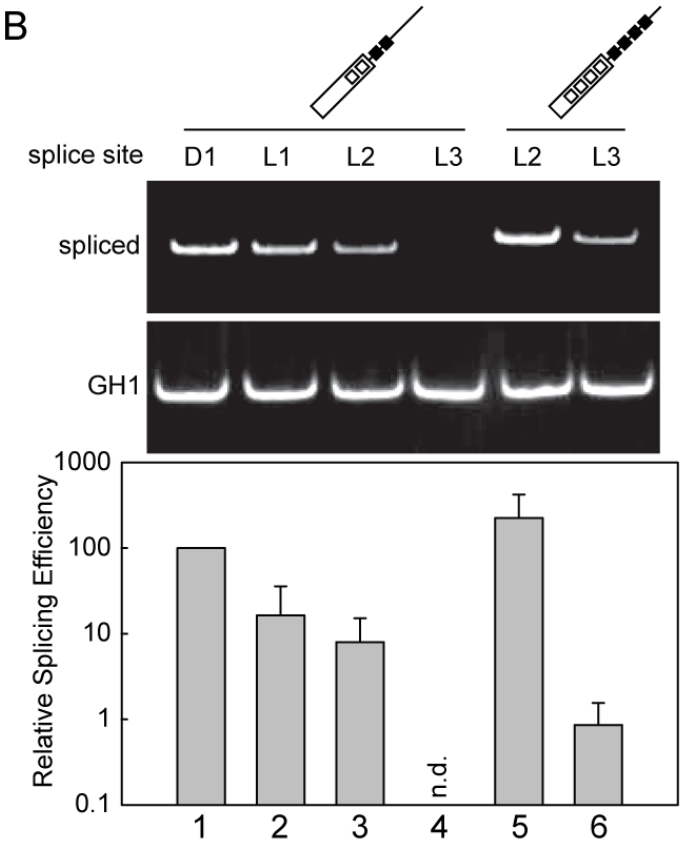
REVISED: Supplemental Figure 3

A

5´ss	sequence	HBS	Maxent
D1	CuG/GUGAGUAc	17.50	10.10
L1	CAc/GUGAGUcc	14.20	9.30
L2	Ccc/GUGAGUcc	12.10	8.40
L3	Cuc/GUAcGUcc	10.70	7.59

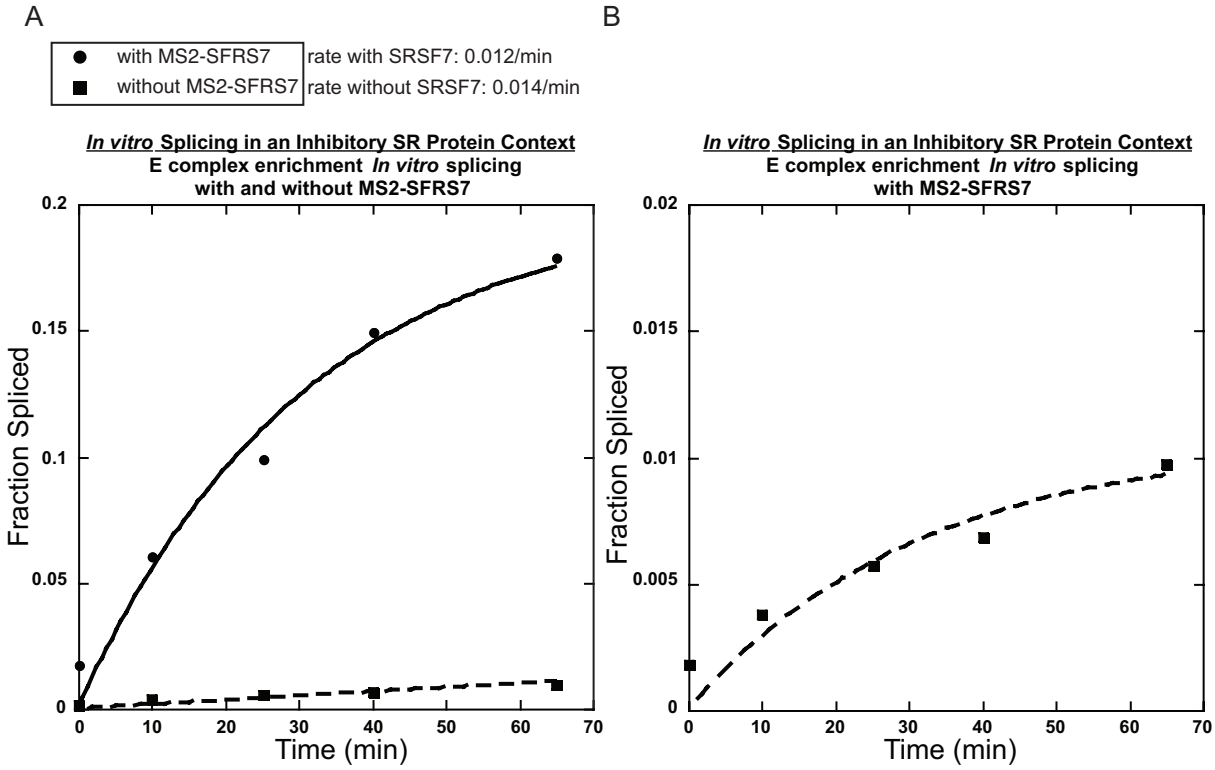
B



Supplemental Figure 3: Multiple PDEs synergize in activating weak 5' splice sites.

To analyze the functional interdependence of the intrinsic strength of a 5´ss defined by its ability to basepair with the U1 snRNA and the sequence surrounding, we mutated the 5´splice site to gradually vary its strength **(A)** and tested it in the context of different numbers of enhancer binding sites in the vicinity. **(B)** Transfection experiments were carried out as described above and samples were subjected to semi-quantitative and quantitative RT-PCR analysis.

REVISED: Supplemental Figure 6



Supplemental Figure 6: Results from E-complex pulse chase experiments in the presence or absence of MS-SRSF7.

E-complex was enriched in the absence of ATP, and the reaction was then chased as described in the Supplemental Materials and Methods. (**A**) Kinetic profiles for both reactions are shown, demonstrating that the presence of MS2-SRSF7 reduces splicing efficiency. (**B**) Blow-up of the reaction in the presence of MS-SRSF7 demonstrating approach to endpoint kinetics. Thus, the reduced kinetics are not due to a drop in the rate of splicing, but due to the drop in the fraction of enriched E-complexes that progress to active spliceosomes.