Supplemental Material

Supplemental Tables

Supplemental Table I: Distinctly IL-1β-induced genes

Accession	Gene	IL-1β Fold Change	PDGF-DD Fold Change
1368128_at	phospholipase A2, group IIA (platelets, synovial fluid), Pla2g2a	4147.1	-7.6
1370964_at	argininosuccinate synthetase 1, Ass1	651.6	1.2
1387715_at	Kallmann syndrome 1, Kal1	408.8	-1.3
1368760_at	chemokine (C-X-C motif) ligand 2, Cxcl2	287.1	1.1
1388032_a_at	chemokine (C-X-C motif) ligand 3, Cxcl3	280.3	1.3
1370634_x_at	chemokine (C-X-C motif) ligand 3, Cxcl3	257.1	1.3
1367939_at	retinol binding protein 1, cellular, Rbp1	250.3	-1.3
1368731_at	orosomucoid 1, Orm1	248.4	-17.2
1369191_at	interleukin 6, Il6	229.6	-1.3
1387667_at	nitric oxide synthase 2, inducible, Nos2	215.3	7.7
1371228_at	colony stimulating factor 2 (granulocyte-macrophage), Csf2	214.6	-5.5
1387648_at	chemokine (C-X-C motif) ligand 5, Cxcl5	186.5	-1.7
1368174_at	EGL nine homolog 3 (C. elegans), Egln3	175.0	1.8
1382181_at	similar to RIKEN cDNA A530088I07 gene, LOC311984	165.5	-1.4
1374594_at	similar to RIKEN cDNA 1600029D21, LOC363060	159.4	1.6
1369529_at	colony stimulating factor 3 (granulocyte), Csf3	134.9	-2.6
1393974_at	mesenchyme homeobox 1 (predicted), Meox1_predicted	134.2	-5.3
1370633_at	chemokine (C-X-C motif) ligand 3, Cxcl3	121.3	1.2
1397729_x_at	similar to RIKEN cDNA 1600029D21, LOC363060	116.7	-2.2
1369983_at	chemokine (C-C motif) ligand 5, Ccl5	104.5	-1.8
1369703_at	endothelial PAS domain protein 1, Epas1	89.9	-1.1
1369393_at	mitogen-activated protein kinase kinase kinase 8, Map3k8	88.0	-3.0
1388204_at	matrix metallopeptidase 13, Mmp13	87.8	-2.0
1398482_at	B-cell leukemia/lymphoma 3, Bcl3	79.0	-1.4
1371732_at	dermatopontin (predicted), Dpt_predicted	74.0	1.6
1392647_at	similar to Serum amyloid A-3 protein precursor, LOC687992	72.9	-1.7
1391946_at	selectin, platelet, Selp	72.8	-2.3
1398333_at	Transcribed locus, ---	69.4	-2.4

1368014_at	prostaglandin E synthase, Ptges	67.2	-4.6
1370367_at	solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), member 1, Slc1a1	66.2	-1.9
1392171_at	chitinase 3-like 1, Chi3l1	64.8	-3.7
1370051_at	transglutaminase 1, K polypeptide, Tgm1	63.1	-1.9
1386739_at	ets variant gene 4 (E1A enhancer binding protein, E1AF) (predicted), Etv4_predicted	61.8	2.9
1369814_at	chemokine (C-C motif) ligand 20, Ccl20	58.9	-20.3
1368271_a_at	fatty acid binding protein 4, adipocyte, Fabp4	56.7	2.5
1393260_at	WDNM1 homolog, LOC360228	56.5	-1.4
1368657_at	matrix metallopeptidase 3, Mmp3	55.8	-2.0
1368342_at	adenosine monophosphate deaminase 3, Ampd3	52.5	-1.7
1383469_at	Transcribed locus, ---	51.9	1.6
1389420_at	signal transducing adaptor family member 2, Stap2	49.6	-2.8
1389470_at	complement component 2	49.5	-8.6
1369764_at	complement component 4 binding protein, alpha, C4bpa	48.4	-5.2
1370154_at	lysozyme, Lyz	47.4	-3.9
1377640_at	Transcribed locus, ---	44.4	1.7
1374989_at	ankyrin repeat and SOCS box-containing protein 12, Asb12	39.0	-11.2
1373947_at	dermatopontin (predicted), Dpt_predicted	38.8	1.4
1392578_at	Transcribed locus, ---	38.1	-1.3
1374452_at	phosphodiesterase 9A, Pde9a	34.8	3.2
1367679_at	CD74 antigen (invariant polypeptide of major histocompatibility complex, class II antigen-associated), Cd74	32.5	-6.1
1370822_at	RT1 class II, locus Ba, RT1-Ba	31.9	-4.7
1379526_at	Transcribed locus, ---	30.6	-7.9
1367612_at	microsomal glutathione S-transferase 1, Mgst1	29.4	1.3
1371033_at	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	28.4	-4.4
1382613_at	Transcribed locus, ---	27.6	3.5
1368626_at	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 3, Kcnn3	27.5	-1.5
1372254_at	serine (or cysteine) peptidase inhibitor, clade G, member 1, Serping1	27.5	-7.5
1368535_at	harakiri, BCL2 interacting protein (contains only BH3 domain), Hrk	26.3	-11.6
1383863_at	LIM domain only 2, Lmo2	26.3	2.7
1368641_at	wingless-related MMTV integration site 4, Wnt4	24.3	-4.6

1368473_at	gap junction membrane channel protein alpha 5, Gja5	22.2	1.8
1368420_at	ceruloplasmin, Cp	21.6	1.0
1368536_at	ectonucleotide pyrophosphatase/phosphodiesterase 2, Enpp2	21.0	-6.0
1370883_at	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	20.9	-4.9
1392280_at	toll-like receptor 2, Tlr2	20.8	-1.4
1388920_at	bone morphogenetic protein 6, Bmp6	20.8	-7.0
1370508_a_at	calcium channel, voltage-dependent, T type, alpha 1G subunit, Cacna1g	20.1	2.4
1393140_at	zinc finger CCCH type containing 12A (predicted), Zc3h12a_predicted	19.9	-1.5
1374119_at	E74-like factor 3, Elf3	19.8	-2.4
1368000_at	complement component 3, C3	19.8	-4.2
1392946_at	Transcribed locus, ---	19.6	1.5
1367701_at	receptor (calcitonin) activity modifying protein 2, Ramp2	19.4	1.2
1367973_at	chemokine (C-C motif) ligand 2, Ccl2	19.3	-1.4
1382590_at	similar to 2310015N21Rik protein (predicted)	18.8	-2.0
1373881_at	Rho, GDP dissociation inhibitor (GDI) beta, Arhgdib	18.7	-1.6
1387868_at	lipopolysaccharide binding protein, Lbp	18.7	-3.8
1375900_at	tumor necrosis factor receptor superfamily, member 9, Tnfrsf9	18.1	-2.4
1390215_at	---	18.1	1.3
1367800_at	plasminogen activator, tissue, Plat	18.0	-1.5
1388033_at	chemokine (C-X-C motif) ligand 3, Cxcl3	17.4	-8.0
1376292_at	ets homologous factor (predicted), Ehf_predicted	17.2	2.3
1368419_at	ceruloplasmin, Cp	17.0	-1.3
1387316_at	chemokine (C-X-C motif) ligand 1, Cxcl1	16.9	-1.6
1393863_at	CD180 antigen (predicted), Cd180_predicted	16.9	1.5
1369294_at	bone marrow stromal cell antigen 1, Bst1	16.7	-1.3
1385464_at	Forkhead box Q1, Foxq1	16.2	3.9
1370383_s_at	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	15.8	-4.0
1395110_at	Transcribed locus, ---	15.7	-4.3
1370750_a_at	interleukin 1 receptor, type I, Il1r1	15.3	1.3
1369255_at	interleukin 1 receptor, type I, Il1r1	15.3	1.0
1374778_at	cathepsin C, Ctsc	15.2	14.5
1384285_at	membrane-associated ring finger (C3HC4) 3, March3	14.8	-1.7
1382950_at	Transcribed locus, ---	14.7	-1.1
1389500_at	CDNA clone IMAGE:7445191, ---	14.5	1.3

1377029_at	RAR-related orphan receptor alpha (predicted), Rora_predicted	14.3	-2.0
1372064_at	chemokine (C-X-C motif) ligand 16, Cxcl16	14.3	-1.1
1372518_at	Fibulin 1 (predicted), Fbln1_predicted	14.3	-1.9
1370516_at	solute carrier family 15, member 3, Slc15a3	14.2	-6.1
1370382_at	RT1 class II, locus Db1, RT1-Db1	14.1	-11.8
1380336_at	interleukin-1 receptor-associated kinase 3 (predicted), Irak3_predicted	13.5	-1.5
1382433_at	Transcribed locus, ---	13.3	-1.5
1376128_at	Transcribed locus, ---	13.3	-2.3
1395887_at	similar to RIKEN cDNA 1600029D21, LOC363060	13.3	-2.7
1370173_at	superoxide dismutase 2, mitochondrial, Sod2	13.1	-2.7
1372440_at	serine (or cysteine) peptidase inhibitor, clade E, member 2, Serpine2	13.0	1.9
1379935_at	chemokine (C-C motif) ligand 7, Ccl7	12.7	-2.2
1369973_at	xanthine dehydrogenase, Xdh	12.5	-3.0
1368200_at	chemokine (C-X3-C motif) ligand 1, Cx3cl1	12.2	1.0
1391593_at	Ras association (RalGDS/AF-6) domain family 4, Rassf4	12.2	-2.8
1374284_at	Ras association (RalGDS/AF-6) domain family 4, Rassf4	12.2	-2.4
1368187_at	glycoprotein (transmembrane) nmb, Gpnmb	11.8	-1.1
1372055_at	similar to P-Rex1 (predicted), RGD1306534_predicted	11.8	-1.4
1388265_x_at	versican, Vcan	11.3	1.9
1391106_at	Transcribed locus, ---	11.3	-1.3
1379564_at	similar to cajalin 2 isoform a (predicted), RGD1565556_predicted	11.2	-2.4
1382685_at	slit homolog 2 (Drosophila), Slit2	11.1	1.6
1394475_at	Transcribed locus, ---	11.1	-3.2
1388201_at	bone morphogenetic protein 6, Bmp6	11.0	-9.2
1368418_a_at	ceruloplasmin, Cp	11.0	-1.4
1378827_at	bone morphogenetic protein 6, Bmp6	10.8	1.9
1385751_at	thrombospondin 2, Thbs2	10.8	-15.9
1385557_at	---	10.8	1.4
1367905_at	ectonucleotide pyrophosphatase/phosphodiesterase 3, Enpp3	10.8	2.1
1391453_at	Epstein-Barr virus induced gene 3 (similar to Interleukin-27 beta chain precursor), Ebi3	10.7	1.5
1370033_at	myosin, light polypeptide 1, Myl1	10.7	-5.7
1388146_at	Brain Ntab mRNA sequence, ---	10.6	-1.0
1370113_at	baculoviral IAP repeat-containing 3, Birc3	10.6	-2.8
1368940_at	purinergic receptor P2Y, G-protein coupled 2,	10.5	1.1

	P2ry2		
1380229_at	Transcribed locus, ---	10.3	1.3
1390866_at	Transcribed locus, ---	10.3	1.7
1387951_at	CD55 antigen, Cd55	10.0	1.3
1368693_at	Gardner-Rasheed feline sarcoma viral (Fgr) oncogene homolog, Fgr	10.0	-3.2
1368209_at	PDZK1 interacting protein 1, Pdzk1ip1	9.9	-8.5
1379022_at	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 8 (predicted), Adamts8_predicted	9.7	2.1
1378321_at	Ras association (RalGDS/AF-6) domain family 4, Rassf4	9.7	-2.2
1369584_at	suppressor of cytokine signaling 3, Socs3	9.6	1.0
1388773_at	tumor necrosis factor, alpha-induced protein 2, Tnfaip2	9.5	1.2
1371237_a_at	metallothionein 1a, Mt1a	9.4	-1.9
1370406_a_at	CD55 antigen, Cd55	9.3	-1.3
1381533_at	Rho family GTPase 1, Rnd1	9.2	-2.7
1393252_at	Transcribed locus, ---	9.1	-4.3
1388720_at	Transcribed locus, ---	9.1	-1.7
1387011_at	lipocalin 2, Lcn2	9.1	-2.1
1367877_at	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2, Slc11a2	9.0	-1.3
1387053_at	flavin containing monooxygenase 1, Fmo1	9.0	-2.4
1379183_at	WD repeat domain 62, Wdr62	8.9	1.2
1388745_at	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4A, Sema4a	8.9	-1.1
1370148_at	haptoglobin, Hp	8.8	-7.4
1368266_at	arginase 1, liver, Arg1	8.7	-1.9
1396472_at	Transcribed locus, ---	8.5	-11.2
1389662_at	WNK lysine deficient protein kinase 4, Wnk4	8.3	1.7
1384816_at	coxsackie virus and adenovirus receptor, Cxadr	8.3	1.5
1369683_at	BH3 interacting domain death agonist, Bid	8.3	1.1
1385380_at	Transcribed locus, ---	8.2	-1.2
1376897_at	similar to Hypothetical protein 4832420M10 (predicted), RGD1560022_predicted	8.1	-4.0
1383910_at	Transcribed locus, ---	7.9	1.9
1372027_at	Transcribed locus, ---	7.9	-2.8
1387221_at	GTP cyclohydrolase 1, Gch1	7.8	-2.0
1382941_at	Transcribed locus, moderately similar to NP_808250.1 MLX interacting protein isoform 1 [Mus musculus], ---	7.8	-1.6
1368813_at	CCAAT/enhancer binding protein (C/EBP), delta,	7.6	-1.5

	Cebpd		
1373207_at	Transcribed locus, ---	7.5	1.9
1389464_at	ligand of numb-protein X 1 (predicted), Lnx1_predicted	7.5	-4.8
1379381_at	Transcribed locus, ---	7.5	-1.6
1370583_s_at	ATP-binding cassette, sub-family B (MDR/TAP), member 1B	7.4	-1.6
1373037_at	ubiquitin-conjugating enzyme E2L 6, Ube2l6	7.4	-1.0
1377092_at	Transcribed locus, ---	7.3	1.3
1374575_at	cAMP responsive element binding protein 3-like 1, Creb3l1	7.3	-2.3
1367755_at	cysteine dioxygenase 1, cytosolic, Cdo1	7.3	-4.2
1386976_at	CD82 antigen, Cd82	7.2	1.7
1387343_at	CCAAT/enhancer binding protein (C/EBP), delta, Cebpd	7.1	-1.7
1384289_at	RELT-like 2, Rell2	7.1	-1.7
1379059_at	MICAL-like 2, Micall2	7.1	-1.2
1388004_at	G protein-coupled receptor 37-like 1, Gpr37l1	7.0	-3.9
1388924_at	angiopoietin-like 4, Angptl4	7.0	-4.6
1382311_at	Traf2 binding protein, T2bp	7.0	-2.2
1367784_a_at	clusterin, Clu	6.9	-1.1
1391255_at	zinc finger, MYND domain containing 15 (predicted), Zmynd15_predicted	6.9	-1.3
1376617_at	Transcribed locus, ---	6.8	-4.2
1391428_at	Transcribed locus, ---	6.8	3.4
1396613_at	Transcribed locus, ---	6.8	-3.0
1368550_at	forkhead box Q1, Foxq1	6.7	1.7
1368480_at	CDW92 antigen, Cdw92	6.7	-1.0
1374246_at	Transcribed locus, ---	6.7	-3.1
1370172_at	superoxide dismutase 2, mitochondrial, Sod2	6.7	-2.0
1389538_at	nuclear factor of kappa light chain gene enhancer in B-cells inhibitor, alpha, Nfkbia	6.7	-1.7
1391925_at	chemokine (C-C motif) ligand 19 (predicted), Ccl19_predicted	6.7	-4.0
1394597_at	DDHD domain containing 1, Ddhd1	6.6	-1.4
1387395_at	adenosine A2B receptor, Adora2b	6.6	-1.1
1389214_at	laminin, alpha 4, Lama4	6.6	-6.8
1386191_a_at	lipoma HMGIC fusion partner-like 2 (predicted), Lhfpl2_predicted	6.5	25.5
1374474_at	copine VIII (predicted), Cpne8_predicted	6.5	-1.2
1374106_at	---	6.4	-2.2
1383605_at	similar to alpha-fetoprotein	6.4	1.3
1368947_at	growth arrest and DNA-damage-inducible 45 alpha, Gadd45a	6.4	1.0

1379371_at	Transcribed locus, ---	6.4	-2.1
1378032_at	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta (predicted), Nfkbiz_predicted	6.3	-1.0
1391046_at	SET and MYND domain containing 3, Smyd3	6.3	-1.2
1370362_at	protein tyrosine phosphatase, receptor type, N, Ptprn	6.3	1.6
1379313_at	---	6.2	1.7
1370445_at	phospholipase A1 member A, Pla1a	6.1	-1.6
1378927_at	---	6.1	-3.3
1392107_at	strawberry notch homolog 2 (Drosophila), Sbno2	6.1	-1.3
1373054_at	CDW92 antigen, Cdw92	6.1	-1.0
1374061_at	CD302 antigen, Cd302	6.1	-2.9
1381376_at	Similar to Tumor necrosis factor, alpha-induced protein 2 (Primary response gene B94 protein), LOC299339	6.1	1.3
1390529_at	CD83 antigen (predicted), Cd83_predicted	6.1	-3.3
1390896_at	Transcribed locus, ---	6.1	-2.9
1368474_at	vascular cell adhesion molecule 1, Vcam1	6.1	-6.4
1373546_at	putative UA20 protein, Ua20	6.0	1.1
1369685_at	twist homolog 2 (Drosophila), Twist2	5.9	1.6
1383489_at	Transcribed locus, ---	5.9	-1.1
1376013_at	tetratricopeptide repeat domain 9, Ttc9	5.8	1.1
1378179_a_at	lipoma HMGIC fusion partner-like 2 (predicted), Lhfpl2_predicted	5.8	1.7
1393003_at	Transcribed locus, ---	5.6	-1.2
1387932_at	solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), member 1, Slc1a1	5.6	1.8
1386981_at	solute carrier family 16 (monocarboxylic acid transporters), member 1, Slc16a1	5.6	1.3
1370260_at	adducin 3 (gamma), Add3	5.6	-1.1
1390585_at	mannan-binding lectin serine peptidase 1, Masp1	5.5	-1.7
1370638_at	ankyrin 3, epithelial, Ank3	5.4	-1.4
1372560_at	Transcribed locus, ---	5.4	-1.2
1373027_at	---	5.4	1.1
1383786_at	RAB32, member RAS oncogene family, Rab32	5.4	1.3
1388036_a_at	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 4, Mllt4	5.4	-1.1
1374429_at	Transcribed locus, ---	5.3	1.4
1383906_at	lung-inducible neuralized-related C3HC4 RING domain protein, Lincr	5.3	1.1

1379770_at	choline phosphotransferase 1, Chpt1	5.3	-1.1
1382269_at	cyclin M2, Cnnm2	5.3	-2.1
1387311_at	NADPH oxidase 1, Nox1	5.3	1.6
1389410_s_at	---	5.2	1.0
1382381_at	Transcribed locus, ---	5.2	1.6
1378003_at	leucine rich repeat containing 8 family, member B, Lrrc8b	5.2	1.4
1383119_at	opioid growth factor receptor-like 1, Ogfrl1	5.2	1.1
1373140_at	Transcribed locus, ---	5.2	-1.2
1377759_at	BH3 interacting domain death agonist, Bid	5.1	1.3
1385950_at	family with sequence similarity 131, member B, Fam131b	5.1	1.8
1399096_at	Transcribed locus, ---	5.1	-1.1
1388059_a_at	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2, Slc11a2	5.0	-1.1
1373233_at	lipoma HMGIC fusion partner-like 2 (predicted), Lhfpl2_predicted	5.0	1.4
1393887_at	choline phosphotransferase 1, Chpt1	5.0	1.0
1370957_at	interleukin 6 signal transducer, Il6st	5.0	1.3
1382069_at	Putative UA20 protein, Ua20	4.9	1.0
1377650_at	Transcribed locus, ---	4.9	1.1
1385497_x_at	ligand of numb-protein X 1 (predicted), Lnx1_predicted	4.9	-2.2
1379631_at	colony stimulating factor 1 (macrophage), Csf1	4.8	1.2
1378130_at	ring finger protein, transmembrane 2, Rnft2	4.8	-1.4
1373666_at	Rap guanine nucleotide exchange factor (GEF) 5, Rapgef5	4.8	-1.2
1385426_at	coiled-coil domain containing 109B, Ccdc109b	4.7	1.3
1395881_at	Death-associated protein, Dap	4.6	1.2
1388271_at	metallothionein 2A, Mt2A	4.6	-1.3
1372403_at	similar to Nuclear membrane binding protein NUCLING (predicted), RGD1560011_predicted	4.6	1.3
1369029_at	phospholipid scramblase 1, Plscr1	4.6	2.0
1370941_at	platelet derived growth factor receptor, alpha polypeptide, Pdgfra	4.6	-1.5
1367568_a_at	matrix Gla protein, Mgp	4.6	-1.4
1376750_at	Transcribed locus, ---	4.5	-4.5
1370728_at	interleukin 13 receptor, alpha 1, Il13ra1	4.5	-1.1
1370882_at	major histocompatibility complex, class II, DM beta, Hla-dmb	4.5	-2.1
1384971_at	DEP domain containing 7, Depdc7	4.5	2.6
1373043_at	stromal cell-derived factor 2-like 1 (predicted), Sdf2l1_predicted	4.5	1.1
1374265_at	Transcribed locus, ---	4.5	1.2

1372293_at	Similar to RIKEN cDNA 1110038F21 (predicted), RGD1562059_predicted	4.4	1.1
1373984_at	solute carrier family 39 (zinc transporter), member 14 (predicted), Slc39a14_predicted	4.4	-1.7
1376661_at	similar to CG11206-PA, LOC313672	4.4	-2.3
1371974_at	phytanoyl-CoA dioxygenase domain containing 1, Phyhd1	4.4	-1.2
1391269_at	---	4.4	1.1
1370963_at	growth arrest specific 7, Gas7	4.4	2.0
1376785_at	Transcribed locus, ---	4.4	1.2
1368754_at	pyrimidinergic receptor P2Y, G-protein coupled, 6, P2ry6	4.4	-2.1
1373882_at	c-fos induced growth factor, Figf	4.4	-3.9
1378126_at	DENN/MADD domain containing 2A, Dennd2a	4.3	1.6
1377214_a_at	hypothetical protein LOC292764, RGD1303117	4.3	1.5
1387087_at	CCAAT/enhancer binding protein (C/EBP), beta, Cebpb	4.3	-1.9
1387599_a_at	NAD(P)H dehydrogenase, quinone 1, Nqo1	4.3	1.2
1376891_at	Transcribed locus, ---	4.3	1.1
1388662_at	Transcribed locus, ---	4.3	-3.6
1375028_at	Transcribed locus, ---	4.3	-1.2
1387392_at	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 4, Mllt4	4.2	1.3
1372213_at	similar to hypothetical protein MGC6835, LOC500300	4.2	-1.1
1367814_at	ATPase, Na+/K+ transporting, beta 1 polypeptide, Atp1b1	4.2	1.1
1392832_at	similar to angiopoietin-like 1, LOC684489	4.2	-1.3
1393730_at	Transcribed locus, ---	4.1	1.2
1376198_at	adipocyte-specific adhesion molecule, Asam	4.1	-2.2
1380696_at	Transcribed locus, ---	4.1	-1.2
1368990_at	cytochrome P450, family 1, subfamily b, polypeptide 1, Cyp1b1	4.1	-1.1
1370301_at	matrix metallopeptidase 2, Mmp2	4.1	-1.2
1370904_at	major histocompatibility complex, class II, DM alpha, Hla-dma	4.1	-1.1
1390292_at	transmembrane protein 8 (five membrane-spanning domains) (predicted), Tmem8_predicted	4.1	1.3
1384099_at	solute carrier family 39 (metal ion transporter), member 6, Slc39a6	4.0	-1.1
1395374_at	Transcribed locus, ---	4.0	-3.7
1370843_at	guanine nucleotide binding protein (G protein), gamma 8, Gng8	4.0	-1.1

1388848_at	similar to hypothetical protein MGC13251, RGD1308350	4.0	1.7
1368605_at	SH2B adaptor protein 2, Sh2b2	4.0	-1.2
1388966_at	Transcribed locus, ---	4.0	1.3
1370942_at	RAS p21 protein activator 3, Rasa3	4.0	-1.1
1368856_at	Janus kinase 2, Jak2	4.0	-1.2
1371926_at	Transcribed locus, ---	3.9	-1.0
1368679_a_at	Yamaguchi sarcoma viral (v-yes-1) oncogene homolog, Lyn	3.9	-1.2
1383229_at	ATP-binding cassette, sub-family A (ABC1), member 7, Abca7	3.9	1.0
1388753_at	sulfatase 2, Sulf2	3.9	-1.9
1368015_at	prostaglandin E synthase, Ptges	3.9	-1.3
1389082_at	---	3.9	1.3
1367712_at	tissue inhibitor of metalloproteinase 1, Timp1	3.9	-1.1
1395307_at	similar to cajalin 2 isoform a (predicted), RGD1565556_predicted	3.8	-1.2
1369044_a_at	phosphodiesterase 4B, cAMP specific, Pde4b	3.8	-2.1
1383330_at	Transcribed locus, ---	3.8	1.4
1367881_at	signal-regulatory protein alpha, Sirpa	3.8	-2.1
1368311_at	O-6-methylguanine-DNA methyltransferase, Mgmt	3.8	1.1
1380583_s_at	colony stimulating factor 1 (macrophage), Csf1	3.8	1.1
1376768_at	Transcribed locus, ---	3.8	-1.1
1369194_a_at	cyclin-dependent kinase inhibitor 2A, Cdkn2a	3.8	1.2
1384408_at	Transcribed locus, ---	3.8	1.1
1376858_at	similar to protein 7 transactivated by hepatitis B virus X antigen, LOC686809	3.7	1.7
1381993_at	chloride intracellular channel 2, Clic2	3.7	-1.4
1371194_at	tumor necrosis factor alpha induced protein 6, Tnfaip6	3.7	1.3
1397929_at	Transcribed locus, ---	3.7	-1.7
1388711_at	interleukin 13 receptor, alpha 1, Il13ra1	3.7	-1.3
1379400_at	Transcribed locus, ---	3.7	1.0
1378153_at	Transcribed locus, ---	3.7	1.6
1372434_at	CASK-interacting protein CIP98, Cip98	3.7	-1.2
1375332_at	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha II polypeptide (predicted), P4ha2_predicted	3.7	-2.7
1384148_at	RAB20, member RAS oncogene family, Rab20	3.6	1.8
1393629_at	H2.0-like homeobox, Hlx	3.6	-2.4
1368771_at	sulfatase 1, Sulf1	3.6	-4.1
1393696_at	fin bud initiation factor, Fibin	3.6	1.2
1378484_at	RAS-like, family 12 (predicted),	3.6	-2.9

	Rasl12_predicted		
1375011_at	Transcribed locus, ---	3.6	-2.7
1369716_s_at	lectin, galactose binding, soluble 5	3.5	-2.1
1379483_at	Basic helix-loop-helix domain containing, class B2, Bhlhb2	3.5	1.6
1368519_at	serine (or cysteine) peptidase inhibitor, clade E, member 1, Serpine1	3.5	-2.1
1394940_at	family with sequence similarity 46, member A, Fam46a	3.5	-1.7
1374273_at	Transcribed locus, ---	3.5	-1.0
1385978_at	Transcribed locus, ---	3.5	1.3
1398905_at	ATPase, H transporting, lysosomal V1 subunit G1 (predicted), Atp6v1g1_predicted	3.5	-1.1
1374174_at	Transcribed locus, ---	3.5	-1.1
1371479_at	methyltransferase like 7A, Mettl7a	3.5	-1.6
1368448_at	latent transforming growth factor beta binding protein 2, Ltbp2	3.5	-1.8
1395279_at	PX domain containing serine/threonine kinase, Pxk	3.5	-1.1
1378334_a_at	Transcribed locus, ---	3.5	-2.3
1392813_at	Transcribed locus, strongly similar to NP_035578.3 SRY-box containing gene 9 [Mus musculus], ---	3.4	1.9
1376740_at	Transcribed locus, ---	3.4	-1.4
1384076_at	Transcribed locus, strongly similar to XP_001479207.1 PREDICTED: similar to Cache domain containing 1 [Mus musculus], ---	3.4	1.1
1377790_at	Transcribed locus, ---	3.4	1.6
1390336_at	similar to Protein C21orf63 homolog precursor (predicted), RGD1307569_predicted	3.4	1.1
1387027_a_at	lectin, galactose binding, soluble 9, Lgals9	3.4	-1.9
1376889_at	Transcribed locus, ---	3.4	1.7
1368541_at	embigin, Emb	3.4	-1.0
1398967_at	mediator complex subunit 24, Med24	3.3	1.2
1387843_at	follistatin, Fst	3.3	-1.2
1369193_at	cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4), Cdkn2b	3.3	3.0
1372362_at	galactokinase 2, Galk2	3.3	-1.0
1377353_a_at	tumor necrosis factor (ligand) superfamily, member 13, Tnfsf13	3.3	-1.3
1375339_at	enthoprotin, Enth	3.3	1.2
1388556_at	syntaxin 6, Stx6	3.3	-1.0
1368914_at	runt related transcription factor 1, Runx1	3.3	1.3
1374433_at	Transcribed locus, ---	3.3	1.4
1387788_at	Jun-B oncogene, Junb	3.3	-1.1

1395442_at	Transcribed locus, ---	3.3	1.1
1379356_at	Transcribed locus, ---	3.3	-1.2
1382291_at	Transcribed locus, strongly similar to NP_035578.3 SRY-box containing gene 9 [Mus musculus], ---	3.2	1.1
1389008_at	Sprouty-related, EVH1 domain containing 2, Spred2	3.2	2.0
1373863_at	mitogen-activated protein kinase kinase kinase kinase 4 (predicted), Map4k4_predicted	3.2	1.3
1368540_at	trophoblast glycoprotein, Tpbg	3.2	1.1
1375874_at	similar to cDNA sequence BC013529 (predicted), RGD1309759_predicted	3.2	-2.7
1377916_at	schlafen 2 (predicted), Slfn2_predicted	3.2	1.8
1391643_at	---	3.2	1.6
1382944_at	Transcribed locus, ---	3.2	-1.2
1370935_at	CDW92 antigen, Cdw92	3.1	-1.4
1384449_at	Transcribed locus, ---	3.1	1.5
1392720_at	cytochrome P450, family 4, subfamily f, polypeptide 17 (predicted), Cyp4f17_predicted	3.1	-1.0
1371019_at	tribbles homolog 1 (Drosophila), Trib1	3.1	1.3
1370065_at	hemopexin, Hpx	3.1	-1.3
1367801_at	endothelin converting enzyme 1, Ece1	3.1	-1.9
1379368_at	B-cell leukemia/lymphoma 6 (predicted), Bcl6_predicted	3.1	-1.4
1393162_at	solute carrier family 39 (metal ion transporter), member 6, Slc39a6	3.1	1.2
1386797_at	solute carrier family 39 (metal ion transporter), member 6, Slc39a6	3.1	1.3
1386660_at	---	3.1	-1.2
1390386_at	caspase 3, apoptosis related cysteine protease, Casp3	3.1	2.0
1381280_at	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2-like (predicted), Mthfd2l_predicted	3.1	1.7
1368025_at	DNA-damage-inducible transcript 4, Ddit4	3.1	-1.5
1374565_at	NIMA (never in mitosis gene a)-related expressed kinase 6, Nek6	3.1	-1.2
1395986_at	slit homolog 2 (Drosophila), Slit2	3.1	1.6
1390326_at	angiogenin, ribonuclease A family, member 1, Ang1	3.1	-1.0
1373407_at	Transcribed locus, ---	3.0	1.4
1388425_at	OAF homolog (Drosophila), Oaf	3.0	1.5
1382745_at	Transcribed locus, ---	3.0	-3.1
1368231_at	signal transducer and activator of transcription 5A, Stat5a	3.0	1.1

1389085_at	Transcribed locus, ---	3.0	-1.9
1392562_at	family with sequence similarity 128, member B, Fam128b	3.0	-1.6
1367677_at	peroxiredoxin 5, Prdx5	3.0	1.2
1395850_at	pseudouridine synthase 3, Pus3	3.0	1.2
1367749_at	lumican, Lum	3.0	-2.6
1377955_at	CDNA clone IMAGE:7383152, ---	3.0	1.2
1378499_at	Transcribed locus, ---	2.9	-1.4
1382919_at	solute carrier family 39 (zinc transporter), member 14 (predicted), Slc39a14_predicted	2.9	-1.6
1374741_at	estrogen related receptor, alpha, Esrra	2.9	1.9
1384756_at	solute carrier family 43, member 2 (predicted), Slc43a2_predicted	2.9	-2.6
1370807_at	transmembrane protein 49, Tmem49	2.9	-1.2
1382948_at	Rho GTPase activating protein 28, Arhgap28	2.9	-1.7
1387202_at	intercellular adhesion molecule 1, Icam1	2.9	-1.6
1371446_at	MAP kinase-activated protein kinase 2, Mapkapk2	2.9	-1.2
1392905_at	Guanine nucleotide binding protein, gamma 2, Gng2	2.9	1.4
1388624_at	similar to Hypothetical UPF0184 protein C9orf16 homolog (predicted), RGD1561113_predicted	2.9	-1.4
1388659_at	calcium regulated heat stable protein 1, Carhsp1	2.9	-1.0
1370358_at	two pore channel 1, Tpcn1	2.9	1.6
1390422_at	PX domain containing serine/threonine kinase, Pxk	2.9	-1.2
1385620_at	heat shock 105kDa/110kDa protein 1, Hsph1	2.9	-1.2
1394965_at	enthoprotin, Enth	2.9	-1.1
1376569_at	Kruppel-like factor 2 (lung) (predicted), Klf2_predicted	2.8	1.3
1380318_at	Transcribed locus, ---	2.8	-2.8
1373452_at	RNA terminal phosphate cyclase-like 1, Rcl1	2.8	1.3
1371536_at	calcium regulated heat stable protein 1, Carhsp1	2.8	-1.2
1382995_at	Transcribed locus, ---	2.8	-1.5
1384525_at	dedicator of cytokinesis 11, Dock11	2.8	1.5
1368106_at	polo-like kinase 2 (Drosophila), Plk2	2.8	1.1
1394020_at	Transcribed locus, ---	2.8	1.8
1368134_a_at	interleukin 4 receptor, alpha, Il4ra	2.8	-2.3
1371108_a_at	ATPase, Na+/K+ transporting, alpha 1 polypeptide, Atp1a1	2.8	1.3
1372599_at	microsomal glutathione S-transferase 2 (predicted), Mgst2_predicted	2.8	1.7
1389742_at	Transcribed locus, ---	2.8	1.4
1373219_at	snail homolog 1 (Drosophila), Snai1	2.8	1.2

1374157_at	Phosphodiesterase 4B, cAMP specific, Pde4b	2.8	-1.7
1389159_at	Transcribed locus, ---	2.8	-4.3
1387109_at	P450 (cytochrome) oxidoreductase, Por	2.8	1.9
1370939_at	acyl-CoA synthetase long-chain family member 1, Acsl1	2.8	1.4
1375526_at	similar to novel protein of unknown function (DUF423) family member (predicted), RGD1563438_predicted	2.8	-1.1
1367943_at	nuclear factor of kappa light chain gene enhancer in B-cells inhibitor, beta, Nfkbib	2.8	-1.4
1388674_at	cyclin-dependent kinase inhibitor 1A, Cdkn1a	2.7	1.4
1376835_at	Solute carrier family 35, member B2, Slc35b2	2.7	-2.0
1379477_at	Transcribed locus, ---	2.7	-1.2
1370906_at	branched chain keto acid dehydrogenase E1, beta polypeptide, Bckdhb	2.7	1.1
1373734_at	Solute carrier organic anion transporter family, member 3a1, Slco3a1	2.7	-1.3
1392971_at	Transcribed locus, ---	2.7	-4.7
1370082_at	transforming growth factor, beta 1, Tgfb1	2.7	1.4
1379663_at	Transcribed locus, strongly similar to XP_001479207.1 PREDICTED: similar to Cache domain containing 1 [Mus musculus], ---	2.7	1.0
1382682_at	Transcribed locus, ---	2.7	-1.3
1373421_at	TG interacting factor 1, Tgif1	2.7	1.4
1388236_x_at	RT1 class I, CE12, RT1-CE12	2.7	-1.5
1378171_at	Transcribed locus, ---	2.7	-1.3
1383149_at	similar to development and differentiation enhancing factor-like 1, LOC684122	2.7	-1.8
1387784_at	CDNA clone MGC:187342 IMAGE:8369120, ---	2.7	-1.3
1376568_at	Transcribed locus, ---	2.7	1.4
1377940_at	family with sequence similarity 101, member B, Fam101b	2.6	-2.1
1393108_at	Transcribed locus, ---	2.6	-1.4
1372443_at	low density lipoprotein receptor-related protein 11 (predicted), Lrp11_predicted	2.6	-1.3
1393143_at	Transcribed locus, ---	2.6	2.0
1393961_at	Transcribed locus, ---	2.6	1.1
1379386_at	G two S phase expressed protein 1, Gtse1	2.6	1.5
1376321_at	family with sequence similarity 38, member A (predicted), Fam38a_predicted	2.6	1.5
1373972_at	similar to neuron navigator 1, LOC685707	2.6	1.8
1368953_at	UDP-glucose ceramide glucosyltransferase-like 1, Ugcgl1	2.6	1.2
1370932_at	low density lipoprotein receptor-related protein 4, Lrp4	2.6	1.0

1387893_at	complement component 1, s subcomponent, C1s	2.6	-2.4
1380110_at	Janus kinase 2, Jak2	2.6	-1.0
1367723_a_at	SH2B adaptor protein 3, Sh2b3	2.6	1.7
1369125_at	5-hydroxytryptamine (serotonin) receptor 2A, Htr2a	2.6	-1.5
1385827_at	cardiotrophin-like cytokine factor 1, Clcf1	2.6	2.5
1380582_at	colony stimulating factor 1 (macrophage), Csf1	2.6	1.2
1387225_at	optic atrophy 1 homolog (human), Opa1	2.6	1.1
1383560_at	Transcribed locus, ---	2.6	-2.7
1377662_at	pirin, Pir	2.6	-1.0
1368207_at	FXYD domain-containing ion transport regulator 5, Fxyd5	2.6	1.6
1387391_at	cyclin-dependent kinase inhibitor 1A, Cdkn1a	2.6	1.8
1384234_at	paired related homeobox 1, Prrx1	2.6	1.2
1369947_at	cathepsin K, Ctsk	2.6	-1.2
1389066_at	regulator of calcineurin 2, Rcan2	2.6	-2.9
1386937_at	ATPase, Na+/K+ transporting, beta 1 polypeptide, Atp1b1	2.6	-1.2
1392587_at	Transcribed locus, ---	2.6	-1.1
1370907_at	beta galactoside alpha 2,6 sialyltransferase 1, St6gal1	2.6	1.3
1390812_a_at	RAS-like, estrogen-regulated, growth-inhibitor, Rerg	2.6	-2.5
1382746_s_at	Transcribed locus, ---	2.5	-3.3
1374849_at	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 7 (predicted), Adamts7_predicted	2.5	-2.0
1375216_at	poliovirus receptor-related 2, Pvrl2	2.5	-1.8
1383860_at	Fos-like antigen 2, Fosl2	2.5	-1.3
1373607_at	ST3 beta-galactoside alpha-2,3-sialyltransferase 3, St3gal3	2.5	-1.6
1368488_at	nuclear factor, interleukin 3 regulated, Nfil3	2.5	-1.6
1376813_at	membrane bound O-acyltransferase domain containing 5, Mboat5	2.5	1.2
1387975_at	UDP-glucose ceramide glucosyltransferase, Ugcg	2.5	-1.3
1397380_at	Transcribed locus, ---	2.5	1.2
1370365_at	glutathione synthetase, Gss	2.5	1.7
1394573_at	Transcribed locus, ---	2.5	-1.7
1392489_at	Transcribed locus, ---	2.5	1.3
1397740_at	sideroflexin 1, Sfxn1	2.5	1.7
1370186_at	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	2.5	1.1
1394483_at	A disintegrin-like and metallopeptidase	2.5	-2.4

	(reprolysin type) with thrombospondin type 1 motif, 5 (aggrecanase-2), Adamts5		
1369961_at	phosphatidic acid phosphatase 2a, Ppap2a	2.5	-2.5
1394948_at	Transcribed locus, ---	2.5	1.3
1385485_x_at	similar to Riken cDNA C230021P08 (predicted), RGD1561571_predicted	2.5	1.6
1384934_at	Solute carrier family 41, member 2 (predicted), Slc41a2_predicted	2.5	1.5
1384997_at	interferon stimulated exonuclease gene 20-like 1 (predicted), Isg20l1_predicted	2.5	1.4
1392923_at	Transcribed locus, ---	2.5	-1.7
1378156_at	similar to cystin 1, LOC690489	2.5	-1.6
1397766_at	Transcribed locus, ---	2.4	1.6
1374019_at	RGD1564379 (predicted), RGD1564379_predicted	2.4	1.2
1367585_a_at	ATPase, Na+/K+ transporting, alpha 1 polypeptide, Atp1a1	2.4	1.1
1372482_at	solute carrier family 39 (metal ion transporter), member 13, Slc39a13	2.4	1.1
1388689_at	similar to Acylphosphatase, muscle type isozyme (Acylphosphate phosphohydrolase), LOC682245	2.4	1.7
1385637_at	Similar to sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1, LOC685899	2.4	-5.2
1388493_at	EGFR-coamplified and overexpressed protein, Ecop	2.4	-1.4
1393891_at	procollagen, type VIII, alpha 1 (predicted), Col8a1_predicted	2.4	1.6
1387925_at	asparagine synthetase, Asns	2.4	1.5
1376379_a_at	similar to RIKEN cDNA 2310004I24 gene, RGD1309906	2.4	-1.2
1373727_at	fin bud initiation factor, Fibin	2.4	1.2
1379271_at	suppressor of cytokine signaling 5, Socs5	2.4	1.5
1372812_at	similar to mKIAA0256 protein (predicted), RGD1559930_predicted	2.4	-1.0
1386870_at	glutamate-ammonia ligase (glutamine synthetase), Glul	2.4	-1.0
1383225_at	Transcribed locus, ---	2.4	-5.6
1397772_at	CDNA clone IMAGE:7320582, ---	2.4	-1.5
1384364_at	F-box protein 4, Fbxo4	2.4	-1.3
1383491_at	interferon stimulated exonuclease gene 20-like 1 (predicted), Isg20l1_predicted	2.4	1.6
1382296_at	Transcribed locus, ---	2.4	-2.4
1383005_at	Transcribed locus, ---	2.4	-1.6

1372273_at	glycophorin C (Gerbich blood group), Gypc	2.4	1.0
1375989_a_at	nuclear factor of kappa light polypeptide gene enhancer in B-cells 2, p49/p100, Nfkb2	2.4	-1.9
1389230_at	Transcribed locus, ---	2.4	1.1
1389973_a_at	surfeit 4, Surf4	2.4	1.3
1370531_a_at	phospholipase D1, Pld1	2.3	-1.7
1367710_at	proteasome (prosome, macropain) 28 subunit, beta, Psme2	2.3	1.0
1383485_at	transformed mouse 3T3 cell double minute 2 homolog (mouse) (predicted), Mdm2_predicted	2.3	1.6
1388153_at	acyl-CoA synthetase long-chain family member 1, Acsl1	2.3	1.2
1379611_at	splA/ryanodine receptor domain and SOCS box containing 1 (predicted), Spsb1_predicted	2.3	-1.5
1369690_at	N-ethylmaleimide sensitive fusion protein, Nsf	2.3	1.0
1369941_at	death-associated protein, Dap	2.3	1.0
1392668_at	recombining binding protein suppressor of hairless (Drosophila) (predicted)	2.3	1.7
1370693_a_at	2',3'-cyclic nucleotide 3' phosphodiesterase, Cnp	2.3	-1.9
1392960_at	similar to RIKEN cDNA 2310004I24 gene, RGD1309906	2.3	1.1
1372653_at	FK506 binding protein 11, Fkbp11	2.3	1.1
1379736_at	solute carrier family 43, member 2 (predicted), Slc43a2_predicted	2.3	-1.6
1373864_at	mitogen-activated protein kinase kinase kinase kinase 4 (predicted), Map4k4_predicted	2.3	1.1
1377639_at	adipocyte-specific adhesion molecule, Asam	2.3	-1.0
1372237_at	Transcribed locus, ---	2.3	1.5
1369931_at	pyruvate kinase, muscle, Pkm2	2.3	1.0
1378168_at	family with sequence similarity 101, member B, Fam101b	2.3	-1.7
1373751_at	Transcribed locus, ---	2.3	-1.3
1392920_at	Elongation factor RNA polymerase II-like 3, Ell3	2.3	1.0
1372818_at	collectin sub-family member 12, Colec12	2.3	-1.7
1370160_at	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble, Xpnpep1	2.3	1.6
1367938_at	UDP-glucose dehydrogenase, Ugdh	2.3	1.4
1371442_at	hypoxia up-regulated 1, Hyou1	2.3	1.4
1372750_at	Transcribed locus, ---	2.3	-1.1
1380402_at	Transcribed locus, ---	2.3	1.2
1372651_at	Transcribed locus, ---	2.3	1.1
1373310_at	Transcribed locus, ---	2.3	-1.8
1372973_at	Lanosterol synthase, Lss	2.3	1.3
1387670_at	glycerol-3-phosphate dehydrogenase 2, mitochondrial, Gpd2	2.3	1.9

1393561_at	Transcribed locus, ---	2.3	-1.1
1388967_at	transcription factor E3 (predicted), Tcfe3_predicted	2.3	1.0
1388909_at	oxidoreductase NAD-binding domain containing 1 (predicted), Oxnad1_predicted	2.3	1.8
1376974_at	tetratricopeptide repeat domain 7, Ttc7	2.3	1.4
1369956_at	interferon gamma receptor 1, Ifngr1	2.3	-1.8
1373062_at	Transcribed locus, ---	2.3	-2.8
1388600_at	CDNA clone IMAGE:7320582, ---	2.3	-1.2
1396263_at	Transcribed locus, ---	2.3	1.3
1389412_at	---	2.3	1.3
1367675_at	calcium and integrin binding 1 (calmyrin), Cib1	2.3	-1.0
1373554_at	splA/ryanodine receptor domain and SOCS box containing 1 (predicted), Spsb1_predicted	2.3	-1.5
1388813_at	ADP-ribosylation factor 2, Arf2	2.3	-1.1
1384295_at	heat shock protein 14, Hspa14	2.3	1.2
1368249_at	Kruppel-like factor 15, Klf15	2.3	-4.3
1370020_at	solute carrier family 25 (mitochondrial carrier; dicarboxylate transporter), member 10, Slc25a10	2.3	1.0
1368322_at	superoxide dismutase 3, extracellular, Sod3	2.2	-2.2
1391456_at	junctional adhesion molecule 3, Jam3	2.2	1.3
1367633_at	glutamate-ammonia ligase (glutamine synthetase), Glul	2.2	-1.0
1389425_at	similar to 5(3)-deoxyribonucleotidase, cytosolic type, LOC688261	2.2	1.6
1393336_at	SWA-70 protein, Swap70	2.2	1.1
1389218_at	Transcribed locus, ---	2.2	-1.0
1390139_a_at	obscurin-like 1, Obsl1	2.2	-1.6
1383978_at	Transcribed locus, ---	2.2	1.0
1378117_at	Transcribed locus, ---	2.2	1.0
1389039_at	Transcribed locus, ---	2.2	-1.6
1389617_at	ELK3, member of ETS oncogene family (predicted), Elk3_predicted	2.2	1.3
1369407_at	tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin), Tnfrsf11b	2.2	1.1
1382277_at	lymphocyte antigen 96, Ly96	2.2	1.5
1368281_at	dipeptidase 1 (renal), Dpep1	2.2	-1.8
1371791_at	surfeit 4, Surf4	2.2	1.3
1367879_at	CDK5 regulatory subunit associated protein 3, Cdk5rap3	2.2	1.4
1388331_at	tumor rejection antigen gp96 (predicted), Tra1_predicted	2.2	1.0
1389404_at	forkhead-like 18 (Drosophila), Fkhl18	2.2	-1.0
1376038_at	testis expressed gene 2, Tex2	2.2	1.1

1376315_at	ER degradation enhancer, mannosidase alpha-like 2, Edem2	2.2	-1.1
1379717_at	similar to ATP-binding cassette, sub-family G (WHITE), member 3, LOC360997	2.2	-1.2
1382074_at	ring finger protein 19B, Rnf19b	2.2	1.9
1376040_at	signal-induced proliferation-associated 1 like 2, Sipa1l2	2.2	1.1
1383315_at	tsukushin, Tsku	2.2	1.4
1371776_at	Transcribed locus, ---	2.2	1.1
1379128_at	Rho guanine nucleotide exchange factor (GEF) 17 (predicted), Arhgef17_predicted	2.2	-1.8
1393367_at	polynucleotide kinase 3'-phosphatase, Pnkp	2.2	1.5
1372471_at	Transcribed locus, ---	2.2	1.2
1376129_at	Transcribed locus, ---	2.2	1.1
1372021_at	nucleoporin 188, Nup188	2.2	1.2
1393713_at	GDP-mannose 4, 6-dehydratase, Gmds	2.2	1.2
1374671_at	Traf3 interacting protein 2, Traf3ip2	2.2	-1.3
1370134_at	solute carrier family 33 (acetyl-CoA transporter), member 1, Slc33a1	2.2	1.2
1389585_at	---	2.2	-1.1
1379885_at	flavin containing monooxygenase 4, Fmo4	2.2	-3.9
1373401_at	Tenascin C, Tnc	2.2	-1.1
1390403_at	family with sequence similarity 43, member A, Fam43a	2.2	-3.8
1380357_a_at	Transcribed locus, ---	2.1	1.2
1392474_at	Unc-51 like kinase 2 (C. elegans) (predicted), Ulk2_predicted	2.1	-1.8
1369906_s_at	multiple coagulation factor deficiency 2, Mcfd2	2.1	1.7
1374538_at	protein O-linked mannose beta1,2-N-acetylglucosaminyltransferase, Pomgnt1	2.1	1.9
1374652_at	Transcribed locus, ---	2.1	1.2
1390555_at	suppressor of cytokine signaling 5, Socs5	2.1	1.6
1390024_at	Transcribed locus, ---	2.1	1.8
1383241_at	complement component 1, r subcomponent, C1r	2.1	-2.8
1370928_at	LPS-induced TN factor, Litaf	2.1	1.2
1374601_at	interferon gamma receptor 2 (predicted), Ifngr2_predicted	2.1	-1.4
1371488_at	similar to SPBPJ4664.02 (predicted)	2.1	-1.3
1370665_at	hypoxia up-regulated 1, Hyou1	2.1	-1.3
1385001_at	gasdermin D, Gsdmd	2.1	1.2
1383500_at	ribosome binding protein 1, Rrbp1	2.1	1.8
1386958_at	thioredoxin reductase 1, Txnrd1	2.1	1.4
1367764_at	cyclin G1, Ccng1	2.1	1.1
1397164_at	Transcribed locus, ---	2.1	1.4

1377614_at	coiled-coil domain containing 95, Ccdc95	2.1	1.2
1376612_at	DTW domain containing 1, Dtwd1	2.1	1.1
1388858_at	mitogen activated protein kinase kinase 3, Map2k3	2.1	1.2
1388325_at	ATPase, H+ transporting, lysosomal V1 subunit D, Atp6v1d	2.1	1.1
1368943_at	ribonuclease, RNase A family 4, Rnase4	2.1	-1.3
1372528_at	N-ethylmaleimide sensitive fusion protein, Nsf	2.1	1.0
1396984_at	Transcribed locus, ---	2.1	-1.1
1370219_at	cytochrome b-245, alpha polypeptide, Cyba	2.1	-1.4
1372231_at	transforming growth factor, beta receptor associated protein 1 (predicted), Tgfbrap1_predicted	2.1	1.2
1374826_at	Transcribed locus, ---	2.1	-1.2
1370931_at	X-ray repair complementing defective repair in Chinese hamster cells 5, Xrcc5	2.1	1.1
1395039_at	Transcribed locus, ---	2.1	-1.1
1373419_at	Protein tyrosine phosphatase, receptor type, G, Ptprg	2.1	1.2
1387076_at	hypoxia inducible factor 1, alpha subunit, Hif1a	2.1	-1.1
1367867_at	growth factor, erv1 (S. cerevisiae)-like (augmenter of liver regeneration), Gfer	2.1	1.1
1388460_at	capping protein (actin filament), gelsolin-like, Capg	2.1	1.1
1368946_at	ADP-ribosylation factor 2, Arf2	2.1	1.0
1372804_at	MMR_HSR1 domain containing protein RGD1359460, RGD1359460	2.1	1.6
1384427_at	transformed mouse 3T3 cell double minute 2 homolog (mouse) (predicted), Mdm2_predicted	2.1	1.3
1374953_at	similar to CG12279-PA, LOC500420	2.1	1.4
1373924_at	similar to C530044N13Rik protein, RGD1306568	2.1	-1.1
1393915_at	membrane bound O-acyltransferase domain containing 5, Mboat5	2.1	1.0
1385999_at	YME1-like 1 (S. cerevisiae), Yme1l1	2.1	-1.9
1374134_at	ELK3, member of ETS oncogene family (predicted), Elk3_predicted	2.1	1.2
1375517_at	tumor protein p53 inducible nuclear protein 2, Trp53inp2	2.1	-2.3
1370869_at	branched chain aminotransferase 1, cytosolic, Bcat1	2.1	1.1
1372951_at	Transcribed locus, ---	2.1	1.0
1389091_at	ubiquitin specific peptidase 3, Usp3	2.1	-1.2
1377743_at	Transcribed locus, ---	2.1	1.2
1371475_at	ribonuclease, RNase A family 4, Rnase4	2.1	-1.1
1375971_at	ceroid-lipofuscinosis, neuronal 5 (predicted),	2.1	-1.1

	Cln5_predicted		
1369743_a_at	purinergic receptor P2X, ligand-gated ion channel 4, P2rx4	2.1	-2.0
1375962_at	Transcribed locus, ---	2.1	-1.0
1399024_at	SCY1-like 1 (S. cerevisiae), Scyl1	2.0	1.0
1377235_a_at	protein phosphatase 2, regulatory subunit B (B56), beta isoform, Ppp2r5b	2.0	1.0
1395468_at	Transcribed locus, ---	2.0	-1.3
1386995_at	B-cell translocation gene 2, anti-proliferative, Btg2	2.0	1.0
1398508_at	similar to polyglutamine-containing protein, RGD1310994	2.0	-1.2
1372704_at	DC2 protein, Dc2	2.0	1.5
1374564_at	deltex 2 homolog (Drosophila), Dtx2	2.0	-1.1
1384724_at	---	2.0	-1.9
1376605_at	solute carrier family 17 (anion/sugar transporter), member 5, Slc17a5	2.0	-1.1
1376680_at	vacuolar protein sorting 37C (yeast) (predicted), Vps37c_predicted	2.0	-1.1
1394304_at	Solute carrier family 33 (acetyl-CoA transporter), member 1, Slc33a1	2.0	1.5
1390905_at	microtubule associated serine/threonine kinase family member 4, Mast4	2.0	1.1
1391871_at	StAR-related lipid transfer (START) domain containing 13, Stard13	2.0	1.6
1376810_at	M-phase phosphoprotein 8, Parp4	2.0	-2.2
1374661_at	aldehyde dehydrogenase 16 family, member A1, Aldh16a1	2.0	1.3
1389483_at	Dpy-19-like 1 (C. elegans) (predicted), Dpy19l1_predicted	2.0	1.2
1387897_at	2',3'-cyclic nucleotide 3' phosphodiesterase, Cnp	2.0	-1.3
1367632_at	glutamate-ammonia ligase (glutamine synthetase), Glul	2.0	-1.2
1393216_at	solute carrier family 33 (acetyl-CoA transporter), member 1, Slc33a1	2.0	1.4
1388243_at	G protein-coupled receptor 176, Gpr176	2.0	-2.2
1372277_at	Transcribed locus, ---	2.0	-1.9
1369940_at	transaldolase 1, Taldo1	2.0	1.4
1368213_at	P450 (cytochrome) oxidoreductase, Por	2.0	1.6
1372776_at	F-box and leucine-rich repeat protein 5 (predicted), Fbxl5_predicted	2.0	1.0
1374215_at	pleckstrin homology domain containing, family J member 1, Plekhj1	2.0	-1.2
1371439_at	erythrocyte membrane protein band 4.1, Epb4.1	2.0	-1.1
1381996_at	Transcribed locus, ---	2.0	1.9

1389525_at	ring finger protein 149, Rnf149	2.0	1.7

Supplemental Table II: Distinctly PDGF-DD-induced genes

Accession Number	Gene	IL-1β Fold Change	PDGF-DD Fold Change
1377112_at	cytidine deaminase (predicted), Cda_predicted	-1.7	41.8
1384253_at	similar to palladin; CGI-151 protein, LOC364558	1.7	19.1
1370834_at	heparan sulfate (glucosamine) 3-O-sulfotransferase 1, Hs3st1	1.2	15.1
1382778_at	Dual specificity phosphatase 6, Dusp6	26.5	12.8
1389413_at	ecotropic viral integration site 2A	3.5	12.8
1389581_at	interleukin 33, Il33	1.1	10.8
1386679_at	Transcribed locus, ---	2.1	10.7
1368124_at	dual specificity phosphatase 5, Dusp5	1.8	10.6
1394600_at	regulator of G-protein signaling 17 (predicted), Rgs17_predicted	1.2	9.9
1384839_at	Transcribed locus, ---	-1.3	9.6
1398483_at	regulator of G-protein signaling 17 (predicted), Rgs17_predicted	-1.2	8.3
1373970_at	interleukin 33, Il33	1.0	7.7
1391083_at	Rho GTPase activating protein 22 (predicted), Arhgap22_predicted	2.0	7.5
1373957_at	reelin, Reln	1.8	7.4
1392547_at	hypothetical LOC302884, MGC105649	4.5	7.2
1370695_s_at	tribbles homolog 3 (Drosophila), Trib3	11.1	6.7
1377113_at	Transcribed locus, ---	1.7	6.5
1377404_at	stanniocalcin 1, Stc1	-1.6	5.9
1371248_at	small proline-rich protein 1A, Sprr1a	1.2	5.8
1370387_at	cytochrome P450, family 3, subfamily a, polypeptide 9, Cyp3a9	6.1	5.7
1392065_at	Transcribed locus, ---	2.1	5.5
1378700_at	Transcribed locus, ---	-1.5	5.3
1375014_at	ADP-ribosylation factor-like 4C, Arl4c	2.8	5.1
1383019_at	Transcribed locus, ---	14.0	5.1
1369006_at	hexokinase 2, Hk2	1.2	5.0
1373403_at	similar to Protein C8orf4 (Thyroid cancer protein 1) (TC-1), LOC684871	2.2	4.9
1370694_at	tribbles homolog 3 (Drosophila), Trib3	4.3	4.9
1369200_at	5' nucleotidase, ecto, Nt5e	5.0	4.9
1394883_at	Transcribed locus, ---	3.6	4.8
1389755_at	cell division cycle associated 7 like, Cdca7l	2.8	4.8
1389528_s_at	Jun oncogene, Jun	-2.1	4.8
1394280_at	regulator of G-protein signaling 17 (predicted),	-3.0	4.7

	Rgs17_predicted		
1395197_at	Transcribed locus, ---	7.3	4.7
1368590_at	matrix metallopeptidase 16, Mmp16	-1.2	4.6
1388891_at	Transcribed locus, ---	3.9	4.5
1375473_at	Transcribed locus, ---	1.8	4.4
1370492_a_at	FMS-like tyrosine kinase 1, Flt1	13.6	4.4
1378936_at	similar to cleavage stimulation factor, 3 pre-RNA subunit 2, LOC683927	-1.2	4.4
1385522_at	origin recognition complex, subunit 1-like (S.cereviaiae), Orc1l	-2.4	4.4
1368321_at	early growth response 1, Egr1	1.3	4.4
1385781_at	excision repair cross-complementing rodent repair deficiency complementation group 6 -like, Ercc6l	1.8	4.3
1393179_at	Transcribed locus, ---	11.2	4.3
1379997_at	Transcribed locus, ---	1.7	4.3
1383589_at	---	-1.3	4.3
1383846_at	similar to Docking protein 5 (Downstream of tyrosine kinase 5) (Protein dok-5) (predicted), RGD1562846_predicted	2.2	4.3
1393684_at	helicase, lymphoid specific, Hells	1.7	4.2
1393235_at	Transcribed locus, ---	2.3	4.2
1386344_at	Progressive ankylosis homolog (mouse), Ank	-1.5	4.2
1381130_at	minichromosome maintenance deficient 8 (S. cerevisiae) (predicted), Mcm8_predicted	-1.5	4.0
1393559_at	Transcribed locus, ---	-1.4	4.0
1367838_at	cystathionase (cystathionine gamma-lyase), Cth	4.7	4.0
1379345_at	collagen, type XV, alpha 1, Col15a1	4.5	4.0
1382960_at	Transcribed locus, ---	1.1	4.0
1388939_at	collagen, type XV, alpha 1, Col15a1	1.8	3.9
1374359_at	cyclin E2, Ccne2	1.1	3.9
1391075_at	regulator of G-protein signaling 17 (predicted), Rgs17_predicted	1.2	3.8
1396101_at	stanniocalcin 1, Stc1	-1.7	3.7
1396214_at	kit ligand, Kitl	-1.7	3.7
1384110_at	---	-1.4	3.7
1372665_at	phosphoserine aminotransferase 1, Psat1	-1.1	3.7
1370047_at	ectonucleotide pyrophosphatase/phosphodiesterase 1, Enpp1	1.0	3.7
1378056_at	geminin (predicted), Gmnn_predicted	1.4	3.6
1377350_at	Transcribed locus, weakly similar to XP_001842288.1 seroreactive antigen BMN1-5 [Culex pipiens quinquefasciatus], ---	1.1	3.6

1397226_at	---	-1.3	3.6
1372843_at	LOC363020 (predicted), RGD1309410_predicted	2.0	3.6
1387389_at	receptor (calcitonin) activity modifying protein 3, Ramp3	3.0	3.5
1368726_a_at	zinc finger protein 347, Zfp347	1.7	3.5
1392061_at	minichromosome maintenance deficient 10 (S. cerevisiae) (predicted), Mcm10_predicted	1.9	3.5
1383581_at	similar to CG3880-PA, LOC680531	-1.3	3.5
1374540_at	cell division cycle associated 7, Cdca7	1.1	3.5
1379510_at	Transcribed locus, ---	-1.2	3.5
1380850_at	Transcribed locus, ---	-2.5	3.5
1392446_at	kelch-like 2, Mayven (Drosophila) (predicted), Klhl2_predicted	1.3	3.5
1386435_at	transcription factor AP4 (predicted), Tcfap4_predicted	1.5	3.4
1378507_at	Transcribed locus, moderately similar to NP_904333.1 ATP synthase F0 subunit 6 [Mus musculus], ---	-1.3	3.4
1387851_at	phosphotriesterase related, Pter	1.2	3.4
1385724_at	hypothetical protein LOC682874, LOC682874	-1.1	3.4
1379619_at	Transcribed locus, ---	2.1	3.4
1387134_at	schlafen 3, Slfn3	1.2	3.4
1379234_a_at	cell division cycle 45 homolog (S. cerevisiae)-like, Cdc45l	1.6	3.3
1371113_a_at	transferrin receptor, Tfrc	1.1	3.3
1394031_at	family with sequence similarity 83, member D, Fam83d	-2.0	3.3
1399032_at	excision repair cross-complementing rodent repair deficiency, complementation group 1 (predicted), Ercc1_predicted	1.8	3.3
1369788_s_at	Jun oncogene, Jun	-1.4	3.3
1375957_at	Transcribed locus, ---	1.8	3.3
1374805_at	defective in sister chromatid cohesion 1 homolog (S. cerevisiae), Dscc1	1.0	3.3
1383084_at	Transcribed locus, ---	2.3	3.3
1381933_at	replication factor C (activator 1) 5 (predicted), Rfc5_predicted	1.2	3.2
1378640_at	ubiquitin-like, containing PHD and RING finger domains, 1, Uhrf1	-1.0	3.2
1389797_at	Transcribed locus, ---	4.3	3.2
1381749_at	Transcribed locus, ---	-1.0	3.2
1390141_at	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like (predicted), Mthfd1l_predicted	1.7	3.2

1391059_at	neuropeptide W, Npw	2.9	3.2
1379448_at	Ttk protein kinase (predicted), Ttk_predicted	-1.7	3.2
1369249_at	progressive ankylosis, Ank	-1.3	3.2
1369625_at	aquaporin 1, Aqp1	-3.8	3.2
1393439_a_at	progressive ankylosis, Ank	-1.6	3.2
1380831_at	Transcribed locus, ---	-3.2	3.1
1390415_at	thyroid hormone receptor interactor 13, Trip13	1.0	3.1
1392274_at	Transcribed locus, ---	-6.0	3.1
1389919_at	parvin, beta (predicted), Parvb_predicted	-1.7	3.1
1370034_at	cell division cycle 25 homolog B (S. pombe), Cdc25b	-1.1	3.1
1389440_at	Transcribed locus, ---	-1.1	3.1
1375377_at	immunoglobulin superfamily, member 3 (predicted), Igsf3_predicted	-2.0	3.0
1378906_at	similar to hypothetical protein FLJ25416 (predicted), RGD1559690_predicted	1.4	3.0
1368677_at	brain derived neurotrophic factor, Bdnf	-1.1	3.0
1380277_at	RAD51 associated protein 1, Rad51ap1	1.5	3.0
1371193_at	tumor necrosis factor alpha induced protein 6, Tnfaip6	2.2	3.0
1387371_at	cell division cycle 25 homolog A (S. pombe), Cdc25a	-1.0	3.0
1393451_at	centromere protein N, Cenpn	1.5	3.0
1389457_at	myeloblastosis oncogene-like 2 (predicted), Mybl2_predicted	-1.0	3.0
1378120_at	Transcribed locus, ---	-1.2	3.0
1396144_at	Similar to Traf2 and NCK interacting kinase, splice variant 4 (predicted), RGD1561817_predicted	-2.2	3.0
1377424_at	Transcribed locus, ---	-1.2	3.0
1377967_at	chromatin licensing and DNA replication factor 1, Cdt1	-1.1	2.9
1369087_at	FMS-like tyrosine kinase 1, Flt1	1.2	2.9
1385723_at	Transcribed locus, ---	1.1	2.9
1381298_at	minichromosome maintenance deficient 10 (S. cerevisiae) (predicted), Mcm10_predicted	1.2	2.9
1393844_at	myeloid leukemia factor 1 interacting protein, Mlf1ip	1.6	2.9
1392829_at	similar to cleavage stimulation factor, 3 pre-RNA subunit 2, LOC683927	-1.0	2.9
1391201_at	WD repeat and HMG-box DNA binding protein 1 (predicted), Wdhd1_predicted	-1.6	2.9
1388856_at	kit ligand, Kitl	-2.3	2.9
1395944_at	Transcribed locus, ---	-1.3	2.9
1368799_at	baculoviral IAP repeat-containing 5, Birc5	1.7	2.9

1383519_at	Hexokinase 2, Hk2	1.4	2.9
1397476_at	Ttk protein kinase (predicted), Ttk_predicted	-4.0	2.9
1393982_at	polymerase (DNA directed), epsilon 2 (p59 subunit) (predicted), Pole2_predicted	-1.4	2.8
1368983_at	heparin-binding EGF-like growth factor, Hbegf	-2.3	2.8
1388618_at	nidogen 2, Nid2	-1.2	2.8
1370422_at	receptor-interacting serine-threonine kinase 3, Ripk3	1.8	2.8
1376027_at	---	-1.6	2.8
1376639_at	ring finger protein 126, Rnf126	-1.0	2.8
1382592_at	coiled-coil domain containing 99, Ccdc99	-1.1	2.8
1395361_at	Deoxyuridine triphosphatase, Dut	1.6	2.8
1368226_at	Nucleoside 2-deoxyribosyltransferase domain containing protein RGD620382, RGD620382	1.5	2.8
1382964_at	---	1.2	2.8
1380895_at	Transcribed locus, ---	1.1	2.8
1368391_at	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1, Slc7a1	1.3	2.8
1382188_at	G patch domain containing 4, Gpatch4	-4.6	2.8
1390481_a_at	ubiquitin-conjugating enzyme E2T (putative) (predicted), Ube2t_predicted	1.2	2.8
1394401_at	ELOVL family member 6, elongation of long chain fatty acids (yeast), Elovl6	-1.4	2.8
1369338_at	roundabout homolog 1 (Drosophila), Robo1	1.7	2.8
1373068_at	interferon-related developmental regulator 2 (predicted), Ifrd2_predicted	-1.4	2.7
1388721_at	heat shock protein 8, Hspb8	1.4	2.7
1382783_at	Bloom syndrome homolog (human) (predicted), Blm_predicted	-1.1	2.7
1376055_at	minichromosome maintenance deficient 5, cell division cycle 46 (S. cerevisiae) (predicted), Mcm5_predicted	-1.2	2.7
1391051_at	Transcribed locus, ---	1.3	2.7
1384268_at	cyclin Y-like 1, Ccnyl1	1.1	2.7
1380030_at	zinc finger protein 593, Zfp593	1.9	2.7
1378556_at	Transcribed locus, ---	-1.4	2.7
1371074_a_at	minichromosome maintenance deficient 6 (MIS5 homolog, S. pombe) (S. cerevisiae), Mcm6	-1.3	2.7
1376065_at	RRS1 ribosome biogenesis regulator homolog (S. cerevisiae) (predicted), Rrs1_predicted	1.2	2.7
1395998_at	nucleolar protein 5A, Nol5a	-1.7	2.7
1379957_at	schlafen 8, Slfn8	1.5	2.7
1378199_at	leucine zipper protein 5 (predicted), Luzp5_predicted	2.3	2.7

1383685_at	HEAT repeat containing 1 (predicted), Heatr1_predicted	-1.0	2.7
1398602_at	MAD2 (mitotic arrest deficient, homolog)-like 1 (yeast) (predicted), Mad2l1_predicted	1.5	2.7
1392449_at	RAD18 homolog (S. cerevisiae) (predicted), Rad18_predicted	-1.5	2.7
1386466_at	Transcribed locus, ---	-1.0	2.7
1397676_at	---	1.2	2.7
1377387_a_at	Transcribed locus, strongly similar to NP_079738.2 endothelin converting enzyme 2 isoform c [Mus musculus], ---	1.8	2.7
1371785_at	tumor necrosis factor receptor superfamily, member 12a, Tnfrsf12a	1.7	2.7
1392576_at	similar to protein C33A12.3, RGD1359508	-1.1	2.7
1383578_at	RAD51 homolog (S. cerevisiae), Rad51	1.1	2.7
1389582_at	CDNA clone MGC:187947 IMAGE:9103164, ---	1.2	2.7
1391518_at	hypothetical protein LOC689399, LOC689399	1.2	2.6
1389450_at	Williams Beuren syndrome chromosome region 22, Wbscr22	1.4	2.6
1393020_at	zinc finger, MYM-type 6, Zmym6	1.1	2.6
1373884_at	kelch-like 2, Mayven (Drosophila) (predicted), Klhl2_predicted	1.4	2.6
1372406_at	minichromosome maintenance deficient 3 (S. cerevisiae) (predicted), Mcm3_predicted	1.2	2.6
1388872_at	Transcribed locus, ---	-1.2	2.6
1380725_at	tetraspanin 5, Tspan5	-1.3	2.6
1377797_at	EMG1 nucleolar protein homolog (S. cerevisiae) (predicted), Emg1_predicted	-1.2	2.6
1383675_at	Transcribed locus, strongly similar to NP_955518.1 ribosomal RNA processing 12 homolog [Mus musculus], ---	1.1	2.6
1373162_at	similar to transmembrane protein 41a, LOC681708	1.1	2.6
1380768_at	Transcribed locus, ---	2.3	2.6
1373786_at	zinc finger protein 703, Zfp703	1.7	2.6
1387848_at	3-hydroxy-3-methylglutaryl-Coenzyme A reductase, Hmgcr	1.4	2.6
1370177_at	poliovirus receptor, PVR	1.4	2.6
1385086_at	budding uninhibited by benzimidazoles 1 homolog (S. cerevisiae) (predicted), Bub1_predicted	-1.3	2.6
1389668_at	SPC25, NDC80 kinetochore complex component, homolog (S. cerevisiae), Spc25	-1.5	2.6
1372156_at	transmembrane protein 97, Tmem97	1.4	2.6
1377689_at	kinetochore associated 1 (predicted),	-1.8	2.6

	Kntc1_predicted		
1385709_x_at	Transcribed locus, ---	-1.6	2.6
1379296_at	Transcribed locus, ---	1.4	2.6
1397567_at	Transcribed locus, ---	1.3	2.6
1374734_at	hypothetical protein LOC680254, LOC680254	1.3	2.6
1371928_at	cell division cycle associated 8, Cdca8	-1.1	2.6
1389542_at	centromere protein E (predicted), Cenpe_predicted	6.9	2.6
1380243_at	Similar to CG14803-PA (predicted), RGD1304693_predicted	1.1	2.6
1368033_at	nucleolar and coiled-body phosphoprotein 1, Nolc1	-1.7	2.6
1388353_at	proliferation-associated 2G4, Pa2g4	1.8	2.6
1374857_at	nucleolar protein family A, member 1 (H/ACA small nucleolar RNPs), Nola1	1.3	2.6
1379235_x_at	cell division cycle 45 homolog (S. cerevisiae)-like, Cdc45l	1.3	2.6
1370910_at	replication factor C (activator 1) 2, Rfc2	1.4	2.6
1373538_at	ubiquitin specific peptdiase 1, Usp1	1.6	2.6
1384231_at	similar to Shc SH2-domain binding protein 1, LOC687121	-2.5	2.6
1385733_at	exonuclease 1 (predicted), Exo1_predicted	-1.4	2.6
1386178_at	Transcribed locus, ---	-1.2	2.6
1381857_at	RAS p21 protein activator 1, Rasa1	1.2	2.6
1378940_at	SHQ1 homolog (S. cerevisiae) (predicted), Shq1_predicted	1.6	2.6
1374404_at	Jun oncogene, Jun	-1.5	2.6
1371133_a_at	protein kinase, cAMP dependent regulatory, type II beta, Prkar2b	-1.1	2.5
1377625_at	tRNA methyltransferase 6 homolog (S. cerevisiae), Trmt6	1.2	2.5
1367894_at	insulin induced gene 1, Insig1	1.5	2.5
1367834_at	spermidine synthase, Srm	1.3	2.5
1376104_at	similar to KIAA0802 protein (predicted), RGD1308319_predicted	-1.2	2.5
1380775_at	M-phase phosphoprotein 1 (predicted), Mphosph1_predicted	-1.2	2.5
1374864_at	sprouty homolog 2 (Drosophila), Spry2	1.8	2.5
1384174_at	---	-1.2	2.5
1375060_at	Transcribed locus, moderately similar to NP_081539.1 apoptosis-inducing, TAF9-like domain 1 [Mus musculus], ---	1.2	2.5
1387048_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39, Ddx39	1.7	2.5
1376026_at	downstream neighbor of SON, Donson	-1.5	2.5

1370258_at	basic leucine zipper and W2 domains 2, Bzw2	1.5	2.5
1389380_at	similar to Folylpolyglutamate synthase, mitochondrial precursor (Folylpoly-gamma-glutamate synthetase), LOC687266	-1.0	2.5
1372318_at	Transcribed locus, ---	-1.4	2.5
1371849_at	5'-nucleotidase domain containing 2, Nt5dc2	1.2	2.5
1390579_at	similar to RIKEN cDNA 1810029B16 (predicted), RGD1305222_predicted	1.0	2.5
1388901_at	FK506 binding protein 5, Fkbp5	1.3	2.5
1390272_at	DPH5 homolog (S. cerevisiae), Dph5	1.2	2.5
1384259_at	Rac GTPase-activating protein 1 (predicted), Racgap1_predicted	-1.4	2.5
1386969_at	neuritin 1, Nrn1	-1.1	2.5
1382511_at	E2F transcription factor 1, E2f1	-2.1	2.5
1388340_at	NS5A (hepatitis C virus) transactivated protein 9, Ns5atp9	1.0	2.5
1384124_at	Transcribed locus, ---	-1.1	2.5
1390383_at	adipose differentiation related protein, Adfp	1.7	2.5
1393848_at	ribonucleotide reductase M2, Rrm2	-1.7	2.5
1398756_at	nucleophosmin 1, Npm1	1.5	2.5
1388341_at	RAN GTPase activating protein 1, Rangap1	1.0	2.5
1382193_at	CDGSH iron sulfur domain 2, Cisd2	1.0	2.5
1372631_at	thymidine kinase 1, Tk1	-1.2	2.5
1393173_at	RAS p21 protein activator 1, Rasa1	1.2	2.5
1376681_at	similar to RIKEN cDNA 1500003O22, RGD1308302	-2.1	2.5
1396086_at	transmembrane protein 97, Tmem97	1.2	2.5
1384068_at	cytoskeleton associated protein 2 (predicted), Ckap2_predicted	1.2	2.5
1383926_at	budding uninhibited by benzimidazoles 1 homolog, beta (S. cerevisiae), Bub1b	-1.2	2.5
1372059_at	similar to RIKEN cDNA 2610528E23, RGD1309437	1.4	2.5
1395635_at	tumor necrosis factor receptor superfamily, member 26 (predicted), Tnfrsf26_predicted	1.7	2.5
1379967_at	zinc finger protein 367, Zfp367	-2.0	2.5
1389081_at	vacuolar protein sorting 37B (yeast) (predicted), Vps37b_predicted	1.1	2.5
1370344_at	heat shock protein 4, Hspa4	-1.1	2.5
1397704_at	---	2.1	2.4
1393128_at	G patch domain containing 4, Gpatch4	1.1	2.4
1388458_at	replication factor C (activator 1) 4 (predicted), Rfc4_predicted	-1.0	2.4
1387926_at	sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S. cerevisae), Sc5d	-1.1	2.4

1372106_at	EH-domain containing 4, Ehd4	1.5	2.4
1377992_at	Transcribed locus, ---	1.7	2.4
1384338_at	cell division cycle 45 homolog (S. cerevisiae)-like, Cdc45l	1.4	2.4
1382459_at	---	2.9	2.4
1381833_at	cell division cycle associated 2, Cdca2	-5.4	2.4
1388436_at	small nuclear ribonucleoprotein polypeptide A, Snrpa	1.3	2.4
1369736_at	epithelial membrane protein 1, Emp1	-1.2	2.4
1372012_at	24-dehydrocholesterol reductase, Dhcr24	1.1	2.4
1392733_at	similar to mirror-image polydactyly 1, LOC687620	-1.1	2.4
1367795_at	interferon-related developmental regulator 1, Ifrd1	-1.3	2.4
1368126_at	acetoacetyl-CoA synthetase, Aacs	-1.0	2.4
1370085_at	RAS p21 protein activator 1, Rasa1	1.0	2.4
1376816_at	Transcribed locus, ---	-1.3	2.4
1394869_at	Transcribed locus, ---	-1.0	2.4
1370875_at	villin 2, Vil2	-1.4	2.4
1388750_at	transferrin receptor, Tfrc	1.3	2.4
1390542_at	Rad51 homolog c (S. cerevisiae), Rad51c	1.7	2.4
1385619_at	kinesin family member 11, Kif11	1.4	2.4
1388622_at	nucleolar protein 5A, Nol5a	1.0	2.4
1386073_at	Similar to T-Brain-1, LOC311078	1.4	2.4
1387280_a_at	solute carrier family 7 (cationic amino acid transporter, y+ system), member 5, Slc7a5	1.1	2.4
1384265_at	polymerase (DNA-directed), delta 3, accessory subunit, Pold3	2.0	2.4
1377619_at	WD repeat domain 36 (predicted), Wdr36_predicted	1.2	2.4
1373224_at	ST3 beta-galactoside alpha-2,3-sialyltransferase 4, St3gal4	1.6	2.4
1375186_at	DPH3, KTI11 homolog (S. cerevisiae), Dph3	1.7	2.4
1370346_at	cyclin B1, Ccnb1	-1.3	2.4
1387196_at	KH domain containing, RNA binding, signal transduction associated 3, Khdrbs3	-1.7	2.4
1383767_at	Transcribed locus, ---	2.0	2.4
1376098_a_at	myosin IG, Myo1g	-1.1	2.4
1377778_at	ischemia related factor vof-16, Vof16	-1.1	2.4
1384326_at	Transcribed locus, ---	-1.3	2.4
1370355_at	stearoyl-Coenzyme A desaturase 1, Scd1	4.2	2.4
1368400_at	translocase of inner mitochondrial membrane 8 homolog a1 (yeast), Timm8a1	-1.0	2.4
1386426_at	ATPase, Ca++ transporting, plasma membrane	1.8	2.4

	1, Atp2b1		
1378489_at	Transcribed locus, ---	1.7	2.4
1390237_at	translocase of inner mitochondrial membrane 8 homolog a1 (yeast), Timm8a1	-1.1	2.4
1387233_at	hydroxysteroid (17-beta) dehydrogenase 7, Hsd17b7	1.2	2.4
1384988_at	F-box protein 5, Fbxo5	-1.3	2.4
1374072_at	Transcribed locus, ---	-1.1	2.4
1393191_at	similar to RIKEN cDNA 2610200G18 (predicted), RGD1561205_predicted	-1.4	2.4
1368275_at	sterol-C4-methyl oxidase-like, Sc4mol	1.2	2.4
1388484_at	ubiquitin-conjugating enzyme E2C (predicted), Ube2c_predicted	1.2	2.4
1388695_at	serine hydroxymethyltransferase 2 (mitochondrial), Shmt2	1.1	2.4
1389430_at	Transcribed locus, ---	-1.1	2.3
1397609_at	TRAF4 associated factor 1, Traf4af1	1.0	2.3
1398553_at	transmembrane emp24 protein transport domain containing 5, Tmed5	1.6	2.3
1371908_at	NTF2-related export protein 1 (predicted), Nxt1_predicted	1.0	2.3
1373439_at	Transcribed locus, ---	1.1	2.3
1392554_a_at	---	-1.2	2.3
1376231_at	GINS complex subunit 1 (Psf1 homolog), Gins1	-1.1	2.3
1392688_at	Ras association (RalGDS/AF-6) domain family 1, Rassf1	1.7	2.3
1373960_at	transmembrane protein 120A, Tmem120a	1.8	2.3
1374794_at	kinesin family member 15, Kif15	-1.7	2.3
1377175_at	Transcribed locus, ---	-2.0	2.3
1370345_at	cyclin B1, Ccnb1	-1.3	2.3
1377299_at	nuclear autoantigenic sperm protein (histone-binding), Nasp	-1.2	2.3
1372729_at	protein C receptor, endothelial, Procr	2.3	2.3
1399077_at	similar to Metaxin 1, isoform 2, LOC295241	1.1	2.3
1373558_at	Transcribed locus, ---	2.4	2.3
1389446_at	---	-1.1	2.3
1392589_at	replication factor C (activator 1) 5 (predicted), Rfc5_predicted	-1.2	2.3
1385109_at	Josephin domain containing 3, Josd3	-1.3	2.3
1369061_at	glutathione reductase, Gsr	1.0	2.3
1376951_at	MAD2 (mitotic arrest deficient, homolog)-like 1 (yeast) (predicted), Mad2l1_predicted	-1.0	2.3
1390321_at	similar to CG14803-PA (predicted), RGD1304693_predicted	-1.3	2.3
1368165_at	phosphoribosyl pyrophosphate synthetase 1,	-1.1	2.3

	Prps1		
1390113_a_at	La ribonucleoprotein domain family, member 1 (predicted), Larp1_predicted	-1.2	2.3
1395828_at	kinesin family member 23 (predicted), Kif23_predicted	-2.6	2.3
1379592_at	solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 13, Slc25a13	1.3	2.3
1368085_at	GTP cyclohydrolase I feedback regulator, Gchfr	1.2	2.3
1391626_at	meiotic nuclear divisions 1 homolog (S. cerevisiae), Mnd1	1.5	2.3
1376737_at	hypothetical protein LOC690243, LOC690243	-1.5	2.3
1389401_at	---	1.5	2.3
1374449_at	cell division cycle associated 3, Cdca3	-1.1	2.3
1392040_at	spindle assembly 6 homolog (C. elegans) (predicted), Sass6_predicted	-2.4	2.3
1370821_at	thiopurine methyltransferase, Tpmt	1.3	2.3
1368100_at	phosphate cytidylyltransferase 2, ethanolamine, Pcyt2	1.2	2.3
1375071_at	nucleoporin 133 (predicted), Nup133_predicted	1.1	2.3
1392881_at	ST3 beta-galactoside alpha-2,3-sialyltransferase 4, St3gal4	1.5	2.3
1368074_at	galactose-4-epimerase, UDP, Gale	1.4	2.3
1388182_at	DNA primase, p49 subunit, Prim1	-1.6	2.3
1377833_at	Rap1 interacting factor 1 homolog (yeast), Rif1	-1.5	2.3
1380100_at	Similar to Traf2 and NCK interacting kinase, splice variant 4 (predicted), RGD1561817_predicted	-2.7	2.3
1375981_a_at	suppressor of variegation 3-9 homolog 1 (Drosophila) (predicted), Suv39h1_predicted	1.1	2.3
1373772_at	DNA methyltransferase (cytosine-5) 1, Dnmt1	-1.8	2.3
1384331_at	sulfiredoxin 1 homolog (S. cerevisiae), Srxn1	2.8	2.3
1373489_at	chromatin assembly factor 1, subunit A (p150), Chaf1a	-1.5	2.3
1383987_at	Transcribed locus, ---	1.5	2.3
1371040_at	solute carrier family 1 (neutral amino acid transporter), member 5, Slc1a5	1.1	2.3
1374354_at	PHD finger protein 19 (predicted), Phf19_predicted	1.9	2.3
1389844_at	FK506 binding protein 4, Fkbp4	-1.3	2.3
1392818_at	growth arrest specific 5, Gas5	-1.5	2.2
1367983_at	flap structure-specific endonuclease 1, Fen1	1.6	2.2
1373767_at	zinc finger, AN1-type domain 2A, Zfand2a	1.4	2.2
1380009_at	vaccinia related kinase 1, Vrk1	1.2	2.2
1374036_at	minichromosome maintenance deficient 2	-1.2	2.2

	mitotin (S. cerevisiae) (predicted), Mcm2_predicted		
1396063_at	DEK oncogene (DNA binding), Dek	-1.0	2.2
1378296_at	non-SMC condensin I complex, subunit H, Ncaph	-1.3	2.2
1384041_at	Transcribed locus, ---	2.3	2.2
1392111_at	exosome component 3 (predicted), Exosc3_predicted	1.2	2.2
1393033_at	tyrosyl-tRNA synthetase 2 (mitochondrial), Yars2	1.2	2.2
1383660_at	Transcribed locus, ---	-1.1	2.2
1392732_at	nucleolar and spindle associated protein 1 (predicted), Nusap1_predicted	-1.4	2.2
1372886_at	transforming, acidic coiled-coil containing protein 3, Tacc3	1.4	2.2
1392499_at	phosphoribosylformylglycinamidine synthase (FGAR amidotransferase) (predicted), Pfas_predicted	1.1	2.2
1373989_at	Ras association (RalGDS/AF-6) domain family 1, Rassf1	1.1	2.2
1367886_at	proprotein convertase subtilisin/kexin type 7, Pcsk7	1.9	2.2
1387017_at	squalene epoxidase, Sqle	1.1	2.2
1381817_at	Transcribed locus, ---	1.4	2.2
1383684_at	ASF1 anti-silencing function 1 homolog B (S. cerevisiae) (predicted), Asf1b_predicted	1.0	2.2
1388108_at	ELOVL family member 6, elongation of long chain fatty acids (yeast), Elovl6	-1.5	2.2
1374775_at	antigen identified by monoclonal antibody Ki-67 (predicted), Mki67_predicted	-1.3	2.2
1374945_at	GCD14/PCMT domain containing protein RGD1359191, RGD1359191	1.3	2.2
1371712_at	similar to snRNP core protein SMX5, LOC684148	1.2	2.2
1385220_at	Zwilch, kinetochore associated, homolog (Drosophila), Zwilch	-1.2	2.2
1368005_at	inositol 1,4,5-triphosphate receptor 3, Itpr3	2.3	2.2
1383323_at	DSN1, MIND kinetochore complex component, homolog (S. cerevisiae), Dsn1	1.1	2.2
1393647_at	histone aminotransferase 1, Hat1	-1.2	2.2
1376831_at	family with sequence similarity 64, member A, Fam64a	-1.0	2.2
1377021_at	tRNA methyltransferase 6 homolog (S. cerevisiae), Trmt6	1.2	2.2
1372009_at	tyrosyl-tRNA synthetase, Yars	-1.1	2.2
1386586_at	PAK1 interacting protein 1, Pak1ip1	1.6	2.2

1379582_a_at	cyclin A2, Ccna2	1.0	2.2
1372389_at	immediate early response 2, Ier2	2.0	2.2
1395118_at	RNA (guanine-9-) methyltransferase domain containing 2, Rg9mtd2	-1.0	2.2
1382661_at	nucleoporin 160 (predicted), Nup160_predicted	-1.5	2.2
1389858_at	thymidine kinase 1, Tk1	1.1	2.2
1370408_at	putative small membrane protein NID67, Nid67	1.0	2.2
1369012_at	inhibin beta-A, Inhba	2.3	2.2
1386913_at	podoplanin, Pdpn	1.6	2.2
1372182_at	phosphofructokinase, platelet, Pfkp	1.5	2.2
1379479_at	kinesin family member 4, Kif4	-1.1	2.2
1383298_at	LOC363015 (predicted), RGD1310444_predicted	2.8	2.2
1390077_at	Translocation associated membrane protein 1, Tram1	-1.2	2.2
1371608_at	mitochondrial ribosomal protein S34 (predicted), Mrps34_predicted	1.4	2.2
1368522_at	timeless homolog (Drosophila), Timeless	-2.6	2.2
1370080_at	heme oxygenase (decycling) 1, Hmox1	1.4	2.2
1375987_at	ceramide kinase (predicted), Cerk_predicted	1.7	2.2
1379989_at	similar to Antxr2 protein, LOC305633	2.0	2.2
1368204_at	ligase I, DNA, ATP-dependent, Lig1	1.0	2.2
1370386_at	RuvB-like protein 1, Ruvbl1	1.5	2.2
1389485_at	transformed mouse 3T3 cell double minute 1, Mdm1	1.3	2.2
1373658_at	Rac GTPase-activating protein 1 (predicted), Racgap1_predicted	-1.6	2.2
1377832_at	polo-like kinase 4 (Drosophila) (predicted), Plk4_predicted	1.5	2.2
1373530_at	cyclin E1, Ccne1	2.3	2.2
1380303_at	similar to Serine/threonine-protein kinase Haspin (Haploid germ cell-specific nuclear protein kinase), LOC687827	1.4	2.2
1389326_at	replication factor C (activator 1) 3, Rfc3	-1.1	2.2
1388397_at	EBNA1 binding protein 2, Ebna1bp2	1.1	2.2
1393581_at	asp (abnormal spindle)-like, microcephaly associated (Drosophila) (predicted), Aspm_predicted	1.3	2.2
1376185_at	kinesin family member C1, Kifc1	-1.2	2.2
1389738_at	uracil-DNA glycosylase, Ung	1.3	2.2
1383805_at	---	-1.8	2.2
1372051_at	rhomboid domain containing 2, Rhbdd2	1.7	2.2
1373114_at	Transcribed locus, ---	-1.0	2.2
1367780_at	pituitary tumor-transforming 1, Pttg1	1.3	2.2

1375612_at	Transcribed locus, ---	1.2	2.2
1373046_at	DAZ associated protein 1, Dazap1	1.2	2.2
1376611_at	Polymerase (DNA directed), alpha 1, Pola1	-1.3	2.2
1387269_s_at	plasminogen activator, urokinase receptor, Plaur	1.4	2.2
1368273_at	mitogen-activated protein kinase 6, Mapk6	1.5	2.2
1390777_at	sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S. cerevisae), Sc5d	-1.3	2.2
1379195_s_at	ligase I, DNA, ATP-dependent, Lig1	1.1	2.1
1375412_at	Transcribed locus, ---	1.5	2.1
1370050_at	ATPase, Ca++ transporting, plasma membrane 1, Atp2b1	2.0	2.1
1387062_a_at	checkpoint kinase 1 homolog (S. pombe), Chek1	-1.1	2.1
1374799_at	non-SMC condensin I complex, subunit D2, Ncapd2	-1.4	2.1
1376039_at	aurora kinase A, Aurka	1.1	2.1
1389421_at	polymerase (DNA directed), epsilon, Pole	-2.2	2.1
1389279_at	Transcribed locus, ---	-1.1	2.1
1375282_at	cerebral cavernous malformation 2 (predicted), Ccm2_predicted	-1.3	2.1
1385606_at	brain protein 16, Brp16	1.0	2.1
1384252_at	similar to hypothetical protein BC015148 (predicted), RGD1309095_predicted	1.1	2.1
1367933_at	S-adenosylmethionine decarboxylase 1, Amd1	1.1	2.1
1376914_at	DEP domain containing 1a (predicted), Depdc1a_predicted	-1.2	2.1
1383741_at	Transcribed locus, ---	1.0	2.1
1376291_at	---	1.8	2.1
1373085_at	carbonyl reductase 3 (predicted), Cbr3_predicted	-1.3	2.1
1371367_at	TAR DNA binding protein, Tardbp	-1.1	2.1
1373677_at	solute carrier family 39 (zinc transporter), member 10 (predicted), Slc39a10_predicted	1.9	2.1
1398439_a_at	origin recognition complex, subunit 6-like (S. cerevisiae), Orc6l	-1.2	2.1
1379337_at	FAST kinase domains 2, Fastkd2	-1.1	2.1
1372903_at	similar to 3000004C01Rik protein, RGD1310360	1.2	2.1
1389017_at	similar to Antxr2 protein, LOC305633	1.8	2.1
1392440_at	---	-3.8	2.1
1373557_at	minichromosome maintenance deficient 4 homolog (S. cerevisiae), Mcm4	1.6	2.1
1371862_at	ribonucleotide reductase M1, Rrm1	-1.1	2.1
1390384_at	H2A histone family, member X, H2afx	1.1	2.1

1370245_at	cathepsin L, Ctsl	1.4	2.1
1391889_at	Transcribed locus, ---	2.0	2.1
1374840_at	similar to peptidyl prolyl isomerase H (predicted), RGD1564921_predicted	1.2	2.1
1373935_at	polymerase (DNA directed), delta 2, regulatory subunit, Pold2	-1.7	2.1
1369617_at	ubiquitin-conjugating enzyme E2N, Ube2n	1.2	2.1
1368031_at	nucleolar and coiled-body phosphoprotein 1, Nolc1	1.1	2.1
1387795_at	polymerase (DNA directed), alpha 2, Pola2	1.7	2.1
1372957_at	Transcribed locus, ---	-3.3	2.1
1398618_s_at	Transcribed locus, ---	-1.1	2.1
1387085_at	phosphoribosyl pyrophosphate synthetase 1, Prps1	-1.2	2.1
1370323_at	thimet oligopeptidase 1, Thop1	1.3	2.1
1388953_at	guanine nucleotide binding protein-like 3 (nucleolar), Gnl3	-1.1	2.1
1374113_at	bromodomain adjacent to zinc finger domain, 1A (predicted), Baz1a_predicted	1.6	2.1
1376084_a_at	extra spindle poles like 1 (S. cerevisiae) (predicted), Espl1_predicted	1.5	2.1
1373741_at	pseudouridine synthase 1, Pus1	1.6	2.1
1377627_at	UTP20, small subunit (SSU) processome component, homolog (yeast), Utp20	1.1	2.1
1373722_at	kinesin family member 20A (predicted), Kif20a_predicted	-1.5	2.1
1397556_at	N-acetyltransferase 13, Nat13	1.3	2.1
1368392_at	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1, Slc7a1	1.0	2.1
1395557_at	Transcribed locus, ---	1.0	2.1
1372942_at	exosome component 5 (predicted), Exosc5_predicted	1.2	2.1
1386762_at	sorting nexin 18, Snx18	1.2	2.1
1390650_at	nucleoporin 85, Nup85	1.1	2.1
1391415_at	partner of NOB1 homolog (S. cerevisiae), Pno1	1.2	2.1
1398394_at	Transcribed locus, ---	1.0	2.1
1389622_at	solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 13, Slc25a13	1.3	2.1
1386888_at	eukaryotic translation initiation factor 4E binding protein 1, Eif4ebp1	1.6	2.1
1393041_at	structural maintenance of chromosomes 2, Smc2	1.0	2.1
1388744_at	minichromosome maintenance deficient 7 (S. cerevisiae), Mcm7	1.0	2.1

1377823_at	Transcribed locus, ---	-1.0	2.1
1388911_at	DNA primase, p58 subunit, Prim2	-1.1	2.1
1374497_at	nicalin homolog (zebrafish), Ncln	1.5	2.1
1384232_at	Transcribed locus, ---	1.8	2.1
1376319_at	Transcribed locus, ---	1.0	2.1
1381163_at	Transcribed locus, ---	1.2	2.1
1372343_at	exosome component 8 (predicted), Exosc8_predicted	-1.2	2.1
1374506_at	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 31 (predicted), Ddx31_predicted	-1.0	2.1
1373701_at	Transcribed locus, ---	-1.4	2.0
1376722_at	nucleoporin 205, Nup205	1.0	2.0
1373280_at	RuvB-like protein 2, Ruvbl2	1.2	2.0
1398308_at	replication protein A3 (predicted), Rpa3_predicted	1.1	2.0
1383486_at	Transcribed locus, ---	2.0	2.0
1374836_at	RRP9, small subunit (SSU) processome component, homolog (yeast), Rrp9	1.1	2.0
1378259_at	TAR DNA binding protein, Tardbp	-1.0	2.0
1376317_at	origin recognition complex, subunit 6-like (S. cerevisiae), Orc6l	-1.6	2.0
1367970_at	profilin 2, Pfn2	-2.6	2.0
1390982_at	chromatin assembly factor 1, subunit B (p60), Chaf1b	1.0	2.0
1368032_at	nucleolar and coiled-body phosphoprotein 1, Nolc1	1.1	2.0
1387151_at	nucleoporin 107, Nup107	1.3	2.0
1393257_at	CUG triplet repeat, RNA binding protein 1, Cugbp1	1.1	2.0
1374323_at	BRCA2 and CDKN1A interacting protein (predicted), Bccip_predicted	1.4	2.0
1395246_at	Transcribed locus, ---	-1.2	2.0
1367811_at	3-phosphoglycerate dehydrogenase, Phgdh	-2.0	2.0
1375972_at	similar to membrane protein expressed in epithelial-like lung adenocarcinoma (predicted), RGD1307493_predicted	-1.0	2.0
1391466_at	---	-1.1	2.0
1394419_at	Rho GTPase activating protein 11A, Arhgap11a	1.2	2.0
1369018_at	forkhead box M1, Foxm1	1.1	2.0
1394854_at	telomeric repeat binding factor 1, Terf1	-1.2	2.0
1382385_at	proteasome (prosome, macropain) 26S subunit, ATPase, 6	-1.0	2.0
1371542_at	tubulin, alpha 4A, Tuba4a	-1.0	2.0
1391317_at	similar to RIKEN cDNA 2810433K01 (predicted), RGD1310784_predicted	-1.7	2.0

1373026_at	SPC24, NDC80 kinetochore complex component, homolog (S. cerevisiae), Spc24	-1.6	2.0
1367495_at	similar to prefoldin 4 (predicted), RGD1560211_predicted	1.1	2.0
1393158_at	centromere protein Q, Cenpq	-1.3	2.0
1383238_at	queuine tRNA-ribosyltransferase 1, Qtrt1	1.2	2.0
1389695_at	family with sequence similarity 20, member C, Fam20c	1.0	2.0
1382370_at	cyclin F, Ccnf	1.1	2.0
1375852_at	3-hydroxy-3-methylglutaryl-Coenzyme A reductase, Hmgcr	1.1	2.0
1389471_at	translocase of outer mitochondrial membrane 34 (predicted), Tomm34_predicted	1.3	2.0
1372043_at	MRT4, mRNA turnover 4, homolog (S. cerevisiae), Mrto4	1.2	2.0
1371839_at	splicing factor, arginine/serine-rich 2 (SC-35), Sfrs2	-1.0	2.0
1374897_at	similar to THO complex subunit 4 (Tho4), LOC688305	1.1	2.0
1368588_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 52, Ddx52	2.0	2.0
1378137_at	leucine rich repeat containing 59, Lrrc59	1.8	2.0
1376001_at	polymerase (RNA) I polypeptide E, Polr1e	1.4	2.0
1374340_at	Transcribed locus, ---	-1.4	2.0
1389756_at	maternal embryonic leucine zipper kinase (predicted), Melk_predicted	-1.3	2.0
1383222_at	CDNA clone IMAGE:7446637, ---	1.7	2.0
1395363_at	---	1.4	2.0
1369499_at	thymidylate synthase, Tyms	1.3	2.0
1370308_at	XTP3-transactivated protein A, Xtp3tpa	1.4	2.0
1384439_at	---	-1.1	2.0
1392514_at	brix domain containing 1 (predicted), Bxdc1_predicted	1.1	2.0

Supplemental Table III: IL-1β and PDGF-DD commonly upregulated genes in SMCs

Accession Number	Gene	IL-1β Fold Change	PDGF-DD Fold Change
1367802_at	serum/glucocorticoid regulated kinase, Sgk	2.4	4.3
1368021_at	alcohol dehydrogenase 1 (class I), Adh1	2.0	4.0
1368078_at	endothelial cell-specific molecule 1, Esm1	48.0	5.8
1368144_at	regulator of G-protein signaling 2, Rgs2	40.6	2.2
1368489_at	fos-like antigen 1, Fosl1	6.1	10.3
1368512_a_at	glutamyl aminopeptidase, Enpep	28.9	2.5
1368527_at	prostaglandin-endoperoxide synthase 2, Ptgs2	6.3	2.3
1368860_at	pleckstrin homology-like domain, family A, member 1, Phlda1	16.1	2.6
1368921_a_at	CD44 antigen, Cd44	21.3	3.2
1369415_at	basic helix-loop-helix domain containing, class B2, Bhlhb2	3.8	2.3
1369534_at	interleukin 11, Il11	32.9	34.7
1370074_at	brain-specific angiogenesis inhibitor 1-associated protein 2, Baiap2	10.6	2.2
1370075_at	dihydrofolate reductase, Dhfr	3.0	2.4
1370281_at	fatty acid binding protein 5, epidermal, Fabp5	10.9	2.7
1370313_at	acyl-CoA thioesterase 7, Acot7	2.1	2.4
1370314_at	solute carrier family 20 (phosphate transporter), member 1, Slc20a1	3.6	2.5
1370374_at	STEAP family member 3, Steap3	2.6	2.1
1370609_a_at	solute carrier family 16 (monocarboxylic acid transporters), member 7, Slc16a7	2.8	3.2
1370817_at	SEC11 homolog C (S. cerevisiae), Sec11c	2.9	3.2
1370902_at	aldo-keto reductase family 1, member B8, Akr1b8	23.9	3.3
1371150_at	cyclin D1, Ccnd1	5.4	4.9
1371232_a_at	versican, Vcan	10.8	2.5
1371643_at	cyclin D1, Ccnd1	6.1	5.1
1371774_at	spermidine/spermine N1-acetyl transferase 1, Sat1	3.1	2.3
1372510_at	sulfiredoxin 1 homolog (S. cerevisiae), Srxn1	2.1	2.7
1372655_at	---	2.7	2.3
1372691_at	uridine phosphorylase 1, Upp1	316.7	3.4
1372805_at	LOC363015 (predicted), RGD1310444_predicted	4.4	2.3
1374117_at	brain-specific angiogenesis inhibitor 1-associated protein 2, Baiap2	5.6	2.9

1374143_at	Eph receptor A2 (predicted), Epha2_predicted	3.8	3.7
1374228_at	similar to Tripartite motif protein 47, Trim47	4.4	2.9
1374845_at	Transcribed locus, ---	4.6	2.6
1375184_at	Transcribed locus, ---	11.0	11.6
1375845_at	androgen-induced 1, Aig1	2.8	3.0
1376362_at	neuronal pentraxin receptor, Nptxr	2.6	3.1
1376435_at	Transcribed locus, ---	34.6	2.4
1376513_a_at	Transcribed locus, ---	3.4	2.6
1376801_at	RGD1564450 (predicted), RGD1564450_predicted	4.6	3.0
1377016_at	cysteine-rich with EGF-like domains 2, Creld2	2.0	2.0
1377064_at	dual specificity phosphatase 6, Dusp6	34.4	10.5
1378001_at	Transcribed locus, ---	4.6	2.4
1378133_at	solute carrier family 7 (cationic amino acid transporter, y+ system), member 11 (predicted), Slc7a11_predicted	10.4	7.0
1378440_at	Transcribed locus, ---	2.6	2.0
1378462_at	Transcribed locus, ---	2.1	3.4
1378552_at	mitogen-activated protein kinase kinase kinase 6 (predicted), Map3k6_predicted	3.1	2.4
1378867_at	Transcribed locus, ---	6.8	8.8
1379714_at	hypothetical protein LOC688459, rCG_43687	5.3	4.1
1379910_at	UDP-N-acetylglucosamine pyrophosphorylase 1, Uap1	2.5	3.0
1380028_at	ADP-ribosylation factor-like 4C, Arl4c	3.3	7.4
1380168_at	ets variant gene 4 (E1A enhancer binding protein, E1AF) (predicted), Etv4_predicted	26.2	3.0
1381279_at	receptor (TNFRSF)-interacting serine-threonine kinase 2, Ripk2	9.4	5.6
1381341_at	hypothetical protein LOC688459, rCG_43687	7.8	3.7
1381986_at	similar to neuron navigator 1, LOC685707	3.2	2.0
1382387_at	transmembrane protein 16A (predicted), Tmem16a_predicted	5.0	5.1
1382688_at	solute carrier family 25, member 37, Slc25a37	4.8	3.6
1383075_at	cyclin D1, Ccnd1	10.7	3.7
1383447_at	ets variant gene 5, Etv5	7.7	3.1
1384112_at	5' nucleotidase, ecto, Nt5e	3.4	6.6
1385150_at	Transcribed locus, ---	3.5	3.9
1385182_at	plakophilin 1 (predicted), Pkp1_predicted	6.7	3.0
1385702_at	interferon activated gene 204, Ifi204	27.3	2.3
1386890_at	S100 calcium binding protein A10 (calpactin), S100a10	2.2	2.3
1386953_at	hydroxysteroid 11-beta dehydrogenase 1, Hsd11b1	55.5	2.1

1387024_at	dual specificity phosphatase 6, Dusp6	6.2	6.7
1387028_a_at	inhibitor of DNA binding 1, Id1	4.8	3.7
1387074_at	regulator of G-protein signaling 2, Rgs2	24.2	2.2
1387101_at	acyl-CoA synthetase long-chain family member 4, Acsl4	4.7	2.5
1387260_at	Kruppel-like factor 4 (gut), Klf4	32.8	3.1
1387273_at	interleukin 1 receptor-like 1, Il1rl1	23.3	3.4
1387566_at	phospholipase A2, group IVA (cytosolic, calcium-dependent), Pla2g4a	2.7	2.0
1387690_at	caspase 3, apoptosis related cysteine protease, Casp3	3.2	2.3
1387952_a_at	CD44 antigen, Cd44	21.1	3.2
1388054_a_at	versican, Vcan	14.0	2.2
1388142_at	versican, Vcan	9.7	2.1
1388309_at	high mobility group AT-hook 1, Hmga1	19.4	7.2
1389355_at	immediate early response 5, Ier5	2.7	2.4
1389463_at	protein kinase, cAMP dependent regulatory, type I, beta, Prkar1b	4.7	2.5
1389862_at	nucleolar protein 12, Nol12	2.1	2.3
1390306_at	Transcribed locus, ---	6.9	3.4
1390502_at	similar to RIKEN cDNA 1700025G04 gene (predicted), RGD1309104_predicted	3.1	2.8
1390659_at	Transcribed locus, ---	15.8	2.6
1393373_at	opsin 3, Opn3	4.1	2.9
1393728_at	Transcribed locus, ---	20.2	2.6
1394527_at	Transcribed locus, ---	8.3	4.3
1395966_at	potassium channel tetramerisation domain containing 14 (predicted), Kctd14_predicted	2.8	2.2
1397644_at	Methylthioadenosine phosphorylase (predicted), Mtap_predicted	2.2	3.5
1397953_at	similar to AMSH-family protein, LOC687696	2.3	2.5
1398295_at	solute carrier family 29 (nucleoside transporters), member 1, Slc29a1	8.5	3.5

Supplemental Table IV: Distinctly IL-1β-repressed genes in SMCs

Accession	Gene	IL-1β Fold Change	PDGF-DD Fold Change
1390783_at	ATP-binding cassette, sub-family A (ABC1), member 8a (predicted), Abca8a_predicted	-227.9	-24.0
1390601_at	Transcribed locus, ---	-221.6	-45.4
1392077_at	putative C11orf8 homolog (human), C11orf8h	-168.7	-1.6
1396933_s_at	aldo-keto reductase family 1, member C14, Akr1c14	-96.3	8.4
1370708_a_at	aldo-keto reductase family 1, member C14, Akr1c14	-89.3	2.1
1377086_at	C1q and tumor necrosis factor related protein 3 (predicted), C1qtnf3_predicted	-78.1	-1.4
1391520_at	Transcribed locus, ---	-67.5	-6.7
1389284_at	Transcribed locus, ---	-43.3	2.8
1387922_at	cysteine-rich secretory protein LCCL domain containing 2, Crispld2	-42.2	-2.6
1376799_a_at	cytokine receptor-like factor 1 (predicted), Crlf1_predicted	-41.2	-2.3
1370563_at	aldo-keto reductase family 1, member C14, Akr1c14	-31.0	-2.8
1376457_at	cysteine-rich secretory protein LCCL domain containing 2, Crispld2	-28.5	-6.5
1387197_at	osteomodulin, Omd	-24.9	-2.8
1379184_at	Transcribed locus, ---	-24.6	-5.5
1368868_at	A kinase (PRKA) anchor protein (gravin) 12, Akap12	-23.4	1.6
1387879_a_at	CUG triplet repeat, RNA binding protein 2, Cugbp2	-23.1	-2.1
1375303_at	LIM domain binding 3, Ldb3	-21.7	-6.3
1370847_at	spondin 2, extracellular matrix protein, Spon2	-18.9	-1.9
1370019_at	sulfotransferase family 1A, phenol-preferring, member 1, Sult1a1	-17.1	-6.6
1374089_at	Transcribed locus, ---	-15.5	-3.3
1385248_a_at	osteoglycin, Ogn	-14.6	-1.7
1370282_at	cysteine and glycine-rich protein 2, Csrp2	-14.6	-1.7
1384080_at	Transcribed locus, ---	-14.4	-1.3
1392295_a_at	Transcribed locus, ---	-14.4	1.1
1394874_at	similar to Dermal papilla derived protein 7 (predicted), RGD1310935_predicted	-13.5	-1.7
1376789_at	Transcribed locus, ---	-12.9	-1.5
1393452_at	carbonic anhydrase 9 (predicted), Car9_predicted	-12.7	-1.1

1397335_at	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3D, Sema3d	-12.2	-1.5
1376632_at	LIM and cysteine-rich domains 1 (predicted), Lmcd1_predicted	-12.0	-1.9
1394740_at	---	-11.9	-1.8
1395052_at	Transcribed locus, ---	-11.5	-4.1
1383263_at	osteoglycin, Ogn	-11.5	-1.8
1390450_a_at	osteoglycin, Ogn	-11.2	-1.9
1388152_at	microtubule-associated protein 2, Mtap2	-11.0	1.4
1385098_at	Transcribed locus, ---	-10.8	-1.8
1376165_at	Solute carrier family 24 (sodium/potassium/calcium exchanger), member 3, Slc24a3	-10.5	-2.5
1372280_at	ankyrin repeat and SOCS box-containing protein 2, Asb2	-10.2	-4.4
1393109_at	CDNA clone IMAGE:7302574, ---	-10.1	-2.0
1376749_at	osteoglycin, Ogn	-9.9	-1.9
1378970_at	Similar to Myosin-binding protein H (MyBP-H) (H-protein), RGD1310511	-9.7	-2.7
1370703_at	MAS-related GPR, member F, Mrgprf	-9.6	-7.1
1372727_at	Transcribed locus, ---	-9.5	-1.1
1394736_at	popeye domain containing 2, Popdc2	-9.4	-3.2
1379452_at	growth arrest-specific 2, Gas2	-9.3	1.1
1387439_at	multiple EGF-like-domains 6, Megf6	-9.3	-4.4
1368375_a_at	interleukin 15, Il15	-9.2	-2.1
1373110_at	Transcribed locus, ---	-8.8	-1.3
1376410_at	matrix metallopeptidase 17 (predicted), Mmp17_predicted	-8.7	-1.3
1394394_at	Transcribed locus, ---	-8.6	-1.8
1380236_at	similar to integrin alpha 9, LOC685004	-8.5	-4.3
1394570_at	Kell blood group precursor (McLeod phenotype) homolog, Xk	-8.5	1.1
1382072_at	olfactomedin-like 2A (predicted), Olfml2a_predicted	-8.5	-10.6
1379497_at	---	-8.4	-3.3
1370135_at	met proto-oncogene, Cav2	-8.3	1.0
1369773_at	bone morphogenetic protein 3, Bmp3	-8.3	-2.6
1368900_at	thrombomodulin, Thbd	-8.2	1.6
1376806_at	Transcribed locus, ---	-7.9	1.2
1389236_at	myosin binding protein H-like, Mybphl	-7.9	-3.5
1398345_at	Transcribed locus, ---	-7.8	1.3
1392963_at	secernin 1, Scrn1	-7.8	1.3
1389198_at	SH2 domain containing 3C (predicted),	-7.8	-2.5

	Sh2d3c_predicted		
1395512_at	cytokine receptor-like factor 1 (predicted), Crlf1_predicted	-7.4	-1.5
1387803_at	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), beta isoform, Ppp2r2b	-7.3	1.7
1398406_at	Transcribed locus, ---	-7.2	1.4
1374241_at	Transcribed locus, ---	-7.1	-1.1
1377058_at	solute carrier family 37 (glycerol-3-phosphate transporter), member 2, Slc37a2	-7.0	1.2
1392221_at	Transcribed locus, ---	-6.8	-1.6
1388145_at	tenascin XA, Tnxa	-6.8	-1.5
1371984_at	Transcribed locus, ---	-6.6	-3.9
1394456_at	Transcribed locus, ---	-6.5	-1.1
1376172_at	ATP-binding cassette, sub-family G (WHITE), member 4, Abcg4	-6.5	-4.3
1377736_at	Transcribed locus, ---	-6.5	-1.1
1372449_at	Transcribed locus, ---	-6.5	1.3
1368869_at	A kinase (PRKA) anchor protein (gravin) 12, Akap12	-6.4	1.4
1377789_at	Transcribed locus, ---	-6.3	-1.5
1369443_at	angiopoietin-like 2, Angptl2	-6.3	1.5
1368989_at	tissue inhibitor of metalloproteinase 3, Timp3	-6.3	-1.2
1378457_at	Transcribed locus, ---	-6.2	-1.2
1394681_at	aldo-keto reductase family 1, member C-like 1 (predicted), Akr1cl1_predicted	-6.2	-1.4
1375638_at	serum deprivation response, Sdpr	-6.2	-1.4
1393943_at	Matrilin 3 (predicted), Matn3_predicted	-6.1	-1.5
1373093_at	ERBB receptor feedback inhibitor 1, Errfi1	-6.1	1.8
1368700_at	phospholipase C-like 1, Plcl1	-6.1	-1.3
1379117_at	Transcribed locus, ---	-6.0	1.0
1392274_at	Transcribed locus, ---	-6.0	3.1
1391563_at	melanoma associated antigen (mutated) 1-like 1, Mum1l1	-6.0	-1.5
1382452_at	serum deprivation response, Sdpr	-5.9	-1.2
1368901_at	thrombomodulin, Thbd	-5.9	-1.1
1370630_a_at	fibroblast growth factor receptor 2, Fgfr2	-5.9	-3.6
1390523_at	Transcribed locus, ---	-5.8	-1.8
1382439_at	integrin, beta 6, Itgb6	-5.8	-2.1
1389720_at	Transcribed locus, strongly similar to XP_001069291.1 PREDICTED: hypothetical protein [Rattus norvegicus], ---	-5.7	-2.1
1367592_at	troponin T2, cardiac, Tnnt2	-5.7	-1.4
1385125_at	transcription factor myocardin, Myocd	-5.7	-1.7
1374574_at	similar to hypothetical protein MGC38960	-5.6	-1.5

	(predicted), RGD1310552_predicted		
1386615_at	carbohydrate sulfotransferase 2 (predicted), Chst2_predicted	-5.6	-1.5
1382351_at	GTP binding protein (gene overexpressed in skeletal muscle) (predicted), Gem_predicted	-5.6	1.1
1369968_at	pleiotrophin, Ptn	-5.5	1.3
1374383_at	Transcribed locus, ---	-5.4	-1.9
1379493_at	Transcribed locus, ---	-5.4	-1.8
1398476_at	vinculin (predicted), Vcl_predicted	-5.4	-2.0
1383280_at	Transcribed locus, ---	-5.3	-1.8
1379300_at	carbohydrate sulfotransferase 2 (predicted), Chst2_predicted	-5.3	-1.8
1395816_at	family with sequence similarity 13, member C1, Fam13c1	-5.3	-6.4
1375982_at	Transcribed locus, strongly similar to NP_001034162.1 LIM domain binding 3 isoform d [Mus musculus], ---	-5.3	-20.4
1387025_at	dynein cytoplasmic 1 intermediate chain 1, Dync1i1	-5.2	1.2
1392637_at	Transcribed locus, ---	-5.2	1.1
1383240_at	Transcribed locus, ---	-5.2	1.1
1384515_at	Hairy/enhancer-of-split related with YRPW motif 2, Hey2	-5.2	-1.6
1388945_at	similar to 1300014I06Rik protein, RGD1311307	-5.1	-1.0
1370048_at	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 2, Edg2	-5.1	-1.3
1379444_at	Transcribed locus, ---	-5.1	-1.1
1369783_a_at	neuregulin 1, Nrg1	-5.0	2.3
1375959_at	Transcribed locus, ---	-5.0	-2.7
1374943_at	similar to RIKEN cDNA 2010011I20 (predicted), RGD1311378_predicted	-4.9	-1.4
1374591_at	similar to protein tyrosine phosphatase, receptor type, D (predicted), RGD1561090_predicted	-4.9	-1.6
1368105_at	tetraspanin 2, Tspan2	-4.9	-1.8
1375951_at	thrombomodulin, Thbd	-4.9	-1.2
1393015_at	similar to hypothetical protein FLJ14146, RGD1310587	-4.8	-3.6
1370023_at	gap junction membrane channel protein alpha 4, Gja4	-4.8	2.0
1379073_at	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 23, Slc25a23	-4.8	-2.8
1394797_at	Transcribed locus, ---	-4.8	-2.1
1387814_at	caveolin 3, Cav3	-4.7	-1.9
1373992_at	similar to interferon-inducible GTPase,	-4.6	1.5

	MGC108823		
1371485_at	Transcribed locus, ---	-4.6	-1.4
1367857_at	fatty acid desaturase 1, Fads1	-4.6	1.8
1377751_at	Transcribed locus, ---	-4.5	-2.1
1367673_at	selenium binding protein 1, Selenbp1	-4.5	-1.5
1398597_at	Transcribed locus, ---	-4.5	2.1
1378094_at	Transcribed locus, ---	-4.5	1.0
1388667_at	---	-4.5	1.1
1382726_at	Transcribed locus, ---	-4.4	1.8
1385815_at	aortic preferentially expressed gene 1	-4.4	-2.4
1389306_at	matrilin 2 (predicted), Matn2_predicted	-4.4	-1.7
1389836_a_at	Tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory), Timp3	-4.4	-1.2
1380312_at	Transcribed locus, ---	-4.4	-1.5
1389867_at	Transcribed locus, ---	-4.4	-1.6
1368001_at	aortic preferentially expressed gene 1, Apeg1	-4.3	-2.5
1372296_at	SH3-binding domain glutamic acid-rich protein, Sh3bgr	-4.3	-4.2
1367859_at	transforming growth factor, beta 3, Tgfb3	-4.3	-1.9
1394727_at	Transcribed locus, ---	-4.3	-2.9
1368513_at	glutamyl aminopeptidase, Enpep	-4.3	-1.4
1381576_at	phosphoinositide-3-kinase, class 2, beta polypeptide (predicted), Pik3c2b_predicted	-4.3	-1.0
1370310_at	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2, Hmgcs2	-4.3	3.5
1370328_at	dickkopf homolog 3 (Xenopus laevis), Dkk3	-4.3	-1.1
1371241_x_at	Tropomyosin 1, alpha, Tpm1	-4.3	-1.5
1391063_at	kinesin family member 23 (predicted), Kif23_predicted	-4.3	2.0
1375230_at	Endogenous retrovirus mRNA, partial sequence, ---	-4.2	-1.3
1368059_at	crystallin, mu, Crym	-4.2	1.1
1372297_at	glutathione S-transferase, alpha 4, Gsta4	-4.2	1.1
1374269_at	Transcribed locus, ---	-4.1	-2.4
1377642_at	caveolin 2, Cav2	-4.1	1.1
1387293_at	zona pellucida glycoprotein 2, Zp2	-4.1	-1.3
1376619_at	similar to protein tyrosine phosphatase, receptor type, D (predicted), RGD1561090_predicted	-4.1	-1.6
1392973_at	Transcribed locus, ---	-4.1	-1.2
1373232_at	CDNA clone MGC:187847 IMAGE:9036094, ---	-4.1	1.2
1370131_at	met proto-oncogene , Cav1	-4.1	-1.1
1389514_at	leucine rich repeat and Ig domain containing 1, Lingo1	-4.1	-1.2

1376082_at	ecotropic viral integration site 1 (predicted), Evi1_predicted	-4.0	-1.0
1381504_at	asporin, Aspn	-4.0	-1.1
1373693_at	G protein-coupled receptor, family C, group 5, member C, Gprc5c	-4.0	-1.6
1376076_at	---	-4.0	1.1
1374016_at	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 2, Edg2	-4.0	-1.1
1382444_at	Transcribed locus, ---	-4.0	1.1
1371394_x_at	---	-4.0	-1.4
1371696_at	G protein-coupled receptor 56, Gpr56	-4.0	1.2
1382802_x_at	---	-4.0	-1.7
1374171_at	Transcribed locus, ---	-3.9	-1.5
1380726_at	Similar to asporin precursor, LOC306805	-3.9	1.2
1390126_at	---	-3.9	1.5
1377695_at	smoothelin-like 2, Smtnl2	-3.9	-12.8
1393860_at	Transcribed locus, ---	-3.8	1.3
1368343_at	potassium voltage-gated channel, subfamily H (eag-related), member 2, Kcnh2	-3.8	-1.9
1369625_at	aquaporin 1, Aqp1	-3.8	3.2
1392074_at	similar to hypothetical protein FLJ21986, LOC500046	-3.8	-2.5
1389698_at	Transcribed locus, ---	-3.8	-1.5
1384617_at	hypothetical LOC310540, MGC72614	-3.8	-1.0
1378006_at	Transcribed locus, ---	-3.8	1.0
1376997_at	Transcribed locus, ---	-3.7	1.3
1380126_at	Transcribed locus, ---	-3.7	-2.7
1392627_x_at	Endogenous retrovirus mRNA, partial sequence, ---	-3.7	-1.4
1380197_at	Transcribed locus, ---	-3.7	-2.5
1393352_at	similar to hypothetical protein MGC38960 (predicted), RGD1310552_predicted	-3.7	-1.4
1378183_at	Transcribed locus, ---	-3.7	1.2
1371518_at	Nidogen 1, Nid1	-3.6	-1.7
1383696_at	protein tyrosine phosphatase-like (proline instead of catalytic arginine), member a, Ptpla	-3.6	-1.0
1383074_at	mannosidase 2, alpha 1, Man2a1	-3.6	1.3
1372226_at	Transcribed locus, strongly similar to NP_001028289.1 SLIT-ROBO Rho GTPase activating protein 3 isoform b [Homo sapiens], ---	-3.6	-1.6
1372598_at	similar to 1190005I06Rik protein (predicted), RGD1309651_predicted	-3.6	-3.2
1387658_at	eukaryotic elongation factor-2 kinase, Eef2k	-3.6	-1.2

1369329_at	Notch gene homolog 3 (Drosophila), Notch3	-3.6	-2.1
1381434_s_at	CDNA clone MGC:187847 IMAGE:9036094, ---	-3.6	1.2
1379157_at	Transcribed locus, ---	-3.6	-1.4
1394101_at	Transcribed locus, ---	-3.6	-1.6
1390681_at	Transcribed locus, ---	-3.5	1.0
1393196_at	kelch-like 23 (Drosophila) (predicted), Klhl23_predicted	-3.5	-1.3
1368133_at	multiple PDZ domain protein, Mpdz	-3.5	-1.0
1367816_at	HOP homeobox, Hopx	-3.5	1.4
1388456_at	S100 calcium binding protein A1, S100a1	-3.5	-2.2
1387137_at	cartilage oligomeric matrix protein, Comp	-3.5	-2.7
1375138_at	tissue inhibitor of metalloproteinase 3, Timp3	-3.5	-1.0
1390800_a_at	met proto-oncogene, Cav2	-3.5	1.8
1392315_at	Transcribed locus, ---	-3.5	-1.8
1389112_at	naked cuticle 1 homolog (Drosophila) (predicted), Nkd1_predicted	-3.5	-2.0
1376989_at	Transcribed locus, ---	-3.5	-1.8
1377375_at	aminoadipate-semialdehyde synthase (predicted), Aass_predicted	-3.4	-1.1
1374910_at	cadherin EGF LAG seven-pass G-type receptor 2, Celsr2	-3.4	-1.5
1388994_at	Transcribed locus, ---	-3.4	1.3
1385876_at	---	-3.4	-1.6
1373592_at	serine (or cysteine) peptidase inhibitor, clade B, member 9, Serpinb9	-3.4	-1.2
1383721_at	frizzled homolog 8 (Drosophila), Fzd8	-3.4	-1.2
1393129_at	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide III, P4ha3	-3.4	-1.7
1387737_at	methionine adenosyltransferase II, alpha, Mat2a	-3.4	1.4
1390051_at	similar to mKIAA0774 protein (predicted), RGD1562533_predicted	-3.4	-2.0
1388539_at	plakophilin 2, Pkp2	-3.4	-1.1
1386333_at	Transcribed locus, ---	-3.4	-2.6
1380064_at	Transcribed locus, ---	-3.3	-1.2
1397634_at	ankyrin repeat and SAM domain containing 1 (predicted), Anks1_predicted	-3.3	1.1
1372381_at	Transcribed locus, ---	-3.3	-1.3
1387130_at	solute carrier family 39 (iron-regulated transporter), member 1, Slc40a1	-3.3	-1.8
1382659_at	phospholipase A2 receptor 1 (predicted), Pla2r1_predicted	-3.3	-2.6
1389990_at	---	-3.3	-1.3
1391481_at	---	-3.3	-1.1

1388453_at	myeloid-associated differentiation marker, Myadm	-3.3	-1.1
1384834_at	cordon-bleu (predicted), Cobl_predicted	-3.3	-1.6
1390828_at	neuropeptide Y receptor Y1, Npy1r	-3.3	-7.5
1383947_at	---	-3.3	-1.7
1384827_at	polymerase (DNA directed), mu, Polm	-3.3	-1.4
1384276_at	similar to procollagen, type IV, alpha 6, LOC363458	-3.3	-1.3
1373776_at	---	-3.3	1.1
1380831_at	Transcribed locus, ---	-3.2	3.1
1372926_at	Tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory), Timp3	-3.2	-1.0
1391290_at	Transcribed locus, ---	-3.2	-1.7
1389779_at	SH2 domain containing 4A, Sh2d4a	-3.2	-1.3
1382017_at	Transcribed locus, moderately similar to XP_995952.1 PREDICTED: hypothetical protein LOC72575 [Mus musculus], ---	-3.2	1.3
1380838_at	Transcribed locus, ---	-3.2	-2.1
1372332_at	Transcribed locus, ---	-3.2	1.2
1387232_at	bone morphogenetic protein 4, Bmp4	-3.2	-1.6
1367929_at	CD59 antigen, Cd59	-3.2	-1.8
1391862_at	Transcribed locus, ---	-3.2	-1.9
1374144_at	Transcribed locus, ---	-3.2	-1.1
1392953_at	protein tyrosine phosphatase-like (proline instead of catalytic arginine), member a, Ptpla	-3.2	-1.3
1375767_at	pleckstrin homology domain containing, family G (with RhoGef domain) member 3, Plekhg3	-3.2	-1.0
1393264_at	similar to 9630058J23Rik protein (predicted), RGD1564833_predicted	-3.2	-1.3
1369097_s_at	guanylate cyclase 1, soluble, beta 3, Gucy1b3	-3.2	1.2
1374771_at	---	-3.2	1.1
1378400_at	family with sequence similarity 122B, Fam122b	-3.1	1.2
1368114_at	fibroblast growth factor 13, Fgf13	-3.1	-1.4
1392597_at	similar to ionized calcium binding adapter molecule 2 (Iba2) (predicted), RGD1305081_predicted	-3.1	-1.5
1379440_at	follistatin-like 3, Fstl3	-3.1	-1.5
1397348_at	Transcribed locus, ---	-3.1	-1.7
1388916_at	Transcribed locus, ---	-3.1	-1.9
1393492_at	Transcribed locus, ---	-3.1	-1.8
1373672_at	Similar to SPI6, MGC94010	-3.1	-1.2
1380057_at	Transcribed locus, ---	-3.1	1.2
1378746_at	---	-3.1	-1.1
1379724_at	pleckstrin homology-like domain, family B,	-3.1	-1.2

	member 2, Phldb2		
1370120_at	follistatin-like 3, Fstl3	-3.1	-1.6
1382482_at	Transcribed locus, ---	-3.0	-1.0
1386805_at	similar to TPR repeat-containing protein KIAA1043, LOC304558	-3.0	-2.8
1374208_at	zinc finger CCCH type containing 7 A (predicted), Zc3h7a_predicted	-3.0	1.2
1375367_at	PDZ and LIM domain 2, Pdlim2	-3.0	-1.9
1370264_at	spectrin repeat containing, nuclear envelope 1, Syne1	-3.0	-1.8
1371350_at	methionine adenosyltransferase II, alpha, Mat2a	-3.0	1.3
1371679_at	synaptopodin 2, Synpo2	-3.0	-1.1
1372820_at	Transcribed locus, ---	-3.0	-1.6
1398387_at	hypothetical LOC310540, MGC72614	-3.0	1.0
1396071_at	Transcribed locus, ---	-3.0	-1.8
1382422_at	Protocadherin 7, Pcdh7	-3.0	-1.8
1369638_at	eukaryotic elongation factor-2 kinase, Eef2k	-3.0	-1.6
1378490_at	Transcribed locus, ---	-3.0	-1.8
1367604_at	cysteine-rich protein 2, Crip2	-3.0	1.1
1384160_at	synaptopodin 2, Synpo2	-3.0	1.1
1383402_at	Transcribed locus, ---	-3.0	-1.5
1386145_at	Transcribed locus, ---	-3.0	-1.1
1391537_at	SERTA domain containing 4, Sertad4	-3.0	-1.3
1373000_at	sushi-repeat-containing protein, X-linked 2 (predicted), Srpx2_predicted	-2.9	-1.4
1370988_at	---	-2.9	-2.2
1383628_at	Transcribed locus, ---	-2.9	-1.3
1376584_at	protein phosphatase 1 (formerly 2C)-like (predicted), Ppm1l_predicted	-2.9	-1.0
1368724_a_at	tropomyosin 1, alpha, Tpm1	-2.9	-1.8
1384380_at	Transcribed locus, ---	-2.9	-1.5
1377950_at	similar to interferon-inducible GTPase, RGD1309362	-2.9	-1.1
1371139_at	plastin 3 (T-isoform), Pls3	-2.8	-1.4
1382591_at	Transcribed locus, ---	-2.8	1.4
1388195_at	CUG triplet repeat, RNA binding protein 2, Cugbp2	-2.8	-1.7
1377795_at	Transcribed locus, ---	-2.8	-1.9
1396085_at	filamin C, gamma (actin binding protein 280) (predicted), Flnc_predicted	-2.8	-1.6
1384062_at	Transcribed locus, ---	-2.8	-1.2
1385314_at	Transcribed locus, ---	-2.8	1.4
1370940_at	tight junction protein 2, Tjp2	-2.8	1.3

1388874_at	metastasis suppressor 1 (predicted), Mtss1_predicted	-2.8	-1.2
1385564_at	LIM domain containing preferred translocation partner in lipoma, Lpp	-2.8	-1.9
1389150_at	Transcribed locus, ---	-2.8	-1.9
1369960_at	FXYD domain-containing ion transport regulator 1, Fxyd1	-2.8	-1.8
1374691_at	sulfotransferase family 5A, member 1 (predicted), Sult5a1_predicted	-2.8	-1.4
1396539_at	Transcribed locus, ---	-2.8	-1.4
1386960_at	solute carrier family 37 (glucose-6-phosphate transporter), member 4, Slc37a4	-2.8	1.3
1374389_at	guanylate cyclase 1, soluble, beta 3, Gucy1b3	-2.7	1.4
1387907_at	inositol 1,4,5-triphosphate receptor 1, Itpr1	-2.7	-1.3
1393281_at	met proto-oncogene, Cav1	-2.7	1.1
1380100_at	Similar to Traf2 and NCK interacting kinase, splice variant 4 (predicted), RGD1561817_predicted	-2.7	2.3
1389680_at	elongation factor RNA polymerase II 2, Ell2	-2.7	1.3
1393170_at	similar to homeobox-containing transcription factor (predicted), RGD1561431_predicted	-2.7	-1.3
1384308_at	similar to myeloid ecotropic viral integration site 1, LOC686117	-2.7	-1.3
1389199_at	CDNA clone IMAGE:7321132, ---	-2.7	1.1
1383697_at	Transcribed locus, ---	-2.7	1.3
1373998_at	Transcribed locus, ---	-2.7	-1.6
1398484_at	similar to TBC1 domain family, member 8 (with GRAM domain); vascular Rab-GAP/TBC-containing (predicted), RGD1308221_predicted	-2.7	1.2
1374028_at	similar to CDNA sequence BC024479, LOC500974	-2.7	1.1
1388889_at	endoplasmic reticulum metallopeptidase 1, Ermp1	-2.7	-1.1
1397866_at	serine (or cysteine) peptidase inhibitor, clade B, member 6b, Serpinb6b	-2.7	-1.6
1376138_at	---	-2.7	-1.7
1370452_at	calcium channel, voltage-dependent, L type, alpha 1C subunit, Cacna1c	-2.7	-1.8
1386577_at	kelch-like 23 (Drosophila) (predicted), Klhl23_predicted	-2.7	-1.5
1393653_at	Transcribed locus, ---	-2.7	-1.5
1398398_at	homeo box A10, Hoxa10	-2.7	-2.0
1378777_at	Transcribed locus, ---	-2.7	-1.8
1371692_at	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to,	-2.7	1.0

	11, Mllt11		
1386296_at	septin 8 (predicted), Sept8_predicted	-2.7	-2.0
1376089_at	Transcribed locus, ---	-2.6	1.6
1373952_at	protein kinase, AMP-activated, gamma 2 non-catalytic subunit, Prkag2	-2.6	-1.4
1390662_at	tripartite motif-containing 24, Trim24	-2.6	1.5
1376554_at	Transcribed locus, strongly similar to NP_780360.1 TatD DNase domain containing 1 [Mus musculus], ---	-2.6	1.0
1367970_at	profilin 2, Pfn2	-2.6	2.0
1379382_at	Transcribed locus, ---	-2.6	-1.0
1383593_at	Transcribed locus, ---	-2.6	1.0
1372180_at	syndecan 3, Sdc3	-2.6	-1.0
1379315_at	Ras association (RalGDS/AF-6) domain family 7 (predicted), Rassf7_predicted	-2.6	-2.5
1393415_at	endothelin receptor type A, Ednra	-2.6	2.1
1383576_at	Transcribed locus, ---	-2.6	-1.8
1385171_s_at	smoothelin-like 2, Smtnl2	-2.6	-4.1
1383353_at	Transcribed locus, ---	-2.6	-1.0
1377042_at	polycomb group ring finger 5, Pcgf5	-2.6	-1.3
1392937_at	cyclin I (predicted), Ccni_predicted	-2.6	-1.1
1376779_at	forkhead box O1, Foxo1	-2.6	-1.3
1392083_at	Similar to Ext1, LOC299907	-2.6	-1.4
1399113_at	Transcribed locus, ---	-2.6	-1.1
1387673_a_at	annexin A6, Anxa6	-2.5	-1.3
1370986_s_at	---	-2.5	-1.5
1371855_at	---	-2.5	-1.9
1396736_at	Transcribed locus, ---	-2.5	-1.2
1372905_at	vinculin (predicted), Vcl_predicted	-2.5	-1.2
1381850_at	protein phosphatase 1, regulatory (inhibitor) subunit 12A, Ppp1r12a	-2.5	-1.5
1371625_at	brain glycogen phosphorylase, Pygb	-2.5	-1.4
1383362_at	Transcribed locus, ---	-2.5	-1.3
1382201_at	unc-5 homolog C (C. elegans), Unc5c	-2.5	1.0
1383228_at	---	-2.5	-1.9
1373624_at	Transcribed locus, ---	-2.5	-1.7
1383641_at	endothelin receptor type A, Ednra	-2.5	2.2
1394451_at	annexin A1, Anxa1	-2.5	-1.3
1376140_at	ATP-binding cassette, sub-family D (ALD), member 1 (predicted), Abcd1_predicted	-2.5	-1.4
1376200_at	hypothetical LOC316976, MGC72974	-2.5	-1.7
1390145_at	Transcribed locus, ---	-2.5	-1.1
1375026_at	Similar to calmodulin-like 4, LOC691455	-2.5	-1.3
1379934_at	Transcribed locus, ---	-2.5	1.4

1398866_at	membrane associated guanylate kinase, WW and PDZ domain containing 3, Magi3	-2.5	-1.0
1389096_at	---	-2.5	-1.1
1375538_at	Vinculin (predicted), Vcl_predicted	-2.4	-1.5
1398294_at	actinin, alpha 1, Actn1	-2.4	-1.5
1388185_at	retinoblastoma 1, Rb1	-2.4	-1.9
1395525_at	WW, C2 and coiled-coil domain containing 2, Wwc2	-2.4	-1.7
1388698_at	extracellular matrix protein 1, Ecm1	-2.4	-1.6
1377679_at	G protein-coupled receptor 125 (predicted), Gpr125_predicted	-2.4	-1.1
1372602_at	starch binding domain 1, Stbd1	-2.4	-1.4
1389656_at	similar to Tetraspanin-15 (Tspan-15) (Transmembrane 4 superfamily member 15) (Tetraspan NET-7), LOC679462	-2.4	-1.5
1388300_at	microsomal glutathione S-transferase 3 (predicted), Mgst3_predicted	-2.4	1.6
1373642_at	---	-2.4	-1.5
1378949_at	endothelin-converting enzyme 2, Ece2	-2.4	-1.8
1374767_at	similar to hypothetical protein FLJ14675, RGD1309592	-2.4	1.2
1371665_at	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3, Smarcd3	-2.4	-1.3
1387279_at	F11 receptor, F11r	-2.4	-1.9
1373749_at	syntrophin, acidic 1, Snta1	-2.4	-1.1
1377118_at	similar to KIAA1712 protein, RGD1308517	-2.4	-1.2
1384521_at	Transcribed locus, ---	-2.4	-1.1
1373448_at	acylphosphatase 1, erythrocyte (common) type (predicted), Acyp1_predicted	-2.4	1.6
1372048_at	podocalyxin-like 2 (predicted), Podxl2_predicted	-2.4	-2.9
1375046_at	NAC alpha domain containing, Nacad	-2.4	-2.1
1383897_at	H2A histone family, member Y2, H2afy2	-2.4	1.2
1376377_at	diaphanous homolog 3 (Drosophila), Diap3	-2.4	1.1
1369953_a_at	CD24 antigen, Cd24	-2.3	1.1
1384182_at	pleckstrin homology domain containing, family C (with FERM domain) member 1, Plekhc1	-2.3	-1.7
1389281_at	Transcribed locus, strongly similar to XP_001077488.1 PREDICTED: similar to ankyrin repeat domain 25 [Rattus norvegicus], ---	-2.3	-1.8
1390444_at	Transcribed locus, ---	-2.3	-1.6
1386061_at	coiled coil domain containing 88A, Ccdc88a	-2.3	1.3
1383025_at	meningioma expressed antigen 5	-2.3	-1.0

	(hyaluronidase), Mgea5		
1368983_at	heparin-binding EGF-like growth factor, Hbegf	-2.3	2.8
1373363_at	microtubule-associated protein 1b, Map1b	-2.3	1.3
1378049_at	zinc finger protein 362, Zscan20	-2.3	-1.8
1387015_at	profilin 2, Pfn2	-2.3	1.6
1372479_at	Transcribed locus, ---	-2.3	-1.0
1397317_at	Transcribed locus, ---	-2.3	1.7
1388906_at	---	-2.3	-1.2
1377427_at	Protein tyrosine phosphatase, non-receptor type 14 (predicted), Ptpn14_predicted	-2.3	-1.5
1371816_at	Transcribed locus, ---	-2.3	1.1
1369735_at	growth arrest specific 6, Gas6	-2.3	-1.9
1383633_at	Transcribed locus, moderately similar to NP_997413.2 oxysterol binding protein-like 1 [Mus musculus], ---	-2.3	1.1
1395779_at	coiled coil domain containing 88A, Ccdc88a	-2.3	1.2
1371043_a_at	POU domain, class 3, transcription factor 3, Pou3f3	-2.3	-1.1
1389555_at	transcription factor 19, Tcf19	-2.3	1.9
1379404_at	Transcribed locus, ---	-2.3	-1.7
1388403_at	isocitrate dehydrogenase 2 (NADP+), mitochondrial, Idh2	-2.3	1.4
1373733_at	Bcl-2-related ovarian killer protein, Bok	-2.3	1.1
1381871_at	Transcribed locus, ---	-2.3	-1.4
1367497_at	phosphatidylserine synthase 1, Ptdss1	-2.3	-1.1
1388496_at	filamin C, gamma (actin binding protein 280) (predicted), Flnc_predicted	-2.3	-1.5
1376747_at	Transcribed locus, strongly similar to NP_001076789.1 membrane associated guanylate kinase, WW and PDZ domain containing 1 isoform b [Mus musculus], ---	-2.3	-2.3
1387113_at	C-terminal binding protein 2, Ctbp2	-2.3	1.1
1377653_at	similar to mKIAA1011 protein, LOC366669	-2.3	-1.3
1391439_at	Transcribed locus, ---	-2.3	-1.9
1383239_at	zinc finger, CCHC domain containing 7 (predicted), Zcchc7_predicted	-2.3	-1.2
1390283_at	transcription factor 3 (predicted), Tcf3_predicted	-2.3	1.0
1373540_at	hypothetical protein LOC685548, LOC685548	-2.3	-1.0
1386827_at	similar to procollagen, type IV, alpha 6, LOC363458	-2.3	-1.4
1379358_at	Sterile alpha motif domain containing 4 (predicted), Samd4_predicted	-2.3	-1.4
1379089_at	Transcribed locus, ---	-2.3	-1.6
1374689_at	phosphatidylinositol 4-kinase, catalytic, beta	-2.3	-1.0

	polypeptide, Pi4kb		
1388856_at	kit ligand, Kitl	-2.3	2.9
1372069_at	ankyrin repeat domain 15, Ankrd15	-2.3	-1.5
1382558_at	transcription factor 3 (predicted), Tcf3_predicted	-2.2	-1.0
1383194_a_at	CDNA clone IMAGE:7379585, ---	-2.2	1.0
1377392_at	Transcribed locus, ---	-2.2	-2.7
1375073_at	similar to hypothetical protein MGC45873 (predicted), RGD1310271_predicted	-2.2	-1.8
1379451_at	Transcribed locus, ---	-2.2	-2.5
1370922_at	cortexin 1, Ctxn1	-2.2	-1.1
1369039_at	phosphatidylinositol 4-kinase, catalytic, beta polypeptide, Pi4kb	-2.2	-1.3
1372895_at	similar to RIKEN cDNA 5730469M10, RGD1309676	-2.2	-1.3
1395203_at	Transcribed locus, ---	-2.2	-1.9
1367880_at	laminin, beta 2, Lamb2	-2.2	-1.7
1371434_at	hypothetical protein LOC691807, rCG_28701	-2.2	-1.1
1379918_at	---	-2.2	-1.5
1388791_at	similar to 2810022L02Rik protein, RGD1309930	-2.2	1.0
1389134_at	Transcribed locus, ---	-2.2	-1.1
1373169_at	1-acylglycerol-3-phosphate O-acyltransferase 5 (lysophosphatidic acid acyltransferase, epsilon) (predicted), Agpat5_predicted	-2.2	1.6
1368927_at	membrane bound C2 domain containing protein, Mbc2	-2.2	1.1
1368287_at	chimerin (chimaerin) 1, Chn1	-2.2	-1.2
1383433_at	kelch-like 23 (Drosophila) (predicted), Klhl23_predicted	-2.2	-1.2
1373812_at	cyclin-dependent kinase inhibitor 1B, Cdkn1b	-2.2	-1.8
1398445_at	Transcribed locus, ---	-2.2	-1.3
1378038_at	Transcribed locus, ---	-2.2	-1.4
1370347_at	PDZ and LIM domain 7, Pdlim7	-2.2	-1.3
1373999_at	Transcribed locus, ---	-2.2	-1.2
1383614_at	NUAK family, SNF1-like kinase, 2, Nuak2	-2.2	-1.5
1391730_at	Transcribed locus, ---	-2.2	-1.6
1388840_at	pleckstrin homology domain containing, family G (with RhoGef domain) member 2 (predicted), Plekhg2_predicted	-2.2	-1.6
1375047_at	spermatogenesis associated 5 (predicted), Spata5_predicted	-2.2	1.6
1389368_at	Cnksr family member 3, Cnksr3	-2.2	1.6
1373569_at	Transcribed locus, ---	-2.2	1.2

1371632_at	coronin, actin binding protein 1C, Coro1c	-2.2	-1.1
1392249_at	Transcribed locus, ---	-2.2	-1.4
1397343_at	---	-2.2	-1.2
1380245_at	Transcribed locus, ---	-2.2	-1.9
1390925_a_at	immunoglobulin superfamily, member 3 (predicted), Igsf3_predicted	-2.2	1.6
1384150_at	Transcribed locus, ---	-2.2	-1.2
1386907_at	enolase 3, beta, muscle, Eno3	-2.2	1.3
1392368_at	---	-2.1	-1.3
1373122_at	ajuba, Jub	-2.1	-1.6
1370017_at	emerin, Emd	-2.1	-1.1
1385933_at	Transcribed locus, ---	-2.1	-1.1
1368827_at	GATA binding protein 6, Gata6	-2.1	-1.6
1377831_at	monoamine oxidase A, Maoa	-2.1	-2.0
1383964_at	ankrin repeat domain 50, Ankrd50	-2.1	1.5
1377879_at	Transcribed locus, ---	-2.1	-1.0
1382441_at	AT rich interactive domain 1B (Swi1 like), Arid1b	-2.1	1.2
1383414_at	similar to 9930012K11Rik protein (predicted), RGD1308117_predicted	-2.1	-1.8
1373874_at	sphingosine-1-phosphate phosphatase 1, Sgpp1	-2.1	-1.0
1373535_at	enabled homolog (Drosophila), Enah	-2.1	1.2
1378373_at	Transcribed locus, ---	-2.1	-1.5
1376996_at	Transcribed locus, ---	-2.1	-1.9
1375231_a_at	CXXC finger 5, Cxxc5	-2.1	1.3
1379953_at	PTC7 protein phosphatase homolog (S. cerevisiae), Pptc7	-2.1	-1.3
1393290_at	similar to myocyte enhancer factor 2C, LOC309957	-2.1	-1.1
1369954_at	isocitrate dehydrogenase 1 (NADP+), soluble, Idh1	-2.1	-1.2
1398366_at	Transcribed locus, ---	-2.1	-1.0
1389424_at	similar to ribosomal protein L22 proprotein, LOC365157	-2.1	-1.2
1373321_at	Transcribed locus, ---	-2.1	-1.5
1372613_at	3-hydroxybutyrate dehydrogenase, type 2 (predicted), Bdh2_predicted	-2.1	-1.3
1376662_at	Transcribed locus, ---	-2.1	-1.5
1379847_at	dysferlin (predicted), Dysf_predicted	-2.1	-1.4
1382628_at	---	-2.1	-1.5
1369942_at	actinin alpha 4, Actn4	-2.1	-1.4
1370247_a_at	peripheral myelin protein 22, Pmp22	-2.1	1.9
1368320_at	neural cell adhesion molecule 1, Ncam1	-2.1	-1.8

1396965_at	Transcribed locus, ---	-2.1	-1.2
1388230_at	ajuba, Jub	-2.1	-1.8
1397767_at	Transcribed locus, ---	-2.1	-1.6
1367902_at	guanine nucleotide binding protein (G protein), gamma 11, Gng11	-2.1	1.0
1383193_at	---	-2.1	-1.7
1379817_at	purine-rich element binding protein G (predicted), Purg_predicted	-2.1	-1.5
1368136_at	thymopoietin, Tmpo	-2.1	2.0
1374161_at	importin 11 (predicted), Ipo11_predicted	-2.1	1.2
1381144_at	Transcribed locus, ---	-2.1	1.1
1389528_s_at	Jun oncogene, Jun	-2.1	4.8
1388522_at	PTC7 protein phosphatase homolog (S. cerevisiae), Pptc7	-2.1	-1.0
1380155_at	Transcribed locus, ---	-2.1	-1.7
1390638_at	Eph receptor A4, Epha4	-2.1	1.4
1380533_at	amyloid beta (A4) precursor protein, App	-2.1	-1.7
1389411_at	Transcribed locus, ---	-2.1	-1.1
1389003_at	Rho-related BTB domain containing 3 (predicted), Rhobtb3_predicted	-2.1	-1.5
1379277_at	Transcribed locus, ---	-2.1	-1.7
1375954_at	S100 calcium binding protein A13 (predicted), S100a13_predicted	-2.1	1.3
1388154_at	E2F transcription factor 5, E2f5	-2.1	1.7
1377522_a_at	similar to KIAA1086 protein (predicted), RGD1304737_predicted	-2.1	-2.0
1384081_at	Transcribed locus, ---	-2.1	-2.6
1376763_at	Transcribed locus, ---	-2.1	-1.7
1375377_at	immunoglobulin superfamily, member 3 (predicted), Igsf3_predicted	-2.0	3.0
1372736_at	amylo-1,6-glucosidase, 4-alpha-glucanotransferase, Agl	-2.0	-1.7
1379541_at	transmembrane and tetratricopeptide repeat containing 4, Tmtc4	-2.0	1.2
1372814_at	SFT2 domain containing 2, Sft2d2	-2.0	-1.5
1376868_at	Cobl-like 1 (predicted), Cobll1_predicted	-2.0	-1.9
1368839_at	Wolfram syndrome 1 homolog (human), Wfs1	-2.0	-1.4
1379294_at	Transcribed locus, ---	-2.0	-1.1
1390440_at	solute carrier family 9 (sodium/hydrogen exchanger), isoform 6, Slc9a6	-2.0	-1.1
1376762_at	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 1, Plekha1	-2.0	1.5
1386569_at	Transcribed locus, ---	-2.0	1.7
1397161_a_at	intersectin 1, Itsn1	-2.0	-1.4

1374572_at	similar to opposite strand transcription unit to Stag3; Gats protein, RGD1304774	-2.0	-1.6
1389367_at	schwannomin interacting protein 1, Schip1	-2.0	-1.1
1371970_at	family with sequence similarity 111, member A, Fam111a	-2.0	1.5
1367811_at	3-phosphoglycerate dehydrogenase, Phgdh	-2.0	2.0
1383501_at	Transcribed locus, ---	-2.0	-1.2
1371382_at	filamin, alpha (predicted), Flna_predicted	-2.0	-1.8
1396009_at	---	-2.0	-1.3
1379274_at	Transcribed locus, ---	-2.0	-1.2
1383883_at	kelch-like 30 (Drosophila), Klhl30	-2.0	-1.2
1378342_at	endothelin receptor type A, Ednra	-2.0	1.7
1383284_at	Transcribed locus, ---	-2.0	-1.3

Supplemental Table V: Distinctly PDGF-DD repressed genes in SMCs

Accession Number	Gene	IL-1β Fold Change	PDGF-DD Fold Change
1376956_at	Transcribed locus, ---	-40.2	-56.8
1374298_at	Transcribed locus, ---	1.6	-41.3
1369814_at	chemokine (C-C motif) ligand 20, Ccl20	58.9	-20.3
1368731_at	orosomucoid 1, Orm1	248.4	-17.2
1385751_at	thrombospondin 2, Thbs2	10.8	-15.9
1384240_at	angiotensin II receptor, type 1a, Agtr1a	6.7	-12.6
1373697_at	myosin binding protein C, fast-type (predicted), Mybpc2_predicted	-3.0	-12.1
1370382_at	RT1 class II, locus Db1, RT1-Db1	14.1	-11.8
1374989_at	ankyrin repeat and SOCS box-containing protein 12, Asb12	39.0	-11.2
1388201_at	bone morphogenetic protein 6, Bmp6	11.0	-9.2
1390037_at	Na+/K+ transporting ATPase interacting 4, Nkain4	-3.4	-8.8
1389470_at	complement component 2	49.5	-8.6
1376105_at	procollagen, type XIV, alpha 1 (predicted), Col14a1_predicted	-1.0	-8.1
1387493_at	A kinase (PRKA) anchor protein 5, Akap5	-2.9	-7.8
1388879_at	similar to ABI gene family, member 3 (NESH) binding protein (predicted), RGD1562717_predicted	-1.1	-7.7
1367862_at	Ras-related associated with diabetes, Rrad	4.1	-7.7
1368128_at	phospholipase A2, group IIA (platelets, synovial fluid), Pla2g2a	4147.1	-7.6
1369291_at	angiotensin II receptor, type 1a, Agtr1a	6.6	-7.4
1370148_at	haptoglobin, Hp	8.8	-7.4
1367700_at	fibromodulin, Fmod	-1.6	-7.2
1388920_at	bone morphogenetic protein 6, Bmp6	20.8	-7.0
1391936_a_at	Transcribed locus, ---	-1.9	-7.0
1374172_at	Transcribed locus, ---	-1.1	-6.8
1389214_at	laminin, alpha 4, Lama4	6.6	-6.8
1373615_at	frizzled-related protein, Frzb	1.9	-6.5
1395153_at	claudin 15 (predicted), Cldn15_predicted	-1.0	-6.4
1370157_at	phospholamban, Pln	-2.7	-6.4
1368474_at	vascular cell adhesion molecule 1, Vcam1	6.1	-6.4
1367679_at	CD74 antigen (invariant polypeptide of major histocompatibility complex, class II antigen-associated), Cd74	32.5	-6.1
1390969_at	Transcribed locus, ---	1.4	-6.0

1376170_at	procollagen, type XIV, alpha 1 (predicted), Col14a1_predicted	-1.2	-6.0
1368536_at	ectonucleotide pyrophosphatase/phosphodiesterase 2, Enpp2	21.0	-6.0
1393084_at	HRAS-like suppressor (predicted), Hrasls_predicted	2.0	-6.0
1375961_at	frizzled-related protein, Frzb	1.5	-5.9
1383225_at	Transcribed locus, ---	2.4	-5.6
1385074_at	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2, Smarca2	-1.7	-5.6
1374352_at	actin, alpha, cardiac 1, Actc1	-2.5	-5.3
1385637_at	Similar to sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1, LOC685899	2.4	-5.2
1369943_at	transglutaminase 2, C polypeptide, Tgm2	1.7	-5.1
1379331_at	tenascin N (predicted), Tnn_predicted	1.9	-5.1
1368201_at	natriuretic peptide receptor 1, Npr1	-1.2	-5.0
1370883_at	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	20.9	-4.9
1392686_at	naked cuticle 2 homolog (Drosophila) (predicted), Nkd2_predicted	1.0	-4.9
1389464_at	ligand of numb-protein X 1 (predicted), Lnx1_predicted	7.5	-4.8
1368147_at	dual specificity phosphatase 1, Dusp1	-1.9	-4.8
1370822_at	RT1 class II, locus Ba, RT1-Ba	31.9	-4.7
1383322_at	RAS-like family 11 member B, Rasl11b	1.2	-4.7
1373345_at	adhesion molecule with Ig like domain 2, Amigo2	1.1	-4.6
1388924_at	angiopoietin-like 4, Angptl4	7.0	-4.6
1373288_at	suppression of tumorigenicity 5 (predicted), St5_predicted	-1.4	-4.6
1376750_at	Transcribed locus, ---	4.5	-4.5
1387241_at	G-protein coupled receptor 88, Gpr88	-1.3	-4.5
1372585_at	RGD1566254 (predicted), RGD1566254_predicted	2.0	-4.4
1393252_at	Transcribed locus, ---	9.1	-4.3
1395110_at	Transcribed locus, ---	15.7	-4.3
1389159_at	Transcribed locus, ---	2.8	-4.3
1373903_at	RCSD domain containing 1 (predicted), Rcsd1_predicted	1.2	-4.3
1368249_at	Kruppel-like factor 15, Klf15	2.3	-4.3
1368000_at	complement component 3, C3	19.8	-4.2
1376617_at	Transcribed locus, ---	6.8	-4.2
1367755_at	cysteine dioxygenase 1, cytosolic, Cdo1	7.3	-4.2

1385354_at	similar to integrin alpha 8 (predicted), RGD1564327_predicted	-1.6	-4.2
1368771_at	sulfatase 1, Sulf1	3.6	-4.1
1370383_s_at	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	15.8	-4.0
1376106_at	transmembrane protein 178, Tmem178	-1.6	-4.0
1374726_at	fibronectin type III domain containing 1, Fndc1	1.4	-4.0
1373882_at	c-fos induced growth factor, Figf	4.4	-3.9
1379885_at	flavin containing monooxygenase 4, Fmo4	2.2	-3.9
1381262_at	Transcribed locus, ---	-1.9	-3.9
1372016_at	growth arrest and DNA-damage-inducible 45 beta, Gadd45b	1.5	-3.9
1373748_at	PDZ domain containing RING finger 3 (predicted), Pdzrn3_predicted	1.8	-3.8
1392590_at	Rho GTPase activating protein 24, Arhgap24	-1.3	-3.8
1370892_at	complement component 4a	1.6	-3.8
1390403_at	family with sequence similarity 43, member A, Fam43a	2.2	-3.8
1373240_at	dehydrogenase/reductase (SDR family) member 3, Dhrs3	-1.3	-3.8
1387868_at	lipopolysaccharide binding protein, Lbp	18.7	-3.8
1370256_at	frizzled homolog 1 (Drosophila), Fzd1	1.3	-3.7
1393295_at	similar to RIKEN cDNA 2610019F03, LOC498662	1.2	-3.7
1387763_at	RAB27A, member RAS oncogene family, Rab27a	-2.6	-3.7
1387898_at	heat shock protein, alpha-crystallin-related, B6, Hspb6	-1.7	-3.7
1395374_at	Transcribed locus, ---	4.0	-3.7
1390536_at	Transcribed locus, ---	1.2	-3.6
1390075_at	olfactomedin-like 2B (predicted), Olfml2b_predicted	1.1	-3.6
1367664_at	ankyrin repeat domain 1 (cardiac muscle), Ankrd1	-1.9	-3.6
1379318_at	Transcribed locus, ---	1.3	-3.6
1387655_at	chemokine (C-X-C motif) ligand 12, Cxcl12	-1.1	-3.5
1389632_at	Rho-related BTB domain containing 1 (predicted), Rhobtb1_predicted	-1.6	-3.5
1384371_at	TEA domain family member 3, Tead3	-1.7	-3.5
1398233_at	Transcribed locus, ---	-1.0	-3.4
1392644_s_at	similar to RIKEN cDNA 2610019F03, LOC498662	1.2	-3.4
1397453_at	Transcribed locus, ---	-1.9	-3.4
1388471_at	t-complex 11 (mouse) like 2, Tcp11l2	1.4	-3.4
1390119_at	secreted frizzled-related protein 2, Sfrp2	1.3	-3.3

1389295_at	olfactomedin-like 2B (predicted), Olfml2b_predicted	-1.4	-3.3
1378927_at	---	6.1	-3.3
1388742_at	---	-1.1	-3.3
1389095_at	biregional cell adhesion molecule-related/down-regulated by oncogenes (Cdon) binding protein (predicted), Boc_predicted	-1.1	-3.3
1382746_s_at	Transcribed locus, ---	2.5	-3.3
1396614_at	secreted frizzled-related protein 2, Sfrp2	1.4	-3.2
1374060_at	Transcribed locus, ---	-1.9	-3.1
1393225_at	Similar to a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 10, LOC314655	-1.5	-3.1
1398622_at	cysteine rich transmembrane BMP regulator 1 (chordin like), Crim1	-1.9	-3.1
1382745_at	Transcribed locus, ---	3.0	-3.1
1376734_at	Transcribed locus, ---	-1.1	-3.1
1374246_at	Transcribed locus, ---	6.7	-3.1
1374971_at	Transcribed locus, ---	-1.2	-3.1
1383173_at	---	1.5	-3.1
1390789_at	acyl-Coenzyme A dehydrogenase family, member 11 (predicted), Acad11_predicted	1.6	-3.1
1368565_at	solute carrier family 1 (glial high affinity glutamate transporter), member 3, Slc1a3	1.0	-3.1
1369973_at	xanthine dehydrogenase, Xdh	12.5	-3.0
1380937_at	CDNA clone IMAGE:7461178, ---	-1.0	-3.0
1369393_at	mitogen-activated protein kinase kinase kinase 8, Map3k8	88.0	-3.0
1368618_at	growth factor receptor bound protein 14, Grb14	-1.2	-3.0
1387454_at	niban protein, Niban	-1.0	-3.0
1371031_at	methionine adenosyltransferase I, alpha, Mat1a	-1.9	-2.9
1378942_at	Transcribed locus, ---	-1.2	-2.9
1392870_at	---	-1.2	-2.9
1370161_at	coiled-coil domain containing 80, Ccdc80	-1.4	-2.9
1396109_at	anthrax toxin receptor 1, Antxr1	-1.7	-2.9
1374061_at	CD302 antigen, Cd302	6.1	-2.9
1383300_at	kelch-like 24 (Drosophila), Klhl24	1.6	-2.9
1370951_at	phosphatidic acid phosphatase type 2B, Ppap2b	-1.3	-2.9
1389066_at	regulator of calcineurin 2, Rcan2	2.6	-2.9
1381654_at	Transcribed locus, ---	-1.3	-2.9
1379868_at	pre-B-cell leukemia transcription factor interacting protein 1, Pbxip1	-1.9	-2.9
1378484_at	RAS-like, family 12 (predicted),	3.6	-2.9

	Rasl12_predicted		
1372027_at	Transcribed locus, ---	7.9	-2.8
1374029_at	---	1.4	-2.8
1370113_at	baculoviral IAP repeat-containing 3, Birc3	10.6	-2.8
1373062_at	Transcribed locus, ---	2.3	-2.8
1396057_at	Transcribed locus, ---	-1.5	-2.8
1380318_at	Transcribed locus, ---	2.8	-2.8
1375910_at	CDC42 effector protein (Rho GTPase binding) 3 (predicted), Cdc42ep3_predicted	-1.8	-2.8
1391593_at	Ras association (RalGDS/AF-6) domain family 4, Rassf4	12.2	-2.8
1383047_at	growth arrest specific 6, Gas6	-1.3	-2.8
1370218_at	lactate dehydrogenase B, Ldhb	1.4	-2.8
1380556_at	F-box protein 10, Fbxo10	-1.8	-2.8
1384287_at	Transcribed locus, ---	-1.2	-2.8
1383241_at	complement component 1, r subcomponent, C1r	2.1	-2.8
1389420_at	signal transducing adaptor family member 2, Stap2	49.6	-2.8
1368883_at	nephroblastoma overexpressed gene, Nov	-1.2	-2.8
1374038_at	Transcribed locus, ---	1.3	-2.8
1370173_at	superoxide dismutase 2, mitochondrial, Sod2	13.1	-2.7
1397837_at	Transcribed locus, ---	3.4	-2.7
1383560_at	Transcribed locus, ---	2.6	-2.7
1387376_at	aldehyde oxidase 1, Aox1	1.2	-2.7
1383069_at	similar to RNA binding motif, single stranded interacting protein 3 isoform 1, LOC680726	-1.7	-2.7
1388494_at	procollagen, type IV, alpha 2 (predicted), Col4a2_predicted	-1.3	-2.7
1370285_at	calcium binding and coiled coil domain 1, Calcoco1	1.0	-2.7
1381533_at	Rho family GTPase 1, Rnd1	9.2	-2.7
1368247_at	heat shock 70kD protein 1A, Hspa1b	-1.4	-2.7
1374235_at	regulator of calcineurin 2, Rcan2	1.8	-2.7
1384852_at	RAB27A, member RAS oncogene family, Rab27a	-1.9	-2.7
1375874_at	similar to cDNA sequence BC013529 (predicted), RGD1309759_predicted	3.2	-2.7
1392784_at	growth arrest specific 6, Gas6	1.1	-2.7
1375011_at	Transcribed locus, ---	3.6	-2.7
1373740_at	---	2.0	-2.7
1371436_at	dimethylarginine dimethylaminohydrolase 2, Ddah2	-1.7	-2.7
1385243_at	Transcribed locus, ---	-1.1	-2.6

1387121_a_at	N-myc downstream regulated gene 2, Ndrg2	-1.4	-2.6
1367957_at	regulator of G-protein signaling 3, Rgs3	1.4	-2.6
1373719_at	mitogen-activated protein kinase kinase kinase kinase 3, Map4k3	-1.9	-2.6
1367570_at	transgelin, Tagln	-2.0	-2.6
1382226_at	Similar to RNA binding motif, single stranded interacting protein 3 isoform 1, LOC680726	-1.8	-2.6
1392525_at	Transcribed locus, ---	1.9	-2.6
1373149_at	similar to yippee-like 3 (predicted), RGD1564579_predicted	1.1	-2.6
1389546_at	Transcribed locus, ---	1.2	-2.6
1367749_at	lumican, Lum	3.0	-2.6
1372325_at	elastin microfibril interfacer 1 (predicted), Emilin1_predicted	1.4	-2.6
1386611_at	kelch-like 24 (Drosophila), Klhl24	1.5	-2.6
1372472_at	similar to Microtubule-associated protein RP/EB family member 2 (APC-binding protein EB2) (End-binding protein 2) (EB2), LOC679221	1.9	-2.6
1382312_at	AT rich interactive domain 5B (Mrf1 like) (predicted), Arid5b_predicted	1.3	-2.5
1369959_at	zinc finger protein 36, C3H type-like 1, Zfp36l1	1.8	-2.5
1378997_at	Eph receptor B6, Ephb6	-1.2	-2.5
1371042_at	mitogen-activated protein kinase kinase kinase kinase 3, Map4k3	-1.9	-2.5
1372439_at	procollagen, type IV, alpha 1, Col4a2_predicted	-1.4	-2.5
1370912_at	heat shock 70kD protein 1B (mapped), Hspa1b	-1.2	-2.5
1391264_at	Transcribed locus, ---	2.4	-2.5
1369961_at	phosphatidic acid phosphatase 2a, Ppap2a	2.5	-2.5
1383110_at	kelch-like 24 (Drosophila), Klhl24	1.4	-2.5
1384188_at	---	1.5	-2.5
1372328_at	kinesin light chain 4, Klc4	-1.2	-2.4
1369633_at	chemokine (C-X-C motif) ligand 12, Cxcl12	-1.2	-2.4
1394483_at	A disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 5 (aggrecanase-2), Adamts5	2.5	-2.4
1372964_at	Transcribed locus, ---	1.2	-2.4
1383531_at	---	1.4	-2.4
1387893_at	complement component 1, s subcomponent, C1s	2.6	-2.4
1372000_at	neuroepithelial cell transforming gene 1, Net1	1.3	-2.4
1374284_at	Ras association (RalGDS/AF-6) domain family 4, Rassf4	12.2	-2.4
1381781_at	Transcribed locus, ---	1.3	-2.4
1381646_at	---	1.8	-2.4

1371916_at	similar to Methionine-R-sulfoxide reductase (Selenoprotein X 1) (Selenoprotein R), MGC105753	-1.3	-2.4
1389145_at	CDC42 effector protein (Rho GTPase binding) 2, Cdc42ep2	1.9	-2.4
1377754_at	Transcribed locus, ---	-1.9	-2.4
1388545_at	SPARC-related modular calcium binding protein 1, Smoc1	-1.9	-2.4
1390323_at	Transcribed locus, ---	-1.2	-2.4
1376615_at	TEA domain family member 3, Tead3	-1.6	-2.4
1379433_at	phosphatidylinositol 3-kinase, C2 domain containing, alpha polypeptide (predicted), Pik3c2a_predicted	-1.5	-2.4
1378842_at	gamma-aminobutyric acid (GABA(A)) receptor-associated protein-like 1 (predicted), MGC125167	1.7	-2.4
1375517_at	tumor protein p53 inducible nuclear protein 2, Trp53inp2	2.1	-2.3
1384728_at	forkhead box N3, Foxn3	-1.6	-2.3
1391630_at	T-box18 (predicted), Tbx18_predicted	-1.2	-2.3
1373245_at	procollagen, type IV, alpha 1, Col4a2_predicted	-1.2	-2.3
1374575_at	cAMP responsive element binding protein 3-like 1, Creb3l1	7.3	-2.3
1392852_at	SPARC-related modular calcium binding protein 1, Smoc1	-1.9	-2.3
1376128_at	Transcribed locus, ---	13.3	-2.3
1374870_at	Procollagen, type XXVII, alpha 1, Col27a1	-1.6	-2.3
1377892_at	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3 F (predicted), Sema3f_predicted	-1.8	-2.3
1369929_at	prosaposin, Psap	-1.3	-2.3
1388492_at	TNFAIP3 interacting protein 1 (predicted), Tnip1_predicted	2.0	-2.3
1388583_at	chemokine (C-X-C motif) ligand 12, Cxcl12	1.1	-2.3
1392893_a_at	Transcribed locus, ---	-1.3	-2.3
1368134_a_at	interleukin 4 receptor, alpha, Il4ra	2.8	-2.3
1387874_at	D site albumin promoter binding protein, Dbp	-1.4	-2.3
1380908_at	Transcribed locus, ---	-1.4	-2.3
1378506_at	phosphatidylinositol 3-kinase, C2 domain containing, alpha polypeptide (predicted), Pik3c2a_predicted	-1.4	-2.3
1387042_at	calcium channel, voltage-dependent, beta 3 subunit, Cacnb3	-1.3	-2.3
1374550_at	MAP kinase-interacting serine/threonine kinase 1, Mknk1	-1.1	-2.3

1369688_s_at	protein tyrosine kinase 2 beta, Ptk2b	-1.4	-2.3
1375958_at	similar to TSC22 domain family protein 4 (TSC22-related-inducible leucine zipper protein 2), LOC686226	-1.3	-2.2
1367842_at	amyloid beta (A4) precursor protein-binding, family B, member 1, Apbb1	-1.3	-2.2
1378321_at	Ras association (RalGDS/AF-6) domain family 4, Rassf4	9.7	-2.2
1385252_at	tripartite motif-containing 6, Trim6	-1.1	-2.2
1383058_at	Transcribed locus, ---	-1.3	-2.2
1373684_at	kelch-like 31 (Drosophila), Klhl31	-2.1	-2.2
1379495_at	Transcribed locus, ---	-1.9	-2.2
1376810_at	M-phase phosphoprotein 8, Parp4	2.0	-2.2
1373104_at	SPECC1-like, Specc1l	-1.4	-2.2
1379935_at	chemokine (C-C motif) ligand 7, Ccl7	12.7	-2.2
1389787_at	PTK7 protein tyrosine kinase 7 (predicted), Ptk7_predicted	1.6	-2.2
1372706_at	hexosaminidase B, Hexb	1.4	-2.2
1379971_at	zinc finger CCCH type containing 6 (predicted), Zc3h6_predicted	-1.1	-2.2
1368702_at	PRKC, apoptosis, WT1, regulator, Pawr	-1.8	-2.2
1382311_at	Traf2 binding protein, T2bp	7.0	-2.2
1386885_at	enoyl coenzyme A hydratase 1, peroxisomal, Ech1	-1.6	-2.2
1390207_at	large tumor suppressor 2 (predicted), Lats2_predicted	-1.6	-2.2
1372468_at	CD97 antigen, Cd97	-1.9	-2.2
1383462_at	zinc finger protein 294, Zfp294	-1.1	-2.2
1388527_at	Transcribed locus, ---	-1.4	-2.2
1370952_at	glutathione S-transferase, mu 2, Gstm2	-1.7	-2.2
1374728_at	Transcribed locus, ---	1.7	-2.2
1396701_at	Transcribed locus, ---	-1.3	-2.2
1393356_at	Transcribed locus, ---	-1.7	-2.2
1371680_at	similar to gamma-aminobutyric acid (GABA(A)) receptor-associated protein-like 1, MGC125167	1.8	-2.2
1374530_at	frizzled homolog 7 (Drosophila) (predicted), Fzd7_predicted	-1.4	-2.2
1392385_at	Nuclear receptor coactivator 3, Ncoa3	1.5	-2.2
1383948_at	similar to TPR repeat-containing protein KIAA1043, LOC304558	-1.5	-2.2
1383201_at	Transcribed locus, strongly similar to NP_031587.1 bone morphogenic protein receptor, type II (serine/threonine kinase) [Mus musculus], ---	1.4	-2.2
1388243_at	G protein-coupled receptor 176, Gpr176	2.0	-2.2

1394550_at	similar to CG1998-PA, LOC691221	-1.4	-2.2
1391476_at	Transcribed locus, ---	-1.5	-2.2
1373922_at	Transcribed locus, ---	-1.9	-2.2
1370202_at	HRAS like suppressor 3, Hrasls3	-1.3	-2.2
1368322_at	superoxide dismutase 3, extracellular, Sod3	2.2	-2.2
1388525_at	phosphoinositide-3-kinase interacting protein 1, Pik3ip1	-1.4	-2.2
1378414_at	Transcribed locus, ---	-1.3	-2.1
1389256_at	Transcribed locus, ---	-1.3	-2.1
1368519_at	serine (or cysteine) peptidase inhibitor, clade E, member 1, Serpine1	3.5	-2.1
1391616_at	---	1.4	-2.1
1392264_s_at	serine (or cysteine) peptidase inhibitor, clade E, member 1, Serpine1	3.6	-2.1
1368172_a_at	lysyl oxidase, Lox	1.1	-2.1
1372719_at	---	1.9	-2.1
1373248_at	Similar to hypothetical protein FLJ20674 (predicted), RGD1565800_predicted	-1.3	-2.1
1379371_at	Transcribed locus, ---	6.4	-2.1
1368754_at	pyrimidinergic receptor P2Y, G-protein coupled, 6, P2ry6	4.4	-2.1
1377940_at	family with sequence similarity 101, member B, Fam101b	2.6	-2.1
1389562_at	Transcribed locus, ---	1.9	-2.1
1373189_at	megakaryoblastic leukemia (translocation) 1, Mkl1	-1.4	-2.1
1376610_a_at	similar to TPR repeat-containing protein KIAA1043, LOC304558	-1.7	-2.1
1387011_at	lipocalin 2, Lcn2	9.1	-2.1
1383952_at	microtubule associated monoxygenase, calponin and LIM domain containing 1 (predicted), Mical1_predicted	-1.8	-2.1
1384250_a_at	Transcribed locus, ---	-1.4	-2.1
1371988_at	mannosidase 1, alpha (predicted), Man1a_predicted	1.0	-2.1
1376282_at	Transcribed locus, ---	1.3	-2.1
1391603_at	Transcribed locus, ---	-1.7	-2.1
1382269_at	cyclin M2, Cnnm2	5.3	-2.1
1374013_at	C1q and tumor necrosis factor related protein 5, C1qtnf5	1.2	-2.1
1374300_at	ectonucleoside triphosphate diphosphohydrolase 4 (predicted), Entpd4_predicted	1.3	-2.1
1388011_a_at	transforming growth factor, beta 2, Tgfb2	-1.6	-2.1
1388700_at	Checkpoint suppressor 1 (predicted),	-2.0	-2.1

	Ches1_predicted		
1370381_at	proline-rich nuclear receptor coactivator 1, Pnrc1	1.2	-2.1
1372935_at	transmembrane protein 119, Tmem119	1.7	-2.1
1395432_at	Transcribed locus, ---	-1.0	-2.1
1385382_at	Transcribed locus, ---	-1.3	-2.1
1370882_at	major histocompatibility complex, class II, DM beta, Hla-dmb	4.5	-2.1
1379441_at	zinc finger protein 294, Zfp294	-1.3	-2.1
1392382_at	Transforming growth factor, beta 2, Tgfb2	-1.5	-2.1
1375898_at	similar to RNA binding protein gene with multiple splicing (predicted), RGD1561067_predicted	-1.1	-2.1
1369044_a_at	phosphodiesterase 4B, cAMP specific, Pde4b	3.8	-2.1
1375869_at	Unc-51 like kinase 1 (C. elegans), Ulk1	-1.7	-2.1
1367881_at	signal-regulatory protein alpha, Sirpa	3.8	-2.1
1372907_at	ATPase, H+ transporting, lysosomal V0 subunit E2, Atp6v0e2	-2.0	-2.1
1375270_at	Transcribed locus, ---	-1.2	-2.1
1374743_at	similar to channel-interacting PDZ domain protein isoform 1 (predicted), RGD1565362_predicted	-1.8	-2.1
1370331_at	interleukin 11 receptor, alpha chain 1, Il11ra1	-1.8	-2.1
1387654_at	myosin IC, Myo1c	-1.6	-2.0
1372392_at	Transcribed locus, ---	-1.0	-2.0
1377011_at	similar to hypothetical protein CG003 (predicted), RGD1307034_predicted	-1.9	-2.0
1374573_at	dynein cytoplasmic 2 light intermediate chain 1, Dync2li1	1.2	-2.0
1389129_at	2-4-dienoyl-Coenzyme A reductase 2, peroxisomal, RGD1308952	1.1	-2.0
1370341_at	enolase 2, gamma, neuronal, Eno2	1.7	-2.0
1369743_a_at	purinergic receptor P2X, ligand-gated ion channel 4, P2rx4	2.1	-2.0
1372380_at	similar to RNA binding protein gene with multiple splicing (predicted), RGD1561067_predicted	1.2	-2.0
1392566_at	Transcribed locus, ---	-1.0	-2.0
1367768_at	latexin, Lxn	-1.5	-2.0
1392704_at	Transcribed locus, ---	1.3	-2.0
1392935_at	Transcribed locus, ---	-1.7	-2.0
1367577_at	heat shock protein 1, Hspb1	-1.4	-2.0
1371510_at	host cell factor C1 regulator 1 (XPO1-dependent), Hcfc1r1	-1.8	-2.0
1373988_at	similar to neuroblastoma-amplified protein,	-1.2	-2.0

	LOC690073		
1368703_at	PDZ and LIM domain 5, Pdlim5	-1.9	-2.0
1387099_at	natriuretic peptide receptor 2, Npr2	-1.0	-2.0
1376843_at	bone morphogenic protein receptor, type II (serine/threonine kinase), Bmpr2	1.7	-2.0
1377687_at	similar to cDNA sequence AK129302 (predicted), RGD1561708_predicted	1.4	-2.0
1394778_at	Transcribed locus, ---	-1.4	-2.0
1398370_at	adenosine deaminase, RNA-specific, B1, Adarb1	-1.8	-2.0
1371029_at	polycystic kidney disease 1 homolog, Pkd1	-1.6	-2.0

Supplemental Table VI: IL-1β and PDGF-DD Commonly Downregulated Genes in SMCs

Accession	Description	IL-1β Fold Change	PDGF-DD Fold Change
1371354_at	troponin C, cardiac/slow skeletal, Tnnc1	-9.0	-14.9
1376937_at	similar to 4631422O05Rik protein (predicted), RGD1565927_predicted	-11.0	-2.3
1393167_at	Transcribed locus, ---	-9.6	-8.6
1391780_at	family with sequence similarity 46, member B, Fam46b	-18.0	-5.2
1388792_at	growth arrest and DNA-damage-inducible 45 gamma, Gadd45g	-10.6	-5.2
1388298_at	myosin, light chain 9, regulatory, Myl9	-8.0	-8.1
1379055_x_at	---	-11.2	-3.1
1390471_at	Transcribed locus, ---	-20.2	-4.0
1381975_at	Transcribed locus, strongly similar to NP_001020144.1 hypothetical protein LOC293823 [Rattus norvegicus], ---	-9.4	-2.1
1367974_at	annexin A3, Anxa3	-5.5	-2.0
1395794_at	tropomyosin 1, alpha, Tpm1	-5.2	-3.3
1378233_at	Transcribed locus, ---	-10.7	-2.4
1387886_at	proline arginine-rich end leucine-rich repeat protein, Prelp	-6.9	-4.6
1367975_at	annexin A3, Anxa3	-17.6	-2.7
1377618_at	Kruppel-like factor 7 (ubiquitous) (predicted), Klf7_predicted	-6.0	-2.4
1368146_at	dual specificity phosphatase 1, Dusp1	-5.4	-4.0
1379936_at	Transcribed locus, ---	-9.0	-5.2
1395753_at	elastin, Eln	-4.4	-3.4
1368104_at	tetraspanin 2, Tspan2	-14.1	-2.1
1367866_at	fibulin 5, Fbln5	-5.1	-2.2
1380933_at	Transcribed locus, ---	-4.2	-2.9
1384818_at	myosin, light polypeptide kinase (predicted), Mylk_predicted	-4.1	-15.4
1371954_at	tensin 1, Tns1	-2.3	-2.7
1383644_at	Transcribed locus, ---	-3.1	-6.2
1389611_at	very low density lipoprotein receptor, Vldlr	-5.2	-4.2
1385008_at	Transcribed locus, ---	-9.1	-2.0
1391753_at	Transcribed locus, ---	-10.9	-4.0
1374643_at	FAT tumor suppressor homolog 4 (Drosophila), Fat4	-3.1	-2.8
1368108_at	ATPase, Ca++ transporting, cardiac muscle, fast twitch 1, Atp2a1	-10.0	-3.3

1380940_at	Transcribed locus, ---	-3.5	-4.7
1376398_at	Transcribed locus, ---	-8.2	-2.1
1370057_at	cysteine and glycine-rich protein 1, Csrp1	-3.4	-2.3
1367650_at	tubulointerstitial nephritis antigen-like 1, Tinagl1	-3.8	-3.9
1376445_at	interleukin 17B, Il17b	-2.1	-5.6
1388422_at	LIM and senescent cell antigen like domains 2, Lims2	-7.7	-12.6
1389376_at	Transcribed locus, ---	-7.7	-3.1
1374542_at	Transcribed locus, ---	-3.5	-7.9
1372316_at	similar to AI115348 protein (predicted), RGD1311939_predicted	-2.6	-2.7
1387402_at	myosin, heavy polypeptide 9, non-muscle, Myh9	-2.6	-2.0
1367858_at	matrix metallopeptidase 11, Mmp11	-13.5	-3.4
1372426_at	ADAMTS-like 4, Adamtsl4	-5.4	-3.2
1370896_a_at	myosin, heavy polypeptide 11, smooth muscle, Myh11	-3.5	-9.2
1387455_a_at	very low density lipoprotein receptor, Vldlr	-4.0	-4.7
1382814_at	odd Oz/ten-m homolog 3 (Drosophila) (predicted), Odz3_predicted	-2.2	-2.7
1396435_at	Transcribed locus, ---	-2.9	-4.0
1369273_a_at	natriuretic peptide receptor 3, Npr3	-8.1	-7.4
1374237_at	leiomodin 1 (smooth muscle) (predicted), Lmod1_predicted	-6.1	-6.4
1373504_at	GLI pathogenesis-related 1 (glioma), Glipr1	-4.0	-2.6
1394838_at	amine oxidase, copper containing 3, Aoc3	-2.6	-10.3
1391448_at	cysteine rich transmembrane BMP regulator 1 (chordin like), Crim1	-5.7	-3.6
1374969_at	phosphoglucomutase 5 (predicted), Pgm5_predicted	-5.4	-4.4
1370613_s_at	UDP glycosyltransferase 1 family, polypeptide A1, Ugt1a9	-4.5	-2.0
1378152_at	Transcribed locus, ---	-5.4	-2.4
1398620_at	Sterile alpha motif domain containing 4 (predicted), Samd4_predicted	-2.4	-2.1
1390153_at	Transcribed locus, ---	-3.6	-2.3
1371566_at	F-box and leucine-rich repeat protein 22, Fbxl22	-5.0	-40.1
1374729_at	Transcribed locus, ---	-3.0	-2.0
1368080_at	response gene to complement 32, Rgc32	-8.9	-5.9
1387018_at	Arg/Abl-interacting protein ArgBP2, Argbp2	-4.2	-3.9
1398380_at	von Willebrand factor A domain containing 1, Vwa1	-4.3	-9.4
1382229_at	Transcribed locus, ---	-2.4	-5.0
1373152_at	protease, serine, 23, Prss23	-7.0	-4.5

1386869_at	actin, gamma 2, smooth muscle, enteric, Actg2	-2.3	-17.5
1391390_at	tensin 1, Tns1	-5.0	-3.3
1387401_at	calsequestrin 2, Casq2	-20.0	-10.0
1371361_at	tensin 1, Tns1	-5.1	-2.5
1394750_at	four and a half LIM domains 1, Fhl1	-2.2	-4.1
1379999_at	Microtubule associated monoxygenase, calponin and LIM domain containing 3, Mical3	-2.0	-2.3
1368988_at	calsequestrin 2, Casq2	-5.2	-5.9
1374417_at	similar to nuclear receptor binding protein, LOC680451	-4.0	-2.8
1377309_at	Transcribed locus, ---	-2.5	-3.5
1395734_at	palmdelphin, Palmd	-5.9	-3.3
1374758_at	Transcribed locus, ---	-3.0	-4.0
1367813_at	protein phosphatase 1, regulatory (inhibitor) subunit 14A, Ppp1r14a	-6.4	-5.4
1379647_at	Transcribed locus, ---	-4.5	-2.4
1384056_at	Fibroblast growth factor receptor 3, Fgfr3	-2.3	-4.5
1369957_at	regulator of G-protein signaling 5, Rgs5	-6.6	-5.4
1380088_at	Transcribed locus, ---	-18.7	-3.6
1370854_at	nexilin, Nexn	-2.9	-5.0
1398390_at	chemokine (C-X-C motif) ligand 13, Cxcl13	-5.5	-4.3
1372728_at	Sortilin 1, Sort1	-3.9	-2.7
1373829_at	fibroblast growth factor receptor 2, Fgfr2	-4.5	-3.1
1391841_at	Transcribed locus, ---	-5.9	-3.2
1396053_at	neural precursor cell expressed, developmentally down-regulated gene 9, Nedd9	-4.8	-2.7
1367648_at	insulin-like growth factor binding protein 2, Igfbp2	-3.2	-2.3
1390049_at	four and a half LIM domains 1, Fhl1	-5.0	-3.3
1370697_a_at	nexilin, Nexn	-12.6	-3.7
1372615_at	amine oxidase, copper containing 3, Aoc3	-4.9	-7.9
1379126_at	Transcribed locus, strongly similar to NP_001020144.1 hypothetical protein LOC293823 [Rattus norvegicus], ---	-2.5	-2.1
1383708_at	integrin, beta-like 1, Itgbl1	-2.4	-2.4
1368003_at	aldehyde dehydrogenase family 1, subfamily A2, Aldh1a2	-2.3	-4.4
1376878_at	similar to RIKEN cDNA 2310022B05 (predicted), RGD1559896_predicted	-2.8	-4.6
1381923_at	similar to LOC387763 protein (predicted), RGD1564664_predicted	-4.3	-4.4
1395413_at	---	-5.3	-2.3
1369098_at	very low density lipoprotein receptor, Vldlr	-3.0	-3.5

1371472_at	Transcribed locus, ---	-2.8	-4.6
1371004_at	sortilin 1, Sort1	-21.1	-2.4
1390682_at	formin binding protein 1, Fnbp1	-7.0	-2.8
1385704_at	tensin 1, Tns1	-4.9	-4.6
1383498_at	Transcribed locus, ---	-3.4	-2.3
1369928_at	actin, alpha 1, skeletal muscle, Acta1	-3.8	-28.3
1369793_a_at	melanoma cell adhesion molecule, Mcam	-2.4	-3.3
1396885_at	smoothelin, Smtn	-2.5	-3.8
1374290_at	Transcribed locus, ---	-4.7	-7.5
1368506_at	regulator of G-protein signaling 4, Rgs4	-2.7	-52.0
1373108_at	protein phosphatase 1, regulatory (inhibitor) subunit 3C, Ppp1r3c	-4.1	-3.8
1394824_at	integrin, alpha 11 (predicted), Itga11_predicted	-3.3	-15.7
1379380_at	sprouty homolog 1 (Drosophila) (predicted), Spry1_predicted	-6.4	-7.9
1391067_at	---	-8.5	-2.0
1394077_at	Rho family GTPase 3, Rnd3	-3.6	-2.0
1374263_at	Transcribed locus, ---	-2.6	-10.8
1379516_at	similar to RIKEN cDNA 2310022B05 (predicted), RGD1559896_predicted	-3.9	-4.1
1392773_at	proprotein convertase subtilisin/kexin type 5, Pcsk5	-4.0	-3.0
1383398_at	similar to integrin alpha 8 (predicted), RGD1564327_predicted	-4.9	-7.2
1382037_at	cysteine rich transmembrane BMP regulator 1 (chordin like), Crim1	-2.0	-2.7
1393615_at	similar to DEP domain containing 6 (predicted), RGD1561030_predicted	-3.9	-3.9
1376481_at	a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 9 (predicted), Adamts9_predicted	-2.1	-7.9
1373485_at	Similar to ring finger protein 122 homolog (predicted), RGD1561238_predicted	-5.1	-3.1
1371700_at	microfibrillar-associated protein 4, Mfap4	-3.1	-3.3
1384211_at	procollagen, type XI, alpha 1, Col11a1	-4.2	-2.1
1383939_at	Transcribed locus, ---	-3.8	-2.0
1376572_a_at	supervillin (predicted), Svil_predicted	-2.3	-2.7
1368806_at	selenoprotein P, plasma, 1, Sepp1	-5.0	-2.8
1380017_at	Transcribed locus, ---	-2.4	-2.4
1372684_at	smoothelin, Smtn	-2.3	-2.7
1374933_at	melanoma cell adhesion molecule, Mcam	-3.2	-3.8
1368824_at	caldesmon 1, Cald1	-2.8	-2.3
1383770_at	Transcribed locus, ---	-3.1	-2.3
1376118_at	OTU domain, ubiquitin aldehyde binding 2	-3.0	-2.5

	(predicted), Otub2_predicted		
1370678_s_at	monoamine oxidase A, Maoa	-2.0	-2.0
1382190_at	MAS-related GPR, member F, Mrgprf	-4.0	-4.5
1376911_at	Transcribed locus, ---	-8.6	-3.5
1392653_at	Transcribed locus, ---	-3.7	-2.1
1374683_at	sarcoglycan, gamma (dystrophin-associated glycoprotein), Sgcg	-2.5	-4.9
1392924_at	Transcribed locus, ---	-2.0	-4.7
1372583_at	Transcribed locus, ---	-7.1	-3.6
1376646_at	popeye domain containing 2, Popdc2	-2.1	-3.7
1392361_at	Transcribed locus, ---	-2.1	-2.1
1374768_at	coiled-coil domain containing 65, Ccdc65	-3.6	-3.7
1378766_at	Transcribed locus, ---	-4.6	-2.0
1369373_at	fibroblast growth factor receptor 3, Fgfr3	-2.1	-3.9
1377663_at	Rho family GTPase 3, Rnd3	-3.3	-2.3
1368505_at	regulator of G-protein signaling 4, Rgs4	-2.2	-97.5
1396249_at	Transcribed locus, ---	-2.2	-4.0
1389913_at	leucine rich repeat (in FLII) interacting protein 1, Lrrfip1	-3.5	-2.1
1390412_at	solute carrier family 39 (iron-regulated transporter), member 1, Slc40a1	-4.1	-2.5
1368725_at	jagged 1, Jag1	-3.3	-2.6
1380964_at	dystrobrevin alpha (predicted), Dtna_predicted	-3.5	-3.6
1382864_at	palmdelphin, Palmd	-2.3	-3.5
1371412_a_at	Neuronal regeneration related protein, Nrep	-2.2	-3.1
1397610_at	Transcribed locus, ---	-2.1	-7.2
1376725_at	low density lipoprotein receptor-related protein 6 (predicted), Lrp6_predicted	-4.0	-2.5
1377669_at	RAB27A, member RAS oncogene family, Rab27a	-3.9	-2.6
1395236_at	protein phosphatase 1, regulatory (inhibitor) subunit 3C, Ppp1r3c	-15.4	-2.5
1387759_s_at	UDP glycosyltransferase 1 family, polypeptide A1, Ugt1a9	-2.9	-2.2
1376924_a_at	palmdelphin, Palmd	-3.5	-5.3
1376066_at	Transcribed locus, ---	-2.4	-2.2
1369182_at	coagulation factor III, F3	-3.0	-3.6
1373286_at	filamin binding LIM protein 1, Fblim1	-3.5	-3.1
1381088_at	podocan (predicted), Podn_predicted	-2.5	-5.2
1371541_at	myosin, light polypeptide kinase (predicted), Mylk_predicted	-2.6	-12.3
1370288_a_at	tropomyosin 1, alpha, Tpm1	-2.7	-2.0
1379719_at	Transcribed locus, ---	-5.5	-2.7
1388111_at	elastin, Eln	-4.5	-5.4

1369518_at	phosphatidylinositol 3 kinase, regulatory subunit, polypeptide 3 (p55), Pik3r3	-4.2	-2.3
1389739_at	neuralized-like 2 (Drosophila) (predicted), Neurl2_predicted	-2.5	-4.6
1373915_at	dystrophia myotonica-protein kinase (predicted), Dmpk_predicted	-2.7	-4.1
1369085_s_at	small nuclear ribonucleoprotein N, Snurf	-2.8	-2.1
1370158_at	myosin, heavy polypeptide 10, non-muscle, Myh10	-3.2	-2.8
1376101_at	Transcribed locus, ---	-2.1	-2.3
1379747_at	Protease, serine, 35, Prss35	-5.0	-2.0
1383914_at	MRV integration site 1 homolog (mouse) (predicted), Mrvi1_predicted	-2.8	-6.1
1374650_at	neural precursor cell expressed, developmentally down-regulated gene 9, Nedd9	-2.6	-2.7
1370375_at	glutaminase 2 (liver, mitochondrial), Gls2	-2.4	-5.8
1392915_at	procollagen, type XI, alpha 1, Col11a1	-2.1	-2.6
1369993_at	calcium/calmodulin-dependent protein kinase II gamma, Camk2g	-2.9	-2.1
1390159_at	RAS, guanyl releasing protein 3 (predicted), Rasgrp3_predicted	-2.7	-3.3
1393806_at	MANSC domain containing 1, Mansc1	-3.7	-2.7
1398304_at	frizzled homolog 2 (Drosophila), Fzd2	-2.2	-2.0
1381363_at	Transcribed locus, moderately similar to XP_001236194.1 PREDICTED: hypothetical protein, partial [Gallus gallus], ---	-2.5	-2.0
1387873_at	WAP four-disulfide core domain 1, Wfdc1	-11.3	-9.7
1375349_at	similar to sorbin and SH3 domain containing 1 isoform 3, LOC678826	-3.2	-6.1
1388935_at	Protein phosphatase 1, regulatory (inhibitor) subunit 12B (predicted), Ppp1r12b_predicted	-2.4	-4.0
1368223_at	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 1, Adamts1	-4.5	-2.1
1379625_at	Similar to RIKEN cDNA 3110050N22 (predicted), RGD1311970_predicted	-2.0	-2.1
1388866_at	sarcospan, Sspn	-4.9	-2.0
1389918_at	Transcribed locus, strongly similar to XP_001053156.1 PREDICTED: similar to palladin [Rattus norvegicus], ---	-3.6	-4.4
1372856_at	Transcribed locus, ---	-2.4	-2.4
1384286_at	Transcribed locus, ---	-2.7	-2.1
1386039_x_at	---	-5.1	-2.8
1367665_at	ankyrin repeat domain 1 (cardiac muscle),	-2.8	-4.1

	Ankrd1		
1367738_at	UNC-119 homolog (C. elegans), Unc119	-2.5	-2.9
1372647_at	---	-2.5	-7.8
1389706_at	Transcribed locus, ---	-3.7	-2.7
1372722_at	Transcribed locus, ---	-2.2	-2.6
1377946_at	Transcribed locus, ---	-2.4	-2.0
1390127_at	DIX domain containing 1, Dixdc1	-4.6	-2.5
1380470_x_at	---	-3.1	-2.2
1396076_at	---	-3.3	-2.6
1367785_at	calponin 1, Cnn1	-3.3	-7.5
1371969_at	Transcribed locus, ---	-8.4	-2.2
1379732_at	syntaxin 11, Stx11	-3.6	-3.1
1393467_at	proprotein convertase subtilisin/kexin type 5, Pcsk5	-2.4	-7.7
1380311_at	Transcribed locus, ---	-3.1	-2.2
1392948_at	Transcribed locus, ---	-2.0	-2.2
1370857_at	smooth muscle alpha-actin, Acta2	-2.2	-7.0

Supplemental Table VII. Gene ontology clustering of distinctly IL-1β-induced genes in SMCs

Gene Ontology Cluster	Enrichment Score	Annotated Genes
Inflammatory Response	11.3	*Arg1, Ass1, Bcl3, Bmp6, Bmp6, Bmp6, C1S, C3, C4Bpa, Casp3, Ccl2, Ccl20, Ccl5, Ccl7, Cd74, Ceacam19, Cfb, Ciita, Clu, Cx3cl1, Cxcl1, Cxcl16, Cxcl2, Cxcl3, Cxcl3, Cxcl3, Cxcl3, Cxcl6, Cyba, Elf3, Elk3, Elk3, Fgr, Gch1, Hif1A, Hp, Il1R1, Il1R1, Il4Ra, Il6, Jak2, Jak2, Lbp, Loc290412, Loc290503, Loc497963, Loc499261, Loc681135, Loc686887, Lyc2, Lyn, Lyz2, Map2k3, Masp1, Mmp2, Mphosph8, Nfkbiz, Nos2, Orm1, Parp4, Pdgfra, Pkm2, Pld1, Ptges, Ptges, Pxk, Pxk, Pxk, Rbpj, Rbpsuh, Rgd1561179, Rgd1561715, Rt1-Ba, Rt1-Da, Selp, Serpine1, Serping1, Sod2, Sod2, Tgfb1, Timp1, Tlr2, Vcam1, Vcan*
Response to lipopolysaccharide	6.8	*Ass1, Bcl3, Casp3, Ccl2, Ccl5, Ceacam19, Cfb, Fgr, Gch1, Hp, Il6, Irak3, Lbp, Loc360228, Loc497963, Loc686887, Lyc2, Lyz2, Mgst1, Mgst2, Nfkb2, Nfkbia, Nos2, Pld1, Ptges, Ptges, Rbpj, Rbpsuh, Selp, Socs3, Tlr2, Trib1*
Adaptive immune response	4.9	*Bcl3, Bcl6, C1S, C3, C4Bpa, Cd74, Ceacam19, Cfb, Hpx, Icam1, Il6, Lbp, Loc686887, Lyn, Masp1, Nfkb2, Nfkbia, Pvrl2, Rgd1561715, Rt1-A1, Rt1-A2, Rt1-A3, Rt1-Ba, Rt1-Ce14, Rt1-Ce16, Rt1-Cl, Rt1-Da, Rt1-Dma, Serping1, Sh2b2, Stat5A, Swap70, Tlr2, Tnfsf13, Traf3Ip2*
Antigen processing and presentation	4.5	*Cd74, Hsph1, Icam1, Loc686172, Loc688090, Psmb9, Psme2, Rt1-A1, Rt1-A2, Rt1-A3, Rt1-Ba, Rt1-Bb, Rt1-Ce1, Rt1-Ce12, Rt1-Ce14, Rt1-Ce16, Rt1-Cl, Rt1-Da, Rt1-Db1, Rt1-Db1, Rt1-Dma, Rt1-Dmb*
Positive regulation of inflammatory response	3.8	*Adora2b, Bcl6, C1S, C3, C4Bpa, Calcrl, Ccl5, Cfb, Cx3Cl1, Fabp4, Hpx, Il6, Jak2, Jak2, Lbp, Lyn, Masp1, Nfkbia, Pvrl2, Rgd1561715, Rt1-A1, Rt1-A2, Rt1-A3, Rt1-Ba, Rt1-Ce14, Rt1-Ce16, Rt1-Cl, Rt1-Da, Rt1-Dma, Sbno2, Selp, Serping1, Sh2b2, Slit2, Slit2, Stat5a, Tgfb1, Tlr2, Tnfsf13*
Response to hormone	3.5	*Acsl1, Acsl1, Asns, Ass1, Bckdhb, Bmp6,*

stimulus		*Bmp6, Bmp6, Btg2, C1s, Casp3, Ccl2, Ccl5, Cd83, Cdkn1a, Cdkn1A, Cdkn2a, Cdkn2b, Cdo1, Cfb, Ciita, Creb3L1, Ctsc, Cxcl16, Cyp1B1, Fabp4, Fosl2, Gch1, Glul, Glul, Glul, Gng2, Gng8, Hif1a, Hp, Il1r1, Il1r1, Il6, Il6st, Il6st, Il6st, Il6st, Irak3, Jak2, Jak2, Junb, Lbp, Loc290412, Loc290503, Loc360228, Loc499261, Loc681135, Lyn, Mgp, Mgp, Mgst1, Mgst2, Mmp13, Mmp2, Mmp3, Nfkb2, Nfkbia, P2rx4, Pdgfra, Pik3R1, Pkm2, Plat, Pld1, Ptges, Ptges, Ptprn, Ramp2, Rerg, Rgd1561179, Rgd1561715, Selp, Sh2b2, Socs3, Stat5a, Tgfb1, Timp1, Tlr2, Tnfrsf11b, Trib1*
Regulation of leukocyte activation	3.3	*Adora2b, Bcl6, Bmp6, Bmp6, Bmp6, C3, Casp3, Ccl5, Cd74, Cd83, Cdkn1a, Cdkn1a, Cdkn2b, Clu, Csf1, Csf1, Csf1, Csf2, Hif1a, Hlx, Hpx, Il13ra1, Il13ra1, Il4ra, Il6, Il6st, Il6st, Il6st, Il6st, Irak3, Jak2, Jak2, Junb, Lbp, Lyn, Pik3r1, Pvrl2, Rt1-A1, Rt1-A2, Rt1-A3, Rt1-Ba, Rt1-Ce14, Rt1-Ce16, Rt1-Cl, Rt1-Dma, Runx1, Serping1, Socs3, Socs5, Socs5, Stat5A, Tgfb1, Tgif1, Tnfsf13, Vcam1, Xrcc5*
Leukocyte homeostasis	3.2	*Adora2b, Bcl6, C1s, C3, C4Bpa, Casp3, Cd74, Cd83, Cdkn1a, Cdkn1a, Cfb, Csf1, Csf1, Csf1, Hlx, Hpx, Icam1, Il13ra1, Il13ra1, Il4ra, Il6, Il6st, Il6st, Il6st, Il6st, Irak3, Jak2, Jak2, Lbp, Lyn, Masp1, Nfkbia, Pvrl2, Rgd1561715, Rt1-A1, Rt1-A2, Rt1-A3, Rt1-Ba, Rt1-Ce14, Rt1-Ce16, Rt1-Cl, Rt1-Da, Rt1-Dma, Selp, Serping1, Sh2b2, Socs5, Socs5, Stat5a, Tgfb1, Tlr2, Tnfsf13, Vcam1*
Regulation of cytokine production	3.2	*Adora2b, Atp1a1, Atp1a1, Bcl3, Bcl6, Bmp6, Bmp6, Bmp6, Ccl2, Ccl5, Cd83, Ceacam19, Cebpb, Csf1, Csf1, Csf1, Cx3cl1, Foxs1, Fst, Fst, Glul, Glul, Glul, Hif1A, Htr2a, Il6, Irak3, Jak2, Jak2, Lbp, Loc686887, Map2k3, Nox1, Stat5A, Tgfb1, Tlr2*
Defense response to bacterium	3.0	*Bcl3, Ceacam19, Fgr, Il6, Lbp, Loc497963, Loc686887, Lyc2, Lyz2, Nos2, Pld1, Rbpj, Rbpsuh, Tlr2*

Supplemental Table VIII: Gene ontology clustering of distinctly PDGF-DD-induced genes in SMCs

Gene Ontology	Enrichment Score	Annotated Genes
Cell cycle	16.7	*Asf1b, Aspm, Aurka, Birc5, Blm, Bub1B, Ccdc99, Ccna2, Ccnb1, Ccnb1, Ccne1, Ccnf, Ccnf-Ps1, Cdc25a, Cdc25b, Cdc45l, Cdc45l, Cdc45l, Cdca3, Cdca5, Cdca8, Chek1, Dnmt1, Dscc1, E2F1, Ercc1, Espl1, Fbxo5, Hat1, Hells, Hjurp, Hjurp, Inhba, Kif11, Kif18A, Kifc1, Lig1, Lig1, Loc290415, Loc300303, Loc317415, Loc364091, Loc684771, Loc686151, Loc689892, Loc692021, Mad2L1, Mad2L1, Mapk6, Mcm2, Mcm6, Mki67, Nasp, Ncapd2, Ncaph, Npm1, Nusap1, Pdpn, Phgdh, Pola1, Pole, Psmc6, Psmd14, Pttg1, Racgap1, Racgap1, Rad51, Rad51c, Ran, Rasa1, Rasa1, Rasa1, Rassf1, Rassf1, Rgd1310778, Rgd1559647, Rgd1560892, Rgd1562067, Rgd1564855, Rgd1565692, Rrs1, Ruvbl1, Ruvbl2, Sass6, Ska1, Ska3, Smc2, Spc25, Suv39H1, Tacc3, Terf1, Timeless, Trip13, Ube2c, Uhrf1*
DNA repair	12.5	*Blm, Ccne1, Ccne2, Cdc25a, Cdc45l, Cdc45l, Cdc45l, Chek1, Dnmt1, Dyrk4, Ercc1, Esco2, Esco2-Ps1, Exo1, Fen1, Gins1, H2afx, Hells, Hmox1, Insig1, Jun, Jun, Jun, Lig1, Lig1, Loc317415, Loc363932, Loc364091, Loc364182, Loc367976, Loc683536, Loc688617, Loc688922, Loc689892, Loc691979, Mcm10, Mcm10, Mcm2, Mcm3, Mcm4, Mcm5, Mcm6, Mcm7, Mcm8, Nasp, Nedd4, Orc1L, Orc6l, Orc6l, Pola1, Pola2, Pold2, Pold3, Pole, Pole2, Prim1, Prim2, Pttg1, Rad18, Rad51, Rad51Ap1, Rad51c, Rfc2, Rfc3, Rfc4, Rfc5, Rfc5, Rgd1559671, Rgd1560892, Rgd1563943, Rgd1564855, Rpa3, Rrm1, Rrm1-Ps1, Rrm2, Ruvbl1, Ruvbl2, Terf1, Timeless, Tk1, Tk1, Trip13, Ube2N, Uhrf1, Ung, Usp1*
Chromosome localization	5.5	*Aspm, Birc5, Ccdc99, Cdca5, Dscc1, Espl1, Kif18A, Loc300303, Loc684771, Loc686151, Mad2L1, Mad2L1, Ncapd2, Ncaph, Npm1, Nusap1, Rrs1, Smc2, Tacc3*
Microtubule cytoskeleton organization	5.0	*Birc5, Ccdc99, Cenpe, Espl1, Ezr, Fbxo5, Kif11, Kif14, Kif15, Kif18A, Kif18B, Kif20A, Kif20B, Kif23, Kifc1, Loc300303, Npm1, Nusap1, Pfn2, Racgap1, Racgap1, Ran, Rasa1, Rasa1, Rasa1, Sass6, Spc25, Tacc3, Tuba4A*
Regulation of cell cycle	4.6	*Birc5, Blm, Ccnb1, Ccnb1, Ccne1, Ccne2, Cdt1, Cenpe, Chek1, E2F1, Fbxo5, Gmnn, H2afx, Inhba, Jun, Jun, Jun, Loc300303, Mad2L1, Mad2L1, Npm1,*

		Nucks1, Nusap1, Plk4, Tacc3, Timeless, Ube2c, Zwilch
DNA duplex unwinding	4.1	*Loc31741, Mcm2, Mcm4, Mcm6, Mcm7, Rad51, Rgd1563943*

Supplemental Table IX: Gene ontology clustering of distinctly PDGF-DD-repressed genes in SMCs

Gene Ontology Cluster	Enrichment Score	Annotated Genes
Antigen processing and presentation	3.3	*C1s, C3, C4b, Cd74, RGD1561715, Rt1-ba, Rt1-da, Rt1-db1, Rt1-db1, Rt1-dmb*