

Table 1. Gene Ontology (GO) classes overrepresented ($P < 0.01$) in the differentially regulated gene lists for treatments with compounds A and B

Overrepresented	GO class	GO class annotation	No. genes*	<i>P</i> value (A)	No. genes*	<i>P</i> value (B)
A and B	GO:0009408	Response to heat	11 (10)	3.25E-14	3 (18)	7.52E-04
	GO:0004364	Glutathione transferase activity	8 (38)	1.96E-07	7 (39)	1.29E-07
	GO:0003700	Transcription factor activity	45 (1,432)	4.52E-07	25 (1,452)	9.75E-04
	GO:0004009	ATP-binding cassette (ABC) transporter activity	11 (110)	9.42E-07	7 (114)	8.85E-05
	GO:0009877	Nodulation	9 (80)	3.84E-06	5 (84)	1.05E-03
	GO:0015706	Nitrate transport	9 (81)	4.22E-06	5 (85)	1.11E-03
	GO:0006824	Cobalt ion transport	9(82)	4.62E-06	5 (86)	1.16E-03
	GO:0008194	UDP-glycosyltransferase activity	9 (83)	5.06E-06	8 (84)	1.34E-06
	GO:0019866	Inner membrane	9 (86)	6.61E-06	5 (90)	1.41E-03
	GO:0017004	Cytochrome biogenesis	9 (90)	9.28E-06	5 (94)	1.69E-03
	GO:0015846	Polyamine transport	8 (79)	2.69E-05	5 (82)	9.50E-04
	GO:0015833	Peptide transport	6 (44)	6.20E-05	5 (45)	7.05E-05
	GO:0006865	Amino acid transport	9 (127)	1.15E-04	5 (131)	6.60E-03
	GO:0009376	HslUV protease complex	2 (2)	1.11E-03	2 (2)	4.40E-04
	GO:0006979	Response to oxidative stress	6 (90)	2.14E-03	5 (91)	1.48E-03
	GO:0016651	Oxidoreductase activity, acting on NADH or NADPH	3 (17)	2.48E-03	3 (17)	6.48E-04
A	GO:0003773	Heat shock protein activity	14 (31)	-5.68E-14	2 (43)	5.76E-02
	GO:0016621	Cinnamoyl-CoA reductase activity	3 (7)	2.89E-04	1 (9)	8.31E-02
	GO:0004219	Pyroglutamyl-peptidase I activity	2 (1)	5.62E-04	0 (3)	NA
	GO:0006810	Transport	18 (574)	1.54E-03	11 (581)	1.41E-02
	GO:0008270	Zinc ion binding	16 (493)	1.98E-03	9 (500)	3.32E-02
	GO:0006457	Protein folding	9 (197)	2.30E-03	2 (204)	5.33E-01
	GO:0009094	L-phenylalanine biosynthesis	2 (4)	2.73E-03	0 (6)	NA
	GO:0004664	Prephenate dehydratase activity	2 (4)	2.73E-03	0 (6)	NA
	GO:0006355	Regulation of transcription, DNA-dependent	28 (1,146)	3.47E-03	16 (1,158)	4.82E-02

Overrepresented	GO class	GO class annotation	No. genes*	P value (A)	No. genes*	P value (B)
	GO:0016758	Transferase activity, transferring hexosyl groups	5 (69)	3.56E-03	3 (71)	2.63E-02
	GO:0016563	Transcriptional activator activity	3 (22)	4.75E-03	2 (23)	1.95E-02
	GO:0009723	Response to ethylene stimulus	2 (7)	6.38E-03	0 (9)	NA
	GO:0005515	Protein binding	15 (512)	6.70E-03	6 (521)	3.04E-01
	GO:0005829	Cytosol	3 (26)	7.25E-03	1 (28)	2.22E-01
B	GO:0016757	Transferase activity, transferring glycosyl groups	10 (302)	1.17E-02	9 (303)	1.62E-03
	GO:0016021	Integral to membrane	14 (622)	5.83E-02	13 (623)	3.66E-03
	GO:0007275	Development	5 (117)	2.70E-02	5 (117)	4.18E-03
	GO:0004564	Beta-fructofuranosidase activity	0 (13)	NA	2 (11)	5.43E-03
	GO:0006400	tRNA modification	2 (11)	1.33E-02	2 (11)	5.43E-03
	GO:0004788	Thiamin diphosphokinase activity	1 (0)	1.38E-02	1 (0)	8.63E-03
	GO:0006772	Thiamin metabolism	1 (0)	1.38E-02	1 (0)	8.63E-03
	GO:0008559	Xenobiotic-transporting ATPase activity	1 (0)	1.38E-02	1 (0)	8.63E-03

NA, not available.

* Number of differentially regulated genes within this GO class (number of genes within this class that are not differentially regulated).