TABLE I

Significant Unique GO Terms (Gene Clusters) Generated by Only Proposed Algorithm

Ontology	Data Sets	Cluster	GO Term / Gene Cluster	P-Value	FDR (%)
Molecular Function	GDS608	8	catalytic activity	2.66E-002	0.00
		17	DNA binding	1.12E-002	6.00
		18	alpha,alpha-trehalose-phosphate synthase (UDP-forming) activity	1.31E-002	2.00
	GDS1013	8	structural constituent of cell wall	1.28E-003	0.00
		15	structural constituent of cell wall	1.01E-002	12.00
	GDS2003	1	transcription regulator activity	3.22E-013	0.00
		6	transferase activity	2.28E-003	0.00
		8	succinate dehydrogenase activity	8.46E-004	0.00
		10	carbon-carbon lyase activity	5.40E-003	12.00
		12	fructose transmembrane transporter activity	2.06E-005	0.00
		13	copper ion binding	1.05E-002	6.00
		23	heme binding	7.27E-005	0.00
	GDS2267	1	actin binding	3.24E-003	0.00
		5	carnitine O-acetyltransferase activity	1.53E-005	0.00
		8	unfolded protein binding	5.66E-004	0.00
		12	hydrolase activity, hydrolyzing O-glycosyl compounds	1.85E-005	0.00
	GDS2712	6	pyrophosphatase activity	7.64E-004	0.00
		11	ubiquitin protein ligase binding	4.28E-002	22.00
		15	pattern binding	9.39E-004	0.00
	GDS2713	5	protein kinase activity	3.74E-002	1.00
		7	nucleoside-triphosphatase activity	3.33E-003	1.00
	GDS2715	1	transcription regulator activity	1.62E-003	0.00
		3	aminoacyl-tRNA ligase activity	7.70E-010	0.00
		4	protein serine/threonine kinase activity	2.67E-003	0.00
		7	monovalent inorganic cation transmembrane transporter activity	5.48E-005	0.00
		14	fructose-2,6-bisphosphate 2-phosphatase activity	8.15E-003	1.00
Biological Process	GDS608	7	cellular transcription	4.03E-002	3.00
		10	proline catabolic process	1.64E-002	7.00
		18	response to temperature stimulus	9.19E-004	0.00
	GDS1013	3	oxidative phosphorylation	6.68E-014	0.00
		4	ribosome biogenesis	4.65E-007	0.00
		13	rRNA export from nucleus	1.43E-004	0.00
		15	pyruvate metabolic process	2.07E-005	0.00
	GDS2003	1	cellular component organization	8.47E-046	0.00
		3	interphase of mitotic cell cycle	2.16E-003	0.00
		8	tricarboxylic acid cycle	2.61E-002	12.00
		9	de novo' IMP biosynthetic process	1.48E-010	0.00
		11	electron transport chain	1.65E-015	0.00
		12	hexose transport	4.76E-008	0.00
		21	alcohol biosynthetic process	9.56E-004	0.00
	GDS2196	15	ribosomal subunit assembly	1.67E-003	0.00
	GDS2267	3	regulation of pH	4.97E-002	22.00
		5	organic acid catabolic process	2.57E-010	0.00
		7	snRNA pseudouridine synthesis	1.66E-004	0.00
		9	cellular amino acid biosynthetic process	7.50E-012	0.00
		12	cytokinesis, completion of separation	1.96E-004	0.00
	GDS2712	13	nucleoside phosphate metabolic process	1.42E-003	0.00
		14	pyruvate metabolic process	9.71E-005	0.00
	GDS2713	12	carboxylic acid metabolic process	3.37E-009	0.00
	GDS2715	5	small molecule metabolic process	1.04E-005	0.00
		6	oxidation reduction	1.46E-004	0.00
		11	cell adhesion	2.04E-003	6.00
		13	positive regulation of cellular transcription	8.82E-003	6.00
Cellular Component	GDS608	1	integral to membrane	2.65E-011	0.00
		18	alpha,alpha-trehalose-phosphate synthase complex (UDP-forming)	1.31E-002	6.00
		21	CCAAT-binding factor complex	2.77E-003	2.00
	GDS1013	15	fungal-type cell wall	2.73E-005	0.00
	GDS2003	11	mitochondrial respiratory chain	2.80E-020	0.00
		12	plasma membrane enriched fraction	1.06E-002	4.00
	GDS2267	4	proteasome complex	2.31E-016	0.00
		6	mitochondrial matrix	2.72E-007	0.00
		10	lipid particle	2.00E-003	0.00
		12	extracellular region	1.70E-004	0.00
	GDS2712	9	mitochondrion	5.56E-004	0.00
		15	fungal-type cell wall	3.20E-003	4.00
	GDS2713	1	organellar large ribosomal subunit	6.28E-004	0.00
		7	cytosolic proteasome complex	4.64E-003	1.00
	GDS2715	1	endomembrane system	5.50E-005	0.00
		7	mitochondrial respiratory chain	3.09E-004	0.00
		13	nuclear nucleosome	1.57E-002	2.00