

**Supplementary Table 1: List of the 316 genes regulated during hyperglycemic euisulinemic clamp in skeletal muscle.**

UGCluster	Name	Symbol	Fold Change	Cytoband
<b><u>Response to stress</u></b>				
Hs.517581	Heme oxygenase (decycling) 1	HMOX1	3.80	22q12
Hs.374950	Metallothionein 1X	MT1X	2.20	16q13
Hs.460867	Metallothionein 1B (functional)	MT1B	1.70	16q13
Hs.148778	Oxidation resistance 1	OXR1	1.60	8q23
Hs.513626	Metallothionein 1F (functional)	MT1F	1.47	16q13
Hs.534330	Metallothionein 2A	MT2A	1.45	16q13
Hs.438462	Metallothionein 1H	MT1H	1.42	16q13
Hs.523836	Glutathione S-transferase pi	GSTP1	-1.74	11q13
Hs.459952	Stannin	SNN	-1.92	16p13
<b><u>Immune response, cytokines &amp; related</u></b>				
Hs.478275	TNF (ligand) superfamily, member 10 (TRAIL)	TNFSF10	1.58	3q26
Hs.278573	CD59 antigen p18-20 (protectin)	CD59	1.49	11p13
Hs.534847	Complement component 4B, telomeric	C4A	1.47	6p21.3
Hs.535668	Immunoglobulin lambda variable 6-57	IGLV6-57	1.40	22q11.2
Hs.529846	Calcium modulating ligand	CAMLG	-1.40	5q23
Hs.193516	B-cell CLL/lymphoma 10	BCL10	-1.40	1p22
Hs.840	Indoleamine-pyrrole 2,3 dioxygenase	INDO	-1.40	8p12-p11
Hs.201083	Mal, T-cell differentiation protein 2	MAL2	-1.44	
Hs.522805	CD99 antigen-like 2	CD99L2	-1.45	Xq28
Hs.50002	Chemokine (C-C motif) ligand 19	CCL19	-1.45	9p13
Hs.350268	Interferon regulatory factor 2 binding protein 2	IRF2BP2	-1.47	1q42.3
Hs.567249	Contactin 1	CNTN1	-1.47	12q11-q12
Hs.132807	MHC class I mRNA fragment 3.8-1	3.8-1	-1.48	6p21.3
Hs.416925	Carcinoembryonic antigen-related cell adhesion molecule 19	CEACAM19	-1.49	19q13.31
Hs.89546	Selectin E (endothelial adhesion molecule 1)	SELE	-1.54	1q22-q25
Hs.436854	Family with sequence similarity 19 (chemokine (C-C motif)-like), member A5	FAM19A5	-1.59	22q13.32
Hs.372679	Fc fragment of IgG, low affinity IIIb, receptor (CD16b)	FCGR3B	-1.59	1q23
Hs.517227	Junctional adhesion molecule 2	JAM2	-1.67	21q21.2
Hs.19413	S100 calcium binding protein A12 (calgranulin C)	S100A12	-1.69	1q21
Hs.534074	Nuclear factor of activated T-cells	NFATC1	-1.71	18q23
Hs.579550	Deleted in colorectal carcinoma	DCC	-1.78	18q21.3
Hs.511748	Sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4D	SEMA4D	-1.93	9q22-q31
<b><u>Circulating active peptides</u></b>				
Hs.2561	Nerve growth factor, beta polypeptide	NGFB	-1.48	1p13.1
Hs.133379	Transforming growth factor, beta 2	TGFB2	-1.53	1q41
Hs.25590	Stanniocalcin 1	STC1	-1.56	8p21-p11.2
Hs.435215	Vascular endothelial growth factor C	VEGFC	-1.69	4q34.1-q34.3
Hs.410092	Coagulation factor II (thrombin)	F2	-1.70	11p11-q12
<b><u>Receptors</u></b>				
Hs.494538	Patched homolog (Drosophila)	PTCH	-1.41	9q22.3
Hs.23582	Tumor-associated calcium signal transducer 2	TACSTD2	-1.44	1p32-p31
Hs.437846	Smoothened homolog (Drosophila)	SMO	-1.44	7q32.3
Hs.381225	Low density lipoprotein receptor (familial hypercholesterolemia)	LDLR	-1.46	19p13.3
Hs.524458	Integrin, beta 7	ITGB7	-1.47	12q13.13
Hs.52931	Adrenergic, alpha-1A-, receptor	ADRA1A	-1.51	8p21-p11.2
Hs.408153	Taste receptor, type 2, member 49	TAS2R49	-1.52	12p13.2
Hs.126667	Endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 2	EDG2	-1.53	9q31.3
Hs.1041	Proto-oncogene tyrosine-protein kinase ROS precursor	ROS1	-1.57	6q22
Hs.293842	Transmembrane protein 71	TMEM71	-1.62	8q24.22
Hs.293917	Poliovirus receptor-related 3	PVRL3	-1.65	3q13
Hs.445000	Prostaglandin E receptor 3 (subtype EP3)	PTGER3	-1.90	1p31.2
Hs.98255	Receptor tyrosine kinase-like orphan receptor 2	ROR2	-2.28	9q22
<b><u>Signaling pathways</u></b>				
<b><u>Protein phosphatases</u></b>				
Hs.79081	Protein phosphatase 1, catalytic subunit, gamma isoform	PPP1CC	1.48	12q24.1-q24.2
Hs.512973	Protein tyrosine phosphatase-like A domain containing 1	PTPLAD1	-1.55	15q22.2
Hs.160871	Protein tyrosine phosphatase, receptor type, O	PTPRO	-1.61	12p13.3-p13.2
Hs.19281	Protein tyrosine phosphatase, non-receptor type 14	PTPN14	-1.71	1q32.2
Hs.146339	Protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform	PPP2R2A	-1.71	8p21.2
Hs.106019	Protein phosphatase 1, regulatory subunit 10	PPP1R10	-2.05	6p21.3
<b><u>Protein kinases</u></b>				
Hs.431850	Mitogen-activated protein kinase 1	MAPK1	1.51	22q11.2
Hs.466987	Protein kinase D2	PRKD2	-1.40	19q13.3
Hs.105818	Cyclin-dependent kinase-like 3	CDKL3	-1.44	5q31
Hs.291623	TAO kinase 2	TAOK2	-1.44	16p11.2
Hs.106015	Tyrosine-protein kinase HCK	DDEF1	-1.45	8q24.1-q24.2
Hs.119882	Cyclin-dependent kinase 6	CDK6	-1.61	7q21-q22

Hs.36566	LIM domain kinase 1	LIMK1	-1.65	7q11.23
Hs.468878	AP2 associated kinase 1	AAK1	-1.88	2p24.3-p14

#### **Others signaling pathways**

Hs.591761	Homer homolog 1 (Drosophila)	HOMER1	1.69	5q14.2
Hs.584744	Calcyphosine	CAPS	1.60	19p13.3
Hs.584507	FYVE, RhoGEF and PH domain containing 1 (faciogenital dysplasia)	FGD1	-1.40	Xp11.21
Hs.333274	Calneuron 1	CALN1	-1.42	7q11
Hs.429434	GRB2-associated binding protein 2	GAB2	-1.43	11q14.1
Hs.213424	Secreted frizzled-related protein 1	SFRP1	-1.44	8p12-p11.1
Hs.188614	Pleckstrin homology domain containing, family A member 5	PLEKHA5	-1.46	12p12
Hs.483784	SH3 domain and tetratricopeptide repeats 2	SH3TC2	-1.47	5q32
Hs.464985	Ras-like without CAAX 2	RIT2	-1.47	18q12.3
Hs.121593	Centaurin, alpha 1	CENTA1	-1.48	7p22.3
Hs.435811	Arrestin, beta 2	ARRB2	-1.48	17p13
Hs.471508	Insulin receptor substrate 1	IRS1	-1.51	2q36
Hs.81328	Nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	NFKBIA	-1.51	14q13
Hs.190977	Ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin)	ENPP2	-1.52	8q24.1
Hs.132121	SH3-domain GRB2-like (endophilin) interacting protein 1	SGIP1	-1.53	1p31.3
Hs.2722	Inositol 1,4,5-trisphosphate 3-kinase A	ITPKA	-1.57	15q14-q21
Hs.113912	Rap guanine nucleotide exchange factor (GEF) 2	RAPGEF2	-1.59	4q32.1
Hs.157351	GTP-binding protein PTD004	PTD004	-1.64	2q31.1
Hs.528993	RalA binding protein 1	RALBP1	-1.68	18p11.3
Hs.591099	RAB27A, member RAS oncogene family	RAB27A	-1.72	15q15-q21.1
Hs.386726	Regulator of G-protein signalling 4	RGS4	-1.72	1q23.3
Hs.567314	Phosphodiesterase 6A, cGMP-specific, rod, alpha	PDE6A	-1.74	5q31.2-q34
Hs.43505	Inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase gamma	IKBKG	-1.75	Xq28
Hs.517216	Phosphoprotein enriched in astrocytes 15	PEA15	-1.92	1q21.1
Hs.483238	Rho GTPase activating protein 29	ARHGAP29	-1.96	1p22.1

#### **Enzymes**

##### **Carbohydrate metabolism**

Hs.513490	Aldolase A, fructose-bisphosphate	ALDOA	1.62	16q22-q24
Hs.154084	Phosphorylase, glycogen; muscle (McArdle syndrome, glycogen storage disease type V)	PYGM	1.51	11q12-q13.2
Hs.590891	Phosphoglucomutase 3	PGM3	-1.40	6q14.1-q15
Hs.54941	Phosphorylase kinase, alpha 2 (liver)	PHKA2	-1.46	Xp22.2-p22.1
Hs.31431	Fructosamine-3-kinase-related protein	FN3KRP	-1.49	17q25.3
Hs.8364	Pyruvate dehydrogenase kinase, isoenzyme 4	PKD4	-2.88	7q21.3-q22.1

##### **Lipid metabolism**

Hs.234898	Acetyl-Coenzyme A carboxylase beta	ACACB	1.40	12q24.1
Hs.512217	Monoacylglycerol O-acyltransferase 3	MOGAT3	-1.43	7q22.1
Hs.105269	Sterol-C4-methyl oxidase-like	SC4MOL	-1.45	4q32-q34
Hs.111256	Arachidonate 15-lipoxygenase, second type	ALOX15B	-1.49	17p13.1
Hs.68864	Lipase, member H	LIPH	-1.56	3q27

##### **ATPase & related**

Hs.291196	ATPase, Na <sup>+</sup> /K <sup>+</sup> transporting, beta 1 polypeptide	ATP1B1	1.46	1q24
Hs.569910	ATPase, Class I, type 8B, member 1	ATP8B1	-1.40	18q21-q22

##### **Others enzymes**

Hs.334347	Creatine kinase, muscle	CKM	1.55	19q13.2-q13.3
Hs.144567	Alanine-glyoxylate aminotransferase (oxalosis I; hyperoxaluria I; glycolicaciduria; serine-pyruvate aminotransferase)	AGXT	1.45	2q36-q37
Hs.484741	Guanosine monophosphate reductase	GMPR	1.43	6p23
Hs.75372	N-acetylgalactosaminidase, alpha-	NAGA	-1.50	22q13-qter
Hs.214142	5,10-methylenetetrahydrofolate reductase (NADPH)	MTHFR	-1.73	1p36.3
Hs.135270	Collapsin response mediator protein 1	CRMP1	-1.88	4p16.1-p15
Hs.272499	Dehydrogenase/reductase (SDR family) member 2	DHRS2	-2.34	14q11.2

##### **Structural proteins & cytoskeleton**

Hs.516105	Actin, gamma 2, smooth muscle, enteric	ACTG2	1.70	2p13.1
Hs.20107	Kinesin 2	KNS2	1.46	14q32.3
Hs.13852	Nexilin (F actin binding protein)	NEXN	1.44	1p31.1
Hs.485903	Myosin binding protein C, slow type	MYBPC1	1.42	12q23.3
Hs.134602	Titin	TTN	1.41	2q31
Hs.516769	EF hand domain family, member D1	EFHD1	-1.43	2q37.1
Hs.590892	Collagen, type IX, alpha 1	COL9A1	-1.44	6q12-q14
Hs.369089	Collagen, type IV, alpha 5 (Alport syndrome)	COL4A5	-1.44	Xq22
Hs.407580	Plakophilin 4	PKP4	-1.44	2q23-q31
Hs.121824	Keratin 5b	K5B	-1.45	12q13.13
Hs.518414	Leucine-rich repeats and calponin homology (CH) domain containing 3	LRCH3	-1.46	3q29
Hs.532824	Microtubule-associated protein, RP/EB family, member 2	MAPRE2	-1.48	18q12.1
Hs.369840	Nidogen 2 (osteonidogen)	NID2	-1.48	14q21-q22
Hs.21213	Myosin VA (heavy polypeptide 12, myosin)	MYO5A	-1.52	15q21

Hs.520554	Tubulin tyrosine ligase-like family, member 2	TLL2	-1.53	6q27
Hs.503178	Spectrin, beta, non-erythrocytic 1	SPTBN1	-1.53	2p21
Hs.436035	Tubulin, alpha 6	TUBA6	-1.54	12q12-q14
Hs.431792	Growth arrest-specific 8	GAS8	-1.56	16q24.3
Hs.34780	Doublecortin; lissencephaly, X-linked (doublecortin)	DCX	-1.62	Xq22.3-q23
Hs.25640	Claudin 3	CLDN3	-1.63	7q11.23
Hs.591727	Sarcoglycan, delta (35kDa dystrophin-associated glycoprotein)	SGCD	-1.65	5q33-q34
Hs.187898	Neurofibromin 2 (bilateral acoustic neuroma)	NF2	-1.67	22q12.2
Hs.175437	Erythrocyte membrane protein band 4.1	EPB41	-1.67	1p33-p32
Hs.104925	Ectodermal-neural cortex (with BTB-like domain)	ENC1	-1.69	5q12-q13.3
Hs.567308	Myosin VB	MYO5B	-1.71	18q21
Hs.497039	Laminin, gamma 1 (formerly LAMB2)	LAMC1	-1.86	1q31
Hs.420269	Collagen, type VI, alpha 2	COL6A2	-2.14	21q22.3

### **Transporters & carriers**

Hs.584756	Fatty acid binding protein 3, muscle and heart (mammary-derived growth inhibitor)	FABP3	-1.40	1p33-p32
Hs.160550	Solute carrier family 43, member 2	SLC43A2	-1.41	17p13.3
Hs.274363	Neuroglobin	NGB	-1.41	14q24
Hs.486508	Solute carrier family 2 (facilitated glucose transporter), member 12	SLC2A12	-1.41	6q23.2
Hs.167317	Synaptosomal-associated protein, 25kDa	SNAP25	-1.44	20p12-p11.2
Hs.14894	Trans-golgi network protein 2	TGOLN2	-1.46	2p11.2
Hs.512681	Sodium channel, nonvoltage-gated 1, delta	SCNN1D	-1.54	1p36.3-p36.2
Hs.167584	Solute carrier family 2 (facilitated glucose transporter), member 2	SLC2A2	-1.55	3q26.1-q26.2
Hs.194816	Stomatin (EPB72)-like 1	STOML1	-1.56	15q24-q25
Hs.30246	Solute carrier family 19 (thiamine transporter), member 2	SLC19A2	-1.61	1q23.3
Hs.444915	Solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), member 1	SLC1A1	-1.65	9p24
Hs.508958	Syntaxin binding protein 6 (amisyn)	STXBP6	-1.76	14q12
Hs.484099	Potassium large conductance calcium-activated channel, subfamily M, beta member 1	KCNMB1	-1.81	5q34
Hs.160264	Hyperpolarization activated cyclic nucleotide-gated potassium channel 4	HCN4	-1.92	15q24-q25
Hs.204238	Lipocalin 2 (oncogene 24p3)	LCN2	-1.93	9q34

### **Transcription and DNA related proteins**

#### ***Transcription factors and transcription regulation***

Hs.507916	TSC22 domain family, member 1	TSC22D1	1.67	13q14
Hs.516176	SET and MYND domain containing 1	SMYD1	1.48	2p11.2
Hs.370666	Forkhead box O1A (rhabdomyosarcoma)	FOXO1A	1.47	13q14.1
Hs.59757	Zinc finger protein 281	ZNF281	1.45	1q32.1
Hs.590886	Retinoid X receptor, alpha	RXRA	1.44	9q34.3
Hs.57687	Four and a half LIM domains 3	FHL3	1.44	1p34
Hs.435369	Four and a half LIM domains 1	FHL1	1.44	Xq26
Hs.167700	SMAD, mothers against DPP homolog 5	SMAD5	-1.40	5q31
Hs.481852	General transcription factor IIB	GTF2B	-1.41	1p22-p21
Hs.280741	Yip1 interacting factor homolog B	YIF1B	-1.42	19q13.2
Hs.258855	Myeloid/lymphoid or mixed-lineage leukemia	MLL	-1.43	11q23
Hs.157883	Zinc finger protein 187	ZNF187	-1.47	6p21.31
Hs.202247	Orthopedia homolog (Drosophila)	OTP	-1.47	5q13.3
Hs.509964	Basic leucine zipper transcription factor, ATF-like	BATF	-1.50	14q24.3
Hs.516922	NK2 transcription factor related, locus 2 (Drosophila)	NKX2-2	-1.50	20pter-q11.23
Hs.444414	AF4/FMR2 family, member 3	AFF3	-1.51	2q11.2-q12
Hs.114246	Zinc finger protein 81 (HFZ20)	ZNF81	-1.54	Xp11.23
Hs.534460	Nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3	NFATC3	-1.55	16q22.2
Hs.435730	Iroquois homeobox protein 5	IRX5	-1.55	16q11.2-q13
Hs.546282	Retinoblastoma binding protein 8	RBBP8	-1.56	18q11.2
Hs.257970	Nuclear factor I/X (CCAAT-binding transcription factor)	NFIX	-1.60	19p13.3
Hs.1545	Caudal type homeo box transcription factor 1	CDX1	-1.61	5q31-q33
Hs.445534	Period homolog 1 (Drosophila)	PER1	-1.66	17p13.1-17p12
Hs.168586	T-cell leukemia, homeobox 2	TLX2	-1.68	2p13.1-p12
Hs.584806	Transcription elongation factor B (SIII), polypeptide 3 (110kDa, elongin A)	TCEB3	-1.73	1p36.1
Hs.184080	Zinc finger protein 138 (clone pHZ-32)	ZNF138	-1.78	7q11.21-q11.23
Hs.535297	AT rich interactive domain 5B (MRF1-like)	ARID5B	-1.79	10q21.2
Hs.15725	Immediate early response 5	IER5	-1.85	1q25.3
Hs.564295	Zinc finger protein 549	ZNF549	-1.85	19q13.43
Hs.25960	V-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian)	MYCN	-1.89	2p24.1
Hs.591091	Paired box gene 5 (B-cell lineage specific activator)	PAX5	-1.96	9p13
Hs.591337	V-myb myeloblastosis viral oncogene homolog (avian)	MYB	-2.21	6q22-q23

#### ***DNA associated proteins***

Hs.475733	Topoisomerase (DNA) II beta 180kDa	TOP2B	-1.45	3p24
Hs.128258	Proliferation-inducing protein 38	RP11-301I17.1	-1.46	13q14.11
Hs.192649	MRE11 meiotic recombination 11 homolog A (S. cerevisiae)	MRE11A	-1.47	11q21
Hs.374043	Additional sex combs like 1 (Drosophila)	ASXL1	-1.52	20q11.1
Hs.535191	Postmeiotic segregation increased 2-like 4	PMS2L4	-1.62	7q11-q22

Hs.440049	ZXD family zinc finger C	ZXDC	-1.71	3q21.2
Hs.436401	Topoisomerase (DNA) III beta	TOP3B	-1.78	22q11.22
Hs.233568	Histone 1, H2a1	HIST1H2AL	-1.88	6p22-p21.3

### **Translation**

#### ***RNA transport and processing***

Hs.478000	Muscleblind-like (Drosophila)	MBNL1	1.46	3q25
Hs.96996	Heterogeneous nuclear ribonucleoprotein A0	HNRPA0	1.42	5q31
Hs.387471	Poly(A) polymerase gamma	PAPOLG	-1.41	2p16.1
Hs.523739	Nuclear RNA export factor 1	NXF1	-1.42	11q12-q13
Hs.516075	TIA1 cytotoxic granule-associated RNA binding protein	TIA1	-1.44	2p13
Hs.591619	Nucleoporin-like protein RIP	HRB	-1.51	2q36.3
Hs.499643	Apobec-1 complementation factor	ACF	-1.55	10q11.23
Hs.190520	LSM6 homolog, U6 small nuclear RNA associated (S. cerevisiae)	LSM6	-1.61	4q31.22

#### ***Translation and post-translational modifications***

Hs.401954	Transmembrane and tetratricopeptide repeat containing 1	TMTC1	1.49	12p11.22
Hs.297304	Glycosyltransferase 8 domain containing 1	GLT8D1	1.48	3p21.1
Hs.400295	Ribosomal protein L30	RPL30	1.41	8q22
Hs.370504	Ribosomal protein S15a	RPS15A	1.40	16p
Hs.501239	Arginyltransferase 1	ATE1	-1.40	10q26.13
Hs.444389	Lysyl oxidase-like 2	LOXL2	-1.41	8p21.3-p21.2
Hs.34180	UDP-glucose ceramide glucosyltransferase-like 1	UGCGL1	-1.41	2q14.3
Hs.301898	Dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit	DPM1	-1.47	20q13.13
Hs.481860	Threonyl-tRNA synthetase	TARS	-1.44	5p13.2
Hs.477498	Eukaryotic elongation factor, selenocysteine-tRNA-specific	EEFSEC	-1.51	3q21.3
Hs.78854	Mannose-P-dolichol utilization defect 1	MPDU1	-1.65	17p13.1-p12
Hs.193226	UDP-glucose ceramide glucosyltransferase-like 2	UGCGL2	-1.67	13q32.1
Hs.592200	Mannosyl (beta-1,4-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase	MGAT3	-1.87	22q13.1
Hs.531642	Phosphatidylinositol N-acetylglucosaminyltransferase GPI1 subunit	PIGQ	-1.91	16p13.3
Hs.131431	Eukaryotic translation initiation factor 2-alpha kinase 2	EIF2AK2	-1.93	2p22-p21

### **Protein catabolism**

#### ***Ubiquitin-proteasome pathway***

Hs.591319	Ubiquitin specific protease 13 (isopeptidase T-3)	USP13	1.63	3q26.2-q26.3
Hs.584916	Ring finger protein 43	RNF43	-1.41	17q22
Hs.546407	Cullin-associated and neddylation-dissociated 1	CAND1	-1.59	12q14

#### ***Proteases and protease inhibitors***

Hs.78977	Proprotein convertase subtilisin/kexin type 1	PCSK1	-1.42	5q15-q21
Hs.591033	Matrix metalloproteinase 19	MMP19	-1.47	12q14
Hs.436564	Prolyl endopeptidase	PREP	-1.47	6q22
Hs.75285	Inter-alpha (globulin) inhibitor H2	ITIH2	-1.51	10p15
Hs.558371	Reelin	RELN	-1.53	7q22
Hs.592083	Crm, cramped-like (Drosophila)	CRAMP1L	-1.55	16p13.3
Hs.75262	Cathepsin O	CTSO	-1.57	4q31-q32
Hs.445857	Protease, serine, 12 (neurotrypsin, motopsin)	PRSS12	-1.78	4q28.1

### **Others and proteins with unknown function**

Hs.432132	Putative lymphocyte G0/G1 switch gene	G0S2	2.84	1q32.2-q41
Hs.475353	LIM and cysteine-rich domains 1	LMCD1	1.58	3p26-p24
Hs.111801	Arsenate resistance protein ARS2	ARS2	1.42	7q21
Hs.104476	Transmembrane protein 125	TMEM125	-1.40	1p34.2
Hs.104672	Downregulated in ovarian cancer 1	DOC1	-1.42	3q12.1
Hs.541894	Ankyrin repeat domain 36	ANKRD36	-1.42	2q11.2
Hs.427232	Vitamin K epoxide reductase complex, subunit 1-like 1	VKORC1L1	-1.42	7q11.21
Hs.448664	Transmembrane protein 80	TMEM80	-1.43	11p15.5
Hs.178703	Mast cell-expressed membrane protein 1	MCEMP1	-1.44	19p13.2
Hs.152913	Endomucin	EMCN	-1.44	4q24
Hs.585433	Kin of IRRE like (Drosophila)	KIRREL	-1.46	1q21-q25
Hs.167741	Butyrophilin, subfamily 3, member A3	BTN3A3	-1.47	6p21.3
Hs.298851	Male sterility domain containing 1	MLSTD1	-1.47	12p11.22
Hs.224008	Fasciculation and elongation protein zeta 1 (zygin I)	FEZ1	-1.49	11q24.2
Hs.585839	Family with sequence similarity 38, member B	FAM38B	-1.51	18p11.22
Hs.165736	WD repeat domain 73	WDR73	-1.53	15q25.2
Hs.141308	Myelin oligodendrocyte glycoprotein	MOG	-1.59	6p22.1
Hs.71040	Family with sequence similarity 32, member A	FAM32A	-1.63	19pter-p13.3
Hs.170904	Growth hormone regulated TBC protein 1	GRTP1	-1.63	13q34
Hs.497369	Neuron navigator 1	NAV1	-1.64	
Hs.91566	Transmembrane protein 115	TMEM115	-1.65	3p21.3
Hs.496459	Torsin A interacting protein 1	TOR1AIP1	-1.65	1q24.2
Hs.169222	Acrosomal vesicle protein 1	ACRV1	-1.74	11p12-q13
Hs.509780	WD repeat domain 22	WDR22	-1.75	14q23-q24.1
Hs.570737	Translocation associated membrane protein 1-like 1	TRAM1L1	-1.79	4q26
Hs.187459	Zinc finger, DHHC domain containing 14	ZDHHC14	-1.90	6q25.3
Hs.567612	Major facilitator superfamily domain containing 7	MFSD7	-2.10	4p16.3
Hs.506663	Huntingtin interacting protein E	HYPE	-2.26	12q24.1

**Hypothetical proteins and EST**

Hs.591954	Hypothetical protein LOC283130	LOC283130	2.23	11q13.1
Hs.536218	Transcribed locus		1.93	
Hs.591724	Transcribed locus		1.60	5q35.3
Hs.374257	Hypothetical protein LOC286167	LOC286167	1.59	8q24.22
Hs.586722	Transcribed locus		1.40	
Hs.460807	Chromosome 20 open reading frame 117	C20orf117	1.40	20q11.23
Hs.25422	Clone 24527 mRNA sequence		-1.40	
Hs.572260	Transcribed locus		-1.41	
Hs.194392	hypothetical protein	LOC147991	-1.41	19q13.11
Hs.160063	FLJ16124 protein	FLJ16124	-1.42	2p14
Hs.303669	Hypothetical protein MGC26694	MGC26694	-1.42	19p13.11
Hs.166551	Chromosome 5 open reading frame 3	C5orf3	-1.43	5q31-q33
Hs.82921	Chromosome 6 open reading frame 165	C6orf165	-1.43	6q15
Hs.4988	Hypothetical protein LOC151162	LOC151162	-1.44	2q21.3
Hs.352541	Chromosome 15 open reading frame 40	C15orf40	-1.45	15q25.2
Hs.119993	Transcribed locus		-1.45	
Hs.600665	Transcribed locus		-1.45	
Hs.480055	Hypothetical protein MGC10646	MGC10646	-1.45	4q21.21
Hs.317190	hypothetical protein H17		-1.45	11q24.2
Hs.600492	Transcribed locus		-1.45	
Hs.597407	Transcribed locus		-1.45	
Hs.604384	Transcribed locus		-1.46	
Hs.432401	Transcribed locus		-1.46	
Hs.26580	Transcribed locus		-1.46	
Hs.8429	Transcribed locus		-1.46	
Hs.530069	Transcribed locus		-1.46	
Hs.404323	Transcribed locus		-1.47	
Hs.192711	Hypothetical gene supported by AK055887	LOC441179	-1.47	6q27
Hs.567379	chromosome 17 open reading frame 35		-1.49	17p11.2
Hs.594218	Transcribed locus		-1.49	
Hs.545117	Transcribed locus		-1.51	
Hs.115140	Hypothetical BC331191_1	LOC163131	-1.51	19q13.2
Hs.502585	Transcribed locus]		-1.52	
Hs.6224	KIAA0895 protein	KIAA0895	-1.52	7p14.2
Hs.520785	Hypothetical protein FLJ12700	FLJ12700	-1.53	7q36.1
Hs.9003	Chromosome 16 open reading frame 58	C16orf58	-1.53	16p11.2
Hs.592376	Full-length cDNA clone CS0DC009YH03		-1.55	
Hs.61587	Transcribed locus		-1.55	
Hs.599547	Transcribed locus		-1.58	
Hs.205572	KIAA0922 protein	KIAA0922	-1.59	4q31.3
Hs.126566	Transcribed locus		-1.60	
Hs.597340	Transcribed locus		-1.60	
Hs.97714	Hypothetical protein FLJ40243	FLJ40243	-1.61	5p13.1
Hs.529860	Hypothetical gene supported by AK024177		-1.61	9q34.11
Hs.262868	Transcribed locus		-1.61	
Hs.429119	Hypothetical protein LOC285043	LOC285043	-1.62	2p23.3
Hs.481936	Hypothetical protein FLJ13231	FLJ13231	-1.63	5p13.2
Hs.229128	Transcribed locus		-1.63	
Hs.592779	Transcribed locus		-1.63	
Hs.490512	Hypothetical protein LOC155060	LOC155060	-1.65	7q36.1
Hs.597567	Full-length cDNA clone CS0DK005YO12		-1.65	
Hs.577789	Transcribed locus		-1.66	
Hs.460217	Hypothetical protein MGC35048	MGC35048	-1.66	16p12.3
Hs.48803	Transcribed locus		-1.69	
Hs.143821	Transcribed locus		-1.72	
Hs.445885	KIAA1217	KIAA1217	-1.72	10p12.1
Hs.471393	Transcribed locus		-1.76	
Hs.124627	Transcribed locus		-1.77	
Hs.134846	Hypothetical protein MGC24381	MGC24381	-1.80	16p13.3
Hs.533644	hypothetical protein FLJ32949	FLJ32949	-1.88	12q14.2
Hs.592254	Chromosome Y open reading frame 15B	CYorf15B	-1.88	Yq11.222
Hs.57870	Transcribed locus		-1.92	
Hs.390738	Hypothetical protein FLJ20366	FLJ20366	-1.96	8q23.2
Hs.37982	Transcribed locus,		-2.34	