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2-Amino-nonyl-6-methoxyl-tetralin muriate activity against *Candida albicans* augments endogenous reactive oxygen species production – a microarray analysis study

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Table S1. Selected genes that are downregulated in 10b-grown *C. albicans* SC5314 as compared with growth without treatment, determined in two independent experiments.

Primary CGDID	**Genename (CandidaDB)**	***S.cerevisiae* homologue name**	**Function**	**Change in fold expression**	
				Ratio1 (D*)	**Ratio2 (D*)**
Generation of precursor metabolites and energy					
CAL0004810	*MBA1*	YBR185C	Aerobic respiration	0.42 (2.38)	0.39 (2.56)
CAL0004098	*GLG21*	YJL137C	Glycogen biosynthesis	0.28 (3.57)	0.28 (3.57)
CAL0000595	*GLC7*	YER133W	Protein described as serine/threonine phosphatase	0.41 (2.44)	0.48 (2.08)
CAL0001531	*PDA1*	YER178W	Pyruvate dehydrogenase (acetyl-transferring) activity	0.13 (7.69)	0.36 (2.78)
CAL0003535	*MRPS9*	YBR146W	Aerobic respiration	0.37 (2.70)	0.31 (3.23)
CAL0005236	*RHR2*	YIL053W	Putative glycerol 3-phosphatase	0.04 (25.00)	0.03 (33.33)
CAL0003394	*GSY1*	YFR015C	Protein described as glycogen synthase	0.12 (8.33)	0.07 (14.29)
CAL0000855	*ACS1*	YAL054C	Putative acetyl-CoA synthetase	0.13 (7.69）	0.19 (5.26)
CAL0004762	*NDE1*	YMR145C	NADH dehydrogenase activity	0.13 (7.69)	0.49 (2.05)
CAL0003526	*RIB3*	YDR487C	3,4-Dihydroxy-2-butanone 4-phosphate synthase	0.13 (7.69)	0.35 (2.86)
ROS scavenge					
CAL0001814	*GPX2*	YBR244W	Glutathione peroxidase activity	0.35 (2.86)	0.36 (2.78)
Glycosis					

CAL0003055	*PFK1*	YGR240C	Alpha subunit of phosphofructokinase (PFK)	0.02 (50.00)	0.07 (14.29)
CAL0003180	*PFK2*	YMR205C	Beta subunit of phosphofructokinase (PFK)	0.08 (12.50)	0.09 (11.11)
CAL0000198	*HXK2*	YGL253W	Protein described as hexokinase II	0.08 (12.50)	0.33 (3.03)
CAL0005977	*CDC19*	YAL038W	Putative pyruvate kinase	0.10 (10.00)	0.17 (5.88)
CAL0003619	*FBA1*	YKL060C	Putative fructose-bisphosphate aldolase	0.05 (20.00)	0.14 (7.14)
CAL0004953	*ENO1*	YGR254W	Enolase (2-phospho-D-glycerate-hydrolyase)	0.08 (12.50)	0.20 (5.00)
CAL0004861	*TPI1*	YDR050C	Triose-phosphate isomerase	0.06 (16.67)	0.14 (7.14)
CAL0001210	*GPM2*	YKL152C	Protein described as phosphoglycerate mutase	0.11 (9.09)	0.09 (11.11)
CAL0003574	*GPM1*	YKL152C	Phosphoglycerate mutase activity	0.13 (7.69)	0.27 (3.70)
CAL0002184	*PGI1*	YBR196C	Protein described as glucose-6-phosphate isomerase	0.14 (7.14)	0.27 (3.70)
Fermentation					
CAL0005202	*PDC11*	YLR044C	Protein similar to pyruvate decarboxylase	0.06 (16.67)	0.06 (16.67)
CAL0002252	*ALD5*	YER073W	Protein described as an aldehyde dehydrogenase	0.19 (5.26)	0.38 (2.63)
CAL0003176	*ADH1*	YMR083W	Alcohol dehydrogenase	0.12 (8.33)	0.30 (3.33)
Respiratory electron transport chain					
CAL0005742	*BCS1*	YDR375C	Chaperone-mediated protein complex assembly	0.41 (2.44)	0.44 (2.27)
CAL0000927	*CYC1*	YJR048W	Mitochondrial electron transport, ubiquinol to	0.36 (2.78)	0.17 (5.88)
CAL0003316	*IPF24060.1*	YHR116W	Mitochondrial respiratory chain complex assembly	0.28 (3.57)	0.41 (2.44)
CAL0000978	*SDH2*	YLL041C	Mitochondrial respiratory chain complex II	0.31 (3.23)	0.50 (2.00)
CAL0004721	*SDH4*	YDR178W	Mitochondrial respiratory chain complex II	0.30 (3.33)	0.38 (2.63)

CAL0006092	*CBP3*	YPL215W	Mitochondrial respiratory chain complex III assembly	0.36 (2.78)	0.26 (3.85)
CAF0007013	*QCR8*	YJL166W	Mitochondrial respiratory chain complex III	0.36 (2.78)	0.31 (3.23)
CAL0003458	*QCR2*	YPR191W	Mitochondrial respiratory chain complex III	0.28 (3.57)	0.40 (2.50)
CAL0005851	*CYT1*	YOR065W	Mitochondrial respiratory chain complex III	0.26 (3.85)	0.41 (2.44)
CAL0003624	*IPF21976.1*	YPR100W	Mitochondrial large ribosomal subunit	0.24 (4.17)	0.31 (3.23)
CAL0002472	*RIP1*	YEL024W	Mitochondrial respiratory chain complex III	0.23 (4.35)	0.27 (3.70)
CAL0004684	*COR1*	YBL045C	Mitochondrial respiratory chain complex III	0.17 (5.88)	0.36 (2.78)
CAF0006913	*COX6*	YHR051W	Mitochondrial respiratory chain complex IV	0.22 (4.55)	0.33 (3.03)
CAL0000422	*COX15*	YER141W	Respiratory chain complex IV assembly	0.21 (4.76)	0.08 (12.5)
CAL0004689	*COX4*	YGL187C	Protein described as subunit IV of cytochrome c oxidase	0.30 (3.33)	0.45 (2.22)
CAL0000236	*IPF690.2*	None	Protein described as NADH-ubiquinone oxidoreductase	0.38 (2.63)	0.41 (2.44）
CAL0000774	*IPF25643.1*	None	Protein described as NADH-ubiquinone oxidoreductase	0.21 (4.76）	0.41 (2.44)
CAL0003145	*NUC2*	None	Protein described as NADH-ubiquinone oxidoreductase	0.15 (6.67)	0.31 (3.23)
CAL0006345	*IPF25079.1*	YGL068W	Aerobic respiration	0.21 (4.76)	0.19 (5.26)
CAL0002635	*GDS1*	YOR355W	Aerobic respiration	0.21 (4.76)	0.25 (4.00)
Lipid metabolic process					
CAL0002977	*URA7*	YBL039C	Phospholipid biosynthetic process	0.48 (2.08)	0.35 (2.86)
CAL0003358	*FAS2*	YPL231W	Alpha subunit of fatty-acid synthase	0.39 (2.56)	0.34 (2.94)
CAL0001206	*FMP44*	YBR004C	GPI anchor biosynthetic process	0.39 (2.56)	0.44 (2.27)
CAL0001431	*IPF20776.1*	YML059C	Putative patatin-like phospholipase	0.19 (5.26)	0.34 (2.94)

CAL0003035	*EBP1*	YHR179W	NADPH oxidoreductase	0.05 (20.00)	0.21 (4.76)
CAL0005104	*ASM3*	None	Putative secreted acid sphingomyelin phosphodiesterase	0.23 (4.35)	0.34 (2.94)
CAL0003509	*IPF12430.2*	YHR067W	Fatty acid biosynthetic process	0.07 (14.29)	0.49 (2.04)
CAL0002903	*IPF22599.1*	YJR013W	GPI anchor biosynthetic process	0.08 (12.50)	0.09 (11.11)
CAL0003066	*SCT1*	YBL011W	Putative glycerol-3-phosphate O-acyltransferase	0.11 (9.09)	0.36 (2.78)
CAL0003358	*FAS2*	YPL231W	Alpha subunit of fatty-acid synthase	0.14 (7.14)	0.34 (2.94)
CAL0005938	*MVD*	YNR043W	Mevalonate diphosphate decarboxylase	0.16 (6.25)	0.47 (2.13)
CAL0005630	*ACC1*	YNR016C	Acetyl-CoA carboxylase activity	0.24 (4.17)	0.35 (2.86)
CAL0000008	*TGL99*	YKL140W	Lipid metabolic process	0..23 (4.35)	0.47 (2.13)
CAL0005333	*LIP6*	None	Secreted lipase	0.25 (4.00)	0.39 (2.56)
CAL0000562	*AYR2*	YIL124W	Acylglycerone-phosphate reductase activity	0.13 (7.69)	0.32 (3.13)
Translation					
CAF0007060	*RPL35*	YDL136W	Ribosomal protein	0.05 (20.00)	0.11 (9.09)
CAF0006876	*RPL6*	YLR448W	Structural constituent of ribosome	0.05 (20.00)	0.22 (4.55)
CAL0003667	*RPL20B*	YMR242C	Predicted ribosomal protein	0.09 (11.11)	0.28 (3.57)
CAF0006944	*RPL2*	YFR031C-A	Structural constituent of ribosome	0.10 (10.00)	0.22 (4.55)
CAL0003181	*RPL5*	YPL131W	Predicted ribosomal protein	0.06 (16.67)	0.31 (3.23)
CAL0006405	*RPL12*	YDR418W	Predicted ribosomal protein	0.11 (9.09)	0.42 (2.38)
CAL0000666	*RPL82*	YLL045C	Predicted ribosomal protein	0.09 (11.11)	0.37 (2.70)
CAF0007000	*RPL43A*	YJR094W-A	Predicted ribosomal protein	0.09 (11.11)	0.20 (5.00)

CAF0006985	*RPL32*	YBL092W	Predicted ribosomal protein	0.07 (14.29)	0.27 (3.70)
CAL0005018	*RPL8B*	YLL045C	Predicted ribosomal protein	0.05 (20.00)	0.23 (4.35）
CAL0003235	*RPL19A*	YBL027W	Predicted ribosomal protein	0.13 (7.69)	0.40 (2.50)
CAF0006907	*RPL37B*	YDR500C	Predicted ribosomal protein	0.14 (7.14)	0.29 (3.45)
CAL0005216	*RPL16A*	YIL133C	Structural constituent of ribosome	0.10 (10.00)	0.40 (2.50)
CAL0005866	*RPL15A*	YLR029C	Putative ribosomal protein;	0.14 (7.14)	0.30 (3.33)
CAL0006240	*RPL11*	YGR085C	Predicted ribosomal protein	0.15 (6.67)	0.26 (3.85)
CAF0006997	*RPL30*	YGL030W	Structural constituent of ribosome	0.27 (3.70)	0.38 (2.63)
CAL0006017	*RPL10*	YLR075W	Putative ribosomal protein;	0.28 (3.57)	0.42 (2.38)
CAL0006678	*RPL29*	YFR032C-A	Ribosomal protein L29	0.29 (3.45)	0.46 (2.17)
CAF0006935	*RPL38*	YLR325C	Predicted ribosomal protein	0.17 (5.88)	0.37 (2.70)
CAL0003449	*RPL18*	YNL301C	Structural constituent of ribosome	0.15 (6.67)	0.44 (2.27)
CAL0002747	*RPL21A*	YBR191W	Putative ribosomal protein;	0.15 (6.67)	0.43 (2.33)
CAL0005770	*RPL23A*	YBL087C	Putative ribosomal protein;	0.15 (6.67)	0.41 (2.44)
CAL0006679	*RPL39*	YMR194W	Ribosomal protein L39;	0.11 (9.09)	0.30 (3.33)
CAL0005037	*RPL10A*	YGL135W	Predicted ribosomal protein	0.13 (7.69)	0.27 (3.70)
CAL0003235	*RPL19A*	YBL027W	Predicted ribosomal protein	0.13 (7.69)	0.40 (2.50)
CAL0006157	*RPL13*	YDL082W	Structural constituent of ribosome	0.18 (5.56)	0.45 (2.22)
CAL0003957	*RPL9B*	YNL067W	Predicted ribosomal protein	0.19 (5.26)	0.29 (3.45)
CAF0006966	*RPL28*	YGL103W	Structural constituent of ribosome	0.18 (5.56)	0.49 (2.04)

CAF0007021	*RPL40B*	YKR094C	Structural constituent of ribosome	0.13 (7.69)	0.29 (3.45)
CAF0007061	*RPS19A*	YOL121C	Structural constituent of ribosome	0.14 (7.14)	0.26 (3.85)
CAF0006970	*RPS16A*	YDL083C	Structural constituent of ribosome	0.17 (5.88)	0.42 (2.38)
CAF0007095	*RPS28B*	YLR264W	Structural constituent of ribosome	0.14 (7.14)	0.27 (3.70)
CAF0006947	*RPS17B*	YDR447C	Structural constituent of ribosome	0.12 (8.33)	0.27 (3.70)
CAF0007074	*RPS14B*	YJL191W	Structural constituent of ribosome	0.17 (5.88)	0.47 (2.13)
CAF0007004	*RPS13*	YDR064W	Structural constituent of ribosome	0.21 (4.76)	0.42 (2.38)
CAL0001384	*RPS20*	YHL015W	Putative ribosomal protein;	0.06 (16.67)	0.34 (2.94)
CAL0005867	*RPS8A*	YBL072C	Putative ribosomal protein;	0.11 (9.09）	0.37 (2.70)
CAL0004156	*RPS42*	YHR203C	Structural constituent of ribosome	0.11 (9.09)	0.22 (4.55)
CAL0005300	*RPS24*	YER074W	Predicted ribosomal protein	0.20 (5.00)	0.31 (3.23)
CAL0000540	*RPS22A*	YJL190C	Predicted ribosomal protein	0.09 (11.11)	0.23 (4.35)
CAL0003305	*RPS15*	YOL040C	Predicted ribosomal protein	0.15 (6.67)	0.20 (5.00)
CAF0006982	*RPS21B*	YJL136C	Structural constituent of ribosome	0.19 (5.26)	0.39 (2.56)
CAL0004119	*RPS21*	YGL123W	Predicted ribosomal protein	0.17 (5.88)	0.22 (4.55)
CAL0004156	*RPS42*	YHR203C	Structural constituent of ribosome	0.17 (5.88)	0.22 (4.55)
CAF0006912	*RPS9B*	YBR189W	Predicted ribosomal protein	0.09 (11.11)	0.27 (3.70)
CAL0000756	*RPS7A*	YOR096W	Predicted ribosomal protein	0.12 (8.33)	0.31 (3.23)
CAL0004310	*RPS4A*	YJR145C	Predicted ribosomal protein	0.12 (8.33)	0.30 (3.33)
CAL0003748	*RPS6A*	YBR181C	Predicted ribosomal protein	0.13 (7.69)	0.36 (2.78)

CAL0006156	*RPP1A*	YDL081C	Conserved acidic ribosomal protein	0.15 (6.67)	0.12 (8.33)
CAL0006683	*RPP2A*	YDR382W	Conserved acidic ribosomal protein	0.20 (5.00)	0.43 (2.33)
CAL0003308	*RPP2B*	YDR382W	Conserved acidic ribosomal protein	0.22 (4.55)	0.22 (4.55)
CAL0002861	*IPF10027.2*	YOL139C	Translation initiation factor activity	0.49 (2.04)	0.37 (2.70)
CAL0005880	*NAM9*	YNL137C	Structural constituent of ribosome	0.28 (3.57)	0.27 (3.70)
CAL0001364	*RSM24*	YDR175C	Structural constituent of ribosome	0.34 (2.94)	0.42 (2.38)
CAL0006187	*IPF25143.1*	YDR237W	Structural constituent of ribosome	0.39 (2.56)	0.34 (2.94)
CAF0006993	*IPF23568.1*	YNR037C	Structural constituent of ribosome	0.40 (2.50)	0.15 (6.67)
CAL0002638	*IMG1*	YCR046C	Structural constituent of ribosome	0.20 (5.00)	0.37 (2.70)
CAL0000338	*IPF26717.1*	YNL252C	Structural constituent of ribosome	0.03 (33.33)	0.12 (8.33)
CAL0004340	*IPF4102.2*	YBL038W	Structural constituent of ribosome	0.33 (3.03)	0.21 (4.76)
CAL0005205	*RML2*	*RML2*	Structural constituent of ribosome	0.33 (3.03)	0.31 (3.23)
CAL0000370	*YST1*	YGR214W	Structural constituent of ribosome	0.07 (14.29)	0.18 (5.56)
CAL0001930	*LPA4*	YPL013C	Structural constituent of ribosome	0.42 (2.38)	0.37 (2.70)
CAF0006992	*IPF23615.1*	YGR034W	Structural constituent of ribosome	0.15 (6.67)	0.30 (3.33)
CAL0005986	*MRPL8*	YJL063C	Structural constituent of ribosome	0.31 (3.23)	0.16 (6.25)
CAL0002038	*EFB1*	YAL003W	Translation elongation factor EF-1 beta	0.42 (2.38)	0.40 (2.50)
CAL0004986	*RPS12*	YOR369C	Protein described as acidic ribosomal protein S12	0.12 (8.33)	0.27 (3.70)
CAF0007073	*IPF20908.1*	YJL189W	Structural constituent of ribosome	0.12 (8.33)	0.24 (4.17)
CAL0001141	*IPF26642.1*	YNL306W	Structural constituent of ribosome	0.10 (10.00)	0.13 (7.69)

CAL0003524	*WRS1*	YOL097C	Putative tRNA-Trp synthetase	0.14 (7.14)	0.30 (3.33)
CAL0002084	*IPF470.1*	YGL245W	Glutamate-tRNA ligase activity	0.14 (7.14)	0.39 (2.56)
CAF0006953	*IPF7197.2*	YGL076C	Structural constituent of ribosome	0.16 (6.25)	0.33 (3.03)
CAL0004282	*GCN1*	YGL195W	Regulation of translational elongation	0.35 (2.86)	0.33 (3.03)
CAL0005746	*CEF3*	YLR249W	Translation elongation factor 3 (EF-3);	0.17 (5.88)	0.25 (4.00)
CAL0000808	*ISM1*	YPL040C	Mitochondrial translation	0.19 (5.26)	0.21 (4.76)
CAL0005153	*MRP21*	YBL090W	Structural constituent of ribosome	0.17 (5.88)	0.22 (4.55)
CAF0006990	*IPF23702.1*	YLR406C	Structural constituent of ribosome	0.18 (5.56)	0.34 (2.94)
CAL0001575	*IPF25529.1*	YER049W	Translational termination	0.20 (5.00)	0.42 (2.38)
CAL0005131	*TUF1*	YOR187W	Putative translation elongation factor	0.22 (4.55)	0.28 (3.57)
CAL0001484	*DOM34*	YNL001W	Nonfunctional rRNA decay	0.25 (4.00)	0.31 (3.23)
CAL0003549	*TYS1*	YGR185C	Putative tRNA-Tyr synthetase	0.25 (4.00)	0.37 (2.70)
CAL0003839	*TIF35*	YDR429C	Putative translation initiation factor	0.26 (3.85)	0.42 (2.38)
CAL0000218	*IPF26811.1*	YCR003W	Structural constituent of ribosome	0.27 (3.70)	0.20 (5.00)
CAL0005820	*IPF23099.1*	YMR188C	Structural constituent of ribosome	0.23 (4.35)	0.33 (3.03)
CAL0002812	*IPF26428.1*	YDR322W	Structural constituent of ribosome	0.25 (4.00)	0.25 (4.00)
CAL0005933	*IPF23746.1*	YGR165W	Structural constituent of ribosome	0.26 (3.85)	0.37 (2.70)
CAL0001217	*IPF20807.1*	YLR312W-A	Structural constituent of ribosome	0.06 (16.67)	0.28 (3.57)
CAF0006916	*IPF26366.1*	YDR115W	Structural constituent of ribosome	0.29 (3.45)	0.21 (4.76)
CAL0004686	*RSM7*	YJR113C	Structural constituent of ribosome	0.32 (3.13)	0.31 (3.23)

CAL0004886	*RSM10*	YDR041W	Structural constituent of ribosome	0.27 (3.70)	0.46(2.17)
CAL0001457	*DPS1-1*	YLL018C	Putative tRNA-Asp synthetase	0.27 (3.70)	0.32 (3.13)
CAL0003469	*CAM1-1*	YPL048W	Translation elongation factor activity	0.11 (9.09)	0.43 (2.33)
CAL0001942	*SSZ1*	YHR064C	Protein described as an HSP70 chaperone	0.22 (4.55)	0.48 (2.08)
CAL0002761	*DIA4*	YHR011W	Serine-tRNA ligase activity	0.30 (3.33)	0.40 (2.50)
Cell wall maintenance					
CAL0003775	*RBE1*	YJL079C	Putative cell wall protein;	0.09 (11.11)	0.08 (12.50)
CAL0001461	*ENG1*	YNR067C	Endo-1,3-beta-glucanase	0.33 (3.03)	0.38 (2.63)
CAL0003597	*IPF21970.1*	None	Putative cell wall protein	0.02 (50.00)	0.08 (12.50)
CAL0004247	*RHD3*	None	GPI-anchored cell wall protein	0.07 (14.29)	0.11 (9.09)
CAL0000839	*UGP1*	YKL035W	1,6-beta-glucan biosynthetic process	0.29 (3.45)	0.44 (2.27)
CAL0000219	*CHT3*	YLR286C	Chitinase, major	0.14 (7.14)	0.16 (6.25)

D* means decreased fold change.

Table S2. Selected genes that are upregulated in 10b-grown *C. albicans* SC5314 as compared with growth without treatment, determined in two independent experiments.

Primary CGDID	**Gene name**	***S. cerevisiae* homologue name**	**Function**	**Change in fold expression**	
				Ratio1	**ratio2**
Generation energy					
CAL0002010	*MRF1*	YBR026C	Protein similar to mitochondrial respiratory proteins	3.34	4.87
CAL0001374	*YMX6*	YMR145C	NADH dehydrogenase	2.47	2.70
CAL0005127	*DLD1*	YDL174C	D-lactate dehydrogenase (cytochrome) activity	3.19	2.11
CAL0005514	*GLG2*	YJL137C	Glycogenin glucosyltransferase activity	4.67	2.25
ROS scavenge					
AL0004456	*SOD5*	None	Cu/zn-containing superoxide dismutase	31.45	31.71
CAL0005271	*SOD6*	None	Copper- and zinc-containing superoxide dismutase	2.56	3.62
CAL0000683	*GPX1*	YIR037W	Glutathione peroxidase	5.91	8.79
Fermentation					
CAL0002620	*ADH3*	YAL060W	Alcohol dehydrogenase (NAD) activity	13.94	38.96
CAL0003363	*ADH5*	YBR145W	Putative alcohol dehydrogenase	3.05	7.99
Translation					

CAF0006909	*RPL25*	YOL127W	Structural constituent of ribosome	3.08	2.89
CAL0003056	*SUI1*	YNL244C	Putative translation initiation factor	2.05	2.13
Lipid metabolic process					
CAL0004893	*ATG15*	YCR068W	Putative lipase	5.06	2.75
CAL0003909	*INP51*	YIL002C	Inositol-polyphosphate 5-phosphatase activity	2.41	3.27
CAL0005049	*LRO1*	YNR008W	Phospholipid:diacylglycerol acyltransferase activity	2.46	3.27
CAL0004027	*SLD1*	None	Sphingolipid delta-8 desaturase	4.66	6.48
CAL0003570	*LCB4*	YOR171C	Putative sphingosine kinase	2.93	3.33
CAL0001256	*PEX11*	YOL147C	Fatty acid oxidation	3.16	2.58
CAL0003504	*TES15*	YJR019C	Fatty acid metabolic process	7.40	7.02
CAL0002240	*DPP3*	YDR284C	Diacylglycerol pyrophosphate phosphatase activity	7.48	5.86
CAL0005073	*ERG2*	YMR202W	C-8 sterol isomerase	38.91	40.11
CAL0002665	*ERG5*	YMR015C	C-22 sterol desaturase	3.20	7.93
CAL0004388	*ERG4*	YGL012W	Sterol C-24 reductase	3.01	4.36
CAL0001165	*ERG25*	YGR060W	C-4 methyl sterol oxidase	8.64	5.06
CAL0006397	*ERG6*	YML008C	Sterol 24-C-methyltransferase	8.49	6.72
CAL0005678	*ERG10*	YPL028W	Acetyl-CoA acetyltransferase	2.39	4.20

CAL0005685	*ERG24*	YNL280C	Delta14-sterol reductase	5.02	3.65
CAL0003665	*ERG251*	YGR060W	C-4 methylsterol oxidase activity	2.00	3.74
CAL0003974	*IPF25962.1*	YNL111C	Sterol biosynthetic process	3.19	3.36
CAL0000465	*CWH8*	YGR036C	Dolichyl pyrophosphate (Dol-P-P) phosphatase	6.05	2.59
CAL0001102	*CHO1*	YER026C	Putative phosphatidylserine synthase	26.17	12.42
CAL0003505	*TES4*	YJR019C	Fatty acid metabolic process	10.20	4.82
CAL0004910	*MIT1*	YPL057C	Sphingolipid biosynthesis	6.92	2.98
CAL0002213	*ECI1*	YLR284C	Fatty acid beta-oxidation	5.97	5.62
CAL0002210	*DCI1*	YLR284C	Fatty acid beta-oxidation	4.94	4.46
CAL0005741	*IPF20283.1*	YNL202W	2,4-dienoyl-CoA reductase (NADPH) activity	2.80	3.17
CAL0004431	*TGL1*	YKL140W	Sterol esterase activity	2.75	2.19
CAL0000760	*FOX3*	YIL160C	Peroxisomal 3-oxoacyl CoA thiolase	2.72	4.17
CAL0004272	*IDI1*	YPL117C	Isopentenyl-diphosphate delta-isomerase activity	2.09	2.22
CAL0003011	*PSD2*	YGR170W	Phosphatidylserine decarboxylase activity	2.00	2.49
CAL0006272	*ARE2*	YGR170W	Acyl CoA:sterol acyltransferase	2.02	4.01
Cell wall maintenance					
CAL0006153	*XOG1*	YLR300W	Exo-1,3-beta-glucanase, major exoglucanase	70.26	30.40

CAL0006391	*CHT1*	YLR286C	Chitinase	9.56	3.26
CAL0005999	*GSC1*	YGR032W	Subunit of beta-1,3-glucan synthase	4.96	3.07
CAL0002219	*TRI4*	YDR402C	Ascospore wall assembly	5.46	2.96
CAL0002655	*CIS303*	YKL163W	Structural constituent of cell wall	47.32	3.29
CAL0004169	*CRH11*	YGR189C	GPI-anchored cell wall protein	15.15	7.92
CAL0004108	*HEX1*	None	Beta-N-acetylhexosaminidase	2.02	2.41
CAL0000299	*IRS4*	YJL083W	Fungal-type cell wall organization	6.70	5.80
CAL0004244	*PGA31*	YIR019C	Putative GPI anchor	8.11	33.75
CAL0003895	*AVO2*	YMR068W	Fungal-type cell wall organization	5.57	4.19
CAL0006050	*EXG2*	YLR300W	GPI-anchored cell wall protein	2.22	2.39
Cell stress					
CAL0003828	*DAG7*	YNL283C	Response to drug	18.04	13.43
CAL0003404	*YPT31*	YGL210W	GTPase activity	2.51	4.43
CAL0005233	*RIM8*	YGL045W	Response to pH	6.16	2.33
CAL0002299	*SGT2*	YOR007C	Response to heat	2.10	2.37
CAL0006364	*GPA2*	YER020W	Response to glucose stimulus	2.22	3.32
CAL0005151	*TTR1*	YDR513W	Response to oxidative stress	2.24	3.46

CAL0000641	*MET15*	YLR303W	Response to drug	2.27	6.80
CAL0005613	*TRP99*	YLR109W	Response to oxidative stress	2.49	3.44
CAL0004546	*SSU81*	YER118C	Predicted adaptor protein, response to oxidative stress	4.49	2.93
CAL0000977	*IPF4952.1*	YDR411C	Endoplasmic reticulum unfolded protein response	8.28	3.02
CAL0001563	*SIP5*	YMR140W	Putative transcription factor	4.47	4.07
CAL0002586	*AUR1*	YKL004W	Inositolphosphorylceramide (IPC) synthase	4.30	2.40
CAL0005739	*IPF11626.2*	YBR014C	Glutathione-disulfide reductase activity	3.04	2.75
CAL0000641	*MET15*	YLR303W	O-acetylhomoserine O-acetylserine sulfhydrylase	2.78	6.80
CAL0001289	*VID27*	YNL212W	Response to drug	2.65	2.18