

**Table 2 : List of the 336 genes regulated in human adipose tissue during 3 hours hyperglycemic clamp**

UGCluster	Name	Symbol	Fold Change	Cytoband
<b><u>Response to stress</u></b>				
Hs.322430	NDRG family member 4	NDRG4	1.41	16q21-q22.1
Hs.9613	Angiopoietin-like 4	ANGPTL4	-1.46	19p13.3
Hs.274363	Neuroglobin	NGB	-1.47	14q24
Hs.433213	Hypoxia-inducible protein 2	HIG2	-1.48	7q32.1
Hs.150837	Thioredoxin domain containing 5	TXNDC5	-1.52	6p24.3
Hs.523836	Glutathione S-transferase pi	GSTP1	-1.54	11q13
Hs.523012	DNA-damage-inducible transcript 4	DDIT4	-1.96	10pter-q26.12
<b><u>Immune response, cytokines &amp; related</u></b>				
Hs.478275	Tumor necrosis factor (ligand) superfamily, member 10	TNFSF10	1.41	3q26
Hs.2164	Pro-platelet basic protein (chemokine (C-X-C motif) ligand 7)	PPBP	1.41	4q12-q13
Hs.375108	CD24 molecule	CD24	1.41	6q21
Hs.534322	Major histocompatibility complex, class II, DR beta 1	HLA-DRB1	1.41	6p21.3
Hs.278391	Toll-like receptor adaptor molecule 2	TICAM2	1.40	5q23.1
Hs.579550	Deleted in colorectal carcinoma	DCC	-1.47	18q21.3
Hs.232543	Programmed cell death 4 (neoplastic transformation inhibitor)	PDCD4	-1.49	10q24
Hs.499674	Mannose-binding lectin (protein C) 2, soluble	MBL2	-1.81	10q11.2-q21
Hs.80395	Mal, T-cell differentiation protein	MAL	-1.89	2cen-q13
Hs.583348	Inhibin, beta A (activin A, activin AB alpha polypeptide)	INHBA	-2.07	7p15-p13
Hs.522572	B-lymphocyte antigen precursor	RP13-297E16.1	-2.52	Xp22.32
Hs.276925	GTP binding protein 1	GTPBP1	-2.24	22q13.1
<b><u>Circulating active peptides</u></b>				
Hs.432400	Agouti signaling protein, nonagouti homolog (mouse)	ASIP	-1.42	20q11.2-q12
Hs.160562	Insulin-like growth factor 1 (somatomedin C)	IGF1	-1.45	12q22-q23
Hs.441047	Adrenomedullin	ADM	-1.45	11p15.4
Hs.11103	Transforming growth factor, beta 1	TGFB1	-1.49	19q13.2
Hs.156979	Interleukin 17B	IL17B	-2.05	5q32-34
Hs.2561	Nerve growth factor, beta polypeptide	NGFB	-2.46	1p13.1
<b><u>Receptors</u></b>				
Hs.369592	Thyroid adenoma associated	THADA	1.46	2p21
Hs.525666	Olfactory receptor, family 4, subfamily N, member 4	OR4N4	1.42	15q11.2
Hs.52931	Adrenergic, alpha-1A-, receptor	ADRA1A	1.40	8p21-p11.2
Hs.101480	AP1 gamma subunit binding protein 1	AP1GBP1	-1.42	17q12
Hs.155048	Basal cell adhesion molecule (Lutheran blood group)	BCAM	-1.43	19q13.2
Hs.438311	Angiotensin II receptor-like 1	AGTRL1	-1.53	11q12
Hs.72550	Hyaluronan-mediated motility receptor (RHAMM)	HMMR	-1.55	5q33.2-qter
Hs.171844	Poliovirus receptor	PVR	-1.60	19q13.2
Hs.525105	SLIT and NTRK-like family, member 6	SLITRK6	-1.68	13q31.1
Hs.515061	Endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 6	EDG6	-1.76	19p13.3
Hs.109514	Ryanodine receptor 2 (cardiac)	RYR2	-1.77	1q42.1-q43
Hs.178066	Membrane-spanning 4-domains, subfamily A, member 5	MS4A5	-1.78	11q12
<b><u>Signaling pathways</u></b>				
<b><u>Protein phosphatases</u></b>				
Hs.19281	Protein tyrosine phosphatase, non-receptor type 14	PTPN14	-1.44	1q32.2
Hs.291000	Protein phosphatase 1K (PP2C domain containing)	PPM1K	-1.46	4q22.1
Hs.584790	Protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), beta isoform	PPP2R1B	-1.60	11q23.2
Hs.106019	Protein phosphatase 1, regulatory subunit 10	PPP1R10	-1.62	6p21.3
Hs.148340	Protein tyrosine phosphatase, receptor type, G	PTPRG	-1.87	3p21-p14
<b><u>Protein kinases</u></b>				
Hs.164267	Dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3	DYRK3	1.46	1q32.1
Hs.7200	NIMA (never in mitosis gene a)- related kinase 9	NEK9	-1.45	14q24.3
Hs.36566	LIM domain kinase 1	LIMK1	-1.47	7q11.23
Hs.431550	Mitogen-activated protein kinase kinase kinase kinase 4	MAP4K4	-1.49	2q11.2-q12
Hs.291623	TAO kinase 2	TAOK2	-1.63	16p11.2
Hs.468878	AP2 associated kinase 1	AAK1	-1.63	2p24.3-p14
Hs.531704	Protein kinase C, alpha	PRKCA	-1.67	17q22-q23.2
Hs.234521	Mitogen-activated protein kinase-activated protein kinase 3	MAPKAPK3	-1.73	3p21.3
Hs.133534	Kinase suppressor of ras 1	KSR1	-1.85	17q11.1
Hs.495984	Calcium/calmodulin-dependent serine protein kinase (MAGUK family)	CASK	-2.16	Xp11.4
Hs.478199	Protein kinase C, iota	PRKCI	-2.28	3q26.3
Hs.541273	V-akt murine thymoma viral oncogene homolog 2	AKT2	-2.46	19q13.1-q13.2
Hs.495731	BMX non-receptor tyrosine kinase	BMX	-2.53	Xp22.2
Hs.466743	Mitogen-activated protein kinase kinase kinase 10	MAP3K10	-3.06	19q13.2

**cAMP Pathway**

Hs.194350	Protein kinase, cAMP-dependent, catalytic, alpha	PRKACA	-1.34	19p13.1
Hs.129493	Adenylate cyclase 5	ADCY5	-1.43	3q13.2-q21
Hs.572993	2'-phosphodiesterase	2'-PDE	-1.46	3p14.3
Hs.132902	CAP, adenylate cyclase-associated protein, 2 (yeast)	CAP2	-1.47	6p22.3
Hs.486483	A kinase (PRKA) anchor protein 7	AKAP7	-1.48	6q23
Hs.170839	Phospholamban	PLN	-1.61	6q22.1

#### **Others signaling pathways**

Hs.6136	Rho GTPase activating protein 20	ARHGAP20	1.47	11q22.3-q23.1
Hs.233495	Pleckstrin homology domain containing, family A member 8	PLEKHA8	1.45	7p21-p11.2
Hs.125293	RasGEF domain family, member 1A	RASGEF1A	1.41	10q11.21
Hs.535257	Centaurin, beta 5	CENTB5	-1.41	
Hs.778	Guanylate cyclase activator 2A (guanylin)	GUCA2A	-1.41	1p35-p34
Hs.469593	LIM and senescent cell antigen-like domains 1	LIMS1	-1.42	2q12.3-q13
Hs.477142	Phosphatidic acid phosphatase type 2B	PPAP2B	-1.43	1pter-p22.1
Hs.121593	Centaurin, alpha 1	CENTA1	-1.43	7p22.3
Hs.465506	Phosphatidic acid phosphatase type 2C	PPAP2C	-1.43	19p13
Hs.531752	RAN binding protein 3	RANBP3	-1.43	19p13.3
Hs.303208	SH2 domain containing 4A	SH2D4A	-1.46	8p21.2
Hs.442344	Insulin receptor substrate 2	IRS2	-1.48	13q34
Hs.225356	CDC42 effector protein (Rho GTPase binding) 1	CDC42EP1	-1.49	22q13.1
Hs.32966	Guanylate cyclase activator 2B (uroguanylin)	GUCA2B	-1.52	1p34-p33
Hs.302435	Centaurin, gamma 1	CENTG1	-1.54	12q14.1
Hs.522378	DAB2 interacting protein	DAB2IP	-1.57	9q33.1-q33.3
Hs.50640	Suppressor of cytokine signaling 1	SOCS1	-1.60	16p13.13
Hs.1116	Pleckstrin homology domain containing, family G (with RhoGef domain) member 6	PLEKHG6	-1.78	12p13.31
Hs.189781	Pleckstrin homology domain containing, family G (with RhoGef domain) member 1	PLEKHG1	-1.82	6q25.1
Hs.515469	Vasodilator-stimulated phosphoprotein	VASP	-1.91	19q13.2-q13.3
Hs.368808	EH-domain containing 3	EHD3	-1.92	2p21
Hs.133044	Raptor	raptor	-2.10	17q25.3
Hs.435019	Neurexophilin 2	NXP2	-2.21	2q22.1
Hs.521482	Src homology 2 domain containing adaptor protein B	SHB	-2.25	9p12-p11

#### **Enzymes**

##### **Carbohydrate metabolism**

Hs.591588	Hexokinase 2	HK2	1.65	2p13
Hs.26010	Phosphofructokinase, platelet	PFKP	1.40	10p15.3-p15.2
Hs.154084	Phosphorylase, glycogen; muscle (McArdle syndrome, glycogen storage disease type V)	PYGM	-1.40	11q12-q13.2
Hs.411695	Hexokinase 3 (white cell)	HK3	-1.70	5q35.2
Hs.8364	Pyruvate dehydrogenase kinase, isozyme 4	PKD4	-2.17	7q21.3-q22.1
Hs.195471	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	PFKFB3	-2.23	10p14-p15
Hs.590891	Phosphoglucomutase 3	PGM3	-2.69	6q14.1-q15

##### **Lipid metabolism**

Hs.122038	Acyl-CoA thioesterase 6	ACOT6	1.46	14q24.3
Hs.128598	3-hydroxyisobutyryl-Coenzyme A hydrolase	HIBCH	1.41	2q32.2
Hs.303980	Cytochrome P450, family 11, subfamily A, polypeptide 1	CYP11A1	-1.45	15q23-q24
Hs.320151	1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid acyltransferase, beta)	AGPAT2	-1.49	9q34.3
Hs.50727	Hydroxysteroid (17-beta) dehydrogenase 1	HSD17B1	-1.51	17q11-q21
Hs.364941	Hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 1	HSD3B1	-1.65	1p13.1

##### **ATPase**

Hs.34114	ATPase, Na <sup>+</sup> /K <sup>+</sup> transporting, alpha 2 (+) polypeptide	ATP1A2	1.58	1q21-q23
Hs.370834	ATPase family, AAA domain containing 2	ATAD2	1.43	8q24.13
Hs.306212	ATPase, Class I, type 8B, member 3	ATP8B3	-1.90	19p13.3

##### **Others enzymes**

Hs.67201	5', 3'-nucleotidase, cytosolic	NT5C	1.48	17q25.1
Hs.524579	Lysozyme (renal amyloidosis)	LYZ	1.48	12q15
Hs.104347	2-amino adipic 6-semialdehyde dehydrogenase	AASDH	1.43	4q12
Hs.284491	Pyridoxal (pyridoxine, vitamin B6) kinase	PDXK	1.42	21q22.3
Hs.75372	N-acetylgalactosaminidase, alpha-	NAGA	-1.47	22q13-qter
Hs.500750	Heparanase 2	HPSE2	-1.49	10q23-q24
Hs.567342	Sulfotransferase family, cytosolic, 1A, phenol-preferring, member 1	SULT1A1	-1.49	16p12.1
Hs.512181	Spermidine/spermine N1-acetyl transferase-like 1	SATL1	-1.57	Xq21.1
Hs.458332	Proline-5-carboxylate reductase 1	PYCR1	-1.81	17q25.3
Hs.369762	Enolase superfamily member 1	ENOSF1	-1.88	18p11.32
Hs.431417	Arylalkylamine N-acetyltransferase	AANAT	-2.30	17q25
Hs.463466	Carbonic anhydrase X	CA10	-2.32	17q21
Hs.159525	Cell growth regulator with EF-hand domain 1	CGREF1	-2.62	2p23.3

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

Hs.520554	Tubulin tyrosine ligase-like family, member 2	TLL2	1.48	6q27
Hs.60480	Keratin associated protein 19-3	KRTAP19-3	1.45	21q22.1
Hs.407580	Plakophilin 4	PKP4	-1.42	2q23-q31
Hs.2785	Keratin 17	KRT17	-1.43	17q12-q21
Hs.418012	Collagen, type IX, alpha 2	COL9A2	-1.46	1p33-p32
Hs.497350	Plakophilin 1 (ectodermal dysplasia/skin fragility syndrome)	PKP1	-1.47	1q32
Hs.432390	Dynein, axonemal, heavy polypeptide 11	DNAH11	-1.51	7p21
Hs.534797	Catenin (cadherin-associated protein), alpha 1, 102kDa	CTNNA1	-1.57	5q31
Hs.1076	Small proline-rich protein 1B (cornifin)	SPRR1B	-1.57	1q21-q22
Hs.381181	Coiled-coil domain containing 96	CCDC96	-1.60	4p16.1
Hs.125133	Hermansky-Pudlak syndrome 6	HPS6	-1.61	10q24.32
Hs.118555	Fascin homolog 2, actin-bundling protein, retinal (Strongylocentrotus purpuratus)	FSCN2	-1.63	17q25
Hs.25640	Claudin 3	CLDN3	-1.67	7q11.23
Hs.487036	Myosin VC	MYO5C	-1.67	15q21
Hs.501928	Microtubule associated monooxygenase, calponin and LIM domain containing 2	MICAL2	-1.67	11p15.3
Hs.446867	Formin 1	FMN1	-1.69	15q13.3
Hs.34780	Doublecortin; lissencephaly, X-linked (doublecortin)	DCX	-1.70	Xq22.3-q23
Hs.499745	Myosin, heavy polypeptide 2, skeletal muscle, adult	MYH2	-1.71	17p13.1
Hs.513915	Claudin 7	CLDN7	-1.71	17p13
Hs.201805	Laminin, gamma 3	LAMC3	-1.82	9q31-q34
Hs.93534	Syntaxin binding protein 5 (tomosyn)	STXBP5	-1.99	6q24.3
Hs.368281	Microtubule-associated protein 2	MAP2	-2.02	2q34-q35
Hs.86492	Small muscle protein, X-linked	SMPX	-2.31	Xp22.1

### **Transporters & carriers**

Hs.443750	Vacuolar protein sorting 45A (yeast)	VPS45A	1.58	1q21-q22
Hs.154433	Cyclic nucleotide gated channel beta 3	CNGB3	1.46	8q21-q22
Hs.524688	Hippocalcin like 4	HPCAL4	-1.42	1p34.2
Hs.160264	Hyperpolarization activated cyclic nucleotide-gated potassium channel 4	HCN4	-1.43	15q24-q25
Hs.61635	Six transmembrane epithelial antigen of the prostate 1	STEAP1	-1.44	7q21
Hs.287827	ATP-binding cassette, sub-family B (MDR/TAP), member 4	ABCB4	-1.46	7q21.1
Hs.194816	Stomatin (EPB72)-like 1	STOML1	-1.47	15q24-q25
Hs.512681	Sodium channel, nonvoltage-gated 1, delta	SCNN1D	-1.51	1p36.3-p36.2
Hs.197116	Solute carrier family 7 (cationic amino acid transporter, y+ system), member 4	SLC7A4	-1.64	22q11.21
Hs.204238	Lipocalin 2 (oncogene 24p3)	LCN2	-1.67	9q34
Hs.14894	Trans-golgi network protein 2	TGOLN2	-1.70	2p11.2
Hs.5476	Solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 25	SLC25A25	-1.71	9q34.11
Hs.2962	S100 calcium binding protein P	S100P	-1.72	4p16
Hs.495674	Chloride channel 4	CLCN4	-1.75	Xp22.3
Hs.23388	Apolipoprotein L domain containing 1	APOLD1	-1.87	12p13.1
Hs.464184	SEC14-like 1 (S. cerevisiae)	SEC14L1	-1.92	17q25.1-17q25.2

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

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

Hs.499205	Iroquois homeobox protein 3	IRX3	1.57	16q12.2
Hs.532277	Zinc finger protein 250	ZNF250	1.43	8q24.3
Hs.547509	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1	SMARCE1	1.42	17q21.2
Hs.501023	MAX interactor 1	MXI1	1.40	10q24-q25
Hs.220971	FOS-like antigen 2	FOSL2	-1.41	2p23.3
Hs.516922	NK2 transcription factor related, locus 2 (Drosophila)	NKX2-2	-1.41	20pter-q11.23
Hs.492740	Activating transcription factor 6	ATF6	-1.41	1q22-q23
Hs.179312	Small nuclear RNA activating complex, polypeptide 1, 43kDa	SNAPC1	-1.42	14q22
Hs.12229	Kruppel-like factor 11	KLF11	-1.42	2p25
Hs.591337	V-myb myeloblastosis viral oncogene homolog (avian)	MYB	-1.43	6q22-q23
Hs.62696	Polymerase (RNA) III (DNA directed) polypeptide B	POLR3B	-1.44	12q23.3
Hs.127950	Bromodomain containing 1	BRD1	-1.50	22q13.33
Hs.440829	CCAAT/enhancer binding protein (C/EBP), delta	CEBPD	-1.52	8p11.2-p11.1
Hs.157883	Zinc finger protein 187	ZNF187	-1.52	6p21.31
Hs.509964	Basic leucine zipper transcription factor, ATF-like	BATF	-1.54	14q24.3
Hs.20879	Zinc finger protein 691	ZNF691	-1.54	1p34.2
Hs.25960	V-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian)	MYCN	-1.54	2p24.1
Hs.532286	Glucocorticoid modulatory element binding protein 1	GMEB1	-1.55	1p35.3
Hs.445534	Period homolog 1 (Drosophila)	PER1	-1.60	17p13.1-17p12
Hs.567425	Androgen-induced proliferation inhibitor	APRIN	-1.61	13q12.3
Hs.413416	Jumonji domain containing 1C	JMJD1C	-1.61	10q21.2
Hs.31746	Scratch homolog 1, zinc finger protein (Drosophila)	SCRT1	-1.66	8q24.3
Hs.371987	Nuclear factor of activated T-cells 5, tonicity-responsive	NFAT5	-1.70	16q22.1
Hs.435413	Metastasis associated 1 family, member 3	MTA3	-1.75	2p21
Hs.584806	Transcription elongation factor B (SIII), polypeptide 3 (110kDa, elongin A)	TCEB3	-1.85	1p36.1
Hs.204475	HIV-1 Tat specific factor 1	HTATSF1	-1.86	Xq26.1-q27.2

Hs.490224	CCR4-NOT transcription complex, subunit 4	CNOT4	-1.87	7q22-qter
Hs.460	Activating transcription factor 3	ATF3	-2.00	1q32.3
Hs.459311	Zinc finger protein 710	ZNF710	-2.08	15q26.1
Hs.558402	Synovial sarcoma, X breakpoint 4	SSX4	-2.14	Xp11.23
Hs.590941	Zinc finger protein 8 (clone HF.18)	ZNF8	-2.20	19q13.43
Hs.569908	Transcription factor 4	TCF4	-2.63	18q21.1

#### **DNA associated proteins**

Hs.133444	PiggyBac transposable element derived 3	PGBD3	1.43	10q11
Hs.389037	MCM3 minichromosome maintenance deficient 3 (S. cerevisiae) associated protein	MCM3AP	1.41	21q22.3
Hs.305985	Polyhomeotic-like 1 (Drosophila)	PHC1	-1.40	12p13
Hs.432948	Origin recognition complex, subunit 5-like (yeast)	ORC5L	-1.49	7q22.1
Hs.410406	SWI/SNF-related, matrix-associated actin-dependent regulator of chromatin, subfamily a, containing DEAD/H box 1	SMARCAD1	-1.50	4q22-q23
Hs.20158	Aprataxin	APTX	-1.53	9p13.3
Hs.443673	R3H domain containing 2	R3HDM2	-1.53	12q13.3
Hs.128258	Proliferation-inducing protein 38	RP11-301117.1	-1.66	13q14.11
Hs.420757	G patch domain containing 2	GPATC2	-1.71	1q41
Hs.435237	Excision repair cross-complementing rodent repair deficiency, complementation group 8	ERCC8	-1.82	5q12.1
Hs.523467	Nuclear receptor interacting protein 3	NRIP3	-1.96	11p15.3
Hs.24485	Chondroitin sulfate proteoglycan 6 (bamacan)	CSPG6	-2.53	10q25
Hs.280987	MutS homolog 3 (E. coli)	MSH3	-2.89	5q11-q12

#### **Translation**

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

Hs.96996	Heterogeneous nuclear ribonucleoprotein A0	HNRPA0	1.44	5q31
Hs.190520	LSM6 homolog, U6 small nuclear RNA associated (S. cerevisiae)	LSM6	-1.40	4q31.22
Hs.387471	Poly(A) polymerase gamma	PAPOLG	-1.41	2p16.1
Hs.482533	Ankyrin repeat domain 31	ANKRD31	-1.41	5q13.3
Hs.499643	ApoBec-1 complementation factor	ACF	-1.45	10q11.23
Hs.496279	Zinc finger CCHC-type and RNA binding motif 1	ZCRB1	-1.46	12q12
Hs.8977	Testis nuclear RNA-binding protein-like	LOC161931	-1.52	16q24.1
Hs.144936	Insulin-like growth factor 2 mRNA binding protein 1	IGF2BP1	-1.58	17q21.32
Hs.279806	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5	DDX5	-1.69	17q21
Hs.248815	WD repeat domain 4	WDR4	-2.19	21q22.3

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

Hs.462640	DnaJ (Hsp40) homolog, subfamily C, member 11	DNAJC11	-1.40	1p36.31
Hs.158304	Carbohydrate (chondroitin 6) sulfotransferase 3	CHST3	-1.40	10q22.1
Hs.237506	DnaJ (Hsp40) homolog, subfamily B, member 5	DNAJB5	-1.44	9p13.3
Hs.158497	ST3 beta-galactoside alpha-2,3-sialyltransferase 3	ST3GAL3	-1.47	1p34.1
Hs.131431	Eukaryotic translation initiation factor 2-alpha kinase 2	EIF2AK2	-1.48	2p22-p21
Hs.158688	Eukaryotic translation initiation factor 5B	EIF5B	-1.50	2p11.1-q11.1
Hs.297304	Glycosyltransferase 8 domain containing 1	GLT8D1	-1.65	3p21.1

#### **Protein catabolism**

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

Hs.251531	Proteasome (prosome, macropain) subunit, alpha type, 4	PSMA4	1.40	15q25.1
Hs.508524	Calcyclin binding protein	CACYBP	-1.44	1q24-q25
Hs.292804	Ring finger protein 34	RNF34	-1.45	12q24.31
Hs.368639	IBR domain containing 1	IBRDC1	-1.47	6q22.31
Hs.189482	Zinc finger protein 179	ZNF179	-1.47	17p11.2
Hs.422688	Ubiquitination factor E4B (UFD2 homolog, yeast)	UBE4B	-1.47	1p36.3
Hs.388364	Ring finger protein 175	RNF175	-1.49	4q31.3

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

Hs.297324	TIMP metalloproteinase inhibitor 3 (Sorsby fundus dystrophy, pseudo-inflammatory)	TIMP3	1.41	22q12.1-q13.2
Hs.75285	Inter-alpha (globulin) inhibitor H2	ITIH2	-1.41	10p15
Hs.511522	Protease, serine, 1 (trypsin 1)	PRSS1	-1.43	7q32-qter
Hs.591033	Matrix metalloproteinase 19	MMP19	-1.44	12q14
Hs.997	26 serine protease	P11	-1.47	12q13.1
Hs.133085	Carboxypeptidase A6	CPA6	-1.48	8q13.2
Hs.524498	Proliferation-associated 2G4, 38kDa	PA2G4	-1.50	12q13
Hs.55279	Serpin peptidase inhibitor, clade B (ovalbumin), member 5	SERPINF5	-1.51	18q21.3
Hs.476604	ADAM metalloproteinase with thrombospondin type 1 motif, 9	ADAMTS9	-1.62	3p14.3-p14.2
Hs.188746	ADAM metalloproteinase with thrombospondin type 1 motif, 18	ADAMTS18	-1.75	16q23
Hs.164226	Thrombospondin 1	THBS1	-1.82	15q15
Hs.191540	Vacuolar protein sorting 13B (yeast)	VPS13B	-1.82	8q22.2

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

Hs.293274	Adenomatous polyposis coli down-regulated 1	APCDD1	1.69	18p11.22
Hs.501857	RAB6 interacting protein 1	RAB6IP1	1.44	11p15.4
Hs.106650	Transmembrane protein 70	TMEM70	1.41	8q21.11
Hs.530904	Cysteine and glycine-rich protein 2	CSRP2	1.41	12q21.1

Hs.580038	Shugoshin-like 2 (S. pombe)	SGOL2	1.40	2q33.1
Hs.483512	RWD domain containing 3	RWDD3	-1.40	1p21.3
Hs.23918	Arginine vasopressin-induced 1	AVP11	-1.40	10q24.2
Hs.194698	Cyclin B2	CCNB2	-1.40	15q22.2
Hs.376071	Cyclin D2	CCND2	-1.41	12p13
Hs.388841	Zona pellucida binding protein	ZBPB	-1.42	7p14.3
Hs.187459	Zinc finger, DHHC-type containing 14	ZDHHC14	-1.46	6q25.3
Hs.478465	MAP6 domain containing 1	MAP6D1	-1.46	3q27.1
Hs.513260	DDHD domain containing 1	DDHD1	-1.47	14q21
Hs.132050	T-complex 11 (mouse) like 2	TCP11L2	-1.50	12q23.3
Hs.496459	Torsin A interacting protein 1	TOR1AIP1	-1.53	1q24.2
Hs.157078	Angel homolog 2 (Drosophila)	ANGEL2	-1.57	1q32.3
Hs.462445	B9 protein	EPPB9	-1.57	17p11.2
Hs.523710	Zinc finger, DHHC-type containing 18	ZDHHC18	-1.60	1p36.11
Hs.444673	Cisplatin resistance related protein CRR9p	CRR9	-2.16	5pter-p15.3

### Hypothetical proteins and EST

Hs.594119	Homo sapiens, clone IMAGE:3881549, mRNA		1.61	
Hs.154652	Chromosome 8 open reading frame 72	C8orf72	1.55	8q12.1
Hs.179260	Chromosome 14 open reading frame 4	C14orf4	1.52	14q24.3
Hs.473374	Transcribed locus		1.49	
Hs.596306	Transcribed locus		1.48	
Hs.606700	Transcribed locus		1.48	
Hs.519749	Hypothetical gene LOC133874	LOC133874	1.47	5q35.1
Hs.175322	Full-length cDNA clone CS0DK012Y110 of HeLa cells Cot 25-normalized of Homo sapiens (human)		1.47	
Hs.128813	Chromosome 17 open reading frame 69	C17orf69	1.47	17q21.31
Hs.570828	Transcribed locus, strongly similar to NP_056208.1 DKFZP564O0823 protein [Homo sapiens]		1.46	
Hs.471582	Transcribed locus, moderately similar to XP_526052.1 PREDICTED: similar to SP140 nuclear body protein isoform 1; nuclear body protein Sp140; lymphoid-specific SP100 homolog [Pan troglodytes]		1.45	
Hs.362702	Hypothetical protein FLJ32745	FLJ32745	1.45	2q13
Hs.596041	Transcribed locus		1.42	
Hs.370287	Clone 23688 mRNA sequence		1.42	
Hs.112680	CDNA FLJ32757 fis, clone TEST12001766		1.41	
Hs.544544	Transcribed locus		1.41	
Hs.604548	Transcribed locus		1.41	
Hs.568874	Transcribed locus, strongly similar to XP_529329.1 PREDICTED: hypothetical protein XP_529329 [Pan troglodytes]		1.40	
Hs.121347	Chromosome 10 open reading frame 82	C10orf82	1.40	10q25.3
Hs.49530	Transcribed locus, strongly similar to XP_293581.4 PREDICTED: similar to seven transmembrane helix receptor [Homo sapiens]		1.40	
Hs.562622	Transcribed locus		1.40	
Hs.288959	Hypothetical protein FLJ20920	FLJ20920	-1.40	17q21.33
Hs.545338	Transcribed locus		-1.40	
Hs.593198	Transcribed locus		-1.40	
Hs.164705	Chromosome 11 open reading frame 63	C11orf63	-1.40	11q24.1
Hs.37517	Transcribed locus, weakly similar to NP_997349.1 FLJ46489 protein [Homo sapiens]		-1.41	
Hs.58185	Full length insert cDNA clone ZD70D07		-1.42	
Hs.128757	Transcribed locus, strongly similar to NP_954587.1 hypothetical protein MGC72075 [Homo sapiens]		-1.42	
Hs.595915	Transcribed locus		-1.42	
Hs.69658	Transcribed locus		-1.43	
Hs.181297	Hypothetical protein LOC283663	LOC283663	-1.43	15q21.3
Hs.91521	Hypothetical protein DKFZP761M1511	DKFZP761M1511	-1.44	5q35.2
Hs.604793	Transcribed locus		-1.44	
Hs.520785	Hypothetical protein FLJ12700	FLJ12700	-1.44	7q36.1
Hs.355747	Hypothetical LOC388610	LOC388610	-1.44	1p36.11
Hs.156506	Similar to RIKEN cDNA A430101B06 gene	MGC13017	-1.44	5q31.1
Hs.591597	Hypothetical protein LOC200609	LOC200609	-1.45	2q37.3
Hs.597340	Transcribed locus		-1.45	
Hs.599805	Transcribed locus		-1.45	
Hs.594466	Transcribed locus		-1.46	
Hs.591027	Small trans-membrane and glycosylated protein	LOC57228	-1.46	12q13.13
Hs.432401	Transcribed locus, strongly similar to NP_821092.1 proline rich membrane anchor 1; acetylcholinesterase membrane anchor precursor PRiMA [Homo sapiens]		-1.46	
Hs.135536	Transcribed locus		-1.46	
Hs.438991	Chromosome 10 open reading frame 61	C10orf61	-1.46	10q23.33
Hs.8429	Transcribed locus		-1.47	
Hs.368296	Chromosome 11 open reading frame 49	C11orf49	-1.48	11p11.2
Hs.579269	GRB2-related adaptor protein-like	LOC400581	-1.48	17p11.2
Hs.585548	KIAA0692	KIAA0692	-1.50	12q24.33

Hs.569494	Clone 23963 mRNA sequence		-1.51	
Hs.529860	Homo sapiens, clone IMAGE:3851018, mRNA		-1.52	
Hs.448889	Hypothetical protein LOC440465	FLJ90757	-1.52	17q25.3
Hs.188825	Full length insert cDNA YQ80D07		-1.52	
Hs.525445	Chromosome 14 open reading frame 168	C14orf168	-1.53	14q24.3
Hs.526528	Transcribed locus		-1.54	
Hs.135282	Transcribed locus, strongly similar to XP_510270.1 PREDICTED: similar to C15orf16 protein [Pan troglodytes]		-1.54	
Hs.591724	Transcribed locus		-1.55	
Hs.92993	Transcribed locus		-1.55	
Hs.432566	Transcribed locus, weakly similar to XP_518535.1 PREDICTED: similar to dJ108C2.1.4 (MCM3 minichromosome maintenance deficient 3 (S. cerevisiae), variant 4) [Pan troglodytes]		-1.55	
Hs.594110	Transcribed locus		-1.56	
Hs.537948	Transcribed locus		-1.56	
Hs.597729	Transcribed locus		-1.56	
Hs.546449	Hypothetical protein MGC4268	MGC4268	-1.57	2q21
Hs.434251	KIAA0690	KIAA0690	-1.58	10q24.1
Hs.348809	Transcribed locus		-1.58	
Hs.190342	Transcribed locus		-1.58	
Hs.519855	Chromosome 6 open reading frame 201	C6orf201	-1.59	6p25.2
Hs.565253	Hypothetical protein LOC148189	LOC148189	-1.59	19q12
Hs.166551	Chromosome 5 open reading frame 3	C5orf3	-1.60	5q31-q33
Hs.30567	Homo sapiens, clone IMAGE:4346533, mRNA		-1.62	
Hs.481936	Hypothetical protein FLJ13231	FLJ13231	-1.63	5p13.2
Hs.592534	Transcribed locus		-1.64	
Hs.59115	Chromosome 8 open reading frame 16	C8orf16	-1.66	8p23.1
Hs.541810	Transcribed locus		-1.69	
Hs.591268	Hypothetical LOC553103	LOC553103	-1.78	
Hs.525826	YDD19 protein	YDD19	-1.81	13q12
Hs.348390	Chromosome 9 open reading frame 26 (NF-HEV)	C9orf26	-1.81	9p24.1
Hs.528335	Hypothetical protein FLJ25477	FLJ25477	-1.83	13q12.13
Hs.124331	Transcribed locus		-1.83	
Hs.93675	Chromosome 10 open reading frame 10	C10orf10	-1.89	10q11.21
Hs.356479	Transcribed locus, strongly similar to NP_004170.1 tryptophan hydroxylase 1; tryptophan 5-monooxygenase; tryptophan hydroxylase (tryptophan 5-monooxygenase) [Homo sapiens]		-2.17	
Hs.382151	Chromosome 20 open reading frame 160	C20orf160	-2.26	20q11.2