

Supplementary Table 4. GO term analysis of genes with downregulated expression in an *ace2* deletion grown as yeast cells.

Terms highlighted in yellow are shown in Fig. 1A.

GO ID	Level(s)	Term	No. In Ref ^a	Freq In Ref ^a	No. In Set ^b	Freq In Set ^b	P value ^c	ENRICHMENT/DEPLETION ^d	Genes In Set
GO:0006096	10,11,8	glycolysis	13	0.0035	6	0.0588	9.13E-06	E	PFK26,GPM1,PFK2,PGI1,FBA1,HXK2
GO:0016052	6	carbohydrate catabolism	32	0.0087	8	0.0784	1.29E-05	E	CTS1,PFK26,GPM1,GPH1,PFK2,PGI1,FBA1,HXK2
GO:0044275	7	cellular carbohydrate catabolism	32	0.0087	8	0.0784	1.29E-05	E	CTS1,PFK26,GPM1,GPH1,PFK2,PGI1,FBA1,HXK2
GO:0005975	5	carbohydrate metabolism	129	0.035	14	0.1373	6.26E-05	E	CTS1,PFK26,GPM1,TPS3,YPI1,GUT2,GPH1,PFK2,PGI1,GLG2,FBA1,DLD1,SMI1,HXK2
GO:0019320	8,9	hexose catabolism	20	0.0054	6	0.0588	6.52E-05	E	PFK26,GPM1,PFK2,PGI1,FBA1,HXK2
GO:0006007	9,10	glucose catabolism	20	0.0054	6	0.0588	6.52E-05	E	PFK26,GPM1,PFK2,PGI1,FBA1,HXK2
GO:0015980	6	energy derivation by oxidation of organic compounds	132	0.0358	14	0.1373	7.81E-05	E	ADH1,PFK26,GPM1,TPS3,YPI1,GPH1,PFK2,PGI1,BDH1,GLG2,ADH3,FBA1,DLD1,HXK2
GO:0046365	7,8	monosaccharide catabolism	24	0.0065	6	0.0588	0.0001524	E	PFK26,GPM1,PFK2,PGI1,FBA1,HXK2
GO:0006807	4	nitrogen compound metabolism	200	0.0543	17	0.1667	0.000186	E	FMS1,ARG3,CPS1,ARO8,CTS1,TRP2,ECM17,LYS2,STT4,LYS1,URE2,AGX1,NPR1,TRP4,HOM2,LPD1,ARO3
GO:0009309	6,7	amine biosynthesis	95	0.0258	11	0.1078	0.0002065	E	ARG3,TRP2,ECM17,LYS2,STT4,LYS1,AGX1,TRP4,HOM2,LPD1,ARO3
GO:0044271	6,5	nitrogen compound biosynthesis	95	0.0258	11	0.1078	0.0002065	E	ARG3,TRP2,ECM17,LYS2,STT4,LYS1,AGX1,TRP4,HOM2,LPD1,ARO3
GO:0046164	6	alcohol catabolism	26	0.0071	6	0.0588	0.0002215	E	PFK26,GPM1,PFK2,PGI1,FBA1,HXK2
GO:0006091	5	generation of precursor metabolites and energy	150	0.0407	14	0.1373	0.0002606	E	ADH1,PFK26,GPM1,TPS3,YPI1,GPH1,PFK2,PGI1,BDH1,GLG2,ADH3,FBA1,DLD1,HXK2
GO:0044262	6	cellular carbohydrate metabolism	120	0.0326	12	0.1176	0.0003786	E	CTS1,PFK26,GPM1,TPS3,YPI1,GPH1,PFK2,PGI1,GLG2,FBA1,SMI1,HXK2
GO:0008652	7,8	amino acid biosynthesis	87	0.0236	10	0.098	0.0004062	E	ARG3,TRP2,ECM17,LYS2,LYS1,AGX1,TRP4,HOM2,LPD1,ARO3
GO:0000920	6	cell separation during cytokinesis	5	0.0014	3	0.0294	0.0010419	E	SCW11,CTS1,DSE4
GO:0007109	7	cytokinesis, completion of separation	5	0.0014	3	0.0294	0.0010419	E	SCW11,CTS1,DSE4
GO:0006006	8,9	glucose metabolism	40	0.0109	6	0.0588	0.0016296	E	PFK26,GPM1,PFK2,PGI1,FBA1,HXK2
GO:0016051	7,6	carbohydrate biosynthesis	40	0.0109	6	0.0588	0.0016296	E	GPM1,TPS3,PGI1,GLG2,FBA1,SMI1
GO:0009308	5	amine metabolism	186	0.0505	14	0.1373	0.0017497	E	FMS1,ARG3,ARO8,CTS1,TRP2,ECM17,LYS2,STT4,LYS1,AGX1,TRP4,HOM2,LPD1,ARO3
GO:0006519	5	amino acid and derivative metabolism	170	0.0461	13	0.1275	0.002161	E	FMS1,ARG3,ARO8,TRP2,ECM17,LYS2,STT4,LYS1,AGX1,TRP4,HOM2,LPD1,ARO3
GO:0009072	7,6,8	aromatic amino acid family metabolism	20	0.0054	4	0.0392	0.0039118	E	ARO8,TRP2,TRP4,ARO3
GO:0006092	7	main pathways of carbohydrate metabolism	49	0.0133	6	0.0588	0.0040619	E	PFK26,GPM1,PFK2,PGI1,FBA1,HXK2
GO:0006576	6,7	biogenic amine metabolism	21	0.0057	4	0.0392	0.0045543	E	FMS1,TRP2,STT4,TRP4
GO:0044264	6,7	cellular polysaccharide metabolism	35	0.0095	5	0.049	0.0046958	E	CTS1,YPI1,GPH1,GLG2,SMI1
GO:0005976	6	polysaccharide metabolism	35	0.0095	5	0.049	0.0046958	E	CTS1,YPI1,GPH1,GLG2,SMI1

GO:0006112		7 energy reserve metabolism	22	0.006	4	0.0392	0.005264	E	TPS3,YPI1,GPH1,GLG2
GO:0019318	7,8	hexose metabolism	52	0.0141	6	0.0588	0.0052785	E	PFK26,GPM1,PFK2,PGI1,FBA1,HXK2
GO:0006113		7 fermentation	11	0.003	3	0.0294	0.0059729	E	ADH1,BDH1,ADH3
GO:0009070	8,9	serine family amino acid biosynthesis	11	0.003	3	0.0294	0.0059729	E	AGX1,HOM2,LPD1
GO:0006826	9,10	iron ion transport	11	0.003	3	0.0294	0.0059729	E	FRE3,FTR1,FET3
GO:0006073	7,8	glucan metabolism	23	0.0062	4	0.0392	0.0060437	E	YPI1,GPH1,GLG2,SMI1
GO:0006575		6 amino acid derivative metabolism	23	0.0062	4	0.0392	0.0060437	E	FMS1,TRP2,STT4,TRP4
GO:0006000	8,9	fructose metabolism	3	0.0008	2	0.0196	0.0070585	E	PFK26,HXK2
GO:0006520	6,7	amino acid metabolism	156	0.0423	11	0.1078	0.0075532	E	ARG3,ARO8,TRP2,ECM17,LYS2,LYS1,AGX1,TRP4,HOM2,LPD1,ARO3
GO:0006090		7 pyruvate metabolism	25	0.0068	4	0.0392	0.0078244	E	GPM1,PGI1,FBA1,LPD1
GO:0005996	6,7	monosaccharide metabolism	58	0.0157	6	0.0588	0.008475	E	PFK26,GPM1,PFK2,PGI1,FBA1,HXK2
GO:0019752		6 carboxylic acid metabolism	242	0.0657	15	0.1471	0.0103609	E	ARG3,ARO8,TRP2,ECM17,GPM1,LYS2,PGI1,LYS1,AGX1,TRP4,FBA1,AYR1,HOM2,LPD1,ARO3
GO:0006082		5 organic acid metabolism	242	0.0657	15	0.1471	0.0103609	E	ARG3,ARO8,TRP2,ECM17,GPM1,LYS2,PGI1,LYS1,AGX1,TRP4,FBA1,AYR1,HOM2,LPD1,ARO3
GO:0006827	10,11	high affinity iron ion transport	4	0.0011	2	0.0196	0.0103936	E	FTR1,FET3
GO:0009073	8,7,9	aromatic amino acid family biosynthesis	15	0.0041	3	0.0294	0.0123234	E	TRP2,TRP4,ARO3
GO:0051171		5 regulation of nitrogen metabolism	5	0.0014	2	0.0196	0.0142851	E	URE2,NPR1
GO:0006808		6 regulation of nitrogen utilization	5	0.0014	2	0.0196	0.0142851	E	URE2,NPR1
GO:0006094	9,10,8	gluconeogenesis	16	0.0043	3	0.0294	0.0143349	E	GPM1,PGI1,FBA1
GO:0019438		6 aromatic compound biosynthesis	16	0.0043	3	0.0294	0.0143349	E	TRP2,TRP4,ARO3
GO:0005977	8,9	glycogen metabolism	17	0.0046	3	0.0294	0.0165204	E	YPI1,GPH1,GLG2
GO:0042401	7,8	biogenic amine biosynthesis	17	0.0046	3	0.0294	0.0165204	E	TRP2,STT4,TRP4
GO:0019878	10,11	lysine biosynthesis via amino adipic acid	6	0.0016	2	0.0196	0.0186995	E	LYS2,LYS1
GO:0000272		7 polysaccharide catabolism	6	0.0016	2	0.0196	0.0186995	E	CTS1,GPH1
GO:0044247	8,7	cellular polysaccharide catabolism	6	0.0016	2	0.0196	0.0186995	E	CTS1,GPH1
GO:0006544	8,9	glycine metabolism	6	0.0016	2	0.0196	0.0186995	E	AGX1,LPD1
GO:0019319	8,9	hexose biosynthesis	18	0.0049	3	0.0294	0.0188812	E	GPM1,PGI1,FBA1
GO:0046364	7,8	monosaccharide biosynthesis	18	0.0049	3	0.0294	0.0188812	E	GPM1,PGI1,FBA1
GO:0007047		6 cell wall organization and biogenesis	91	0.0247	7	0.0686	0.0191737	E	ECM17,DSE1,PIR1,SLA1,ECM4,SMI1,ECM33
GO:0045229		5 external encapsulating structure organization and bio	91	0.0247	7	0.0686	0.0191737	E	ECM17,DSE1,PIR1,SLA1,ECM4,SMI1,ECM33
GO:0046165		6 alcohol biosynthesis	19	0.0052	3	0.0294	0.0214178	E	GPM1,PGI1,FBA1
GO:0042398	7,6	amino acid derivative biosynthesis	19	0.0052	3	0.0294	0.0214178	E	TRP2,STT4,TRP4
GO:0009085	9,10	lysine biosynthesis	7	0.0019	2	0.0196	0.023605	E	LYS2,LYS1
GO:0006553	8,9	lysine metabolism	7	0.0019	2	0.0196	0.023605	E	LYS2,LYS1
GO:0007039	8,9	vacuolar protein catabolism	7	0.0019	2	0.0196	0.023605	E	APE3,LAP4
GO:0009069	7,8	serine family amino acid metabolism	20	0.0054	3	0.0294	0.0241304	E	AGX1,HOM2,LPD1
GO:0009250	9,8	glucan biosynthesis	8	0.0022	2	0.0196	0.028971	E	GLG2,SMI1
GO:0010038		6 response to metal ion	8	0.0022	2	0.0196	0.028971	E	URE2,FET3
GO:0009096	9,8,10	aromatic amino acid family biosynthesis, anthranilate	9	0.0024	2	0.0196	0.0347685	E	TRP2,TRP4
GO:0042430		6 indole and derivative metabolism	9	0.0024	2	0.0196	0.0347685	E	TRP2,TRP4
GO:0006586	7,8	indolalkylamine metabolism	9	0.0024	2	0.0196	0.0347685	E	TRP2,TRP4
GO:0006568	8,9,7	tryptophan metabolism	9	0.0024	2	0.0196	0.0347685	E	TRP2,TRP4
GO:0042435	8,6	indole derivative biosynthesis	9	0.0024	2	0.0196	0.0347685	E	TRP2,TRP4
GO:0042434		7 indole derivative metabolism	9	0.0024	2	0.0196	0.0347685	E	TRP2,TRP4

GO:0046219	8,9,7	indolalkylamine biosynthesis	9	0.0024	2	0.0196	0.0347685	E	TRP2,TRP4
GO:0000162	10,9,8,11	tryptophan biosynthesis	9	0.0024	2	0.0196	0.0347685	E	TRP2,TRP4
GO:0006769	9,8	nicotinamide metabolism	25	0.0068	3	0.0294	0.0403087	E	GUT2,PGI1,POS5
GO:0006066	5	alcohol metabolism	108	0.0293	7	0.0686	0.04048	E	PFK26,GPM1,PFK2,PGI1,STT4,FBA1,HXK2
GO:0000147	10,9	actin cortical patch assembly	10	0.0027	2	0.0196	0.0409695	E	SLA1,ARC15
GO:0006739	10,9	NADP metabolism	10	0.0027	2	0.0196	0.0409695	E	PGI1,POS5
GO:0019740	5	nitrogen utilization	10	0.0027	2	0.0196	0.0409695	E	URE2,NPR1
GO:0010035	5	response to inorganic substance	10	0.0027	2	0.0196	0.0409695	E	URE2,FET3
GO:0006493	10,9	protein amino acid O-linked glycosylation	11	0.003	2	0.0196	0.0475472	E	PMT4,PMT6
GO:0030866	9,8	cortical actin cytoskeleton organization and biogenesis	11	0.003	2	0.0196	0.0475472	E	SLA1,ARC15
GO:0030865	7	cortical cytoskeleton organization and biogenesis	11	0.003	2	0.0196	0.0475472	E	SLA1,ARC15
GO:0044265	6	cellular macromolecule catabolism	197	0.0535	11	0.1078	0.0478614	E	CTS1,PFK26,APE3,GPM1,GPH1,LAP4,PFK2,PGI1,UBX7,FBA1,HXK2
GO:0051276	6	chromosome organization and biogenesis	219	0.0594	1	0.0098	0.0441564	D	CST6
GO:0019538	5	protein metabolism	897	0.2434	14	0.1373	0.04316	D	CPS1,RTS1,PRD1,APE3,YKL171W,TPK2,YPI1,PMT4,LAP4,MNN2,UPL1,UBX7,PMT6,CMK1
GO:0007001	7	chromosome organization and biogenesis (sensu Eukarya)	210	0.057	1	0.0098	0.0428306	D	CST6
GO:0051649	6,5	establishment of cellular localization	397	0.1077	3	0.0294	0.0168414	D	URE2,PIR1,CUP5
GO:0046907	7,5,6	intracellular transport	391	0.1061	3	0.0294	0.016455	D	URE2,PIR1,CUP5
GO:0006259	6	DNA metabolism	334	0.0906	2	0.0196	0.0162733	D	CST6,RNR2
GO:0006139	5	nucleobase, nucleoside, nucleotide and nucleic acid metabolism	986	0.2676	12	0.1176	0.0048226	D	YHR087W,ACE2,GUT2,PGI1,STP2,ASH1,CST6,SIP3,POS5,MSN4,HXK2,RNR2
GO:0016043	4	cell organization and biogenesis	1135	0.308	13	0.1275	0.0016052	D	ARP3,ECM17,STT4,DSE1,URE2,PIR1,CST6,SLA1,ECM4,CUP5,SMI1,ECM33,ARC15
GO:0016070	6	RNA metabolism	378	0.1026	1	0.0098	0.0013322	D	YHR087W
GO:0006996	5	organelle organization and biogenesis	726	0.197	6	0.0588	0.0013053	D	ARP3,STT4,CST6,SLA1,CUP5,ARC15

^a Reference data: 3685 *S. cerevisiae* orthologues of *C. albicans* genes represented on the microarrays

^b Data set: 102 *S. cerevisiae* orthologues of *C. albicans* genes with reduced expression in yeast cells

^c Terms with a p value of less than or equal to 0.05 are shown.

^d E: GO term over-represented in data set; D: GO term under-represented in data set

Supplementary Table 5. GO term analysis of genes with upregulated expression in an *ace2* deletion grown as yeast cells.

Terms highlighted in yellow are shown in Fig. 1A.

GO ID	Level(s)	Term	No. In Ref ^a	Freq In Ref ^a	No. In Set ^b	Freq In Set ^b	P value ^c	ENRICHMENT/D EPLETION ^d	Genes In Set
GO:0006412	7,6	protein biosynthesis	359	0.0974	64	0.3536	3.21E-14	E	RSM18,MSS51,MRPS5,CAX4,RSM10,MRPL4,CBP6,MRPS28,NAM9,MRPL36,MRPS17,RSM24,MRPS35,YPL183W,A_GCD10,MRPL17,MNN11,MRPL28,MRPS8,MRP51,MRPL11,IMG1,MRPL38,RSM26,MNP1,MRPL1,SWS2,MRP1,MRPL9,MRPL3,MRPL31,MRPL49,MRP7,TUF1,MEF1,MRPL7,IFM1,MRPL37,RSM23,TIF5,MRPS16,MRPL40,MRPL15,YDR115W,FAA4,MRP4,PET123,CLU1,RML2,RSM27,MRPL19,MRPL51,MRPL16,IMG2,MRPL22,MRPL35,ISM1,RSM25,NAM2,RSM7,YML6,MRPL24,DPS1,YNR036C
GO:0009059	6,5	macromolecule biosynthesis	396	0.1075	64	0.3536	1.72E-12	E	RSM18,MSS51,MRPS5,CAX4,RSM10,MRPL4,CBP6,MRPS28,NAM9,MRPL36,MRPS17,RSM24,MRPS35,YPL183W-A_GCD10,MRPL17,MNN11,MRPL28,MRPS8,MRP51,MRPL11,IMG1,MRPL38,RSM26,MNP1,MRPL1,SWS2,MRP1,MRPL9,MRPL3,MRPL31,MRPL49,MRP7,TUF1,MEF1,MRPL7,IFM1,MRPL37,RSM23,TIF5,MRPS16,MRPL40,MRPL15,YDR115W,FAA4,MRP4,PET123,CLU1,RML2,RSM27,MRPL19,MRPL51,MRPL16,IMG2,MRPL22,MRPL35,ISM1,RSM25,NAM2,RSM7,YML6,MRPL24,DPS1,YNR036C
GO:0009058	4	biosynthesis	671	0.1821	83	0.4586	3.07E-10	E	MEU1,ERG24,RSM18,PUT2,MSS51,MRPS5,CAX4,RSM10,URA3,ADE4,MRPL4,CBP6,MRPS28,NAM9,MRPL36,CHO2,MRPS17,YAH1,RSM24,MRPS35,YPL183,A_GCD10,MRPL17,MNN11,ERG2,MRPL28,MRPS8,MRP51,MRPL11,IMG1,PRS3,FAS2,MRPL38,PIS1,RSM26,MNP1,YDR531W,MRPL1,SWS2,MRP1,MRPL9,IMG3,MRPL3,MRPL31,MRPL49,MRP7,TUF1,MEF1,MRPL7,IFM1,MRPL37,SUR4,RSM23,TIF5,MRPS16,MRPL40,MRPL15,ERG10,YDR115W,CYB5,ERG28,FAA4,MRP4,PET123,CLU1,RML2,RSM27,MRPL19,MRPL51,MRPL16,IMG2,MRPL22,FAS1,MRPL35,ISM1,RSM25,NAM2,ACC1,RSM7,YML6,MRPL24,DPS1,YNR036C
GO:0044249	5	cellular biosynthesis	610	0.1655	76	0.4199	8.86E-10	E	MEU1,RSM18,PUT2,MSS51,MRPS5,CAX4,RSM10,URA3,ADE4,MRPL4,CBP6,MRPS28,NAM9,MRPL36,MRPS17,YAH1,RSM24,MRPS35,YPL183W-A_GCD10,MRPL17,MNN11,MRPL28,MRPS8,MRP51,MRPL11,IMG1,PRS3,FAS2,MRPL38,RSM26,MNP1,YDR531W,MRPL1,SWS2,MRP1,MRPL9,IMG3,MRPL3,MRPL31,MRPL49,MRP7,TUF1,MEF1,MRPL7,IFM1,MRPL37,SUR4,RSM23,TIF5,MRPS16,MRPL40,MRPL15,ERG10,YDR115W,CYB5,ERG28,FAA4,MRP4,PET123,CLU1,RML2,RSM27,MRPL19,MRPL51,MRPL16,IMG2,MRPL22,FAS1,MRPL35,ISM1,RSM25,NAM2,ACC1,RSM7,YML6,MRPL24,DPS1,YNR036C
GO:0006626	10,8,9	protein targeting to mitochondrion	40	0.0109	16	0.0884	6.32E-09	E	TIM17,TOM7,TIM9,TIM50,MIA40,OCT1,YTA12,MRS11,PAM16,TIM8,TIM44,TOM40,MGE1,OXA1,PAM17,TIM54
GO:0009060	8	aerobic respiration	62	0.0168	15	0.0829	3.77E-06	E	MRPS17,RSM24,MRPS35,MBA1,MAM33,COQ5,MNP1,MRPL1,MDL2,COX11,FUM1,YDR115W,MRPL51,MRPL22,SDH4
GO:0045333	7	cellular respiration	63	0.0171	15	0.0829	4.45E-06	E	MRPS17,RSM24,MRPS35,MBA1,MAM33,COQ5,MNP1,MRPL1,MDL2,COX11,FUM1,YDR115W,MRPL51,MRPL22,SDH4
GO:0017038	6,7	protein import	79	0.0214	16	0.0884	1.29E-05	E	TIM17,TOM7,TIM9,TIM50,MIA40,OCT1,YTA12,MRS11,PAM16,TIM8,TIM44,TOM40,MGE1,OXA1,PAM17,TIM54,ACC1
GO:0044267	6	cellular protein metabolism	798	0.2166	75	0.4144	1.37E-05	E	RSM18,MSS51,MRPS5,CAX4,RSM10,MRPL4,CBP6,MRPS28,NAM9,MRPL36,MRPS17,QRI7,HSP10,RSM24,MRPS35,YPL183W-A_GCD10,MRPL17,MNN11,MRPL28,MRPS8,MRP51,MRPL11,IMG1,PRS3,FAS2,MRPL38,RSM26,MNP1,MRPL1,SWS2,MRP1,MRPL9,IMG3,MRPL3,MRPL31,MRPL49,MRP7,TUF1,MEF1,MRPL7,IFM1,MRPL37,RSM23,TIF5,MRPS16,MRPL40,MRPL15,YDR115W,FAA4,MRP4,PET123,CLU1,RML2,RSM27,MRPL19,CYT2,MRPL51,MRPL16,IMG2,MRPL22,MRPL35,ISM1,RSM25,NAM2,PIM1,RSM7,SEC23,YML6,MRPL24,DPS1,YNR036C
GO:0030150	11,9,7,10,8	protein import into mitochondrial matrix	18	0.0049	8	0.0442	1.96E-05	E	TIM17,TOM7,TIM50,PAM16,TIM44,TOM40,MGE1,PAM17
GO:0019538	5	protein metabolism	897	0.2434	80	0.442	3.39E-05	E	RSM18,MSS51,MRPS5,CAX4,COX18,RSM10,MRPL4,CBP6,MRPS28,NAM9,MRPL36,MRPS17,QRI7,HSP10,RSM24,MRPS35,YPL183W-A_GCD10,MRPL17,MNN11,OCT1,MRPL28,MRPS8,MRP51,MRPL11,YTA12,IMG1,FAS2,BUD32,MRPL38,RSM26,MNP1,MRPL1,TMA108,SWS2,MRP1,PRE9,MRPL9,MRPL3,MRPL31,MRPL49,MRP7,TUF1,COX11,MEF1,MRPL7,IFM1,MRPL37,RSM23,TIF5,MRPS16,MRPL40,MRPL15,YDR115W,FAA4,MRP4,PET123,CLU1,ATP11,RML2,RSM27,MRPL19,CYT2,MRPL51,MRPL16,IMG2,NSR1,MRPL22,MRPL35,ISM1,RSM25,NAM2,PIM1,RSM7,SEC23,YML6,MRPL24,DPS1,YNR036C
GO:0044260	5	cellular macromolecule metabolism	826	0.2242	75	0.4144	3.56E-05	E	RSM18,MSS51,MRPS5,CAX4,RSM10,MRPL4,CBP6,MRPS28,NAM9,MRPL36,MRPS17,QRI7,HSP10,RSM24,MRPS35,YPL183W-A_GCD10,MRPL17,MNN11,OCT1,MRPL28,MRPS8,MRP51,MRPL11,YTA12,IMG1,FAS2,BUD32,MRPL38,RSM26,MNP1,MRPL1,TMA108,SWS2,MRP1,PRE9,MRPL9,MRPL3,MRPL31,MRPL49,MRP7,TUF1,MEF1,MRPL7,IFM1,MRPL37,RSM23,TIF5,MRPS16,MRPL40,MRPL15,YDR115W,FAA4,MRP4,PET123,CLU1,RML2,RSM27,MRPL19,CYT2,MRPL51,MRPL16,IMG2,MRPL22,MRPL35,ISM1,RSM25,NAM2,PIM1,RSM7,SEC23,YML6,MRPL24,DPS1,YNR036C
GO:0007006	6,7	mitochondrial membrane organization and biogenesis	16	0.0043	7	0.0387	6.99E-05	E	TOM7,TIM9,MBA1,MRS11,TIM8,OXA1,TIM54
GO:0007007	7,8	inner mitochondrial membrane organization and biogenesis	12	0.0033	6	0.0331	0.000131	E	TIM9,MBA1,MRS11,TIM8,OXA1,TIM54
GO:0045039	11,8,9,7,10	protein import into mitochondrial inner membrane	9	0.0024	5	0.0276	0.000337	E	TIM9,MRS11,TIM8,OXA1,TIM54
GO:0007005	6	mitochondrion organization and biogenesis	76	0.0206	12	0.0663	0.001012	E	TOM7,TIM9,MBA1,GGC1,MHR1,MRS11,RIM2,TIM8,RPO41,CLU1,OXA1,TIM54
GO:0006633	8,7,6	fatty acid biosynthesis	10	0.0027	4	0.0221	0.003436	E	FAS2,SUR4,FAS1,ACC1
GO:0015980	6	energy derivation by oxidation of organic compounds	132	0.0358	15	0.0829	0.00544	E	MRPS17,RSM24,MRPS35,MBA1,MAM33,COQ5,MNP1,MRPL1,MDL2,COX11,FUM1,YDR115W,MRPL51,MRPL22,SDH4
GO:0008610	6,5,7	lipid biosynthesis	96	0.0261	12	0.0663	0.005606	E	ERG24,CAX4,CHO2,ERG2,FAS2,PIS1,SUR4,ERG10,CYB5,ERG28,FAS1,ACC1
GO:0046394	7	carboxylic acid biosynthesis	13	0.0035	4	0.0221	0.007281	E	FAS2,SUR4,FAS1,ACC1
GO:0016053	6	organic acid biosynthesis	13	0.0035	4	0.0221	0.007281	E	FAS2,SUR4,FAS1,ACC1
GO:0006091	5	generation of precursor metabolites and energy	150	0.0407	16	0.0884	0.008502	E	MRPS17,RSM24,MRPS35,MBA1,MAM33,COQ5,MNP1,MRPL1,MDL2,CYC1,COX11,FUM1,YDR115W,MRPL51,MRPL22,SDH4
GO:0006631	6,7	fatty acid metabolism	32	0.0087	6	0.0331	0.008541	E	ACB1,FAS2,SUR4,RML2,FAS1,ACC1
GO:0006390	8	transcription from mitochondrial promoter	2	0.0005	2	0.011	0.012528	E	RPO41,MTF1
GO:0006629	5	lipid metabolism	174	0.0472	17	0.0939	0.014513	E	ERG24,CAX4,CHO2,YBR030W,ERG2,ACB1,FAS2,PIS1,YPL206C,SUR4,ERG10,CYB5,ERG28,FAA4,RML2,FAS1,ACC1
GO:0016126	7,8,9	sterol biosynthesis	27	0.0073	5	0.0276	0.016515	E	ERG24,ERG2,ERG10,CYB5,ERG28
GO:0044255	5,6	cellular lipid metabolism	165	0.0448	16	0.0884	0.019482	E	ERG24,CAX4,CHO2,YBR030W,ERG2,ACB1,FAS2,PIS1,YPL206C,SUR4,ERG10,CYB5,ERG28,RML2,FAS1,ACC1
GO:0043037	8,7	translation	101	0.0274	11	0.0608	0.021822	E	MSS51,GCD10,MRP51,MNP1,TUF1,MEF1,IFM1,TIF5,CLU1,ISM1,NAM2

GO:0009451		7 RNA modification		53	0.0144	7	0.0387	0.023217	E	TRM2,PUS7,NHP2,GCD10,MRM1,TAN1,CCA1
GO:0006605	9,7,8	protein targeting		181	0.0491	17	0.0939	0.02551	E	TIM17,TOM7,TIM9,TIM50,MIA40,OCT1,YTA12,MRS11,PAM16,TIM8,TIM44,TOM40,MGE1,OXA1,PAM17,TIM54,ACC1
GO:0006399		7 tRNA metabolism		88	0.0239	10	0.0552	0.025949	E	TRM2,LHP1,PUS7,GCD10,MTR4,POP3,TAN1,ISM1,NAM2,CCA1
GO:0006694	7,6,8	steroid biosynthesis		31	0.0084	5	0.0276	0.026426	E	ERG24,ERG2,ERG10,CYB5,ERG28
GO:0000002		7 mitochondrial genome maintenance		21	0.0057	4	0.0221	0.02858	E	GGC1,MHR1,RIM2,RPO41
GO:0006862	6,7	nucleotide transport		4	0.0011	2	0.011	0.029387	E	GGC1,RIM2
GO:0043170		4 macromolecule metabolism		1533	0.416	100	0.5525	0.031766	E	URB2,RSM18,MSS51,MRPS5,TRM2,LHP1,YJR096W,CAX4,COX18,PUS7,RSM10,MRPL4,CBP6,MRPS28,NAM9,MRPL36,NHP2,FAF1,MRPS17,QRI7,HSP10,RSM24,SUV3,MRPS35,YPL183W-A,GCD10,MRPL17,MNN11,OCT1,MTR4,MRPL28,MRPS8,MRP51,MRPL11,YTA12,IMG1,FAS2,BUD32,MRPL38,RSM26,MNP1,MRPL1,TMA108,SWS2,MRP1,RRP5,PRES9,NOP7,MRPL9,COX17,MRPL3,MRPL31,MRPL49,MRP7,TUF1,COX11,MEF1,SNU13,MRPL7,IFM1,FUM1,POP3,MRM1,MRPL37,RSM23,TIF5,MRPS16,MRPL40,MRPL15,YDR115W,TAN1,FAA4,MRP4,PET123,RRP42,CLU1,ATP11,DDR48,RML2,RSM27,MRPL19,CYT2,MRPL51,MRPL16,IMG2,NSR1,MRPL22,MRPL35,ISM1,RSM25,NAM2,PIM1,RSM7,SEC23,CCA1,YML6,MRPL24,DPS1,SDH4,YNR036C
GO:0006886	8,6,7	intracellular protein transport		194	0.0526	17	0.0939	0.03231	E	TIM17,TOM7,TIM9,TIM50,MIA40,OCT1,YTA12,MRS11,PAM16,TIM8,TIM44,TOM40,MGE1,OXA1,PAM17,TIM54,ACC1
GO:0016125	6,7,8	sterol metabolism		33	0.009	5	0.0276	0.032542	E	ERG24,ERG2,ERG10,CYB5,ERG28
GO:0006400		8 tRNA modification		35	0.0095	5	0.0276	0.039469	E	TRM2,PUS7,GCD10,TAN1,CCA1
GO:0006413	9,8	translational initiation		35	0.0095	5	0.0276	0.039469	E	GCD10,MRP51,IFM1,TIF5,CLU1
GO:0001522		8 pseudouridine synthesis		5	0.0014	2	0.011	0.03986	E	PUS7,NHP2
GO:0015680	8,6,10,7,11	intracellular copper ion transport		5	0.0014	2	0.011	0.03986	E	COX17,COX11
GO:0006696	8,9,10	ergosterol biosynthesis		24	0.0065	4	0.0221	0.041346	E	ERG24,ERG2,ERG10,ERG28
GO:0008204	7,8,9	ergosterol metabolism		24	0.0065	4	0.0221	0.041346	E	ERG24,ERG2,ERG10,ERG28
GO:0008202	6,7	steroid metabolism		37	0.01	5	0.0276	0.04722	E	ERG24,ERG2,ERG10,CYB5,ERG28
GO:0044237		4 cellular metabolism		2152	0.584	134	0.7403	0.048087	E	URB2,MEU1,ERG24,RSM18,PUT2,MSS51,MRPS5,TRM2,LHP1,YJR096W,CAX4,PUS7,RSM10,URA3,ADE4,CAR1,MRPL4,CBP6,MRPS28,NAM9,MRPL36,NHP2,FAF1,CHO2,MRPS17,QRI7,HSP10,YAH1,YBR030W,RSM24,ACH1,SUV3,MRPS35,YPL183W-A,GCD10,MRPL17,MNN11,OCT1,MTR4,ERG2,ACB1,MRPL28,ADH7,MBA1,MRPS8,MRP51,MRPL11,YTA12,SVF1,IMG1,MAM33,PRS3,FAS2,BUD32,MRPL38,PIS1,COQ5,RSM26,MNP1,YDR531W,MRPL1,YPL206C,TMA108,SWS2,MRP1,RRP5,PRES9,NOP7,MDL2,MRPL9,IMD3,MRPL3,MRPL31,MRPL49,MRP7,TUF1,CYC1,COX11,PUF6,MEF1,SNU13,MRPL7,IFM1,FUM1,POP3,MRM1,MRPL37,SUR4,RSM23,TIF5,MRPS16,RPO41,MRPL40,MRPL15,ERG10,YDR115W,CYB5,ERG28,TAN1,FAA4,MRP4,PET123,RRP42,CLU1,DDR48,RRN7,RML2,RSM27,MRPL19,CYT2,MRPL51,SNQ2,MRPL16,IMG2,NSR1,MRPL22,FAS1,COQ4,MRPL35,ISM1,RSM25,NAM2,PIM1,ACC1,RSM7,MTF1,SEC23,CCA1,RPC19,YML6,MRPL24,DPS1,SDH4,YNR036C
GO:0015031	5,6	protein transport		199	0.054	17	0.0939	0.048207	E	TIM17,TOM7,TIM9,TIM50,MIA40,OCT1,YTA12,MRS11,PAM16,TIM8,TIM44,TOM40,MGE1,OXA1,PAM17,TIM54,ACC1
GO:0008152		3 metabolism		2216	0.6014	137	0.7569	0.050178	E	URB2,MEU1,ERG24,RSM18,PUT2,MSS51,MRPS5,TRM2,LHP1,YJR096W,CAX4,COX18,PUS7,RSM10,URA3,ADE4,CAR1,MRPL4,CBP6,MRPS28,NAM9,MRPL36,NHP2,FAF1,CHO2,MRPS17,QRI7,HSP10,YAH1,YBR030W,RSM24,ACH1,SUV3,MRPS35,YPL183W-A,GCD10,MRPL17,MNN11,OCT1,MTR4,ERG2,ACB1,MRPL28,ADH7,MBA1,MRPS8,MRP51,MRPL11,YTA12,SVF1,IMG1,MAM33,PRS3,FAS2,BUD32,MRPL38,PIS1,COQ5,RSM26,MNP1,YDR531W,MRPL1,YPL206C,TMA108,SWS2,MRP1,RRP5,PRES9,NOP7,MDL2,MRPL9,COX17,IMD3,MRPL3,MRPL31,MRPL49,MRP7,TUF1,CYC1,COX11,PUF6,MEF1,SNU13,MRPL7,IFM1,FUM1,POP3,MRM1,MRPL37,SUR4,RSM23,TIF5,MRPS16,RPO41,MRPL40,MRPL15,ERG10,YDR115W,CYB5,ERG28,TAN1,FAA4,MRP4,PET123,RRP42,CLU1,ATP11,DDR48,RRN7,RML2,RSM27,MRPL19,CYT2,MRPL51,SNQ2,MRPL16,IMG2,NSR1,MRPL22,FAS1,COQ4,MRPL35,ISM1,RSM25,NAM2,PIM1,ACC1,RSM7,MTF1,SEC23,CCA1,RPC19,YML6,MRPL24,DPS1,SDH4,YNR036C
GO:0045041	11,9,7,10,8	protein import into mitochondrial intermembrane space		6	0.0016	2	0.011	0.051497	E	MIA40,YTA12
GO:0006281	7,5	DNA repair		113	0.0307	1	0.0055	0.06379	D	DDR48
GO:0045045	5,6	secretory pathway		157	0.0426	2	0.011	0.048317	D	SUR4,SEC23
GO:0042221		4 response to chemical stimulus		150	0.0407	2	0.011	0.046664	D	SVF1,SNQ2
GO:0000004		2 biological process unknown		615	0.1669	18	0.0994	0.036738	D	FMP35,YLR168C,FYV4,FMP38,YGL220W,OMS1,YMR295C,NCS6,FMP31,YMR002W,FMP36,FMP25,YIL110W,YJR129C,YIRO35C,PGA3,YNR020C,YAL046C
GO:0009628		3 response to abiotic stimulus		199	0.054	3	0.0166	0.034651	D	SVF1,SNQ2,PIM1
GO:0046903		5 secretion		163	0.0442	2	0.011	0.033469	D	SUR4,SEC23
GO:0006974		4 response to DNA damage stimulus		131	0.0355	1	0.0055	0.030475	D	DDR48
GO:0009719		3 response to endogenous stimulus		136	0.0369	1	0.0055	0.020522	D	DDR48
GO:0006464		7 protein modification		369	0.1001	8	0.0442	0.018113	D	CAX4,MNN11,OCT1,YTA12,FAS2,BUD32,FAA4,CYT2
GO:0006139		5 nucleobase, nucleoside, nucleotide and nucleic acid metabolism		986	0.2676	30	0.1657	0.015038	D	URB2,TRM2,LHP1,PUS7,URA3,ADE4,NHP2,FAF1,SUV3,GCD10,MTR4,PRS3,RRP5,NOP7,IMD3,PUF6,SNU13,POP3,MRM1,RPO41,TAN1,RRP42,DDR48,RRN7,NSR1,ISM1,NAM2,MTF1,CCA1,RPC19
GO:0007010		6 cytoskeleton organization and biogenesis		151	0.041	1	0.0055	0.014686	D	ABP140
GO:0007275		2 development		289	0.0784	5	0.0276	0.012402	D	YAH1,LAS1,PRS3,BUD32,PUF6
GO:0000003		2 reproduction		170	0.0461	1	0.0055	0.006927	D	LAS1
GO:0006351		7 transcription, DNA-dependent		313	0.0849	5	0.0276	0.006607	D	PUF6,RPO41,RRN7,MTF1,RPC19
GO:0006950		3 response to stress		286	0.0776	4	0.0221	0.00471	D	SVF1,DDR48,SNQ2,PIM1
GO:0043283		5 biopolymer metabolism		1113	0.302	31	0.1713	0.003301	D	URB2,TRM2,LHP1,CAX4,PUS7,NHP2,FAF1,SUV3,GCD10,MNN11,OCT1,MTR4,YTA12,FAS2,BUD32,RRP5,PRES9,NOP7,SNU13,POP3,MRM1,TAN1,FAA4,RRP42,DDR48,CYT2,NSR1,ISM1,NAM2,SEC23,CCA1
GO:0016192	5,6	vesicle-mediated transport		229	0.0621	2	0.011	0.002733	D	SUR4,SEC23
GO:0006350		6 transcription		344	0.0934	5	0.0276	0.002467	D	PUF6,RPO41,RRN7,MTF1,RPC19

GO:0031323	5	regulation of cellular metabolism	272	0.0738	3	0.0166	0.002201	D	MSS51,PUF6,TIF5
GO:0006355	8	regulation of transcription, DNA-dependent	202	0.0548	1	0.0055	0.001405	D	PUF6
GO:0019222	4	regulation of metabolism	291	0.079	3	0.0166	0.001073	D	MSS51,PUF6,TIF5
GO:0045449	7	regulation of transcription	214	0.0581	1	0.0055	0.000963	D	PUF6
GO:0019219	6	regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	236	0.064	1	0.0055	0.000453	D	PUF6
GO:0050896	2	response to stimulus	377	0.1023	4	0.0221	0.000198	D	SVF1,DDR48,SNQ2,PIM1
GO:0007049	4	cell cycle	260	0.0706	1	0.0055	0.000129	D	PIS1
GO:0050794	3	regulation of cellular process	396	0.1075	3	0.0166	2.44E-05	D	MSS51,PUF6,TIF5
GO:0051244	4	regulation of cellular physiological process	395	0.1072	3	0.0166	2.44E-05	D	MSS51,PUF6,TIF5
GO:0050791	3	regulation of physiological process	406	0.1102	3	0.0166	1.65E-05	D	MSS51,PUF6,TIF5
GO:0050789	2	regulation of biological process	414	0.1123	3	0.0166	1.12E-05	D	MSS51,PUF6,TIF5
GO:0006259	6	DNA metabolism	334	0.0906	1	0.0055	7.62E-06	D	DDR48

^a Reference data: 3685 *S. cerevisiae* orthologues of *C. albicans* genes represented on the microarrays

^b Data set: 181 *S. cerevisiae* orthologues of *C. albicans* genes with increased expression in yeast cells

^c Terms with a p value of less than or equal to 0.05 are shown.

^d E: GO term over-represented in data set. D: GO term under-represented in data set

Supplementary Table 6. GO term analysis of genes with downregulated expression in an *ace2* deletion grown as hyphal cells.

Terms highlighted in yellow are shown in Fig. 1A.

GO ID	Level(s)	Term	No. In Ref ^a	Freq In Ref ^a	No. In Set ^b	Freq In Set ^b	P value ^c	ENRICHMENT /DEPLETION ^d	Genes In Set ^b
GO:0006096	10,11,8	glycolysis	13	0.0035	8	0.069	1.40E-07	E	ENO1,TDH3,PFK1,GPM1,PGI1,FBA1,HXK2,PGK1
GO:0006066	5	alcohol metabolism	108	0.0293	18	0.1552	1.55E-07	E	DAP1,ENO1,ERG25,PSA1,TDH3,PFK1,GPM1,ERG5,PGI1,ARE2,DOG2,DAK2,ERG11,FBA1,ERG1,PYC2,HXK2,PGK1
GO:0016051	7,6	carbohydrate biosynthesis	40	0.0109	11	0.0948	5.03E-07	E	ENO1,PSA1,TDH3,GPM1,TPS3,PGI1,GLG2,FBA1,GSY1,PYC2,PGK1
GO:0019319	8,9	hexose biosynthesis	18	0.0049	8	0.069	9.28E-07	E	ENO1,PSA1,TDH3,GPM1,PGI1,FBA1,PYC2,PGK1
GO:0046364	7,8	monosaccharide biosynthesis	18	0.0049	8	0.069	9.28E-07	E	ENO1,PSA1,TDH3,GPM1,PGI1,FBA1,PYC2,PGK1
GO:0046164	6	alcohol catabolism	26	0.0071	9	0.0776	1.07E-06	E	ENO1,TDH3,PFK1,GPM1,PGI1,DAK2,FBA1,HXK2,PGK1
GO:0046165	6	alcohol biosynthesis	19	0.0052	8	0.069	1.28E-06	E	ENO1,PSA1,TDH3,GPM1,PGI1,FBA1,PYC2,PGK1
GO:0019320	8,9	hexose catabolism	20	0.0054	8	0.069	1.74E-06	E	ENO1,TDH3,PFK1,GPM1,PGI1,FBA1,HXK2,PGK1
GO:0006007	9,10	glucose catabolism	20	0.0054	8	0.069	1.74E-06	E	ENO1,TDH3,PFK1,GPM1,PGI1,FBA1,HXK2,PGK1
GO:0006006	8,9	glucose metabolism	40	0.0109	10	0.0862	3.33E-06	E	ENO1,TDH3,PFK1,GPM1,PGI1,DOG2,FBA1,PYC2,HXK2,PGK1
GO:0016052	6	carbohydrate catabolism	32	0.0087	9	0.0776	4.45E-06	E	ENO1,CTS1,TDH3,PFK1,GPM1,PGI1,FBA1,HXK2,PGK1
GO:0044275	7	cellular carbohydrate catabolism	32	0.0087	9	0.0776	4.45E-06	E	ENO1,CTS1,TDH3,PFK1,GPM1,PGI1,FBA1,HXK2,PGK1
GO:0019318	7,8	hexose metabolism	52	0.0141	11	0.0948	4.51E-06	E	ENO1,PSA1,TDH3,PFK1,GPM1,PGI1,DOG2,FBA1,PYC2,HXK2,PGK1
GO:0006094	9,10,8	gluconeogenesis	16	0.0043	7	0.0603	4.80E-06	E	ENO1,TDH3,GPM1,PGI1,FBA1,PYC2,PGK1
GO:0046365	7,8	monosaccharide catabolism	24	0.0065	8	0.069	5.24E-06	E	ENO1,TDH3,PFK1,GPM1,PGI1,FBA1,HXK2,PGK1
GO:0005975	5	carbohydrate metabolism	129	0.035	17	0.1466	5.55E-06	E	EXG1,ENO1,AMS1,CTS1,PSA1,TDH3,PFK1,GPM1,TPS3,PGI1,DOG2,GLG2,FBA1,GSY1,PYC2,HXK2,PGK1
GO:0006790	5	sulfur metabolism	45	0.0122	10	0.0862	8.15E-06	E	CYS3,MET2,ECM17,MET22,MET3,MET14,YHR112C,MET17,SAM4,MET10
GO:0044262	6	cellular carbohydrate metabolism	120	0.0326	16	0.1379	8.77E-06	E	EXG1,ENO1,CTS1,PSA1,TDH3,PFK1,GPM1,TPS3,PGI1,DOG2,GLG2,FBA1,GSY1,PYC2,HXK2,PGK1
GO:0005996	6,7	monosaccharide metabolism	58	0.0157	11	0.0948	1.11E-05	E	ENO1,PSA1,TDH3,PFK1,GPM1,PGI1,DOG2,FBA1,PYC2,HXK2,PGK1
GO:0006090	7	pyruvate metabolism	25	0.0068	7	0.0603	5.10E-05	E	ENO1,TDH3,GPM1,PGI1,FBA1,PYC2,PGK1
GO:0006082	5	organic acid metabolism	242	0.0657	22	0.1897	6.05E-05	E	CYS3,ENO1,SCS7,MET2,TDH3,ECM17,GPM1,HIS4,MET22,MET3,PGI1,LYS1,ACB1,MET14,LYS12,FAS2,MET17,FBA1,AYR1,PYC2,PGK1,SAM4
GO:0019752	6	carboxylic acid metabolism	242	0.0657	22	0.1897	6.05E-05	E	CYS3,ENO1,SCS7,MET2,TDH3,ECM17,GPM1,HIS4,MET22,MET3,PGI1,LYS1,ACB1,MET14,LYS12,FAS2,MET17,FBA1,AYR1,PYC2,PGK1,SAM4
GO:0006791	6	sulfur utilization	10	0.0027	5	0.0431	6.87E-05	E	ECM17,MET22,MET3,MET14,MET10
GO:0000103	7	sulfate assimilation	10	0.0027	5	0.0431	6.87E-05	E	ECM17,MET22,MET3,MET14,MET10
GO:0000096	7,8,6	sulfur amino acid metabolism	27	0.0073	7	0.0603	7.70E-05	E	CYS3,MET2,MET22,MET3,MET14,MET17,SAM4
GO:0006092	7	main pathways of carbohydrate metabolism	49	0.0133	9	0.0776	8.19E-05	E	ENO1,TDH3,PFK1,GPM1,PGI1,FBA1,PYC2,HXK2,PGK1
GO:0009066	7,8	aspartate family amino acid metabolism	36	0.0098	7	0.0603	0.0003577	E	MET2,MET22,MET3,LYS1,MET14,LYS12,MET17
GO:0015980	6	energy derivation by oxidation of organic compounds	132	0.0358	13	0.1121	0.0007744	E	ENO1,ADH1,TDH3,PFK1,GPM1,TPS3,PGI1,GLG2,FBA1,GSY1,PYC2,HXK2,PGK1
GO:0016125	6,7,8	sterol metabolism	33	0.009	6	0.0517	0.0012556	E	DAP1,ERG25,ERG5,ARE2,ERG11,ERG1
GO:0006555	8,9,7	methionine metabolism	22	0.006	5	0.0431	0.0013416	E	MET2,MET22,MET3,MET14,MET17
GO:0044255	5,6	cellular lipid metabolism	165	0.0448	14	0.1207	0.0018541	E	DAP1,SCS7,ERG25,ERG5,SUR2,ARE2,ACB1,PLB2,ERG11,FAS2,ERG1,AYR1,SPO14,PLB3
GO:0008202	6,7	steroid metabolism	37	0.01	6	0.0517	0.0021041	E	DAP1,ERG25,ERG5,ARE2,ERG11,ERG1

GO:0006091	5	generation of precursor metabolites and energy	150	0.0407	13	0.1121	0.002194	E	ENO1,ADH1,TDH3,PFK1,GPM1,TPS3,PGI1,GLG2,FBA1,GSY1,PYC2,HXK2,PGK1
GO:0009067	8,9	aspartate family amino acid biosynthesis	15	0.0041	4	0.0345	0.00249	E	MET2,MET22,LYS1,LYS12
GO:0000097	8,9,7	sulfur amino acid biosynthesis	8	0.0022	3	0.0259	0.0040747	E	MET2,MET22,MET17
GO:0006807	4	nitrogen compound metabolism	200	0.0543	15	0.1293	0.0045351	E	CYS3,CTS1,MET2,ECM17,DCG1,HIS4,MET22,MET3,LYS1,URE2,ATO2,MET14,LYS12,MET17,SAM4
GO:0006629	5	lipid metabolism	174	0.0472	14	0.1207	0.0045711	E	DAP1,SCS7,ERG25,ERG5,SUR2,ARE2,ACB1,PLB2,ERG11,FAS2,ERG1,AYR1,SPO14,PLB3
GO:0030503	6,5	regulation of cell redox homeostasis	9	0.0024	3	0.0259	0.0053063	E	GRX1,AHP1,PRX1
GO:0045454	5	cell redox homeostasis	9	0.0024	3	0.0259	0.0053063	E	GRX1,AHP1,PRX1
GO:0006739	10,9	NADP metabolism	10	0.0027	3	0.0259	0.0067378	E	PGI1,POS5,PYC2
GO:0006696	8,9,10	ergosterol biosynthesis	24	0.0065	4	0.0345	0.0104942	E	ERG25,ERG5,ERG11,ERG1
GO:0008204	7,8,9	ergosterol metabolism	24	0.0065	4	0.0345	0.0104942	E	ERG25,ERG5,ERG11,ERG1
GO:0044272	6	sulfur compound biosynthesis	13	0.0035	3	0.0259	0.0122969	E	MET2,MET22,MET17
GO:0005978	10,9	glycogen biosynthesis	4	0.0011	2	0.0172	0.0131694	E	GLG2,GSY1
GO:0006534	8,9,7	cysteine metabolism	4	0.0011	2	0.0172	0.0131694	E	CYS3,MET17
GO:0016126	7,8,9	sterol biosynthesis	27	0.0073	4	0.0345	0.0149674	E	ERG25,ERG5,ERG11,ERG1
GO:0009086	9,10,8	methionine biosynthesis	5	0.0014	2	0.0172	0.0180571	E	MET2,MET22
GO:0006520	6,7	amino acid metabolism	156	0.0423	11	0.0948	0.02084	E	CYS3,MET2,ECM17,HIS4,MET22,MET3,LYS1,MET14,LYS12,MET17,SAM4
GO:0006694	7,6,8	steroid biosynthesis	31	0.0084	4	0.0345	0.0225597	E	ERG25,ERG5,ERG11,ERG1
GO:0009092	8,9	homoserine metabolism	6	0.0016	2	0.0172	0.0235813	E	CYS3,MET2
GO:0006972	5	hyperosmotic response	6	0.0016	2	0.0172	0.0235813	E	MET22,GPD1
GO:0008652	7,8	amino acid biosynthesis	87	0.0236	7	0.0603	0.0278749	E	MET2,ECM17,HIS4,MET22,LYS1,LYS12,MET17
GO:0007039	8,9	vacuolar protein catabolism	7	0.0019	2	0.0172	0.0296974	E	APE3,LAP4
GO:0006553	8,9	lysine metabolism	7	0.0019	2	0.0172	0.0296974	E	LYS1,LYS12
GO:0009085	9,10	lysine biosynthesis	7	0.0019	2	0.0172	0.0296974	E	LYS1,LYS12
GO:0005976	6	polysaccharide metabolism	35	0.0095	4	0.0345	0.0321183	E	EXG1,CTS1,GLG2,GSY1
GO:0044264	6,7	cellular polysaccharide metabolism	35	0.0095	4	0.0345	0.0321183	E	EXG1,CTS1,GLG2,GSY1
GO:0009069	7,8	serine family amino acid metabolism	20	0.0054	3	0.0259	0.0330569	E	CYS3,MET2,MET17
GO:0006767	6	water-soluble vitamin metabolism	53	0.0144	5	0.0431	0.0340311	E	SNZ1,PGI1,POS5,PYC2,RIB4
GO:0006766	5	vitamin metabolism	53	0.0144	5	0.0431	0.0340311	E	SNZ1,PGI1,POS5,PYC2,RIB4
GO:0009308	5	amine metabolism	186	0.0505	12	0.1034	0.0340643	E	CYS3,CTS1,MET2,ECM17,HIS4,MET22,MET3,LYS1,MET14,LYS12,MET17,SAM4
GO:0010038	6	response to metal ion	8	0.0022	2	0.0172	0.0363631	E	URE2,AHP1
GO:0009250	9,8	glucan biosynthesis	8	0.0022	2	0.0172	0.0363631	E	GLG2,GSY1
GO:0044271	6,5	nitrogen compound biosynthesis	95	0.0258	7	0.0603	0.0405759	E	MET2,ECM17,HIS4,MET22,LYS1,LYS12,MET17
GO:0009309	6,7	amine biosynthesis	95	0.0258	7	0.0603	0.0405759	E	MET2,ECM17,HIS4,MET22,LYS1,LYS12,MET17
GO:0006112	7	energy reserve metabolism	22	0.006	3	0.0259	0.041001	E	TPS3,GLG2,GSY1
GO:0008610	6,5,7	lipid biosynthesis	96	0.0261	7	0.0603	0.042387	E	ERG25,ERG5,SUR2,ERG11,FAS2,ERG1,AYR1
GO:0006740	11,10	NADPH regeneration	9	0.0024	2	0.0172	0.0435384	E	PGI1,PYC2
GO:0006733	7	oxidoreduction coenzyme metabolism	39	0.0106	4	0.0345	0.0437024	E	PGI1,COQ6,POS5,PYC2
GO:0006073	7,8	glucan metabolism	23	0.0062	3	0.0259	0.0452983	E	EXG1,GLG2,GSY1
GO:0006865	6,7,8	amino acid transport	23	0.0062	3	0.0259	0.0452983	E	MUP1,CAN1,GAP1
GO:0006519	5	amino acid and derivative metabolism	170	0.0461	11	0.0948	0.0461677	E	CYS3,MET2,ECM17,HIS4,MET22,MET3,LYS1,MET14,LYS12,MET17,SAM4

GO:0019740	5	nitrogen utilization	10	0.0027	2	0.0172	0.0511848	E	URE2,ATO2
GO:0010035	5	response to inorganic substance	10	0.0027	2	0.0172	0.0511848	E	URE2,AHP1
GO:0019219	6	regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	236	0.064	2	0.0172	0.0461418	D	HXK2,SPT5
GO:0019222	4	regulation of metabolism	291	0.079	3	0.0259	0.0456999	D	URE2,HXK2,SPT5
GO:0043170	4	macromolecule metabolism	1533	0.416	32	0.2759	0.0433995	D	YHR087W,EXG1,ENO1,AMS1,CTS1,POA1,PRD1,SNF5,PSA1,TDH3,PFK1,APE3,GPM1,TPS3,HSH49,LAP4,SSA4,PGI1,SET3,DOG2,GLG2,ATG18,FAS2,FBA1,SAD1,BUD32,GSY1,PYC2,HXK2,RNR2,SPT5,PGK1
GO:0006366	8	transcription from RNA polymerase II promoter	198	0.0537	1	0.0086	0.0296671	D	SPT5
GO:0031323	5	regulation of cellular metabolism	272	0.0738	2	0.0172	0.0232016	D	HXK2,SPT5
GO:0016070	6	RNA metabolism	378	0.1026	4	0.0345	0.0230061	D	YHR087W,POA1,HSH49,SAD1
GO:0043412	6	biopolymer modification	431	0.117	5	0.0431	0.0216354	D	PSA1,SET3,ATG18,FAS2,BUD32
GO:0044260	5	cellular macromolecule metabolism	826	0.2242	13	0.1121	0.0145586	D	EXG1,CTS1,PRD1,PSA1,APE3,LAP4,SSA4,SET3,GLG2,ATG18,FAS2,BUD32,GSY1
GO:0006351	7	transcription, DNA-dependent	313	0.0849	2	0.0172	0.0077532	D	HXK2,SPT5
GO:0043283	5	biopolymer metabolism	1113	0.302	18	0.1552	0.0066101	D	YHR087W,EXG1,CTS1,POA1,SNF5,PSA1,APE3,HSH49,LAP4,SET3,GLG2,ATG18,FAS2,SAD1,BUD32,GSY1,RNR2,SPT5
GO:0007049	4	cell cycle	260	0.0706	1	0.0086	0.0064414	D	SET3
GO:0016043	4	cell organization and biogenesis	1135	0.308	18	0.1552	0.0050098	D	EXG1,MON1,SNF5,LDB19,PSA1,ECM17,YOR084W,SSA4,URE2,SET3,PIR1,ATG18,SUN4,CCC2,BUD32,ECM3,SPT5,ARC15
GO:0006350	6	transcription	344	0.0934	2	0.0172	0.0036784	D	HXK2,SPT5
GO:0006996	5	organelle organization and biogenesis	726	0.197	8	0.069	0.0017831	D	SNF5,LDB19,YOR084W,SET3,ATG18,SUN4,SPT5,ARC15
GO:0006139	5	nucleobase, nucleoside, nucleotide and nucleic acid metabolism	986	0.2676	13	0.1121	0.0013697	D	YHR087W,POA1,SNF5,PSA1,HSH49,PGI1,SET3,POS5,SAD1,PYC2,HXK2,RNR2,SPT5
GO:0044267	6	cellular protein metabolism	798	0.2166	9	0.0776	0.0011543	D	PRD1,PSA1,APE3,LAP4,SSA4,SET3,ATG18,FAS2,BUD32
GO:0006412	7,6	protein biosynthesis	359	0.0974	1	0.0086	0.0006072	D	PSA1
GO:0019538	5	protein metabolism	897	0.2434	9	0.0776	0.0002005	D	PRD1,PSA1,APE3,LAP4,SSA4,SET3,ATG18,FAS2,BUD32
^a Reference data: 3685 <i>S. cerevisiae</i> orthologues of <i>C. albicans</i> genes represented on the microarrays									
^b Data set: 116 <i>S. cerevisiae</i> orthologues of <i>C. albicans</i> genes with reduced expression in hyphal cells									
^c Terms with a p value of less than or equal to 0.05 are shown									
^d E: GO term over-represented in data set; D: GO term under-represented in data set									

Supplementary Table 7. GO term analysis of genes with upregulated expression in an *ace2* deletion grown as hyphal cells.

GO ID	Level(s)	Term	No. In Ref ^a	Freq In Ref ^a	No. In Set ^b	Freq In Set ^b	P value ^c	ENRICHMENT /DEPLETION ^d	Genes in set
GO:0006091	5	generation of precursor metabolites and energy	150	0.0407	32	0.2424	5.40E-13	E	CYT1,RSM24,LSC1,IDH2,MRPS35,ATP1,MBA1,REG1,MNP1,MRPL1,COR1,ATP2,RIP1,FUM1,TIM11,ATP5,FBP1,PET9,NPA3,QCR2,ATP4,IDH1,MCR1,PCK1,KGD1,MRPL51,ATP7,MRPL22,ACO1,CIT1,IDP2,NDE1
GO:0009060	8	aerobic respiration	62	0.0168	19	0.1439	9.36E-11	E	RSM24,LSC1,IDH2,MRPS35,MBA1,MNP1,MRPL1,COR1,RIP1,FUM1,PET9,NPA3,QCR2,IDH1,KGD1,MRPL51,MRPL22,ACO1,CIT1
GO:0045333	7	cellular respiration	63	0.0171	19	0.1439	1.17E-10	E	RSM24,LSC1,IDH2,MRPS35,MBA1,MNP1,MRPL1,COR1,RIP1,FUM1,PET9,NPA3,QCR2,IDH1,KGD1,MRPL51,MRPL22,ACO1,CIT1
GO:0015980	6	energy derivation by oxidation of organic compounds	132	0.0358	24	0.1818	4.13E-09	E	RSM24,LSC1,IDH2,MRPS35,MBA1,REG1,MNP1,MRPL1,COR1,RIP1,FUM1,FBP1,PET9,NPA3,QCR2,IDH1,PCK1,KGD1,MRPL51,MRPL22,ACO1,CIT1,IDP2,NDE1
GO:0006100	8	tricarboxylic acid cycle intermediate metabolism	14	0.0038	8	0.0606	5.32E-07	E	LSC1,IDH2,FUM1,IDH1,KGD1,ACO1,CIT1,IDP2
GO:0006119	6,8	oxidative phosphorylation	25	0.0068	9	0.0682	2.20E-06	E	CYT1,ATP1,ATP2,RIP1,TIM11,ATP5,QCR2,ATP4,ATP7
GO:0007028	5	cytoplasm organization and biogenesis	211	0.0573	25	0.1894	2.67E-06	E	NOP15,NOP4,NOP9,TIF6,MRPS28,FAF1,NOG1,ESF1,NMD3,NOP2,NSA1,MRH4,NOP7,ARX1,EMG1,KRR1,UTP18,ENP1,NOP58,NSR1,NOP1,RRP1,YML6,RRP14,RIO2
GO:0042254	6	ribosome biogenesis and assembly	211	0.0573	25	0.1894	2.67E-06	E	NOP15,NOP4,NOP9,TIF6,MRPS28,FAF1,NOG1,ESF1,NMD3,NOP2,NSA1,MRH4,NOP7,ARX1,EMG1,KRR1,UTP18,ENP1,NOP58,NSR1,NOP1,RRP1,RRP14,RIO2
GO:0007046	7	ribosome biogenesis	184	0.0499	23	0.1742	2.80E-06	E	NOP15,NOP4,NOP9,TIF6,FAF1,NOG1,ESF1,NMD3,NOP2,NSA1,MRH4,NOP7,ARX1,EMG1,KRR1,UTP18,ENP1,NOP58,NSR1,NOP1,RRP1,RRP14,RIO2
GO:0046356	8	acetyl-CoA catabolism	13	0.0035	7	0.053	3.68E-06	E	LSC1,IDH2,FUM1,IDH1,KGD1,ACO1,CIT1
GO:0006099	9,8	tricarboxylic acid cycle	13	0.0035	7	0.053	3.68E-06	E	LSC1,IDH2,FUM1,IDH1,KGD1,ACO1,CIT1
GO:0009142	7,8	nucleoside triphosphate biosynthesis	14	0.0038	7	0.053	5.34E-06	E	YNK1,ATP1,ATP2,TIM11,ATP5,ATP4,ATP7
GO:0009141	7	nucleoside triphosphate metabolism	15	0.0041	7	0.053	7.59E-06	E	YNK1,ATP1,ATP2,TIM11,ATP5,ATP4,ATP7
GO:0009109	7	coenzyme catabolism	15	0.0041	7	0.053	7.59E-06	E	LSC1,IDH2,FUM1,IDH1,KGD1,ACO1,CIT1
GO:0015672	7,8	monovalent inorganic cation transport	16	0.0043	7	0.053	1.06E-05	E	ATP1,ENA2,ATP2,TIM11,ATP5,ATP4,ATP7
GO:0051187	6	cofactor catabolism	16	0.0043	7	0.053	1.06E-05	E	LSC1,IDH2,FUM1,IDH1,KGD1,ACO1,CIT1
GO:0015986	9,11,8,10,7	ATP synthesis coupled proton transport	10	0.0027	6	0.0455	1.16E-05	E	ATP1,ATP2,TIM11,ATP5,ATP4,ATP7
GO:0006754	8,10,7,9,11	ATP biosynthesis	10	0.0027	6	0.0455	1.16E-05	E	ATP1,ATP2,TIM11,ATP5,ATP4,ATP7
GO:0015985	7,9,8,10	energy coupled proton transport, down electrochemical gradient	10	0.0027	6	0.0455	1.16E-05	E	ATP1,ATP2,TIM11,ATP5,ATP4,ATP7
GO:0046034	6,10	ATP metabolism	10	0.0027	6	0.0455	1.16E-05	E	ATP1,ATP2,TIM11,ATP5,ATP4,ATP7
GO:0006753	8	nucleoside phosphate metabolism	10	0.0027	6	0.0455	1.16E-05	E	ATP1,ATP2,TIM11,ATP5,ATP4,ATP7
GO:0006732	6	coenzyme metabolism	97	0.0263	15	0.1136	1.33E-05	E	UTR1,LSC1,IDH2,ATP1,ATP2,FUM1,TIM11,ATP5,ATP4,IDH1,KGD1,ATP7,ACO1,CIT1,NDE1
GO:0009205	9	purine ribonucleoside triphosphate metabolism	11	0.003	6	0.0455	1.74E-05	E	ATP1,ATP2,TIM11,ATP5,ATP4,ATP7
GO:0009145	8,9	purine nucleoside triphosphate biosynthesis	11	0.003	6	0.0455	1.74E-05	E	ATP1,ATP2,TIM11,ATP5,ATP4,ATP7
GO:0009144	8	purine nucleoside triphosphate metabolism	11	0.003	6	0.0455	1.74E-05	E	ATP1,ATP2,TIM11,ATP5,ATP4,ATP7
GO:0006537	9,10	glutamate biosynthesis	11	0.003	6	0.0455	1.74E-05	E	MEU1,IDH2,IDH1,ACO1,CIT1,IDP2
GO:0009206	9,10	purine ribonucleoside triphosphate biosynthesis	11	0.003	6	0.0455	1.74E-05	E	ATP1,ATP2,TIM11,ATP5,ATP4,ATP7
GO:0006084	7	acetyl-CoA metabolism	18	0.0049	7	0.053	1.94E-05	E	LSC1,IDH2,FUM1,IDH1,KGD1,ACO1,CIT1
GO:0044249	5	cellular biosynthesis	610	0.1655	48	0.3636	2.09E-05	E	MEU1,RSM18,SSZ1,RPS2,RSM10,MNT2,MRPS28,YNK1,RSM24,IDH2,MRPS35,MRPL17,ATP1,MRPL28,PRS3,MRPL32,MNP1,MRPL1,MRP1,MRP17,TUF1,ATP2,MEF1,MRPL7,TIM11,ATP5,FBP1,MRPS16,MRPL40,MSF1,ATP4,IDH1,PCK1,MRPL51,ATP7,MRPL22,MRP2,RSM22,MRPL35,RSM25,ACO1,SUI3,YML6,MRPL24,DPS1,MTD1,CIT1,IDP2
GO:0009199	8	ribonucleoside triphosphate metabolism	12	0.0033	6	0.0455	2.53E-05	E	ATP1,ATP2,TIM11,ATP5,ATP4,ATP7
GO:0009201	8,9	ribonucleoside triphosphate biosynthesis	12	0.0033	6	0.0455	2.53E-05	E	ATP1,ATP2,TIM11,ATP5,ATP4,ATP7

GO:0009058	4	biosynthesis	671	0.1821	51	0.3864	2.87E-05	E	MEU1,RSM18,SSZ1,RPS2,RSM10,MNT2,MRPS28,CHO2,YNK1,RSM24,IDH2,MRPS35,MRPL17,ATP1,MRPL28,PRS3,MRPL32,MNP1,MRPL1,MRP1,MRP17,TUF1,ATP2,MEF1,MRPL7,TIM11,ATP5,FBP1,MRPS16,MRPL40,LAC1,MSF1,ATP4,IDH1,MCR1,PCK1,MRPL51,ATP7,MRPL22,MRP2,RSM22,MRPL35,RSM25,ACO1,SUI3,YML6,MRPL24,DPS1,MTD1,CIT1,IDP2
GO:0015992	6,8,7,9	proton transport	13	0.0035	6	0.0455	3.58E-05	E	ATP1,ATP2,TIM11,ATP5,ATP4,ATP7
GO:0006818	5,6	hydrogen transport	13	0.0035	6	0.0455	3.58E-05	E	ATP1,ATP2,TIM11,ATP5,ATP4,ATP7
GO:0006164	7,8	purine nucleotide biosynthesis	29	0.0079	8	0.0606	3.93E-05	E	YNK1,ATP1,PRS3,ATP2,TIM11,ATP5,ATP4,ATP7
GO:0006092	7	main pathways of carbohydrate metabolism	49	0.0133	10	0.0758	4.28E-05	E	LSC1,IDH2,FUM1,FBP1,IDH1,PCK1,KGD1,ACO1,CIT1,IDP2
GO:0006536	8,9	glutamate metabolism	14	0.0038	6	0.0455	4.96E-05	E	MEU1,IDH2,IDH1,ACO1,CIT1,IDP2
GO:0006163	7	purine nucleotide metabolism	32	0.0087	8	0.0606	7.09E-05	E	YNK1,ATP1,PRS3,ATP2,TIM11,ATP5,ATP4,ATP7
GO:0006412	7,6	protein biosynthesis	359	0.0974	31	0.2348	8.04E-05	E	RSM18,SSZ1,RPS2,RSM10,MNT2,MRPS28,RSM24,MRPS35,MRPL17,MRPL28,MRPL32,MNP1,MRPL1,MRP1,MRP17,TUF1,MEF1,MRPL7,MRPS16,MRPL40,MSF1,MRPL51,MRPL22,MRP2,RSM22,MRPL35,RSM25,SUI3,YML6,MRPL24,DPS1
GO:0009059	6,5	macromolecule biosynthesis	396	0.1075	33	0.25	9.72E-05	E	RSM18,SSZ1,RPS2,RSM10,MNT2,MRPS28,RSM24,MRPS35,MRPL17,MRPL28,MRPL32,MNP1,MRPL1,MRP1,MRP17,TUF1,MEF1,MRPL7,MRPS16,MRPL40,MSF1,PCK1,MRPL51,MRPL22,MRP2,RSM22,MRPL35,RSM25,SUI3,YML6,MRPL24,DPS1
GO:0009152	8,9	purine ribonucleotide biosynthesis	25	0.0068	7	0.053	0.0001087	E	ATP1,PRS3,ATP2,TIM11,ATP5,ATP4,ATP7
GO:0009260	7,8	ribonucleotide biosynthesis	26	0.0071	7	0.053	0.0001336	E	ATP1,PRS3,ATP2,TIM11,ATP5,ATP4,ATP7
GO:0051186	5	cofactor metabolism	123	0.0334	15	0.1136	0.0001473	E	UTR1,LSC1,IDH2,ATP1,ATP2,FUM1,TIM11,ATP5,ATP4,IDH1,KGD1,ATP7,ACO1,CIT1,NDE1
GO:0009150	8	purine ribonucleotide metabolism	27	0.0073	7	0.053	0.000163	E	ATP1,PRS3,ATP2,TIM11,ATP5,ATP4,ATP7
GO:0016072	7	rRNA metabolism	155	0.0421	17	0.1288	0.0001838	E	NOP4,NOP9,TIF6,FAF1,ESF1,NOP2,NOP7,EMG1,KRR1,UTP18,PAP2,ENP1,NOP58,NSR1,NOP1,RRP1,RIO2
GO:0042273	8	ribosomal large subunit biogenesis	19	0.0052	6	0.0455	0.0001941	E	NOP15,TIF6,NSA1,NOP7,ARX1,RRP14
GO:0009259	7	ribonucleotide metabolism	28	0.0076	7	0.053	0.0001974	E	ATP1,PRS3,ATP2,TIM11,ATP5,ATP4,ATP7
GO:0006812	6,7	cation transport	62	0.0168	10	0.0758	0.0002363	E	SMF1,FRE3,ATP1,ENA2,ATP2,TIM11,ATP5,ATP4,PHO84,ATP7
GO:0006364	8	rRNA processing	147	0.0399	16	0.1212	0.0002951	E	NOP4,NOP9,TIF6,FAF1,ESF1,NOP2,NOP7,EMG1,KRR1,UTP18,ENP1,NOP58,NSR1,NOP1,RRP1,RIO2
GO:0009165	6,7	nucleotide biosynthesis	41	0.0111	8	0.0606	0.0003104	E	YNK1,ATP1,PRS3,ATP2,TIM11,ATP5,ATP4,ATP7
GO:0009084	8,9	glutamine family amino acid biosynthesis	22	0.006	6	0.0455	0.0003761	E	MEU1,IDH2,IDH1,ACO1,CIT1,IDP2
GO:0009117	6	nucleotide metabolism	69	0.0187	10	0.0758	0.0005031	E	UTR1,YNK1,ATP1,PRS3,ATP2,TIM11,ATP5,ATP4,ATP7,NDE1
GO:0006811	5,6	ion transport	76	0.0206	10	0.0758	0.0009807	E	SMF1,FRE3,ATP1,ENA2,ATP2,TIM11,ATP5,ATP4,PHO84,ATP7
GO:0006102	9,7	isocitrate metabolism	4	0.0011	3	0.0227	0.0013572	E	IDH2,IDH1,IDP2
GO:0006752	7	group transfer coenzyme metabolism	32	0.0087	6	0.0455	0.0020243	E	ATP1,ATP2,TIM11,ATP5,ATP4,ATP7
GO:0016310	7	phosphorylation	101	0.0274	11	0.0833	0.0022518	E	CYT1,YNK1,ATP1,ATP2,RIP1,TIM11,ATP5,QCR2,ATP4,ATP7,RCK1
GO:0044262	6	cellular carbohydrate metabolism	120	0.0326	12	0.0909	0.0028141	E	LSC1,IDH2,GAL7,REG1,FUM1,FBP1,IDH1,PCK1,KGD1,ACO1,CIT1,IDP2
GO:0006122	9,11,8	mitochondrial electron transport, ubiquinol to cytochrome c	6	0.0016	3	0.0227	0.0030873	E	CYT1,RIP1,QCR2
GO:0009064	7,8	glutamine family amino acid metabolism	36	0.0098	6	0.0455	0.0034029	E	MEU1,IDH2,IDH1,ACO1,CIT1,IDP2
GO:0005975	5	carbohydrate metabolism	129	0.035	12	0.0909	0.0047586	E	LSC1,IDH2,GAL7,REG1,FUM1,FBP1,IDH1,PCK1,KGD1,ACO1,CIT1,IDP2
GO:0006101	9,7	citrate metabolism	2	0.0005	2	0.0152	0.0069927	E	ACO1,CIT1
GO:0006118	6,5	electron transport	19	0.0052	4	0.0303	0.0078915	E	CYT1,RIP1,QCR2,MCR1
GO:0009108	7	coenzyme biosynthesis	46	0.0125	6	0.0455	0.0097445	E	ATP1,ATP2,TIM11,ATP5,ATP4,ATP7
GO:0000002	7	mitochondrial genome maintenance	21	0.0057	4	0.0303	0.0106547	E	GGC1,MHR1,RPO41,ACO1
GO:0042255	7	ribosome assembly	53	0.0144	6	0.0455	0.0174674	E	NOP15,MRPS28,NMD3,NSR1,NOP1,YML6
GO:0042773	7,9,6	ATP synthesis coupled electron transport	14	0.0038	3	0.0227	0.0202154	E	CYT1,RIP1,QCR2
GO:0042775	8,10,7	ATP synthesis coupled electron transport (sensitive to phosphorylation)	14	0.0038	3	0.0227	0.0202154	E	CYT1,RIP1,QCR2
GO:0006796	6	phosphate metabolism	137	0.0372	11	0.0833	0.0207562	E	CYT1,YNK1,ATP1,ATP2,RIP1,TIM11,ATP5,QCR2,ATP4,ATP7,RCK1
GO:0006793	5	phosphorus metabolism	137	0.0372	11	0.0833	0.0207562	E	CYT1,YNK1,ATP1,ATP2,RIP1,TIM11,ATP5,QCR2,ATP4,ATP7,RCK1
GO:0030490	9	processing of 20S pre-rRNA	41	0.0111	5	0.0379	0.0222446	E	FAF1,NOP7,NOP58,NOP1,RIO2
GO:0042257	8	ribosomal subunit assembly	43	0.0117	5	0.0379	0.0262215	E	MRPS28,NMD3,NSR1,NOP1,YML6
GO:0007005	6	mitochondrion organization and biogenesis	76	0.0206	7	0.053	0.0273189	E	MBA1,MDM35,GGC1,MHR1,RPO41,OXA1,ACO1
GO:0051188	6	cofactor biosynthesis	60	0.0163	6	0.0455	0.0285763	E	ATP1,ATP2,TIM11,ATP5,ATP4,ATP7
GO:0006828	9,10	manganese ion transport	7	0.0019	2	0.0152	0.0372994	E	SMF1,PHO84
GO:0006450	10,9,8	regulation of translational fidelity	7	0.0019	2	0.0152	0.0372994	E	SSZ1,RPS2

GO:0006365		9	35S primary transcript processing	65	0.0176	6	0.0455	0.0388353	E	EMG1,KRR1,UTP18,ENP1,NOP58,NOP1
GO:0006879	8,9		iron ion homeostasis	20	0.0054	3	0.0227	0.0450162	E	FRE3,UTR1,GGC1
GO:0000028		9	ribosomal small subunit assembly and maintenance	8	0.0022	2	0.0152	0.0455507	E	MRPS28,NSR1
GO:0008652	7,8		amino acid biosynthesis	87	0.0236	7	0.053	0.0482823	E	MEU1,IDH2,PRS3,IDH1,ACO1,CIT1,IDP2
GO:0045449		7	regulation of transcription	214	0.0581	2	0.0152	0.0475607	D	REG1,ELP2
GO:0007049		4	cell cycle	260	0.0706	3	0.0227	0.0470589	D	MSH5,PAP2,RCK1
GO:0000003		2	reproduction	170	0.0461	1	0.0076	0.0452553	D	SPS19
GO:0051641	5,4		cellular localization	416	0.1129	7	0.053	0.0443124	D	NOG1,NMD3,YTA12,SSC1,PET9,TOM40,OXA1
GO:0000278		5	mitotic cell cycle	163	0.0442	1	0.0076	0.0434235	D	PAP2
GO:0006350		6	transcription	344	0.0934	5	0.0379	0.0406338	D	RPC34,REG1,RPO41,ELP2,RPC19
GO:0000004		2	biological process unknown	615	0.1669	11	0.0833	0.0269418	D	YFR011C,YGL050W,YLR168C,YOR227W,FMP13,YLR243W,YLR063W,YMR002W,YML030W,KRE33,NOP13
GO:0019219		6	regulation of nucleobase, nucleoside, nucleotide	236	0.064	2	0.0152	0.0233204	D	REG1,ELP2
GO:0050896		2	response to stimulus	377	0.1023	5	0.0379	0.0222606	D	TRM9,AGP2,ALO1,YHB1,MCR1
GO:0043412		6	biopolymer modification	431	0.117	6	0.0455	0.0151356	D	TRM9,MNT2,YTA12,NOP58,NOP1,RCK1
GO:0051276		6	chromosome organization and biogenesis	219	0.0594	1	0.0076	0.0098583	D	PAP2
GO:0006259		6	DNA metabolism	334	0.0906	3	0.0227	0.0060488	D	YNK1,MSH5,PAP2
GO:0050791		3	regulation of physiological process	406	0.1102	4	0.0303	0.0045246	D	SSZ1,RPS2,REG1,ELP2
GO:0051244		4	regulation of cellular physiological process	395	0.1072	4	0.0303	0.0044252	D	SSZ1,RPS2,REG1,ELP2
GO:0050794		3	regulation of cellular process	396	0.1075	4	0.0303	0.0044197	D	SSZ1,RPS2,REG1,ELP2
GO:0050789		2	regulation of biological process	414	0.1123	4	0.0303	0.0031243	D	SSZ1,RPS2,REG1,ELP2
GO:0006464		7	protein modification	369	0.1001	3	0.0227	0.0029975	D	MNT2,YTA12,RCK1
^a Reference data: 3685 <i>S. cerevisiae</i> orthologues of <i>C. albicans</i> genes represented on the microarrays										
^b Data set: 132 <i>S. cerevisiae</i> orthologues of <i>C. albicans</i> genes with increased expression in hyphal cells										
^d E: GO term over-represented in data set; D: GO term under-represented in data set										