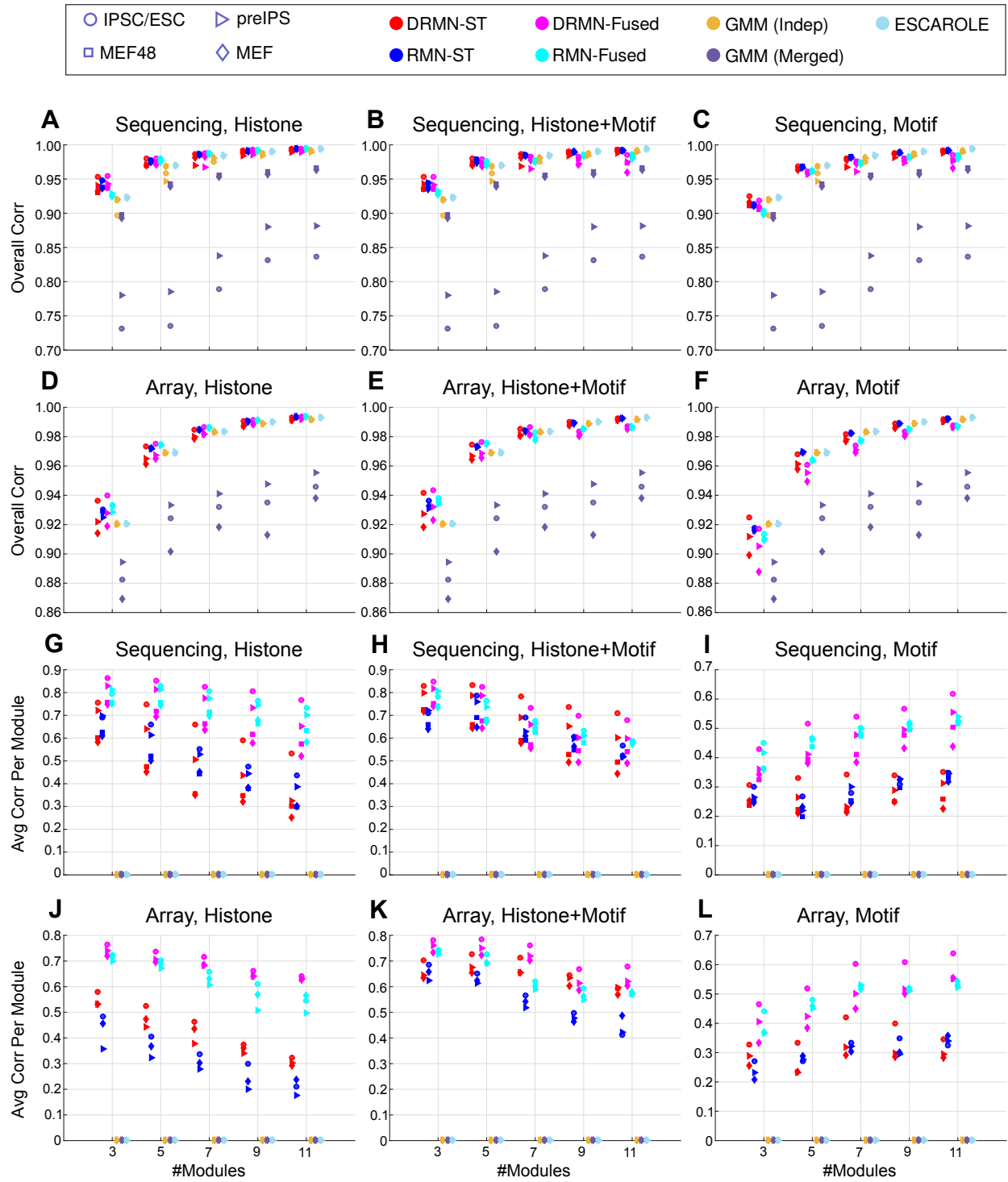




Supplemental Figure S5. Comparing RMN and DRMN's expression predictions to expression-based baseline approaches. Each panel compares seven algorithms on the basis of one correlation metric (y-axis) across a range of k (x-axis) for a particular feature type. Each dot represents the results for one cell type averaged over three-fold cross validation. **A-F.** Comparison based on Pearson's correlation of predicted to true expression for held-aside genes. **G-L.** Comparison based on per-module correlation coefficients, averaged across k modules. Note, for expression prediction the generative models need the information about the observed expression.