

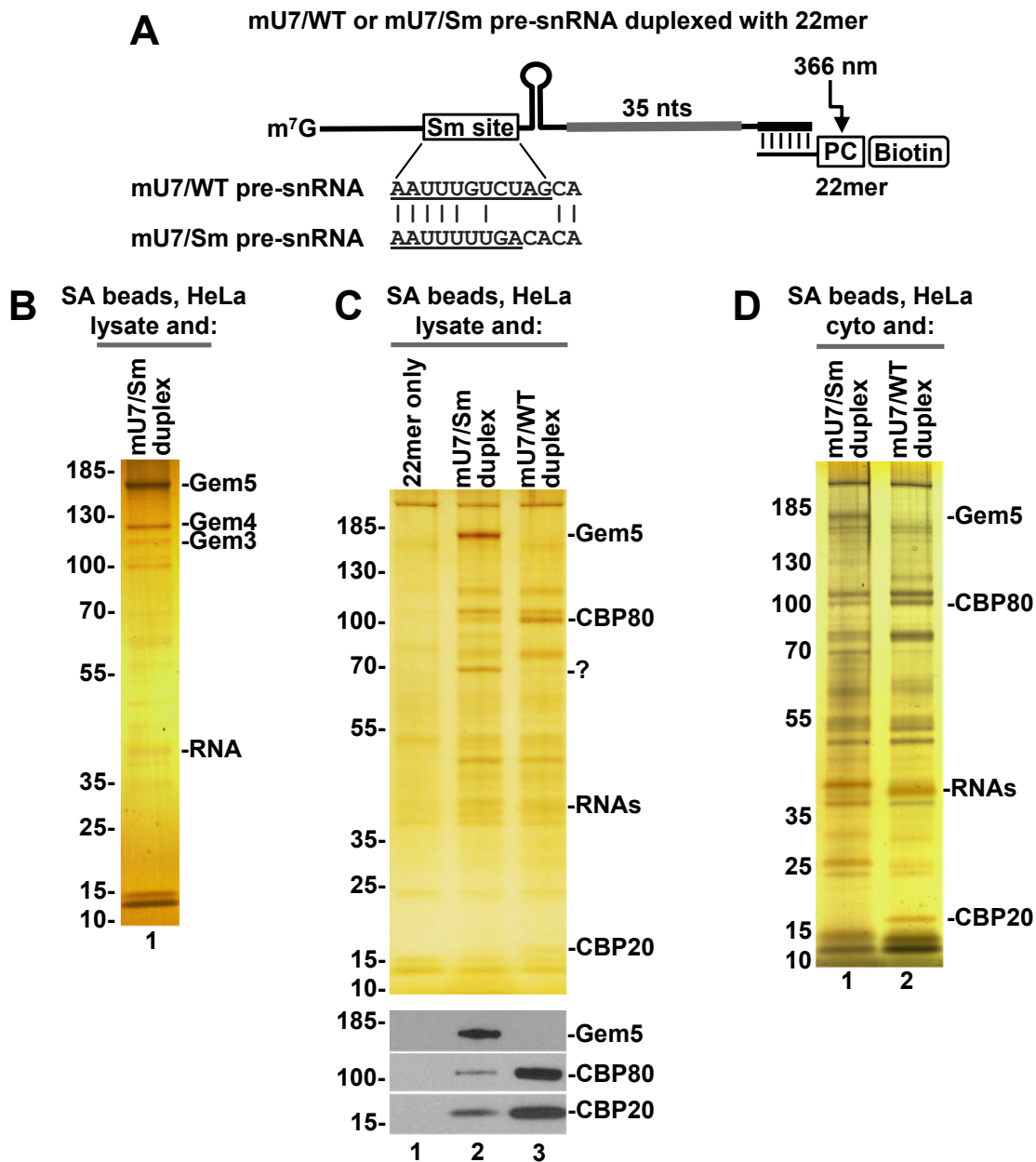


Fig. S1. Purification of human proteins bound to mouse WT U7 pre-snRNA using UV-mediated elution. **A.** A diagram of the duplex formed between the 22mer containing a photocleavable linker and biotin at the 5' end and either WT mouse U7 pre-snRNA or its mutant within the Sm site. The thick line indicates a 35-nucleotide extension at the 3' end of U7 pre-snRNA that is exonucleolytically removed upon completion of the Sm ring. Nucleotide substitutions that convert the U7-specific Sm site in mU7/WT pre-snRNA to its U4 counterpart in mU7/Sm pre-snRNA are shown below. **B-D.** Proteins of HeLa whole cell lysates (panels B and C) or a HeLa cytoplasmic extract (panel D) bound to either mU7/WT or mU7/Sm pre-snRNAs were released from streptavidin beads via UV elution, separated by electrophoresis in a 4-12% SDS/polyacrylamide gel and detected by silver staining. Protein identities determined by mass spectrometry and/or Western blotting are indicated to the right of each panel. The question mark indicates a protein of unknown identity that predominantly binds to mU7/Sm pre-snRNA.

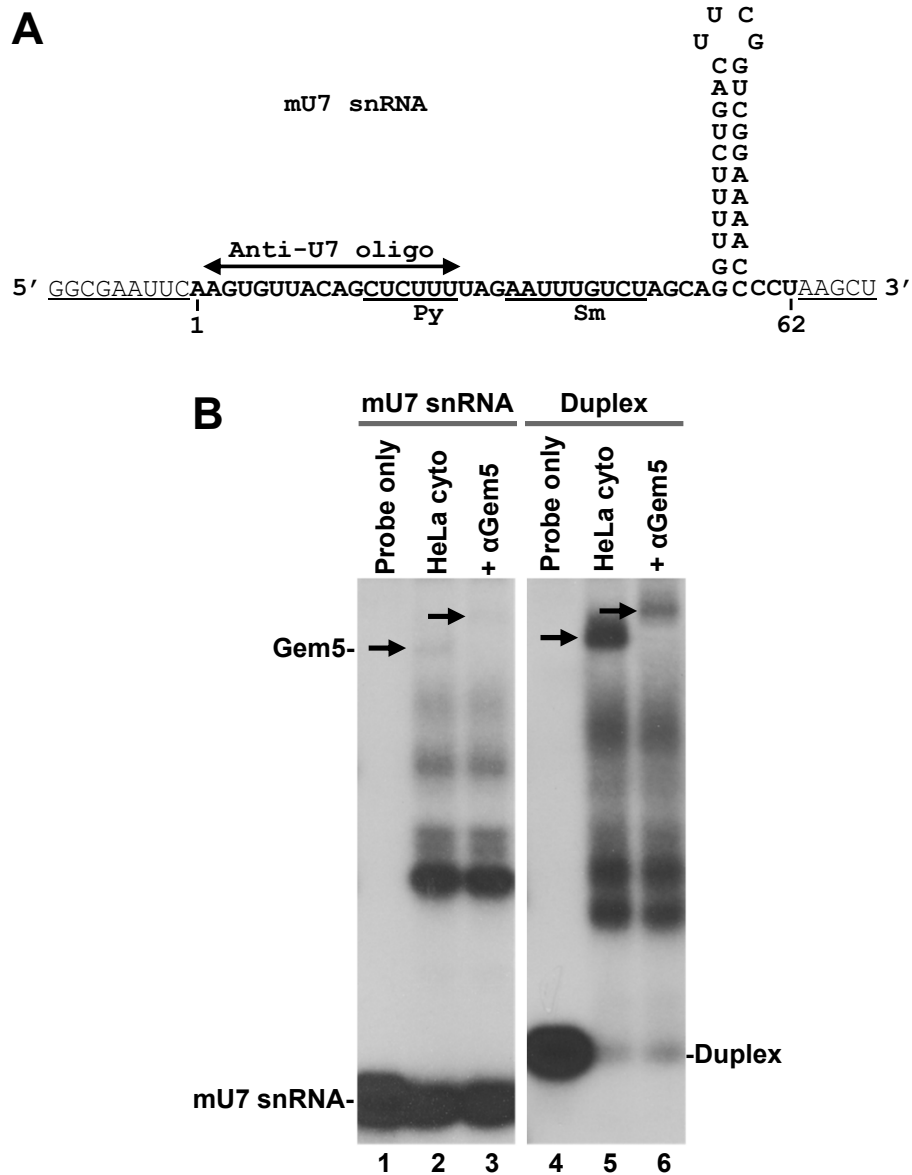


Fig. S2. Blocking the 5' end of mouse U7 snRNA (mU7 snRNA) by a complementary oligonucleotide promotes Gemin5 interaction. **A.** Nucleotides of mouse U7 snRNA (1-62) are indicated with bold fonts. The Py and Sm sites are underlined, and the region that base pairs with the anti-U7 oligonucleotide is shown above. Nucleotides indicated with thin fronts at the 5' and 3' ends are of vector origin. **B.** EMSA with a HeLa cytoplasmic extract and mouse U7 snRNA (mU7 snRNA) alone or pre-annealed to the anti-U7 oligonucleotide (duplex). Lane 3 and 6 contain anti-Gemin5 antibody. The arrows indicate the positions of Gemin5-containing complexes.

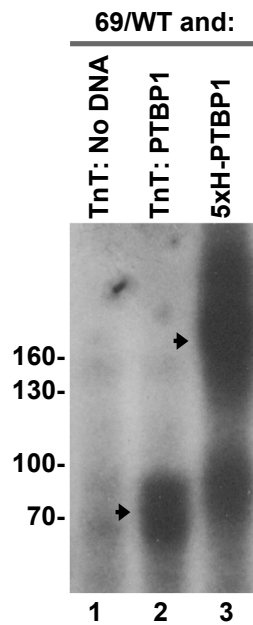


Fig. S3. UV-cross-linking of PTBP1 to 69/WT RNA. TnT-expressed PTBP1 (lane 2) or 5xH-tagged recombinant PTBP1 (lane 3) were UV irradiated and separated by PAGE. In lane 1, UV-crosslinking was carried out with a control TnT lysate lacking PTBP1 cDNA. Proteins covalently attached to radioactively labeled RNA were detected by autoradiography. Arrows indicate the positions of the PTBP1 monomer and dimer cross-linked to 69/WT probe.

Gemin2 interaction			
Hs	17	DSVLFRRGTGQSDSDIWDDTALIKAYDKAVASFKHALKNGDICETSGKPKTTPKRKPAK	76
		+ V+F RGTGQSDSDIWDDTALIKAYDKAVASFK+ALK D KRK K	
Dr	6	EDVVFCRGTGQSDSDIWDDTALIKAYDKAVASFKNALKGEDGATPQENDNPGKKRKNK	65
Tudor domain			
Hs	77	KNKSQKKNTAASLQQWKVGDKCSAIWSEDGCIYPATIASIDFKRETCTVVVYTGYNREEQ	136
		KNKS+K+ AA ++W+VGD C A WSEDG +Y ATI S+D ++ TCVV YT YGN EEQ	
Dr	66	KNKSRKRCNAAPDKEWQVGDSCYAFWSEDGNLYTATITSVDQEGTCTVVFYTDYGNEEQ	125
		142 146	
Hs	137	NLSDLLSPICEVANNIEQNAQENENESQVSTDESENSRSPGNKSDNIKPKS-----AP	189
		NLSDLL+ ++ + + A E ES ST+ES+ S +P KS + K KS P	
Dr	126	NLSDLLTEPPDMDDEDALKTANVKETES--STEESDRSFTP-QKSGHAKHKSKSNFPMGPP	182
		194 230	
Hs	190	WNSFLPPPPPPMPGRLGPGKPLKFNGLPPPPPPPPPHLLSCWLPPFPSPGPPPIPPPPPI	249
		PP P P P G + GP P P W P P GPP+IPPPPP+	
Dr	183	SWFPSFPPGPPPPPPHFKKMDGRRGEGPGPSFPG-----WPPMIPLGPPMIPPPPPM	234
YG box			
Hs	250	CPDSLDDADALGSMLISWYMSGYHTGYIMGFRONQKEGRCS	290
		PD +D +ALGSMLISWYMSGYHTGYIMG RQ +KE S	
Dr	235	SPDFGEDDEALGSMLISWYMSGYHTGYIMGRLRQGRKEAAS	275

Fig. S4. Domain conservation between human and *Danio rerio* SMN proteins.

Amino acid BLAST alignment of human (top) and *Danio rerio* (bottom) SMN proteins. Known domains are underlined in the human sequence, and the boundaries of deletion mutants are indicated with amino acid numbers. Amino acids substitutions that are unlikely to change the overall protein structure, as determined by the BLOSUM62 scoring matrix, are marked by “+”.