Table 1. Relative changes of gene expression comparing opaque to white cell [a].

Probe set	12h	18h	24h	48h	Gene names and descriptions
Carbohydrate metabolism					
orf6.1691	5.3	2.7	5.8	30	IDP2; NADP-dependent isocitrate dehydrogenase
orf6.8733	3.1	2.2	1.6	2.8	MDH1; mitochondrial malate dehydrogenase precursor
orf6.8594	5.8	9	4.1	1.8	GLG2; self-glucosylating initiator of glycogen synthesis
orf6.1915	3.5	4.2	7.4	11.9	SFC1; mitochondrial succinate-fumarate transporter
orf6.2470	3.2	14.1	17.2	4.5	NAG1; glucosamine-6-phosphate deaminase
orf6.2470	10	8.9	7.3	5.3	NAG1; glucosamine-6-phosphate deaminase
orf6.9016	3.8	3.6	5.1	12.6	CaMAL2; alpha-D-glucosidase/maltase
orf6.3107	6.9	37.2	27.1	-2	MNN1; alpha-1,3-mannosyltransferase
orf6.3042	4	3.8	8.4	4	RKI1; D-ribose-5-phosphate ketol-isomerase
orf6.991	4	3.9	14	5.9	JEN1; carboxylic acid transporter (essential for pyruvate & lactate uptake)
orf6.8009	1.8	7.1	3.4	5.1	CYB2; lactate dehydrogenase cytochrome b2
orf6.4131	16.3	6.4	11	2.1	ALD6; cytosolic acetaldehyde dehydrogenase
orf6.1674	2.4	5.7	3.2	3.3	ESB6; putative monocarboxylate permease.
orf6.7053	7.9	34.8	19.5	2.3	similar to malate permease
orf6.7053	3.3	17.1	3.9	2.4	similar to malate permease
orf6.5328	1.4	2.1	2.3	3.1	AYR1; 1-acyl dihydroxyacetone phosphate reductase
orf6.725	3.1	2.8	6.5	1.3	AYR1; 1-acyl dihydroxyacetone phosphate reductase
orf6.725	6.3	2	2.9	3.3	AYR1; 1-acyl dihydroxyacetone phosphate reductase
orf6.7378	1.7	4.6	4.7	10.1	MLS1; malate synthase 1
orf6.6087	2	3.4	2.4	3.3	YNL274; potential alpha-ketoisocaproate reductase; similar to glycerate- & formate-dehydrogenase
orf6.6337	61.5	32.1	13.2	8.5	ADH2; alcohol dehydrogenase II
orf6.4197	114.4	42.9	94.5	268	ADH3; alcohol dehydrogenase III
orf6.2378	-3.5	-3.6	-6.4	-2.9	HXT3; low-affinity hexose transporter
orf6.2379	-38.2	-6.8	-29.3	-96.9	HXT4; moderate- to low-affinity hexose transporter
orf6.187	-3.1	-1.8	-5	-3.4	HXT7; high-affinity hexose transporter
orf6.2377	-35.3	-5.1	-10.3	-50	HXT7; high-affinity hexose transporter
orf6.5097	-9	-1.7	-3.4	-4.3	HXK1; hexokinase I
orf6.5274	-3.3	-2.1	-4.9	-5.9	PFK2; 6-phosphofructokinase (beta-subunit)
orf6.5754	-2.7	-1	-2.4	-18.2	CDC19; pyruvate kinase
orf6.4133	-5.5	1.1	-2.6	-2.4	GDB1; glycogen debranching enzyme(similarity to human 4-alpha-glucanotransferase)
orf6.6537	-3.1	1.4	-2.2	-2.4	TPS1; trehalose-6-P synthase 56kD subunit
orf6.7775	-2.9	-1.6	-4.5	-5	TPS2; trehalose-6-phosphate phosphatase
orf6.8114	-4.4	-3.5	-8.4	-12.2	YBR056; homolog to glucan-1,3--beta-glucosidase
orf6.8673	-8.7	-1.2	-3.6	-26.8	RHR2; DL-glycerol-3-phosphatase
orf6.8815	-5.2	-3.3	-9.9	-2.9	YJR096; putative oxidoreductase
orf6.6126	-3.6	-4	-2.7	-2.5	SOU1; short-chain alcohol dehydrogenase homolog; sorbose utilization
orf6.1009	-2.2	-2.5	-6.4	-2.8	YAL060; possible stereo specific (2R,3R)-2,3-butanediol dehydrogenase; potentail dehydrogenase
orf6.3827	-36.4	-28.3	-38	-4.6	YAL060; possible stereo-specific (2R,3R)-2,3-butanediol dehydrogenase; potential dehydrogenase
orf6.2004	-3.9	1.2	-10.2	-14.1	YPL088; putative aryl alcohol dehydrogenase
orf6.2004	-9	1.2	-20	-44.2	YPL088; putative aryl alcohol dehydrogenase
orf6.2130	-2.2	1.2	-5.4	-6.3	LPG20; putative aryl alcohol dehydrogenase
orf6.4277	-5.7	-1.2	-2.5	-2.6	ADH2; alcohol dehydrogenase II
Lipid and fatty acid metabolism					
orf6.8539	2.9	1.7	7.9	4.4	FAA2; fatty acid activator 2; long chain fatty acid-CoA ligase (Acyl-CoA synthetase)
orf6.1284	2.9	3.1	2.4	6.6	AEH1; acyl-CoA dehydrogenases / epoxide hydrolases
orf6.3796	2.4	3.5	13.3	4.8	POX1; fatty-acyl CoA oxidase
orf6.3140	3.8	5.1	37.7	18.7	POX1; fatty-acyl Co-A oxidase
orf6.7811	3.8	3.1	8.9	4.4	ECI1; delta 3-cis-delta2-trans-enoyl-CoA isomerase
orf6.7766	1.2	4.2	9.3	5.5	YDR036; member of enoyl-coA hydratase/isomerase family
orf6.8801	2	3.7	10.3	21.7	YDR036; member of enoyl-coA hydratase/isomerase family

orf6.1167	1.1	2.3	6.2	3.4	FOX2; peroxisomal hydratase-dehydrogenase-epimerase
orf6.3123	2.2	2.3	10.4	7.8	FOX3; 3-ketoacyl-CoA thiolase B (peroximal acetyl-CoA C-acyltransferase)
orf6.9116	2.2	2.3	2.7	3.2	YPR128/ANT1; peroxisomal ADP/ATP carrier
orf6.2269	2.7	4.5	7.1	4.6	YPR128/ANT1; peroxisomal ADP/ATP carrier
orf6.2269	6.1	7.4	15.2	2.9	YPR128/ANT1; peroxisomal ADP/ATP carrier
orf6.2621	5	2.3	4	2.1	SPS19; peroxisomal 2,4-dienoyl-CoA reductase
orf6.2495	8.6	3.3	20	4.2	SPS19; peroxisomal 2,4-dienoyl-CoA reductase
orf6.3118	8.1	3.8	4.8	5.4	PXP18; lipid transfer; sterol carrier protein 2; similar to *Candida tropicalis* non-specific lipid-transfer protein
orf6.6697	1.9	6.6	5.1	2.8	YAT1; carnitine acetyltransferase
orf6.4584	4	3.8	2.6	2.1	YAT2/YER024; carnitine acetyltransferase
orf6.5671	5.4	6.8	9.1	13.2	FAO1; long chain fatty acid oxidase
orf6.5913	3.2	4	19.3	7.4	FAD1; delta-12 fatty acid desaturase
orf6.3337	3	1.5	32.6	25	POX18; peroxisomal lipid carrier
orf6.3337	4.6	I 2	80.1	42.7	POX18; peroxisomal lipid carrier
orf6.3192	6.5	6.4	21.4	13.8	TES99; peroxisomal acyl-CoA thioesterase; possible role in fatty acid oxidation
orf6.3930	2.2	1.8	2.8	4.6	ERG2; sterol C8-C7 isomerase
orf6.4879	4.8	2.5	4.7	3.2	OSH3; similar to human oxysterol-binding protein (OSBP)
orf6.2606	-1.7	2.4	2.7	7.3	EBP1; estrogen-binding protein; likely NADH oxidoreductase isoform 2 (old yellow enzyme isoform1)
orf6.1227	4.2	5.8	21.2	9.2	MOC1; similar to bacterial cyclohexa monooxygenases (Flavin-binding monooxygenase)
orf6.1104	-4.9	-3.2	-3.5	-9.7	DAK2; dihydroxyacetone kinase (glycerolipid metabolism)
orf6.4041	-12.4	-3.2	-2	-2.7	SUR2; hydroxylase involved in sphingolipid metabolism;required for the hydroxylation of C-4 of the sphingoid moiety of ceramide
orf6.2481	-13.2	-10	-9.2	-24.4	GIT1; inositol metabolism; glycerophosphoinositol transporter
orf6.2054	-4.3	-2.6	-1.4	-2.3	ERG25; sterol C-4 methyl oxidase (ergosterol biosynthesis pathway)
Nitrogen, sulfur and amino acid metabolism					
orf6.6107	2.2	3.9	4	4.4	RAF1; arginase/agmatinase family protein (arginine degradation)
orf6.1912	1.5	3.8	5.4	4.4	CAR1; arginase (arginine degradation)
orf6.8395	6.8	8.6	7.3	20.7	CDG1; similar to cysteine dioxygenases (cysteine degradation)
orf6.7802	1.6	2.3	2.9	4	DAO1; D-amino acid oxidase
orf6.6363	9.3	9	5.5	35.5	CHA1; L-serine/L-threonine dehydratase
orf6.6363	9.9	15.1	7.1	74.9	CHA1; L-serine/L-threonine dehydratase
orf6.766	21.6	10	3.9	118.1	CHA2; L-serine/L-threonine dehydratase
orf6.4764	1	6	8	4.7	ARO8; aromatic amino acid (tyr or asp) aminotransferase
orf6.5956	2.3	1.8	2.2	5.9	DFR1; dihydrofolate reductase
orf6.945	2.2	2.6	6.6	3.3	HIS3; imidazole glycerol phosphate dehydratase.
orf6.744	2.2	1.2	4.2	37.9	GCV1; T subunit of glycine decarboxylase (glycine degradation)
orf6.3099	2.2	3.4	2.2	2.2	HQD2; similar to bacterial hydroxyquinol 1,2-dioxygenase
orf6.6152	3.8	8.2	6	2.3	UGA4; GABA-specific high affinity permease; amino acid permease
orf6.9043	1.5	2.7	6.1	4.8	RHB1; regulation of arginine & lysine uptake; GTP-binding protein, ras family; involved in growth regulation
orf6.4694	5.8	10.2	16.2	22.2	SUL2; high-affinity sulfate transport protein
orf6.6967	7.7	13.2	14.5	13.4	AMD2; possible amidase
orf6.1742	5.2	10.5	6.6	3.5	AMO2; peroxisomal amine oxidase (allows the cells to utilize various amines as C- & N-sources)
orf6.8360	2.3	5	2.5	5.9	NIT2; nitrilase superfamily member
orf6.1137	-5.3	-2.2	1.4	-2.8	BAT1; branched-chain amino acid transaminase
orf6.2072	-6.9	-3.5	2.2	-3.6	CAN3; basic amino acid permease
orf6.6768	-3.6	-3.7	-24.7	-9.4	GAP1; general amino acid permease
orf6.5457	-35.3	-24.1	-11.3	-15	AGP2; general amino acid (asp, gln) permease; carnitine transport
Phosphate metabolism					
orf6.897	3.4	3.9	4.2	2.3	PHO11; secreted acid phosphatase family
orf6.8482	19.6	39.5	50.1	9.8	PHO84; high-affinity inorganic phosphate/H+ symporter
orf6.3437	1.4	5.8	8.2	2.6	PHO84; high-affinity inorganic phosphate/H+ symporter
orf6.7898	112.9	152.6	53	1.3	PHO89; probable Na+-coupled phosphate transport protein, high-affinity
orf6.8691	3.4	2.8	2.3	2	VTC1; similar to *S. pombe* Nrf1; negative regulator of CDC42
orf6.6326	2.6	4.7	4.9	4.9	VTC2; putative polyphosphate synthetase (vacuolar polyphosphate accumulation)

orf6.8394	3.4	6.4	4.6	1.8	SSU1; involved in sulfite efflux; major facilitator superfamily protein; sulfite sensitivity protein
orf6.293	-6.7	-4.4	-3.8	-9.2	PHO87; inorganic phosphate permease
orf6.1540	-14.8	-3.1	-3.1	-10.5	PHO98; low-affinity phosphate permease
Nucleotide metabolism					
orf6.307	2.7	2.1	1.4	5.1	AAH1; adenine aminohydrolase; adenosine deaminase (purine/adenosine salvage pathway)
orf6.7032	2.4	2.7	3.9	12.6	URH1; uridine ribohydrolase (pyrimidine salvage pathway)
orf6.7558	2.6	3.3	5.4	1.7	NUP3; purine nucleoside permease
orf6.4050	8.4	8.2	8	4.4	RNY1; ribonuclease
orf6.726	2.4	5.9	8.1	6.2	RNH1; similar to ribonuclease H
orf6.8435	1.3	2.1	2.7	4.2	ADK2; adenylate kinase (mitochondrial GTP:AMP phosphotransferase)
orf6.2547	2.3	3.4	6.5	3.5	YPR011; Grave's disease carrier protein; similar to mitochondrial ADP/ATP carrier proteins
orf6.4254	-2.8	-6.1	-1.1	-3.2	YGL186; purine/cytosine permease
orf6.332	-5.4	-2.7	-2.5	1.1	FCY2; purine/cytosine permease
orf6.7052	-9.1	-4.1	-12.7	-12.4	RNR2; small subunit of ribonucleotide reductase
Vitamin, cofactor and prosthetic group metabolism					
orf6.2440	-2.3	-2	-2.9	-3.7	RIB3; 3,4-dihydroxy-2-butanone 4-phosphate synthase
orf6.6669	-8.2	-5.2	-2.1	-19	SNZ99; stationary-phase-induced; putative pyridoxine (Vit B6) biosynthesis enzyme
Energy					
orf6.3525	22.2	7.4	2.7	19.4	FDH1; possible formate dehydrogenase
orf6.2662	16.6	2.6	3.3	15	FDH1; possible formate dehydrogenase
orf6.3469	14.5	6.7	4.9	9.1	FDH1; possible formate dehydrogenase
orf6.485	8	2.7	4.3	5	FDH1; possible formate dehydrogenase
orf6.7642	2.4	4.5	4.9	4.6	YMR110; similar to aldehyde dehydrogenases
orf6.7610	4.2	4.3	4.5	2	YMR110; similar to aldehyde dehydrogenases
orf6.3984	14.3	25.5	8.9	-1	AXO2; alternative oxidase (cyanide-resistant respiratory pathway)
orf6.3792	7.9	4.4	80.3	71.3	ALK1; n-alkane-inducible cytochrome p-450
orf6.1706	2.5	4.6	3.9	-2.7	ALK8; n-alkane inducible cytochrome P-450
orf6.8764	2.1	8.2	39.4	12.2	ALK3; cytochrome P450
orf6.8765	3.3	9.3	24.2	13.3	ALK2; cytochrome P450
Cell fate (cell growth, differentiation, cell surface and adhesion)					
orf6.5914	35.3	67.1	66.7	41	OP4; opaque phase-specific protein
orf6.8184	16.4	19.5	21.3	13.1	AGA1; weak similarity to anchorage subunit of a-agglutinin
orf6.4005	4.6	8.7	14.3	5.1	SCW4; cell wall protein
orf6.5529	2.6	3	2.5	1.2	MUC1; cell surface flocculin
orf6.5529	10.2	9.8	15.9	2.6	MUC1; cell surface flocculin
orf6.8769	1.8	5.3	20.6	11.5	CHT1; chitinase
orf6.4498	3.7	3	5.2	3.8	ALG5; dolichol-P-glucose synthetase
orf6.8847	4.3	9.1	17.2	15.2	similat to hypothetical serine-rich secreted protein
orf6.7834	10	16.4	5	2.4	weak similar to mucin protein
orf6.6744	5.8	3.3	10.3	27.6	TIR1; serine-rich cell wall protein
orf6.6587	-2.1	-2.1	-2.2	-12.3	FLO1; cell wall protein involved in flocculation
orf6.8596	-2.9	-2.5	-3.4	-3.7	AAF1; adhesion and aggregation mediating surface antigen
orf6.1310	-51.4	-9.3	-13.3	-32.6	ALS1; agglutinin-like protein
orf6.1311	-25.7	-12.6	-22.9	-227	ALS2; agglutinin-like protein
orf6.1377	-3	-2.9	-1.9	-3.1	ALS3; agglutinin-like protein
orf6.2760	-4.4	-2.5	-5	-3.5	ALS99; agglutinin-like protein
orf6.3000	-18.4	-9.5	-29.2	-37.1	ALS99; agglutinin-like protein
orf6.3074	-18.6	-19	-29.5	-40.5	ALS99; agglutinin-like protein
orf6.3075	-66.6	-17.1	-23.7	-156.7	ALS99; agglutinin-like protein
orf6.4390	-5.4	-3.2	-8.4	-15.2	MNN4; transfer mannosylphosphate to core & other chain of N-linked oligosaccharide mannan synthesis defective

orf6.2497	-3.3	-1.7	-4.2	-2.1	CAX4; generation of mannoprotein layer of the cell wall
orf6.1361	-2.2	-2.9	-7.6	-27.3	VAN1; mannosyltransferase: vanadate resistance protein
orf6.2428	-5	-11.1	-11.2	-24	YOR009; possible cell wall mannoprotein
Stress response/Drug resistance					
orf6.1092	2	2.2	2.9	5.2	GST3; glutathione s-transferase
orf6.271	8.6	43.5	20.6	33.1	C terminal of ORF6.1092; glutathione S-transferase
orf6.6924	35.5	28.3	8.8	6.6	similar to glutathione-S-transferase (*S. pombe*)
orf6.7240	4	9.8	27.1	41.4	similar to glutathione-S-transferase
orf6.7744	5.7	9.2	22.2	4.5	GTT1; glutathione s-transferase
orf6.5229	2.3	1.7	3.8	8	YBR014; glutaredoxin
orf6.7493	13.9	28.4	3.6	5.7	SOD1; superoxide dismutase
orf6.4875	4.6	6.4	7.2	18.1	CDR3; opaque-specific putative ABC transporter
orf6.8417	9.5	53.9	25.2	2.5	YBR293; MFS efflux transporter
orf6.1559	-34.7	-18.3	-4.6	-4	HYR1; glutathione-peroxidase
orf6.2088	-15.6	-3.2	-23.2	-8.3	YPR156; member of drug-resistant 12-spanner family of MFS-MDR
orf6.3649	-4	-2.6	-15.6	-2.8	YGR138; member of drug-resistant MFS-MDR family
orf6.7063	-10.7	-7.4	-38.5	-39.8	QDR1; member of drug-resistant 12-spanner family of the MFS-MDR
orf6.6297	-6.8	-4.4	-18	-18.8	CDR4; ABC transporter
orf6.1668	-4.6	-1.7	-4.7	-4.1	HSP12; 12kd Heat Shock Protein
orf6.2627	-6.1	-2.6	-10.1	-28.3	HSP70; heat shock protein of HSP70 family
orf6.474	-3.9	-1.9	-3.6	-11.8	HSP150/PIR1; role in cell wall organization and biogenesis; required for tolerance to heat shock
orf6.4208	-29	-5.3	-29.9	-23.3	DHN6; dehydrin
Mitochondrial proteins					
orf6.2738	1.8	3.4	2.8	4.6	YHM2; membrane transporter of mitochondrial carrier family
orf6.3644	4.4	2.2	2.3	-2.3	MMM1; establishment & maintain mitochondrial shape & structure
Protein synthesis					
orf6.4732	-2.9	-2.4	-1.6	-2.4	MSR1; mitochondrial arginyl-tRNA synthetase
SAPs & LIPs					
orf6.4644	223.3	204.6	173.1	238	SAP1; secreted aspartyl proteinase
orf6.9036	8.2	22.5	66.7	456.8	SAP3; secreted aspartyl proteinase
orf6.1902	9	24.5	62.1	252	SAP99; secreted aspartyl proteinase
orf6.1902	26.4	48.9	78.6	407.3	SAP99; secreted aspartyl proteinase
orf6.288	4.3	3.4	6.1	2.1	LIP4; secretory lipase
Transcription					
orf6.9028	4.5	4.1	2.7	4.1	CTA215; putative transcriptional activator
orf6.1952	2.8	4.3	3.7	3.6	SUA7; transcription factor TFIIB
orf6.2403	3.8	3.5	3.4	1.8	YIL130; putative transcription factor with fungal Zn(2)-Cys(6) binuclear cluster domain
orf6.9045	3.5	4.3	4.1	5.3	CTF1; potential fungal Zn(2)-Cys(6) binuclear cluster domain
orf6.3344	10	7.5	3	1.2	HAP3; transcriptional activator of respiratory genes
orf6.8756	1.7	3.7	3.9	7	SRP40; nucleolar snoRNP component
orf6.1556	8.1	10.3	8.1	5	ZF097; putative zinc finger protein
orf6.9062	1.4	2.5	3.1	3.9	ADR1; transcriptional factor of ADH2 and peroxisomal protein genes
orf6.2094	2.3	9.5	5.3	5.9	similar to transcription factor KIYAPI (*Kluyveromyces lactis*)
orf6.1107	-3	-2.5	-2.4	-7.6	CTA8; putative transcription factor
orf6.3986	-5.7	-2.2	-1.4	-4.3	CTA8; putative transcription factor
orf6.1367	-2.8	1.2	-5.8	-4.1	CTA226; putative transcription factor
orf6.5412	-3	1.2	-4.7	-3.8	CTA223; putative transcription factor
orf6.5530	-2.8	1.1	-4.5	-3.8	CTA221; putative transcription factor
orf6.8027	-2.9	1.2	-5	-3.2	CTA227; putative transcription factor

orf6.1954	-2.3	1.2	-3.9	-3.6	CTA222; putative transcription factor
orf6.4578	-2.6	1.2	-5	-4.5	CTA224; putative transcription factor
orf6.8534	-2.4	-2.8	-3.3	-5.9	OAF1; zinc-finger transcription factor
orf6.8814	-4.8	-2.2	-4.1	-6.3	FCR1; potential Zn(2)-Cys(6)binuclear cluster domain; activation of sphingolipid biosynthesis
orf6.5885	-6.7	-2.9	-3	-2.9	HSH49; spliceosome associated protein
orf6.8011	-2.9	-3.9	-3.5	-2.8	TEA1; associated with Ty1 expression; Ty1 enhancer activator of Gal4-type DNA-binding protein
orf6.2978	-25.7	-5.8	-5.9	-4.3	EFG2; transcription factor in PKA signal transduction pathway; regulator of morphogenesis
orf6.4821	-11.2	-12.6	-13.3	-8.2	EFG1; transcription factor in PKA signal transduction pathway; regulator of morphogenesis
orf6.1414	-7.3	-2.3	-1.9	-6	ECM22; involved in cell wall biogenesis; potential fungal Zn(2)-Cys(6) cluster domain
orf6.8739	-2.3	-2.1	-8.8	-5.2	RRT98; reverse transcripases
orf6.1793	-6.1	-2.3	-9.9	-48.7	NUP100; nuclear pore complex subunit
orf6.8468	-2	-2.1	-2.1	-4.1	GLE1; contains nuclear-export-signal (NES)
orf6.8519	-4.5	-2.1	-1.7	-8.9	CRZ1; calcineurin responsive zinc-finger transcriptional factor
Signaling					
orf6.9126	-11	-4	-8.3	-20.2	CMK1; Ca++/calmodulin-dependent ser/thr protein kinase I
orf6.6480	-3.1	-4.3	-4.4	-1.7	STK99; serine/threonine protein kinase
orf6.5024	-1.2	-2.3	-3	-6.7	RHO4; rho family in Ras superfamily; GTP-binding protein
orf6.6451	-2.3	-2.1	-2.4	-2	GPA2; similar to G-alpha protein, glucose-induced activation of plasma membrane ATPase; role in pseudohyphal growth and sexual cycle
orf6.5310	-3.6	-2.2	-2	-3.6	YCR079; protein phosphatase of the PP2C family
orf6.7197	-2.3	1	-2.6	-3.4	GAC1; putative phosphatase
Ionic homeostasis					
orf6.8406	4	14.6	I 1.9	2.5	SCO1; inner mitochondrial membrane protein; possible role in Cu transport or insert Cu into cytochrome oxidase
orf6.6966	2.3	4.1	2.7	-1.6	ENA2; P-type ATPase involved in Na+ efflux
orf6.7646	-10.2	-3.8	-2.7	-5.5	CUP9; copper homeostasis & peptide import regulation
orf6.2939	-28.1	-11.7	-6.5	-6.2	FET35; cell surface multicopper ferroxidase
orf6.4145	-2.9	1.4	-2.9	-9.2	PMA1; H+ transporting P-type ATPase
orf6.7614	-7.3	-4.1	-3.2	-4.3	ENA2; P-type ATPase involved in Na+ efflux
orf6.1885	-3.7	-1.8	-2.3	-4.3	YOR291; cation translocating P-type ATPase
Mating type & cell cycle					
orf6.4306	170.6	153.2	87.3	100.9	putative alpha-factor
orf6.6173	7.6	9	7.1	22.2	STE3; a factor receptor
orf6.4399	4.9	3.8	5.1	6.6	MATALPHA1; Mating-type regulatory protein
orf6.2854	1.7	3.6	2.5	6.4	FUS3; Serine/threonine protein kinase of MAP kinase family (required for cell cycle arrest & for cell fusion during mating)
orf6.1819	1.9	3.5	7.1	2.6	FUS3; mitogen-activated protein kinase(MAP kinase) (required for cell cycle arrest & for cell fusion during mating)
orf6.975	4.3	7.2	12.4	13.9	PRY2; pathogen related in Sc, homology to plant PR-1 class of pathogen related proteins;possible role in mating efficiency
orf6.4742	-3.1	-3.8	-2.6	-9.2	NDT80; Meiosis-specific protein (required for exit from pachytene)
orf6.706	-2.4	-2.8	-2.8	-2.2	SWE1; serine/tyrosine dual-specifity protein kinase
orf6.1592	-5.7	-5.9	-5.2	-3	CDC25; mitotic inducer phosphatase
Protein fate					
orf6.8365	-20.2	-11.3	-32.6	-38.7	USO1; integrin analogue
Transporters					
orf6.1364	16	21.1	37.6	23	OPT23; oligopeptide transporter
orf6.2912	13.3	20.6	38.6	19.8	OPT25; oligopeptide transporter
orf6.6090	-2.2	-2.1	-3.6	-1.2	MAF1; nuclear-cytoplasmic transport
orf6.4943	-2.2	1.7	-2.2	-2.5	AQY1; aquaporin water channel protein
Unclassified & unknown					
orf6.2295	1.4	10.5	15.6	2.9	similar to complex 1 intermediate associated protein CIA30 of Neurospora crassa

orf6.2484	2	2.6	3.5	6.5	similar to glycerol-3-phosphate acyltransferase of *Caenorhabditis elegans*
orf6.2833	9.6	4	4.8	9.8	similar to mammalian globins
orf6.2871	3.6	6.5	13.8	16.3	similar to hydrolase (*Streptomyces coelicolor*)
orf6.311	11	16.1	15	14.5	STO99; Ser/Thr-rich Orf
orf6.3214	76.4	92.4	79.8	9.6	weak similarity to ras-interacting protein RIPA
orf6.3438	94.3	109.9	95.4	79.6	similar to S-adenosylmethionine: diacylglycerol 3-amino-3-carboxypropyl transferase
orf6.4641	2.3	2.1	4	4.9	CSR1; unknown function
orf6.4690	9.5	18.5	30	26.3	SCD99; similar to SPCC736.13, short chain dehydrogenase
orf6.4976	2.3	4.7	4.4	9.6	YPL206; possible glycerophosphoryl phosphodiesterase
orf6.5522	4.2	14.4	19.3	38.7	AOF1001; unknown function
orf6.5845	2.8	2.6	3.3	2.9	PCP6; phylogeneticaly conserved protein
orf6.5958	2.9	4.9	2.4	1.2	similar to MSV016 leucine-rich repeat gene family protein
orf6.6858	3.2	7.5	13.4	31.7	similar to epoxide hydrolase
orf6.8945	4	21.8	7.4	6.7	PMU3; possible phosphoglycerate mutase family
orf6.1019	33.5	20.3	37.5	38.6	Ca38F10.05; hypothetical protein
orf6.1020	14.3	22.8	20.3	54.4	Ca38F10.05; hypothetical protein
orf6.3709	12.9	12.6	9.2	11.7	Ca38F10.05; hypothetical protein
orf6.3709	7	5.9	3.4	5.6	Ca38F10.05; hypothetical protein
orf6.3710	21.7	20.5	20.5	32	Ca38F10.05; hypothetical protein
orf6.3932	16.1	63.3	96.9	7	Ca38F10.05; hypothetical protein
orf6.8292	15	20.2	12.5	2.1	Ca38F10.05; hypothetical protein
orf6.7278	5.7	3	5.5	11.3	similar to *Drosophila melanogaste* CG3792 gene product
orf6.1289	-1.6	3.5	2.8	5	YOR049; similar to *S. cerevisiae* YOR049c
orf6.1342	2.7	1.4	3	5.1	YDL124; similar to *S. cerevisiae* YDL124w
orf6.1342	4.1	1.3	2.2	3.3	YDL124; similar to *S. cerevisiae* YDL124w
orf6.1741	2.4	3.2	3.6	2.8	YGL157; similar to *S.cerevisiae* YGL157w
orf6.1805	2.4	1.6	3.6	9	YGR263; similar to *S. cerevisiae* YGR263c
orf6.1848	2.5	4.1	6.2	3.4	YPR009; similar to *S. cerevisiae* YPR009w
orf6.2236	2	8	18.9	4	YOR246; similar to *S. cerevisaie* YOR246c
orf6.2296	6.5	4	9	3	YOR246; similar to *S. cerevisiae* YOR246c
orf6.2517	6	6.5	7.8	10.6	YOR059; similar to *S. cerevisiae* YOR059c
orf6.3050	30.3	22.9	27.2	3.3	YEL007; similar to *S. cerevisiae* YEL007w
orf6.3138	2.3	2.1	1.2	3.4	YHR140; similar to *S. cerevisiae* YHR140w
orf6.5146	8.8	5	8	2.5	YNR061; similar to *S. cerevisiae* YNR061c
orf6.6461	7.8	4.9	3.4	5.9	YKR105; similar to *S. cerevisiae* YKR105c
orf6.7617	1.1	2.7	2.4	7.6	YLR205; similar to *S. cerevisiae* YLR205c; induced during aerobic growth
orf6.7819	2.3	2.2	3.4	2.2	YGR243; similar to *S. cerevisiae* YGR243W
orf6.8826	5.4	9.6	6.7	4.4	YDR089; similar to *S. cerevisiae* YDR089W
orf6.8890	6.2	2.4	5	3.1	YLR414; similar to *S. cerevisiae* YLR414C
orf6.9029	2.5	2.3	3.4	30.2	YLL032; similar to *S. cerevisiae* YLL032C
orf6.7284	31	71.3	78	86.1	YMR317; similar to *S. cerevisiae* YMR317w
orf6.4494	6	8	8.4	1.3	YMR317; similar to S. cerevisiae YMR317w
orf6.9034	1.5	6.6	5.4	3.2	YMR317; similar to S. cerevisiae YMR317w
orf6.143	5.7	8.8	45	15.7	no significant homologies
orf6.1048	8.5	3.5	2.6	3.1	no significant homologies
orf6.105	2.3	3.1	2.5	8.2	no significant homologies
orf6.1051	2.7	2.8	1.8	3.9	no significant homologies
orf6.113	2.1	10.4	14.2	11.3	no significant homologies
orf6.1148	12.7	21.4	60.7	98.3	no significant homologies
orf6.1148	54	94.1	107.8	252.4	no significant homologies
orf6.1151	3.2	-1.3	9.9	16.7	no significant homologies
orf6.1199	1.9	3.7	2.2	4.8	no significant homologies
orf6.1970	1.5	2.2	2.4	5	no significant homologies
orf6.2406	2.9	2.7	2.2	8.6	no significant homologies
orf6.2490	20.1	40.4	78.9	138.4	no significant homologies

orf6.2644	2.6	1.4	4.7	2.9	no significant homologies
orf6.294	2.1	3.9	11.8	5.8	no significant homologies
orf6.3209	11.7	15.8	26.2	63	no significant homologies
orf6.3419	5.6	9.5	7.6	2.4	no significant homologies
orf6.3562	22.6	27.7	35.1	3.2	no significant homologies
orf6.3646	8.5	14.5	7.7	-1.3	no significant homologies
orf6.4000	4.7	2.2	5.2	4.1	no significant homologies
orf6.4069	3.4	1.5	2.3	4.7	no significant homologies
orf6.4069	2.7	1.6	3.5	3.4	no significant homologies
orf6.4255	3.6	6	6.8	2.4	no significant homologies
orf6.4304	1.7	2.7	3.2	2.7	no significant homologies
orf6.4535	2.2	4.2	4.3	4.5	no significant homologies
orf6.4918	11.1	10.5	6	2.1	no significant homologies
orf6.501	8.2	8.4	12.1	4.6	no significant homologies
orf6.5361	2.4	3.8	2.6	4.5	no significant homologies
orf6.5489	8.8	13.9	6.4	71	no significant homologies
orf6.5533	3.1	3.3	7.2	2.7	no significant homologies
orf6.5893	5.1	10.3	21.3	6.5	no significant homologies
orf6.5899	4.1	5.1	5.4	2.9	no significant homologies
orf6.6033	9.5	9.4	4.3	4.1	no significant homologies
orf6.6258	2.9	3	2.9	5.5	no significant homologies
orf6.6383	1.5	2.4	4	2.6	no significant homologies
orf6.6419	4.2	2.4	2.8	9.2	no significant homologies
orf6.6524	1.9	2.9	2.8	6.2	no significant homologies
orf6.6743	8.5	2.3	3.3	21	no significant homologies
orf6.6787	1.7	2.4	7.6	17.1	no significant homologies
orf6.6880	3	7.5	4.1	17.6	no significant homologies
orf6.7060	3.9	5.8	9.8	4.5	no significant homologies
orf6.7906	8.1	8.9	7.2	14.4	no significant homologies
orf6.7968	2.9	7.7	4.8	7.3	no significant homologies
orf6.8030	3.4	2.9	1.8	3.2	no significant homologies
orf6.821	3.4	5.8	8.3	6.8	no significant homologies
orf6.8291	35.2	20.2	30.4	61.5	no significant homologies
orf6.8291	14.8	23.2	36.7	66.4	no significant homologies
orf6.8294	3.9	4.1	4.6	14.3	no significant homologies
orf6.864	4	2.4	2.8	2.7	no significant homologies
orf6.8692	5.4	4	2.6	2.2	no significant homologies
orf6.8773	5.5	4.2	4.5	-1.2	no significant homologies
orf6.8807	3.1	3	4.7	-2	no significant homologies
orf6.8956	1.4	3.2	6.9	6.6	no significant homologies
orf6.9117	4.2	4.5	2.1	-1.1	no significant homologies
orf6.979	1.7	3.7	2.2	2.8	no significant homologies
orf6.979	1.4	2.7	2.2	2.6	no significant homologies
orf6.1219	-4.4	-3.6	-5	-16.9	PIB2; phosphatidylinositol 3-phosphate binding
orf6.3242	-2.3	-2.1	-1.2	-2.6	similar to C. elegans Y55B1BR.3 of unknown function
orf6.3677	-2.3	-2.3	-4	-4.8	YNL134; similar to *C.carbonum* toxD
orf6.461	-5.2	-4.7	-3.6	-2.3	SRO99; serine-rich Orf
orf6.4675	-4.2	-2.4	-3.1	-6.6	CHP98; conserved hypothetical protein
orf6.4772	-10.1	-5.1	-4.5	-2.5	GAG2; GAG poly protein
orf6.495	-1	-2.2	-3.7	-7.3	YOR019; UspA family of putative nucleotide binding proteins
orf6.5509	-1.8	-3.2	-4.9	-6.1	YMR221; integral membrane protein
orf6.568	-3	-2.3	-10.7	-11.4	LRR9; 9 leucine-rich repeats
orf6.6464	-9.5	-2.8	-2	-7.2	AFF10; ady2-Fun34 like family, possible transmembrane acetate facilitor/sensor
orf6.6793	-10.4	-8.3	-12.1	-124	PNC1; pyrazinamidase/nicotinamidase
orf6.6793	-3.2	-2.5	-1.6	-14.3	PNC1; pyrazinamidase/nicotinamidase

orf6.72	-15.7	-4.5	-6.2	2.6	similar to *E. coli* ada
orf6.72	-12.6	-2.9	-4.9	-4	similar to *E. coli* ada
orf6.2588	-24.2	-8.1	-23.9	-38.4	similar to *E. coli* ada
orf6.8861	-3.6	-4.8	-9.4	-4.4	ENT4; cytoskeletal adaptor
orf6.3978	-5.9	-2.2	-3.1	-3.5	YKR70; similar to *S. cerevisiae* YKR70w; similar to *S. pombe* phosphatidyl synthase
orf6.1262	-3.2	-1.5	-5.1	-3	YHR087; similar to *S. cerevisiae* YHR087w
orf6.2518	-18.2	-9	-10	-2.1	YKL051; similar to *S. cerevisiae* YKL051w
orf6.328	-5.9	-2.1	-1.9	-3.1	YOR104; similar to *S. cerevisiae* YOR104w
orf6.3754	-2.4	-1.1	-2.6	-10.2	YCR061; similar to *S. cerevisiae* YCR061w
orf6.5589	-3.7	-2.6	-3.4	-1.9	YDR365; similar to S. cerevisiae YDR365c
orf6.5917	-4.9	-6.4	-8.4	-5.7	YOR049; similar to *S. cerevisiae* YOR049c
orf6.5917	-2.5	-5	-6.2	-3.3	YOR049; similar to *S. cerevisiae* YOR049c
orf6.5918	-25.3	-17.5	-8.5	-6.1	YOR049; similar to *S. cerevisiae* YOR049c
orf6.664	-1.5	-2.2	-4.5	-5.4	YBR101; similar to *S. cerevisiae* YBR101c
orf6.8127	-2.4	-3.7	-6.2	-2.6	YFR003; similar to *S. cerevisiae* YKR017c
orf6.8391	-39.9	-3.6	-22.5	-9.1	YML128; similar to *S. cerevisiae* YML128c
orf6.1116	-9.3	-5.8	-15.2	-16.6	no significant homologies
orf6.1265	-11.5	-7.1	-5.8	3.5	no significant homologies
orf6.1467	-3.9	1.4	-5.9	-4.4	no significant homologies
orf6.2000	-2.3	-1.8	-4.5	-4.8	no significant homologies
orf6.2206	-3.5	-3.5	-2.5	-1.5	no significant homologies
orf6.264	-12.9	-7.1	-6.6	-1.3	no significant homologies
orf6.2657	-2.1	-2.1	1.1	-4.3	no significant homologies
orf6.2682	-2.1	-1.7	-3.7	-5.7	no significant homologies
orf6.2940	-22.8	-20.6	-13.4	-11.2	no significant homologies
orf6.296	-9.1	-5.7	-21.5	-34.9	no significant homologies
orf6.3127	-9.1	-1.5	-5	-3	no significant homologies
orf6.3447	-5.4	-1.8	-5.8	-8.2	no significant homologies
orf6.3950	-4.2	1.7	-4.5	-9	no significant homologies
orf6.3979	-2.4	-3.9	-2.5	-4.4	no significant homologies
orf6.402	-4.1	-9.3	-7.1	-3.2	no significant homologies
orf6.4552	-12.2	-25.7	-24.7	-10.1	no significant homologies
orf6.4564	-4.5	1.2	-4.8	-8.3	no significant homologies
orf6.477	-1.5	-2.1	-2.8	-5.7	no significant homologies
orf6.4785	-5.1	-4.3	-4.3	-9.3	no significant homologies
orf6.4944	-2.7	-2.7	-9.7	-6.9	no significant homologies
orf6.4945	-5	-6	-5.4	-1.9	no significant homologies
orf6.502	-2.2	-6.6	-11.1	-3.1	no significant homologies
orf6.5927	1.1	-2.5	-10.6	-5.8	no significant homologies
orf6.6489	-2.1	-2.6	-2.7	-3.5	no significant homologies
orf6.6713	-15.8	-1.2	-8.9	-2.6	no significant homologies
orf6.7231	-7.3	-3.5	-4.9	-5.9	no significant homologies
orf6.7387	-3.2	-3.3	-5.1	-8.3	no significant homologies
orf6.7660	-11.4	-6.1	-4	-9.5	no significant homologies
orf6.7922	-4.8	-3.4	-1.7	-8.3	no significant homologies
orf6.8140	-1.4	-2.7	-5.1	-6.7	no significant homologies
orf6.8303	-4	-9.3	-25.7	-6.3	no significant homologies
orf6.861	-24.6	-18.9	-18.3	-19.5	no significant homologies

[a] Relative changes of gene expression are represented by fold changes comparing O to W cells.

The positive and negative (shaded) values represent a higher expression of transcript in O and W cells, respectively.