

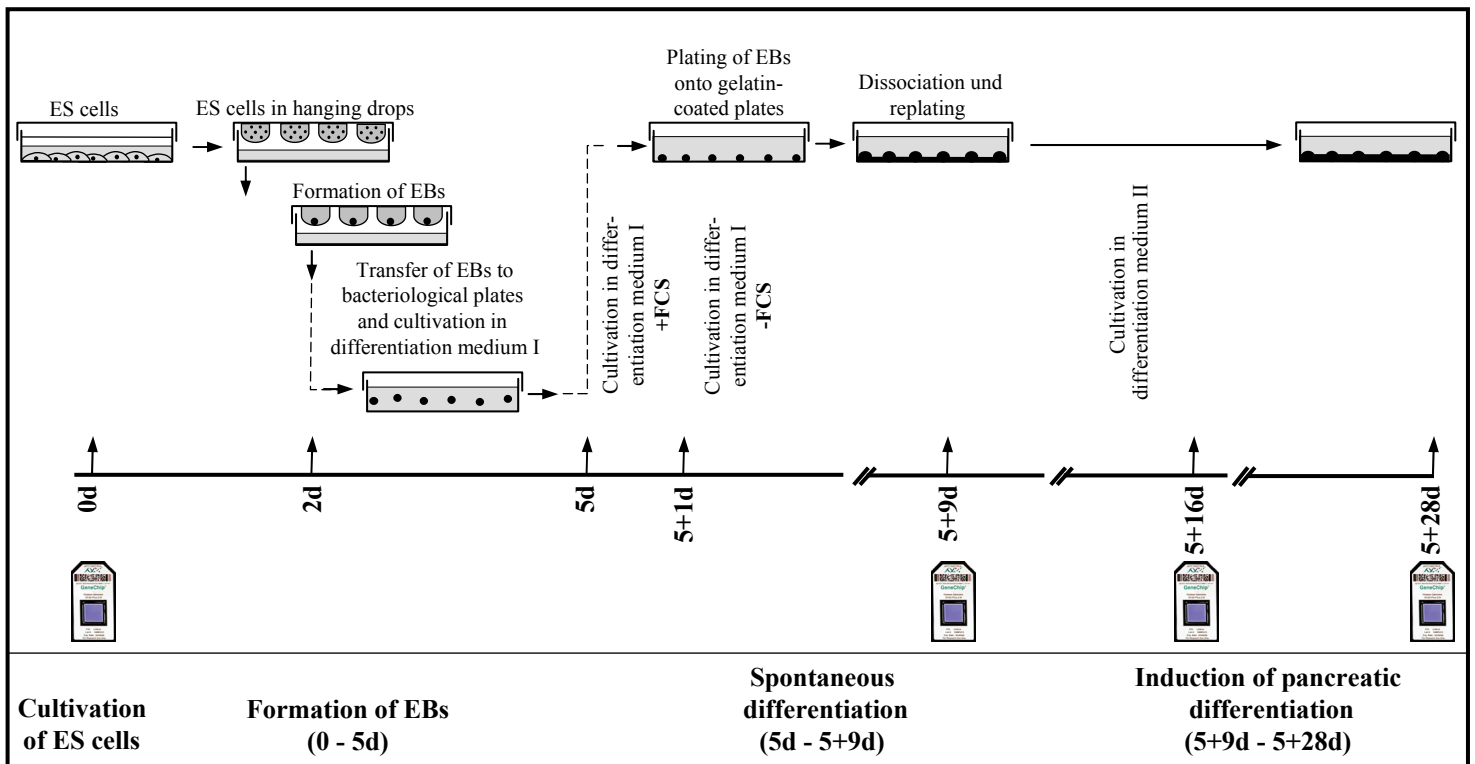
SUPPLEMENTARY MATERIAL

corresponding to:

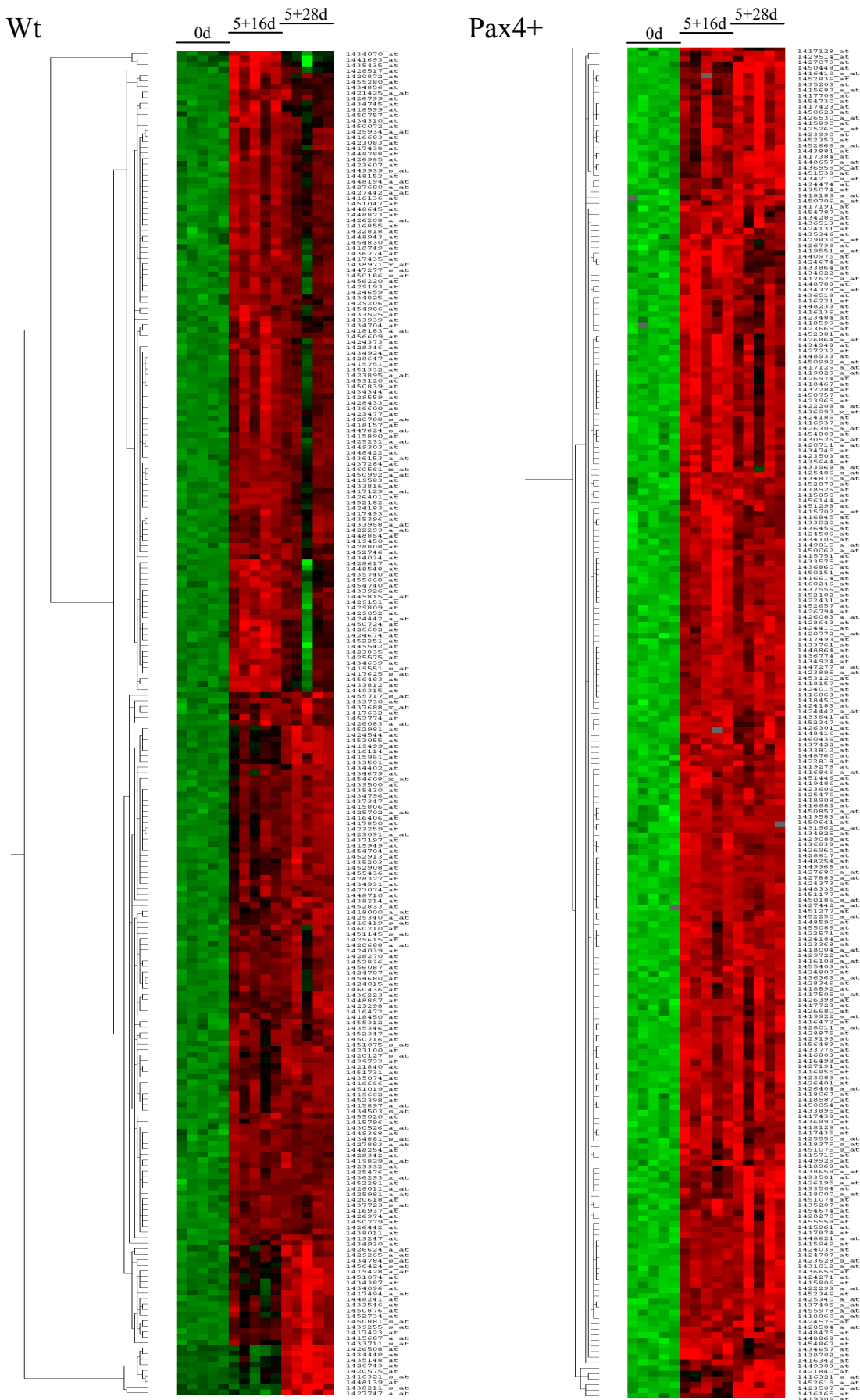
Characterization of mouse embryonic stem cell differentiation into the pancreatic lineage *in vitro* by transcriptional profiling, quantitative RT-PCR and immunocytochemistry

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NORBERT HUEBNER and ANNA M. WOBUS

Suppl. Figure S1: Differentiation protocol for wt and Pax4+ ES cells into the pancreatic lineage (Blyszczuk et al., 2004; Schroeder et al., 2006) and cell stages used for Affymetrix analysis (symbol) at days 0, 5+9 (only wt cells), 5+16 and 5+28.

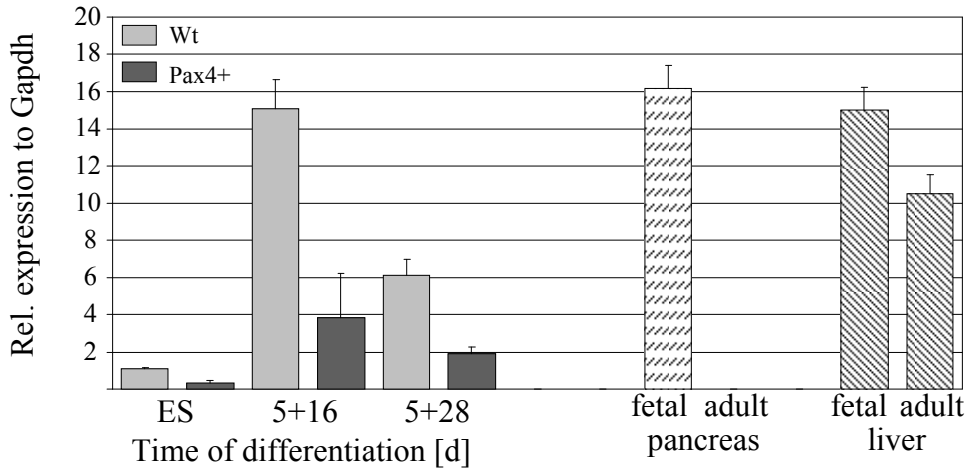


Suppl. Figure S2: Hierarchical clustering of probe sets two or more fold up-regulated

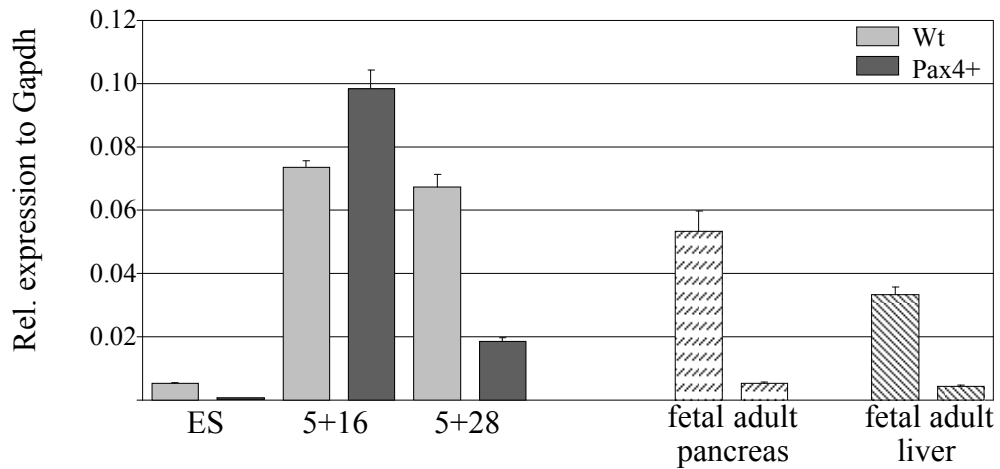


Transcriptional regulation:

Foxa1

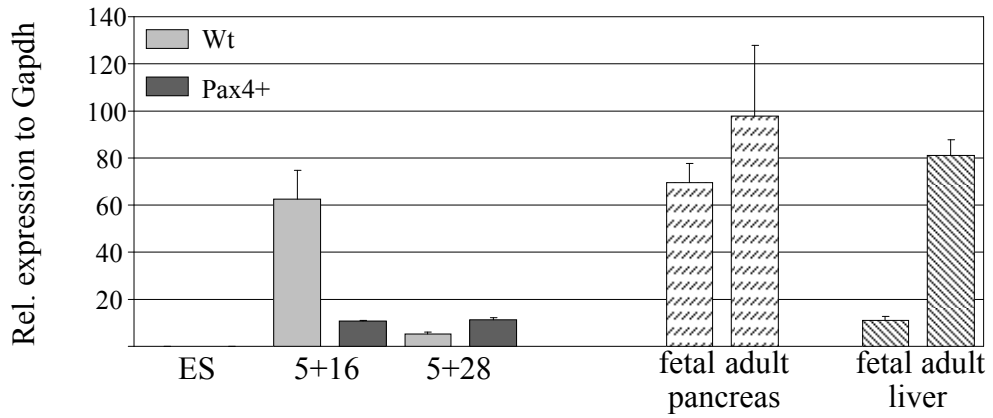


Hoxb2

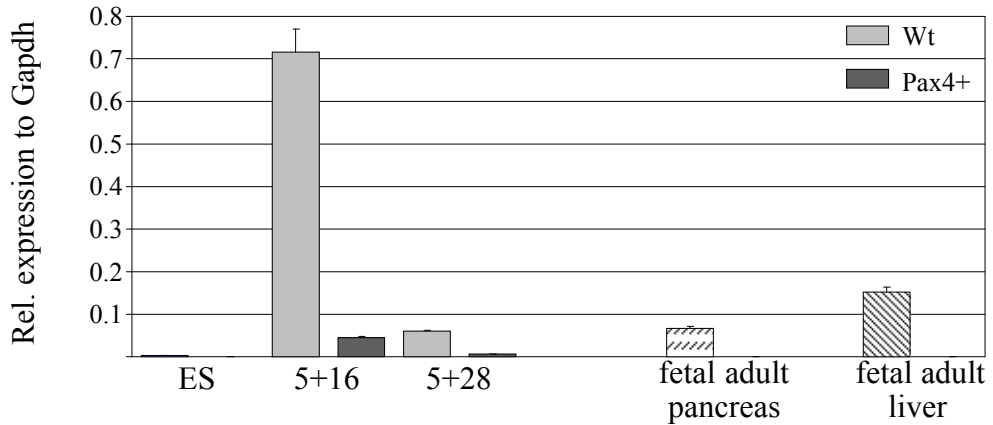


Signaling, growth factors:

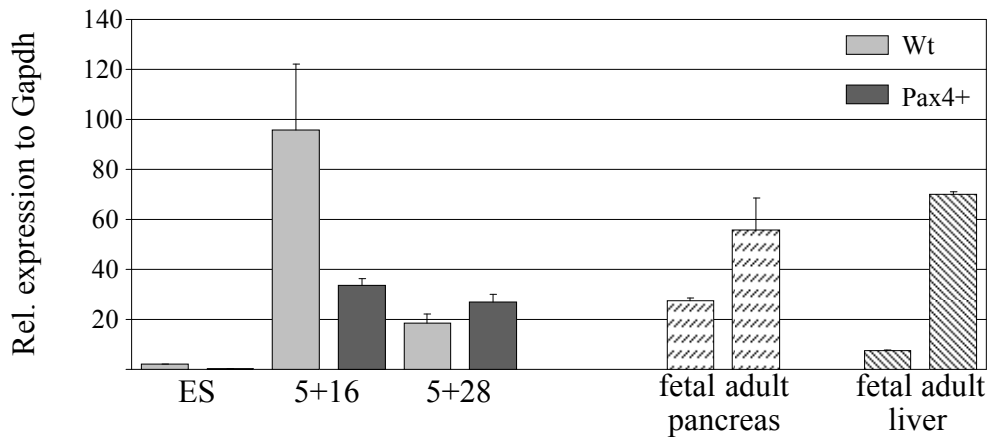
Igf1



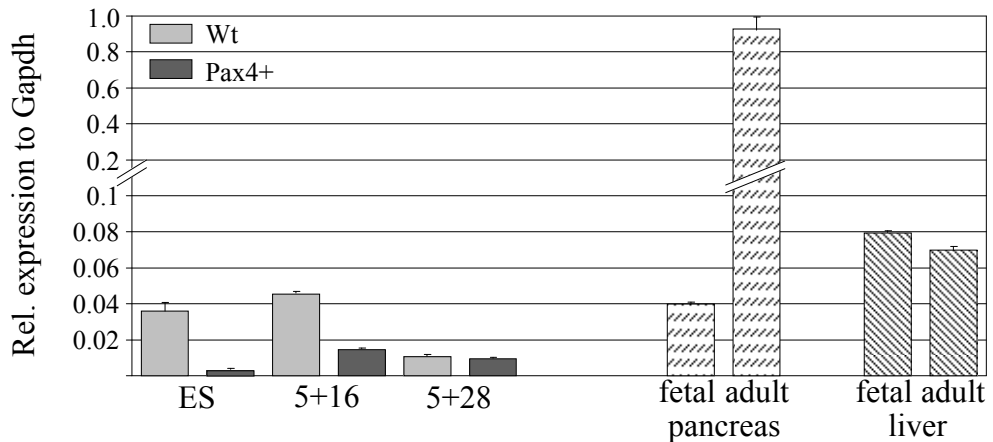
Igf2



Igfbp7

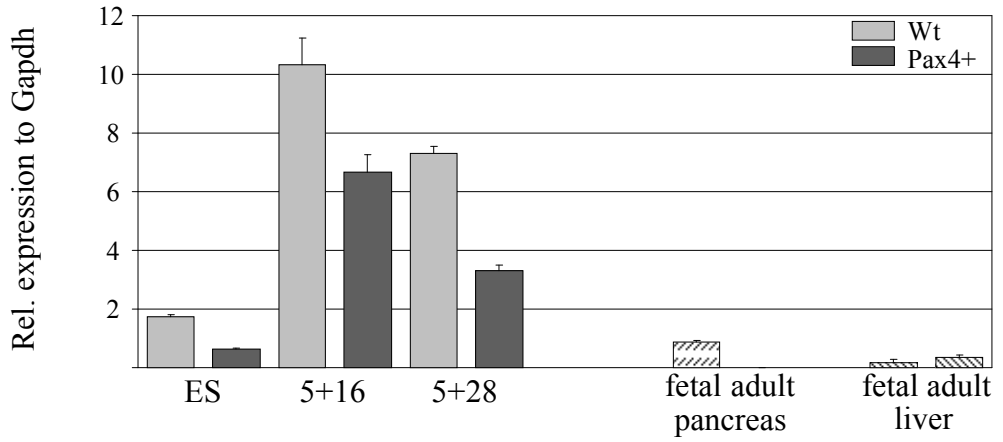


Irs1

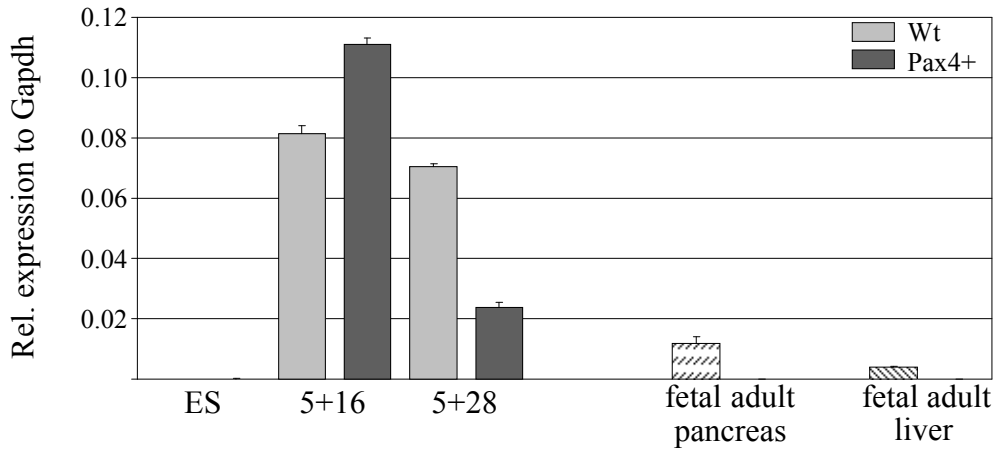


Signaling, growth factors:

Pik3r3

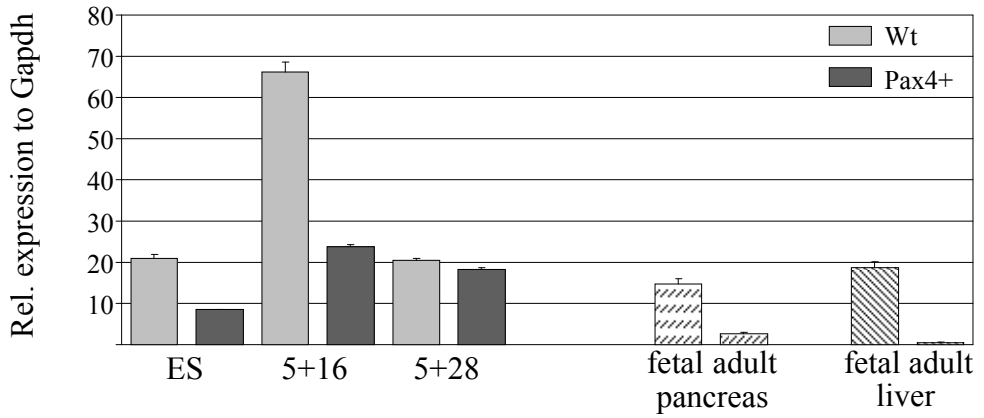


Ptn

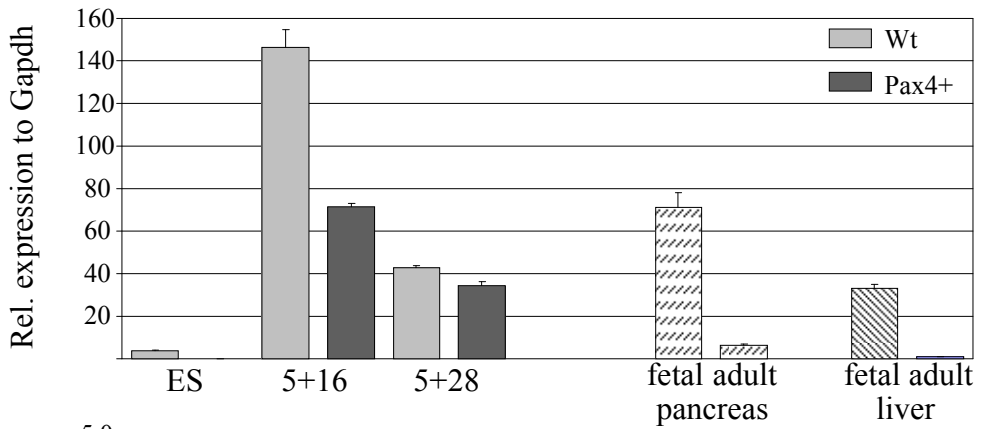


Adhesion, extracellular matrix:

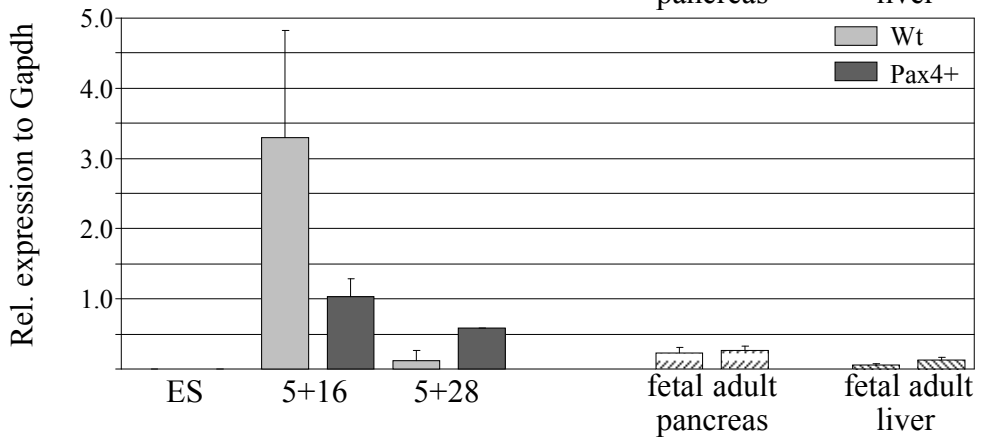
Col1a2



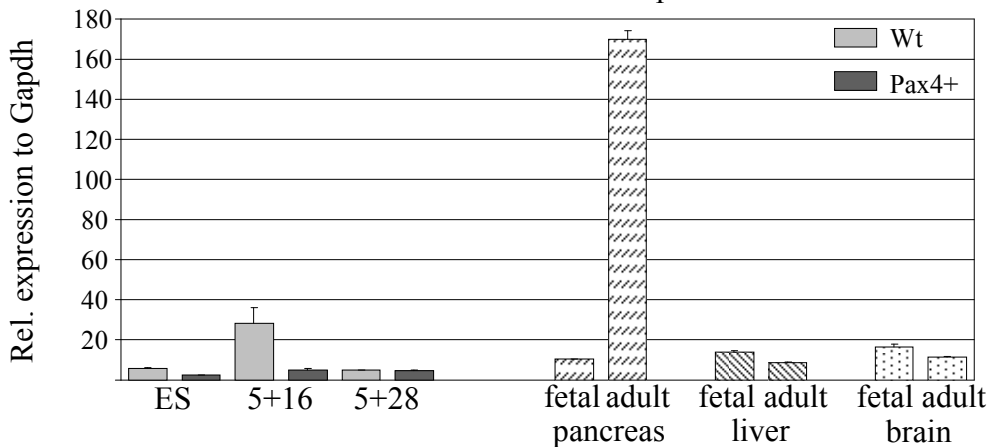
Col3a1



Dcn

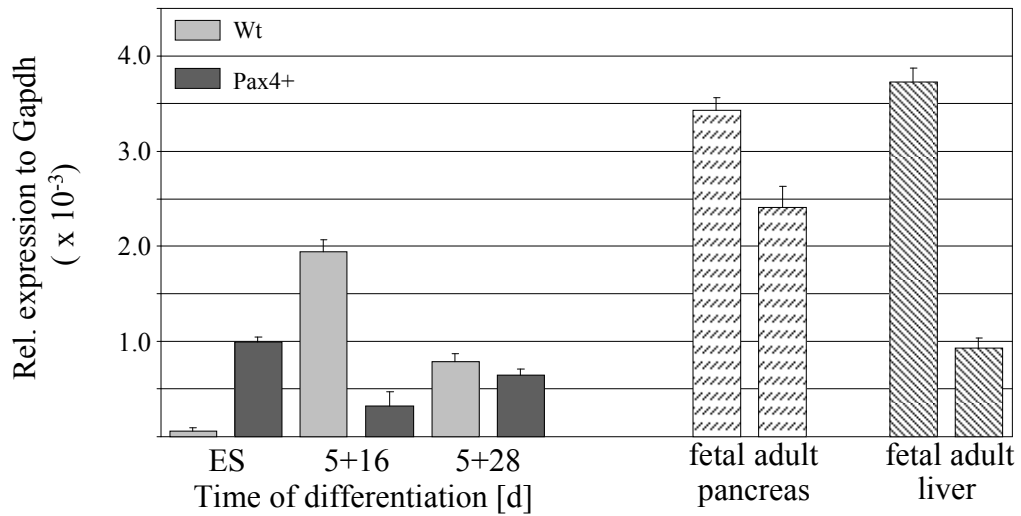


Serpine 2

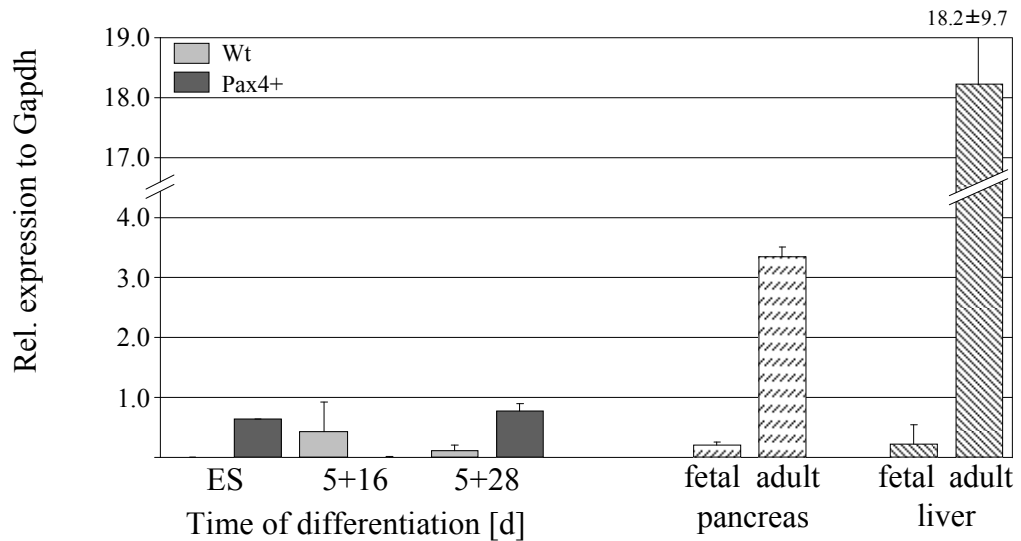


Membrane, transport:

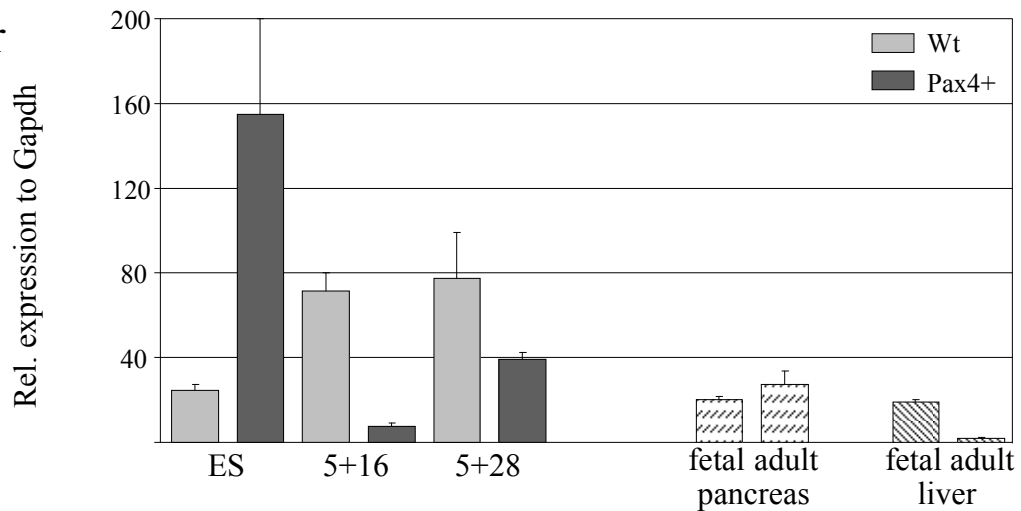
Chgb



Ttr

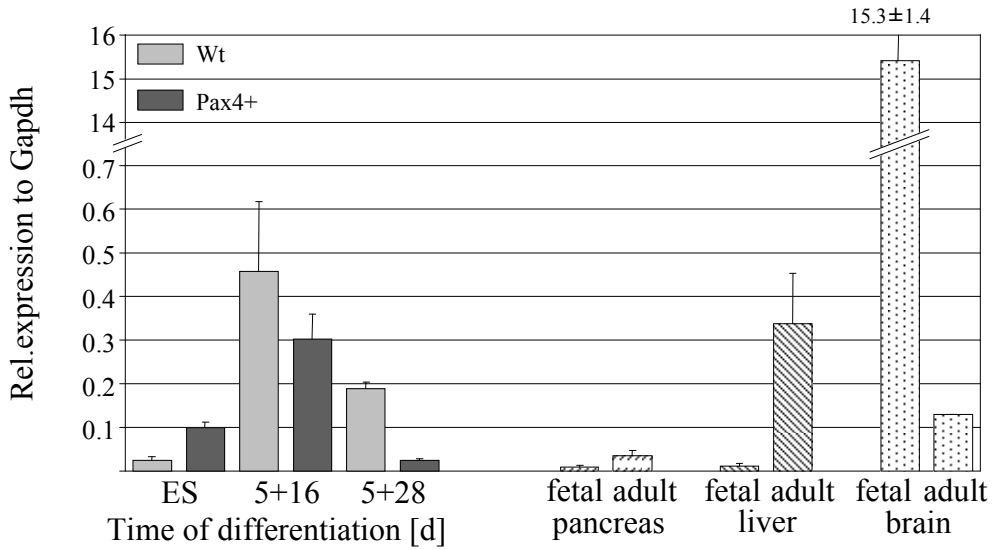


Vldlr

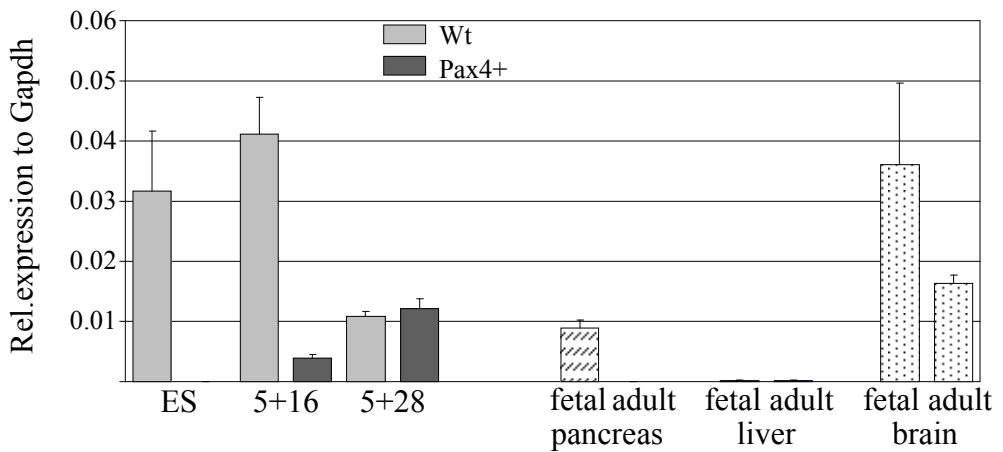


Organogenesis:

Nnat

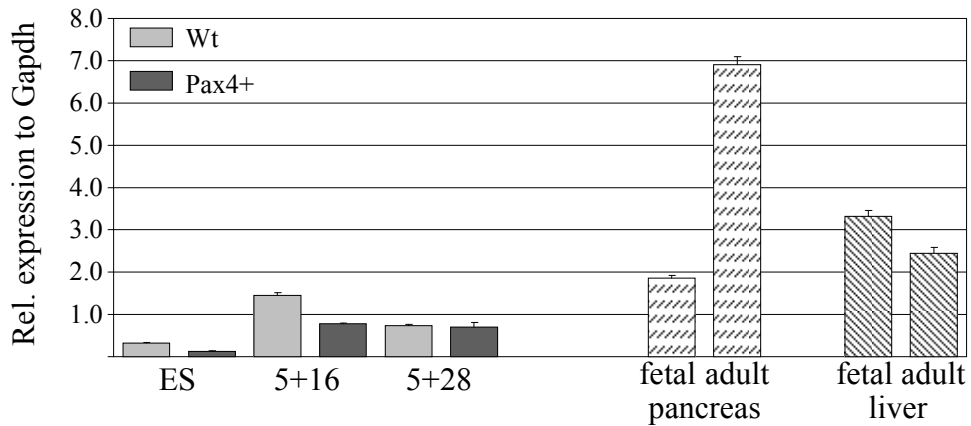


Nrp1

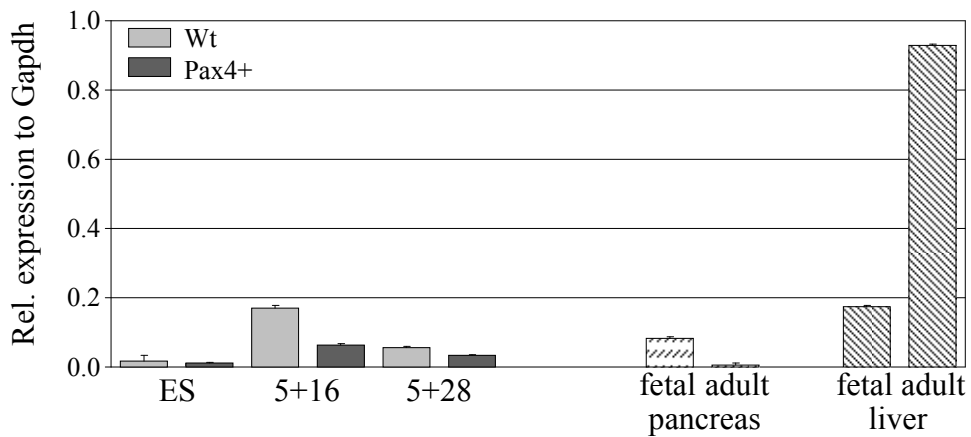


Metabolism, peroxisome:

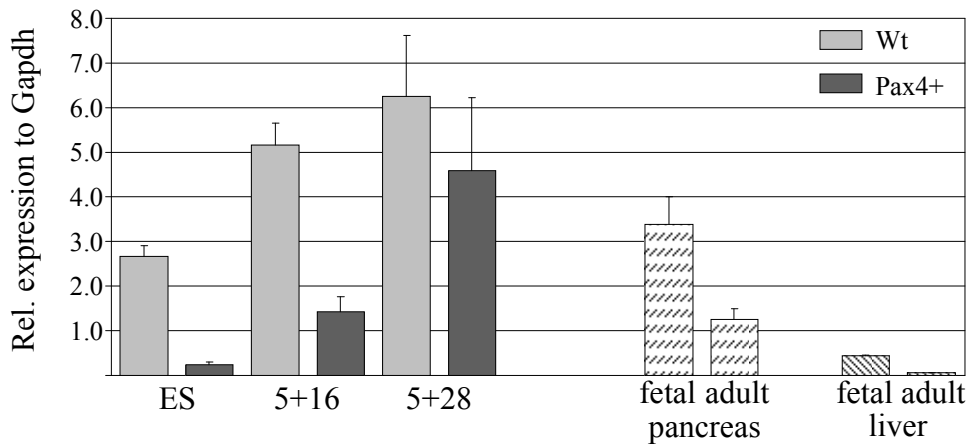
Ctsb



Ctsf

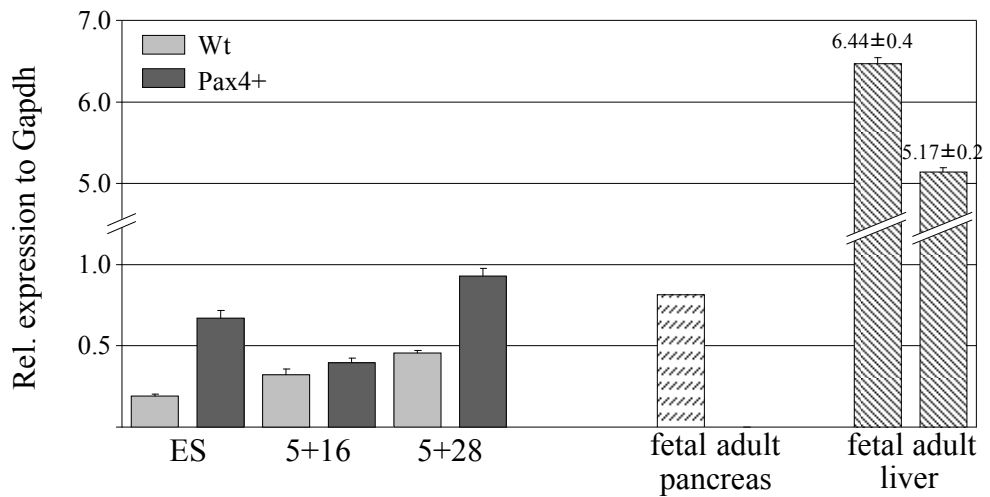


Cpe

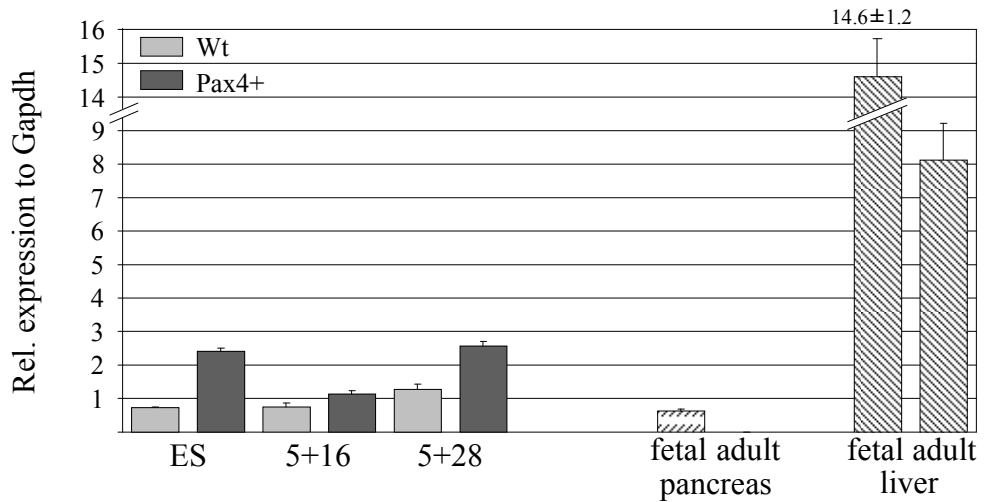


Metabolism, peroxisome:

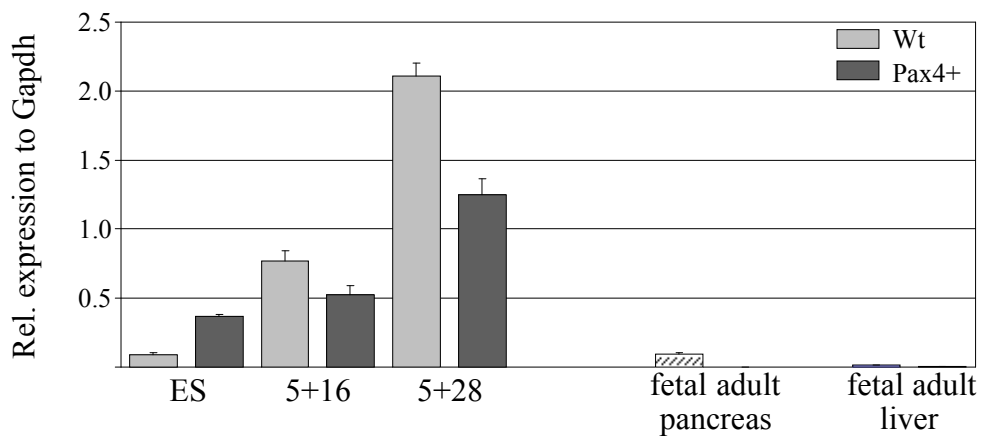
Mt1



Mt2

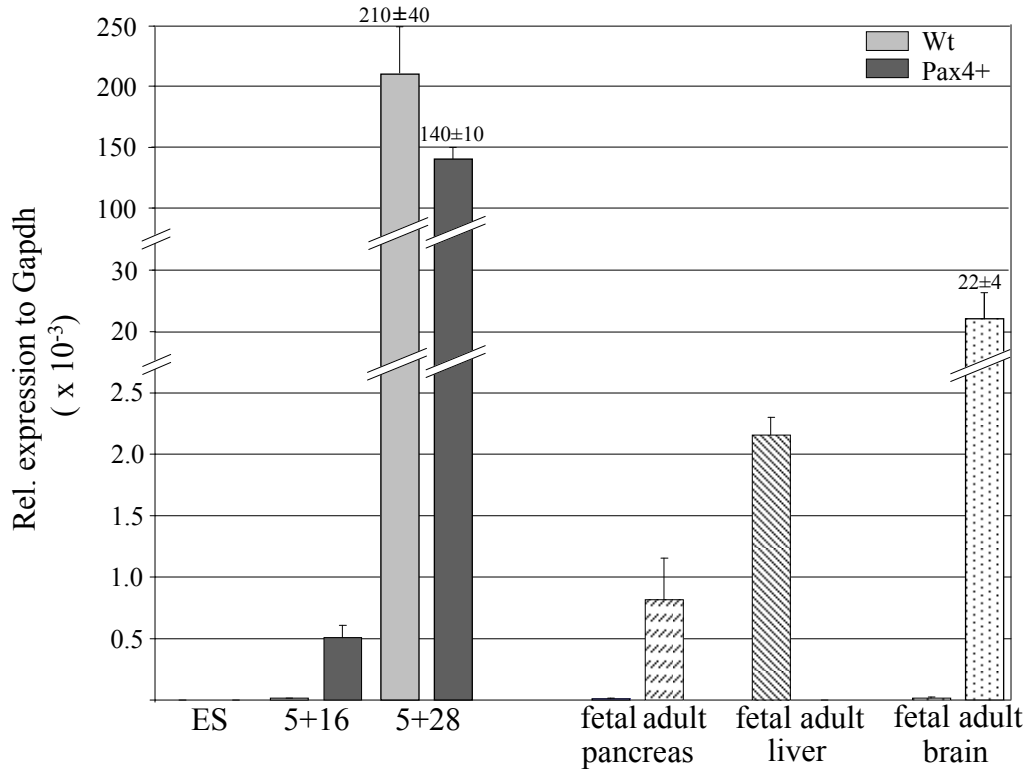


Mt3

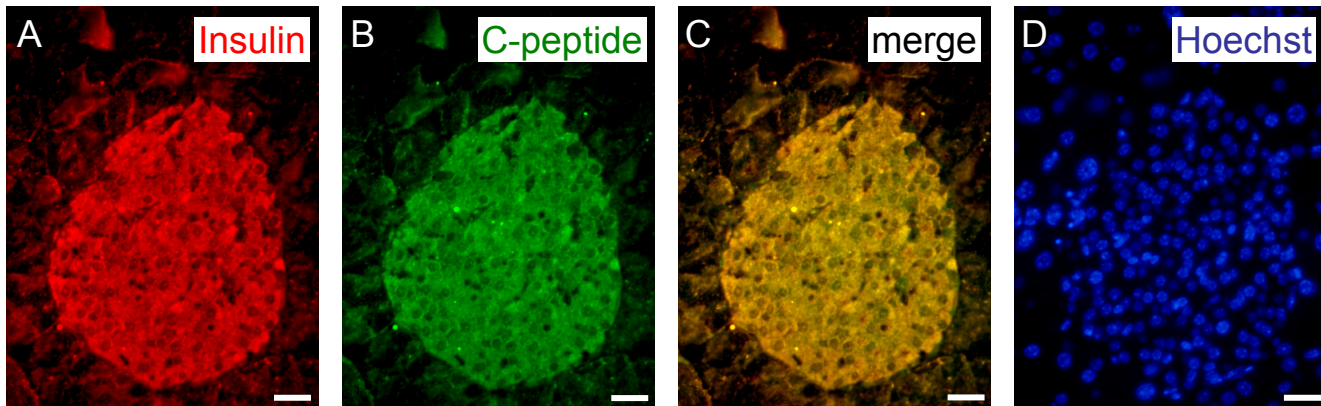


Cytoskeleton, intermediate filaments:

Gfap



Suppl. Figure S4: Immunofluorescence staining of adult (8 weeks) mouse pancreas tissue section as positive control. Significant labeling of islet cells is shown. (A) mouse anti-insulin, (B) sheep anti-C-peptide, (C) merge of A and B, and (D) Hoechst visualizing cell nuclei (Bar= 20 μ m).



Suppl. Table S1: Primer sets employed for real time RT-PCR analysis

Gene	Sense (5'-3')	Antisense (5'-3')
Foxa1	CCA GTG GAT CAT GGA CCT CTT C	CCT TGA CGA AAC AAT CGT TGA A
HoxB2	CGC GTC GCG TCG AGA T	TCA TGC GTC GGT TCT GGA A
Ttr	CGT ACT GGA AGA CAC TTG GCA TT	CGT TGG CTG TGA AAA CCA CAT
ChgB	CCC GCT GGC TGA ACT TTT C	GAG TTC TGA CGG CGG AAG AG
Vldlr	CCA AGA GGA AGT TCC TGT TTA ATT CT	GCC CGA CAA CGG ATC CA
Col3a1	TTG ATG TGC AGC TGG CAT TC	GCC ACT GGC CTG ATC CAT AT
Col1a2	CAC GTG CCG GGA CTT AAG AC	CAT AGT ACA TCC TTG GTT AGG GTC AA
Dcn	TCC AGG TCG TCT ACC TTC ACA AC	ACA GCC GAG TAG GAA GCC TTT
Serpine 2	GAT CGC CCT GCC AAC AGA	TCC AGC TAT CAA TGG TCT TGG TAG T
Igf-1	GAT CTG AGG AGA CTG GAG ATG TAC TG	CTT CTG AGT CTT GGG CAT GTC A
Igf-2	ACG TTC ACT CTG TCT CTC TCA CTA TCT CT	GCG GGC CAG ATA TTG TAC TTT C
Igfbp-7	GGA GGA CGC TGG AGA GTA TGA G	TGG AGG GCA TCA ACC ACT GTA
Irs-1	CGG GCT GAC TCC AAG AAC AA	TCG CTA TCC GCG GCA AT
Pik3r3	TTA TTA ACC ACT ACC ACC ACG AGT CT	TGG AAT CTG GAT ACT GGG TAC GT
Ctsb	TTG TTC CAG ATC CAT TAG AAT ACA GAA	AGC GCT CTC ACT TCC ACT ACC ACA GAG C
Ctsf	ACG GGA TTG CTC ACC CAT T	TGT TAG AGC GGT TGC CAT AGC
Cpe	TGA GAC ACG GAG CGG TAC TG	CGC GCG AGC CAA GCT
Nnat	GGA GCA ACC CTC GAG ATA TGG	TTG ATG GGC TGT TCG ATC TTC
Gfap	CGT TTC TCC TTG TCT CGA ATG A	TCG CCC GTG TCT CCT TGA
Ptn	GAG CAT CAG CCA GCG ATA CC	ACT AGC TGG CTG CCT TTG TTG
Mt-1	CGT GCT GTG CCT GAT GTG A	AAC AGG GTG GAA CTG TAT AGG AAG A
Mt-2	ATA GAC CAT GTA GAA GCC TAG CCT TTT	GGC TTT TAT TGT CAG TTA CAT GCT TTA TAG
Mt-3	GCA GAG GCC GAG AAA TGC	CAG GGA CAC CCA GCA CTA TTT AC
Nrp1	AAG CGC TTC TCG CGA ATT	CCG CCT AAG AAC CAT AAA ATC CT
Gapdh	CCT GCA CCA CCA ACT GCT TA	TCA TGA GCC CTT CCA CCA TG

Suppl. Table S2. List of transcripts five- or more-fold up-regulated in wt and Pax4+ cells (FC: fold change)

S2a: Wt ES cells (0d) vs. committed progenitor cells at 5+16d

Probe ID	FC	Gene Symbol	Gene Title
Transcriptional regulation			
1423477_at	77.0	Zic1	zinc finger protein of the cerebellum 1
1418157_at	48.0	Nr2f1	nuclear receptor subfamily 2, group F, member 1
1450533_a_at	42.9	Plagl1	pleiomorphic adenoma gene-like 1
1450928_at	29.2	Irbp4	inhibitor of DNA binding 4
1434102_at	22.5	Nfib	nuclear factor I/B
1421163_a_at	21.3	Nfia	nuclear factor I/A
1450992_a_at	17.6	Meis1	myeloid ecotropic viral integration site 1
1416158_at	17.0	Nr2f2	nuclear receptor subfamily 2, group F, member 2
1444615_x_at	11.7	Cbfa2t1h	CBFA2T1 identified gene homolog (human)
1437556_at	11.7	Zfhx4	zinc finger homeodomain 4
1419583_at	11.1	Cbx4	chromobox homolog 4 (Drosophila Pc class)
1417447_at	10.8	Tcf21	transcription factor 21
1436363_a_at	10.0	Nfix	nuclear factor I/X
1436931_at	9.8	Rfx4	regulatory factor X, 4 (influences HLA class II expression)
1428433_at	9.8	Hipk2	homeodomain interacting protein kinase 2
1447624_s_at	9.7	Stox2	storkhead box 2
1430526_a_at	8.8	Smarca2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2
1434856_at	8.4	Ankrd44	ankyrin repeat domain 44
1421072_at	7.7	Irx5	Iroquois related homeobox 5 (Drosophila)
1424029_at	7.5	Tspyl4	TSPY-like 4
1418496_at	7.3	Foxa1	forkhead box A1
1418517_at	7.3	Irx3	Iroquois related homeobox 3 (Drosophila)
1455121_at	7.0	Mlr2	Mblk1-related protein-2
1429138_at	7.0	Npas3	Neuronal PAS domain protein 3
1435078_at	6.5	Tanc2	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 2
1460006_at	6.4	Atbf1	AT motif binding factor 1
1454906_at	6.2	Rarb	retinoic acid receptor, beta
1447864_s_at	5.8	Pogk	pogo transposable element with KRAB domain
1429205_at	5.8	Mllt3	myeloid/lymphoid or mixed lineage-leukemia translocation to 3 homolog (Drosophila)
1416149_at	5.7	Olig1	oligodendrocyte transcription factor 1
1460324_at	5.7	Dnmt3a	DNA methyltransferase 3A
1416390_at	5.6	Chc11	chromosome condensation 1-like
1437598_at	5.5	Zbtb20	zinc finger and BTB domain containing 20
1425383_a_at	5.2	Pbx1	pre B-cell leukemia transcription factor 1
1438930_s_at	5.1	Mecp2	methyl CpG binding protein 2
1429088_at	5.1	Lbh	limb-bud and heart
1428939_s_at	5.0	Gnaq	guanine nucleotide binding protein, alpha q polypeptide
Signaling, growth factors			
1448254_at	160.9	Ptn	pleiotrophin
1456741_s_at	144.4	Gpm6a	glycoprotein m6a
1437347_at	76.8	Ednrb	endothelin receptor type B
1425575_at	37.9	Epha3	Eph receptor A3
1419248_at	23.2	Rgs2	regulator of G-protein signaling 2
1456379_x_at	20.0	Dner	delta/notch-like EGF-related receptor
1423091_a_at	19.4	Gpm6b	glycoprotein m6b
1452114_s_at	18.6	Igfbp5	insulin-like growth factor binding protein 5

1434413_at	18.0	Igf1	Insulin-like growth factor 1
1436736_x_at	17.3	D0H4S114	DNA segment, human D4S114
1433968_a_at	15.8	Megf9	Multiple EGF-like-domains 9
1459749_s_at	15.5	Fat4	FAT tumor suppressor homolog 4 (Drosophila)
1456609_at	13.2	Camk2n1	calcium/calmodulin-dependent protein kinase II inhibitor 1
1452251_at	11.6	Nbea	neurobeachin
1420858_at	11.4	Pkia	protein kinase inhibitor, alpha
1433434_at	11.2	AW551984	expressed sequence AW551984
1421425_a_at	11.1	Dscr111	Down syndrome critical region gene 1-like 1
1434881_s_at	10.7	Kctd12	potassium channel tetramerisation domain containing 12
1448152_at	10.5	Igf2	insulin-like growth factor 2
1448933_at	10.5	Pcdhb17	protocadherin beta 17
1437284_at	10.0	Fzd1	frizzled homolog 1 (Drosophila)
1455893_at	8.4	Rspo2	R-spondin 2 homolog (Xenopus laevis)
1438664_at	7.9	Prkar2b	protein kinase, cAMP dependent regulatory, type II beta
1423756_s_at	7.8	Igfbp4	insulin-like growth factor binding protein 4
1451289_at	7.7	Dcamk1	Double cortin and calcium/calmodulin-dependent protein kinase-like 1
1435977_at	7.4	Hdgfrp3	hepatoma-derived growth factor, related protein 3
1416846_a_at	6.9	Pdzrn3	PDZ domain containing RING finger 3
1448117_at	6.7	Kitl	kit ligand
1456482_at	6.4	Pik3r3	phosphatidylinositol 3 kinase, regulatory subunit, polypeptide 3 (p55)
1460187_at	6.3	Sfrp1///2210415 K03Rik	secreted frizzled-related sequence protein 1 /// RIKEN cDNA 2210415K03 gene
1424007_at	6.1	Gdf10	growth differentiation factor 10
1454604_s_at	5.9	Tm4sf12	transmembrane 4 superfamily member 12
1415806_at	5.8	Plat	plasminogen activator, tissue
1452398_at	5.8	Plce1	phospholipase C, epsilon 1
1460419_a_at	5.8	Prkcb1	protein kinase C, beta 1
1436309_at	5.8	Neto2	neuropilin (NRP) and tolloid (TLL)-like 2
1435787_at	5.6	Ppm1l	protein phosphatase 1 (formerly 2C)-like
1419829_a_at	5.4	Gab2	Growth factor receptor bound protein 2-associated protein 2
1450700_at	5.4	Cdc42ep3	CDC42 effector protein (Rho GTPase binding) 3
1453282_at	5.4	Cxadr	coxsackievirus and adenovirus receptor
1435184_at	5.3	Npr3	natriuretic peptide receptor 3
1422504_at	5.3	Glrb	glycine receptor, beta subunit
1437422_at	5.2	Sema5a	sema domain, seven thrombospondin repeats (type 1 and type 1-like) 5A transmembrane domain (TM) and short cytoplasmic domain (semaphorin)
1455970_at	5.1	Pde5a	Phosphodiesterase 5A, cGMP-specific
1426992_at	5.1	Xpr1	xenotropic and polytropic retrovirus receptor 1
1441693_at	5.0	Adamts3	ADAM metallopeptidase with thrombospondin type 1 motif, 3

Adhesion, extracellular matrix

1427884_at	102.5	Col3a1	procollagen, type III, alpha 1
1419663_at	45.2	Ogn	osteoglycin
1449368_at	30.8	Dcn	decorin
1423607_at	29.2	Lum	lumican
1425476_at	22.3	Col4a5	procollagen, type IV, alpha 5
1449154_at	20.7	Col11a1	procollagen, type XI, alpha 1
1454830_at	18.2	Fbn2	fibrillin2
1435486_at	17.8	Pak3	P21 (CDKN1A)-activated kinase 3
1416114_at	16.8	Sparcl1	SPARC-like 1 (mast9, hevin)
1436223_at	14.5	Itgb8	Integrin beta 8
1420798_s_at	13.9	Pcdha8/Pcdha6	protocadherin alpha 8 /// protocadherin alpha 6 /// protocadherin

		/// Pcdha9	alpha 9 /// protocadherin alpha 5 /// protocadherin alpha 4
1425425_a_at	13.5	Wif1	Wnt inhibitory factor 1
1435120_at	13.4	Cdh11	Cadherin 11
1455622_at	13.2	Podxl2	podocalyxin-like 2
1455280_at	9.5	Frem1	Fras1 related extracellular matrix protein 1
1424010_at	8.9	Mfap4	microfibrillar-associated protein 4
1434679_at	8.5	Cspg3	chondroitin sulfate proteoglycan 3
1455978_a_at	8.3	Matn2	matrilin 2
1437467_at	7.9	Alcam	activated leukocyte cell adhesion molecule
1416136_at	7.8	Mmp2	matrix metalloproteinase 2
1448590_at	7.0	Col6a1	procollagen, type VI, alpha 1
1429310_at	6.4	Flrt3	fibronectin leucine rich transmembrane protein 3
1418815_at	6.1	Cdh2	cadherin 2
1449583_at	6.0	Pcdhb20	protocadherin beta 20
1452035_at	5.9	Col4a1	procollagen, type IV, alpha 1
1438532_at	5.7	Hmcn1	hemicentin 1
1417359_at	5.7	Mfap2	microfibrillar-associated protein 2
1455494_at	5.6	Col1a1	procollagen, type I, alpha 1
1436920_at	5.6	Pcdh17	protocadherin 17
1436678_at	5.3	---	Similar to beta-sarcoglycan
1435637_at	5.3	Itfg1	integrin alpha FG-GAP repeat containing 1
1424051_at	5.2	Col4a2	procollagen, type IV, alpha 2

Membrane, transport

1450779_at	155.4	Fabp7	fatty acid binding protein 7, brain
1455913_x_at	65.9	Ttr	transthyretin (prealbumin)
1423608_at	21.8	Itm2a	integral membrane protein 2A
1415885_at	16.2	Chgb	chromogranin B
1436719_at	15.5	Slc35f1	solute carrier family 35, member F1
1449264_at	9.2	Syt11	synaptotagmin 11
1433509_s_at	9.1	Reep1	receptor accessory protein 1
1450708_at	8.7	Scg2	secretogranin II
1445268_at	8.6	Copg2	Coatamer protein complex, subunit gamma 2
1455176_a_at	8.0	Syt11	synaptotagmin 11
1419186_a_at	8.0	Siat8d	sialyltransferase 8 (alpha-2, 8-sialyltransferase) D
1434728_at	7.8	Gria3	RIKEN cDNA E430013K19 gene
1438698_at	7.4	Tmem132C	transmembrane protein 132C
1455169_at	6.7	Rab11fip2	RAB11 family interacting protein 2 (class I)
1448734_at	6.4	Cp	ceruloplasmin
1448211_at	5.8	Atp6v0e2	ATPase, H+ transporting, lysosomal V0 subunit E2
1435396_at	5.7	Stxbp6	syntaxin binding protein 6 (amisyn)
1429809_at	5.6	Tmtc2	transmembrane and tetratricopeptide repeat containing 2

Organogenesis

1423506_a_at	39.4	Nnat	neuronatin
1449939_s_at	35.8	Dlk1	delta-like 1 homolog (Drosophila)
1455426_at	29.1	MGI:2662731	ES neuronal differentiation 3
1456060_at	20.3	Maf	avian musculoaponeurotic fibrosarcoma (v-maf) AS42 oncogene homolog
1451154_a_at	20.2	Cugbp2	CUG triplet repeat, RNA binding protein 2
1457632_s_at	13.8	Mrg1	myeloid ecotropic viral integration site-related gene 1
1420872_at	13.0	Gucy1b3	guanylate cyclase 1, soluble, beta 3
1448943_at	10.2	Nrp1	neuropilin 1
1448733_at	9.5	Bmi1	B lymphoma Mo-MLV insertion region 1
1429178_at	9.0	Odz3	odd Oz/ten-m homolog 3 (Drosophila)
1448201_at	8.7	Sfrp2	secreted frizzled-related sequence protein 2

1452913_at	8.4	Pcp41	Purkinje cell protein 4-like 1
1424659_at	8.4	Slit2	slit homolog 2 (Drosophila)
1418004_a_at	8.4	Tmem176B	transmembrane protein 176B
1423561_at	8.2	Nell2	nel-like 2 homolog (chicken)
1460359_at	8.0	Armxc3	armadillo repeat containing, X-linked 3
1422818_at	7.7	Nedd9	neural precursor cell expressed, developmentally down-regulated gene 9
1452792_at	6.3	Dzip1	DAZ interacting protein 1
1451691_at	7.4	Ednra	endothelin receptor type A
1456700_x_at	7.2	Marcks	Myristoylated alanine rich protein kinase C substrate
1448416_at	7.2	Mglap	matrix gamma-carboxyglutamate (gla) protein
1420621_a_at	6.4	App	amyloid beta (A4) precursor protein
1433716_x_at	6.1	Gfra2	glial cell line derived neurotrophic factor family receptor alpha 2
1429506_at	5.7	Nkd1	naked cuticle 1 homolog (Drosophila)
1421917_at	5.2	Pdgfra	platelet derived growth factor receptor, alpha polypeptide
1417073_a_at	5.0	Qk	quaking

Metabolism, peroxisome

1415897_a_at	13.8	Mgst1	microsomal glutathione S-transferase 1
1433428_x_at	9.3	Tgm2	transglutaminase 2, C polypeptide
1447903_x_at	9.0	Ap1s2	adaptor-related protein complex 1, sigma 2 subunit
1433551_at	8.1	Al427515	expressed sequence Al427515
1438413_at	7.7	Senp7	SUMO1/sentrin specific protease 7
1415949_at	7.6	Cpe	carboxypeptidase E
1438665_at	7.6	Smpd3	sphingomyelin phosphodiesterase 3, neutral
1450716_at	6.8	Adamts1	a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 1
1437339_s_at	6.4	Pcsk5	Proprotein convertase subtilisin/kexin type 5
1428718_at	6.0	Scrn1	secernin 1
1450105_at	5.4	Adam10	a disintegrin and metalloprotease domain 10
1423294_at	5.0	Mest	mesoderm specific transcript
1421840_at	5.0	Abca1	ATP-binding cassette, sub-family A (ABC1), member 1

Cytoskeleton, intermediate filaments

1418726_a_at	45.1	Tnnt2	troponin T2, cardiac
1437197_at	14.2	Sorbs2	sorbin and SH3 domain containing 2
1425506_at	8.0	Mylk	myosin, light polypeptide kinase
1418209_a_at	7.3	Pfn2	profilin 2
1435435_at	5.0	Ctnbp2	cortactin binding protein 2

Inflammatory response, cytokine

1448823_at	31.6	Cxcl12	chemokine (C-X-C motif) ligand 12
1417625_s_at	14.1	Cmkor1	chemokine orphan receptor 1
1448710_at	10.7	Cxcr4	chemokine (C-X-C motif) receptor 4
1417574_at	10.0	Cxcl12	chemokine (C-X-C motif) ligand 12

Enzymes, metalloproteinases

1424886_at	10.5	Ptprd	Protein tyrosine phosphatase, receptor type, D
1426621_a_at	9.6	Ppp2r2b	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52) beta isoform
1433855_at	9.5	Abat	4-aminobutyrate aminotransferase
1425452_s_at	5.4	Ptprj/AW125753	protein tyrosine phosphatase, receptor type, J /// expressed sequence AW125753

Cell cycle, cell growth

1423100_at	13.9	Fos	FBJ osteosarcoma oncogene
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1448494_at	13.8	Gas1	growth arrest specific 1
1448229_s_at	9.0	Ccnd2	cyclin D2
1455792_x_at	8.0	Ndn	necdin
1449303_at	5.4	Sesn3	sestrin 3
1417649_at	5.4	Cdkn1c	cyclin-dependent kinase inhibitor 1C (P57)
1416406_at	5.2	Pea15	phosphoprotein enriched in astrocytes 15

Others

1436600_at	29.5	Tnrc9	trinucleotide repeat containing 9
1418450_at	28.3	Islr	immunoglobulin superfamily containing leucine-rich repeat
1427320_at	17.5	Copg2as2	coatomer protein complex, subunit gamma 2, antisense 2
1448788_at	13.6	Cd200 /// 2300009N04Rik	Cd200 antigen /// RIKEN cDNA 2300009N04 gene
1451332_at	12.3	Zfp521	zinc finger protein 521
1448194_a_at	8.3	H19	H19 fetal liver mRNA
1423835_at	8.2	Zfp503	zinc finger protein 503
1434639_at	7.3	Kbtbd9	Kelch repeat and BTB (POZ) domain containing 9
1436938_at	7.1	Rbms3	RNA binding motif, single stranded interacting protein
1454822_x_at	7.1	Apcdd1	adenomatosis polyposis coli down-regulated 1
1437152_at	6.3	Rkhd3	ring finger and KH domain containing 3
1454867_at	5.9	LOC433938	Similar to dJ353E16.2 (meningioma (disrupted in balanced translocation) 1)
1456220_at	5.4	Fbxl7	F-box and leucine-rich repeat protein 7
1456063_at	5.3	Orf34	open reading frame 34
1456961_at	5.3	Eny2	enhancer of yellow 2 homolog (Drosophila)
1423672_at	5.0	Ttc30b	tetratricopeptide repeat domain 30B

RIKEN cDNA, unknown ESTs

1436293_x_at	17.6	D1Ert471e	DNA segment, Chr 1, ERATO Doi 471, expressed
1428097_at	14.4	2510009E07Rik	RIKEN cDNA 2510009E07 gene
1439990_at	10.1	---	12 days embryo spinal ganglion cDNA, RIKEN full-length enriched library, cl.:D130065P14 product:unknown EST, full insert sequence
1434788_at	9.3	D930050A07Rik	RIKEN cDNA D930050A07 gene
1455249_at	8.1	---	Hypothetical gene supported by AK029001
1436221_at	7.8	D1Ert471e	DNA segment, Chr 1, ERATO Doi 471, expressed
1435468_at	7.7	C76566	expressed sequence C76566
1436570_at	7.7	---	Transcribed locus
1455101_at	7.6	---	Mus musculus, clone IMAGE:2647821, mRNA
1454965_at	7.2	D430039N05Rik	RIKEN cDNA D430039N05 gene
1438989_s_at	7.0	B130021B11Rik	RIKEN cDNA B130021B11 gene
1455160_at	6.6	2610203C20Rik	RIKEN cDNA 2610203C20 gene
1443847_x_at	6.4	---	Transcribed locus
1428647_at	6.2	2310056B04Rik	RIKEN cDNA 2310056B04 gene
1436546_at	6.1	6330549D23Rik	RIKEN cDNA 6330549D23 gene
1453120_at	6.1	D2Bwg1356e	DNA segment, Chr 2, Brigham & Women's Genetics 1356 express.
1426766_at	6.1	6330403K07Rik	RIKEN cDNA 6330403K07 gene
1438531_at	6.1	A730054J21Rik	RIKEN cDNA A730054J21 gene
1435464_at	6.1	5430439C17Rik	RIKEN cDNA 5430439C17 gene
1455686_at	6.0	---	---
1460465_at	5.7	A930038C07Rik	RIKEN cDNA A930038C07 gene
1435087_at	5.6	BC039093	CDNA sequence BC039093
1438007_at	5.5	AI851790	expressed sequence AI851790
1439794_at	5.4	---	Transcribed locus
1433939_at	5.3	A730046J16	hypothetical protein A730046J16
1452762_at	5.3	8430436O14Rik	RIKEN cDNA 8430436O14 gene
1436246_at	5.3	---	Adult male medulla oblongata cDNA, RIKEN full-length enriched sequence library, cl.:6330566A22 product:unclassifiable, full insert

1428541_at	5.1	3321401G04Rik	RIKEN cDNA 3321401G04 gene
1436150_at	5.0	2310028H24Rik	RIKEN cDNA 2310028H24 gene

S2b: Pax4+ ES cells (0d) vs. committed progenitor cells at 5+16d

Probe ID	FC	Gene Symbol	Gene Title
Transcriptional regulation			
1418157_at	52.4	Nr2f1	nuclear receptor subfamily 2, group F, member 1
1436363_a_at	36.2	Nfix	nuclear factor I/X
1416158_at	32.8	Nr2f2	nuclear receptor subfamily 2, group F, member 2
1450533_a_at	30.6	Plagl1	pleiomorphic adenoma gene-like 1
1427680_a_at	27.7	Nfib	nuclear factor I/B
1450992_a_at	20.2	Meis1	myeloid ecotropic viral integration site 1
1429088_at	19.0	Lbh	limb-bud and heart
1427233_at	16.3	Sdccag33	Serologically defined colon cancer antigen 33
1437556_at	16.3	Zfhx4	zinc finger homeodomain 4
1421163_a_at	13.3	Nfia	nuclear factor I/A
1430526_a_at	13.3	Smarca2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2
1419583_at	12.0	Cbx4	chromobox homolog 4 (Drosophila Pc class)
1428433_at	11.9	Hipk2	homeodomain interacting protein kinase 2
1417447_at	11.0	Tcf21	transcription factor 21
1434856_at	10.3	Ankrd44	ankyrin repeat domain 44
1439774_at	9.4	Prrx1	paired related homeobox 1
1444615_x_at	9.2	Cbfa2t1h	CBFA2T1 identified gene homolog (human)
1449314_at	8.9	Zfpm2	zinc finger protein, multitype 2
1434298_at	8.2	Zeb2	zinc finger E-box binding homeobox 2
1423259_at	7.9	Irb4	inhibitor of DNA binding 4
1436994_a_at	7.8	Hist1h1c	histone 1, H1c
1421027_a_at	7.7	Mef2c	myocyte enhancer factor 2C
1448926_at	7.4	Hoxa5	homeo box A5
1421072_at	7.3	Irx5	Iroquois related homeobox 5 (Drosophila)
1416614_at	7.2	Cri1	CREBBP/EP300 inhibitory protein 1
1418733_at	7.1	Twist1	twist gene homolog 1 (Drosophila)
1424261_at	7.0	Zfp672	zinc finger protein 672
1429722_at	6.8	Zbtb4	zinc finger and BTB domain containing 4
1424029_at	6.7	Tspyl4	TSPY-like 4
1435078_at	6.6	Tanc2	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 2
1435866_s_at	6.4	Hist3h2a	histone 3, H2a
1427433_s_at	6.2	Hoxa3	homeo box A3
1449397_at	6.2	Hoxb2	homeo box B2
1418496_at	6.0	Foxa1	forkhead box A1
1447643_x_at	6.0	Snai2 = slug	snail homolog 2 (Drosophila)
1437598_at	5.9	Zbtb20	zinc finger and BTB domain containing 20
1452381_at	5.8	Creb3l2	cAMP responsive element binding protein 3-like 2
1460246_at	5.3	Mecp2	methyl CpG binding protein 2
1421908_a_at	5.3	Tcf12	transcription factor 12
Signaling, growth factors			
1448254_at	218.9	Ptn	pleiotrophin
1437347_at	64.9	Ednrb	endothelin receptor type B
1456741_s_at	53.9	Gpm6a	glycoprotein m6a
1452114_s_at	41.8	Igfbp5	insulin-like growth factor binding protein 5
1423091_a_at	38.9	Gpm6b	glycoprotein m6b
1434413_at	32.4	Igf1	insulin-like growth factor (Igf1)
1425575_at	32.2	Epha3	Eph receptor A3

1436659_at	24.1	Dcamk1l	Double cortin and calcium/calmodulin-dependent protein kinase-like 1
1423584_at	20.1	Igfbp7	insulin-like growth factor binding protein 7
1416846_a_at	20.1	Pdzrn3	PDZ domain containing RING finger 3
1433968_a_at	19.5	Megf9	Multiple EGF-like-domains 9
1434881_s_at	18.6	Kctd12	potassium channel tetramerisation domain containing 12
1415806_at	16.0	Plat	plasminogen activator. tissue
1436736_x_at	15.5	D0H4S114	DNA segment. human D4S114
1438658_a_at	15.3	Edg3	endothelial differentiation. sphingolipid G-protein-coupled recept. 3
1456609_at	14.8	Camk2n1	calcium/calmodulin-dependent protein kinase II inhibitor 1
1448152_at	14.1	Igf2	insulin-like growth factor 2
1436791_at	13.9	Wnt5a	wingless-related MMTV integration site 5A
1437284_at	13.6	Fzd1	frizzled homolog 1 (Drosophila)
1448259_at	13.4	Fstl1	follistatin-like 1
1418379_s_at	11.9	Gpr124	G protein-coupled receptor 124
1420859_at	11.6	Pkia	protein kinase inhibitor. alpha
1423756_s_at	11.1	Igfbp4	insulin-like growth factor binding protein 4
1426397_at	10.6	Tgfbr2	transforming growth factor. beta receptor II
1420512_at	10.4	Dkk2	dickkopf homolog 2 (Xenopus laevis)
1418049_at	10.1	Ltbp3	latent transforming growth factor beta binding protein 3
1451446_at	9.0	Antxr1	anthrax toxin receptor 1
1448933_at	8.8	Pcdhb17	protocadherin beta 17
1419248_at	8.5	Rgs2	regulator of G-protein signaling 2
1438664_at	8.0	Prkar2b	protein kinase. cAMP dependent regulatory. type II beta
1421045_at	7.6	Mrc2	mannose receptor. C type 2
1418892_at	7.5	Rhoj	ras homolog gene family. member J
1422890_at	7.3	Pcdh18	protocadherin 18
1419922_s_at	7.3	Atrnl1	RIKEN cDNA E430016L07 gene
1421425_a_at	7.2	Dscr11l	Down syndrome critical region gene 1-like 1
1433434_at	7.1	AW551984	expressed sequence AW551984
1423104_at	6.7	Irs1	insulin receptor substrate 1
1450047_at	6.7	Hs6st2	heparan sulfate 6-O-sulfotransferase 2
1423805_at	6.7	Dab2	disabled homolog 2 (Drosophila)
1422293_a_at	6.6	Kctd1	potassium channel tetramerisation domain containing 1
1452251_at	6.5	Nbea	neurobeachin
1423825_at	6.2	Gpr177	G protein-coupled receptor 177
1449893_a_at	6.1	Lrig1	leucine-rich repeats and immunoglobulin-like domains 1
1420406_at	5.6	Peg12	paternally expressed 12
1437409_s_at	5.5	Gpr126	G protein-coupled receptor 126
1454675_at	5.4	Thra	thyroid hormone receptor alpha
1427191_at	5.4	Npr2	natriuretic peptide receptor 2
1428603_at	5.4	Glcci1	glucocorticoid induced transcript 1
1452014_a_at	5.2	Igf1	insulin-like growth factor 1

Adhesion, extracellular matrix

1427883_a_at	240.1	Col3a1	procollagen. type III. alpha 1
1450757_at	117.0	Cdh11	cadherin 11
1449368_at	70.0	Dcn	decorin
1419663_at	55.3	Ogn	osteoglycin
1423607_at	50.2	Lum	lumican
1423110_at	46.3	Col1a2	procollagen. type I. alpha 2
1423606_at	42.6	Postn	periostin. osteoblast specific factor
1423669_at	39.7	Col1a1	procollagen. type I. alpha 1
1425476_at	35.3	Col4a5	procollagen. type IV. alpha 5
1448162_at	34.4	Vcam1	vascular cell adhesion molecule 1
1448228_at	31.9	Lox	lysyl oxidase

1455978_a_at	29.8	Matn2	matrilin 2
1448590_at	26.7	Col6a1	procollagen. type VI. alpha 1
1449154_at	23.6	Col11a1	procollagen. type XI. alpha 1
1416405_at	22.0	Bgn	biglycan
1416342_at	20.3	Tnc	tenascin C
1416114_at	19.3	Sparcl1	SPARC-like 1 (mast9. hevin)
1454830_at	16.5	Fbn2	fibrillin2
1426865_a_at	15.9	Ncam1	neural cell adhesion molecule 1
1422437_at	15.8	Col5a2	procollagen. type V. alpha 2
1460208_at	14.7	Fbn1	fibrillin 1
1455096_at	14.4	Flrt2	fibronectin leucine rich transmembrane protein 2
1455627_at	14.0	Col8a1	procollagen. type VIII. alpha 1
1437467_at	13.3	Alcam	activated leukocyte cell adhesion molecule
1456214_at	13.1	Pcdh7	protocadherin 7
1452250_a_at	12.3	Col6a2	procollagen. type VI. alpha 2
1422571_at	11.7	Thbs2	thrombospondin 2
1437360_at	11.0	Pcdh19	Protocadherin 19
1456250_x_at	10.6	Tgfb1	transforming growth factor. beta induced
1424010_at	9.8	Mfap4	microfibrillar-associated protein 4
1416740_at	9.4	Col5a1	procollagen. type V. alpha 1
1424131_at	8.6	Col6a3	procollagen. type VI. alpha 3
1424807_at	8.5	Lama4	laminin. alpha 4
1451342_at	8.3	Spon1	spondin 1. (f-spondin) extracellular matrix protein
1416136_at	8.2	Mmp2	matrix metalloproteinase 2
1455688_at	7.9	Ddr2	discoidin domain receptor family. member 2
1424051_at	7.7	Col4a2	procollagen. type IV. alpha 2
1418815_at	7.4	Cdh2	cadherin 2
1452035_at	6.9	Col4a1	procollagen. type IV. alpha 1
1431375_s_at	6.2	Parva	parvin. alpha
1433586_at	6.1	Rgmb	RGM domain family. member B
1416666_at	5.8	Serpine2	serine (or cysteine) proteinase inhibitor. clade E. member 2
1437417_s_at	5.5	Gpc6	glypican 6
1417359_at	5.4	Mfap2	microfibrillar-associated protein 2
1436920_at	5.3	Pcdh17	protocadherin 17
1456392_at	5.1	Negr1	neuronal growth regulator 1

Membrane, transport

1450779_at	115.0	Fabp7	fatty acid binding protein 7. brain
1417900_a_at	10.7	Vldlr	very low density lipoprotein receptor
1416612_at	10.5	Cyp1b1	cytochrome P450. family 1. subfamily b. polypeptide 1
1416803_at	8.0	Fkbp7	FK506 binding protein 7
1452357_at	6.4	Gp1bb /// Sept5	glycoprotein Ib. beta polypeptide /// septin 5
1445268_at	6.2	Copg2	Coatomer protein complex. subunit gamma 2
1436566_at	5.9	Rab40b	Rab40b. member RAS oncogene family
1433481_at	5.3	Fkbp14	FK506 binding protein 14
1429809_at	5.2	Tmtc2	transmembrane and tetratricopeptide repeat containing 2
1415986_at	5.1	Clcn4-2	chloride channel 4-2
1416343_a_at	5.0	Lamp2	lysosomal membrane glycoprotein 2
1415961_at	5.0	Itn2c	integral membrane protein 2C
1448972_at	5.0	Gria1	glutamate receptor. ionotropic. AMPA1 (alpha 1)

Organogenesis

1448943_at	35.9	Nrp1	neuropilin 1
1448416_at	26.4	Mglap	matrix gamma-carboxyglutamate (gla) protein
1441137_at	14.9	Bicc1	Bicaudal C homolog 1 (Drosophila)
1417129_a_at	13.5	Mrg1	myeloid ecotropic viral integration site-related gene 1

1418004_a_at	17.8	Tmem176B	transmembrane protein 176B
1456060_at	11.5	Maf	avian musculoaponeurotic fibrosarcoma (v-maf) AS42 oncogene homolog
1424659_at	11.3	Slit2	slit homolog 2 (Drosophila)
1425603_at	10.9	Tmem176A	transmembrane protein 176A
1451691_at	9.9	Ednra	endothelin receptor type A
1420621_a_at	9.8	App	amyloid beta (A4) precursor protein
1448733_at	9.3	Bmi1	B lymphoma Mo-MLV insertion region 1
1454674_at	8.9	Fez1	fasciculation and elongation protein zeta 1 (zygin I)
1422818_at	8.8	Neddd9	neural precursor cell expressed. developmentally down-regulated gene 9
1423561_at	8.7	Nell2	nel-like 2 homolog (chicken)
1460359_at	8.5	Armcx3	armadillo repeat containing. X-linked 3
1415973_at	7.7	Marcks	Myristoylated alanine rich protein kinase C substrate
1454974_at	7.5	Ntn1	netrin 1
1454613_at	7.5	Dpysl3	Dihydropyrimidinase-like 3
1448475_at	7.4	Olfml3	olfactomedin-like 3
1451154_a_at	7.1	Cugbp2	CUG triplet repeat.RNA binding protein 2
1417073_a_at	7.0	Qk	quaking
1436970_a_at	6.9	Pdgfrb	platelet derived growth factor receptor. beta polypeptide
1434106_at	6.6	Epm2aip1	EPM2A (laforin) interacting protein 1
1428393_at	6.0	Nrn1	neuritin 1
1417847_at	5.9	Ulk2	Unc-51 like kinase 2 (C. elegans)
1455812_x_at	5.6	Slit2	Slit-like 2 (Drosophila)
1426869_at	5.5	Boc	biregional cell adhesion molecule-related/down-regulated by oncogenes (Cdon) binding protein
1426680_at	5.3	Seprn1	selenoprotein N. 1
1418285_at	5.2	Efnb1	ephrin B1
1453622_s_at	5.2	Mllt3	myeloid/lymphoid or mixed lineage-leukemia translocation to 3 homolog (Drosophila)
1436959_x_at	5.0	Nelf	nasal embryonic LHRH factor

Metabolism, peroxisome

1415897_a_at	10.5	Mgst1	microsomal glutathione S-transferase 1
1415949_at	10.0	Cpe	carboxypeptidase E
1433428_x_at	9.1	Tgm2	transglutaminase 2. C polypeptide
1447903_x_at	8.0	Ap1s2	adaptor-related protein complex 1. sigma 2 subunit
1450843_a_at	7.5	Serpinh1	serine (or cysteine) proteinase inhibitor. clade H. member 1
1417492_at	7.2	Ctsb	cathepsin B
1438413_at	7.0	Senp7	SUMO1/sentrin specific protease 7
1450716_at	6.4	Adamts1	a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif. 1
1454997_at	6.0	Msrb3	methionine sulfoxide reductase B3
1437568_at	5.7	Mmp16	matrix metalloproteinase 16
1428791_at	5.6	Ube2h	ubiquitin-conjugating enzyme E2H
1433501_at	5.1	Ctso	cathepsin O

Cytoskeleton, intermediate filaments

1418726_a_at	26.1	Tnnt2	troponin T2. cardiac
1415927_at	15.0	Actc1	actin. alpha. cardiac
1425506_at	10.8	Mylk	myosin. light polypeptide kinase
1437197_at	9.0	Sorbs2	sorbin and SH3 domain containing 2
1418209_a_at	8.5	Pfn2	profilin 2
1440990_at	6.3	Kif26b	kinesin family member 26B

Inflammatory response, cytokine

1448823_at	22.2	Cxcl12	chemokine (C-X-C motif) ligand 12
1417625_s_at	9.0	Cmkor1	chemokine orphan receptor 1

Enzymes, metalloproteinases

1449335_at	12.3	Timp3	tissue inhibitor of metalloproteinase 3
1454677_at	12.1	Timp2	tissue inhibitor of metalloproteinase 2
1416498_at	5.1	Ppic	peptidylprolyl isomerase C
1426621_a_at	5.0	Ppp2r2b	protein phosphatase 2 (formerly 2A). regulatory subunit B (PR 52). beta isoform

Cell cycle, cell growth

1416855_at	28.9	Gas1	growth arrest specific 1
1434745_at	21.3	Ccnd2	cyclin D2
1448233_at	8.4	Prnp	prion protein
1455792_x_at	7.8	Ndn	neclin
1437101_at	6.5	Lats2	Large tumor suppressor 2
1417399_at	6.4	Gas6	growth arrest specific 6
1448655_at	6.0	Lrp1	low density lipoprotein receptor-related protein 1
1416406_at	5.0	Pea15	phosphoprotein enriched in astrocytes 15

Others

1418450_at	44.2	Islr	immunoglobulin superfamily containing leucine-rich repeat
1448788_at	16.5	Cd200 /// 2300009N04Rik	Cd200 antigen /// RIKEN cDNA 2300009N04 gene
1436938_at	14.9	Rbms3	RNA binding motif, single stranded interacting protein
1424186_at	13.5	Ccdc80	coiled-coil domain containing 80
1451332_at	12.8	Zfp521	zinc finger protein 521
1423835_at	11.2	Zfp503	zinc finger protein 503
1428187_at	10.3	Cd47	CD47 antigen (Rh-related antigen, integrin-associated signal transducer)
1433776_at	9.9	Lhfp	lipoma HMGIC fusion partner
1449070_x_at	9.7	Apcdd1	adenomatous polyposis coli down-regulated 1
1454867_at	7.5	LOC433938	Similar to dJ353E16.2 (meningioma (disrupted in balanced translocation) 1)
1454630_at	6.5	Samd14	sterile alpha motif domain containing 14
1434825_at	6.2	Zfp469	Zinc finger protein 469
1426306_a_at	6.2	Maged2	melanoma antigen, family D, 2
1422064_a_at	5.5	Zbtb20	zinc finger and BTB domain containing 20
1424970_at	5.2	Purg	purine-rich element binding protein G
1421871_at	5.1	Sh3bgrl	SH3-binding domain glutamic acid-rich protein like
1416401_at	5.1	Kai1	kangai 1 (suppression of tumorigenicity 6, prostate)
1433812_at	5.0	Lix1l	Lix1-like
1419584_at	5.0	Ttc28	tetratricopeptide repeat domain 28
1423672_at	5.0	Ttc30b	tetratricopeptide repeat domain 30B

RIKEN cDNA, unknown ESTs

1427932_s_at	34.1	1200016E24Rik/// 1200015M12Rik/// 1200003I10Rik	RIKEN cDNA 1200016E24 gene /// RIKEN cDNA 1200015M12 gene /// RIKEN cDNA 1200003I10 gene
1435137_s_at	32.7	1200015M12Rik	RIKEN cDNA 1200015M12 gene
1455160_at	19.1	2610203C20Rik	RIKEN cDNA 2610203C20 gene
1436223_at	17.1	---	0 day neonate kidney cDNA. RIKEN full-length enriched library. clone:D630049N15 product:unknown EST, full insert sequence
1436546_at	12.9	6330549D23Rik	RIKEN cDNA 6330549D23 gene
1438531_at	12.9	A730054J21Rik	RIKEN cDNA A730054J21 gene
1428097_at	10.8	2510009E07Rik	RIKEN cDNA 2510009E07 gene

1428861_at	10.7	4631422O05Rik	RIKEN cDNA 4631422O05 gene
1456130_at	10.5	---	CDNA clone IMAGE:6741091
1452762_at	9.1	8430436O14Rik	RIKEN cDNA 8430436O14 gene
1453266_at	8.1	9230111I22Rik	RIKEN cDNA 9230111I22 gene
1455249_at	7.7	---	Hypothetical gene supported by AK029001
1428432_at	7.6	2310047A01Rik	RIKEN cDNA 2310047A01 gene
1451127_at	7.5	AW146242	expressed sequence AW146242
1435087_at	7.1	BC039093	CDNA sequence BC039093
1427108_at	7.0	9530068E07Rik	RIKEN cDNA 9530068E07 gene
1426766_at	6.9	6330403K07Rik	RIKEN cDNA 6330403K07 gene
1428541_at	6.8	3321401G04Rik	RIKEN cDNA 3321401G04 gene
1439990_at	6.7	---	12 days embryo spinal ganglion cDNA, RIKEN full-length enriched Library, clone:D130065P14 product:unknown EST, full insert seq.
1435468_at	6.6	C76566	expressed sequence C76566
1424099_at	6.3	2310016C16Rik	RIKEN cDNA 2310016C16 gene
1448648_at	6.2	9130005N14Rik	RIKEN cDNA 9130005N14 gene
1443847_x_at	5.8	---	Transcribed locus
1429281_at	5.5	2610008E11Rik	RIKEN cDNA 2610008E11 gene
1436150_at	5.2	2310028H24Rik	RIKEN cDNA 2310028H24 gene
1453208_at	5.2	2700089E24Rik	RIKEN cDNA 2700089E24 gene
1428647_at	5.1	2310056B04Rik	RIKEN cDNA 2310056B04 gene
1434423_at	5.1	---	Transcribed locus
1437291_at	5.1	2700081O15Rik	RIKEN cDNA 2700081O15 gene
1436570_at	5.0	---	Transcribed locus
1429065_at	5.0	1700023M03Rik	RIKEN cDNA 1700023M03 gene
1439496_at	5.0	4921524J06Rik	RIKEN cDNA 4921524J06 gene
1428103_at	5.0	---	---

Suppl. Table S3. List of transcripts two- or more-fold up-regulated in wt ES cells (6d) vs. multilineage progenitor cells at 5-9d (FC: fold change)

Probe ID	Gene symbol	Gene title	FC wt-ESC (6d) vs. wt-5-9d gpph	gccc	gocm	unigene	refseqp	refseqt	test_wt-ESC (6d) vs. wt-5-9d signal	wt-ESC (6d) signal	wt-5-9d signal
148254_a	Ptn	pliotropin	76.2	74 / regulation of cell cycle // in 5578 / extracellular matrix // 18033 / growth factor activity	MM.27960	NP_030499.NM_008973	9.36537e-006	43.0	327.4	389.3	
148284_a	Cc3h1	procollagen, type III, alpha 1	75.6	6817 / phosphatase transport // in 5578 / troponin complex // 15007 / structural constituent of muscle	MM.24740	NP_034060.NM_009390	1.001747e-007	30.0	52.0	38.0	
1481726_a	Tnnc2	troponin T, cardiac	67.4	6936 / muscle contraction // in 5578 / troponin complex // 15007 / structural constituent of muscle	MM.24740	NP_030749.NM_011619	4.19026e-006	18.7	126.0	13.0	
1483747_a	Ednrb	endothelin receptor type B	59.7	1755 / neural crest cell migrates // 5615 / extracellular space // 1584 / rhodopsin-like receptor	MM.22952	NP_031930.NM_007904	4.7024e-009	20.3	120.9	23.0	
1483872_a	Gucy1b3	guanylate cyclase 1, soluble, beta-3	42.7	6182 / cGMP biosynthesis // in 5578 / cytoplasm // in 5578 / guanylate cyclase	MM.24545	NP_030442.NM_017469	6.02094e-004	21.0	89.2	69.2	
1450533_a	Plagl1	pleiomorphic adenoma gene-like 1	38.1	74 / regulation of cell cycle // in 5578 / extracellular space // 15059 / calcium ion binding // in 5578	MM.28787	NP_033564.NM_009538	3.21202e-006	60.6	230.2	120.2	
1449939_a	DK1	delta-1-like protein (Drosophila)	38.2	---	---	---	3.94822e-006	399.1	15227.8	15227.8	
1483041_a	---	---	30.9	---	---	---	1.41722e-006	56.8	174.7	56.8	
1453351_a	RIKEN cDNA 943001M06 gene	---	27.9	---	---	---	3.61476e-006	28.6	74.2	28.6	
1423607_a	Lum	luciferin	27.8	---	---	---	0.0011956	144.8	403.5	144.8	
1418157_a	NC21	nucleus receptor subfamily 2, group F, member 1	29.2	74 / regulation of cell cycle // in 5578 / extracellular matrix // 18033 / growth factor activity	MM.14297	NP_034061.NM_010151	0.000794775	50.0	789.2	50.0	
1424867_a	Tnnc2	troponin T, cardiac	25.4	6936 / muscle contraction // in 5578 / troponin complex // 15007 / structural constituent of muscle	MM.24740	NP_030749.NM_011619	2.68884e-006	45.4	112.1	45.4	
1454881_a	Ubp3c	ubiquitin 3	25.0	---	---	---	0.000743072	70.3	1759.0	70.3	
1423596_a	Nnt1	nucleoside diphosphate kinase 1	23.8	770 / development // in 5578 / endoplasmic reticulum	MM.23669	NP_030503.NM_010023	7.12281e-006	21.2	519.0	21.2	
1452575_a	Epha3	Eph receptor A3	22.0	6468 / protein amino acid phosphatase // 4672 / protein kinase activity	MM.1977	NP_034270.NM_010140	7.65313e-007	23.2	51.2	23.2	
1448823_a	Cxcl12	chemokine (C-X-C motif) ligand 12	21.0	6935 / chemokines // in 5578 / extracellular region // 5125 / cytokine activity	MM.30321	NP_0010124.NM_0010124	1.74034e-007	59.8	1253.2	59.8	
1423422_a	Ast4	arabinoside repeat and SOCS box-containing protein 4	20.5	6355 / regulation of transcription // in 5578 / DNA binding // in 5578 / nuclear acid binding	MM.51340	NP_075535.NM_022048	0.001155118	22.2	454.3	22.2	
1417574_a	Cxcl12	chemokine (C-X-C motif) ligand 12	20.3	6935 / chemokines // in 5578 / extracellular region // 5125 / cytokine activity	MM.30321	NP_0010124.NM_0010124	1.37514e-008	47.9	97.0	47.9	
1455426_a	MGI2662731	ES neuron differentiation 3	19.9	---	---	---	8.92211e-006	25.0	496.1	25.0	
1423919_a	Ast4	arabinoside repeat and SOCS box-containing protein 4	19.1	6355 / regulation of transcription // in 5578 / DNA binding // in 5578 / nuclear acid binding	MM.51340	NP_075535.NM_022048	7.59949e-007	31.3	596.4	31.3	
1424890_a	Bnc1	basonuclin 1	18.8	6350 / transcription // in 5578 / nucleus // in 5578 / protein kinase activity	MM.24802	NP_031588.NM_007562	0.80690e-005	57.2	1075.1	57.2	
1423608_a	Imn2a	integral membrane protein 2A	18.7	---	---	---	4.74869e-007	46.6	871.8	46.6	
1436001_a	Tnnc3	troponin C, cardiac	18.0	5534 / nucleus // in 5578 / troponin complex // 15007 / structural constituent of muscle	MM.20275	NP_065010.NM_127313	0.004008979	33.7	603.5	33.7	
1457532_a	Mrg1	myeloid ectopic viral integration site-related gene 1	17.9	1654 / eye morphogenesis // in 5578 / nucleus // in 5578 / DNA binding // in 5578 / protein kinase activity	MM.24756	NP_034955.NM_010825	2.14064e-008	78.7	1405.6	78.7	
1418486_a	Vnn1	vanin 1	17.7	6807 / nitrogen compound meta-5615 / extracellular space // 16787 / hydrolase activity	MM.27154	NP_038343.NM_011704	0.000275632	37.1	655.6	37.1	
1449342_a	Myh6	myosin heavy polypeptide 6, cardiac muscle, alpha	16.8	1525 / angiogenesis // in 5578 / plasma membrane // 4872 / receptor activity	MM.25174	NP_032763.NM_008737	3.31327e-005	340.3	571.1	340.3	
1425454_a	Gta6b	GATA binding protein 6	16.6	6350 / transcription // in 5578 / nucleus // in 5578 / DNA binding // in 5578 / protein kinase activity	MM.32927	NP_034358.NM_010258	3.33856e-006	116.5	1535.6	116.5	
1417129_a	Mrg1	myeloid ectopic viral integration site-related gene 1	16.2	1654 / eye morphogenesis // in 5578 / nucleus // in 5578 / DNA binding // in 5578 / protein kinase activity	MM.24756	NP_034955.NM_010825	5.62882e-009	100.5	1629.1	100.5	
1448826_a	Myh6	myosin heavy polypeptide 6, cardiac muscle, alpha	16.1	6941 / striated muscle contract-5858 / cytoskeleton // in 5578 / motor activity	MM.30063	NP_034986.NM_010856	0.001017221	55.7	868.2	55.7	
1452463_a	Gta6b	GATA binding protein 6	15.8	1525 / angiogenesis // in 5578 / plasma membrane // 4872 / receptor activity	MM.25174	NP_032763.NM_008737	6.82596e-005	199.2	442.2	199.2	
1450922_a	Mes1	myeloid ectopic viral integration site 1	15.8	6355 / regulation of transcription // in 5578 / nucleus // in 5578 / DNA binding // in 5578 / protein kinase activity	MM.35678	NP_034919.NM_010789	0.003450747	47.1	743.4	47.1	
1416211_a	Pln	pleiotrophin	15.8	74 / regulation of cell cycle // in 5578 / extracellular matrix // 18033 / growth factor activity	MM.27960	NP_030919.NM_008973	8.05666e-007	127.5	2009.9	127.5	
1417625_a	Ctscr1	cutaneous melanocyte stem cell receptor 1	15.4	6935 / cell adhesion // in 5578 / extracellular matrix // 18033 / growth factor activity	MM.20722	NP_049716.NM_009432	1.94974e-006	92.0	524.3	92.0	
1426208_a	Plagl1	Pleiomorphic adenoma gene-like 1	15.3	74 / regulation of cell cycle // in 5578 / extracellular matrix // 18033 / growth factor activity	MM.28787	NP_033564.NM_009538	2.28948e-005	123.4	1885.6	123.4	
1428571_a	Col1a1	collagen, type I, alpha 1	15.2	6817 / phosphatase transport // in 5578 / extracellular matrix // 1518 / structural molecule acM	MM.54662	NP_031766.NM_007740	5.50092e-005	47.6	72.1	47.6	
1425478_a	Ubp3c	ubiquitin 3	15.2	1155 / ubiquitin conjugation // in 5578 / extracellular matrix // 1518 / structural molecule acM	MM.29884	NP_031874.NM_007376	0.002934573	160.1	250.1	160.1	
1455280_a	Frem1	Fra1 related extracellular matrix protein 1	14.9	7160 / cell-matrix adhesion // in 5578 / plasma membrane // 4872 / receptor activity	MM.24672	NP_080531.NM_177863	1.84341e-006	19.1	283.5	19.1	
1418094_a	Nrp1	neuropilin 1	14.2	1525 / angiogenesis // in 5578 / plasma membrane // 4872 / receptor activity	MM.27145	NP_032763.NM_008737	1.03926e-006	233.0	331.4	233.0	
1422580_a	My4	myosin I, alpha 1	14.2	7010 / cytoskeleton organization // in 5578 / cytoskeleton // in 5578 / motor activity	MM.21929	NP_030949.NM_010969	9.30649e-005	69.8	442.2	69.8	
1450078_a	Nrk	Nrk related kinase	14.2	6468 / protein amino acid phosphatase // 4672 / protein kinase activity	MM.22367	NP_038752.NM_013724	0.93866e-005	48.4	685.4	48.4	
1451047_a	Imn2a	integral membrane protein 2A	14.0	---	---	---	9.02441e-006	58.4	819.2	58.4	
1423922_a	Kc2f7	transmembrane 2, basic, gene 7	13.1	7010 / cytoskeleton organization // in 5578 / cytoskeleton // in 5578 / motor activity	MM.23678	NP_040526.NM_009873	2.15464e-009	29.9	442.2	29.9	
1452141_a	Sepp1	selenoprotein P, plasma, 1	13.3	1887 / selenium metabolism // in 5578 / extracellular region // 5125 / cytokine activity	MM.29269	NP_033181.NM_009155	0.000918233	260.4	3471.0	260.4	
1452114_a	Igf5b5	insulin-like growth factor binding protein 5	13.2	1558 / regulation of cell growth // in 5578 / extracellular region // 5125 / insulin-like growth factor	MM.30917	NP_034648.NM_010518	0.000418018	246.0	3299.2	246.0	
1449844_a	Nrp1	neuropilin 1	12.8	1525 / angiogenesis // in 5578 / plasma membrane // 4872 / receptor activity	MM.27145	NP_032763.NM_008737	3.82374e-007	205.1	205.1	205.1	
1436736_a	---	---	12.6	---	---	---	0.000349551	354.5	4475.9	354.5	
1427883_a	Col3a1	collagen, type III, alpha 1	12.5	6817 / phosphatase transport // in 5578 / extracellular matrix // 1518 / structural molecule acM	MM.24955	NP_034060.NM_009390	2.30033e-006	136.8	1667.4	136.8	
1416761_a	Col3a1	collagen, type III, alpha 1	12.4	---	---	---	8.26237e-009	132.0	1841.6	132.0	
1418157_a	Itih3	Itih3 related homeobox 3 (Drosophila)	12.2	6355 / regulation of transcription // in 5578 / nucleus // in 5578 / DNA binding // in 5578 / protein kinase activity	MM.23044	NP_032419.NM_008393	4.43898e-005	11.8	1239.0	11.8	
1451342_a	Spon11	spondin 1, (spondin) extracellular matrix protein	12.2	7155 / cell adhesion // in 5578 / extracellular matrix // 5515 / protein binding // in 5578 / protein kinase activity	MM.31410	NP_063659.NM_145584	0.000394746	46.8	569.1	46.8	
1450839_a	DNM3H11	dishevelled homolog 11	12.1	7015 / regulation of transcription // in 5578 / nucleus // in 5578 / DNA binding // in 5578 / protein kinase activity	MM.25174	NP_032763.NM_008737	6.82596e-005	199.2	442.2	199.2	
1450079_a	Nrk	Nrk related kinase	11.8	6468 / protein amino acid phosphatase // 4672 / protein kinase activity	MM.22367	NP_038752.NM_013724	1.16124e-005	101.0	1203.2	101.0	
1417447_a	Tcf21	transcription factor 21	11.8	6350 / transcription // in 5578 / nucleus // in 5578 / DNA binding // in 5578 / protein kinase activity	MM.16497	NP_030675.NM_011545	1.83273e-005	45.3	534.5	45.3	
1433026_a	Tgm2	transglutaminase 2, C polypeptide	11.7	6508 / proteolysis and peptidolysis // 5737 / cytoplasm // in 5578 / protein-glutamine gamma-glutamyl	MM.30754	NP_033399.NM_009373	0.000399111	99.3	2304.0	99.3	
1456502_a	Mal2	avian myeloblastosis-oncogene (fms-like) 2	11.6	74 / regulation of cell cycle // in 5578 / extracellular matrix // 18033 / growth factor activity	MM.27549	NP_030919.NM_008973	0.000037949	86.9	1003.6	86.9	
1454530_a	Flnb2	fibronectin 2	11.5	30326 / embryonic limb morph-1527 / microtubul // traceab // 5509 / calcium ion binding // in 5578	MM.20271	NP_034311.NM_010171	0.000034581	106.6	1228.7	106.6	
1448494_a	Gas1	growth arrest specific 1	11.5	7049 / cell cycle // in 5578 / membrane // in 5578 / protein binding // in 5578 / protein kinase activity	MM.22701	NP_032112.NM_008086	2.10105e-007	181.5	2086.7	181.5	
1448154_a	Col11a1	collagen, type XI, alpha 1	11.5	1520 / cytoskeleton organization // in 5578 / cytoskeleton // in 5578 / motor activity	MM.20728	NP_030949.NM_010969	8.61956e-005	92.0	524.3	92.0	
1429206_a	Rhoib1	Rho-related BTB domain containing 1	11.5	7264 / cell-matrix adhesion // in 5578 / plasma membrane // 4872 / receptor activity	MM.28659	XP_125637.XM_125637	2.00087e-007	65.9	758.3	65.9	
1450646_a	Ctfr1	complement component 1, a subcomponent, receptor 1	11.5	6952 / defense response // in 5578 / extracellular space // 4872 / receptor activity	MM.681	NP_034870.NM_010740	1.79786e-006	45.8	525.7	45.8	
1450250_a	Tgfr	transforming growth factor 20	11.5	6952 / defense response // in 5578 / extracellular space // 4872 / receptor activity	MM.681	NP_034870.NM_010740	1.79786e-006	45.8	525.7	45.8	
1419248_a	Rgs2	regulator of G-protein signaling 2	11.5	7049 / cell cycle // in 5578 / membrane // in 5578 / protein binding // in 5578 / protein kinase activity	MM.22701	NP_032112.NM_008086	2.10105e-007	181.5	2086.7	181.5	
1419599_a	Ctfr1	complement component 1, a subcomponent, receptor 1	11.0	6952 / defense response // in 5578 / extracellular space // 4872 / receptor activity	MM.681	NP_034870.NM_010740	1.79786e-006	45.8	525.7	45.8	
1419599_a	Bcl1	Bcl1 related kinase	10.7	6355 / regulation of transcription // in 5578 / nucleus // in 5578 / DNA binding // in 5578 / protein kinase activity	MM.29884	NP_031874.NM_007376	0.002934573	160.1	250.1	160.1	
1437277_a	Tgm2	transglutaminase 2, C polypeptide	10.7	6508 / proteolysis and peptidolysis // 5737 / cytoplasm // in 5578 / protein-glutamine gamma-glutamyl	MM.330731	NP_033399.NM_009373	1.27294e-005	211.6	2263.4	211.6	
1416855_a	Gas1	growth arrest specific 1	10.7	7049 / cell cycle // in 5578 / membrane // in 5578 / protein binding // in 5578 / protein kinase activity	MM.22701	NP_032112.NM_008086	1.62425e-007	377.2	3810.6	377.2	
1416855_a	NC22	nucleus receptor subfamily 2, group F, member 2	10.7	1764 / cell adhesion // in 5578 / extracellular matrix // 18033 / growth factor activity	MM.25174	NP_032763.NM_008737	6.82596e-005	199.2	442.2	199.2	
1420871_a	Gucy1b3	guanylate cyclase 1, soluble, beta 3	10.3	6182 / cGMP biosynthesis // in 5578 / cytoplasm // in 5578 / guanylate cyclase	MM.24545	NP_030442.NM_017469	0.000217178	74.1	765.9	74.1	
1447849_a	Mal2	avian myeloblastosis-oncogene (fms-like) 2	10.3	74 / regulation of cell cycle // in 5578 / extracellular matrix // 18033 / growth factor activity	MM.27549	NP_030919.NM_008973	0.000162599	28.9	296.3	28.9	
1421027_a	Bcl1	Bcl1 related kinase	10.2	6350 / transcription // in 5578 / nucleus // in 5578 / DNA binding // in 5578 / protein kinase activity	MM.29884	NP_031874.NM_007376	0.002934573	160.1	250.1	160.1	
1418450_a	Isr	immunoglobulin superfamily containing leucine-rich repeat 10	10.1	---	---	---	8.08988e-006	49.1	497.1	49.1	
1436399_a	Nrk	Nrk related kinase	10.1	6468 / protein amino acid phosphatase // 4672 / protein kinase activity	MM.22367	NP_038752.NM_013724	0.51196e-006	81.6	81		

1425475_at	Ccl45b	proctolin, type IV, alpha 5	6.1	7155 // cell adhesion // inferred: 5578 // extracellular matrix // 1518 // structural molecule // acMm.286802	NP_031762.1NM_007736	0.00014689	222.1	1554.3	
1428349_at	Ebn3	early B-cell factor 3	6.1	6350 // transcription // inferred: 5578 // nucleus // inferred: 3677 // DNA binding // inferMeM.258708	NP_034226.1NM_010096	9.11527e-005	40.5	245.5	
1454604_x_at	Tspan2	tetraspanin 2	6.1	---	Mm.21950	2.486e-006	25.1	152.5	
1423110_at	Ccl42	chemokine (C-C motif) type 42	6.0	6817 // phosphate transport // inferred: 5578 // extracellular matrix // 1518 // structural molecule // acMm.275742	NP_031769.1NM_007743	0.00043644	40.5	1485.8	
1455447_at	D430019H16R1	choline channel cation activated 1 // chloride channel c	6.0	---	Mm.21950	0.00079374	79.3	477.6	
1460259_at	Cla2a	chloride channel cation activated 1 // chloride channel c	6.0	6817 // chloride transport // inferred: 5578 // integral to plasma m // 5229 // integral to calcium acMm.275745	NP_034029.2NM_008999	---	36.1	217.3	
1438413_at	Serp7	SUMO1/serpin specific protease	6.0	---	Mm.22515	1.0047e-005	33.4	200.5	
1421072_at	Irf5	interferon related factor 5 (Drosophila)	5.9	6355 // regulation of transcription // 5634 // nucleus // inferred: 3677 // DNA binding // inferMeM.258708	NP_0010309.NM_010039	0.00017703	79.0	477.6	
1460292_at	Smarc1	SMN1/serpin related, matrix associated, actin dependent reg	5.9	16568 // chromatin modification // 5634 // nucleus // inferred: 3677 // DNA binding // inferMeM.258708	NP_000123.1NM_000123	1.9559e-005	190.2	1130.8	
1448798_at	Cd200	Cd200 antigen	5.9	---	NP_034948.2NM_010118	0.00010232	58.1	344.9	
1418373_at	Gpr124	G protein-coupled receptor 124	5.9	7165 // signal transduction // inferred: 5578 // plasma membrane // 4871 // signal transducer // acMm.265444	NP_037655.1NM_050444	3.6281e-006	27.6	150.7	
1433968_x_at	---	---	5.9	---	---	6.28994e-005	27.6	163.3	
1428336_at	Zfp503	zinc finger protein 503	5.9	---	Mm.29241	0.00258112	113.8	668.3	
1424134_at	BC025872	cDNA sequence BC025872	5.9	---	Mm.29241	7.0814e-005	122.4	719.8	
1416401_at	Kai1	kangal1 (suppression of tumorigenicity 6, prostate)	5.8	---	Mm.42661	0.00221818	126.9	800.6	
1456707_at	Marcks	Myristoylated alanine rich protein kinase C substrate	5.8	---	NP_032654.1NM_008588	5.63646e-006	938.2	5488.2	
1417092_at	Pbr1	patencyrod homone receptor 1	5.8	1501 // skeletal development // inferred: 5578 // membrane // inferred: 3677 // DNA binding // inferMeM.258708	NP_030329.1NM_011159	1.02634e-005	133.5	774.8	
1450757_at	Cdh11	cadherin 11	5.8	7155 // cell adhesion // inferred: 5737 // cytoplasm // inferred: 5509 // calcium ion binding // Mm.1571	NP_033998.2NM_009636	5.13678e-005	795.9	4614.4	
1434678_at	A061274	expressed sequence A061274	5.8	---	---	3.47546e-005	88.6	513.6	
1427233_at	Sca3g3	serologically defined colon cancer antigen 33	5.8	6355 // regulation of transcription // ---	NP_129060.1NM_129060	2.0493e-006	82.5	467.5	
1436937_at	Rbm3c	RNA binding motif, single stranded interacting protein	5.8	---	NP_036777.1NM_018660	2.53487e-006	62.9	361.6	
1433795_at	Tgfb3	transforming growth factor, beta receptor III	5.8	---	NP_035708.2NM_011578	3.6424e-005	237.2	1364.0	
1450723_at	Iat1	ISL1 transcription factor, LIM/homeobox (talet 1)	5.7	6891 // generation of precursor // 5634 // nucleus // inferred: 3677 // DNA binding // inferMeM.258708	NP_047434.2NM_021458	0.00019803	35.9	285.6	
1417111_at	Man1a	mannosidase 1, alpha	5.7	5975 // carbohydrate metabolism // 138 // Golgi membrane // inferred: 3677 // DNA binding // inferMeM.258708	NP_035274.1NM_008548	0.01741e-007	174.4	954.0	
1423204_at	Meat	mesoderm specific transcript	5.7	6508 // proteolysis and peptidolysis // 5615 // extracellular space // 4177 // aminopeptidase activity // Mm.1089	NP_032616.1NM_008590	1.3181e-005	135.2	7693.9	
1416864_at	Gab2	GATA binding protein 4	5.7	1701 // protein synthesis and biogenesis // 5634 // nucleus // inferred: 3677 // DNA binding // inferMeM.258708	NP_032118.2NM_008092	0.00038513	70.4	403.6	
1447890_at	Ron1	retrospondin 1	5.7	5615 // extracellular space // 1509 // calcium ion binding // Mm.4876	NP_030363.1NM_009037	0.00013473	41.3	235.1	
1448785_at	Cla2a2	CFBZAT1 identified gene homolog (human)	5.7	6350 // transcription // inferred: 5634 // nucleus // inferred: 3677 // DNA binding // inferMeM.4909	NP_033952.2NM_009882	2.81145e-006	57.4	328.1	
1417110_x_at	Fus2	filamentous temperature sensitive 2 (Drosophila)	5.7	6488 // carbohydrate metabolism // 138 // Golgi membrane // inferred: 3677 // DNA binding // inferMeM.258708	NP_035113.1NM_010548	0.00019709	115.5	645.4	
142572_x_at	Cla1c	chloride channel cation activated 1	5.7	6817 // chloride transport // inferred: 5578 // integral to plasma m // 5229 // integral to calcium acMm.275745	NP_034029.2NM_008999	7.47878e-005	44.2	250.1	
1428766_at	R330430K7R1	RIKEN cDNA 63304030707 gene	5.6	---	Mm.27768	1.86873e-007	159.9	901.9	
1428433_at	Hpk2	homocysteine interacting protein kinase 2	5.6	122 // negative regulation of tra // 5634 // nucleus // inferred: 3714 // transcription corepressor // Mm.23790	NP_045653.1NM_010433	3.64167e-006	94.0	527.7	
1439648_at	R430550H18R1	RIKEN cDNA 62565091202 gene	5.6	---	NP_766518.1NM_172390	0.00019239	10.0	57.7	
1417149_at	P4ha2	procollagen-proline, 2-oxoglutarate 4-dioxygenase (prolin	5.6	18401 // peptidyl-proline hydrolase // 5615 // extracellular space // 4656 // procollagen-proline // Acm.3705	NP_030161.1NM_011031	0.00027675	118.3	1220.4	
1428531_at	R730964Z1R1	RIKEN cDNA A73055421 gene	5.6	---	Mm.12927	0.0007165	107.7	588.8	
1435027_at	BC039093	cDNA sequence BC039093	5.6	---	NP_131700.3NM_131700	0.00029153	21.5	114.7	
1428284_at	R430427H17R1	RIKEN cDNA 6430247417 gene	5.6	---	Mm.50660	0.003744e-005	103.2	573.8	
1425603_at	D61001104R1	RIKEN cDNA 601011104 gene	5.6	---	Mm.27061	0.0796222NM_025236	6.93486e-006	88.6	492.8
1417466_at	---	---	5.5	---	---	2.46374e-006	93.2	167.3	
1438698_at	463245D07R1	RIKEN cDNA 463245D07 gene	5.5	---	Mm.370296	0.00125555	78.4	156.9	
1418496_at	Foxa1	forkhead box A1	5.5	6350 // cell adhesion // inferred: 5634 // nucleus // inferred: 3677 // DNA binding // inferMeM.4978	NP_032285.1NM_008259	9.37067e-005	24.6	112.0	
1449313_at	Pchrb17	proctolin receptor subunit 17	5.5	1155 // cell adhesion // inferred: 5615 // extracellular space // 1509 // calcium ion binding // Mm.21950	NP_047434.2NM_021458	0.00019803	35.9	285.6	
1437502_x_at	Cd24a	CD24 antigen	5.5	---	Mm.28742	0.00045622	717.8	3956.9	
1433691_at	Ppp1f3c	protein phosphatase 1, regulatory (inhibitor) subunit 3C	5.5	5977 // glycolysis and gluconeogenesis // 5615 // integral to plasma m // 5229 // integral to calcium acMm.275745	NP_035050.1NM_018684	1.33826e-006	43.1	246.9	
1419117_at	Ccno	connexin 43	5.5	6508 // proteolysis and peptidolysis // 5634 // nucleus // inferred: 3677 // DNA binding // inferMeM.258708	NP_030363.1NM_009037	0.00038513	70.4	403.6	
1427442_x_at	App	amyloid beta (A4) precursor protein	5.5	6897 // endocytosis // inferred: 5578 // coated pi // inferred: 4666 // endopeptidase inhibitor // Mm.27765	NP_031497.2NM_007471	1.67248e-007	117.9	670.4	
1448182_x_at	Cd24a	CD24 antigen	5.5	---	Mm.28742	0.00016805	151.8	834.0	
1435920_at	Adams2	Adams2 and metalloprotease (neprosin type) w/	5.5	6897 // proteolysis and peptidolysis // 5634 // nucleus // inferred: 3677 // DNA binding // inferMeM.258708	NP_030363.1NM_009037	0.00038513	70.4	403.6	
1448405_x_at	Cri1	CREBBP1/EBP30 inhibitor protein 1	5.5	122 // negative regulation of tra // 5634 // nucleus // inferred: 3677 // DNA binding // inferMeM.4244	NP_078989.1NM_025613	1.91821e-009	50.3	274.7	
1452107_x_at	Nprt	nephrocytin	5.5	7160 // cell-matrix adhesion // inferred: 5578 // extracellular matrix // 1518 // integrin binding // inferMeM.279310	NP_077060.1NM_030523	0.00011891	46.7	254.9	
1437326_at	Pcds5	protein disulfide isomerase like protein type 5	5.5	6488 // protein amino acid phosphatase // 5615 // extracellular space // 1509 // cytoskeletal endopeptidase // Mm.32491	NP_129214.2NM_129214	0.00019709	115.5	645.4	
1420621_x_at	App	amyloid beta (A4) precursor protein	5.4	6897 // endocytosis // inferred: 5578 // coated pi // inferred: 4666 // endopeptidase inhibitor // Mm.27765	NP_031497.2NM_007471	1.65455e-005	735.8	3981.8	
1448395_at	Shp1	secreted frizzled-related sequence protein 1	5.4	7275 // development // inferred: 5578 // extracellular space // 4688 // transmembrane receptor // Mm.21950	NP_038862.1NM_013834	4.35405e-008	41.3	220.8	
1440201_at	Shp2	secreted frizzled-related sequence protein 2	5.4	7275 // development // inferred: 5578 // extracellular space // 4688 // transmembrane receptor // Mm.21950	NP_038862.1NM_013834	0.000302795	138.2	748.8	
1434102_at	EO3302010R1	RIKEN cDNA EO3302010 gene	5.3	---	Mm.37483	0.00018237	67.4	360.2	
1450429_at	Capn9	capain 9	5.3	6508 // proteolysis and peptidolysis // 5634 // nucleus // inferred: 3677 // DNA binding // inferMeM.30290	NP_031629.2NM_007603	4.47822e-005	244.2	1304.7	
1416933_at	Rbck	ribonucleoside C	5.3	6350 // transcription // inferred: 5634 // nucleus // inferred: 3677 // DNA binding // inferMeM.4909	NP_035113.1NM_010548	0.00019709	115.5	645.4	
1441019_at	Ilnar2	interleukin (alpha and beta) receptor 2	5.3	6357 // regulation of transcription // 5615 // extracellular space // 4872 // receptor activity // inferMeM.6834	NP_034356.1NM_010598	0.00066868	17.9	95.4	
1455844_at	---	Transcribed locus	5.3	---	Mm.368594	---	3.66464e-005	1215.6	6472.6
1448554_x_at	Myh6	myosin heavy polypeptide 6, cardiac muscle, alpha	5.3	6841 // striated muscle contract // 5856 // cytoskeleton // inferred: 3714 // motor activity // inferMeM.29003	NP_034986.1NM_010658	0.00034844	98.2	523.0	
1435078_at	R3204623R1	RIKEN cDNA 620420202 gene	5.3	6841 // regulation of transcription // ---	NP_3677.1NM_3677	0.00073466	20.9	108.9	
1447050_at	Cd42ep3	CD42c receptor protein (Rho GTPase binding) 3	5.3	---	NP_080790.1NM_026514	0.00034844	119.3	633.0	
1422561_at	Adams5	a disintegrin-like and metalloprotease (neprosin type) w/	5.3	6508 // proteolysis and peptidolysis // 5634 // nucleus // inferred: 3677 // DNA binding // inferMeM.12923	NP_035912.1NM_011782	0.000196262	90.2	478.4	
1427650_at	Nfb	nucleofactin	5.3	6360 // DNA replication // inferred: 5622 // intracellular // inferred: 3677 // DNA binding // inferMeM.27947	NP_030625.1NM_010689	0.00029153	21.5	114.7	
1424112_at	Igf2r	insulin-like growth factor 2 receptor	5.3	6810 // transcription // inferred: 5615 // extracellular space // 4872 // receptor activity // inferMeM.26553	NP_034645.1NM_010515	0.00042356	69.6	366.4	
1416072_at	Cd34	CD34 antigen	5.3	7155 // cell adhesion // inferred: 5887 // external side of plas // 515 // protein binding // inferMeM.2978	NP_088415.1NM_133654	0.00045283	69.1	362.2	
1426233_at	D1Erat47	DNA segment, Chr 1, ERATO D41, expressed endonuclease receptor type 4	5.2	---	Mm.101743	---	1.30674e-007	82.7	327.6
1418370_at	Tnct1	Tnct1, cardiac/bone skeletal	5.2	6937 // regulation of muscle con // 588 // tropoin complex // 15200 // structural constituent // Mm.712	NP_034149.1NM_009393	2.73227e-005	118.6	617.6	
1437107_at	R43004107R1	RIKEN cDNA R43004107 gene	5.2	---	NP_030363.1NM_009037	0.00038513	70.4	403.6	
1415973_at	Marcks	Myristoylated alanine rich protein kinase C substrate	5.2	---	NP_032654.1NM_008588	5.63646e-006	107.2	5433.9	
1417355_at	Pep3	patently expressed 3	5.2	6355 // regulation of transcription // 5634 // nucleus // inferred: 3676 // nucleus // inferMeM.7852	NP_0010109NM_010109	0.00011787	147.0	7623.6	
1417105_at	Pep4	patently expressed 4	5.2	6355 // regulation of transcription // 5634 // nucleus // inferred: 3676 // nucleus // inferMeM.7852	NP_0010109NM_010109	0.00011787	147.0	7623.6	
1418934_x_at	Mat2i2	mat-2-like 2 (C. elegans)	5.2	1747 // eye morphogenesis (see ---) // ---	Mm.214385	0.00015884	245.6	1286.5	
1438993_x_at	Pfn2	profilin 2	5.2	7010 // cytoskeleton organization // 5856 // cytoskeleton // inferred: 3714 // actin binding // inferMeM.27144	NP_062283.1NM_019410	1.42422e-005	299.4	1543.6	
1416209_at	Pfn1	profilin 1	5.2	7010 // cytoskeleton organization // 5856 // cytoskeleton // inferred: 3714 // actin binding // inferMeM.27144	NP_062283.1NM_019410	0.00013802	116.7	617.6	
1448733_x_at	Bmi1	B lymphoma Mo-MuLV insertion region 1	5.2	1501 // skeletal development // inferred: 5578 // ubiquitin ligase complex // 4842 // ubiquitin-protein ligase // Mm.28954	NP_031578.2NM_007552	3.66505e-005	36.4	187.7	
1416034_x_at	Cd24a	CD24 antigen	5.1	---	NP_033976.1NM_009846	0.000593133	95.7	493.0	
1440066_at	Erb3	early B-cell factor 3	5.1	6350 // transcription // inferred: 5634 // nucleus // inferred: 3677 // DNA binding // inferMeM.4909	NP_035113.1NM_010548	0.00019709	115.5	645.4	
1426057_at	EphA3	Eph receptor A3	5.1	6468 // protein amino acid phosphatase // 5615 // extracellular space // 1509 // cytoskeletal endopeptidase // Mm.1977	NP_034270.1NM_011454	0.00017941	40.5	208.8	
1447864_x_at	Pogk	pogo transposable element with KRAB domain	5.1	6355 // regulation of transcription // 5622 // intracellular // inferred: 3676 // nucleus // acMm.29294	NP_780379.1NM_175170	1.04478e-005	77.4	392.9	
1422593_at	R430430D4R1	RIKEN cDNA R430430D4 gene	5.1	---	NP_030363.1NM_009037	0.00038513	70.4	403.6	
1416414_at	Erm1n1	elastin microfibrin interacting	5.1	---	NP_035584.1NM_011454	0.00045346	84.3	427.5	
1438570_at	---	Transcribed locus	5.1	---	Mm.20855	0.00015403	71.4	361.5	
1416025_at	Serp1ng1	serpin (or cysteine) proteinase inhibitor, clade G, member 5	5.1	7229 // the integrin-mediated sign // ---	Mm.18021	0.00017388	44.0	222.5	
1425545_at	Thx2	Thx2	5.1	6817 // phosphate transport // inferred: 5578 // extracellular matrix // 1515 // structural molecule // inferMeM.286375	NP_089679.1NM_198738	0.00010311	180.0	890.9	
1438664_at	Pkar2b	protein kinase, cAMP dependent regulatory, type II beta	5.1	---	Mm.23897	1.61847e-00			

1415923	Ndn	neudin	4.2	1558 // regulation of cell growth 5634 // nucleus // inferred 3677 // DNA binding // inferred	Mm.250919	NP_035012.2NM_010882	1.12897e-005	760.2	3223.8
1428136	Mt4p	microtubulin-associated protein 4	4.2	---	---	---	1.7518e-008	504.0	2132.9
1428101	Mt4p	microtubulin-associated protein 4	4.2	7155 // cell adhesion // inferred 1527 // microtubule // inferred	Mm.272278	NP_083844.1NM_029568	1.18289e-007	274.0	1162.1
1438732	LOC343423	LOC343423	4.2	---	---	---	4.41898e-006	25.3	107.1
1424849	Mend	monocyte to macrophage differentiation-associated 1	4.2	19835 // cytolytic // inferred from 16021 // integral to membra 4872 // receptor activity // inferred	Mm.275718	NP_084654.1NM_028178	4.6824e-006	147.5	592.2
1434566	---	Transcribed locus, strongly similar to XP_510031.1 similia	4.2	---	---	---	1.6041e-006	44.6	187.2
1427985	963004297RfR	RKEN CDNA 963004297 gene	4.2	7276 // gonemesis // inferred	Mm.112025	NP_048868.1NM_178753	1.529e-007	51.3	215.1
1417423	Glna	glutamine synthetase, N-methyl-D-aspartate-ase	4.2	6468 // protein amino acid phosph 5615 // extracellular space 4872 // protein kinase activity // inferred	Mm.6804	NP_075622.1NM_021648	2.30406e-007	741.1	3049.2
1421841	FgR3	fibroblast growth factor receptor 3	4.2	---	---	---	4.98004e-005	139.2	580.0
1422771	---	---	4.2	---	---	---	7.52508e-006	180.0	749.4
1447624	493340907RfR	RKEN CDNA 493340907 gene	4.2	---	---	---	2.51088e-005	342.1	1404.0
1439794	---	Transcribed locus	4.1	---	---	---	2.51025e-005	53.3	221.2
1425274	Eph3a	Eph receptor A3	4.1	6468 // protein amino acid phosph 5615 // extracellular space 4872 // protein kinase activity // inferred	Mm.1778	NP_034270.1NM_010140	3.81708e-005	71.5	296.4
1429840	181001IN17RfR	RKEN CDNA 181001017 gene	4.1	---	---	---	4.08115e-005	57.2	237.0
1460574	1460574	RKEN CDNA 603410K14 gene	4.1	---	---	---	3.02599e-007	49.2	203.5
1456720	---	---	4.1	---	---	---	0.000667871	84.9	351.3
1431004	Lmo2	lysoyl oxidase-like 2	4.1	---	---	---	0.002232633	327.2	1322.3
1417061	Slc40a1	solute carrier family 40 (iron-regulated transporter), memt	4.1	6810 // transport // inferred from 5743 // mitochondrial inner 5831 // iron ion transporter act	Mm.28756	NP_058613.1NM_016917	0.000416835	181.9	750.4
1429585	Mesp1	mannan-6-binding lectin serine protease 1	4.1	6508 // proteolysis and peptidol 5615 // extracellular space 4422 // serine-type endopept Mm.1213	NP_032981.1NM_008555	0.000429895	163.0	672.5	
1417535	111111	11 receptor, alpha chain 1 // interleukin 11 rec	4.1	1775 // natural killer cell killer 5807 // integrat to plasma r 4872 // receptor activity // infer	Mm.130451	NP_034679.1NM_010549	3.95041e-006	187.5	770.1
1438665	Smpd3	sphingomyelin phosphodiesterase 3, neutral	4.1	6684 // sphingomyelin metabolism 5745 // Golgi apparatus // i 4767 // sphingomyelin phosp	Mm.23298	NP_067466.1NM_021491	9.03193e-006	106.7	437.8
1418286	Ehrlb1	ehrin B1	4.1	1755 // neural crest cell migrate 5615 // extracellular space 5515 // protein binding // infer	Mm.3374	NP_034240.1NM_010110	7.42826e-007	470.7	1930.2
1417644	Sapn	sarcospan	4.1	74 // regulation of cell cycle // inferred 5522 // intracellular // inferred	Mm.26898	NP_034786.1NM_010566	0.000896228	35.7	146.3
1417137	Dact1	dapper homolog 1, antagonist of beta-catenin (xenopus)	4.1	---	---	---	7.6703e-006	236.0	964.4
1417359	Mt2p	microtubulin-associated protein 2	4.1	---	---	---	0.000187748	654.5	2673.7
1432055	Sema3d	semaphorin 3, class D, member 3	4.1	7275 // cell development // inferred 16021 // integral to membra 4872 // receptor activity // infer	Mm.330359	NP_076125.2NM_172537	4.52748e-006	244.7	958.8
1434740	Scurl2	scavenger receptor class F, member 2	4.1	7155 // cell adhesion // inferred 16021 // integral to membra 4872 // receptor activity // infer	Mm.194500	NP_022465.1NM_153790	2.58006e-006	176.2	717.7
1437458	Clu	clusterin	4.1	8219 // cell death // inferred from 5615 // extracellular space	Mm.200608	NP_038520.1NM_013492	0.000202961	1300.4	5292.1
1416498	Ppic	peptidyl-prolyl isomerase C	4.1	6457 // protein folding // inferred 5615 // extracellular space 3755 // peptidyl-prolyl cis-tran	Mm.4587	NP_032934.1NM_008908	0.00041414	349.2	1404.0
144354	---	---	4.0	---	---	---	4.29393e-006	59.8	241.9
1447900	Emp24	ectonucleoside triphosphate diphosphohydrolase 4	4.0	---	---	---	3.82055e-005	34.2	138.0
1421405	Zm1	zinc finger, imprinted 1	4.0	6355 // regulation of transcript 5622 // intracellular // inferred 3678 // nuclear acid bindin	Mm.89976	NP_038899.1NM_025613	0.000897274	35.9	145.5
1428112	AV146242	expressed sequence AV146242	4.0	---	---	---	0.000166274	65.3	787.0
1451475	PlexD1	plexin D1	4.0	1569 // patterning of blood vess 5888 // plasma membra 4872 // receptor activity // infer	Mm.30385	NP_080652.1NM_026376	1.38567e-008	152.6	614.4
1422987	9930013L23RfR	RKEN CDNA 9930013L23 gene	4.0	---	---	---	0.00014901	56.6	228.6
1426819	---	---	4.0	---	---	---	1.08317e-006	39.4	158.8
1416343	Lamp2	lysosomal membrane glycoprotein 2	4.0	6418 // rRNA aminoacylation for 5624 // membrane fraction 4812 // RNA ligase activity // Mm.486	NP_034815.2NM_010685	3.93811e-006	163.1	1451.2	
1450294	Hsp93p	hepatoma-derived growth factor, related protein 3	4.0	6283 // cell proliferation // infer 5634 // nucleus // inferred 476	Mm.28887	NP_038914.2NM_013886	0.000596867	65.8	263.7
1439871	Ube2n	ubiquitin-conjugating enzyme E2n	4.0	6484 // ubiquitin conjugation // inferred 5840 // ubiquitin conjugation // infer	Mm.20769	NP_034429.1NM_010949	4.44478e-006	198.9	799.0
1448429	Gy1	glycogenin 1	4.0	5978 // glycogen biosynthesis // infer	Mm.6375	NP_038783.1NM_013755	1.6844e-005	257.0	1023.4
1436184	B430302C24RfR	RKEN CDNA B430302C24 gene	4.0	---	---	---	3.7428e-007	135.0	542.5
1439407	FgR2	fibroblast growth factor receptor 2	4.0	6468 // protein amino acid phosph 5615 // extracellular space 4872 // protein kinase activity // infer	Mm.14530	NP_034337.1NM_010207	1.3543e-006	177.1	701.0
1423140	Lip1	lysosomal acid lipase 1	4.0	6629 // lipid metabolism // infer 5615 // extracellular space 3824 // catalytic activity // infer	Mm.15745	NP_067435.2NM_021460	0.0001285	180.2	711.8
1444512	B13001701RfR	RKEN CDNA B13001701 gene	3.9	7242 // intracellular signaling ca	5096 // GTPase activator act	Mm.226267	1.7825e-006	96.4	380.7
1430734	---	---	3.9	---	---	---	1.6394e-006	66.7	268.9
1451619	Rab11p2	RAB11 family interactor protein 2 (class I)	3.9	---	---	---	8.24167e-007	44.4	174.8
1447774	573046910RfR	RKEN CDNA 573046910 gene	3.9	---	---	---	0.000398983	129.3	506.7
1427108	353008020RfR	RKEN CDNA 353008020 gene	3.9	---	---	---	0.000129189	119.8	469.0
1466148	Crisp2	cysteine-rich secretory protein LCCL domain containing 2	3.9	---	---	---	0.00037737	67.4	655.0
1419814	Cr1	CR1/CR2/CR3/CR4/CR5/CR6/CR7/CR8/CR9/CR10/CR11/CR12/CR13/CR14/CR15/CR16/CR17/CR18/CR19/CR20/CR21/CR22/CR23/CR24/CR25/CR26/CR27/CR28/CR29/CR30/CR31/CR32/CR33/CR34/CR35/CR36/CR37/CR38/CR39/CR40/CR41/CR42/CR43/CR44/CR45/CR46/CR47/CR48/CR49/CR50/CR51/CR52/CR53/CR54/CR55/CR56/CR57/CR58/CR59/CR60/CR61/CR62/CR63/CR64/CR65/CR66/CR67/CR68/CR69/CR70/CR71/CR72/CR73/CR74/CR75/CR76/CR77/CR78/CR79/CR80/CR81/CR82/CR83/CR84/CR85/CR86/CR87/CR88/CR89/CR90/CR91/CR92/CR93/CR94/CR95/CR96/CR97/CR98/CR99/CR100/CR101/CR102/CR103/CR104/CR105/CR106/CR107/CR108/CR109/CR110/CR111/CR112/CR113/CR114/CR115/CR116/CR117/CR118/CR119/CR120/CR121/CR122/CR123/CR124/CR125/CR126/CR127/CR128/CR129/CR130/CR131/CR132/CR133/CR134/CR135/CR136/CR137/CR138/CR139/CR140/CR141/CR142/CR143/CR144/CR145/CR146/CR147/CR148/CR149/CR150/CR151/CR152/CR153/CR154/CR155/CR156/CR157/CR158/CR159/CR160/CR161/CR162/CR163/CR164/CR165/CR166/CR167/CR168/CR169/CR170/CR171/CR172/CR173/CR174/CR175/CR176/CR177/CR178/CR179/CR180/CR181/CR182/CR183/CR184/CR185/CR186/CR187/CR188/CR189/CR190/CR191/CR192/CR193/CR194/CR195/CR196/CR197/CR198/CR199/CR200/CR201/CR202/CR203/CR204/CR205/CR206/CR207/CR208/CR209/CR210/CR211/CR212/CR213/CR214/CR215/CR216/CR217/CR218/CR219/CR220/CR221/CR222/CR223/CR224/CR225/CR226/CR227/CR228/CR229/CR230/CR231/CR232/CR233/CR234/CR235/CR236/CR237/CR238/CR239/CR240/CR241/CR242/CR243/CR244/CR245/CR246/CR247/CR248/CR249/CR250/CR251/CR252/CR253/CR254/CR255/CR256/CR257/CR258/CR259/CR260/CR261/CR262/CR263/CR264/CR265/CR266/CR267/CR268/CR269/CR270/CR271/CR272/CR273/CR274/CR275/CR276/CR277/CR278/CR279/CR280/CR281/CR282/CR283/CR284/CR285/CR286/CR287/CR288/CR289/CR290/CR291/CR292/CR293/CR294/CR295/CR296/CR297/CR298/CR299/CR300/CR301/CR302/CR303/CR304/CR305/CR306/CR307/CR308/CR309/CR310/CR311/CR312/CR313/CR314/CR315/CR316/CR317/CR318/CR319/CR320/CR321/CR322/CR323/CR324/CR325/CR326/CR327/CR328/CR329/CR330/CR331/CR332/CR333/CR334/CR335/CR336/CR337/CR338/CR339/CR340/CR341/CR342/CR343/CR344/CR345/CR346/CR347/CR348/CR349/CR350/CR351/CR352/CR353/CR354/CR355/CR356/CR357/CR358/CR359/CR360/CR361/CR362/CR363/CR364/CR365/CR366/CR367/CR368/CR369/CR370/CR371/CR372/CR373/CR374/CR375/CR376/CR377/CR378/CR379/CR380/CR381/CR382/CR383/CR384/CR385/CR386/CR387/CR388/CR389/CR390/CR391/CR392/CR393/CR394/CR395/CR396/CR397/CR398/CR399/CR400/CR401/CR402/CR403/CR404/CR405/CR406/CR407/CR408/CR409/CR410/CR411/CR412/CR413/CR414/CR415/CR416/CR417/CR418/CR419/CR420/CR421/CR422/CR423/CR424/CR425/CR426/CR427/CR428/CR429/CR430/CR431/CR432/CR433/CR434/CR435/CR436/CR437/CR438/CR439/CR440/CR441/CR442/CR443/CR444/CR445/CR446/CR447/CR448/CR449/CR450/CR451/CR452/CR453/CR454/CR455/CR456/CR457/CR458/CR459/CR460/CR461/CR462/CR463/CR464/CR465/CR466/CR467/CR468/CR469/CR470/CR471/CR472/CR473/CR474/CR475/CR476/CR477/CR478/CR479/CR480/CR481/CR482/CR483/CR484/CR485/CR486/CR487/CR488/CR489/CR490/CR491/CR492/CR493/CR494/CR495/CR496/CR497/CR498/CR499/CR500/CR501/CR502/CR503/CR504/CR505/CR506/CR507/CR508/CR509/CR510/CR511/CR512/CR513/CR514/CR515/CR516/CR517/CR518/CR519/CR520/CR521/CR522/CR523/CR524/CR525/CR526/CR527/CR528/CR529/CR530/CR531/CR532/CR533/CR534/CR535/CR536/CR537/CR538/CR539/CR540/CR541/CR542/CR543/CR544/CR545/CR546/CR547/CR548/CR549/CR550/CR551/CR552/CR553/CR554/CR555/CR556/CR557/CR558/CR559/CR560/CR561/CR562/CR563/CR564/CR565/CR566/CR567/CR568/CR569/CR570/CR571/CR572/CR573/CR574/CR575/CR576/CR577/CR578/CR579/CR580/CR581/CR582/CR583/CR584/CR585/CR586/CR587/CR588/CR589/CR590/CR591/CR592/CR593/CR594/CR595/CR596/CR597/CR598/CR599/CR600/CR601/CR602/CR603/CR604/CR605/CR606/CR607/CR608/CR609/CR610/CR611/CR612/CR613/CR614/CR615/CR616/CR617/CR618/CR619/CR620/CR621/CR622/CR623/CR624/CR625/CR626/CR627/CR628/CR629/CR630/CR631/CR632/CR633/CR634/CR635/CR636/CR637/CR638/CR639/CR640/CR641/CR642/CR643/CR644/CR645/CR646/CR647/CR648/CR649/CR650/CR651/CR652/CR653/CR654/CR655/CR656/CR657/CR658/CR659/CR660/CR661/CR662/CR663/CR664/CR665/CR666/CR667/CR668/CR669/CR670/CR671/CR672/CR673/CR674/CR675/CR676/CR677/CR678/CR679/CR680/CR681/CR682/CR683/CR684/CR685/CR686/CR687/CR688/CR689/CR690/CR691/CR692/CR693/CR694/CR695/CR696/CR697/CR698/CR699/CR700/CR701/CR702/CR703/CR704/CR705/CR706/CR707/CR708/CR709/CR710/CR711/CR712/CR713/CR714/CR715/CR716/CR717/CR718/CR719/CR720/CR721/CR722/CR723/CR724/CR725/CR726/CR727/CR728/CR729/CR730/CR731/CR732/CR733/CR734/CR735/CR736/CR737/CR738/CR739/CR740/CR741/CR742/CR743/CR744/CR745/CR746/CR747/CR748/CR749/CR750/CR751/CR752/CR753/CR754/CR755/CR756/CR757/CR758/CR759/CR760/CR761/CR762/CR763/CR764/CR765/CR766/CR767/CR768/CR769/CR770/CR771/CR772/CR773/CR774/CR775/CR776/CR777/CR778/CR779/CR780/CR781/CR782/CR783/CR784/CR785/CR786/CR787/CR788/CR789/CR790/CR791/CR792/CR793/CR794/CR795/CR796/CR797/CR798/CR799/CR800/CR801/CR802/CR803/CR804/CR805/CR806/CR807/CR808/CR809/CR810/CR811/CR812/CR813/CR814/CR815/CR816/CR817/CR818/CR819/CR820/CR821/CR822/CR823/CR824/CR825/CR826/CR827/CR828/CR829/CR830/CR831/CR832/CR833/CR834/CR835/CR836/CR837/CR838/CR839/CR840/CR841/CR842/CR843/CR844/CR845/CR846/CR847/CR848/CR849/CR850/CR851/CR852/CR853/CR854/CR855/CR856/CR857/CR858/CR859/CR860/CR861/CR862/CR863/CR864/CR865/CR866/CR867/CR868/CR869/CR870/CR871/CR872/CR873/CR874/CR875/CR876/CR877/CR878/CR879/CR880/CR881/CR882/CR883/CR884/CR885/CR886/CR887/CR888/CR889/CR890/CR891/CR892/CR893/CR894/CR895/CR896/CR897/CR898/CR899/CR900/CR901/CR902/CR903/CR904/CR905/CR906/CR907/CR908/CR909/CR910/CR911/CR912/CR913/CR914/CR915/CR916/CR917/CR918/CR919/CR920/CR921/CR922/CR923/CR924/CR925/CR926/CR927/CR928/CR929/CR930/CR931/CR932/CR933/CR934/CR935/CR936/CR937/CR938/CR939/CR940/CR941/CR942/CR943/CR944/CR945/CR946/CR947/CR948/CR949/CR950/CR951/CR952/CR953/CR954/CR955/CR956/CR957/CR958/CR959/CR960/CR961/CR962/CR963/CR964/CR965/CR966/CR967/CR968/CR969/CR970/CR971/CR972/CR973/CR974/CR975/CR976/CR977/CR978/CR979/CR980/CR981/CR982/CR983/CR984/CR985/CR986/CR987/CR988/CR989/CR990/CR991/CR992/CR993/CR994/CR995/CR996/CR997/CR998/CR999/CR1000/CR1001/CR1002/CR1003/CR1004/CR1005/CR1006/CR1007/CR1008/CR1009/CR1010/CR1011/CR1012/CR1013/CR1014/CR1015/CR1016/CR1017/CR1018/CR1019/CR1020/CR1021/CR1022/CR1023/CR1024/CR1025/CR1026/CR1027/CR1028/CR1029/CR1030/CR1031/CR1032/CR1033/CR1034/CR1035/CR1036/CR1037/CR1038/CR1039/CR1040/CR1041/CR1042/CR1043/CR1044/CR1045/CR1046/CR1047/CR1048/CR1049/CR1050/CR1051/CR1052/CR1053/CR1054/CR1055/CR1056/CR1057/CR1058/CR1059/CR1060/CR1061/CR1062/CR1063/CR1064/CR1065/CR1066/CR1067/CR1068/CR1069/CR1070/CR1071/CR1072/CR1073/CR1074/CR1075/CR1076/CR1077/CR1078/CR1079/CR1080/CR1081/CR1082/CR1083/CR1084/CR1085/CR1086/CR1087/CR1088/CR1089/CR1090/CR1091/CR1092/CR1093/CR1094/CR1095/CR1096/CR1097/CR1098/CR1099/CR1100/CR1101/CR1102/CR1103/CR1104/CR1105/CR1106/CR1107/CR1108/CR1109/CR1110/CR1111/CR1112/CR1113/CR1114/CR1115/CR1116/CR1117/CR1							

1423159	463149011R1A	RKEN_CDNA_463149011 gene	3.4	---	---	---	Mm.2395	---	0.00052474	36.9	123.9		
1423413	Nbr1	N-myrc downstream regulated gene 1	3.4	45576	// mast cell activation // ir	---	Mm.30837	NP_030514.NM_010884	0.00047947	206.6	694.3		
1435464	11100030E1R1A	RKEN_CDNA_11100030E1 gene	3.4	---	16021	// integral to membra	Mm.10709	NP_598458.NM_133697	1.57121-005	74.9	251.0		
1438910	Bmp7	bone morphogenetic protein 7	3.4	7389	// part specification // in 5615 / extracellular space / 4822 // cytokine activity // ir	nmM.595	NP_031563.NM_020757	0.00022144	84.0	215.0			
1439103	---	---	3.4	---	---	---	---	---	1.06474-005	164.0	226.0		
1426448	Pja1	praja1, RING-H2 motif containing	3.4	6512	// ubiquitin cycle // inferred 151 / ubiquitin ligase comp 4842 // ubiquitin-protein ligase	Mm.8211	NP_032879.NM_008853	1.49171-005	108.9	365.6			
1439202	Sema3c	sema domain, immunoglobulin domain (fg), transmembr	3.4	7275	// development // inferred 15615 / extracellular space / 4872 // receptor activity // ir	nmM.2958	NP_129653.NM_129653	1.03326-005	143.0	479.5			
1437744	---	---	3.4	---	---	---	---	---	0.00246868	43.7	146.3		
1429712	Etoh1	ethanol induced 1	3.3	---	---	---	Mm.33062	XP_485125.NM_485125	3.82016-006	91.4	304.9		
1427186	Ma2a	myocyte enhancer factor 2A	3.3	6350	// transcription // inferred 15634 // nucleus // Unknown	3077	NP_038625.NM_013937	1.87947-005	63.1	209.6			
1434651	Kc1d12	potassium channel tetramer domain containing 12	3.3	---	---	---	Mm.24546	NP_038633.NM_177716	0.00048483	100.9	329.2		
1447693	---	---	3.3	---	---	---	---	---	1.47796-006	283.4	874.2		
1437351	Cxoc4	CXCR4 ligand 4	3.3	16055	// Wnt receptor signaling 5737 // cytoplasm // inferred	---	Mm.24814	NP_00104308.NM_001043	0.00050081	70.0	223.0		
1430177	Cond2	cyclin D2	3.3	74	// regulation of cell cycle // in 5634 // nucleus // inferred	5515 // protein binding // ir	nmM.33340	NP_033959.NM_006929	0.000634238	836.5	2704.0		
1428898	---	---	3.3	---	---	---	---	---	0.000414923	53.5	176.1		
1423488	Mmd	monocyte to macrophage differentiation-associated	3.3	19835	// catalysis // inferred 16021 // integral to membra 4872 // receptor activity // ir	nmM.27618	NP_080454.NM_026178	9.28486-006	519.8	1711.3			
1416474	Nsep	neighbor of Puro E11	3.3	7155	// cell adhesion // inferred 5887 // integral to membra 4872 // protein binding // ir	nmM.25961	NP_030229.NM_020043	2.42525-006	180.5	594.1			
1433504	Pygb	brin glycoprotein phosphatase	3.3	5975	// catalytic activity // ir	nmM.22584	NP_722476.NM_153781	0.00017323	37.8	124.1			
1435106	---	---	3.3	---	---	---	---	---	0.000627108	45.7	150.2		
1417847	Ume2	UmeO1 like kinase 2 (C. elegans)	3.3	---	---	---	Mm.36087	NP_038909.NM_013881	1.50291-005	187.0	613.6		
1451978	Lov1	lysyl oxidase-like 1	3.3	6464	// protein modification // in 5676 // extracellular region / 4702 // protein-lysine 6-oxida	Mm.250462	NP_034859.NM_010729	0.000059495	65.9	216.5			
1442774	2610042G18RA	RKEN_CDNA_2610042G18 gene	3.3	---	---	---	Mm.274159	NP_899003.NM_183180	5.14478-006	206.0	675.7		
1428965	Cugp2	CUG triplet repeat RNA binding protein 2	3.3	6376	// mRNA splicing site selected 5634 // nucleus // inferred	---	Mm.147081	NP_034236.NM_010160	0.008993038	216.4	707.8		
1416727	11100030E1R1A	RKEN_CDNA_11100030E1 gene	3.3	---	16021	// integral to membra	Mm.10709	NP_598458.NM_133697	7.78086-006	555.8	1817.0		
1460561	Sepw1	serenoprotein W, muscle 1	3.3	---	---	---	Mm.42828	NP_033182.NM_009156	2.13474-006	196.1	642.1		
1433565	Abat	4-aminobutyrate aminotransferase	3.3	42135	// neurotransmitter catabolism 5739 // mitochondrion // in 5643 // transaminase activity	Mm.25915	NP_765545.NM_127991	2.08699-005	60.7	197.9			
1416122	Cond2	cyclin D2	3.3	74	// regulation of cell cycle // in 5634 // nucleus // inferred	5515 // protein binding // ir	nmM.33340	NP_033959.NM_006929	9.01238-005	980.5	3940.9		
1421433	Zhu4	zinc finger homeodomain 4	3.3	---	5634	// nucleus // inferred 3677 // DNA binding // ir	nmM.41522	NP_109633.NM_030708	0.000398119	49.3	160.4		
1421433	Zhu4	zinc finger homeodomain 4	3.3	---	---	---	---	---	0.000192222	22.0	397.2		
1410422M04RA	RKEN_CDNA_10422M04RA gene	3.3	7283	// spermatogenesis // in 5634 // nucleus // inferred	---	---	Mm.29150	NP_080025.NM_025975	8.78438-005	557.2	1812.2		
1458554	Tce11	H-complex-associated-testis-expressed-1-like	3.3	---	---	---	---	---	1.47826-005	129.9	422.3		
1418159	Nr22	nuclear receptor subunit 2, group F, member 2	3.3	1764	// nuclear migration // in 5634 // nucleus // inferred 3677 // DNA binding // ir	nmM.27019	NP_038827.NM_009697	1.47826-005	127.8	412.1			
1433939	A73046J16	hypothetical protein A73046J16	3.2	---	---	---	Mm.27008	NP_038827.NM_009697	9.8966-005	127.8	412.1		
1452913	Poc41	Purkinje cell protein 4-like 1	3.2	---	---	---	Mm.89404	XP_484833.NM_484833	4.4804-006	84.2	247.3		
1448688	Podd	podocalyxin-like	3.2	---	5615	// extracellular space	Mm.89118	NP_038751.NM_013723	0.00025126	73.1	237.6		
1437198	Gabbr1	Gamma-aminobutyric acid (GABA-B) receptor, 1	3.2	7165	// signal transduction // in 5737 // cytoplasm // inferred 4871 // signal transducer activator	Mm.32191	NP_062312.NM_019439	4.98716-006	80.4	261.1			
1416221	Fat1	Fatty acid transferase 1	3.2	6350	// regulation of cell cycle // in 5634 // nucleus // inferred	5515 // protein binding // ir	nmM.33340	NP_033959.NM_006929	8.70234-005	980.5	3940.9		
1423083	Rab33b	RAB33b, member of RAS oncogene family	3.2	6810	// transport // inferred from 5622 // intracellular // in 5652 // GTP binding // ir	nmM.16884	NP_058554.NM_016888	1.07436-005	21.3	70.1			
1421552	Gnao1	guanine nucleotide binding protein, alpha 0	3.2	7165	// signal transduction // in 5634 // membrane fraction / 3924 // GTPase activity // ir	nmM.36740	NP_034438.NM_010308	3.34729-007	93.7	303.2			
1434796	Vamp4	VAMP4, vesicle-mediated transport 4	3.2	6192	// vesicle-mediated transport 16021 // integral to membra	---	---	NP_034438.NM_010308	2.1154-006	127.4	424.2		
1419033	2610180G18RA	RKEN_CDNA_2610180G18 gene	3.2	6468	// protein amino acid phos	---	4672	// protein kinase activity // ir	nmM.46254	NP_588480.NM_132748	0.000464743	330.4	1068.2
1425716	5730A6M10RA	RKEN_CDNA_5730A6M10 gene	3.2	---	---	---	Mm.27227	NP_081740.NM_027646	0.00033404	301.9	975.5		
1435563	Ment16	metalloendopeptidase 16	3.2	6508	// proteolysis and peptidolysis 5578 // extracellular matrix / 4222 // metalloendopeptidase	2042	NP_062858.NM_019274	1.08070-005	140.0	84.0			
1449383	Adra1	adenylosuccinate synthetase like 1	3.2	6163	// purine nucleotide metab	---	287	// magnesium ion binding // nm	3.440	NP_031447.NM_007421	0.000526109	129.5	416.6
1424207	Gdf10	growth differentiation factor 10	3.2	---	5615	// extracellular space / 5125 // cytokine activity // ir	nmM.40323	NP_068684.NM_145741	0.000025158	88.8	294.8		
1416123	Cond2	cyclin D2	3.2	74	// regulation of cell cycle // in 5634 // nucleus // inferred	5515 // protein binding // ir	nmM.33340	NP_033959.NM_006929	9.01238-005	980.5	3940.9		
1451890	MGI2384865	O-acetyltransferase 1	3.2	---	---	---	---	---	1.94256-006	327.2	1046.8		
1455178	Sytl1	synaptotagmin 1	3.2	6810	// transport // inferred from 5887 // integral to plasma m 5215 // transference activity // ir	Mm.37035	NP_061274.NM_018904	7.51889-005	131.4	419.4			
1450747	---	---	3.2	910	// cytokinesis // inferred from 5634 // nucleus // inferred 5515 // protein binding // ir	nmM.28588	NP_034438.NM_010308	2.1154-006	127.4	424.2			
1414816	Rb2	retinoblastoma-like 2	3.2	6350	// transcription // inferred 15634 // nucleus // inferred 3677 // DNA binding // ir	nmM.30550	NP_033830.NM_011250	0.00031585	89.3	283.6			
1434704	---	---	3.2	---	---	---	---	---	1.07916-005	343.9	1091.9		
1434937	Cdon	cell adhesion molecule-related-down-regulated by oncog	3.2	7155	// cell adhesion // inferred 15615 // extracellular space / 5615 // protein binding // ir	nmM.35500	NP_067314.NM_021338	0.00045812	282.3	895.3			
1433770	Dysl2	dytropyrimidine-like 2	3.2	5739	// mitochondrion // in 5676 // hydrolyase activity // ir	Mm.235823	NP_034085.NM_009955	3.78816-006	182.3	678.2			
1429177	Socx17	SRY-box containing gene 17	3.2	6350	// transcription // inferred 15634 // nucleus // inferred 3677 // DNA binding // ir	nmM.27903	NP_035571.NM_011441	1.39106-006	20.9	58.2			
1428300	Alcam	cell surface glycoprotein cell adhesion molecule	3.2	7155	// cell adhesion // inferred 15634 // nucleus // inferred 5515 // protein binding // ir	nmM.33340	NP_033959.NM_006929	9.01238-005	980.5	3940.9			
1424039	181004SK07RA	RKEN_CDNA_181004SK07 gene	3.2	---	16021	// integral to membra	Mm.29053	NP_080708.NM_026432	8.11906-005	418.5	3744.6		
1450967	493342803R1A	RKEN_CDNA_493342803 gene	3.2	---	16021	// integral to membra	Mm.374811	NP_080036.NM_025760	0.000124821	20.1	63.0		
1448649	9130002M14RA	RKEN_CDNA_9130002M14 gene	3.2	---	---	---	Mm.255145	NP_080943.NM_026967	0.000702626	120.5	716.5		
1455001	3222402P14RA	RKEN_CDNA_3222402P14 gene	3.1	---	---	---	Mm.35388	NP_135153.NM_135153	3.52566-005	44.0	138.3		
1422504	Glb	glycine receptor, beta subunit	3.1	6810	// transport // inferred from 5615 // extracellular space / 3964 // DNA-directed DNA pm	Mm.275639	NP_034428.NM_010298	0.000924202	13.4	42.0			
1421172	Adam2	a disintegrin and metalloproteinase domain 2 (metrin a)	3.1	6508	// proteolysis and peptidolysis 5578 // extracellular matrix / 4222 // metalloendopeptidase	Mm.32601	NP_031426.NM_007400	0.00130184	249.5	657.1			
1436592	Nef	neuropilin-1, LHRF factor	3.1	6350	// regulation of cell cycle // in 5634 // nucleus // inferred	5515 // protein binding // ir	nmM.33340	NP_033959.NM_006929	9.01238-005	980.5	3940.9		
1428342	Rcor3	REST corepressor 3	3.1	---	---	---	Mm.207457	NP_069063.NM_144814	2.27709-006	129.2	405.1		
1423685	Ehfb3	ehrin B3	3.1	7275	// development // inferred 15615 // extracellular space /	---	---	---	0.000729233	233.0	729.7		
1447640	Pho3	phorbol cell leukemia transcription factor 3	3.1	6350	// regulation of cell cycle // in 5634 // nucleus // inferred	5515 // protein binding // ir	nmM.33340	NP_033959.NM_006929	9.01238-005	980.5	3940.9		
1437445	Cond2	cyclin D2	3.1	74	// regulation of cell cycle // in 5634 // nucleus // inferred	5515 // protein binding // ir	nmM.33340	NP_033959.NM_006929	9.01238-005	980.5	3940.9		
1425702	Enp5	ectonucleotide pyrophosphatase/phosphodiesterase 5	3.1	9117	// nucleotide metabolism // in 5615 // extracellular space / 4551 // nucleotide diphosph	Mm.30145	NP_143921.NM_032003	7.99106-005	80.9	190.5			
1419554	Cat7	CAT7 antigen (Rb-related antigen, integrin-associated sign	3.1	7292	// vesicle-mediated transport 16021 // integral to membra	---	---	---	2.1154-006	127.4	424.2		
1418499	Amc1	amphiphilic alanine rich nuclear kinase C substrate	3.1	6810	// transport // inferred from 8076 // voltage-gated potas 5216 // ion channel activity // ir	Mm.28238	NP_065599.NM_020574	0.000556557	17.5	54.7			
1447227	Zp467	zinc finger protein 467	3.1	45448	// regulation of transcription 5634 // nucleus // inferred 3677 // DNA binding // ir	nmM.30985	NP_066114.NM_020589	1.27524-005	45.7	142.6			
1455563	Ment16	metalloendopeptidase 16	3.1	6508	// proteolysis and peptidolysis 5578 // extracellular matrix / 4222 // metalloendopeptidase	Mm.27429	NP_062858.NM_019274	1.08070-005	140.0	84.0			
1436475	Nr22	nuclear receptor subunit 2, group F, member 2	3.1	1764	// nuclear migration // in 5634 // nucleus // inferred 3677 // DNA binding // ir	nmM.27019	NP_038827.NM_009697	1.47826-005	127.8	412.1			
1417030	2310280G22RA	RKEN_CDNA_2310280G22 gene	3.1	---	---	---	Mm.283630	NP_080140.NM_025864	0.000661172	50.6	157.2		
1451766	493364D19RA	RKEN_CDNA_493364D19 gene	3.1	---	16021	// integral to membra	Mm.236300	NP_080140.NM_025864	0.000661172	50.6	157.2		
1436897	Mha1a	malignant glioma histiocytoma amplified sequence 1	3.1	---	---	---	Mm.103246	XP_356068.2X_356068	0.8776-005	28.2	87.6		
1431339	Ehmd2	Erf hand domain containing 2	3.1	7517	// muscle development // in 16459 // myosin // inferred 17374 // motor activity // ir	Mm.17917	NP_080270.NM_025994	0.000513486	49.8	138.0			
1426401	Pyg3a3	pyruvate kinase, cytosolic, alpha, alpha isoform	3.1	82	// G1/S transition of mitotic cell cycle // protein serine/threo	---	---	---	0.00154571	97.9	319.0		
1436918	181003B18RA	RKEN_CDNA_181003B18 gene	3.1	---	---	---	Mm.45566	XP_483571.NM_483571	9.30084-008	281.8	872.8		
1429566	Rhhb1	Rho-related BTB domain containing 1	3.1	7264	// small GTPase mediated	---	5515 // protein binding // ir	nmM.28659	NP_125637.NM_125637	0.000103005	38.8	119.9	
1455112	Sfhd2	serpin H2	3.1	---	---	---	Mm.24833	NP_047468.NM_132007	0.00113525	243.0	789.0		
1456057	111000615R1A	RKEN_CDNA_111000615 gene	3.1	---	5615	// extracellular space	Mm.25180	NP_589803.NM_134142	0.000193027	29.6	90.2		
1423078	672047519R1A	RKEN_CDNA_672047519 gene	3.1	---	---	---	Mm.29177	---	0.000207573	25.5	78.1		
1434805	Pyg113b	pyruvate kinase, cytosolic, beta (inhibitor) subunit 13B	3.1	6855	// regulation of transcription 5634 // nucleus // inferred 3677 // DNA binding // ir	nmM.31628	NP_067314.NM_021338	0.00045812	282.3	895.3			
141008	Tme3	transmembrane emp24 carrier containing protein 3	3.1	6886	// intracellular transport protein 5615 // extracellular space / 8320 // protein carrier activity	Mm.27066	NP_079638.NM_010260	7.28001-006	376.1	1156.8			
1447725	0C03004E14RA	RKEN_CDNA_0C03004E14 gene	3.1	---	---	---	Mm.256423	---	2.42022-005	30.9	94.8		
1428107	Sh3bp3	SH3-binding domain glutamic acid-rich protein like	3.1	6810	// transport // inferred from 5615 // extracellular space / 3964 // DNA-directed DNA pm	Mm.275639	NP_034428.NM_010298	0.000924202					

143708_x1	111000615R1K	RIKEN cDNA 111000615 gene	2,9	--	5615 // extracellular space //	Mm.25180	NP_089893.NM.134142	7.05e-005	3882	1107.0	
1434504_x1	Phz2	PHD finger protein 2	2,9	6355 // regulation of transcription 5634 // nucleus // inferred 3777 // DNA binding // inferredMm.212554	NP_030208.NM.010178	4.73003e-007	2269	646.9	1209.4	646.9	
1420928_x1	Stlg91	beta galactosidase alpha 2.6 sialyltransferase 1	2,9	6486 // protein amino acid glycosyl 574 // Golgi apparatus // in 3835 // beta-galactosidase alphaMm.149029	NP_066045.NM.145933	0.002003829	4243	1209.4	646.9	1209.4	
1434455_x1	Vhr1	very low density lipoprotein receptor	2,9	6629 // lipid metabolism // inferred 5634 // extracellular space // 4872 // receptor activity // inferredMm.4141	NP_038731.NM.013703	0.000314824	1628	98.7	463.3	463.3	
1426909_x1	483341Y06RA	RIKEN cDNA 483341Y06 gene	2,8	--	--	--	--	--	--	--	
1438931_x1	Seat1	sestin 1	2,8	7050 // cell cycle arrest // inferred 5634 // nucleus // inferred 7	Mm.139418	XP_125538.ZM.125538	0.000303513	92.0	262.0	262.0	
1426018_x1	Soaf1	SRF-box containing gene 3	2,8	6350 // transcription // inferred 5634 // nucleus // Unknown 3677 // DNA binding // inferredMm.323065	NP_030575.NM.011445	2.1377e-005	55.7	158.4	89.2	89.2	
1417252_x1	Mmp23	matrix metalloproteinase 23	2,8	6508 // proteolysis and peptidolysis 5578 // extracellular matrix // inferred 5634 // nucleus // inferred 3677 // DNA binding // inferredMm.011986	NP_030399.NM.011986	0.001985137	310.9	892.2	619.7	619.7	
1436028_x1	Tmem33	transmembrane protein 33	2,8	--	16021 // integral to membra-	Mm.23217	NP_083251.NM.028975	2.471e-005	254.4	721.6	
1448396_x1	Pp22	ribosomal protein L22	2,8	6412 // protein biosynthesis // in 5622 // intracellular // inferred 3723 // RNA binding // inferredMm.307846	NP_030105.NM.009379	1.23696e-005	895.2	1971.3	1971.3	1971.3	
1429205_x1	Pnc1	pancreatic polypeptide 1	2,8	6276 // development // inferred 5615 // extracellular space // 4887 // serine-type endopeptidaseMm.226422	NP_061857.NM.019789	0.000260502	47.3	134.0	134.0	134.0	
1445583_x1	Rh22	protodiscardin beta 2	2,8	7155 // cell adhesion // inferred 1620 // membrane // inferred 5599 // calcium ion binding // Mm.172449	NP_044375.NM.051345	1.45048e-005	267.7	75.5	75.5	75.5	
1431890_x1	Mk3	myeloid/lymphoid or mixed-lineage leukemia translocator scavenger receptor class B, member 1	2,8	6355 // regulation of transcription 5634 // nucleus // inferred 7	Mm.28888	NP_081602.NM.027328	0.00036103	87.2	169.7	169.7	
1437378_x1	Scat1	serpin-1	2,8	7155 // cell adhesion // inferred 299 // integral to membrane // 4872 // receptor activity // inferredMm.225242	NP_030037.ZM.000346	0.000307477	327.8	643.3	643.3	643.3	
1451271_x1	Acat1	acyl-Coenzyme A acyltransferase 1	2,8	--	5739 // mitochondrion // in 3985 // acetyl-CoA C-acyltransferaseMm.293233	NP_059033.NM.144784	0.000297005	315.6	891.2	891.2	
1428011_x1	Enk2p	Enk2 interacting protein	2,8	6605 // protein targeting // inferred 1623 // basolateral plasma 5515 // protein binding // inferredMm.277354	NP_00100598.NM.001058	5.37948e-006	332.4	937.6	937.6	937.6	
1452763_x1	Fnc3b	fibronectin type III domain containing 3B	2,8	--	Mm.38882	NP_176274.NM.173162	5.31098e-005	361.1	1017.5	1017.5	
1417525_x1	Hand1	heart and neural crest derivatives expressed transcript 1	2,8	1525 // angiogenesis // inferred 5634 // nucleus // inferred 3777 // DNA binding // inferredMm.4746	NP_032239.NM.008213	9.28286e-005	252.3	710.1	710.1	710.1	
1434832_x1	---	---	2,8	--	Mm.101841	---	9.93867e-005	33.9	95.4	95.4	
1438321_x1	373241Z022R	RIKEN cDNA 373241Z022 gene	2,8	--	--	--	0.000383781	157.1	442.0	442.0	
1450843_x1	Serp1n1	serpin (or cysteine) proteinase inhibitor, clade H, member 2	2,8	6457 // protein folding // inferred 5615 // extracellular space // 4866 // endopeptidase inhibMm.22708	NP_033955.NM.009825	0.000493976	2584.9	7271.1	7271.1	7271.1	
1456220_x1	---	---	2,8	--	--	--	3.65129e-005	52.4	147.4	147.4	
1430739_x1	E1En459b	DNA segment, chr 11, ERATO D01 49b, expressed	2,8	--	Mm.35817	NP_080522.NM.145840	6.80714e-005	89.5	251.6	251.6	
142442_x1	P9a2	p9a2, a RING-H2 motif containing	2,8	6512 // ubiquitin cycle // inferred --	5515 // protein binding // inferredMm.41711	NP_059108.NM.144859	6.5486e-005	586.0	1644.7	1644.7	
1449124_x1	Rg1	rat guanine nucleotide dissociation stimulator, like 1	2,8	7165 // signal transduction // in 1620 // membrane // 4872 // receptor activity // inferredMm.245270	NP_058542.NM.016848	2.58246e-006	103.2	289.0	289.0	289.0	
1425153_x1	Zmynd11	zinc finger, MYND domain containing 11	2,8	122 // regulation of transcription 5634 // nucleus // inferred 3677 // DNA binding // inferredMm.258773	NP_033039.NM.144516	6.82329e-005	439.2	1226.8	1226.8	1226.8	
1436357_x1	Zfp629	zinc finger protein 629	2,8	6877 // DNA binding // inferredMm.156718	NP_178600.NM.177226	7.8416e-006	196.2	548.1	548.1	548.1	
1428122_x1	2610528K11R	RIKEN cDNA 2610528K11 gene	2,8	--	Mm.284914	NP_178033.NM.159184	1.77809e-005	140.0	391.1	391.1	
143334_x1	Rhnc	rat heat shock cognate 1, member C	2,8	7204 // small GTPase mediated --	5515 // GTP binding // inferredMm.207148	NP_030110.NM.007148	1.9521e-005	177.1	485.2	485.2	
1452056_x1	Pp3ca	protein phosphatase 3, catalytic subunit, alpha isoform	2,8	82 // G1S transition of mitosis 8287 // protein serine/threo 158 // protein phosphataseMm.331389	NP_032939.NM.008913	4.82191e-005	296.9	828.8	828.8	828.8	
1421711_x1	Adam12	adrenomedullin and metalloproteinase domain 12 (metrin alpha)	2,8	6508 // proteolysis and peptidolysis 5578 // extracellular matrix // 4222 // metalloendopeptidaseMm.323601	NP_031426.NM.107514	0.000207311	124.4	354.5	354.5	354.5	
1425050_x1	Rtn	retin (RGS-Stearin-binding class-expressed intermediate filament associated protein 2)	2,8	6350 // transcription // inferred 5634 // nucleus // Unknown 3677 // DNA binding // inferredMm.241109	NP_067379.NM.019706	3.18948e-006	24.7	67.8	67.8	67.8	
1426911_x1	Riz2	cell heparan sulfate proteoglycan 2	2,8	6350 // transcription // inferred 5634 // nucleus // inferred 3677 // DNA binding // inferredMm.025562	NP_030629.NM.011256	0.000264965	134.6	369.3	369.3	369.3	
1456388_x1	Atp11a	ATPase, class VI, type 11A	2,8	6812 // calcium transport // inferred 1620 // membrane // inferred 287 // magnesium ion bindingMm.257837	NP_056619.NM.015804	0.000854563	260.4	724.1	724.1	724.1	
1426295_x1	R430427H17R	RIKEN cDNA R430427H17 gene	2,8	--	Mm.50600	NP_001019189.NM.001019	5.69189e-005	100.3	278.6	278.6	
1435717_x1	Ppp1r1	protein phosphatase 1, regulatory subunit 2C, like 1	2,8	165 // MAPK/JNK cascade // inferred --	587 // magnesium ion binding // inferredMm.44781	NP_049811.NM.178728	1.29481e-005	132	369.3	369.3	
1450978_x1	Ndg1	N-myristeamine regulated gene 1	2,8	4576 // mast cell activation // in 7	Mm.30037	NP_030514.NM.010884	0.00084236	76.8	208.6	208.6	
1456739_x1	Armc2	armadillo repeat containing, X-linked 2	2,8	--	16021 // integral to membra-	Mm.286969	NP_080415.NM.028139	3.40086e-007	1550.9	4304.0	
1426951_x1	Crm1	small GTP-binding protein 1	2,8	6350 // regulation of cell growth 5515 // extracellular space // 4867 // serine-type endopeptidaseMm.19388	NP_032723.NM.011912	0.000299693	304.0	839.2	839.2	839.2	
1421612_x1	H2afy3 // H2afy3/H2A histone family, member Y2 // H2A histone family, member Y2	2,8	7549 // dosage compensation // 788 // nucleus // inferred 3777 // DNA binding // inferredMm.272870	NP_080506.NM.026230	0.000235858	499.4	1385.4	1385.4	1385.4		
1449404_x1	Pp3k2a	phosphatidylinositol-3-kinase type 2, alpha isoform	2,8	187 // activation of MAPK // in 5615 // extracellular space // 1630 // kinase activity // inferredMm.312977	NP_030871.NM.010845	0.000239336	100.2	277.7	277.7	277.7	
1416895_x1	Elna1	epithelial sodium channel 1	2,8	747 // activation of MAPK // in 5615 // extracellular space // 1630 // kinase activity // inferredMm.312977	NP_030871.NM.010845	0.000239336	100.2	277.7	277.7	277.7	
1451462_x1	Inra2	intra-2, alpha (beta) and beta 2 receptor 2	2,8	6357 // regulation of transcription 5615 // extracellular space // 4872 // receptor activity // inferredMm.6834	NP_034639.NM.010559	0.00080436	308.8	849.8	849.8	849.8	
1418928_x1	Zhu1a	zinc finger homeobox 1a	2,8	6350 // transcription // inferred 5634 // nucleus // inferred 3677 // nucleic acid binding // inferredMm.3629	NP_030676.NM.011948	1.47858e-007	524.7	1452.8	1452.8	1452.8	
1425163_x1	3110041P15R	RIKEN cDNA 3110041P15 gene	2,8	--	Mm.331498	NP_030634.NM.194371	2.98871e-005	316.8	818.8	818.8	
1418049_x1	Ltp3	latent transforming growth factor beta binding protein 3	2,8	1501 // skeletal development // in 5578 // extracellular region // 5509 // calcium ion binding // Mm.123396	NP_032546.NM.008520	0.0018999	373.6	1003.3	1003.3	1003.3	
1417806_x1	Podp2	poeype domain containing 2	2,8	1620 // membrane // in 1620 // membrane // in 1620 // membrane // inferredMm.28688	NP_071713.NM.022318	3.55225e-005	146.2	403.6	403.6	403.6	
1427185_x1	Mad2	small GTP-binding protein 2	2,8	6350 // transcription // inferred 5634 // nucleus // Unknown 3677 // DNA binding // inferredMm.133788	NP_038825.NM.013597	9.38767e-006	304.0	839.2	839.2	839.2	
1437853_x1	Ndn	necdin	2,8	1558 // regulation of cell growth 5634 // nucleus // inferred 3777 // DNA binding // inferredMm.250919	NP_030512.NM.010884	7.27785e-006	820.3	2261.6	2261.6	2261.6	
1429312_x1	Ror1	receptor tyrosine kinase like orphan receptor 1	2,8	6486 // protein amino acid glycosyl 5615 // extracellular space // 4872 // receptor activity // inferredMm.5752	NP_038873.NM.013845	0.000964384	32.6	89.8	89.8	89.8	
1433723_x1	Seaf2	Small EDRK-related factor 2	2,8	6486 // protein amino acid glycosyl 5615 // extracellular space // 4872 // receptor activity // inferredMm.5752	NP_038873.NM.013845	0.000964384	32.6	89.8	89.8	89.8	
1433488_x1	Grs	guanine nucleotide- (N-acetyl)-S-sulfatase	2,8	6027 // glycosaminoglycan catab 5764 // lysosome // inferred 4449 // N-acetylglucosaminaseMm.207683	NP_083640.NM.002813	0.00020133	316.7	870.4	870.4	870.4	
1417999_x1	Itih2b	integrin membrane protein 2b	2,7	--	5624 // membrane fraction // 5524 // ATP binding // inferredMm.4266	NP_032436.NM.008410	6.14249e-005	1435.4	3942.5	3942.5	
1422510_x1	Ctsp1	cathepsin B, cytosolic, lysosomal, RNA polymerase II, poly	2,7	--	5634 // nucleus // inferred 7	Mm.22542	NP_030629.NM.011256	0.000264965	134.6	369.3	
1428617_x1	1700129L13R	RIKEN cDNA 1700129L13 gene	2,7	--	--	--	0.000400605	120.0	318.8	318.8	
1455262_x1	---	---	2,7	--	--	--	0.00011897	102.9	282.3	282.3	
1430737_x1	Socb1	small EDRK-related factor 1	2,7	6810 // transport // inferred from 1205 // stress fiber // inferred 5515 // protein binding // in 5615 // extracellular space // 4872 // receptor activity // inferredMm.259122	NP_033152.NM.009106	0.000267006	177.1	485.2	485.2	485.2	
1418860_x1	Lem1	LETM1 domain containing 1	2,7	6355 // regulation of transcription 5615 // extracellular space // 4872 // receptor activity // inferredMm.292168	NP_080684.NM.134093	4.6538e-006	139.5	382.5	382.5	382.5	
1424399_x1	Scn3p	synuclein, alpha interacting protein (synphin)	2,7	6355 // regulation of transcription 5615 // extracellular space // 4872 // receptor activity // inferredMm.292168	NP_080684.NM.134093	4.6538e-006	139.5	382.5	382.5	382.5	
1418037_x1	Tspr	tyrosin sulfatase-deficient lymphoplasma, receptor	2,7	--	5615 // extracellular space // 4872 // receptor activity // inferredMm.307171	NP_057924.NM.016715	0.00020889	472.3	1293.1	1293.1	
1420143_x1	Tca	transcription factor 1, cytosolic, member C	2,7	187 // activation of MAPK // in 5615 // extracellular space // 1630 // kinase activity // inferredMm.156718	NP_178600.NM.177226	7.8416e-006	196.2	548.1	548.1	548.1	
1448510_x1	Elna1	epithelial sodium channel 1	2,7	187 // activation of MAPK // in 5615 // extracellular space // 1630 // kinase activity // inferredMm.156718	NP_178600.NM.177226	7.8416e-006	196.2	548.1	548.1	548.1	
1452761_x1	R430436D14R	RIKEN cDNA R430436D14 gene	2,7	--	--	--	0.000716445	251.3	687.0	687.0	
1428965_x1	Cd9p2	C9orf2 antigen-like 2	2,7	--	5615 // extracellular space //	Mm.283879	NP_012182.NM.138309	6.70898e-005	63.4	172.9	172.9
1458341_x1	---	---	2,7	--	--	Mm.134911	---	2.00016228	2068.3	5616.4	
1425740_x1	Myh10	myosin, heavy polypeptide 10, non-muscle	2,7	902 // cellular morphology // 1725 // stress fiber // inferred 3774 // motor activity // inferredMm.218233	NP_178469.NM.175260	0.00149228	2068.3	5616.4	5616.4	5616.4	
1448700_x1	---	---	2,7	--	--	Mm.24979	---	0.000199693	115.9	318.8	
1442434_x1	D8Erd82e	DNA segment, chr 8, ERATO D01 82, expressed	2,7	--	5524 // ATP binding // inferredMm.244971	NP_176649.NM.172911	0.000149708	554.0	1510.0	1510.0	
1434222_x1	Sema5a	sema domain, seven transmembrane repeats type 1 and 2	2,7	7275 // development // inferred 5615 // extracellular space // 4872 // receptor activity // inferredMm.260374	NP_033180.NM.009154	1.84696e-005	112.5	306.2	306.2	306.2	
1417272_x1	3110002N14R	RIKEN cDNA 3110002N14 gene	2,7	--	Mm.26545	NP_038825.NM.013597	9.38767e-006	304.0	839.2	839.2	
1427206_x1	Tcn2	transcobalamin 2	2,7	6810 // transport // inferred 5615 // extracellular space // 488 // binding // inferred fromMm.20948	NP_056584.NM.015749	1.02003e-005	589.0	1592.7	1592.7	1592.7	
1427236_x1	Mis5	myeloid/lymphoid or mixed-lineage leukemia 5	2,7	6355 // regulation of transcription --	3677 // DNA binding // inferredMm.205100	NP_045570.NM.045570	1.74438e-005	358.0	971.6	971.6	
1420270_x1	Cd81b1	glycoprotein IIb/IIIa 8 domain containing 1									

1448392	Sparc	secreted acidic cysteine rich glycoprotein	2.6	---	5578 // extracellular matrix 15509 // calcium ion binding // Uni.M.21442	NP_033568.1NM_029242	0.0001487	4551.6	11676.7
1449198	Slc6a5	ST3 beta-galactoside alpha-2,6-sialyltransferase 5	2.6	6486 // protein amino acid phosphorylation // Golgi apparatus // in 5373 // sialyltransferase actvMm.38248	NP_035055.1NM_011375	---	1.40336e-006	445.8	1141.4
1420725	Tm6he	trimethyllysine hydroxylase, epsilon	2.6	45329 // carnitine biosynthesis 5739 // methionine // in 16491 // oxidoreductase actvMm.139078	NP_056564.1NM_015749	---	1.20256e-005	86.4	2217.2
1447800	Tnc2	Transcortinin 2	2.6	6810 // transport // inferred from 5615 // extracellular space 5488 // binding // inferred from 26949	NP_056564.1NM_015749	---	0.000215138	866.4	2217.2
141648	Ctspg	141648	2.6	74 // regulation of cell cycle // in 5789 // cyclin-dependent kinase 2	NP_031611.1NM_020757	---	0.000093034	325	830.6
1415780	Ammc2	ammiolip repeat containing, X-linked 2	2.6	---	NP_080415.2NM_026139	---	2.02005e-005	340.0	3408.0
1414948	Tex27	testis expressed protein 27	2.5	---	NP_220972	---	0.00010448	463.4	1109.0
1434108	Epm2af1	EPH2A (also known as EPHA2) protein	2.5	5783 // endoplasmic reticulum 5513 // protein binding // inferred from 25949	NP_083726.1NM_148526	---	4.42824e-005	188.1	479.8
1416418	Gabaraip1	gamma-aminobutyric acid (GABA(A)) receptor-associated	2.5	5786 // aromatic amino acid biosynthesis 8092 // cytoskeletal protein b.Mm.14638	NP_065615.1NM_020590	---	0.0008835	303.1	769.9
1452208	Z008082R2AR	RKEN1 DNA Z0080824 gene	2.5	---	NP_281762	---	1.45846e-005	350.5	889.6
1425241	Wnt1	Wnt1 (also known as Wnt1) non-covalently associated	2.5	742 // intracellular signaling ca. ---	NP_030328.1NM_019853	---	2.74383e-002	145.0	350.9
1427727	Poyvnt1	prenyltransferase oxidase 1	2.5	30328 // protein tyrosine kinase 5615 // extracellular space 1735 // prenyltransferase oxidaseMm.20383	NP_080099.1NM_025823	---	1.17516e-007	87.0	2207.2
1417471	D1E0222e	DNA segment, chr 1, ERATO D01 622, expressed	2.5	---	NP_12309	---	0.000681622	37.6	95.2
1452162	Gsn2	UDP-N-acetyl-alpha-D-glucosaminyl-polyphosphate N-acetyl	2.5	6483 // O-linked glycosylation // 5794 // Golgi apparatus // in 4653 // polypeptide N-acetyltransferase	NP_044678.1NM_135072	---	0.00012097	100.0	254.3
1456603	150005K14R	RKEN1 DNA 150005K14 gene	2.5	---	NP_341311	---	5.0334e-005	210.7	538.1
1448744	---	---	2.5	---	NP_27742	---	8.89998e-008	247.6	626.3
1435074	Z31008Z2R2R	RKEN1 DNA Z31008Z22 gene	2.5	---	NP_082268.1NM_027992	---	9.4866e-006	394.4	997.0
1422313	Igf1bp5	insulin-like growth factor binding protein 5	2.5	1558 // regulation of cell growth 5576 // extracellular region 5520 // insulin-like growth factorMm.309617	NP_034648.1NM_010518	---	4.64416e-006	511.6	1292.5
1455901	Chp1	choline phosphotransferase 1	2.5	---	NP_089887	---	0.00012751	20.9	52.9
1436447	AL004037	expressed sequence AL004037	2.5	16021 // integral to membrane 16740 // transferase activity // Mm.288887	NP_059056.2NM_144807	---	0.000221983	58.4	147.4
1416845	Hsp90a1	heat shock 70kDa protein 5 binding protein 1	2.5	6457 // protein folding // inferred 16021 // integral to membrane ---	NP_27387	---	0.000175809	61.5	154.0
1426648	Mapkapk2	MAP kinase-activated protein kinase 2	2.5	6488 // protein amino acid phosph 5634 // nucleus // inferred // 4672 // protein kinase activityMm.221205	NP_032577.1NM_008551	---	0.000828974	653.3	1643.0
1438423	Sap2	single-stranded DNA binding protein 2	2.5	7242 // intracellular signaling ca. ---	NP_033028.2NM_020836	---	0.000297637	18.7	46.9
1434034	Cerk	ceramide kinase	2.5	6672 // ceramide metabolism 5624 // membrane fraction 287 // magnesium ion bindingMm.228685	NP_063450.3NM_145475	---	0.000898263	102.0	255.9
1435198	---	---	2.5	---	---	---	8.9421e+006	52.3	131.3
1419383	Ahgef17	Rho guanine nucleotide exchange factor (GEF) 17	2.5	30036 // actin cytoskeleton org. ---	NP_133692.1NM_133692	---	3.48723e-005	115.7	293.2
1418840	Ptd4a	programmed cell death 4	2.5	16853 // isomerase activity // Mm.1050	NP_035180.1NM_011050	---	1.59458e-005	740.0	1866.0
1448645	Mu31	male-specific lethal 3 (Drosophila)	2.5	6333 // chromatin assembly or 788 // chromatin // inferred // 1862 // chromatin binding // inMm.24248	NP_034962.2NM_010832	---	2.00272e-007	273.3	584.8
1428387	Nst1	N-deacetylase-N-sulfotransferase (heparan glucosaminyl)	2.5	271 // polysaccharide biosynthesis 5794 // Golgi apparatus // in 4197 // cytoskeleton type endosMm.181862	NP_033232.2NM_020836	---	5.64931e+005	231.3	680.1
1416483	Tlc3	tetraspanin repeat domain 3	2.5	---	NP_213408	---	6.87851e-007	866.8	2178.5
1428283	MCL2448259	neuritin	2.5	7155 // cell adhesion // inferred ---	NP_05151 // protein binding // inMm.283138	---	1.6438e-006	60.5	151.4
1419693	Colec12	collin sub-family member 12	2.5	6910 // transcription, recognition 16020 // membrane // inferred // 472 // receptor activity // inMm.218571	NP_089716.1NM_130449	---	0.000403265	200.5	502.0
1427635	Nccl1	Nucleo-cytoplasmic factor 2 (family 3, group C, member 1)	2.5	6910 // transcription // inferred // 5634 // nucleus // inferred // 472 // receptor activity // inMm.204473	NP_033028.2NM_020836	---	0.00018096	80.0	197.5
1429722	92301112R1R	RKEN1 DNA 923011122 gene	2.5	---	NP_33277	---	0.000177416	10.6	26.67
1448750	Nr1	heart and neural crest derivatives expressed transcript 1	2.5	1525 // angiogenesis // inferred // 5634 // nucleus // inferred // 3677 // DNA binding // inMm.4746	NP_032329.1NM_008213	---	1.60134e-005	189.8	474.6
1437478	Ehr2	ERH2 nuclear core factor 2	2.5	7517 // muscle development // in 1659 // myosin // inferred // 571 // motor activity // inMm.1258	NP_0010584.1NM_011917	---	0.000150845	194.9	487.2
145624	Yar2	phospholipid transfer protein	2.5	6810 // transport // inferred // 5615 // extracellular space 5289 // lipid binding // inMm.6105	NP_032555.1NM_011125	---	3.89179e-005	622.8	4057.9
143970	Pdghfr	platelet derived growth factor receptor, beta polypeptide	2.5	6488 // protein amino acid phosph 5615 // extracellular space 4672 // receptor activity // inMm.4148	NP_032835.1NM_008909	---	0.00015215	293.4	731.9
1433730	Ehr1	ERH1 nuclear core factor 1	2.5	7517 // muscle development // in 1659 // myosin // inferred // 571 // motor activity // inMm.1258	NP_048651.1NM_17878	---	6.16296e-005	394.9	850.9
1421916	Pdghra	platelet derived growth factor receptor, alpha polypeptide	2.5	6488 // protein amino acid phosph 5615 // extracellular space 4672 // receptor activity // inMm.221403	NP_035188.1NM_011058	---	0.000735242	160.9	401.0
1417612	Irf5	interferon response factor 5	2.5	---	NP_124266	---	0.000147916	377.7	941.4
1450151	Zfp116	Zfp116 zinc finger protein 316	2.5	6810 // transport // inferred // 16020 // membrane // in 5215 // transporter activity // inMm.209497	NP_059451.1NM_020497	---	1.40493e-005	118.6	298.0
1417073	Ok	quaking	2.5	1570 // vasculogenesis // inferred // 5634 // nucleus // traceable 3676 // nucleic acid binding // inMm.262394	NP_068881.1NM_021881	---	0.00050464	332.2	824.9
1418481	---	---	2.5	---	NP_364795	---	1.5284e-005	74.8	185.7
1447223	MCL1930686	Transcript MCL1930686	2.5	---	---	---	5.29298e-002	105.9	268.1
1448434	Rf103	ringer finger protein 103	2.5	16587 // protein ubiquitination // in 151 // ubiquitin ligase complex 3676 // nucleic acid binding // inMm.310	NP_033569.1NM_009543	---	0.00063187	203.9	505.7
1415961	Ihm2c	integral membrane protein 2C	2.5	5624 // membrane fraction 5524 // ATP binding // inMm.28870	NP_071862.1NM_022417	---	1.5688e-006	1377.6	3412.0
1417201	Tid1a1a	ubiquitin receptor factor superfamily, member 1a	2.5	6963 // prostaglandin metabolism 5615 // extracellular space 4672 // receptor activity // inMm.15189	NP_037042.1NM_011578	---	0.000391711	40.5	101.2
1419550	Slk39	serine/threonine kinase 39, STE20/SPK1 homolog (yeast)	2.5	6488 // protein amino acid phosph ---	NP_058582.1NM_016886	---	0.000673116	168.6	417.3
1423222	Cap2	CAP, adenylate cyclase-associated protein 2 (yeast)	2.5	16020 // membrane // inMm.44259	NP_080332.1NM_020956	---	1.28151e-005	72.9	190.7
1425620	Tgfb3	transforming growth factor, beta receptor III	2.5	5615 // extracellular space 5615 // extracellular space 4672 // receptor activity // inMm.15189	NP_037042.1NM_011578	---	2.89939e-005	221.5	548.7
1424634	Tceal1	transcription elongation factor A (SII)-like 1	2.5	---	NP_066348.1NM_142326	---	9.1926e-005	107.5	265.6
1454704	Scarb2	scavenger receptor class B, member 2	2.5	7155 // cell adhesion // inferred // 5615 // extracellular space 4672 // receptor activity // inMm.297914	NP_031670.1NM_00744	---	4.95846e-007	750.6	1853.8
1424201	Scarb1	scavenger receptor class B, member 1	2.5	7155 // cell adhesion // inferred // 5615 // extracellular space 4672 // receptor activity // inMm.297914	NP_031670.1NM_00744	---	0.001450205	194.4	487.2
1445057	Cd47	CD47 antigen (Rb-related antigen, integrin-associated sig	2.5	7223 // integrin-mediated signal 5615 // extracellular space 5615 // protein binding // inMm.3110	NP_034711.1NM_170811	---	0.000102783	599.6	1479.7
1455550	---	---	2.5	---	---	---	0.000692755	144.8	358.4
1452650	Tm62	titinlike motif-containing protein 2	2.5	---	NP_313553	---	0.000297531	40.5	89.8
1456790	AA407452	EST AA407452	2.5	---	NP_84441	---	2.95888e-005	34.8	84.8
1454978	Thy13	twenty homolog 3 (Drosophila)	2.5	16021 // integral to membrane 5254 // chloride channel actvMm.28947	NP_780483.1NM_175274	---	0.000300331	885.3	2161.5
1435167	Ranbp6	RAN binding protein 6	2.5	6910 // transport // inferred from 5634 // nucleus // inferred // 7	NP_083899.2NM_177721	---	0.0000066	52.4	129.1
1414702	Slc44	solute carrier family 4 (anion exchanger), member 4	2.5	6488 // protein amino acid phosph ---	NP_039515.1NM_011785	---	0.000189713	394.9	971.7
1433925	Dnc2	dynamin, cytoplasmic, light intermediate polypeptide 2	2.5	---	NP_289983	---	1.1145e-006	415.8	1022.8
1434096	Slc44a	solute carrier family 4 (anion exchanger), member 4	2.5	6810 // transport // inferred from 5634 // nucleus // inferred // 7	NP_039515.1NM_011785	---	0.000189713	394.9	971.7
1423399	Yar2	Yar2 associated factor 2	2.5	6810 // transport // inferred from 5634 // nucleus // inferred // 7	NP_039515.1NM_011785	---	5.28305e-007	47.0	116.0
1418067	Clr2	collin 2, zinc finger	2.5	---	NP_033276	---	5.3227e-006	1438.0	3529.9
1455146	E430011P2R2R	RKEN1 DNA E430011P22 gene	2.5	---	NP_037174.1NM_007888	---	0.000141248	78.0	190.8
141519	Fbn1	fibulin 1	2.5	5576 // extracellular region 5509 // calcium ion binding // Uni.M.287992	NP_034310.1NM_010180	---	1.19955e-005	839.9	2058.6
1434328	Coro2b	coronin, actin binding protein, 2B	2.5	7165 // signal transduction // inferred // 5634 // nucleus // inferred // 3779 // actin binding // inMm.335229	NP_700693.1NM_175484	---	2.04854e-005	89.7	219.8
1416419	Gabaraip1	gamma-aminobutyric acid (GABA(A)) receptor-associated	2.5	5786 // aromatic amino acid biosynthesis 8092 // cytoskeletal protein b.Mm.14638	NP_065615.1NM_020590	---	1.28657e-005	303.1	769.9
1457139	Ausz2	autism susceptibility candidate 2	2.4	---	NP_217323	---	1.18657e-006	188.9	461.9
1460319	Fub1	ubiquitin transferase 6	2.4	---	NP_058589.2NM_016893	---	5.17426e-005	419.5	1023.3
142562	DK004017R2R	RKEN1 DNA DK0040172 gene	2.4	---	NP_145033.1NM_145033	---	3.24262e-005	128.9	324.8
1456022	Hpk2	homeodomain interacting protein kinase 2	2.4	122 // negative regulation of transcription // in 314 // transcription corepMm.23790	NP_034563.1NM_010433	---	5.37426e-005	116.9	285.5
1455009	Cpd	carboxypeptidase 2	2.4	6508 // proteolysis and peptidolysis 5615 // extracellular space 4180 // carboxypeptidase actMm.276738	NP_031780.1NM_007754	---	0.000495941	171.2	417.5
1428372	Scd5	suppression of tumorigenicity 5 (Drosophila)	2.4	---	NP_262303	---	7.33424e-004	348.9	845.9
1419684	Sir	serine racemase	2.4	3824 // catalytic activity // inMm.131443	NP_038789.1NM_013761	---	3.84307e-005	59.7	145.4
1422208	Grb5	guanine nucleotide binding protein, beta 5	2.4	7165 // signal transduction // inferred // 5634 // heterotrimeric G-protein 3924 // GTPase activity // inMm.17604	NP_034443.1NM_010313	---	8.68811e-005	207.2	503.8
1437766	---	---	2.4	---	---	---	0.000430448	249.8	618.4
1429006	AK	AK serine/threonine kinase 1	2.4	---	NP_6415 // acyltransferase actvMm.273155	---	0.000282526	95.9	232.8
1449089	Nr1	nuclear receptor interacting protein 1	2.4	122 // negative regulation of transcription // in 314 // transcription corepMm.274711	NP_075616.1NM_173440	---	0.000999184	190.0	461.3
1424053	RKEN1 DNA Z008082R2R	RKEN1 DNA Z0080824 gene	2.4	6096 // cell wall catabolism // in ---	NP_790420.1NM_175215	---	2.71328e-005	101.3	251.3
1428779	983013G2R2R	RKEN1 DNA 983013G207 gene	2.4	---	NP_766231.1NM_172643	---	1.95948e-006	154.6	375.0
1448899	Slc38a4	solute carrier family 38, member 4	2.4	6910 // transport // inferred from 16020 // membrane // in 5215 // transporter activity // inMm.209497	NP_081328.1NM_027052	---	0.00089516	1375.8	3338.7
1437234	Hmrl1	heterogeneous ribonucleoprotein methyltransferase class 1	2.4	6380 // RNA processing // inferred // 5634 // nucleus // inferred // 678 // methyltransferase actvMm.20200	NP_073461.1NM_133162	---	6.1734e-005	60.3	90.3

1451019_a.t	Csf1	---	---	6508 // proteolysis and peptidolysis 5615 // extracellular space / 4197 // cysteine-type endopeptidase	Mm.29561	NP_063914.NM_191861	0.000131283	235.7	548.0
1437490_a.t	---	---	---	---	---	---	0.000983809	289.2	669.6
1450881_a.t	Tm7f1	transmembrane 7 superfamily member 1	2.3	---	Mm.35677	NP_114388.NM_031999	1.12334-005	182.9	433.7
1452653_a.t	181030824R	RIKEN cDNA 181030824 gene	2.3	---	Mm.8606	NP_060486.NM_020210	0.45068-006	665.7	1540.4
1436514_a.t	Cdc19	CDC28 protein kinase 19	2.3	910 // cytokinesis // inferred from 16201 // integral to membra	Mm.6923	NP_099201.NM_018944	1.9528-001	47.2	109.9
1433694_a.t	Pde3b	phosphodiesterase 3B, cGMP-inhibited	2.3	1165 // signal transduction // inferred from 5634 // nucleus // inferred from 3677 // DNA binding // infer	Mm.103319	NP_030518.NM_011055	0.63786-006	210.4	486.3
1427500_a.t	Slx5	sex locus-related homeobox 5 homolog (Drosophila)	2.3	6350 // transcription // inferred from 5634 // nucleus // inferred from 3677 // DNA binding // infer	Mm.34110	NP_030518.NM_011055	3.44037-007	197.9	458.8
1481853_a.t	Lamnt1	lamin A, type 1	2.3	2011 // morphogenesis of an ep	Mm.42007	NP_020506.NM_008480	0.000138444	100.9	509.3
1454646_a.t	E45400E19RA	RIKEN cDNA E45400E19 gene	2.3	---	Mm.28142	NP_066120.NM_146008	0.00023643	91.7	211.6
1427524_a.t	Slp17	synaptotagmin 17	2.3	---	Mm.17134	NP_060619.NM_026343	2.93256-007	84.3	194.4
1434044_a.t	Repr1	repression initiator 1	2.3	6954 // inflammation of response // 5576 // extracellular region // 5125 // cytokine activity // infer	Mm.25193	NP_060619.NM_026343	9.62951-005	201.9	463.8
144510_a.t	Znf467	zinc finger protein 467	2.3	45449 // regulatory transcript // 5634 // nucleus // inferred from 3677 // DNA binding // infer	Mm.306885	NP_066614.NM_020589	0.21051-005	126.3	291.1
1433333_a.t	Hf2p2	infection regulatory factor 2 binding protein 2	2.3	122 // negative regulation of tra	Mm.334918	NP_284454.XM_284454	1.71242e-005	264.6	609.7
1416472_a.t	Syp1	synapse associated protein 1	2.3	5634 // nucleus // inferred fr	Mm.44207	NP_080208.NM_025932	4.97179-009	406.9	937.5
1428692_a.t	111003309RA	RIKEN cDNA 111003309 gene	2.3	---	Mm.21171	NP_081088.NM_026812	1.8667-005	168.9	388.9
1428540_a.t	3321401G0AR	RIKEN cDNA 3321401G0A gene	2.3	---	Mm.24652	NP_084206.NM_029390	1.3738e-006	395.5	910.4
1426790_a.t	Rab1b	RAB8B, member RAS oncogene family	2.3	160 // two-component signal tra	Mm.9677	NP_075589.NM_174113	0.000908009	367.7	845.6
1448442_a.t	Cd61	cysteine dioxygenase 1, cytosolic	2.3	19452 // iron homeostasis // 5739 // mitochondrial // 1164 // iron binding // infer	Mm.241056	NP_149026.NM_030303	0.63826-007	162.8	374.3
1451520_a.t	Dnm1	dynamitin 1	2.3	6897 // endocytosis // inferred from 30117 // membrane coat // 13774 // motor activity // infer	Mm.4738	NP_034195.NM_010065	4.2714-005	394.3	903.9
1460365_a.t	Cnm1	adenylyl kinase 3	2.3	8652 // anti-oxidant biosynthesis // 5739 // mitochondrial // 1164 // iron binding // infer	Mm.196067	NP_082774.NM_021299	1.55315e-005	394.1	905.2
1428683_a.t	Rbm	RNA binding motif protein, subfamily H (eag-related)	2.3	5634 // nucleus // inferred from 3676 // nucleic acid binding // infer	Mm.28275	NP_038382.NM_011252	0.000654474	115.6	265.5
1451912_a.t	Fgfr1	fibroblast growth factor receptor-like 1	2.3	7168 // cell surface receptor like	Mm.240361	NP_073412.NM_054079	3.72302e-005	233.7	538.5
1435790_a.t	Psd	pleckstrin and Sec7 domain containing protein voltage-gated channel, subfamily H (eag-related)	2.3	160 // two-component signal tra	Mm.6539	NP_038597.NM_013569	6.1788e-006	235.7	540.8
1449544_a.t	Korh2	soluble carrier family 1 (glial high affinity glutamate transp	2.3	6005 // protein targeting // infer	Mm.5343	NP_037401.NM_148398	1.5772e-005	95.6	219.4
1424201_a.t	Gria2	glutamate receptor ionotropic, AMPA 2	2.3	6629 // lipid metabolism // infer	Mm.28707	NP_034429.NM_010299	6.18449e-005	428.6	953.6
1439089_a.t	883013207BR	RIKEN cDNA 883013207 gene	2.3	---	Mm.19171	NP_076231.NM_172643	0.000134033	109.9	252.2
1429230_a.t	Hr23	invariant polydiphosphate 2 (NAOP+), mitochondrial	2.3	6029 // main pathway of carbon	Mm.173011	NP_060486.NM_020210	0.000431623	161.0	361.3
1454642_a.t	COMM3	COMM domain containing 3	2.3	160 // two-component signal tra	Mm.249586	NP_080087.NM_147778	0.00068393	552.3	1265.8
1419062_a.t	Epd4.1b3	erythrocyte protein band 4.1-like 3	2.3	30866 // cytosolic actin cytoskeleton // 5737 // cytoplasm // inferred from 3779 // actin binding // infer	Mm.13135	NP_038841.NM_013813	2.28114e-005	430.8	987.0
1436853_a.t	Snc	synuclein, alpha	2.3	44849 // synaptic vesicle transp	Mm.17484	NP_033247.NM_020221	0.00019889	21.1	53.0
1435772_a.t	Kctd1b	keratin-like domain containing 1B	2.3	7017 // microtubule-based proc	Mm.249586	NP_080087.NM_147778	0.000431623	161.0	361.3
1419081_a.t	Appl10	autophagy 10-like (S. cerevisiae)	2.3	6512 // ubiquitin cycle // infer	Mm.5515	NP_036717.NM_018628	1.37342e-005	70.3	161.0
1434572_a.t	Trf2	transferrin locus 2	2.3	4457 // protein folding // infer	Mm.377036	NP_030297.NM_016783	0.000397378	20.4	46.8
1433451_a.t	Fkbp14	FKBP binding protein 14	2.3	6512 // ubiquitin cycle // infer	Mm.377036	NP_030297.NM_016783	0.000397378	20.4	46.8
1448389_a.t	Tal1	T cell acute lymphocytic leukemia 1	2.3	6350 // transcription // infer	Mm.37979	NP_036567.NM_011527	2.30287e-005	65.7	150.3
1448548_a.t	Tup4	tubulin like protein 4	2.3	7242 // intracellular signaling ca	Mm.28251	NP_073381.NM_054040	0.000116889	48.1	110.3
1415989_a.t	Hsp1	heat shock protein of 90 kDa class B member 1	2.3	1370 // escapologenes // infer	Mm.249586	NP_080087.NM_147778	0.000431623	161.0	361.3
1460307_a.t	At3	thymoma viral protein oncogene 3	2.3	6468 // protein amino acid phos	Mm.235194	NP_035915.NM_011785	0.000225758	172.2	393.3
1458370_a.t	Bmp2c	BMP2 inducible kinase	2.3	6468 // protein amino acid phos	Mm.281490	NP_054239.NM_060708	0.000129661	90.8	207.3
1429624_a.t	Vangl3	vanilloid-associated membrane protein 3	2.3	6192 // vesicle-mediated transp	Mm.101674	NP_050742.NM_016784	5.525e-008	174.2	528.8
1426897_a.t	5430417L22RA	RIKEN cDNA 5430417L22 gene	2.3	---	Mm.19666	---	1.17815e-005	121.7	277.8
1418455_a.t	Cop2	coatamer protein complex, subunit zeta 2	2.3	6810 // transport // infer	Mm.22144	NP_063930.NM_019877	0.000195951	289.3	660.6
1429837_a.t	Tnc1c5	tropomyosin containing 15	2.3	---	Mm.23065	NP_066224.NM_146112	3.42876e-005	167.2	374.3
1451146_a.t	Scgb	sarcoglycan, beta (dystrophin-associated glycoprotein)	2.3	7010 // cytoskeleton organizati	Mm.38868	NP_036200.NM_011890	1.0247e-005	93.3	212.7
1449566_a.t	Pnce	phosphatidylethanolamine N-transferase	2.3	6468 // protein amino acid phos	Mm.27860	NP_028234.NM_017683	0.00012328	118.2	270.0
1420726_a.t	Tmhe	trimethyllysine hydroxylase, epsilon	2.3	45329 // cAMP biosynthesis // 5739 // mitochondrial // 1164 // iron binding // infer	Mm.139078	NP_020097.NM_013878	2.3424e-005	85.5	87.6
1422258_a.t	Zfp361	zinc finger protein 36, C3H type-like 1	2.3	5634 // nucleus // inferred from 3676 // nucleic acid binding // infer	Mm.235132	NP_031590.NM_007564	0.000496631	89.0	195.7
1424189_a.t	Pcp1	CP1 nuclear biosynthesis factor 1	2.3	6006 // GTPi nuclear biosynthesis	Mm.249586	NP_080087.NM_147778	0.000431623	161.0	361.3
1431012_a.t	Peci	peroxisomal delta3, delta2-acyl-Coenzyme A isomerase	2.3	7010 // peroxisome organization // 5777 // peroxisome // infer	Mm.28883	NP_035988.NM_011888	4.1611e-005	415.3	945.4
1423500_a.t	Sox5	SRF-box containing gene 5	2.3	6350 // transcription // infer	Mm.1752	NP_035744.NM_011444	0.00098268	32.9	74.8
1450910_a.t	Cag2	CAP, adenylate cyclase-associated protein, 2 (yeast)	2.3	1600 // membrane // infer	Mm.249586	NP_080087.NM_147778	0.000431623	161.0	361.3
1425854_a.t	---	---	2.3	---	---	---	---	---	---
1431375_a.t	Panva	parvin, alpha	2.3	7155 // cell adhesion // infer	Mm.14363	NP_066531.NM_020606	5.97398e-005	480.8	1092.6
1453989_a.t	2610005L07RA	RIKEN cDNA 2610005L07 gene	2.3	---	Mm.157800	NP_480359.NM_480359	1.38203e-005	846.0	1913.0
1455591_a.t	---	---	2.3	---	---	---	0.000116031	146.8	333.2
1425701_a.t	Rgs3	regulator of G-protein signaling 3	2.3	7165 // signal transduction // infer	Mm.286753	NP_082365.NM_019492	0.000218931	186.7	423.2
1418987_a.t	Sif7	Suppression of tumorigenicity 7	2.3	---	Mm.12051	NP_071727.NM_022332	6.7284e-005	112.1	254.1
1438532_a.t	PncB	penicillinase, beta-lactamase	2.3	---	Mm.24652	NP_084206.NM_029390	1.3738e-006	395.5	910.4
1423729_a.t	AK123302	cDNA sequence AK123302	2.3	---	Mm.336158	NP_0010039.NM_0010039	2.65955e-005	246.4	532.4
1451731_a.t	Abca3	ATP-binding cassette, sub-family A (ABC1), member 3	2.3	6810 // transport // infer	Mm.239470	NP_038883.NM_013855	1.4474e-005	280.0	632.8
1433844_a.t	Lp12	lipoteichoic acid-related protein 12	2.3	6192 // endocytosis // infer	Mm.5205	NP_069602.NM_122814	8.59679e-005	39.0	89.0
1404147_a.t	Lg2	leucine-rich repeat, LGI family, member 2	2.3	---	Mm.44721	NP_059194.NM_144945	1.87197e-005	42.4	95.8
1451075_a.t	Ctdp2	CTD (carboxy-terminal domain, RNA polymerase II, poly	2.3	5625 // soluble fractin // infer	Mm.28490	NP_066124.NM_146012	5.01658e-005	1332.3	3007.1
1423725_a.t	Pnc3	penicillinase, beta-lactamase	2.3	---	Mm.34842	NP_069602.NM_122814	8.59679e-005	39.0	89.0
1455729_a.t	Gnaq	guanine nucleotide binding protein, alpha 4 polypeptide	2.3	1501 // skeletal development // 1583 // heterotrimeric G-pro	Mm.3924	NP_032165.NM_008139	0.000778e-006	177.8	402.7
1428272_a.t	1500010M16RA	RIKEN cDNA 1500010M16 gene	2.3	6412 // protein biosynthesis // infer	Mm.28753	NP_081168.NM_026892	0.000075008	769.0	1727.0
1429317_a.t	Zfp37	zinc finger protein 37	2.3	6350 // transcription // infer	Mm.1112	NP_035744.NM_011444	0.00098268	32.9	74.8
1420617_a.t	Cpeb4	cytoplasmic polyadenylation element binding protein 4	2.3	3676 // nucleic acid binding // infer	Mm.339792	NP_080528.NM_026252	0.00075008	367.7	367.4
1455688_a.t	6720423E03	hypothetical protein 6720423E03	2.3	---	---	---	6.72794e-007	187.2	424.1
1429237_a.t	1810010N17RA	RIKEN cDNA 1810010N17 gene	2.3	---	Mm.35837	NP_079731.NM_102545	0.00012328	118.2	270.0
1435018_a.t	5930434B04RA	RIKEN cDNA 5930434B04 gene	2.3	16021 // integral to membra	Mm.150270	NP_084138.NM_029862	2.90761e-005	312.5	700.9
1448550_a.t	Lbp	lipopolysaccharide binding protein	2.3	6810 // transport // infer	Mm.218446	NP_032515.NM_008489	6.6256e-005	130.7	293.1
1454080_a.t	Erf1	ETS transcription factor family class 1 member 1	2.3	5209 // ion channel binding // infer	Mm.27979	NP_030376.NM_020100	0.00012328	118.2	270.0
1434018_a.t	BC043098	cDNA sequence BC043098	2.3	---	Mm.12051	NP_077812.NM_174997	0.57657e-005	593.5	1330.1
1428938_a.t	Gnaq	guanine nucleotide binding protein, alpha 4 polypeptide	2.3	1501 // skeletal development // 1583 // heterotrimeric G-pro	Mm.3924	NP_032165.NM_008139	0.000171222	186.8	418.6
1429845_a.t	---	---	2.3	---	Mm.34842	NP_069602.NM_122814	8.59679e-005	39.0	89.0
1416950_a.t	Trifap8	tumor necrosis factor, alpha-induced protein 8	2.3	---	Mm.27740	NP_058882.NM_134131	2.0002e-005	180.3	403.5
1426241_a.t	Sornh1	sex comb on midleg homolog 1	2.3	6350 // transcription // infer	Mm.28924	NP_038911.NM_013883	0.000419631	220.6	493.3
1428972_a.t	281041L24RA	RIKEN cDNA 281041L24 gene	2.3	---	Mm.28753	NP_081168.NM_026892	0.000075008	769.0	1727.0
1454586_a.t	Isvl1	iVb (bacterial acetoacetate synthase)-like	2.3	5615 // extracellular space	Mm.26444	NP_077612.NM_137351	0.00014241	322.8	721.5
1433907_a.t	---	---	2.3	---	---	---	0.000970329	159.1	355.6
1439064_a.t	4303550W12RA	RIKEN cDNA 4303550W12 gene	2.3	---	Mm.27979	NP_058162.NM_172390	0.000075008	769.0	1727.0
1418020_a.t	Cod	carboxypeptidase D	2.3	6508 // proteolysis and peptidolysis 5615 // extracellular space / 4180 // carboxypeptidase ac	Mm.7898	NP_031780.NM_007754	0.00012328	148.5	331.8
1426282_a.t	M2C2446259	neurotrophin	2.3	7155 // cell adhesion // infer	Mm.28138	NP_078484.NM_122890	0.000182428	75.8	169.3
1428966_a.t	5930430B19RA	RIKEN cDNA							

1455045_at	Ort	serine racemase	2.0	6520 // amino acid metabolism // ---	3824 // catalytic activity // inferMm.131443	NP_038789.1NM_013761	7.14735e-005	152.8	358.8	
1454708_at	Abim1	actin-binding LIM protein 1	2.0	7010 // cytoskeleton organization 5556 // cytoskeleton // ---	3824 // catalytic activity // inferMm.217161	NP_848803.2NM_176688	0.0013712	167.5	338.3	
1427125_s_at	D630045E04R4	RIKEN cDNA D630045E04 gene	2.0	6512 // ubiquitin cycle // inferred ---	Mm.260796	NP_705741.1NM_153521	4.7749e-005	609.2	1230.4	
1434520_at	Ssd1	sterol-C5-desaturase (lungal ERG3, delta-5-desaturase) 1	2.0	6694 // steroid biosynthesis // in 5763 // endoplasmic reticu.3824 // catalytic activity // inferMm.32700	NP_786357.1NM_172769	XP_146033.4XM_146034	4.11365e-005	136.5	273.5	
1434613_at	1810013L24R4	RIKEN cDNA 1810013L24 gene	2.0	---	Mm.201706	XP_148044.1NM_148044	0.00042605	296.7	598.6	
1422473_at	Pde4b	phosphodiesterase 4B, cAMP specific	2.0	6939 // smooth muscle contracti---	4115 // cAMP-specific phosphMm.20181	NP_062814.1NM_019840	0.00032062	110.2	222.3	
1418100_at	A03009H04R4	RIKEN cDNA A03009H04 gene	2.0	---	Mm.5324	NP_065616.1NM_020591	0.000891032	55.0	111.0	
1417554_at	Gkap1	G kinase anchoring protein 1	2.0	7199 // G-protein signaling, cou.5615 // extracellular space // 5515 // protein binding // inferMm.294625	NP_062608.1NM_019332	XP_146033.4XM_146033	0.00448025	492.1	810.6	
1448657_s_at	Dnajb10	DnaJ (Hsp40) homolog, subfamily B, member 10	2.0	6457 // protein folding // inferred---	31072 // heat shock protein b.Mm.248776	NP_064662.1NM_020266	2.1485e-007	189.6	382.0	
1439453_at	D63004G17R4	RIKEN cDNA D63004G17 gene	2.0	---	Mm.48724	XP_146033.4XM_146033	7.95198e-005	138.3	276.5	
1427050_at	573040B2R4	RIKEN cDNA 573040B22 gene	2.0	6118 // electron transport // infer---	Mm.28129	NP_768185.1NM_172597	1.07808e-005	138.2	279.2	
1433854_at	AW547186	Expressed sequence AW547186	2.0	---	Mm.248648	NP_808260.2NM_177592	0.000204567	261.9	527.1	
1424876_s_at	Spg20	spastic paraplegia 20, spartin (Troyer syndrome) homolog	2.0	---	5615 // extracellular space // ---	Mm.235523	NP_659144.1NM_144895	0.000482169	359.6	720.9
1429654_at	Croc6	CCR4-NOT transcription complex, subunit 6	2.0	6350 // transcription // inferred 5634 // nucleus // inferred fr 297 // magnesium ion bindingMm.247113	NP_597649.1NM_212484	---	0.000202661	451.0	906.7	
1422466_at	---	---	2.0	---	---	---	7.0655e-005	129.9	261.1	
1429175_at	2810417M05R4	RIKEN cDNA 2810417M05 gene	2.0	---	Mm.357108	NP_060792.1NM_020516	0.00053155	39.2	78.8	
1455960_at	Egfr5	EGF-like domain, multiple 5	2.0	---	16021 // integral to membra 5198 // structural molecule actMm.251189	NP_786282.1NM_172994	0.0000392525	44.3	88.9	
1455143_at	Ngap2	neuroigin 2	2.0	7155 // cell adhesion // inferred 16021 // integral to membra 5515 // protein binding // inferMm.151293	NP_842562.2NM_198882	---	1.6558e-005	386.4	775.7	
1438455_at	C330050A14R4	RIKEN cDNA C330050A14 gene	2.0	---	Mm.119234	---	1.25941e-005	20.4	41.0	
1418059_at	Ena1	EGF, integrin seven transmembrane domain containing	2.0	7165 // signal transduction // int.16020 // membrane // infer 4871 // signal transducer actMm.317261	NP_573485.1NM_133222	---	6.18387e-006	22.7	45.5	
1438185_at	A1314180	expressed sequence A1314180	2.0	---	5634 // nucleus // inferred fr ---	Mm.234801	NP_759013.2NM_172381	0.000850413	109.1	218.9
1435075_at	2310036D22R4	RIKEN cDNA 2310036D22 gene	2.0	---	Mm.27742	NP_062268.1NM_027992	0.000337731	132.4	265.7	
1434378_s_at	Max4	Max dimerization protein 4	2.0	6350 // transcription // inferred 5634 // nucleus // inferred fr 2677 // DNA binding // inferMm.252680	NP_034863.2NM_010763	---	0.000154773	140.8	282.5	
1426404_s_at	Rrf11	ring finger protein 11	2.0	6511 // ubiquitin-dependent prot 151 // ubiquitin ligase comp 4842 // ubiquitin-protein ligasMm.172605	NP_038904.1NM_013876	---	5.8838e-005	612.3	1227.7	
1436650_at	5730485H21R4	RIKEN cDNA 5730485H21 gene	2.0	---	Mm.23049	XP_486240.1XM_486240	0.000379934	93.6	187.6	
1415735_at	9130011J15R4	RIKEN cDNA 9130011J15 gene	2.0	---	Mm.22565	NP_765984.1NM_172396	0.000165764	433.3	863.7	
1419358_at	Sorsc5	scotin-related VPS10 domain containing receptor 2	2.0	6886 // intracellular protein trans 5615 // extracellular space // 5529 // sugar binding // inferMm.34113	NP_112151.1NM_020886	---	0.000425319	184.7	370.2	
1428259_at	2310075M15R4	RIKEN cDNA 2310075M15 gene	2.0	---	16491 // oxidoreductase actMm.251774	XP_283052.2XM_283052	0.000284861	1005.3	2014.4	
1418658_at	2410050I01R4	RIKEN cDNA 2410050I01 gene	2.0	---	Mm.257603	NP_079752.3NM_025476	0.000100042	106.0	212.4	
1415715_at	2410015I15R4	RIKEN cDNA 2410015I15 gene	2.0	---	---	---	2.28715e-006	180.6	361.7	
1434802_s_at	Nf3	neurotrophin 3	2.0	7274 // neuromuscular synaptic 5576 // extracellular region 5186 // neurotrophin p75 recMm.267570	NP_032768.1NM_008742	---	5.04053e-005	25.4	50.9	
1428801_at	Sept8	septin 8	2.0	7049 // cell cycle // inferred from ---	5525 // GTP binding // inferMm.274399	NP_149156.1NM_033144	3.62575e-006	332.8	665.9	
1452002_at	Pnc2a	phosphodiesterase 2A, cGMP-stimulated	2.0	7165 // signal transduction // int.16020 // membrane // infer 4114 // 3',5'-cyclic nucleotideMm.247564	NP_0010385.NM_0010385	---	0.00017104	87.1	174.3	
1484441_s_at	Wsp1	WW domain binding protein 1	2.0	---	16021 // integral to membra 5515 // protein binding // inferMm.1109	NP_058037.1NM_016757	0.000371543	544.4	1089.2	
1457736_at	Wbsc24	Williams-Beuren syndrome chromosome region 24 homol	2.0	---	Mm.44356	NP_808242.1NM_177574	0.000288404	165.3	330.8	
1436593_at	Vglr	very low density lipoprotein receptor	2.0	6629 // lipid metabolism // inferMm.5615 // extracellular space // 4872 // receptor activity // inferMm.4141	NP_038731.1NM_013703	---	0.000568065	76.4	150.9	

Suppl. Table S4: List of transcripts two- or more-fold up-regulated in wt and Pax4+ cells**S4a: Wt cells 5+16d vs. 5+28d**

Probe ID	FC	Gene Symbol	Gene Title
Transcriptional regulation			
1438211_s_at	3.2	Dbp	D site albumin promoter binding protein
1426743_at	2.8	Dip3b	Dip3 beta
1420337_at	2.7	Gbx2	gastrulation brain homeobox 2
1424034_at	2.1	Rora	RAR-related orphan receptor alpha
Signaling, growth factors			
1435495_at	4.1	Adora1	adenosine A1 receptor
1433769_at	2.6	Als2cl	ALS2 C-terminal like
1439255_s_at	2.0	Tm7sf1	transmembrane 7 superfamily member 1
Adhesion, extracellular matrix			
1416114_at	6.4	Sparcl1	SPARC-like 1 (mast9, hevin)
1416321_s_at	6.2	Prelp	proline arginine-rich end leucine-rich repeat
Membrane, transport			
1434449_at	61.5	Aqp4	aquaporin 4
1448735_at	10.7	Cp	ceruloplasmin
1435148_at	6.0	Atp1b2	ATPase, Na ⁺ /K ⁺ transporting, beta 2 polypeptide
1427747_a_at	3.9	Lcn2	lipocalin 2
1448690_at	3.2	Kcnk1	potassium channel, subfamily K, member 1
1417963_at	2.3	Pltp	phospholipid transfer protein
Organogenesis			
1448139_at	12.3	Mlc1	megalencephalic leukoencephalopathy with subcortical cysts 1 homolog (human)
Metabolism, peroxisome			
1420575_at	10.4	Mt3	metallothionein 3
1448507_at	6.9	Efhd1	EF hand domain containing 1
1422557_s_at	4.8	Mt1	metallothionein 1
1428942_at	4.7	Mt2	metallothionein 2
1454858_x_at	2.3	Mettl7a	methyltransferase like 7A
1426236_a_at	2.1	Glul	glutamate-ammonia ligase (glutamine synthase)
Cytoskeleton, intermediate filaments			
1426509_s_at	46.4	Gfap	glial fibrillary acidic protein
1435504_at	2.9	Rsnl2	Restin-like 2
1417307_at	2.3	Dmd	dystrophin, muscular dystrophy
RIKEN cDNA, unknown ESTs			
1453119_at	3.2	Otud1	OTU domain containing 1
1432198_at	2.5	---	---
1427878_at	2.3	0610010O12Rik	RIKEN cDNA 0610010O12 gene

S4b: Pax4+ cells 5+16d vs. 5+28d

Probe ID FC Gene Symbol Gene Title

Membrane, transport

1435154_at 3.2 LOC245128 similar to solute carrier family 7 (cationic amino acid transporter, y+ system), member 3

Organogenesis

1423429_at 3.9 Pem placentae and embryos oncofetal gene

Metabolism, peroxisome

1428942_at 2.3 Mt2 metallothionein 2

Apoptosis

1436990_s_at 3.0 Ndg2 Nur77 downstream gene 2

1450752_at 2.1 Cyct cytochrome c, testis

Suppl. Table 5: Transcripts two- or more-fold up-regulated in wt and Pax4+ cells at the committed progenitor stage (0d vs. 5+16d) compared to tissue samples (according to Gu et al., 2004)

S5a: Transcripts enriched in endoderm vs. meso- and ectoderm at E7.5

Gene Symbol	FC wt cells	FC Pax4+ cells	Gene Title
Growth factors, receptors, and signaling molecules			
Cmkor1	14.1	9.0	Chemokine orphan receptor 1
Igf2	10.5	14.1	Insulin-like growth factor 2
Igfbp5	18.6	41.8	Insulin-like growth factor binding protein 5
Kitl	6.7	4.8	Kit ligand
Nrp (Nrp1)	10.2	35.9	Neuropilin
Nedd9	7.7	8.8	neural precursor cell expressed, developmentally down-regulated gene 9
Pthr (pthr1)	2.7	-	Parathyroid hormone receptor 1
Transcriptional regulators and other nuclear factors			
Dab2	-	6.7	Disabled homolog 2 (Drosophila)
Foxa1	7.3	6.0	Forkhead box A1
Msx1	2.4	2.0	Homeo box, msh-like 1
Nr2f2	17.0	32.8	Nuclear receptor subfamily 2, group F, member 2
Cell surface, adhesion, matrix, cytoskeletal protein			
App	6.4	9.8	Amyloid beta (A4) precursor protein
Col4a1	5.9	6.9	Procollagen, type IV, alpha 1
Col4a2	5.2	7.2	Procollagen, type IV, alpha 2
Itm2b	3.7	3.8	Integral membrane protein 2B
Xpr1	5.1	4.4	Xenotropic and polytropic retrovirus receptor 1
Hormones, proteases, and secretory apparatus			
Cpd	-	3.0	Carboxypeptidase D
Serpinh	3.3	7.5	Serine (or cysteine) proteinase inhibitor, clade H, member 1
Cell cycle associated genes			
Cdkn1c	5.4	-	Cyclin-dependent kinase inhibitor 1C (P57)
Gas6	-	6.4	Growth arrest specific 6
Cell death			
Capn6	4.2	4.3	Calpain 6
Pea15	5.2	5.0	Phosphoprotein enriched in astrocytes 15
Others			
H19	8.3	-	H19 fetal liver
Pon2	-	2.4	Paraoxonase 2

S5b: Transcripts enriched in Pdx1+ pancreatic cells vs. Pdx1+ cells in stomach and duodenum at E10.5

Gene Symbol	FC wt cells	FC Pax4+ cells	Gene Title
Growth factors, receptors, and signaling molecules			
Amfr	2.6	2.5	Autocrine motility factor receptor
Dlk1	35.8	-	Delta-like 1 homolog (Drosophila)
Notch1	2.5	-	Notch gene homolog 1 (Drosophila)
Rgs2	23.2	3.5	Regulator of G-protein signaling 2
Sos2	2.2	-	Son of sevenless homolog 2 (Drosophila)

Transcriptional regulators and other nuclear factors

Idb3	2.6	-	Inhibitor of DNA binding 3
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Cell surface, adhesion, matrix, cytoskeletal protein

App	6.4	-	Amyloid beta (A4) precursor protein
Prkcb	5.8	-	Protein kinase C, beta 1 (Prkcb1)
Vim	-	4.0	Vimentin

Hormones, proteases, and secretory apparatus

Chgb	16.2	-	Chromogranin B
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Cell cycle associated genes

Cdkn1c	5.4	-	Cyclin-dependent kinase inhibitor 1C (P57)
Dp1	2.9	-	Deleted in polyposis 1

Transport proteins

Abca1	5.0	4.8	ATP-binding cassette, sub-family A (ABC1), member 1
Atp1a	-	2.7	Atp1a2 (ATPase, Na ⁺ /K ⁺ transporting, alpha 2 polypeptide)
Pltp	2.3	-	Phospholipid transfer protein

Others

BC003940	2.0	-	Phosphotyrosyl phosphatase activator
Hrc	-	4.5	Histidine rich calcium binding protein
Mest	5.0	-	Mesoderm specific transcript
Sparc	-	4.1	Secreted acidic cysteine rich glycoprotein

S5c: Transcripts enriched in endocrine progenitors (Ngn3-/GFP+) vs. non-endocrine progenitor cells (Ngn3-/GFP-) at E13.5

Gene	FC wt cells	FC Pax4+ cells	Gene Title
Ddr1	4.0	2.2	Discoidin domain receptor family, member 1
Mafb	3.5	-	v-maf musculoaponeurotic fibrosarcoma oncogene

Transcriptional regulators and other nuclear factors

Cbfa2t1h	11.7	9.2	CBFA2T1 identified gene homolog (human)
Cut11	4.2	-	Cut-like 1 (Drosophila)

Cell surface, adhesion, matrix, cytoskeletal protein

App	6.4	-	Amyloid beta (A4) precursor protein
Vamp2	3.4	-	Vesicle-associated membrane protein 2

Hormones, proteases, and secretory apparatus

Chgb	16.2	-	Chromogranin B
Cpe	7.6	10.0	Carboxypeptidase E
Ctsf	2.5	-	Cathepsin F
Spint1	2.7	3.1	Serine protease inhibitor, Kunitz type 1

Cell cycle associated genes

Npdc1	3.3	3.2	Neural proliferation, differentiation and control gene 1
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Others

Btg2	3.7	-	B-cell translocation gene 2, anti-proliferative
Galnt2	3.1	3.0	UDP-N-acetyl-alpha-D-galactosamine:poly-peptide N-acetyl-galactosaminyltransferase 2
Pam	2.3	4.0	Peptidylglycine alpha-amidating monooxygenase
Prnp	4.9	8.4	Prion protein

S5d: Transcripts enriched in E7.5 endoderm compared to pancreatic tissue from other developmental stages

Gene	FC wt cells	FC Pax4+ cells	Gene Title
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Growth factors, receptors, and signaling molecules

Kitl	6.7	4.8	Kit ligand
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Transcriptional regulators and other nuclear factors

Dab2	-	6.7	Disabled homolog 2 (Drosophila)
Foxa1	7.3	6.0	Forkhead box A1
Idb3	2.3	-	Inhibitor of DANN binding 3
Irx3	7.3	-	Iroquois related homeobox 3

S5e: Transcripts enriched in Pdx1+ cells compared to pancreatic tissue from other developmental stages

Gene Symbol	FC wt cells	FC Pax4+ cells	Gene Title
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Growth factors, receptors, and signaling molecules

Dlk1	35.8	-	Delta-like 1 homolog (Drosophila)
Gas1	13.8	28.9	Growth arrest specific 1
Igfbp5	18.6	41.8	Insulin-like growth factor binding protein 5
Sfrp1	6.3	-	Secreted frizzled-related protein 1

Transcriptional regulators and other nuclear factors

Mfap2	5.7	5.4	Microfibrillar-associated protein 2
Meis1	17.6	20.2	Myeloid ecotropic viral integration site 1

Cell surface, adhesion, matrix, cytoskeletal protein

Mfap2	5.7	5.4	Microfibrillar-associated protein 2
Meis1	17.6	20.2	Myeloid ecotropic viral integration site 1
Col1a1	-	39.7	Procollagen, type I, alpha 1
Col1a2	-	46.3	Procollagen, type I, alpha 2
Col5a2	-	15.8	Procollagen, type V, alpha 2
Tnc	-	20.3	Tenascin C

Hormones, proteases, and secretory apparatus

Capn6	4.2	4.3	Calpain 6
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Others

Ptn	160.9	218.9	Pleiotrophin
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S5f: Transcripts enriched in Ngn3+ cells compared to pancreatic tissue from other developmental stages

Gene Symbol	FC wt cells	FC Pax4+ cells	Gene Title
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Transcriptional regulators and other nuclear factors

Mafb	3.5	-	v-maf musculoaponeurotic fibrosarcoma oncogene
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Others

Ogn	45.2	55.3	Osteoglycin
Pik3r1	4.4	4.1	Phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 1

S5g: Transcripts enriched in mature islets compared to pancreatic tissue of early stages

Gene Symbol	FC wt cells	FC Pax4+ cells	Gene Title
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Growth factors, receptors, and signaling molecules

Inha	2.0	-	Inhibin alpha
Thra	-	5.4	Thyroid hormone receptor alpha

Transcriptional regulators and other nuclear factors

STAT5B	2.0	-	Musculus partial STAT5B gene, exons 6-9
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Hormones, proteases, and secretory apparatus

SgII 8.7 -

Mus musculus SgII gene for secretogranin II, exon 2

Suppl. Table S6: Transcripts two- or more-fold up-regulated in wt and/or Pax4+ cells (0d vs. 5+16d) compared with Pdx1 (E10.5)- and Ngn3 (E13.5)- negative cells *in vivo* (according to Gu et al., 2004)

S6a: Transcripts upregulated in ES-derived cells (0d vs. 5+16d) compared to those of Pdx1-negative cells (E10.5)

Gene Symbol	FC wt cells	FC Pax4+ cells	Gene Title
Growth factors, receptors, and signaling molecules			
Basp1	2.5	2.5	Brain abundant, membrane attached signal protein 1
Bmp1	-	3.7	Bone morphogenetic protein 1
Cmkor1	14.1	9.0	Chemokine orphan receptor 1
Dlk1	35.8	-	Delta-like 1 homolog (Drosophila)
Il11ra1//Il11ra2	3.4	3.9	Interleukin 11 receptor, alpha chain 1
Nr2f1	48.0	52.4	Nuclear receptor subfamily 2, group F, member 1
Pdgfra	5.2	-	Platelet derived growth factor receptor, alpha
Snai2	-	6.0	Snail homolog 2 (Drosophila)
Sfrp1	6.3	-	Secreted frizzled-related protein 1
Sfrp2	8.7	-	Secreted frizzled-related protein 2
Tgfb1	-	10.6	Transforming growth factor, beta induced, 68 kDa

Transcriptional regulators and other nuclear factors

Cutl1	4.2	-	Cut-like 1 (Drosophila)
Dab2	-	6.7	Disabled homolog 2 (Drosophila)
Foxa1	7.3	6.0	Forkhead box A1
Lmo4	2.1	2.7	LIM domain only 4
Pbx1	5.2	4.5	Pre B-cell leukaemia transcription factor 1
Tcf21	10.8	11.0	Transcription factor 21
Zfhx1a	-	4.4	Zinc finger homeobox 1a

Cell surface, adhesion, matrix, cytoskeletal protein

Bgn	-	22.0	Biglycan
Cd81	-	2.1	CD 81 antigen
Col1a2	-	46.3	Procollagen, type I, alpha 2
Col5a1	-	15.8	Procollagen, type V, alpha 1
Col5a2	5.2	7.2	Procollagen, type V, alpha 2
Cdh11	13.4	11.7	Cadherin 11
Fbn2	-	16.5	Fibrillin 2
Flna	18.2	-	Filamin, alpha
Efnb1	4.8	5.2	Ephrin B1
Efnb2	2.2	2.9	Ephrin B2
Eln	-	3.9	elastin
Itm2a	21.8	-	Integral membrane protein 2A
Nid1	2.3	-	Nidogen 1
Tnc	-	20.3	Tenascin C
Tubb2	3.8	-	Tubulin, beta 2

Cell cycle associated genes

Ccnd2	9.0	21.3	Cyclin D2
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Others

Adcy6	2.1	2.6	Adenylat cyclase 6
Plat	5.8	16.0	Plasminogen activator, tissue
Ppic	3.5	5.1	Peptidyl isomerase C

Smoc2	-	4.0	SPARC related modular calcium binding 2
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S6b: Transcripts up-regulated in ES-derived cells (0d vs. 5+16d) compared to those present or enriched in Ngn3-negative cells vs. Ngn3-positive cells (E13.5)

Gene	FC wt cells	FC Pax4+ cells	Gene Title
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Symbol

Growth factors, receptors, and signaling molecules

Basp1	2.5	2.5	Brain abundant, membrane attached signal protein 1
Epha3	37.9	32.2	Eph receptor A3
Igfbp5	18.6	41.8	Insulin-like growth factor binding protein 5
Igfbp4	7.8	11.1	Insulin-like growth factor binding protein 4
Il11ra1//Il11ra2	3.4	3.9	Interleukin 11 receptor, alpha chain 2
Igf1	18.0	32.4	Insulin-like growth factor 1
Igf2	10.5	14.1	Insulin-like growth factor 2
Notch1	2.5	-	Notch gene homolog 1, (Drosophila)
Nr2f2	17.0	32.8	Nuclear receptor subfamily 2, group F, member 2
Sfrp1	6.3	-	Secreted frizzled-related protein 1
Sfrp2	8.7	-	Secreted frizzled-related protein 2
Snai2	-	6.0	Snail homolog 2 (Drosophila)
Tgfb1	-	10.6	Transforming growth factor, beta induced, 68 kDa

Transcriptional regulators and other nuclear factors

Lmo4	2.1	2.7	LIM domain only 4
Nfib	22.5	27.7	Nuclear factor I/B
Tbx2	4.5	-	T-box 2
Tcf21	10.8	11.0	Transcription factor 21
Zfhx1a	-	4.4	Zinc finger homeobox 1a
Zfp275	2.1	-	Zinc finger protein 275
Zfp36l1	2.7	3.0	Zinc finger protein 36, C3H type-like 1
Zfp422	3.4	-	Zinc finger protein 422

Cell surface, adhesion, matrix, cytoskeletal protein

Col1a1	5.6	39.7	Procollagen, type I, alpha 1
Col1a2	-	46.3	Procollagen, type I, alpha 2
Col3a1	102.5	240.1	Procollagen, type III, alpha 1
Col5a1	-	15.8	Procollagen, type V, alpha 1
Col5a2	5.2	7.2	Procollagen, type V, alpha 2
Col6a3	-	8.6	Procollagen, type VI, alpha 3
Cspg2	-	3.3	Chondroitin sulfate proteoglycan 2
Dcn	30.8	70.0	Decorin
Eln	-	3.9	elastin
Fbn1	-	14.7	Fibrillin 1
Islr	28.3	44.2	Immunoglobulin superfamily containing leucine-rich repeat
Itm2a	21.8	-	Integral membrane protein 2A
Lama4	-	8.5	Laminin, alpha 4
Lum	29.2	50.2	Lumican
Mfap2	5.7	5.4	Microfibrillar-associated protein 2
Nrp	10.2	35.9	Neuropilin

Cell cycle associated genes

Cdkn1c	5.4	-	Cyclin-dependent kinase inhibitor 1C (P57)
Cks	2.6	2.3	CDC28 protein kinase 1
Gas1	13.8	28.9	Growth arrest specific 1

Hormones, proteases, and secretory apparatus

Capn6	4.2	4.3	Calpain 6
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Others

Enpp5	4.1	2.6	Ectonucleotide pyrophosphatase/phosphodiesterase 5
Hic1	2.7	3.5	Hypermethylated in cancer 1
Lsp1	-	3.4	Lymphocyte specific 1
Meis1	17.6	20.2	Myeloid ecotropic viral integration site 1
Ppic	3.5	5.1	Peptidyl isomerase C
Pygb	3.3	2.3	Brain glycogen phosphorylase
Qk	5.0	7.0	Quaking
Sparc	-	4.1	Secreted acidic cysteine rich glycoprotein