Table S1. Significantly enriched DAVID terms (BH-adjusted *p*-val < 0.05) for post-filtering biclusters.

Metabolic biclusters

	Categories	Term	Count	%	BH-adjusted *p*-val
B1	GOTERM_BP_3	response to wounding	32	26.20	3.10E-16
	GOTERM_BP_3	chemotaxis	15	12.30	6.90E-09
	PANTHER_BP_ALL	Immunity and defense	37	30.3	9.70E-10
B3		*No enrichment*			
B4	GOTERM CC2	cell fraction	22	13.40	1.80E-03
	GOTERM CC3	membrane fraction	18	11.00	1.60E-02
	GOTERM CC4	vesicular fraction	10	6.10	7.20E-03
	GOTERM CC4	membrane fraction	18	11.00	2.20E-02
	GOTERM CC5	microsome	10	6.10	6.90E-03
	GOTERM CC5	vesicular fraction	10	6.10	4.30E-03
	GOTERM_MF_3	transferase activity, transferring glycosyl groups	12	7.30	7.20E-03
	GOTERM_MF_4	UDP-glycosyltransferase activity	11	6.70	1.70E-05
	GOTERM_MF_4	transferase activity, transferring hexosyl groups	11	6.70	1.00E-03
	GOTERM_MF_5	glucuronosyltransferase activity	10	6.10	7.10E-10
	PANTHER_BP	Carbohydrate metabolism	15	9.10	2.80E-03
	PANTHER_BP	Immunity and defense	23	14.00	4.40E-02
	PANTHER_BP	G-protein mediated signaling	38	23.20	4.10E-02
	PANTHER_MF_ALL	Glycosyltransferase	25	15.00	6.20E-05
	PANTHER_MF_ALL	Nucleic acid binding	68	41.50	1.10E-02
B5		*No enrichment*			
B6		*No enrichment*			

B8	GOTERM BP_3	circulatory system process	6	14.3	3.50E-02
B9	GOTERM BP_1	developmental process	16	39.00	3.30E-02
	GOTERM BP_1	multicellular organismal process	17	41.50	2.40E-02
	GOTERM BP_1	biological regulation	20	48.80	3.30E-02
B11		*No enrichment*			
B13		*No enrichment*			
B14	GOTERM_BP_1	developmental process	13	40.60	4.10E-02
B15		*No enrichment*			

Neuronal biclusters

	Categories	**Term**	**Count**	**%**	**BH-adjusted *p*-val**
B1	GOTERM_BP_2	anatomical structure development	55	17.57	2.67E-04
	GOTERM_BP_2	multicellular organismal development	57	18.21	7.26E-04
	GOTERM_BP_2	multicellular organismal development	36	11.50	2.20E-03
	GOTERM_BP_2	multicellular organismal development	46	14.70	5.30E-03
	GOTERM_BP_2	multicellular organismal development	31	9.90	3.70E-02
	GOTERM_BP_3	axon ensheathment	8	2.56	3.53E-04
	GOTERM_BP_3	regulation of action potential	8	2.56	7.43E-04
	GOTERM_BP_3	system development	50	15.97	7.62E-04
	GOTERM_BP_3	neurogenesis	18	5.75	5.10E-03
	GOTERM_BP_3	cell differentiation	46	14.70	2.90E-02
	GOTERM_BP_3	cell-cell signaling	16	5.11	3.90E-02
	GOTERM_BP_4	nervous system development	33	10.54	5.47E-06

	GOTERM_BP_4	ensheathment of neurons	8	2.56	4.44E-04
	GOTERM_BP_4	myelination	7	2.24	3.60E-03
	GOTERM_BP_4	cell development	36	11.50	4.20E-02
B2	GOTERM_BP_3	neuron projection development	14	4.7	2.60E-03
	GOTERM_BP_3	cell motion	19	6.3	4.30E-03
	GOTERM_MF_3	diacylglycerol binding	9	3	2.00E-04
	GOTERM_MF_3	calmodulin binding	11	3.7	9.40E-06
	PANTHER_BP_ALL	Synaptic transmission	20	8.90E-09	1.20E-06
	PANTHER_BP_ALL	Developmental processes	59	19.7	2.20E-05
B3	GOTERM_BP_1	developmental process	92	24.40	7.60E-07
	GOTERM_BP_1	biological adhesion	27	7.16	1.20E-03
	GOTERM_BP_1	establishment of localization	67	17.77	1.20E-02
	GOTERM_BP_1	localization	80	21.22	9.85E-04
	GOTERM_BP_2	death	26	6.90	2.63E-02
	GOTERM_BP_2	multicellular organismal development	65	17.24	2.76E-03
	GOTERM_BP_2	ensheathment of neurons	5	1.33	4.62E-02
	GOTERM_BP_2	cellular developmental process	58	15.38	8.19E-04
	GOTERM_BP_2	cell adhesion	27	7.16	5.75E-03
	GOTERM_BP_2	anatomical structure development	68	18.04	4.79E-05
	GOTERM_BP_2	cell development	45	11.94	4.26E-04
	GOTERM_BP_2	transport	66	17.51	3.89E-02
	GOTERM_BP_2	anatomical structure morphogenesis	38	10.08	1.43E-02
	GOTERM_BP_2	cell proliferation	20	5.31	4.83E-02
	GOTERM_BP_2	establishment of localization	67	17.77	4.26E-02
	GOTERM_BP_3	cell differentiation	58	15.40	1.60E-02

GOTERM_BP_4	cell development	45	11.90	9.40E-03
GOTERM_CC_1	extracellular matrix	14	3.71	1.56E-02
GOTERM_CC_1	extracellular region	81	21.49	7.02E-08
GOTERM_CC_1	extracellular region part	76	20.16	7.00E-08
GOTERM_CC_2	extracellular region part	76	20.16	4.90E-07
GOTERM_CC_2	extracellular space	70	18.57	2.91E-06
GOTERM_CC_2	membrane	168	44.56	1.09E-02
GOTERM_CC_2	proteinaceous extracellular matrix	14	3.71	4.00E-02
GOTERM_CC_3	extracellular space	70	18.57	2.71E-05
GOTERM_CC_3	plasma membrane	65	17.24	1.90E-03
GOTERM_CC_3	membrane	168	44.56	4.98E-02
GOTERM_CC_4	plasma membrane	65	17.20	2.80E-03
GOTERM_MF_1	motor activity	9	2.39	4.71E-02
GOTERM_MF_1	binding	219	58.09	3.23E-02
GOTERM_MF_1	structural molecule activity	23	6.10	2.74E-02
GOTERM_MF_2	lipid binding	19	5.00	2.70E-02
PANTHER_BP_ALL	Cell structure and motility	58	15.38	1.81E-10
PANTHER_BP_ALL	Cell structure	88	23.34	2.61E-07
PANTHER_BP_ALL	Lipid, fatty acid and steroid metabolism	31	8.22	4.16E-04
PANTHER_BP_ALL	Signal transduction	88	23.34	4.75E-03
PANTHER_BP_ALL	Protein disulfide-isomerase reaction	19	5.04	7.70E-03
PANTHER_BP_ALL	mRNA transcription regulation	169	44.83	1.54E-02
PANTHER_BP_ALL	Neuronal activities	13	3.45	2.79E-02
PANTHER_BP_ALL	Developmental processes	45	11.94	2.96E-02

	PANTHER_BP_ALL	Cell communication	24	6.37	3.07E-02
	PANTHER_BP_ALL	Receptor mediated endocytosis	15	3.98	3.38E-02
	PANTHER_BP_ALL	Intracellular signaling cascade	25	6.63	3.95E-02
	PANTHER_BP_ALL	Amino acid biosynthesis	15	3.98	4.36E-02
	PANTHER_BP_ALL	Protein modification	57	15.12	4.42E-02
	PANTHER_BP_ALL	Vitamin biosynthesis	8	2.12	4.58E-02
	PANTHER_MF_ALL	Cytoskeletal protein	33	8.75	1.01E-05
	PANTHER_MF_ALL	Cell junction protein	15	3.98	1.35E-03
	PANTHER_MF_ALL	Actin binding cytoskeletal protein	39	10.34	5.28E-03
	PANTHER_MF_ALL	Other receptor	22	5.84	7.27E-03
	PANTHER_MF_ALL	Non-motor actin binding protein	60	15.92	7.85E-03
	PANTHER_MF_ALL	Signaling molecule	23	6.10	9.85E-03
	PANTHER_MF_ALL	Other G-protein modulator	63	16.71	1.55E-02
	PANTHER_MF_ALL	Membrane-bound signaling molecule	9	2.39	2.90E-02
	PANTHER_MF_ALL	Non-receptor serine/threonine protein kinase	86	22.81	3.32E-02
	PANTHER_MF_ALL	Other cell junction protein	11	2.92	3.48E-02
	PANTHER_MF_ALL	Protein kinase	38	10.08	4.08E-02
	PANTHER_MF_ALL	Cadherin	15	3.98	4.21E-02
	PANTHER_MF_ALL	Non-motor microtubule binding protein	29	7.69	4.26E-02
	PANTHER_MF_ALL	Guanyl-nucleotide exchange factor	48	12.73	4.76E-02
B4	GOTERM_BP_1	metabolic process	100	42.40	3.10E-03
	GOTERM_BP_3	cellular lipid metabolic process	18	7.60	2.90E-02
	GOTERM_CC_1	organelle	96	40.70	4.20E-02
	GOTERM_CC_2	intracellular part	116	49.20	1.00E-02
	GOTERM_CC_2	intracellular	119	50.40	2.10E-02
	GOTERM_CC_3	cytoplasm	89	37.70	5.10E-04

	GOTERM_CC_3	cytoplasmic part	57	24.20	1.30E-02
	GOTERM_CC_3	intracellular part	116	49.20	1.60E-02
	GOTERM_CC_4	cytoplasm	89	37.70	1.10E-02
	GOTERM_CC_5	cytoplasm	89	37.70	1.30E-02
	PANTHER_BP_ALL	Lipid, fatty acid and steroid metabolism	23	9.70	8.00E-04
	PANTHER_BP_ALL	Protein phosphorylation	41	17.40	4.70E-04
	PANTHER_BP_ALL	mRNA transcription regulation	107	45.30	2.40E-02
	PANTHER_MF_ALL	Actin binding cytoskeletal protein	26	11.02	1.90E-02
	PANTHER_MF_ALL	Actin and actin related protein	18	7.63	2.00E-02
	PANTHER_MF_ALL	Transferase	34	14.41	2.00E-02
	PANTHER_MF_ALL	Voltage-gated potassium channel	25	10.59	3.60E-02
	PANTHER_MF_ALL	Non-motor actin binding protein	38	16.10	3.70E-02
B5	GOTERM_CC_3	cytoplasm	70	49.6	1.70E-03
B8	PANTHER_BP_ALL	Intracellular protein traffic	26	10.7	1.80E-02
B9	GOTERM_CC_3	intracellular part	176	60.9	3.70E-04
	PANTHER_BP_ALL	Intracellular protein traffic	29	10	1.40E-02
B12		*No enrichment*			
B14	GOTERM_BP_3	protein localization	29	9.2	4.60E-02
	GOTERM_MF_2	protein binding	129	40.8	6.20E-05
	PANTHER_BP_ALL	Intracellular protein traffic	30	9.5	3.30E-02
B15		*No enrichment*			
B17	GOTERM_MF_3	passive transmembrane transporter activity	8	9.3	3.40E-02
	PANTHER_BP_ALL	Calcium mediated signaling	7	8.1	4.30E-04

B18		*No enrichment*			
B19		*No enrichment*			
B20		*No enrichment*			
B23		*No enrichment*			
B24		*No enrichment*			
B25		*No enrichment*			
B26		*No enrichment*			
B27		*No enrichment*			
B28		*No enrichment*			
B29		*No enrichment*			
B30		*No enrichment*			
B31		*No enrichment*			
B32		*No enrichment*			
B33		*No enrichment*			

Developmental biclusters

	Categories	**Term**	**Count**	**%**	**BH-adjusted *p*-val**
B2	GOTERM_BP_3	reproductive developmental process	23	3.4	2.30E-03
	GOTERM_BP_3	macromolecule catabolic process	40	5.80	6.90E-03
	GOTERM_MF_3	cytoskeletal protein binding	28	4.1	2.70E-02
	GOTERM_MF_4	tubulin binding	12	1.8	5.90E-03

	GOTERM_CC_5	nucleus	186	27.2	2.60E-04
B3	GOTERM_BP_3	system development	126	17.6	9.10E-07
	GOTERM_BP_3	organ morphogenesis	81	11.3	6.70E-07
	GOTERM_BP_3	anatomical structure morphogenesis			
	GOTERM_MF_3	growth factor binding	12	1.7	1.10E-02
	PANTHER_BP_ALL	Developmental processes	107	15	3.40E-02
	PANTHER_MF_ALL	Select calcium binding protein	23	3.2	2.90E-02
B4	GOTERM_BP_1	multi-organism process	16	3.40	6.40E-03
	GOTERM_BP_1	immune system process	34	7.30	5.00E-03
	GOTERM_BP_2	defense response	36	7.80	4.30E-04
	GOTERM_BP_2	response to other organism	15	3.20	1.50E-03
	GOTERM_BP_2	immune response	26	5.60	1.10E-02
	GOTERM_BP_2	response to biotic stimulus	15	3.20	4.40E-02
	GOTERM_BP_2	response to external stimulus	22	4.70	4.70E-02
	GOTERM_BP_3	response to other organism	15	3.20	1.50E-02
	GOTERM_BP_3	lipid metabolic process	30	6.50	3.30E-02
	GOTERM_BP_3	digestive system process	5	1.10	3.00E-02
	GOTERM_BP_3	cellular lipid metabolic process	27	5.80	2.30E-02
	GOTERM_BP_3	inflammatory response	15	3.20	4.10E-02
	GOTERM_BP_3	Lipid transport	13	2.90	3.63E-02
	GOTERM_CC_1	extracellular region	106	22.80	5.10E-12
	GOTERM_CC_1	extracellular region part	91	19.60	1.30E-08
	GOTERM_CC_2	extracellular space	88	19.00	1.30E-08
	GOTERM_CC_2	extracellular region part	91	19.60	1.20E-08

GOTERM_CC_2	apical part of cell	12	2.60	3.50E-05
GOTERM_CC_2	membrane	204	44.00	1.30E-03
GOTERM_CC_3	extracellular space	88	19.00	5.80E-08
GOTERM_CC_3	apical part of cell	12	2.60	2.40E-04
GOTERM_CC_3	membrane	204	44.00	8.30E-03
GOTERM_CC_3	plasma membrane	70	15.10	2.00E-02
GOTERM_CC_4	plasma membrane	70	15.10	1.30E-02
GOTERM_CC_4	integral to membrane	153	33.00	1.70E-02
GOTERM_CC_4	intrinsic to membrane	153	33.00	1.40E-02
GOTERM_CC_4	membrane part	164	35.30	1.10E-02
GOTERM_CC_4	apicolateral plasma membrane	10	2.20	1.80E-02
GOTERM_CC_4	plasma membrane part	54	11.60	3.60E-02
GOTERM_CC_5	integral to membrane	153	33.00	9.00E-03
GOTERM_CC_5	intrinsic to membrane	153	33.00	5.50E-03
GOTERM_CC_5	apical junction complex	10	2.20	2.70E-02
GOTERM_CC_5	apicolateral plasma membrane	10	2.20	2.30E-02
GOTERM_CC_5	plasma membrane part	54	11.60	3.00E-02
GOTERM_CC_5	intercellular junction	12	2.60	3.60E-02
GOTERM_MF_2	lipid binding	21	4.50	2.50E-02
GOTERM_MF_3	receptor binding	29	6.20	4.20E-02
GOTERM_MF_5	chemokine receptor binding	7	1.50	3.20E-02
PANTHER_BP_ALL	Lipid, fatty acid and steroid metabolism	36	7.80	1.20E-03
PANTHER_BP_ALL	Receptor protein tyrosine kinase signaling pathway	22	4.70	1.40E-02

	PANTHER_MF_ALL	Transporter	33	7.10	3.10E-05
	PANTHER_MF_ALL	Signaling molecule	33	7.10	6.50E-05
	PANTHER_MF_ALL	Peptide hormone	23	5.00	4.20E-04
	PANTHER_MF_ALL	Apolipoprotein	19	4.10	7.10E-03
	PANTHER_MF_ALL	Transferase	59	12.70	1.00E-02
	PANTHER_MF_ALL	Chemokine	11	2.40	9.40E-03
B5	GOTERM_BP_3	regulation of primary metabolic process	118	20.2	5.40E-05
	GOTERM_BP_3	reproductive developmental process	21	3.6	2.80E-03
	GOTERM_MF_3	cation binding	149	25.5	1.20E-03
B7		*No enrichment*			
B13	GOTERM_BP_3	cellular nitrogen compound metabolic process	89	22.1	4.00E-02
B17	GOTERM_BP_1	developmental process	85	20.40	9.00E-04
	GOTERM_BP_1	metabolic process	179	42.90	2.80E-03
	GOTERM_BP_1	reproduction	20	4.80	1.30E-02
	GOTERM_BP_1	biological regulation	109	26.10	1.20E-02
	GOTERM_BP_1	reproductive process	12	2.90	2.40E-02
	GOTERM_BP_1	gene expression	77	18.50	3.90E-02
	GOTERM_BP_1	biological adhesion	22	5.30	4.60E-02
	GOTERM_BP_2	multicelular organismal development	72	17.30	4.50E-04
	GOTERM_BP_2	reproductive developmental process	11	2.60	1.50E-03
	GOTERM_BP_2	anatomical structure development	63	15.10	2.50E-03
	GOTERM_BP_2	cellular metabolic process	166	39.80	1.90E-03
	GOTERM_BP_2	cellular developmental process	57	13.70	3.30E-03
	GOTERM_BP_2	cell development	41	9.80	8.20E-03
	GOTERM_BP_2	regulation of cellular process	96	23.00	1.10E-02
	GOTERM_BP_2	primary metabolic process	160	38.40	1.50E-02
	GOTERM_BP_2	regulation of metabolic process	70	16.80	2.70E-02

GOTERM_BP_2	regulation of biological process	101	24.20	2.70E-02
GOTERM_BP_2	embryonic development	19	4.60	3.00E-02
GOTERM_BP_2	anatomical structure morphogenesis	37	8.90	2.90E-02
GOTERM_BP_2	ensheathment of neurons	5	1.20	4.10E-02
GOTERM_BP_3	system development	59	14.15	4.50E-03
GOTERM_BP_3	reproductive developmental process	11	2.64	8.00E-03
GOTERM_BP_3	sex differentiation	10	2.40	1.30E-02
GOTERM_BP_3	cell differentiation	57	13.67	2.20E-02
GOTERM_BP_3	reproductive structure development	8	1.92	2.60E-02
GOTERM_BP_3	male sex differentiation	6	1.44	2.90E-02
GOTERM_BP_3	development of primary sexual characteristics	8	1.92	3.30E-02
GOTERM_BP_5	male gonad development	6	1.40	4.90E-02
GOTERM_CC_2	intracellular part	187	44.80	3.80E-02
GOTERM_MF_1	binding	237	56.80	3.60E-02
GOTERM_MF_1	transcription regulator activity	39	9.40	2.40E-02
PANTHER_BP_ALL	Nucleoside, nucleotide and nucleic acid metabolism	78	18.71	3.40E-03
PANTHER_BP_ALL	Proteolysis	113	27.10	3.80E-03
PANTHER_BP_ALL	mRNA transcription regulation	184	44.12	6.50E-03
PANTHER_BP_ALL	MHCII-mediated immunity	36	8.63	7.50E-03
PANTHER_BP_ALL	Cation transport	85	20.38	9.20E-03
PANTHER_BP_ALL	Ion transport	51	12.23	4.80E-02
PANTHER_MF_ALL	Non-motor actin binding protein	64	15.30	2.70E-02
PANTHER_MF_ALL	Nucleic acid binding	152	36.50	4.40E-02
PANTHER_MF_ALL	Transcription cofactor	21	5.00	3.40E-02

B20	GOTERM_BP_1	metabolic process	162	41.00	5.30E-03
	GOTERM_BP_1	reproduction	19	4.80	1.40E-02
	GOTERM_BP_1	gene expression	72	18.20	3.40E-02
	GOTERM_BP_2	establishment of RNA localization	8	2.03	5.20E-03
	GOTERM_BP_2	cellular metabolic process	151	38.23	8.60E-03
	GOTERM_BP_2	primary metabolic process	147	37.22	1.60E-02
	GOTERM_BP_2	cell cycle	26	6.58	1.90E-02
	GOTERM_BP_2	cell cycle process	23	5.82	2.10E-02
	GOTERM_BP_2	transcription	59	14.94	3.50E-02
	GOTERM_BP_2	macromolecule metabolic process	129	32.66	3.80E-02
	GOTERM_BP_3	biopolymer metabolic process	118	29.87	4.80E-05
	GOTERM_BP_3	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	95	24.05	9.30E-05
	GOTERM_BP_3	cell cycle phase	18	4.56	3.80E-03
	GOTERM_BP_3	RNA localization	8	2.03	1.00E-02
	GOTERM_BP_3	nucleobase, nucleoside, nucleotide and nucleic acid transport	8	2.03	1.30E-02
	GOTERM_BP_3	establishment of RNA localization	8	2.03	1.30E-02
	GOTERM_BP_3	RNA transport	8	2.03	1.30E-02
	GOTERM_BP_3	cell cycle process	23	5.82	3.80E-02
	GOTERM_BP_3	meiotic cell cycle	8	2.03	3.80E-02
	GOTERM_BP_4	mRNA transport	8	2.03	2.50E-02
	GOTERM_BP_4	establishment of RNA localization	8	2.03	2.60E-02
	GOTERM_BP_4	RNA transport	8	2.03	2.60E-02
	GOTERM_BP_4	nucleic acid transport	8	2.03	2.60E-02
	GOTERM_BP_4	nucleobase, nucleoside, nucleotide and nucleic acid transport	8	2.03	2.70E-02
	GOTERM_BP_4	RNA metabolic process	72	18.23	2.80E-02

GOTERM_BP_4	M phase	15	3.80	3.00E-02
GOTERM_BP_4	cell cycle phase	18	4.56	3.20E-02
GOTERM_CC_1	organelle	149	37.70	6.30E-04
GOTERM_CC_2	intracellular	193	48.86	9.90E-08
GOTERM_CC_2	intracellular part	182	46.08	7.80E-07
GOTERM_CC_2	membrane-bound organelle	137	34.68	4.70E-04
GOTERM_CC_2	intracellular organelle	149	37.72	9.10E-04
GOTERM_CC_3	intracellular	193	48.86	4.60E-07
GOTERM_CC_3	intracellular part	182	46.08	3.61E-06
GOTERM_CC_3	intracellular membrane-bound organelle	137	34.68	2.10E-03
GOTERM_CC_3	intracellular organelle	149	37.72	4.20E-03
GOTERM_CC_4	nucleus	113	28.61	3.33E-07
GOTERM_CC_4	intracellular part	182	46.08	3.06E-05
GOTERM_CC_4	intracellular membrane-bound organelle	137	34.68	1.70E-02
GOTERM_CC_4	intracellular organelle	149	37.72	3.50E-02
GOTERM_CC_5	nucleus	113	28.60	4.10E-07
GOTERM_CC_5	intracellular membrane-bound organelle	137	34.70	3.10E-02
GOTERM_MF_1	binding	228	57.70	1.20E-05
GOTERM_MF_2	nucleic acid binding	90	22.80	1.10E-04
GOTERM_MF_2	nucleotide binding	61	15.40	5.90E-04
GOTERM_MF_3	purine nucleotide binding	52	13.16	2.70E-02
GOTERM_MF_3	hydrolase activity, acting on acid anhydrides	24	6.08	2.80E-02
GOTERM_MF_3	ribonucleotide binding	52	13.16	3.00E-02

	GOTERM_MF_3	RNA binding	24	6.08	3.30E-02
	GOTERM_MF_3	DNA binding	55	13.92	4.30E-02
	GOTERM_MF_4	purine ribonucleotide binding	52	13.20	4.50E-02
	GOTERM_MF_4	hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides	24	6.10	3.80E-02
	PANTHER_BP_ALL	Nucleoside, nucleotide and nucleic acid metabolism	97	24.56	7.65E-09
	PANTHER_BP_ALL	mRNA transcription	126	31.90	8.30E-03
	PANTHER_BP_ALL	Ion transport	54	13.67	1.50E-02
	PANTHER_BP_ALL	Cation transport	84	21.27	1.50E-02
	PANTHER_BP_ALL	Cell adhesion-mediated signaling	17	4.30	1.50E-02
	PANTHER_BP_ALL	rRNA metabolism	18	4.56	2.30E-02
	PANTHER_BP_ALL	Protein modification	62	15.70	3.30E-02
	PANTHER_BP_ALL	Cell structure	72	18.23	3.60E-02
	PANTHER_BP_ALL	Sulfur metabolism	21	5.32	4.00E-02
	PANTHER_BP_ALL	Other metabolism	64	16.20	4.40E-02
	PANTHER_MF_ALL	Nucleic acid binding	163	41.27	6.47E-04
	PANTHER_MF_ALL	Actin binding motor protein	34	8.61	6.70E-03
B21	GOTERM_CC_2	intracellular	115	47.10	4.60E-02
	PANTHER_BP_ALL	Ion transport	38	15.60	1.90E-02
	PANTHER_BP_ALL	Cell structure	49	20.10	3.70E-02
	PANTHER_BP_ALL	Nucleoside, nucleotide and nucleic acid metabolism	48	19.70	2.90E-02
	PANTHER_BP_ALL	rRNA metabolism	13	5.30	4.40E-02
	PANTHER_MF_ALL	Non-motor actin binding protein	47	19.30	9.30E-04

B25	*No enrichment*