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Supplemental Data

Competition between the ATPase Prp5 and Branch Region-U2 snRNA Pairing Modulates the Fidelity of Spliceosome Assembly

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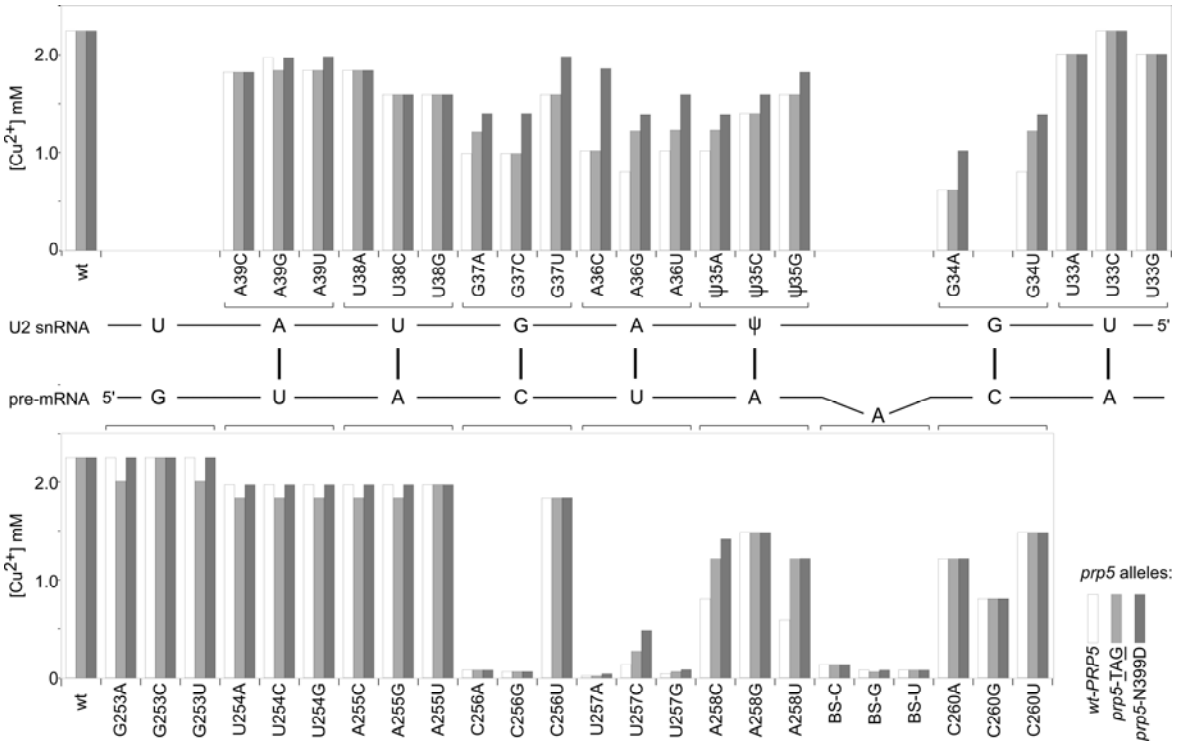

Figure S1. Summary of growth on copper of strains carrying either intron branch region mutants, or wt reporter in the presence of U2 snRNA mutants. *prp5*-TAG *and* -N399D alleles improve overall splicing of wt reporter in the presence of U2 snRNA alleles mutated at positions G34, ψ35, A36, and G37 (upper), and improve splicing of intron branch region mutants at two positions, U257 and A258 (lower).

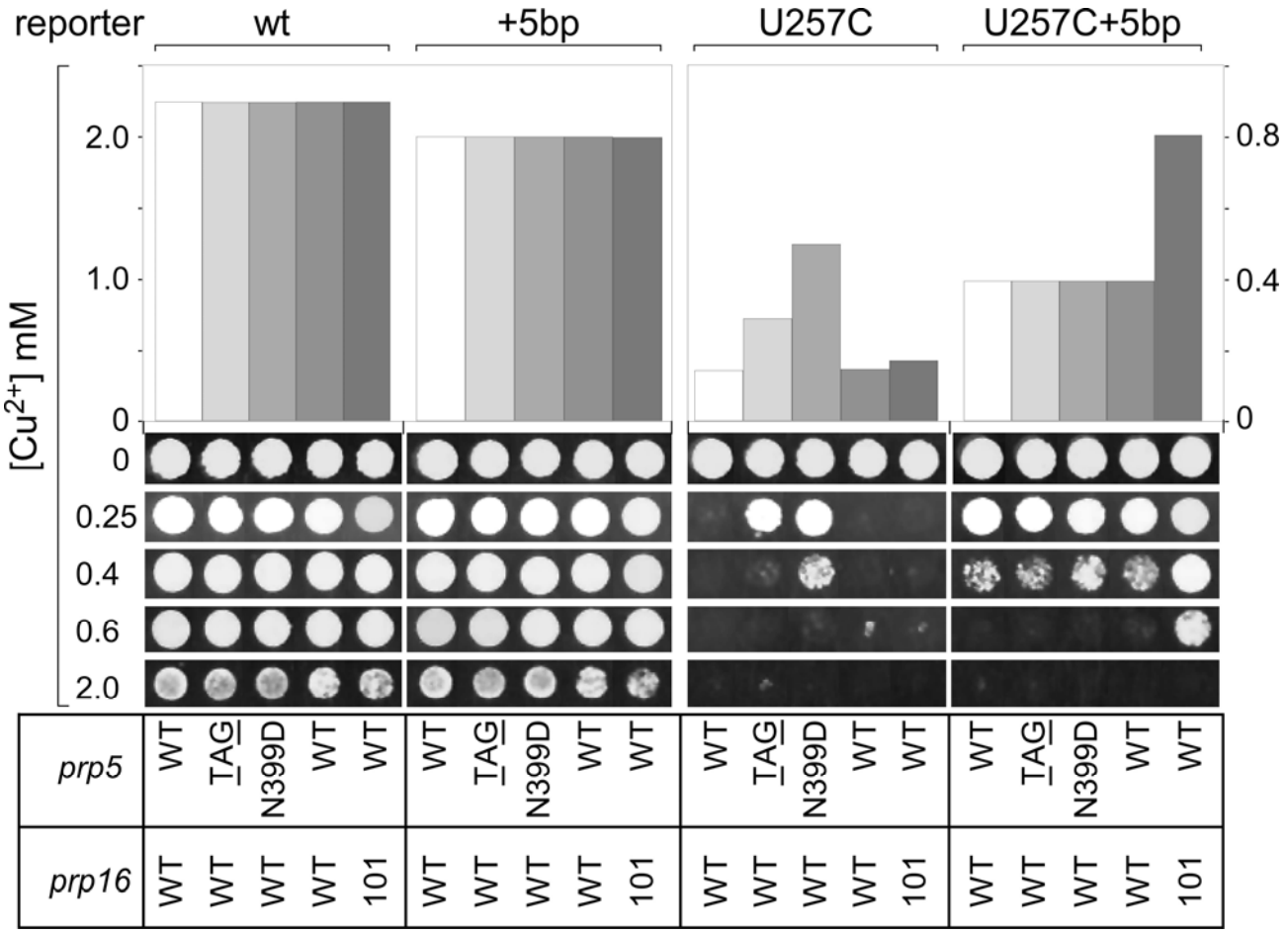

Figure S2. *prp5* and *prp16* alleles have distinct effects on splicing of suboptimal branch region mutants.

(Upper) Graph of maximum copper concentration that allows cell growth. (Lower) Cell growth on selected copper plates, as indicated. *prp5*-TAG and -N399D alleles improve splicing of branch region mutant U257C, but provide no additional improvement to branch region mutant (U257C+5bp) that contains extended pairing to U2 snRNA. In contrast, the *prp16-101* allele provides only slight improvement to the U257C reporter, but provides significant additional improvement to the U257C+5bp mutant.