

Supplementary Material Vinciguerra et al.

Materials and Methods

Plasmid and strain constructions

Plasmids and strains used in this study are summarised in supplementary Table II and Table III. To obtain the mutant strain GFP-*yra1-8*, the *yra1-8* coding sequence (Zenklusen *et al*, 2002) was amplified by PCR and cloned as a Sall fragment into pPS808-GAL-GFP (URA3, 2 μ). GAL-GFP-*yra1-8* was subcloned as a BamHI/EcoRI fragment into YcPLac22 (TRP1, CEN) to generate pFS1975. GFP-*yra1-8* was subsequently subcloned as an XhoI PCR fragment behind the *YRA1* promoter in YcPLac22-HA-YRA1 \pm 500 (Zenklusen *et al*, 2001; Zenklusen *et al*, 2002) to generate pFS2581. HA-GFP-*yra1-8* \pm 500 was subcloned as a BamHI fragment in YcPLac111 to generate pFS2554.

Deletions of *MLP1*, *MLP2* or *RRP6* in the *YRA1* shuffle strain (*yra1::HIS3*, pURA3-*YRA1*) were obtained using PCR based homologous recombination as described (Longtine *et al*, 1998). The double deletion strain Δ *mlp1/2* strain was obtained by crossing the single deletion *YRA1* shuffle *mlp1::TRP1* and *YRA1* shuffle *mlp2::TRP1* strains and analysis of segregants by PCR. The Mlp1-ProtA (FSY1567) and Mlp2-ProtA (FSY1351) strains were obtained by genomic tagging of *MLP1* and *MLP2* with a ProtA-TRP1 cassette in the *YRA1* shuffle background as described (Zenklusen *et al*, 2002).

The strains used in Table I have been obtained as following. *MLP1* and *MLP2* were deleted in NAB2 shuffle (ACY429) (Green *et al*, 2002) using a TRP1 marker to generate NAB2 shuffle Δ *mlp1* (FSY2081) and NAB2 shuffle Δ *mlp2* (FSY2082). The same marker was used in SUB2 shuffle (FSY1465) (Jensen *et al*, 2001) to obtain SUB2 shuffle Δ *mlp1* (FSY1555) and SUB2 shuffle Δ *mlp2* (FSY1556), in Δ *cbp20* (FSY265) (Colot *et al*, 1996) and Δ *cbp80* (FSY211) (Fortes *et al*, 1999) to obtain Δ *cbp20 Δ *mlp1* (FSY2024), Δ *cbp20 Δ *mlp2* (FSY2025) and Δ *cbp80 Δ *mlp1* (FSY2026), Δ *cbp80 Δ *mlp2* (FSY2027), in *rna14-1* (FSY582)****

and *rna15-1* (FSY538) (Minvielle-Sebastia *et al*, 1991) to obtain *rna14-1Δmlp1* (FSY2071), *rna14-1Δmlp2* (FSY2072) and *rna15-1Δmlp1* (FSY2073), *rna15-1Δmlp2* (FSY2074), in *pap1-1* (FSY1968) (Patel and Butler, 1992) to obtain *pap1-1Δmlp1* (FSY1986) and *pap1-1Δmlp2* (FSY1987), in *npl3-1* (FSY1175) (Henry *et al*, 1996) to obtain *npl3-1Δmlp1* (FSY1825) and *npl3-1Δmlp2* (FSY1826), in *mex67-5* (FSY1982) (Jimeno *et al*, 2002) to generate *mex67-5Δmlp1* (FSY1983) and *mex67-5Δmlp2* (FSY1984), in *rat8-2* (FSY535) (Snay-Hodge *et al*, 1998) to generate *rat8-2Δmlp1* (FSY2022) and *rat8-2Δmlp2* (FSY2023). *MLP1* and *MLP2* were also deleted in *Δhpr1* (FSY1624) (Zenklusen *et al*, 2002) using a HIS3 marker to generate *Δhpr1Δmlp1* (FSY1626) and *Δhpr1Δmlp2* (FSY1627). Only *MLP2* was deleted in *rat7-1* (FSY138) (Gorsch *et al*, 1995) using a HIS3 marker to generate *rat7-1Δmlp2* (FSY2021). Finally *RRP6* was deleted in *Δmlp1* (FSY1822) using a KAN resistance marker to generate *Δmlp1Δrrp6* (FSY1842) and in *Δmlp2* (FSY1823) to generate *Δmlp2Δrrp6* (FSY1843).

Antibodies and Western blotting

Western blots were performed according to standard procedures. The anti-Yra1p antibody was used at a 1:2000 dilution, anti-Yra2p at 1:1500, anti-Nab2p (a gift from A. Corbett) at 1:10000, anti-Mex67p (a gift from C. Dargemont) at 1:10000 and anti-Crm1p at a 1:500 dilution. The protein signals were revealed with Super Signal West Pico substrate or West Femto Chemiluminescent substrate (Pierce).

Primer pairs used for chromatin immunoprecipitation (ChIP) analysis

Immuno-precipitated DNA was analysed by quantitative PCR using the following primer pairs for the GAL1 promoter: OFS884 (5' GCCCCACAAACCTTCAAATTAACG 3') and OFS885 (5' CTTCGCTGATTAATTACCCAGAAATAA 3'), and for the intergenic

region, OFS710 (5' CGCATTACCAGACGGAGATGT 3') and OFS711 (5' CAAGCAAGCCTTGTGCATAAGA 3').

Global analysis of transcript levels with Affymetrix DNA microarrays

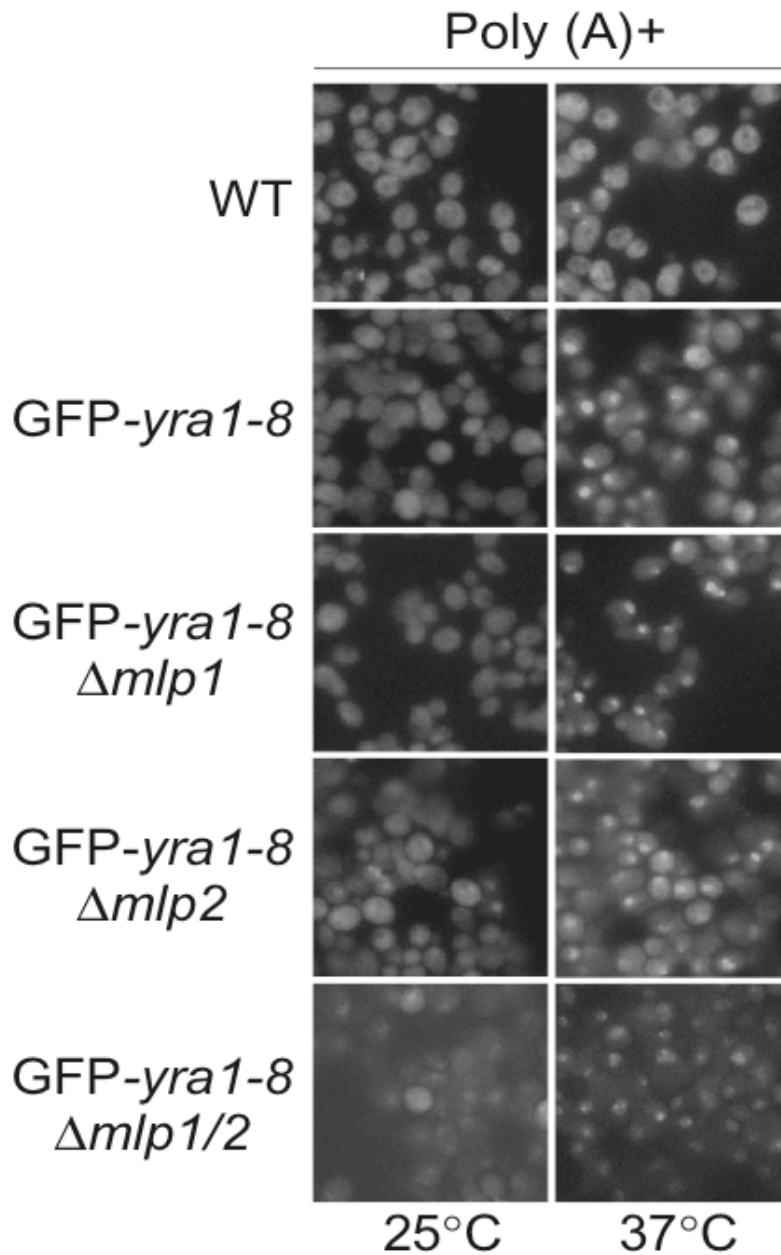
The wild-type *YRA1*, *YRA1Δmlp2*, *GFP-yra1-8* and *GFP-yra1-8Δmlp2* strains were grown at 25°C to $OD_{600}=0.6$ ($0.5 \cdot 10^6$ cells/ml) in synthetic complete medium and shifted to 37°C for 2.5h. Total RNA was prepared using the hot phenol extraction procedure. Total RNA labelling and microarray hybridization was performed using the Affymetrix Gene Chip Yeast Genome S98 Array and protocols described by Affymetrix, Inc. (Santa Clara, CA). For each strain, the experiment was performed in duplicate using independent cultures and RNA preparations. Data were analyzed using Affymetrix Microarray suite 5.. To identify genes differentially expressed in *GFP-yra1-8*, each gene chip was compared to the two wild-type *YRA1* chips. A transcript was considered to decrease in *GFP-yra1-8* if (i) it scored as “decreased” in 3 out of 4 comparisons and if (ii) the four comparisons gave a mean expression change of at least two-fold, i.e., the median log ratio of the 4 comparisons was equal or less than -1 as calculated by the Affymetrix software. 194 transcripts met these criteria (Supplementary Table I, column 3). The expression levels (mean intensity values of two gene chips) of these 194 transcripts in the four strains analyzed are also shown as such (columns 4-7) or as a percentage of wild-type *YRA1* (columns 8-11). The 58 transcripts for which the intensity or expression level ratio in *GFP-yra1-8Δmlp2* versus *GFP-yra1-8* was equal or higher to 1.5, were considered as significantly rescued by the loss of Mlp2p, i.e. significantly down-regulated by Mlp2p in *GFP-yra1-8* (columns 12-13, dark green). The 194 genes/transcripts have been numbered according to increasing *GFP-yra1-8Δmlp2/GFP-yra1-8* ratios.

Raw data are available at <http://www.ebi.ac.uk/arrayexpress/query/entry>, accession number E-MEXP-130.

References for supplementary material, Vinciguerra et al.

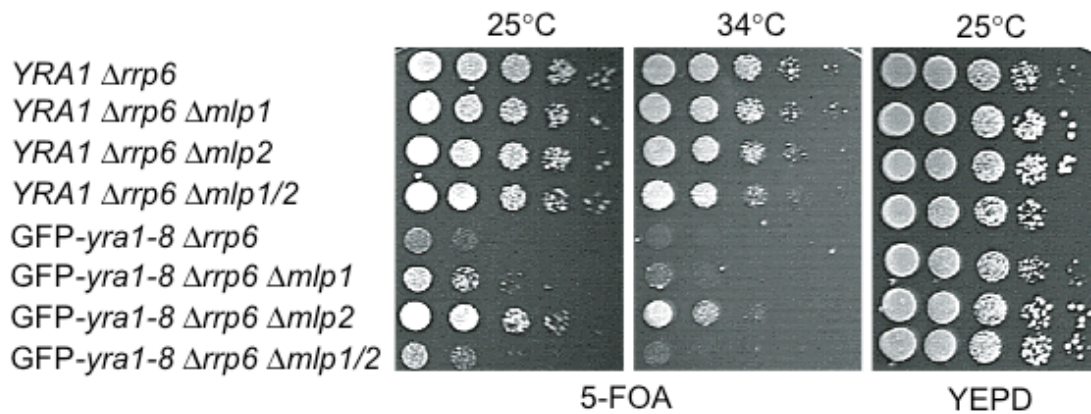
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Supplementary Figure 1 Vinciguerra et al.

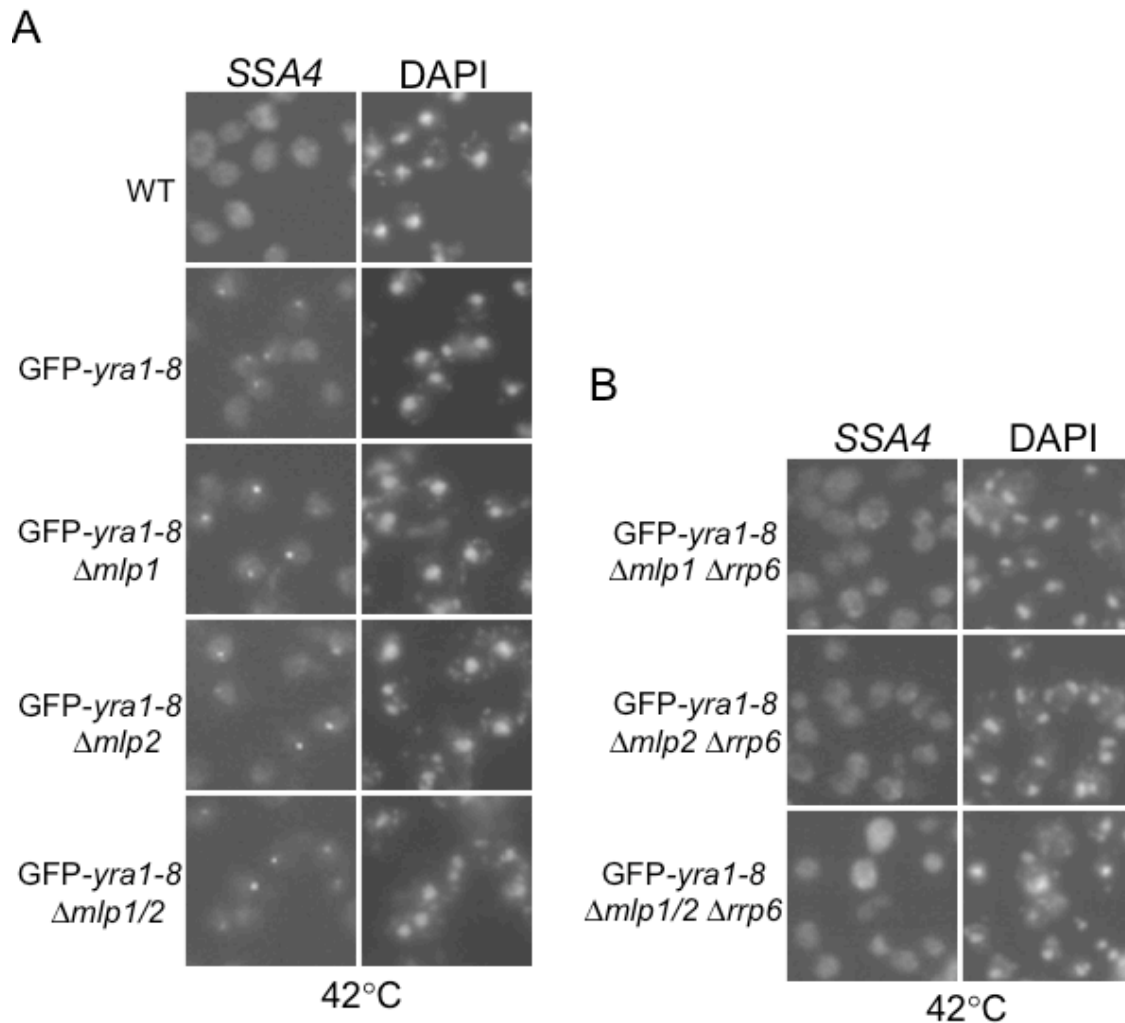


Loss of Mlp1p or Mlp2p does not rescue the poly (A)+ RNA export defect of the GFP-*yra1-8* mutant strain. Wild-type, GFP-*yra1-8*, GFP-*yra1-8* $\Delta mlp1$, GFP-*yra1-8* $\Delta mlp2$ or GFP-*yra1-8* $\Delta mlp1/2$ were grown at 25°C and either kept at 25°C or shifted to 37°C for 1h. After fixation, the distribution of poly(A)+ RNA was examined by in situ hybridization with Cy3-labelled oligodT₍₅₅₎.

Supplementary Figure 2 Vinciguerra et al.



The synthetic interaction between GFP-*yra1-8* and $\Delta rrp6$ is alleviated in the context of $\Delta mlp2$, $\Delta mlp1$ or $\Delta mlp1/2$. The YRA1 shuffle strain (*yra1::HIS3*, pURA3-YRA1) as such or deleted for *RRP6* and combined with $\Delta mlp1$, $\Delta mlp2$ or $\Delta mlp1/2$ was transformed with wild-type *YRA1* or the GFP-*yra1-8* plasmids. Transformants were grown in selective medium and 10-fold dilutions spotted on YEPD to control for cell number or on 5-FOA to select against the wild-type pURA3-YRA1 plasmid. Plates were incubated for 3 days at 25°C and 34°C.



Loss of Mlp1p, Mlp2p or both in GFP-*yra1-8* does not suppress accumulation of newly synthesized *SSA4* heat shock transcripts within nuclear foci. (A) Wild-type *YRA1* or GFP-*yra1-8* strains in combination with $\Delta mlp1$, $\Delta mlp2$ or $\Delta mlp1/2$ were shifted to 42°C for 30 min. After fixation, the distribution of *SSA4* transcripts was examined by in situ hybridization with Cy3-labelled oligonucleotide probes specific for *SSA4*. (B) The accumulation of *SSA4* transcripts in nuclear foci depends on Rrp6p. *RRP6* was deleted in the above-mentioned GFP-*yra1-8* $\Delta mlp1$, GFP-*yra1-8* $\Delta mlp2$ and GFP-*yra1-8* $\Delta mlp1/2$ strains. Cells were shifted to 42°C for 30 min and processed as described in (A).

Supplementary Table I Vinciguerra et al.

no	affymetrix code	med log ratio	expression level				expression level (% of YRA1)			
		GFP- <i>yra1-8</i> vs YRA1	YRA1	YRA1 Δ <i>mlp2</i>	GFP- <i>yra1-8</i>	GFP- <i>yra1-8</i> Δ <i>mlp2</i>	YRA1	YRA1 Δ <i>mlp2</i>	GFP- <i>yra1-8</i>	GFP- <i>yra1-8</i> Δ <i>mlp2</i>
1	10400_at	-3.34	1.85	0.6	0.05	0.6	100	32.4	2.7	32.4
2	7044_at	-1.28	3.55	2.55	0.95	3.95	100	71.8	26.8	111.3
3	7895_at	-1.49	4.35	3.95	1.35	5.15	100	90.8	31.0	118.4
4	8050_at	-2.03	3.6	3.3	0.7	2.65	100	91.7	19.4	73.6
5	5414_i_at	-4.93	1.4	0.05	0.05	0.15	100	3.6	3.6	10.7
6	5216_at	-1.72	147.55	130.75	37.45	112.25	100	88.6	25.4	76.1
7	10399_at	-1.66	4.9	4.1	1.25	3.3	100	83.7	25.5	67.3
8	9280_at	-1.69	4.65	6	1.4	3.6	100	129.0	30.1	77.4
9	8785_at	-2.38	2.4	2.45	0.5	1.25	100	102.1	20.8	52.1
10	5330_at	-2.18	8.5	7.05	2.4	5.95	100	82.9	28.2	70.0
11	9232_at	-2.2	3.2	3.55	0.8	1.9	100	110.9	25.0	59.4
12	5323_at	-1.31	94.4	114.6	32.15	72.85	100	121.4	34.1	77.2
13	9640_at	-1.27	5.65	4	2.1	4.75	100	70.8	37.2	84.1
14	5177_at	-1.58	7.75	7.55	2.25	5	100	97.4	29.0	64.5
15	9554_at	-2.05	8.95	7.15	1.95	4	100	79.9	21.8	44.7
16	11240_s_at	-1.95	4.05	0.65	1.45	2.9	100	16.0	35.8	71.6
17	2605_s_at	-1.63	92.8	66.35	30.4	60.35	100	71.5	32.8	65.0
18	10809_g_at	-1.5	10.4	12.1	3.4	6.55	100	116.3	32.7	63.0
19	4224_at	-1.4	12.2	10.35	4.25	8.05	100	84.8	34.8	66.0
20	11273_at	-1.96	9.1	10.6	2.7	5.05	100	116.5	29.7	55.5
21	8915_at	-1.16	37	41.35	14.3	26.65	100	111.8	38.6	72.0
22	5683_at	-1.22	13.3	7.95	4.45	8.2	100	59.8	33.5	61.7
23	11276_at	-2.35	4	0.6	0.9	1.65	100	15.0	22.5	41.3
24	9866_i_at	-1.41	6.95	3.3	1.8	3.25	100	47.5	25.9	46.8
25	2233_at	-1.47	8.85	5.6	3.55	6.4	100	63.3	40.1	72.3
26	4582_at	-1.49	74.3	54.05	26.4	47.5	100	72.7	35.5	63.9
27	8153_at	-1.84	22.15	15.95	6.7	12.05	100	72.0	30.2	54.4
28	2606_s_at	-1.82	268.1	176.3	84.65	151.75	100	65.8	31.6	56.6
29	10689_at	-2.35	796.6	531.1	201.15	358.65	100	66.7	25.3	45.0
30	4641_s_at	-1.31	11.75	10	4.6	8.2	100	85.1	39.1	69.8
31	8753_at	-1.79	5.15	2.4	2.05	3.65	100	46.6	39.8	70.9
32	3808_s_at	-1.21	298.75	235.3	114.8	203.9	100	78.8	38.4	68.3
33	7821_at	-1.43	15.85	13.6	5.6	9.9	100	85.8	35.3	62.5
34	5413_at	-1.19	202.65	204.3	75.65	133.05	100	100.8	37.3	65.7
35	5382_at	-1.17	149.3	127.75	64.8	112.6	100	85.6	43.4	75.4
36	2184_s_at	-1.13	132.7	133.1	61.05	105.4	100	100.3	46.0	79.4
37	11079_at	-1.43	134.6	123.7	36.7	62.45	100	91.9	27.3	46.4
38	4431_at	-2.28	6.55	3.1	1.6	2.7	100	47.3	24.4	41.2
39	7546_at	-1	65.55	65.5	33.45	55.7	100	99.9	51.0	85.0
40	7828_at	-1.62	349.15	358.7	107.4	178.7	100	102.7	30.8	51.2
41	4430_at	-3.26	417.8	249.5	33.9	55.65	100	59.7	8.1	13.3
42	7290_at	-1.41	958.35	657.35	346.1	564.7	100	68.6	36.1	58.9
43	9575_at	-1.46	34.95	25.9	10.6	17.25	100	74.1	30.3	49.4
44	5929_at	-1.29	10.25	10.85	5.45	8.85	100	105.9	53.2	86.3
45	7499_at	-1.09	25.15	14.05	10.9	17.3	100	55.9	43.3	68.8
46	7973_at	-1.23	848.55	600.3	351.05	556.75	100	70.7	41.4	65.6
47	10294_at	-1.48	12.4	8.9	4.45	7.05	100	71.8	35.9	56.9
48	3204_at	-1.07	20.3	13.25	6.25	9.85	100	65.3	30.8	48.5
49	5089_at	-1.03	12.4	12	5.9	9.2	100	96.8	47.6	74.2
50	7547_at	-1	17.55	19.95	9.95	15.45	100	113.7	56.7	88.0
51	2607_s_at	-1.11	819.5	703	366.35	563.45	100	85.8	44.7	68.8
52	8173_at	-1.07	437.35	419.5	213.95	327.25	100	95.9	48.9	74.8
53	10623_at	-1.33	156.85	106	57.75	87.5	100	67.6	36.8	55.8
54	6896_at	-1.66	232	200.8	82.3	124.55	100	86.6	35.5	53.7
55	7075_at	-1.29	8.85	7.2	4.05	6.1	100	81.4	45.8	68.9
56	8864_at	-1.25	951.4	817.6	379.45	569.35	100	85.9	39.9	59.8
57	8444_at	-1.08	32.3	27.35	16.15	24.2	100	84.7	50.0	74.9
58	11181_at	-1.07	108.7	109.2	46.4	69.5	100	100.5	42.7	63.9
59	11369_at	-1.01	321.25	309.95	158.5	236.45	100	96.5	49.3	73.6
60	5381_at	-1.23	104.95	75.7	45.6	66.95	100	72.1	43.4	63.8
61	4009_at	-1.27	65.5	53.55	28.7	41.85	100	81.8	43.8	63.9
62	3646_s_at	-2.64	12.45	7.9	3.8	5.5	100	63.5	30.5	44.2
63	9227_i_at	-1.34	308.35	375.55	111.15	159.85	100	121.8	36.0	51.8
64	5643_at	-1.06	396.25	280.2	173.6	248.45	100	70.7	43.8	62.7
65	8778_at	-1.22	11.8	9.25	5.25	7.5	100	78.4	44.5	63.6
66	4028_at	-1.14	10.1	8.2	3.75	5.35	100	81.2	37.1	53.0
67	4451_at	-1.22	69.4	53.7	30.65	43.5	100	77.4	44.2	62.7
68	8186_at	-1.29	90.35	76.7	39.45	54.4	100	84.9	43.7	60.2

GFP- <i>yra1-8</i> Δ <i>mlp2</i> / GFP- <i>yra1-8</i>	
12.00	non-annotated SAGE orf Found forward in NC_001143 between 173981 and 174175
4.16	non-annotated SAGE orf Found reverse in NC_001134 between 164788 and 164997
3.81	<i>SPO19</i> YPL130W
3.79	non-annotated SAGE orf Found forward in NC_001147 between 1071000 and 1071164 w
3.00	CEN5 Centromere
3.00	<i>MIG2</i> YGL209W
2.64	non-annotated SAGE orf Found reverse in NC_001143 between 137683 and 137847
2.57	non-annotated SAGE orf Found reverse in NC_001145 between 433097 and 433231
2.50	<i>CPD1</i> YNR074C
2.48	YFR032C
2.38	non-annotated SAGE orf Found forward in NC_001145 between 733313 and 733531
2.27	YFR026C
2.26	YMR018W
2.22	<i>RCK1</i> YGL158W
2.05	<i>NAT4</i> YMR069W
2.00	non-annotated SAGE orf Found reverse in NC_001133 between 219555 and 219719
1.99	chromosome XVI. Found forward in NC_001148 between 111147 and 112146
1.93	non-annotated SAGE orf Found forward in NC_001142 between 471954 and 472142
1.89	<i>CSM2</i> YIL132C
1.87	non-annotated SAGE orf Found forward in NC_001133 between 73444 and 73614
1.86	<i>RNH35</i> YNL072W
1.84	<i>MIG3</i> YER028C
1.83	non-annotated SAGE orf Found reverse in NC_001133 between 3170 and 3394
1.81	<i>BSC3</i> YLR465C
1.80	chromosome VI. Found forward in NC_001138 between 73614 and 74613
1.80	YHL026C
1.80	non-annotated SAGE orf Found forward in NC_001147 between 33183 and 33335
1.79	chromosome XVI. Found forward in NC_001148 between 112147 and 113146
1.78	<i>CWP1</i> YKL096W
1.78	non-annotated SAGE orf Found forward in NC_001139 between 319845 and 319982
1.78	non-annotated SAGE orf Found forward in NC_001146 between 547109 and 547366
1.78	RDN37-1 35S ribosomal RNA
1.77	YPL068C
1.76	RPR1 RNase P RNA
1.74	YFL006W
1.73	chromosome VII. Found forward in NC_001139 between 138050 and 139047
1.70	<i>PRY3</i> YJL078C
1.69	YHR095W
1.67	<i>OPT2</i> YPR194C
1.66	<i>ALD6</i> YPL061W
1.64	<i>HXT1</i> YHR094C
1.63	<i>TIP1</i> YBR067C
1.63	<i>ARG80</i> YMR042W
1.62	non-annotated SAGE orf Found reverse in NC_001136 between 340810 and 340977
1.59	non-annotated SAGE orf Found reverse in NC_001148 between 678411 and 678614
1.59	<i>FAS2</i> YPL231W
1.58	YLR042C
1.58	YHRCDELTA4
1.56	<i>PUS2</i> YGL063W
1.55	YPR195C
1.54	chromosome XVI. Found forward in NC_001148 between 113147 and 113815
1.53	<i>ALD4</i> YOR374W
1.52	<i>MAE1</i> YKL029C
1.51	<i>GFD2</i> YCL036W
1.51	YBR219C
1.50	<i>ACC1</i> YNR016C
1.50	<i>RGS2</i> YOR107W
1.50	<i>FAR1</i> YJL157C
1.49	<i>CLN3</i> YAL040C
1.47	<i>BLM3</i> YFL007W
1.46	non-annotated SAGE orf Found forward in NC_001141 between 26990 and 27169
1.45	<i>YRF1-6</i> YNL339C
1.44	non-annotated SAGE orf Found reverse in NC_001145 between 671528 and 671701
1.43	<i>RNR1</i> YER070W
1.43	YNR066C
1.43	non-annotated SAGE orf Found reverse in NC_001141 between 231169 and 231306
1.42	<i>TRM5</i> YHR070W
1.38	YOR342C

69	5184_at	-1.05	106.35	91.5	56.4	77.7	100	86.0	53.0	73.1
70	9796_at	-1.72	49.35	43.65	15.7	21.6	100	88.4	31.8	43.8
71	3762_s_at	-1.39	183.05	163.3	74.9	102.75	100	89.2	40.9	56.1
72	10831_s_a	-1.12	30.3	28.55	14.5	19.85	100	94.2	47.9	65.5
73	10391_at	-1.23	147.95	119.35	64.7	88.35	100	80.7	43.7	59.7
74	4019_at	-1.38	16.8	14.05	7.95	10.75	100	83.6	47.3	64.0
75	11101_at	-1.33	33.85	35.5	13.95	18.85	100	104.9	41.2	55.7
76	8713_at	-1.64	16.65	14.35	6.7	9.05	100	86.2	40.2	54.4
77	7346_at	-1.12	7.9	8.1	4	5.4	100	102.5	50.6	68.4
78	4600_at	-1.74	27.6	28.2	9.75	13.15	100	102.2	35.3	47.6
79	9229_i_at	-1.04	8.85	5.15	3.9	5.25	100	58.2	44.1	59.3
80	8981_at	-1.15	443	405.1	183.65	246.2	100	91.4	41.5	55.6
81	6906_at	-1.18	18.8	15.15	8.15	10.9	100	80.6	43.4	58.0
82	8922_at	-1.14	466.2	369.2	200.9	265.8	100	79.2	43.1	57.0
83	10282_at	-1.11	152.25	132	88.2	116.2	100	86.7	57.9	76.3
84	3718_s_at	-1.33	996.7	726.85	440.5	577.55	100	72.9	44.2	57.9
85	9293_at	-1.25	91.35	123.35	40.9	53.45	100	135.0	44.8	58.5
86	8726_at	-2.19	148.05	277.05	31.6	41.2	100	187.1	21.3	27.8
87	4942_at	-1.06	149.8	126.3	76.55	99.65	100	84.3	51.1	66.5
88	6373_g_at	-1.09	167.5	145.2	81.65	106.2	100	86.7	48.7	63.4
89	3114_s_at	-1.15	72.2	48.75	37.2	48.1	100	67.5	51.5	66.6
90	9020_at	-1.32	10.8	10.9	3.7	4.75	100	100.9	34.3	44.0
91	7015_at	-1.16	10.65	8.25	5.65	7.25	100	77.5	53.1	68.1
92	5173_at	-1.21	10.9	8.05	4.45	5.7	100	73.9	40.8	52.3
93	5758_at	-1.15	44.4	33.25	19.15	24.5	100	74.9	43.1	55.2
94	2253_s_at	-1.27	724.2	1061.65	328.05	419.55	100	146.6	45.3	57.9
95	10895_at	-1.09	21.5	16.6	9.45	12.05	100	77.2	44.0	56.0
96	10471_at	-1.48	75	68.75	33.05	41.9	100	91.7	44.1	55.9
97	10778_at	-1	405	410.05	200.4	252.05	100	101.2	49.5	62.2
98	4477_at	-1.09	27.65	21.1	11.8	14.8	100	76.3	42.7	53.5
99	7601_at	-1.23	16.4	16.75	7.1	8.9	100	102.1	43.3	54.3
100	5841_at	-1.08	6.65	6	2.6	3.25	100	90.2	39.1	48.9
101	2604_s_at	-1.8	14.9	8.25	5.6	7	100	55.4	37.6	47.0
102	10382_at	-1	241.05	222.6	117.35	146.35	100	92.3	48.7	60.7
103	4164_at	-1.28	739.15	601.9	308.7	384.45	100	81.4	41.8	52.0
104	8477_at	-1.09	61.95	51.95	31.05	38.65	100	83.9	50.1	62.4
105	8185_at	-1	349.25	272.95	167.15	207.5	100	78.2	47.9	59.4
106	10818_at	-1.12	15.4	8.55	5.65	7	100	55.5	36.7	45.5
107	5029_at	-1.89	3.4	1.45	0.85	1.05	100	42.6	25.0	30.9
108	8721_at	-1.43	6	5.3	2.35	2.9	100	88.3	39.2	48.3
109	2252_g_at	-1.17	933.05	1166.5	413.7	509.6	100	125.0	44.3	54.6
110	8730_g_at	-1.45	457.9	488.25	173.5	211.75	100	106.6	37.9	46.2
111	7476_at	-1.57	41.9	33.35	14.25	17.35	100	79.6	34.0	41.4
112	9967_at	-1.82	27.15	23.35	8.95	10.85	100	86.0	33.0	40.0
113	5807_at	-1.39	223.2	155.65	78.6	95.15	100	69.7	35.2	42.6
114	3115_at	-1.55	7.95	2.05	3.35	4.05	100	25.8	42.1	50.9
115	10758_at	-1.03	20.95	23.2	9.65	11.65	100	110.7	46.1	55.6
116	4660_i_at	-1.01	13.95	7.9	7.25	8.7	100	56.6	52.0	62.4
117	5465_f_at	-1.36	107.2	70.55	35.1	42	100	65.8	32.7	39.2
118	7609_at	-1.03	28.1	24.15	13.55	16.15	100	85.9	48.2	57.5
119	9189_at	-1.22	245.45	264.05	110.4	131.3	100	107.6	45.0	53.5
120	3834_s_at	-1.33	276.55	174	104.8	124.45	100	62.9	37.9	45.0
121	4324_s_at	-1.13	270.8	218.35	131.65	156.3	100	80.6	48.6	57.7
122	4534_at	-1.05	55.55	52.3	22.25	26.4	100	94.1	40.1	47.5
123	7932_at	-1.08	104.1	117.95	54.6	64.75	100	113.3	52.4	62.2
124	5600_at	-1.25	86.2	66.25	38.85	46	100	76.9	45.1	53.4
125	10292_at	-1.22	30.55	28.5	14.5	17.1	100	93.3	47.5	56.0
126	5467_f_at	-1.19	893.05	934.9	366.5	430.9	100	104.7	41.0	48.3
127	4832_at	-1.37	96.5	102.9	38.25	44.95	100	106.6	39.6	46.6
128	2183_s_at	-1.26	77.15	59.9	32.4	37.95	100	77.6	42.0	49.2
129	6980_at	-1.49	13.2	12.3	4.4	5.15	100	93.2	33.3	39.0
130	10877_at	-1	52.45	50.8	29.45	34.45	100	96.9	56.1	65.7
131	9192_at	-1.88	23.35	15.1	3.85	4.5	100	64.7	16.5	19.3
132	5116_at	-1.16	235.95	246.45	115.65	134.3	100	104.5	49.0	56.9
133	4392_at	-1.24	668.6	673.45	263.25	305.25	100	100.7	39.4	45.7
134	10662_at	-1.02	49.6	44.2	25.45	29.3	100	89.1	51.3	59.1
135	2947_s_at	-1.16	71	41.4	32.85	37.75	100	58.3	46.3	53.2
136	9998_at	-1	6.6	8.8	4.05	4.65	100	133.3	61.4	70.5
137	8775_at	-1.28	6.25	4.3	3.4	3.9	100	68.8	54.4	62.4
138	5922_s_at	-1.02	146.25	119.3	75.6	85.2	100	81.6	51.7	58.3
139	9236_at	-1.21	67	90.35	29.1	32.75	100	134.9	43.4	48.9
140	10583_at	-1.01	718.05	505.85	366.45	412.3	100	70.4	51.0	57.4
141	10763_at	-1.15	47.45	39.15	22.7	25.4	100	82.5	47.8	53.5

1.38	<i>GCN1</i>	YGL195W
1.38		SNR55 snRNA
1.37		chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 941478 and 942778
1.37		non-annotated SAGE orf Found reverse in NC_001142 between 731735 and 731896
1.37	<i>VPS13</i>	YLL040C
1.35		non-annotated SAGE orf Found reverse in NC_001141 between 385816 and 385959
1.35	<i>ZAP1</i>	YJL056C
1.35		SNR19 snRNA
1.35		YBR032W
1.35		non-annotated SAGE orf Found forward in NC_001139 between 1012179 and 1012379
1.35		non-annotated SAGE orf Found forward in NC_001145 between 733267 and 733455
1.34	<i>RPS7B</i>	YNL096C
1.34	<i>FRM2</i>	YCL026C-A
1.32	<i>SUN4</i>	YNL066W
1.32		YLR073C
1.31		chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 942777 and 946791
1.31	<i>HUG1</i>	YML058w-a
1.30	<i>ZPS1</i>	YOL154W
1.30	<i>ADE6</i>	YGR061C
1.30	<i>DNF2</i>	YDR093W
1.29		chromosome X, complete chromosome sequence. Found forward in NC_001142 between 15138 and 15624
1.28	<i>ALF1</i>	YNL148C
1.28		non-annotated SAGE orf Found reverse in NC_001134 between 143662 and 143892
1.28	<i>SUT1</i>	YGL162W
1.28	<i>MCM3</i>	YEL032W
1.28		chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 21307 and 21608
1.28	<i>HMS2</i>	YJR147W
1.27	<i>SRP40</i>	YKR092C
1.26	<i>ASH1</i>	YKL185W
1.25		YHR048W
1.25		YPR157W
1.25		non-annotated SAGE orf Found forward in NC_001136 between 1022913 and 1023059
1.25		chromosome XVI, complete chromosome sequence. Found forward in NC_001148 between 110147 and 111146
1.25	<i>YBT1</i>	YLL048C
1.25	<i>RHR2</i>	YIL053W
1.24	<i>RK11</i>	YOR095C
1.24	<i>RPA190</i>	YOR341W
1.24		non-annotated SAGE orf Found forward in NC_001142 between 322217 and 322453
1.24	<i>HOP2</i>	YGL033W
1.23		YOL160W
1.23		chromosome VII, complete chromosome sequence. Found forward in NC_001139 between 20307 and 21306
1.22		non-annotated SAGE orf Found forward in NC_001146 between 89212 and 89394
1.22		SNR41 snRNA
1.21		YLR343W
1.21		SNR13 snRNA
1.21		chromosome X, complete chromosome sequence. Found forward in NC_001142 between 41889 and 42888
1.21		YKL161C
1.20		non-annotated SAGE orf Found forward in NC_001139 between 783944 and 784078
1.20		non-annotated SAGE orf Found reverse in NC_001137 between 52351 and 52515
1.19		YPR123C
1.19		SNR77 snRNA
1.19		YLL067C
1.19		YHR218W
1.19	<i>MIP6</i>	YHR015W
1.19		YPL183C
1.18	<i>SPR6</i>	YER115C
1.18		YLR040C
1.18		non-annotated SAGE orf Found reverse in NC_001137 between 52391 and 52549
1.18	<i>ATF2</i>	YGR177C
1.17		chromosome VII, forward in NC_001139 between 137050 and 138049 with 100% identity.
1.17		non-annotated SAGE orf Found reverse in NC_001134 between 376102 and 376293
1.17		YJR129C
1.17		SNR74 snRNA
1.16	<i>SCS3</i>	YGL126W
1.16	<i>DSE2</i>	YHR143W
1.15	<i>DHR2</i>	YKL078W
1.15		chromosome XII, complete chromosome sequence. Found forward in NC_001144 between 103543 and 104542
1.15	<i>REC102</i>	YLR329W
1.15		non-annotated SAGE orf Found forward in NC_001146 between 89019 and 89186
1.13		YDL184w-a
1.13		non-annotated SAGE orf Found forward in NC_001145 between 434355 and 434564
1.13	<i>URA6</i>	YKL024C
1.12	<i>TOR2</i>	YKL203C

142	2591_s_at	-1.25	8.7	4.9	3.85	4.3	100	56.3	44.3	49.4
143	3187_s_at	-1.38	117.75	76.1	49.8	55.5	100	64.6	42.3	47.1
144	3737_s_at	-1.46	27.45	15.7	10.75	11.95	100	57.2	39.2	43.5
145	10526_at	-1.05	73.35	52.15	36.05	40	100	71.1	49.1	54.5
146	7762_at	-1.12	269.4	204.45	123.45	135.4	100	75.9	45.8	50.3
147	11272_at	-1.03	32.05	56.65	14.25	15.6	100	176.8	44.5	48.7
148	5034_at	-1.32	100.9	90.4	42.6	46.5	100	89.6	42.2	46.1
149	6725_at	-2.36	53.05	47.5	8.85	9.65	100	89.5	16.7	18.2
150	8749_at	-1.2	12	7.75	4.7	5.1	100	64.6	39.2	42.5
151	3476_f_at	-1.21	41.45	40.2	20.7	22.35	100	97.0	49.9	53.9
152	10658_at	-1	85.35	77.2	41.35	44.45	100	90.5	48.4	52.1
153	3734_s_at	-1.32	35.8	25.75	18.9	20.3	100	71.9	52.8	56.7
154	6346_at	-1.07	26.6	18.35	11.8	12.6	100	69.0	44.4	47.4
155	4422_at	-1.07	357.9	276.9	161.2	171.95	100	77.4	45.0	48.0
156	10203_at	-1.21	80.8	79.25	39.5	41.85	100	98.1	48.9	51.8
157	3794_f_at	-1.38	56.9	44.8	23.6	25	100	78.7	41.5	43.9
158	4385_at	-1.38	9.05	7.45	2.8	2.95	100	82.3	30.9	32.6
159	3924_f_at	-1.2	52.3	44.25	24.15	25.15	100	84.6	46.2	48.1
160	3418_f_at	-1.18	55	45.65	23.25	24.15	100	83.0	42.3	43.9
161	3361_f_at	-1.31	52.35	44.15	22.8	23.4	100	84.3	43.6	44.7
162	8285_at	-1.03	23.2	20.15	11.9	12.2	100	86.9	51.3	52.6
163	4288_at	-2.3	85	87.9	20.9	21.4	100	103.4	24.6	25.2
164	7475_at	-1.04	213.6	188.75	107.4	109.4	100	88.4	50.3	51.2
165	3707_f_at	-1.25	53	41.05	24	24.4	100	77.5	45.3	46.0
166	9203_at	-1.26	357.6	286.85	147.05	146.75	100	80.2	41.1	41.0
167	3743_f_at	-1.2	73.95	43.6	34.25	34.05	100	59.0	46.3	46.0
168	3243_at	-1.18	39.5	24.25	16	15.9	100	61.4	40.5	40.3
169	8777_at	-1.08	319.45	323.8	167.2	162.25	100	101.4	52.3	50.8
170	4698_at	-1	35.8	37.15	15.3	14.75	100	103.8	42.7	41.2
171	3710_f_at	-1.04	62	42.3	32.65	31.35	100	68.2	52.7	50.6
172	3819_f_at	-1.17	75.25	43.65	35.1	33.65	100	58.0	46.6	44.7
173	9193_at	-2.4	120.4	113.95	16.3	15.45	100	94.6	13.5	12.8
174	3840_f_at	-1.16	51.7	43	23.55	22.05	100	83.2	45.6	42.6
175	3733_s_at	-1.19	24.6	13.5	10.25	9.55	100	54.9	41.7	38.8
176	4736_at	-1.39	274.65	231.75	94.7	87.95	100	84.4	34.5	32.0
177	3830_f_at	-1.08	82.25	51	44.1	40.7	100	62.0	53.6	49.5
178	9798_at	-1.07	154.05	134.65	80.15	73.95	100	87.4	52.0	48.0
179	8049_at	-2.48	7.15	3.95	1.85	1.7	100	55.2	25.9	23.8
180	3885_f_at	-1.3	89.35	51.15	35.5	32.1	100	57.2	39.7	35.9
181	3113_s_at	-1.41	42	46.05	28.4	25.6	100	109.6	67.6	61.0
182	5947_at	-1.17	11.2	7.45	5.85	5.25	100	66.5	52.2	46.9
183	3514_f_at	-1.04	53.5	42.9	23.75	20.85	100	80.2	44.4	39.0
184	5412_at	-1.73	6.9	5.55	2.4	2.1	100	80.4	34.8	30.4
185	3473_f_at	-1.07	78.4	51.4	38.35	32.2	100	65.6	48.9	41.1
186	3681_s_at	-1.85	3.7	2.15	1.25	1	100	58.1	33.8	27.0
187	3688_f_at	-1.01	76.9	43.5	37.65	30	100	56.6	49.0	39.0
188	5838_at	-1	55.3	46.05	31.95	25.3	100	83.3	57.8	45.8
189	9279_at	-1.07	9.45	8.5	4.1	3.2	100	89.9	43.4	33.9
190	9762_at	-1.8	532.25	557	160.6	118.55	100	104.7	30.2	22.3
191	8115_f_at	-1.13	38.85	33.25	20.65	15.2	100	85.6	53.2	39.1
192	8783_at	-1.15	4.7	1.75	2.1	1.35	100	37.2	44.7	28.7
193	6619_at	-2.14	7.15	2.6	2.7	1.65	100	36.4	37.8	23.1
194	10457_at	-1.08	3.95	2.5	1.65	0.8	100	63.3	41.8	20.3

1.12		chromosome XV, complete chromosome sequence. Found forward in NC_001147 between 962693 and 963692
1.11		YHL050C
1.11	<i>YRF1-5</i>	YLR467W
1.11	<i>DYN1</i>	YKR054C
1.10	<i>RPA135</i>	YPR010C
1.09		non-annotated SAGE orf Found reverse in NC_001133 between 222994 and 223152
1.09	<i>SCW11</i>	YGL028C
1.09	<i>HO</i>	YDL227C
1.09		non-annotated SAGE orf Found forward in NC_001146 between 116677 and 116865
1.08		TS(AGA)D1 tRNA-Ser
1.07	<i>TEF4</i>	YKL081W
1.07	<i>YRF1-4</i>	YLR466W
1.07		YDR111C
1.07	<i>FUR1</i>	YHR128W
1.06	<i>DIP2</i>	YLR129W
1.06		TS(AGA)L tRNA-Ser
1.05	<i>SPL2</i>	YHR136C
1.04		TS(AGA)A tRNA-Ser
1.04		TS(AGA)D2 tRNA-Ser
1.03		TS(AGA)E tRNA-Ser
1.03	<i>DSE3</i>	YOR264W
1.02		non-annotated SAGE orf Found reverse in NC_001140 between 34593 and 34790
1.02		SNR70 snRNA
1.02		TS(AGA)M tRNA-Ser
1.00	<i>EGT2</i>	YNL327W
0.99		TA(AGC)L tRNA-Ala
0.99		TL(GAG)G tRNA-Leu
0.97		YNR065C
0.96		non-annotated SAGE orf Found reverse in NC_001139 between 366397 and 366531
0.96		TA(AGC)M1 tRNA-Ala
0.96		TA(AGC)K1 tRNA-Ala
0.95		SNR73 snRNA
0.94		TS(AGA)J tRNA-Ser
0.93		YLR464W
0.93	<i>TNA1</i>	YGR260W
0.92		TA(AGC)K2 tRNA-Ala
0.92		SNR44 snRNA
0.92		non-annotated SAGE orf Found forward in NC_001147 between 1070794 and 1071003
0.90		TA(AGC)J tRNA-Ala
0.90		chromosome X, complete chromosome sequence. Found forward in NC_001142 between 14138 and 15137
0.90	<i>SPS1</i>	YDR523C
0.88		TS(AGA)B tRNA-Ser
0.88		SNR53 snRNA
0.84		TA(AGC)D tRNA-Ala
0.80		YMRWDELTA15
0.80		TA(AGC)M2 tRNA-Ala
0.79		non-annotated SAGE orf Found reverse in NC_001136 between 678003 and 678185
0.78		non-annotated SAGE orf Found reverse in NC_001145 between 297849 and 297983
0.74	<i>PHO84</i>	YML123C
0.74		non-annotated SAGE orf Found forward in NC_001147 between 464469 and 464630
0.64		YNR071C
0.61		YDL156W
0.48		non-annotated SAGE orf Found forward in NC_001143 between 145707 and 145880

List of the 194 transcripts that decrease more than two-fold in GFP-*yra1-8* versus wild-type *YRA1*. The levels of the 194 transcripts were compared in the four indicated strains as described in supplementary Materials and Methods section.