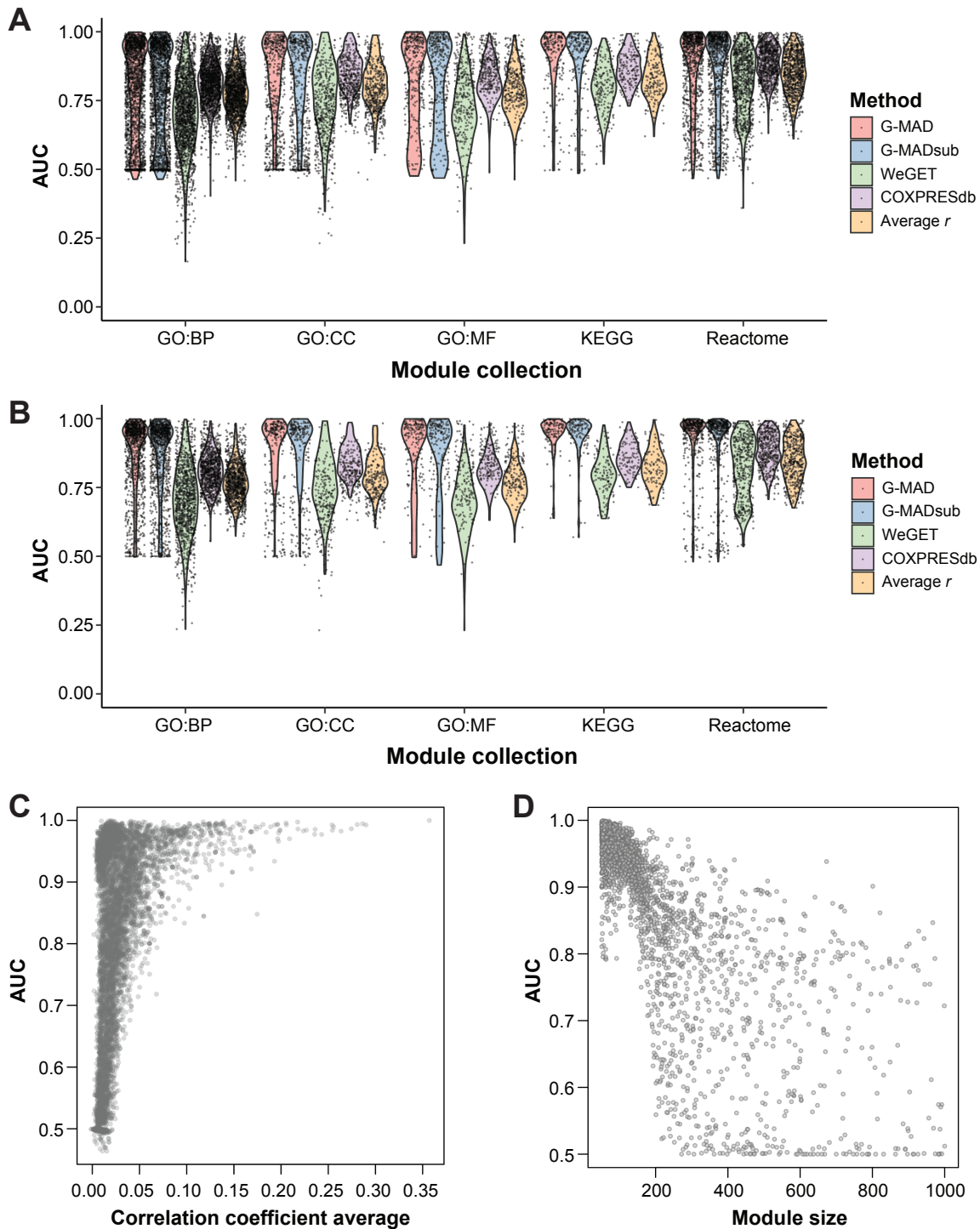# Figure S3

Figure S3. Comparison of the predictive performance of G-MAD with available methods.
A, B, The performances of G-MAD, as well as other existing methods in all modules (**A**) or modules with more than 50 genes (**B**) are summarized based on the collection source of the modules. The predictive performance of G-MAD is compared to WeGET and COXPRESdb, as well as a simpler method based on average of correlation coefficient (average *r*) using the same expression compendium of G-MAD, using cross-validation. In addition, we repeated G-MAD with a subset (G-MADsub, using 800 datasets) of the datasets to test if the number of datasets brought the higher performance than WeGET, which has around 1,000 datasets. Cross validation evaluates the robustness of the methods by removing the genes from the query module and test the performance in redetecting them. Performance of the method is computed as the area under the receiver operating characteristic curve (AUC) for each module. A high AUC indicates that most of the genes in the module are rediscovered when they are removed from the module in the analysis.
C, D, The intergene correlations (correlation coefficient average) (**C**) and module size (**D**) have strong influence on the predictive performance of modules.