Supplemental Tables and Figures

Table S1: *Schizosaccharomyces pombe* strains used in this study

Strain	Genotype	Figure	Source
OHI246	*h- leu1-32 ura4-D18 ade6-M210*	2, 3, 4, 5, 6, 7	K. Gould[a]
OHI408	*h- cwf10 2-127Δ ade6-M21X leu1-32 ura4-D18*	2, 3, 4, 5, 6, 7, Table 2	This work
OHI479	*h+ brr2-HA::kanR ade6-M210 leu1-32 ura4-D18*	2	Adapted from K. Gould[a]
OHI480	*h+ prp3-linker3XV5 cwf10 2-127Δ ade6-M21X leu1-32 ura4-D18*	2	This work
OHI371	*h+ prp3-linker3XV5*	2	This work
OHI482	*h- brr2-HA::kanR cwf10 2-127Δ ade6-M21X leu1-32 ura4-D18*	2, S3	This work
OHI323	*h- prp1-myc13X::kanR ade6-M210 leu1-32 ura4-D18*	2, 4	(1)
OHI439	*h- prp1-myc13X::kanR cwf10 2-127Δ ade6-M21X leu1-32 ura4-D18*	2, 4	This work
OHI448	*h- cwf10 2-127Δ::kanR ade6-M21X leu1-32 ura4-D18*	5	This work
OHI463	*h+ cdc28-P8*	5	Adapted from (2)
OHI467	*h+ cdc28-P8 cwf10 2-127Δ::kanR ade6-M21X ura4-D18*	5	This work
OHI464	*h+ prp10-1*	5	Adapted from (3)
OHI468	*h+ prp10-1 cwf10 2-127Δ::kanR*	5	This work
OHI466	*h+ spp42-1::kanR leu1-32*	5	Adapted from (4)
OHI465	*h+ spp41-1::kanR leu1-32 ura4-D18*	5	Adapted from (4)
OHI471	*h+ spp41-1::kanR cwf10 2-127Δ ade6-M21X leu1-32 ura4-D18*	5	This work
OHI322	*h+ prp1-4 ura4-D18*	5	Adapted from (3)
OHI321	*h+ prp4-73 leu1-32 ura4-294*	5	Adapted from (5)
OHI462	*h- prp4-73 cwf10 2-127Δ::kanR leu1-32 ura4-D18 or -294*	5	This work
OHI478	*h+ aar2::kanR ade6-M216 leu1-32 ura4-D18*	5	(6)
OHI481	*h- aar2::kanR cwf10 2-127Δ ade6-M21X leu1-*	5	This work

	32 ura4-D18		
OHI483	*h+ cwf10 2-23Δ ade6-M21X leu1-32 ura4-D18*	6	This work
OHI260	*h- cdc5-TAP::kanR*	Tables 1, 2	Adapted from (7)
OHI491	*h- cdc5-TAP::kanR cwf10 2-127Δ leu1-32*	Table 1	This work
OHI383	*h-/h+ cwf10+/cwf10::ura4+ ade6-M210/ade6-M216 leu1-32/leu1-32 ura4-D18/ura4-D18*	integrant construction	This work

[a]Vanderbilt University School of Medicine, Nashville, TN.

Table S2: Primers used in this study

Analysis	Name	Purpose	Primer sequence(s) (5'-3')
RT-PCR	tbp1_a F BL365	amplify first *tbp1* intron	CGCTTTACCCACCACGGCCTCGCAAG
RT-PCR	tbp1_a R BL366	amplify first *tbp1* intron	TTCTGCATTACGTGCATGTAGCGC
RT-PCR	mrps16_b F BL541	amplify second *mrps16* intron	AAAGCACCTCAAGCCAAACCTATCGA
RT-PCR	mrps16_b R BL542	amplify second *mrps16* intron	TCAAGAAACGGGTTTTTTAGGAAGCAACT
Northern	BL432	hybridize U1	ATAACTGAGTCTCCACAATTCTTGTG
Northern	BL429	hybridize U2	AGAACAGATACTACACTTGATCTAAG
Northern	BL433	hybridize U4	AAAAGTTCCTCACTGATAAGCGTAAT
Northern	BL434	hybridize U5	ACAGTCAAATTAGCACACCTTACAAA
Northern	BL435	hybridize U6	TCTTCTCTGTATCGTTTCAATTTGAC

Table S3. Pre-mRNA splicing factors co-purifying with TAP-NTE in a *cwf10*-Δ*NTE* background at either 150 or 75 mM NaCl detected by 1D liquid chromatography-tandem mass spectrometry (LC-MS/MS).

	S. pombe	ORF number	TAP-NTE from *cwf10*-Δ*NTE*				*S. cerevisiae*	*H. sapiens*
			150 mM NaCl[a]		75 mM NaCl			
			I	II	I	II		
Core snRNP	Smb1	SPAC26A3.08	4[b]	3	4	3	Smb1	SMB/B'
	Smd1	SPAC27D7.07c	1	3	3	3	Smd1	SMD1
	Smd2	SPAC2C4.03c	6	3	5	6	Smd2	SMD2
	Smd3	SPBC19C2.14	3	1	4	5	Smd3	SMD3
	Sme1	SPBC11G11.06c	1	1	2	3	Sme1	SME1
	Smf1	SPBC3E7.14	5	3	4	3	Smf1	SMF1
	Smg1	SPBC4B4.05	---[c]	3	2	3	Smg2	SMG1
U2	Lea1	SPBC1861.08c	9	3	15	8	Lea1	U2A'
	Msl1	SPBC8D2.09c	1	---	3	1	Msl1	U2B"
	Prp10	SPAC27F1.09c	---	---	1	---	Hsh155	SF3B160
U5	Cwf10-ΔNTE	SPBC215.12	60	42	71	65	Snu114	U5-116
	Brr2	SPAC9.03c	---	---	---	----	Brr2	U5-200
	Spp42	SPAC4F8.12c	57	33	77	75	Prp8	U5-220
	Cwf17/Spf38	SPBC1289.11	9	4	16	12	UNK[d]	U5-40
NTC core	Cdc5	SPAC644.12	34	13	39	42	Cef1	CDC5
	Cwf2	SPAC3A12.11c	13	5	14	15	Cwc2	RBM22
	Cwf7	SPBC28F2.04c	10	6	14	8	Snt309	SPF27
	Cwf15	SPBC337.06c	6	1	9	7	Cwc15	AD002
	Prp5	SPBP22H7.07	14	8	22	22	Prp46	PRL1
	Prp19	SPAC29A4.08c	18	17	16	25	Prp19	PRP19
NTC-associated	Cwf3	SPBC211.02c	26	9	32	36	Syf1	SYF1
	Cwf4	SPBC31F10.11c	21	11	28	25	Clf1	CRN1
	Cwf5/Ecm2	SPCC550.02c	12	10	21	22	Ecm2/Slt11	RBM22
	Cwf12	SPBC32F12.05c	6	6	8	7	Isy1	ISY1
	Prp45	SPCC188.11	3	3	10	11	Prp45	SKIP
	Prp17	SPBC6B1.10	17	15	25	31	Prp17	hPRP17
	Syf2	SPBC3E7.13c	10	5	10	9	Syf2	SYF2
Other	Cwf11	SPBC646.02	36	17	52	50	UNK	hCWF11
	Cwf14	SPBC24C6.11	8	4	10	11	Cwc14	G10
	Cwf18	SPCP1E11.07c	6	5	8	5	UNK	MGC23918
	Cwf19	SPAC30D11.09	11	3	15	19	UNK	hCWF19L2
	Cwf21	SPAC4A8.09c	1	---	5	2	Cwc21	SRm300
	Cwf22	SPBC13E7.01	2	1	4	6	Cwc22	hCWC22
	Cyp1	SPAC57A10.03	5	1	5	5	UNK	PPIL1
	Mug161	SPAC1F3.09	---	---	---	---	YGR093W	CWF19L1
	Prp16	SPBC1711.17	---	---	---	---	Prp16	PRP16
	Prp43	SPBC16H5.10c	---	---	---	---	Prp43	hPRP43
	Prp22	SPAC10F6.02c	---	---	1	---	Prp22	hPRP22
	Saf4	SPBC18H10.10c	3	3	7	4	UNK	CCDC130

	Slu7	SPBC365.05c	---	---	---	---	Slu7	SLU7
	Sum3	SPCC1795.11	7	1	2	1	Ded1	DDX3
	unnamed	SPAC20H4.09	---	---	---	---	UNK	DHX35
	Pab1	SPAC57A7.04c	---	---	6	6	Pab1	PABC1
	Ubp10	SPBC577.07	---	---	1	4	Sad1	USP39

[a]Results for purifications done at 150 mM NaCl are the same as shown in Table 2 and are included again in this table to make comparison easier. [b]Peptide counts of identified proteins in each biological replicate (I and II), [c] --- indicates no peptides identified, [d]UNK indicates that an ortholog is unknown or not present.

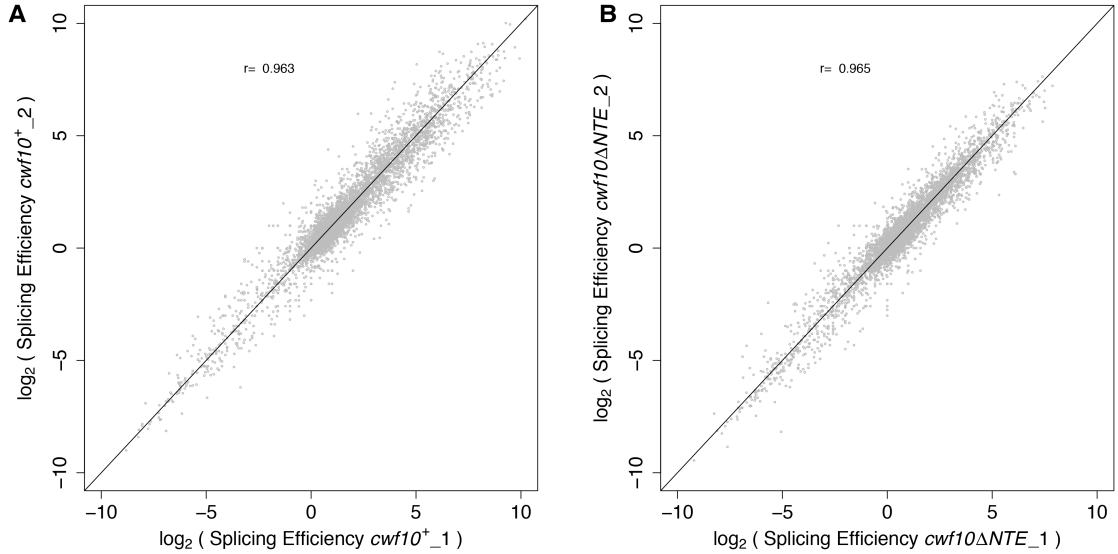

Figure S1. Reproducibility of splicing efficiency in replicates. Each point represents an intron (5,361 in total; 'r' Pearson's correlation coefficient; $\log_2$ scale). (A) Two wild-type replicates. (B) Two *cwf10*-Δ*NTE* replicates.

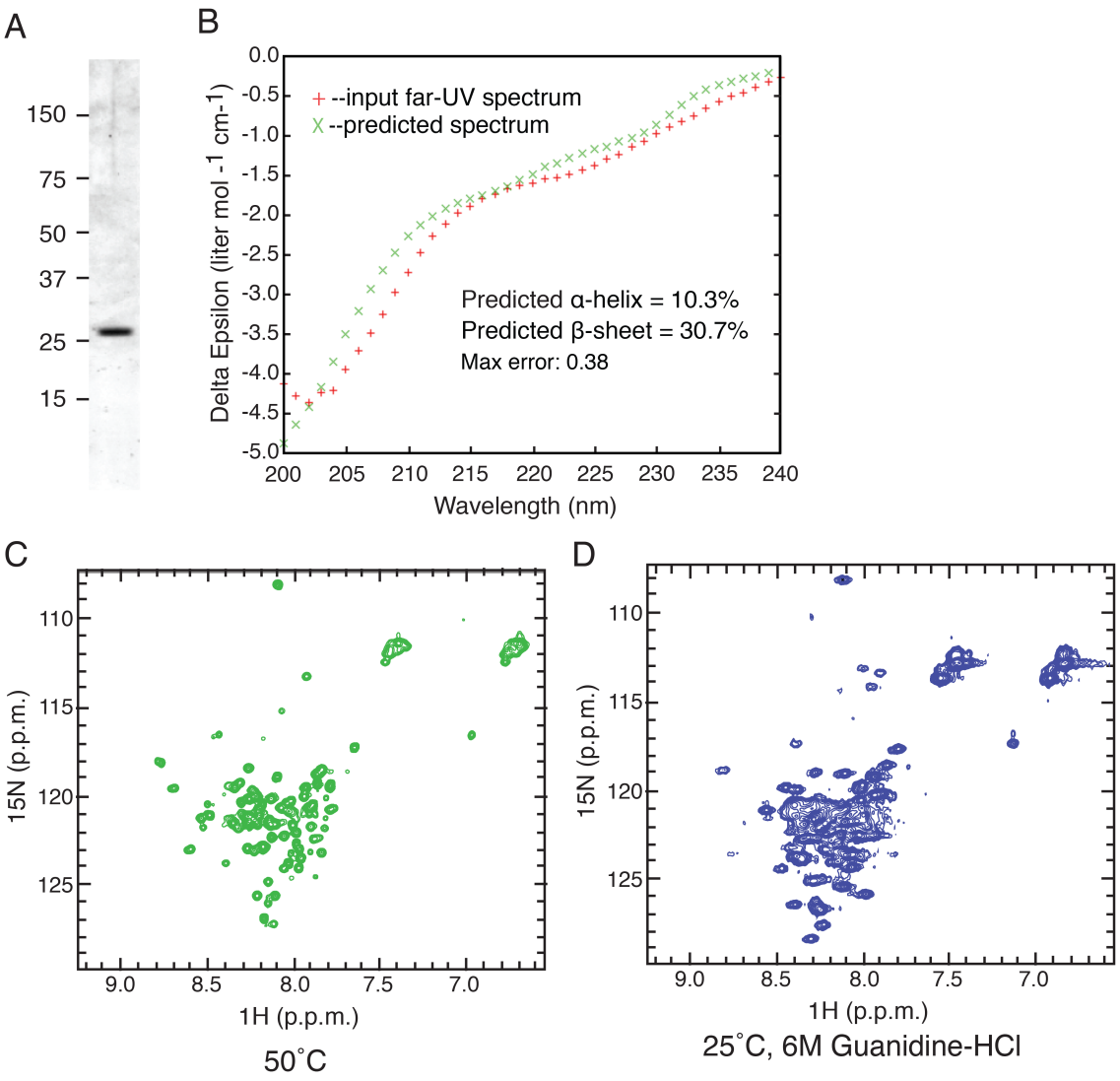

Figure S2. Analysis of recombinant Cwf10(1-135)His$_6$. (A) Coomassie stained SDS-PAGE gel of recombinant Cwf10(1-135)His$_6$. Molecular weight markers in kilodaltons are shown on left. (B) Predicted secondary structure calculated from the Far-UV spectrum seen in Fig. 6E using the program K2D2 (1). (C) ^{15}N-^{1}H HSQC spectrum of Cwf10(1-135)His$_6$ at 50°C. (D) ^{15}N-^{1}H HSQC spectrum of Cwf10(1-135)His$_6$ in 6 M Guanidine-HCl.

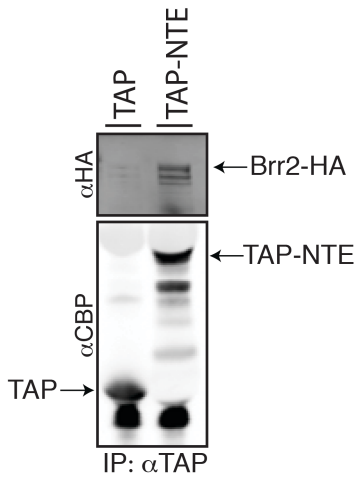

Figure S3. TAP-NTE co-immunoprecipitates Brr2-HA. *pREP41 NTAP* or *pREP41 NTAP-NTE* were expressed in *cwf10-ΔNTE brr2-HA* cells. TAP and TAP-NTE were immunoprecipitated with IgG-Sepharose beads and then immunoblotted with anti-HA antibodies. Positions of proteins on the immunoblot are labeled.

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