

SUPPLEMENTARY FIGURE LEGENDS

Figure S1. Base-pairing between 5.8S rRNA and 25S rRNA.

Secondary structure of domains I, II, and III of yeast LSU rRNA (<http://www.rna.cccb.utexas.edu>, Canone et al, 2002). 5.8S rRNA sequences is highlighted in yellow. Helices 2, 4, and 10 formed by base-pairing between 5.8S and 25S rRNAs are shown within red boxes. Based on the binding sites of bacterial r-proteins on 23S rRNA, binding sites of four r-proteins rpL17, rpL26, rpL35, and rpL37 on 5.8S and 25S rRNAs are indicated by black boxes.

Figure S2. Changes in protein composition in A₃ Factor mutants

- (A) Levels of Nop7 are diminished in preribosomes in the absence of other interdependent A₃ factors.** Preribosomes were purified from yeast cultures grown in galactose or shifted to glucose for 16h to deplete the A₃ factor. Western blotting of Nop7 in preribosomes purified from indicated strains are shown.
- (B) Bar graph demonstrating changes in levels of proteins in preribosomes determined by iTRAQ when Rlp7 is depleted.** Each bar on the x-axis corresponds to a specific protein identified in this study. The y-axis represents the ratio of the amount of a protein in preribosomes purified from cells in which Rlp7 was depleted to that in preribosomes purified from wildtype cells.
- (C) Relative abundance of other proteins in Rlp7-depleted cells determined by iTRAQ.** The ratio of other proteins (not shown in Figure 5) from Rlp7-depleted cells and Rlp7-expressed cells (Glu/Gal). SEM are given.

Figure S3. ~10 nt 5'-truncated pre-rRNAs are unique to the absence of rpL17.

Indicated strains were grown in either galactose or shifted to glucose for 16 hours, to a density of 3×10^7 cells. RNAs were extracted from whole cell lysates and subject to primer extension using an oligonucleotide that hybridizes within ITS2. * indicates RNA degradation products that are observed sometimes as an artifact of the extraction process.

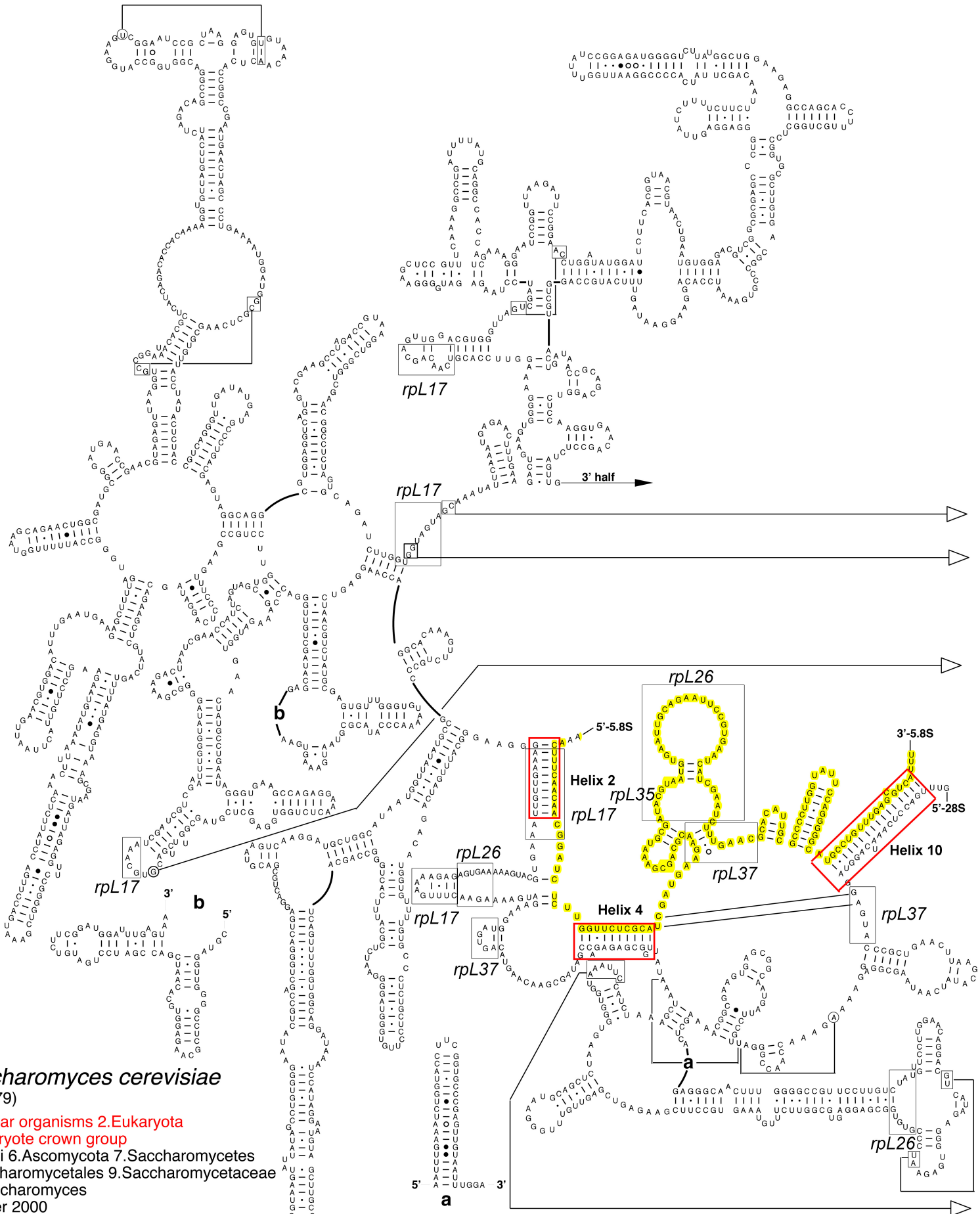
Figure S4. Association of r-proteins with preribosomes is affected in the absence of other interdependent A₃ factors.

Indicated yeast strains were grown in galactose or shifted to glucose for 16h to deplete the A₃ factor and harvested in the mid-log phase ($3 \cdot 10^7$ cells/ml). Western blotting of HA-tagged r-proteins and rpL17 in preribosomes is shown.

Supplementary References

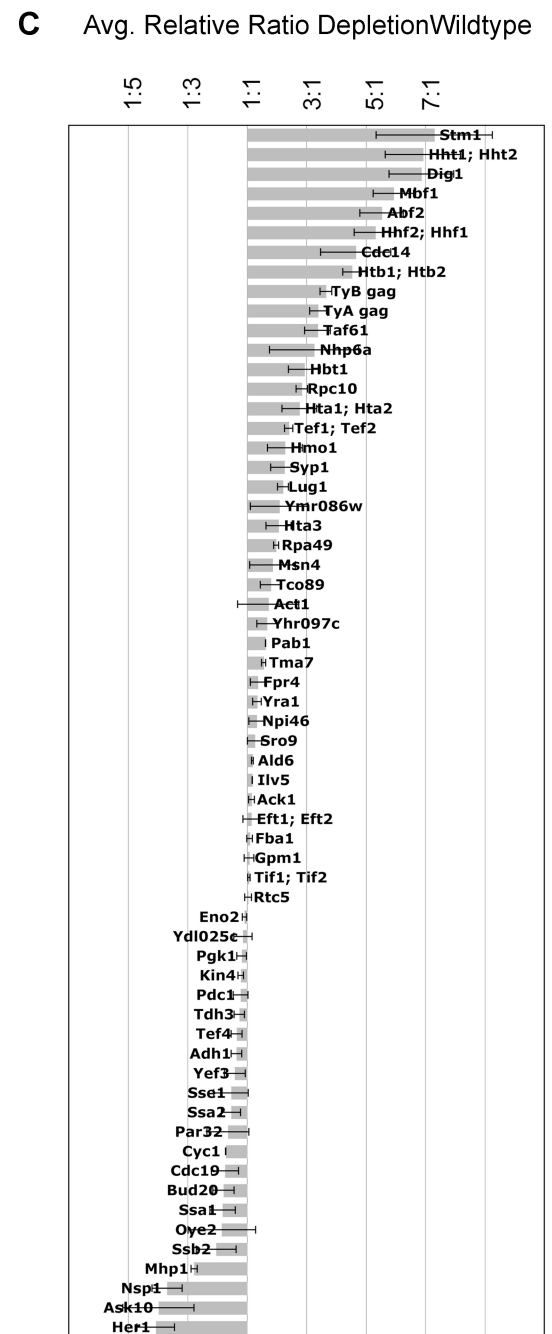
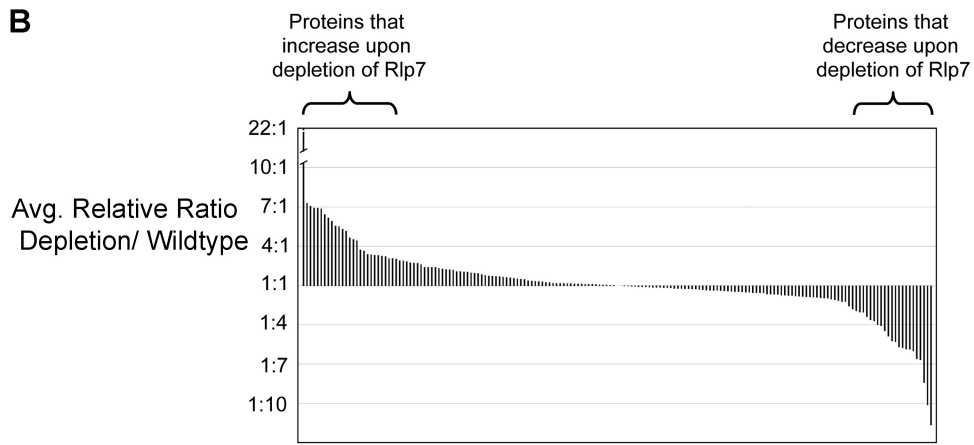
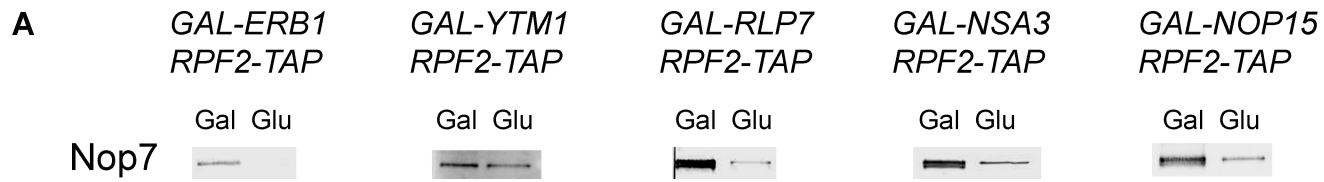
Canone JJ, Subramanian S, Schnare MN, Collett JR, D'Souza LM, Du Y, Feng B, Lin N, Madabusi LV, Müller KM, Pande N, Shang Z, Yu N, Gutell RR (2002) The comparative RNA Web (CRW) site: An online database of comparative sequence and structure information for ribosomal, intron, and other RNAs. *BMC Bioinformatics* **3**:2

Secondary Structure: large subunit ribosomal RNA - 5' half

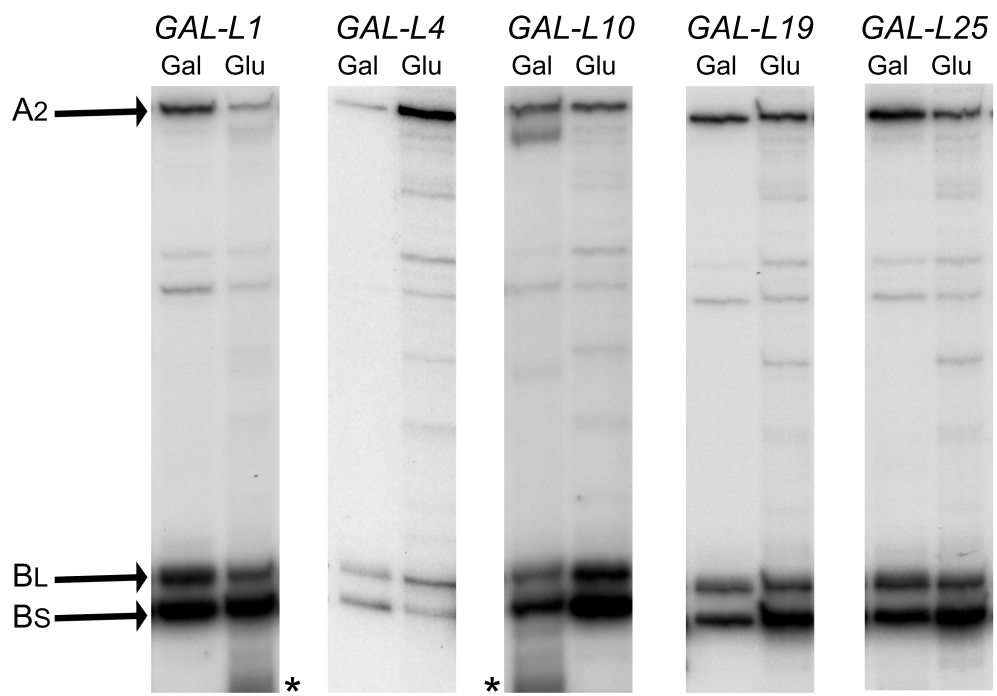


Saccharomyces cerevisiae
(U53879)

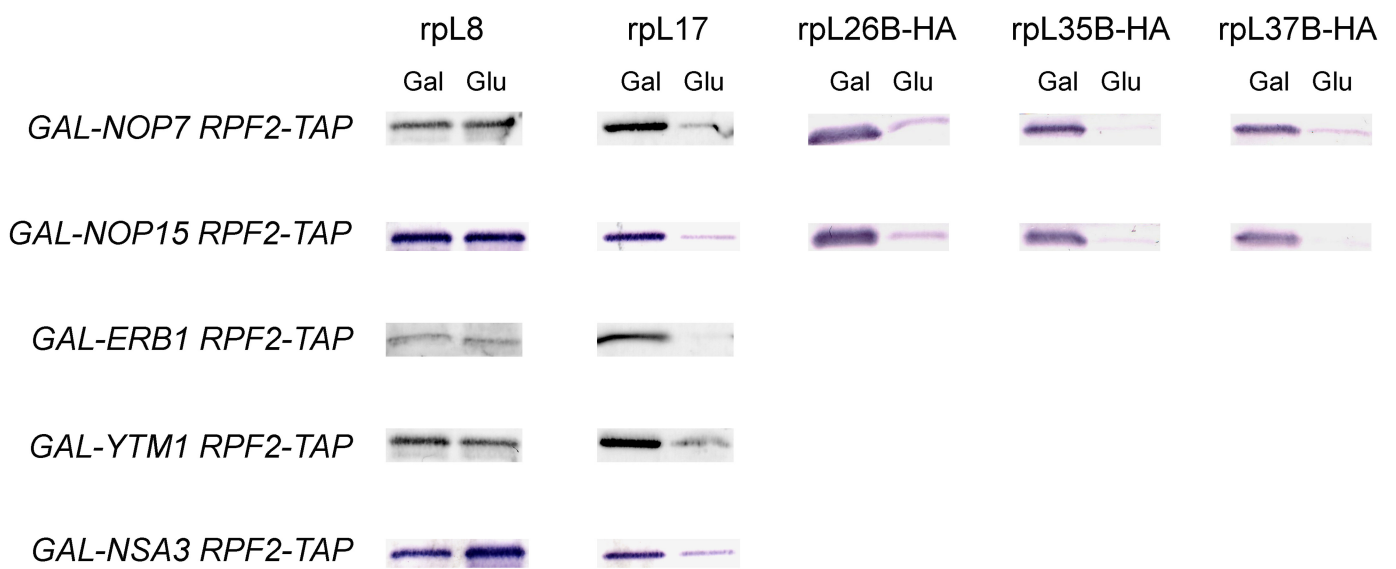
1. cellular organisms
 2. Eukaryota
 3. eukaryote crown group
 5. Fungi
 6. Ascomycota
 7. Saccharomycetes
 8. Saccharomycetales
 9. Saccharomycetaceae
 10. Saccharomyces
- October 2000



Supplementary Figure 2



Sahasranaman et al., Supplementary Figure S3



Sahasranaman et al, Figure S4

Supplementary Table 1: Relative iTRAQ Ratios for Proteins in Preribosomes in Wildtype Versus Rlp7-Depleted Yeast (Two Replicates)

Gene name	Accession	Total peptides ^a	Unique peptides ^b	Sequence coverage (%) ^c	Glu/Gal	SEM	Glu/Gal	SEM
Abf2	gi 6323717	17	14	56.83	4.80 : 1	0.69	5.53 : 1	0.73
Ack1	gi 6319998	2	2	5.14	01:01.3	0.12	1.15 : 1	0.1
Act1	gi 6321069	2	2	7.73	01:01.1	0.11	1.71 : 1	1.03
Adh1	gi 6324486	8	5	16.67	1.07 : 1	0.08	01:01.4	0.18
Alb1	gi 6322339	2	2	18.86	01:18.5	15.57	01:05.7	3.33
Ald6	gi 6325196	3	3	7.6	1.11 : 1	0.08	1.18 : 1	0.03
Ask10	gi 6321534	4	3	3.93	01:04.9	0.95	01:04.0	1.19
Brx1	gi 6324496	16	7	27.84	01:01.2	0.07	1.12 : 1	0.04
Bud20	gi 6323103	2	2	14.46	01:02.0	0.35	01:01.8	0.36
Bud21	gi 6324652	2	2	12.62	3.75 : 1	1.44	6.17 : 1	1.13
Cdc14	gi 6321141	3	3	6.17	7.46 : 1	0.06	4.66 : 1	1.18
Cdc19	gi 6319279	9	6	15.8	01:01.7	0.47	01:01.7	0.46
Cgr1	gi 6321409	10	4	25	01:13.3	3.36	01:10.1	2.64
Cyc1	gi 6322508	3	2	21.1	01:01.7	0.25	01:01.7	0.01
Dbp10	gi 6320173	11	7	6.83	01:04.0	0.49	01:04.9	1.03
Dbp9	gi 6323306	10	8	11.28	1.16 : 1	0.06	1.61 : 1	0.1
Dig1	gi 6325208	3	2	7.52	3.86 : 1	0.67	6.86 : 1	1.08
Ebp2	gi 6322676	9	9	16.86	01:01.1	0.06	1.17 : 1	0.1
Eft1; Eft2	gi 6324707; gi 6320593	3	3	4.99	1.13 : 1	0.09	1.13 : 1	0.28
Eno2	gi 6321968	9	7	20.82	1.09 : 1	0.19	01:01.1	0.08
Enp1	gi 6319724	2	2	7.87	3.44 : 1	0.45	21.70 : 1	14.19
Fba1	gi 6322790	3	2	8.08	1.18 : 1	0.15	1.08 : 1	0.09
Fcf1	gi 6320546	2	2	8.99	2.89 : 1	0.64	5.17 : 1	1.69
Fpr4	gi 6323482	3	3	8.93	01:01.3	0.15	1.35 : 1	0.24
Gpm1	gi 6322697	4	4	22.27	1.20 : 1	0.05	1.07 : 1	0.17
Has1	gi 6323947	7	6	14.26	01:02.4	0.26	01:01.7	0.25
Her1	gi 6324801	20	12	11.96	01:06.0	1.04	01:04.1	0.63
Hhf2/ Hhf1	gi 6324298; gi 6319481	20	5	50.49	3.93 : 1	0.35	5.31 : 1	0.71
Hht1/ Hht2	gi 6324297; gi 6319482	10	4	25.74	4.15 : 1	0.5	6.91 : 1	1.27
Hmo1	gi 6320379	10	4	21.54	2.66 : 1	0.74	2.27 : 1	0.59
Hta1; Hta2	gi 6320431; gi 6319470	5	2	12.12	1.91 : 1	0.24	2.75 : 1	0.59
Hta3	gi 6324562	4	2	12.69	1.79 : 1	0.34	2.06 : 1	0.42
Htb1; Htb2	gi 6320430; gi 6319471	15	6	35.11	2.77 : 1	0.35	4.53 : 1	0.32
Ilv5	gi 6323387	2	2	5.32	01:01.5	0.21	1.17 : 1	0.01
Imp3	gi 6321942	8	7	39.34	3.00 : 1	0.29	4.43 : 1	0.62

Imp4	gi 6324254	4	3	11.72	2.19 : 1	0.29	3.07 : 1	0.41
Kin4	gi 6324807	2	2	4	01:01.5	0.05	01:01.2	0.09
Krr1	gi 6319791	7	6	18.67	1.63 : 1	0.21	2.32 : 1	0.3
Lcp5	gi 6320974	3	3	7.28	1.77 : 1	0.32	1.75 : 1	0.03
Loc1	gi 6321113	62	14	48.53	01:01.5	0.05	01:01.2	0.04
Lug1	gi 6319930	3	2	13.07	1.61 : 1	0.21	2.20 : 1	0.18
Mak21	gi 6320265	2	2	1.95	1.71 : 1	0.11	2.08 : 1	0.08
Mbf1	gi 6324873	8	3	63.79	3.61 : 1	0.45	5.92 : 1	0.68
Mhp1	gi 6322419	4	3	2.43	01:02.6	1	01:02.8	0.1
Mrt4	gi 6322843	3	3	13.14	01:02.4	0.39	01:01.7	0.17
Msn4	gi 6322788	2	2	5.56	1.42 : 1	0.53	1.86 : 1	0.77
Nhp2	gi 6319993	4	3	23.12	01:01.3	0.14	01:01.0	0.06
Nhp6a	gi 6325309	2	2	9.78	2.96 : 1	0.55	3.26 : 1	1.5
Noc2	gi 6324780	2	2	2.68	01:01.4	0.22	1.00 : 1	0.17
Nog1	gi 6325164	10	8	12.83	01:01.4	0.09	01:01.4	0.15
Nog2	gi 6324381	3	3	6.58	01:02.1	0.38	01:01.7	0.23
Nop1	gi 6320190	4	4	13.76	1.10 : 1	0.08	1.38 : 1	0.11
Nop10	gi 7839181	5	4	53.45	01:01.4	0.1	1.05 : 1	0.08
Nop12	gi 6324532	6	5	13.29	2.06 : 1	0.35	1.94 : 1	0.29
Nop15	gi 6324219	2	2	7.73	01:02.4	0.02	01:01.9	0.13
Nop16	gi 6320838	10	9	36.36	01:05.3	0.57	01:04.5	0.63
Nop2	gi 6324268	5	3	6.8	01:01.3	0.19	01:01.5	0.08
Nop4	gi 6325213	5	5	8.47	1.97 : 1	0.27	2.89 : 1	0.51
Nop53	gi 6325111	6	5	10.55	01:03.6	0.71	01:03.0	0.61
Nop58	gi 6324886	2	2	7.05	01:01.3	0.09	01:01.9	0.88
Nop6	gi 6319988	8	5	33.33	2.57 : 1	0.37	2.92 : 1	0.54
Nop7	gi 6321540	2	2	3.14	01:02.7	0.51	01:02.2	0.65
Npi46	gi 6323566	3	3	9.25	01:01.4	0.11	1.32 : 1	0.26
Nsa2	gi 6320973	6	6	24.9	01:06.3	1.74	01:05.9	1.61
Nsa3	gi 6321843	20	13	30.59	01:02.0	0.13	01:01.5	0.09
Nsp1	gi 6322420	7	4	13.97	01:05.1	0.37	01:03.7	0.51
Nug1	gi 6320842	3	3	5	01:02.1	0.1	01:02.6	0.78
Oye2	gi 6321973	2	2	5.75	1.05 : 1	0.15	01:01.8	1.14
Pab1	gi 6321013	2	2	4.68	1.33 : 1	0.01	1.62 : 1	0.01
Par32	gi 6320028	2	2	7.46	01:02.0	0.63	01:01.7	0.71
Pdc1	gi 6323073	7	5	10.83	1.01 : 1	0.14	01:01.2	0.24
Pgk1	gi 6319857	13	8	26.44	1.12 : 1	0.08	01:01.2	0.16
Rlp7	gi 6324326	5	3	9.63	01:05.8	2.05	01:03.6	1.37
Rpa49	gi 6324081	2	2	5.3	1.39 : 1	0.34	1.97 : 1	0.08
Rpc10	gi 6321937	2	2	38.57	2.04 : 1	0.02	2.84 : 1	0.19
Rpf1	gi 6321880	10	6	21.69	01:02.3	0.36	01:02.1	0.29
Rpf2	gi 6322934	6	3	9.88	1.03 : 1	0.17	1.11 : 1	0.09
rpL10	gi 6323104	3	2	8.6	1.69 : 1	0.6	01:01.2	0.3

rpL11AB	gi 6325359; gi 6321522	4	3	20.11	01:01.3	0.32	1.20 : 1	0.37
rpL12AB	gi 6320781; gi 6320625	10	5	44.85	01:01.4	0.12	01:01.1	0.1
rpL13B	gi 6323791	63	18	64.82	01:01.6	0.08	1 : 1.39	0.06
rpL14A	gi 6322847	21	10	50.72	01:02.4	0.14	01:01.9	0.1
rpL14B	gi 6321786	20	8	50.72	01:02.4	0.14	01:01.9	0.1
rpL15A	gi 6323057	41	11	41.18	01:01.7	0.07	01:01.3	0.05
rpL16A	gi 6322058	18	13	48.74	01:01.4	0.08	01:01.1	0.07
rpL16B	gi 6324260	25	11	41.41	01:01.3	0.08	01:01.1	0.05
rpL17A	gi 6322668	15	5	33.7	01:08.0	1.33	01:05.9	0.9
rpL17B	gi 6322284	15	5	33.7	01:08.2	1.38	01:05.7	0.9
rpL18AB	gi 6324452; gi 6324028	28	10	47.85	01:01.2	0.06	1.00 : 1	0.04
rpL19AB	gi 6319559; gi 6319444	24	7	29.1	01:03.5	0.4	01:02.9	0.26
rpL1AB	gi 6325036; gi 6321303	14	7	30.88	01:02.2	0.19	01:01.8	0.16
rpL20AB	gi 6324888; gi 6323898	20	9	45.4	01:01.9	0.19	01:01.5	0.08
rpL23AB	gi 6320963; gi 6319384	16	6	42.34	01:01.4	0.07	01:01.1	0.06
Rpl24	gi 6323037	5	4	12.56	01:01.8	0.15	01:01.5	0.09
rpL25	gi 6324445	9	4	32.39	01:01.4	0.2	01:01.1	0.1
rpL26A	gi 6323376	18	10	47.24	01:09.4	1.73	01:06.6	1.02
rpL26B	gi 6321471	24	11	47.29	01:07.4	1.13	01:06.0	0.82
rpL27AB	gi 6321798; gi 6320679	30	9	57.35	01:01.7	0.09	01:01.4	0.07
rpL2AB	gi 6322171; gi 6321145	6	4	16.93	01:02.4	0.58	01:02.2	0.42
rpL3	gi 6324637	9	5	14.99	01:01.5	0.36	01:01.3	0.18
rpL30	gi 6321408	8	2	27.62	1.44 : 1	0.54	1 : 1.65	0.21
rpL31AB	gi 6323438; gi 6320128	6	4	31.86	01:02.7	0.6	01:02.1	0.56
rpL32	gi 6319378	19	6	41.54	01:01.8	0.28	01:01.3	0.07
rpL33A	gi 6325114	3	3	32.71	01:02.0	0.03	01:01.9	0.46
rpL34AB	gi 9755331; gi 6322137	8	4	32.23	01:02.1	0.25	01:01.8	0.14
rpL35AB	gi 6320065; gi 6320010	17	10	49.17	01:07.1	1.24	01:05.2	0.83
rpL36A	gi 6323848	39	7	50	01:01.7	0.08	01:01.5	0.06
rpL36B	gi 6325006	43	7	50	01:01.8	0.09	01:01.5	0.05
rpL37A	gi 6323214	5	3	31.82	01:07.2	1.72	01:05.3	1.42

rpL37B	gi 6320708	3	3	22.73	01:08.7	2.39	01:06.7	1.47
rpL38	gi 6323357	4	2	11.22	01:03.4	0.76	01:03.4	0.55
rpL39	gi 6322272	2	2	21.57	1.49 : 1	1.3	01:03.0	1.75
rpL4A	gi 6319505	15	9	23.2	01:01.4	0.07	1.02 : 1	0.05
rpL4B	gi 6320215	15	9	23.2	01:01.4	0.14	01:01.0	0.06
rpL5	gi 6325126	7	3	11.45	01:01.6	0.07	01:01.2	0.08
rpL6A	gi 6323567	32	13	68.18	01:01.8	0.1	01:01.4	0.07
rpL6B	gi 6323481	34	15	72.16	01:01.7	0.09	01:01.3	0.06
rpL7A	gi 6321362	51	16	58.2	01:01.2	0.04	1.15 : 1	0.04
rpL7B	gi 6325058	51	14	58.2	01:01.2	0.04	1.13 : 1	0.04
rpL8A	gi 6321754	82	19	62.89	01:01.4	0.03	01:01.1	0.03
rpL8B	gi 6322984	90	22	66.41	01:01.4	0.03	01:01.1	0.02
rpPO	gi 6323371	4	3	11.22	2.26 : 1	0.53	01:01.5	0.55
rpS0AB	gi 6323077; gi 6321653	3	2	11.9	1.16 : 1	0.12	01:01.0	0.02
rpS11AB	gi 6320228; gi 6319522	4	3	23.72	2.14 : 1	0.51	2.04 : 1	0.57
rpS13	gi 6320269	5	4	23.84	1.92 : 1	0.43	2.60 : 1	0.9
rpS14AB	gi 6322270; gi 6319879	7	4	26.09	2.86 : 1	0.76	2.70 : 1	0.89
rpS17AB	gi 6323617; gi 6320655	13	6	47.06	2.94 : 1	0.42	6.94 : 1	1.92
rpS18AB	gi 6323615; gi 6320658	9	4	32.88	1.10 : 1	0.24	1.52 : 1	0.45
rpS20	gi 6321772	6	5	29.75	01:01.4	0.25	01:01.3	0.26
rpS22B	gi 6323399	13	6	47.69	2.89 : 1	0.32	5.56 : 1	1.24
rpS24B	gi 6322120; gi 6320918	11	6	28.15	3.37 : 1	0.38	2.41 : 1	0.53
rpS31	gi 6323196	10	5	29.61	1.10 : 1	0.09	1.29 : 1	0.15
rpS4AB	gi 6322605; gi 6321997	11	8	26.82	2.81 : 1	0.47	3.33 : 1	0.74
rpS5	gi 6322583	4	3	17.78	1.72 : 1	0.29	1.12 : 1	0.44
rpS6AB	gi 9755341; gi 6320120	15	7	56.64	2.51 : 1	0.4	2.73 : 1	0.5
rpS6AB	gi 6325167; gi 6319658	8	5	21.61	2.43 : 1	0.28	3.30 : 1	0.32
rpS7A	gi 6324670	13	8	36.32	5.16 : 1	0.84	6.44 : 1	1.25
rpS7B	gi 6324233	10	6	29.47	4.89 : 1	0.93	7.08 : 1	1.38
rpS8AB	gi 6320949; gi 6319399	7	4	23	2.71 : 1	0.7	2.40 : 1	0.85
rpS9B	gi 6319666	9	7	34.36	2.24 : 1	0.55	3.04 : 1	0.93
rpSAB	gi 6323577; gi 6323474	5	3	10.2	1.60 : 1	0.28	1.96 : 1	0.39

Rrp15	gi 6325400	10	7	22.4	1.27 : 1	0.09	1.69 : 1	0.07
Rrp17	gi 6320620	2	2	6.81	1.11 : 1	0.33	01:01.9	0.51
Rrp5	gi 6323885	4	4	2.83	2.08 : 1	0.3	2.40 : 1	0.28
Rrs1	gi 6324868	5	4	29.06	01:01.0	0.11	1.13 : 1	0.08
Rtc5	gi 6324692	2	2	3.17	01:01.2	0.05	1.03 : 1	0.11
Sas10	gi 6320049	4	3	7.38	2.25 : 1	0.35	3.22 : 1	0.68
Sik1	gi 6323226	9	8	17.46	1.03 : 1	0.09	1.25 : 1	0.09
Snu13	gi 6320809	3	2	14.29	1.21 : 1	0.06	1.49 : 1	0.06
Spb1	gi 6319796	3	2	3.92	01:12.7	6.15	01:08.4	3.82
Sro9	gi 6319812	3	3	12.88	01:01.8	0.39	1.26 : 1	0.24
Ssa1	gi 6319314	12	10	19.63	1.19 : 1	0.19	01:01.8	0.43
Ssa2	gi 6323004	11	10	19.72	1.05 : 1	0.13	01:01.5	0.33
Ssb2	gi 6324120	9	8	16.8	1.96 : 1	0.49	01:02.0	0.67
Sse1	gi 6325151	2	2	3.61	1.89 : 1	1.06	01:01.5	0.58
Stm1	gi 6323179	10	8	34.43	3.47 : 1	0.71	7.30 : 1	1.95
Syp1	gi 6319878	4	3	4.6	1.85 : 1	0.22	2.25 : 1	0.46
Taf61	gi 6320349	2	2	4.45	3.17 : 1	1.12	3.37 : 1	0.43
Tco89	gi 6325077	3	3	5.76	1.76 : 1	0.38	1.80 : 1	0.35
Tdh3	gi 6321631	12	7	24.1	1.12 : 1	0.2	1 : 1.26	0.17
Tef1; Tef2	gi 6325337; gi 6319594	43	20	32.72	1.74 : 1	0.08	2.40 : 1	0.14
Tef4	gi 6322769	2	2	5.1	2.18 : 1	1.3	01:01.4	0.18
Tif1; Tif2	gi 6322912; gi 6322323	2	2	5.57	01:01.2	0.14	1.06 : 1	0.04
Tma7	gi 6323292	4	3	39.06	1.25 : 1	0.12	1.56 : 1	0.07
Utp11	gi 6322750	5	3	13.67	2.45 : 1	0.57	3.08 : 1	0.87
Utp14	gi 6323546	5	5	7.12	3.07 : 1	0.54	3.74 : 1	0.61
Utp30	gi 6322913	2	2	8.03	1.77 : 1	0.75	2.22 : 1	0.57
Utpo6	gi 6320657	2	2	3.41	2.11 : 1	0.33	1.73 : 1	0.2
Ybl028c	gi 6319443	19	10	44.34	01:37.3	13.15	01:11.6	2.92
Ydl025c	gi 6320179	2	2	3.55	01:01.5	0.25	01:01.1	0.31
Yef3	gi 6323278	2	2	2.39	01:01.5	0.44	01:01.4	0.35
Ygr038c-b; Ydr098c-b	gi 7839173; gi 7839152	3	2	1.77	4.65 : 1	1.64	3.65 : 1	0.2
Yhr097c	gi 6321889	2	2	9.56	1.09 : 1	0.3	1.66 : 1	0.34

Ypr158w-a; Ypr137c-a; Yor142w-a; Ynl054w-a; Yml045w-a; Ygr161c-c; Yer159c-a; Ydr316w-a; Ydr261c-c	gi 7839208; gi 7839206; gi 7839198; gi 7839195; gi 7839191; gi 7839177; gi 7839168; gi 7839161; gi 7839159; gi 6862572; gi 6323695; gi 6322488; gi 6319485; gi 6319324	4	3	9.32	2.89 : 1	0.27	3.39 : 1	0.28
Yra1	gi 6320589	13	7	32.3	1.12 : 1	0.08	1.33 : 1	0.14

^a Total peptides with at least 95% confidence.

^b The total number unique peptides with at least 95% confidence.

^c The number of amino acids spanned by the assigned peptides divided by the sequence length.

Supplementary Table 2: Strain List

Strain	Genotype	Source or Reference
JWY 8243	<i>MATa ura3-52 trp1-Δ101 lys2-801 his3-Δ200 leu2-Δ1 nop7::GAL-3HA-NOP7 TRP1</i>	This study
JWY 8271	<i>MATa ura3-52 trp1-Δ101 lys2-801 his3-Δ200 leu2-Δ1 nop7::GAL-3HA-NOP7 TRP1 rpf2::RPF2-TAP URA3</i>	This study
JWY 8267	<i>MATa ura3Δ0 his3Δ1 leu2Δ0 lys2Δ0 met15Δ0 erb1::URA3 [CEN LEU pGAL-HA-ERB1] rpf2::RPF2-TAP URA3</i>	This study
JWY 8238	<i>MATa ura3-52 trp1-Δ101 lys2-801 his3-Δ200 leu2-Δ1 ytm1::GAL-3HA-YTMI TRP1</i>	This study
JWY 8268	<i>MATa ura3-52 trp1-Δ101 lys2-801 his3-Δ200 leu2-Δ1 ytm1::GAL-3HA-YTMI TRP1 rpf2::RPF2-TAP URA3</i>	This study
JWY 8275	<i>MATa ura3-52 trp1-Δ101 lys2-801 his3-Δ200 leu2-Δ1 rlp7::GAL-3HA-RLP7 TRP1</i>	This study
JWY 8277	<i>MATa ura3-52 trp1-Δ101 lys2-801 his3-Δ200 leu2-Δ1 rlp7::GAL-3HA-RLP7 TRP1 rpf2::RPF2-TAP URA3</i>	This study
JWY 7050	<i>MATa ura3-52 lys2-801^{amber} ade2-101^{ochre} his3-Δ200 leu2-Δ1 rlp7::HIS3 trp1::KANMX6 nop7::NOP7-TAP Kl. TRP1 [pGAD3-RLP7 (GAL-RLP7 ADE2 URA3 CEN6 ARSH4)]</i>	This study
JWY 8278	<i>MATa ura3-52 trp1-Δ101 lys2-801 his3-Δ200 leu2-Δ1 cic1::GAL-CIC1 TRP1</i>	This study
JWY 8280	<i>MATa ura3-52 trp1-Δ101 lys2-801 his3-Δ200 leu2-Δ1 cic1::GAL-CIC1 TRP1 rpf2::RPF2-TAP URA3</i>	This study
JWY 8292	<i>MATa ura3-52 trp1-Δ101 lys2-801 his3-Δ200 leu2-Δ1 nop15::GAL-3HA-NOP15 TRP1</i>	This study
JWY 8294	<i>MATa ura3-52 trp1-Δ101 lys2-801 his3-Δ200 leu2-Δ1 nop15::GAL-3HA-NOP15 TRP1 rpf2::RPF2-TAP URA3</i>	This study
JWY 8293	<i>MATa ura3-52 trp1-Δ101 lys2-801 his3-Δ200 leu2-Δ1 rrp1::GAL-3HA-RRP1 TRP1</i>	This study
JWY 8295	<i>MATa ura3-52 trp1-Δ101 lys2-801 his3-Δ200 leu2-Δ1 rrp1::GAL-3HA-RRP1 TRP1 rpf2::RPF2-TAP URA3</i>	This study
JWY 8110	<i>MATα trp1 lys2-801 ura3-52 his3Δ200 pep4::HIS3 prb1Δ1.6R can rpf2::GAL-3HA-RPF2 TRP1 Gal⁺</i>	Zhang et al, 2007
JWY 8141	<i>MATα trp1 lys2-801 ura3-52 his3Δ200 pep4::HIS3 prb1Δ1.6R can rpf2::GAL-3HA-RPF2 TRP1 nop7::NOP7-TAP URA3</i>	Zhang et al., 2007
JWY 7419	<i>MATa leu2-Δ1 trp1Δ63 ura3-52 ebp2-1. KAN</i>	Huber et al, 2000

JWY 9013	<i>MATa leu2-Δ1 trp1Δ63 ura3-52 ebp2-1. KAN rpf2::RPF2-TAP URA3</i>	This study
JWY 8832	<i>MATa ura3Δ0 his3Δ1 met15Δ0 leu2Δ0</i>	Ghaemmaghmi et al, 2003
JWY 8849	<i>MATa ura3Δ0 his3Δ1 met15Δ0 leu2Δ0 rlp7::RLP7-TAP HIS3MX6</i>	Ghaemmaghmi et al, 2003
JWY 8840	<i>MATa ura3Δ0 his3Δ1 met15Δ0 leu2Δ0 nsa3::NSA3-TAP HIS3MX6</i>	Ghaemmaghmi et al, 2003
JWY 8856	<i>MATa ura3Δ0 his3Δ1 met15Δ0 leu2Δ0 ytm1::YTM1-TAP HIS3MX6</i>	Ghaemmaghmi et al, 2003
JWY 8306	<i>MATa ura3-52 trp1-Δ101 lys2-801 his3-Δ200 leu2-Δ1 rlp7::GAL-3HA-RLP7 TRP1 rpf2::RPF2-TAP URA3 rat1::RAT1-3HA HIS3</i>	This study
JWY 8307	<i>MATa ura3-52 trp1-Δ101 lys2-801 his3-Δ200 leu2-Δ1 rrp1::GAL-3HA-RRP1 TRP1 rpf2::RPF2-TAP URA3 rat1::RAT1-3HA HIS3</i>	This study
JWY8312	<i>MATa ura3-52 trp1-Δ101 lys2-801 his3-Δ200 leu2-Δ1 rlp7::GAL-3HA-RLP7 TRP1 rpf2::RPF2-TAP URA3 xrn1::XRN1-GFP HIS3</i>	This study
JWY 8392	<i>MATa ura3-52 trp1-Δ101 lys2-801 his3-Δ200 leu2-Δ1 rlp7::GAL-3HA-RLP7 TRP1 rpf2::RPF2-TAP URA3 rrp17::RRP17-3HA KANMX6</i>	This study
JWY 8308	<i>MATa ura3-52 trp1-Δ101 lys2-801 his3-Δ200 leu2-Δ1 rpf2::RPF2-TAP URA3</i>	This study
JWY 8352	<i>MATa ura3-52 trp1-Δ101 lys2-801 his3-Δ200 leu2-Δ1 rail::KANMX6 rat1::RAT1-3HA HIS3 rpf2::RPF2-TAP URA3</i>	This study
JWY 8378	<i>MATa ura3-52 trp1-Δ101 lys2-801 his3-Δ200 leu2-Δ1 rpf2::RPF2-TAP URA3 rat1::RAT1-3HA HIS3 pop3::GAL-3HA-POP3 KANMX6</i>	This study
JWY 8887	<i>MATa ura3Δ0 his3Δ1 met15Δ0 leu2Δ0 rat1::RAT1-TAP HIS3MX6</i>	Ghaemmaghmi et al, 2003
JWY 8383	<i>MATa ura3-52 trp1-Δ101 lys2-801 his3-Δ200 leu2-Δ1 rlp7::GAL-3HA-RLP7 TRP1 rpf2::RPF2-TAP URA3 rpL17b::RPL17B-3HA KANMX6</i>	This study
JWY 8385	<i>MATa ura3-52 trp1-Δ101 lys2-801 his3-Δ200 leu2-Δ1 rlp7::GAL-3HA-RLP7 TRP1 rpf2::RPF2-TAP URA3 rpL26a::RPL26A-3HA KANMX6</i>	This study
JWY 8387	<i>MATa ura3-52 trp1-Δ101 lys2-801 his3-Δ200 leu2-Δ1 rlp7::GAL-3HA-RLP7 TRP1 rpf2::RPF2-TAP URA3 rpL26b::RPL26B-3HA KANMX6</i>	This study
JWY 8398	<i>MATa ura3-52 trp1-Δ101 lys2-801 his3-Δ200 leu2-Δ1 rlp7::GAL-3HA-RLP7 TRP1 rpf2::RPF2-TAP URA3 rpL35b::RPL35B-3HA KANMX6</i>	This study
JWY 8389	<i>MATa ura3-52 trp1-Δ101 lys2-801 his3-Δ200 leu2-Δ1 rlp7::GAL-3HA-RLP7 TRP1 rpf2::RPF2-TAP URA3</i>	This study

JWY 8389	<i>MATa ura3-52 trp1-Δ101 lys2-801 his3-Δ200 leu2-Δ1 rlp7::GAL-3HA-RLP7 TRP1 rpf2::RPF2-TAP URA3 rpl37a::RPL37A-3HA KANMX6</i>	This study
JWY 8390	<i>MATa ura3-52 trp1-Δ101 lys2-801 his3-Δ200 leu2-Δ1 rlp7::GAL-3HA-RLP7 TRP1 rpf2::RPF2-TAP URA3 rpl37b::RPL37B-3HA KANMX6</i>	This study
JWY 8394	<i>MATa ura3-52 trp1-Δ101 lys2-801 his3-Δ200 leu2-Δ1 rlp7::GAL-3HA-RLP7 TRP1 rpf2::RPF2-TAP URA3 rpl19a::RPL19A-3HA KANMX6</i>	This study
JWY 8396	<i>MATa ura3-52 trp1-Δ101 lys2-801 his3-Δ200 leu2-Δ1 rlp7::GAL-3HA-RLP7 TRP1 rpf2::RPF2-TAP URA3 rpl19b::RPL19B-3HA KANMX6</i>	This study
JWY 9027	<i>MATa ura3-52 trp1-Δ101 lys2-801 his3-Δ200 leu2-Δ1 rlp7::GAL-3HA-RLP7 rpf2::RPF2-TAP URA3 rpl4a::RPL4A-3HA KANMX6</i>	This study
JWY 7159	<i>MATa ura3Δ0 his3Δ1 met15Δ0 leu2Δ0 rpl17b::RPL17B-TAP HIS3MX6</i>	Ghaemmaghmi et al, 2003
JWY 9021	<i>MAT? pra1-1 prb1-1 prc1-1 cps1-3 Dhis3 leu2-3,112 Dura3 trp1::LEU2 NPA2-TAP::kURA3</i>	Rosado et al, 2007
JWY 8814	<i>MATa ura3Δ0 his3Δ1 met15Δ0 leu2Δ0 nsa1::NSA1-TAP HIS3MX6</i>	Ghaemmaghmi et al, 2003
JWY 8809	<i>MATa ura3Δ0 his3Δ1 met15Δ0 leu2Δ0 nog2::NOG2-TAP HIS3MX6</i>	Ghaemmaghmi et al, 2003
JWY 9092	<i>Mat a, ade2-1, trp1-1, can1-100, leu2-3, 112, his3-11, 15, ura3Δ, GAL psi+, ssd1-Δ2, Met::rat1 HIS3 xrn1Δ::Nat GAL::HA3-rrp17- KanMX6 rpf2::RPF2-TAP URA3</i>	This study
JWY 9087	<i>MATa ura3-52 leu2Δ1 his3Δ200 trp1Δ63 rat1-1^{ts} rpl17b::HIS3 rpl17a::GAL-3HA-RPL17A KAN</i>	This study
JWY 7767	<i>MATa ura3Δ0 his3Δ1 met15Δ0 leu2Δ0 enp1::ENP1-TAP HIS3MX6</i>	Ghaemmaghmi et al, 2003
JWY 9094	<i>MATa ura3-52 trp1-Δ101 lys2-801 his3-Δ200 leu2-Δ1 nop7::GAL-3HA-NOP7 TRP1 rpf2::RPF2-TAP URA3 rpl26b::RPL26B-3HA KAN</i>	This study
JWY 9095	<i>MATa ura3-52 trp1-Δ101 lys2-801 his3-Δ200 leu2-Δ1 nop7::GAL-3HA-NOP7 TRP1 rpf2::RPF2-TAP URA3 rpl35b::RPL35B-3HA KAN</i>	This study
JWY 9096	<i>MATa ura3-52 trp1-Δ101 lys2-801 his3-Δ200 leu2-Δ1 nop7::GAL-3HA-NOP7 TRP1 rpf2::RPF2-TAP URA3 rpl37b::RPL37B-3HA KAN</i>	This study
JWY 9097	<i>MATa ura3-52 trp1-Δ101 lys2-801 his3-Δ200 leu2-Δ1 nop15::GAL-3HA-NOP15 TRP1 rpf2::RPF2-TAP URA3 rpl26b::RPL26B-3HA KAN</i>	This study
JWY 9098	<i>MATa ura3-52 trp1-Δ101 lys2-801 his3-Δ200 leu2-Δ1 nop15::GAL-3HA-NOP15 TRP1 rpf2::RPF2-TAP URA3</i>	This study

JWY 9099	<i>MATa ura3-52 trp1-Δ101 lys2-801 his3-Δ200 leu2-Δ1 nop15::GAL-3HA-NOP15 TRP1 rpf2::RPF2-TAP URA3 rpl37b::RPL37B-3HA KAN</i>	This study
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Supplementary Table 3: Ratios from Figure 1B

RNA	Lane	Lane Name	AU-BG	A3/A2	fold change	A3/total B	fold change	B1S/total B	fold change
A2	1	EBP2, GAL	163505	0.56		0.14		0.66	
A3	1		92132						
B1L	1		222223						
B1S	1		434210						
A2	2	EBP2, GLU	664013	0.08	-7.00	0.36	2.57	0.43	-1.53
A3	2		53562						
B1L	2		84404						
B1S	2		64733						
A2	3	TIF6, GAL	156865	0.57		0.08		0.56	
A3	3		89506						
B1L	3		489033						
B1S	3		618229						
A2	4	TIF6, GLU	462720	0.14	-4.07	0.03	-2.67	0.64	1.14
A3	4		63597						
B1L	4		689373						
B1S	4		1218074						
A2	5	NOP7, GAL	248459	0.22		0.03		0.52	
A3	5		53756						
B1L	5		883127						
B1S	5		968154						
A2	6	NOP7, GLU	548950	0.74	3.36	0.43	14.33	0.34	-1.53
A3	6		405994						
B1L	6		630004						
B1S	6		321181						
A2	7	YTM1, GAL	366115	0.20		0.03		0.52	
A3	7		72491						
B1L	7		1039738						
B1S	7		1140389						
A2	8	YTM1, GLU	394454	0.92	4.60	0.30	10.00	0.45	-1.16
A3	8		364144						
B1L	8		658622						
B1S	8		545538						
A2	9	WT, GAL	304784	0.19		0.03		0.54	
A3	9		58374						
B1L	9		798635						
B1S	9		945577						
A2	10	WT, GLU	463583	0.12	-1.58	0.03	1.00	0.64	1.19
A3	10		57376						
B1L	10		590986						
B1S	10		1070473						
A2	11	RLP7, GAL	447558	0.17		0.03		0.50	
A3	11		74506						
B1L	11		1220907						
B1S	11		1236275						
A2	12	RLP7, GLU	963037	0.67	3.94	0.43	14.33	0.32	-1.56
A3	12		647905						
B1L	12		1040166						
B1S	12		480102						
A2	13	NSA3, GAL	417407	0.10		0.02		0.57	
A3	13		43507						
B1L	13		899484						
B1S	13		1177607						
A2	14	NSA3, GLU	968337	0.62	6.20	0.44	22.00	0.28	-2.04
A3	14		601226						
B1L	14		993828						
B1S	14		387041						
A2	15	NOP15, GAL	217147	0.19		0.03		0.52	
A3	15		40909						
B1L	15		691689						
B1S	15		741163						
A2	16	NOP15, GLU	886082	0.66	3.47	0.47	15.67	0.24	-2.17
A3	16		586740						
B1L	16		954269						
B1S	16		297864						
A2	17	RRP1, GAL	224433	0.28		0.04		0.48	
A3	17		61914						
B1L	17		838308						
B1S	17		772866						
A2	18	RRP1, GLU	531090	0.32	1.14	0.17	4.25	0.54	1.13
A3	18		169453						
B1L	18		473710						
B1S	18		548511						
A2	21	ERB1, GAL	616488	0.15		0.03		0.65	
A3	21		91063						
B1L	21		966541						
B1S	21		1784975						
A2	22	ERB1, GLU	1931788	0.57	3.80	0.42	14.00	0.32	-2.03
A3	22		1100706						
B1L	22		1784742						
B1S	22		852006						