Supplemental Table 1. Primers and probes for real time RT-PCR

Gene	ABI* Catalog #	Amplicon length (bp)	Context sequence (of probe)	Exons
18S	Hs99999901_s1	187	TCCATTGGAGGGCAAGTCTGGTGCC	
SP-A	Hs00831305_s1	164	AGCCCCCTGACCTGAAGACAGCCAG	5
SP-B	Hs00167036_m1	100	GATTCCCAAGGGTGCGCTAGCTGTG	6-8
SP-C	Hs00161628_m1	73	AGAGCCCGCCGGACTACTCCGCAGC	4, 5
TTF-1	Hs00163037_m1	96	CCGCCATCTCCCGCTTCATGGGCCC	2, 3
CEBPd	Hs00270931_s1	107	TGGCGCAGCCAGAGCCGCCGGGTGC	1
PGC	Hs00160052_m1	83	AGCAGTGGTCAAAGTGCCCCTGAAG	1, 2
DC-LAMP	Hs00180880_m1	72	TTTGGAAATGTGGATGAGTGCTCGT	5, 6
ABCA3	Hs00184543_m1	77	GAAGTCTTCCTTCGGGTCGGGAAGC	17-19
DUOX1	Hs00213694_m1	87	TCTGTGTCAAAGGGGTGGAGGTGCC	19-23
ADFP	Hs00605340_m1	139	TACTGTTCACCTGATTGAATTTGCC	6, 7
CEACAM6	Hs00366002_m1	80	CAGGAAGACTGGCAGATTGGACCAG	5, 6

* TAQMAN Gene Expression Assay primer sets from Applied Biosystems, Inc.
All primers are inventoried sets.

Supplemental Table 2. Genes expressed ≥10-fold higher in adult versus fetal type II cells

Gene Title	Gene Symbol	mRNA Abundance Adult (f.u.)	Fetal/ Adult	GO Biological Response /Molecular Functiion
secretoglobin, family 1A, member 1 (uteroglobin)	SCGB1A1	10924	0.002	signal transduction/cytokine activity
chemokine (C-X-C motif) ligand 2	CXCL2	9035	0.03	chemotaxis
secretory leukocyte peptidase inhibitor	SLPI	8190	0.06	---
interleukin 8	IL8	6491	0.02	angiogenesis/cytokine activity
heat shock 70kDa protein 1A / 1B	HSPA1A /B	5492	0.10	protein folding
chemokine (C-C motif) ligand 20	CCL20	4833	0.004	chemotaxis/chemokine activity
superoxide dismutase 2, mitochondrial	SOD2	3805	0.02	response to superoxide
chemokine (C-X-C motif) ligand 1	CXCL1	3694	0.02	chemotaxis/chemokine activity
S100 calcium binding protein A8	S100A8	3167	0.01	inflammatory response/Ca ion binding
surfactant, pulmonary-associated protein D	SFTPD	2759	0.06	Regulate cytokine production/Ca ion binding
chemokine (C-C motif) ligand 2	CCL2	2674	0.09	protein aa phosphorylation/chemokine activity
heat shock 70kDa protein 6 (HSP70B')	HSPA6	2647	0.01	protein folding
lipocalin 2 (oncogene 24p3)	LCN2	2456	0.01	transport
peptidase inhibitor 3, skin-derived (SKALP)	PI3	2430	0.01	/endopeptidase inhibitor activity
S100 calcium binding protein A2	S100A2	2355	0.09	calcium ion binding
ribosomal protein S4, Y-linked 1	RPS4Y1	2216	0.01	protein biosynthesis/RNA binding
hypothetical protein MGC5618	MGC5618	2059	0.05	---
proteoglycan 1, secretory granule	PRG1	2057	0.01	---
tumor necrosis factor, alpha-induced protein 3	TNFAIP3	2054	0.09	ubiquitin cycle/DNA binding
serine peptidase inhibitor, Kazal type 1	SPINK1	1793	0.06	serine-type endopeptidase inhibitor activity
Major histocompatibility complex, class II, DR beta 3	HLA-DRB5	1792	0.03	immune response
chemokine (C-X-C motif) ligand 3	CXCL3	1791	0.02	chemotaxis/chemokine activity
CD74 antigen	CD74	1449	0.07	prostaglandin biosynthesis/cytokine binding
v-fos FBJ murine osteosarcoma viral oncogene homolog	FOS	1436	0.05	DNA methylation/ DNA binding
interleukin 1 receptor antagonist	IL1RN	1417	0.01	inflammatory response
defensin, beta 4	DEFB4	1347	0.01	chemotaxis
chemokine (C-X-C motif) ligand 5	CXCL5	1278	0.03	chemotaxis/chemokine activity
major histocompatibility complex, class II, DR beta 1	HLA-DRB1	1264	0.02	immune response
S100 calcium binding protein A9	S100A9	1234	0.02	inflammatory response/signal transduction
cytochrome P450, family 4 B, polypeptide 1	CYP4B1	1210	0.04	electron transport/monooxygenase activity
chromosome 8 open reading frame 4	C8orf4	1209	0.06	---

complement component 4 binding protein, alpha	C4BPA	1152	0.02	immune response
stratifin	SFN	1152	0.02	cell cycle/PKC inhibitor activity
v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	LYN	1086	0.08	protein aa phosphorylation/nucleotide binding
carcinoembryonic antigen-related cell adhesion molecule 5	CEACAM5	1020	0.10	---
BCL2-related protein A1	BCL2A1	1012	0.02	anti-apoptosis
immunoglobulin heavy constant alpha 1 /A2/ MGC27165	IGHA1 /A2 /MGC27165	1001	0.02	immune response/antigen binding
palate, lung and nasal epithelium carcinoma associated	PLUNC	1000	0.02	innate immune response/lipid binding
matrix metallopeptidase 7 (matrilysin, uterine)	MMP7	979	0.02	proteolysis
chemokine (C-C motif) ligand 3	CCL3/3L1/3L3	965	0.02	inflammatory response/signal transduction
PDZK1 interacting protein 1	PDZK1IP1	941	0.02	---
tumor necrosis factor (ligand) superfamily 10	TNFSF10	937	0.04	apoptosis/signal transducer activity
tryptase beta 2	TPSB2	936	0.02	proteolysis/ endopeptidase activity
arachidonate 5-lipoxygenase-activating protein	ALOX5AP	934	0.02	inflammatory response/enzyme activator
serpin peptidase inhibitor, clade B 2	SERPINB2	918	0.02	anti-apoptosis/ endopeptidase inhibitor
major histocompatibility complex, class II, DR alpha	HLA-DRA	912	0.02	immune response
interleukin 1, beta	IL1B	893	0.03	inflammatory response/signal transduction
aldo-keto reductase family 1, C3	AKR1C3	840	0.03	lipid metabolism/transporter activity
chromosome 10 open reading frame 116	C10orf116	833	0.02	---
Ras-related associated with diabetes	RRAD	828	0.02	small GTPase mediated signal transduction
regulator of G-protein signalling 1	RGS1	812	0.02	immune response/signal transduction
FBJ murine osteosarcoma viral oncogene homolog B	FOSB	794	0.03	regulation of progression through cell cycle
CD83 antigen	CD83	775	0.03	humoral immune response
hemoglobin, alpha 2	HBA2	775	0.03	transport/oxygen transporter activity
chemokine (C-X-C motif) ligand 6	CXCL6	759	0.03	inflammatory response/cytokine activity
tryptase alpha/beta 1	TPSAB1	725	0.03	defense response/endopeptidase activity
lactotransferrin	LTF	716	0.03	iron ion transport/endopeptidase activity
immunoglobulin kappa constant /kappa variable 1-5	IGKC /V1-5	714	0.03	immune response/antigen bindin
chemokine (C-C motif) ligand 4	CCL4	684	0.03	inflammatory response/chemokine activity
aquaporin 9	AQP9	683	0.03	water transport
lysosomal associated multispanning membrane protein 5	LAPTM5	667	0.04	---
G protein-coupled receptor 109B	GPR109B	658	0.03	G-protein coupled signaling pathway
Rho GDP dissociation inhibitor (GDI) beta	ARHGDIB	642	0.03	immune response
interleukin 6 (interferon, beta 2)	IL6	622	0.09	acute-phase response
C-type lectin domain family 2, B	CLEC2B	616	0.09	antimicrobial humoral response
immunoglobulin lambda locus	IGL@	610	0.03	immune response/antigen binding

/Mcg/Kern-Oz/variable 3-25 / 2-14	/C1/C2/V3-25/V2-14			
CD53 antigen	CD53	590	0.10	antimicrobial humoral response
carboxypeptidase A3	CPA3	584	0.03	proteolysis
haptoglobin //haptoglobin-related protein	HP / HPR	582	0.03	defense response/ endopeptidase activity
major histocompatibility complex, class II, DP alpha 1	HLA-DPA1	575	0.05	immune response
cylindromatosis	CYLD	570	0.04	ubiquitin cycle/ endopeptidase activity
DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y-linked	DDX3Y	570	0.04	---
chloride intracellular channel 2	CLIC2	565	0.04	ion transport
Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide	FCER1G	557	0.04	immune response/receptor activity
formyl peptide receptor 1	FPR1	552	0.04	inflammatory response/receptor activity
ras-related C3 botulinum toxin substrate 2	RAC2	541	0.04	intracellular protein transport
B-factor, properdin	BF	530	0.04	immune response/complement binding
defensin, alpha 1 /alpha 3	DEFA1 /3	525	0.04	defense response
phosphatidylinositol glycan, class A	PIGA	524	0.08	biosynthesis
zinc finger CCCH-type containing 12A	ZC3H12A	521	0.04	---
v-maf musculoaponeurotic fibrosarcoma oncogene homolog F	MAFF	511	0.04	transcription
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baculoviral IAP repeat-containing 3	BIRC3	510	0.04	anti-apoptosis/ubiquitin ligase activity
cathepsin S	CTSS	488	0.04	immune response/endopeptidase activity
microseminoprotein, beta	MSMB	475	0.05	---
hemoglobin, beta	HBB	471	0.06	oxygen transport
aquaporin 1	AQP1	470	0.10	water transport
inhibitor of DNA binding 2/ 2B	ID2 /2B	468	0.07	regulation of transcription
hydroxysteroid (17-beta) dehydrogenase 6	HSD17B6	465	0.05	metabolism/oxidoreductase activity
hemoglobin, alpha 1 /alpha 2	HBA1 /2	463	0.05	oxygen transport
toll-like receptor 2	TLR2	463	0.04	inflammatory response
Rho family GTPase 1	RND1	459	0.04	regulation of cell adhesion/GTPase activity
fibroblast growth factor binding protein 1	FGFBP1	459	0.06	negative regulation of cell proliferation
fatty acid binding protein 4, adipocyte	FABP4	442	0.05	transport/ lipid binding
zinc finger protein 165	ZNF165	442	0.10	transcription
interferon-related developmental regulator 1	IFRD1	438	0.05	cell differentiation
kynureninase	KYNU	436	0.05	nucleotide biosynthesis/peptidase activity
SAM domain, SH3 domain and nuclear localisation signals, 1	SAMSN1	429	0.05	---
v-maf musculoaponeurotic fibrosarcoma oncogene homolog B	MAFB	428	0.05	transcription
hexokinase 2	HK2	424	0.05	regulation of progression through cell cycle

v-jun sarcoma virus 17 oncogene homolog (avian)	JUN	412	0.05	transcription
CASP8 and FADD-like apoptosis regulator	CFLAR	406	0.05	proteolysis/signal transducer activity
immunoglobulin heavy locus /G1/G2/G3/mu	IGH@ /G1 /G2 /G3 /M	400	0.05	immune response/antigen binding
CD69 antigen	CD69	386	0.05	defense response/transmembrane receptor
proline rich Gla (G-carboxyglutamic acid) 4	PRRG4	377	0.05	---
cytochrome P450, family 2, B7 pseudogene 1	CYP2B7P1	376	0.05	---
transporter 1, ATP-binding cassette B	TAP1	376	0.05	transport
deleted in malignant brain tumors 1	DMBT1	368	0.05	innate immune response/scavenger receptor
phorbol-12-myristate-13-acetate-induced protein 1	PMAIP1	362	0.06	---
complement component 3a receptor 1	C3AR1	356	0.06	cellular defense response
Solute carrier family 30 (zinc transporter), member 1	SLC30A1	352	0.06	transport
activity-regulated cytoskeleton-associated protein	ARC	351	0.06	---
guanylate binding protein 1, interferon-inducible	GBP1	345	0.06	immune response
major histocompatibility complex, class II, DQ beta 1	HLA-DQB1	344	0.06	immune response
colony stimulating factor 1	CSF1	344	0.06	cell proliferation/cytokine activity
lysozyme / leukocyte immunoglobulin-like receptor, subfamily B1	LYZ / LILRB1	343	0.06	immune response
S100 calcium binding protein A12	S100A12	343	0.06	inflammatory response
guanylate binding protein 2, interferon-inducible	GBP2	331	0.06	immune response
orosomucoid 1 /2	ORM1 /ORM2	325	0.06	inflammatory response
RRS1 ribosome biogenesis regulator homolog (S. cerevisiae)	RRS1	322	0.06	ribosome biogenesis
lymphocyte cytosolic protein 1 (L-plastin)	LCP1	320	0.06	---
complement component 2	C2	312	0.06	immune response/ endopeptidase activity
thyroid hormone receptor, alpha/nuclear receptor 1D1	THRA /NR1D1	311	0.07	transcription/steroid hormone receptor activity
target of myb1-like 1 (chicken)	TOM1L1	304	0.07	protein transport
colony stimulating factor 2 receptor, beta	CSF2RB	304	0.07	antimicrobial humoral response/receptor
Ras-related GTP binding D	RRAGD	300	0.07	---
chemokine (C-C motif) receptor-like 2	CCRL2	300	0.07	antimicrobial humoral response/receptor
ceruloplasmin (ferroxidase)	CP	299	0.07	ion transport
complement component 4A /4B	C4A /B	297	0.07	inflammatory response/endopeptidase inhibitor
tryptophanyl-tRNA synthetase	WARS	292	0.07	protein biosynthesis
orosomucoid 1	ORM1	290	0.07	inflammatory response

protein kinase, interferon-inducible dsRNA dependent activator	PRKRA	286	0.07	immune response
proteasome beta t8	PSMB8	286	0.07	immune response/endopeptidase activity
pleckstrin	PLEK	286	0.07	intracellular signaling cascade/Ca ion binding
neurogranin (protein kinase C substrate, RC3)	NRGN	286	0.07	signal transduction
carcinoembryonic antigen-related cell adhesion molecule 1	CEACAM1	280	0.07	homophilic cell adhesion/receptor activity
acid phosphatase 1, soluble	ACP1	277	0.07	protein aa dephosphorylation
KIAA0674	KIAA0674	276	0.07	protein folding
mucin 4, tracheobronchial	MUC4	276	0.07	cell-matrix adhesion
ankyrin repeat domain 12	ANKRD12	273	0.07	---
CD163 antigen	CD163	272	0.08	antimicrobial humoral response
tumor necrosis factor, alpha-induced protein 2	TNFAIP2	269	0.07	cell differentiation
CD44 antigen	CD44	268	0.07	cell-matrix adhesion/receptor activity
lymphocyte cytosolic protein 2	LCP2	263	0.07	immune response
selectin E (endothelial adhesion molecule 1)	SELE	262	0.08	inflammatory response
major histocompatibility complex, class II, DQ alpha 1	HLA-DQA1/A2	262	0.08	immune response
---	---	260	0.08	---
ecotropic viral integration site 2B	EVI2B	259	0.08	---
tripartite motif-containing 29	TRIM29	257	0.08	transcription
trefoil factor 3 (intestinal)	TFF3	257	0.08	defense response
peroxisome proliferative activated receptor, delta	PPARD	253	0.08	transcription/steroid hormone receptor
cerebellar degeneration-related protein 2, 62kDa	CDR2	252	0.08	translation
spectrin repeat containing, nuclear envelope 1	SYNE1	251	0.08	nuclear organization and biogenesis
mitochondrial ribosomal protein L17	MRPL17	250	0.08	protein biosynthesis
fibrinogen gamma chain	FGG	250	0.08	signal transduction
protein tyrosine phosphatase, receptor type, C	PTPRC	246	0.08	protein aa dephosphorylation
adenosine A2b receptor	ADORA2B	244	0.08	cellular defense response
mitogen-activated protein kinase kinase kinase 8	MAP3K8	240	0.08	protein aa phosphorylation
major histocompatibility complex, class II, DR beta 4	HLA-DRB4	237	0.08	immune response
TNFAIP3 interacting protein 3	TNIP3	236	0.08	---
TYRO protein tyrosine kinase binding protein	TYROBP	236	0.08	cellular defense response/receptor signaling
serpin peptidase inhibitor, clade A3	SERPINA3	235	0.09	inflammatory response/endopeptidase inhibitor
Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog	FGR	231	0.09	protein aa phosphorylation
small trans-membrane and glycosylated protein	LOC57228	230	0.09	---
DNA-damage-inducible transcript 3	DDIT3	228	0.09	transcription

homeo box D1	HOXD1	224	0.09	regulation of transcription
proteasome beta10	PSMB10	223	0.09	humoral immune response/endopeptidase activity
hematopoietic cell-specific Lyn substrate 1	HCLS1	223	0.09	regulation of transcription
ecotropic viral integration site 2A	EVI2A	221	0.09	---
apolipoprotein C-I	APOC1	220	0.09	lipoprotein metabolism
v-rel reticuloendotheliosis viral oncogene homolog (avian)	REL	217	0.09	transcription
sulfotransferase family, cytosolic, 1A 2	SULT1A2	217	0.09	lipid metabolism
CD300A antigen	CD300A	215	0.09	cell adhesion/receptor activity
hypothetical protein FLJ20152	FLJ20152	215	0.09	---
deoxyribonuclease II, lysosomal	DNASE2	213	0.09	DNA metabolism
Ubiquitin-conjugating enzyme E2D 2 (UBC4/5 homolog, yeast)	UBE2D2	212	0.09	ubiquitin cycle
nuclear receptor subfamily 4,A1	NR4A1	211	0.09	transcription
mahogunin, ring finger 1	MGRN1	211	0.09	protein ubiquitination
hypothetical protein FLJ20323	FLJ20323	211	0.09	---
growth arrest and DNA-damage-inducible, gamma	GADD45G	209	0.10	response to stress
small proline-rich protein 2B	SPRR2B	209	0.10	epidermis development/structural molecule
chitinase 3-like 1	CHI3L1	209	0.10	carbohydrate metabolism/hydrolase activity
aquaporin 3	AQP3	206	0.10	transport
interferon (alpha, beta and omega) receptor 2	IFNAR2	206	0.10	cell surface receptor signal transduction
ficolin (collagen/fibrinogen domain containing) 3\	FCN3	205	0.10	phosphate transport
Nuclear receptor coactivator 2	NCOA2	201	0.10	transcription
lectin, galactoside-binding, soluble, 8 (galectin 8)	LGALS8	200	0.10	---

Data are mean values for 5 experiments comparing transcript abundance in adult cells with level in fetal cells (**Wade KC, Guttentag SH, Gonzales LW, Maschhoff KL, Gonzales J, Kolla V, Singhal S, and Ballard PL.** Gene Induction during Differentiation of Human Pulmonary Type II Cells In Vitro. *Am J Respir Cell Mol Biol* 34: 727-737, 2006).

---, no gene designation for probe sequence or GO category assigned

Supplemental Table 3: Genes expressed >10-fold higher abundance in fetal vs adult type II cells

		Abundance (f.u.)			
Gene Title	Gene Symbol	Fetal cells	Adult cells	Fetal/ Adult	GO Biological Process /Cellular Component
collagen, type IV, alpha 2	COL4A2	3974	200	19.9	extracell matrix organization/collagen
collagen, type I, alpha 1	COL1A1	3890	80	48.8	skeletal development/collagen
collagen, type I, alpha 2	COL1A2	3711	46	80.7	skeletal development/collagen
collagen, type III, alpha 1	COL3A1	3454	72	48.0	phosphate transport /collagen
insulin-like growth factor binding protein 5	IGFBP5	3401	97	35.2	regulation cell growth/extracell region
collagen, type IV, alpha 1	COL4A1	2965	165	18.0	phosphate transport /lcollagen
transforming growth factor,	TGFBI	2935	113	26.0	cell adhesion/extracell matrix
actin, alpha 2, smooth muscle, aorta	ACTA2	2357	95	24.8	muscle development/ cytoskeleton
chromosome 5 open reading frame 13	C5orf13	1789	128	14.0	---
serpin peptidase inhibitor (nexin, PAI type 1)	SERPINE2	1717	51	33.6	cell differentiation/extracell region
secreted protein, acidic, cysteine-rich (osteonectin)	SPARC	1478	117	12.7	ossification/extracellular matrix
Cyclin-dependent kinase inhibitor 1C (p57, Kip2)	CDKN1C	1092	75	14.6	cell cycle/nucleus
matrix metallopeptidase 2 (gelatinase A,)	MMP2	1078	51	21.2	peptidoglycan metab/extracell matrix
chondroitin sulfate proteoglycan 2 (versican)	CSPG2	995	46	21.6	development/extracell matrix
matrix-remodelling associated 8	MXRA8	915	41	22.2	---
collagen, type VI, alpha 1	COL6A1	865	59	14.8	phosphate transport /collagen
peroxidasin homolog (Drosophila)	PXDN	853	67	12.7	immune response
monocyte to macrophage differentiation-associated	MMD	846	71	11.9	cytolysis/membrane fraction
myeloid/lymphoid or mixed-lineage leukemia	MLLT11	756	73	10.4	---
Ca/calmodulin-dependent protein kinase II inhibitor 1	CAMK2N1	708	49	14.3	---
endothelin receptor type A	EDNRA	606	56	10.7	s muscle contraction/plasma membrane
DNA segment on chromosome 4	D4S234E	478	18	27.3	dopamine receptor signaling pathway
forkhead box F1	FOXF1	387	33	11.6	transcription/nucleus
collagen, type XVIII, alpha 1	COL18A1	365	34	10.8	phosphate transport /collagen

Data are mean values for 5 experiments comparing transcript abundance in adult cells with level in fetal cells (**Wade KC, Guttentag SH, Gonzales LW, Maschhoff KL, Gonzales J, Kolla V, Singhal S, and Ballard PL.** Gene Induction during Differentiation of Human Pulmonary Type II Cells In Vitro. *Am J Respir Cell Mol Biol* 34: 727-737, 2006).

---, no gene designation for probe sequence or GO category assigned

Supplemental Table 4. Genes induced ≥1.5 fold by hormone treatment

		DCI-Treated/Control	
Gene Title	Gene Symbol	Mean	GO Biological Process
progastricsin (pepsinogen C)	PGC	59.1 ± 20.6	proteolysis
zinc finger and BTB domain containing 16	ZBTB16	24.8 ± 23.8	transcription
dual oxidase 1	DUOX1	21.8 ± 13.8	electron transport/hydrogen peroxide biosynthesis
palate, lung and nasal epithelium carcinoma associated	PLUNC	20.1 ± 16.4	response to pathogenic bacteria
citron (rho-interacting, serine/threonine kinase 21)	CIT	10.1 ± 3.3	protein phosphorylation/signal transduction
cartilage acidic protein 1	CRTAC1	9.7 ± 9.4	cell adhesion /
WNT inhibitory factor 1	WIF1	7.4 ± 4.2	signal transduction
ATP-binding cassette, sub-family A (ABC1), member 3	ABCA3	7.4 ± 2.5	transport
phospholipase A2, group X	PLA2G10	6.8 ± 0.9	lipid catabolism
chemokine (C-C motif) ligand 20	CCL20	6.4 ± 6.7	chemotaxis/ inflammatory response
low density lipoprotein-related protein 2	LRP2	6.1 ± 5.3	protein glycosylation/receptor mediated endocytosis
Phosphodiesterase 4D, cAMP-specific	PDE4D	6.0 ± 1.4	signal transduction
N-acetylneuraminate pyruvate lyase (dihydrodipicolinate synthase)	NPL	5.8 ± 4.3	carbohydrate metabolic process
secretory leukocyte peptidase inhibitor	SLPI	5.6 ± 2.5	anti-inflammatory
surfactant protein C	SFTPC	5.4 ± 2.4	respiratory gaseous exchange
fatty acid synthase	FASN	5.4 ± 1.1	fatty acid biosynthesis
fatty acid binding protein 5	FABP5	5.3 ± 4.7	lipid metabolism
carbonic anhydrase XII	CA12	5.3 ± 3.1	one-carbon compound metabolism
period homolog 1 (Drosophila)	PER1	5.3 ± 3.2	transcription
hypothetical protein FLJ20366	FLJ20366	5.0 ± 1.9	---
alpha-2-glycoprotein 1, zinc	AZGP1	5.0 ± 2.6	cell adhesion/cell proliferation/lipid catabolism
fibrinogen gamma chain	FGG	4.9 ± 5.8	signal transduction
transforming, acidic coiled-coil containing protein 2	TACC2	4.7 ± 0.6	---
lysosomal-associated membrane protein 3	LAMP3	4.6 ± 2.4	cell proliferation/lamellar body membrane
lipoprotein lipase	LPL	4.5 ± 2.0	fatty acid metabolism
fatty acid desaturase 1	FADS1	4.5 ± 1.1	fatty acid biosynthesis
SH3-domain binding protein 5 (BTK-associated)	SH3BP5	4.5 ± 2.3	signal transduction
monoamine oxidase A	MAOA	4.4 ± 1.5	electron transport/catecholamine metabolism
phospholipase A2, group IB (pancreas)	PLA2G1B	4.3 ± 3.0	actin filament organization/lipid catabolism
family with sequence similarity 13, member A1	FAM13A1	4.3 ± 0.9	signal transduction
TSC22 domain family, member 3	TSC22D3	4.3 ± 2.1	regulation of transcription
CCAAT/enhancer binding protein (C/EBP), delta	CEBPD	4.3 ± 1.9	\transcription
N-myc downstream regulated gene 1	NDRG1	4.2 ± 1.7	response to metal ion
Rho-related BTB domain containing 2	RHOBTB2	4.2 ± 2.8	small GTPase mediated signal transduction
chromosome 14 open reading frame 147	C14orf147	4.1 ± 1.3	---
uracil-DNA glycosylase 2	UNG2	4.1 ± 3.1	cell cycle /carbohydrate metabolism

FLJ41131 protein	FLJ41131	4.0	±	1.2	---
solute carrier family 6 (amino acid transporter), member 14	SLC6A14	3.9	±	0.8	amino acid metabolism/transport /
phosphatidylinositol-specific phospholipase C, X domain containing 1	PLCXD1	3.8	±	1.6	signal transduction
alkaline phosphatase, liver/bone/kidney	ALPL	3.8	±	0.9	ossification/metabolism
metallothionein 1G	MT1G	3.6	±	2.6	---
S100 calcium binding protein P	S100P	3.6	±	1.5	---
dicarbonyl/L-xylulose reductase	DCXR	3.6	±	1.4	carbohydrate metabolism
A kinase (PRKA) anchor protein 13	AKAP13	3.5	±	1.3	intracellular signaling cascade
MID1 interacting protein 1 (gastrulation specific G12-like)	MID1IP1	3.5	±	1.5	negative regulation of microtubule depolymerization
hypothetical protein MGC11242	MGC11242	3.5	±	1.6	---
regulator of G-protein signalling 16	RGS16	3.5	±	2.1	negative regulation of signal transduction
GTP binding protein overexpressed in skeletal muscle	GEM	3.5	±	1.1	immune response/signal transduction
interferon stimulated exonuclease gene 20kDa	ISG20	3.4	±	1.8	cell proliferation
ubiquitin specific peptidase 13 (isopeptidase T-3)	USP13	3.4	±	1.1	ubiquitin cycle
---	---	3.4	±	2.8	---
ATPase, aminophospholipid transporter Class I, 8A,1	ATP8A1	3.4	±	1.3	cation transport/ metabolism /
titin	TTN	3.4	±	2.1	regulation of actin filament length/muscle development
calcium channel, voltage-dependent, alpha 2/delta subunit 2	CACNA2D2	3.4	±	1.5	---
5-methyltetrahydrofolate-homocysteine methyltransferase reductase	MTRR	3.3	±	1.3	electron transport/amino acid biosynthesis
arachidonate 15-lipoxygenase, second type	ALOX15B	3.3	±	1.6	lipid metabolism /negative regulation of growth /
proprotein convertase subtilisin/kexin type 2	PCSK2	3.3	±	1.1	proteolysis/cell-cell signaling
sushi, nidogen and EGF-like domains 1	SNED1	3.3	±	1.2	cell-matrix adhesion
selenium binding protein 1	SELENBP1	3.2	±	2.0	---
serum/glucocorticoid regulated kinase	SGK	3.2	±	1.8	protein amino acid phosphorylation/sodium ion transport
protocadherin 9	PCDH9	3.2	±	1.2	cell adhesion
GTP cyclohydrolase I feedback regulator	GCHFR	3.2	±	1.2	nitric oxide biosynthesis
transcription factor CP2-like 1	TFCP2L1	3.2	±	1.0	regulation of transcription
colony stimulating factor 3 receptor	CSF3R	3.1	±	0.8	defense response /cell adhesion
methylenetetrahydrofolate dehydrogenase (NADP+ dept) 2-like	MTHFD2L	3.1	±	0.9	folic acid and derivative biosynthesis
phosphatidylinositol glycan, class A	PIGA	3.1	±	1.0	biosynthesis
nicotinamide N-methyltransferase	NNMT	3.1	±	2.1	---
v-ets erythroblastosis virus E26 oncogene homolog 2 (avian)	ETS2	3.0	±	0.8	regulation of transcription
metallothionein 1M	MT1M	3.0	±	2.5	---
---	---	3.0	±	1.2	---
dehydrogenase/reductase (SDR family) member 3	DHRS3	3.0	±	1.2	fatty acid metabolism
ribonuclease, RNase A family, 4	RNASE4	3.0	±	0.9	mRNA cleavage/development
rabphilin 3A-like (without C2 domains)	RPH3AL	3.0	±	0.8	intracellular protein transport
protein kinase C, alpha	PRKCA	3.0	±	2.2	cell cycle /intracellular signaling cascade
sphingomyelin phosphodiesterase, acid-like	SMPDL3A	3.0	±	1.2	carbohydrate metabolism

3A

surfactant protein B	SFTPB	2.9	±	1.3	respiratory gaseous exchange
calpain 3, (p94)	CAPN3	2.9	±	1.3	proteolysis
regulator of G-protein signalling 2, 24kDa	RGS2	2.9	±	1.0	cell cycle/negative regulation of signal transduction
DKFZP564O0823 protein	DKFZP564O0823	2.8	±	0.3	---
FN5 protein	FN5	2.8	±	0.5	---
serine hydroxymethyltransferase 1 (soluble)	SHMT1	2.8	±	2.0	one-carbon compound metabolism
metallothionein 1H	MT1H	2.8	±	1.5	---
Hypothetical protein FLJ11127	FLJ11127	2.8	±	1.3	---
HIRA interacting protein 3	HIRIP3	2.8	±	1.6	chromatin assembly or disassembly
flavin containing monooxygenase 5	FMO5	2.8	±	1.8	protein folding
cystathionase (cystathionine gamma-lyase)	CTH	2.8	±	1.1	amino acid biosynthesis
KIAA0703 gene product	KIAA0703	2.7	±	0.7	cation transport
melanophilin	MLPH	2.7	±	0.3	intracellular protein transport
Similar to 60S ribosomal protein L35	RPL35	2.7	±	1.6	protein biosynthesis
protein kinase C binding protein 1	PRKCBP1	2.7	±	0.4	regulation of transcription
Kruppel-like factor 9	KLF9	2.7	±	0.8	regulation of transcription,
ceruloplasmin (ferroxidase)	CP	2.7	±	1.1	ion transport
aldehyde dehydrogenase 6 A1	ALDH6A1	2.7	±	1.0	metabolism
serpin peptidase inhibitor, 1	SERPINF1	2.7	±	1.3	development/cell proliferation
endothelial PAS domain protein 1	EPAS1	2.6	±	0.7	cell differentiation /angiogenesis
dihydropyrimidine dehydrogenase	DPYD	2.6	±	1.1	thymidine catabolism
KIAA0256 gene product	KIAA0256	2.6	±	0.8	---
potassium inwardly-rectifying channel, J, 8	KCNJ8	2.6	±	0.9	ion transport
chromosome 1 open reading frame 121	C1orf121	2.6	±	0.4	---
chitinase 3-like 1 (cartilage glycoprotein-39)	CHI3L1	2.6	±	1.0	carbohydrate metabolism
methylcrotonoyl-Coenzyme A carboxylase 1 (alpha)	MCCC1	2.6	±	1.0	leucine catabolism
complement component 2	C2	2.5	±	1.0	immune response/proteolysis
DEP domain containing 6	DEPDC6	2.5	±	0.7	intracellular signaling cascade
cytochrome P450, family 1, A1	CYP1A1	2.5	±	0.8	electron transport
metallothionein 1F (functional)	MT1F	2.5	±	1.1	---
MRNA; cDNA DKFZp762M127 (from clone DKFZp762M127)	---	2.5	±	0.4	---
Transcribed locus, weakly similar to XP_496299	---	2.5	±	0.7	---
glutathione S-transferase A4	GSTA4	2.5	±	0.9	response to stress/metabolism
Mitochondrial ribosomal protein S6	MRPS6	2.4	±	1.1	protein biosynthesis
metallothionein 1X	MT1X	2.4	±	1.2	response to metal ion/electron transport
patched homolog (Drosophila)	PTCH	2.4	±	0.7	cell cycle/signal transduction
solute carrier family 24 (sodium/potassium/calcium exchanger), 3	SLC24A3	2.4	±	1.3	ion transport
dynamin 2	DNM2	2.4	±	0.5	mitotic cell cycle/regulation of transcription
solute carrier family 27 (fatty acid transporter), member 3	SLC27A3	2.4	±	0.7	lipid metabolism
surfactant protein D	SFTPD	2.4	±	1.0	regulation of cytokine/macrophage chemotaxis

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tensin like C1 domain containing phosphatase (tensin 2)	TENC1	2.4	±	1.1	intracellular signaling cascade
solute carrier family 5 (inositol transporters), 3	SLC5A3	2.4	±	1.0	ion transport
Hypothetical LOC388388	---	2.4	±	1.0	---
response gene to complement 32	RGC32	2.4	±	0.8	regulation of cyclin dependent protein kinase activity
suppression of tumorigenicity 7	ST7	2.4	±	0.9	---
phosphodiesterase 4B, cAMP-specific	PDE4B	2.4	±	0.5	signal transduction
high-mobility group box 2	HMGB2	2.4	±	0.5	DNA replication/regulation of transcription
family with sequence similarity 46, member A	FAM46A	2.4	±	1.0	---
inhibin, beta B (activin AB beta polypeptide)	INHBB	2.3	±	0.7	response to external stimulus/cell differentiation
insulin-like growth factor binding protein 5	IGFBP5	2.3	±	0.6	regulation of cell growth
aldo-keto reductase 1, C1	AKR1C1/C2	2.3	±	0.5	lipid metabolism/transport
death-associated protein kinase 2	DAPK2	2.3	±	0.9	protein aa phosphorylation/induction apoptosis
ribosomal protein S6 kinase, 90kDa, polypeptide 2	RPS6KA2	2.3	±	0.4	protein aa phosphorylation/signal transduction
NFK light polypeptide gene enhancer in B-cells inhibitor, a	NFKBIA	2.3	±	0.5	apoptosis/response to pathogenic bacteria
3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)	HMGCS1	2.3	±	0.8	lipid biosynthesis
interferon induced transmembrane protein 1 (9-27)	IFITM1	2.3	±	1.2	immune response/cell proliferation
B-cell CLL/lymphoma 6 (zinc finger protein 51)	BCL6	2.3	±	0.8	inflammatory response/transcription
inositol 1,4,5-triphosphate receptor, type 2	ITPR2	2.3	±	0.6	cation transport
syntrophin, beta 1	SNTB1	2.3	±	1.0	muscle contraction
nuclear receptor subfamily 4, A, 2	NR4A2	2.3	±	0.7	transcription
glycoprotein M6B	GPM6B	2.3	±	1.4	development
adipose differentiation-related protein	ADFP	2.3	±	1.0	---
high-mobility group box 3	HMGB3	2.3	±	1.0	development/regulation of transcription,
DKFZP434C171 protein	DKFZP434C171	2.2	±	0.6	---
glycerol-3-phosphate dehydrogenase 1-like	GPD1L	2.2	±	0.4	carbohydrate metabolism
sodium channel, nonvoltage-gated 1, beta (Liddle syndrome)	SCNN1B	2.2	±	0.6	ion transport
cell division cycle 25B	CDC25B	2.2	±	0.5	cell division
Rap guanine nucleotide exchange factor (GEF) 5	RAPGEF5	2.2	±	1.0	transcription
CCR4-NOT transcription complex, subunit 8	CNOT8	2.2	±	0.9	transcription
cytochrome P450, 2, B, 7, 1	CYP2B7P1	2.2	±	0.7	---
peroxisomal membrane protein 4, 24kDa	PXMP4	2.2	±	0.9	---
ST6	ST6GALNAC4	2.2	±	0.6	protein amino acid glycosylation
ATPase, Na+/K+ transporting, alpha 1 polypeptide	ATP1A1	2.2	±	0.3	cation transport
acyl-Coenzyme A dehydrogenase, long chain	ACADL	2.2	±	0.7	lipid metabolism
isopentenyl-diphosphate delta isomerase 1	IDI1	2.2	±	0.4	lipid biosynthesis
lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase)	LSS	2.2	±	0.8	lipid biosynthesis
prostate stem cell antigen	PSCA	2.2	±	0.7	---
solute carrier family 7, 8	SLC7A8	2.2	±	0.6	amino acid transport

dolichyl-phosphate mannosyltransferase polypeptide 3	DPM3	2.2	±	0.2	carbohydrate metabolism
solute carrier organic anion transporter family, member 4C1	SLCO4C1	2.2	±	0.4	transport
MOCO sulphurase C-terminal domain containing 1	MOSC1	2.2	±	0.8	---
CCAAT/enhancer binding protein (C/EBP), beta	CEBPB	2.2	±	0.3	inflammatory response/transcription
insulin induced gene 1	INSIG1	2.1	±	0.7	metabolism/cell proliferation
ATP-binding cassette, sub-family C (CFTR/MRP), member 4	ABCC4	2.1	±	0.8	ion transport
arginase, type II	ARG2	2.1	±	0.4	urea cycle/nitric oxide biosynthesis
egl nine homolog 2 (C. elegans)	EGLN2	2.1	±	0.6	regulation of cell growth /protein metabolism
3'-phosphoadenosine 5'-phosphosulfate synthase 2	PAPSS2	2.1	±	0.7	nucleoside, nucleotide and nucleic acid metabolism
Poly(rC) binding protein 2	PCBP2	2.1	±	0.7	mRNA metabolism
Metallothionein 1M	MT1K	2.1	±	0.7	---
aldehyde dehydrogenase 3 family, member B1	ALDH3B1	2.1	±	0.7	alcohol metabolism/lipid metabolism
hypothetical protein DKFZp434C0328	DKFZp434C0328	2.1	±	0.8	---
neural precursor cell expressed, development down-regulated 4-like	NEDD4L	2.1	±	0.8	sodium ion transport/protein modification
EF-hand calcium binding domain 2	EFCAB2	2.1	±	1.0	---
interleukin 6 receptor	IL6R	2.1	±	0.4	immune response/development
choline phosphotransferase 1	CHPT1	2.1	±	0.6	regulation of cell growth/lipid metabolism
myosin regulatory light chain interacting protein	MYLIP	2.1	±	0.7	cell motility/ubiquitin cycle
metallothionein 2A	MT2A	2.0	±	0.9	copper ion homeostasis
kinesin family member 13B	KIF13B	2.0	±	0.8	protein targeting/ microtubule-based movement
uronyl-2-sulfotransferase	UST	2.0	±	0.5	protein amino acid sulfation
stearoyl-CoA desaturase (delta-9-desaturase)	SCD	2.0	±	0.6	fatty acid biosynthesis
sodium channel, nonvoltage-gated 1 alpha	SCNN1A	2.0	±	0.4	ion transport
LETM1 domain containing 1	LETMD1	2.0	±	0.3	---
apoptosis-inducing, TAF9-like domain 1	APITD1	2.0	±	0.6	---
epoxide hydrolase 1, microsomal (xenobiotic)	EPHX1	2.0	±	0.4	xenobiotic metabolism
fibroblast growth factor receptor 2	FGFR2	2.0	±	0.4	protein amino acid phosphorylation
N-acetylneuraminic acid synthase (sialic acid synthase)	NANS	2.0	±	0.2	carbohydrate biosynthesis
DKFZP564J102 protein	DKFZP564J102	2.0	±	0.3	---
DKFZP586A0522 protein	DKFZP586A0522	2.0	±	0.6	---
acetyl-Coenzyme A acetyltransferase 1	ACAT1	2.0	±	0.5	---
chaperone, ABC1 activity of bc1 complex like (S. pombe)	CABC1	2.0	±	0.7	protein folding
acetyl-Coenzyme A carboxylase alpha	ACACA	2.0	±	0.3	fatty acid biosynthesis
chromosome 1 open reading frame 25	C1orf25	2.0	±	0.7	tRNA processing
cellular repressor of E1A-stimulated genes 1	CREG1	2.0	±	0.1	regulation of cell growth/transcription
protein tyrosine phosphatase type IVA, member 1	PTP4A1	2.0	±	0.4	protein aa dephosphorylation/development
KIAA1280 protein	KIAA1280	2.0	±	0.4	---
phosphomannomutase 1	PMM1	1.9	±	0.4	metabolism
phosphatidylinositol-4-phosphate 5-kinase,	PIP5K1B	1.9	±	0.4	---

type I, beta					
brain protein 44-like	BRP44L	1.9	±	0.4	---
unc-13 homolog B (C. elegans)	UNC13B	1.9	±	0.6	exocytosis/induction of apoptosis
PDZ domain containing 3	PDZK3	1.9	±	0.7	cell adhesion
chromosome 5 open reading frame 4	C5orf4	1.9	±	0.4	metabolism
CD44 antigen	CD44	1.9	±	0.7	cell-matrix
polymerase (RNA) I polypeptide D, 16kDa	POLR1D	1.9	±	0.2	transcription
ER degradation enhancer, mannosidase alpha-like 1	EDEM1	1.9	±	0.7	protein amino acid N-linked glycosylation
hydroxysteroid (17-beta) dehydrogenase 4	HSD17B4	1.9	±	0.3	lipid metabolism
propionyl Coenzyme A carboxylase, alpha polypeptide	PCCA	1.9	±	0.5	fatty acid metabolism
chromosome 6 open reading frame 48	C6orf48	1.9	±	0.2	---
ubiquitin domain containing 1	UBTD1	1.9	±	0.6	protein modification
heat-responsive protein 12	HRSP12	1.9	±	0.3	regulation of translational termination
chromosome 14 open reading frame 94	C14orf94	1.9	±	0.7	---
mal, T-cell differentiation protein-like	MALL	1.9	±	0.3	cholesterol homeostasis
syntaxin binding protein 1	STXBP1	1.9	±	0.5	vesicle-mediated transport
programmed cell death 4 (neoplastic transformation inhibitor)	PDCD4	1.9	±	0.5	---
two pore segment channel 1	TPCN1	1.9	±	0.6	ion transport
anterior gradient 2 homolog (Xenopus laevis)	AGR2	1.9	±	0.1	---
X-box binding protein 1	XBP1	1.9	±	0.3	immune response/transcription
FXYD domain containing ion transport regulator 3	FXYD3	1.9	±	0.5	ion transport
ATP-binding cassette, sub-family C (CFTR/MRP), member 6	ABCC6	1.9	±	0.5	transport
protein kinase, AMP-activated, beta 1 non-catalytic subunit	PRKAB1	1.9	±	0.3	carbohydrate metabolism/lipid biosynthesis
nucleosome assembly protein 1-like 1	NAP1L1	1.9	±	0.4	DNA replication
adenylate kinase 1	AK1	1.9	±	0.2	nucleoside, nucleotide and nucleic acid metabolism
endonuclease G	ENDOG	1.9	±	0.6	DNA metabolism
WD repeat domain 19	WDR19	1.9	±	0.3	---
surfactant protein A2	SFTPA2	1.9	±	0.7	respiratory gaseous exchange
RNA binding protein with multiple splicing	RBPMS	1.9	±	0.4	RNA processing
ribonuclease, RNase A family, 1 (pancreatic)	RNASE1	1.8	±	0.9	---
ribosomal protein S6 kinase, 90kDa, polypeptide 5	RPS6KA5	1.8	±	0.5	transcription,/protein amino acid phosphorylation
arginine vasopressin-induced 1	AVPI1	1.8	±	0.4	---
chromosome 6 open reading frame 60	C6orf60	1.8	±	0.4	---
24-dehydrocholesterol reductase	DHCR24	1.8	±	0.3	lipid biosynthesis
protein tyrosine phosphatase type IVA, member 2	PTP4A2	1.8	±	0.6	protein amino acid dephosphorylation
Down syndrome critical region gene 5	DSCR5	1.8	±	0.5	---
7-dehydrocholesterol reductase	DHCR7	1.8	±	0.2	lipid biosynthesis
hypothetical protein FLJ23560	FLJ23560	1.8	±	0.8	protein folding
insulin receptor	INSR	1.8	±	0.3	carbohydrate metabolism
B-cell translocation gene 1, anti-proliferative	BTG1	1.8	±	0.4	negative regulation of cell proliferation/transcription

succinate-CoA ligase, GDP-forming, beta subunit	SUCLG2	1.8	±	0.4	tricarboxylic acid cycle
BTG family, member 3	BTG3	1.8	±	0.2	regulation of progression through cell cycle
Mannosidase, alpha, class 1A, member 1	MAN1A1	1.8	±	0.8	carbohydrate metabolism
branched chain aminotransferase 2, mitochondrial	BCAT2	1.8	±	0.4	metabolism/amino acid biosynthesis
sorting nexin 1	SNX1	1.8	±	0.5	intracellular protein transport
sin3-associated polypeptide, 18kDa	SAP18	1.8	±	0.3	transcription
WAP four-disulfide core domain 2	WFDC2	1.8	±	0.2	proteolysis
REST corepressor 1	RCOR1	1.8	±	0.2	regulation of transcription
Sec23 homolog B (S. cerevisiae)	SEC23B	1.8	±	0.4	intracellular protein transport
solute carrier family 1 (neutral amino acid transporter), member 5	SLC1A5	1.8	±	0.2	transport
nebulette	NEBL	1.8	±	0.3	regulation of actin filament length
p10-binding protein	Cep70	1.8	±	0.4	---
La ribonucleoprotein domain family, member 5	LARP5	1.8	±	0.5	---
P450 (cytochrome) oxidoreductase	POR	1.8	±	0.2	electron transport
cystathionine-beta-synthase	CBS	1.8	±	0.5	amino acid biosynthesis
ring finger protein 128	RNF128	1.8	±	0.3	proteolysis/protein ubiquitination
solute carrier family 7, 11	SLC7A11	1.8	±	0.3	transport
enthoprotin	ENTH	1.7	±	0.4	endocytosis
metallothionein 1E (functional)	MT1E	1.7	±	0.4	---
insulin receptor substrate 2	IRS2	1.7	±	0.3	glucose metabolism/cell proliferation
biliverdin reductase B (flavin reductase (NADPH))	BLVRB	1.7	±	0.5	nucleotide-sugar metabolism
selenoprotein P, plasma, 1	SEPP1	1.7	±	0.3	response to oxidative stress
hypothetical protein LOC339229	LOC339229	1.7	±	0.1	---
signal transducer and activator of transcription 3	STAT3	1.7	±	0.3	acute-phase response/regulation of transcription,
transcription factor-like 5 (basic helix-loop-helix)	TCFL5	1.7	±	0.5	regulation of transcription,/development
cAMP responsive element binding protein-like 2	CREBL2	1.7	±	0.2	regulation of transcription,
par-3 partitioning defective 3 homolog (C. elegans)	PARD3	1.7	±	0.6	cell division/protein complex assembly
serpin peptidase inhibitor, clade A, 1	SERPINA1	1.7	±	0.3	acute-phase response
lipin 2	LPIN2	1.7	±	0.4	---
H3 histone, family 3B (H3.3B)	H3F3B	1.7	±	0.3	nucleosome assembly
enolase superfamily member 1	ENOSF1	1.7	±	0.4	metabolism
lipoma HMGIC fusion partner-like 2	LHFPL2	1.7	±	0.3	---
Coenzyme A synthase	COASY	1.7	±	0.4	biosynthesis
sema, immunoglobulin, short basic domain, secreted, semaphorin 3B	SEMA3B	1.7	±	0.6	cell-cell signaling/development
lipin 1	LPIN1	1.7	±	0.5	fat cell differentiation
cAMP responsive element binding protein 3-like 1	CREB3L1	1.7	±	0.4	regulation of transcription
lysophosphatidic acid acyltransferase, beta	AGPAT2	1.7	±	0.4	phospholipid biosynthesis
VAMP (vesicle-associated membrane protein)-associated protein A	VAPA	1.7	±	0.1	exocytosis

transmembrane protein 80	TMEM80	1.7	±	0.5	---
emopamil binding protein (sterol isomerase)	EBP	1.7	±	0.1	lipid biosynthesis
glutamate-ammonia ligase (glutamine synthetase)	GLUL	1.7	±	0.1	nitrogen compound metabolism
KIAA1102 protein	KIAA1102	1.7	±	0.3	actomyosin structure organization and biogenesis
ecotropic viral integration site 1	EVI1	1.7	±	0.4	development
intersectin 2	ITSN2	1.7	±	0.2	endocytosis
superoxide dismutase 3, extracellular	SOD3	1.7	±	0.3	superoxide metabolism
Methionine adenosyltransferase II, alpha	MAT2A	1.7	±	0.5	one-carbon compound metabolism
autism susceptibility candidate 2	AUTS2	1.7	±	0.3	---
forkhead box O1A (rhabdomyosarcoma)	FOXO1A	1.7	±	0.7	transcription
zinc finger protein 42 (myeloid-specific retinoic acid-responsive)	ZNF42	1.7	±	0.3	transcription
calcium binding protein P22	CHP	1.7	±	0.1	potassium ion transport
mitochondrial ribosomal protein S18B	MRPS18B	1.7	±	0.4	protein biosynthesis
phosphoinositide-3-kinase, catalytic, beta polypeptide	PIK3CB	1.6	±	0.3	regulation of cell cycle/chemotaxis
frequently rearranged in advanced T-cell lymphomas 2	FRAT2	1.6	±	0.4	cell proliferation/development
LIM domain only 3 (rhombotin-like 2)	LMO3	1.6	±	0.3	transcription
zinc finger protein 36, C3H type, homolog (mouse)	ZFP36	1.6	±	0.2	mRNA catabolism
hypothetical protein FLJ11259	FLJ11259	1.6	±	0.1	---
Bernardinelli-Seip congenital lipodystrophy 2 (seipin)	BSCL2 / HNRPUL2	1.6	±	0.4	---
laminin, beta 2 (laminin S)	LAMB2	1.6	±	0.5	cell adhesion
pleckstrin homology domain containing, B (evectins) 1	PLEKHB1	1.6	±	0.3	phototransduction
SNF1-like kinase	SNF1LK	1.6	±	0.7	cell cycle/evelopment
chromosome 10 open reading frame 77	C10orf77	1.6	±	0.5	---
sterol-C4-methyl oxidase-like	SC4MOL	1.6	±	0.1	ipid biosynthesis
THAP domain containing 11	THAP11	1.6	±	0.3	---
hyaluronoglucosaminidase 1	HYAL1	1.6	±	0.3	carbohydrate metabolism
solute carrier family 19 (thiamine transporter), member 2	SLC19A2	1.6	±	0.1	transport
chromosome 14 open reading frame 109	C14orf109	1.6	±	0.2	---
Similar to lymphocyte-specific protein 1	---	1.6	±	0.3	---
hypothetical protein MAC30	MAC30	1.6	±	0.3	regulation of cell growth
syntaxin 12	STX12	1.6	±	0.3	intracellular protein transport
low density lipoprotein receptor (familial hypercholesterolemia)	LDLR	1.6	±	0.1	lipid transport
MOCO sulphurase C-terminal domain containing 2	MOSC2	1.6	±	0.3	---
GULP, engulfment adaptor PTB domain containing 1	GULP1	1.6	±	0.2	phagocytosis,
dual specificity phosphatase 1	DUSP1	1.6	±	0.3	protein aa dephosphorylation/cell cycle
MAX-like protein X	MLX	1.6	±	0.4	transcription
aldo-keto reductase 1, C2	AKR1C2	1.6	±	0.3	lipid metabolism
IMP (inosine monophosphate) dehydrogenase2	IMPDH2	1.5	±	0.2	purine nucleotide biosynthesis

CD59 antigen p18-20	CD59	1.5	±	0.2	immune response
ornithine aminotransferase (gyrate atrophy)	OAT	1.5	±	0.5	amino acid metabolism
poly(A)-specific ribonuclease (deadenylation nuclease)	PARN	1.5	±	0.2	transcription/mRNA catabolism
CD97 antigen	CD97	1.5	±	0.4	inflammatory response/cell motility
UDP-GlcNAc:bGal beta-1,3-N-acetylglucosaminyltransferase 6	B3GNT6	1.5	±	0.2	poly-N-acetyllactosamine biosynthesis
kallikrein 11	KLK11	1.5	±	0.6	proteolysis
phosphodiesterase 4D interacting protein (myomegalin)	PDE4DIP	1.5	±	0.5	protein biosynthesis
RING1 and YY1 binding protein	RYBP	1.5	±	0.1	transcription /apoptosis

Data are mean±SD for 5 experiments comparing transcript abundance after 5 days culture without (control) or with (treated) dexamethasone+8-Br-cAMP+isobuthylmethylxanthine

---, no gene designation for probe sequence or GO category assigned