

Additional file 14A - GO term enrichment analysis of genes down-regulated in a upc

Legend

GOID	Gene ontology Identifier
GO_term	Gene ontology term description
terms in differentially expressed genes	Cluster Frequency of the set of genes tested
frequency of GO terms in entire dataset	Cluster Frequency of the gene background
Corrected P_value rate	the whole genome that are annotated to that GO Term. correction for multiple-testing
Gene(s) annotated to the term	List of genes annotated to each single GO term

GOID	GO_term	frequency of GO terms in differentially expressed genes	frequency of GO terms in entire dataset	Corrected P-value
16126	sterol biosynthetic p	19 out of 62 genes,	27 out of 5214 bac	5.86E-30
6694	steroid biosynthetic	19 out of 62 genes,	27 out of 5214 bac	5.86E-30
16125	sterol metabolic proc	19 out of 62 genes,	35 out of 5214 bac	1.00E-26
8202	steroid metabolic pro	19 out of 62 genes,	35 out of 5214 bac	1.00E-26
16129	phytosteroid biosynth	16 out of 62 genes,	23 out of 5214 bac	1.00E-24
44108	cellular alcohol biosy	16 out of 62 genes,	23 out of 5214 bac	1.00E-24
6696	ergosterol biosynthes	16 out of 62 genes,	23 out of 5214 bac	1.00E-24
16128	phytosteroid metabol	16 out of 62 genes,	25 out of 5214 bac	8.21E-24
44107	cellular alcohol meta	16 out of 62 genes,	25 out of 5214 bac	8.21E-24
8204	ergosterol metabolic	16 out of 62 genes,	25 out of 5214 bac	8.21E-24
8610	lipid biosynthetic pro	24 out of 62 genes,	124 out of 5214 bac	1.09E-21
44283	small molecule biosy	28 out of 62 genes,	213 out of 5214 bac	5.10E-21
44281	small molecule metal	38 out of 62 genes,	661 out of 5214 bac	3.40E-17
46165	alcohol biosynthetic	16 out of 62 genes,	55 out of 5214 bac	9.29E-17
6629	lipid metabolic proce	25 out of 62 genes,	223 out of 5214 bac	1.28E-16
6066	alcohol metabolic pr	20 out of 62 genes,	148 out of 5214 bac	2.33E-14
9058	biosynthetic process	39 out of 62 genes,	1030 out of 5214 ba	2.14E-11
44249	cellular biosynthetic	38 out of 62 genes,	1010 out of 5214 ba	7.73E-11
16053	organic acid biosynth	13 out of 62 genes,	146 out of 5214 bac	2.15E-06
46394	carboxylic acid biosy	13 out of 62 genes,	146 out of 5214 bac	2.15E-06
19752	carboxylic acid metal	16 out of 62 genes,	298 out of 5214 bac	4.77E-05
43436	oxoacid metabolic pr	16 out of 62 genes,	298 out of 5214 bac	4.77E-05
6082	organic acid metabol	16 out of 62 genes,	299 out of 5214 bac	5.00E-05
42180	cellular ketone metal	16 out of 62 genes,	310 out of 5214 bac	8.22E-05
6633	fatty acid biosynthesi	6 out of 62 genes, 9	28 out of 5214 bac	0.00015
8152	metabolic process	48 out of 62 genes,	2524 out of 5214 ba	0.00054
42493	response to drug	15 out of 62 genes,	318 out of 5214 bac	0.00064
6631	fatty acid metabolic	7 out of 62 genes, 1	56 out of 5214 bac	0.00077
32787	monocarboxylic acid	8 out of 62 genes, 1	80 out of 5214 bac	0.00082
44238	primary metabolic pr	43 out of 62 genes,	2177 out of 5214 ba	0.00204
44255	cellular lipid metabol	11 out of 62 genes,	187 out of 5214 bac	0.00213
44237	cellular metabolic pr	43 out of 62 genes,	2281 out of 5214 ba	0.00826
42398	cellular modified ami	4 out of 62 genes, 6	17 out of 5214 bac	0.00849
44271	cellular nitrogen com	11 out of 62 genes,	242 out of 5214 bac	0.02351
9987	cellular process	52 out of 62 genes,	3254 out of 5214 ba	0.03998
42221	response to chemical	16 out of 62 genes,	508 out of 5214 bac	0.04489

6575	cellular modified ami	4 out of 62 genes, 6	26 out of 5214 back	0.04923
8652	cellular amino acid b	7 out of 62 genes, 1	111 out of 5214 bac	0.06785
6720	isoprenoid metabolic	3 out of 62 genes, 4	12 out of 5214 back	0.07213
8299	isoprenoid biosynthe	3 out of 62 genes, 4	12 out of 5214 back	0.07213
9309	amine biosynthetic p	7 out of 62 genes, 1	115 out of 5214 bac	0.08433
15677	copper ion import	2 out of 62 genes, 3	3 out of 5214 backg	0.09154

Δ2 deletion in the RNA-seq experiment.

False discovery
rate

Gene(s) annotated to the term

0.00%	PDR16:HMG1:ERG7:ERG10:ERG24:ERG6:ERG27:ERG9:ERG25:UPC2:ERG1:I
0.00%	PDR16:HMG1:ERG7:ERG10:ERG24:ERG6:ERG27:ERG9:ERG25:UPC2:ERG1:I
0.00%	PDR16:HMG1:ERG7:ERG10:ERG24:ERG6:ERG27:ERG9:ERG25:UPC2:ERG1:I
0.00%	PDR16:HMG1:ERG7:ERG10:ERG24:ERG6:ERG27:ERG9:ERG25:UPC2:ERG1:I
0.00%	ERG7:ERG10:ERG24:ERG6:ERG27:ERG9:ERG25:UPC2:ERG1:ERG5:ERG4:EI
0.00%	ERG7:ERG10:ERG24:ERG6:ERG27:ERG9:ERG25:UPC2:ERG1:ERG5:ERG4:EI
0.00%	ERG7:ERG10:ERG24:ERG6:ERG27:ERG9:ERG25:UPC2:ERG1:ERG5:ERG4:EI
0.00%	ERG7:ERG10:ERG24:ERG6:ERG27:ERG9:ERG25:UPC2:ERG1:ERG5:ERG4:EI
0.00%	ERG7:ERG10:ERG24:ERG6:ERG27:ERG9:ERG25:UPC2:ERG1:ERG5:ERG4:EI
0.00%	ERG7:ERG10:ERG24:ERG6:ERG27:ERG9:ERG25:UPC2:ERG1:ERG5:ERG4:EI
0.00%	PDR16:HMG1:ERG7:ERG10:ERG24:ERG6:SLD1:ERG27:ERG9:ERG25:UPC2:I
0.00%	ERG7:ERG10:ERG24:orf19.163:ERG6:orf19.2286:MET6:SLD1:THI6:MET13:ER
0.00%	PDR16:HMG1:ERG7:ERG10:ERG24:orf19.163:ERG6:URA3:IMH3:orf19.2286:UF
0.00%	ERG7:ERG10:ERG24:ERG6:ERG27:ERG9:ERG25:UPC2:ERG1:ERG5:ERG4:EI
0.00%	PDR16:HMG1:ERG7:ERG10:ERG24:ERG6:SLD1:ERG27:ERG9:ERG25:UPC2:I
0.00%	PDR16:HMG1:ERG7:ERG10:ERG24:ERG6:orf19.276:ERG27:ERG9:ERG25:UPC
0.00%	PDR16:HMG1:ERG7:ERG10:ERG24:orf19.163:ERG6:URA3:IMH3:orf19.2286:UF
0.00%	HMG1:ERG7:ERG10:ERG24:orf19.163:ERG6:URA3:IMH3:orf19.2286:URA2:ME
0.00%	orf19.163:orf19.2286:MET6:SLD1:MET13:ERG25:HIS1:DES1:FET3:ERG251:orf
0.00%	orf19.163:orf19.2286:MET6:SLD1:MET13:ERG25:HIS1:DES1:FET3:ERG251:orf
0.00%	orf19.163:orf19.2286:URA2:MET6:SLD1:MET13:ACH1:ERG25:HIS1:DES1:ERG
0.00%	orf19.163:orf19.2286:URA2:MET6:SLD1:MET13:ACH1:ERG25:HIS1:DES1:ERG
0.00%	orf19.163:orf19.2286:URA2:MET6:SLD1:MET13:ACH1:ERG25:HIS1:DES1:ERG
0.00%	SLD1:ERG25:DES1:FET3:ERG251:ERG3
0.00%	PDR16:HMG1:ERG7:ERG10:ERG24:orf19.163:ERG6:URA3:IMH3:orf19.2286:UF
0.00%	PDR16:HMG1:ERG24:ERG6:IMH3:ERG27:UPC2:ERG1:FET3:TPO4:ERG2:orf19
0.00%	SLD1:ERG25:DES1:ERG1:FET3:ERG251:ERG3
0.00%	SLD1:ACH1:ERG25:DES1:ERG1:FET3:ERG251:ERG3
0.07%	PDR16:HMG1:ERG7:ERG10:ERG24:orf19.163:ERG6:URA3:IMH3:orf19.2286:UF
0.06%	HMG1:SLD1:ERG25:DES1:ERG1:FET3:ERG251:LRO1:MVD:ERG13:ERG3
0.19%	HMG1:ERG7:ERG10:ERG24:orf19.163:ERG6:URA3:IMH3:orf19.2286:URA2:ME
0.18%	orf19.163:orf19.2286:orf19.6057:SAM2
0.29%	orf19.163:URA3:IMH3:orf19.2286:URA2:MET6:THI6:MET13:HIS1:orf19.6057:SA
0.40%	HMG1:RBT1:ECM3:ERG7:ERG10:ERG24:orf19.163:ERG6:URA3:IMH3:orf19.22
0.44%	PDR16:HMG1:ERG24:ERG6:IMH3:ERG27:UPC2:ERG1:FET3:TPO4:ERG2:YPS

0.49% orf19.163:orf19.2286:orf19.6057:SAM2
0.68% orf19.163:orf19.2286:MET6:MET13:HIS1:orf19.6057:SAM2
0.67% HMG1:MVD:ERG13
0.65% HMG1:MVD:ERG13
0.68% orf19.163:orf19.2286:MET6:MET13:HIS1:orf19.6057:SAM2
0.76% CTR1:orf19.7077

ERG5:ERG4:ERG2:MVD:CYB5:ERG13:ERG3:ERG11
ERG5:ERG4:ERG2:MVD:CYB5:ERG13:ERG3:ERG11
ERG5:ERG4:ERG2:MVD:CYB5:ERG13:ERG3:ERG11
ERG5:ERG4:ERG2:MVD:CYB5:ERG13:ERG3:ERG11
RG2:CYB5:ERG13:ERG3:ERG11
RG2:CYB5:ERG13:ERG3:ERG11
RG2:CYB5:ERG13:ERG3:ERG11
RG2:CYB5:ERG13:ERG3:ERG11
RG2:CYB5:ERG13:ERG3:ERG11
RG2:CYB5:ERG13:ERG3:ERG11
DES1:ERG1:FET3:ERG251:ERG5:ERG4:LRO1:ERG2:MVD:CYB5:ERG13:ERG3:ERG11
G27:ERG9:ERG25:UPC2:HIS1:DES1:ERG1:FET3:ERG251:ERG5:ERG4:ERG2:orf19.6057:SAM2:CYB5:EF
RA2:MET6:SLD1:orf19.276:THI6:MET13:ACH1:ERG27:ERG9:ERG25:UPC2:SAH1:HIS1:DES1:ERG1:FET3:
RG2:CYB5:ERG13:ERG3:ERG11
DES1:ERG1:FET3:ERG251:orf19.4982:ERG5:ERG4:LRO1:ERG2:MVD:CYB5:ERG13:ERG3:ERG11
C2:ERG1:ERG5:ERG4:ERG2:MVD:CYB5:ERG13:ERG3:ERG11
RA2:MET6:SLD1:THI6:MET13:RPP1A:ERG27:ERG9:ERG25:UPC2:HIS1:DES1:ERG1:FET3:ERG251:ERG
T6:SLD1:THI6:MET13:RPP1A:ERG27:ERG9:ERG25:UPC2:HIS1:DES1:ERG1:FET3:ERG251:ERG5:ERG4
19.6057:SAM2:ERG3
19.6057:SAM2:ERG3
1:FET3:ERG251:orf19.6057:SAM2:ERG3
1:FET3:ERG251:orf19.6057:SAM2:ERG3
1:FET3:ERG251:orf19.6057:SAM2:ERG3
1:FET3:ERG251:orf19.6057:SAM2:ERG3

RA2:MET6:SLD1:orf19.276:THI6:MET13:RPP1A:ACH1:ERG27:ERG9:ERG25:UPC2:SAH1:HIS1:DES1:ER
)7197:ERG13:ERG3:ERG11

RA2:MET6:SLD1:MET13:RPP1A:ERG27:ERG9:ERG25:UPC2:HIS1:DES1:ERG1:FET3:ERG251:orf19.4736

T6:SLD1:THI6:MET13:RPP1A:ACH1:ERG27:ERG9:ERG25:UPC2:SAH1:HIS1:DES1:ERG1:FET3:ERG251

M2
86:URA2:MET6:SLD1:THI6:MET13:RPP1A:ACH1:ERG27:orf19.3547:ERG9:CTR1:ERG25:UPC2:SAH1:HI
7:orf19.7197:ERG13:ERG3:ERG11

RG13:ERG3:ERG11

3:ERG251:ERG5:ERG4:LRO1:ERG2:orf19.6057:MVD:SAM2:CYB5:ERG13:ERG3:ERG11

5:ERG4:LRO1:ERG2:orf19.6057:MVD:RPS27:SAM2:CYB5:RPP1B:orf19.7197:ERG13:ERG3:ERG11

1:LRO1:ERG2:orf19.6057:MVD:RPS27:SAM2:CYB5:RPP1B:orf19.7197:ERG13:ERG3:ERG11

G1:FET3:ERG251:orf19.4738:orf19.4982:ERG5:ERG4:LRO1:ERG2:orf19.6057:MVD:SEC61:RPS27:YPS7:

3:orf19.4982:ERG5:ERG4:LRO1:ERG2:orf19.6057:MVD:SEC61:RPS27:YPS7:SAM2:CYB5:RPP1B:orf19.7:

:orf19.4738:ERG5:ERG4:LRO1:ERG2:orf19.6057:MVD:SEC61:RPS27:SAM2:CYB5:RPP1B:orf19.7197:SE

S1:DES1:ERG1:FET3:HXT5:ERG251:HGT17:TPO4:orf19.4738:ERG5:ERG4:LRO1:ERG2:orf19.6057:MVD

:SAM2:CYB5:orf19.7077:RPP1B:orf19.7197:SET3:ERG13:ERG3:ERG11

197:SET3:ERG13:ERG3:ERG11

T3:ERG13:ERG3:ERG11

:SEC61:RPS27:YPS7:SAM2:CYB5:orf19.7077:RPP1B:orf19.7197:SET3:ERG13:ERG3:ERG11

Additional file 14B - GO term enrichment analysis of genes down-regulated in a up

Legend

GOID Gene ontology Identifier
 GO_term Gene ontology term description
 terms in differentially expressed genes Cluster Frequency of the set of genes tested
 frequency of GO terms in entire dataset Cluster Frequency of the gene background genome that are annotated to that GO Term.
 Corrected P_value rate correction for multiple-testing
 Gene(s) annotated to the term List of genes annotated to each single GO term

GOID	GO_term	frequency of GO terms in differentially expressed genes	frequency of GO terms in entire dataset	Corrected P-value
15691	cadmium ion transpo	2 out of 36 genes, 5	2 out of 5214 backg	0.0075

c2 deletion in the RNA-seq experiment.

False discovery rate	Gene(s) annotated to the term
0.00%	SMF12:CRP1