**File S2 for Rounds *et al.*, 2021, *Genetics*.**

**Legends for Tables S1, S3, and S4.**

**TABLE S1. Software, version numbers, and exact parameters used in RIP-Seq analyses.** As a supplement to the in-text *Materials and Methods*, this table details software names, version numbers, and exact parameters or settings used in our RIP-Seq analysis pipeline. Descriptions cover software used for, among other functions, read mapping, count normalization, gene ontology analysis, and sequence motif analysis. Tools are divided into three subcategories—*Galaxy software…*, *Gene Ontology (GO) software…*, and *Sequence Motif Analyses, MEME Suite*. For each software tool described, the tool name, version number, access data (where appropriate) is given in one column, and the exact parameters or settings used are given in a second.

**TABLE S3.** **Identities, enrichment values, and significance testing for *Both Nab2 and Atx2*-associated transcripts, *Only Nab2*-associated transcripts, *Only Atx2*-associated transcripts, and all other transcripts in the RIP-Seq testable set.** The gene symbols, IP/Input control-normalized enrichment values, and results of statistical significance testing are provided for all 5,760 transcripts in the RIP-Seq testable set, including the 28 *Both Nab2 and Atx2*-associated transcripts, the 113 *Nab2 Only*-associated transcripts, and the 75 *Atx2 Only*-associated transcripts. For each transcript, the first three columns present *Control-normalized IP/Input* (i.e. Fold Enrichment) values, which quantify how effectively a transcript was enriched by IP. These are derived by calculating IP/Input values from *DESeq2*-normalized counts for each control and epitope-tag sample and then setting the average of control values to 1. The next two columns display results from significance testing by gene-by-gene one-way ANOVAs, Dunnett’s post hoc tests, and within-gene multiple hypothesis testing adjustment. Transcripts with *Dun. Adj. p*-values < 0.05 are considered statistically significantly enriched by IP and thus were found to be associated with the relevant RBP. The next column categorizes the transcript by which RBP, if any, it was found to be significantly associated with. The next three columns detail the standard error of the mean (SEM) of the *Control-normalized IP/Input* values. The last two columns list Dunnett values calculated in the course of significance testing.

**TABLE S4. Identities of all RBP-associated transcripts annotated under the overrepresented GO terms reported herein.** Figure 4 and Supplemental Figure 4 report the top 3 independent (see *Methods*) *Molecular Function* and *Cellular Component* GO terms, and the top 6 independent *Biological Process* GO terms, that among the three sets of RBP-associated transcripts (*Both Nab2 and Atx2*, *Nab2 Only*, and *Atx2 Only*) are most overrepresented by fold enrichment compared to the entire testable transcript set. The identities of a few RBP-associated transcripts annotated under these GO terms are reported in-text; all such transcripts are reported in this table. GO terms are categorized by RBP-associated transcript set (first column), further categorized by top-level GO term, and then listed in descending order of fold enrichment (second column). GO accessions are provided for each term to annotate and unambiguously identify it. RBP-associated transcripts within each set and annotated under each GO term are listed in the third through sixth columns. Some transcripts are listed multiple times, reflecting their annotation under multiple top independent GO terms.