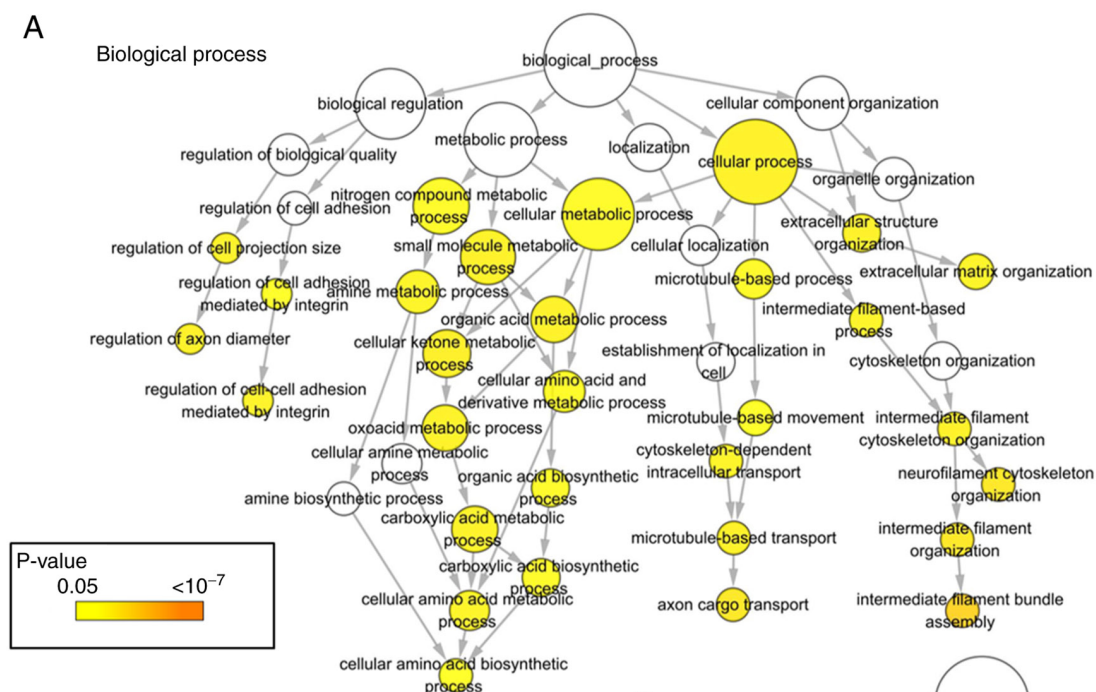


Figure S1. Gene ontology enrichment of the (A) biological processes, (B) molecular function and (C) cellular component in clusters of the differentia proteins. (A) A total of 30 terms including regulation of axon diameter, amino acid metabolic process, axon cargo transport and neurofilament organization were over-represented ($P < 0.05$) in the biological process category. (B) A total of eight terms were over-represented ($P < 0.05$) in the molecular function category. (C) A total of 16 terms were over-represented ($P < 0.05$) in the cellular component category. Terms are depicted as nodes connected by arrows that represent hierarchies and relationships between terms. Node size is proportional to the number of proteins assigned to a given ontology term, whereas node color represents the corrected P-value (Benjamin Hochberg false discovery rate correction).

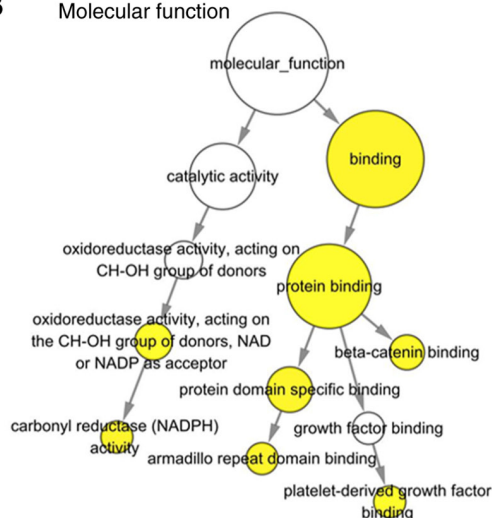
A

Biological process



B

Molecular function



C

Cellular component

