Supplemental data

Table S1. Sixty-three differentially regulated transcripts computed with the Significance Analysis of Microarrays (SAM) method sorted by fold–change values. The number of permutations in the SAM method was set to twenty-thousand and a false discovery rate of 2.5% was selected.

Accession No.	**Gensymbol**	**Name**	**Biological Process**	**Fold change**
AI017691	TMEM174	Transmembrane protein 174		-3.49
AA962549	SLC6A19	Solute carrier family 6 (neutral amino acid transporter), member 19	Transport, Amino acid metabolism	-3.48
AA743923		CDNA FLJ32283 fis, clone PROST2000212		-3.34
AA878637		Transcribed locus		-3.29
AA864848	TMEM174	Transmembrane protein 174		-3.20
AA962194	UGT2B7	UDP glucuronosyltransferase 2 family, polypeptide B7	Steroid hormone metabolism, Steroid metabolism, Lipid, fatty acid and steroid metabolism	-3.19
H93381	GLYATL1	Glycine-N-acyltransferase-like 1	Lipid, fatty acid and steroid metabolism	-3.10
AA872711	SLC5A12	Solute carrier family 5 (sodium/glucose cotransporter), member 12	Transport	-2.98
AI253164		Transcribed locus		-2.90
AA988580	GPR155	G protein-coupled receptor 155		-2.85
R86241	SULT1C2	Sulfotransferase family, cytosolic, 1C, member 2	Steroid hormone metabolism, Steroid metabolism, Lipid, fatty acid and steroid metabolism	-2.74
AA456975	APOD	Apolipoprotein D	Transport, Coenzyme and prosthetic group metabolism	-2.62
AA917550		Transcribed locus		-2.41
N68871		CDNA FLJ43400 fis, clone OCBBF2010281		-2.35
AA994816	SLC5A12	Solute carrier family 5 (sodium/glucose cotransporter), member 12	Transport	-2.31
AA496149	HMGCS2	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 (mitochondrial)	Coenzyme and prosthetic group metabolism, Steroid metabolism, Lipid, fatty acid and steroid metabolism	-2.27
AA705032		Transcribed locus		-2.20
AA894763	MGAM	Maltase-glucoamylase (alpha-glucosidase)		-2.19
R15785	PREPL	Prolyl endopeptidase-like	Protein metabolism and modification	-2.18
AI792934	LOC155006	Hypothetical protein LOC155006		-2.17
W85883	SLC47A1	Solute carrier family 47, member 1		-2.15

Accession No.	Gensymbol	Name	Biological Process	Fold change
AA973279	AMN	Amnionless homolog (mouse)	Transport, Lipid, fatty acid and steroid metabolism	-2.14
N69913	CRIP3	Cysteine-rich protein 3		-2.14
R40400	CHL1	Cell adhesion molecule with homology to L1CAM (close homolog of L1)	Determination of dorsal/ventral axis	-2.13
H02884	CDH5	Cadherin 5, type 2, VE-cadherin (vascular epithelium)		-2.11
H38650	SLC2A5	Solute carrier family 2 (facilitated glucose/fructose transporter), member 5	Transport	-2.11
AA999881	LOC202051	Hypothetical protein LOC202051		-2.07
AA972434	SLC39A5	Solute carrier family 39 (metal ion transporter), member 5	Transport	-2.05
AA058341	FAHD1	Fumarylacetoacetate hydrolase domain containing 1	Amino acid metabolism	-2.03
AA879452		CDNA clone IMAGE:5270438		-2.03
W35369	PRLR	Prolactin receptor	Lactation, mammary development	-2.01
AI989344	USH1C	Usher syndrome 1C (autosomal recessive, severe)		-2.01
N29639	CMAH	Cytidine monophosphate-N-acetylneuraminic acid hydroxylase (CMP-N-acetylneuraminate monooxygenase) pseudogene		-1.97
AA975301	CALCRL	Calcitonin receptor-like		-1.96
AA917621		Transcribed locus		-1.95
AI264620	LOC201229	Hypothetical protein LOC201229		-1.89
AA458652		Transcribed locus		-1.87
R06256		Transcribed locus		-1.85
AA496110		Transcribed locus, strongly similar to NP_115821.1 multiple EGF-like-domains 11 [Homo sapiens]		-1.84
T99793	CTAGE5	CTAGE family, member 5		-1.83
AA705720	ALAD	Aminolevulinate, delta-, dehydratase	Coenzyme and prosthetic group metabolism, Porphyrin metabolism	-1.81
AA182796	RHOBTB1	Rho-related BTB domain containing 1		-1.80
AA009593	MPP7	Membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7)	Asymmetric protein localization	-1.79
R09729	SDPR	Serum deprivation response (phosphatidylserine binding protein)	mRNA transcription termination	-1.78
AI123255	DHRSX	Dehydrogenase/reductase (SDR family) X-linked		-1.78
AA450353	ELMOD1	ELMO/CED-12 domain containing 1		-1.75
AI668706		Transcribed locus		-1.75
T49816	LOC643008	PP12104		-1.73
R85643		Data not found		-1.72
H62009		Transcribed locus		-1.72
N66734	EMCN	Endomucin		-1.72
AA983558	SLC12A1	Solute carrier family 12 (sodium/potassium/chloride transporters), member 1	Transport	-1.72

Accession No.	**Gensymbol**	**Name**	**Biological Process**	**Fold change**
AA233564	PDE8A	Phosphodiesterase 8A		-1.70
AA862485		Data not found		-1.70
N79823	LCN2	Lipocalin 2	Transport	-1.65
AA058566		Data not found		-1.65
H67900		Transcribed locus, moderately similar to XP_001372821.1 PREDICTED: similar to Choline/ethanolamine phosphotransferase 1 [Monodelphis domestica]		-1.64
H90761	IL17RB	Interleukin 17 receptor B		-1.63
AA188785	KIAA1549	KIAA1549		-1.62
H73410		Data not found		-1.62
W37841		CDNA clone IMAGE:4902949		-1.57
N35894		Data not found		-1.56
AA399405	SNX30	Sorting nexin family member 30		-1.50

Table S2. 147 differentially regulated transcripts computed with the Student's t-Test sorted by fold-change values. The p-value threshold was set to < 0.05 with fold-change values greater than two.

Accession No.	**Gensymbol**	**Name**	**Biological Process**	**Fold change**
T94626	FGG	Fibrinogen gamma chain	Blood circulation and gas exchange, Blood clotting, Immunity and defense, Cell proliferation and differentiation	4.92
AA865707	FGA	Fibrinogen alpha chain	Blood circulation and gas exchange, Blood clotting, Immunity and defense, Cell proliferation and differentiation	3.19
R14976		Data not found		3.16
AA704242	SERPINA3	Serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3		2.84
T72915	SOCS3	Suppressor of cytokine signaling 3	JAK-STAT cascade, Inhibition of apoptosis	2.72
AA457138	FZD8	Frizzled homolog 8 (Drosophila)		2.54
AI003775	LOC387763	Hypothetical LOC387763		2.48
H53340	MT1G	Metallothionein 1G		2.44
AW029498	SERPINA3	Serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3		2.42
AI922872	SOCS3	Suppressor of cytokine signaling 3		2.42
AA055946	CD3D	CD3d molecule, delta (CD3-TCR complex)	Immunity and defense	2.12
AA678021	SNRPE	Small nuclear ribonucleoprotein polypeptide E		2.01
AA704995	GLYAT	Glycine-N-acyltransferase	Lipid, fatty acid and steroid metabolism, Fatty acid metabolism	-4.71
AI253049	TINAG	Tubulointerstitial nephritis antigen	Cell adhesion	-4.01
AA932134		CDNA FLJ32283 fis, clone PROST2000212		-3.90
R97050		CDNA clone IMAGE:4610527		-3.78

Accession No.	Gensymbol	Name	Biological Process	Fold change
AA994816	SLC5A12	Solute carrier family 5 (sodium/glucose cotransporter), member 12	Transport	-3.68
AA877253	RNF186	Ring finger protein 186	Proteolysis	-3.63
AA885603		Transcribed locus		-3.52
AI017691	TMEM174	Transmembrane protein 174		-3.50
AA962549	SLC6A19	Solute carrier family 6 (neutral amino acid transporter), member 19	Transport, Amino acid metabolism, Amino acid transport	-3.48
W85851	ACSM2B	Acyl-CoA synthetase medium-chain family member 2B		-3.38
AA743923		CDNA FLJ32283 fis, clone PROST2000212		-3.34
AA878637		Transcribed locus		-3.29
AA864848	TMEM174	Transmembrane protein 174		-3.21
AA919149	HAO2	Hydroxyacid oxidase 2 (long chain)	Carbohydrate metabolism	-3.20
AA962194	UGT2B7	UDP glucuronosyltransferase 2 family, polypeptide B7	Lipid, fatty acid and steroid metabolism, Steroid hormone metabolism, Steroid metabolism, Carbohydrate metabolism, Other polysaccharide metabolism	-3.19
N74025	DIO1	Deiodinase, iodothyronine, type I		-3.17
AI017796	SLC5A12	Solute carrier family 5 (sodium/glucose cotransporter), member 12	Transport	-3.15
H93381	GLYATL1	Glycine-N-acyltransferase-like 1	Lipid, fatty acid and steroid metabolism, Fatty acid metabolism	-3.09
H88329	CALB1	Calbindin 1, 28kDa	Homeostasis	-3.04
AA872711	SLC5A12	Solute carrier family 5 (sodium/glucose cotransporter), member 12	Transport	-2.98
AI017796	SLC5A12	Solute carrier family 5 (sodium/glucose cotransporter), member 12	Transport	-2.96
AI335086	ANGPTL3	Angiopoietin-like 3		-2.93

Accession No.	**Gensymbol**	**Name**	**Biological Process**	**Fold change**
AI245843		Transcribed locus, strongly similar to NP_001011880.1 hypothetical protein LOC497190 [Homo sapiens]		-2.91
AI253164		Transcribed locus		-2.90
AI264674	SLC16A12	Solute carrier family 16, member 12 (monocarboxylic acid transporter 12)	Transport, Ion transport, Cation transport	-2.88
AA988580	GPR155	G protein-coupled receptor 155		-2.85
R08178	LOC100129488	Hypothetical protein LOC100129488		-2.85
AA864183	RHCG	Rh family, C glycoprotein	Transport	-2.82
AA928710	SLC6A19	Solute carrier family 6 (neutral amino acid transporter), member 19	Transport, Amino acid metabolism, Amino acid transport	-2.74
R86241	SULT1C2	Sulfotransferase family, cytosolic, 1C, member 2	Lipid, fatty acid and steroid metabolism, Steroid hormone metabolism, Steroid metabolism, Sulfur metabolism	-2.74
AA456001	NOX4	NADPH oxidase 4	Electron transport	-2.70
N36136	EMCN	Endomucin	Cell adhesion	-2.69
AA416585	ACE2	Angiotensin I converting enzyme (peptidyl-dipeptidase A) 2	Proteolysis	-2.68
AI241028		Data not found		-2.68
AA994857	ZNF552	Zinc finger protein 552	Nucleoside, nucleotide and nucleic acid metabolism, mRNA transcription	-2.67
AA514359	RNF186	Ring finger protein 186	Proteolysis	-2.66
AA456975	APOD	Apolipoprotein D	Transport, Coenzyme and prosthetic group metabolism, Vitamin/cofactor transport	-2.62
AI301528	HNF4A	Hepatocyte nuclear factor 4, alpha		-2.60
T70353	ACMSD	Aminocarboxymuconate semialdehyde decarboxylase		-2.58

Accession No.	**Gensymbol**	**Name**	**Biological Process**	**Fold change**
N53031	UGT2B4	UDP glucuronosyltransferase 2 family, polypeptide B4	Lipid, fatty acid and steroid metabolism, Steroid hormone metabolism, Steroid metabolism, Carbohydrate metabolism, Other polysaccharide metabolism	-2.57
W81603		Data not found		-2.56
AA902897		Transcribed locus		-2.53
R16259		Data not found		-2.53
H44449	LRP2	Low density lipoprotein-related protein 2		-2.51
AA878939		Transcribed locus		-2.51
R63647	PRLR	Prolactin receptor	Lactation, mammary development	-2.49
H18608	SLC22A8	Solute carrier family 22 (organic anion transporter), member 8	Transport, Ion transport, Extracellular transport and import, Anion transport	-2.45
AI245812	KCNJ15	Potassium inwardly-rectifying channel, subfamily J, member 15	Transport, Ion transport, Cation transport	-2.42
AA918008	SLC28A1	Solute carrier family 28 (sodium-coupled nucleoside transporter), member 1	Transport, Ion transport, Cation transport, Nucleoside, nucleotide and nucleic acid metabolism	-2.42
AA932134		CDNA FLJ32283 fis, clone PROST2000212		-2.42
AA932135		Transcribed locus		-2.41
AA917550		Transcribed locus		-2.41
AI015991	CLDN2	Claudin 2		-2.40
AA746229	UGT2B7	UDP glucuronosyltransferase 2 family, polypeptide B7	Lipid, fatty acid and steroid metabolism, Steroid hormone metabolism, Steroid metabolism, Carbohydrate metabolism, Other polysaccharide metabolism	-2.40

Accession No.	Gensymbol	Name	Biological Process	Fold change
T50951	UGT2B15	UDP glucuronosyltransferase 2 family, polypeptide B15	Lipid, fatty acid and steroid metabolism, Steroid hormone metabolism, Steroid metabolism, Carbohydrate metabolism, Other polysaccharide metabolism	-2.39
N53031	UGT2B4	UDP glucuronosyltransferase 2 family, polypeptide B4	Lipid, fatty acid and steroid metabolism, Steroid hormone metabolism, Steroid metabolism, Carbohydrate metabolism, Other polysaccharide metabolism	-2.38
AI222515	BBOX1	Butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) 1	Coenzyme and prosthetic group metabolism	-2.37
AI264674	SLC16A12	Solute carrier family 16, member 12 (monocarboxylic acid transporter 12)	Transport, Ion transport, Cation transport	-2.35
N68871		CDNA FLJ43400 fis, clone OCBBF2010281		-2.35
R98936	MME	Membrane metallo-endopeptidase	Proteolysis	-2.34
AI261833	SLC7A9	Solute carrier family 7 (cationic amino acid transporter, y+ system), member 9	Transport, Amino acid metabolism, Amino acid transport	-2.34
AA878391	GPC5	Glypican 5	Cell adhesion	-2.31
AA994816	SLC5A12	Solute carrier family 5 (sodium/glucose cotransporter), member 12	Transport	-2.31
R43597		Data not found		-2.31
AA918729		Transcribed locus		-2.30
R08912		Data not found		-2.30
AA703222		CDNA FLJ12088 fis, clone HEMBB1002545		-2.30
AA676742	DMGDH	Dimethylglycine dehydrogenase	Electron transport	-2.27

Accession No.	**Gensymbol**	**Name**	**Biological Process**	**Fold change**
AA496149	HMGCS2	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 (mitochondrial)	Lipid, fatty acid and steroid metabolism, Steroid metabolism, Coenzyme and prosthetic group metabolism	-2.27
W56753	KIAA1276	KIAA1276 protein		-2.27
AA947621	ATP6V1G3	ATPase, H+ transporting, lysosomal 13kDa, V1 subunit G3	Transport, Ion transport, Cation transport, Nucleoside, nucleotide and nucleic acid metabolism	-2.26
AA858019	SLC13A1	Solute carrier family 13 (sodium/sulfate symporters), member 1	Transport, Ion transport, Cation transport	-2.26
AA862436	FAM151A	Family with sequence similarity 151, member A		-2.25
R10885	ACY3	Aspartoacylase (aminocyclase) 3	Amino acid metabolism, Other amino acid metabolism	-2.24
AA287032	TBC1D8B	TBC1 domain family, member 8B (with GRAM domain)		-2.24
R98070		Data not found		-2.23
R40176	CXCL14	Chemokine (C-X-C motif) ligand 14		-2.22
AA971563	SGSM3	Small G protein signaling modulator 3		-2.22
AA026754	SNTA1	Syntrophin, alpha 1 (dystrophin-associated protein A1, 59kDa, acidic component)		-2.22
AI253036		Transcribed locus		-2.20
AA705032		Transcribed locus		-2.20
AA894763	MGAM	Maltase-glucoamylase (alpha-glucosidase)		-2.19
AI344372	SLC26A7	Solute carrier family 26, member 7	Transport, Ion transport, Extracellular transport and import, Anion transport, Sulfur metabolism	-2.19

Accession No.	**Gensymbol**	**Name**	**Biological Process**	**Fold change**
T47312	INSR	Insulin receptor	Carbohydrate metabolism, Regulation of carbohydrate metabolism, Other developmental process	-2.18
AI792934	LOC155006	Hypothetical protein LOC155006		-2.18
AA705112	MOCS1	Molybdenum cofactor synthesis 1	Coenzyme and prosthetic group metabolism, Pterin metabolism	-2.18
R15785	PREPL	Prolyl endopeptidase-like	Proteolysis	-2.18
AI015652	SLC13A1	Solute carrier family 13 (sodium/sulfate symporters), member 1	Transport, Ion transport, Cation transport	-2.18
W85883	SLC47A1	Solute carrier family 47, member 1		-2.15
AA971425	USP2	Ubiquitin specific peptidase 2	Proteolysis	-2.15
AA973279	AMN	Amnionless homolog (mouse)	Transport, Lipid, fatty acid and steroid metabolism	-2.14
AA677185	ANK3	Ankyrin 3, node of Ranvier (ankyrin G)		-2.14
AI733138	BHMT2	Betaine-homocysteine methyltransferase 2	Amino acid metabolism	-2.14
AA886349		Data not found		-2.14
R66006	ACADL	Acyl-Coenzyme A dehydrogenase, long chain	Lipid, fatty acid and steroid metabolism, Fatty acid metabolism, Electron transport	-2.13
R40400	CHL1	Cell adhesion molecule with homology to L1CAM (close homolog of L1)	Cell adhesion	-2.13
N69913	CRIP3	Cysteine-rich protein 3		-2.13
N92901	FABP4	Fatty acid binding protein 4, adipocyte	Transport, Lipid, fatty acid and steroid metabolism, Coenzyme and prosthetic group metabolism, Vitamin/cofactor transport	-2.13
H50623	HLA-DRB1	Major histocompatibility complex, class II, DR beta 3		-2.13
H27752	AQP7	Aquaporin 7	Transport, Homeostasis	-2.12
AA256291		Transcribed locus		-2.12
AI263210		Transcribed locus		-2.12

Accession No.	**Gensymbol**	**Name**	**Biological Process**	**Fold change**
H02884	CDH5	Cadherin 5, type 2, VE-cadherin (vascular epithelium)	Cell adhesion	-2.11
H38650	SLC2A5	Solute carrier family 2 (facilitated glucose/fructose transporter), member 5	Transport, Carbohydrate metabolism	-2.11
AA865572		Transcribed locus		-2.11
AA111975	CMBL	Carboxymethylenebutenolidase homolog (Pseudomonas)	Carbohydrate metabolism	-2.10
AA775223	HPGD	Hydroxyprostaglandin dehydrogenase 15-(NAD)	Lipid, fatty acid and steroid metabolism, Steroid metabolism	-2.10
AA485893	RNASE1	Ribonuclease, RNase A family, 1 (pancreatic)	Nucleoside, nucleotide and nucleic acid metabolism	-2.10
AI815076	SLC7A7	Solute carrier family 7 (cationic amino acid transporter, y+ system), member 7	Transport, Amino acid metabolism, Amino acid transport	-2.10
W72294	CXCL14	Chemokine (C-X-C motif) ligand 14		-2.09
H78003	IYD	Iodotyrosine deiodinase	Electron transport	-2.09
H18456	LOC644662	Similar to hCG2042541		-2.09
AA682293	PAH	Phenylalanine hydroxylase	Amino acid metabolism, Other amino acid metabolism	-2.09
R07484		Data not found		-2.09
AA452278	SLC4A4	Solute carrier family 4, sodium bicarbonate cotransporter, member 4	Transport, Ion transport, Cation transport, Homeostasis	-2.08
AA677050	AFM	Afamin	Transport	-2.07
AA999881	LOC202051	Hypothetical protein LOC202051		-2.07
AI279830	PPP1R16B	Protein phosphatase 1, regulatory (inhibitor) subunit 16B		-2.07
AA855158	CA4	Carbonic anhydrase IV		-2.06
AI383171	LDB3	LIM domain binding 3	Nucleoside, nucleotide and nucleic acid metabolism, mRNA transcription, Other developmental process	-2.06
AA452826	PCP4	Purkinje cell protein 4		-2.06
AA972434	SLC39A5	Solute carrier family 39 (metal ion transporter), member 5	Transport, Ion transport	-2.05

Accession No.	**Gensymbol**	**Name**	**Biological Process**	**Fold change**
AI300876	FAM150B	Family with sequence similarity 150, member B		-2.04
AA058341	FAHD1	Fumarylacetoacetate hydrolase domain containing 1	Amino acid metabolism	-2.03
AA932696	FAM107A	Family with sequence similarity 107, member A		-2.03
AA872397	LGALS2	Lectin, galactoside-binding, soluble, 2	Cell adhesion	-2.03
AI000188	UGT2B7	UDP glucuronosyltransferase 2 family, polypeptide B7	Lipid, fatty acid and steroid metabolism, Steroid hormone metabolism, Steroid metabolism, Carbohydrate metabolism, Other polysaccharide metabolism	-2.03
W35369	PRLR	Prolactin receptor	Lactation, mammary development	-2.02
AA680349	PROZ	Protein Z, vitamin K-dependent plasma glycoprotein	Proteolysis	-2.02
AA879452		CDNA clone IMAGE:5270438		-2.02
H99932	CRYL1	Crystallin, lambda 1	Lipid, fatty acid and steroid metabolism, Carbohydrate metabolism, Fatty acid metabolism	-2.01
H02824	LYVE1	Lymphatic vessel endothelial hyaluronan receptor 1		-2.01
AA579186	TMPRSS2	Transmembrane protease, serine 2	Proteolysis	-2.01
R68997	PRLR	Prolactin receptor	Lactation, mammary development	-2.00
AI989344	USH1C	Usher syndrome 1C (autosomal recessive, severe)		-2.00