Supplementary Table 3.

E1

GOID	GO_term	Cluster frequency	Background frequency	P-value	FDR	Expected FP	Gene(s) annotated to the term
7165	signal transduction	9 out of 23 genes, 39.1%	224 out of 6359 background genes, 3.5%	8.32E-06	0	0	*GPB2,RGT2,SNF3,MTH1,CYR1,SSK1,HOG1,RAS2,SSK2*
23052	signaling	9 out of 23 genes, 39.1%	230 out of 6359 background genes, 3.6%	1.04E-05	0	0	*GPB2,RGT2,SNF3,MTH1,CYR1,SSK1,HOG1,RAS2,SSK2*
7154	cell communication	10 out of 23 genes, 43.5%	329 out of 6359 background genes, 5.2%	1.65E-05	0	0	*GPB2,RGT2,SNF3,MTH1,DAL81,CYR1,SSK1,HOG1,RAS2,SSK2*
50794	regulation of cellular process	15 out of 23 genes, 65.2%	1090 out of 6359 background genes, 17.1%	8.10E-05	0	0	*GPB2,SED4,RGT2,SNF3,MTH1,RIM15,DAL81,CYR1,RGT1,SSK1,HOG1,RAS2,SSK2,CIN5,SWI1*
50789	regulation of biological process	15 out of 23 genes, 65.2%	1125 out of 6359 background genes, 17.7%	0.00012	0	0	*GPB2,SED4,RGT2,SNF3,MTH1,RIM15,DAL81,CYR1,RGT1,SSK1,HOG1,RAS2,SSK2,CIN5,SWI1*
65007	biological regulation	16 out of 23 genes, 69.6%	1322 out of 6359 background genes, 20.8%	0.00014	0	0	*GPB2,SED4,RGT2,SNF3,MTH1,RIM15,DAL81,CYR1,RGT1,VPS13,SSK1,HOG1,RAS2,SSK2,CIN5,SWI1*
15758	glucose transport	3 out of 23 genes, 13.0%	10 out of 6359 background genes, 0.2%	0.00107	0	0	*SNF3,MTH1,RGT1*
34284	response to monosaccharide stimulus	3 out of 23 genes, 13.0%	10 out of 6359 background genes, 0.2%	0.00107	0	0	*GPB2,RGT2,SNF3*
9746	response to hexose stimulus	3 out of 23 genes, 13.0%	10 out of 6359 background genes, 0.2%	0.00107	0	0	*GPB2,RGT2,SNF3*
9749	response to glucose stimulus	3 out of 23 genes, 13.0%	10 out of 6359 background genes, 0.2%	0.00107	0	0	*GPB2,RGT2,SNF3*
9743	response to carbohydrate stimulus	3 out of 23 genes, 13.0%	11 out of 6359 background genes, 0.2%	0.00147	0	0	*GPB2,RGT2,SNF3*
42221	response to chemical stimulus	8 out of 23 genes, 34.8%	352 out of 6359 background genes, 5.5%	0.00422	0	0	*GPB2,RGT2,SNF3,RIM15,DAL81,HOG1,RAS2,CIN5*
50896	response to stimulus	12 out of 23 genes, 52.2%	925 out of 6359 background genes, 14.5%	0.00528	0	0.02	*GPB2,RGT2,SNF3,MTH1,RIM15,DAL81,CYR1,SSK1,HOG1,RAS2,SSK2,CIN5*
51716	cellular response to stimulus	11 out of 23 genes, 47.8%	766 out of 6359 background genes, 12.0%	0.00545	0	0.02	*GPB2,RGT2,SNF3,MTH1,RIM15,DAL81,CYR1,SSK1,HOG1,RAS2,SSK2*
7231	osmosensory signaling pathway	3 out of 23 genes, 13.0%	17 out of 6359 background genes, 0.3%	0.00598	0	0.02	*SSK1,HOG1,SSK2*
34287	detection of monosaccharide stimulus	2 out of 23 genes, 8.7%	3 out of 6359 background genes, 0.0%	0.00824	0	0.02	*RGT2,SNF3*
51594	detection of glucose	2 out of 23 genes, 8.7%	3 out of 6359 background genes, 0.0%	0.00824	0	0.02	*RGT2,SNF3*
51606	detection of stimulus	2 out of 23 genes, 8.7%	3 out of 6359 background genes, 0.0%	0.00824	0	0.02	*RGT2,SNF3*
9593	detection of chemical stimulus	2 out of 23 genes, 8.7%	3 out of 6359 background genes, 0.0%	0.00824	0	0.02	*RGT2,SNF3*
9730	detection of carbohydrate stimulus	2 out of 23 genes, 8.7%	3 out of 6359 background genes, 0.0%	0.00824	0	0.02	*RGT2,SNF3*
9732	detection of hexose stimulus	2 out of 23 genes, 8.7%	3 out of 6359 background genes, 0.0%	0.00824	0	0.02	*RGT2,SNF3*

E2

GOID	GO_term	Cluster frequency	Background frequency	P-value	FDR	Expected FP	Gene(s) annotated to the term
7165	signal transduction	8 out of 24 genes, 33.3%	224 out of 6359 background genes, 3.5%	0.00018	0	0	*GPB2,RGT2,SNF3,AFR1,MTH1,PBS2,SSK1,SSK2*
23052	signaling	8 out of 24 genes, 33.3%	230 out of 6359 background genes, 3.6%	0.00022	0	0	*GPB2,RGT2,SNF3,AFR1,MTH1,PBS2,SSK1,SSK2*
7154	cell communication	9 out of 24 genes, 37.5%	329 out of 6359 background genes, 5.2%	0.00029	0	0	*GPB2,RGT2,SNF3,AFR1,MTH1,PBS2,VPS25,SSK1,SSK2*
15749	monosaccharide transport	4 out of 24 genes, 16.7%	24 out of 6359 background genes, 0.4%	0.0003	0	0	*SNF3,MTH1,HXT6,RGT1*
8645	hexose transport	4 out of 24 genes, 16.7%	24 out of 6359 background genes, 0.4%	0.0003	0	0	*SNF3,MTH1,HXT6,RGT1*
15758	glucose transport	3 out of 24 genes, 12.5%	10 out of 6359 background genes, 0.2%	0.00105	0	0	*SNF3,MTH1,RGT1*
34284	response to monosaccharide stimulus	3 out of 24 genes, 12.5%	10 out of 6359 background genes, 0.2%	0.00105	0	0	*GPB2,RGT2,SNF3*
9746	response to hexose stimulus	3 out of 24 genes, 12.5%	10 out of 6359 background genes, 0.2%	0.00105	0	0	*GPB2,RGT2,SNF3*
9749	response to glucose stimulus	3 out of 24 genes, 12.5%	10 out of 6359 background genes, 0.2%	0.00105	0	0	*GPB2,RGT2,SNF3*
50896	response to stimulus	13 out of 24 genes, 54.2%	925 out of 6359 background genes, 14.5%	0.00119	0	0	*GPB2,BPH1,RGT2,SNF3,AFR1,MTH1,RIM15,PBS2,VPS25,SSK1,SSK2,WHI2,ARP8*
9743	response to carbohydrate stimulus	3 out of 24 genes, 12.5%	11 out of 6359 background genes, 0.2%	0.00144	0	0	*GPB2,RGT2,SNF3*
8643	carbohydrate transport	4 out of 24 genes, 16.7%	41 out of 6359 background genes, 0.6%	0.00271	0	0	*SNF3,MTH1,HXT6,RGT1*
7231	osmosensory signaling pathway	3 out of 24 genes, 12.5%	17 out of 6359 background genes, 0.3%	0.00583	0	0	*PBS2,SSK1,SSK2*
51716	cellular response to stimulus	11 out of 24 genes, 45.8%	766 out of 6359 background genes, 12.0%	0.00767	0	0	*GPB2,RGT2,SNF3,AFR1,MTH1,RIM15,PBS2,VPS25,SSK1,SSK2,ARP8*
34287	detection of monosaccharide stimulus	2 out of 24 genes, 8.3%	3 out of 6359 background genes, 0.0%	0.00768	0	0.02	*RGT2,SNF3*
51594	detection of glucose	2 out of 24 genes, 8.3%	3 out of 6359 background genes, 0.0%	0.00768	0	0.02	*RGT2,SNF3*
51606	detection of stimulus	2 out of 24 genes, 8.3%	3 out of 6359 background genes, 0.0%	0.00768	0	0.02	*RGT2,SNF3*
9593	detection of chemical stimulus	2 out of 24 genes, 8.3%	3 out of 6359 background genes, 0.0%	0.00768	0	0.02	*RGT2,SNF3*
9730	detection of carbohydrate stimulus	2 out of 24 genes, 8.3%	3 out of 6359 background genes, 0.0%	0.00768	0	0.02	*RGT2,SNF3*
9732	detection of hexose stimulus	2 out of 24 genes, 8.3%	3 out of 6359 background genes, 0.0%	0.00768	0	0.02	*RGT2,SNF3*

E3

GOID	GO_term	Cluster frequency	Background frequency	P-value	FDR	Expected FP	Gene(s) annotated to the term
50789	regulation of biological process	20 out of 37 genes, 54.1%	1125 out of 6359 background genes, 17.7%	0.00019	0	0	*GPB2,CDC15,IRA1,UBC13,MTH1,GLC7,RIM15,CDC55,OSH3,DAL81,BCK1,LCB3,VPS25,BYE1,ACE2,HSP60,IRA2,PDE2,NDD1,GAL4*
50794	regulation of cellular process	19 out of 37 genes, 51.4%	1090 out of 6359 background genes, 17.1%	0.00062	0	0	*GPB2,CDC15,IRA1,UBC13,MTH1,GLC7,RIM15,CDC55,OSH3,DAL81,BCK1,LCB3,VPS25,BYE1,ACE2,IRA2,PDE2,NDD1,GAL4*
65007	biological regulation	20 out of 37 genes, 54.1%	1322 out of 6359 background genes, 20.8%	0.00266	0.01	0.02	*GPB2,CDC15,IRA1,UBC13,MTH1,GLC7,RIM15,CDC55,OSH3,DAL81,BCK1,LCB3,VPS25,BYE1,ACE2,HSP60,IRA2,PDE2,NDD1,GAL4*
	negative regulation of Ras protein						
46580	signal transduction	3 out of 37 genes, 8.1%	8 out of 6359 background genes, 0.1%	0.00327	0.01	0.02	*GPB2,IRA1,IRA2*
	negative regulation of small GTPase						
51058	mediated signal transduction	3 out of 37 genes, 8.1%	8 out of 6359 background genes, 0.1%	0.00327	0	0.02	*GPB2,IRA1,IRA2*
7154	cell communication	10 out of 37 genes, 27.0%	329 out of 6359 background genes, 5.2%	0.00392	0	0.02	*GPB2,IRA1,MTH1,DAL81,BCK1,LCB3,VPS25,IRA2,PDE2,GAL4*
50896	response to stimulus	16 out of 37 genes, 43.2%	925 out of 6359 background genes, 14.5%	0.00735	0	0.02	*GPB2,IRA1,UBC13,MTH1,GLC7,RIM15,DAL81,BCK1,LCB3,POL32,VPS25,MNN4,IRA2,PDE2,GAL4,ATH1*