

**Supplementary Table S1. Decay rates of isoforms associated with specific Gene Ontology terms.**

**Supplementary Table S2. Results from ANOVA followed pair-wise t-tests on the decay rates of isoforms belonging to each of the eight transcript isoform categories in Figure 4 .**

**Supplementary Table S3. Isoform pairs with significantly different decay rates in wild-type yeast.**

**Supplementary Table S4. Stabilities for isoforms with and without RBP motif for genes with RBP motif.**

**Supplementary Table S5. Stabilities of PUF3-bound isoforms in wild-type yeast and their relative stabilities in *puf3Δ*.**

**Supplemental File S1. Sweave document with a detailed computational top-down analysis pipeline that can be used to reproduce our MIST-Seq analysis and easily adapted for future studies.**