

Table 1A. Genes enriched as over-expressed in DPM treatment group

Affy Probeset	Gene Name	mRNA Accession	Gene Description	Fold Change
10538247	Npy	NM_023456	Mus musculus neuropeptide Y (Npy), mRNA.	2.0024
10598062	---	NC_005089	gi 34538597 ref NC_005089.1 :11546-11612, tRNA-His	2.0562
10462618	Ifit3	NM_010501	Mus musculus interferon-induced protein with tetratricopeptide repeats 3 (Ifit3), mRNA.	2.0574
10598071	---	NC_005089	gi 34538597 ref NC_005089.1 :15289-15355, tRNA-Thr	2.0601
10539263	Loxl3	NM_013586	Mus musculus lysyl oxidase-like 3 (Loxl3), mRNA.	2.0733
10381809	Itgb3	NM_016780	Mus musculus integrin beta 3 (Itgb3), mRNA.	2.0891
10566358	Trim30	NM_009099	Mus musculus tripartite motif-containing 30 (Trim30), mRNA.	2.1749
10407327	Emb	NM_010330	Mus musculus embigin (Emb), mRNA.	2.1802
10582888	---	ENSMUST0000099042	cdna:known chromosome:NCBIM37:9:3001070:3002330:1 gene:ENSMUSG00000074566	2.1835
10400967	Six1	NM_009189	Mus musculus sine oculis-related homeobox 1 homolog (Drosophila) (Six1), mRNA.	2.1864
10467826	Hpse2	BC158131	Mus musculus similar to Heparanase-2 (Hpa2), mRNA (cDNA clone MGC:190011 IMAGE:9088198), complete cds.	2.2208
10410931	Vcan	NM_00108129	Mus musculus versican (Vcan), transcript variant 1, mRNA.	2.2243
10467766	Loxl4	BC053925	Mus musculus cDNA clone IMAGE:6311688, partial cds.	2.2390
10522919	Smr2	NM_021289	Mus musculus submaxillary gland androgen regulated protein 2 (Smr2), mRNA.	2.2531
10489429	Wfdc5	NM_145369	Mus musculus WAP four-disulfide core domain 5 (Wfdc5), mRNA.	2.2985
10366546	Cpm	NM_027468	Mus musculus carboxypeptidase M (Cpm), mRNA.	2.3140
10552488	Klk10	NM_133712	Mus musculus kallikrein related-peptidase 10 (Klk10), mRNA.	2.3985
10492355	Mme	NM_008604	Mus musculus membrane metallo endopeptidase (Mme), mRNA.	2.6674
10575211	---	mmu-mir-140	MI0000165 Mus musculus miR-140 stem-loop	2.8980
10522934	Amtn	ENSMUST0000073363	Amelotin gene:ENSMUSG00000029282	3.6794
10513514	Mup5	NM_008649	Mus musculus major urinary protein 5 (Mup5), mRNA.	4.1283
10485357	---	ENSMUST0000099683	cdna:known chromosome:NCBIM37:2:98506704:98507458:-1 gene:ENSMUSG00000075014	4.2577
10598064	---	NC_005089 // NC_005089	gi 34538597 ref NC_005089.1 :11613-11671, tRNA-Ser // gi 34538597 ref NC_005089.1 :11671-11741, tRNA-Leu	4.3329
10421853	Lect1	NM_010701	Mus musculus leukocyte cell derived chemotaxin 1 (Lect1), mRNA.	4.3854

Table 1B. Genes enriched as under-expressed in DPM treatment group

Affy Probeset	Gene Name	mRNA Accession	Gene Description	Fold Change
10386683	Slc47a1	NM_026183	solute carrier family 47, member 1 (Slc47a1).	0.3068
10477512	BC018465	NM_144890	cDNA sequence BC018465 (BC018465).	0.3103
10513512	Mup1	NM_001163011	major urinary protein 1 (Mup1), transcript variant 1.	0.3276
10513497	Mup2	NM_001045550	major urinary protein 2 (Mup2), transcript variant 2.	0.3402
10477495	U46068	NM_001012392	cDNA sequence U46068 (U46068), transcript variant 1.	0.3657
10420362	Gjb2	NM_008125	gap junction protein, beta 2 (Gjb2).	0.3666
10513437	Mup2	NM_008647	major urinary protein 2 (Mup2), transcript variant 1.	0.3910
10442115	Vmn2r96	NM_001104547	vomer nasal 2, receptor 96 (Vmn2r96).	0.4081
10513420	Mup7	NM_001134675	predicted gene 12546 (Gm12546).	0.4202
10410007	Fbp1	NM_019395	fructose biphosphatase 1 (Fbp1).	0.4296
10415081	EG665955	FJ556972	endogenous virus Friend spleen focus-forming virus (SFFVp) cell-line DS19-sc9 envelope glycoprotein 52 mRNA, complete cds.	0.4563
10569008	Cox8b	NM_007751	cytochrome c oxidase, subunit VIIIb (Cox8b), nuclear gene encoding mitochondrial protein.	0.4682
10565609	Thrsp	NM_009381	thyroid hormone responsive SPOT14 homolog (Rattus) (Thrsp).	0.4769
10543017	Pdk4	NM_013743	pyruvate dehydrogenase kinase, isoenzyme 4 (Pdk4).	0.4841

Table 2A. Functional enrichment (based on GO Biological Process) of genes over-expressed in DPM treatment group using DAVID.

Annotation Cluster 1	Enrichment Score: 4.4	Count	P_Value	Benjamin i
SP_PIR_KEYWORDS	signal	43	8.7E-8	1.7E-5
UP_SEQ_FEATURE	signal peptide	43	5.4E-7	2.6E-4
SP_PIR_KEYWORDS	glycoprotein	42	3.9E-5	2.5E-3
SP_PIR_KEYWORDS	disulfide bond	32	8.7E-5	4.2E-3
UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...)	41	1.6E-4	3.7E-2
UP_SEQ_FEATURE	disulfide bond	31	3.7E-4	5.8E-2
Annotation Cluster 2	Enrichment Score: 4.53	Count	P_Value	Benjamin i
GOTERM_CC_FAT	extracellular region	31	1.0E-6	1.6E-4
SP_PIR_KEYWORDS	Secreted	24	2.0E-5	1.9E-3
GOTERM_CC_FAT	extracellular region part	15	1.2E-3	4.4E-2
Annotation Cluster 3	Enrichment Score: 3.47	Count	P_Value	Benjamin i
GOTERM_BP_FAT	cell adhesion	14	6.9E-5	5.1E-2
GOTERM_BP_FAT	biological adhesion	14	7.1E-5	2.6E-2
SP_PIR_KEYWORDS	cell adhesion	10	6.5E-4	2.5E-2
INTERPRO	EGF-like region, conserved site	8	4.1E-3	2.9E-1

Table 2B. Functional enrichment (based on GO Biological Process) of genes under-expressed in DPM treatment group using DAVID.

Annotation Cluster 1	Enrichment Score: 4.4	Count	P_Value	Benjamin i
GOTERM_CC_FAT	extracellular region	27	1.3E-9	9.1E-8
SP_PIR_KEYWORDS	Secreted	21	1.0E-7	1.6E-5
SP_PIR_KEYWORDS	signal	30	1.7E-7	1.3E-5
UP_SEQ_FEATURE	signal peptide	30	1.1E-6	3.0E-4
SP_PIR_KEYWORDS	disulfide bond	18	7.2E-3	1.6E-1
UP_SEQ_FEATURE	disulfide bond	18	1.2E-2	8.0E-1
SP_PIR_KEYWORDS	glycoprotein	21	3.3E-2	4.6E-1
UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...)	20	8.9E-2	9.8E-1

Table 3. Cell growth, proliferation and migration related functions of those genes differentially-enriched in the DPM treatment group

Gene Function	Up-regulated Gene	Down-regulated Gene
Cell adhesion	Mme, Edil3, Lypd3, Amtn, Vcan, Ccdc80, Col11a1, Dsg3, Emb, Flrt3, Itgb4, Itgb3, Lgals3bp, Llg12, Pcdh9, Tubb2b, Tnc, Thbs	Cldn2, Dsc1
Negative regulation of cell proliferation	H19, Npy	
Apoptosis	Sap30bp, Casp1, Casp12, Casp1, Xaf1, Slc5a8	
Autophagy	Wipi1	
Anti-angiogenesis	Lect1	
MAPKKK cascade	Gadd45b, Plce1, Prkca, Map3k3	
Tumorigenesis	Klk10	

** Bold font indicates gene validated by qPCR and by western blotting*

Table 4. Comparison of gene expression fold changes between microarray and qPCR.

Up-regulated Gene from Microarray			Down-regulated Gene from Microarray		
Gene Name	Fold Change (RT-qPCR)	Fold Change (microarray)	Gene Name	Fold Change (RT-qPCR)	Fold Change (microarray)
Npy	9.5889	2.0024	Slc47a1	1.8024	0.3068
Ifit3	2.9347	2.0574	BC018465	2.1201	0.3103
Loxl3	4.7443	2.0733	Mup1	13.4641	0.3276
Itgb3	4.7117	2.0891	Mup2 (transcript variant 2)	4.1853	0.3402
Trim30	1.3263	2.1749	U46068	1.8993	0.3657
Emb	3.7531	2.1802	Gjb2	0.4993	0.3666
Six1	14.4140	2.1864	Mup2 (transcript variant 1)	12.1766	0.3910
Hpse2	7.0131	2.2208	Vmn2r96	1.3226	0.4081
Vcan	3.4556	2.2243	Mup7	2.1216	0.4202
Loxl4	1.4325	2.2390	Fbp1	0.6392	0.4296
Smr2	0.4123	2.2531	EG665955	1.1455	0.4563
Wfdc5	12.5628	2.2985	Cox8b	0.3432	0.4682
Cpm	3.6211	2.3140	Thrsp	0.3835	0.4769
Klk10	30.5677	2.3985	Pdk4	0.6708	0.4841
Mme	4.2186	2.6674			
Amtn	11.3662	3.6794			
Mup5	23.5264	4.1283			
Lect1	16.8956	4.3854			

Table 5. Differentially expressed miRNAs in DPM treatment group

Affy Probeset	Up-regulated		Affy Probeset	Down-regulated	
	Fold Change (qPCR)	Fold Change (array)		Fold Change (qPCR)	Fold Change (array)
mmu-miR-455-star_st	N.D.	3.6571	mmu-miR-322_st	N.D.	0.6643
v11_mmu-miR-685_st	1.4507	3.4884	mmu-miR-148b_st	N.D.	0.6547
mmu-miR-140-star_st	59.0232	3.0054	mmu-miR-139-5p_st	N.D.	0.6491
mmu-miR-1937b_st	1.7365	2.9470	mmu-miR-181a-1-star_st	N.D.	0.6445
mmu-miR-140_st	4.71232	2.8451	mmu-let-7d-star_st	N.D.	0.6428
v11_mmu-miR-699_st	N.D.	2.6581	mmu-miR-101b_st	N.D.	0.6299
mmu-miR-1937a_st	1.9141	2.6132	mmu-miR-148a-star_st	N.D.	0.6288
mmu-miR-455_st	8.7503	2.6124	mmu-miR-10b_st	N.D.	0.6129
mmu-miR-711_st		2.5429	mmu-miR-203_st	1.1972	0.6005
mmu-miR-10a_st	N.D. N.D.	2.3127	mmu-miR-466b-3p_st	N.D.	0.5953
mmu-miR-1274a_st	N.D.	2.0029	mmu-miR-532-3p_st	N.D.	0.5879
hp_mmu-mir-465c-2_s_st	N.D.	1.9301	mmu-miR-434-3p_st	N.D.	0.5836
mmu-miR-712_st	N.D.	1.8635	mmu-miR-466e-3p_st	N.D.	0.5820
mmu-miR-503_st	N.D.	1.8343	mmu-miR-98_st	N.D.	0.5793
mmu-miR-1931_st	N.D.	1.7642	mmu-miR-375_st	N.D.	0.5412
mmu-miR-298_st	N.D.	1.7481	mmu-miR-193_st	N.D.	0.5407
mmu-miR-1949_st	1.3557	1.7196	mmu-miR-329_st	N.D.	0.5405
mmu-miR-1839-3p_st	N.D.	1.6043	mmu-miR-128_st	N.D.	0.5375
mmu-miR-2133_st	N.D.	1.5995	mmu-miR-1895_st	N.D.	0.5295
hp_mmu-mir-465c-1_s_st	N.D.	1.5710	mmu-miR-148a_st	0.8957	0.5251
mmu-miR-214_st	1.9402	1.5704	mmu-miR-467e_st	N.D.	0.5186
mmu-miR-326_st	N.D.	1.5668	v11_mmu-miR-467a-str_st	N.D.	0.4786
mmu-miR-351_st	3.3836	1.5661	mmu-miR-15b_st	28.2102	0.4770
mmu-miR-762_st	1.0757	1.5623	mmu-miR-125a-5p_st	3.2956	0.4483
mmu-miR-150_st	N.D.	1.5286	mmu-miR-374_st	N.D.	0.2218
mmu-miR-133a_st	N.D.	1.5211	mmu-miR-34c-star_st	N.D.	0.1489
mmu-miR-690_st	0.8865	1.5051		N.D.	

N.D. = not determined, or not detectable by qPCR