Supplemental Material to:

Anita Nag and Joan A. Steitz. Tri-snRNP-associated proteins interact with subunits of the TRAMP and nuclear exosome complexes, linking RNA decay and pre-mRNA splicing. RNA Biology 2012. 9(3); http://dx.doi.org/10.4161/rna.9.3.19431; http://www.landesbioscience.com/journals/rnabiology/article/19431

Supplemental Table S1

List of proteins identified by mass spectrometric analysis of Trf4-1 IP

Human Protein Identified	# Unique Peptides	NCBI Accession #	MW, kD
Heat shock cognate 71 kDa protein	20	HSP7C_HUMAN	70.85
Heat shock 70 kDa protein 1	20	HSP71_HUMAN	70.01
Tubulin beta-2C chain	14	TBB2C_HUMAN	49.79
Actin, cytoplasmic 1	13	ACTB_HUMAN	41.71
DNA polymerase sigma/ Trf4-1	13	POLS_HUMAN	59.84
Tubulin beta chain	9	TBB5_HUMAN	49.64
Tubulin alpha-1C chain	7	TBA1C_HUMAN	49.86
Tubulin alpha-1A chain	7	TBA1A_HUMAN	50.10
Actin, arotic smooth muscle	6	ACTA_HUMAN	41.98
Heterogeneous nuclear ribonucleoprotein M	6	HNRPM_HUMAN	77.46
Tubulin beta-4 chain	4	TBB4_HUMAN	49.55
Ubiquitin	3	UBIQ_HUMAN	8.56
Heterogeneous nuclear ribonucleoprotein H	2	HNRH_HUMAN	49.19
60S ribosomal protein L7a	2	RL7A_HUMAN	29.97
Methylosome protein 50	2	MEP50_HUMAN	36.70
Heat shock protein HSP 90-beta	2	HS90B_HUMAN	83.21
40S ribosomal protein S3	2	RS3_HUMAN	26.67
Positive; Score >60, expect <1e-4, good y-ion series			
60S ribosomal protein L11	1	RL11_HUMAN	20.24
78 kDa glucose-regulated protein	1	GRP78_HUMAN	72.28
40S ribosomal protein SA	1	RSSA_HUMAN	32.83
14-3-3 protein epsilon	1	1433E_HUMAN	29.15
Vimentin	1	VIME_HUMAN	53.61
60S ribosomal protein L4	1	RL4_HUMAN	47.66
Probable; Score >50, expect <0.01, good y-ion series			
Stress-70 protein	1	GRP75_HUMAN	73.63
U4/U6 small nuclear ribonucleoprotein Prp31	1	PRP31_HUMAN	55.42
Elongation factor 1-alpha 1	1	EF1A1_HUMAN	50.11
Possible; Score >30, expect <0.1, good y-ion series			
Component of gems 4	1	GEMI4_HUMAN	119.91
40S ribosomal protein S18	1	RS18_HUMAN	17.70
60S ribosomal protein L17	1	RL17_HUMAN	21.38
Heterogeneous nuclear ribonucleoproteins C1/C2	1	HNRPC_HUMAN	33.65
Heat shock protein HSP 90-alpha	1	HS90A_HUMAN	84.60
Protein KIAA1967	1	K1967_HUMAN	102.83
60S acidic ribosomal protein P0	1	RLA0_HUMAN	34.25
40S ribosomal protein S25	1	RS25_HUMAN	13.73

RNA-binding protein 10	1	RBM10_HUMAN	103.39

Supplemental Table S2

Oligonucleotide sequences for PCR amplification and mutation of reported plasmids

Oligonucleotide #	**Oligonucleotide sequence**
AN101	CCGCGCCCAAGCTTATGTCCCCTTGTCCTGAAGAAGCAGC
AN102	GGCGCGGGAAGCTTCCATTATCTGCTGAGGCTCACGGG
AN110	CGGCCGCTCGAGCTACAAGTAGAGGCTGGCAGCAAACACAATATCTC
AN189	CGCCGCGGATCCGCCACCATGTCTCTGGCAGATGAGCTCTTAGC
AN190	CGGCGGCTCGAGTCACTTGTCATCGTCGTCCTTGTAGTCGGTGGACATAAGGCCACTCTT
AN202	CCAAGCACCGCATCGCCGAGTATGTGGAGTCC
AN203	CCAAGCACCGCATCGCCGAGTATGTGGAGTCC
AN204	GCCCCACACCGGCGCCATCGCCCACAGTGACATCG
AN205	GCCCCACACCGGCGCCATCGCCCACAGTGACATCG
AN206	CGTATATGGCGGGAAGGCCGCCATCCGCGACC
AN207	GGTCGCGGATGGCGGCCTTCCCGCCATATACG
AN210	CGTGGCCTTCGCCCCACTCCAGGGCC
AN211	GGCCCTGGAGTGGGGCGAAGGCCACG
AN225	CGGCGGCTCGAGTCACTTGTCATCGTCGTCCTTGTAGTCCATGCTGGAGAAATACTTCTGGTTGGCC
AN226	CGGCGGCTCGAGTCACTTGTCATCGTCGTCCTTGTAGTCCTTCCCGCCATATACGACGCTCTGC
AN232	CCGGCCGCTCGAGCATGGCGGACGCATTCGGAGATGAGC
AN244	ATCGCTTCTCGGCCTTTTGGC
AN245	TGGTGCACCGTTCCTGGAGG
AN246	CGCTTCGGCAGCACATATAC
AN247	AGGGGCCATGCTAATCTTCT