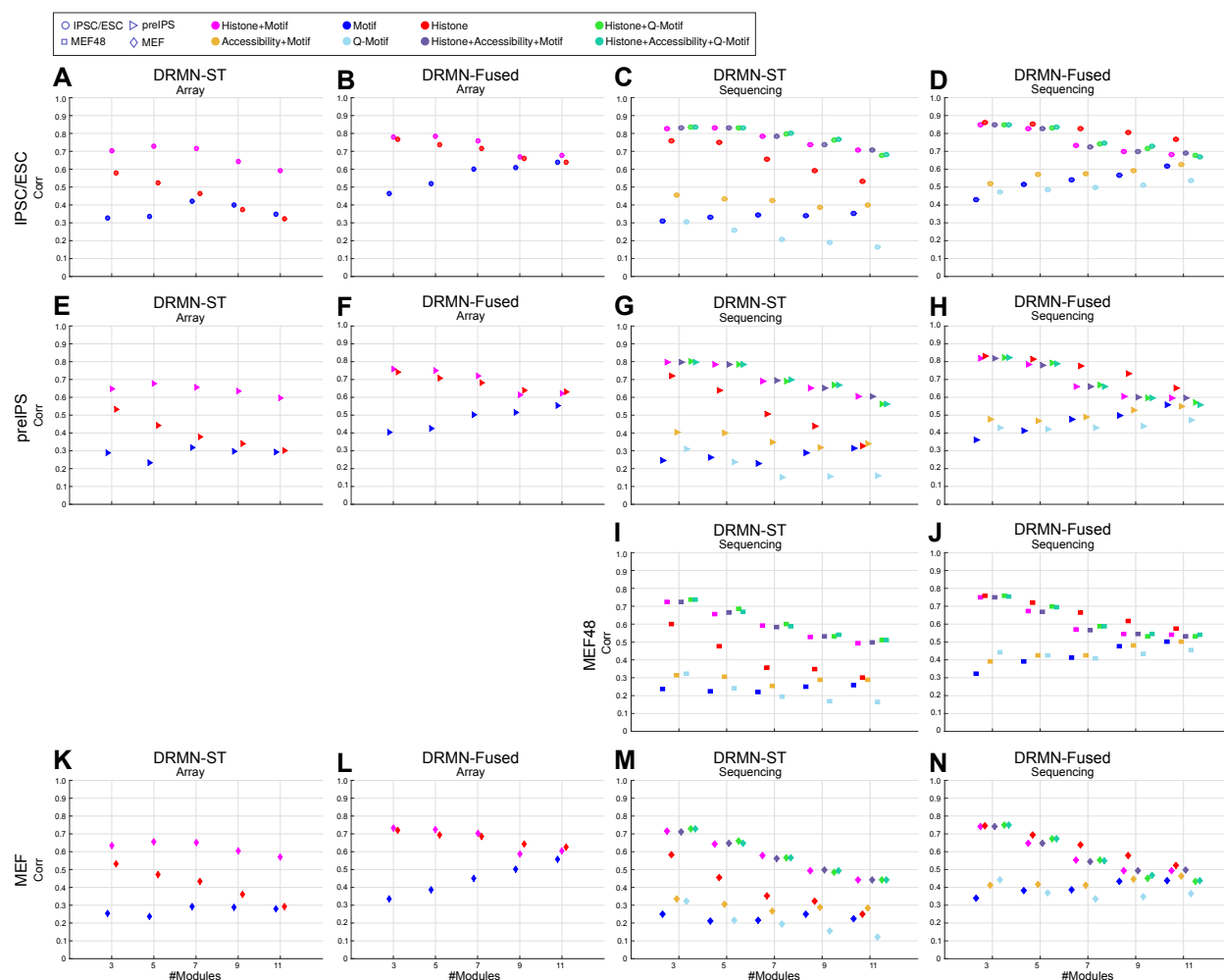




Supplemental Figure S1. Average per-module correlation as a function of different number of modules for DRMN and RMN models using the reprogramming datasets. Each row and marker shape corresponds to a cell state from the array or sequencing dataset. Different colors correspond to different feature types. Results in the main paper **Figure. 2** shows all the cell states together. **A-D.** ESC/IPSC. **E-H.** pre-IPSC. **I, J.** MEF 48 hours (only for sequencing dataset). **K-N** MEF. Each column corresponds to DRMN-ST or DRMN-FUSED versions on a dataset (**A, E, K** for DRMN-ST on array dataset, **B, F, L** for DRMN-FUSED on array dataset, **C, G, I, M** for DRMN-ST on sequencing dataset, and **D, H, J, N** for DRMN-FUSED on sequencing dataset). Note, for expression prediction the generative models need the information about the observed expression.