

**Supplementary Table S5.**

List of genes differentially expressed between sole +8 versus cytogenetically normal de novo acute myeloid leukemia patients

Symbol	Name	EntrezID	Fold-change	Parametric p-value
DPYSL2	dihydropyrimidinase-like 2	1808	2,07	2,66E-05
APP	amyloid beta (A4) precursor protein	351	2,06	3,19E-05
BAALC	brain and acute leukemia, cytoplasmic	79870	2,04	2,14E-05
GJA1	gap junction protein, alpha 1, 43kDa	2697	2,01	8,73E-05
RBPMS	RNA binding protein with multiple splicing	11030	1,97	5,30E-06
ADM	adrenomedullin	133	1,94	7,52E-05
EPS8	epidermal growth factor receptor pathway substrate 8	2059	1,88	2,84E-05
FZD6	frizzled family receptor 6	8323	1,86	1,71E-05
BEND4	BEN domain containing 4	389206	1,86	0,0001169
CPNE3	copine III	8895	1,85	< 1e-07
ADAMTSL4	ADAMTS-like 4	54507	1,85	3,00E-07
FAM169A	family with sequence similarity 169, member A	26049	1,82	2,00E-07
LY96	lymphocyte antigen 96	23643	1,82	6,36E-05
H1FO	H1 histone family, member 0	3005	1,82	0,0001257
KLF9	Kruppel-like factor 9	687	1,81	< 1e-07
GPR124	G protein-coupled receptor 124	25960	1,8	4,50E-06
ABCB1	ATP-binding cassette, sub-family B (MDR/TAP), member 1	5243	1,79	0,0001236
ID1	inhibitor of DNA binding 1, dominant negative helix-loop-helix	3397	1,78	1,41E-05
PLSCR4	phospholipid scramblase 4	57088	1,76	6,00E-06
SCRN1	secernin 1	9805	1,75	0,0006492
MFHAS1	malignant fibrous histiocytoma amplified sequence 1	9258	1,74	< 1e-07
CXCR7	chemokine (C-X-C motif) receptor 7	57007	1,73	1,02E-05
SPAG1	sperm associated antigen 1	6674	1,72	< 1e-07
CKAP4	cytoskeleton-associated protein 4	10970	1,72	2,41E-05
CLIC2	chloride intracellular channel 2	1193	1,7	0,0004149
MN1	meningioma (disrupted in balanced translocation) 1	4330	1,7	0,0004839
NID1	nidogen 1	4811	1,66	0,0003085
BAG3	BCL2-associated athanogene 3	9531	1,66	0,0003494
MRPL15	mitochondrial ribosomal protein L15	29088	1,65	< 1e-07
SDC2	syndecan 2	6383	1,65	0,0006866
LAMC1	laminin, gamma 1 (formerly LAMB2)	3915	1,64	< 1e-07
F2RL1	coagulation factor II (thrombin) receptor-like 1	2150	1,64	< 1e-07
LPL	lipoprotein lipase	4023	1,64	2,00E-07
TMEM55A	transmembrane protein 55A	55529	1,63	< 1e-07
EMP1	epithelial membrane protein 1	2012	1,63	0,0002095
PDP1	pyruvate dehydrogenase phosphatase catalytic subunit	54704	1,62	< 1e-07
EMR1	egf-like module containing, mucin-like, hormone receptor-like 1	2015	1,62	5,90E-06
THBD	thrombomodulin	7056	1,62	0,0001521
GBP1	guanylate binding protein 1, interferon-inducible	2633	1,62	0,0001632
AK4	adenylate kinase 4	205	1,61	< 1e-07
PLS3	plastin 3	5358	1,61	3,52E-05
SLC25A37	solute carrier family 25 (mitochondrial iron transporter)	51312	1,61	0,000258
LOC100127983	uncharacterized LOC100127983	100127983	1,61	0,0003816
PLEKHA2	pleckstrin homology domain containing, family A (phosphoinositide 3-kinase)	59339	1,6	< 1e-07
NAT1	N-acetyltransferase 1 (arylamine N-acetyltransferase)	9	1,6	< 1e-07
SPARC	secreted protein, acidic, cysteine-rich (osteonectin)	6678	1,6	8,28E-05
RRM2B	ribonucleotide reductase M2 B (TP53 inducible)	50484	1,59	< 1e-07
TRPS1	trichorhinophalangeal syndrome I	7227	1,59	< 1e-07
EGR3	early growth response 3	1960	1,59	0,000103
DDIT4	DNA-damage-inducible transcript 4	54541	1,59	0,0001132

<i>ALDH2</i>	aldehyde dehydrogenase 2 family (mitochondrial)	217	1,59	0,0008205
<i>SETD7</i>	SET domain containing (lysine methyltransferase) 7	80854	1,58	1,00E-07
<i>ARAP2</i>	ArfGAP with RhoGAP domain, ankyrin repeat and PH	116984	1,58	2,08E-05
<i>CTSB</i>	cathepsin B	1508	1,57	< 1e-07
<i>GGH</i>	gamma-glutamyl hydrolase (conjugase, folylpolygamn	8836	1,57	3,00E-07
<i>PTK2</i>	PTK2 protein tyrosine kinase 2	5747	1,57	7,92E-05
<i>FHL1</i>	four and a half LIM domains 1	2273	1,57	0,0003448
<i>CCNE2</i>	cyclin E2	9134	1,56	1,40E-06
<i>MT1G</i>	metallothionein 1G	4495	1,56	1,80E-06
<i>THSD7A</i>	thrombospondin, type I, domain containing 7A	221981	1,56	0,0001088
<i>FAM213A</i>	family with sequence similarity 213, member A	84293	1,56	0,0005141
<i>WWP1</i>	WW domain containing E3 ubiquitin protein ligase 1	11059	1,55	< 1e-07
<i>TPD52</i>	tumor protein D52	7163	1,55	3,00E-06
<i>ADAM9</i>	ADAM metallopeptidase domain 9	8754	1,54	4,33E-05
<i>FOXO1</i>	forkhead box O1	2308	1,54	8,89E-05
<i>SHCBP1</i>	SHC SH2-domain binding protein 1	79801	1,54	0,0001225
<i>TCEB1</i>	transcription elongation factor B (SIII), polypeptide 1 (	6921	1,53	< 1e-07
<i>UBE2V2</i>	ubiquitin-conjugating enzyme E2 variant 2	7336	1,53	< 1e-07
<i>TMEM70</i>	transmembrane protein 70	54968	1,52	< 1e-07
<i>HOOK3</i>	hook homolog 3 (Drosophila)	84376	1,52	< 1e-07
<i>EIF2C2</i>	eukaryotic translation initiation factor 2C, 2	27161	1,52	< 1e-07
<i>ARHGEF10</i>	Rho guanine nucleotide exchange factor (GEF) 10	9639	1,52	7,00E-07
<i>MTMR11</i>	myotubularin related protein 11	10903	1,52	0,0002842
<i>ANKRD46</i>	ankyrin repeat domain 46	157567	1,51	7,00E-07
<i>ASAP1-IT1</i>	ASAP1 intronic transcript 1 (non-protein coding)	29065	1,51	3,10E-06
<i>TNS3</i>	tensin 3	64759	1,51	8,48E-05
<i>GNPDA1</i>	glucosamine-6-phosphate deaminase 1	10007	1,51	0,0001282
<i>VPS37A</i>	vacuolar protein sorting 37 homolog A (S. cerevisiae)	137492	1,5	< 1e-07
<i>CHCHD7</i>	coiled-coil-helix-coiled-coil-helix domain containing 7	79145	1,5	< 1e-07
<i>MTHFD2</i>	methylenetetrahydrofolate dehydrogenase (NADP+ de	10797	1,5	< 1e-07
<i>PLCB4</i>	phospholipase C, beta 4	5332	1,5	2,80E-06
<i>EBAG9</i>	estrogen receptor binding site associated, antigen, 9	9166	1,49	< 1e-07
<i>TM2D2</i>	TM2 domain containing 2	83877	1,49	< 1e-07
<i>SNX16</i>	sorting nexin 16	64089	1,49	< 1e-07
<i>CPQ</i>	carboxypeptidase Q	10404	1,49	< 1e-07
<i>FBXO6</i>	F-box protein 6	26270	1,49	1,91E-05
<i>KBTBD8</i>	kelch repeat and BTB (POZ) domain containing 8	84541	1,49	4,99E-05
<i>ADORA2B</i>	adenosine A2b receptor	136	1,48	1,73E-05
<i>TCTEX1D1</i>	Tctex1 domain containing 1	200132	1,48	1,91E-05
<i>ZAK</i>	sterile alpha motif and leucine zipper containing kinas	51776	1,48	0,0001229
<i>ST3GAL1</i>	ST3 beta-galactoside alpha-2,3-sialyltransferase 1	6482	1,47	< 1e-07
<i>SLITRK4</i>	SLIT and NTRK-like family, member 4	139065	1,47	6,48E-05
<i>MRPL13</i>	mitochondrial ribosomal protein L13	28998	1,46	< 1e-07
<i>HEATR7A</i>	HEAT repeat containing 7A	727957	1,46	< 1e-07
<i>MTERFD1</i>	MTERF domain containing 1	51001	1,46	< 1e-07
<i>LACTB2</i>	lactamase, beta 2	51110	1,46	2,00E-07
<i>KBTBD11</i>	kelch repeat and BTB (POZ) domain containing 11	9920	1,46	0,0003231
<i>AURKA</i>	aurora kinase A	6790	1,46	0,0004788
<i>VDAC3</i>	voltage-dependent anion channel 3	7419	1,45	< 1e-07
<i>ZNF706</i>	zinc finger protein 706	51123	1,45	< 1e-07
<i>GRINA</i>	glutamate receptor, ionotropic, N-methyl D-aspartate-r	2907	1,45	< 1e-07
<i>PTP4A3</i>	protein tyrosine phosphatase type IVA, member 3	11156	1,45	3,70E-06
<i>TET2</i>	tet methylcytosine dioxygenase 2	54790	1,45	5,60E-06
<i>SGMS1</i>	sphingomyelin synthase 1	259230	1,45	0,0001103
<i>RUNX3</i>	runt-related transcription factor 3	864	1,45	0,0001234

<i>KLRB1</i>	killer cell lectin-like receptor subfamily B, member 1	3820	1,45	0,0005792
<i>ERLIN2</i>	ER lipid raft associated 2	11160	1,44	< 1e-07
<i>CORO2A</i>	coronin, actin binding protein, 2A	7464	1,44	1,00E-07
<i>BMPR2</i>	bone morphogenetic protein receptor, type II (serine/thr	659	1,44	1,00E-07
<i>CDCA2</i>	cell division cycle associated 2	157313	1,44	1,70E-06
<i>SRD5A1</i>	steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo	6715	1,44	1,90E-06
<i>SERPINI1</i>	serpin peptidase inhibitor, clade I (neuroserpin), mem	5274	1,44	5,70E-06
<i>HRSP12</i>	heat-responsive protein 12	10247	1,44	1,34E-05
<i>PLAG1</i>	pleiomorphic adenoma gene 1	5324	1,44	2,96E-05
<i>PPP1R3B</i>	protein phosphatase 1, regulatory subunit 3B	79660	1,44	4,51E-05
<i>TSPYL5</i>	TSPY-like 5	85453	1,44	0,0003941
<i>UTP23</i>	UTP23, small subunit (SSU) processome component,	84294	1,43	< 1e-07
<i>COPS5</i>	COP9 constitutive photomorphogenic homolog subun	10987	1,43	< 1e-07
<i>MCPH1</i>	microcephalin 1	79648	1,43	< 1e-07
<i>ATAD2</i>	ATPase family, AAA domain containing 2	29028	1,43	< 1e-07
<i>PHF20L1</i>	PHD finger protein 20-like 1	51105	1,43	< 1e-07
<i>RB1CC1</i>	RB1-inducible coiled-coil 1	9821	1,43	4,00E-07
<i>SPIRE1</i>	spire homolog 1 (Drosophila)	56907	1,43	3,50E-06
<i>MXI1</i>	MAX interactor 1	4601	1,43	2,08E-05
<i>LOC100996552</i>	uncharacterized LOC100996552	100996552	1,43	0,0001007
<i>BCL2L11</i>	BCL2-like 11 (apoptosis facilitator)	10018	1,43	0,0001148
<i>F2R</i>	coagulation factor II (thrombin) receptor	2149	1,43	0,0002752
<i>EPB41L2</i>	erythrocyte membrane protein band 4.1-like 2	2037	1,43	0,0003131
<i>ITGB5</i>	integrin, beta 5	3693	1,43	0,0005519
<i>ARMC1</i>	armadillo repeat containing 1	55156	1,42	< 1e-07
<i>FAM82B</i>	family with sequence similarity 82, member B	51115	1,42	< 1e-07
<i>PTDSS1</i>	phosphatidylserine synthase 1	9791	1,42	< 1e-07
<i>EFR3A</i>	EFR3 homolog A (S. cerevisiae)	23167	1,42	< 1e-07
<i>B4GALT5</i>	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase,	9334	1,42	2,10E-06
<i>PSD3</i>	pleckstrin and Sec7 domain containing 3	23362	1,42	3,80E-06
<i>MS4A4A</i>	membrane-spanning 4-domains, subfamily A, membe	51338	1,42	0,0009992
<i>TTI2</i>	TELO2 interacting protein 2	80185	1,41	< 1e-07
<i>PPP3CC</i>	protein phosphatase 3, catalytic subunit, gamma isoz	5533	1,41	< 1e-07
<i>SDCBP</i>	syndecan binding protein (syntenin)	6386	1,41	< 1e-07
<i>GINS4</i>	GINS complex subunit 4 (Sld5 homolog)	84296	1,41	< 1e-07
<i>TNFRSF10A</i>	tumor necrosis factor receptor superfamily, member 1	8797	1,41	< 1e-07
<i>OXR1</i>	oxidation resistance 1	55074	1,41	2,00E-07
<i>OSGIN2</i>	oxidative stress induced growth inhibitor family memb	734	1,41	3,00E-07
<i>PLEKHA1</i>	pleckstrin homology domain containing, family A (phos	59338	1,41	8,20E-06
<i>KLF10</i>	Kruppel-like factor 10	7071	1,41	2,50E-05
<i>C5orf25</i>	chromosome 5 open reading frame 25	375484	1,41	2,64E-05
<i>SGPP1</i>	sphingosine-1-phosphate phosphatase 1	81537	1,41	0,0003557
<i>PLOD2</i>	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 2	5352	1,41	0,0004123
<i>C4orf32</i>	chromosome 4 open reading frame 32	132720	1,41	0,0004674
<i>GBP2</i>	guanylate binding protein 2, interferon-inducible	2634	1,41	0,0008197
<i>ENY2</i>	enhancer of yellow 2 homolog (Drosophila)	56943	1,4	< 1e-07
<i>C8orf40</i>	chromosome 8 open reading frame 40	114926	1,4	< 1e-07
<i>ZFAND1</i>	zinc finger, AN1-type domain 1	79752	1,4	< 1e-07
<i>OTUD6B</i>	OTU domain containing 6B	51633	1,4	1,00E-07
<i>LOC100506342</i>	uncharacterized LOC100506342	100506342	1,4	2,00E-07
<i>SIAE</i>	sialic acid acetyltransferase	54414	1,4	2,00E-07
<i>CKAP2</i>	cytoskeleton associated protein 2	26586	1,4	5,00E-07
<i>PNMA1</i>	paraneoplastic Ma antigen 1	9240	1,4	7,00E-07
<i>PROSC</i>	proline synthetase co-transcribed homolog (bacterial)	11212	1,4	2,60E-06
<i>ASAP1</i>	ArfGAP with SH3 domain, ankyrin repeat and PH dom	50807	1,4	3,60E-06

<i>HINT3</i>	histidine triad nucleotide binding protein 3	135114	1,4	2,97E-05
<i>SLC16A1</i>	solute carrier family 16, member 1 (monocarboxylic ac	6566	1,4	3,78E-05
<i>MT1F</i>	metallothionein 1F	4494	1,4	4,09E-05
<i>NDFIP1</i>	Nedd4 family interacting protein 1	80762	1,4	7,45E-05
<i>GPR160</i>	G protein-coupled receptor 160	26996	1,4	0,0002081
<i>LRP12</i>	low density lipoprotein receptor-related protein 12	29967	1,4	0,000254
<i>FAM49B</i>	family with sequence similarity 49, member B	51571	1,39	< 1e-07
<i>WDYHV1</i>	WDYHV motif containing 1	55093	1,39	< 1e-07
<i>THAP1</i>	THAP domain containing, apoptosis associated protei	55145	1,39	< 1e-07
<i>KAT6A</i>	K(lysine) acetyltransferase 6A	7994	1,39	< 1e-07
<i>CLN8</i>	ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressiv	2055	1,39	< 1e-07
<i>NRBP2</i>	nuclear receptor binding protein 2	340371	1,39	5,00E-07
<i>LOC100507303</i>	uncharacterized LOC100507303	100507303	1,39	2,14E-05
<i>ENDOD1</i>	endonuclease domain containing 1	23052	1,39	6,70E-05
<i>SACS</i>	spastic ataxia of Charlevoix-Saguenay (sacsin)	26278	1,39	0,0002131
<i>CAMK2D</i>	calcium/calmodulin-dependent protein kinase II delta	817	1,39	0,000414
<i>PPAP2B</i>	phosphatidic acid phosphatase type 2B	8613	1,39	0,0006423
<i>TGFBR3</i>	transforming growth factor, beta receptor III	7049	1,39	0,0009878
<i>UBE2W</i>	ubiquitin-conjugating enzyme E2W (putative)	55284	1,38	< 1e-07
<i>ZNF7</i>	zinc finger protein 7	7553	1,38	< 1e-07
<i>LOC100505812</i>	uncharacterized LOC100505812	100505812	1,38	6,80E-06
<i>SLC30A1</i>	solute carrier family 30 (zinc transporter), member 1	7779	1,38	3,46E-05
<i>LY6E</i>	lymphocyte antigen 6 complex, locus E	4061	1,38	0,0001636
<i>RNF139</i>	ring finger protein 139	11236	1,37	< 1e-07
<i>PEX2</i>	peroxisomal biogenesis factor 2	5828	1,37	< 1e-07
<i>TACC1</i>	transforming, acidic coiled-coil containing protein 1	6867	1,37	< 1e-07
<i>DCAF13</i>	DDB1 and CUL4 associated factor 13	25879	1,37	< 1e-07
<i>FAM43A</i>	family with sequence similarity 43, member A	131583	1,37	< 1e-07
<i>PDLIM2</i>	PDZ and LIM domain 2 (mystique)	64236	1,37	9,30E-06
<i>RRAGD</i>	Ras-related GTP binding D	58528	1,37	2,02E-05
<i>DBNDD2</i>	dysbindin (dystrobrevin binding protein 1) domain con	55861	1,37	5,27E-05
<i>SYS1-DBNDD2</i>	SYS1-DBNDD2 readthrough (non-protein coding)	767557	1,37	5,27E-05
<i>C8orf76</i>	chromosome 8 open reading frame 76	84933	1,36	< 1e-07
<i>REEP4</i>	receptor accessory protein 4	80346	1,36	< 1e-07
<i>DDHD2</i>	DDHD domain containing 2	23259	1,36	< 1e-07
<i>ATP6V1C1</i>	ATPase, H <sup>+</sup> transporting, lysosomal 42kDa, V1 subun	528	1,36	3,60E-06
<i>FAM57A</i>	family with sequence similarity 57, member A	79850	1,36	8,30E-06
<i>SLC18A2</i>	solute carrier family 18 (vesicular monoamine), memb	6571	1,36	3,21E-05
<i>PRKCH</i>	protein kinase C, eta	5583	1,36	0,0001959
<i>WASF3</i>	WAS protein family, member 3	10810	1,36	0,000344
<i>C3orf14</i>	chromosome 3 open reading frame 14	57415	1,36	0,0006522
<i>TNFRSF10B</i>	tumor necrosis factor receptor superfamily, member 10	8795	1,35	5,10E-06
<i>ASAH1</i>	N-acylsphingosine amidohydrolase (acid ceramidase)	427	1,35	8,70E-06
<i>PTPRO</i>	protein tyrosine phosphatase, receptor type, O	5800	1,35	1,29E-05
<i>LYN</i>	v-yes-1 Yamaguchi sarcoma viral related oncogene ho	4067	1,35	1,41E-05
<i>LOC100996579</i>	uncharacterized LOC100996579	100996579	1,35	5,08E-05
<i>SGK223</i>	homolog of rat pragma of Rnd2	157285	1,35	7,88E-05
<i>ACPL2</i>	acid phosphatase-like 2	92370	1,35	0,0006012
<i>CDC42</i>	cell division cycle 42 (GTP binding protein, 25kDa)	998	1,35	0,0007366
<i>SGK3</i>	serum/glucocorticoid regulated kinase family, member	23678	1,34	1,00E-07
<i>TSTA3</i>	tissue specific transplantation antigen P35B	7264	1,34	2,43E-05
<i>AP3M2</i>	adaptor-related protein complex 3, mu 2 subunit	10947	1,34	4,64E-05
<i>AGTBP1</i>	ATP/GTP binding protein 1	23287	1,34	0,000164
<i>MPP6</i>	membrane protein, palmitoylated 6 (MAGUK p55 subf	51678	1,34	0,0003198
<i>ARG2</i>	arginase, type II	384	1,34	0,0004309

<i>RNASE4</i>	ribonuclease, RNase A family, 4	6038	1,34	0,0006554
<i>CMTM4</i>	CKLF-like MARVEL transmembrane domain containin	146223	1,33	< 1e-07
<i>EMC2</i>	ER membrane protein complex subunit 2	9694	1,33	1,00E-07
<i>WDR47</i>	WD repeat domain 47	22911	1,33	2,00E-07
<i>TMEM68</i>	transmembrane protein 68	137695	1,33	3,00E-07
<i>LETM2</i>	leucine zipper-EF-hand containing transmembrane pr	137994	1,33	1,20E-06
<i>KIAA1551</i>	KIAA1551	55196	1,33	3,50E-06
<i>RALA</i>	v-ral simian leukemia viral oncogene homolog A (ras r	5898	1,33	0,000166
<i>GNG2</i>	guanine nucleotide binding protein (G protein), gamma	54331	1,33	0,000174
<i>SLC25A32</i>	solute carrier family 25 (mitochondrial folate carrier) , t	81034	1,32	< 1e-07
<i>GNRH1</i>	gonadotropin-releasing hormone 1 (luteinizing-releasi	2796	1,32	< 1e-07
<i>AKT3</i>	v-akt murine thymoma viral oncogene homolog 3 (pro	10000	1,32	4,00E-07
<i>TRMT12</i>	tRNA methyltransferase 12 homolog (S. cerevisiae)	55039	1,32	1,00E-06
<i>TRIQQ</i>	triple QxxK/R motif containing	286144	1,32	5,20E-06
<i>C14orf129</i>	chromosome 14 open reading frame 129	51527	1,32	1,22E-05
<i>IL7</i>	interleukin 7	3574	1,32	6,03E-05
<i>MANSC1</i>	MANSC domain containing 1	54682	1,32	0,0006185
<i>KIF18A</i>	kinesin family member 18A	81930	1,32	0,0007483
<i>PLEC</i>	plectin	5339	1,32	0,0008809
<i>SORBS3</i>	sorbin and SH3 domain containing 3	10174	1,31	< 1e-07
<i>NEIL2</i>	nei endonuclease VIII-like 2 (E. coli)	252969	1,31	< 1e-07
<i>PPAPDC1B</i>	phosphatidic acid phosphatase type 2 domain contain	84513	1,31	< 1e-07
<i>ATP6V1B2</i>	ATPase, H+ transporting, lysosomal 56/58kDa, V1 sul	526	1,31	5,00E-07
<i>LYPLA1</i>	lysophospholipase I	10434	1,31	6,10E-06
<i>DNAJB9</i>	DnaJ (Hsp40) homolog, subfamily B, member 9	4189	1,31	7,00E-06
<i>CPED1</i>	cadherin-like and PC-esterase domain containing 1	79974	1,31	4,72E-05
<i>KLHDC7B</i>	kelch domain containing 7B	113730	1,31	0,0001792
<i>CYB5A</i>	cytochrome b5 type A (microsomal)	1528	1,31	0,0002164
<i>DDIT4L</i>	DNA-damage-inducible transcript 4-like	115265	1,31	0,0008158
<i>UBXN2B</i>	UBX domain protein 2B	137886	1,3	< 1e-07
<i>UBR5</i>	ubiquitin protein ligase E3 component n-recognin 5	51366	1,3	< 1e-07
<i>BAG4</i>	BCL2-associated athanogene 4	9530	1,3	6,00E-07
<i>RDH10</i>	retinol dehydrogenase 10 (all-trans)	157506	1,3	7,20E-06
<i>LRR8C</i>	leucine rich repeat containing 8 family, member C	84230	1,3	2,05E-05
<i>MRPS28</i>	mitochondrial ribosomal protein S28	28957	1,3	5,28E-05
<i>LOC1009965</i>	uncharacterized LOC100996537	100996537	1,3	0,0001204
<i>RAP2A</i>	RAP2A, member of RAS oncogene family	5911	1,3	0,0001218
<i>MCM4</i>	minichromosome maintenance complex component 4	4173	1,3	0,0004175
<i>C8orf82</i>	chromosome 8 open reading frame 82	414919	1,3	0,0004281
<i>NUDT4</i>	nudix (nucleoside diphosphate linked moiety X)-type r	11163	1,3	0,0005372
<i>LOC1009964</i>	uncharacterized LOC100996412	100996412	1,3	0,0007649
<i>PPP1R27</i>	protein phosphatase 1, regulatory subunit 27	116729	1,3	0,0009549
<i>RNF19A</i>	ring finger protein 19A, E3 ubiquitin protein ligase	25897	1,29	< 1e-07
<i>LOC1005073</i>	uncharacterized LOC100507316	100507316	1,29	< 1e-07
<i>MTRF1</i>	mitochondrial fission regulator 1	9650	1,29	< 1e-07
<i>SPCS2</i>	signal peptidase complex subunit 2 homolog (S. cerev	9789	1,29	2,00E-07
<i>DCTN6</i>	dynactin 6	10671	1,29	4,00E-07
<i>RBM12B</i>	RNA binding motif protein 12B	389677	1,29	6,00E-07
<i>IMPA1</i>	inositol(myo)-1(or 4)-monophosphatase 1	3612	1,29	3,80E-06
<i>LOC1001288</i>	uncharacterized LOC100128822	100128822	1,29	1,20E-05
<i>TBL2</i>	transducin (beta)-like 2	26608	1,29	2,15E-05
<i>SESN3</i>	sestrin 3	143686	1,29	3,46E-05
<i>ADCY9</i>	adenylate cyclase 9	115	1,29	0,000114
<i>F8</i>	coagulation factor VIII, procoagulant component	2157	1,29	0,0001509
<i>SAMD9</i>	sterile alpha motif domain containing 9	54809	1,29	0,0004403

<i>KIF13B</i>	kinesin family member 13B	23303	1,28	< 1e-07
<i>FNTA</i>	farnesyltransferase, CAAX box, alpha	2339	1,28	< 1e-07
<i>VPS13B</i>	vacuolar protein sorting 13 homolog B (yeast)	157680	1,28	1,70E-06
<i>ANKRD6</i>	ankyrin repeat domain 6	22881	1,28	6,08E-05
<i>CMTM8</i>	CKLF-like MARVEL transmembrane domain containin	152189	1,28	8,38E-05
<i>C12orf29</i>	chromosome 12 open reading frame 29	91298	1,28	0,0002642
<i>TMEM45A</i>	transmembrane protein 45A	55076	1,28	0,0003373
<i>MICAL2</i>	microtubule associated monooxygenase, calponin and	9645	1,28	0,0004686
<i>PRDX4</i>	peroxiredoxin 4	10549	1,28	0,000612
<i>CRTAM</i>	cytotoxic and regulatory T cell molecule	56253	1,28	0,0007397
<i>REEP5</i>	receptor accessory protein 5	7905	1,28	0,0007711
<i>AGPAT5</i>	1-acylglycerol-3-phosphate O-acyltransferase 5 (lysop	55326	1,28	0,0009867
<i>MED30</i>	mediator complex subunit 30	90390	1,27	1,00E-07
<i>PPP2R2A</i>	protein phosphatase 2, regulatory subunit B, alpha	5520	1,27	1,00E-07
<i>C8orf59</i>	chromosome 8 open reading frame 59	401466	1,27	2,80E-06
<i>DECR1</i>	2,4-dienoyl CoA reductase 1, mitochondrial	1666	1,27	3,90E-06
<i>LYPLAL1</i>	lysophospholipase-like 1	127018	1,27	4,90E-06
<i>GAN</i>	gigaxonin	8139	1,27	2,67E-05
<i>PRKDC</i>	protein kinase, DNA-activated, catalytic polypeptide	5591	1,27	3,56E-05
<i>YTHDF3</i>	YTH domain family, member 3	253943	1,27	4,62E-05
<i>PODXL</i>	podocalyxin-like	5420	1,27	8,15E-05
<i>SLC16A10</i>	solute carrier family 16, member 10 (aromatic amino a	117247	1,27	0,000215
<i>SBF2</i>	SET binding factor 2	81846	1,27	0,000255
<i>DGAT2</i>	diacylglycerol O-acyltransferase 2	84649	1,27	0,000276
<i>ZBTB41</i>	zinc finger and BTB domain containing 41	360023	1,27	0,000451
<i>MB21D1</i>	Mab-21 domain containing 1	115004	1,27	0,0008142
<i>ANKRD28</i>	ankyrin repeat domain 28	23243	1,27	0,0009003
<i>LRRCC1</i>	leucine rich repeat and coiled-coil centrosomal protein	85444	1,27	0,0009174
<i>CNOT7</i>	CCR4-NOT transcription complex, subunit 7	29883	1,26	1,00E-07
<i>TRIM35</i>	tripartite motif containing 35	23087	1,26	3,00E-07
<i>MTMR9</i>	myotubularin related protein 9	66036	1,26	1,60E-06
<i>C8orf44-SGK3</i>	C8orf44-SGK3 readthrough	100533105	1,26	2,00E-06
<i>FBXO25</i>	F-box protein 25	26260	1,26	3,90E-06
<i>ERI1</i>	exoribonuclease 1	90459	1,26	1,14E-05
<i>PHTF2</i>	putative homeodomain transcription factor 2	57157	1,26	1,57E-05
<i>TATDN3</i>	TatD DNase domain containing 3	128387	1,26	2,02E-05
<i>NUDT19</i>	nudix (nucleoside diphosphate linked moiety X)-type r	390916	1,26	2,26E-05
<i>FBXO8</i>	F-box protein 8	26269	1,26	2,65E-05
<i>SQLE</i>	squalene epoxidase	6713	1,26	0,0001325
<i>EIF4EBP1</i>	eukaryotic translation initiation factor 4E binding prote	1978	1,26	0,0001528
<i>TMEM64</i>	transmembrane protein 64	169200	1,26	0,0002045
<i>KLHDC8B</i>	kelch domain containing 8B	200942	1,26	0,0002854
<i>ZBED6</i>	zinc finger, BED-type containing 6	100381270	1,26	0,0003178
<i>XPO7</i>	exportin 7	23039	1,26	0,000319
<i>BNIP3L</i>	BCL2/adenovirus E1B 19kDa interacting protein 3-like	665	1,26	0,0005603
<i>CD3E</i>	CD3e molecule, epsilon (CD3-TCR complex)	916	1,26	0,0006372
<i>CHSY1</i>	chondroitin sulfate synthase 1	22856	1,26	0,0006855
<i>ZNF34</i>	zinc finger protein 34	80778	1,25	9,00E-07
<i>TATDN1</i>	TatD DNase domain containing 1	83940	1,25	3,40E-06
<i>SEC62</i>	SEC62 homolog (S. cerevisiae)	7095	1,25	4,10E-06
<i>NAA30</i>	N(alpha)-acetyltransferase 30, NatC catalytic subunit	122830	1,25	3,35E-05
<i>KIAA0232</i>	KIAA0232	9778	1,25	4,12E-05
<i>PNOC</i>	prepronociceptin	5368	1,25	8,09E-05
<i>RIPK2</i>	receptor-interacting serine-threonine kinase 2	8767	1,25	8,86E-05
<i>CHST2</i>	carbohydrate (N-acetylglucosamine-6-O) sulfotransfer	9435	1,25	0,0002641

<i>TNFRSF10D</i>	tumor necrosis factor receptor superfamily, member 10	8793	1,25	0,0004812
<i>ZNF395</i>	zinc finger protein 395	55893	1,25	0,0005219
<i>KCTD3</i>	potassium channel tetramerisation domain containing 3	51133	1,25	0,0005358
<i>SLC17A5</i>	solute carrier family 17 (anion/sugar transporter), member 5	26503	1,25	0,0007034
<i>OLFML3</i>	olfactomedin-like 3	56944	1,25	0,0007414
<i>SOCS6</i>	suppressor of cytokine signaling 6	9306	1,25	0,000816
<i>PRRG4</i>	proline rich Gla (G-carboxyglutamic acid) 4 (transmembrane protein)	79056	1,25	0,0008639
<i>ERGIC2</i>	ERGIC and golgi 2	51290	1,24	7,00E-06
<i>MUT</i>	methylmalonyl CoA mutase	4594	1,24	1,28E-05
<i>RNF14</i>	ring finger protein 14	9604	1,24	2,45E-05
<i>NBN</i>	nibrin	4683	1,24	2,54E-05
<i>SREK1IP1</i>	SREK1-interacting protein 1	285672	1,24	3,72E-05
<i>RNF141</i>	ring finger protein 141	50862	1,24	6,63E-05
<i>SLC16A7</i>	solute carrier family 16, member 7 (monocarboxylic acid transporter)	9194	1,24	0,0001432
<i>SH3RF1</i>	SH3 domain containing ring finger 1	57630	1,24	0,0001546
<i>SNTB1</i>	syntrophin, beta 1 (dystrophin-associated protein A1, 4)	6641	1,24	0,0001936
<i>AIM2</i>	absent in melanoma 2	9447	1,24	0,0003731
<i>HSPA13</i>	heat shock protein 70kDa family, member 13	6782	1,24	0,000504
<i>KPNA2</i>	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)	3838	1,24	0,0009012
<i>CISH</i>	cytokine inducible SH2-containing protein	1154	1,24	0,0009656
<i>GPAAL1</i>	glycosylphosphatidylinositol anchor attachment protein 1	8733	1,23	6,00E-07
<i>INTS9</i>	integrator complex subunit 9	55756	1,23	7,00E-07
<i>FAM175B</i>	family with sequence similarity 175, member B	23172	1,23	4,40E-06
<i>KIFC2</i>	kinesin family member C2	90990	1,23	3,08E-05
<i>MSRA</i>	methionine sulfoxide reductase A	4482	1,23	4,19E-05
<i>LSM5</i>	LSM5 homolog, U6 small nuclear RNA associated (S. cerevisiae)	23658	1,23	4,28E-05
<i>CEP85L</i>	centrosomal protein 85kDa-like	387119	1,23	4,74E-05
<i>SEMA4C</i>	sema domain, immunoglobulin domain (Ig), transmembrane protein	54910	1,23	0,0001424
<i>C6orf57</i>	chromosome 6 open reading frame 57	135154	1,23	0,0001929
<i>NCOA2</i>	nuclear receptor coactivator 2	10499	1,23	0,0002288
<i>IPW</i>	imprinted in Prader-Willi syndrome (non-protein coding)	3653	1,23	0,0003932
<i>SUMO1</i>	SMT3 suppressor of mif two 3 homolog 1 (S. cerevisiae)	7341	1,23	0,0005031
<i>IMPACT</i>	Impact homolog (mouse)	55364	1,23	0,0009004
<i>INTS6</i>	integrator complex subunit 6	26512	1,23	0,0009318
<i>ZNF252P</i>	zinc finger protein 252, pseudogene	286101	1,22	3,00E-06
<i>MAK16</i>	MAK16 homolog (S. cerevisiae)	84549	1,22	7,00E-06
<i>LOC100506295</i>	uncharacterized LOC100506295	100506295	1,22	2,41E-05
<i>SLC39A14</i>	solute carrier family 39 (zinc transporter), member 14	23516	1,22	2,47E-05
<i>ZNF596</i>	zinc finger protein 596	169270	1,22	2,50E-05
<i>FAM116A</i>	family with sequence similarity 116, member A	201627	1,22	4,23E-05
<i>TXNDC9</i>	thioredoxin domain containing 9	10190	1,22	5,08E-05
<i>ELP3</i>	elongator acetyltransferase complex subunit 3	55140	1,22	5,56E-05
<i>INIP</i>	INTS3 and NABP interacting protein	58493	1,22	8,78E-05
<i>RBM43</i>	RNA binding motif protein 43	375287	1,22	9,07E-05
<i>UBXN8</i>	UBX domain protein 8	7993	1,22	0,0001048
<i>WBP2</i>	WW domain binding protein 2	23558	1,22	0,0001699
<i>LEMD3</i>	LEM domain containing 3	23592	1,22	0,0002068
<i>GSTA4</i>	glutathione S-transferase alpha 4	2941	1,22	0,000208
<i>SERAC1</i>	serine active site containing 1	84947	1,22	0,0002268
<i>STXBP3</i>	syntaxin binding protein 3	6814	1,22	0,0002573
<i>COL4A3BP</i>	collagen, type IV, alpha 3 (Goodpasture antigen) binding protein	10087	1,22	0,0002911
<i>LPHN1</i>	latrophilin 1	22859	1,22	0,0003464
<i>RBMXL1</i>	RNA binding motif protein, X-linked-like 1	494115	1,22	0,0006018
<i>PSAT1</i>	phosphoserine aminotransferase 1	29968	1,22	0,0006332
<i>DNAJC3</i>	DnaJ (Hsp40) homolog, subfamily C, member 3	5611	1,22	0,0006627

<i>TSPAN14</i>	tetraspanin 14	81619	1,22	0,0007143
<i>CSPP1</i>	centrosome and spindle pole associated protein 1	79848	1,21	1,74E-05
<i>DGAT1</i>	diacylglycerol O-acyltransferase 1	8694	1,21	5,48E-05
<i>PPDPF</i>	pancreatic progenitor cell differentiation and proliferation	79144	1,21	7,90E-05
<i>SLU7</i>	SLU7 splicing factor homolog ( <i>S. cerevisiae</i> )	10569	1,21	9,08E-05
<i>MRAS</i>	muscle RAS oncogene homolog	22808	1,21	9,21E-05
<i>ZNF143</i>	zinc finger protein 143	7702	1,21	0,0001588
<i>HELB</i>	helicase (DNA) B	92797	1,21	0,0001663
<i>INTS10</i>	integrator complex subunit 10	55174	1,21	0,0002032
<i>SMC3</i>	structural maintenance of chromosomes 3	9126	1,21	0,0002438
<i>ASS1</i>	argininosuccinate synthase 1	445	1,21	0,0003064
<i>GOLGA5</i>	golgin A5	9950	1,21	0,0005105
<i>CSTF2T</i>	cleavage stimulation factor, 3' pre-RNA, subunit 2, 64kDa	23283	1,21	0,0005641
<i>SDHD</i>	succinate dehydrogenase complex, subunit D, integral membrane	6392	1,21	0,0007262
<i>CTNNA1</i>	catenin (cadherin-associated protein), alpha 1, 102kDa	1495	1,21	0,0008518
<i>RFWD3</i>	ring finger and WD repeat domain 3	55159	1,21	0,00089
<i>RNF166</i>	ring finger protein 166	115992	1,21	0,0008909
<i>ALDH9A1</i>	aldehyde dehydrogenase 9 family, member A1	223	1,2	1,32E-05
<i>EIF3E</i>	eukaryotic translation initiation factor 3, subunit E	3646	1,2	5,93E-05
<i>HIGD1A</i>	HIG1 hypoxia inducible domain family, member 1A	25994	1,2	6,67E-05
<i>BCL9L</i>	B-cell CLL/lymphoma 9-like	283149	1,2	0,0001401
<i>DHX29</i>	DEAH (Asp-Glu-Ala-His) box polypeptide 29	54505	1,2	0,0001807
<i>ZNF426</i>	zinc finger protein 426	79088	1,2	0,0002077
<i>LEPROTL1</i>	leptin receptor overlapping transcript-like 1	23484	1,2	0,0002795
<i>LOC100506100</i>	uncharacterized LOC100506100	100506100	1,2	0,0002947
<i>MAP1S</i>	microtubule-associated protein 1S	55201	1,2	0,0002958
<i>RAB7L1</i>	RAB7, member RAS oncogene family-like 1	8934	1,2	0,0004074
<i>CNTLN</i>	centlein, centrosomal protein	54875	1,2	0,0004193
<i>SLK</i>	STE20-like kinase	9748	1,2	0,0004723
<i>USP8</i>	ubiquitin specific peptidase 8	9101	1,2	0,0004723
<i>MICB</i>	MHC class I polypeptide-related sequence B	4277	1,2	0,0005133
<i>SGTB</i>	small glutamine-rich tetratricopeptide repeat (TPR)-containing	54557	1,2	0,0006688
<i>ACAT1</i>	acetyl-CoA acetyltransferase 1	38	1,2	0,0007354
<i>PEX12</i>	peroxisomal biogenesis factor 12	5193	1,19	7,68E-05
<i>ZBTB2</i>	zinc finger and BTB domain containing 2	57621	1,19	8,94E-05
<i>INTS8</i>	integrator complex subunit 8	55656	1,19	0,0001513
<i>KIAA1715</i>	KIAA1715	80856	1,19	0,0001525
<i>GLO1</i>	glyoxalase I	2739	1,19	0,0004594
<i>GNG10</i>	guanine nucleotide binding protein (G protein), gamma 10	2790	1,19	0,0005344
<i>DNAJC25-GNG10</i>	DNAJC25-GNG10 readthrough	552891	1,19	0,0005344
<i>SLC31A1</i>	solute carrier family 31 (copper transporters), member 1	1317	1,19	0,0007022
<i>KBTBD3</i>	kelch repeat and BTB (POZ) domain containing 3	143879	1,19	0,0007528
<i>PLEKHF2</i>	pleckstrin homology domain containing, family F (with forkhead)	79666	1,19	0,000753
<i>PALM</i>	paralemmin	5064	1,19	0,0007542
<i>ZNF552</i>	zinc finger protein 552	79818	1,19	0,0008303
<i>TMEM69</i>	transmembrane protein 69	51249	1,19	0,0008512
<i>CASP7</i>	caspase 7, apoptosis-related cysteine peptidase	840	1,19	0,0009789
<i>TBC1D15</i>	TBC1 domain family, member 15	64786	1,18	4,48E-05
<i>DSN1</i>	DSN1, MIND kinetochore complex component, homologous to	79980	1,18	8,11E-05
<i>MCMBP</i>	minichromosome maintenance complex binding protein	79892	1,18	0,0002301
<i>ATL3</i>	atlastin GTPase 3	25923	1,18	0,0003477
<i>VHL</i>	von Hippel-Lindau tumor suppressor, E3 ubiquitin protein	7428	1,18	0,0004144
<i>XAB2</i>	XPA binding protein 2	56949	1,18	0,0005441
<i>KCTD18</i>	potassium channel tetramerisation domain containing 18	130535	1,18	0,0005833
<i>07-Mar</i>	membrane-associated ring finger (C3HC4) 7, E3 ubiquitin	64844	1,18	0,0008059



<i>DCUN1D5</i>	DCN1, defective in cullin neddylation 1, domain conta	84259	1,17	0,0002026
<i>PTK2B</i>	PTK2B protein tyrosine kinase 2 beta	2185	1,17	0,000262
<i>ACN9</i>	ACN9 homolog (S. cerevisiae)	57001	1,17	0,0005377
<i>ENTPD4</i>	ectonucleoside triphosphate diphosphohydrolase 4	9583	1,17	0,0006375
<i>CYP3A5</i>	cytochrome P450, family 3, subfamily A, polypeptide 5	1577	1,17	0,0006437
<i>CBR3</i>	carbonyl reductase 3	874	1,17	0,0009724
<i>SDHC</i>	succinate dehydrogenase complex, subunit C, integra	6391	1,17	0,0009971
<i>AKIP1</i>	A kinase (PRKA) interacting protein 1	56672	1,16	0,0004523
<i>ASH2L</i>	ash2 (absent, small, or homeotic)-like (Drosophila)	9070	1,16	0,0004553
<i>UCHL5</i>	ubiquitin carboxyl-terminal hydrolase L5	51377	1,16	0,0005263
<i>MBIP</i>	MAP3K12 binding inhibitory protein 1	51562	1,16	0,0006635
<i>HPS5</i>	Hermansky-Pudlak syndrome 5	11234	1,16	0,0007002
<i>ZC3H3</i>	zinc finger CCCH-type containing 3	23144	1,16	0,0007225
<i>USP31</i>	ubiquitin specific peptidase 31	57478	1,16	0,0007829
<i>EXOC5</i>	exocyst complex component 5	10640	1,16	0,0008463
<i>CCDC90B</i>	coiled-coil domain containing 90B	60492	1,16	0,0008748
<i>PRKCA</i>	protein kinase C, alpha	5578	1,15	0,0009343
<i>SPG7</i>	spastic paraplegia 7 (pure and complicated automa	6687	0,87	0,0003797
<i>ZNF496</i>	zinc finger protein 496	84838	0,87	0,0003927
<i>CLK2</i>	CDC-like kinase 2	1196	0,87	0,0005333
<i>ZNF428</i>	zinc finger protein 428	126299	0,87	0,0005392
<i>MIA-RAB4B</i>	MIA-RAB4B readthrough	100529262	0,87	0,0005737
<i>LRRC23</i>	leucine rich repeat containing 23	10233	0,87	0,0007427
<i>CABIN1</i>	calcineurin binding protein 1	23523	0,87	0,0009965
<i>LOC10013283</i>	PMS2 postmeiotic segregation increased 2 (S. cerevis	100132832	0,86	0,000299
<i>CDK11B</i>	cyclin-dependent kinase 11B	984	0,86	0,0003009
<i>CHKA</i>	choline kinase alpha	1119	0,86	0,0003741
<i>ALDH16A1</i>	aldehyde dehydrogenase 16 family, member A1	126133	0,86	0,0003757
<i>TTL3</i>	tubulin tyrosine ligase-like family, member 3	26140	0,86	0,0003845
<i>FAM219B</i>	family with sequence similarity 219, member B	57184	0,86	0,0004392
<i>NR1H2</i>	nuclear receptor subfamily 1, group H, member 2	7376	0,86	0,0004402
<i>PDDC1</i>	Parkinson disease 7 domain containing 1	347862	0,86	0,0004485
<i>AKT1</i>	v-akt murine thymoma viral oncogene homolog 1	207	0,86	0,0005124
<i>DCAF4</i>	DDB1 and CUL4 associated factor 4	26094	0,86	0,0005423
<i>SAP25</i>	Sin3A-associated protein, 25kDa	100316904	0,86	0,000554
<i>SUGP2</i>	SURP and G patch domain containing 2	10147	0,86	0,0006294
<i>HP07349</i>	uncharacterized LOC100652853	100652853	0,86	0,0006499
<i>COMMD1</i>	copper metabolism (Murr1) domain containing 1	150684	0,86	0,0006729
<i>KIAA0100</i>	KIAA0100	9703	0,86	0,000723
<i>ANKMY1</i>	ankyrin repeat and MYND domain containing 1	51281	0,86	0,0007327
<i>NSUN5</i>	NOP2/Sun domain family, member 5	55695	0,86	0,0007654
<i>SYNCRIP</i>	synaptotagmin binding, cytoplasmic RNA interacting p	10492	0,86	0,0008918
<i>PPIB</i>	peptidylprolyl isomerase B (cyclophilin B)	5479	0,86	0,0009342
<i>EEF2K</i>	eukaryotic elongation factor-2 kinase	29904	0,86	0,0009444
<i>LYPLA2</i>	lysophospholipase II	11313	0,86	0,0009454
<i>PTBP1</i>	polypyrimidine tract binding protein 1	5725	0,85	6,30E-05
<i>LOC100507424</i>	uncharacterized LOC100507424	100507424	0,85	7,63E-05
<i>PRPF3</i>	PRP3 pre-mRNA processing factor 3 homolog (S. cer	9129	0,85	7,87E-05
<i>SEC24C</i>	SEC24 family, member C (S. cerevisiae)	9632	0,85	9,52E-05
<i>DKC1</i>	dyskeratosis congenita 1, dyskerin	1736	0,85	0,0001548
<i>CIB1</i>	calcium and integrin binding 1 (calmyrin)	10519	0,85	0,0001581
<i>AGBL5</i>	ATP/GTP binding protein-like 5	60509	0,85	0,0001726
<i>HNRNPA2B1</i>	heterogeneous nuclear ribonucleoprotein A2/B1	3181	0,85	0,0001867
<i>MOGS</i>	mannosyl-oligosaccharide glucosidase	7841	0,85	0,0002136
<i>MFGE8</i>	milk fat globule-EGF factor 8 protein	4240	0,85	0,0002181

<i>BMS1</i>	BMS1 homolog, ribosome assembly protein (yeast)	9790	0,85	0,000244
<i>SRSF6</i>	serine/arginine-rich splicing factor 6	6431	0,85	0,0002941
<i>GAL3ST4</i>	galactose-3-O-sulfotransferase 4	79690	0,85	0,0003037
<i>BCAS3</i>	breast carcinoma amplified sequence 3	54828	0,85	0,0003071
<i>TRIM45</i>	tripartite motif containing 45	80263	0,85	0,0003123
<i>SLC25A28</i>	solute carrier family 25 (mitochondrial iron transporter)	81894	0,85	0,0003241
<i>C10orf2</i>	chromosome 10 open reading frame 2	56652	0,85	0,0004131
<i>ZNF26</i>	zinc finger protein 26	7574	0,85	0,0004715
<i>LOC1002875</i>	zinc finger protein 26-like	100287515	0,85	0,0004715
<i>POLG2</i>	polymerase (DNA directed), gamma 2, accessory subunit	11232	0,85	0,0005455
<i>APOC4-APOC2</i>	APOC4-APOC2 readthrough	100533990	0,85	0,0008569
<i>SAPCD1</i>	suppressor APC domain containing 1	401251	0,85	0,0008669
<i>AKD1</i>	adenylate kinase domain containing 1	221264	0,85	0,0008714
<i>C19orf45</i>	chromosome 19 open reading frame 45	374877	0,85	0,0008728
<i>TMEM160</i>	transmembrane protein 160	54958	0,85	0,0009188
<i>CCDC22</i>	coiled-coil domain containing 22	28952	0,85	0,0009834
<i>COPG1</i>	coatamer protein complex, subunit gamma 1	22820	0,84	7,70E-06
<i>TBC1D9B</i>	TBC1 domain family, member 9B (with GRAM domain)	23061	0,84	1,23E-05
<i>SNRNP70</i>	small nuclear ribonucleoprotein 70kDa (U1)	6625	0,84	1,24E-05
<i>TMEM198B</i>	transmembrane protein 198B, pseudogene	440104	0,84	2,65E-05
<i>DIDO1</i>	death inducer-obliterator 1	11083	0,84	3,17E-05
<i>DNAJC17</i>	DnaJ (Hsp40) homolog, subfamily C, member 17	55192	0,84	3,17E-05
<i>ASPSCR1</i>	alveolar soft part sarcoma chromosome region, candidate 1	79058	0,84	4,58E-05
<i>MGEA5</i>	meningioma expressed antigen 5 (hyaluronidase)	10724	0,84	4,86E-05
<i>ARPC4</i>	actin related protein 2/3 complex, subunit 4, 20kDa	10093	0,84	4,87E-05
<i>TMEM91</i>	transmembrane protein 91	641649	0,84	5,25E-05
<i>NAP1L4</i>	nucleosome assembly protein 1-like 4	4676	0,84	5,76E-05
<i>IFI27L2</i>	interferon, alpha-inducible protein 27-like 2	83982	0,84	9,23E-05
<i>LIMD1</i>	LIM domains containing 1	8994	0,84	9,81E-05
<i>GLMN</i>	glomulin, FKBP associated protein	11146	0,84	0,0001366
<i>SPATA7</i>	spermatogenesis associated 7	55812	0,84	0,0001433
<i>DCUN1D2</i>	DCN1, defective in cullin neddylation 1, domain containing 2	55208	0,84	0,0001557
<i>LOC100996421</i>	uncharacterized LOC100996421	100996421	0,84	0,0001713
<i>WRNIP1</i>	Werner helicase interacting protein 1	56897	0,84	0,0001769
<i>CRIPAK</i>	cysteine-rich PAK1 inhibitor	285464	0,84	0,0001849
<i>FAM212A</i>	family with sequence similarity 212, member A	389119	0,84	0,0002246
<i>DKFZP586I1420</i>	uncharacterized protein DKFZp586I1420	222161	0,84	0,0002261
<i>BCL2L2</i>	BCL2-like 2	599	0,84	0,000246
<i>MFSD12</i>	major facilitator superfamily domain containing 12	126321	0,84	0,0002564
<i>CDK11A</i>	cyclin-dependent kinase 11A	728642	0,84	0,0002704
<i>SWSAP1</i>	SWIM-type zinc finger 7 associated protein 1	126074	0,84	0,0002907
<i>SUOX</i>	sulfite oxidase	6821	0,84	0,0003795
<i>ABCC2</i>	ATP-binding cassette, sub-family C (CFTR/MRP), member 2	1244	0,84	0,0003848
<i>VILL</i>	villin-like	50853	0,84	0,0004557
<i>SLC33A1</i>	solute carrier family 33 (acetyl-CoA transporter), member 1	9197	0,84	0,000459
<i>CDK19</i>	cyclin-dependent kinase 19	23097	0,84	0,000488
<i>MSH5-SAPCD1</i>	MSH5-SAPCD1 readthrough (non-protein coding)	100532732	0,84	0,0005116
<i>MPZL1</i>	myelin protein zero-like 1	9019	0,84	0,0005311
<i>LSM2</i>	LSM2 homolog, U6 small nuclear RNA associated (S. cerevisiae)	57819	0,84	0,0005825
<i>FUS</i>	fused in sarcoma	2521	0,84	0,0005869
<i>PPIEL</i>	peptidylprolyl isomerase E-like pseudogene	728448	0,84	0,0006301
<i>PMS2P3</i>	postmeiotic segregation increased 2 pseudogene 3	5387	0,84	0,0007017
<i>IFT172</i>	intraflagellar transport 172 homolog (Chlamydomonas reinhardtii)	26160	0,84	0,0007215
<i>DNAJC2</i>	DnaJ (Hsp40) homolog, subfamily C, member 2	27000	0,84	0,0007919
<i>LTB4R</i>	leukotriene B4 receptor	1241	0,84	0,0009473

<i>LIG3</i>	ligase III, DNA, ATP-dependent	3980	0,83	2,80E-06
<i>ATXN2L</i>	ataxin 2-like	11273	0,83	4,50E-06
<i>TELO2</i>	TEL2, telomere maintenance 2, homolog (S. cerevisia	9894	0,83	6,70E-06
<i>THOC1</i>	THO complex 1	9984	0,83	1,01E-05
<i>ARHGAP4</i>	Rho GTPase activating protein 4	393	0,83	1,40E-05
<i>TEKT4P2</i>	tektin 4 pseudogene 2	100132288	0,83	2,59E-05
<i>PMS2P1</i>	postmeiotic segregation increased 2 pseudogene 1	5379	0,83	2,65E-05
<i>ADPGK</i>	ADP-dependent glucokinase	83440	0,83	3,19E-05
<i>PHKA2</i>	phosphorylase kinase, alpha 2 (liver)	5256	0,83	4,12E-05
<i>FLJ23867</i>	uncharacterized protein FLJ23867	200058	0,83	4,52E-05
<i>MBD6</i>	methyl-CpG binding domain protein 6	114785	0,83	5,29E-05
<i>ZDHHC11</i>	zinc finger, DHHC-type containing 11	79844	0,83	6,59E-05
<i>ARHGEF1</i>	Rho guanine nucleotide exchange factor (GEF) 1	9138	0,83	6,80E-05
<i>PTTG1IP</i>	pituitary tumor-transforming 1 interacting protein	754	0,83	7,50E-05
<i>CCDC28B</i>	coiled-coil domain containing 28B	79140	0,83	7,53E-05
<i>CAPN11</i>	calpain 11	11131	0,83	9,66E-05
<i>RPS6KL1</i>	ribosomal protein S6 kinase-like 1	83694	0,83	0,0001063
<i>IFT122</i>	intraflagellar transport 122 homolog (Chlamydomonas	55764	0,83	0,0001087
<i>LOC728537</i>	uncharacterized LOC728537	728537	0,83	0,0001449
<i>DYX1C1</i>	dyslexia susceptibility 1 candidate 1	161582	0,83	0,000161
<i>PCGF3</i>	polycomb group ring finger 3	10336	0,83	0,0002403
<i>GOLGA2P5</i>	golgin A2 pseudogene 5	55592	0,83	0,0004384
<i>THOC6</i>	THO complex 6 homolog (Drosophila)	79228	0,83	0,0005134
<i>ZSCAN2</i>	zinc finger and SCAN domain containing 2	54993	0,83	0,0005611
<i>POLR3E</i>	polymerase (RNA) III (DNA directed) polypeptide E (8	55718	0,83	0,000565
<i>RNPEP</i>	arginyl aminopeptidase (aminopeptidase B)	6051	0,83	0,0007249
<i>PVRL1</i>	poliovirus receptor-related 1 (herpesvirus entry media	5818	0,83	0,0007315
<i>AHI1</i>	Abelson helper integration site 1	54806	0,83	0,0007958
<i>KCNMB3</i>	potassium large conductance calcium-activated chanr	27094	0,83	0,0009812
<i>C16orf58</i>	chromosome 16 open reading frame 58	64755	0,82	1,80E-06
<i>CCDC94</i>	coiled-coil domain containing 94	55702	0,82	2,40E-06
<i>FUBP1</i>	far upstream element (FUSE) binding protein 1	8880	0,82	2,80E-06
<i>OSGEP</i>	O-sialoglycoprotein endopeptidase	55644	0,82	3,80E-06
<i>NONO</i>	non-POU domain containing, octamer-binding	4841	0,82	4,30E-06
<i>MDFI</i>	MyoD family inhibitor	4188	0,82	4,40E-06
<i>C17orf65</i>	chromosome 17 open reading frame 65	339201	0,82	5,10E-06
<i>LOC1002331</i>	tektin 4 pseudogene	100233156	0,82	5,90E-06
<i>RABEP2</i>	rabaptin, RAB GTPase binding effector protein 2	79874	0,82	7,00E-06
<i>STAT2</i>	signal transducer and activator of transcription 2, 113k	6773	0,82	9,70E-06
<i>RALGAPA2</i>	Ral GTPase activating protein, alpha subunit 2 (cataly	57186	0,82	1,40E-05
<i>DUS3L</i>	dihydrouridine synthase 3-like (S. cerevisiae)	56931	0,82	1,89E-05
<i>LOC1005075</i>	uncharacterized LOC100507577	100507577	0,82	4,96E-05
<i>RADIL</i>	Ras association and DIL domains	55698	0,82	6,32E-05
<i>USP43</i>	ubiquitin specific peptidase 43	124739	0,82	7,81E-05
<i>C1QTNF3</i>	C1q and tumor necrosis factor related protein 3	114899	0,82	0,0001331
<i>DOCK2</i>	dedicator of cytokinesis 2	1794	0,82	0,0001466
<i>SLC45A3</i>	solute carrier family 45, member 3	85414	0,82	0,000399
<i>LOC1002722</i>	uncharacterized LOC100272228	100272228	0,82	0,0005538
<i>RRN3P3</i>	RNA polymerase I transcription factor homolog (S. cer	100131998	0,82	0,0008589
<i>NCBP2</i>	nuclear cap binding protein subunit 2, 20kDa	22916	0,81	2,00E-07
<i>NXF5</i>	nuclear RNA export factor 5	55998	0,81	3,00E-07
<i>KRT3</i>	keratin 3	3850	0,81	4,00E-07
<i>PCDHB18</i>	protocadherin beta 18 pseudogene	54660	0,81	7,00E-07
<i>CLSTN3</i>	calsyntenin 3	9746	0,81	1,10E-06
<i>YY1AP1</i>	YY1 associated protein 1	55249	0,81	4,30E-06

<i>NADSYN1</i>	NAD synthetase 1	55191	0,81	4,40E-06
<i>WDR6</i>	WD repeat domain 6	11180	0,81	6,60E-06
<i>GMPPA</i>	GDP-mannose pyrophosphorylase A	29926	0,81	7,30E-06
<i>MZF1</i>	myeloid zinc finger 1	7593	0,81	8,10E-06
<i>ASB3</i>	ankyrin repeat and SOCS box containing 3	51130	0,81	1,43E-05
<i>AMT</i>	aminomethyltransferase	275	0,81	1,94E-05
<i>LOC100506057</i>	uncharacterized LOC100506057	100506057	0,81	2,18E-05
<i>NOP56</i>	NOP56 ribonucleoprotein homolog (yeast)	10528	0,81	2,21E-05
<i>AHSA2</i>	AHA1, activator of heat shock 90kDa protein ATPase	130872	0,81	4,07E-05
<i>CDK2</i>	cyclin-dependent kinase 2	1017	0,81	5,71E-05
<i>EPHB6</i>	EPH receptor B6	2051	0,81	7,31E-05
<i>RASSF1</i>	Ras association (RalGDS/AF-6) domain family memb	11186	0,81	7,93E-05
<i>TMEM44</i>	transmembrane protein 44	93109	0,81	0,0001056
<i>ZCCHC11</i>	zinc finger, CCHC domain containing 11	23318	0,81	0,0002328
<i>HIST1H2BB</i>	histone cluster 1, H2bb	3018	0,81	0,0003787
<i>PAK6</i>	p21 protein (Cdc42/Rac)-activated kinase 6	56924	0,81	0,0004274
<i>GTF2I</i>	general transcription factor Iii	2969	0,81	0,0005971
<i>IL3RA</i>	interleukin 3 receptor, alpha (low affinity)	3563	0,81	0,0006455
<i>SUPT3H</i>	suppressor of Ty 3 homolog (S. cerevisiae)	8464	0,81	0,0006496
<i>FARSA</i>	phenylalanyl-tRNA synthetase, alpha subunit	2193	0,81	0,000961
<i>FAM193B</i>	family with sequence similarity 193, member B	54540	0,8	< 1e-07
<i>LEPRE1</i>	leucine proline-enriched proteoglycan (leprecan) 1	64175	0,8	6,00E-07
<i>ITIH4</i>	inter-alpha-trypsin inhibitor heavy chain family, membe	3700	0,8	1,60E-06
<i>RASAL3</i>	RAS protein activator like 3	64926	0,8	3,50E-06
<i>TRMT1</i>	tRNA methyltransferase 1 homolog (S. cerevisiae)	55621	0,8	6,50E-06
<i>TP53BP1</i>	tumor protein p53 binding protein 1	7158	0,8	7,30E-06
<i>CDRT15L2</i>	CMT1A duplicated region transcript 15-like 2	256223	0,8	1,08E-05
<i>RCC2</i>	regulator of chromosome condensation 2	55920	0,8	1,30E-05
<i>CHTF18</i>	CTF18, chromosome transmission fidelity factor 18 hc	63922	0,8	1,63E-05
<i>UCN</i>	urocortin	7349	0,8	1,68E-05
<i>EBLN2</i>	endogenous Bornavirus-like nucleoprotein 2	55096	0,8	3,06E-05
<i>RANBP1</i>	RAN binding protein 1	5902	0,8	3,22E-05
<i>AFF1</i>	AF4/FMR2 family, member 1	4299	0,8	3,63E-05
<i>ALYREF</i>	Aly/REF export factor	10189	0,8	3,82E-05
<i>TBC1D2B</i>	TBC1 domain family, member 2B	23102	0,8	5,46E-05
<i>AMD1</i>	adenosylmethionine decarboxylase 1	262	0,8	7,01E-05
<i>RGL2</i>	ral guanine nucleotide dissociation stimulator-like 2	5863	0,8	8,00E-05
<i>FGFR1OP</i>	FGFR1 oncogene partner	11116	0,8	0,0001222
<i>SLC25A29</i>	solute carrier family 25 (mitochondrial carnitine/acylca	123096	0,8	0,0002284
<i>ZNF790-AS1</i>	ZNF790 antisense RNA 1	284408	0,8	0,0003209
<i>HHAT</i>	hedgehog acyltransferase	55733	0,8	0,00044
<i>WDR52</i>	WD repeat domain 52	55779	0,8	0,0006801
<i>C19orf81</i>	chromosome 19 open reading frame 81	342918	0,79	< 1e-07
<i>P4HTM</i>	prolyl 4-hydroxylase, transmembrane (endoplasmic re	54681	0,79	1,00E-07
<i>CHKB</i>	choline kinase beta	1120	0,79	1,00E-07
<i>CCNL2</i>	cyclin L2	81669	0,79	2,00E-07
<i>WDFY2</i>	WD repeat and FYVE domain containing 2	115825	0,79	4,90E-06
<i>GDF11</i>	growth differentiation factor 11	10220	0,79	8,30E-06
<i>PMCHL1</i>	pro-melanin-concentrating hormone-like 1, pseudoger	5369	0,79	8,60E-06
<i>CCDC84</i>	coiled-coil domain containing 84	338657	0,79	1,36E-05
<i>PMS2P5</i>	postmeiotic segregation increased 2 pseudogene 5	5383	0,79	1,59E-05
<i>LOC100996753</i>	postmeiotic segregation increased 2-like protein 5-like	100996753	0,79	1,59E-05
<i>RASGRP2</i>	RAS guanyl releasing protein 2 (calcium and DAG-rec	10235	0,79	3,56E-05
<i>ZNF767</i>	zinc finger family member 767	79970	0,79	3,94E-05
<i>UBA7</i>	ubiquitin-like modifier activating enzyme 7	7318	0,79	8,77E-05

<i>HIST1H4D</i>	histone cluster 1, H4d	8360	0,79	0,0001439
<i>LCN6</i>	lipocalin 6	158062	0,79	0,000186
<i>NEAT1</i>	nuclear paraspeckle assembly transcript 1 (non-protein-coding)	283131	0,79	0,0003254
<i>USP54</i>	ubiquitin specific peptidase 54	159195	0,79	0,0003829
<i>HHIP-AS1</i>	HHIP antisense RNA 1	646576	0,79	0,0008366
<i>RNF220</i>	ring finger protein 220	55182	0,78	< 1e-07
<i>RAMP2-AS1</i>	RAMP2 antisense RNA 1	100190938	0,78	< 1e-07
<i>KDM1A</i>	lysine (K)-specific demethylase 1A	23028	0,78	2,00E-07
<i>GPR75-ASB3</i>	GPR75-ASB3 readthrough	100302652	0,78	5,00E-07
<i>POU5F1P4</i>	POU class 5 homeobox 1 pseudogene 4	645682	0,78	6,00E-07
<i>POLR1C</i>	polymerase (RNA) I polypeptide C, 30kDa	9533	0,78	9,00E-07
<i>ACAP1</i>	ArfGAP with coiled-coil, ankyrin repeat and PH domain	9744	0,78	2,90E-06
<i>ST3GAL4</i>	ST3 beta-galactoside alpha-2,3-sialyltransferase 4	6484	0,78	4,50E-06
<i>IRF3</i>	interferon regulatory factor 3	3661	0,78	8,90E-06
<i>NOP2</i>	NOP2 nucleolar protein homolog (yeast)	4839	0,78	9,00E-06
<i>EGFL8</i>	EGF-like-domain, multiple 8	80864	0,78	1,01E-05
<i>PPT2-EGFL8</i>	PPT2-EGFL8 readthrough	100532746	0,78	1,01E-05
<i>LOC100996496</i>	uncharacterized LOC100996496	100996496	0,78	2,35E-05
<i>FANK1</i>	fibronectin type III and ankyrin repeat domains 1	92565	0,78	4,93E-05
<i>EFHC1</i>	EF-hand domain (C-terminal) containing 1	114327	0,78	5,85E-05
<i>TSPAN32</i>	tetraspanin 32	10077	0,78	9,48E-05
<i>HOXB4</i>	homeobox B4	3214	0,78	0,0001196
<i>DROSHA</i>	drosha, ribonuclease type III	29102	0,78	0,0001317
<i>DAZ4</i>	deleted in azoospermia 4	57135	0,78	0,0002801
<i>DAZ2</i>	deleted in azoospermia 2	57055	0,78	0,0002801
<i>DAZ1</i>	deleted in azoospermia 1	1617	0,78	0,0002801
<i>DAZ3</i>	deleted in azoospermia 3	57054	0,78	0,0002801
<i>ZNF385C</i>	zinc finger protein 385C	201181	0,78	0,0003901
<i>PIEZO1</i>	piezo-type mechanosensitive ion channel component	9780	0,78	0,0004305
<i>SLC17A9</i>	solute carrier family 17, member 9	63910	0,78	0,0008571
<i>SAA1</i>	serum amyloid A1	6288	0,77	< 1e-07
<i>TOMM22</i>	translocase of outer mitochondrial membrane 22 homolog	56993	0,77	< 1e-07
<i>HIST1H2AK</i>	histone cluster 1, H2ak	8330	0,77	< 1e-07
<i>CDK5RAP3</i>	CDK5 regulatory subunit associated protein 3	80279	0,77	< 1e-07
<i>PYROXD2</i>	pyridine nucleotide-disulphide oxidoreductase domain	84795	0,77	2,00E-07
<i>GAGE10</i>	G antigen 10	643832	0,77	3,30E-06
<i>MYO15B</i>	myosin XVb pseudogene	80022	0,77	5,30E-06
<i>SERF1B</i>	small EDRK-rich factor 1B (centromeric)	728492	0,77	5,62E-05
<i>SERF1A</i>	small EDRK-rich factor 1A (telomeric)	8293	0,77	5,62E-05
<i>SH3D21</i>	SH3 domain containing 21	79729	0,77	5,82E-05
<i>ISYNA1</i>	inositol-3-phosphate synthase 1	51477	0,77	0,000194
<i>LOC153684</i>	uncharacterized LOC153684	153684	0,77	0,0004064
<i>FBXW4P1</i>	F-box and WD repeat domain containing 4 pseudogene	26226	0,77	0,000774
<i>UGGT2</i>	UDP-glucose glycoprotein glucosyltransferase 2	55757	0,77	0,0007977
<i>ZDHHC8P1</i>	zinc finger, DHHC-type containing 8 pseudogene 1	150244	0,76	< 1e-07
<i>TUSC5</i>	tumor suppressor candidate 5	286753	0,76	< 1e-07
<i>STK11IP</i>	serine/threonine kinase 11 interacting protein	114790	0,76	< 1e-07
<i>TMEM151A</i>	transmembrane protein 151A	256472	0,76	< 1e-07
<i>JSRP1</i>	junctional sarcoplasmic reticulum protein 1	126306	0,76	< 1e-07
<i>GAB3</i>	GRB2-associated binding protein 3	139716	0,76	2,80E-06
<i>PILRB</i>	paired immunoglobulin-like type 2 receptor beta	29990	0,76	9,80E-06
<i>KIAA1683</i>	KIAA1683	80726	0,76	1,22E-05
<i>MYCN</i>	v-myc myelocytomatosis viral related oncogene, neuro	4613	0,76	1,62E-05
<i>SOGA2</i>	SOGA family member 2	23255	0,76	2,83E-05
<i>GNMT</i>	glycine N-methyltransferase	27232	0,76	4,19E-05

<i>FOXP1-IT1</i>	FOXP1 intronic transcript 1 (non-protein coding)	100506815	0,76	9,92E-05
<i>METTL3</i>	methyltransferase like 3	56339	0,76	0,0005141
<i>CATSPER2</i>	cation channel, sperm associated 2	117155	0,75	< 1e-07
<i>KIFC3</i>	kinesin family member C3	3801	0,75	< 1e-07
<i>OGT</i>	O-linked N-acetylglucosamine (GlcNAc) transferase	8473	0,75	7,00E-07
<i>INTS3</i>	integrator complex subunit 3	65123	0,75	4,80E-05
<i>COPG2IT1</i>	COPG2 imprinted transcript 1 (non-protein coding)	53844	0,75	0,0001167
<i>LTC4S</i>	leukotriene C4 synthase	4056	0,75	0,0001699
<i>ACCS</i>	1-aminocyclopropane-1-carboxylate synthase homolo	84680	0,75	0,0002815
<i>C21orf56</i>	chromosome 21 open reading frame 56	84221	0,75	0,0007073
<i>AK2</i>	adenylate kinase 2	204	0,75	0,0008129
<i>CRYBB2P1</i>	crystallin, beta B2 pseudogene 1	1416	0,74	< 1e-07
<i>MYO1G</i>	myosin IG	64005	0,74	0,000332
<i>SAA2</i>	serum amyloid A2	6289	0,73	< 1e-07
<i>OSBPL5</i>	oxysterol binding protein-like 5	114879	0,73	< 1e-07
<i>BAHCC1</i>	BAH domain and coiled-coil containing 1	57597	0,73	5,00E-07
<i>HIST1H2BH</i>	histone cluster 1, H2bh	8345	0,73	9,00E-07
<i>ATP2A3</i>	ATPase, Ca <sup>++</sup> transporting, ubiquitous	489	0,73	2,50E-06
<i>HCST</i>	hematopoietic cell signal transducer	10870	0,73	1,20E-05
<i>HIST1H2AM</i>	histone cluster 1, H2am	8336	0,73	8,17E-05
<i>IL12A</i>	interleukin 12A (natural killer cell stimulatory factor 1, $\gamma$	3592	0,73	0,0001393
<i>BEX4</i>	brain expressed, X-linked 4	56271	0,73	0,0006705
<i>LTB4R2</i>	leukotriene B4 receptor 2	56413	0,72	< 1e-07
<i>HNRNPH1</i>	heterogeneous nuclear ribonucleoprotein H1 (H)	3187	0,72	< 1e-07
<i>AP1G2</i>	adaptor-related protein complex 1, gamma 2 subunit	8906	0,72	3,00E-07
<i>CEL</i>	carboxyl ester lipase (bile salt-stimulated lipase)	1056	0,72	6,30E-06
<i>HIST1H2BK</i>	histone cluster 1, H2bk	85236	0,72	7,29E-05
<i>LPPR3</i>	lipid phosphate phosphatase-related protein type 3	79948	0,72	9,42E-05
<i>LOC100507520</i>	uncharacterized LOC100507520	100507520	0,72	0,0001004
<i>HOXA3</i>	homeobox A3	3200	0,72	0,0006867
<i>TCF15</i>	transcription factor 15 (basic helix-loop-helix)	6939	0,71	< 1e-07
<i>CYP11B2</i>	cytochrome P450, family 11, subfamily B, polypeptide	1585	0,71	< 1e-07
<i>MBOAT1</i>	membrane bound O-acyltransferase domain containin	154141	0,71	< 1e-07
<i>PIK3R6</i>	phosphoinositide-3-kinase, regulatory subunit 6	146850	0,71	6,40E-06
<i>P2RX1</i>	purinergic receptor P2X, ligand-gated ion channel, 1	5023	0,71	6,50E-06
<i>SOX4</i>	SRY (sex determining region Y)-box 4	6659	0,71	0,0007905
<i>TARBP1</i>	TAR (HIV-1) RNA binding protein 1	6894	0,7	5,00E-07
<i>MAT2A</i>	methionine adenosyltransferase II, alpha	4144	0,7	8,00E-07
<i>HIST1H2BO</i>	histone cluster 1, H2bo	8348	0,7	3,10E-06
<i>FAM185A</i>	family with sequence similarity 185, member A	222234	0,69	< 1e-07
<i>C16orf93</i>	chromosome 16 open reading frame 93	90835	0,69	1,00E-07
<i>DUSP10</i>	dual specificity phosphatase 10	11221	0,69	1,20E-06
<i>MICALL2</i>	MICAL-like 2	79778	0,69	5,99E-05
<i>ATAT1</i>	alpha tubulin acetyltransferase 1	79969	0,68	< 1e-07
<i>LTK</i>	leukocyte receptor tyrosine kinase	4058	0,68	8,00E-07
<i>NSUN5P2</i>	NOP2/Sun domain family, member 5 pseudogene 2	260294	0,68	6,25E-05
<i>NSUN5P1</i>	NOP2/Sun domain family, member 5 pseudogene 1	155400	0,67	4,00E-07
<i>C1orf186</i>	chromosome 1 open reading frame 186	440712	0,66	2,71E-05
<i>CTSW</i>	cathepsin W	1521	0,66	0,0001499
<i>TCN1</i>	transcobalamin I (vitamin B12 binding protein, R binder	6947	0,66	0,0003309
<i>HIST1H2BE</i>	histone cluster 1, H2be	8344	0,65	< 1e-07
<i>CD33</i>	CD33 molecule	945	0,65	7,40E-05
<i>TIE1</i>	tyrosine kinase with immunoglobulin-like and EGF-like	7075	0,65	0,0001286
<i>ZNF69</i>	zinc finger protein 69	7620	0,64	< 1e-07
<i>HNRNPCL1</i>	heterogeneous nuclear ribonucleoprotein C-like 1	343069	0,64	< 1e-07

<i>FAM46A</i>	family with sequence similarity 46, member A	55603	0,64	5,00E-07
<i>HIST1H2BI</i>	histone cluster 1, H2bi	8346	0,63	3,00E-07
<i>HIST1H2BD</i>	histone cluster 1, H2bd	3017	0,63	0,0003915
<i>C1orf228</i>	chromosome 1 open reading frame 228	339541	0,62	1,83E-05
<i>CSF2RB</i>	colony stimulating factor 2 receptor, beta, low-affinity (	1439	0,62	3,79E-05
<i>HIST1H2BF</i>	histone cluster 1, H2bf	8343	0,61	1,37E-05
<i>RASGRP3</i>	RAS guanyl releasing protein 3 (calcium and DAG-reg	25780	0,6	0,0002793
<i>HDC</i>	histidine decarboxylase	3067	0,57	2,44E-05
<i>LOC285758</i>	uncharacterized LOC285758	285758	0,56	6,92E-05
<i>HIST1H3D</i>	histone cluster 1, H3d	8351	0,55	7,40E-06
<i>HIST2H2BE</i>	histone cluster 2, H2be	8349	0,54	8,00E-07
<i>HIST1H2AD</i>	histone cluster 1, H2ad	3013	0,53	2,00E-07
<i>DPY19L2</i>	dpy-19-like 2 ( <i>C. elegans</i> )	283417	0,51	1,89E-05
<i>MPO</i>	myeloperoxidase	4353	0,51	0,0008496
<i>LGALS3BP</i>	lectin, galactoside-binding, soluble, 3 binding protein	3959	0,5	0,0001763
<i>CLC</i>	Charcot-Leyden crystal protein	1178	0,49	0,0002768