

Figure S1

A. StringDB PPI interaction networks for module M1 across the three clusters; genes color-coded by limma t-value; upper right subpanel indicates number of DEGs within the module for each AD cluster. **B.** Highly enriched pathways and TFs for each comodule (hypergeometric test).

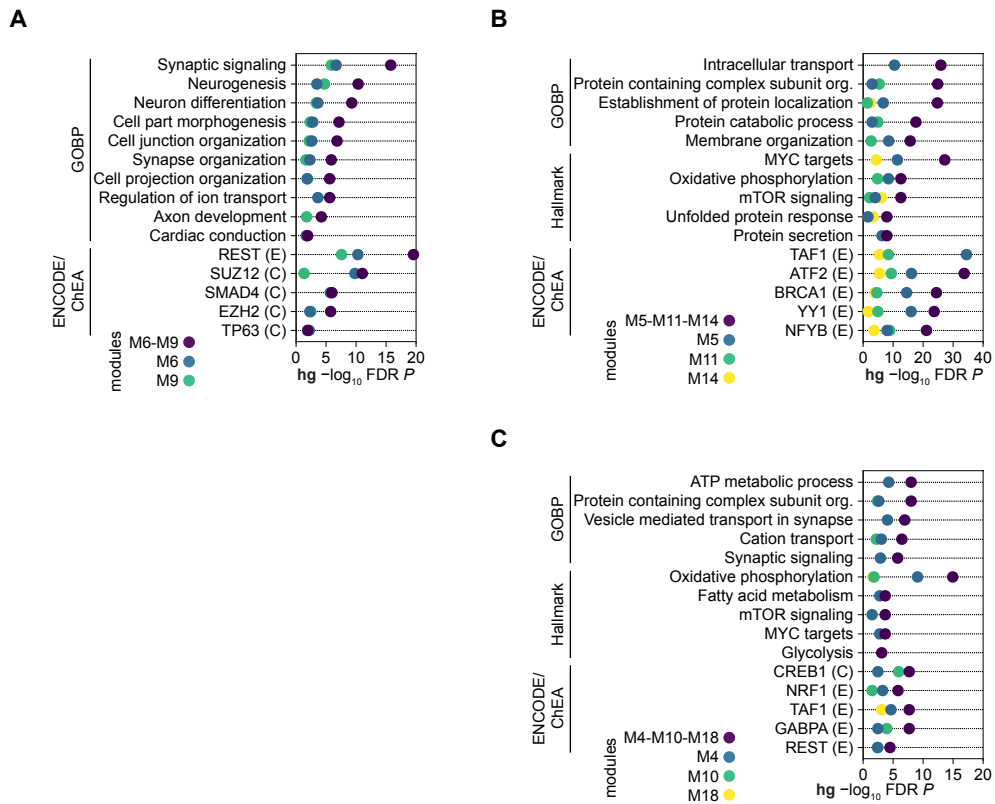


Figure S2

A-C Hypergeometric enrichment (hg) of modules and combined comodules using the Gene Ontology – Biological Process (GOBP), Hallmark, and ENCODE-ChEA Consensus databases for comodule **A** M6-M9, **B** M5-M11-M14, **C** M4-M10-M18.