

Supplementary Material 2.

List of GenMAPPs and gene ontologies significantly changed in mouse tumours by OPP.

This file contains one worksheet which shows lists of GenMAPPs and gene ontologies significantly changed in tumours of mice supplemented with OPP.

All GenMAPPs and gene ontologies 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.

UP-REGULATED - GENMAPP (TREATMENT VERSUS CONTROL)									
No.	MAPP Name		Number Changed	Number Measured	Number on MAPP	Percent Changed	Percent Present	Z Score	Permuted P Value
1	Mm_Translation_Factors		5	49	50	10.2041	98.0000	3.7540	0.0040
2	Mm_mRNA_processing_binding_Reactome		19	426	551	4.4601	77.3140	3.2030	0.0050
3	Mm_Ovarian_Infertility_Genes		3	31	31	9.6774	100.0000	2.7820	0.0300
4	Mm_Selenoamino_acid_metabolism		2	13	26	15.3846	50.0000	3.1820	0.0330
5	Mm_Folate_biosynthesis		2	13	31	15.3846	41.9355	3.1820	0.0380
UP-REGULATED - GENE ONTOLOGY (TREATMENT VERSUS CONTROL)									
No.	GO Name	GO Type	Number Changed	Number Measured	Number in GO	Percent Changed	Percent Present	Z Score	Permuted P Value
1	negative regulation of complement activation	P	2	2	2	100.0000	100.0000	9.4150	0.0000
2	amino acid biosynthesis	P	6	42	46	14.2857	91.3043	5.3370	0.0000
3	biosynthesis	P	49	1154	1428	4.2461	80.8123	4.9130	0.0000
4	metabolism	P	191	6705	7938	2.8486	84.4671	4.8490	0.0000
5	ubiquitin cycle	P	21	437	511	4.8055	85.5186	3.7550	0.0010
6	mRNA processing	P	11	173	198	6.3584	87.3737	3.7390	0.0010
7	protein folding	P	13	200	227	6.5000	88.1057	4.1620	0.0020
8	protein ubiquitination	P	10	147	173	6.8027	84.9711	3.8130	0.0030
9	'de novo' pyrimidine base biosynthesis	P	2	5	5	40.0000	100.0000	5.7540	0.0050
10	positive regulation of I-kappaB kinase/NF-kappaB cascade	P	5	56	61	8.9286	91.8033	3.4310	0.0070
11	nuclear mRNA splicing\, via spliceosome	P	7	118	135	5.9322	87.4074	2.7660	0.0080
12	regulation of cell volume	P	2	6	7	33.3333	85.7143	5.1910	0.0110
13	N-glycan processing	P	2	8	8	25.0000	100.0000	4.3900	0.0110
14	cell division	P	9	168	178	5.3571	94.3820	2.7960	0.0160
15	autophagic vacuole formation	P	2	9	10	22.2222	90.0000	4.0890	0.0170
16	sterol biosynthesis	P	3	25	27	12.0000	92.5926	3.3360	0.0170
17	apoptosis	P	21	572	617	3.6713	92.7066	2.4320	0.0180
18	negative regulation of protein kinase activity	P	4	46	49	8.6957	93.8776	3.0010	0.0190
19	chaperone cofactor dependent protein folding	P	2	9	10	22.2222	90.0000	4.0890	0.0200
20	steroid biosynthesis	P	5	70	74	7.1429	94.5946	2.8180	0.0200
21	chromatin remodeling	P	4	48	52	8.3333	92.3077	2.8940	0.0210
22	chloride transport	P	4	51	52	7.8431	98.0769	2.7450	0.0230
23	chromatin silencing	P	2	11	12	18.1818	91.6667	3.6080	0.0250
24	protein modification	P	44	1476	1665	2.9810	88.6487	2.1350	0.0320
25	acyl-CoA metabolism	P	2	13	13	15.3846	100.0000	3.2360	0.0390
26	cartilage development	P	3	32	32	9.3750	100.0000	2.7630	0.0430
27	amino acid metabolism	P	10	245	273	4.0816	89.7436	2.0150	0.0470
28	negative regulation of cell migration	P	2	15	16	13.3333	93.7500	2.9350	0.0490
29	ubiquitin-protein ligase activity	F	15	219	259	6.8493	84.5560	4.7120	0.0000
30	ligase activity	F	20	382	449	5.2356	85.0780	4.0830	0.0000
31	catalytic activity	F	137	4686	5420	2.9236	86.4576	4.0470	0.0000
32	unfolded protein binding	F	9	146	159	6.1644	91.8239	3.2720	0.0050
33	RNA binding	F	19	466	548	4.0773	85.0365	2.7940	0.0060
34	protein kinase binding	F	5	53	62	9.4340	85.4839	3.5880	0.0100
35	transcription cofactor activity	F	12	264	281	4.5455	93.9502	2.6100	0.0100
36	histone deacetylase binding	F	2	8	8	25.0000	100.0000	4.3900	0.0150
37	cyclin-dependent protein kinase activity	F	2	10	10	20.0000	100.0000	3.8320	0.0170
38	protein carrier activity	F	2	8	8	25.0000	100.0000	4.3900	0.0180
39	transcription factor binding	F	13	325	350	4.0000	92.8571	2.2260	0.0310
40	hydrolase activity\, acting on glycosyl bonds	F	6	110	125	5.4545	88.0000	2.3280	0.0320
41	ubiquitin conjugating enzyme activity	F	3	33	38	9.0909	86.8421	2.6950	0.0350

42	transferase activity	F	46	1559	1757	2.9506	88.7308	2.1150	0.0430
43	GTP binding	F	12	301	335	3.9867	89.8508	2.1240	0.0440
44	endoplasmic reticulum	C	30	528	561	5.6818	94.1177	5.5360	0.0000
45	cytoplasm	C	115	3484	3969	3.3008	87.7803	5.0320	0.0000
46	intracellular	C	196	6933	8118	2.8271	85.4028	4.8340	0.0000
47	autophagic vacuole	C	2	5	5	40.0000	100.0000	5.7540	0.0060
48	cyclin-dependent protein kinase holoenzyme complex	C	2	7	7	28.5714	100.0000	4.7500	0.0060
49	eukaryotic translation initiation factor 4F complex	C	2	5	5	40.0000	100.0000	5.7540	0.0090
50	ubiquitin ligase complex	C	9	152	182	5.9211	83.5165	3.1340	0.0120
51	mitochondrion	C	26	730	822	3.5616	88.8078	2.5570	0.0150
52	chromatin silencing complex	C	2	7	8	28.5714	87.5000	4.7500	0.0160
53	signal recognition particle (sensu Eukaryota)	C	2	10	12	20.0000	83.3333	3.8320	0.0230
54	cytosol	C	14	344	383	4.0698	89.8172	2.3800	0.0260
55	ribonucleoprotein complex	C	14	355	550	3.9437	64.5455	2.2550	0.0310
56	perinuclear region	C	3	37	40	8.1081	92.5000	2.4470	0.0450
57	nucleoplasm	C	13	343	376	3.7901	91.2234	2.0200	0.0460

DOWN-REGULATED - GENMAPP (TREATMENT VERSUS CONTROL)

No.	MAPP Name	Number Changed	Number Measured	Number on MAPP	Percent Changed	Percent Present	Z Score	Permuted P Value
1	Mm_Striated_muscle_contraction	13	42	45	30.9524	93.3333	9.7000	0.0000
2	Mm_2-Tissues-Muscle_Fat_Bone_and_Connective	8	51	55	15.6863	92.7273	4.7460	0.0010
3	Mm_Aminosugars_metabolism	4	24	50	16.6667	48.0000	3.5070	0.0090
4	Mm_Translation_Factors	5	49	50	10.2041	98.0000	2.5560	0.0180
5	Mm_Cell_Cycle_KEGG	7	80	86	8.7500	93.0233	2.5650	0.0210
6	Mm_Purine_metabolism	8	92	146	8.6957	63.0137	2.7260	0.0220
7	Mm_Electron_Transport_Chain	6	66	83	9.0909	79.5181	2.4780	0.0270
8	Mm_mRNA_processing_binding_Reactome	23	426	551	5.3991	77.3140	2.2220	0.0290
9	Mm_Pyrimidine_metabolism	5	51	87	9.8039	58.6207	2.4520	0.0480

DOWN-REGULATED - GENE ONTOLOGY (TREATMENT VERSUS CONTROL)

No.	GO Name	GO Type	Number Changed	Number Measured	Number in GO	Percent Changed	Percent Present	Z Score	Permuted P Value
1	muscle contraction	P	20	132	142	15.1515	92.9578	9.6440	0.0000
2	embryonic hemopoiesis	P	2	2	3	100.0000	66.6667	9.0390	0.0000
3	striated muscle contraction	P	6	20	22	30.0000	90.9091	8.0900	0.0000
4	regulation of muscle contraction	P	7	33	36	21.2121	91.6667	7.0880	0.0000
5	mitosis	P	15	136	146	11.0294	93.1507	6.6280	0.0000
6	muscle development	P	14	149	161	9.3960	92.5466	5.6280	0.0000
7	cell division	P	14	168	178	8.3333	94.3820	5.0730	0.0000
8	regulation of striated muscle contraction	P	3	7	7	42.8571	100.0000	7.0120	0.0010
9	chromosome organization and biogenesis (sensu Eukaryota)	P	14	252	332	5.5556	75.9036	3.3190	0.0010
10	cell cycle	P	27	629	681	4.2925	92.3642	3.1940	0.0010
11	DNA replication	P	10	145	160	6.8966	90.6250	3.5710	0.0020
12	generation of precursor metabolites and energy	P	25	598	722	4.1806	82.8255	2.9280	0.0020
13	purine nucleotide biosynthesis	P	6	75	96	8.0000	78.1250	3.1890	0.0050
14	sarcomere alignment	P	2	4	8	50.0000	50.0000	6.2360	0.0060
15	embryonic development (sensu Mammalia)	P	5	56	58	8.9286	96.5517	3.2100	0.0060
16	germ cell migration	P	2	6	6	33.3333	100.0000	4.9640	0.0070
17	cytoskeleton organization and biogenesis	P	18	385	431	4.6753	89.3272	2.9760	0.0070
18	RNA splicing	P	9	144	167	6.2500	86.2276	3.0480	0.0090
19	gluconeogenesis	P	3	20	20	15.0000	100.0000	3.6950	0.0100
20	heart development	P	7	101	104	6.9307	97.1154	2.9990	0.0110
21	protein polyubiquitination	P	2	6	8	33.3333	75.0000	4.9640	0.0120

22	protein homooligomerization	P	3	23	23	13.0435	100.0000	3.3480	0.0140
23	protein complex assembly	P	12	245	320	4.8980	76.5625	2.5920	0.0190
24	synaptic vesicle exocytosis	P	2	11	11	18.1818	100.0000	3.4310	0.0220
25	actin filament organization	P	4	45	47	8.8889	95.7447	2.8590	0.0220
26	galactose metabolism	P	2	8	8	25.0000	100.0000	4.1880	0.0230
27	DNA-dependent DNA replication	P	5	69	73	7.2464	94.5206	2.6480	0.0230
28	negative regulation of microtubule depolymerization	P	2	10	10	20.0000	100.0000	3.6480	0.0250
29	nucleosome assembly	P	5	67	128	7.4627	52.3438	2.7250	0.0250
30	nuclear mRNA splicing\, via spliceosome	P	7	118	135	5.9322	87.4074	2.5300	0.0270
31	mRNA processing	P	9	173	198	5.2023	87.3737	2.4370	0.0270
32	viral genome replication	P	2	11	13	18.1818	84.6154	3.4310	0.0280
33	regulation of progression through cell cycle	P	15	375	410	4.0000	91.4634	2.0680	0.0420
34	cellular respiration	P	3	34	34	8.8235	100.0000	2.4590	0.0480
35	ER to Golgi vesicle-mediated transport	P	4	53	59	7.5472	89.8305	2.4630	0.0490
36	structural constituent of muscle	F	10	30	34	33.3333	88.2353	11.1090	0.0000
37	cytoskeletal protein binding	F	21	315	344	6.6667	91.5698	5.0240	0.0000
38	ATPase activity	F	19	312	360	6.0897	86.6667	4.3250	0.0000
39	binding	F	253	9103	10565	2.7793	86.1619	3.9390	0.0000
40	nucleotide binding	F	63	1750	1959	3.6000	89.3313	3.5320	0.0000
41	actin binding	F	15	207	230	7.2464	90.0000	4.6080	0.0010
42	RNA binding	F	23	466	548	4.9356	85.0365	3.6570	0.0010
43	ATPase activity\, coupled	F	15	266	301	5.6391	88.3721	3.5020	0.0010
44	motor activity	F	9	121	148	7.4380	81.7568	3.6510	0.0020
45	nucleoside-triphosphatase activity	F	24	498	565	4.8193	88.1416	3.6120	0.0020
46	structural constituent of cytoskeleton	F	7	84	98	8.3333	85.7143	3.5770	0.0020
47	uridine kinase activity	F	2	5	5	40.0000	100.0000	5.5070	0.0030
48	microfilament motor activity	F	3	11	12	27.2727	91.6667	5.4060	0.0030
49	adenylate kinase activity	F	2	6	8	33.3333	75.0000	4.9640	0.0040
50	creatine kinase activity	F	2	4	4	50.0000	100.0000	6.2360	0.0050
51	actin filament binding	F	3	19	20	15.7895	95.0000	3.8270	0.0070
52	RNA polymerase III transcription factor activity	F	2	5	6	40.0000	83.3333	5.5070	0.0100
53	ATP binding	F	41	1180	1331	3.4746	88.6551	2.5450	0.0100
54	calcium-transporting ATPase activity	F	2	6	9	33.3333	66.6667	4.9640	0.0110
55	threonine endopeptidase activity	F	3	18	21	16.6667	85.7143	3.9680	0.0130
56	cytochrome-c oxidase activity	F	3	21	27	14.2857	77.7778	3.5720	0.0150
57	tropomyosin binding	F	2	10	10	20.0000	100.0000	3.6480	0.0160
58	nucleic acid binding	F	82	2710	3327	3.0258	81.4548	2.4010	0.0170
59	transaminase activity	F	3	28	32	10.7143	87.5000	2.8870	0.0200
60	histone binding	F	2	13	13	15.3846	100.0000	3.0690	0.0280
61	helicase activity	F	7	121	136	5.7851	88.9706	2.4560	0.0280
62	structural molecule activity	F	24	632	893	3.7975	70.7727	2.3690	0.0280
63	DNA-directed RNA polymerase activity	F	3	32	36	9.3750	88.8889	2.5900	0.0300
64	ATP-dependent helicase activity	F	6	98	109	6.1224	89.9083	2.4280	0.0320
65	two-component sensor activity	F	2	11	13	18.1818	84.6154	3.4310	0.0330
66	protein binding	F	132	4716	5185	2.7990	90.9547	2.2330	0.0340
67	RNA polymerase II transcription factor activity	F	9	194	208	4.6392	93.2692	2.0650	0.0430
68	striated muscle thin filament	C	6	10	12	60.0000	83.3333	11.9320	0.0000
69	muscle myosin	C	6	12	18	50.0000	66.6667	10.8030	0.0000
70	DNA-directed RNA polymerase I complex	C	3	5	5	60.0000	100.0000	8.4360	0.0000
71	actin cytoskeleton	C	21	206	229	10.1942	89.9563	7.3860	0.0000
72	myosin	C	8	50	58	16.0000	86.2069	6.3120	0.0000
73	intracellular	C	224	6934	8118	3.2305	85.4151	6.3020	0.0000

74	cytoskeleton	C	41	742	859	5.5256	86.3795	5.7400	0.0000
75	cytoplasm	C	127	3484	3969	3.6452	87.7803	5.5540	0.0000
76	protein complex	C	74	1751	2202	4.2262	79.5186	5.3610	0.0000
77	troponin complex	C	2	3	4	66.6667	75.0000	7.2900	0.0010
78	striated muscle thick filament	C	3	8	9	37.5000	88.8889	6.5040	0.0010
79	proteasome complex (sensu Eukaryota)	C	6	37	42	16.2162	88.0952	5.5140	0.0010
80	chromosome	C	15	280	364	5.3571	76.9231	3.2830	0.0010
81	respiratory chain complex IV (sensu Eukaryota)	C	2	4	4	50.0000	100.0000	6.2360	0.0020
82	Z disc	C	4	19	25	21.0526	76.0000	5.3300	0.0020
83	nucleus	C	108	3275	3798	3.2977	86.2296	3.8590	0.0020
84	transcription factor TFIIIC complex	C	2	2	3	100.0000	66.6667	9.0390	0.0030
85	sarcoplasmic reticulum	C	3	13	14	23.0769	92.8571	4.8860	0.0070
86	exocyst	C	2	6	6	33.3333	100.0000	4.9640	0.0110
87	proteasome core complex (sensu Eukaryota)	C	3	18	21	16.6667	85.7143	3.9680	0.0120
88	cytosol	C	15	344	383	4.3605	89.8172	2.4220	0.0150
89	smooth endoplasmic reticulum	C	2	8	8	25.0000	100.0000	4.1880	0.0170
90	chromatin	C	8	141	217	5.6738	64.9770	2.5660	0.0200
91	actin filament	C	3	25	27	12.0000	92.5926	3.1490	0.0220
92	signal recognition particle (sensu Eukaryota)	C	2	10	12	20.0000	83.3333	3.6480	0.0250
93	ribonucleoprotein complex	C	15	355	550	4.2254	64.5455	2.2930	0.0300
94	spliceosome complex	C	5	71	78	7.0423	91.0256	2.5730	0.0340
95	mitochondrial matrix	C	5	74	76	6.7568	97.3684	2.4660	0.0350