S12 Text: Stability of Denoising.

SCRaPL: A Bayesian hierarchical framework for detecting technical associates in single cell multiomics data.

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In the main text we looked the extend to which SCRaPL could be used as a denoising tool, to perform data integration at the level of latent space instead of raw data done by Seurat. Since denoising involves sampling from the posterior, we verify the consistency across different trials. As evident from Figs AA,AC and AE a tiny fraction of cells vary across trials, which implies that results are stable.

(A)

(B)

(C)

(D)

(E)

(F)
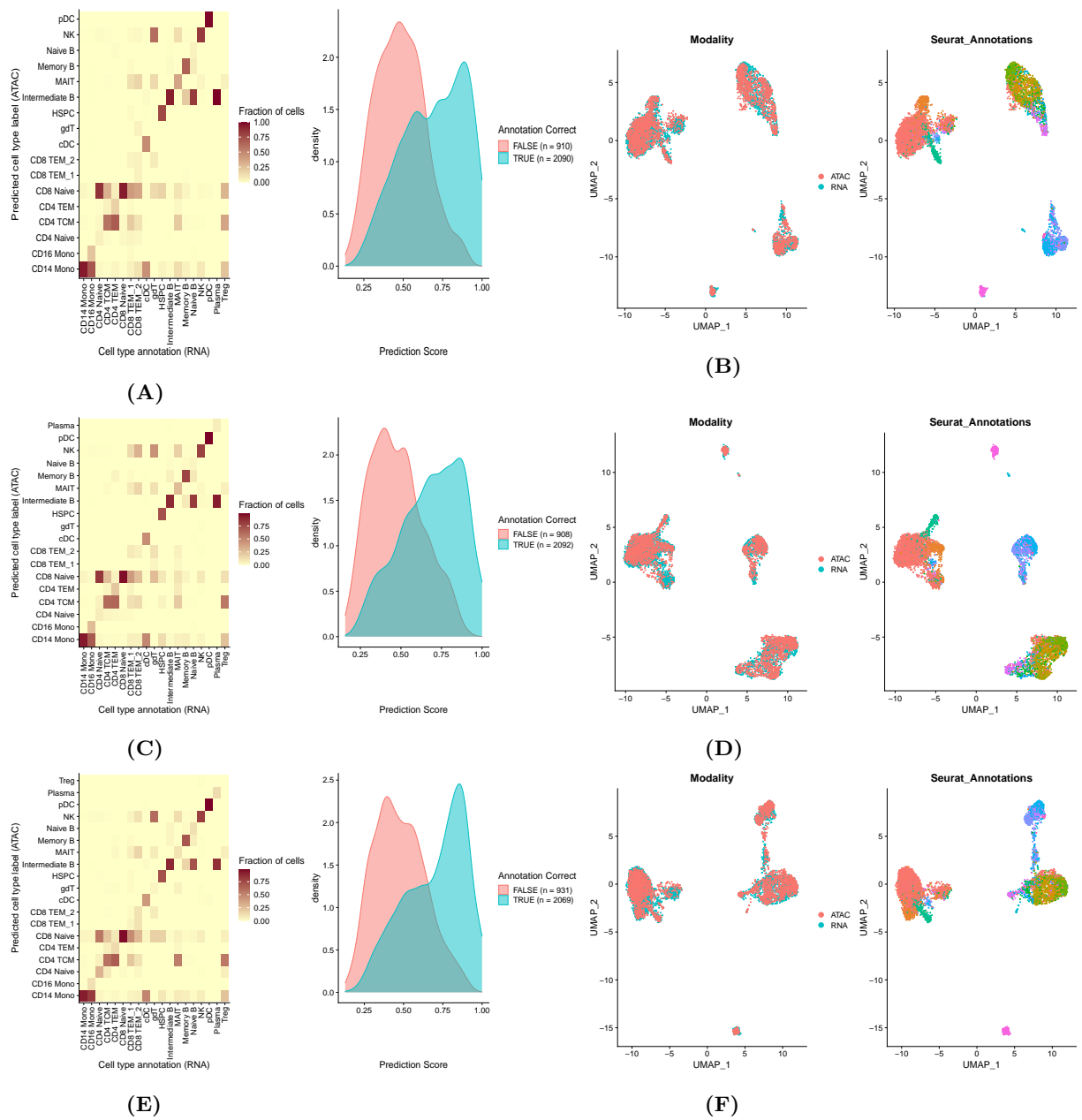
Fig A. Stability analysis of cell integration using SCRaPL as a denoising tool
Panel summarizing label transfer from expression to accessibility in trials 2(AA), 3 (AC) and 4 (AE) along with respective latent plot visualizations (AB,AD,AE) of sc-RNA and scATAC