Supplemental Table 1. Candidate fetal genes in whole blood

Gene	Probe set ID	Gene Symbol	Accession Number	Biological function	p value[A]	p value[B]	Count[C]
S-phase kinase-associated protein 1A (p19A)	200719_at	SKP1A	NM_006930	Ubiquitin cycle, may be involved in transcription regulation for development or maintenance of specialized functions of the inner ear	0.0186	0.0000	9 of 10
Family with sequence similarity 120A	200767_s_at	FAM120A	NM_014612	ATP biosynthesis, transport, ion transport, ATP synthesis coupled proton transport, proton transport, generation of precursor metabolites and energy	0.0411	0.0425	8 of 10
CTD small phosphatase-like	201906_s_at	CTDSPL	NM_005808	Biological function unknown	0.0114	0.0358	8 of 10
Upstream transcription factor 2, c-fos interacting	202152_x_at	USF2	NM_003367	Regulation of transcription, DNA-dependent regulation of transcription, transcription	0.0143	0.0000	9 of 10
Tumor-associated calcium signal transducer 2	202286_s_at	TACSTD2	J04152	Cell surface receptor linked signal transduction, visual perception, cell proliferation, response to stimulus, regulation of progression through cell cycle	0.0216	0.0002	8 of 10
Dehydrogenase/reductase member 3	202481_at	DHRS3	NM_004753	Visual perception, metabolism, retinol metabolism	0.0000	0.0001	9 of 10
Adenylate kinase 1	202588_at	AK1	NM_000476	Nucleobase, nucleoside, nucleotide and nucleic acid metabolism, ATP metabolism	0.0274	0.0000	7 of 10
Cyclin B2	202705_at	CCNB2	NM_004701	Regulation of progression through cell cycle, cell cycle mitosis, cell division, protein biosynthesis, translational initiation, regulation of translational initiation, distinct pattern of expression during spermatogenesis	0.0000	0.0016	8 of 10
Integral membrane protein 2A	202747_s_at	ITM2A	NM_004867	Seen to be expressed in outer perichondrial rim of postnatal mandibular condyle	0.0495	0.0118	7 of 10
Neuroblastoma-amplified protein	202926_at	NAG	NM_015909	Upregulated in neuroblastoma	0.0023	0.0003	10 of 10
Mevalonate (diphospho) decarboxylase	203027_s_at	MVD	NM_002461	Cholesterol, lipid, sterol and isoprenoid biosynthesis, phosphorylation	0.0000	0.0000	10 of 10
Myotubularin related protein 2	203212_s_at	MTMR2	NM_016156	Protein amino acid and phospholipid dephosphorylation	0.0036	0.0466	7 of 10
Frizzled homolog 6 (Drosophila)	203987_at	FZD6	NM_003506	Establishment of tissue polarity, cell surface receptor linked signal transduction, G-protein coupled receptor protein signaling pathway, frizzled signaling pathway, development, signal transduction development, Wnt receptor signaling pathway	0.0489	0.0012	7 of 10
Arylsulfatase A	204443_at	ARSA	NM_000487	Lipid and sphinogolipid metabolism, metabolism	0.0000	0.0000	10 of 10
Nuclear pore complex interacting protein	204538_x_at	NPIP	NM_006985	Neuropeptide signaling pathway	0.0011	0.0295	8 of 10

Natriuretic peptide receptor A/guanlyate cyclase A	204648_at	NPR1	NM_000906	cGMP biosynthesis, protein amino acid phosphorylation, cell surface receptor linked signal transduction, intracellular signaling cascade, fluid secretion, blood pressure regulation, negative regulation of cell growth, vascular permeability and angiogenesis, diuresis, natriuresis, vasodilation, cyclic nucleotide biosynthesis	0.0095	0.0005	8 of 10
Protoporphyrinogen oxidase	204788_s_at	PPOX	NM_000309	Electron transport, heme and porphyrin biosynthesis	0.0062	0.0028	7 of 10
Zinc finger protein 646	204876_at	ZNF646	NM_014699	Transcription regulation of transcription, DNA dependent	0.0479	0.0237	8 of 10
Neuralized-like (Drosophila)	204888_s_at	NEURL	NM_004210	Nervous system development, involved in determination of cell fate in neurogenic region of embryo	0.0000	0.0080	9 of 10
AP2 associated kinase 1	205435_s_at	AAK1	NM_014911	Protein amino acid phosphorylation	0.0324	0.0365	7 of 10
Kallikrein-related peptidase 11	205470_s_at	KLK11	NM_006853	Proteolysis	0.0000	0.0000	10 of 10
Bactericidal/permeability-increasing protein	205557_at	BPI	NM_001725	Immune response, response to pest, pathogen or parasite, defense response to bacteria	0.0094	0.0103	8 of 10
Gamma-glutamyltransferase-like activity 1	205582_s_at	GGTLA1	NM_004121	Amino acid metabolism, glutathione and leukotriene biosynthesis	0.0004	0.0013	8 of 10
Cathespsin G	205653_at	CTSG	NM_001911	Proteolysis, immune response, killing and engulfing of pathogens	0.0041	0.0000	9 of 10
Gamma-aminobutyric acid (GABA) A receptor, beta 3	205850_s_at	GABRB3	NM_000814	Ion transport, signal transduction, transport	0.0414	0.0028	9 of 10
RNA binding motif protein 19	206019_at	RBM19	NM_014852	RNA, nucleic acid, and nucleotide binding	0.0026	0.0094	8 of 10
Interleukin 3 receptor, alpha (low affinity)	206148_at	IL3RA	NM_002183	Protein amino acid phosphorylation, development	0.0298	0.0176	8 of 10
Exostoses (multiple)-like 1	206329_at	EXTL1	NM_004455	Skeletal development	0.0260	0.0000	9 of 10
ELAV (embryonic lethal, abnormal vision, Dropsophila)-like 3 (Hu antigen C)	206338_at	ELAVL3	NM_001420	Nervous system development, cell differentiation, development	0.0233	0.0023	7 of 10
Solute carrier organic anion transporter family, member 1B3[D]	206354_at	SLCO1B3	NM_019844	Transport, ion, decarboxylic acid and organic acid transport	0.0234	0.0043	7 of 10
Chemokine (C motif) ligand 2[D]	206366_x_at	XCL2	U23772	Chemotaxis, immune response, signal transduction, cell-cell signaling, circulation, calcium ion homeostasis, chemotaxis, cell-cell signaling antimicrobial humoral response (sensu Vertebrata)	0.0141	0.0364	8 of 10
CD19 molecule	206398_s_at	CD19	NM_001770	Cellular defense response, cell surface receptor linked signal transduction	0.0069	0.0006	10 of 10
Neural retina leucine zipper	206597_at	NRL	NM_006177	Transcription, regulation of transcription, DNA-dependent transcription from RNA polymerase II promoter regulation of rhodopsin gene activity, visual perception, response to stimulus, photoceptor development and function, preferentially expressed in rod photoreceptors	0.0048	0.0000	7 of 10
IQ motif containing C[E]	206650_at	IQCC	NM_018134	Biological function unknown	0.0370	0.0002	8 of 10

Elastase 2, neutrophil[D]	206871_at	ELA2	NM_001972	Proteolysis, calcium ion homeostasis, response to UV, protein catabolism, anti-inflammatory response, positive regulation of MAPD activity, negative regulation of chemokine biosynthesis, interleukin-8, inflammatory response, and chemotaxis, biosynthesis, positive regulation of interleukin 8, and smooth muscle cell proliferation	0.0045	0.0268	10 of 10
Complement factor H-related 2	206910_x_at	CFHR2	NM_005666	Immune Response	0.0174	0.0160	9 of 10
Histone 1, H4e[D]	206951_at	HIST1H4E	NM_003545	Nucleosome assembly, chromosome organization and biogenesis (sensu Eukaryota), establishment and/or maintenance of chromatin architecture, phosphoinositide-mediated signaling	0.0008	0.0370	8 of 10
Defensin, alpha 4, corticostatin[D]	207269_at	DEFA4	NM_001925	Xenobiotic metabolism, response to pest, pathogen or parasite, defense response to bacteria and fungi, defense response	0.0444	0.0019	9 of 10
Aspartate beta-hydroxylase	207284_s_at	ASPH	NM_020164	Muscle contraction, peptidyl-amino acid modification	0.0346	0.0345	6 of 10
GIPC PDZ domain containing family member 1	207525_s_at	GIPC1	NM_005716	G-protein coupled receptor protein signaling pathway, nuclear mRNA splicing, via spliceosome mRNA processing and metabolism, RNA splicing, spliceosome assembly	0.0083	0.0000	9 of 10
Arginine vasopressin	207848_at	AVP	NM_000490	Generation of precursor metabolites and energy, water transport, signal transduction, cell-cell signaling, vasoconstriction, regulation of blood vessel size, direct antidiuretic action on kidney, contraction of smooth muscle during parturition and lactation. Involved in cognition tolerance adaptation and complex sexual and maternal behavior.	0.0000	0.0169	8 of 10
Rho guanine exchange facotr (GEF) 16	208009_s_at	ARHGEF16	NM_014448	Regulation of Rho protein signal transduction	0.0046	0.0217	5 of 10
Neuregulin 1	208232_x_at	NRG1	L12260	Nervous system development, embryonic development, negative regulation of transcription, cell differentiation	0.0277	0.0002	7 of 10
Protein phosphatase, EF-hand calcium binding domain 2	208411_x_at	PPEF2	NM_006239	Protein amino acid dephosphorylation, visual perception, response to stimulus, detection of stimulus during sensory perception	0.0410	0.0016	9 of 10
RAS p21 protein activator 4	208534_s_at	RASA4	NM_006989	Intracellular signaling cascade, regulation of small GTPase mediated signal transduction	0.0001	0.0081	7 of 10
Acidic (leucine-rich) nuclear phosphoprotein 32 family, member C[D]	208538_at	ANP32C	NM_012403	Tumor suppressor activity	0.0345	0.0037	7 of 10
Interferon-related developmental regulator 2	209100_at	IFRD2	BC001327	Cell proliferation and differentiation	0.0032	0.0499	9 of 10

Aurora kinase B	209464_at	AURKB	AB011446	Protein amino acid phosphorylation, cell cycle mitosis, cell division	0.0011	0.0000	9 of 10
Adenosine monophosphate deaminase (isoform E)	209491_s_at	AMPD3	NM_000480	AMP catabolism, nucleotide metabolism, purine ribonucleoside monophosphate biosynthesis	0.0001	0.0014	9 of 10
Paraneoplastic antigen MA2	209598_at	PNMA2	AB020690	Biological function unknown	0.0026	0.0275	6 of 10
S100 calcium binding protein, beta (neural)[D]	209686_at	S100B	BC001766	Energy reserve metabolism, calcium ion homeostasis, induction of apoptosis, axonogenesis, central nervous system development, learning and/or memory cell proliferation, regulation of cytokine biosynthesis, positive regulation of complement activation, astrocyte activation, hyperphosphorylation, regulation of long-term neuronal synaptic plasticity, regulation of protein, biosynthesis	0.0082	0.0006	8 of 10
Sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3F	209730_at	SEMA3F	U38276	Development	0.0256	0.0004	9 of 10
Mannosyl (beta-1, 4)-glycoprotein beta-1, 4-N-acetylglucosaminyl transferase	209764_at	MGAT3	NM_002409	Protein amino acid glycosylation, protein amino acid N-linked glycosylation	0.0164	0.0004	10 of 10
Leucine rich repeat, neuronal 3	209840_s_at	LRRN3	NM_018334	Biological function unknown	0.0000	0.0000	10 of 10
Amyloid beta (A4) precursor protein-binding, family A, member 2 (X11-like)	209871_s_at	APBA2	NM_005503	Nervous system development, protein transport, transport	0.0086	0.0069	8 of 10
Synuclein, gamma (breast cancer-specific protein 1)	209877_at	SNCG	AF010126	Protein metabolism, believed to be involved in pathogenesis of neurodegenerative diseases, high levels seen in advanced breast carcinoma	0.0159	0.0000	9 of 10
Musculin (activated B-Cell factor-1)	209928_s_at	MSC	AF060154	Regulation of transcription, DNA-dependent transcription from RNA polymerase II promoter, transcription. Protein members of this family are required for a number of different developmental pathways, specifically myogenesis	0.0161	0.0020	9 of 10
Cytochrome P450, family 2, subfamily E, polypeptide 1	209976_s_at	CYP2E1	AF182276	Electron transport	0.0014	0.0002	9 of 10
Inositol 1,3,4-triphosphate 5/6 kinase	210197_at	ITPK1	BC003622	Signal transduction	0.0005	0.0000	9 of 10
Cathelicidin antimicrobial peptide	210244_at	CAMP	U19970	Response to pest, pathogen or parasite, defense response to bacteria	0.0141	0.0000	8 of 10
Acetylcholinesterase (Yt blood group)	210332_at	ACHE	M55040	Acetylcholine catabolism in synaptic cleft, DNA replication, cell adhesion, synaptogenesis, muscle development, cell proliferation, response to wounding, neurotransmitter catabolism, amyloid precursor, protein metabolism, positive regulation of protein secretion, nervous system development	0.0365	0.0015	8 of 10
Glutamate dehydrogenase 2[F]	210447_at	GLUD2	BC005111	Electron transport, amino acid and glutamate metabolism	0.0350	0.0009	9 of 10
Pyruvate kinase, liver and RBC[D]	210451_at	PKLR	M15465	Glycolysis	0.0076	0.0344	8 of 10

High mobility group AT-hook 1	210457_x_at	HMGA1	AF176039	DNA unwinding during replication, nucleosome disassembly, loss of chromatin, silencing, transcription regulation of transcription, DNA-dependent regulation of transcription, DNA-dependent protein complex assembly chromosome organization and biogenesis (sensu Eukaryota), transmembrane receptor protein tyrosine kinase signaling pathway, positive regulation of transcription	0.0298	0.0000	9 of 10
Nuclear distribution gene C homolog (A. nidulans)	210575_at	NUDC	AF241788	Cell cycle mitosis, cell division	0.0285	0.0000	9 of 10
Peroxisome proliferative activated receptor, delta	210636_at	PPARD	BC002715	Negative regulation of transcription from RNA polymerase II promoter, glucose metabolism, generation of precursor metabolites and energy, transcription, lipid metabolism, fatty acid beta oxidation, apoptosis, embryo implantation, cholesterol metabolism, cell proliferation, nerve ensheathment, epidermis development, fatty acid catabolism, glucose and fatty acid transport, positive regulation of fat cell differentiation, decidualization, regulation of insulin secretion, cellular physiological process regulation of transcription, DNA-dependent regulation of transcription from RNA polymerase II promoter	0.0461	0.0239	8 of 10
Regucalcin (senescence marker protein-30)	210751_s_at	RGN	D31815	Calcium ion binding, enzyme regulator activity	0.0059	0.0232	8 of 10
Cysteine and glycine-rich protein 2	211126_s_at	CSRP2	U46006	Muscle development, cell proliferation, organ morphogenesis, cell growth and differentiation, development	0.0076	0.0000	7 of 10
Killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 4	211242_x_at	KIR2DL4	AF276292	Cellular defense response, signal transduction	0.0010	0.0028	8 of 10
Interferon, alpha 2	211338_at	IFNA2	NM_000605	Induction of apoptosis, defense response, inflammatory response, cell surface receptor linked signal transduction, cell-cell signaling, response to virus	0.0241	0.0011	7 of 10
Leucine rich repeat containing 21	211353_at	LRRC21	AB031547	Biological function unknown	0.0076	0.0023	7 of 10
	211459_at		AF234262	Biological function unknown	0.0000	0.0016	10 of 10
Receptor-associated protein of the synapse, 43kD^{D}	211570_s_at	RAPSN	BC004196	Synaptic transmission	0.0309	0.0420	6 of 10
Killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail	211688_x_at	KIR3DL2	AF263617	Immune response, natural killer cell activation, negative regulation of natural killer cell activity, cellular defense response, signal transduction	0.0087	0.0002	9 of 10

Prostaglandin D2 syntase 21kDa (brain) prostaglandin D2 synthase 21kDa (brain)	211748_x_at	PTGDS	BC005939	Prostaglandin and fatty acid biosynthesis, lipid metabolism, transport regulation of circadian sleep/wake clycle, sleep prostaglandin biosynthesis and metabolism, transport	0.0003	0.0037	8 of 10
Complement factor B Complement factor B	211920_at	CFB	AF349679	Proteolysis, complement activation alternative pathway, innate immune response	0.0022	0.0035	7 of 10
Chromosome 16 open reading frame 34	212115_at	C16orf34	AK023154	DNA binding, transcription regulator activity	0.0013	0.0000	10 of 10
Neuropilin 1	212298_at	NRP1	NM_001024628	Angiogenesis, cell adhesion, signal transduction, cell-cell signaling, nervous system development, axon guidance, positive regulation of cell proliferation, organ morphogenesis, cell differentiation, development	0.0264	0.0213	7 of 10
Eukaryotic translation initiation factor 2B, subunit 5 epsilon, 82kDa	212351_at	EIF2B5	U23028	Protein biosynthesis, regulation of translation initiation, amino acid metabolism	0.0226	0.0010	10 of 10
Transcription factor 4	212382_at	TCF4	NM_003199	Negative regulation of transcription from RNA polymerase II promoter, transcription, DNA-dependent regulation of transcription	0.0001	0.0001	9 of 10
SET binding factor 1	212393_at	SBF1	AL096767	Protein amino acid and phospholipid dephosphorylation	0.0030	0.0313	8 of 10
Rho-related BTB domain containing 1	212651_at	RHOBTB1	AB018283	Small GTPase mediated signal transduction	0.0249	0.0003	6 of 10
RAS p21 protein activator 4 hypothetical protein FLJ21767	212707_s_at	RASA4, FLJ21767	NM_006989	Intracellular signaling cascade, regulation of small GTPase mediated signal transduction	0.0030	0.0365	9 of 10
Growth arrest and DNA-damage-inducible, gamma interacting protein 1	212891_s_at	GADD45GIP1	XM_379820	Cell cycle	0.0013	0.0000	10 of 10
Dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 4	212954_at	DYRK4	NM_052850	Protein amino acid phosphorylation, plays key role in cell proliferation, survival and development	0.0013	0.0079	8 of 10
CD3d molecule, delta (CD3-TCR complex)	213539_at	CD3D	NM_000732	Protein complex assembly, cell surface receptor linked signal transduction, T cell activation, positive thymic T cell selection	0.0009	0.0491	9 of 10
CREB/ATF bZIP transcription factor	213584_s_at	CREBZF	NM_001039618	Transcription, regulation of transcription DNA dependent, response to virus, negative regulation of transcription and gene expression, epigenetic regulation of transcription factor activity	0.0000	0.0414	8 of 10
Tubulin, beta 2C	213726_x_at	TUBB2C	NM_006088	Micro-tubule-based movement, natural killer cell mediated cytotoxicity, protein polymerization	0.0315	0.0109	9 of 10
Phosphodiesterase 4D interacting protein (myomegalin)	214099_s_at	PDE4DIP	AK001619	Protein biosynthesis, cytoskeleton organization and biogenesis, actin cytoskeleton organization and biogenesis	0.0294	0.0039	8 of 10

Collagen, type VIII, alpha 1	214587_at	COL8A1	NM_001850	Phosphate transport, cell adhesion, somatic muscle development, major component of basement membrane of corneal epithelium	0.0096	0.0290	8 of 10
Somatostatin receptor 2	214597_at	SSTR2	NM_001050	Signal transduction G-protein signaling, coupled to cyclic nucleotide second messenger, cell-cell signaling, response to nutrient digestion, negative regulation of cell proliferation, G-protein coupled receptor protein signaling pathway	0.0094	0.0095	7 of 10
Spectrin, alpha, nonerythrocytic 1 (alpha-fodrin)	214925_s_at	SPTAN1	NM_003127	Barbed-end actin filament capping	0.0000	0.0000	10 of 10
Nucleoporin 62kDa interleukin 4 induced 1	214935_at	NUP62, IL4I1	NM_012346, NM_172374	Transport, cell surface receptor linked signal transduction, cell death, negative regulation of cell proliferation, hormone-mediated signaling, negative regulation of apoptosis, negative regulation of non-apoptotic programmed cell death, positive regulation of I-kappaB kinase/NF-kappaB cascade, positive regulation of epidermal growth factor receptor signaling pathway, regulation of Ras protein signal transduction, electron transport, cell adhesion	0.0181	0.0017	8 of 10
ST6 beta-galactosamide alpha-2,6-sialyltransferase 1	214970_s_at	ST6GAL1	X17247	Protein amino acid glycosylation, humoral immune response, development, oligosaccharide metabolism, growth, protein modification	0.0115	0.0287	9 of 10
G-rich RNA sequence binding factor 1	215030_at	GRSF1	AK023187	mRNA polyadenylylation	0.0188	0.0085	8 of 10
RAB GTPase activating protein 1	215070_x_at	RABGAP1	AK022408	Signal transduction, G-protein coupled receptor protein signaling pathway	0.0107	0.0058	9 of 10
Nuclear receptor co-repressor 2	215205_x_at	NCOR2	S83390	Regulation of transcription, DNA-dependent regulation of transcription, transcription	0.0106	0.0014	8 of 10
Solute carrier family 8 (sodium-calcium exchanger), member 2[D]	215267_s_at	SLC8A2	NM_015063	Ion transport, sodium and calcium ion transport, cell communication transport	0.0256	0.0011	8 of 10
mRNA sequence, IMAGE clone 446411[D]	215477_at		H49077	Biological function unknown	0.0459	0.0003	8 of 10
Zinc finger UBR1 type 1	215636_at	UBR1	AK022322	Ubiquitin cycle	0.0439	0.0000	9 of 10
Transcription factor AP-2 beta (activating enhancer binding protein 2 beta)	215686_x_at	TFAP2B	AL031224	Transcription, regulation of transcription from RNA polymerase II promoter, nervous system development, regulation of transcription, DNA-dependent. Thought to stimulate cell proliferation and suppress terminal differentiation of specific cell types during embryonic development.	0.0360	0.0301	5 of 10
	215799_at		AK024971	Biological function unknown	0.0048	0.0000	8 of 10
Similar to bK246H3.1 (immunoglobulin lambdalike polypeptide 1, pre-B-cell specific)	215816_at	LOC91316	L02326	Carbohydrate metabolism, small GTPase mediated signal transduction	0.0022	0.0018	9 of 10
Spectrin, beta, nonerythrocytic 1	215918_s_at	SPTBN1	NM_003128	Barbed-end actin filament capping	0.0105	0.0123	7 of 10
Hypothetical protein LOC731501	216053_x_at	LOC731501	XM_001133525	Biological function unknown	0.0350	0.0158	7 of 10

GTPase activating Rap/RanGap domain-like 3	216165_at	GARNL3	NM_032293	GTPase activator activity, small GTPase regulator activity	0.0296	0.0002	7 of 10
Pleckstrin homology domain containing, family M (with RUN domain) member 1	216200_at	PLEKHM1	NM_014798	Intracellular signaling cascade	0.0104	0.0001	7 of 10
Jerky homolog (mouse)	216309_x_at	JRK	AF072467	Regulation of transcription	0.0274	0.0000	8 of 10
Tenascin XA pseudogene tenascin XB	216339_s_at	TNXA, TNXB	NR_001284, NM_019105	Cell adhesion, cell-matrix adhesion	0.0020	0.0000	9 of 10
cDNA: FLJ21769 fis, clone COLF7354	216429_at		AK025422	Biological function unknown	0.0158	0.0051	9 of 10
LOC642150 similar to cationic trypsin III precursor (pretrypsinogen III)	216597_at	LOC642150	XR_018089	Biological function unknown	0.0059	0.0000	9 of 10
Transmembrane 6 superfamily member 2[E]	216736_at	TM6SF2	AK024515	Biological function unknown	0.0123	0.0036	7 of 10
Keratin 84	217031_at	KRT84	Y19209	Structural molecule activity, structural constituent of epidermis, heterodimers with type 1 keratin to form hair and nails	0.0490	0.0002	7 of 10
Protease, serine 7 (enterokinase)	217269_s_at	PRSS7	NM_002772	Proteolysis	0.0320	0.0024	8 of 10
PRAME family member 10	217273_at	PRAMEF10	AL022101	Biological function unknown	0.0470	0.0021	8 of 10
Serine hydroxymethyltransferase 1 (soluble)	217304_at	SHMT1	Y14488	Glycine metabolism, L-serine metabolism and catabolism, one-carbon compound metabolism	0.0116	0.0031	8 of 10
Interleukin 23, alpha subunit p19	217328_at	IL23A	NM_016584	Inflammatory and immune response, response to virus, tissue development, innate immune response	0.0082	0.0002	8 of 10
Basic transcription factor 3	217461_x_at	BTF3	NM_001207	Transcription, regulation of transcription, DNA-dependent transcription from RNA polymerase II promoter	0.0480	0.0357	7 of 10
Olfactory receptor, family 7, subfamily e, member 37 pseudogene[G]	217499_x_at	OR7E37P	AW874308	Sensory perception of smell	0.0003	0.0000	10 of 10
Cation channel, sperm associated 2 cation channel, sperm associated 2 pseudogene[D]	217588_at	CATSPER2, CARSPER2P1	NM_054020, NR_002318	Ion transport, transport. Specific to spermatazoa, particularly the flagellum	0.0446	0.0297	4 of 10
Desmoglein 2	217901_at	DSG2	NM_001943	Cell adhesion, homophilic cell adhesion	0.0273	0.0176	7 of 10
Mitochondrial ribosomal protein L4	218105_s_at	MRPL4	NM_015956	Protein biosynthesis	0.0480	0.0202	5 of 10
Fanconi anemia, complementation group L	218397_at	FANCL	NM_018062	DNA repair, ubiquitin cycle, response to DNA damage stimulus	0.0254	0.0002	9 of 10
TBC1 domain family, member 13	218596_at	TBC1D13	NM_018201	GTPase activator activity, Rab GTPase activator activity	0.0410	0.0015	7 of 10
Phospholipid scramblase 3	218828_at	PLSCR3	NM_020360	Phospholipid scrambling	0.0198	0.0208	9 of 10
Chromosome 2 open reading frame 43	219008_at	C2orf43	NM_021925	Hydrolase activity	0.0358	0.0001	9 of 10
Brevican	219107_at	BCAN	NM_021948	Cell adhesion	0.0059	0.0000	8 of 10
SLAM family member 8[F]	219386_s_at	SLAMF8	NM_020125	Immune response, lymphocyte activation, may function during B cell lineage commitment	0.0046	0.0000	9 of 10
Placenta-specific 1[H]	219702_at	PLAC1	NM_021796	Placenta development	0.0141	0.0003	9 of 10
Galactose-3-O-sulfotransferase 4	219815_at	GAL3ST4	NM_024637	Sulfur metabolism, cell-cell signaling, biosynthesis, glycoprotein metabolism, oligosaccharide metabolism, proteoglycan biosynthesis	0.0057	0.0000	10 of 10
Glycerophosphodiester phosphodiesterase domain containing 2[E]	220291_at	GDPD2	NM_017711	Glycerol metabolism	0.0079	0.0067	8 of 10

Signal-regulatory protein gamma[D]	220485_s_at	SIRPG	NM_018556	Intracellular signaling cascade, cell-cell signaling, negative regulation of cell proliferation	0.0235	0.0104	7 of 10
Testis-specific kinase substrate	220545_s_at	TSKS	NM_021733	Protein binding. Gene may play a role in testicular physiology, spermatogenesis, or spermiogeneisis	0.0163	0.0006	7 of 10
Hypothetical protien FLJ11783	220546_at	FLJ11783	NM_024891	Biological function unknown	0.0485	0.0002	7 of 10
Disabled homolog 1 (Drosophila)	220611_at	DAB1	NM_021080	Nervous system development, cell differentiation, development	0.0339	0.0033	7 of 10
	220687_at		NM_018175	Biological function unknown	0.0002	0.0002	9 of 10
Roundabout homolog 4, magic roundabout (Drosophila)[E]	220758_s_at	ROBO4	NM_019055	Angiogenesis, cell differentiation, regulation of cell migration, angiogenesis, development	0.0480	0.0000	7 of 10
hCG 1732469	220823_at	hCG_1732469	NM_017624	Biological function unknown	0.0368	0.0125	8 of 10
WD repeats and SOF 1 domain containing	220843_s_at	WDSOF1	NM_014156	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	0.0275	0.0276	8 of 10
Unc-51-like kinase 4 (C elegans)	220958_at	ULK4	NM_017886	Protein amino acid phosphorylation	0.0065	0.0002	9 of 10
Integral membrane protein 2C integral membrane protein 2C	221004_s_at	ITM2C	NM_030926	ATP binding	0.0017	0.0000	9 of 10
Natural cytotoxicity triggering receptor 2[D]	221074_at	NCR2	NM_004828	Cellular defense response, signal transduction	0.0254	0.0158	7 of 10
2-oxoglutarate and iron-dependent oxygenase domain containing 1	221090_s_at	OGFOD1	NM_018233	Protein metabolism	0.0371	0.0421	8 of 10
Growth differentiation factor 9[D]	221314_at	GDF9	NM_005260	Transforming growth factor beta receptor, signaling pathway, female gamete generation	0.0244	0.0426	6 of 10
Cholinergic receptor, muscarinic 5[D]	221347_at	CHRM5	NM_012125	Nervous system development, signal transduction, muscarinic acetylcholine receptor, adenylate cyclase inhibiting pathway, acetylcholine receptor signaling muscarinic pathway, cell proliferation, G-protein coupled receptor protein signaling pathway	0.0068	0.0001	8 of 10
Hypothetical protein LOC339047	221501_x_at	LOC339047	AF229069	Neuropeptide signaling pathway	0.0109	0.0017	7 of 10
Par-3 partitioning defective 3 homolog (C elegans)	221526_x_at	PARD3	NM_019619	Protein complex assembly cell cycle establishment and/or maintenance of cell polarity, protein kinase C activation, axonogenesis, asymmetric cell division, cell division	0.0389	0.0000	8 of 10
MAP/microtubule affinity-regulating kinase 4	221560_at	MARK4	AB049127	Microtubule bundle formation, protein amino acid phosphorylation, nervous system development, positive regulation of programmed cell death, microtubule cytoskeleton organization and biogenesis, positive regulation of cell proliferation, Wnt receptor signaling pathway	0.0005	0.0001	9 of 10
RRN3 RNA polymerase 1 transcription factor homolog (S. cerevisiae) pseudogene	221714_s_at	LOC730092	BC006441	Biological function unknown	0.0455	0.0001	7 of 10
Zinc finger protein 512B	221869_at	ZNF512B	NM_020713	Transcription, regulation of transcription, DNA-dependent	0.0007	0.0000	10 of 10

aarF domain containing kinase 2	222117_s_at	ADCK2	NM_052853	ATP binding, kinase activity, nucleotide binding, transferase activity	0.0000	0.0109	8 of 10
Similar to Zinc finger protein 418	222135_at	LOC73051	XR_015766	Regulation of transcription, DNA-dependent	0.0462	0.0004	8 of 10
Splicing factor 3a, subunit 2, 66kDa	37462_i_at	SF3A2	L21990	Nuclear mRNA 3'-splice site recognition, nuclear mRNA splicing, via spliceosome RNA splicing mRNA processing	0.0353	0.0231	6 of 10
Hydroxysteroid (17-beta) dehydrogenase 6 homolog (mouse)	37512_at	HSD17B6	U89281	Androgen biosynthesis, catabolism and metabolism	0.0014	0.0226	7 of 10
CD22 molecule/myelin-associated glyocoprotein	38521_at	CD22MAG	X59350	Involved in the process of myelination, cell adhesion, cell-cell adhesion, antimicrobial humoral response (sensu Vertebrata)	0.0007	0.0406	8 of 10
Acetyl-Coenzyme A carboxylase beta	49452_at	ACACB	NM_001093	Fatty acid biosynthesis metabolism, lipid biosynthesis	0.0193	0.0105	7 of 10
	AFFX-BioDn-3_at			Biotin biosynthesis metabolism, biosynthesis, cobalamin biosynthesis	0.0365	0.0101	7 of 10

[A] Adjusted p values for antepartum vs. postpartum samples

[B] Adjusted p values for umbilical vs. postpartum samples

[C] Proportion of cases with expresssion values where antepartum>postpartum and umbilical>postpartum

[D] Fetal specific expression patterr

[E] Embryo specific expression pattern

[F] Neonate specific expression patterr

[G] Expression pattern restricted to embryc

[H] Placental/fetal specific expression patterr

Supplemental Table 2. Real-time RT-PCR Data. All samples were run in triplicate and the value listed is the mean quantity expressed as ng/mL of whole blood. Coefficient of variation values, (CV), are also provided. *GAPDH* was included as a housekeeping gene.

	GAPDH ng/mL (CV)	*DEFA1, DEFA3* ng/mL (CV)	*TRBV19, TRBC1* ng/mL (CV)	*MYL4* ng/mL *(CV)*
2A	3,122 (19.8)	18,352 (10.2)	54,192 (12.2)	1,538 (65.2)
2U	24,788 (5.30	2,505,424 (42.6)	312,320 (36.3)	33,104 (59)
2P	5,956 (18.5)	51,456 (14.6)	280,288 (66.1)	15,792 (30.5)
3A	1,780 (3.4)	52,192 (9.8)	133,248 (17.7)	7,872 (20.5)
3U	10,796 (23.2)	1,248,576 (9.4)	452,864 (5.5)	29,680 (23.5)
3P	3,104 (23.4)	43,920 (19.8)	198,336 (17.5)	15,396 (7.4)
4A	7,968 (27.5)	107,104 (9.6)	99,840 (8.9)	6,386 (12)
4Ua	9,564 (4.5)	109,536 (0.7)	397,216 (0.2)	69,644 (36.6)
4Ub	69,874 (8.7)	99,312 (4.4)	266,368 (10.7)	28,480 (25.6)
4P	2,022 (6.3)	7,040 (22)	36,912 (9.7)	909 (10.7)
5A	7,740 (21.9)	47,200 (15.1)	89,584 (40.7)	2,713 (42.2)
5U	29,340 (13.9)	3,189,760 (12.5)	522,464 (2)	52,688 (21.4)
5P	26,772 (9.3)	53,888 (4.1)	159,632 (7)	5,018 (17.5)
6A	3,080 (6.2)	40,944 (20)	72,432 (7.2)	1,062 (39)
6U	11,052 (23.9)	198,400 (10.4)	268,208 (6.9)	13,783 (10.2)
6P	18,420 (22.6)	52,208 (9.8)	79,232 (2.2)	1,375 (19.7)

A=Antepartum; U=Umbilical; P=Postpartum
Sample 3Ua=Twin A; Sample 3Ub= Twin B

Supplemental Table 3. Maternal and Fetal Genotyping for SNP Analysis. Two of the three informative pairs for *KIR3DL2, rs21168*, revealed evidence of fetal RNA trafficking. *CD19, rs2904880,* was positive for fetal trafficking in a retrospective analysis of original stored cDNA samples.

Genotype (Maternal/Fetal)	***SNP CD19, rs2904880***	***SNP KIR3DL2, rs21168***
Homozygous/Homozygous	6/11 (55%)	5/11 (45%)
Heterozygous/Heterozygous	2/11 (18%)	2/11 (18%)
Heterozygous/Homozygous	2/11 (18%)	1/11 (9%)
Homozygous/Heterozygous*	**1/11 (9%)**	**3/11 (27%)**

*Informative Maternal-Fetal Pair

Supplemental Table 4. Candidate fetal genes in plasma

Gene	Probe set ID	Gene Symbol	Accession Number	Biological function	p value^A	p value^B
Ribosomal protein L27	200025_s_at	RPL27	NM_000988	Protein biosynthesis	0.0146	0.0451
DEAD (Asp-Glu-Ala-Asp) box polypeptide 5	200033_at	DDX5	NM_004396	Cell growth. Some members of this family are believed to be involved in embryogenesis, spermatogenesis and cellular growth	0.0000	0.0130
ADP-ribosylation factor 1	200065_s_at	ARF1	AF052179	rRNA processing, ER to Golgi vesicle-mediated transport, small GTPase mediated signal transduction, protein transport, transport, ribosome biogenesis	0.0313	0.0000
Heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa)	200073_s_at	HNRPD	M94630	Telomere maintenance, transcription, regulation of transcription, DNA-dependent RNA processing, RNA catabolism, mRNA catabolism	0.0000	0.0000
Dynein, light chain, LC8-type 1	200703_at	DYNLL1	NM_003746	Microtubule-based process. Physically interacts with and inhibits the activity of neuronal NO synthesase dimer. Female gamete generation, morphogenesis, actin cytoskeleton, organization and biogenesis	0.0000	0.0249
Methionine adenosyltransferase II, alpha	200768_s_at	MAT2A	BC001686	One-carbon compound metabolism, S-adenosylmethionine biosynthesis	0.0469	0.0461
Proteasome (prosome, macropain) 26S subunit, non-ATPase 8	200820_at	PSMD8	NM_002812	Regulation of progression through cell cycle proteolysis	0.0056	0.0000
Lysyl-tRNA synthetase	200840_at	KARS	NM_005548	Protein biosynthesis, lysyl-tRNA aminoacylation, tRNA processing, tRNA aminoacylation for protein translation, protein biosynthesis	0.0206	0.0477
RAB14, member RAS oncogene family	200928_s_at	RAB14	AL162081	Golgi to endosome transport, small GTPase mediated signal transduction, neurotransmitter secretion, protein transport, vesicle-mediated transport, intracellular transport	0.0000	0.0002
Ribophorin I	201011_at	RPN1	NM_002950	Protein amino acid gylcosylation, protein amino acid N-linked gylcosylation via asparagine protein modification	0.0051	0.0001
NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae)	201077_s_at	NHP2L1	AF155235	Regulation of progression through cell cycle, nuclear mRNA splicing, via spliceosome, ribosome biogenesis and assembly mRNA processing	0.0018	0.0000
Carboxypeptidase E	201116_s_at	CPE	NM+001873	Protein modification, proteolysis, neuropeptide signaling pathway, metabolism	0.0000	0.0002
Ribosome binding protein 1 homolog 180kDa (dog)	201203_s_at	RRBP1	NM_001042576	Protein biosynthesis, protein targeting, signal transduction, protein transport, transport endocytosis	0.0000	0.0044
Topoisomerase (DNA) II alpha 170kDa	201291_s_at	TOP2A	NM_001067	DNA replication, topological change, unwinding during replication, repair, phosphoinositide-mediated signaling, metabolism	0.0000	0.0057
Protein phosphatase 1, catalytic subunit, beta isoform	201409_s_at	PPP1CB	NM_002709	Carbohydrate and glycogen metabolism, cell cycle, cell division	0.0001	0.0000
Ubiquitin-like 3	201535_at	UBL3	NM_007106	Protein modification	0.0000	0.0214
Eukaryotic translation termination factor 1	201573_s_at	ETF1	M75715	Protein biosynthesis, translational termination	0.0073	0.0404
Protein phosphatase 1, regulatory (inhibitor) subunit 12A	201603_at	PPP1R12A	NM_002480	Regulation of muscle contraction	0.0029	0.0004
Fragile X mental retardation, autosomal homolog 1	201635_s_at	FXR1	NM_001013438	Apoptosis, striated muscle development, cell differentiation, development	0.0232	0.0380
Cleavage and polyadenylation specific factor 1, 160kDa	201639_s_at	CPSF1	NM_013291	mRNA polyadenylylation, cleavage and processing	0.0073	0.0480
Integrin, alpha 6	201656_at	ITGA6	NM_000210	Cell-substrate junction assembly, cell adhesion, cell-matrix adhesion, integrin-mediated signaling pathway	0.0000	0.0003

Oxysterol binding protein	201800_s_at	OSBP	AF185696	Lipid transport, steroid metabolism, transport	0.0296	0.0000
SEC63-like (S. cerevisiae)	201916_s_at	SEC63	NM_007214	Protein folding, protein targeting to membrane, protein transport	0.0422	0.0130
Plakophilin 4	201928_at	PKP4	NM_001005476	Cell adhesion	0.0000	0.0001
Optineurin	202074_s_at	OPTN	NM_021980	Protein C-terminus binding	0.0295	0.0030
Nucleoporin 153kDa	202097_at	NUP153	NM_005124	Transport, ATP synthesis, couple proton transport	0.0002	0.0000
Zinc finger, MYND domain containing 11	202137_s_at	ZMYND11	NM_006624	Negative regulation of transcription from RNA polymerase II promoter, transcription, regulation of transcription, DNA-dependent cell cycle cell proliferation	0.0008	0.0499
COP9 constitutive photomorphogenic homolog subunit 8 (Arabidopsis)	202143_s_at	COPS8	NM_006710	Metabolism	0.0438	0.0000
Transmembrane emp24 protein transport domain containing 5	202194_at	TMED5	AL117354	Transport	0.0049	0.0179
Integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51)	202351_at	ITGAV	NM_002210	Cell adhesion, cell-matrix adhesion, integrin-mediated signaling pathway	0.0000	0.0000
Brain abundant membrane attached signal protein 1	202391_at	BASP1	NM_006317		0.0000	0.0271
Endosulfine alpha	202596_at	ENSA	BC000436	Transport, response to nutrient	0.0053	0.0000
Serine threonine kinase 39 (STE20/SPS1 homolog, yeast)	202786_at	STK39	NM_013233	Protein amino acid phosphorylation, response to stress	0.0000	0.0094
Developmentally regulated GTP binindg protein 1	202810_at	DRG1	NM_004147	Transcription, development	0.0000	0.0253
Bromodomain adjacent to zinc finger domain, 2B	203080_s_at	BAZ2B	NM_013450	Transcription, regulation of transcription, DNA-dependent	0.0122	0.0011
MAD2 mitotic arrest deficient-like 1 (yeast)	203362_s_at	MAD2L1	NM_002358	Cell cycle mitosis, mitotic checkpont, cell division mitosis	0.0401	0.0054
Potassium voltage-gated channel, shaker-related subfamily, beta member 2	203402_at	KCNAB2	NM_003636	Ion transport, potassium ion transport, transport	0.0000	0.0000
2,3-bisphosphoglycerate mutase	203502_at	BPGM	NM_001724	Carbohydrate metabolism, glycolysis, respiratory gaseous exchange, metabolism	0.0000	0.0419
ADP-ribosylation factor-like 4D	203587_at	ARL4D	NM_001661	rRNA processing, small GTPase mediated signal transduction, protein secretion, ribosome biogenesis	0.0278	0.0000
Pericentrin (kendrin)	203660_s_at	PCNT	NM_006031	Cilium biogenesis	0.0251	0.0000
Vascular cell adhesion molecule 1	203868_s_at	VCAM1	NM_001078	Cell-cell adhesion, cell adhesion	0.0480	0.0000
Arginase, type II	203945_at	ARG2	NM_001172	Urea cycle arginine catabolism, nitric oxide biosynthesis, arginine metabolism	0.0161	0.0025
ZW10 interactor	204026_s_at	ZWINT	NM_007057	Cell cycle spindle organization and biogenesis, phosphoinositide-mediated signaling	0.0007	0.0000
Solute carrier family 5 (sodium-dependent vitamin transporter), member 6	204087_s_at	SLC5A6	NM_021095	Ion transport, sodium ion transport, transport	0.0189	0.0282
SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3	204099_at	SMARCD3	NM_003078	Chromatin remodeling, transcription, regulation of transcription for RNA polymerase II promoter, positive regulation of transcription, DNA-dependent regulation of transcription, DNA-dependent chromatin modification	0.0131	0.0000
Cyclin-dependent kinase 2	204252_at	CDK2	M68520	G2/M transition of mitotic cell cycle, regulation of DNA replication, protein amino acid phosphorylation, cell cycle mitosis, traversing start control point of mitotic cell cycle; positive regulation of cell proliferation, cell division	0.0073	0.0000
Regulator of G-protein signaling 10	204319_s_at	RGS10	NM_002925	Negative regulation of signal transduction	0.0003	0.0014
LIM domain only 3 (rhombotin-like 2)	204424_s_at	LMO3	AL050152	Transcription, regulation of transcription, DNA-dependent	0.0111	0.0010
	204536_s_at		NM_005612	Regulation of transcription, DNA-dependent	0.0429	0.0000
Cell adhesion molecule with homology to L1CMA (close homolog of L1)	204591_at	CHL1	NM_006614	Cell adhesion, signal transduction, nervous system development, cell differentiation, cell adhesion, development	0.0002	0.0000
Folate receptor 2 (fetal)	204829_s_at	FOLR2	NM_000803	Folic acid transport	0.0000	0.0026

Vaccinia related kinase 2	205126_at	VRK2	NM_006296	Protein amino acid phosphorylation, response to stress	0.0000	0.0000
POU domain, class 2, associating factor 1	205267_at	POU2AF1	NM_006235	Transcription, regulation of transcription, DNA-dependent, transcription from RNA polymerase II promoter, humoral immune response, cell cycle arrest, negative regulation of cell proliferation, neuron differentiation	0.0000	0.0000
Proline-rich protein HaeIII subfamily 1; proline-rich protein HaeIII subfamily 2	205272_s_at	PRH1, PRH2	NM_006250	G-protein coupled receptor protein signaling pathway	0.0251	0.0012
BAI1-associated protein 2	205293_x_at	BAIAP2	AB017120	Rho protein signal transduction, axonogenesis, insulin receptor signaling pathway	0.0000	0.0013
Claudin 10	205328_at	CLDN10	NM_006984	Cell adhesion, calcium-independent cell-cell adhesion	0.0000	0.0360
Neuropeptide Y receptor Y1	205440_s_at	NPY1R	NM_000909	Signal transduction G-protein signaling, coupled to cyclic nucleotide second messenger G-protein signaling, adenylate cyclase inhibiting pathway, neuropeptide signaling pathway, feeding behavior, G-protein coupled receptor protein signaling pathway	0.0000	0.0005
Fragile histidine triad gene	206492_at	FHIT	NM_002012	Cell cycle, nucleotide metabolism, negative regulation of progression through cell cycle	0.0010	0.0000
SET domain and mariner transposase fusion gene	206554_x_at	SETMAR	NM_006515	Transposition, DNA-mediated chromatin modification, regulation of transcription	0.0033	0.0000
Coagulation factor II (thrombin) receptor-like 2	206795_at	F2RL2	NM_004101	Signal transduction, G-protein signaling pathway, blood coagulation, response to wounding	0.0006	0.0000
Alanine-glyoxylate aminotransferase	206957_at	AGXT	NM_016236	Metabolism	0.0000	0.0000
ATPase, Ca++ transporting, plasma memberane 3	207026_s_at	ATP2B3	NM_021949	Cation transport, calcium ion transport, metabolism, transport, ion transport, transport	0.0000	0.0000
Distal-less homeobox 2	207147_at	DLX2	NM_004405	Regulation of transcription, DNA-dependent, development, brain development, regulation of transcription	0.0001	0.0109
NADPH oxidase 1	207217_s_at	NOX1	NM_013955	Electron, proton and ion transport, NADP and FADH2 metabolism	0.0019	0.0000
Solute carrier family 17 (sodium phosphate), member 3	207298_at	SLC17A3	NM_006632	Phosphate metabolism, ion and sodium ion transport, transport	0.0335	0.0000
	207478_at		NM_018546	Biological function unknown	0.0004	0.0049
POU class 1, homeobox 1	207846_at	POU1F1	NM_000306	Regulation of transcription, DNA-dependent transcription from RNA polymerase II promoter, negative regulation of cell proliferation, organ morphogenesis	0.0000	0.0213
H2B histone family, member S	208579_x_at	H2BFS	NM_017445	Nucleosome assembly, chromosome organization and biogenesis (sensu Eukaryota), response to bacteria, pest, pathogen or parasite	0.0001	0.0349
Villin 2 (ezrin)	208621_s_at	VIL2	NM_003379	Cytoskeletal anchoring, regulation of cell shape, actin filament bundle formation	0.0008	0.0000
Serine incorporator 1	208671_at	SERINC1	AF164794	Phosphatidylserine metabolism, sphingolipid metabolism, L-serine transport positive regulation of transferase activity	0.0001	0.0001
Melanoma antigen family D, 2	208682_s_at	MAGED2	AF126181	Protein biosynthesis	0.0000	0.0000
Sin3A-associated protein, 18kDa	208742_s_at	SAP18	U78303	Transcription, regulation of transcription from RNA polymerase II promoter, regulation of transcription, DNA-dependent	0.0416	0.0000

High-mobility group box 2	208808_s_at	HMGB2	BC000903	DNA ligation, replication and unwinding during replication, DNA repair, base-excision repair, establishment and/or maintenance of chromatin architecture, nucleosome assembly, regulation of transcription from RNA polymerase II promoter, phosphoinositide-mediated signaling, regulation of transcription, DNA-dependent	0.0049	0.0128
Topoisomerase (DNA) 1	208901_s_at	TOP1	J03250	DNA topological change, DNA unwinding during replication	0.0000	0.0019
Platelet/endothelial cell adhesion molecule (CD31 antigen)	208982_at	PECAM1	NM_000442	Cell motility, adhesion, recognition, signal transduction	0.0000	0.0117
Heterogeneous nuclear ribonucleoprotein H3 (2H9)	208990_s_at	HNRPH3	AF132362	Nuclear mRNA splicing, via spliceosome, RNA splicing and processing, mRNA processing	0.0000	0.0036
GABA (A) receptor-associated protein-like 2	209046_s_at	GABARAPL2	AB030710	Protein targeting and transport, synaptic transmission,	0.0003	0.0002
Hepatoma-derived growth factor, related protein 3	209526_s_at	HDGFRP3	AB029156	Cell proliferation	0.0000	0.0000
Integrin, alpha 7	209663_s_at	ITGA7	AF072132	Cell adhesion, homophilic cell adhesion, cell-matrix adhesion, integrin-mediated signaling pathway, muscle development, regulation of cell shape	0.0023	0.0000
Annexin A2	210427_x_at	ANXA2	BC001388	Skeletal development	0.0000	0.0075
Colony stimulating factor 1 (macrophage)	210557_x_at	CSF1	M76453	Cell proliferation and differentiation, positive regulation of cell proliferation, hemopoiesis, macrophage differentiation	0.0351	0.0014
Tachykinin receptor 1	210637_at	TACR1	M81797	Inflammatory response, signal transduction, G-protein coupled receptor protein signaling pathway, G-protein signaling, coupled to IP3 second messenger (phospholipase C activation) tachykinin signaling pathway, mechanosensory behavior, detection of abiotic stimulus, behavior	0.0000	0.0001
Regucalcin (senescence marker protein-30)	210751_s_at	RGN	D31815	Calcium ion binding, enzyme regulator activity	0.0000	0.0000
Tubulin tyrosine ligase-like family, member 5	210806_at	TTLL5	AL136808	Protein modification	0.0196	0.0063
Hepatocyte growth factor (hepapoietin A; scatter factor)	210997_at	HGF	M77227	Proteolysis, mitosis, blood coagulation	0.0156	0.0000
Pyruvate dehydrogenase (lipoamide) beta	211023_at	PDHB	AL117618	Glucose metabolism, glycolysis, tricarboxylic acid cycle	0.0000	0.0000
Glycogenin 1	211275_s_at	GYG1	AF087942	Glycogen and carbohydrate biosynthesis	0.0000	0.0000
CDKN1A interacting zinc finger protein 1	211358_s_at	CIZ1	AF234161	Regulation of progression through cell cycle	0.0204	0.0113
Sperm associated antigen 11B	211381_x_at	SPAG11B	AF168617	Defense response, response to pest, pathogen or parasite, spermatogenesis	0.0000	0.0000
POZ (BTB) and AT hook containing zinc finger	211392_s_at	PATZ1	AF242522	Transcription, regulation of transcription, DNA-dependent	0.0002	0.0000
Aminolevulinate, delta-,synthase 2 (sideroblastic/hypochromic anemia)	211560_s_at	ALAS2	NM_000032	Heme biosynthesis, metabolism	0.0000	0.0060
RNA guanylyltransferase and 5'-phosphatase	211849_s_at	RNGTT	AB009023	mRNA capping protein amino acid dephosphorylation	0.0021	0.0003
CDNA: FLJ22515 fis, clone HRC12122, highly similar to AF052101 Homo sapiens clone 23872 mRNA sequence	211976_at		AK026168	Biological function unknown	0.0109	0.0000
LSM14, SCD6 homolog A (S. cerevisiae)	212132_at	LSM14A	NM_015578	Biological function unknown	0.0009	0.0096
Suppressor of zeste 12 homolog (Drosophila)	212287_at	SUZ12	NM_015355	Transcription, regulation of transcription, DNA-dependent, chromatin modification	0.0000	0.0004
Yip1 domain family, member 6	212341_at	YIPF6	NM_173834	Biological function unknown	0.0037	0.0434
Amine oxidase (flavin containing) domain 2	212348_s_at	AOF2	AB011173	Electron transport, transcription, regulation of transcription, DNA-dependent, chromatin modification	0.0000	0.0000
Structural maintenance of chromosomes flexible hinge domain containing 1	212577_at	SMCHD1	XM_113962	Chromosome organization and biogenesis	0.0060	0.0000
EH domain binding protein 1	212650_at	EHBP1	NM_015252	Biological function unknown	0.0400	0.0000
Hypothetical protein TI-227H taurine upregulated gene 1	212725_s_at	TI-227H, TUG1	NR_002323	Biological function unknown	0.0001	0.0001
Chromosome 1 open reading 216	212791_at	C1ORF216	NM_152374	Biological function unknown	0.0000	0.0004

KIAA1033	212794_s_at	KIAA1033	AK001728	Biological function unknown	0.0160	0.0073
TAF4 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 135kDa	213090_s_at	TAF4	NM_003185	Transcription, transcription initiation, regulation of transcription, DNA-dependent	0.0030	0.0000
Bicaudal D homolog 2 (Drosophila)	213154_s_at	BICD2	NM_001003800	Vesicle mediated transport	0.0408	0.0066
Keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris	213287_s_at	KRT10	X14487	Epidermis development	0.0073	0.0000
NIMA (never in mitosis gene a)-related kinase 1	213331_s_at	NEK1	NM_012224	Protein amino acid phosphorylation, cell cycle mitosis and division	0.0045	0.0027
Stonin 1	213413_at	STON1	NM_006873	Regulation of endocytosis, intracellular protein, transport, endocytosis	0.0122	0.0070
	213642_at		BE312027	Translation	0.0028	0.0461
Regeneration associated muscle protease	213661_at	DKFZP586H2123	NM_001001991	Proteolysis	0.0162	0.0008
Integrin, beta 5	214020_x_at	ITGB5	NM_002213	Cell adhesion, cell-matrix adhesion, integrin-mediated signaling pathway, development	0.0286	0.0000
Aldehyde dehydrogenase 1 family, member A3	214073_at	ALDH1A3	NM_005231	Alcohol, lipid and retinoic metabolism, metabolism, positive regulation of apoptosis, embryonic eye morphogenesis	0.0202	0.0116
Chromosome 1 open reading frame 107	214193_s_at	C1orf107	NM_014388	Development	0.0002	0.0003
Immunity-related GTPase family, cinema	214392_at	IRGC	NM_019612	Cell communication, signal transduction	0.0001	0.0066
Protein inhibitor of activated STAT, 2	214593_at	PIAS2	NM_004671	Transcription, ubiquitin cycle androgen receptor signaling pathway, positive regulation of transcription, DNA-dependent	0.0267	0.0080
Reticulon 4	214629_x_at	RTN4	AF320999	Negative regulation of anti-apoptosis, negative regulation of axon extension, regulation of apoptosis, apoptosis	0.0007	0.0368
Syntrophin, beta 1 (dystrophin-associated protein A1, 59kDa, basic component 1)	214708_at	SNTB1	NM_021021	Muscle contraction	0.0000	0.0000
Zinc finger protein 451	215012_at	ZNF451	NM_001031623	Transcription, regulation of transcription, DNA-dependent, phosphoenolpyruvate-dependent sugar phosphotransferase system	0.0001	0.0013
Paraspeckle component 1	215083_at	PSPC1	AL049263	Regulationof nucleobase, nucleoside, nucleotide, and necleic acid metabolism	0.0089	0.0003
Lymphocyte antigen 9	215967_s_at	LY9	NM_001033667	Cell adhesion, humoral defense mechanism (sensu Vertebrata)	0.0000	0.0215
Dishevelled associated activator of morphogenesis 1	216060_s_at	DAAM1	NM_014992	Cell organization and biogenesis, actin cytoskeleton organization and biogenesis	0.0000	0.0000
Leupaxin	216250_s_at	LPXN	NM_004881	Protein complex assembly, cell adhesion, signal transduction	0.0000	0.0000
Erythropoietin receptor	216999_at	EPOR	X97671	Signal transduction, small GTPase mediated signal transduction	0.0003	0.0001
Similar to alpha-2-glycoprotein 1, zinc	217013_at	LOC646282	AC004522	Biological function unknown	0.0272	0.0181
Similar to putative transcription factor ZNF131	217306_at	LOC645749	AL031119	Biological function unknown	0.0000	0.0000
Transmembrane BAX inhibitor motif containing 1	217730_at	TMBIM1	NM_022152	Biological function unknown	0.0022	0.0000
YKT6 v-SNARE homolog (S. cerevisiae)	217784_at	YKT6	NM_006555	ER to Golgi vesicle-mediated transport, vesicle targeting, vesicle docking during exocytosis, transport	0.0052	0.0000
ATP syntase, H+ transporting, mitochondrial F1 complex, epsilon subunit	217801_at	ATP5E	NM_006886	Ion and proton transport, ATP synthesis coupled proton transport	0.0002	0.0498
Glioma tumor suppressor candidate region gene 2	217807_s_at	GLTSCR2	NM_015710		0.0162	0.0068
Suppressor of Ty 16 homolog (S. cerevisiae)	217815_at	SUPT16H	NM_007192	DNA replication and repair, nucleosome disassembly, transcription, regulation of transcription, DNA-dependent, transcription from RNA polymerase II, promoter proteolysis, response to DNA damage stimulus	0.0166	0.0000

Golgi autoantigen, golgin subfamily a, 7	217819_at	GOLGA7	NM_016099	Lactation, lipid and triacylglycerol biosynthesis, activation of NF-kappaB transcription factor, B cell homeostasis, protein modification, protein amino acid phophorylation, I-kappaB phosphorylation, DNA replication and repair, base-excision repair, gap filling, anti-apoptosis, response to DNA damage stimulus, cell death, transport, intracellular protein transport, ion transport, synaptic transmission metabolism, synaptic transmission, cholinergic adenine transport	0.0339	0.0063
Leucine aminopeptidase 3	217933_s_at	LAP3	NM_015907	Proteolysis, protein metabolism	0.0000	0.0296
Mitogen-activated protein kinase kinase 1 interacting protein 1	217971_at	MAP2K1Ip1	NM_021970	Cell communication, signal transduction	0.0000	0.0003
RNA-binding protein	218035_s_at	FLJ20273	NM_019027	Nucleotide, nucleic acid and RNA binding	0.0122	0.0008
CDC42 effector protein (Rho GTPase binding) 4	218063_s_at	CDC42EP4	AF099664	Regulation of cell shape, positive regulation of pseudopodium formation	0.0000	0.0000
Cytoskeleton associated protein 2	218252_at	CKAP2	NM_018204	Apoptosis, cell cycle	0.0000	0.0002
RAB guanine nucleotide exchange factor (GEF) 1	218310_at	RABGEF1	NM_014504	Endocytosis, protein transport, transport	0.0000	0.0161
Fanconi anemia, complementation group L	218397_at	FANCL	NM_018062	DNA repair, ubiquitin cycle, response to DNA damage stimulus	0.0000	0.0000
Sorting nexin 10	218404_at	SNX10	NM_013322	Intracellular signaling cascade, protein transport, transport	0.0041	0.0495
Chromosome 1 open reading frame 115	218546_at	C1orf115	NM_024709	Biological function unknown	0.0009	0.0000
Immediate early response 5	218611_at	IER5	NM_016545	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	0.0000	0.0000
Hypothetical protein MGC2752	218624_s_at	MGC2752	NM_023939	Biological function unknown	0.0000	0.0000
Vacuolar protein sorting 28 homolog (S. cerevisiae)	218679_s_at	VPS28	NM_016208	Protein transport, transport	0.0000	0.0381
Hypothetical protein FLJ20920	218844_at	FLJ20920	NM_025149	Metabolism	0.0000	0.0001
NFU1 iron-sulfur cluster scaffold homolog (S. cerevesiae)	218946_at	NFU1	NM_015700	Iron-sulfur cluster assembly	0.0152	0.0000
Mediator of cell motility 1	219065_s_at	MEMO1	NM_015955	Biological function unknown	0.0197	0.0002
Development and differentiation enhancing factor-like 1	219103_at	DDEFL1	NM_017707	Regulation of GTPase activity	0.0032	0.0035
tRNA-histidine guanylyl transferase 1-like (S. cerevesiae)	219122_s_at	THG1L	NM_017872	tRNA modification and processing	0.0009	0.0031
Chromosome 2 open reading frame 47	219176_at	C2ORF47	NM_024520	Biological function unknown	0.0000	0.0074
RNA binding motif protein 15	219286_s_at	RBM15	NM_022768	Regulation of transcription	0.0003	0.0000
Alpha 1,4-galactosyltransferase (globotriaosylceramide syntase)	219488_at	A4GALT	NM_017436	Glycosphingolipid biosynthesis, plasma membrane organization and biogenesis, lipid biosynthesis	0.0002	0.0229
Erythroid associated factor	219672_at	ERAF	NM_016633	Protein folding, hemoglobin metabolism, hemopoiesis	0.0000	0.0000
Tetratricopeptide repeat domain 23	219838_at	TTC23	NM_022905	Biological function unknown	0.0047	0.0001
Hypothetical protein FLJ13197	219871_at	FLJ13197	NM_024614	Biological function unknown	0.0000	0.0000
Calcium binding tyrosine-(Y)-phosphorylation regulated (fibrousheathin 2)	219928_s_at	CABYR	NM_012189	Signal transduction	0.0116	0.0004
Family with sequence similarity 60, member A	220147_s_at	FAM60A	NM_021238	Biological function unknown	0.0000	0.0000
Chromosome 10 open reading frame 95	220152_at	C10orf95	NM_024886	Biological function unknown	0.0002	0.0333
Ral GEF with PH domain and SH3 binidng motif 2	220338_at	RALGPS2	NM_018037	Small GTPase mediated signal transduction	0.0000	0.0404
SEMK homolog 1, supressor of mek1 (Dictyostelium)	220368_s_at	SMEK1	NM_017936	Biological function unknown	0.0000	0.0001
	220687_at		NM_018175	Biological function unknown	0.0000	0.0030
Membrane-spanning 4-domains, subfamily A, member 12	220834_at	MS4A12	NM_017716	Electron transport, signal transduction	0.0000	0.0000
ATPase, Class V, type 10B	220920_at	ATP10B	NM_025153	Cation transport	0.0000	0.0000
Chromosome 21 open reading frame 91	220941_s_at	C21orf91	NM_017447	Biological function unknown	0.0000	0.0000
Kelch domain containing 4	221219_s_at	KLHDC4	NM_017566	Cell growth and/or maintenance	0.0001	0.0046
Atonal homolog 1 (Drosophila)	221336_at	ATOH1	NM_005172	Regulation of transcription, DNA-dependent, transcription from RNA polymerase II promoter, central nervous system development, regulation of transcription, transcription	0.0185	0.0159
Iron-sulfa cluster assembly 1 homolog (S. cerevesiae)	221425_s_at	ISCA1	NM_030940	Biological function unknown	0.0008	0.0000
CDC14 cell division cycle 14 homolg B (S. cerevisiae)	221556_at	CDC14B	NM_001077181	Protein amino acid dephosphorylation	0.0354	0.0004
Immunoglobulin kappa constant, immunoglobulin kappa variable 1-5, immunogolbulin kappa variable 2-24	221651_x_at	IGKC, IGKV1-5, IGKV2 24	3514, 28299, 28923	Immune response, antigen presentation, endogenous antigen via MHC class I	0.0125	0.0068

Immunoglobulin kappa constant, immunoglobulin kappa variable 1-5, immunogolbulin kappa variable 2-24	221671_x_at	IGKC, IGKV1-5, IGKV2 24	3514, 28299, 28923	Immune response, antigen presentation, endogenous antigen via MHC class I	0.0090	0.0000
Cylindromatosis (turban tumor syndrome)	221903_s_at	CYLD	NM_001042355	Protein biosynthesis, ubiquitin-dependent protein catabolism, cell cycle negative regulation of progression through cell cycle, ubiquitin-dependent protein catabolism, ubiquitin cycle	0.0358	0.0000
Family with sequence similarity 131, member A	221904_at	FAM131A	NM_144635	Biological function unknown	0.0381	0.0000
Matrix metallopeptidase 24 (membrane-inserted)	49679_s_at	MMP24	NM_006690	Peptidoglycan metabolism, proteolysis	0.0000	0.0000
Potassium channel tetramerisation domain containing 14	58916_at	KCTD14	NM_023930	Potassium ion transport	0.0000	0.0003
Similar to Zinc finger protein 418, zinc finger protein 814	60794_f_at	LOC730051, ZNF814	XR_015766	Regulation of transcription, DNA-dependent	0.0124	0.0058
Leucine-rich repeats and calponin homology (CH) domain containing 4	90610_at	LRCH4	NM_002319	Nervous system development	0.0026	0.0100
	AFFX-r2-Bs-dap-5_at			Transcript, regulation of transcription, DNA-dependent, protein modification, amino acid biosynthesis, lysine biosynthesis, lysine biosynthesis via diaminopimelate, diaminopimelate biosynthesis, tRNA 3'-terminal CCA addition, RNA and tRNA processing, RNA repair, methylglyoxal biosynthesis, biosynthesis	0.0325	0.0043

[A] Adjusted p values for antepartum vs. postpartum samples

[B] Adjusted p values for umbilical vs. postpartum samples

Supplemental Table 5. Umbilical cord blood gene expression levels

Gene	UNIQID	1U		2U		3U		4UA		4UB		5U		6U		7U		8U		9U	
S-phase kinase-associated protein 1A (p19A)	200719_at	95.5	++	76.8	++	127.5	+++	101.7	+++	147.4	+++	95.8	++	103.3	+++	35.4	++	60.1	++	55.1	++
Family with sequence similarity 120A	200767_s_at	17.9	++	24.6	++	16.6	++	26.6	++	28.5	++	23.1	++	18.7	++	39.3	++	20.5	++	43.7	++
CTD small phosphatase-like	201906_s_at	44.7	++	16.1	++	50.5	++	37.0	++	38.1	++	35.5	++	16.5	++	16.3	++	17.2	++	19.8	++
Upstream transcription factor 2, c-fos interacting	202152_x_at	51.7	++	21.4	++	7.8	+	86.4	++	24.5	++	32.4	++	34.6	++	80.9	++	67.3	++	107.5	+++
Tumor-associated calcium signal transducer 2	202286_s_at	11.2	++	11.0	++	16.7	++	4.7	+	8.4	+	10.6	++	6.6	+	6.6	+	13.1	++	9.8	+
Dehydrogenase/reductase member 3	202481_at	29.6	++	27.5	++	30.9	++	4.7	+	22.1	++	20.2	++	38.8	++	26.8	++	13.9	++	44.7	++
Adenylate kinase 1	202588_at	45.2	++	16.2	++	5.6	+	38.9	++	14.4	++	41.9	++	41.2	++	25.1	++	13.0	++	33.7	++
Cyclin B2	202705_at	26.9	++	17.8	++	12.7	++	4.2		6.7	+	14.2	++	14.7	++	22.8	++	24.4	++	21.3	++
Integral membrane protein 2A	202747_s_at	50.6	++	65.4	++	190.3	+++	18.1	++	104.7	+++	506.9	+++	340.8	++	202.0	+++	119.3	+++	100.9	+++
Neuroblastomal-amplified protein	202926_at	19.6	++	31.4	++	20.0	++	26.7	++	19.7	++	14.8	++	14.3	++	31.7	++	33.7	++	16.4	++
Mevalonate (diphospho) decarboxylase	203027_s_at	10.5	++	14.2	++	2.9	+	85.0	++	14.8	++	21.8	++	2.4	+	25.9	++	27.4	++	29.9	++
Myotubularin related protein 2	203212_s_at	47.2	++	25.6	++	27.4	++	5.6	+	21.9	++	8.2	+	6.3	+	18.0	++	7.1	+	10.5	++
Frizzled homolog 6 (Drosophila)	203987_at	13.1	++	4.6	+	7.4	+	20.6	++	16.3	++	13.9	++	8.0	+	7.0	+	16.7	++	8.3	+
Arylsulfatase A	204443_at	26.0	++	37.6	++	16.5	++	18.9	++	15.1	++	23.6	++	24.1	++	14.7	++	21.9	++	15.4	++
Nuclear pore complex interacting protein	204538_x_at	81.6	++	33.6	++	72.8	++	13.0	++	55.4	++	83.0	++	75.2	++	49.2	++	104.2	+++	77.2	++
Natriuretic peptide receptor A/guanlyate cyclase A	204648_at	54.3	++	21.8	++	5.4	+	3.6	+	9.9	+	28.1	++	20.2	++	12.3	++	27.2	++	39.6	++
Protoporphyrinogen oxidase	204788_s_at	171.6	+++	85.5	++	97.1	++	58.0	++	61.7	++	66.0	++	103.4	+++	21.4	++	65.8	++	30.9	++
Zinc finger protein 646	204876_at	34.7	++	19.6	++	4.8	+	3.9		5.8	+	5.0	+	19.4	++	12.4	++	20.4	++	25.2	++
Neuralized-like (Drosophila)	204888_s_at	5.3	+	9.3		15.2	++	11.9	++	3.7	+	3.5	+	3.2	+	10.1	++	9.6	+	20.8	++
AP2 associated kinase 1	205435_s_at	27.0	++	29.0	++	16.2	++	22.9	++	18.3	++	23.4	++	22.8	++	28.9	++	19.4	++	34.1	++
Kallikrein-related peptide 11	205470_s_at	5.3	+	14.3	++	19.4	++	19.0	++	12.6	++	20.1	++	6.0	+	12.3	++	11.2	++	15.9	++
Bactericidal/permeability-increasing protein	205557_at	89.2	++	357.5	+++	154.4	+++	27.0	++	24.9	++	52.3	++	51.6	++	58.3	++	43.0	++	26.7	++
Gamma-glutamyltransferase-like activity 1	205582_s_at	9.7	+	4.8	+	5.8	+	4.0	+	1.3	+	1.3	+	5.3	+	24.0	++	10.2	++	20.7	++
Cathespsin G	205653_at	27.9	++	145.3	+++	45.2	++	6.7	+	3.9	+	74.3	++	18.5	++	28.6	++	59.3	++	44.5	++
Gamma-aminobutyric acid (GABA) A receptor, beta 3	205850_s_at	3.7	+	2.7	+	1.2	+	15.7	++	19.6	++	7.2	+	8.9	+	3.8	+	15.4	++	12.7	++
RNA binding motif protein 19	206019_at	7.1	+	4.9	+	8.2	+	30.6	++	4.2	+	19.2	++	5.0	+	17.5	++	2.2	+	5.0	+
Interleukin 3 receptor, alpha (low affinity)	206148_at	40.8	++	9.8	+	2.3	+	6.1	+	8.2	+	17.2	++	2.5	+	2.2	+	3.6	+	7.0	+
Exostoses (multiple)-like 1	206329_at	13.6	++	17.6	++	6.9	+	21.2	++	21.9	++	27.9	++	31.4	++	16.4	++	28.9	++	29.9	++
ELAV (embryonic lethal, abnormal vision, Dropsophila)-like 3 (Hu antigen C)	206338_at	19.2	++	43.1	++	4.8	+	9.5	+	10.7	++	21.0	++	13.8	++	17.2	++	3.1	+	31.0	++
Solute carrier organic anion transporter family, member 1B3	206354_at	9.5	+	3.3	+	2.6	+	4.8	+	14.6	++	10.3	++	1.2	+	1.2	+	5.8	+	1.4	+
Chemokine (C motif) ligand 2	206366_x_at	85.6	++	35.3	++	56.1	++	39.1	++	54.3	++	75.3	++	55.6	++	35.6	++	8.1	+	19.3	++
CD19 molecule	206398_s_at	48.3	++	36.9	++	27.7	++	14.5	++	28.3	++	18.3	++	59.1	++	17.6	++	48.0	++	28.1	++
Neural retina leucine zipper	206597_at	34.6	++	5.1	+	1.9	+	39.8	++	21.7	++	4.5	+	3.0	+	16.3	++	18.1	++	16.1	++
IQ motif containing C	206650_at	20.1	++	31.3	++	27.3	++	30.4	++	13.4	++	52.8	++	32.2	++	17.5	++	5.0		8.4	+
Elastase 2, neutrophil	206871_at	96.3	++	256.3	+++	73.3	++	13.6	++	21.8	++	26.0	++	65.7	++	10.8	++	14.4	++	9.1	+
Complement factor H-related 2	206910_x_at	23.3	++	6.2	+	9.7	+	17.6	++	8.1	+	12.7	++	3.1	+	11.6	++	22.3	++	19.4	++
Histone 1, H4e	206951_at	12.3	++	29.7	++	12.4	++	4.0	+	32.8	++	5.9	+	3.1	+	14.7	++	4.8	+	13.0	++
Defensin, alpha 4, corticostatin	207269_at	315.6	+++	573.9	+++	1337.9	++++	171.0	+++	101.3	+++	817.6	+++	414.8	++	253.8	+++	913.7	+++	232.8	+++
Aspartate beta-hydroxylase	207284_s_at	0.4	<1	4.6	+	1.2	+	22.6	++	1.2		14.0	++	0.7	<1	2.9	+	4.8	+	15.5	++
GIPC PDZ domain containing family member 1	207525_s_at	33.7	++	33.0	++	23.5	++	42.3	++	47.6	++	48.3	++	22.8	++	28.8	++	28.3	++	33.6	++
Arginine vasopressin	207848_at	3.4	+	4.8	+	1.6	+	35.7	++	2.5	+	2.9		7.7	+	24.7	++	13.5	++	21.6	++
Rho guanine exchange facotr (GEF) 16	208009_s_at	6.2	+	6.3	+	2.7	+	37.4	++	4.4	+	22.7	++	3.9	+	25.3	++	19.7	++	23.4	++
Neuregulin 1	208232_x_at	3.9	+	15.0	++	2.7	+	26.6	++	4.5	+	24.8	++	2.7	+	21.8	++	21.4	++	28.6	++
Protein phosphatase, EF-hand calcium binding domain 2	208411_x_at	1.2	+	4.7	+	0.8	<1	0.5	<1	1.1	+	1.6	+	0.6	<1	1.5	+	1.9	+	5.7	+
RAS p21 protein activator 4	208534_s_at	12.2	++	9.7	+	9.8	+	26.8	++	22.1	++	25.2	++	14.1	++	5.9	+	2.7	+	1.5	+
Acidic (leucine-rich) nuclear phosphoprotein 32 family, member C	208538_at	22.7	++	1.7	+	2.4	+	6.9	+	9.5	+	2.9	+	3.0	+	4.5	+	2.4	+	14.5	++
Interferon-related developmental regulator 2	209100_at	98.9	++	72.9	++	60.5	++	43.3	++	83.1	++	39.3	++	83.8	++	37.7	++	39.7	++	42.7	++
Aurora kinase B	209464_at	21.5	++	19.4	++	3.2	+	4.9	+	10.8	++	18.0	++	14.2	++	6.7	+	24.8	++	15.0	++
Adenosine monophosphate deaminase (isoform E)	209491_s_at	30.4	++	21.5	++	17.1	++	5.8	+	5.5	+	25.0	++	4.9	+	19.1	++	26.9	++	28.2	++
Paraneoplastic antigen MA2	209598_at	0.6	<1	0.5	<1	0.5	<1	9.8	+	3.4	+	13.6	++	10.6	++	6.0	+	4.6	+	21.2	++
S100 calcium binding protein, beta (neural)	209686_at	6.5	+	15.0	++	12.5	++	1.9	+	12.4	++	1.7		1.1	+	3.0	+	5.4	+	4.4	+
Sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3F	209730_at	2.4	+	3.1	+	5.4	+	27.8	++	3.7	+	20.0	++	3.2	+	21.6	++	7.0	+	10.4	++
Mannosyl (beta-1,4)-glyocoprotein beta-1, 4-N-acetylgluocosaminyltransferase	209764_at	37.0	++	26.4	++	3.8	+	34.7	++	11.1	++	36.8	++	31.2	++	26.6	++	21.4	++	38.1	++
Leucine rich repeat	209840_s_at	59.2	++	35.4	++	98.1	++	79.8	++	120.6	+++	115.8		243.1	+++	105.9	+++	109.6	+++	50.2	++
Amyloid beta (A4) precursor protein-binding, family A, member 2 (X11-like)	209871_s_at	26.5	++	34.9	++	31.9	++	51.2	++	22.2	++	32.4	++	32.9	++	13.7	++	9.3	+	2.8	+
Synuclein, gamma (breast cancer-specific protein 1)	209877_at	28.5	++	14.0	++	3.7	+	11.8	++	11.2	++	22.8	++	3.9	+	12.6	++	23.9	++	20.4	++
Musculin (activated B-Cell factor-1)	209928_s_at	8.6	+	11.9	++	1.3	+	0.6	<1	3.1	+	6.3	+	5.6	+	13.4	++	15.6	++	12.7	++
Cytochrome P450, family 2, subfamily E, polypeptide 1	209976_s_at	13.0	++	6.0	+	1.0	+	34.2	++	13.8	++	3.1	+	9.2	+	7.4	+	2.7	+	20.4	++
Inositol 1,3,4-triphosphate 5/6 kinase	210197_at	44.2	++	24.9	++	24.0	++	25.9	++	15.8	++	16.0	++	20.7	++	13.9	++	20.4	++	31.7	++
Cathelicidin antimicrobial peptide	210244_at	463.7	+++	784.9	+++	675.6	+++	200.8	+++	188.4	+++	783.3	+++	431.8	+++	252.4	+++	358.9	+++	168.6	+++
Acetylcholinesterase (Yt blood group)	210332_at	12.4	++	16.6	++	1.7	+	34.9	++	12.4	++	28.8	++	3.7	+	28.6	++	14.0	++	12.8	++
Glutamate dehydrogenase 2	210447_at	0.8		5.4	+	1.3	+	1.9	+	17.2	++	7.0	+	4.8	+	8.6	+	7.8	+	8.4	+
Pyruvate kinase, liver and RBC	210451_at	21.5	++	8.2	+	7.1	+	0.7	<1	8.1	+	1.3	+	3.3	+	13.3	++	6.4	+	13.8	++

High mobility group AT-hook 1	210457_x_at	26.2	++	25.2	++	7.5	+	26.7	++	25.6	++	46.7	++	2.5	+	16.6	++	24.1	++	33.7	++
Nuclear distribution gene C homolog (A. nidulans)	210575_at	10.5	++	0.7	<0.1	2.0	+	9.9	+	6.0	+	40.4	++	9.1	+	1.6	+	5.7	+	17.3	++
Peroxisome proliferative activated receptor, delta	210636_at	5.8	+	0.7	<0.1	6.7	+	4.2	+	0.9	<1	1.9	+	5.5	+	2.9	+	2.5	+	1.1	+
Regucalcin (senescence marker protein-30)	210751_s_at	16.4	++	24.5	++	9.4	+	3.3	+	9.8	+	4.3	+	6.4	+	8.6	+	16.8	++	20.7	++
Cysteine and glycine-rich protein 2	211126_s_at	19.7	++	21.2	++	3.7	+	15.9	++	33.2	++	21.5	++	12.8	++	9.5	+	22.5	++	12.0	++
Killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 4	211242_x_at	19.5	++	20.9	++	1.3	+	16.3	++	3.3	+	22.6	++	12.0	++	17.8	++	23.2	++	13.0	++
Interferon, alpha 2	211338_at	0.7	<0.1	6.2	+	1.0	+	3.9	+	1.8	+	13.0	++	1.3	+	4.1	+	5.8	+	7.3	+
Leucine rich repeat containing 21	211353_at	6.7	16.9	0.9	<0.1	1.8	+	3.1	+	3.4	+	4.7	+	2.7	+	3.6	+	11.4	++	14.9	++
	211459_at	5.3	16.9	5.1	+	1.1	+	14.8	++	17.4	++	1.0	+	10.1	++	3.4	+	4.2	+	6.1	+
Receptor-associated protein of the synapse, 43kD	211570_s_at	9.0	16.9	13.9	++	16.0	++	6.9	+	2.5	+	31.9	++	11.0	++	5.8	+	3.8	+	19.5	++
Killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail	211688_x_at	4.0	16.9	3.3	+	11.9	++	51.8	++	16.4	++	4.1	+	9.4	+	3.7	+	4.6	+	11.8	++
Prostaglandin D2 syntase 21kDa (brain) prostaglandin D2 synthase 21kDa (brain)	211748_x_at	57.3	++	41.9	++	8.5	+	24.5	++	16.2	++	41.1	++	10.0	++	39.5	++	16.5	++	32.4	++
Complement factor B	211920_at	5.8	16.9	6.2	+	3.0	+	39.1	++	2.9	+	7.5	+	4.0	+	15.3	++	16.0	++	23.9	++
Chromosome 16 open reading frame 34	212115_at	2.4	16.9	13.1	++	26.5	++	19.4	++	4.4	+	40.1	++	33.0	++	26.0	++	5.0	+	17.2	++
Neuropilin 1	212298_at	9.3	16.9	1.1	+	2.6	+	1.0	+	0.7	<1	0.5	<1	0.4	<1	1.8	+	9.4	+	1.0	+
Eukaryotic translation initiation factor 2B, subunit 5 epsilon, 82kDa	212351_at	36.2	++	14.4	++	33.2	++	29.0	++	22.8	++	57.0	++	24.4	++	20.2	++	30.1	++	23.0	++
Transcription factor 4	212382_at	20.3	++	8.5	+	11.9	++	7.1	+	11.4	++	8.1	+	18.0	++	14.5	++	23.6	++	24.2	++
SET binding factor 1	212393_at	18.0	++	11.1	++	3.0	+	8.0	+	9.6	+	10.0	++	3.1	+	25.9	++	16.2	++	23.8	++
Rho-related BTB domain containing 1	212651_at	1.0		2.8	+	11.5	++	4.0	+	12.5	++	1.1	+	7.3	+	6.6	+	14.4	++	7.8	+
RAS p21 protein activator 4 hypothetical protein FLJ21767	212707_s_at	21.2	++	21.8	++	41.5	++	10.0	++	27.3	++	26.9	++	21.5	++	9.9	+	22.0	++	26.1	++
Growth arrest and DNA-damage-inducible, gamma interacting protein 1	212891_s_at	30.2	++	27.0	++	35.0	++	3.7	+	25.2	++	14.7	++	49.2	++	12.4	++	20.1	++	15.0	++
Dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 4	212954_at	42.5	++	20.9	++	33.9	++	11.0	++	33.7	++	9.8	+	23.9	++	21.5	++	36.3	++	28.3	++
CD3d molecule, delta (CD3-TCR complex)	213539_at	331.1	+++	258.0	+++	646.2	+++	427.3	+++	629.9	+++	333.5	+++	509.8	+++	173.3	+++	280.5	+++	103.9	+++
CREB/ATF bZIP transcription factor	213584_s_at	9.6	+	11.5	++	4.9	+	2.3	+	11.4	++	27.3	++	9.4	+	17.4	++	17.0	++	18.1	++
Tubulin, beta 2C	213726_x_at	237.2	+++	175.7	+++	92.9	++	114.5	+++	108.9		481.8	+++	293.5	+++	116.2	+++	264.1	+++	56.8	++
Phosphodiesterase 4D interacting protein (myomegalin)	214099_s_at	3.2	+	8.4	+	3.7	+	34.1	++	16.1	++	4.3	+	4.0	+	6.4	+	19.6	++	2.7	+
Collagen, type VIII, alpha 1	214587_at	6.2	+	9.7	+	2.1	+	4.2	+	11.9	++	6.5	+	3.7	+	8.2	+	0.4	<1	17.8	++
Somatostatin receptor 2	214597_at	1.9	+	1.9	+	5.5	+	5.6	+	3.9	+	7.3	+	2.8	+	10.2	++	8.1	+	11.2	++
Spectrin, alpha, nonerythrocytic 1 (alpha-fodrin)	214925_s_at	5.4	+	17.5	++	0.6	<1	16.1	++	7.5	+	8.1	+	4.3	+	11.1	++	9.5	+	11.8	++
Nucleoporin 62kDa interleukin 4 induced 1	214935_at	9.5	+	14.1	++	2.6	+	11.4	++	15.9	++	2.4	+	3.2	+	7.9	+	2.6	+	1.7	+
ST6 beta-galactosamide alpha-2,6-sialyltransferase 1	214970_s_at	3.0	+	1.5	+	2.4	+	17.8	++	1.7	+	0.9	<1	2.3	+	2.7	+	4.2	+	9.2	+
G-rich RNA sequence binding factor 1	215030_at	11.4	++	6.5	+	12.6	++	17.6	++	20.0	++	13.7	++	7.6	+	8.7	+	1.9	+	10.6	++
RAB GTPase activating protein 1	215070_x_at	10.6	++	6.7	+	14.3	++	4.3	+	16.9	++	23.6	++	3.2	+	8.6	+	14.4	++	14.6	++
Nuclear receptor co-repressor 2	215205_x_at	6.6	+	7.2	+	4.0	+	10.1	++	2.8	+	1.1	+	9.3	+	19.5	++	4.1	+	23.3	++
Solute carrier family 8 (sodium-calcium exchanger), member 2	215267_s_at	2.0	+	10.2	++	2.4	+	18.1	++	16.8	++	1.6	+	3.3	+	16.3	++	20.4	++	19.4	++
MRNA sequence, IMAGE clone 446411	215477_at	14.4	++	1.2	+	23.7	++	34.2	++	3.2		19.4	++	5.9	+	15.7	++	13.2	++	21.2	++
Zinc finger UBR1 type 1	215636_at	2.0	+	14.0	++	13.7	++	21.1	++	13.8	++	4.2		15.1	++	4.6	+	11.3	++	16.9	++
Transcription factor AP-2 beta (activating enhancer binding protein 2 beta)	215686_x_at	14.8	++	24.1	++	16.4	++	23.3	++	12.0	++	14.7	++	3.0	+	1.4	+	25.0	++	10.7	++
	215799_x_at	9.4	+	6.1	+	3.1	+	7.8	+	5.2	+	4.4	+	4.3	+	3.0	+	2.9	+	1.8	+
Similar to bK246H3.1 (immunoglobulin lambdalike polypeptide 1, pre-B-cell specific)	215816_at	6.6	+	5.3	+	8.9	+	6.4	+	9.7	+	4.0	+	3.2	+	19.3	++	3.1	+	20.1	++
Spectrin, beta, nonerythrocytic 1	215918_s_at	2.4		12.3	++	2.1	+	4.4	+	20.9	++	8.6	+	9.4	+	2.7	+	3.8	+	19.6	++
Hypothetical protein LOC731501	216053_x_at	18.7	++	14.9	++	2.1	+	11.5	++	20.3	++	4.5	+	2.5	+	13.2	++	5.7	+	11.9	++
GTPase activating Rap/RanGap domain-like 3	216165_at	11.3	++	4.8	+	1.9	+	14.7	++	14.2	++	4.7	+	5.7	+	7.3	+	5.8	+	1.0	+
Pleckstrin homology domain containing, family M (with RUN domain) member 1	216200_at	2.9	+	21.0	++	13.6	++	6.9	+	20.0	++	30.7	++	13.0	++	9.0	+	12.2	++	8.4	+
Jerky homolog (mouse)	216309_x_at	32.7	++	16.0	++	8.3	+	54.7	++	10.2	++	57.7	++	92.1	++	68.4	++	49.7	++	71.1	++
Tenascin XA pseudogene tenascin XB	216339_s_at	3.8	+	12.2	++	3.4	+	1.5	+	2.3	+	3.5	+	2.4	+	1.8	+	2.3	+	6.4	+
CDNA: FLJ21769 fis, clone COLF7354	216429_at	6.3	+	19.9	++	18.9	++	23.2	++	20.3	++	28.1	++	10.2	++	27.6	++	17.5	++	45.6	++
LOC642150 similar to cationic trypsin III precursor (pretrypsinogen III)	216597_at	7.0	+	1.9	+	1.3	+	16.9	++	5.1	+	15.2	++	11.4	++	13.9	++	10.1	++	13.9	++
Transmembrane 6 superfamily member 2	216736_at	29.5	++	18.0	++	4.8	+	52.9	++	23.3	++	51.4	++	3.0	+	35.0	++	32.1	++	40.0	++
Keratin 84	217031_at	4.2		2.2	+	1.3	+	4.5	+	1.3	+	17.1	++	1.4	+	5.3	+	6.5	+	5.3	+
Protease, serine 7 (enterokinase)	217269_s_at	26.7	++	54.6	++	42.8	++	72.8	++	44.0	++	71.2	++	56.8	++	42.1	++	33.3	++	33.9	++
PRAME family member 10	217273_at	12.1	++	5.8	+	1.7	+	11.5	++	0.7	<1	2.2	+	2.5	+	6.2	+	3.3	+	16.6	++
Serine hydroxymethyltransferase 1 (soluble)	217304_at	15.1	++	26.8	++	29.7	++	15.8	++	25.3	++	7.8	+	8.8	+	6.5	+	16.3	++	25.9	++
Interleukin 23, alpha subunit p19	217328_at	19.8	++	21.5	++	10.7	++	65.2	++	19.2	++	26.9	++	17.1	++	17.7	++	13.0	++	27.4	++
Basic transcription factor 3	217461_x_at	20.7	++	2.6	+	16.0	++	32.0	++	14.6	++	13.4	+	10.2	++	7.5	+	25.4	++	2.4	+

Olfactory receptor, family 7, subfamily e, member 37 pseudogene	217499_x_at	68.0	++	43.8	++	64.1	++	84.5	++	66.8	++	122.8	+++	91.6	++	63.8	++	101.9	+++	66.4	++
Cation channel, sperm associated 2 cation channel, sperm associated 2 pseudogene	217588_at	23.2	++	22.5	++	15.4	++	20.2	++	18.9	++	34.0	++	4.0	+	26.2	++	15.4	++	29.8	++
Desmoglein 2	217901_at	0.4	<0.1	6.3	+	5.1	+	26.8	++	6.2	+	8.6	+	1.9	+	6.3	+	14.3	++	18.1	++
Mitochondrial ribosomal protein L4	218105_s_at	17.6	++	6.3	+	3.4	+	26.4	++	5.0	+	17.4	++	2.9	+	1.8	+	3.6	+	25.4	++
Fanconi anemia, complementation group L	218397_at	14.0	++	9.6	+	11.5	++	7.5	+	16.8	++	3.7	+	8.5	++	10.7	++	8.0	+	12.8	++
TBC1 domain family, member 13	218596_at	6.5		4.4	+	7.3	+	2.0	+	5.9	+	6.7	+	2.5	+	11.1	++	2.8	+	9.5	+
Phospholipid scramblase 3	218828_at	24.0	++	16.5	++	8.6	+	70.5	++	123.5	+++	75.6	++	98.7	++	78.5	++	67.2	++	64.8	++
Chromosome 2 open reading frame 43	219008_at	4.1		5.9	+	12.0	++	18.1	++	8.5	+	21.0	++	19.7	++	16.2	++	17.2	++	17.7	++
Brevican	219107_at	32.2	++	29.2	++	24.2	++	8.6	+	5.5	+	23.2	++	18.1	++	37.0	++	9.5	+	49.9	++
SLAM family member 8	219386_s_at	10.2	++	4.3	+	2.4		6.6	+	6.6	+	1.9	+	2.1		10.5	++	13.3	++	3.9	+
Placenta-specific 1	219702_at	22.0	++	13.4	++	19.1	++	2.8	+	13.0	++	13.5	++	2.5		1.3		17.0	++	6.6	+
Galactose-3-O-sulfotransferase 4	219815_at	26.6	++	26.1	++	41.5	++	60.1	++	14.9	++	23.2	++	23.5	++	36.3	++	33.9	++	43.2	++
Glycerophosphodiester phosphodiesterase domain containing 2	220291_at	25.6	++	5.0	+	4.3	+	27.1	++	3.0	+	5.5	+	6.0	+	58.0	++	6.6	+	25.2	++
Signal-regulatory protein gamma	220485_s_at	45.1	++	32.5	++	47.9	++	46.8	++	69.5	++	67.4	++	78.0	++	29.6	++	30.9	++	28.4	++
Testis-specific kinase substrate	220545_s_at	18.8	++	9.1	+	2.0	+	8.5	+	4.4	+	13.0	++	4.1	+	9.4	+	13.8	++	10.9	++
Hypothetical protien FLJ11783	220546_at	5.6	+	4.3	+	8.7	+	6.7	+	17.8	++	13.0	++	3.0	+	7.9	+	13.0	++	6.5	+
Disabled homolog 1 (Drosophila)	220611_at	11.9	++	15.3	++	1.3	+	37.1	++	2.8	+	10.7	++	0.9	<1	16.3	++	7.4	+	18.2	++
	220687_at	12.2	++	13.2	++	4.5	+	29.6	++	4.7	+	1.1	+	7.0		3.6		10.9	++	15.5	++
Roundabout homolog 4, magic roundabout (Drosophila)	220758_s_at	26.4	++	28.3	++	21.5	++	45.5	++	64.1	++	36.7	++	28.0	++	48.6	++	65.6	++	56.2	++
hCG 1732469	220823_at	17.3	++	10.7	++	17.2	++	2.4	+	24.4	++	18.9	++	15.2	++	20.5	++	21.9	++	20.3	++
WD repeats and SOF 1 domain containing	220843_s_at	1.0	+	12.0	++	11.1	++	7.6	+	11.4	++	14.4	++	3.8	+	11.1	++	4.0	+	10.5	++
Unc-51-like kinase 4 (C elegans)	220958_at	9.0	+	2.6	+	0.9	<1	3.2	+	2.3	+	10.4	++	7.4	+	14.1	++	14.6	++	7.2	+
Integral membrane protein 2C	221004_s_at	72.5	++	39.6	++	60.8	++	27.5	++	20.2	++	15.1	++	32.9	++	9.9	+	26.9	++	16.2	++
Natural cytotoxicity triggering receptor 2	221074_at	10.3	++	2.9	+	5.0	+	1.9	+	9.7	+	3.3	+	1.6	+	9.9	+	9.5	+	8.8	+
2-oxoglutarate and iron-dependent oxygenase domain containing 1	221090_s_at	14.0	++	13.5	++	10.0	++	16.7	++	14.8	++	25.0	++	24.3	++	7.9	+	17.3	++	20.3	++
Growth differentiation factor 9	221314_at	3.6	+	14.6	++	8.6	+	23.0	++	21.9	++	6.3	+	12.7	++	29.2	++	26.1	++	41.3	++
Cholinergic receptor, muscarinic 5	221347_at	2.7	+	17.6	++	2.6	+	12.7	++	12.2	++	38.1	++	15.3	++	18.0	++	28.2	++	32.4	++
Hypothetical protein LOC339047	221501_x_at	80.0	++	68.0	++	74.9	++	170.8	+++	91.6	++	126.1	+++	58.5	++	75.1	++	201.7	+++	37.6	++
Par-3 partitioning defective 3 homolog (C elegans)	221526_x_at	8.6	+	17.8	++	7.9	+	23.0	++	45.3	++	5.1	+	6.7		11.6	++	16.7	++	20.7	++
MAP/microtubule affinity-regulating kinase 4	221560_at	4.0	+	8.7	+	2.7	+	12.8	++	5.2	+	40.1	++	15.2	++	44.0	++	26.2	++	32.2	++
RRN3 RNA polymerase 1 transcription factor homolog (S. cerevisiae) pseudogene	221714_s_at	2.6	+	2.1	+	11.4	++	12.9	++	2.6	+	20.6	++	9.9	+	21.3	++	21.1	++	10.8	++
Zinc finger protein 512B	221869_at	9.4	+	4.7	+	1.1	+	3.1	+	2.9	+	10.9	++	1.2	+	3.4	+	3.8	+	2.0	+
aarF domain containing kinase 2	222117_s_at	15.6	++	17.9	++	4.8	+	20.6	++	11.8	++	2.4	+	7.8	+	13.7	++	2.4	+	17.7	++
Similar to Zinc finger protein 418	222135_at	9.8	+	0.9	<1	8.5	+	1.6	+	3.2	+	12.4	++	5.9	+	1.6	+	15.7	++	14.7	++
Splicing factor 3a, subunit 2, 66kDa	37462_i_at	63.3	++	4.3	+	34.1	++	4.8	+	1.6	+	26.8	++	43.9	++	25.4	++	36.8	++	15.0	++
Hydroxysteroid (17-beta) dehydrogenase 6 homolog (mouse)	37512_at	7.8	+	4.7	+	7.4	+	19.2	++	1.7	+	0.3	<1	0.2	<1	0.8	<1	5.8	+	3.4	+
CD22 molecule, myelin-associated glycoprotein	38521_at	45.7	++	38.5	++	38.6	++	20.1	++	9.2	+	55.0	++	22.2	++	29.2	++	49.9	++	11.4	++
Acetyl-Coenzyme A carboxylase beta	49452_at	6.5	+	3.6	+	3.0	+	2.0	+	3.1	+	3.6	+	3.1	+	13.3	++	7.7	+	7.8	+
	AFFX-BioDn-3_at	2999.7	++++	1074.0	++++	1182.4	++++	3810.2	++++	1570.2	++++	4362.5	++++	1854.7	++++	224.2	+++	3063.2	++++	695.7	+++