Supplementary Information

Mass spectrometry-based relative quantification of proteins in pre-catalytic and catalytically active spliceosomes by metabolic labeling (SILAC), chemical labeling (iTRAQ), and label-free spectral count

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Supplementary Table 1: Proteins without clear assignment after quantification. For these proteins, B:C protein ratios fluctuate between the three quantification approaches. The average value of two biological replicates after SILAC, iTRAQ or spectral count quantification is shown. An average protein ratio was calculated for each protein. Proteins that lack an assigned value could not be quantified by the respective approach. Proteins quantified by only one approach are not shown. For proteins identified solely in the B complex or the C complex (indicated with "OSB", only spectra B complex, or "OSC", only spectra C complex), no B:C protein ratio could be calculated by spectral count. Proteins are grouped according to their initial classification by Bessonov *et al*. (2008). Proteins labeled with an * are defined to be major components of the human spliceosome and to be abundant in A, B, C or B^{act} complexes according to Agafonov *et al*. (2011).

			B:C protein ratios			**Aver. Protein ratio**
Protein	**MW [kDa]**	**accession no.**	**SILAC**	**iTRAQ**	**spectral count**	**SILAC/iTRAQ/spectral count**
Proteins previously assigned to B complexes						
PPIL2 $*^{Bact}$	59.5	gi|7657473	0.64	2.15	1.23	1.34
hPRP2 (DDX16) $*^{Bact, C}$	119.2	gi|4503293	0.31	1.32	0.58	0.74
hPRP4-Kinase	117.1	gi|89276756	1.41	0.48	0.85	0.91
PABP1	70.5	gi|46367787	0.3	3.21	1.44	1.65
SKIV2L2	117.8	gi|39930353	3.34	1.14	0.54	1.67
PABPN1	32.6	gi|4758876	0.72	1.00	1.67	1.13
RNF113A $*^{Bact}$	38.8	gi|5902158	0.43	0.81	1.00	0.75
hsp27	22.8	gi|4504517	0.25	0.74	0.88	0.62
GCFC	104.7	gi|22035565	1.55	1.74	2.08	1.79
MGC20398 $*^{Bact}$	42	gi|49472814	0.57	1.16	0.93	0.88
MGC23918 $*^{Bact}$	19.2	gi|21389497	0.28	0.52	1.00	0.60
Proteins previously assigned to C complexes						
WDR70	73.2	gi|8922301		1.19	OSC	1.19
EJC/mRNP proteins						
RNPS1	34.2	gi|6857826	1.45	1.36	0.63	1.14
Acinus	151.8	gi|7662238	1.63	1.60	1.42	1.55
SAP18 $*^{Bact, C}$	17.4	gi|5032067	2.25	1.28	1.86	1.80
Aly/REF (THOC4)	26.9	gi|55770864	2.09	1.11	1.17	1.46

TREX						
THOC1	75.6	gi|154448890	0.07	1.45	1.00	0.84
THOC2	169.6	gi|125656165	1.79	1.08	0.36	1.08
KIAA0983 (THOC5)	78.4	gi|50959110	3.15	1.40	0.83	1.79
WDR58 (THOC6)	37.4	gi|31543164	1.25	1.00	0.67	0.97
pre-mRNA/mRNA binding proteins						
CBP20	18	gi|110349727	1.04	0.82	0.79	0.88
CBP80	91.8	gi|4505343	1.04	1.21	0.87	1.04
NF45	43	gi|24234747	3.88	1.94	3.33	3.05
ZC3H18	104	gi|31377595	3.95	1.19	1.38	2.17
YB-1 *[A, B, Bact, C]	35.9	gi|34098946	0.45	1.91	1.27	1.21
ELG	38.9	gi|8923771	5.93	2.10	0.84	2.96
DDX3	73.3	gi|87196351	4.71	1.05	3.00	2.92
ASR2B *[A, B, Bact, C]	100	gi|33383233	3.73	1.28	1.37	2.12
BCLAF1	107.2	gi|7661958	6.54	1.92	3.15	3.87
RBM7	30.5	gi|4503293		1.14	0.25	0.70
proteins previously assigned as "micelleneous"						
BAG2	23.4	gi|4757834	0.50	0.50	0.33	0.44
RBBP6	197.2	gi|33620716	1.93	1.38	0.57	1.29

Supplementary Table 2: Quantification of spliceosomal B and C complexes by SILAC. The B:C protein ratio, the standard deviation (StDev), and the number of peptides used to calculate the protein ratio (#) are given for two replicates (SILAC #1 and SILAC #2). The mean B:C protein ratio and the corresponding standard deviation were calculated from the two replicates (SILAC mean). Proteins without assigned values could not be quantified.

Protein	MW [kDa]	accession no.	SILAC #1			SILAC #2			SILAC mean	
			B:C	**StDev**	**#**	**B:C**	**StDev**	**#**	**B:C**	**StDev**
U1 snRNP										
U1-A	31.3	gi|4759156	22.18	3.04	3	29.73		1	25.95	5.34
U1-C	17.4	gi|4507127				27.15		1	27.15	
U1-70K	51.6	gi|29568103	3.19	1.40	5	11.83	0.41	6	7.51	6.11
17S U2 snRNP										
U2A′	28.4	gi|50593002	1.07	0.12	24	0.78	0.03	25	0.92	0.21
U2B′′	25.4	gi|4507123	0.96	0.45	14	0.90	0.03	7	0.93	0.04
SF3a120	88.9	gi|5032087	3.14	0.04	11	3.15	0.12	32	3.15	0.00
SF3a66	49.3	gi|21361376	3.04	0.59	13	3.30	0.01	2	3.17	0.19
SF3a60	58.5	gi|5803167	3.16	0.77	37	3.35	0.18	9	3.26	0.13
SF3b155	145.8	gi|54112117	3.24	0.42	32	4.60	1.41	71	3.92	0.96
SF3b145	100.2	gi|55749531	3.29	0.25	25	2.95	0.20	42	3.12	0.24
SF3b130	135.5	gi|54112121	3.40	0.35	31	3.40	0.14	94	3.40	0.00
SF3b49	44.4	gi|5032069	3.58	0.27	6	2.83	0.03	3	3.20	0.54
SF3b14a (p14)	14.6	gi|7706326	5.01	0.65	6	2.80	0.09	10	3.90	1.56
SF3b14b	12.4	gi|14249398				3.88	0.11	4	3.88	
SF3b10	10.1	gi|13775200				3.43	0.11	4	3.43	
17S U2-related										
U2AF65	53.5	gi|6005926	1.51		1				1.51	
U2AF35	27.9	gi|5803207	2.86		1				2.86	
hPRP43	90.9	gi|68509926	4.69	0.65	51	4.15	0.20	25	4.42	0.38
SPF45	45.0	gi|14249678	10.09	0.00	7	10.78	0.41	5	10.43	0.49
SR140	118.2	gi|122937227	12.48	3.02	52	12.23	3.32	13	12.35	0.18
CHERP	100.0	gi|119226260	4.12	0.00	10	10.60	0.54	5	7.36	4.58
SF3b125	103.0	gi|45446747	5.15	0.00	1	17.58	1.46	3	11.36	8.79
U5 snRNP										
220K	273.3	gi|3661610	0.98	0.02	107	1.13	0.07	179	1.05	0.10
200K	244.5	gi|45861372	1.00	0.14	128	1.10	0.06	229	1.05	0.07

116K	109.4	gi|41152056	0.93	0.12	92	1.08	0.05	65	1.00	0.11
40K	39.3	gi|4758560	0.94	0.13	6	1.05	0.07	23	0.99	0.08
102K	106.9	gi|40807485	3.32	0.24	18	3.48	0.40	53	3.40	0.11
15K	16.8	gi|5729802				13.85	1.99	2	13.85	
100K	95.6	gi|41327771	2.78	0.68	28	2.38	0.18	23	2.58	0.29
52K	37.6	gi|5174409	2.02	0.54	10	2.33	0.08	8	2.17	0.21
U4/U6 snRNP										
90K	77.6	gi|4758556	16.28	7.39	42	19.38	1.84	24	17.83	2.19
60K	58.4	gi|45861374	14.21	5.44	16	17.08	0.93	4	15.64	2.02
20K	20.0	gi|5454154	7.17	1.90	5	10.18	0.36	8	8.67	2.12
61K	55.4	gi|40254869	17.30	7.67	13	21.88	1.49	3	19.59	3.23
15.5K	14.2	gi|4826860				21.50	1.02	2	21.50	
U4/U6.U5 snRNP										
110K	90.2	gi|13926068	7.25	1.72	51	10.78	0.67	29	9.01	2.50
65K	65.4	gi|56550051	3.22	0.33	35	3.28	0.12	11	3.25	0.04
27K (RY1)	18.9	gi|24307919				6.25	0.22	3	6.25	
hPRP38	37.5	gi|24762236				2.70	0.67	11	2.70	
TFIP11	96.8	gi|8393259	1.71	0.18	11	1.45	0.04	8	1.58	0.18
LSm Proteins										
LSm2	10.8	gi|10863977	23.42		1	18.35	0.77	7	20.88	3.58
LSm3	11.8	gi|7657315	4.04	0.00	2	14.13	0.29	3	9.08	7.13
LSm4	15.4	gi|6912486	9.60	4.06	3	16.35	0.91	3	12.98	4.77
LSm5	9.9									
LSm6	9.1	gi|5919153	15.80	0.00	2	19.85	1.58	6	17.82	2.87
LSm7	11.6	gi|7706423	19.62	8.34	2				19.62	
LSm8	10.4	gi|7706425	10.70	5.53	5				10.70	
Sm Proteins										
B	24.6	gi|4507125	1.70	0.09	5	1.50	0.15	19	1.60	0.14
D1	13.3	gi|5902102	1.96	0.28	11	1.70	0.07	8	1.83	0.18
D2	13.5	gi|29294624	1.98	0.25	21	1.50	0.06	21	1.74	0.34
D3	13.9	gi|4759160	1.89	0.24	17	1.73	0.06	9	1.81	0.12
E	10.8	gi|4507129	2.03	0.23	8	1.73	0.04	7	1.88	0.21
F	9.7	gi|4507131	1.82	0.00	2	1.73	0.04	7	1.77	0.07
G	8.5	gi|4507133	1.94	0.00	2	1.78	0.03	8	1.86	0.12

hPRP19/CDC5L complex										
hPrp19	55.2	gi|7657381	0.35	0.07	59	0.38	0.06	29	0.36	0.02
CDC5L	92.2	gi|11067747	0.41	0.13	38	0.43	0.16	66	0.42	0.01
SPF27	21.5	gi|5031653	0.33	0.07	28	0.35	0.01	17	0.34	0.01
PRL1	57.2	gi|4505895	0.33	0.10	26	0.33	0.01	11	0.33	0.01
Hsp70	70.4	gi|5729877	0.19	0.12	21	0.15	0.01	4	0.17	0.03
AD-002	26.6	gi|7705475	0.21	0.02	8	0.33	0.01	9	0.27	0.08
CTNNBL1	65.1	gi|18644734	0.59	0.05	4	0.75	0.02	10	0.67	0.11
Npw38BP	70.0	gi|7706501	3.10	0.49	2	3.95	0.15	2	3.53	0.60
Npw38	30.5	gi|74735456				3.55		1	3.55	
hPRP19/CDC5L-related										
hSYF1	100.0	gi|55770906	0.22	0.04	86	0.28	0.05	42	0.25	0.04
CRNKL1	100.6	gi|30795220	0.27	0.10	78	0.25	0.01	44	0.26	0.02
hIsy1	33.0	gi|20149304	0.17	0.17		0.23	0.02	15	0.20	0.04
SKIP	51.1	gi|6912676	0.29	0.05	85	0.33	0.03	34	0.31	0.03
RBM22	46.9	gi|8922328	0.28	0.10	20	0.30	0.02	14	0.29	0.02
Cyp-E	33.4	gi|5174637	0.18	0.01	16	0.23	0.01	10	0.20	0.03
PPIL1	18.2	gi|7706339	0.25	0.03	8	0.38	0.02	21	0.31	0.09
KIAA0560	171.3	gi|38788372	0.22	0.07	122	0.28	0.06	86	0.25	0.04
G10	17.0	gi|32171175								
hRES complex proteins										
SNIP1	45.8	gi|21314720				0.73	0.03	7	0.73	
MGC12135	70.5	gi|14249338	0.74	0.07	10	0.75	0.03	14	0.75	0.01
CGI-79	39.7	gi|4929627	0.52	0.06	8	0.73	0.02	6	0.62	0.15
Proteins recruited to A complex										
RBM39	59.4	gi|4757926	3.32	0.75	17	3.65	0.11	5	3.48	0.24
p68 (DDX5)	69.2	gi|4758138	3.38	0.23	5	3.05	0.39	4	3.21	0.23
ELAV-like 1 (HuR)	36.1	gi|38201714	9.86	4.68	28	10.50	0.76	16	10.18	0.45
p72/DDX17	80.5	gi|3122595	2.90		1				2.90	

Proteins recruited to B complex										
MFAP1	51.9	gi|50726968	2.13	0.24	10	3.18	0.16	11	2.65	0.74
RED	65.6	gi|10835234	5.62	0.88	11	5.40	0.16	11	5.51	0.15
hSmu-1	57.5	gi|8922679	2.74	0.32	9	9.50	0.27	8	6.12	4.78
PPIL2	59.5	gi|7657473	0.48	0.14	12	0.80	0.03	17	0.64	0.23
hPRP2 (DDX16)	119.2	gi|4503293	0.04		1	0.58	0.02	23	0.31	0.38
hPRP4-Kinase	117.1	gi|89276756	1.41	0.24	15				1.41	
THRAP3	108.6	gi|4827040	3.56	0.57	5	16.85	1.17	11	10.21	9.39
PABP1	70.5	gi|46367787	0.30	0.04	7				0.30	
SKIV2L2	117.8	gi|39930353	3.98	0.72	13	2.70	0.06	7	3.34	0.91
PABPN1	32.6	gi|4758876	0.36	0.01	4	1.08	0.03	6	0.72	0.51
RNF113A	38.8	gi|5902158				0.43	0.02	8	0.43	
NY-CO-10	53.8	gi|64276486	0.33	0.10	8	0.70	0.04	8	0.51	0.26
KIAA1604	105.5	gi|55749769	0.16	0.05	17	0.23	0.02	26	0.19	0.04
hsp27	22.8	gi|4504517				0.25	0.00	2	0.25	
GCFC	104.7	gi|22035565	1.60	0.26	10	1.50	0.09	11	1.55	0.07
UBL5	8.5	gi|13236510								
CCDC16	42.0	gi|49472814	0.41	0.06	5	0.73	0.04	5	0.57	0.22
CCDC12	19.2	gi|21389497				0.28	0.07	13	0.28	
HsKin17	45.2	gi|13124883	1.25	0.14	7	1.40	0.06	5	1.33	0.10
Step 2 factors										
hPRP22	139.3	gi|4826690	0.14	0.10	49	0.10	0.07	48	0.12	0.03
hPRP18	39.9	gi|4506123				0.10		1	0.10	
hPRP17	65.5	gi|7706657	0.29	0.10	28	0.23	0.02	29	0.26	0.04
hPRP16	140.5	gi|17999539				0.48	0.01	2	0.48	
hSLU7	68.4	gi|27477111	0.24	0.08	6	0.40	0.53	14	0.32	0.11
Proteins recruited to C complex										
Abstrakt	69.8	gi|21071032	0.19	0.06	25	0.13	0.15	24	0.16	0.05
GCIP p29	28.7	gi|46371998	0.02	0.20	11	0.15	0.15	18	0.09	0.09
DDX35	78.9	gi|20544129	0.07	0.08	13	0.05	0.01	15	0.06	0.01
Q9BRR8	103.3	gi|74732921				0.05	0.01	7	0.05	
c19orf29 (NY-REN-24)	88.6	gi|126723149				0.05	0.02	21	0.05	
PPIase-like 3b	18.6	gi|19557636	0.01	0.00	2	0.03	0.01	7	0.02	0.01

PPWD1	73.6	gi|24308049	0.08	0.03	18	0.08	0.05	18	0.08	0.00
MORG1	34.3	gi|153791298	0.07	0.01	2	0.05	0.00	5	0.06	0.02
FRG1	29.2	gi|4758404	0.22	0.02	3	0.23	0.01	2	0.22	0.00
NOSIP	33.2	gi|7705716				0.10	0.05	2	0.10	
GPKOW	52.1	gi|15811782	0.09	0.04	5	0.33	0.04	12	0.21	0.17
C1orf55	39.3	gi|148664216	0.19	0.00	2	0.05	0.03	25	0.12	0.10
FAM32A	13.1	gi|7661696	0.12		1	0.03	0.02	4	0.07	0.07
RACK1 (GNB2L1)	35.1	gi|5174447								
Tip-49	50.2	gi|4506753				0.13	0.01	3	0.13	
Potential C complex specific proteins										
PPIG	88.5	gi|42560244	0.54	0.15	2	0.20	0.06	5	0.37	0.24
FAM50A	40.1	gi|4758220	0.15		1	0.03	0.00	7	0.09	0.09
FAM50B	38.6	gi|6912326				0.05	0.03	2	0.05	
C9orf78	33.7	gi|7706557	0.04	0.01	2	0.03	0.01	2	0.03	0.01
C10orf4	37.5	gi|24432067				0.10	0.05	5	0.10	
CXorf56	25.6	gi|11545813	0.18	0.07	3	0.08	0.06	8	0.13	0.08
DGCR14	52.4	gi|13027630	0.25	0.07	8	0.03	0.01	8	0.14	0.16
CCDC130	44.7	gi|13540614				0.10	0.02	2	0.10	
TOE1	56.4	gi|156564398								
NKAP	47.0	gi|13375676	0.10		1	0.03	0.00	5	0.06	0.05
ZCCHC10	18.4	gi|8923106	0.16	0.00	2	0.08	0.03	2	0.12	0.06
CDK10	35.4	gi|16950647				0.10	0.04	6	0.10	
TTC14	88.2	gi|33457330	0.34		1	0.08	0.02	8	0.21	0.19
WDR70	73.2	gi|8922301								
NFKBIL1	43.1	gi|26787991				0.08	0.01	3	0.08	
JUP	81.6	gi|12056468	0.08	0.08	4				0.08	
EJC/mRNP										
eIF4A3	46.9	gi|7661920	0.26	0.08	18	0.23	0.02	21	0.24	0.03
Magoh	17.2	gi|4505087	0.21	0.01	6	0.28	0.00	3	0.24	0.04
Y14	19.9	gi|4826972	0.13	0.13	2	0.18	0.04	2	0.15	0.03
Pinin	81.6	gi|33356174	0.31		1	1.23	0.02	4	0.77	0.65
RNPS1	34.2	gi|6857826	0.63	0.02	3	2.28	0.08	5	1.45	1.17
Acinus	151.8	gi|7662238	0.50	0.11	11	2.75	0.33	13	1.63	1.59
SAP18	17.4	gi|5032067				2.25	0.03	2	2.25	
Aly/REF (THOC4)	26.9	gi|55770864	0.98	0.26	2	3.20	0.07	5	2.09	1.57

UAP56	49.1	gi|18375623	0.28	0.03	5	6.08	0.07	4	3.18	4.10
TREX										
THOC1	75.6	gi|154448890	0.07	0.02	2				0.07	
THOC2	169.6	gi|125656165	0.15	0.02	5	3.43	0.09	3	1.79	2.31
THOC3	38.8	gi|14150171								
KIAA0983 (THOC5)	78.4	gi|50959110				3.15		1	3.15	
WDR58 (THOC6)	37.4	gi|31543164				1.25	0.11	3	1.25	
pre-mRNA/mRNA binding proteins										
CBP20	18.0	gi|110349727	0.88	0.06	10	1.20	0.02	7	1.04	0.23
CBP80	91.8	gi|4505343	0.89	0.11	64	1.20	0.07	53	1.04	0.22
NF45	43.0	gi|24234747	2.86	0.44	12	4.90	0.22	3	3.88	1.44
ZC3H18	104.0	gi|31377595	3.74	0.54	13	4.15	0.17	7	3.95	0.29
YB-1	35.9	gi|34098946	0.56	0.12	14	0.35	0.02	11	0.45	0.15
ELG	38.9	gi|8923771	1.37	0.07	5	10.50	0.06	3	5.93	6.46
DDX3	73.3	gi|87196351	4.71	1.13	4				4.71	
ASR2B	100.0	gi|33383233	3.29	0.55	51	4.18	0.32	22	3.73	0.63
BCLAF1	107.2	gi|7661958	0.29		1	12.80	0.33	2	6.54	8.85
DBPA	40.1	gi|20070160				0.33		1	0.33	
RBM7	30.5	gi|4503293								
HSP70	70.0	gi|5123454	0.19	0.12	21	0.15	0.01	4	0.17	0.03
Miscelleneous proteins										
BAG2	23.4	gi|4757834				0.50	0.01	5	0.50	
RBBP6	197.2	gi|33620716				1.93	0.10	2	1.93	
RBM42	50.3	gi|21359951	12.35	12.21	2				12.35	
SR-related proteins										
SRm160	102.5	gi|42542379	0.14	0.05	3	0.50	0.06	3	0.32	0.25
SRm300	300.0	gi|4759098	0.26	0.12	13	0.40	0.09	26	0.33	0.10
SR proteins										
SF2/ASF	27.8	gi|5902076	1.62	0.23	44	5.43	0.73	23	3.52	2.69
9G8	27.4	gi|72534660	1.91	0.32	14	3.98	0.98	19	2.94	1.46
SRp20	19.4	gi|4506901	2.89	0.00	2	9.15	0.00	2	6.02	4.42
SRp30c	25.5	gi|4506903	1.33	0.12	16	1.30	0.25	18	1.32	0.02
SRp38	31.3	gi|5730079	0.95	0.18	6				0.95	
SRp40	31.3	gi|3929378	0.70	0.19	10	1.90	0.58	10	1.30	0.85

SRp46	31.2	gi|15055543				4.15	0.15	2	4.15	
SRp55	39.6	gi|20127499	1.41	0.83	4	1.58	0.44	15	1.49	0.12
SRp75	56.8	gi|21361282				5.93	0.17	2	5.93	
SC35 (SFRS2)	25.5	gi|47271443								
hTra-2 alpha	32.7	gi|9558733	2.90		15	4.33	0.15	6	3.61	1.01
hTra-2 beta (SFRS109	33.7	gi|4759098	3.97	0.94	2	5.53	0.97	16	4.75	1.10
hnRNP										
hnRNP A1	38.7	gi|4504445	12.92	4.92		12.13	1.44	12	12.52	0.56
hnRNP A3	39.6	gi|34740329	5.83	2.37	4	5.03	0.11	3	5.43	0.57
hnRNP AB	36.0	gi|12803583	7.38	0.05	3	7.05	0.68	3	7.21	0.23
hnRNP A2/B1	37.4	gi|14043072	2.93		1	9.28	1.75	8	6.10	4.49
hnRNP C	33.3	gi|4758544	1.34	0.14	41	1.68	0.11	28	1.51	0.24
hnRNP D	38.4	gi|14110420	9.75	0.00	2	10.40	2.42	2	10.08	0.46
hnRNP F	45.7	gi|148470406				3.85	0.07	2	3.85	
hnRNP G	47.4	gi|56699409	3.30	0.66	19	3.75	0.12	11	3.52	0.32
hnRNP G-T	42.7	gi|153252068				0.08		1	0.08	
hnRNP H1	49.1	gi|5031753	2.63	0.89	3	2.65	0.16	6	2.64	0.01
hnRNP H3	36.9	gi|14141157								
hnRNP K	51.0	gi|14165435	12.05	4.94	13				12.05	
hnRNP M	77.5	gi|14141152	4.30	1.59	8	2.83		1	3.56	1.04
hnRNP Q	69.6	gi|15809590	2.49	0.07	3				2.49	
hnRNP R	70.9	gi|5031755	0.87	0.15	12	1.23	0.07	4	1.05	0.25
hnRNP U	90.6	gi|14141161	12.82	0.00	2	9.65	1.39	2	11.24	2.24
PCBP1	37.5	gi|5453854	5.32	1.27	11	5.53	0.08	2	5.42	0.14
PCBP2	38.1	gi|14141166	5.44	0.81	12	3.50	0.01	2	4.47	1.37
RALY	32.5	gi|8051631				1.25	0.11	8	1.25	

Supplementary Table 3: Additional proteins identified and quantified by SILAC. The B:C protein ratio, the standard deviation (StDev), and the number of peptides used for quantification are shown for two replicates (SILAC #1 and SILAC #2). Note that not all proteins were identified in both replicates. Proteins highlighted in gray were added to the respective list of B- and C-complex-specific proteins.

				SILAC #1			**SILAC #2**		
Protein	**Protein accession no.**	**Protein database description**	**Protein mass [Da]**	**B:C protein ratio**	**StDev**	**#**	**B:C protein ratio**	**StDev**	**#**
AKAP8	gi|4884374	hypothetical protein [Homo sapiens]	39914				5.550	0.090	2
ALB	gi|122920512	Chain A. Human Serum Albumin Complexed With Myristate And Aspirin	66412				0.075	0.060	7
ALG-2	gi|7019485	programmed cell death 6 [Homo sapiens]	21855				3.050	0.060	4
Anti-Ifn-Gamma	gi|4139695	Chain L. Comparison Of The Three-Dimensional Structures Of A Humanized And A Chimeric Fab Of An Ant	23394				0.150		1
BAT4	gi|15042961	HLA-B associated transcript 4 [Homo sapiens]	39518	3.504		1			
C1orf77	gi|28875797	hypothetical protein LOC26097 [Homo sapiens]	26380				6.850		1
Cactin	gi|3253120	R31449_3 [Homo sapiens]	93849	0.286	0.330	8			
CCAR1	gi|27497118	death inducer with SAP domain DIS [Homo sapiens]	133308	1.320		1			
CCDC55	gi|119571605	coiled-coil domain containing 55. isoform CRA_a [Homo sapiens]	60405				3.150		1
CLK1	gi|119590621	CDC-like kinase 1. isoform CRA_a [Homo sapiens]	58120				1.950		1
CTD-binding protein SR-like rA9	gi|20987470	KIAA1542 protein [Homo sapiens]	117316	1.488		1			
DCD	gi|16751921	dermcidin preproprotein [Homo sapiens]	11391	0.077	0.070	12	0.175	0.010	3
DDX21	gi|50659095	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21 [Homo sapiens]	87804	0.463	0.000	2	1.675	0.050	4
DDX29	gi|33440541	DEAH (Asp-Glu-Ala-His) box polypeptide 29 [Homo sapiens]		0.804		1			

DDX34	gi|38158022	DEAH (Asp-Glu-Ala-His) box polypeptide 34 [Homo sapiens]	128040				0.100	0.020	5
DDX9	gi|307383	RNA helicase A	143405	2.178	0.380	4			
DSG1	gi|416917	Desmoglein-1 precursor (Desmosomal glycoprotein 1) (DG1) (DGI) (Pemphigus foliaceus antigen)	114670	0.055	0.040	3			
DSP	gi|1147813	desmoplakin I [Homo sapiens]	334023	0.176	0.240	8	0.175	0.040	7
E1B-AP5	gi|21536320	E1B-55kDa-associated protein 5 isoform d [Homo sapiens]	85311	4.202	0.910	6	1.250	0.020	3
eEF2	gi|4503483	eukaryotic translation elongation factor 2 [Homo sapiens]	96246	1.584		1			
eIF2AK2	gi|4506103	eukaryotic translation initiation factor 2-alpha kinase 2 [Homo sapiens]	62512	10.439		1			
EXOSC10	gi|119592084	exosome component 10. isoform CRA_b [Homo sapiens]	101453	2.750	0.790	2			
EXOSC2	gi|514266	unknown [Homo sapiens]	29187				2.350		1
EXOSC4	gi|9506689	exosome component 4 [Homo sapiens]	26366				2.300		1
EXOSC5	gi|122920910	Chain D. Structure Of The Human Rna Exosome Composed Of Rrp41. Rrp45. Rrp46. Rrp43. Mtr3. Rrp42. Cs	25433				2.600		1
FAM58A	gi|119593258	family with sequence similarity 58. member A. isoform CRA_b [Homo sapiens]	19165				0.125	0.040	5
FAM82C	gi|14270766	putative TCPTP-interacting protein [Homo sapiens]	44443	0.444		1			
FBP11	gi|5360087	NY-REN-6 antigen [Homo sapiens]	50793	4.334		1			
FBP21	gi|6005948	WW domain-containing binding protein 4 [Homo sapiens]	42652	8.195		1	33.250	0.430	2
FLG2	gi|62122917	filaggrin family member 2 [Homo sapiens]	247928				0.175		1
FNBP4	gi|20521728	KIAA1014 protein [Homo sapiens]	113560				3.275		1
FUSE3	gi|1575609	FUSE binding protein 3 [Homo sapiens]	64239	6.226	2.790	6	5.925	0.140	3
GPATC3	gi|21739398	hypothetical protein [Homo sapiens]	59644				0.300		1

GU2	gi|13129006	nucleolar protein GU2 [Homo sapiens]	83084	0.583	0.050	2	0.950	0.020	5
hnRNP A0	gi|1911429	A0=heterogeneous nuclear ribonucleoprotein [human. placenta. Peptide. 305 aa]	30882				3.600	0.200	2
hnRNP U-like 2	gi|52545896	hypothetical protein [Homo sapiens]	72891	3.844	1.860	3			
hp2-alpha	gi|306880	preprohaptoglobin	38427				0.200		1
hPRP38	gi|24762236	PRP38 pre-mRNA processing factor 38 (yeast) domain containing A [Homo sapiens]	37453				2.700	0.670	11
IFIT1	gi|116534937	interferon-induced protein with tetratricopeptide repeats 1 isoform 2 [Homo sapiens]	55325				0.450	0.020	6
IFIT2	gi|119570530	interferon-induced protein with tetratricopeptide repeats 2 [Homo sapiens]	51751				0.425	0.020	5
IGHA1	gi|229585	Ig A1 Bur	73331				0.050	0.020	3
IGHG1	gi|15825647	Chain H. Crystal Structure Of The Intact Human Igg B12 With Broad And Potent Activity Against Prima	50385				0.075	0.020	5
immunoglobulin	gi|263261	nestin=intermediate filament [human. Peptide. 1618 aa]	177170	0.228	0.000	2			
KIAA1404	gi|7243189	KIAA1404 protein [Homo sapiens]	220837				0.175	0.070	4
LRC	gi|24308289	leukocyte receptor cluster (LRC) member 1 [Homo sapiens]	30511				0.025	0.010	3
MGC138493	gi|27462066	MSTP054 [Homo sapiens]	128079				12.050	1.280	2
NCL	gi|21750187	unnamed protein product [Homo sapiens]	32900				8.825	0.330	2
NFAR	gi|1770458	M-phase phosphoprotein 4 [Homo sapiens]	67102	6.831	0.840	4			
NFAR-2	gi|5762315	nuclear factor associated with dsRNA NFAR-2 [Homo sapiens]	95325				27.325	2.120	2
NIP30	gi|13376429	hypothetical protein LOC80011 [Homo sapiens]	28895				0.025		1
NOP58	gi|6841462	HSPC120 [Homo sapiens]	52462				0.175		1
NUFIP1	gi|6912542	nuclear fragile X mental retardation protein interacting protein 1 [Homo sapiens]	56732	0.055		1	0.025		1
PABPC1	gi|693937	polyadenylate binding protein II [Homo sapiens]	58481				2.025	0.050	2

PABPC4	gi|4504715	poly A binding protein. cytoplasmic 4 [Homo sapiens]	71080	0.198		1			
PIP	gi|4505821	prolactin-induced protein [Homo sapiens]	16847	0.066		1			
PPIL3	gi|14043400	Peptidylprolyl isomerase (cyclophilin)-like 3 [Homo sapiens]	18385	0.204		1			
PPIL4	gi|20911035	peptidylprolyl isomerase-like 4 [Homo sapiens]	57703	0.297	0.030	2	3.050	0.070	3
PRKRIP1	gi|13375901	PRKR interacting protein 1 (IL11 inducible) [Homo sapiens]	20984	0.174	0.080	4	0.075	0.030	6
PTCRA	gi|553734	putative [Homo sapiens]	2212				0.050	0.020	29
PUF60	gi|1809248	siah binding protein 1 [Homo sapiens]	58131	6.226	1.620	7	6.675	0.560	3
PURA	gi|62089471	Purine-rich element binding protein A [Homo sapiens]	34917				0.150	0.010	2
RBM15(OTT)	gi|14161371	putative RNA-binding motif protein 15 short form plus alternative exon [Homo sapiens]	107001				21.050	2.290	6
RBM4	gi|157881813	Chain A. Solution Structure Of The Second Rna Binding Domain In Rna- Binding Protein 30	10160	4.169	0.800	2			
RBM5/LUCA15	gi|62087206	RNA binding motif protein 5 variant [Homo sapiens]	56076	12.266	7.350	7			
RBMXL1	gi|82802769	RBM1 [Homo sapiens]	41440				3.325		1
RSRC1	gi|14714462	RSRC1 protein [Homo sapiens]	31510				1.875	0.090	3
S100 A7	gi|400892	Protein S100-A7 (S100 calcium-binding protein A7) (Psoriasin)	11450				0.275	0.080	2
S100 A9	gi|4506773	S100 calcium-binding protein A9 [Homo sapiens]	13291	0.022	0.020	7			
SAFB-like	gi|62244004	modulator of estrogen induced transcription isoform b [Homo sapiens]	115625	5.511	0.030	2	10.900		1
SEMGI	gi|487420	SEMGI	52143	0.066		1			
SERPINB3	gi|239552	squamous cell carcinoma antigen; SCC antigen [Homo sapiens]	44507				0.175	0.090	2
SF3b125	gi|15930131	DDX42 protein [Homo sapiens]	90298	5.148		1			
SFRS12	gi|21040255	splicing factor. arginine/serine-rich 12 isoform b [Homo sapiens]	59345				10.075		1

SHRM3	gi|74716122	Protein Shroom3 (Shroom) (Shroom-related protein) (hShrmL)	218125	0.078	0.000	13			
SMN2	gi|736411	putative open reading frame; duplicate of the functional spinal muscular atrophy gene. cDNA clone B	31697				10.750		1
SMT3	gi|89062887	PREDICTED: similar to SMT3 suppressor of mif two 3 homolog 2 [Homo sapiens]	10807	0.108	0.030	6			
SON3	gi|119630224	SON DNA binding protein. isoform CRA_e [Homo sapiens]	264566	2.728	0.570	7	2.050	0.320	11
SPF30	gi|5032113	survival motor neuron domain containing 1 [Homo sapiens]	26694				10.075	0.290	5
TARDBP	gi|6678271	TAR DNA binding protein [Homo sapiens]	45053	4.727	0.020	3			
TCERG1	gi|21327715	transcription elongation regulator 1 isoform 1 [Homo sapiens]	124051	1.540	0.220	3	2.525	0.060	2
TF IIB	gi|8392875	transcription factor IIB [Homo sapiens]	22931	4.312		1	5.450	0.400	2
TFIP11	gi|8393259	tuftelin interacting protein 11 [Homo sapiens]	96758				1.450	0.040	8
THOC7	gi|34783006	THOC7 protein [Homo sapiens]	23039				3.350	0.100	4
TIP-48	gi|4506753	RuvB-like 1 [Homo sapiens]	50538	0.220		1	0.175	0.010	2
TLS/FUS	gi|1040970	fus-like protein	53345				13.275	0.760	2
TRIP3	gi|703110	thyroid receptor interactor	17307				0.025	0.000	2
U11/U12-48K	gi|48427636	TPA: TPA_exp: U11/U12 snRNP 48K [Homo sapiens]	40125				3.400		1
USP25	gi|6941888	ubiquitin-specific processing protease [Homo sapiens]	125670	0.132	0.100	10			
ZC3H11A	gi|29387160	ZC3H11A protein [Homo sapiens]	68688				6.300	0.410	2
ZFR	gi|119631196	zinc finger RNA binding protein. isoform CRA_c [Homo sapiens]	115705	17.82		1			

Supplementary Table 4: Quantification of spliceosomal B and C complexes by iTRAQ. The protein B:C protein ratio, the standard deviation (StDev), and the peptide number used to calculate the protein ratio (#) are shown for two replicates (iTRAQ #1 and iTRAQ #2). The mean B:C protein ratio and the corresponding standard deviation were calculated from the two replicates (iTRAQ mean). Proteins without assigned values could not be quantified.

Protein	**MW [kDa]**	**accession no.**	**iTRAQ #1**			**iTRAQ #2**			**iTRAQ mean**	
			B:C	**StDev**	**#**	**B:C**	**StDev**	**#**	**B:C**	**StDev**
U1 snRNP										
U1-A	31.3	gi|4759156				22.35	7.32	5	22.35	
U1-C	17.4	gi|4507127								
U1-70K	51.6	gi|29568103	3.24	1.42	12	7.08	1.10	7	5.16	2.71
17S U2 snRNP										
U2A′	28.4	gi|50593002	0.48	0.18	23	1.39	0.20	24	0.93	0.65
U2B′′	25.4	gi|4507123	0.53	0.25	14	1.74	0.42	12	1.14	0.86
SF3a120	88.9	gi|5032087	2.66	0.58	26	2.64	0.44	29	2.65	0.01
SF3a66	49.3	gi|21361376	3.94	0.71	7	8.09	0.43	6	6.02	2.93
SF3a60	58.5	gi|5803167	4.91	1.28	24	6.68	0.65	14	5.80	1.25
SF3b155	145.8	gi|54112117	3.98	2.36	68	3.66	2.15	118	3.82	0.22
SF3b145	100.2	gi|55749531	4.63	1.53	21	4.13	0.93	34	4.38	0.35
SF3b130	135.5	gi|54112121	5.01	1.85	98	3.52	0.72	49	4.27	1.05
SF3b49	44.4	gi|5032069	5.67	1.26	2	5.33	2.56	4	5.50	0.24
SF3b14a (p14)	14.6	gi|7706326	4.25	1.31	11	4.37	0.60	14	4.31	0.08
SF3b14b	12.4	gi|14249398	3.75	1.04	10	2.00	0.25	2	2.87	1.23
SF3b10	10.1	gi|13775200								
17S U2 related										
U2AF65	53.5	gi|6005926	3.63	0.80	2				3.63	
U2AF35	27.9	gi|5803207	5.59	2.69	8				5.59	
hPRP43	90.9	gi|68509926	5.98	2.21	28	2.59	0.35	37	4.28	2.39
SPF45	45.0	gi|14249678	5.38	1.25	5	6.22	0.84	6	5.80	0.60
SR140	118.2	gi|122937227	3.04	0.17	3	4.82	0.80	5	3.93	1.26
CHERP	100.0	gi|119226260	5.36	0.05	2	4.27	1.06	5	4.82	0.77
SF3b125	103.0	gi|45446747	10.06	4.64	6	6.19	2.07	6	8.12	2.73
U5 snRNP										
220K	273.3	gi|3661610	1.18	0.20	154	1.00	0.15	158	1.09	0.13
200K	244.5	gi|45861372	1.05	0.24	211	1.06	0.20	168	1.05	0.01

116K	109.4	gi|41152056	0.96	0.28	52	1.09	0.27	73	1.03	0.10
40K	39.3	gi|4758560	1.03	0.18	20	1.33	0.18	16	1.18	0.22
102K	106.9	gi|40807485	2.77	0.78	55	1.81	0.54	64	2.29	0.68
15K	16.8	gi|5729802	7.03	1.46	3	4.73	0.45	3	5.88	1.63
100K	95.6	gi|41327771	1.57	0.38	48	1.09	0.16	33	1.33	0.34
52K	37.6	gi|5174409	1.06	0.57	3	3.50	1.17	5	2.28	1.72
U4/U6 snRNP										
90K	77.6	gi|4758556	8.27	3.88	37	4.37	1.59	39	6.32	2.75
60K	58.4	gi|45861374	8.18	2.98	26	5.83	0.85	20	7.00	1.66
20K	20.0	gi|5454154	2.50	0.33	3	2.55	0.40	4	2.53	0.04
61K	55.4	gi|40254869	7.43	3.30	26	5.50	1.46	29	6.46	1.37
15.5K	14.2	gi|4826860	9.12	2.96	2	16.96	0.28	2	13.04	5.54
U4/U6.U5 snRNP										
110K	90.2	gi|13926068	4.50	1.96	23	3.60	1.09	19	4.05	0.63
65K	65.4	gi|56550051	1.78	0.36	21	1.63	0.21	19	1.70	0.11
27K (RY1)	18.9	gi|24307919								
hPRP38	37.5	gi|24762236	4.95	1.88	11	4.04	0.85	7	4.50	0.64
hSnu23	28.8	gi|13385046	5.478	1.948	2	12.221	3.172	4	8.85	4.77
TFIP11	96.8	gi|8393259	6.50	1.91	12	1.01	0.08	22	3.75	3.88
LSm Proteins										
LSm2	10.8	gi|10863977	5.24	1.28	4	4.47	0.39	8	4.86	0.54
LSm3	11.8	gi|7657315	3.45		1	3.21		1	3.33	0.17
LSm4	15.4	gi|6912486	4.78	1.60	8	5.52	2.31	2	5.15	0.53
LSm5	9.9									
LSm6	9.1	gi|5919153	5.64	2.12	4	6.16	1.02	3	5.90	0.36
LSm7	11.6	gi|7706423	6.61	3.62	8	3.70	0.08	2	5.15	2.06
LSm8	10.4	gi|7706425	3.55	1.53	3	4.14	0.70	2	3.85	0.41
Sm Proteins										
B	24.6	gi|4507125	1.69	0.28	13	1.70	0.29	15	1.70	0.01
D1	13.3	gi|5902102	1.39	0.26	6	1.86	0.51	7	1.62	0.34
D2	13.5	gi|29294624	1.62	0.66	35	1.88	0.30	22	1.75	0.18
D3	13.9	gi|4759160	1.40	0.32	32	2.08	0.44	19	1.74	0.48
E	10.8	gi|4507129	1.20	0.17	11	2.03	0.47	7	1.61	0.59
F	9.7	gi|4507131	2.91	0.93	2	1.40	0.37	6	2.15	1.07
G	8.5	gi|4507133	1.52	0.44	4	1.19	0.09	5	1.36	0.23

hPRP19/CDC5L complex										
hPrp19	55.2	gi|7657381	0.62	0.36	61	0.57	0.12	62	0.60	0.04
CDC5L	92.2	gi|11067747	0.23	0.14	45	0.19	0.12	30	0.21	0.03
SPF27	21.5	gi|5031653	0.53	0.13	18	0.55	0.12	15	0.54	0.01
PRL1	57.2	gi|4505895	0.69	0.22	33	1.06	0.22	6	0.87	0.26
Hsp70	70.4	gi|5729877								
AD-002	26.6	gi|7705475	0.22	0.08	6	0.15	0.08	3	0.18	0.05
CTNNBL1	65.1	gi|18644734	1.44	0.46	4	2.29	0.34	11	1.86	0.60
Npw38BP	70.0	gi|7706501	7.31	0.72	6	8.77	2.32	17	8.04	1.04
Npw38	30.5	gi|74735456				7.68	1.60	3	7.68	
hPRP19/CDC5L related										
hSYF1	100.0	gi|55770906	0.27	0.09	62	0.38	0.08	65	0.33	0.08
CRNKL1	100.6	gi|30795220	0.47	0.52	88	0.32	0.07	82	0.39	0.11
hIsy1	33.0	gi|20149304	0.20	0.07	16	0.61	0.10	17	0.40	0.28
SKIP	51.1	gi|6912676	0.58	0.17	58	0.63	0.10	42	0.60	0.03
RBM22	46.9	gi|8922328	0.45	0.13	35	0.53	0.11	39	0.49	0.06
Cyp-E	33.4	gi|5174637	0.13	0.05	8	0.58	0.14	5	0.36	0.32
PPIL1	18.2	gi|7706339	0.42	0.18	10	0.45	0.08	8	0.43	0.02
KIAA0560	171.3	gi|38788372	0.09	0.05	96	0.39	0.13	186	0.24	0.21
G10	17.0	gi|32171175	0.39	0.19	14	0.88	0.02	4	0.64	0.35
hRES complex proteins										
SNIP1	45.8	gi|21314720	0.80	0.11	10	1.66	0.15	2	1.23	0.61
MGC12135	70.5	gi|14249338	1.97	0.71	10	0.94	0.38	10	1.46	0.73
CGI-79	39.7	gi|4929627	0.76	0.11	3	1.36	0.10	2	1.06	0.42
Proteins recruited to A complex										
RBM39	59.4	gi|4757926	4.08	0.89	17	4.07	0.73	13	4.07	0.01
p68 (DDX5)	69.2	gi|4758138	1.52	0.55	8	2.30	0.45	15	1.91	0.55
ELAV-like 1 (HuR)	36.1	gi|38201714	4.76	2.29	27	5.65	0.82	18	5.20	0.63
p72/DDX17	80.5	gi|3122595	1.07		1	2.30	0.73	2	1.69	0.87
Proteins recruited to B complex										
MFAP1	51.9	gi|50726968	3.54	1.00	38	4.77	0.56	11	4.15	0.87

RED	65.6	gi|10835234	4.64	2.17	23	7.21	2.03	20	5.92	1.82
hSmu-1	57.5	gi|8922679	5.67	2.36	44	4.00	0.65	4	4.83	1.18
PPIL2	59.5	gi|7657473	1.33	0.88	19	2.96	0.74	32	2.15	1.15
hPRP2 (DDX16)	119.2	gi|4503293	0.54	0.16	19	2.10	0.29	20	1.32	1.10
hPRP4-Kinase	117.1	gi|89276756	0.59	0.19	25	0.37	0.07	18	0.48	0.15
THRAP3	108.6	gi|4827040	2.04	0.67	30	1.19	0.08	4	1.62	0.60
PABP1	70.5	gi|46367787	1.70	0.48	8	4.72	2.46	4	3.21	2.13
SKIV2L2	117.8	gi|39930353	1.13	0.20	12	1.15	0.19	8	1.14	0.01
PABPN1	32.6	gi|4758876	1.21	0.09	3	0.79	0.00	2	1.00	0.29
RNF113A	38.8	gi|5902158	0.43	0.15	2	1.20	0.13	3	0.81	0.55
NY-CO-10	53.8	gi|64276486	0.63	0.22	12	0.68	0.05	2	0.66	0.03
KIAA1604	105.5	gi|55749769	0.35	0.15	25	0.46	0.23	27	0.40	0.08
hsp27	22.8	gi|4504517	1.02		1	0.47	0.02	2	0.74	0.39
GCFC	104.7	gi|22035565	2.12	0.42	16	1.36	0.26	24	1.74	0.54
UBL5	8.5	gi|13236510	17.04		1	10.08	6.92	2	13.56	4.92
CCDC16	42.0	gi|49472814	0.93	0.37	11	1.38	0.25	22	1.16	0.31
CCDC12	19.2	gi|21389497	0.53	0.17	6	0.51	0.05	4	0.52	0.02
HsKin17	45.2	gi|13124883	3.10	1.36	6	2.99	0.57	8	3.04	0.08
Step 2 factors										
hPRP22	139.3	gi|4826690	0.13	0.12	55	0.29	0.15	89	0.21	0.11
hPRP18	39.9	gi|4506123	0.38		1	0.39	0.18	4	0.39	0.01
hPRP17	65.5	gi|7706657	0.19	0.08	32	0.45	0.15	57	0.32	0.19
hPRP16	140.5	gi|17999539				0.43	0.11	12	0.43	
hSLU7	68.4	gi|27477111	0.10	0.10	19	0.20	0.09	38	0.15	0.07
Proteins recruited to C complex										
Abstrakt	69.8	gi|21071032	0.08	0.06	48	0.17	0.14	90	0.12	0.06
GCIP p29	28.7	gi|46371998	0.18	0.14	11	0.18	0.07	7	0.18	0.00
DDX35	78.9	gi|20544129	0.32	0.17	28	0.17	0.07	22	0.25	0.11
Q9BRR8	103.3	gi|74732921	0.40	0.09	3	0.19	0.07	9	0.29	0.15
c19orf29 (NY-REN-24)	88.6	gi|126723149	0.17	0.13	21	0.17	0.08	35	0.17	0.00
PPIase-like 3b	18.6	gi|19557636	0.17	0.14	8	0.31	0.19	3	0.24	0.10
PPWD1	73.6	gi|24308049	0.10	0.12	39	0.20	0.09	53	0.15	0.07
MORG1	34.3	gi|153791298	0.10		1	0.69	0.09	3	0.39	0.42
FRG1	29.2	gi|4758404				0.58	0.17	6	0.58	

NOSIP	33.2	gi|7705716	0.11	0.08	9	0.19	0.09	3	0.15	0.05
GPKOW	52.1	gi|15811782	0.66	0.21	6				0.66	
C1orf55	39.3	gi|148664216	0.08	0.04	19	0.13	0.06	14	0.10	0.03
FAM32A	13.1	gi|7661696	0.11	0.06	2				0.11	
RACK1 (GNB2L1)	35.1	gi|5174447								
Tip-49	50.2	gi|4506753								
Potential C complex specific proteins										
PPIG	88.5	gi|42560244	0.20	0.09	6				0.20	
FAM50A	40.1	gi|4758220	0.15	0.08	15	0.29	0.12	5	0.22	0.10
FAM50B	38.6	gi|6912326	0.13	0.03	2	0.36	0.05	3	0.25	0.16
C9orf78	33.7	gi|7706557	0.14	0.05	6	0.26	0.01	2	0.20	0.09
C10orf4	37.5	gi|24432067	0.10	0.06	2	0.11	0.05	6	0.10	0.01
CXorf56	25.6	gi|11545813	0.08	0.08	12	0.24	0.13	11	0.16	0.11
DGCR14	52.4	gi|13027630	0.09	0.03	3	0.29	0.16	8	0.19	0.14
CCDC130	44.7	gi|13540614								
TOE1	56.4	gi|156564398	0.84	0.37	3				0.84	
NKAP	47.0	gi|13375676	0.22	0.11	6				0.22	
ZCCHC10	18.4	gi|8923106	0.66	0.71	2				0.66	
CDK10	35.4	gi|16950647	0.20	0.09	3	0.24	0.10	4	0.22	0.03
TTC14	88.2	gi|33457330	0.22	0.14	8	0.32	0.10	11	0.27	0.07
WDR70	73.2	gi|8922301				1.19	0.18	5	1.19	
NFKBIL1	43.1	gi|26787991								
JUP	81.6	gi|12056468								
EJC/mRNP										
eIF4A3	46.9	gi|7661920	0.15	0.07	31	0.55	0.06	9	0.35	
Magoh	17.2	gi|4505087	0.15	0.06	10	0.20	0.05	5	0.18	0.04
Y14	19.9	gi|4826972	0.40	0.14	7	0.11	0.03	2	0.25	0.20
Pinin	81.6	gi|33356174	2.11	0.58	5	1.89	0.06	3	2.00	0.15
RNPS1	34.2	gi|6857826	0.63	0.17	2	2.09		1	1.36	1.04
Acinus	151.8	gi|7662238	1.35	0.42	13	1.84	0.38	17	1.60	0.34
SAP18	17.4	gi|5032067	1.37	0.21	6	1.19	0.17	6	1.28	0.13
Aly/REF (THOC4)	26.9	gi|55770864	1.11	0.27	4				1.11	
UAP56	49.1	gi|18375623	2.01	0.44	11	4.54	1.00	3	3.28	1.79

TREX										
THOC1	75.6	gi|154448890	1.13	0.42	4	1.77	0.17	3	1.45	0.45
THOC2	169.6	gi|125656165	0.62	0.17	13	1.54	0.26	7	1.08	0.65
THOC3	38.8	gi|14150171								
KIAA0983 (THOC5)	78.4	gi|50959110	1.44	0.46	5	1.35	0.26	5	1.40	0.07
WDR58 (THOC6)	37.4	gi|31543164	0.51	0.25	2	1.50		1	1.00	0.70
pre-mRNA/mRNA binding proteins										
CBP20	18.0	gi|110349727	0.71	0.16	8	0.93	0.16	10	0.82	0.16
CBP80	91.8	gi|4505343	1.41	0.41	33	1.01	0.12	32	1.21	0.28
NF45	43.0	gi|24234747				1.94	0.32	4	1.94	
ZC3H18	104.0	gi|31377595	0.71	0.42	11	1.68	0.36	27	1.19	0.68
YB-1	35.9	gi|34098946	1.55	0.69	9	2.27	0.02	2	1.91	0.51
ELG	38.9	gi|8923771	3.11	0.54	5	1.08		1	2.10	1.44
DDX3	73.3	gi|87196351	1.05	0.16	2				1.05	
ASR2B	100.0	gi|33383233	1.00	0.27	15	1.55	0.20	32	1.28	0.39
BCLAF1	107.2	gi|7661958	1.61	0.24	23	2.23	0.31	6	1.92	0.44
DBPA	40.1	gi|20070160								
RBM7	30.5	gi|4503293	1.14		1				1.14	
HSP70	70.0	gi|5123454	0.25	0.14	15	1.19	0.22	10	0.72	0.67
Miscelleneous proteins										
BAG2	23.4	gi|4757834				0.50		1	0.50	
RBBP6	197.2	gi|33620716	1.38		1				1.38	
RBM42	50.3	gi|21359951								
SR related proteins										
SRm160	102.5	gi|42542379	1.12	0.16	5				1.12	
SRm300	300.0	gi|4759098	0.31	0.13	7	1.63	0.85	4	0.97	0.93
SR proteins										
SF2/ASF	27.8	gi|5902076	0.80	0.19	14	2.46	0.37	8	1.63	1.17
9G8	27.4	gi|72534660	1.16	0.32	24	2.58	0.38	9	1.87	1.00
SRp20	19.4	gi|4506901	1.65	0.44	8	2.53		1	2.09	0.62
SRp30c	25.5	gi|4506903	0.99	0.20	16	0.53		1	0.76	0.33
SRp38	31.3	gi|5730079	0.91	0.52	15	1.44	0.32	7	1.18	0.38
SRp40	31.3	gi|3929378	0.85	0.07	4	1.83	0.26	5	1.34	0.70

SRp46	31.2	gi|15055543	1.85	1.08	2				1.85	
SRp55	39.6	gi|20127499	1.35	0.23	17	0.88	0.18	7	1.11	0.33
SRp75	56.8	gi|21361282				1.16	0.17	2	1.16	
SC35 (SFRS2)	25.5	gi|47271443								
hTra-2 alpha	32.7	gi|9558733	1.44	0.70	9	2.80	0.47	2	2.12	0.97
hTra-2 beta (SFRS109	33.7	gi|4759098	1.37	1.30	22	1.22	0.37	9	1.30	0.10
hnRNP										
hnRNP A1	38.7	gi|4504445	3.44	1.81	6	5.21	0.13	2	4.32	1.25
hnRNP A3	39.6	gi|34740329	4.62	1.12	6	5.14		1	4.88	0.37
hnRNP AB	36.0	gi|12803583								
hnRNP A2/B1	37.4	gi|14043072	4.63	1.96	6	3.60	0.18	4	4.11	0.73
hnRNP C	33.3	gi|4758544	1.72	0.47	23	1.97	0.30	16	1.84	0.17
hnRNP D	38.4	gi|14110420								
hnRNP F	45.7	gi|148470406				2.94		1	2.94	
hnRNP G	47.4	gi|56699409	1.52	0.59	32	2.21	0.35	6	1.87	0.49
hnRNP G-T	42.7	gi|153252068								
hnRNP H1	49.1	gi|5031753	1.27	0.30	4	1.84	0.27	13	1.56	0.40
hnRNP H2	49.3	gi|74099697								
hnRNP H3	36.9	gi|14141157								
hnRNP K	51.0	gi|14165435	2.97		1	4.01	0.73	2	3.49	0.74
hnRNP M	77.5	gi|14141152	1.32	0.31	8	1.37	0.38	4	1.34	0.04
hnRNP Q	69.6	gi|15809590								
hnRNP R	70.9	gi|5031755	0.88	0.32	8	1.09		1	0.98	0.15
hnRNP U	90.6	gi|14141161	3.86	2.17	10				3.86	
PCBP1	37.5	gi|5453854	5.02	1.56	5	4.66	1.45	10	4.84	0.26
PCBP2	38.1	gi|14141166	2.58	0.29	4	3.71	1.04	16	3.15	0.80
RALY	32.5	gi|8051631	0.80	0.20	4	2.48	0.68	3	1.64	1.19

Supplementary Table 5: Additional proteins identified and quantified by iTRAQ. The B:C protein ratio, the standard deviation (StDev) and the number of peptides used for quantification are given for two replicates (iTRAQ #1 and iTRAQ #2). Note that not all proteins were identified in both replicates. Proteins highlighted in gray were added to the respective list of B- and C-complex-specific proteins.

				iTRAQ #1			**iTRAQ #2**		
Protein	**Protein accesion no.**	**Protein database description**	**Protein mass [Da]**	**B:C protein ratio**	**StDev**	**#**	**B:C protein ratio**	**StDev**	**#**
ALB	gi|28592	serum albumin [Homo sapiens]	79864				7.905	0.974	3
alpha tubulin	gi|340021	alpha-tubulin	53554				1.143	0.197	26
BCR	gi|116666695	Chain A. Crystal Structure Of Full-Length 3~-Exonuclease	45012				1.380		1
beta-tubulin	gi|1297274	beta-tubulin [Homo sapiens]	53303				0.669	0.103	5
BRIX	gi|55770900	BRIX [Homo sapiens]	47945				1.391	0.313	2
Cas-Br-M	gi|13376204	Cas-Br-M (murine) ecotropic retroviral transforming sequence-like 1 [Homo sapiens]	57712				1.944	0.081	2
CCAR1	gi|27497118	death inducer with SAP domain DIS [Homo sapiens]	147586				5.017	1.242	2
CCDC55	gi|14149807	coiled-coil domain containing 55 isoform 1 [Homo sapiens]	76765				1.172		1
CCNK	gi|8980825	cyclin K [Homo sapiens]	44722				2.555		1
CIP29	gi|119617243	hCG2016179. isoform CRA_d [Homo sapiens]	25459	3.571		1			
CLK1	gi|67551261	CDC-like kinase 1 [Homo sapiens]	63472	1.081	0.446	4			
CLK4	gi|10190706	CDC-like kinase 4 [Homo sapiens]	62901	0.848		1			
CUG	gi|5729794	CUG triplet repeat. RNA-binding protein 1 isoform 1 [Homo sapiens]	55437	1.967	0.022	2	3.420	0.532	7
Cyclin M	gi|88989669	PREDICTED: similar to CG31232-PA. isoform A [Homo sapiens]	27359				0.184	0.025	2
DDX21	gi|2135315	RNA helicase Gu - human (fragment)	103155	1.666	0.575	7			
DDX9	gi|33878473	DHX9 protein [Homo sapiens]	73628	1.343		1	1.427	0.141	3
DHX34	gi|38158022	DEAH (Asp-Glu-Ala-His) box polypeptide 34 [Homo sapiens]	135588	0.487	0.334	7	0.260	0.170	20

E1B-AP5	gi|3319956	E1B-55kDa-associated protein [Homo sapiens]	101542				1.619	0.104	4
Ecm29	gi|2224677	KIAA0368 [Homo sapiens]	175362				1.771	0.169	2
eEF1A1	gi|31092	unnamed protein product [Homo sapiens]	57288	0.320	0.146	4	1.065	0.506	2
ERH	gi|4758302	enhancer of rudimentary homolog [Homo sapiens]	13542	2.036	0.531	5			
EXOSC2	gi|19923403	exosome component 2 [Homo sapiens]	35402	0.396	0.168	3			
EXOSC4	gi|9506689	exosome component 4 [Homo sapiens]	27317				1.671		1
EXOSC5	gi|14043511	Exosome component 5 [Homo sapiens]	27406	0.516		1	0.856		1
EXOSC7	gi|473949	KIAA0116 [Homo sapiens]	34928				2.510		1
FBP11	gi|34222504	Pre-mRNA-processing factor 40 homolog A (Formin-binding protein 3) (Formin-binding protein 11) (Huntingtin-interacting protein HYPA) (Huntingtin yeast partner A) (Fas ligand-associated factor 1) (NY-REN-6 antigen)	123665	1.259	0.205	4	2.701	0.504	4
FNBP4	gi|6808095	hypothetical protein [Homo sapiens]	119110				2.711	0.290	4
FUSE3	gi|1575609	FUSE binding protein 3 [Homo sapiens]	67621	3.176	1.538	4	3.784	0.650	17
GU2	gi|5174447	guanine nucleotide binding protein (G protein). beta polypeptide 2-like 1 [Homo sapiens]	38016	0.847		1			
H2A	gi|32111	unnamed protein product [Homo sapiens]	16181	1.233		1			
hnRNP A0	gi|1911429	A0=heterogeneous nuclear ribonucleoprotein [human. placenta. Peptide. 305 aa]	33758	1.247	0.671	2			
hnRNP L	gi|133274	Heterogeneous nuclear ribonucleoprotein L (hnRNP L)	64788	5.835		1			
hnRNP Q2	gi|15809588	hnRNP Q2 [Homo sapiens]	72196	0.841	0.117	3	0.964	0.438	2
LOC150383	gi|49533621	hypothetical protein LOC150383 [Homo sapiens]	15480				0.070		1
LOC540543	gi|84000355	hypothetical protein LOC540543 [Bos taurus]	38096				2.447	1.214	2
LRC	gi|24308289	leukocyte receptor cluster (LRC) member 1 [Homo sapiens]	33537				0.373		1
LUC7A	gi|8922297	LUC7-like isoform a [Homo sapiens]	42306				4.196	0.875	2

Matrin3	gi|57162250	novel protein [Homo sapiens]	16315				1.085		1
NCL	gi|189306	nucleolin	89313				1.296		1
N-myc and STAT inetractor	gi|4758814	N-myc and STAT interactor [Homo sapiens]	39988	4.030	1.192	4	4.957		1
NUFIP1	gi|6912542	nuclear fragile X mental retardation protein interacting protein 1 [Homo sapiens]	64004	0.223		1	0.330	0.019	2
Numa 1	gi|35119	NuMA protein [Homo sapiens]	260907				3.112		1
NY-REN-37	gi|10433149	unnamed protein product [Homo sapiens]	51438	1.162		1			
PABPC4	gi|4504715	poly A binding protein. cytoplasmic 4 [Homo sapiens]	77931	1.524	0.351	4	0.992		1
plakophilin	gi|6005830	plakophilin 3 [Homo sapiens]	91432				2.485		1
PPIL4	gi|20911035	peptidylprolyl isomerase-like 4 [Homo sapiens]	65817				2.907		1
PRCC	gi|14714625	Papillary renal cell carcinoma (translocation-associated) [Homo sapiens]	57721				2.944	0.176	4
PRKRIP1	gi|13375901	PRKR interacting protein 1 (IL11 inducible) [Homo sapiens]	24875	0.134	0.089	7	0.111	0.056	4
PUF60	gi|1809248	siah binding protein 1 [Homo sapiens]	62853	2.341		1	4.261	1.354	19
RBM10	gi|34785044	RBM10 protein [Homo sapiens]	64274	6.494		1	5.088	1.051	4
RBM14	gi|5454064	RNA binding motif protein 14 [Homo sapiens]	72469	1.260		1			
RBM15(OTT)	gi|10433990	unnamed protein product [Homo sapiens]	108615	1.406	0.186	2	1.914	0.262	9
RBM18	gi|14916461	RNA binding motif protein 18 [Homo sapiens]	25042				0.423		1
RBM5/LUCA	gi|1244404	putative tumor suppressor	100212	4.986	0.356	2	6.732	0.864	2
RSRC1	gi|14714462	RSRC1 protein [Homo sapiens]	35833				1.685	0.535	4
S100 A9	gi|4506773	S100 calcium-binding protein A9 [Homo sapiens]	15009				89.373		1
S164	gi|55741709	RNA binding motif protein 25 [Homo sapiens]	113081	0.725	0.345	3	3.218	0.475	4
SAFB-like	gi|62825862	SLTM protein [Homo sapiens]	86766	4.104	0.836	5			
SEMG I	gi|487420	SEMGI	58184				14.259	5.786	4
SEMG II	gi|4506885	semenogelin II precursor [Homo sapiens]	73999				28.488		1
SFRS11	gi|4759100	splicing factor. arginine/serine-rich 11 [Homo sapiens]	61240				3.212		1

SFRS12	gi|28703790	Similar to expressed sequence AI450757 [Homo sapiens]	46956	6.408		1	2.799	0.587	6
SFRS17A	gi|187242	550 amino acids MW=61kDa. glycosylated=75 kDa; expressed on endothelium. activated lymphocytes and syncytiotrophoblast. contains leucine zipper and basic region homologous to myc; 721P	71752	1.357	0.199	4	0.408	0.013	2
SON3	gi|17046381	SON DNA binding protein isoform E [Homo sapiens]	240773	1.129	0.221	5	1.382	0.059	2
Spen	gi|14790190	spen homolog. transcriptional regulator [Homo sapiens]	440442	4.774	1.530	16	7.310	2.566	4
SPF30	gi|5032113	survival motor neuron domain containing 1 [Homo sapiens]	31300	30.159		1			
TARDBP	gi|6678271	TAR DNA binding protein [Homo sapiens]	48013	0.994	0.327	3	5.256	1.777	2
tat SF1	gi|1667611	Tat-SF1 [Homo sapiens]	96255				1.131		1
TCERG1	gi|21327715	transcription elongation regulator 1 isoform 1 [Homo sapiens]	138273	2.099	0.263	3	4.518	0.710	6
TCP1	gi|1800303	HIV-1 Nef interacting protein [Homo sapiens]	50858	0.358	0.132	3	0.637	0.093	2
TF IIB	gi|8392875	transcription factor IIB [Homo sapiens]	25348				3.614		1
THOC7	gi|34783006	THOC7 protein [Homo sapiens]	26105				1.808	0.465	2
tubulin alpha-2	gi|34740335	tubulin. alpha 2 [Mus musculus]	53554	0.726	0.113	2	1.087	0.219	33
tubulin beta	gi|18088719	Tubulin. beta [Homo sapiens]	52313	0.926	0.231	2			
tubulin beta-2	gi|5174735	tubulin. beta. 2 [Homo sapiens]	52473				1.152		1
tubulin beta-5	gi|7106439	tubulin. beta 5 [Mus musculus]	52313				0.940	0.246	29
UKp68	gi|40804742	nuclear protein UKp68 isoform 1 [Homo sapiens]	91387				1.054	0.232	6
USP36	gi|7023072	unnamed protein product [Homo sapiens]	114660				0.300		1
USP42	gi|79750944	ubiquitin specific protease 42 [Homo sapiens]	158266	0.589	0.351	7	0.571	0.172	5
YT521	gi|16551831	unnamed protein product [Homo sapiens]	82609	0.976	0.335	2			
ZBT46	gi|30354537	ZBTB46 protein [Homo sapiens]	69412				1.143		1

ZC3H11A	gi|29387160	ZC3H11A protein [Homo sapiens]	83552	2.636	1.360	2			
ZCCHC19	gi|51243065	zinc finger CCHC-type and RNA binding motif 1 [Homo sapiens]	29083	0.482	0.211	4	1.381	0.006	2
ZCCHC8	gi|7018505	hypothetical protein [Homo sapiens]	55697	1.147	0.153	2	0.940	0.091	6
ZNF	gi|14330434	putative zinc finger protein [Homo sapiens]	127231				0.568		1
ZNF432	gi|40788368	KIAA0798 protein [Homo sapiens]	89866				1.193		1

Supplementary Table 6: Quantification of spliceosomal proteins by peptide and spectral count. The peptide count quantification was performed manually (Bessonov *et al.* 2008). Peptide numbers from two replicates of purified B and C complexes are given. The average number of peptides for B and C complexes was used to calculate the B:C protein ratio. The spectral count was performed using the software Scaffold 2. Spectra number for the two replicates of purified B and C complexes is shown, and the average spectral number was used to calculate the B:C protein ratio. When proteins were identified only in B or C complexes, the B:C protein ratio is denoted with “OSB” (“only spectra B complex”) or “OSC” (“only spectra C complex”).

			Peptide count according to Bessonov *et al.* (2008): manual data analysis							Spectral count using Scaffold 2: software-based data analysis						
Protein	**MW [kDa]**	**accession no.**	B #1	B #2	**B**	C #1	C #2	**C**	**B:C protein ratio**	B #1	B #2	**B**	C #1	C #2	**C**	**B:C protein ratio**
U1 snRNP																
U1-A	31.3	gi|4759156	17	8	12.5				OSB	7	8	7.5	6	1	3.5	2.14
U1-C	17.4	gi|4507127		1	0.5				OSB		1	0.5				OSB
U1-70K	51.6	gi|29568103		11	5.5				OSB	4	5	4.5	1	1	1	4.50
17S U2 snRNP																
U2A′	28.4	gi|50593002	55	12	33.5	39	18	28.5	1.18	48	12	30	26	18	22	1.36
U2B′′	25.4	gi|4507123	25	15	20	13	14	13.5	1.48	17	14	15.5	14	12	13	1.19
SF3a120	88.9	gi|5032087	84	47	65.5	11	13	12	5.46	59	45	52	17	11	14	3.71
SF3a66	49.3	gi|21361376	18	25	21.5		3	1.5	14.33	9	23	16	2	2	2	8.00
SF3a60	58.5	gi|5803167	39	42	40.5	7	10	8.5	4.76	32	41	36.5	7	9	8	4.56
SF3b155	145.8	gi|54112117	153	119	136	22	28	25	5.44	130	114	122	30	24	27	4.52
SF3b145	100.2	gi|55749531	82	61	71.5	16	13	14.5	4.93	52	65	58.5	10	13	11.5	5.09
SF3b130	135.5	gi|54112121	209	254	231.5	26	67	46.5	4.98	161	236	198.5	29	63	46	4.32
SF3b49	44.4	gi|5032069	8	1	4.5	1	1	1	4.50	6	1	3.5	2	1	1.5	2.33
SF3b14a (p14)	14.6	gi|7706326		17	8.5	7	7	7	1.21	15	15	15	6	7	6.5	2.31
SF3b14b	12.4	gi|14249398	19	22	20.5	8	9	8.5	2.41	14	20	17	3	9	6	2.83
17S U2 related																
U2AF65	53.5	gi|6005926	8	4	6				OSB	5	2	3.5	1		0.5	7.00
U2AF35	27.9	gi|5803207		1	0.5				OSB	1	1	1				OSB
hPRP43	90.9	gi|68509926	51	54	52.5	7	27	17	3.09	36	56	46	26	32	29	1.59
SPF45	45	gi|14249678	19	9	14				OSB	4	8	6				OSB
SR140	118.2	gi|122937227	34	17	25.5		1	0.5	51.00	9	13	11	1	1	1	11.00
CHERP	100	gi|119226260	14	7	10.5				OSB	8	5	6.5				OSB
SF3b125	103	gi|45446747	29	10	19.5				OSB	12	10	11	1		0.5	22.00
U5 snRNP																
220K	273.7	gi|3661610	408	335	371.5	299	261	280	1.33	345	316	330.5	153	240	196.5	1.68
200K	244.5	gi|45861372	267	375	321	334	329	331.5	0.97	226	355	290.5	155	314	234.5	1.24

116K	109.4	gi|41152056	169	168	168.5	212	133	172.5	0.98	140	159	149.5	127	128	127.5	1.17
40K	39.3	gi|4758560	23	37	30	29	29	29	1.03	21	36	28.5	9	29	19	1.50
102K	106.9	gi|40807485	90	170	130	15	50	32.5	4.00	67	159	113	13	45	29	3.90
15K	16.8	gi|5729802	6	11	8.5				OSB	6	11	8.5		1	0.5	17.00
100K	95.6	gi|41327771	47	107	77	11	51	31	2.48	28	100	64	14	49	31.5	2.03
52K	37.6	gi|5174409	18	5	11.5		4	2	5.75	11	4	7.5	1	3	2	3.75
U4/U6 snRNP																
90K	77.6	gi|4758556	63	75	69	3	11	7	9.86	49	73	61	3	12	7.5	8.13
60K	58.4	gi|45861374	37	57	47		10	5	9.40	36	55	45.5	2	7	4.5	10.11
20K	20	gi|5454154	24	14	19	6	8	7	2.71	27	16	21.5	7	7	7	3.07
61K	55.4	gi|40254869	27	60	43.5		10	5	8.70	19	58	38.5	1	9	5	7.70
15.5K	14.2	gi|4826860	7	9	8		2	1	8.00	12	9	10.5		2	1	10.50
U4/U6.U5 snRNP																
110K	90.2	gi|13926068	65	57	61		11	5.5	11.09	48	56	52	5	11	8	6.50
65K	65.4	gi|56550051	26	48	37	7	25	16	2.31	19	45	32	9	26	17.5	1.83
hPRP38	37.5	gi|24762236	17	30	23.5	4	8	6	3.92	13	28	20.5		6	3	6.83
hSnu23	28.8	gi|13385046								8	2	5				OSB
TFIP11	96.8	gi|8393259		12	6	7	10	8.5	0.71	7	12	9.5	9	10	9.5	1.00
LSm proteins																
LSm2	10.8	gi|10863977	20	10	15		2	1	15.00	14	10	12		2	1	12.00
LSm3	11.8	gi|7657315		3	1.5		2	1	1.50	3	3	3		2	1	3.00
LSm4	15.4	gi|6912486	13	19	16				OSB	7	12	9.5				OSB
LSm6	9.1	gi|5919153		12	6		2	1	6.00	17	11	14		1	0.5	28.00
LSm7	11.6	gi|7706423	10	5	7.5				OSB	4	4	4	1		0.5	8.00
LSm8	10.4	gi|7706425	10	18	14		2	1	14.00	10	16	13		2	1	13.00
Sm proteins																
B	24.6	gi|4507125	34	22	28	26	18	22	1.27	33	20	26.5	26	15	20.5	1.29
D1	13.3	gi|5902102	18	20	19	10	22	16	1.19	15	21	18	9	20	14.5	1.24
D2	13.5	gi|29294624	24	60	42	30	68	49	0.86	27	59	43	20	59	39.5	1.09
D3	13.9	gi|4759160	22	35	28.5	26	46	36	0.79	15	35	25	15	44	29.5	0.85
E	10.8	gi|4507129	24	23	23.5	10	25	17.5	1.34	21	18	19.5	10	22	16	1.22
F	9.7	gi|4507131	21	23	22	4	11	7.5	2.93	3	19	11	2	11	6.5	1.69
G	8.5	gi|4507133	7	11	9	5	3	4	2.25	7	10	8.5	5	3	4	2.13
hPRP19/CDC5L complex																
hPRP19	55.2	gi|7657381	39	96	67.5	167	138	152.5	0.44	29	87	58	72	125	98.5	0.59
CDC5L	92.2	gi|11067747	70	53	61.5	118	109	113.5	0.54	52	49	50.5	126	103	114.5	0.44
SPF27	21.5	gi|5031653	21	11	16	34	9	21.5	0.74	17	11	14	33	9	21	0.67

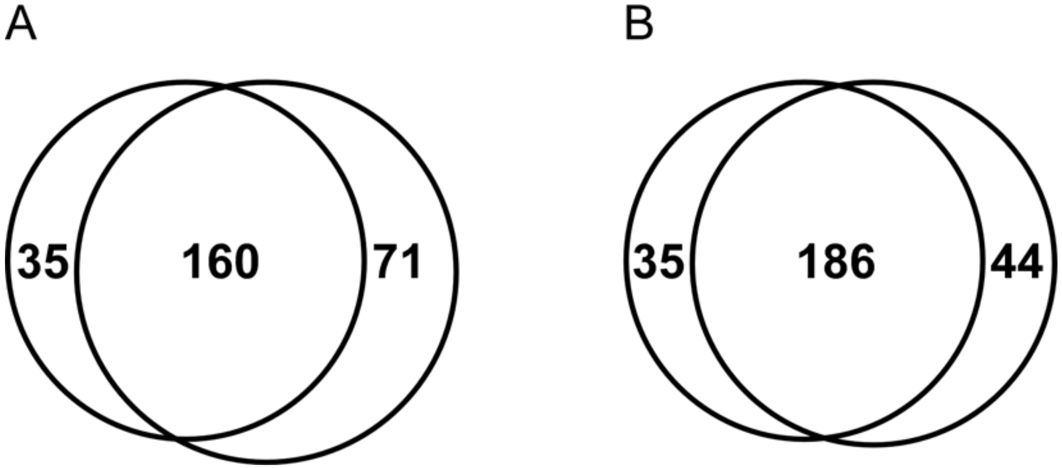
PRL1	57.2	gi|4505895	22	28	25	63	44	53.5	0.47	15	24	19.5	40	43	41.5	0.47
Hsp70	70.4	gi|5729877		8	4	7	20	13.5	0.30	3	7	5	19	17	18	0.28
AD-002	26.6	gi|7705475	10	1	5.5	16	7	11.5	0.48	7	1	4	11	7	9	0.44
CTNNBL1	65.1	gi|18644734	21	13	17	6	8	7	2.43	11	10	10.5	6	8	7	1.50
Npw38BP	70	gi|7706501	17	10	13.5				OSB	15	9	12	1		0.5	24.00
Npw38	30.5	gi|151301228		7	3.5		1	0.5	7.00	5	1	3				OSB
hPrp19/CDC5L related proteins																
hSYF1	100	gi|55770906	53	36	44.5	151	98	124.5	0.36	53	31	42	97	91	94	0.45
CRNKL1	100.6	gi|30795220	66	86	76	143	176	159.5	0.48	43	80	61.5	112	174	143	0.43
hIsy1	33	gi|20149304	19	4	11.5	3	24	13.5	0.85	4	4	4	23	22	22.5	0.18
SKIP	51.1	gi|6912676	37	60	48.5	66	82	74	0.66	27	58	42.5	68	79	73.5	0.58
RBM22	46.9	gi|8922328	29	11	20	54	44	49	0.41	25	8	16.5	48	44	46	0.36
Cyp-E	33.4	gi|5174637	13	6	9.5	20	13	16.5	0.58	10	6	8	23	11	17	0.47
PPIL1	18.2	gi|7706339	7	15	11	19	23	21	0.52	7	14	10.5	14	22	18	0.58
KIAA0560	171.3	gi|38788372	41	44	42.5	203	163	183	0.23	32	41	36.5	131	156	143.5	0.25
G10	17	gi|32171175	9	10	9.5	24	24	24	0.40	13	8	10.5	26	24	25	0.42
hRES complex proteins																
SNIP1	45.8	gi|21314720	10	12	11	10	11	10.5	1.05	7	11	9	4	9	6.5	1.38
MGC13125	70.5	gi|14249338	44	17	30.5	14	16	15	2.03	19	17	18	13	16	14.5	1.24
CGI-79	39.7	gi|4929627		6	3	13	5	9	0.33	2	6	4	2	5	3.5	1.14
Proteins recruited to A complex																
RBM39	59.4	gi|4757926	10	48	29	3	10	6.5	4.46	9	44	26.5	2	10	6	4.42
p68 (DDX5)	69.2	gi|4758138	14	14	14		6	3	4.67	9	21	15	5	7	6	2.50
ELAV (HuR)	36.1	gi|38201714	52	77	64.5	21	14	17.5	3.69	36	77	56.5	14	14	14	4.04
p72/DDX17	80.5	gi|3122595	6	23	14.5		7	3.5	4.14	3	21	12	1	6	3.5	3.43
Proteins recruited to B complex																
MFAP1	51.9	gi|50726968	37	49	43	2	10	6	7.17	25	45	35	4	10	7	5.00
RED	65.6	gi|10835234	43	58	50.5		6	3	16.83	32	54	43	3	5	4	10.75
hSmu-1	57.5	gi|8922679	47	79	63	5	16	10.5	6.00	51	76	63.5	2	15	8.5	7.47
PPIL2	59.5	gi|7657473	22	26	24	7	14	10.5	2.29	16	22	19	17	14	15.5	1.23
hPRP2 (DDX16)	119.2	gi|4503293	38	12	25	35	27	31	0.81	17	14	15.5	20	33	26.5	0.58
hPRP4-Kinase	117.1	gi|89276756	19	34	26.5		43	21.5	1.23	6	34	20	5	42	23.5	0.85
THRAP3	108.6	gi|4827040	42	48	45	1	17	9	5.00	17	51	34	5	14	9.5	3.58
PABP1	70.5	gi|46367787	29	16	22.5	1	8	4.5	5.00	8	15	11.5	9	7	8	1.44

SKIV2L2	117.8	gi|39930353	18	9	13.5	3	13	8	1.69	6	8	7	15	11	13	0.54
PABPN1	32.6	gi|4758876	4	5	4.5	3	3	3	1.50	1	4	2.5	1	2	1.5	1.67
RNF113A	38.8	gi|5902158	9	1	5	7	4	5.5	0.91	6	1	3.5	3	4	3.5	1.00
NY-CO-10	53.8	gi|64276486	8	7	7.5		2	1	7.50	4	6	5	13	2	7.5	0.67
KIAA1604	105.5	gi|55749769	42	8	25	67	55	61	0.41	20	8	14	50	53	51.5	0.27
hsp27	22.8	gi|4504517	6	3	4.5	1	3	2	2.25	4	3	3.5	5	3	4	0.88
GCFC	104.7	gi|22035565		19	9.5	4	15	9.5	1.00	8	19	13.5		13	6.5	2.08
UBL5	8.5	gi|13236510	2	10	6				OSB	3	9	6				OSB
CCDC16	42	gi|49472814	22	3	12.5	6	10	8	1.56	10	3	6.5	5	9	7	0.93
CCDC12	19.2	gi|21389497	18	7	12.5		10	5	2.50	12	6	9	10	8	9	1.00
HsKin17	45.2	gi|13124883	18	10	14		1	0.5	28.00	13	8	10.5		1	0.5	21.00
Step 2 factors																
hPRP22	139.3	gi|4826690		7	3.5	129	169	149	0.02	4	9	6.5	97	160	128.5	0.05
hPRP18	39.9	gi|4506123				6	3	4.5	OSC				2	3	2.5	OSC
hPRP17	65.5	gi|7706657	19	21	20	73	52	62.5	0.32	11	20	15.5	44	47	45.5	0.34
hPRP16	140.5	gi|17999539				1	5	3	OSC		1	0.5	1	5	3	0.17
hSLU7	68.4	gi|27477111				31	53	42	OSC				31	50	40.5	OSC
Proteins recruited to C-complex																
Abstrakt	69.8	gi|21071032		3	1.5	71	94	82.5	0.02	1	2	1.5	75	89	82	0.02
GCIP p29	28.7	gi|46371998				28	21	24.5	OSC	2		1	25	20	22.5	0.04
DDX35	78.9	gi|20544129		7	3.5	11	40	25.5	0.14	2	5	3.5	28	36	32	0.11
Q9BRR8	103.3	gi|74732921				14	10	12	OSC		1	0.5	13	10	11.5	0.04
c19orf29 (NY-REN-24)	88.6	gi|126723149				37	61	49	OSC		1	0.5	20	56	38	0.01
PPIase-like 3b	18.6	gi|19557636				11	12	11.5	OSC				10	11	10.5	OSC
PPWD1	73.6	gi|24308049				24	54	39	OSC	1		0.5	31	50	40.5	0.01
MORG1	34.3	gi|153791298		1	0.5	19	3	11	0.05		1	0.5	11	3	7	0.07
FRG1	29.2	gi|4758404				16	1	8.5	OSC				8	3	5.5	OSC
NOSIP	33.2	gi|7705716				18	5	11.5	OSC				17	4	10.5	OSC
GPKOW	52.1	gi|15811782				33	8	20.5	OSC	3	1	2	7	8	7.5	0.27
C1orf55	39.3	gi|148664216				18	24	21	OSC				18	23	20.5	OSC
FAM32A	13.1	gi|7661696				11	6	8.5	OSC		1	0.5	6	5	5.5	0.09
RACK1 (GNB2L1)	35.1	gi|5174447				5		2.5	OSC		2	1	2		1	1.00
TIP-49	50.2	gi|4506753				1	8	4.5	OSC	1		0.5	1	3	2	0.25

Potential C-complex specific proteins																
PPIG	88.5	gi|42560244		2	1	22	14	18	0.06		2	1	4	13	8.5	0.12
FAM50A	40.1	gi|4758220				13	16	14.5	OSC	1		0.5	15	21	18	0.03
FAM50B	38.6	gi|6912326				8	12	10	OSC				5	14	9.5	OSC
C9orf78	33.7	gi|7706557				11	9	10	OSC				8	8	8	OSC
C10orf4	37.5	gi|24432067				20	4	12	OSC		1	0.5	7	4	5.5	0.09
CXorf56	25.6	gi|11545813				17	34	25.5	OSC		1	0.5	21	30	25.5	0.02
DGCR14	52.4	gi|13027630				5	4	4.5	OSC				18	6	12	OSC
CCDC130	44.7	gi|13540614				6	5	5.5	OSC				2	5	3.5	OSC
TOE1	56.4	gi|156564398				2	2	2	OSC							
NKAP	47	gi|13375676				7	13	10	OSC				3	11	7	OSC
ZCCHC10	18.4	gi|8923106				4	10	7	OSC				5	12	8.5	OSC
CDK10	35.4	gi|16950647					10	5	OSC					9	4.5	OSC
TTC14	88.2	gi|33457330					16	8	OSC				3	16	9.5	OSC
WDR70	73.2	gi|8922301					1	0.5	OSC				3	1	2	OSC
NFKBIL1 (IKBL)	43.1	gi|26787991				10		5	OSC	1		0.5	4	1	2.5	0.20
JUP	81.6	gi|12056468				2		1	OSC							
EJC/mRNP																
eIF4A3	46.9	gi|7661920	27	18	22.5	61	67	64	0.35	17	16	16.5	42	62	52	0.32
Magoh	17.2	gi|4505087		4	2		18	9	0.22	1	4	2.5	8	17	12.5	0.20
Y14	19.9	gi|4826972	4	2	3	7	8	7.5	0.40	4	2	3	5	8	6.5	0.46
Pinin	81.6	gi|33356174		11	5.5	9	3	6	0.92	8	9	8.5	2	2	2	4.25
RNPS1	34.2	gi|6857826		6	3	1	9	5	0.60		5	2.5	1	7	4	0.63
Acinus	151.8	gi|7662238	44	33	38.5	11	21	16	2.41	22	29	25.5	15	21	18	1.42
SAP18		gi|5032067	10	6	8	2	3	2.5	3.20	7	6	6.5	4	3	3.5	1.86
Aly/REF (THOC4)	26.9	gi|55770864		5	2.5	6	4	5	0.50	2	5	3.5	3	3	3	1.17
UAP56	49.1	gi|18375623	11	21	16	10	9	9.5	1.68	5	18	11.5	6	9	7.5	1.53
TREX																
THOC1	75.6	gi|154448890	12	5	8.5	9	6	7.5	1.13	9	5	7	7	7	7	1.00
THOC2	169.6	gi|125656165		2	1	14	3	8.5	0.12	3	2	2.5	10	4	7	0.36
THOC3	38.8	gi|14150171	7		3.5	7		3.5	1.00	2		1		1	0.5	2.00
KIAA0983 (THOC5)	78.4	gi|50959110		10	5	5	8	6.5	0.77	6	13	9.5	7	16	11.5	0.83
WDR58 (THOC6)	37.4	gi|31543164		2	1	13	2	7.5	0.13	1	3	2	4	2	3	0.67

pre-mRNA/mRNA binding proteins																
CBP20	18	gi|110349727	14	25	19.5	15	38	26.5	0.74	12	25	18.5	15	32	23.5	0.79
CBP80	91.8	gi|4505343	47	95	71	46	108	77	0.92	41	87	64	48	99	73.5	0.87
NF45	43	gi|24234747	12	10	11		2	1	11.00	10	10	10	4	2	3	3.33
ZC3H18	104	gi|31377595	28	4	16	5	4	4.5	3.56	8	3	5.5	5	3	4	1.38
YB-1	35.9	gi|34098946	10	15	12.5	30	8	19	0.66	4	15	9.5	7	8	7.5	1.27
ELG	38.9	gi|8923771	8	4	6	4	6	5	1.20	11	10	10.5	13	12	12.5	0.84
DDX3	73.3	gi|87196351	24	9	16.5		4	2	8.25	5	10	7.5		5	2.5	3.00
ASR2B	100	gi|33383233	31	20	25.5	9	20	14.5	1.76	22	19	20.5	12	18	15	1.37
BCLAF1	107.2	gi|7661958	25	34	29.5		13	6.5	4.54	8	33	20.5	2	11	6.5	3.15
DBPA	40.1	gi|20070160		1	0.5	7		3.5	0.14							
RBM7	30.5	gi|4503293		2	1	6	2	4	0.25		2	1	6	2	4	0.25
HSP70	70	gi|5123454	17	8	12.5		20	10	1.25							
Miscelleneous proteins																
BAG2	23.4	gi|4757834	10		5	11	3	7	0.71	3		1.5	6	3	4.5	0.33
RBBP6	197.2	gi|33620716		3	1.5		3	1.5	1.00	1	3	2	5	2	3.5	0.57
RBM42	50.3	gi|21359951		2	1		2	1	1.00		2	1		1	0.5	2.00
SR related proteins																
SRm160	102.5	gi|42542379		2	1	4	1	2.5	0.40	2	1	1.5	1	1	1	1.50
SRm300	300	gi|4759098	52		26	33	25	29	0.90	10		5	63	22	42.5	0.12
SR proteins																
SF2/ASF	27.8	gi|5902076	42	18	30	32	29	30.5	0.98	32	18	25	24	28	26	0.96
9G8	27.4	gi|72534660	57	76	66.5	39	61	50	1.33	48	68	58	23	54	38.5	1.51
SRp20	19.4	gi|4506901	15	18	16.5	4	6	5	3.30	12	23	17.5	12	11	11.5	1.52
SRp30c	25.5	gi|4506903	32	23	27.5	34	13	23.5	1.17	22	20	21	24	12	18	1.17
SRp38	31.3	gi|5730079	18	27	22.5	40	33	36.5	0.62	16	25	20.5	25	36	30.5	0.67
SRp40	31.3	gi|3929378	24	21	22.5	3	32	17.5	1.29	8	27	17.5	8	20	14	1.25
SRp46	31.2	gi|15055543					5	2.5	OSC	3	1	2		4	2	1.00
SRp55	39.6	gi|20127499	20	23	21.5	26	23	24.5	0.88	11	36	23.5	10	30	20	1.18
SRp75	56.8	gi|21361282		3	1.5	1	5	3	0.50							
SC35 (SFRS2)	25.5	gi|47271443				2		1	OSC							
hTra-2 alpha	32.7	gi|9558733	16	18	17	6	9	7.5	2.27	13	18	15.5	11	8	9.5	1.63
hTra-2 beta (SFRS10)	33.7	gi|4759098	21	32	26.5	34	35	34.5	0.77	16	29	22.5	12	29	20.5	1.10
hnRNP																
hnRNP A1	38.7	gi|4504445	11	19	15	1	1	1	15.00	5	17	11	1	1	1	11.00

hnRNP A3	39.6	gi|34740329		15	7.5		2	1	7.50	2	15	8.5		1	0.5	17.00
hnRNP AB	36	gi|12803583	5	7	6				OSB	2	6	4				
hnRNP A2/B1	37.4	gi|14043072	15	20	17.5		3	1.5	11.67	3	18	10.5		3	1.5	7.00
hnRNP C	33.3	gi|4758544	43	51	47	51	27	39	1.21	27	50	38.5	31	26	28.5	1.35
hnRNP D	38.4	gi|14110420		3	1.5		2	1	1.50	1	3	2		1	0.5	4.00
hnRNP F	45.7	gi|148470406		2	1		3	1.5	0.67		3	1.5	1	3	2	0.75
hnRNP G	47.4	gi|56699409	35	34	34.5	29	13	21	1.64	16	33	24.5	26	12	19	1.29
hnRNP G-T	42.7	gi|153252068		2	1				OSB							
hnRNP H1	49.1	gi|5031753		5	2.5		4	2	1.25		5	2.5	1	3	2	1.25
hnRNP H2	49.3	gi|74099697				8		4	OSC							
hnRNP H3	36.9	gi|14141157		3	1.5				OSB		4	2				OSB
hnRNP K	51	gi|14165435	17	12	14.5				OSB	12	12	12				OSB
hnRNP M	77.5	gi|14141152	31	32	31.5	11	14	12.5	2.52	10	29	19.5	1	12	6.5	3.00
hnRNP Q	69.6	gi|15809590	15	6	10.5		4	2	5.25	5	12	8.5	3	6	4.5	1.89
hnRNP R	70.9	gi|5031755		22	11		12	6	1.83	2	21	11.5	4	12	8	1.44
hnRNP U	90.6	gi|14141161	14	4	9				OSB	5	3	4	2	2	2	2.00
PCBP1	37.5	gi|5453854	13	42	27.5	17	7	12	2.29							
PCBP2	38.1	gi|14141166		11	5.5		7	3.5	1.57	20	32	26	11	8	9.5	2.74
RALY	32.5	gi|8051631	15	7	11	14	6	10	1.10	4	6	5	12	6	9	0.56



Supplementary Figure 1: Venn diagrams comparing the numbers of proteins identified in the biological replicates by SILAC and iTRAQ. (A) Venn diagram of proteins quantified in two independent biological replicates analyzed by SILAC. **(B)** Venn diagram of proteins quantified in two independent biological replicates analyzed by iTRAQ.

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