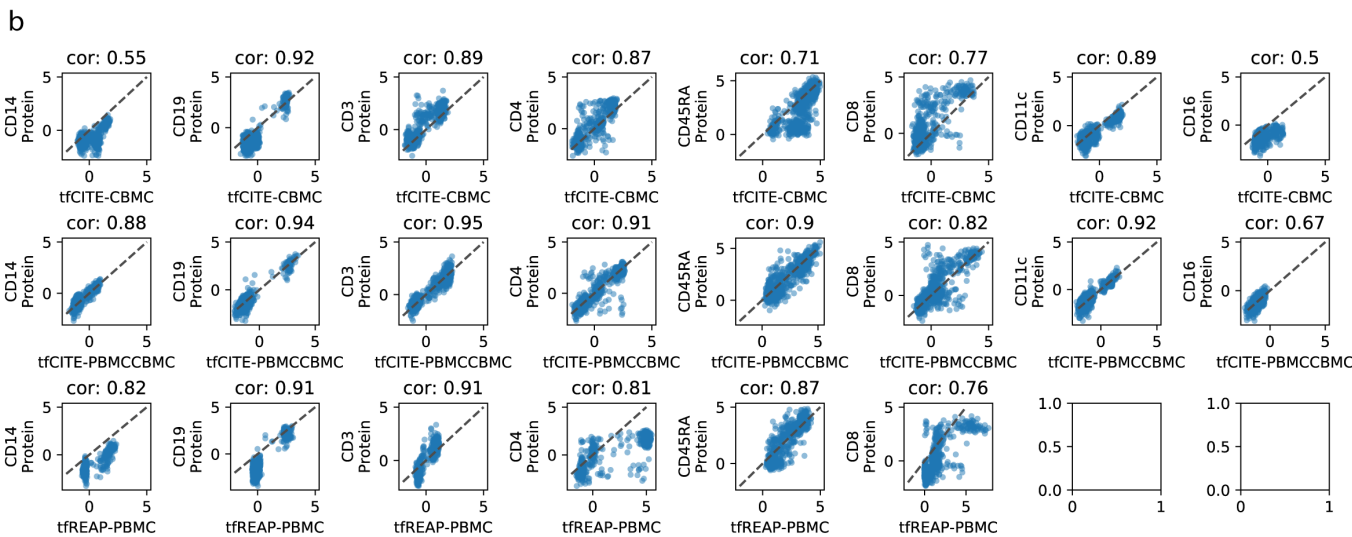
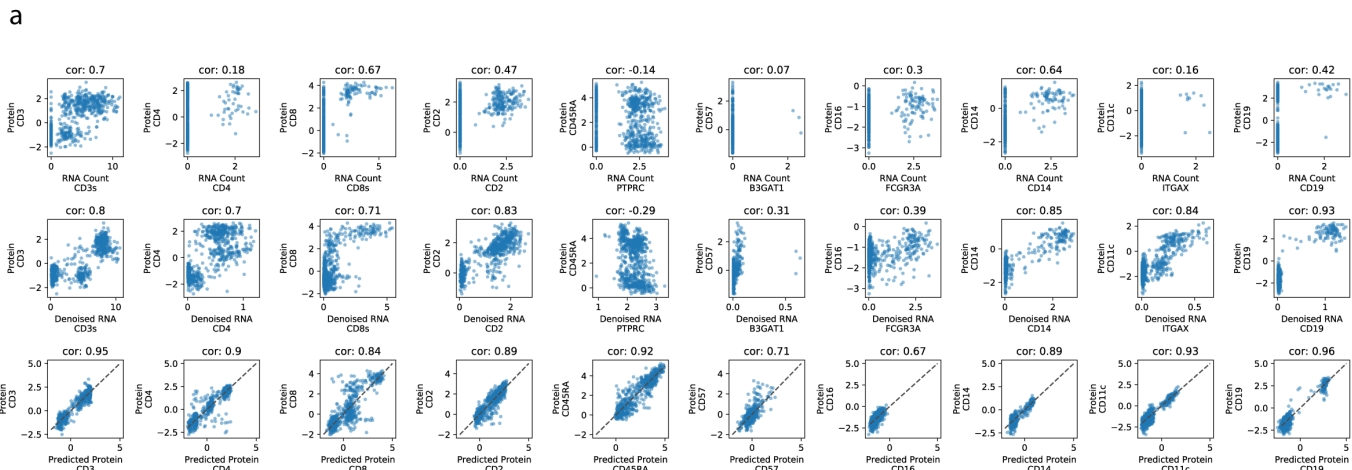
Neural network architecture of the cTP-net.

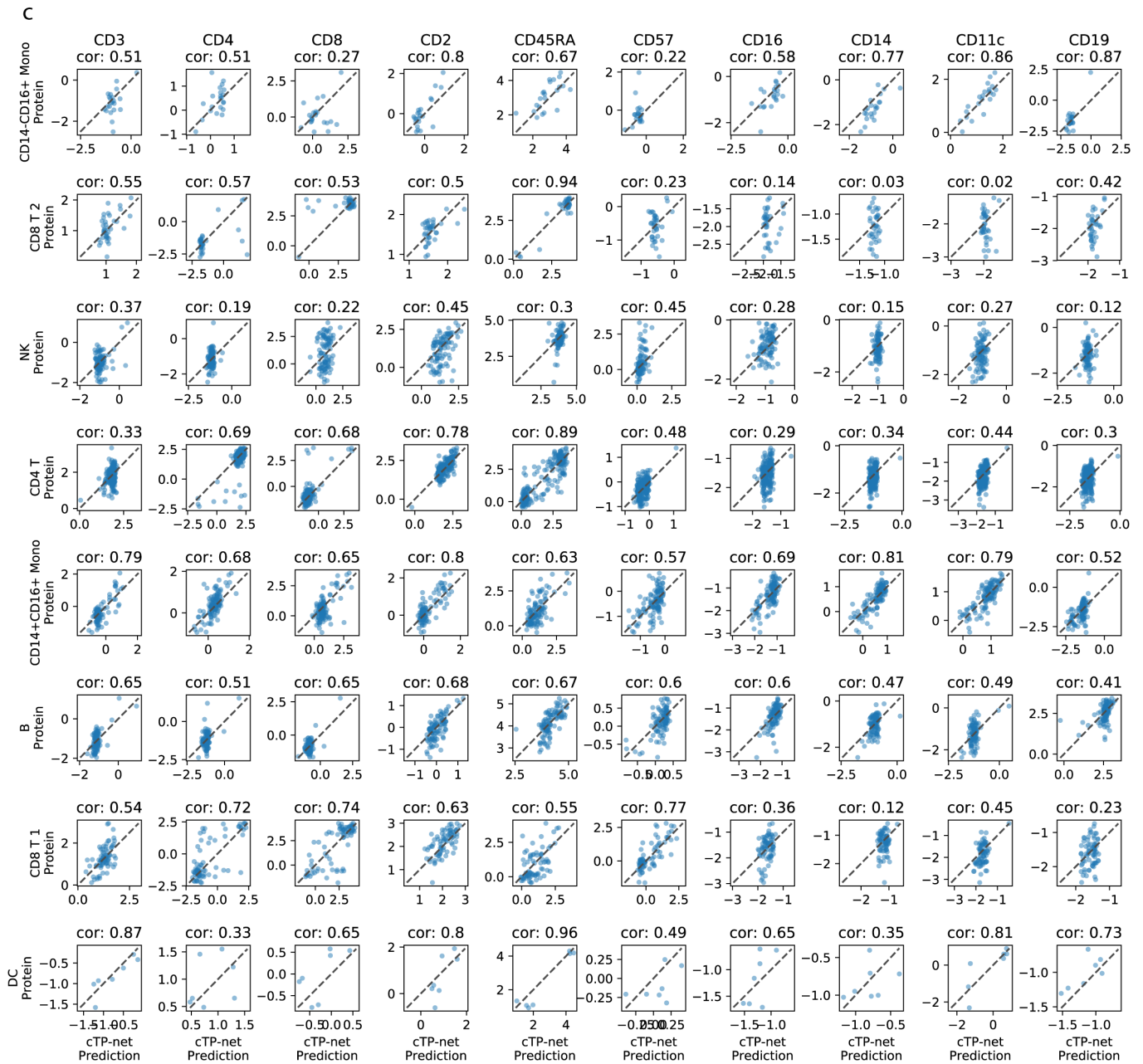


Supplementary Figure 2

Benchmark procedure.

(a) Holdout method validation scheme. (b) Out-of-cell-type benchmark scheme.



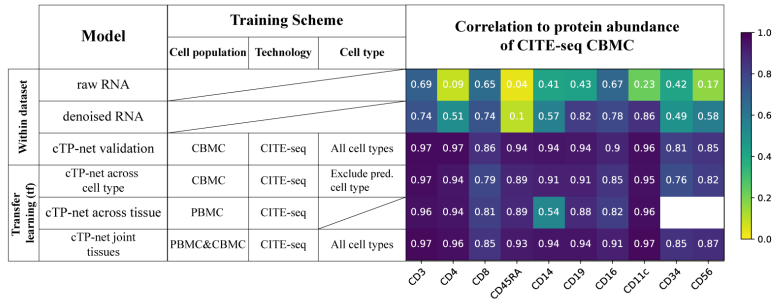


Supplementary Figure 3

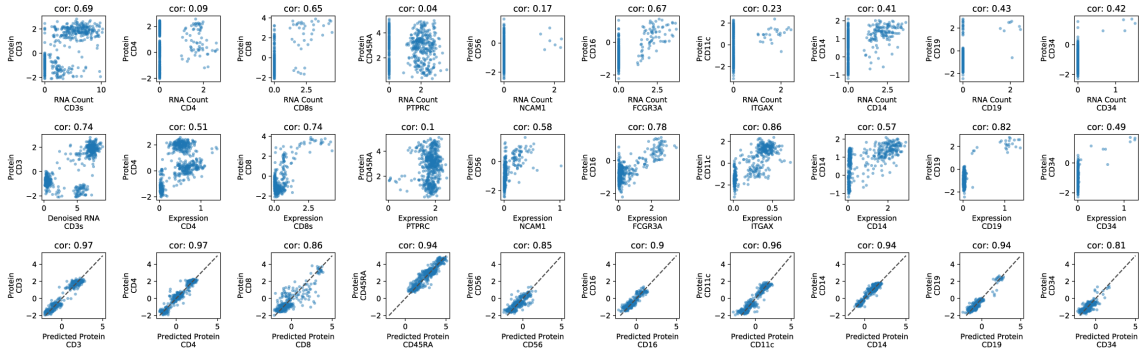
Benchmark evaluation of cTP-net on CITE-PBMC data set.

(a) Benchmark correlation of true protein level vs. (1) Raw RNA count, (2) SAVER-X denoised RNA level, and (3) cTP-net predicted protein abundance in holdout method. (b) Benchmark correlation of truth protein level vs. (1) transfer learning from CITE-CBMC, (2) transfer learning from CITE-PBMC+CBMC, and (3) transfer learning from REAP-PBMC. (c) Benchmark correlation of true protein level vs. cTP-net prediction in holdout method for each cell type.

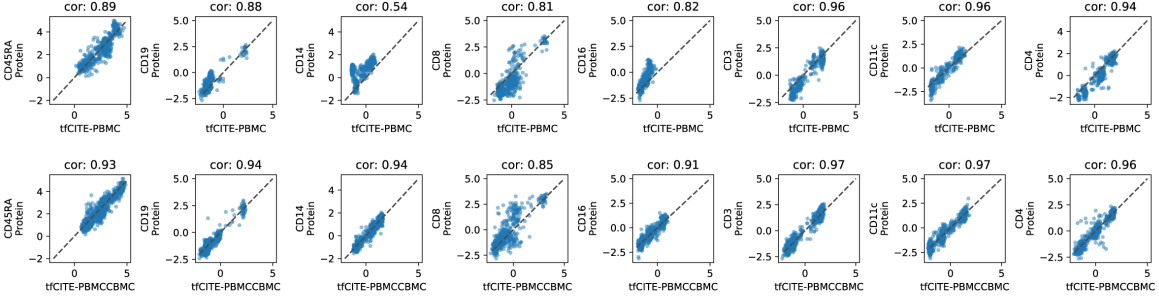
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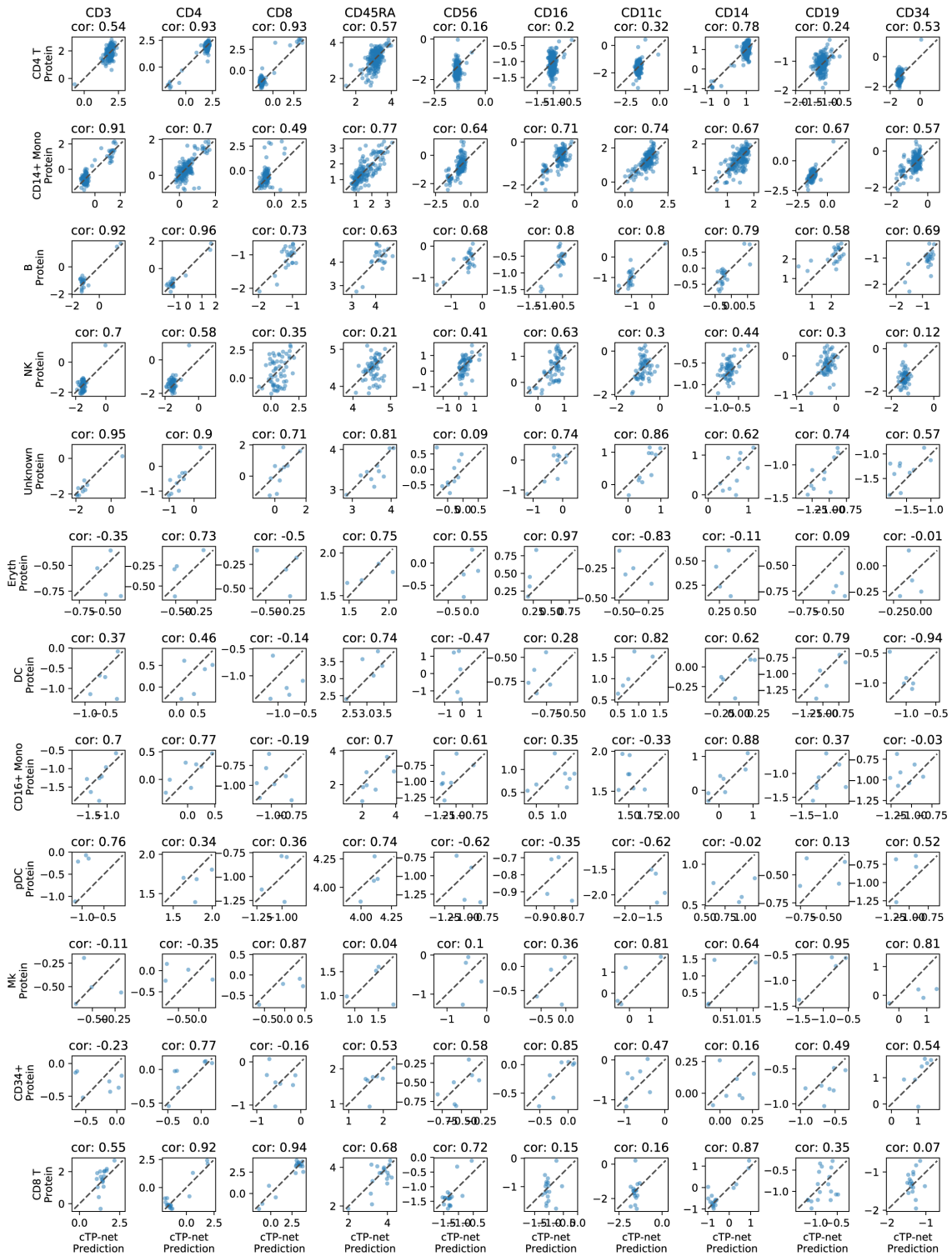
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c



d

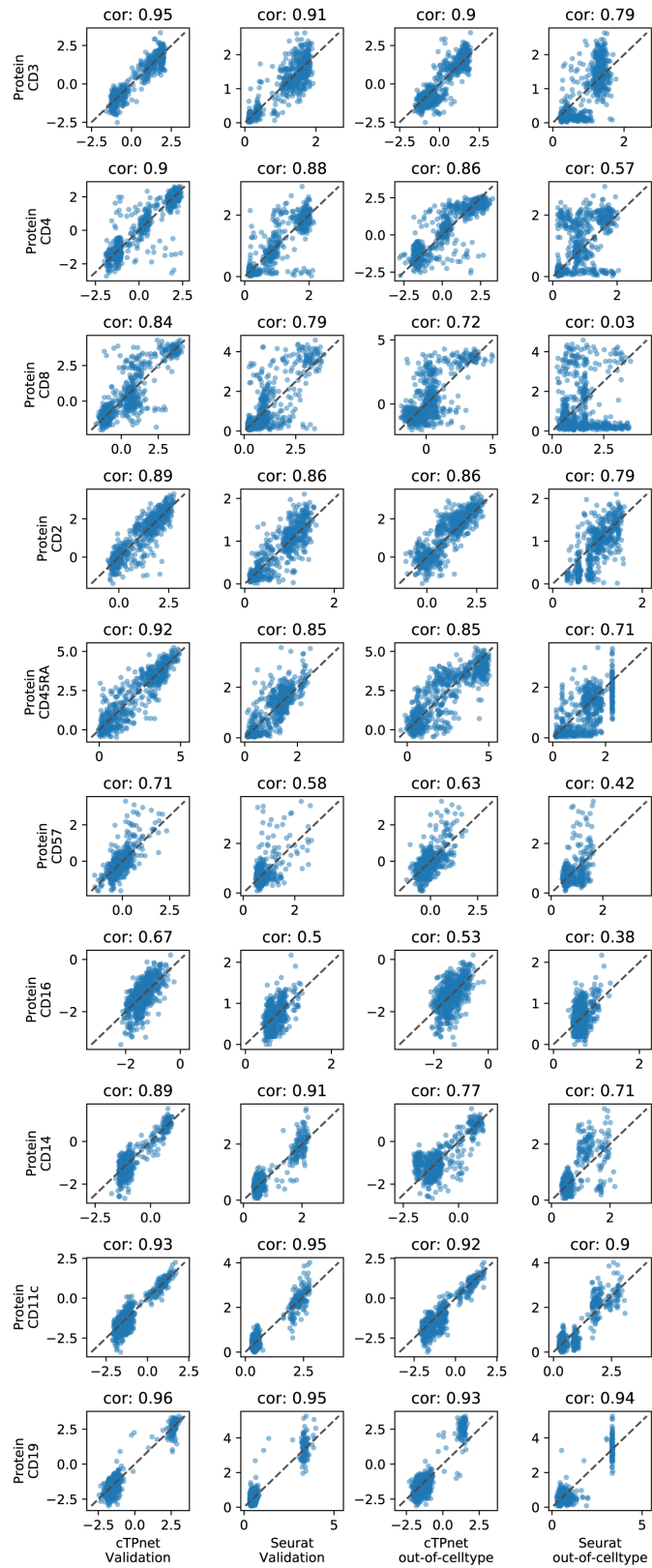


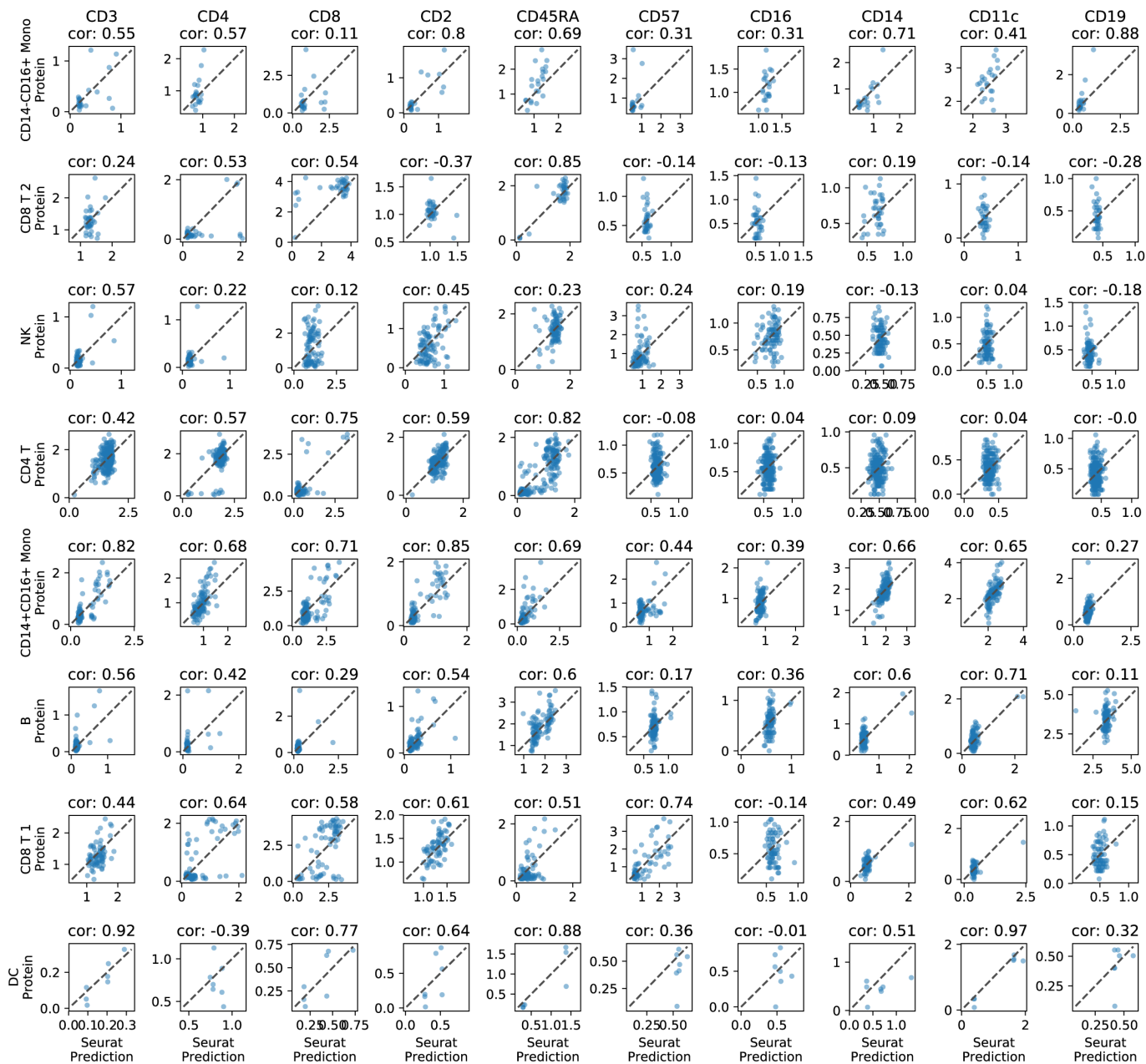
Supplementary Figure 4

Benchmark evaluation of cTP-net on CITE-CBMC data set.

(a) Benchmark evaluation heatmap of cTP-net and comparison with Seurat v3. The table on the left captures the detailed training scheme and model name of each test. **(b)** Benchmark correlation of true protein level vs. (1) Raw RNA count, (2) SAVER-X denoised RNA level, and (3) cTP-net predicted protein abundance in holdout method. **(c)** Benchmark correlation of truth protein level vs. (1) transfer learning from CITE-PBMC, and (2) transfer learning from CITE-PBMCCBMC. **(d)** Benchmark correlation of true protein level vs. cTP-net prediction in holdout method for each cell type.

a

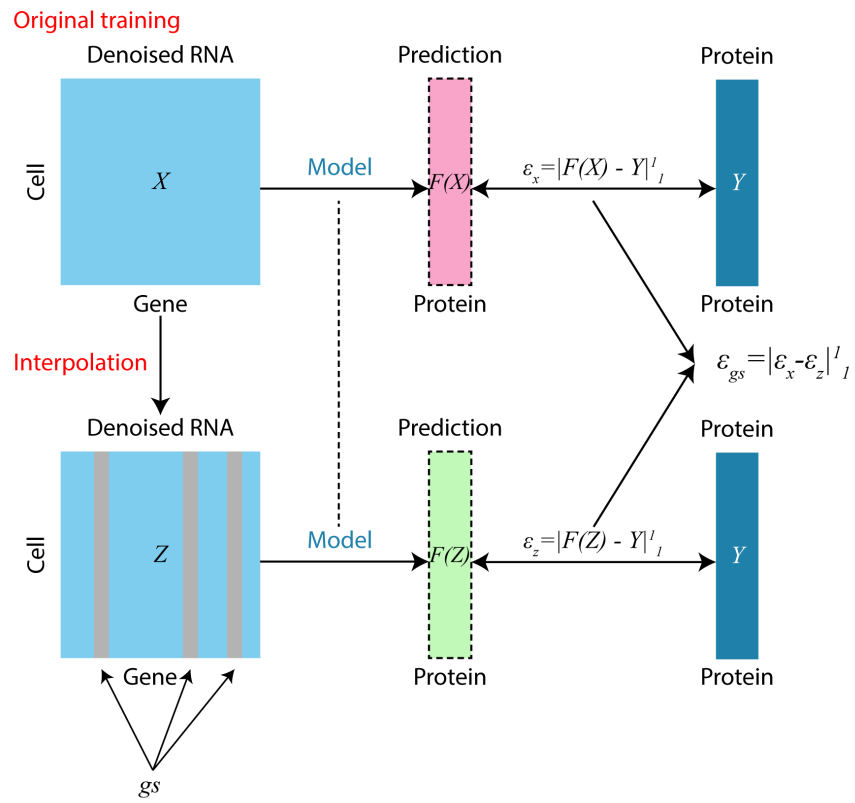


b

Supplementary Figure 5

Benchmark evaluation of Seurat v3 on CITE-PBMC data set.

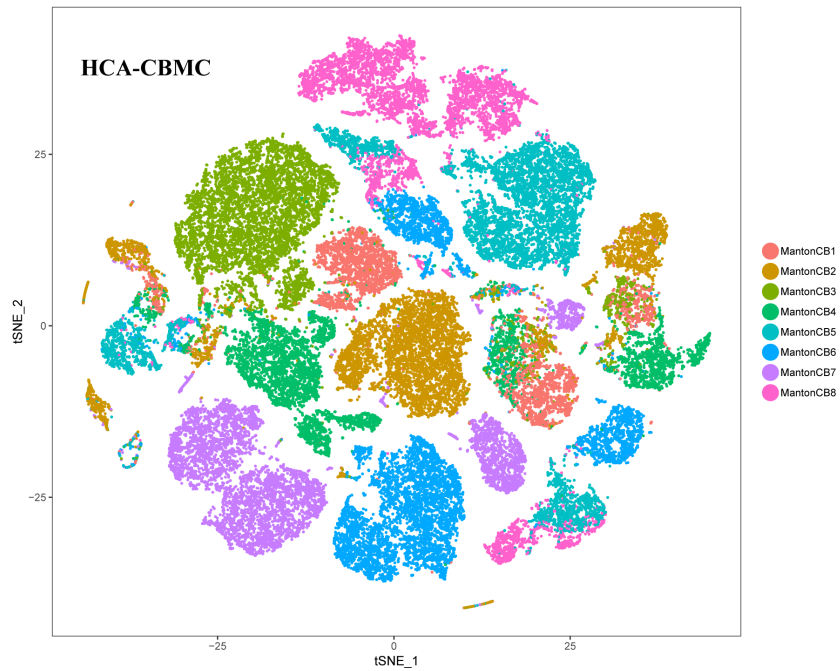
(a) Benchmark correlation of true protein level vs. (1) cTP-net predicted protein abundance in holdout method, (2) Seurat v3 predicted protein abundance in holdout method, (3) out-of-cell-type cTP-net predicted protein abundance, and (4) out-of-cell-type Seurat v3 predicted protein abundance. **(b)** Benchmark correlation of truth protein level vs. (1) transfer learning from CITE-PBMC, and (2) transfer learning from CITE-PBMCCBMC. **(c)** Benchmark correlation of true protein level vs. cTP-net prediction in holdout method for each cell type.



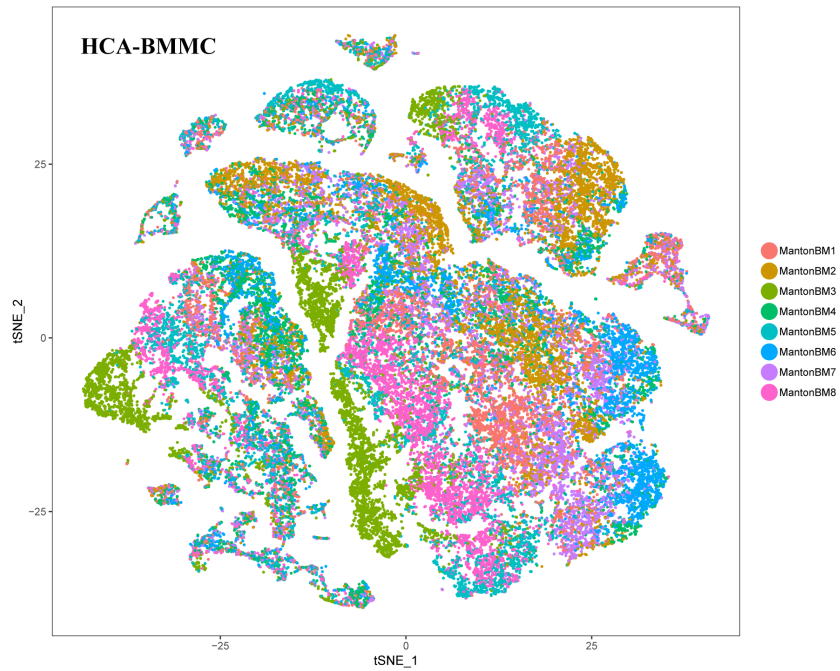
Supplementary Figure 6

Interpolation procedure.

a



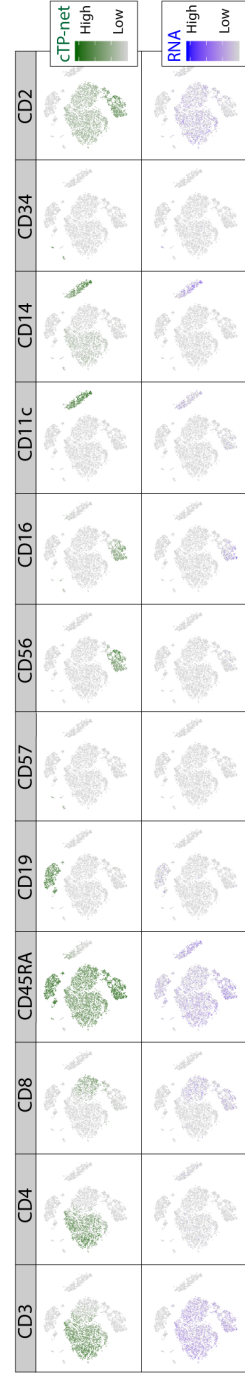
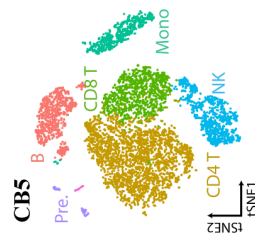
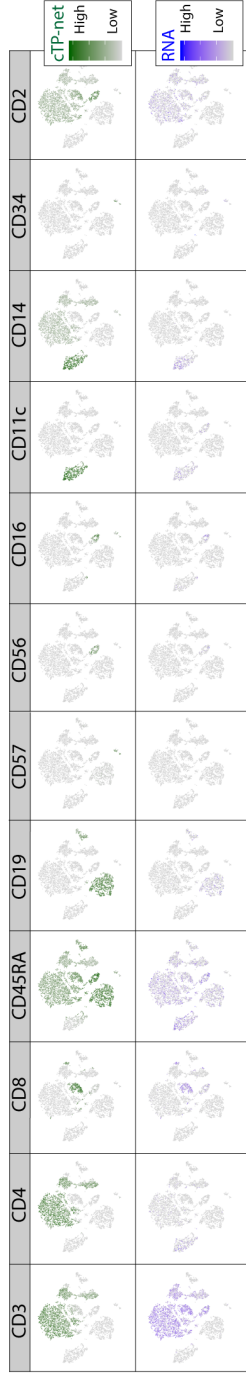
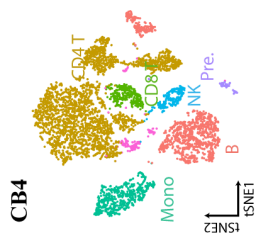
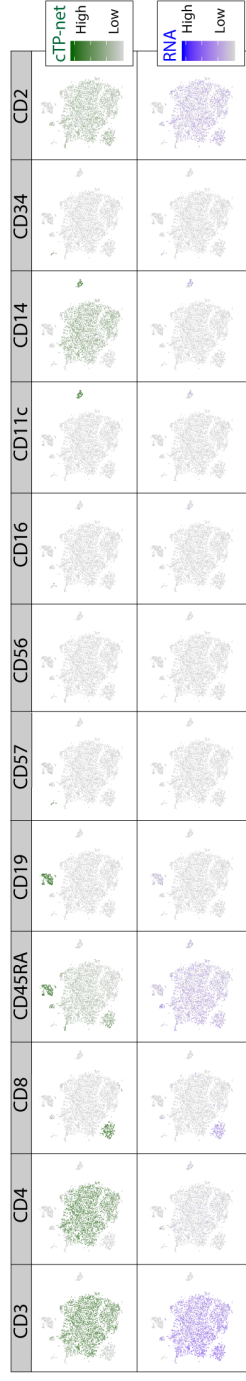
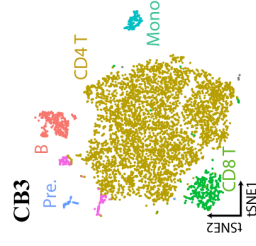
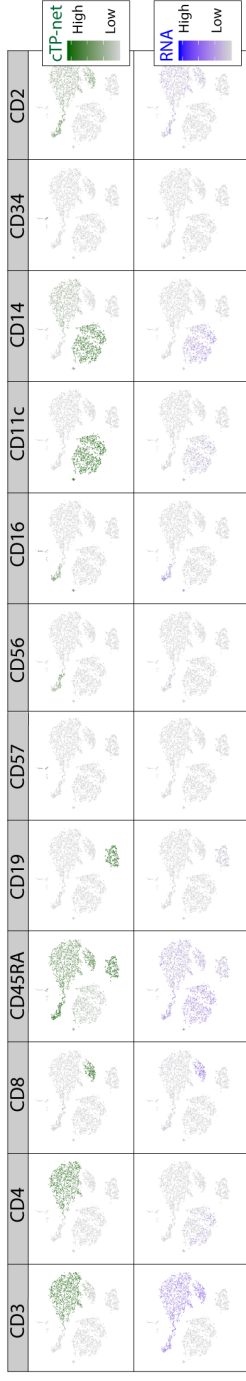
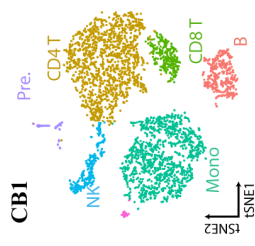
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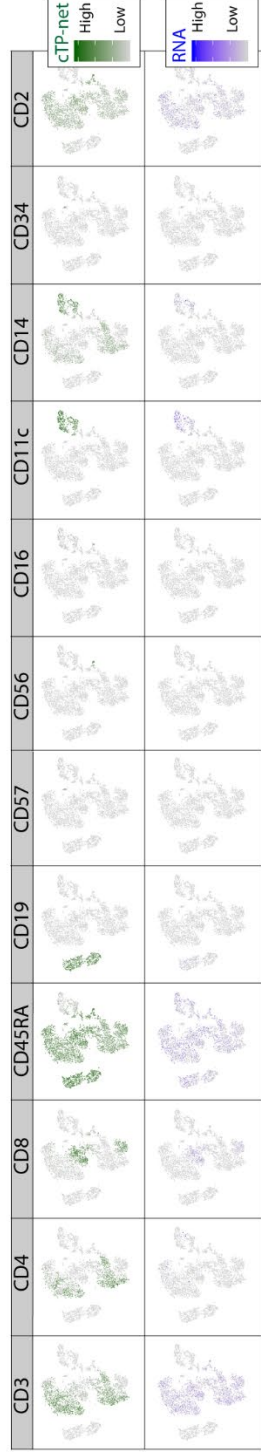
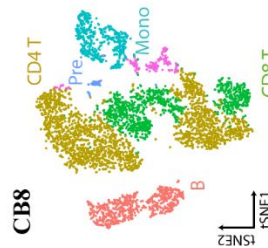
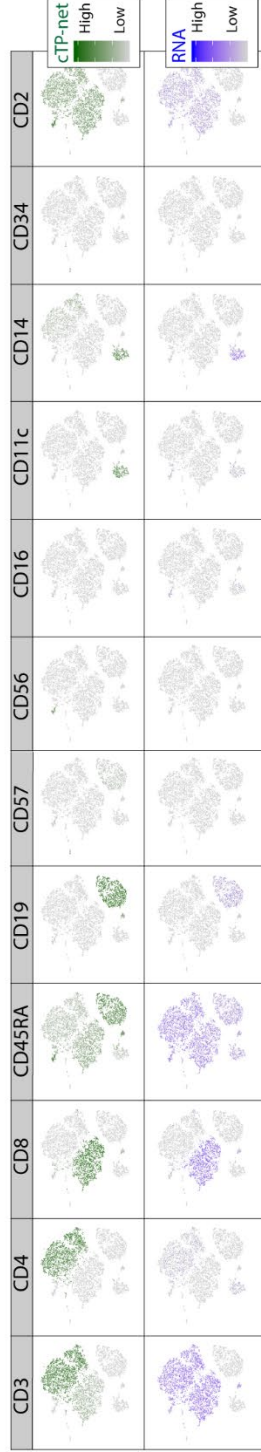
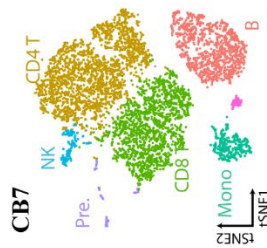
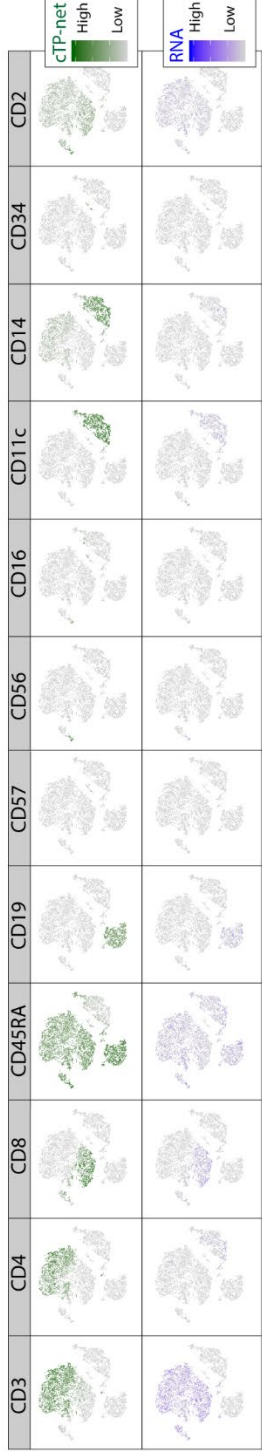
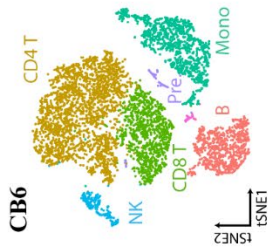


Supplementary Figure 7

Human Cell Atlas t-SNE plot based on normalized expression.

(a) t-SNE plot on Human Cell Atlas CBMCs based on normalized expression. Color indicates sample IDs. **(b)** t-SNE plot on Human Cell Atlas BMMCs based on normalized expression. Color indicates sample IDs. Strong batch effects observed in both data sets.

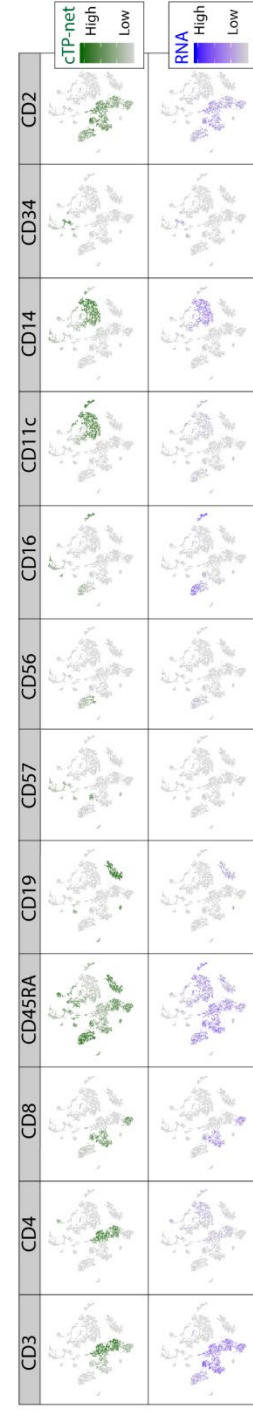
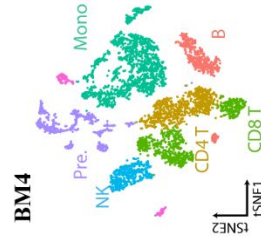
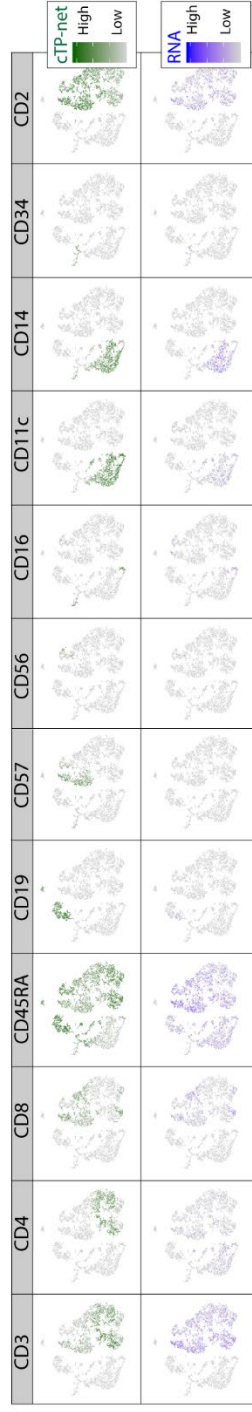
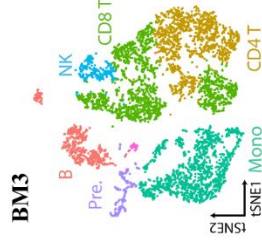
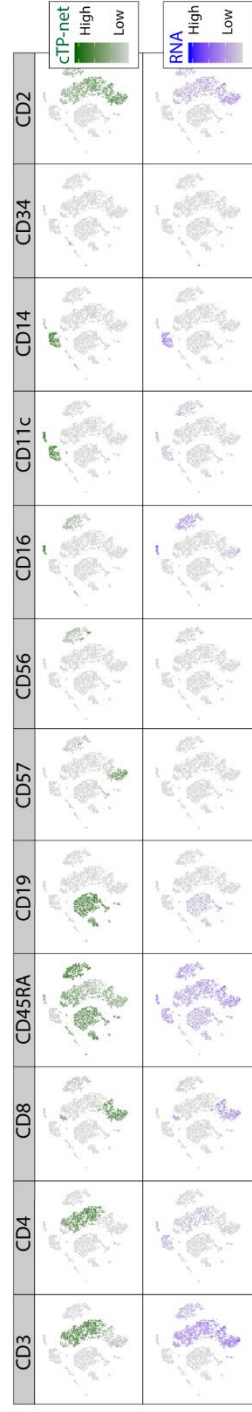
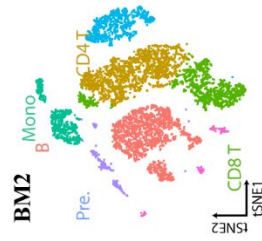
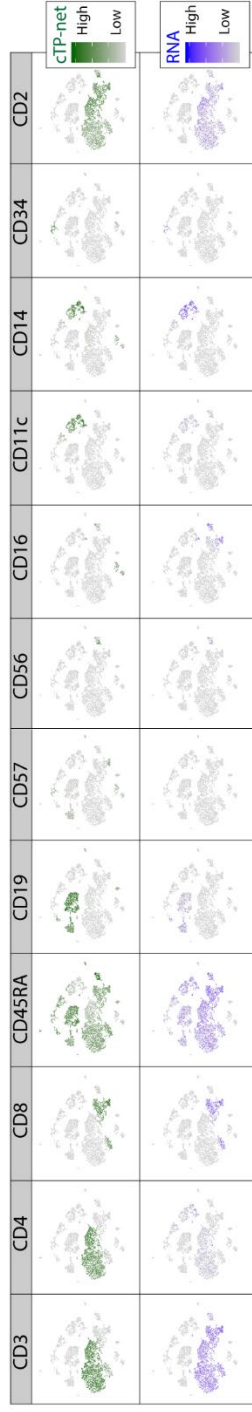
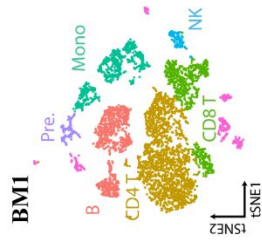


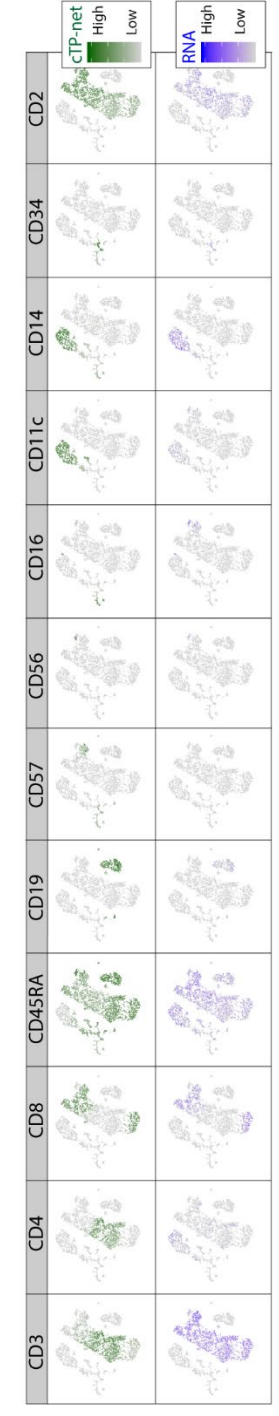
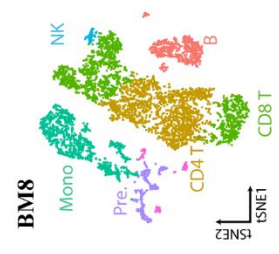
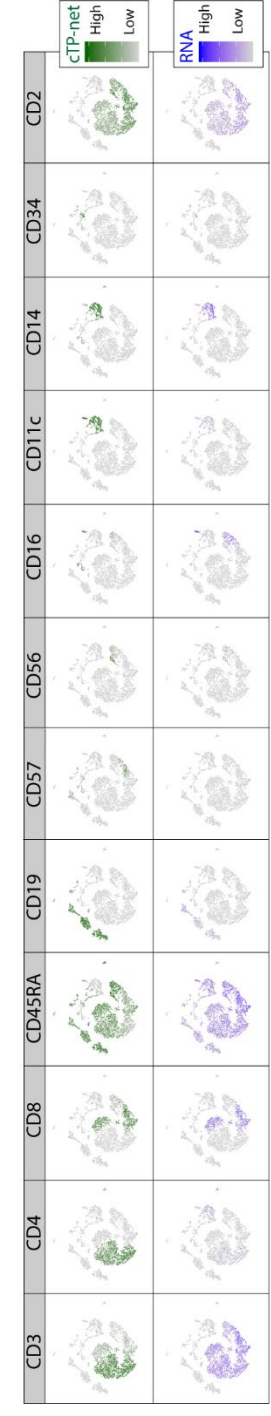
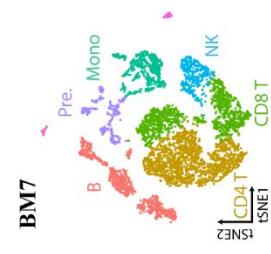
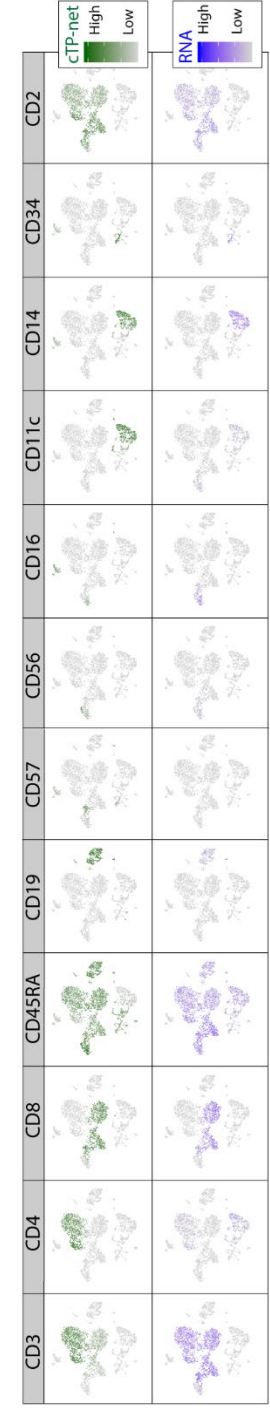
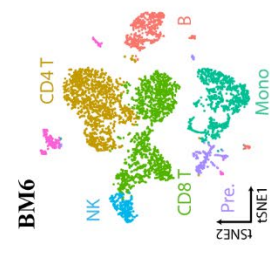
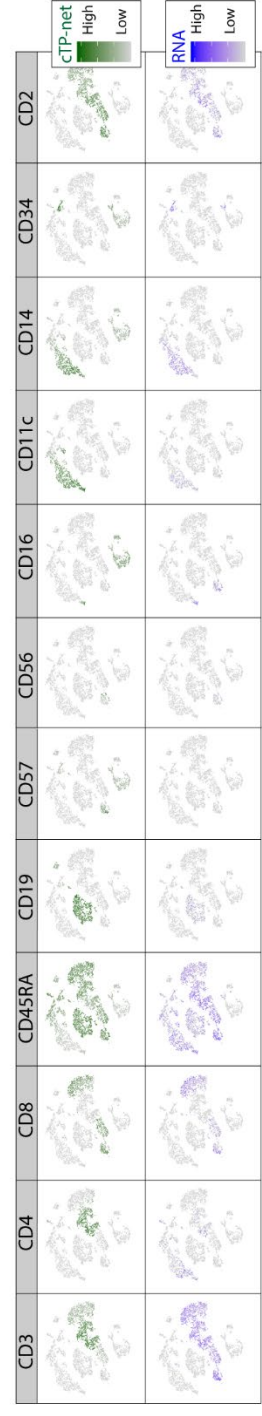
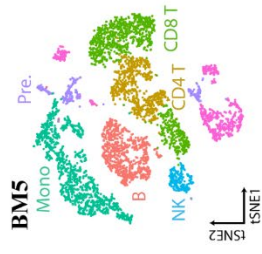


Supplementary Figure 8

cTP-net prediction on Human Cell Atlas CBMCs by individual.

For each individual, we show (1) t-SNE visualization of HCA CBMCs based on expression. B: B cells; CD4 T: CD4 T cells; CD8 T: CD8 T cells; Mono: Monocyte; NK: Nature killer cells; Pre.: Precursors. (2) cTP-net imputed protein abundance and RNA of its cognate gene across 12 different surface proteins.





Supplementary Figure 9

cTP-net prediction on Human Cell Atlas BMMCs by individual.

For each individual, we show (1) t-SNE visualization of HCA BMMCs based on expression. B: B cells; CD4 T: CD4 T cells; CD8 T: CD8 T cells; Mono: Monocyte; NK: Nature killer cells; Pre.: Precursors. (2) cTP-net imputed protein abundance and RNA of its cognate gene across 12 different surface proteins.