

Table 11. Functional categorization of cluster II using BiNGO

GO-ID	p-value	corr p-value	# selected	Genes in test set	# total	Description
6951	1.15E-22	2.55E-20	17	75	75	response to heat
9266	2.25E-17	2.48E-15	19	209	209	response to temperature stimulus
6950	6.22E-17	4.58E-15	31	823	823	response to stress
6457	2.23E-11	1.23E-09	13	165	165	protein folding
50896	1.21E-10	5.33E-09	35	1792	1792	response to stimulus
9628	3.80E-10	1.40E-08	28	1210	1210	response to abiotic stimulus
9615	1.70E-06	5.37E-05	4	15	15	response to virus
51707	6.01E-05	1.59E-03	10	354	354	response to other organism
9613	6.47E-05	1.59E-03	9	287	287	response to pest, pathogen or parasite
6118	8.45E-05	1.87E-03	8	231	231	electron transport
19538	1.42E-04	2.86E-03	22	1559	1559	protein metabolism
44267	2.69E-04	4.70E-03	21	1516	1516	cellular protein metabolism
6091	2.76E-04	4.70E-03	9	348	348	generation of precursor metabolites and energy
44237	3.21E-04	5.06E-03	43	4407	4407	cellular metabolism
44260	4.96E-04	7.30E-03	21	1586	1586	cellular macromolecule metabolism
8152	1.02E-03	1.41E-02	44	4783	4783	metabolism
9607	1.31E-03	1.70E-02	11	615	615	response to biotic stimulus
43170	1.51E-03	1.85E-02	25	2225	2225	macromolecule metabolism
8151	1.67E-03	1.94E-02	50	5803	5803	cellular physiological process
9404	2.45E-03	2.57E-02	3	44	44	toxin metabolism
9407	2.45E-03	2.57E-02	3	44	44	toxin catabolism
9626	4.20E-03	4.22E-02	2	16	16	hypersensitive response
9987	4.81E-03	4.62E-02	50	6065	6065	cellular process
9636	5.10E-03	4.70E-02	3	57	57	response to toxin
7582	6.02E-03	4.83E-02	51	6283	6283	physiological process
51131	6.11E-03	4.83E-02	1	1	1	chaperone-mediated protein complex assembly
9413	6.11E-03	4.83E-02	1	1	1	response to flooding
43335	6.11E-03	4.83E-02	1	1	1	protein unfolding

Parameters

File created with BiNGO (c) on 23-nov-2006 at 9:49:26

ontology: process

curator: GO

Selected ontology file : R:\Mol-Bio\cytoscape_2.3.2\plugins\BiNGO\GO_Biological_Process

Selected annotation file : R:\Mol-Bio\Cytoscape_2.3.2\plugins\BiNGO\A_thaliana_ATH1_ORF_TAIR_230606

Overrepresentation

Selected statistical test : Hypergeometric test

Selected correction : Benjamini & Hochberg False Discovery Rate (FDR) correction

Selected significance level : 0.05

Testing option : Test cluster versus complete annotation

Number of genes selected : 95

Total number of genes in annotation : 15538