Supplemental Materials and Methods

Animals: All animal investigations were performed in compliance with Northwestern University’s institutional guidelines and under the National Research Council's criteria for humane care as outlined in the "Guide for the Care and Use of Laboratory Animals". Female New Zealand White rabbits (3-4kg) were purchased from Covance (Princeton, NJ) and were acclimated for a minimum of 7 days prior to enrollment in experiments. Anesthesia included intramuscular ketamine (45mg/kg) and xylasine (7mg/kg), or inhaled isofluorane (1-2%), as well as a local anesthetic (1% lidocaine HCl and 1:100,000 epinephrine). Post-operative analgesia was achieved by the administration of 0.05mg/kg buprenorphine every 6-12 hours for up to 3 days following surgery.

Skin and mucosal incisional grid model: The ventral surface of each ear and the vaginal introitus, perineum, and surrounding area was depilated and a surgical scrub was performed (N=8 per time point). On each ear, a 2cm x 2cm grid of shallow (30-50µm deep) perpendicular incisions was made with a maximum distance of 1mm between incisions. These wounds were covered with a semi-occlusive Tegaderm dressing (3M, St Paul, MN) until complete re-epithelialization occurred. In the vagina of the same animals, a series of shallow (30-50µm deep), parallel, longitudinal incisions was made from the introitus into the vagina (length = 3cm). The incisions were made around the entire circumference of the vagina, with a maximum distance of 1mm between incisions. At defined intervals (12 hours, 24 hours, 3 days, 5 days) after injury, the animals were euthanized and samples of the cutaneous and mucosal wounds and uninjured tissue were taken. Each animal was used for one time point only.

Hypertrophic scar model: A reproducible model of cutaneous hypertrophic scar formation in the New Zealand White rabbit was utilized as previously described (Kloeters et al. 2008). Briefly, the ventral surface of each ear was depilated and a surgical scrub was performed. At each of six sites per ear, a 7mm diameter biopsy punch was used to score the skin to the depth of the cartilage, and the epidermis and dermis was removed, leaving the perichondrium intact. All wounds were dressed with Tegaderm dressing (3M, St Paul, MN), and the dressings were replaced as necessary until complete re-epithelialization was observed on post-operative day 18. On post-operative days 20, 25, and 30, 7.5mg (50µL) of the interleukin-1 receptor antagonist Anakinra (Kineret TM) (Amgen, Thousand Oaks, CA), or vehicle control was injected subcutaneously at the site of each wound site (N=4 animals, 24-48 wounds per treatment). The dose of IL-1RA utilized was equivalent to the human daily therapeutic dose of 1-2mg/kg, but the treatment was administered at a reduced frequency due to the need to anesthetize the animals for each therapeutic treatment. All animals were euthanized at 35 days post-surgery and samples of wounded and control tissue were taken.

Histology: Following euthanasia, full thickness samples of all wounds and from normal skin and mucosa were taken and fixed overnight in 10% zinc formalin for histological analysis. All samples were embedded in paraffin (Paraplast X-tra, Fisher Scientific, Houston, TX) and were sectioned at 5µm thickness through the center of each wound. Sections were de-paraffinized and stained with hematoxylin and eosin, and were photographed under 10x or 20x magnification. The epithelial thickness (number of cells and absolute thickness in µm) was determined for all incisional wounds. The total scar area (scar elevation index, SEI) (Kloeters et al. 2008) of all full thickness punch wounds was determined using ImageJ software (NIH, Bethessa, MD). A SEI value of 1 indicates that the scar dermis is of an equivalent height to the dermis of the adjacent normal, unwounded skin.A SEI value of 2 indicates that the height of the scar dermis is twice that of unwounded skin.

RNA extraction: Following euthanasia, samples of all wounds were frozen in RNAlater (Ambion, Austin, TX) at -80oC for molecular analysis. The epithelium of all incisional grid samples was mechanically separated from the underlying mesenchymal tissue using a single-edged razor blade (Schierle et al. 2007). The cutaneous dermis was further separated from the underlying cartilage, and the cartilage was discarded. All full thickness punch wounds were separated from the underlying cartilage and were processed intact (epidermis and dermis together). Each tissue compartment (epithelium, connective tissue, or whole skin) was homogenized independently in RLT buffer (Qiagen, Valencia, CA) with 1% beta- mercaptoethanol using a PowerGen Model 500 Homogenizer (Fisher Scientific, Houston, TX). Total RNA was extracted and purified using the RNeasy kit (Qiagen, Valencia, CA) as previously described (Reno et al. 1997). RNA quality was determined using the Agilent Bioanalyzer (Agilent Technologies, Santa Clara, CA)

Microarray: A subset of paired rabbit skin and mucosal epithelial RNA samples (N=5-6 per time point) plus four common control (pooled) samples were chosen for microarray analysis based on the histologic analysis of each sample and on the RNA quality (A260/A280 ratio, 28s/18s RNA ratio, RNA integrity number). All 60 samples were labeled with the One-Color Quick-Amp Labeling Kit (Agilent Technologies, Santa Clara, CA) and then were hybridized to an Agilent custom rabbit microarray containing 4 sets of 44,000 probes per slide (23679 unique probes, Amadid #017132) (Agilent Technologies, Santa Clara, CA). All labeling and hybridization was performed at the University of Florida Interdisciplinary Center for Biotechnology Research according to standard Agilent recommended protocols.

Data preprocessing was performed using the Bioconductor Agi4x44PreProcess package. The Agilent Feature Extraction (AFE) algorithm was used for image analysis and background correction. Quantile normalization was then used to correct for the non-biological variations across arrays. Probes were filtered based on the criteria that at least 5 of the 60 samples must have a signal level above background and negative controls. Duplicated probes were combined using their median intensities. As the gene expression level of unwounded skin and mucosal epithelium were quite different, in order to detect gene expression changes over time in response to injury, the data were normalized against the unwounded tissue by subtracting the respective tissue T=0 sample mean (in log2 scale) from each value.To identify differentially expressed genes, we applied routines implemented in the Bioconductor Limma package to fit linear models to the normalized expression values (Smyth 2005). The variance used in the t-score calculation was corrected by an empirical Bayesian method for better estimation under small sample size.

To control for the effects of multiple testing and to minimize false positives, a subset of statistically significant transcripts was selected for further analysis based on the following filtering criteria: 1) absolute fold change >2, 2) p value <0.01, and 3) Benjamini &

Hochberg FDR <0.05. The data were analyzed to identify 1) temporal changes in gene expression over time in each tissue, and 2) genes whose expression differed between the two tissues. The latter utilized an F test, which identified a total of 1075 genes which had a significantly different fold change (normalized to unwounded tissue) between skin and mucosa at at least one time point. The gene profiles were then scaled to a standard deviation of 1 without shifting the mean of the profile, thereby keeping the direction of the fold-change unchanged. Next, hierarchical clustering was applied to get an overview of the cluster distribution. A cutoff threshold was visually selected to define initial clusters. Based on these initial clusters, K-Means clustering was performed. Five clusters of genes with different temporal expression patterns were identified. Functional analysis was performed on the genes which were differentially expressed over time in each tissue and on the genes that were located in the five clusters. First, the outlier genes which are were located far away from the cluster centers were filtered out. Then the over-represented functionalities of the genes were identified by using the Hypergeometric test based on the Gene Ontology database (Ashburner et al. 2000).

Raw and processed microarray data can be accessed at the Gene Expression Omnibus accession number (http://www.ncbi.nlm.nih.gov/geo/ , GSE25261).

Quantitative RT-PCR: Reverse transcription was performed using one microgram of total RNA and M-MLV Reverse Transcriptase (Promega, Madison, WI) as per the manufacturer's instructions. Quantitative real-time PCR was performed on an ABI Prism 7000 Sequence Detection System (Applied Biosystems, Foster City, CA). Each PCR reaction was run in triplicate and contained 0.03⌠g cDNA template along with 900nM primers and 250nM probe and Taq Man Universal Master Mix (Applied Biosystems, Foster City, CA) in a final reaction volume of 25⌠L. Cycling parameters were: 50°C for 2 minutes, 95°C for 10 minutes to activate DNA polymerase, and then 40 cycles of 95°C for 15 seconds and 60°C for 1 minute. No-template controls were run in parallel to evaluate for amplification of genomic DNA. After thermal cycling, the relative mRNA expression of each amplicon was calculated by normalizing its Ct value relative to a housekeeping molecule (18s) and then expressing the value as a proportion of baseline levels (unwounded skin)(2-ΔΔCt). All parameters were assessed using a one-sided ANOVA or using a paired t-test, with a p value of <0.05 indicating significance.

Referecnces:

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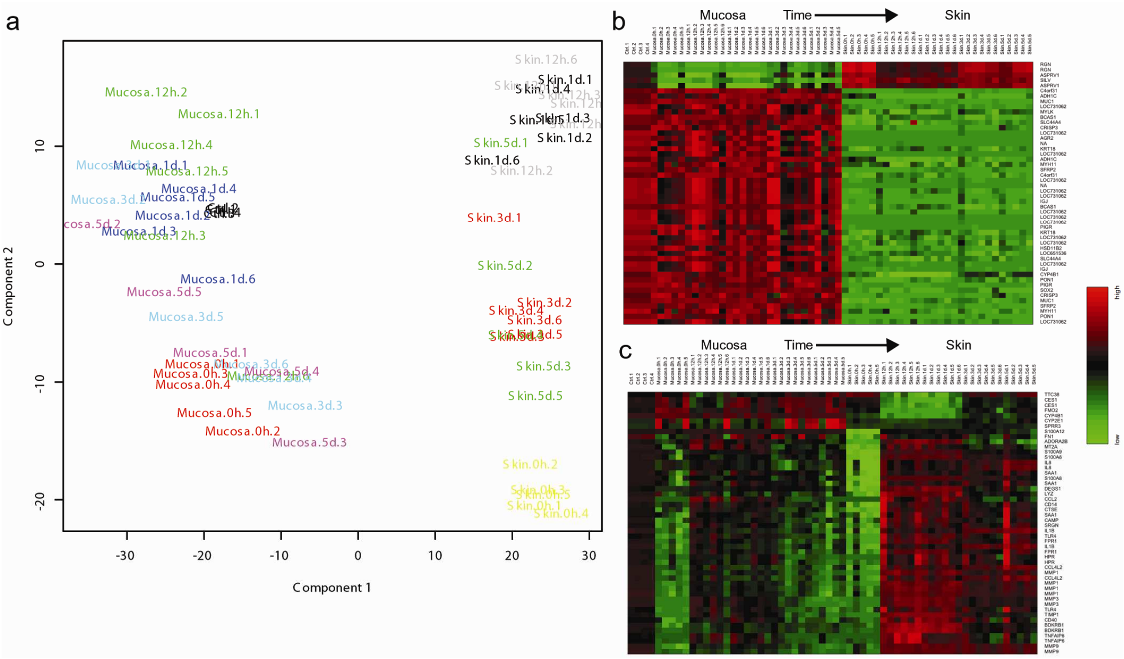
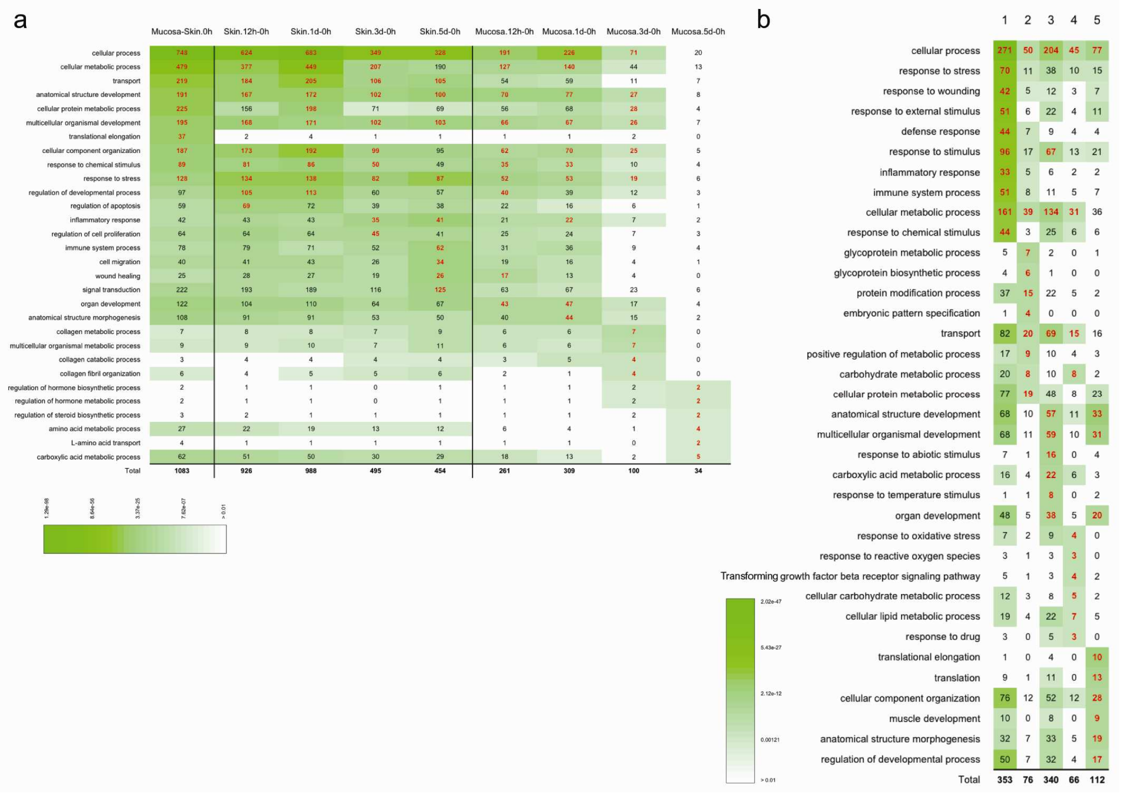
Supplemental Figure 1: Microarray analysis of injured epithelium: Major differences in gene expression between wounded skin and mucosa

Microarray analysis of cutaneous and mucosal epithelium at various times post-wounding (unwounded, 12 hours, 1 day, 3 days, 5 days, N=5) indicates that there are significant differences in how the two tissues respond to injury. Principal component analysis of 14647 probes that met the preprocessing criteria (A) indicates that the two biggest sources of variability in the data are tissue type (principal component 1), and time post-injury (principal component 2). A heatmap of the top 50 probes in the first principal component (B) indicates that gene expression in the skin and mucosal epithelium is significantly different prior to injury, and that many of those differences persist over time. A heatmap of the top 50 probes in the second principal component (C) indicates that injury results in a change of expression of a number of molecules involved in epithelial proliferation and differentiation, inflammation, and extracellular matrix synthesis and reorganization. Furthermore, it is evident that the cutaneous epithelium responds more strongly to injury, and that injury-associated gene expression changes persist for a longer period of time in the skin.



Supplemental Figure 2: Functional analysis: Inflammation, response to stress, and anabolic processes (structure development) pathways are differentially upregulated in skin and mucosal epithelium following injury

Functional analysis of the genes which are differentially expressed over time in each tissue (A) and which are identified in each cluster (B) was performed using the Gene Ontology database. Gene functionalities, which are significantly overexpressed in healing skin as compared to mucosa, include response to wounding, response to stress, inflammation, structure development. These functionalities are more highly enriched in the skin samples, and are overexpressed for a longer following injury. All numbers in red indicate the top 10 GO categories for each sample group. The intensity of the background color corresponds to the p-value of enrichment tests.



	Mucosa-Skin.0h	Skin.12h-0h	Skin.1d-0h	Skin.3d-0h	Skin.5d-0h	Mucosa.12h-0h	Mucosa.1d-0h	Mucosa.3d-0h	Mucosa.5d-0h
cellular process	748	624	683	349	328	191	226	71	20
cellular metabolic process	479	377	449	207	190	127	140	44	13
transport	219	184	205	106	105	54	59	11	7
anatomical structure development	191	167	172	102	100	70	77	27	8
cellular protein metabolic process	225	156	198	71	69	56	68	28	4
multicellular organismal development	195	168	171	102	103	66	67	26	7
translational elongation	37	2	4	1	1	1	1	2	0
cellular component organization	187	173	192	99	95	62	70	25	5
response to chemical stimulus	89	81	86	50	49	35	33	10	4
response to stress	128	134	138	82	87	52	53	19	6
regulation of developmental process	97	105	113	60	57	40	39	12	3
regulation of apoptosis	59	69	72	39	38	22	16	6	1
inflammatory response	42	43	43	35	41	21	22	7	2
regulation of cell proliferation	64	64	64	45	41	25	24	7	3
immune system process	78	79	71	52	62	31	36	9	4
cell migration	40	41	43	26	34	19	16	4	1
wound healing	25	28	27	19	26	17	13	4	0
signal transduction	222	193	189	116	125	63	67	23	6
organ development	122	104	110	64	67	43	47	17	4
anatomical structure morphogenesis	108	91	91	53	50	40	44	15	2
collagen metabolic process	7	8	8	7	9	6	6	7	0
multicellular organismal metabolic process	9	9	10	7	11	6	6	7	0
collagen catabolic process	3	4	4	4	4	3	5	4	0
collagen fibril organization	6	4	5	5	6	2	1	4	0
regulation of hormone biosynthetic process	2	1	1	0	1	1	1	2	2
regulation of hormone metabolic process	2	1	1	0	1	1	1	2	2
regulation of steroid biosynthetic process	3	2	1	1	1	1	1	2	2
amino acid metabolic process	27	22	19	13	12	6	4	1	4
L-amino acid transport	4	1	1	1	1	1	1	0	2
carboxylic acid metabolic process	62	51	50	30	29	18	13	2	5
Total	**1083**	**926**	**988**	**495**	**454**	**261**	**309**	**100**	**34**

	1	2	3	4	5
cellular process	271	50	204	45	77
response to stress	70	11	38	10	15
response to wounding	42	5	12	3	7
response to external stimulus	51	6	22	4	11
defense response	44	7	9	4	4
response to stimulus	96	17	67	13	21
inflammatory response	33	5	6	2	2
immune system process	51	8	11	5	7
cellular metabolic process	161	39	134	31	36
response to chemical stimulus	44	3	25	6	6
glycoprotein metabolic process	5	7	2	0	1
glycoprotein biosynthetic process	4	6	1	0	0
protein modification process	37	15	22	5	2
embryonic pattern specification	1	4	0	0	0
transport	82	20	69	15	16
positive regulation of metabolic process	17	9	10	4	3
carbohydrate metabolic process	20	8	10	8	2
cellular protein metabolic process	77	19	48	8	23
anatomical structure development	68	10	57	11	33
multicellular organismal development	68	11	59	10	31
response to abiotic stimulus	7	1	16	0	4
carboxylic acid metabolic process	16	4	22	6	3
response to temperature stimulus	1	1	8	0	2
organ development	48	5	38	5	20
response to oxidative stress	7	2	9	4	0
response to reactive oxygen species	3	1	3	3	0
Transforming growth factor beta receptor signaling pathway	5	1	3	4	2
cellular carbohydrate metabolic process	12	3	8	5	2
cellular lipid metabolic process	19	4	22	7	5
response to drug	3	0	5	3	0
translational elongation	1	0	4	0	10
translation	9	1	11	0	13
cellular component organization	76	12	52	12	28
muscle development	10	0	8	0	9
anatomical structure morphogenesis	32	7	33	5	19
regulation of developmental process	50	7	32	4	17
Total	**353**	**76**	**340**	**66**	**112**

Supplemental Figure 3: Alignment of Human and Rabbit IL-1RA sequences
In order to determine if a human interleukin-1 receptor antagonist would maintain its biological function if used in a rabbit, a multiple sequence alignment was performed between the human and rabbit IL-1RA sequence. Based on the work of Schreuder (Schreuder, Tardif et al. 1997), it is clear that all but one of the 17 amino acids that are responsible for IL-1RA binding to the IL-1 receptor are identical between human and rabbit.

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                 1                                                    50
Human  AAB41943  MEICRGLRSH LITLLLFLFH SETICRPSGR KSSKMQAFRI WDVNQKTFYL
Rabbit BAA04860  MRPSRSTRRH LISLLLFLFH SETACRPSGK RPCRMQAFRI WDVNQKTFYL
      Consensus  MricRglRrH LIsLLLFLFH SETaCRPSGr rpcrMQAFRI WDVNQKTFYL

                 51                                                  100
Human  AAB41943  RNNQLVAGYL QGPNVNLEEK IDVVPIEPHA LFLGIHGGKM CLSCVKSGDE
Rabbit BAA04860  RNNQLVAGYL QGPNAKLEER IDVVPLEPQL LFLGIQRGKL CLSCVKSGDK
      Consensus  RNNQLVAGYL QGPNanLEEr IDVVPiEPqa LFLGIqrGK$ CLSCVKSGDe

                 101                                                 150
Human  AAB41943  TRLQLEAVNI TDLSENRKQD KRFAFIRSDS GPTTSFESAA CPGWFLCTAM
Rabbit BAA04860  MKLHLEAVNI TDLGKNKEQD KRFTFIRSNS GPTTTFESAS CPGWFLCTAL
      Consensus  mrLqLEAVNI TDLgeNreQD KRFaFIRS#S GPTTsFESAa CPGWFLCTA$

                 151                       177
Human  AAB41943  EADQPVSLTN MPDEGVMVTK FYFQEDE
Rabbit BAA04860  EADQPVSLTN TPDDSIVVTK FYFQEDQ
      Consensus  EADQPVSLTN mPD#g!mVTK FYFQED#

Interactions with IL-1 receptor
Mismatch

Consensus symbols:
 ! is anyone of IV
 $ is anyone of LM
 % is anyone of FY
 # is anyone of NDQEBZ
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Supplemental Table 1: Genes identified in each cluster

Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5
2',3'-cyclic nucleotide 3' phosphodiesterase	acyl-CoA synthetase long-chain family member 1	3-hydroxyisobutyryl-Coenzyme A hydrolase	ADAM metallopeptidase domain 9 (meltrin gamma)	A kinase (PRKA) anchor protein 12
2'-5'-oligoadenylate synthetase-like	ankyrin 3, node of Ranvier (ankyrin G)	3-oxoacid CoA transferase 1	adaptor-related protein complex 3, beta 2 subunit	acid phosphatase 6, lysophosphatidic
3-hydroxy-3-methylglutaryl-Coenzyme A reductase	ATPase, Na+/K+ transporting, beta 1 polypeptide	5'-nucleotidase domain containing 2	adipose differentiation-related protein	ADAM metallopeptidase with thrombospondin type 1 motif, 9
acetoacetyl-CoA synthetase	beta-site APP-cleaving enzyme 2	abhydrolase domain containing 8	aldehyde dehydrogenase 1 family, member A1	ADP-ribosylation factor-like 3
actin related protein 2/3 complex, subunit 4, 20kDa	BMI1 polycomb ring finger oncogene	aconitase 2, mitochondrial	aldo-keto reductase family 1, member D1 (delta 4-3-ketosteroid-5-beta-reductase)	angiogenin, ribonuclease, RNase A family, 5
actinin, alpha 3	bone morphogenetic protein 6	actin binding LIM protein family, member 3	alpha 1,3-galactosyltransferase 2	annexin A5
actinin, alpha 4	calpain 5	acyl-CoA synthetase family member 2	ankyrin repeat domain 13A	annexin A6
activating transcription factor 4 (tax-responsive enhancer element B67)	catenin (cadherin-associated protein), beta 1, 88kDa	acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain	anti-Mullerian hormone receptor, type II	annexin A8
acyl-CoA synthetase long-chain family member 3	cell division cycle and apoptosis regulator 1	acyl-Coenzyme A dehydrogenase, long chain	arginyl aminopeptidase (aminopeptidase B)	apoptosis, caspase activation inhibitor
acyloxyacyl hydrolase (neutrophil)	chloride channel 3	adenosylmethionine decarboxylase 1	aspartate beta-hydroxylase domain containing 1	ATP-binding cassette, sub-family C (CFTR/MRP), member 9
adaptor-related protein complex 1, gamma 1 subunit	chromosome 1 open reading frame 63	adenylate cyclase 10 (soluble)	bleomycin hydrolase	bone morphogenetic protein 4
adenosine A2b receptor	chromosome 16 open reading frame 13	alanyl (membrane) aminopeptidase	BTB (POZ) domain containing 3	caldesmon 1
adenosine monophosphate deaminase (isoform E)	chromosome 4 open reading frame 49	alcohol dehydrogenase 1C (class I), gamma polypeptide	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit	caprin family member 2

adenosylmethionine decarboxylase 1	claudin 5	aldehyde dehydrogenase 9 family, member A1	chromosome 10 open reading frame 58	carnitine palmitoyltransferase 1C
ADP-ribosyltransferase 1	collagen, type VIII, alpha 2	aldolase C, fructose-bisphosphate	chromosome 4 open reading frame 3	caveolin 1, caveolae protein, 22kDa
amidohydrolase domain containing 2	complement component 3	amylo-1, 6-glucosidase, 4-alpha-glucanotransferase	DNA-damage-inducible transcript 3	centromere protein N
ankyrin repeat domain 22	cysteine-rich secretory protein 3	androgen receptor	enolase 3 (beta, muscle)	ceruloplasmin (ferroxidase)
annexin A1	cytochrome P450, family 3, subfamily A, polypeptide 4	angiomotin like 2	G protein-coupled receptor 1	coagulation factor III (thromboplastin, tissue factor)
annexin A11	dual specificity phosphatase 4	ankylosis, progressive homolog (mouse)	galactosidase, beta 1	coiled-coil domain containing 80
annexin A3	E74-like factor 1 (ets domain transcription factor)	apolipoprotein A-I binding protein	glutathione S-transferase mu 3 (brain)	collagen, type V, alpha 1
apolipoprotein B mRNA editing enzyme, catalytic polypeptide 1	family with sequence similarity 20, member C	apolipoprotein E	glutathione synthetase	collagen, type V, alpha 2
archain 1	F-box protein 34	aquaporin 5	glycogenin 1	collagen, type VI, alpha 1
ArfGAP with coiled-coil, ankyrin repeat and PH domains 2	fibronectin type III domain containing 3B	arginine vasopressin-induced 1	G-protein signaling modulator 2 (AGS3-like, C. elegans)	collagen, type VI, alpha 2
arginase, liver	flavin containing monooxygenase 3	ATP synthase 6; ATPase subunit 6	hexamethylene bis-acetamide inducible 1	collagen, type XII, alpha 1
arginine vasopressin-induced 1	flavin containing monooxygenase 5	ATPase, aminophospholipid transporter (APLT), class I, type 8A, member 1	high-mobility group box 2	complement component 4A (Rodgers blood group)
ARP3 actin-related protein 3 homolog (yeast)	fructose-1,6-bisphosphatase 1	baculoviral IAP repeat-containing 7	kinesin family member 20B	CUG triplet repeat, RNA binding protein 2
asparagine-linked glycosylation 2, alpha-1,3-mannosyltransferase homolog (S. cerevisiae)	furin (paired basic amino acid cleaving enzyme)	Bardet-Biedl syndrome 9	lactalbumin, alpha-	cysteine and glycine-rich protein 2
aspartate beta-hydroxylase	glucose-fructose	basal cell adhesion	LIM and SH3 protein 1	deoxyuridine

domain containing 1	oxidoreductase domain containing 2	molecule (Lutheran blood group)		triphosphatase
ataxia telangiectasia and Rad3 related	glutamate-cysteine ligase, catalytic subunit	basic transcription factor 3	lipocalin 2	desmin
ATP synthase 6; ATPase subunit 6	glutathione peroxidase 3 (plasma)	BH3 interacting domain death agonist	macrophage migration inhibitory factor (glycosylation-inhibiting factor)	dickkopf homolog 1 (Xenopus laevis)
ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	golgi phosphoprotein 3 (coat-protein)	biliverdin reductase B (flavin reductase (NADPH))	major histocompatibility complex, class II, DO beta	dickkopf homolog 3 (Xenopus laevis)
ATPase, Ca++ transporting, plasma membrane 1	hyaluronoglucosaminidase 2	bobby sox homolog (Drosophila)	matrix metallopeptidase 12 (macrophage elastase)	dihydrofolate reductase
ATPase, class VI, type 11B	inositol(myo)-1(or 4)-monophosphatase 1	bone marrow stromal cell antigen 2	matrix metallopeptidase 13 (collagenase 3)	dysbindin (dystrobrevin binding protein 1) domain containing 2
ATPase, Na+/K+ transporting, alpha 1 polypeptide	insulin-like growth factor 2 receptor	brain expressed X-linked 2	NEDD4 binding protein 2-like 2	EH domain binding protein 1
ATP-binding cassette, sub-family C (CFTR/MRP), member 3	Kruppel-like factor 5 (intestinal)	brain protein I3	nidogen 2 (osteonidogen)	eukaryotic translation elongation factor 1 beta 2
bactericidal/permeability-increasing protein	leucine rich repeat (in FLII) interacting protein 2	branched chain keto acid dehydrogenase E1, beta polypeptide	nitric oxide synthase 2, inducible	eukaryotic translation elongation factor 1 gamma
BCL2-associated X protein	lipase A, lysosomal acid, cholesterol esterase	bromodomain containing 3	nucleosome assembly protein 1-like 1	eukaryotic translation initiation factor 2A, 65kDa
beaded filament structural protein 1, filensin	meningioma expressed antigen 5 (hyaluronidase)	calcium and integrin binding family member 2	oviductal glycoprotein 1, 120kDa	fasciculation and elongation protein zeta 1 (zygin I)
bradykinin receptor B1	mitogen-activated protein kinase kinase 3	calcium channel, voltage-dependent, beta 3 subunit	patatin-like phospholipase domain containing 6	fibroblast activation protein, alpha
breast carcinoma amplified sequence 1	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog,	calcium/calmodulin-dependent protein kinase ID	phosphoenolpyruvate carboxykinase 2 (mitochondrial)	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1

	Drosophila); translocated to, 3			
cadherin 16, KSP-cadherin	myosin VB	calsequestrin 2 (cardiac muscle)	phosphoglucomutase 1	guanosine monophosphate reductase
calcitonin-related polypeptide beta	NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase)	calsyntenin 1	pleckstrin homology domain containing, family G (with RhoGef domain) member 2	heat shock 22kDa protein 8
calpain 2, (m/II) large subunit	neuropeptide Y receptor Y2	caprin family member 2	proline-rich protein BstNI subfamily 3	heat shock 70kDa protein 2
calpain, small subunit 1	orosomucoid 2	carboxylesterase 1 (monocyte/macrophage serine esterase 1)	protein phosphatase 1, regulatory (inhibitor) subunit 12A	HtrA serine peptidase 1
calpastatin	phosphatidylinositol-5-phosphate 4-kinase, type II, alpha	carnitine O-octanoyltransferase	RAP1, GTP-GDP dissociation stimulator 1	hypothetical protein FLJ10357
canopy 3 homolog (zebrafish)	phytanoyl-CoA 2-hydroxylase	casein kinase 2, alpha prime polypeptide	relaxin 2	immunoglobulin lambda-like polypeptide 1
carbonic anhydrase XII	polymeric immunoglobulin receptor	catalase	S100 calcium binding protein A6	insulin-like growth factor binding protein 2, 36kDa
cartilage acidic protein 1	programmed cell death 6 interacting protein	catenin, beta interacting protein 1	sodium channel, nonvoltage-gated 1, beta	insulin-like growth factor binding protein 6
cathelicidin antimicrobial peptide	protein kinase C, delta	CD81 molecule	solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2	insulin-like growth factor binding protein 7
cathepsin E	protein kinase C, eta	CD82 molecule	solute carrier family 2 (facilitated glucose transporter), member 1	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)
cathepsin L1	protein phosphatase 1, catalytic subunit, beta isoform	CDC-like kinase 1	solute carrier family 22, member 23	interleukin 11 receptor, alpha
cathepsin L2	protein phosphatase 1, regulatory (inhibitor) subunit 9B	centrosome and spindle pole associated protein 1	sortilin-related receptor, L(DLR class) A repeats-containing	lactate dehydrogenase A
CCR4-NOT transcription	protein phosphatase 4,	chromosome 1 open	sulfotransferase family 4A,	laminin, alpha 2

complex, subunit 8	regulatory subunit 2	reading frame 102	member 1	
CD14 molecule	quiescin Q6 sulfhydryl oxidase 1	chromosome 12 open reading frame 29	sushi, nidogen and EGF-like domains 1	laminin, alpha 4
CD1a molecule	RAB11 family interacting protein 1 (class I)	chromosome 16 open reading frame 13	tetraspanin 15	LIM domain binding 2
CD2 (cytoplasmic tail) binding protein 2	Ras-related GTP binding D	chromosome 17 open reading frame 63	thymosin beta 15B	lysyl oxidase-like 3
CD40 molecule, TNF receptor superfamily member 5	secreted phosphoprotein 1	chromosome 19 open reading frame 42	transcription elongation factor A (SII), 2	matrix Gla protein
CD63 molecule	secretogranin II (chromogranin C)	chromosome 20 open reading frame 108	transforming, acidic coiled-coil containing protein 3	matrix metallopeptidase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collagenase)
cell division cycle 42 (GTP binding protein, 25kDa)	selenium binding protein 1	chromosome 20 open reading frame 152	translocator protein (18kDa)	melanoma cell adhesion molecule
cellular retinoic acid binding protein 2	serpin peptidase inhibitor, clade B (ovalbumin), member 11 (gene/pseudogene)	chromosome 3 open reading frame 1	transmembrane protein 41B	methyltransferase like 12
chaperonin containing TCP1, subunit 3 (gamma)	sodium channel, nonvoltage-gated 1 alpha	chromosome 4 open reading frame 27	troponin I type 2 (skeletal, fast)	myosin, heavy chain 11, smooth muscle
chaperonin containing TCP1, subunit 5 (epsilon)	solute carrier family 12 (sodium/potassium/chloride transporters), member 2	chromosome 5 open reading frame 4	ubiquitin-conjugating enzyme E2C	NA
chaperonin containing TCP1, subunit 7 (eta)	solute carrier family 17 (sodium phosphate), member 1	chromosome 5 open reading frame 53	v-fos FBJ murine osteosarcoma viral oncogene homolog	nestin
chemokine (C-C motif) ligand 4-like 2	solute carrier family 3 (cystine, dibasic and neutral amino acid transporters, activator of cystine, dibasic and neutral amino acid transport), member 1	claudin 5	zinc finger CCCH-type containing 7A	peroxisome proliferator-activated receptor gamma
chemokine (C-X-C motif)	ST3 beta-galactoside	coiled-coil domain	zinc finger protein 295	phosphorylase kinase,

ligand 2	alpha-2,3-sialyltransferase 4	containing 91		alpha 2 (liver)
chemokine (C-X-C motif) ligand 5	T, brachyury homolog (mouse)	cold shock domain protein A	zinc finger, FYVE domain containing 16	platelet-derived growth factor receptor-like
chimerin (chimaerin) 1	TAP binding protein (tapasin)	collagen, type V, alpha 1		pleckstrin homology domain containing, family O member 1
chromatin modifying protein 6	TNFAIP3 interacting protein 1	collagen, type VIII, alpha 1		podocalyxin-like
chromosome 1 open reading frame 107	TraB domain containing	complement component 8, gamma polypeptide		polymerase (RNA) I polypeptide D, 16kDa
chromosome 16 open reading frame 72	transmembrane protein 68	cortactin binding protein 2		potassium channel, subfamily K, member 1
chromosome 4 open reading frame 31	two pore segment channel 1	coxsackie virus and adenovirus receptor		PQ loop repeat containing 3
chromosome 6 open reading frame 153	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 2	crystallin, alpha A		procollagen C-endopeptidase enhancer
chromosome 6 open reading frame 66	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 3 (GalNAc-T3)	crystallin, alpha B		prostaglandin reductase 1
CNDP dipeptidase 2 (metallopeptidase M20 family)	uroplakin 2	CSRP2 binding protein		RAB34, member RAS oncogene family
coagulation factor II (thrombin)	von Hippel-Lindau tumor suppressor	C-type lectin domain family 11, member A		Rho GTPase activating protein 24
coatomer protein complex, subunit beta 2 (beta prime)	zonadhesin	cullin 9		ribosomal protein L22-like 1
coiled-coil domain containing 58		cyclin I		ribosomal protein L23a
collagen, type I, alpha 2		cyclin-dependent kinase inhibitor 2D (p19, inhibits CDK4)		ribosomal protein L5

collagen, type II, alpha 1		cystatin C		ribosomal protein S16
complement component 1, q subcomponent, A chain		cysteine-rich protein 2		ribosomal protein S26
complement component 3		cytochrome b5 reductase 3		ribosomal protein S3
component of oligomeric golgi complex 6		cytochrome c oxidase III		ribosomal protein S5
copine VI (neuronal)		cytochrome P450, family 27, subfamily A, polypeptide 1		ribosomal protein S8
coronin, actin binding protein, 1A		cytochrome P450, family 4, subfamily B, polypeptide 1		ribosomal protein, large, P0
creatine kinase, brain		D site of albumin promoter (albumin D-box) binding protein		sarcoglycan, gamma (35kDa dystrophin-associated glycoprotein)
creatine kinase, mitochondrial 1B		dehydrogenase/reductase (SDR family) member 1		secreted protein, acidic, cysteine-rich (osteonectin)
crystallin, gamma S		dehydrogenase/reductase (SDR family) member 4		secretoglobin, family 2A, member 2
cyclin D3		DENN/MADD domain containing 2A		serine carboxypeptidase 1
cyclin-dependent kinase inhibitor 1C (p57, Kip2)		diacylglycerol kinase, theta 110kDa		signal sequence receptor, delta (translocon-associated protein delta)
cysteine-rich with EGF-like domains 2		dickkopf homolog 3 (Xenopus laevis)		similar to immunoglobulin iota chain preproprotein
cytochrome b		DiGeorge syndrome critical region gene 2		similar to Immunoglobulin omega chain precursor (VpreB2 protein)
cytochrome b-245, alpha polypeptide		disrupted in renal carcinoma 2		solute carrier family 22 (extraneuronal monoamine transporter), member 3
DCN1, defective in cullin neddylation 1, domain containing 5 (S. cerevisiae)		DNL-type zinc finger		solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 4
DEAD (Asp-Glu-Ala-Asp)		dopamine receptor D1		solute carrier family 4,

box polypeptide 27				anion exchanger, member 3
degenerative spermatocyte homolog 1, lipid desaturase (Drosophila)		dual specificity phosphatase 26 (putative)		solute carrier family 8 (sodium/calcium exchanger), member 1
Der1-like domain family, member 1		dynein, cytoplasmic 2, heavy chain 1		splicing factor 3b, subunit 4, 49kDa
DnaJ (Hsp40) homolog, subfamily B, member 1		ectonucleoside triphosphate diphosphohydrolase 2		stathmin 1/oncoprotein 18
DnaJ (Hsp40) homolog, subfamily B, member 11		EH domain binding protein 1		syntrophin, alpha 1 (dystrophin-associated protein A1, 59kDa, acidic component)
DnaJ (Hsp40) homolog, subfamily B, member 6		endothelin 2		tachykinin, precursor 1
DnaJ (Hsp40) homolog, subfamily B, member 9		epoxide hydrolase 1, microsomal (xenobiotic)		TEA domain family member 4
DnaJ (Hsp40) homolog, subfamily C, member 10		epoxide hydrolase 2, cytoplasmic		tetraspanin 4
dolichyl-diphosphooligosaccharide-protein glycosyltransferase		erythrocyte membrane protein band 4.1 like 4B		thrombospondin 2
Down syndrome critical region gene 3		family with sequence similarity 114, member A2		transforming growth factor, beta-induced, 68kDa
dyskeratosis congenita 1, dyskerin		family with sequence similarity 84, member A		transgelin
early growth response 1		F-box protein 9		transmembrane phosphoinositide 3-phosphatase and tensin homolog 2
endonuclease G		fibroblast growth factor (acidic) intracellular binding protein		tropomyosin 2 (beta)
EPH receptor A2		fibroblast growth factor receptor 2		troponin T type 1 (skeletal, slow)

eukaryotic translation initiation factor 3, subunit B		FK506 binding protein 1B, 12.6 kDa		tubulin, alpha 1a
eukaryotic translation initiation factor 4E		FK506 binding protein 4, 59kDa		tumor necrosis factor receptor superfamily, member 11b
eukaryotic translation initiation factor 5B		FK506 binding protein 9, 63 kDa		vascular cell adhesion molecule 1
exportin 6		flavin containing monooxygenase 2 (non-functional)		very low density lipoprotein receptor
Fas (TNF receptor superfamily, member 6)		fms-related tyrosine kinase 4		vesicle amine transport protein 1 homolog (T. californica)-like
fatty acid desaturase 3		frizzled-related protein		
fem-1 homolog b (C. elegans)		FXYD domain containing ion transport regulator 6		
ferritin, heavy polypeptide 1		glutaminyl-tRNA synthetase		
ferritin, light polypeptide		glutathione S-transferase alpha 1		
fibroblast growth factor 5		glyoxalase domain containing 4		
fibronectin 1		glyoxalase domain containing 5		
filamin B, beta (actin binding protein 278)		GNAS complex locus		
formyl peptide receptor 1		growth arrest-specific 6		
fructosamine 3 kinase related protein		growth differentiation factor 1		
fusion (involved in t(12;16) in malignant liposarcoma)		guanine nucleotide binding protein (G protein) alpha 12		
FXYD domain containing ion transport regulator 5		heat shock 22kDa protein 8		
FYVE, RhoGEF and PH domain containing 4		heat shock 27kDa protein 1		

G patch domain containing 4		heat shock 70kDa protein 1A		
G protein-coupled receptor 37 like 1		heat shock protein family B (small), member 11		
G1 to S phase transition 2		helicase-like transcription factor		
gap junction protein, alpha 10, 62kDa		hemochromatosis		
gastrokine 1		hexosaminidase B (beta polypeptide)		
GLI pathogenesis-related 1		high mobility group nucleosomal binding domain 3		
glutathione peroxidase 1		hippocampus abundant transcript-like 1		
glutathione S-transferase mu 3 (brain)		histone cluster 1, H2bh		
glutathione S-transferase pi 1		histone deacetylase 5		
glyceraldehyde-3-phosphate dehydrogenase		HSPB (heat shock 27kDa) associated protein 1		
glycerophosphodiester phosphodiesterase 1		hyaluronoglucosaminidase 1		
GM2 ganglioside activator		hydroxyacyl-Coenzyme A dehydrogenase		
growth associated protein 43		hydroxypyruvate isomerase homolog (E. coli)		
growth hormone receptor		hydroxysteroid (17-beta) dehydrogenase 4		
GrpE-like 1, mitochondrial (E. coli)		hypothetical protein FLJ22184		
guanine nucleotide binding protein (G protein), gamma 2		hypothetical protein LOC389203		
haptoglobin-related protein		immunoglobulin lambda-		

		like polypeptide 1		
heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)		immunoglobulin superfamily, member 10		
hemopexin		inhibitor of DNA binding 1, dominant negative helix-loop-helix protein		
heparin-binding EGF-like growth factor		inhibitor of DNA binding 3, dominant negative helix-loop-helix protein		
heterogeneous nuclear ribonucleoprotein D-like		inhibitor of growth family, member 4		
HLA-B associated transcript 2		inositol 1,4,5-triphosphate receptor, type 3		
hypothetical protein LOC731467		insulin-like growth factor binding protein 2, 36kDa		
hypoxia inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)		insulin-like growth factor binding protein 5		
immunoglobulin superfamily, member 8		integrin alpha FG-GAP repeat containing 1		
integrin alpha FG-GAP repeat containing 3		integrin, alpha 2b (platelet glycoprotein IIb of IIb/IIIa complex, antigen CD41)		
integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor)		integrin, beta 5		
integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12)		interleukin 18 (interferon-gamma-inducing factor)		
integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)		jagged 2		
interleukin 1 receptor		junctophilin 2		

antagonist				
interleukin 1, alpha		kelch domain containing 3		
interleukin 1, beta		kelch repeat and BTB (POZ) domain containing 3		
interleukin 8		KIAA0649		
interleukin 8 receptor, alpha		KIAA1009		
IQ motif containing GTPase activating protein 2		KIAA1614		
isopentenyl-diphosphate delta isomerase 1		kinesin family member 16B		
keratin 6A		Kv channel interacting protein 4		
kinesin family member 19		lactamase, beta 2		
kinesin family member 5C		LAG1 homolog, ceramide synthase 4		
kinesin light chain 1		laminin, beta 2 (laminin S)		
lactalbumin, alpha-		LEM domain containing 2		
leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 4		leucine rich repeat containing 49		
leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3		leucine zipper, putative tumor suppressor 2		
lipoma HMGIC fusion partner		ligand of numb-protein X 1		
lipopolysaccharide-induced TNF factor		like-glycosyltransferase		
low density lipoprotein receptor		LIM domain binding 1		
lymphocyte antigen 96		LY6/PLAUR domain containing 2		
lysozyme (renal		lymphocyte antigen 6		

amyloidosis)		complex, locus E		
major histocompatibility complex, class I, B		LYR motif containing 5		
major histocompatibility complex, class II, DQ alpha 1		lysyl oxidase-like 1		
major vault protein		MACRO domain containing 1		
MAP kinase interacting serine/threonine kinase 1		MAF1 homolog (S. cerevisiae)		
MARCKS-like 1		mannosidase, alpha, class 2A, member 2		
matrix metallopeptidase 1 (interstitial collagenase)		MAP7 domain containing 2		
matrix metallopeptidase 3 (stromelysin 1, progelatinase)		matrilin 2		
matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 92kDa type IV collagenase)		matrix metallopeptidase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collagenase)		
MAX dimerization protein 1		McKusick-Kaufman syndrome		
Mdm2 p53 binding protein homolog (mouse)		melanoma antigen family D, 2		
metallothionein 2A		metallothionein 3		
mevalonate (diphospho) decarboxylase		methylmalonyl Coenzyme A mutase		
microtubule associated monoxygenase, calponin and LIM domain containing 1		mitochondrial carrier homolog 1 (C. elegans)		
mitochondrial ribosomal protein L33		mitochondrial tumor suppressor 1		
mitochondrial ribosomal protein S31		MORC family CW-type zinc finger 2		

mitogen-activated protein kinase 14		MYC binding protein 2		
myosin binding protein C, fast type		myosin IXA		
NA		myosin, heavy chain 3, skeletal muscle, embryonic		
Na+/H+ exchanger domain containing 2		myosin, heavy chain 6, cardiac muscle, alpha		
NAD(P)H dehydrogenase, quinone 2		NA		
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa		NA		
NADH dehydrogenase, subunit 2 (complex I)		N-acetylglucosamine kinase		
NCK-associated protein 1-like		N-acetyltransferase 6 (GCN5-related)		
neuregulin 1		NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4-like 2		
neuroblastoma RAS viral (v-ras) oncogene homolog		nascent polypeptide-associated complex alpha subunit		
neutrophil cytosolic factor 1		nephronophthisis 4		
neutrophil cytosolic factor 2		neural precursor cell expressed, developmentally down-regulated 4-like		
neutrophil cytosolic factor 4, 40kDa		neural proliferation, differentiation and control, 1		
NOP14 nucleolar protein homolog (yeast)		nicolin 1		
NOP2 nucleolar protein homolog (yeast)		N-terminal asparagine amidase		

NOP58 ribonucleoprotein homolog (yeast)		nuclear mitotic apparatus protein 1		
Notch homolog 2 (Drosophila)		nuclear receptor coactivator 7		
nuclear import 7 homolog (S. cerevisiae)		nuclear receptor subfamily 2, group F, member 1		
nucleolar complex associated 2 homolog (S. cerevisiae)		obscurin-like 1		
nucleolar protein 12		olfactomedin 1		
nucleoredoxin		paraoxonase 3		
nucleotide-binding oligomerization domain containing 1		PDZ and LIM domain 4		
ornithine decarboxylase 1		PDZ domain containing 1		
osteoclast associated, immunoglobulin-like receptor		period homolog 1 (Drosophila)		
oxysterol binding protein-like 6		peroxiredoxin 2		
PAK1 interacting protein 1		peroxisomal biogenesis factor 11 alpha		
parathyroid hormone-like hormone		peroxisomal biogenesis factor 3		
parvin, beta		phosphatidic acid phosphatase type 2B		
paxillin		phosphatidylinositol transfer protein, membrane-associated 1		
peptidylprolyl isomerase (cyclophilin)-like 4		phosphoglucomutase 2-like 1		
peroxisome proliferator-activated receptor delta		phosphoserine aminotransferase 1		
phosphogluconate dehydrogenase		pleckstrin homology domain containing, family B (evectins) member 1		

phosphoglycerate kinase 1		pleckstrin homology domain containing, family G (with RhoGef domain) member 3		
phosphoglycerate mutase 2 (muscle)		plexin domain containing 2		
phosphoglycolate phosphatase		poly(A) binding protein interacting protein 2		
pituitary tumor-transforming 1 interacting protein		polymerase (RNA) III (DNA directed) polypeptide G (32kD)-like		
plasminogen activator, tissue		polymerase (RNA) III (DNA directed) polypeptide K, 12.3 kDa		
platelet factor 4		potassium large conductance calcium-activated channel, subfamily M, beta member 1		
platelet-activating factor receptor		pre-B-cell leukemia homeobox interacting protein 1		
plexin A2		premature ovarian failure, 1B		
potassium inwardly-rectifying channel, subfamily J, member 3		prion protein		
pre-B lymphocyte 1		proline-rich protein BstNI subfamily 1		
programmed cell death 6 interacting protein		proline-rich protein BstNI subfamily 2		
proline-serine-threonine phosphatase interacting protein 1		prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)		

prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)		protease, serine, 23		
proteasome (prosome, macropain) 26S subunit, non-ATPase, 14		protein phosphatase 2 (formerly 2A), regulatory subunit B", gamma		
protein disulfide isomerase family A, member 4		protein S (alpha)		
protein disulfide isomerase family A, member 6		PTEN induced putative kinase 1		
protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1)		purinergic receptor P2X, ligand-gated ion channel, 4		
protein tyrosine phosphatase, non-receptor type 11		putative homeodomain transcription factor 1		
protocadherin gamma subfamily A, 2		RALBP1 associated Eps domain containing 1		
purinergic receptor P2Y, G-protein coupled, 2		RAS-like, family 11, member A		
putative homeodomain transcription factor 2		regucalcin (senescence marker protein-30)		
RAB11A, member RAS oncogene family		reticulocalbin 2, EF-hand calcium binding domain		
RAD51 homolog (RecA homolog, E. coli) (S. cerevisiae)		retinal outer segment membrane protein 1		
RAN binding protein 3		Rh family, B glycoprotein (gene/pseudogene)		
ras homolog gene family, member C		RhoA/RAC/CDC42 exchange factor		
RCD1 required for cell differentiation1 homolog		ribonuclease, RNase A family, 4		

(S. pombe)				
regulatory solute carrier protein, family 1, member 1		ribosomal protein L28		
replication initiator 1		ribosomal protein L35		
Rho family GTPase 3		ribosomal protein L5		
ribosomal protein S19 binding protein 1		ribosomal protein S18		
ribosomal protein S6 kinase, 90kDa, polypeptide 1		ring finger protein 7		
ring finger protein 41		rogdi homolog (Drosophila)		
RuvB-like 1 (E. coli)		RUN and SH3 domain containing 2		
S100 calcium binding protein A10		scavenger receptor class B, member 1		
S100 calcium binding protein A11		sclerostin domain containing 1		
S100 calcium binding protein A12		secretoglobin, family 1D, member 2		
S100 calcium binding protein A6		selenium binding protein 1		
S100 calcium binding protein A8		selenoprotein P, plasma, 1		
S100 calcium binding protein A9		serine incorporator 3		
schwannomin interacting protein 1		serine peptidase inhibitor-like, with Kunitz and WAP domains 1 (eppin)		
Sec23 homolog B (S. cerevisiae)		serpin peptidase inhibitor, clade I (neuroserpin), member 1		
secretory leukocyte peptidase inhibitor		short coiled-coil protein		
selenoprotein T		signal transducer and activator of transcription 1,		

		91kDa		
selenoprotein X, 1		silver homolog (mouse)		
serglycin		similar to immunoglobulin iota chain preproprotein		
serine incorporator 2		similar to Immunoglobulin omega chain precursor (VpreB2 protein)		
serine palmitoyltransferase, long chain base subunit 2		sirtuin (silent mating type information regulation 2 homolog) 2 (S. cerevisiae)		
serine/threonine kinase 17a		SLIT and NTRK-like family, member 6		
serpin peptidase inhibitor, clade B (ovalbumin), member 2		SLIT-ROBO Rho GTPase activating protein 2		
serpin peptidase inhibitor, clade B (ovalbumin), member 6		small nuclear ribonucleoprotein polypeptide N		
serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2		SNAP-associated protein		
serum amyloid A1		solute carrier family 15, member 4		
serum/glucocorticoid regulated kinase 1		solute carrier family 19, member 3		
signal peptide peptidase 3		solute carrier family 22 (organic anion transporter), member 7		
signal sequence receptor, alpha		solute carrier family 23 (nucleobase transporters), member 2		
signal-regulatory protein alpha		solute carrier family 24, member 5		
similar to immunoglobulin iota chain preproprotein		solute carrier family 25 (carnitine/acylcarnitine		

		translocase), member 20		
similar to Immunoglobulin omega chain precursor (VpreB2 protein)		solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 4		
similar to phosphoglycerate mutase processed protein		solute carrier family 25, member 37		
Sjogren syndrome antigen B (autoantigen La)		solute carrier family 37 (glycerol-3-phosphate transporter), member 2		
small nuclear ribonucleoprotein 25kDa (U11/U12)		solute carrier family 39 (zinc transporter), member 10		
small nuclear ribonucleoprotein polypeptide A'		solute carrier family 4, sodium bicarbonate cotransporter, member 4		
small optic lobes homolog (Drosophila)		solute carrier family 46 (folate transporter), member 1		
sodium channel, nonvoltage-gated 1, beta		solute carrier family 5 (sodium/glucose cotransporter), member 10		
sodium channel, voltage-gated, type I, beta		sorting nexin 1		
solute carrier family 2 (facilitated glucose transporter), member 3		SPARC-like 1 (hevin)		
solute carrier family 29 (nucleoside transporters), member 2		spastic paraplegia 7 (pure and complicated autosomal recessive)		
solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2		sperm specific antigen 2		
solute carrier family 7		staufen, RNA binding		

(cationic amino acid transporter, y+ system), member 5		protein, homolog 2 (Drosophila)		
solute carrier family 7 (cationic amino acid transporter, y+ system), member 7		sterile alpha motif domain containing 1		
solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 1		sterile alpha motif domain containing 11		
sorcin		sterol carrier protein 2		
splicing factor, arginine/serine-rich 18		storkhead box 2		
splicing factor, arginine/serine-rich 7, 35kDa		stromal interaction molecule 2		
stearoyl-CoA desaturase (delta-9-desaturase)		synuclein, beta		
sterol regulatory element binding transcription factor 1		TEA domain family member 2		
sterol-C4-methyl oxidase-like		tetratricopeptide repeat domain 38		
sulfiredoxin 1 homolog (S. cerevisiae)		thioredoxin interacting protein		
sulfotransferase family 4A, member 1		threonyl-tRNA synthetase-like 2		
surfeit 4		thrombospondin 1		
syndecan 4		thymocyte nuclear protein 1		
syndecan binding protein (syntenin)		transcription elongation factor A (SII), 3		
TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1		transcription elongation factor A (SII)-like 1		

thioredoxin		transient receptor potential cation channel, subfamily V, member 5		
thioredoxin-like 4A		transmembrane 7 superfamily member 2		
thioredoxin-related transmembrane protein 1		transmembrane protein 42		
thrombospondin 1		transmembrane protein 59		
thrombospondin, type I, domain containing 1		tripartite motif-containing 47		
THUMP domain containing 3		tropomyosin 1 (alpha)		
thymosin beta 4, X-linked		TSC22 domain family, member 3		
TIMP metallopeptidase inhibitor 1		tubby like protein 2		
TIMP metallopeptidase inhibitor 2		tubulin polymerization-promoting protein family member 3		
toll-like receptor 2		tubulin, alpha 1a		
toll-like receptor 4		tumor protein D52-like 1		
transformer 2 beta homolog (Drosophila)		tumor protein p53 binding protein 1		
transforming growth factor, beta 1		tweety homolog 1 (Drosophila)		
transforming growth factor, beta receptor II (70/80kDa)		tyrosinase (oculocutaneous albinism IA)		
transgelin 2		tyrosinase-related protein 1		
transgelin 3		tyrosylprotein sulfotransferase 1		
translocase of inner mitochondrial membrane 17 homolog A (yeast)		ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase)		
translocase of outer		UBX domain protein 6		

mitochondrial membrane 40 homolog (yeast)				
transmembrane protein 140		UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 1		
transmembrane protein 170B		UDP-glucose pyrophosphorylase 2		
transmembrane protein 2		unc-119 homolog (C. elegans)		
transmembrane protein 33		unconventional SNARE in the ER 1 homolog (S. cerevisiae)		
transmembrane protein 8 (five membrane-spanning domains)		vacuolar protein sorting 13 homolog A (S. cerevisiae)		
tubulin, beta 6		vacuolar protein sorting 33 homolog B (yeast)		
tumor necrosis factor (TNF superfamily, member 2)		viral DNA polymerase-transactivated protein 6		
tumor necrosis factor, alpha-induced protein 6		vitronectin		
ubiquitin carboxyl-terminal hydrolase L5		voltage-dependent anion channel 1		
ubiquitin specific peptidase 14 (tRNA-guanine transglycosylase)		WD repeat domain 45		
ubiquitin-fold modifier 1		Williams Beuren syndrome chromosome region 27		
UDP-galactose-4-epimerase		Wilms tumor 1 interacting protein		
UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 8		WW domain binding protein 1		
UDP-glucose		zinc finger CCCH-type		

dehydrogenase		containing 6		
UHRF1 binding protein 1-like		zinc finger protein 260		
uncoupling protein 2 (mitochondrial, proton carrier)		zinc finger protein 358		
UTP14, U3 small nucleolar ribonucleoprotein, homolog A (yeast)		zinc finger protein 532		
uveal autoantigen with coiled-coil domains and ankyrin repeats		zinc finger protein 64 homolog (mouse)		
valosin-containing protein		zinc finger protein 706		
vanin 1		zinc finger, MYM-type 5		
vascular endothelial growth factor A				
v-ets erythroblastosis virus E26 oncogene homolog 1 (avian)				
vinculin				
v-ral simian leukemia viral oncogene homolog B (ras related; GTP binding protein)				
WD repeat domain 1				
WD repeat domain 12				
WD repeat domain 60				
WD repeat domain 77				
wingless-type MMTV integration site family, member 7A				
WW and C2 domain containing 2				
Yip1 interacting factor homolog B (S. cerevisiae)				
zinc finger protein 642				

zinc finger, MYND-type containing 19				