

**A compensatory link between cleavage/polyadenylation and mRNA turnover
regulates steady-state mRNA levels in yeast**

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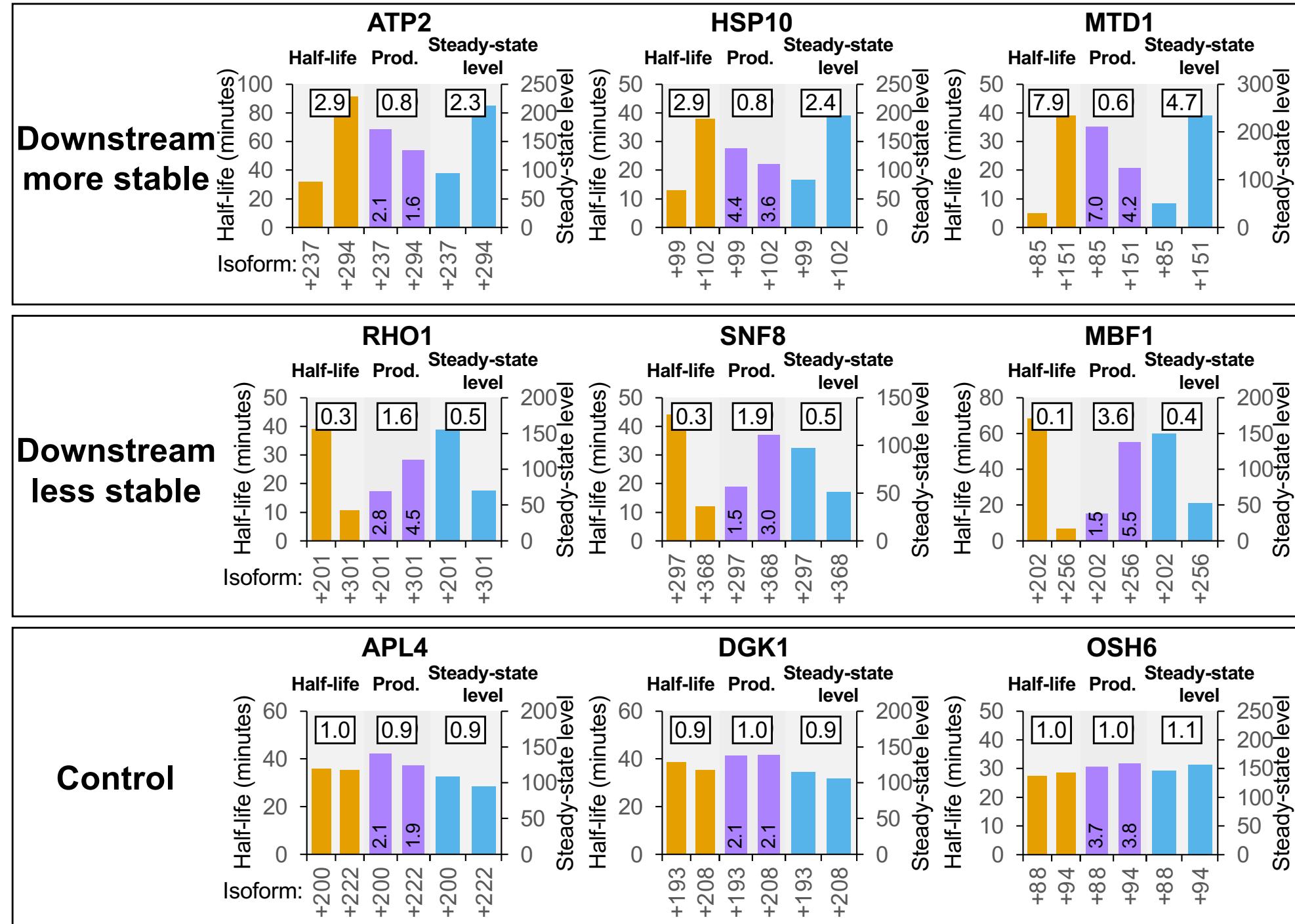
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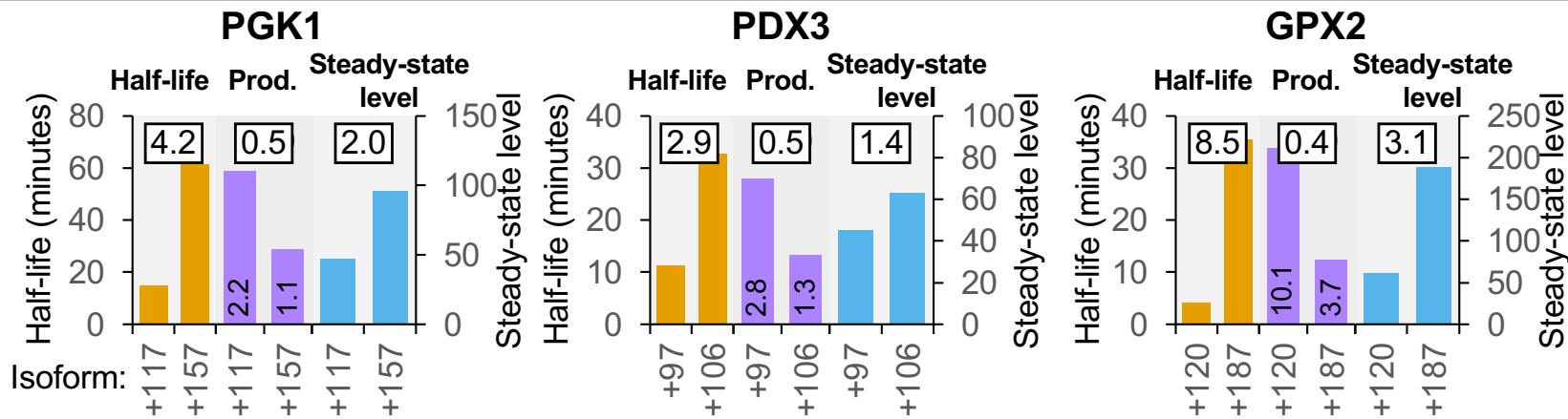
SI Appendix

Moqtaderi et al. Figure S1

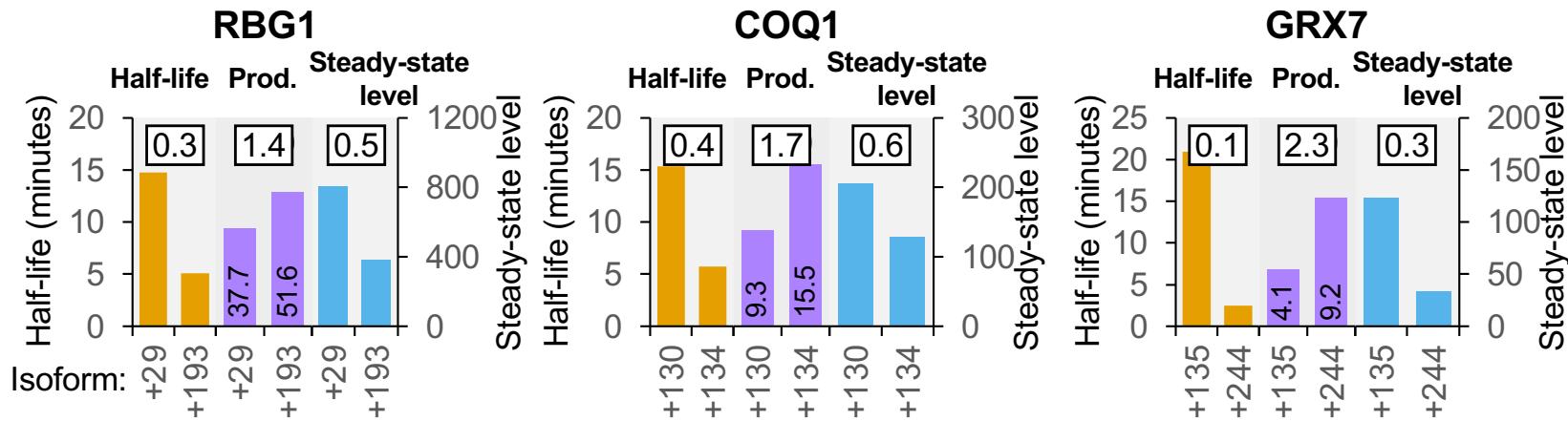


Moqtaderi et al. Figure S2A

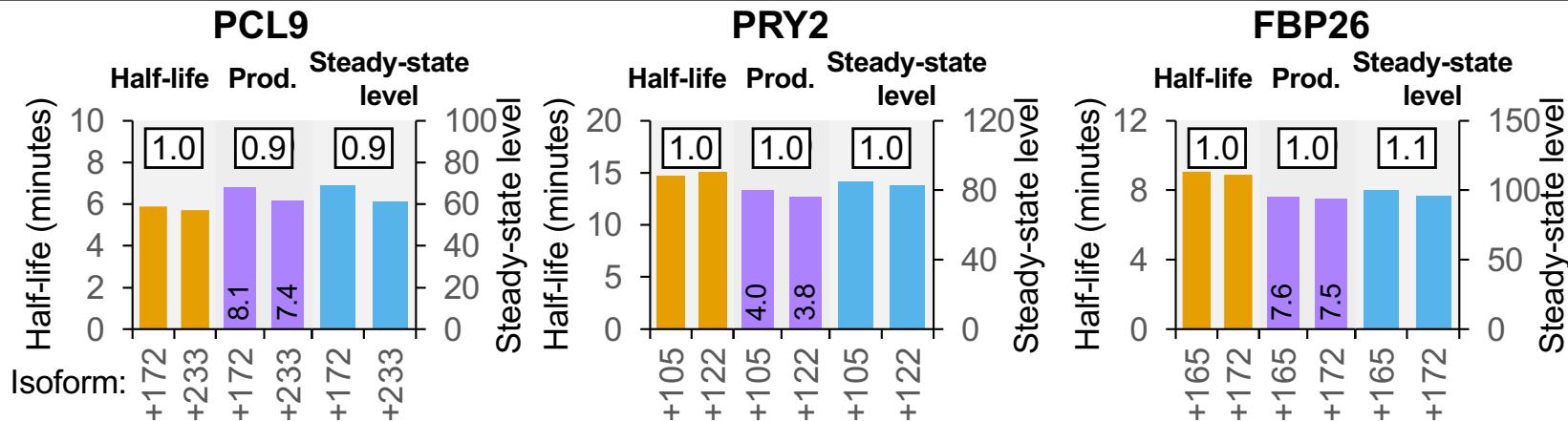
Downstream more stable



Downstream less stable



Control



Moqtaderi et al. Figure S2B

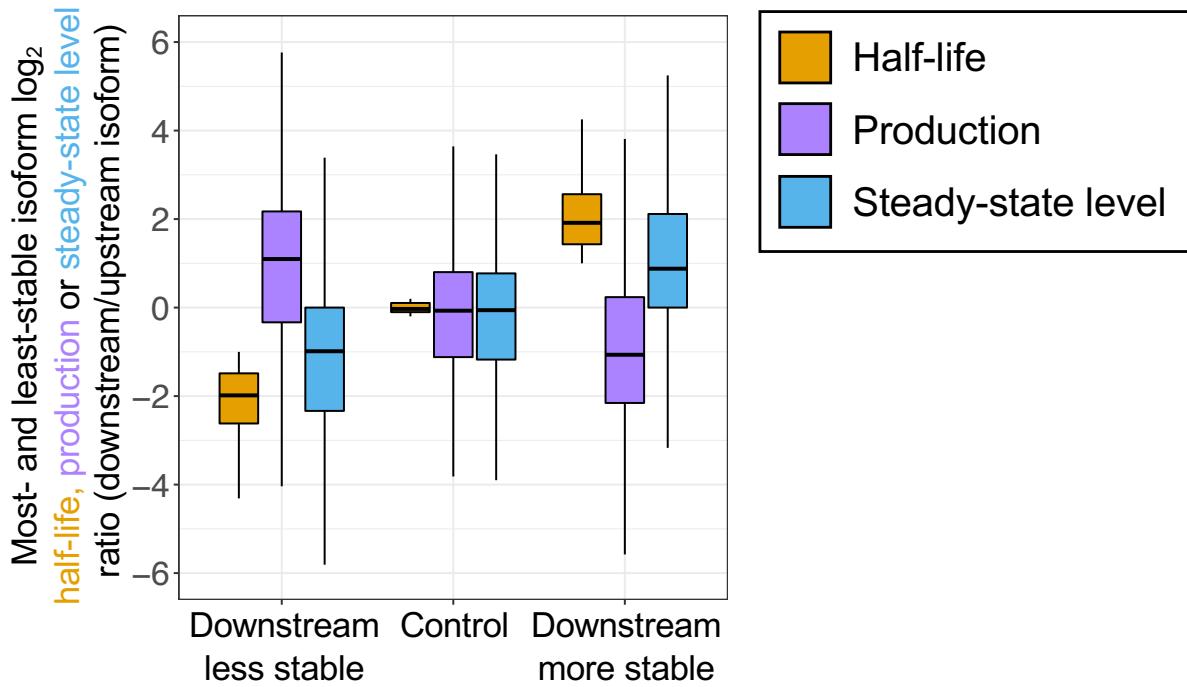
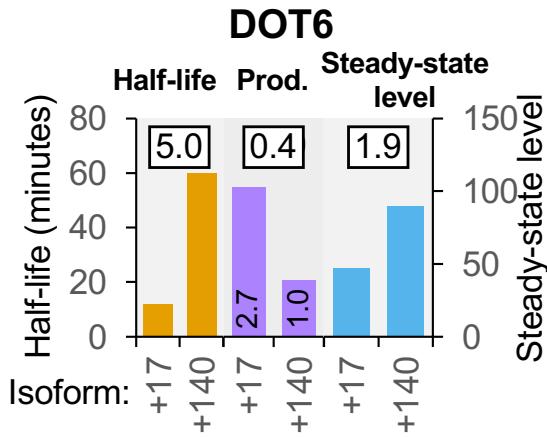
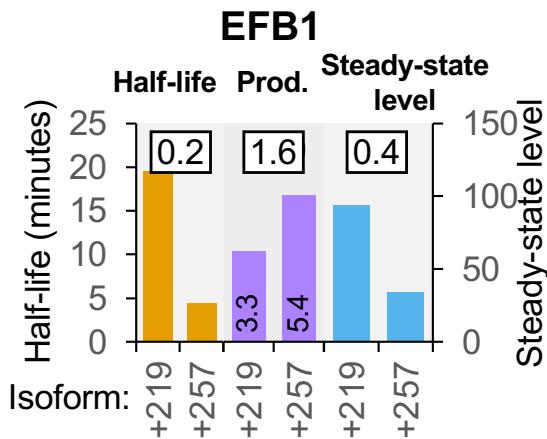


Figure S3

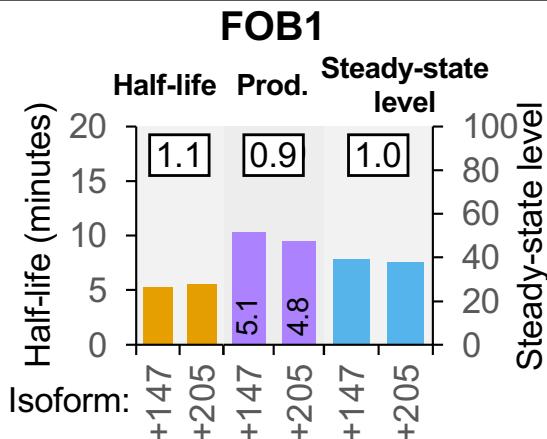
Downstream more stable



Downstream less stable

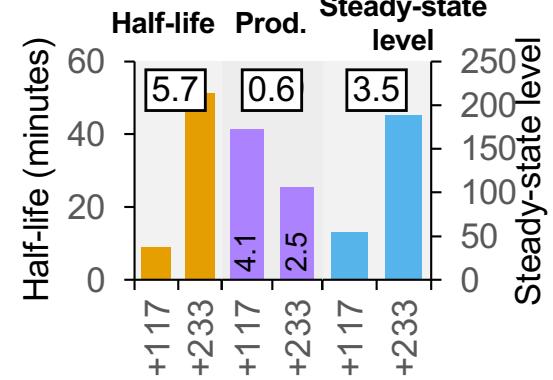


Control

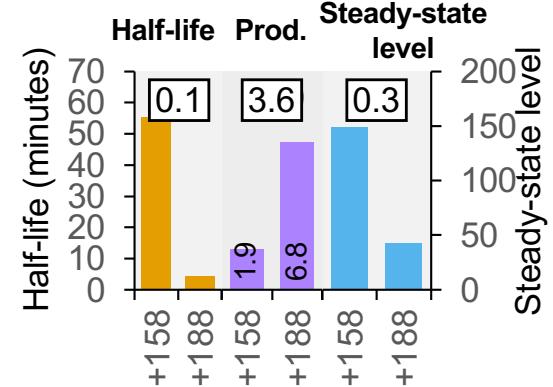


Minimal

TUB2



GDT1



RPC31

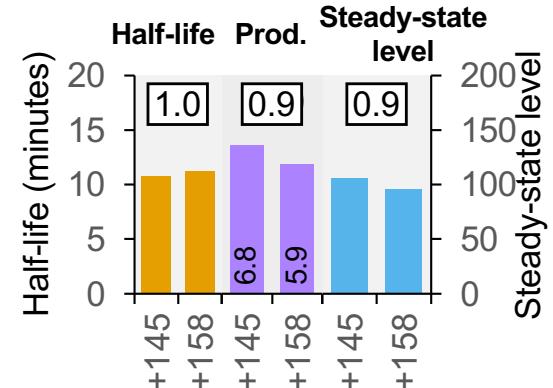
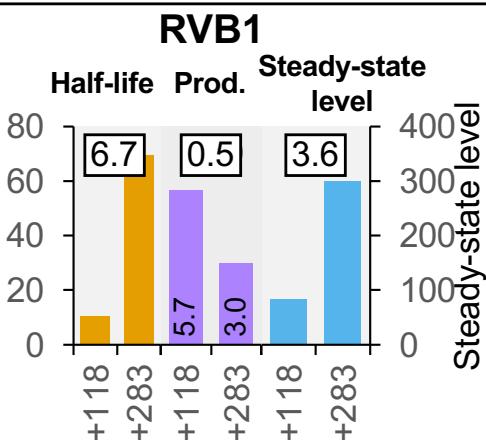
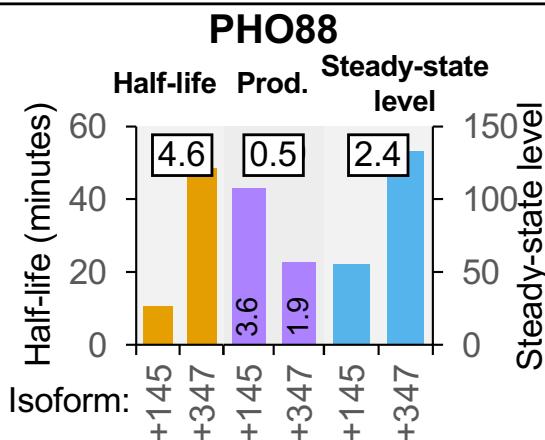


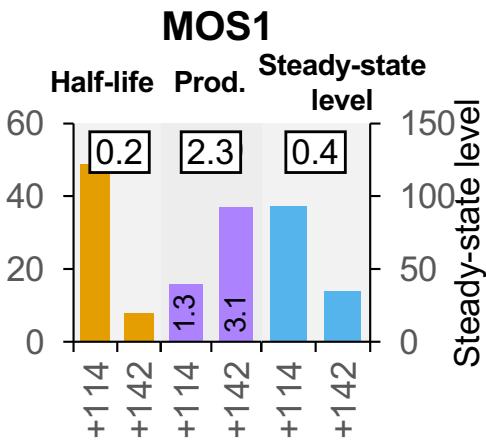
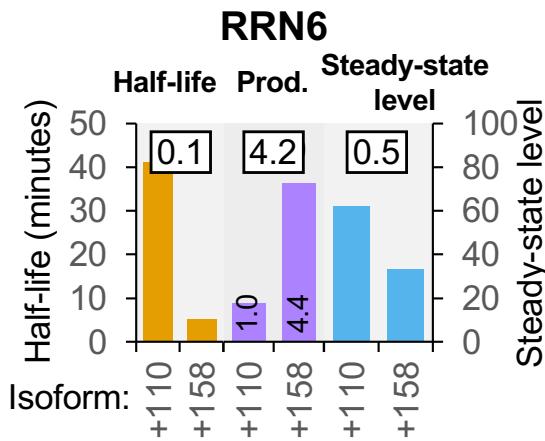
Figure S4

YPD

**Downstream
more stable**



**Downstream
less stable**



Control

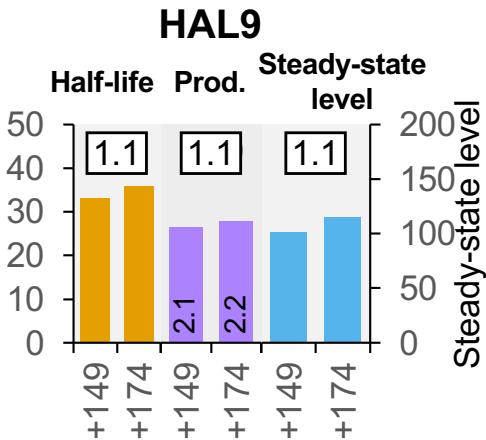
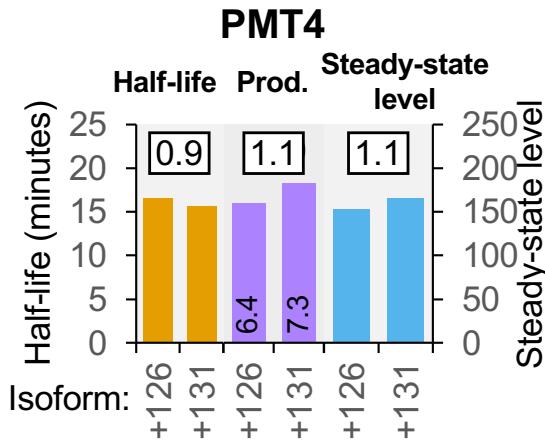


Figure S5

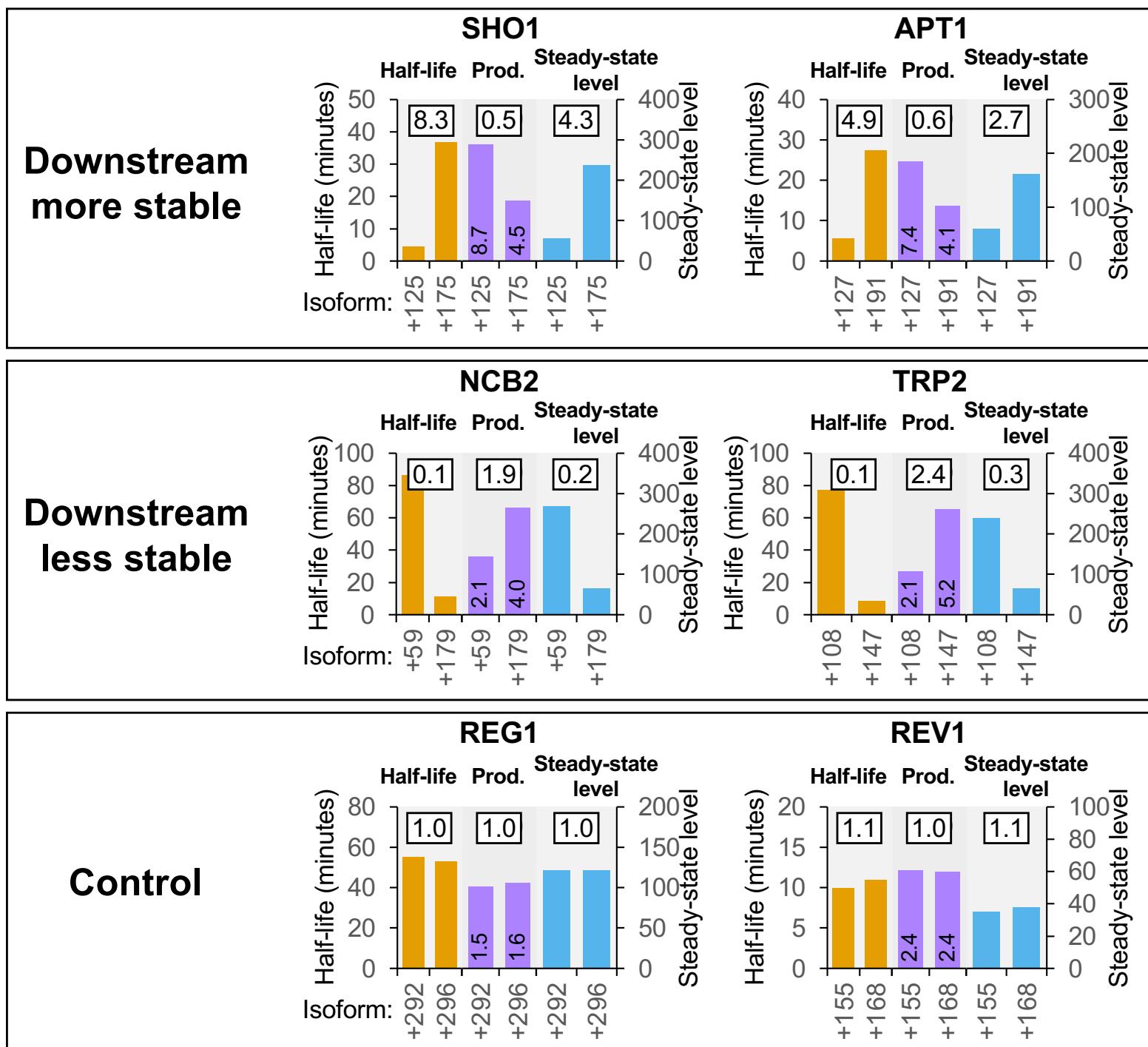
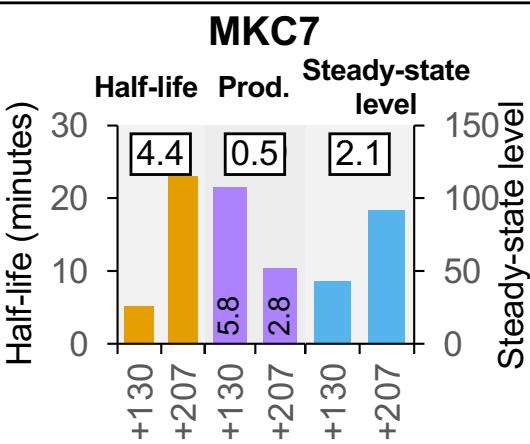
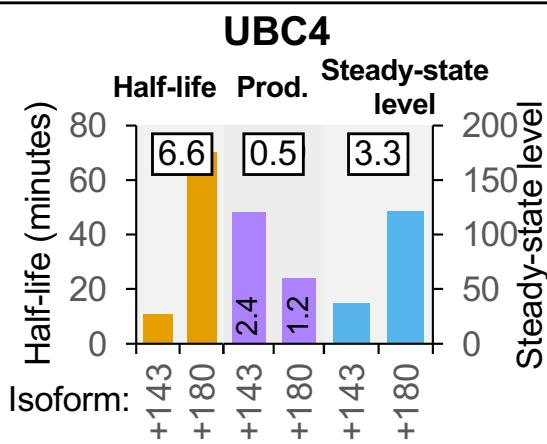
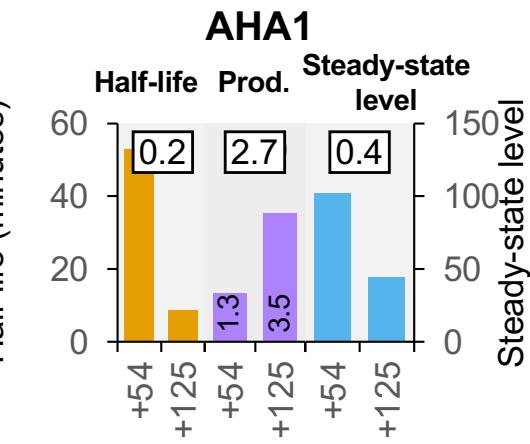
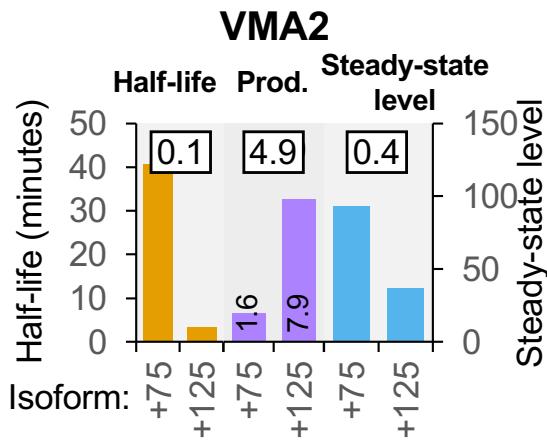


Figure S6

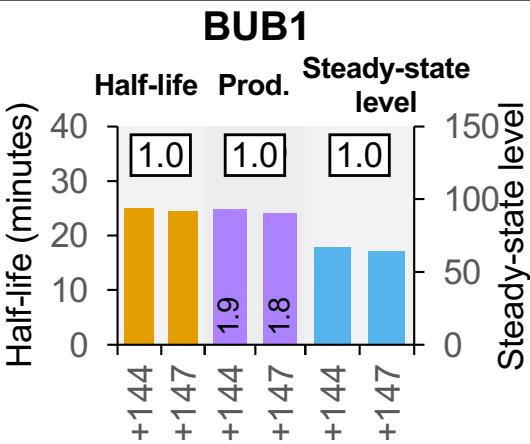
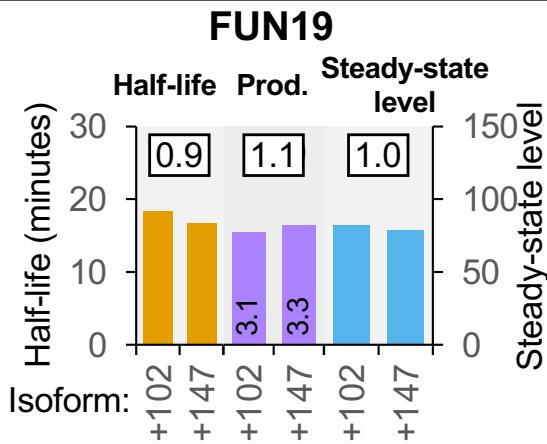
**Downstream
more stable**



**Downstream
less stable**



Control



SUPPLEMENTARY LEGENDS

Supplementary Figure 1. Additional examples from a published dataset (10) showing compensation between cleavage/polyadenylation and mRNA stability in YPD medium. For each gene, the most- and least-stable isoforms are compared with respect to isoform stability (orange bars, values on left y-axis), relative production rate (purple bars, values printed on the bars), and steady-state level (blue bars, values on right y-axis). Three additional examples are shown for each of the “downstream less stable,” “downstream more stable,” and “control” 3’ UTR categories. Boxed numbers above the bars represent the ratio of values for the two isoforms (expressed as downstream/upstream isoform value).

Supplementary Figure 2. Compensatory effect is independent of strain background, Pol II inactivation methodology, and RNA assay/sequencing procedure. (A) Examples of compensation between cleavage/polyadenylation and mRNA stability in a strain harboring a temperature-sensitive allele of Pol II grown in YPD (11). Isoform stability (orange bars, values on left y-axis), production rates (purple bars, values printed on the bars), and steady-state expression levels (blue bars, values on right y-axis) are shown for the least- and most-stable same-gene isoform pairs in the “downstream less stable,” “downstream more stable,” and “control” categories. Boxed numbers above each pair of bars represent the ratio of values for the isoform pair (downstream/upstream isoform). (B) Median distal/proximal steady-state isoform production ratios in a strain harboring a temperature-sensitive allele of Pol II are inversely related to the corresponding median stability ratios for the most- and least-stable isoforms of each gene. Three classes of isoform pairs are considered, based on whether the downstream isoform is more stable (“downstream more stable”), less stable (“downstream less stable”), or comparably stable (“Control”) relative to the upstream isoform. For each group, distributions of production rate ratios (purple boxes) and steady-state expression ratios (at $t =$

0; blue boxes) are shown alongside the half-life distributions of the same isoforms (gold boxes). Data (11) are tabulated in Supplemental File 1.

Supplementary Figure 3. Additional examples of compensation between cleavage/polyadenylation and mRNA stability in Minimal medium. Isoform stability (orange bars, values on left y-axis), steady-state expression (blue bars, values on right y-axis), and production rates (purple bars, values printed on the bars) are shown for the most-and least-stable isoform pairs from genes in the “downstream less stable,” “downstream more stable,” and “control” categories. Boxed numbers above each pair of bars represent the ratio of values for the downstream to the isoform pair (always expressed as downstream/upstream isoform values).

Supplementary Figure 4. Additional examples of compensation between cleavage/polyadenylation and mRNA stability in YPD medium. Isoform stability (orange bars, values on left y-axis), production rates (purple bars, values printed on the bars), and steady-state expression levels (blue bars, values on right y-axis) are shown for the most- and least-stable isoform pairs from 3' UTRs in the “downstream less stable,” “downstream more stable,” and “control” categories. Boxed numbers above each pair of bars represent the ratio of values for the isoform pair (always expressed as downstream/upstream isoform values).

Supplementary Figure 5. Additional examples of compensation between cleavage/polyadenylation and mRNA stability in medium containing Sorbitol. Isoform stability (orange bars, values on left y-axis), production rates (purple bars, values printed on the bars), and steady-state expression (blue bars, values on right y-axis) are shown for most- and least-stable isoform pairs from genes in the “downstream less stable,” “downstream more stable,” and “control” categories. Boxed numbers above each pair of bars represent the ratio of values for the isoform pair (always expressed as downstream/upstream isoform values).

Supplementary Figure 6. Additional examples of compensation between cleavage/polyadenylation and mRNA stability in YPGal medium. Isoform stability (orange bars, values on left y-axis), production rates (purple bars, values printed on the bars), and steady-state expression (blue bars, values on right y-axis) are shown for most- and least-stable isoform pairs from genes in the “downstream less stable,” “downstream more stable,” and “control” categories. Boxed numbers above each pair of bars represent the ratio of values for the isoform pair (always expressed as downstream/upstream isoform values).

Supplementary file 1

Ratios (\log_2) of half-lives, production rates and steady-state expression levels of same-gene 3' mRNA isoforms (defined by position downstream of the ORF) with the minimal or maximal half-life for all datasets.