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Supplemental Information

Condensation of Ded1p Promotes a Translational Switch from Housekeeping to Stress Protein Production

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Table S1: Overview of 5’UTR characteristics of differentially translated genes. Related to Figures 1 and 6 and Figures S1 and S6. Median and means of PARS scores, calculated MFEs and length of all known yeast 5’UTRs in comparison to the PARS scores, calculated MFEs and length of 5’UTRs of differentially translated genes between wildtype Ded1p and Ded1-IDR$_m$ at 30°C, 40°C and 42°C. Significance of differences between the conditions were determined using a two-sided Wilcoxon test.

comparison	**PARS adj p value**	**PARS mean**	**PARS median**	**gene count***	**MFE adj p value**	**MFE mean**	**MFE median**	**length adj p value**	**length mean**	**length median**	**gene count****
All genes		7.78	3.77	2674		-11.41	-5.00		81	53	4358
WT_40_<_WT_42	0.868	6.56	6.84	99	3.93E-06	-6.32	-1.61	8.46E-07	53	34	118
WT_40_>_WT_42	3.68E-04	20.84	10.00	177	8.19E-04	-17.11	-7.10	2.29E-10	123	78	240
WT_40_<_IDRm_40	0.934	13.89	3.01	71	0.659	-12.31	-5.50	0.059	100	64	93
WT_40_>_IDRm_40	0.064	14.14	8.44	96	0.002	-17.30	-8.40	2.67E-04	110	72	110
WT_42_<_IDRm_42	0.209	11.45	6.93	138	0.091	-10.88	-3.79	0.482	89	55	235
WT_42_>_IDRm_42	0.009	15.15	6.34	190	3.59E-06	-14.84	-9.30	4.01E-05	96	74	249

* the gene count corresponds to the number of genes differentially expressed for which the PARS score was experimentally determined.

** the gene count corresponds to the number of genes differentially expressed for which the 5'UTR sequence is known.

Table S2: Overview of *in vitro* translation assay reporter transcripts. Related to Figure 6. The likelihood of an mRNA to fold was measured with the program RNAfold from the ViennaRNA Package (Lorenz et al., 2011) by calculating the minimum free energy and the partition function. The more negative the free energy for a given RNA, the more likely it is to be folded. The *GIS2* 5'UTR was used as the unstructured baseline control for the *in vitro* translation assays. The "high" Ded1p induction is defined as a greater than 10-fold increase in the translation of the respective mRNA upon addition of 0.8 µM Ded1p in the *in vitro* translation reaction after 90 minutes. A "low" induction is defined as a less than 10-fold increase in the *in vitro* translation of the respective mRNA.

Gene	**Description**	**Minimum free energy (kcal/mol)**	**Ensemble free energy (kcal/mol)**	**Centroid free energy (kcal/mol)**	**5'UTR length (nt)**	**Ded1p induction**
GIS2	IRES activator	0	0	0	14	Low
HSP12	Heat induced small Hsp	0	-0.01	0	39	Low
HSP104	Heat induced disaggregase	0	-0.4	0	40	Low
SSA4	Heat induced Hsp70	0	-0.38	0	55	Low
DED1	RNA helicase	-0.8	-1.13	-0.8	21	Low
SSA1	Housekeeping Hsp70	-2.7	-3.95	-0.3	64	High
SBE22	Involved in bud growth	-12.84	-13.72	-12.84	81	High
PAB1	Poly(A)-binding protein	-12.5	-15.46	-9.3	133	High
SSK2	MAPKKK of HOG1 signaling pathway.	-16.83	-19.55	-4.18	98	High

Table S3: Overview of the maximum growth temperature of fungi species and T_{onset} for Ded1p phase separation. Related for Figure 7. The T_{onset} of purified Ded1p homologues was assessed using DLS.

Species	**Max. growth temperature (°C)**	**T_{onset} (°C)**
S. kudriavzevii	36 (Salvadó et al., 2011)	34
S. cerevisiae (W303)	42 (Observation, growth on plates)	40
T. terrestris	50 (Samson et al., 1977)	46