

Supplemental data, Table 2

Analysis was performed using the Bioconductor program for R, with the Affymetrix linear modeling Graphical User Interface (affymGUI) package

Fold change is calculated from the log₂-fold change

M=log₂-fold change

A=(log signal for vehicle samples + log signal for treated samples)/2

t=moderated t-statistic

P.Value (adjusted for multiple testing) <0.05 is used as threshold for significantly changed expression

B=the posterior log-odds of differential expression

Genes increased after treatment with 1.0 mg/kg PPT

	ID	Symbol	Name	Fold change	M	A	t	P.Value	B
4000	1419669_at	Prtn3	proteinase 3	69.3	6.1	8.1	27.1	0.000004	11.6
9413	1425107_a_at	Lifr	leukemia inhibitory factor receptor	34.8	5.1	10.7	38.3	0.000001	12.9
4035	1419704_at	Cyp3a41	cytochrome P450, family 3, subfamily a, polypeptide 41	21.6	4.4	9.3	11.0	0.000870	5.8
5381	1421075_s_at	Cyp7b1	cytochrome P450, family 7, subfamily b, polypeptide 1	14.2	3.8	7.9	15.0	0.000142	8.1
22960	1438654_x_at	Mmd2	monocyte to macrophage differentiation-associated 2	14.0	3.8	9.0	28.0	0.000004	11.7
3348	1419017_at	Corin	corin	13.3	3.7	7.2	19.1	0.000039	9.7
5975	1421669_at	Sult3a1	sulfotransferase family 3A, member 1	12.9	3.7	10.2	9.8	0.001606	4.9
13450	1429144_at	Prei4	preimplantation protein 4	12.6	3.7	10.6	39.1	0.000001	13.0
5380	1421074_at	Cyp7b1	cytochrome P450, family 7, subfamily b, polypeptide 1	12.5	3.6	8.8	15.7	0.000110	8.5
10007	1425701_a_at	Rgs3	regulator of G-protein signaling 3	12.2	3.6	6.7	16.7	0.000091	8.9
22259	1437953_at	Prei4	preimplantation protein 4	11.2	3.5	5.9	21.1	0.000021	10.3
8840	1424534_at	Mmd2	monocyte to macrophage differentiation-associated 2	11.1	3.5	9.0	32.6	0.000002	12.4
13945	1429639_at	Prei4	preimplantation protein 4	10.6	3.4	8.7	23.7	0.000008	10.9
13283	1428977_at	Chst8	carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 8	10.2	3.4	5.7	15.4	0.000123	8.3
26656	1442350_at	NA	NA	9.9	3.3	5.6	16.4	0.000098	8.7
34840	1450545_a_at	Dntt	deoxynucleotidyltransferase, terminal	9.7	3.3	8.3	26.1	0.000004	11.4
20717	1436411_at	Atp13a5	ATPase type 13A5	9.4	3.2	4.9	16.2	0.000101	8.7
34056	1449757_x_at	Dntt	deoxynucleotidyltransferase, terminal	8.9	3.2	8.3	29.0	0.000003	11.9
42038	1457743_at	D13Bwg1146e	DNA segment, Chr 13, Brigham & Women's Genetics 1146 expressed	8.8	3.1	4.8	10.1	0.001434	5.1
10460	1426154_s_at	Mup3	major urinary protein 3	8.6	3.1	9.7	6.9	0.010023	2.1
37208	1452913_at	Pcp4l1	Purkinje cell protein 4-like 1	8.1	3.0	6.9	20.5	0.000025	10.1
24749	1440443_at	Prei4	preimplantation protein 4	7.0	2.8	7.3	11.0	0.000874	5.8

ID	Symbol	Name	Fold change	M	A	t	P.Value	B	
308	1415977_at	Isyna1	myo-inositol 1-phosphate synthase A1	6.8	2.8	8.1	18.8	0.000044	9.6
28548	1444242_at	Slco2a1	solute carrier organic anion transporter family, member 2a1	6.7	2.8	6.3	19.4	0.000038	9.8
11658	1427352_at	BC031593	cDNA sequence BC031593	6.7	2.7	6.5	9.6	0.001885	4.8
23478	1439172_at	Atp13a5	ATPase type 13A5	6.5	2.7	4.9	10.1	0.001431	5.1
21865	1437559_at	D13Bwg1146e	DNA segment, Chr 13, Brigham & Women's Genetics 1146 expressed	6.1	2.6	5.2	8.7	0.003164	3.9
3166	1418835_at	Phlda1	pleckstrin homology-like domain, family A, member 1	6.0	2.6	8.1	13.5	0.000264	7.4
37159	1452864_at	Med12l	mediator of RNA polymerase II transcription, subunit 12 homolog (yeast)-li	5.9	2.6	5.8	17.6	0.000069	9.2
1185	1416854_at	Slc34a2	solute carrier family 34 (sodium phosphate), member 2	5.8	2.5	8.8	9.9	0.001521	5.0
42996	1458701_at	Prei4	preimplantation protein 4	5.5	2.5	6.5	9.4	0.002083	4.6
20001	1435695_a_at	A030007L17Ri	RIKEN cDNA A030007L17 gene	5.4	2.4	9.2	26.9	0.000004	11.6
34327	1450032_at	Slco2a1	solute carrier organic anion transporter family, member 2a1	5.0	2.3	7.8	12.6	0.000373	6.9
8166	1423860_at	Ptgds	prostaglandin D2 synthase (brain)	4.9	2.3	6.7	8.1	0.004724	3.4
25421	1441115_at	Rnf125	ring finger protein 125	4.9	2.3	5.1	5.3	0.027965	0.2
33667	1449367_at	Trex2	three prime repair exonuclease 2	4.8	2.3	6.8	9.1	0.002443	4.3
11039	1426733_at	Itpk1	inositol 1,3,4-triphosphate 5/6 kinase	4.8	2.3	9.4	24.8	0.000006	11.2
42829	1458534_at	D13Bwg1146e	DNA segment, Chr 13, Brigham & Women's Genetics 1146 expressed	4.7	2.2	5.2	6.6	0.012630	1.8
2159	1417828_at	Aqp8	aquaporin 8	4.5	2.2	11.7	15.8	0.000110	8.5
28576	1444270_at	Rshl3	radial spokehead-like 3	4.4	2.2	7.2	11.2	0.000767	6.0
5219	1420913_at	Slco2a1	solute carrier organic anion transporter family, member 2a1	4.4	2.1	9.1	13.3	0.000274	7.3
33669	1449369_at	Tmprss2	transmembrane protease, serine 2	4.4	2.1	7.5	6.9	0.009930	2.1
12790	1428484_at	Osbpl3	oxysterol binding protein-like 3	4.4	2.1	8.6	14.3	0.000199	7.8
39279	1454984_at	A230075M04R	RIKEN cDNA A230075M04 gene	4.3	2.1	9.9	14.0	0.000229	7.6
40195	1455900_x_at	Tgm2	transglutaminase 2, C polypeptide	4.3	2.1	10.9	14.3	0.000202	7.8
15199	1430893_at	Mup1	major urinary protein 1	4.3	2.1	6.3	9.4	0.002127	4.5
21583	1437277_x_at	Tgm2	transglutaminase 2, C polypeptide	4.1	2.0	10.6	12.0	0.000523	6.5
35883	1451588_at	1810022C23Ri	RIKEN cDNA 1810022C23 gene	4.1	2.0	6.4	17.6	0.000069	9.2
23167	1438861_at	Bnc2	basonuclin 2	4.0	2.0	4.9	11.6	0.000627	6.2
32561	1448261_at	Cdh1	cadherin 1	4.0	2.0	6.9	4.7	0.044241	-0.7
8165	1423859_a_at	Ptgds	prostaglandin D2 synthase (brain)	4.0	2.0	7.7	6.5	0.013045	1.7
22779	1438473_at	Arl15	ADP-ribosylation factor-like 15	3.9	2.0	6.8	11.8	0.000567	6.4
11717	1427411_s_at	Dleu2	deleted in lymphocytic leukemia, 2	3.9	2.0	5.6	7.3	0.007706	2.6
1730	1417399_at	Gas6	growth arrest specific 6	3.9	2.0	9.6	16.2	0.000101	8.6
9602	1425296_a_at	Rgs3	regulator of G-protein signaling 3	3.9	2.0	8.3	9.9	0.001521	5.0
17734	1433428_x_at	Tgm2	transglutaminase 2, C polypeptide	3.9	2.0	11.0	10.4	0.001172	5.4

ID	Symbol	Name	Fold change	M	A	t	P.Value	B	
23030	1438724_at	Osbpl3	oxysterol binding protein-like 3	3.8	1.9	6.9	10.7	0.001043	5.6
42642	1458347_s_at	Tmprss2	transmembrane protease, serine 2	3.8	1.9	6.0	7.3	0.007930	2.5
44241	1459948_at	Ghr	growth hormone receptor	3.7	1.9	6.1	5.2	0.031863	0.0
1831	1417500_a_at	Tgm2	transglutaminase 2, C polypeptide	3.7	1.9	11.1	13.2	0.000283	7.2
3485	1419154_at	Tmprss2	transmembrane protease, serine 2	3.7	1.9	7.2	8.3	0.004166	3.6
4485	1420166_at	Dntt	deoxynucleotidyltransferase, terminal	3.7	1.9	5.3	10.5	0.001145	5.5
18416	1434110_x_at	Mup1	major urinary protein 1	3.6	1.9	11.0	6.3	0.014160	1.5
7236	1422930_at	Icam4	intercellular adhesion molecule 4, Landsteiner-Wiener blood group	3.6	1.8	5.6	16.8	0.000091	8.9
17948	1433642_at	Arl15	ADP-ribosylation factor-like 15	3.5	1.8	7.4	16.1	0.000101	8.6
10310	1426004_a_at	Tgm2	transglutaminase 2, C polypeptide	3.4	1.8	9.2	13.6	0.000263	7.4
43127	1458832_at	Ghr	growth hormone receptor	3.4	1.8	5.7	7.2	0.008030	2.5
18474	1434168_at	Peo1	progressive external ophthalmoplegia 1 (human)	3.4	1.7	8.9	11.9	0.000529	6.4
34502	1450207_at	Lifr	leukemia inhibitory factor receptor	3.4	1.7	5.9	13.5	0.000264	7.4
3280	1418949_at	Gdf15	growth differentiation factor 15	3.3	1.7	8.9	7.2	0.008482	2.4
5775	1421469_a_at	Stat5a	signal transducer and activator of transcription 5A	3.3	1.7	8.1	7.8	0.005509	3.1
34796	1450501_at	Itga2	integrin alpha 2	3.3	1.7	5.1	10.4	0.001172	5.4
32906	1448606_at	Edg2	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptc	3.2	1.7	6.5	15.0	0.000142	8.1
41353	1457058_at	Adamts2	a disintegrin-like and metallopeptidase (repolysin type) with thrombosponc	3.2	1.7	6.6	9.1	0.002449	4.3
34554	1450259_a_at	Stat5a	signal transducer and activator of transcription 5A	3.2	1.7	7.1	8.0	0.004847	3.3
1080	1416749_at	Htra1	HtrA serine peptidase 1	3.2	1.7	6.3	8.2	0.004267	3.5
4771	1420465_s_at	Mup1	major urinary protein 1	3.2	1.7	13.5	13.4	0.000274	7.3
11716	1427410_at	Dleu2	deleted in lymphocytic leukemia, 2	3.2	1.7	6.5	5.4	0.027088	0.3
13573	1429267_at	Acot11	acyl-CoA thioesterase 11	3.1	1.6	6.1	4.5	0.048915	-0.9
44610	1460318_at	Csrp3	cysteine and glycine-rich protein 3	3.1	1.6	9.2	15.9	0.000110	8.5
18603	1434297_at	E130304F04Ri	RIKEN cDNA E130304F04 gene	3.1	1.6	5.6	8.3	0.004170	3.6
3446	1419115_at	Alg14	asparagine-linked glycosylation 14 homolog (yeast)	3.0	1.6	6.9	13.3	0.000274	7.2
17752	1433446_at	Hmgcs1	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1	2.9	1.5	10.9	10.6	0.001083	5.5
11217	1426911_at	Dsc2	desmocollin 2	2.9	1.5	8.0	12.3	0.000446	6.7
353	1416022_at	Fabp5	fatty acid binding protein 5, epidermal	2.9	1.5	8.8	8.2	0.004259	3.5
21182	1436876_at	D13Bwg1146e	DNA segment, Chr 13, Brigham & Women's Genetics 1146 expressed	2.9	1.5	7.0	8.0	0.004841	3.3
5462	1421156_a_at	Dsc2	desmocollin 2	2.9	1.5	8.4	17.1	0.000083	9.0
24164	1439858_at	NA	NA	2.8	1.5	7.3	11.7	0.000603	6.3
17749	1433443_a_at	Hmgcs1	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1	2.8	1.5	12.4	11.2	0.000766	6.0
31533	1447227_at	Slc40a1	solute carrier family 40 (iron-regulated transporter), member 1	2.8	1.5	7.3	10.6	0.001083	5.5

ID	Symbol	Name	Fold change	M	A	t	P.Value	B	
1701	1417370_at	Tff3	trefoil factor 3, intestinal	2.8	1.5	6.7	7.1	0.008807	2.3
22700	1438394_x_at	Krt4	keratin 4	2.8	1.5	5.3	6.6	0.012195	1.8
37025	1452730_at	1110033J19Ri	RIKEN cDNA 1110033J19 gene	2.7	1.5	8.4	13.2	0.000280	7.2
40184	1455889_at	Mlstd1	male sterility domain containing 1	2.7	1.4	4.6	10.6	0.001108	5.5
37318	1453023_at	Ankhd1	ankyrin repeat and KH domain containing 1	2.7	1.4	9.3	4.9	0.036982	-0.3
2683	1418352_at	Hsd17b2	hydroxysteroid (17-beta) dehydrogenase 2	2.6	1.4	11.2	11.8	0.000584	6.3
24101	1439795_at	Gpr64	G protein-coupled receptor 64	2.6	1.4	6.4	5.9	0.018790	0.9
6766	1422460_at	Mad21	MAD2 (mitotic arrest deficient, homolog)-like 1 (yeast)	2.6	1.4	8.0	7.9	0.005255	3.2
32382	1448080_at	E2f8	E2F transcription factor 8	2.6	1.4	7.8	4.7	0.042177	-0.6
41099	1456804_at	Av381130	NA	2.6	1.4	5.6	5.5	0.023911	0.5
6253	1421947_at	Gng12	guanine nucleotide binding protein (G protein), gamma 12	2.6	1.4	9.4	8.6	0.003269	3.9
8834	1424528_at	Cgref1	cell growth regulator with EF hand domain 1	2.6	1.4	7.3	6.9	0.009608	2.2
352	1416021_a_at	Fabp5	fatty acid binding protein 5, epidermal	2.5	1.4	10.1	7.9	0.005237	3.2
483	1416152_a_at	Sfrs3	splicing factor, arginine/serine-rich 3 (SRp20)	2.5	1.3	7.3	7.2	0.008030	2.5
2838	1418507_s_at	Socs2	suppressor of cytokine signaling 2	2.5	1.3	6.3	5.9	0.018944	0.9
5210	1420904_at	Il17ra	interleukin 17 receptor A	2.5	1.3	6.9	13.3	0.000274	7.3
36555	1452260_at	Cidec	cell death-inducing DFFA-like effector c	2.5	1.3	9.5	5.8	0.019584	0.9
5211	1420905_at	Il17ra	interleukin 17 receptor A	2.5	1.3	7.6	12.0	0.000523	6.5
3475	1419144_at	Cd163	CD163 antigen	2.5	1.3	7.3	6.0	0.016886	1.1
37338	1453043_at	0610012H03Ri	RIKEN cDNA 0610012H03 gene	2.5	1.3	9.1	16.5	0.000098	8.8
33041	1448741_at	Slc3a1	solute carrier family 3, member 1	2.5	1.3	8.7	8.3	0.004033	3.6
1474	1417143_at	Edg2	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptc	2.5	1.3	5.7	13.4	0.000274	7.3
17751	1433445_x_at	Hmgcs1	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1	2.5	1.3	12.3	10.1	0.001426	5.1
19017	1434711_at	BC030867	cDNA sequence BC030867	2.4	1.3	6.1	8.7	0.003216	3.9
2660	1418329_at	Pgpep1	pyroglutamyl-peptidase I	2.4	1.3	9.2	12.9	0.000328	7.0
3445	1419114_at	Alg14	asparagine-linked glycosylation 14 homolog (yeast)	2.4	1.3	9.3	9.9	0.001521	5.0
12287	1427981_a_at	Csad	cysteine sulfinic acid decarboxylase	2.4	1.3	11.3	9.6	0.001885	4.8
18395	1434089_at	Synpo	synaptopodin	2.4	1.2	6.5	5.4	0.025477	0.4
482	1416151_at	Sfrs3	splicing factor, arginine/serine-rich 3 (SRp20)	2.3	1.2	6.5	9.2	0.002371	4.4
36083	1451788_at	F11	coagulation factor XI	2.3	1.2	8.7	7.1	0.008562	2.4
10913	1426607_at	Grik5	glutamate receptor, ionotropic, kainate 5 (gamma 2)	2.3	1.2	7.5	6.5	0.013045	1.7
32705	1448405_a_at	Cri1	CREBBP/EP300 inhibitory protein 1	2.3	1.2	6.6	6.0	0.018071	1.0
14601	1430295_at	Gna13	guanine nucleotide binding protein, alpha 13	2.3	1.2	7.9	10.5	0.001168	5.4
39384	1455089_at	Gng12	guanine nucleotide binding protein (G protein), gamma 12	2.3	1.2	9.2	7.0	0.009257	2.2

ID	Symbol	Name	Fold change	M	A	t	P.Value	B	
33052	1448752_at	Car2	carbonic anhydrase 2	2.3	1.2	9.2	10.1	0.001401	5.2
12853	1428547_at	Nt5e	5' nucleotidase, ecto	2.3	1.2	9.4	8.7	0.003041	4.0
8835	1424529_s_at	Cgref1	cell growth regulator with EF hand domain 1	2.3	1.2	7.8	8.2	0.004267	3.5
2359	1418028_at	Dct	dopachrome tautomerase	2.3	1.2	9.1	9.4	0.002083	4.6
17750	1433444_at	Hmgcs1	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1	2.2	1.2	11.9	6.5	0.012929	1.7
9287	1424981_at	Nln	neurolysin (metallopeptidase M3 family)	2.2	1.2	8.5	13.9	0.000236	7.6
5220	1420914_at	Slco2a1	solute carrier organic anion transporter family, member 2a1	2.2	1.2	5.9	7.1	0.008619	2.4
7222	1422916_at	Fgf21	fibroblast growth factor 21	2.2	1.2	9.2	7.1	0.008807	2.3
10175	1425869_a_at	Psen2	presenilin 2	2.2	1.2	12.0	11.3	0.000731	6.0
24892	1440586_at	B430203I24Rik	RIKEN cDNA B430203I24 gene	2.2	1.2	5.2	5.8	0.020278	0.8
28351	1444045_at	A430107O13R	RIKEN cDNA A430107O13 gene	2.2	1.1	5.3	13.6	0.000263	7.4
23606	1439300_at	Chic1	cysteine-rich hydrophobic domain 1	2.2	1.1	6.2	4.9	0.038325	-0.4
18755	1434449_at	Aqp4	aquaporin 4	2.2	1.1	9.3	7.6	0.006338	2.9
34906	1450611_at	Orm3	orosomucoid 3	2.2	1.1	8.2	7.5	0.006697	2.8
15954	1431648_at	4930528F23Rik	RIKEN cDNA 4930528F23 gene	2.2	1.1	6.2	4.7	0.044553	-0.7
33278	1448978_at	Ngef	neuronal guanine nucleotide exchange factor	2.2	1.1	7.1	10.9	0.000920	5.7
8160	1423854_a_at	Rasl11b	RAS-like, family 11, member B	2.2	1.1	7.4	5.2	0.030364	0.0
34647	1450352_at	Mtnr1a	melatonin receptor 1A	2.2	1.1	7.7	9.6	0.001965	4.7
2574	1418243_at	Fcna	ficolin A	2.1	1.1	8.9	7.0	0.009195	2.3
37183	1452888_at	1110034G24Rik	RIKEN cDNA 1110034G24 gene	2.1	1.1	6.2	7.0	0.009022	2.3
43719	1459424_at	Tmem56	transmembrane protein 56	2.1	1.1	6.6	6.8	0.011149	2.0
2309	1417978_at	Eif4e3	eukaryotic translation initiation factor 4E member 3	2.1	1.1	7.1	7.7	0.006092	3.0
35858	1451563_at	Emr4	EGF-like module containing, mucin-like, hormone receptor-like sequence	2.1	1.1	7.1	5.0	0.034182	-0.2
2198	1417867_at	Cfd	complement factor D (adipsin)	2.1	1.1	5.3	4.7	0.043043	-0.7
24158	1439852_at	NA	NA	2.1	1.1	4.2	10.0	0.001471	5.1
35850	1451555_at	Nln	neurolysin (metallopeptidase M3 family)	2.1	1.1	8.5	11.3	0.000736	6.0
18790	1434484_at	1100001G20Rik	RIKEN cDNA 1100001G20 gene	2.1	1.1	12.5	5.2	0.031863	0.0
41698	1457403_at	9130409I23Rik	RIKEN cDNA 9130409I23 gene	2.1	1.0	8.5	5.1	0.033681	-0.2
8595	1424289_at	BC010311	cDNA sequence BC010311	2.1	1.0	5.1	9.4	0.002083	4.6
9821	1425515_at	Pik3r1	phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 1 (p85 alpha	2.1	1.0	8.0	7.0	0.009195	2.3
22245	1437939_s_at	Ctsc	cathepsin C	2.0	1.0	5.4	6.6	0.012474	1.8
35794	1451499_at	Cadps2	Ca ²⁺ -dependent activator protein for secretion 2	2.0	1.0	7.2	11.3	0.000736	6.0
39288	1454993_a_at	Sfrs3	splicing factor, arginine/serine-rich 3 (SRp20)	2.0	1.0	7.8	6.5	0.013164	1.6
30674	1446368_at	9130221J18Rik	RIKEN cDNA 9130221J18 gene	2.0	1.0	6.6	5.9	0.019103	0.9

ID	Symbol	Name	Fold change	M	A	t	P.Value	B	
36385	1452090_a_at	Olfm3	olfactomedin 3	2.0	1.0	5.6	9.1	0.002449	4.3
6136	1421830_at	Ak3l1	adenylate kinase 3 alpha-like 1	2.0	1.0	9.4	9.4	0.002083	4.6
28266	1443960_at	NA	NA	2.0	1.0	6.7	6.6	0.012711	1.7
8702	1424396_a_at	Asrgl1	asparaginase like 1	2.0	1.0	8.2	9.2	0.002357	4.4
3151	1418820_s_at	Zcchc10	zinc finger, CCHC domain containing 10	2.0	1.0	5.4	6.4	0.013933	1.5
8938	1424632_a_at	Rev3l	REV3-like, catalytic subunit of DNA polymerase zeta RAD54 like (S. cerev	2.0	1.0	8.2	8.9	0.002785	4.1
18319	1434013_at	Ablim3	actin binding LIM protein family, member 3	2.0	1.0	5.7	7.1	0.008807	2.3
39729	1455434_a_at	Ktn1	kinectin 1	2.0	1.0	9.2	9.0	0.002492	4.2
28931	1444625_at	LOC545822	NA	2.0	1.0	6.3	7.8	0.005643	3.1
15006	1430700_a_at	Pla2g7	phospholipase A2, group VII (platelet-activating factor acetylhydrolase, pla	2.0	1.0	7.5	6.5	0.013055	1.6
3241	1418910_at	Bmp7	bone morphogenetic protein 7	2.0	1.0	4.7	6.0	0.017740	1.1
13064	1428758_at	Tmem86a	transmembrane protein 86A	2.0	1.0	8.8	7.1	0.008807	2.3
24125	1439819_at	AU015263	expressed sequence AU015263	2.0	1.0	5.8	4.6	0.045537	-0.8
10832	1426526_s_at	Ovgp1	oviductal glycoprotein 1	2.0	1.0	4.8	10.1	0.001401	5.2
44883	1460591_at	Esr1	estrogen receptor 1 (alpha)	2.0	1.0	9.0	9.5	0.002044	4.6
9322	1425016_at	Ephb2	Eph receptor B2	2.0	1.0	5.6	5.6	0.023894	0.5
2308	1417977_at	Eif4e3	eukaryotic translation initiation factor 4E member 3	2.0	1.0	7.4	6.3	0.014038	1.5
18393	1434087_at	Mthfr	5,10-methylenetetrahydrofolate reductase	2.0	1.0	7.4	4.5	0.049808	-1.0
10204	1425898_x_at	Olfm3	olfactomedin 3	2.0	1.0	6.3	8.5	0.003448	3.8
36071	1451776_s_at	Hod	homeobox only domain	2.0	1.0	10.0	9.9	0.001521	5.0
9688	1425382_a_at	Aqp4	aquaporin 4	2.0	1.0	9.0	7.9	0.005143	3.2
1671	1417340_at	Txnl2	thioredoxin-like 2	2.0	1.0	9.0	8.0	0.004876	3.3
11287	1426981_at	Pcsk6	proprotein convertase subtilisin/kexin type 6	2.0	1.0	9.7	7.3	0.007772	2.6

Genes decreased after treatment with 1.0 mg/kg PPT

ID	Symbol	Name	Fold change	M	A	t	P.Value	B	
33825	1449525_at	Fmo3	flavin containing monooxygenase 3	-18.0	-4.2	8.6	-13.6	0.000263	7.4
15712	1431406_at	Agxt2l1	alanine-glyoxylate aminotransferase 2-like 1	-5.8	-2.5	7.5	-5.0	0.036909	-0.3
22517	1438211_s_at	Dbp	D site albumin promoter binding protein	-4.5	-2.2	8.2	-4.7	0.042238	-0.6
10143	1425837_a_at	Ccrn4l	CCR4 carbon catabolite repression 4-like (S. cerevisiae)	-4.3	-2.1	7.8	-5.2	0.031100	0.0

ID	Symbol	Name	Fold change	M	A	t	P.Value	B	
18802	1434496_at	Plk3	polo-like kinase 3 (Drosophila)	-4.3	-2.1	7.2	-6.0	0.017740	1.1
2505	1418174_at	Dbp	D site albumin promoter binding protein	-4.0	-2.0	7.3	-5.4	0.026251	0.3
480	1416149_at	Olig1	oligodendrocyte transcription factor 1	-3.9	-2.0	6.6	-15.5	0.000123	8.3
23683	1439377_x_at	Cdc20	cell division cycle 20 homolog (S. cerevisiae)	-3.5	-1.8	5.7	-5.5	0.024008	0.5
33433	1449133_at	Sprr1a	small proline-rich protein 1A	-3.4	-1.8	6.2	-8.2	0.004308	3.5
5347	1421041_s_at	Gsta2	glutathione S-transferase, alpha 2 (Yc2)	-3.4	-1.8	10.4	-11.9	0.000529	6.4
33453	1449153_at	Mmp12	matrix metalloproteinase 12	-3.2	-1.7	5.2	-5.3	0.029475	0.1
2231	1417900_a_at	Vldlr	very low density lipoprotein receptor	-3.1	-1.6	6.4	-13.7	0.000263	7.5
36010	1451715_at	Mafb	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein B (avian	-3.1	-1.6	6.4	-6.6	0.012521	1.8
2356	1418025_at	Bhlhb2	basic helix-loop-helix domain containing, class B2	-3.1	-1.6	9.2	-12.6	0.000378	6.8
36011	1451716_at	Mafb	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein B (avian	-3.0	-1.6	7.9	-6.8	0.010904	2.0
15520	1431214_at	1300007C21Ri	RIKEN cDNA 1300007C21 gene	-3.0	-1.6	9.6	-7.5	0.006513	2.8
2152	1417821_at	D17H6S56E-5	DNA segment, Chr 17, human D6S56E 5	-2.9	-1.5	6.1	-5.7	0.020791	0.7
19494	1435188_at	Gm129	gene model 129, (NCBI)	-2.9	-1.5	7.2	-7.6	0.006228	2.9
6124	1421818_at	Bcl6	B-cell leukemia/lymphoma 6	-2.9	-1.5	6.8	-15.0	0.000142	8.1
35215	1450920_at	Ccnb2	cyclin B2	-2.8	-1.5	5.7	-7.0	0.009195	2.3
1396	1417065_at	Egr1	early growth response 1	-2.8	-1.5	6.5	-7.2	0.008220	2.5
12189	1427883_a_at	Col3a1	procollagen, type III, alpha 1	-2.8	-1.5	7.8	-7.4	0.007212	2.7
11537	1427231_at	Robo1	roundabout homolog 1 (Drosophila)	-2.7	-1.5	6.1	-13.0	0.000320	7.1
44549	1460256_at	Car3	carbonic anhydrase 3	-2.7	-1.4	12.6	-10.2	0.001364	5.2
995	1416664_at	Cdc20	cell division cycle 20 homolog (S. cerevisiae)	-2.7	-1.4	6.5	-6.0	0.017418	1.1
180	1415849_s_at	Stmn1	stathmin 1	-2.6	-1.4	7.7	-9.0	0.002450	4.3
36780	1452485_at	Phospho1	phosphatase, orphan 1	-2.6	-1.4	6.8	-11.4	0.000729	6.1
6158	1421852_at	Kcnk5	potassium channel, subfamily K, member 5	-2.6	-1.4	7.2	-11.2	0.000787	5.9
36814	1452519_a_at	Zfp36	zinc finger protein 36	-2.6	-1.4	9.4	-6.6	0.012579	1.8
836	1416505_at	Nr4a1	nuclear receptor subfamily 4, group A, member 1	-2.6	-1.4	7.3	-9.1	0.002443	4.3
2784	1418453_a_at	Atp1b1	ATPase, Na ⁺ /K ⁺ transporting, beta 1 polypeptide	-2.6	-1.4	9.2	-8.5	0.003506	3.8
15519	1431213_a_at	1300007C21Ri	RIKEN cDNA 1300007C21 gene	-2.6	-1.4	11.0	-4.8	0.041618	-0.6
40520	1456225_x_at	Trib3	tribbles homolog 3 (Drosophila)	-2.6	-1.4	6.6	-4.6	0.046537	-0.8
1258	1416927_at	Trp53inp1	transformation related protein 53 inducible nuclear protein 1	-2.6	-1.4	8.1	-6.4	0.013859	1.5
1257	1416926_at	Trp53inp1	transformation related protein 53 inducible nuclear protein 1	-2.6	-1.4	10.7	-5.8	0.020558	0.8
23342	1439036_a_at	Atp1b1	ATPase, Na ⁺ /K ⁺ transporting, beta 1 polypeptide	-2.5	-1.3	9.5	-9.1	0.002428	4.3
6863	1422557_s_at	Mt1	metallothionein 1	-2.5	-1.3	12.7	-4.5	0.049950	-1.0
1740	1417409_at	Jun	Jun oncogene	-2.5	-1.3	7.5	-11.4	0.000731	6.1

ID	Symbol	Name	Fold change	M	A	t	P.Value	B	
4655	1420349_at	Ptgr	prostaglandin F receptor	-2.5	-1.3	4.8	-4.7	0.042327	-0.6
33709	1449409_at	Sult1c2	sulfotransferase family, cytosolic, 1C, member 2	-2.4	-1.3	6.4	-6.0	0.017718	1.1
35447	1451152_a_at	Atp1b1	ATPase, Na+/K+ transporting, beta 1 polypeptide	-2.4	-1.3	8.3	-12.7	0.000365	6.9
18771	1434465_x_at	Vldlr	very low density lipoprotein receptor	-2.4	-1.3	7.4	-14.6	0.000172	7.9
12658	1428352_at	Arrdc2	arrestin domain containing 2	-2.3	-1.2	6.3	-6.5	0.013049	1.7
2651	1418320_at	Prss8	protease, serine, 8 (prostasin)	-2.3	-1.2	6.0	-6.6	0.012521	1.8
8196	1423890_x_at	Atp1b1	ATPase, Na+/K+ transporting, beta 1 polypeptide	-2.3	-1.2	8.6	-7.7	0.005916	3.0
2926	1418595_at	S3-12	plasma membrane associated protein, S3-12	-2.3	-1.2	9.3	-7.1	0.008619	2.4
9951	1425645_s_at	Cyp2b10	cytochrome P450, family 2, subfamily b, polypeptide 10	-2.3	-1.2	8.5	-6.4	0.014025	1.5
5346	1421040_a_at	Gsta2	glutathione S-transferase, alpha 2 (Yc2)	-2.3	-1.2	10.3	-9.5	0.001985	4.7
407	1416076_at	Ccnb1-rs1	cyclin B1, related sequence 1	-2.3	-1.2	4.7	-4.7	0.042774	-0.6
9334	1425028_a_at	Tpm2	tropomyosin 2, beta	-2.3	-1.2	7.2	-5.7	0.020791	0.7
36335	1452040_a_at	Cdca3	cell division cycle associated 3	-2.3	-1.2	5.8	-4.9	0.037260	-0.4
10770	1426464_at	Nr1d1	nuclear receptor subfamily 1, group D, member 1	-2.2	-1.2	7.8	-5.9	0.018595	1.0
7719	1423413_at	Ndrp1	N-myc downstream regulated gene 1	-2.2	-1.2	6.8	-12.1	0.000496	6.6
6563	1422257_s_at	Cyp2b10	cytochrome P450, family 2, subfamily b, polypeptide 10	-2.2	-1.2	7.7	-5.9	0.019318	0.9
13829	1429523_a_at	Slc39a5	solute carrier family 39 (metal ion transporter), member 5	-2.2	-1.1	7.6	-8.1	0.004529	3.4
34146	1449851_at	Per1	period homolog 1 (Drosophila)	-2.2	-1.1	7.0	-9.3	0.002174	4.5
34693	1450398_at	Kcnk5	potassium channel, subfamily K, member 5	-2.2	-1.1	6.8	-9.3	0.002261	4.5
7303	1422997_s_at	Acot2	acyl-CoA thioesterase 2	-2.2	-1.1	10.8	-5.3	0.028465	0.2
30622	1446316_at	Lpin2	lipin 2	-2.2	-1.1	5.7	-6.5	0.013164	1.6
38219	1453924_a_at	Ptgr	prostaglandin F receptor	-2.2	-1.1	4.7	-5.1	0.033207	-0.1
25153	1440847_at	Mtss1	metastasis suppressor 1	-2.2	-1.1	7.0	-6.3	0.014727	1.4
35152	1450857_a_at	Col1a2	procollagen, type I, alpha 2	-2.2	-1.1	7.6	-5.4	0.025423	0.4
8584	1424278_a_at	Birc5	baculoviral IAP repeat-containing 5	-2.2	-1.1	4.7	-5.6	0.023773	0.5
10270	1425964_x_at	Hspb1	heat shock protein 1	-2.2	-1.1	7.2	-7.6	0.006419	2.9
36559	1452264_at	Tenc1	tensin like C1 domain-containing phosphatase	-2.2	-1.1	7.3	-8.4	0.003692	3.7
5066	1420760_s_at	Ndr1	N-myc downstream regulated-like	-2.1	-1.1	7.8	-12.8	0.000356	6.9
36122	1451827_a_at	Nox4	NADPH oxidase 4	-2.1	-1.1	7.2	-4.9	0.037656	-0.4
153	1415822_at	Scd2	stearoyl-Coenzyme A desaturase 2*	-2.1	-1.1	6.7	-4.6	0.045581	-0.8
40469	1456174_x_at	Ndrp1	N-myc downstream regulated gene 1	-2.1	-1.1	7.1	-9.1	0.002449	4.3
33125	1448825_at	Pdk2	pyruvate dehydrogenase kinase, isoenzyme 2	-2.1	-1.1	8.6	-6.5	0.012874	1.7
40300	1456005_a_at	Bcl2l11	BCL2-like 11 (apoptosis facilitator)	-2.1	-1.0	6.9	-7.6	0.006228	2.9
20599	1436293_x_at	D1Ert471e	DNA segment, Chr 1, ERATO Doi 471, expressed	-2.1	-1.0	9.1	-11.0	0.000870	5.8

ID	Symbol	Name	Fold change	M	A	t	P.Value	B	
1933	1417602_at	Per2	period homolog 2 (Drosophila)	-2.1	-1.0	5.6	-8.6	0.003388	3.8
3189	1418858_at	Aox3	aldehyde oxidase 3	-2.0	-1.0	10.2	-6.4	0.013398	1.6
13899	1429593_at	Slc38a2	solute carrier family 38, member 2	-2.0	-1.0	8.5	-4.8	0.040134	-0.5
34183	1449888_at	Epas1	endothelial PAS domain protein 1	-2.0	-1.0	7.0	-6.1	0.016255	1.2
8418	1424112_at	Igf2r	insulin-like growth factor 2 receptor	-2.0	-1.0	7.3	-6.4	0.013762	1.5
24652	1440346_at	Jmjd3	jumonji domain containing 3	-2.0	-1.0	7.1	-6.6	0.012149	1.9
26355	1442049_at	Trf	transferrin	-2.0	-1.0	7.9	-5.1	0.032119	-0.1
33365	1449065_at	Acot1	acyl-CoA thioesterase 1	-2.0	-1.0	10.4	-5.6	0.022634	0.6
5234	1420928_at	St6gal1	beta galactoside alpha 2,6 sialyltransferase 1	-2.0	-1.0	9.4	-10.9	0.000919	5.7
34676	1450381_a_at	Bcl6	B-cell leukemia/lymphoma 6	-2.0	-1.0	6.4	-11.9	0.000529	6.4
22222	1437916_at	NA	NA	-2.0	-1.0	6.2	-7.3	0.007706	2.6
9587	1425281_a_at	Tsc22d3	TSC22 domain family 3	-2.0	-1.0	9.6	-5.5	0.025250	0.4
11608	1427302_at	Enpp3	ectonucleotide pyrophosphatase/phosphodiesterase 3	-2.0	-1.0	8.5	-9.2	0.002399	4.4
39037	1454742_at	Rasgef1b	RasGEF domain family, member 1B	-2.0	-1.0	7.6	-5.6	0.022634	0.6
2211	1417880_at	G6pc	glucose-6-phosphatase, catalytic	-2.0	-1.0	12.0	-5.6	0.023071	0.6
8824	1424518_at	BC020489	cDNA sequence BC020489	-2.0	-1.0	7.3	-6.1	0.016071	1.2
4069	1419738_a_at	Tpm2	tropomyosin 2, beta	-2.0	-1.0	8.2	-8.5	0.003519	3.8
20861	1436555_at	Slc7a2	solute carrier family 7 (cationic amino acid transporter, y+ system), membe	-2.0	-1.0	10.5	-6.9	0.009971	2.1
21200	1436894_at	D1Ert471e	DNA segment, Chr 1, ERATO Doi 471, expressed	-2.0	-1.0	6.3	-11.5	0.000675	6.2
33791	1449491_at	Card10	caspase recruitment domain family, member 10	-2.0	-1.0	7.3	-8.8	0.002807	4.1
5078	1420772_a_at	Tsc22d3	TSC22 domain family 3	-2.0	-1.0	10.0	-5.4	0.025542	0.4
8313	1424007_at	Gdf10	growth differentiation factor 10	-2.0	-1.0	5.3	-7.9	0.005146	3.2
35266	1450971_at	Gadd45b	growth arrest and DNA-damage-inducible 45 beta	-2.0	-1.0	6.8	-4.6	0.046107	-0.8
33615	1449315_at	Odz3	odd Oz/ten-m homolog 3 (Drosophila)	-2.0	-1.0	8.4	-5.6	0.022400	0.6
9433	1425127_at	Hsd3b2	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomeras	-2.0	-1.0	6.3	-6.5	0.013049	1.7
3362	1419031_at	Fads2	fatty acid desaturase 2	-2.0	-1.0	10.6	-4.7	0.042691	-0.6
524	1416193_at	Car1	carbonic anhydrase 1	-2.0	-1.0	6.0	-6.8	0.010322	2.1

* The annotation for probeset 1415822_at was manually corrected to Scd2 (it was originally misannotated as Scd1 using this program)