Supplemental Data

Structure-function analysis and genetic interactions of the Luc7 subunit of the *Saccharomyces cerevisiae* U1 snRNP

Radhika Agarwal, Beate Schwer, and Stewart Shuman

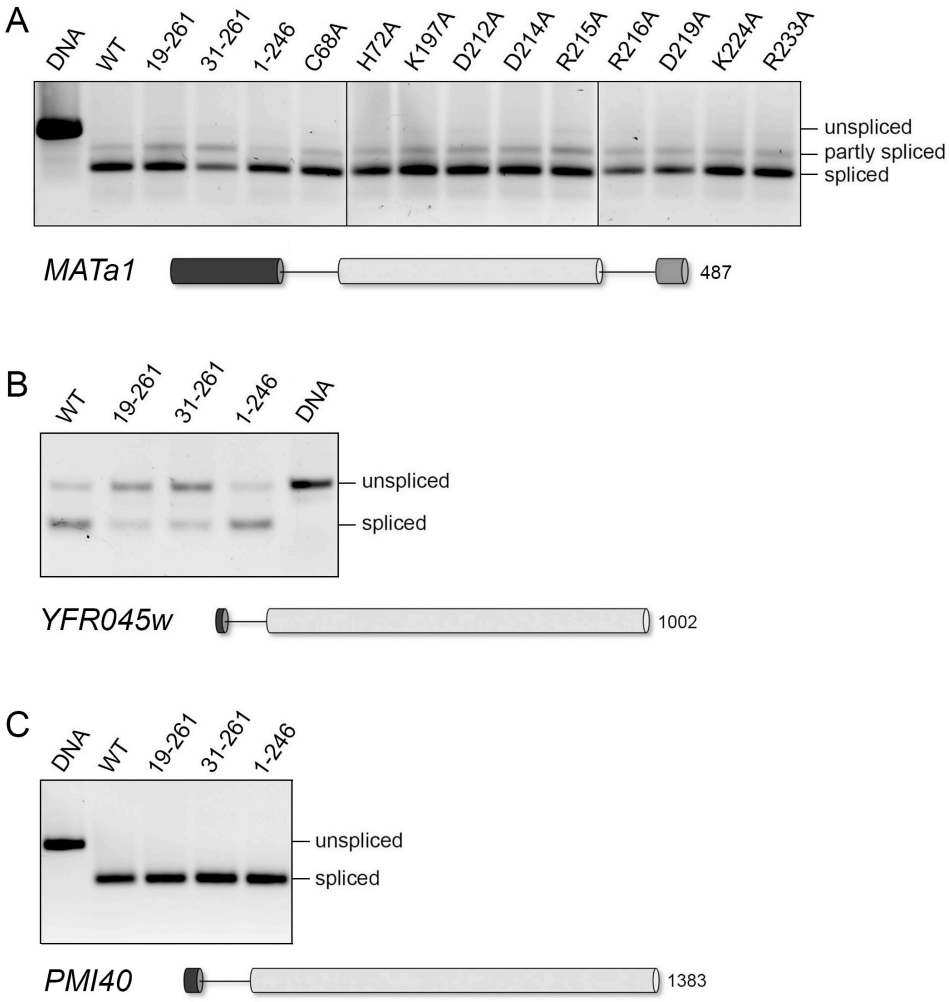

Figure S1. **Effect of Luc7 mutations on splicing of *MATa1, YFR045w*, and *PMI40* pre-mRNAs**. RNA isolated from the indicated *LUC7* strains was reverse transcribed with an oligo(dT) primer. cDNAs were PCR-amplified with gene-specific sense and antisense primer pairs derived from the first and last exons of the *MATa1* (panel A), *YFR045w* (panel B) and *PMI40* (panel C) genes (Jacewicz et al. 2015). The exon-intron organizations of the pre-mRNAs are shown, with exons depicted as horizontal cylinders. The PCR products were resolved by native agarose gel electrophoresis and visualized by staining with ethidium bromide. The products of PCR amplification of genomic DNA with the same primer pairs are shown in lanes labeled "DNA". The RT-PCR products of unspliced, partly spliced, and fully spliced transcripts are specified on the *right*.