

Supplementary Table S1: Factors identified in primary screen for inhibitors of poly-(A⁺) export

Gene	GO	Function(s)	Human Homolog
Bx42	PE	Splicing factor, associates with snRNP U5 components, also involved in transcriptional regulation	SNW1
Cap-G	CM	Condensin subunit, mitotic chromosome condensation	NCAPG
Cas	NT	Nuclear protein transport, Importin- α 3 export factor	CSE1L
CG10059/MAGE*	U	Unknown	MAGE; NDNL2
CG11198/ACC1	O	Acetyl Co-A carboxylase	ACAC
CG12236*	U	Unknown	ZNF295
CG14641	PE	Splicing factor, spliceosome component	RBM22
CG14701	U	Unknown	ZCLS2; DPH3
CG18591	PE	Splicing factor, snRNP component	SNRPE
CG2063	U	Unknown	SAP30BP
CG2685	U	Unknown	WBP11
CG2807	PE	Splicing factor, snRNP U2 component	SF3B1
CG2921*	U	Unknown	C6orf211
CG30376	U	Unknown	-
CG31126	U	Unknown	BOLA1
CG32267	U	Unknown	-
CG5451*	U	Unknown	SMU1
CG5931	PE	Splicing factor, DEAD-box RNA helicase	ASCC3L1
CG6694	U	Unknown	ZC3H3
CG7214	U	Unknown	-
CG7351/dmPCID2	O	Immune response, TNF family member protein, phospholipase 2A activity	PCID2
CycD	CM	Cell cycle control, G1 cyclin	CCND2
CycE	CM	Cell cycle control, G1/S transition	CCNE1
DebB	PE	Splicing factor, snRNP component	SNRPF
emb	NT	Nuclear protein transport, Importin- β 3 import factor	XPO1
Fs*	O	Follistatin, inhibitor of activin, affects growth factor signalling	FST
Hel25E/UAP56	PE	mRNA splicing and export factor, DEAD-box RNA helicase	BAT1
Hpr1	PE	Component of the TREX complex, couples transcription to mRNA splicing and export	THOC1
Karybeta3	NT	Nuclear protein transport, Importin- β 3 import factor	RanBP5
l(1)10Bb	U	Unknown	EDG2
lig	O	Required for insect copulation, molecular function unknown	UBAP2
Mtr3	PE	Exosome component, 3'-5' exoribonuclease activity	EXOSC6
Nedd4	O	Ubiquitin E3 ligase	NEDD4
noi	PE	Splicing factor, snRNP U2 component	SP3A3; SAP61; SF3a60
Nup153	NT	Nuclear pore complex component	NUP153
Nup154	NT	Nuclear pore complex component	NUP155
Nup358	NT	Nuclear pore complex component	NUP358; RanBP2
Nup98	NT	Nuclear pore complex component	NUP98
Nxt1/p15	PE	mRNA export factor, as a heterodimer with sbr/Nxf1	NXT1
Pabp2	PE	Nuclear mRNA polyadenylation factor	PABPN1
pcx	O	Membrane-associated protein involved in neurogenesis, molecular function unknown	PCNX
Pitslre	CM	Cdc2-related Cyclin-dependent kinase	CDC2L1; CDK11
pum*	O	Translational repression of specific mRNA targets involved in the growth, function and morphology of neurons	PUM1
Rae1	CM	G1 phase regulator, participates in cell cycle progression	RAE1
ran*	NT	Nuclear protein transport, GTP-dependent	RAN
RnrS	O	Ribonucleotide reductase, small subunit, nucleotide biosynthesis	RRM2
RplI215	O	RNA polymerase II subunit, 215 kDa	POLR2A; RBP1
RpL12	RP	Ribosomal protein, large subunit	RPL12
RpL18	RP	Ribosomal protein, large subunit	RPL18
RpL22	RP	Ribosomal protein, large subunit	RPL22
RpL36	RP	Ribosomal protein, large subunit	RPL36
RpL7	RP	Ribosomal protein, large subunit	RPL7
RpLP0	RP	Ribosomal protein, large subunit	RPLP0
RpS14b	RP	Ribosomal protein, small subunit	RPS14
RpS16*	RP	Ribosomal protein, small subunit	RPS16
RpS24	RP	Ribosomal protein, small subunit	RPS24
RpS26*	RP	Ribosomal protein, small subunit	RPS26
RpS3A	RP	Ribosomal protein, small subunit	RPS3A
RpS4	RP	Ribosomal protein, small subunit	RPS4X; CCG2; SCAR
Rrp6	PE	Exosome component, 3'-5' exonuclease activity	EXOSC10; RRP6
sbr/NXF1	PE	mRNA export factor, as a heterodimer with Nxt1/p15	NXF1/TAP
sip1	O	Septin interacting protein, molecular function uncertain	C3orf10; MDS207; HSPC300
SmD3	PE	Splicing factor, snRNP component	SNRPD3; SMD3
Socs36E*	O	Suppressor of cytokine signalling, JAK/STAT pathway	SOCS1
Ssrp	PE	Single-stranded RNA/DNA binding protein, regulation of chromatin structure	SSRP1; FACT
stg	CM	Cdc25, regulation of cell cycle, G2/M transition	CDC25A
swm	CM	Required for entry into S-phase, molecular function unknown	RBM26*
synaptogyrin*	O	Synaptic vesicle transport in neurons	SYNGR1
Tho2	PE	Component of the TREX complex, couples transcription to mRNA splicing and export	THOC2
tsr/Cofilin	CM	Actin binding protein, involved in cytokinesis, centrosome migration and contractile ring formation	CFL2
U2A	PE	Splicing factors, snRNP U2 component	SNRPA1
xmas-2	U	Unknown	MCM3AP; GANP; MAP80

Gene Ontology (GO) categories: CM - cell cycle and mitosis; PE - mRNA processing and export; NT - nuclear transport; RP - ribosomal protein; O - other; U - unknown.

* <50% penetrance of nuclear accumulation phenotype

All human homologs were derived from the eukaryotic Orthology database (http://www.sanger.ac.uk/PostGenomics/S_pombe/YOBY/index.shtml) or Homologene[®] from NCBI (<http://www.ncbi.nlm.nih.gov/Homologene>).

Supplementary Table S2: A comparison of mRNA export factor requirements in *S. cerevisiae* and *Drosophila*

<i>S.cerevisiae</i> mRNA export factor	<i>Drosophila</i> Homolog	<i>Drosophila</i> gene result in mRNA export screen	Identity (%)	Similarity (%)	Gaps (%)	Score [†]
Arg82	CG10082	-	12.8	19.8	69.2	396
Cdc31	CG31802	-	40.2	57.2	21.1	341
Dbp5	DBP80	-	43.8	62.5	10.1	1011
Gle1	CG14749	-	22.5	36.2	44	459
Lrp1	CG8928	-	97.8	97.8	2.2	890
Mtr4	l(2)35Df	-	50	68.4	10.5	2864
Mtr10	Trn-SR	-	26.7	43.7	26	994
Nab2	CG5720	-	11.6	18.3	70	405
Npl3	SRp55	-	18.7	26.8	52.8	298.5
Nup133	Nup133	-	21.7	35.6	39.7	721.5
Nup159	Nup214	-	21.2	31.9	46.5	867
Nup49	Nup58	-	24.4	36.9	45.5	402.5
Pap1	hrg/PAP	-	33.2	47.8	31.9	1121
Pcf11	l(2)K08015	-	9.7	15.4	73.7	433.5
Prp20	Bj1	-	26.3	37.5	42.4	598
Rna1	RanGAP	-	23.2	37.9	40.3	521
Rna14	su(f)	-	24.8	41.1	33.5	716.5
Rna15	CstF-64	-	23.1	38.1	42.5	333
Sus1	e(y)2	-	30.3	50.5	20.2	132.5
Tom1	CG8184	-	21.8	34.1	46.8	2881.5
Yra1	REF (Aly)	-	28.8	43.4	29.2	259.5
Acc1	dmAcc1 (CG11198)	+	40.8	57	21.3	5095.5
Crm1	emb	+	43.4	63.8	8.8	2431
Gle2	Rae1	+	41.8	56.7	16.8	825
Gsp1	Ran	+*	76.8	88.2	2.3	930
Hpr1	Hpr1	+	21.4	36.4	42.2	448.5
Mex67	sbr (dmNXF1)	+	24.1	40.5	33.4	533.5
Mtr2	Nxt1 (p15)	+	19.5	29.5	55.9	82.5
Mtr3	Mtr3	+	20.1	30.1	48	160.5
Nup1	Nup153	+	21.4	29	56	995.5
Nup145	Nup98	+	22.9	34.2	44.9	1339.5
Nup157	Nup154	+	19.8	31.2	51.4	858
Pse1	Kary-beta 3 (CG1059)	+	32.6	50.6	19.3	1599
Rrp6	Rrp6	+	28	48.9	31.8	1075.5
Rsp5	Nedd4	+	39.9	54.9	21	1702.5
Sac3	Xmas-2	+	22.7	36.1	40.5	943.5
Sub2	Hel25E (dmUAP56)	+	60.3	75.9	6	1422
Tho2	Tho2	+	22.9	37.9	37.9	1207.5
Thp1	CG7351	+	22.9	37	40.5	317
Apq12	none found	n/a				
Mft1	none found	n/a				
Nup116	none found	n/a				
Nup120	none found	n/a				
Nup42	none found	n/a				
Slx9	none found	n/a				

+ >50% penetrance of nuclear poly(A⁺) RNA accumulation phenotype

+* <50% penetrance of nuclear poly(A⁺) RNA accumulation phenotype

- no nuclear poly(A⁺) RNA accumulation phenotype

n/a not applicable

[†] Score was determined by BLOSUM62 matrix with a Gap penalty = 5.0 and Extend penalty = 0.5.

Totals: 45 *S. cerevisiae* mRNA export factors, 18 positive *Drosophila* homologs