

LEGENDS TO SUPPLEMENTAL FIGURES

Figure S1. Representative examples of protein quantitation data from tau1-441 interactome study. The graphs depict relative quantitations of peptides underlying the identifications of three proteins and depict data from three biological replicates of tau1-441-EGFP versus EGFP control interactomes. All relative quantitations are presented as ratios of enrichment, with the respective peptide levels observed in one of the three EGFP control affinity capture experiments serving as denominators in all direct comparisons. The plots exemplify proteins, which (A) served as the affinity capture bait (tau), (B) were robustly co-enriched (60S ribosomal protein L35) with the bait; or (C) purified unspecifically with both bait and control matrices (myosin-9).

Figure S2. Workflow of comparative interactome analysis of N- and C-terminal tau constructs, tau1-255-EGFP and tau256-441-EGFP. This study was based on four-plex iTRAQ-labeling and contained two additional negative controls, i.e., tau1-255-EGFP and EGFP, to facilitate the direct comparison of binders of full-length and truncated expression constructs.

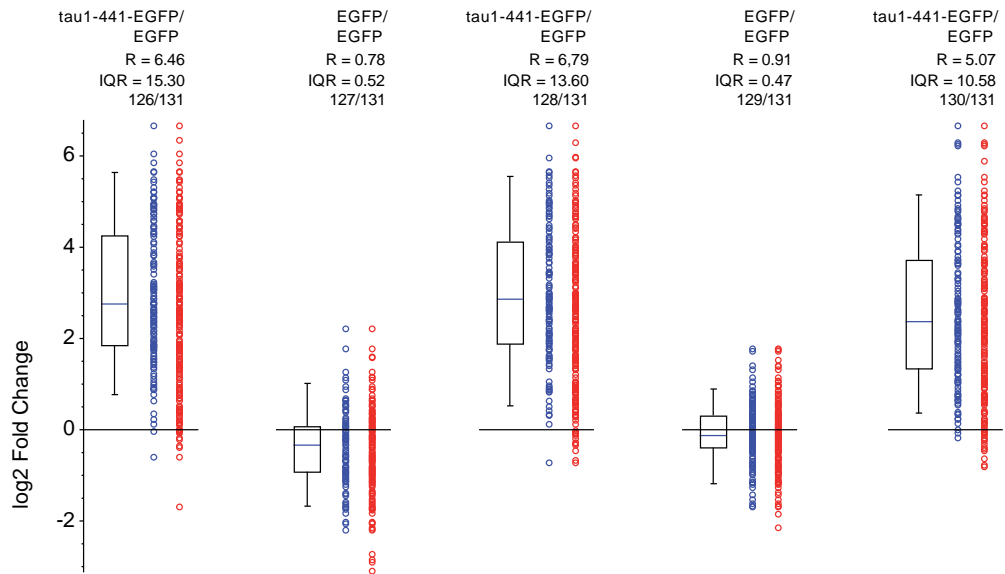
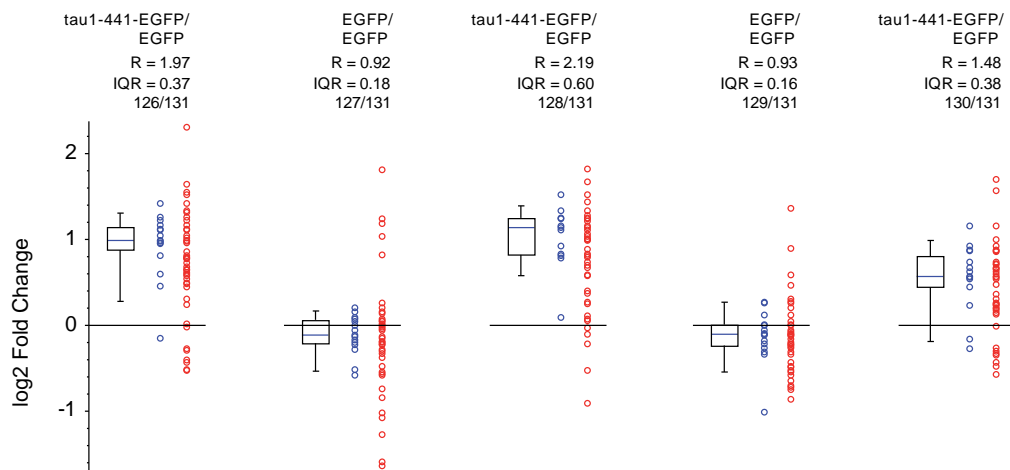
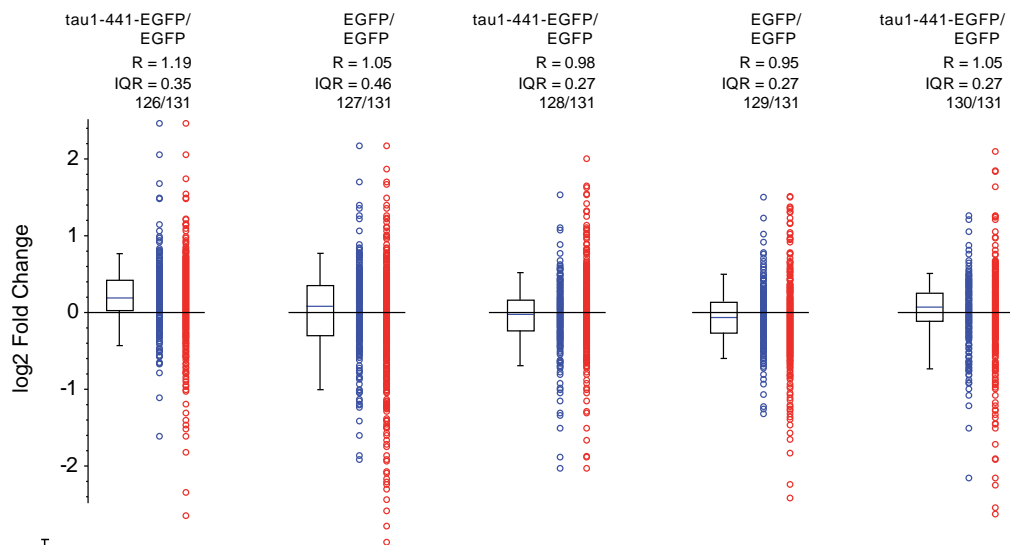
Figure S3. Representative examples of protein quantitation data observed in the four separate tau interactome experiments described in this report. Note that in contrast to Fig. S1, biological replicates are not shown in this panel. Instead, each subpanel depicts the enrichment ratios for a protein of interest in one of the interactome studies conducted (as indicated in the headers of individual data columns). Each of the subfigures A-C represents a detailed data representation of a single data row in Table S3. The plots depict relative peptide enrichment distributions of (A) Hsp90 and (B) STIP1, which bind tau in a manner that is facilitated by (Hsp90) or independent (STIP1) of the presence of RNA, involves preferential interaction with the C-terminal half of tau and exhibit reduced binding to tau1-441(P301L) tau.

(C) Graphs in this panel identified Fus as a candidate tau interactor, whose binding to tau is promoted in the absence of RNA, is directed toward the tau N-terminus and is slightly enhanced toward P301L mutant tau.

Figure S4. Examples of protein quantitation data in global proteome analysis.

(A) The identification and quantitation of tau confirmed the reproducible expression of this protein only in HEK-293 lysates, which had been transiently transfected with the tau1-255-EGFP expression construct. (B) Evidence of reproducibly increased cystatin B levels in cells that express tau1-255-EGFP. (C) Myosin-9 levels are not affected by tau1-255-EGFP or EGFP expression. Highly similar levels of this protein in all cell lysates are shown as an example to illustrate the technical reproducibility of the method. See **Fig. S1** for explanation of symbols.

Figure S5. Summary of experiments, data tables and raw data files generated in this study.

Figure S1**A** isoform Tau-F of microtubule-associated protein tau (IPI00025499.3)**B** 60S ribosomal protein L35 (IPI00412607.6)**C** isoform 1 of myosin-9 (IPI00019502.3)

○ Peptides not used for quantification
 ● Peptides used for quantification

R = Median Peptide Ratio (not in log2)
 IQR = Inter Quartile Range (not in log2)

Figure S2

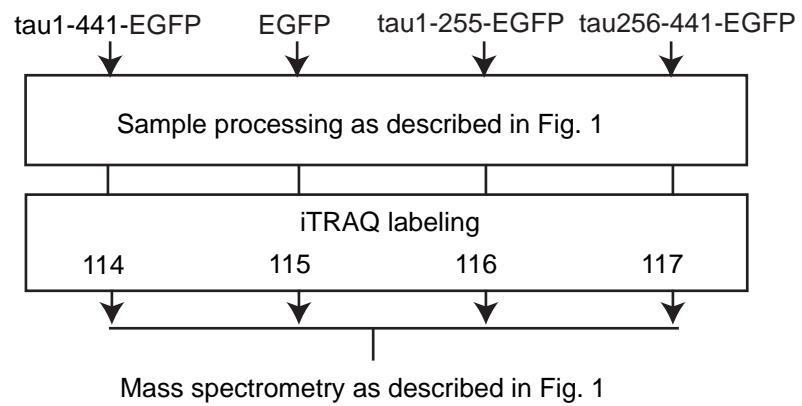
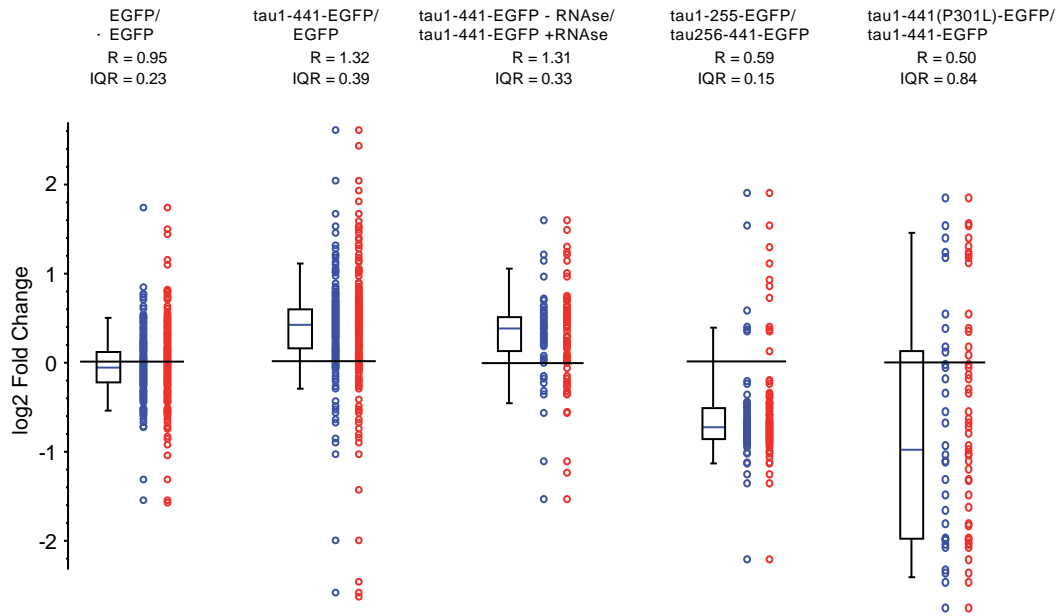
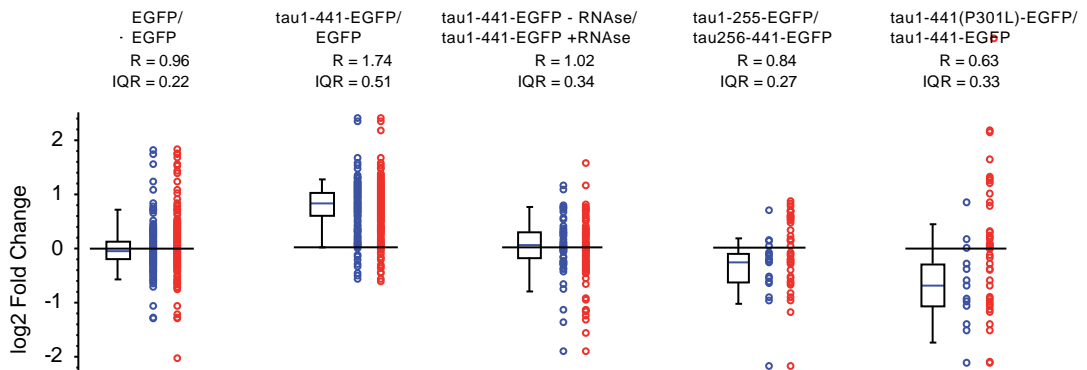


Figure S3

A Heat shock protein HSP 90-beta (IPI00414676.6)



B STIP1 protein (IPI00479946.4)



C RNA-binding protein FUS isoform 3 (IPI00645208.3)

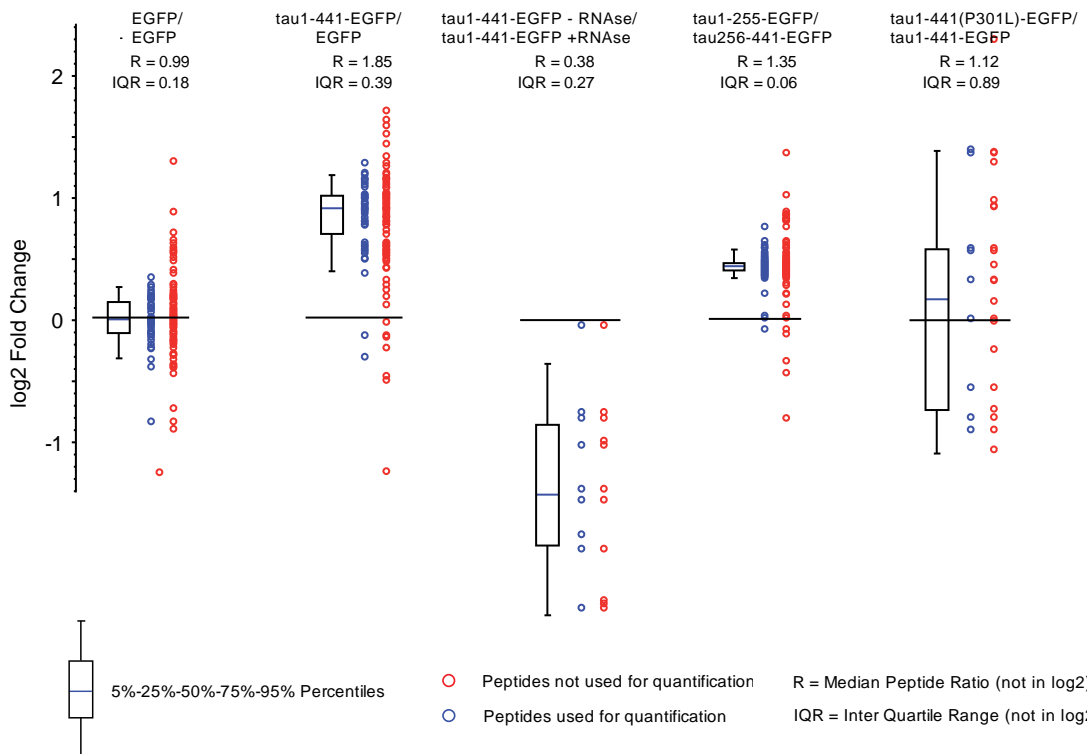


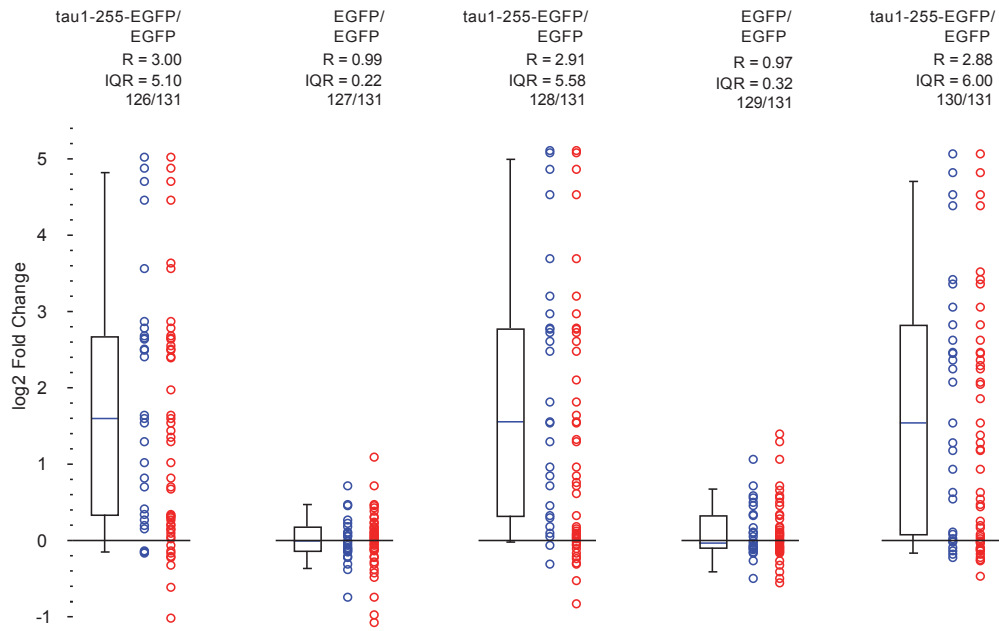
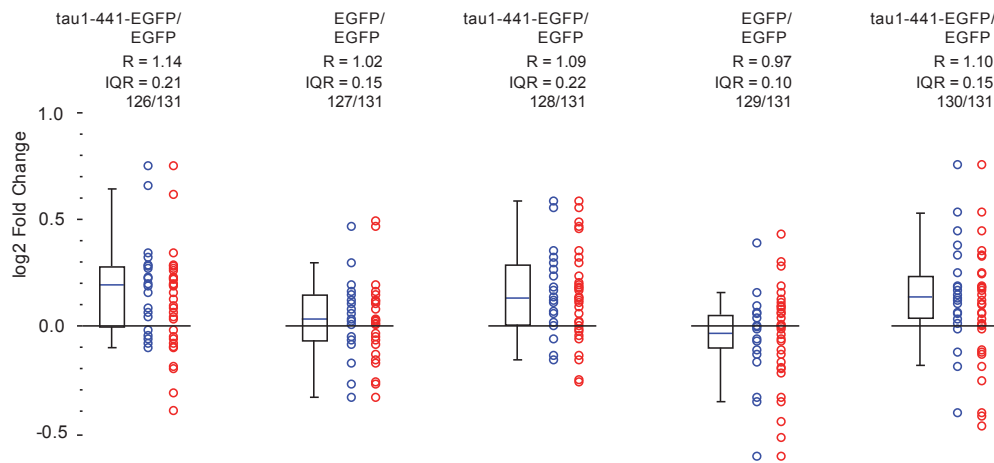
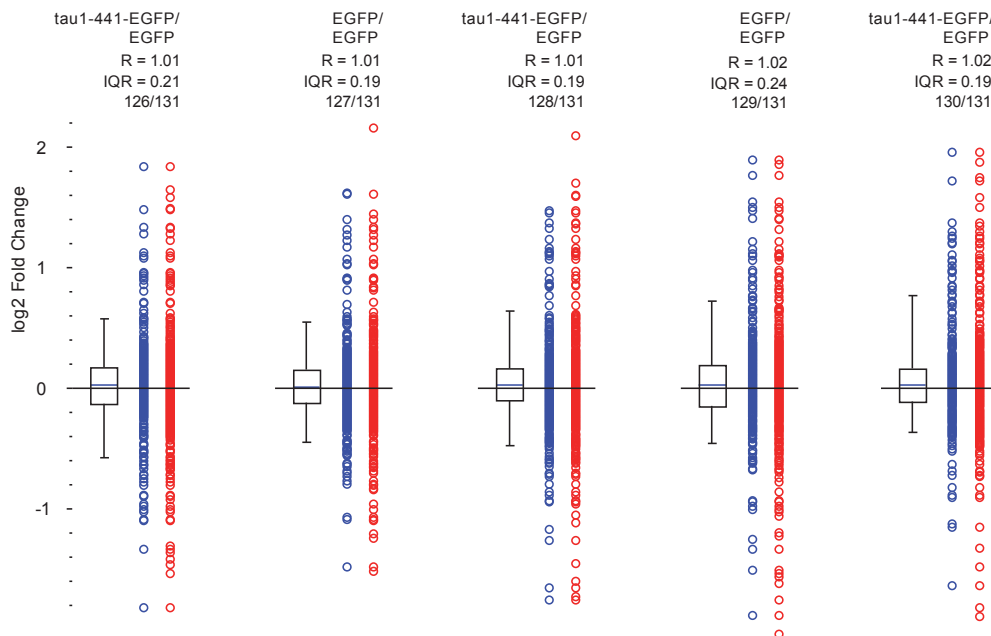
Figure S4**A** isoform Tau-C of microtubule-associated protein tau (IPI00220174.4)**B** Cystatin B (IPI00021828.1)**C** isoform 1 of myosin-9 (IPI00019502.3)

Figure S5. Summary of experiments, data tables and raw data files generated in this study

experiment number	host cell	comparison		affinity capture matrix	type of study	Suppl. Table (data column)
		samples	controls			
1	SH-SY5Y	tau1-441-EGFP	EGFP	GBP ^b	interactome	S1, S2, S3(1)
2	SH-SY5Y	tau1-255-EGFP	tau256-441-EGFP ¹	GBP	interactome	S3 (2)
3	SH-SY5Y	tau1-441-EGFP	tau1-441 + RNase	GBP	interactome	S3 (3)
4	SH-SY5Y	tau1-441(P301L)-EGFP	tau1-441-EGFP	GBP	interactome	S3 (4)
5	HEK293	tau1-255-EGFP	EGFP	N/A	global	S4

experiment number	isobaric label	isobaric label assignments				number of deposited raw data files ^c	
		samples	controls	additional controls ^a		C18	SCX
1	6-plex TMT	126, 128, 130	127, 129, 131	N/A	N/A	3	3
2	4-plex iTRAQ	116	117	114	115	3	2
3	6-plex TMT	126, 128, 130	127, 129, 131	N/A	N/A	3	3
4	6-plex TMT	127, 129, 131	126, 128, 130	N/A	N/A	3	-
5	6-plex TMT	126, 128, 130	127, 129, 131	N/A	N/A	3	3

^asee also **Fig. S2** for nature of additional controls

^bGFP binding protein (GBP)

^cC18 or SCX refers to ZipTip clean-up method applied to peptide mixtures before mass spectrometry analysis

Table S2: Tau candidate interactors comprising one or more RNA recognition motif (RRM) domains

Accession	Description	Symbol	Chromosome	Amino acids
IPI00909622.1	Cleavage stimulation factor, 3' pre-RNA, subunit 2	CSTF2	Xq22.1	553
IPI00290460.3	Eukaryotic translation initiation factor 3 subunit G	EIF3G	19p13.2	320
IPI00893431.2	Eukaryotic translation initiation factor 3, subunit B	EIF3B	7p22.3	738
IPI01022506.1	Eukaryotic translation initiation factor 4B isoform 1	EIF4B	12q13.13	616
IPI00260715.5	Fus-like protein, partial	FUS	16p11.2	528
IPI00011913.1	Heterogeneous nuclear ribonucleoprotein A0	HNRNPA0	5q31	305
IPI00909232.1	Heterogeneous nuclear ribonucleoprotein C	HNRNPC	14q11.2	288
IPI00027834.3	Heterogeneous nuclear ribonucleoprotein L isoform a	HNRNPL	19q13.2	589
IPI00383296.5	Heterogeneous nuclear ribonucleoprotein M isoform b	HNRNPM	19p13.2	691
IPI00018140.3	Heterogeneous nuclear ribonucleoprotein Q isoform 1	SYNCRIP	6q14-q15	623
IPI00414696.1	Heterogeneous nuclear ribonucleoproteins A2/B1 isoform A2	HNRNPA2B1	7p15	341
IPI00607677.1	HUD4	ELAVL4	1p34	383
IPI00658000.3	Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3	7p11	579
IPI00009032.1	Lupus La protein	SSB	2q31.1	408
IPI00789551.1	Matrin-3	MATR3	5q31.2	895
IPI00154590.6	MKI67 FHA domain-interacting nucleolar phosphoprotein	NIFK,MKI67IP	2q14.3	293
IPI00304596.3	Non-POU domain-containing octamer-binding protein isoform 1	NONO	Xq13.1	471
IPI00604620.3	Nucleolin	NCL	2q37.1	710
IPI00008524.1	Polyadenylate-binding protein 1	PABPC1	8q22.2-q23	636
IPI00642904.1	Polyadenylate-binding protein 4 isoform 1	PABPC4	1p34.2	660
IPI00179964.5	Polypyrimidine tract-binding protein 1 isoform c	PTBP1	19p13.3	531
IPI00012442.1	Ras GTPase-activating protein-binding protein 1	G3BP1	5q33.1	466
IPI00009057.2	Ras GTPase-activating protein-binding protein 2 isoform a	G3BP2	4q21.1	482
IPI00304692.1	RNA-binding motif protein, X chromosome isoform 1	RBMX	Xq26.3	391
IPI00010740.1	Splicing factor, proline- and glutamine-rich	SFPQ	1p34.3	707
IPI00971018.1	TAR DNA-binding protein 43	TARDBP	1p36.22	414
IPI00910884.1	Unnamed protein product	MSI2	17q22	324

IP0002639.1	Isomorf 1 of Protein LMS1 homolog B	72.216	8	2	32	223	1.242	25.0	14	1.156	22.7	4	1.620	14.8	9	1.542	9.4	2	385	42.0	9.69	
IP0064181.5	MARCKS-related protein 2	72.216	1	1	209	1.029	1.0	27	1.029	7.5	3	0.708	1.0	9	0.913	2.7	1.227	49.6	65	31.5	4.67	
IP0021930.7	Methylated-lysine rich C-tail subunit	66.676	1	10	16	295	1.361	22.7	47	1.815	25.4	5	1.815	8.7	7	1.651	56.2	24	332	31.5	4.45	
IP0080007.2	Microtubule-associated protein 8	66.676	9	7	174	952	1.709	34.5	85	0.785	47.1	25	0.831	187	63	1.352	39.4	31	2297	245.3	6.23	
IP0000864.4	Microtubule-associated protein 8B	62.164	9	7	174	952	1.709	34.5	85	0.785	47.1	25	0.831	187	63	1.352	39.4	31	2297	245.3	6.23	
IP0002113.1	Isomorf 2 of Microtubule-associated protein 8	75.086	1	1	84	662	1.710	35.1	73	0.940	55.9	21	1.241	171	55	1.550	33.5	30	979	102.8	5.47	
IP0001759.3	Microtubule-associated protein RP/EB family member 1	73.306	5	9	26	142	0.962	13.2	24	0.612	34.9	5	1.017	31	2	0.648	43.4	2	288	30.0	5.14	
IP0004630.4	Peptidyl-prolyl cis-trans isomerase B	74.148	1	13	23	142	1.164	18.1	19	0.543	39.1	1	1.070	9.2	4	0.881	124.0	1	216	23.7	7.91	
IP0002415.1	Proteinase K	85.276	4	18	31	168	1.268	23.3	39	0.727	123.9	21	2.088	6.8	107	2.288	6.8	27	242	23.7	25.2	
IP0001610.2	Poly(I:C)-binding protein 1	96.316	10	14	37	979	1.126	18.1	194	1.433	26.7	56	1.171	30.1	17	0.638	70.0	2	356	37.5	7.09	
IP0002581.1	Isomorf 1 of Poly(I:C)-binding protein 1	91.676	21	26	63	1133	1.063	26.3	145	0.967	36.5	65	1.039	16.3	145	0.967	36.5	65	636	70.0	9.50	
IP0005740.7	Isomorf 2 of Poly(I:C)-binding protein 1	87.166	16	67	58	1.508	25.3	50	1.012	10.1	2.028	12.9	1.039	12.6	65	0.797	27.0	11	611	65.5	6.92	
IP0017094.5	Isomorf 1 of Poly(I:C)-binding protein 1	90.906	10	18	39	868	1.654	14.1	58	1.007	29.0	32	1.039	12.6	23	0.526	84.6	7	931	57.2	11.7	
IP0000002.3	Protein subunit 7	79.276	1	9	15	258	1.414	17.9	19	0.313	4.3	0.073	37.3	50	0.682	57.4	14	129	146	16.6	8.88	
IP0005671.1	Protein subunit 6	82.956	2	11	120	245	1.530	17.7	19	1.642	5.0	0.376	9.1	23	1.030	113.0	1	129	146	16.6	8.88	
IP0000968.1	Pre-mRNA-processing factor 19	55.956	3	14	24	228	1.184	29.5	21	1.163	25.6	10	1.179	13.2	9	1.328	29.2	3	504	55.1	6.61	
IP0000968.4	Pre-mRNA-processing factor 19B	58.896	4	30	149	596	1.160	19.0	46	0.978	38.3	23	0.841	73.6	9	0.913	11.7	235	274.2	8.84	8.84	
IP0001972.2	Proteinase 3 subunit 1	86.146	4	12	25	256	1.374	7.7	44	1.152	25.1	14	0.779	31.4	43	1.011	68.7	2	267	30.9	6.11	
IP0021845.1	Isomorf 2 of 26S proteasome non-ATPase regulatory subunit 1	70.526	6	35	72	437	1.308	20.2	77	1.148	15.5	18	0.824	26.5	19	0.559	166.7	2	953	100.9	5.39	
IP0001228.3	26S proteasome non-ATPase regulatory subunit 2	73.466	9	30	63	437	1.364	16.1	86	1.235	20.3	17	0.868	15	0.467	159.0	2	908	100.9	5.39		
IP0001163.2	26S proteasome non-ATPase regulatory subunit 3	85.526	4	30	70	506	1.448	18.9	89	1.220	26.4	27	0.532	60.6	24	0.733	72.3	6	354	60.9	8.44	
IP0001839.4	26S protease regulatory subunit 7	84.726	5	14	25	217	1.224	20.1	89	1.221	25.4	0.652	54.5	10	0.841	89.9	3	377	40.7	4.79		
IP0001112.6	26S protease regulatory subunit 8	79.076	3	25	301	1.373	13.2	87	1.112	10.0	0.629	50.5	10	0.629	50.5	10	0.629	50.5	10	440	82.2	9.21
IP0001839.4	26S protease regulatory subunit 6A	79.956	10	22	36	361	1.436	12.7	76	1.218	18.6	17	0.465	32.9	16	0.535	104.2	2	439	49.2	5.24	
IP0002439.3	26S protease regulatory subunit 7	86.146	3	25	301	1.373	13.2	87	1.112	10.0	0.629	50.5	10	0.629	50.5	10	0.629	50.5	10	440	82.2	9.21
IP0007450.2	26S protease regulatory subunit 8 isomorf 2	74.476	8	19	42	239	1.313	12.0	55	1.447	27.2	9	0.438	51.0	9	0.837	18.0	3	423	47.5	4.68	
IP0001058.3	Proteinase 26S non-ATPase subunit 11 variant (Fragment)	82.026	2	15	48	213	1.409	13.0	31	1.408	43.1	7	0.500	97.3	4	0.844	147.7	2	456	52.9	7.65	
IP0001839.4	Isomorf 2 of 26S proteasome non-ATPase regulatory subunit 13	74.476	1	8	21	133	1.352	20.5	23	1.141	26.1	5	0.753	24.6	4	0.657	48.3	6	310	34.6	5.12	
IP0002482.1	Isomorf Long of Proteasome subunit alpha type 1	78.076	4	17	29	301	1.509	23.7	52	1.206	35.2	13	0.529	23.9	12	0.643	99.4	2	269	30.2	7.43	
IP0001242.4	Protein subunit alpha type 2	59.406	4	9	12	137	1.294	50.3	13	1.343	31.1	1	0.729	11.2	1	0.729	11.2	1	248	74.3	7.43	
IP0002800.1	Protein subunit beta type 2	58.716	4	4	12	83	1.530	23.9	15	1.509	26.9	2	1.502	57.8	4	0.853	91.6	2	201	22.8	7.02	
IP0001473.3	Isomorf 1 of Proteasome subunit alpha type 2	69.356	9	11	24	180	1.464	17.0	38	1.021	27.6	4	0.866	70.6	6	0.847	55.9	4	248	27.9	8.44	
IP0002312.3	Protein subunit beta type 2	64.896	7	12	19	142	1.429	18.9	17	1.429	18.9	17	1.429	18.9	17	1.429	18.9	17	277	63.1	9.44	
IP0000000.2	Isomorf Long of Double-stranded RNA-binding protein Staufen homolog 1	80.486	16	14	56	375	1.520	22.3	51	1.109	86.9	12	1.432	21.4	9	0.745	68.8	8	538	59.0	9.55	
IP00014481.2	Isomorf 2 of Double-stranded RNA-binding protein Staufen homolog 1	80.486	16	14	56	375	1.520	22.3	51	1.109	86.9	12	1.432	21.4	9	0.745	68.8	8	538	59.0	9.55	
IP0001268.2	CDNA FL27422, highly similar to RNA-binding protein, autoantigenic, transcript variant 1	65.136	1	1	26	146	1.313	15.6	11	1.558	11.1	1	1.385	10.1	1	0.911	60.1	1	476	52.2	5.43	
IP0004579.1	Cold inducible RNA-binding protein, isoform CMA_C	53.544	5	10	26	488	1.450	12.0	14	0.617	41.8	2	1.361	9.5	78	1.075	28.8	8	297	31.9	9.61	
IP0002430.1	Purative RNA-binding protein	59.636	1	6	16	89	1.574	14.7	9	0.936	121.9	2	1.502	70.8	6	1.014	28.8	1	157	17.2	8.91	
IP0000187.8	RNA-binding protein 28	57.076	18	1	16	136	1.364	47.8	6	1.146	6.1	1	1.146	6.1	1	1.146	6.1	1	749	72.9	9.22	
IP0008792.1	RNA-binding protein EVS isoform 3	35.426	9	9	34	345	1.864	20.2	38	0.446	60.1	9	1.299	25.6	17	1.355	27.5	8	655	68.3	9.33	
IP0004208.3	RNA-binding protein HUS isoform 3	45.986	7	7	32	516	1.864	12.9	42	0.376	58.4	10	1.351	11	1.009	1.122	36.8	11	522	53.2	9.36	
IP0002442.1	Ras GTPase-activating protein-binding protein 1	71.446	11	1	23	149	1.931	35.8	8	1.411	61.2	27	1.404	21	1.404	21	1.404	21	466	62.6	11.4	
IP0000684.3	Ras-related protein Rab-18	74.836	43	6	20	148	1.814	23.4	24	1.514	11.2	2	0.538	34.8	8	1.051	38.2	2	201	22.2	5.73	
IP00011169.1	Ras-related protein Rab-2A	77.836	8	3	19	2	1.382	19.2	13	1.791	15.1	4	1.138	20.4	3	1.006	266.1	2	212	23.5	6.54	
IP0001244.1	Uncharacterized protein	72.936	1	1	1	163	1.410	35.8	8	1.410	35.8	8	1.410	35.8	8	1.410	35.8	8	207	23.5	6.70	
IP0001169.1	Ras-related protein Rab-7a	74.886	7	14	20	204	1.352	19.2	30	1.591	5.0	2	0.538	34.8	8	1.051	50.2	7	207	23.5	6.70	
IP0000248.4	Isomorf 1 of RNA polymerase II-associated protein 3	70.086	3	31	55	445	1.542	17.3	90	0.896	57.7	21	1.023	27.7	15	0.675	69.8	10	665	75.7	6.84	
IP0002093.3	CDNA FL27422, highly similar to RNA polymerase II-associated protein 3	74.706	1	1	1	137	1.474	16.0	49	1.474	16.0	49	1.474	16.0	49	1.474	16.0	49	247	24.7	6.84	
IP0002117.4	Isomorf 1 of RuvB-like 1	84.656	5	23	39	307	1.420	13.6	70	1.195	26.3	13	0.782	26.4	26	0.442	6.5	4	456	50.2	6.42	
IP0000210.7	RuvB-2	80.956	3	24	44	351	1.478	19.8	77	1.541	16.2	11	0.698	29.9	13	0.888	36.0	7	463	51.1	5.64	
IP0001970.7	Isomorf 2 of Septin-1	53.756	1	1	1	111	1.609	11.1	1	1.058	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.8	463	41.5	6.60	
IP0001970.7	Isomorf 1 of Septin-1	81.446	18	20	32	345	1.361	26.0	70	0.842	14.4	12	0.828	15.8	18	0.508	48.4	6	361	41.5	6.60	
IP0002163.9	Isomorf 1 of Septin-6	85.556	8	5	34	279	1.502	16.7	22	0.943	22.9	5	0.956	14.8	13	0.792	21.8	2	427	48.6	8.81	
IP0001090.1	Uncharacterized protein	81.096	1	26	27	148	1.433	27.2	22	0.943	22.9	5	0.956	14.8	13	0.792	21.8	2	427	48.6	8.81	
IP0007461.1	Septin-9 isomorf 4	82.256	8																			

IP00550746.4	Nuclear migration protein nuuC	70.39%	4	16	32	243	1.380	16.9	39	1.296	45.2	4	0.744	38.4	9	0.797	107.6	7	331	38.2	5.38
IP00031812.3	Nucleic-acid-sensitive element binding protein 1	70.73%	5	9	30	2027	0.783	24.3	154	0.244	198.6	30	1.151	12.6	179	1.240	21.9	16	324	35.9	9.28
IP00216654.2	Isoform Beta of Nuclear and coiled-body phosphoprotein 1	49.51%	3	15	50	180	1.954	9.8	5	1.699	66.3	6	0.809	11.3	14	1.946	55.1	11	709	24.7	9.47
IP00604620.3	Nucleolin	79.58%	11	58	101	2519	1.628	18.8	102	0.659	55.8	53	1.103	6.7	623	1.726	18.0	48	710	76.6	4.70
IP00549246.4	Isoform 1 of Nucleophosmin	84.01%	5	23	33	1092	1.595	13.2	72	1.379	27.6	38	1.364	5.1	214	1.151	37.8	24	294	32.6	4.78
IP00941461.1	Nucleosome assembly protein 1-like 4	75.73%	15	17	30	389	1.228	14.3	105	0.860	28.1	7	0.729	37.2	5	0.869	52.2	4	375	42.8	4.69
IP00305092.7	Isoform 1 of Partner of Y14 and mago	86.70%	2	10	18	221	1.426	29.2	21	0.941	165.5	9	1.152	25.8	13	1.503	35.1	8	204	22.6	9.45
IP00709005.2	PEST proteolytic signal containing nuclear protein, isoform CRA_a	66.83%	3	6	19	122	1.369	25.1	20	1.472	24.8	6	1.321	14.8	3	0.869	5.7	3	199	20.9	8.27
IP00006167.1	Protein phosphatase 5G	55.13%	3	18	34	194	1.078	20.2	34	0.835	5.3	3	0.938	22.3	6	1.582	67.8	3	546	59.2	4.36
IP00470497.3	Isoform 2 of Plasminogen activator inhibitor 1 RNA-binding protein	72.14%	2	3	42	862	1.890	25.5	80	0.969	51.8	34	2.449	7.4	160	1.347	23.4	14	402	44.2	8.66
IP00214088.3	Isoform 1 of Pleckstrin	57.00%	12	37	206	925	0.817	27.8	68	1.544	37.3	21	2.028	6.5	15	0.816	54.3	2	4668	511.5	5.96
IP00409040.5	Poly (ADP-ribose) polymerase 1	71.10%	5	44	91	1234	1.170	19.7	137	0.792	46.9	32	1.179	18.7	7	1.128	42.1	4	1014	113.0	8.88
IP00739539.6	POE1 ankyrin domain family member F	61.77%	7	1	65	752	1.061	18.7	50	0.785	46.9	16	0.747	7.4	175	1.397	40.9	7	1075	121.4	6.20
IP00299000.5	Proliferation-associated protein 2G4	89.14%	7	25	38	778	1.078	36.0	69	0.970	132.1	46	2.026	7.2	147	1.218	24.1	19	394	41.8	9.56
IP00081761.5	Isoform 7 of Protein PRC2C	50.14%	11	41	152	608	1.486	31.2	59	1.181	32.9	24	1.411	56.6	7	1.743	41.1	4	2898	316.9	9.13
IP0046044.2	Protein RCC2	57.85%	1	14	33	192	1.361	19.7	21	0.727	72.2	10	1.023	20.3	16	1.243	65.7	4	522	56.0	8.78
IP00159072.3	regulator of differentiation 1 Isoform 2	45.43%	12	1	21	132	1.546	29.9	7	1.120	27.3	3	2.096	24.4	6	0.941	177.0	4	524	56.8	9.20
IP00399170.1	Isoform 2 of Regulator of nonsense transcripts 1	50.27%	2	27	63	317	1.313	35.7	43	1.152	30.0	18	1.782	26.1	6	0.825	56.7	2	1118	123.0	6.48
IP0017412.1	Isoform 1 of Replication factor C subunit 2	72.03%	3	9	23	126	1.272	11.7	16	1.652	28.6	5	0.950	8.5	6	0.804	144.3	2	354	39.1	6.44
IP00031521.1	Replication factor C subunit 3	36.18%	4	7	26	163	1.846	19.9	17	1.091	23.6	3	0.575	2.8	2	0.717	31.7	3	358	40.5	8.94
IP00902661.1	Isoform 5 of Rib. guanine nucleotide exchange factor 7	75.65%	8	9	67	489	1.147	21.0	105	1.012	55.9	7	0.582	30.2	13	1.776	134.1	4	731	82.5	8.84
IP00782592.3	Isoform 1 of Serine/arginine repetitive matrix protein 2	74.64%	5	15	280	794	0.989	13.1	7	0.176	4.0	5	0.991	83.4	3	1.716	38.1	4	2752	299.4	12.06
IP00102041.1	Serine/arginine-rich splicing factor 3	68.95%	4	6	17	251	1.888	18.7	14	0.612	54.5	4	1.829	8.6	28	1.144	84.4	3	164	19.3	11.65
IP00554737.3	Serine/threonine protein phosphatase 2A 65 kDa regulatory subunit A alpha Isoform	75.38%	9	17	46	298	1.024	18.3	85	1.912	23.1	17	0.579	31.2	18	0.773	21.5	3	589	65.3	5.11
IP00848328.1	Similar to Peroxisomal enoyl-coenzyme A hydratase-like protein	69.69%	4	1	23	94	1.476	17.8	10	1.004	5.7	2	1.555	26.9	5	1.144	9.2	3	320	35.9	7.42
IP00794202.5	Similar to Y8-1 protein	44.51%	1	1	17	391	0.768	22.3	20	0.706	42.2	9	1.117	11.5	94	1.158	14.9	4	346	38.4	10.07
IP00217961.1	Small nuclear ribonucleoprotein Sm D2	79.66%	2	8	14	110	1.324	21.5	17	1.175	1.8	3	1.091	10.5	18	0.914	10.1	2	118	13.5	9.95
IP00841765.1	Isoform 3 of Spectrin alpha chain, brain	90.46%	3	2	287	2956	1.292	19.0	724	0.986	30.7	55	0.764	32.1	24	0.961	54.8	35	2452	282.1	5.34
IP00140420.4	Staphylococcal nuclease domain-containing protein 1	73.63%	4	32	79	585	1.369	14.8	66	1.375	28.4	16	2.061	19.1	59	0.749	61.8	11	910	101.9	7.17
IP00411559.2	Isoform 1 of Structural maintenance of chromosomes protein 4	68.56%	10	37	119	645	1.217	18.8	64	1.426	30.8	31	0.824	31.1	9	1.027	62.7	16	1208	147.3	6.79
IP00219299.4	Talin-2	62.90%	4	16	152	608	1.051	16.1	37	1.566	31.2	5	1.990	1.7	7	1.138	1.2	3	2542	271.4	5.57
IP00305692.5	Thioredoxin-like protein 1	62.98%	2	12	16	173	1.284	34.9	40	1.192	19.1	11	0.612	17.6	9	1.203	18.3	2	289	32.2	4.96
IP00381461.5	Isoform 1 of Thymocyte nuclear protein 1	88.00%	3	6	24	97	1.456	47.4	10	0.880	117.0	2	1.699	15.7	5	1.216	71.8	3	225	25.7	9.25
IP00104050.3	Thyroid hormone receptor-associated protein 3	66.70%	2	11	96	312	1.708	32.8	12	3.448	24.3	8	0.726	32.1	10	0.768	27.8	3	955	108.6	10.15
IP00001159.1	Transcriptional activator GCN1	71.43%	1	79	199	865	1.178	18.7	68	2.026	65.1	56	1.491	24.5	54	1.629	37.5	1	2671	292.6	7.47
IP00815712.2	Uncharacterized protein	61.84%	10	33	119	721	1.424	30.9	27	1.264	81.8	18	0.771	36.1	22	1.264	99.1	31	1526	156.0	8.97
IP00018434.1	Isoform 1 of Tumor susceptibility gene 101 protein	60.00%	3	13	30	206	1.441	11.0	43	1.289	16.1	6	0.447	80.9	4	1.547	65.1	2	390	43.9	6.46
IP00514689.2	Uncharacterized protein	74.75%	2	1	29	232	1.242	25.0	16	1.321	4.8	3	1.529	26.7	9	0.842	18.9	3	305	33.0	9.89
IP00031526.3	Uncharacterized protein C1orf43	50.57%	1	5	13	82	1.399	16.8	8	1.148	57.1	3	0.956	20.6	5	0.852	127.6	2	176	18.4	9.44
IP00031651.1	Uncharacterized protein C1orf50	56.70%	4	7	10	133	0.611	21.9	19	0.646	60.6	9	1.120	31.1	11	1.246	34.3	5	194	22.1	9.64
IP00107104.1	UPF3B8 protein Ciof26	68.67%	2	14	22	124	1.398	18.2	30	1.195	23.9	4	0.779	13.3	2	0.497	60.9	4	233	26.0	4.79
IP00011997.4	Isoform 1 of UPF048 protein Ciof33	84.28%	2	8	20	139	1.321	34.3	5	0.934	38.0	32	0.938	13.5	5	0.921	2.1	3	229	25.0	9.95
IP00006980.1	UPF058 protein C1orf166	86.07%	6	17	25	272	1.698	13.5	42	1.152	29.5	15	1.355	26.5	32	1.635	200.5	2	244	28.1	6.65
IP00412244.2	WD repeat-containing protein 11	58.88%	2	19	65	285	1.163	22.8	41	1.278	18.0	10	1.024	14.1	3	0.793	60.9	2	1224	136.6	6.92
IP00910815.2	WNA FLJ6104, highly similar to WW domain-binding protein 11	52.88%	3	17	42	229	1.468	31.2	23	0.819	24.0	5	1.179	21.8	14	0.618	114.6	3	607	66.8	8.07
IP00250153.8	Y-box binding protein 2	69.23%	2	2	21	238	1.734	26.4	26	0.706	42.2	5	1.051	5.8	62	1.271	14.9	2	364	38.5	10.80
IP00306043.1	Isoform 1 of YTH domain family protein 2	45.60%	5	12	33	235	1.308	25.0	31	1.073	45.1	8	2.148	8.5	10	1.158	165.4	2	579	62.3	8.79
IP01010975.1	Uncharacterized protein	52.81%	6	10	32	147	1.598	9.9	11	0.641	116.9	9	1.181	13.5	3	1.556	65.1	3	392	44.9	7.36
IP00218866.2	Isoform 2 of Zinc finger Ran-binding domain-containing protein 2	73.13%	2	7	31	174	1.067	48.7	5	1.937	7.2	2	1.429	147.3	4	1.283	17.0	3	320	36.3	9.76

