Bracken. Supplementary Table 3.

A complete list of all significantly enriched PcG target genes in human embryonic fibroblasts

			anti-HA		anti-CBX8		anti-SUZ12		anti-K27me3		
Gene name	**Description**	**Gene ID**	**MEAN**	**Std Dev**	**MEAN**	**Std Dev**	**MEAN**	**Std Dev**	**MEAN**	**Std Dev**	**Biological Process (Information extracted from DAVID http://apps1.niaid.nih.gov/david/)**
HOXD12	homeo box D12	NM_021193			4.446	0.319	3.574	0.529	2.945	0.528	Regulation of transcription, DNA-dependent. Development.
HOXA11	homeobox protein A11	NM_005523			4.406	0.241	3.205	0.362	3.273	0.477	Regulation of transcription, DNA-dependent. Morphogenesis.
OLIG2	oligodendrocyte lineage transcription factor 2	BC047511			4.117	0.379	3.189	0.244	2.999	0.386	Transcription. Regulation of transcription, DNA-dependent. Development.
PHOX2B	paired-like homeobox 2b	NM_003924			4.685	0.233	2.869	0.706	2.721	0.316	Regulation of transcription, DNA-dependent. Development. Neurogenesis.
SIM1	single-minded homolog 1	NM_005068			4.42	0.327	2.943	0.336	2.538	0.7	Transcription. Regulation of transcription, DNA-dependent. Signal transduction. Development. Neurogenesis.
HOXA13	homeobox protein A13	NM_000522			3.728	0.517	3.166	0.696	2.958	0.979	Skeletal development. Regulation of transcription, DNA-dependent. Development.
ZIC5	zinc finger protein of the cerebellum 5	NM_033132			4.279	0.315	2.562	0.479	2.95	0.613	
LHX9	LIM homeobox 9	NM_020204			4.219	0.227	2.966	0.549	2.488	0.594	
N/A	Unknown (protein for MGC:15427)	BC008699			4.286	0.463	2.298	0.379	2.934	0.495	
HOXD13	homeo box D13	NM_000523			3.976	0.472	2.657	0.484	2.779	0.806	Skeletal development. Regulation of transcription, DNA-dependent. Transcription from RNA polymerase II promoter. Development,
PAX3	paired box gene 3 isoform PAX3d	NM_181458			4.171	0.497	2.296	0.523	2.795	0.31	Regulation of transcription, DNA-dependent. Transcription from RNA polymerase II promoter. Apoptosis. Development. Neurogenes
PRDM13	PR domain containing 13	NM_021620			4.037	0.305	2.658	0.424	2.557	0.488	Transcription. Regulation of transcription, DNA-dependent.
OLIG3	oligodendrocyte transcription factor 3	NM_175747			4.127	0.39	2.328	0.763	2.592	0.953	
TAL1	T-cell acute lymphocytic leukemia 1	NM_003189	1.791	1.534	4.186	0.292	2.842	0.392	1.978	0.333	Transcription. Regulation of transcription, DNA-dependent. Cell proliferation . Cell differentiation.
NKX2-5	" NK2 transcription factor related, locus 5"	NM_004387			3.508	0.478	2.692	0.303	2.804	0.565	Negative regulation of transcription from RNA polymerase II promoter. Development. Heart development.
HOXB9	homeo box B9	NM_024017			3.711	0.414	2.664	0.42	2.625	0.683	Regulation of transcription, DNA-dependent. Development.
PAX-9	N/A	U59628			3.894	0.437	2.958	0.354	2.102	0.587	Transcription. Regulation of transcription, DNA-dependent. Development.
TLX3	" T-cell leukemia, homeobox 3"	NM_021025			4.151	0.468	2.629	0.611	2.139	0.598	Regulation of transcription, DNA-dependent. Development.
CYP26A1	" cytochrome P450, family 26, subfamily A, polypeptide 1 isof	NM_057157			3.753	0.492	2.663	0.571	2.49	0.671	Electron transport. Metabolism.
LGI3	leucine-rich glioma inactivated protein 3	AJ487518			3.615	0.555	2.582	0.658	2.684	0.556	
N/A	N/A	AK026075			4.276	0.349	2.669	0.436	1.888	0.681	Regulation of cell cycle. Cytokinesis. Carbohydrate metabolism. Base-excision repair.
FLJ32063	hypothetical protein FLJ32063	NM_153031			3.836	0.403	2.266	0.333	2.715	0.612	
MEOX2	mesenchyme homeo box 2	NM_005924			4.075	0.534	2.148	0.429	2.542	0.545	Regulation of transcription, DNA-dependent. Development. Circulation.
LHX1	LIM homeobox protein 1	NM_005568			3.811	0.442	2.903	0.796	2.009	0.906	Regulation of transcription, DNA-dependent. Neurogenesis.
ZIC4	zinc finger protein of the cerebellum 4	NM_032153			4.079	0.383	2.701	0.549	1.928	0.878	
N/A	progesterone receptor B isoform	AY382152			3.489	0.694	2.549	0.771	2.651	0.57	
EVX1	even-skipped homeo box 1	NM_001989			3.661	0.429	2.078	0.223	2.917	0.543	
SIX6	SIX6 protein	BC065831			3.46	0.452	2.413	0.437	2.765	0.473	Regulation of transcription, DNA-dependent. Development. Visual perception. Organogenesis.
CROC4	transcriptional activator of the c-fos promoter	NM_006365			3.3	0.478	2.169	0.694	3.154	0.78	
VGLL2	vestigial-like 2 isoform 1	NM_182645			3.986	0.503	2.279	0.619	2.342	0.709	Regulation of transcription.
BARX1	BARX1 protein	BC064363			2.831	1.001	2.992	0.765	2.767	0.89	Regulation of transcription, DNA-dependent. Regulation of transcription, DNA-dependent. Development.
TLX2	" T-cell leukemia, homeobox 2 isoform 1"	NM_016170			4.067	0.366	2.262	0.438	2.24	0.61	Regulation of transcription, DNA-dependent. Development.
N/A	N/A	AK021601			4.357	0.32	1.46	0.537	2.713	0.386	
FLJ20171	FLJ20171 protein	BC067098			3.331	0.396	2.536	0.276	2.616	0.35	
WT1	WT1 protein	BC046461			3.819	0.629	2.266	0.576	2.365	0.745	Transcription. Regulation of transcription, DNA-dependent. Regulation of transcription, DNA-dependent. Cell cycle.
KCNA1	" potassium voltage-gated channel, shaker-related subfamily,	NM_000217			3.287	0.54	2.432	0.607	2.685	0.678	Cation transport. Potassium ion transport. Muscle contraction. Synaptic transmission.
PAX5	paired box 5	NM_016734			4.161	0.515	2.602	0.692	1.637	0.757	Transcription. Regulation of transcription, DNA-dependent. Transcription from RNA polymerase II promoter. Humoral immune response.
GJB6	" gap junction protein, beta 6 (connexin 30)"	NM_006783			3.07	0.59	2.551	0.835	2.751	0.798	Cell communication. Perception of sound.
FOXB1	forkhead box B1	NM_012182			3.445	0.572	2.555	0.362	2.323	0.562	Transcription. Regulation of transcription, DNA-dependent.
N/A	Unknown (protein for MGC:70702)	BC059780			2.688	0.434	2.38	0.312	3.225	0.449	
HOXD9	homeo box D9	NM_014213			3.422	0.361	2.416	0.349	2.45	0.506	Regulation of transcription, DNA-dependent. Development.
NR2E1	" nuclear receptor subfamily 2, group E, member 1"	NM_003269			3.413	0.65	2.545	0.453	2.317	0.577	Transcription. Regulation of transcription, DNA-dependent. Development. Neurogenesis.
HOXD8	homeo box D8	NM_019558			3.861	0.711	2.087	0.76	2.309	1.187	Regulation of transcription, DNA-dependent. Development. Determination of anterior/posterior axis, embryo.
HCK	hemopoietic cell kinase isoform p61HCK	NM_002110			2.534	0.629	3.012	0.865	2.693	0.799	Protein amino acid phosphorylation. Intracellular signaling cascade. Mesoderm development.
NEUROD1	neurogenic differentiation 1	NM_002500			3.588	0.313	2.044	0.392	2.524	0.681	Transcription. Regulation of transcription, DNA-dependent. Neurogenesis. Cell differentiation.
LPL	lipoprotein lipase precursor	NM_000237			3.848	0.625	2.304	0.786	1.99	0.925	Fatty acid metabolism. Circulation. Lipid catabolism.
ARX	aristaless related homeobox	NM_139058			3.24	0.465	2.566	0.502	2.268	0.779	Regulation of transcription, DNA-dependent. Development.
HAND1	basic helix-loop-helix transcription factor HAND1	NM_004821			3.306	0.248	2.599	0.237	2.153	0.442	Regulation of transcription, DNA-dependent. Transcription from RNA polymerase II promoter. Development.

NKX2-3	" NK2 transcription factor related, locus 3"	NM_145285			3.129	0.629	2.155	0.291	2.759	0.494	
TBX1	T-box 1 isoform C	NM_080647			2.408	1.12	2.72	0.424	2.87	0.753	Regulation of transcription from RNA polymerase II promoter. Heart development. Morphogenesis.
SNCB	beta-synuclein	NM_001001502			4.054	0.805	1.082	0.328	2.862	0.921	
WIT-1	Wilms tumor associated protein	NM_015855			3.713	0.417	2.208	0.421	2.068	0.334	Cell proliferation.
N/A	N/A	AK125569			3.132	0.636	2.144	0.435	2.687	0.729	
EN2	engrailed homolog 2	NM_001427			3.475	0.934	1.801	0.418	2.685	0.477	Regulation of transcription, DNA-dependent. Development.
N/A	N/A	AK126665			2.745	0.419	2.61	0.552	2.588	0.449	
N/A	N/A	AK123661			3.227	0.58	2.248	0.436	2.46	0.433	
SIDT1	" SID1 transmembrane family, member 1"	NM_017699			4.454	0.454	1.193	0.697	2.178	0.568	
KIAA0322	N/A	AB002320			3.263	0.56	2.043	0.796	2.519	0.689	Ubiquitin cycle.
SPON1	" spondin 1, extracellular matrix protein"	NM_006108			2.742	0.893	2.433	0.945	2.65	0.948	Cell adhesion. Development.
BCAN	brevican isoform 1	NM_021948			3.29	0.551	1.853	0.667	2.679	0.603	Cell adhesion.
N/A	N/A	AK022595			3.709	0.534	2.414	0.548	1.679	0.583	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism. Metabolism.
DLX5	distal-less homeo box 5	NM_005221			3.162	0.899	1.925	0.487	2.687	0.889	Skeletal development. Regulation of transcription, DNA-dependent. Development. Neurogenesis.
PRAC	small nuclear protein PRAC	NM_032391			3.769	0.483	1.915	0.83	2.089	0.578	
FOXL2	forkhead box L2	NM_023067			3.344	0.696	2.237	0.665	2.184	0.575	Transcription. Regulation of transcription, DNA-dependent.
ROBO3	" roundabout, axon guidance receptor, homolog 3"	NM_022370			3.396	0.354	1.85	0.488	2.516	0.416	Chemotaxis. Neurogenesis. Sensory perception. Cell differentiation.
NEUROG2	neurogenin 2	NM_024019			3.672	0.656	2.33	0.879	1.723	0.788	
LHX5	LIM homeobox protein 5	NM_022363			2.848	0.605	2.069	0.498	2.784	0.451	Regulation of transcription, DNA-dependent. Central nervous system development.
HOXD4	homeo box D4	NM_014621			2.936	0.551	2.081	0.464	2.681	0.381	Regulation of transcription, DNA-dependent. Development.
FEV	FEV (ETS oncogene family)	NM_017521			2.494	0.71	2.128	0.559	3.074	0.454	Regulation of transcription, DNA-dependent. Transcription from RNA polymerase II promoter.
CHX10	ceh-10 homeo domain containing homolog	NM_182894			3.114	0.409	1.908	0.827	2.623	0.504	
IPF1	" insulin promoter factor 1, homeodomain transcription factor"	NM_000209	1.327	1.266	3.809	0.669	2.059	0.504	1.772	0.66	Generation of precursor metabolites and energy. Regulation of transcription, DNA-dependent. Development. Organogenesis.
ZNF312	zinc finger protein 312	NM_018008			3.207	0.272	2.31	0.26	2.086	0.449	
DKFZp686B14266	hypothetical proteincDNA DKFZp686B14266 (from clone DKFZ	BX640762			3.324	0.622	1.994	0.88	2.274	0.657	
HOXC11	homeo box C11	NM_014212			2.651	0.652	2.299	0.523	2.632	0.489	Regulation of transcription, DNA-dependent. Development. Endoderm development.
PRDM12	PR domain containing 12	NM_021619			2.484	0.652	2.88	0.754	2.21	0.86	Transcription. Regulation of transcription, DNA-dependent.
KIAA1788	KIAA1788 protein	AB058691			3.346	0.581	2.213	0.375	2.007	0.53	Skeletal development. Skeletal development. Regulation of transcription, DNA-dependent. Development.
N/A	N/A	AK123662	1.111	0.692	2.764	0.316	2.011	0.442	2.79	0.326	
HOXC12	homeo box C12	NM_173860			3.233	0.412	1.98	0.477	2.347	0.426	
HOXA10	homeobox protein A10 isoform a	NM_018951			3.088	0.339	2.146	0.503	2.317	0.642	Regulation of transcription, DNA-dependent. Development. Spermatogenesis.
SIX3	sine oculis homeobox homolog 3	NM_005413	1.002	1.309	3.107	0.28	2.298	0.331	2.139	0.459	Regulation of transcription, DNA-dependent. Brain development. Visual perception.
GDF7	growth differentiation factor 7	NM_182828			3.053	0.582	2.669	0.668	1.814	0.729	
EN1	engrailed homolog 1	NM_001426			2.923	0.417	2.069	0.388	2.506	0.325	Skeletal development. Regulation of transcription, DNA-dependent. Morphogenesis.
OG12	homeodomain protein	AF022654			3.509	0.499	1.784	0.349	2.191	0.664	Skeletal development. Regulation of transcription, DNA-dependent. Development. Neurogenesis. Heart development.
CART1	cartilage paired-class homeoprotein 1	NM_006982			3.292	0.547	1.912	0.676	2.277	0.463	Cartilage condensation. Regulation of transcription, DNA-dependent. Transcription from RNA polymerase II promoter. Brain Development.
MSI1	musashi 1	NM_002442			2.596	0.594	2.354	0.414	2.529	0.881	Neurogenesis.
POMC	proopiomelanocortin	NM_000939			2.984	0.657	1.654	0.553	2.832	0.75	Generation of precursor metabolites and energy. Signal transduction. Neuropeptide signaling pathway. Cell-cell signaling.
FKHL15	DNA binding protein FKHL15	U89995			3.393	0.92	2.101	0.849	1.949	0.739	Negative regulation of transcription from RNA polymerase II promoter. Transcription.
SLC6A20	X transporter protein 3 isoform 1	NM_020208			3.506	0.356	1.97	0.431	1.959	0.542	Neurotransmitter transport.
C6orf141	hypothetical protein MGC46457	NM_153344			3.444	0.606	2.189	0.441	1.772	0.552	
KCNN1	" potassium intermediate/small conductance calcium-activatec	NM_002248			2.747	0.481	2.37	0.445	2.287	0.348	Ion transport. Potassium ion transport. Synaptic transmission.
TFCP2L4	TFCP2L4 protein	BC036890			3.252	0.282	1.592	0.495	2.557	0.547	
CDX2	caudal type homeo box transcription factor 2	NM_001265			3.111	0.814	1.941	0.777	2.341	0.802	
CCND2	cyclin D2	NM_001759			3.299	0.562	2.276	0.999	1.816	0.623	Regulation of cell cycle. Cytokinesis.
HOXD3	homeo box D3	NM_006898			2.903	0.556	1.666	0.495	2.82	0.696	Regulation of transcription, DNA-dependent. Morphogenesis.
C20orf103	chromosome 20 open reading frame 103 precursor	NM_012261			3.245	0.41	1.727	0.39	2.415	0.673	
EMX1	empty spiracles homolog 1	NM_004097	1.601	1.226	3.243	0.55	2.578	0.492	1.55	0.543	Regulation of transcription, DNA-dependent. Development.
CKMT1	" ubiquitous mitochondrial creatine kinase, precursor"	BC001926			2.234	0.893	2.406	0.572	2.71	0.481	
BARHL1	BarH-like 1	NM_020064			2.894	0.934	2.365	0.842	2.089	0.607	Regulation of transcription, DNA-dependent.
DLX4	DLX4 protein	BC014419			2.411	0.567	2.588	0.465	2.346	0.606	Regulation of transcription, DNA-dependent. Regulation of transcription, DNA-dependent. Development.
HPX-6	N/A	X74863			3.288	0.707	2.068	0.491	1.985	0.801	
MGC16664	hypothetical protein MGC16664	NM_173509			2.736	0.817	2.245	0.982	2.355	0.579	
MT1G	MT1G protein	BC020757			2.662	0.488	2.071	0.537	2.588	0.633	
LBX1	transcription factor similar to D. melanogaster homeodomain p	NM_006562			2.849	0.419	2.623	0.77	1.839	0.595	Regulation of transcription, DNA-dependent. Morphogenesis.
RHBDL4	" rhomboid, veinlet-like 4"	NM_138328	1.096	1.345	2.438	1.143	2.38	0.985	2.465	1.073	

HOXC9	homeo box C9	NM_006897	2.695	0.507	2.456	0.777	2.132	0.498	Regulation of transcription, DNA-dependent. Development.
HRK	harakiri	NM_003806	3.089	0.898	1.38	0.682	2.809	0.784	Induction of apoptosis. Negative regulation of survival gene product activity. Regulation of apoptosis
LOC222171	hypothetical protein LOC222171	NM_175887	2.548	0.205	2.491	0.299	2.231	0.327	
DMRT3	doublesex and mab-3 related transcription factor 3	NM_021240	3.107	1.427	2.188	1.111	1.963	1.152	Regulation of transcription, DNA-dependent. Sex differentiation.
FLJ25477	FLJ25477 protein	BC032653	2.503	0.866	2.198	0.599	2.552	0.886	
N/A	N/A	AK075440	3.565	0.653	1.11	0.993	2.573	0.69	
NRN1	" neuritin, precursor"	BC042019	3.535	0.507	1.586	0.831	2.119	0.628	
FLJ32447	hypothetical protein FLJ32447	NM_153038	3.693	0.334	1.195	0.353	2.344	0.521	
KIAA1465	KIAA1465 protein	AB040898	2.581	0.788	2.563	0.826	2.076	0.799	
NFIB	nuclear factor I/B	NM_005596	3.719	0.491	2.084	0.549	1.396	0.577	DNA replication. Transcription. Regulation of transcription, DNA-dependent.
ZIC1	zinc finger protein of the cerebellum 1	NM_003412	3.583	0.574	1.916	0.622	1.696	0.648	Pattern specification. Brain development. Behavior. Regulation of smoothened signaling pathway
N/A	N/A	AK002097	3.136	0.781	2.004	0.595	2.05	0.89	
ZBTB16	zinc finger and BTB domain containing 16	NM_006006	2.35	0.827	2.41	0.472	2.396	0.565	Regulation of transcription, DNA-dependent. Mesoderm development.
MEGF11	MEGF11 protein	NM_032445	2.99	0.552	1.81	0.477	2.329	0.637	
CKMT1	" ubiquitous mitochondrial creatine kinase, precursor"	BC001926	2.003	0.926	2.406	0.572	2.71	0.481	
N/A	homeobox protein	AJ004949	3.079	0.7	1.99	0.57	2.049	0.791	
DUOX1	dual oxidase 1 precursor	NM_017434	2.521	0.529	2.17	0.449	2.42	0.507	Electron transport. Superoxide release. Hydrogen peroxide biosynthesis.
FOXD4	forkhead box D4 protein	AF452724	2.684	0.413	2.022	0.427	2.398	0.346	Transcription. Regulation of transcription, DNA-dependent.
FLJ43965	FLJ43965 protein	NM_207406	2.865	0.582	2.024	0.613	2.213	0.45	
PAX7	paired box gene 7 isoform 1	NM_002584	2.809	0.847	2.138	0.479	2.15	0.712	Regulation of transcription, DNA-dependent. Anti-apoptosis. Morphogenesis.
BARHL2	BarH-like 2	NM_020063	3.27	1.068	1.946	0.712	1.88	0.986	
MGC26690	hypothetical protein MGC26690	NM_152450	3.239	0.883	1.726	0.663	2.123	0.756	
LOC164153	similar to RIKEN cDNA 4930522D07	NM_203412	1.944	0.37	1.922	0.316	3.203	0.457	
VAX1	ventral anterior homeobox 1	NM_199131	2.761	0.775	2.057	0.691	2.222	0.891	
ADRA1A	alpha 1A adrenoceptor isoform 5b	AY491780	1.93	0.759	2.429	0.524	2.675	0.483	
FLJ46347	hypothetical LOC389064	NM_001005303	3.913	0.37	1.306	0.643	1.808	0.668	
SLC26A10	" solute carrier family 26, member 10"	NM_133489	2.102	0.654	2.452	0.406	2.437	0.32	Regulation of transcription, DNA-dependent.
FOXG1B	forkhead box G1B	BC050072	4.068	0.322	1.288	0.356	1.63	0.549	Transcription. Regulation of transcription, DNA-dependent. Regulation of transcription, DNA-dependent. Brain development.
GPR145	G protein-coupled receptor 145	NM_032503	3.235	0.572	1.779	0.516	1.964	0.517	Signal transduction. G-protein coupled receptor protein signaling pathway.
HOXD11	homeo box D11	NM_021192	3.179	0.469	2.065	0.579	1.724	0.616	Regulation of transcription, DNA-dependent. Development.
ATOH1	atonal homolog 1	NM_005172	3.675	0.722	1.318	0.572	1.968	0.99	Regulation of transcription, DNA-dependent. Central nervous system development.
RAX	RAX protein	BC051901	2.566	0.285	2.56	0.486	1.813	0.675	Transcription, DNA-dependent. Development. Visual perception.
EMX2	empty spiracles homolog 2	NM_004098	3.016	0.38	1.973	0.473	1.941	0.232	Regulation of transcription, DNA-dependent. Development.
TFAP2C	transcription factor AP-2 gamma	NM_003222	2.921	1.035	1.701	0.757	2.306	0.853	Transcription. Regulation of transcription from RNA polymerase II promoter. Cell-cell signaling.
N/A	PRO2206	AF119866	2.515	0.427	2.174	0.603	2.238	0.431	
HOXB13	homeo box B13	NM_006361	3.136	0.568	1.799	0.38	1.964	0.469	Regulation of transcription, DNA-dependent. Development. Epidermis development. Response to wounding.
CYP24A1	" cytochrome P450, family 24 precursor"	NM_000782	2.957	1.253	2.084	1.039	1.854	0.999	Electron transport.
N/A	N/A	AK125426	3.939	0.419	1.024	0.403	1.927	0.613	Protein ubiquitination.
N/A	CCK-B/gastrin receptoralternatively spliced.	AF239668	2.299	0.661	2.007	0.431	2.584	0.464	Phospholipase C activation. Phospholipase C activation. Positive regulation of cytosolic calcium ion concentration.
EFNA1	ephrin A1 isoform a precursor	NM_004428	3.016	0.551	1.738	0.507	2.132	0.615	Cell-cell signaling.
N/A	N/A	AK098343	2.366	0.943	2	0.547	2.491	0.905	
JPH3	JPH3 protein	BC008690	2.384	0.501	2.336	0.514	2.133	0.672	
N/A	choline acetyltransferase isoform S	AF305908	1.582	0.683	2.53	0.433	2.739	0.37	Synaptic transmission. Neurotransmitter biosynthesis.
NKX6-1	" NK6 transcription factor related, locus 1"	NM_006168	3.34	0.772	2.212	0.743	1.292	0.43	Regulation of transcription, DNA-dependent. Development. Organogenesis.
N/A	sodium dependent phosphate transporter isoform NaPi-IIb	AF146796	3.048	0.745	1.566	0.452	2.192	0.92	Phosphate metabolism. Phosphate transport.
SORL1	sortilin-related receptor containing LDLR class A repeats prepr	NM_003105	2.515	0.486	2.251	0.924	2.038	1.054	Lipid metabolism. Lipid transport. Receptor mediated endocytosis. Steroid metabolism. Cholesterol metabolism.
N/A	N/A	AK124550	2.533	0.303	1.637	0.25	2.625	0.28	
EOMES	eomesodermin	NM_005442	3.571	0.967	1.541	0.704	1.681	0.863	Transcription. Regulation of transcription, DNA-dependent. Morphogenesis.
GATA4	GATA binding protein 4	NM_002052	1.986	0.608	2.485	0.7	2.321	0.586	Regulation of transcription, DNA-dependent. Development.
CACNG4	voltage-dependent calcium channel gamma-4 subunit	NM_014405	3.143	1.173	1.335	0.385	2.31	0.931	Ion transport. Calcium ion transport.
GFRA1	GDNF family receptor alpha 1 isoform a preproprotein	NM_005264	3.134	0.302	1.684	0.638	1.966	0.458	Cell surface receptor linked signal transduction,
THBS4	thrombospondin 4 precursor	NM_003248	3.839	0.503	1.128	0.389	1.814	0.333	Substrate-bound cell migration, cell extension. Cell adhesion.
LHX2	LIM homeobox protein 2	NM_004789	3.019	0.795	1.824	0.645	1.918	0.698	Regulation of transcription, DNA-dependent.
TFCP2L3	transcription factor CP2-like 3	NM_024915	2.485	0.814	1.793	0.529	2.478	0.53	
HOXA9	homeobox protein A9 isoform a	NM_152739	3.518	0.436	1.769	0.588	1.458	0.343	Transcription. Regulation of transcription, DNA-dependent. Development.
TRIM36	tripartite motif protein 36	NM_018700	3.839	0.325	1.279	0.568	1.604	0.521	Protein ubiquitination.

RIPK4	ankyrin repeat domain 3	NM_020639			3.663	0.365	1.359	0.396	1.699	0.549	Protein amino acid phosphorylation. Protein amino acid phosphorylation.
PRDM6	PR-domain zinc finger protein 6 isoform Aalternatively spliced.	AF272898			2.959	0.275	1.758	0.677	2.003	0.421	Transcription. Regulation of transcription, DNA-dependent
ZAR1	zygote arrest 1	NM_175619			3.069	0.763	1.744	0.641	1.901	0.966	
HOXC10	homeo box C10	NM_017409			2.635	1.123	1.916	0.774	2.162	0.659	Regulation of transcription, DNA-dependent. Positive regulation of cell proliferation. Morphogenesis.
IRX3	iroquois homeobox protein 3	NM_024336			2.517	0.895	1.982	0.82	2.197	0.782	Regulation of transcription, DNA-dependent.
DMRTA2	doublesex-mab-3 (DM) domain	AJ301580			2.873	0.596	1.739	0.608	2.08	0.781	
MASS1	very large G-protein coupled receptor 1	NM_032119			3.562	0.479	1.554	0.381	1.57	0.887	Cell communication. Neuropeptide signaling pathway. Neurogenesis. Cell-cell adhesion.
COL25A1	COL25A1 protein	BC036669			3.117	0.436	2.053	0.57	1.507	0.416	Phosphate transport. Cell adhesion.
HOXB8	homeo box B8	NM_024016			3.903	0.312	1.441	0.585	1.332	0.4	Regulation of transcription, DNA-dependent. Development.
HOXC8	homeo box C8	NM_022658			2.74	0.624	1.829	0.542	2.093	0.777	Regulation of transcription, DNA-dependent. Development.
sox-10	SOX-10	X65666			2.737	0.726	2.222	0.716	1.701	0.819	
GRID2	" glutamate receptor, ionotropic, delta 2"	NM_001510			3.383	0.615	1.667	0.696	1.61	0.316	Ion transport. Glutamate signaling pathway. Synaptic transmission
MT1J	metallothionein 1J	NM_175622			2.866	0.418	1.688	0.457	2.105	0.556	
COL2A1	alpha 1 type II collagen isoform 1	NM_001844			2.637	0.734	2.06	0.682	1.958	0.815	Skeletal development. Phosphate transport. Cell adhesion. Perception of sound.
ALX3	aristaless-like homeobox 3	NM_006492			3.077	1.194	1.335	0.546	2.239	0.949	Regulation of transcription, DNA-dependent. Development.
COLEC12	collectin sub-family member 12 isoform II	NM_030781			3.132	0.947	1.98	0.861	1.534	0.84	Phosphate transport. Phagocytosis, recognition. Carbohydrate mediated signaling.
ALOX15	arachidonate 15-lipoxygenase	NM_001140			2.241	0.251	2.004	0.221	2.393	0.48	Electron transport. Lipid metabolism. Inflammatory response. Leukotriene biosynthesis.
LIPG	endothelial lipase	NM_006033			2.463	0.462	2.104	0.652	2.052	0.592	Lipid metabolism. Lipid catabolism.
N/A	N/A	AK127166			2.943	0.306	1.949	0.587	1.7	0.775	
GABRA2	GABRA2 protein	BC022488			2.801	0.966	1.971	0.908	1.814	1.015	
H2AFY2	core histone macroH2A2.2	BC016172			2.472	0.546	1.731	0.511	2.379	0.461	Nucleosome assembly. Chromosome organization and biogenesis (sensu Eukaryota).
N/A	winged helix transcription factor beta	AF343006			2.523	0.597	1.857	0.492	2.202	0.311	
N/A	N/A	AK096981			2.963	0.522	1.711	0.45	1.906	0.478	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
DLX3	distal-less homeo box 3	NM_005220			2.569	0.735	1.621	0.412	2.381	0.633	Skeletal development. Regulation of transcription, DNA-dependent. Development.
NPR1	natriuretic peptide receptor A/guanylate cyclase A (atrionatriure	NM_000906	1.312	1.738	1.225	0.405	2.914	0.379	2.427	0.513	CGMP biosynthesis. Protein amino acid phosphorylation. Cell surface receptor linked signal transduction.
T	transcription factor T	NM_003181			2.009	0.685	2.205	0.547	2.349	0.47	Regulation of transcription, DNA-dependent. Signal transduction. Mesoderm.
PAX2	paired box protein 2 isoform c	NM_003988			2.536	0.577	2.167	0.438	1.857	0.489	GTP biosynthesis. UTP biosynthesis. CTP biosynthesis. Regulation of transcription.
TBR1	" T-box, brain, 1"	NM_006593			3.568	0.878	1.308	0.791	1.683	0.942	Transcription. Regulation of transcription, DNA-dependent. Brain development.
LOC405753	similar to Numb-interacting homolog protein	NM_207581			1.571	0.78	2.442	0.443	2.541	0.38	
N/A	N/A	AK125088			2.973	0.204	1.804	0.599	1.771	0.561	
N/A	N/A	AK126468			2.053	0.767	1.833	0.845	2.654	0.555	CAMP biosynthesis. Intracellular signaling cascade.
LRP2	low density lipoprotein-related protein 2	NM_004525			2.749	0.452	1.546	0.345	2.239	0.501	Protein amino acid glycosylation. Lipid metabolism. Receptor mediated endocytosis.
SFRP2	secreted frizzled-related protein 2 precursor	NM_003013			2.901	0.817	1.535	0.644	2.078	0.789	Wnt receptor signaling pathway. Cell differentiation.
N/A	N/A	M23102			2.328	0.668	2.178	0.473	1.998	0.735	Protein amino acid phosphorylation. Transmembrane receptor protein tyrosine kinase signaling pathway.
CXCL14	small inducible cytokine B14 precursor	NM_004887			2.221	0.732	1.813	0.675	2.47	0.749	Chemotaxis. Inflammatory response. Signal transduction. Cell-cell signaling.
N/A	Unknown (protein for MGC:24860)	BC031812			2.223	0.643	1.761	0.633	2.512	0.659	
SCNN1B	" sodium channel, nonvoltage-gated 1, beta"	BC036352			2.331	0.74	2.028	0.574	2.129	0.437	Ion transport. Sodium ion transport. Excretion. Sensory perception.
DLK1	delta-like homolog	NM_003836			1.904	0.912	1.626	0.705	2.956	0.756	Development.
MGC10561	hypothetical protein MGC10561	BC004252			3.659	1.302	1.688	0.975	1.127	0.689	Chromatin assembly or disassembly. Regulation of transcription, DNA-dependent. Negative regulation of transcription.
ZBTB8	zinc finger and BTB domain containing 8	NM_144621			3.546	1.04	1.458	0.466	1.459	0.676	Transcription. Regulation of transcription, DNA-dependent
DKFZp434H168	hypothetical proteincDNA DKFZp434H168 (from clone DKFZp	AL117580			2.636	1.259	1.426	0.425	2.392	0.726	
HOXD1	homeo box D1	NM_024501			2.73	1.14	1.86	0.641	1.857	0.631	Regulation of transcription, DNA-dependent. Development.
WNT3	" wingless-type MMTV integration site family, member 3"	NM_030753			2.032	0.747	2.667	0.364	1.747	0.588	Frizzled-2 signaling pathway. Cell-cell signaling. Morphogenesis.
SPAG6	sperm associated antigen 6 isoform 1	NM_012443			3.267	0.57	1.567	0.287	1.606	0.479	Spermatid cell development.
N/A	Unknown (protein for MGC:75260)	BC067110			2.325	0.579	1.908	0.483	2.205	0.591	
WNT6	" wingless-type MMTV integration site family, member 6 precu	NM_006522			1.979	0.843	2.19	0.977	2.268	0.933	Frizzled-2 signaling pathway. Cell-cell signaling. Development.
MYH11	smooth muscle myosin heavy chain 11 isoform SM2	NM_022844			2.895	0.472	1.929	0.397	1.612	0.565	Striated muscle contraction. Muscle development.
HOXD10	homeo box D10	NM_002148			2.408	0.503	1.782	0.331	2.225	0.679	Regulation of transcription, DNA-dependent. Development.
N/A	N/A	AK125319			2.627	0.522	2.157	0.436	1.621	0.437	
FLJ33651	hypothetical protein FLJ33651	NM_182590			2.773	0.504	1.189	0.491	2.441	0.763	
NEUROG1	neurogenin 1	NM_006161			2.25	0.799	1.995	0.639	2.153	0.692	Transcription. Regulation of transcription from RNA polymerase II promoter. Neurogenesis. Cell differentiation.
OCLN	occludin	NM_002538			3.46	1.403	1.659	0.71	1.276	0.745	Protein complex assembly.
IRS4	insulin receptor substrate 4	NM_003604			2.977	0.795	1.896	0.737	1.514	0.706	Signal transduction.
JPH4	junctophilin 4	NM_032452			2.109	0.49	1.655	0.563	2.614	0.411	
TCF2	transcription factor 2 isoform bLF-B3 " variant hepatic nuclear f	NM_006481			2.42	0.44	1.702	0.686	2.25	0.545	Regulation of transcription, DNA-dependent. Positive regulation of transcription.
N/A	" prostaglandin E receptor, subtype EP3C"	X83860			2.74	0.516	1.779	0.516	1.85	0.697	Transcription, DNA-dependent. Signal transduction. G-protein coupled receptor protein signaling pathway.

LECT1	LECT1 protein	BC025659			2.318	0.553	1.738	0.275	2.305	0.383	Skeletal development. Proteoglycan metabolism. Cell differentiation.
LMO1	LIM domain only 1	NM_002315			2.531	0.505	2.36	0.562	1.463	0.498	Development. Cell proliferation.
TITF1	thyroid transcription factor 1	NM_003317			2.823	0.477	1.869	0.541	1.643	0.703	Regulation of transcription, DNA-dependent. Regulation of transcription, DNA-dependent.
SP7	osterix	NM_152860			1.465	0.837	2.093	0.45	2.775	0.5	
KIAA0644	KIAA0644 protein	AB014544			2.877	0.754	1.124	0.412	2.332	0.937	
FLJ13236	hypothetical protein FLJ13236	NM_024902			3.03	0.408	1.955	0.606	1.335	0.546	Protein folding.
N/A	N/AcDNA DKFZp761F169 (from clone DKFZp761F169).	AL833884			2.222	0.559	1.265	1.133	2.831	0.29	
RARB	" retinoic acid receptor, beta isoform 1"	NM_000965			3.554	0.884	1.17	1.096	1.576	0.725	Transcription. Regulation of transcription, DNA-dependent. Signal transduction.
MT1A	metallothionein 1A	NM_005946			2.572	0.601	1.688	0.355	2.037	0.425	
N/A	N/A	AK125488			3.039	0.481	1.378	0.54	1.861	0.36	
N/A	Unknown (protein for IMAGE:6023106)	BC040697			3.16	0.573	1.625	0.403	1.491	0.687	
FLJ44881	FLJ44881 protein	NM_207461			2.112	0.742	1.632	0.698	2.524	0.514	
FOXA1	forkhead box A1	NM_004496			3.325	0.498	1.283	0.646	1.657	0.675	Transcription. Regulation of transcription, DNA-dependent.
RUNX3	runt-related transcription factor 3	NM_004350			3.117	1.134	1.707	0.648	1.437	0.809	Regulation of transcription, DNA-dependent. Transcription from RNA polymerase II promoter. Cell proliferation.
CR1	complement component (3b/4b) receptor 1 isoform S	NM_000651			3.455	0.627	1.055	0.313	1.75	0.629	Immune response. Complement activation, classical pathway.
KCNA5	" potassium voltage-gated channel, shaker-related subfamily,	NM_002234			2.725	0.539	1.419	0.533	2.11	0.621	Cation transport. Potassium ion transport.
COCH	" coagulation factor C homolog, cochlin precursor"	NM_004086			2.697	0.819	1.502	0.874	2.045	1.113	Perception of sound.
GATA2	GATA binding protein 2	NM_032638			2.903	0.407	1.422	0.521	1.916	0.748	Transcription. Regulation of transcription, DNA-dependent. Transcription from RNA polymerase II promoter. Phagocytosis.
MLN	motilin	NM_002418			2.298	0.411	1.545	0.534	2.38	0.538	G-protein coupled receptor protein signaling pathway. Cell-cell signaling. Regulation of physiological process.
RTN4RL2	reticulon 4 receptor-like 2	NM_178570	1.263	1.051	2.751	0.999	2	1.05	1.467	1.06	
MT1F	metallothionein 1F	NM_005949			2.681	0.338	1.736	0.427	1.783	0.492	
NKX2-2	" NK2 transcription factor related, locus 2"	NM_002509			3.152	0.473	1.457	0.576	1.576	0.687	Regulation of transcription, DNA-dependent. Development. Brain development.
GRIN2D	N-methyl-D-aspartate receptor subunit 2D precursor	NM_000836			1.786	0.946	2.151	0.685	2.24	0.528	Ion transport. Signal transduction. Synaptic transmission.
NKX2-8	" NK2 transcription factor related, locus 8"	NM_014360			2.585	0.927	1.797	0.676	1.788	0.366	Regulation of transcription, DNA-dependent. Transcription from RNA polymerase II promoter. Development.
VSX1	visual system homeobox 1 protein isoform a	NM_014588			2.22	0.678	1.783	0.657	2.158	0.774	Regulation of transcription, DNA-dependent. Development. Sensory perception. Visual perception.
GRP	gastrin-releasing peptide	NM_002091			2.152	0.479	2.027	0.731	1.98	0.665	Signal transduction. Neuropeptide signaling pathway.
SLC17A7	" solute carrier family 17, member 7"	NM_020309			2.822	0.623	1.008	0.587	2.317	0.833	Transport. Phosphate transport.
KIF12	kinesin family member 12	NM_138424			2.21	0.892	1.591	0.383	2.336	0.521	
KIAA1355	KIAA1355 protein	AB037776			2.412	0.478	1.301	0.455	2.424	0.718	
OTX2	orthodenticle 2 isoform a	NM_021728			2.768	0.77	1.479	0.604	1.883	0.338	Regulation of transcription, DNA-dependent. Regulation of transcription, DNA-dependent. Development. Development.
SEMA5B	semaphorin 5B	NM_018987			3.069	0.444	1.103	0.739	1.956	0.563	Development. Neurogenesis. Cell differentiation.
AARSL	AARSL protein	BC040881			1.861	0.718	2.079	1.13	2.182	1.201	
SELV	selenoprotein V	NM_182704			2.023	0.686	2.241	0.675	1.856	0.45	
RFX4	regulatory factor X4 isoform c	NM_213594			2.399	0.467	1.907	0.456	1.793	0.465	Regulation of transcription, DNA-dependent.
MMP24	matrix metalloproteinase 24 (membrane-inserted)	NM_006690			2.004	0.741	1.696	0.625	2.394	0.623	Proteolysis and peptidolysis.
N/A	N/A	AK095610			1.749	0.722	1.655	0.406	2.69	0.432	
N/A	metallothionein	AF136177			2.678	0.63	1.667	0.574	1.739	0.75	
WNT10A	" wingless-type MMTV integration site family, member 10A, pr	BC052234			1.903	0.51	1.979	0.627	2.19	0.853	Frizzled-2 signaling pathway. Development.
PPP1R1B	" protein phosphatase 1, regulatory (inhibitor) subunit 1B"	NM_032192			1.753	0.561	1.869	0.649	2.446	0.474	Signal transduction.
ESR1	estrogen receptor 1	NM_000125			2.136	0.83	1.492	0.817	2.429	0.855	Regulation of transcription, DNA-dependent. Signal transduction. Cell growth.
HLF	hepatic leukemia factor	NM_002126			2.47	0.683	1.484	0.947	2.098	0.991	Regulation of transcription, DNA-dependent. Transcription from RNA polymerase II promoter. Development.
ACHE	acetylcholinesterase isoform E4-E5 precursor	NM_015831			2.1	0.922	2.239	0.943	1.712	0.698	Acetylcholine catabolism in synaptic cleft. DNA replication. Cell adhesion. Synaptogenesis. Muscle development.
FOXN4	forkhead box N4	NM_213596			2.835	0.865	1.591	0.525	1.612	0.582	Transcription. Regulation of transcription, DNA-dependent.
N/A	N/A	AK096323			2.62	0.758	1.217	0.641	2.2	0.537	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
POU2F3	POU transcription factor	NM_014352			1.987	0.798	1.782	0.683	2.263	0.803	Regulation of transcription from RNA polymerase II promoter. Epidermis development.
ITGB2	" integrin beta chain, beta 2 precursor" " macrophage antigen	NM_000211			2.159	0.733	1.281	0.73	2.587	0.546	Apoptosis. Inflammatory response. Leukocyte cell adhesion. Cell-matrix adhesion. Integrin-mediated signaling pathway.
N/A	N/A	AK096196			2.624	1.063	1.648	0.532	1.735	0.625	
KIF5A	kinesin family member 5A	NM_004984			2.673	0.592	1.212	0.384	2.122	0.497	Electron transport. Microtubule-based movement. Synaptic transmission.
GABRA4	" gamma-aminobutyric acid A receptor, alpha 4 precursor"	NM_000809			3.226	0.625	1.53	0.486	1.247	0.669	Ion transport. Chloride transport. Gamma-aminobutyric acid signaling pathway.
N/A	N/A	AK097430			2.295	0.923	1.693	0.68	2.008	0.905	
N/A	N/A	AK091698			1.724	0.564	2.071	0.54	2.19	1.009	
N/A	N/A	AK096088			2.043	0.494	1.63	0.841	2.309	0.589	Phosphate metabolism. Ion transport. Sodium ion transport. Phosphate transport. Fluid secretion.
EVA1	epithelial V-like antigen 1 precursor	NM_005797			2.173	0.544	1.386	0.454	2.418	0.331	Cell adhesion. Homophilic cell adhesion. Morphogenesis.
MYOD1	myogenic factor 3	NM_002478			1.079	0.739	2.291	0.493	2.599	0.837	Regulation of transcription, DNA-dependent.
FLJ42875	FLJ42875 protein	NM_001004337			3.019	0.738	1.228	0.445	1.721	0.609	
PTGIS	prostaglandin I2 (prostacyclin) synthase	NM_000961			2.105	0.643	1.47	0.633	2.374	0.902	Prostaglandin biosynthesis. Electron transport. Lipid metabolism. Fatty acid biosynthesis.

HOXC4	homeo box C4	NM_014620			3.217	0.493	1.265	0.5	1.462	0.747	Regulation of transcription, DNA-dependent. Development.
NMNAT2	nicotinamide mononucleotide adenylyltransferase 2 isoform 1	NM_015039			2.558	1.151	1.653	1.085	1.732	0.995	Phospholipid biosynthesis. Biosynthesis. NAD biosynthesis.
N/A	N/A	AK098068			1.86	0.837	1.853	0.608	2.227	0.862	
HEY2	hairy/enhancer-of-split related with YRPW motif 2	NM_012259			3.145	1.069	1.497	0.956	1.296	0.979	Regulation of transcription, DNA-dependent. Neurogenesis.
TBX20	T-box transcription factor TBX20	NM_020417			2.978	0.668	1.196	0.707	1.76	0.661	
PAX4	paired box gene 4	NM_006193			2.081	0.826	1.374	0.431	2.474	0.471	Regulation of transcription, DNA-dependent. Organogenesis. Cell differentiation.
N/A	N/A	AK125823			2.197	0.489	1.489	0.596	2.23	0.443	
SOX14	SRY-box 14	NM_004189			1.517	0.628	1.919	0.642	2.477	0.55	Transcription. Regulation of transcription, DNA-dependent. Neurogenesis.
N/A	EG-VEGF	AY358683			2.311	0.646	1.046	0.546	2.548	0.433	Regulation of cell cycle. Cell proliferation.
LOC283514	LOC283514 protein	BC041372			1.814	0.747	1.328	0.774	2.754	0.945	
HOXC13	homeo box C13	NM_017410			2.018	0.849	1.465	0.394	2.413	0.616	Regulation of transcription, DNA-dependent. Morphogenesis.
HBM	hemoglobin mu chain	NM_001003938			1.526	0.351	2.508	0.487	1.85	0.477	Transport. Oxygen transport.
N/A	N/A	AK129645			3.371	0.245	1.21	0.414	1.299	0.512	
GJB2	" gap junction protein, beta 2, 26kDa (connexin 26)"	NM_004004			2.918	1.203	1.635	0.685	1.325	0.848	Transport. Cell-cell signaling. Perception of sound.
NPAS3	neuronal PAS domain protein 3	NM_022123			3.26	0.994	1.082	0.517	1.535	0.687	Transcription. Regulation of transcription, DNA-dependent. Signal transduction.
ACOXL	ACOXL protein	BC022268			2.143	0.461	1.541	0.443	2.193	0.508	
VIAAT	vesicular inhibitory amino acid transporter	NM_080552			2.281	0.573	1.439	0.896	2.15	0.974	Neurotransmitter transport. Amino acid transport.
LAD1	ladinin 1	NM_005558			2.001	0.492	1.865	0.563	2.003	0.733	
POU4F2	" POU domain, class 4, transcription factor 2"	NM_004575			1.849	0.573	1.827	0.526	2.187	0.705	Negative regulation of transcription from RNA polymerase II promoter. Eye morphogenesis. Neurogenesis.
METH2	METH2 protein	AF060153			2.805	0.641	1.035	0.636	2.023	0.615	Proteolysis and peptidolysis. Negative regulation of cell proliferation.
SP8	Sp8 transcription factor isoform 2	NM_198956			2.309	0.615	1.154	0.724	2.396	0.635	
PKD2L1	polycystic kidney disease 2-like 1	NM_016112			1.416	0.878	2.152	0.396	2.288	0.541	Cation transport. Cation transport. Signal transduction.
SPOCK2	" sparc/osteonectin, cwcv and kazal-like domains proteoglyca	NM_014767			2.681	0.898	1.173	1.301	2	0.56	Synaptogenesis. Extracellular matrix organization and biogenesis. Regulation of cell differentiation.
DKFZp686L1857	hypothetical proteincDNA DKFZp686L1857 (from clone DKFZ	BX538158			2.862	0.592	1.126	0.617	1.858	0.358	Neurotransmitter transport. Intracellular protein transport.
FLJ42220	FLJ42220 protein	NM_207441			2.396	0.625	1.386	0.691	2.061	0.738	
PROK2	prokineticin 2	NM_021935			2.661	1.221	1.141	0.556	2.039	1.07	Activation of MAPK. Angiogenesis. Anti-apoptosis. Chemotaxis. Inflammatory response.
PLA2G7	" phospholipase A2, group VII"	NM_005084			2.222	0.611	1.802	0.754	1.811	0.643	Inflammatory response. Lipid catabolism.
PKP1	plakophilin 1 isoform 1b	NM_000299			1.803	0.48	1.527	0.715	2.503	0.595	Cell adhesion. Signal transduction. Cell-cell signaling.
INSM1	insulinoma-associated 1	NM_002196			2.394	0.772	1.79	0.872	1.646	0.603	Transcription. Regulation of transcription, DNA-dependent.
N/A	N/A	AK091777			2.699	0.878	1.478	0.588	1.639	0.639	ATP-dependent proteolysis. Protein ubiquitination.
TBC1D1	" TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1"	NM_015173	1.044	1.099	2.153	0.766	1.717	0.616	1.943	0.717	
GAD1	glutamate decarboxylase 1 isoform GAD67	NM_000817			2.66	0.309	1.44	0.317	1.713	0.536	Amino acid metabolism. Glutamate decarboxylation to succinate. Synaptic transmission. Protein-pyridoxal-5-phosphate linkage.
N/A	N/A	AK126839			1.679	0.75	1.999	1.102	2.134	1.055	
KCNAB1	" potassium voltage-gated channel, shaker-related subfamily,	NM_172159			2.187	0.693	1.577	0.751	2.047	0.59	Ion transport. Potassium ion transport. Potassium ion transport.
PHOX2A	paired-like homeobox 2a	NM_005169			1.765	0.454	2.1	0.744	1.945	0.868	Regulation of transcription, DNA-dependent. Neurotransmitter metabolism.
NPPC	natriuretic peptide precursor C	NM_024409			1.817	0.666	2.002	0.579	1.988	0.625	Regulation of blood pressure. Regulation of vasoconstriction.
LRAT	lecithin:retinol acyltransferase isoform 1	AY546085			2.265	0.59	1.498	0.574	2.037	0.629	Sensory perception. Visual perception.
N/A	forkhead homolog	L12142			2.665	0.564	1.597	0.617	1.535	0.578	
FLJ10052	hypothetical protein FLJ10052	NM_017982			2.355	1.062	1.824	0.748	1.613	0.597	
SYT6	synaptotagmin VI	NM_205848			1.871	0.695	1.915	0.487	2.003	0.52	Transport.
CDO1	" cysteine dioxygenase, type I"	NM_001801			2.206	0.748	1.921	0.82	1.656	0.522	L-cysteine metabolism.
HOXC5	homeo box C5	NM_018953			2.469	0.5	1.022	0.33	2.291	0.423	Regulation of transcription from RNA polymerase II promoter. Development.
N/A	hepatocyte growth factor-like protein homolog	U28055			1.606	0.353	1.614	0.251	2.558	0.29	Proteolysis and peptidolysis. Negative regulation of blood coagulation.
CCK	cholecystokinin preproprotein	NM_000729			1.621	1.151	1.755	0.422	2.394	0.451	Signal transduction.
HRLP5	HRLP5 protein	BC034222			2.888	0.979	1.408	0.724	1.473	0.809	
KCNQ4	potassium voltage-gated channel KQT-like protein 4 isoform a	NM_004700			2.432	0.735	1.904	0.682	1.43	0.52	Cation transport. Potassium ion transport. Perception of sound.
FLJ00220	FLJ00220 protein	AK074147			1.959	1.014	1.441	0.695	2.366	1.238	Skeletal development. Development.
MCTP1	multiple C2-domains with two transmembrane regions 1 isofor	NM_024717			2.568	0.807	1.651	0.847	1.545	0.72	
TNK1	" tyrosine kinase, non-receptor, 1"	NM_003985	1.105	1.558	1.726	1.395	1.437	0.485	2.599	0.578	Autophosphorylation.
DKFZp686P24273	hypothetical proteincDNA DKFZp686P24273 (from clone DKFZ	BX538083			2.339	0.276	1.23	0.264	2.19	0.622	
SIX2	SIX2	AF332197			2.572	0.828	1.64	0.763	1.542	0.916	Regulation of transcription, DNA-dependent. Transcription from RNA polymerase II promoter. Morphogenesis.
N/A	N/A	AK093202			2.271	0.357	1.464	0.235	2.016	0.29	
CLIC6	chloride channel form Balternatively spliced.	AF448439			1.968	0.837	1.641	0.407	2.135	0.693	Ion transport. Chloride transport.
N/A	N/A	AK123969			1.818	0.923	1.492	0.569	2.432	0.773	Carbohydrate metabolism. Glycogen metabolism. Signal transduction.
FLJ33655	hypothetical protein FLJ33655	BC067734			1.429	0.608	1.939	0.501	2.373	0.631	
RDH13	retinol dehydrogenase 13 (all-trans and 9-cis)	NM_138412			1.873	1.235	1.566	1.318	2.299	1.339	Metabolism.

ROPN1	AKAP-binding sperm protein ropporin	NM_017578			2.587	0.556	1.022	0.406	2.128	0.921	Cytokinesis. Signal transduction. Rho protein signal transduction. Spermatogenesis. Acrosome reaction.
KCNK10	" potassium channel, subfamily K, member 10 isoform 1"	NM_021161			2.214	0.86	1.422	0.754	2.101	0.694	Ion transport. Potassium ion transport. Signal transduction.
N/A	MU-MB-20.220	AY130010			2.545	0.929	1.66	0.493	1.528	0.926	Transcription. Regulation of transcription, DNA-dependent.
VAX2	ventral anterior homeobox 2	NM_012476			2.471	0.959	1.133	0.66	2.118	1.046	Regulation of transcription, DNA-dependent. Transcription from RNA polymerase II promoter. Ectoderm development.
DUOX2	dual oxidase 2 precursor	NM_014080			1.46	0.58	2.143	0.437	2.113	0.598	Electron transport. Superoxide release. Hydrogen peroxide biosynthesis.
ZDHHC22	" zinc finger, DHHC domain containing 22"	NM_174976			1.901	0.861	1.693	0.725	2.118	0.635	
KIAA1963	KIAA1963 protein	AB075843			2.093	0.997	1.988	0.654	1.629	0.557	
BHMT	betaine-homocysteine methyltransferase	BC012616			1.802	0.335	1.734	0.392	2.171	0.437	Protein amino acid methylation. Regulation of homocysteine metabolism.
INSRR	insulin receptor-related receptor precursor	NM_014215			1.904	0.528	2.04	0.37	1.761	0.485	Protein amino acid phosphorylation. Transmembrane receptor protein tyrosine kinase signaling pathway.
CXCR4	chemokine receptor CXCR4-Lo	AF147204			2.166	0.463	1.77	0.531	1.768	0.771	Signal transduction. G-protein coupled receptor protein signaling pathway.
ZNFN1A3	" zinc finger protein, subfamily 1A, 3 (Aiolos) isoform 1"	NM_012481	1.421	1.186	3.152	0.581	1.382	0.701	1.168	0.291	
THPO	thrombopoietin isoform 1 precursor	NM_000460			1.743	1.053	1.628	0.602	2.326	0.716	Development. Cell proliferation.
N/A	N/A	AK126633			1.133	0.865	2.147	0.353	2.411	0.513	
MTE	MTE	AF348997			2.388	0.433	1.163	0.491	2.138	0.376	
TRAD	serine/threonine kinase with Dbl- and pleckstrin homology dom	NM_007064			2.563	1.09	1.541	0.398	1.572	0.658	
FLJ23191	hypothetical protein FLJ23191	NM_024574			2.862	0.769	1.116	0.818	1.696	0.748	
HOXC6	homeo box C6 isoform 2	NM_153693	1.042	1.323	2.971	0.65	1.39	0.539	1.311	0.761	Regulation of transcription from RNA polymerase II promoter. Development.
FOXD4L2	FOXD4-like 2	NM_199135			2.264	0.39	1.347	0.244	2.046	0.178	Transcription. Regulation of transcription, DNA-dependent.
HBA2	HBA2 protein	BC005931	1.538	1.572	1.62	0.399	1.81	0.351	2.225	0.512	Transport. Oxygen transport.
LHX8	LIM homeobox 8	NM_001001933			1.398	0.515	1.644	0.852	2.609	0.424	
IHH	IHH protein	BC034757			1.51	0.573	2.138	1.291	1.99	1.046	Proteolysis and peptidolysis. Cell-cell signaling. Development. Intein-mediated protein splicing.
FAM43B	" family with sequence similarity 43, member B"	NM_207334			1.742	0.633	1.644	0.551	2.246	0.616	
FOXD4b	forkhead box protein D4b	NM_199244			2.335	0.45	1.32	0.42	1.976	0.246	Regulation of transcription, DNA-dependent.
CX36	connexin-36	NM_020660			1.984	0.721	1.801	0.401	1.842	0.774	Cell communication.
SLC7A10	" solute carrier family 7, member 10"	NM_019849			1.571	0.628	2.225	0.7	1.83	0.468	Transport. Neutral amino acid transport.
IL12RB2	" interleukin 12 receptor, beta 2 precursor"	NM_001559			1.484	0.218	1.958	0.844	2.182	1.269	Cell surface receptor linked signal transduction. Positive regulation of cell proliferation.
GPR49	G protein-coupled receptor 49	NM_003667			2.644	0.544	1.36	0.314	1.616	0.314	Signal transduction. G-protein coupled receptor protein signaling pathway.
GHSR	growth hormone secretagogue receptor isoform 1a	NM_198407			1.527	0.502	1.609	0.342	2.484	0.42	Signal transduction. G-protein coupled receptor protein signaling pathway.
POU3F2	" POU domain, class 3, transcription factor 2"	NM_005604	1.444	0.876	2.771	0.716	1.829	0.698	1.019	0.63	Regulation of transcription, DNA-dependent.
RXRG	" retinoid X receptor, gamma"	NM_006917			2.038	0.516	1.491	0.317	2.085	0.359	Transcription. Regulation of transcription, DNA-dependent.
LRRN6D	leucine rich repeat neuronal 6D	NM_001004432			1.933	0.418	1.185	0.459	2.495	0.452	
KIAA0473	KIAA0473 protein	AB007942			1.86	0.291	1.345	0.425	2.403	0.619	Protein folding. Protein amino acid dephosphorylation. Cell cycle. Negative regulation of cell cycle.
FOXD3	forkhead box D3	NM_012183			2.814	0.451	1.469	0.469	1.323	0.384	Negative regulation of transcription from RNA polymerase II promoter. Embryonic development (sensu Mammalia).
NODAL	nodal-related protein	NM_018055			1.494	0.715	1.97	0.496	2.138	0.415	
N/A	homeodomain protein (50 AA)	X52402			1.892	0.775	1.703	0.772	2.006	0.51	Regulation of transcription from RNA polymerase II promoter. Development.
FOXD4L1	forkhead box D4-like 1	NM_012184			2.25	0.275	1.37	0.318	1.98	0.304	Transcription. Regulation of transcription, DNA-dependent.
ICSBP1	interferon consensus sequence binding protein 1	NM_002163			2.815	0.639	1.2	0.436	1.58	0.448	Negative regulation of transcription from RNA polymerase II promoter. DNA-dependent. Immune response.
ADMP	ADMP	NM_145035			3.036	0.673	1.022	0.384	1.533	0.782	
TNNT1	TNNT1 protein	BC022086			2.027	0.787	1.463	0.331	2.096	0.637	Regulation of muscle contraction. Muscle development.
KAL1	Kallmann syndrome 1 protein	NM_000216			1.442	0.653	1.405	0.696	2.732	1.12	Cell motility. Chemotaxis. Cell adhesion. Axon guidance.
NXPH2	neurexophilin 2	NM_007226			2.016	1.138	1.582	0.782	1.98	1.526	Neuropeptide signaling pathway.
OTP	orthopedia	NM_032109			2.698	0.491	1.36	0.519	1.516	0.469	Regulation of transcription, DNA-dependent. Development.
RGMA	" RGM domain family, member A"	NM_020211			2.033	0.562	2.07	1.095	1.468	0.775	
SHH	sonic hedgehog preproprotein	NM_000193			2.393	0.387	1.531	0.602	1.638	0.577	Proteolysis and peptidolysis. Cell-cell signaling. Development. Ventral midline development. Mesoderm cell fate dete.
SLITRK3	slit and trk like 3 protein	NM_014926			2.516	0.661	1.446	0.408	1.597	0.361	
TNFRSF11A	" tumor necrosis factor receptor superfamily, member 11a prec	NM_003839			2.719	0.647	1.425	0.367	1.411	0.463	Immune response. Signal transduction. Cell-cell signaling. Perception of sound. Positive regulation of cell proliferation.
WNT1	" wingless-type MMTV integration site family, member 1 precu	NM_005430			1.486	0.706	1.971	0.284	2.097	0.444	Frizzled-2 signaling pathway. Spermatogenesis. Central nervous system development. Morphogenesis.
SIAT8D	sialyltransferase 8D isoform a	NM_005668			2.389	0.799	1.788	0.874	1.377	0.718	Protein amino acid glycosylation. N-glycan processing. Neurogenesis. Oligosaccharide metabolism.
TNFRSF8	" tumor necrosis factor receptor superfamily, member 8 isoforr	NM_001243			1.441	0.298	2.158	0.46	1.954	0.526	Signal transduction. Negative regulation of cell proliferation.
soxB	N/A	X71137			1.958	0.879	1.934	0.836	1.661	0.625	
N/A	N/A	AK056317			1.975	0.636	1.458	0.473	2.118	0.732	Proteolysis and peptidolysis. Proteolysis and peptidolysis. Development.
UCP1	uncoupling protein 1	NM_021833	1.303	1.168	2.638	0.504	1.421	0.356	1.486	0.644	Generation of precursor metabolites and energy. Transport. Mitochondrial transport. Proton transport.
MTM	metallothionein M	NM_175620			1.945	0.634	1.438	0.38	2.146	0.541	
FOXE3	forkhead box E3	NM_012186			1.769	0.317	1.638	0.623	2.122	0.684	Transcription. Regulation of transcription, DNA-dependent. Development.
KIAA1914	KIAA1914 protein isoform 1	NM_001001936			2.485	0.832	1.248	0.354	1.775	0.906	
SLC5A5	" solute carrier family 5 (sodium iodide symporter), member 5"	NM_000453			1.899	0.701	1.645	0.783	1.962	0.596	Ion transport. Sodium ion transport.

SP5	SP5 protein	BC069026			1.987	0.725	1.836	0.309	1.679	0.509	
MAP6	microtubule-associated protein 6 isoform 2	NM_207577			2.418	0.697	1.554	0.46	1.524	0.505	
SLC6A4	solute carrier family 6 member 4	NM_001045			2.986	0.674	1.232	0.772	1.272	0.36	Neurotransmitter uptake. Serotonin transport.
CDH3	" cadherin 3, type 1, preproprotein"	BC041846			2.076	0.382	1.504	0.67	1.906	0.441	Cell adhesion. Homophilic cell adhesion. Sensory perception. Visual perception.
ONECUT2	" one cut domain, family member 2"	NM_004852			2.259	1.008	1.32	0.624	1.901	0.876	Regulation of transcription, DNA-dependent. Organogenesis.
ARHGEF7	Rho guanine nucleotide exchange factor 7 isoform b	NM_145735			2.828	0.577	1.295	0.48	1.351	0.827	Signal transduction.
FLJ46156	FLJ46156 protein	NM_198499			2.569	0.713	1.479	0.555	1.424	0.623	
RFXDC1	regulatory factor X domain containing 1	NM_173560			1.706	0.486	1.501	0.491	2.264	0.618	
ONECUT1	" one cut domain, family member 1"	NM_004498			2.332	0.661	1.3	0.628	1.839	0.517	Regulation of transcription, DNA-dependent.
PUNC	putative neuronal cell adhesion molecule	NM_004884			2.209	1.037	1.318	0.939	1.941	0.94	
TCF15	TCF15 protein	BC067836			2.233	1.313	1.366	0.614	1.862	1.121	Regulation of transcription from RNA polymerase II promoter. Mesoderm development.
N/A	N/A	AK056896			1.987	0.84	1.334	0.571	2.14	0.662	
RNF39	HZFw1 protein isoform 1	NM_025236			2.421	0.348	1.462	0.52	1.577	0.478	Protein ubiquitination.
GSH1	homeobox protein Gsh-1	NM_145657			2.199	0.77	1.386	0.5	1.862	0.622	Regulation of transcription, DNA-dependent. Development.
KIAA1916	KIAA1916 protein	AB067503			1.544	0.742	1.862	0.378	2.035	0.635	
N/A	N/A	AK124544			3.238	0.768			2.198	0.423	
KIAA1247	KIAA1247 protein	AB033073			1.798	0.487	1.826	0.393	1.809	0.655	Amino acid metabolism. Metabolism. Heparan sulfate proteoglycan metabolism.
SLC10A4	" solute carrier family 10 (sodium/bile acid cotransporter family	NM_152679			3.066	0.644			2.365	0.749	Sodium ion transport.
C20orf127	chromosome 20 open reading frame 127	NM_080757			2.048	0.734	1.33	0.673	2.052	0.748	
WNT3A	" wingless-type MMTV integration site family, member 3A"	NM_033131			2.044	0.728	1.586	0.462	1.797	0.645	
MGC35555	hypothetical protein MGC35555	NM_178565			2.55	0.434	1.467	0.594	1.405	0.703	
N/A	MSTP061	AF117225			1.722	0.671	1.625	0.598	2.069	0.795	
CG-6	brain protein	AF155065			2.633	0.593	1.263	0.639	1.513	0.787	
N/A	N/A	AK126846			1.851	0.598	1.352	0.518	2.204	0.425	Signal transduction. Transmembrane receptor protein tyrosine kinase signaling pathway. Neurogenesis.
MCF2L2	Rho family guanine-nucleotide exchange factor	NM_015078			2.417	0.448	1.712	0.324	1.275	0.484	
LOC126248	hypothetical protein LOC126248	NM_173479	3.265	0.315	2.145	0.223	1.856	0.272	1.401	0.192	
N/A	N/A	AK125200			1.58	0.23	1.894	0.693	1.925	0.425	
PTH2	phosphatase and tensin homolog 2	AF019083			3.149	0.458	1.028	0.346	1.213	0.69	Protein amino acid dephosphorylation. Cell cycle. Negative regulation of cell cycle.
SSTR2	somatostatin receptor 2	NM_001050			2.167	0.642	1.311	0.478	1.907	0.717	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism. Metabolism.
GRIN2C	N-methyl-D-aspartate receptor subunit 2C precursor	NM_000835			1.138	0.495	2.373	0.642	1.871	0.779	Ion transport. Glutamate signaling pathway. Synaptic transmission.
DMRT1	doublesex and mab-3 related transcription factor 1	NM_021951			2.065	0.593	1.349	0.591	1.967	0.451	Regulation of transcription, DNA-dependent. Sex determination. Sex differentiation. Male gonad development.
PTPRZ1	" protein tyrosine phosphatase, receptor-type, Z polypeptide 1	NM_002851			2.832	1.031	1.197	0.715	1.349	0.919	Protein amino acid dephosphorylation. One-carbon compound metabolism. Central nervous system development.
LOC349136	LOC349136 protein	BC047921			1.53	0.738	2.018	0.621	1.821	0.834	Electron transport.
GAL	galanin preproprotein	NM_015973			1.457	1.05	1.732	0.74	2.172	0.868	Smooth muscle contraction. Neuropeptide signaling pathway. Insulin secretion. Growth hormone secretion.
FLJ44815	FLJ44815 protein	NM_207454			1.451	0.86	1.867	0.673	2.041	0.629	
FBXO39	F-box protein 39	NM_153230			1.834	0.874	1.477	0.437	2.047	0.681	
B4GalNac-T3	" beta 1,4-N-acetylgalactosaminyltransferase-transferase-III"	NM_173593			2.217	0.858	1.277	0.432	1.862	0.978	
N/A	N/A	AK124198			1.215	0.921	2.286	0.674	1.85	0.468	
R-spondin	hypothetical protein FLJ40906	NM_173640			2.393	1.059	1.382	0.719	1.574	0.797	Electron transport.
SOX7	SRY-box 7	NM_031439			2.331	0.709	1.745	0.515	1.272	0.605	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism. Metabolism.
MT1B	metallothionein 1B	NM_005947			1.914	0.612	1.258	0.35	2.176	0.257	
N/A	chordin Like	AY358522			2.192	1.065	1.1	0.524	2.055	0.881	Cell differentiation.
N/A	N/A	AK128329			1.674	0.678	1.692	0.713	1.971	0.65	
IGFBP2	insulin-like growth factor binding protein 2 (36kD)	NM_000597			1.813	0.828	1.426	0.894	2.095	0.844	Regulation of cell growth.
EPN3	epsin 3	NM_017957			1.808	0.679	1.296	0.285	2.229	0.608	
N/A	Unknown (protein for IMAGE:4819956)	BC018035			1.541	0.718	1.949	0.569	1.838	0.889	
OVOL1	OVO-like 1 binding protein	NM_004561			1.732	0.37	1.944	0.473	1.647	0.478	Regulation of transcription, DNA-dependent. Spermatogenesis.
BIK	BCL2-interacting killer	NM_001197			2.234	0.993	1.494	0.458	1.592	0.778	
FOXQ1	forkhead box Q1	NM_033260			2.41	0.545	1.171	0.305	1.732	0.534	Regulation of transcription, DNA-dependent.
LRFN5	leucine rich repeat and fibronectin type III domain containing 5	NM_152447			1.704	1.384	1.374	0.912	2.234	0.829	
N/A	N/A	AK125333			1.278	0.548	1.8	0.497	2.219	0.481	
JPH3	junctophilin 3	NM_020655			1.965	0.693	1.359	0.371	1.973	0.987	
CAM-KIIN	CaM-KII inhibitory protein	NM_033259			2.317	0.923	1.628	0.797	1.35	0.611	Proteolysis and peptidolysis. Cell-cell signaling. Cell-cell signaling. Brain development.
EFCBP1	EF hand calcium binding protein 1	NM_022351			2.168	1.036	1.124	0.384	1.992	0.454	Antibiotic biosynthesis.
N/A	G protein-coupled receptor PGR10	AY255534			2.239	0.664	1.411	0.37	1.612	0.324	
NEUROG3	neurogenin 3	NM_020999			1.809	0.693	1.46	0.321	1.992	0.574	Transcription. Central nervous system development. Peripheral nervous system development.

C20orf86	chromosome 20 open reading frame 86	NM_080674			2.649	0.927	1.527	0.724	1.083	0.53	Protein modification.
SPATS1	" spermatogenesis associated, serine-rich 1"	NM_145026			2.172	0.678	1.327	0.447	1.756	0.772	
ESX1L	" extraembryonic, spermatogenesis, homeobox 1-like"	NM_153448			2.726	0.571	1.118	0.533	1.409	0.429	
C1QTNF4	C1q and tumor necrosis factor related protein 4	NM_031909			1.396	0.529	1.395	0.597	2.461	0.749	
NOL4	nucleolar protein 4	NM_003787			2.226	0.522	1.502	0.82	1.522	0.727	
TBX21	T-box 21	NM_013351			1.798	0.979	1.605	0.441	1.84	0.717	Transcription. Regulation of transcription, DNA-dependent. Development.
ASTN	astrotactin isoform 1	NM_004319			3.016	0.387			2.227	0.515	Cell adhesion. Neuronal cell adhesion. Cell migration.
PRPH	peripherin	BC032703			1.68	0.428	1.424	0.375	2.131	0.304	
GPR12	G protein-coupled receptor 12	NM_005288			2.12	1.048	1.632	0.754	1.481	0.943	Signal transduction. G-protein coupled receptor protein signaling pathway.
GPR101	G protein-coupled receptor 101	NM_054021			1.2	0.393	2.259	0.464	1.774	0.506	
KCNA2	" potassium voltage-gated channel, shaker-related subfamily,	NM_004974			1.264	0.432	1.868	0.749	2.1	0.776	Cation transport. Potassium ion transport. Potassium ion transport.
GNG4	" guanine nucleotide binding protein (G protein), gamma 4"	NM_004485			2.583	0.814	1.43	0.435	1.217	0.509	Signal transduction. Regulation of G-protein coupled receptor protein signaling pathway.
TNL	TRIM9-like protein TNL	NM_001004342			2.278	1.198	1.138	0.693	1.809	0.897	
C10orf71	chromosome 10 open reading frame 71	NM_199459			1.619	0.44	1.387	0.375	2.217	0.657	Transport.
MGC35308	hypothetical protein MGC35308	NM_175922			1.531	0.407	1.728	0.171	1.954	0.469	
APOL3	apolipoprotein L3 isoform 3	NM_145641			2.771	0.429	1.167	0.548	1.275	0.502	Lipid metabolism. Lipid transport. Acute-phase response. Development. Cholesterol metabolism.
NMU	neuromedin U	NM_006681			2.539	0.519	1.21	0.586	1.463	0.325	Regulation of smooth muscle contraction. Signal transduction. Neuropeptide signaling pathway. Digestion.
LOC221711	hypothetical protein LOC221711	NM_194299			2.725	0.62	1.163	0.531	1.322	0.34	
ALOX5	arachidonate 5-lipoxygenase	NM_000698			2.173	0.872	1.018	0.601	2.019	0.767	Electron transport. Inflammatory response. Leukotriene biosynthesis.
LOC90525	hypothetical protein BC007586	NM_138356			2.441	0.679	1.015	0.708	1.753	0.6	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism. Metabolism.
SYT3	synaptotagmin 3	NM_032298			1.008	0.456	1.078	0.488	3.122	0.317	Transport.
FLJ16008	FLJ16008 protein	NM_001001665			2.461	0.625	1.364	0.81	1.38	0.764	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism. Metabolism.
N/A	unknown	AF289589			1.466	0.934	1.389	0.663	2.317	0.612	
BSND	barttin	NM_057176			1.561	0.724	1.435	0.652	2.172	0.359	
DOK5	DOK5 protein isoform a	NM_018431			1.425	0.617	1.63	0.478	2.113	0.557	
C15orf27	chromosome 15 open reading frame 27	NM_152335			2.899	0.398	1	0.563	1.267	0.474	
PCSK2	proprotein convertase subtilisin/kexin type 2	NM_002594			2.494	0.747	1.003	0.635	1.664	0.457	Proteolysis and peptidolysis. Cell-cell signaling.
TMEM16B	transmembrane protein 16B	NM_020373			1.967	0.617	1.051	0.72	2.14	0.752	
N/A	Unknown (protein for MGC:71509)	BC060765			2.692	0.736	1.305	0.485	1.151	0.621	Cation transport.
GPR73	G protein-coupled receptor 73	NM_138964			1.489	1	1.134	0.507	2.521	0.423	Signal transduction. G-protein coupled receptor protein signaling pathway.
ATP5G2	" ATP synthase, H+ transporting, mitochondrial F0 complex, s	NM_001002031			2.515	0.697	1.616	0.535	1.009	0.523	Ion transport. ATP synthesis coupled proton transport. Proton transport.
HAMP	hepcidin antimicrobial peptide	NM_021175			1.801	0.627	1.558	0.631	1.781	0.736	Xenobiotic metabolism. Iron ion homeostasis. Immune response. Defense response to bacteria. Response to pathogen.
PTPRO	receptor-type protein tyrosine phosphatase O isoform a precur	NM_030667			2.035	0.616	1.284	0.535	1.818	0.536	Protein amino acid dephosphorylation. Protein amino acid dephosphorylation.
N/A	Unknown (protein for MGC:75440)	BC063642			2.318	0.29			2.817	0.586	
ATP1B2	Na+/K+ -ATPase beta 2 subunit	NM_001678			1.95	0.597	1.322	0.529	1.851	0.58	Transport. Potassium ion transport. Sodium ion transport.
SEMA6A	semaphorin 6A1	NM_020796			2.216	0.676	1.296	0.841	1.604	0.731	Apoptosis. Cytoskeleton organization and biogenesis. Signal transduction. Development. Neurogenesis.
RGS6	regulator of G-protein signalling 6	NM_004296			2.219	1.071	1.269	0.684	1.624	0.958	Intracellular signaling cascade. Regulation of G-protein coupled receptor protein signaling pathway.
POU3F3	" POU domain, class 3, transcription factor 3"	NM_006236			2.485	1.211	1.225	0.681	1.399	0.781	Regulation of transcription, DNA-dependent. Central nervous system development.
CNFN	cornifelin	NM_032488			1.698	0.721	1.244	0.659	2.166	0.643	
SLC30A2	" solute carrier family 30, member 2 isoform 1"	NM_001004434			1.561	0.555	1.651	0.898	1.894	0.698	Transport. Cation transport. Zinc ion transport.
MSX2	msh homeo box homolog 2	NM_002449			2.881	1.038			2.221	1.04	Skeletal development. Regulation of transcription, DNA-dependent. Development.
NPY2R	neuropeptide Y receptor Y2	NM_000910			1.866	0.431	1.054	0.392	2.181	0.886	
KIAA0522	KIAA0522 protein	AB011094			2.226	0.87	1.37	1.053	1.502	0.671	
N/A	FGF17	AY358869			1.3	0.477	1.478	0.477	2.314	0.904	Signal transduction. Cell-cell signaling. Neurogenesis.
SSTR3	somatostatin receptor 3	NM_001051	2.132	1.429	2.067	0.5	1.249	0.524	1.774	0.666	G-protein signaling, coupled to cyclic nucleotide second messenger. Cell-cell signaling. Negative regulation of cell proliferation.
N/A	protease serine 4 isoform B	AY052783			1.674	0.746	1.571	0.345	1.844	0.659	Proteolysis and peptidolysis. Digestion. Negative regulation of blood coagulation.
DSCAML1	Down syndrome cell adhesion molecule like 1	NM_020693			1.649	0.864	1.533	0.38	1.906	0.52	Cell adhesion.
SYT2	synaptotagmin II	NM_177402			1.582	0.464	2.003	0.573	1.502	0.566	
N/A	N/A	AK022284			1.902	0.609	1.629	0.589	1.55	0.654	Regulation of transcription, DNA-dependent.
LOC401097	LOC401097 protein	BC031660			2.682	0.499	1.247	0.397	1.15	0.847	
C19orf4	brain-specific membrane-anchored protein precursor	NM_012109			1.913	1.232	1.549	0.896	1.617	1.052	
B3GNT5	" beta-1,3-N-acetylglucosaminyltransferase bGnT-5"	NM_032047			2.874	1.076	1.109	0.782	1.089	0.671	Protein amino acid glycosylation. Central nervous system development. Glycolipid biosynthesis.
LOC113828	hypothetical protein BC011204	NM_138435			1.766	0.317	1.167	0.391	2.134	0.408	
N/A	MCP-1 receptor	X95583			2.441	1.012			2.622	0.595	Chemotaxis. Inflammatory response. Cellular defense response. Signal transduction.
CRABP1	cellular retinoic acid binding protein 1	NM_004378			1.888	0.915	1.047	0.358	2.128	0.683	Transport. Signal transduction. Development,
C10orf48	chromosome 10 open reading frame 48	NM_173576			2.636	0.957	1.296	0.647	1.128	0.388	Regulation of transcription, DNA-dependent.

CHL1	cell adhesion molecule with homology to L1CAM precursor	NM_006614			2.562	0.773	1.304	0.612	1.191	0.715	Cell adhesion. Signal transduction.
CA4	" carbonic anhydrase IV, precursor"	BC057792			1.381	0.515	1.683	0.457	1.992	0.501	One-carbon compound metabolism.
N/A	N/A	AK127156			2.031	0.635	1.43	0.65	1.594	0.613	
GPR25	G protein-coupled receptor 25	NM_005298			1.797	0.645	1.295	0.538	1.953	0.796	Signal transduction. G-protein coupled receptor protein signaling pathway.
N/A	" cyclin-dependent kinase 5, regulatory subunit 2 (p39)"	BT007437			1.906	0.743	1.749	0.854	1.389	0.83	
C21orf29	chromosome 21 open reading frame 29	NM_144991			1.472	1.205	1.827	0.678	1.741	0.709	
DKFZp686I0554	hypothetical proteincDNA DKFZp686I0554 (from clone DKFZp	BX640900			1.487	0.897	1.454	0.56	2.098	0.607	
VIPR1	vasoactive intestinal peptide receptor 1	NM_004624			1.441	0.759	1.584	0.265	2.013	0.581	Muscle contraction. Immune response. Signal transduction. G-protein signaling, coupled to cyclic nucleotide second messenger.
SOX21	SRY-box 21	NM_007084			2.268	0.819	1.602	0.655	1.168	0.429	Establishment and/or maintenance of chromatin architecture. Transcription.
mop-1	MOP-1	AB014771	2.425	2.281	2.979	0.622			2.059	0.909	Cytokinesis. Small GTPase mediated signal transduction.
ADCYAP1	adenylate cyclase activating polypeptide precursor	NM_001117	1.222	1.407	1.928	0.551	1.177	0.356	1.93	0.676	Adenylate cyclase activation. Cell-cell signaling. Pregnancy.
ALDH1A2	aldehyde dehydrogenase 1A2 isoform 1	NM_003888			2.003	0.653	1.389	0.554	1.642	0.599	Vitamin A metabolism. Metabolism.
UNQ3030	ELLP3030	NM_198565			1.483	0.439	1.522	0.583	2.028	0.578	
NEFL	NEFL protein	BC039237			1	1.202	1.722	0.442	2.311	0.418	
KREMEN2	kringle-containing transmembrane protein 2 isoform c precurs	NM_145348			1.35	0.838	1.976	0.666	1.701	0.467	Wnt receptor signaling pathway.
CD38	CD38 antigen	NM_001775			2.551	0.617			2.475	0.441	Generation of precursor metabolites and energy. Signal transduction. Induction of apoptosis by extracellular signals.
IRF5	interferon regulatory factor 5 isoform a	NM_002200			1.861	0.488	1.353	0.542	1.809	0.569	Regulation of transcription, DNA-dependent.
GUCY2D	" guanylate cyclase 2D, membrane (retina-specific)"	NM_000180			1.918	0.867	1.644	0.676	1.448	0.746	CGMP biosynthesis. Protein amino acid phosphorylation. Receptor guanylyl cyclase signaling pathway.
LHFPL3	lipoma HMGIC fusion partner-like 3	NM_199000			1.409	0.634	1.611	0.579	1.983	0.662	
ELAVL3	ELAV-like protein 3 isoform 1	NM_001420			1.193	0.648	1.634	0.626	2.165	0.451	Neurogenesis. Cell differentiation.
KIRREL2	kin of IRRE-like 2 isoform c	NM_199180			1.567	0.758	1.591	0.783	1.832	0.968	Cell adhesion.
KIAA0514	KIAA0514 protein	NM_014696			1.276	0.435	1.477	0.437	2.234	0.45	
DKFZp779E2271	hypothetical proteincDNA DKFZp779E2271 (from clone DKFZ	BX537865			2.02	0.416	1.223	0.522	1.744	0.532	
CR2	complement receptor	X68990			2.342	0.343	1.298	0.493	1.346	0.394	
ESPN	espin	NM_031475			1.19	0.597	1.711	0.782	2.079	0.837	Cell adhesion.
ADRB3	" adrenergic, beta-3-, receptor"	NM_000025			1.748	0.405	1.085	0.449	2.145	0.687	Carbohydrate metabolism. Generation of precursor metabolites and energy. Energy reserve metabolism. Signal transduction.
N/A	protein tyrosine phosphatase non-receptor type substrate prot	AY424277			1.705	0.7	1.221	0.497	2.049	0.469	
GJB3	connexin 31	AF052692			1.817	0.505	1.283	0.467	1.874	0.393	Cell communication. Perception of sound.
KRT4	keratin 4	NM_002272			1.768	0.443	1.512	0.309	1.687	0.746	Cytoskeleton organization and biogenesis.
SLC27A2	" solute carrier family 27 (fatty acid transporter), member 2"	NM_003645			1.943	0.889	1.146	0.982	1.874	0.862	Very-long-chain fatty acid metabolism. Lipid metabolism.
WNT11	" wingless-type MMTV integration site family, member 11 prec	NM_004626			1.898	0.815	1.54	0.708	1.522	0.895	Signal transduction. Frizzled-2 signaling pathway. Cell-cell signaling. Development. Morphogenesis.
FGF19	fibroblast growth factor 19 precursor	NM_005117			1.919	0.588	1.314	0.728	1.725	0.7	Neurogenesis.
N/A	N/AcDNA DKFZp434J193 (from clone DKFZp434J193).	AL080137			1.513	0.831	1.058	0.513	2.385	0.327	
FGF3	fibroblast growth factor 3 precursor	NM_005247			1.288	0.443	1.602	0.752	2.066	0.537	Regulation of cell cycle. Signal transduction. Cell-cell signaling. Cell proliferation. Morphogenesis.
MGC39715	hypothetical protein MGC39715	NM_152628			2.216	0.626	1.316	0.429	1.42	0.686	Intracellular signaling cascade. Protein transport.
FLJ25037	hypothetical protein FLJ25037	NM_182596			2.152	0.706	1.463	0.663	1.328	0.628	Mitotic chromosome condensation.
LOC124842	hypothetical protein LOC124842	NM_207313			1.501	0.65	1.714	0.667	1.725	0.703	
FLJ16517	FLJ16517 protein	NM_001004317			3.573	0.855			1.367	1.203	Regulation of transcription, DNA-dependent
OTX1	orthodenticle 1	NM_014562			2.792	0.988	1.053	0.768	1.094	0.602	Regulation of transcription, DNA-dependent. Development.
DKFZp686E13109	hypothetical proteincDNA DKFZp686E13109 (from clone DKF	BX648771			2.151	1.039	1.147	0.854	1.638	0.998	Protein amino acid dephosphorylation. Phosphate metabolism.
LHX3	LIM homeobox protein 3 isoform b	NM_014564			1.133	0.428	1.893	0.885	1.906	0.775	Regulation of transcription, DNA-dependent. Organogenesis.
HLXB9	homeo box HB9	NM_005515			1.75	0.778	1.542	0.611	1.64	0.77	Regulation of transcription from RNA polymerase II promoter. Humoral immune response. Morphogenesis.
KCNJ9	potassium inwardly-rectifying channel subfamily J9	NM_004983			2.342	0.298	1.144	0.657	1.443	0.255	Ion transport. Potassium ion transport.
GFRA4	GDNF family receptor alpha 4 isoform b precursor	NM_145762			1.777	0.453	1.039	0.601	2.112	0.612	
LOC120224	hypothetical protein BC016153	NM_138788			1.141	0.439	1.5	0.574	2.283	0.685	
N/A	N/A	BX161496			1.53	0.647	1.727	0.587	1.666	0.613	
ACDC	adiponectin precursor	NM_004797	2.302	0.854	2.135	0.504	1.145	0.729	1.639	0.817	Generation of precursor metabolites and energy. Phosphate transport.
N/A	N/A	AK026773			1.385	0.671	1.76	0.872	1.767	0.949	Transport.
SLC6A7	" solute carrier family 6, member 7"	NM_014228			1.243	0.337	1.495	0.538	2.169	0.465	Neurotransmitter transport. Amino acid transport. Synaptic transmission. L-proline transport.
FOXA2	forkhead box A2	NM_021784			1.338	0.864	1.638	1.106	1.93	1.151	Transcription. Regulation of transcription, DNA-dependent.
CXCR4	chemokine (C-X-C motif) receptor 4	NM_003467			1.899	0.844	1.234	0.652	1.772	0.632	Signal transduction. G-protein coupled receptor protein signaling pathway.
OTOP3	otopetrin 3	NM_178233			1.407	0.407	1.361	0.43	2.13	0.762	
SOX2	sex-determining region Y-box 2	NM_003106			1.572	0.431	1.316	0.457	2.005	0.852	Establishment and/or maintenance of chromatin architecture. Transcription. Regulation of transcription, DNA-dependent.
CHR3SYT	chr3 synaptotagmin	NM_031913			2.033	0.457	1.192	0.31	1.668	0.542	
ADCY1	brain adenylate cyclase 1	NM_021116			1.762	0.769	1.263	1.237	1.864	1.168	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism. Metabolism.
JPH1	JPH1 protein	BC049372			1.797	0.645	1.513	0.798	1.578	0.524	

PALM	paralemmin	NM_002579			1.565	1.29	1.304	0.947	2.016	0.837	Cell motility. Regulation of cell shape.
SOX3	SRY (sex determining region Y)-box 3	NM_005634			1.82	0.746	1.574	0.639	1.489	0.915	Transcription. Regulation of transcription, DNA-dependent. Central nervous system development.
CDS1	phosphatidate cytidylyltransferase 1	NM_001263			1.846	0.91	1.572	0.753	1.463	0.613	Lipid metabolism. Signal transduction. Visual perception. Phospholipid biosynthesis.
PTCHD1	patched domain containing 1	NM_173495			2.225	0.844	1.401	0.456	1.251	0.732	
ABCC8	" ATP-binding cassette, sub-family C, member 8"	NM_000352			2.54	0.726			2.333	0.757	Carbohydrate metabolism. Transport. Potassium ion transport.
CLIC5	chloride intracellular channel 5	BC035968			1.665	0.545	1.158	0.339	2.048	0.389	Ion transport. Chloride transport. Pregnancy.
CADPS	Ca2+-dependent secretion activator isoform 1	NM_003716			1.547	0.365	1.261	0.861	2.06	0.898	Exocytosis.
PTGFRN	prostaglandin F2 receptor negative regulator	NM_020440			1.986	0.516	1.044	0.445	1.837	0.498	Negative regulation of protein biosynthesis.
CRLF1	cytokine receptor-like factor 1	NM_004750			1.635	0.494	1.869	0.508	1.362	0.613	Antimicrobial humoral response.
SHD	src homology 2 domain-containing transforming protein D	NM_020209			1.99	1.255	1.331	0.719	1.543	0.683	Intracellular signaling cascade.
PAQR9	progestin and adipoQ receptor family member IX	NM_198504			2.237	0.876	1.406	1.045	1.217	0.864	
KIT	v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homol	NM_000222			1.747	0.579	1.907	0.748	1.206	0.482	Signal transduction. Transmembrane receptor protein tyrosine kinase signaling pathway.
NALP6	" NACHT, leucine rich repeat and PYD containing 6"	NM_138329			1.685	0.665	1.079	0.226	2.093	0.747	
C6orf85	ion transporter protein	NM_021945			2.548	0.41			2.307	0.639	Transport.
N/A	N/A	AK095054			1.207	0.929	1.789	0.69	1.855	0.51	
FLJ39237	FLJ39237 protein	NM_198571			1.541	0.355	1.985	0.514	1.325	0.377	
C14orf25	C14orf25 protein	BC038110			1.669	0.572	1.384	0.382	1.796	0.333	
Wnt10B	Wnt10B	U81787			1.565	0.646	1.492	0.502	1.788	0.346	Signal transduction. Frizzled-2 signaling pathway. Development.
PCSK1	proprotein convertase subtilisin/kexin type 1 preproprotein	NM_000439			1.871	1.009	1.123	0.664	1.85	1.069	Proteolysis and peptidolysis. Cell-cell signaling. Metabolism.
VSNL1	visinin-like 1	NM_003385			3.078	0.47			1.76	0.888	
IFNA2	" interferon, alpha 2"	NM_000605			3.228	0.42			1.609	0.333	Defense response. Cell-cell signaling. Response to virus.
KRT9	keratin 9	NM_000226			1.439	0.758	1.294	0.744	2.101	0.449	Epidermis development.
FLJ39630	hypothetical protein FLJ39630	NM_173688			1.659	0.619	1.552	0.613	1.622	0.783	
FBXO27	F-box protein 27	NM_178820			2.252	0.386	1.135	0.385	1.446	0.35	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism. Metabolism.
FGF11	fibroblast growth factor 11	NM_004112			1.357	0.676	1.586	0.624	1.887	0.584	Signal transduction. Cell-cell signaling. Neurogenesis.
MGAT3	" mannosyl (beta-1,4-)-glycoprotein beta-1,4-N-acetylglucosar	NM_002409			1.053	0.652	1.538	0.368	2.238	0.582	N-linked glycosylation.
CACNA1S	" calcium channel, voltage-dependent, L type, alpha 1S subun	NM_000069			1.304	0.501	1.28	0.67	2.239	0.95	Cation transport. Calcium ion transport. Muscle contraction.
TP73	tumor protein p73	NM_005427			1.359	0.412	1.901	0.692	1.554	0.882	Mismatch repair. Transcription. Regulation of transcription, DNA-dependent. Apoptosis. Cell cycle.
OTOF	otoferlin isoform a	NM_194248			1.381	0.467	1.268	0.358	2.162	0.386	Membrane fusion. Perception of sound.
N/A	N/A	AK096006			1.843	0.464	1.174	0.49	1.79	0.528	
RAB6B	" RAB6B, member RAS oncogene family"	NM_016577			1.521	0.922	1.135	0.303	2.151	0.908	Intracellular protein transport. Retrograde transport, Golgi to ER. Small GTPase mediated signal transduction.
PYC1	pyrin-domain containing protein	AF467809			1.692	0.342	1.557	0.604	1.558	0.471	
KIAA0845	KIAA0845 protein	AB020652			1.957	0.572	1.077	0.391	1.763	0.728	Nucleosome assembly. Neurogenesis.
N/A	apoptosis related protein APR-2	AF143236			1.333	0.698	1.341	0.579	2.122	0.523	Electron transport. Apoptosis.
AGC1	aggrecan 1 isoform 2 precursor	NM_013227			1.853	1.289	1.533	0.575	1.409	0.825	Cell adhesion.
ZMYND15	" zinc finger, MYND domain containing 15"	NM_032265	1.673	1.507	2.074	1.491	1.456	0.762	1.264	0.837	
TLX1	" T-cell leukemia, homeobox 1"	NM_005521			2.359	0.395			2.434	0.855	Regulation of transcription, DNA-dependent. Development.
N/A	N/A	AK127178			1.893	0.737	1.591	0.604	1.309	0.4	
N/A	precursor (AA -19 to 692)	X53961			1.57	0.551	1.179	0.423	2.035	0.602	Transport. Iron ion transport. Iron ion homeostasis. Humoral immune response. Defense response to bacteria.
SPTB	" spectrin, beta, erythrocytic (includes spherocytosis, clinical t	NM_000347			2.148	0.989	1.165	0.523	1.466	0.645	
SCAP1	src family associated phosphoprotein 1	BC047870			1.804	0.968	1.335	1.07	1.64	0.954	Immune response. Signal transduction.
MGC42367	similar to 2010300C02Rik protein	NM_207362			2.258	0.792	1.351	0.525	1.168	0.472	
GATA-6	GATA-6 DNA binding protein	X95701			3.328	1.344			1.449	0.688	Transcription. Regulation of transcription, DNA-dependent. Muscle development. Positive regulation of transcription.
N/A	interferon alpha 2b	AY255838			3.168	0.465			1.606	0.297	Defense response. Cell-cell signaling. Response to virus.
N/A	N/A	AK130238			1.015	0.539	1.573	0.588	2.181	0.639	
GSH-2	homeobox protein GSH-2	NM_133267			1.254	0.384	1.39	0.639	2.122	0.526	Regulation of transcription, DNA-dependent. Development.
ADRA2A	alpha-2A-adrenergic receptor	NM_000681			1.977	0.913	1.479	0.377	1.309	0.646	Activation of MAPK. Cell motility. Signal transduction. G-protein coupled receptor protein signaling pathway.
PGA5	" pepsinogen 5, group I (pepsinogen A)"	BC029055			2.11	0.321			2.655	0.197	
N/A	N/A	AK128180			1.426	0.729			3.336	0.275	
N/A	N/A	BC035798			1.761	1.139	1.544	1.087	1.453	0.494	
FLJ20619	hypothetical protein FLJ20619	NM_017904			1.285	0.443	1.372	0.497	2.099	0.585	
SATB2	SATB family member 2	NM_015265			3.72	0.65	1.035	0.491			Regulation of transcription, DNA-dependent.
PENK	proenkephalin	NM_006211			1.445	0.653	1.209	0.493	2.1	0.435	Signal transduction. Neuropeptide signaling pathway. Cell-cell signaling.
TIP39	tuberoinfundibular 39 residue protein precursor	NM_178449			1.705	0.965	1.116	0.565	1.929	0.806	
NXPH4	neurexophilin 4	NM_007224	1.457	1.341	1.337	0.759	1.013	0.626	2.399	1.002	Neuropeptide signaling pathway.
RTN1	reticulon 1 isoform A	NM_021136			2.166	0.38	1.392	0.627	1.186	0.879	Signal transduction. Neuron cell differentiation.

MGC50844	hypothetical protein MGC50844	NM_178562			2.659	0.987			2.083	0.848	
FBXO16	F-box only protein 16	NM_172366			2.955	0.761			1.783	0.683	Ubiquitin cycle.
HCN4	hyperpolarization activated cyclic nucleotide-gated potassium c	NM_005477			1.609	0.834	1.416	0.363	1.709	0.728	Cation transport. Potassium ion transport. Sodium ion transport. Muscle contraction. Circulation.
RODH-4	microsomal NAD+-dependent retinol dehydrogenase 4	NM_003708			1.84	0.219	1.025	0.23	1.868	0.254	Lipid metabolism. Metabolism.
DKFZp761H171	hypothetical proteincDNA DKFZp761H171 (from clone DKFZp7	AL137502	1.055	0.625	1.724	0.235	1.35	0.565	1.647	0.707	
CRYBA2	" crystallin, beta A2"	NM_057093			1.336	0.81	1.643	0.467	1.739	0.531	
HBA2	alpha 2 globin	NM_000517	1.794	1.616	1.207	0.459	1.642	0.39	1.866	0.472	
N/A	N/A	BX248251			2.304	1.17	1.118	0.547	1.286	0.799	
N/A	N/A	AK095915			1.433	0.916	1.127	0.531	2.148	0.733	Protein amino acid phosphorylation.
FGF4	fibroblast growth factor 4 precursor	NM_002007			1.408	0.64	1.445	0.52	1.854	0.63	Regulation of cell cycle. Mitosis. Signal transduction. Cell-cell signaling. Cell proliferation.
GRAP2	GRB2-related adaptor protein 2	NM_004810			2.855	0.793			1.85	0.473	Intracellular signaling cascade. Ras protein signal transduction. Cell-cell signaling. Antimicrobial humoral response.
AMACO	A-domain containing protein similar to matrilin and collagen	NM_198496			1.779	0.522	1.309	0.232	1.617	0.237	
CDH22	cadherin 22 precursor	NM_021248			1.246	0.983	1.439	0.67	2.019	0.712	Cell adhesion. Homophilic cell adhesion.
FLJ40319	hypothetical protein FLJ40319	NM_182564	1.115	0.833	2.489	0.668	2.212	0.41			
MK2S4	protein kinase substrate MK2S4	NM_052862			2.679	0.775			2.018	0.453	
FLJ42461	FLJ42461 protein	NM_198501			1.462	0.593	1.663	0.295	1.571	0.644	
N/A	Unknown (protein for IMAGE:4694038)	BC020891			2.084	0.515	1.011	0.54	1.598	0.663	
GALR2	galanin receptor 2	NM_003857			1.318	0.601	1.507	0.653	1.867	0.832	Muscle contraction. G-protein coupled receptor protein signaling pathway.
GCM2	glial cells missing homolog 2	NM_004752			1.861	0.526	1.265	0.443	1.553	0.607	Transcription. Regulation of transcription, DNA-dependent. Development.
MOS	v-mos Moloney murine sarcoma viral oncogene homolog	NM_005372			2.203	0.715	1.1	0.403	1.374	0.646	Regulation of cell cycle. Protein amino acid phosphorylation.
N/A	N/A	AK094219			1.67	0.64	1.204	0.62	1.799	0.784	
CR2	complement component (3d/Epstein Barr virus) receptor 2 isofo	NM_001006658			2.257	0.41	1.094	0.451	1.313	0.186	Immune response. Complement activation, classical pathway.
N/A	N/A	AK126643	1.605	1.221	1.313	0.861	1.492	0.364	1.848	0.701	
DKFZp434M202	hypothetical protein DKFZp434M202	NM_182499			2.136	0.561			2.514	0.496	
C6orf189	C6orf189 protein	BC038997			2.099	0.685	1.341	0.43	1.21	0.343	
KIAA0466	KIAA0466 protein	AB007935			2.076	0.874			2.569	0.901	
N/A	alpha2i-subunit of soluble guanylyl cyclase	Z50053			1.852	0.549	1.329	0.415	1.462	0.621	CGMP biosynthesis. Intracellular signaling cascade.
HTR2C	5-hydroxytryptamine (serotonin) receptor 2C	NM_000868			1.053	0.97	1.55	0.684	2.035	0.701	Signal transduction. Serotonin receptor signaling pathway. Synaptic transmission. Feeding behavior.
LOC255743	hypothetical protein LOC255743	NM_198278			1.503	0.756	1.538	0.578	1.595	1.01	
SLCO2B1	" solute carrier organic anion transporter family, member 2B1"	NM_007256			2.086	1.165			2.55	0.914	Ion transport.
FLJ00030	FLJ00030 protein	AK024440			1.388	0.411	1.411	0.403	1.836	0.592	Metabolism.
C20orf46	chromosome 20 open reading frame 46	NM_018354			1.482	0.926	1.262	0.566	1.885	1.13	
HBF-3	N/A	X74144			2.22	0.826	1.075	0.475	1.331	0.699	Regulation of transcription, DNA-dependent. Brain development.
DKFZp547A0817	hypothetical proteincDNA DKFZp547A0817 (from clone DKFZp	AL832541			1.286	0.984	1.015	0.329	2.324	0.579	
CDK5R2	" cyclin-dependent kinase 5, regulatory subunit 2"	NM_003936			2.251	0.849			2.374	0.773	Regulation of cyclin dependent protein kinase activity.
C14orf39	chromosome 14 open reading frame 39	NM_174978			2.499	0.558	1.068	0.598	1.051	0.631	
N/A	susceptibility protein NSG-x	AF211119	1.086	0.746	2.426	0.314	1.018	0.496	1.171	0.444	
COL9A2	alpha 2 type IX collagen	NM_001852			1.222	0.599	1.726	0.596	1.666	0.598	Skeletal development. Phosphate transport.
CNTFR	ciliary neurotrophic factor receptor preproprotein	NM_147164			1.277	0.544	1.699	0.414	1.633	0.479	Signal transduction. Neurogenesis.
BTNL2	butyrophilin-like 2	NM_019602			2.468	0.397			2.14	0.314	
CACNA1A	" calcium channel, alpha 1A subunit isoform 2"	NM_023035			1.831	1.372	1.238	0.852	1.537	0.868	Regulation of transcription, DNA-dependent. Cation transport. Calcium ion transport.
CHRNB2	" cholinergic receptor, nicotinic, beta polypeptide 2 (neuronal)"	NM_000748			1.068	0.551	1.557	0.679	1.979	0.737	Ion transport. Signal transduction. Synaptic transmission.
RIPK3	RIPK3 protein	BC041668			2.339	0.768			2.264	0.521	Protein amino acid phosphorylation.
N/A	Unknown (protein for MGC:78661)	BC068080			1.66	1.221	1.473	0.835	1.469	1.059	
IL22RA1	" interleukin 22 receptor, alpha 1"	NM_021258			1.402	1.237	1.762	1.462	1.432	0.452	
DLL3	delta-like 3 protein isoform 1 precursor	NM_016941			1.512	0.591	1.327	0.769	1.757	0.877	Skeletal development. Embryonic development. Cell fate determination. Notch signaling pathway.
PTGDR	prostaglandin D2 receptor	NM_000953			1.695	0.568	1.607	0.789	1.293	0.34	Signal transduction. G-protein coupled receptor protein signaling pathway.
N/A	N/A	AK094626			2.264	0.463			2.325	0.47	
SOX17	SRY-box 17	NM_022454			2.241	0.762	1.256	0.803	1.082	0.72	Regulation of transcription, DNA-dependent.
COL27A1	" collagen, type XXVII, alpha 1"	NM_032888			1.393	0.886	1.747	0.982	1.436	0.925	Phosphate transport. Cell adhesion.
HAP1	huntingtin-associated protein 1 isoform 1	NM_003949			1.834	0.644	1.476	0.304	1.265	0.403	Synaptic transmission. Development.
CNDP1	carnosinase 1	NM_032649			1.372	0.404	1.362	0.496	1.84	0.392	Proteolysis and peptidolysis.
GBX2	gastrulation brain homeo box 2	NM_001485			2.322	1.062	1.117	0.831	1.132	0.656	Regulation of transcription, DNA-dependent. Neurogenesis. Antimicrobial humoral response.
COL4A4	alpha 4 type IV collagen precursor	NM_000092	1.413	0.877	1.476	0.409	1.651	0.366	1.444	0.659	Phosphate transport. Long-term strengthening of neuromuscular junction.
WDR8	WDR8 protein	BC002611			1.81	0.718	1.359	0.75	1.398	0.782	
IRF4	lymphocyte specific interferon regulatory factor/interferon regul	U52682			1.361	0.712	1.864	0.585	1.342	0.632	Transcription. Regulation of transcription, DNA-dependent. T-cell activation.

SCN4B	" sodium channel, voltage-gated, type IV, beta"	NM_174934			1.643	0.484	1.232	0.579	1.689	0.258	Ion transport. Sodium ion transport. Synaptic transmission.
NTRK3	" neurotrophic tyrosine kinase, receptor, type 3"	NM_002530			1.269	0.456	1.565	0.523	1.727	0.652	Protein amino acid phosphorylation. Transmembrane receptor protein tyrosine kinase signaling pathway.
MGC33600	hypothetical protein MGC33600	NM_182539			1.522	0.749	1.312	0.463	1.726	0.632	
ACTA1	alpha 1 actin precursor	NM_001100			1.175	0.415	1.606	0.794	1.779	0.755	Muscle development.
NT5C1A	" 5'-nucleotidase, cytosolic IA"	NM_032526			1.895	0.624	1.276	0.488	1.384	0.416	Nucleoside metabolism. Nucleotide metabolism.
MGC52498	hypothetical protein MGC52498	NM_182621			1.8	0.751	1.016	0.564	1.729	1.076	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism. Metabolism.
FLJ43826	FLJ43826 protein	NM_198502			1.866	0.471	1.041	0.395	1.631	0.589	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism. Metabolism.
EPB49	erythrocyte membrane protein band 4.9 (dematin)	NM_001978			1.269	0.738	1.363	0.56	1.904	0.411	Cytoskeleton organization and biogenesis. Actin filament bundle formation.
SOST	sclerosteosis	NM_025237			1.98	0.979	1.044	0.404	1.51	0.413	Negative regulation of ossification.
N/A	N/A	AK093672			1.477	0.565	1.124	0.262	1.933	0.449	
N/A	Unknown (protein for MGC:46433)	BC036837			1.714	0.675	1.262	0.693	1.553	0.588	
OTOS	otospiralin	NM_148961			1.057	0.598	1.141	0.493	2.324	0.327	
CYP26B1	" cytochrome P450, family 26, subfamily b, polypeptide 1"	NM_019885	1.067	0.879	2.306	1.053	1.148	0.53	1.066	0.535	Electron transport.
MG29	mitsugumin 29	NM_001006603			2.085	0.627			2.432	0.55	Transport.
KIAA0474	KIAA0474 protein	AB007943			1.707	0.788	1.172	0.446	1.635	0.802	Signal transduction.
DMRT2	doublesex and mab-3 related transcription factor 2	NM_006557			1.621	0.361	1.335	0.47	1.558	0.749	Transcription. Regulation of transcription, DNA-dependent. Sex determination. Sex differentiation. Male gonad development.
KIAA0945	KIAA0945 protein	AB023162			1.246	0.47	1.206	0.538	2.062	0.557	
GPR7	G protein-coupled receptor 7	NM_005285			1.587	0.506	1.162	0.468	1.764	0.595	
KIAA1772	KIAA1772	NM_024935			2.086	0.911	1.098	0.573	1.325	0.861	Proteolysis and peptidolysis.
CD8B1	CD8 antigen beta polypeptide 1 isoform 1 precursor	NM_172099			2.08	0.731			2.429	0.609	Immune response. Transmembrane receptor protein tyrosine kinase signaling pathway. T-cell activation.
FLJ33790	hypothetical protein FLJ33790	NM_173583			1.743	1.417	1.45	1.066	1.313	1.21	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
LGI1	" leucine-rich, glioma inactivated 1, precursor"	BC022500			2.193	0.729			2.309	0.718	Neurogenesis. Cell proliferation.
CPVL	serine carboxypeptidase vitellogenic-like	NM_019029			1.492	1.119	1.088	0.262	1.92	0.415	Proteolysis and peptidolysis.
PLXNC1	plexin C1	NM_005761			1.636	1.135	1.325	0.684	1.537	1.14	Cell adhesion. Development.
KIAA1222	KIAA1222 protein	AB033048			2.439	0.585			2.056	0.254	Neurogenesis. Cell differentiation.
RASGRP2	RAS guanyl releasing protein 2 isoform 1	NM_005825			1.364	0.914	1.509	0.582	1.621	0.843	Regulation of cell growth. Small GTPase mediated signal transduction. Ras protein signal transduction.
IL17RB	interleukin 17B receptor isoform 2 precursor	NM_172234			1.076	0.594	1.543	0.69	1.875	0.765	Regulation of cell growth. Defense response.
ATF3	activating transcription factor 3 delta Zip isoform	NM_004024			2.381	1.629	1.091	1.087	1.021	0.734	Transcription. Regulation of transcription, DNA-dependent.
N/A	docking protein 1-like protein	AF229166			1.953	0.694			2.539	0.614	
N/A	galanin-related peptide	AF077047			1.489	1.129	1.061	0.704	1.937	1.004	
NPY5R	neuropeptide Y receptor Y5	NM_006174			1.414	0.921	1.28	0.519	1.792	0.501	Signal transduction. G-protein coupled receptor protein signaling pathway.
CHRDL1	chordin-like 1	NM_145234			1.801	1.359	1.075	0.561	1.608	0.518	Development.
SIM2	single-minded homolog 2 long isoform	NM_005069			1.985	0.681	1.191	0.675	1.3	0.75	Transcription. Regulation of transcription, DNA-dependent. Signal transduction. Neurogenesis. Cell differentiation.
TLR2	TLR2 protein	BC033756			1.442	0.681	1.192	0.481	1.84	0.875	Induction of apoptosis. Inflammatory response. Signal transduction.
N/A	N/A	AK124891			2.144	0.415			2.33	0.533	
HLA-G	" major histocompatibility complex, class I, G precursor"	NM_002127			1.718	0.58	1.024	0.937	1.728	0.638	Antigen presentation, endogenous antigen. Antigen processing, endogenous antigen via MHC class I.
LOC199964	hypothetical protein LOC199964	NM_182532			1.936	0.837	1.008	0.385	1.524	0.612	
C2orf23	chromosome 2 open reading frame 23	NM_022912			1.704	0.858	1.035	0.661	1.727	0.947	
N/A	N/A	AK075014			1.064	0.689	1.773	0.585	1.628	0.694	Transport. Amino acid transport.
NOPE	DDM36	NM_020962			1.609	0.684	1.008	0.623	1.846	0.982	Cell adhesion.
TRAF5	TNF receptor-associated factor 5	NM_004619			3.297	0.434			1.163	0.631	Apoptosis. Signal transduction. Protein ubiquitination. Positive regulation of I-kappaB kinase/NF-kappaB cascade.
N/A	calcitonin receptor	L00587			1.156	0.783	1.5	0.518	1.803	0.452	Ossification. Signal transduction. G-protein coupled receptor protein signaling pathway. Adenylate cyclase activation.
SYT15	synaptotagmin XV isoform a	NM_031912			1.105	0.21	1.386	0.457	1.967	0.774	
NRCAM	neuronal cell adhesion molecule	NM_005010			1.867	0.637	1.343	0.368	1.245	0.499	Neuronal migration. Axonal fasciculation. Synaptogenesis. Central nervous system development. Cell-cell adhesion.
GDA	guanine deaminase	NM_004293			1.869	0.391	1.151	0.4	1.431	0.361	Nucleobase, nucleoside, nucleotide and nucleic acid metabolism. Neurogenesis.
N/A	FP18279	AY203929			1.439	0.613	1.239	0.646	1.771	0.431	
CRTAC1	cartilage acidic protein 1	NM_018058			1.298	0.722	1.572	0.691	1.577	0.772	Cell-matrix adhesion.
OXCT2	3-oxoacid CoA transferase 2	NM_022120			1.511	0.727	1.055	0.365	1.874	0.637	Metabolism.
MDS1	myelodysplasia syndrome protein 1	NM_004991			3.046	1.012			1.393	0.935	
NPY	neuropeptide Y	BC029497	1.095	1.105	1.534	0.963	1.358	0.526	1.544	0.71	Calcium ion transport. Cell motility. G-protein signaling. Neuropeptide signaling pathway.
N/A	Fc gamma receptor I	L03419			2.188	0.28			2.248	0.446	
N/A	N/A	AK127534			1.346	0.813	1.333	0.567	1.749	0.418	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
IL5RA	" interleukin 5 receptor, alpha isoform 1 precursor"	NM_000564			1.635	0.777	1.317	1.014	1.473	0.623	Signal transduction. Cell proliferation.
MEGF10	MEGF10 protein	NM_032446			1.98	1.138	1.343	0.35	1.098	0.307	
PRKAG2	PRKAG2 protein	BC068598			2.411	0.464			2	0.596	Fatty acid biosynthesis. Cholesterol biosynthesis.
N/A	serine protease prostase	AF113140			1.956	0.296			2.451	0.46	Proteolysis and peptidolysis.

CKLFSF8	chemokine-like factor superfamily 8	NM_178868			1.12	0.803	1.282	0.58	2.005	0.763	Chemotaxis. Sensory perception.
KIAA0227	N/A	D86980			2.746	0.784			1.656	0.552	
DUSP9	dual specificity phosphatase 9	NM_001395			1.348	0.799	1.431	0.992	1.623	1.038	Inactivation of MAPK. Protein amino acid dephosphorylation. JNK cascade.
MGC35338	hypothetical protein MGC35338	NM_152389			2.846	0.604			1.553	0.505	
SYN2	synapsin II isoform IIb	NM_003178			1.358	0.757	1.053	0.884	1.987	0.733	Synaptic transmission. Neurotransmitter secretion.
SLC6A2	SLC6A2 protein	BC060831			1.159	0.555	1.362	0.851	1.877	0.64	Neurotransmitter transport. Synaptic transmission.
LRRN6A	leucine-rich repeat neuronal 6A	NM_032808			1.624	0.794	1.506	0.57	1.266	0.61	
N/A	FP1188	AF370365			1.363	0.901	1.257	0.576	1.774	0.724	
CGREF1	cell growth regulator with EF hand domain 1	NM_006569			1.169	0.676	1.393	0.575	1.827	0.658	Response to stress. Cell cycle. Cell cycle arrest. Negative regulation of cell proliferation.
CART	cocaine- and amphetamine-regulated transcript	NM_004291	1.352	0.981	1.39	0.479	1.135	0.545	1.859	0.417	Signal transduction. Neuropeptide signaling pathway. Cell-cell signaling. Synaptic transmission.
FRAS1	Fraser syndrome 1 isoform 1	NM_025074			2.758	0.617	1.622	0.591			Cell communication.
GUCY1B2	" guanylate cyclase 1, soluble, beta 2"	NM_004129			1.483	1.12	1.03	0.749	1.866	0.293	CGMP biosynthesis. Intracellular signaling cascade.
AP2E	" adaptor-related protein complex 2, epsilon subunit"	NM_178548			2.901	0.472			1.476	0.628	
DACH1	dachshund homolog 1 isoform a	NM_080759			3.254	0.991	1.116	0.945			Transcription. Regulation of transcription, DNA-dependent. Development. Eye morphogenesis.
N/A	unknown	AF466366			1.602	0.721	1.377	0.613	1.39	0.466	
N/A	N/A	AK130688			1.521	0.429	1.155	0.349	1.692	0.421	
N/A	thrombospondin	AF251057			2.135	0.815	1.226	0.605	1.007	0.55	Electron transport.
SLC13A2	" solute carrier family 13 (sodium-dependent dicarboxylate tra	NM_003984			1.958	0.488			2.409	0.451	Ion transport. Sodium ion transport.
CITED1	" Cbp/p300-interacting transactivator, with Glu/Asp-rich carbo	NM_004143			2.977	1.197	1.388	0.894			Regulation of transcription from RNA polymerase II promoter.
KCNC4	Shaw-related voltage-gated potassium channel protein 4 isofo	NM_004978			1.175	0.628	1.889	1.334	1.287	1.074	Cation transport. Potassium ion transport. Potassium ion transport. Synaptic transmission.
OXT	oxytocin-neurophysin I preproprotein	NM_000915			1.449	0.788	1.104	0.408	1.788	0.368	Signal transduction. Parturition.
PPP1R14C	" protein phosphatase 1, regulatory (inhibitor) subunit 14C"	NM_030949			2.265	1.013			2.072	0.663	
N/A	unknown	AF036977			1.122	0.498	1.169	0.226	2.046	0.72	
COMP	COMP protein	BC033676			1.606	0.543	1.376	0.352	1.352	0.481	Skeletal development. Cell adhesion.
KRTHA5	type I hair keratin 5	NM_002280			2.16	0.613			2.174	0.474	Morphogenesis.
NEURL	neuralized-like	NM_004210			1.864	0.839	1.307	0.768	1.161	0.623	Neurogenesis. Protein ubiquitination.
HPCAL4	hippocalcin-like protein 4	BC030827			1.359	0.783	1.454	0.369	1.514	0.351	Central nervous system development.
DGKG	" diacylglycerol kinase, gamma 90kDa"	NM_001346			1.498	0.857	1.363	0.515	1.465	0.436	Protein kinase C activation. Intracellular signaling cascade.
MAL	" T-lymphocyte maturation-associated protein, isoform a"	BC000458			1.468	0.47	1.336	0.507	1.517	0.823	Signal transduction. Central nervous system development. Hemocyte development.
STAC	SH3 and cysteine rich domain	NM_003149			1.323	0.49	1.363	0.512	1.634	0.397	Intracellular signaling cascade.
CCNA1	cyclin A1	NM_003914			2.123	0.561	1.182	0.44	1.014	0.476	Regulation of cyclin dependent protein kinase activity. Cytokinesis. Mitosis. Meiosis. Male meiosis I.
N/A	Unknown (protein for MGC:33592)	BC022082			1.662	0.671	1.212	0.657	1.444	0.781	
C13orf18	C13orf18 protein	BC032311			1.329	0.397	1.271	0.584	1.715	0.882	
KIAA0273	N/A	D87463			1.128	0.517	1.144	0.511	2.036	0.568	
TUB	tubby isoform a	NM_003320			1.74	1.168			2.567	0.514	
ITGA8	" integrin, alpha 8"	NM_003638			2.033	1.004	1.217	0.76	1.056	0.473	Cell-matrix adhesion. Integrin-mediated signaling pathway. Cell-cell adhesion.
ZNF80	zinc finger protein 80 (pT17)	NM_007136			2.461	0.971			1.843	0.996	Transcription. Regulation of transcription, DNA-dependent.
FLJ45803	FLJ45803 protein	NM_207429			2.292	0.653			2.009	0.792	
ADAMTS18	" a disintegrin-like and metalloprotease (reprolysin type) with t	NM_199355			2.068	0.626			2.225	0.771	Proteolysis and peptidolysis.
N/A	N/A	AK123485			1.797	0.67	1.355	0.546	1.138	0.352	
COL23A1	" collagen, type XXIII, alpha 1"	NM_173465			1.083	0.631	1.328	0.784	1.879	0.327	Phosphate transport. Cell adhesion.
LOC200420	LOC200420	NM_145300			1.731	0.856			2.548	0.549	
N/A	N/A	AK126812			1.142	0.65	1.239	0.435	1.891	0.441	
KL	klotho isoform b	NM_153683			1.799	0.428	1.168	0.387	1.305	0.393	Carbohydrate metabolism.
CRMP1	collapsin response mediator protein 1	NM_001313			2.095	1.324			2.176	1.086	Nucleobase, nucleoside, nucleotide and nucleic acid metabolism. Neurogenesis.
N/A	N/A	AK056971	1.085	0.796	1.728	0.463	1.073	0.508	1.469	0.51	
MYCN	" v-myc myelocytomatosis viral related oncogene, neuroblasto	NM_005378			1.346	0.678	1.241	0.625	1.674	0.523	Regulation of transcription from RNA polymerase II promoter.
PITPNM3	PITPNM family member 3	NM_031220			1.512	0.778	1.397	0.997	1.348	0.499	Phosphoinositide metabolism.
N/A	unknown	AF450484			1.686	0.395	1.227	0.468	1.341	0.617	
GSCL	goosecoid-like	NM_005315			1.146	1.072	1.253	0.691	1.854	1.05	Regulation of transcription from RNA polymerase II promoter. Morphogenesis,
N/A	N/A	AK126852			2.619	0.525			1.63	0.782	
N/A	N/A	BC038293			2.808	0.37			1.44	0.799	
COL4A3	" alpha 3 type IV collagen isoform 1, precursor"	NM_000091			1.829	0.664	1.336	0.422	1.082	0.507	
C14orf8	chromosome 14 open reading frame 8	NM_173846			1.466	0.491			2.779	0.741	
FLJ20152	hypothetical protein FLJ20152	NM_019000			1.676	0.494	1.413	0.387	1.151	0.55	
N/A	N/A	AK126160			1.992	0.61			2.247	0.72	Proteolysis and peptidolysis. Protein catabolism.

DKFZp451C1317	hypothetical proteincDNA DKFZp451C1317 (from clone DKFZ	AL832601			1.26	0.398	1.434	0.434	1.545	0.509	
N/A	N/A	AK130282			1.338	0.337	1.284	0.197	1.611	0.187	
kIAA0367	N/A	AB002365			1.589	0.603			2.641	0.669	Apoptosis.
EMILIN3	elastin microfibril interfacer 3	NM_052846			1.069	0.642	1.21	0.929	1.948	1.073	
LOC145741	hypothetical LOC145741	NM_207322			2.733	0.388			1.49	0.489	
N/A	STRA6	AY358748			2.038	1.007			2.184	0.57	
RASGRF1	Ras protein-specific guanine nucleotide-releasing factor 1 isof	NM_002891			1.199	0.333	1.194	0.371	1.827	0.604	Small GTPase mediated signal transduction. Long-term memory.
TCF7	" transcription factor 7 (T-cell specific, HMG-box) isoform 1"	NM_003202			1.184	0.519	1.079	0.458	1.953	0.583	Transcription. Regulation of transcription, DNA-dependent. Immune response.
WFDC2	WAP four-disulfide core domain 2 isoform 3 precursor	NM_080733	1.789	1.416			2.101	0.664	2.113	0.722	Proteolysis and peptidolysis. Spermatogenesis.
N/A	peptide YY precursor	D13902			1.432	0.618	1.196	0.556	1.586	0.36	Cell motility. Cytoskeleton organization and biogenesis. Cell-cell signaling. Digestion.
N/A	putative tumor suppressor gene 26 protein alpha 2 delta calciu	AF040709			1.152	0.758	1.343	0.632	1.718	0.935	Ion transport. Calcium ion transport.
KIAA1855	KIAA1855 protein	AB058758			1.983	0.707			2.229	0.713	Protein amino acid phosphorylation.
N/A	N/A	AK128290			1.172	0.482	1.182	0.691	1.85	0.606	
CECR6	" cat eye syndrome chromosome region, candidate 6"	NM_031890			1.021	1.046	1.361	0.768	1.814	1.068	
SLC22A7	solute carrier family 22 member 7 isoform b	NM_153320			1.286	0.74	1.07	0.448	1.838	0.332	Ion transport. Sodium ion transport. Organic anion transport.
GFRA2	GDNF family receptor alpha 2 preproprotein	NM_001495			1.609	1.401	1.341	1.124	1.243	0.645	Transmembrane receptor protein tyrosine kinase signaling pathway.
KIAA0437	N/A	AB007897			2.147	1.244	1.037	0.655	1.008	0.607	
EDARADD	EDAR-associated death domain isoform B	NM_080738			1.663	1.106	1.199	0.95	1.329	0.644	
N/A	Unknown (protein for MGC:11077)	BC006530			1.328	0.318	1.362	0.508	1.495	0.33	
RHCG	" Rhesus blood group, C glycoprotein"	BC030965			1.352	0.54	1.248	0.473	1.584	0.644	Transport. Ammonium transport.
LHX6	LIM homeobox protein 6 isoform 1	NM_014368			2.44	0.645			1.74	0.85	Regulation of transcription, DNA-dependent. Brain development.
GAS2	GAS2 protein	BC013326			2.51	0.788			1.667	0.577	Cellular morphogenesis. Apoptosis. Cell cycle. Cell cycle arrest.
N/A	N/A	AK123049			2.625	0.481			1.551	0.37	
FLJ00138	FLJ00138 protein	AK074067			1.697	1.157	1.329	0.899	1.148	0.793	Intracellular signaling cascade.
N/A	PRSS22	AY358396			1.078	0.653	1.411	0.629	1.684	0.66	Proteolysis and peptidolysis.
CNTNAP3	cell recognition molecule CASPR3	NM_033655			1.07	0.262	1.333	0.658	1.76	0.521	Cell adhesion. Cell recognition.
POU4F1	" POU domain, class 4, transcription factor 1"	NM_006237			2.821	0.81			1.334	0.585	Regulation of transcription from RNA polymerase II promoter. Development. Axonogenesis. Synaptogenesis.
LOC284013	secretory protein LOC284013	NM_182566			1.819	0.479	1.11	0.243	1.226	0.597	
GPR103	G protein-coupled receptor 103	NM_198179			1.092	0.451	1.641	0.59	1.422	0.725	
CFC1	cryptic	NM_032545			2.123	0.975			2.029	0.488	
S100B	" S100 calcium-binding protein, beta"	NM_006272			1.682	0.837	1.099	0.96	1.37	0.741	Energy reserve metabolism. Calcium ion homeostasis. Induction of apoptosis. Axonogenesis.
DKFZp761H039	hypothetical protein DKFZp761H039	NM_018711					1.337	0.818	2.805	0.227	Ion transport.
GALNT9	polypeptide N-acetylgalactosaminyltransferase 9	NM_021808			1.195	0.358	1.141	0.739	1.804	0.596	O-linked glycosylation.
RANBP2L1	RAN-binding protein 2-like 1 isoform 2	NM_032260			2.216	0.27			1.911	0.461	
NKD1	naked cuticle homolog 1	NM_033119			1.714	0.618	1.389	0.721	1.021	0.627	
PSD2	pleckstrin and Sec7 domain containing 2	NM_032289			1.225	1.074	1.078	0.607	1.82	1.222	
CUTL2	cut-like 2	NM_015267			1.169	0.539	1.77	0.925	1.182	0.489	Regulation of transcription, DNA-dependent.
N/A	Unknown (protein for IMAGE:4798313)	BC030761			1.321	0.927	1.015	0.955	1.778	0.626	
APOBEC3A	phorbolin 1	NM_145699			1.911	0.968			2.191	0.666	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism. Metabolism.
NPHS2	podocin	NM_014625			1.181	1.11	1.439	0.69	1.476	0.671	Excretion.
N/A	LP6728	AY203947			1.854	0.544			2.241	0.576	
PMP22	peripheral myelin protein 22	NM_000304			2.323	0.509			1.772	0.505	Synaptic transmission. Peripheral nervous system development. Perception of sound. Mechanosensory behavior.
FKSG58	FKSG58	AF336885			2.319	0.804			1.775	0.445	
GNAO1	GNAO1 protein	BC030027			1.252	0.487	1.453	0.678	1.387	0.615	Muscle contraction. Signal transduction. G-protein coupled receptor protein signaling pathway. Neurogenesis. Axon guidance.
N/A	N/A	AK092418			1.667	0.352			2.425	0.324	
MEGF4	MEGF4	AB011537					1.753	0.7	2.336	0.578	
N/A	HCTP4-binding protein	AY390431					1.918	0.852	2.17	1.041	
N/A	N/A	AK092393			2.756	0.632	1.324	0.435			
N/A	N/A	AK125833			1.137	0.517	1.139	0.605	1.798	0.507	
DPYS	dihydropyrimidinase	NM_001385			1.24	0.591	1.081	0.635	1.752	0.841	Nucleobase, nucleoside, nucleotide and nucleic acid metabolism. Response to toxin.
FLT3	fms-related tyrosine kinase 3	NM_004119			1.878	0.728	1.034	0.439	1.16	0.847	Protein amino acid phosphorylation. Positive regulation of cell proliferation.
PACSIN1	PACSIN1 protein	BC040228					1.445	0.571	2.626	0.522	Endocytosis.
LOC283439	hypothetical protein LOC283439	NM_199460			2.454	0.742			1.612	0.891	
NGFR	" nerve growth factor receptor, precursor"	BC050309			1.501	0.563	1.014	0.622	1.55	0.872	Apoptosis. Signal transduction. Neurogenesis. Cell differentiation.
N/A	HSPC080	AF161343					1.321	0.633	2.743	0.798	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
MGC4766	testis-specific protein TES101RP	NM_031451			1.659	0.204			2.404	0.426	

N/A	N/A	AK125190			2.335	0.41			1.724	0.508	
NINJ2	ninjurin 2	NM_016533			2.155	0.765			1.903	0.775	Cell adhesion. Neuronal cell adhesion. Neurogenesis. Tissue regeneration.
GDF2	growth differentiation factor 2	NM_016204			1.686	0.779			2.372	0.432	Growth.
FLJ46354	FLJ46354 protein	NM_198547			1.627	0.485	1.063	0.345	1.368	0.394	Mitotic chromosome condensation.
B3GNT3	beta-1,3-N-acetylglucosaminyltransferase bGnT-3"	NM_014256					1.749	0.869	2.306	0.603	Protein amino acid glycosylation.
FLJ00202	FLJ00202 protein	AK122580			1.606	0.595			2.444	0.464	Metabolism.
FLJ00330	FLJ00330 protein	AK090421			1.017	0.662	1.145	0.604	1.884	0.649	
TNFSF8	" tumor necrosis factor (ligand) superfamily, member 8"	NM_001244			2.396	0.589			1.648	0.479	Induction of apoptosis. Immune response. Signal transduction. Cell-cell signaling. Cell proliferation.
PDGFB	c-sis/platelet-derived growth factor 2	M12783			1.433	0.922	1.021	0.798	1.584	0.47	
KIAA1013	KIAA1013 protein	AB023230			1.29	0.525	1.076	0.461	1.664	0.346	
N/A	N/A	AK130422			1.013	0.516	1.17	0.544	1.847	0.536	
DKK-2	dickkopf-2	AF177395			2.592	0.678			1.434	0.855	Development. Negative regulation of Wnt receptor signaling pathway.
OR6B3	" olfactory receptor, family 6, subfamily B, member 3"	NM_173351			1.1	0.688			2.921	0.58	
N/A	interferon	V00541			2.065	0.541			1.956	0.361	Defense response.
KIAA1119	KIAA1119 protein	AB032945			2.42	1.439			1.601	0.992	
ADD2	adducin 2 isoform e	NM_017488			1.396	1.12	1.089	0.765	1.535	0.451	
PDE8B	" 3',5' cyclic nucleotide phosphodiesterase 8B"	NM_003719			1.746	0.721	1.028	0.509	1.233	0.694	Signal transduction. Cyclic nucleotide metabolism.
RPP25	ribonuclease P 25kDa subunit	NM_017793			1.494	0.347	1.123	0.678	1.386	0.82	
OTOP1	otopetrin 1	NM_177998					1.896	0.538	2.099	0.483	
TNFRSF9	" tumor necrosis factor receptor superfamily, member 9 precur	NM_001561			2.575	0.339			1.419	0.248	Induction of apoptosis. Immune response. Negative regulation of cell proliferation.
KRTHA2	type I hair keratin 2	NM_002278			1.978	0.474			2.01	0.468	Epidermis development.
FLJ42133	hypothetical FLJ42133	NM_001001690			1.687	1.277			2.294	0.936	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism. Metabolism.
MSMB	beta-microseminoprotein isoform a precursor	NM_002443	1.195	1.545	2.08	0.307			1.899	0.458	
TGM7	transglutaminase 7	NM_052955			2.202	0.615			1.773	0.495	Peptide cross-linking.
N/A	KTSR5831	AY358206			1.666	0.905	1.012	0.381	1.292	0.995	
BAMBI	BMP and activin membrane-bound inhibitor	NM_012342			2.732	1.641			1.23	0.823	
LOC286359	hypothetical protein LOC286359	NM_182600	1.499	0.236	2.308	0.647			1.653	0.235	
LOC146206	LOC146206 protein	BC043154			1.087	0.526	1.067	0.274	1.807	0.686	
CHRNB4	" cholinergic receptor, nicotinic, beta polypeptide 4"	NM_000750			1.302	0.672	1.08	0.571	1.578	0.75	Ion transport. Signal transduction. Synaptic transmission.
SFTPC	" surfactant, pulmonary-associated protein C"	NM_003018			1.807	0.735			2.152	0.394	Respiratory gaseous exchange. Regulation of liquid surface tension.
DKFZp434B1231	eEF1A2 binding protein	NM_178275			1.179	0.922			2.78	0.493	Striated muscle contraction. Cell adhesion. Muscle development.
DNAJB8	" DnaJ homolog, subfamily B, member 8"	NM_153330			1.709	0.477			2.248	0.497	Protein folding.
B3GNT7	" UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransfer	NM_145236			1.27	0.575	1.289	0.485	1.395	0.821	Protein amino acid glycosylation.
C10orf49	chromosome 10 open reading frame 49	NM_145314			2.168	0.767			1.783	0.72	
CRHR1	corticotropin releasing hormone receptor 1	NM_004382			1.078	0.52	1.425	0.624	1.438	0.647	Immune response. Signal transduction. G-protein coupled receptor protein signaling pathway.
FLJ38379	hypothetical protein FLJ38379	NM_178530			1.863	0.3			2.077	0.572	
IL17E	interleukin 17E isoform 1 precursor	NM_022789			1.801	0.503			2.138	0.417	Inflammatory response.
ZAN	zonadhesin isoform 1	NM_173055			1.755	0.387			2.183	0.377	Cell adhesion. Binding of sperm to zona pellucida. Binding of sperm to zona pellucida. Cell recognition.
TECTA	tectorin alpha precursor	NM_005422			1.583	0.58			2.351	0.509	Cell-matrix adhesion. Perception of sound.
N/A	N/A	AK123428			1.128	0.452	1.623	0.661	1.183	0.53	
GPR144	G protein-coupled receptor 144	NM_182611			1.023	0.471	1.211	0.865	1.697	0.618	Signal transduction. Neuropeptide signaling pathway.
GCKR	glucokinase regulatory protein	NM_001486			2.546	1.317			1.381	0.63	
C18orf1	chromosome 18 open reading frame 1 isoform gamma 1	NM_001003674			1.238	0.702	1.102	0.455	1.587	0.578	
MDFI	MyoD family inhibitor	BC007836			1.048	0.506	1.589	0.635	1.284	0.535	Embryonic development. Cell differentiation. Cytoplasmic sequestering of transcription factor.
GALGT2	" sda beta-1,4-GalNAc transferase"	AJ517770			1.575	0.463	1.121	0.638	1.222	0.594	
LOC374946	hypothetical gene supported by AK075558Homo sapiens hypo	NM_198545			1.063	0.585	1.077	0.497	1.777	0.715	
c-erbB-3	ErbB-3 R35	U88360			1.66	0.249			2.257	0.366	
HPSE2	heparanase 2	NM_021828			1.651	0.469			2.264	0.516	
PPP2R2C	" gamma isoform of regulatory subunit B55, protein phosphata	NM_020416			1.332	0.766	1.062	0.52	1.52	0.975	Signal transduction.
MGC26733	hypothetical protein MGC26733	NM_144992			2.571	0.948			1.343	0.73	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
N/A	hypothetical protein	AJ291678			1.706	0.386			2.205	0.352	
SLC26A9	" solute carrier family 26, member 9 isoform a"	NM_052934			1.434	0.873			2.475	0.372	Sulfate transport.
PDE2A	" phosphodiesterase 2A, cGMP-stimulated"	NM_002599			1.385	0.445			2.522	0.65	Signal transduction.
LHX4	LIM homeobox protein 4	NM_033343			2.771	0.963	1.132	0.969			
LOR	loricrin	NM_000427					1.639	0.698	2.263	0.473	
N/A	N/A	AK094090			1.999	0.732			1.9	0.435	Electron transport. Lipid metabolism. C21-steroid hormone biosynthesis. Glucocorticoid biosynthesis.

CYB5R2	cytochrome b5 reductase b5R.2 isoform 2	NM_001001336			1.341	0.704	1.243	0.717	1.305	0.616	Electron transport. Electron transport. Cholesterol biosynthesis.
PAK1	p21-activated kinase 1	NM_002576			2.422	0.536			1.461	0.93	Protein amino acid phosphorylation. Protein amino acid phosphorylation. Apoptosis. JNK cascade.
IL20RA	" interleukin 20 receptor, alpha"	NM_014432			2.607	0.414			1.272	0.197	Blood coagulation.
RAMP2	receptor (calcitonin) activity modifying protein 2 precursor	NM_005854			1.312	0.624	1.027	0.428	1.539	0.951	Intracellular protein transport. Receptor mediated endocytosis. Cell surface receptor linked signal transduction.
N/A	N/A	AK091426			2.151	0.556			1.722	0.661	
POU4F3	POU domain, class 4, transcription factor 3"	NM_002700					1.522	0.34	2.35	0.508	Eye morphogenesis. Regulation of transcription, DNA-dependent. Neurogenesis. Visual perception. Perception of sound.
PTF1A	" pancreas specific transcription factor, 1a"	NM_178161			1.114	0.878	1.166	0.484	1.588	0.582	
CYS1	cilia-associated protein	AF544983			1.61	0.537	1.079	0.331	1.178	0.716	
GADD45G	" growth arrest and DNA-damage-inducible, gamma"	NM_006705			1.4	0.63	1.09	0.489	1.374	0.643	Activation of MAPKKK. DNA repair. Apoptosis. Response to stress. Cell differentiation.
GFI1	growth factor independent 1	NM_005263			2.818	0.539			1.045	0.541	G1/S-specific transcription in mitotic cell cycle. Transcription. Regulation of transcription, DNA-dependent. Viral life cycle.
CACNG2	voltage-dependent calcium channel gamma-2 subunit	NM_006078			1.54	0.905	1.268	0.687	1.055	0.395	Ion transport. Calcium ion transport.
N/A	N/A	AK128759			2.055	0.981			1.804	0.585	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism. Metabolism.
FLJ45983	FLJ45983 protein	NM_207423			2.754	0.547			1.103	0.785	
FLJ30469	FLJ30469 protein	BC057816			1.842	0.995			2.013	0.455	
N/A	N/A	AK127934			1.666	0.941			2.188	0.391	
OR1I1	" olfactory receptor, family 1, subfamily I, member 1"	NM_001004713			1.988	0.473			1.859	0.678	Signal transduction. G-protein coupled receptor protein signaling pathway. Perception of smell.
NPM2	nucleoplasmin 2 variant 1	AY262113			1.09	0.449	1.37	0.465	1.387	0.355	Chromatin remodeling. Regulation of translation. Regulation of exit from mitosis. Fertilization. Embryonic development.
SLC24A5	" solute carrier family 24 (sodium/potassium/calcium exchange	NM_205850			2.338	0.814			1.508	0.741	
N/A	N/A	AK124493			1.016	0.566			2.829	0.562	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
AMN	amnionless protein	NM_030943			1	0.548	1.099	0.401	1.742	0.41	Development.
ADRA2B	alpha-2B-adrenergic receptor	NM_000682			1.056	0.529	1.334	0.559	1.449	0.797	Signal transduction. G-protein coupled receptor protein signaling pathway. Cell-cell signaling.
CASQ2	cardiac calsequestrin 2	BC022288			2.029	1.053			1.809	0.816	Striated muscle contraction. Heart development. Muscle development.
FMOD	fibromodulin precursor	NM_002023			2.151	0.786			1.679	0.687	Transforming growth factor beta receptor complex assembly.
AXIN2	axin 2	NM_004655			1.604	0.449			2.226	0.537	Signal transduction. Frizzled signaling pathway. Development.
SIGLEC9	sialic acid binding Ig-like lectin 9	NM_014441			2.103	0.661			1.718	1.101	Cell adhesion.
UBXD3	UBX domain containing 3	NM_152376					1.293	0.29	2.524	0.651	
CRHR2	corticotropin releasing hormone receptor 2	NM_001883			1.005	0.528	1.235	0.246	1.577	0.655	Signal transduction. G-protein coupled receptor protein signaling pathway.
PDYN	beta-neoendorphin-dynorphin preproprotein	NM_024411			1.964	0.635			1.846	0.613	Neuropeptide signaling pathway. Synaptic transmission.
LOC283868	LOC283868 protein	BC033227			1.181	0.572	1.012	0.647	1.617	0.46	
N/A	N/A	AK026786			1.572	0.392			2.236	0.124	
G0S2	putative lymphocyte G0/G1 switch gene	NM_015714			1.197	0.983	1.115	0.675	1.496	0.598	Regulation of cell cycle.
HTR6	5-hydroxytryptamine (serotonin) receptor 6	NM_000871			1.18	0.599	1.324	0.589	1.303	0.628	Signal transduction. G-protein signaling, coupled to cyclic nucleotide second messenger. Synaptic transmission.
NAT8	N-acetyltransferase 8	NM_003960			1.672	0.543			2.13	0.355	Response to drug.
TNFSF7	" tumor necrosis factor ligand superfamily, member 7"	NM_001252			1.81	0.264			1.989	0.462	Apoptosis. Immune response. Signal transduction. Cell-cell signaling. Cell proliferation.
WIF1	Wnt inhibitory factor-1 precursor	NM_007191			2.033	0.406			1.765	0.403	Signal transduction. Cell-cell signaling. Development. Wnt receptor signaling pathway.
HMX1	homeo box (H6 family) 1	NM_018942			1.053	0.621	1.149	0.417	1.596	0.66	Regulation of transcription, DNA-dependent.
CELL	carboxyl ester lipase-like protein	L14813	1.096	1.477	1.538	0.492			2.254	0.528	
RARRES2	retinoic acid receptor responder (tazarotene induced) 2	NM_002889			1.809	0.691			1.982	0.952	Retinoid metabolism.
CCR5	chemokine (C-C motif) receptor 5	NM_000579			2.145	0.353			1.645	0.539	G-protein coupled receptor protein signaling pathway.
DKFZp566F223	hypothetical proteincDNA DKFZp566F223 (from clone DKFZp5	AL050056			1.633	0.812			2.155	0.667	Microtubule-based movement. Protein polymerization.
MGAT4A	" mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosa	NM_012214			2.714	0.332			1.072	0.513	Carbohydrate metabolism. N-glycan processing.
GRIA1	" glutamate receptor, ionotropic, AMPA 1"	NM_000827			2.09	0.47			1.69	0.54	Ion transport. Potassium ion transport. Signal transduction. Synaptic transmission.
TMOD2	tropomodulin 2 (neuronal)	NM_014548			2.634	1.031			1.145	0.433	Neurogenesis.
N/A	N/A	AK091259			1.298	0.351			2.481	0.437	
MGC34741	hypothetical protein MGC34741	NM_153356			1.657	0.783			2.114	0.453	
LEMD1	LEM domain containing 1	NM_001001552			1.986	0.535			1.779	0.456	
N/A	N/A	AF035316			1.72	0.719			2.036	0.652	Microtubule-based movement. Protein polymerization.
SIAT8F	" alpha-2, 8-sialyltransferase"	NM_001004470			1.506	1.036	1.161	0.67	1.089	0.863	Protein amino acid glycosylation.
N/A	RhoGEF protein	AF433662			1.238	0.538	1.22	0.312	1.289	0.701	Rho protein signal transduction.
LOC400696	eosinophil lysophospholipase-like	NM_207646			2.009	0.67			1.736	0.611	
FLJ44186	FLJ44186 protein	NM_198508			1.203	0.553	1.289	0.566	1.245	0.447	
N/A	N/A	AK096803			1.651	0.578			2.081	0.401	
N/A	myosin	L29144			2.359	0.688			1.372	0.482	
KRT25C	keratin 25C	NM_181537	2.456	2.04	2.53	0.378			1.201	0.485	
CPA6	carboxypeptidase B precursor	NM_020361			2.523	0.933	1.206	0.439			Proteolysis and peptidolysis.
ALDH3B2	aldehyde dehydrogenase 3B2	NM_000695			1.686	0.737			2.043	0.45	Alcohol metabolism. Lipid metabolism.

LMX1B	" LIM homeobox transcription factor 1, beta"	NM_002316			1.621	0.698	1.041	0.484	1.065	0.681	Embryonic development. Regulation of transcription, DNA-dependent. Dorsal/ventral pattern formation.
UPB1	beta-ureidopropionase	NM_016327			1.207	0.736	1.017	0.731	1.496	0.314	Nitrogen compound metabolism.
KIAA1130	KIAA1130 protein	AB032956			1.311	0.933	1.068	0.77	1.337	1.136	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
PAX8	paired box gene 8 isoform PAX8A	NM_003466			2.281	0.333			1.434	0.433	GTP biosynthesis. UTP biosynthesis. CTP biosynthesis. Transcription. Regulation of transcription.
SYN3	synapsin III isoform IIIa	NM_003490			2.353	0.452			1.357	0.955	Neurotransmitter secretion. Neurotransmitter secretion.
TPPP	brain-specific protein p25 alpha	NM_007030			1.234	0.639	1.094	0.598	1.378	0.979	
KRTHB3	keratin, hair, basic, 3"	NM_002282					1.393	0.361	2.313	0.378	Epidermis development.
STRC	stereocilin	NM_153700			1.778	0.805			1.928	0.696	Perception of sound.
N/A	hypothetical protein	AJ311357					1.15	0.579	2.554	0.345	Transport.
CRYM	" crystallin, mu"	BC018061			2.312	0.681			1.389	0.558	Visual perception.
TRIM31	tripartite motif protein 31 isoform alpha	NM_007028			1.863	0.452			1.837	0.454	Protein ubiquitination.
MYOG	myogenin	BC053899			1.352	0.631			2.348	0.562	Regulation of transcription, DNA-dependent. Transcription from RNA polymerase II promoter. Myogenesis. Cell differentiation.
FBP1	" fructose-1,6-bisphosphatase 1"	NM_000507			1.081	0.637	1.305	0.558	1.311	0.307	Carbohydrate metabolism. Fructose metabolism. Gluconeogenesis.
KIAA0167	KIAA0167 protein	D79989			2.394	0.567			1.302	0.577	Signal transduction. Small GTPase mediated signal transduction.
KIAA1006	KIAA1006 protein	AB023223			1.332	0.383			2.355	1.149	Vesicle-mediated transport.
PLP1	proteolipid protein 1 isoform 1	NM_000533			1.993	0.932			1.69	0.617	
PGF	" placental growth factor, vascular endothelial growth factor-re	NM_002632			1.121	1.033	1.088	0.72	1.452	0.59	Regulation of cell cycle. Angiogenesis. Signal transduction. Cell-cell signaling. Cell proliferation.
FCGR2B	" Fc fragment of IgG, low affinity IIb, receptor for (CD32) isofor	NM_004001			1.553	0.364			2.108	0.406	Immune response.
PCDH21	protocadherin 21 precursor	NM_033100			1.287	0.864	1.027	0.347	1.343	0.503	Homophilic cell adhesion.
N/A	N/A	AK126716					1.208	0.404	2.448	0.902	Germ cell development. Embryonic development. RNA interference.
NPPB	natriuretic peptide precursor B	NM_002521					1.624	0.489	2.03	0.381	Signal transduction. Fluid secretion. Regulation of blood pressure. Negative regulation of angiogenesis.
PLA2G2A	" phospholipase A2, group IIA"	NM_000300			1.377	1.001			2.273	0.444	Lipid catabolism.
KCNK4	potassium channel, subfamily K, member 4 isoform 1"	NM_016611					1.765	0.593	1.881	0.681	Potassium ion transport.
SMO	smoothened	NM_005631			2.252	1.089			1.391	0.832	G-protein coupled receptor protein signaling pathway. Development.
MT3	metallothionein 3	NM_005954			1.522	0.456			2.121	0.422	Response to hypoxia. Metal ion homeostasis. Removal of superoxide radicals. Negative regulation of cell growth.
ANGPT4	angiopoietin 4	NM_015985	1.107	1.941	1.738	0.854			1.905	0.381	
THRB	" thyroid hormone receptor, beta"	NM_000461			1.049	0.244	1.188	0.422	1.405	0.7	Regulation of transcription, DNA-dependent. Perception of sound.
WFDC5	WAP four-disulfide core domain 5 precursor	NM_145652			1.512	0.804			2.129	0.438	
N/A	N/A	AK075214			1.571	0.659			2.069	0.675	Cell cycle.
KCNA6	" potassium voltage-gated channel, shaker-related subfamily,	NM_002235			1.029	0.536	1.06	0.597	1.55	0.4	Cation transport. Potassium ion transport.
RGS8	regulator of G-protein signalling 8	NM_033345			1.525	0.595			2.114	0.435	Signal transduction.
FLJ21511	hypothetical protein FLJ21511	NM_025087			1.165	0.587	1.315	0.437	1.157	0.478	
CACNA1E	calcium channel, voltage-dependent, alpha 1E subunit"	NM_000721					1.13	0.406	2.507	0.601	Calcium ion transport. Synaptic transmission.
FLJ14050	hypothetical protein FLJ14050	NM_024869			1.824	0.792			1.809	0.579	
N/A	N/A	AK095622			1.686	0.359			1.946	0.593	
PTPN3	PTPN3 protein	BC063287			1.369	0.84	1.128	0.908	1.133	1.019	
CRYGC	" crystallin, gamma C"	NM_020989			2.602	0.517			1.026	0.307	
DCNP1	dendritic cell nuclear protein 1	NM_130848			1.784	0.8			1.841	0.399	
ENPP2	ectonucleotide pyrophosphatase/phosphodiesterase 2 (autota	NM_006209			2.428	0.397	1.196	0.512			Phosphate metabolism. Cell motility. Chemotaxis. G-protein coupled receptor protein signaling pathway. Nucleotide metabolism.
CELSR1	cadherin EGF LAG seven-pass G-type receptor 1	NM_014246			1.274	0.774	1.286	0.956	1.062	0.712	Cell adhesion. Homophilic cell adhesion. Signal transduction. Neuropeptide signaling pathway. Development.
MGC50104	Similar to RIKEN cDNA 1810046K07 gene	NM_198498			2.579	0.51	1.042	0.556			
DKFZp761B1219	hypothetical proteincDNA DKFZp761B1219 (from clone DKFZ	AL831923			1.006	1.443	1.406	0.516	1.201	0.636	
IRX4	iroquois homeobox protein 4	NM_016358			1.375	0.641	1.153	0.506	1.082	0.439	Regulation of transcription, DNA-dependent. Heart development.
LIN28	lin-28 homolog	NM_024674			2.162	0.694			1.438	0.822	Regulation of transcription, DNA-dependent.
TNNI1	" troponin I, skeletal, slow"	NM_003281			1.821	0.665			1.774	0.536	Regulation of striated muscle contraction. Muscle development.
N/A	N/A	AK024257			1.223	0.886	1.277	0.394	1.093	0.455	Cell adhesion.
TLP	thymus LIM protein TLP-A	NM_206922			1.602	0.748			1.989	0.421	
AP1G2	" adaptor-related protein complex 1, gamma 2 subunit"	NM_080545			2.129	1.128			1.459	0.899	Protein complex assembly. Intracellular protein transport. Endocytosis.
PRLR	prolactin receptor	NM_000949			2.424	0.571			1.162	0.579	Steroid biosynthesis. Steroid biosynthesis. Anti-apoptosis. Anti-apoptosis.
GSC	goosecoid	NM_173849			2.161	0.721			1.422	0.465	
INA	" internexin neuronal intermediate filament protein, alpha"	NM_032727			2.038	0.636			1.541	0.489	Neurogenesis. Cell differentiation.
CLECSF13	C-type lectin, superfamily member 13"	NM_173535					1.196	0.901	2.381	0.551	
SLC14A2	" solute carrier family 14 (urea transporter), member 2"	NM_007163			1.868	0.563			1.708	0.494	Transport. Urea transport. Urea transport.
SCGB1D1	lipophilin A	NM_006552			1.838	0.433			1.736	0.407	
ADORA1	adenosine A1 receptor	NM_000674			1.513	0.891			2.061	0.824	Phagocytosis. Inflammatory response. G-protein coupled receptor protein signaling pathway. Cell-cell signaling.
KIAA1154	KIAA1154 protein	AB032980			2.154	0.522			1.417	0.407	Cellular defense response. Intracellular signaling cascade.

N/A	YPLR6490	AY358209			2.344	0.92	1.221	0.478			
N/A	N/A	AK128772			1.617	0.36			1.947	0.366	Neuropeptide signaling pathway.
N/A	N/A	AK056949					1.007	0.601	2.551	0.372	
CAMK2B	calcium/calmodulin-dependent protein kinase IIB isoform 1	NM_001220					1.365	0.428	2.193	0.832	Protein amino acid phosphorylation. Protein amino acid phosphorylation. Signal transduction.
ECEL1	endotheline-converting enzyme ECEL1	AB030579			1.109	0.649	1.005	0.553	1.443	0.749	Proteolysis and peptidolysis. Neuropeptide signaling pathway.
NDRG4	NDRG family member 4	NM_020465	1.04	0.68	1.336	0.876	1.126	0.626	1.093	0.765	Response to stress. Cell growth. Cell differentiation.
SIGLEC11	sialic acid binding Ig-like lectin 11	NM_052884			1.742	0.268			1.812	0.267	
TFF3	trefoil factor 3 precursor	NM_003226			1.334	1.122			2.211	0.644	Defense response. Digestion.
N/A	N/A	AK128146			1.493	0.54			2.052	0.464	
TRIM40	TRIM40 protein	BC060785			2.245	0.729			1.299	0.668	
FLJ00136	FLJ00136 protein	AK074065					1.198	0.648	2.342	0.815	
N/A	N/A	AK126028			1.379	0.787	1.088	0.824	1.071	0.636	
IGFL4	insulin growth factor-like family member 4	NM_001002923			1.387	0.65			2.148	0.648	
FXYD6	FXYD6 protein	BC018652			1.38	0.63			2.153	0.712	Ion transport.
LOC339047	LOC339047 protein	BC008178			1.526	0.368			2.005	0.146	Neuropeptide signaling pathway.
OR6B2	" olfactory receptor, family 6, subfamily B, member 2"	NM_001005853			1.351	0.835			2.178	0.356	
FCGR1A	" Fc fragment of IgG, high affinity Ia, receptor for (CD64)"	NM_000566			1.744	0.603			1.784	0.243	Phagocytosis, engulfment. Immune response. Signal transduction.
KIAA0631	KIAA0631 protein	AB014531			1.721	0.586			1.806	0.525	
MARK1	MAP/microtubule affinity-regulating kinase 1	NM_018650			2.407	0.856			1.118	0.475	Protein amino acid phosphorylation. Cytoskeleton organization and biogenesis. Protein kinase cascade.
IFNA5	" interferon, alpha 5"	NM_002169			1.768	0.775			1.756	0.383	Defense response.
TNRC4	trinucleotide repeat containing 4	NM_007185			1.603	0.582			1.918	0.338	Nuclear mRNA splicing, via spliceosome. Neurogenesis.
N/A	hypothetical protein	AJ311358			1.238	0.788			2.283	0.5	Transport.
GPR81	G protein-coupled receptor 81	NM_032554			2.03	0.617			1.483	0.895	Proteolysis and peptidolysis. Proteolysis and peptidolysis. Anti-apoptosis. Apoptotic program. Regulation of apoptosis.
N/A	protein phosphatase inhibitor 2	AF275684			2.368	0.303			1.139	0.453	
N/A	testis-specific protein NYD-TSP1	AF333098			1.877	0.45			1.623	0.67	
SIAT7A	" GalNAc alpha-2, 6-sialyltransferase I"	NM_018414			1.388	0.376			2.111	0.557	Protein amino acid glycosylation. Protein amino acid glycosylation.
IGFBP1	insulin-like growth factor binding protein 1	NM_000596			2.079	0.705			1.418	0.215	Regulation of cell growth. Signal transduction.
PLCXD3	" phosphatidylinositol-specific phospholipase C, X domain con	NM_001005473			1.946	0.795			1.547	0.549	Intracellular signaling cascade.
NHLH2	nescient helix loop helix 2	NM_005599			2.435	0.998			1.056	0.96	Transcription. Regulation of transcription, DNA-dependent. Central nervous system development. Cell differentiation.
N/A	N/A	AK125618	3.755	0.301	1.714	0.553	1.775	0.305			Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism. Metabolism.
RP1L1	retinitis pigmentosa 1-like 1	NM_178857			1.83	0.476			1.657	0.678	
N/A	N/A	AK127467			1.549	0.543			1.938	0.936	
N/A	Unknown (protein for MGC:87634)	BC066987			2.147	0.793			1.339	0.438	
N/A	N/A	AK125695			1.738	0.556			1.748	0.459	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism. Metabolism.
CSTL1	cystatin-like 1 precursor	NM_138283			1.806	0.886			1.677	0.57	
CNNM1	cyclin M1	NM_020348			1.017	0.442	1.102	0.4	1.358	0.833	Fatty acid biosynthesis.
EMID2	putative emu2	NM_133457			1.103	0.327	1.178	0.511	1.195	0.651	Phosphate transport.
CST8	cystatin 8 precursor	NM_005492			1.303	0.6			2.172	0.599	
IL8RA	interleukin 8 receptor alpha	NM_000634			2.126	0.849			1.346	0.637	
N/A	N/A	AK098147			1.297	0.429			2.174	0.681	
N/A	TMC2	AY358613			2.023	0.689			1.447	0.584	
EFNA3	ephrin A3	NM_004952			1.683	0.591			1.785	0.49	Cell-cell signaling.
HCG9	HLA complex group 9	NM_005844			1.715	0.622			1.752	0.478	
RAET1L	retinoic acid early transcript 1L	NM_130900			2.447	0.652			1.016	0.372	Antigen presentation. Natural killer cell activation.
N/A	N/A	X64979			1.84	0.554			1.622	1.05	
N/A	N/A	AK098759			2.062	0.689			1.399	0.405	
HSPC105	NAD(P) dependent steroid dehydrogenase-like	NM_145168			1.856	0.453			1.604	0.796	
DKFZp434B1222	hypothetical proteincDNA DKFZp434B1222 (from clone DKFZ	AL133624			1.991	0.415			1.468	0.451	Signal transduction.
N/A	N/A	BC028736			2.15	1.161			1.302	0.765	Ion transport. Potassium ion transport. Signal transduction. Synaptic transmission.
SESN3	sestrin 3	NM_144665			2.403	1.134			1.048	0.79	Cell cycle arrest.
DKFZp564G2082	hypothetical protein	AL833943					1.514	0.445	1.937	0.685	
DKFZp761O1810	hypothetical proteincDNA DKFZp761O1810 (from clone DKFZ	AL713706			2.184	0.482			1.266	0.292	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism. Metabolism.
SIAT8A	sialyltransferase 8A	NM_003034			2.192	0.568	1.253	0.234			Carbohydrate metabolism. Protein amino acid glycosylation. Glycosphingolipid biosynthesis.
N/A	N/A	AK092134			2.399	1.073			1.046	0.61	
CYP19A1	" cytochrome P450, family 19"	NM_031226			1.562	0.693			1.88	0.39	Electron transport. Steroid biosynthesis. Transport.
PROP1	" prophet of Pit1, paired-like homeodomain transcription factor	NM_006261			1.862	0.535			1.579	0.595	Regulation of transcription, DNA-dependent. Central nervous system development.

KRT13	keratin 13 isoform a	NM_153490			1.921	0.799			1.52	0.853	Epidermis development.
GRIK1	" Glutamate receptor, ionotropic, kainate 1 isoform 2 precurso	NM_175611			1.676	0.644			1.76	0.492	Ion transport. Potassium ion transport. Glutamate signaling pathway. Synaptic transmission. Central nervous system development.
RBP4	N/A	NM_006744			2.066	0.719			1.368	0.588	Transport. Sensory perception. Visual perception-
MUC3	mucin	AF007194			1.078	0.547			2.351	0.454	
OR4D6	" olfactory receptor, family 4, subfamily D, member 6"	NM_001004708			2.124	0.909	1.298	0.88			
SERPING1	complement component 1 inhibitor precursor	NM_000062			1.855	0.564			1.567	0.548	Immune response. Complement activation, classical pathway. Blood coagulation. Circulation.
GPR74	G protein-coupled receptor 74	NM_004885			1.745	0.829			1.676	0.808	Signal transduction. G-protein coupled receptor protein signaling pathway. Detection of abiotic stimulus.
TEKT1	tektin 1	NM_053285			2.054	0.611			1.367	0.752	Microtubule cytoskeleton organization and biogenesis.
FLJ35171	FLJ35171 protein	NM_199338			1.758	0.387			1.662	0.48	
MGC35206	hypothetical protein MGC35206	NM_178552					1.11	1.352	2.307	0.625	
CNGB1	cyclic nucleotide gated channel beta 1	NM_001297			2.186	0.628			1.231	0.268	Ion transport. Potassium ion transport.
LBP	lipopolysaccharide-binding protein precursor	NM_004139			1.368	0.436			2.048	0.756	Lipid transport. Acute-phase response. Cellular defense response. Response to pathogenic bacteria
GATA3	GATA binding protein 3 isoform 1	NM_001002295			2.38	0.578			1.035	0.718	Regulation of transcription, DNA-dependent. Transcription from RNA polymerase II promoter. Defense response.
FLJ14001	hypothetical protein FLJ14001	NM_024677			2.23	0.79	1.183	0.679			
MMP9	matrix metalloproteinase 9 preproprotein	NM_004994			1.63	0.618			1.783	0.3	Collagen catabolism.
WNT8B	" wingless-type MMTV integration site family, member 8B prec	NM_003393			2.132	0.537			1.278	0.295	Signal transduction. Frizzled-2 signaling pathway. Cell-cell signaling. Development. Neurogenesis.
N/A	Unknown (protein for IMAGE:4825217)	BC034818			2.157	0.507			1.252	0.416	
LOC90139	tetraspanin similiar to uroplakin 1	NM_130783			1.776	0.848			1.633	0.48	
KCND3	Sha1-related potassium channel Kv4.3	AF120491			1.102	0.372	1.129	0.644	1.173	0.647	Cation transport. Potassium ion transport.
N/A	N/A	AK096973			1.772	0.879			1.631	0.663	
hCT2	carnitine transporter 2	AB055798			2.099	0.742	1.303	0.398			Transport. Spermatid cell development. Spermatid cell development. Fertilization.
SH3BGRL2	SH3 domain binding glutamic acid-rich protein like 2	NM_031469			2.182	0.803			1.218	0.674	
KCNK13	" potassium channel, subfamily K, member 13"	BC012779			1.291	0.537	1.045	0.684	1.063	0.718	Ion transport. Potassium ion transport.
DKFZP564O0823	DKFZP564O0823 protein	NM_015393			1.874	0.379			1.521	0.606	
CALC	calcitonin	X02330			2.088	0.605			1.304	0.585	Skeletal development. G-protein signaling, coupled to cAMP nucleotide second messenger.
AVPR1B	arginine vasopressin receptor 1B	NM_000707			1.44	0.576			1.952	0.701	Signal transduction. Phospholipase C activation. Positive regulation of cytosolic calcium ion concentration.
KRTAP5-11	keratin associated protein 5-11	AJ628247			1.372	0.579			2.019	0.856	
SH3GL2	SH3GL2 protein	BC032825			1.714	0.622			1.674	1.146	Signal transduction. Central nervous system development.
KIAA1384	KIAA1384 protein	AB037805			1.341	1.004			2.045	1.162	
KIAA1264	KIAA1264 protein	AB033090			1.571	0.779			1.814	0.879	Protein amino acid phosphorylation.
FLJ41327	FLJ41327 protein	NM_207485			1.35	0.365			2.034	0.642	
N/A	SFVP2550	AY358815	1.465	1.14	2.068	1.236			1.315	0.686	
KIAA2015	KIAA2015 protein	AB095935			1.092	0.754	1.164	0.426	1.126	0.453	
PLEKHA7	" pleckstrin homology domain containing, family A member 2"	NM_175058			1.113	0.894	1.137	0.552	1.131	0.819	
KIAA1392	KIAA1392 protein	AB037813			1.27	0.562			2.11	0.294	
FLJ40083	hypothetical protein FLJ40083	NM_182628					1.242	0.65	2.137	0.679	
KIAA0220	KIAA0220 protein	BC061522			1.33	0.329			2.047	0.206	Neuropeptide signaling pathway.
ZNF383	zinc finger protein 383	NM_152604	3.043	0.734	1.571	0.77	1.806	0.65			Regulation of transcription, DNA-dependent.
SLC6A12	" solute carrier family 6 (neurotransmitter transporter, betaine/	NM_003044			1.166	0.572			2.211	0.669	Neurotransmitter transport. Amino acid transport.
N/A	N/A	AK124156			2.137	0.516	1.238	0.486			Transmembrane receptor protein tyrosine kinase signaling pathway. Cellular defense response. T-cell activation.
MCOLN2	mucolipin 2	NM_153259			2.295	0.928			1.08	0.496	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism. Metabolism.
PIGR	polymeric immunoglobulin receptor	NM_002644			1.652	0.583			1.722	0.373	Protein secretion.
TMPRSS6	" transmembrane protease, serine 6"	NM_153609			1.03	1.102			2.342	0.567	Angiogenesis. Proteolysis and peptidolysis. Intracellular signaling cascade.
UNC5B	unc-5 homolog B	NM_170744			2.265	1.277			1.106	1.012	Apoptosis. Signal transduction. Development.
LOC342897	similar to F-box only protein 2	NM_001001414			1.583	0.933			1.788	0.793	
FLJ30707	FLJ30707 protein	BC051771			1.947	1.099			1.423	0.627	
OXGR1	oxoglutarate (alpha-ketoglutarate) receptor 1	NM_080818			1.683	0.431			1.685	0.482	
N/A	N/A	AK128705			1.509	0.47			1.855	0.618	
C9orf65	chromosome 9 open reading frame 65	NM_138818			1.993	0.62			1.37	0.697	
OR13J1	" olfactory receptor, family 13, subfamily J, member 1"	NM_001004487			1.915	0.75			1.447	0.449	
KIAA1442	KIAA1442 protein	AB037863			1.839	0.819			1.514	0.661	Proteolysis and peptidolysis.
FLJ00254	FLJ00254 protein	AK074181	2.742	0.037	1.622	0.629	1.73	0.375			Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
NOS3	nitric oxide synthase 3 (endothelial cell)	NM_000603			1.726	0.683			1.623	0.618	Electron transport. Amino acid metabolism. Nitric oxide biosynthesis. Cell motility.
DKFZp761P211	similar to hypothetical protein Y97E10AL.1	NM_001003665			1.905	0.774	1.444	0.849			
NBL1	" neuroblastoma, suppression of tumorigenicity 1 precursor"	NM_182744			2.304	0.372	1.045	0.531			Cell cycle. Negative regulation of cell cycle.
N/A	N/A	AK075525			1.797	0.547			1.55	0.729	

CABP1	CABP1 protein	BC015006			1.189	0.697			2.156	0.472	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
TGM5	transglutaminase 5 isoform 1	NM_201631			1.297	0.527			2.048	0.554	Epidermis development. Peptide cross-linking.
PODXL2	endoglycan	BC052585			1.924	0.839			1.421	1.194	
KRT6IRS	keratin 6 irs	NM_033448			1.011	0.558			2.334	0.411	
SCGB1D4	secretoglobin family 1D member 4	NM_206998			1.531	0.581			1.813	0.478	
VENTX2	VENT-like homeobox 2	NM_014468					1.838	0.688	1.502	0.931	Regulation of transcription, DNA-dependent.
CILP	cartilage intermediate layer protein	NM_003613			1.737	0.583			1.601	0.34	Nucleobase, nucleoside, nucleotide and nucleic acid metabolism.
N/A	N/A	AK055704			1.52	0.542			1.815	0.478	Protein amino acid dephosphorylation.
ASCL2	achaete-scute complex homolog-like 2	NM_005170			1.67	1.197			1.665	0.879	Transcription. Central nervous system development. Peripheral nervous system development. Cell differentiation.
N/A	N/A	AK125859			1.61	0.774			1.722	0.6	
RAP140	retinoblastoma-associated protein 140	NM_015224	2.313		1.589		1.741				
FP14381	unknown	AF461895			1.791	0.493			1.539	0.613	
KCNK17	potassium channel, subfamily K, member 17"	NM_031460					1.295	0.687	2.032	0.742	Ion transport. Potassium ion transport.
TFAP2B	transcription factor AP-2 beta (activating enhancer binding prot	NM_003221			1.901	0.481			1.425	0.664	Transcription. Regulation of transcription from RNA polymerase II promoter. Neurogenesis.
SCIN	SCIN protein	BC021090			2.142	0.851			1.18	0.872	
NBC4	sodium bicarbonate cotransporter NBC4c	AF293337			1.438	1.48			1.884	0.488	Anion transport. Bicarbonate transport.
N/A	N/A	AK129827			2.261	0.851			1.061	0.632	
FAM46C	FLJ20202 protein	NM_017709			1.723	0.934	1.599	1.096			
CYP21A2	" cytochrome P450, family 21, subfamily A, polypeptide 2"	NM_000500			1.725	0.53			1.596	0.533	Electron transport. C21-steroid hormone biosynthesis.
N/A	PRO2769	AF116713			1.231	0.642			2.09	0.503	Hyaluronan metabolism. Immune cell activation.
KIAA1159	KIAA1159 protein	AB032985			1.655	0.777			1.661	0.742	Neuropeptide signaling pathway.
N/A	hypothetical protein	AJ295984			1.364	0.654			1.951	0.536	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
MGC33309	hypothetical protein MGC33309	NM_152413			1.645	0.546			1.67	0.632	
CD244	NK cell type I receptor protein 2B4	AF363452			1.412	0.598			1.902	0.917	
LOC387700	similar monocarboxylate transporter	NM_213606			1.739	0.864			1.573	0.775	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism. Metabolism.
N/A	N/A	AK124496			1.542	0.196			1.769	0.368	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
CA8	carbonic anhydrase VIII	NM_004056			1.752	0.537			1.559	0.56	One-carbon compound metabolism.
FLJ38723	hypothetical protein FLJ38723	NM_173805	1.232	1.823	1.773	0.754			1.537	0.707	
PVALB	parvalbumin	NM_002854			1.203	0.472			2.104	0.692	Muscle development.
HAPLN2	brain link protein-1	NM_021817			2.065	0.776			1.241	0.575	Cell adhesion.
CHRM1	" cholinergic receptor, muscarinic 1"	NM_000738			1.295	0.986			2.011	0.678	Protein modification. Signal transduction. Protein kinase C activation. Muscarinic acetylcholine receptor.
N/A	N/A	AK074473			1.95	0.529			1.355	0.643	
RASEF	RAS and EF hand domain containing	NM_152573			1.957	0.941	1.345	0.842			Small GTPase mediated signal transduction. Protein transport.
GCA	" grancalcin, EF-hand calcium binding protein"	NM_012198			2.158	0.483			1.143	0.597	Membrane fusion.
CACNG8	voltage-dependent calcium channel gamma-8 subunit	NM_031895			1.13	0.906			2.17	0.607	Ion transport. Calcium ion transport.
DKFZp761B107	hypothetical protein DKFZp761B107	NM_173463			1.956	0.93			1.341	0.466	
CHD7	chromodomain helicase DNA binding protein 7	NM_017780			2.234	1.082	1.063	0.839			Chromatin assembly or disassembly.
LRRTM1	leucine rich repeat transmembrane neuronal 1	NM_178839			1.452	0.543			1.84	0.593	
FLJ42486	FLJ42486 protein	NM_207379					1.487	0.592	1.804	0.37	
N/A	Unknown (protein for IMAGE:4724389)	BC020909			1.805	0.438			1.484	0.468	
LRP5	low density lipoprotein receptor-related protein 5	NM_002335					1.493	0.347	1.794	0.531	Lipid metabolism. Endocytosis. Signal transduction. Development. Positive regulation of cell proliferation.
CD1D	" CD1D antigen, d polypeptide"	NM_001766			1.944	0.833			1.342	0.729	Detection of bacteria. T-cell selection. Positive regulation of innate immune response.
N/A	N/A	AK126297			1.487	0.721			1.796	0.452	
N/A	N/A	AK056716					1.641	0.687	1.642	0.865	
FLJ39743	hypothetical protein FLJ39743	NM_182562					1.388	0.92	1.891	0.798	
N/A	X2 box repressor	U22680			2.239	1.097			1.039	0.81	
PSCDBP	" pleckstrin homology, Sec7 and coiled-coil domains, binding p	NM_004288			2.005	0.933			1.269	0.739	
ZPBP2	zona pellucida binding protein 2 isoform 1	NM_198844			1.236	0.662			2.037	0.908	Binding of sperm to zona pellucida.
CD86	CD86 antigen isoform 2 precursor	NM_006889			1.637	0.496			1.635	0.54	Immune response. Positive regulation of cell proliferation. T-cell activation.
N/A	AKAP-binding sperm protein ropporin	AF231410			1.947	0.473			1.318	0.741	Cytokinesis. Signal transduction. Rho protein signal transduction. Spermatogenesis. Acrosome reaction.
FLJ00197	FLJ00197 protein	AK074125			2.24	0.926			1.022	0.922	
DMBT1	deleted in malignant brain tumors 1 isoform b precursor	NM_007329			1.331	0.795			1.93	0.407	Epithelial cell differentiation. Induction of bacterial agglutination. Innate immune response.
KRTAP9-4	keratin associated protein 9-4	NM_033191					1.169	0.339	2.09	0.557	
UNC5C	unc5C	NM_003728			2.017	0.629			1.24	0.64	Apoptosis. Signal transduction. Development. Axon guidance. Brain development.
PDE1B	phosphodiesterase 1B, calmodulin-dependent"	NM_000924					1.412	0.712	1.843	0.501	Apoptosis. Signal transduction.
COAS2	cyclophilin-LC	NM_178230			1.759	0.252			1.49	0.191	Protein folding.

PRKCG	" protein kinase C, gamma"	NM_002739			2.163	0.679			1.084	0.232	Protein amino acid phosphorylation. Intracellular signaling cascade.
MOG	MOG protein	BC035938			1.761	0.682			1.482	0.583	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism. Metabolism.
IL1R2	" interleukin 1 receptor, type II precursor"	NM_004633			1.361	0.444			1.881	0.62	Immune response.
ALDH5A1	" aldehyde dehydrogenase 5A1 precursor, isoform 1"	NM_170740			1.941	1.295			1.299	0.621	Metabolism. Gamma-aminobutyric acid metabolism. Gamma-aminobutyric acid catabolism. Dopamine metabolism.
CML2	putative N-acetyltransferase Camello 2	NM_016347			1.23	0.807			2.009	0.467	Response to drug.
N/A	N/A	AK125438					1.274	0.718	1.963	0.321	
MYH6	myosin heavy chain 6	NM_002471			1.574	0.713			1.661	0.39	Striated muscle contraction. Muscle development.
FCA/MR	Fc alpha/mu receptor	NM_032029			1.469	0.375			1.764	0.827	
KIAA0837	KIAA0837 protein	AB020644					1.368	0.606	1.861	0.584	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
GFI1B	" growth factor independent 1B (potential regulator of CDKN1	NM_004188			1.959	0.666			1.267	0.376	G1-specific transcription in mitotic cell cycle. Negative regulation of transcription. Cell proliferation.
KCNN3	small conductance calcium-activated potassium channel protei	NM_002249			1.935	0.468			1.289	0.796	Ion transport. Potassium ion transport. Potassium ion transport. Synaptic transmission. Neurogenesis.
MGC34827	hypothetical protein MGC34827	NM_152693			1.56	0.487			1.661	0.614	
LSECtin	liver and lymph node sinusoidal endothelial cell C-type lectin	NM_198492			1.353	0.81			1.865	0.723	
FLJ37927	CDC20-like protein	NM_152623			3.21	1.18					
ITGB1BP3	integrin beta 1 binding protein 3	NM_170678			1.507	0.528			1.701	0.845	Pyridine nucleotide biosynthesis.
NDRG2	N-myc downstream-regulated gene 2 isoform a	NM_201535			1.683	0.472			1.523	0.609	Cell differentiation. Cell differentiation.
N/A	prothymosin a14	AF170294			1.705	0.936			1.501	0.878	
N/A	N/A	AK074442			1.077	0.476			2.127	0.753	Muscle contraction.
BPI	bactericidal/permeability-increasing protein precursor	NM_001725			1.714	0.539			1.489	0.264	Immune response. Defense response to bacteria.
C1QR1	" complement component 1, q subcomponent, receptor 1"	NM_012072			1.93	0.871			1.272	0.669	Phagocytosis. Antimicrobial humoral response (sensu Protostomia). Cell-cell adhesion. Macrophage activation,
COL19A1	alpha 1 type XIX collagen precursor	NM_001858			1.894	0.679			1.307	0.493	Skeletal development. Phosphate transport. Cell adhesion. Cell-cell adhesion. Extracellular matrix organization and biogenesis.
N/A	N/A	AK125708			1.391	1.209			1.809	0.983	
DPCR1	diffuse panbronchiolitis critical region 1 protein	NM_080870			1.092	0.272			2.106	0.398	
N/A	N/A	AK056484			1.752	0.447			1.441	0.607	
N/A	skin-antimicrobial peptide 1 (SAP1)	Z71389			1.642	0.765			1.55	0.329	Chemotaxis. Immune response. G-protein coupled receptor protein signaling pathway. Response to pest, pathogen or parasite.
NKX6-2	" NK6 transcription factor related, locus 2"	NM_177400			1.948	0.53	1.241	0.531			Regulation of transcription, DNA-dependent.
N/A	N/A	AK125166			1.169	0.328			2.02	0.39	
FLJ90165	hypothetical protein FLJ90165	NM_153338			1.221	0.492			1.968	0.401	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
MGC26988	hypothetical protein MGC26988	NM_130899					1.089	0.904	2.097	1.208	
OR8B4	" olfactory receptor, family 8, subfamily B, member 4"	NM_001005196			1.223	0.436			1.962	0.485	
HLA-DOA	" major histocompatibility complex, class II, DO alpha"	NM_002119			1.824	0.573			1.36	0.631	Immune response. Antigen presentation, exogenous antigen. Antigen processing, exogenous antigen via MHC class II.
AGXT2L1	alanine-glyoxylate aminotransferase 2-like 1	NM_031279			2.092	0.802			1.092	0.369	Amino acid metabolism.
ADRB1	beta-1-adrenergic receptor	NM_000684			1.616	0.87			1.568	1.005	Signal transduction. G-protein coupled receptor protein signaling pathway. Adenylate cyclase activation.
N/A	N/A	AK093839					1.591	0.547	1.589	0.588	
CHRNA2	" cholinergic receptor, nicotinic, alpha polypeptide 2 (neuronal)	NM_000742			1.079	0.795			2.098	0.3	Ion transport. Signal transduction. Synaptic transmission.
DKFZp434P162	hypothetical proteincDNA DKFZp434P162 (from clone DKFZp	AL833871			1.125	0.226			2.051	0.437	
JACOP	likely ortholog of mouse junction-associated coiled-coil protein	NM_032866			1.035	0.589	1.057	0.907	1.084	0.995	
P2RX2	purinergic receptor P2X2 isoform D	NM_170683			2.083	0.893	1.092	0.423			Ion transport.
KIF1A	axonal transport of synaptic vesicles	NM_004321			1.025	0.578	1.066	0.542	1.083	0.576	Microtubule-based movement. Anterograde axon cargo transport.
FLJ25169	hypothetical protein FLJ25169	NM_152568			1.159	0.4			2.015	0.569	
DKFZp434B1612	hypothetical proteincDNA DKFZp434B1612 (from clone DKFZ	AL157436			2.033	0.996	1.141	0.964			MRNA processing. MRNA-nucleus export. Protein-nucleus import. Transport. Development.
TBX4	T-box 4	NM_018488			1.494	0.84			1.679	0.617	Transcription. Regulation of transcription, DNA-dependent. Development.
N/A	N/A	AK098018			1.31	0.523			1.863	0.734	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
PTTG2	pituitary tumor-transforming 2	NM_006607			2.093	0.794			1.078	0.412	DNA replication and chromosome cycle. DNA metabolism.
PP3227	unknown	AF193053			1.645	0.292			1.526	0.335	
GPR8	G protein-coupled receptor 8	NM_005286			1.338	0.706			1.833	0.593	Signal transduction. G-protein coupled receptor protein signaling pathway.
DHDH	dimeric dihydrodiol dehydrogenase	NM_014475	2.865	0.331	1.852	0.402			1.319	0.363	Carbohydrate metabolism. Electron transport. Metabolism.
N/A	N/A	AK093877			1.405	0.859			1.764	0.284	Carbohydrate metabolism. Aldehyde metabolism.
CTNNA3	" catenin, alpha 3"	NM_013266			2.001	0.573			1.168	0.643	Cell adhesion.
FLJ00278	FLJ00278 protein	AK090401			1.232	0.194			1.936	0.368	
KRTAP12-4	keratin associated protein 12-4	NM_198698			1.017	0.685			2.151	0.626	
KIAA0656	KIAA0656 protein	AB014556			1.776	1.281			1.391	0.985	
N/A	PP10566	AF370395			1.446	0.681			1.715	0.645	
FLJ00292	FLJ00292 protein	AK131088			1.748	0.431			1.413	0.3	
ABCG4	" ATP-binding cassette, subfamily G, member 4"	NM_022169			1.5	1.319			1.661	0.752	Transport.
N/A	N/A	M21389			1.357	1.069			1.797	0.44	Ectoderm development.

GALR1	galanin receptor 1	NM_001480			1.73	0.67			1.423	0.559	Ion transport. Signal transduction. Negative regulation of adenylate cyclase activity. Neuropeptide signaling pathway.
BMP7	bone morphogenetic protein 7 precursor	NM_001719					1.076	0.694	2.076	0.97	Skeletal development. Cell differentiation. Growth.
CCR1	chemokine (C-C motif) receptor 1	NM_001295			2.119	0.938			1.032	0.536	Chemotaxis. Inflammatory response. Cell adhesion. G-protein signaling, coupled to cyclic nucleotide second messenger.
N/A	N/A	AK126834					1.471	0.43	1.679	0.833	
NPL	N-acetylneuraminate pyruvate lyase	NM_030769			1.912	0.599			1.238	0.516	Lysine biosynthesis. Diaminopimelate biosynthesis.
TRIM29	tripartite motif protein TRIM29 isoform alpha	NM_012101			1.233	0.595			1.916	0.491	Transcription from RNA polymerase II promoter.
FLJ33387	hypothetical protein FLJ33387	NM_182526			1.703	0.925			1.445	0.883	
NFASC	neurofascin isoform 1	NM_001005388			1.262	0.891			1.884	1.123	Cell adhesion.
ARHGEF15	Rho guanine exchange factor 15	NM_173728			1.057	0.703			2.084	0.442	
NOTCH4	notch4 preproprotein	NM_004557			1.604	1.083			1.536	0.373	Patterning of blood vessels. Cell fate determination. Transcription. Notch signaling pathway.
N/A	N/A	AK130194			1.399	0.766			1.741	0.899	
FLJ37118	hypothetical protein FLJ37118	NM_173507			1.85	0.825			1.287	0.656	
KRTAP10-6	keratin associated protein 10-6	NM_198688			1.512	0.492			1.624	0.345	
INHBB	inhibin beta B subunit precursor	NM_002193	1.06	0.924	1.89	0.979	1.246	0.691			Ovarian follicle development. Defense response. Response to external stimulus. Cell differentiation. Growth.
N/A	N/A	AK126832	1.385	1.749	1.463	0.56			1.671	0.408	
N/A	Unknown (protein for IMAGE:4105361)	BC016338	2.383	1.32	1.135	1			1.997	0.772	
N/A	N/A	AK130933			1.752	0.258			1.38	0.476	
DKFZp434E1119	hypothetical proteincDNA DKFZp434E1119 (from clone DKFZ	AL834516			1.664	0.568			1.467	0.736	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism. Metabolism.
N/A	amyloid lambda 6 light chain variable region PIP	AF267874			1.826	0.38			1.302	0.64	
KRTAP12-1	keratin associated protein 12-1	NM_181686			1.646	0.848			1.482	0.282	
N/A	NPD009	AF237813			1.309	0.578			1.817	0.581	Synaptic transmission. Gamma-aminobutyric acid metabolism. Neurotransmitter catabolism.
FLJ00278	FLJ00278 protein	AK090401			1.19	0.315			1.936	0.368	
KRTAP10-7	keratin associated protein KAP10.7	AJ566385			1.707	0.421			1.417	0.568	
DKFZP564J102	DKFZP564J102 protein	NM_015398			1.749	1.028			1.375	0.564	
CA14	carbonic anhydrase XIV precursor	NM_012113			1.917	0.475			1.207	0.865	One-carbon compound metabolism.
KIAA1511	KIAA1511 protein	AB040944	1.065	1.166	1.96	0.806			1.159	0.704	
N/A	Unknown (protein for MGC:71567)	BC059370			1.495	0.599			1.623	0.359	
N/A	N/A	AK057390			1.999	0.61			1.119	0.54	Microtubule cytoskeleton organization and biogenesis.
FLJ44006	FLJ44006 protein	NM_001001696			1.479	0.819			1.637	1.027	
UNC5A	UNC5A protein	BC009333			1.424	0.635			1.692	0.407	Apoptosis. Signal transduction. Development.
MST148	MST148 protein	AF184211					1.222	0.323	1.893	0.538	
N/A	Unknown (protein for IMAGE:4477067)	BC012029			1.376	0.689			1.738	0.56	
HLA-DPB1	" major histocompatibility complex, class II, DP beta 1 precurs	NM_002121			2.071	0.629			1.042	0.478	Immune response. Pathogenesis. Detection of pest, pathogen or parasite. Antigen presentation, exogenous antigen.
DLGAP4	disks large-associated protein 4 isoform a	NM_014902			1.067	0.53			2.046	0.656	Cell-cell signaling.
KCNA7	potassium voltage-gated channel, shaker-related subfamily, me	NM_031886					1.083	0.307	2.026	0.44	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
GRM4	" glutamate receptor, metabotropic 4"	NM_000841			1.526	0.994			1.583	0.489	G-protein coupled receptor protein signaling pathway. Negative regulation of adenylate cyclase activity. Synaptic transmission.
N/A	N/A	AK127720	1.601	1.877	1.937	0.716			1.17	0.803	
SLC16A10	" solute carrier family 16, member 10"	NM_018593			3.106	1.053					Transport.
DKFZp686O2282	hypothetical protein	BX537382					1.463	0.326	1.643	0.777	Sodium ion transport. Amino acid transport. L-asparagine transport. L-glutamine transport.
N/A	N/A	AK128620			1.344	0.762			1.757	0.698	
EFHD1	EF hand domain containing 1	NM_025202			2.043	0.73	1.058	0.694			
LZLP	leucine zipper-like protein	AF159055			1.882	0.386			1.216	0.47	
WFDC12	WAP four-disulfide core domain 12 precursor	NM_080869			1.562	0.587			1.535	0.544	
N/A	putative microtubule-binding protein	AJ251708			3.096	0.47					DNA repair. Transcription. Regulation of transcription, DNA-dependent. Chromatin modification.
FLJ43806	hypothetical protein FLJ43806	NM_201628			1.676	0.418			1.417	0.481	
UNQ467	KIPV467	NM_207392			1.352	0.737			1.736	0.735	
SFTPA2	" surfactant, pulmonary-associated protein A2"	NM_006926			1.504	0.753			1.584	0.638	Phosphate transport. Respiratory gaseous exchange. Regulation of liquid surface tension.
PNPLA5	patatin-like phospholipase domain containing 5	NM_138814					1.539	0.454	1.549	0.563	
RAMP3	receptor (calcitonin) activity modifying protein 3 precursor	NM_005856	1.04	0.977			1.205	0.872	1.882	0.785	Intracellular protein transport. Receptor mediated endocytosis. Cell surface receptor linked signal transduction.
N/A	N/A	BC032235			1.82	0.875			1.266	0.306	
SPINT1	hepatocyte growth factor activator inhibitor 1 isoform 1 precurs	NM_181642			1.71	1.059			1.375	0.754	
N/A	PCOLCE2	AY358557			2.002	0.781			1.08	0.669	
KCNA4	" potassium voltage-gated channel, shaker-related subfamily,	NM_002233			1.501	0.738			1.576	0.653	Cation transport. Potassium ion transport.
IFNA8	" interferon, alpha 8"	NM_002170			1.274	0.447			1.803	0.346	Defense response.
RIMS4	regulating synaptic membrane exocytosis 4	NM_182970					1.21	0.881	1.865	1.103	Neurotransmitter transport. Exocytosis.
PPM1E	protein phosphatase 1E	NM_014906			1.929	0.67			1.145	0.421	Protein amino acid dephosphorylation.

OR13A1	" olfactory receptor, family 13, subfamily A, member 1"	NM_001004297	1.066	0.759	1.799	0.579	1.275	0.305			
E2F3	E2F3 protein	BC016847			1.981	0.546			1.089	0.588	Regulation of cell cycle. Transcription. Regulation of transcription, DNA-dependent.
N/A	Unknown (protein for IMAGE:5093011)	BC068999			1.703	0.586			1.365	0.645	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
C14orf166B	chromosome 14 open reading frame 166B	NM_194287			1.859	0.728			1.209	0.564	
N/A	DAP-1 alpha	AF131778					1.297	0.474	1.771	1.179	Cell-cell signaling.
MGC33846	hypothetical protein MGC33846	NM_175885			1.473	0.856			1.592	0.784	
LPHN3	latrophilin 3	NM_015236					1.393	0.519	1.669	0.58	Signal transduction. Neuropeptide signaling pathway.
KIAA1276	KIAA1276 protein	AB033102					1.319	0.474	1.741	0.783	
TNFAIP2	tumor necrosis factor, alpha-induced protein 2"	NM_006291					1.538	0.871	1.518	0.473	Angiogenesis. Cell differentiation.
SFTPA2	" surfactant, pulmonary-associated protein A2"	NM_006926			1.568	0.607			1.488	0.656	Phosphate transport. Respiratory gaseous exchange. Regulation of liquid surface tension.
APOL4	apolipoprotein L4 isoform 1	NM_030643	1.025	1.647	1.484	0.28			1.571	0.345	Lipid transport. Lipoprotein metabolism.
SLC37A1	glycerol 3-phosphate permease	AF311320			1.591	0.53			1.462	0.814	Transport.
SLC11A1	" solute carrier family 11 (proton-coupled divalent metal ion tra	NM_000578			1.151	0.248			1.902	0.083	Transport. Transport. Iron ion transport. Response to bacteria.
PR1	PR1 protein	BC046362			1.187	0.766			1.866	0.392	
RIBC2	RIB43A domain with coiled-coils 2	NM_015653					1.283	0.445	1.768	0.628	
POU3F1	" POU domain, class 3, transcription factor 1"	NM_002699	1.511	0.982	1.114	0.691	1.936	1.665			Regulation of transcription, DNA-dependent. Nerve ensheathment.
FLJ41423	FLJ41423 protein	NM_001001679			1.586	0.728			1.463	0.655	
N/A	myosin-reactive immunoglobulin light chain variable region	AF035038			1.383	0.49			1.663	0.504	
TERT	telomerase reverse transcriptase isoform 1	NM_003219					1.507	0.574	1.535	0.674	RNA-dependent DNA replication. Telomerase-dependent telomere maintenance.
N/A	N/A	AK124823					1.135	0.332	1.905	0.614	
KLF14	Kruppel-like factor 14	NM_138693			3.04	1.479					Transcription. Regulation of transcription, DNA-dependent.
SMC1L2	SMC1 structural maintenance of chromosomes 1-like 2	NM_148674					1.223	0.747	1.816	0.891	
N/A	N/A	AK124125					1.357	0.399	1.682	0.84	Protein modification.
DKFZp667J0810	hypothetical proteincDNA DKFZp667J0810 (from clone DKFZ	AL713800			1.377	0.649			1.661	0.409	
SLC6A5	" solute carrier family 6 (neurotransmitter transporter, glycine),	NM_004211			1.159	0.829			1.873	0.665	Neurotransmitter transport. Synaptic transmission.
GPR114	G-protein coupled receptor 114	NM_153837			1.435	0.662			1.597	0.425	Signal transduction. Neuropeptide signaling pathway.
TMEM34	transmembrane protein 34	NM_018241			1.47	1.591	1.561	0.843			
DKFZp434M131	hypothetical proteincDNA DKFZp434M131 (from clone DKFZp	AL080179			1.309	0.447			1.722	0.399	
POU2F2	" POU domain, class 2, transcription factor 2"	NM_002698			1.072	0.723			1.957	0.483	Regulation of transcription, DNA-dependent. Humoral immune response.
KIAA1257	KIAA1257 protein	AB033083			1.095	1.008			1.932	0.988	
P-Rex2	P-Rex2 protein	AJ437636			1.953	0.724			1.071	0.467	Intracellular signaling cascade.
N/A	N/A	AK125854			1.855	0.929			1.167	0.781	Lipid metabolism. Intracellular signaling cascade.
LOC150236	similar to hypothetical protein DKFZp434K191	NM_131915			1.959	0.37			1.062	0.316	
SIAT1	sialyltransferase 1 isoform a	NM_173216			1.543	0.641			1.476	0.693	Protein amino acid glycosylation. Humoral immune response. Oligosaccharide metabolism. Growth.
ERAF	erythroid associated factor	NM_016633			1.695	1.002			1.322	0.667	Protein folding. Hemoglobin metabolism. Hemopoiesis.
FKSG68	FKSG68	AF338196	1.886	1.221	1.875	0.999			1.14	0.509	
HPGD	hydroxyprostaglandin dehydrogenase 15-(NAD)	NM_000860			3.014	0.598					Lipid metabolism. Fatty acid metabolism. Prostaglandin metabolism. Metabolism.
KIAA1183	KIAA1183 protein	AB033009			1.083	0.517			1.93	0.33	
SLC22A14	organic cation transporter like 4	NM_004803			1.647	1.032	1.365	0.589			Transport.
BCL11A	B-cell CLL/lymphoma 11A isoform 1	NM_022893			1.874	0.52	1.138	0.386			Transcription. Regulation of transcription, DNA-dependent. Hemopoiesis.
G6PC	" glucose-6-phosphatase, catalytic"	NM_000151			1.152	0.609			1.857	0.805	Glycogen metabolism. Glycogen biosynthesis. Glucose metabolism. Transport.
FLJ10748	hypothetical protein FLJ10748	NM_018203			1.885	0.723			1.12	0.367	
MYOM2	myomesin 2	NM_003970			1.765	0.734			1.239	0.592	Striated muscle contraction. Muscle development.
HPCA	hippocalcin	NM_002143			1.006	0.36			1.997	0.886	
PAPOLB	poly(A) polymerase beta (testis specific)	NM_020144			1.729	0.98			1.271	0.671	Transcription. mRNA processing.
HFSE-1	HFSE-1	AF072164	1.629	1.933	1.642	1.308	1.358	1.602			
GLDC	glycine dehydrogenase (decarboxylatingHomo sapiens glycine	NM_000170			1.684	0.662			1.316	0.53	Glycine catabolism.
TNFSF11	" tumor necrosis factor ligand superfamily, member 11 isoform	NM_003701			1.205	0.753			1.79	0.649	Immune response. Cell differentiation. Osteoclast differentiation.
N/A	Unknown (protein for IMAGE:4797124)	BC022565			1.658	0.712	1.334	0.66			Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism. Metabolism.
SLC1A3	" solute carrier family 1 (glial high affinity glutamate transporte	NM_004172			2.991	0.504					Neurotransmitter uptake. Transport. Dicarboxylic acid transport. Synaptic transmission. L-glutamate transport.
GPR73L1	G protein-coupled receptor 73-like 1	NM_144773			1.115	0.651			1.876	0.805	Signal transduction. G-protein coupled receptor protein signaling pathway.
IL28RA	" interleukin 28 receptor, alpha isoform 1"	NM_170743			1.756	0.5			1.233	0.851	
KDR	kinase insert domain receptor (a type III receptor tyrosine kina	NM_002253			1.968	0.604			1.019	0.613	Angiogenesis. Transmembrane receptor protein tyrosine kinase signaling pathway. Cell differentiation.
TLS-ERG	N/A	S77574			1.088	0.57			1.894	1.178	
PODXL	podocalyxin-like precursor	NM_005397			1.702	0.745			1.278	0.477	
LY6G6E	lymphocyte antigen 6 complex G6E isoform 2	NM_001003721			1.304	0.469			1.674	0.32	

MYL3	MYL3 protein " ventricular, skeletal, slow, mRNA (cDNA clone	BC009790					1.054	0.479	1.923	0.518	Muscle contraction. Muscle development.
KIAA1976	KIAA1976 protein	AB075856			1.317	0.539			1.66	0.459	Apoptosis. Signal transduction. Development.
SALPR	G-protein coupled receptor SALPR	NM_016568			1.926	0.962	1.048	0.79			Signal transduction. G-protein coupled receptor protein signaling pathway.
pp12613	unknown	AF318325			1.816	0.469			1.157	0.68	
KRT25B	keratin 25B	NM_181539			1.891	1.361			1.082	1.17	
SIAT7B	sialyltransferase 7	NM_006456			1.419	0.933			1.553	0.86	Protein amino acid glycosylation.
N/A	N/A	AK128824			1.387	0.696			1.577	0.737	
ENPP5	ectonucleotide pyrophosphatase/phosphodiesterase 5 (putativ	NM_021572			1.708	0.673			1.255	0.515	Nucleotide metabolism.
ULBP1	UL16 binding protein 1	AF425265			2.961	0.414					Antigen presentation. Natural killer cell activation.
DKFZp564L1878	hypothetical proteincDNA DKFZp564L1878 (from clone DKFZ	AL157430			2.961	0.785					
DMRTC1	DMRTC1 protein	BC029799			1.431	0.47			1.528	0.589	
N/A	N/A	AK127522	3.128	0.568	1.154	0.604			1.805	0.427	
PCK1	cytosolic phosphoenolpyruvate carboxykinase 1	NM_002591					1.224	1.076	1.734	0.466	Gluconeogenesis.
N/A	N/A	AK002043			1.149	0.7			1.809	0.331	
LGR6	leucine-rich repeat-containing G protein-coupled receptor 6	NM_021636					1.34	0.593	1.616	0.727	Signal transduction. G-protein coupled receptor protein signaling pathway.
RHBG	RHBG protein	BC065218			1.321	0.717			1.63	0.802	Transport.
BENE	BENE protein	NM_005434			1.793	0.507			1.156	0.632	
NYD-SP25	protein kinase NYD-SP25 isoform 1	NM_033516			1.146	1.054			1.801	0.536	
C20orf58	chromosome 20 open reading frame 58	NM_152864	1.094	1.109			1.166	0.568	1.781	0.832	
RORB	RAR-related orphan receptor B	NM_006914			1.791	0.514			1.15	0.778	Transcription. Regulation of transcription, DNA-dependent,
MRGX1	G protein-coupled receptor MRGX1	NM_147199			1.359	0.646			1.581	0.498	
N/A	N/A	BX161445			1.075	0.796			1.864	0.493	
CHRFAM7A	CHRNA7-FAM7A fusion isoform 1	NM_139320			1.642	0.525			1.297	0.317	Activation of MAPK. Ion transport. Signal transduction. Synaptic transmission.
OCA2	P protein	NM_000275			1.787	0.313			1.15	0.549	Eye pigment biosynthesis. Transport.
MLNR	motilin receptor	NM_001507			1.711	0.806			1.225	0.758	Smooth muscle contraction. Signal transduction. G-protein coupled receptor protein signaling pathway.
N/A	pps22-1 protein	AY498718					1.332	0.204	1.603	0.311	
CCL3	chemokine (C-C motif) ligand 3	NM_002983			1.69	1.172			1.245	0.887	Calcium ion homeostasis. Exocytosis. Cell motility. Chemotaxis. Inflammatory response. Cytoskeleton organization.
N/A	FEX2	AY311388			1.911	0.839			1.022	1.132	
SLC22A8	solute carrier family 22 member 8	NM_004254			1.222	0.886			1.71	0.485	Transport. Ion transport. Organic anion transport.
N/A	N/A	AK098562			1.872	0.636			1.059	0.42	
DKFZp434E092	hypothetical proteincDNA DKFZp434E092 (from clone DKFZp	AL834175			1.889	0.582			1.042	0.364	
TREML4	triggering receptor expressed on myeloid cells-like 4	NM_198153			1.169	0.642			1.761	0.727	
NUDT10	nudix (nucleoside diphosphate linked moiety X)-type motif 10	NM_153183			1.44	1.288			1.489	0.708	Intracellular signaling cascade. Calcium-mediated signaling. Cyclic-nucleotide-mediated signaling.
N/A	Unknown (protein for MGC:62031)	BC056262			1.138	0.353			1.791	0.369	Transport.
LOC115648	similar to hypothetical protein FLJ13659	NM_145326			1.013	0.644	1.915	0.616			Regulation of transcription, DNA-dependent.
zf31	zinc finger protein zfp31	U71600			1.83	0.6			1.096	0.622	
DKFZp667N0215	hypothetical proteincDNA DKFZp667N0215 (from clone DKFZ	BX640915			1.848	0.842	1.078	0.867			
OTOP2	otopetrin 2	NM_178160					1.681	0.587	1.244	0.563	
N/A	N/A	AK094783			1.494	0.596			1.431	0.345	
N/A	hypothetical protein	AL035288			1.011	0.594			1.91	0.408	
USH1G	Usher syndrome 1G protein	NM_173477					1.694	0.755	1.219	0.623	
FLJ35429	hypothetical protein FLJ35429	NM_001003807			1.374	0.764			1.538	0.395	
C20orf39	chromosome 20 open reading frame 39	NM_024893					1.156	0.483	1.754	0.887	
KCNS3	potassium voltage-gated channel delayed-rectifier protein S3	NM_002252	1.196	0.826	1.575	1.003			1.334	0.998	Cation transport. Potassium ion transport.
GFRA3	GDNF family receptor alpha 3 preproprotein	NM_001496					1.192	0.664	1.714	0.389	Signal transduction. Peripheral nervous system development.
DKFZp686O1754	hypothetical proteincDNA DKFZp686O1754 (from clone DKFZ	BX640902			1.728	1.281			1.178	0.967	
BPESC1	" blepharophimosis, epicanthus inversus and ptosis, candidat	NM_021812			1.14	0.628			1.766	0.543	
EPHA8	ephrin receptor EphA8 precursor	NM_020526			1.158	0.804			1.747	0.763	Protein amino acid phosphorylation. Protein amino acid phosphorylation.
PITX2	paired-like homeodomain transcription factor 2 isoform c	NM_000325			2.905	0.667					Regulation of transcription, DNA-dependent. Development. Determination of left/right symmetry. Organogenesis.
CYP2S1	" cytochrome P450, family 2, subfamily S, polypeptide 1"	NM_030622	1.179	0.705	1.891	0.806			1.012	0.681	Electron transport. Transport.
C13orf25	chromosome 13 open reading frame 25 isoform B	NM_213723			2.901	1.485					
N/A	N/A	BX640632					1.873	0.684	1.025	0.749	
EDAR	ectodysplasin A receptor	NM_022336			1.25	0.459			1.648	0.415	Apoptosis. Signal transduction. Epidermis development. Cell differentiation.
MRC1	mannose receptor C type 1 precursor	NM_002438			1.472	0.519			1.425	0.381	Receptor mediated endocytosis. Pinocytosis.
CDH5	" cadherin 5, type 2 preproprotein"	NM_001795			1.533	0.499			1.363	0.504	Cell adhesion. Homophilic cell adhesion,
MGC17299	hypothetical protein MGC17299	NM_144626			1.638	0.538			1.257	0.549	

TMIE	transmembrane inner ear protein	NM_147196					1.153	0.483	1.741	0.68	
POU3F1	transcriptional regulator	S81257			1.595	0.902	1.297	0.576			Regulation of transcription, DNA-dependent. Nerve ensheathment.
HCRTR2	orexin receptor 2	NM_001526			1.641	1.135			1.251	0.693	Signal transduction. Neuropeptide signaling pathway. Synaptic transmission. Feeding behavior.
GPR128	G protein-coupled receptor 128	NM_032787			1.42	1.031			1.47	0.362	
OLIG1	oligodendrocyte transcription factor 1	BC033290			1.738	0.561			1.151	0.727	Regulation of transcription, DNA-dependent. Development.
N/A	N/A	AK124823					1.135	0.332	1.752	0.735	
CALML5	calmodulin-like skin protein	BC039172							2.883	0.376	Signal transduction. Epidermis development.
CABP7	calcium binding protein 7	NM_182527					1.164	0.581	1.711	0.929	
SLC9A3	solute carrier family 9 (sodium/hydrogen exchanger), isoform 3	NM_004174					1.216	0.877	1.655	0.977	Sodium ion transport. Regulation of pH.
N/A	neurogenic extracellular slit protein Slit2	AF055585			1.784	0.527			1.085	0.585	Ureteric bud development. Chemotaxis. Cell adhesion. G-protein coupled receptor protein signaling pathway.
ARMCX2	ALEX2 protein	NM_177949			1.669	0.482			1.199	0.945	
TACR1	tachykinin receptor 1 isoform long	NM_001058	1.172	1.335	1.841	0.944	1.026	0.666			Inflammatory response. Signal transduction. G-protein coupled receptor protein signaling pathway.
ADRBK2	beta adrenergic receptor kinase 2	NM_005160			1.184	0.542			1.683	0.656	Protein amino acid phosphorylation. Signal transduction.
N/A	carbonic anhydrase VII short form	AY075020			1.018	0.599			1.848	0.724	One-carbon compound metabolism.
CSEN	Kv channel interacting protein 3	NM_013434	1.996	1.732	1.078	0.876			1.786	0.739	Regulation of transcription. Signal transduction.
PRKCZ	" protein kinase C, zeta"	NM_002744			1.312	0.778			1.549	0.834	Protein amino acid phosphorylation. Anti-apoptosis. Intracellular signaling cascade.
HAO2	hydroxyacid oxidase 2	NM_001005783			1.748	1.305			1.112	0.667	Fatty acid alpha-oxidation. Electron transport.
KIAA0711	KIAA0711 protein	AB018254			1.693	0.789			1.166	0.654	
GLP1R	glucagon-like peptide 1 receptor	NM_002062					1.194	0.499	1.663	0.7	Generation of precursor metabolites and energy. Signal transduction. Adenylate cyclase activation.
KIAA0523	KIAA0523 protein	NM_015253					1.153	0.622	1.701	0.977	
CCR9	chemokine (C-C motif) receptor 9 isoform A	NM_031200			1.407	0.77			1.447	0.815	Chemotaxis. Cellular defense response. Signal transduction. G-protein coupled receptor protein signaling pathway.
N/A	N/A	AK090863			1.094	0.801			1.758	0.664	
KCNQ1DN	KCNQ1 downstream neighbor	NM_018722			1.627	1.095			1.224	0.652	
hp51CN	inositol polyphosphate 5- phosphatase	X98429			1.735	0.359			1.116	0.318	Phosphate metabolism. Intracellular signaling cascade.
RDH12	retinol dehydrogenase 12 (all-trans and 9-cis)	NM_152443			1.818	0.493	1.031	0.617			Sensory perception. Metabolism. Retinol metabolism. Photoreceptor maintenance.
DLEU7	deleted in lymphocytic leukemia 7	NM_198989					1.047	0.547	1.802	0.688	
NPHS1	nephrin	NM_004646			1.189	0.647			1.659	0.434	Cell adhesion. Excretion.
SCN2B	" sodium channel, voltage-gated, type II, beta"	BC036793			1.249	0.548			1.594	0.555	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
HUMCYT2A	cytokeratin 2	NM_015848			1.223	1			1.619	0.308	Cytoskeleton organization and biogenesis.
N/A	neurocalcin	AF251061	1.63	1.594	1.692	0.489			1.149	0.568	Vesicle-mediated transport.
IFNA17	" interferon, alpha 17"	NM_021268			1.827	0.371			1.011	0.539	Defense response. Cell-cell signaling. Response to virus.
C21orf63	chromosome 21 open reading frame 63	NM_058187			1.427	0.424			1.41	0.48	
PADI4	" peptidyl arginine deiminase, type IV"	NM_012387			1.025	0.804			1.808	0.723	Protein modification. Protein modification.
CRYGD	" crystallin, gamma D"	NM_006891			1.544	0.345			1.288	0.612	Sensory perception. Visual perception.
ASCL1	achaete-scute complex homolog-like 1	BC004425			1.276	0.831			1.556	0.837	Regulation of transcription from RNA polymerase II promoter. Neurogenesis. Cell differentiation.
D4S234E	brain neuron cytoplasmic protein 1	NM_014392					1.433	0.497	1.398	0.854	Dopamine receptor signaling pathway.
DKFZp434N092	hypothetical proteincDNA DKFZp434N092 (from clone DKFZp	AL713690			1.433	1.079	1.396	0.686			
C14orf162	chromosome 14 open reading frame 162	NM_020181			1.236	0.714			1.592	0.591	
FLJ11127	hypothetical protein FLJ11127	NM_019018			1.512	0.712			1.314	0.701	
FLJ44790	FLJ44790 protein	NM_001001691			1.003	0.484			1.823	0.795	
ZG16	zymogen granule protein 16	BC029149							2.824	0.756	
N/A	N/A	AK128214			1.105	0.855			1.718	0.438	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
N/A	SAMK3000	AY358539	2.035	1.445	1.251	0.766			1.57	0.826	
SLC16A11	solute carrier family 16, member 11"	NM_153357					1.337	0.576	1.483	0.427	Transport.
N/A	N/A	AK097437			1.156	0.748			1.663	0.609	
FIGLA	factor in the germline alpha	NM_001004311			1.755	0.256	1.064	0.462			
N/A	Unknown (protein for MGC:64921)	BC058890			1.085	0.382			1.733	0.183	
NOS2A	nitric oxide synthase 2A isoform 1	NM_000625					1.34	0.698	1.477	0.478	Electron transport. Superoxide metabolism. Nitric oxide biosynthesis. Inflammatory response.
DKFZp434I0916	hypothetical proteincDNA DKFZp434I0916 (from clone DKFZp	AL136772			1.644	0.9			1.173	0.451	Apoptosis. Metabolism. Heparan sulfate proteoglycan metabolism.
MRC1	mannose receptor C type 1 precursor	NM_002438			1.547	0.522			1.269	0.47	Receptor mediated endocytosis. Pinocytosis.
DKFZp451N061	hypothetical proteincDNA DKFZp451N061 (from clone DKFZp	BX537998			1.791	1.241			1.025	0.48	Carbohydrate metabolism. Protein amino acid phosphorylation. Regulation of striated muscle contraction.
LOC401498	similar to RIKEN A930001M12	NM_212558					1.415	0.407	1.399	0.827	
KIAA1747	KIAA1747 protein	AB051534			1.058	0.428			1.755	0.35	
DKFZp547G0215	hypothetical protein DKFZp547G0215	NM_173643			1.601	0.789			1.212	0.482	
DKFZp761G0122	hypothetical proteincDNA DKFZp761G0122 (from clone DKFZ	AL713743			1.787	0.739	1.023	0.657			
BARX2	BarH-like homeobox 2	NM_003658			1.714	0.545			1.091	0.462	Regulation of transcription, DNA-dependent. Transcription from RNA polymerase II promoter.

LYZL4	lysozyme-like 4	NM_144634			1.764	0.419			1.039	0.281	Carbohydrate metabolism. Cell wall catabolism. Cytolysis. Defense response to bacteria.
ERAS	small GTPase protein E-Ras	NM_181532			1.012	0.364			1.789	0.754	
RAG1	recombination activating gene 1	NM_000448			1.664	0.601			1.136	0.449	DNA recombination. Immune response. Hemocyte development. Protein ubiquitination.
UNQ5792	INPE5792	NM_207375			2.798	0.369					
DEFB4	" defensin, beta 4 precursor"	NM_004942			1.3	1.12			1.498	0.308	Chemotaxis. Immune response. G-protein coupled receptor protein signaling pathway. Response to pest, pathogen or parasite.
C10orf118	CTCL tumor antigen L14-2	NM_018017			2.797	0.621					
STAC2	SH3 and cysteine rich domain 2	NM_198993			1.203	0.514			1.592	0.612	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
KRT2A	keratin 2a	NM_000423			1.319	1.032			1.475	0.703	Epidermis development.
GIPC2	PDZ domain protein GIPC2	NM_017655			1.662	1.404			1.132	0.611	
MOGAT1	monoacylglycerol O-acyltransferase 1	NM_058165			1.735	0.862			1.058	0.638	
N/A	Unknown (protein for IMAGE:4271781)	BC017937			1.16	0.527			1.632	0.356	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
N/A	G protein-coupled receptor PGR27	AY255609			1.534	0.304			1.258	0.483	
N/A	N/A	AK124560					1.218	0.422	1.574	0.421	
FZD3	frizzled 3	NM_017412			1.76	0.956			1.032	0.691	G-protein coupled receptor protein signaling pathway. Frizzled signaling pathway. Development. Cell proliferation.
TRAR4	trace amine receptor 4	NM_175067			1.685	0.974			1.105	0.749	
N/A	N/A	AK125849			1.014	0.486			1.774	0.594	
N/A	N/A	AK125824			1.473	0.579			1.315	0.464	Amino acid metabolism.
SNCA	alpha-synuclein isoform NACP140	NM_000345			2.786	0.919					Anti-apoptosis. Central nervous system development.
OB1	odd homeobox 1 protein isoform Aalternatively spliced.	AF492675			2.785	0.677					Regulation of transcription, DNA-dependent. Development.
N/A	N/A	AK127451			1.542	1.045			1.243	0.688	
CLPS	colipase preproprotein	NM_001832			1.269	0.57			1.515	0.573	Digestion. Lipid catabolism.
IRX5	iroquois homeobox protein 5	NM_005853			1.37	0.466			1.413	0.879	Regulation of transcription, DNA-dependent.
EGFL9	EGF-like-domain, multiple 9"	NM_023932					1.582	0.565	1.201	0.698	
PRODH	proline dehydrogenase (oxidase) 1	NM_016335			1.375	0.756			1.408	0.459	Glutamate biosynthesis. Proline catabolism. Induction of apoptosis by oxidative stress.
KRTAP5-9	keratin associated protein 5-9	AJ628246			1.229	0.662			1.553	0.504	
FUT3	fucosyltransferase 3 (galactoside 3(4)-L-fucosyltransferase, Le	NM_000149					1.009	0.526	1.773	0.441	Carbohydrate metabolism. Protein amino acid glycosylation.
TRH	thyrotropin-releasing hormone	NM_007117					1.332	0.721	1.445	0.654	Signal transduction. Cell-cell signaling. Hormone-mediated signaling.
TRAR5	G protein-coupled receptor 102	NM_053278			1.39	1.116			1.387	1.001	
LRG1	leucine-rich alpha-2-glycoprotein 1	NM_052972					1.016	0.349	1.761	0.733	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
LOC284680	hypothetical protein LOC284680	NM_182581			1.519	0.477			1.258	0.482	
IFNA21	" interferon, alpha 21"	NM_002175			1.744	0.649			1.031	0.709	Defense response. Cell-cell signaling. Response to virus.
CRYBB2	" crystallin, beta B2"	NM_000496			1.364	1.412			1.41	0.816	Sensory perception. Visual perception.
SFTPA1	SFTPA1 protein	BC026229			1.144	0.709			1.629	0.393	Phosphate transport. Respiratory gaseous exchange. Regulation of liquid surface tension.
CEL	bile salt-activated lipase	M54994	1.094	1.404	1.109	0.47			1.663	0.675	
MGC44903	telomeric TBC1 domain family member 3-like	NM_001001418			1.07	0.266			1.699	0.163	
FLJ45273	FLJ45273 protein	NM_198461			1.581	0.528			1.187	0.413	
MGC33951	hypothetical protein MGC33951	NM_152448			1.542	0.547			1.225	0.226	
CX40.1	connexin40.1	NM_153368			1.213	1.203			1.553	0.36	Cell communication.
ACADL	" acyl-Coenzyme A dehydrogenase, long chain precursor"	NM_001608			1.766	0.684			1	0.437	Electron transport. Lipid metabolism. Fatty acid metabolism.
LOC253012	hypothetical protein LOC253012	NM_198151			1.183	0.488			1.582	0.933	
IFNA7	" interferon, alpha 7"	NM_021057			1.215	0.312			1.547	0.22	Defense response. Cell-cell signaling. Response to virus.
BCL11B	B-cell CLL/lymphoma 11B isoform 1	NM_138576			1.681	0.675			1.078	0.629	Regulation of transcription, DNA-dependent.
ADCY8	adenylate cyclase 8	NM_001115					1.302	0.458	1.457	0.477	CAMP biosynthesis. Intracellular signaling cascade. Learning and/or memory.
TRIM43	tripartite motif-containing 43	NM_138800			1.472	0.739			1.287	0.782	
MTUS1	mitochondrial tumor suppressor 1 isoform 3	NM_001001927			1.646	1.096			1.11	0.712	
BTK	Bruton agammaglobulinemia tyrosine kinase	NM_000061			1.595	1.035			1.16	0.385	Protein amino acid phosphorylation. Mesoderm development. Induction of apoptosis by extracellular signals.
TIAM1	T-cell lymphoma invasion and metastasis 1	NM_003253	1.078	0.792	1.043	0.751			1.708	1.235	Intracellular signaling cascade.
WNT16	" wingless-type MMTV integration site family, member 16 isofc	NM_057168			1.179	0.483			1.57	0.363	Frizzled-2 signaling pathway. Cell-cell signaling. Development.
FAM26A	" family with sequence similarity 26, member A"	NM_182494			1.679	0.782			1.07	0.776	
FLJ46608	FLJ46608 protein	NM_001004308			1.537	0.382			1.209	0.227	
CHST13	carbohydrate (chondroitin 4) sulfotransferase 13	NM_152889			1.234	0.379			1.51	0.916	Carbohydrate metabolism. Chondroitin sulfate biosynthesis.
N/A	N/A	AK127184			1.665	0.541			1.078	0.225	
SSB4	SPRY domain-containing SOCS box protein SSB-4	NM_080862	1.049	0.861	1.238	0.638			1.505	0.99	Intracellular signaling cascade.
CHST1	carbohydrate (keratan sulfate Gal-6) sulfotransferase 1	NM_003654			1.033	0.74			1.71	0.92	Polysaccharide metabolism. Galactose metabolism. Inflammatory response. Keratan sulfate metabolism.
SLC6A13	" solute carrier family 6 (neurotransmitter transporter, GABA),	NM_016615			1.006	0.725			1.736	0.758	Neurotransmitter transport. Amino acid transport.
KRTAP10-2	keratin associated protein 10-2	NM_198693			1.092	0.767			1.647	0.681	

STK32A	serine/threonine kinase 32A	NM_145001			1.466	0.478			1.269	0.509	
ADCYAP1R1	type I adenylate cyclase activating polypeptide receptor precur	NM_001118					1.193	0.962	1.541	1.04	G-protein coupled receptor protein signaling pathway. Spermatogenesis. Cell differentiation.
SIGLEC7	sialic acid binding Ig-like lectin 7	NM_014385			1.155	0.745			1.576	0.738	Cell adhesion.
VDR	" vitamin D (1,25- dihydroxyvitamin D3) receptor"	NM_000376			1.495	0.612			1.23	0.531	Transcription. Regulation of transcription, DNA-dependent. Signal transduction.
PNCK	pregnancy upregulated non-ubiquitously expressed CaM kinas	NM_198452			1.129	0.624			1.595	0.73	Protein amino acid phosphorylation.
ACCN1	neuronal amiloride-sensitive cation channel 1 isoform 1	NM_183377					1.127	0.517	1.595	0.478	Ion transport. Sodium ion transport. Synaptic transmission. Central nervous system development.
ABCG5	sterolin 1	NM_022436			1.023	0.695			1.698	0.902	Transport. Cholesterol absorption.
PALMD	palmdelphin	NM_017734			1.468	0.809	1.25	0.984			Regulation of cell shape.
MOGAT3	monoacylglycerol O-acyltransferase 3	NM_178176			1.383	0.517			1.334	0.668	
SPAG11	N/A	NM_016512			1.27	0.608			1.445	0.97	Defense response. Spermatogenesis. Response to pest, pathogen or parasite.
N/A	N/A	AK091660			1.254	1.003			1.459	0.901	
N/A	N/A	AK095603					1.594	0.434	1.112	0.391	
MAST1	microtubule associated serine/threonine kinase 1	NM_014975			1.327	0.822			1.379	0.615	DNA metabolism. Apoptosis. Development.
KCNJ10	potassium inwardly-rectifying channel J10	NM_002241			1.675	0.877			1.031	0.747	Ion transport. Potassium ion transport.
KRTAP5-2	keratin associated protein 5-2	NM_001004325			1.097	0.408			1.605	0.505	
PRKWNK3	" protein kinase, lysine deficient 3 isoform 1"	NM_020922			1.286	0.466			1.414	0.499	Protein amino acid phosphorylation. Protein amino acid phosphorylation. Protein kinase cascade.
KIAA1144	KIAA1144 protein	AB032970			1.36	0.783			1.338	0.955	Cation transport. Potassium ion transport.
RBP7	RBP7 protein	BC033883			1.255	0.558			1.442	0.692	Transport.
OPRL1	OPRL1 protein	BC038433			1.482	0.855			1.214	0.786	Signal transduction. G-protein coupled receptor protein signaling pathway. Positive regulation.
MGC75556	hypothetical gene supported by BC063653	NM_001004350					1.1	0.427	1.595	0.425	
KLF15	Kruppel-like factor 15	NM_014079			1.645	0.451			1.05	1.097	Transcription. Regulation of transcription, DNA-dependent.
FLJ31952	hypothetical protein FLJ31952	NM_144682			2.695	0.566					Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
SPDEF	SAM pointed domain containing ets transcription factor	BC021299			1.549	0.793			1.145	0.6	Regulation of transcription, DNA-dependent. Development.
TOM1L1	target of myb1-like 1	NM_005486			1.691	1.562			1.002	0.777	Intracellular protein transport. Intra-Golgi transport.
SLC4A11	solute carrier family 4 member 11	NM_032034					1.482	0.682	1.209	0.871	Anion transport.
NCF4	" neutrophil cytosolic factor 4 (40kD), isoform 2"	BC002798			1.23	0.327			1.46	0.518	Electron transport. Defense response. Intracellular signaling cascade.
N/A	N/A	AK124965			1.545	0.385			1.144	0.395	
N/A	N/A	AJ007292					1.233	0.424	1.456	0.689	Cell-cell signaling.
ATP12A	" ATPase, H+/K+ transporting, nongastric, alpha polypeptide"	NM_001676			1.574	0.392			1.115	0.506	Potassium ion transport. Metabolism. Proton transport.
GPR45	G protein-coupled receptor 45	NM_007227			1.191	1.023			1.497	0.531	Signal transduction. G-protein coupled receptor protein signaling pathway. Neurogenesis.
CSPG2	chondroitin sulfate proteoglycan 2 (versican)	NM_004385			2.688	0.561					Development. Cell recognition.
HPX-5	N/A	X74862			1.067	0.406			1.621	0.395	
C1QL2	complement component 1, q subcomponent-like 2"	NM_182528					1.163	0.524	1.524	0.451	
KCNG4	" potassium voltage-gated channel, subfamily G, member 4 is	NM_133490			1.028	0.847			1.658	0.47	
DKFZp434B2328	hypothetical proteincDNA DKFZp434B2328 (from clone DKFZ	AL137448			1.223	0.501			1.462	0.669	
IGFL1	insulin growth factor-like family member 1	NM_198541							2.683	0.571	
KRTHB5	keratin, hair, basic, 5"	NM_002283							2.681	0.383	Epidermis development.
KRTAP10-2	keratin associated protein KAP10.2	AJ566381			1.013	0.815			1.667	0.49	
CCL4L	chemokine (C-C motif) ligand 4-like precursor	NM_001001435			1.179	0.398			1.501	0.757	Cell motility. Chemotaxis. Inflammatory response. Cell adhesion. Establishment and/or maintenance of cell polarity.
CD22	CD22 antigen	NM_001771							2.678	0.626	Immune response. Cell-cell adhesion. Antimicrobial humoral response.
PLEKHK1	" pleckstrin homology domain containing, family K member 1"	NM_145307			1.618	0.904			1.058	0.843	Signal transduction.
HLA-Dw12	cell surface glycoprotein	M57650			1.134	0.944			1.542	1.159	Immune response. Antigen presentation, exogenous antigen.
KIAA1900	KIAA1900	NM_052904			1.629	0.58	1.042	0.689			
KIAA1210	KIAA1210 protein	AB033036			1.588	0.921			1.083	0.685	
DCAMKL1	doublecortin and CaM kinase-like 1	NM_004734			1.564	0.77			1.107	0.899	Protein amino acid phosphorylation. Intracellular signaling cascade. Central nervous system development. Endosome transport.
N/A	Unknown (protein for MGC:34907)	BC027486			1.018	0.873			1.652	0.702	
N/A	N/A	AK095339			1.108	0.398			1.562	0.351	
N/A	N/A	AK026467							2.67	0.659	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
CHST4	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 4	NM_005769			1.608	0.494			1.062	0.478	Carbohydrate metabolism. N-acetylglucosamine metabolism. Sulfur metabolism. Inflammatory response.
N/A	N/A	AK095105			1.178	0.256			1.489	0.355	
HLA-DQB2	" major histocompatibility complex, class II, DQ beta 2"	NM_182549			1.46	0.422			1.206	0.46	Immune response. Immune response. Antigen presentation, exogenous antigen.
GPR63	G protein-coupled receptor 63	NM_030784	2.31	1.582	1.634	0.701			1.03	0.909	Signal transduction. G-protein coupled receptor protein signaling pathway.
AAA1	AAA1 protein isoform IV	NM_207286			2.66	0.643					
N/A	VDLS1900	AY358358			1.12	1.226			1.539	0.292	
THBD	thrombomodulin precursor	NM_000361			1.406	0.75			1.252	0.396	Blood coagulation.
LOC283677	LOC283677 protein	BC055412			1.254	1.081			1.404	0.431	

N/A	Rhesus polypeptide XIII	X63097			1.418	0.311			1.239	0.587	
KIAA1394	KIAA1394 protein	AB037815					1.188	0.859	1.469	0.703	
CAST	cytomatrix protein p110	NM_015576			1.319	0.867			1.338	0.804	
KCNJ5	potassium inwardly-rectifying channel J5	NM_000890			1.586	0.871	1.069	0.398			
HAND2	basic helix-loop-helix transcription factor HAND2	NM_021973			2.655	0.632					Angiogenesis. Transcription. Regulation of transcription, DNA-dependent. Cell differentiation.
N/A	N/A	AK055830			1.321	1.183			1.333	0.718	
KIAA0087	N/A	D42038			1.226	0.7			1.428	0.728	
NETO1	neuropilin- and tolloid-like protein 1 isoform 3 precursor	NM_138966					1.051	0.516	1.602	0.877	
N/A	N/A	AK091901			1.256	0.529			1.397	0.354	
ARGBP2	Arg/Abl-interacting protein 2 isoform 2	NM_021069			1.605	0.394			1.047	0.507	
FLJ38377	hypothetical protein FLJ38377	NM_152698			1.158	0.643			1.491	0.701	
N/A	N/A	AK125274			1.127	0.384			1.521	0.799	Antigen presentation, endogenous antigen. Antigen processing.
CSHL1	chorionic somatomammotropin hormone-like 1 isoform 1 precu	NM_022579			1.098	0.424			1.549	0.4	
N/A	Unknown (protein for IMAGE:4610447)	BC022390			1.029	0.438			1.615	0.537	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
N/A	N/A	AK095266			2.644	0.915					
N/A	PPRR6495	AY358177			1.02	0.957			1.622	0.43	
SPTBN2	" spectrin, beta, non-erythrocytic 2"	NM_006946			1.075	0.528			1.561	0.439	Vesicle-mediated transport.
RNF28	ring finger protein 28	AJ291713			1.016	0.656			1.617	0.445	Signal transduction. Protein ubiquitination.
N/A	N/A	AK128846					1.015	0.506	1.618	0.351	
GPR83	G protein-coupled receptor 83	NM_016540			1.309	0.713			1.324	0.806	Signal transduction. G-protein coupled receptor protein signaling pathway.
C20orf160	chromosome 20 open reading frame 160	NM_080625			1.189	0.587			1.444	0.525	
SRY	sex determining region Y	NM_003140			2.631	1.237					Transcription. Regulation of transcription, DNA-dependent. Sex differentiation. Male sex determination.
NELL1	nel-like 1 precursor	NM_006157					1.105	0.389	1.525	0.665	Tricarboxylic acid cycle. Cell adhesion. Neurogenesis. Metabolism.
N/A	Similar to prostaglandin E receptor 4 (subtype EP4)	BC042539			1.462	0.226			1.167	0.274	G-protein coupled receptor protein signaling pathway.
LYZL6	LYZL6 protein	BC054481			1.048	0.53			1.581	0.394	Carbohydrate metabolism. Cell wall catabolism. Cytolysis. Defense response to bacteria.
N/A	N/A	AK055759	2.077	2.259	1.414	0.547			1.214	0.482	Protein ubiquitination.
KRT20	keratin 20	NM_019010			1.472	1.128			1.153	0.606	
SLC7A8	" solute carrier family 7 (cationic amino acid transporter, y+ sy	NM_012244			2.624	1.41					Protein complex assembly. Amino acid metabolism. Amino acid transport.
LILRB2	LILRB2 protein	BC041708			1.192	0.874			1.432	0.474	
CXCL16	chemokine (C-X-C motif) ligand 16	NM_022059			1.396	0.46			1.228	0.91	Receptor mediated endocytosis. Chemotaxis. Sensory perception. Lymphocyte chemotaxis.
N/A	N/A	AK124840			1.139	0.692			1.483	0.687	
DKFZp451F1716	hypothetical proteincDNA DKFZp451F1716 (from clone DKFZ	AL832580			1.274	0.638			1.347	0.902	Protein ubiquitination.
LAPTM5	Lysosomal-associated multispanning membrane protein-5	NM_006762			1.373	0.38			1.246	0.614	
FLJ33718	hypothetical protein FLJ33718	NM_173660					1.175	0.48	1.444	0.716	
FGF23	fibroblast growth factor 23 precursor	NM_020638					1.127	0.812	1.491	0.562	Cell differentiation.
UCN3	urocortin 3	NM_053049			1.258	0.678			1.359	0.762	
N/A	N/A	AK124561			1.013	0.459			1.603	0.508	
MGC15619	hypothetical protein MGC15619	NM_032369			1.321	0.755			1.294	0.766	Cation transport.
CGM1b	CD66d	D90278			1.226	0.57			1.388	0.615	Defense response. Pregnancy. Pregnancy.
AZGP1	" alpha-2-glycoprotein 1, zinc"	NM_001185			1.199	0.619			1.415	0.455	Regulation of transcription, DNA-dependent.
RAB3C	" RAB3C, member RAS oncogene family"	NM_138453			2.613	1.377					
DOC2B	" double C2-like domains, beta"	NM_003585			1.078	0.97			1.535	0.582	Transport.
SLC18A3	solute carrier family 18 (vesicular acetylcholine), member 3"	NM_003055					1.176	0.549	1.435	0.776	Acetylcholine transport.
N/A	golgi autoantigen golgin subfamily a2-like	AF332229			1.396	0.354			1.215	0.583	
IFNA10	" interferon, alpha 10"	NM_002171			1.603	0.592			1.008	0.489	Defense response. Response to virus.
C1orf32	chromosome 1 open reading frame 32	NM_199351			1.557	1.016			1.054	0.832	
FBXL16	F-box and leucine-rich repeat protein 16	NM_153350					1.121	0.607	1.489	0.705	Ubiquitin cycle.
DRD1IP	dopamine receptor D1 interacting protein	NM_015722					1.365	0.371	1.242	0.199	Dopamine receptor signaling pathway. Synaptic transmission.
SIAT8B	sialyltransferase 8B	NM_006011					1.098	0.769	1.506	0.457	Carbohydrate metabolism. Protein amino acid glycosylation. N-glycan processing. Neurogenesis.
FETUB	fetuin B	NM_014375			1.265	0.889			1.339	0.608	
REM1	RAS-like GTP-binding protein REM	NM_014012					1.091	0.353	1.512	0.72	Small GTPase mediated signal transduction.
N/A	N/AcDNA DKFZp564K1522 (from clone DKFZp564K1522).	AL050397			1.338	0.993			1.265	0.501	Lipid metabolism. Synaptic transmission. Neurogenesis. Vesicle-mediated transport.
TRIM10	tripartite motif-containing 10 isoform 2	NM_052828			1.032	0.353			1.569	0.523	Protein ubiquitination. Hemopoiesis.
SLC4A10	" solute carrier family 4, sodium bicarbonate transporter-like, n	NM_022058			1.017	0.974			1.584	0.7	Anion transport. Chloride transport. Bicarbonate transport.
NXF	HLH-PAS transcription factor NXF	NM_178864	1.079	1.604			1.252	0.583	1.349	0.654	Regulation of transcription, DNA-dependent. Signal transduction.
TEPP	testis/prostate/placenta-expressed protein isoform 1	NM_199046			1.088	0.629			1.512	0.377	

FCER2	" Fc fragment of IgE, low affinity II, receptor for (CD23A)"	NM_002002			1.25	1.012			1.348	0.497	
SPTBN4	" spectrin, beta, non-erythrocytic 4"	NM_025213			1.399	0.737			1.198	0.682	Cytoskeletal anchoring. Vesicle-mediated transport.
PCDH17	protocadherin 17	NM_014459			1.321	0.905			1.276	0.536	Cell adhesion. Homophilic cell adhesion.
EYA2	eyes absent 2 isoform b	NM_172113			1.107	0.591			1.489	0.653	Eye morphogenesis. Regulation of transcription, DNA-dependent. Development.
L3MBTL4	l(3)mbt-like 4	NM_173464			1.106	0.623			1.489	0.815	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
MPO	myeloperoxidase	NM_000250			1.39	0.795			1.205	0.494	Anti-apoptosis. Defense response. Response to oxidative stress.
FLJ16139	FLJ16139 protein	NM_001004329			1.067	0.675			1.528	0.582	
N/A	ADAM 21	AF029900			1.392	0.85			1.2	0.537	Proteolysis and peptidolysis. Fertilization.
KIAA1643	KIAA1643 protein	AB046863			1.521	0.876			1.071	0.685	
DOCK3	dedicator of cytokinesis 3	NM_004947			1.043	0.754			1.548	1.038	
ADAM5	ADAM5 protein	BC067864			1.586	1.042			1.005	0.298	
CBX4	chromobox homolog 4	NM_003655			1.345	0.569	1.245	1.005			Chromatin assembly or disassembly. Transcription. Regulation of transcription, DNA-dependent. Anti-apoptosis.
EFNB3	ephrin-B3 precursor	NM_001406			1.416	0.593			1.172	0.446	Cell-cell signaling. Neurogenesis. Cell differentiation.
NDP	Norrie disease protein	NM_000266			2.587	0.702					Vacuole organization and biogenesis. Signal transduction. Cell-cell signaling. Neurogenesis. Sensory perception.
UMP-CMPK	UMP-CMP kinase	NM_016308			1.431	0.887	1.156	0.615			Nucleobase, nucleoside, nucleotide and nucleic acid metabolism. Pyrimidine ribonucleotide biosynthesis.
IL29	interleukin 29	NM_172140			1.32	0.44			1.267	0.514	
GABRD	" gamma-aminobutyric acid (GABA) A receptor, delta"	NM_000815			1.117	1.01			1.47	0.654	Ion transport. Signal transduction. Synaptic transmission.
CPLX1	complexin 1	NM_006651			1.145	0.632	1.442	0.504			Neurotransmitter transport. Exocytosis. Synaptic transmission.
N/A	N/A	AK126221			1.52	0.6	1.066	0.391			
SAA2	serum amyloid A2	NM_030754			1.152	1.485			1.431	0.475	Acute-phase response. Acute-phase response. Positive regulation of cytosolic calcium ion concentration.
SLC24A3	solute carrier family 24 (sodium/potassium/calcium exchanger)	NM_020689					1.063	0.393	1.515	0.703	Potassium ion transport. Sodium ion transport. Calcium ion transport.
KIAA0449	KIAA0449 protein	AB007918			1.022	0.564			1.554	0.647	Microtubule-based movement.
N/A	N/A	AK096387					1.332	0.464	1.243	0.671	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
SLC8A3	solute carrier family 8 member 3 isoform C precursor	NM_183002			1.54	0.394	1.034	0.499			
IFNA14	interferon, alpha 14"	NM_002172					1.36	0.68	1.213	0.568	Defense response.
NKG7	natural killer cell group 7 sequence	NM_005601							2.573	0.486	
N/A	Unknown (protein for IMAGE:3543874)	BC001607	1.087	0.754			1.208	0.782	1.364	0.533	
KLK1	kallikrein 1 isoform 3 preproprotein	AY429508	1.342	1.308	1.227	0.374			1.345	0.365	Proteolysis and peptidolysis.
KIAA1804	mixed lineage kinase 4	NM_032435	1.227	1.343	1.12	0.313	1.452	1.021			Protein amino acid phosphorylation.
IL5	interleukin 5 precursor	NM_000879			1.429	0.765	1.142	0.766			Inflammatory response. Positive regulation of cell proliferation.
CLECSF14	CLECSF14 protein	BC027858			1.504	0.68			1.065	0.254	Endocytosis. Immune response.
MRIP2	MRIP2	AF411132			1.204	0.446			1.364	0.407	
MGC12197	BM-011 protein	NM_016625	1.18	1.112	2.567	0.589					
PPP1R16B	protein phosphatase 1 regulatory inhibitor subunit 16B	NM_015568			1.045	0.346			1.521	0.815	Signal transduction.
FLJ10847	hypothetical protein FLJ10847	NM_018242			1.057	0.538			1.505	0.569	Multidrug transport.
Shax3	Snf7 homologue associated with Alix 3	NM_152284			1.505	0.457			1.053	0.637	
N/A	eosinophil preperoxidase (AA -127 to 575)	X14346			1.012	0.914			1.542	0.574	Response to oxidative stress.
RYR1	ryanodine receptor 1 (skeletal)	NM_000540					1.521	1.292	1.033	0.418	Regulation of cell cycle. Protein folding. Cation transport. Calcium ion transport.
N/A	ISLR	AY358871			1.363	0.499			1.19	0.501	Cell adhesion.
FLJ39739	FLJ39739 protein	NM_207400			2.55	0.793					
FGR	Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homol	NM_005248			1.532	1.023			1.017	0.419	Protein amino acid phosphorylation. Intracellular signaling cascade. Response to virus.
N/A	Unknown (protein for IMAGE:5218466)	BC030533			1.054	0.574			1.494	0.497	Immune response.
N/A	Unknown (protein for IMAGE:4181241)	BC012202			1.031	0.701			1.517	0.661	
HAS1	hyaluronan synthase 1	BC035837			1.359	0.52			1.189	0.419	Glycosaminoglycan biosynthesis. Substrate-bound cell migration. Cell adhesion.
AK3	adenylate kinase 3	NM_001005353			1.329	0.617			1.219	1.18	Nucleobase, nucleoside, nucleotide and nucleic acid metabolism. Amino acid biosynthesis.
OR8B8	" olfactory receptor, family 8, subfamily B, member 8"	NM_012378			1.392	0.688			1.155	0.621	
N/A	trace amine receptor 3	AY183469			1.502	0.98			1.044	0.559	
CNTN1	contactin 1 isoform 1 precursor	NM_001843					1.451	0.713	1.088	0.622	Cell adhesion.
DMRTA1	DMRT-like family A1	NM_022160			1.15	0.855			1.388	0.564	Regulation of transcription, DNA-dependent. Sex differentiation.
LOC375616	kielin-like	NM_199349					1.08	0.329	1.457	0.371	
sGC	soluble guanylyl cyclase	Y15723			1.26	0.684	1.275	1.029			CGMP biosynthesis. Nitric oxide mediated signal transduction. Circulation.
TAFA4	TAFA4 protein	NM_182522			1.118	0.634			1.416	0.647	
N/A	N/A	AK125454			1.064	0.671			1.469	0.412	
UBE2Q	ubiquitin-conjugating enzyme E2Q	NM_017582			1.094	0.982	1.431	0.684			Ubiquitin cycle.
N/A	N/A	AK056520			1.101	0.756			1.424	0.442	
FLJ37078	hypothetical protein FLJ37078	NM_153043					1.247	0.461	1.277	0.377	

EZI	likely ortholog of mouse zinc finger protein EZI	NM_207336					1.167	0.571	1.355	0.665	
GJA8	gap junction protein, alpha 8, 50kDa (connexin 50)"	NM_005267					1.103	0.615	1.416	1.018	Transport. Cell communication. Visual perception.
ATP6V1B1	" ATPase, H+ transporting, lysosomal 56/58kD, V1 subunit B,	BC063411			1.188	0.718			1.33	0.537	Ion transport. Excretion. Perception of sound. ATP synthesis coupled proton transport.
adam23	Adam23 protein	AJ005580			1.355	1.188			1.163	0.868	Proteolysis and peptidolysis. Cell adhesion. Central nervous system development.
PRKCH	" protein kinase C, eta"	NM_006255			1.32	0.53			1.194	0.495	Protein amino acid phosphorylation. Intracellular signaling cascade.
HES2	HES2 protein	BC012091					1.212	0.771	1.3	0.423	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
PKD1L2	polycystin 1-like 2 isoform a	NM_052892			1.145	0.24			1.364	0.521	Cation transport. Neuropeptide signaling pathway.
POU2AF1	" POU domain, class 2, associating factor 1"	NM_006235			1.293	0.535			1.216	0.566	Transcription. Regulation of transcription, DNA-dependent. Humoral immune response.
C7orf29	chromosome 7 open reading frame 29	NM_138434			1.454	0.39			1.055	0.384	
PTHR1	parathyroid hormone receptor 1 precursor	NM_000316			1.127	0.615			1.381	0.477	Skeletal development. Signal transduction. G-protein coupled receptor protein signaling pathway.
HOXA7	homeobox protein A7	NM_006896			1.396	0.623	1.11	0.577			
N/A	N/A	AK125302							2.505	0.577	
N/A	Unknown (protein for MGC:34009)	BC031108			1.319	0.793			1.185	0.515	
N/A	NGNL6975	AY358255			1.446	1.007			1.058	0.485	
PRKG2	" protein kinase, cGMP-dependent, type II"	NM_006259			1.471	0.73	1.032	0.591			Regulation of cell cycle. Protein amino acid phosphorylation. Signal transduction.
FLJ11273	hypothetical protein FLJ11273	NM_018374			2.502	1.267					
ACO	serine protease homologue	X75363			1.062	0.673			1.44	0.835	Proteolysis and peptidolysis. Proteolysis and peptidolysis.
GRIA3	glutamate receptor 3 isoform flop precursor	NM_000828					1.032	1.14	1.469	0.653	Ion transport. Potassium ion transport. Glutamate signaling pathway. Synaptic transmission.
KIAA1910	KIAA1910 protein	AB067497			2.501	0.564					
N/A	1C7 precursor	AF031136			1.475	0.592			1.024	0.45	Inflammatory response. Cellular defense response.
TNNI3	troponin I, cardiac"	NM_000363					1.011	0.655	1.487	0.676	Muscle development. Regulation of heart contraction rate. Negative regulation of angiogenesis.
ECRG4	ECRG4 protein	BC021742							2.497	0.892	
CLDN3	claudin 3	NM_001306					1.115	0.381	1.382	0.467	Calcium-independent cell-cell adhesion.
K6IRS4	keratin 6 irs4	NM_175053			1.183	0.451			1.313	0.773	Ectoderm development.
NTN4	netrin 4	NM_021229			2.493	0.904					
EEF1A2	eukaryotic translation elongation factor 1 alpha 2	NM_001958			1.074	0.509			1.418	0.461	Protein biosynthesis. Translational elongation.
C4BPB	" complement component 4 binding protein, beta"	BC005378			1.334	1.012			1.158	0.535	Immune response. Complement activation, classical pathway. Blood coagulation.
KCNE2	" potassium voltage-gated channel, Isk-related family, membe	NM_172201			1.26	0.41			1.23	0.465	Ion transport. Potassium ion transport. Muscle contraction. Regulation of heart contraction rate.
PLA2G2D	" phospholipase A2, group IID"	NM_012400	1.412	1.249	1.298	0.973			1.189	0.453	Phospholipid metabolism. Inflammatory response. Lipid catabolism.
DBH	dopamine beta-hydroxylase precursor	NM_000787							2.486	0.559	Synaptic transmission. Catecholamine biosynthesis.
GNG13	guanine nucleotide binding protein (G protein), gamma 13"	NM_016541					1.085	0.524	1.397	0.638	Signal transduction. G-protein coupled receptor protein signaling pathway.
N/A	N/A	AK097632			2.481	0.504					
KIAA1872	KIAA1872 protein	AB058775			1.076	0.624			1.405	0.584	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
PGC	progastricsin (pepsinogen C)	NM_002630			1.111	0.994			1.368	0.359	Proteolysis and peptidolysis. Proteolysis and peptidolysis. Digestion.
DKFZp686B1195	hypothetical proteincDNA DKFZp686B1195 (from clone DKFZ	BX537594			2.479	0.372					
LY6H	lymphocyte antigen 6 complex, locus H"	BC028894					1.01	0.564	1.467	1.171	Cellular defense response. Neurogenesis.
DSCR6	Down syndrome critical region protein 6	NM_018962					1.081	0.427	1.396	0.57	
N/A	Unknown (protein for IMAGE:3356192)	BC001200					1.33	0.466	1.146	0.483	
GNA14	guanine nucleotide binding protein (G protein), alpha 14"	NM_004297					1.071	0.749	1.405	0.596	Protein amino acid ADP-ribosylation. Signal transduction. G-protein coupled receptor protein signaling pathway.
CXCL1	chemokine (C-X-C motif) ligand 1	NM_001511			1.426	0.675			1.047	0.638	Chemotaxis. Inflammatory response. Intracellular signaling cascade. Neurogenesis.
N/A	group III secreted phospholipase A2	AF220490			1.002	1.104			1.47	0.549	Phospholipid metabolism. Lipid catabolism.
TRPM3	" transient receptor potential cation channel, subfamily M, mer	NM_206946			1.374	0.392			1.096	0.527	Cation transport. Calcium ion transport.
N/A	N/A	AK127208			1.026	0.209			1.441	0.397	
LOC63928	hepatocellular carcinoma antigen gene 520	NM_022097			1.056	0.905			1.41	0.705	
CKM	muscle creatine kinase	BC007462					1.104	0.61	1.362	0.474	
CD3D	CD3D antigen, delta polypeptide (TiT3 complex)"	NM_000732							2.465	0.81	Protein complex assembly. Cell surface receptor linked signal transduction. T-cell activation. Positive thymic T-cell selection.
CASKIN1	CASK interacting protein 1	NM_020764					1.166	0.831	1.299	0.77	
MIST	mast cell immunoreceptor signal transducer	NM_052964			1.343	0.443			1.121	0.707	
N/A	N/A	AK128498			1.328	0.45			1.135	0.689	Cell death.
C6orf117	chromosome 6 open reading frame 117	NM_138409					1.088	0.796	1.373	0.594	
SYCP1	synaptonemal complex protein 1	NM_003176			1.418	0.543			1.042	0.293	Cytokinesis. Cell cycle. Meiosis. Synaptonemal complex formation. Meiotic recombination.
C21orf69	chromosome 21 open reading frame 69 isoform 2	NM_058189			1.145	0.636			1.31	0.603	
CNTN2	contactin 2 precursor	NM_005076			1.005	0.861			1.447	0.532	Cell adhesion.
PCLO	piccolo	NM_033026							2.45	0.5	
CACNG6	voltage-dependent calcium channel gamma-6 subunit isoform	NM_145814					1.292	0.493	1.157	0.478	Ion transport. Calcium ion transport.
MYH7	myosin, heavy polypeptide 7, cardiac muscle, beta"	NM_000257							2.447	0.447	Striated muscle contraction. Muscle development.

MN1	meningioma1	NM_002430			1.307	0.81	1.14	0.799			Cell cycle. Negative regulation of cell cycle.
EMILIN2	elastin microfibril interfacer 2	NM_032048			2.447	0.651					Cell adhesion.
WRN	Werner syndrome protein	NM_000553			1.148	0.282			1.298	0.58	DNA metabolism. Aging.
N/A	N/A	BX161470					1.299	0.885	1.147	0.878	
CDCP1	CUB domain-containing protein 1 isoform 1	NM_022842			1.288	1.589			1.158	1.152	
FKSG64	FKSG64	AF338199	2.468	1.137	1.351	0.402	1.094	0.62			
N/A	N/A	AK128819			1.362	0.901	1.082	0.742			
N/A	N/A	AK074650			1.432	0.561			1.012	0.365	
MAP7	microtubule-associated protein 7	NM_003980			2.444	1.125					Microtubule cytoskeleton organization and biogenesis. Establishment and/or maintenance of cell polarity.
FUT1	fucosyltransferase 1	NM_000148					1.286	0.601	1.157	0.617	Carbohydrate metabolism. Protein amino acid glycosylation. L-fucose catabolism.
KRTAP10-1	keratin associated protein 10-1	NM_198691			1.125	0.504			1.317	0.382	
HCN2	hyperpolarization activated cyclic nucleotide-gated potassium c	NM_001194					1.13	0.868	1.312	0.524	Cation transport. Potassium ion transport. Sodium ion transport. Muscle contraction. Cell-cell signaling.
CCR7	chemokine (C-C motif) receptor 7 precursor	NM_001838			1.144	0.396			1.297	0.562	Chemotaxis. Inflammatory response. Signal transduction. G-protein coupled receptor protein signaling pathway.
N/A	N/A	AK025855			1.167	0.619			1.272	0.528	Cell adhesion. Homophilic cell adhesion.
TREML2	triggering receptor expressed on myeloid cells-like 2	NM_024807					1.231	0.623	1.207	0.551	
N/A	Unknown (protein for MGC:87051)	BC067760			1.283	0.613			1.152	0.644	Protein amino acid phosphorylation.
ZNFN1A1	zinc finger protein, subfamily 1A, 1 (Ikaros)"	NM_006060					1.123	0.661	1.31	0.91	Regulation of transcription, DNA-dependent. Mesoderm development.
N/A	uterine-derived 14 kDa protein	AF305836					1.286	0.698	1.147	0.753	
KIAA1617	KIAA1617 protein	AB046837			2.431	0.682					
N/A	VLCS3029	AY358806	1.941	2.177	1.398	0.532			1.031	0.452	
N/A	Unknown (protein for IMAGE:3631157)	BC008048	1.408	1.34	1.415	0.798			1.012	0.649	
TNFRSF10C	" tumor necrosis factor receptor superfamily, member 10c prec	NM_003841			1.168	0.888			1.259	0.49	Apoptosis. Signal transduction.
MST078	MSTP078	AF170491	1.186	1.172	1.066	0.694			1.36	0.537	
KIAA1727	KIAA1727 protein	NM_033393			1.408	0.528			1.013	0.55	Cell organization and biogenesis.
MIXL1	Mix-like homeobox protein 1	NM_031944					1.127	0.839	1.291	1.043	Regulation of transcription, DNA-dependent.
TGFA	" transforming growth factor, alpha"	NM_003236			1.029	0.798			1.385	0.907	Regulation of cell cycle. Cell-cell signaling. Cell proliferation.
N/A	N/A	AK130550	1.154	1.273	1.236	1.026			1.176	0.822	
DNAJA4	" DnaJ (Hsp40) homolog, subfamily A, member 4"	NM_018602			1.088	0.852			1.323	0.501	Protein folding.
N/A	N/A	AK126788			1.35	0.661			1.06	0.532	
UBQLN3	ubiquilin 3	BC036743			1.314	0.719			1.094	0.382	Ubiquitin cycle.
FGF13	fibroblast growth factor 13 isoform 1y1v	AF108756			1.108	0.473	1.299	0.408			
NPTXR	neuronal pentraxin receptor isoform 1	NM_014293			1.203	0.582			1.203	0.704	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
N/A	CD33L1	D86358			1.101	0.646			1.305	0.379	
N/A	DEFB127	AY358796	1.604	1.301	2.404	0.635					Defense response to bacteria.
AQP5	aquaporin 5	BC032946					1.174	0.49	1.23	0.807	Water transport. Excretion.
PCDH1	protocadherin 1 isoform 2 precursor	NM_032420			1.073	0.532			1.322	0.522	Regulation of transcription, DNA-dependent. Cell adhesion. Homophilic cell adhesion. Cell-cell signaling. Neurogenesis.
CSMD3	CUB and Sushi multiple domains 3 isoform 1	NM_198123			1.101	0.861			1.294	1.247	
UPK2	uroplakin 2	NM_006760					1.121	0.696	1.272	0.928	Development. Membrane organization and biogenesis.
TNF	tumor necrosis factor alpha	NM_000594							2.393	0.469	Regulation of transcription, DNA-dependent. Anti-apoptosis. Inflammatory response. Leukocyte cell adhesion.
CCL4	chemokine (C-C motif) ligand 4 precursor	NM_002984			1.013	0.589			1.376	0.741	Cell motility. Chemotaxis. Inflammatory response. Cell adhesion. Establishment and/or maintenance of cell polarity.
N/A	QLGT871	AY358417			1.185	0.881			1.202	0.481	
XCR1	G protein-coupled receptor 5	NM_005283			1.253	0.581			1.133	0.293	Chemotaxis. Inflammatory response. Signal transduction. G-protein signaling, coupled to cyclic nucleotide second messenger.
NR5A1	" nuclear receptor subfamily 5, group A, member 1"	NM_004959			1.307	0.596			1.079	0.441	Transcription. Regulation of transcription from RNA polymerase II promoter. Signal transduction. Cell-cell signaling.
DIO3	DIO3 protein	BC017717					1.235	0.847	1.151	0.896	
CHD5	chromodomain helicase DNA binding protein 5	NM_015557					1.162	0.889	1.224	0.89	Chromatin assembly or disassembly. Chromatin remodeling. Regulation of transcription, DNA-dependent.
PNOC	prepronociceptin	NM_006228							2.383	0.702	Neuropeptide signaling pathway. Synaptic transmission. Sensory perception.
N/A	N/A	AK128573			1.183	1.229	1.197	1.054			Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
SLC30A10	" solute carrier family 30 (zinc transporter), member 10 isoforn	NM_001004433			1.18	0.383			1.199	0.591	Cation transport.
CA5A	" carbonic anhydrase VA, mitochondrial precursor"	NM_001739			1.084	0.61			1.293	0.348	One-carbon compound metabolism.
APC2	adenomatosis polyposis coli 2	NM_005883			1.06	0.892			1.315	0.778	Protein complex assembly. Signal transduction. Wnt receptor signaling pathway. Negative regulation of cell cycle.
AOC3	copper containing amine oxidase 3 precursor	NM_003734			1.28	0.612			1.095	0.599	Inflammatory response. Cell adhesion. Amine metabolism.
KRT1	keratin 1	NM_006121			1.135	0.895			1.238	0.421	Complement activation, lectin pathway. Response to oxidative stress. Epidermis development. Fibrinolysis.
KCNIP1	Kv channel interacting protein 1	NM_014592			1.028	0.448			1.343	0.716	Calcium ion sensing. Signal transduction. Synaptic transmission.
N/A	LP2209	AY203950			2.367	0.877					
MMP26	matrix metalloproteinase 26 preproprotein	NM_021801			2.367	1.039					Collagen catabolism.
STRBP	spermatid perinuclear RNA-binding protein	NM_018387			1.203	0.969			1.163	0.966	Regulation of transcription, DNA-dependent.

BEX2	brain expressed X-linked 2	NM_032621			1.162	0.495			1.204	0.783	
ZNF239	zinc finger protein 239	NM_005674			2.365	0.311					Transcription. Regulation of transcription, DNA-dependent.
N/A	thrombopoietin	AB014683			1.329	0.591			1.034	0.394	Development. Cell proliferation.
HAPIP	huntingtin-associated protein interacting protein	NM_003947			1.129	1.084			1.234	0.546	Protein amino acid phosphorylation. Signal transduction. Intracellular signaling cascade. Neurogenesis.
CLDN9	claudin 9	NM_020982			1.069	0.496			1.294	0.415	Calcium-independent cell-cell adhesion.
RAI2	RAI2 protein	BC027937	1.108	0.854	1.093	1.078			1.268	1.196	Embryonic development.
N/A	N/A	AK124722			1.074	1.039			1.287	0.841	
DNAH11	" dynein, axonemal, heavy polypeptide 11"	NM_003777			1.189	0.44			1.171	0.363	Microtubule-based movement.
GATM	glycine amidinotransferase (L-arginine:glycine amidinotransfera	BC004141			2.36	0.741					Creatine biosynthesis.
ARHGAP6	Rho GTPase activating protein 6 isoform 2	NM_001174			2.36	0.872					Rho protein signal transduction. Actin filament polymerization.
HMGCS2	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 (mitochon	NM_005518	1.048	1.695			1.181	0.939	1.178	0.622	Acetyl-CoA metabolism. Cholesterol biosynthesis.
N/A	N/A	AK095331			1.156	0.551			1.202	0.467	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
IMP-1	IGF-II mRNA-binding protein 1	NM_006546			2.357	1.194					
CTSE	cathepsin E isoform a preproprotein	NM_001910			1.015	0.507			1.342	0.47	Proteolysis and peptidolysis. Digestion. Antigen processing, exogenous antigen via MHC class II. Cell-mediated immune response.
N/A	N/A	AK056241			1.269	0.591			1.087	0.616	Protein amino acid glycosylation.
C1orf36	chromosome 1 open reading frame 36	BC065541							2.356	0.277	
N/A	N/A	AK000420							2.351	0.648	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
KIAA0574	KIAA0574 protein	AB011146	1.132	1.303			1.047	0.434	1.304	0.518	
ATP6V0A4	" ATPase, H+ transporting, lysosomal V0 subunit a isoform 4"	NM_020632			1.003	0.522			1.347	0.426	Ion transport. Regulation of pH. Proton transport.
HFE	hemochromatosis splice variant 838-2283del	AF144239			1.068	1.054	1.281	0.492			Protein complex assembly. Iron ion homeostasis. Receptor mediated endocytosis.
C20orf185	antimicrobial peptide RYA3	NM_182658							2.348	0.444	
SCUBE3	" signal peptide, CUB domain, EGF-like 3"	NM_152753			1.024	0.762			1.32	1.316	
LOC284804	LOC284804 protein	BC065483			1.125	0.428			1.219	0.782	
N/A	AH-related protein	AF331033			1.018	1.136	1.325	0.811			CAMP biosynthesis. Intracellular signaling cascade.
N/A	N/A	AK126237			1.338	0.77			1.004	0.584	
N/A	ncaml	AF241539			2.341	0.255					
SLC6A3	solute carrier family 6 (neurotransmitter transporter, dopamine)	NM_001044					1.099	0.495	1.241	0.505	Neurotransmitter transport.
N/A	N/A	AK127935			1.321	1.023			1.016	0.53	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
N/A	Unknown (protein for IMAGE:5260398)	BC068579			1.136	0.668			1.2	0.421	
MGC35212	hypothetical protein MGC35212	NM_152764			2.336	0.488					
RYD5	ligand binding protein RYD5	NM_145651			1.243	0.794			1.092	0.623	
PAX1	paired box gene 1	NM_006192					1.146	0.333	1.189	0.553	Skeletal development. Regulation of transcription, DNA-dependent.
N/A	N/A	AK130623			1.004	0.581			1.331	0.536	
IFNA13	" interferon, alpha 13"	NM_006900			1.016	0.43			1.319	0.627	Defense response.
FABP1	" fatty acid binding protein 1, liver"	NM_001443			1.285	0.463			1.05	0.273	Fatty acid metabolism. Transport. Cell-cell signaling. Organogenesis.
HOXA3	homeobox A3 protein isoform a	NM_153631			2.334	0.696					Regulation of transcription, DNA-dependent. Development.
RYD5	ligand binding protein RYD5	NM_145651			1.241	0.554			1.092	0.623	
N/A	N/A	AK128007			1.109	0.452			1.223	0.699	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
ZNF541	zinc finger protein 541	NM_032255			1.147	0.556			1.183	0.58	Regulation of transcription, DNA-dependent.
DKFZp434A1727	hypothetical proteincDNA DKFZp434A1727 (from clone DKFZ	AL133657			1.31	0.683			1.019	0.408	
N/A	N/A	AK127982					1.062	0.206	1.266	0.32	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
N/A	G protein-coupled receptor GPR112	AY255581			2.326	1.352					
DRD1	dopamine receptor D1	NM_000794			1.087	0.615			1.239	0.453	Signal transduction. G-protein signaling, coupled to cyclic nucleotide second messenger. Dopamine receptor.
MGC35366	hypothetical protein MGC35366	NM_152435			1.175	0.487	1.15	0.898			Histidine catabolism to glutamate and formamide.
FLJ11164	hypothetical protein FLJ11164	NM_018346	1.079	1.333	1.289	0.917	1.035	0.64			Porphyrin biosynthesis.
N/A	N/A	BX161461			1.261	0.736			1.061	0.498	
BTN2A2	" butyrophilin, subfamily 2, member A2 isoform a"	NM_006995			2.32	0.981					
N/A	N/A	AK125400							2.318	0.695	
N/A	N/A	AK126775			1.072	0.599			1.244	0.346	
N/A	PRO2949	AF119907			1.05	0.971			1.264	0.539	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
KIAA0362	N/A	AB002360							2.314	0.728	Electron transport. Intracellular signaling cascade.
CHN2	chimerin (chimaerin) 2	NM_004067	1.201	1.159			1.16	0.533	1.154	0.673	Intracellular signaling cascade.
IGFL3	insulin growth factor-like family member 3	NM_207393							2.313	0.566	
SALL2	sal-like 2	NM_005407			1.211	0.513	1.1	0.421			Regulation of transcription, DNA-dependent.
MUSP1	MUSP1	AF384996							2.311	0.162	
N/A	small intestine aquaporin	AF159174			1.02	0.512			1.29	0.741	

LOC388161	LOC388161 protein	BC054509			2.309	0.379					
N/A	N/A	AK126237			1.3	0.72			1.004	0.584	
N/A	Unknown (protein for MGC:20989)	BC014249			2.303	0.234					Transcription. Regulation of transcription, DNA-dependent.
FLJ00415	FLJ00415 protein	AK122590							2.303	0.292	
N/A	Unknown (protein for MGC:32654)	BC030984			1.127	0.885			1.173	0.579	
C20orf51	chromosome 20 open reading frame 51	NM_022099	1.312	1.686	1.071	0.358			1.229	0.48	
XKRX	" X Kell blood group precursor-related, X-linked"	NM_212559			1.272	0.547			1.026	0.384	
KIAA1427	KIAA1427 protein	AB037848			1.039	0.769			1.259	0.661	Transport.
N/A	PRO1787	AF116668							2.295	0.273	Development.
KIAA0475	KIAA0475 protein	AB007944			1.18	1.133	1.115	0.773			Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
CYP2B7P1	CYP2B7P1 protein	BC041174					1.091	0.99	1.204	0.589	Electron transport. Transport.
GJB4	gap junction protein, beta 4"	NM_153212					1.017	0.847	1.277	0.356	Cell communication. Perception of sound.
NTF5	neurotrophin 5 preproprotein	NM_006179					1.072	0.271	1.219	0.439	
TUSC5	LOST1	NM_172367			1.123	0.971			1.168	0.479	
NSBP1	nucleosomal binding protein 1	NM_030763			1.113	0.833	1.176	0.601			Transcription. Regulation of transcription, DNA-dependent.
PLA2G12B	" phospholipase A2, group XIIB"	NM_032562			1.164	1.281			1.124	0.598	Lipid catabolism.
N/A	Unknown (protein for IMAGE:4821006)	BC034423			2.287	0.393					
HS6ST3	heparan sulfate 6-O-sulfotransferase 3	NM_153456			2.285	1.26					
CDC42L1	CDC42-like GTPase	AF211836			1.276	0.98	1.008	0.582			Small GTPase mediated signal transduction.
CPAMD8	C3 and PZP-like, alpha-2-macroglobulin domain containing 8"	NM_015692					1.034	0.506	1.248	0.638	
N/A	Unknown (protein for IMAGE:4663898)	BC026176			1.189	0.788			1.092	0.347	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
N/A	N/A	AK055534			1.241	0.368			1.04	0.507	
RNASE3	" ribonuclease, RNase A family, 3 (eosinophil cationic protein)'	NM_002935			1.043	1.018			1.237	0.563	RNA catabolism. Defense response to bacteria.
FLJ25660	hypothetical protein FLJ25660	NM_152481			1.068	0.644			1.212	0.309	
RDS	retinal degeneration slow protein	NM_000322					1.094	0.34	1.184	0.3	Cell adhesion. Sensory perception. Visual perception.
CFTR	" cystic fibrosis transmembrane conductance regulator, ATP-bi	NM_000492			1.068	0.271			1.21	0.495	Ion transport. Respiratory gaseous exchange.
FGF8	fibroblast growth factor 8 isoform F precursor	NM_033163					1.006	0.422	1.269	0.569	Regulation of cell cycle. Signal transduction. Cell-cell signaling. Gastrulation. Cell proliferation. Morphogenesis.
KIAA1864	KIAA1864 protein	AB058767					1.015	0.843	1.258	0.178	
KIAA0550	KIAA0550 protein	AB011122					1.199	0.611	1.073	0.309	Signal transduction. Neuropeptide signaling pathway.
N/A	N/A	AK075134			2.272	0.975					Cytokinesis.
N/A	neuronal protein 22	AF303058			1.26	1.309	1.011	0.91			Central nervous system development. Muscle development.
AVPR1A	arginine vasopressin receptor 1A	NM_000706			1.016	0.792			1.254	0.929	Generation of precursor metabolites and energy. Signal transduction. G-protein coupled receptor protein signaling pathway.
Gup1	GRINL1A complex upstream protein	NM_152451			1.035	0.608			1.234	0.969	
naaladase	NAALADase II protein	AJ012370			2.267	0.33					Proteolysis and peptidolysis. Proteolysis and peptidolysis.
FRMPD1	FERM and PDZ domain containing 1	NM_014907			1.266	0.8			1.001	0.927	
N/A	N/A	BC027961			1.018	0.446			1.248	0.97	
N/A	N/A	AK126788			1.206	0.385			1.06	0.532	
N/A	pparl	AF242527			2.265	0.457					
PSMA1	proteasome alpha 1 subunit isoform 1	NM_148976			1.187	0.565	1.077	0.542			Ubiquitin-dependent protein catabolism.
TCBA1	T-cell lymphoma breakpoint-associated target 1	NM_153355					1.231	0.513	1.03	0.617	
N/A	unknown	AF451986							2.261	0.405	
HLA-B	" major histocompatibility complex, class I, B"	NM_005514			2.261	1.228					Antigen presentation, endogenous antigen. Antigen processing, endogenous antigen via MHC class I.
RET	ret proto-oncogene isoform a	NM_020975					1.053	0.498	1.206	0.867	Protein amino acid phosphorylation. Protein amino acid phosphorylation. Homophilic cell adhesion. Signal transduction.
FLJ45686	FLJ45686 protein	NM_001005210							2.258	0.503	
FLJ26056	hypothetical protein LOC375127	NM_201401			1.066	0.585			1.192	0.273	
PKIB	cAMP-dependent protein kinase inhibitor beta	NM_181795			2.257	1.201					Negative regulation of protein kinase activity.
C20orf102	chromosome 20 open reading frame 102	NM_080607			1.025	0.724			1.232	1.052	
N/A	N/A	AK124203			1.233	1.248	1.022	0.813			
h461	ribonuclease-like protein 9	NM_001001673			1.233	0.548			1.019	0.462	
GPX7	glutathione peroxidase 7	NM_015696			1.213	0.557			1.039	0.758	Response to oxidative stress.
CIDEA	cell death-inducing DFFA-like effector a isoform 2	NM_198289			1.154	0.597			1.096	0.644	DNA fragmentation during apoptosis. Apoptosis. DNA damage response.
HFE2	hemojuvelin isoform a	NM_213653			2.249	0.493					
N/A	N/A	AK127971					1.011	0.348	1.237	0.453	
N/A	N/A	AK098599							2.247	0.229	
N/A	N/A	AK125712							2.245	0.231	
LOC255330	LOC255330 protein	BC042038							2.245	0.811	

CXorf41	chromosome X open reading frame 41	NM_173494			2.245	0.565					
GRIK5	glutamate receptor KA2 precursor	NM_002088							2.243	0.803	Potassium ion transport. Synaptic transmission.
CTSH	cathepsin H isoform a preproprotein	NM_004390	1.037	1.182	1.011	0.475			1.23	0.85	Proteolysis and peptidolysis. Proteolysis and peptidolysis.
ST14	matriptase	NM_021978							2.24	0.884	Proteolysis and peptidolysis.
N/A	N/A	AK096998	1.865	1.277			1.197	0.207	1.043	0.866	
GPR54	hypogonadotropin-1	AY253982					1.175	0.465	1.065	0.395	Signal transduction. G-protein coupled receptor protein signaling pathway.
SSTR4	somatostatin receptor 4	NM_001052					1.048	0.59	1.191	0.534	Signal transduction. Neuropeptide signaling pathway. Negative regulation of cell proliferation.
PIPOX	PIPOX protein	BC008960			1.15	0.503			1.087	0.405	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
GPR92	putative G protein-coupled receptor 92	NM_020400			1.139	0.986			1.093	0.276	Signal transduction. G-protein coupled receptor protein signaling pathway.
SCML2	sex comb on midleg-like 2	BC064617			2.231	1.043					Regulation of transcription, DNA-dependent. Morphogenesis.
SLC4A1	solute carrier family 4, anion exchanger, member 1 (erythrocyt	NM_000342							2.229	0.551	Anion transport. Cell ion homeostasis.
HDC	histidine decarboxylase	NM_002112			1.035	0.305			1.192	0.891	Amino acid metabolism. Histidine metabolism. Catecholamine biosynthesis.
KIAA1215	KIAA1215 protein	AB033041			1.1	0.487			1.126	0.856	Development.
ZNF396	zinc finger protein 396	NM_145756			2.224	0.863					
MRIP2	MRIP2	AF411132			1.204	0.446			1.019	0.449	
CTTNBP2	cortactin binding protein 2	NM_033427			2.221	1.049					
CCHL1A1	calcium channel alpha-1D subunit	M76558			1.218	0.512			1.003	0.544	Cation transport. Calcium ion transport.
CYP2J2	" cytochrome P450, family 2, subfamily J, polypeptide 2"	BC032594			1.083	0.808			1.131	0.338	Electron transport. Icosanoid metabolism. Transport. Regulation of heart contraction rate.
CLECSF7	C-type lectin, superfamily member 7 isoform 1"	NM_130441					1.029	0.245	1.185	0.275	
BMP8B	bone morphogenetic protein 8B preproprotein	NM_001720			1.093	0.457			1.119	0.481	Skeletal development. Cell differentiation. Growth.
DHX32	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 32	NM_018180			1.19	0.732	1.021	0.535			
CD209	CD209 antigen	NM_021155			1.145	0.807			1.062	0.298	Endocytosis. Cell adhesion. Leukocyte cell adhesion. Intracellular signaling cascade. Pathogenesis.
SYK	spleen tyrosine kinase	NM_003177			1.012	0.556			1.194	0.695	Protein complex assembly. Protein amino acid phosphorylation. Leukocyte cell adhesion. Integrin-mediated signaling pathway.
N/A	N/A	AK057899							2.206	0.382	Electron transport. Intracellular signaling cascade.
LAMA3	laminin alpha 3 subunit isoform 1	NM_198129			2.206	1.075					Epidermis development. Regulation of cell adhesion. Regulation of cell migration. Regulation of embryonic development.
N/A	N/A	AK122979			1.013	1.316	1.192	0.825			Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
IL28A	interleukin 28A	NM_172138							2.203	0.288	
S100A9	S100 calcium-binding protein A9	NM_002965							2.199	0.83	Inflammatory response. Cell-cell signaling.
NPTX1	neuronal pentraxin I precursor	NM_002522			1.068	0.689	1.13	0.656			Transport. Synaptic transmission. Central nervous system development.
PCTK3	PCTK3 protein	BC040529			1.011	0.625			1.183	0.39	Protein amino acid phosphorylation. Protein amino acid phosphorylation. Signal transduction.
CDH23	cadherin related 23 isoform 1 precursor	NM_022124			1.143	0.477			1.051	0.499	Cell adhesion. Homophilic cell adhesion. Sensory perception. Visual perception. Perception of sound.
AATF	apoptosis antagonizing transcription factor	NM_012138			2.194	0.972					Anti-apoptosis.
N/A	N/A	AK130044			1.018	0.683			1.174	0.963	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
C21orf129	chromosome 21 open reading frame 129	NM_152506							2.192	0.654	
DGAT2	diacylglycerol O-acyltransferase homolog 2	NM_032564			1.151	0.783			1.039	0.607	Triacylglycerol biosynthesis.
GRIN1	NMDA receptor 1 isoform NR1-3 precursor	NM_007327							2.189	0.424	Cation transport. Potassium ion transport. Calcium ion homeostasis.
FLJ00287	FLJ00287 protein	AK090403			1.065	0.68			1.124	0.497	
N/A	N/A	AK126077			1.032	0.454			1.156	0.61	
KRTAP10-12	keratin associated protein 10-12	NM_198699							2.187	0.705	
N/A	N/A	AK125932			1.041	0.521			1.145	0.396	
SLC12A8	solute carrier family 12, member 8"	NM_024628					1.157	0.738	1.028	0.658	Transport. Amino acid transport.
HPX-153	N/A	X76978			1.164	0.267	1.021	0.411			
NTSR2	neurotensin receptor 2	NM_012344	2.518	1.415	1.085	0.452			1.097	0.477	G-protein coupled receptor protein signaling pathway. Sensory perception.
TAS1R2	" taste receptor, type 1, member 2"	NM_152232			1.023	0.734			1.158	0.456	
LEP	leptin precursor	NM_000230			1.007	0.937			1.173	0.569	Energy reserve metabolism. Signal transduction. Cell-cell signaling.
N/A	unknown	AF289604			1.148	0.531	1.031	1.213			
HSPA12B	heat shock 70kD protein 12B	NM_052970			1.091	0.367			1.086	0.319	
KIAA1754L	KIAA1754-like	NM_178495			1.166	0.743	1.01	0.657			
KIAA0984	KIAA0984 protein	AB023201			1.114	0.579			1.06	0.81	
GPR55	G protein-coupled receptor 55	NM_005683	1.416	1.822	1.084	0.745			1.089	0.208	
FLJ14213	hypothetical protein FLJ14213	NM_024841			2.171	0.523					
RGS14	regulator of G-protein signalling 14	NM_006480	1.046	0.742	1.121	0.257			1.049	0.579	Signal transduction. Regulation of G-protein coupled receptor protein signaling pathway.
KIAA0681	KIAA0681 protein	AB014581			1.047	0.764			1.12	0.68	Regulation of transcription, DNA-dependent. Chromatin modification.
FA2H	fatty acid 2-hydroxylase	NM_024306			1.074	0.408			1.092	0.59	Electron transport. Transport. Metabolism.
LOC146853	LOC146853	NM_145272					1.012	0.787	1.153	0.604	
GPHB5	glycoprotein beta 5	NM_145171			1.127	0.523			1.036	0.445	

DAAM1	dishevelled-associated activator of morphogenesis 1	NM_014992			2.163	1.399					Cell organization and biogenesis. Actin cytoskeleton organization and biogenesis.
FY	Duffy blood group	NM_002036							2.162	0.258	Defense response. Signal transduction. G-protein coupled receptor protein signaling pathway.
N/A	collagen type XIV	Y11709			1.117	1.133			1.042	0.853	
N/A	N/A	AK127725			1.131	0.529			1.027	0.491	
N/A	N/A	AK074886			1.047	0.27			1.108	0.651	
KIAA0515	KIAA0515 protein	BC002969			1.131	1.003	1.022	0.976			
N/A	silencer element	D50375							2.152	0.814	Intracellular signaling cascade. Neuron cell differentiation.
MGC27121	MGC27121 protein	NM_001001343					1.116	0.522	1.034	0.461	
FOXD2	forkhead box D2	NM_004474			2.15	0.982					Transcription. Regulation of transcription, DNA-dependent.
PUS3	pseudouridylate synthase 3	NM_031307			1.056	0.466	1.093	0.756			tRNA processing.
LOC348840	hypothetical protein LOC348840	NM_182631			1.006	0.544			1.143	0.556	
AHSG	alpha-2-HS-glycoprotein	BC048198							2.148	0.457	Regulation of transcription, DNA-dependent.
SIGLEC5	sialic acid binding Ig-like lectin 5	NM_003830			1.111	0.694			1.037	0.489	Cell adhesion.
N/A	N/A	AK095925					1.015	0.737	1.132	0.553	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
INSM2	insulinoma-associated protein IA-6	NM_032594			2.146	0.991					
N/A	N/A	AK127489							2.145	0.472	
CALCB	calcitonin-related polypeptide, beta"	NM_000728							2.145	0.625	Skeletal development. G-protein signaling, coupled to cAMP nucleotide second messenger. Adenylate cyclase activation.
MGC34728	hypothetical protein MGC34728	NM_152533	1.109	1.095	1.083	0.693			1.061	0.352	
MT4	metallothionein IV	NM_032935			1.052	0.649			1.09	0.433	
VIL1	villin 1	NM_007127							2.14	0.724	Protein complex assembly. Cytoskeleton organization and biogenesis. Actin filament severing. Actin filament bundle formation.
TGM3	transglutaminase 3 precursor	NM_003245			1.04	0.907			1.1	0.643	Peptide cross-linking.
SPINT1	serine protease inhibitor Kunitz type 1	AY372172			1.002	0.675			1.137	0.716	
FLJ10901	hypothetical protein FLJ10901	NM_018265			1.034	0.631	1.1	0.547			
N/A	N/A	AK130578			1.003	0.83			1.127	0.541	
FAM26C	family with sequence similarity 26, member C"	NM_001001412							2.129	0.203	
N/A	N/A	AK127288			1.04	0.211			1.087	0.413	Inflammatory response.
MYH13	" myosin, heavy polypeptide 13, skeletal muscle"	NM_003802			2.12	1.451					Striated muscle contraction. Muscle development.
LOC89944	hypothetical protein BC008326	NM_138342			1.059	0.695			1.06	0.866	Carbohydrate metabolism.
NNMT	nicotinamide N-methyltransferase	BC000234							2.116	0.778	
LOC205251	hypothetical protein LOC205251	NM_174925			2.116	0.487					
NEF3	neurofilament 3 (150kDa medium)	NM_005382					1.017	0.176	1.095	0.379	
KIAA1680	KIAA1680 protein	AB051467			1.033	0.749			1.078	0.32	
N/A	Unknown (protein for IMAGE:3867347)	BC010635							2.108	0.244	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
OR1J2	" olfactory receptor, family 1, subfamily J, member 2"	NM_054107			1.101	0.992			1.004	0.256	
GNAS	guanine nucleotide binding protein, alpha stimulating activity p	NM_080425					1.099	0.613	1.006	0.474	G-protein coupled receptor protein signaling pathway.
LOC284861	hypothetical gene supported by BC039313	NM_201565			1.03	0.489			1.074	0.311	
MARCO	macrophage receptor with collagenous structure	NM_006770			1.018	0.6			1.083	0.336	Phosphate transport. Cell surface receptor linked signal transduction. Response to pathogenic bacteria.
N/A	N/A	AK055043			1.053	0.543			1.046	0.686	Neurotransmitter transport. Vesicle docking during exocytosis.
IFNA1	" interferon, alpha 1"	NM_024013			1.03	0.365			1.069	0.278	Defense response.
N/A	breast cancer suppressor element Ishmael Upper RP2	U50403							2.098	0.421	
C21orf77	chromosome 21 open reading frame 77	NM_018277			1.046	0.726			1.045	0.647	
A4GNT	alpha-1,4-N-acetylglucosaminyltransferase"	NM_016161							2.09	0.587	Carbohydrate metabolism. O-linked glycosylation.
DEFB104	" defensin, beta 104"	NM_080389			1.039	0.604			1.05	0.653	
TFAP2A	TFAP2A protein	BC017754			2.088	0.828					Transcription. Regulation of transcription, DNA-dependent. Signal transduction.
N/A	N/A	AK090868			2.088	0.784					Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism. Metabolism.
B2-bradykinin	N/A	X86163			2.087	0.43					Smooth muscle contraction. Inflammatory response. Transmembrane receptor protein tyrosine kinase signaling pathway.
PJCG2	olfactory-like receptor PJCG2	AF238487			1.012	0.466			1.073	0.6	
JAM2	junctional adhesion molecule 2 precursor	NM_021219			2.085	0.416					Cell-cell adhesion.
N/A	N/A	AK127761			1.026	0.6			1.056	0.447	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
HSD11B1	11-beta-hydroxysteroid dehydrogenase 1	NM_181755			2.081	0.667					Lipid metabolism. Metabolism. Glucocorticoid metabolism.
HEMGN	hemogen	NM_018437			2.079	0.261					
PPP4R2	protein phosphatase 4 regulatory subunit 2	AJ271448			1.056	1.048	1.021	0.947			Protein modification.
HA-1	minor histocompatibility antigen HA-1	NM_012292			1.018	0.578			1.059	0.511	Intracellular signaling cascade.
AGT	angiotensinogen precursor	NM_000029			2.077	0.487					Cell surface receptor linked signal transduction. Cell-cell signaling. Pregnancy. Regulation of blood pressure.
N/A	vitelliform macular dystrophy 2-like protein 1	AF440756							2.076	0.48	Ion transport.
CCBP2	chemokine binding protein 2	NM_001296	3.1	1.291	2.075	0.335					Chemotaxis. Immune response. Signal transduction. G-protein coupled receptor protein signaling pathway. Development.

DKFZp451K1917	hypothetical proteincDNA DKFZp451K1917 (from clone DKFZ	AL832613			1.037	0.701			1.034	0.415	Transport.
FLJ20130	hypothetical protein FLJ20130	BC016327			2.069	0.811					
N/A	N/A	AK130404	1.55	1.777					2.068	0.446	
MGC42951	MGC42951 protein	BC031958							2.068	0.455	
FLJ90680	FLJ90680 protein	NM_207475							2.068	1.114	
IL9	interleukin 9 precursor	NM_000590			2.067	1.153					Inflammatory response. Cell-cell signaling. Positive regulation of cell proliferation.
N/A	N/A	AK127681					2.066	0.183			Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
N/A	N/A	AK093303			2.065	0.269					Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism. Metabolism.
GPR41	G protein-coupled receptor 41	NM_005304							2.064	0.232	Signal transduction. G-protein coupled receptor protein signaling pathway.
FLJ00087	FLJ00087 protein	AK024488			1.046	0.568			1.017	0.391	
C4BPA	" complement component 4 binding protein, alpha"	NM_000715			1.054	1.021			1.008	0.532	Immune response. Complement activation, classical pathway.
N/A	N/A	AK098728							2.061	0.406	
FLJ12650	hypothetical protein FLJ12650	NM_024522							2.059	0.51	
N/A	N/A	AK127751							2.056	0.791	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
LOC375295	LOC375295 protein	BC013438			2.056	0.578					
PRG3	proteoglycan 3	NM_006093			1.032	0.547			1.022	0.39	Histamine biosynthesis. Negative regulation of protein biosynthesis. Leukotriene biosynthesis. Neutrophil activation.
N/A	N/A	AK074433			1.036	1.212			1.016	0.664	
KIAA1981	KIAA1981 protein	AB075861			2.048	0.368					
ITGAL	integrin alpha L precursor " alpha polypeptide) (ITGAL), mRNA	NM_002209							2.048	0.276	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
FLJ00376	FLJ00376 protein	AK090455			2.047	0.658					
FLJ00097	FLJ00097 protein	AK074042							2.046	0.648	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
RFPL3	ret finger protein-like 3	NM_006604			1.014	0.404			1.029	0.336	Protein ubiquitination.
N/A	FP588	AF370382							2.043	1.064	
DKFZp434P0216	hypothetical protein	AL834139							2.043	0.804	
TDRD1	tudor domain containing 1	NM_198795			2.038	0.277					
N/A	N/A	AK124803			2.037	0.728					
UPK3A	uroplakin 3A	NM_006953			2.033	0.572					
AMPD3	adenosine monophosphate deaminase (isoform E)	NM_000480	1.037	0.752	1.021	0.841			1.011	0.414	AMP catabolism. Nucleotide metabolism. Purine ribonucleoside monophosphate biosynthesis.
ACR	acrosin precursor	NM_001097							2.032	0.417	Proteolysis and peptidolysis. Acrosome reaction.
N/A	N/A	AK056734			2.03	0.584					
IL2RG	interleukin 2 receptor, gamma precursor"	NM_000206							2.03	0.477	Protein complex assembly. Immune response. Signal transduction. Cell proliferation.
N/A	hypothetical protein, similar to (NP_006139.1) LASP-1, LIM an	AL365412							2.028	0.415	
DKFZp686J1593	hypothetical protein	BX537502					1.026	0.748	1.002	0.584	Cell surface receptor linked signal transduction. Sensory perception. Rhodopsin mediated signaling.
OR52W1	" olfactory receptor, family 52, subfamily W, member 1"	NM_001005178			1.002	0.849			1.025	0.588	
FLJ00331	FLJ00331 protein	AK090422			2.025	0.643					
MMP28	matrix metalloproteinase 28 preproprotein isoform 2	NM_032950			2.024	0.632					Proteolysis and peptidolysis. Proteolysis and peptidolysis.
FLJ32949	hypothetical protein FLJ32949	NM_173812			2.024	0.813					
CACNG7	voltage-dependent calcium channel gamma-7 subunit	NM_031896	2.653	1.227					2.024	0.803	Ion transport. Calcium ion transport.
FLJ39155	hypothetical protein FLJ39155 isoform 2	NM_182798			2.019	0.398					Cell adhesion.
OR4D1	" olfactory receptor, family 4, subfamily D, member 1"	NM_012374			1.016	0.938			1.002	0.634	
LEF1	lymphoid enhancer binding factor-1	BC020624			2.018	0.608					Transcription. Regulation of transcription, DNA-dependent. Wnt receptor signaling pathway.
PIK3CD	" phosphoinositide-3-kinase, catalytic, delta polypeptide"	NM_005026			2.017	0.998					Protein amino acid phosphorylation. Signal transduction. Signal transduction.
KIAA1313	KIAA1313 protein	AB037734							2.016	0.407	Cell adhesion. Homophilic cell adhesion.
SLC5A8	solute carrier family 5 (iodide transporter), member 8"	NM_145913							2.012	0.63	Transport.
N/A	PRO2605	AF116709							2.009	0.651	
DKFZp686O1389	hypothetical protein	BX537525							2.009	0.662	
COLQ	acetylcholinesterase collagen-like tail subunit isoform VI precu	NM_080542			2.008	1.089					Acetylcholine catabolism in synaptic cleft. Phosphate transport. Asymmetric protein localization. Neurotransmitter catabolism.
ALK	anaplastic lymphoma kinase Ki-1	NM_004304							2.005	0.907	Protein amino acid phosphorylation. Transmembrane receptor protein tyrosine kinase signaling pathway. Neurogenesis.
N/A	N/A	Z22814			2.002	2.219					Central nervous system development.
GPR42	G protein-coupled receptor 42	NM_005305							2.001	0.634	Signal transduction. G-protein coupled receptor protein signaling pathway.
IL28B	interleukin 28B	AY129149							2	0.331	
N/A	placenta copper monamine oxidase	AF054985							1.994	0.544	Inflammatory response. Cell adhesion. Amine metabolism.
N/A	N/A	AK125949							1.993	0.563	
WAS	Wiskott-Aldrich syndrome protein	NM_000377							1.992	1.339	Defense response. Blood coagulation. Actin polymerization and/or depolymerization. Epidermis development.
C20orf152	chromosome 20 open reading frame 152	NM_080834			1.992	0.345					
TRIM15	tripartite motif protein 15 isoform alpha	NM_033229			1.99	1.12					Mesoderm cell fate determination. Protein ubiquitination.

PRSS1	protease, serine, 1 preproprotein"	NM_002769			1.987	0.678	Proteolysis and peptidolysis. Proteolysis and peptidolysis. Digestion. Negative regulation of blood coagulation
AKAP14	A-kinase anchor protein 28	NM_178813	1.987	0.69			
ARSF	arylsulfatase F precursor	NM_004042	1.985	0.663			Metabolism.
MGC34923	hypothetical protein MGC34923	NM_144717	1.983	0.806			
CYP2A7	cytochrome P450, family 2, subfamily A, polypeptide 7 isoform	NM_000764			1.98	0.475	Electron transport.
TSHR	thyroid stimulating hormone receptor	NM_000369	1.979	0.863			Signal transduction. Cell-cell signaling. Positive regulation of cell proliferation.
CAPON	C-terminal PDZ domain ligand of neuronal nitric oxide synthas	NM_014697	1.978	0.872			Neurotransmitter secretion. Regulation of nitric-oxide synthase activity.
SATB1	special AT-rich sequence binding protein 1	NM_002971	1.976	0.646			Establishment and/or maintenance of chromatin architecture. Regulation of transcription, DNA-dependent.
TF	transferrin	NM_001063			1.975	0.687	Iron ion transport. Iron ion homeostasis.
PSD4	PSD4 protein	BC035307			1.974	0.381	
N/A	N/A	AK128685	1.974	0.45			
SLC25A18	solute carrier	NM_031481	1.973	0.172			Transport.
FLJ32934	hypothetical protein FLJ32934	NM_144622			1.971	0.605	
ZNF238	zinc finger protein 238 isoform 1	NM_205768	1.97	0.372			Negative regulation of transcription from RNA polymerase II promoter.
N/A	G protein-coupled receptor PGR26	AY255601			1.969	0.396	
DKFZp547K146	hypothetical protein	AL834459			1.969	0.732	
N/A	N/A	AK130024	1.968	0.811			
ZCCHC12	" zinc finger, CCHC domain containing 12"	BC036572	1.962	0.65			
GAB3	Gab3 protein	NM_080612	1.962	0.983			
TRP-2	tyrosinase-related protein-2	AJ000503	1.961	1.319			Melanin metabolism. Melanin biosynthesis from tyrosine. Epidermis development.
APOB	apolipoprotein B precursor	NM_000384			1.955	0.862	Lipid metabolism. Lipid transport. Signal transduction. Circulation. Steroid metabolism.
CMYA4	cardiomyopathy associated 4	NM_173167			1.952	0.739	Regulation of transcription, DNA-dependent. Mitotic chromosome condensation. Chromatin modification.
KCNH5	" potassium voltage-gated channel, subfamily H, member 5 is	NM_139318	1.949	1.021			Two-component signal transduction system (phosphorelay). Cation transport. Potassium ion transport.
OR10P1	olfactory receptor, family 10, subfamily P, member 1"	NM_206899			1.944	0.267	
GALNT14	GALNT14 protein	BC010659			1.944	0.547	
IFP38	IFP38	NM_031943			1.943	0.67	
N/A	SIGLEC5	AY358369	1.942	0.719			
BDNF	brain-derived neurotrophic factor BDNF1	AY054392	1.94	1.098			Neurogenesis.
OR51T1	" olfactory receptor, family 51, subfamily T, member 1"	NM_001004759	1.938	0.78			
N/A	placenta expressed transcript 1	AY364431	1.938	0.441			
BTNL3	butyrophilin-like 3 isoform a	NM_197975	1.938	0.536			
N/A	N/A	AK125908			1.937	0.47	
ERO1LB	endoplasmic reticulum oxidoreductin 1-Lbeta	NM_019891	1.937	1.078			Electron transport. Protein folding. Transport.
tpcr25	putative olfactory receptor	X89672	1.935	0.704			
N/A	N/A	AK127400	1.934	1.001			Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism. Metabolism.
LOC112885	hypothetical protein BC012187	NM_138415	1.929	1.431			Regulation of transcription, DNA-dependent.
CST11	cystatin 11 isoform 1 precursor	NM_130794			1.927	0.497	
CRX	cone-rod homeobox protein	NM_000554			1.926	0.407	Regulation of transcription, DNA-dependent. Sensory perception. Visual perception. Organogenesis.
N/A	N/A	AK128800	1.925	0.321			
N/A	Unknown (protein for IMAGE:4246623)	BC063134	1.924	0.488			
Hox-2.2	homeobox protein	AJ270993	1.924	0.649			Regulation of transcription, DNA-dependent. Development. Determination of anterior/posterior axis, embryo.
SLC9A2	" solute carrier family 9 (sodium/hydrogen exchanger), isoform	NM_003048	1.922	1.263			
N/A	N/A	AK055463			1.922	0.51	
LOC51066	LOC51066 protein	BC052614			1.922	0.519	
PARP8	" poly (ADP-ribose) polymerase family, member 8"	NM_024615	1.921	0.964			Protein amino acid ADP-ribosylation.
N/A	Unknown (protein for IMAGE:5206951)	BC030522			1.919	0.291	
KRTAP10-3	keratin associated protein KAP10.3	AJ566383			1.919	0.315	
CYP2A6	cytochrome P450, family 2, subfamily A, polypeptide 6"	NM_000762			1.918	0.358	Electron transport. Transport.
FLJ38819	hypothetical protein FLJ38819	NM_145865			1.917	0.631	
N/A	N/A	AK125751			1.912	0.352	
KRT6B	keratin 6B	BC034535			1.91	0.88	Ectoderm development.
PGLYRP4	peptidoglycan recognition protein-I-beta precursor	NM_020393			1.909	0.397	Peptidoglycan catabolism. Detection of bacteria. Innate immune response. Defense response to Gram-positive bacteria.
TNF-alpha	tumor necrosis factor alpha	AJ251878			1.907	0.349	
OR10J3	" olfactory receptor, family 10, subfamily J, member 3"	NM_001004467	1.907	0.552			
N/A	Unknown (protein for IMAGE:4814381)	BC022493	1.907	0.607			
FLJ00275	FLJ00275 protein	AK090399			1.904	0.452	Immune response. Response to virus.

FLJ46419	FLJ46419 protein	NM_001004314			1.903	1.295					
SPANXB2	" sperm protein associated with the nucleus, X chromosome, f	NM_145664					1.902	0.794			Spermatid cell development.
IVD	isovaleryl Coenzyme A dehydrogenase	NM_002225			1.902	0.984					Electron transport.
N/A	Unknown (protein for IMAGE:3454279)	BC000825			1.9	0.566					
DKFZp547M202	hypothetical proteincDNA DKFZp547M202 (from clone DKFZp	AL512724			1.899	0.895					
CYP11A1	cytochrome P450, subfamily XIA precursor"	NM_000781							1.899	0.471	Electron transport. Lipid metabolism. C21-steroid hormone biosynthesis. Androgen biosynthesis. Steroid metabolism.
CYP17A1	" cytochrome P450, family 17"	NM_000102			1.898	0.333					Electron transport. C21-steroid hormone biosynthesis. Transport. Sex differentiation.
GPR154	G protein-coupled receptor 154 isoform A	NM_207172			1.894	0.731					
FLJ22795	FLJ22795 protein	BC007811			1.893	0.68					
CYP2A13	cytochrome P450, family 2, subfamily A, polypeptide 13"	NM_000766							1.891	0.506	Electron transport.
N/A	N/A	AK126866							1.888	0.572	
N/A	heat shock protein 86	M30627	1.08	1.211	1.886	0.487					Protein folding. Response to unfolded protein.
KRTHB4	keratin, hair, basic, 4"	NM_033045							1.886	0.489	
FLJ43870	FLJ43870 protein	NM_001001686							1.886	0.463	
TM4SF5	transmembrane 4 superfamily member 5	NM_003963							1.885	0.8	N-linked glycosylation.
PPY2	pancreatic polypeptide 2	NM_021092							1.885	0.542	
K6IRS2	keratin protein K6irs	NM_080747							1.884	0.313	
FLJ42654	FLJ42654 protein	NM_198447			1.883	1.108					Vesicle-mediated transport.
ZNF574	zinc finger protein 574	NM_022752							1.882	0.622	
ROR2	receptor tyrosine kinase-like orphan receptor 2 precursor	NM_004560			1.882	0.563					Protein amino acid phosphorylation. Signal transduction. Development.
ProSAPiP1	ProSAPiP1 protein	NM_014731							1.882	0.378	
MUSK	" muscle, skeletal, receptor tyrosine kinase"	NM_005592			1.882	0.426					Protein amino acid phosphorylation. Muscle development.
PSME3	proteasome activator subunit 3 isoform 2 " Ki) (PSME3), transc	NM_176863			1.88	0.816					
N/A	unknown	AF289571			1.879	0.757					
FOXO1A	forkhead box O1A	NM_002015			1.878	0.75					Transcription. Regulation of transcription from RNA polymerase II promoter. Anti-apoptosis.
EDA2R	X-linked ectodysplasin receptor	BC034919			1.878	1.212					Epidermis development. Embryonic development. Cell differentiation. Positive regulation of JNK cascade.
PRRG4	proline rich Gla (G-carboxyglutamic acid) 4 (transmembrane)	NM_024081	1.213	1.083	1.877	0.663					
NRG2	neuregulin 2 isoform 3	NM_013982			1.877	0.324					Anti-apoptosis. Signal transduction. Cell-cell signaling. Embryonic development.
KIAA1127	KIAA1127 protein	AB032953			1.876	0.766					
N/A	N/A	AK027267			1.875	1.063					Small GTPase mediated signal transduction.
FLJ43339	FLJ43339 protein	NM_207380			1.873	0.797					
LOC144347	hypothetical protein LOC144347	NM_181709			1.871	0.879					
CCL22	small inducible cytokine A22 precursor	NM_002990							1.871	0.532	Chemotaxis. Inflammatory response. Signal transduction. Cell-cell signaling. Sensory perception.
DKFZp686J24109	hypothetical proteincDNA DKFZp686J24109 (from clone DKFZ	BX641153			1.87	0.668					
ShrmL	Shroom-related protein	NM_020859			1.868	0.477					
MPP6	" membrane protein, palmitoylated 6"	NM_016447			1.868	0.777					Protein complex assembly.
IL1RAPL2	interleukin 1 receptor accessory protein-like 2	NM_017416							1.868	0.438	Central nervous system development.
IL1F6	interleukin 1 family, member 6 (epsilon)"	NM_014440							1.865	0.32	Inflammatory response.
FLJ12455	hypothetical protein FLJ12455	NM_022078			1.864	0.29					
SLCO2A1	solute carrier organic anion transporter family, member 2A1"	NM_005630							1.863	0.796	Lipid transport.
RLN2	relaxin 2 isoform 2	NM_005059			1.862	0.361					Pregnancy. Physiological process.
N/A	N/A	AK127271			1.862	0.733					
CBX7	chromobox homolog 7	NM_175709			1.858	0.812					Chromatin assembly or disassembly. Transcription. Regulation of transcription, DNA-dependent. Chromatin modification.
LOC129531	hypothetical protein BC018453	NM_138798			1.854	1.701					
LAMP3	lysosomal-associated membrane protein 3	NM_014398			1.854	0.975					Cell proliferation.
C9orf87	chromosome 9 open reading frame 87	NM_018112			1.854	1.343					
N/A	N/A	AK127186			1.851	0.773					
HRG	histidine-rich glycoprotein precursor	NM_000412							1.851	0.31	
FLJ25421	hypothetical protein FLJ25421	NM_152512							1.847	0.435	
RYR3	ryanodine receptor 3	NM_001036							1.843	0.503	Cation transport. Calcium ion transport. Calcium ion homeostasis.
OR2D2	" olfactory receptor, family 2, subfamily D, member 2"	NM_003700			1.843	0.905					
HLA-DQA1	MHC class II antigen	AF533931							1.843	0.57	
DKFZp434L2319	hypothetical proteincDNA DKFZp434L2319 (from clone DKFZp	AL833908			1.843	0.482					
SGEF	DKFZP434D146 protein	NM_015595			1.842	0.784					
AQP2	aquaporin 2	NM_000486							1.835	0.407	Transport. Water transport. Excretion.
UNQ473	DMC	NM_198477							1.834	0.656	

ZP2	zona pellucida glycoprotein 2 preproprotein	NM_003460							1.833	0.791	Fertilization. Binding of sperm to zona pellucida.
pyruvate	pyruvate dehydrogenase alpha subunit	S57358	1.311	1.534			1.833	0.93			Acetyl-CoA metabolism. Glycolysis.
PCSK6	paired basic amino acid cleaving system 4 isoform a preproprc	NM_002570							1.83	0.816	Proteolysis and peptidolysis. Cell-cell signaling.
FBP2	fructose-1,6-bisphosphatase 2"	NM_003837							1.829	0.387	Carbohydrate metabolism. Fructose metabolism. Gluconeogenesis.
N/A	N/A	AK125451							1.828	1.113	
OR5AR1	" olfactory receptor, family 5, subfamily AR, member 1"	NM_001004730	1.144	1.477			1.827	1.2			
ELA1	" elastase 1, pancreatic"	NM_001971			1.827	0.868					Proteolysis and peptidolysis.
OR1J4	" olfactory receptor, family 1, subfamily J, member 4"	NM_001004452			1.826	0.551					
HNF4A	hepatocyte nuclear factor 4 alpha isoform b	NM_000457							1.826	0.459	Regulation of transcription, DNA-dependent. Lipid metabolism.
FCN1	ficolin 1 precursor	NM_002003							1.826	0.382	Phosphate transport. Cell adhesion. Opsonization.
N/A	protease serine 2 isoform B	AY052784							1.825	0.391	Proteolysis and peptidolysis. Digestion. Negative regulation of blood coagulation.
CPN1	carboxypeptidase N, polypeptide 1, 50kD, precursor"	BC027897							1.823	0.737	Proteolysis and peptidolysis.
ADAMTS19	" a disintegrin-like and metalloprotease (reprolysin type) with t	NM_133638			1.823	0.936					
PROX1	prospero-related homeobox 1	NM_002763			1.822	1.185					
GUCA2B	guanylate cyclase activator 2B (uroguanylin)	NM_007102							1.822	0.77	Excretion.
N/A	N/A	AK127499							1.82	0.422	
N/A	unknown	AF218021			1.82	0.597					
KRT6A	keratin 6A	BC008807							1.82	0.421	Ectoderm development. Cytoskeleton organization and biogenesis.
N/A	N/A	AK128402							1.819	0.527	
N/A	N/A	AK128106			1.818	0.38					
N/A	GHRH receptor splice variant 1	AF282259							1.818	0.519	Skeletal development. Signal transduction. G-protein coupled receptor protein signaling pathway.
MUC4	mucin 4 isoform a	NM_018406							1.818	0.584	Cell-matrix adhesion.
MGC15730	hypothetical protein MGC15730	NM_032880							1.817	0.767	Cell adhesion.
IL1F9	interleukin 1 family, member 9"	NM_019618							1.816	0.691	Inflammatory response. Cell-cell signaling.
TDGF1	teratocarcinoma-derived growth factor 1	NM_003212			1.815	0.377					Activation of MAPK. Branching morphogenesis. Heart development. Positive regulation of cell proliferation.
SPARCL1	SPARC-like 1	NM_004684			1.812	0.712					
LPO	lactoperoxidase	NM_006151			1.812	0.905					Response to oxidative stress.
UCN	urocortin preproprotein	NM_003353							1.811	0.746	G-protein coupled receptor protein signaling pathway.
DKFZp434J1027	hypothetical proteincDNA DKFZp434J1027 (from clone DKFZp	AL133084			1.811	0.694					
CARD14	caspase recruitment domain protein 14 isoform 1	NM_024110							1.811	0.35	Activation of NF-kappaB-inducing kinase. Regulation of apoptosis.
BAPX1	bagpipe homeobox 1	NM_001189			1.811	0.717					Skeletal development. Regulation of transcription, DNA-dependent. Transcription from RNA polymerase II promoter.
ADAM2	a disintegrin and metalloproteinase domain 2 proprotein	NM_001464			1.811	0.915					Proteolysis and peptidolysis. Cell adhesion. Fusion of sperm to egg plasma membrane.
SPG3A	atlastin	NM_181598			1.81	0.544					Immune response.
AP1M2	adaptor-related protein complex 1, mu 2 subunit"	BC005021							1.81	0.283	Protein targeting. Endocytosis. Vesicle targeting.
NDRF	neuroD-related factor	AB021742							1.809	0.767	Transcription. Neurogenesis. Cell differentiation.
DKFZp686O08126	hypothetical protein	BX641066							1.809	0.696	Regulation of transcription, DNA-dependent.
TEX15	testis expressed sequence 15	NM_031271			1.808	0.956					
N/A	FKBP14	AY358643			1.808	1.397					Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism. Metabolism.
APOF	apolipoprotein F precursor	NM_001638			1.808	0.899					Lipid metabolism. Lipid transport. Steroid metabolism. Cholesterol metabolism.
N/A	myosin	L29147							1.807	0.511	
LOC90167	hypothetical protein LOC90167	NM_194277			1.807	0.256					
N/A	IL20	AY358320			1.806	0.655					Immune response. Hemopoiesis. Positive regulation of tyrosine phosphorylation of Stat3 protein.
N/A	OBP2B	AY358981							1.805	0.4	Chemosensory behavior. Electron transport. Perception of smell.
N/A	N/A	AK125132			1.803	0.505					
N/A	N/A	AK124469							1.803	0.957	
5-HTR3B	5-hydroxytryptamine 3 receptor B subunit	AF169255			1.803	0.436					Ion transport. Synaptic transmission.
WASF3	WASF3 protein	BC050283			1.802	0.737					Protein complex assembly. Actin filament polymerization.
UNQ9433	RPLK9433	NM_207413			1.798	0.732					
FLJ00167	FLJ00167 protein	AK074096							1.798	0.565	
IL2RB	interleukin 2 receptor beta precursor	NM_000878							1.795	0.496	Protein complex assembly. Immune response. Signal transduction.
CENTB1	centaurin beta1	NM_014716							1.795	1.089	Intracellular signaling cascade. Regulation of GTPase activity.
TTN	titin isoform N2-A	NM_133378	1.153	0.909	1.794	0.674					Carbohydrate metabolism. Protein amino acid phosphorylation. Striated muscle contraction.
GAC1	glioma amplified on chromosome 1 protein	AF030435							1.793	0.801	Cell adhesion. Signal transduction.
RPE65	retinal pigment epithelium-specific protein 65kDa	NM_000329			1.791	0.64					Vitamin A metabolism. Sensory perception. Visual perception.
FLJ25770	hypothetical protein FLJ25770	NM_178555			1.791	0.602					
CSH1	chorionic somatomammotropin hormone 1 isoform 2	NM_022640							1.791	0.439	

N/A	G protein-coupled receptor MRGG	AY255583							1.789	0.53	
N/A	N/A	AK096781	1.246						1.789		
FLJ00400	FLJ00400 protein	AK090478							1.787	0.871	
CRYBB3	crystallin, beta B3"	NM_004076							1.785	0.308	Visual perception.
SNFT	Jun dimerization protein p21SNFT	NM_018664			1.781	0.945					Regulation of transcription, DNA-dependent. Response to pest, pathogen or parasite.
N/A	N/A	AK126047							1.78	0.547	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
BMP3	bone morphogenetic protein 3 (osteogenic) precursor	NM_001201			1.78	0.345					Skeletal development. Cell-cell signaling. Cell differentiation.
N/A	N/A	AK122638							1.779	0.337	
FLJ33708	hypothetical protein FLJ33708	NM_173675			1.778	0.515					
HLA-DPA1	major histocompatibility complex, class II, DP alpha 1 precurso	NM_033554							1.777	0.884	Immune response. Antigen presentation, exogenous antigen. Antigen processing.
SPINLW1	" serine protease inhibitor-like, with Kunitz and WAP domains	NM_181502	1.884	1.37					1.776	0.874	
RGS7	regulator of G-protein signalling 7	NM_002924			1.775	0.873					Intracellular signaling cascade. Regulation of G-protein coupled receptor protein signaling pathway.
SLC6A1	solute carrier family 6 (neurotransmitter transporter, GABA), m	NM_003042							1.774	1.156	Neurotransmitter transport. Synaptic transmission.
PIK3R4	" phosphoinositide-3-kinase, regulatory subunit 4, p150"	NM_014602			1.774	1.095					Protein amino acid phosphorylation. Mitotic chromosome condensation. Meiosis.
GDF10	growth differentiation factor 10 precursor	NM_004962							1.774	1.123	Skeletal development. Transforming growth factor beta receptor signaling pathway.
APP	" amyloid beta A4 protein precursor, isoform a"	NM_000484			1.774	1.217					Copper ion homeostasis. Endocytosis. Apoptosis. Cell adhesion. Signal transduction. Cell death.
PCDH8	protocadherin 8 isoform 1 precursor	NM_002590							1.773	0.55	Cell adhesion. Homophilic cell adhesion. Cell-cell signaling.
LTA	lymphotoxin alpha precursor	NM_000595							1.773	0.679	Induction of apoptosis. Immune response. Signal transduction. Cell-cell signaling.
C21orf89	C21orf89 protein	AF426268							1.771	0.601	
LOC136306	hypothetical protein LOC136306	NM_174959			1.769	0.833					
FERD3L	nephew of atonal 3	NM_152898							1.767	0.642	
ZNF423	zinc finger protein 423	NM_015069							1.764	0.483	
RPL24	ribosomal protein L24	NM_000986			1.763	1.015					Protein biosynthesis.
RGR	retinal G protein coupled receptor	NM_002921							1.763	0.745	Signal transduction. G-protein coupled receptor protein signaling pathway.
LR8	LR8 protein	NM_014020							1.761	0.439	Organogenesis.
LRP11	LRP11 protein	BC016788			1.76	1.147					
GLUT10	glucose transporter	AF248053			1.76	1.241					Carbohydrate transport. Glucose transport.
FLJ00411	FLJ00411 protein	AK122586							1.76	0.57	Inflammatory response. Cell-matrix adhesion. Cell-cell adhesion.
SEC14L3	SEC14-like 3	NM_174975							1.759	0.348	Transport. Intracellular protein transport.
LY9	lymphocyte antigen 9 precursor	AF055708							1.759	0.443	Cell adhesion. Humoral defense mechanism.
KIAA1719	KIAA1719 protein	AB051506							1.759	0.846	
C14orf66	sphingolipid C4-hydroxylase/delta 4-desaturase	NM_206918							1.758	0.849	
N/A	N/A	AK127689							1.757	0.565	
RND1	GTP-binding protein RHO6	NM_014470			1.756	0.846					Actin filament organization. Negative regulation of cell adhesion. Neuronal remodeling.
SFTPD	surfactant, pulmonary-associated protein D"	NM_003019							1.755	0.499	Regulation of cytokine production. Oxygen and reactive oxygen species metabolism.
c-myb	v-myb myeloblastosis viral oncogene homologue (avian)	AJ606319			1.755	0.981					Regulation of transcription, DNA-dependent.
STK22D	spermiogenesis associated serine/threonine kinase 22D	NM_032028			1.754	1.102					
RORC	RAR-related orphan receptor C isoform a	NM_005060							1.754	0.745	Regulation of transcription, DNA-dependent.
N/A	apolipoprotein A-IV precursor	X13629							1.754	0.626	Lipid metabolism.
C14orf115	chromosome 14 open reading frame 115	BC053325	1.479	1.217					1.754	0.735	DNA transposition.
LOC400120	hypothetical LOC400120	NM_203451							1.753	0.663	
MUC15	mucin 15	NM_145650			1.752	0.331					
NKp44RG2	N/A	AJ010100							1.751	0.568	Cellular defense response. Signal transduction.
N/A	Unknown (protein for MGC:33988)	BC029542							1.751	0.384	
N/A	N/A	AK057244							1.751	0.492	
DBCCR1L	DBCCR1-like	NM_199051			1.749	1.061					
FLJ46361	FLJ46361 protein	NM_198577			1.748	0.743					
FGF20	fibroblast growth factor 20	NM_019851			1.748	1.331					Signal transduction. Cell-cell signaling.
ZDHHC21	" zinc finger, DHHC domain containing 21"	NM_178566			1.746	0.775					
CIB3	DNA-dependent protein kinase catalytic subunit-interacting pro	NM_054113							1.746	0.775	
FLJ32785	hypothetical protein FLJ32785	NM_152494							1.745	0.502	Protein ubiquitination.
N/A	Unknown (protein for MGC:70902)	BC065260			1.743	0.814					
N/A	Unknown (protein for MGC:18299)	BC008624			1.742	0.854					
KIAA1359	KIAA1359 protein	AB037780							1.741	0.316	
GRB14	growth factor receptor-bound protein 14	NM_004490			1.741	0.811					Intracellular signaling cascade.
SPANXB2	" sperm protein associated with the nucleus, X chromosome, f	NM_145664					1.739	0.768			Spermatid cell development.

NGEF	neuronal guanine nucleotide exchange factor	NM_019850					1.739	0.513	
N/A	Unknown (protein for IMAGE:4944653)	BC060318					1.738	0.891	
N/A	N/A	AK127768					1.738	0.422	
FLJ30934	hypothetical protein FLJ30934	NM_152760					1.737	0.855	Intracellular signaling cascade. Protein transport.
LCN2	lipocalin 2 (oncogene 24p3)	NM_005564					1.736	0.457	Transport.
pp9974	unknown	AF318382					1.735	0.683	
N/A	N/A	AK097143	1.01	1.168	1.735	0.566			
N/A	N/A	AK094872					1.735	0.497	Aromatic compound metabolism.
CCL17	small inducible cytokine A17 precursor	NM_002987					1.734	0.17	Chemotaxis. Inflammatory response. G-protein coupled receptor protein signaling pathway. Cell-cell signaling. Development.
DKFZp686F10110	hypothetical proteincDNA DKFZp686F10110 (from clone DKFZ	BX640641			1.733	0.872			Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
N/A	N/A	AK127849			1.732	1.08			
PAPLN	papilin	NM_173462					1.731	0.771	
Nbla00761	RIM short form	AB045726			1.731	0.553			
N/A	N/A	AK124375					1.731	0.32	
IL1F10	interleukin 1 family, member 10"	NM_032556					1.731	0.909	Inflammatory response.
N/A	Similar to RIKEN cDNA 4933430H15 gene	BC033790			1.729	0.519			
C6orf52	C6orf52 protein	BC016820			1.729	0.709			
SLC16A14	" solute carrier family 16 (monocarboxylic acid transporters), n	NM_152527			1.728	0.472			Transport.
BMPR1B	" bone morphogenetic protein receptor, type IB"	NM_001203			1.725	0.83			Skeletal development. Cartilage condensation. Ovarian cumulus expansion. Eye morphogenesis.
SALL4	sal-like 4	NM_020436			1.72	0.757			Regulation of transcription, DNA-dependent.
USH3A	USH3A protein isoform a	NM_174878			1.719	0.758			
LSR68	lipopolysaccharide specific response-68 protein	AF147723			1.718	0.651			Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism. Metabolism.
KIAA0883	KIAA0883 protein	AB020690					1.718	0.707	
MGC11242	hypothetical protein MGC11242	NM_024320					1.717	0.328	
RDH-E2	retinal short chain dehydrogenase reductase	NM_138969					1.715	0.752	Metabolism.
GRB7	growth factor receptor-bound protein 7	NM_005310					1.715	0.813	Signal transduction. Epidermal growth factor receptor signaling pathway. Intracellular signaling cascade.
N/A	N/A	AK094751					1.714	0.526	
FLJ41287	FLJ41287 protein	NM_207381			1.712	0.656			Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism. Metabolism.
FLJ13798	hypothetical protein FLJ13798	NM_024773			1.712	0.599			
N/A	N/A	AK127951					1.711	0.388	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
N/A	N/A	AK074597					1.71	0.521	Extracellular matrix organization and biogenesis.
RBP3	N/A	NM_002900					1.707	0.563	Proteolysis and peptidolysis. Lipid metabolism. Transport. Visual perception.
N/A	N/A	AK095511			1.707	0.403			
MLC1	MLC1 protein	BC010518					1.707	0.42	Protein biosynthesis. Ion transport.
TRADD	TNFRSF1A-associated via death domain isoform 2	NM_153425					1.706	0.414	Induction of apoptosis. Signal transduction. Positive regulation of I-kappaB kinase/NF-kappaB.
SLC13A4	" solute carrier family 13 (sodium/sulfate symporters), membe	BC030689			1.706	1.02			Ion transport. Sodium ion transport. Sulfate transport. Response to pest, pathogen or parasite.
PTH	parathyroid hormone preproprotein	NM_000315	1.597	1.519	1.702	0.79			Skeletal development. Calcium ion homeostasis. G-protein coupled receptor protein signaling pathway. Cell-cell signaling.
N/A	genethonin 3	AF177292			1.701	0.328			
LOC167127	hypothetical protein LOC167127	NM_174914					1.701	0.803	Metabolism.
CEACAM8	carcinoembryonic antigen-related cell adhesion molecule 8	NM_001816					1.698	0.608	Immune response. Pregnancy.
NFE2L3	nuclear factor (erythroid-derived 2)-like 3	NM_004289			1.696	1.344			Regulation of transcription, DNA-dependent.
MYL2	MYL2 protein	BC015821					1.695	0.37	Regulation of striated muscle contraction. Muscle development.
ERRB2	nuclear receptor ERRB2	AF094517					1.693	0.399	Regulation of transcription, DNA-dependent.
SPIC	SPI-C transcription factor	AF518404			1.692	1.153			
SLC5A10	" solute carrier family 5 (sodium/glucose cotransporter), memb	NM_152351	1.744	2.16			1.692	0.322	Transport.
SLC13A5	solute carrier family 13 (sodium-dependent citrate transporter),	NM_177550					1.691	0.893	Sodium ion transport.
KRTAP9-3	keratin associated protein 9.3	NM_031962					1.69	0.554	
FLJ14721	hypothetical protein FLJ14721	NM_032829			1.687	0.426			
PRDM7	PR-domain zinc finger protein 7 isoform A	AF274347					1.686	0.438	Regulation of transcription, DNA-dependent.
LOC134548	hypothetical protein LOC134548	NM_175873			1.686	0.927			
GAS2L2	growth arrest-specific 2 like 2	NM_139285					1.686	0.431	
CACNB2	" calcium channel, voltage-dependent, beta 2 subunit isoform	NM_000724			1.685	0.473			Calcium ion transport. Neuromuscular junction development.
N/A	N/A	M19154			1.684	1.045			Regulation of cell cycle. Cell proliferation. Cell growth.
MGC52423	hypothetical protein MGC52423	NM_182517					1.684	0.358	
SIAT10	" alpha2,3-sialyltransferase VI"	NM_006100			1.682	0.833			Amino sugar metabolism. Protein amino acid glycosylation.
N/A	N/A	AK098288			1.682	1.336			

DLL1	delta-like 1	NM_005618			1.682	0.601					Embryonic development (sensu Mammalia). Cell fate determination. Cell communication. Notch signaling pathway.
rab1c	small GTP-binding protein	U66622							1.681	0.7	
N/A	LD78 alpha beta	D63785							1.681	0.614	Calcium ion homeostasis. Exocytosis. Cell motility. Chemotaxis. Inflammatory response. Cytoskeleton organization.
R3HDML	R3H domain (binds single-stranded nucleic acids) containing-li	NM_178491							1.68	0.574	
K5B	keratin 5b	NM_173352							1.68	0.297	
FLJ10884	hypothetical protein FLJ10884	NM_019079							1.679	0.379	
DKFZp434O0527	hypothetical protein DKFZp434O0527	NM_194302							1.678	0.356	
C14orf78	C14orf78 protein	BC011859							1.678	0.673	
HRC	histidine-rich calcium-binding protein precursor	NM_002152							1.677	0.376	Electron transport. Muscle contraction.
N/A	N/A	AK126065			1.676	0.855					
KIAA1679	KIAA1679 protein	AB051466			1.674	0.985					
DDIT4L	DNA-damage-inducible transcript 4-like	NM_145244			1.674	1.059					
N/A	N/A	AK126276			1.673	0.849					
N/A	GIQT3049	AY359026			1.672	0.612					Electron transport. Cholesterol biosynthesis.
N/A	N/A	AK093351	2.067	2.023					1.672	0.566	
LY75	lymphocyte antigen 75	NM_002349			1.671	0.611					Endocytosis. Inflammatory response.
CLGN	calmegin	NM_004362			1.671	0.609					Protein folding. Fertilization.
FSTL4	follistatin-like 4	NM_015082							1.669	0.873	
N/A	G protein-coupled receptor KIAA0758 protein	AY255552							1.666	0.701	
N/A	N/A	AK127825							1.665	0.773	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
N/A	interleukin-1 homolog 2	AF200494							1.664	0.463	Immune response.
N/A	N/A	AK128517			1.663	0.477					
MGC71745	similar to embigin	NM_198449			1.663	0.817					
KIAA0976	KIAA0976 protein	AB023193							1.662	0.589	Neurogenesis. Axonogenesis. Cell differentiation.
C14orf147	chromosome 14 open reading frame 147	NM_138288					1.662	0.333			
ADAM28	a disintegrin and metalloproteinase domain 28 isoform 1 prepr	NM_014265			1.662	0.87					Proteolysis and peptidolysis. Spermatogenesis.
TRIM9	tripartite motif protein 9 isoform 1	NM_015163			1.661	1.036					Protein ubiquitination.
FLJ90013	hypothetical protein FLJ90013	NM_153365			1.661	1.456					
FLJ00054	FLJ00054 protein	AK054562							1.661	0.616	
N/A	PRO1257	AF116629			1.66	0.613					Electron transport.
CYP3A7	cytochrome P450, family 3, subfamily A, polypeptide 7"	NM_000765							1.66	0.404	Electron transport. Xenobiotic metabolism.
N/A	N/A	AK126399							1.659	0.502	
GP9	glycoprotein IX (platelet)	NM_000174							1.659	0.494	Cell adhesion. Blood coagulation.
SYNE1	nesprin 1 longest	NM_182961			1.658	1.259					Nuclear organization and biogenesis. Golgi organization and biogenesis. Muscle cell differentiation.
N/A	N/A	AK022209			1.658	0.406					Electron transport.
N/A	N/A	AK128039			1.657	0.388					
UGT1A6	" UDP glycosyltransferase 1 family, polypeptide A6 isoform 1	NM_001072			1.656	0.314					Xenobiotic metabolism. Metabolism.
TAS2R40	" taste receptor, type 2, member 40"	NM_176882			1.656	0.648					
N/A	N/A	AK124894							1.656	0.369	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
PLEKHB1	pleckstrin homology domain containing, family B (evectins) me	NM_021200							1.654	0.557	Signal transduction. Phototransduction.
N/A	N/A	X51602			1.654	0.506					Angiogenesis. Transmembrane receptor protein tyrosine kinase signaling pathway. Pregnancy.
N/A	N/A	AK098637			1.653	0.515					
OR10AD1	olfactory receptor, family 10, subfamily AD, member 1"	NM_001004134							1.652	1.372	
N/A	N/A	AK128040			1.651	0.847					
N/A	N/A	AK127300							1.651	0.484	Transport. Cation transport. Zinc ion transport.
N/A	N/A	AK026211			1.651	0.677					
LOC285679	LOC285679 protein	BC043435							1.651	0.719	
N/A	Unknown (protein for IMAGE:5192302)	BC048278			1.65	0.609					
SIAT9	sialyltransferase 9 " GM3 synthase) (SIAT9), mRNA."	NM_003896			1.649	1.254					Ganglioside biosynthesis. Carbohydrate metabolism. Protein amino acid glycosylation.
C9orf42	chromosome 9 open reading frame 42	NM_138333			1.649	1.126					
N/A	Similar to hypothetical protein FLJ21394	BC013935							1.648	0.376	
LSP1	lymphocyte-specific protein 1	NM_002339							1.648	0.422	Cell motility. Cellular defense response. Signal transduction.
CD4	CD4 receptor	S79267							1.648	0.606	Immune response. Cell adhesion. Transmembrane receptor protein tyrosine kinase signaling pathway. T-cell differentiation.
C20orf166	chromosome 20 open reading frame 166	NM_178463							1.648	0.798	
ZNF19	zinc finger protein 19	NM_006961							1.647	0.742	Regulation of transcription, DNA-dependent.
SLCO5A1	organic anion transporter polypeptide-related protein 4	NM_030958							1.647	0.822	Transport.

PEBP4	hypothetical protein MGC22776	NM_144962							1.647	0.372	
N/A	N/A	AK092741							1.647	0.766	Cell proliferation. Antimicrobial humoral response.
PDGFRL	platelet-derived growth factor receptor-like protein	NM_006207			1.646	0.896					
C21orf37	chromosome 21 open reading frame 37	NM_001005521			1.646	0.47					
PRICKLE1	prickle-like 1	NM_153026			1.645	0.637					
N/A	N/A	M28586			1.645	0.476					Defense response. Cell-cell signaling. Response to virus.
N/A	N/A	AK024389			1.645	0.724					
ALPI	intestinal alkaline phosphatase precursor	NM_001631							1.645	0.719	Metabolism. Phosphorylation.
ZNF232	zinc finger protein 232	NM_014519							1.644	0.591	Regulation of transcription, DNA-dependent.
N/A	Unknown (protein for IMAGE:2988019)	BC001521			1.644	0.739					
FBN3	fibrillin 3	NM_032447							1.643	0.822	
WNT2	wingless-type MMTV integration site family member 2 precurs	NM_003391			1.642	0.46					Frizzled-2 signaling pathway. Development.
N/A	N/A	AK091509							1.642	0.496	
BCORL1	BCL6 co-repressor-like 1	NM_021946			1.641	0.811					
tpcr16	putative olfactory receptor	X89670							1.638	0.899	
PDK4	" pyruvate dehydrogenase kinase, isoenzyme 4"	NM_002612			1.638	0.748					Glucose metabolism. Protein amino acid phosphorylation.
MYT1	MYT1	AB028973							1.638	0.397	Protein modification.
CHRNA5	" cholinergic receptor, nicotinic, alpha polypeptide 5"	NM_000745			1.636	0.567					Ion transport. Signal transduction. Synaptic transmission.
SLIC1	selectin ligand interactor cytoplasmic-1	NM_153337			1.635	0.961					Intracellular signaling cascade. Protein transport.
IGF2AS	" insulin-like growth factor 2, antisense"	NM_016412			1.635	1.052					
FLJ00143	FLJ00143 protein	AK074072			1.635	0.342					Intracellular signaling cascade.
APOA4	apolipoprotein A-IV precursor	NM_000482							1.635	0.679	Lipid metabolism. Lipid transport. Lipid transport. Circulation.
N/A	Unknown (protein for IMAGE:3866238)	BC008648							1.633	0.278	Nucleosome assembly. Neurogenesis.
MRGX2	G protein-coupled receptor MRGX2	NM_054030							1.633	0.593	
PHOSPHO1	" phosphatase, orphan 1"	NM_178500			1.632	0.85					Metabolism.
N/A	N/A	AK124895			1.632	0.793					
FLJ42842	FLJ42842 protein	NM_001004335	1.37	1.775					1.631	0.562	
VLDLR	very low density lipoprotein receptor	NM_003383			1.63	0.979					Lipid metabolism. Lipid transport. Endocytosis. Signal transduction. Neurogenesis.
KRTHB2	keratin, hair, basic, 2"	NM_033033							1.63	0.443	
IQGAP2	IQ motif containing GTPase activating protein 2	NM_006633			1.63	0.797					Signal transduction. Small GTPase mediated signal transduction.
HLA-C	" major histocompatibility complex, class I, C precursor"	NM_002117			1.627	0.749					
DKFZp686A1395	hypothetical protein	BX537436							1.627	0.52	Ion transport. Calcium ion transport.
GAL3ST1	galactose-3-O-sulfotransferase 1	NM_004861							1.626	0.596	N-linked glycosylation. Biosynthesis.
ZCCHC13	" zinc finger, CCHC domain containing 13"	NM_203303			1.621	0.272					
N/A	N/A	BX248746			1.621	0.792					
DKFZp547E052	DKFZp547E052 protein	BC062636			1.621	1.066					
PCBD	pterin-4 alpha-carbinolamine dehydratase isoform 1 precursor	NM_000281					1.62	0.997			Tetrahydrobiopterin biosynthesis.
env	HERV-E envelope glycoprotein	AF026246							1.619	0.252	
KRTAP9.5	keratin associated protein 9.5	AJ406949							1.617	0.774	
GH2	growth hormone 2 isoform 2	NM_022557							1.617	0.59	
N/A	hunc18b2	AB002559							1.616	0.532	Intracellular protein transport. Vesicle docking during exocytosis. Vesicle-mediated transport.
CSH2	chorionic somatomammotropin hormone 2 isoform 2	NM_022644							1.616	0.362	Signal transduction. Cell-cell signaling. Pregnancy.
N/A	TAC3	AY358679							1.615	0.387	Tachykinin signaling pathway. Neuropeptide signaling pathway. Synaptic transmission. Pregnancy.
DKFZp434P0111	hypothetical protein	AL157492							1.615	0.242	
GSTA1	glutathione S-transferase A1	BC053578							1.612	0.642	Metabolism.
DKFZp667D092	hypothetical proteincDNA DKFZp667D092 (from clone DKFZp	AL713683			1.612	0.791					
N/A	N/A	AK095342							1.608	0.639	Epidermis development.
N/A	N/A	AK126380							1.607	0.715	
ATP1A3	Na+/K+ -ATPase alpha 3 subunit	NM_152296							1.607	0.807	Potassium ion transport. Sodium ion transport. Metabolism. ATP hydrolysis coupled.
YPEL5	yippee-like 5	NM_016061			1.605	0.827					
FLJ00240	FLJ00240 protein	AK074167							1.605	0.402	
KNG1	kininogen 1	NM_000893							1.604	0.398	Smooth muscle contraction. Inflammatory response. Negative regulation of cell adhesion. Blood coagulation.
CATX-2	unknown	AF083118			1.604	0.874					
KIAA1045	KIAA1045 protein	AB028968			1.603	1.214					
GUCY2F	guanylate cyclase 2F	NM_001522			1.603	0.811					Protein amino acid phosphorylation. Receptor guanylyl cyclase signaling pathway. Intracellular signaling cascade.
N/A	alkaline phosphatase	AB012642							1.602	0.445	Metabolism. Phosphorylation.

N/A	KSP37	AY358978							1.601	0.8	
CD72	CD72 antigen	NM_001782							1.601	0.651	Cell adhesion. Antimicrobial humoral response.
N/A	N/A	AK058066			1.6	0.725					
CBFA2T3	myeloid translocation gene-related protein 2 isoform MTG16a '	NM_005187							1.6	0.297	Regulation of transcription, DNA-dependent. Cell proliferation.
N/A	PRO1900	AF118081							1.599	0.566	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
C21orf125	chromosome 21 open reading frame 125	NM_194309							1.599	0.557	
PLXDC2	plexin domain containing 2 precursor	NM_032812			1.598	0.911					Development.
HOOK1	hook homolog 1	NM_015888			1.598	0.47					Microtubule cytoskeleton organization and biogenesis. Spermatogenesis. Cell differentiation.
GRM2	glutamate receptor, metabotropic 2 precursor"	NM_000839							1.598	0.584	Signal transduction. Negative regulation of adenylate cyclase activity. Synaptic transmission.
SNCAIP	synuclein alpha interacting protein	NM_005460			1.597	1.153					
FLJ45079	FLJ45079 protein	NM_001001685							1.596	0.612	
RRP22	RRP22 protein	BC050739							1.594	0.941	Small GTPase mediated signal transduction.
ATP2B2	plasma membrane calcium ATPase 2 isoform a	NM_001001331							1.594	0.545	Cation transport. Calcium ion transport. Metabolism.
N/A	N/A	AK092699			1.593	0.731					
KCNJ6	potassium inwardly-rectifying channel J6	NM_002240			1.593	0.914					Ion transport. Potassium ion transport.
TRIM4	tripartite motif protein TRIM4 isoform alpha	NM_033017							1.592	0.217	Protein ubiquitination.
TRPM6	" transient receptor potential cation channel, subfamily M, mer	NM_017662			1.591	0.413					Protein amino acid phosphorylation. Cation transport. Calcium ion transport.
ST18	suppression of tumorigenicity 18	NM_014682							1.591	0.676	Regulation of transcription, DNA-dependent.
SEC22L1	vesicle trafficking protein sec22b	NM_004892			1.591	0.428					ER to Golgi transport. Protein transport. Vesicle-mediated transport.
N/A	N/A	AK090695							1.591	1.102	
KCNQ2	potassium voltage-gated channel KQT-like protein 2 isoform c	NM_004518							1.591	0.746	Cation transport. Potassium ion transport. Potassium ion transport. Synaptic transmission. Neurogenesis.
GHRH-R	N/A	S79912							1.591	0.618	
EPHA3	ephrin receptor EphA3 isoform a precursor	NM_005233			1.591	0.541					Protein amino acid phosphorylation. Signal transduction. Transmembrane receptor protein tyrosine kinase signaling pathway.
OR51F2	" olfactory receptor, family 51, subfamily F, member 2"	NM_001004753			1.59	1.672					
N/A	N/A	AK127341					1.59	0.93			Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
PIWIL2	piwi-like 2	NM_018068			1.589	0.937					
KRTAP9-2	keratin associated protein 9.2	NM_031961			1.588	0.872					
BCL2	B-cell lymphoma protein 2 alpha isoform	NM_000633			1.588	0.353					Regulation of cell cycle. Release of cytochrome c from mitochondria. Anti-apoptosis. Humoral immune response.
FLJ21128	hypothetical protein FLJ21128	NM_025083			1.587	0.937					
ASS	argininosuccinate synthetase	NM_054012							1.587	0.584	Urea cycle. Arginine biosynthesis. Amino acid biosynthesis.
TRIP3	thyroid hormone receptor interactor 3	NM_004773			1.586	0.926					Regulation of transcription, DNA-dependent.
GPR51	G protein-coupled receptor 51	NM_005458							1.584	0.444	
SLC36A2	" solute carrier family 36 (proton/amino acid symporter), meml	NM_181776			1.583	1.311					Protein biosynthesis. Transport. Amino acid transport.
ETV7	Ets transcription factor TEL-2b	NM_016135			1.582	0.475					Transcription. Regulation of transcription, DNA-dependent. Transcription from RNA polymerase II promoter. Organogenesis.
N/A	N/A	AK126199							1.58	0.46	
LYG2	lysozyme-like	NM_175735			1.58	1.16					
N/A	N/A	AK091161							1.579	0.122	
N/A	Unknown (protein for IMAGE:4749202)	BC033372							1.578	0.677	
N/A	N/A	AK024943							1.578	0.327	Intracellular signaling cascade. Sensory perception. Visual perception. Perception of sound.
MSP	mosaic serine protease	NM_032046							1.578	0.465	Proteolysis and peptidolysis.
HRH3	histamine receptor H3	NM_007232							1.578	0.954	Signal transduction. G-protein coupled receptor protein signaling pathway.
ZMYND10	" zinc finger, MYND domain-containing 10"	NM_015896			1.577	0.3					
N/A	N/A	AK123235							1.577	0.589	
OR13H1	" olfactory receptor, family 13, subfamily H, member 1"	NM_001004486			1.576	0.905					
N/A	N/A	AK093103			1.576	1.01					
SCGB1A1	" secretoglobin, family 1A, member 1 (uteroglobin)"	NM_003357	1.566	1.735	1.575	0.95					Signal transduction. Embryo implantation. Organogenesis.
KIAA1957	KIAA1957 protein	AB075837							1.575	0.859	
DKFZp761K058	hypothetical protein	AL833940							1.575	0.465	
CEACAM4	carcinoembryonic antigen-related cell adhesion molecule 4	NM_001817							1.575	0.794	
MGC5391	hypothetical protein MGC5391	NM_032740					1.574	0.313			
LOC404266	LOC404266 protein	BC010732			1.574	0.689					
KIAA1783	KIAA1783 protein	AB058686							1.574	0.339	ATP synthesis coupled proton transport.
N/A	N/A	AK124069							1.573	1.02	
N/A	N/A	AK057762			1.573	0.588					
LAIR1	leukocyte-associated Ig-like receptor 1 isoform a precursor	NM_002287			1.573	1.154					
CHST11	carbohydrate (chondroitin 4) sulfotransferase 11	NM_018413			1.573	0.64					Carbohydrate metabolism. Chondroitin sulfate biosynthesis.

SP6	Sp6 transcription factor	NM_199262			1.572	0.856					
FLJ00165	FLJ00165 protein	AK074094							1.571	0.382	Positive regulation of cytokine production. Inflammatory response. Cell surface receptor linked signal transduction.
DPT	dermatopontin precursor	NM_001937			1.571	0.708					Cell adhesion.
N/A	N/A	AK097513							1.57	0.831	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
GLRA2	" glycine receptor, alpha 2"	NM_002063			1.57	0.884					Ion transport. Chloride transport. Cell surface receptor linked signal transduction. Synaptic transmission.
GABRR1	gamma-aminobutyric acid (GABA) receptor, rho 1"	NM_002042							1.57	0.639	Ion transport. Gamma-aminobutyric acid signaling pathway. Synaptic transmission.
HSD17B12	steroid dehydrogenase homolog	NM_016142			1.569	0.491					Metabolism.
FLJ32955	hypothetical protein FLJ32955	NM_153041					1.569	1.003			
N/A	seminal plasma protein-like protein	AF279147			1.568	0.941					
LOC129285	smooth muscle myosin heavy chain 11 isoform SM1-like	NM_152994			1.567	0.877					
KIAA1622	HEAT-like repeat-containing protein isoform 1	NM_058237			1.567	1.001					
CX3CL1	chemokine (C-X3-C motif) ligand 1	NM_002996							1.567	0.428	Immune response. Cell adhesion. Cytokine and chemokine mediated signaling pathway. Immune cell chemotaxis.
ATP2B3	plasma membrane calcium ATPase 3 isoform 3a	NM_021949							1.567	0.787	Cation transport. Calcium ion transport. Metabolism.
SCGB1D2	lipophilin B	NM_006551							1.566	0.563	
PIK4CB	PIK4CB protein	BC040300			1.566	0.601					Phosphatidylinositol biosynthesis. Receptor mediated endocytosis. Signal transduction.
OR2B11	olfactory receptor, family 2, subfamily B, member 11"	NM_001004492							1.566	0.593	
N/A	N/A	AK130379							1.566	0.331	
N/A	N/A	AK095136							1.566	0.935	Small GTPase mediated signal transduction.
TRALPUSH	TRALPUSH	NM_053002			1.565	0.564					
N/A	N/A	K00830							1.565	0.545	
N/A	N/A	AK022399			1.565	0.965					Protein biosynthesis. Translational initiation. Biosynthesis. Response to virus.
KIAA1573	KIAA1573 protein	NM_020925			1.565	0.579					Ion transport. Calcium ion transport.
N/A	N/A	K00830							1.564	0.518	
CACNG1	voltage-dependent calcium channel gamma-1 subunit	NM_000727							1.564	0.857	Ion transport. Calcium ion transport. Muscle contraction.
FLJ45651	FLJ45651 protein	NM_198442							1.563	0.511	
ATP7B	" ATPase, Cu++ transporting, beta polypeptide"	NM_000053			1.563	0.811					Copper ion transport. Copper ion transport. Metabolism. Metal ion transport.
PKLR	pyruvate kinase, liver and RBC isoform 1"	NM_000298							1.562	0.542	Glycolysis.
PRES	prestin isoform a	NM_198999			1.561	0.531					
DKFZp667F0711	hypothetical protein	AL713753							1.561	0.288	
NKX3-1	" NK3 transcription factor related, locus 1"	NM_006167			1.56	0.587					Regulation of transcription, DNA-dependent. Development.
N/A	N/A	AK126772			1.56	1.056					
TRY1	trypsin X3	NM_001001317					1.559	0.273			Proteolysis and peptidolysis.
S100A7	S100 calcium-binding protein A7	NM_002963							1.559	1.027	Epidermis development.
MGC16186	hypothetical protein MGC16186	NM_032372							1.559	0.64	
CPT1C	CPT1C protein	BC029104			1.559	1.118					Lipid metabolism. Fatty acid metabolism.
OR6V1	olfactory receptor, family 6, subfamily V, member 1"	NM_001001667							1.558	0.321	
N/A	Unknown (protein for MGC:45823)	BC033184							1.558	0.475	
DEFB107	beta-defensin 107	AF540979	1.024	0.504	1.558	0.75					
N/A	L-alanine:glyoxylate aminotransferase	S71388							1.557	0.233	
SCGB2A1	secretoglobin, family 2A, member 1"	NM_002407							1.556	0.84	
LOC130576	hypothetical protein LOC130576	NM_177964							1.556	0.545	
IFP38	IFP38	NM_031943							1.556	0.64	
PGR	progesterone receptor	NM_000926			1.554	0.54					
N/A	interleukin-1 receptor-associated kinase	L76191			1.554	1.094					Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
N/A	N/A	AK128205			1.554	0.51					
CREB5	cAMP responsive element binding protein 5	NM_182898			1.554	0.987					Positive regulation of transcription.
prepro-NPW	prepro-Neuropeptide W polypeptide	AB084276							1.553	0.443	Neuropeptide signaling pathway.
PRDM5	PR domain containing 5	NM_018699			1.552	0.591					Regulation of transcription, DNA-dependent
N/A	N/A	AK127243							1.551	0.238	
MUC5AC	MUC5AC protein	AJ001402							1.551	0.347	Cell adhesion.
N/A	Unknown (protein for IMAGE:5268331)	BC036665							1.549	0.644	
EGLN3	egl nine homolog 3	NM_022073			1.549	0.623					Apoptosis. Protein metabolism.
ART5	ADP-ribosyltransferase 5 precursor	NM_053017			1.548	0.881					
TRAR1	trace amine receptor 1	NM_138327	1.012	1.134	1.547	1.188					
SAA1	serum amyloid A1 isoform 1	NM_000331							1.547	0.45	Acute-phase response.
NALP11	" NACHT, leucine rich repeat and PYD containing 11"	NM_145007			1.547	0.753					

DKFZp564F1062	hypothetical proteincDNA DKFZp564F1062 (from clone DKFZ	AL713790			1.547	1.126					
ORM2	orosomucoid 2	NM_000608							1.545	0.513	Transport. Acute-phase response.
N/A	Unknown (protein for IMAGE:4778855)	BC031359			1.545	0.419					
N/A	N/A	AK091818			1.545	1.108					Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
TAS2R7	" taste receptor, type 2, member 7"	NM_023919			1.543	0.456					Signal transduction. G-protein coupled receptor protein signaling pathway. Sensory perception. Perception of taste.
ITM2C	integral membrane protein 3	NM_030926			1.543	0.826					
FLT4	fms-related tyrosine kinase 4 isoform 1	NM_182925			1.543	0.851					Protein amino acid phosphorylation. Transmembrane receptor protein tyrosine kinase signaling pathway.
DKFZp586O1922	hypothetical proteincDNA DKFZp586O1922 (from clone DKFZ	AL117471			1.542	0.66					
IL16	interleukin 16 isoform 2	NM_172217			1.541	1.149					Chemotaxis. Immune response. Sensory perception.
HOMER1	homer 1	NM_004272			1.541	1.208					Metabotropic glutamate receptor, phospholipase C activating pathway. Synaptic transmission.
N/A	HSPC062	AF161547	1.07	0.701	1.539	1.108					
N/A	PRO2369	AF119879			1.539	1.201					Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
TMEM35	transmembrane protein 35	NM_021637			1.538	0.569					
PAK3	p21-activated kinase 3	NM_002578			1.538	0.585					Protein amino acid phosphorylation.
NIFIE	seven transmembrane domain protein	Y18007			1.538	0.607					
N/A	N/A	AK128158							1.538	0.744	
XB	tenascin-X	Y17868							1.537	0.322	
N/A	N/A	BC043414							1.536	0.771	
MRPS16	mitochondrial ribosomal protein S16	NM_016065			1.536	1.016					Protein biosynthesis.
SC5DL	SC5DL protein	BC012333			1.535	1.102					Lipid metabolism. Sterol biosynthesis.
MHC2TA	MHC class II transactivator	NM_000246							1.534	0.44	Regulation of transcription, DNA-dependent. Immune response. Detection of pest, pathogen or parasite.
N/A	N/A	AK125965							1.533	0.351	
FLJ25818	hypothetical protein FLJ25818	NM_173503	1.259	1.37	1.533	0.588					
PCDHY	protocadherin	AJ564971			1.532	0.765					Cell adhesion. Homophilic cell adhesion.
RORA	RAR-related orphan receptor A isoform b	NM_134260			1.531	0.37					Transcription. Regulation of transcription, DNA-dependent. Signal transduction.
IFIT3	IFIT3 protein	BC001383			1.531	0.681					Immune response.
N/A	Unknown (protein for IMAGE:3354783)	BC009522	1.031	1.336	1.53	0.691					Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
N/A	N/A	AK125852							1.53	0.667	
N/A	hypothetical protein	AF428259							1.53	0.388	
TNXB	tenascin XB isoform 1	NM_019105							1.529	0.687	Cell-matrix adhesion.
OR7C1	" olfactory receptor, family 7, subfamily C, member 1"	NM_198944			1.527	0.505					
N/A	INM04	AY194294			1.527	0.586					
MX1	myxovirus resistance protein 1	NM_002462			1.527	0.265					Induction of apoptosis. Immune response. Signal transduction.
FCN2	ficolin 2 isoform d precursor	NM_015839							1.527	0.372	
PEX5L	PXR2b protein	NM_016559			1.526	0.899					
MGC35154	hypothetical protein MGC35154	NM_152614							1.526	0.659	
ROR1	receptor tyrosine kinase-like orphan receptor 1	NM_005012			1.524	0.891					Protein amino acid phosphorylation. Transmembrane receptor protein tyrosine kinase signaling pathway. Development.
N/A	N/A	AK023750							1.524	0.498	
KIAA0207	N/A	D86962			1.524	1.02					Intracellular signaling cascade. Cell-cell signaling. Insulin receptor signaling pathway.
TSLL1	TSLC1-like 1	AF363367							1.523	0.691	
MGC62094	similar to PAGE-5 protein	NM_207339			1.522	0.758					
LOC152195	hypothetical protein LOC152195	NM_194289			1.522	0.962					
SLC5A12	" solute carrier family 5 (sodium/glucose cotransporter), memb	NM_178498			1.52	0.852					Transport.
LOC285192	LOC285192 protein	BC041460							1.52	0.496	
FLJ22662	hypothetical protein FLJ22662	NM_024829	2.294	1.29					1.52	0.891	
CTLA4	cytotoxic T-lymphocyte-associated protein 4	NM_005214							1.52	0.896	Immune response. Immune response.
TLR1	toll-like receptor 1	NM_003263			1.519	1.062					Inflammatory response. Signal transduction. Activation of NF-kappaB-inducing kinase. Macrophage activation.
N/A	N/A	AK128367			1.519	0.516					Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
N/A	N/A	AK096051							1.519	0.328	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
EPB41L4B	erythrocyte membrane protein band 4.1 like 4B	NM_019114			1.519	1.16					
UNQ9366	GPAD9366	NM_198444							1.518	0.835	
KIAA0599	KIAA0599 protein	AB011171			1.518	0.705					
BJ-TSA-9	hypothetical protein MGC14128 isoform a	NM_032899	3.114	1.486					1.518	0.657	
TDRKH	tudor and KH domain-containing protein	AF227192			1.517	0.693					
RNF128	ring finger protein 128 isoform 1	NM_194463			1.517	0.759					Proteolysis and peptidolysis. Apoptosis. Protein ubiquitination.
N/A	N/AcDNA DKFZp451P074 (from clone DKFZp451P074).	AL832035			1.517	1.27					

N/A	N/A	AK130385							1.517	0.199	
APLP1	amyloid beta (A4) precursor-like protein 1	NM_005166							1.517	0.651	Endocytosis. Apoptosis. Cell adhesion. Neurogenesis.
NEFH	neurofilament heavy subunit	S66488							1.515	0.422	
CYP11B2	cytochrome P450, subfamily XIB polypeptide 2 precursor"	NM_000498							1.515	0.645	Electron transport. Lipid metabolism. C21-steroid hormone biosynthesis. Glucocorticoid biosynthesis.
ZHX2	zinc fingers and homeoboxes 2	NM_014943			1.514	0.516					Negative regulation of transcription, DNA-dependent.
SCRT2	scratch 2 protein	NM_033129							1.512	0.421	
SYT9	synaptotagmin IX	NM_175733							1.511	0.799	Transport.
PGDS	prostaglandin-D synthase	BC020734			1.511	0.724					Prostaglandin biosynthesis. Fatty acid biosynthesis. Signal transduction. Cell-cell signaling. Locomotory behavior.
OR2W5	" olfactory receptor, family 2, subfamily W, member 5"	NM_001004698			1.511	0.972					
LOC127540	HMG2 like	NM_145205			1.511	1.076					Regulation of transcription, DNA-dependent.
GPX5	glutathione peroxidase 5 precursor, isoform 1"	NM_001509							1.511	0.856	Lipid metabolism. Response to oxidative stress.
N/A	N/A	AK128062							1.51	0.817	
N/A	N/A	AK125726							1.51	0.282	
KRT15	keratin 15	NM_002275			1.51	0.964					Epidermis development.
KLRG1	" killer cell lectin-like receptor subfamily G, member 1"	NM_005810			1.509	0.562					Inflammatory response. Cellular defense response. Cell surface receptor linked signal transduction.
N/A	N/A	AK124155			1.508	1.45					
N/A	N/A	AK123197					1.508	0.442			
N/A	N/A	AK125470			1.506	0.555					
FABP5	fatty acid binding protein 5 (psoriasis-associated)	BC019385			1.506	0.432					Lipid metabolism. Transport. Epidermis development.
DLNB27	N/A	AB094096							1.506	0.625	Ion transport. Water transport. Receptor guanylyl cyclase signaling pathway. Response to toxin. CGMP-mediated signaling.
AIF1	allograft inflammatory factor 1 isoform 2	NM_004847							1.506	0.632	Response to stress. Inflammatory response. Cell cycle arrest. Negative regulation of cell proliferation.
N/A	Unknown (protein for MGC:71934)	BC062217			1.505	0.784					
ADAMTS9	a disintegrin and metalloproteinase with thrombospondin motif	NM_182920			1.505	0.789					Glycoprotein catabolism. Development.
N/A	N/A	AK124971			1.504	0.365					
DKFZp547K152	hypothetical proteincDNA DKFZp547K152 (from clone DKFZp	AL834238			1.504	0.85					
N/A	N/A	AK055963			1.503	0.635					
TLH6	alanine-glyoxylate aminotransferase homolog	AF191687							1.502	0.375	Metabolism.
OLFML1	olfactomedin-like 1	NM_198474							1.502	0.458	
CNN3	calponin 3	NM_001839			1.502	0.785					Smooth muscle contraction.
LOC340529	LOC340529 protein	BC041956							1.5	0.967	
SDR-O	orphan short-chain dehydrogenase / reductase	NM_148897							1.499	0.641	
OPN1LW	opsin 1 (cone pigments), long-wave-sensitive (color blindness,	NM_020061							1.499	0.599	Signal transduction. G-protein coupled receptor protein signaling pathway. Sensory perception. Visual perception.
N/A	zinc finger protein	AF024701					1.499	0.544			
GPR158L1	GPR158-like 1	NM_001004334							1.499	0.483	
FLJ23703	hypothetical protein FLJ23703	NM_182534	1.018	1.035	1.499	1.095					
N/A	acidic mammalian chitinase precursor	AF290004			1.497	0.843					Polysaccharide catabolism. Response to acid. Carbohydrate metabolism. Cell wall chitin metabolism.
SLC16A8	solute carrier family 16, member 8"	NM_013356							1.496	0.367	Transport. Organic anion transport. Lactate transport.
OR2C1	olfactory receptor, family 2, subfamily C, member 1"	NM_012368							1.496	0.969	Signal transduction. G-protein coupled receptor protein signaling pathway. Perception of smell.
N/A	N/A	BC013816			1.496	0.215					
KHDRBS3	" KH domain containing, RNA binding, signal transduction ass	NM_006558			1.496	0.435					Spermatogenesis.
N/A	N/A	AK126619			1.495	0.928					
N/A	N/A	AK125828							1.495	0.548	
N/A	ACAH3104	AY358109							1.493	0.884	
N/A	N/A	AL137353							1.493	0.81	
N/A	HOM-TES-85 tumor antigen	AF124430			1.493	0.986					
KCNA3	potassium voltage-gated channel, shaker-related subfamily, m	NM_002232							1.493	0.933	Cation transport. Potassium ion transport.
ASB10	ankyrin repeat and SOCS box-containing protein 10	NM_080871							1.493	0.468	
GR6	putative GR6 protein	NM_007354							1.492	0.544	
GH1	growth hormone 1 isoform 1	NM_000515							1.492	0.697	Signal transduction.
FLJ30726	hypothetical protein FLJ30726	NM_153018							1.492	0.231	
N/A	N/A	AK130931			1.49	0.769					
FLJ11017	hypothetical protein FLJ11017	NM_018302			1.488	0.586					
DFNB31	CASK-interacting protein CIP98	NM_015404			1.488	0.809					Perception of sound.
CYP3A4	cytochrome P450, subfamily IIIA, polypeptide 4"	NM_017460							1.488	0.495	Electron transport. Lipid metabolism. Xenobiotic metabolism. Xenobiotic metabolism.
N/A	N/A	AK123276							1.487	0.346	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism. Metabolism.
GIF	gastric intrinsic factor (vitamin B synthesis)	NM_005142							1.487	0.693	Ion transport. Cobalt ion transport.

CXorf36	chromosome X open reading frame 36	NM_024689							1.487	0.57	
GPR123	G protein-coupled receptor 123	NM_032422							1.486	0.623	Signal transduction. G-protein coupled receptor protein signaling pathway.
GALR3	galanin receptor 3	NM_003614							1.485	0.482	Signal transduction. Negative regulation of adenylate cyclase activity. Neuropeptide signaling pathway. Synaptic transmission.
CD207	CD207 antigen, langerin"	NM_015717							1.485	0.421	
N/A	N/A	AK097864							1.484	0.387	Apoptosis. Inflammatory response. Leukocyte cell adhesion. Cell-matrix adhesion. Integrin-mediated signaling pathway.
GDAP1L1	ganglioside-induced differentiation-associated protein 1-like 1	NM_024034							1.484	0.452	
C20orf17	chromosome 20 open reading frame 17	NM_173485							1.484	0.457	Regulation of transcription, DNA-dependent.
SLC2A7	intestinal facilitative glucose transporter 7	NM_207420			1.483	0.408					
IGFBP5	IGFBP5 protein	BC008099			1.483	1.413					Regulation of cell growth. Signal transduction.
DKFZp686D09174	hypothetical proteincDNA DKFZp686D09174 (from clone DKFZ	BX641097			1.483	0.855					Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
CHST6	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 6	NM_021615			1.483	0.611					
CCNJ	cyclin J	NM_019084	1.061	1.289	1.483	1.565					Regulation of cell cycle.
FLJ39553	hypothetical protein FLJ39553	NM_173549			1.482	0.468					
DKFZP566M1046	hypothetical protein DKFZp566M1046	NM_032127			1.482	1.109					
RNF30	ring finger protein 30 isoform 1	NM_032546			1.481	0.83					Microtubule-based process. Negative regulation of microtubule depolymerization. Signal transduction. Protein ubiquitination.
N/A	N/A	AK092825							1.481	0.723	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism. Metabolism.
C1orf37	C1orf37 protein	BC067775			1.481	0.303					
ULBP2	UL16 binding protein 2	NM_025217			1.48	1.457					Antigen presentation. Natural killer cell activation.
KIAA1423	KIAA1423 protein	AB037844			1.48	0.586					
GRIN2B	N-methyl-D-aspartate receptor subunit 2B precursor	NM_000834							1.479	0.519	
FLJ40121	hypothetical protein FLJ40121	NM_175904							1.479	0.973	
CAGLP	calglandulin-like protein	NM_138705							1.479	0.639	
FOXP3	forkhead box P3	NM_014009			1.478	0.518					Transcription. Regulation of transcription, DNA-dependent. Immune response.
UBASH3A	UBASH3A protein	BC028138							1.477	0.393	Metabolism.
OR4D9	olfactory receptor, family 4, subfamily D, member 9"	NM_001004711							1.477	1.126	
KRTHA1	type I hair keratin 1	NM_002277							1.477	0.511	Epidermis development.
GHRH	growth hormone releasing hormone preproprotein	NM_021081							1.477	0.382	Signal transduction. G-protein signaling, coupled to cAMP nucleotide second messenger. Cell-cell signaling.
N/A	N/A	BX161411			1.476	0.594					
N/A	N/A	AK127347							1.476	0.444	
N/A	N/A	AK055082							1.476	0.621	
N/A	testis-specific PTP-BL related Y protein	AF517635			1.476	1.118					
IL3	interleukin 3 precursor	NM_000588							1.476	0.461	Immune response. Cell-cell signaling. Neurogenesis. Positive regulation of cell proliferation.
FLJ36980	hypothetical protein FLJ36980	NM_182598							1.475	0.537	
ACTL7A	actin-like 7A	BC014610					1.475	0.835			
RIMS2	regulating synaptic membrane exocytosis 2	NM_014677			1.474	0.712					Intracellular protein transport.
N/A	Unknown (protein for IMAGE:6141205)	BC050733			1.474	0.647					Transport. Transport. Sensory perception. Visual perception. Response to drug.
FLJ23834	hypothetical protein FLJ23834	NM_152750							1.474	0.381	Cell adhesion. Homophilic cell adhesion.
SRMS	src-related kinase lacking C-terminal regulatory tyrosine and N	NM_080823							1.473	0.655	Regulation of transcription, DNA-dependent.
N/A	N/A	AK126351							1.473	0.401	
CYP8b1	sterol 12-alpha hydroxylase CYP8B1	AF090318							1.473	0.705	Electron transport. Transport.
C10orf58	chromosome 10 open reading frame 58	NM_032333							1.473	0.657	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
ZNF493	zinc finger protein 493	NM_175910	1.013	0.757			1.472	0.906			Regulation of transcription, DNA-dependent. Negative regulation of protein kinase activity. I-kappaB kinase/NF-kappaB cascade.
FLJ35848	FLJ35848 protein	BC041481			1.472	0.761					
BMP6	bone morphogenetic protein 6 precursor	NM_001718			1.472	0.709					Skeletal development. Cell differentiation. Growth.
SRrp35	serine-arginine repressor protein (35 kDa)	NM_080743			1.471	0.772					Assembly of spliceosomal tri-snRNP. Regulation of alternative nuclear mRNA splicing, via spliceosome.
N/A	Unknown (protein for IMAGE:3849975)	BC015216			1.471	0.766					Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism. Metabolism.
LOC199675	hypothetical protein LOC199675	NM_174918							1.471	0.546	
KNP3	N/A	AB001535							1.471	0.33	Cation transport. Sodium ion transport. Calcium ion transport.
GPR6	G protein-coupled receptor 6	NM_005284							1.471	0.899	Signal transduction. G-protein coupled receptor protein signaling pathway.
DDX25	DEAD (Asp-Glu-Ala-Asp) box polypeptide 25	NM_013264							1.471	0.962	
DKFZp434O2417	hypothetical protein	AL133015							1.47	0.407	Protein biosynthesis. One-carbon compound metabolism. Biosynthesis. 10-formyltetrahydrofolate catabolism.
TRAF1	TNF receptor-associated factor 1	NM_005658			1.468	1.179					Protein complex assembly. Apoptosis.
KRT24	keratin 24	NM_019016			1.468	0.774					
IF	I factor (complement)	NM_000204			1.467	0.723					Proteolysis and peptidolysis. Immune response. Complement activation, classical pathway.
N/A	Similar to RIKEN cDNA 4930442L21 gene	BC036722							1.466	0.337	
N/A	N/A	AK127997			1.466	1.258					Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.

CLCNKB	chloride channel Kb	NM_000085							1.466	0.707	Ion transport. Chloride transport. Excretion.
N/A	molybdenum cofactor biosynthesis protein A	AF034374			1.464	0.713					Mo-molybdopterin cofactor biosynthesis. Mo-molybdopterin cofactor biosynthesis.
N/A	Unknown (protein for IMAGE:5755761)	BC064595							1.463	1.053	
N/A	N/A	AK130927			1.463	1.452					
HEM1	hematopoietic protein 1	NM_005337							1.463	0.427	
N/A	N/A	AK127597							1.46	0.527	
EPHA7	ephrin receptor EphA7	NM_004440			1.459	0.854					Protein amino acid phosphorylation. Transmembrane receptor protein tyrosine kinase signaling pathway.
N/A	N/A	AK124875							1.458	0.603	Neurotransmitter transport.
MGC20579	hypothetical protein MGC20579	NM_182614			1.458	0.695					
DKFZp434M0927	hypothetical proteincDNA DKFZp434M0927 (from clone DKFZ	AL133660			1.458	0.696					Protein folding.
KIAA0605	KIAA0605 protein	AB011177							1.457	0.432	
GPR50	G protein-coupled receptor 50	NM_004224							1.457	0.656	Signal transduction. G-protein coupled receptor protein signaling pathway. Cell-cell signaling.
RRN3	RRN3 RNA polymerase I transcription factor homolog	NM_018427			1.456	0.438					Transcription from RNA polymerase I promoter.
MYO15B	MYO15B protein	BC027875							1.456	0.395	ATP synthesis coupled proton transport.
FLJ14503	hypothetical protein FLJ14503	NM_152780							1.456	0.625	
CHRM4	cholinergic receptor, muscarinic 4"	NM_000741							1.456	0.243	Acetylcholine receptor signaling, muscarinic pathway. Synaptic transmission. Cell proliferation.
P2RX3	purinergic receptor P2X3	NM_002559							1.455	0.559	Ion transport. Signal transduction.
C20orf71	chromosome 20 open reading frame 71	NM_178466							1.455	0.506	
KCNIP4	potassium channel-interacting protein 4 isoform 3	NM_147182							1.454	1.103	
TAFA1	TAFA1 protein	NM_213609					1.453	0.742			
FLJ00299	FLJ00299 protein	AK090408			1.453	0.926					Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
N/A	diamine oxidase, copper/topa quinone containing"	U11863							1.452	0.515	Metabolism.
IL1RN	interleukin 1 receptor antagonist isoform 4	NM_173843							1.452	0.443	Inflammatory response.
SEMA3A	semaphorin 3A	NM_006080			1.451	0.881					Neurogenesis. Cell differentiation.
N/A	Unknown (protein for MGC:40403)	BC030520			1.451	0.625					
ATOH7	atonal homolog 7	NM_145178			1.451	0.779					
ABCA2	" ATP-binding cassette, sub-family A, member 2 isoform a"	NM_001606	1.053	0.968	1.451	0.876					Lipid metabolism. Transport.
N/A	Unknown (protein for MGC:34223)	BC058862			1.45	0.497					
MGC14436	MGC14436 protein	BC007821							1.45	0.646	
CH25H	cholesterol 25-hydroxylase	NM_003956			1.45	0.495					Lipid metabolism. Metabolism.
HBZ	zeta globin	NM_005332							1.449	0.534	Transport. Oxygen transport.
PACSIN3	protein kinase C and casein kinase substrate in neurons 3	NM_016223			1.448	0.762					Endocytosis. Negative regulation of endocytosis.
SPATA3	testis and spermatogenesis cell apoptosis related protein 1	NM_139073							1.447	0.467	
GJB1	gap junction protein, beta 1, 32kDa (connexin 32, Charcot-Mar	NM_000166							1.447	0.636	Transport. Cell-cell signaling. Neurogenesis.
DKFZp667H0215	hypothetical proteincDNA DKFZp667H0215 (from clone DKFZ	AL834507					1.447	0.384			
N/A	Unknown (protein for MGC:45541)	BC033839			1.446	0.256					
c-myc	N/A	X66258			1.446	0.696					Transcription. Iron ion homeostasis. Cell cycle arrest. Cell proliferation.
GALP	galanin-like peptide precursor	NM_033106							1.445	0.65	Neuropeptide signaling pathway.
DDC	dopa decarboxylase (aromatic L-amino acid decarboxylase)	NM_000790							1.445	0.587	Amino acid metabolism. Catecholamine biosynthesis.
CA13	carbonic anhydrase XIII	NM_198584			1.445	0.48					One-carbon compound metabolism.
N/A	N/A	AK125612			1.444	1					
N/A	N/A	AK091683			1.444	0.929					
N/A	N/A	AK127132			1.443	1.195					Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
hIAN6	immune associated nucleotide 6	NM_175571							1.443	0.33	
FLJ20315	hypothetical protein FLJ20315	NM_017763			1.442	0.415					Protein ubiquitination.
DKFZp451G182	hypothetical proteincDNA DKFZp451G182 (from clone DKFZp	AL831966			1.442	0.545					
OR2AT4	olfactory receptor, family 2, subfamily AT, member 4"	NM_001005285							1.441	0.189	
N/A	N/A	AK129856			1.441	0.967					Amino acid metabolism. Aspartate catabolism. Biosynthesis.
LOC132200	LOC132200 protein	BC015210			1.441	1.066					
FLJ40142	FLJ40142 protein	NM_207435			1.441	0.424					
TUBA4	" tubulin, alpha 4"	NM_025019	2.985	1.845	1.44	0.766					Microtubule-based movement. Protein polymerization.
NKD2	NKD2 protein	BC012176							1.44	0.79	
NSE2	breast cancer membrane protein 101	NM_174911			1.438	1.254					Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
N/A	N/A	AK123188							1.438	0.685	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
GPR97	G protein-coupled receptor 97	NM_170776							1.438	0.509	Signal transduction. Neuropeptide signaling pathway.
FLJ00176	FLJ00176 protein	AK074105							1.437	0.844	Biosynthesis. Chaperone cofactor dependent protein folding.

TTBK1	TTBK1 protein	BC036764							1.436	0.539	Protein amino acid phosphorylation.
ANP32B	" acidic (leucine-rich) nuclear phosphoprotein 32 family, memb	NM_006401			1.436	0.63					
S100A3	S100 calcium binding protein A3	NM_002960			1.435	1.219					
LHCGR	luteinizing hormone/choriogonadotropin receptor precursor	NM_000233							1.435	0.618	Signal transduction. Male gonad development. Male genitalia morphogenesis.
KIAA1457	KIAA1457 protein	AB040890			1.434	1.075					Transport. Metabolism.
FGD5	" FYVE, RhoGEF and PH domain containing 5"	NM_152536	1.176	1.95					1.434	0.397	Cytoskeleton organization and biogenesis. Regulation of cell shape. Actin cytoskeleton organization and biogenesis.
OR2T2	" olfactory receptor, family 2, subfamily T, member 2"	NM_001004136			1.433	0.293					
GRM1	glutamate receptor, metabotropic 1"	NM_000838							1.433	0.869	Signal transduction. G-protein coupled receptor protein signaling pathway. Synaptic transmission.
NALP12	PYRIN-containing APAF1-like protein 7	NM_144687							1.432	0.412	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
RGS16	regulator of G-protein signalling 16	NM_002928			1.431	0.467					Signal transduction. Visual perception. Regulation of G-protein coupled receptor protein signaling pathway.
IFNA16	" interferon, alpha 16"	NM_002173	1.033	1.443	1.431	0.605					Defense response.
ATF3deltaZip2exonl	ATF3deltaZip2	AB078028			1.431	0.994					
C12orf14	chromosome 12 open reading frame 14	NM_021238			1.43	0.814					
RASGEF1C	RasGEF domain family, member 1C"	NM_175062							1.429	0.35	Small GTPase mediated signal transduction.
HAS2	hyaluronan synthase 2	NM_005328			1.429	0.779					
SLC28A1	solute carrier family 28 (sodium-coupled nucleoside transporte	NM_004213							1.428	0.594	Nucleobase, nucleoside, nucleotide and nucleic acid metabolism. Transport. Nucleoside transport.
ROS1	proto-oncogene c-ros-1 protein precursor	NM_002944			1.428	0.967					Protein amino acid phosphorylation. Signal transduction. Transmembrane receptor protein tyrosine kinase signaling pathway.
RAB11FIP4	RAB11 family interacting protein 4 (class II)	NM_032932							1.428	0.664	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
FLJ32028	hypothetical protein FLJ32028	NM_152680			1.428	0.365					
MGC34761	hypothetical protein MGC34761	NM_173619							1.427	0.466	
FAM45B	" family with sequence similarity 45, member B"	NM_018472			1.427	1.183					
SH2D4B	SH2 domain containing 4B	NM_207372							1.426	0.446	
N/A	N/A	AK125739							1.426	0.489	
N/A	N/A	AK125480							1.424	0.613	
MYO1A	myosin IA	NM_005379							1.424	0.479	Perception of sound. Actin filament-based movement.
FLJ32011	hypothetical protein FLJ32011	NM_182516							1.424	0.516	
PFKFB1	6-phosphofructo-2-kinase/fructose-2, 6-biphosphatase 1"	NM_002625							1.423	0.522	Fructose 2,6-bisphosphate metabolism.
N/A	Unknown (protein for MGC:34845)	BC023973			1.423	1.097					
MUC4	mucin 4	AF058803							1.423	0.406	
FGF6	fibroblast growth factor 6 precursor	NM_020996							1.422	0.393	Regulation of cell cycle. Angiogenesis. Signal transduction. Cell-cell signaling. Cell proliferation.
ASB13	ASB13 protein	BC012056			1.422	1.008					Intracellular signaling cascade.
REN	renin precursor	NM_000537			1.421	0.465					Proteolysis and peptidolysis. Regulation of blood pressure.
IL18	interleukin 18 proprotein	NM_001562			1.421	0.602					Angiogenesis. Immune response. Cell-cell signaling. Induction of apoptosis via death domain receptors.
CHRNA6	cholinergic receptor, nicotinic, alpha polypeptide 6"	NM_004198							1.421	0.591	Ion transport. Signal transduction. Synaptic transmission.
C10orf64	chromosome 10 open reading frame 64	NM_173524							1.421	0.415	
SERPINB7	" serine (or cysteine) proteinase inhibitor, clade B (ovalbumin),	NM_003784					1.42	0.597			
GRASP	GRP1 (general receptor for phosphoinositides 1)-associated sc	NM_181711			1.42	1.044					
HUR	N/A	X98307			1.419	0.659					
FAM13C1	" family with sequence similarity 13, member C1 isoform 1"	NM_198215			1.419	0.438					
DKFZp547I048	hypothetical proteincDNA DKFZp547I048 (from clone DKFZp5	AL834414	1.397	1.613					1.419	0.834	
DEFB124	defensin beta 124	AY122476							1.417	0.441	
TNFRSF5	TNFRSF5 protein	BC064518							1.416	0.418	Protein complex assembly. Apoptosis. Inflammatory response. Immune response. Signal transduction.
TH	tyrosine hydroxylase isoform a	NM_199292			1.416	0.839					Synaptic transmission. Aromatic amino acid family metabolism. Morphogenesis. Neurotransmitter biosynthesis.
MAT1A	methionine adenosyltransferase I, alpha"	BC018359							1.416	0.702	Amino acid metabolism. One-carbon compound metabolism.
FP15529	unknown	AF495723							1.416	0.677	
AP1S1	" adaptor-related protein complex 1, sigma 1 subunit isoform 2	NM_057089	1.312	1.174	1.416	0.848					Intracellular protein transport. Receptor mediated endocytosis.
NELL2	NELL2 protein	BC020544			1.415	0.462					Cell adhesion.
GYLTL1B	glycosyltransferase-like 1B	NM_152312							1.415	0.56	Glycosphingolipid biosynthesis. Synaptic transmission. Perception of sound. Glycoprotein biosynthesis.
FLJ00404	FLJ00404 protein	AK090482			1.415	0.979					
COL17A1	alpha 1 type XVII collagen	NM_000494	1.076	1.675					1.415	0.993	Electron transport. Phosphate transport. Cell-matrix adhesion. Epidermis development.
ANKRD20A	ankyrin repeat domain 20A	NM_032250							1.415	0.315	
ZA20D3	" zinc finger, A20 domain containing 3"	NM_019006			1.414	0.741					
NAGK	N-Acetylglucosamine kinase	NM_017567			1.414	0.513					N-acetylglucosamine metabolism. N-acetylmannosamine metabolism.
MTP	microsomal triglyceride transfer protein large subunit precursor	NM_000253			1.414	0.493					
MGC24047	hypothetical protein MGC24047	NM_178840			1.414	1.042					
FLJ45880	FLJ45880 protein	NM_207404					1.414	0.398			Regulation of transcription, DNA-dependent.

CHSY2	chodroitin synthase 2	AJ578034			1.414	0.83			
LOC387763	LOC387763 protein	BC052560			1.413	0.621			
KRN1	" keratin, cuticle, ultrahigh sulphur 1"	NM_005553			1.413	0.836			Epidermis development.
N/A	N/A	AK123889			1.412	0.732			Ciliary or flagellar motility.
LY64	lymphocyte antigen 64 homolog, radioprotective 105kDa"	NM_005582					1.412	0.355	Inflammatory response.
KIAA1876	KIAA1876 protein	AB058779			1.412	1.276			Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
IFI44	" interferon-induced, hepatitis C-associated microtubular aggre	NM_006417			1.412	0.562			Response to virus.
TAFA2	TAFA2 protein	NM_178539	1.446	1.58	1.411	0.545			
N/A	N/A	AK093042					1.411	0.566	
FRMPD2	FERM and PDZ domain containing 2	NM_152428					1.411	0.562	
CYP27B1	CYP27B1 protein	BC001776					1.411	0.486	Electron transport. Lipid metabolism. Transport. Calcium ion homeostasis. Vitamin biosynthesis.
WDFY3	WD repeat and FYVE domain containing 3 isoform 1	NM_014991			1.41	0.764			
S100A8	S100 calcium-binding protein A8	NM_002964					1.41	0.357	Inflammatory response.
CDH13	cadherin 13 preproprotein	NM_001257			1.41	0.462			Cell adhesion. Homophilic cell adhesion.
MUC12	transmembrane mucin 12	AF147790					1.409	0.427	
KIAA0863	KIAA0863 protein	NM_014913			1.409	0.833			Regulation of transcription, DNA-dependent.
OR52A4	" olfactory receptor, family 52, subfamily A, member 4"	NM_001005222			1.408	1.784			
N/A	Unknown (protein for MGC:45495)	BC032733			1.408	1.035			Immune response.
GPR84	inflammation-related G protein-coupled receptor EX33	BC020614			1.408	0.425			G-protein coupled receptor protein signaling pathway.
ESM1	endothelial cell-specific molecule 1 precursor	NM_007036			1.408	0.449			Regulation of cell growth.
ASB8	ankyrin repeat and SOCS box-containing 8	NM_024095			1.408	0.818			Intracellular signaling cascade.
KRT16	keratin 16	NM_005557					1.407	0.446	Epidermis development.
DSP	desmoplakin	NM_004415			1.407	0.468			Epidermis development.
SLC36A3	solute carrier family 36 (proton/amino acid symporter), membe	NM_181774					1.406	0.486	
GADD45A	" growth arrest and DNA-damage-inducible, alpha"	NM_001924			1.406	0.989			Regulation of cyclin dependent protein kinase activity. DNA repair. Apoptosis. Cell cycle arrest.
FGFBP1	fibroblast growth factor binding protein 1	NM_005130					1.406	0.843	Signal transduction. Cell-cell signaling. Negative regulation of cell proliferation.
OR8D2	" olfactory receptor, family 8, subfamily D, member 2"	NM_001002918	1.155	1.408	1.405	0.53			Signal transduction. G-protein coupled receptor protein signaling pathway. Perception of smell.
N/A	N/A	U82319					1.404	1.025	
HARSL	histidyl-tRNA synthetase-like	NM_012208			1.404	0.713			Protein biosynthesis. Histidyl-tRNA aminoacylation.
B7-H4	immune costimulatory protein B7-H4	NM_024626			1.404	1.066			
L1CAM	L1 cell adhesion molecule isoform 1 precursor	NM_000425					1.403	0.779	Cell adhesion. Neurogenesis. Cell differentiation.
KCNK3	potassium channel, subfamily K, member 3"	NM_002246					1.403	0.824	Potassium ion transport. Synaptic transmission.
CD79B	CD79B antigen isoform 1 precursor	NM_000626					1.403	0.484	Immune response. Cell surface receptor linked signal transduction.
MGC87693	similar to ZP1 precursor	NM_207341					1.402	0.326	Fertilization.
ITM2B	integral membrane protein 2B	NM_021999			1.402	0.784			Neurogenesis. Perception of sound.
EBF	early B-cell factor	NM_024007			1.402	1.155			Transcription. Regulation of transcription, DNA-dependent. Development.
RPS6KA1	" ribosomal protein S6 kinase, 90kDa, polypeptide 1"	NM_002953			1.401	0.883			Protein amino acid phosphorylation. Signal transduction.
EB-1	cajalin 2 isoform a	NM_152788			1.401	0.809			
TCF21	transcription factor 21	NM_198392			1.399	0.711			Transcription. Regulation of transcription, DNA-dependent. Mesoderm development.
OR2T35	" olfactory receptor, family 2, subfamily T, member 35"	NM_001001827			1.399	0.423			
N/A	N/A	AK127627			1.399	0.778			
KIAA0418	N/A	AB007878					1.399	0.678	Intracellular signaling cascade. Metabolism. Protein transport.
PADI6	peptidylarginine deiminase type 6	NM_207421					1.398	0.385	
Beta4GalNAc-T4	" beta1,4-N-acetylgalactosaminyltransferases IV"	NM_178537			1.398	0.75			
PCDH12	protocadherin 12 precursor	NM_016580					1.397	0.496	Cell adhesion. Homophilic cell adhesion. Neuronal cell recognition.
ELA3B	elastase 3B	NM_007352					1.397	0.249	Proteolysis and peptidolysis. Cholesterol metabolism.
OR5AU1	" olfactory receptor, family 5, subfamily AU, member 1"	NM_001004731			1.396	0.864			
GPR10	G protein-coupled receptor 10	NM_004248					1.396	0.379	Signal transduction. G-protein coupled receptor protein signaling pathway. Pregnancy.
FLJ12057	hypothetical protein FLJ12057	NM_024768					1.396	0.29	
N/A	myosin-reactive immunoglobulin light chain variable region	AF035044			1.395	0.923			
KCNK15	" potassium family, subfamily K, member 15"	NM_022358			1.395	0.494			Ion transport. Potassium ion transport.
COLM	collomin	NM_181789			1.395	0.985			Phosphate transport. Cell adhesion.
ALOX5AP	arachidonate 5-lipoxygenase-activating protein	NM_001629			1.395	0.809			Inflammatory response. Leukotriene biosynthesis.
N/A	N/AcDNA DKFZp434M0320 (from clone DKFZp434M0320).	AL137560			1.394	0.83			Protein amino acid dephosphorylation.
N/A	N/A	AK056450			1.394	1.113			
PMCHL2	pro-melanin-concentrating hormone-like 2	NM_031888			1.393	0.831			Synaptic transmission. Behavior.

IGLL1	immunoglobulin lambda-like polypeptide 1 isoform a precursor	NM_020070	1.064	0.819					1.393	0.684	Immune response.
DKFZp434I099	hypothetical protein DKFZp434I099	NM_032269							1.393	0.591	
TRAR3	trace amine receptor 3	NM_175057			1.391	0.992					
FLJ13955	hypothetical protein FLJ13955	NM_024759			1.389	0.874					
XTP7	protein 7 transactivated by hepatitis B virus X antigen	NM_138568							1.388	0.94	
LYZ	lysozyme precursor	NM_000239							1.388	0.775	Carbohydrate metabolism. Cell wall catabolism. Cytolysis. Defense response to bacteria. Immune response.
TUBA8	tubulin, alpha 8"	NM_018943							1.387	0.788	Microtubule-based movement. Protein polymerization.
FABP6	gastrotropin	NM_001445							1.387	0.801	Lipid metabolism. Transport. Negative regulation of cell proliferation.
N/A	N/A	AK130702					1.386	0.577			Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
FAM12B	human epididymis-specific 3 beta precursor	NM_022360							1.386	0.457	Spermatid cell development.
tre	oncogene	X63547							1.385	0.377	Ubiquitin-dependent protein catabolism. Ubiquitin cycle.
SLC10A1	solute carrier family 10 (sodium/bile acid cotransporter family),	NM_003049							1.385	0.819	Ion transport. Sodium ion transport. Organic anion transport.
KRTAP10-7	keratin associated protein 10-7	NM_198689			1.385	0.761					
FGF14	fibroblast growth factor 14 isoform 1B	NM_175929							1.385	0.513	Signal transduction. Cell-cell signaling. Neurogenesis.
NTF3	neurotrophin 3 precursor	NM_002527			1.384	0.864					Anti-apoptosis. Cell motility. Signal transduction. Cell-cell signaling. Neurogenesis.
TENS1	tensin-like SH2 domain containing 1	NM_022748			1.383	0.95					Protein amino acid dephosphorylation. Cell cycle. Intracellular signaling cascade.
N/A	N/A	AK128478			1.383	0.875					
N/A	N/A	AK126488			1.383	0.375					Nuclear mRNA splicing, via spliceosome. MRNA processing. RNA splicing.
HC6	HC6	AF269286					1.383	0.306			Cell adhesion.
DKFZp434H0735	hypothetical protein	AL117509							1.383	0.67	
BNC1	basonuclin 1	NM_001717			1.383	0.593					Transcription. Regulation of transcription, DNA-dependent. Positive regulation of cell proliferation. Epidermis development.
N/A	N/A	AK128281			1.382	0.634					
KIAA1579	hypothetical protein FLJ10770	NM_018211			1.382	1.116					
GABRQ	gamma-aminobutyric acid (GABA) receptor, theta precursor"	NM_018558							1.382	0.667	Ion transport. Signal transduction. Synaptic transmission.
FLJ31846	hypothetical protein FLJ31846	NM_144974			1.382	0.887					Protein ubiquitination.
N/A	Unknown (protein for IMAGE:4154275)	BC018318							1.381	0.481	
MGC35140	hypothetical protein MGC35140	NM_152759							1.381	0.344	
FLJ26443	FLJ26443 protein	NM_207440							1.381	0.683	
CAMP	cathelicidin antimicrobial peptide	NM_004345							1.381	0.292	Response to pest, pathogen or parasite. Defense response to bacteria.
DKFZp434H1419	hypothetical proteincDNA DKFZp434H1419 (from clone DKFZ	AL137534			1.38	0.26					
TACSTD2	tumor-associated calcium signal transducer 2 precursor	NM_002353			1.379	0.587					Cell surface receptor linked signal transduction. Sensory perception. Visual perception. Cell proliferation.
N/A	Unknown (protein for MGC:29947)	BC019830					1.379	0.393			
N/A	N/A	AK129980							1.379	0.087	
GSDM1	gasdermin 1	NM_178171							1.379	0.765	
GPR88	G-protein coupled receptor 88	NM_022049			1.379	0.457					Signal transduction. G-protein coupled receptor protein signaling pathway.
FKSG48	FKSG48	AF336875			1.379	1.252					
CAMK1G	calcium/calmodulin-dependent protein kinase IG	NM_020439	1.64	2.277					1.379	0.61	Protein amino acid phosphorylation.
APCDD1	adenomatosis polyposis coli down-regulated 1	AB104887							1.379	0.737	
N/A	interleukin 30	BC062422							1.378	0.623	
N/A	N/A	AK128707			1.378	1.005					
CSF2RB	colony stimulating factor 2 receptor, beta, low-affinity (granuloc	NM_000395							1.378	0.316	Signal transduction. Respiratory gaseous exchange. Cytokine and chemokine mediated signaling pathway.
KIAA1503	KIAA1503 protein	AB040936			1.377	0.889					
WFDC8	WAP four-disulfide core domain 8 precursor	NM_181510							1.376	0.597	
NKCC2	Na-K-2Cl cotransporter isoform IV	AB032527							1.376	0.721	
FLJ00050	FLJ00050 protein	AK024458							1.376	0.551	
THSD1	thrombospondin type I domain-containing 1 isoform 1	NM_018676			1.375	0.578					
N/A	Unknown (protein for IMAGE:4042121)	BC015977			1.375	1.146					
KIAA0277	N/A	D87467			1.375	0.652					Small GTPase mediated signal transduction. Neurogenesis.
N/A	N/A	AK092212	1.016	0.934					1.374	0.446	
N/A	N/A	AK055571							1.374	0.672	
TLR6	toll-like receptor 6	NM_006068			1.373	0.353					Signal transduction. Activation of NF-kappaB-inducing kinase. T-helper 1 type immune response.
OR8A1	olfactory receptor, family 8, subfamily A, member 1"	NM_001005194							1.373	1.012	
Na/Pi-4	renal Na+-dependent phosphate cotransporter	D28532			1.373	0.589					Ion transport. Sodium ion transport. Phosphate transport.
N/A	" Similar to phospholipase A2, group IVB (cytosolic)"	BC035335	1.016	1.553			1.373	0.706			Phospholipid catabolism.
SSTR1	somatostatin receptor 1	NM_001049			1.372	0.811					G-protein signaling, coupled to cyclic nucleotide second messenger. Cell-cell signaling. Response to nutrients. Digestion.
NUP210	nucleoporin 210	NM_024923							1.372	0.905	Development.

N/A	N/A	AK124132							1.372	0.514	
HRIHFB2099	N/A	AB015334							1.372	0.509	
FLJ39501	hypothetical protein FLJ39501	NM_173483							1.372	0.436	Electron transport.
FLJ20225	hypothetical protein FLJ20225	NM_019062			1.372	1.219					Protein ubiquitination.
C20orf53	chromosome 20 open reading frame 53	NM_178472			1.372	0.213					
ZNF100	zinc finger protein 100	NM_173531			1.371	0.39					
SLC39A8	" solute carrier family 39 (zinc transporter), member 8"	NM_022154			1.371	0.415					Transport. Metal ion transport.
PDE3B	phosphodiesterase 3B, cGMP-inhibited"	NM_000922							1.371	0.681	Signal transduction.
N/A	polymerase	AF080232			1.371	0.267					
BRF2	RNA polymerase III transcription initiation factor BRF2	NM_018310			1.371	1.238					Cell cycle.
DKFZp547F072	hypothetical protein DKFZp547F072	NM_032274					1.37	0.757			
N/A	N/A	AK074401							1.369	0.584	
N/A	Similar to GPI-gamma 4	BC036784	1.232	1.124	1.368	0.785					
MERTK	c-mer proto-oncogene tyrosine kinase	NM_006343			1.368	1.066					Protein amino acid phosphorylation. Cell surface receptor linked signal transduction. Cell-cell signaling. Sensory perception.
HS3ST4	heparan sulfate D-glucosaminyl 3-O-sulfotransferase 4	NM_006040							1.368	0.621	Heparan sulfate proteoglycan metabolism.
FLJ30594	hypothetical protein FLJ30594	NM_153011			1.368	0.971					
PMSP	Papillomavirus minor structural protein interacting protein	AJ437509							1.367	0.784	
N/A	N/A	AK123156			1.366	0.838					
LASS3	LAG1 longevity assurance homolog 3	NM_178842							1.366	0.81	
DGKH	" diacylglycerol kinase, eta isoform 2"	NM_178009			1.366	1.34					
ISL1	ISL1 protein	BC031213							1.365	0.454	Regulation of transcription, DNA-dependent. Development.
ARF3	ADP-ribosylation factor 3	NM_001659			1.365	0.973					Intracellular protein transport. Small GTPase mediated signal transduction.
AKR7A3	" aldo-keto reductase family 7, member A3"	NM_012067			1.365	0.65					Aldehyde metabolism.
OPRD1	opioid receptor, delta 1"	NM_000911							1.364	0.978	Immune response. Signal transduction. G-protein signaling, coupled to cyclic nucleotide second messenger. Sensory perception.
N/A	ALIN3064	AY358107							1.364	0.571	
PXT1	peroxisomal, testis specific 1"	NM_152990							1.363	0.717	
NAG13	NAG13	AF194537					1.363	0.203			
EAT2	SH2 domain-containing molecule EAT2	NM_053282							1.363	0.62	
SEMA4A	semaphorin B	NM_022367							1.362	1.032	Neurogenesis. Cell differentiation.
KIAA1365	densin-180	NM_020794			1.362	0.645					
CRHBP	corticotropin releasing hormone binding protein	NM_001882							1.362	0.552	Signal transduction. Pregnancy. Learning and/or memory.
MAGEE2	" melanoma antigen, family E, 2"	NM_138703					1.361	0.544			
IRTA1	immunoglobulin superfamily receptor translocation associated	NM_031282					1.361	0.701			
ETV5	ets variant gene 5 (ets-related molecule)	NM_004454			1.361	1.147					Regulation of transcription, DNA-dependent.
ABCG1	ATP-binding cassette sub-family G member 1 isoform 1	NM_207630							1.361	0.584	Lipid transport. Cholesterol metabolism. Detection of hormone stimulus. Response to organic substance.
RRAD	Ras-related associated with diabetes	BC057815			1.36	0.48					Small GTPase mediated signal transduction.
KLHL6	kelch-like 6	NM_130446					1.36	0.337			
CCL25	small inducible cytokine A25 isoform 1 precursor	NM_005624							1.36	0.699	Chemotaxis. Inflammatory response. G-protein coupled receptor protein signaling pathway. Sensory perception.
C14orf6	chromosome 14 open reading frame 6	NM_145250							1.36	0.433	
N/A	N/A	AK075117							1.359	0.494	Inflammatory response. I-kappaB kinase/NF-kappaB cascade. Detection of virus. Innate immune response.
MYOC	myocilin	BC029261			1.359	1.114					Visual perception. Morphogenesis.
N/A	N/A	AK094921							1.358	0.233	
KIAA0441	N/A	AB007901			1.358	1.086					Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
GOLPH2	golgi phosphoprotein 2	NM_016548			1.358	0.644					
SH3GL3	SH3-domain GRB2-like 3	NM_003027			1.357	0.628					Signal transduction. Central nervous system development.
RBPSUHL	recombining binding protein L	NM_014276			1.357	0.622					Transcription. Regulation of transcription, DNA-dependent. Signal transduction.
N/A	Go protein	Y18213							1.357	0.485	Muscle contraction. Signal transduction. G-protein coupled receptor protein signaling pathway. Neurogenesis. Axon guidance.
MT6-MMP	membrane type matrix metalloproteinase number 6	AJ272137			1.357	0.317					Proteolysis and peptidolysis. Inflammatory response.
GCM1	glial cells missing homolog a	NM_003643							1.357	0.57	Regulation of transcription, DNA-dependent. Morphogenesis.
FLJ36870	hypothetical protein FLJ36870	NM_173658							1.357	0.566	
DKFZp451P2311	hypothetical protein	BX537997							1.357	0.386	
CACNA1H	calcium channel, voltage-dependent, alpha 1H subunit isoform	NM_021098							1.357	0.951	Cation transport. Calcium ion transport. Muscle contraction. Muscle development. Myoblast fusion.
UNQ541	GSGL541	NM_205854							1.355	0.764	
N/A	myosin	L29137			1.355	0.343					
N/A	N/A	AK127800	1.033	1.246	1.355	0.815					Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism. Metabolism.
N/A	cyclin-dependent kinase inhibitor	AF488410			1.355	0.632					Regulation of cyclin dependent protein kinase activity. Cell cycle. Cell cycle arrest. Negative regulation of cell proliferation.

KRTAP10-10	keratin associated protein 10-10	NM_181688					1.355	0.512	
APOBEC3B	" apolipoprotein B mRNA editing enzyme, catalytic polypeptide	NM_004900			1.355	1.176			
WSB2	WD SOCS-box protein 2	NM_018639			1.354	1.105			Intracellular signaling cascade.
tpcr24	putative olfactory receptor	X89671			1.354	0.836			
IL1F7	interleukin 1 family, member 7 isoform 1 proprotein"	NM_014439					1.354	0.379	Immune response.
APXL	apical protein of Xenopus-like	NM_001649			1.354	1.152			
TNFRSF13B	tumor necrosis factor receptor 13B	NM_012452					1.353	0.411	Immune response. Cell surface receptor linked signal transduction.
DKFZp761I217	hypothetical protein	AL834260					1.353	0.585	
C20orf85	chromosome 20 open reading frame 85	NM_178456					1.353	0.506	
N/A	N/A	AK126956			1.352	0.036			
FLJ44082	FLJ44082 protein	NM_207416			1.351	0.816			
CDH16	cadherin 16 precursor	NM_004062					1.351	0.501	Cell adhesion. Homophilic cell adhesion.
KIAA0994	KIAA0994 protein	AB023211					1.35	0.576	
GGT2	gamma-glutamyl transpeptidase small subunit	M30474			1.349	0.435			Amino acid metabolism. Glutathione biosynthesis. Glutathione biosynthesis.
CDW52	CDW52 antigen (CAMPATH-1 antigen)	BC000644			1.349	0.785			
PRKAG3	AMP-activated protein kinase, non-catalytic gamma-3 subunit"	NM_017431					1.348	0.592	Generation of precursor metabolites and energy. Fatty acid biosynthesis. Protein kinase cascade.
HSD3B1	" hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid	NM_000862			1.348	0.705			C21-steroid hormone biosynthesis.
FLJ25084	FLJ25084 protein	BC031997					1.348	0.534	Proteolysis and peptidolysis. Fatty acid biosynthesis.
ZNF495	zinc finger protein 495	NM_024303			1.347	1.05			Regulation of transcription, DNA-dependent.
N/A	PDE4C-426	U66347					1.347	0.611	Signal transduction. Signal transduction.
N/A	N/A	AK125960					1.347	0.761	
SOX18	SRY-box 18	NM_018419					1.346	0.702	Regulation of transcription.
N/A	Unknown (protein for MGC:42059)	BC040177	1.201	1.436	1.346	0.608			Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
N/A	N/A	AK129567					1.346	0.292	
h-erg	putative potassium channel subunit	U04270					1.346	0.673	Two-component signal transduction system. Cation transport. Potassium ion transport. Muscle contraction.
OAS1	" 2',5'-oligoadenylate synthetase 1 isoform E18"	NM_016816			1.345	0.784			Nucleobase, nucleoside, nucleotide and nucleic acid metabolism. Immune response. Response to virus.
N/A	PRO0386	AF116603					1.345	0.577	Protein complex assembly. Epidermal growth factor receptor signaling pathway.
SLC12A5	solute carrier family 12 member 5	NM_020708					1.344	0.419	Potassium ion transport. Sodium ion transport. Chloride transport. Amino acid transport.
GPR40	G protein-coupled receptor 40	NM_005303					1.344	0.439	Signal transduction. G-protein coupled receptor protein signaling pathway.
FLJ31300	hypothetical protein FLJ31300	NM_144639					1.344	0.355	
FLJ22573	hypothetical protein FLJ22573	NM_024660			1.344	0.999			
LMO3	LIM domain only 3	NM_018640			1.343	0.701			Transcription. Regulation of transcription, DNA-dependent.
CLEC1	C-type lectin-like receptor-1	BC067746			1.343	0.572			
KRTAP5-1	keratin associated protein 5-1	NM_001005922					1.342	0.476	
GPR43	G protein-coupled receptor 43	NM_005306					1.342	0.467	Signal transduction. G-protein coupled receptor protein signaling pathway.
TSGA13	" testis specific, 13"	NM_052933			1.341	0.609			
LEC1	lectomedin-1 alpha	AF104266			1.341	0.552			Signal transduction. Neuropeptide signaling pathway.
N/A	apolipoprotein B fragment	X03324			1.34	0.551			
N/A	Unknown (protein for MGC:45681)	BC033102					1.34	0.269	
N/A	N/A	AK126330					1.339	0.741	
DKFZp434J212	hypothetical protein	AL137395					1.339	0.625	
N/A	folate binding protein	AF000380					1.338	0.488	Folic acid transport.
GPRC5B	" G protein-coupled receptor, family C, group 5, member B pre	NM_016235			1.338	0.496			Signal transduction. G-protein coupled receptor protein signaling pathway. Visual perception.
FLJ37964	hypothetical protein FLJ37964	NM_182578					1.338	0.663	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
N/A	N/A	AK130519					1.337	0.454	
N/A	N/A	AK127293					1.337	0.688	Cell-matrix adhesion.
LOC124220	similar to common salivary protein 1	NM_145252					1.337	0.351	
CD58	" CD58 antigen, (lymphocyte function-associated antigen 3)"	NM_001779			1.337	0.844			Cell-cell adhesion. Antimicrobial humoral response.
N/A	N/A	AK097032			1.336	0.949			Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
GPR48	G protein-coupled receptor 48	NM_018490			1.336	1.619			Signal transduction. G-protein coupled receptor protein signaling pathway.
GARNL4	GTPase activating Rap/RanGAP domain-like 4	NM_015085					1.336	0.525	
CNR2	cannabinoid receptor 2 (macrophage)	NM_001841			1.336	0.696			Immune response. Signal transduction. G-protein signaling, coupled to cyclic nucleotide second messenger.
KRT3	keratin 3	NM_057088					1.335	0.535	Cytoskeleton organization and biogenesis.
DEFB1	" defensin, beta 1 preproprotein"	NM_005218			1.335	1.16			Response to pest, pathogen or parasite. Defense response to bacteria. Innate immune response.
ZFHX4	zinc finger homeodomain 4	NM_024721			1.334	0.766			Regulation of transcription, DNA-dependent.
TSC	hypothetical protein FLJ20607	NM_017899					1.334	0.553	

N/A	N/A	AK125730							1.334	0.548	
KIAA1220	KIAA1220 protein	AB033046			1.334	0.719					Ion transport. Synaptic transmission.
CSRP3	cysteine and glycine-rich protein 3	NM_003476			1.334	1.23					Myogenesis. Cell differentiation.
CABP2	calcium binding protein 2 isoform 1	NM_016366							1.334	0.661	Signal transduction.
ALOX12B	arachidonate 12-lipoxygenase, 12R type"	NM_001139							1.334	0.354	Electron transport. Lipid metabolism. Epidermis development. Leukotriene biosynthesis.
N/A	G protein-coupled receptor PGR19	AY255595					1.333	1.24			Signal transduction. Neuropeptide signaling pathway.
N/A	N/A	AK074614			1.332	0.533					
FLJ25006	hypothetical protein FLJ25006	NM_144610					1.332	0.851			Protein amino acid phosphorylation.
C10orf99	chromosome 10 open reading frame 99	NM_207373							1.332	0.479	
SNF1LK	SNF1-like kinase	NM_173354			1.331	1.161					Protein amino acid phosphorylation. Cell cycle. Protein kinase cascade. Regulation of mitotic cell cycle.
NPR3	natriuretic peptide receptor C/guanylate cyclase C (atrionatriur	NM_000908			1.331	0.226					Skeletal development.
NIN	ninein isoform 2	NM_020921			1.331	0.917					
N/A	Unknown (protein for MGC:71953)	BC062691			1.331	0.695					
N/A	N/A	AK127674							1.331	0.689	
N/A	PRO2987	AF116719			1.331	0.798					Transport. Oxygen transport.
RFXANK	regulatory factor X-associated ankyrin-containing protein isofor	NM_003721			1.33	0.403					Transcription. Regulation of transcription, DNA-dependent. Humoral immune response.
KIAA1516	KIAA1516 protein	AB040949			1.33	0.539					Activation of MAPK. Activation of MAPK. Regulation of cell growth. Regulation of cell growth. Lipid m
N/A	PRO1483	AF116635			1.329	0.599					
LCN1	lipocalin 1 precursor	NM_002297	2.098	1.061					1.329	0.429	Proteolysis and peptidolysis. Transport. Sensory perception. Antimicrobial humoral response.
STX7	syntaxin 7	NM_003569			1.328	0.546					Intracellular protein transport. Post-Golgi transport.
GPR15	G protein-coupled receptor 15	NM_005290	1.94	2.1	1.328	0.443					Signal transduction. G-protein coupled receptor protein signaling pathway.
FKSG61	FKSG61	AF338190					1.328	0.476			
DNAH8	truncated axonemal dynein heavy chain 8 isoform 4	AF527623							1.328	0.638	
SFRP5	secreted frizzled-related protein 5	AF117758							1.327	0.56	Wnt receptor signaling pathway. Cell differentiation.
NAALADL1	N-acetylated alpha-linked acidic dipeptidase-like 1	NM_005468							1.327	0.364	Proteolysis and peptidolysis.
N/A	Unknown (protein for IMAGE:4837157)	BC034593			1.326	0.554					
N/A	ARVP6125	AY358247							1.326	0.496	
N/A	PP11646	AF370405							1.326	0.972	
LCE3E	late cornified envelope 3E	NM_178435			1.326	1.103					
FLJ32942	hypothetical protein FLJ32942	NM_144594			1.326	0.236					
N/A	N/A	AK093227			1.325	1.039					
MAGEC3	" melanoma antigen, family C, 3 protein isoform 1"	NM_138702			1.325	0.718					
KCNQ3	potassium voltage-gated channel KQT-like protein 3	NM_004519							1.325	0.959	Cation transport. Potassium ion transport. Synaptic transmission.
C20orf75	chromosome 20 open reading frame 75	NM_152611							1.325	0.674	
OR2AG1	" olfactory receptor, family 2, subfamily AG, member 1"	NM_001004489			1.324	0.846					
N/A	Unknown (protein for IMAGE:3935553)	BC013933			1.324	1.612					
N/A	N/A	AK127462			1.324	0.301					
DAO	D-amino-acid oxidase	NM_001917							1.324	0.402	Electron transport.
PTCRA	pre T-cell antigen receptor alpha	NM_138296			1.323	0.32					
GPR68	G protein-coupled receptor 68	NM_003485							1.323	0.676	Inflammatory response. Signal transduction. G-protein coupled receptor protein signaling pathway.
FOXP2	forkhead box P2 isoform III	NM_148900			1.323	0.676					
PPFIBP2	PPFIBP2 protein	BC021714			1.322	0.482					Cell communication.
N/A	N/A	AK075513							1.322	0.827	
KIAA1671	KIAA1671 protein	AB051458							1.322	0.51	
DKFZp434M0519	hypothetical proteincDNA DKFZp434M0519 (from clone DKFZ	AL137727					1.322	0.722			
BTLA	B and T lymphocyte associated	NM_181780			1.322	0.559					
MYL7	myosin light chain 2a	NM_021223							1.321	0.766	Smooth muscle contraction. Muscle development. Actin filament-based movement.
GAPDS	" glyceraldehyde-3-phosphate dehydrogenase, spermatogenic	NM_014364			1.321	0.749					Glucose metabolism. Glycolysis.
FLJ00013	FLJ00013 protein	AK024424			1.321	0.894					Metabolism.
ELOVL4	" elongation of very long chain fatty acids (FEN1/Elo2, SUR4/	NM_022726			1.321	0.646					Fatty acid biosynthesis. Sensory perception. Visual perception.
P5-1	N/A	L06175							1.32	0.632	Defense response.
LRCH1	leucine-rich repeats and calponin homology (CH) domain conta	NM_015116			1.32	1.209					
FLJ35424	hypothetical protein FLJ35424	NM_173661							1.32	0.457	
DPM3	dolichyl-phosphate mannosyltransferase polypeptide 3 isoform	NM_018973			1.32	1.065					Carbohydrate metabolism.
N/A	protein-serine/threonine kinase	Z25433			1.319	1.22					Regulation of cell cycle. Protein amino acid phosphorylation.
N/A	N/A	AK097495			1.319	0.862					

GCK	glucokinase isoform 1	NM_000162							1.319	0.216	Glycolysis.
FLJ31842	hypothetical protein FLJ31842	NM_152487	1.064	1.218	1.319	0.822					Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
ZFR	zinc finger RNA binding protein	NM_016107			1.318	0.262					
UQCR	ubiquinol-cytochrome c reductase (6.4kD) subunit	NM_006830			1.318	1.029					Electron transport. Transport.
MYO5A	" myosin VA (heavy polypeptide 12, myoxin)"	NM_000259			1.318	1.201					Transport. Actin filament-based movement.
N/A	N/A	BX247965			1.317	0.261					
N/A	N/A	AK127005			1.317	0.265					Carbohydrate metabolism. N-linked glycosylation. Oligosaccharide metabolism.
KIAA1568	KIAA1568 protein	AB046788			1.317	0.989					Ureteric bud development. Chemotaxis. Cell adhesion. Homophilic cell adhesion. Brain development.
ERN2	endoplasmic reticulum to nucleus signalling 2	NM_033266							1.317	0.333	Electron transport. Regulation of transcription, DNA-dependent. mRNA processing.
APG3L	APG3L protein	BC002830			1.317	0.56					Autophagy. Protein transport. Protein ubiquitination.
PTPNS1L2	protein tyrosine phosphatase, non-receptor type substrate 1-lik	NM_178460							1.316	0.415	
P53AIP1	p53-regulated apoptosis-inducing protein 1	NM_022112							1.316	0.276	Apoptosis.
N/A	N/A	AK057813							1.316	0.506	Proteolysis and peptidolysis. Fatty acid biosynthesis.
STCH	" stress 70 protein chaperone, microsome-associated, 60kDa	NM_006948			1.315	0.956					
MGC35361	hypothetical protein MGC35361	NM_147194			1.315	0.475					
N/A	PRO0195	AF090901			1.314	0.759					Nucleobase, nucleoside, nucleotide and nucleic acid metabolism. Response to toxin.
FLJ25811	FLJ25811 protein	NM_001005214			1.313	0.616					
FLJ36116	FLJ36116 protein	NM_207399					1.312	0.531			
FAT2	FAT tumor suppressor 2 precursor	NM_001447							1.312	0.624	Cell adhesion. Homophilic cell adhesion.
DYSF	dysferlin	NM_003494							1.312	0.677	Muscle contraction.
DKFZp434H0735	hypothetical protein	AL117509							1.312	0.454	
PEPP-2	homeobox protein from AL590526	NM_032498			1.311	0.814					Regulation of transcription, DNA-dependent.
N/A	N/A	U52830			1.311	0.938					
N/A	BCL2 protein	AF401211			1.311	0.729					
N/A	PRO0352	AF090920							1.311	0.274	Cell communication.
MGC35450	hypothetical protein MGC35450	BC065202			1.311	0.538					
LOC161577	LOC161577 protein	NM_198524			1.311	0.364					
FLJ40457	hypothetical protein FLJ40457	NM_173628							1.311	0.684	
FLJ32833	hypothetical protein FLJ32833	NM_152488			1.311	0.289					
FLJ25084	hypothetical protein FLJ25084	NM_152792							1.311	0.465	Proteolysis and peptidolysis. Fatty acid biosynthesis.
D-GPCR	Dresden-G-protein-coupled receptor	NM_152430			1.311	0.507					Signal transduction. G-protein coupled receptor protein signaling pathway. Perception of smell.
ABHD1	alpha/beta hydrolase domain containing protein 1 isoform 1	NM_032604			1.311	0.671					
N/A	N/A	AK128173			1.31	0.801					Protein amino acid phosphorylation.
PLAC8	PLAC8 protein	BC012205			1.309	0.898					
N/A	Similar to potassium inwardly-rectifying channel, subfamily J, n	BC040617							1.309	0.643	Ion transport. Potassium ion transport.
MIP	major intrinsic protein of lens fiber	NM_012064							1.309	0.585	Transport. Cell-cell signaling. Sensory perception. Visual perception.
CD34	CD34 antigen	NM_001773							1.309	0.493	Cell adhesion.
ACF	apobec-1 complementation factor isoform 3	NM_138933			1.309	0.712					MRNA editing. Protein stabilization.
N/A	Unknown (protein for IMAGE:5200632)	BC027847	1.047	1.083			1.308	0.75			
N/A	N/A	AK096041			1.308	0.974					Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
CALML3	calmodulin-like 3	NM_005185							1.308	0.491	
BTN1A1	" butyrophilin, subfamily 1, member A1"	NM_001732			1.308	1.254					
ARMC4	armadillo repeat containing 4	NM_018076			1.308	0.623					Mitotic chromosome condensation. Cell adhesion.
N/A	N/A	AK128528							1.307	0.816	
N/A	N/A	AK023180			1.307	1.08					
KRTHB6	keratin, hair, basic, 6"	NM_002284							1.307	0.658	Cytoskeleton organization and biogenesis.
FLJ00317	FLJ00317 protein	AK131095	1.006	1.272					1.307	0.317	Proteolysis and peptidolysis. Integrin-mediated signaling pathway.
SMPDL3B	acid sphingomyelinase-like phosphodiesterase 3B	NM_014474							1.306	0.327	Carbohydrate metabolism.
KIAA1717	KIAA1717 protein	AB051504			1.306	0.959					
NKPD1	NTPase, KAP family P-loop domain containing 1"	NM_198478							1.305	0.843	
N/A	N/A	AK126863							1.305	0.291	
KIAA0527	KIAA0527 protein	AB011099			1.305	1.099					Cell adhesion.
GPR61	G protein-coupled receptor 61	NM_031936							1.305	0.349	Signal transduction. G-protein coupled receptor protein signaling pathway.
IL26	interleukin 26 precursor	NM_018402			1.304	0.837					Immune response. Cell-cell signaling. Antimicrobial humoral response.
GPR126	G protein-coupled receptor 126 beta 1	NM_198569			1.304	0.827					Signal transduction. Neuropeptide signaling pathway.
CKLFSF5	chemokine-like factor superfamily 5 isoform b	NM_181618							1.304	0.335	Chemotaxis. Sensory perception.

N/A	Similar to RIKEN cDNA 1700074P13 gene	BC047233			1.302	0.656					
N/A	N/A	AK094329			1.302	0.652					Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
N/A	N/A	AK090752			1.302	1.199					Protein amino acid phosphorylation. Signal transduction. Spermatid cell development. Wnt receptor signaling pathway.
GPR120	G protein-coupled receptor 120	NM_181745							1.302	0.259	
ENPEP	glutamyl aminopeptidase (aminopeptidase A)	NM_001977			1.302	0.721					Proteolysis and peptidolysis. Cell-cell signaling. Cell proliferation.
N/A	N/A	AK126211			1.301	0.543					Mo-molybdopterin cofactor biosynthesis. Sulfur metabolism.
N/A	PRO2796	AF116714					1.301	0.014			
HOMER2	homer 2 isoform 2	NM_199330			1.301	0.822					Metabotropic glutamate receptor signaling pathway.
CREG1	cellular repressor of E1A-stimulated genes	NM_003851			1.301	0.628					Regulation of cell growth. Regulation of transcription from RNA polymerase II promoter. Development. Cell proliferation.
PARVG	parvin, gamma"	BC034406							1.3	0.453	Cell-matrix adhesion.
N/A	Wnt4	AY358947			1.3	0.97					Frizzled-2 signaling pathway. Cell-cell signaling. Development.
LMX1A	LIM homeobox transcription factor 1, alpha isoform 6A"	NM_177398							1.3	0.668	Regulation of transcription, DNA-dependent. Development
MUC7	" mucin 7, salivary"	NM_152291					1.299	0.455			
CDX4	caudal type homeo box transcription factor 4	NM_005193							1.299	0.52	Regulation of transcription, DNA-dependent. Development.
SLC35A5	" solute carrier family 35, member A5"	NM_017945			1.298	0.799					Nucleotide-sugar transport.
HS747E2A	hypothetical protein HS747E2A	NM_015370							1.298	0.476	
GRIN3A	glutamate receptor, ionotropic, N-methyl-D-aspartate 3A"	NM_133445							1.298	0.407	Protein biosynthesis. Ion transport. Synaptic transmission.
TRPA1	ankyrin-like protein 1	NM_007332			1.297	0.656					Cation transport. Sensory perception.
FOLR1	folate receptor 1 precursor	NM_016730							1.297	0.384	Receptor mediated endocytosis. Folic acid transport.
DLNB26	N/A	AB094095			1.297	1.166					
C6orf60	chromosome 6 open reading frame 60	NM_024581			1.297	0.741					
KIAA1984	KIAA1984 protein	AB075864							1.296	0.629	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
KIAA0090	N/A	D42044			1.296	1.047					
IL27RA	class I cytokine receptor	NM_004843							1.296	0.843	
N/A	Unknown (protein for IMAGE:4825733)	BC032027							1.295	0.755	
GDF11	growth differentiation factor 11	NM_005811			1.295	0.61					Skeletal development. Neurogenesis. Mesoderm development.
PEG1/MEST	N/A	D87367			1.294	0.698					Xenobiotic metabolism. Mesoderm development.
FKSG62	FKSG62	AF338191	2.163	1.116	1.294	1.183					
CD3E	CD3E antigen, epsilon polypeptide (TiT3 complex)"	NM_000733							1.294	0.7	Signal complex formation. G-protein coupled receptor protein signaling pathway. Positive regulation of T-cell proliferation.
N/A	N/A	AK027480			1.293	0.519					Regulation of transcription, DNA-dependent.
DKFZp547J2313	hypothetical protein	AL512688							1.293	0.41	Fatty acid metabolism. Transport. Neurogenesis. Negative regulation of cell proliferation.
SMAD3	" MAD, mothers against decapentaplegic homolog 3"	NM_005902			1.292	1.173					Transcription. Transforming growth factor beta receptor signal.
N/A	N/A	AK026266			1.292	0.876					
ORM1	orosomucoid 1 precursor	NM_000607							1.291	0.279	Transport. Acute-phase response. Inflammatory response.
N/A	N/A	AK130172							1.291	0.354	
MYLIP	myosin regulatory light chain interacting protein	NM_013262			1.291	0.467					Cell motility. Neurogenesis. Protein ubiquitination.
MRPL22	mitochondrial ribosomal protein L22	NM_014180			1.291	0.48					Protein biosynthesis.
C9orf138	chromosome 9 open reading frame 138	NM_153707			1.291	0.884					
AQP1	aquaporin 1	NM_198098	1.023	0.567					1.291	0.284	Transport. Water transport. Excretion.
TU3A	downregulated in renal cell carcinoma	NM_007177							1.29	0.474	Regulation of cell growth.
N/A	CTAGE-3 protein	AF338231							1.29	0.305	RNA processing.
MGC40178	hypothetical protein MGC40178	NM_152325							1.29	0.505	
N/A	N/A	AK097908			1.289	0.773					
N/A	N/A	AK093450							1.289	0.512	
IL15	interleukin 15 isoform 1 precursor	NM_172174			1.289	1.307					Immune response. Signal transduction. Cell-cell signaling. Positive regulation of cell proliferation.
CDIE	leukocyte differentiation antigen	X79518							1.289	0.532	Immune response.
SDCCAG33	serologically defined colon cancer antigen 33	NM_005786			1.288	0.614					Regulation of transcription, DNA-dependent.
N/A	HSA250839	AY358353	4.152	1.227	1.288	1.169					
N/A	N/A	AK123899							1.288	0.583	
N/A	N/A	AK054946							1.288	0.569	
TGM6	transglutaminase 6	NM_198994							1.287	0.34	Peptide cross-linking.
RFPL1	ret finger protein-like 1	NM_021026			1.287	0.721					Protein ubiquitination.
GUCA1A	guanylate cyclase activator 1A (retina)	NM_000409							1.286	0.441	Signal transduction. Sensory perception. Visual perception.
PNUTL2	peanut-like 2 isoform 4	NM_080417			1.285	0.521					Cytokinesis. Cell cycle. Regulation of apoptosis.
LOC339742	LOC339742 protein	BC045732			1.285	0.489					
SULT1A1	sulfotransferase family, cytosolic, 1A, phenol-preferring, memb	NM_177534							1.284	0.406	Catecholamine metabolism. Lipid metabolism. Steroid metabolism. Amine metabolism.

OR52B2	" olfactory receptor, family 52, subfamily B, member 2"	NM_001004052			1.284	0.545					
N/A	N/A	AK130265							1.284	0.308	
LOC387646	hypothetical LOC387646	NM_001006604							1.284	0.635	
CGB5	N/A	NM_033043							1.284	0.405	Signal transduction. Cell-cell signaling. Sex determination. Male gonad development.
TFR2	transferrin receptor 2	NM_003227			1.283	0.819					Proteolysis and peptidolysis. Iron ion transport.
CHRNA4	cholinergic receptor, nicotinic, alpha polypeptide 4 precursor"	NM_000744							1.283	0.691	Ion transport. Signal transduction. Synaptic transmission. Neurogenesis.
CCR2	chemokine (C-C motif) receptor 2 isoform A	NM_000647							1.283	0.327	Chemotaxis. Inflammatory response. Cellular defense response. Signal transduction.
AGTRL1	angiotensin II receptor-like 1	NM_005161							1.283	0.671	Signal transduction. G-protein coupled receptor protein signaling pathway.
TFG	TRK-fused gene	NM_006070			1.282	1.043					Protein amino acid phosphorylation. Positive regulation of I-kappaB kinase/NF-kappaB cascade.
NB1	NB1 glycoprotein	AJ310433							1.282	0.469	
N/A	Unknown (protein for IMAGE:4907098)	BC025357							1.282	0.675	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
N/A	unknown	AY129023							1.282	0.521	
DEFB129	beta defensin 129 precursor	NM_080831			1.282	1.22					Defense response to bacteria.
MGC26816	hypothetical protein MGC26816	NM_152613							1.281	0.597	
PCDHX	protocadherin	AJ564947			1.28	1.007					Cell adhesion. Homophilic cell adhesion.
N/A	N/A	AK126655			1.28	0.818					Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
N/A	N/A	AK057649			1.28	0.47					Amino acid metabolism. Biosynthesis.
FUT6	" fucosyltransferase 6 (alpha (1,3) fucosyltransferase)"	NM_000150			1.28	0.513					Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
DKFZp686H1615	hypothetical proteincDNA DKFZp686H1615 (from clone DKFZ	BX537882			1.28	0.826					
DKFZp547K059	hypothetical protein	AL713786							1.28	0.534	
ali	alivin 1	AB079074			1.28	1.25					
ACVR1C	" activin A receptor, type IC"	NM_145259			1.28	0.975					
N/A	Similar to LOC149651	BC025345							1.279	0.362	
N/A	N/A	AK055758							1.279	0.418	Multidrug transport.
MGC26963	hypothetical protein MGC26963	NM_152621			1.279	0.309					Lipid metabolism. Sphingolipid metabolism. Sphingomyelin biosynthesis.
CGA	" glycoprotein hormones, alpha polypeptide, precursor"	BC020782			1.279	0.589					Signal transduction. Cell-cell signaling.
PABPC3	" poly(A) binding protein, cytoplasmic 3"	NM_030979			1.278	0.51					MRNA metabolism.
N/A	Unknown (protein for IMAGE:5242623)	BC028099			1.278	0.864					
N/A	N/A	AK130278							1.278	1.054	
EDIL3	EGF-like repeats and discoidin I-like domains-containing protei	NM_005711			1.278	0.824					Cell adhesion. Development.
MGC10233	hypothetical protein MGC10233	NM_152715			1.277	0.937					Protein modification.
KIAA0735	KIAA0735 protein	AB018278			1.277	0.483					Neurotransmitter transport.
RPP30	ribonuclease P (30kD)	NM_006413			1.276	0.78					tRNA processing.
PTPRN	protein tyrosine phosphatase, receptor type, N precursor"	NM_002846							1.276	0.643	Protein amino acid dephosphorylation.
N/A	N/A	AK126053							1.276	0.597	
KRT14	keratin 14	NM_000526							1.276	0.481	Epidermis development.
FLJ26850	FLJ26850 protein	NM_001001687	1.262	1.12	1.276	0.478					
N/A	Unknown (protein for IMAGE:3162384)	BC000537							1.275	0.657	Electron transport. Protein folding. Protein-ER retention.
TPTEps1	TPTEps1 protein	BC041842							1.274	0.458	
FRG2	FSHD region gene 2 protein	NM_001005217							1.274	0.446	
N/A	N/A	AK126917							1.272	0.255	Electron transport.
N/A	N/A	AK123224	1.599	1.455					1.272	0.242	
HS3ST1	heparan sulfate D-glucosaminyl 3-O-sulfotransferase 1 precurs	NM_005114							1.272	0.799	
GABRP	" gamma-aminobutyric acid (GABA) A receptor, pi"	NM_014211			1.272	0.663					Ion transport. Synaptic transmission.
FLJ10178	hypothetical protein FLJ10178	BC011483			1.272	0.719					
TMEM26	transmembrane protein 26	NM_178505			1.271	0.748					
PYCARD	PYD and CARD domain containing isoform a	NM_013258			1.271	0.522					Induction of apoptosis. Caspase activation. Cell cycle. Signal transduction. Regulation of apoptosis.
N/A	LHLC1946	AY358228							1.27	0.604	
N/A	N/A	AK023435					1.27	0.48			
GALC	galactosylceramidase precursor	NM_000153					1.27	0.511			Carbohydrate metabolism. Galactosylceramide catabolism.
FLJ39531	FLJ39531 protein	NM_207445			1.27	0.837					
N/A	N/A	AK095606							1.269	0.505	Development.
SULT1A2	sulfotransferase family, cytosolic, 1A, phenol-preferring, memb	NM_177528							1.268	0.418	Catecholamine metabolism. Lipid metabolism. Steroid metabolism. Amine metabolism.
N/A	zinc finger protein	AF024694			1.268	0.699					
K6IRS3	keratin 6 irs3	NM_175068							1.268	0.453	Ectoderm development.
FLJ35843	hypothetical protein FLJ35843	NM_152591							1.268	0.697	

TNFSF13B	" tumor necrosis factor (ligand) superfamily, member 13b"	NM_006573			1.267	0.69					Immune response. Signal transduction. Cell proliferation. Positive regulation of cell proliferation.
SLC24A2	" solute carrier family 24 (sodium/potassium/calcium exchang	NM_020344			1.267	0.68					Potassium ion transport. Sodium ion transport. Calcium ion transport. Sensory perception.
GLT25D2	glycosyltransferase 25 domain containing 2	NM_015101			1.267	0.303					Lipopolysaccharide biosynthesis.
FLJ32855	FLJ32855 protein	BC031684			1.267	1.016					
C9orf37	chromosome 9 open reading frame 37	NM_032937			1.267	0.962					
YPEL2	yippee-like 2	NM_001005404			1.266	0.807					
KIAA1713	KIAA1713 protein	AB051500			1.265	0.71					
HOXA4	homeobox protein A4	NM_002141			1.264	1.151					Regulation of transcription, DNA-dependent. Morphogenesis.
FMO5	flavin containing monooxygenase 5	NM_001461			1.264	0.302					Electron transport.
FBXL21	FBXL21 protein	BC044938			1.264	0.536					
CALCRL	calcitonin receptor-like	NM_005795	1.041	0.8	1.264	0.866					Signal transduction. G-protein signaling, coupled to cyclic nucleotide second messenger.
VWF	von Willebrand factor precursor	NM_000552							1.263	0.463	Cell adhesion. Response to wounding. Platelet activation.
OR9A2	" olfactory receptor, family 9, subfamily A, member 2"	NM_001001658			1.263	0.916					
NMUR1	neuromedin U receptor 1	NM_006056							1.263	0.353	Calcium ion transport. Smooth muscle contraction. G-protein signaling, coupled to IP3 second messenger
N/A	polymerase	U87591	1.041	0.875	1.263	0.222					
KRT6E	keratin 6 isoform K6e	NM_173086							1.263	0.379	Ectoderm development.
IRAK3	interleukin-1 receptor-associated kinase 3	BC057800			1.263	0.652					Protein amino acid phosphorylation. Signal transduction. Cytokine and chemokine mediated signaling pathway.
IQCF2	IQ motif containing F2	NM_203424							1.263	0.259	
FLJ30313	hypothetical protein FLJ30313	NM_152757							1.263	0.428	
IL1F5	interleukin 1 family, member 5"	NM_012275							1.262	0.655	Inflammatory response.
C10orf13	hypothetical protein MGC39320	NM_152429			1.262	0.751					
HTR3C	5-hydroxytryptamine receptor 3 subunit C	NM_130770			1.261	0.426					
ACVRL1	activin A receptor type II-like 1	NM_000020	1.514	1.37	1.261	1.158					Protein amino acid phosphorylation. Transforming growth factor beta receptor signaling pathway.
MMP15	matrix metalloproteinase 15 preproprotein	NM_002428							1.26	0.377	Protein modification. Proteolysis and peptidolysis.
erg-3	Erg-3	S68130			1.26	0.623					
ALDH1A3	aldehyde dehydrogenase 1A3	NM_000693			1.26	1.077					Alcohol metabolism. Lipid metabolism.
LOC149830	M8 protein	NM_177549							1.259	0.718	
KIAA1509	KIAA1509 protein	AB040942			1.259	0.613					
DKFZp547J226	hypothetical protein	AL834457							1.259	0.93	
RAB3IL1	RAB3A interacting protein (rabin3)-like 1	NM_013401			1.257	0.775					
PRM2	protamine 2	NM_002762			1.257	0.61					DNA packaging. Chromosome organization and biogenesis. Mitotic chromosome condensation. Spermatogenesis.
NHLH1	nescient helix loop helix 1	NM_005598							1.257	0.272	Transcription. Regulation of transcription, DNA-dependent. Central nervous system development. Cell differentiation.
FOXP4	forkhead box P4	NM_138457			1.257	0.82					Regulation of transcription, DNA-dependent.
P2RY2	purinergic receptor P2Y2	NM_176072							1.256	0.504	Cell ion homeostasis. Signal transduction. G-protein signaling, coupled to IP3 second messenger (phospholipase C activating).
N/A	CLECSF1	AY358376							1.256	0.957	Skeletal development.
N/A	N/A	AK128534							1.256	0.667	
KPNA6	karyopherin alpha 6	NM_012316					1.255	0.477			NLS-bearing substrate-nucleus import. Intracellular protein transport.
GDF8	growth differentiation factor 8	NM_005259					1.255	1.122			Transforming growth factor beta receptor signaling pathway. Muscle development. Growth.
N/A	Unknown (protein for IMAGE:30345306)	BC066345			1.254	1.005					
N/A	Unknown (protein for IMAGE:5242289)	BC036877							1.254	0.432	
N/A	Similar to major histocompatibility complex, class II, DP beta 1'	BC017967							1.254	0.793	
N/A	casein kinase II alpha subunit	AY112721							1.254	0.467	Protein amino acid phosphorylation.
N/A	N/A	AK130758							1.254	0.429	
ACOX1	" acyl-Coenzyme A oxidase, isoform a"	BC008767			1.254	0.705					Electron transport. Lipid metabolism. Fatty acid beta-oxidation. Prostaglandin metabolism.
N/A	N/A	AK125981			1.253	0.718					
N/A	N/A	AK096009							1.253	0.455	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
KIAA0895	KIAA0895 protein	AB020702			1.252	0.923					
CYP1A2	cytochrome P450, family 1, subfamily A, polypeptide 2"	NM_000761							1.252	0.451	Electron transport. Transport.
CTGLF1	centaurin, gamma-like family, member 1"	NM_133446							1.252	0.351	
N/A	N/A	AK124987							1.251	0.446	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
FKSG42	FKSG42	NM_032032			1.251	0.215					
C20orf179	chromosome 20 open reading frame 179	NM_178477							1.251	0.522	
C20orf173	chromosome 20 open reading frame 173	NM_080828					1.251	0.669			
C2	complement component 2 precursor	NM_000063			1.251	0.947					Proteolysis and peptidolysis. Immune response. Complement activation, classical pathway,
ZNF133	zinc finger protein 133	BC001887			1.25	1.099					Transcription. Regulation of transcription, DNA-dependent.
FLJ46836	FLJ46836 protein	NM_207509							1.25	0.3	

FLJ13842	hypothetical protein FLJ13842	NM_024645			1.25	0.788					
EFEMP1	EGF-containing fibulin-like extracellular matrix protein 1 isofor	NM_004105			1.25	0.576					Visual perception.
GNG7	guanine nucleotide binding protein (G protein), gamma 7"	NM_052847							1.249	0.582	Signal transduction. Regulation of G-protein coupled receptor protein signaling pathway.
FXYD7	FXYD domain-containing ion transport regulator 7	NM_022006							1.249	0.624	Ion transport.
CLECSF12	" C-type lectin, superfamily member 12 isoform h"	NM_197953			1.249	0.445					Phagocytosis, recognition. Cell recognition. Carbohydrate mediated signaling. Antibacterial humoral response.
KRTAP10-5	keratin associated protein KAP10.5	AJ566384							1.248	0.829	
KIAA1157	KIAA1157 protein	AB032983			1.248	0.645					
FLJ40321	FLJ40321 protein	NM_198479							1.248	0.324	
FLJ40235	hypothetical protein FLJ40235	NM_173635					1.248	0.562			
VGF	VGF nerve growth factor inducible precursor	NM_003378							1.247	0.961	
PFKP	" phosphofructokinase, platelet"	BC029138			1.247	0.925					Glycolysis.
ARHGEF4	Rho guanine nucleotide exchange factor 4 isoform b	NM_032995							1.247	0.604	Intracellular signaling cascade.
LCN10	lipocalin 10	NM_001001712							1.246	0.422	
EML1	EML1 protein	BC033043			1.246	0.879					Visual perception.
ChGn	ChGn protein	BC060772			1.246	1.286					Neurogenesis. Cell recognition. Cell proliferation. Morphogenesis. Heparan sulfate proteoglycan biosynthesis.
BTC	betacellulin	BC011618			1.246	0.302					Regulation of cell cycle. Positive regulation of cell proliferation.
AUTS2	autism susceptibility candidate 2	NM_015570			1.246	0.378					
OBPIIa	putative odorant binding protein ag	AJ251024							1.245	0.495	Perception of smell. Chemosensory behavior. Electron transport.
N/A	Similar to hypothetical protein FLJ21463	BC019703			1.245	1.246					
N/A	N/A	AK125806							1.245	0.374	
DKFZp686C05222	hypothetical proteincDNA DKFZp686C05222 (from clone DKF	BX538342	1.086	1.491	1.245	1.008					
C20orf35	uncharacterized hypothalamus protein HSMNP1	NM_018478			1.245	0.615					Protein transport.
N/A	N/A	AK023998			1.244	0.716					
CST6	cystatin M precursor	NM_001323							1.244	0.712	Morphogenesis.
ARMC3	armadillo repeat containing 3	NM_173081							1.244	0.399	
TCEAL8	transcription elongation factor A (SII)-like 8	NM_153333			1.243	0.665					
SORCS3	VPS10 domain receptor protein SORCS 3	NM_014978							1.243	0.504	Intracellular protein transport. Neuropeptide signaling pathway.
NFE2L2	nuclear factor (erythroid-derived 2)-like 2	NM_006164			1.243	0.624					Regulation of transcription, DNA-dependent. Transcription from RNA polymerase II promoter.
KCNK12	" potassium channel, subfamily K, member 12"	BC047749					1.243	0.825			Potassium ion transport.
HIG1	DKFZP564K247 protein	NM_014056			1.243	0.611					
ELOVL3	elongation of very long chain fatty acids like 3	NM_152310			1.243	0.373					Fatty acid biosynthesis.
PLSCR2	phospholipid scramblase 2	NM_020359			1.242	1.224					Phospholipid scrambling.
GFPT2	glutamine-fructose-6-phosphate transaminase 2	BC000012			1.242	0.812					Fructose 6-phosphate metabolism. Energy reserve metabolism. Glutamine metabolism.
ZNRD1	" zinc ribbon domain containing, 1"	NM_170783			1.241	1.06					Nucleobase, nucleoside, nucleotide and nucleic acid metabolism. RNA elongation. Regulation of transcription, DNA-dependent.
WFDC6	WAP four-disulfide core domain 6 precursor	NM_080827							1.241	0.609	
TRPM5	transient receptor potential cation channel, subfamily M, memb	NM_014555							1.241	0.377	Cation transport.
TESK1	testis-specific protein kinase 1	NM_006285			1.241	0.748					Protein amino acid phosphorylation. Spermatogenesis.
STAG3	stromal antigen 3	NM_024070			1.241	0.946					Cell cycle. Chromosome segregation. Meiosis. Synaptonemal complex formation.
N/A	N/A	AK092564			1.241	1.188					
LRRTM4	leucine rich repeat transmembrane neuronal 4	NM_024993			1.241	1.476					
ITGA9	" integrin, alpha 9 precursor"	NM_002207			1.241	0.743					Cell-matrix adhesion. Integrin-mediated signaling pathway.
F12	coagulation factor XII precursor	NM_000505			1.241	0.361					Proteolysis and peptidolysis. Blood coagulation. Negative regulation of blood coagulation.
CYP2B6	cytochrome P450, family 2, subfamily B, polypeptide 6"	NM_000767							1.241	0.771	Electron transport.
PADI1	peptidylarginine deiminase type I	NM_013358							1.239	0.353	Protein modification.
GPR1	G protein-coupled receptor 1	BC067833			1.239	0.6					Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
FXYD3	FXYD domain containing ion transport regulator 3 isoform 2 pr	NM_021910							1.239	0.544	Chloride transport.
DKFZp434A1520	hypothetical proteincDNA DKFZp434A1520 (from clone DKFZ	AL137544			1.239	1.066					
ASTL	astacin-like metalloendopeptidase (M12 family)	NM_001002036							1.239	0.388	
NOSTRIN	nitric oxide synthase trafficking	NM_052946			1.238	0.426					
N/A	PRO1992	AF118086			1.238	1.261					
MMEL2	membrane metallo-endopeptidase-like 2	NM_033467							1.238	0.504	
CRYGN	gammaN-crystallin variant	NM_144727							1.238	0.714	
BUCS1	acetyl-Coenzyme A synthetase 3	NM_052956							1.238	0.671	Lipid metabolism. Metabolism. Energy derivation by oxidation of organic compounds. Benzoate metabolism.
ZDHHC19	ZDHHC19 protein	BC034801							1.237	0.247	
PNR	putative neurotransmitter receptor	NM_003967			1.237	0.747					Signal transduction. G-protein coupled receptor protein signaling pathway. Synaptic transmission.
N/A	unknown	AY044233			1.237	0.667					Transport.

N/A	N/A	AK095544	1.327	1.047	1.237	0.55					
GLULD1	glutamate-ammonia ligase (glutamine synthase) domain conta	NM_016571			1.237	1.082					
ACP5	tartrate resistant acid phosphatase 5 precursor	NM_001611			1.237	1.014					
SARG	specifically androgen-regulated protein	NM_023938			1.236	0.456					
DAPK1	death-associated protein kinase 1	NM_004938			1.236	0.611					Protein amino acid phosphorylation. Apoptosis. Signal transduction. Protein kinase cascade.
ZCSL3	" zinc finger, CSL domain containing 3"	NM_181706			1.235	0.83					Protein folding.
N/A	extracellular calcium-sensing receptor	U20760							1.235	0.404	Ossification. Calcium ion sensing. Calcium ion homeostasis. Signal transduction.
N/A	N/A	AK075158			1.235	0.725					
FRMD4A	FERM domain containing 4A	NM_018027							1.234	0.4	
DNAJC5G	DnaJ (Hsp40) homolog, subfamily C, member 5 gamma"	NM_173650							1.234	0.497	
HIAT1	hippocampus abundant transcript 1	NM_033055			1.233	0.442					Transport. Tetracycline transport.
AMIGO2	AMIGO2 protein	BC014103			1.233	1.236					
CEACAM7	carcinoembryonic antigen-related cell adhesion molecule 7	NM_006890	1.188	1.405					1.232	0.709	
ADAM22	a disintegrin and metalloproteinase domain 22 isoform 1 prepr	NM_021723			1.232	0.813					Proteolysis and peptidolysis. Negative regulation of cell adhesion. Central nervous system development.
SLC7A9	" solute carrier family 7 (cationic amino acid transporter, y+ sy	NM_014270			1.231	0.969					Protein complex assembly. Amino acid metabolism.
RGS12	regulator of G-protein signalling 12 isoform 2	NM_002926			1.231	0.787					Signal transduction. Regulation of G-protein coupled receptor protein signaling pathway. Protein transport.
N/A	Unknown (protein for IMAGE:5223216)	BC025775	1.751	0.802					1.231	0.46	
KRTAP5-3	keratin associated protein 5-3	AJ628243							1.231	0.432	
FOLR3	folate receptor 3 precursor	NM_000804							1.23	0.314	Folic acid transport.
FGF9	fibroblast growth factor 9 precursor	NM_002010			1.23	1.071					Regulation of cell cycle. Signal transduction. Cell-cell signaling. Cell proliferation. Cell differentiation.
PON1	paraoxonase 1	NM_000446							1.229	0.357	Response to external stimulus.
N/A	hypothetical protein	AJ276510							1.229	0.4	
KCNB2	potassium voltage-gated channel, Shab-related subfamily, mer	NM_004770							1.229	0.869	Cation transport. Potassium ion transport. Regulation of smooth muscle contraction.
C1QB	complement component 1, q subcomponent, beta polypeptide	NM_000491							1.229	0.137	Phosphate transport. Immune response. Complement activation, classical pathway.
N/A	N/A	AK130364			1.228	0.47					
N/A	N/A	AK055569							1.228	0.498	Proteolysis and peptidolysis.
AS3MT	arsenic (+3 oxidation state) methyltransferase	NM_020682							1.228	0.478	Toxin metabolism. Arsonoacetate metabolism.
MGC:13379	HSPC244	NM_016499							1.227	0.588	
SRD5A2	3-oxo-5 alpha-steroid 4-dehydrogenase 2	NM_000348							1.226	0.413	Cell-cell signaling. Sex determination. Sex differentiation. Androgen metabolism. Male gonad development.
RLN1	relaxin 1 preproprotein	NM_006911			1.226	0.634					Signal transduction. Pregnancy. Physiological process.
N/A	N/A	AK127471					1.226	0.683			
N/A	N/A	AK125068							1.226	0.368	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
FKSG53	FKSG53	AF336880			1.226	0.772					
ZNF75A	zinc finger protein 75a	NM_153028					1.225	1.732			
N/A	N/A	AK127109			1.225	0.197					Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
FCGR3A	Fc fragment of IgG, low affinity IIIa, receptor for (CD16)"	NM_000569							1.225	0.459	Immune response.
N/A	unknown	AF353675					1.224	0.557			
KRT1B	keratin 1B	NM_175078							1.224	0.573	
KRT25A	keratin 25A	NM_181534			1.223	0.834					
KIAA1446	KIAA1446 protein	AB040879							1.223	0.564	
ADAM30	a disintegrin and metalloproteinase domain 30 preproprotein	NM_021794			1.223	0.562					Proteolysis and peptidolysis.
THSD3	" thrombospondin, type I domain containing 3 isoform 2"	NM_199265					1.222	0.606			
N/A	LP3428	AY203949							1.222	0.432	
N/A	galectin-12 isoform b	AF244975							1.222	0.823	Apoptosis.
HB6	E-type ATPase	AF034840							1.222	0.642	
C1orf21	chromosome 1 open reading frame 21	NM_030806			1.222	0.772					
UNC5CL	unc-5 homolog C-like	NM_173561							1.221	0.737	Signal transduction.
N/A	N/A	AK074560			1.221	0.732					Chromatin assembly or disassembly. Transcription. Regulation of transcription, DNA-dependent. Chromatin modification.
LOC201191	LOC201191 protein	BC047081			1.221	0.687					
FLJ00256	FLJ00256 protein	AK074183							1.221	0.68	
PSMB4	proteasome beta 4 subunit	BC017486			1.22	0.38					Ubiquitin-dependent protein catabolism.
N/A	replicative senescence downregulated leo1-like protein	AY302186			1.22	0.518					
N/A	N/A	AK093639							1.22	0.722	
N/A	myosin-reactive immunoglobulin light chain variable region	AF035032							1.22	0.517	
MGC3020	hypothetical protein MGC3020	NM_024048							1.22	0.535	
KIAA1137	KIAA1137 protein	AB032963			1.22	0.581					Cation transport.

FLJ25369	hypothetical protein FLJ25369	NM_152670			1.22	0.667					
VNN1	vanin 1 precursor	NM_004666			1.219	0.331					Nitrogen compound metabolism. Cell motility.
TRPC4	transient receptor potential 4	NM_016179			1.219	0.411					Cation transport. Calcium ion transport.
MGC40214	hypothetical protein MGC40214	NM_152416			1.219	1.028					
GPR32	G protein-coupled receptor 32	NM_001506							1.219	0.344	Signal transduction. G-protein coupled receptor protein signaling pathway.
FLJ25410	hypothetical protein FLJ25410	NM_144605							1.219	0.689	Cell cycle.
N/A	N/A	X06180			1.218	0.468					Calcium ion transport. Transmembrane receptor protein tyrosine kinase signaling pathway. T-cell activation.
N/A	Unknown (protein for MGC:35232)	BC031626			1.218	0.388					
N/A	N/A	AK090684							1.218	0.518	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
MEGF5	MEGF5	AB011538							1.218	0.378	
HLA-DOB		BC006097							1.218	0.531	Immune response. Antigen presentation, exogenous antigen. Antigen processing.
VPS24	vacuolar protein sorting 24 isoform 1	NM_016079			1.217	1.011					
N/A	PRO1512	AF130109					1.217	0.344			Ubiquitin-dependent protein catabolism.
FLJ25735	hypothetical protein FLJ25735	NM_152577			1.217	1.125					
NGFB	nerve growth factor, beta polypeptide"	NM_002506							1.216	1.029	Cell-cell signaling. Development.
N/A	unknown	U82313							1.216	0.652	
N/A	N/A	AK126016							1.216	0.719	
N/A	N/A	AK123848					1.216	0.946			
PPEF2	serine/threonine protein phosphatase with EF-hand motifs 2 is	NM_152933			1.215	0.357					Protein amino acid dephosphorylation. Sensory perception. Visual perception.
MAG	myelin associated glycoprotein isoform b precursor	NM_080600							1.215	0.505	Cell adhesion.
BC008967	hypothetical gene BC008967	NM_033201	1.039	1.089	1.215	0.252					
ARHGAP21	ARHGAP21 protein	BC022931			1.215	0.879					
N/A	N/A	AK075037							1.214	0.431	
KRTHA7	type I hair keratin 7	NM_003770							1.214	0.551	
PTPN13	" protein tyrosine phosphatase, non-receptor type 13 isoform	NM_080685			1.213	0.874					Protein amino acid dephosphorylation.
LOC375323	lipoma HMGIC fusion partner-like protein 4	NM_198560							1.213	0.606	
DKFZp564I122	hypothetical proteincDNA DKFZp564I122 (from clone DKFZp5	AL080062					1.213	0.529			
ARHGEF19	Rho guanine nucleotide exchange factor (GEF) 19	NM_153213							1.213	0.473	
ALPPL2	placental-like alkaline phosphatase preproprotein	NM_031313							1.213	0.411	Metabolism. Phosphorylation.
RUNX2	runt-related transcription factor 2	NM_004348			1.212	0.771					Ossification. Regulation of transcription, DNA-dependent.
PGLYRP3	peptidoglycan recognition protein-I-alpha precursor	NM_052891							1.212	0.457	
CMIP	c-Maf-inducing protein C-mip isoform	NM_198390			1.212	0.478					
ARHGAP27	Rho GTPase activating protein 27	NM_199282							1.212	0.895	
FLJ25989	FLJ25989 protein	NM_198512					1.211	0.795			
STX10	STX10 protein	BC017237			1.21	0.654					Intracellular protein transport.
N/A	RAN-binding protein 2-like 1 short isoform	AY354203			1.21	0.311					
KRTAP23-1	keratin associated protein 23-1	NM_181624			1.21	0.87					
C9orf47	chromosome 9 open reading frame 47	NM_001001938			1.21	1.054					
BYSL	bystin	NM_004053			1.21	1.29					Cell adhesion. Pregnancy.
RBMS2	" RNA binding motif, single stranded interacting protein 2"	NM_002898					1.209	1.262			RNA processing. Regulation of translation.
PIN1L	protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting 1	NM_006222	1.072	1.32	1.209	1.153					
PERP	" PERP, TP53 apoptosis effector"	NM_022121			1.209	0.895					
N/A	N/A	AK127126							1.209	0.563	
N/A	unknown	AF452715							1.209	0.369	
FLJ00402	FLJ00402 protein	AK090480					1.209	1.001			
OR6S1	olfactory receptor, family 6, subfamily S, member 1"	NM_001001968							1.208	0.742	
RAB39B	RAB39B, member RAS oncogene family"	NM_171998							1.207	0.505	Small GTPase mediated signal transduction. Protein transport.
OR10G2	olfactory receptor, family 10, subfamily G, member 2"	NM_001005466							1.207	0.619	
HSF1	heat shock transcription factor 1	NM_005526			1.207	0.696					Transcription. Regulation of transcription, DNA-dependent. Protein folding.
EGR4	early growth response 4	NM_001965			1.207	0.55					Transcription. Regulation of transcription, DNA-dependent. Positive regulation of cell proliferation.
N/A	N/A	AK124982							1.206	0.483	
DKFZp586D0922	hypothetical protein	AL050169							1.206	0.466	Transport. Development.
SCNN1G	" sodium channel, nonvoltage-gated 1, gamma"	NM_001039			1.205	0.355					Ion transport. Sodium ion transport. Excretion. Sensory perception.
N/A	Unknown (protein for IMAGE:3681106)	BC014579			1.205	0.623					
N/A	N/A	AK097976							1.205	0.391	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
N/A	N/A	AK000130			1.205	0.99					

MGC71999	alpha-NAC protein	NM_199290			1.205	0.826					
IRF6	interferon regulatory factor 6	NM_006147							1.205	1.001	Regulation of transcription, DNA-dependent.
N/A	N/A	L32537							1.204	0.584	
LOC57821	hypothetical protein LOC57821	NM_021179			1.204	0.581					
CASC1	cancer susceptibility candidate 1	NM_018272					1.204	0.954			
C7orf9	chromosome 7 open reading frame 9	NM_022150			1.204	1.398					Neuropeptide signaling pathway.
BCL2L14	BCL2-like 14 isoform 2	NM_030766							1.204	0.666	Regulation of apoptosis.
TPD52	tumor protein D52	NM_005079							1.203	0.612	Morphogenesis.
SORBS1	sorbin and SH3 domain containing 1	NM_015385			1.203	0.702					Transport. Insulin receptor signaling pathway. Glucose transport. Stress fiber formation.
N/A	N/A	AK056842					1.203	0.214			Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism. Metabolism.
FLJ32825	hypothetical protein FLJ32825	NM_152492							1.203	0.441	
N/A	N/A	AK124944			1.202	0.622					
N/A	N/A	AK095177			1.202	1.183					Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
INPP4A	INPP4A protein	BC028361			1.202	1.025					Signal transduction.
IL8RB	interleukin 8 receptor beta	NM_001557							1.201	0.372	Cell motility. Chemotaxis. Inflammatory response. Cellular defense response. G-protein signaling.
ENO1P	ENO1P protein	BC046928							1.201	0.272	
CXCL6	chemokine (C-X-C motif) ligand 6 (granulocyte chemotactic pr	NM_002993			1.201	0.408					RNA-dependent DNA replication. Chemotaxis. Inflammatory response. Signal transduction.
SCGF	stem cell growth factor precursor " lymphocyte secreted C-typ	NM_002975							1.2	0.41	Positive regulation of cell proliferation.
OR1N2	olfactory receptor, family 1, subfamily N, member 2"	NM_001004457							1.2	0.614	
N/A	N/A	AK124599			1.2	0.943					
APOE	apolipoprotein E precursor	NM_000041			1.2	0.388					Response to reactive oxygen species. Lipid transport. Induction of apoptosis. Cytoskeleton organization and biogenesis.
ADAM11	a disintegrin and metalloprotease domain 11 isoform 1 preprop	NM_002390							1.2	0.606	Proteolysis and peptidolysis. Integrin-mediated signaling pathway.
TECTB	tectorin beta	NM_058222							1.199	1.296	
N/A	N/A	AK124147							1.199	0.258	
LAMC3	laminin gamma 3 chain precursor	AF041835							1.199	0.864	Cell adhesion.
FLJ35816	FLJ35816 protein	NM_207489							1.199	0.281	
EIF3S3	" eukaryotic translation initiation factor 3, subunit 3 gamma, 4	BC000386					1.199	0.6			Protein biosynthesis. Regulation of translational initiation.
CCL16	small inducible cytokine A16 precursor	NM_004590							1.199	0.553	Chemotaxis. Inflammatory response. Cell-cell signaling. Sensory perception. Antimicrobial humoral response.
N/A	Unknown (protein for MGC:72083)	BC062442			1.198	0.572					
N/A	Unknown (protein for IMAGE:5313099)	BC036083							1.198	0.554	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
N/A	N/A	AK095678			1.198	0.621					
N/A	N/A	AK090830			1.198	1.283					
KIAA1599	KIAA1599 protein	AB046819							1.198	0.72	
AKAP	protein kinase	M90359			1.198	0.753					Protein targeting. Signal transduction. Synaptic transmission.
ABCC13	ATP-binding cassette protein C13 isoform a	NM_138726							1.198	0.481	Transport.
N/A	N/A	AK124635	1.257	1.126					1.197	0.43	Proteolysis and peptidolysis. Lipid metabolism. Steroid metabolism. Cholesterol metabolism.
ALOX15B	arachidonate 15-lipoxygenase, second type"	NM_001141							1.197	0.522	Electron transport. Lipid metabolism. Fatty acid metabolism. Induction of apoptosis. Negative regulation of cell proliferation.
PLA2G1B	phospholipase A2, group IB"	NM_000928							1.196	0.674	Actin filament organization. Signal transduction. Lipid catabolism.
KIAA1266	KIAA1266 protein	AB033092			1.196	0.627					Regulation of transcription, DNA-dependent.
DKFZp434K0322	hypothetical protein	AL137708							1.196	0.631	
CD3Z	T-cell receptor zeta chain isoform 1 precursor	NM_198053							1.196	0.684	Cell surface receptor linked signal transduction.
WARS2	mitochondrial tryptophanyl tRNA synthetase 2 isoform 2 precur	NM_201263					1.195	0.988			Protein biosynthesis. Tryptophanyl-tRNA aminoacylation.
N/A	brain my048 protein	AF063606					1.195	0.918			
LOC388937	LOC388937 protein	BC065041							1.195	0.356	
LOC348645	hypothetical protein LOC348645	NM_198851			1.195	0.476					
FLJ10916	hypothetical protein FLJ10916	NM_018271							1.195	0.496	Metabolism.
FGF16	fibroblast growth factor 16	NM_003868					1.195	0.547			Signal transduction. Cell-cell signaling. Metabolism. Response to temperature. Organogenesis.
PDPR	pyruvate dehydrogenase phosphatase regulatory subunit	NM_017990			1.194	0.657					Electron transport. Glycine catabolism.
N/A	AHPA9419	AY358263			1.194	0.445					
N/A	HSPC295	AF161413			1.194	0.631					
HSPA6	heat shock 70kDa protein 6 (HSP70B')	NM_002155			1.194	0.989					Protein folding. Response to unfolded protein.
FLJ41841	FLJ41841 protein	NM_207499							1.194	0.546	
MUC5B	mucin	AF086604	1.217	1.146					1.193	0.464	
ICA1	islet cell autoantigen 1 isoform 1	NM_022307	1.042	0.97	1.193	0.627					Neurotransmitter transport. Regulation of neurotransmitter secretion.
EIF2C2	" eukaryotic translation initiation factor 2C, 2"	NM_012154			1.193	0.719					Protein biosynthesis.
DCDC1	doublecortin domain containing 1	NM_181807			1.193	0.951					

CD3G	CD3G gamma precursor	NM_000073							1.193	0.507	Establishment and/or maintenance of cell polarity. Cell surface receptor linked signal transduction. Protein transport.
AGER	advanced glycosylation end product-specific receptor isoform	NM_001136			1.193	1.004					Inflammatory response. Cell surface receptor linked signal transduction.
ORMDL1	ORM1-like 1	NM_016467			1.192	0.919					
N/A	Similar to hypothetical gene LOC118703	BC031882			1.192	0.71					
MFRP	membrane frizzled-related protein	NM_031433			1.192	0.544					Development. Embryonic development.
N/A	N/A	AK092739							1.191	0.452	Electron transport. Intracellular signaling cascade.
MAOA	monoamine oxidase A	NM_000240							1.191	0.603	Electron transport. Catecholamine metabolism. Behavior. Neurotransmitter catabolism.
DKFZp434P185	hypothetical protein	AL834225							1.191	0.407	Potassium ion transport. Sodium ion transport. Calcium ion transport.
DKFZp434B172	hypothetical protein	AL117530							1.191	0.588	
BLVRB	biliverdin reductase B (flavin reductase (NADPH))	NM_000713			1.191	0.848					Nucleotide-sugar metabolism.
N/A	N/A	AK125674							1.19	0.213	
FLJ25005	FLJ25005 protein	NM_152334	1.03	1.097	1.19	1.169					Electron transport. Protein biosynthesis. Threonyl-tRNA aminoacylation.
CREB3L3	cAMP responsive element binding protein 3-like 3	NM_032607							1.19	0.458	Regulation of transcription, DNA-dependent.
CLCNKA	chloride channel Ka	BC053869			1.19	1.12					Ion transport. Chloride transport. Excretion. Excretion.
CDH1	cadherin 1, type 1 preproprotein"	NM_004360							1.19	0.491	Cell adhesion. Homophilic cell adhesion. Homophilic cell adhesion.
ADAM21	a disintegrin and metalloproteinase domain 21 preproprotein	NM_003813			1.19	0.83					Proteolysis and peptidolysis. Fertilization.
TRPM1	transient receptor potential cation channel, subfamily M, memb	NM_002420							1.189	0.624	Cation transport.
NAGLU	alpha-N-acetylglucosaminidase	NM_000263			1.189	0.142					Carbohydrate metabolism. Neurogenesis. Glycosaminoglycan metabolism.
N/A	zinc finger protein C2H2-25	U38904							1.189	0.761	Regulation of transcription, DNA-dependent.
N/A	N/A	AK127527							1.189	0.288	
MYO3B	myosin IIIB	NM_138995			1.189	1.04					Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
DKFZp434H0735	hypothetical protein	AL117509							1.189	0.563	
PDZK4	PDZ domain containing 4	NM_032512							1.188	0.583	
N/A	N/A	AK126747							1.188	0.626	
N/A	PRO0641	AF090939			1.188	0.882					
MGC10715	novel C2H2 type zinc finger protein	NM_024325	1.163	1.033			1.188	0.828			Regulation of transcription, DNA-dependent.
FLJ12242	hypothetical protein FLJ12242	NM_024681			1.188	0.845					Potassium ion transport.
DIRAS1	small GTP-binding tumor suppressor 1	NM_145173			1.188	0.798					Small GTPase mediated signal transduction.
ABLIM2	actin binding LIM protein family, member 2"	NM_032432							1.188	1.039	Cytoskeleton organization and biogenesis.
ZNF556	zinc finger protein 556	NM_024967			1.187	1.168					Regulation of transcription, DNA-dependent.
SCG3	secretogranin III	NM_013243							1.187	0.492	
N/A	MAS-related G protein-coupled receptor	AY255572							1.187	0.453	
N/A	N/A	AK094417							1.187	0.293	
N/A	N/A	AK057335							1.187	0.633	
MRPL30	mitochondrial ribosomal protein L30 isoform a	NM_145212			1.187	1.603					Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
COX6A2	cytochrome c oxidase subunit VIa polypeptide 2 precursor	NM_005205			1.187	0.824					Electron transport.
MPP2	palmitoylated membrane protein 2	NM_005374			1.186	0.689					Protein complex assembly. Signal transduction.
LRRC21	retina specific protein PAL	NM_015613			1.186	0.593					
FLJ46365	FLJ46365 protein	NM_207504			1.186	0.651					Immune response. Signal transduction.
C11orf21	N/A	AB029488							1.186	0.432	
SLC39A2	solute carrier family 39 (zinc transporter), member 2"	NM_014579							1.185	0.563	Zinc ion transport.
BCLP	beta-casein-like protein	NM_033504			1.185	0.777					Glycolysis.
NUDT4	nudix (nucleoside diphosphate linked moiety X)-type motif 4 is	NM_199040			1.184	0.864					Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
N/A	N/A	AK094447							1.184	0.537	
DKFZp434H0512	hypothetical proteincDNA DKFZp434H0512 (from clone DKFZ	AL137620			1.184	0.778					
CYP8B1	cytochrome P450, family 8, subfamily B, polypeptide 1"	NM_004391							1.184	0.636	Electron transport.
N/A	N/A	AK128231			1.183	0.701					Generation of precursor metabolites and energy. Transport. Water transport. Excretion. Glycerol transport.
N/A	N/A	AK124497	1.295	2.165	1.183	1.276					
IL10RA	" interleukin 10 receptor, alpha precursor"	NM_001558			1.183	0.288					
GGT2	gamma-glutamyl transpeptidase small subunit	M30474			1.183	0.364					Amino acid metabolism. Glutathione biosynthesis. Glutathione biosynthesis.
MAP1D	methionine aminopeptidase 1D	NM_199227			1.182	0.825					
KLK2	kallikrein 2, prostatic isoform 2"	NM_001002231							1.182	0.605	Proteolysis and peptidolysis.
GPC3	glypican 3	NM_004484			1.182	0.497					Morphogenesis.
FLJ32569	hypothetical protein FLJ32569	NM_152491			1.182	0.59					Proteolysis and peptidolysis.
SST	somatostatin	NM_001048							1.181	0.29	
SLC6A15	" solute carrier family 6 (neurotransmitter transporter), membe	NM_182767			1.181	0.789					Neurotransmitter transport. Neurotransmitter transport.

RAB9B	RAB9-like protein	NM_016370	1.181	0.723					
PMCHL1	pro-melanin-concentrating hormone-like 1	NM_031887	1.181	0.714					Synaptic transmission. Behavior.
N/A	N/A	AK128864					1.181	0.444	
N/A	N/A	AK123892	1.181	0.523					Protein amino acid phosphorylation.
FCGBP	Fc fragment of IgG binding protein	NM_003890					1.181	0.268	Cell adhesion. Binding of sperm to zona pellucida.
VGLL1	vestigial like 1	NM_016267	1.18	0.632					Regulation of transcription, DNA-dependent.
USF1	upstream stimulatory factor 1 isoform 1	NM_007122			1.18	0.74			Regulation of transcription, DNA-dependent.
TRPC5	" transient receptor potential cation channel, subfamily C, men	NM_012471	1.18	0.712					Cation transport. Calcium ion transport. Neurogenesis.
KIAA1030	KIAA1030 protein	AB028953					1.18	0.601	
PGLYRP2	peptidoglycan recognition protein L precursor	NM_052890	1.179	0.805					Peptidoglycan catabolism. Detection of bacteria. Detection of bacteria. Innate immune response.
N/A	NOX5	AY358983	1.179	0.746					
EPHA10	hypothetical protein FLJ33655	NM_001004338					1.179	0.52	Protein amino acid phosphorylation. Transmembrane receptor protein tyrosine kinase signaling pathway.
PIP	prolactin-induced protein	BC010951			1.177	0.482			
MC3R	melanocortin 3 receptor	NM_019888					1.177	0.38	Signal transduction. G-protein signaling, coupled to cyclic nucleotide second messenger.
KLF1	Kruppel-like factor 1 (erythroid)	NM_006563					1.177	0.511	Regulation of transcription, DNA-dependent. Organogenesis.
KIAA1490	KIAA1490 protein	AB040923			1.177	0.422			Actin cytoskeleton organization and biogenesis.
ZNF365	zinc finger protein 365 isoform D	NM_199452	1.176	0.619					
N/A	triiodothyronine receptor	M24900	1.176	0.469					Regulation of transcription, DNA-dependent.
N/A	N/A	AK125786	1.176	0.746					
N/A	N/A	AK001998	1.176	0.672					Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
CFL2	cofilin 2	NM_138638	1.176	0.59					
ADAMTS3	" a disintegrin-like and metalloprotease (reprolysin type) with t	NM_014243	1.176	0.586					Collagen fibril organization. Collagen catabolism.
TAC1	tachykinin 1 isoform beta precursor	NM_003182			1.175	0.591			Tachykinin signaling pathway. Neuropeptide signaling pathway. Cell-cell signaling. Synaptic transmission.
SCN11A	sodium channel, voltage-gated, type XI, alpha"	NM_014139					1.175	0.919	Cation transport. Sodium ion transport. Synaptic transmission.
GPR153	G protein-coupled receptor 153	NM_207370					1.175	0.591	G-protein coupled receptor protein signaling pathway.
SEMG2	semenogelin II precursor	NM_003008					1.174	0.696	Sexual reproduction.
N/A	unknown	AF390030	1.174	0.739					
EOS	EOS protein	BC036846					1.174	0.412	
PNPLA4	GS2 gene	NM_004650	1.173	0.831					
OGDHL	oxoglutarate dehydrogenase-like	NM_018245	1.173	1.107					Glycolysis. Metabolism.
N/A	N/A	AK124340			1.173	0.438			
KIAA2017	KIAA2017 protein	AB095937					1.173	0.493	Microtubule-based movement.
CD48	CD48 protein	BC030224					1.173	0.408	Defense response.
N/A	N/A	AK126528	1.172	0.464					
RGSL2	regulator of G-protein signalling like 2	NM_032267					1.171	0.9	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
N/A	" UDP-Gal:glucosylceramide beta-1,4-galactosyltransferase"	AF097159	1.171	0.753					Carbohydrate metabolism.
HCRT	orexin precursor	NM_001524			1.171	0.537			Neuropeptide signaling pathway. Synaptic transmission. Feeding behavior.
H3F3A	" H3 histone, family 3A"	BC038989	1.171	0.498					
FLJ90661	hypothetical protein FLJ90661	NM_173502					1.171	0.432	
FLJ12681	hypothetical protein FLJ12681	NM_022773	1.171	0.864					
cPLA2	cytosolic phospholipase A2 delta	AB090876	1.171	1.097					
OR52M1	" olfactory receptor, family 52, subfamily M, member 1"	NM_001004137	1.17	0.898					
N/A	N/A	AK130383	1.17	0.73					
N/A	N/A	AK094364					1.17	0.698	
LOC136288	LOC136288 protein	BC031107	1.17	1.361					
KIAA0726	KIAA0726 protein	AB018269	1.17	1.22					Cell adhesion. Homophilic cell adhesion.
HLA-DQA2	major histocompatibility complex, class II, DQ alpha 2"	NM_020056					1.17	0.804	Immune response. Antigen presentation, exogenous antigen. Antigen processing, exogenous antigen via MHC class II.
GLP	golgin-like protein	AF263742	1.17	0.693					
PNMA6A	paraneoplastic antigen like 6A	NM_032882					1.169	0.626	
EPO	erythropoietin	NM_000799					1.169	0.603	Response to stress. Signal transduction. Cell-cell signaling. Development. Circulation.
SEC14L4	SEC14p-like protein TAP3	NM_174977					1.168	0.506	Transport. Intracellular protein transport.
N/A	guanylate cyclase-coupled enterotoxin receptor	S57551	1.168	0.797					CGMP biosynthesis. Protein amino acid phosphorylation. Receptor guanylyl cyclase signaling pathway.
N/A	erythroid membrane-associated protein	AF311284	1.168	0.52					
GPR27	G protein-coupled receptor 27	NM_018971			1.168	0.929			Signal transduction. G-protein coupled receptor protein signaling pathway.
DKFZp686P23184	hypothetical proteincDNA DKFZp686P23184 (from clone DKFZ	BX538327	1.168	0.431					Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
DKFZP586B1621	DKFZP586B1621 protein	NM_015533	1.168	1.352					Glycerol metabolism

ARS	ARS component B precursor	NM_020427	1.168	1.161					Cell activation. Cell adhesion.
ADCY5	adenylate cyclase 5	NM_183357	1.168	0.639					CAMP biosynthesis. Intracellular signaling cascade.
TUBB5	tubulin, beta, 5"	NM_006087					1.167	0.608	Microtubule-based movement. Protein polymerization.
KREMEN1	KREMEN1 protein	BC063787	1.167	0.715					Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
CRYGB	crystallin, gamma B"	NM_005210					1.167	0.649	
SH2D3C	SH2 domain containing 3C	NM_170600	1.166	0.473					JNK cascade. Small GTPase mediated signal transduction.
RASAL1	RAS protein activator like 1	NM_004658					1.166	0.349	Intracellular signaling cascade.
PPL	periplakin	NM_002705					1.166	0.68	
N/A	N/A	AK092426	1.166	0.625					
KRT23	keratin 23 isoform a	NM_015515	1.166	1.115					
JAG2	jagged 2 isoform a precursor	NM_002226					1.166	0.598	Cell fate determination. Cell cycle. Notch signaling pathway. Cell-cell signaling. Spermatogenesis.
FOXH1	forkhead box H1	NM_003923			1.166	0.59			Regulation of transcription, DNA-dependent. Signal transduction.
FAM14A	TLH29 protein precursor	NM_032036	1.166	0.365					Response to pest, pathogen or parasite.
N/A	calcium channel L-type alpha 1 subunit	AF070589	1.165	0.828					
KIAA1170	KIAA1170 protein	AB032996	1.165	1.626					
FLJ10996	hypothetical protein FLJ10996	BC005078			1.165	0.591			
CRNKL1	crooked neck-like 1 protein	NM_016652	1.165	0.691					Spliceosome assembly.
N/A	N/A	AK094481			1.164	0.536			Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
DDEF1	development and differentiation enhancing factor 1	NM_018482			1.164	0.477			Regulation of GTPase activity.
CLMN	calponin like transmembrane domain protein	NM_024734	1.164	0.587					
BASE	breast cancer and salivary gland expression gene	NM_173859					1.164	0.426	
PRPF18	PRP18 pre-mRNA processing factor 18 homolog	NM_003675	1.163	0.82					Nuclear mRNA splicing, via spliceosome.
N/A	N/A	BC001051	1.163	0.804					Intracellular protein transport. Small GTPase mediated signal transduction.
N/A	N/A	AK124777	1.163	0.587					
GSTA3	glutathione S-transferase A3	NM_000847	1.163	0.822					Response to stress. Metabolism.
KIAA0611	KIAA0611 protein	AB014511	1.162	1.315					Cation transport. Metabolism.
FLJ13639	hypothetical protein FLJ13639	NM_024705	1.162	0.745					
ADRA2C	alpha-2C-adrenergic receptor	NM_000683					1.162	0.51	Activation of MAPK. Signal transduction. G-protein coupled receptor protein signaling pathway. Cell-cell signaling.
PNMA1	paraneoplastic antigen MA1	NM_006029	1.161	1.032					Spermatogenesis. Central nervous system development.
PKHD1L1	fibrocystin L	NM_177531	1.161	0.553					
N/A	N/A	AK093047					1.16	0.583	
MRGPRD	MAS-related GPR, member D"	NM_198923					1.16	0.56	
GLYCAM1	glycosylation-dependent cell adhesion molecule 1	AJ489592					1.16	0.512	
ZNF488	zinc finger protein 488	NM_153034	1.159	0.844					
XAGE-4	XAGE-4 protein	AJ318895	1.159	1.325					
tpcr86	putative olfactory receptor	X89676	1.159	0.702					
NTSR1	neurotensin receptor 1	NM_002531					1.159	0.567	Signal transduction. G-protein coupled receptor protein signaling pathway. Synaptic transmission.
IFNA4	" interferon, alpha 4"	NM_021068	1.159	0.704					Defense response. Cell-cell signaling. Response to virus.
ZFH4	ZFH4 protein	BC047745			1.158	1.14			Regulation of transcription, DNA-dependent.
NHS	Nance-Horan syndrome protein	NM_198270	1.158	0.594					
MAGE-E1c	N/A	AB040529	1.158	0.68					
F7	" coagulation factor VII precursor, isoform a"	NM_000131	1.158	0.789					Proteolysis and peptidolysis. Blood coagulation.
DKFZp727A071	hypothetical protein	AL117473					1.158	0.475	
OSTbeta	organic solute transporter beta	NM_178859	1.157	0.566					
NDST3	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 3	NM_004784	1.157	0.811					Protein amino acid deacetylation. Protein amino acid sulfation.
N/A	N/A	AK093145	1.157	0.645					
LOC90353	LOC90353	NM_145232	1.157	0.612					
LOC387882	hypothetical protein	NM_207376	1.157	1.006					
LMO2	LIM domain only 2	NM_005574					1.157	0.723	Development.
OLFML2B	olfactomedin-like 2B	NM_015441	1.156	0.665					
N/A	N/A	AK127606	1.156	0.448					Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
N/A	N/A	AK098749	1.155	0.62					
FLJ44861	FLJ44861 protein	NM_207389					1.155	0.3	
DELGEF	deafness locus associated putative guanine nucleotide exchan	NM_012139	1.155	0.666					Signal transduction.
SIAT8E	sialyltransferase 8E	NM_013305					1.154	0.583	Carbohydrate metabolism. Protein amino acid glycosylation. Glycosphingolipid biosynthesis.
PAM	" peptidylglycine alpha-amidating monooxygenase isoform a,	NM_000919	1.154	1.298					Peptide amidation. Protein modification.

N/A	N/A	AK125136							1.154	0.357	
N/A	unknown	AF462446							1.154	0.395	
MST068	MSTP068	AF163259			1.154	1.026					
MGC34799	hypothetical protein MGC34799	NM_182575					1.154	1.09			
DEFA1	defensin, alpha 1 preproprotein"	NM_004084							1.154	0.319	Xenobiotic metabolism. Response to pest, pathogen or parasite. Defense response to bacteria. Defense response to fungi.
SEPT3	septin 3 isoform B	NM_019106							1.154	0.965	Cytokinesis. Cell cycle.
ZP4	zona pellucida glycoprotein 4 preproprotein	NM_021186					1.153	0.492			Fertilization.
POLR3C	polymerase (RNA) III (DNA directed) polypeptide C (62kD)	NM_006468			1.153	0.967					Transcription. Regulation of transcription.
OR2T34	" olfactory receptor, family 2, subfamily T, member 34"	NM_001001821			1.153	0.796					
N/A	PRO0117	AF090895					1.153	0.972			
MGC43036	hypothetical gene supported by BC031966	NM_001004323					1.153	0.38			
LOC220594	TL132 protein	NM_145809			1.153	0.535					Ubiquitin-dependent protein catabolism. Ubiquitin cycle.
FMO1	FMO1 protein	BC047129					1.153	0.591			Electron transport.
EGFL7	EGF-like-domain, multiple 7"	NM_201446							1.153	0.267	Angiogenesis. Blood vessel development. Vasculogenesis. Regulation of cell migration.
DPEP1	dipeptidase 1 (renal)	NM_004413							1.153	0.646	Proteolysis and peptidolysis.
CHD6	chromodomain helicase DNA binding protein 6	NM_032221			1.153	1.163					Chromatin assembly or disassembly.
CDC27	cell division cycle protein 27	NM_001256					1.153	0.467			Mitotic metaphase/anaphase transition. Cell proliferation.
CCL3L1	chemokine (C-C motif) ligand 3-like 1 precursor	NM_021006							1.153	0.554	Calcium ion homeostasis. Exocytosis. Cell motility. Chemotaxis. Inflammatory response. Cytoskeleton organization.
RGS13	regulator of G-protein signalling 13	BC056866			1.152	1.177					Signal transduction.
LHFPL2	lipoma HMGIC fusion partner-like 2	NM_005779			1.152	0.497					
DIRAS2	Di-Ras2	NM_017594							1.152	0.651	Small GTPase mediated signal transduction.
N/A	tissue plasminogen activator	U63828							1.151	0.613	
LOC91752	similar to C630007C17Rik protein	NM_194250			1.151	0.93					
TMPRSS2	transmembrane protease, serine 2"	NM_005656							1.15	0.728	Proteolysis and peptidolysis.
N/A	N/A	AK126025							1.15	0.545	
N/A	N/A	AK125816			1.15	1.195					
N/A	SH2 domain-containing phosphatase anchor protein 2d	AF416904					1.15	0.494			
N/A	PRO1084	AF116621							1.15	0.601	
KIAA1336	KIAA1336 protein	AB037757			1.15	0.408					
CCR4	chemokine (C-C motif) receptor 4	NM_005508							1.15	0.676	Chemotaxis. Inflammatory response. Signal transduction. G-protein coupled receptor protein signaling pathway.
ABCG8	sterolin 2	NM_022437							1.15	0.429	Transport.
N/A	N/A	BX161457							1.149	0.692	
KRTAP4-4	keratin associated protein 4.4	NM_032524			1.149	0.573					
HOMER3	" Homer, neuronal immediate early gene, 3"	NM_004838			1.149	0.758					Protein targeting. Metabotropic glutamate receptor signaling pathway.
FLJ42925	FLJ42925 protein	NM_198511							1.149	0.503	
DKFZp686O12114	hypothetical protein	BX537916							1.149	0.53	
AP1S2	adaptor-related protein complex 1 sigma 2 subunit	NM_003916			1.149	1.15					Transport. Intracellular protein transport. Receptor mediated endocytosis.
KCNH3	potassium voltage-gated channel, subfamily H (eag-related), m	NM_012284							1.148	0.762	Two-component signal transduction system. Cation transport. Potassium ion transport.
IL13	interleukin 13 precursor	NM_002188			1.148	0.719					Cell motility. Inflammatory response. Signal transduction. Cell-cell signaling. Cell proliferation.
GPR78	G protein-coupled receptor 78	NM_080819					1.148	0.705			
CCKAR	cholecystokinin A receptor	NM_000730							1.148	0.531	Smooth muscle contraction. Signal transduction. Positive regulation of cytosolic calcium ion concentration. Response to nutrients. Digestion.
SORCS2	VPS10 domain receptor protein SORCS 2	NM_020777			1.147	0.598					Intracellular protein transport. Neuropeptide signaling pathway.
N/A	hypothetical protein	AL049689							1.147	0.273	Cell growth. Cell migration.
N/A	N/A	AK127492							1.147	0.669	Cation transport. Potassium ion transport.
LCP1	L-plastin	NM_002298							1.147	0.538	
FAM3B	family with sequence similarity 3, member B isoform a"	NM_058186							1.147	0.625	Insulin secretion.
ARHGDIG	Rho GDP dissociation inhibitor (GDI) gamma	NM_001176	1.221	0.981					1.147	0.617	Negative regulation of cell adhesion. Rho protein signal transduction.
UBE1DC1	ubiquitin-activating enzyme E1-domain containing 1 isoform 2	NM_198329					1.146	0.757			L-serine biosynthesis.
TTPA	tocopherol (alpha) transfer protein (ataxia (Friedreich-like) with	NM_000370			1.146	1.084					Lipid metabolism. Transport.
N/A	N/A	AK097698							1.146	0.56	
N/A	PRO1808	AF118077	1.349	0.907	1.146	0.982					
KRTAP10-11	keratin associated protein 10-11	NM_198692							1.146	0.83	
HIST1H2AE	" H2A histone family, member A"	NM_021052			1.146	1.384					Nucleosome assembly. Chromosome organization and biogenesis.
OR5K4	" olfactory receptor, family 5, subfamily K, member 4"	NM_001005517			1.145	1.316					
N/A	C6orf37	AF350451			1.145	0.647					
FLJ00040	FLJ00040 protein	AK054561			1.145	0.667					

ETNK2	ETNK2 protein	BC010082			1.145	0.651					
CPB2	plasma carboxypeptidase B2 isoform a preproprotein	NM_001872							1.145	0.614	Proteolysis and peptidolysis.
N/A	N/A	AK125766							1.144	0.449	
N/A	N/A	AK096219							1.144	0.468	
MTAC2D1	membrane targeting (tandem) C2 domain containing 1	NM_152332							1.144	0.429	Transport.
MGC45491	hypothetical protein MGC45491	NM_153246			1.144	0.404					
LOC388394	similar to candidate mediator of the p53-dependent G2 arrest	NM_203400							1.144	0.473	
AKR1C4	" aldo-keto reductase family 1, member C4" " 3-alpha hydroxy	NM_001818			1.144	0.768					Xenobiotic metabolism.
TAF15	TBP-associated factor 15 isoform 1	NM_139215					1.143	0.91			
PTHR2	parathyroid hormone receptor 2 precursor	NM_005048							1.143	0.433	Signal transduction. G-protein coupled receptor protein signaling pathway.
N/A	N/A	AK057355							1.143	0.173	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
KIAA1274	KIAA1274	NM_014431							1.143	0.351	
UNQ430	RGTR430	NM_205545							1.142	0.369	
SYT5	synaptotagmin V	NM_003180							1.142	0.634	Transport. Synaptic transmission.
N/A	unknown	U79275							1.142	0.533	
N/A	Unknown (protein for IMAGE:4252124)	BC017997	2.233	1.036					1.142	0.452	
N/A	UHS KERB-like protein	AY360461							1.142	0.506	
MGC14289	hypothetical protein MGC14289	NM_080660			1.142	0.898					
KIAA0653	KIAA0653 protein	AB014553			1.142	0.478					Immune response. Hyperosmotic response. Signal transduction. Positive regulation of activated T-cell proliferation.
BTNL8	butyrophilin-like 8	NM_024850			1.142	0.793					
SLC25A4	solute carrier family 25 (mitochondrial carrierHomo sapiens sol	NM_001151			1.141	0.984					Mitochondrial genome maintenance. Generation of precursor metabolites and energy. Mitochondrial transport.
SLC18A1	SLC18A1 protein	BC006317							1.141	0.437	Monoamine transport. Drug transport.
POLG	" polymerase (DNA directed), gamma"	NM_002693					1.141	0.832			DNA-dependent DNA replication.
PLA2G10	phospholipase A2, group X"	NM_003561							1.141	0.425	Lipid catabolism.
N/A	N/A	AK096705			1.141	0.898					
N/A	pol protein	AF109183			1.141	0.513					
ITIH5L	inter-alpha (globulin) inhibitor H5-like	NM_198510							1.141	0.465	Hyaluronan metabolism.
FLJ20628	hypothetical protein FLJ20628	NM_017910			1.141	0.801					
DTX1	deltex homolog 1	NM_004416	1	0.789					1.141	0.561	Transcription. Cell surface receptor linked signal transduction. Regulation of Notch signaling pathway. Protein ubiquitination.
CD99L2	CD99L2 protein	BC025729			1.141	0.408					
USH1C	harmonin isoform b3	NM_153676							1.14	0.568	Intracellular signaling cascade. Sensory perception. Visual perception. Perception of sound.
STEERIN2	steerin2 protein	AJ488203			1.14	0.917					
PEX7	PEX7 protein	BC031606			1.14	0.877					Protein transport.
N/A	N/A	AK095016			1.14	0.421					
N/A	unknown	AF143328			1.14	0.557					G-protein coupled receptor protein signaling pathway.
LOC400451	hypothetical gene supported by AK075564	NM_207446							1.14	0.512	
DKFZp451P181	hypothetical proteincDNA DKFZp451P181 (from clone DKFZp4	BX640730			1.14	1.059					Ion transport.
SKIV2L	superkiller viralicidic activity 2-like homolog	NM_006929			1.139	1.032					Regulation of translation.
OLFM2	olfactomedin 2	NM_058164							1.139	0.478	
N/A	N/A	AK096379			1.139	1.039					
N/A	N/A	AK000374			1.139	0.819					
N/A	RAG2	AF080577			1.139	0.895					DNA recombination. Generation of antibody gene diversity.
FLJ90586	hypothetical protein FLJ90586	NM_153345			1.139	0.483					
UHSKerB	keratin, ultrahigh sulfur, B"	NM_021046							1.138	0.515	
THEG	testicular haploid expressed gene product isoform 1	NM_016585							1.138	0.249	Spermatogenesis. Chaperone-mediated protein complex assembly.
SLC22A15	" solute carrier family 22 (organic cation transporter), member	NM_018420			1.138	0.665					Transport.
FAIM2	neuromembrane protein 35	NM_012306	1.411	1.3	1.138	0.474					Anti-apoptosis.
CLDN5	claudin 5	NM_003277							1.138	0.404	Calcium-independent cell-cell adhesion.
CCR2	chemokine (C-C motif) receptor 2 isoform A	NM_000647							1.138	0.337	Chemotaxis. Inflammatory response. Cellular defense response. Signal transduction.
C10orf27	chromosome 10 open reading frame 27	NM_152710							1.138	0.577	
N/A	C21orf108	AF231919			1.137	0.584					
MST4	serine/threonine protein kinase MASK	NM_016542			1.137	0.923					Protein amino acid phosphorylation.
FLJ16641	FLJ16641 protein	NM_001004316			1.137	1.484					
EPC2	enhancer of polycomb homolog 2	NM_015630			1.137	0.6					
CST7	cystatin F	NM_003650							1.137	0.512	Immune response.
N/A	Unknown (protein for IMAGE:4715570)	BC020899			1.136	1.273					

ITPR2	" inositol 1,4,5-triphosphate receptor, type 2"	NM_002223			1.136	0.737					Cation transport. Calcium ion transport. Signal transduction.
FSTL3	follistatin-like 3glycoprotein	BC005839	1.278	1.596					1.136	0.624	
CXorf9	chromosome X open reading frame 9	NM_018990							1.136	0.606	
CCL11	small inducible cytokine A11 precursor	NM_002986							1.136	0.767	Protein amino acid phosphorylation. Calcium ion homeostasis. Chemotaxis. Inflammatory response. Cellular defense response.
PLEKHA6	PLEKHA6 protein	BC010522			1.135	0.784					
NGFRAP1	nerve growth factor receptor (TNFRSF16) associated protein 1	NM_206915					1.135	0.66			Apoptosis. Development.
N/A	N/A	AK125870							1.135	0.348	
KIAA0853	KIAA0853	NM_015070			1.135	0.596					
PKD2	polycystin 2	NM_000297			1.134	0.754					Cation transport. Cell-matrix adhesion. Organogenesis.
N/A	FGF21	AY359086							1.134	0.313	Signal transduction. Cell-cell signaling.
N/A	N/A	AK128224							1.134	0.531	
N/A	N/A	AK023947					1.134	0.659			Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
muc20S	transmembrane mucin MUC20S	AB098731							1.134	0.468	
SARDH	sarcosine dehydrogenase	NM_007101			1.133	0.631					Electron transport. Glycine catabolism.
RHOV	" ras homolog gene family, member V"	NM_133639			1.133	0.726					Small GTPase mediated signal transduction.
N/A	Unknown (protein for IMAGE:4070464)	BC016719			1.133	0.807					
KIAA1510	KIAA1510 protein	AB040943							1.133	0.558	Phosphate transport. Cell adhesion.
KIAA1026	KIAA1026 protein	AB028949			1.133	0.592					
IQCF1	IQCF1 protein	BC034228					1.133	0.616			
DEFB126	beta defensin 126 preproprotein	NM_030931							1.133	0.668	Proteolysis and peptidolysis. Defense response to bacteria.
MARCKS	myristoylated alanine-rich protein kinase C substrate	NM_002356			1.132	0.471					Cell motility.
DNASE1L1	DNASE1L1 protein	BC028092			1.132	0.503					DNA catabolism.
TYR	tyrosinase precursor	M27160					1.131	0.897			Melanin biosynthesis from tyrosine. Eye pigment biosynthesis. Visual perception. Perception of sound.
N/A	N/A	AK097656							1.131	0.866	
MT1E	metallothionein 1E	NM_175617			1.131	0.876					
CXADR	coxsackie virus and adenovirus receptor precursor	NM_001338			1.131	0.623					
BRS3	bombesin-like receptor 3	NM_001727			1.131	0.793					Glucose metabolism. Smooth muscle contraction. Signal transduction. G-protein coupled receptor protein signaling pathway.
ATP11C	" ATPase, Class VI, type 11C"	NM_173694					1.131	0.515			Cation transport.
PCDHX	protocadherin	AJ564937					1.13	0.797			Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
MGC39545	hypothetical protein LOC403312	NM_203452			1.13	0.745					Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
IMAGE:4907098	beta-1,3-N-acetylglucosaminyltransferase protein"	NM_138706							1.13	0.674	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
FLJ45910	FLJ45910 protein	NM_207390	1.208	1.26					1.13	0.383	
XG	XG glycoprotein precursor	NM_175569	2.48	2.057	1.129	0.68					
SUV39H1	suppressor of variegation 3-9 homolog 1	NM_003173			1.129	0.879					DNA replication and chromosome cycle. Chromatin assembly or disassembly. Chromatin modification.
N/A	Unknown (protein for MGC:71925)	BC062680			1.129	0.725					
LOC51136	PTD016 protein	NM_016125			1.129	0.564					Protein ubiquitination.
PPP3R2	protein phosphatase 3 regulatory subunit B, beta isoform"	NM_147180							1.128	0.506	
ATP8A1	" ATPase, aminophospholipid transporter (APLT), class I, type	NM_006095			1.128	0.715					Cation transport. Metabolism. Aminophospholipid transport.
PNMT	phenylethanolamine N-methyltransferase	NM_002686							1.127	0.433	Catecholamine biosynthesis.
NXF3	nuclear RNA export factor 3	NM_022052							1.127	0.637	mRNA processing. mRNA-nucleus export. Protein-nucleus import.
F9	coagulation factor IX	NM_000133					1.127	0.46			Proteolysis and peptidolysis. Blood coagulation.
KIAA1952	KIAA1952 protein	AB075832			1.126	0.916					
KIAA1200	KIAA1200 protein	AB033026			1.126	0.35					
FGD3	" FGD1 family, member 3"	NM_033086	4.055	0.766					1.126	0.452	Cytoskeleton organization and biogenesis. Regulation of cell shape. Actin cytoskeleton organization and biogenesis.
ALDOB	aldolase B	NM_000035			1.126	0.652					Fructose metabolism. Glycolysis.
PRDM16	PR domain containing 16 isoform 1	NM_022114							1.125	0.617	Regulation of transcription, DNA-dependent.
PF6	projection protein PF6	NM_206996			1.125	0.777					Transcription.
NTN1	netrin 1	NM_004822							1.125	0.696	Apoptosis. Cell motility. Cell-cell signaling. Neurogenesis.
KIAA0027	KIAA0027 protein	D25217			1.125	1.06					Protein biosynthesis. Ion transport.
DHRS2	dehydrogenase/reductase (SDR family) member 2 isoform 1	NM_182908							1.125	0.602	Carbohydrate metabolism. Metabolism.
XYLT2	xylosyltransferase II	NM_022167			1.124	0.532					Glycosaminoglycan biosynthesis,
TLR3	toll-like receptor 3	NM_003265	1.153	1.2			1.124	0.807			Inflammatory response. Hyperosmotic response. Signal transduction. Activation of NF-kappaB-inducing kinase. Detection of virus.
NBEA	neurobeachin	NM_015678			1.124	0.693					Post-Golgi transport.
N/A	Unknown (protein for IMAGE:4155919)	BC027465			1.124	0.677					
N/A	N/A	AK127147					1.124	0.369			
LOC196264	hypothetical protein LOC196264	NM_198275			1.124	0.661					

GRCA	" gene rich cluster, A isoform 2"	NM_019858			1.124	0.946					G-protein coupled receptor protein signaling pathway. Protein metabolism
FLJ00113	FLJ00113 protein	AK024504			1.124	1.132					Protein amino acid phosphorylation.
AQP9	aquaporin 9	NM_020980							1.124	0.6	Water transport. Water transport. Purine transport. Purine transport. Immune response.
NR1D2	" nuclear receptor subfamily 1, group D, member 2"	NM_005126			1.123	0.876					Transcription. Regulation of transcription, DNA-dependent. Regulation of transcription, DNA-dependent.
N/A	N/A	AK025280					1.123	0.695			
N/A	GRIP1 protein	AJ133439			1.123	1.17					Intracellular signaling cascade. Synaptic transmission.
KLC2L	kinesin light chain 2-like isoform a	NM_177417							1.123	0.375	
FP3214	unknown	AF447874			1.123	0.883					
DKFZp686C12204	hypothetical proteincDNA DKFZp686C12204 (from clone DKFZ	BX538331			1.123	0.618					
DKFZp434M1820	hypothetical proteincDNA DKFZp434M1820 (from clone DKFZ	AL136803			1.123	0.569					Transport. Mitochondrial transport.
CRARF	precursor of P100 serine protease of Ra-reactive factor	D17525			1.123	0.728					Proteolysis and peptidolysis. Immune response. Complement activation. Complement activation, classical pathway.
N/A	N/A	AK128511					1.122	0.431			Lipid metabolism. Hormone-mediated signaling. Fatty acid oxidation.
MGC33835	hypothetical protein MGC33835	NM_182548	1.07	1.046	1.122	0.64					
CXCL10	interferon gamma-inducedprecursor	NM_001565			1.122	0.831					Cell motility. Chemotaxis. Inflammatory response. Cell surface receptor linked signal transduction. Cell-cell signaling.
TREM1	triggering receptor expressed on myeloid cells 1	NM_018643	1.532	1.599					1.121	0.803	Humoral immune response. Intracellular signaling cascade.
SSX6	synovial sarcoma, X breakpoint 6"	NM_173357							1.121	0.755	
SLC35D3	SLC35D3 protein	BC067217							1.121	0.362	
PPP1R14D	protein phosphatase 1, regulatory subunit 14D"	NM_017726							1.121	0.732	
N/A	N/A	AK128718							1.121	0.502	
N/A	hypotetical protein	AJ237663							1.121	0.409	Transport.
N/A	PRO3077	AF119913			1.121	0.637					
LOC130951	hypothetical protein BC014602	NM_138804			1.121	0.42					
KIAA2027	KIAA2027 protein	AB095947	1.668	0.739	1.121	0.964					
GGTLA4	gamma-glutamyltransferase-like activity 4	NM_080920			1.121	0.33					Amino acid metabolism. Glutathione biosynthesis. Glutathione biosynthesis.
ZCCHC5	" zinc finger, CCHC domain containing 5"	NM_152694	1.252	1.265			1.12	0.843			
KIAA1583	KIAA1583 protein	AB046803			1.12	0.615					
CRSP8	" cofactor required for Sp1 transcriptional activation, subunit 8	NM_004269					1.12	0.633			Transcription initiation from RNA polymerase II promoter.
MAGEH1	" melanoma antigen, family H, 1 protein"	NM_014061					1.119	0.859			Apoptosis.
FGF10	fibroblast growth factor 10 precursor	NM_004465			1.119	1.437					Protein-nucleus import, translocation. Regulation of cell cycle. Response to stress. Signal transduction.
DKFZp586A1123	hypothetical proteincDNA DKFZp586A1123 (from clone DKFZp	AL050181			1.119	0.891					
PI15	protease inhibitor 15 preproprotein	NM_015886			1.118	1.012					
NT5C2L1	" 5'-nucleotidase, cytosolic II-like 1 protein"	NM_152729			1.118	0.891					
N/A	calcium and DAG-regulated guanine nucleotide exchange fact	AF081195							1.118	0.607	Small GTPase mediated signal transduction. Ras protein signal transduction.
SLC15A1	solute carrier family 15 (oligopeptide transporter), member 1"	NM_005073							1.117	0.503	Transport. Oligopeptide transport. Digestion.
N/A	Unknown (protein for IMAGE:4813419)	BC037837			1.117	0.46					Neurogenesis. Cell differentiation.
N/A	PRO2289	AF116698			1.117	0.561					
GAS	proprotein	NM_000805							1.117	0.475	Smooth muscle contraction. Signal transduction.
TXNDC8	thioredoxin domain containing 8	NM_001003936			1.116	0.794					
PART1	prostate androgen-regulated transcript 1 protein	NM_016590	2.079	2.147			1.116	0.558			
N/A	TMEM9	AY359012			1.116	0.605					Transport.
N/A	N/A	AK090929			1.116	0.176					
KIAA1653	KIAA1653 protein	AB051440							1.116	0.344	Glutamate biosynthesis. Proline catabolism.
DKFZp686E1183	hypothetical proteincDNA DKFZp686E1183 (from clone DKFZp	BX537393			1.116	0.854					Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
DKFZp451F173	hypothetical proteincDNA DKFZp451F173 (from clone DKFZp4	AL831982					1.116	0.903			Induction of apoptosis. Caspase activation.
CRYBA4	" crystallin, beta A4"	NM_001886			1.116	0.677					Visual perception.
C11orf11	chromosome 11 open reading frame 11	NM_006133							1.116	1.068	Lipid metabolism.
B3GAT1	beta-1,3-glucuronyltransferase 1"	NM_054025							1.116	0.731	Carbohydrate metabolism. Protein amino acid glycosylation.
MEOX1	mesenchyme homeo box 1 isoform 1	NM_004527			1.115	1.032					Regulation of transcription, DNA-dependent. Development.
KCNH4	potassium voltage-gated channel, subfamily H, member 4"	NM_012285							1.115	0.545	Two-component signal transduction system (phosphorelay). Cation transport. Potassium ion transport.
FBXW11	F-box and WD-40 domain protein 1B isoform C	NM_012300					1.115	0.628			Wnt receptor signaling pathway. Protein ubiquitination.
CASK	CASK	AF035582			1.115	1.104					Protein amino acid phosphorylation. Cell adhesion.
ATP4A	ATPase, H+/K+ exchanging, alpha polypeptide"	NM_000704							1.115	0.532	Potassium ion transport. Metabolism. Proton transport.
OPN1MW	" opsin 1 (cone pigments), medium-wave-sensitive (color blind	NM_000513			1.114	0.284					Signal transduction. G-protein coupled receptor protein signaling pathway. Sensory perception. Visual perception.
N/A	N/A	AK123256			1.114	0.73					
IGF2	insulin-like growth factor 2 (somatomedin A)	NM_000612			1.114	0.786					Regulation of cell cycle. Skeletal development. Imprinting. Development. Physiological process.
FLJ00260	FLJ00260 protein	AK131074							1.114	0.575	Positive regulation of I-kappaB kinase/NF-kappaB cascade.

DKFZp761I2312	hypothetical protein	AL161971							1.114	0.607	
N/A	N/A	AK097925			1.113	0.747					Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism. Metabolism.
MGC42090	hypothetical protein MGC42090	NM_152774			1.113	1.009					
MGC11324	hypothetical protein MGC11324	NM_032717			1.113	0.443					Metabolism.
GPR89	GPR89 protein	BC067816			1.113	0.46					Positive regulation of I-kappaB kinase/NF-kappaB cascade.
CYP1A1	cytochrome P450, family 1, subfamily A, polypeptide 1"	NM_000499							1.113	0.657	Electron transport. Transport.
B3GALT2	" UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase 2"	BC022507	1.904	1.263	1.113	0.754					Protein amino acid glycosylation.
AKAP13	A-kinase anchor protein 13 isoform 1	NM_006738			1.113	0.981					
N/A	PPRR2488	AY358843			1.112	0.567					Metabolism. Lipid catabolism.
N/A	N/A	AK129701			1.112	0.85					Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
N/A	N/A	AK094116			1.112	0.874					
KIAA0664	KIAA0664 protein	NM_015229			1.112	1.146					Protein biosynthesis. Metabolism.
FLJ16030	FLJ16030 protein	NM_198494			1.112	0.941					
CD80	CD80 antigen (CD28 antigen ligand 1, B7-1 antigen)"	NM_005191							1.112	0.643	Immune response. Intracellular signaling cascade. Cell-cell signaling. Positive regulation of signal transduction. T-cell activation.
C1QTNF3	C1q and tumor necrosis factor related protein 3	NM_181435	2.694	1.892	1.112	1.086					Phosphate transport.
RAB11FIP2	RAB11 family interacting protein 2 (class I)	NM_014904			1.111	1.034					
N/A	plasminogen-related protein A	U67178							1.111	0.433	
N/A	N/A	AK128589			1.111	0.611					Protein folding. Apoptosis, inferred from expression pattern. Spermatogenesis.
N/A	N/A	AK090879			1.111	0.687					
MDS018	hypothetical protein MDS018	NM_021823					1.111	0.365			
KSR2	kinase suppressor of Ras-2	NM_173598			1.111	0.792					
COMMD9	COMM domain containing 9	NM_014186			1.111	0.706					
CLECSF2	" C-type lectin, superfamily member 2"	NM_005127			1.111	0.619					Antimicrobial humoral response.
SPATS2	" spermatogenesis associated, serine-rich 2"	NM_023071			1.11	0.959					
N/A	N/A	AK027208							1.11	0.342	
KIAA0531	KIAA0531 protein	AB011103			1.11	1.119					Organelle organization and biogenesis. Microtubule-based movement.
INSL6	insulin-like 6 precursor	NM_007179							1.11	0.64	Physiological process.
ZNF334	zinc finger protein 334 isoform b	NM_199441			1.109	0.296					Regulation of transcription, DNA-dependent.
KIAA0865	KIAA0865 protein	AB020672			1.109	0.757					
KIAA0748	KIAA0748 protein	AB018291			1.109	0.402					
CCL24	small inducible cytokine A24 precursor	NM_002991			1.109	1.204					Chemotaxis. Inflammatory response. Signal transduction. Cell-cell signaling. Sensory perception.
ABCC6	" ATP-binding cassette, sub-family C, member 6"	NM_001171			1.109	0.429					Transport. Transport. Sensory perception. Visual perception. Response to drug.
MMP20	matrix metalloproteinase 20 preproprotein	NM_004771			1.108	0.938					Proteolysis and peptidolysis.
MGC26979	hypothetical protein MGC26979	NM_153704			1.108	1.181					
FLJ23554	hypothetical protein FLJ23554 isoform 1	NM_024806			1.108	0.166					
DKFZp779M2348	hypothetical protein	BX640689							1.108	0.412	Regulation of striated muscle contraction. Muscle development.
C21orf86	chromosome 21 open reading frame 86	NM_153454	1.389	0.547			1.108	0.832			
N/A	N/A	AK128065							1.107	0.347	Microtubule-based movement.
N/A	N/A	AK090911							1.107	0.386	
MGC10992	hypothetical protein LOC92922	NM_033212			1.107	0.76					
FBL	fibrillarin	BC019260					1.107	0.5			rRNA processing.
DKFZp667B0210	early B-cell factor 3	NM_001005463			1.107	0.734					Regulation of transcription, DNA-dependent. Development.
BPY2B	" basic charge, Y-linked, 2B"	NM_001002760			1.107	0.349					Fertilization.
ZNF266	ZNF266 protein	BC017407			1.106	0.554					Regulation of transcription, DNA-dependent.
TSGA10	" testis specific, 10"	NM_025244			1.106	0.51					Spermatogenesis.
TLR9	toll-like receptor 9 isoform B	NM_138688							1.106	0.577	Inflammatory response. Defense response to bacteria.
PRF1	perforin 1 precursor	NM_005041							1.106	0.347	Programmed cell death, transformed cells. Cellular defense response. Pathogenesis. Cytolysis.
N/A	HGS_RE408	AY359108					1.106	0.27			
TTL	tubulin tyrosine ligase	NM_153712			1.105	0.815					Protein modification.
N/A	interferon-induced protein with tetratricopeptide repeats 1	BT006667					1.105	0.572			Immune response.
N/A	N/A	AK127601							1.105	0.369	
N/A	hypothetical protein	AF429967			1.105	1					
FNDC5	fibronectin type III domain containing 5	NM_153756							1.105	0.56	
ATP1A2	Na+/K+ -ATPase alpha 2 subunit proprotein	NM_000702					1.105	0.395			Potassium ion transport. Sodium ion transport. Metabolism. ATP hydrolysis coupled proton transport.
TBX10	T-box 10	NM_005995							1.104	0.28	Transcription. Morphogenesis.
N/A	Unknown (protein for MGC:71640)	BC063295			1.104	0.286					

KIAA0773	KIAA0773 gene product	NM_014690			1.104	0.565					
ID4	" inhibitor of DNA binding 4, dominant negative helix-loop-heli	NM_001546			1.104	0.979					Regulation of transcription.
CYYR1	cysteine and tyrosine-rich 1 protein precursor	NM_052954	1.032	0.832	1.104	0.778					
MGC51082	hypothetical protein MGC51082	NM_182498			1.103	0.637					
N/A	N/A	AK123987							1.102	0.384	
KIAA1232	KIAA1232 protein	AB033058					1.102	0.588			Negative regulation of cell proliferation.
FP6765	unknown	AF495727							1.102	0.618	
FLJ00179	FLJ00179 protein	AK074108			1.102	0.529					
DKFZp779N1944	hypothetical proteincDNA DKFZp779N1944 (from clone DKFZ	BX538100	1.453	1.076	1.102	0.799					
ACSL1	acyl-CoA synthetase long-chain family member 1	NM_001995			1.102	0.979					Lipid metabolism. Fatty acid metabolism. Digestion.
RAD51AP1	RAD51AP1 protein	BC016330			1.101	0.543					DNA repair.
N/A	N/A	AK027500							1.101	0.401	
LOC204010	LOC204010 protein	BC058822			1.101	1.014					
BMX	BMX non-receptor tyrosine kinase	NM_203281							1.101	0.498	Protein amino acid phosphorylation. Intracellular signaling cascade. Mesoderm development.
N/A	LP3317	AY203941							1.1	0.338	
MTNR1A	melatonin receptor Mel1a	AF435588			1.1	0.475					Signal transduction. G-protein signaling, coupled to cyclic nucleotide second messenger. Mating behavior. Circadian rhythm.
LGALS3BP	galectin 3 binding protein	NM_005567			1.1	0.605					Cellular defense response. Cell adhesion. Signal transduction.
N/A	E2F-5	U31556	1.04	1.294	1.099	0.622					Regulation of cell cycle. Regulation of transcription, DNA-dependent.
N/A	N/A	AK128181							1.099	0.597	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
HSPB7	" heat shock 27kDa protein family, member 7 (cardiovascular)	NM_014424	2.295	1.9	1.099	0.923					Protein folding. Response to unfolded protein. Regulation of heart contraction rate.
GAGED2	" G antigen, family D, 2 isoform 1c"	NM_133431					1.099	0.62			
FLJ14494	hypothetical protein FLJ14494	BC014131			1.099	0.882					RNA processing.
FLJ00311	FLJ00311 protein	AK090413					1.099	1.025			Glutathione biosynthesis.
DKFZP434O047	DKFZP434O047 protein	NM_015594	1.295	1.051					1.099	0.422	
AIM1	non-lens beta gamma-crystallin like protein	U83115			1.099	0.871					
PDE4D	cAMP-specific phosphodiesterase 4D	NM_006203			1.098	1.144					Signal transduction. Cyclic nucleotide metabolism.
CTNNB1	" catenin (cadherin-associated protein), beta 1, 88kDa"	NM_001904			1.098	0.594					Transcription. Cell adhesion. Wnt receptor signaling pathway.
PRTFDC1	phosphoribosyl transferase domain containing 1	NM_020200			1.097	0.956					Purine ribonucleoside salvage. Nucleoside metabolism.
N-cym	N/A	S49953							1.097	0.659	Development.
N/A	ESRM828	AY358534	1.085	1.379			1.097	0.819			
N/A	N/A	AK127359			1.097	0.817					Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
MGC4266	hypothetical protein MGC4266	NM_032680			1.097	0.523					
KCNC2	Shaw-related voltage-gated potassium channel protein 2 isofor	NM_139136					1.097	0.825			Cation transport. Potassium ion transport.
CSF3R	colony stimulating factor 3 receptor isoform c precursor	NM_156039							1.097	0.442	Defense response. Cell adhesion. Signal transduction.
TRPC6	" transient receptor potential cation channel, subfamily C, men	NM_004621			1.095	0.703					Cation transport. Calcium ion transport.
NYD-SP18	testes development-related NYD-SP18	NM_032599							1.095	0.752	
N/A	N/A	AK127144					1.095	0.221			
DNMT3L	cytosine-5-methyltransferase 3-like protein isoform 1	NM_013369							1.095	0.381	DNA methylation. Imprinting. Spermatogenesis.
CACNA1G	voltage-dependent calcium channel alpha 1G subunit isoform	NM_198396			1.095	0.493					Cation transport. Calcium ion transport.
N/A	unknown	AF452719			1.094	0.943					
HABP2	hyaluronan binding protein 2	NM_004132			1.094	0.989					Proteolysis and peptidolysis. Cell adhesion.
DKFZp564A026	hypothetical proteincDNA DKFZp564A026 (from clone DKFZp	AL050367					1.094	0.638			
SOSTDC1	cystine knot-containing secreted protein	NM_015464					1.093	0.699			Wnt receptor signaling pathway.
SLC15A3	solute carrier family 15, member 3"	NM_016582							1.093	0.733	Oligopeptide transport.
KIAA2011	KIAA2011 protein	AB095931							1.093	0.632	
GMNN	geminin	NM_015895			1.093	0.461					Negative regulation of DNA replication. Negative regulation of cell cycle.
DKFZp451P134	hypothetical proteincDNA DKFZp451P134 (from clone DKFZp	AL832032					1.093	0.557			
COMMD3	COMM domain containing 3	BC022898			1.093	0.401					Two-component signal transduction system.
AANAT	arylalkylamine N-acetyltransferase	NM_001088							1.093	0.566	Circadian rhythm.
CNR1	central cannabinoid receptor isoform b	NM_033181							1.092	0.697	Signal transduction. G-protein signaling, coupled to cyclic nucleotide second messenger. Behavior.
VTI1A	SNARE Vti1a-beta protein	NM_145206			1.091	0.885					
DKFZp686C07187	hypothetical protein	BX640713							1.091	0.488	Regulation of transcription, DNA-dependent.
CLECSF5	" C-type lectin, superfamily member 5"	NM_013252			1.091	0.636					Cellular defense response. Signal transduction.
CCL28	small inducible cytokine A28 precursor	NM_019846			1.091	0.988					Chemotaxis. Immune response. Sensory perception.
SULT4A1	sulfotransferase family 4A, member 1 isoform b"	NM_176874							1.09	0.594	Lipid metabolism. Steroid metabolism.
OPRK1	opioid receptor, kappa 1"	NM_000912							1.09	0.963	Immune response. Signal transduction. G-protein coupled receptor protein signaling pathway.

MGC33367	hypothetical protein MGC32905	NM_144602							1.09	0.437	
KIAA2036	KIAA2036 protein	AB111888							1.09	0.366	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
FLJ25102	hypothetical protein FLJ25102	NM_182626			1.09	0.443					Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
FLJ10199	FLJ10199 protein	BC005177	1.051	0.772	1.09	1.047					
RERG	" RAS-like, estrogen-regulated, growth inhibitor"	NM_032918			1.089	0.762					Small GTPase mediated signal transduction. Negative regulation of cell proliferation. Response to hormone stimulus.
N/A	N/A	M19734			1.089	1.016					
LOC165186	similar to RIKEN cDNA 4632412N22 gene	NM_199280					1.089	0.498			Mitotic chromosome condensation.
CXCL5	chemokine (C-X-C motif) ligand 5 precursor	NM_002994			1.089	0.853					Chemotaxis. Inflammatory response. Signal transduction. Cell-cell signaling. Positive regulation of cell proliferation.
C9orf127	chromosome 9 open reading frame 127	NM_016446					1.089	0.484			
UBD	diubiquitin	NM_006398							1.088	0.636	Proteolysis and peptidolysis. Ubiquitin cycle. Antimicrobial humoral response.
TLR7	toll-like receptor 7	AF240467			1.088	0.96					Protein amino acid phosphorylation. Signal transduction.
RNF29	ring finger protein 29 isoform 2	NM_033058					1.088	0.921			Signal transduction. Protein ubiquitination.
RASIP1	Ras-interacting protein 1	NM_017805							1.088	0.335	Signal transduction.
N/A	CD24 antigen (small cell lung carcinoma cluster 4 antigen)	BC007674			1.088	0.416					Humoral immune response.
LOC158435	hypothetical protein BC008050	NM_138497							1.088	0.407	
KIAA1760	KIAA1760 protein	AB051547							1.088	0.473	Protein amino acid phosphorylation. Protein kinase cascade.
IKBKE	IKK-related kinase epsilon	NM_014002					1.088	0.651			Protein amino acid phosphorylation. Immune response. Positive regulation of I-kappaB kinase/NF-kappaB cascade.
HNRPK	heterogeneous nuclear ribonucleoprotein K isoform a	NM_002140	1.159	1.519	1.088	1.041					
FOXJ1	forkhead box J1	BC046460							1.088	0.497	Transcription. Regulation of transcription, DNA-dependent. Spermatogenesis.
PTPN7	" protein tyrosine phosphatase, non-receptor type 7 isoform 2"	NM_080588	1.635	1.685					1.087	0.618	Protein amino acid dephosphorylation.
N/A	Unknown (protein for IMAGE:4248887)	BC017893					1.087	0.433			
N/A	N/A	AK128004	1.014	1.096	1.087	0.659					
MGC45922	MGC45922 protein	BC033237							1.087	0.373	
MGC35434	LOC148872 protein	NM_198543					1.087	0.479			
LOC399888	LOC399888 protein	BC065704			1.087	0.664					
IFI30	interferon gamma-inducible protein 30	AF401212							1.087	0.357	
FLJ00325	FLJ00325 protein	AK090417					1.087	0.884			Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
DKFZp586M0622	hypothetical proteincDNA DKFZp586M0622 (from clone DKFZ	AL117396			1.087	0.541					
DKFZp434K028	hypothetical proteincDNA DKFZp434K028 (from clone DKFZp	AL117582			1.087	0.855					
ZBTB2	zinc finger and BTB domain containing 2	NM_020861	1.161	1.019	1.086	0.798					Regulation of transcription, DNA-dependent.
N/A	N/A	AK128308							1.086	0.215	
MTCH1	MTCH1 protein	BC040659			1.086	0.827					Transport. Caspase activation. Regulation of signal transduction. Positive regulation of apoptosis.
KRTHA3B	type I hair keratin 3B	BC009971							1.086	0.476	
CYP1B1	" cytochrome P450, family 1, subfamily B, polypeptide 1"	NM_000104			1.086	0.83					Eye morphogenesis. Electron transport. Visual perception.
N/A	CRB1 isoform III	AY043323			1.085	1.067					Cell adhesion. Establishment and/or maintenance of cell polarity. Cell-cell signaling. Sensory perception. Visual perception.
MCC	MCC	BX537952			1.085	0.943					Cell cycle. Signal transduction. Negative regulation of cell cycle.
FLJ33590	hypothetical protein FLJ33590	NM_173821							1.085	0.434	
COBLL1	COBL-like 1	NM_014900			1.085	1.622					
PTP4A3	protein tyrosine phosphatase type IVA, member 3 isoform 1"	NM_032611							1.084	0.407	Protein amino acid dephosphorylation.
N/A	N/A	AK025111			1.084	0.816					
HYAL1	hyaluronoglucosaminidase 1 isoform 1	NM_007312			1.084	1.188					Carbohydrate metabolism.
ERGIC53	N/A	X71661			1.084	0.485					Protein folding. ER to Golgi transport. Blood coagulation. Protein transport.
DKFZp434I245	hypothetical proteincDNA DKFZp434I245 (from clone DKFZp4	AL833931			1.084	0.929					
SCPEP1	serine carboxypeptidase 1 precursor protein	NM_021626			1.083	0.697					Proteolysis and peptidolysis.
OR56A1	" olfactory receptor, family 56, subfamily A, member 1"	NM_001001917					1.083	0.484			
NEB	nebulin	NM_004543			1.083	1.34					Somatic muscle development. Regulation of actin filament length.
N/A	N/A	AK122631							1.083	0.192	
N/A	HSPC107	AF161370					1.083	0.884			
GAFA3	FGF-2 activity-associated protein 3	AF220235			1.083	0.935					
CYP2E1	cytochrome P450, family 2, subfamily E, polypeptide 1"	NM_000773							1.083	0.628	Electron transport.
N/A	N/A	AK001950			1.082	1.399					Protein transport.
ITGB4	integrin beta 4 isoform 1 precursor	NM_000213							1.082	0.672	Cell-matrix adhesion. Integrin-mediated signaling pathway.
FLJ00041	FLJ00041 protein	AK024449							1.082	0.617	
N/A	N/A	AK054957			1.081	1.258					
FOXN1	winged-helix nude	NM_003593							1.081	0.234	Transcription. Defense response. Development. Epidermis development.
CHRND	nicotinic acetylcholine receptor delta polypeptide precursor	NM_000751							1.081	0.402	Ion transport. Muscle contraction. Signal transduction. Synaptic transmission.

WIG1	p53 target zinc finger protein isoform 1	NM_022470			1.08	0.49					
NRF1	nuclear respiratory factor 1	NM_005011			1.08	1.065					Generation of precursor metabolites and energy. Regulation of transcription, DNA-dependent.
N/A	hypothetical C4orf11 protein variant 2	AY316302			1.08	0.357					
N/A	N/A	AK127224							1.08	0.5	
KCNJ1	potassium inwardly-rectifying channel J1 isoform b	NM_153767					1.08	0.523			Potassium ion transport. Excretion.
FST	follistatin isoform FST317 precursor	NM_006350			1.08	0.639					Development. Negative regulation of follicle-stimulating hormone secretion.
FLJ42102	FLJ42102 protein	NM_001001680							1.08	0.7	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
FLJ23263	hypothetical protein FLJ23263	NM_025115			1.08	0.385					
CRADD	CASP2 and RIPK1 domain containing adaptor with death dom	NM_003805					1.08	1.2			Signal transduction. Induction of apoptosis via death domain receptors. Regulation of apoptosis.
BMI1	B lymphoma Mo-MLV insertion region	NM_005180			1.08	0.823					Regulation of transcription, DNA-dependent. Segment specification. Protein ubiquitination.
PYY2	peptide YY, 2 (seminalplasmin)"	NM_021093							1.079	0.439	
N/A	Unknown (protein for MGC:59785)	BC053319			1.079	0.993					Cell adhesion.
N/A	N/A	AK128416			1.079	0.757					
N/A	N/A	AK027752			1.079	0.561					Protein ubiquitination.
N/A	PRO2219	AF116694			1.079	0.906					Chemotaxis. Sensory perception.
KCNJ13	potassium inwardly-rectifying channel J13	NM_002242	1.042	1.14			1.079	0.817			Potassium ion transport.
RNASE7	ribonuclease 7	NM_032572			1.078	0.56					Defense response to bacteria. Innate immune response.
OR52E5	" olfactory receptor, family 52, subfamily E, member 5"	NM_001005166			1.078	1.232					
NOXO1	NADPH oxidase organizer 1 isoform a	NM_144603							1.078	0.342	Intracellular signaling cascade.
N/A	orphan G-protein coupled receptor Dez isoform a	U79526							1.078	0.683	Skeletal development. Chemotaxis. Immune response. Signal transduction.
N/A	N/A	M35069			1.078	0.614					
N/A	Unknown (protein for IMAGE:4794937)	BC030093			1.078	0.98					Immune response. Synaptic transmission. Central nervous system development. Nerve ensheathment.
KIAA0799	KIAA0799 protein	AB018342			1.078	0.817					Signal transduction.
JAK3	Janus kinase 3	NM_000215							1.078	0.544	Protein amino acid phosphorylation. Intracellular signaling cascade. Mesoderm development.
FLJ45909	FLJ45909 protein	NM_198445			1.078	0.476					Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
DKFZp434O0320	hypothetical proteincDNA DKFZp434O0320 (from clone DKFZ	AL137562			1.078	0.907					
COL11A2	collagen, type XI, alpha 2 isoform 1 preproprotein"	NM_080680							1.078	0.66	Skeletal development. Phosphate transport. Cell adhesion. Perception of sound. Collagen fibril organization.
CD53	CD53 antigen	NM_000560							1.078	0.661	Signal transduction. Antimicrobial humoral response.
BMP4	bone morphogenetic protein 4 preproprotein	NM_001202			1.078	0.626					Skeletal development. Mesoderm development. Cell differentiation.
RTN4RL1	reticulon 4 receptor-like 1	NM_178568							1.077	0.343	
RPA2	" replication protein A2, 32kDa"	NM_002946			1.077	0.344					DNA-dependent DNA replication.
N/A	Unknown (protein for MGC:75009)	BC063390							1.077	0.692	
MGC42630	hypothetical protein MGC42630	NM_175923							1.077	0.19	
FLJ10970	hypothetical protein FLJ10970	NM_018286			1.077	0.406					
DKFZp434E1512	hypothetical proteincDNA DKFZp434E1512 (from clone DKFZ	AL157437			1.077	0.572					Protein modification.
C9orf48	chromosome 9 open reading frame 48	NM_194313	1.268	1.656			1.077	1.326			
SERPINB13	" serine (or cysteine) proteinase inhibitor, clade B (ovalbumin),	NM_012397	1.224	1.466	1.076	0.757					Response to UV. Regulation of proteolysis and peptidolysis.
PCDHB10	protocadherin beta 10 precursor	NM_018930							1.076	0.685	Cell adhesion. Homophilic cell adhesion. Synaptic transmission. Synaptogenesis. Calcium-dependent cell-cell adhesion.
N/A	N/A	AK128227							1.076	0.598	
N/A	caspase recruitment domain protein 12	AF376061					1.076	0.655			
N/A	Nck-associated protein NAP5	AB005217					1.076	0.939			
MAGEB1	" melanoma antigen, family B, 1"	NM_002363					1.075	0.67			
HNRNPG-T	testes-specific heterogenous nuclear ribonucleoprotein G-T	BC057796			1.075	0.428					
GDI2	GDP dissociation inhibitor 2	NM_001494			1.075	0.777					Protein transport. Regulation of GTPase activity.
FLJ12684	FLJ12684 protein	BC067527							1.075	0.297	
ZNF219	zinc finger protein 219	NM_016423			1.074	0.783					Regulation of transcription, DNA-dependent.
N/A	Unknown (protein for MGC:33652)	BC021741			1.074	0.738					
DKFZp686K2089	hypothetical proteincDNA DKFZp686K2089 (from clone DKFZ	BX537524			1.074	0.863					
DKFZp566K0524	hypothetical protein	AL050040							1.074	0.367	Protein amino acid dephosphorylation.
SLC1A1	" solute carrier family 1, member 1"	NM_004170	1.074	1.064	1.073	0.499					Transport. Dicarboxylic acid transport. Synaptic transmission. L-glutamate transport.
OR10J5	" olfactory receptor, family 10, subfamily J, member 5"	NM_001004469			1.073	1.059					
N/A	N/A	AK130204							1.073	0.219	
MGC16028	MGC16028 similar to RIKEN cDNA 1700019E19 gene	NM_052873			1.073	1.07					
LOC346673	STRA8	NM_182489			1.073	1.116					
CLCA2	calcium activated chloride channel 2	NM_006536			1.073	0.641					Transport. Chloride transport.
ABI3	NESH protein	NM_016428							1.073	0.775	Cell motility.

N/A	N/A	AK126977							1.072	0.404	
FLJ45422	FLJ45422 protein	NM_001004349			1.072	0.935					Antigen presentation. Antigen presentation, endogenous antigen.
FLJ43860	FLJ43860 protein	NM_207414							1.072	0.657	
CSAG1	chondrosarcoma associated gene 1 isoform a	NM_153478							1.072	0.823	Response to drug.
CCL19	small inducible cytokine A19 precursor	NM_006274							1.072	0.486	Calcium ion homeostasis. Chemotaxis. Inflammatory response. Signal transduction. Sensory perception.
AFAP	actin filament associated protein	NM_021638			1.072	1.03					
TACSTD1	tumor-associated calcium signal transducer 1 precursor	NM_002354			1.071	0.65					
N/A	N/A	AK097971							1.071	0.33	Positive regulation of cytokine production. Inflammatory response. Cell surface receptor linked signal transduction.
N/A	PNAS-119	AF277177			1.071	1.058					
MS4A2	" membrane-spanning 4-domains, subfamily A, member 2" " b	NM_000139	1.123	1.379			1.071	1.123			Humoral immune response. Signal transduction. G-protein coupled receptor protein signaling pathway. Cell proliferation.
KRTAP10-4	keratin associated protein 10-4	NM_198687	1.298	1.52					1.071	0.44	
UNQ827	KFLL827	NM_207469			1.07	0.874					Defense response to bacteria.
LOC284739	hypothetical protein LOC284739	NM_207349							1.07	0.42	
TMOD1	tropomodulin 1	NM_003275					1.069	0.485			Cytoskeleton organization and biogenesis.
TCP10L	T-complex 10A-2	NM_144659							1.069	0.664	
MGC33894	transcript expressed during hematopoiesis 2	NM_152914			1.069	1.042					
FKBP9L	similar to FK506 binding protein 9	NM_182827							1.069	0.288	Protein folding.
EBI2	EBV-induced G protein-coupled receptor 2	NM_004951	1.187	0.848			1.069	0.782			Immune response. Signal transduction. G-protein coupled receptor protein signaling pathway.
DSG4	desmoglein 4	NM_177986			1.069	0.801					
DAB2IP	DAB2 interacting protein	NM_032552			1.069	0.557					
CLDN20	claudin 20	NM_001001346			1.069	1.328					
SH2D4A	SH2 domain containing 4A	NM_022071			1.068	0.765					Intracellular signaling cascade.
N/A	PINK1	AY358957			1.068	0.648					Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
MGC40069	hypothetical protein MGC40069	NM_182615					1.068	0.518			
LOC375449	similar to microtubule associated testis specific serine/threonin	NM_198828							1.068	0.645	
LOC255177	LOC255177 protein	BC031230			1.068	0.392					
MGC8685	tubulin, beta polypeptide paralog"	NM_178012							1.067	0.362	Microtubule-based movement. Protein polymerization.
LOC285682	LOC285682 protein	BC027302							1.067	0.381	
PRPS2	phosphoribosyl pyrophosphate synthetase 2	NM_002765			1.066	0.851					Nucleoside metabolism. Ribonucleoside monophosphate biosynthesis.
N/A	albumin	X51365			1.066	0.812					
pp9964	unknown	AF318381					1.065	0.575			
OR4F5	" olfactory receptor, family 4, subfamily F, member 5"	NM_001005484			1.065	0.89					
FLJ00265	FLJ00265 protein	AK122581			1.065	0.912					
CGI-07	CGI-07 protein	NM_015938			1.065	1.124					
RCV1	recoverin	NM_002903			1.064	0.509					Signal transduction. Sensory perception. Visual perception.
N/A	G2	U10991					1.064	1.028			
N/A	brain my050 protein	AF063608							1.064	0.328	Electron transport. Microtubule-based movement. Synaptic transmission.
MCM5	minichromosome maintenance deficient protein 5	NM_006739			1.064	0.731					Regulation of cell cycle. DNA replication. DNA replication initiation. Transcription.
LMOD3	leiomodin 3 (fetal)	NM_198271			1.064	0.689					Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
DEFB105	" defensin, beta 105"	NM_152250					1.064	0.36			
N/A	N/A	BC008814					1.063	0.379			
N/A	RVLA1944	AY358202							1.063	0.686	
N/A	N/A	AK096928			1.063	0.55					
MTMR9	myotubularin-related protein 9	NM_015458					1.063	0.876			Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
LST001	SLTP001	AF111704			1.063	0.794					
KIAA0386	N/A	AB002384			1.063	0.794					
GAL3ST3	galactose-3-O-sulfotransferase 3	NM_033036							1.063	0.515	Monosaccharide metabolism. Sulfur metabolism. Biosynthesis. Oligosaccharide metabolism.
FLJ46481	FLJ46481 protein	NM_207405							1.063	0.715	
N/A	N/A	AK000159			1.062	0.628					
LOC388906	LOC388906 protein	BC039496					1.062	0.802			
KIAA0894	KIAA0894 protein	AB020701			1.062	0.614					Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
ASB18	ankyrin repeat and SOCS box-containing 18	NM_212556			1.062	0.529					
TULP1	tubby related protein 1 TULP1	U82468							1.061	0.453	Sensory perception. Visual perception.
sycl	syntenin	AF000652			1.061	0.762					Protein-membrane targeting. Substrate-bound cell migration, cell extension. Intracellular signaling cascade.
LOC284367	LOC284367 protein	BC050999							1.061	0.676	
KLK9	kallikrein 9	NM_012315							1.061	0.526	Proteolysis and peptidolysis.

FLJ40113	FLJ40113 protein	NM_198079							1.061	0.438	
AMOTL2	angiomotin like 2	NM_016201			1.061	0.639					
OR1G1	olfactory receptor, family 1, subfamily G, member 1"	NM_003555							1.06	0.625	Signal transduction. G-protein coupled receptor protein signaling pathway. Perception of smell.
N/A	N/A	AK125175			1.06	1.151					
MGC13159	hypothetical protein MGC13159	NM_032927					1.06	0.842			
BCORL2	BCL6 co-repressor-like 2	NM_173700							1.06	0.464	
BCL9	B-cell CLL/lymphoma 9	NM_004326			1.06	0.592					Wnt receptor signaling pathway.
ZNF452	zinc finger protein 452	NM_052923							1.059	0.575	DNA recombination. Regulation of transcription, DNA-dependent.
SFMBT1	Scm-like with four mbt domains 1	NM_001005159			1.059	0.711					Regulation of transcription, DNA-dependent. Regulation of transcription.
NYX	nyctalopin	NM_022567					1.059	0.525			Sensory perception. Visual perception.
N/A	N/A	AK130490							1.059	0.407	
N/A	N/A	AK126123							1.059	0.637	
N/A	N/A	AK096466			1.059	1.355					
N/A	cystatin 9	AF494536							1.059	0.558	
HT008	uncharacterized hypothalamus protein HT008	NM_018469			1.059	0.415					Phosphoenolpyruvate-dependent sugar phosphotransferase system.
FSHPRH1	follicle-stimulating hormone primary response protein 1	NM_006733							1.059		Spermatogenesis. Female gamete generation. Sex differentiation.
CNP	" 2',3'-cyclic nucleotide 3' phosphodiesterase"	NM_033133			1.059	0.592					Synaptic transmission. Cyclic nucleotide catabolism.
ANXA9	annexin A9	NM_003568			1.059	0.627					Actin filament organization. Cell-cell adhesion.
SCOC	short coiled-coil protein	NM_032547			1.058	0.823					
N/A	N/A	AK094114			1.058	0.502					
UNQ830	ASCL830	NM_206895			1.057	0.955					
TAFA3	TAFA3 protein isoform 2	NM_001004440							1.057	0.76	
N/A	N/A	AK094480			1.057	1.517					
CORO2A	coronin, actin binding protein, 2A"	NM_003389							1.057	0.407	Glutamine biosynthesis. Nitrogen compound metabolism. Intracellular signaling cascade.
AIPL1	aryl hydrocarbon receptor interacting protein-like 1	NM_014336			1.057	0.749					Protein folding. Sensory perception. Visual perception.
N/A	N/A	AK025278					1.056	0.987			
N/A	unknown	AF119045							1.056	0.603	Protein amino acid dephosphorylation.
NCAM1	NCAM1 protein	BC014205							1.054	0.837	Cell adhesion. Cell-cell signaling. Synaptic transmission.
FGG	fibrinogen, gamma chain isoform gamma-B precursor"	NM_021870							1.054	0.761	Angiogenesis. Signal transduction. Regulation of blood pressure. Positive regulation of cell proliferation. Platelet activation.
CYP2F1	cytochrome P450, family 2, subfamily F, polypeptide 1"	NM_000774							1.054	0.655	Electron transport.
AARSL	alanyl-tRNA synthetase like	NM_020745			1.054	0.705					Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
TMEM2	transmembrane protein 2	NM_013390			1.053	0.623					
SLC7A7	" solute carrier family 7 (cationic amino acid transporter, y+ sy	NM_003982			1.053	1.085					Protein complex assembly. Amino acid metabolism. Amino acid transport.
PITX1	paired-like homeodomain transcription factor 1	NM_002653					1.053	0.695			Skeletal development. Regulation of transcription, DNA-dependent. Morphogenesis.
PDE4A	phosphodiesterase 4A, cAMP-specific (phosphodiesterase E2	NM_006202							1.053	0.633	Signal transduction. Signal transduction. Cyclic nucleotide metabolism.
NONO	" non-POU domain containing, octamer-binding"	NM_007363					1.053	0.753			mRNA processing. RNA splicing.
NNT	nicotinamide nucleotide transhydrogenase	NM_012343					1.053	0.462			Electron transport. Proton transport.
FLJ11078	hypothetical protein FLJ11078	NM_018316							1.053	0.64	
ACY3	aspartoacylase (aminocyclase) 3	NM_080658	2.419	1.113	1.053	0.461					Metabolism.
RLBP1	retinaldehyde binding protein 1	NM_000326							1.052	0.769	Vitamin A metabolism. Transport. Sensory perception. Visual perception.
NAG	neuroblastoma-amplified protein	NM_015909			1.052	1.008					
N/A	N/A	AK056288					1.052	0.504			
N/A	N/A	AK023691					1.052	1.156			Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism. Metabolism.
LETMD1	cervical cancer 1 protooncogene protein p40	NM_015416			1.052	0.534					
ITIH1	inter-alpha (globulin) inhibitor H1	NM_002215							1.052	0.269	Hyaluronan metabolism. Immune cell activation.
FAM40A	" family with sequence similarity 40, member A"	NM_033088			1.052	0.754					
IGFBP3	insulin-like growth factor binding protein 3	NM_000598			1.051	0.534					Regulation of cell growth. Positive regulation of myoblast differentiation.
NEU4	sialidase 4	BC012899	1.361	0.783					1.05	0.451	Carbohydrate metabolism.
N/A	SR rich protein	AF314185			1.05	1.037					
LOC163782	hypothetical protein LOC163782	NM_181712							1.05	0.444	
FLJ45537	FLJ45537 protein	NM_001001709			1.05	0.414					
DC-UbP	dendritic cell-derived ubiquitin-like protein	NM_152277					1.05	0.446			Protein modification.
USP26	ubiquitin-specific protease 26	NM_031907			1.049	1.005					Ubiquitin-dependent protein catabolism. Ubiquitin cycle.
SCUBE2	CEGP1 protein	NM_020974					1.049	0.823			
SALL1	sal-like 1	NM_002968	1.164	1.144	1.049	0.455					Transcription. Regulation of transcription, DNA-dependent. Morphogenesis.
RNASEL	ribonuclease L	NM_021133			1.049	0.922					mRNA processing. Protein amino acid phosphorylation.

N/A	N/A	AK025871							1.049	0.918	
N/A	OVN6-2	AF230200					1.049	1.057			Regulation of transcription, DNA-dependent. Negative regulation of transcription.
HZF8	zinc finger protein	X78931			1.049	0.746					Regulation of transcription, DNA-dependent.
ARL5	ADP-ribosylation factor-like 5 isoform 1	NM_012097			1.049	0.565					Intracellular protein transport. Small GTPase mediated signal transduction.
ANXA7	annexin VII isoform 2	NM_004034	1.027	1.506			1.049	0.984			Negative regulation of coagulation.
SNX10	sorting nexin 10	NM_013322							1.048	0.434	Intracellular signaling cascade. Protein transport.
PIGA	phosphatidylinositol N-acetylglucosaminyltransferase subunit A	NM_002641			1.048	1.249					Biosynthesis.
N/A	N/A	AK126791					1.048				
LOC253827	hypothetical protein LOC253827	NM_198080					1.048	0.913			Protein repair.
KIAA0867	KIAA0867 protein	AB020674			1.048	0.757					
HK1	hexokinase 1 isoform HKI-td	NM_033500					1.048	0.709			Glycolysis.
FLJ37183	FLJ37183 protein	NM_198466							1.048	0.463	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
FLJ00017	FLJ00017 protein	AK024428			1.048	0.573					
N/A	Unknown (protein for MGC:71807)	BC063312	1.081	1.175	1.047	0.729					
N/A	Unknown (protein for MGC:47828)	BC039725			1.047	0.682					
N/A	N/A	AK127460							1.047	0.191	
N/A	N/A	AK125754							1.047	0.529	
N/A	N/A	AK096702	1.319	1.392	1.047	1.07					Regulation of transcription, DNA-dependent.
N/A	N/A	AK075415					1.047	0.39			Biosynthesis. Coenzyme A biosynthesis.
F379	hypothetical protein	AF346307			1.047	0.252					
CLDN7	claudin 7	NM_001307							1.047	0.37	Calcium-independent cell-cell adhesion.
CD5L	CD5 antigen-like (scavenger receptor cysteine rich family)	NM_005894			1.047	1.271					Apoptosis. Cellular defense response.
C1QL1	" complement component 1, q subcomponent-like 1"	NM_006688			1.047	0.531					Phosphate transport. Locomotory behavior.
ZAP70	zeta-chain associated protein kinase 70kDa isoform 1	NM_001079			1.046	0.378					Protein amino acid phosphorylation. Immune response. Protein kinase cascade.
N/A	EPA6	AY358738							1.046	0.426	
N/A	N/A	AK074645			1.046	1.168					Lipid transport. Lipid transport. Lipoprotein metabolism.
MGC29671	hypothetical protein MGC29671	NM_182538							1.046	0.377	Transport.
KCNMB2	large conductance calcium-activated potassium channel beta2	AF209747	1.124	0.836			1.046	0.578			Regulation of action potential. Calcium ion sensing. Potassium ion transport. Smooth muscle contraction.
BCAS1	breast carcinoma amplified sequence 1	NM_003657			1.046	0.879					
SLPI	secretory leukocyte protease inhibitor precursor	NM_003064							1.045	0.356	
NDST4	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 4	NM_022569					1.045	0.407			
MBD6	methyl-CpG binding domain protein 6	NM_052897			1.045	1.222					
LOC144233	hypothetical protein LOC144233	NM_181708					1.045	0.68			
KIAA1866	KIAA1866 protein	AB058769							1.045	1.026	
GPR58	G protein-coupled receptor 58	NM_014626							1.045	0.701	Signal transduction. G-protein coupled receptor protein signaling pathway.
COG2	component of oligomeric golgi complex 2	BC014960							1.045	0.73	Protein amino acid glycosylation. Intracellular protein transport. Intra-Golgi transport. Golgi organization and biogenesis.
ASTN2	astrotactin 2 isoform c	NM_198187							1.045	0.486	
ZNF179	zinc finger protein 179	BC053989			1.044	0.598					Immune response. Protein ubiquitination.
UBH1	ubiquitin hydrolyzing enzyme 1	AF022793					1.044	0.348			
OR1L8	olfactory receptor, family 1, subfamily L, member 8"	NM_001004454							1.044	0.881	
KIAA1145	KIAA1145 protein	NM_020698			1.044	0.366					
K6HF	cytokeratin type II	NM_004693							1.044	0.429	
FLJ00394	FLJ00394 protein	AK090473					1.044	1.259			
CNR1	central cannabinoid receptor isoform a	NM_016083							1.044	0.844	Signal transduction. G-protein signaling, coupled to cyclic nucleotide second messenger. Behavior.
TNFRSF11B	osteoprotegerin precursor	NM_002546			1.043	1.02					Skeletal development. Apoptosis. Signal transduction.
TAF9L	TBP-associated factor 9L	NM_015975			1.043	0.98					Transcription initiation. Regulation of transcription, DNA-dependent.
SPR	" sepiapterin reductase (7,8-dihydrobiopterin:NADP+ oxidored	NM_003124					1.043	0.783			Tetrahydrobiopterin biosynthesis. Metabolism.
OR2A12	" olfactory receptor, family 2, subfamily A, member 12"	NM_001004135			1.043	1.197					
MGC4734	hypothetical protein MGC4734	NM_145051							1.043	0.465	Protein ubiquitination.
FLJ00247	FLJ00247 protein	AK074174			1.043	0.968					Development.
VPREB1	immunoglobulin iota chain preproprotein	NM_007128			1.042	0.717					Immune response.
SGK2	serum/glucocorticoid regulated kinase 2 isoform beta	NM_016276			1.042	0.683					Protein amino acid phosphorylation. Response to oxidative stress. Protein kinase cascade.
PRRX2	paired related homeobox 2	NM_016307			1.042	0.477					Regulation of transcription, DNA-dependent. Development.
OR7A17	" olfactory receptor, family 7, subfamily A, member 17"	NM_030901			1.042	1.277					Signal transduction. G-protein coupled receptor protein signaling pathway. Perception of smell.
N/A	N/A	AK125236							1.042	0.446	Regulation of muscle contraction. Muscle development. Regulation of heart contraction rate.
IFNA6	" interferon, alpha 6"	NM_021002			1.042	1.034					Defense response. Response to virus.

CRISP1	acidic epididymal glycoprotein-like 1 isoform 1 precursor	NM_001131	1.02	1.119	1.042	0.969					Spermatogenesis. Fusion of sperm to egg plasma membrane.
CAMK2G	calcium/calmodulin-dependent protein kinase II gamma isoforn	NM_172171			1.042	0.566					Protein amino acid phosphorylation. Signal transduction. Insulin secretion.
N/A	Unknown	AF131852	1.285	0.817	1.041	0.616					
MARLIN1	multiple coiled-coil GABABR1-binding protein	NM_144720							1.041	0.909	
ITGAX	integrin alpha X precursor	NM_000887					1.041	0.786			Cell-matrix adhesion. Integrin-mediated signaling pathway. Organogenesis.
IL22RA2	interleukin 22-binding protein isoform 1	NM_052962			1.041	0.292					
ST7	suppression of tumorigenicity 7 isoform b	NM_021908			1.04	1.585					
RAB6C	" RAB6C, member RAS oncogene family"	NM_032144					1.04	0.498			Small GTPase mediated signal transduction. Protein transport. Small GTPase mediated signal transduction. Response to drug.
OR9Q1	" olfactory receptor, family 9, subfamily Q, member 1"	NM_001005212					1.04	0.972			
N/A	N/A	AK124538							1.04	0.437	
GPR82	G protein-coupled receptor 82	NM_080817	1.201	1.184			1.04	0.973			
CROCC	" ciliary rootlet coiled-coil, rootletin"	NM_014675	3.123	0.665	1.04	0.424					
PRDX4	thioredoxin peroxidase	BC016770					1.039	0.616			I-kappaB phosphorylation.
N/A	N/A	AK126061							1.039	0.248	
KCNG3	" potassium voltage-gated channel, subfamily G, member 3 is	NM_133329					1.039	0.747			
HAAO	3-hydroxyanthranilate 3,4-dioxygenase"	NM_012205							1.039	0.512	Metabolism.
GSTA2	glutathione S-transferase A2	NM_000846							1.039	0.503	Metabolism.
ENPP6	ectonucleotide pyrophosphatase/phosphodiesterase 6	NM_153343							1.039	0.319	Nucleotide metabolism.
SSX3	" synovial sarcoma, X breakpoint 3 isoform a"	NM_021014			1.038	0.365					Transcription. Regulation of transcription, DNA-dependent.
SHBG	sex hormone-binding globulin	NM_001040			1.038	0.509					Hormone transport.
N/A	N/A	M94046			1.038	0.89					Transcription. Regulation of transcription, DNA-dependent.
MGC71735	MGC71735 protein	BC059396							1.038	0.392	Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
LOC51249	LOC51249 protein	BC013608			1.038	1.446					
FLJ32312	hypothetical protein FLJ32312	NM_144709					1.038	0.746			
DKFZp547B028	hypothetical proteincDNA DKFZp547B028 (from clone DKFZp	AL831887			1.038	1.173					
SCTR	secretin receptor precursor	NM_002980							1.037	0.374	Signal transduction. G-protein coupled receptor protein signaling pathway. Digestion. Excretion.
PLXDC1	plexin domain containing 1 precursor	NM_020405			1.037	0.901					Angiogenesis. Development.
N/A	Unknown (protein for MGC:35221)	BC029877			1.037	0.652					
MYBPC1	myosin binding protein C, slow type isoform 1"	NM_002465							1.037	0.59	Striated muscle contraction. Cell adhesion. Muscle development.
KCNMB1	KCNMB1 protein	BC025707			1.037	0.451					
HCFC1R1	host cell factor C1 regulator 1 (XPO1 dependant) isoform 1	NM_017885			1.037	0.384					
FRMD3	FERM domain containing 3	NM_174938							1.037	0.498	Metabolism.
SLC29A2	solute carrier family 29 (nucleoside transporters), member 2"	NM_001532							1.036	0.613	Nucleobase, nucleoside, nucleotide and nucleic acid metabolism. Transport. Cell proliferation. Nucleoside transport.
N/A	N/A	AK127642							1.036	0.741	
CCL23	small inducible cytokine A23 isoform CKbeta8-1 precursor	NM_005064							1.036	0.341	Calcium ion homeostasis. Chemotaxis. Inflammatory response. Signal transduction.
CAMK4	calcium/calmodulin-dependent protein kinase IV	NM_001744			1.036	0.724					Protein amino acid phosphorylation. Signal transduction.
WARP	von Willebrand factor A domain-related protein isoform 1	NM_022834			1.035	0.917					
ROCK2	" Rho-associated, coiled-coil containing protein kinase 2"	NM_004850			1.035	0.675					Cytokinesis. Protein amino acid phosphorylation. Muscle contraction.
N/A	N/A	AK126656			1.035	1.065					
N/A	N/A	AK126320	1.072	0.702			1.035	1.071			
LOC374676	similar to golgi autoantigen, golgin subfamily a, 2 Homo sapien	BC041854							1.035	0.506	
EIF2AK3	eukaryotic translation initiation factor 2-alpha kinase 3	NM_004836			1.035	0.365					Translational initiation. Regulation of translation. Protein amino acid phosphorylation.
COL15A1	alpha 1 type XV collagen precursor	NM_001855			1.035	0.406					Phosphate transport. Cell adhesion. Cell adhesion.
N/A	N/A	AK096849			1.034	0.806					
GPR35	G protein-coupled receptor 35	NM_005301							1.034	0.439	Signal transduction. G-protein coupled receptor protein signaling pathway.
DKFZp686I18166	hypothetical proteincDNA DKFZp686I18166 (from clone DKFZ	BX641032			1.034	0.882					
CES4	carboxylesterase 4-like	NM_016280							1.034	0.365	Xenobiotic metabolism. Morphogenesis.
SATL1	SATL1 protein	BC043215							1.033	0.678	
N/A	N/A	AK092641			1.033	0.977					Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
N/A	hepatocellular carcinoma-associated antigen HCA108	AF447583							1.033	0.768	Regulation of transcription, DNA-dependent.
CBLN1	cerebellin	NM_004352							1.033	0.452	Synaptic transmission. Neurogenesis.
TCAM-1	testicular cell adhesion molecule 1	AB026156			1.032	1.205					
SSBP1	SSBP1 protein	BC008402					1.032	0.451			DNA replication.
BPIL3	bactericidal/permeability-increasing protein-like 3	NM_174897							1.032	0.43	
YPEL4	YPEL4 protein	BC029228					1.031	0.949			
RPS26	ribosomal protein S26	BC002604					1.031	0.551			Protein biosynthesis.

NGB	neuroglobin	NM_021257							1.031	0.307	Transport. Oxygen transport.
N/A	N/A	AK023679			1.031	0.632					
MIDORI	KIAA1330 protein	NM_020778			1.031	0.57					Protein amino acid phosphorylation. Heart development.
LOC399851	hypothetical gene supported by AY129010	NM_207427							1.031	1.286	
LOC388650	hypothetical LOC388650	NM_001006605			1.031	1.252					
HRASLS2	HRAS-like suppressor 2	NM_017878							1.031	0.973	
FLJ23311	FLJ23311 protein	NM_024680			1.031	0.781					Regulation of cell cycle. Regulation of transcription, DNA-dependent.
APEH	N-acylaminoacyl-peptide hydrolase	NM_001640			1.031	0.636					Proteolysis and peptidolysis.
TDRD5	tudor domain containing 5	NM_173533							1.03	0.431	
SAMD11	SAMD11 protein	BC024295							1.03	0.54	
PEMT	phosphatidylethanolamine N-methyltransferase isoform 2	NM_007169					1.03	0.391			Lipid metabolism. Phospholipid metabolism. Phosphatidylcholine biosynthesis. Cell proliferation.
OR10V1	" olfactory receptor, family 10, subfamily V, member 1"	NM_001005324			1.03	0.959					
MOBP	myelin-associated oligodendrocyte basic protein	NM_182935			1.03	0.479					Neurogenesis.
KRTAP17-1	keratin associated protein 17-1	NM_031964							1.03	0.182	
KIAA1639	KIAA1639 protein	AB046859							1.03	0.479	Protein amino acid phosphorylation.
KIAA0264	N/A	D87453					1.03	0.677			
NFATC1	" nuclear factor of activated T-cells, cytosolic component 1 iso	NM_006162			1.029	0.427					Regulation of transcription, DNA-dependent.
KIAA1502	KIAA1502 protein	AB040935							1.029	0.248	
DRD2	dopamine receptor D2 isoform long	NM_000795							1.029	0.662	Signal transduction. Dopamine receptor, adenylate cyclase inhibiting pathway. Synaptic transmission. Neurogenesis.
SLC38A5	amino acid transport system N2	NM_033518					1.028	0.537			Amino acid transport.
PARP14	" poly (ADP-ribose) polymerase family, member 14"	NM_017554					1.028	0.961			Protein amino acid ADP-ribosylation.
NR3C2	" nuclear receptor subfamily 3, group C, member 2"	NM_000901			1.028	0.494					Transcription. Regulation of transcription, DNA-dependent. Sodium ion homeostasis. Signal transduction. Excretion.
N/A	N/A	AK057427			1.028	0.392					
N/A	N/A	AK027333							1.028	0.554	Protein amino acid dephosphorylation.
N/A	N/A	AK000838			1.028	0.953					
LOC84643	kinesin protein	NM_032559			1.028	0.632					Microtubule-based movement.
LOC339457	hypothetical protein LOC339457	NM_001003808							1.028	0.387	
KIAA1087	KIAA1087 protein	AB029010							1.028	0.268	Sodium ion transport. Calcium ion transport. Cell communication.
KCNS1	potassium voltage-gated channel delayed-rectifier protein S1	NM_002251					1.028	0.467			Cation transport. Potassium ion transport.
NTN2L	netrin 2-like	NM_006181							1.027	0.558	Axon guidance.
N/A	G protein-coupled receptor PGR23	AY255611							1.027	0.482	
N/A	N/A	AK097510			1.027	0.988					
N/A	PRO2613	AF119888			1.027	0.982					
N/A	PRO1873	AF119859					1.027	0.532			
IFRG28	28kD interferon responsive protein	NM_022147			1.027	0.417					
H2AFJ	" H2A histone family, member J isoform 1"	NM_018267			1.027	0.449					Nucleosome assembly. Chromosome organization and biogenesis.
ELK4	ELK4 protein isoform b	NM_021795			1.027	0.779					Regulation of transcription, DNA-dependent.
BCGF1	B-cell growth factor	M15530			1.027	0.704					Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
ZDHHC11	zinc finger, DHHC domain containing 11"	NM_024786							1.026	0.533	
UNQ3045	AAAL3045	NM_207409							1.026	0.585	
OKL38	pregnancy-induced growth inhibitor	NM_013370							1.026	0.463	Cell differentiation. Negative regulation of cell growth.
N/A	N/A	M13150					1.026	0.624			Signal transduction. G-protein coupled receptor protein signaling pathway. Cell proliferation. Morphogenesis.
N/A	N/A	AK128159			1.026	1.005					
MUC	mucin	AF015521			1.026	0.687					
KIAA1246	KIAA1246 protein	AB033072			1.026	0.422					
FLJ45224	FLJ45224 protein	NM_207510							1.026	0.544	
FLJ10569	hypothetical protein FLJ10569	NM_018142			1.026	0.617					
COL21A1	alpha 1 type XXI collagen precursor	NM_030820					1.026	0.458			Phosphate transport. Cell adhesion.
TLR5	toll-like receptor 5	NM_003268			1.025	0.605					Inflammatory response.
SPAG4L	sperm associated antigen 4-like	NM_080675			1.025	0.576					Spermatogenesis.
N/A	N/A	AK097772					1.025	0.601			
KIAA1234	KIAA1234 protein	AB033060	2.184	1.696					1.025	0.434	Apoptosis. Induction of apoptosis by extracellular signals. Regulation of transcription, DNA-dependent. Signal transduction.
DKFZp761P0212	hypothetical protein	AL162045							1.025	0.314	
ABCB6	" ATP-binding cassette, sub-family B, member 6"	NM_005689			1.025	0.606					Transport. Iron ion homeostasis.
YBX2	germ cell specific Y-box binding protein	NM_015982			1.024	0.551					
TAGAP	T-cell activation Rho GTPase-activating protein isoform b	NM_054114			1.024	0.516					

SPACA4	sperm acrosomal membrane protein 14	NM_133498			1.024	0.222					
RHBDF1	rhomboid family 1	NM_022450					1.024	0.922			
PTGS1	prostaglandin-endoperoxide synthase 1 isoform 1 precursor	NM_000962			1.024	0.746					Prostaglandin biosynthesis. Lipid metabolism. Fatty acid biosynthesis. Physiological process.
N/A	GLPG464	AY358510			1.024	0.831					
MMP2	matrix metalloproteinase 2 preproprotein	NM_004530			1.024	0.525					Collagen catabolism.
FLJ00370	FLJ00370 protein	AK090449			1.024	0.545					
OR7G2	" olfactory receptor, family 7, subfamily G, member 2"	NM_001005193	1.293	1.206	1.023	1.237					
N/A	N/A	AK128261							1.023	0.393	
AMBP	alpha-1-microglobulin/bikunin precursor	NM_001633							1.023	0.414	Transport. Cell adhesion. Pregnancy. Anti-inflammatory response. Heme catabolism.
TAF2	TBP-associated factor 2	NM_003184					1.022	0.4			Transcription initiation from RNA polymerase II promoter.
OR8S1	olfactory receptor, family 8, subfamily S, member 1"	NM_001005203							1.022	0.67	
N/A	N/Adynactin light chain.	AK091661			1.022	0.704					Protein amino acid phosphorylation. Signal transduction. Intracellular signaling cascade.
N/A	N/A	AK091044							1.022	0.317	
N/A	N/A	AK058065					1.022	1.213			
KLK13	kallikrein 13 precursor	NM_015596			1.022	0.501					Proteolysis and peptidolysis. Proteolysis and peptidolysis.
IL17D	interleukin 17D precursor	NM_138284			1.022	0.49					Inflammatory response.
FLJ31265	hypothetical protein FLJ31265	NM_152395			1.022	1.185					
C7orf13	chromosome 7 open reading frame 13	NM_032625			1.022	0.996					Metal ion transport.
C20orf42	chromosome 20 open reading frame 42	NM_017671			1.022	0.758					
PDE6B	phosphodiesterase 6B, cGMP-specific, rod, beta"	NM_000283							1.021	0.412	Signal transduction. Sensory perception. Visual perception. Phototransduction, visible light.
OSBPL5	oxysterol-binding protein-like protein 5 isoform a	NM_020896			1.021	0.467					Lipid transport. Golgi to plasma membrane transport. Steroid metabolism. Cholesterol metabolism.
N/A	N/AcDNA DKFZp451H072 (from clone DKFZp451H072).	AL831967					1.021	0.769			
N/A	PRO1722	AF119851			1.021	1.02					
DKFZp547C1010	hypothetical protein	AL831941							1.021	0.586	
SFRP1	SFRP1 protein	BC036503			1.02	0.485					Wnt receptor signaling pathway. Cell differentiation.
MGC4268	hypothetical protein MGC4268	NM_031445			1.02	0.436					
CHURC1	churchill domain containing 1	NM_145165			1.02	0.817					Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
SCN7A	" sodium channel, voltage-gated, type VII, alpha"	NM_002976					1.019	1.072			Cation transport. Sodium ion transport. Muscle contraction.
N/A	Unknown (protein for MGC:17708)	BC008667					1.019	0.658			Coenzyme A biosynthesis.
GNGT2	guanine nucleotide binding protein-gamma transducing activity	NM_031498							1.019	0.852	Signal transduction. G-protein coupled receptor protein signaling pathway. Phototransduction.
DEFB28	beta-defensin 28 precursor	AF525930			1.019	0.812					
bA9F11.1	hypothetical LOC255349	NM_001001663					1.019	0.379			
TNR-CFTR	N/A	S82430			1.018	0.509					
MTA1	metastasis associated protein	NM_004689			1.018	0.5					Regulation of transcription, DNA-dependent. Signal transduction.
LGALS7	galectin 7	BC061588			1.018	0.661					Apoptosis. Heterophilic cell adhesion.
KIAA0598	KIAA0598 protein	AB011170							1.018	0.501	Regulation of DNA recombination. Hexose biosynthesis. Hexose biosynthesis. Regulation of B-cell differentiation.
HS3ST3A1	heparan sulfate D-glucosaminyl 3-O-sulfotransferase 3A1	NM_006042			1.018	0.695					
FLJ21963	FLJ21963 protein	NM_024560							1.018	0.819	Lipid metabolism. Fatty acid metabolism.
DPAGT1	UDP-N-acetylglucosamine-dolichyl-phosphate N-acetylglucosa	NM_001382					1.018	1.421			Lipid metabolism.
DP58	cytosolic phosphoprotein DP58	NM_001004441							1.018	0.444	
C14orf127	chromosome 14 open reading frame 127	BC024919			1.018	0.527					Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
TSBP	testis specific basic protein	U60665			1.017	0.44					
SNTG2	" syntrophin, gamma 2"	NM_018968			1.017	0.783					Central nervous system development.
FLJ10781	hypothetical protein FLJ10781	NM_018215			1.017	0.622					
N/A	N/A	AK124578			1.016	0.214					Protein ubiquitination.
MGC26597	hypothetical protein MGC26597	NM_152700			1.016	0.882					
KRTAP12-2	keratin associated protein 12-2	NM_181684			1.016	0.46					
DKFZp434N062	hypothetical protein DKFZp434N062	NM_199336			1.016	0.768					Metabolism.
CX62	connexin 62	NM_032602			1.016	0.816					
WFDC10A	WAP four-disulfide core domain 10A precursor	NM_080753			1.015	0.72					
VAV3	vav 3 oncogene	NM_006113							1.015	0.645	Intracellular signaling cascade. Small GTPase mediated signal transduction.
SCYL1	SCY1-like 1	NM_020680	1.124	1.004	1.015	0.823					Protein amino acid phosphorylation. Mitotic chromosome condensation.
N/A	Similar to spinster-like protein	BC041772			1.015	0.677					Transport.
N/A	N/A	AK023875							1.015	0.507	
N/A	unknown	AF007157	1.042	1.208	1.015	0.998					
LIF	leukemia inhibitory factor (cholinergic differentiation factor)	NM_002309			1.015	0.56					Immune response. Cell-cell signaling. Development. Positive regulation of cell proliferation.

FSCN2	fascin 2	NM_012418							1.015	0.525	Sensory perception. Visual perception. Morphogenesis. Actin filament bundle formation.
FLJ45966	FLJ45966 protein	NM_001001700							1.015	0.486	
CNN1	" calponin 1, basic, smooth muscle"	NM_001299			1.015	0.585					Regulation of smooth muscle contraction.
PRKY	" protein kinase, Y-linked"	NM_002760			1.014	0.727					Protein amino acid phosphorylation.
GPR172B	G protein-coupled receptor 172B	NM_017986			1.014	0.262					
FLJ23231	hypothetical protein FLJ23231	NM_025079			1.014	0.542					
DKFZp434L142	hypothetical protein DKFZp434L142	NM_016613			1.014	1.02					
DEDD2	death effector domain-containingDNA binding protein 2	NM_133328			1.014	1.318					Regulation of transcription, DNA-dependent. RNA processing. Intracellular signaling cascade.
NEU2	sialidase 2	NM_005383							1.013	0.461	Carbohydrate metabolism.
N/A	N/A	AK123170							1.013	0.478	Regulation of transcription, DNA-dependent. Cell adhesion.
GYLZ-RCC18	nucleoporin	AY064415							1.013	0.757	
GIPR	gastric inhibitory polypeptide receptor	NM_000164			1.013	0.56					Generation of precursor metabolites and energy. G-protein coupled receptor protein signaling pathway.
PPP2R2B	" beta isoform of regulatory subunit B55, protein phosphatase	NM_004576			1.012	0.758					Signal transduction.
LOC253724	LOC253724 protein	BC064342			1.012	0.632					
GPR160	G protein-coupled receptor 160	NM_014373			1.012	0.569					Signal transduction. G-protein coupled receptor protein signaling pathway.
GLT25D2	GLT25D2 protein	BC019709			1.012	0.757					Lipopolysaccharide biosynthesis.
DKFZp434I0428	hypothetical proteincDNA DKFZp434I0428 (from clone DKFZp	AL133092			1.012	0.624					
CXorf33	chromosome X open reading frame 33	NM_198450					1.012	0.441			
AP1S3	" adaptor-related protein complex 1, sigma 3 subunit"	NM_178814			1.012	0.657					Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
SPINK2	" serine protease inhibitor, Kazal type 2 (acrosin-trypsin inhibit	BC022514			1.011	0.364					
N/A	voltage-gated potassium channel	L02840					1.011	0.744			Cation transport. Potassium ion transport.
N/A	N/A	AK022991					1.011	0.665			Endocytosis. Signal transduction. Regulation of growth.
LOC388962	similar to RIKEN 1810056O20	NM_212552			1.011	0.751					
CST9L	" cystatin 9-like, precursor"	BC029656			1.011	0.667					
ABO	ABO blood group (transferase A, alpha 1-3-N-acetylgalactosan	NM_020469							1.011	0.483	Carbohydrate metabolism. Protein amino acid glycosylation. Biosynthesis.
PFC	" properdin P factor, complement"	NM_002621					1.01	0.891			Immune response. Complement activation, alternative pathway. Defense response to bacteria.
N/A	Unknown (protein for MGC:87657)	BC067891	3.165	0.63	1.01	0.965					Protein biosynthesis.
DLL4	delta-like 4 protein precursor	NM_019074					1.01	0.759			Signal transduction. Notch signaling pathway. Circulation. Cell differentiation.
DKFZp434L187	hypothetical proteincDNA DKFZp434L187 (from clone DKFZp4	AL117445			1.01	0.594					
OR5A1	" olfactory receptor, family 5, subfamily A, member 1"	NM_001004728			1.009	1.025					
N/A	N/A	AK127470			1.009	0.93					
MSX1	msh homeo box homolog 1	NM_002448			1.009	0.651					Skeletal development. Regulation of transcription, DNA-dependent.
MSLN	megakaryocyte potentiating factor, precursor"	BC003512							1.009	0.651	Cell adhesion.
OR8G1P	" olfactory receptor, family 8, subfamily G, member 1"	NM_001002905			1.008	0.787					
N/A	WGAR9166	AY358775			1.008	0.759					
N/A	N/A	AK128839			1.008	0.652					Steroid biosynthesis. Metabolism.
HUMTCHIT	chitinase	U58515			1.008	0.632					Metabolism.
HB92	cervical cancer homeoprotein 92	AF426412			1.008	1.051					
SCNN1A	amiloride-sensitive epithelial sodium channel alpha subunitalte	AY365119			1.007	0.98					Ion transport. Sodium ion transport. Excretion. Sensory perception.
KIAA0779	KIAA0779 protein	NM_015008			1.007	0.809					
FLJ46321	FLJ46321 protein	NM_001001670			1.007	0.296					
CLTCL1	" clathrin, heavy polypeptide-like 1 isoform b"	NM_007098			1.007	1.124					Receptor mediated endocytosis. Morphogenesis.
TLR10	toll-like receptor 10 precursor	NM_030956			1.006	0.488					Inflammatory response.
N/A	PRO2300	AF130086	1.095	0.688	1.006	0.799					Protein amino acid phosphorylation. Cell cycle. Signal transduction.
LOC81558	C/EBP-induced protein	NM_030802			1.006	0.318					
TD-60	RCC1-like	NM_018715			1.005	1.049					
N/A	N/A	AK127907					1.005	0.736			Protein amino acid phosphorylation. Signal transduction. Alcohol metabolism. Lipid metabolism.
N/A	N/A	AK123974			1.005	0.702					Regulation of muscle contraction. Muscle development.
N/A	PRO1068	AF116620			1.005	1.266					
PCSK5	proprotein convertase subtilisin/kexin type 5 preproprotein	NM_006200			1.004	1.123					Proteolysis and peptidolysis. Proteolysis and peptidolysis. Cell-cell signaling.
CHD1L	chromodomain helicase DNA binding protein 1-like	NM_004284			1.004	0.707					
SNAI1	snail 1 homolog	NM_005985			1.003	0.567					Cartilage condensation. Development. Neurogenesis.
RNASE8	" RNase 8, placental"	NM_138331			1.003	1.42					Defense response to bacteria. Innate immune response.
ME4	cadherin	D88797			1.003	0.79					
COL9A3	alpha 3 type IX collagen	NM_001853			1.003	0.465					Phosphate transport.
RBBP7	retinoblastoma binding protein 7	NM_002893			1.002	0.54					Development. Cell proliferation.

FLJ13273	hypothetical protein FLJ13273	NM_024751	1.002	0.484			
CXorf43	chromosome X open reading frame 43	NM_144657			1.002	0.603	
ACTR1A	" ARP1 actin-related protein 1 homolog A, centractin alpha"	NM_005736	1.002	1.039			
XK	" McLeod syndrome-associated, Kell blood group protein"	NM_021083	1.001	1.27			Amino acid transport.
SLC26A7	" solute carrier family 26, member 7 isoform a"	NM_052832	1.001	1			
N/A	VCEW9374	AY358216	1.001	0.939			
N/A	N/A	AK090827	1.001	0.709			
KIAA0255	N/A	D87444			1.001	0.562	Transport.
SNRPF	SNRPF protein	BC002505	1	1.06			Nuclear mRNA splicing, via spliceosome.
PXMP2	PXMP2 protein	BC009836			1	0.239	
MOV10L1	MOV10-like 1	NM_018995			1	0.721	Development. Germ cell development. Spermatogenesis.