

Supplementary Table 2. GO term analysis.

(A) GO term (process) analysis of genes with increased expression following exposure to farnesol.									
GO_ID	Levels	TERM	No. in ref <sup>a</sup>	Freq in ref <sup>a</sup>	No in set <sup>b</sup>	Freq in set <sup>b</sup>	P value <sup>c</sup>	Enrichment/Depletion <sup>d</sup>	Genes in set
GO:0007	7	ribosome biogenesis	138	0.0510	23	0.0943	0.001295	E	BMS1,DIP2,NOC2,MTR4,DBP7,HAS1,MRH4,ARX1,RAT1,LSM1,SOF1,LOC1,TSR1,DBP8,MRT4,RVB2,ERB1,NUG1,CSL4,SPB1,TSR2,RRP14,RIO2
GO:0008	6,7	steroid metabolism	30	0.0111	8	0.0328	0.003047	E	ERG7,ATG26,ERG6,NCP1,ERG4,MCR1,MVD1,OSH3
GO:0007	5	cytoplasm organization and bio	152	0.0562	23	0.0943	0.004081	E	BMS1,DIP2,NOC2,MTR4,DBP7,HAS1,MRH4,ARX1,RAT1,LSM1,SOF1,LOC1,TSR1,DBP8,MRT4,RVB2,ERB1,NUG1,CSL4,SPB1,TSR2,RRP14,RIO2
GO:0042	6	ribosome biogenesis and assem	152	0.0562	23	0.0943	0.004081	E	BMS1,DIP2,NOC2,MTR4,DBP7,HAS1,MRH4,ARX1,RAT1,LSM1,SOF1,LOC1,TSR1,DBP8,MRT4,RVB2,ERB1,NUG1,CSL4,SPB1,TSR2,RRP14,RIO2
GO:0006	7,6,8	steroid biosynthesis	25	0.0092	7	0.0287	0.004094	E	ERG7,ERG6,NCP1,ERG4,MCR1,MVD1,OSH3
GO:0006	8,9	glutamate metabolism	14	0.0052	5	0.0205	0.004986	E	PUT2,GLT1,PUT1,GDH1,UGA2
GO:0006	8	rRNA processing	111	0.0410	18	0.0738	0.005025	E	BMS1,DIP2,MTR4,DBP7,HAS1,RAT1,LSM1,SOF1,TSR1,DBP8,MRT4,RVB2,ERB1,NUG1,CSL4,SPB1,TSR2,RIO2
GO:0008	7,8,9	ergosterol metabolism	20	0.0074	6	0.0246	0.005392	E	ERG7,ERG6,NCP1,ERG4,MCR1,MVD1
GO:0006	8,9,10	ergosterol biosynthesis	20	0.0074	6	0.0246	0.005392	E	ERG7,ERG6,NCP1,ERG4,MCR1,MVD1
GO:0008	5	intracellular mRNA localization	5	0.0018	3	0.0123	0.006014	E	HEK2,SCP160,LOC1
GO:0044	5,6	cellular lipid metabolism	132	0.0488	20	0.0820	0.006628	E	ERG7,ATG26,SPS19,CHO2,ERG6,LRO1,ACP1,NCP1,POX1,DNF2,LAG1,ERG4,STT4,MCR1,MVD1,OSH3,RSB1,ACC1,POT1,PLB3
GO:0008	3	metabolism	1620	0.5987	161	0.6598	0.006721	E	PTC2,GLN1,SCL1,SET2,RPN2,PUT2,SOH1,ADH1,PRP8,SEN2,GCD1,ERG7,MUM2,ZRC1,MNT4,ATG26,SPS19,BMS1,NAR1,UGA1,YMR226C,ISW2,HSP78,PRB1,DIP2,STH1,MLH3,CYS4,HMT1,KIP2,ALG3,UBP2,CDC20,MRPS17,CHO2,NOC2,GSF2,ILV5,ACH1,SPT6,RAD1,RPC53,HTS1,RPS6A,ICL1,RPB2,OCT1,UBI4,MTR4,ECM2,ADO1,ADH7,ERG6,YNL247W,PUS4,LRO1,ACP1,DBP7,HAS1,CHS5,PDB1,RPST4,GLT1,GRE3,PUT1,MOD5,KEX2,REG1,TAL1,BRE1,NAT1,SNF1,GTS1,RPN1,NCP1,DBP2,SWI3,SCH9,WR51,POX1,STP1,HOM6,CDC60,HTZ1,MRC1,RAT1,DCP2,LSM1,GDH1,TUF1,KEK1,CTS1,ATP2,SOF1,YHR113W,TPD3,TRM10,CTA1,SSL1,RBA50,DNF2,RET1,MRP20,GCN1,DCD1,TSR1,DBP8,UBA4,MRT4,RSC8,LAG1,ERG4,MNN2,RVB2,POL5,CCT5,ERB1,IKI3,STT4,MCR1,CTI6,GCN3,HOG1,KIP3,NUG1,ESA1,TIF4631,GCD14,HSC82,RSC58,SI52,PRT1,RTF1,SGN1,UGA2,CSL4,DUS4,MVD1,NFS1,OSH3,SNZ2,ALD5,GCV1,GDB1,NGG1,PIM1,SPB1,RSB1,ACC1,TSR2,MSS116,POT1,CMK2,HAT1,CPR3,NPL4,RPS22A,PLB3,ALG2,NDE1,RIO2
GO:0016	7	rRNA metabolism	115	0.0425	18	0.0738	0.006963	E	BMS1,DIP2,MTR4,DBP7,HAS1,RAT1,LSM1,SOF1,TSR1,DBP8,MRT4,RVB2,ERB1,NUG1,CSL4,SPB1,TSR2,RIO2
GO:0044	4	cellular metabolism	1588	0.5868	158	0.6475	0.007052	E	PTC2,GLN1,SCL1,SET2,RPN2,PUT2,SOH1,ADH1,PRP8,SEN2,GCD1,ERG7,MUM2,ZRC1,MNT4,ATG26,SPS19,BMS1,NAR1,ISW2,HSP78,DIP2,STH1,MLH3,CYS4,HMT1,KIP2,ALG3,UBP2,CDC20,MRPS17,CHO2,NOC2,GSF2,ILV5,ACH1,SPT6,RAD1,RPC53,HTS1,RPS6A,ICL1,RPB2,OCT1,UBI4,MTR4,ECM2,ADO1,ADH7,ERG6,YNL247W,PUS4,LRO1,ACP1,DBP7,HAS1,CHS5,PDB1,RPST4,GLT1,GRE3,PUT1,MOD5,KEX2,REG1,TAL1,BRE1,NAT1,SNF1,GTS1,RPN1,NCP1,DBP2,SWI3,SCH9,WR51,POX1,STP1,HOM6,CDC60,HTZ1,MRC1,RAT1,DCP2,LSM1,GDH1,TUF1,KEK1,CTS1,ATP2,SOF1,YHR113W,TPD3,TRM10,CTA1,SSL1,RBA50,DNF2,RET1,MRP20,GCN1,DCD1,TSR1,DBP8,UBA4,MRT4,RSC8,LAG1,ERG4,MNN2,RVB2,POL5,CCT5,ERB1,IKI3,STT4,MCR1,CTI6,GCN3,HOG1,KIP3,NUG1,ESA1,TIF4631,GCD14,HSC82,RSC58,SI52,PRT1,RTF1,SGN1,UGA2,CSL4,DUS4,MVD1,NFS1,OSH3,SNZ2,ALD5,GCV1,GDB1,NGG1,PIM1,SPB1,RSB1,ACC1,TSR2,MSS116,POT1,CMK2,HAT1,CPR3,NPL4,RPS22A,PLB3,ALG2,NDE1,RIO2
GO:0016	6	RNA metabolism	275	0.1016	35	0.1434	0.007517	E	PRP8,SEN2,BMS1,DIP2,HTS1,MTR4,ECM2,YNL247W,PUS4,DBP7,HAS1,MOD5,DBP2,WR51,STP1,CDC60,RAT1,DCP2,LSM1,SOF1,TRM10,TSR1,DBP8,MRT4,RVB2,ERB1,NUG1,GCD14,SGN1,CSL4,DUS4,SPB1,TSR2,MSS116,RIO2
GO:0016	6,7,8	sterol metabolism	28	0.0103	7	0.0287	0.007638	E	ERG7,ATG26,ERG6,NCP1,ERG4,MCR1,MVD1
GO:0044	4	primary metabolism	1481	0.5473	148	0.6066	0.008038	E	PTC2,GLN1,SCL1,SET2,RPN2,PUT2,SOH1,ADH1,PRP8,SEN2,GCD1,ERG7,MUM2,MNT4,ATG26,SPS19,BMS1,ISW2,HSP78,PRB1,DIP2,STH1,MLH3,CYS4,HMT1,KIP2,ALG3,UBP2,CDC20,MRPS17,CHO2,NOC2,GSF2,ILV5,SPT6,RAD1,RPC53,HTS1,RPS6A,ICL1,RPB2,OCT1,UBI4,MTR4,ECM2,ADO1,ERG6,YNL247W,PUS4,LRO1,ACP1,DBP7,HAS1,CHS5,RPST4,GLT1,GRE3,PUT1,MOD5,KEX2,REG1,TAL1,BRE1,NAT1,SNF1,GTS1,RPN1,NCP1,DBP2,SWI3,SCH9,WR51,POX1,STP1,HOM6,CDC60,HTZ1,MRC1,RAT1,DCP2,LSM1,GDH1,TUF1,KEK1,CTS1,ATP2,SOF1,YHR113W,TPD3,TRM10,SSL1,RBA50,DNF2,RET1,MRP20,GCN1,DCD1,TSR1,DBP8,UBA4,MRT4,RSC8,LAG1,ERG4,MNN2,RVB2,POL5,CCT5,ERB1,IKI3,STT4,MCR1,CTI6,GCN3,HOG1,KIP3,NUG1,ESA1,TIF4631,GCD14,HSC82,RSC58,PR1,RTF1,SGN1,UGA2,CSL4,DUS4,MVD1,OSH3,GCV1,GDB1,NGG1,PIM1,SPB1,RSB1,ACC1,TSR2,MSS116,POT1,CMK2,HAT1,CPR3,NPL4,RPS22A,PLB3,ALG2,NDE1,RIO2
GO:0006	9,10	N-acetylglucosamine catabolism	2	0.0007	2	0.0082	0.0081	E	CHS5,CTS1
GO:0046	7,8	amino sugar catabolism	2	0.0007	2	0.0082	0.0081	E	CHS5,CTS1
GO:0006	10,11,9,8	chitin catabolism	2	0.0007	2	0.0082	0.0081	E	CHS5,CTS1
GO:0010	10,9,11	proline catabolism to glutamate	2	0.0007	2	0.0082	0.0081	E	PUT2,PUT1
GO:0006	8,9	glucosamine catabolism	2	0.0007	2	0.0082	0.0081	E	CHS5,CTS1
GO:0016	7,8,9	sterol biosynthesis	23	0.0085	6	0.0246	0.010631	E	ERG7,ERG6,NCP1,ERG4,MCR1,MVD1
GO:0000	6,7	polysaccharide catabolism	6	0.0022	3	0.0123	0.010955	E	CHS5,CTS1,GDB1
GO:0044	8,7	cellular polysaccharide catabolism	6	0.0022	3	0.0123	0.010955	E	CHS5,CTS1,GDB1
GO:0006	9,10	glutamate biosynthesis	11	0.0041	4	0.0164	0.011114	E	PUT2,GLT1,PUT1,GDH1
GO:0006	5	lipid metabolism	140	0.0517	20	0.0820	0.011357	E	ERG7,ATG26,SPS19,CHO2,ERG6,LRO1,ACP1,NCP1,POX1,DNF2,LAG1,ERG4,STT4,MCR1,MVD1,OSH3,RSB1,ACC1,POT1,PLB3
GO:0008	6,5,7	lipid biosynthesis	78	0.0288	13	0.0533	0.011664	E	ERG7,CHO2,ERG6,LRO1,ACP1,NCP1,LAG1,ERG4,STT4,MCR1,MVD1,OSH3,ACC1
GO:0006	7	tRNA metabolism	72	0.0266	12	0.0492	0.014608	E	SEN2,HTS1,MTR4,YNL247W,PUS4,MOD5,WR51,STP1,CDC60,TRM10,GCD14,DUS4,DNF2,RSB1
GO:0045	7,8,9	phospholipid translocation	3	0.0011	2	0.0082	0.022126	E	DNF2,RSB1
GO:0007	6	plasma membrane organization	3	0.0011	2	0.0082	0.022126	E	DNF2,RSB1
GO:0006	8,9,7	cysteine metabolism	3	0.0011	2	0.0082	0.022126	E	CYS4,YNL247W
GO:0000	10,11	deadenylation-dependent dec	3	0.0011	2	0.0082	0.022126	E	DCP2,LSM1
GO:0009	8,9	glutamine family amino acid cat	8	0.0030	3	0.0123	0.025442	E	PUT2,PUT1,UGA2
GO:0009	8,9	glutamine family amino acid bio	21	0.0078	5	0.0205	0.026417	E	GLN1,PUT2,GLT1,PUT1,GDH1
GO:0042	8	ribosomal large subunit biogen	15	0.0055	4	0.0164	0.03165	E	ARX1,LOC1,MRT4,RRP14
GO:0009	7,8	serine family amino acid metabi	15	0.0055	4	0.0164	0.03165	E	CYS4,YNL247W,HOM6,GCV1
GO:0043	5	biopolymer metabolism	838	0.3097	83	0.3402	0.031885	E	PTC2,SCL1,SET2,RPN2,SOH1,PRP8,SEN2,MUM2,MNT4,BMS1,ISW2,PRB1,DIP2,STH1,MLH3,HMT1,ALG3,UBP2,CDC20,SPT6,RAD1,HTS1,OCT1,UBI4,MTR4,ECM2,YNL247W,PUS4,DBP7,HAS1,CHS5,MOD5,KEX2,REG1,BRE1,NAT1,SNF1,RPN1,DBP2,SWI3,SCH9,WR51,STP1,CDC60,HTZ1,MRC1,RAT1,DCP2,LSM1,KEK1,CTS1,SOF1,TPD3,TRM10,SSL1,TSR1,DBP8,UBA4,MRT4,RSC8,MNN2,RVB2,ERB1,STT4,HOG1,NUG1,ESA1,GCD14,RSC58,RTF1,SGN1,CSL4,DUS4,GDB1,NGG1,SPB1,TSR2,MSS116,CMK2,HAT1,NPL4,ALG2,RIO2
GO:0043	4	macromolecule metabolism	1106	0.4087	107	0.4385	0.033066	E	PTC2,SCL1,SET2,RPN2,SOH1,PRP8,SEN2,MUM2,MNT4,BMS1,ISW2,HSP78,PRB1,DIP2,STH1,MLH3,HMT1,KIP2,ALG3,UBP2,CDC20,MRPS17,NOC2,GSF2,SPT6,RAD1,HTS1,RPS6A,ICL1,OCT1,UBI4,MTR4,ECM2,YNL247W,PUS4,DBP7,HAS1,CHS5,RPST4,GLT1,GRE3,PUT1,MOD5,KEX2,REG1,TAL1,BRE1,NAT1,SNF1,RPN1,DBP2,SWI3,SCH9,WR51,STP1,CDC60,HTZ1,MRC1,RAT1,DCP2,LSM1,TUF1,KEK1,CTS1,SOF1,YHR113W,TPD3,TRM10,SSL1,MRP20,GCN1,TSR1,DBP8,UBA4,MRT4,RSC8,MNN2,RVB2,CCT5,ERB1,STT4,GCN3,HOG1,KIP3,NUG1,ESA1,TIF4631,GCD14,HSC82,RSC58,PR1,RTF1,SGN1,CSL4,DUS4,GDB1,NGG1,PIM1,SPB1,TSR2,MSS116,CMK2,HAT1,CPR3,NPL4,RPS22A,ALG2,RIO2
GO:0043	8,7	translation	65	0.0240	10	0.0410	0.034496	E	GCD1,HTS1,YNL247W,WR51,CDC60,TUF1,GCN1,GCN3,TIF4631,PR1,SET2,HEK2,SAC6,ARP3,BMS1,ISW2,HSP78,DIP2,STH1,KIP2,CDC20,NOC2,ILV5,VTC2,SPT6,MTR4,YNL313C,DBP7,HAS1,BRE1,MRH4,SWI3,CDC12,HTZ1,ARX1,MRC1,RAT1,LSM1,SOF1,PXL1,TPD3,MYO2,LOC1,PEX29,TSR1,DBP8,MRT4,RSC8,SEC8,RVB2,CCT5,SPC110,ERB1,STT4,KIP3,NUG1,ESA1,VP54,PEP3,RSC58,RTF1,CSL4,CDC42,NGG1,SPB1,ACC1,TSR2,HAT1,RRP14,RIO2
GO:0006	5	organelle organization and bio	592	0.2188	60	0.2459	0.035518	E	PRP8,SEN2,BMS1,DIP2,MTR4,ECM2,DBP7,HAS1,STP1,RAT1,LSM1,SOF1,TSR1,DBP8,MRT4,RVB2,ERB1,NUG1,CSL4,SPB1,TSR2,MSS116,RIO2
GO:0006	7	RNA processing	194	0.0717	23	0.0943	0.035868	E	ERG7,ATG26,ADH7,ERG6,GRE3,TAL1,SNF1,NCP1,ERG4,STT4,MCR1,MVD1,NDE1
GO:0006	5	alcohol metabolism	94	0.0347	13	0.0533	0.036398	E	

GO:0009	4	catabolism	206	0.0761	24	0.0984	0.037807	E	SCL1, RPN2, PUT2, SPS19, PRB1, CDC20, MTR4, CHS5, GRE3, PUT1, REG1, TAL1, RPN1, D
GO:0007	10,8	microtubule depolymerization	4	0.0015	2	0.0082	0.04029	E	BP2, DCP2, LSM1, CTS1, MRT4, UGA2, CSL4, GCV1, GDB1, NPL4, PLB3
GO:0006	9,10	proline catabolism	4	0.0015	2	0.0082	0.04029	E	KIP2, KIP3
GO:0006	7	acetate metabolism	4	0.0015	2	0.0082	0.04029	E	PUT2, PUT1
GO:0031	9	microtubule polymerization or d	4	0.0015	2	0.0082	0.04029	E	ACH1, ALD5
GO:0007	5,4	cell aging	24	0.0089	5	0.0205	0.041712	E	KIP2, KIP3
GO:0007	4	cell adhesion	10	0.0037	3	0.0123	0.045212	E	SNF1, GTS1, SCH9, ATP2, LAG1
GO:0007	2	development	202	0.0746	23	0.0943	0.045943	E	FLO1, MUC1, SNF1
GO:0006	7	RNA catabolism	33	0.0122	6	0.0246	0.045995	E	SAC6, SPS19, ISW2, PRB1, RAD1, UBI4, CHS5, BRE1, SNF1, GTS1, SCH9, CDC12, HTZ1, M
GO:0044	5	cellular catabolism	192	0.0710	22	0.0902	0.046781	E	RC1, ATP2, PXL1, MYO2, LAG1, SEC8, CDC42, HAT1, RRP14, KIC1
GO:0006	9	35S primary transcript processi	51	0.0188	8	0.0328	0.047327	E	MTR4, DBP2, DCP2, LSM1, MRT4, CSL4
GO:0008	4	cell death	25	0.0092	5	0.0205	0.047494	E	SCL1, RPN2, PUT2, SPS19, CDC20, MTR4, CHS5, GRE3, PUT1, TAL1, RPN1, DBP2, DCP2, L
GO:0007	3,4	aging	25	0.0092	5	0.0205	0.047494	E	SM1, CTS1, MRT4, UGA2, CSL4, GCV1, GDB1, NPL4, PLB3
GO:0009	5	macromolecule catabolism	151	0.0558	18	0.0738	0.048547	E	BMS1, MTR4, DBP7, RAT1, SOF1, DBP8, RVB2, CSL4
GO:0006	8	mRNA processing	63	0.0233	2	0.0082	0.048531	D	SNF1, GTS1, SCH9, ATP2, LAG1
GO:0006	7	DNA replication	63	0.0233	2	0.0082	0.048531	D	SNF1, GTS1, SCH9, ATP2, LAG1
GO:0045	5	establishment of protein localiza	154	0.0569	9	0.0369	0.045007	D	SCL1, RPN2, PRB1, CDC20, MTR4, CHS5, GRE3, REG1, TAL1, RPN1, DBP2, DCP2, LSM1, C
GO:0006	8,6,7	intracellular protein transport	144	0.0532	8	0.0328	0.041373	D	TS1, MRT4, CSL4, GDB1, NPL4
GO:0006	9,7,8	protein targeting	132	0.0488	7	0.0287	0.040645	D	PRP8, ECM2
GO:0015	5,6	protein transport	148	0.0547	8	0.0328	0.03518	D	MUM2, MLH3
GO:0006	8	DNA-dependent DNA replicatio	53	0.0196	1	0.0041	0.034066	D	HSP78, NOC2, OCT1, VPS9, DNF2, CSE1, STT4, TOM40, ACC1
GO:0051	3	localization	556	0.2055	43	0.1762	0.033744	D	HSP78, NOC2, OCT1, VPS9, DNF2, CSE1, TOM40, ACC1
GO:0046	5	secretion	129	0.0477	6	0.0246	0.025765	D	HSP78, NOC2, OCT1, VPS9, CSE1, TOM40, ACC1
GO:0051	5,4	cellular localization	314	0.1160	20	0.0820	0.01834	D	HSP78, NOC2, OCT1, VPS9, DNF2, CSE1, TOM40, ACC1
GO:0048	8,6,7	Golgi vesicle transport	94	0.0347	3	0.0123	0.017015	D	MLH3
GO:0045	5,6	secretory pathway	124	0.0458	5	0.0205	0.016228	D	HEK2, SAC6, SMF1, ZRC1, ARP3, ENA5, HSP78, HMT1, KIP2, NPL3, NOC2, GSF2, VTC2, SC
GO:0046	7,5,6	intracellular transport	297	0.1098	18	0.0738	0.01412	D	P160, OCT1, MTR4, VPS9, CHS5, GTS1, GDI1, ATP2, VCX1, MYO2, LOC1, DNF2, ALR1, CSE
GO:0016	5,6	vesicle-mediated transport	183	0.0676	9	0.0369	0.0132	D	1, SEC8, STT4, MCR1, TOM40, KIP3, VPS4, PEP3, GTR1, EPS1, DAL5, CDC42, PDR5, ALD5, CTR2, RSB1, ACC1
GO:0051	4	establishment of localization	529	0.1955	37	0.1516	0.01303	D	CHS5, SEC8, PEP3
GO:0051	6,5	establishment of cellular localiz	301	0.1112	18	0.0738	0.012198	D	GSF2, CHS5, SEC8, PEP3, CDC42
GO:0006	4,5	transport	521	0.1925	36	0.1475	0.011703	D	HSP78, HMT1, KIP2, NPL3, NOC2, OCT1, MTR4, VPS9, CHS5, DNF2, CSE1, SEC8, TOM40, K
									IP3, VPS4, PEP3, CTR2, ACC1
									SAC6, CHS5, GDI1, MYO2, DNF2, SEC8, VPS4, PEP3, CDC42
									SAC6, SMF1, ZRC1, ENA5, HSP78, HMT1, KIP2, NPL3, NOC2, GSF2, OCT1, MTR4, VPS9, CH
									S5, GTS1, GDI1, ATP2, VCX1, MYO2, DNF2, ALR1, CSE1, SEC8, STT4, MCR1, TOM40, KIP3,
									VPS4, PEP3, GTR1, DAL5, CDC42, PDR5, ALD5, CTR2, RSB1, ACC1
									HSP78, HMT1, KIP2, NPL3, NOC2, OCT1, MTR4, VPS9, CHS5, DNF2, CSE1, SEC8, TOM40, K
									IP3, VPS4, PEP3, CTR2, ACC1
									SAC6, SMF1, ZRC1, ENA5, HSP78, HMT1, KIP2, NPL3, NOC2, GSF2, OCT1, MTR4, VPS9, CH
									S5, GTS1, GDI1, ATP2, VCX1, MYO2, DNF2, ALR1, CSE1, SEC8, MCR1, TOM40, KIP3, VPS4,
									PEP3, GTR1, DAL5, CDC42, PDR5, ALD5, CTR2, RSB1, ACC1
(B) GO term (process) analysis of genes with decreased expression following exposure to farnesol.									
GO_ID	Levels	TERM	No. in ref <sup>a</sup>	Freq in ref <sup>a</sup>	No in set <sup>b</sup>	Freq in set <sup>b</sup>	P value <sup>c</sup>	Enrichment/Depletion <sup>d</sup>	Genes in set
GO:0006	5	alcohol metabolism	94	0.0347	15	0.0765	0.001659	E	YJR096W, PFK26, PDC2, GID8, GAL7, CAT8, GAL10, ERG25, FBP1, PFK1, YAT1, PCK1, GUP
GO:0005	6,7	monosaccharide metabolism	50	0.0185	9	0.0459	0.005938	E	1, ERG9, ERG1
GO:0019	7,8	hexose metabolism	44	0.0163	8	0.0408	0.008564	E	YJR096W, PFK26, GID8, GAL7, CAT8, GAL10, FBP1, PFK1, PCK1
GO:0030	9,10	phosphoinositide metabolism	20	0.0074	5	0.0255	0.009779	E	PFK26, GID8, GAL7, CAT8, GAL10, FBP1, PFK1, PCK1
GO:0006	10,11	GPI anchor metabolism	13	0.0048	4	0.0204	0.009842	E	GP12, PIK1, GP13, GP12, GP11
GO:0006	10,11,9,11	GPI anchor biosynthesis	13	0.0048	4	0.0204	0.009842	E	GP12, GP13, GP12, GP11
GO:0046	10,9,11	phosphoinositide biosynthesis	14	0.0052	4	0.0204	0.012796	E	GP12, GP13, GP12, GP11
GO:0006	8	riboflavin metabolism	3	0.0011	2	0.0102	0.014541	E	GP12, GP13, GP12, GP11
GO:0009	8,9	riboflavin biosynthesis	3	0.0011	2	0.0102	0.014541	E	RIB1, RIB2
GO:0042	8	riboflavin and derivative biosynt	3	0.0011	2	0.0102	0.014541	E	RIB1, RIB2
GO:0042	7	riboflavin and derivative metabo	3	0.0011	2	0.0102	0.014541	E	RIB1, RIB2
GO:0051	4	establishment of localization	529	0.1955	48	0.2449	0.014615	E	VTI1, KRE11, MON1, MTH1, NUP159, SRP68, PHO91, SEC39, MDM1, MOG1, JEN1, PTR2, YI
GO:0051	3	localization	556	0.2055	50	0.2551	0.014972	E	P1, PIK1, ADP1, TOR2, YPR011C, SMF2, AVT4, APM4, SFC1, ASM4, EMP47, VPS68, SIW14,
GO:0006	4,5	transport	521	0.1925	47	0.2398	0.016495	E	MSN5, CCS1, DUR3, SFT2, CYB2, NDC1, GSG1, TRS120, SDS22, ORT1, QCR2, SOL1, ARF3,
GO:0043	8,7,6	regulation of carbohydrate bios	9	0.0033	3	0.0153	0.020167	E	QDR3, SCO1, ARR3, BOS1, GUP1, TPC1, OPT2, ANT1, HOL1, RAV2
GO:0006	9,10,8	gluconeogenesis	17	0.0063	4	0.0204	0.024365	E	VTI1, KRE11, MON1, MTH1, NUP159, SRP68, PHO91, SEC39, ERD2, MDM1, MOG1, JEN1, P
GO:0044	5,6	cellular lipid metabolism	132	0.0488	15	0.0765	0.024601	E	TR2, YIP1, PIK1, ADP1, TOR2, YPR011C, SMF2, AVT4, APM4, SFC1, ASM4, EMP47, VPS68,
GO:0006	8,9	glucose metabolism	35	0.0129	6	0.0306	0.025989	E	SIW14, MSN5, CCS1, DUR3, SFT2, CYB2, NDC1, GSG1, TRS120, SDS22, ORT1, QCR2, SOL
GO:0016	6	carbohydrate catabolism	26	0.0096	5	0.0255	0.026642	E	1, ARF3, QDR3, SCO1, ARR3, BOS1, MDM2, GUP1, TPC1, OPT2, ANT1, HOL1, RAV2
GO:0044	7	cellular carbohydrate catabolism	26	0.0096	5	0.0255	0.026642	E	VTI1, KRE11, MON1, MTH1, NUP159, SRP68, PHO91, SEC39, MOG1, JEN1, PTR2, YIP1, PIK
GO:0040	8	regulation of meiosis	10	0.0037	3	0.0153	0.026749	E	1, ADP1, TOR2, YPR011C, SMF2, AVT4, APM4, SFC1, ASM4, EMP47, VPS68, SIW14, MSN5,
GO:0006	8,9	galactose metabolism	4	0.0015	2	0.0102	0.026994	E	CCS1, DUR3, SFT2, CYB2, NDC1, GSG1, TRS120, SDS22, ORT1, QCR2, SOL1, ARF3, QDR3
GO:0015	5,6	peptide transport	4	0.0015	2	0.0102	0.026994	E	, SCO1, ARR3, BOS1, GUP1, TPC1, OPT2, ANT1, HOL1, RAV2
GO:0009	5	regulation of catabolism	4	0.0015	2	0.0102	0.026994	E	GID8, CAT8, PCL7
GO:0008	6,5,7	lipid biosynthesis	78	0.0288	10	0.0510	0.02925	E	GID8, CAT8, FBP1, PCK1
GO:0006	7,8	phospholipid metabolism	47	0.0174	7	0.0357	0.031893	E	GID8, CAT8, FBP1, PCK1
GO:0046	6	alcohol biosynthesis	19	0.0070	4	0.0204	0.034215	E	GP12, ERG25, SCT1, GP113, TSC11, GP112, GP111, ERG9, ERG1, CRD1, PDX3,
GO:0046	7,8	monosaccharide biosynthesis	19	0.0070	4	0.0204	0.034215	E	GP12, PIK1, SCT1, GP113, GP112, GP111, DPP1
GO:0019	8,9	hexose biosynthesis	19	0.0070	4	0.0204	0.034215	E	GID8, CAT8, FBP1, PCK1
GO:0006	5	lipid metabolism	140	0.0517	15	0.0765	0.034821	E	GID8, CAT8, FBP1, PCK1
GO:0046	7,6,8	membrane lipid biosynthesis	38	0.0140	6	0.0306	0.035422	E	GP12, SPS19, PIK1, ERG25, SCT1, GP113, TSC11, GP112, GP111
GO:0007	4	signal transduction	93	0.0344	11	0.0561	0.035987	E	GP12, SCT1, GP113, TSC11, GP112, GP111
GO:0000	2	biological process unknown	427	0.1578	37	0.1888	0.036617	E	RLM1, MTH1, SIP2, PIK1, TRL1, TOR2, TEM1, RCK2, RGT2, STE3, DPP1
GO:0046	6	alcohol catabolism	20	0.0074	4	0.0204	0.039713	E	YMR247C, YKL207W, YMR258C, YOL138C, YPR098C, YJR116W, YDR109C, YJL163C, YJ
GO:0007	3	cell communication	107	0.0395	12	0.0612	0.03999	E	R107W, PTC4, YJL055W, SKG3, YLR352W, YER130C, YDR438W, RMD11, OYE3, YMR262
GO:0006	6,7	membrane lipid metabolism	61	0.0225	8	0.0408	0.040811	E	W, NSG2, YIL067C, YIL057C, YCL047C, YHR177W, YBL055C, YIL110W, YNL224C, YDL183
GO:0051	6	negative regulation of cell organ	5	0.0018	2	0.0102	0.04176	E	C, YIL001W, YHR140W, YGR110W, UBX3, YPR003C, PMU1, YBR281C, YNR018W, PHS1, Y
GO:0006	8,9	glycerophospholipid metabolism	30	0.0111	5	0.0255	0.042932	E	OR175C
GO:0008	8,7,9	phospholipid biosynthesis	30	0.0111	5	0.0255	0.042932	E	YJR096W, PFK26, PFK1, GUP1
GO:0046	9,8,10	glycerophospholipid biosynthes	21	0.0078	4	0.0204	0.04555	E	RLM1, MTH1, SIP2, MUC1, PIK1, TRL1, TOR2, TEM1, RCK2, RGT2, STE3, DPP1
GO:0016	4	cell organization and biogenesis	840	0.3104	56	0.2857	0.048088	D	GP12, PIK1, SCT1, GP113, TSC11, GP112, GP111, DPP1
GO:0006	5	amino acid and derivative meta	146	0.0540	6	0.0306	0.044929	D	MHP1, CAP1
									GP12, PIK1, GP113, GP112, GP111
									GP12, SCT1, GP113, GP112, GP111
									GP12, GP113, GP112, GP111
									VTI1, KCS1, KRE11, RLM1, MON1, NUP159, SRP68, MYO1, FIG4, MDM1, MOG1, CDC27, NU
									P192, MOB2, MHP1, YIP1, PIK1, TOR2, APM4, ASM4, EMP47, VPS68, SBE2, SIW14, MSN5, C
									CS1, PEX6, HPA3, UME6, SFT2, NDC1, BUD4, GSG1, BEI1, TRS120, SNF4, SDS22, RIA1, O
									RT1, RPO41, SWD1, SOL1, ARF3, CAP1, CDC50, HOS2, TSC11, BOS1, DBP6, MDM20, CRD
									1, ANT1, APC1, RAV2, YDR089W, TRA1
									MES1, LEU4, GCV2, ORT1, SPE4, YAT1

GO:0006	7	proteolysis	99	0.0366	3	0.0153	0.041954	D	CDC27, RPN3, APC1
GO:0016	9	chromatin modification	117	0.0432	4	0.0204	0.039802	D	HPA3, SWD1, HOS2, TRA1
									ORM1, VTI1, KCS1, YJL103C, KRE11, RLM1, UBA2, MON1, AMS1, MTH1, NUP159, SRP68, COQ9, MYO1, GPI2, PHO91, MES1, SEC39, YJR096W, PRP28, SIP2, ERD2, PFK26, IME4, FIG4, SPS19, JLP1, UBP7, MDM1, MOG1, CDC27, PDC2, NUP192, MOB2, JEN1, PTR2, MHP1, RIB1, YIP1, PIK1, ADP1, TRL1, TOR2, CCC1, YPR011C, SMM1, GID8, SMF2, TEM1, LEU4, GAL7, PRX1, RPN3, POL30, APM4, ELP3, SFC1, ASM4, MED8, CAT8, RCK2, EMP47, MAF1, GAL10, GCV2, VPS68, SBE2, SIW14, MSN5, PHO80, NFU1, RIM9, RIM21, CCS1, CBP3, PEX6, DUR3, HPA3, UME6, SFT2, RGT2, TFA1, STE3, CYB2, RAD5, NDC1, BUD4, RIB2, GSG1, YAK1, BEM1, ERG25, TRS120, SNF4, PCL7, SDS22, FBP1, RIA1, PFK1, ORT1, YHB1, FES1, RPO41, QCR2, SPE4, ESP1, SWD1, SCT1, PIN4, SOL1, ARF3, CAP1, GP113, CDC50, RNA14, QDR3, YAT1, SCO1, HOS2, ARR3, PCK1, TSC11, GPI12, ADK2, SWP1, TFC3, BOS1, DBP6, KEL2, MDM20, SNQ2, GUP1, GPI11, ERG9, RIM13, UBR2, ERG1, CRD1, PDX3, DPP1, TPC1, OPT2, ANT1, SLD5, HOL1, DPB2, RTT106, APC1, RAV2, MSH6, HEM2, YDR089W, TRA1, PSF3
GO:0007	2	physiological process	2262	0.8359	158	0.8061	0.038974	D	MES1
GO:0043	8,7	translation	65	0.0240	1	0.0051	0.036957	D	HPA3, UME6, SWD1, HOS2, TRA1
GO:0007	7	chromosome organization and	139	0.0514	5	0.0255	0.031791	D	HPA3, SWD1, HOS2, TRA1
GO:0006	8	establishment and/or maintain	125	0.0462	4	0.0204	0.028065	D	HPA3, SWD1, HOS2, TRA1
GO:0006	7	DNA packaging	125	0.0462	4	0.0204	0.028065	D	HPA3, SWD1, HOS2, TRA1
GO:0006	6	DNA metabolism	254	0.0939	12	0.0612	0.027599	D	POL30, HPA3, UME6, RAD5, SWD1, HOS2, SLD5, DPB2, RTT106, MSH6, TRA1, PSF3
GO:0009	5	amine metabolism	160	0.0591	6	0.0306	0.026608	D	MES1, LEU4, GCV2, ORT1, SPE4, YAT1
GO:0009	6,5	macromolecule biosynthesis	256	0.0946	12	0.0612	0.025996	D	GPI2, MES1, GID8, CAT8, PCL7, FBP1, FES1, GPI13, PCK1, GPI12, SWP1, GPI11
GO:0051	6	chromosome organization and	144	0.0532	5	0.0255	0.025829	D	HPA3, UME6, SWD1, HOS2, TRA1
GO:0009	4	biosynthesis	468	0.1729	26	0.1327	0.024072	D	COQ9, GPI2, MES1, PDC2, RIB1, GID8, LEU4, CAT8, RIB2, ERG25, PCL7, FBP1, ORT1, FES1, SPE4, SCT1, GPI13, PCK1, TSC11, GPI12, SWP1, GPI11, ERG9, ERG1, CRD1, HEM2
									VTI1, KCS1, YJL103C, KRE11, RLM1, UBA2, MON1, AMS1, MTH1, NUP159, SRP68, COQ9, MYO1, GPI2, PHO91, MES1, SEC39, YJR096W, PRP28, SIP2, PFK26, IME4, FIG4, SPS19, JLP1, UBP7, MDM1, MUC1, MOG1, CDC27, PDC2, NUP192, MOB2, JEN1, PTR2, MHP1, RIB1, YIP1, PIK1, ADP1, TRL1, TOR2, CCC1, YPR011C, SMM1, GID8, SMF2, TEM1, LEU4, GAL7, PRX1, RPN3, AVT4, POL30, APM4, ELP3, SFC1, ASM4, MED8, CAT8, RCK2, EMP47, MAF1, GAL10, GCV2, VPS68, SBE2, SIW14, MSN5, PHO80, NFU1, RIM9, RIM21, CCS1, CBP3, PEX6, DUR3, HPA3, UME6, SFT2, RGT2, TFA1, STE3, CYB2, RAD5, NDC1, BUD4, RIB2, GSG1, YAK1, BEM1, ERG25, TRS120, SNF4, PCL7, SDS22, FBP1, RIA1, PFK1, ORT1, FES1, RPO41, QCR2, SPE4, ESP1, SWD1, SCT1, PIN4, SOL1, ARF3, CAP1, GPI13, CDC50, RNA14, QDR3, YAT1, SCO1, HOS2, ARR3, PCK1, TSC11, GPI12, ADK2, SWP1, TFC3, BOS1, DBP6, KEL2, MDM20, SNQ2, GUP1, GPI11, ERG9, RIM13, UBR2, ERG1, CRD1, PDX3, DPP1, TPC1, OPT2, ANT1, SLD5, HOL1, DPB2, RTT106, APC1, RAV2, MSH6, HEM2, YDR089W, TRA1, PSF3
GO:0009	2	cellular process	2227	0.8230	153	0.7806	0.020897	D	VTI1, KCS1, YJL103C, KRE11, RLM1, UBA2, MON1, AMS1, MTH1, NUP159, SRP68, COQ9, MYO1, GPI2, PHO91, MES1, SEC39, YJR096W, PRP28, SIP2, PFK26, IME4, FIG4, SPS19, JLP1, UBP7, MDM1, MUC1, MOG1, CDC27, PDC2, NUP192, MOB2, JEN1, PTR2, MHP1, RIB1, YIP1, PIK1, ADP1, TRL1, TOR2, CCC1, YPR011C, SMM1, GID8, SMF2, TEM1, LEU4, GAL7, PRX1, RPN3, AVT4, POL30, APM4, ELP3, SFC1, ASM4, MED8, CAT8, RCK2, EMP47, MAF1, GAL10, GCV2, VPS68, SBE2, SIW14, MSN5, PHO80, NFU1, RIM9, RIM21, CCS1, CBP3, PEX6, DUR3, HPA3, UME6, SFT2, TFA1, STE3, CYB2, RAD5, NDC1, BUD4, RIB2, GSG1, YAK1, BEM1, ERG25, TRS120, SNF4, PCL7, SDS22, FBP1, RIA1, PFK1, ORT1, FES1, RPO41, QCR2, SPE4, ESP1, SWD1, SCT1, PIN4, SOL1, ARF3, CAP1, GPI13, CDC50, RNA14, QDR3, YAT1, SCO1, HOS2, ARR3, PCK1, TSC11, GPI12, ADK2, SWP1, TFC3, BOS1, DBP6, KEL2, MDM20, SNQ2, GUP1, GPI11, ERG9, RIM13, UBR2, ERG1, CRD1, PDX3, DPP1, TPC1, OPT2, ANT1, SLD5, HOL1, DPB2, RTT106, APC1, RAV2, MSH6, HEM2, YDR089W, TRA1, PSF3
GO:0050	3	cellular physiological process	2207	0.8156	151	0.7704	0.018149	D	VTI1, KCS1, YJL103C, KRE11, RLM1, UBA2, MON1, AMS1, MTH1, NUP159, SRP68, COQ9, MYO1, GPI2, PHO91, MES1, SEC39, YJR096W, PRP28, SIP2, PFK26, IME4, FIG4, SPS19, JLP1, UBP7, MDM1, MUC1, MOG1, CDC27, PDC2, NUP192, MOB2, JEN1, PTR2, MHP1, RIB1, YIP1, PIK1, ADP1, TRL1, TOR2, CCC1, YPR011C, SMM1, GID8, SMF2, TEM1, LEU4, GAL7, PRX1, RPN3, AVT4, POL30, APM4, ELP3, SFC1, ASM4, MED8, CAT8, RCK2, EMP47, MAF1, GAL10, GCV2, VPS68, SBE2, SIW14, MSN5, PHO80, NFU1, RIM9, RIM21, CCS1, CBP3, PEX6, DUR3, HPA3, UME6, SFT2, TFA1, STE3, CYB2, RAD5, NDC1, BUD4, RIB2, GSG1, YAK1, BEM1, ERG25, TRS120, SNF4, PCL7, SDS22, FBP1, RIA1, PFK1, ORT1, FES1, RPO41, QCR2, SPE4, ESP1, SWD1, SCT1, PIN4, SOL1, ARF3, CAP1, GPI13, CDC50, RNA14, QDR3, YAT1, SCO1, HOS2, ARR3, PCK1, TSC11, GPI12, ADK2, SWP1, TFC3, BOS1, DBP6, KEL2, MDM20, SNQ2, GUP1, GPI11, ERG9, RIM13, UBR2, ERG1, CRD1, PDX3, DPP1, TPC1, OPT2, ANT1, SLD5, HOL1, DPB2, RTT106, APC1, RAV2, MSH6, HEM2, YDR089W, TRA1, PSF3
GO:0006	4	nitrogen compound metabolism	171	0.0632	6	0.0306	0.01697	D	MES1, LEU4, GCV2, ORT1, SPE4, YAT1
GO:0006	6,7	amino acid metabolism	136	0.0503	4	0.0204	0.016841	D	MES1, LEU4, GCV2, ORT1
GO:0006	10	chromatin remodeling	79	0.0292	1	0.0051	0.015305	D	SWD1
GO:0007	7	ribosome biogenesis	138	0.0510	4	0.0204	0.015295	D	NUP159, TOR2, RIA1, DBP6
GO:0006	5	organelle organization and biog	592	0.2188	33	0.1684	0.014861	D	VTI1, KCS1, NUP159, MYO1, MDM1, CDC27, NUP192, MOB2, MHP1, TOR2, ASM4, SIW14, PEX6, HPA3, UME6, SFT2, NDC1, BUD4, BEM1, SNF4, RIA1, RPO41, SWD1, ARF3, CAP1, CDC50, HOS2, DBP6, MDM20, CRD1, ANT1, APC1, TRA1
GO:0006	7	rRNA processing	194	0.0717	7	0.0357	0.013278	D	PRP28, TRL1, SMM1, RIA1, SOL1, RNA14, DBP6
GO:0006	8	rRNA processing	111	0.0410	2	0.0102	0.008017	D	RIA1, DBP6
GO:0042	6	ribosome biogenesis and assem	152	0.0562	4	0.0204	0.007594	D	NUP159, TOR2, RIA1, DBP6
GO:0007	5	cytoplasm organization and bio	152	0.0562	4	0.0204	0.007594	D	NUP159, TOR2, RIA1, DBP6
GO:0044	5	cellular biosynthesis	422	0.1559	20	0.1020	0.007288	D	COQ9, GPI2, MES1, PDC2, RIB1, GID8, LEU4, CAT8, RIB2, PCL7, FBP1, ORT1, FES1, SPE4, GPI13, PCK1, GPI12, SWP1, GPI11, HEM2
GO:0016	7	rRNA metabolism	115	0.0425	2	0.0102	0.006307	D	RIA1, DBP6
GO:0044	6	cellular protein metabolism	610	0.2254	31	0.1582	0.00419	D	UBA2, GPI2, MES1, PRP28, SIP2, UBP7, CDC27, MOB2, MHP1, RPN3, RCK2, SIW14, CBP3, HPA3, YAK1, FES1, SWD1, CAP1, GPI13, SCO1, HOS2, GPI12, SWP1, DBP6, MDM20, GPI11, RIM13, UBR2, APC1, RAV2, TRA1
GO:0006	7,6	protein biosynthesis	222	0.0820	7	0.0357	0.003824	D	GPI2, MES1, FES1, GPI13, GPI12, SWP1, GPI11
GO:0044	5	cellular macromolecule metabol	632	0.2336	32	0.1633	0.003418	D	UBA2, GPI2, MES1, PRP28, SIP2, UBP7, CDC27, MOB2, MHP1, RPN3, RCK2, SIW14, CBP3, HPA3, YAK1, PCL7, FES1, SWD1, CAP1, GPI13, SCO1, HOS2, GPI12, SWP1, DBP6, MDM20, GPI11, RIM13, UBR2, APC1, RAV2, TRA1
GO:0019	5	protein metabolism	627	0.2317	31	0.1582	0.002476	D	UBA2, GPI2, MES1, PRP28, SIP2, UBP7, CDC27, MOB2, MHP1, RPN3, RCK2, SIW14, CBP3, HPA3, YAK1, FES1, SWD1, CAP1, GPI13, SCO1, HOS2, GPI12, SWP1, DBP6, MDM20, GPI11, RIM13, UBR2, APC1, RAV2, TRA1
GO:0016	6	RNA metabolism	275	0.1016	9	0.0459	0.001761	D	MES1, PRP28, IME4, TRL1, SMM1, RIA1, SOL1, RNA14, DBP6
GO:0044	4	cellular metabolism	1588	0.5868	94	0.4796	0.000428	D	YJL103C, RLM1, UBA2, AMS1, COQ9, GPI2, MES1, YJR096W, PRP28, SIP2, PFK26, IME4, SPS19, JLP1, UBP7, CDC27, PDC2, MOB2, MHP1, RIB1, PIK1, TRL1, SMM1, GID8, LEU4, GAL7, RPN3, POL30, ELP3, MED8, CAT8, RCK2, MAF1, GAL10, GCV2, SIW14, PHO80, CBP3, HP A3, UME6, TFA1, CYB2, RAD5, RIB2, YAK1, ERG25, SNF4, PCL7, FBP1, RIA1, PFK1, ORT1, FES1, RPO41, QCR2, SPE4, SWD1, SCT1, SOL1, CAP1, GPI13, CDC50, RNA14, YAT1, SCO1, HOS2, PCK1, TSC11, GPI12, ADK2, SWP1, TFC3, DBP6, MDM20, SNQ2, GUP1, GPI11, ERG9, RIM13, UBR2, ERG1, CRD1, PDX3, DPP1, ANT1, SLD5, DPB2, RTT106, APC1, RAV2, MSH6, HEM2, TRA1, PSF3
GO:0043	5	biopolymer metabolism	838	0.3097	41	0.2092	0.000346	D	UBA2, GPI2, MES1, PRP28, SIP2, IME4, UBP7, CDC27, MOB2, PIK1, TRL1, SMM1, RPN3, POL30, RCK2, SIW14, HPA3, UME6, RAD5, YAK1, PCL7, RIA1, SWD1, SOL1, CDC50, RNA14, HOS2, ADK2, TFC3, DBP6, SLD5, DPB2, RTT106, MSH6, TRA1, PSF3
GO:0008	3	metabolism	1620	0.5987	95	0.4847	0.00022	D	YJL103C, RLM1, UBA2, AMS1, COQ9, GPI2, MES1, YJR096W, PRP28, SIP2, PFK26, IME4, SPS19, JLP1, UBP7, CDC27, PDC2, MOB2, MHP1, RIB1, PIK1, TRL1, SMM1, GID8, YMR010W, LEU4, GAL7, RPN3, POL30, ELP3, MED8, CAT8, RCK2, MAF1, GAL10, GCV2, SIW14, PHO80, CBP3, HP A3, UME6, TFA1, CYB2, RAD5, RIB2, YAK1, ERG25, SNF4, PCL7, FBP1, RIA1, PFK1, ORT1, FES1, RPO41, QCR2, SPE4, SWD1, SCT1, SOL1, CAP1, GPI13, CDC50, RNA14, YAT1, SCO1, HOS2, PCK1, TSC11, GPI12, ADK2, SWP1, TFC3, DBP6, MDM20, SNQ2, GUP1, GPI11, ERG9, RIM13, UBR2, ERG1, CRD1, PDX3, DPP1, ANT1, SLD5, DPB2, RTT106, APC1, RAV2, MSH6, HEM2, TRA1, PSF3
GO:0006	5	nucleobase, nucleoside, nucleo	732	0.2705	33	0.1684	0.000173	D	RLM1, MES1, PRP28, IME4, PDC2, TRL1, SMM1, POL30, ELP3, MED8, CAT8, MAF1, HPA3, UME6, TFA1, RAD5, SNF4, RIA1, RPO41, SWD1, SOL1, CDC50, RNA14, HOS2, ADK2, TFC3, DBP6, SLD5, DPB2, RTT106, MSH6, TRA1, PSF3
GO:0043	4	macromolecule metabolism	1106	0.4087	57	0.2908	0.000117	D	UBA2, AMS1, GPI2, MES1, YJR096W, PRP28, SIP2, PFK26, IME4, UBP7, CDC27, MOB2, MHP1, PIK1, TRL1, SMM1, GID8, GAL7, RPN3, POL30, ELP3, MED8, CAT8, RCK2, MAF1, GAL10, GCV2, SIW14, CBP3, HPA3, UME6, TFA1, RAD5, YAK1, ERG25, SNF4, PCL7, FBP1, RIA1, PFK1, ORT1, FES1, RPO41, SPE4, SWD1, SCT1, SOL1, CAP1, GPI13, CDC50, RNA14, YAT1, SCO1, HOS2, PCK1, TSC11, GPI12, ADK2, SWP1, TFC3, DBP6, MDM20, SNQ2, GUP1, GPI11, ERG9, RIM13, UBR2, ERG1, CRD1, PDX3, DPP1, ANT1, SLD5, DPB2, RTT106, APC1, RAV2, MSH6, TRA1, PSF3
GO:0044	4	primary metabolism	1481	0.5473	83	0.4235	8.95E-05	D	RLM1, UBA2, AMS1, GPI2, MES1, YJR096W, PRP28, SIP2, PFK26, IME4, SPS19, UBP7, CDC27, PDC2, MOB2, MHP1, PIK1, TRL1, SMM1, GID8, LEU4, GAL7, RPN3, POL30, ELP3, MED8, CAT8, RCK2, MAF1, GAL10, GCV2, SIW14, CBP3, HPA3, UME6, TFA1, RAD5, YAK1, ERG25, SNF4, PCL7, FBP1, RIA1, PFK1, ORT1, FES1, RPO41, SPE4, SWD1, SCT1, SOL1, CAP1, GPI13, CDC50, RNA14, YAT1, SCO1, HOS2, PCK1, TSC11, GPI12, ADK2, SWP1, TFC3, DBP6, MDM20, SNQ2, GUP1, GPI11, ERG9, RIM13, UBR2, ERG1, CRD1, PDX3, DPP1, ANT1, SLD5, DPB2, RTT106, APC1, RAV2, MSH6, TRA1, PSF3

\*Reference data: 2764 *S. cerevisiae* orthologues of *C. parapsilosis* genes represented on the microarrays

<sup>b</sup> Data set: 244 <i>S. cerevisiae</i> orthologues of <i>C. parapsilosis</i> genes with increased expression and 196 <i>S. cerevisiae</i> orthologues of <i>C. parapsilosis</i> genes with reduced expression in farnesol-treated cells.
<sup>c</sup> Terms with a p value of less than or equal to 0.05 are shown.
<sup>d</sup> E: GO term over-represented in data set; D: GO term under-represented in data set