Supplemental Figure 2. Gene ontology analysis for all modules. Functional annotations derived from gene ontology analyses of all 25 co-expression network modules, conducted using g:Profiler. Only 22 contained functional enrichments that exceeded significance thresholds, and they are depicted here. The top six most significant gene ontology (GO) biological process and/or molecular function terms per module are displayed (y-axis), against their respective -log10 p-values (x-axis). A) Gene ontology results against a custom background of all SomaLogic-quantified proteins, adjusted using the default multiple comparison algorithm (g:SCS). B) Gene ontology results against a custom background of all SomaLogic-quantified proteins, adjusted using FDR correction. C) Gene ontology results against a background of all annotated genes, adjusted using the default multiple comparison algorithm (g:SCS).