Supplementary material

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21 **Table E1.** 1378 significantly differentially expressed genes in asthmatic patients

	CA vs. Ctrl		SA vs. CA		SA vs. Ctrl						
ID	**FC**	**adj. p***	**FC**	**adj. p***	**FC**	**adj. p***	**AveExpr**	**F adj.p***	**Chr**	**Symbol**	**Gene name or Transcript description**
8130628	1,22	2,92E-02	-1,05	5,88E-01	1,16	8,93E-02	6,74	1,79E-02	6	*AGPAT4*	1-acylglycerol-3-phosphate O-acyltransferase 4 (lysophosphatidic acid acyltransferase, delta)
8007188	1,02	8,92E-01	-1,16	1,30E-02	-1,13	3,79E-02	8,36	1,19E-02	17	*CNP*	2',3'-cyclic nucleotide 3' phosphodiesterase
7975066	1,54	4,70E-02	-1,07	7,82E-01	1,44	6,82E-02	6,00	2,46E-02	14	*AKAP5*	A kinase (PRKA) anchor protein 5
8008185	1,29	3,31E-02	-1,20	9,66E-02	1,08	6,39E-01	8,35	2,06E-02	17	*ABI3*	ABI family, member 3
7963646	1,08	4,07E-01	-1,22	1,18E-03	-1,13	3,54E-02	8,23	7,68E-04	12	*AAAS*	achalasia, adrenocortical insufficiency, alacrimia (Allgrove, triple-A)
7947815	1,10	5,36E-01	-1,19	2,41E-02	-1,09	3,83E-01	7,62	3,88E-02	11	*ACP2*	acid phosphatase 2, lysosomal
8103518	-1,06	7,03E-01	1,19	9,29E-03	1,13	8,76E-02	7,80	1,00E-02	4	*ANP32C*	acidic (leucine-rich) nuclear phosphoprotein 32 family, member C
8073430	1,08	2,48E-01	-1,16	2,85E-03	-1,07	1,80E-01	8,87	2,76E-03	22	*ACO2*	aconitase 2, mitochondrial
8143766	1,27	5,51E-02	1,00	9,88E-01	1,27	2,69E-02	5,78	1,73E-02	7	*ARP11*	actin-related Arp11
8075285	1,04	9,35E-01	-1,33	2,80E-02	-1,29	6,21E-02	11,56	2,91E-02	22	*ASCC2*	activating signal cointegrator 1 complex subunit 2
8178727	1,05	6,99E-01	-1,12	3,00E-02	-1,07	2,84E-01	9,24	4,99E-02	6	*ATF6B*	activating transcription factor 6 beta
7930498	1,09	2,96E-01	-1,17	5,83E-03	-1,08	2,65E-01	8,99	6,23E-03	10	*ACSL5*	acyl-CoA synthetase long-chain family member 5
8065444	1,07	5,87E-01	-1,16	1,27E-02	-1,09	2,04E-01	7,32	1,80E-02	20	*ACSS1*	acyl-CoA synthetase short-chain family member 1
7924701	-1,05	6,89E-01	-1,14	1,18E-02	-1,19	2,33E-04	9,40	5,63E-04	1	*ACBD3*	acyl-Coenzyme A binding domain containing 3
7979927	1,09	6,73E-01	1,16	1,21E-01	1,27	1,02E-02	5,23	1,98E-02	14	*ADAM20*	ADAM metallopeptidase domain 20
8033635	1,17	3,81E-02	-1,12	9,20E-02	1,04	6,88E-01	7,27	2,34E-02	19	*ADAMTS10*	ADAM metallopeptidase with thrombospondin type 1 motif, 10
8084345	1,08	5,68E-01	-1,27	8,98E-04	-1,18	9,97E-03	10,22	3,13E-04	3	*AP2M1*	adaptor-related protein complex 2, mu 1 subunit
8093643	1,05	7,07E-01	-1,13	2,78E-02	-1,08	2,56E-01	9,36	4,55E-02	4	*ADD1*	adducin 1 (alpha)

7946201	1,04	7,62E-01	-1,13	1,32E-02	-1,09	9,85E-02	7,19	1,71E-02	11	*ARFIP2*	ADP-ribosylation factor interacting protein 2
7941104	1,11	2,84E-01	-1,16	2,29E-02	-1,05	6,32E-01	8,17	3,09E-02	11	*ARL2*	ADP-ribosylation factor-like 2
7996012	-1,04	8,16E-01	-1,14	5,38E-02	-1,18	9,28E-03	9,26	1,44E-02	16	*ARL2BP*	ADP-ribosylation factor-like 2 binding protein
7999834	-1,06	6,68E-01	-1,08	1,62E-01	-1,14	1,55E-02	12,29	2,91E-02	16	*ARL6IP1*	ADP-ribosylation factor-like 6 interacting protein 1
8109086	1,22	5,19E-02	-1,09	3,79E-01	1,12	2,91E-01	7,51	4,05E-02	5	*ADRB2*	adrenergic, beta-2-, receptor, surface
8043993	1,10	8,26E-01	1,37	4,69E-02	1,51	8,19E-03	4,75	1,21E-02	2	*UNQ9419*	AHPA9419
8128034	-1,18	7,13E-02	1,14	9,66E-02	-1,04	8,00E-01	9,99	3,78E-02	6	*AKIRIN2*	akirin 2
8002347	1,11	3,40E-01	-1,17	2,80E-02	-1,05	6,19E-01	7,97	4,04E-02	16	*AARS*	alanyl-tRNA synthetase
7935230	1,08	6,66E-01	-1,25	6,83E-03	-1,16	7,61E-02	7,21	6,76E-03	10	*ALDH18A1*	aldehyde dehydrogenase 18 family, member A1
7901110	1,04	8,26E-01	-1,18	1,55E-02	-1,13	7,56E-02	7,87	1,79E-02	1	*AKR1A1*	aldo-keto reductase family 1, member A1 (aldehyde reductase)
8180376	1,30	5,60E-03	-1,17	8,46E-02	1,11	3,21E-01	5,35	4,14E-03	10	*AKR1C1*	aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase)
7925929	1,96	1,23E-03	-1,51	2,68E-02	1,29	2,33E-01	6,03	3,28E-04	10	*AKR1C3*	aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, type II)
8005399	-1,05	7,28E-01	-1,11	5,34E-02	-1,16	4,57E-03	9,16	8,43E-03	17	*ALKBH5*	alkB, alkylation repair homolog 5 (E. coli)
8131374	1,09	4,50E-01	-1,15	2,88E-02	-1,06	5,09E-01	7,98	4,59E-02	7	*AIMP2*	aminoacyl tRNA synthetase complex-interacting multifunctional protein 2
8053214	1,05	4,81E-01	-1,11	1,32E-02	-1,05	2,90E-01	9,48	1,96E-02	2	*AUP1*	ancient ubiquitous protein 1
7922598	1,12	4,41E-01	1,13	1,74E-01	1,26	5,32E-03	3,75	1,19E-02	1	*ANGPTL1*	angiopoietin-like 1
8164572	1,08	5,13E-01	-1,14	2,78E-02	-1,06	4,46E-01	7,89	4,52E-02	9	*ASB6*	ankyrin repeat and SOCS box-containing 6
8054054	1,29	5,32E-02	1,04	7,83E-01	1,34	8,96E-03	9,16	8,54E-03	2	*ANKRD36B*	ankyrin repeat domain 36B
8057990	1,07	4,03E-01	1,06	3,10E-01	1,13	1,29E-02	10,46	2,52E-02	2	*ANKRD44*	ankyrin repeat domain 44
7919729	-1,03	8,92E-01	-1,18	1,18E-02	-1,21	1,80E-03	8,52	2,32E-03	1	*APH1A*	anterior pharynx defective 1 homolog A (C. elegans)
7937020	-1,08	7,09E-01	-1,16	1,26E-01	-1,26	1,43E-02	6,45	2,61E-02	10	*MKI67*	antigen identified by monoclonal antibody Ki-67
8167854	1,09	3,16E-01	-1,14	2,67E-02	-1,04	6,34E-01	7,03	3,67E-02	X	*APEX2*	APEX nuclease (apurinic/apyrimidinic endonuclease) 2

7973056	-1,03	8,86E-01	-1,14	6,52E-02	-1,18	2,24E-02	9,99	2,81E-02	14	*APEX1*	APEX nuclease (multifunctional DNA repair enzyme) 1
7906185	1,14	1,34E-01	-1,21	7,12E-03	-1,06	5,25E-01	7,85	6,40E-03	1	*APOA1BP*	apolipoprotein A-I binding protein
8073068	1,18	8,61E-02	-1,27	3,87E-03	-1,08	4,71E-01	9,75	3,11E-03	22	*APOBEC3C*	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3C
8073072	1,15	1,88E-01	-1,17	4,97E-02	-1,02	9,27E-01	8,92	4,90E-02	22	*APOBEC3D*	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3D
8073081	1,14	1,86E-01	-1,23	7,23E-03	-1,08	4,51E-01	8,75	7,27E-03	22	*APOBEC3F*	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3F
8180374	1,25	1,46E-02	-1,21	2,19E-02	1,03	8,62E-01	8,39	5,14E-03	22	*APOBEC3F*	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3F
8073088	1,38	1,44E-02	-1,32	2,32E-02	1,05	8,43E-01	8,55	5,14E-03	22	*APOBEC3G*	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3G
8027117	1,12	1,27E-01	-1,13	4,54E-02	-1,00	9,74E-01	7,03	3,53E-02	19	*ARMC6*	armadillo repeat containing 6
8131614	-1,22	9,00E-02	-1,01	9,51E-01	-1,23	3,52E-02	9,29	2,63E-02	7	*AHR*	aryl hydrocarbon receptor
7993071	1,09	2,35E-01	-1,14	1,65E-02	-1,04	6,06E-01	7,71	2,10E-02	16	*ALG1*	asparagine-linked glycosylation 1, beta-1,4-mannosyltransferase homolog (S. cerevisiae)
8076851	1,03	8,00E-01	-1,11	2,42E-02	-1,08	1,49E-01	7,72	3,50E-02	22	*ALG12*	asparagine-linked glycosylation 12, alpha-1,6-mannosyltransferase homolog (S. cerevisiae)
8092457	1,05	7,64E-01	-1,21	5,83E-03	-1,15	3,67E-02	9,28	4,84E-03	3	*ALG3*	asparagine-linked glycosylation 3, alpha-1,3-mannosyltransferase homolog (S. cerevisiae)
7951633	1,04	8,31E-01	-1,15	2,22E-02	-1,11	1,10E-01	7,90	2,90E-02	11	*ALG9*	asparagine-linked glycosylation 9, alpha-1,2-mannosyltransferase homolog (S. cerevisiae)
8150988	-1,12	4,83E-01	1,26	1,28E-02	1,13	2,84E-01	6,64	1,88E-02	8	*ASPH*	aspartate beta-hydroxylase
8059222	1,07	5,69E-01	-1,16	1,66E-02	-1,08	2,78E-01	7,62	2,67E-02	2	*DNPEP*	aspartyl aminopeptidase
8124040	-1,00	9,92E-01	1,14	4,93E-02	1,14	6,21E-02	8,43	4,47E-02	6	*ATXN1*	ataxin 1
8142098	-1,08	7,07E-01	-1,15	1,17E-01	-1,23	1,26E-02	8,28	2,30E-02	7	*ATXN7L1*	ataxin 7-like 1
8077858	1,07	7,50E-01	1,16	9,33E-02	1,24	1,14E-02	8,34	2,00E-02	3	*ATG7*	ATG7 autophagy related 7 homolog (S. cerevisiae)
7948997	1,06	7,52E-01	-1,19	1,74E-02	-1,12	1,46E-01	7,91	2,56E-02	11	*ATL3*	atlastin GTPase 3
8015460	1,06	3,99E-01	-1,11	1,85E-02	-1,04	4,53E-01	9,26	2,81E-02	17	*ACLY*	ATP citrate lyase
7964234	1,06	5,87E-01	-1,15	7,12E-03	-1,09	1,11E-01	11,46	7,59E-03	12	*ATP5B*	ATP synthase, H+ transporting, mitochondrial F1 complex, beta polypeptide

8037037	-1,02	9,31E-01	-1,14	5,76E-02	-1,16	2,98E-02	7,94	3,29E-02	19	*ATP5SL*	ATP5S-like
8165345	1,21	4,38E-02	-1,14	1,36E-01	1,06	6,09E-01	7,61	3,14E-02	9	*ABCA2*	ATP-binding cassette, sub-family A (ABC1), member 2
8018038	1,13	5,28E-01	1,12	3,13E-01	1,27	2,43E-02	6,77	4,41E-02	17	*ABCA5*	ATP-binding cassette, sub-family A (ABC1), member 5
8084360	1,09	3,64E-01	-1,14	3,01E-02	-1,05	6,12E-01	7,34	4,46E-02	3	*ABCF3*	ATP-binding cassette, sub-family F (GCN20), member 3
8133233	1,26	2,25E-02	-1,13	1,92E-01	1,11	3,52E-01	6,23	1,76E-02	7	*AUTS2*	autism susceptibility candidate 2
7901418	1,00	9,91E-01	-1,14	3,61E-02	-1,14	4,36E-02	10,10	2,95E-02	1	*BTF3L4*	basic transcription factor 3-like 4
8069561	-1,02	9,37E-01	-1,15	4,87E-02	-1,17	2,49E-02	8,47	2,56E-02	1	*BTF3L4*	basic transcription factor 3-like 4
7969933	-1,01	9,86E-01	-1,18	3,00E-02	-1,19	2,50E-02	6,95	1,93E-02	13	*BIVM*	basic, immunoglobulin-like variable motif containing
8160260	1,52	1,77E-02	-1,25	1,79E-01	1,21	3,28E-01	5,44	1,40E-02	9	*BNC2*	basonuclin 2
8140061	-1,02	9,12E-01	-1,13	8,52E-02	-1,16	4,03E-02	8,87	4,71E-02	7	*BCL7B*	B-cell CLL/lymphoma 7B
8125766	1,15	1,58E-01	-1,19	2,42E-02	-1,03	8,15E-01	8,08	2,45E-02	6	*BAK1*	BCL2-antagonist/killer 1
8160647	1,02	9,57E-01	-1,27	4,22E-02	-1,24	7,80E-02	9,21	4,41E-02	9	*BAG1*	BCL2-associated athanogene
8065569	1,03	9,47E-01	-1,28	4,31E-02	-1,24	9,02E-02	12,02	4,82E-02	20	*BCL2L1*	BCL2-like 1
8047538	1,06	7,74E-01	-1,18	2,87E-02	-1,12	1,98E-01	8,42	4,48E-02	2	*BMPR2*	bone morphogenetic protein receptor, type II (serine/threonine kinase)
7995040	-1,06	7,44E-01	-1,14	1,05E-01	-1,21	1,30E-02	7,66	2,32E-02	16	*BCKDK*	branched chain ketoacid dehydrogenase kinase
8087885	-1,01	9,59E-01	-1,10	5,32E-02	-1,11	3,82E-02	8,37	3,55E-02	3	*BAP1*	BRCA1 associated protein-1 (ubiquitin carboxy-terminal hydrolase)
7958352	-1,10	5,21E-01	-1,10	2,73E-01	-1,21	1,78E-02	6,85	3,39E-02	12	*BTBD11*	BTB (POZ) domain containing 11
8068105	-1,09	5,56E-01	1,19	2,96E-02	1,09	4,20E-01	9,16	4,96E-02	21	*BACH1*	BTB and CNC homology 1, basic leucine zipper transcription factor 1
8158725	1,02	9,13E-01	-1,13	1,65E-02	-1,11	4,27E-02	6,99	1,61E-02	9	*ABL1*	c-abl oncogene 1, receptor tyrosine kinase
8063761	-1,06	5,80E-01	1,14	1,85E-02	1,07	2,90E-01	5,27	3,04E-02	20	*CDH26*	cadherin-like 26
8123230	-1,07	8,48E-01	1,30	2,83E-02	1,22	1,29E-01	7,85	3,90E-02	6	*LOC729603*	calcium binding protein P22 pseudogene
8020653	1,09	3,13E-01	1,04	5,06E-01	1,13	2,30E-02	4,95	3,59E-02	18	*CABYR*	calcium binding tyrosine-(Y)-phosphorylation regulated
8087691	1,35	1,07E-02	-1,26	3,78E-02	1,08	6,62E-01	6,80	5,25E-03	3	*CACNA2D2*	calcium channel, voltage-dependent, alpha 2/delta subunit 2

7913237	1,04	8,73E-01	-1,21	3,32E-02	-1,16	1,28E-01	6,63	4,41E-02	1	*CAMK2N1*	calcium/calmodulin-dependent protein kinase II inhibitor 1
8029831	1,03	7,92E-01	-1,11	2,29E-02	-1,08	1,47E-01	10,31	3,33E-02	19	*CALM3*	calmodulin 3 (phosphorylase kinase, delta)
8165046	-1,10	2,98E-01	-1,06	3,69E-01	-1,16	1,04E-02	7,42	1,97E-02	9	*CAMSAP1*	calmodulin regulated spectrin-associated protein 1
8028172	1,06	5,81E-01	-1,20	1,89E-03	-1,13	3,26E-02	10,55	1,69E-03	19	*CAPNS1*	calpain, small subunit 1
7995712	1,09	7,88E-01	1,21	1,36E-01	1,32	2,76E-02	5,89	4,36E-02	16	*CAPNS2*	calpain, small subunit 2
8026106	1,07	4,10E-01	-1,13	2,64E-02	-1,05	5,25E-01	9,71	4,05E-02	19	*CALR*	calreticulin
8155096	1,04	8,53E-01	-1,18	1,67E-02	-1,13	7,56E-02	7,72	2,05E-02	9	*CREB3*	cAMP responsive element binding protein 3
7962112	1,04	8,86E-01	-1,21	3,39E-02	-1,17	1,17E-01	7,28	4,41E-02	12	*CAPRIN2*	caprin family member 2
8147112	1,10	7,14E-01	-1,28	2,78E-02	-1,17	2,45E-01	6,47	4,52E-02	8	*CA13*	carbonic anhydrase XIII
8110971	-1,38	2,00E-01	-1,14	5,42E-01	-1,57	1,31E-02	5,84	2,05E-02	5	*CMBL*	carboxymethylenebutenolidase homolog (Pseudomonas)
8164535	1,05	8,86E-01	-1,25	3,45E-02	-1,19	1,18E-01	7,80	4,47E-02	9	*CRAT*	carnitine acetyltransferase
8133938	1,20	3,02E-02	-1,10	2,17E-01	1,09	3,74E-01	6,48	2,35E-02	7	*CROT*	carnitine O-octanoyltransferase
8089261	1,23	3,88E-02	-1,11	2,84E-01	1,11	3,44E-01	9,37	3,26E-02	3	*CBLB*	Cas-Br-M (murine) ecotropic retroviral transforming sequence b
8076056	1,08	5,25E-01	-1,15	2,19E-02	-1,07	3,71E-01	7,86	3,50E-02	22	*CSNK1E*	casein kinase 1, epsilon
8179298	1,07	6,68E-01	-1,17	2,21E-02	-1,10	2,48E-01	10,90	3,51E-02	6	*CSNK2B*	casein kinase 2, beta polypeptide
8137874	1,19	1,93E-02	-1,17	2,47E-02	1,02	8,78E-01	8,33	6,90E-03	7	*CARD11*	caspase recruitment domain family, member 11
8103389	1,11	5,80E-01	-1,26	2,18E-02	-1,13	3,14E-01	7,22	3,47E-02	4	*CTSO*	cathepsin O
8001693	1,03	8,07E-01	-1,10	2,48E-02	-1,07	1,48E-01	10,53	3,55E-02	16	*CNOT1*	CCR4-NOT transcription complex, subunit 1
7921677	1,36	3,69E-02	-1,20	1,82E-01	1,14	4,68E-01	8,53	2,71E-02	1	*CD244*	CD244 molecule, natural killer cell receptor 2B4
7922040	1,48	3,11E-03	-1,21	1,26E-01	1,23	1,24E-01	9,55	1,75E-03	1	*CD247*	CD247 molecule, CD3
7953428	-1,04	8,30E-01	-1,21	8,42E-03	-1,26	5,30E-04	10,21	7,85E-04	12	*CD4*	CD4 molecule
7939341	-1,03	7,53E-01	-1,06	1,15E-01	-1,10	1,61E-02	11,43	2,76E-02	11	*CD44*	CD44 molecule (Indian blood group)
7947425	-1,15	1,63E-01	-1,04	6,54E-01	-1,20	1,69E-02	8,29	2,22E-02	11	*CD59*	CD59 molecule, complement regulatory protein

8081564	1,19	4,48E-02	-1,16	6,36E-02	1,03	8,26E-01	10,15	2,34E-02	3	*CD96*	CD96 molecule
8173217	1,11	5,11E-01	-1,21	2,22E-02	-1,10	3,91E-01	7,86	3,53E-02	X	*ARHGEF9*	Cdc42 guanine nucleotide exchange factor (GEF) 9
7918911	1,03	9,05E-01	1,15	6,43E-02	1,19	2,69E-02	7,20	3,18E-02	1	---	cdna:Genscan chromosome:GRCh37:1:117075558:117076621:-1 /// cdna:pseudogene chromosome:GRCh37:1:117075558:117076714:-1 gene:ENSG00000177173
7898673	1,00	9,91E-01	-1,11	3,90E-02	-1,11	4,87E-02	7,04	3,35E-02	1	---	cdna:Genscan chromosome:GRCh37:1:21710086:21724749:1 /// cdna:pseudogene chromosome:GRCh37:1:21724483:21724833:1 gene:ENSG00000236216
7925128	-1,01	9,41E-01	-1,11	7,31E-02	-1,12	4,36E-02	7,77	4,65E-02	1	---	cdna:Genscan chromosome:GRCh37:1:234492450:234492887:-1 /// cdna:pseudogene chromosome:GRCh37:1:234492450:234492887:-1 gene:ENSG00000235605
7935054	-1,03	8,65E-01	1,18	1,03E-02	1,14	3,40E-02	5,45	8,26E-03	10	---	cdna:Genscan chromosome:GRCh37:10:94428529:94429500:-1 /// cdna:pseudogene chromosome:GRCh37:10:94428502:94429500:-1 gene:ENSG00000236493 /// cdna:pseudogene chromosome:GRCh37:10:94428529:94429500:-1 gene:ENSG00000236493
7974617	1,04	8,65E-01	1,16	6,36E-02	1,21	1,69E-02	5,11	2,32E-02	14	---	cdna:Genscan chromosome:GRCh37:14:58751643:58752182:1 /// cdna:pseudogene chromosome:GRCh37:14:58751491:58752113:1 gene:ENSG00000180189
7979925	1,09	6,68E-01	1,14	1,68E-01	1,24	1,64E-02	3,65	3,08E-02	14	---	cdna:Genscan chromosome:GRCh37:14:70935739:70937933:-1 /// cdna:pseudogene chromosome:GRCh37:14:70935877:70937825:-1 gene:ENSG00000176082 /// Homo sapiens, clone IMAGE:5170866, mRNA.
8073293	1,02	9,26E-01	1,12	6,16E-02	1,14	3,10E-02	4,93	3,44E-02	22	---	cdna:Genscan chromosome:GRCh37:22:40965292:40965436:1 /// cdna:pseudogene chromosome:GRCh37:22:40965290:40965899:1

8105739	1,05	7,19E-01	1,09	1,65E-01	1,15	2,30E-02	6,63	3,95E-02	5	---	gene:ENSG00000172912 /// cdna:pseudogene chromosome:GRCh37:22:40965292:40965904:1 gene:ENSG00000172912 cdna:Genscan chromosome:GRCh37:5:65867887:65868429:1 /// cdna:pseudogene chromosome:GRCh37:5:65867887:65868380:1 gene:ENSG00000234838
8116571	1,29	7,93E-02	1,13	3,68E-01	1,45	1,42E-03	6,50	3,06E-03	6	---	cdna:Genscan chromosome:GRCh37:6:583776:602526:1
8159873	1,01	9,59E-01	-1,16	4,68E-02	-1,14	8,37E-02	5,87	4,93E-02	9	---	cdna:Genscan chromosome:GRCh37:9:2875850:2923272:-1 /// cdna:pseudogene chromosome:GRCh37:9:2875449:2876427:-1 gene:ENSG00000236496
8159959	1,05	9,08E-01	1,36	1,57E-02	1,42	3,76E-03	5,05	4,16E-03	9	---	cdna:Genscan chromosome:GRCh37:9:5084999:5086381:-1 /// cdna:pseudogene chromosome:GRCh37:9:5084995:5086065:-1 gene:ENSG00000182347 /// cdna:pseudogene chromosome:GRCh37:9:5084999:5086112:-1 gene:ENSG00000182347
7903389	1,13	4,80E-01	1,17	1,15E-01	1,32	3,03E-03	7,22	7,27E-03	1	---	cdna:known chromosome:GRCh37:1:101455761:101457653:1 gene:ENSG00000236517 /// Homo sapiens cDNA FLJ20139 fis, clone COL07179.
7904693	1,55	4,32E-02	1,20	3,77E-01	1,87	7,45E-04	6,60	1,63E-03	1	---	cdna:known chromosome:GRCh37:1:144989309:144991365:1 gene:ENSG00000236192 /// Homo sapiens cDNA: FLJ21272 fis, clone COL01753.
7927597	1,05	7,75E-01	1,12	8,75E-02	1,18	1,28E-02	4,21	2,15E-02	10	---	cdna:known chromosome:GRCh37:10:52152766:52154321:1 gene:ENSG00000232016
7937876	-1,01	9,82E-01	1,19	3,90E-02	1,18	5,40E-02	7,01	3,50E-02	11	---	cdna:known chromosome:GRCh37:11:3436152:3436887:1 gene:ENSG00000182139 /// Homo sapiens cDNA clone MGC:15478 IMAGE:2967661, complete cds.
7956419	1,08	4,73E-01	1,07	3,34E-01	1,16	2,10E-02	4,72	3,85E-02	12	---	cdna:known chromosome:GRCh37:12:57810198:57810536:1 gene:ENSG00000225061 /// Homo sapiens clone HQ0470 PRO0470 mRNA, complete cds.
8104731	1,22	5,69E-02	1,06	5,95E-01	1,29	3,66E-03	4,11	4,91E-03	5	---	cdna:known chromosome:GRCh37:5:32149194:32149403:1 gene:ENSG00000230760 /// Homo sapiens clone HQ0255 PRO0255 mRNA, complete cds.
8145529	1,09	8,04E-01	1,25	1,08E-01	1,37	2,10E-02	7,30	3,34E-02	8	---	cdna:known chromosome:GRCh37:8:27204526:27205143:1 gene:ENSG00000197825 /// Homo sapiens cDNA FLJ90149 fis, clone HEMBB1001978.

8174889	1,16	8,76E-02	-1,14	7,29E-02	1,02	9,06E-01	4,99	3,92E-02	X	---	cdna:known chromosome:GRCh37:X:122249960:122251634:-1 gene:ENSG00000224236
8165888	1,23	1,10E-01	1,10	3,93E-01	1,35	2,48E-03	4,82	4,84E-03	X	---	cdna:known chromosome:GRCh37:X:7922621:7924183:1 gene:ENSG00000235465
7909102	1,21	4,32E-02	-1,01	9,58E-01	1,20	2,88E-02	5,47	1,54E-02	1	---	cdna:pseudogene chromosome:GRCh37:1:205320375:205320599:1 gene:ENSG00000235363
8003800	-1,08	6,06E-01	1,17	2,68E-02	1,08	3,46E-01	5,69	4,47E-02	17	---	cdna:pseudogene chromosome:GRCh37:17:3019721:3020751:1 gene:ENSG00000142163
8067860	1,15	6,28E-02	1,07	3,30E-01	1,23	8,58E-04	3,12	1,89E-03	21	---	cdna:pseudogene chromosome:GRCh37:21:15373248:15373421:1 gene:ENSG00000183249 /// cdna:pseudogene chromosome:GRCh37:21:15373248:15377600:1 gene:ENSG00000183249
8093974	1,00	9,99E-01	1,28	4,31E-02	1,28	4,61E-02	5,56	3,46E-02	4	---	cdna:pseudogene chromosome:GRCh37:4:6852339:6852678:1 gene:ENSG00000214696 /// Homo sapiens clone FLB3535 PRO0898 mRNA, complete cds.
8149345	1,04	8,55E-01	1,12	1,12E-01	1,16	3,31E-02	6,94	4,70E-02	8	---	cdna:pseudogene chromosome:GRCh37:8:11786293:11786940:-1 gene:ENSG00000206014 /// cdna:pseudogene chromosome:GRCh37:2:159731154:159732182:1 gene:ENSG00000188668
8162247	1,03	9,05E-01	1,22	1,17E-02	1,25	1,97E-03	7,17	2,45E-03	9	---	cdna:pseudogene chromosome:GRCh37:9:92054926:92055245:-1 gene:ENSG00000176993 /// Homo sapiens clone pp6489 unknown mRNA.
8000706	-1,02	9,28E-01	-1,15	3,45E-02	-1,17	1,37E-02	9,70	1,49E-02	16	*CDIPT*	CDP-diacylglycerol--inositol 3-phosphatidyltransferase (phosphatidylinositol synthase)
8046488	-1,12	3,44E-01	-1,06	4,80E-01	-1,18	2,43E-02	5,15	3,94E-02	2	*CDCA7*	cell division cycle associated 7
8094988	-1,06	3,94E-01	1,10	3,21E-02	1,03	5,95E-01	3,72	4,83E-02	4	*CWH43*	cell wall biogenesis 43 C-terminal homolog (S. cerevisiae)
8040578	1,16	3,88E-02	-1,17	1,56E-02	-1,01	9,50E-01	6,47	8,26E-03	2	*CENPO*	centromere protein O
8156026	1,42	4,51E-02	-1,22	2,32E-01	1,17	4,47E-01	7,73	3,56E-02	9	*CEP78*	centrosomal protein 78kDa
8144279	1,13	1,01E-01	1,07	2,97E-01	1,22	1,23E-03	7,60	2,97E-03	8	*CLN8*	ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental retardation)

7920984	1,11	1,24E-01	-1,13	1,65E-02	-1,02	7,85E-01	8,53	1,58E-02	1	*CCT3*	chaperonin containing TCP1, subunit 3 (gamma)
8042720	1,15	1,34E-01	-1,18	2,80E-02	-1,02	8,82E-01	8,83	2,56E-02	2	*CCT7*	chaperonin containing TCP1, subunit 7 (eta)
7966089	1,61	1,14E-02	-1,32	1,22E-01	1,22	3,56E-01	7,85	8,53E-03	12	*CMKLR1*	chemokine-like receptor 1
8148467	-1,04	8,05E-01	-1,14	3,45E-02	-1,19	4,08E-03	8,93	6,51E-03	8	*CHRAC1*	chromatin accessibility complex 1
7978187	-1,05	7,03E-01	1,18	1,39E-03	1,13	1,16E-02	6,43	8,04E-04	14	*CHMP4A*	chromatin modifying protein 4A
7901675	1,23	2,36E-02	-1,08	4,16E-01	1,14	1,48E-01	4,87	1,74E-02	1	*C1orf177*	chromosome 1 open reading frame 177
7908161	1,46	1,46E-02	-1,17	2,95E-01	1,24	1,70E-01	7,44	1,14E-02	1	*C1orf21*	chromosome 1 open reading frame 21
7909561	-1,13	1,56E-01	-1,02	8,65E-01	-1,15	4,12E-02	4,67	3,85E-02	1	*C1orf97*	chromosome 1 open reading frame 97
7929719	1,06	7,80E-01	1,13	1,52E-01	1,19	3,02E-02	7,53	4,90E-02	10	*C10orf28*	chromosome 10 open reading frame 28
7939723	1,08	2,80E-01	-1,14	1,08E-02	-1,06	4,08E-01	6,37	1,22E-02	11	*C11orf49*	chromosome 11 open reading frame 49
7942783	1,11	7,13E-02	-1,02	7,37E-01	1,08	1,13E-01	5,79	3,94E-02	11	*C11orf67*	chromosome 11 open reading frame 67
7967109	1,01	9,61E-01	-1,11	3,51E-02	-1,10	5,88E-02	7,46	3,39E-02	12	*C12orf43*	chromosome 12 open reading frame 43
7958950	1,03	8,15E-01	-1,12	1,74E-02	-1,09	1,01E-01	6,95	2,34E-02	12	*C12orf52*	chromosome 12 open reading frame 52
7958253	1,29	6,60E-02	-1,15	2,71E-01	1,13	4,56E-01	8,61	4,96E-02	12	*C12orf75*	chromosome 12 open reading frame 75
7971134	1,01	9,70E-01	-1,17	1,56E-02	-1,16	1,93E-02	8,65	1,00E-02	13	*C13orf23*	chromosome 13 open reading frame 23
7980309	1,16	1,04E-01	-1,20	1,56E-02	-1,03	7,95E-01	9,86	1,36E-02	14	*C14orf1*	chromosome 14 open reading frame 1
7975989	1,09	6,74E-01	-1,23	2,13E-02	-1,13	2,35E-01	9,43	3,35E-02	14	*C14orf156*	chromosome 14 open reading frame 156
7975595	1,03	8,06E-01	-1,13	2,18E-02	-1,09	1,28E-01	7,51	2,98E-02	14	*C14orf169*	chromosome 14 open reading frame 169
7979721	1,33	3,88E-02	-1,34	1,66E-02	-1,01	9,69E-01	6,53	8,79E-03	14	*C14orf83*	chromosome 14 open reading frame 83
7977868	-1,05	6,49E-01	-1,07	2,34E-01	-1,13	2,59E-02	6,95	4,59E-02	14	*C14orf93*	chromosome 14 open reading frame 93
7990027	1,10	7,57E-01	1,21	1,33E-01	1,33	2,08E-02	6,96	3,50E-02	15	*C15orf28*	chromosome 15 open reading frame 28
7985253	-1,10	3,67E-01	1,17	2,34E-02	1,06	5,38E-01	6,78	3,46E-02	15	*C15orf37*	chromosome 15 open reading frame 37
7990636	1,16	3,66E-02	1,02	8,28E-01	1,18	6,97E-03	4,28	5,78E-03	15	*C15orf5*	chromosome 15 open reading frame 5

7984405	-1,05	8,01E-01	-1,11	1,31E-01	-1,16	2,85E-02	6,68	4,41E-02	15	*C15orf61*	chromosome 15 open reading frame 61
7993159	-1,08	3,48E-01	1,14	1,57E-02	1,05	4,55E-01	9,39	2,22E-02	16	*C16orf72*	chromosome 16 open reading frame 72
8005305	-1,03	9,21E-01	-1,27	1,55E-02	-1,31	4,15E-03	8,07	4,29E-03	17	*C17orf39*	chromosome 17 open reading frame 39
8008795	1,01	9,70E-01	-1,19	4,58E-02	-1,17	7,36E-02	6,33	4,58E-02	17	*C17orf71*	chromosome 17 open reading frame 71
8011462	1,05	7,37E-01	1,09	1,34E-01	1,14	1,87E-02	8,16	3,27E-02	17	*C17orf85*	chromosome 17 open reading frame 85
8022941	1,11	6,66E-01	-1,28	2,18E-02	-1,16	2,45E-01	9,64	3,44E-02	18	*C18orf10*	chromosome 18 open reading frame 10
8021152	1,00	9,93E-01	1,13	3,45E-02	1,13	3,15E-02	4,43	2,39E-02	18	*C18orf12*	chromosome 18 open reading frame 12
8032127	-1,01	9,69E-01	-1,21	6,49E-02	-1,22	5,38E-02	11,78	4,96E-02	19	*C19orf22*	chromosome 19 open reading frame 22
8026698	1,08	6,95E-01	-1,23	1,30E-02	-1,14	1,43E-01	8,68	1,80E-02	19	*C19orf62*	chromosome 19 open reading frame 62
8040698	1,03	8,59E-01	-1,16	1,47E-02	-1,13	5,86E-02	7,83	1,59E-02	2	*C2orf18*	chromosome 2 open reading frame 18
8050115	1,75	3,22E-03	-1,11	6,01E-01	1,57	9,43E-03	6,60	1,24E-03	2	*C2orf46*	chromosome 2 open reading frame 46
8062286	1,04	7,53E-01	-1,18	1,74E-03	-1,13	1,08E-02	8,14	1,09E-03	20	*C20orf4*	chromosome 20 open reading frame 4
8065280	-1,01	9,57E-01	1,18	1,35E-02	1,17	1,98E-02	9,05	8,91E-03	20	*C20orf74*	chromosome 20 open reading frame 74
8060977	1,17	4,70E-02	-1,02	8,29E-01	1,14	5,66E-02	7,17	2,29E-02	20	*C20orf94*	chromosome 20 open reading frame 94
8068664	1,01	9,43E-01	1,10	7,68E-02	1,11	4,67E-02	4,52	4,98E-02	21	*C21orf130*	chromosome 21 open reading frame 130
8068202	1,14	7,34E-02	-1,09	1,81E-01	1,05	6,22E-01	7,14	4,96E-02	21	*C21orf63*	chromosome 21 open reading frame 63
8076826	1,03	8,87E-01	1,17	4,58E-02	1,21	1,32E-02	6,13	1,70E-02	22	*C22orf34*	chromosome 22 open reading frame 34
8100532	-1,04	7,09E-01	-1,10	4,88E-02	-1,15	3,19E-03	8,49	6,30E-03	4	*C4orf14*	chromosome 4 open reading frame 14
8093456	1,08	7,47E-01	-1,27	1,18E-02	-1,18	9,31E-02	7,84	1,43E-02	4	*C4orf42*	chromosome 4 open reading frame 42
8113113	-1,02	9,82E-01	1,39	4,93E-02	1,37	7,13E-02	5,32	4,78E-02	5	*C5orf36*	chromosome 5 open reading frame 36
8125850	1,04	7,57E-01	-1,14	1,63E-02	-1,09	1,30E-01	8,13	2,30E-02	6	*C6orf106*	chromosome 6 open reading frame 106
8130982	-1,04	6,79E-01	1,11	2,26E-02	1,06	2,45E-01	3,85	3,56E-02	6	*C6orf123*	chromosome 6 open reading frame 123
8129649	-1,16	4,45E-01	-1,21	9,65E-02	-1,41	1,83E-03	7,87	4,84E-03	6	*C6orf192*	chromosome 6 open reading frame 192

8130641	1,25	4,30E-03	-1,01	9,44E-01	1,24	2,10E-03	5,81	8,04E-04	6	*C6orf59*	chromosome 6 open reading frame 59
8133192	-1,01	9,20E-01	-1,07	6,68E-02	-1,09	3,26E-02	9,97	3,67E-02	7	*C7orf42*	chromosome 7 open reading frame 42
8135902	1,37	2,13E-02	1,19	1,73E-01	1,63	4,10E-05	5,93	1,44E-04	7	*C7orf54*	chromosome 7 open reading frame 54
8138088	-1,02	9,15E-01	-1,15	1,66E-02	-1,18	4,63E-03	8,10	4,84E-03	7	*C7orf70*	chromosome 7 open reading frame 70
8149315	1,18	3,30E-01	1,29	2,22E-02	1,53	6,80E-05	5,01	2,77E-04	8	*C8orf15*	chromosome 8 open reading frame 15
8180229	1,13	3,10E-01	1,14	1,15E-01	1,29	1,17E-03	4,88	3,23E-03	8	*C8orf16*	chromosome 8 open reading frame 16
8157144	-1,11	2,61E-01	-1,08	2,52E-01	-1,21	3,66E-03	7,76	8,26E-03	9	*C9orf6*	chromosome 9 open reading frame 6
8163348	1,03	8,73E-01	1,12	6,51E-02	1,16	1,88E-02	3,11	2,54E-02	9	*C9orf84*	chromosome 9 open reading frame 84
7996891	1,03	9,15E-01	-1,29	2,27E-03	-1,25	2,95E-03	9,14	7,97E-04	16	*CIRH1A*	cirrhosis, autosomal recessive 1A (cirhin)
8089062	-1,05	6,81E-01	-1,07	2,17E-01	-1,12	2,69E-02	10,42	4,74E-02	3	*CLDND1*	claudin domain containing 1
8029560	1,01	9,61E-01	-1,14	2,38E-02	-1,13	3,75E-02	9,30	1,99E-02	19	*CLPTM1*	cleft lip and palate associated transmembrane protein 1
7950142	1,07	4,43E-01	-1,15	1,08E-02	-1,07	2,57E-01	7,41	1,35E-02	11	*CLPB*	ClpB caseinolytic peptidase B homolog (E. coli)
8021727	1,09	5,40E-01	-1,23	7,12E-03	-1,13	1,40E-01	8,77	8,41E-03	18	*CNDP2*	CNDP dipeptidase 2 (metallopeptidase M20 family)
8106393	1,30	1,61E-02	-1,18	9,95E-02	1,10	4,88E-01	8,20	1,16E-02	5	*F2R*	coagulation factor II (thrombin) receptor
8176245	-1,05	5,69E-01	-1,07	1,39E-01	-1,13	7,32E-03	10,36	1,50E-02	X	*F8A1*	coagulation factor VIII-associated (intronic transcript) 1
7955896	1,05	7,09E-01	-1,19	5,76E-03	-1,13	4,63E-02	9,70	4,84E-03	12	*COPZ1*	coatomer protein complex, subunit zeta 1
8056359	1,10	5,87E-01	1,11	2,37E-01	1,22	1,88E-02	3,98	3,53E-02	2	*COBLL1*	COBL-like 1
8161575	1,18	6,85E-01	1,26	2,21E-01	1,49	2,83E-02	6,30	4,93E-02	9	*CBWD5*	COBW domain containing 5
8094190	1,00	9,91E-01	1,19	3,40E-02	1,19	3,02E-02	4,28	2,32E-02	4	*CC2D2A*	coiled-coil and C2 domain containing 2A
7994362	1,06	7,19E-01	-1,17	1,81E-02	-1,11	1,69E-01	8,39	2,73E-02	16	*CCDC101*	coiled-coil domain containing 101
8055208	1,02	9,19E-01	-1,15	2,64E-02	-1,13	6,58E-02	7,66	2,81E-02	2	*CCDC115*	coiled-coil domain containing 115
7900555	1,01	9,58E-01	1,16	3,62E-02	1,18	2,22E-02	5,77	2,02E-02	1	*CCDC30*	coiled-coil domain containing 30
7967486	1,14	1,86E-01	-1,17	2,84E-02	-1,03	8,15E-01	8,41	3,08E-02	12	*CCDC92*	coiled-coil domain containing 92

8057620	-1,08	3,58E-01	1,12	3,45E-02	1,04	6,50E-01	4,65	4,96E-02	2	*COL5A2*	collagen, type V, alpha 2
8065637	1,08	3,97E-01	-1,16	1,39E-02	-1,07	3,71E-01	8,23	1,97E-02	20	*COMMD7*	COMM domain containing 7
7909390	-1,11	7,04E-01	-1,18	1,61E-01	-1,31	1,91E-02	8,71	3,49E-02	1	*CR1L*	complement component (3b/4b) receptor 1-like
8002381	1,09	4,62E-01	-1,16	2,62E-02	-1,07	4,77E-01	8,62	4,16E-02	16	*COG4*	component of oligomeric golgi complex 4
8000263	1,06	6,71E-01	-1,15	2,93E-02	-1,08	3,04E-01	6,50	4,91E-02	16	*COG7*	component of oligomeric golgi complex 7
8002272	1,02	8,73E-01	-1,10	2,78E-02	-1,08	1,09E-01	7,78	3,57E-02	16	*COG8*	component of oligomeric golgi complex 8
8134699	1,06	6,94E-01	-1,16	2,26E-02	-1,09	2,35E-01	9,49	3,55E-02	7	*COPS6*	COP9 constitutive photomorphogenic homolog subunit 6 (Arabidopsis)
7953395	1,01	9,60E-01	-1,15	2,00E-02	-1,14	3,10E-02	8,59	1,61E-02	12	*COPS7A*	COP9 constitutive photomorphogenic homolog subunit 7A (Arabidopsis)
8049088	1,03	8,25E-01	-1,12	2,59E-02	-1,09	1,36E-01	7,82	3,61E-02	2	*COPS7B*	COP9 constitutive photomorphogenic homolog subunit 7B (Arabidopsis)
7986049	-1,09	5,94E-01	-1,10	2,67E-01	-1,20	2,48E-02	9,04	4,48E-02	15	*CRTC3*	CREB regulated transcription coactivator 3
8006019	1,01	9,39E-01	1,11	4,97E-02	1,13	2,69E-02	4,33	2,71E-02	17	*CRYBA1*	crystallin, beta A1
7970455	-1,03	8,99E-01	-1,13	8,20E-02	-1,16	3,32E-02	6,95	4,09E-02	13	*CRYL1*	crystallin, lambda 1
7936904	-1,03	8,92E-01	1,14	3,23E-02	1,11	1,03E-01	6,39	3,98E-02	10	*CTBP2*	C-terminal binding protein 2
8174794	-1,12	1,97E-01	1,15	3,84E-02	1,02	8,65E-01	8,50	4,05E-02	X	*CUL4B*	cullin 4B
7951447	1,15	1,97E-01	1,06	4,83E-01	1,22	9,78E-03	6,83	1,64E-02	11	*CWF19L2*	CWF19-like 2, cell cycle control (S. pombe)
8023344	1,06	5,77E-01	-1,12	2,93E-02	-1,06	3,98E-01	7,22	4,93E-02	18	*CXXC1*	CXXC finger 1 (PHD domain)
8113010	1,04	8,59E-01	1,15	6,46E-02	1,20	1,65E-02	7,85	2,32E-02	5	*CCNH*	cyclin H
8101212	-1,05	6,52E-01	-1,10	4,01E-02	-1,15	1,55E-03	11,92	3,70E-03	4	*CCNI*	cyclin I
7956076	1,05	7,26E-01	-1,15	2,41E-02	-1,10	2,07E-01	7,21	3,71E-02	12	*CDK2*	cyclin-dependent kinase 2
7923378	1,06	7,64E-01	-1,22	1,17E-02	-1,15	8,00E-02	8,38	1,29E-02	1	*CSRP1*	cysteine and glycine-rich protein 1
8113641	-1,05	7,09E-01	1,14	2,52E-02	1,09	2,34E-01	4,74	4,08E-02	5	*CDO1*	cysteine dioxygenase, type I
8041447	1,26	3,88E-02	-1,23	4,34E-02	1,03	8,90E-01	6,80	1,71E-02	2	*CRIM1*	cysteine rich transmembrane BMP regulator 1 (chordin-like)
8003824	1,01	9,57E-01	-1,20	1,56E-02	-1,18	2,42E-02	7,42	1,12E-02	17	*CTNS*	cystinosis, nephropathic

8079993	1,09	4,58E-01	-1,15	2,78E-02	-1,06	4,94E-01	7,16	4,42E-02	3	*CYB561D2*	cytochrome b-561 domain containing 2
8001552	1,02	9,41E-01	-1,15	2,93E-02	-1,13	6,17E-02	7,59	3,03E-02	16	*CIAPIN1*	cytokine induced apoptosis inhibitor 1
7947694	1,09	3,81E-01	-1,15	2,42E-02	-1,06	5,34E-01	7,90	3,57E-02	11	*CKAP5*	cytoskeleton associated protein 5
7948534	1,08	5,80E-01	-1,23	3,68E-03	-1,14	5,87E-02	9,38	3,44E-03	11	*DDB1*	damage-specific DNA binding protein 1, 127kDa
8088128	-1,06	6,77E-01	-1,10	1,55E-01	-1,17	1,51E-02	8,62	2,81E-02	3	*DCP1A*	DCP1 decapping enzyme homolog A (S. cerevisiae)
7973545	1,04	8,18E-01	-1,17	2,00E-02	-1,12	1,11E-01	8,40	2,65E-02	14	*DCAF11*	DDB1 and CUL4 associated factor 11
7979849	1,12	1,33E-01	-1,12	4,34E-02	-1,01	9,58E-01	9,59	3,52E-02	14	*DCAF5*	DDB1 and CUL4 associated factor 5
7979223	1,18	8,36E-02	1,00	9,72E-01	1,18	3,63E-02	8,23	2,56E-02	14	*DDHD1*	DDHD domain containing 1
7904000	-1,06	7,88E-01	-1,15	8,69E-02	-1,22	1,37E-02	7,68	2,30E-02	1	*DDX20*	DEAD (Asp-Glu-Ala-Asp) box polypeptide 20
7962869	1,13	2,13E-01	-1,15	4,69E-02	-1,02	8,90E-01	8,74	4,94E-02	12	*DDX23*	DEAD (Asp-Glu-Ala-Asp) box polypeptide 23
8116096	1,07	5,14E-01	-1,15	1,03E-02	-1,08	2,03E-01	8,84	1,27E-02	5	*DDX41*	DEAD (Asp-Glu-Ala-Asp) box polypeptide 41
8027100	-1,00	9,91E-01	-1,10	4,97E-02	-1,10	4,94E-02	7,31	3,94E-02	19	*DDX49*	DEAD (Asp-Glu-Ala-Asp) box polypeptide 49
7921793	-1,05	7,03E-01	-1,09	1,07E-01	-1,14	1,02E-02	9,17	1,93E-02	1	*DEDD*	death effector domain containing
8065552	1,10	2,24E-01	1,03	6,82E-01	1,13	2,95E-02	3,52	3,74E-02	20	*DEFB116*	defensin, beta 116
7912537	1,21	7,80E-02	-1,23	2,00E-02	-1,02	9,08E-01	7,85	1,49E-02	1	*DHRS3*	dehydrogenase/reductase (SDR family) member 3
7909568	1,07	8,49E-01	-1,29	3,26E-02	-1,21	1,45E-01	6,26	4,56E-02	1	*DTL*	denticleless homolog (Drosophila)
8034454	1,10	3,84E-01	-1,17	2,42E-02	-1,06	5,30E-01	8,01	3,58E-02	19	*DHPS*	deoxyhypusine synthase
8152628	1,03	8,73E-01	-1,14	1,57E-02	-1,11	5,79E-02	9,86	1,71E-02	8	*DERL1*	Der1-like domain family, member 1
8005313	1,08	5,20E-01	-1,16	1,89E-02	-1,07	3,47E-01	8,00	3,07E-02	17	*DRG2*	developmentally regulated GTP binding protein 2
7986685	1,05	8,08E-01	-1,20	1,18E-02	-1,15	6,33E-02	8,42	1,28E-02	16	*DEXI*	Dexi homolog (mouse)
7999419	1,04	8,48E-01	-1,28	3,03E-03	-1,22	8,67E-03	7,13	1,63E-03	16	*DEXI*	Dexi homolog (mouse)
8168691	1,09	6,87E-01	1,14	1,74E-01	1,24	1,91E-02	6,84	3,53E-02	X	*DIAPH2*	diaphanous homolog 2 (Drosophila)
8019376	1,07	4,69E-01	-1,13	1,55E-02	-1,06	3,32E-01	7,85	2,30E-02	17	*DUS1L*	dihydrouridine synthase 1-like (S. cerevisiae)

7941621	1,09	4,50E-01	-1,17	2,25E-02	-1,07	4,48E-01	7,71	3,51E-02	11	*DPP3*	dipeptidyl-peptidase 3
8032871	1,10	2,69E-01	-1,15	2,52E-02	-1,04	6,74E-01	7,41	3,35E-02	19	*DPP9*	dipeptidyl-peptidase 9
7910559	1,05	7,69E-01	1,12	9,15E-02	1,18	1,29E-02	6,20	2,19E-02	1	*DISC1*	disrupted in schizophrenia 1
7904131	-1,08	6,52E-01	-1,14	8,50E-02	-1,23	5,07E-03	6,58	1,05E-02	1	*DCLRE1B*	DNA cross-link repair 1B (PSO2 homolog, S. cerevisiae)
7912303	1,02	9,23E-01	-1,13	3,58E-02	-1,11	8,95E-02	7,37	4,11E-02	1	*DFFA*	DNA fragmentation factor, 45kDa, alpha polypeptide
7963935	1,04	7,89E-01	-1,20	5,76E-03	-1,15	2,91E-02	7,93	4,34E-03	12	*DNAJC14*	DnaJ (Hsp40) homolog, subfamily C, member 14
7898192	1,01	9,57E-01	-1,14	3,84E-02	-1,13	7,12E-02	8,24	3,95E-02	1	*DNAJC16*	DnaJ (Hsp40) homolog, subfamily C, member 16
7952185	1,02	9,21E-01	-1,26	2,27E-03	-1,23	2,75E-03	8,63	7,85E-04	11	*DPAGT1*	dolichyl-phosphate (UDP-N-acetylglucosamine) N-acetylglucosaminephosphotransferase 1 (GlcNAc-1-P transferase)
8164336	1,05	8,86E-01	-1,29	2,86E-02	-1,23	1,00E-01	8,40	3,57E-02	9	*DPM2*	dolichyl-phosphate mannosyltransferase polypeptide 2, regulatory subunit
8154128	1,02	9,51E-01	1,20	5,14E-02	1,22	3,15E-02	3,31	3,14E-02	NA	*DSERG1*	Down syndrome encephalopathy related protein 1
7900911	1,06	6,78E-01	-1,16	2,14E-02	-1,09	2,33E-01	6,73	3,35E-02	1	*DPH2*	DPH2 homolog (S. cerevisiae)
8068551	-1,11	1,27E-01	-1,02	7,81E-01	-1,14	2,22E-02	10,11	2,35E-02	21	*DYRK1A*	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A
8053107	1,03	8,35E-01	-1,10	2,52E-02	-1,08	1,23E-01	8,47	3,47E-02	2	*DCTN1*	dynactin 1 (p150, glued homolog, Drosophila)
7964466	1,01	9,54E-01	-1,14	1,60E-02	-1,13	2,69E-02	8,74	1,24E-02	12	*DCTN2*	dynactin 2 (p50)
7938128	1,25	3,88E-02	-1,13	2,03E-01	1,10	4,56E-01	6,85	3,08E-02	11	*DNHD1*	dynein heavy chain domain 1
7938133	1,16	7,34E-02	-1,02	8,24E-01	1,13	8,40E-02	6,40	3,53E-02	11	*DNHD1*	dynein heavy chain domain 1
7933872	-1,33	8,77E-03	1,11	3,10E-01	-1,19	1,04E-01	6,31	6,07E-03	10	*EGR2*	early growth response 2
8149720	-1,39	3,78E-02	1,20	2,09E-01	-1,15	4,35E-01	6,23	2,88E-02	8	*EGR3*	early growth response 3
8037621	1,12	5,80E-02	-1,05	3,89E-01	1,07	3,00E-01	6,30	4,49E-02	19	*EML2*	echinoderm microtubule associated protein like 2
8112615	1,37	4,37E-02	-1,31	5,33E-02	1,05	8,59E-01	6,72	2,10E-02	5	*ENC1*	ectodermal-neural cortex (with BTB-like domain)
8126750	1,53	3,66E-02	-1,32	1,27E-01	1,16	5,77E-01	5,89	2,48E-02	6	*ENPP5*	ectonucleotide pyrophosphatase/phosphodiesterase 5 (putative function)
8016099	1,09	4,08E-01	-1,16	1,95E-02	-1,06	4,51E-01	9,26	2,99E-02	17	*EFTUD2*	elongation factor Tu GTP binding domain containing 2

7915504	1,01	9,79E-01	-1,16	2,41E-02	-1,16	3,15E-02	10,01	1,86E-02	1	*ELOVL1*	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 1
8167305	1,14	2,86E-01	-1,23	1,74E-02	-1,07	5,64E-01	7,18	2,43E-02	X	*EBP*	emopamil binding protein (sterol isomerase)
7996685	1,06	4,89E-01	-1,12	1,60E-02	-1,06	3,32E-01	8,28	2,45E-02	16	*EDC4*	enhancer of mRNA decapping 4
8005994	1,06	7,71E-01	-1,22	1,17E-02	-1,15	7,56E-02	8,64	1,24E-02	17	*ERAL1*	Era G-protein-like 1 (E. coli)
8062174	-1,00	9,95E-01	-1,19	8,99E-03	-1,20	4,63E-03	9,49	3,06E-03	20	*ERGIC3*	ERGIC and golgi 3
7988033	1,11	8,25E-01	-1,48	2,53E-02	-1,33	1,34E-01	9,54	3,54E-02	15	*EPB42*	erythrocyte membrane protein band 4.2
8153457	-1,03	8,85E-01	1,18	2,12E-02	1,14	7,12E-02	6,25	2,37E-02	8	*EEF1D*	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)
7968411	1,07	4,83E-01	1,07	2,30E-01	1,14	1,07E-02	7,00	2,18E-02	13	*EEF1DP3*	eukaryotic translation elongation factor 1 delta pseudogene 3
8083333	-1,04	7,53E-01	-1,09	1,46E-01	-1,13	2,31E-02	8,91	3,88E-02	3	*EIF2A*	eukaryotic translation initiation factor 2A, 65kDa
8084303	1,10	1,74E-01	-1,11	3,39E-02	-1,02	8,72E-01	6,97	3,37E-02	3	*EIF2B5*	eukaryotic translation initiation factor 2B, subunit 5 epsilon, 82kDa
8072946	-1,02	9,04E-01	-1,08	8,78E-02	-1,10	3,82E-02	11,50	4,63E-02	22	*EIF3L*	eukaryotic translation initiation factor 3, subunit L
7928119	-1,05	7,19E-01	-1,09	1,08E-01	-1,14	1,21E-02	10,72	2,18E-02	10	*EIF4EBP2*	eukaryotic translation initiation factor 4E binding protein 2
8075507	1,02	8,95E-01	-1,10	1,66E-02	-1,09	5,11E-02	8,08	1,74E-02	22	*EIF4ENIF1*	eukaryotic translation initiation factor 4E nuclear import factor 1
7928630	-1,11	7,65E-01	-1,23	1,27E-01	-1,37	2,08E-02	8,61	3,47E-02	10	*EIF5AL1*	eukaryotic translation initiation factor 5A-like 1
8072206	1,00	9,92E-01	1,09	5,36E-02	1,09	5,57E-02	8,27	4,52E-02	22	*EWSR1*	Ewing sarcoma breakpoint region 1
8037537	1,08	4,98E-01	-1,25	1,18E-03	-1,15	2,44E-02	7,49	7,32E-04	19	*ERCC2*	excision repair cross-complementing rodent repair deficiency, complementation group 2
8110685	-1,04	8,12E-01	-1,14	1,56E-02	-1,18	1,30E-03	7,20	2,11E-03	5	*EXOC3*	exocyst complex component 3
8136293	1,13	4,32E-02	-1,06	3,03E-01	1,06	3,36E-01	8,23	3,47E-02	7	*EXOC4*	exocyst complex component 4
8079294	1,12	1,50E-01	1,02	8,22E-01	1,14	3,24E-02	6,65	3,33E-02	3	*EXOSC7*	exosome component 7
8126588	1,08	5,28E-01	-1,18	1,41E-02	-1,09	2,68E-01	7,41	2,07E-02	6	*XPO5*	exportin 5
8127391	1,11	7,86E-01	1,29	9,00E-02	1,43	1,44E-02	4,19	2,37E-02	6	*EYS*	eyes shut homolog (Drosophila)
7905831	1,07	1,65E-01	-1,08	5,50E-02	-1,00	9,72E-01	6,89	4,90E-02	1	*FLAD1*	FAD1 flavin adenine dinucleotide synthetase homolog (S. cerevisiae)

7904948	1,32	2,76E-02	-1,29	2,44E-02	1,02	9,32E-01	10,34	8,75E-03	19	*FAM108A1*	family with sequence similarity 108, member A1
8074842	1,29	1,03E-02	-1,20	4,41E-02	1,07	6,13E-01	9,29	5,47E-03	19	*FAM108A1*	family with sequence similarity 108, member A1
7924230	1,20	3,42E-02	-1,12	1,74E-01	1,08	4,63E-01	8,16	2,50E-02	19	*FAM108A1*	family with sequence similarity 108, member A1
8026751	1,07	4,60E-01	-1,14	1,76E-02	-1,06	3,87E-01	7,28	2,79E-02	19	*FAM125A*	family with sequence similarity 125, member A
8170009	-1,02	9,15E-01	-1,13	4,46E-02	-1,15	1,78E-02	8,40	1,99E-02	X	*FAM127A*	family with sequence similarity 127, member A
8140942	1,15	3,53E-01	1,15	1,61E-01	1,33	2,74E-03	7,52	6,63E-03	7	*FAM133B*	family with sequence similarity 133, member B
8048468	-1,06	7,53E-01	-1,11	1,69E-01	-1,17	2,87E-02	8,51	4,74E-02	2	*FAM134A*	family with sequence similarity 134, member A
8015655	1,09	2,51E-01	-1,15	9,38E-03	-1,06	4,15E-01	9,27	1,07E-02	17	*FAM134C*	family with sequence similarity 134, member C
8112649	1,24	9,39E-02	-1,19	1,12E-01	1,04	8,23E-01	6,43	4,99E-02	5	*FAM169A*	family with sequence similarity 169, member A
7932285	1,16	6,60E-02	-1,01	8,82E-01	1,14	5,94E-02	7,02	2,82E-02	10	*FAM188A*	family with sequence similarity 188, member A
7908612	-1,04	8,07E-01	1,16	1,50E-02	1,12	8,63E-02	6,65	1,81E-02	1	*FAM58B*	family with sequence similarity 58, member B
7987536	1,14	1,51E-01	-1,19	1,65E-02	-1,04	7,29E-01	7,84	1,73E-02	15	*FAM82A2*	family with sequence similarity 82, member A2
7982574	1,14	2,01E-01	1,02	8,03E-01	1,17	4,33E-02	6,02	4,63E-02	15	*FAM98B*	family with sequence similarity 98, member B
8097288	1,24	8,19E-02	-1,04	7,83E-01	1,19	1,09E-01	4,50	4,36E-02	4	*FAT4*	FAT tumor suppressor homolog 4 (Drosophila)
8029693	-1,98	8,45E-03	1,08	7,97E-01	-1,83	1,02E-02	7,45	2,86E-03	19	*FOSB*	FBJ murine osteosarcoma viral oncogene homolog B
8071713	1,17	3,88E-02	-1,08	2,59E-01	1,08	3,67E-01	7,48	3,09E-02	22	*FBXW4P1*	F-box and WD repeat domain containing 4 pseudogene 1
8165319	1,11	2,75E-01	-1,16	2,47E-02	-1,05	6,62E-01	8,84	3,32E-02	9	*FBXW5*	F-box and WD repeat domain containing 5
7925996	-1,02	8,93E-01	-1,14	1,74E-02	-1,16	3,93E-03	8,42	4,64E-03	10	*FBXO18*	F-box protein, helicase, 18
7906475	1,62	6,60E-02	-1,45	1,02E-01	1,12	7,73E-01	9,50	3,66E-02	1	*FCRL6*	Fc receptor-like 6
8024898	1,01	9,61E-01	-1,16	4,05E-02	-1,15	6,97E-02	6,95	4,09E-02	19	*FEM1A*	fem-1 homolog a (C. elegans)
7984470	-1,06	3,74E-01	-1,07	9,62E-02	-1,13	1,30E-03	8,74	3,58E-03	15	*FEM1B*	fem-1 homolog b (C. elegans)
8003056	1,18	1,84E-01	1,14	1,79E-01	1,34	9,85E-04	5,38	2,76E-03	16	*GAFA2*	FGF-2 activity-associated protein 2
8099807	1,07	8,13E-01	1,18	1,13E-01	1,27	2,44E-02	4,92	3,70E-02	4	*GAFA3*	FGF-2 activity-associated protein 3

8099471	1,74	3,69E-02	-1,36	2,09E-01	1,28	4,27E-01	9,51	2,76E-02	4	*FGFBP2*	fibroblast growth factor binding protein 2
8013307	-1,08	6,70E-01	-1,13	1,73E-01	-1,22	1,75E-02	12,08	3,28E-02	17	*FOXO3B*	forkhead box O3B pseudogene
7963092	1,25	8,82E-03	-1,22	1,57E-02	1,03	8,47E-01	7,50	3,11E-03	12	*FMNL3*	formin-like 3
7969794	1,23	2,98E-01	1,12	4,46E-01	1,37	1,59E-02	6,14	2,69E-02	13	*UNQ1829*	FRSS1829
8100292	1,15	1,86E-01	1,11	2,08E-01	1,28	1,30E-03	7,86	3,53E-03	4	*FRYL*	FRY-like
8167270	1,04	8,12E-01	-1,16	1,22E-02	-1,12	6,37E-02	7,74	1,34E-02	X	*FTSJ1*	FtsJ homolog 1 (E. coli)
8119198	1,08	6,42E-01	-1,25	3,68E-03	-1,16	4,35E-02	8,01	3,11E-03	6	*FTSJD2*	FtsJ methyltransferase domain containing 2
7995069	1,09	3,89E-01	1,08	2,49E-01	1,18	7,83E-03	9,96	1,64E-02	16	*FUS*	fusion (involved in t(12;16) in malignant liposarcoma)
8128956	1,14	8,49E-02	-1,11	1,09E-01	1,03	8,08E-01	9,85	4,63E-02	6	*FYN*	FYN oncogene related to SRC, FGR, YES
8172548	1,09	2,48E-01	-1,14	1,41E-02	-1,05	5,36E-01	7,79	1,75E-02	X	*GPKOW*	G patch domain and KOW motifs
8010747	1,07	4,38E-01	-1,15	1,11E-02	-1,07	2,68E-01	8,77	1,40E-02	17	*GPS1*	G protein pathway suppressor 1
7996064	1,32	2,56E-02	-1,19	1,45E-01	1,12	4,66E-01	8,25	1,92E-02	16	*GPR114*	G protein-coupled receptor 114
8091503	1,20	5,06E-01	-1,38	2,80E-02	-1,16	4,55E-01	7,39	4,59E-02	3	*GPR171*	G protein-coupled receptor 171
8157727	1,54	5,19E-03	1,25	1,34E-01	1,93	4,00E-06	6,43	1,37E-05	9	*GPR21*	G protein-coupled receptor 21
7907531	1,47	1,16E-02	1,28	8,36E-02	1,89	4,00E-06	6,77	2,08E-05	1	*GPR52*	G protein-coupled receptor 52
7996081	1,74	2,41E-02	-1,51	6,46E-02	1,15	6,88E-01	9,42	1,42E-02	16	*GPR56*	G protein-coupled receptor 56
7983616	1,17	2,94E-02	-1,06	3,88E-01	1,10	1,89E-01	7,56	2,18E-02	15	*GALK2*	galactokinase 2
8027169	1,05	7,13E-01	-1,14	2,44E-02	-1,08	2,22E-01	9,35	3,85E-02	19	*GATAD2A*	GATA zinc finger domain containing 2A
8123562	1,11	7,52E-02	1,01	8,86E-01	1,12	2,07E-02	7,13	1,74E-02	6	*GMDS*	GDP-mannose 4,6-dehydratase
8150103	1,10	5,86E-01	1,13	1,51E-01	1,25	9,00E-03	7,79	1,84E-02	8	*GTF2E2*	general transcription factor IIE, polypeptide 2, beta 34kDa
8000425	1,09	1,85E-01	-1,10	3,71E-02	-1,01	8,78E-01	7,79	3,75E-02	16	*GTF3C1*	general transcription factor IIIC, polypeptide 1, alpha 220kDa
8158961	1,07	5,11E-01	-1,15	1,27E-02	-1,08	2,56E-01	7,38	1,80E-02	9	*GTF3C5*	general transcription factor IIIC, polypeptide 5, 63kDa
8165684	-1,25	4,01E-01	-1,17	3,77E-01	-1,46	1,88E-02	9,16	3,44E-02	M	---	gi|17981852|ref|NC_001807.4|:12267-12337; gene=TRNL2; product=tRNA-Leu

7996211	1,05	7,19E-01	-1,14	2,95E-02	-1,08	2,52E-01	5,95	4,87E-02	16	*GINS3*	GINS complex subunit 3 (Psf3 homolog)
7917676	1,22	2,34E-01	1,08	5,70E-01	1,32	1,91E-02	5,73	2,85E-02	1	*GLMN*	glomulin, FKBP associated protein
8131496	1,01	9,34E-01	-1,11	3,62E-02	-1,10	8,41E-02	8,99	4,05E-02	7	*GLCCI1*	glucocorticoid induced transcript 1
7899504	-1,06	5,80E-01	-1,09	1,28E-01	-1,16	6,97E-03	7,84	1,42E-02	1	*GMEB1*	glucocorticoid modulatory element binding protein 1
8007561	1,07	6,97E-01	-1,19	1,41E-02	-1,12	1,51E-01	7,71	1,97E-02	17	*G6PC3*	glucose 6 phosphatase, catalytic, 3
8027621	1,06	7,39E-01	-1,18	2,87E-02	-1,11	2,32E-01	9,45	4,63E-02	19	*GPI*	glucose phosphate isomerase
7948744	1,07	5,82E-01	-1,18	7,27E-03	-1,11	1,21E-01	9,62	8,43E-03	11	*GANAB*	glucosidase, alpha; neutral AB
8139859	1,07	5,17E-01	-1,14	2,53E-02	-1,06	4,23E-01	8,06	4,14E-02	7	*GUSB*	glucuronidase, beta
8177544	1,29	5,19E-02	1,08	5,67E-01	1,40	2,83E-03	9,44	4,21E-03	5	*SMA4*	glucuronidase, beta pseudogene
8124469	1,23	1,23E-01	1,07	5,78E-01	1,32	8,17E-03	9,04	1,17E-02	6	*GUSBL1*	glucuronidase, beta-like 1
8111455	1,25	5,19E-02	-1,01	9,20E-01	1,23	4,18E-02	8,58	2,09E-02	6	*GUSBL1*	glucuronidase, beta-like 1
7934852	1,02	9,11E-01	-1,13	1,93E-02	-1,11	5,12E-02	9,88	1,97E-02	10	*GLUD1*	glutamate dehydrogenase 1
7935627	1,13	1,72E-01	-1,28	8,98E-04	-1,13	7,43E-02	7,37	3,44E-04	10	*GOT1*	glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase 1)
8018673	1,03	8,38E-01	1,09	6,68E-02	1,12	1,49E-02	5,87	2,21E-02	17	*QRICH2*	glutamine rich 2
8087271	1,05	7,39E-01	-1,15	1,85E-02	-1,10	1,61E-01	9,61	2,76E-02	3	*QRICH1*	glutamine-rich 1
8065817	1,12	2,24E-01	-1,15	3,34E-02	-1,03	7,98E-01	7,38	3,77E-02	20	*GSS*	glutathione synthetase
8091120	1,38	7,41E-03	-1,07	6,25E-01	1,29	1,97E-02	6,40	3,28E-03	3	*GK5*	glycerol kinase 5 (putative)
8038261	1,05	6,79E-01	-1,14	2,19E-02	-1,08	2,38E-01	7,66	3,47E-02	19	*GYS1*	glycogen synthase 1 (muscle)
8037152	-1,02	9,30E-01	-1,14	3,39E-02	-1,16	1,37E-02	9,87	1,48E-02	19	*GSK3A*	glycogen synthase kinase 3 alpha
7922029	-1,15	3,57E-01	-1,11	3,18E-01	-1,27	1,07E-02	7,37	2,10E-02	1	*GPA33*	glycoprotein A33 (transmembrane)
8148715	1,07	4,05E-01	-1,12	1,93E-02	-1,05	4,52E-01	8,89	2,95E-02	8	*GPAA1*	glycosylphosphatidylinositol anchor attachment protein 1 homolog (yeast)
8155250	1,05	8,32E-01	-1,22	1,82E-02	-1,16	9,11E-02	7,38	2,35E-02	9	*GRHPR*	glyoxylate reductase/hydroxypyruvate reductase
7987027	1,35	1,51E-02	-1,10	4,62E-01	1,23	8,80E-02	7,70	1,05E-02	15	*GOLGA9P*	golgi autoantigen, golgin subfamily a, 9 pseudogene

7987139	1,50	2,97E-02	-1,20	2,93E-01	1,24	2,73E-01	7,40	2,32E-02	15	*GOLGA9P*	golgi autoantigen, golgin subfamily a, 9 pseudogene
7985472	1,01	9,74E-01	1,22	6,14E-02	1,23	5,33E-02	6,99	4,75E-02	15	*FLJ40113*	golgi autoantigen, golgin subfamily a-like pseudogene
8041000	1,15	1,80E-01	-1,20	1,60E-02	-1,05	6,81E-01	7,18	1,80E-02	2	*GPN1*	GPN-loop GTPase 1
8101757	1,24	3,02E-02	-1,11	2,66E-01	1,12	3,03E-01	8,19	2,35E-02	4	*GPRIN3*	GPRIN family member 3
8043236	1,53	1,46E-02	-1,22	2,37E-01	1,25	2,22E-01	10,63	1,13E-02	2	*GNLY*	granulysin
7978366	1,73	3,06E-03	-1,29	1,27E-01	1,34	1,02E-01	8,55	1,36E-03	14	*GZMB*	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1)
8023977	1,30	7,41E-03	-1,17	9,71E-02	1,12	3,14E-01	8,54	4,84E-03	19	*GZMM*	granzyme M (lymphocyte met-ase 1)
8176163	1,16	7,80E-02	-1,12	1,15E-01	1,03	7,73E-01	8,44	4,41E-02	X	*GAB3*	GRB2-associated binding protein 3
8137865	1,05	8,78E-01	-1,26	2,44E-02	-1,20	9,11E-02	8,55	3,03E-02	7	*GNA12*	guanine nucleotide binding protein (G protein) alpha 12
7974341	1,18	6,60E-02	-1,01	9,05E-01	1,17	5,39E-02	9,50	2,68E-02	14	*GNG2*	guanine nucleotide binding protein (G protein), gamma 2
8046515	-1,05	6,16E-01	1,13	1,18E-02	1,08	1,65E-01	12,05	1,54E-02	1	*H3F3A*	H3 histone, family 3A
7905733	1,01	9,73E-01	-1,24	1,27E-02	-1,22	1,45E-02	7,43	7,37E-03	1	*HAX1*	HCLS1 associated protein X-1
7915659	1,09	4,98E-01	-1,17	2,49E-02	-1,07	4,37E-01	8,25	4,04E-02	1	*HECTD3*	HECT domain containing 3
8090193	1,29	3,58E-02	-1,30	1,60E-02	-1,01	9,78E-01	7,59	7,71E-03	3	*HEG1*	HEG homolog 1 (zebrafish)
8028104	1,29	2,38E-02	-1,26	2,44E-02	1,02	9,16E-01	9,13	8,26E-03	19	*HCST*	hematopoietic cell signal transducer, DAP10
8115455	1,16	1,85E-01	-1,18	4,97E-02	-1,01	9,34E-01	4,98	4,78E-02	5	*HAVCR1*	hepatitis A virus cellular receptor 1
8119525	1,07	7,11E-01	1,12	1,86E-01	1,20	2,69E-02	5,41	4,59E-02	6	*HCRP1*	hepatocellular carcinoma-related HCRP1
8083282	1,01	9,84E-01	-1,15	3,17E-02	-1,14	4,18E-02	9,34	2,60E-02	3	*HPS3*	Hermansky-Pudlak syndrome 3
7933192	-1,03	8,90E-01	1,14	3,47E-02	1,11	1,15E-01	6,21	4,47E-02	10	*HNRNPA3P1*	heterogeneous nuclear ribonucleoprotein A3 pseudogene 1
8117377	1,17	2,44E-02	-1,10	1,50E-01	1,07	4,49E-01	12,76	1,87E-02	6	*HIST1H1E*	histone cluster 1, H1e
8124402	-1,12	5,69E-01	1,28	1,99E-02	1,14	3,08E-01	4,29	3,21E-02	6	*HIST1H1T*	histone cluster 1, H1t
8124531	1,10	4,45E-01	-1,19	2,19E-02	-1,08	4,44E-01	10,82	3,39E-02	6	*HIST1H3I*	histone cluster 1, H3i
8145636	1,15	8,61E-02	1,00	9,72E-01	1,15	3,85E-02	7,69	2,68E-02	8	*HMBOX1*	homeobox containing 1

7919131	1,16	2,70E-01	1,14	1,63E-01	1,32	1,58E-03	6,58	4,33E-03	1	---	Homo sapiens cDNA clone IMAGE:4249212.
7907568	1,05	7,35E-01	1,09	1,81E-01	1,15	2,90E-02	4,33	4,92E-02	1	---	Homo sapiens cDNA clone IMAGE:5296077.
8020650	1,02	9,42E-01	1,22	3,62E-02	1,25	1,77E-02	5,43	1,78E-02	18	---	Homo sapiens cDNA clone MGC:21733 IMAGE:4517792, complete cds.
7902848	1,18	4,05E-01	1,11	4,57E-01	1,31	2,95E-02	8,11	4,90E-02	1	---	Homo sapiens cDNA FLJ13538 fis, clone PLACE1006617.
8063449	-1,05	8,62E-01	1,21	3,39E-02	1,15	1,42E-01	6,68	4,68E-02	20	---	Homo sapiens cDNA FLJ14031 fis, clone HEMBA1004335.
8061414	-1,28	1,31E-01	1,37	1,55E-02	1,07	7,40E-01	6,04	1,47E-02	20	---	Homo sapiens cDNA FLJ33142 fis, clone UTERU1000192.
7926894	1,12	4,75E-01	1,09	3,44E-01	1,22	2,25E-02	5,15	4,05E-02	10	---	Homo sapiens cDNA FLJ35060 fis, clone OCBBF2018828.
8075190	-1,03	8,71E-01	1,15	2,71E-02	1,11	1,08E-01	4,79	3,52E-02	22	---	Homo sapiens cDNA FLJ38169 fis, clone DFNES2008280.
8093330	1,32	1,63E-01	1,06	7,51E-01	1,41	2,64E-02	6,88	2,92E-02	4	---	Homo sapiens cDNA FLJ38191 fis, clone FCBBF1000243. /// Homo sapiens cDNA FLJ42172 fis, clone THYMU2029676.
8101990	1,22	4,93E-01	1,58	6,22E-03	1,94	2,90E-05	5,80	1,10E-04	4	---	Homo sapiens cDNA FLJ39766 fis, clone SPLEN2000307.
8144569	1,24	4,98E-01	1,20	3,20E-01	1,49	2,16E-02	4,84	3,95E-02	8	---	Homo sapiens cDNA FLJ42545 fis, clone BRACE3004783.
7994570	1,16	4,91E-01	1,16	2,59E-01	1,35	1,36E-02	6,76	2,69E-02	16	---	Homo sapiens cDNA: FLJ23497 fis, clone LNG02604.
8002102	1,15	5,05E-01	1,13	2,95E-01	1,30	1,88E-02	5,62	3,53E-02	16	---	Homo sapiens clone HQ0113 PRO0113 mRNA, complete cds.
7935863	1,05	6,12E-01	1,11	3,56E-02	1,17	1,06E-03	3,59	2,57E-03	10	---	Homo sapiens clone HQ0483$ PRO0483 mRNA, complete cds.
8081254	1,13	2,96E-01	1,09	3,33E-01	1,23	8,29E-03	5,27	1,64E-02	3	---	Homo sapiens clone HQ0641 PRO0641 mRNA, complete cds.
8020321	1,15	4,11E-01	1,17	1,38E-01	1,35	2,94E-03	5,67	7,10E-03	18	---	Homo sapiens clone HQ0644 PRO0644 mRNA, complete cds.
8089295	1,32	4,23E-02	-1,03	8,69E-01	1,29	4,33E-02	6,83	1,86E-02	3	---	Homo sapiens HC1 (HC1) mRNA, complete cds.
8165932	1,02	9,61E-01	1,29	3,05E-02	1,31	1,88E-02	3,81	1,67E-02	X	---	Homo sapiens HCV-NS5ATP5 binding protein 1 mRNA, complete cds.
8055016	1,08	8,41E-01	1,43	1,47E-02	1,55	1,55E-03	7,43	2,45E-03	2	---	Homo sapiens IL-1beta-regulated neutrophil survival protein mRNA, complete cds.
8005829	1,45	1,34E-01	1,49	4,28E-02	2,16	4,10E-05	5,33	1,68E-04	17	---	Homo sapiens lung squamous cell carcinoma related protein-2 mRNA, complete cds.
7975457	1,21	3,60E-01	1,30	4,92E-02	1,58	3,67E-04	8,04	1,24E-03	14	---	Homo sapiens mRNA for FLJ00399 protein.
8168727	1,17	1,25E-01	1,10	2,50E-01	1,29	1,09E-03	4,67	2,78E-03	X	---	Homo sapiens mRNA for HEIL2, complete cds.

7958207	1,41	1,44E-01	1,36	1,00E-01	1,91	2,11E-04	7,13	7,68E-04	12	---	Homo sapiens mRNA similar to hypothetical protein FLJ21394 (cDNA clone IMAGE:3950761).
8152865	1,13	7,31E-01	1,35	4,33E-02	1,52	3,08E-03	7,77	5,86E-03	8	---	Homo sapiens OK/SW-cl.41 mRNA, complete cds.
7939374	1,63	1,95E-02	1,20	3,77E-01	1,96	2,33E-04	6,69	5,07E-04	11	---	Homo sapiens PNAS-17 mRNA, complete cds.
7985266	1,09	7,45E-01	1,31	1,66E-02	1,44	8,58E-04	6,41	1,69E-03	15	---	Homo sapiens PP1200 mRNA, complete cds.
8132513	1,05	8,86E-01	1,28	4,69E-02	1,35	1,36E-02	5,38	1,75E-02	7	---	Homo sapiens uncharacterized gastric protein ZG12P mRNA, complete cds.
7919787	-1,09	8,79E-01	1,51	2,12E-02	1,39	7,58E-02	6,48	2,43E-02	1	*HORMAD1*	HORMA domain containing 1
8175947	1,03	9,04E-01	-1,17	2,39E-02	-1,14	6,75E-02	8,50	2,61E-02	X	*HCFC1*	host cell factor C1 (VP16-accessory protein)
8093685	1,16	2,38E-02	-1,09	1,40E-01	1,06	4,61E-01	7,87	1,79E-02	4	*HTT*	huntingtin
8132245	1,03	8,92E-01	1,12	9,59E-02	1,15	3,89E-02	4,19	4,90E-02	7	*FLJ20712*	hypothetical FLJ20712
7961097	1,00	9,93E-01	1,19	1,66E-02	1,19	1,28E-02	5,76	8,54E-03	12	*FLJ46363*	hypothetical FLJ46363
7951140	1,23	5,22E-01	1,35	7,92E-02	1,66	2,06E-03	7,66	5,10E-03	11	*UNQ6228*	hypothetical LOC100131541
8061483	1,17	4,37E-02	-1,01	8,81E-01	1,15	4,30E-02	6,13	1,92E-02	20	*CTD-2514C3.1*	hypothetical LOC100134868
8148982	1,12	6,11E-01	1,18	1,47E-01	1,32	9,92E-03	6,56	1,99E-02	8	*LOC389607*	hypothetical LOC389607
8023868	-1,18	3,88E-02	1,07	3,95E-01	-1,10	2,34E-01	5,97	3,10E-02	18	*LOC400657*	hypothetical LOC400657
8084739	1,10	5,00E-01	1,12	1,40E-01	1,23	4,81E-03	5,86	1,09E-02	3	*FLJ42393*	hypothetical LOC401105
8135931	-1,12	5,49E-01	1,28	1,28E-02	1,15	2,34E-01	7,71	1,87E-02	7	*tcag7.907*	hypothetical LOC402483
7976828	-1,05	7,69E-01	1,17	1,74E-02	1,11	1,32E-01	5,44	2,53E-02	14	*FLJ41170*	hypothetical LOC440200
7919596	1,12	6,68E-01	1,17	2,11E-01	1,32	2,39E-02	5,19	4,29E-02	1	*LOC440570*	hypothetical LOC440570
7912194	1,14	6,49E-01	1,35	2,44E-02	1,54	7,28E-04	6,45	1,72E-03	1	*DKFZp566H0824*	hypothetical LOC54744
8137483	1,18	2,16E-01	1,10	3,54E-01	1,30	5,37E-03	5,63	1,07E-02	7	*FLJ16734*	hypothetical LOC641928
8159732	1,06	7,52E-01	1,14	7,69E-02	1,20	8,86E-03	7,12	1,56E-02	9	*FLJ40292*	hypothetical LOC643210
8111922	-1,01	9,38E-01	-1,15	1,40E-02	-1,16	4,35E-03	7,16	4,16E-03	5	*LOC648987*	hypothetical LOC648987
8113071	-1,03	8,90E-01	1,19	1,18E-02	1,16	3,19E-02	7,56	9,53E-03	5	*LOC729040*	hypothetical LOC729040

7985431	1,14	8,09E-01	-1,63	1,66E-02	-1,43	1,00E-01	6,53	2,25E-02	15	*LOC80154*	hypothetical LOC80154
8008700	1,02	9,24E-01	1,15	2,93E-02	1,17	1,12E-02	5,52	1,17E-02	17	*FLJ11710*	hypothetical protein FLJ11710
8017344	1,17	1,86E-01	1,02	8,44E-01	1,20	4,46E-02	7,02	4,48E-02	17	*LOC100129112*	hypothetical protein LOC100129112
7971965	1,04	9,08E-01	1,20	6,33E-02	1,24	2,76E-02	5,38	3,21E-02	13	*LOC100129884*	hypothetical protein LOC100129884
8105189	1,02	9,56E-01	1,21	5,12E-02	1,23	3,32E-02	4,81	3,28E-02	5	*LOC100287671*	hypothetical protein LOC100287671
7978917	1,09	5,78E-01	1,11	1,84E-01	1,22	1,20E-02	6,04	2,36E-02	14	*LOC196913*	hypothetical protein LOC196913
8063793	1,14	5,69E-01	1,15	2,70E-01	1,30	2,24E-02	5,64	4,12E-02	20	*LOC284757*	hypothetical protein LOC284757
7957242	-1,03	9,01E-01	-1,15	5,71E-02	-1,19	2,22E-02	8,46	2,64E-02	12	*LOC552889*	hypothetical protein LOC552889
7952145	1,11	2,95E-01	-1,15	3,76E-02	-1,04	7,46E-01	7,60	4,96E-02	11	*HYOU1*	hypoxia up-regulated 1
7936826	-1,16	3,03E-01	-1,06	5,89E-01	-1,23	3,15E-02	8,34	4,59E-02	10	*IKZF5*	IKAROS family zinc finger 5 (Pegasus)
7981737	-1,22	6,27E-01	-1,28	2,31E-01	-1,57	2,24E-02	7,14	4,09E-02	14	*IGHA1*	immunoglobulin heavy constant alpha 1
8071658	-1,26	3,14E-01	-1,10	5,88E-01	-1,39	3,29E-02	5,39	4,83E-02	22	*IGLV7-46*	immunoglobulin lambda variable 7-46 (gene/pseudogene)
8045171	1,05	7,24E-01	-1,17	8,65E-03	-1,11	6,85E-02	8,08	8,53E-03	2	*IMP4*	IMP4, U3 small nucleolar ribonucleoprotein, homolog (yeast)
7900888	1,12	1,14E-01	-1,13	3,39E-02	-1,01	9,40E-01	6,62	2,67E-02	1	*IPO13*	importin 13
7978132	1,07	4,87E-01	-1,12	2,93E-02	-1,05	4,85E-01	7,18	4,77E-02	14	*IPO4*	importin 4
8118734	1,18	1,36E-01	-1,18	5,27E-02	-1,00	9,86E-01	7,64	4,24E-02	6	*ITPR3*	inositol 1,4,5-triphosphate receptor, type 3
8043791	1,16	5,60E-03	-1,06	2,57E-01	1,09	9,70E-02	9,28	4,16E-03	2	*INPP4A*	inositol polyphosphate-4-phosphatase, type I, 107kDa
8011062	1,06	6,69E-01	-1,15	2,95E-02	-1,08	3,08E-01	8,75	4,96E-02	17	*INPP5K*	inositol polyphosphate-5-phosphatase K
8059470	-1,09	4,96E-01	-1,10	1,98E-01	-1,19	8,69E-03	5,62	1,80E-02	2	*IRS1*	insulin receptor substrate 1
7986383	-1,26	3,88E-02	1,36	3,68E-03	1,08	6,17E-01	7,20	2,09E-03	15	*IGF1R*	insulin-like growth factor 1 receptor
8102162	-1,02	8,98E-01	-1,15	1,17E-02	-1,17	1,77E-03	6,22	2,17E-03	4	*INTS12*	integrator complex subunit 12
8150014	1,12	2,57E-01	-1,20	1,27E-02	-1,07	4,94E-01	7,64	1,57E-02	8	*INTS9*	integrator complex subunit 9
7994826	1,16	9,08E-02	-1,15	4,76E-02	1,00	9,85E-01	10,51	3,08E-02	16	*ITGAL*	integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide)

7963614	1,19	1,34E-01	-1,24	2,12E-02	-1,04	8,17E-01	9,68	1,99E-02	12	*ITGB7*	integrin, beta 7
8017547	1,22	2,08E-02	-1,12	1,40E-01	1,08	4,35E-01	9,76	1,56E-02	17	*ICAM2*	intercellular adhesion molecule 2
7925161	-1,13	2,08E-01	-1,03	7,34E-01	-1,16	3,35E-02	9,41	3,98E-02	1	*IRF2BP2*	interferon regulatory factor 2 binding protein 2
7921110	1,02	9,24E-01	-1,16	1,47E-02	-1,14	3,13E-02	8,76	1,21E-02	1	*ISG20L2*	interferon stimulated exonuclease gene 20kDa-like 2
7944152	1,16	6,60E-02	-1,19	1,27E-02	-1,03	8,39E-01	10,50	8,75E-03	11	*IL10RA*	interleukin 10 receptor, alpha
8035380	1,16	3,88E-02	-1,18	1,27E-02	-1,01	9,14E-01	8,09	6,90E-03	19	*IL12RB1*	interleukin 12 receptor, beta 1
7902205	1,45	2,38E-02	-1,18	3,07E-01	1,23	2,29E-01	6,51	1,91E-02	1	*IL12RB2*	interleukin 12 receptor, beta 2
8097553	1,14	3,26E-01	1,08	4,50E-01	1,23	1,89E-02	5,19	3,29E-02	4	*IL15*	interleukin 15
8075886	1,58	1,46E-02	-1,29	1,47E-01	1,22	3,50E-01	9,91	1,14E-02	22	*IL2RB*	interleukin 2 receptor, beta
7994292	1,15	1,31E-01	-1,17	2,98E-02	-1,02	8,99E-01	7,34	2,64E-02	16	*IL21R*	interleukin 21 receptor
7960559	1,14	3,45E-02	-1,03	6,87E-01	1,11	7,06E-02	7,21	1,89E-02	12	*IFFO1*	intermediate filament family orphan 1
7975705	-1,04	7,45E-01	-1,09	5,17E-02	-1,13	4,63E-03	8,06	8,52E-03	14	*ISCA2*	iron-sulfur cluster assembly 2 homolog (S. cerevisiae)
7991374	1,08	5,44E-01	-1,17	2,51E-02	-1,08	3,92E-01	8,63	4,13E-02	15	*IDH2*	isocitrate dehydrogenase 2 (NADP+), mitochondrial
7985134	-1,04	8,90E-01	-1,20	2,84E-02	-1,25	7,54E-03	9,39	8,58E-03	15	*IDH3A*	isocitrate dehydrogenase 3 (NAD+) alpha
8064522	1,05	7,52E-01	-1,14	2,38E-02	-1,09	1,86E-01	8,65	3,55E-02	20	*IDH3B*	isocitrate dehydrogenase 3 (NAD+) beta
7911993	1,09	3,45E-01	-1,17	7,68E-03	-1,08	2,75E-01	7,30	8,75E-03	1	*ICMT*	isoprenylcysteine carboxyl methyltransferase
8114938	1,39	5,81E-02	-1,12	5,14E-01	1,24	2,07E-01	5,75	4,18E-02	5	*JAKMIP2*	janus kinase and microtubule interacting protein 2
7998267	1,07	5,48E-01	-1,18	7,12E-03	-1,10	1,35E-01	8,25	8,26E-03	16	*JMJD8*	jumonji domain containing 8
8038683	1,02	8,90E-01	1,10	9,65E-02	1,13	3,83E-02	5,40	4,89E-02	19	*KLK6*	kallikrein-related peptidase 6
8019737	-1,03	8,92E-01	-1,15	7,06E-02	-1,19	2,69E-02	8,44	3,33E-02	17	*KPNA2*	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)
8038078	-1,00	9,96E-01	-1,17	1,74E-02	-1,17	1,52E-02	8,08	1,01E-02	19	*KDELR1*	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1
8138108	1,01	9,85E-01	-1,15	3,30E-02	-1,15	4,27E-02	9,14	2,68E-02	7	*KDELR2*	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2
8119648	1,04	8,48E-01	-1,18	1,22E-02	-1,14	5,03E-02	9,19	1,21E-02	6	*KLHDC3*	kelch domain containing 3

8003283	1,16	5,68E-02	-1,04	6,10E-01	1,12	1,48E-01	6,79	3,67E-02	16	*KLHDC4*	kelch domain containing 4
8098177	-1,24	2,22E-01	1,31	3,70E-02	1,05	8,33E-01	7,54	4,16E-02	4	*KLHL2*	kelch-like 2, Mayven (Drosophila)
7991173	-1,00	9,95E-01	1,13	3,96E-02	1,13	4,59E-02	5,91	3,30E-02	15	*KLHL25*	kelch-like 25 (Drosophila)
8154725	1,17	1,97E-01	1,03	7,96E-01	1,21	4,12E-02	6,98	4,41E-02	12	*KRT18*	keratin 18
7963427	1,22	5,24E-02	-1,02	8,63E-01	1,20	5,40E-02	5,87	2,39E-02	12	*KRT5*	keratin 5
7963459	1,34	1,03E-02	-1,22	6,15E-02	1,10	5,14E-01	6,04	6,38E-03	12	*KRT72*	keratin 72
7963471	1,57	4,30E-03	-1,41	1,95E-02	1,11	6,47E-01	5,42	1,89E-03	12	*KRT73*	keratin 73
7963359	-1,03	8,87E-01	1,18	2,19E-02	1,15	7,23E-02	5,73	2,48E-02	12	*KRT83*	keratin 83
8093230	1,12	9,39E-02	-1,10	1,02E-01	1,02	8,47E-01	8,39	4,83E-02	3	*KIAA0226*	KIAA0226
7915882	1,03	8,65E-01	-1,13	2,67E-02	-1,10	1,11E-01	9,70	3,49E-02	1	*KIAA0494*	KIAA0494
8097148	1,01	9,76E-01	1,12	5,27E-02	1,13	4,47E-02	9,42	3,94E-02	4	*KIAA1109*	KIAA1109
8021496	1,07	6,80E-01	1,09	2,27E-01	1,17	2,88E-02	8,81	4,99E-02	18	*KIAA1468*	KIAA1468
8121525	1,18	1,81E-01	1,02	8,76E-01	1,20	5,08E-02	7,55	4,77E-02	6	*KIAA1919*	KIAA1919
8031297	1,60	5,19E-02	-1,21	4,25E-01	1,33	2,54E-01	6,91	3,95E-02	19	*KIR2DL1*	killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 1
8039829	1,84	3,71E-02	-1,42	1,94E-01	1,30	4,50E-01	7,66	2,76E-02	19	*KIR2DL2*	killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 2
7961059	1,50	2,06E-02	-1,42	2,87E-02	1,06	8,59E-01	9,41	8,09E-03	12	*KLRB1*	killer cell lectin-like receptor subfamily B, member 1
7953949	1,54	3,78E-02	-1,22	3,17E-01	1,27	2,87E-01	9,26	2,89E-02	12	*KLRD1*	killer cell lectin-like receptor subfamily D, member 1 (CD94)
7953892	2,08	1,46E-02	-1,34	3,17E-01	1,55	1,54E-01	8,65	1,12E-02	12	*KLRF1*	killer cell lectin-like receptor subfamily F, member 1
7953835	1,58	4,11E-02	-1,22	3,68E-01	1,30	2,65E-01	9,70	3,31E-02	12	*KLRG1*	killer cell lectin-like receptor subfamily G, member 1
8150036	1,16	4,51E-02	-1,02	8,28E-01	1,14	5,48E-02	7,51	2,19E-02	8	*KIF13B*	kinesin family member 13B
7962274	1,28	3,05E-02	-1,10	3,81E-01	1,16	2,01E-01	5,37	2,32E-02	12	*KIF21A*	kinesin family member 21A
7991296	-1,07	6,09E-01	1,16	1,27E-02	1,09	1,91E-01	6,05	1,80E-02	15	*KIF7*	kinesin family member 7
7982326	-1,04	8,20E-01	-1,09	1,25E-01	-1,13	3,08E-02	9,45	4,65E-02	15	*KLF13*	Kruppel-like factor 13

8163002	-1,39	3,02E-02	-1,02	9,30E-01	-1,41	9,73E-03	7,38	6,52E-03	9	*KLF4*	Kruppel-like factor 4 (gut)
7969414	-1,16	1,35E-01	-1,01	9,41E-01	-1,17	5,12E-02	7,49	4,09E-02	13	*KLF5*	Kruppel-like factor 5 (intestinal)
7931810	-1,18	3,88E-02	1,06	4,88E-01	-1,11	1,72E-01	9,22	2,92E-02	10	*KLF6*	Kruppel-like factor 6
7916130	-1,02	9,41E-01	-1,22	1,03E-02	-1,24	2,48E-03	7,99	2,52E-03	1	*KTI12*	KTI12 homolog, chromatin associated (S. cerevisiae)
8109438	-1,05	6,95E-01	-1,09	9,16E-02	-1,15	7,62E-03	9,28	1,45E-02	5	*LARP1*	La ribonucleoprotein domain family, member 1
7910096	1,01	9,67E-01	1,15	5,11E-02	1,17	3,96E-02	4,80	3,53E-02	1	*LBR*	lamin B receptor
8034783	1,07	4,63E-01	-1,14	1,85E-02	-1,06	3,95E-01	7,54	2,95E-02	19	*LPHN1*	latrophilin 1
7994237	1,04	7,31E-01	-1,14	1,11E-02	-1,09	8,90E-02	7,70	1,24E-02	16	*LCMT1*	leucine carboxyl methyltransferase 1
8049536	1,01	9,85E-01	1,16	5,36E-02	1,17	5,12E-02	8,81	4,33E-02	2	*LRRFIP1*	leucine rich repeat (in FLII) interacting protein 1
8049530	1,10	8,59E-01	1,48	3,70E-02	1,63	7,61E-03	8,71	1,01E-02	2	*LRRFIP1*	leucine rich repeat (in FLII) interacting protein 1
8049532	-1,05	9,32E-01	1,42	3,30E-02	1,35	7,58E-02	7,07	3,53E-02	2	*LRRFIP1*	leucine rich repeat (in FLII) interacting protein 1
7933484	1,04	8,29E-01	1,16	3,90E-02	1,21	6,63E-03	4,62	9,16E-03	10	*LRRC18*	leucine rich repeat containing 18
7986394	1,07	7,00E-01	-1,18	2,35E-02	-1,11	2,33E-01	8,06	3,69E-02	15	*LRRC28*	leucine rich repeat containing 28
7915827	1,04	7,75E-01	-1,17	7,12E-03	-1,12	4,38E-02	8,20	6,52E-03	1	*LRRC41*	leucine rich repeat containing 41
8137215	1,08	3,81E-01	-1,15	1,16E-02	-1,07	3,23E-01	7,41	1,44E-02	7	*LRRC61*	leucine rich repeat containing 61
8098924	1,07	5,34E-01	-1,14	1,74E-02	-1,07	3,14E-01	7,35	2,78E-02	4	*LETM1*	leucine zipper-EF-hand containing transmembrane protein 1
7908816	1,44	5,19E-03	-1,22	1,13E-01	1,18	2,38E-01	6,22	3,82E-03	1	*LGR6*	leucine-rich repeat-containing G protein-coupled receptor 6
8136315	1,15	5,29E-02	-1,09	1,96E-01	1,06	5,32E-01	4,15	3,95E-02	7	*LRGUK*	leucine-rich repeats and guanylate kinase domain containing
8071466	1,13	4,32E-02	-1,08	1,88E-01	1,05	5,03E-01	7,37	3,35E-02	22	*LZTR1*	leucine-zipper-like transcription regulator 1
8039257	1,17	2,27E-01	-1,22	3,02E-02	-1,05	7,76E-01	9,02	3,53E-02	19	*LAIR1*	leukocyte-associated immunoglobulin-like receptor 1
8084742	1,20	2,67E-02	1,05	5,84E-01	1,26	1,30E-03	9,14	1,89E-03	3	*LPP*	LIM domain containing preferred translocation partner in lipoma
7994541	1,14	3,80E-01	-1,23	3,01E-02	-1,07	5,96E-01	9,49	4,52E-02	16	*LAT*	linker for activation of T cells
8130598	1,38	2,97E-02	-1,14	3,67E-01	1,21	2,07E-01	5,86	2,25E-02	6	*LPAL2*	lipoprotein, Lp(a)-like 2 pseudogene

7904742	1,03	8,05E-01	-1,11	2,70E-02	-1,08	1,61E-01	8,82	3,97E-02	1	*LIX1L*	Lix1 homolog (mouse)-like
8085429	1,06	7,05E-01	1,14	5,31E-02	1,21	3,67E-03	6,80	7,10E-03	3	*UNQ6487*	LMNE6487
8150206	-1,03	8,90E-01	-1,14	5,42E-02	-1,18	1,87E-02	10,32	2,32E-02	17	*LSM12*	LSM12 homolog (S. cerevisiae)
8037061	-1,08	5,80E-01	1,17	2,32E-02	1,09	3,35E-01	4,88	3,76E-02	19	*LYPD4*	LY6/PLAUR domain containing 4
7941769	-1,10	5,87E-02	1,03	5,78E-01	-1,07	1,69E-01	9,55	3,98E-02	11	*KDM2A*	lysine (K)-specific demethylase 2A
8154333	1,19	4,70E-02	-1,08	3,74E-01	1,10	2,81E-01	8,54	3,69E-02	9	*KDM4C*	lysine (K)-specific demethylase 4C
8110841	1,23	7,80E-02	-1,05	6,80E-01	1,17	1,48E-01	9,18	4,63E-02	5	*LPCAT1*	lysophosphatidylcholine acyltransferase 1
8148737	1,09	5,39E-01	-1,22	1,11E-02	-1,12	1,97E-01	8,25	1,40E-02	8	*MAF1*	MAF1 homolog (S. cerevisiae)
7955729	1,06	6,97E-01	-1,18	1,84E-02	-1,11	1,98E-01	7,37	2,86E-02	12	*MFSD5*	major facilitator superfamily domain containing 5
8180086	-1,03	9,08E-01	-1,15	7,41E-02	-1,18	3,26E-02	9,73	3,88E-02	6	*HLA-DMA*	major histocompatibility complex, class II, DM alpha
8180100	-1,04	8,96E-01	-1,22	2,78E-02	-1,27	7,64E-03	12,15	8,54E-03	6	*HLA-DPA1*	major histocompatibility complex, class II, DP alpha 1
8178891	1,00	9,94E-01	-1,25	2,42E-02	-1,25	2,67E-02	11,96	1,71E-02	6	*HLA-DPA1*	major histocompatibility complex, class II, DP alpha 1
8133690	1,02	8,97E-01	-1,13	3,56E-02	-1,10	1,12E-01	10,03	4,51E-02	7	*MDH2*	malate dehydrogenase 2, NAD (mitochondrial)
8053158	1,10	2,02E-01	-1,13	3,40E-02	-1,02	8,32E-01	7,98	3,67E-02	2	*MOGS*	mannosyl-oligosaccharide glucosidase
7939767	1,09	3,47E-01	-1,13	3,23E-02	-1,04	6,49E-01	9,34	4,61E-02	11	*MADD*	MAP-kinase activating death domain
8180377	1,79	8,12E-02	-1,67	6,88E-02	1,07	9,03E-01	7,12	3,53E-02	17	*MXRA7*	matrix-remodelling associated 7
7912412	1,07	4,04E-01	-1,13	1,71E-02	-1,05	4,32E-01	8,31	2,64E-02	1	*MTOR*	mechanistic target of rapamycin (serine/threonine kinase)
8014925	1,09	2,08E-01	-1,19	1,74E-03	-1,08	1,61E-01	8,21	1,69E-03	17	*MED24*	mediator complex subunit 24
8032682	1,37	3,31E-02	-1,20	1,83E-01	1,14	4,43E-01	7,26	2,44E-02	19	*MATK*	megakaryocyte-associated tyrosine kinase
8076894	1,30	3,87E-02	-1,17	1,70E-01	1,11	5,04E-01	7,97	2,83E-02	22	*MLC1*	megalencephalic leukoencephalopathy with subcortical cysts 1
8167815	1,16	8,12E-02	-1,19	1,68E-02	-1,02	8,71E-01	7,35	1,36E-02	X	*MAGED2*	melanoma antigen family D, 2
8025421	1,08	7,69E-01	-1,28	1,60E-02	-1,19	1,17E-01	9,11	2,18E-02	19	*MARCH2*	membrane-associated ring finger (C3HC4) 2
7948696	1,09	4,25E-01	-1,17	1,28E-02	-1,08	3,27E-01	9,70	1,83E-02	11	*MTA2*	metastasis associated 1 family, member 2

7955441	-1,05	8,68E-01	-1,18	1,03E-01	-1,24	3,27E-02	8,51	4,51E-02	12	*METTL7A*	methyltransferase like 7A
8060734	-1,04	9,33E-01	1,38	2,57E-02	1,33	5,82E-02	5,18	2,63E-02	20	*MIR103-2AS /// MIR103-2*	microRNA 103-2-as /// microRNA 103-2
7903717	-1,01	9,83E-01	1,26	1,11E-02	1,25	9,77E-03	7,76	4,91E-03	1	*MIR197*	microRNA 197
7987097	-1,04	8,77E-01	1,24	6,25E-03	1,20	1,70E-02	6,95	4,16E-03	15	*MIR211*	microRNA 211
8164438	1,01	9,57E-01	1,12	5,01E-02	1,13	3,31E-02	5,14	3,22E-02	9	*MIR219-2*	microRNA 219-2
8084755	1,12	3,34E-01	1,09	3,15E-01	1,22	9,12E-03	3,23	1,80E-02	3	*MIR28*	microRNA 28
7923974	1,01	9,84E-01	1,40	4,01E-02	1,42	3,42E-02	6,62	2,76E-02	1	*MIR29C*	microRNA 29c
8127498	-1,10	7,03E-01	1,26	2,96E-02	1,15	2,75E-01	4,29	4,93E-02	6	*MIR30C2*	microRNA 30c-2
8020419	-1,01	9,57E-01	1,19	2,83E-02	1,17	5,03E-02	4,69	2,64E-02	18	*MIR320C1*	microRNA 320c-1
8175261	-1,13	3,24E-01	1,20	2,51E-02	1,06	6,08E-01	5,50	3,53E-02	X	*MIR503*	microRNA 503
8031029	-1,13	1,87E-01	-1,03	7,56E-01	-1,16	3,22E-02	2,50	3,65E-02	19	*MIR520B /// MIR520C*	microRNA 520b /// microRNA 520c
8156523	-1,11	3,13E-01	1,16	3,62E-02	1,04	7,19E-01	6,36	4,92E-02	9	*MIRLET7D*	microRNA let-7d
7963064	1,07	4,60E-01	-1,15	1,56E-02	-1,07	3,43E-01	7,79	2,32E-02	12	*MCRS1*	microspherule protein 1
7900235	1,19	4,32E-02	-1,03	7,64E-01	1,16	6,82E-02	9,07	2,33E-02	1	*MACF1*	microtubule-actin crosslinking factor 1
7900336	1,24	4,32E-02	1,04	7,26E-01	1,30	5,27E-03	6,27	5,51E-03	1	*MACF1*	microtubule-actin crosslinking factor 1
8020878	1,11	1,74E-01	-1,13	3,86E-02	-1,02	8,99E-01	9,37	3,74E-02	18	*MAPRE2*	microtubule-associated protein, RP/EB family, member 2
8018343	1,08	6,37E-01	-1,23	5,76E-03	-1,15	7,23E-02	7,35	5,41E-03	17	*MIF4GD*	MIF4G domain containing
7967987	1,01	9,82E-01	-1,13	3,77E-02	-1,13	5,33E-02	6,17	3,39E-02	13	*MRP63*	mitochondrial ribosomal protein 63
7901601	-1,01	9,58E-01	-1,12	3,00E-02	-1,13	1,74E-02	9,10	1,56E-02	1	*MRPL37*	mitochondrial ribosomal protein L37
8071206	1,04	8,39E-01	-1,15	1,99E-02	-1,12	9,31E-02	6,98	2,52E-02	22	*MRPL40*	mitochondrial ribosomal protein L40
7941164	1,06	8,16E-01	-1,29	7,81E-03	-1,21	3,59E-02	7,92	6,52E-03	11	*MRPL49*	mitochondrial ribosomal protein L49
7920047	1,08	6,12E-01	-1,18	2,02E-02	-1,10	2,79E-01	8,49	3,29E-02	1	*MRPL9*	mitochondrial ribosomal protein L9
7934326	1,03	8,68E-01	-1,16	1,18E-02	-1,13	4,27E-02	8,40	1,11E-02	10	*MRPS16*	mitochondrial ribosomal protein S16

8063427	-1,01	9,85E-01	-1,21	5,01E-02	-1,22	4,59E-02	6,30	3,85E-02	20	*MOCS3*	molybdenum cofactor synthesis 3
7904050	1,16	7,52E-02	-1,20	1,18E-02	-1,03	7,88E-01	8,18	8,53E-03	1	*MOV10*	Mov10, Moloney leukemia virus 10, homolog (mouse)
8051066	1,03	9,14E-01	-1,19	1,63E-02	-1,16	4,12E-02	10,16	1,54E-02	2	*MPV17*	MpV17 mitochondrial inner membrane protein
7926565	-1,03	8,80E-01	-1,11	5,38E-02	-1,14	1,61E-02	8,43	2,10E-02	10	*MLLT10*	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 10
8139433	1,20	3,22E-02	-1,20	1,71E-02	1,00	9,99E-01	9,41	7,84E-03	7	*MYO1G*	myosin IG
7965812	1,29	5,69E-02	-1,18	1,61E-01	1,09	6,08E-01	8,68	3,95E-02	12	*GNPTAB*	N-acetylglucosamine-1-phosphate transferase, alpha and beta subunits
7940824	1,20	4,93E-02	-1,20	2,57E-02	-1,00	9,99E-01	7,38	1,42E-02	11	*NAT11*	N-acetyltransferase 11 (GCN5-related, putative)
8079772	1,06	6,88E-01	-1,16	1,66E-02	-1,10	1,91E-01	8,13	2,60E-02	3	*APEH*	N-acylaminoacyl-peptide hydrolase
8170590	1,08	4,77E-01	-1,15	3,06E-02	-1,06	5,03E-01	7,47	4,96E-02	X	*NSDHL*	NAD(P) dependent steroid dehydrogenase-like
8031097	1,14	1,18E-01	-1,13	6,51E-02	1,01	9,59E-01	8,72	4,37E-02	19	*NDUFA3*	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 3, 9kDa
8079707	1,13	3,66E-02	-1,09	8,36E-02	1,03	7,03E-01	9,06	2,14E-02	3	*NDUFAF3*	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 3
8031387	1,59	9,12E-03	-1,20	3,02E-01	1,32	1,15E-01	7,58	6,61E-03	19	*NCR1*	natural cytotoxicity triggering receptor 1
8179773	1,57	9,49E-04	-1,35	1,30E-02	1,16	3,05E-01	7,80	1,68E-04	6	*NCR3*	natural cytotoxicity triggering receptor 3
8038809	1,46	4,17E-02	-1,38	5,29E-02	1,06	8,52E-01	11,44	2,00E-02	19	*NKG7*	natural killer cell group 7 sequence
7919854	1,04	9,08E-01	1,31	1,47E-02	1,36	3,40E-03	6,95	3,79E-03	1	---	ncrna:misc_RNA chromosome:GRCh37:1:150854927:150855011:-1 gene:ENSG00000212512
7899560	1,03	9,15E-01	1,21	4,16E-02	1,25	1,59E-02	6,12	1,79E-02	1	---	ncrna:misc_RNA chromosome:GRCh37:1:29312222:29312322:1 gene:ENSG00000206704
7914665	-1,20	5,34E-01	1,45	1,57E-02	1,22	2,87E-01	6,25	2,39E-02	1	---	ncrna:misc_RNA chromosome:GRCh37:1:33802167:33802465:-1 gene:ENSG00000222112
7901443	1,01	9,63E-01	1,15	1,26E-02	1,16	5,40E-03	6,56	4,29E-03	1	---	ncrna:misc_RNA chromosome:GRCh37:1:52615776:52616089:1 gene:ENSG00000222221
7901477	-1,02	9,23E-01	1,15	3,84E-02	1,13	9,65E-02	4,56	4,55E-02	1	---	ncrna:misc_RNA chromosome:GRCh37:1:53180071:53180370:1

										gene:ENSG00000223289
7933976	1,06	7,89E-01	1,22	1,30E-02	1,29	8,47E-04	8,20	1,42E-03	10	--- ncrna:misc_RNA chromosome:GRCh37:10:69767477:69767774:-1 gene:ENSG00000223114
7934297	1,01	9,82E-01	1,29	1,24E-02	1,30	6,97E-03	5,30	4,79E-03	10	--- ncrna:misc_RNA chromosome:GRCh37:10:74842252:74842353:-1 gene:ENSG00000201047
7928489	1,23	5,36E-01	1,85	1,18E-03	2,29	3,00E-06	7,56	1,36E-05	10	--- ncrna:misc_RNA chromosome:GRCh37:10:76311150:76311251:1 gene:ENSG00000206756
7947989	1,14	3,79E-01	1,10	3,69E-01	1,25	1,61E-02	7,59	2,96E-02	11	--- ncrna:misc_RNA chromosome:GRCh37:11:47748446:47748544:-1 gene:ENSG00000200090
7965429	1,07	8,87E-01	1,33	6,32E-02	1,43	2,13E-02	4,24	2,68E-02	12	--- ncrna:misc_RNA chromosome:GRCh37:12:92564129:92564229:-1 gene:ENSG00000199895
7970567	1,06	6,10E-01	1,06	2,71E-01	1,12	2,81E-02	3,19	4,96E-02	13	--- ncrna:misc_RNA chromosome:GRCh37:13:23726725:23726825:-1 gene:ENSG00000207157
7971482	-1,10	7,58E-01	1,48	4,01E-03	1,34	2,64E-02	8,44	3,14E-03	13	--- ncrna:misc_RNA chromosome:GRCh37:13:46743594:46743883:-1 gene:ENSG00000222074
7969091	1,35	4,05E-01	1,41	1,24E-01	1,89	2,35E-03	4,92	5,92E-03	13	--- ncrna:misc_RNA chromosome:GRCh37:13:49669527:49669628:1 gene:ENSG00000199788
7969671	1,03	9,05E-01	1,16	5,81E-02	1,19	2,37E-02	6,91	2,76E-02	13	--- ncrna:misc_RNA chromosome:GRCh37:13:96821800:96822099:1 gene:ENSG00000222656
7981872	-1,05	7,76E-01	1,17	2,41E-02	1,11	1,64E-01	6,96	3,53E-02	15	--- ncrna:misc_RNA chromosome:GRCh37:15:23263708:23263986:1 gene:ENSG00000238846
7983677	-1,00	9,96E-01	1,18	1,17E-02	1,17	8,54E-03	5,09	4,85E-03	15	--- ncrna:misc_RNA chromosome:GRCh37:15:50981097:50981382:1 gene:ENSG00000222751
7989249	1,17	4,65E-01	1,21	1,17E-01	1,41	2,94E-03	5,22	7,04E-03	15	--- ncrna:misc_RNA chromosome:GRCh37:15:58996036:58996353:-1 gene:ENSG00000199730
7999382	1,08	5,28E-01	1,15	2,52E-02	1,23	3,51E-04	8,08	9,96E-04	16	--- ncrna:misc_RNA

7994343	1,09	6,68E-01	1,15	1,31E-01	1,25	1,14E-02	3,34	2,19E-02	16	---	chromosome:GRCh37:16:10315632:10315930:-1 gene:ENSG00000222479 ncrna:misc_RNA
8001231	1,12	4,75E-01	1,15	1,27E-01	1,28	3,67E-03	5,20	8,53E-03	16	---	chromosome:GRCh37:16:28194639:28194751:1 gene:ENSG00000200138 ncrna:misc_RNA
8011110	1,10	7,63E-01	1,21	1,23E-01	1,33	1,91E-02	6,90	3,30E-02	17	---	chromosome:GRCh37:16:47346938:47347032:-1 gene:ENSG00000222767 ncrna:misc_RNA
8003771	1,03	8,78E-01	1,18	7,12E-03	1,21	6,46E-04	6,93	7,85E-04	17	---	chromosome:GRCh37:17:1507670:1507966:-1 gene:ENSG00000222655 ncrna:misc_RNA
8017702	1,06	8,58E-01	1,20	1,00E-01	1,27	2,94E-02	4,63	4,09E-02	17	---	chromosome:GRCh37:17:2584242:2584528:1 gene:ENSG00000222785 ncrna:misc_RNA
8022623	-1,00	9,85E-01	1,12	4,69E-02	1,11	6,37E-02	6,67	4,39E-02	18	---	chromosome:GRCh37:17:62867610:62867902:-1 gene:ENSG00000222273 ncrna:misc_RNA
8020086	1,09	7,18E-01	1,34	5,76E-03	1,45	9,20E-05	6,31	1,98E-04	18	---	chromosome:GRCh37:18:23398200:23398496:-1 gene:ENSG00000222577 ncrna:misc_RNA
8026298	-1,09	5,49E-01	1,19	1,57E-02	1,10	2,74E-01	6,04	2,36E-02	19	---	chromosome:GRCh37:18:9250108:9250209:1 gene:ENSG00000207092 ncrna:misc_RNA
8054870	-1,05	9,04E-01	1,34	2,32E-02	1,28	6,54E-02	7,28	2,54E-02	2	---	chromosome:GRCh37:19:14323864:14324141:1 gene:ENSG00000223021 ncrna:misc_RNA
8056100	1,13	7,62E-01	1,50	1,30E-02	1,69	6,46E-04	5,03	1,22E-03	2	---	chromosome:GRCh37:2:121798186:121798286:-1 gene:ENSG00000201584 ncrna:misc_RNA
8040614	1,05	7,52E-01	1,09	1,60E-01	1,15	2,64E-02	5,06	4,39E-02	2	---	chromosome:GRCh37:2:160392755:160392857:-1 gene:ENSG00000207117 ncrna:misc_RNA
8065903	1,16	2,51E-01	1,05	6,52E-01	1,22	3,19E-02	6,08	4,29E-02	20	---	chromosome:GRCh37:2:25280901:25281196:1 gene:ENSG00000223095 ncrna:misc_RNA chromosome:GRCh37:20:33969297:33969610:-1 gene:ENSG00000223240

8069446	1,25	3,88E-02	-1,00	9,90E-01	1,25	2,10E-02	5,85	1,21E-02	21	---	ncrna:misc_RNA chromosome:GRCh37:21:47955709:47956003:1 gene:ENSG00000222201
8074789	1,28	6,29E-02	-1,09	5,15E-01	1,18	2,15E-01	4,82	4,44E-02	22	---	ncrna:misc_RNA chromosome:GRCh37:22:22077172:22077471:-1 gene:ENSG00000222425
8074890	1,07	5,55E-01	1,12	5,36E-02	1,20	1,47E-03	5,32	3,70E-03	22	---	ncrna:misc_RNA chromosome:GRCh37:22:23603974:23604258:-1 gene:ENSG00000222211
8074057	-1,02	9,46E-01	1,24	1,66E-02	1,21	3,13E-02	5,43	1,41E-02	22	---	ncrna:misc_RNA chromosome:GRCh37:22:50809639:50809923:1 gene:ENSG00000222793
8081546	1,04	9,47E-01	1,35	5,75E-02	1,40	3,49E-02	4,06	3,53E-02	3	---	ncrna:misc_RNA chromosome:GRCh37:3:110445868:110445968:1 gene:ENSG00000201426
8082570	1,02	9,50E-01	1,24	2,39E-02	1,27	1,10E-02	4,50	1,01E-02	3	---	ncrna:misc_RNA chromosome:GRCh37:3:129537775:129537876:1 gene:ENSG00000202412
8083445	1,24	3,49E-01	1,25	1,45E-01	1,55	2,12E-03	9,41	5,45E-03	3	---	ncrna:misc_RNA chromosome:GRCh37:3:152167061:152167173:1 gene:ENSG00000201217
8083933	1,36	6,97E-02	1,30	6,63E-02	1,77	3,70E-05	6,87	1,53E-04	3	---	ncrna:misc_RNA chromosome:GRCh37:3:171955116:171955381:1 gene:ENSG00000222342
8092312	1,02	8,91E-01	1,10	6,23E-02	1,12	2,23E-02	2,90	2,74E-02	3	---	ncrna:misc_RNA chromosome:GRCh37:3:180454196:180454491:-1 gene:ENSG00000222360
8092957	1,01	9,80E-01	1,44	1,18E-03	1,45	1,13E-04	6,26	1,10E-04	3	---	ncrna:misc_RNA chromosome:GRCh37:3:195140165:195140275:-1 gene:ENSG00000207368
8078260	1,08	7,76E-01	1,26	3,23E-02	1,37	2,93E-03	6,07	4,91E-03	3	---	ncrna:misc_RNA chromosome:GRCh37:3:23315298:23315401:1 gene:ENSG00000206728
8079149	1,05	9,08E-01	1,27	5,44E-02	1,33	2,31E-02	9,01	2,64E-02	3	---	ncrna:misc_RNA chromosome:GRCh37:3:43356443:43356745:1 gene:ENSG00000222330
8079368	1,49	1,33E-02	-1,13	4,49E-01	1,32	8,11E-02	5,65	8,75E-03	3	---	ncrna:misc_RNA chromosome:GRCh37:3:45784167:45784460:1 gene:ENSG00000223285

8097470	1,02	9,45E-01	1,23	1,16E-02	1,26	3,05E-03	5,82	3,05E-03	4	---	ncrna:misc_RNA chromosome:GRCh37:4:140021531:140021815:1 gene:ENSG00000223000
8102936	1,41	1,92E-01	1,08	7,70E-01	1,52	3,52E-02	4,74	3,95E-02	4	---	ncrna:misc_RNA chromosome:GRCh37:4:141621989:141622096:-1 gene:ENSG00000207155
8097743	1,09	6,02E-01	1,18	5,20E-02	1,29	1,72E-03	5,11	4,16E-03	4	---	ncrna:misc_RNA chromosome:GRCh37:4:148730077:148730358:1 gene:ENSG00000222217
8094717	1,15	3,30E-01	1,20	5,93E-02	1,38	4,30E-04	4,08	1,42E-03	4	---	ncrna:misc_RNA chromosome:GRCh37:4:39762620:39762921:1 gene:ENSG00000223178
8095159	1,10	7,47E-01	1,26	5,02E-02	1,38	4,57E-03	7,41	8,26E-03	4	---	ncrna:misc_RNA chromosome:GRCh37:4:56278803:56278905:1 gene:ENSG00000239040
8101585	-1,06	8,40E-01	1,30	1,35E-02	1,23	5,92E-02	5,50	1,47E-02	4	---	ncrna:misc_RNA chromosome:GRCh37:4:85608890:85609152:-1 gene:ENSG00000222903
8128604	1,16	2,03E-01	1,11	2,66E-01	1,29	2,48E-03	5,39	5,75E-03	6	---	ncrna:misc_RNA chromosome:GRCh37:6:106731290:106731586:-1 gene:ENSG00000238396
8121884	1,40	1,73E-02	1,05	7,58E-01	1,48	1,85E-03	6,88	2,00E-03	6	---	ncrna:misc_RNA chromosome:GRCh37:6:126196314:126196628:1 gene:ENSG00000222445
8119078	1,05	7,15E-01	1,09	1,43E-01	1,15	1,82E-02	4,70	3,26E-02	6	---	ncrna:misc_RNA chromosome:GRCh37:6:36489968:36490275:1 gene:ENSG00000238332
8119856	1,12	2,02E-02	-1,07	1,49E-01	1,05	4,06E-01	2,72	1,52E-02	6	---	ncrna:misc_RNA chromosome:GRCh37:6:43511881:43512007:1 gene:ENSG00000238338
8127660	1,13	2,15E-01	1,08	2,70E-01	1,22	2,90E-03	5,48	6,49E-03	6	---	ncrna:misc_RNA chromosome:GRCh37:6:76364686:76365015:-1 gene:ENSG00000200091
8121085	-1,03	8,63E-01	1,16	2,68E-02	1,12	1,13E-01	4,08	3,53E-02	6	---	ncrna:misc_RNA chromosome:GRCh37:6:89800665:89800959:1 gene:ENSG00000222699
8136889	1,09	5,56E-01	1,10	2,71E-01	1,20	2,10E-02	7,19	3,94E-02	7	---	ncrna:misc_RNA chromosome:GRCh37:7:142987708:142988004:1 gene:ENSG00000222498

8147650	1,30	1,92E-01	1,26	1,21E-01	1,64	5,05E-04	5,74	1,67E-03	8	---	ncrna:misc_RNA chromosome:GRCh37:8:100540054:100540155:1 gene:ENSG00000206699
8148329	-1,07	6,15E-01	1,16	2,19E-02	1,08	2,88E-01	6,94	3,49E-02	8	---	ncrna:misc_RNA chromosome:GRCh37:8:130303229:130303531:1 gene:ENSG00000222755
8145887	-1,09	5,10E-01	1,19	1,61E-02	1,09	3,14E-01	5,44	2,52E-02	8	---	ncrna:misc_RNA chromosome:GRCh37:8:37766252:37766553:1 gene:ENSG00000222502
8146305	1,11	7,51E-01	1,25	1,16E-01	1,39	1,59E-02	6,66	2,73E-02	8	---	ncrna:misc_RNA chromosome:GRCh37:8:43008119:43008197:1 gene:ENSG00000238589
8151411	1,02	9,51E-01	1,31	1,74E-03	1,33	2,35E-04	7,65	1,84E-04	8	---	ncrna:misc_RNA chromosome:GRCh37:8:74746010:74746277:-1 gene:ENSG00000222948
8146955	1,04	9,08E-01	1,26	5,06E-02	1,31	2,04E-02	8,88	2,35E-02	8	---	ncrna:misc_RNA chromosome:GRCh37:8:75288922:75289028:1 gene:ENSG00000207417
8151869	1,04	8,16E-01	1,16	3,50E-02	1,21	4,63E-03	5,55	7,06E-03	8	---	ncrna:misc_RNA chromosome:GRCh37:8:95725943:95726040:-1 gene:ENSG00000199701
8163015	1,05	6,84E-01	1,08	1,60E-01	1,14	1,65E-02	5,67	3,09E-02	9	---	ncrna:misc_RNA chromosome:GRCh37:9:110573898:110574195:-1 gene:ENSG00000223122
8163105	1,11	3,13E-01	1,11	1,15E-01	1,24	1,19E-03	4,27	3,28E-03	9	---	ncrna:misc_RNA chromosome:GRCh37:9:111804666:111804767:-1 gene:ENSG00000199331
8163426	-1,05	7,85E-01	1,19	2,02E-02	1,13	1,34E-01	6,84	2,82E-02	9	---	ncrna:misc_RNA chromosome:GRCh37:9:115034868:115035111:-1 gene:ENSG00000222882
8155246	1,20	4,26E-01	1,26	1,03E-01	1,51	1,83E-03	6,56	4,84E-03	9	---	ncrna:misc_RNA chromosome:GRCh37:9:37160134:37160234:1 gene:ENSG00000200502
8161737	1,30	2,85E-01	1,11	5,88E-01	1,44	2,89E-02	5,87	4,13E-02	9	---	ncrna:misc_RNA chromosome:GRCh37:9:74517371:74517466:-1 gene:ENSG00000200922
8171193	1,27	1,33E-01	1,05	7,31E-01	1,34	1,88E-02	5,67	2,18E-02	X	---	ncrna:misc_RNA chromosome:GRCh37:X:3559484:3559596:-1 gene:ENSG00000207320

8166948	-1,05	9,36E-01	1,49	3,61E-02	1,41	8,23E-02	9,02	3,98E-02	X	---	ncrna:misc_RNA chromosome:GRCh37:X:44260849:44260950:1 gene:ENSG00000200702
8173607	1,51	8,77E-03	1,26	1,18E-01	1,90	5,00E-06	9,43	2,08E-05	X	---	ncrna:misc_RNA chromosome:GRCh37:X:73462445:73462741:-1 gene:ENSG00000222195
7922456	1,01	9,73E-01	1,29	2,68E-02	1,31	1,82E-02	6,20	1,50E-02	1	---	ncrna:rRNA chromosome:GRCh37:1:173938456:173938574:-1 gene:ENSG00000200755
7915202	-1,01	9,67E-01	1,19	8,19E-03	1,18	8,04E-03	5,20	3,70E-03	1	---	ncrna:rRNA chromosome:GRCh37:1:39619863:39619968:-1 gene:ENSG00000222378
7932017	1,01	9,75E-01	1,13	4,79E-02	1,14	3,90E-02	2,88	3,37E-02	10	---	ncrna:rRNA chromosome:GRCh37:10:8698679:8698794:-1 gene:ENSG00000212505
7942645	1,11	7,88E-01	1,25	1,46E-01	1,39	3,02E-02	6,34	4,84E-02	11	---	ncrna:rRNA chromosome:GRCh37:11:75645975:75646083:1 gene:ENSG00000223013
8112070	1,17	6,52E-01	1,25	1,74E-01	1,47	1,61E-02	6,36	3,06E-02	5	---	ncrna:rRNA chromosome:GRCh37:11:97528464:97528582:1 gene:ENSG00000199315 /// ncrna:rRNA chromosome:GRCh37:5:54480742:54480855:-1 gene:ENSG00000201369
7961960	1,16	5,86E-01	1,30	5,00E-02	1,51	1,50E-03	5,78	3,76E-03	12	---	ncrna:rRNA chromosome:GRCh37:12:26526557:26526666:-1 gene:ENSG00000212549
7965150	1,42	1,77E-01	1,36	1,18E-01	1,93	3,91E-04	4,57	1,33E-03	12	---	ncrna:rRNA chromosome:GRCh37:12:80272085:80272199:-1 gene:ENSG00000201942
7971013	1,07	8,02E-01	1,22	5,64E-02	1,30	8,71E-03	5,72	1,39E-02	13	---	ncrna:rRNA chromosome:GRCh37:13:37372412:37372515:-1 gene:ENSG00000199873
7969370	-1,04	8,03E-01	1,18	9,29E-03	1,13	4,93E-02	5,92	8,54E-03	13	---	ncrna:rRNA chromosome:GRCh37:13:72552226:72552344:1 gene:ENSG00000200037
8003087	1,08	8,24E-01	1,28	4,78E-02	1,38	8,13E-03	6,54	1,21E-02	16	---	ncrna:rRNA chromosome:GRCh37:16:84073523:84073638:-1 gene:ENSG00000199350
8004219	-1,03	8,80E-01	1,16	3,17E-02	1,12	1,15E-01	4,29	4,10E-02	17	---	ncrna:rRNA chromosome:GRCh37:17:6890784:6890903:1 gene:ENSG00000222165
8045347	1,43	7,13E-02	-1,01	9,59E-01	1,41	4,39E-02	4,70	2,56E-02	2	---	ncrna:rRNA chromosome:GRCh37:2:134988766:134988883:1 gene:ENSG00000222921
8041223	-1,09	4,56E-01	1,19	1,18E-02	1,09	2,81E-01	5,99	1,65E-02	2	---	ncrna:rRNA chromosome:GRCh37:2:31451178:31451287:1 gene:ENSG00000201671
8078603	1,25	1,35E-01	1,08	5,93E-01	1,35	1,02E-02	6,00	1,46E-02	3	---	ncrna:rRNA chromosome:GRCh37:3:37383140:37383257:1 gene:ENSG00000222208
8095214	1,16	2,91E-01	1,09	3,80E-01	1,27	1,07E-02	7,27	1,98E-02	4	---	ncrna:rRNA chromosome:GRCh37:4:56963556:56963670:1 gene:ENSG00000200741

8113035	1,02	9,53E-01	1,21	4,76E-02	1,23	2,90E-02	5,81	2,76E-02	5	---	ncrna:rRNA chromosome:GRCh37:5:87570075:87570193:-1 gene:ENSG00000207129
8143385	-1,07	7,04E-01	1,24	5,76E-03	1,16	5,24E-02	7,19	5,13E-03	7	---	ncrna:rRNA chromosome:GRCh37:7:140086581:140086707:-1 gene:ENSG00000202472
8139055	1,08	8,04E-01	1,23	8,71E-02	1,33	1,53E-02	6,96	2,44E-02	7	---	ncrna:rRNA chromosome:GRCh37:7:36633278:36633375:-1 gene:ENSG00000222789
8163326	1,14	3,22E-01	1,15	1,28E-01	1,31	1,50E-03	6,37	4,16E-03	9	---	ncrna:rRNA chromosome:GRCh37:9:114173914:114174022:-1 gene:ENSG00000223238
8156599	1,06	8,31E-01	1,21	5,50E-02	1,29	1,11E-02	7,05	1,65E-02	9	---	ncrna:rRNA chromosome:GRCh37:9:98667287:98667402:1 gene:ENSG00000199202
7904048	-1,04	9,28E-01	1,43	9,29E-03	1,37	1,47E-02	7,57	5,09E-03	1	---	ncrna:snoRNA chromosome:GRCh37:1:113195210:113195310:1 gene:ENSG00000238975
7898294	1,02	9,15E-01	1,16	2,21E-02	1,19	6,97E-03	2,82	7,06E-03	1	---	ncrna:snoRNA chromosome:GRCh37:1:16237392:16237492:1 gene:ENSG00000238818
7913185	1,01	9,58E-01	1,17	1,17E-02	1,19	4,15E-03	5,32	3,58E-03	1	---	ncrna:snoRNA chromosome:GRCh37:1:19858664:19858768:-1 gene:ENSG00000239027
7909839	1,10	5,55E-01	1,18	4,16E-02	1,30	9,61E-04	3,89	2,50E-03	1	---	ncrna:snoRNA chromosome:GRCh37:1:220310506:220310608:1 gene:ENSG00000238576
7933731	-1,01	9,85E-01	1,45	1,27E-02	1,44	1,26E-02	4,16	6,67E-03	10	---	ncrna:snoRNA chromosome:GRCh37:10:59998418:59998521:-1 gene:ENSG00000238970
7928216	1,11	2,88E-01	1,10	1,54E-01	1,22	1,62E-03	5,87	4,44E-03	10	---	ncrna:snoRNA chromosome:GRCh37:10:73085085:73085188:1 gene:ENSG00000238918
7937913	1,11	3,25E-01	1,15	4,53E-02	1,27	2,33E-04	6,36	8,04E-04	11	---	ncrna:snoRNA chromosome:GRCh37:11:3943797:3943933:1 gene:ENSG00000206976
7941563	1,18	5,21E-01	1,44	9,29E-03	1,69	5,50E-05	6,23	1,64E-04	11	---	ncrna:snoRNA chromosome:GRCh37:11:65920092:65920196:1 gene:ENSG00000238763
7958015	1,16	1,82E-01	1,08	3,93E-01	1,26	5,03E-03	5,50	9,51E-03	12	---	ncrna:snoRNA chromosome:GRCh37:12:102183593:102183693:1 gene:ENSG00000238940
7957159	-1,04	8,25E-01	1,18	1,41E-02	1,13	6,92E-02	5,00	1,64E-02	12	---	ncrna:snoRNA chromosome:GRCh37:12:72033135:72033263:1 gene:ENSG00000212461

7969675	1,05	8,05E-01	1,11	1,41E-01	1,16	3,19E-02	3,60	4,96E-02	13	---	ncrna:snoRNA chromosome:GRCh37:13:97709633:97709734:1 gene:ENSG00000238522
7999884	1,25	1,31E-01	1,25	5,36E-02	1,55	6,40E-05	5,66	2,44E-04	16	---	ncrna:snoRNA chromosome:GRCh37:16:18881488:18881591:-1 gene:ENSG00000238329
8000690	1,49	3,22E-03	1,09	5,71E-01	1,62	6,80E-05	9,37	1,22E-04	16	---	ncrna:snoRNA chromosome:GRCh37:16:18881488:18881591:-1 gene:ENSG00000238329 /// ncrna:snoRNA chromosome:GRCh37:16:21468647:21468750:-1 gene:ENSG00000238954 /// ncrna:snoRNA chromosome:GRCh37:16:21900888:21900991:-1 gene:ENSG00000238712 /// ncrna:snoRNA chromosome:GRCh37:16:22492795:22492898:1 gene:ENSG00000239172 /// ncrna:snoRNA chromosome:GRCh37:16:29448818:29448921:-1 gene:ENSG00000238639 /// ncrna:snoRNA chromosome:GRCh37:16:29550583:29550686:-1 gene:ENSG00000239193 /// ncrna:snoRNA chromosome:GRCh37:16:30290569:30290672:-1 gene:ENSG00000239114 /// ncrna:snoRNA chromosome:GRCh37:16:70266882:70266985:-1 gene:ENSG00000238734
8002342	1,40	3,88E-02	1,07	7,20E-01	1,49	4,49E-03	6,44	4,84E-03	16	---	ncrna:snoRNA chromosome:GRCh37:16:18881488:18881591:-1 gene:ENSG00000238329 /// ncrna:snoRNA chromosome:GRCh37:16:21468647:21468750:-1 gene:ENSG00000238954 /// ncrna:snoRNA chromosome:GRCh37:16:21900888:21900991:-1 gene:ENSG00000238712 /// ncrna:snoRNA chromosome:GRCh37:16:22492795:22492898:1 gene:ENSG00000239172 /// ncrna:snoRNA chromosome:GRCh37:16:29448818:29448921:-1 gene:ENSG00000238639 /// ncrna:snoRNA chromosome:GRCh37:16:29550583:29550686:-1 gene:ENSG00000239193 /// ncrna:snoRNA chromosome:GRCh37:16:30290569:30290672:-1 gene:ENSG00000239114 /// ncrna:snoRNA chromosome:GRCh37:16:70266882:70266985:-1

											gene:ENSG00000238734
8001371	1,10	6,87E-01	1,15	2,14E-01	1,26	2,69E-02	5,60	4,74E-02	16	---	ncrna:snoRNA chromosome:GRCh37:16:50386100:50386203:-1 gene:ENSG00000238544
7996759	1,10	4,96E-01	1,09	3,23E-01	1,20	2,15E-02	6,05	3,95E-02	16	---	ncrna:snoRNA chromosome:GRCh37:16:68223190:68223324:1 gene:ENSG00000212445
8003769	-1,00	9,95E-01	1,28	1,18E-02	1,28	9,28E-03	6,96	5,27E-03	17	---	ncrna:snoRNA chromosome:GRCh37:17:2558973:2559076:1 gene:ENSG00000239024
8016431	1,16	5,21E-01	1,15	3,12E-01	1,33	2,30E-02	3,95	4,17E-02	17	---	ncrna:snoRNA chromosome:GRCh37:17:46459734:46459948:-1 gene:ENSG00000200538
8016787	1,00	9,93E-01	1,33	3,03E-03	1,34	1,05E-03	7,32	5,69E-04	17	---	ncrna:snoRNA chromosome:GRCh37:17:49175535:49175639:-1 gene:ENSG00000238815
8010285	-1,02	8,90E-01	1,15	1,65E-02	1,12	5,24E-02	6,65	1,73E-02	17	---	ncrna:snoRNA chromosome:GRCh37:17:76396016:76396144:1 gene:ENSG00000200063
8057439	-1,01	9,73E-01	1,24	4,41E-02	1,22	6,85E-02	5,20	4,35E-02	2	---	ncrna:snoRNA chromosome:GRCh37:2:180799128:180799265:-1 gene:ENSG00000202216
8050472	1,07	2,52E-01	-1,09	3,61E-02	-1,02	7,79E-01	2,51	4,41E-02	2	---	ncrna:snoRNA chromosome:GRCh37:2:18221872:18221999:-1 gene:ENSG00000212455
8058518	1,02	9,57E-01	1,22	5,09E-02	1,24	3,46E-02	4,45	3,32E-02	2	---	ncrna:snoRNA chromosome:GRCh37:2:208938785:208938886:-1 gene:ENSG00000238582
8041170	1,11	7,53E-01	1,26	9,93E-02	1,40	1,28E-02	7,57	2,24E-02	2	---	ncrna:snoRNA chromosome:GRCh37:2:29150849:29150926:1 gene:ENSG00000212326
8050213	-1,01	9,79E-01	1,34	2,29E-02	1,32	2,97E-02	7,50	1,75E-02	2	---	ncrna:snoRNA chromosome:GRCh37:2:9672371:9672474:-1 gene:ENSG00000238462
8070081	-1,01	9,80E-01	1,12	4,74E-02	1,11	6,95E-02	6,32	4,59E-02	21	---	ncrna:snoRNA chromosome:GRCh37:21:34214171:34214305:-1 gene:ENSG00000207098
8084124	1,02	8,60E-01	-1,10	2,78E-02	-1,07	1,18E-01	2,52	3,67E-02	3	---	ncrna:snoRNA chromosome:GRCh37:3:180260489:180260624:1 gene:ENSG00000201810
8116577	1,03	8,50E-01	1,12	6,30E-02	1,15	1,49E-02	3,35	2,14E-02	6	---	ncrna:snoRNA chromosome:GRCh37:6:1186753:1186855:1

											gene:ENSG00000238438
8117286	1,03	8,98E-01	1,18	1,65E-02	1,21	3,67E-03	5,73	4,29E-03	6	---	ncrna:snoRNA chromosome:GRCh37:6:25435508:25435611:1 gene:ENSG00000238322
8121062	1,09	4,53E-01	1,10	1,81E-01	1,21	6,11E-03	3,25	1,33E-02	6	---	ncrna:snoRNA chromosome:GRCh37:6:88430633:88430736:1 gene:ENSG00000238628
8128075	1,16	3,81E-01	1,15	2,18E-01	1,33	5,63E-03	5,40	1,24E-02	6	---	ncrna:snoRNA chromosome:GRCh37:6:89423961:89424149:-1 gene:ENSG00000222145
8139083	1,16	2,88E-01	1,18	9,02E-02	1,36	6,46E-04	6,44	2,00E-03	7	---	ncrna:snoRNA chromosome:GRCh37:7:37209283:37209384:-1 gene:ENSG00000238772
8131335	1,11	3,21E-01	1,07	3,92E-01	1,19	1,32E-02	3,10	2,43E-02	7	---	ncrna:snoRNA chromosome:GRCh37:7:5525026:5525132:1 gene:ENSG00000238394
8152863	1,25	4,67E-01	1,44	3,96E-02	1,80	5,05E-04	7,52	1,54E-03	8	---	ncrna:snoRNA chromosome:GRCh37:8:130880836:130880962:-1 gene:ENSG00000200075
8150862	1,04	9,49E-01	1,66	2,85E-03	1,72	3,91E-04	5,75	2,88E-04	8	---	ncrna:snoRNA chromosome:GRCh37:8:56815282:56815414:-1 gene:ENSG00000199405
8158684	-1,04	8,78E-01	1,20	3,35E-02	1,15	1,23E-01	4,35	4,41E-02	9	---	ncrna:snoRNA chromosome:GRCh37:9:133325241:133325342:1 gene:ENSG00000238298
8174592	1,04	7,34E-01	1,10	7,58E-02	1,14	7,97E-03	2,78	1,42E-02	X	---	ncrna:snoRNA chromosome:GRCh37:X:112244247:112244356:-1 gene:ENSG00000238811
7925607	1,17	1,86E-01	1,06	5,55E-01	1,24	1,27E-02	3,93	1,92E-02	1	---	ncrna:snRNA chromosome:GRCh37:1:246352316:246352420:-1 gene:ENSG00000202184
7901383	-1,03	8,12E-01	1,15	9,29E-03	1,11	4,46E-02	2,71	8,26E-03	1	---	ncrna:snRNA chromosome:GRCh37:1:51847980:51848086:1 gene:ENSG00000206595
7916743	1,03	8,25E-01	1,13	1,70E-02	1,17	1,77E-03	5,02	3,01E-03	1	---	ncrna:snRNA chromosome:GRCh37:1:64494566:64494668:-1 gene:ENSG00000207190
7932635	1,44	3,78E-02	1,30	9,61E-02	1,87	2,90E-05	5,90	1,35E-04	10	---	ncrna:snRNA chromosome:GRCh37:10:27079469:27079575:-1 gene:ENSG00000206605
7944525	1,17	3,48E-01	1,27	2,22E-02	1,49	7,50E-05	6,88	2,88E-04	11	---	ncrna:snRNA chromosome:GRCh37:11:119527021:119527126:1 gene:ENSG00000199217
7940580	1,09	5,69E-01	1,18	3,39E-02	1,28	7,25E-04	6,12	1,88E-03	11	---	ncrna:snRNA chromosome:GRCh37:11:61705366:61705472:1

										gene:ENSG00000200898
7965838	1,20	3,40E-01	1,15	2,67E-01	1,38	6,97E-03	5,04	1,43E-02	12	--- ncrna:snRNA chromosome:GRCh37:12:102190188:102190296:-1 gene:ENSG00000222932
7966223	1,12	4,78E-01	1,09	3,65E-01	1,23	2,62E-02	6,01	4,55E-02	12	--- ncrna:snRNA chromosome:GRCh37:12:110005780:110005920:-1 gene:ENSG00000200274
7959014	1,15	3,75E-01	1,18	9,85E-02	1,37	1,30E-03	3,62	3,70E-03	12	--- ncrna:snRNA chromosome:GRCh37:12:116520375:116520481:1 gene:ENSG00000200665
7961420	1,06	8,59E-01	1,21	6,94E-02	1,28	1,83E-02	3,06	2,54E-02	12	--- ncrna:snRNA chromosome:GRCh37:12:13612604:13612710:-1 gene:ENSG00000201909
7955248	1,05	6,55E-01	1,07	2,03E-01	1,12	2,10E-02	3,27	3,84E-02	12	--- ncrna:snRNA chromosome:GRCh37:12:49986887:49986996:1 gene:ENSG00000199237
7955419	1,14	6,90E-01	1,29	6,72E-02	1,46	4,57E-03	6,62	8,83E-03	12	--- ncrna:snRNA chromosome:GRCh37:12:51050756:51050861:1 gene:ENSG00000200183
8132830	1,13	6,94E-01	1,29	6,28E-02	1,46	4,15E-03	6,01	8,29E-03	7	--- ncrna:snRNA chromosome:GRCh37:12:51556684:51556790:1 gene:ENSG00000199824 /// ncrna:snRNA chromosome:GRCh37:7:50503078:50503184:1 gene:ENSG00000200815
7964640	1,41	4,05E-01	1,23	4,60E-01	1,74	2,96E-02	5,24	4,93E-02	12	--- ncrna:snRNA chromosome:GRCh37:12:62727872:62727978:-1 gene:ENSG00000200814
7952984	1,12	8,16E-01	1,45	3,45E-02	1,61	4,50E-03	6,01	6,87E-03	12	--- ncrna:snRNA chromosome:GRCh37:12:890297:890365:1 gene:ENSG00000221439
7967872	-1,01	9,61E-01	1,16	1,88E-02	1,15	2,94E-02	4,55	1,50E-02	13	--- ncrna:snRNA chromosome:GRCh37:13:19454194:19454297:1 gene:ENSG00000206787
7968295	1,39	1,75E-01	1,66	7,12E-03	2,31	3,00E-06	4,27	1,37E-05	13	--- ncrna:snRNA chromosome:GRCh37:13:28806638:28806744:1 gene:ENSG00000200840
7971996	1,12	5,21E-01	1,20	5,36E-02	1,34	1,23E-03	4,64	3,12E-03	13	--- ncrna:snRNA chromosome:GRCh37:13:73455246:73455352:-1 gene:ENSG00000199381
7976874	1,14	5,60E-01	1,23	7,00E-02	1,39	2,13E-03	4,24	5,13E-03	14	--- ncrna:snRNA chromosome:GRCh37:14:102269564:102269668:1 gene:ENSG00000207208

7975770	1,11	5,33E-02	-1,00	9,91E-01	1,11	2,94E-02	2,62	1,79E-02	14	---	ncrna:snRNA chromosome:GRCh37:14:75487464:75487570:1 gene:ENSG00000206924
7987066	1,11	8,81E-01	1,61	3,71E-02	1,79	9,31E-03	7,08	1,19E-02	15	---	ncrna:snRNA chromosome:GRCh37:15:31248451:31248553:-1 gene:ENSG00000212526
7983761	1,20	3,35E-01	1,29	4,49E-02	1,55	2,38E-04	6,20	8,32E-04	15	---	ncrna:snRNA chromosome:GRCh37:15:52199397:52199502:1 gene:ENSG00000202323
7989144	1,17	5,96E-01	1,24	1,54E-01	1,45	9,77E-03	4,08	1,97E-02	15	---	ncrna:snRNA chromosome:GRCh37:15:56566728:56566834:-1 gene:ENSG00000199784
7990564	1,16	5,87E-01	1,18	2,37E-01	1,37	1,88E-02	5,76	3,54E-02	15	---	ncrna:snRNA chromosome:GRCh37:15:76271133:76271280:-1 gene:ENSG00000201630
7991171	1,06	8,40E-01	1,23	3,84E-02	1,30	6,97E-03	3,90	9,60E-03	15	---	ncrna:snRNA chromosome:GRCh37:15:86194753:86194859:-1 gene:ENSG00000202081
7996258	1,08	4,16E-01	1,08	2,02E-01	1,18	6,14E-03	4,95	1,34E-02	16	---	ncrna:snRNA chromosome:GRCh37:16:59574030:59574170:1 gene:ENSG00000200062
7993112	1,04	7,69E-01	1,09	1,35E-01	1,13	2,34E-02	3,20	3,83E-02	16	---	ncrna:snRNA chromosome:GRCh37:16:6923900:6924006:1 gene:ENSG00000200869
7997164	-1,02	9,54E-01	1,26	6,22E-03	1,24	7,04E-03	4,79	2,94E-03	16	---	ncrna:snRNA chromosome:GRCh37:16:71699994:71700100:1 gene:ENSG00000199301
8013013	1,09	7,26E-01	1,26	3,20E-02	1,38	1,83E-03	4,50	3,82E-03	17	---	ncrna:snRNA chromosome:GRCh37:17:16041082:16041186:-1 gene:ENSG00000199674
8174195	1,20	2,65E-01	1,14	2,61E-01	1,37	4,00E-03	6,81	8,75E-03	X	---	ncrna:snRNA chromosome:GRCh37:17:46274042:46274148:-1 gene:ENSG00000207306
8112894	1,33	2,70E-01	1,22	2,96E-01	1,62	5,37E-03	5,20	1,13E-02	5	---	ncrna:snRNA chromosome:GRCh37:17:46274042:46274148:-1 gene:ENSG00000207306 /// ncrna:snRNA chromosome:GRCh37:5:79661545:79661651:-1 gene:ENSG00000206774 /// ncrna:snRNA chromosome:GRCh37:4:54131628:54131734:-1 gene:ENSG00000207385
8128886	1,24	5,49E-01	1,36	1,04E-01	1,67	3,85E-03	5,46	8,54E-03	6	---	ncrna:snRNA chromosome:GRCh37:17:46274042:46274148:-1 gene:ENSG00000207306 /// ncrna:snRNA chromosome:GRCh37:6:111043453:111043551:-1 gene:ENSG00000200522 /// ncrna:snRNA chromosome:GRCh37:2:39111701:39111807:-1 gene:ENSG00000207295

8008596	1,09	5,69E-01	1,12	1,46E-01	1,22	7,84E-03	3,85	1,64E-02	17	---	ncrna:snRNA chromosome:GRCh37:17:53629171:53629281:1 gene:ENSG00000200107
8017251	1,02	9,59E-01	1,25	2,17E-02	1,27	1,13E-02	4,11	9,51E-03	17	---	ncrna:snRNA chromosome:GRCh37:17:58739694:58739798:-1 gene:ENSG00000200013
8018814	1,03	9,48E-01	1,35	3,63E-02	1,40	1,88E-02	6,79	1,86E-02	17	---	ncrna:snRNA chromosome:GRCh37:17:75148643:75148756:-1 gene:ENSG00000222808
8021372	1,03	9,56E-01	1,32	5,00E-02	1,36	3,24E-02	4,49	3,15E-02	18	---	ncrna:snRNA chromosome:GRCh37:18:55422626:55422732:1 gene:ENSG00000202159
8046626	-1,01	9,68E-01	1,12	3,94E-02	1,11	6,31E-02	2,76	3,85E-02	2	---	ncrna:snRNA chromosome:GRCh37:2:178903629:178903731:1 gene:ENSG00000206788
8048993	1,14	3,58E-01	1,13	2,28E-01	1,29	5,46E-03	2,85	1,21E-02	2	---	ncrna:snRNA chromosome:GRCh37:2:231616856:231616962:1 gene:ENSG00000201044
8049042	1,05	8,66E-01	1,17	9,95E-02	1,22	3,08E-02	3,76	4,24E-02	2	---	ncrna:snRNA chromosome:GRCh37:2:231998176:231998344:1 gene:ENSG00000201574
8040576	1,28	1,26E-01	1,22	1,22E-01	1,57	2,33E-04	5,79	8,04E-04	2	---	ncrna:snRNA chromosome:GRCh37:2:24899178:24899284:1 gene:ENSG00000206732
8040630	1,01	9,90E-01	1,37	4,74E-02	1,38	4,48E-02	3,93	3,59E-02	2	---	ncrna:snRNA chromosome:GRCh37:2:26265544:26265650:1 gene:ENSG00000199872
8051394	1,11	6,18E-01	1,24	3,84E-02	1,38	1,24E-03	4,82	3,01E-03	2	---	ncrna:snRNA chromosome:GRCh37:2:32439525:32439631:-1 gene:ENSG00000201113
8041568	1,06	5,49E-01	1,06	3,09E-01	1,12	2,62E-02	2,64	4,65E-02	2	---	ncrna:snRNA chromosome:GRCh37:2:39309730:39309833:1 gene:ENSG00000206985
8052231	1,30	4,33E-01	1,43	7,75E-02	1,86	1,30E-03	5,10	3,56E-03	2	---	ncrna:snRNA chromosome:GRCh37:2:55241554:55241656:-1 gene:ENSG00000200086
8065853	1,17	3,24E-01	1,11	3,73E-01	1,30	1,26E-02	3,34	2,31E-02	20	---	ncrna:snRNA chromosome:GRCh37:20:33618120:33618219:-1 gene:ENSG00000202150
8069517	1,01	9,69E-01	1,20	4,69E-02	1,21	3,49E-02	5,28	3,12E-02	21	---	ncrna:snRNA chromosome:GRCh37:21:15340810:15340916:-1 gene:ENSG00000223287 /// ncrna:snRNA chromosome:GRCh37:13:19443325:19443431:-1 gene:ENSG00000223024
8069444	1,36	3,32E-02	-1,08	6,18E-01	1,26	8,94E-02	4,00	1,99E-02	21	---	ncrna:snRNA chromosome:GRCh37:21:47945531:47945635:1 gene:ENSG00000202239

8075306	-1,00	9,94E-01	1,15	5,11E-02	1,15	6,47E-02	5,66	4,77E-02	22	---	ncrna:snRNA chromosome:GRCh37:22:30295576:30295682:-1 gene:ENSG00000207455
8075479	-1,01	9,85E-01	1,39	5,00E-02	1,37	7,22E-02	4,20	4,93E-02	22	---	ncrna:snRNA chromosome:GRCh37:22:31618731:31618839:-1 gene:ENSG00000199695
8089928	1,12	5,49E-01	1,31	9,29E-03	1,47	6,40E-05	10,07	1,78E-04	3	---	ncrna:snRNA chromosome:GRCh37:3:121374316:121374451:-1 gene:ENSG00000222057
8090934	1,04	9,08E-01	1,30	1,71E-02	1,35	4,63E-03	5,33	4,91E-03	3	---	ncrna:snRNA chromosome:GRCh37:3:136148919:136149025:-1 gene:ENSG00000200571
8083144	1,15	2,23E-02	-1,03	6,64E-01	1,12	5,33E-02	2,75	1,21E-02	3	---	ncrna:snRNA chromosome:GRCh37:3:141864296:141864397:1 gene:ENSG00000206604
8093126	-1,01	9,84E-01	1,48	4,22E-03	1,46	2,75E-03	5,96	1,36E-03	3	---	ncrna:snRNA chromosome:GRCh37:3:196120579:196120683:-1 gene:ENSG00000206644
8097116	1,15	7,34E-01	1,37	6,67E-02	1,57	6,82E-03	5,30	1,19E-02	4	---	ncrna:snRNA chromosome:GRCh37:4:120288717:120288874:1 gene:ENSG00000201186 /// ncrna:snRNA chromosome:GRCh37:4:166173732:166173889:1 gene:ENSG00000200974
8098193	1,02	9,73E-01	1,42	5,86E-02	1,46	5,02E-02	5,61	4,48E-02	4	---	ncrna:snRNA chromosome:GRCh37:4:166173732:166173889:1 gene:ENSG00000200974
8093683	1,10	4,75E-01	1,13	1,14E-01	1,24	2,94E-03	4,93	7,02E-03	4	---	ncrna:snRNA chromosome:GRCh37:4:3045828:3045934:1 gene:ENSG00000199335
8094739	1,10	6,06E-01	1,15	1,37E-01	1,27	8,57E-03	4,29	1,74E-02	4	---	ncrna:snRNA chromosome:GRCh37:4:40079494:40079602:1 gene:ENSG00000200455
8100227	1,26	4,78E-01	1,20	3,57E-01	1,50	2,49E-02	5,78	4,41E-02	4	---	ncrna:snRNA chromosome:GRCh37:4:48108098:48108205:-1 gene:ENSG00000200269
8107348	1,07	7,53E-01	1,15	1,15E-01	1,23	1,59E-02	5,16	2,71E-02	5	---	ncrna:snRNA chromosome:GRCh37:5:112114060:112114166:1 gene:ENSG00000212370
8111358	1,17	8,52E-02	-1,00	9,83E-01	1,17	4,70E-02	3,49	3,00E-02	5	---	ncrna:snRNA chromosome:GRCh37:5:32234872:32234981:-1 gene:ENSG00000199731
8112041	1,00	9,95E-01	1,17	1,27E-02	1,18	8,96E-03	5,98	5,45E-03	5	---	ncrna:snRNA chromosome:GRCh37:5:53207850:53207953:-1 gene:ENSG00000222960
8105577	1,08	6,16E-01	1,11	1,73E-01	1,21	1,30E-02	3,69	2,56E-02	5	---	ncrna:snRNA chromosome:GRCh37:5:61739003:61739109:1 gene:ENSG00000199279

8129899	1,07	7,76E-01	1,21	4,47E-02	1,30	4,78E-03	3,04	8,26E-03	6	---	ncrna:snRNA chromosome:GRCh37:6:139180164:139180270:-1 gene:ENSG00000206856
8130011	1,04	7,71E-01	1,08	1,54E-01	1,12	2,89E-02	3,44	4,66E-02	6	---	ncrna:snRNA chromosome:GRCh37:6:145784374:145784535:-1 gene:ENSG00000201119
8130181	1,12	6,37E-01	1,16	1,96E-01	1,31	1,78E-02	4,35	3,35E-02	6	---	ncrna:snRNA chromosome:GRCh37:6:150647759:150647899:-1 gene:ENSG00000201628
8117018	1,72	6,41E-02	1,90	1,18E-02	3,27	3,00E-06	5,48	1,36E-05	6	---	ncrna:snRNA chromosome:GRCh37:6:15315151:15315257:1 gene:ENSG00000201367
8119235	1,10	6,40E-01	1,26	2,18E-02	1,39	5,32E-04	5,76	1,33E-03	6	---	ncrna:snRNA chromosome:GRCh37:6:37883372:37883518:1 gene:ENSG00000200597
8120600	1,03	8,54E-01	1,12	6,67E-02	1,15	1,66E-02	4,69	2,35E-02	6	---	ncrna:snRNA chromosome:GRCh37:6:71892315:71892421:1 gene:ENSG00000207180
8127658	1,00	9,94E-01	1,12	3,09E-02	1,12	2,89E-02	7,02	2,12E-02	6	---	ncrna:snRNA chromosome:GRCh37:6:76183454:76183610:-1 gene:ENSG00000201291
8127822	1,22	3,78E-02	-1,00	9,99E-01	1,22	1,88E-02	4,77	1,11E-02	6	---	ncrna:snRNA chromosome:GRCh37:6:82920055:82920153:-1 gene:ENSG00000223044
8142979	-1,03	9,08E-01	1,17	2,82E-02	1,14	7,84E-02	7,49	3,27E-02	7	---	ncrna:snRNA chromosome:GRCh37:7:130739645:130739751:-1 gene:ENSG00000199627
8143365	1,16	3,58E-01	1,16	1,63E-01	1,34	2,94E-03	3,60	7,06E-03	7	---	ncrna:snRNA chromosome:GRCh37:7:139909363:139909471:-1 gene:ENSG00000199971
8138795	1,05	6,62E-01	1,09	1,17E-01	1,15	9,09E-03	2,60	1,79E-02	7	---	ncrna:snRNA chromosome:GRCh37:7:28157732:28157838:-1 gene:ENSG00000206623
8148309	1,18	3,02E-01	1,12	3,46E-01	1,32	9,28E-03	4,55	1,79E-02	8	---	ncrna:snRNA chromosome:GRCh37:8:126913195:126913298:1 gene:ENSG00000206695
8144512	1,10	5,69E-02	1,07	1,38E-01	1,18	9,20E-05	2,81	3,44E-04	8	---	ncrna:snRNA chromosome:GRCh37:8:8753323:8753428:1 gene:ENSG00000200713
8163147	-1,03	8,92E-01	1,15	3,45E-02	1,12	1,12E-01	5,41	4,40E-02	9	---	ncrna:snRNA chromosome:GRCh37:9:111958481:111958589:-1 gene:ENSG00000200106
8154572	1,02	9,20E-01	1,12	5,95E-02	1,14	2,88E-02	3,11	3,21E-02	9	---	ncrna:snRNA chromosome:GRCh37:9:20418319:20418434:1 gene:ENSG00000222202
8174646	1,05	7,74E-01	1,11	1,15E-01	1,16	1,88E-02	4,08	3,14E-02	X	---	ncrna:snRNA chromosome:GRCh37:X:115532007:115532113:-1

											gene:ENSG00000207033
8172305	1,31	1,01E-01	1,27	7,52E-02	1,66	6,80E-05	3,09	2,85E-04	X	---	ncrna:snRNA chromosome:GRCh37:X:47211242:47211348:-1 gene:ENSG00000201450
7977621	1,00	9,95E-01	-1,16	2,48E-02	-1,15	2,70E-02	7,53	1,76E-02	14	*NDRG2*	NDRG family member 2
8066051	1,08	5,20E-01	-1,16	1,41E-02	-1,08	2,76E-01	9,22	2,06E-02	20	*NDRG3*	NDRG family member 3
7898337	-1,02	9,18E-01	-1,13	2,12E-02	-1,15	6,73E-03	10,02	6,67E-03	1	*NECAP2*	NECAP endocytosis associated 2
7986969	-1,00	9,95E-01	-1,12	4,16E-02	-1,12	4,27E-02	7,46	3,23E-02	15	*NDNL2*	necdin-like 2
8037913	1,12	5,05E-01	-1,29	9,29E-03	-1,15	1,89E-01	9,20	1,08E-02	19	*NAPA*	N-ethylmaleimide-sensitive factor attachment protein, alpha
7985983	1,06	6,44E-01	-1,16	1,66E-02	-1,09	2,20E-01	7,22	2,60E-02	15	*NGRN*	neugrin, neurite outgrowth associated
7943892	1,56	2,44E-02	-1,21	3,30E-01	1,29	2,11E-01	7,07	1,93E-02	11	*NCAM1*	neural cell adhesion molecule 1
7918813	-1,05	7,02E-01	-1,08	1,23E-01	-1,14	1,27E-02	9,95	2,33E-02	1	*NRAS*	neuroblastoma RAS viral (v-ras) oncogene homolog
8152119	1,43	5,19E-03	-1,28	4,01E-02	1,12	4,82E-01	7,46	3,01E-03	8	*NCALD*	neurocalcin delta
7925954	-1,11	3,56E-01	-1,08	3,16E-01	-1,19	1,04E-02	6,75	2,05E-02	10	*NET1*	neuroepithelial cell transforming 1
8059720	1,50	2,23E-02	-1,26	1,64E-01	1,19	3,98E-01	7,66	1,71E-02	2	*NMUR1*	neuromedin U receptor 1
8007197	-1,02	9,29E-01	-1,15	5,67E-02	-1,18	2,90E-02	8,35	3,14E-02	17	*NKIRAS2*	NFKB inhibitor interacting Ras-like 2
8085852	1,08	6,07E-01	1,08	2,72E-01	1,17	2,75E-02	8,17	4,90E-02	3	*NGLY1*	N-glycanase 1
7906576	-1,06	6,99E-01	-1,11	1,32E-01	-1,18	1,36E-02	9,46	2,55E-02	1	*NCSTN*	nicastrin
8022531	1,25	3,66E-02	-1,15	1,58E-01	1,09	5,08E-01	8,86	2,60E-02	18	*NPC1*	Niemann-Pick disease, type C1
7960253	1,18	1,19E-01	-1,25	1,18E-02	-1,06	6,83E-01	7,89	1,01E-02	12	*NINJ2*	ninjurin 2
8151952	-1,04	8,82E-01	-1,20	4,12E-02	-1,25	1,10E-02	7,51	1,41E-02	8	*NIPAL2*	NIPA-like domain containing 2
7998983	1,17	4,88E-02	-1,11	1,47E-01	1,05	6,05E-01	7,29	3,47E-02	16	*NLRC3*	NLR family, CARD domain containing 3
8007715	1,03	8,97E-01	-1,15	3,79E-02	-1,12	1,19E-01	8,51	4,92E-02	17	*NMT1*	N-myristoyltransferase 1
8059071	1,05	7,81E-01	-1,17	1,42E-02	-1,12	9,31E-02	8,02	1,79E-02	2	*NHEJ1*	nonhomologous end-joining factor 1
8168280	1,06	5,86E-01	-1,16	1,11E-02	-1,09	1,69E-01	9,97	1,39E-02	X	*NONO*	non-POU domain containing, octamer-binding

8043363	1,42	9,62E-02	1,17	4,08E-01	1,66	2,32E-03	5,64	4,60E-03	2	*NCRNA00152*	non-protein coding RNA 152
7925561	1,16	5,94E-01	1,22	1,68E-01	1,41	1,10E-02	7,80	2,21E-02	1	*NCRNA00201*	non-protein coding RNA 201
7960575	1,10	3,81E-01	-1,16	2,93E-02	-1,05	5,88E-01	7,68	4,42E-02	12	*NOP2*	NOP2 nucleolar protein homolog (yeast)
8060484	1,06	6,48E-01	-1,15	2,66E-02	-1,08	3,03E-01	7,23	4,41E-02	20	*NOP56*	NOP56 ribonucleoprotein homolog (yeast)
7904702	1,08	5,68E-01	1,12	1,08E-01	1,21	4,57E-03	10,71	9,98E-03	1	*NOTCH2NL*	Notch homolog 2 (Drosophila) N-terminal like
8064438	-1,10	2,39E-01	-1,02	7,20E-01	-1,12	3,96E-02	9,10	4,83E-02	20	*NSFL1C*	NSFL1 (p97) cofactor (p47)
8008087	-1,04	8,24E-01	-1,14	2,96E-02	-1,19	3,95E-03	8,27	5,88E-03	17	*NFE2L1*	nuclear factor (erythroid-derived 2)-like 1
8067040	1,27	4,93E-02	-1,22	5,45E-02	1,03	8,71E-01	9,07	2,32E-02	20	*NFATC2*	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2
8096635	-1,13	4,37E-02	1,01	8,83E-01	-1,12	4,27E-02	9,44	1,92E-02	4	*NFKB1*	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1
8000131	1,12	2,50E-01	1,05	5,67E-01	1,17	2,13E-02	11,65	3,21E-02	16	*NPIPL3*	nuclear pore complex interacting protein-like 3
7960331	1,02	9,38E-01	1,15	3,39E-02	1,17	1,50E-02	5,59	1,54E-02	12	*NRIP2*	nuclear receptor interacting protein 2
7911359	1,10	3,53E-01	-1,19	7,12E-03	-1,09	2,49E-01	8,15	7,96E-03	1	*NOC2L*	nucleolar complex associated 2 homolog (S. cerevisiae)
8160682	1,06	6,96E-01	-1,18	1,27E-02	-1,11	1,36E-01	6,90	1,73E-02	9	*NOL6*	nucleolar protein family 6 (RNA-associated)
8158446	1,12	1,99E-01	-1,15	3,49E-02	-1,02	8,45E-01	7,93	3,74E-02	9	*NUP188*	nucleoporin 188kDa
7973826	1,20	8,13E-02	1,01	9,59E-01	1,21	3,31E-02	5,21	2,39E-02	14	*NUBPL*	nucleotide binding protein-like
7993467	-1,05	7,09E-01	-1,09	1,65E-01	-1,15	2,15E-02	9,27	3,79E-02	16	*NDE1*	nudE nuclear distribution gene E homolog 1 (A. nidulans)
7934299	1,03	9,20E-01	1,16	5,85E-02	1,19	2,82E-02	6,41	3,12E-02	10	*NUDT13*	nudix (nucleoside diphosphate linked moiety X)-type motif 13
8179683	-1,08	6,80E-01	-1,13	1,57E-01	-1,22	1,59E-02	7,91	2,92E-02	6	*NRM*	nurim (nuclear envelope membrane protein)
7911231	-1,00	9,98E-01	-1,56	1,10E-02	-1,56	6,97E-03	9,47	4,20E-03	1	*OR2W3*	olfactory receptor, family 2, subfamily W, member 3
7937942	1,28	2,46E-01	1,17	3,23E-01	1,50	5,57E-03	6,24	1,14E-02	11	*OR52K1*	olfactory receptor, family 52, subfamily K, member 1
7959294	1,08	4,35E-01	-1,16	1,03E-02	-1,08	2,54E-01	8,60	1,26E-02	12	*ORAI1*	ORAI calcium release-activated calcium modulator 1
8014916	1,16	1,04E-01	-1,16	5,38E-02	1,01	9,74E-01	7,93	3,59E-02	17	*ORMDL3*	ORM1-like 3 (S. cerevisiae)
8157450	1,12	5,02E-01	1,17	1,06E-01	1,31	2,95E-03	5,91	7,06E-03	9	*ORM2*	orosomucoid 2

8147262	1,20	2,62E-02	1,01	9,15E-01	1,21	7,77E-03	7,62	5,13E-03	8	*OTUD6B*	OTU domain containing 6B
7917433	1,20	9,08E-02	-1,01	9,24E-01	1,18	6,71E-02	6,32	3,74E-02	1	*ODF2L*	outer dense fiber of sperm tails 2-like
7908861	1,51	1,77E-01	1,67	2,68E-02	2,52	2,90E-05	7,67	1,40E-04	1	*OCR1*	ovarian cancer-related protein 1
7973314	-1,02	9,06E-01	-1,12	7,99E-02	-1,14	3,52E-02	10,63	4,20E-02	14	*OXA1L*	oxidase (cytochrome c) assembly 1-like
8138613	1,21	6,15E-02	-1,01	9,43E-01	1,20	4,27E-02	7,02	2,32E-02	7	*OSBPL3*	oxysterol binding protein-like 3
7945831	1,45	5,52E-03	-1,27	6,19E-02	1,15	3,88E-01	7,28	3,70E-03	11	*OSBPL5*	oxysterol binding protein-like 5
8134789	1,16	1,17E-02	-1,11	5,81E-02	1,05	5,68E-01	8,86	7,27E-03	7	*PILRB*	paired immunoglobin-like type 2 receptor beta
7915286	-1,08	8,02E-01	-1,19	1,22E-01	-1,27	2,56E-02	11,37	3,94E-02	1	*PPT1*	palmitoyl-protein thioesterase 1
8162533	1,38	7,32E-02	-1,30	8,47E-02	1,06	8,44E-01	7,50	3,58E-02	9	*PTCH1*	patched homolog 1 (Drosophila)
8063097	1,04	7,72E-01	-1,14	1,57E-02	-1,10	1,14E-01	8,45	2,11E-02	20	*PCIF1*	PDX1 C-terminal inhibiting factor 1
8175860	1,30	8,56E-02	-1,23	1,22E-01	1,06	7,78E-01	6,46	4,95E-02	X	*PDZD4*	PDZ domain containing 4
7915910	1,01	9,88E-01	-1,47	2,42E-02	-1,45	2,89E-02	9,84	1,78E-02	1	*PDZK1IP1*	PDZK1 interacting protein 1
8067978	1,11	4,87E-02	-1,13	1,41E-02	-1,01	9,02E-01	10,60	8,43E-03	7	*PPIA*	peptidylprolyl isomerase A (cyclophilin A)
7919162	1,09	7,39E-01	1,18	1,43E-01	1,29	2,07E-02	7,34	3,53E-02	1	*PPIAL4B*	peptidylprolyl isomerase A (cyclophilin A)-like 4B
7919407	1,10	5,37E-01	1,12	2,21E-01	1,23	1,30E-02	5,79	2,60E-02	1	*PPIAL4B*	peptidylprolyl isomerase A (cyclophilin A)-like 4B
7900354	1,13	1,06E-01	-1,12	6,75E-02	1,01	9,41E-01	7,34	4,17E-02	1	*PPIE*	peptidylprolyl isomerase E (cyclophilin E)
7934161	1,76	2,66E-03	-1,39	4,93E-02	1,26	2,38E-01	10,57	1,03E-03	10	*PRF1*	perforin 1 (pore forming protein)
7911720	1,00	9,96E-01	-1,11	3,62E-02	-1,11	4,00E-02	6,87	2,78E-02	1	*PEX10*	peroxisomal biogenesis factor 10
7921571	-1,00	9,95E-01	-1,17	1,17E-02	-1,17	7,52E-03	8,03	4,69E-03	1	*PEX19*	peroxisomal biogenesis factor 19
8075406	1,02	9,15E-01	-1,13	1,65E-02	-1,11	4,06E-02	6,93	1,54E-02	22	*PES1*	pescadillo homolog 1, containing BRCT domain (zebrafish)
8081348	-1,06	7,09E-01	-1,11	1,24E-01	-1,17	1,37E-02	10,09	2,55E-02	3	*PCNP*	PEST proteolytic signal containing nuclear protein
7971563	-1,02	9,19E-01	-1,14	4,35E-02	-1,16	1,79E-02	9,83	1,97E-02	3	*PCNP*	PEST proteolytic signal containing nuclear protein
8134098	-1,04	9,00E-01	1,29	9,29E-03	1,24	2,14E-02	7,86	6,37E-03	7	*PFTK1*	PFTAIRE protein kinase 1

8080306	-1,03	8,79E-01	-1,15	3,51E-02	-1,18	8,54E-03	6,12	1,07E-02	3	*PHF7*	PHD finger protein 7
7899455	1,03	8,88E-01	-1,17	1,75E-02	-1,14	5,88E-02	8,95	1,97E-02	1	*PHACTR4*	phosphatase and actin regulator 4
8013641	1,03	8,68E-01	-1,15	1,57E-02	-1,11	5,94E-02	9,19	1,73E-02	17	*PIGS*	phosphatidylinositol glycan anchor biosynthesis, class S
8062981	1,10	2,78E-01	-1,14	3,62E-02	-1,03	7,56E-01	8,81	4,65E-02	20	*PIGT*	phosphatidylinositol glycan anchor biosynthesis, class T
8065762	1,06	6,84E-01	-1,22	3,68E-03	-1,15	3,59E-02	8,09	3,06E-03	20	*PIGU*	phosphatidylinositol glycan anchor biosynthesis, class U
8147447	-1,00	9,86E-01	-1,16	1,27E-02	-1,16	7,79E-03	9,81	5,13E-03	8	*PTDSS1*	phosphatidylserine synthase 1
7904965	1,26	1,31E-01	1,33	2,15E-02	1,67	1,30E-05	6,42	8,32E-05	1	*PDE4DIP*	phosphodiesterase 4D interacting protein
8112220	1,28	1,03E-02	-1,09	4,00E-01	1,18	7,83E-02	7,63	6,67E-03	5	*PDE4D*	phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila)
7934271	-1,10	2,27E-01	1,14	1,99E-02	1,04	6,68E-01	5,90	2,43E-02	10	*PLA2G12B*	phospholipase A2, group XIIB
8060854	1,25	6,99E-02	-1,03	8,27E-01	1,21	7,91E-02	7,19	3,38E-02	20	*PLCB1*	phospholipase C, beta 1 (phosphoinositide-specific)
8169240	1,06	6,90E-01	-1,25	1,74E-03	-1,17	1,74E-02	8,09	1,30E-03	X	*PRPS1*	phosphoribosyl pyrophosphate synthetase 1
8166049	-1,04	8,47E-01	-1,15	3,60E-02	-1,19	6,65E-03	8,50	8,75E-03	X	*PRPS2*	phosphoribosyl pyrophosphate synthetase 2
8095221	-1,03	9,15E-01	-1,19	2,48E-02	-1,22	8,17E-03	7,61	8,53E-03	4	*PAICS*	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase
8061447	1,07	6,77E-01	-1,18	2,38E-02	-1,10	2,56E-01	8,48	3,77E-02	20	*PYGB*	phosphorylase, glycogen; brain
8094596	1,19	5,77E-01	1,37	5,15E-02	1,63	1,50E-03	5,60	3,76E-03	4	*PTTG2*	pituitary tumor-transforming 2
8101429	1,18	3,42E-02	-1,17	2,84E-02	1,01	9,34E-01	11,24	1,15E-02	4	*PLAC8*	placenta-specific 8
7951351	1,56	1,60E-02	-1,27	1,70E-01	1,23	3,30E-01	7,20	1,27E-02	11	*PDGFD*	platelet derived growth factor D
7913883	1,25	4,74E-02	-1,13	2,43E-01	1,11	4,40E-01	7,66	3,74E-02	1	*PAFAH2*	platelet-activating factor acetylhydrolase 2, 40kDa
8081590	1,41	5,19E-03	-1,15	2,45E-01	1,23	9,77E-02	5,29	3,79E-03	3	*PHLDB2*	pleckstrin homology-like domain, family B, member 2
7907024	1,01	9,51E-01	-1,11	4,39E-02	-1,10	8,82E-02	8,02	4,85E-02	1	*POGK*	pogo transposable element with KRAB domain
8134777	1,23	4,21E-02	-1,14	1,40E-01	1,07	5,91E-01	8,83	3,00E-02	7	*PVRIG*	poliovirus receptor related immunoglobulin domain containing
8082086	1,35	4,32E-02	-1,17	2,75E-01	1,16	3,72E-01	8,44	3,50E-02	3	*PARP15*	poly (ADP-ribose) polymerase family, member 15

7941214	1,10	1,96E-01	-1,17	4,54E-03	-1,07	3,21E-01	7,08	4,44E-03	11	*POLA2*	polymerase (DNA directed), alpha 2 (70kD subunit)
8139299	1,02	9,42E-01	-1,17	1,57E-02	-1,15	2,94E-02	7,55	1,25E-02	7	*POLD2*	polymerase (DNA directed), delta 2, regulatory subunit 50kDa
8163525	-1,02	9,17E-01	-1,12	4,68E-02	-1,14	1,91E-02	7,76	2,16E-02	9	*POLE3*	polymerase (DNA directed), epsilon 3 (p17 subunit)
8013588	1,02	8,96E-01	-1,17	1,58E-03	-1,15	2,28E-03	9,10	5,13E-04	17	*POLDIP2*	polymerase (DNA-directed), delta interacting protein 2
7968254	-1,06	8,30E-01	-1,20	6,32E-02	-1,26	1,29E-02	9,66	1,93E-02	13	*POLR1D*	polymerase (RNA) I polypeptide D, 16kDa
8055089	-1,02	9,08E-01	-1,11	8,93E-02	-1,13	4,12E-02	7,38	4,91E-02	2	*POLR2D*	polymerase (RNA) II (DNA directed) polypeptide D
7934653	1,14	1,44E-01	-1,15	4,69E-02	-1,01	9,59E-01	6,95	3,92E-02	10	*POLR3A*	polymerase (RNA) III (DNA directed) polypeptide A, 155kDa
8024019	1,03	8,38E-01	-1,14	1,22E-02	-1,11	5,33E-02	10,26	1,24E-02	19	*PTBP1*	polypyrimidine tract binding protein 1
7903188	1,17	1,72E-01	1,07	4,91E-01	1,26	8,17E-03	7,76	1,34E-02	1	*PTBP2*	polypyrimidine tract binding protein 2
8071877	-1,06	7,44E-01	1,21	9,29E-03	1,15	6,84E-02	6,75	9,16E-03	22	*POM121L9P*	POM121 membrane glycoprotein-like 9 (rat) pseudogene
8167287	1,11	4,73E-01	-1,20	2,38E-02	-1,09	4,41E-01	7,46	3,72E-02	X	*PORCN*	porcupine homolog (Drosophila)
7937892	-1,07	6,51E-01	-1,09	2,36E-01	-1,16	2,69E-02	8,48	4,75E-02	11	*PGAP2*	post-GPI attachment to proteins 2
8133754	1,12	7,17E-02	-1,01	9,35E-01	1,11	5,11E-02	7,62	2,75E-02	7	*PMS2L11*	postmeiotic segregation increased 2-like 11 pseudogene
7966202	1,20	5,77E-02	-1,13	1,59E-01	1,06	6,15E-01	7,78	3,98E-02	12	*KCTD10*	potassium channel tetramerisation domain containing 10
8023914	-1,01	9,77E-01	-1,14	5,72E-02	-1,15	5,11E-02	7,99	4,47E-02	18	*PQLC1*	PQ loop repeat containing 1
8172531	-1,02	9,34E-01	-1,16	7,47E-02	-1,19	4,25E-02	8,03	4,58E-02	X	*PRAF2*	PRA1 domain family, member 2
7960984	1,20	3,66E-02	-1,04	7,12E-01	1,16	6,68E-02	5,00	1,94E-02	12	*PZP*	pregnancy-zone protein
7991465	1,06	9,04E-01	1,41	2,94E-02	1,50	9,00E-03	5,22	1,01E-02	15	---	PRO0800 gene:ENSG00000233726
7927550	1,19	2,51E-01	1,16	1,80E-01	1,37	1,71E-03	8,20	4,54E-03	10	*LOC100133130 /// LOC728407 /// BMS1P4*	PRO1102 /// poly(ADP-ribose) glycohydrolase pseudogene /// BMS1 pseudogene 4
8141688	1,09	3,82E-01	-1,17	1,17E-02	-1,08	3,29E-01	7,68	1,50E-02	7	*PLOD3*	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3
7904974	1,08	1,16E-01	-1,07	5,27E-02	1,00	9,90E-01	12,07	3,71E-02	1	*C1orf152*	profilin 1 pseudogene
7930226	1,09	3,24E-01	-1,14	2,68E-02	-1,04	6,27E-01	7,17	3,77E-02	10	*PDCD11*	programmed cell death 11
8016552	1,11	2,37E-01	-1,16	2,28E-02	-1,04	6,85E-01	9,02	2,80E-02	17	*PHB*	prohibitin

7960716	1,03	8,96E-01	-1,16	2,17E-02	-1,13	6,45E-02	9,15	2,35E-02	12	*PHB2*	prohibitin 2
8117922	1,02	9,15E-01	-1,13	3,48E-02	-1,11	9,31E-02	7,14	4,12E-02	6	*PRR3*	proline rich 3
8073705	1,15	8,56E-02	-1,18	1,27E-02	-1,03	7,74E-01	8,43	9,95E-03	22	*PRR5*	proline rich 5 (renal)
7939383	1,47	1,17E-02	-1,38	2,68E-02	1,07	7,80E-01	8,68	5,12E-03	11	*PRR5L*	proline rich 5 like
8145854	1,03	8,59E-01	-1,14	1,10E-02	-1,11	3,79E-02	8,89	8,88E-03	8	*PROSC*	proline synthetase co-transcribed homolog (bacterial)
8121076	-1,08	2,96E-01	-1,03	5,74E-01	-1,12	2,90E-02	10,65	4,24E-02	6	*PNRC1*	proline-rich nuclear receptor coactivator 1
7961259	1,25	3,88E-02	-1,12	2,53E-01	1,11	3,79E-01	6,72	3,12E-02	12	*PRH1*	proline-rich protein HaeIII subfamily 1
8128572	1,21	8,66E-03	-1,14	4,63E-02	1,06	5,44E-01	7,31	4,60E-03	6	*PREP*	prolyl endopeptidase
8043522	-1,08	3,16E-01	1,13	1,47E-02	1,05	4,73E-01	5,72	1,99E-02	2	*PROM2*	prominin 2
7969835	1,19	1,13E-02	-1,05	4,78E-01	1,13	6,05E-02	6,23	7,01E-03	13	*PCCA*	propionyl Coenzyme A carboxylase, alpha polypeptide
8082886	1,07	4,92E-01	-1,17	7,12E-03	-1,09	1,66E-01	7,64	8,43E-03	3	*PCCB*	propionyl Coenzyme A carboxylase, beta polypeptide
7974363	1,64	5,74E-02	-1,23	4,11E-01	1,34	2,80E-01	8,59	4,41E-02	14	*PTGDR*	prostaglandin D2 receptor (DP)
8159521	1,28	3,54E-02	-1,14	2,35E-01	1,12	3,73E-01	6,63	2,66E-02	9	*PTGDS*	prostaglandin D2 synthase 21kDa (brain)
8105067	-1,11	3,03E-01	-1,07	3,46E-01	-1,19	9,28E-03	9,35	1,80E-02	5	*PTGER4*	prostaglandin E receptor 4 (subtype EP4)
8028756	1,12	1,74E-01	-1,17	1,27E-02	-1,05	6,27E-01	9,24	1,39E-02	19	*PSMC4*	proteasome (prosome, macropain) 26S subunit, ATPase, 4
8006392	1,03	8,16E-01	-1,17	3,76E-03	-1,13	1,49E-02	8,60	2,52E-03	17	*PSMD11*	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11
8006984	1,05	6,44E-01	-1,15	6,66E-03	-1,09	8,29E-02	8,47	6,75E-03	17	*PSMD3*	proteasome (prosome, macropain) 26S subunit, non-ATPase, 3
7973564	1,05	6,63E-01	-1,13	2,22E-02	-1,07	2,55E-01	10,12	3,53E-02	14	*PSME1*	proteasome (prosome, macropain) activator subunit 1 (PA28 alpha)
8053797	1,28	2,39E-01	1,12	4,85E-01	1,43	1,34E-02	6,74	2,25E-02	2	*LOC400986*	protein immuno-reactive with anti-PTH polyclonal antibodies
7974835	1,22	2,89E-02	-1,21	1,84E-02	1,01	9,79E-01	10,90	7,63E-03	14	*PRKCH*	protein kinase C, eta
7931930	1,18	9,82E-02	-1,16	5,75E-02	1,01	9,58E-01	8,97	3,62E-02	10	*PRKCQ*	protein kinase C, theta
8061706	1,04	7,94E-01	-1,12	3,05E-02	-1,08	1,90E-01	6,37	4,71E-02	20	*POFUT1*	protein O-fucosyltransferase 1
7908841	1,11	6,15E-01	1,15	1,69E-01	1,28	1,26E-02	7,41	2,43E-02	1	*PPP1R12B*	protein phosphatase 1, regulatory (inhibitor) subunit 12B

7981460	1,09	4,16E-01	-1,17	1,59E-02	-1,07	3,93E-01	7,16	2,37E-02	14	*PPP1R13B*	protein phosphatase 1, regulatory (inhibitor) subunit 13B
8051119	1,01	9,75E-01	-1,15	1,18E-02	-1,14	1,23E-02	8,82	6,04E-03	2	*PPM1G*	protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform
8030881	1,06	6,38E-01	-1,16	1,66E-02	-1,09	2,27E-01	9,53	2,65E-02	19	*PPP2R1A*	protein phosphatase 2 (formerly 2A), regulatory subunit A, alpha isoform
8114900	1,35	2,25E-02	-1,23	8,91E-02	1,10	5,88E-01	6,57	1,50E-02	5	*PPP2R2B*	protein phosphatase 2 (formerly 2A), regulatory subunit B, beta isoform
8119627	1,04	7,61E-01	-1,14	1,56E-02	-1,10	1,17E-01	7,67	2,04E-02	6	*PPP2R5D*	protein phosphatase 2, regulatory subunit B', delta isoform
8158523	1,11	2,26E-01	-1,20	4,16E-03	-1,08	2,75E-01	8,02	4,16E-03	9	*PPP2R4*	protein phosphatase 2A activator, regulatory subunit 4
7990511	1,07	6,79E-01	-1,20	9,29E-03	-1,13	1,02E-01	8,09	1,07E-02	15	*PTPN9*	protein tyrosine phosphatase, non-receptor type 9
8060539	1,07	1,46E-01	-1,11	9,29E-03	-1,03	5,68E-01	7,97	8,54E-03	20	*PTPRA*	protein tyrosine phosphatase, receptor type, A
8180272	-1,11	6,12E-01	1,24	2,94E-02	1,12	3,64E-01	3,91	4,96E-02	5	*PCDHA6*	protocadherin alpha 6
7926283	1,00	9,98E-01	1,26	3,53E-02	1,26	3,60E-02	8,41	2,62E-02	10	*PRPF18*	PRP18 pre-mRNA processing factor 18 homolog (S. cerevisiae)
8157283	1,09	3,78E-01	-1,19	8,42E-03	-1,09	2,60E-01	8,48	9,60E-03	9	*PRPF4*	PRP4 pre-mRNA processing factor 4 homolog (yeast)
7934178	1,02	9,54E-01	-1,15	4,47E-02	-1,14	8,76E-02	6,50	4,90E-02	10	*PCBD1*	pterin-4 alpha-carbinolamine dehydratase/dimerization cofactor of hepatocyte nuclear factor 1 alpha
8177026	1,05	8,21E-01	-1,23	1,22E-02	-1,17	5,94E-02	9,19	1,28E-02	c("X", "Y")	*P2RY8*	purinergic receptor P2Y, G-protein coupled, 8
8069003	1,08	3,67E-01	-1,15	1,18E-02	-1,06	3,55E-01	7,11	1,57E-02	21	*PWP2*	PWP2 periodic tryptophan protein homolog (yeast)
8008064	1,01	9,62E-01	-1,15	2,93E-02	-1,14	4,76E-02	7,94	2,63E-02	17	*PNPO*	pyridoxamine 5'-phosphate oxidase
7906386	1,44	8,77E-03	-1,15	3,16E-01	1,25	1,02E-01	8,79	6,07E-03	1	*PYHIN1*	pyrin and HIN domain family, member 1
7939329	-1,00	9,96E-01	-1,14	5,21E-02	-1,14	5,86E-02	8,91	4,53E-02	11	*PDHX*	pyruvate dehydrogenase complex, component X
8008263	-1,01	9,78E-01	-1,23	1,31E-02	-1,24	7,45E-03	7,81	5,13E-03	17	*PDK2*	pyruvate dehydrogenase kinase, isozyme 2
7978239	1,08	3,97E-01	-1,17	7,12E-03	-1,08	2,22E-01	7,56	8,26E-03	14	*RABGGTA*	Rab geranylgeranyltransferase, alpha subunit
7967456	-1,28	2,66E-02	1,19	9,07E-02	-1,08	6,14E-01	9,26	1,73E-02	12	*RILPL2*	Rab interacting lysosomal protein-like 2
8074880	1,03	8,70E-01	1,10	9,16E-02	1,13	2,87E-02	5,26	3,82E-02	22	*RAB36*	RAB36, member RAS oncogene family
8028930	1,06	6,77E-01	-1,14	2,19E-02	-1,08	2,40E-01	8,42	3,47E-02	19	*RAB4B*	RAB4B, member RAS oncogene family

7923812	1,20	3,17E-02	-1,13	1,12E-01	1,06	5,88E-01	8,60	2,10E-02	1	*RAB7L1*	RAB7, member RAS oncogene family-like 1
8085665	1,19	3,81E-02	-1,12	1,21E-01	1,06	6,04E-01	8,15	2,56E-02	3	*RFTN1*	raftlin, lipid raft linker 1
8164810	1,15	2,08E-01	-1,23	1,28E-02	-1,07	5,74E-01	7,73	1,50E-02	9	*RALGDS*	ral guanine nucleotide dissociation stimulator
8164692	1,20	2,23E-01	1,18	1,50E-01	1,42	1,01E-03	5,35	2,93E-03	9	*RAPGEF1*	Rap guanine nucleotide exchange factor (GEF) 1
7962623	1,00	9,95E-01	1,13	5,49E-02	1,13	6,02E-02	5,94	4,87E-02	12	*RAPGEF3*	Rap guanine nucleotide exchange factor (GEF) 3
7989365	1,26	1,46E-02	-1,03	7,83E-01	1,22	2,10E-02	8,97	5,74E-03	15	*RORA*	RAR-related orphan receptor A
8087640	1,21	4,45E-02	-1,07	4,91E-01	1,13	1,87E-01	7,85	3,35E-02	3	*RASSF1*	Ras association (RalGDS/AF-6) domain family member 1
7963009	1,15	3,88E-02	-1,08	2,45E-01	1,07	3,91E-01	4,36	3,10E-02	12	*RHEBL1*	Ras homolog enriched in brain like 1
7918593	1,28	6,70E-02	-1,22	8,91E-02	1,05	8,14E-01	8,67	3,51E-02	1	*RHOC*	ras homolog gene family, member C
7967202	1,14	1,77E-01	-1,19	1,47E-02	-1,05	6,59E-01	9,32	1,61E-02	12	*RHOF*	ras homolog gene family, member F (in filopodia)
8035050	1,20	5,07E-02	-1,13	1,64E-01	1,07	5,80E-01	8,59	3,62E-02	19	*RASAL3*	RAS protein activator like 3
8116740	-1,09	1,06E-01	-1,02	7,26E-01	-1,12	1,37E-02	7,79	1,64E-02	6	*RREB1*	ras responsive element binding protein 1
8154523	-1,04	7,70E-01	-1,09	8,71E-02	-1,12	1,24E-02	7,59	2,05E-02	9	*RRAGA*	Ras-related GTP binding A
7930205	1,14	2,70E-01	1,07	4,83E-01	1,22	1,63E-02	4,79	2,68E-02	10	*hCG_2024410*	rcRPE
7905938	1,05	7,83E-01	-1,23	4,22E-03	-1,17	2,33E-02	8,89	3,31E-03	1	*RAG1AP1*	recombination activating gene 1 activating protein 1
7905185	-1,03	8,82E-01	-1,17	1,66E-02	-1,20	2,95E-03	9,16	3,89E-03	1	*RPRD2*	regulation of nuclear pre-mRNA domain containing 2
8009277	1,47	1,83E-02	-1,32	6,15E-02	1,11	6,42E-01	6,14	1,08E-02	17	*RGS9*	regulator of G-protein signaling 9
7919971	1,03	8,90E-01	-1,16	1,60E-02	-1,13	4,97E-02	8,08	1,64E-02	1	*RFX5*	regulatory factor X, 5 (influences HLA class II expression)
8110437	1,06	6,87E-01	-1,17	1,17E-02	-1,11	1,24E-01	7,57	1,45E-02	5	*RMND5B*	required for meiotic nuclear division 5 homolog B (S. cerevisiae)
7937275	1,09	1,96E-01	-1,16	5,12E-03	-1,06	3,44E-01	8,34	4,84E-03	11	*RIC8A*	resistance to inhibitors of cholinesterase 8 homolog A (C. elegans)
7940781	-1,06	8,04E-01	1,23	2,44E-02	1,16	1,48E-01	8,18	3,52E-02	11	*RTN3*	reticulon 3
7940775	1,25	2,36E-02	-1,16	1,13E-01	1,08	5,26E-01	8,15	1,68E-02	11	*RARRES3*	retinoic acid receptor responder (tazarotene induced) 3
7906163	-1,06	6,52E-01	1,13	2,52E-02	1,07	2,90E-01	5,46	4,17E-02	1	*RHBG*	Rh family, B glycoprotein (gene/pseudogene)

8133662	-1,02	9,13E-01	-1,14	6,60E-02	-1,17	2,95E-02	9,42	3,46E-02	7	*RHBDD2*	rhomboid domain containing 2
7977507	1,01	9,83E-01	1,17	5,14E-02	1,18	4,64E-02	10,51	3,94E-02	14	*RPPH1*	ribonuclease P RNA component H1
8130768	-1,16	2,90E-01	1,23	3,05E-02	1,06	6,96E-01	8,27	4,06E-02	6	*RNASET2*	ribonuclease T2
8130783	-1,04	8,39E-01	1,25	5,83E-03	1,19	2,10E-02	7,13	4,16E-03	6	*RNASET2*	ribonuclease T2
8062349	1,04	7,64E-01	-1,13	2,71E-02	-1,08	1,97E-01	9,69	4,21E-02	20	*RPN2*	ribophorin II
8024299	1,04	7,64E-01	-1,12	2,78E-02	-1,08	2,00E-01	10,53	4,36E-02	19	*RPS15*	ribosomal protein S15
7950626	1,02	9,61E-01	1,24	4,39E-02	1,27	2,95E-02	8,19	2,68E-02	11	*RPS20P27*	ribosomal protein S20 pseudogene 27
7922504	1,03	9,19E-01	1,22	4,93E-02	1,26	2,13E-02	8,89	2,36E-02	1	*RFWD2*	ring finger and WD repeat domain 2
8178244	1,09	2,43E-01	-1,12	3,45E-02	-1,03	7,81E-01	7,67	4,14E-02	6	*RING1*	ring finger protein 1
8021120	1,31	3,85E-02	-1,15	2,49E-01	1,14	3,79E-01	6,10	3,02E-02	18	*RNF165*	ring finger protein 165
7913206	-1,03	8,78E-01	1,13	3,45E-02	1,10	1,28E-01	6,38	4,63E-02	1	*RNF186*	ring finger protein 186
7944510	-1,05	8,38E-01	-1,20	2,67E-02	-1,25	3,89E-03	8,12	5,45E-03	11	*RNF26*	ring finger protein 26
8179472	1,11	3,73E-01	-1,24	5,76E-03	-1,11	1,92E-01	7,27	5,84E-03	6	*RNF5*	ring finger protein 5
7941694	1,15	5,74E-02	-1,16	1,60E-02	-1,02	9,08E-01	8,48	1,07E-02	11	*RBM14*	RNA binding motif protein 14
8080093	-1,04	8,31E-01	-1,11	1,16E-01	-1,15	2,96E-02	7,05	4,41E-02	3	*RBM15B*	RNA binding motif protein 15B
8027908	1,09	1,79E-01	-1,09	5,22E-02	-1,01	9,49E-01	7,46	4,90E-02	19	*RBM42*	RNA binding motif protein 42
8085233	1,11	2,38E-01	-1,16	1,66E-02	-1,05	6,10E-01	7,99	2,17E-02	3	*RPUSD3*	RNA pseudouridylate synthase domain containing 3
8060895	1,13	4,01E-01	1,12	2,33E-01	1,26	7,37E-03	5,90	1,54E-02	20	*RNU105B*	RNA, U105B small nucleolar
7967028	1,56	3,07E-01	1,57	1,24E-01	2,45	1,30E-03	7,07	3,70E-03	12	*RNU4-2*	RNA, U4 small nuclear 2
7913805	1,19	1,77E-01	-1,22	4,25E-02	-1,02	9,08E-01	9,41	4,06E-02	1	*RUNX3*	runt-related transcription factor 3
8014257	1,36	3,22E-03	-1,19	7,31E-02	1,14	2,32E-01	8,76	1,89E-03	17	*SLFN12L*	schlafen family member 12-like
8014248	1,26	3,32E-02	-1,10	3,42E-01	1,14	2,43E-01	7,78	2,53E-02	17	*SLFN13*	schlafen family member 13
7931951	1,21	2,13E-02	-1,06	5,02E-01	1,14	9,56E-02	8,06	1,42E-02	10	*SFMBT2*	Scm-like with four mbt domains 2

8108099	-1,01	9,58E-01	-1,11	5,07E-02	-1,12	3,49E-02	8,43	3,34E-02	5	*SEC24A*	SEC24 family, member A (S. cerevisiae)
8101376	1,05	6,24E-01	-1,15	1,08E-02	-1,09	1,43E-01	10,25	1,28E-02	4	*SEC31A*	SEC31 homolog A (S. cerevisiae)
8082408	1,04	7,02E-01	-1,12	2,21E-02	-1,07	2,19E-01	9,67	3,47E-02	3	*SEC61A1*	Sec61 alpha 1 subunit (S. cerevisiae)
7990417	1,04	7,75E-01	-1,14	2,78E-02	-1,09	1,91E-01	10,08	4,29E-02	15	*SCAMP2*	secretory carrier membrane protein 2
8054004	1,26	1,14E-02	-1,23	1,65E-02	1,03	8,78E-01	6,85	3,89E-03	2	*SEMA4C*	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4C
7956401	-1,01	9,68E-01	-1,16	3,57E-02	-1,17	2,49E-02	8,80	2,14E-02	12	*SHMT2*	serine hydroxymethyltransferase 2 (mitochondrial)
8062908	1,01	9,48E-01	1,10	2,80E-02	1,11	1,33E-02	10,75	1,28E-02	20	*STK4*	serine/threonine kinase 4
8123609	1,08	7,09E-01	-1,28	7,12E-03	-1,19	6,27E-02	9,87	7,10E-03	6	*SERPINB9*	serpin peptidase inhibitor, clade B (ovalbumin), member 9
8003667	1,21	6,78E-02	-1,15	1,24E-01	1,05	7,19E-01	6,24	4,10E-02	17	*SERPINF1*	serpin peptidase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium derived factor), member 1
8052669	-1,14	2,28E-01	-1,03	7,58E-01	-1,17	4,27E-02	8,48	4,91E-02	2	*SERTAD2*	SERTA domain containing 2
8001306	1,00	9,96E-01	1,18	1,69E-02	1,18	1,45E-02	6,91	9,60E-03	16	*SIAH1*	seven in absentia homolog 1 (Drosophila)
7915363	1,07	6,33E-01	-1,18	1,24E-02	-1,10	1,67E-01	7,46	1,71E-02	1	*SCMH1*	sex comb on midleg homolog 1 (Drosophila)
8142036	1,01	9,78E-01	1,14	3,45E-02	1,15	2,69E-02	9,21	2,18E-02	7	*SRPK2*	SFRS protein kinase 2
7921900	1,79	3,88E-02	-1,20	5,22E-01	1,49	1,49E-01	9,24	2,68E-02	1	*SH2D1B*	SH2 domain containing 1B
7921144	1,54	2,35E-03	-1,30	3,71E-02	1,18	2,46E-01	8,02	6,92E-04	1	*SH2D2A*	SH2 domain protein 2A
7994603	1,20	1,33E-01	-1,20	4,97E-02	-1,00	9,85E-01	9,15	3,94E-02	16	*SPN*	sialophorin
8081710	1,24	3,02E-02	-1,24	1,81E-02	1,00	9,87E-01	8,12	7,84E-03	3	*SIDT1*	SID1 transmembrane family, member 1
7944049	1,01	9,88E-01	-1,27	4,77E-02	-1,26	6,27E-02	9,15	4,41E-02	11	*SIDT2*	SID1 transmembrane family, member 2
7929919	1,08	4,45E-01	-1,17	9,29E-03	-1,08	2,35E-01	7,68	1,17E-02	10	*SFXN3*	sideroflexin 3
7967091	-1,02	9,15E-01	-1,10	4,26E-02	-1,11	1,64E-02	9,28	1,85E-02	12	*UNQ1887*	signal peptide peptidase 3
7952557	1,06	5,67E-01	-1,15	9,29E-03	-1,08	1,61E-01	10,35	1,15E-02	11	*SRPR*	signal recognition particle receptor (docking protein)
8057771	1,36	4,30E-03	-1,11	3,23E-01	1,22	5,33E-02	9,47	2,98E-03	2	*STAT4*	signal transducer and activator of transcription 4
8059672	1,10	4,69E-01	-1,19	2,22E-02	-1,08	4,30E-01	9,32	3,51E-02	2	*LOC645870*	similar to barrier-to-autointegration factor

7986428	1,17	1,29E-01	1,03	7,51E-01	1,21	1,91E-02	7,39	2,18E-02	15	*LOC400464*	similar to FLJ43276 protein
8081808	1,15	5,46E-01	1,31	2,78E-02	1,51	4,30E-04	4,19	1,25E-03	3	*LOC100128175*	similar to PRO2591
7957606	1,08	5,89E-01	1,09	2,03E-01	1,18	1,45E-02	5,07	2,83E-02	12	*LOC283398*	similar to sucb
7912861	1,08	6,23E-01	1,10	2,55E-01	1,19	2,68E-02	6,31	4,76E-02	1	*LOC644634*	similar to UPF0627 protein ENSP00000358171
7990487	-1,05	6,52E-01	-1,09	1,06E-01	-1,15	7,46E-03	9,24	1,46E-02	15	*SIN3A*	SIN3 homolog A, transcription regulator (yeast)
7945377	1,17	1,00E-01	-1,15	8,00E-02	1,02	9,07E-01	8,58	4,41E-02	11	*SIGIRR*	single immunoglobulin and toll-interleukin 1 receptor (TIR) domain
7906613	1,43	3,62E-02	-1,32	6,67E-02	1,08	7,55E-01	8,40	1,92E-02	1	*SLAMF7*	SLAM family member 7
8023191	1,01	9,82E-01	1,27	4,73E-02	1,28	4,09E-02	8,20	3,43E-02	18	*SMAD2*	SMAD family member 2
8023220	1,21	1,63E-01	-1,25	3,66E-02	-1,03	8,99E-01	6,65	3,50E-02	18	*SMAD7*	SMAD family member 7
8021181	1,25	3,78E-02	-1,13	2,28E-01	1,11	4,06E-01	10,47	2,91E-02	18	*SCARNA17*	small Cajal body-specific RNA 17
8021183	1,29	3,78E-02	-1,20	9,27E-02	1,07	6,83E-01	10,01	2,32E-02	18	*SCARNA17*	small Cajal body-specific RNA 17
8053909	1,10	1,88E-01	-1,17	4,73E-03	-1,06	3,37E-01	9,99	4,54E-03	2	*SNRNP200*	small nuclear ribonucleoprotein 200kDa (U5)
8028916	1,01	9,58E-01	-1,15	2,21E-02	-1,14	3,60E-02	9,16	1,86E-02	19	*SNRPA*	small nuclear ribonucleoprotein polypeptide A
8154394	1,19	1,29E-01	1,00	9,97E-01	1,19	6,20E-02	9,13	4,44E-02	9	*SNAPC3*	small nuclear RNA activating complex, polypeptide 3, 50kDa
7948900	-1,06	8,75E-01	-1,23	1,02E-01	-1,31	3,42E-02	7,82	4,63E-02	11	*SNORD30*	small nucleolar RNA, C/D box 30
7975453	1,29	6,18E-01	1,67	3,61E-02	2,15	1,13E-03	4,92	2,76E-03	14	*SNORD56B*	small nucleolar RNA, C/D box 56B
7951030	1,09	8,40E-01	1,36	4,94E-02	1,49	9,78E-03	8,20	1,42E-02	11	*SNORD6*	small nucleolar RNA, C/D box 6
7951032	-1,05	9,43E-01	1,74	9,29E-03	1,65	1,32E-02	7,17	4,91E-03	11	*SNORA1*	small nucleolar RNA, H/ACA box 1
7962827	1,13	7,15E-01	1,50	6,46E-03	1,69	1,03E-04	5,31	2,44E-04	12	*SNORA2A*	small nucleolar RNA, H/ACA box 2A
7920873	1,12	7,82E-01	1,38	4,74E-02	1,55	5,57E-03	8,57	9,04E-03	1	*SNORA42*	small nucleolar RNA, H/ACA box 42
7915227	1,06	7,61E-01	1,18	2,91E-02	1,24	2,11E-03	6,72	4,14E-03	1	*SNORA55*	small nucleolar RNA, H/ACA box 55
8005626	1,09	5,93E-01	1,11	2,28E-01	1,22	1,83E-02	6,31	3,47E-02	1	*SNORA59A*	small nucleolar RNA, H/ACA box 59A
8052524	1,24	2,59E-01	1,20	1,89E-01	1,50	1,88E-03	5,38	4,91E-03	2	*SNORA70B*	small nucleolar RNA, H/ACA box 70B (retrotransposed)

7964830	1,12	7,43E-01	1,25	1,21E-01	1,41	1,64E-02	6,70	2,84E-02	12	*SNORA70G*	small nucleolar RNA, H/ACA box 70G (retrotransposed)
8108420	1,11	5,55E-01	1,18	8,80E-02	1,31	2,95E-03	5,63	6,93E-03	5	*SNORA74A*	small nucleolar RNA, H/ACA box 74A
7920217	1,06	7,19E-01	1,13	1,01E-01	1,20	1,08E-02	8,05	1,97E-02	1	*SPRR2G*	small proline-rich protein 2G
7994006	1,13	3,68E-01	1,10	3,03E-01	1,23	1,02E-02	11,43	2,02E-02	16	*SMG1*	SMG1 homolog, phosphatidylinositol 3-kinase-related kinase (C. elegans)
8000834	1,07	5,85E-01	1,08	2,70E-01	1,15	2,42E-02	11,23	4,41E-02	16	*SMG1*	SMG1 homolog, phosphatidylinositol 3-kinase-related kinase (C. elegans)
8000638	1,14	4,02E-01	1,10	3,79E-01	1,26	1,91E-02	11,20	3,47E-02	16	*SMG1*	SMG1 homolog, phosphatidylinositol 3-kinase-related kinase (C. elegans)
8002333	1,13	2,85E-01	1,10	2,30E-01	1,24	3,42E-03	11,18	7,96E-03	16	*SMG1*	SMG1 homolog, phosphatidylinositol 3-kinase-related kinase (C. elegans)
8000823	1,14	3,25E-01	1,07	5,11E-01	1,21	2,58E-02	10,78	3,98E-02	16	*SMG1*	SMG1 homolog, phosphatidylinositol 3-kinase-related kinase (C. elegans)
8000651	1,13	3,87E-01	1,11	2,35E-01	1,26	6,97E-03	7,87	1,46E-02	16	*SMG1*	SMG1 homolog, phosphatidylinositol 3-kinase-related kinase (C. elegans)
8044499	1,20	3,88E-02	-1,08	3,84E-01	1,12	2,42E-01	9,21	3,11E-02	2	*SLC20A1*	solute carrier family 20 (phosphate transporter), member 1
8123232	-1,07	7,65E-01	1,23	2,69E-02	1,15	1,96E-01	6,04	4,17E-02	6	*SLC22A1*	solute carrier family 22 (organic cation transporter), member 1
8056766	1,15	1,28E-01	-1,15	6,88E-02	1,01	9,64E-01	7,79	4,74E-02	2	*SLC25A12*	solute carrier family 25 (mitochondrial carrier, Aralar), member 12
8033190	1,03	8,39E-01	-1,12	3,04E-02	-1,09	1,45E-01	6,14	4,33E-02	19	*SLC25A23*	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 23
8018352	1,06	5,79E-01	-1,14	1,35E-02	-1,08	2,23E-01	6,58	1,98E-02	17	*SLC25A19*	solute carrier family 25 (mitochondrial thiamine pyrophosphate carrier), member 19
8012450	1,07	5,38E-01	-1,16	1,18E-02	-1,08	2,21E-01	6,01	1,64E-02	17	*SLC25A35*	solute carrier family 25, member 35
7940717	1,09	5,79E-01	-1,18	2,55E-02	-1,09	3,62E-01	8,24	4,26E-02	11	*SLC3A2*	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2
8108558	1,07	5,86E-01	-1,17	1,50E-02	-1,09	2,34E-01	9,25	2,22E-02	5	*SLC35A4*	solute carrier family 35, member A4
7939590	1,03	8,81E-01	-1,20	3,78E-03	-1,17	8,83E-03	7,36	2,00E-03	11	*SLC35C1*	solute carrier family 35, member C1
8066697	1,04	7,75E-01	-1,12	2,26E-02	-1,08	1,59E-01	8,25	3,35E-02	20	*SLC35C2*	solute carrier family 35, member C2
8068810	1,06	6,18E-01	-1,18	8,65E-03	-1,11	1,17E-01	7,50	9,55E-03	21	*SLC37A1*	solute carrier family 37 (glycerol-3-phosphate transporter), member 1
8145122	1,11	1,02E-01	-1,13	2,52E-02	-1,01	9,08E-01	6,19	2,05E-02	8	*SLC39A14*	solute carrier family 39 (zinc transporter), member 14

8095585	1,44	1,23E-02	-1,22	1,49E-01	1,18	3,18E-01	6,52	9,60E-03	4	*SLC4A4*	solute carrier family 4, sodium bicarbonate cotransporter, member 4
7923824	1,08	5,11E-01	-1,18	9,29E-03	-1,10	1,91E-01	7,40	1,15E-02	1	*SLC41A1*	solute carrier family 41, member 1
7948249	1,06	7,44E-01	-1,21	1,03E-02	-1,15	7,72E-02	8,03	1,08E-02	11	*SLC43A1*	solute carrier family 43, member 1
7948229	-1,03	8,68E-01	-1,14	4,97E-02	-1,18	1,26E-02	8,84	1,70E-02	11	*SLC43A3*	solute carrier family 43, member 3
7955055	-1,01	9,92E-01	-1,27	5,27E-02	-1,28	5,38E-02	8,52	4,38E-02	12	*SLC48A1*	solute carrier family 48 (heme transporter), member 1
8172280	-1,06	8,19E-01	-1,17	8,67E-02	-1,23	1,78E-02	7,17	2,68E-02	X	*SLC9A7*	solute carrier family 9 (sodium/hydrogen exchanger), member 7
8040908	1,14	1,70E-01	-1,15	5,06E-02	-1,01	9,53E-01	9,75	4,61E-02	2	*SNX17*	sorting nexin 17
8105328	-1,04	8,56E-01	1,20	1,66E-02	1,15	7,33E-02	8,05	2,02E-02	5	*SNX18*	sorting nexin 18
8107613	-1,02	9,08E-01	-1,14	5,50E-02	-1,17	2,35E-02	9,95	2,68E-02	5	*SNX2*	sorting nexin 2
7993281	-1,08	5,55E-01	-1,10	2,04E-01	-1,18	1,26E-02	8,23	2,48E-02	16	*SNX29*	sorting nexin 29
8131709	1,08	4,21E-01	-1,14	2,83E-02	-1,05	5,34E-01	9,35	4,42E-02	7	*SP4*	Sp4 transcription factor
8130211	1,39	1,13E-02	-1,03	8,52E-01	1,35	1,16E-02	8,13	3,82E-03	6	*SYNE1*	spectrin repeat containing, nuclear envelope 1
7974920	1,29	3,11E-03	1,04	7,10E-01	1,33	9,90E-05	8,86	1,29E-04	14	*SYNE2*	spectrin repeat containing, nuclear envelope 2
8104856	1,12	2,07E-01	1,04	6,15E-01	1,16	1,96E-02	4,46	2,73E-02	5	*SPEF2*	sperm flagellar 2
7912374	1,03	8,96E-01	-1,17	2,00E-02	-1,14	6,02E-02	9,21	2,18E-02	1	*SRM*	spermidine synthase
7990582	1,11	3,70E-01	1,06	4,47E-01	1,18	2,36E-02	7,38	3,94E-02	15	*SCAPER*	S-phase cyclin A-associated protein in the ER
8055183	1,04	8,62E-01	-1,19	1,57E-02	-1,15	6,22E-02	7,98	1,75E-02	2	*SMPD4*	sphingomyelin phosphodiesterase 4, neutral membrane (neutral sphingomyelinase-3)
8048717	-1,14	2,97E-02	-1,01	9,34E-01	-1,15	9,59E-03	5,73	6,37E-03	2	*SGPP2*	sphingosine-1-phosphate phosphotase 2
8034043	1,36	1,14E-02	-1,17	1,81E-01	1,16	2,55E-01	8,48	8,75E-03	19	*S1PR5*	sphingosine-1-phosphate receptor 5
8173208	1,15	1,44E-01	-1,16	4,46E-02	-1,01	9,50E-01	7,33	3,77E-02	X	*SPIN4*	spindlin family, member 4
8035581	1,17	1,60E-02	-1,05	4,85E-01	1,12	8,39E-02	7,82	1,08E-02	19	*SFRS14*	splicing factor, arginine/serine-rich 14
8098870	1,74	8,77E-03	-1,35	1,28E-01	1,28	2,79E-01	7,81	6,05E-03	4	*SPON2*	spondin 2, extracellular matrix protein
7956257	1,03	8,96E-01	-1,19	2,48E-02	-1,15	7,74E-02	7,25	2,86E-02	12	*SPRYD4*	SPRY domain containing 4

8138689	-1,05	8,12E-01	1,22	1,61E-02	1,16	9,16E-02	10,33	2,06E-02	7	*SKAP2*	src kinase associated phosphoprotein 2
8066038	1,31	8,77E-03	-1,21	4,39E-02	1,08	5,82E-01	8,82	4,84E-03	20	*SLA2*	Src-like-adaptor 2
8021349	1,00	9,94E-01	1,11	4,31E-02	1,11	4,27E-02	3,70	3,30E-02	18	*ST8SIA3*	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 3
8135876	1,12	1,16E-01	-1,13	3,17E-02	-1,01	9,28E-01	9,05	2,56E-02	7	*SND1*	staphylococcal nuclease and tudor domain containing 1
8053890	1,06	6,42E-01	-1,22	8,98E-04	-1,16	4,88E-03	9,79	2,05E-04	2	*STARD7*	StAR-related lipid transfer (START) domain containing 7
8129482	1,38	6,63E-02	-1,05	7,99E-01	1,31	8,51E-02	8,42	3,37E-02	6	*SAMD3*	sterile alpha motif domain containing 3
7928516	-1,08	6,94E-01	1,31	2,85E-03	1,21	2,69E-02	8,62	2,17E-03	10	*SAMD8*	sterile alpha motif domain containing 8
8160968	1,11	4,18E-01	-1,18	2,93E-02	-1,07	5,47E-01	8,47	4,57E-02	9	*STOML2*	stomatin (EPB72)-like 2
8133215	1,19	6,60E-02	-1,11	2,33E-01	1,07	5,12E-01	7,03	4,86E-02	7	*STAG3L4*	stromal antigen 3-like 4
7937900	1,05	7,19E-01	-1,13	2,52E-02	-1,08	2,25E-01	8,55	4,03E-02	11	*STIM1*	stromal interaction molecule 1
8019877	-1,02	9,33E-01	1,18	2,57E-02	1,15	5,82E-02	11,26	2,63E-02	18	*SMCHD1*	structural maintenance of chromosomes flexible hinge domain containing 1
7948192	1,03	8,78E-01	-1,15	3,23E-02	-1,12	1,19E-01	7,11	4,24E-02	11	*SSRP1*	structure specific recognition protein 1
8091811	1,02	8,84E-01	1,07	8,72E-02	1,08	3,06E-02	3,15	3,95E-02	3	*SI*	sucrase-isomaltase (alpha-glucosidase)
7962760	1,01	9,60E-01	-1,15	3,45E-02	-1,14	5,86E-02	8,78	3,35E-02	12	*SENP1*	SUMO1/sentrin specific peptidase 1
8167347	-1,02	9,13E-01	-1,11	6,01E-02	-1,13	2,69E-02	6,41	3,09E-02	X	*SUV39H1*	suppressor of variegation 3-9 homolog 1 (Drosophila)
8163383	1,18	7,34E-02	-1,13	1,16E-01	1,04	7,58E-01	9,06	4,24E-02	9	*SUSD1*	sushi domain containing 1
7966172	1,04	7,64E-01	1,09	1,52E-01	1,14	2,69E-02	4,92	4,41E-02	12	*SVOP*	SV2 related protein homolog (rat)
7955331	1,02	8,82E-01	-1,16	7,12E-03	-1,13	1,89E-02	8,50	4,84E-03	12	*SMARCD1*	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 1
8017460	-1,01	9,70E-01	-1,11	6,39E-02	-1,12	5,34E-02	8,12	4,90E-02	17	*SMARCD2*	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 2
8123006	1,10	3,11E-01	-1,15	2,39E-02	-1,05	6,08E-01	6,75	3,33E-02	6	*SYNJ2*	synaptojanin 2
7950810	1,49	2,66E-03	-1,13	3,59E-01	1,32	1,79E-02	6,25	8,04E-04	11	*SYTL2*	synaptotagmin-like 2
8063839	-1,02	9,02E-01	1,10	2,84E-02	1,09	8,55E-02	6,39	3,39E-02	20	*SS18L1*	synovial sarcoma translocation gene on chromosome 18-like 1
7948864	1,01	9,61E-01	-1,13	2,78E-02	-1,12	4,47E-02	8,60	2,47E-02	11	*STX5*	syntaxin 5

8016600	-1,01	9,70E-01	1,15	4,05E-02	1,14	6,33E-02	6,29	3,94E-02	17	*TAC4*	tachykinin 4 (hemokinin)
8006573	1,12	1,61E-01	1,08	2,39E-01	1,20	1,36E-03	8,89	3,56E-03	17	*TAF15*	TAF15 RNA polymerase II, TATA boxbinding protein (TBP)-associated factor, 68kDa
8141425	1,04	8,10E-01	-1,15	1,18E-02	-1,11	6,17E-02	7,53	1,25E-02	7	*TAF6*	TAF6 RNA polymerase II, TATA boxbinding protein (TBP)-associated factor, 80kDa
7901091	-1,04	8,32E-01	-1,15	6,49E-02	-1,20	1,36E-02	7,82	2,04E-02	1	*TOE1*	target of EGR1, member 1 (nuclear)
7961275	1,32	8,45E-03	1,04	7,59E-01	1,37	7,28E-04	4,14	6,87E-04	12	*TAS2R13*	taste receptor, type 2, member 13
7961279	1,61	3,22E-03	1,08	6,82E-01	1,74	1,07E-04	6,09	1,40E-04	12	*TAS2R14*	taste receptor, type 2, member 14
7961287	1,58	3,88E-02	1,05	8,58E-01	1,66	9,28E-03	5,57	7,63E-03	12	*TAS2R19*	taste receptor, type 2, member 19
7961285	1,68	3,22E-03	-1,01	9,72E-01	1,66	1,30E-03	5,42	5,13E-04	12	*TAS2R20*	taste receptor, type 2, member 20
7961291	1,47	8,27E-02	1,01	9,69E-01	1,48	3,52E-02	5,62	2,52E-02	12	*TAS2R31*	taste receptor, type 2, member 31
8136645	1,27	3,35E-01	1,24	2,03E-01	1,58	3,67E-03	5,17	8,53E-03	7	*TAS2R4*	taste receptor, type 2, member 4
8180320	1,06	9,02E-01	1,45	2,46E-02	1,54	6,98E-03	5,04	7,70E-03	12	*TAS2R45*	taste receptor, type 2, member 45
7961293	1,43	1,14E-01	1,12	6,05E-01	1,60	8,66E-03	3,56	1,18E-02	12	*TAS2R46*	taste receptor, type 2, member 46
8136647	1,12	2,78E-01	1,07	4,22E-01	1,20	1,26E-02	5,40	2,21E-02	7	*TAS2R5*	taste receptor, type 2, member 5
7961281	1,57	9,51E-03	1,02	9,31E-01	1,61	2,48E-03	4,82	1,67E-03	12	*TAS2R50*	taste receptor, type 2, member 50
8158406	1,07	4,04E-01	-1,11	2,93E-02	-1,04	5,61E-01	8,20	4,51E-02	9	*TBC1D13*	TBC1 domain family, member 13
8094476	1,27	2,25E-02	-1,10	3,79E-01	1,16	1,65E-01	7,04	1,73E-02	4	*TBC1D19*	TBC1 domain family, member 19
8064336	1,07	4,98E-01	-1,17	8,75E-03	-1,09	1,85E-01	8,70	1,02E-02	20	*TBC1D20*	TBC1 domain family, member 20
8116348	1,08	4,98E-01	-1,17	1,57E-02	-1,08	3,17E-01	7,40	2,39E-02	5	*TBC1D9B*	TBC1 domain family, member 9B (with GRAM domain)
8092627	1,13	1,47E-01	-1,13	5,72E-02	-1,00	9,90E-01	7,17	4,68E-02	3	*TBCCD1*	TBCC domain containing 1
8008029	1,36	2,70E-02	-1,23	1,12E-01	1,11	5,56E-01	7,82	1,86E-02	17	*TBX21*	T-box 21
8180367	1,28	2,10E-01	-1,42	1,57E-02	-1,11	6,29E-01	10,51	1,88E-02	7	*TARP*	TCR gamma alternate reading frame protein
7935251	1,10	4,22E-01	-1,23	4,07E-03	-1,12	1,26E-01	7,84	4,28E-03	10	*TCTN3*	tectonic family member 3
8002289	1,00	9,84E-01	-1,09	3,63E-02	-1,08	4,95E-02	7,99	3,21E-02	16	*TERF2*	telomeric repeat binding factor 2

8135585	1,29	2,27E-01	1,09	6,24E-01	1,41	2,38E-02	5,89	3,30E-02	7	*LOC100128868*	testin-related protein TRG
8135576	1,17	7,90E-03	-1,08	2,04E-01	1,09	1,62E-01	10,48	5,21E-03	7	*TES*	testis derived transcript (3 LIM domains)
8052925	-1,02	9,36E-01	-1,13	3,62E-02	-1,15	1,64E-02	8,88	1,71E-02	2	*TEX261*	testis expressed 261
7915718	-1,10	2,63E-01	-1,05	4,48E-01	-1,16	1,30E-02	7,79	2,27E-02	1	*TESK2*	testis-specific kinase 2
7928705	1,03	8,41E-01	-1,15	1,75E-02	-1,11	8,41E-02	9,96	2,22E-02	10	*TSPAN14*	tetraspanin 14
7956613	1,06	7,27E-01	-1,19	1,02E-02	-1,13	8,14E-02	8,98	1,08E-02	12	*TSPAN31*	tetraspanin 31
7937782	1,20	1,77E-02	-1,07	3,46E-01	1,12	1,58E-01	8,44	1,37E-02	11	*TSPAN32*	tetraspanin 32
8056995	-1,23	8,56E-02	1,03	8,12E-01	-1,19	1,01E-01	4,91	4,39E-02	2	*TTC30B*	tetratricopeptide repeat domain 30B
8042874	1,11	3,14E-01	-1,17	2,21E-02	-1,05	5,87E-01	6,99	3,09E-02	2	*TTC31*	tetratricopeptide repeat domain 31
8073842	1,49	3,11E-03	-1,22	1,19E-01	1,23	1,29E-01	7,64	1,72E-03	22	*TTC38*	tetratricopeptide repeat domain 38
7996675	1,02	8,89E-01	-1,14	1,74E-02	-1,11	5,84E-02	8,25	1,96E-02	16	*THAP11*	THAP domain containing 11
7904726	-1,03	6,62E-01	-1,04	2,36E-01	-1,07	2,81E-02	13,18	4,93E-02	1	*TXNIP*	thioredoxin interacting protein
7976037	-1,11	4,71E-02	1,05	2,96E-01	-1,05	3,64E-01	4,04	3,77E-02	14	*TSHR*	thyroid stimulating hormone receptor
8026341	1,01	9,48E-01	-1,14	2,19E-02	-1,12	4,19E-02	9,58	1,97E-02	19	*TECR*	trans-2,3-enoyl-CoA reductase
8101622	1,12	2,13E-01	-1,22	4,78E-03	-1,09	3,12E-01	9,00	4,79E-03	19	*TECR*	trans-2,3-enoyl-CoA reductase
8016739	-1,14	5,25E-01	-1,14	2,71E-01	-1,30	1,80E-02	9,59	3,44E-02	17	*TOB1*	transducer of ERBB2, 1
8139468	1,12	2,02E-01	-1,15	4,39E-02	-1,02	8,89E-01	7,65	4,56E-02	7	*TBRG4*	transforming growth factor beta regulator 4
7917649	1,64	1,09E-02	-1,34	1,04E-01	1,22	3,87E-01	8,63	7,70E-03	1	*TGFBR3*	transforming growth factor, beta receptor III
7971104	-1,08	2,24E-01	1,10	4,25E-02	1,02	8,59E-01	3,84	4,66E-02	13	*TRPC4*	transient receptor potential cation channel, subfamily C, member 4
8005171	1,22	1,16E-02	-1,16	4,59E-02	1,05	6,38E-01	7,49	6,52E-03	17	*TRPV2*	transient receptor potential cation channel, subfamily V, member 2
8003627	1,05	7,50E-01	-1,16	2,47E-02	-1,10	1,97E-01	8,79	3,83E-02	17	*TIMM22*	translocase of inner mitochondrial membrane 22 homolog (yeast)
8028705	1,06	6,26E-01	-1,14	2,48E-02	-1,07	3,09E-01	8,48	4,09E-02	19	*TIMM50*	translocase of inner mitochondrial membrane 50 homolog (S. cerevisiae)

8073032	-1,00	9,98E-01	-1,21	3,30E-03	-1,21	1,29E-03	6,72	6,92E-04	22	*TOMM22*	translocase of outer mitochondrial membrane 22 homolog (yeast)
7978166	1,01	9,50E-01	-1,15	1,66E-02	-1,13	3,06E-02	8,79	1,42E-02	14	*TM9SF1*	transmembrane 9 superfamily member 1
7955277	-1,02	9,05E-01	-1,12	3,90E-02	-1,15	1,32E-02	11,89	1,56E-02	12	*TMBIM6*	transmembrane BAX inhibitor motif containing 6
8010212	1,14	1,02E-01	-1,13	7,75E-02	1,02	9,15E-01	9,24	4,41E-02	17	*TMC8*	transmembrane channel-like 8
8012383	1,04	7,88E-01	-1,14	1,82E-02	-1,10	1,22E-01	6,63	2,56E-02	17	*TMEM107*	transmembrane protein 107
7940372	1,09	5,75E-01	-1,24	6,22E-03	-1,14	1,02E-01	9,75	6,48E-03	11	*TMEM109*	transmembrane protein 109
8087685	-1,02	9,08E-01	-1,12	5,68E-02	-1,14	2,43E-02	8,49	2,77E-02	3	*TMEM115*	transmembrane protein 115
7954985	1,14	8,40E-02	-1,11	1,04E-01	1,03	8,19E-01	5,63	4,48E-02	12	*TMEM117*	transmembrane protein 117
7940473	1,10	5,51E-02	-1,15	1,18E-03	-1,05	2,89E-01	8,68	6,92E-04	11	*TMEM138*	transmembrane protein 138
8091546	1,21	5,44E-01	1,26	1,71E-01	1,52	8,83E-03	6,41	1,81E-02	3	*TMEM14E*	transmembrane protein 14E
8114536	1,09	5,06E-01	-1,18	2,29E-02	-1,08	4,03E-01	8,78	3,65E-02	5	*TMEM173*	transmembrane protein 173
8123062	1,25	4,30E-03	-1,13	1,07E-01	1,11	2,16E-01	9,21	3,06E-03	6	*TMEM181*	transmembrane protein 181
8175621	1,04	8,47E-01	-1,18	2,24E-02	-1,13	1,02E-01	7,25	2,87E-02	X	*TMEM185A*	transmembrane protein 185A
8165486	1,02	9,45E-01	-1,20	6,22E-03	-1,18	8,04E-03	8,27	3,06E-03	9	*TMEM203*	transmembrane protein 203
8142912	1,01	9,56E-01	-1,20	1,03E-02	-1,19	1,28E-02	9,34	5,23E-03	7	*TMEM209*	transmembrane protein 209
7899675	1,06	5,17E-01	-1,12	2,44E-02	-1,05	4,10E-01	7,28	3,94E-02	1	*TMEM39B*	transmembrane protein 39B
8092534	1,11	2,83E-01	-1,15	3,86E-02	-1,03	7,68E-01	7,70	4,96E-02	3	*TMEM41A*	transmembrane protein 41A
7901135	-1,04	8,35E-01	-1,15	4,97E-02	-1,20	9,77E-03	8,10	1,43E-02	1	*TMEM69*	transmembrane protein 69
7982507	1,11	2,52E-01	-1,17	1,81E-02	-1,05	6,08E-01	9,69	2,39E-02	15	*TMEM85*	transmembrane protein 85
8040365	1,09	6,63E-01	-1,21	2,70E-02	-1,12	2,94E-01	8,63	4,49E-02	2	*TRIB2*	tribbles homolog 2 (Drosophila)
8162729	1,10	3,54E-01	-1,17	2,44E-02	-1,06	5,67E-01	8,35	3,53E-02	9	*TRIM14*	tripartite motif-containing 14
7938057	-1,19	4,94E-02	1,09	2,73E-01	-1,09	4,03E-01	4,30	3,94E-02	11	*TRIM22*	tripartite motif-containing 22
7911218	-1,04	9,39E-01	-1,29	5,34E-02	-1,33	2,95E-02	10,63	3,09E-02	1	*TRIM58*	tripartite motif-containing 58

7945979	1,07	7,53E-01	-1,23	2,71E-02	-1,14	2,09E-01	7,52	4,29E-02	11	*TRIM68*	tripartite motif-containing 68
7908147	1,16	6,93E-02	-1,02	7,85E-01	1,13	9,14E-02	8,04	3,53E-02	1	*TSEN15*	tRNA splicing endonuclease 15 homolog (S. cerevisiae)
8009832	1,27	3,50E-03	-1,14	8,06E-02	1,11	2,47E-01	7,87	2,52E-03	17	*TSEN54*	tRNA splicing endonuclease 54 homolog (S. cerevisiae)
7920472	1,08	7,65E-01	1,19	9,20E-02	1,28	1,28E-02	7,54	2,18E-02	1	*TPM3*	tropomyosin 3
8129099	-1,02	9,19E-01	-1,10	6,54E-02	-1,12	3,15E-02	9,88	3,53E-02	6	*TSPYL1*	TSPY-like 1
8129089	-1,07	5,36E-01	-1,07	2,71E-01	-1,15	1,89E-02	7,07	3,56E-02	6	*TSPYL4*	TSPY-like 4
8167790	1,05	8,25E-01	-1,21	1,60E-02	-1,16	8,29E-02	7,33	1,97E-02	X	*TSR2*	TSR2, 20S rRNA accumulation, homolog (S. cerevisiae)
8095868	1,14	3,25E-01	1,06	5,67E-01	1,20	3,23E-02	4,20	4,87E-02	4	*UNQ3028*	TSSP3028
7953135	1,14	3,21E-01	-1,24	1,50E-02	-1,09	4,71E-01	6,59	2,03E-02	12	*TULP3*	tubby like protein 3
8179174	1,02	9,13E-01	-1,12	3,91E-02	-1,10	1,09E-01	11,51	4,90E-02	6	*TUBB*	tubulin, beta
8007302	1,07	5,23E-01	-1,19	3,76E-03	-1,11	7,81E-02	7,88	3,70E-03	17	*TUBG1*	tubulin, gamma 1
8007312	1,04	8,00E-01	-1,14	2,41E-02	-1,09	1,48E-01	6,79	3,47E-02	17	*TUBG2*	tubulin, gamma 2
8163629	-1,12	3,90E-01	-1,08	3,62E-01	-1,21	1,65E-02	9,88	3,08E-02	9	*TNFSF8*	tumor necrosis factor (ligand) superfamily, member 8
8149749	-1,16	1,47E-02	-1,02	7,87E-01	-1,19	1,83E-03	7,64	1,88E-03	8	*TNFRSF10D*	tumor necrosis factor receptor superfamily, member 10d, decoy with truncated death domain
8012257	1,07	7,27E-01	-1,20	2,17E-02	-1,13	1,87E-01	8,92	3,29E-02	17	*TP53*	tumor protein p53
8087669	1,22	2,25E-02	-1,13	1,21E-01	1,08	4,90E-01	7,32	1,64E-02	3	*TUSC4*	tumor suppressor candidate 4
8100210	1,38	8,77E-03	-1,08	5,52E-01	1,28	3,55E-02	8,55	4,84E-03	4	*TXK*	TXK tyrosine kinase
8075106	1,18	8,77E-03	-1,13	4,47E-02	1,05	5,76E-01	9,17	4,84E-03	22	*TPST2*	tyrosylprotein sulfotransferase 2
7914563	1,10	3,78E-01	-1,22	7,12E-03	-1,10	2,35E-01	8,17	8,26E-03	1	*YARS*	tyrosyl-tRNA synthetase
8167924	-1,03	8,25E-01	-1,08	6,48E-02	-1,11	1,28E-02	9,35	1,93E-02	X	*UBQLN2*	ubiquilin 2
8087100	1,01	9,71E-01	-1,14	3,81E-02	-1,13	5,92E-02	6,98	3,56E-02	3	*UQCRC1*	ubiquinol-cytochrome c reductase core protein I
7993872	-1,00	9,85E-01	-1,10	2,68E-02	-1,10	2,12E-02	10,53	1,64E-02	16	*UQCRC2*	ubiquinol-cytochrome c reductase core protein II
7905700	1,01	9,26E-01	-1,10	2,98E-02	-1,09	7,26E-02	9,79	3,32E-02	1	*UBAP2L*	ubiquitin associated protein 2-like

7976336	-1,00	9,96E-01	-1,23	3,39E-02	-1,23	3,35E-02	7,07	2,43E-02	14	*UBR7*	ubiquitin protein ligase E3 component n-recognin 7 (putative)
8167125	1,17	5,77E-02	-1,20	1,17E-02	-1,03	8,22E-01	8,52	7,27E-03	X	*USP11*	ubiquitin specific peptidase 11
7906671	1,02	9,08E-01	-1,14	2,80E-02	-1,11	7,83E-02	8,30	3,24E-02	1	*USP21*	ubiquitin specific peptidase 21
7951752	1,28	5,19E-02	-1,26	3,51E-02	1,01	9,62E-01	8,31	1,79E-02	11	*USP28*	ubiquitin specific peptidase 28
8058940	1,04	8,10E-01	-1,15	2,82E-02	-1,10	1,62E-01	7,20	4,16E-02	2	*USP37*	ubiquitin specific peptidase 37
8043218	1,05	6,87E-01	-1,14	1,55E-02	-1,08	1,69E-01	8,11	2,21E-02	2	*USP39*	ubiquitin specific peptidase 39
7953483	1,10	2,40E-01	-1,20	3,68E-03	-1,09	2,21E-01	6,93	3,54E-03	12	*USP5*	ubiquitin specific peptidase 5 (isopeptidase T)
8008139	1,06	6,29E-01	-1,16	1,11E-02	-1,10	1,47E-01	9,50	1,39E-02	17	*UBE2Z*	ubiquitin-conjugating enzyme E2Z
7990361	1,06	6,48E-01	-1,20	4,93E-03	-1,13	5,99E-02	8,91	4,77E-03	15	*UBL7*	ubiquitin-like 7 (bone marrow stromal cell-derived)
8087485	1,09	2,86E-01	-1,14	1,65E-02	-1,05	5,41E-01	9,20	2,25E-02	3	*UBA7*	ubiquitin-like modifier activating enzyme 7
8146544	-1,11	6,10E-01	1,25	2,93E-02	1,12	3,63E-01	9,15	4,93E-02	8	*UBXN2B*	UBX domain protein 2B
7921806	-1,01	9,64E-01	-1,16	3,73E-02	-1,18	2,59E-02	9,10	2,25E-02	1	*B4GALT3*	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 3
8086352	1,19	2,36E-02	1,01	9,15E-01	1,21	6,97E-03	6,60	4,73E-03	3	*ULK4*	unc-51-like kinase 4 (C. elegans)
7950307	1,09	3,53E-01	-1,14	3,35E-02	-1,04	6,50E-01	11,43	4,79E-02	11	*UCP2*	uncoupling protein 2 (mitochondrial, proton carrier)
7958455	1,13	1,56E-01	-1,15	3,66E-02	-1,02	9,06E-01	6,14	3,44E-02	12	*UNG*	uracil-DNA glycosylase
8067756	1,05	6,97E-01	-1,14	2,42E-02	-1,08	2,44E-01	7,56	3,89E-02	20	*UCKL1*	uridine-cytidine kinase 1-like 1
7936937	1,03	8,70E-01	-1,14	3,39E-02	-1,11	1,34E-01	7,96	4,59E-02	10	*UROS*	uroporphyrinogen III synthase
8122464	1,17	6,54E-02	1,02	8,36E-01	1,20	1,36E-02	9,71	1,26E-02	6	*UTRN*	utrophin
7944382	1,10	2,37E-01	-1,19	3,87E-03	-1,08	2,45E-01	8,94	3,92E-03	11	*VPS11*	vacuolar protein sorting 11 homolog (S. cerevisiae)
8007355	1,04	7,94E-01	-1,16	1,28E-02	-1,12	7,94E-02	8,26	1,54E-02	17	*VPS25*	vacuolar protein sorting 25 homolog (S. cerevisiae)
7987840	-1,04	6,26E-01	-1,06	2,04E-01	-1,10	1,80E-02	9,43	3,41E-02	15	*VPS39*	vacuolar protein sorting 39 homolog (S. cerevisiae)
8180123	1,15	7,80E-02	-1,15	3,79E-02	1,00	9,95E-01	8,92	2,36E-02	6	*VPS52*	vacuolar protein sorting 52 homolog (S. cerevisiae)
8036840	1,03	8,38E-01	-1,12	2,22E-02	-1,09	1,05E-01	9,53	2,87E-02	19	*AKT2*	v-akt murine thymoma viral oncogene homolog 2

8165658	-1,02	9,56E-01	-1,24	6,73E-02	-1,28	4,62E-02	8,15	4,64E-02	7	*VIPR2*	vasoactive intestinal peptide receptor 2
8164967	-1,10	5,13E-01	-1,12	1,74E-01	-1,24	7,83E-03	6,77	1,64E-02	9	*VAV2*	vav 2 guanine nucleotide exchange factor
8115732	1,08	6,05E-01	1,19	1,81E-02	1,29	3,31E-04	4,99	8,09E-04	5	*UNQ9374*	VCEW9374
8055060	1,08	6,34E-01	1,10	2,33E-01	1,20	2,35E-02	9,29	4,28E-02	2	*WDR33*	WD repeat domain 33
8178939	1,11	1,74E-01	-1,15	2,19E-02	-1,03	7,69E-01	7,24	2,32E-02	6	*WDR46*	WD repeat domain 46
8002802	1,10	2,26E-01	-1,13	3,02E-02	-1,03	7,79E-01	7,61	3,53E-02	16	*WDR59*	WD repeat domain 59
8021312	1,18	1,51E-02	-1,05	5,26E-01	1,13	6,69E-02	8,48	9,60E-03	18	*WDR7*	WD repeat domain 7
7948881	1,08	6,31E-01	-1,19	2,17E-02	-1,10	2,72E-01	8,44	3,44E-02	11	*WDR74*	WD repeat domain 74
8006906	1,29	1,48E-02	-1,16	1,41E-01	1,12	3,67E-01	6,48	1,15E-02	17	*ERBB2*	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian)
7930524	1,12	6,15E-02	1,05	4,29E-01	1,17	1,52E-03	7,93	3,06E-03	10	*VTI1A*	vesicle transport through interaction with t-SNAREs homolog 1A (yeast)
8068593	-1,29	2,23E-02	1,13	2,70E-01	-1,15	2,49E-01	8,81	1,75E-02	21	*ETS2*	v-ets erythroblastosis virus E26 oncogene homolog 2 (avian)
8000998	1,08	5,61E-01	-1,17	1,66E-02	-1,09	2,83E-01	9,70	2,64E-02	16	*VKORC1*	vitamin K epoxide reductase complex, subunit 1
8066266	-1,21	7,07E-02	1,05	6,87E-01	-1,16	1,33E-01	7,70	4,15E-02	20	*MAFB*	v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian)
8122202	-1,08	6,16E-01	-1,11	1,70E-01	-1,20	1,28E-02	7,54	2,48E-02	6	*MYB*	v-myb myeloblastosis viral oncogene homolog (avian)
8151101	1,62	3,22E-03	-1,19	2,64E-01	1,35	5,08E-02	9,07	1,85E-03	8	*MYBL1*	v-myb myeloblastosis viral oncogene homolog (avian)-like 1
8053599	1,02	9,09E-01	-1,12	2,00E-02	-1,10	5,33E-02	8,61	2,03E-02	2	*WBP1*	WW domain binding protein 1
8033392	1,09	3,52E-01	-1,17	1,12E-02	-1,07	3,46E-01	8,48	1,39E-02	19	*XAB2*	XPA binding protein 2
7936284	1,18	5,19E-02	-1,20	1,47E-02	-1,02	9,02E-01	8,58	8,91E-03	10	*XPNPEP1*	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble
7949577	1,03	8,59E-01	-1,14	1,41E-02	-1,11	5,60E-02	7,90	1,49E-02	11	*YIF1A*	Yip1 interacting factor homolog A (S. cerevisiae)
8074780	1,32	1,13E-02	-1,24	3,61E-02	1,07	6,89E-01	7,70	5,45E-03	22	*YPEL1*	yippee-like 1 (Drosophila)
8008819	-1,15	4,94E-02	-1,01	8,89E-01	-1,17	1,37E-02	8,90	1,12E-02	17	*YPEL2*	yippee-like 2 (Drosophila)
8067593	-1,03	7,69E-01	-1,07	1,47E-01	-1,11	2,69E-02	9,18	4,36E-02	20	*YTHDF1*	YTH domain family, member 1
8043725	1,29	1,83E-02	-1,22	4,97E-02	1,06	7,00E-01	9,01	9,68E-03	2	*ZAP70*	zeta-chain (TCR) associated protein kinase 70kDa

8132062	1,06	4,47E-01	1,05	2,94E-01	1,12	1,43E-02	8,61	2,78E-02	7	*ZNRF2*	zinc and ring finger 2
8089701	1,22	1,13E-01	1,02	8,59E-01	1,25	2,78E-02	7,64	2,52E-02	3	*ZBTB20*	zinc finger and BTB domain containing 20
7907486	1,13	2,39E-01	1,11	1,46E-01	1,26	1,13E-03	7,37	3,11E-03	1	*ZBTB37*	zinc finger and BTB domain containing 37
8073397	1,05	4,51E-01	-1,13	4,22E-03	-1,07	1,19E-01	8,43	4,54E-03	22	*ZC3H7B*	zinc finger CCCH-type containing 7B
8055639	1,56	1,95E-02	1,30	1,48E-01	2,02	2,90E-05	6,89	1,22E-04	2	*ZEB2*	zinc finger E-box binding homeobox 2
8143733	1,13	2,35E-01	1,05	6,08E-01	1,19	2,36E-02	7,83	3,34E-02	7	*ZNF767*	zinc finger family member 767
7923183	-1,24	2,06E-02	1,03	8,12E-01	-1,21	2,68E-02	8,78	8,36E-03	1	*ZNF281*	zinc finger protein 281
8120992	1,01	9,54E-01	1,12	5,27E-02	1,14	3,42E-02	9,43	3,37E-02	6	*ZNF292*	zinc finger protein 292
8065517	1,17	8,56E-02	-1,02	8,37E-01	1,14	9,23E-02	6,81	4,19E-02	20	*ZNF337*	zinc finger protein 337
8028652	-1,24	2,06E-02	-1,01	9,56E-01	-1,25	7,58E-03	10,48	4,54E-03	19	*ZFP36*	zinc finger protein 36, C3H type, homolog (mouse)
7899870	1,03	8,77E-01	-1,15	2,68E-02	-1,11	1,01E-01	8,01	3,43E-02	1	*ZNF362*	zinc finger protein 362
7975645	1,07	6,21E-01	-1,16	2,26E-02	-1,08	2,90E-01	7,93	3,62E-02	14	*ZNF410*	zinc finger protein 410
8040985	-1,11	4,56E-01	-1,08	4,01E-01	-1,19	2,87E-02	8,38	4,90E-02	2	*ZNF512*	zinc finger protein 512
8099364	-1,17	9,76E-02	1,01	9,33E-01	-1,15	6,85E-02	8,52	3,94E-02	4	*ZNF518B*	zinc finger protein 518B
8029182	-1,01	9,58E-01	-1,13	2,42E-02	-1,15	1,29E-02	7,03	1,14E-02	19	*ZNF574*	zinc finger protein 574
8031522	-1,07	4,93E-01	-1,06	2,97E-01	-1,13	1,80E-02	6,44	3,43E-02	19	*ZNF581*	zinc finger protein 581
8067094	1,03	8,21E-01	-1,13	2,83E-02	-1,09	1,52E-01	6,69	4,09E-02	20	*ZFP64*	zinc finger protein 64 homolog (mouse)
7900461	1,09	3,58E-01	-1,15	1,65E-02	-1,06	4,60E-01	4,53	2,40E-02	1	*ZNF684*	zinc finger protein 684
8073943	-1,12	1,44E-01	-1,04	5,69E-01	-1,16	9,78E-03	7,40	1,46E-02	22	*ZBED4*	zinc finger, BED-type containing 4
8144758	1,01	9,72E-01	-1,25	2,07E-02	-1,24	2,87E-02	9,69	1,56E-02	8	*ZDHHC2*	zinc finger, DHHC-type containing 2
7940051	-1,02	9,03E-01	-1,09	5,90E-02	-1,11	2,38E-02	8,68	2,79E-02	11	*ZDHHC5*	zinc finger, DHHC-type containing 5
8173457	1,02	8,91E-01	-1,13	3,68E-02	-1,10	1,20E-01	7,25	4,83E-02	X	*ZMYM3*	zinc finger, MYM-type 3
8090364	-1,00	9,91E-01	1,20	3,86E-02	1,19	4,82E-02	6,35	3,31E-02	3	*ZXDC*	ZXD family zinc finger C

7928547	-1,02	9,44E-01	1,17	2,02E-02	1,15	4,03E-02	10,38	1,82E-02	10	---	---
8180418	1,01	9,56E-01	-1,14	3,90E-02	-1,13	7,47E-02	9,69	4,09E-02	---	---	---
7995328	-1,03	9,15E-01	1,20	3,06E-02	1,17	8,21E-02	8,52	3,51E-02	16	---	---
7919129	1,19	5,26E-01	1,20	2,34E-01	1,42	1,35E-02	8,49	2,68E-02	1	---	---
7995330	-1,03	9,11E-01	1,17	3,97E-02	1,14	1,12E-01	8,32	4,98E-02	16	---	---
7989218	-1,13	7,84E-01	1,84	1,33E-03	1,62	5,71E-03	8,31	6,57E-04	15	---	---
8003465	-1,01	9,75E-01	1,16	1,27E-02	1,15	1,37E-02	8,27	7,04E-03	16	---	---
8063549	-1,05	8,30E-01	1,22	1,65E-02	1,16	8,23E-02	8,12	2,02E-02	20	---	---
8154227	1,25	4,83E-01	1,29	1,60E-01	1,62	5,67E-03	8,01	1,26E-02	9	---	---
8100962	1,02	9,45E-01	1,17	2,51E-02	1,19	1,13E-02	7,94	1,08E-02	4	---	---
7897661	1,00	9,90E-01	1,12	4,39E-02	1,12	4,12E-02	7,85	3,29E-02	1	---	---
7970565	-1,01	9,71E-01	1,19	1,18E-02	1,18	1,28E-02	7,74	6,23E-03	13	---	---
8154207	1,29	2,41E-01	1,32	8,27E-02	1,71	3,82E-04	7,73	1,32E-03	9	---	---
7977103	-1,03	9,05E-01	1,27	4,78E-03	1,23	8,83E-03	7,73	2,58E-03	14	---	---
7911047	1,00	9,85E-01	1,13	5,85E-02	1,13	5,71E-02	7,52	4,87E-02	1	---	---
8042306	1,15	6,93E-01	1,42	2,29E-02	1,63	8,58E-04	7,37	1,89E-03	2	---	---
8154209	1,24	3,18E-01	1,16	3,49E-01	1,44	1,03E-02	7,37	1,98E-02	9	---	---
8164694	1,10	8,32E-01	1,34	8,27E-02	1,47	1,87E-02	7,23	2,72E-02	9	---	---
8175438	1,02	9,56E-01	1,22	4,62E-02	1,24	2,89E-02	7,21	2,70E-02	X	---	---
8154868	-1,05	9,11E-01	1,47	1,17E-02	1,40	2,50E-02	7,19	8,26E-03	9	---	---
8091809	-1,02	9,43E-01	1,23	1,56E-02	1,21	2,90E-02	7,18	1,23E-02	3	---	---
8163424	1,06	8,48E-01	1,25	2,94E-02	1,32	4,81E-03	7,18	6,76E-03	9	---	---
7979127	1,01	9,61E-01	1,22	5,76E-03	1,24	1,50E-03	7,09	1,23E-03	14	---	---

8105321	1,18	2,33E-01	1,22	4,22E-02	1,44	9,20E-05	6,84	3,81E-04	5	---	---
7934717	1,27	2,02E-01	1,32	4,13E-02	1,68	6,80E-05	6,76	2,88E-04	---	---	---
8013915	1,01	9,58E-01	1,18	1,16E-02	1,19	3,99E-03	6,76	3,42E-03	17	---	---
8099668	-1,02	9,58E-01	1,27	2,78E-02	1,24	4,80E-02	6,75	2,56E-02	4	---	---
8071595	1,00	9,95E-01	1,16	3,62E-02	1,17	3,52E-02	6,58	2,63E-02	22	---	---
7972215	1,31	1,51E-01	1,30	7,29E-02	1,69	1,10E-04	6,47	5,07E-04	13	---	---
7974479	1,02	9,64E-01	1,22	4,25E-02	1,24	2,95E-02	6,46	2,63E-02	14	---	---
8098547	1,25	1,69E-01	1,07	6,54E-01	1,34	1,75E-02	6,43	2,31E-02	4	---	---
8129675	1,00	9,85E-01	1,14	3,72E-02	1,15	3,17E-02	6,28	2,54E-02	6	---	---
8117698	-1,01	9,58E-01	1,16	1,71E-02	1,15	2,83E-02	6,26	1,39E-02	6	---	---
7917672	1,02	9,10E-01	1,16	9,29E-03	1,18	1,55E-03	6,21	1,75E-03	1	---	---
7995346	-1,08	5,46E-01	1,17	1,57E-02	1,09	2,79E-01	6,20	2,39E-02	16	---	---
7933113	1,01	9,94E-01	1,35	3,39E-02	1,36	3,07E-02	6,15	2,32E-02	10	---	---
7975455	1,06	8,83E-01	1,33	1,85E-02	1,40	3,66E-03	6,11	4,55E-03	14	---	---
8059578	1,17	3,41E-01	1,12	3,37E-01	1,31	1,11E-02	6,10	2,15E-02	2	---	---
8114898	1,63	1,52E-02	-1,25	2,49E-01	1,30	2,22E-01	6,02	1,24E-02	5	---	---
7945069	1,02	9,33E-01	1,16	1,41E-02	1,19	4,15E-03	5,94	4,16E-03	11	---	---
7933634	1,30	2,86E-01	1,46	2,48E-02	1,90	6,70E-05	5,85	2,47E-04	10	---	---
8142405	1,05	8,36E-01	1,17	8,72E-02	1,24	2,08E-02	5,83	3,04E-02	7	---	---
7969772	1,01	9,83E-01	1,14	6,03E-02	1,15	5,71E-02	5,81	4,93E-02	13	---	---
8104607	1,02	9,82E-01	2,22	1,18E-03	2,27	2,31E-04	5,80	1,40E-04	5	---	---
8174977	1,01	9,57E-01	1,13	4,53E-02	1,14	2,90E-02	5,79	2,68E-02	X	---	---
8124055	1,05	8,55E-01	1,20	4,93E-02	1,25	1,07E-02	5,77	1,50E-02	6	---	---

8146328	1,10	5,69E-01	1,11	2,60E-01	1,23	2,10E-02	5,77	3,89E-02	8	---	---
8173162	1,10	7,81E-01	1,23	1,35E-01	1,35	2,62E-02	5,76	4,13E-02	X	---	---
8027429	1,30	2,13E-01	1,05	7,89E-01	1,37	4,35E-02	5,71	4,80E-02	19	---	---
8001680	-1,06	7,90E-01	1,22	2,23E-02	1,15	1,44E-01	5,62	3,23E-02	16	---	---
8100941	1,23	7,43E-01	1,43	1,80E-01	1,75	2,95E-02	5,60	4,96E-02	4	---	---
8151764	1,07	7,75E-01	1,21	3,61E-02	1,29	3,37E-03	5,58	5,74E-03	8	---	---
8180252	1,02	9,00E-01	1,13	3,12E-02	1,16	9,28E-03	5,57	1,07E-02	---	---	---
8091552	1,05	7,09E-01	1,10	1,28E-01	1,15	1,49E-02	5,49	2,68E-02	3	---	---
7950762	-1,04	8,76E-01	1,22	2,68E-02	1,16	1,03E-01	5,45	3,47E-02	11	---	---
8097472	-1,05	7,75E-01	1,19	1,42E-02	1,13	9,75E-02	5,33	1,80E-02	4	---	---
8102869	1,02	9,41E-01	1,14	6,23E-02	1,16	3,56E-02	5,21	3,74E-02	4	---	---
8128549	1,14	2,29E-01	1,04	6,32E-01	1,19	2,54E-02	5,15	3,44E-02	6	---	---
8047241	-1,03	9,30E-01	1,24	2,68E-02	1,21	6,18E-02	4,96	2,77E-02	2	---	---
7989193	1,09	8,75E-01	1,37	6,48E-02	1,49	1,88E-02	4,94	2,53E-02	15	---	---
8026420	-1,00	9,93E-01	1,15	4,93E-02	1,15	6,21E-02	4,90	4,48E-02	19	---	---
8159961	1,49	1,24E-01	1,18	4,73E-01	1,76	4,63E-03	4,88	7,99E-03	9	---	---
8142464	1,05	8,90E-01	1,36	1,18E-02	1,43	1,83E-03	4,88	2,42E-03	7	---	---
7907966	1,00	9,94E-01	1,23	2,41E-02	1,23	2,07E-02	4,87	1,48E-02	1	---	---
8008038	1,13	6,11E-01	1,20	1,28E-01	1,36	8,09E-03	4,86	1,64E-02	17	---	---
8166351	-1,05	8,17E-01	1,19	2,43E-02	1,14	1,34E-01	4,85	3,43E-02	X	---	---
8121269	1,14	3,66E-02	1,10	9,04E-02	1,26	2,90E-05	4,83	1,22E-04	6	---	---
7945942	1,06	8,75E-01	1,22	9,15E-02	1,30	2,94E-02	4,78	3,94E-02	11	---	---
7925448	1,12	5,27E-01	1,16	1,49E-01	1,30	6,65E-03	4,77	1,40E-02	1	---	---

8154217	1,22	2,35E-01	1,08	5,59E-01	1,33	1,86E-02	4,74	2,76E-02	9	---	---
8136059	-1,00	9,94E-01	1,16	3,50E-02	1,16	4,12E-02	4,70	2,76E-02	7	---	---
7948033	1,01	9,63E-01	1,18	5,70E-02	1,20	4,36E-02	4,69	4,06E-02	11	---	---
8171203	-1,01	9,64E-01	1,20	1,56E-02	1,19	2,10E-02	4,67	1,05E-02	X	---	---
8129390	1,12	7,37E-01	1,38	2,60E-02	1,55	1,50E-03	4,65	3,06E-03	6	---	---
7932612	-1,03	9,02E-01	1,16	2,67E-02	1,13	7,93E-02	4,64	3,09E-02	10	---	---
8120756	1,28	6,26E-01	1,38	1,92E-01	1,76	1,63E-02	4,61	3,11E-02	6	---	---
8157281	1,04	8,92E-01	1,16	9,06E-02	1,20	3,58E-02	4,54	4,52E-02	9	---	---
8146788	1,00	9,96E-01	1,21	3,49E-02	1,21	3,52E-02	4,54	2,56E-02	8	---	---
7934883	1,00	9,94E-01	1,14	3,38E-02	1,15	3,06E-02	4,54	2,32E-02	10	---	---
8180204	1,12	8,63E-02	1,03	6,64E-01	1,15	8,71E-03	4,50	1,08E-02	---	---	---
8136932	1,13	6,79E-01	1,21	1,44E-01	1,37	1,36E-02	4,48	2,58E-02	7	---	---
8051462	1,24	2,08E-01	1,04	7,85E-01	1,29	4,23E-02	4,44	4,60E-02	2	---	---
8168731	1,08	6,79E-01	1,12	2,01E-01	1,21	2,31E-02	4,39	4,12E-02	X	---	---
7962246	1,02	9,28E-01	1,16	5,02E-02	1,19	2,43E-02	4,35	2,60E-02	12	---	---
7925056	1,03	9,70E-01	1,61	2,29E-02	1,65	1,39E-02	4,35	1,15E-02	1	---	---
7948037	1,15	5,20E-01	1,16	2,24E-01	1,32	1,21E-02	4,29	2,39E-02	11	---	---
8155528	1,33	3,74E-01	1,28	2,41E-01	1,71	6,89E-03	4,19	1,43E-02	9	---	---
7923440	1,14	8,90E-01	1,90	3,76E-02	2,16	1,07E-02	4,17	1,30E-02	1	---	---
7997498	-1,04	7,93E-01	1,15	2,85E-02	1,10	1,78E-01	4,14	4,37E-02	16	---	---
7959144	1,06	6,62E-01	1,08	1,97E-01	1,14	2,07E-02	4,11	3,74E-02	12	---	---
8139778	-1,01	9,71E-01	1,23	1,11E-02	1,22	1,11E-02	3,98	5,14E-03	7	---	---
8097809	1,04	7,39E-01	1,10	6,95E-02	1,15	7,32E-03	3,97	1,28E-02	4	---	---

8143599	1,18	4,33E-01	1,16	2,76E-01	1,37	1,21E-02	3,91	2,37E-02	7	---	---
7916725	-1,05	8,28E-01	1,19	2,52E-02	1,14	1,29E-01	3,78	3,51E-02	1	---	---
7907964	1,22	4,24E-01	1,18	2,98E-01	1,44	1,32E-02	3,73	2,58E-02	1	---	---
8142169	1,12	4,62E-01	1,19	4,69E-02	1,32	6,46E-04	3,60	1,89E-03	7	---	---
7979414	1,11	3,54E-01	1,09	2,46E-01	1,22	6,36E-03	3,30	1,34E-02	14	---	---
8045559	1,02	9,70E-01	1,42	2,17E-02	1,45	1,28E-02	3,27	1,03E-02	2	---	---
7942985	1,05	7,59E-01	1,10	1,40E-01	1,16	2,29E-02	3,22	3,79E-02	11	---	---
7946328	1,14	5,87E-01	1,16	2,23E-01	1,32	1,71E-02	3,15	3,31E-02	11	---	---
7942525	1,00	9,94E-01	1,15	4,41E-02	1,16	4,37E-02	3,01	3,43E-02	11	---	---
8082572	1,05	8,61E-01	1,28	1,43E-02	1,35	1,72E-03	2,88	2,58E-03	3	---	---
8055594	1,08	8,04E-01	1,30	2,00E-02	1,41	1,72E-03	2,82	3,06E-03	2	---	---
8114213	-1,20	1,94E-01	-1,14	2,24E-01	-1,36	1,57E-03	2,82	4,16E-03	5	---	---
8151205	-1,11	2,59E-01	-1,04	6,08E-01	-1,16	2,81E-02	2,78	3,89E-02	8	---	---
8053364	-1,03	8,02E-01	1,12	3,05E-02	1,08	1,83E-01	2,72	4,66E-02	2	---	---

Abbreviations in order of appearance: CA, controlled asthma; Ctrl, healthy controls; SA, severe asthma; FC, fold change; AveExpr, average expression value; F, F-test statistics, Chr, chromosome. *Benjamini and Hochberg's correction for multiple testing.