Supplementary Note 1

***DAPK1* reporter cell line generation**

Context-dependent assembly (CoDA) of Zinc Finger Nucleases:

ZiFiT software version (4.215)[1] was used to design Genome Editing Nucleases targeting GACAGCCACCAATCAGTTGATTGT on human chr9:90225669-90225692, downstream of *DAPK1* exon3 according to the CoDA method[2]. The underlined sequence indicates the 6nt spacer adjacent to the 2x9nt binding sequence. The predicted ZFN target sequence was checked by blast nucleotide search for lack of predicted additional targets.

ZFN-synthesis and reporter construct cloning:

Left and right ZFN-coding plasmid was synthesized by GeneArt® (Life technologies) into the standard cloning vector pANY (sequences are available upon request). Left and right ZFN-sequences were subcloned via BamHI + XhoI overhangs into the ZFN-expression vectors pAC.HA.nIL2RGL.hNeeai_1140 and pAC.HA.nIL2RGR.hNqkiv_1141, respectively, and sequence-verified by Sanger sequencing. pAC.HA.nIL2RGL.hNeeai_1140 and pAC.HA.nIL2RGR.hNqkiv_1141 were kindly provided by Prof. Cathomen (University Medical Centre, Freiburg). Standard molecular cloning techniques were used to create the reporter construct. The reporter was cloned into pBluescript II KS(-) as follows: First, PCR-amplification and subcloning of EGFP-Neo from LeGO-G/Neo-opt, mCherry-Zeo from LeGO-C/Zeo , SFFV-promoter from LeGO-C/Zeo (see Weber at al.[3] for vector details), BGH-polyA from pcDNA™5/FRT/TO (Invitrogen), SV40 polyA and CMV-TO from pT-Rex-DEST30 (Invitrogen), Spliceacceptor+self-cleaving peptide (SA-2A, synthesized as in AAVS1-SA-2A-puro-pA donor 19) and HSV-TK (from PL253 20) into pBluescript II KS(-). Next, the sequence-verified elements were excised from the plasmids, gel purified, and then step-wise ligated by T4-ligase to create the full reporter construct. After cloning, the 9.7 kb full-size dual-fluorescence/resistance reporter construct was partially re-sequenced at critical components to assure sequence correctness. Finally, left (chr9:90224925+90225674) and right (>chr9:90225687+90226448) homology arms of ~750 bp were PCR-amplified from NCI-H1299 genomic DNA and adjacently cloned into the donor plasmid. For details on restriction enzymes and primers used and further cloning details, see **Supplementary Table 6** and **Supplementary Fig. 2a and B**.

ZFN-mediated targeting of the endogenous DAPK1 locus:

NCI-H1299 cells grown in RPMI 1640 supplemented with 10% FCS were seeded in T75 flasks at a density of 12000 cells/cm² and expanded for 24 h. Thereafter, transfection with 2 µg of left and right ZFN-encoding plasmid and 16 µg of donor plasmid using Trans-IT LT1 (Mirus Bio) was performed. Fresh media containing 100 µg/ml Zeocin (Invitrogen) was applied 48 h after transfection. After 10 d of Zeocin selection, integration positive polyconal cell pools were subjected to monoclonal cell line generation by FACS-mediated single-cell cloning. For this purpose, mCherry-positive cells were sorted into 96 well plates by the DKFZ FACS core facility using the FACSAria III machine (BD Biosciences). Two weeks after initial seeding and expansion under positive (100 µg/ml Zeocin) and negative (10µg/ml Ganciclovir, Sigma) selection pressure, surviving clones were further expanded. Correct reporter construct integration was validated by "In-Out" PCR and Southern-Blotting.

Genotyping polymerase chain reaction

Genomic DNA from polyclonal and monoclonal NCI-H1299 cell lines was isolated using the DNeasy Blood & Tissue Kit (Qiagen) according to the manufacturer's protocol. Genotyping PCRs were performed with 50 ng template DNA in 96well format using Phusion High-Fidelity DNA-Polymerase (Thermo Scientific). One DAPK1-locus specific primer and one primer binding the reporter construct were applied for integration specific amplification. PCR-products of both 5` and 3` integration were visualized by Ethidium-Bromide stain on 1.5% Agarose gels to determine correct integration and sequence-verified in case of positively genotyped monoclonal cells. Primers used for cell line genotyping are listed in **Supplementary Table 7.**

Southern blotting

Genomic DNA (10 µg) was isolated by Phenol-chloroform extraction and separated on a 0.8% agarose gel after overnight digest with 100 U BamHI (NEB). Depurinated and denatured gel was then capillary transferred over-night to a nylon membrane (Amersham Hybond NX) and finally hybridized with ^{32}P-labeled (Megaprime DNA Labeling System, Amersham) probes against genomic DAPK1 loci upstream (chr9:90,224,318-90,224,820) or downstream (chr9:90,228,320-90,229,358) of the ZFN-mediated integration site. Probing was carried out in Church's buffer (7% SDS, 1 mM EDTA, 0.5 M NaPi pH 7.2) supplemented with 100 µg/ml salmon sperm DNA (Invitrogen).

Epigenetic compound viability screen

Epigenetic compound screen in NCI-H1299 reporter cells was performed using the Epigenetics Screening Library (Cayman Chemical) in 96 well format with modifications. Compound concentrations were cross-referenced with commonly used cell-culture concentrations and adjusted to have maximum cytotoxic effects of 50 % viability reduction after 72 h of treatment. For details on

compounds and used concentrations, see **Supplementary Table 8**. Media containing the compound was refreshed every 24 h for 72h. G418-selection of DAPK1-reactivated cells was carried out in media containing 800 µg/ml G418 (Sigma) for 10 d and cell viability was quantified using the Calcein-AM assay. In brief, cells were grown in fresh media containing 0.8 µM Calcein-AM for 1 h and then lysed with PBS containing 3% Triton-X (Sigma) and fluorescent signal intensity was measured on a Spectramax M5e plate reader (at ex494 nm and em530 nm).

5' Rapid amplification of cDNA ends (5' RACE)

5'RACE was essentially performed as described previously[4]. Firstly, cDNA was synthesized using 10 pmol gene-specific primer 1 (GSP1) and Thermoscript Reverse Transcriptase with 1 µg DNA-free template RNA for 50 min at 61 °C in 20 µl reaction volume. After heat inactivation at 80 °C for 5 min, RNA from cDNA-RNA hybrids was specifically digested by adding 1 µl of RNase H for 30 min at 37 °C. Next, RNase H was heat inactivated at 70 °C for 10 min. To purify the now single-stranded cDNA, DNA was precipitated by addition of 0.1 vol. 3 M sodium acetate, 2 µg Glycogen and 2.5 vol. 100% ethanol. After centrifugation at 13,000 g, the DNA pellet was washed in 500 µl 70% ethanol and then air dried before it was resuspended in 50 µl of H_20. To tail the 3'end of the newly synthesized cDNA, single-stranded cDNA was incubated with 30 U TdT and 100 pmol dATP at 37 °C for 15 min in a 20 µl reaction, followed by heat inactivation at 70 °C for 10 min and finally diluted by addition of 30 µl H_20. The first amplification PCR was carried out using the High Fidelity PCR system with 3 pmol primer Q_T, 25 pmol primer Q_0 and 25 pmol primer GSP2 in a 50 µl reaction using 1.5 µl of tailed and diluted cDNA under the following cycling conditions: 2 min initial denaturation at 95 °C, 2 min annealing of primer Q_T, 40 min of linear amplification with primer Q_T at 68 °C. Next, linearly amplified and Q_T tagged cDNA was then exponentially amplified by 10 touchdown cycles of 15 s at 94 °C, 30 s at 60 °C (-0.5 °C per cycle) and 1 min extension at 68 °C followed by 30 PCR-cycles at 55 °C annealing temperature and 1 min extension time. For the second PCR, 1.5 µl of 1:20 diluted PCR product from the first amplification was amplified employing 10 pmol Primer Q_1 and 10 pmol GSP3 primer with the same PCR protocol (touchdown 10+30 cycles) as for the first PCR, but lacking the initial steps of linear amplification. Finally, the PCR products were separated on a 1.5 % agarose gel and then gel-purified for subcloning, utilizing the TOPO TA Cloning Kit according to the manufacturer's protocol (Invitrogen). Cloned PCR-products from single blue-white selected colonies were Sanger-sequenced (GATC, Konstanz, Germany) to identify the cloned transcripts. For details on the used primers see **Supplementary Table 9**.

Supplementary Tables

Supplementary Table 2: Filtering procedure of StringTie assembled transcripts

	DAC	SB939	DAC+SB
Total	453	744	3627
Overlap protein-coding exon	98	105	571
Longest isoform only	87	97	474
Highest coverage only	71	81	376
Translated (*in silico* prediction)	62	61	327

Supplementary Table 6: Oligonucleotides used for reporter construct and ZFN cloning

Primer/Target	Forward (5' -> 3')	Reverse (5' -> 3')	Details
HA_3'4_Left	CTAGCTAGGCGGCCGCACTGCCACTGACCCAAAAAG	CTAGCTAGTCTAGAGCTGTCCCTTCGGGGTGG	Cloning of the ~750 bp ZFN3'4 associated homology arm upstream (left) of the ZFN target site tagged with NotI (Forward, bold) and XbaI (Reverse, bold) recognition sites.
HA_3'4ight	CTAGCTAGCTCGAGGATTGTTCCTGTGTGTAATTTTGGAT	CTAGCTAGGGTACCTGAGCTATGATTGCACCACTG	Cloning of the ~750 bp ZFN3'4 associated homology arm downstream (left) of the ZFN target site tagged with XhoI (Forward, bold) and KpnI (Reverse, bold) recognition sites.
SA-T2A	CTAGCTAGTCTAGACTGACCTCTTCTCTTCCTCCCAC	CTAGCTAGGGATCCCTCGAGCCTAGGGCCGG	Cloning of the Spliceacceptor-T2A cassette from the synthesized ZFN vector tagged with XbaI (Forward, bold) and BamHI (Reverse, bold) recognition sites.
EGFP-NEO	AAAGGATCCATCAGTCAGCGTACGATGGTGAGCAAGGGCGA	AAAGAATTCACTAGCTAGTCCGGATCAGAAGAACTCGTCCAGCAG	Cloning of the EGFP-NEO cassette from the LeGO-G/Neo-opt vector tagged with BamHI (Forward, bold) and EcoRI (Reverse, bold) recognition sites.
BGH-PolyA	CTAGCTAGGAATTCCCTCGACTGTGCCTTCTAGTT	CTAGCTAGAAGCTTCCATAGAGCCCACCGCAT	Cloning of the BGH-pA cassette from the pcDNA™5/FRT/TO vector tagged with EcoRI (Forward, bold) and HindIII (Reverse, bold) recognition sites.
CMV-TO	CTAGCTAGAAGCTTATGCATGTCGTTACAT	CTAGCTAGATCGATTCCCGGTGTCTTCT	Cloning of the CMV-TO cassette from the pT-Rex-DEST30 vector tagged with HindIII

	AACTTACG	ATGGAG	(Forward, bold) and ClaI (Reverse, bold) recognition sites.
Cherry-Zeo	AAAATCGATACTAGCTAGACGCGTAATCCCGCCACCATGGTGA	AAAGTCGACACTAGCTAGCCCGGGTCAGTCCTGCTCCTCGGC	Cloning of the Cherry-Zeo cassette from the LeGO-C/Zeo vector tagged with ClaI (Forward, bold) and SalI (Reverse, bold) recognition sites.
SV40-PolyA	CTAGCTAGGTCGACAACTTGTTTATTGCAGCTTATAATGGT	CTAGCTAGCTCGAGGCCGATTCATTAATGCAGGA	Cloning of the SV40-pA cassette from the pT-Rex-DEST30 vector tagged with SalI (Forward, bold) and XhoI (Reverse, bold) recognition sites.
SFFV	CTAGCTAGGGTACCCTGAAAGACCCCACCTGTAGG	CTAGCTAGATCGATGGGCGACTCAGTCAATCG	Cloning of the SFFV promoter from the LeGO-C/Zeo vector tagged with KpnI (Forward, bold) and ClaI (Reverse, bold) recognition sites.
HSV-TK	CTAGATCGATAATCCCGCCACCATGGCTTCGTACCCCGG	CTAGACATGTTCAGTTAGCCTCCCCCATCT	Cloning of the HSV-TK cassette from the PL253 vector tagged with ClaI (Forward, bold) and PciI (Reverse, bold) recognition sites.
ZFN-left	GAAAAAAATCTAGACCCGGGG	CAGGAAACAGCTATGACCGG	Cloning of the ZFN "left" pairs from the synthesized ZFN plasmids into pAC.HA.nIL2RGL.hNeeai_1140.
ZFN-right	GAAAAAAATCTAGACCCGGGG	GCAATGTAACATCAGAGATGGATC	Cloning of the ZFN "right" pairs from the synthesized ZFN plasmids and pAC.HA.nIL2RGR.hNqkiv_1141.

Supplementary Table 7: Genotyping primers

Primer/Target	Forward (5' -> 3')	Reverse (5' -> 3')	Details
ZFN3'4 genotyping_Left	GAACTTCCTCTGAGGGTTAGTG	GTGGGAGGAAGAGAAGAGGTCA	Forward primer binds genomic sequence upstream ofZFN3'4 target site. Reverse primer binds SA-2A sequence.
ZFN3'4 genotyping_Right	GACTTCGTGGAGGACGACTT	AAAAAGGAAAAATTGAAATTCTGG	Reverse primer binds genomic sequence downstream ofZFN3'4 target site. Forward primer binds Zeo cassette.

Supplementary Table 8: Epigenetic compound library

Compound	Target group	Primary target proteins	IC50 in NCI-H1299 H2 cells	Concentration used [nM]
Zebularine	DNMT	DNMT1	>50µM	50000
RG-108	DNMT	DNMT1	>50µM	50000
2',3',5'-triacetyl-5-Azacytidine	DNMT	DNMT1	>50µM	50000
Decitabine	DNMT	DNMT1	>50µM	1000
5-Azacytidine	DNMT	DNMT1	7.5µM	5000
Delphinidin chloride	HATS	HATs,	25µM	50000
Anacardic Acid	HATS	HATs,p300;PCAF	>50µM	50000
Garcinol	HATS	HATs,p300;PCAF	6µM	5000
SB939	HDAC	HDAC pan	700nM	500
CAY10398	HDAC	HDAC1	7.5µM	5000
MS-275	HDAC	HDAC1	120nM	100
Suberohydroxamic Acid	HDAC	HDAC1 , HDAC3	20µM	10000
CBHA	HDAC	HDAC1, 3	4000nM	1000
M 344	HDAC	HDAC1, 3,6	1µM	500
Tubastatin A (trifluoroacetate salt)	HDAC	HDAC6	15µM	1000
CAY10603	HDAC	HDAC6	1µM	500
Valproic Acid (sodium salt)	HDAC	HDACs pan	>50µM	50000
Chidamide	HDAC	HDACs pan	5µM	5000
HNHA	HDAC	HDACs pan	>50µM	5000
(S)-HDAC-42	HDAC	HDACS pan	0.5µM	500
VPA	HDAC	HDACS pan	1600µM	50000
HC Toxin	HDAC	HDACs 1,2,3,8	40nM	50
Scriptaid	HDAC	HDACs 1,2,8	1µM	1000
Oxamflatin	HDAC	HDACs 3,6	100nM	50
Pimelic Diphenylamide 106	HDAC	HDACs Class I	16µM	10000
Sodium Butyrate	HDAC	HDACS Class I, Iia	>50µM	50000
Apicidin	HDAC	HDACs Class I,II	200nM	100
Trichostatin A	HDAC	HDACs Class I,II	50nM	50

SAHA	HDAC	HDACs Class I+II, IV	3-4µM	1000
4-iodo-SAHA	HDAC	HDACs Class I+II, IV	0.6µM	500
Chaetocin	HMTS	SU(VAR)3-9; G9a/GLP	< 20nm	5000
3-Deazaneplanocin A	HMTS	EZH2, other HMTs	>50µM	10000
BIX01294 (hydrochloride hydrate)	HMTS	G9a	10µM	5000
UNC0321 (trifluoroacetate salt)	HMTS	G9a, GLP	>50µM	1000
UNC0638	HMTS	G9A,GLP	15µM	1000
UNC0224	HMTS	G9a,GLP	20µM	1000
2-PCPA (hydrochloride)	HDM	LSD1, MAOA, MAOB	>50µM	50000
Genistein	OTHER	various	7.5µM	5000
Nicotinamide	OTHER	various	>50µM	50000
Suramin (sodium salt)	OTHER	various	>50µM	50000
EGCG	OTHER	various	50µM	50000
IOX1	OTHER	2OG	10µM	10000
Gemcitabine	OTHER	Gadd45a	70nM	50
2,4-DPD	OTHER	HIF-PH	>50µM	5000
SP600125	OTHER	JNK	>5µM	5000
Phthalazinone pyrazole	OTHER	Aurora-A-Kinase	>50µM	1000
(+)-JQ1	OTHER	BETs, BRD4	500nM	1000
(-)-JQ1	OTHER	None, inactive	25µM	1000
Flavopiridol	OTHER	CDKs	70nM	50
Tunicamycin	OTHER	Cell cycle	200ng/ml	100ng/ml
trans-Resveratrol	OTHER	COX, Sirts	25µM	10000
Ellagic Acid	OTHER	CytP450	10µM	10000
Fludarabine	OTHER	DNA-Synthesis inhibition	30nM	50
DMOG	OTHER	HIF-PH	>50µM	50000

PD03259	OTHER	MAPK	4.1nM	1
Mirin	OTHER	MRN; ATM	50µM	50000
SB202190	OTHER	p38a , p38b	>5µM	5000
F-Amidine (trifluoroacetate salt)	OTHER	PAD4	>50µM	50000
Cl-Amidine	OTHER	PAD4	>50µM	50000
Phorbol-12-myristat-13-acetat (TPA)	OTHER	PKC activation	2µg/ml	1ng/ml
Isoliquiritigenin	OTHER	Quinone reductase-1	7.5µM	5000
ATRA	OTHER	RAR	25µM	10000
CCG-100602	OTHER	Rho signaling	4.5µM	5000
Anisomycin	OTHER	Ribosome	100nM	100
Etoposide	OTHER	Topoisomerase	800nM	1000
Curcumin	OTHER	various	3µM	1000
Xanthohumol	OTHER	various	6µM	3000
BSI-201	PARP	PARP-1	>50µM	50000
AG-014699	PARP	PARP-1	10µM	1000
3-amino Benzamide	PARP	PARP-1	>50µM	50000
(-)-Neplanocin A	SAH	SAH	600 nM	500
S-Adenosylhomocysteine	SAH	SAH	>50µM	50000
Splitomicin	SIRTUINS	Sir2p	>50µM	50000
EX-527	SIRTUINS	Sirt1	>50µM	50000
Sirtinol	SIRTUINS	SIRT1; SIRT2	10µM	5000
AGK2	SIRTUINS	SIRT2	>50µM	50000
JGB1741	SIRTUINS	SIRTs	50µM	50000
Salermide	SIRTUINS	SIRTs	5µM	5000
Tenovin-6	SIRTUINS	SIRTs	3µM	1000
Tenovin-1	SIRTUINS	Sirts	1.5µM	1000

Information on inhibited proteins for the individual compounds was derived from http://www.caymanchem.com

Supplementary Table 9: 5'RACE primers

Primer/Target	**Forward (5’ -> 3’)**	**Details**
Q_T	CCAGTGAGCAGAGTGACGAGGACTCGAGCT	5’ RACE standard primer.

	CAAGCTTTTTTTTTTTTTTTTT	
Q_0	CCAGTGAGCAGAGTGACG	5’ RACE standard primer.
Q_1	GAGGACTCGAGCTCAAGC	5’ RACE standard primer.
GSP1	GGTCAGGGTGGTCACGAG	Binds EGFP.
GSP2	GCCCTTGCTCACCATCGTA	Binds SA-2A sequence.
GSP3	CACGTCACCGCATGTTAGA	Binds SA-2A sequence.

Supplementary Table 10: Oligonucleotides used for shRNA cloning into pRSI9

Primer/Target	Forward (5’ -> 3’)	Reverse (5’ -> 3’)
shDNMT1-3	accgggcccaatgagattgacattaagttaata ttcatagcttgatgtcagtctcattgggctttt	cgaaaaaagcccaatgagactgacatcaagctatgaatattaa cttaatgtcaatctcattgggcc
shLuc2	accggcttcgaaatgttcgtttggttgttaatatt catagcaaccgaacggacatttcgaagtttt	cgaaaaaacttcgaaatgtccgttcggttgctatgaatattaac aaccaaacgaacatttcgaagc

Supplementary Table 11: Primer sequences

Sequence 5’ -> 3’	Target	Target	Orientation	Application
GCAGGAAAACGTGGATGATT	DAPK1	Exon 2	Forward	qRT-PCR
CATTTCTTCACAACCGCAAA	DAPK1	Exon 3	Reverse	qRT-PCR
TGCAAGAAATACGAAGCCAGA	DAPK1	3’ UTR	Forward	qRT-PCR
GGTTGGGTCCATTGAGCTT	DAPK1	3’ UTR	Reverse	qRT-PCR
ACGGACGTCATCCTGATCTT	DAPK1	Exon 3	Forward	qRT-PCR
CACGTCACCGCATGTTAGA	DAPK1	EGFP construct	Reverse	qRT-PCR
GGACTGTGAGTTTTCTGAGGGTA	DAPK1	α-transcript	Forward	qRT-PCR
CATTTCTTCACAACCGCAAA	DAPK1	α-transcript	Reverse	qRT-PCR
GGAAATTGGAGCTTCCAAAAG	DAPK1	β-transcript	Forward	qRT-PCR
CATTTCTTCACAACCGCAAA	DAPK1	β-transcript	Reverse	qRT-PCR
TACCTTGAGACGGGAGGAGA	DAPK1	γ-transcript	Forward	qRT-PCR
CATTTCTTCACAACCGCAAA	DAPK1	γ-transcript	Reverse	qRT-PCR
aggaagagagAGTTTAGTAATGTGTTATAGGTG	DAPK1	Promoter CpG island	Forward	MassARRAY
cagtaatacgactcactatagggagaaggctA	DAPK1 CGI	Promoter CpG	Reverse	MassARRAY

CCAATAAAAACCCTACAAAC		island		
AGCCACATCGCTCAGACAC	GAPDH	Housekeeper	Forward	qRT-PCR
GCCCAATACGACCAAATCC	GAPDH	Housekeeper	Reverse	qRT-PCR
TGACCTTGATTTATTTTGCATACC	HPRT1	Housekeeper	Forward	qRT-PCR
CGAGCAAGACGTTCAGTCCT	HPRT1	Housekeeper	Reverse	qRT-PCR
CAACGAGTCTGGCTTTGAGA	DNMT1	Housekeeper	Forward	qRT-PCR
GACACAGGTGACCGTGCTTA	DNMT1	Housekeeper	Reverse	qRT-PCR
ATTGGCAATGAGCGGTTC	beta-Actin	Housekeeper	Forward	qRT-PCR
GGATGCCACAGGACTCCAT	beta-Actin	Housekeeper	Reverse	qRT-PCR
ATGGGCCGCCTTAAGAGTAA	NAALAD2	TINAT	Forward	qRT-PCR
GCAATGCTTCTCTCCTGGA	NAALAD2	Exon	Reverse	qRT-PCR
TGATTTTCTCTTGCTGCCGC	ERC1	TINAT	Forward	qRT-PCR
CGCAATTCATCCTGGAGAGC	ERC1	Exon	Reverse	qRT-PCR
AGCTCTCATCTGGTCTGCTG	CRADD	TINAT	Forward	qRT-PCR
CTGGTTAATCTGCCGGTCTG	CRADD	Exon	Reverse	qRT-PCR
AACGCATCGGAAGCAAGA	FMN1	TINAT	Forward	qRT-PCR
CTCTGTTGGGAAGGTCTTTAGG	FMN1	Exon	Reverse	qRT-PCR
GAACAACCTCCAGACGCG	DNAH3	TINAT	Forward	qRT-PCR
TGGAAATGATATTCAGATGGCGA	DNAH3	Exon	Reverse	qRT-PCR
CTCCCAACACATCCGACCAT	DNAH12	TINAT	Forward	qRT-PCR
TTTTCCTGTGCCTGCTGG	DNAH12	Exon	Reverse	qRT-PCR
TCCTCATTTTCTCTTGTCACCAC	FARS2	TINAT	Forward	qRT-PCR
TGCGTAATTCTCAGAGGGCA	FARS2	Exon	Reverse	qRT-PCR
TCACTGTGAGGGTCCGCG	CPED1	TINAT	Forward	qRT-PCR
GTGGCTGCTGTATTTCTGGT	CPED1	Exon	Reverse	qRT-PCR
ACGCGCTGCCTTTTAGAAC	COL28A1	TINAT	Forward	qRT-PCR
AATCCTTCTCCGGGTAAGCC	COL28A1	Exon	Reverse	qRT-PCR
ACTGTCCTACGGGCTAGAGA	FBP2	TINAT	Forward	qRT-PCR
ACCATGTTGATCACCAGGGA	FBP2	Exon	Reverse	qRT-PCR
TTCTTCTGGTGTCCTGTGGA	BCAS1	TINAT	Forward	qRT-PCR
TGGTAAGTCTCTGCTTCTGGT	BCAS1	Exon	Reverse	qRT-PCR
GCTCCATTCATGATCACCTTCT	CRYGC	TINAT	Forward	qRT-PCR
TTGGTAGTTGGGACGCTCAT	CRYGC	Exon	Reverse	qRT-PCR
GCTCCATTCATGATCACCTTCT	ATP6V1H	TINAT	Forward	qRT-PCR

TTGGTAGTTGGGACGCTCAT	ATP6V1H	Exon	Reverse	qRT-PCR
GGGTGTGTTTTCTTCCCCTT	PON2	TINAT	Forward	qRT-PCR
ATTCCCGTGCCCTTGGTTTT	PON2	Exon	Reverse	qRT-PCR
GGTCAGCAAAATGCATGGAG	AVEN	TINAT	Forward	qRT-PCR
TCTGCATCGCTGTCATCTTC	AVEN	Exon	Reverse	qRT-PCR
ACCAATTCTGGACACACTGG	CACUL1	TINAT	Forward	qRT-PCR
TGATCTATGGCACCATCCAA	CACUL1	Exon	Reverse	qRT-PCR
TGGGAGATGGAGATCTCTGG	CERCAM	TINAT	Forward	qRT-PCR
CTGATGGCACTGCTGTTGAG	CERCAM	Exon	Reverse	qRT-PCR
CATGGTTTTTGGCTTCACCT	CFLAR	TINAT	Forward	qRT-PCR
GCAAATTGGCCAAGAATCTG	CFLAR	Exon	Reverse	qRT-PCR
CGGATGAAGGACCAGTGTG	CLU	TINAT	Forward	qRT-PCR
TTCCTGGTCAACCTCTCAGC	CLU	Exon	Reverse	qRT-PCR
CATGGCTCCCCTCATCCT	CPSF1	TINAT	Forward	qRT-PCR
AAAGCGGACTTTGAGATTGC	CPSF1	Exon	Reverse	qRT-PCR
CCCAACACATCCGACCAT	DNAH12	TINAT	Forward	qRT-PCR
TAGCCAAGTCCTTGGTGGTT	DNAH12	Exon	Reverse	qRT-PCR
GGAAGATGCACTGACTAGAACTG	DNAJC1	TINAT	Forward	qRT-PCR
CAGGAAATTCAGGTTTTGGTTT	DNAJC1	Exon	Reverse	qRT-PCR
TATTCATCCATGGGCCAGAT	FANCC	TINAT	Forward	qRT-PCR
CCCAAGACCTTGAGTGAAAAG	FANCC	Exon	Reverse	qRT-PCR
GCATGGAGTACCTGGAGAGC	FES	TINAT	Forward	qRT-PCR
GGGACATCCCAAAGTCACTG	FES	Exon	Reverse	qRT-PCR
TCCGGACACAATGGTACAAA	FMN1	TINAT	Forward	qRT-PCR
TTCTTTGTGCTCCCTCTTCAA	FMN1	Exon	Reverse	qRT-PCR
GAATTCATTGCTTGGCTGGT	GCG	TINAT	Forward	qRT-PCR
CGGCCAAGTTCTTCAACAAT	GCG	Exon	Reverse	qRT-PCR
ATGCACGACTTGAAGACACG	IGF2R	TINAT	Forward	qRT-PCR
CAATGCTGCTCTGGACTCTG	IGF2R	Exon	Reverse	qRT-PCR
TTGCTCCTCATTTGCCTTCT	INTS7	TINAT	Forward	qRT-PCR

AAAGTCTGGGAAAGCGAACA	INTS7	Exon	Reverse	qRT-PCR
GGAGCAAACTCCAGACACG	JHDM1D	TINAT	Forward	qRT-PCR
CAGCATGATGTTCTTCTACTCC	JHDM1D	Exon	Reverse	qRT-PCR
ATGTGCTCCTGCAGAAAAGG	MYO5C	TINAT	Forward	qRT-PCR
GAGAGAGGGGCTCCAAAGTT	MYO5C	Exon	Reverse	qRT-PCR
TCTGCCACCATGTGAAATGT	OSMR	TINAT	Forward	qRT-PCR
GGTAAGTCCTCAAGGACAGCA	OSMR	Exon	Reverse	qRT-PCR
GGAACCCTGACCTGTACGAT	PIH1D1	TINAT	Forward	qRT-PCR
ATGTTCTGCTGCGAGATGG	PIH1D1	Exon	Reverse	qRT-PCR
GTGAAGCGGTTGAGTTCCTT	PRKCG	TINAT	Forward	qRT-PCR
AACTTGCCCAGCTGTTGAAT	PRKCG	Exon	Reverse	qRT-PCR
CAGCAGGAGGGGAACTACCT	RBCK1	TINAT	Forward	qRT-PCR
AAGGTGTGCAGACACTCACG	RBCK1	Exon	Reverse	qRT-PCR
TCTCTCTGGCCAAGACCACT	SFN	TINAT	Forward	qRT-PCR
TGATGAGGGTGCTGTCTTTG	SFN	Exon	Reverse	qRT-PCR
AACCACCACCAAAAACCTCA	SRSF6	TINAT	Forward	qRT-PCR
CGAACAGGTGGTCCGTATTT	SRSF6	Exon	Reverse	qRT-PCR
AGAAGGACGTGTTTGCTTCC	STPG1	TINAT	Forward	qRT-PCR
GCCAGTGCGTTCATTTTTCT	STPG1	Exon	Reverse	qRT-PCR
TTGCCTGGGAGGTACAGTTC	TFCP2L1	TINAT	Forward	qRT-PCR
GCGAGCACATCACTGAGCTA	TFCP2L1	Exon	Reverse	qRT-PCR
TTCCGGACACCCTATCAGAG	TP63	TINAT	Forward	qRT-PCR
ATGAGCTGGGGTTTCTACGA	TP63	Exon	Reverse	qRT-PCR
CAGAAAGGGAATCTTCAGTCG	ZNF236	TINAT	Forward	qRT-PCR
ACCCATATGCATCTTGCTGA	ZNF236	Exon	Reverse	qRT-PCR
TCATGCAGAACTTGCTCGAC	ZNF546	TINAT	Forward	qRT-PCR
TTCCGTTTGAAGACGAAAGG	ZNF546	Exon	Reverse	qRT-PCR

GCCAGTGACAATGCCTTCAT	ZNF582	TINAT	Forward	qRT-PCR
TGGGTCAGCTTCTCTGAGGT	ZNF582	Exon	Reverse	qRT-PCR
TCACTCTTTGGGTCCACACT	LTR12C_1	Consensus	Forward	qRT-PCR
TGGAGTTGTTCGTTCCTCCC	LTR12C_1	Consensus	Reverse	qRT-PCR
GAAGGCTCATGGCAAGAAGG	Rabbit beta-Globin	Housekeeper	Forward	qRT-PCR
ATGATGAGACAGCACAATAACCAG	Rabbit beta-Globin	Housekeeper	Reverse	qRT-PCR
CTGAACTCGCATCATCCGTG	CRYGC	5’UTR	Forward	In vitro transcription
CTCACTGACTCACCCAGAGC	CRYGC	TINAT	Forward	In vitro transcription
TGGGAAATTGGTAGTGTTAAGCT	CRYGC	3’UTR	Reverse	In vitro transcription
CCGTTTGGGTCTCTTTCC	FBP2	TINAT	Forward	In vitro transcription
GCTTCCAAACCTGTCGTAAG	FBP2	3’UTR	Reverse	In vitro transcription
TCATTCTTCTGGTGTCCTGTGG	BCAS1	TINAT	Forward	In vitro transcription
TTCCCTCCCTTTCCTGCTTG	BCAS1	3’UTR	Reverse	In vitro transcription

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