Supplementary Data

Dynamics of the yeast transcriptome during bread dough fermentation

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Figure S1 and Tables S1, S2

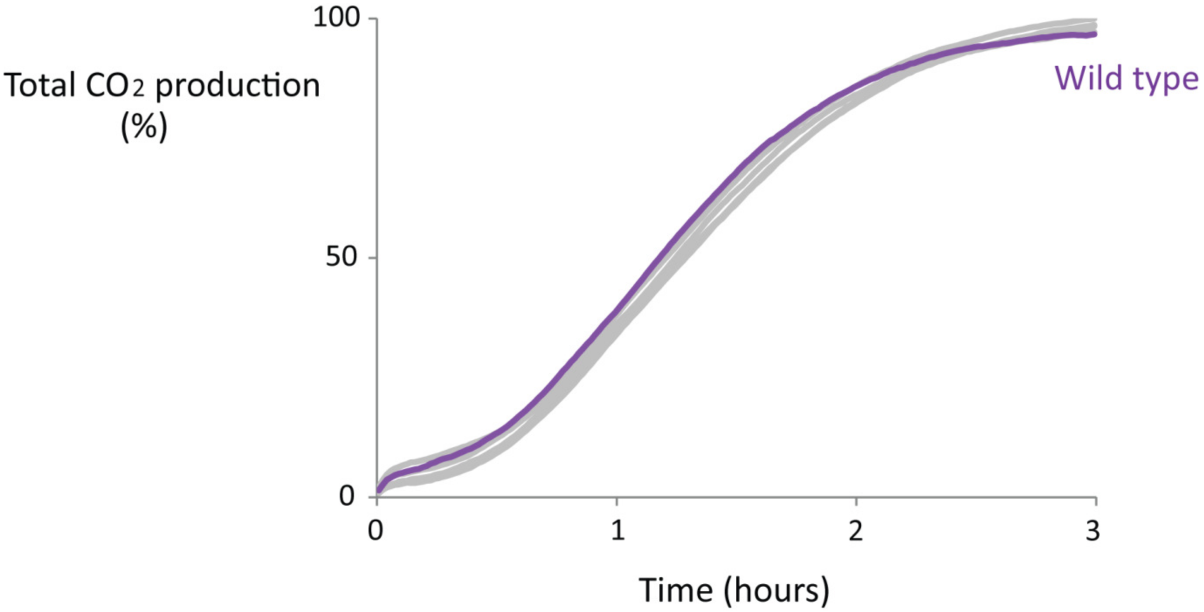

Fig. S1: None of the mutants showed differences in activity compared to the wild type during fermentation of standard rich medium (YPD). Shown is the CO_2 production during dough fermentation, which serves as a proxy for the fermentation efficiency.

Table S1: Top 50 Gene Ontology terms for transiently up (cluster 2 and 3 figure 3) and down regulated (cluster 5 and 6 figure 3) genes in all three strains.

2728		**2730**		**2930**	
GO Term	FDR	GO Term	FDR	GO Term	FDR
Transiently up-regulated					
GO:0042254~ribosome biogenesis	1.48E-86	GO:0042254~ribosome biogenesis	1.24E-90	GO:0042254~ribosome biogenesis	2.2E-99
GO:0022613~ribonucleoprotein complex biogenesis	4.62E-82	GO:0022613~ribonucleoprotein complex biogenesis	1.56E-82	GO:0016072~rRNA metabolic process	4.21E-84
GO:0034470~ncRNA processing	6E-78	GO:0034470~ncRNA processing	1.94E-82	GO:0022613~ribonucleoprotein complex biogenesis	1.37E-83
GO:0034660~ncRNA metabolic process	1.46E-77	GO:0034660~ncRNA metabolic process	6.15E-79	GO:0006364~rRNA processing	3.78E-83
GO:0016072~rRNA metabolic process	9.51E-67	GO:0006364~rRNA processing	6.77E-75	GO:0034470~ncRNA processing	3.59E-82
GO:0006364~rRNA processing	1.18E-65	GO:0016072~rRNA metabolic process	7.69E-74	GO:0034660~ncRNA metabolic process	2.01E-79
GO:0006396~RNA processing	5.64E-60	GO:0006396~RNA processing	7.74E-55	GO:0006396~RNA processing	2.41E-46
GO:0030490~maturation of SSU-rRNA	8.82E-29	GO:0000462~maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	2.36E-32	GO:0000462~maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	5.69E-40
GO:0000462~maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	5.83E-28	GO:0030490~maturation of SSU-rRNA	1.52E-31	GO:0030490~maturation of SSU-rRNA	9.32E-40
GO:0009451~RNA modification	2.94E-25	GO:0009451~RNA modification	2.76E-27	GO:0042255~ribosome assembly	6.6E-28
GO:0000466~maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	2.99E-22	GO:0042273~ribosomal large subunit biogenesis	4E-25	GO:0042273~ribosomal large subunit biogenesis	7.88E-28
GO:0000460~maturation of 5.8S rRNA	2.99E-22	GO:0000466~maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	1.06E-22	GO:0000460~maturation of 5.8S rRNA	1.44E-26
GO:0006417~regulation of translation	8.64E-22	GO:0000460~maturation of 5.8S rRNA	1.06E-22	GO:0000466~maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	1.44E-26
GO:0042273~ribosomal large subunit biogenesis	1.72E-21	GO:0042255~ribosome assembly	1.06E-22	GO:0009451~RNA modification	1.23E-23
GO:0032268~regulation of cellular protein metabolic process	7.25E-20	GO:0000469~cleavages during rRNA processing	2.98E-18	GO:0042257~ribosomal subunit assembly	1.79E-22
GO:0042255~ribosome assembly	2.88E-19	GO:0042257~ribosomal subunit assembly	1.89E-17	GO:0000469~cleavages during rRNA processing	2.31E-20
GO:0000469~cleavages during rRNA processing	3.27E-18	GO:0006417~regulation of translation	3.78E-16	GO:0000479~endonucleolytic cleavage of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	8.66E-18
GO:0010608~posttranscriptional regulation of gene expression	6.08E-18	GO:0022618~ribonucleoprotein complex assembly	2.32E-14	GO:0000478~endonucleolytic cleavages during rRNA processing	8.66E-18
GO:0006399~tRNA metabolic process	8.97E-17	GO:0032268~regulation of cellular protein metabolic process	2.61E-14	GO:0006417~regulation of translation	3.15E-17

GO:0022618~ribonucleoprotein complex assembly	8.17E-15	GO:0000479~endonucleolytic cleavage of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	3.06E-14	GO:0042274~ribosomal small subunit biogenesis	9.87E-17
GO:0042257~ribosomal subunit assembly	9.2E-15	GO:0000478~endonucleolytic cleavages during rRNA processing	3.06E-14	GO:0000447~endonucleolytic cleavage in ITS1 to separate SSU-rRNA from 5.8S rRNA and LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	1.73E-16
GO:0042274~ribosomal small subunit biogenesis	3.89E-13	GO:0006399~tRNA metabolic process	9.28E-14	GO:0032268~regulation of cellular protein metabolic process	5.09E-16
GO:0006913~nucleocytoplasmic transport	5.77E-13	GO:0010608~posttranscriptional regulation of gene expression	1.89E-13	GO:0010608~posttranscriptional regulation of gene expression	2.13E-15
GO:0051169~nuclear transport	5.77E-13	GO:0000447~endonucleolytic cleavage in ITS1 to separate SSU-rRNA from 5.8S rRNA and LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	1.89E-13	GO:0008652~cellular amino acid biosynthetic process	3.16E-15
GO:0051168~nuclear export	1.54E-12	GO:0000027~ribosomal large subunit assembly	1.89E-13	GO:0000027~ribosomal large subunit assembly	4.65E-15
GO:0000479~endonucleolytic cleavage of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	3.65E-12	GO:0042274~ribosomal small subunit biogenesis	3.89E-13	GO:0006412~translation	1.69E-14
GO:0000478~endonucleolytic cleavages during rRNA processing	3.65E-12	GO:0000966~RNA 5'-end processing	1.13E-09	GO:0009309~amine biosynthetic process	1.89E-13
GO:0000447~endonucleolytic cleavage in ITS1 to separate SSU-rRNA from 5.8S rRNA and LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	2.44E-11	GO:0009309~amine biosynthetic process	1.63E-09	GO:0022618~ribonucleoprotein complex assembly	1.88E-12
GO:0008033~tRNA processing	5.56E-11	GO:0008652~cellular amino acid biosynthetic process	1.92E-09	GO:0046394~carboxylic acid biosynthetic process	1.54E-11
GO:0006400~tRNA modification	3.31E-10	GO:0006400~tRNA modification	2.09E-09	GO:0016053~organic acid biosynthetic process	1.54E-11
GO:0000027~ribosomal large subunit assembly	7.33E-10	GO:0016032~viral reproduction	2.17E-09	GO:0000967~rRNA 5'-end processing	1.02E-10
GO:0034621~cellular macromolecular complex subunit organization	5.06E-09	GO:0034471~ncRNA 5'-end processing	3.2E-09	GO:0034471~ncRNA 5'-end processing	1.02E-10
GO:0000966~RNA 5'-end processing	3.93E-08	GO:0000967~rRNA 5'-end processing	3.2E-09	GO:0000472~endonucleolytic cleavage to generate mature 5'-end of SSU-rRNA from (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	4.35E-10
GO:0034471~ncRNA 5'-end processing	9.85E-08	GO:0046797~viral procapsid maturation	5.52E-09	GO:0000966~RNA 5'-end processing	4.95E-10
GO:0000967~rRNA 5'-end processing	9.85E-08	GO:0019068~virion assembly	5.52E-09	GO:0000480~endonucleolytic cleavage in 5'-ETS of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	7.72E-09
GO:0032774~RNA biosynthetic process	1.48E-07	GO:0019058~viral infectious cycle	5.52E-09	GO:0009067~aspartate family amino acid biosynthetic process	1.1E-07
GO:0006351~transcription, DNA-dependent	1.51E-07	GO:0010927~cellular component assembly involved in morphogenesis	5.52E-09	GO:0009066~aspartate family amino acid metabolic process	3.21E-07
GO:0000472~endonucleolytic cleavage to generate mature	2.46E-07	GO:0019069~viral capsid assembly	5.52E-09	GO:0044271~nitrogen compound biosynthetic	4.59E-07

5'-end of SSU-rRNA from (SSU-rRNA, 5.8S rRNA, LSU-rRNA)				process	
GO:0043144~snoRNA processing	1.08E-06	GO:0022415~viral reproductive process	5.52E-09	GO:0033753~establishment of ribosome localization	4.98E-07
GO:0043628~ncRNA 3'-end processing	1.09E-06	GO:0021700~developmental maturation	5.52E-09	GO:0000054~ribosome export from nucleus	4.98E-07
GO:0016032~viral reproduction	1.47E-06	GO:0019067~viral assembly, maturation, egress, and release	5.52E-09	GO:0033750~ribosome localization	4.98E-07
GO:0000480~endonucleolytic cleavage in 5'-ETS of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	1.53E-06	GO:0051168~nuclear export	8.09E-09	GO:0051168~nuclear export	7.74E-07
GO:0006350~transcription	2.01E-06	GO:0000472~endonucleolytic cleavage to generate mature 5'-end of SSU-rRNA from (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	9.07E-09	GO:0006399~tRNA metabolic process	8.26E-07
GO:0043933~macromolecular complex subunit organization	2.43E-06	GO:0015074~DNA integration	1.47E-08	GO:0000463~maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	1.08E-06
GO:0006412~translation	2.62E-06	GO:0008033~tRNA processing	1.83E-08	GO:0000470~maturation of LSU-rRNA	1.08E-06
GO:0019068~virion assembly	3.21E-06	GO:0006913~nucleocytoplasmic transport	4.78E-08	GO:0051169~nuclear transport	3.74E-06
GO:0019069~viral capsid assembly	3.21E-06	GO:0051169~nuclear transport	4.78E-08	GO:0006913~nucleocytoplasmic transport	3.74E-06
GO:0021700~developmental maturation	3.21E-06	GO:0000480~endonucleolytic cleavage in 5'-ETS of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	7.24E-08	GO:0043628~ncRNA 3'-end processing	4.72E-06
GO:0010927~cellular component assembly involved in morphogenesis	3.21E-06	GO:0009066~aspartate family amino acid metabolic process	1.18E-07	GO:0000097~sulfur amino acid biosynthetic process	1.08E-05
GO:0022415~viral reproductive process	3.21E-06	GO:0009067~aspartate family amino acid biosynthetic process	2.26E-07	GO:0006400~tRNA modification	2.45E-05
Transiently down-regulated					
GO:0007039~vacuolar protein catabolic process	4.09E-38	GO:0030163~protein catabolic process	8.61E-45	GO:0007039~vacuolar protein catabolic process	4E-53
GO:0030163~protein catabolic process	2.23E-36	GO:0044257~cellular protein catabolic process	8.64E-44	GO:0009266~response to temperature stimulus	9.05E-42
GO:0044257~cellular protein catabolic process	1.73E-35	GO:0007039~vacuolar protein catabolic process	6.69E-42	GO:0009408~response to heat	5.53E-36
GO:0009266~response to temperature stimulus	7.17E-29	GO:0009266~response to temperature stimulus	1.61E-32	GO:0034605~cellular response to heat	3.84E-35
GO:0009628~response to abiotic stimulus	4.04E-25	GO:0009408~response to heat	5.11E-29	GO:0055114~oxidation reduction	1.17E-34
GO:0009408~response to heat	6.38E-25	GO:0034605~cellular response to heat	4E-28	GO:0009628~response to abiotic stimulus	7.29E-31
GO:0034605~cellular response to heat	1.11E-22	GO:0009628~response to abiotic stimulus	5.26E-28	GO:0006091~generation of precursor metabolites and energy	2.6E-28
GO:0055114~oxidation reduction	5.25E-18	GO:0009057~macromolecule catabolic process	3.27E-22	GO:0030163~protein catabolic process	3.11E-25
GO:0009057~macromolecule catabolic process	2.33E-17	GO:0044265~cellular macromolecule catabolic process	2.14E-21	GO:0044257~cellular protein catabolic process	3.65E-24
GO:0044265~cellular macromolecule catabolic process	2.6E-16	GO:0006914~autophagy	6.15E-20	GO:0015980~energy derivation by oxidation of organic compounds	5.76E-22
GO:0006914~autophagy	1.22E-14	GO:0007005~mitochondrion organization	5.76E-19	GO:0009057~macromolecule catabolic process	8.98E-15

GO:0006091~generation of precursor metabolites and energy	1.24E-14	GO:0055114~oxidation reduction	1.03E-17	GO:0044265~cellular macromolecule catabolic process	1.89E-13
GO:0015980~energy derivation by oxidation of organic compounds	1.28E-14	GO:0015980~energy derivation by oxidation of organic compounds	6.72E-16	GO:0045333~cellular respiration	5.55E-13
GO:0006508~proteolysis	1.31E-11	GO:0006091~generation of precursor metabolites and energy	1.64E-14	GO:0005996~monosaccharide metabolic process	1.11E-12
GO:0051603~proteolysis involved in cellular protein catabolic process	1.54E-09	GO:0051603~proteolysis involved in cellular protein catabolic process	6.36E-14	GO:0006119~oxidative phosphorylation	2.41E-12
GO:0019941~modification-dependent protein catabolic process	5.56E-08	GO:0006508~proteolysis	1.34E-12	GO:0033554~cellular response to stress	2.6E-12
GO:0006511~ubiquitin-dependent protein catabolic process	2.76E-07	GO:0019941~modification-dependent protein catabolic process	6.53E-12	GO:0019318~hexose metabolic process	6.29E-12
GO:0045333~cellular respiration	8.84E-07	GO:0006511~ubiquitin-dependent protein catabolic process	3.84E-11	GO:0006006~glucose metabolic process	5.01E-10
GO:0006112~energy reserve metabolic process	2.79E-05	GO:0045333~cellular respiration	5.07E-09	GO:0044275~cellular carbohydrate catabolic process	2.43E-09
GO:0043632~modification-dependent macromolecule catabolic process	3.59E-05	GO:0043632~modification-dependent macromolecule catabolic process	1.52E-08	GO:0016052~carbohydrate catabolic process	4.66E-09
GO:0009060~aerobic respiration	3.63E-05	GO:0016044~membrane organization	2.28E-08	GO:0006914~autophagy	4.96E-09
GO:0006084~acetyl-CoA metabolic process	5.38E-05	GO:0009060~aerobic respiration	9.01E-08	GO:0042775~mitochondrial ATP synthesis coupled electron transport	5.35E-09
GO:0033554~cellular response to stress	6.77E-05	GO:0006112~energy reserve metabolic process	7.09E-06	GO:0042773~ATP synthesis coupled electron transport	5.35E-09
GO:0019318~hexose metabolic process	6.82E-05	GO:0005984~disaccharide metabolic process	1.08E-05	GO:0009060~aerobic respiration	5.71E-09
GO:0005996~monosaccharide metabolic process	0.000117	GO:0007034~vacuolar transport	1.2E-05	GO:0051186~cofactor metabolic process	1.15E-08
GO:0007005~mitochondrion organization	0.000166	GO:0033554~cellular response to stress	1.52E-05	GO:0006099~tricarboxylic acid cycle	4.73E-08
GO:0016044~membrane organization	0.000203	GO:0032543~mitochondrial translation	6.17E-05	GO:0046356~acetyl-CoA catabolic process	4.73E-08
GO:0006119~oxidative phosphorylation	0.000219	GO:0030435~sporulation resulting in formation of a cellular spore	9.98E-05	GO:0008219~cell death	6.82E-08
GO:0008219~cell death	0.000315	GO:0043934~sporulation	9.98E-05	GO:0016265~death	6.82E-08
GO:0016265~death	0.000315	GO:0009991~response to extracellular stimulus	0.000101	GO:0006084~acetyl-CoA metabolic process	1.72E-07
GO:0007034~vacuolar transport	0.000824	GO:0033108~mitochondrial respiratory chain complex assembly	0.000159	GO:0009109~coenzyme catabolic process	1.72E-07
GO:0016310~phosphorylation	0.000924	GO:0051186~cofactor metabolic process	0.000189	GO:0016310~phosphorylation	2.58E-07
GO:0006006~glucose metabolic process	0.000988	GO:0006623~protein targeting to vacuole	0.000203	GO:0022904~respiratory electron transport chain	3.13E-07
GO:0051186~cofactor metabolic process	0.001352	GO:0031667~response to nutrient levels	0.000392	GO:0051187~cofactor catabolic process	3.96E-07
GO:0006099~tricarboxylic acid cycle	0.001522	GO:0010324~membrane invagination	0.000498	GO:0046365~monosaccharide catabolic process	5.85E-07
GO:0046356~acetyl-CoA catabolic process	0.001522	GO:0031668~cellular response to extracellular stimulus	0.000805	GO:0006793~phosphorus metabolic process	8.16E-07
GO:0006732~coenzyme metabolic process	0.001581	GO:0006084~acetyl-CoA metabolic process	0.000878	GO:0022900~electron transport chain	1.1E-06
GO:0009991~response to extracellular stimulus	0.001766	GO:0016265~death	0.001659	GO:0006732~coenzyme metabolic process	1.32E-06
GO:0006793~phosphorus	0.00202	GO:0008219~cell death	0.00165	GO:0046164~alcohol	1.35E-

metabolic process	5		9	catabolic process	06
GO:0009109~coenzyme catabolic process	0.00253	GO:0016310~phosphorylation	0.002221	GO:0006112~energy reserve metabolic process	7.09E-06
GO:0007031~peroxisome organization	0.002964	GO:0031669~cellular response to nutrient levels	0.003063	GO:0019320~hexose catabolic process	1.26E-05
GO:0006623~protein targeting to vacuole	0.003294	GO:0007031~peroxisome organization	0.003356	GO:0006796~phosphate metabolic process	2.52E-05
GO:0010324~membrane invagination	0.004182	GO:0006099~tricarboxylic acid cycle	0.00382	GO:0005984~disaccharide metabolic process	3.54E-05
GO:0016052~carbohydrate catabolic process	0.004269	GO:0046356~acetyl-CoA catabolic process	0.00382	GO:0006007~glucose catabolic process	9.75E-05
GO:0044275~cellular carbohydrate catabolic process	0.005104	GO:0006732~coenzyme metabolic process	0.00467	GO:0005978~glycogen biosynthetic process	0.00063
GO:0048308~organelle inheritance	0.005816	GO:0009109~coenzyme catabolic process	0.005102	GO:0006733~oxidoreduction coenzyme metabolic process	0.001162
GO:0031667~response to nutrient levels	0.005952	GO:0006793~phosphorus metabolic process	0.00617	GO:0031668~cellular response to extracellular stimulus	0.002228
GO:0051187~cofactor catabolic process	0.006495	GO:0042594~response to starvation	0.006783	GO:0016054~organic acid catabolic process	0.002653
GO:0042773~ATP synthesis coupled electron transport	0.007733	GO:0016197~endosome transport	0.009463	GO:0046395~carboxylic acid catabolic process	0.002653
GO:0042775~mitochondrial ATP synthesis coupled electron transport	0.007733	GO:0006119~oxidative phosphorylation	0.010654	GO:0009991~response to extracellular stimulus	0.006525

Table S2: List of mutants that were tested based on RNA-seq data (see the text). The list contains deletion of genes with high up-regulation in earliest time point (30 min) and genes with key role in osmotic stress response. Performance of these mutants during dough fermentation was tested to investigate the importance of the genes for proper dough fermentation. Note that mutants with impaired growth or fermentation on standard rich medium (YPD) were excluded from study.

Mutant	Gene Systematic Name	Gene Name Description
*Δhog1**	YLR113W	High Osmolarity Glycerol response
*Δhot1**	YMR172W	High-Osmolarity-induced Transcription
*Δpbs2**	YJL128C	Polymyxin B Sensitivity
*Δsho1**	YER118C	Transmembrane osmosensor
*Δste20**	YHL007C	STErile
Δgpp1^*	YIL053W	glycerol-1-phosphatase
Δgpp2^*	YER062C	Glycerol-1-phosphatase
Δstl1^*	YDR536W	Sugar Transporter-Like protein
Δgpd1^*	YDL022W	Glycerol-3-Phosphate Dehydrogenase
Δgre2^*	YOL151W	Stress responsive gene
*Δfsf1^*	YOR271C	Fungal SideroFlexin
*Δfre4^*	YNR060W	Ferric REductase
*Δaqr1^*	YNL065W	Acids Quinidine Resistance
*Δari1^*	YGL157W	Aldehyde Reductase Intermediate
*Δstd1^*	YOR047C	Suppressor of Tbp Deletion
*Δsul2^*	YLR092W	SULfate metabolism
*Δaco2^*	YJL200C	ACOnitase
*Δhlr1^*	YDR528W	Homologue of LRe1
*Δctp1^*	YBR291C	Citrate Transport Protein

*The gene is regulated by HOG pathway

^ The gene was highly up-regulated at earliest time point