

Table 10. Functional categorization of cluster I using BiNGO

GO-ID	p-value	corr p-value	# selected	Genes in test set	# total	Description
7582	2.56E-05	3.68E-03	44	6283		physiological process
8151	6.19E-05	3.68E-03	41	5803		cellular physiological process
9987	7.42E-05	3.68E-03	42	6065		cellular process
8152	7.61E-05	3.68E-03	36	4783		metabolism
9156	1.82E-04	3.68E-03	2	5		ribonucleoside monophosphate biosynthesis
9161	1.82E-04	3.68E-03	2	5		ribonucleoside monophosphate metabolism
9168	1.82E-04	3.68E-03	2	5		purine ribonucleoside monophosphate biosynthesis
9167	1.82E-04	3.68E-03	2	5		purine ribonucleoside monophosphate metabolism
9127	1.82E-04	3.68E-03	2	5		purine nucleoside monophosphate biosynthesis
9126	1.82E-04	3.68E-03	2	5		purine nucleoside monophosphate metabolism
9124	1.82E-04	3.68E-03	2	5		nucleoside monophosphate biosynthesis
9123	1.82E-04	3.68E-03	2	5		nucleoside monophosphate metabolism
44237	2.32E-04	4.33E-03	33	4407		cellular metabolism
44249	2.61E-04	4.53E-03	14	1125		cellular biosynthesis
9926	3.81E-04	5.79E-03	3	33		auxin polar transport
9914	3.81E-04	5.79E-03	3	33		hormone transport
6979	4.49E-04	6.42E-03	4	83		response to oxidative stress
6091	7.30E-04	9.57E-03	7	348		generation of precursor metabolites and energy
6800	7.49E-04	9.57E-03	4	95		oxygen and reactive oxygen species metabolism
9058	8.44E-04	9.88E-03	14	1264		biosynthesis
9404	8.94E-04	9.88E-03	3	44		toxin metabolism
9407	8.94E-04	9.88E-03	3	44		toxin catabolism
50896	1.25E-03	1.32E-02	17	1792		response to stimulus
9636	1.90E-03	1.92E-02	3	57		response to toxin
9260	2.39E-03	2.15E-02	2	17		ribonucleotide biosynthesis
9150	2.39E-03	2.15E-02	2	17		purine ribonucleotide metabolism
9152	2.39E-03	2.15E-02	2	17		purine ribonucleotide biosynthesis
9259	2.68E-03	2.33E-02	2	18		ribonucleotide metabolism
6810	3.07E-03	2.48E-02	12	1135		transport
6163	3.31E-03	2.48E-02	2	20		purine nucleotide metabolism
6164	3.31E-03	2.48E-02	2	20		purine nucleotide biosynthesis
51234	3.37E-03	2.48E-02	12	1148		establishment of localization
51179	3.37E-03	2.48E-02	12	1148		localization
6188	4.31E-03	2.91E-02	1	1		IMP biosynthesis
46040	4.31E-03	2.91E-02	1	1		IMP metabolism
6189	4.31E-03	2.91E-02	1	1		'de novo' IMP biosynthesis
42364	5.15E-03	3.39E-02	2	25		water-soluble vitamin biosynthesis
42221	6.63E-03	4.24E-02	9	791		response to chemical stimulus
9165	6.90E-03	4.30E-02	2	29		nucleotide biosynthesis
15980	7.10E-03	4.32E-02	3	91		energy derivation by oxidation of organic compounds
6950	8.52E-03	4.65E-02	9	823		response to stress
6207	8.61E-03	4.65E-02	1	2		'de novo' pyrimidine base biosynthesis
6206	8.61E-03	4.65E-02	1	2		pyrimidine base metabolism
19856	8.61E-03	4.65E-02	1	2		pyrimidine base biosynthesis
8535	8.61E-03	4.65E-02	1	2		cytochrome c oxidase complex assembly
9110	9.40E-03	4.97E-02	2	34		vitamin biosynthesis

Parameters

File created with BiNGO (c) on 23-nov-2006 at 9:40:37

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 : 67

Total number of genes in annotation : 15538