Supplementary Materials

Supplementary Methods

Phylogenetic analysis

43 amino acid sequences of Dis3, Dis3L and Dis3L2 proteins, including the SPAC2C4.07c gene product, used in the phylogenetic analyses, were obtained from NCBI Entrez and the Genome Portal of the Department of Energy Joint Genome Institute (Grigoriev et al, 2012) and are described in Supplementary Table 3.

CLANS (Frickey & Lupas, 2004) was used to visualize the relationships between different Dis3 proteins according to their pairwise sequence similarities with P-value cutoff at 10^{-10}.

Sequences were aligned using SeaView (Gouy et al, 2010). To estimate phylogenetic relationships the protein sequences were analysed using the Neighbour Joining (NJ), Maximum Parsimony (MP) and Bayesian inference (BI) methods. NJ analysis was performed using BioNJ (Gascuel, 1997) with the Kimura or Poisson distance and 1000 bootstrap replicates. For MP analysis PAUP* (Swofford, 2003) version 4.0b10 was used, with 1000 bootstrap replicates to assess the reliability of nodes. Consensus tree (50%) with bootstrap support values was calculated using the SumTrees program of the DendroPy package version 3.12.0 (Sukumaran & Holder, 2010). Bayesian inference analysis was performed using MrBayes version 3.1.2 (Ronquist & Huelsenbeck, 2003) with 500 000 generations of each MCMC search sampled every 10 generations, and mixed fixed-rate models. Burnin values corresponded to 25% of the samples. Trees were visualized using Dendroscope (Huson et al, 2007).

Microarray analysis

Yeasts were grown up to early exponential phase at YES media and total RNA was extracted as described. The quality was assessed with a BioAnalyzer (Agilent Technology). RNA was processed for use on GeneChip Yeast Genome 2.0 Array from Affymetrix, according to the manufacturer's protocol. Three independent biological samples were analysed for each strain. Hybridization, scanning and detection procedures were done at the Genomics Unit of the Instituto Gulbenkian de Ciência.

Subsequent exploration, normalization, summarization and analyses of the generated Affymetrix CEL files were performed using R free statistical software (http://cran.r-project.org/) and its associated tool for high-throughput genomic data, Bioconductor (http://www.bioconductor.org/).

The reliability of the data set, before and after normalization, was estimated through its statistical exploration. For each strain, the summarized probe set intensities were calculated using the Robust MultiArray Averaging (RMA) method (Bolstad et al, 2003; Irizarry et al, 2003). The empirical Bayes statistics was used to analyze the data because it provides a robust estimate of variance for each gene. It indeed assumes that genes expressed at similar levels exhibit similar variance which leads to the smoothing of standard errors associated to the fold-change logs (Hatfield et al, 2003). The multiple testing issue was furthermore taken into account through the calculation of the False Discovery Rate (FDR) according to Benjamini-Hochberg method (Benjamini et al, 2001).

pFA6a TAP Kan MX6 plasmid construction

GFP sequence was removed from the pFA6a GFP kan MX6 vector using restriction enzymes PacI AscI (Fermentas). The TAP tag sequence was then cloned into the plasmid using SLIC method according to the protocol (Li & Elledge, 2007). TAP tag sequence was amplified using pJL72 vector template. Primers used are listed in Supplementary Table 2.

Dis3L2 protein purification

Proteins were expressed in BL(21) pRIL cells grown in full media at 37°C until OD_{600} 0.6 and then expression was induced for overnight at 20°C, subsequently cells were harvested, resuspended in lysis buffer (300mM NaCl, 1mMDTT, 50mM Phosphate buffer pH 7) and lysed using French press. Lysates were clarified by ultracentrifugation and protein purification was performed using GST-trap column according to manufacturer's instructions (GE Healthcare). The proteins were additionally purified using cation exchange column (HiTrap SP HP) according to manufacturer's instructions (GE Healthcare). After purification the proteins were concentrated to about 100 µg/µl using viva spin 500 columns (Sartorius stedim). The concentration of proteins was monitored using Bradford method and SDS-PAGE gels. Protein solutions were finally diluted until 50% in glycerol and kept at -80°C.

Substrate labeling

For all assays described in the text HPLC, purified RNA or DNA oligonucleotides were used (http://www.stabvida.net/). Oligonucleotides were 5' labeled with radioactive phosphate using PNK (Fermentas) and γP^{32}ATP and the substrate purified using G-50 columns (GE Healthcare). Substrates were then added to the reactions directly or supplemented with a known concentration of the non-labeled oligonucleotide. To create double-stranded substrates a complementary non-labeled DNA oligonucleotide was mixed with the radioactive oligo in a 2:1 molar ratio, samples were then denatured and cooled down slowly for annealing. Integrity of the double-stranded substrates was checked using native acrylamide gels (Malecki et al, 2010).

For the synthesis of the internally labeled substrate, in vitro transcription was carried out using the purified PCR product as template in the presence of an excess of [32P]-α-UTP over unlabeled UTP with 'Riboprobe in vitro Transcription System' (Promega) and T7 RNA polymerase. Radioactive transcripts were purified by electrophoresis on an denaturing polyacrylamide gel. The gel slice was crushed and the RNA eluted with elution buffer (3 M ammonium acetate pH 5.2, 1mM EDTA, 2.5% (v/v) phenol pH 4.3), overnight at room temperature. The RNA was ethanol precipitated and resuspended in RNase free water.

RNA isolation

Cells were thawed on ice, resuspended in the cold AES buffer (0.5 % SDS, 50mM NaAc pH 5.2, 10mM EDTA) and then transferred to the tubes containing phenol solution and glass beads (Sigma 425-600 µm). Cells were lysed in phenol using FastPrep-24 equipment (MP Biomedicals) – 3 times maximum speed for 25 s. Subsequently the solution was incubated in 65°C for 30 min with vortex every 10 min, than centrifuged and aqueous fraction was transferred to the fresh tube with phenol. Solution was vortex for 5 min, centrifuged and the aqueous fraction was transferred to the fresh tube with chlorophorm: isoamyl alcohol solution (24:1). Solution was vortex for 5 min, centrifuged and aqueous fraction was transferred to the fresh tube. Subsequently NaAc (pH 5.3) was added to 300 mM and RNA was precipitated with ethanol.

Supplementary Figures

Supplementary Figure 1

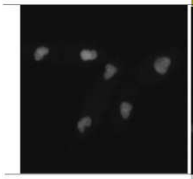
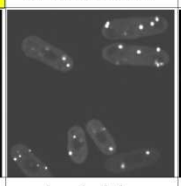
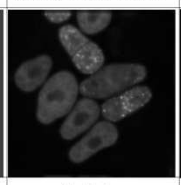
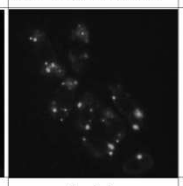
SPBC26H8.10	SPAC2C4.07c	SPBC609.01	SPCC16C4.09	SPCC23B6.06	systematic name
					localisation of overexpressed GFP fusion (data from RIKEN www.riken.jp/SPD/)
inviable	viable	inviable	viable	viable	deletion phenotype
Dis3	-	-	Ssd1	Dss1	*S. cerevisiae* orthologs
yes	yes	no	no	yes	conservation of exoribonucleolytic active site

Figure S1 Listed *S. pombe* genes that encode proteins with RNase II/R domain, with localization data from (Matsuyama et al, 2006). Phenotype and budding yeast homologue information from Pombase (http://www.pombase.org/) (Wood et al, 2012).

Supplementary Figure 2

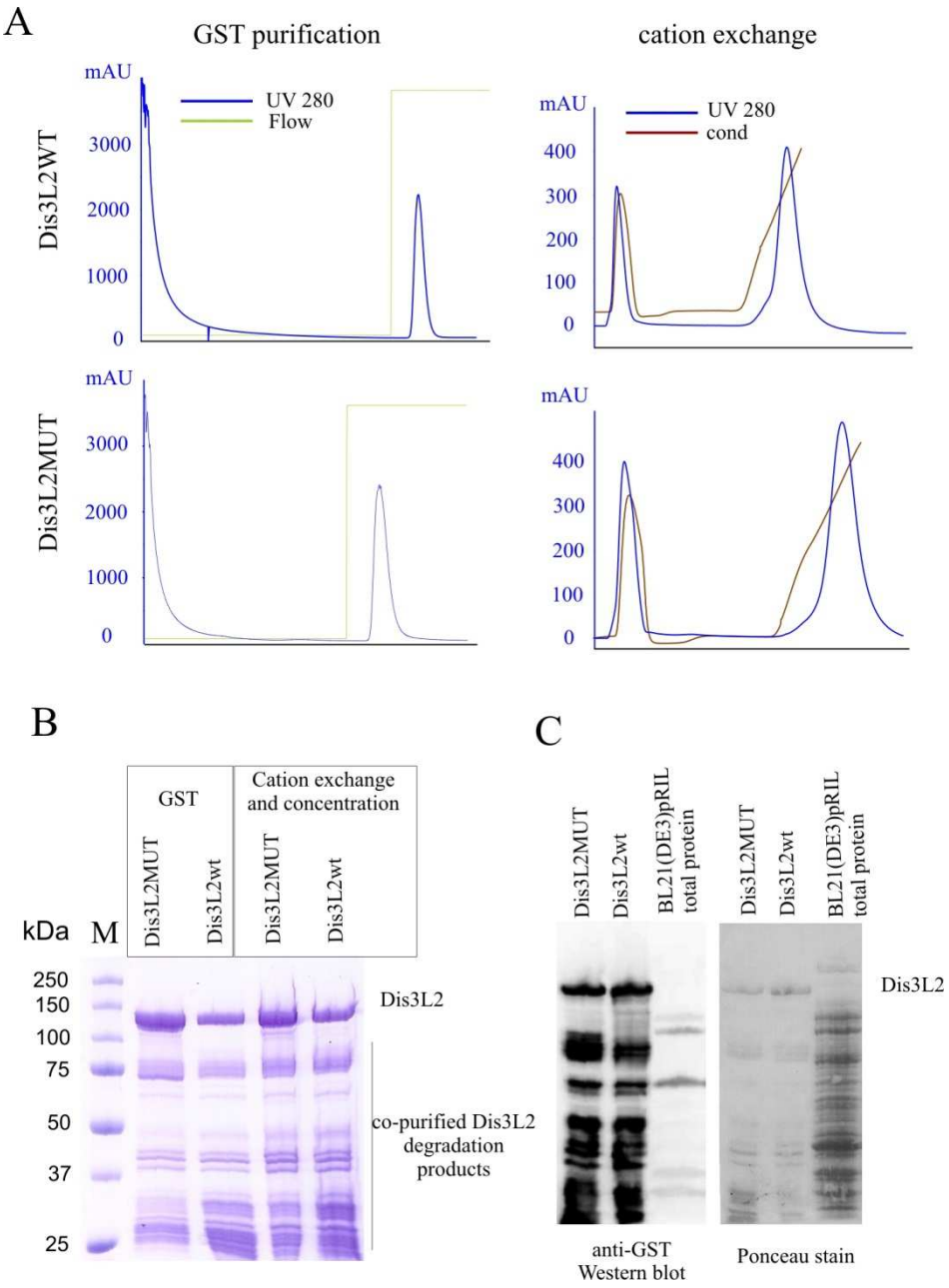


Figure S2 Dis3L2 purification. **(A)** GST fusions of Dis3L2 wild type (Dis3L2WT) and mutated version (Dis3L2MUT) were purified using GST affinity chromatography followed by cation exchange chromatography. **(B)** SDS-PAGE analysis of purification products. The size of the full length Dis3L2 protein is indicated on the right. Preparations obtained after cation exchange and protein concentration were used in the assays. **(C)** Purified protein preparations were subjected to Western blot analysis against GST to investigate the nature of lower molecular weight contaminants. Contaminations consisted on Dis3L2-GST protein degradation by-products as indicated in the picture. The total protein extract from the bacteria used for protein expression was used (BL21(DE3)pRIL) as control. The weaker signal of target protein in Western blot is due to signal saturation.

Supplementary Figure 3

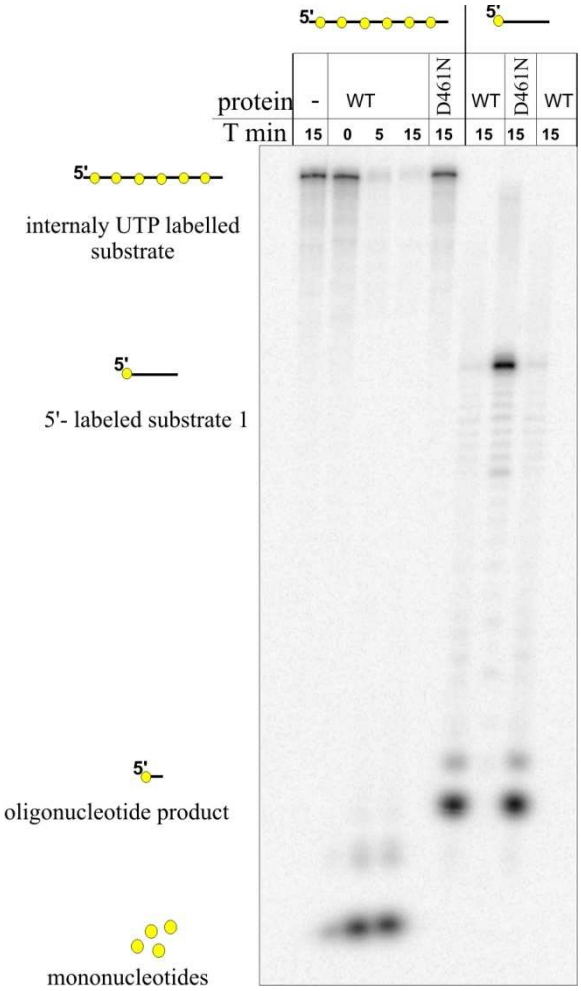
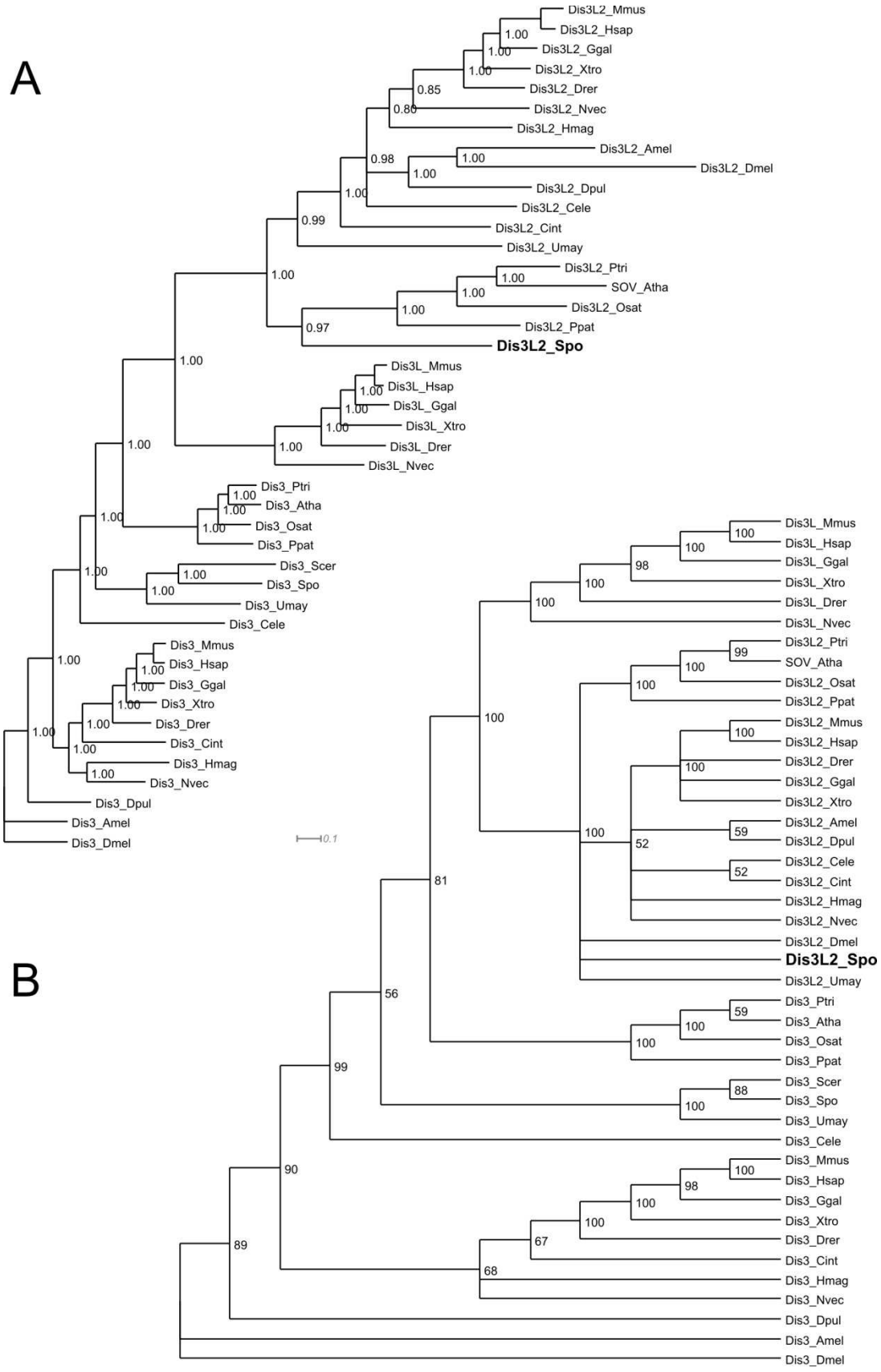


Figure S3 Dis3L2 is a processive 3-5’ exonuclease. Around 0.5 pmols of purified wild type protein Dis3L2 (WT) and its mutated version (D461N) were incubated with 0.2 pmols of either an internally labeled RNA substrate (see Supplementary Table 2) or a 5’-end labeled substrate (substrate 1). Reactions were stopped at the indicated times and products were separated on denaturing polyacrylamide gel. The size of the different substrates and reaction products are indicated.

Supplementary Figure 4



C

Figure S4 Phylogenetic analyses of the Dis3 homologues in eukaryotes. Three distinct groups, corresponding to Dis3, Dis3L and Dis3L2 are apparent in all trees, and the SPAC2C4.07c gene product of *S. pombe* (Dis3L2_Spo) is consistently classified with the Dis3L2 group. (**A**) 50% majority-rule consensus tree from 1000 bootstrap replicates of a maximum parsimony (MP) analysis, bootstrap support values shown for nodes. (**B**) Bayesian inference (BI) tree, with posterior probabilities of each node. (C) Conservation of active site consensus between different Dis3 like proteins.

Supplementary Figure 5

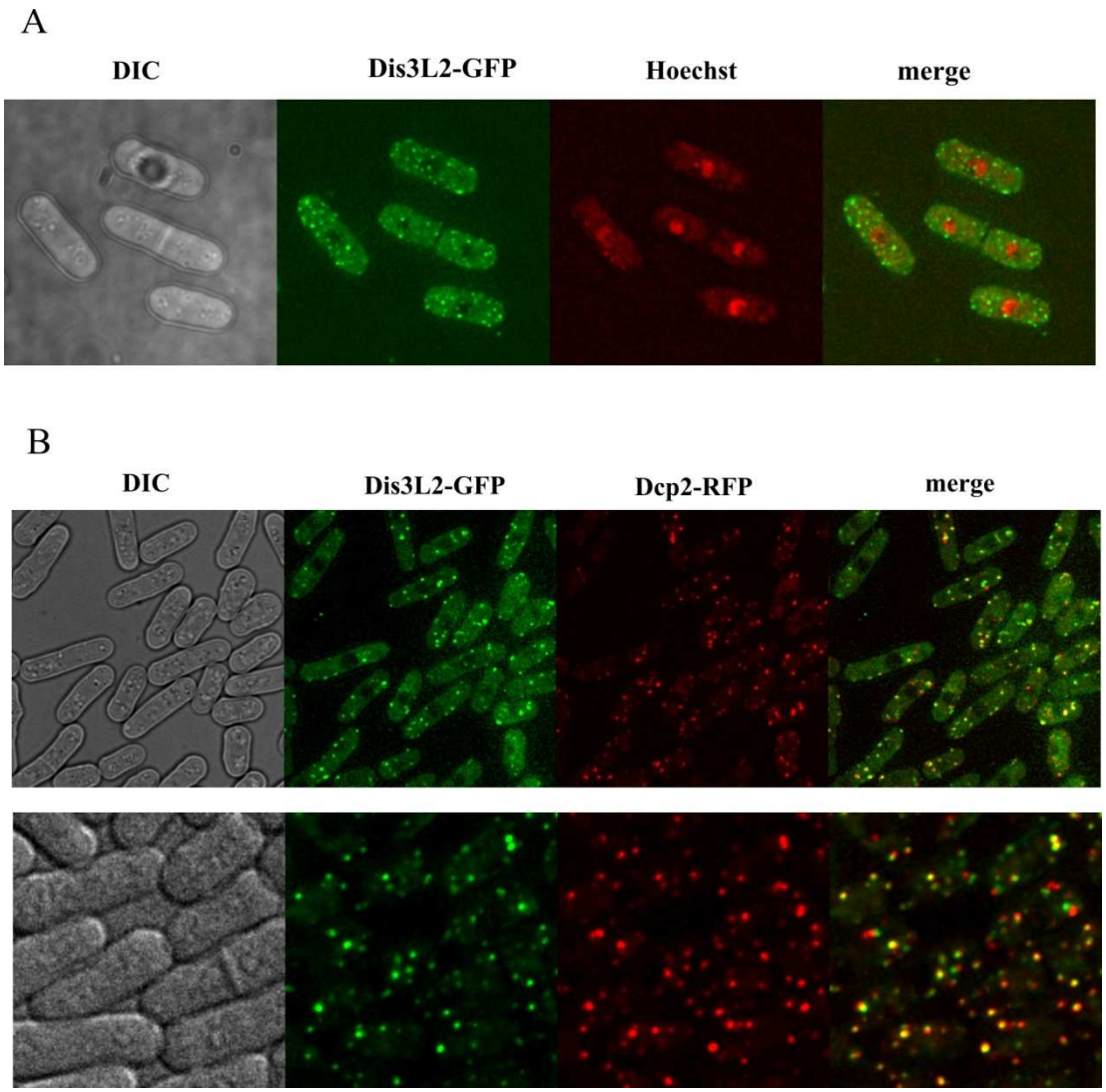


Figure S5 Dis3L2 localizes in the cytoplasm and cytoplasmic foci. **(A)** Cells expressing Dis3L2-GFP were grown to mid-log phase in minimal medium (EMM) and the localization of epitope tagged protein was determined by fluorescence microscopy. Nucleus were stained with Hoechst and its co-localisation with Dis3L2-GFP signal was was examined. **(B)** Dis3L2-GFP was examined for co-localization with Dcp2-RFP. Cells expressing Dis3L2-GFP and Dcp2-RFP were grown to mid-log phase in minimal medium (EMM) and than immediately subjected to microscopy.

Supplementary Figure 6

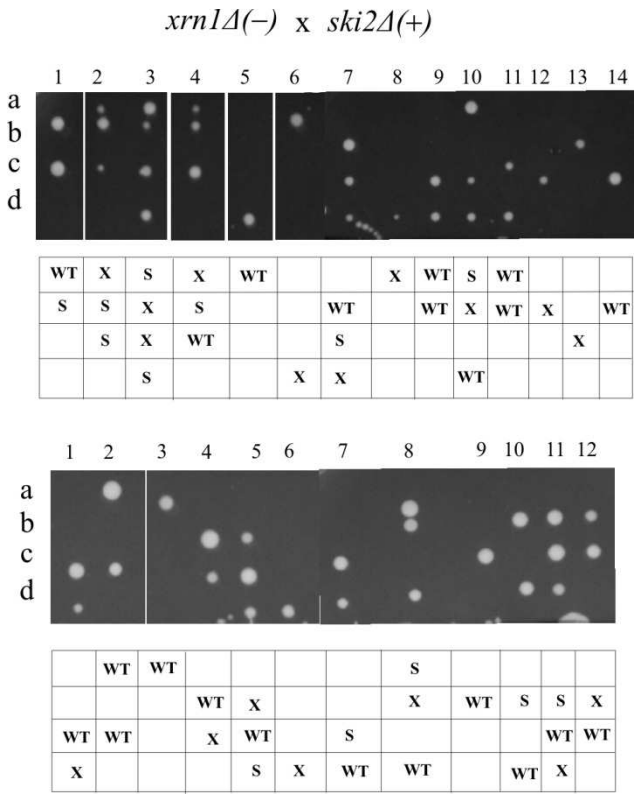


Figure S6 *xrn1*$^{+}$ deletion is synthetically lethal with deletion of *ski2*$^{+}$. Haploid *ski2*$^{+}$*::hph* cells were crossed with *xrn1*$^{+}$*::hph* strain. Resulting diploids were sporulated and tetrads were dissected on YES plates. Genotypes of the spores were analyzed by colony PCR and are described in the bottom tables: WT- wild type strain, X- *xrn1Δ*, S- *ski2Δ*.

Supplementary Figure 7

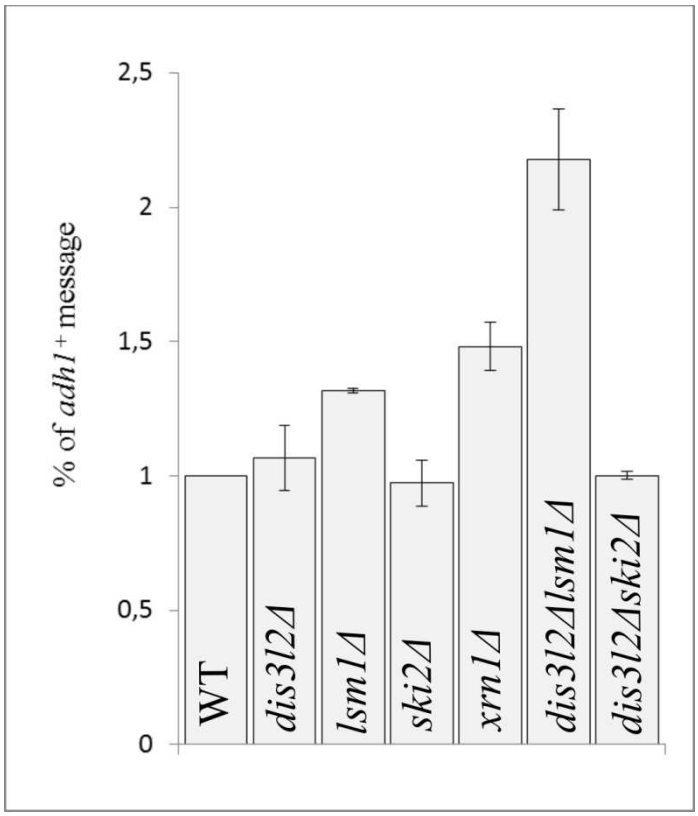


Figure S7 *adh1*$^{+}$ transcript levels accumulates in a *dis3l2Δlsm1Δ* background. Graph represents Northern blot results of *adh1*$^{+}$ mRNA analysis over total RNA from the wild type and different deletion mutant strains, from three independent experiments. Error bars represent standard deviation.

Supplementary Figure 8

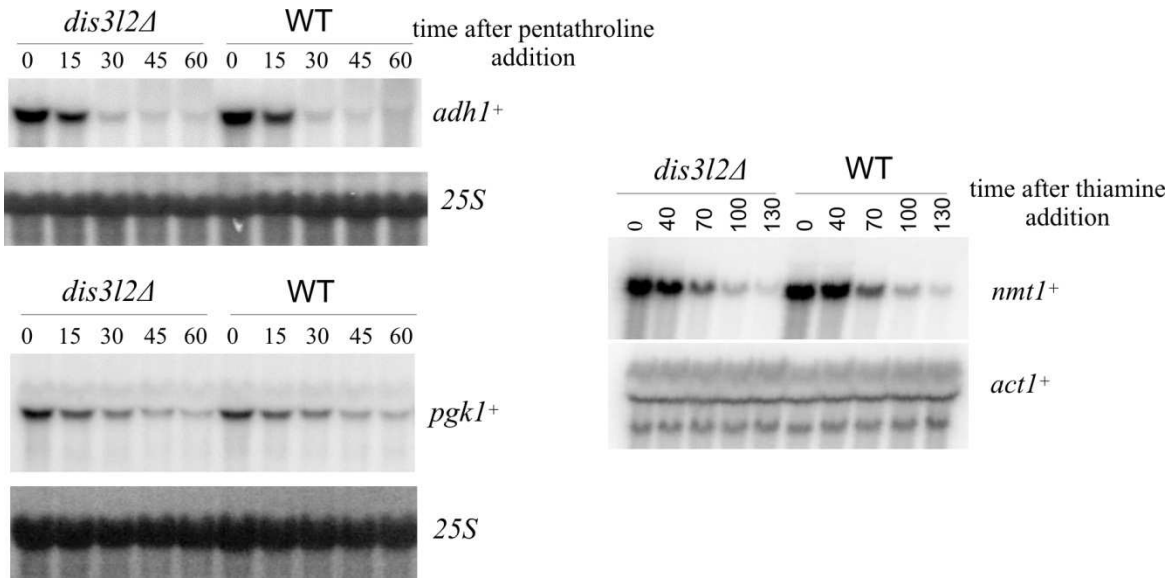


Figure S8 No detectable difference was observed in mRNAs degradation rates between wild type yeast strain (WT) and *dis3l2Δ* mutant. Wild type and *dis3l2Δ* strains were grown in the full media (for *adh1*$^+$ and *pgk1*$^+$) or minimal media (for *nmt1*$^+$) until mid-log phase, subsequently transcription was stopped by either 1,10-penanthroline (for *adh1*$^+$ and *pgk1*$^+$) or thiamine (for *nmt1*$^+$) addition. Cells were harvested at the indicated time points after transcriptional arrest, total RNA was isolated and mRNA decay analyzed by Northern blot.

Supplementary Figure 9

WT

CCCATCCTTTAAAAAAAAAAAAAAAA (15)

CCCATCCTTTAAAAAAAAAAAAAAAAAAAAAAAAAAA (28)

CCCATCCTTTAAAAAAAAAAAAAAAAAAAA 21

CCCATCCTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA (31)

CCCATCCTTTAAAAAAAAAAAAAAAAAAA (19)

CCCATCCTTTAAAAAAAAAAAAAAAAAAAAA (21)

CCCAAAAAAAAAAAAAAAAACAAAAAAAAAAAT (30)

CCCATCCTTAAAAAAAAAAAAAAAAAAAAAAAAAAA (27)

CCCATCCTTTAAAAAAAAAAAAAAAAAAAA (21)

CCCATCCTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA (31)

CCCATCCTTAAAAAAAAAAAAAAAAAAA (19)

CCCATCCTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA (31)

CCCATCCTTTAAAAAAAAAAAAAA (14)

CCCATCCTTTAAAAAAAAAAAAAAAAT (17)

CCCATCCTTTAAAAAAAAAAAAAAT (14)

dis3l2Δ

CCCATCCTTTAAAAAAAAAAAAAAAAAAAAAAAT (23)

CCCATCCTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA (34)

CCCATCCTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA (49)

CCCATCCTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAT (29)

CCCATCCTTTAAAAAAAAAAAAAAAAAAAAAAA (23)

CCCATCCTTTAAAAAAAAAAT (12)

CCCAAAAAAAAAAAAAA (15)

CCCATCCTTTAAAAAAAAAAAAAT (13)

CCCAAAAAAAAAAAAAAAAAAAAAAAA (25)

CCCAAAAAAAAAT (9)

CCCATCCTTTAAAAAAAAAAAAAAT (14)

CCCATCCTTTAAAAAAAAAAAAAAAAA (18)

lsm1Δ

CTTTTCTTTTCTTCCTCCTCCTCGTTCAT (-171)

CAAACCATCTCGGGGTTAGAGT (-246)

CCCATCCTTTAAAAAAAT (7)

CCCATCCTTTAAAAAAAAAAAAAATT (14)

CCCATCCTTTAAAAAAAAAAAATT (12)

CCCATCCTTTAAAAAAAAAAT (10)

CCCATCCTTTAAAAAAT (6)

CCCATCCTTTAAAAAAAAAA (10)

CCCATCCTTTAAAAAAAAAAAAAAAAAAAAAAAAA (26)

CCCATCCTTTAAAAAAAAAAT (10)

CCCATCCTTTAAAAAAAAAAAAAAAAAAAAAAAAA (26)

CCCATCCTTTAAAAAAAAAAAAAAAAAA (18)

CCCATCCTTTAAAAATT (5)

CCCATCCTTTAAAAAAAAAAAAT (13)

CCCATCCTTTAAAATT (4)

CCCATCCTTTAAAAAAAAT (8)

dis3l2Δ lsm1Δ

TGTTTTGTATAGAAATCAATGTTTT (-20)

GGACGATTGTACCTTTGAAAATTTT (-55)

GATTGTACCTTTGAAAACCAATT (-52)

GGACGATTGTACCTTTGAAAACCAACT (-50)

TGTTTTGTATAGAAATCAATGT (-20)

TGTTTTGTATAGAAATTTTT (-25)

CCTTTGAAAATTTT (-55)

TTTTGCATGTTTTTTTATT (-35)

CCCATCCTTTAAAAAAAAAAAAAAAAAT (18)

CAACTACTTTTGCATGTTTT (-34)

CCCATCCTTTAAAAAAAAAGAAAAAAAT (17)

TTAGAATCCCATT (-4)

CAACTACTTTTGCATGTTTT (-34)

TTTTGTATAGAAATC (-23)

TTAGAATCCCATT (-4)

TTTTGCATGTTCTTTTT (-36)

TTAGAATCCCATTTTTTTT (-4)

CCCATCCTTTAAAAAAAATTT (8)

Figure S9 Sequences of 3'-ends of *adh1*$^{+}$ transcripts obtained in 3' RACE experiment from different yeast strains. The non-genome encoded thymines are colored in red. Length of poly(A) tail is represented by the positive values in the brackets, and the extension of the 3'-end trimming is represented by the negative value. Nucleotides were counted from polyadenylation site (zero point).

Supplementary Figure 10

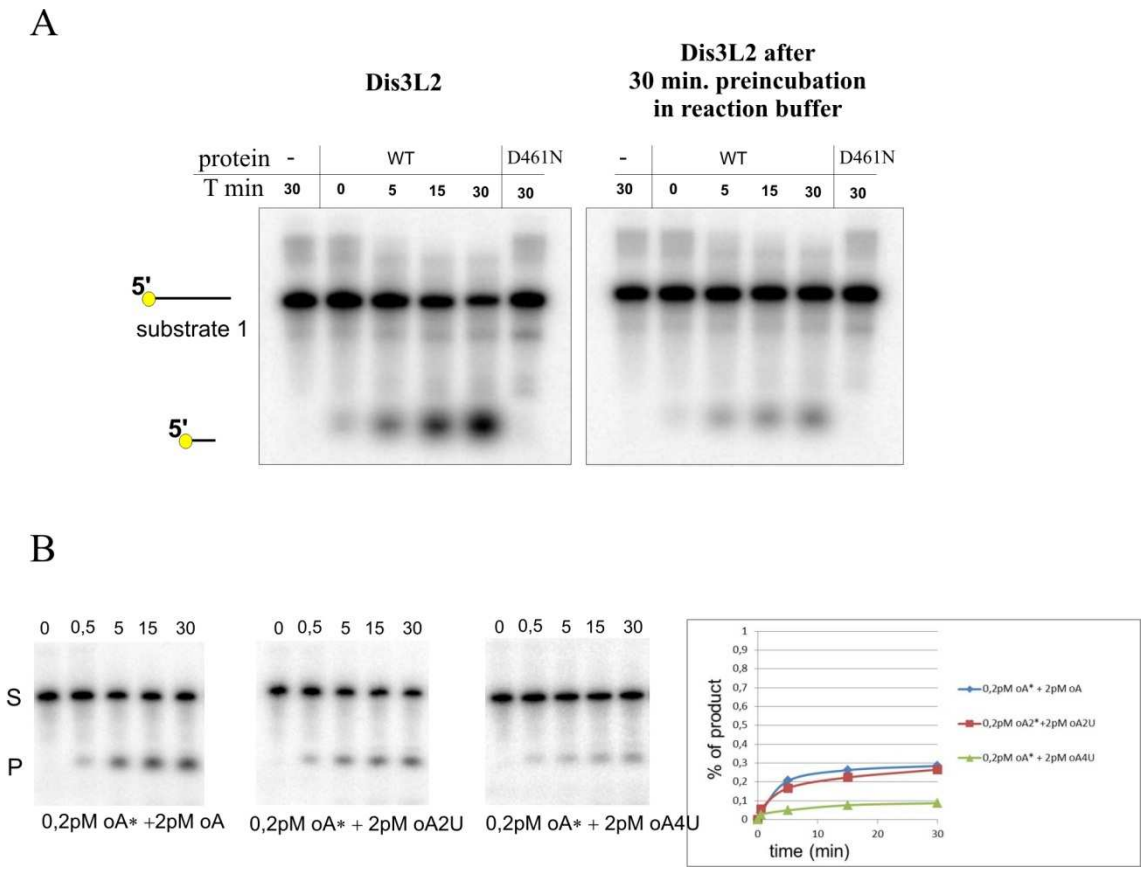


Figure S10 (A) Dis3L2 loses its activity over time in the reaction conditions. 0.5 pmols of Dis3L2 or mutated protein version (D461N) were incubated with 2pmols of 5' labeled substrate 1 for 30 minutes or first pre-incubated 30 minutes in reaction buffer in 30^0C and subsequently supplemented with the substrate and incubated another 30 minutes. Reactions were stopped at indicated times and products were separated on denaturing polyacrylamide gels **(B)** Uracil residues added to the 3' end can effectively target RNA substrates for degradation by Dis3L2 *in vitro*. Addition of non-labeled uridylated substrates inhibits degradation of labeled adenylated RNAs. Equal amounts of Dis3L2 protein were incubated with the indicated amounts of different RNA substrates (RNA oligonucleotides sequence in Fig.7 and Supplementary Table 1). Reactions with radioactive substrates (labeled with *) were supplemented with non-labeled oligonucleotides. Reactions were stopped at the indicated time points (top of the gels) and separated on denaturing polyacrylamide gels. Graphs on the right side depict the accumulation of the reaction product at different time points as calculated using Image Quant.

Supplementary Tables

Supplementary Table 1 Strains used in this study

Strain	Genotype	Creator
MGF10	*h- ade6-M210 his3-D1 leu1-32 ura4-D18*	J Cooper
MGF11	*h- ade6-M210 his3-D1 leu1-32 ura4-D18*	J Cooper
MGF1	*h-*	
MGF2	*h+*	
MGF3	*h- ade6-M210 his3-D1 leu1-32 ura4-D18 dis3l2::KanMX4*	Bioneer
MM1	*h- ade6-M210 his3-D1 leu1-32 ura4-D18 dis3l2::dis3l2-GFP-KanMS6*	this study
MM2	*h- ade6-M210 his3-D1 leu1-32 ura4-D18 dis3l2::dis3l2-GFP-KanMS6 dcp2::dcp2-mRFP-hph*	this study
MM3	*h- ade6-M210 his3-D1 leu1-32 ura4-D18 dis3l2::dis3l2-GFP-KanMS6 pabp::pabp-mRFP-hph*	this study
MM4	*h- ade6-M210 his3-D1 leu1-32 ura4-D18 dis3l2::dis3l2-GFP-KanMS6 dis3::dis3-mRFP-hph*	this study
MM5	*h- ade6-M210 his3-D1 leu1-32 ura4-D18 dis3::dis3-GFP-KanMS6*	this study
MM6	*h- ade6-M210 his3-D1 leu1-32 ura4-D18 rrp43::rrp43-GFP-KanMS6*	this study
MM7	*h- ade6-M210 his3-D1 leu1-32 ura4-D18 dis3::dis3-TAPtag-KanMS6*	this study
MM8	*h- ade6-M210 his3-D1 leu1-32 ura4-D18 rrp43::rrp43-TAPtag-KanMS6*	this study
MM9	*h- ade6-M210 his3-D1 leu1-32 ura4-D18 dis3l2::dis3l2-TAPtag-KanMS6*	this study
MM10	*h- dis3l2::KanMS6*	this study
MM11	*h- dis3l2::hph*	this study
MM12	*h+ dis3l2::hph*	this study
MM13	*h- xrn1::hph*	this study
MM14	*h+ xrn1::hph*	this study
MM15	*h- dis3l2::KanMS6 ski2::hph*	this study
MM16	*h- ski2::hph*	this study
MM17	*h- dis3l2::KanMS6 lsm1::hph*	this study
MM18	*h- lsm1::hph*	this study
MM19	*h- dcp2::dcp2-GFP-KanMS6*	this study
MM20	*h- dis3l2::hph dcp2::dcp2-GFP-KanMS6*	this study

Supplementary Table 2 Oligonucleotides and substrates used in this study.

RNA substrates	
Substrate 1	GUUUUGUAUAGAAAUCAAUG
Substrate 2	CCCGACACCAACCACUAAAAAAAAAAAAAA
oA	CACCAACCACUAAAAAAAAAAAAA
oA2U	CACCAACCACUAAAAAAAAAAAUU
oA4U	CACCAACCACUAAAAAAAAAAUUUU
Poli(U)	UUUUUUUUUUUUUUUUUUUUUUUUUUUUUU
Poli(A)	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
Internally labeled substrate	GAAAUAUUUGUAAUUGCAACUUAAUUUUCCUGUAACAUAGUGUGAUUAAUUUU CAGUAGGGGGUUAUAAAAAUUGAAGGAUAAGAUUAUUGAUAACGCAA UAACCUUAUUUUCAGAG
DNA oligonucleotides	
Substrate3 (DNA)	AGTGGTTGGTGTCGGG
18SrRNAprobe	ACCAGACTTGCCCTCCAATTGTTCC
25SrRNAprobe	ACCTTGGAGACCTGCTGCGGTTATG
Primers	
L_fba1_probe	CATCCCTGCCATTAACGTCAC
R_fba1_probe	GACGTAGGCGAATTGGGTATC
L_pabp_probe	TACTCGCCGTTCTTTGGG
R_pabp_probe	ACCTGCTTCCTGCTTTCC
L_hsc1_probe	AGGGCAATGCTCGTCCTAC
R_hsc1_probe	GAGGCAGCCAAACCAGAAC
L_pyk1_probe	CTCCGTGATGCTGGTATG
R_pyk1_probe	GCTGGTGGACAAGACAAC
L_pgk1_probe	CACCAACAATGCCCGTATCG
R_pgk1_probe	TCCACAGTCCAAACCCATCC
L_act1_probe	CTATGTATCCCGGTATTGCC
R_act1_probe	GGAGCTTAGAAGCACTTACG
L_rrg1_probe	CACGAACAGCCTTCTTACTC
R_rrg1_probe	GAGCCAAAGTCTTCTTCACC
L_adh1_probe	CACCGATTTACACGCTCTTC
R_adh1_probe	GAAAGGTCCAAGACGATACG
L_pik1_probe	GCTGGTAAAAATGTTGTTAC
R_pik1_probe	TAGTAAATTCCGTTCG
L_nmt1_probe	TATGAGCGTGAAGGGATTGAG
R_nmt1_probe	CGACATAACGAAGTGAGTTGC
1st_adh_PASE	CAAGATTGCCGGCCGTATCG
2nd_adh_PASE	TTTCACCACACGTTTATACC
L_TAPtagSLIC	CGCTGCAGGTCGACGGATCCCCGGGTTAATTAACATGG AAAAGAGAAGATGGA
R_TAPtagSLIC	TAAGAAATTCGCTTATTTAGAAGTGGCGCGCCTCAGGT TGACTTCCCCGCGG
L_mut_Dis3l2	CAGCTCGAGACTTGAATGATGCTGTTTC
P_mut_Dis3l2	GAAACAGCATCATTCAAGTCTCGAGCTG
L_clon_Dis3l2	ATGAATTCATGGATTTAAAACCAAATATTAG
P_clon_Dis3l2	TACTCGAGTTAATTCAAAGAAACTAGAC

*all the primers used for *S. pombe* gene deletions and integrations were designed using PPP: Pombe PCR Primer Programs tool (Penkett et al, 2006) and are not included in this list, as well as primers used for checking integration in the obtained strains.

Standard primers for 3' linker used in PASE reaction (Alexander et al, 2010) are not included in the table.

Supplementary Table 3 Sequences used in protein comparison and phylogenetic analyzes. Accession numbers from NCBI Entrez with the exception of *.

Name	Family	Species	Accession#
Dis3_Amel	Dis3	*Apis mellifera*	XP_397381
Dis3L2_Amel	Dis3_L2	*Apis mellifera*	XP_624734
Dis3_Cele	Dis3	*Caenorhabditis elegans*	NP_501835
Dis3L2_Cele	Dis3_L2	*Caenorhabditis elegans*	NP_498160
Dis3_Cint	Dis3	*Ciona intestinalis*	XP_002132066
Dis3L2_Cint	Dis3_L2	*Ciona intestinalis*	XP_002119190
Dis3_Drer	Dis3	*Danio rerio*	XP_001336850
Dis3L_Drer	Dis3L	*Danio rerio*	NP_001103928
Dis3L2_Drer	Dis3L2	*Danio rerio*	XR_084214
Dis3_Dpul	Dis3	*Daphnia pulex*	EFX89559
Dis3L2_Dpul	Dis3L2	*Daphnia pulex*	EFX64669
Dis3_Dmel	Dis3	*Drosophila melanogaster*	NP_651246
Dis3L2_Dmel	Dis3L2	*Drosophila melanogaster*	NP_728490
Dis3_Ggal	Dis3	*Gallus gallus*	XP_417016
Dis3L_Ggal	Dis3L	*Gallus gallus*	XP_003641875
Dis3L2_Ggal	Dis3L2	*Gallus gallus*	XP_422741
Dis3_Hmag	Dis3	*Hydra magnipapillata*	XR_053815
Dis3L2_Hmag	Dis3L2	*Hydra magnipapillata*	XP_002154262
Dis3_Mmus	Dis3	*Mus musculus*	NP_082591
Dis3L_Mmus	Dis3L	*Mus musculus*	NP_001001295
Dis3L2_Mmus	Dis3L2	*Mus musculus*	NP_705758
Dis3L_Nvec	Dis3L	*Nematostella vectensis*	XP_001632370
Dis3L2_Nvec	Dis3L2	*Nematostella vectensis*	XP_001634492
Dis3_Nvec	Dis3	*Nematostella vectensis*	10544|gw.129.26.1*
Dis3_Osat	Dis3	*Oryza sativa*	EEE58267
Dis3L2_Osat	Dis3L2	*Oryza sativa*	NP_001048152
Dis3_Ppat	Dis3	*Physcomitrella patens*	XP_001766083
Dis3L2_Ppat	Dis3L2	*Physcomitrella patens*	XP_001773680
Dis3_Scer	Dis3	*Saccharomyces cerevisiae*	NP_014621
Dis3_Spo	Dis3	*Schizosaccharomyces pombe*	NP_596653
Dis3L2_Spo	Dis3_L2	*Schizosaccharomyces pombe*	NP_594510
Dis3_Umay	Dis3	*Ustilago maydis*	XP_759849
Dis3L2_Umay	Dis3L2	*Ustilago maydis*	XP_757367
Dis3_Xtro	Dis3	*Xenopus (Silurana) tropicalis*	NP_001120564
Dis3L_Xtro	Dis3L	*Xenopus (Silurana) tropicalis*	NP_001072835
Dis3L2_Xtro	Dis3L2	*Xenopus (Silurana) tropicalis*	NP_001072804
Dis3L_Hsap	Dis3L	*Homo sapiens*	NP_001137160
Dis3_Hsap	Dis3	*Homo sapiens*	NP_055768
Dis3L2_Hsap	Dis3L2	*Homo sapiens*	NP_689596
Dis3_Ptri	Dis3	*Populus trichocarpa*	XP_002303419
Dis3L2_Ptri	Dis3L2	*Populus trichocarpa*	XP_002302251
Dis3_Atha	Dis3	*Arabidopsis thaliana*	NP_565418
SOV_Atha	Dis3_L2	*Arabidopsis thaliana*	NP_177891

* Sequence not available in NCBI Entrez at the time of writing. Protein ID and Name from the Genome Portal of the Department of Energy Joint Genome Institute (Grigoriev et al, 2012) provided instead.

Supplementary Table 4 Proteins co-purified with Dis3TAP or Rrp43TAP and identified by mass-spectrometry.
Protein or gene names are listed by score order. Known exosome complex subunits and interacting proteins are underlined

Dis3TAP	Rrp43TAP
dis3	dis3
tdh1	rrp45
rrp46	rrp4
rrp45	rrp42
rrp42	rrp46
rrp4	fas2
rrp40	rrp40
fas2	rrp43
rrp43	fas1
rrp41	rrp41
fas1	rrp6
gpm1	mtr3
rpl4a	csl4
csl4	sks2
tef1a	act1
mtr3	ssa2
pyk1	rpp201
tef3	tef1b
eno101	gpd3
egd2	rpa5
ssa2	SPAC24C9.12c
pgk1	gua1
pda1	ura1
swo1	pda1
SPBC16A3.08c	rpl4b
gua1	arg5
act1	SPAP8A3.05
rpp201	SPACUNK4.11c
rrp6	pdb1
SPCC794.07	SPCC794.07
his1	rps18a
pdb1	hsp60
rpl7c	rpp203
ura1	rpl14
SPAC1F8.07c	SPCC1235.01
rpp203	rpl25a
adh1	rps7
rpa5	rpp202
rps3	rpl30a
hsp60	SPCC1827.03c
fba1	SPCC1739.07
sce3	rpl18b
rps2	cct4
wis2	fta5
cct2	rps23a
rps7	cct5
SPBC8D2.18c	rpl28e
rps18a	
vas2	
sgt2	
arg5	
rpa1	
rps6a	
cdc48	
rps5b	
sla1	
rpl6	
rps0b	
SPCC1739.07	
rpl1201	
rpl25a	
rpl18a	
lys4	
rps22a	
cdc48	

fta5	sla1
tef-1	tif471
ssp1	ssp1
rps19a	htb1
SPCC1259.09c	puf6
SPAC9.09	eft1
gpd1	SPCC364.06
eft1	rpl27a
SPAC24C9.12c	rpl7c
SPAC22A12.16	SPAC222.08c
ilv5	rpp0
btf3	rpt3
rpl11a	hsp10
SPBC24C6.04	rpl35
eca39	rpl7b
rpl30a	swo1
pab1	pfk1
mbf1	SPAC12G12.07c
sua1	rpl37b
cof1	cct6
SPCC1827.03c	mlo3
rps16a	tea3
rpl23a	rpn7
SPAC1782.11	rps4c
rpl7b	btf3
rpl14	rps14a
cct6	rpl22
SPAP8A3.05	dld1
SPCC1235.01	rpl6
rpl27a	rps15b
rpl28e	tfs1
p23fy	rps102
vma10	tif213
rps6b	ubi3
krs1	rpl8
SPCC1223.14	rps2
rps0a	rpl17b
rpp202	rpc19
rps14a	rps5b
SPCC191.02c	tif211
gly1	rpl13
hsp10	rpl36a
rps102	rpl16a
rpl35	SPAC1F8.07c
rpl18b	rpl1201
cut6	SPBC1734.11
rpl24b	tcg1
sti1	cut6
SPAC12G12.07c	ppt1
SPBC354.10	
rps20	
rps4c	
rps23a	
SPCC584.01c	
SPAPB1E7.07	
srp2	
aro4	
SPBC660.16	
tif211	
rpp0	
rpl13	
rps21	
rps12a	
but2	
mge1	
SPCC364.06	
sir1	
rpl2a	
SPAC222.08c	
rki1	
inh1	
rpl31	
cdc37	
ura5	
rpl36a	

gpx1
cdc8
rpl10b
htb1
SPBP8B7.05c
SPAC26F1.13c
nup61
arg4
mlo3
rps4b
rpn2
rpl17b
SPAC1805.02c
fim1
rps17a
rpt3
tea3
SPAC4F10.19c
arg1
dbp2
rps9a
hub1
rps0b
SPAC17A5.15c
atp2
pmt3
tif1
SPAC24H6.10c
SPBC1711
lys3
rpl37b
rps101
SPBC1703.07
SPBC19C7.06
SPBC18E5.07
rpl28a
rps10b
pmp20
SPAC8C9.04
mmf1
rpl22
rad25
tim13
rpb4
rpl15b
erg10
SPBC2F12.05c
bip1
hsp9
SPBC21B10.03c
cct8
cct4
SPAPB24D3.07c
rpl5a
tif471
ypt1
rkp1
hts1
tal1
lys1
SPBC1539.06
grx4
rpl20a
rad24
SPBC776.15c
SPCC1183.02
rpl3b
cpy1
dld1
shm2
plb1
shg1
tpx1
SPBC713.03
rps8b

rps27
cyc1
rpl8
ubi3
SPBC1734.11
rps30a
tpi1
sui1
clc1
mpd2
tef3
mri1
eif3f
SPBC1271.04c
SPAC10F6.16
rps13
tif213
pan1
SPBC359.05
SPCC965.06
SPAC25G10.08
SPAC29E6.06c
SPAC13G7.06
arc4
vip1
SPBC1198.05
tif11
rps15a
SPBC776.03
tcg1
SPAC1F5.11c
ppt1
cct5
rps24b
rpl16a
SPAC9E9.09c
utp22
SPAC1F5.06
mug125
mts2
eif3m
hmt2
rrf1
nhp6
SPAC22E12.19
SPAC23H3.15c
uba2
dps1
SPBP4H10.15
srp54
hxk1
hrq1
aru1
SPAC5H10.03
SPBC30D10.05c
SPBC14C8.04
ino80
SPBC29A3.16
rhb1
mdn1
srp72
ded1
SPAC926.08c
prs3
SPAC458.04c
let1
SPBC337.07c
smd1
utp20
SPMIT.03

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