X3P ID	UniGene ID	Gene Title	Gene Symbol	A	M	*p-fdr*
Hs.326557.0.S1_3p_s_at	Hs.264750	ectonucleotide pyrophosphatase/phosphodiesterase 3	ENPP3	8.3	26.1	0.001
g4557322_3p_at	Hs.534305	apolipoprotein C-III	APOC3	10.9	16.8	0.003
g4758153_3p_a_at	Hs.304365	deafness. autosomal dominant 5	DFNA5	8.7	15.7	0.012
Hs.26691.1.S1_3p_at	---	---	---	8.2	13.5	0.009
Hs2.343553.2.S1_3p_at	Hs.534621	similar to RIKEN cDNA 1110002C08 gene	MGC9564	9.9	12.7	0.013
g189084_3p_at	Hs.466814	carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen)	CEACAM6	10.1	12.5	0.011
g8051574_3p_a_at	Hs.369055	ATP-binding cassette. sub-family G (WHITE). member 1	ABCG1	8.3	12.3	0.029
g4503144_3p_a_at	Hs.1355	cathepsin E	CTSE	10.3	12.2	0.048
g13477106_3p_s_at	Hs.466814	carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen)	CEACAM6	7.9	11.4	0.016
g4557320_3p_a_at	Hs.93194	apolipoprotein A-I	APOA1	12.3	10.1	0.021
Hs.43577.0.S1_3p_at	Hs.43577	ATPase. Class I. type 8B. member 2	ATP8B2	7.8	9.9	0.035
g6996012_3p_at	Hs.90708	granzyme A (granzyme 1. cytotoxic T-lymphocyte-associated serine esterase 3)	GZMA	9.3	9.1	0.006
g4505792_3p_a_at	Hs.297681	serine (or cysteine) proteinase inhibitor. clade A (alpha-1 antiproteinase. antitrypsin). member 1	SERPINA1	9.8	7.7	0.002
Hs2.343553.1.S2_3p_a_at	Hs.534621	similar to RIKEN cDNA 1110002C08 gene	MGC9564	9.6	7.7	0.020
g4504664_3p_at	Hs.75596	interleukin 2 receptor. beta	IL2RB	8.2	7.4	0.017
222938_3p_x_at	Hs.264750	ectonucleotide pyrophosphatase/phosphodiesterase 3	ENPP3	9.0	7.0	0.000
Hs.73849.1.A1_3p_at	---	---	---	8.1	6.6	0.002
Hs.21351.0.A1_3p_at	Hs.379930	MAX dimerization protein 1	MAD	8.3	6.6	0.033
g4759113_3p_at	Hs.351306	solute carrier family 16 (monocarboxylic acid transporters). member 4	SLC16A4	7.5	6.4	0.039
g181183_3p_a_at	Hs.439776	stomatin	STOM	9.3	6.3	0.010
g13241283_3p_s_at	Hs.336429	GABA(A) receptor-associated protein like 1	GABARAPL1	8.5	6.1	0.006
g13376573_3p_at	Hs.287702	hypothetical protein FLJ22595	FLJ22595	9.3	6.1	0.025

g13375570_3p_a_at	Hs.336429	GABA(A) receptor-associated protein like 1	GABARAPL1	9.4	6.1	0.002
Hs.21858.2.A1_3p_at	Hs.21858	serine (or cysteine) proteinase inhibitor. clade E (nexin. plasminogen activator inhibitor type 1). member 2	SERPINE2	7.6	5.8	0.040
g6857799_3p_at	Hs.105434	interferon stimulated gene 20kDa	ISG20	8.7	5.8	0.005
g5730074_3p_at	Hs.351808	fibrinogen-like 2	FGL2	8.9	5.7	0.036
g4557710_3p_a_at	Hs.83450	laminin. alpha 3	LAMA3	8.9	5.7	0.004
Hs.23016.0.S1_3p_at	Hs.231853	chemokine orphan receptor 1	CMKOR1	7.9	5.7	0.005
g4507016_3p_at	Hs.24030	solute carrier family 31 (copper transporters). member 2	SLC31A2	8.0	5.7	0.024
g13435385_3p_at	Hs.442527	cytochrome P450. family 3. subfamily A. polypeptide 4	CYP3A4	11.0	5.6	0.012
g6470134_3p_s_at	Hs.442527	cytochrome P450. family 3. subfamily A. polypeptide 4	CYP3A4	11.1	5.5	0.006
Hs.11169.2.S2_3p_at	Hs.11169	mitogen-inducible gene 6	MIG-6	9.3	5.5	0.033
Hs.264750.0.A1_3p_s_at	Hs.264750	ectonucleotide pyrophosphatase/phosphodiesterase 3	ENPP3	8.3	5.5	0.001
Hs.5940.0.A1_3p_a_at	Hs.5940	mucin 13. epithelial transmembrane	MUC13	8.3	5.4	0.042
Hs.150164.0.A1_3p_at	---	---	---	7.6	5.4	0.003
g623041_3p_at	Hs.97087	CD3Z antigen. zeta polypeptide (TiT3 complex)	CD3Z	7.2	5.3	0.033
g8922199_3p_s_at	Hs.128738	absent in melanoma 1-like	AIM1L	7.5	5.3	0.000
Hs2.343553.1.S1_3p_a_at	Hs.534621	similar to RIKEN cDNA 1110002C08 gene	MGC9564	8.2	5.2	0.028
g9506666_3p_at	Hs.512618	ras homolog gene family. member F (in filopodia)	RHOF	8.7	5.2	0.002
g5901909_3p_at	Hs.81743	CD160 antigen	CD160	8.0	5.1	0.033
g13787191_3p_at	Hs.37009	alkaline phosphatase. intestinal	ALPI	10.2	5.0	0.001
g6912363_3p_at	Hs.132753	F-box protein 2	FBXO2	7.2	4.9	0.021
g13787191_3p_x_at	Hs.37009	alkaline phosphatase. intestinal	ALPI	10.2	4.9	0.001
g4501944_3p_at	Hs.441047	adrenomedullin	ADM	8.0	4.9	0.024
g5174773_3p_x_at	Hs.1247	apolipoprotein A-IV	APOA4	13.0	4.9	0.002
g5174550_3p_at	Hs.194777	meprin A. beta	MEP1B	11.9	4.8	0.011
Hs.326779.0.A1_3p_s_at	---	---	---	10.2	4.7	0.016
g4557544_3p_a_at	Hs.1408	endothelin 3	EDN3	9.6	4.7	0.014
g12056470_3p_at	Hs.194691	retinoic acid induced 3	RAI3	8.9	4.6	0.012
Hs.21364.0.A1_3p_at	---	---	---	7.3	4.5	0.042

g4759111_3p_s_at	Hs.386678	solute carrier family 16 (monocarboxylic acid transporters). member 3	SLC16A3	8.3	4.5	0.032
g7705707_3p_at	Hs.113019	fls485	LOC51066	8.0	4.4	0.041
g4557358_3p_at	Hs.513489	bradykinin receptor B2	BDKRB2	7.6	4.4	0.005
g4758379_3p_a_at	Hs.306834	FK506 binding protein 1B. 12.6 kDa	FKBP1B	9.8	4.4	0.033
g510702_3p_at	Hs.436983	laminin. beta 3	LAMB3	8.5	4.4	0.005
220289_3p_s_at	Hs.128738	absent in melanoma 1-like	AIM1L	7.6	4.4	0.000
g12862475_3p_at	Hs.76507	lipopolysaccharide-induced TNF factor	LITAF	8.9	4.4	0.037
g186929_3p_a_at	Hs.232432	lysosomal-associated membrane protein 2	LAMP2	8.4	4.4	0.031
g6857799_3p_s_at	Hs.105434	interferon stimulated gene 20kDa	ISG20	9.3	4.3	0.002
g5478215_3p_x_at	---	major histocompatibility complex. class II. DR beta 1	HLA-DRB1	10.6	4.3	0.040
g4758899_3p_a_at	Hs.195471	6-phosphofructo-2-kinase/fructose-2.6-biphosphatase 3	PFKFB3	9.4	4.3	0.022
g7705770_3p_at	Hs.19385	abhydrolase domain containing 5	ABHD5	7.8	4.3	0.016
g12061050_3p_a_at	Hs.110571	growth arrest and DNA-damage-inducible. beta	GADD45B	8.2	4.3	0.008
Hs.279930.1.S1_3p_x_at	---	major histocompatibility complex. class II. DR beta 1	HLA-DRB1	10.0	4.3	0.041
g12803628_3p_at	Hs.7644	histone 1. H1c	HIST1H1C	6.4	4.3	0.021
Hs.280892.0.S1_3p_at	Hs.280892	Hypothetical gene supported by AK026416	---	9.4	4.2	0.017
g11386202_3p_a_at	Hs.370771	cyclin-dependent kinase inhibitor 1A (p21. Cip1)	CDKN1A	10.7	4.2	0.006
Hs.110341.0.A2_3p_at	Hs.212787	KIAA0303 protein	KIAA0303	6.4	4.1	0.032
g5174773_3p_at	Hs.1247	apolipoprotein A-IV	APOA4	13.2	4.1	0.002
g8393364_3p_at	Hs.212172	beta-carotene 15.15'-monooxygenase 1	BCMO1	7.0	4.1	0.028
Hs.167529.3.S1_3p_a_at	Hs.418127	cytochrome P450. family 2. subfamily C. polypeptide 9	CYP2C9	10.5	4.1	0.024
g4507450_3p_at	Hs.350470	trefoil factor 1 (breast cancer. estrogen-inducible sequence expressed in)	TFF1	8.8	4.1	0.034
g8051580_3p_a_at	Hs.5057	carboxypeptidase D	CPD	7.7	4.0	0.031
Hs.44021.0.S1_3p_at	Hs.386140	Bcl2 modifying factor	BMF	8.0	4.0	0.005
Hs.119663.0.S1_3p_a_at	Hs.278573	CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5. EJ16. EJ30. EL32 and G344)	CD59	8.4	4.0	0.044

g11545806_3p_at	Hs.375023	cell death-inducing DFFA-like effector c	CIDEC	11.1	4.0	0.024
Hs.17998.0.S1_3p_at	---	---	---	9.2	4.0	0.044
g4504436_3p_at	Hs.202833	heme oxygenase (decycling) 1	HMOX1	9.9	4.0	0.012
g4758683_3p_at	Hs.481028	lecithin retinol acyltransferase (phosphatidylcholine--retinol O-acyltransferase)	LRAT	5.1	3.9	0.011
Hs.184367.0.S2_3p_at	Hs.534502	HSPC047 protein /// RAS p21 protein activator 4	HSPC047 /// RASA4	7.4	3.9	0.044
g8923525_3p_x_at	Hs.272805	HRAS-like suppressor 2	HRASLS2	11.0	3.9	0.016
220017_3p_x_at	Hs.418127	cytochrome P450. family 2. subfamily C. polypeptide 9	CYP2C9	10.8	3.9	0.046
g8923121_3p_s_at	Hs.4205	protocadherin LKC	PC-LKC	9.9	3.9	0.005
213716_3p_s_at	Hs.95655	secreted and transmembrane 1	SECTM1	8.9	3.8	0.003
g181569_3p_a_at	Hs.44926	dipeptidylpeptidase 4 (CD26. adenosine deaminase complexing protein 2)	DPP4	9.5	3.8	0.014
g8923525_3p_at	Hs.272805	HRAS-like suppressor 2	HRASLS2	11.0	3.8	0.018
Hs.84063.0.S1_3p_at	Hs.84063	BCL2-like 11 (apoptosis facilitator)	BCL2L11	7.6	3.8	0.033
Hs.271819.0.S1_3p_at	Hs.271819	mucin 17	MUC17	10.8	3.8	0.032
214421_3p_x_at	Hs.418127	cytochrome P450. family 2. subfamily C. polypeptide 9	CYP2C9	10.0	3.8	0.043
g5921993_3p_at	Hs.560	apolipoprotein B mRNA editing enzyme. catalytic polypeptide 1	APOBEC1	10.9	3.8	0.024
g4827007_3p_at	Hs.489180	solute carrier family 15 (oligopeptide transporter). member 1	SLC15A1	10.9	3.7	0.009
216025_3p_x_at	---	---	---	10.5	3.7	0.038
g11545786_3p_a_at	Hs.443906	egl nine homolog 3 (C. elegans)	EGLN3	7.5	3.7	0.018
g188469_3p_at	Hs.446471	CD74 antigen (invariant polypeptide of major histocompatibility complex. class II antigen-associated)	CD74	11.3	3.7	0.023
g8922813_3p_at	Hs.120946	hypothetical protein FLJ11000	FLJ11000	8.0	3.6	0.013
g9845492_3p_s_at	Hs.458453	gamma-glutamyltransferase-like 4 /// gamma-glutamyltransferase 1 /// gamma-glutamyltransferase-like activity 4	GGTL4 /// GGT1 /// GGTLA4	7.2	3.6	0.024
212221_3p_x_at	Hs.522169	iduronate 2-sulfatase (Hunter syndrome)	IDS	9.4	3.6	0.047
g13259502_3p_at	Hs.427055	nuclear receptor subfamily 0. group B. member 2	NR0B2	9.8	3.6	0.006
Hs.167529.2.S1_3p_x_at	---	---	---	11.5	3.6	0.034
g4506324_3p_at	Hs.198288	protein tyrosine phosphatase. receptor type. R	PTPRR	7.1	3.6	0.010

g306748_3p_s_at	Hs.458453	gamma-glutamyltransferase-like 4 /// gamma-glutamyltransferase 1 /// gamma-glutamyltransferase-like activity 4	GGTL4 /// GGT1 /// GGTLA4	7.3	3.6	0.039
g7657042_3p_a_at	Hs.282326	Down syndrome critical region gene 1	DSCR1	8.6	3.6	0.030
208306_3p_x_at	Hs.520049	Major histocompatibility complex. class II. DR beta 4	HLA-DRB3	11.0	3.6	0.041
Hs.133083.0.S1_3p_at	Hs.405755	dihydrodiol dehydrogenase (dimeric)	DHDH	9.2	3.5	0.042
Hs.13377.0.S1_3p_at	Hs.464526	abhydrolase domain containing 3	ABHD3	10.3	3.5	0.029
g13477232_3p_at	Hs.389311	hypothetical protein MGC13057	MGC13057	10.7	3.5	0.024
g13699817_3p_x_at	Hs.418127	cytochrome P450. family 2. subfamily C. polypeptide 9	CYP2C9	11.9	3.5	0.031
g4507530_3p_at	Hs.29499	toll-like receptor 3	TLR3	8.2	3.5	0.013
g4503722_3p_a_at	Hs.8302	four and a half LIM domains 2	FHL2	9.7	3.5	0.039
g4507538_3p_at	Hs.184194	transmembrane 4 superfamily member 5	TM4SF5	11.5	3.5	0.008
g188469_3p_x_at	Hs.446471	CD74 antigen (invariant polypeptide of major histocompatibility complex. class II antigen-associated)	CD74	11.4	3.4	0.024
Hs.2056.1.S1_3p_s_at	Hs.124112	UDP glycosyltransferase 1 family. polypeptide A3 /// UDP glycosyltransferase 1 family. polypeptide A6 /// UDP glycosyltransferase 1 family. polypeptide A1 /// UDP glycosyltransferase 1 family. polypeptide A10 /// UDP glycosyltransferase 1 family. polypeptide A7 /// UDP glycosyltransferase 1 family. polypeptide A5 /// UDP glycosyltransferase 1 family. polypeptide A8 /// UDP glycosyltransferase 1 family. polypeptide A9 /// UDP glycosyltransferase 1 family. polypeptide A4	UGT1A3 /// UGT1A6 /// UGT1A1 /// UGT1A10 /// UGT1A7 /// UGT1A5 /// UGT1A8 /// UGT1A9 /// UGT1A4	10.9	3.4	0.036
Hs.289098.0.S1_3p_x_at	Hs.458453	gamma-glutamyltransferase-like 4 /// gamma-glutamyltransferase 1 /// gamma-glutamyltransferase-like activity 4	GGTL4 /// GGT1 /// GGTLA4	8.5	3.4	0.034
g8051633_3p_at	Hs.17466	retinoic acid receptor responder (tazarotene induced) 3	RARRES3	9.8	3.4	0.031
g13699817_3p_a_at	Hs.418127	cytochrome P450. family 2. subfamily C. polypeptide 9	CYP2C9	11.5	3.4	0.033

g10880125_3p_a_at	Hs.57922	X-prolyl aminopeptidase (aminopeptidase P) 2. membrane-bound	XPNPEP2	11.5	3.4	0.039
g12240160_3p_a_at	Hs.49753	uveal autoantigen with coiled-coil domains and ankyrin repeats	UACA	8.0	3.4	0.039
g4502404_3p_x_at	Hs.512682	carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein)	CEACAM1	8.2	3.4	0.009
Hs.95898.0.S1_3p_at	---	---	---	8.6	3.4	0.005
g13376256_3p_a_at	Hs.31297	cytochrome b reductase 1	CYBRD1	9.9	3.3	0.014
Hs.167529.2.S1_3p_a_at	Hs.418127	cytochrome P450. family 2. subfamily C. polypeptide 9	CYP2C9	11.5	3.3	0.035
g13699814_3p_s_at	Hs.1360	cytochrome P450. family 2. subfamily B. polypeptide 6	CYP2B6	9.9	3.3	0.018
g5032096_3p_at	Hs.388375	solute carrier family 6 (neurotransmitter transporter. creatine). member 8	SLC6A8	9.9	3.3	0.032
Hs.83883.0.S2_3p_at	Hs.83883	transmembrane. prostate androgen induced RNA	TMEPAI	7.3	3.3	0.020
g9961350_3p_at	Hs.361463	coagulation factor X	F10	8.4	3.3	0.025
Hs.167529.1.S1_3p_a_at	Hs.418127	cytochrome P450. family 2. subfamily C. polypeptide 9	CYP2C9	11.5	3.3	0.033
Hs.20196.0.S2_3p_at	Hs.20196	adenylate cyclase 9	ADCY9	9.1	3.3	0.045
g8922531_3p_at	Hs.23025	hypothetical protein FLJ10579	FLJ10579	9.5	3.3	0.010
4855867C_3p_at	Hs.234642	aquaporin 3	AQP3	12.2	3.3	0.039
g6006024_3p_at	Hs.422215	membrane protein. palmitoylated 1. 55kDa	MPP1	9.6	3.3	0.033
Hs.2014.2.S1_3p_a_at	Hs.2014	T cell receptor delta diversity 3 /// T cell receptor delta locus	TRDD3 /// TRD@	7.5	3.3	0.039
Hs.234234.0.S2_3p_at	Hs.315235	aldolase B. fructose-bisphosphate	ALDOB	10.8	3.2	0.046
g4502152_3p_a_at	Hs.280226	apolipoprotein B (including Ag(x) antigen)	APOB	12.8	3.2	0.021
Hs.69388.1.S1_3p_at	Hs.69388	chromosome 6 open reading frame 145	C6orf145	10.0	3.2	0.006
g4507728_3p_at	Hs.512712	tubulin. beta polypeptide	TUBB	9.8	3.1	0.023
g4501900_3p_at	Hs.334707	aminoacylase 1	ACY1	10.1	3.1	0.014
g12082808_3p_a_at	Hs.308638	cytochrome P450. family 3. subfamily A. polypeptide 7	CYP3A7	5.9	3.1	0.016
Hs.16732.0.A1_3p_at	---	---	---	6.2	3.1	0.044
Hs.285976.2.S1_3p_a_at	Hs.285976	LAG1 longevity assurance homolog 2 (S. cerevisiae)	LASS2	10.8	3.1	0.006
Hs.191034.0.A1_3p_at	---	---	---	9.8	3.1	0.039
g10947055_3p_a_at	Hs.440478	ankyrin 3. node of Ranvier (ankyrin G)	ANK3	10.9	3.1	0.049

Hs.16950.0.S1_3p_at	Hs.517761	KIAA0342 gene product	KIAA0342	8.0	3.1	0.033
Hs.30213.0.S1_3p_a_at	Hs.30213	ceroid-lipofuscinosis. neuronal 5	CLN5	7.9	3.1	0.029
g4885066_3p_s_at	Hs.179735	ras homolog gene family. member C	RHOC	10.9	3.1	0.021
g12803250_3p_at	Hs.90753	HIV-1 Tat interactive protein 2. 30kDa	HTATIP2	11.3	3.1	0.018
g4504956_3p_at	Hs.232432	lysosomal-associated membrane protein 2	LAMP2	8.5	3.1	0.004
g13376165_3p_at	Hs.156652	hypothetical protein FLJ22800	FLJ22800	12.2	3.1	0.050
g10835152_3p_x_at	Hs.528402	interleukin 15	IL15	6.3	3.0	0.040
Hs.91109.0.A1_3p_at	Hs.91109	hypothetical protein LOC222171	LOC222171	8.5	3.0	0.043
g4502404_3p_a_at	Hs.512682	carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein)	CEACAM1	9.3	3.0	0.005
Hs.264915.0.S2_3p_at	---	---	---	8.8	3.0	0.042
g13375833_3p_at	Hs.434247	hypothetical protein FLJ23186	FLJ23186	6.0	3.0	0.032
g179723_3p_at	Hs.1285	complement component 8. gamma polypeptide	C8G	7.7	3.0	0.013
g7706171_3p_at	Hs.159651	tumor necrosis factor receptor superfamily. member 21	TNFRSF21	9.2	3.0	0.029
g11225608_3p_a_at	Hs.178098	angiotensin I converting enzyme (peptidyl-dipeptidase A) 2	ACE2	12.3	3.0	0.012
g7669480_3p_at	Hs.60389	BCL2/adenovirus E1B 19kDa interacting protein 3	BNIP3	7.7	3.0	0.038
g4759051_3p_at	Hs.510225	ribosomal protein S6 kinase. 90kDa. polypeptide 5	RPS6KA5	5.9	3.0	0.037
Hs2.337588.1.S1_3p_a_at	Hs.337588	liver-expressed antimicrobial peptide 2	LEAP-2	8.8	3.0	0.021
g4507144_3p_a_at	Hs.267812	sorting nexin 4	SNX4	7.7	3.0	0.024
g5442445_3p_a_at	Hs.28988	glutaredoxin (thioltransferase)	GLRX	8.7	3.0	0.042
Hs.104114.0.S1_3p_s_at	Hs.493275	tripartite motif-containing 31	TRIM31	8.3	3.0	0.024
g9790904_3p_at	Hs.80409	growth arrest and DNA-damage-inducible. alpha	GADD45A	9.6	2.9	0.023
Hs.296259.0.S1_3p_at	Hs.440967	paraoxonase 3	PON3	7.8	2.9	0.024
g4501850_3p_a_at	Hs.437420	amiloride binding protein 1 (amine oxidase (copper-containing))	ABP1	10.4	2.9	0.036
g4507054_3p_a_at	Hs.194693	solute carrier family 7 (cationic amino acid transporter. y+ system). member 7	SLC7A7	11.7	2.9	0.009
g13376180_3p_at	Hs.163079	tubulin. alpha-like 3	TUBAL3	9.6	2.9	0.037
209728_3p_at	Hs.534337	major histocompatibility complex. class II. DR beta 4	HLA-DRB4	8.2	2.9	0.042
Hs.310525.0.S1_3p_at	---	---	---	7.0	2.9	0.016

Hs.264750.0.A1_3p_a_at	Hs.264750	ectonucleotide pyrophosphatase/phosphodiesterase 3	ENPP3	6.1	2.9	0.019
Hs.12942.0.S2_3p_at	Hs.12942	SEC22 vesicle trafficking protein-like 3 (S. cerevisiae)	SEC22L3	10.3	2.9	0.032
g13569890_3p_s_at	Hs.133988	Hypothetical gene supported by BC012394; BC053611	---	9.4	2.9	0.046
Hs.5672.0.S2_3p_at	Hs.5672	golgi membrane protein SB140	SMAP-5	9.7	2.9	0.021
g5032094_3p_at	Hs.83974	solute carrier organic anion transporter family. member 2A1	SLCO2A1	7.0	2.8	0.009
g5453735_3p_a_at	Hs.134859	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	MAF	8.4	2.8	0.037
Hs.77522.1.S1_3p_a_at	Hs.351279	major histocompatibility complex. class II. DM alpha	HLA-DMA	9.9	2.8	0.048
Hs.90291.1.S1_3p_a_at	Hs.439726	laminin. beta 2 (laminin S)	LAMB2	6.5	2.8	0.049
g4503228_3p_s_at	Hs.442527	cytochrome P450. family 3. subfamily A. polypeptide 4	CYP3A4	12.6	2.8	0.015
Hs.95835.0.A1_3p_at	Hs.95835	OCIA domain containing 2	OCIAD2	9.3	2.8	0.026
Hs.184598.0.S1_3p_at	Hs.335798	rhophilin. Rho GTPase binding protein 2	RHPN2	9.8	2.8	0.014
g5453735_3p_at	Hs.134859	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	MAF	10.6	2.8	0.039
g885925_3p_at	---	NADH dehydrogenase 5	MTND5	12.2	2.8	0.021
g5729841_3p_at	Hs.268849	glyoxalase I	GLO1	11.8	2.8	0.012
Hs.108169.0.S1_3p_at	Hs.370774	ankyrin repeat and BTB (POZ) domain containing 2	ABTB2	8.8	2.7	0.036
Hs.26216.0.S1_3p_at	---	---	---	10.8	2.7	0.029
Hs.267566.0.S1_3p_a_at	Hs.267566	chromosome 14 open reading frame 58	C14orf58	8.6	2.7	0.015
g9961350_3p_x_at	Hs.361463	coagulation factor X	F10	8.5	2.7	0.018
g2460168_3p_at	Hs.437606	HMG-box transcription factor 1	HBP1	9.3	2.7	0.044
g8922761_3p_at	Hs.502773	membrane-type 1 matrix metalloproteinase cytoplasmic tail binding protein-1	MTCBP-1	10.5	2.7	0.023
g4507030_3p_at	Hs.1964	solute carrier family 5 (sodium/glucose cotransporter). member 1	SLC5A1	11.1	2.7	0.047
g4503366_3p_at	Hs.44926	dipeptidylpeptidase 4 (CD26. adenosine deaminase complexing protein 2)	DPP4	11.5	2.7	0.048
g5031908_3p_at	Hs.179704	meprin A. alpha (PABA peptide hydrolase)	MEP1A	11.9	2.7	0.040

g13376444_3p_x_at	Hs.390817	myosin XVB. pseudogene	MYO15B	9.3	2.7	0.037
Hs.29002.0.S2_3p_at	Hs.412318	KIAA1706 protein	KIAA1706	8.6	2.7	0.037
g13027587_3p_at	Hs.28368	low density lipoprotein receptor-related protein 10	LRP10	10.4	2.7	0.022
g2645728_3p_a_at	Hs.35052	testis enhanced gene transcript (BAX inhibitor 1)	TEGT	11.4	2.7	0.004
g5174516_3p_at	Hs.370849	SMAD. mothers against DPP homolog 7 (Drosophila)	SMAD7	6.4	2.6	0.042
Hs.163323.0.A1_3p_at	Hs.127748	Solute carrier family 6 (neurotransmitter transporter). member 19	SLC6A19	9.3	2.6	0.008
g5901963_3p_x_at	Hs.252351	HERV-H LTR-associating 2	HHLA2	12.3	2.6	0.045
g12655216_3p_a_at	Hs.502773	membrane-type 1 matrix metalloproteinase cytoplasmic tail binding protein-1	MTCBP-1	10.7	2.6	0.026
Hs.82240.0.S3_3p_at	Hs.82240	syntaxin 3A	STX3A	9.7	2.6	0.014
Hs.121849.0.S1_3p_a_at	Hs.356061	microtubule-associated protein 1 light chain 3 beta	MAP1LC3B	7.9	2.6	0.040
g12803984_3p_x_at	Hs.130853	histone 1. H2bd	HIST1H2BD	8.3	2.6	0.047
g4504024_3p_at	Hs.28988	glutaredoxin (thioltransferase)	GLRX	11.9	2.6	0.029
Hs.234234.2.A1_3p_a_at	Hs.315235	Aldolase B. fructose-bisphosphate	ALDOB	8.6	2.6	0.044
g9295326_3p_at	Hs.79025	SNF-1 related kinase	SNRK	9.2	2.6	0.004
g7662019_3p_at	Hs.82426	KIAA0247	KIAA0247	11.0	2.6	0.008
Hs.108530.1.S1_3p_a_at	Hs.108530	transmembrane protein 30A	TMEM30A	6.0	2.6	0.033
g12240160_3p_s_at	Hs.49753	uveal autoantigen with coiled-coil domains and ankyrin repeats	UACA	9.6	2.6	0.021
g4504106_3p_x_at	Hs.433951	glutathione peroxidase 4 (phospholipid hydroperoxidase)	GPX4	10.5	2.6	0.008
Hs.8136.0.S2_3p_at	Hs.8136	endothelial PAS domain protein 1	EPAS1	10.6	2.6	0.021
Hs.20726.0.A1_3p_at	---	---	---	7.5	2.6	0.018
Hs.26860.0.S1_3p_at	Hs.369679	progestin and adipoQ receptor family member III	PAQR3	8.2	2.6	0.038
g12313878_3p_a_at	Hs.165619	mucin and cadherin-like	MUCDHL	10.6	2.6	0.021
Hs.24359.0.S1_3p_at	Hs.24359	Transcribed locus. weakly similar to XP_375099.1 hypothetical protein LOC283585 [Homo sapiens]	---	10.5	2.6	0.004
g13325115_3p_a_at	Hs.279518	amyloid beta (A4) precursor-like protein 2	APLP2	9.9	2.5	0.009
Hs.167835.3.S1_3p_a_at	Hs.379991	acyl-Coenzyme A oxidase 1. palmitoyl	ACOX1	9.6	2.5	0.034
g8923197_3p_at	Hs.131776	pyroglutamyl-peptidase I	PGPEP1	8.0	2.5	0.033
Hs.266662.0.S1_3p_at	Hs.129208	death-associated protein kinase 2	DAPK2	8.0	2.5	0.030

g13537296_3p_s_at	Hs.334305	diacylglycerol O-acyltransferase homolog 2 (mouse)	DGAT2	7.7	2.5	0.007
g11055999_3p_at	Hs.521443	PDZ and LIM domain 2 (mystique)	PDLIM2	9.2	2.5	0.038
g4758087_3p_at	Hs.17958	galactose-3-O-sulfotransferase 1	GAL3ST1	8.7	2.5	0.021
211843_3p_x_at	Hs.308638	cytochrome P450. family 3. subfamily A. polypeptide 7	CYP3A7	9.4	2.5	0.012
g4758867_3p_at	Hs.104772	procollagen-proline. 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase). alpha polypeptide II	P4HA2	8.2	2.5	0.031
Hs.18878.0.A1_3p_a_at	Hs.443906	egl nine homolog 3 (C. elegans)	EGLN3	7.7	2.5	0.010
Hs.224630.0.A1_3p_at	Hs.224630	hypothetical protein FLJ33318	FLJ33318	8.7	2.5	0.006
g5360207_3p_s_at	Hs.522169	iduronate 2-sulfatase (Hunter syndrome)	IDS	7.0	2.5	0.009
g306441_3p_a_at	Hs.110	solute carrier family 3 (cystine. dibasic and neutral amino acid transporters. activator of cystine. dibasic and neutral amino acid transport). member 1	SLC3A1	11.6	2.5	0.008
Hs.50732.0.S1_3p_at	Hs.50732	protein kinase. AMP-activated. beta 2 non-catalytic subunit	PRKAB2	5.8	2.5	0.038
g1079575_3p_s_at	Hs.25363	presenilin 2 (Alzheimer disease 4)	PSEN2	9.0	2.5	0.022
Hs.75124.0.S2_3p_at	Hs.112906	cerebellar degeneration-related protein 2. 62kDa	CDR2	10.0	2.5	0.039
g11967982_3p_a_at	Hs.57988	rhomboid family 1 (Drosophila)	RHBDF1	8.2	2.5	0.005
Hs.9834.0.A1_3p_at	Hs.388715	hypothetical protein LOC285733	LOC285733	7.7	2.5	0.014
Hs.79299.0.S1_3p_at	Hs.79299	lipoma HMGIC fusion partner-like 2	LHFPL2	9.7	2.4	0.037
g4507574_3p_a_at	Hs.159	tumor necrosis factor receptor superfamily. member 1A	TNFRSF1A	10.7	2.4	0.006
Hs.232604.0.S1_3p_at	Hs.232604	Hypothetical gene supported by AK026328	---	10.4	2.4	0.008
Hs.287995.0.S1_3p_s_at	Hs.75626	CD58 antigen. (lymphocyte function-associated antigen 3)	CD58	8.8	2.4	0.014
g10952525_3p_a_at	Hs.512618	ras homolog gene family. member F (in filopodia)	RHOF	7.1	2.4	0.009
g12313880_3p_at	Hs.165619	mucin and cadherin-like	MUCDHL	11.0	2.4	0.014
Hs.148367.0.A1_3p_at	Hs.127748	Solute carrier family 6 (neurotransmitter transporter). member 19	SLC6A19	10.0	2.4	0.029
Hs.9788.0.S1_3p_a_at	Hs.9788	Nedd4 family interacting protein 1	NDFIP1	8.3	2.4	0.026
Hs.79402.1.A1_3p_at	Hs.279832	polymerase (RNA) II (DNA directed) polypeptide C. 33kDa	POLR2C	10.3	2.4	0.011
Hs.127748.0.A1_3p_at	---	---	---	9.0	2.4	0.036
g13376867_3p_x_at	Hs.335355	chromosome 6 open reading frame 29	C6orf29	9.8	2.4	0.045

g13129033_3p_at	---	hypothetical protein MGC5395	MGC5395	7.5	2.4	0.029
Hs.15951.1.A1_3p_a_at	Hs.15951	proline-rich acidic protein 1	PRAP1	9.5	2.4	0.021
g881502_3p_a_at	Hs.389536	sulfotransferase family. cytosolic. 1A. phenol-preferring. member 2 /// sulfotransferase family. cytosolic. 1A. phenol-preferring. member 1	SULT1A2 /// SULT1A1	10.0	2.4	0.028
g9257247_3p_at	Hs.6441	tissue inhibitor of metalloproteinase 2	TIMP2	7.9	2.4	0.040
g4507302_3p_a_at	Hs.389536	sulfotransferase family. cytosolic. 1A. phenol-preferring. member 2 /// sulfotransferase family. cytosolic. 1A. phenol-preferring. member 1	SULT1A2 /// SULT1A1	9.9	2.4	0.027
g9910497_3p_a_at	Hs.83883	transmembrane. prostate androgen induced RNA	TMEPAI	6.7	2.4	0.015
Hs.25220.1.S1_3p_a_at	Hs.25220	like-glycosyltransferase	LARGE	8.3	2.4	0.002
206514_3p_s_at	Hs.106242	cytochrome P450. family 4. subfamily F. polypeptide 3 /// cytochrome P450. family 4. subfamily F. polypeptide 2	CYP4F3 /// CYP4F2	7.5	2.4	0.018
g4504106_3p_at	Hs.433951	glutathione peroxidase 4 (phospholipid hydroperoxidase)	GPX4	10.7	2.4	0.009
Hs.173484.0.S2_3p_s_at	Hs.173484	leucine rich repeat containing 8	LRRC8	9.9	2.4	0.028
Hs.301723.0.S1_3p_x_at	Hs.433297	Chromosome 10 open reading frame 75	C10orf75	7.7	2.4	0.024
g13383475_3p_at	Hs.182454	NEDD8 ultimate buster-1	NYREN18	9.9	2.4	0.048
Hs.149429.0.A1_3p_at	Hs.1964	solute carrier family 5 (sodium/glucose cotransporter). member 1	SLC5A1	11.2	2.3	0.047
Hs.283378.0.S1_3p_at	Hs.283378	hypothetical protein LOC253981	LOC253981	10.2	2.3	0.027
Hs.18593.0.A1_3p_at	Hs.409314	solute carrier family 36 (proton/amino acid symporter). member 1	SLC36A1	7.5	2.3	0.035
g4504850_3p_a_at	Hs.444448	potassium channel. subfamily K. member 5	KCNK5	9.7	2.3	0.027
Hs.9788.0.S3_3p_at	Hs.9788	Nedd4 family interacting protein 1	NDFIP1	9.6	2.3	0.008
g5174596_3p_at	Hs.118630	MAX interactor 1	MXI1	9.5	2.3	0.049
g5454115_3p_a_at	Hs.14894	trans-golgi network protein 2	TGOLN2	8.6	2.3	0.040
g5453681_3p_a_at	Hs.15299	HMBA-inducible	HIS1	9.0	2.3	0.034
g13097653_3p_s_at	Hs.534537	docking protein 4	DOK4	11.5	2.3	0.011
g4507014_3p_at	---	---	---	9.6	2.3	0.024
g1890049_3p_at	Hs.18069	legumain	LGMN	10.2	2.3	0.048
Hs.127748.0.A1_3p_x_at	---	---	---	9.2	2.3	0.046
g11139543_3p_x_at	Hs.534552	chemokine (C-X-C motif) ligand 16	CXCL16	8.7	2.3	0.039
g4507576_3p_at	Hs.256278	tumor necrosis factor receptor superfamily. member 1B	TNFRSF1B	9.2	2.3	0.005

g4758571_3p_at	Hs.416495	chromosome 1 open reading frame 8	C1orf8	11.8	2.3	0.030
4844495C_3p_s_at	Hs.158654	KIAA1196 protein	KIAA1196	5.3	2.3	0.046
Hs.54037.0.S1_3p_a_at	Hs.54037	ectonucleotide pyrophosphatase/phosphodiesterase 4 (putative function)	ENPP4	8.5	2.3	0.042
Hs.102926.0.A1_3p_at	Hs.417068	JM11 protein	JM11	8.9	2.3	0.029
g12053214_3p_at	Hs.42635	hypothetical protein DKFZp434K2435	DKFZp434K2435	8.4	2.3	0.022
g4503138_3p_a_at	Hs.135226	cathepsin B	CTSB	10.6	2.3	0.022
Hs.91052.0.A1_3p_at	Hs.380389	chromosome 9 open reading frame 77	C9orf77	8.3	2.3	0.038
g4502024_3p_a_at	Hs.78712	aminolevulinate. delta-. synthase 1	ALAS1	9.1	2.3	0.010
g306754_3p_x_at	Hs.458453	gamma-glutamyltransferase-like 4 /// gamma-glutamyltransferase 1	GGTL4 /// GGT1	8.7	2.3	0.033
Hs.117865.1.S2_3p_at	Hs.117865	solute carrier family 17 (anion/sugar transporter). member 5	SLC17A5	9.5	2.2	0.042
g11321600_3p_at	Hs.26010	phosphofructokinase. platelet	PFKP	9.9	2.2	0.023
Hs.11638.0.S1_3p_a_at	Hs.11638	acyl-CoA synthetase long-chain family member 5	ACSL5	12.5	2.2	0.045
g2078324_3p_a_at	Hs.198288	protein tyrosine phosphatase. receptor type. R	PTPRR	6.7	2.2	0.018
Hs.20894.0.S3_3p_at	Hs.20894	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1	NDST1	9.5	2.2	0.038
Hs.8068.2.S1_3p_a_at	Hs.505806	pre-B-cell leukemia transcription factor interacting protein 1	PBXIP1	9.0	2.2	0.038
g5802975_3p_at	Hs.74120	chromosome 10 open reading frame 116	C10orf116	10.2	2.2	0.041
Hs.167529.1.A1_3p_a_at	---	---	---	7.0	2.2	0.028
Hs.240767.0.S1_3p_at	Hs.438872	chromosome 6 open reading frame 72	C6orf72	7.9	2.2	0.009
g4503802_3p_at	Hs.576	fucosidase. alpha-L- 1. tissue	FUCA1	11.3	2.2	0.009
g4507576_3p_x_at	Hs.256278	tumor necrosis factor receptor superfamily. member 1B	TNFRSF1B	8.4	2.2	0.005
g11139543_3p_at	Hs.534552	chemokine (C-X-C motif) ligand 16	CXCL16	8.7	2.2	0.047
Hs.209061.0.S3_3p_at	Hs.209061	RIO kinase 3 (yeast)	RIOK3	11.6	2.2	0.042
g340067_3p_x_at	Hs.183704	ubiquitin C	UBC	12.1	2.2	0.034

g13487899_3p_s_at	Hs.124112	UDP glycosyltransferase 1 family. polypeptide A3 /// UDP glycosyltransferase 1 family. polypeptide A6 /// UDP glycosyltransferase 1 family. polypeptide A1 /// UDP glycosyltransferase 1 family. polypeptide A10 /// UDP glycosyltransferase 1 family. polypeptide A7 /// UDP glycosyltransferase 1 family. polypeptide A5 /// UDP glycosyltransferase 1 family. polypeptide A8 /// UDP glycosyltransferase 1 family. polypeptide A9 /// UDP glycosyltransferase 1 family. polypeptide A4	UGT1A3 /// UGT1A6 /// UGT1A1 /// UGT1A10 /// UGT1A7 /// UGT1A5 /// UGT1A8 /// UGT1A9 /// UGT1A4	8.1	2.2	0.040
Hs.149846.1.S1_3p_a_at	Hs.149846	integrin. beta 5	ITGB5	8.9	2.2	0.021
g12655188_3p_a_at	Hs.129129	testis derived transcript (3 LIM domains)	TES	7.5	2.2	0.045
g12803610_3p_a_at	Hs.4187	intraflagellar transport protein IFT20	LOC90410	10.1	2.2	0.018
Hs.234234.2.A1_3p_x_at	Hs.315235	Aldolase B. fructose-bisphosphate	ALDOB	8.6	2.2	0.036
g12654738_3p_at	Hs.23131	kinesin family member C3	KIFC3	10.1	2.2	0.037
g4503106_3p_at	Hs.304682	cystatin C (amyloid angiopathy and cerebral hemorrhage)	CST3	9.3	2.2	0.030
Hs.296670.0.S1_3p_at	Hs.493302	Transcribed locus. weakly similar to XP_375099.1 hypothetical protein LOC283585 [Homo sapiens]	---	7.1	2.2	0.021
Hs.268551.0.S1_3p_at	Hs.268551	receptor-interacting serine-threonine kinase 3	RIPK3	8.3	2.2	0.032
g181623_3p_at	Hs.436928	deoxyribonuclease I	DNASE1	9.2	2.2	0.015
g7657014_3p_at	Hs.273213	hypothetical protein HSPC117	HSPC117	11.7	2.1	0.043
Hs2.35406.1.S1_3p_at	Hs.223296	GPI-mannosyltransferase subunit	FLJ20522	7.2	2.1	0.035
Hs.288924.0.S1_3p_at	Hs.147663 /// Hs.444436	Protein tyrosine phosphatase. non-receptor type 9 /// AF464140	PTPN9 /// LOC163590	10.1	2.1	0.021
Hs.264915.0.S1_3p_at	---	---	---	8.2	2.1	0.034
209919_3p_x_at	Hs.352119	gamma-glutamyltransferase 1	GGT1	8.0	2.1	0.023
Hs.20524.0.S1_3p_at	Hs.445459	hypothetical protein FLJ22761	FLJ22761	10.1	2.1	0.032
g7657594_3p_a_at	Hs.475792	small membrane protein 1	SMP1	9.5	2.1	0.043
g12652742_3p_s_at	Hs.438972	chromosome 9 open reading frame 28	C9orf28	7.7	2.1	0.040

g13376444_3p_at	Hs.390817	myosin XVB. pseudogene	MYO15B	9.6	2.1	0.020
Hs.64179.2.S1_3p_a_at	Hs.439652	syndecan binding protein (syntenin) 2	SDCBP2	11.0	2.1	0.048
g4507544_3p_at	Hs.15791	transmembrane 7 superfamily member 1 (upregulated in kidney)	TM7SF1	6.9	2.1	0.023
g2647407_3p_a_at	Hs.183704	ubiquitin C	UBC	13.0	2.1	0.044
g8923529_3p_s_at	Hs.232459	chromosome 9 open reading frame 95	C9orf95	9.8	2.1	0.029
g4501864_3p_s_at	Hs.387567	ATP citrate lyase	ACLY	11.1	2.1	0.019
g13259538_3p_at	Hs.26458	methionine sulfoxide reductase A	MSRA	10.4	2.1	0.016
g9506568_3p_a_at	Hs.207134	erythrocyte membrane protein band 4.1 like 4B	EPB41L4B	11.8	2.1	0.040
Hs.103158.0.A1_3p_at	Hs.444424	chromosome 9 open reading frame 103	C9orf103	8.7	2.1	0.045
g4759139_3p_at	Hs.396783	solute carrier family 9 (sodium/hydrogen exchanger). isoform 3 regulator 1	SLC9A3R1	11.4	2.1	0.011
g4505558_3p_at	Hs.339	purinergic receptor P2Y. G-protein coupled. 2	P2RY2	7.2	2.1	0.010
Hs.15299.0.S1_3p_s_at	Hs.15299	HMBA-inducible	HIS1	9.5	2.1	0.024
Hs.4984.1.S1_3p_a_at	Hs.356823	KIAA0828 protein	KIAA0828	6.6	2.1	0.042
g4505570_3p_s_at	Hs.310781	sequestosome 1	SQSTM1	11.5	2.1	0.004
Hs.795.1.S1_3p_x_at	Hs.417332	histone 2. H2aa	HIST2H2AA	9.1	2.1	0.011
Hs.209061.0.S1_3p_a_at	Hs.209061	RIO kinase 3 (yeast)	RIOK3	6.8	2.0	0.014
Hs.99175.0.S1_3p_at	Hs.390817	myosin XVB. pseudogene	MYO15B	10.5	2.0	0.011
g5031560_3p_at	Hs.437229	glycoprotein A33 (transmembrane)	GPA33	12.3	2.0	0.014
g13375941_3p_at	Hs.526404	Hypothetical protein FLJ22938	FLJ22938	7.0	2.0	0.026
Hs.214783.0.S2_3p_at	Hs.423523	forkhead box O3A	FOXO3A	9.8	2.0	0.046
g6005943_3p_at	Hs.534392	villin 1	VIL1	10.4	2.0	0.033
Hs.83992.0.S1_3p_at	---	---	---	11.4	2.0	0.038
g4503142_3p_at	Hs.121575	cathepsin D (lysosomal aspartyl protease)	CTSD	8.3	2.0	0.027
g13654271_3p_s_at	Hs.473855	hypothetical protein HT036	HT036	8.9	2.0	0.047
Hs.99175.0.S1_3p_x_at	Hs.390817	myosin XVB. pseudogene	MYO15B	10.2	2.0	0.014
g7705816_3p_s_at	Hs.374485	HSPC038 protein	LOC51123	11.0	2.0	0.039
g13376740_3p_at	---	---	---	8.7	2.0	0.024
Hs.135056.0.S1_3p_at	Hs.135056	chromosome 20 open reading frame 139	C20orf139	8.4	2.0	0.018
Hs.236522.0.S1_3p_at	Hs.441550	chromosome 20 open reading frame 22	C20orf22	8.5	2.0	0.009

g4506760_3p_s_at	Hs.143873	S100 calcium binding protein A10 (annexin II ligand. calpactin I. light polypeptide (p11))	S100A10	12.4	2.0	0.042
g13236537_3p_at	Hs.132380	fatty acid 2-hydroxylase	FA2H	7.6	2.0	0.043
Hs.302810.0.S1_3p_at	Hs.130463	chromosome 20 open reading frame 35	C20orf35	7.9	2.0	0.029
Hs.155606.2.S1_3p_s_at	Hs.443452	paired related homeobox 1 /// similar to rat tricarboxylate carrier-like protein	PRRX1 /// BA108L7.2	9.7	2.0	0.043
g5531846_3p_a_at	Hs.284296	surfeit 4	SURF4	9.4	2.0	0.018
g11968026_3p_at	Hs.380897	fused toes homolog (mouse)	FTS	7.4	2.0	0.025
Hs.198689.0.S1_3p_a_at	Hs.443518	dystonin	DST	7.8	2.0	0.027
g5729771_3p_a_at	Hs.30213	ceroid-lipofuscinosis. neuronal 5	CLN5	7.4	2.0	0.044
g4507164_3p_at	Hs.371696	Nuclear antigen Sp100	SP100	9.7	2.0	0.036
g5031782_3p_at	Hs.409200	interferon gamma receptor 2 (interferon gamma transducer 1)	IFNGR2	11.2	2.0	0.034
Hs.110771.0.S2_3p_at	Hs.14894	trans-golgi network protein 2	TGOLN2	11.7	1.9	0.023
Hs.44175.1.S1_3p_at	Hs.44175	SEC15-like 2 (S. cerevisiae)	SEC15L2	6.0	1.9	0.042
Hs.178186.1.S1_3p_a_at	---	---	---	7.9	1.9	0.002
217144_3p_at	---	---	---	9.3	1.9	0.040
g4503142_3p_x_at	Hs.121575	cathepsin D (lysosomal aspartyl protease)	CTSD	10.1	1.9	0.021
Hs.173135.1.S1_3p_s_at	Hs.173135	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2	DYRK2	8.6	1.9	0.041
Hs.178738.1.A1_3p_at	---	---	---	8.3	1.9	0.003
224624_3p_at	Hs.173484	leucine rich repeat containing 8	LRRC8	8.8	1.9	0.045
g5597012_3p_a_at	Hs.429658	ceroid-lipofuscinosis. neuronal 2. late infantile (Jansky-Bielschowsky disease)	CLN2	9.7	1.9	0.026
Hs.8852.0.A1_3p_at	Hs.8852	Zinc finger. A20 domain containing 1	ZA20D1	5.1	1.9	0.038
g179094_3p_a_at	Hs.77813	sphingomyelin phosphodiesterase 1. acid lysosomal (acid sphingomyelinase)	SMPD1	8.3	1.9	0.008
Hs.40112.0.A1_3p_at	Hs.352250	GATA binding protein 5	GATA5	7.0	1.9	0.039
Hs.130714.0.S1_3p_at	Hs.130714	Similar to HSPC323	---	12.4	1.9	0.024
Hs.98992.0.A1_3p_at	---	---	---	7.4	1.9	0.028
Hs2.344350.1.S1_3p_at	Hs.344350	Homo sapiens. clone IMAGE:5303182. mRNA	---	9.4	1.9	0.008
g178752_3p_at	Hs.170222	solute carrier family 9 (sodium/hydrogen exchanger). isoform 1 (antiporter. Na+/H+. amiloride sensitive)	SLC9A1	9.9	1.9	0.028

Hs.75216.0.S2_3p_a_at	Hs.75216	protein tyrosine phosphatase. receptor type. F	PTPRF	11.3	1.9	0.040
4850925C_3p_x_at	Hs.390817	myosin XVB. pseudogene	MYO15B	7.4	1.9	0.035
g13436385_3p_s_at	Hs.437475	signal transducer and activator of transcription 6. interleukin-4 induced	STAT6	9.0	1.9	0.020
200766_3p_at	Hs.121575	cathepsin D (lysosomal aspartyl protease)	CTSD	7.6	1.9	0.039
Hs.129782.2.S1_3p_x_at	Hs.489354	mucin 3B	MUC3B	10.2	1.9	0.011
g6042199_3p_a_at	Hs.259047	membrane metallo-endopeptidase (neutral endopeptidase. enkephalinase. CALLA. CD10)	MME	11.9	1.9	0.045
212196_3p_at	Hs.71968	Interleukin 6 signal transducer (gp130. oncostatin M receptor)	IL6ST	7.5	1.9	0.040
Hs.61469.0.S2_3p_at	Hs.61469	chromosome X open reading frame 9	CXorf9	6.6	1.9	0.045
g7110714_3p_at	Hs.430576	SEC14-like 2 (S. cerevisiae)	SEC14L2	7.4	1.9	0.016
Hs.101490.0.A1_3p_a_at	---	---	---	6.7	1.9	0.008
g7657004_3p_s_at	Hs.129208	death-associated protein kinase 2	DAPK2	8.8	1.9	0.007
g4502678_3p_at	Hs.445570	CD63 antigen (melanoma 1 antigen)	CD63	11.5	1.9	0.022
g5453915_3p_a_at	Hs.9071	progesterone receptor membrane component 2	PGRMC2	11.9	1.9	0.033
g13375714_3p_at	Hs.334854	adiponectin receptor 2	ADIPOR2	10.2	1.9	0.022
Hs2.172702.2.S1_3p_at	Hs.396533	folliculin	FLCN	7.2	1.8	0.026
g4505876_3p_s_at	Hs.79706	plectin 1. intermediate filament binding protein 500kDa	PLEC1	10.0	1.8	0.043
208284_3p_x_at	Hs.352119	gamma-glutamyltransferase 1	GGT1	7.9	1.8	0.016
g967208_3p_a_at	Hs.32956	fucosyltransferase 6 (alpha (1.3) fucosyltransferase)	FUT6	8.7	1.8	0.042
g13376122_3p_at	Hs.145717	hypothetical protein FLJ13798	FLJ13798	8.5	1.8	0.033
Hs.178186.0.S1_3p_a_at	---	---	---	7.9	1.8	0.005
g10863968_3p_s_at	Hs.82520	polymerase (DNA-directed). delta 4	POLD4	8.6	1.8	0.017
g8922698_3p_a_at	Hs.149185	CNDP dipeptidase 2 (metallopeptidase M20 family)	CNDP2	12.4	1.8	0.015
g13436070_3p_at	Hs.11184	ubiquitin-conjugating enzyme E2R 2	UBE2R2	8.1	1.8	0.021
g4507746_3p_at	Hs.501739	thioredoxin reductase 1	TXNRD1	11.0	1.8	0.039
Hs2.182081.1.S1_3p_s_at	Hs.182081	KIAA1811 protein	KIAA1811	9.8	1.8	0.014
g12641848_3p_s_at	Hs.6518	GABA(A) receptor-associated protein-like 2	GABARAPL2	11.8	1.8	0.024
Hs.180236.0.A1_3p_at	Hs.180236	Testis expressed sequence 10	TEX10	5.7	1.8	0.043
g7328089_3p_a_at	Hs.422334	nuclear receptor coactivator 4	NCOA4	13.0	1.8	0.036
g11967980_3p_s_at	Hs.44278	RAB17. member RAS oncogene family	RAB17	11.9	1.8	0.049

g1165218_3p_at	Hs.405474	PTK2B protein tyrosine kinase 2 beta	PTK2B	7.2	1.8	0.040
Hs.247891.0.S1_3p_at	Hs.356190	ubiquitin B	UBB	9.7	1.8	0.041
g12654942_3p_at	Hs.414241	phosphatidylinositol glycan. class S	PIGS	11.9	1.8	0.014
g1165218_3p_x_at	Hs.405474	PTK2B protein tyrosine kinase 2 beta	PTK2B	7.3	1.8	0.023
Hs.274701.0.S2_3p_at	Hs.274701	thymidine kinase 2. mitochondrial	TK2	8.3	1.8	0.025
g4758091_3p_a_at	Hs.513557	chitobiase. di-N-acetyl-	CTBS	5.9	1.8	0.049
g4885508_3p_s_at	Hs.439671	neuroblastoma. suppression of tumorigenicity 1	NBL1	11.4	1.8	0.009
Hs2.376047.1.S1_3p_s_at	Hs.376047	hypothetical protein FLJ20847	FLJ20847	9.9	1.8	0.049
Hs.7934.2.S1_3p_at	Hs.7934	secretory carrier membrane protein 5	SCAMP5	8.8	1.8	0.019
g4506310_3p_a_at	Hs.75216	protein tyrosine phosphatase. receptor type. F	PTPRF	11.2	1.8	0.019
g5453745_3p_at	Hs.118131	5.10-methenyltetrahydrofolate synthetase (5-formyltetrahydrofolate cyclo-ligase)	MTHFS	9.5	1.8	0.040
g4885350_3p_x_at	Hs.103502	glutamic-pyruvate transaminase (alanine aminotransferase)	GPT	9.2	1.8	0.033
Hs.75216.0.S1_3p_a_at	Hs.75216	protein tyrosine phosphatase. receptor type. F	PTPRF	7.7	1.8	0.025
Hs.60371.0.A1_3p_at	---	---	---	7.4	1.8	0.048
g4504610_3p_a_at	Hs.76473	insulin-like growth factor 2 receptor	IGF2R	9.9	1.8	0.049
Hs.247891.0.S1_3p_x_at	Hs.356190	ubiquitin B	UBB	9.9	1.8	0.049
Hs.49500.0.S1_3p_at	Hs.49500	KIAA0746 protein	KIAA0746	8.5	1.8	0.004
Hs.98401.0.S1_3p_at	Hs.438669	Insulin receptor	INSR	9.8	1.8	0.039
Hs.102471.0.S1_3p_a_at	Hs.102471	phosphatase and actin regulator 2	PHACTR2	5.5	1.8	0.041
g5931954_3p_a_at	Hs.295137	autocrine motility factor receptor	AMFR	9.0	1.8	0.036
218280_3p_x_at	Hs.417332	histone 2. H2aa	HIST2H2AA	7.6	1.7	0.050
g13375671_3p_at	Hs.5366	EPS8-like 3	EPS8L3	9.9	1.7	0.036
g4557881_3p_at	Hs.84	interleukin 2 receptor. gamma (severe combined immunodeficiency)	IL2RG	8.1	1.7	0.045
g12653928_3p_at	Hs.44468	chromosome 6 open reading frame 80	C6orf80	9.7	1.7	0.018
Hs.218212.0.A1_3p_at	Hs.85950	hypothetical protein MGC33648	MGC33648	8.4	1.7	0.008
Hs.236522.0.S1_3p_x_at	Hs.441550	chromosome 20 open reading frame 22	C20orf22	8.4	1.7	0.038
g7669500_3p_x_at	Hs.150101	lysosomal-associated membrane protein 1	LAMP1	11.3	1.7	0.036
Hs.10346.0.S2_3p_at	Hs.10346	chromosome 10 open reading frame 26	C10orf26	10.0	1.7	0.029

g7669500_3p_a_at	Hs.150101	lysosomal-associated membrane protein 1	LAMP1	12.9	1.7	0.005
Hs.103419.1.S1_3p_a_at	Hs.258563	fasciculation and elongation protein zeta 2 (zygin II)	FEZ2	10.4	1.7	0.045
Hs.64239.0.A1_3p_s_at	Hs.128366	IBR domain containing 3	IBRDC3	7.5	1.7	0.036
g9506762_3p_a_at	Hs.13011	GTP binding protein 2	GTPBP2	9.8	1.7	0.033
g4504776_3p_at	Hs.1741	integrin. beta 7	ITGB7	7.9	1.7	0.045
g13279166_3p_a_at	Hs.103665	villin-like	VILL	8.1	1.7	0.038
Hs.74614.1.S1_3p_a_at	Hs.74614	tight junction protein 1 (zona occludens 1)	TJP1	6.8	1.7	0.044
g4557614_3p_at	Hs.75641	galactose-1-phosphate uridylyltransferase	GALT	8.9	1.7	0.031
Hs.2014.1.S1_3p_at	Hs.2014	T cell receptor delta locus	TRD@	8.4	1.7	0.036
g11024713_3p_at	Hs.356190	ubiquitin B	UBB	13.4	1.7	0.018
Hs.279518.4.S1_3p_a_at	Hs.279518	amyloid beta (A4) precursor-like protein 2	APLP2	9.6	1.7	0.037
g5360209_3p_at	Hs.183986	poliovirus receptor-related 2 (herpesvirus entry mediator B)	PVRL2	7.9	1.7	0.030
g6031182_3p_a_at	Hs.120870	mannosyl (alpha-1.3-)-glycoprotein beta-1.2-N-acetylglucosaminyltransferase	MGAT1	9.1	1.7	0.015
g967208_3p_x_at	Hs.32956	fucosyltransferase 6 (alpha (1.3) fucosyltransferase)	FUT6	7.7	1.7	0.039
207131_3p_x_at	Hs.352119	gamma-glutamyltransferase 1	GGT1	7.9	1.7	0.027
g11415023_3p_at	Hs.172690	diacylglycerol kinase. alpha 80kDa	DGKA	9.9	1.7	0.043
g4503456_3p_a_at	Hs.75794	endothelial differentiation. lysophosphatidic acid G-protein-coupled receptor. 2	EDG2	7.3	1.7	0.038
219173_3p_at	Hs.390817	myosin XVB. pseudogene	MYO15B	7.8	1.7	0.018
g13375755_3p_at	Hs.422676	hypothetical protein FLJ22709	FLJ22709	9.0	1.6	0.045
g13477108_3p_x_at	Hs.271599	yippee-like 3 (Drosophila)	YPEL3	9.0	1.6	0.019
Hs.37477.0.A1_3p_at	Hs.37477	FLJ42654 protein	FLJ42654	8.4	1.6	0.034
g9910225_3p_s_at	Hs.416456	FN5 protein	FN5	10.1	1.6	0.034
g4505306_3p_s_at	Hs.370421	myosin VIIA (Usher syndrome 1B (autosomal recessive. severe))	MYO7A	7.2	1.6	0.014
Hs.12320.0.A1_3p_at	Hs.6920	hypothetical protein MGC45562	MGC45562	5.3	1.6	0.041
g8922156_3p_s_at	Hs.426359	DKFZp564J157 protein	DKFZp564J157	12.6	1.6	0.039
g2804283_3p_a_at	Hs.41682	killer cell lectin-like receptor subfamily D. member 1	KLRD1	6.1	1.6	0.039
Hs.197613.0.A1_3p_at	Hs.197613	Similar to RIKEN cDNA 1110035L05	---	8.5	1.6	0.017
59375_3p_at	Hs.390817	myosin XVB. pseudogene	MYO15B	7.8	1.6	0.021
Hs.279832.1.A1_3p_a_at	Hs.534537	docking protein 4	DOK4	6.3	1.6	0.046

g5174578_3p_x_at	Hs.239663	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog. Drosophila); translocated to. 7	MLLT7	9.0	1.6	0.014
g7656921_3p_a_at	Hs.12107	putative breast adenocarcinoma marker (32kD)	BC-2	11.2	1.6	0.030
g13445909_3p_at	Hs.154628	radial spokehead-like 2	RSHL2	6.3	1.6	0.024
g6005763_3p_at	Hs.534435	GABA(A) receptor-associated protein	GABARAP	11.8	1.6	0.043
g5006272_3p_s_at	Hs.274329	TP53 activated protein 1	TP53AP1	8.2	1.6	0.020
Hs2.323265.1.S1_3p_at	---	hypothetical protein LOC283639	LOC283639	8.5	1.6	0.039
g4758343_3p_at	Hs.433300	Fc fragment of IgE. high affinity I. receptor for; gamma polypeptide	FCER1G	7.5	1.6	0.020
Hs.75334.0.S1_3p_a_at	Hs.75334	exostoses (multiple) 2	EXT2	8.7	1.6	0.030
g829622_3p_at	Hs.511744	myosin regulatory light chain MRLC2	MRLC2	13.1	1.6	0.048
Hs.14478.0.S1_3p_at	Hs.14478	hypothetical protein DKFZp762H185	DKFZp762H185	7.2	1.6	0.032
Hs.184029.0.S1_3p_a_at	Hs.444460	hypothetical protein DKFZp761A052	DKFZp761A052	7.0	1.6	0.019
g4557432_3p_at	Hs.652	tumor necrosis factor (ligand) superfamily. member 5 (hyper-IgM syndrome)	TNFSF5	6.1	1.6	0.041
Hs.198278.1.A1_3p_at	Hs.198278	6-phosphofructo-2-kinase/fructose-2.6-biphosphatase 4	PFKFB4	7.7	1.6	0.045
g13236513_3p_x_at	Hs.300691	chromosome 6 open reading frame 106	C6orf106	5.1	1.6	0.042
g8923274_3p_at	Hs.440401	all-trans-13.14-dihydroretinol saturase	FLJ20296	12.5	1.6	0.048
Hs.82719.0.S2_3p_at	Hs.82719	hypothetical protein MGC21416	MGC21416	7.8	1.6	0.024
214020_3p_x_at	---	---	---	6.4	1.6	0.030
Hs.55947.0.S1_3p_at	Hs.55947	pecanex homolog (Drosophila)	PCNX	6.3	1.6	0.040
g8922634_3p_s_at	Hs.3376	TBC1 domain family. member 13	TBC1D13	8.8	1.6	0.038
g4929600_3p_a_at	Hs.433760	calcium binding protein 39	CAB39	6.2	1.6	0.021
g4103319_3p_a_at	Hs.355816	CTD (carboxy-terminal domain. RNA polymerase II. polypeptide A) small phosphatase 2	CTDSP2	8.1	1.6	0.037
Hs.291623.0.A1_3p_at	Hs.291623	hypothetical protein BC017488	LOC124446	7.8	1.6	0.048
g7657612_3p_at	Hs.118725	selenophosphate synthetase 2	SEPHS2	12.6	1.5	0.048
g5031600_3p_s_at	Hs.433506	actin related protein 2/3 complex. subunit 1B. 41kDa	ARPC1B	10.3	1.5	0.049
g306752_3p_x_at	Hs.355394	gamma-glutamyltransferase-like activity 4	GGTLA4	8.7	1.5	0.034
g13528689_3p_a_at	Hs.3989	plexin B2	PLXNB2	9.5	1.5	0.018
g6005781_3p_s_at	Hs.251399	histamine receptor H3	HRH3	8.6	1.5	0.012
Hs.293834.0.S1_3p_at	Hs.436082	hypothetical protein MGC24039	MGC24039	5.6	1.5	0.028

g1002922_3p_s_at	Hs.415067	coronin. actin binding protein. 1A	CORO1A	7.5	1.5	0.033
218596_3p_at	Hs.3376	TBC1 domain family. member 13	TBC1D13	7.8	1.5	0.005
Hs2.348672.2.S1_3p_at	---	---	---	9.0	1.5	0.026
Hs2.8728.2.A1_3p_a_at	Hs.8728	filamin-binding LIM protein-1	FBLP-1	7.4	1.5	0.027
g13259520_3p_at	Hs.9028	histone deacetylase 5	HDAC5	6.7	1.5	0.042
Hs.173864.0.S1_3p_x_at	Hs.173864	Microtubule associated serine/threonine kinase 3	MAST3	8.9	1.5	0.018
g13112058_3p_s_at	Hs.446438	G protein-coupled receptor. family C. group 5. member C	GPRC5C	9.0	1.5	0.041
g10092596_3p_s_at	Hs.417402	mucolipin 1	MCOLN1	8.0	1.5	0.034
g8922367_3p_a_at	Hs.356096	hypothetical protein FLJ10350	FLJ10350	9.0	1.5	0.038
g5174578_3p_at	Hs.239663	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog. Drosophila); translocated to. 7	MLLT7	9.0	1.5	0.018
g4502098_3p_at	Hs.79172	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator). member 5	SLC25A5	12.1	1.5	0.033
Hs.61661.0.A1_3p_at	Hs.403933	F-box protein 32	FBXO32	6.6	1.5	0.043
g13375692_3p_at	Hs.458374	chondroitin polymerizing factor	CHPF	7.4	1.5	0.045
Hs.86386.1.A2_3p_at	---	---	---	5.5	1.5	0.030
g11386146_3p_s_at	Hs.406455	prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy)	PSAP	11.8	1.5	0.045
g8922156_3p_x_at	Hs.426359	DKFZp564J157 protein	DKFZp564J157	13.3	1.5	0.044
Hs.6983.0.S1_3p_at	Hs.467614	transcriptional adaptor 2 (ADA2 homolog. yeast)-beta	MGC21874	8.3	1.5	0.043
Hs2.406933.1.S1_3p_at	Hs.499548	hypothetical protein MGC23284	MGC23284	6.4	1.5	0.011
Hs.17558.0.A1_3p_at	Hs.17558	hypothetical protein FLJ90586	FLJ90586	7.7	1.5	0.015
Hs2.50651.1.S2_3p_s_at	Hs.309244	Janus kinase 1 (a protein tyrosine kinase)	JAK1	5.6	1.5	0.038
206540_3p_at	Hs.181173	galactosidase. beta 1-like	GLB1L	7.3	1.5	0.032
g4885524_3p_s_at	Hs.439645	SH2 domain containing 3A	SH2D3A	6.5	1.5	0.045
Hs.46319.1.S1_3p_a_at	Hs.46319	sex hormone-binding globulin	SHBG	7.0	1.5	0.040
Hs.189658.0.S1_3p_a_at	Hs.512608	vacuolar protein sorting 24 (yeast)	VPS24	10.1	1.5	0.035
g8922455_3p_s_at	Hs.534537	docking protein 4	DOK4	6.5	1.5	0.025
g7262293_3p_at	Hs.88251	arylsulfatase A	ARSA	6.0	1.5	0.049
217117_3p_x_at	---	---	---	8.8	1.4	0.015
g4504768_3p_a_at	Hs.85266	integrin. beta 4	ITGB4	8.7	1.4	0.044
Hs.173864.0.S1_3p_at	Hs.173864	Microtubule associated serine/threonine kinase 3	MAST3	8.6	1.4	0.028
g12803668_3p_at	Hs.269898	SERTA domain containing 1	SERTAD1	9.2	1.4	0.049

Hs2.12764.1.S1_3p_at	Hs.12764	CDNA clone IMAGE:5541046. partial cds	---	9.1	1.4	0.025
Hs2.287418.1.A1_3p_at	Hs.34790	F-box and leucine-rich repeat protein 18	FBXL18	8.6	1.4	0.026
g8922462_3p_a_at	Hs.272838	lipocalin-interacting membrane receptor	LIMR	9.0	1.4	0.050
Hs.36353.0.S1_3p_a_at	Hs.301242	likely ortholog of mouse myocytic induction/differentiation originator	MIDORI	8.2	1.4	0.028
Hs.178186.0.S1_3p_x_at	---	---	---	7.9	1.4	0.041
g12803230_3p_s_at	Hs.194673	phosphoprotein enriched in astrocytes 15	PEA15	7.4	1.4	0.024
Hs2.348672.2.S1_3p_x_at	---	---	---	9.2	1.4	0.029
g12803692_3p_a_at	Hs.181046	dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related)	DUSP3	6.7	1.4	0.040
g306754_3p_s_at	Hs.458453	gamma-glutamyltransferase-like 4 /// gamma-glutamyltransferase 1 /// gamma-glutamyltransferase-like activity 4	GGTL4 /// GGT1 /// GGTLA4	9.5	1.4	0.049
Hs.50925.0.A1_3p_at	---	---	---	6.2	1.4	0.041
Hs.302183.0.S1_3p_at	---	---	---	5.4	1.4	0.045
g13376545_3p_at	Hs.287623	hypothetical protein FLJ14100	FLJ14100	8.9	1.4	0.037
g4507268_3p_at	Hs.74597	stromal interaction molecule 1	STIM1	8.2	1.4	0.039
Hs2.8107.2.S1_3p_s_at	Hs.8107	guanine nucleotide binding protein (G protein). gamma 12	GNG12	5.1	1.4	0.039
Hs.50716.1.S1_3p_a_at	Hs.50716	signal-regulatory protein beta 2	SIRPB2	8.2	1.4	0.049
Hs.128095.0.A1_3p_at	Hs.367799	glutamate receptor. ionotropic. kainate 5	GRIK5	11.1	1.4	0.025
1556533_3p_at	Hs.211530	hypothetical protein LOC283994	LOC283994	7.6	1.4	0.034
g12408683_3p_s_at	Hs.356358	FCH domain only 2 /// chorionic somatomammotropin hormone-like 1 /// chorionic somatomammotropin hormone 1 (placental lactogen) /// growth hormone 1 /// growth hormone 2 /// chorionic somatomammotropin hormone 2	FCHO2 /// CSHL1 /// CSH1 /// GH1 /// GH2 /// CSH2	4.0	1.4	0.048
Hs.194293.0.A1_3p_at	Hs.335599	Hypothetical protein FLJ38348	FLJ38348	6.6	1.3	0.029
Hs.173638.0.S1_3p_s_at	Hs.214039	transcription factor 7-like 2 (T-cell specific. HMG-box)	TCF7L2	7.7	1.3	0.040
g13506660_3p_a_at	Hs.214099	brother of CDO	BOC	6.7	1.3	0.018
Hs.201201.0.A1_3p_at	Hs.135229	Similar to ataxin 2-binding protein 1 isoform 4; hexaribonucleotide binding protein 1	---	7.9	1.3	0.029
g11094314_3p_a_at	Hs.233325	hemochromatosis	HFE	9.6	1.3	0.021

Hs.20707.1.S1_3p_at	Hs.303669	hypothetical protein MGC26694	MGC26694	8.7	1.3	0.045
g11231178_3p_a_at	Hs.407964	leukocyte-associated Ig-like receptor 1	LAIR1	7.0	1.3	0.037
Hs2.435302.1.S1_3p_at	Hs.298119	myeloid/lymphoid or mixed-lineage leukemia 3	MLL3	9.9	1.3	0.039
g4505140_3p_a_at	Hs.79748	solute carrier family 3 (activators of dibasic and neutral amino acid transport). member 2	SLC3A2	9.6	1.3	0.049
g11024695_3p_a_at	Hs.283764	F-box protein 24	FBXO24	6.0	1.3	0.028
Hs2.356664.3.S1_3p_a_at	Hs.534611	homolog of Drosophila Numb-interacting protein	NIP	7.1	1.3	0.047
Hs2.370852.1.A1_3p_at	Hs.370852	Homo sapiens. clone IMAGE:5273088. mRNA	---	8.4	1.3	0.044
g4126973_3p_at	Hs.428446	carbonic anhydrase XI	CA11	8.9	1.3	0.039
Hs.301745.0.A1_3p_at	---	---	---	5.2	1.3	0.033
g6382065_3p_x_at	Hs.446610	amino-terminal enhancer of split	AES	8.5	1.3	0.033