



Figure S6 The stability of the spliced 3'UTR intron-containing *y14* mRNA is affected by NMD, EJC and CBC mutations.

(A-C) Half-lives of mRNA were measured by 4TU RNA pulse-chase as described in Figure 2 to analyze the effects of NMD, EJC and CBC mutations on *y14* transcript stability. 4TU RNA was from the same samples used for analyses of other RNAs in other figures (A) wt, $\Delta upf1$, $\Delta upf1$ *his-3::upf1*, $\Delta upf1$ *his-3::upf1-3XFLAG*, $\Delta upf2$, $\Delta upf2$ *his-3::upf2-3XFLAG* and $\Delta upf2$, *his-3::upf2-HAT-FLAG* strains (B) wt, $\Delta mago$ and $\Delta mago$ *mago[Bar^r]* strains (C) wt, $\Delta cbp20$, $\Delta cbp20$ *cbp20[Bar^r]*, $\Delta cbp80$, $\Delta cbp80$ *cbp80[Bar^r]* strains. (D) Measurement of mRNA levels of *y14*, *eif4a3*, *erf1*, *arg-2*, *eif5* and *cox-5* in total RNA in wt, $\Delta upf1$, $\Delta upf2$, $\Delta y14$, $\Delta mago$, $\Delta cbp20$ and $\Delta cbp80$ strains. The data for total RNA levels show the average and standard deviations from four independent RNA preparations (mRNA levels were normalized to 25S rRNA levels in each case and all then all calculated relative to the normalized level in wt).