Supplementary Information

AK2 deficiency compromises the mitochondrial energy metabolism required for differentiation of human neutrophil and lymphoid lineages

Emmanuelle Six, Chantal Lagresle-Peyrou, Sandrine Susini, Corinne De Chappedelaine, Nelly Sigrist, Hanem Sadek, Myriam Chouteau, Nicolas Cagnard, Michaela Fontenay, O Hermine, Christine Chomienne, Pascal Reynier, Alain Fischer, Isabelle André-Schmutz, Naig Gueguen, Marina Cavazzana.

Supplementary Methods

Constructs and vectors

We used the following target sequences for the shRNA: shAK2 #1 (ATGGTAGTGGAGCTCATTGAG), shAK2 #2 (GAAACTGGTGAGTGATGAAAT), shCont (CAACAAGATGAAGAGCACCAA). We generated pLKO-mCherry variants of the shAK2 #2 and shCont vectors by replacing the puromycin resistance cassette (BamHI and KpnI sites) by the mCherry reporter. hAK1 or hBcl2 cDNA were cloned into the pWPI lentiviral vector as previously described [1].

Double transduction of human CD34+ progenitor cells and the HL60 cell line

Cord blood CD34+ cells were cultured overnight (as previously described[1]) and transduced first with the pWPI supernatant and then twice with the pLKO-mCherry supernatant. Two days later, the GFP+mCherry+ cells were sorted on a FACSAria (BD Biosciences) prior to *in vitro* differentiation.

The HL60 cell line was transduced twice with pWPI supernatant in the presence of polybrene (4 µg/ml, Sigma Aldrich). In order to select cells expressing the lentiviral vector, GFP+ cells were sorted on a FACSAria (BD Biosciences). The HL60-GFP cell line was then transduced with the pLKO.1 lentiviral vector.

mRNA quantification

Total RNA was isolated with the RNeasy Micro Kit (Qiagen) and then reverse-transcribed using a High-capacity cDNA Reverse Transcription Kit (Life Technologies). Diluted cDNA was used as a template for quantitative, real-time polymerase chain reaction (PCR) reactions in TaqMan gene expression assays for AK2, AK1 and Bcl-2 (Hs01123132, Hs00176119 and Hs 00608023 respectively, Life Technologies). The transcript levels were normalized against the human glyceraldehyde-3-phosphate dehydrogenase (*GAPDH*, Hs02758991*)*. The PCRs were performed on a ViiA7 Real-Time PCR System (Applied Biosystems), according to the manufacturer's instructions.

Electron microscopy

Cells were fixed in medium and cultured for 15 min at 37◦C by the addition of an equal volume of 2x fixative solution [5% glutaraldehyde in PHEM buffer (60 mM Pipes, 25 mM Hepes, 10 mM EGTA and 2 mM MgCl2, pH=6.9)] and medium. Then cells were collected by centrifugation for 5 min at 2000 g and fixation was continued for 1 h at room temperature with fresh fixative [2,5% (w/v) glutaraldehyde in PHEM buffer]. Then the cells were washed with PHEM buffer, and resuspended in 2,5% (w/v) glutaraldehyde in PHEM buffer and stored at 4◦C overnight. Cells were washed three times with PHEM buffer and were postfixed with 1% osmium tetroxide for 1 h at room temperature, dehydrated in ethanol gradient, and embedded in Epon. Thin sections were cut with a Leica EM UC7 Microtome, stained with uranyl acetate and lead citrate. The samples were observed under Tecnai T12 (FEI company) at 120 kV accelerating voltage. Images were recorded using Eagle camera and Tia software.

Bibliography

1 Lagresle-Peyrou C, Six EM, Picard C et al. Human adenylate kinase 2 deficiency causes a profound hematopoietic defect associated with sensorineural deafness. Nat Genet 2009;41:106-111.

Supplementary Figure 1

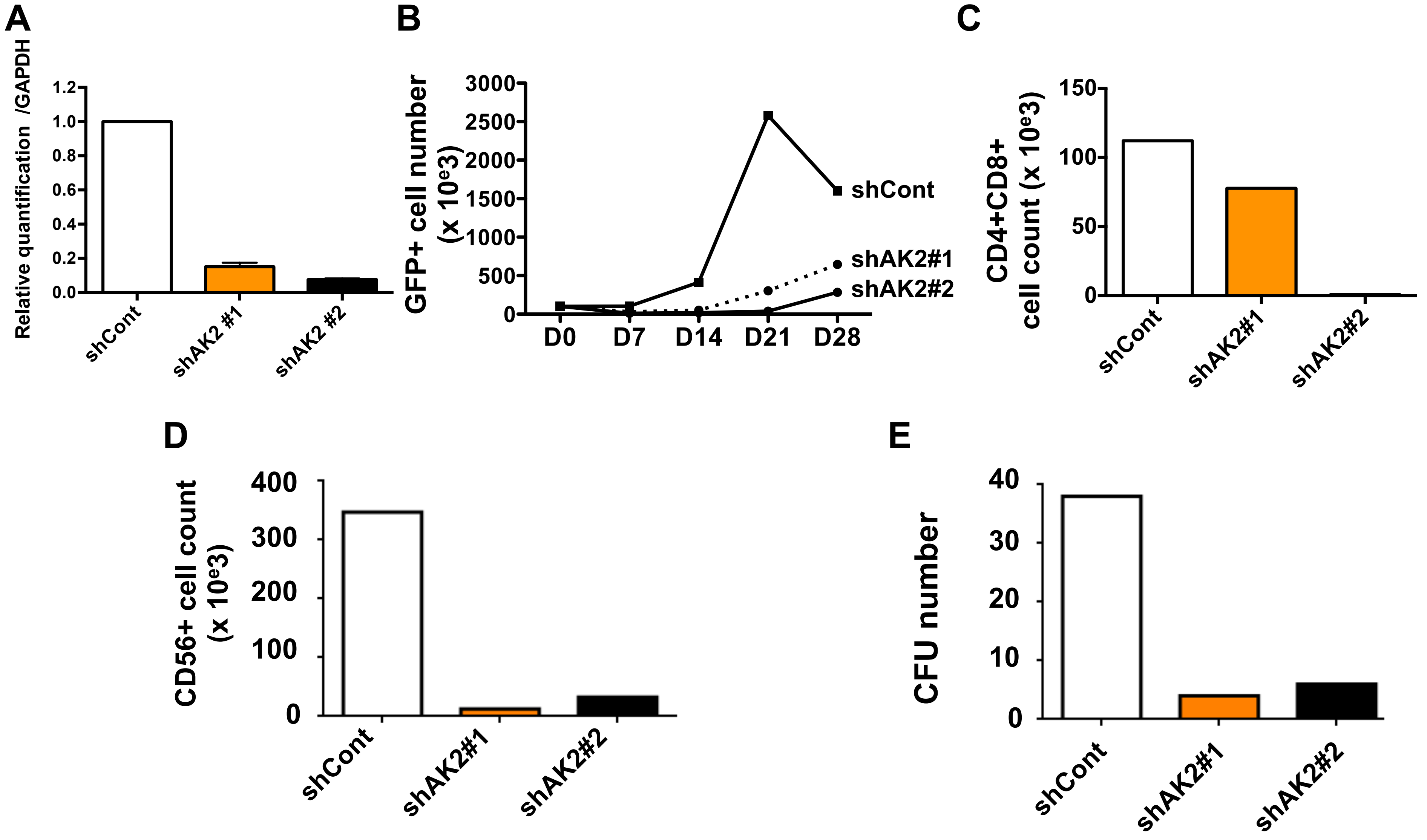

Figure S1

Two independent shAK2 approaches reveals similar degrees of inhibition of lymphoid and myeloid differentiation

Cord blood CD34+ progenitors were transduced with shAK2 #1, shAK2 #2 or shCont, sorted for GFP+ cells and cultured in transduction medium for 1 week (A) on OP9-hDelta1 cells until D28 (B-C), in NK cell differentiation medium until D21 (D) or seeded on methylcellulose until D12 (E).

(A) RT-qPCRs were performed on cell samples, in order to measure the level of AK2 inhibition.

(B) The change over time in the GFP+ cell count for shCont-transduced cells (black squares) or shAK2-transduced cells (shAK2 #1: dashed line black circles; shAK2#2: solid line black circles).

(C) The DP CD4+CD8+ cell count was determined under shCont, shAK2 #1 or shAK2#2 conditions after differentiation on OP9-hDelta1

(D) The CD56+ cell count was determined under shCont, shAK2 #1 or shAK2#2 condition after NK cell differentiation.

(E) The number of colony-forming units (CFUs) was evaluated in a methylcellulose assay under shCont, shAK2 #1 and shAK2#2 conditions. The CFUs include both CFU-G and CFU-M colonies.

Supplementary Figure 2

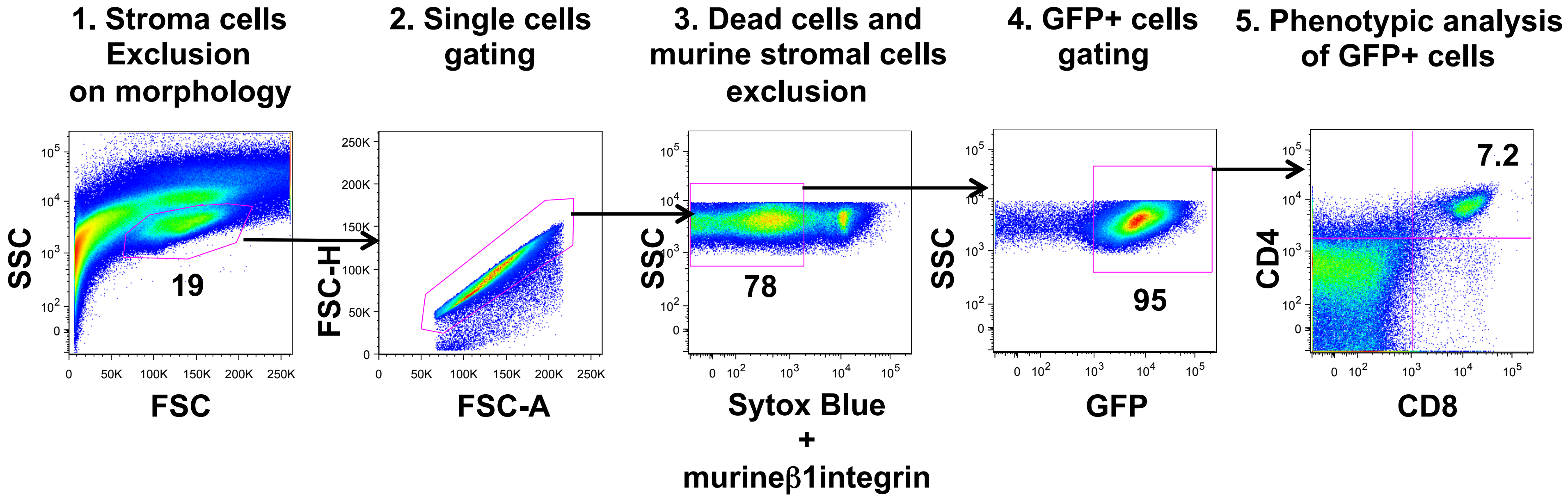

Figure S2

Flow cytometry gating strategy for T cell differentiation analysis of the GFP+ transduced cells.

Cord blood CD34+ progenitors were transduced with shCont, sorted for GFP+ cells and cultured for 28 days on OP9-hDelta1 stromal cell (to monitor T-cell differentiation).

In order to guarantee the removal of stromal cells (which are also GFP+), the flow cytometry analysis of the T-cell differentiation used a gating strategy with an antibody against murine b1 integrin. Dead cells were removed using Sytox Blue staining.

Supplementary Figure 3

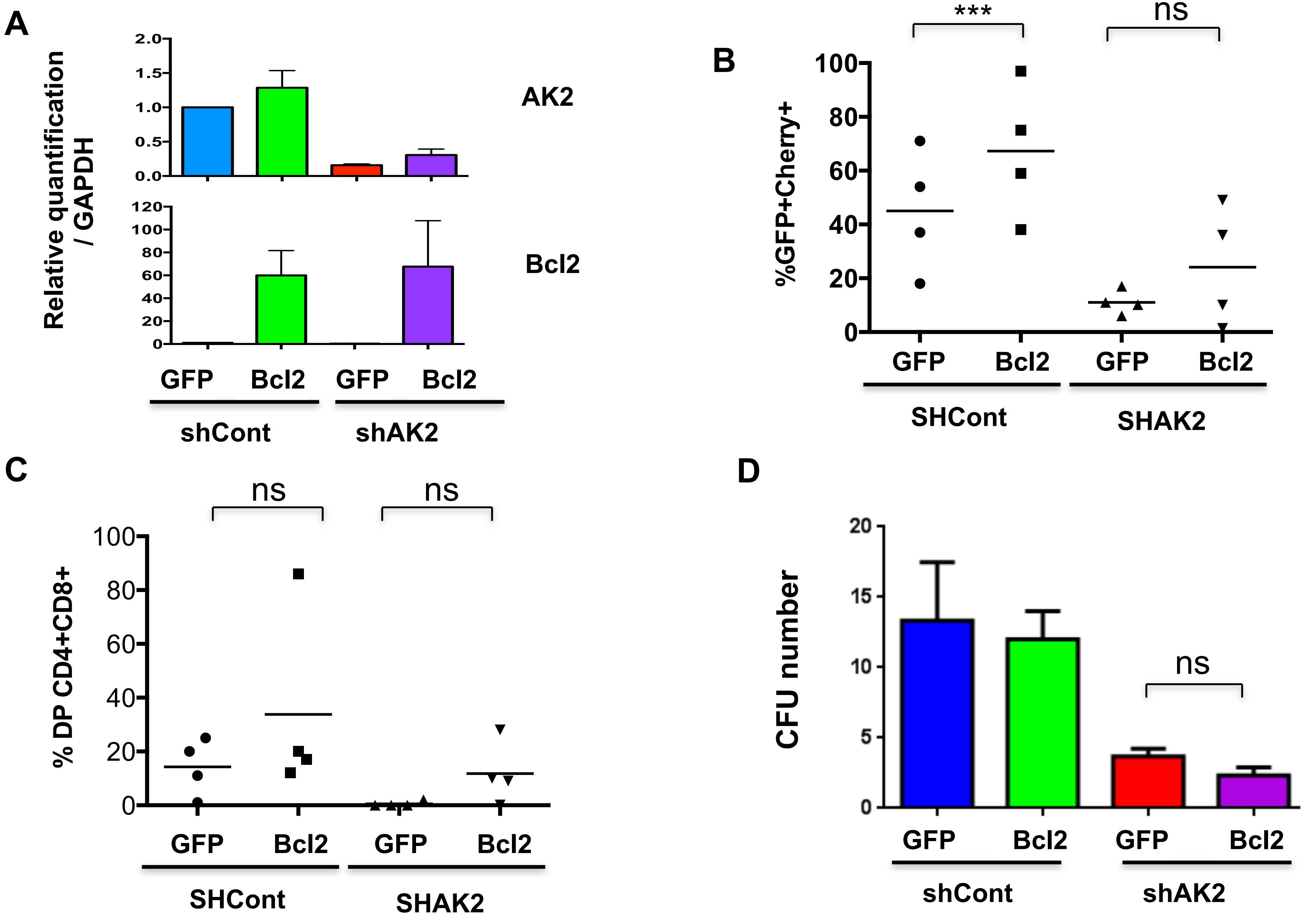

Figure S3

Bcl2 does not rescue survival and differentiation of AK2 knock-down progenitors.

Cord blood CD34+ progenitors were double-transduced with Bcl2 and shAK2 or shCont, sorted for GFP+mCherry+ cells and cultured in the transduction medium for 1 week (A), plated on OP9-hDelta1cells until D42 (B and C) or plated on methylcellulose for 12 days (D)

(A) RT-qPCRs were performed on cell samples, in order to measure the level of AK2 inhibition (upper panel, the slight increase in AK2 upon adition of Bcl2 is not significant) and monitor the expression of Bcl2 (lower panel)

(B) Percentage of GFP+mCherry+ cells 42 days after initiation of T cell differentiation under the shAK2 and shCont conditions ($p=0.0002$ between shCont+GFP and shCont + Bcl2).

(C) Percentage of DP CD4+CD8+ T cells 42 days after the initiation of T cell differentiation.

(D) The number of CFUs was evaluated in the shCont+GFP, shCont+Bcl2, shAK2+GFP and shAK2+Bcl2 conditions. The CFUs include both CFU-G and CFU-M colonies.

ns : not significant differences

Supplementary Figure 4

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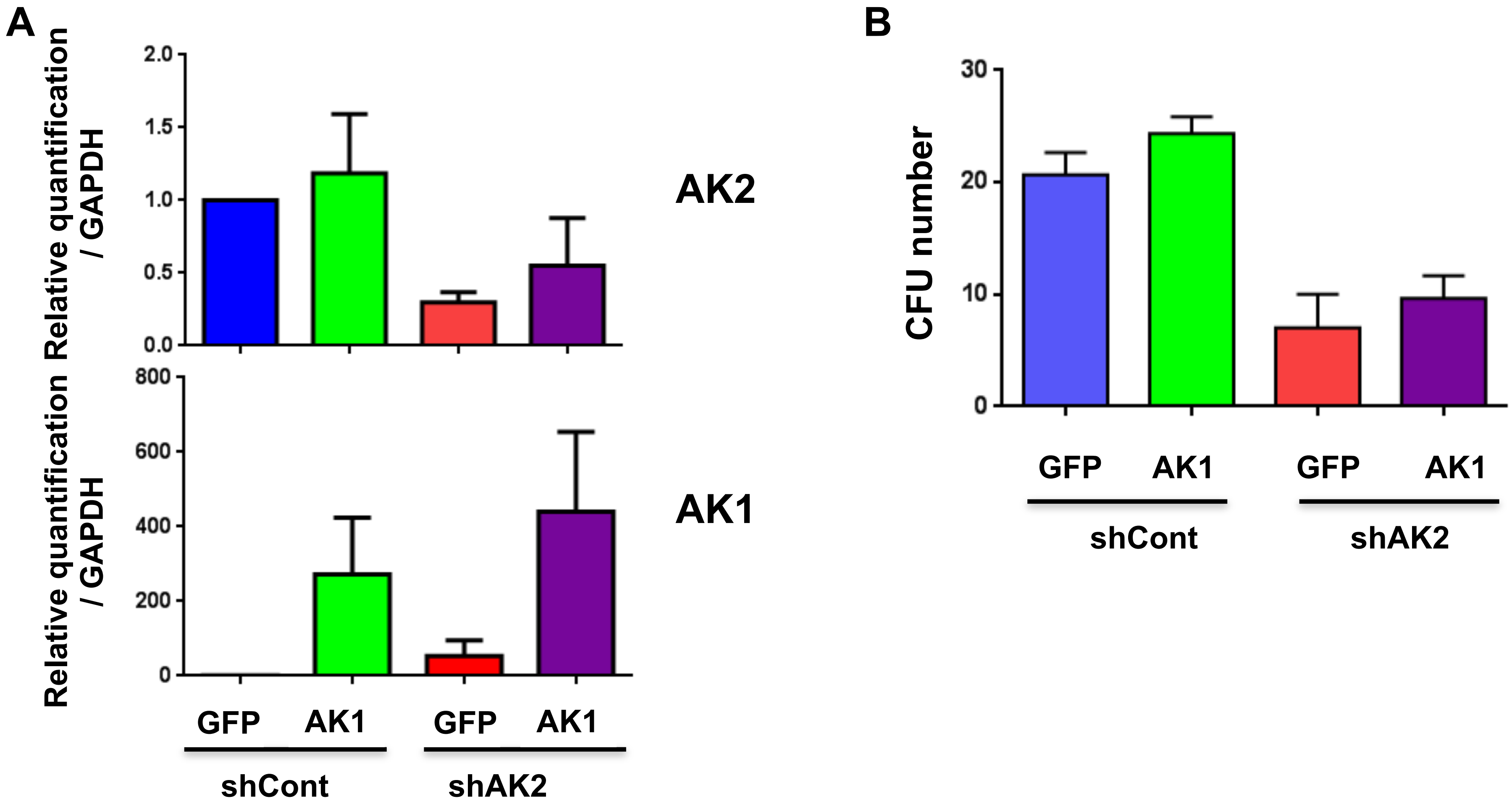

Figure S4

AK1 does not rescue survival and differentiation of AK2 knock-down progenitors

Cord blood CD34+ progenitors were double-transduced with AK1 and shAK2 or shCont, sorted for GFP+mCherry+ cells and cultured in the transduction medium for 1 week (A), or cultured on methylcellulose for 12 days (n=3) (B).

(A) RT-qPCR were performed on cell samples, in order to measure the level of AK2 inhibition (upper panel) and monitor the expression of AK1 (lower panel) under the shCont+GFP, shCont+AK1, shAK2+GFP and shAK2+AK1 conditions.

(B) The number of CFUs was evaluated under the shCont+GFP, shCont+AK1, shAK2+GFP and shAK2+AK1 conditions. The CFUs include both CFU-G and CFU-M colonies.

Supplementary Figure 5

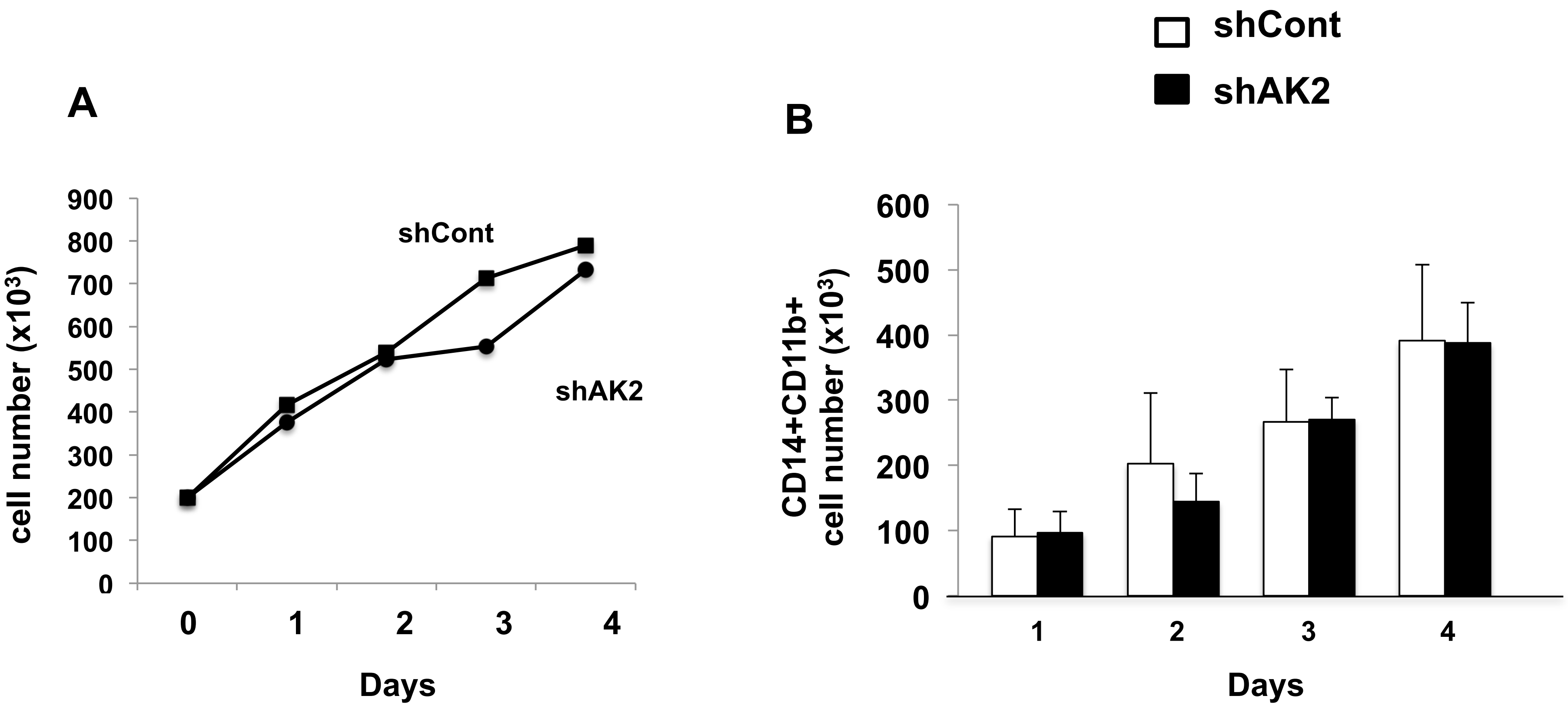

Figure S5

Monocyte differentiation is not impaired in the AK2-deficient HL60 cell line.

HL60 cells were transduced with shAK2 or shCont, sorted for GFP+ cells and seeded in culture with 100nM vitamin D3 (to induce monocyte differentiation).

(A) The change over time in the total cell count over 4 days of monocyte differentiation (n=4) under the shAK2 (black round) and shCont (black square) conditions.

(B) The CD14+CD11b+ monocyte count was measured for 4 days under the shAK2 (black bar) and shCont (white bar) conditions

Supplementary Figure S6

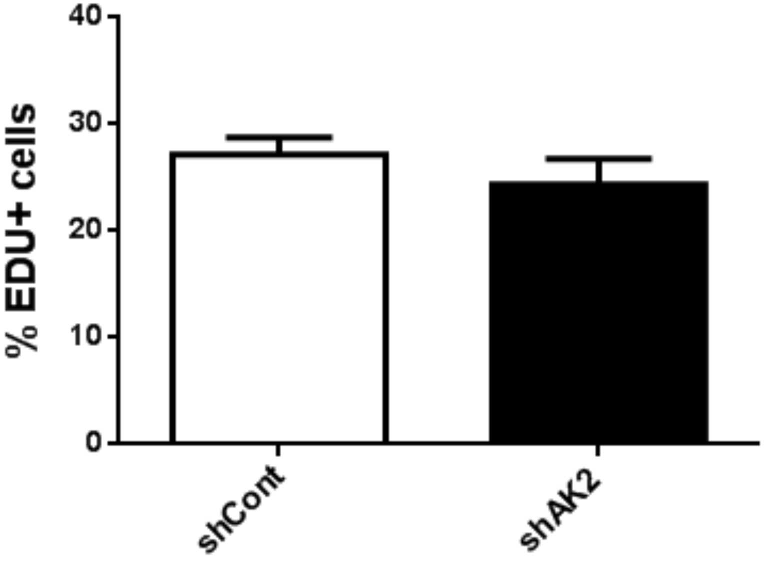

Figure S6

The proliferation of CD34 progenitors is not affected by AK2 knock-down

Cord blood CD34+ progenitors were transduced with shAK2 or shCont, sorted for GFP+ cells and cultured in the presence of SCF+TPO+FLT3-L+IL-3 (a cytokine cocktail commonly used to induce CD34+ cell proliferation). Cell proliferation (incorporation of EdU) was analyzed four days after the initiation of the culture under the shCont and shAK2 conditions ($p>0.05$, $n=3$).

Supplementary Figure 7

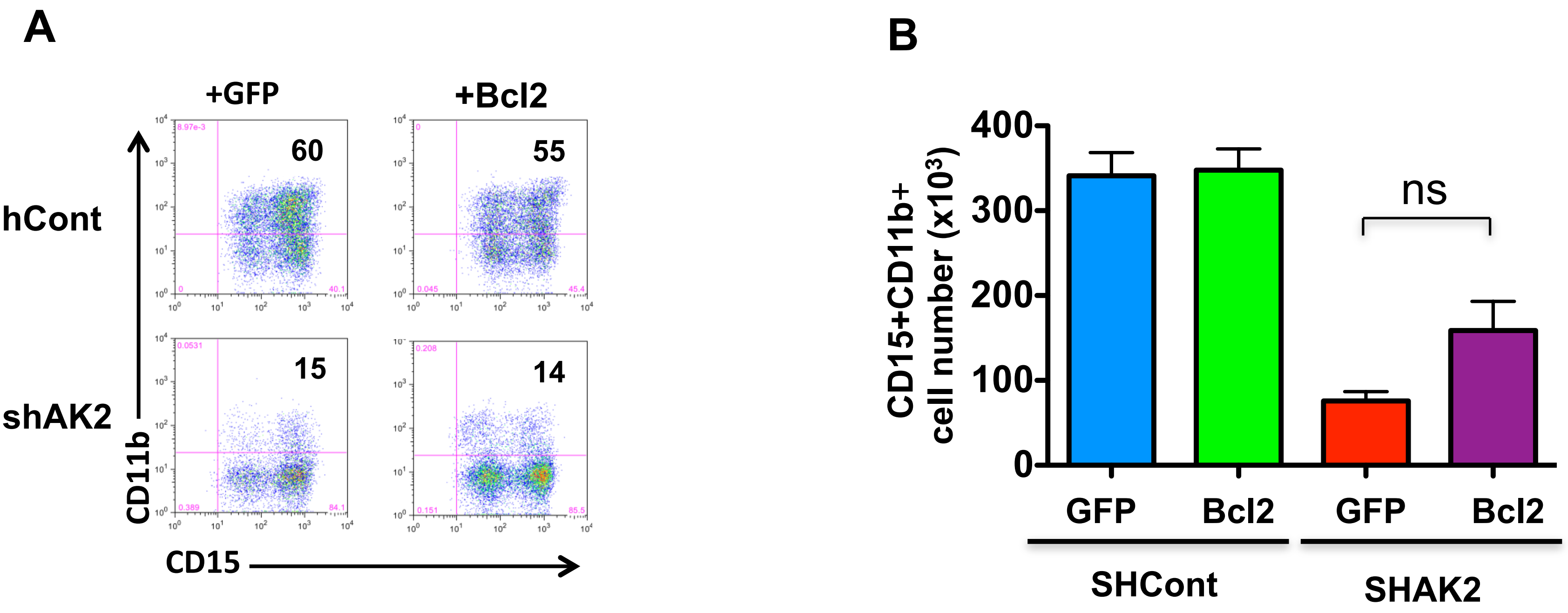

Figure S7

Bcl2 does not restore neutrophil differentiation of AK2-deficient HL60 cells.

HL60 cells were transduced with Bcl2 and shAK2 or shCont, selected for GFP+ and puromycin resistance and cultured with 10uM ATRA (to induce granulocyte differentiation).

(A) Flow cytometry analysis of GFP+ cells after 4 days of culture under shAK2 and shCont conditions.

(B) The CD15+CD11b+ granulocyte count was measured after 4 days under the shCont+GFP, shCont+Bcl2, shAK2+GFP and shAK2+Bcl2 conditions.

Supplementary Figure 8

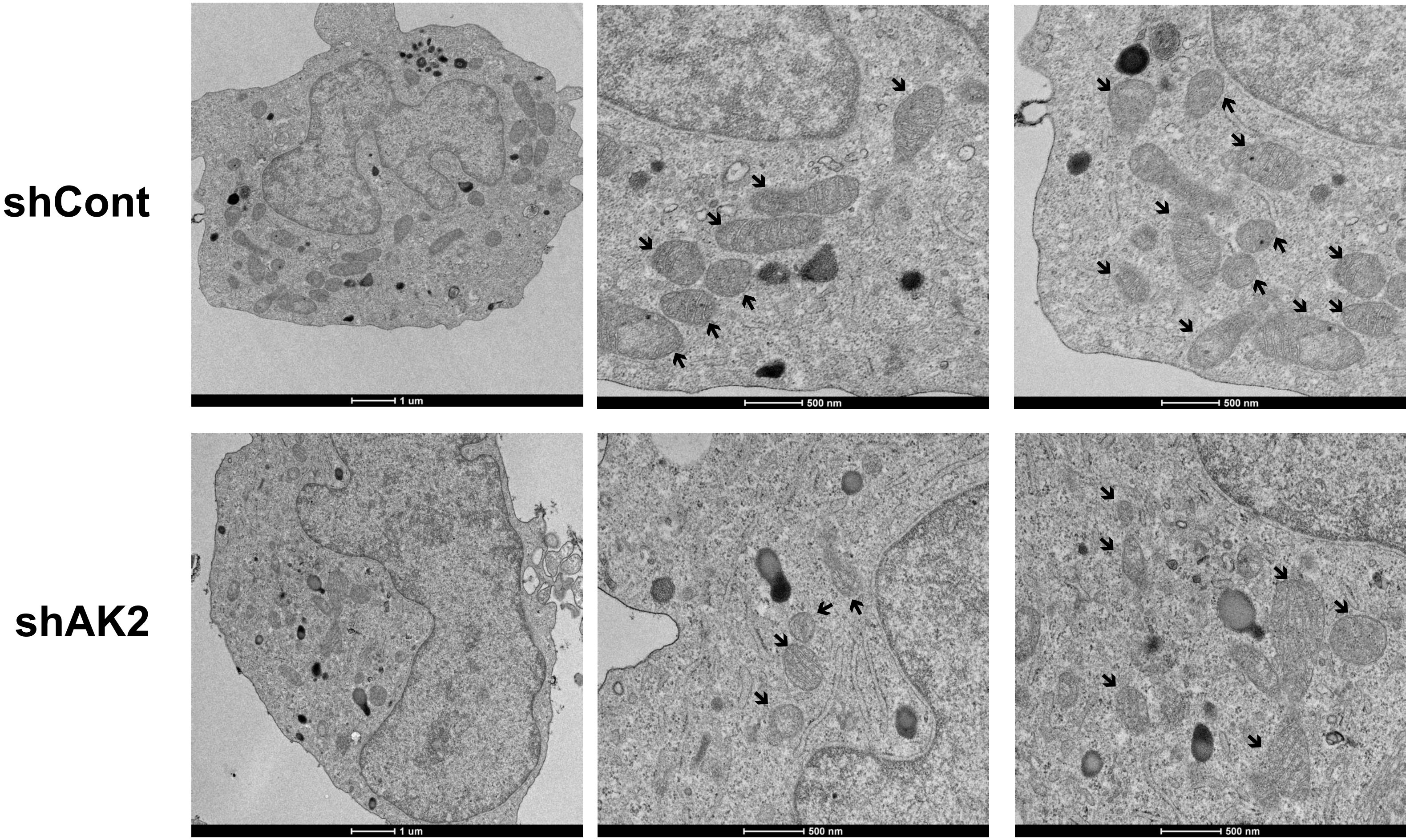

Figure S8

Mitochondria ultrastructure in AK2-deficient HL60 cells.

HL60 cells were transduced with shAK2 or shCont, selected for puromycin resistance and cultured with 10uM ATRA for 4 days (to induce granulocyte differentiation). Transmission electron microscopy revealed the mitochondrial ultrastructure. Arrow highlight mitochondria.

Supplementary Table S1

(the fold change (FC) and pvalue between shAK2 and shCont is shown for shAK2 #1 and shAK2 #2, upregulated genes are shown in bold type)

Gene Symbol	Entrez Gene Name	FC #1	FC #2	pvalue #1	pvalue #2
AACS	acetoacetyl-CoA synthetase	0.72	0.66	0.016	0.026
ABCF2	ATP-binding cassette, sub-family F (GCN20), member 2	0.62	0.78	0.035	0.032
ABHD14A /// ACY1	abhydrolase domain containing 14A /// aminoacylase 1	0.57	0.75	0.019	0.011
ABHD14B	abhydrolase domain containing 14B	0.81	0.61	0.037	0.033
ACAD9	acyl-CoA dehydrogenase family, member 9	0.80	0.71	0.027	0.011
ACP5	acid phosphatase 5, tartrate resistant	**4.43**	**7.22**	0.003	0.000
ACSL3	acyl-CoA synthetase long-chain family member 3	0.39	0.58	0.003	0.041
ACSL5	acyl-CoA synthetase long-chain family member 5	0.53	0.72	0.030	0.028
ACSM3	acyl-CoA synthetase medium-chain family member 3	**1.45**	**5.12**	0.042	0.003
ACSS1	acyl-CoA synthetase short-chain family member 1	0.58	0.62	0.040	0.043
ACY3	aspartoacylase (aminocyclase) 3	**1.30**	**3.54**	0.013	0.041
ADCK2	aarF domain containing kinase 2	0.65	0.53	0.022	0.011
ADD2	adducin 2 (beta)	0.18	0.13	0.009	0.004
ADRBK2	adrenergic, beta, receptor kinase 2	0.62	0.74	0.033	0.029
AFF4	AF4/FMR2 family, member 4	**1.30**	**2.16**	0.038	0.026
AFG3L2	AFG3 ATPase family gene 3-like 2 (S, cerevisiae)	0.73	0.76	0.008	0.020
AHCYL1	adenosylhomocysteinase-like 1	0.69	0.76	0.027	0.023
AHSP	alpha hemoglobin stabilizing protein	0.31	0.27	0.012	0.013
AK2	adenylate kinase 2	0.13	0.12	0.001	0.000
AK7	adenylate kinase 7	0.40	0.50	0.003	0.030
AKAP13	A kinase (PRKA) anchor protein 13	**1.28**	**1.35**	0.022	0.026
AKIRIN1	akirin 1	**1.56**	**1.54**	0.018	0.008
AKR1C1	aldo-keto reductase family 1, member C1	0.21	0.19	0.014	0.013
AKR1C2	aldo-keto reductase family 1, member C2	0.30	0.24	0.033	0.016
AKT3	v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma)	**1.71**	**1.92**	0.038	0.038
ALAD	aminolevulinate dehydratase	0.51	0.50	0.001	0.004
ALAS2	aminolevulinate, delta-, synthase 2	0.10	0.09	0.003	0.005
ALOX5	arachidonate 5-lipoxygenase	0.37	0.18	0.009	0.029
AMMECR1	Alport syndrome, mental retardation, midface hypoplasia and elliptocytosis chromosomal region gene 1	0.34	0.17	0.003	0.016
ANK1	ankyrin 1, erythrocytic	0.62	0.63	0.024	0.018
ANKLE1	ankyrin repeat and LEM domain containing 1	0.33	0.53	0.013	0.012
ANKRD44	ankyrin repeat domain 44	**1.84**	**1.57**	0.028	0.037
ANPEP	alanyl (membrane) aminopeptidase	**2.05**	**2.27**	0.004	0.041
AP1M1	adaptor-related protein complex 1, mu 1 subunit	0.80	0.82	0.032	0.023
APOA1BP	apolipoprotein A-I binding protein	0.58	0.80	0.001	0.007
APOBEC3C	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3C	0.68	0.83	0.025	0.005
APOC1	apolipoprotein C-I	0.21	0.31	0.005	0.027
APOOL	apolipoprotein O-like	0.70	0.69	0.012	0.030
APP	amyloid beta (A4) precursor protein	**1.66**	**1.49**	0.033	0.012
APPL1	adaptor protein, phosphotyrosine interaction, PH domain and leucine zipper containing 1	**1.52**	**1.86**	0.050	0.022
ARHGAP19	Rho GTPase activating protein 19	0.68	0.57	0.007	0.030
ARHGEF3	Rho guanine nucleotide exchange factor (GEF) 3	**2.42**	**3.05**	0.007	0.002
ARHGEF37	Rho guanine nucleotide exchange factor (GEF) 37	0.24	0.27	0.007	0.005
ARID1A	AT rich interactive domain 1A (SWI-like)	0.71	0.79	0.042	0.041
ARPC3	actin related protein 2/3 complex, subunit 3, 21kDa	**2.14**	**1.44**	0.030	0.043
ARRDC2	arrestin domain containing 2	**1.38**	**1.60**	0.025	0.047
ARSB	arylsulfatase B	0.56	0.53	0.042	0.037

ASAH1	N-acylsphingosine amidohydrolase (acid ceramidase) 1	**1.57**	**1.98**	0.034	0.008
ASNA1	arsA arsenite transporter, ATP-binding, homolog 1 (bacterial)	0.83	0.62	0.034	0.002
ASPM	asp (abnormal spindle) homolog, microcephaly associated (Drosophila)	0.76	0.61	0.025	0.007
ASRGL1	asparaginase like 1	0.57	0.54	0.035	0.024
ATAD3A	ATPase family, AAA domain containing 3A	0.80	0.80	0.017	0.023
ATAD3B	ATPase family, AAA domain containing 3B	0.77	0.76	0.045	0.031
ATP8B4	ATPase, class I, type 8B, member 4	**2.04**	**1.48**	0.038	0.036
ATPIF1	ATPase inhibitory factor 1	0.49	0.43	0.031	0.010
AUH	AU RNA binding protein/enoyl-CoA hydratase	**1.40**	**1.52**	0.006	0.014
AURKA	aurora kinase A	0.78	0.59	0.012	0.005
AVL9	AVL9 homolog (S, cerevisiase)	0.70	0.49	0.049	0.008
B2M	beta-2-microglobulin	**1.30**	**1.25**	0.023	0.050
BAALC	brain and acute leukemia, cytoplasmic	**2.45**	**4.27**	0.040	0.004
BANF1	barrier to autointegration factor 1	0.70	0.70	0.009	0.017
BAZ2B	bromodomain adjacent to zinc finger domain, 2B	**2.04**	**2.26**	0.031	0.019
BCL2L11	BCL2-like 11 (apoptosis facilitator)	0.61	0.43	0.014	0.018
BCS1L	BCS1-like (S, cerevisiae)	0.74	0.61	0.019	0.013
BIRC2	baculoviral IAP repeat-containing 2	**1.29**	**1.42**	0.042	0.027
BLVRB	biliverdin reductase B (flavin reductase (NADPH))	0.26	0.18	0.002	0.011
BOLA3	bolA homolog 3 (E, coli)	0.26	0.69	0.001	0.002
BOP1	block of proliferation 1	0.66	0.65	0.030	0.026
BRP44	brain protein 44	0.53	0.42	0.000	0.032
BTBD11	BTB (POZ) domain containing 11	**1.71**	**1.87**	0.008	0.019
BTBD6	BTB (POZ) domain containing 6	0.70	0.62	0.018	0.038
BTG1	B-cell translocation gene 1, anti-proliferative	**1.57**	**1.55**	0.002	0.026
C10orf46	chromosome 10 open reading frame 46	**1.58**	**1.46**	0.000	0.030
C12orf43	chromosome 12 open reading frame 43	0.69	0.73	0.024	0.041
C12orf52	chromosome 12 open reading frame 52	0.61	0.79	0.011	0.008
C14orf135	chromosome 14 open reading frame 135	0.55	0.55	0.022	0.028
C16orf88	chromosome 16 open reading frame 88	0.62	0.69	0.022	0.007
C17orf90	chromosome 17 open reading frame 90	0.79	0.71	0.032	0.006
C17orf99	chromosome 17 open reading frame 99	0.18	0.14	0.006	0.005
C18orf10	chromosome 18 open reading frame 10	0.50	0.57	0.011	0.026
C1orf135	chromosome 1 open reading frame 135	0.83	0.79	0.027	0.006
C1orf162	chromosome 1 open reading frame 162	0.52	0.65	0.033	0.023
C1orf198	chromosome 1 open reading frame 198	0.51	0.50	0.002	0.007
C1orf93	chromosome 1 open reading frame 93	0.57	0.62	0.038	0.039
C1QBP	complement component 1, q subcomponent binding protein	0.76	0.77	0.002	0.004
C20orf108	chromosome 20 open reading frame 108	0.40	0.38	0.009	0.005
C20orf194	chromosome 20 open reading frame 194	**2.02**	**2.66**	0.017	0.027
C21orf91	chromosome 21 open reading frame 91	**1.60**	**1.94**	0.023	0.010
C22orf13	chromosome 22 open reading frame 13	0.66	0.66	0.002	0.009
C3orf17	chromosome 3 open reading frame 17	**1.23**	**1.30**	0.010	0.000
C3orf39	chromosome 3 open reading frame 39	0.50	0.54	0.009	0.047
C5orf33	chromosome 5 open reading frame 33	0.69	0.53	0.039	0.039
C5orf62	chromosome 5 open reading frame 62	**2.35**	**1.69**	0.012	0.027
C6orf108	chromosome 6 open reading frame 108	0.52	0.61	0.032	0.013
C6orf89	chromosome 6 open reading frame 89	0.47	0.46	0.018	0.034
C7orf44	chromosome 7 open reading frame 44	0.43	0.66	0.004	0.025
C8orf30A	chromosome 8 open reading frame 30A	0.75	0.74	0.016	0.039
C8orf82	chromosome 8 open reading frame 82	0.68	0.62	0.027	0.022
C9orf86	chromosome 9 open reading frame 86	0.58	0.43	0.008	0.007
CACNA2D4	calcium channel, voltage-dependent, alpha 2/delta subunit 4	0.61	0.62	0.023	0.043
CALML4	calmodulin-like 4	**1.92**	**1.71**	0.019	0.023
CAND1	cullin-associated and neddylation-dissociated 1	0.60	0.46	0.041	0.020
CARKD	carbohydrate kinase domain containing	0.69	0.57	0.022	0.001
CARS2	cysteinyl-tRNA synthetase 2, mitochondrial (putative)	0.80	0.65	0.017	0.005

CAST	calpastatin	0.37	0.45	0.005	0.014
CBARA1	calcium binding atopy-related autoantigen 1	0.70	0.68	0.040	0.037
CBX5	chromobox homolog 5	0.68	0.77	0.028	0.049
CCDC77	coiled-coil domain containing 77	0.81	0.51	0.025	0.020
CCDC90B	coiled-coil domain containing 90B	**1.64**	**2.51**	0.010	0.006
CCNA1	cyclin A1	**4.09**	**1.70**	0.001	0.026
CCNE1	cyclin E1	0.64	0.41	0.001	0.003
CCNF	cyclin F	0.63	0.49	0.020	0.035
CCR2	chemokine (C-C motif) receptor 2	0.56	0.49	0.009	0.049
CCT5	chaperonin containing TCP1, subunit 5 (epsilon)	0.43	0.50	0.007	0.007
CCT7	chaperonin containing TCP1, subunit 7 (eta)	0.82	0.83	0.008	0.014
CD109	CD109 molecule	**2.08**	**7.22**	0.005	0.014
CD1D	CD1d molecule	**1.79**	**2.83**	0.044	0.015
CD200	CD200 molecule	**2.91**	**9.96**	0.007	0.028
CD300A	CD300a molecule	**1.21**	**1.43**	0.048	0.019
CD302	CD302 molecule	**1.47**	**1.36**	0.007	0.029
CD34	CD34 molecule	**1.88**	**2.67**	0.001	0.036
CD44	CD44 molecule (Indian blood group)	**1.43**	**1.88**	0.038	0.037
CD48	CD48 molecule	**1.48**	**1.79**	0.019	0.025
CDC20	cell division cycle 20 homolog (S, cerevisiae)	0.62	0.46	0.043	0.002
CDC27	cell division cycle 27 homolog (S, cerevisiae)	0.78	0.37	0.003	0.007
CDC45	cell division cycle 45 homolog (S, cerevisiae)	0.67	0.50	0.030	0.017
CDC6	cell division cycle 6 homolog (S, cerevisiae)	0.59	0.55	0.020	0.019
CDH1	cadherin 1, type 1, E-cadherin (epithelial)	0.47	0.09	0.027	0.002
CDK10	cyclin-dependent kinase 10	0.57	0.72	0.003	0.038
CDK5RAP2	CDK5 regulatory subunit associated protein 2	0.59	0.52	0.009	0.032
CDKN1C	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	**4.17**	**8.12**	0.001	0.002
CEBPB	CCAAT/enhancer binding protein (C/EBP), beta	**1.42**	**1.87**	0.022	0.010
CENPN	centromere protein N	0.82	0.73	0.041	0.041
CENPV	centromere protein V	0.42	0.60	0.004	0.045
CEP72	centrosomal protein 72kDa	0.50	0.60	0.029	0.045
CFH	complement factor H	**4.52**	**3.23**	0.008	0.005
CFH /// CFHR1	complement factor H /// complement factor H-related 1	**2.75**	**10.89**	0.002	0.001
CHCHD4	coiled-coil-helix-coiled-coil-helix domain containing 4	0.78	0.67	0.023	0.014
CHD7	chromodomain helicase DNA binding protein 7	0.58	0.74	0.028	0.039
CHEK2	CHK2 checkpoint homolog (S, pombe)	0.71	0.66	0.018	0.015
CHPT1	choline phosphotransferase 1	0.75	0.54	0.048	0.011
CKAP2L	cytoskeleton associated protein 2-like	0.73	0.58	0.046	0.046
CLC	Charcot-Leyden crystal protein	0.25	0.06	0.009	0.017
CLDN10	claudin 10	**2.71**	**3.41**	0.012	0.006
CLEC2B	C-type lectin domain family 2, member B	**3.70**	**3.53**	0.006	0.020
CLIC4	chloride intracellular channel 4	**1.71**	**1.54**	0.007	0.001
CLN6	ceroid-lipofuscinosis, neuronal 6, late infantile, variant	0.59	0.72	0.006	0.027
CLU	clusterin	0.48	0.66	0.017	0.018
CMAH	cytidine monophosphate-N-acetylneuraminic acid hydroxylase (CMP-N-acetylneuraminate monooxygenase) pseudogene	**4.04**	**3.34**	0.043	0.042
CNST	consortin, connexin sorting protein	**1.73**	**2.72**	0.031	0.026
COASY	CoA synthase	0.71	0.75	0.050	0.003
COCH	coagulation factor C homolog, cochlin (Limulus polyphemus)	0.27	0.31	0.013	0.023
COPS6	COP9 constitutive photomorphogenic homolog subunit 6 (Arabidopsis)	0.56	0.68	0.010	0.030
COQ3	coenzyme Q3 homolog, methyltransferase (S, cerevisiae)	0.60	0.66	0.023	0.023
COTL1	coactosin-like 1 (Dictyostelium)	0.63	0.59	0.008	0.008
COX5A	cytochrome c oxidase subunit Va	0.55	0.57	0.012	0.047
CPNE8	copine VIII	**1.56**	**2.52**	0.013	0.018
CRHBP	corticotropin releasing hormone binding protein	**3.63**	**19.17**	0.011	0.019
CRIM1	cysteine rich transmembrane BMP regulator 1 (chordin-like)	**1.80**	**3.21**	0.026	0.024

CRYZL1	crystallin, zeta (quinone reductase)-like 1	**1.38**	**1.38**	0.028	0.007
CSRP1	cysteine and glycine-rich protein 1	0.75	0.77	0.007	0.037
CTHRC1	collagen triple helix repeat containing 1	**3.88**	**2.96**	0.012	0.038
CTNNAL1	catenin (cadherin-associated protein), alpha-like 1	0.72	0.43	0.041	0.018
CTNNB1	catenin (cadherin-associated protein), beta 1, 88kDa	**2.46**	**2.13**	0.014	0.016
CTSC	cathepsin C	0.71	0.55	0.025	0.019
CTSE	cathepsin E	0.30	0.27	0.032	0.048
CTTN	cortactin	0.16	0.25	0.005	0.025
CUL4B	cullin 4B	**1.75**	**1.33**	0.026	0.006
CXADR	coxsackie virus and adenovirus receptor	0.21	0.30	0.003	0.026
CYP1B1	cytochrome P450, family 1, subfamily B, polypeptide 1	**2.06**	**4.68**	0.044	0.029
CYSLTR1	cysteinyl leukotriene receptor 1	**1.94**	**2.34**	0.042	0.031
CYYR1	cysteine/tyrosine-rich 1	**2.13**	**4.87**	0.044	0.009
DAAM1	dishevelled associated activator of morphogenesis 1	0.38	0.36	0.022	0.014
DAZAP1	DAZ associated protein 1	0.77	0.70	0.039	0.028
DCBLD2	Discoidin, CUB and LCCL domain containing 2	**4.28**	**4.04**	0.008	0.027
DCLRE1B	DNA cross-link repair 1B	0.77	0.63	0.027	0.006
DCUN1D5	DCN1, defective in cullin neddylation 1, domain containing 5 (S, cerevisiae)	0.80	0.59	0.049	0.031
DDAH2	dimethylarginine dimethylaminohydrolase 2	**1.75**	**2.18**	0.008	0.014
DDI2	DNA-damage inducible 1 homolog 2 (S, cerevisiae)	0.46	0.45	0.009	0.025
DDX11 /// DDX12 /// LOC642846	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 /// DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 12 /// DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11-like	0.76	0.39	0.010	0.002
DDX24	DEAD (Asp-Glu-Ala-Asp) box polypeptide 24	0.74	0.79	0.010	0.003
DDX39	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39	0.69	0.59	0.013	0.006
DDX41	DEAD (Asp-Glu-Ala-Asp) box polypeptide 41	0.78	0.70	0.025	0.007
DHCR7	7-dehydrocholesterol reductase	0.60	0.51	0.009	0.004
DHFR	dihydrofolate reductase	0.62	0.73	0.001	0.034
DHRS11	dehydrogenase/reductase (SDR family) member 11	0.14	0.22	0.002	0.006
DHX35	DEAH (Asp-Glu-Ala-His) box polypeptide 35	0.68	0.69	0.028	0.039
DLD	dihydrolipoamide dehydrogenase	0.67	0.60	0.034	0.017
DLST	dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex)	0.68	0.80	0.001	0.005
DMXL2	Dmx-like 2	**3.32**	**1.69**	0.009	0.015
DNAJA4	DnaJ (Hsp40) homolog, subfamily A, member 4	0.35	0.30	0.017	0.014
DNAJC10	DnaJ (Hsp40) homolog, subfamily C, member 10	**1.75**	**1.78**	0.035	0.019
DNAJC11	DnaJ (Hsp40) homolog, subfamily C, member 11	0.71	0.76	0.007	0.009
DNAJC19	DnaJ (Hsp40) homolog, subfamily C, member 19	0.66	0.78	0.018	0.018
DNAJC9	DnaJ (Hsp40) homolog, subfamily C, member 9	0.80	0.74	0.025	0.044
DNASE2	deoxyribonuclease II, lysosomal	**1.40**	**2.66**	0.030	0.045
DOK4	docking protein 4	**2.58**	**4.43**	0.014	0.011
DOLPP1	dolichyl pyrophosphate phosphatase 1	0.72	0.77	0.027	0.026
DONSON	downstream neighbor of SON	0.68	0.50	0.027	0.001
DPH5	DPH5 homolog (S, cerevisiae)	**1.61**	**1.87**	0.015	0.010
DPP3	dipeptidyl-peptidase 3	0.66	0.77	0.027	0.048
DPP7	Dipeptidyl-peptidase 7	0.23	0.23	0.000	0.005
DPYSL2	dihydropyrimidinase-like 2	0.70	0.50	0.030	0.019
DRG1	developmentally regulated GTP binding protein 1	0.82	0.82	0.017	0.007
DSC2	desmocollin 2	**4.35**	**2.51**	0.029	0.045
DTYMK	deoxythymidylate kinase (thymidylate kinase)	0.61	0.57	0.023	0.036
EARS2	glutamyl-tRNA synthetase 2, mitochondrial (putative)	0.66	0.67	0.046	0.046
EEFSEC	eukaryotic elongation factor, selenocysteine-tRNA-specific	0.59	0.71	0.007	0.018
EHD4	EH-domain containing 4	0.70	0.53	0.036	0.002
EIF2AK1	eukaryotic translation initiation factor 2-alpha kinase 1	0.58	0.70	0.001	0.002
EIF3B	eukaryotic translation initiation factor 3, subunit B	0.73	0.71	0.024	0.029
EIF6	eukaryotic translation initiation factor 6	0.57	0.80	0.003	0.022
ELOVL1	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 1	0.73	0.70	0.040	0.038

EME1	essential meiotic endonuclease 1 homolog 1 (S, pombe)	0.60	0.62	0.005	0.009
EMP2	epithelial membrane protein 2	0.31	0.35	0.006	0.012
ENDOD1	endonuclease domain containing 1	0.43	0.61	0.002	0.039
ENDOG	endonuclease G	0.69	0.58	0.025	0.008
ENO3	enolase 3 (beta, muscle)	0.73	0.58	0.032	0.018
ENOSF1	enolase superfamily member 1	0.60	0.56	0.013	0.006
EPB42	erythrocyte membrane protein band 4,2	0.25	0.29	0.023	0.031
EPC2	enhancer of polycomb homolog 2 (Drosophila)	**1.35**	**1.58**	0.012	0.013
EPCAM	epithelial cell adhesion molecule	0.18	0.17	0.007	0.023
EPM2AIP1	EPM2A (laforin) interacting protein 1	0.79	0.71	0.008	0.013
EPOR	erythropoietin receptor	0.33	0.30	0.009	0.007
EPS15L1	epidermal growth factor receptor pathway substrate 15-like 1	0.64	0.47	0.031	0.019
ERAL1	Era G-protein-like 1 (E, coli)	0.57	0.79	0.013	0.049
ERG	v-ets erythroblastosis virus E26 oncogene homolog (avian)	**1.74**	**3.43**	0.020	0.018
ERI1	exoribonuclease 1	0.50	0.56	0.003	0.016
ERMAP	erythroblast membrane-associated protein (Scianna blood group)	0.47	0.62	0.001	0.045
ETV6	ets variant 6	**1.38**	**1.64**	0.036	0.023
EXOSC2	exosome component 2	0.72	0.78	0.038	0.026
EXOSC4	exosome component 4	0.68	0.82	0.025	0.049
EZR	ezrin	0.54	0.67	0.011	0.022
F2RL1	coagulation factor II (thrombin) receptor-like 1	**1.34**	**6.65**	0.037	0.011
FADS1	fatty acid desaturase 1	0.61	0.63	0.018	0.009
FAF1	Fas (TNFRSF6) associated factor 1	0.79	0.62	0.005	0.002
FAM178B	family with sequence similarity 178, member B	0.33	0.34	0.005	0.006
FAM26F	family with sequence similarity 26, member F	**1.31**	**2.06**	0.016	0.035
FAM46C	family with sequence similarity 46, member C	0.58	0.28	0.012	0.003
FAM60A	family with sequence similarity 60, member A	**1.34**	**1.53**	0.029	0.012
FAM82A2	family with sequence similarity 82, member A2	0.76	0.65	0.021	0.003
FAM89A	family with sequence similarity 89, member A	0.19	0.32	0.006	0.005
FANCD2	Fanconi anemia, complementation group D2	0.69	0.46	0.008	0.024
FANCI	Fanconi anemia, complementation group I	0.71	0.53	0.009	0.017
FARSB	phenylalanyl-tRNA synthetase, beta subunit	0.74	0.60	0.021	0.023
FBXL4	F-box and leucine-rich repeat protein 4	**1.58**	**1.43**	0.037	0.030
FBXO4	F-box protein 4	0.58	0.69	0.008	0.006
FBXO7	F-box protein 7	0.59	0.57	0.035	0.035
FBXO9	F-box protein 9	0.66	0.70	0.005	0.013
FBXW2	F-box and WD repeat domain containing 2	0.80	0.82	0.014	0.024
FCGR1B	Fc fragment of IgG, high affinity Ib, receptor (CD64)	**2.76**	**3.68**	0.007	0.000
FDPS	farnesyl diphosphate synthase	0.68	0.63	0.006	0.004
FECH	ferrochelatase	0.34	0.20	0.010	0.003
FGFR3	fibroblast growth factor receptor 3	0.28	0.38	0.003	0.012
FIBP	fibroblast growth factor (acidic) intracellular binding protein	0.58	0.81	0.015	0.008
FKBP4	FK506 binding protein 4, 59kDa	0.54	0.67	0.009	0.044
FKBP5	FK506 binding protein 5	0.78	0.77	0.048	0.019
FKBPL	FK506 binding protein like	0.61	0.64	0.000	0.035
FLI1	Friend leukemia virus integration 1	**1.76**	**2.49**	0.032	0.011
FLOT2	flotillin 2	0.36	0.69	0.011	0.024
FN3KRP	fructosamine 3 kinase related protein	0.64	0.65	0.001	0.015
FOXM1	forkhead box M1	0.36	0.49	0.013	0.001
FTH1	ferritin, heavy polypeptide 1	0.75	0.58	0.015	0.022
FZD3	frizzled homolog 3 (Drosophila)	0.44	0.43	0.021	0.022
GALNT14	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14 (GalNAc-T14)	**1.37**	**2.15**	0.006	0.031
GARS	glycyl-tRNA synthetase	0.68	0.70	0.005	0.001
GAS2L1	growth arrest-specific 2 like 1	0.42	0.42	0.037	0.032
GATA1	GATA binding protein 1 (globin transcription factor 1)	0.27	0.30	0.004	0.010
GBAP1	glucosidase, beta, acid pseudogene 1	0.55	0.70	0.014	0.029

GBGT1	globoside alpha-1,3-N-acetylgalactosaminyltransferase 1	0.30	0.55	0.008	0.005
GBP2	guanylate binding protein 2, interferon-inducible	**4.67**	**3.87**	0.002	0.002
GBP3	guanylate binding protein 3	**2.69**	**4.30**	0.005	0.005
GFI1	growth factor independent 1 transcription repressor	**1.66**	**2.46**	0.013	0.003
GFI1B	growth factor independent 1B transcription repressor	0.25	0.45	0.012	0.037
GGA2	golgi-associated, gamma adaptin ear containing, ARF binding protein 2	0.80	0.82	0.007	0.016
GIMAP1	GTPase, IMAP family member 1	**2.07**	**2.29**	0.043	0.002
GIMAP4	GTPase, IMAP family member 4	**2.84**	**4.24**	0.007	0.023
GIMAP5	GTPase, IMAP family member 5	**2.84**	**5.03**	0.008	0.000
GIMAP6	GTPase, IMAP family member 6	**1.88**	**4.39**	0.029	0.012
GIMAP7	GTPase, IMAP family member 7	**2.29**	**3.35**	0.009	0.000
GIMAP8	GTPase, IMAP family member 8	**2.67**	**5.99**	0.004	0.018
GINS2	GINS complex subunit 2 (Psf2 homolog)	0.61	0.53	0.005	0.014
GLCCI1	glucocorticoid induced transcript 1	0.46	0.49	0.029	0.024
GLIPR1	GLI pathogenesis-related 1	**1.53**	**1.86**	0.019	0.030
GLRX	glutaredoxin (thioltransferase)	0.71	0.78	0.023	0.025
GLRX5	glutaredoxin 5	0.68	0.73	0.029	0.029
GLT25D2	glycosyltransferase 25 domain containing 2	0.71	0.70	0.018	0.017
GNAI1	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 1	**2.54**	**3.67**	0.036	0.016
GNS	glucosamine (N-acetyl)-6-sulfatase	**1.54**	**3.76**	0.010	0.019
GOSR2	golgi SNAP receptor complex member 2	0.73	0.77	0.003	0.018
GOT2	glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2)	0.67	0.80	0.012	0.017
GPD1L	glycerol-3-phosphate dehydrogenase 1-like	0.66	0.78	0.021	0.026
GPX1	glutathione peroxidase 1	**1.23**	**1.34**	0.001	0.010
GRK6	G protein-coupled receptor kinase 6	0.79	0.76	0.043	0.033
GRTP1	growth hormone regulated TBC protein 1	0.15	0.12	0.003	0.001
GSS	glutathione synthetase	0.66	0.78	0.021	0.008
GTDC1	glycosyltransferase-like domain containing 1	**1.24**	**1.72**	0.031	0.031
GTSE1	G-2 and S-phase expressed 1	0.53	0.52	0.006	0.012
GUCY1A3	guanylate cyclase 1, soluble, alpha 3	**2.97**	**4.67**	0.006	0.016
GYPA	glycophorin A (MNS blood group)	0.15	0.16	0.017	0.019
HAGH	hydroxyacylglutathione hydrolase	0.52	0.44	0.039	0.000
HBA1 /// HBA2	hemoglobin, alpha 1 /// hemoglobin, alpha 2	0.07	0.02	0.005	0.001
HBB	hemoglobin, beta	0.19	0.04	0.014	0.027
HBD	hemoglobin, delta	0.18	0.05	0.015	0.016
HBG1 /// HBG2	hemoglobin, gamma A /// hemoglobin, gamma G	0.05	0.04	0.008	0.030
HBP1	HMG-box transcription factor 1	**1.46**	**1.84**	0.002	0.003
HBS1L	HBS1-like (S, cerevisiae)	0.59	0.55	0.017	0.013
HDHD3	haloacid dehalogenase-like hydrolase domain containing 3	0.54	0.60	0.028	0.005
HEBP1	heme binding protein 1	0.51	0.36	0.000	0.002
HEBP2	heme binding protein 2	**1.20**	**1.51**	0.043	0.026
HERC6	hect domain and RLD 6	**1.31**	**2.42**	0.033	0.036
HIRIP3	HIRA interacting protein 3	0.72	0.58	0.043	0.002
HIST3H2A	histone cluster 3, H2a	0.54	0.56	0.044	0.047
HJURP	Holliday junction recognition protein	0.80	0.60	0.019	0.020
HK1	hexokinase 1	0.59	0.73	0.001	0.027
HLA-DQB1 /// LOC100133583	major histocompatibility complex, class II, DQ beta 1 /// HLA class II histocompatibility antigen, DQ beta 1 chain-like	0.61	0.22	0.025	0.003
HMGA1	high mobility group AT-hook 1	0.61	0.73	0.026	0.018
HMGCR	3-hydroxy-3-methylglutaryl-CoA reductase	0.72	0.44	0.048	0.002
HNMT	histamine N-methyltransferase	**2.29**	**2.58**	0.011	0.013
HOMER2	homer homolog 2 (Drosophila)	0.50	0.34	0.045	0.025
HOMER3	homer homolog 3 (Drosophila)	**2.34**	**2.66**	0.026	0.008
HOOK1	hook homolog 1 (Drosophila)	0.36	0.32	0.031	0.024
HOXA10 /// HOXA9	homeobox A10 /// homeobox A9	**1.89**	**1.83**	0.013	0.027

HP1BP3	heterochromatin protein 1, binding protein 3	0.57	0.56	0.030	0.042
HPDL	4-hydroxyphenylpyruvate dioxygenase-like	0.30	0.30	0.001	0.006
HSDL2	hydroxysteroid dehydrogenase like 2	0.64	0.37	0.019	0.011
ICAM4	intercellular adhesion molecule 4 (Landsteiner-Wiener blood group)	0.25	0.39	0.004	0.033
IDH2	isocitrate dehydrogenase 2 (NADP+), mitochondrial	0.81	0.71	0.014	0.003
IER2	immediate early response 2	**1.42**	**1.22**	0.012	0.020
IFI44L	interferon-induced protein 44-like	**3.16**	**6.71**	0.020	0.021
IGHM	immunoglobulin heavy constant mu	**1.87**	**2.19**	0.039	0.047
IGLL1	immunoglobulin lambda-like polypeptide 1	0.78	0.40	0.014	0.026
IKBIP	IKBKB interacting protein	**2.46**	**1.48**	0.035	0.046
IL5RA	interleukin 5 receptor, alpha	0.53	0.57	0.027	0.007
ILF3	interleukin enhancer binding factor 3, 90kDa	0.83	0.75	0.005	0.019
IRAK1	interleukin-1 receptor-associated kinase 1	0.68	0.45	0.046	0.000
IRF1	interferon regulatory factor 1	**1.72**	**2.16**	0.005	0.004
IRF2BP2	interferon regulatory factor 2 binding protein 2	**1.32**	**1.27**	0.027	0.029
ITGA5	integrin, alpha 5 (fibronectin receptor, alpha polypeptide)	**1.28**	**2.14**	0.010	0.027
ITGA6	integrin, alpha 6	**3.25**	**5.41**	0.028	0.024
ITGA9	integrin, alpha 9	**1.72**	**3.39**	0.012	0.020
ITLN1	intelectin 1 (galactofuranose binding)	0.08	0.13	0.003	0.005
JAM3	junctional adhesion molecule 3	**1.24**	**3.03**	0.029	0.034
JAZF1	JAZF zinc finger 1	0.49	0.38	0.037	0.002
JUP	junction plakoglobin	**1.43**	**2.33**	0.003	0.026
KCNH2	potassium voltage-gated channel, subfamily H (eag-related), member 2	0.20	0.31	0.005	0.007
KCNK5	potassium channel, subfamily K, member 5	0.53	0.49	0.030	0.046
KDM1B	lysine (K)-specific demethylase 1B	**1.44**	**1.79**	0.045	0.035
KDM3A	lysine (K)-specific demethylase 3A	**2.11**	**2.02**	0.007	0.001
KDM5B	lysine (K)-specific demethylase 5B	**1.80**	**2.05**	0.045	0.014
KEL	Kell blood group, metallo-endopeptidase	0.22	0.27	0.009	0.031
KIAA0040	KIAA0040	0.56	0.47	0.013	0.013
KIAA0101	KIAA0101	0.79	0.66	0.010	0.028
KIAA0114	KIAA0114	0.60	0.60	0.028	0.035
KIAA0125	KIAA0125	**2.22**	**4.32**	0.012	0.029
KIF14	kinesin family member 14	0.82	0.41	0.024	0.014
KIF22	kinesin family member 22	0.76	0.52	0.040	0.042
KIFC1	kinesin family member C1	0.64	0.54	0.033	0.018
KLF1	Kruppel-like factor 1 (erythroid)	0.15	0.23	0.004	0.040
KLHL24	kelch-like 24 (Drosophila)	**2.52**	**3.10**	0.017	0.013
KRT13	keratin 13	0.09	0.08	0.001	0.003
L3MBTL2	l(3)mbt-like 2 (Drosophila)	0.65	0.72	0.038	0.030
LACTB	lactamase, beta	**1.32**	**1.35**	0.007	0.040
LAMP2	lysosomal-associated membrane protein 2	**2.95**	**1.46**	0.048	0.026
LAPTM4A	lysosomal protein transmembrane 4 alpha	**1.66**	**1.82**	0.001	0.000
LAPTM4B	lysosomal protein transmembrane 4 beta	**1.28**	**2.08**	0.034	0.032
LCA5	Leber congenital amaurosis 5	0.26	0.27	0.006	0.011
LEPROTL1	leptin receptor overlapping transcript-like 1	**1.85**	**1.75**	0.028	0.025
LOC100288525	hypothetical protein LOC100288525	0.32	0.27	0.007	0.009
LOC100505633	hypothetical LOC100505633	0.20	0.14	0.012	0.005
LOC150776 /// SMPD4	sphingomyelin phosphodiesterase 4, neutral membrane pseudogene /// sphingomyelin phosphodiesterase 4, neutral membrane (neutral sphingomyelinase-3)	0.75	0.57	0.041	0.019
LOC158402	hypothetical protein LOC158402	0.58	0.52	0.007	0.047
LOC541471 /// NCRNA00152	hypothetical LOC541471 /// non-protein coding RNA 152	0.61	0.57	0.001	0.045
LOC728855	hypothetical LOC728855	**1.31**	**1.99**	0.041	0.023
LPCAT3	lysophosphatidylcholine acyltransferase 3	0.44	0.47	0.006	0.002
LRPAP1	low density lipoprotein receptor-related protein associated protein 1	0.61	0.39	0.008	0.009

LRPPRC	leucine-rich PPR-motif containing	0.69	0.83	0.029	0.045
LRRC59	leucine rich repeat containing 59	0.70	0.73	0.018	0.016
LSM11	LSM11, U7 small nuclear RNA associated	0.64	0.66	0.036	0.040
LSM4	LSM4 homolog, U6 small nuclear RNA associated (S, cerevisiae)	0.78	0.73	0.047	0.036
LSS	lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase)	0.72	0.66	0.039	0.028
LTBP1	latent transforming growth factor beta binding protein 1	0.33	0.38	0.014	0.017
MACF1	microtubule-actin crosslinking factor 1	**1.70**	**1.92**	0.006	0.021
MAF	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	**1.62**	**2.21**	0.041	0.006
MAFK	v-maf musculoaponeurotic fibrosarcoma oncogene homolog K (avian)	**1.93**	**1.57**	0.017	0.039
MAGEE1	melanoma antigen family E, 1	0.69	0.64	0.007	0.005
MAN2A1	mannosidase, alpha, class 2A, member 1	0.69	0.33	0.043	0.018
MAP2K6	mitogen-activated protein kinase kinase 6	0.60	0.49	0.025	0.018
MAPK6	mitogen-activated protein kinase 6	**1.54**	**1.57**	0.010	0.001
MAST4	microtubule associated serine/threonine kinase family member 4	**1.41**	**3.45**	0.008	0.030
MBOAT2	membrane bound O-acyltransferase domain containing 2	0.41	0.52	0.007	0.027
MCFD2	multiple coagulation factor deficiency 2	0.63	0.26	0.049	0.006
MCM10	minichromosome maintenance complex component 10	0.56	0.61	0.036	0.016
MCM2	minichromosome maintenance complex component 2	0.76	0.55	0.034	0.022
MCM3	minichromosome maintenance complex component 3	0.74	0.26	0.027	0.002
MCM7	minichromosome maintenance complex component 7	0.71	0.60	0.030	0.009
MCTP1	multiple C2 domains, transmembrane 1	**1.42**	**2.07**	0.005	0.005
MED16	mediator complex subunit 16	0.61	0.61	0.028	0.018
MEF2C	myocyte enhancer factor 2C	**1.50**	**2.08**	0.019	0.011
MEIS1	Meis homeobox 1	**1.63**	**4.24**	0.007	0.002
METTL13	methyltransferase like 13	0.71	0.65	0.025	0.002
METTL2A /// METTL2B	methyltransferase like 2A /// methyltransferase like 2B	0.74	0.66	0.012	0.016
MGA	MAX gene associated	**1.66**	**1.67**	0.022	0.022
MGAT3	mannosyl (beta-1,4-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase	0.55	0.66	0.034	0.026
MGC21881	hypothetical locus MGC21881	0.49	0.45	0.003	0.009
MGST3	microsomal glutathione S-transferase 3	0.63	0.50	0.029	0.009
MICAL2	microtubule associated monoxygenase, calponin and LIM domain containing 2	0.39	0.48	0.006	0.036
MKI67	antigen identified by monoclonal antibody Ki-67	0.69	0.40	0.045	0.009
MKRN1	makorin ring finger protein 1	**1.26**	**1.34**	0.034	0.008
MLF1IP	MLF1 interacting protein	0.61	0.58	0.029	0.016
MLKL	mixed lineage kinase domain-like	**1.50**	**2.35**	0.029	0.034
MPP1	membrane protein, palmitoylated 1, 55kDa	0.58	0.72	0.016	0.020
MRM1	mitochondrial rRNA methyltransferase 1 homolog (S, cerevisiae)	0.60	0.76	0.011	0.031
MRPL12	mitochondrial ribosomal protein L12	0.62	0.79	0.001	0.013
MRPL27	mitochondrial ribosomal protein L27	0.73	0.75	0.024	0.018
MRPL35	mitochondrial ribosomal protein L35	0.62	0.58	0.002	0.012
MRPL36	mitochondrial ribosomal protein L36	0.77	0.76	0.008	0.039
MRPL37	mitochondrial ribosomal protein L37	0.77	0.73	0.006	0.017
MRPS17 /// ZNF713	mitochondrial ribosomal protein S17 /// zinc finger protein 713	0.68	0.75	0.000	0.042
MRTO4	mRNA turnover 4 homolog (S, cerevisiae)	0.73	0.78	0.006	0.029
MSI2	musashi homolog 2 (Drosophila)	**1.48**	**2.33**	0.037	0.012
MT1F	metallothionein 1F	0.56	0.63	0.005	0.011
MTF2	metal response element binding transcription factor 2	**1.59**	**1.71**	0.010	0.015
MTHFD1	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1, methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase	0.76	0.70	0.010	0.004
MTHFR	methylenetetrahydrofolate reductase (NAD(P)H)	0.61	0.56	0.014	0.013

MTMR12	myotubularin related protein 12	0.64	0.59	0.015	0.022
MTMR14	myotubularin related protein 14	0.81	0.70	0.043	0.040
MXD1	MAX dimerization protein 1	0.36	0.43	0.019	0.018
MYBL2	v-myb myeloblastosis viral oncogene homolog (avian)-like 2	0.69	0.52	0.003	0.017
MYH10	myosin, heavy chain 10, non-muscle	0.27	0.45	0.005	0.028
MYL4	myosin, light chain 4, alkali; atrial, embryonic	0.42	0.39	0.011	0.015
MYO19	myosin XIX	0.74	0.76	0.050	0.010
NASP	nuclear autoantigenic sperm protein (histone-binding)	0.79	0.64	0.011	0.018
NBAS	neuroblastoma amplified sequence	0.71	0.68	0.005	0.017
NCAPH	non-SMC condensin I complex, subunit H	0.71	0.45	0.001	0.016
NCOA1	nuclear receptor coactivator 1	0.66	0.73	0.012	0.027
NCOA3	nuclear receptor coactivator 3	**1.78**	**1.56**	0.013	0.020
NCRNA00275	non-protein coding RNA 275	**1.29**	**1.94**	0.039	0.023
NDUFB6	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6, 17kDa	0.74	0.75	0.008	0.044
NDUFB9	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9, 22kDa	0.80	0.82	0.024	0.048
NDUFS7	NADH dehydrogenase (ubiquinone) Fe-S protein 7, 20kDa (NADH-coenzyme Q reductase)	0.67	0.59	0.035	0.005
NEK2	NIMA (never in mitosis gene a)-related kinase 2	0.82	0.33	0.041	0.005
NEK6	NIMA (never in mitosis gene a)-related kinase 6	**1.52**	**2.19**	0.013	0.015
NFIA	nuclear factor I/A	0.35	0.40	0.009	0.013
NIPA2	non imprinted in Prader-Willi/Angelman syndrome 2	0.61	0.62	0.005	0.007
NOG	noggin	**4.84**	**11.16**	0.012	0.004
NOTCH1	notch 1	**1.59**	**1.24**	0.023	0.001
NPL	N-acetylneuraminate pyruvate lyase (dihydrodipicolinate synthase)	0.38	0.45	0.016	0.039
NPRL3	nitrogen permease regulator-like 3 (S, cerevisiae)	0.48	0.56	0.006	0.018
NRIP1	nuclear receptor interacting protein 1	**1.66**	**2.35**	0.033	0.020
NT5DC2	5-nucleotidase domain containing 2	0.68	0.58	0.032	0.006
NUDT21	nudix (nucleoside diphosphate linked moiety X)-type motif 21	0.67	0.49	0.046	0.050
NUP62	nucleoporin 62kDa	0.79	0.82	0.029	0.019
OAT	ornithine aminotransferase	0.68	0.63	0.045	0.030
OBFC2A	oligonucleotide/oligosaccharide-binding fold containing 2A	**1.85**	**1.73**	0.010	0.015
OGFOD2	2-oxoglutarate and iron-dependent oxygenase domain containing 2	0.71	0.70	0.043	0.015
OGT	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase)	**1.52**	**1.52**	0.028	0.025
OSTM1	osteopetrosis associated transmembrane protein 1	**2.01**	**2.30**	0.047	0.020
P2RY8	purinergic receptor P2Y, G-protein coupled, 8	**1.49**	**2.30**	0.004	0.007
P4HB	prolyl 4-hydroxylase, beta polypeptide	0.76	0.73	0.034	0.038
PA2G4	proliferation-associated 2G4, 38kDa	0.67	0.68	0.002	0.008
PAFAH1B3	platelet-activating factor acetylhydrolase 1b, catalytic subunit 3 (29kDa)	0.55	0.65	0.001	0.028
PAIP2	poly(A) binding protein interacting protein 2	**1.23**	**1.39**	0.006	0.032
PAQR7	progestin and adipoQ receptor family member VII	**1.42**	**1.69**	0.012	0.002
PARP14	poly (ADP-ribose) polymerase family, member 14	**1.52**	**1.37**	0.007	0.037
PBK	PDZ binding kinase	0.26	0.34	0.003	0.003
PCCB	propionyl CoA carboxylase, beta polypeptide	0.47	0.68	0.007	0.020
PCGF5	polycomb group ring finger 5	0.47	0.47	0.037	0.035
PCMTD1	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1	**1.48**	**1.62**	0.009	0.016
PCNX	pecanex homolog (Drosophila)	**2.50**	**1.70**	0.049	0.039
PDK3	pyruvate dehydrogenase kinase, isozyme 3	0.53	0.68	0.004	0.025
PDLIM1	PDZ and LIM domain 1	0.71	0.58	0.023	0.031
PDLIM5	PDZ and LIM domain 5	**1.34**	**2.22**	0.035	0.022
PDSS1	prenyl (decaprenyl) diphosphate synthase, subunit 1	0.79	0.62	0.030	0.006
PECAM1	platelet/endothelial cell adhesion molecule	**2.11**	**3.17**	0.011	0.004

PECI	peroxisomal D3,D2-enoyl-CoA isomerase	0.62	0.28	0.010	0.011
PFDN6	prefoldin subunit 6	0.72	0.73	0.042	0.031
PGP	phosphoglycolate phosphatase	0.58	0.53	0.021	0.018
PHF10	PHD finger protein 10	0.82	0.73	0.032	0.010
PHGDH	phosphoglycerate dehydrogenase	0.62	0.80	0.037	0.037
PHTF1	putative homeodomain transcription factor 1	**2.32**	**1.82**	0.032	0.012
PIGC	phosphatidylinositol glycan anchor biosynthesis, class C	0.59	0.79	0.008	0.027
PIGH	phosphatidylinositol glycan anchor biosynthesis, class H	0.44	0.62	0.000	0.033
PIGV	phosphatidylinositol glycan anchor biosynthesis, class V	0.48	0.74	0.038	0.017
PIK3AP1	phosphoinositide-3-kinase adaptor protein 1	**1.50**	**1.38**	0.001	0.004
PIN1	peptidylprolyl cis/trans isomerase, NIMA-interacting 1	0.72	0.73	0.035	0.033
PIP4K2A	phosphatidylinositol-5-phosphate 4-kinase, type II, alpha	0.74	0.65	0.018	0.019
PISD	phosphatidylserine decarboxylase	0.80	0.75	0.017	0.015
PITPNB	phosphatidylinositol transfer protein, beta	0.79	0.55	0.026	0.006
PKLR	pyruvate kinase, liver and RBC	0.12	0.10	0.000	0.001
PLA2G12A	phospholipase A2, group XIIA	0.70	0.43	0.042	0.018
PLAU	plasminogen activator, urokinase	**1.95**	**2.50**	0.008	0.019
PLCB4	phospholipase C, beta 4	**1.73**	**3.93**	0.001	0.042
PLD1	phospholipase D1, phosphatidylcholine-specific	0.52	0.72	0.015	0.021
PLEKHA5	pleckstrin homology domain containing, family A member 5	**1.81**	**1.72**	0.040	0.011
PLK1	polo-like kinase 1	0.67	0.43	0.034	0.023
PNMT	phenylethanolamine N-methyltransferase	0.22	0.35	0.002	0.018
PNPO	pyridoxamine 5-phosphate oxidase	0.42	0.51	0.005	0.001
PNRC1	proline-rich nuclear receptor coactivator 1	**1.55**	**1.66**	0.002	0.031
POGK	pogo transposable element with KRAB domain	**1.50**	**1.31**	0.011	0.023
POLD1	polymerase (DNA directed), delta 1, catalytic subunit 125kDa	0.72	0.65	0.012	0.016
POLD2	polymerase (DNA directed), delta 2, regulatory subunit 50kDa	0.75	0.60	0.014	0.013
POLDIP2	polymerase (DNA-directed), delta interacting protein 2	0.75	0.73	0.033	0.011
POLR2C	polymerase (RNA) II (DNA directed) polypeptide C, 33kDa	0.62	0.69	0.002	0.009
POLR2F	polymerase (RNA) II (DNA directed) polypeptide F	0.70	0.76	0.044	0.014
POLR2L	polymerase (RNA) II (DNA directed) polypeptide L, 7,6kDa	0.78	0.76	0.027	0.030
POP7	processing of precursor 7, ribonuclease P/MRP subunit (S, cerevisiae)	0.62	0.61	0.021	0.017
PPCS	phosphopantothenoylcysteine synthetase	**1.85**	**1.55**	0.011	0.017
PPIL2	peptidylprolyl isomerase (cyclophilin)-like 2	0.72	0.75	0.019	0.022
PPM1A	protein phosphatase, Mg2+/Mn2+ dependent, 1A	0.69	0.64	0.012	0.022
PPME1	protein phosphatase methylesterase 1	0.58	0.65	0.030	0.034
PPOX	protoporphyrinogen oxidase	0.32	0.33	0.001	0.016
PPP1R3D	protein phosphatase 1, regulatory (inhibitor) subunit 3D	**1.58**	**1.53**	0.029	0.021
PPT2	palmitoyl-protein thioesterase 2	0.48	0.39	0.011	0.027
PRC1	protein regulator of cytokinesis 1	0.69	0.53	0.001	0.009
PRDX2	peroxiredoxin 2	0.30	0.29	0.002	0.014
PRICKLE1	prickle homolog 1 (Drosophila)	**2.71**	**1.78**	0.027	0.009
PRKAB1	protein kinase, AMP-activated, beta 1 non-catalytic subunit	0.40	0.80	0.012	0.001
PRKAG2	protein kinase, AMP-activated, gamma 2 non-catalytic subunit	**1.95**	**1.48**	0.028	0.033
PRKAR2B	protein kinase, cAMP-dependent, regulatory, type II, beta	0.27	0.33	0.033	0.040
PRKCH	protein kinase C, eta	**1.86**	**3.63**	0.036	0.002
PROM1	prominin 1	**2.67**	**8.50**	0.044	0.026
PRPF31	PRP31 pre-mRNA processing factor 31 homolog (S, cerevisiae)	0.80	0.81	0.011	0.044
PRPS1	phosphoribosyl pyrophosphate synthetase 1	0.68	0.77	0.043	0.043
PSAT1	phosphoserine aminotransferase 1	0.79	0.56	0.012	0.015
PSMD11	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11	0.83	0.34	0.032	0.006
PSMD13	proteasome (prosome, macropain) 26S subunit, non-ATPase, 13	0.75	0.67	0.028	0.039
PSMD8	proteasome (prosome, macropain) 26S subunit, non-ATPase, 8	0.62	0.75	0.001	0.022
PSME3	proteasome (prosome, macropain) activator subunit 3 (PA28 gamma; Ki)	0.63	0.70	0.034	0.008

PTEN	phosphatase and tensin homolog	**1.48**	**1.35**	0.020	0.034
PTEN /// PTENP1	phosphatase and tensin homolog /// phosphatase and tensin homolog pseudogene 1	**1.62**	**1.30**	0.003	0.015
PTPN18	protein tyrosine phosphatase, non-receptor type 18 (brain-derived)	0.74	0.63	0.043	0.029
PUS1	pseudouridylate synthase 1	0.73	0.75	0.018	0.047
PVT1	Pvt1 oncogene (non-protein coding)	0.07	0.30	0.004	0.035
PYGL	phosphorylase, glycogen, liver	**1.58**	**1.83**	0.049	0.002
RAB8B	RAB8B, member RAS oncogene family	**1.55**	**1.89**	0.049	0.035
RABGAP1L	RAB GTPase activating protein 1-like	0.64	0.59	0.026	0.000
RACGAP1	Rac GTPase activating protein 1	0.51	0.60	0.000	0.015
RAD23A	RAD23 homolog A (S, cerevisiae)	0.53	0.57	0.030	0.023
RANBP1	RAN binding protein 1	0.78	0.79	0.012	0.022
RARRES3	retinoic acid receptor responder (tazarotene induced) 3	**1.92**	**4.00**	0.014	0.027
RAVER1	ribonucleoprotein, PTB-binding 1	0.58	0.55	0.012	0.005
RBM22	RNA binding motif protein 22	**1.27**	**1.24**	0.006	0.029
RBMS1	RNA binding motif, single stranded interacting protein 1	**1.33**	**1.76**	0.024	0.010
RCCD1	RCC1 domain containing 1	0.73	0.45	0.010	0.001
RDBP	RD RNA binding protein	0.71	0.63	0.007	0.020
RECK	reversion-inducing-cysteine-rich protein with kazal motifs	**3.43**	**5.35**	0.019	0.001
REXO2	REX2, RNA exonuclease 2 homolog (S, cerevisiae)	0.37	0.38	0.000	0.004
RFC2	replication factor C (activator 1) 2, 40kDa	0.77	0.71	0.038	0.001
RFC4	replication factor C (activator 1) 4, 37kDa	0.76	0.54	0.011	0.010
RFESD	Rieske (Fe-S) domain containing	0.22	0.19	0.010	0.008
RHAG	Rh-associated glycoprotein	0.07	0.17	0.004	0.022
RHOBTB1	Rho-related BTB domain containing 1	**1.85**	**1.84**	0.012	0.015
RILP	Rab interacting lysosomal protein	0.20	0.58	0.001	0.005
RILPL2	Rab interacting lysosomal protein-like 2	**1.42**	**1.20**	0.004	0.012
RIT1	Ras-like without CAAX 1	**1.66**	**1.66**	0.014	0.026
RMND5B	required for meiotic nuclear division 5 homolog B (S, cerevisiae)	0.27	0.73	0.002	0.008
RNASE1	ribonuclease, RNase A family, 1 (pancreatic)	0.18	0.18	0.002	0.010
RNASE4	ribonuclease, RNase A family, 4	0.24	0.44	0.020	0.000
RNASEH2A	ribonuclease H2, subunit A	0.68	0.53	0.018	0.015
RNF113A	ring finger protein 113A	**1.30**	**1.45**	0.038	0.045
RNF121	ring finger protein 121	0.54	0.68	0.028	0.009
RNF123	ring finger protein 123	0.56	0.51	0.025	0.017
RNF126	ring finger protein 126	0.38	0.80	0.002	0.038
RNF149	ring finger protein 149	**1.47**	**1.44**	0.000	0.006
RNF26	ring finger protein 26	0.48	0.47	0.045	0.011
RNF34	ring finger protein 34	0.61	0.45	0.028	0.020
RPP21 /// TRIM39 /// TRIM39R	ribonuclease P/MRP 21kDa subunit /// tripartite motif-containing 39 /// TRIM39-like protein	0.71	0.81	0.038	0.010
RPRD1A	regulation of nuclear pre-mRNA domain containing 1A	0.43	0.51	0.031	0.030
RPS6KL1	ribosomal protein S6 kinase-like 1	0.48	0.44	0.006	0.002
RRAGD	Ras-related GTP binding D	**1.45**	**1.85**	0.026	0.015
RTP4	receptor (chemosensory) transporter protein 4	**2.16**	**4.76**	0.017	0.004
RUVBL2	RuvB-like 2 (E, coli)	0.67	0.68	0.019	0.026
RYR3	ryanodine receptor 3	0.38	0.57	0.019	0.033
SAMM50	sorting and assembly machinery component 50 homolog (S, cerevisiae)	0.54	0.69	0.003	0.004
SAP130	Sin3A-associated protein, 130kDa	0.61	0.64	0.017	0.015
SAP30BP	SAP30 binding protein	0.73	0.76	0.030	0.005
SARNP	SAP domain containing ribonucleoprotein	0.70	0.67	0.011	0.032
SARS	seryl-tRNA synthetase	0.73	0.72	0.037	0.013
SART1	squamous cell carcinoma antigen recognized by T cells	0.75	0.80	0.033	0.019
SATB1	SATB homeobox 1	**1.42**	**1.96**	0.048	0.034
SBF2	SET binding factor 2	**1.88**	**2.93**	0.031	0.041

SCPEP1	serine carboxypeptidase 1	**1.52**	**1.76**	0.002	0.037
SDHA	succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	0.70	0.71	0.043	0.003
SEC14L2	SEC14-like 2 (S, cerevisiae)	0.59	0.70	0.034	0.025
SEC22C	SEC22 vesicle trafficking protein homolog C (S, cerevisiae)	0.72	0.58	0.013	0.035
SEC62	SEC62 homolog (S, cerevisiae)	**1.41**	**1.35**	0.012	0.001
SEL1L3	sel-1 suppressor of lin-12-like 3 (C, elegans)	**2.31**	**1.79**	0.005	0.017
SELENBP1	selenium binding protein 1	0.05	0.09	0.001	0.002
SEMA4D	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4D	**1.94**	**2.67**	0.042	0.015
SEPP1	selenoprotein P, plasma, 1	**6.08**	**3.52**	0.009	0.004
SERPINB1	serpin peptidase inhibitor, clade B (ovalbumin), member 1	**1.45**	**1.58**	0.026	0.012
SESN1	sestrin 1	**1.73**	**1.89**	0.001	0.004
SETD8	SET domain containing (lysine methyltransferase) 8	0.69	0.57	0.017	0.006
SFXN1	sideroflexin 1	0.67	0.45	0.030	0.014
SGPL1	sphingosine-1-phosphate lyase 1	**1.95**	**1.26**	0.016	0.036
SHB	Src homology 2 domain containing adaptor protein B	**1.41**	**1.89**	0.046	0.009
SHKBP1	SH3KBP1 binding protein 1	0.49	0.66	0.016	0.006
SHMT2	serine hydroxymethyltransferase 2 (mitochondrial)	0.73	0.75	0.024	0.013
SIAH2	seven in absentia homolog 2 (Drosophila)	0.66	0.78	0.013	0.001
SIGMAR1	sigma non-opioid intracellular receptor 1	0.50	0.60	0.009	0.009
SLC12A6	solute carrier family 12 (potassium/chloride transporters), member 6	0.48	0.53	0.014	0.014
SLC16A9	solute carrier family 16, member 9 (monocarboxylic acid transporter 9)	0.19	0.16	0.003	0.011
SLC17A5	solute carrier family 17 (anion/sugar transporter), member 5	**1.50**	**1.58**	0.017	0.017
SLC22A23	solute carrier family 22, member 23	0.29	0.30	0.010	0.011
SLC25A1	solute carrier family 25 (mitochondrial carrier; citrate transporter), member 1	0.58	0.61	0.008	0.012
SLC25A11	solute carrier family 25 (mitochondrial carrier; oxoglutarate carrier), member 11	0.72	0.78	0.007	0.004
SLC25A12	solute carrier family 25 (mitochondrial carrier, Aralar), member 12	**3.21**	**1.31**	0.025	0.035
SLC25A17	solute carrier family 25 (mitochondrial carrier; peroxisomal membrane protein, 34kDa), member 17	0.62	0.47	0.041	0.009
SLC25A21	solute carrier family 25 (mitochondrial oxodicarboxylate carrier), member 21	0.11	0.05	0.001	0.006
SLC25A28	solute carrier family 25, member 28	0.78	0.75	0.032	0.019
SLC25A37	solute carrier family 25, member 37	0.47	0.41	0.017	0.013
SLC25A39	solute carrier family 25, member 39	0.61	0.43	0.004	0.006
SLC26A2	solute carrier family 26 (sulfate transporter), member 2	0.45	0.33	0.010	0.011
SLC29A1	solute carrier family 29 (nucleoside transporters), member 1	0.55	0.72	0.019	0.028
SLC29A2	solute carrier family 29 (nucleoside transporters), member 2	0.68	0.77	0.023	0.026
SLC31A1	solute carrier family 31 (copper transporters), member 1	0.73	0.68	0.011	0.010
SLC35A4	solute carrier family 35, member A4	0.52	0.64	0.018	0.015
SLC35D2	solute carrier family 35, member D2	**1.96**	**3.62**	0.015	0.005
SLC37A4	solute carrier family 37 (glucose-6-phosphate transporter), member 4	0.49	0.48	0.011	0.017
SLC38A5	solute carrier family 38, member 5	0.29	0.33	0.000	0.015
SLC41A2	solute carrier family 41, member 2	0.44	0.25	0.009	0.015
SLC43A3	solute carrier family 43, member 3	0.56	0.48	0.002	0.014
SLC9A3R1	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 1	**1.30**	**1.52**	0.010	0.006
SLX1A /// SLX1B	SLX1 structure-specific endonuclease subunit homolog A (S, cerevisiae) /// SLX1 structure-specific endonuclease subunit homolog B (S, cerevisiae)	0.62	0.60	0.013	0.019
SMURF2	SMAD specific E3 ubiquitin protein ligase 2	**1.76**	**1.73**	0.032	0.038
SNHG1	small nucleolar RNA host gene 1 (non-protein coding)	0.83	0.75	0.041	0.028
SNRK	SNF related kinase	**1.87**	**1.88**	0.033	0.009
SNRNP27	small nuclear ribonucleoprotein 27kDa (U4/U6,U5)	0.67	0.71	0.008	0.044
SNX9	sorting nexin 9	0.66	0.74	0.048	0.001

SORBS1	sorbin and SH3 domain containing 1	0.26	0.29	0.016	0.035
SORL1	sortilin-related receptor, L(DLR class) A repeats-containing	**2.36**	**2.97**	0.003	0.016
SOX4	SRY (sex determining region Y)-box 4	**1.52**	**2.34**	0.007	0.008
SP1	Sp1 transcription factor	**1.78**	**1.25**	0.017	0.033
SPAG5	sperm associated antigen 5	0.75	0.59	0.015	0.029
SPARC	secreted protein, acidic, cysteine-rich (osteonectin)	**2.24**	**4.54**	0.003	0.021
SPCS3	signal peptidase complex subunit 3 homolog (S, cerevisiae)	**1.23**	**1.28**	0.013	0.003
SPIN1	spindlin 1	**1.28**	**1.63**	0.013	0.015
SPNS1	spinster homolog 1 (Drosophila)	0.73	0.59	0.045	0.004
SPOP	speckle-type POZ protein	**1.32**	**1.35**	0.001	0.001
SPTA1	spectrin, alpha, erythrocytic 1 (elliptocytosis 2)	0.19	0.12	0.023	0.019
SPTBN1	spectrin, beta, non-erythrocytic 1	**2.07**	**2.81**	0.029	0.018
SPTLC2	Serine palmitoyltransferase, long chain base subunit 2	**1.56**	**1.28**	0.038	0.036
SRBD1	S1 RNA binding domain 1	**1.82**	**1.88**	0.024	0.008
SRD5A1	steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 1)	0.69	0.51	0.038	0.022
SRP14	signal recognition particle 14kDa (homologous Alu RNA binding protein)	**1.25**	**1.23**	0.014	0.029
SRXN1	sulfiredoxin 1	0.42	0.66	0.011	0.049
SSRP1	structure specific recognition protein 1	0.79	0.58	0.017	0.005
SSX2IP	synovial sarcoma, X breakpoint 2 interacting protein	0.61	0.66	0.034	0.021
ST3GAL6	ST3 beta-galactoside alpha-2,3-sialyltransferase 6	**2.74**	**1.76**	0.006	0.003
STAP1	signal transducing adaptor family member 1	**1.70**	**2.97**	0.048	0.011
STK35	serine/threonine kinase 35	**1.74**	**1.58**	0.019	0.021
STRA13	stimulated by retinoic acid 13 homolog (mouse)	0.68	0.70	0.018	0.016
STUB1	STIP1 homology and U-box containing protein 1, E3 ubiquitin protein ligase	0.66	0.79	0.019	0.006
STX2	syntaxin 2	0.59	0.32	0.044	0.014
SUPT6H	suppressor of Ty 6 homolog (S, cerevisiae)	0.75	0.67	0.006	0.029
SWAP70	SWAP switching B-cell complex 70kDa subunit	**1.62**	**1.47**	0.000	0.042
SYNGR2	synaptogyrin 2	0.75	0.74	0.011	0.000
SYNJ2BP	synaptojanin 2 binding protein	**2.35**	**2.40**	0.029	0.007
TAB2	TGF-beta activated kinase 1/MAP3K7 binding protein 2	**1.34**	**2.23**	0.020	0.024
TATDN3	TatD DNase domain containing 3	**1.61**	**1.66**	0.021	0.011
TBC1D2B	TBC1 domain family, member 2B	**1.63**	**1.55**	0.012	0.010
TBCD	tubulin folding cofactor D	0.78	0.83	0.023	0.014
TBL1X	transducin (beta)-like 1X-linked	0.51	0.71	0.009	0.020
TBL3	transducin (beta)-like 3	0.78	0.72	0.027	0.002
TBXAS1	thromboxane A synthase 1 (platelet)	**1.47**	**1.75**	0.045	0.013
TCEAL4	transcription elongation factor A (SII)-like 4	**1.33**	**1.68**	0.050	0.033
TCEB2	transcription elongation factor B (SIII), polypeptide 2 (18kDa, elongin B)	0.74	0.57	0.013	0.015
TCF7L2	transcription factor 7-like 2 (T-cell specific, HMG-box)	**1.67**	**2.91**	0.036	0.015
TELO2	TEL2, telomere maintenance 2, homolog (S, cerevisiae)	0.78	0.80	0.032	0.043
TEX261	testis expressed 261	0.76	0.62	0.045	0.002
TFEC	transcription factor EC	**2.18**	**2.36**	0.001	0.009
TFR2	transferrin receptor 2	0.21	0.34	0.006	0.009
TFRC	transferrin receptor (p90, CD71)	0.64	0.60	0.026	0.034
TH1L	TH1-like (Drosophila)	0.69	0.79	0.007	0.006
TIMELESS	timeless homolog (Drosophila)	0.80	0.66	0.042	0.016
TIMM50	translocase of inner mitochondrial membrane 50 homolog (S, cerevisiae)	0.64	0.62	0.019	0.022
TIMM8B	translocase of inner mitochondrial membrane 8 homolog B (yeast)	0.76	0.80	0.020	0.033
TIMP2	TIMP metallopeptidase inhibitor 2	**2.13**	**1.60**	0.008	0.046
TK1	thymidine kinase 1, soluble	0.78	0.46	0.049	0.020
TLE4	transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila)	**1.71**	**1.46**	0.036	0.030
TM7SF3	transmembrane 7 superfamily member 3	0.79	0.30	0.036	0.006
TMCO6	transmembrane and coiled-coil domains 6	0.65	0.66	0.027	0.026

TMED5	transmembrane emp24 protein transport domain containing 5	**1.56**	**1.66**	0.021	0.008
TMEM138	transmembrane protein 138	0.72	0.52	0.021	0.003
TMEM141	transmembrane protein 141	0.41	0.49	0.001	0.009
TMEM14B	transmembrane protein 14B	0.37	0.66	0.002	0.005
TMEM14B /// TMEM14C	transmembrane protein 14B /// transmembrane protein 14C	0.54	0.75	0.000	0.049
TMEM14C	transmembrane protein 14C	0.52	0.63	0.001	0.039
TMEM156	transmembrane protein 156	**2.23**	**1.29**	0.001	0.031
TMEM165	transmembrane protein 165	0.73	0.63	0.008	0.000
TMEM177	transmembrane protein 177	0.67	0.80	0.018	0.003
TMEM19	transmembrane protein 19	0.56	0.33	0.029	0.014
TMEM30A	transmembrane protein 30A	**2.12**	**2.09**	0.045	0.017
TMEM56	transmembrane protein 56	0.13	0.06	0.008	0.000
TMEM97	transmembrane protein 97	0.56	0.47	0.016	0.032
TMF1	TATA element modulatory factor 1	0.54	0.59	0.017	0.029
TMOD1	tropomodulin 1	0.32	0.52	0.027	0.030
TNFRSF10D	tumor necrosis factor receptor superfamily, member 10d, decoy with truncated death domain	**2.13**	**3.63**	0.006	0.000
TNFRSF19	tumor necrosis factor receptor superfamily, member 19	0.26	0.37	0.029	0.042
TNFRSF1A	tumor necrosis factor receptor superfamily, member 1A	**1.64**	**1.93**	0.046	0.020
TNFSF4	tumor necrosis factor (ligand) superfamily, member 4	**3.17**	**2.91**	0.014	0.027
TOMM40	translocase of outer mitochondrial membrane 40 homolog (yeast)	0.69	0.77	0.044	0.011
TOP3A	topoisomerase (DNA) III alpha	0.71	0.68	0.021	0.018
TP53	tumor protein p53	0.75	0.78	0.026	0.011
TP53INP1	tumor protein p53 inducible nuclear protein 1	**2.68**	**2.86**	0.010	0.013
TPM1	tropomyosin 1 (alpha)	0.29	0.51	0.013	0.028
TPP2	tripeptidyl peptidase II	**1.53**	**1.53**	0.042	0.029
TPX2	TPX2, microtubule-associated, homolog (Xenopus laevis)	0.63	0.60	0.004	0.004
TRAK2	trafficking protein, kinesin binding 2	0.48	0.76	0.008	0.037
TRAP1	TNF receptor-associated protein 1	0.68	0.73	0.020	0.015
TROAP	trophinin associated protein (tastin)	0.69	0.55	0.037	0.016
TSFM	Ts translation elongation factor, mitochondrial	0.76	0.75	0.047	0.016
TSPAN5	tetraspanin 5	0.29	0.40	0.008	0.021
TST	thiosulfate sulfurtransferase (rhodanese)	0.55	0.53	0.013	0.011
TSTA3	tissue specific transplantation antigen P35B	0.81	0.74	0.029	0.003
TTC13	tetratricopeptide repeat domain 13	0.72	0.50	0.018	0.000
TTLL11	tubulin tyrosine ligase-like family, member 11	0.61	0.66	0.013	0.018
TTLL12	tubulin tyrosine ligase-like family, member 12	0.64	0.59	0.004	0.005
TUBB2A	tubulin, beta 2A	0.31	0.12	0.020	0.006
TUBB3	tubulin, beta 3	0.73	0.76	0.042	0.032
TUBB6	tubulin, beta 6	0.57	0.51	0.019	0.003
TUBG1	tubulin, gamma 1	0.62	0.57	0.024	0.028
TXLNG	taxilin gamma	0.72	0.57	0.022	0.013
U2AF2	U2 small nuclear RNA auxiliary factor 2	0.66	0.81	0.010	0.024
UBAC1	UBA domain containing 1	0.64	0.62	0.020	0.007
UBE2F	ubiquitin-conjugating enzyme E2F (putative)	0.71	0.76	0.014	0.002
UBE2H	ubiquitin-conjugating enzyme E2H (UBC8 homolog, yeast)	**1.69**	**1.81**	0.013	0.018
UBE2J2	ubiquitin-conjugating enzyme E2, J2 (UBC6 homolog, yeast)	0.73	0.81	0.018	0.047
UBE2L3	ubiquitin-conjugating enzyme E2L 3	0.65	0.43	0.023	0.013
UBE3B	ubiquitin protein ligase E3B	0.45	0.36	0.041	0.007
UBL7	ubiquitin-like 7 (bone marrow stromal cell-derived)	0.45	0.55	0.025	0.021
UCA1	urothelial cancer associated 1 (non-protein coding)	0.12	0.11	0.000	0.003
UGGT1	UDP-glucose glycoprotein glucosyltransferase 1	0.68	0.64	0.008	0.021
UMPS	uridine monophosphate synthetase	0.49	0.55	0.025	0.020
UQCR10	ubiquinol-cytochrome c reductase, complex III subunit X	0.67	0.76	0.004	0.038
UROD	uroporphyrinogen decarboxylase	0.41	0.32	0.018	0.022
UROS	uroporphyrinogen III synthase	0.54	0.55	0.002	0.020

UXS1	UDP-glucuronate decarboxylase 1	**1.51**	**2.07**	0.041	0.012
VGLL4	vestigial like 4 (Drosophila)	**1.27**	**1.40**	0.002	0.035
VPS25	vacuolar protein sorting 25 homolog (S, cerevisiae)	0.75	0.81	0.001	0.049
VPS37B	vacuolar protein sorting 37 homolog B (S, cerevisiae)	0.49	0.69	0.021	0.045
WBP11	WW domain binding protein 11	0.68	0.70	0.024	0.007
WDR18	WD repeat domain 18	0.70	0.75	0.007	0.010
WDR61	WD repeat domain 61	0.83	0.78	0.013	0.033
WDR7	WD repeat domain 7	0.50	0.53	0.030	0.030
WHSC1	Wolf-Hirschhorn syndrome candidate 1	0.65	0.70	0.041	0.018
WHSC1L1	Wolf-Hirschhorn syndrome candidate 1-like 1	0.83	0.70	0.027	0.040
WIBG	within bgcn homolog (Drosophila)	0.66	0.40	0.032	0.034
WIPF1	WAS/WASL interacting protein family, member 1	**1.66**	**1.86**	0.030	0.030
XBP1	X-box binding protein 1	**1.36**	**1.97**	0.045	0.026
XK	X-linked Kx blood group (McLeod syndrome)	0.15	0.21	0.021	0.011
XPO5	exportin 5	0.58	0.67	0.005	0.017
XPR1	xenotropic and polytropic retrovirus receptor 1	0.59	0.47	0.034	0.037
XRCC5	X-ray repair complementing defective repair in Chinese hamster cells 5 (double-strand-break rejoining)	0.78	0.83	0.029	0.008
YIF1A	Yip1 interacting factor homolog A (S, cerevisiae)	0.79	0.62	0.040	0.001
YIF1B	Yip1 interacting factor homolog B (S, cerevisiae)	0.59	0.62	0.038	0.003
YPEL5	yippee-like 5 (Drosophila)	**1.59**	**1.60**	0.016	0.033
ZDHHC14	zinc finger, DHHC-type containing 14	0.49	0.37	0.001	0.010
ZFAND5	zinc finger, AN1-type domain 5	**1.39**	**1.36**	0.040	0.049
ZMAT3	zinc finger, matrin-type 3	**2.11**	**2.50**	0.043	0.027
ZMYM4	zinc finger, MYM-type 4	**1.39**	**1.60**	0.023	0.003
ZMYM5	zinc finger, MYM-type 5	**1.48**	**1.49**	0.004	0.007
ZMYND19	zinc finger, MYND-type containing 19	0.73	0.77	0.002	0.017
ZNF24	zinc finger protein 24	**1.49**	**1.47**	0.040	0.037
ZNF280B	zinc finger protein 280B	**1.73**	**1.84**	0.039	0.014
ZNF519	zinc finger protein 519	0.53	0.55	0.010	0.008
ZNF655	zinc finger protein 655	0.63	0.54	0.046	0.009
ZSCAN16	zinc finger and SCAN domain containing 16	0.79	0.64	0.033	0.025
ZSCAN18	zinc finger and SCAN domain containing 18	**1.21**	**1.81**	0.025	0.036

Supporting Information Table S2
Alteration of metabolic pathways in AK2-deficient cells

(the fold change between shAK2 and shCont is shown for shAK2 #1 and shAK2 #2, upregulated genes are shown in bold type)

OXPHOS genes		**#1**	**#2**
ATPIF1	ATPase inhibitory factor 1 (**regulator of CxV activity**)	0.49	0.43
BCS1L	BCS1-like (**assembly factor of CxIII**)	0.74	0.61
BOLA3	bolA homolog 3 (**production of respiratory chain Fe-S clusters**)	0.26	0.69
COX5A	cytochrome c oxidase subunit Va (**CxIV subunit**)	0.55	0.57
GLRX5	glutaredoxin 5 (**production of respiratory chain Fe-S clusters**)	0.68	0.73
NDUFB6	NADH dehydrogenase (ubiquinone) 1 beta 6 (**CxI subunit**)	0.74	0.76
NDUFB9	NADH dehydrogenase (ubiquinone) 1 beta 9 **(CxI subunit**)	0.80	0.82
NDUFS7	NADH dehydrogenase (ubiquinone) Fe-S protein 7 (**CxI subunit**)	0.67	0.59
SDHA	succinate dehydrogenase complex. subunit A. flavoprotein (Fp) (**CxII subunit**)	0.70	0.71
UQCR10	ubiquinol-cytochrome c reductase subunit X (**CxIII subunit**)	0.67	0.76

Mitochondrial translation		**#1**	**#2**
CARS2	cysteinyl-tRNA synthetase 2. mitochondrial (putative)	0.81	0.66
EARS2	glutamyl-tRNA synthetase 2. mitochondrial (putative)	0.66	0.67
GARS	glycyl-tRNA synthetase	0.68	0.70
LRPPRC	leucine-rich PPR-motif containing	0.69	0.83
MRM1	mitochondrial rRNA methyltransferase 1 homolog	0.60	0.76
MRPL12	mitochondrial ribosomal protein L12	0.62	0.79
MRPL27	mitochondrial ribosomal protein L27	0.73	0.76
MRPL35	mitochondrial ribosomal protein L35	0.62	0.58
MRPL36	mitochondrial ribosomal protein L36	0.77	0.76
MRPL37	mitochondrial ribosomal protein L37	0.77	0.73
PUS1	pseudouridylate synthase 1	0.73	0.75
TSFM	Ts translation elongation factor. mitochondrial	0.76	0.75

Mitochondrial protein import		**#1**	**#2**
TIMM50	translocase of inner mitochondrial membrane 50 homolog	0.64	0.62
TIMM8B	translocase of inner mitochondrial membrane 8 homolog B	0.76	0.80
TOMM40	translocase of outer mitochondrial membrane 40 homolog	0.69	0.77
SAMM50	sorting and assembly machinery component 50 homolog	0.54	0.69

Mitochondrial metabolites import		**#1**	**#2**
SLC25A1	solute carrier family 25 (mitochondrial citrate transporter) member 1	0.58	0.61
SLC25A11	solute carrier family 25 (mitochondrial oxoglutarate carrier) member 11	0.72	0.78
SLC25A12	solute carrier family 25 (mitochondrial carrier. Aralar) member 12	**3.21**	**1.31**
SLC25A21	solute carrier family 25 (mitochondrial oxodicarboxylate carrier) member 21	0.11	0.05
SLC25A17	solute carrier family 25 (mitochondrial carrier; peroxisomal membrane protein) member 17	0.62	0.47
SLC25A37	solute carrier family 25 member 37 (iron transport)	0.47	0.41
SLC25A28	solute carrier family 25 member 28 (iron transport)	0.78	0.75

Fatty acid metabolism		**#1**	**#2**
AACS	acetoacetyl-CoA synthetase	0.72	0.66
ACAD9	acyl-CoA dehydrogenase family. member 9	0.80	0.71
ACSL3	acyl-CoA synthetase long-chain family member 3	0.39	0.58
ACSL5	acyl-CoA synthetase long-chain family member 5	0.53	0.72
ACSM3	acyl-CoA synthetase medium-chain family member 3	**1.45**	**5.12**
ACSS1	acyl-CoA synthetase short-chain family member 1	0.58	0.62
AUH	AU RNA binding protein/enoyl-CoA hydratase	**1.40**	**1.52**
FADS1	fatty acid desaturase 1	0.61	0.63
GPD1L	glycerol-3-phosphate dehydrogenase 1-like	0.66	0.78

Other mitochondrial metabolic pathways		**#1**	**#2**
ADCK2	aarF domain containing kinase 2 (**CoQ10 synthesis**)	0.65	0.53
COASY	CoA synthase (**biosynthesis of Coenzyme A**)	0.71	0.76
COQ3	coenzyme Q3 homolog. methyltransferase (**CoQ10 synthesis**)	0.60	0.66
DLD	dihydrolipoamide dehydrogenase (**pyruvate dehydrogenase and TCA cycle**)	0.67	0.60
DLST	dihydrolipoamide S-succinyltransferase (**pyruvate dehydrogenase and TCA cycle**)	0.68	0.81
FDPS	farnesyl diphosphate synthase (**CoQ10 synthesis**)	0.68	0.63
GOT2	glutamic-oxaloacetic transaminase 2. mitochondrial (**aminoacids metabolism**)	0.67	0.80
IDH2	isocitrate dehydrogenase 2 (NADP+). mitochondrial (**TCA cycle**)	0.81	0.71
OGFOD2	2-oxoglutarate iron-dependent oxygenase domain 2 (**TCA cycle**)	0.71	0.70
PDK3	pyruvate dehydrogenase kinase. isozyme 3 (**pyruvate dehydrogenase**)	0.53	0.68
PPCS	phosphopantothenoylcysteine synthetase (**biosynthesis of Coenzyme A**)	**1.85**	**1.55**

Metabolism and transport of nucleotides		**#1**	**#2**
DTYMK	deoxythymidylate kinase (thymidylate kinase)	0.61	0.57
DPYSL2	dihydropyrimidinase-like 2	0.70	0.50
GUCY1A3	guanylate cyclase 1. soluble. alpha 3	**2.97**	**4.67**
NT5DC2	5-nucleotidase domain containing 2	0.68	0.58
OGT	O-linked N-acetylglucosamine (GlcNAc) transferase	**1.52**	**1.52**
P2RY8	purinergic receptor P2Y. G-protein coupled. 8	**1.49**	**2.30**
PNPO	pyridoxamine 5-phosphate oxidase	0.42	0.51
POP7	processing of precursor 7. ribonuclease P/MRP subunit	0.62	0.61
PRPS1	phosphoribosyl pyrophosphate synthetase 1	0.68	0.77
PUS1	pseudouridylate synthase 1	0.73	0.75
RAVER1	ribonucleoprotein. PTB-binding 1	0.58	0.55
SLC29A1	solute carrier family 29 (nucleoside transporters). member 1	0.55	0.72
SLC29A2	solute carrier family 29 (nucleoside transporters). member 2	0.68	0.77
TK1	thymidine kinase 1. soluble	0.78	0.46
UGGT1	UDP-glucose glycoprotein glucosyltransferase 1	0.68	0.64
UMPS	uridine monophosphate synthetase	0.49	0.55
UXS1	UDP-glucuronate decarboxylase 1	**1.51**	**2.07**