Article Title: Gene Expression Changes in Spleens and Livers of Tumour-Bearing Mice Suggest Anti-Inflammatory Effects of Oil Palm Phenolics in Delaying Tumour Growth.
Journal Name: Journal of Nutrigenetics and Nutrigenomics.
Author Names: Soon-Sen Leow, Shamala Devi Sekaran, Kalyana Sundram, YewAi Tan, Ravigadevi Sambanthamurthi.
Corresponding Author: Ravigadevi Sambanthamurthi; Malaysian Palm Oil Board, No. 6, Persiaran Institusi, Bandar Baru Bangi, 43000 Kajang, Selangor, Malaysia; E-mail: raviga@mpob.gov.my.

SUPPLEMENTARY MATERIAL 2.

List of GenMAPPs and gene ontologies significantly changed across time in spleens and livers of mice supplemented with OPP (Treatment group versus control group in mice injected with J558 myeloma cells at three time points). Genes classified as up-regulated or down-regulated with time by K-means clustering were analysed separately. All GenMAPPs and gene ontologies identified as significant had Permuted P Values of less than 0.05, Numbers of Genes Changed of more than or equal to 2 and Z Scores of more than 2.

(A) GenMAPPs and gene ontologies significantly changed across time in spleens.

(B) GenMAPPs and gene ontologies significantly changed across time in livers.

A

UP-REGULATED - GENMAPP

No.	MAPP Name	Number Changed	Number Measured	Number on MAPP	Percent Changed	Percent Present	Z Score	Permuted P Value
1	Mm_Ribosomal_Proteins	34	78	80	43.5897	97.5000	6.7320	0.0000
2	Mm_Electron_Transport_Chain	29	66	83	43.9394	79.5181	6.2620	0.0000
3	Mm_mRNA_processing_binding_Reactome	106	426	551	24.8826	77.3140	5.3120	0.0000
4	Mm_RNA_transcription_Reactome	17	40	41	42.5000	97.5610	4.6100	0.0000
5	Mm_Translation_Factors	19	49	50	38.7755	98.0000	4.3920	0.0000
6	Mm_Proteasome_Degradation	25	73	81	34.2466	90.1235	4.3100	0.0000
7	Mm_Ubiquinone_biosynthesis	9	17	43	52.9412	39.5349	4.1760	0.0010
8	Mm_TNF-alpha-NF-kB_NetPath_9	43	166	176	25.9036	94.3182	3.5770	0.0010
9	Mm_DNA_replication_Reactome	14	40	41	35.0000	97.5610	3.3090	0.0030
10	Mm_Unsaturated_Fatty_Acid_Beta_Oxidation_BiGCaT	4	6	6	66.6667	100.0000	3.3970	0.0060
11	Mm_Galactose_metabolism	8	19	46	42.1053	41.3044	3.1230	0.0080
12	Mm_Krebs-TCA_Cycle	10	29	29	34.4828	100.0000	2.7370	0.0080
13	Mm_Fructose_and_mannose_metabolism	10	30	77	33.3333	38.9610	2.6120	0.0100
14	Mm_Mitochondrial_fatty_acid_betaoxidation	6	16	16	37.5000	100.0000	2.3600	0.0220

UP-REGULATED - GENE ONTOLOGY

No.	GO Name	GO Type	Number Changed	Number Measured	Number in GO	Percent Changed	Percent Present	Z Score	Permuted P Value
1	oxidative phosphorylation	P	32	66	97	48.4849	68.0412	8.9960	0.0000
2	cellular biosynthesis	P	210	1016	1277	20.6693	79.5615	8.4770	0.0000
3	intracellular transport	P	144	648	740	22.2222	87.5676	7.9130	0.0000
4	protein localization	P	138	644	714	21.4286	90.1961	7.2600	0.0000
5	nucleotide biosynthesis	P	33	129	155	25.5814	83.2258	4.6360	0.0000
6	glucose catabolism	P	16	57	89	28.0702	64.0449	3.6480	0.0000
7	phosphate metabolism	P	127	790	902	16.0760	87.5832	3.3670	0.0000
8	physiological process	P	1379	9941	11632	13.8718	85.4625	8.6240	0.0000
9	proteasomal ubiquitin-dependent protein catabolism	P	11	20	22	55.0000	90.9091	5.8330	0.0000
10	ribosome biogenesis and assembly	P	33	86	105	38.3721	81.9048	7.4070	0.0000
11	purine nucleotide biosynthesis	P	26	75	96	34.6667	78.1250	5.9340	0.0000
12	ATP biosynthesis	P	18	49	64	36.7347	76.5625	5.2340	0.0000
13	nucleocytoplasmic transport	P	29	117	130	24.7863	90.0000	4.1500	0.0000
14	biosynthesis	P	236	1154	1428	20.4506	80.8123	8.8440	0.0000
15	pentose-phosphate shunt	P	6	8	10	75.0000	80.0000	5.4130	0.0000
16	generation of precursor metabolites and energy	P	111	598	722	18.5619	82.8255	4.8020	0.0000
17	RNA processing	P	88	329	371	26.7477	88.6792	8.1070	0.0000
18	ER-associated protein catabolism	P	7	12	12	58.3333	100.0000	4.8700	0.0000
19	protein catabolism	P	45	190	215	23.6842	88.3721	4.8360	0.0000
20	ribosome biogenesis	P	28	79	84	35.4430	94.0476	6.3020	0.0000
21	vesicle docking during exocytosis	P	9	19	20	47.3684	95.0000	4.6700	0.0000
22	cellular physiological process	P	1318	8916	10403	14.7824	85.7061	11.5850	0.0000
23	mitochondrial electron transport\, NADH to ubiquinone	P	10	14	25	71.4286	56.0000	6.7550	0.0000
24	nucleotide metabolism	P	50	194	236	25.7732	82.2034	5.7800	0.0000
25	protein modification	P	231	1476	1665	15.6504	88.6487	4.1940	0.0000
26	translational initiation	P	22	58	72	37.9310	80.5556	5.9750	0.0000
27	mRNA export from nucleus	P	12	26	32	46.1539	81.2500	5.2760	0.0000
28	regulation of translational initiation	P	12	30	30	40.0000	100.0000	4.6390	0.0000
29	nucleobase\, nucleoside\, nucleotide and nucleic acid metabolism	P	425	2803	3355	15.1623	83.5469	5.2170	0.0000
30	RNA splicing	P	44	144	167	30.5556	86.2276	6.7300	0.0000
31	ATP synthesis coupled proton transport	P	17	45	60	37.7778	75.0000	5.2290	0.0000
32	proton transport	P	21	74	92	28.3784	80.4348	4.2400	0.0000
33	mRNA processing	P	49	173	198	28.3237	87.3737	6.4830	0.0000
34	ER to Golgi vesicle-mediated transport	P	20	53	59	37.7359	89.8305	5.6670	0.0000
35	rRNA processing	P	22	65	70	33.8462	92.8571	5.3200	0.0000
36	vesicle-mediated transport	P	82	379	406	21.6359	93.3498	5.6420	0.0000
37	nuclear mRNA splicing\, via spliceosome	P	36	118	135	30.5085	87.4074	6.0710	0.0000
38	ubiquitin-dependent protein catabolism	P	38	132	149	28.7879	88.5906	5.8190	0.0000
39	regulation of progression through cell cycle	P	70	375	410	18.6667	91.4634	3.8360	0.0000
40	protein folding	P	50	200	227	25.0000	88.1057	5.5340	0.0000
41	intracellular protein transport	P	93	415	463	22.4096	89.6328	6.3990	0.0000
42	metabolism	P	1022	6705	7938	15.2424	84.4671	10.1070	0.0000
43	protein transport	P	133	589	654	22.5806	90.0612	7.8000	0.0000
44	cell cycle	P	115	629	681	18.2830	92.3642	4.7120	0.0000
45	ubiquitin cycle	P	96	437	511	21.9680	85.5186	6.2860	0.0000
46	transport	P	386	2540	2884	15.1969	88.0721	4.9710	0.0000
47	protein biosynthesis	P	146	588	801	24.8299	73.4082	9.4900	0.0000
48	cell death	P	101	603	650	16.7496	92.7692	3.4370	0.0010
49	purine ribonucleoside salvage	P	3	3	3	100.0000	100.0000	4.6350	0.0020
50	protein sumoylation	P	4	6	9	66.6667	66.6667	4.0650	0.0020
51	DNA replication	P	32	145	160	22.0690	90.6250	3.6220	0.0020
52	DNA metabolism	P	92	543	682	16.9429	79.6188	3.3950	0.0030
53	tricarboxylic acid cycle	P	8	24	24	33.3333	100.0000	3.1520	0.0030
54	cell redox homeostasis	P	6	14	16	42.8571	87.5000	3.4930	0.0040
55	chaperone cofactor dependent protein folding	P	5	9	10	55.5556	90.0000	3.9630	0.0040
56	cell division	P	34	168	178	20.2381	94.3820	3.1740	0.0040
57	ameboidal cell migration	P	3	4	4	75.0000	100.0000	3.8270	0.0050
58	Rac protein signal transduction	P	4	7	7	57.1429	100.0000	3.6220	0.0050
59	response to unfolded protein	P	13	46	55	28.2609	83.6364	3.3160	0.0050

60	protein targeting	P	43	227	261	18.9427	86.9732	3.0970	0.0050
61	biological process unknown	P	57	319	357	17.8683	89.3557	3.0910	0.0050
62	apoptotic program	P	14	56	61	25.0000	91.8033	2.9140	0.0060
63	peroxisome organization and biogenesis	P	6	17	18	35.2941	94.4444	2.8980	0.0060
64	DNA-dependent DNA replication	P	16	69	73	23.1884	94.5206	2.7760	0.0060
65	tRNA processing	P	11	38	41	28.9474	92.6829	3.1420	0.0060
66	regulation of cyclin dependent protein kinase activity	P	10	35	40	28.5714	87.5000	2.9470	0.0060
67	apoptosis	P	94	572	617	16.4336	92.7066	3.1090	0.0060
68	RNA catabolism	P	9	28	30	32.1429	93.3333	3.2120	0.0070
69	regulation of translation	P	17	71	76	23.9437	93.4211	3.0110	0.0070
70	regulation of protein biosynthesis	P	30	148	155	20.2703	95.4839	2.9890	0.0070
71	electron transport	P	63	386	461	16.3212	83.7310	2.4690	0.0090
72	intra-Golgi vesicle-mediated transport	P	5	11	12	45.4545	91.6667	3.3590	0.0100
73	spliceosome assembly	P	8	25	30	32.0000	83.3333	3.0130	0.0100
74	chaperonin-mediated tubulin folding	P	2	2	2	100.0000	100.0000	3.7840	0.0110
75	nucleoside metabolism	P	8	27	44	29.6296	61.3636	2.7560	0.0120
76	response to DNA damage stimulus	P	39	223	239	17.4888	93.3054	2.4020	0.0130
77	Golgi organization and biogenesis	P	4	9	9	44.4444	100.0000	2.9460	0.0130
78	aldehyde metabolism	P	4	9	10	44.4444	90.0000	2.9460	0.0140
79	post-Golgi vesicle-mediated transport	P	5	13	16	38.4615	81.2500	2.8830	0.0140
80	DNA repair	P	34	185	198	18.3784	93.4343	2.5560	0.0140
81	copper ion homeostasis	P	3	5	5	60.0000	100.0000	3.2560	0.0150
82	endosome transport	P	9	32	35	28.1250	91.4286	2.7410	0.0150
83	mRNA catabolism\, nonsense-mediated decay	P	5	13	14	38.4615	92.8571	2.8830	0.0160
84	suckling behavior	P	2	2	2	100.0000	100.0000	3.7840	0.0170
85	regulation of Wnt receptor signaling pathway	P	6	18	19	33.3333	94.7368	2.7290	0.0170
86	protein ubiquitination	P	28	147	173	19.0476	84.9711	2.5240	0.0170
87	internal protein amino acid acetylation	P	2	2	2	100.0000	100.0000	3.7840	0.0180
88	ceramide metabolism	P	7	24	24	29.1667	100.0000	2.5290	0.0180
89	snRNA export from nucleus	P	2	2	2	100.0000	100.0000	3.7840	0.0190
90	vesicle transport along microtubule	P	3	5	5	60.0000	100.0000	3.2560	0.0190
91	glycerol-3-phosphate metabolism	P	3	6	8	50.0000	75.0000	2.8200	0.0200
92	microtubule cytoskeleton organization and biogenesis	P	14	62	69	22.5806	89.8551	2.4850	0.0200
93	positive regulation of cytotoxic T cell differentiation	P	2	2	2	100.0000	100.0000	3.7840	0.0210
94	protein desumoylation	P	2	2	2	100.0000	100.0000	3.7840	0.0220
95	small GTPase mediated signal transduction	P	51	305	344	16.7213	88.6628	2.4040	0.0220
96	mitochondrion organization and biogenesis	P	8	30	35	26.6667	85.7143	2.4100	0.0230
97	pyrimidine nucleotide biosynthesis	P	6	19	22	31.5790	86.3636	2.5700	0.0240
98	germ cell migration	P	3	6	6	50.0000	100.0000	2.8200	0.0240
99	translational elongation	P	7	23	28	30.4348	82.1429	2.6610	0.0240
100	phagocytosis\, engulfment	P	4	10	13	40.0000	76.9231	2.6760	0.0270
101	apoptotic mitochondrial changes	P	5	15	16	33.3333	93.7500	2.4910	0.0270
102	endocytosis	P	30	167	181	17.9641	92.2652	2.2630	0.0290
103	establishment and/or maintenance of epithelial cell polarity	P	3	6	6	50.0000	100.0000	2.8200	0.0300
104	fatty acid beta-oxidation	P	6	20	20	30.0000	100.0000	2.4220	0.0300
105	phenylalanyl-tRNA aminoacylation	P	2	3	3	66.6667	100.0000	2.8740	0.0330
106	chromatin remodeling	P	11	48	52	22.9167	92.3077	2.2560	0.0330
107	cell proliferation	P	92	609	648	15.1067	93.9815	2.1920	0.0330
108	regulation of cell redox homeostasis	P	3	6	6	50.0000	100.0000	2.8200	0.0340
109	DNA replication initiation	P	6	21	21	28.5714	100.0000	2.2820	0.0340
110	mitochondrial electron transport\, ubiquinol to cytochrome c	P	2	3	5	66.6667	60.0000	2.8740	0.0350
111	arginyl-tRNA aminoacylation	P	2	3	3	66.6667	100.0000	2.8740	0.0370
112	vesicle targeting	P	4	11	12	36.3636	91.6667	2.4390	0.0380
113	membrane fusion	P	8	31	34	25.8065	91.1765	2.3030	0.0380
114	sphingosine metabolism	P	2	3	3	66.6667	100.0000	2.8740	0.0390
115	nuclear membrane organization and biogenesis	P	2	3	3	66.6667	100.0000	2.8740	0.0390
116	ribosomal protein import into nucleus	P	2	3	3	66.6667	100.0000	2.8740	0.0390
117	mitosis	P	25	136	146	18.3824	93.1507	2.1890	0.0390
118	redox signal response	P	2	3	3	66.6667	100.0000	2.8740	0.0430
119	zinc ion homeostasis	P	3	7	7	42.8571	100.0000	2.4700	0.0430
120	negative regulation of tyrosine phosphorylation of Stat3 protein	P	2	3	3	66.6667	100.0000	2.8740	0.0440
121	mitochondrial fission	P	2	3	3	66.6667	100.0000	2.8740	0.0440
122	regulation of glycolysis	P	2	3	3	66.6667	100.0000	2.8740	0.0440
123	dephosphorylation	P	24	132	149	18.1818	88.5906	2.0860	0.0440
124	G2 phase of mitotic cell cycle	P	2	3	3	66.6667	100.0000	2.8740	0.0450
125	protein import into mitochondrial inner membrane	P	2	3	8	66.6667	37.5000	2.8740	0.0450
126	mitotic spindle assembly	P	2	3	4	66.6667	75.0000	2.8740	0.0460
127	GPI anchor biosynthesis	P	5	17	19	29.4118	89.4737	2.1580	0.0460
128	glucose metabolism	P	19	100	135	19.0000	74.0741	2.0640	0.0470
129	spindle organization and biogenesis	P	5	17	20	29.4118	85.0000	2.1580	0.0490
130	morphogenesis of embryonic epithelium	P	8	33	33	24.2424	100.0000	2.1020	0.0490
131	electron carrier activity	F	24	67	80	35.8209	83.7500	5.8960	0.0000
132	ubiquitin-like conjugating enzyme activity	F	5	6	9	83.3333	66.6667	5.3100	0.0000
133	purine nucleotide binding	F	227	1505	1695	15.0831	88.7906	3.5310	0.0000
134	translation regulator activity	F	37	127	151	29.1339	84.1060	5.8260	0.0000
135	hydrogen ion transporter activity	F	29	104	130	27.8846	80.0000	4.8780	0.0000
136	protein serine/threonine phosphatase activity	F	13	32	36	40.6250	88.8889	4.8990	0.0000
137	threonine endopeptidase activity	F	9	18	21	50.0000	85.7143	4.8860	0.0000
138	NADH dehydrogenase (ubiquinone) activity	F	16	27	39	59.2593	69.2308	7.4550	0.0000
139	hydrogen-transporting ATP synthase activity\, rotational mechanism	F	16	43	56	37.2093	76.7857	4.9970	0.0000

140	NADH dehydrogenase activity	F	18	31	43	58.0645	72.0930	7.7860	0.0000
141	hydrogen-transporting ATPase activity\, rotational mechanism	F	17	45	58	37.7778	77.5862	5.2290	0.0000
142	translation initiation factor activity	F	22	66	86	33.3333	76.7442	5.2340	0.0000
143	structural molecule activity	F	115	632	893	18.1962	70.7727	4.6560	0.0000
144	isomerase activity	F	31	136	153	22.7941	88.8889	3.7650	0.0000
145	protein transporter activity	F	30	120	132	25.0000	90.9091	4.2750	0.0000
146	catalytic activity	F	697	4686	5420	14.8741	86.4576	6.6220	0.0000
147	unfolded protein binding	F	41	146	159	28.0822	91.8239	5.8610	0.0000
148	structural constituent of ribosome	F	75	183	354	40.9836	51.6949	11.9260	0.0000
149	binding	F	1206	9101	10565	13.2513	86.1429	4.6900	0.0000
150	RNA binding	F	116	466	548	24.8927	85.0365	8.4540	0.0000
151	hydrolase activity	F	278	1924	2234	14.4491	86.1235	3.1480	0.0000
152	nucleotide binding	F	282	1750	1959	16.1143	89.3313	5.2450	0.0000
153	protein binding	F	672	4715	5185	14.2524	90.9354	5.0730	0.0000
154	protein phosphatase type 1 activity	F	6	9	10	66.6667	90.0000	4.9790	0.0010
155	nucleoside-triphosphatase activity	F	84	498	565	16.8675	88.1416	3.1930	0.0010
156	ubiquitin conjugating enzyme activity	F	10	33	38	30.3030	86.8421	3.1650	0.0010
157	molecular function unknown	F	73	404	455	18.0693	88.7912	3.6140	0.0010
158	oxidoreductase activity	F	105	662	775	15.8610	85.4194	2.8950	0.0010
159	SUMO conjugating enzyme activity	F	3	3	6	100.0000	50.0000	4.6350	0.0020
160	nucleotidyltransferase activity	F	23	105	117	21.9048	89.7436	3.0260	0.0020
161	RNA splicing factor activity\, transesterification mechanism	F	8	20	23	40.0000	86.9565	3.7860	0.0020
162	DNA-directed RNA polymerase activity	F	11	32	36	34.3750	88.8889	3.8200	0.0020
163	ligase activity	F	69	382	449	18.0628	85.0780	3.5070	0.0020
164	ubiquitin-protein ligase activity	F	44	219	259	20.0913	84.5560	3.5630	0.0020
165	GTP binding	F	53	301	335	17.6080	89.8508	2.8620	0.0020
166	acetyl-CoA C-acyltransferase activity	F	3	3	3	100.0000	100.0000	4.6350	0.0030
167	hydrolase activity\, acting on acid anhydrides\	F	28	136	161	20.5882	84.4721	2.9770	0.0040
168	electron transporter activity	F	32	175	195	18.2857	89.7436	2.4480	0.0040
169	ATP binding	F	175	1180	1331	14.8305	88.6551	2.8130	0.0040
170	insulin-like growth factor receptor binding	F	4	7	7	57.1429	100.0000	3.6220	0.0050
171	phosphoinositide binding	F	15	58	64	25.8621	90.6250	3.1660	0.0050
172	intracellular transporter activity	F	8	24	28	33.3333	85.7143	3.1520	0.0060
173	ATPase activity\, coupled to transmem. movement of substances	F	27	134	158	20.1493	84.8101	2.8000	0.0060
174	tRNA binding	F	6	14	22	42.8571	63.6364	3.4930	0.0070
175	rRNA binding	F	6	15	18	40.0000	83.3333	3.2790	0.0080
176	cytochrome-c oxidase activity	F	7	21	27	33.3333	77.7778	2.9480	0.0080
177	dynein binding	F	3	4	5	75.0000	80.0000	3.8270	0.0090
178	TPR domain binding	F	2	2	2	100.0000	100.0000	3.7840	0.0100
179	4 iron\, 4 sulfur cluster binding	F	5	13	13	38.4615	100.0000	2.8830	0.0100
180	cholestenol delta-isomerase activity	F	2	2	2	100.0000	100.0000	3.7840	0.0110
181	disulfide oxidoreductase activity	F	6	17	19	35.2941	89.4737	2.8980	0.0110
182	ATPase activity\, coupled	F	47	266	301	17.6692	88.3721	2.7180	0.0110
183	syntaxin binding	F	5	11	13	45.4545	84.6154	3.3590	0.0110
184	translation release factor activity	F	3	5	5	60.0000	100.0000	3.2560	0.0120
185	pseudouridylate synthase activity	F	4	9	11	44.4444	81.8182	2.9460	0.0120
186	ATPase activity	F	53	312	360	16.9872	86.6667	2.5770	0.0120
187	hydrogen-exporting ATPase activity\, phosphorylative mechanism	F	7	23	27	30.4348	85.1852	2.6610	0.0130
188	thiol-disulfide exchange intermediate activity	F	3	5	5	60.0000	100.0000	3.2560	0.0140
189	ceramide glucosyltransferase activity	F	2	2	2	100.0000	100.0000	3.7840	0.0150
190	dephospho-CoA kinase activity	F	2	2	2	100.0000	100.0000	3.7840	0.0160
191	protein phosphatase type 2A regulator activity	F	5	14	14	35.7143	100.0000	2.6780	0.0160
192	long-chain-acyl-CoA dehydrogenase activity	F	2	2	2	100.0000	100.0000	3.7840	0.0170
193	acetyl-CoA C-acetyltransferase activity	F	3	5	5	60.0000	100.0000	3.2560	0.0170
194	6-phosphogluconolactonase activity	F	2	2	3	100.0000	66.6667	3.7840	0.0180
195	Ral GTPase binding	F	2	2	2	100.0000	100.0000	3.7840	0.0180
196	protein phosphatase type 2C activity	F	4	9	10	44.4444	90.0000	2.9460	0.0220
197	myosin phosphatase activity	F	3	5	5	60.0000	100.0000	3.2560	0.0230
198	translation release factor activity\, codon specific	F	2	3	3	66.6667	100.0000	2.8740	0.0290
199	transferase activity	F	217	1559	1757	13.9192	88.7308	2.1190	0.0320
200	phenylalanine-tRNA ligase activity	F	2	3	3	66.6667	100.0000	2.8740	0.0330
201	protein phosphatase type 1 regulator activity	F	2	3	3	66.6667	100.0000	2.8740	0.0330
202	arginine-tRNA ligase activity	F	2	3	3	66.6667	100.0000	2.8740	0.0370
203	protein phosphatase type 2A activity	F	3	6	6	50.0000	100.0000	2.8200	0.0380
204	phosphoric monoester hydrolase activity	F	36	211	239	17.0616	88.2845	2.1450	0.0380
205	racemase and epimerase activity\	F	2	3	3	66.6667	100.0000	2.8740	0.0390
206	Wnt-protein binding	F	2	3	3	66.6667	100.0000	2.8740	0.0410
207	cAMP-dependent protein kinase activity	F	2	3	3	66.6667	100.0000	2.8740	0.0410
208	6-phosphofructokinase activity	F	2	3	3	66.6667	100.0000	2.8740	0.0420
209	CTD phosphatase activity	F	3	6	6	50.0000	100.0000	2.8200	0.0420
210	isocitrate dehydrogenase (NAD+) activity	F	2	3	3	66.6667	100.0000	2.8740	0.0430
211	hematopoietin/interferon-class (D200-domain) cytokine receptor	F	2	3	3	66.6667	100.0000	2.8740	0.0440
212	ribosome binding	F	3	7	7	42.8571	100.0000	2.4700	0.0470
213	single-stranded DNA binding	F	7	28	32	25.0000	87.5000	2.0590	0.0470
214	mitochondrial envelope	C	73	280	329	26.0714	85.1064	7.1180	0.0000
215	large ribosomal subunit	C	14	29	42	48.2759	69.0476	5.9210	0.0000
216	dynactin complex	C	5	6	7	83.3333	85.7143	5.3100	0.0000
217	small ribosomal subunit	C	17	32	45	53.1250	71.1111	7.0580	0.0000
218	respiratory chain complex I (sensu Eukaryota)	C	6	8	14	75.0000	57.1429	5.4130	0.0000
219	mitochondrial electron transport chain	C	13	30	40	43.3333	75.0000	5.1960	0.0000

220	signalosome complex	C	6	9	10	66.6667	90.0000	4.9790	0.0000
221	mitochondrial small ribosomal subunit	C	6	9	9	66.6667	100.0000	4.9790	0.0000
222	proteasome complex (sensu Eukaryota)	C	18	37	42	48.6487	88.0952	6.7590	0.0000
223	mitochondrial ribosome	C	17	35	37	48.5714	94.5946	6.5600	0.0000
224	nuclear envelope	C	24	97	111	24.7423	87.3874	3.7630	0.0000
225	proteasome core complex (sensu Eukaryota)	C	9	18	21	50.0000	85.7143	4.8860	0.0000
226	mitochondrial matrix	C	26	74	76	35.1351	97.3684	6.0170	0.0000
227	endosome	C	25	96	104	26.0417	92.3077	4.1330	0.0000
228	proton-transporting two-sector ATPase complex	C	18	47	61	38.2979	77.0492	5.4530	0.0000
229	protein complex	C	383	1750	2202	21.8857	79.4732	13.0880	0.0000
230	nucleolus	C	41	133	147	30.8271	90.4762	6.5610	0.0000
231	Golgi apparatus	C	80	435	471	18.3908	92.3567	3.9620	0.0000
232	ribonucleoprotein complex	C	122	355	550	34.3662	64.5455	12.8600	0.0000
233	mitochondrial inner membrane	C	62	232	275	26.7241	84.3636	6.7740	0.0000
234	ribosome	C	73	176	345	41.4773	51.0145	11.8930	0.0000
235	cytosol	C	78	344	383	22.6744	89.8172	5.9630	0.0000
236	endoplasmic reticulum	C	94	528	561	17.8030	94.1177	3.9590	0.0000
237	intracellular	C	1151	6933	8118	16.6018	85.4028	15.1710	0.0000
238	mitochondrion	C	195	730	822	26.7123	88.8078	12.2180	0.0000
239	cytoplasm	C	698	3484	3969	20.0344	87.7803	16.0260	0.0000
240	nucleus	C	498	3274	3798	15.2108	86.2033	5.8490	0.0000
241	exocyst	C	5	6	6	83.3333	100.0000	5.3100	0.0010
242	small nucleolar ribonucleoprotein complex	C	10	24	32	41.6667	75.0000	4.3970	0.0010
243	protein serine/threonine phosphatase complex	C	9	26	29	34.6154	89.6552	3.4800	0.0020
244	DNA-directed RNA polymerase I complex	C	4	5	5	80.0000	100.0000	4.6200	0.0020
245	nucleoplasm	C	60	343	376	17.4927	91.2234	2.9930	0.0020
246	nuclear pore	C	13	40	46	32.5000	86.9565	3.9100	0.0020
247	muscle thin filament tropomyosin	C	3	3	4	100.0000	75.0000	4.6350	0.0030
248	vesicle membrane	C	18	76	82	23.6842	92.6829	3.0460	0.0030
249	cytosolic large ribosomal subunit (sensu Eukaryota)	C	6	13	18	46.1539	72.2222	3.7290	0.0030
250	nuclear matrix	C	7	18	19	38.8889	94.7368	3.4480	0.0030
251	Golgi stack	C	52	289	310	17.9931	93.2258	3.0040	0.0040
252	cyclin-dependent protein kinase holoenzyme complex	C	4	7	7	57.1429	100.0000	3.6220	0.0050
253	coated pit	C	11	38	38	28.9474	100.0000	3.1420	0.0050
254	nuclear lamina	C	5	9	9	55.5556	100.0000	3.9630	0.0060
255	nuclear inner membrane	C	5	11	13	45.4545	84.6154	3.3590	0.0060
256	cytosolic small ribosomal subunit (sensu Eukaryota)	C	6	14	16	42.8571	87.5000	3.4930	0.0060
257	endoplasmic reticulum membrane	C	23	104	109	22.1154	95.4128	3.0770	0.0060
258	spliceosome complex	C	17	71	78	23.9437	91.0256	3.0110	0.0060
259	cell cortex	C	11	41	44	26.8293	93.1818	2.8500	0.0070
260	mitochondrial large ribosomal subunit	C	5	12	14	41.6667	85.7143	3.1080	0.0070
261	Golgi transport complex	C	3	4	4	75.0000	100.0000	3.8270	0.0080
262	glycerol-3-phosphate dehydrogenase complex	C	2	2	4	100.0000	50.0000	3.7840	0.0090
263	proton-transporting ATP synthase complex\, coupling factor F(o)	C	4	8	13	50.0000	61.5385	3.2560	0.0110
264	spindle midzone	C	2	2	2	100.0000	100.0000	3.7840	0.0120
265	mediator complex	C	7	22	24	31.8182	91.6667	2.8000	0.0140
266	clathrin vesicle coat	C	10	36	40	27.7778	90.0000	2.8440	0.0140
267	collagen type VI	C	2	2	2	100.0000	100.0000	3.7840	0.0170
268	protein phosphatase type 2A complex	C	5	13	13	38.4615	100.0000	2.8830	0.0180
269	lamin filament	C	3	5	5	60.0000	100.0000	3.2560	0.0190
270	peroxisome	C	15	68	71	22.0588	95.7747	2.4710	0.0200
271	endoplasmic reticulum lumen	C	5	14	14	35.7143	100.0000	2.6780	0.0210
272	eukaryotic translation initiation factor 4F complex	C	3	5	5	60.0000	100.0000	3.2560	0.0220
273	proton-transporting ATP synthase complex\, catalytic core F(1)	C	3	6	6	50.0000	100.0000	2.8200	0.0240
274	cytoplasmic dynein complex	C	3	6	7	50.0000	85.7143	2.8200	0.0240
275	ruffle	C	7	23	26	30.4348	88.4615	2.6610	0.0280
276	cellular component unknown	C	60	368	404	16.3044	91.0891	2.3990	0.0280
277	outer membrane	C	15	69	75	21.7391	92.0000	2.4080	0.0290
278	nuclear inclusion body	C	2	3	3	66.6667	100.0000	2.8740	0.0310
279	NuRD complex	C	3	7	9	42.8571	77.7778	2.4700	0.0330
280	peroxisomal membrane	C	6	21	22	28.5714	95.4545	2.2820	0.0340
281	Golgi cis-face	C	3	7	9	42.8571	77.7778	2.4700	0.0350
282	DNA replication factor C complex	C	2	3	4	66.6667	75.0000	2.8740	0.0380
283	polytene chromosome chromocenter	C	2	3	5	66.6667	60.0000	2.8740	0.0400
284	translocon complex	C	2	3	3	66.6667	100.0000	2.8740	0.0410
285	6-phosphofructokinase complex	C	2	3	3	66.6667	100.0000	2.8740	0.0420
286	replication fork	C	6	22	24	27.2727	91.6667	2.1500	0.0420
287	mitochondrial intermembrane space protein transporter complex	C	2	3	8	66.6667	37.5000	2.8740	0.0450
288	COPI-coated vesicle	C	3	8	8	37.5000	100.0000	2.1780	0.0450
289	anaphase-promoting complex	C	4	11	14	36.3636	78.5714	2.4390	0.0450
290	ubiquitin ligase complex	C	27	152	182	17.7632	83.5165	2.0820	0.0490

DOWN-REGULATED - GENMAPP

No.	MAPP Name	Number Changed	Number Measured	Number on MAPP	Percent Changed	Percent Present	Z Score	Permuted P Value
1	Mm_T-Cell-Receptor_NetPath_11	31	124	126	25.0000	98.4127	6.5360	0.0000
2	Mm_B_Cell_Receptor_NetPath_12	31	147	150	21.0884	98.0000	5.4230	0.0000
3	Mm_TNF-alpha-NF-kB_NetPath_9	33	166	176	19.8795	94.3182	5.2130	0.0000
4	Mm_Ribosomal_Proteins	18	78	80	23.0769	97.5000	4.5470	0.0000
5	Mm_Signaling_of_Hepatocyte_Growth_Factor_Receptor	9	30	34	30.0000	88.2353	4.1540	0.0010
6	Mm_IL-3_NetPath_15	19	95	96	20.0000	98.9583	3.9520	0.0010

7	Mm_IL-5_NetPath_17	14	62	66	22.5806	93.9394	3.9070	0.0010
8	Mm_IL-2_NetPath_14	15	72	73	20.8333	98.6301	3.6850	0.0010
9	Mm_Integrin-mediated_cell_adhesion_KEGG	17	90	98	18.8889	91.8367	3.4670	0.0010
10	Mm_IL-1_NetPath_13	9	37	37	24.3243	100.0000	3.3870	0.0030
11	Mm_Focal_adhesion_KEGG	26	181	190	14.3646	95.2632	2.7640	0.0030
12	Mm_EGFR1_NetPath_4	26	166	171	15.6627	97.0760	3.2470	0.0040
13	Mm_IL-6_NetPath_18	17	96	97	17.7083	98.9691	3.1680	0.0040
14	Mm_Kit-Receptor_NetPath_6	13	64	65	20.3125	98.4615	3.3220	0.0060
15	Mm_MAPK_signaling_pathway_KEGG	21	131	136	16.0305	96.3235	3.0240	0.0060
16	Mm_MAPK_Cascade	7	27	29	25.9259	93.1035	3.1860	0.0110
17	Mm_TGF_Beta_Signaling_Pathway	9	50	51	18.0000	98.0392	2.3480	0.0170
18	Mm_IL-4_NetPath_16	10	55	59	18.1818	93.2203	2.5120	0.0180
19	Mm_IL-7_NetPath_19	8	42	43	19.0476	97.6744	2.3920	0.0220
20	Mm_S1P_Signaling	5	21	22	23.8095	95.4545	2.4630	0.0300
21	Mm_Insulin_Signaling	21	152	159	13.8158	95.5975	2.2790	0.0360
22	Mm_1-Tissue-Blood_and_Lymph	4	16	17	25.0000	94.1177	2.3180	0.0380
23	Mm_ESC_Pluripotency_Pathways	15	106	109	14.1509	97.2477	2.0170	0.0410
24	Mm_Aminosugars_metabolism	5	24	50	20.8333	48.0000	2.1150	0.0430
25	Mm_IL-9_NetPath_20	5	23	24	21.7391	95.8333	2.2250	0.0470

DOWN-REGULATED - GENE ONTOLOGY

No.	GO Name	GO Type	Number Changed	Number Measured	Number in GO	Percent Changed	Percent Present	Z Score	Permuted P Value
1	antigen processing	P	11	35	44	31.4286	79.5455	5.3800	0.0000
2	cellular physiological process	P	749	8916	10403	8.4006	85.7061	5.1260	0.0000
3	protein metabolism	P	264	2842	3423	9.2892	83.0266	4.0250	0.0000
4	humoral immune response	P	22	134	142	16.4179	94.3662	3.9360	0.0000
5	protein kinase cascade	P	45	305	322	14.7541	94.7205	4.8580	0.0000
6	I-kappaB kinase/NF-kappaB cascade	P	20	95	100	21.0526	95.0000	5.0300	0.0000
7	humoral defense mechanism (sensu Vertebrata)	P	18	93	101	19.3548	92.0792	4.3530	0.0000
8	vesicle-mediated transport	P	48	379	406	12.6649	93.3498	3.8650	0.0000
9	defense response	P	90	828	915	10.8696	90.4918	3.7860	0.0000
10	positive regulation of I-kappaB kinase/NF-kappaB cascade	P	14	56	61	25.0000	91.8033	4.9800	0.0000
11	protein transport	P	66	589	654	11.2054	90.0612	3.4820	0.0000
12	immune response	P	81	731	793	11.0807	92.1816	3.7670	0.0000
13	intracellular signaling cascade	P	124	1104	1204	11.2319	91.6944	4.8910	0.0000
14	peroxisome fission	P	3	4	4	75.0000	100.0000	5.1250	0.0010
15	cell death	P	64	603	650	10.6136	92.7692	2.9620	0.0010
16	protein modification	P	147	1476	1665	9.9594	88.6487	3.7780	0.0010
17	metabolism	P	568	6705	7938	8.4713	84.4671	4.0810	0.0010
18	phosphate metabolism	P	84	790	902	10.6329	87.5832	3.4340	0.0020
19	phosphorylation	P	70	648	743	10.8025	87.2140	3.2620	0.0020
20	microtubule nucleation	P	4	8	9	50.0000	88.8889	4.5640	0.0020
21	sequestering of lipid	P	4	9	9	44.4444	100.0000	4.2080	0.0020
22	antigen presentation	P	11	52	63	21.1539	82.5397	3.7440	0.0020
23	transmembrane receptor protein tyrosine kinase signaling pathway	P	23	162	172	14.1975	94.1860	3.2530	0.0020
24	histone phosphorylation	P	2	2	2	100.0000	100.0000	4.9660	0.0030
25	cell organization and biogenesis	P	155	1659	1897	9.3430	87.4539	3.0210	0.0030
26	antigen presentation\, exogenous antigen via MHC class II	P	4	10	12	40.0000	83.3333	3.9020	0.0030
27	small GTPase mediated signal transduction	P	37	305	344	12.1312	88.6628	3.1010	0.0030
28	protein amino acid phosphorylation	P	62	560	622	11.0714	90.0322	3.2690	0.0030
29	positive regulation of long-term neuronal synaptic plasticity	P	2	2	3	100.0000	66.6667	4.9660	0.0040
30	response to antibiotic	P	2	2	3	100.0000	66.6667	4.9660	0.0040
31	aromatic amino acid family biosynthesis	P	2	2	2	100.0000	100.0000	4.9660	0.0040
32	cholesterol transport	P	4	9	9	44.4444	100.0000	4.2080	0.0040
33	cholesterol homeostasis	P	4	11	11	36.3636	100.0000	3.6350	0.0040
34	antigen processing\, exogenous antigen via MHC class II	P	4	9	13	44.4444	69.2308	4.2080	0.0050
35	lipid transport	P	12	68	76	17.6471	89.4737	3.1830	0.0050
36	apoptosis	P	60	572	617	10.4895	92.7066	2.7660	0.0050
37	ATP-dependent proteolysis	P	3	5	7	60.0000	71.4286	4.4570	0.0060
38	antigen presentation\, endogenous antigen	P	6	22	25	27.2727	88.0000	3.5230	0.0060
39	antimicrobial humoral response (sensu Vertebrata)	P	9	48	51	18.7500	94.1177	2.9630	0.0060
40	endocytosis	P	22	167	181	13.1737	92.2652	2.7980	0.0080
41	intracellular protein transport	P	47	415	463	11.3253	89.6328	2.9990	0.0080
42	negative regulation of anti-apoptosis	P	2	2	2	100.0000	100.0000	4.9660	0.0090
43	regulation of neuronal synaptic plasticity	P	3	7	9	42.8571	77.7778	3.5520	0.0110
44	integrin-mediated signaling pathway	P	11	68	77	16.1765	88.3117	2.7220	0.0110
45	peptidyl-serine phosphorylation	P	3	6	6	50.0000	100.0000	3.9520	0.0120
46	intra-Golgi vesicle-mediated transport	P	4	11	12	36.3636	91.6667	3.6350	0.0120
47	B cell receptor signaling pathway	P	3	7	7	42.8571	100.0000	3.5520	0.0160
48	cytoskeleton organization and biogenesis	P	41	385	431	10.6494	89.3272	2.3750	0.0160
49	antigen processing\, endogenous antigen via MHC class I	P	5	20	23	25.0000	86.9565	2.9720	0.0170
50	regulation of fatty acid metabolism	P	3	8	8	37.5000	100.0000	3.2220	0.0180
51	response to stress	P	96	1014	1107	9.4675	91.5989	2.4620	0.0180
52	MAPKKK cascade	P	17	131	140	12.9771	93.5714	2.3890	0.0210
53	heart development	P	14	101	104	13.8614	97.1154	2.4340	0.0220
54	sperm axoneme assembly	P	2	4	4	50.0000	100.0000	3.2270	0.0270
55	mannose metabolism	P	3	9	9	33.3333	100.0000	2.9430	0.0290
56	telomere maintenance	P	5	24	28	20.8333	85.7143	2.4810	0.0300
57	regulation of muscle contraction	P	6	33	36	18.1818	91.6667	2.3310	0.0310
58	peptidyl-threonine phosphorylation	P	2	4	4	50.0000	100.0000	3.2270	0.0330

59	glial cell migration	P	2	4	4	50.0000	100.0000	3.2270	0.0330
60	release of sequestered calcium ion into cytosol	P	2	4	4	50.0000	100.0000	3.2270	0.0330
61	response to pest\, pathogen or parasite	P	50	502	553	9.9602	90.7776	2.1270	0.0340
62	actin polymerization and/or depolymerization	P	8	52	54	15.3846	96.2963	2.1610	0.0360
63	actin filament-based movement	P	4	18	18	22.2222	100.0000	2.3720	0.0360
64	negative regulation of transcription factor activity	P	2	5	6	40.0000	83.3333	2.7590	0.0370
65	activation of NF-kappaB-inducing kinase	P	3	11	11	27.2727	100.0000	2.4900	0.0370
66	protein amino acid O-linked glycosylation	P	4	18	21	22.2222	85.7143	2.3720	0.0370
67	activation of MAPKKK activity	P	2	5	5	40.0000	100.0000	2.7590	0.0380
68	calcium-mediated signaling	P	5	26	29	19.2308	89.6552	2.2720	0.0380
69	antigen presentation\, exogenous antigen	P	4	17	21	23.5294	80.9524	2.5100	0.0390
70	response to pathogenic bacteria	P	4	19	20	21.0526	95.0000	2.2440	0.0390
71	cotranslational protein targeting to membrane	P	3	12	13	25.0000	92.3077	2.3020	0.0400
72	cell proliferation	P	59	609	648	9.6880	93.9815	2.0910	0.0400
73	heparan sulfate proteoglycan metabolism	P	3	11	12	27.2727	91.6667	2.4900	0.0440
74	antigen presentation\, exogenous peptide antigen	P	2	5	6	40.0000	83.3333	2.7590	0.0450
75	transport	P	215	2540	2884	8.4646	88.0721	2.0240	0.0480
76	actin filament severing	P	2	5	5	40.0000	100.0000	2.7590	0.0490
77	negative regulation of axon extension	P	2	5	5	40.0000	100.0000	2.7590	0.0490
78	protein binding\, bridging	F	13	59	64	22.0339	92.1875	4.2460	0.0000
79	cytoskeletal protein binding	F	44	315	344	13.9683	91.5698	4.4040	0.0000
80	receptor signaling protein activity	F	21	137	148	15.3285	92.5676	3.4940	0.0000
81	SH3/SH2 adaptor activity	F	11	39	42	28.2051	92.8571	4.9140	0.0000
82	actin binding	F	28	207	230	13.5266	90.0000	3.3140	0.0000
83	binding	F	763	9101	10565	8.3837	86.1429	5.1640	0.0000
84	protein binding	F	440	4715	5185	9.3319	90.9354	5.7840	0.0000
85	casein kinase I activity	F	3	3	3	100.0000	100.0000	6.0820	0.0010
86	transcriptional repressor activity	F	27	203	212	13.3005	95.7547	3.1580	0.0020
87	phospholipid binding	F	17	107	117	15.8879	91.4530	3.3050	0.0030
88	protein serine/threonine kinase activity	F	50	435	488	11.4943	89.1393	3.2080	0.0030
89	v-SNARE activity	F	2	2	2	100.0000	100.0000	4.9660	0.0040
90	phosphotyrosine binding	F	3	5	5	60.0000	100.0000	4.4570	0.0040
91	structural constituent of ribosome	F	24	183	354	13.1148	51.6949	2.9000	0.0040
92	protein kinase activity	F	59	545	612	10.8257	89.0523	3.0010	0.0050
93	nucleotide binding	F	158	1750	1959	9.0286	89.3313	2.5820	0.0050
94	myosin binding	F	3	7	7	42.8571	100.0000	3.5520	0.0070
95	kinase activity	F	78	786	887	9.9237	88.6133	2.6490	0.0070
96	chromatin binding	F	13	81	88	16.0494	92.0455	2.9280	0.0080
97	protein-tyrosine kinase activity	F	37	317	340	11.6719	93.2353	2.8490	0.0080
98	calmodulin binding	F	14	98	102	14.2857	96.0784	2.5580	0.0090
99	protein kinase binding	F	10	53	62	18.8679	85.4839	3.1470	0.0100
100	protein tyrosine phosphatase activity	F	11	68	79	16.1765	86.0760	2.7220	0.0110
101	intracellular calcium activated chloride channel activity	F	2	3	3	66.6667	100.0000	3.8900	0.0130
102	MHC class II receptor activity	F	3	7	11	42.8571	63.6364	3.5520	0.0130
103	SH2 domain binding	F	4	15	15	26.6667	100.0000	2.8190	0.0130
104	lipoprotein binding	F	6	24	26	25.0000	92.3077	3.2570	0.0140
105	prenylated protein tyrosine phosphatase activity	F	3	8	10	37.5000	80.0000	3.2220	0.0150
106	antigen binding	F	7	34	63	20.5882	53.9683	2.9000	0.0170
107	hematopoietin/interferon-class (D200-domain) cytokine receptor	F	2	3	3	66.6667	100.0000	3.8900	0.0190
108	MAP kinase activity	F	4	14	14	28.5714	100.0000	2.9940	0.0200
109	lipid binding	F	29	249	274	11.6466	90.8759	2.5040	0.0220
110	GTP binding	F	33	301	335	10.9635	89.8508	2.3030	0.0230
111	phosphatidylinositol transporter activity	F	2	4	5	50.0000	80.0000	3.2270	0.0270
112	translation activator activity	F	2	4	4	50.0000	100.0000	3.2270	0.0310
113	non-membrane spanning protein tyrosine kinase activity	F	3	12	12	25.0000	100.0000	2.3020	0.0310
114	thyroid hormone receptor binding	F	4	17	18	23.5294	94.4444	2.5100	0.0320
115	catalytic activity	F	382	4686	5420	8.1519	86.4576	2.0450	0.0320
116	oxygen transporter activity	F	4	17	21	23.5294	80.9524	2.5100	0.0330
117	hematopoietin/interferon-class (D200-domain) cytokine receptor	F	9	58	60	15.5172	96.6667	2.3220	0.0340
118	1-alkyl-2-acetylglycerophosphocholine esterase activity	F	2	4	4	50.0000	100.0000	3.2270	0.0350
119	phosphoinositide 3-kinase regulator activity	F	2	5	5	40.0000	100.0000	2.7590	0.0390
120	SH3 domain binding	F	4	18	18	22.2222	100.0000	2.3720	0.0400
121	sulfuric ester hydrolase activity	F	3	11	12	27.2727	91.6667	2.4900	0.0480
122	GTPase activator activity	F	15	119	132	12.6050	90.1515	2.1220	0.0480
123	retinoid X receptor binding	F	2	5	5	40.0000	100.0000	2.7590	0.0490
124	Golgi membrane	C	18	102	104	17.6471	98.0769	3.9030	0.0000
125	Golgi apparatus	C	55	435	471	12.6437	92.3567	4.1320	0.0000
126	cytosol	C	44	344	383	12.7907	89.8172	3.7680	0.0000
127	endoplasmic reticulum	C	63	528	561	11.9318	94.1177	3.9350	0.0000
128	intracellular	C	651	6933	8118	9.3899	85.4028	8.2010	0.0000
129	cytoplasm	C	341	3484	3969	9.7876	87.7803	5.8600	0.0000
130	ribosome	C	24	176	345	13.6364	51.0145	3.1080	0.0020
131	nucleus	C	286	3274	3798	8.7355	86.2033	3.0380	0.0020
132	Golgi stack	C	34	289	310	11.7647	93.2258	2.7780	0.0040
133	immunological synapse	C	9	44	51	20.4546	86.2745	3.2660	0.0050
134	vacuole	C	20	141	148	14.1844	95.2703	3.0270	0.0050
135	cytosolic small ribosomal subunit (sensu Eukaryota)	C	5	14	16	35.7143	87.5000	4.0090	0.0050
136	cytoplasmic membrane-bound vesicle	C	27	206	221	13.1068	93.2127	3.0750	0.0050
137	MHC class II protein complex	C	2	2	2	100.0000	100.0000	4.9660	0.0070
138	external side of plasma membrane	C	12	76	80	15.7895	95.0000	2.7500	0.0120

139	insoluble fraction	C	5	20	21	25.0000	95.2381	2.9720	0.0140
140	cell surface	C	20	156	164	12.8205	95.1220	2.5350	0.0150
141	peroxisomal membrane	C	5	21	22	23.8095	95.4545	2.8390	0.0160
142	lysosome	C	17	123	129	13.8211	95.3488	2.6710	0.0160
143	Arp2/3 protein complex	C	3	8	8	37.5000	100.0000	3.2220	0.0190
144	female pronucleus	C	2	3	3	66.6667	100.0000	3.8900	0.0210
145	clathrin vesicle coat	C	7	36	40	19.4444	90.0000	2.7230	0.0220
146	unconventional myosin	C	2	4	4	50.0000	100.0000	3.2270	0.0250
147	actin cytoskeleton	C	24	206	229	11.6505	89.9563	2.2760	0.0280
148	chromosome	C	30	279	364	10.7527	76.6484	2.0810	0.0320
149	DNA-directed RNA polymerase I complex	C	2	5	5	40.0000	100.0000	2.7590	0.0360
150	focal adhesion	C	5	24	26	20.8333	92.3077	2.4810	0.0360
151	integral to peroxisomal membrane	C	3	11	11	27.2727	100.0000	2.4900	0.0370
152	cellular component unknown	C	38	368	404	10.3261	91.0891	2.0830	0.0460

B

UP-REGULATED - GENMAPP

No.	MAPP Name	Number Changed	Number Measured	Number on MAPP	Percent Changed	Percent Present	Z Score	Permuted P Value
1	Mm_Cholesterol_Biosynthesis	8	15	15	53.3333	100.0000	9.2890	0.0000
2	Mm_Tyrosine_metabolism	6	32	82	18.7500	39.0244	3.9920	0.0010
3	Mm_Methionine_metabolism	3	8	26	37.5000	30.7692	4.5860	0.0020
4	Mm_Selenoamino_acid_metabolism	4	13	26	30.7692	50.0000	4.6610	0.0030
5	Mm_Synthesis_and_degradation_of_ketone_bodies	2	3	7	66.6667	42.8571	5.2780	0.0080
6	Mm_Galactose_metabolism	4	19	46	21.0526	41.3044	3.5630	0.0120
7	Mm_TNF-alpha-NF-kB_NetPath_9	14	166	176	8.4337	94.3182	2.6100	0.0170
8	Mm_Steroid_Biosynthesis	3	13	13	23.0769	100.0000	3.3030	0.0180
9	Mm_IL-9_NetPath_20	4	23	24	17.3913	95.8333	3.0610	0.0190
10	Mm_Mitochondrial_fatty_acid_betaoxidation	3	16	16	18.7500	100.0000	2.8180	0.0260
11	Mm_Circadian_Exercise	6	48	49	12.5000	97.9592	2.7690	0.0270
12	Mm_Alkaloid_biosynthesis_I	2	6	38	33.3333	15.7895	3.4710	0.0280
13	Mm_Cysteine_metabolism	2	7	26	28.5714	26.9231	3.1330	0.0320
14	Mm_Aminophosphonate_metabolism	2	7	19	28.5714	36.8421	3.1330	0.0330
15	Mm_Glycerolipid_metabolism	7	72	122	9.7222	59.0164	2.2390	0.0360
16	Mm_Proteasome_Degradation	7	73	81	9.5890	90.1235	2.1980	0.0370
17	Mm_Androgen_and_estrogen_metabolism	4	28	42	14.2857	66.6667	2.5740	0.0380

UP-REGULATED - GENE ONTOLOGY

No.	GO Name	GO Type	Number Changed	Number Measured	Number in GO	Percent Changed	Percent Present	Z Score	Permuted P Value
1	sterol biosynthesis	P	11	25	27	44.0000	92.5926	11.4690	0.0000
2	retrograde protein transport\, ER to cytosol	P	3	4	4	75.0000	100.0000	8.0730	0.0000
3	RNA processing	P	26	329	371	7.9027	88.6792	4.7860	0.0000
4	steroid biosynthesis	P	15	70	74	21.4286	94.5946	8.5700	0.0000
5	ER-associated protein catabolism	P	4	12	12	33.3333	100.0000	5.8620	0.0000
6	biosynthesis	P	76	1154	1428	6.5858	80.8123	6.6100	0.0000
7	mRNA processing	P	15	173	198	8.6705	87.3737	4.0230	0.0000
8	response to unfolded protein	P	10	46	55	21.7391	83.6364	7.0600	0.0000
9	amino acid metabolism	P	19	245	273	7.7551	89.7436	3.9870	0.0000
10	cholesterol biosynthesis	P	9	20	22	45.0000	90.9091	10.5080	0.0000
11	lipid metabolism	P	35	581	616	6.0241	94.3182	3.8170	0.0000
12	protein transport	P	37	589	654	6.2818	90.0612	4.2030	0.0000
13	metabolism	P	286	6705	7938	4.2655	84.4671	6.2400	0.0000
14	ubiquitin cycle	P	28	437	511	6.4073	85.5186	3.7510	0.0000
15	establishment of protein localization	P	37	617	684	5.9968	90.2047	3.8990	0.0010
16	glycogen metabolism	P	5	28	28	17.8571	100.0000	4.3480	0.0010
17	aromatic compound metabolism	P	11	101	108	10.8911	93.5185	4.3260	0.0010
18	RNA splicing	P	13	144	167	9.0278	86.2276	3.9090	0.0010
19	ER to Golgi vesicle-mediated transport	P	8	53	59	15.0943	89.8305	4.8540	0.0010
20	nuclear mRNA splicing\, via spliceosome	P	12	118	135	10.1695	87.4074	4.2360	0.0010
21	intracellular protein transport	P	26	415	463	6.2651	89.6328	3.4870	0.0010
22	protein folding	P	17	200	227	8.5000	88.1057	4.1930	0.0010
23	ubiquitin-dependent protein catabolism	P	11	132	149	8.3333	88.5906	3.2900	0.0020
24	retrograde axon cargo transport	P	2	4	4	50.0000	100.0000	5.2590	0.0030
25	positive regulation of nitric oxide biosynthesis	P	2	4	4	50.0000	100.0000	5.2590	0.0040
26	catecholamine metabolism	P	4	17	20	23.5294	85.0000	4.7030	0.0050
27	unfolded protein response	P	3	9	9	33.3333	100.0000	5.0760	0.0050
28	nitric oxide biosynthesis	P	4	18	19	22.2222	94.7368	4.5280	0.0060
29	protein modification	P	65	1476	1665	4.4038	88.6487	2.5930	0.0060
30	transport	P	106	2540	2884	4.1732	88.0721	2.8290	0.0060
31	response to sterol depletion	P	2	4	4	50.0000	100.0000	5.2590	0.0070
32	mRNA splice site selection	P	3	13	15	23.0769	86.6667	4.0210	0.0090
33	ribosome biogenesis	P	8	79	84	10.1266	94.0476	3.4400	0.0110
34	protein polymerization	P	5	43	50	11.6279	86.0000	3.0900	0.0120
35	negative regulation of apoptosis	P	11	161	171	6.8323	94.1521	2.5600	0.0150
36	microtubule-based movement	P	8	89	114	8.9888	78.0702	3.0470	0.0150
37	regulation of cell redox homeostasis	P	2	6	6	33.3333	100.0000	4.1450	0.0160
38	phosphatidylinositol biosynthesis	P	2	5	5	40.0000	100.0000	4.6220	0.0170
39	protein sumoylation	P	2	6	9	33.3333	66.6667	4.1450	0.0170
40	NLS-bearing substrate import into nucleus	P	2	7	7	28.5714	100.0000	3.7680	0.0170
41	galactose metabolism	P	2	8	8	25.0000	100.0000	3.4600	0.0200
42	rRNA processing	P	6	65	70	9.2308	92.8571	2.7120	0.0210
43	embryo implantation	P	3	20	21	15.0000	95.2381	2.9540	0.0250
44	anti-apoptosis	P	9	124	134	7.2581	92.5373	2.5120	0.0250
45	vesicle-mediated transport	P	20	379	406	5.2770	93.3498	2.2320	0.0260
46	chaperone cofactor dependent protein folding	P	2	9	10	22.2222	90.0000	3.2010	0.0290
47	cell cycle	P	30	629	681	4.7695	92.3642	2.1690	0.0290
48	glycine metabolism	P	2	10	11	20.0000	90.9091	2.9780	0.0320
49	protein amino acid N-linked glycosylation via asparagine	P	2	10	11	20.0000	90.9091	2.9780	0.0380
50	protein amino acid methylation	P	3	23	25	13.0435	92.0000	2.6400	0.0400
51	CTP biosynthesis	P	2	10	12	20.0000	83.3333	2.9780	0.0420
52	UTP biosynthesis	P	2	10	12	20.0000	83.3333	2.9780	0.0420
53	response to oxidative stress	P	5	59	63	8.4746	93.6508	2.2560	0.0430
54	cell aging	P	2	10	10	20.0000	100.0000	2.9780	0.0450
55	microtubule-based process	P	10	157	190	6.3694	82.6316	2.2000	0.0450
56	isoprenoid biosynthesis	P	2	12	16	16.6667	75.0000	2.6130	0.0470

57	translational initiation	P	5	58	72	8.6207	80.5556	2.2990	0.0480
58	TPR domain binding	F	2	2	2	100.0000	100.0000	7.6970	0.0000
59	protein carrier activity	F	4	8	8	50.0000	100.0000	7.4390	0.0000
60	catalytic activity	F	210	4686	5420	4.4814	86.4576	5.6700	0.0000
61	unfolded protein binding	F	14	146	159	9.5890	91.8239	4.3200	0.0000
62	RNA binding	F	31	466	548	6.6524	85.0365	4.1800	0.0000
63	transferase activity	F	77	1559	1757	4.9391	88.7308	3.9310	0.0000
64	nucleotide binding	F	82	1750	1959	4.6857	89.3313	3.5600	0.0000
65	1-phosphatidylinositol 4-kinase activity	F	2	2	2	100.0000	100.0000	7.6970	0.0010
66	protein transporter activity	F	11	120	132	9.1667	90.9091	3.6520	0.0010
67	ligase activity	F	24	382	449	6.2827	85.0780	3.3610	0.0010
68	3-beta-hydroxy-delta5-steroid dehydrogenase activity	F	3	9	11	33.3333	81.8182	5.0760	0.0030
69	protein serine/threonine phosphatase activity	F	5	32	36	15.6250	88.8889	3.9380	0.0030
70	selenium binding	F	4	25	27	16.0000	92.5926	3.5850	0.0040
71	Janus kinase activity	F	2	4	4	50.0000	100.0000	5.2590	0.0060
72	protein phosphatase type 1 activity	F	3	9	10	33.3333	90.0000	5.0760	0.0060
73	isomerase activity	F	10	136	153	7.3529	88.8889	2.6940	0.0080
74	magnesium ion binding	F	16	253	273	6.3241	92.6740	2.7610	0.0090
75	MAP kinase phosphatase activity	F	3	10	10	30.0000	100.0000	4.7580	0.0100
76	ATP binding	F	54	1180	1331	4.5763	88.6551	2.6410	0.0120
77	snoRNA binding	F	2	6	6	33.3333	100.0000	4.1450	0.0130
78	binding	F	323	9101	10565	3.5491	86.1429	2.4610	0.0130
79	protein kinase C binding	F	2	7	8	28.5714	87.5000	3.7680	0.0140
80	acyltransferase activity	F	10	134	149	7.4627	89.9329	2.7460	0.0140
81	nuclear localization sequence binding	F	2	7	7	28.5714	100.0000	3.7680	0.0150
82	oxidoreductase activity	F	33	662	775	4.9849	85.4194	2.5470	0.0160
83	nitric-oxide synthase regulator activity	F	2	5	6	40.0000	83.3333	4.6220	0.0170
84	inositol or phosphatidylinositol kinase activity	F	4	29	33	13.7931	87.8788	3.1930	0.0170
85	phosphoric monoester hydrolase activity	F	13	211	239	6.1611	88.2845	2.3830	0.0170
86	kinase activity	F	37	786	887	4.7074	88.6133	2.3370	0.0170
87	FK506 binding	F	2	7	7	28.5714	100.0000	3.7680	0.0180
88	ribosome binding	F	2	7	7	28.5714	100.0000	3.7680	0.0210
89	guanylate kinase activity	F	2	6	8	33.3333	75.0000	4.1450	0.0220
90	porin activity	F	3	19	19	15.7895	100.0000	3.0730	0.0220
91	Wnt receptor activity	F	2	7	7	28.5714	100.0000	3.7680	0.0240
92	insulin-like growth factor receptor binding	F	2	7	7	28.5714	100.0000	3.7680	0.0240
93	protein kinase binding	F	5	53	62	9.4340	85.4839	2.5310	0.0240
94	protein domain specific binding	F	6	72	74	8.3333	97.2973	2.4250	0.0320
95	steroid delta-isomerase activity	F	2	9	10	22.2222	90.0000	3.2010	0.0330
96	dolichyl-diphosphooligosaccharide-protein glycotransferase	F	2	9	10	22.2222	90.0000	3.2010	0.0330
97	nucleoside diphosphate kinase activity	F	2	10	12	20.0000	83.3333	2.9780	0.0420
98	methyltransferase activity	F	9	138	160	6.5217	86.2500	2.1620	0.0490
99	protein complex	C	82	1750	2202	4.6857	79.4732	3.5600	0.0000
100	ribonucleoprotein complex	C	26	355	550	7.3239	64.5455	4.3550	0.0000
101	intracellular	C	298	6933	8118	4.2983	85.4028	6.6490	0.0000
102	soluble fraction	C	17	173	183	9.8266	94.5355	4.8840	0.0000
103	endoplasmic reticulum	C	43	528	561	8.1439	94.1177	6.4230	0.0000
104	mitochondrion	C	42	730	822	5.7534	88.8078	3.8790	0.0000
105	cytoplasm	C	187	3484	3969	5.3674	87.7803	7.9880	0.0000
106	COPII vesicle coat	C	3	7	7	42.8571	100.0000	5.8950	0.0010
107	endoplasmic reticulum membrane	C	11	104	109	10.5769	95.4128	4.2100	0.0010
108	nucleus	C	136	3274	3798	4.1539	86.2033	3.2430	0.0010
109	peroxisome	C	8	68	71	11.7647	95.7747	3.9520	0.0030
110	microsome	C	12	138	148	8.6957	93.2432	3.6060	0.0030
111	integral to endoplasmic reticulum membrane	C	5	34	35	14.7059	97.1429	3.7570	0.0040
112	perinuclear region	C	5	37	40	13.5135	92.5000	3.5110	0.0080
113	spliceosome complex	C	7	71	78	9.8592	91.0256	3.1330	0.0080
114	oligosaccharyl transferase complex	C	2	9	10	22.2222	90.0000	3.2010	0.0330
115	nuclear pore	C	4	40	46	10.0000	86.9565	2.4000	0.0410

DOWN-REGULATED - GENMAPP

No.	MAPP Name	Number Changed	Number Measured	Number on MAPP	Percent Changed	Percent Present	Z Score	Permuted P Value
1	Mm_Insulin_Signaling	8	152	159	5.2632	95.5975	3.7220	0.0000
2	Mm_Nuclear_Receptors	4	38	38	10.5263	100.0000	4.4550	0.0010
3	Mm_Adipogenesis	8	129	132	6.2016	97.7273	4.2890	0.0010
4	Mm_B_Cell_Receptor_NetPath_12	8	147	150	5.4422	98.0000	3.8360	0.0030
5	Mm_Riboflavin_metabolism	2	8	17	25.0000	47.0588	5.3300	0.0040
6	Mm_IL-6_NetPath_18	6	96	97	6.2500	98.9691	3.7240	0.0040
7	Mm_Delta-Notch_NetPath_3	5	77	80	6.4935	96.2500	3.5010	0.0050
8	Mm_Pantothenate_and_CoA_biosynthesis	2	10	30	20.0000	33.3333	4.6880	0.0070
9	Mm_IL-7_NetPath_19	3	42	43	7.1429	97.6744	2.9150	0.0250
10	Mm_Circadian_Exercise	3	48	49	6.2500	97.9592	2.6180	0.0380
11	Mm_Apoptosis	4	83	83	4.8193	100.0000	2.4000	0.0380
12	Mm_EGFR1_NetPath_4	6	166	171	3.6145	97.0760	2.1550	0.0450

DOWN-REGULATED - GENE ONTOLOGY

No.	GO Name	GO Type	Number Changed	Number Measured	Number in GO	Percent Changed	Percent Present	Z Score	Permuted P Value
1	S-adenosylmethionine biosynthesis	P	2	2	2	100.0000	100.0000	11.5930	0.0000
2	Golgi to plasma membrane transport	P	2	3	4	66.6667	75.0000	9.3950	0.0010
3	embryonic cleavage	P	2	4	4	50.0000	100.0000	8.0760	0.0010

4	vesicle transport along microtubule	P	2	5	5	40.0000	100.0000	7.1690	0.0020
5	metabolism	P	123	6705	7938	1.8345	84.4671	3.3960	0.0020
6	apoptotic program	P	4	56	61	7.1429	91.8033	3.5400	0.0030
7	zinc ion homeostasis	P	2	7	7	28.5714	100.0000	5.9670	0.0050
8	nitric oxide mediated signal transduction	P	2	7	7	28.5714	100.0000	5.9670	0.0070
9	response to cold	P	2	10	10	20.0000	100.0000	4.8770	0.0090
10	acyl-CoA metabolism	P	2	13	13	15.3846	100.0000	4.1760	0.0110
11	electron transport	P	11	386	461	2.8497	83.7310	2.2910	0.0210
12	nucleotide metabolism	P	7	194	236	3.6082	82.2034	2.4980	0.0240
13	protein amino acid phosphorylation	P	15	560	622	2.6786	90.0322	2.4330	0.0310
14	regulation of exocytosis	P	2	17	17	11.7647	100.0000	3.5340	0.0330
15	response to pathogenic bacteria	P	2	19	20	10.5263	95.0000	3.2870	0.0360
16	cell division	P	6	168	178	3.5714	94.3820	2.2830	0.0360
17	response to oxidative stress	P	3	59	63	5.0847	93.6508	2.3170	0.0440
18	ligand-dependent nuclear receptor activity	F	5	51	53	9.8039	96.2264	4.9620	0.0000
19	thyroid hormone receptor activity	F	3	7	8	42.8571	87.5000	9.1120	0.0000
20	2'-phosphotransferase activity	F	2	2	2	100.0000	100.0000	11.5930	0.0020
21	nucleotide diphosphatase activity	F	2	6	6	33.3333	100.0000	6.4950	0.0030
22	steroid hormone receptor activity	F	4	49	50	8.1633	98.0000	3.9060	0.0040
23	ephrin receptor binding	F	2	7	7	28.5714	100.0000	5.9670	0.0060
24	transforming growth factor beta receptor activity	F	2	13	14	15.3846	92.8571	4.1760	0.0150
25	sodium ion binding	F	4	66	69	6.0606	95.6522	3.1120	0.0190
26	kinase activity	F	20	786	887	2.5445	88.6133	2.5840	0.0210
27	protein kinase activity	F	15	545	612	2.7523	89.0523	2.5450	0.0220
28	microtubule binding	F	3	42	44	7.1429	95.4545	3.0650	0.0230
29	subtilase activity	F	2	20	21	10.0000	95.2381	3.1770	0.0370
30	protein serine/threonine kinase activity	F	12	435	488	2.7586	89.1393	2.2760	0.0370
31	GTPase activator activity	F	5	119	132	4.2017	90.1515	2.4920	0.0400
32	ubiquitin-protein ligase activity	F	7	219	259	3.1963	84.5560	2.1460	0.0410
33	magnesium ion binding	F	8	253	273	3.1621	92.6740	2.2630	0.0420
34	binding	F	148	9101	10565	1.6262	86.1429	2.0500	0.0430
35	presynaptic membrane	C	2	10	10	20.0000	100.0000	4.8770	0.0140
36	synaptic vesicle membrane	C	2	11	12	18.1818	91.6667	4.6130	0.0180
37	microsome	C	5	138	148	3.6232	93.2432	2.1180	0.0430