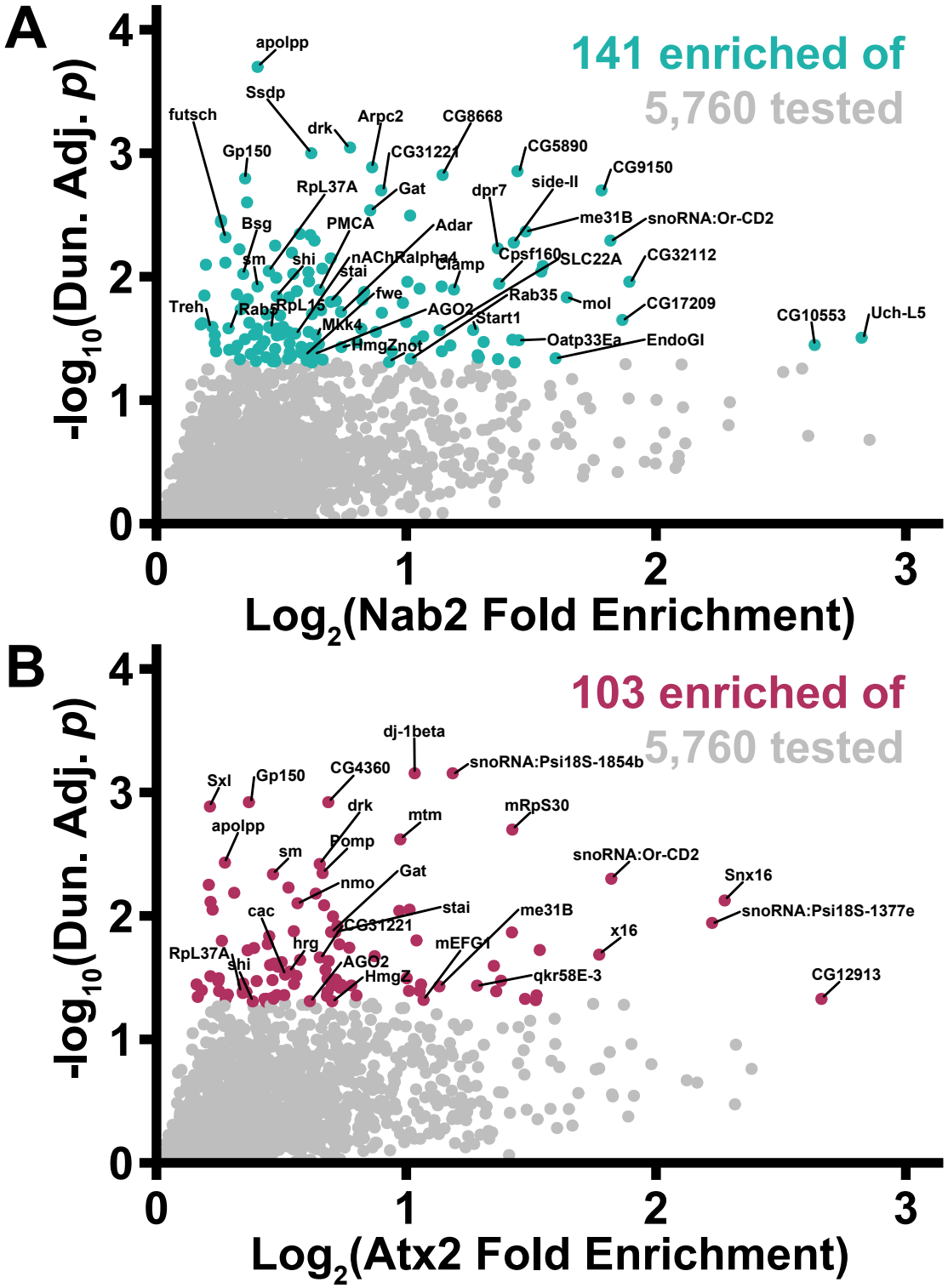

Figure S3 (Associated with Figure 4). RIP-Seq analysis reveals diverse sets of overlapping transcripts associate with Nab2-FLAG and Atx2-3xFLAG. (A-B) Scatter plots of all transcripts within the 5,760 of the testable set with positive (A) *log_2(Nab2 Fold Enrichment)* or (B) *log_2(Atx2 Fold Enrichment)* values. *Fold Enrichment* values quantify how effectively a transcript was enriched by IP and are derived by calculating IP/Input (i.e. percent input) values for control and epitope-tag samples and setting the average of control values to 1 (i.e. 0 on the logarithmic scale used here). Y-axes display results of significance testing, conducted by gene-by-gene one-way ANOVA, Dunnett's post-hoc test, and within-gene multiple hypothesis testing adjustment (*Dun. Adj. p*). Statistically significant transcripts (*Dun. Adj. p* < 0.05) are colored. On each plot, labels identify many transcripts of interest chosen by both objective and subjective means. Labels are shown for many transcripts among the "top" RBP-specific RBP-associated transcripts, the shared RBP-associated transcripts, the transcripts emphasized by GO analyses (see *Results* for details), and others of subjective interest. RBP-associated transcripts of interest not included in the main text include *Treh* and *Bsg* in (A), *qkr58E-3* and *cac* in (B), and *RpL37A* and *Gp150* in both panels.