

Table S1 The differential expression of genes putatively involved in antioxidant mechanisms

Gene ID	Expression level (stress)	Expression level (control)	<i>P</i> value NOIseq result	Description of gene
Antioxidant enzymes				
F481_00620	133.652	37.2397	0.8188962	Fe, Mn SOD
F481_03410	111.807	16.5827	0.8548361	Dyp-type peroxidase
F481_06421	1736	241.976	0.8575301	Thioredoxin peroxidase
Thioredoxin				
F481_02467	178.849	57.3289	0.811306	Thioredoxin-like
F481_00656	76.0089	21.1075	0.8181803	Thioredoxin-like
F481_01980	182.066	47.6827	0.8203169	Thioredoxin-like
F481_08492	1597.84	360.593	0.8392459	Thioredoxin-like
F481_05562	312.111	61.7746	0.8498087	Thioredoxin-like
F481_06439	150.386	26.333	0.8501366	Thioredoxin-like
F481_06421	1736	241.976	0.8575301	Thioredoxin-like
Glutathione metabolism				
F481_04800	277.84	39.4006	0.8574372	Spermine synthase
F481_00649	76.9356	22.0064	0.8180874	Orn/DAP/Arg decarboxylase 2
F481_04824	67.4564	0.759665	0.9395464	Glutathione S-transferase (GST), C-terminal domain
F481_08200	46.3625	10.2666	0.8378251	Glutathione S-transferase (GST), C-terminal domain
F481_07895	109.164	1.96135	0.8594645	Glutathione S-transferase (GST), C-terminal domain
F481_02789	227.393	69.5137	0.8124645	Glutathione S-transferase (GST), C-terminal domain
F481_08392	408.741	102.843	0.8204863	Glutathione S-transferase (GST), C-terminal domain
Vitamin B6 metabolism				
F481_02092	14.9954	3.74325	0.8014973	Pyridoxal kinase
F481_04633	269.188	20.5525	0.8596339	Glutamine amidotransferase subunit PdxT
F481_00300	94.5512	14.6913	0.8545574	Phosphoserine aminotransferase
F481_00322	1206.83	91.5978	0.8597213	Vitamin B6 biosynthesis protein

Table S2 The differential expression of genes putatively involved in osmotic regulation

Gene ID	Expression level (stress)	Expression level (control)	<i>P</i> value NOIseq result	Description of gene
F481_02188	28.3869	36.6172	0.3861257	Trehalose-6-phosphate synthase
F481_01316	61.1314	37.7043	0.5700601	Trehalose-6-phosphate synthase
F481_05299	60.0955	90.5713	0.5480328	Trehalose-6-phosphate synthase

Table S3 The differential expression of genes putatively involved in post-translational processing

Gene ID	Expression level (stress)	Expression level (control)	P value NOIseq result	Description of gene
Molecular chaperone				
F481_07985	76.8372	19.9212	0.8195027	HSP70, peptide-binding domain
F481_03297	81.6759	18.2611	0.8384098	GroEL equatorial domain-like
F481_03442	261.088	73.9599	0.8190601	HSP20-like chaperones
F481_03823	318.409	98.4233	0.8118579	GroEL equatorial domain-like
F481_04859	1888.11	334.144	0.8503934	HSP20-like chaperones
F481_05104	99.6631	13.5011	0.8571093	Chaperonin Cpn60/TCP-1
F481_05773	1284.79	178.943	0.8575301	Chaperonin Cpn10
F481_05858	107.333	34.6502	0.8109399	Chaperonin Cpn60/TCP-1
F481_07753	314.865	63.8575	0.8408743	Heat shock protein 70
F481_07169	133.129	26.8154	0.8406667	Chaperonin Cpn60/TCP-1
F481_07646	227.953	30.6375	0.8573934	HSP20-like chaperones
Proteasome				
F481_00698	259.579	86.4416	0.8113552	Proteasome, alpha-subunit, conserved site
F481_01693	250.25	83.1821	0.8113552	Proteasome component (PCI) domain
F481_05836	144.295	44.9356	0.811612	Proteasome, subunit alpha/beta
F481_03277	286.402	86.1234	0.8125355	Proteasome, subunit alpha/beta
F481_08863	234.24	67.5561	0.8142459	Proteasome, subunit alpha/beta
F481_08894	128.83	32.81	0.8202186	Proteasome, alpha-subunit, conserved site
F481_07919	149.141	35.4908	0.8384481	Proteasome component (PCI) domain
F481_04019	270.363	45.7194	0.8502951	Proteasome, alpha-subunit, conserved site
F481_04061	399.412	62.1101	0.8549891	Proteasome, subunit alpha/beta
F481_03276	552.606	69.6354	0.8575301	Proteasome, subunit alpha/beta

Table S4 The differential expression of genes putatively involved in signal transduction pathway

Gene ID	Expression level (stress)	Expression level (control)	P value NOIseq result	Description gene name	KEGG
F481_01624	83.3915	1272.32	0.8597596	RNA-binding domain, RBD	Calcium-mediated signaling
F481_07285	16.095	77.0356	0.8400383	Protein kinase-like (PK-like)	MAPK signaling pathway-yeast
F481_01068	102.82	375.341	0.8201475	SH3-domain	MAPK signaling pathway-yeast
F481_04996	30.1677	90.3552	0.810612	Protein kinase-like (PK-like)	MAPK signaling pathway-yeast

Table S5 The differential expression of genes putatively involved in transcriptional factor

Gene ID	Expression level (stress)	Expression level (control)	P value NOIseq result	Description of gene
F481_00089	93.1442	24.409	0.819852	Transcription factor MEIS1
F481_02736	1046.45	84.2267	0.859661	Transcription initiation factor IIA, gamma subunit
F481_05516	525.801	170.193	0.811475	Transcription factor containing NAC and TS-N domains
F481_06822	68.3807	11.728	0.849333	Transcription regulator HTH, Myb-type, DNA-binding
F481_01683	326.008	75.0766	0.839142	Basic-leucine zipper (bZIP) transcription factor
F481_00773	100.533	25.149	0.83818	transcription factor NusA, alpha-helical
F481_06073	513.9	135.927	0.820437	Transcription factor CBF/NF-Y/archaeal histone
F481_05070	5.58272	97.1436	0.859366	Transcription factor, Zinc finger
F481_00825	18.1091	190.474	0.85929	Transcription factor GATA
F481_04641	97.2342	915.777	0.85918	Transcription factor, Zinc finger
F481_05788	5.35411	25.7508	0.830393	Transcription factor, Zinc finger
F481_06075	36.5055	182.367	0.849689	Transcription factor, Zinc finger
F481_05695	10.2929	39.3274	0.815836	Transcription factor, Zinc finger
F481_05940	17.0715	101.768	0.85459	Transcription factor, Zinc finger
F481_00435	27.8409	84.5152	0.810475	Transcription factor, Zinc finger
F481_04136	6.37078	191.472	0.859596	Transcription factor GATA
F481_05314	20.0335	152.595	0.857328	Heat shock transcription factor
F481_00923	21.0427	144.521	0.854934	Transcription factor, MADS-box
F481_03680	41.3724	136.544	0.812301	p53-like transcription factor, DNA-binding
F481_06048	20.8409	77.8524	0.81923	p53-like transcription factor, DNA-binding
F481_05425	8.48359	28.7934	0.803749	Disco-Interaction protein 2 (DIP2)
F481_04647	14.4786	48.9945	0.811011	Basic-leucine zipper (bZIP) transcription factor
F481_02977	4.62576	19.5786	0.815579	Transcription factor, fork head
F481_03547	9.16494	35.7164	0.814612	Transcription factor Cmr1
F481_08590	23.4431	80.2297	0.813361	Transcription factor HOXA13-related

Table S6 The differential expression of genes putatively involved in pyrimidine and purine metabolism

Gene ID	Expression level (stress)	Expression level (control)	P value NOIseq result	Description of gene
F481_00378	51.4458	13.8088	0.8175355	RBP11-like subunits of RNA polymerase
F481_00591	237.652	47.0825	0.8497322	Phosphoribosyltransferase
F481_00852	172.976	48.645	0.8189672	RPB6/omega subunit-like
F481_00996	26.0738	5.35128	0.8303934	Ribulose-phosphate binding barrel
F481_01824	35.5948	8.60985	0.8327814	FMN-linked oxidoreductases
F481_02044	43.8035	12.8512	0.8100546	Adenine nucleotide alpha hydrolases-like
F481_02100	108.252	17.3186	0.8546448	dUTPase-like
F481_02859	65.5124	10.2141	0.8539617	DNA-directed RNA polymerase III subunit Rpc34
F481_03929	33.4423	9.26456	0.8122077	DNA primase large subunit
F481_03930	30.7324	6.73684	0.8335738	DNA primase large subunit
F481_04004	346.212	45.6313	0.8574863	RBP11-like subunits of RNA polymerase
F481_04191	170.204	36.9914	0.840459	Ribokinase-like
F481_04442	68.2026	17.5823	0.8192077	RNA polymerase III subunit RPC82
F481_04766	87.5185	24.5384	0.8183607	Phosphoribosyltransferase
F481_04793	24.8847	5.1517	0.8291093	Amidohydrolase 2
F481_05270	161.737	35.5567	0.8404426	Amidophospho ribosyltransferase
F481_06583	676.361	97.3217	0.8551639	Alpha-D-phosphohexomutase
F481_07842	32.7267	8.59177	0.8134262	SAICAR synthase
F481_08135	59.957	17.7257	0.8122404	L-aspartase

Table S7 The differential expression of genes putatively involved in oxidative phosphorylation

Gene ID	Expression level (stress)	Expression level (control)	P value NOIseq result	Description of gene
F481_00136	553.667	128.76	0.8387924	mitochondrial F1F0-ATP synthase g subunit
F481_00917	61.2199	10.8894	0.8490164	ATPase, F1 complex
F481_01557	1274.81	329.341	0.8205519	Cytochrome c oxidase subunit h
F481_01979	179.287	29.3143	0.854847	NADH-ubiquinone oxidoreductase 18 kDa subunit
F481_02166	815.057	121.74	0.8551694	mitochondrial ATPase subunit ATP4
F481_02259	112.726	29.7592	0.8200109	NADH-ubiquinone oxidoreductase subunit
F481_02589	276.419	47.9046	0.8503005	Ubiquinone-binding protein QP-C of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
F481_03248	452.52	101.044	0.8391803	ACP-like
F481_03249	120.135	21.6156	0.8500273	4Fe-4S ferredoxins
F481_04003	242.525	49.5297	0.8408033	NADH-ubiquinone oxidoreductase B14 subunit
F481_04075	220.653	35.6603	0.8548852	NAD(P)-binding Rossmann-fold domains
F481_04567	563.264	103.779	0.8499399	cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
F481_04674	1003	191.519	0.8498798	Inorganic pyrophosphatase
F481_04739	172.274	37.4484	0.8404699	NADH:ubiquinone oxidoreductase
F481_07096	573.978	185.099	0.8114918	ATPase, F0 complex, subunit H
F481_07436	378.455	83.2792	0.840612	NADH:ubiquinone oxidoreductase, NDUF9/B22 subunit
F481_08015	98.5059	20.9437	0.8403989	Cytochrome c oxidase assembly protein CtaG/Cox11

Table S8 The differential expression of genes putatively involved in nitrogen and carbon metabolism

Gene ID	Expression level (stress)	Expression level (control)	P value NOIseq result	Description of gene
Nitrogen metabolism				
F481_06302	14.3953	124.632	0.8583716	Glutamate synthase
F481_04501	15.527	77.3965	0.849	Acetamidase/Formamidase
F481_07075	3.40505	158.605	0.8595574	Nitrite/sulphitereductase
F481_03490	4.17401	26.1543	0.8456776	2-nitropropane dioxygenase, NPD
F481_08559	2.84208	21.7508	0.8440874	Asparagine synthase
F481_08558	2.62624	16.5703	0.8282077	Asparagine synthase
Glutathione metabolism				
F481_05520	4.09442	25.6	0.8456776	Hydantoinase/oxoprolinase
F481_04800	277.84	39.4006	0.8574372	S-adenosyl-L-methionine-dependent methyltransferases
F481_04824	67.4564	0.759665	0.9395464	Glutathione S-transferase
F481_00649	76.9356	22.0064	0.8180874	Alanine racemase C-terminal domain-like
F481_08200	46.3625	10.2666	0.8378251	Glutathione S-transferase (GST)
F481_07895	109.164	1.96135	0.8594645	Glutathione S-transferase (GST)
Galactose metabolism				
F481_05966	7.7875	31.8316	0.8316175	Galactose oxidase
F481_03176	10.0886	159.008	0.8595574	Galactose dehydratase
F481_03285	14.5811	312.735	0.8596831	NAD-dependent epimerase/dehydratase
Nucleotide sugar metabolism				
F481_02076	85.4894	19.903	0.838071	Chitin synthase
F481_07291	145.625	29.9006	0.8406721	Nucleotidyltransferase
F481_06583	676.361	97.3217	0.8551639	Phosphoglucomutase
F481_07290	127.409	39.4175	0.8115519	Nucleotide-diphospho-sugar transferases
F481_07556	444.86	25.0018	0.8597158	Eukaryotic phosphomannomutase
F481_00358	238.396	64.8396	0.8200492	Acyl-CoA N-acyltransferases (Nat)
F481_06056	2.54855	0.257281	0.5090656	Metallo-dependent hydrolases