



Figure S4 (Associated with Figure 5). PANTHER GO analyses of transcripts associating only with Nab2-FLAG or Atx2-3xFLAG by RIP-Seq identify functions each RBP may regulate independent of the other. (A-B) The independent *Molecular Function* (red), *Biological Process* (green), and *Cellular Component* (blue) Gene Ontology (GO) terms most overrepresented among the (A) Nab2-specific or (B) Atx2-specific associated transcripts as compared to the entire testable transcript set. GO term independence was determined by “Hierarchical Selection” (see *Methods*). The number of GO term members within the RBP-associated transcripts and within the entire testable transcript set (*Genes enriched / Genes in total*) are reported to the right of each bar. Terms enriched among Nab2-associated transcripts include *positive regulation of microtubule polymerization* and *exosomal secretion*, while terms enriched among Atx2-associated transcripts include *regulation of ATP metabolic process* and *retrograde vesicle-mediated transport, Golgi to endoplasmic reticulum*. These GO terms may reflect processes within domains such as cytoskeletal organization, metabolism, and vesicle transport that Nab2 and Atx2 regulate independently of one another.