S11 Text: Macroscopic analysis of SCRaPL's behavior compared to Pearson and Spearman Correlation.

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

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In this section we provide evidence in favor of the arguments presented in section "SCRaPL associations are influenced by data sparsity and are 152 robust to outliers. ", about the differences between SCRaPL and different frequentist approaches considered in this work. More precisely, we argued that high CpG coverage and low inflation contribute in the reduction of discrepancy between SCRaPL's posterior correlation and Pearson/Spearman correlations. By regressing correlation discrepancy against these parameters we generate Fig A along with figure $3d$ presented in the main text which perfectly demonstrate the point.

(A)

(B)
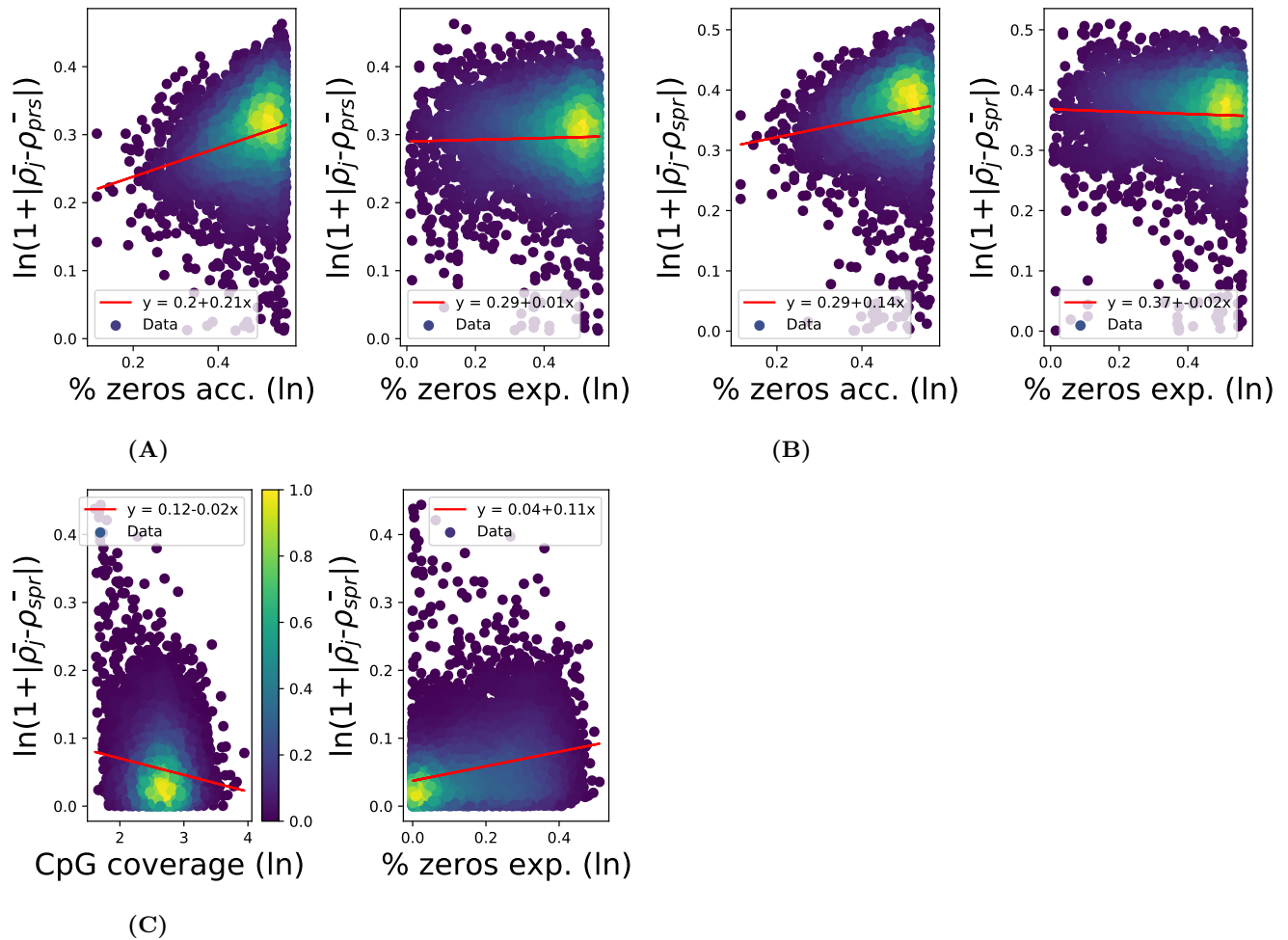
(C)

Fig A. SCRaPL's behavior compared to Pearson/Spearman correlation in micro and macro scale. (AA) Scatter plots to demonstrate the positive relationship between alternative correlation estimates (Pearson and SCRaPL) and % zeros in accessibility and expression respectively. (AB) Scatter plots to demonstrate the positive relationship between alternative correlation estimates (Spearman and SCRaPL) and % zeros in accessibility and expression respectively. (AC) Scatter plots to demonstrate the negative/positive relationship between alternative correlation estimates and CpG coverage/% zeros in expression respectively.