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