

Name		Nucleotide sequence (5'→3')	Used in the	
PGK1	Forward	GTTGCAGACAAGATCCAGGTC	quantification of mRNA expression	
	Reverse	GAAGTGGCAATTCATGTTG		
CHERP	Forward	CCAATGTGCTACTCGGAT	quantification of mRNA expression	
	Reverse	TGTACTCGTGATCTCCAGCTT		
iRNA	Forward	TGCAACGTTGATCATGAGATGCCGCTGC	construction of expression vector wild-type	
	Reverse	GCCACTGTGCTGATCTACTACCTGTCCTGG		
U6 snRNA	Forward	GTAGTGTGGCGSAGTGGTTAAG	confirmation of the fractionation	
	Reverse	GTAGTCGGCAGATTGGAAC		
E2F8	Forward	GTGCTCCCTCGCGAAGCACTTACACTAAA	confirmation of the fractionation	
	Reverse	CTCAAAAAGGAATGCTTCAAAATTGCCT		
CANT1	Forward	CGGGGAGGAGAATAAGTACG	confirmation of the fractionation	
	Reverse	CTTGCTTTTGGGGCTGTTTA		
RSGR	Forward	CCTTCCCTCACTAGCTTCC	quantification of increased intron inclusion	
	Reverse	GGTCAGGTAGCCCTTTTTC		
RGR	Forward	GACGAGGATACAGCTCTTA	quantification of increased intron inclusion	
	Reverse	TTGAATCCTCTGCTCCTTCC		
RGR	Forward	CGCGGATCCAAACAACAACAATTGGGGAAGTGA	construction of minigene wild-type	
	Reverse	ATATCCGCTCGAGCTCTGCTTTTGTCTGTAAAGTCACTGTGATA		
RGR	Forward	AGATGAGGAAGCAGGTAAGGACACAGGCCA	construction of minigene mutant for 5' splice site	1st PCR
	Reverse	TGGCCTGTGCTTACCTGCTTCTCATC		2nd PCR
RGR	Forward	CGCGGATCCAAACAACAACAATTGGGGAAGTGA	construction of minigene mutant for 3' splice site	1st PCR
	Reverse	ATATCCGCTCGAGCTCTGCTTTTGTCTGTAAAGTCACTGTGATA		2nd PCR
RSRP1	Forward	GTGATCTTTTACAGTATCCAGAGGAGAAGGAAGG	quantification of increased intron inclusion	
	Reverse	CCTTCTCTCTCTGGGATACGAAAAGATCAC		
DVL3	Forward	CGCGGATCCAAACAACAACAATTGGGGAAGTGA	quantification of decreased intron inclusion	
	Reverse	ATATCCGCTCGAGCTCTGCTTTTGTCTGTAAAGTCACTGTGATA		
PODXL	Forward	GTGATCTTTTACAGTATCCAGAGGAGAAGGAAGG	quantification of decreased intron inclusion	
	Reverse	CCTTCTCTCTCTGGGATACGAAAAGATCAC		
SUPT7L	Forward	CGCGGATCCAAACAACAACAATTGGGGAAGTGA	quantification of decreased intron inclusion	
	Reverse	ATATCCGCTCGAGCTCTGCTTTTGTCTGTAAAGTCACTGTGATA		
ARAP2	Forward	GAACAACCAACTTGACTTGC	quantification of increased intron inclusion	
	Reverse	CTTTGCTGGTAGGTTTTTC		
DVL3	Forward	TGAGCAGTGAAGTGGAGACC	quantification of decreased intron inclusion	
	Reverse	CGCGCTTGTGCTTCTCATC		
PODXL	Forward	ACCTACCCTGCCAGAGACCA	quantification of decreased intron inclusion	
	Reverse	AGGACGAGCTTCTCACTC		
SUPT7L	Forward	TTTGACCGACAGAAAGGCTG	quantification of decreased intron inclusion	
	Reverse	AGTGTACGAAAAGTGTAGGACCA		
ARAP2	Forward	TGGCCTTGTGCTTTTCTATCC	quantification of exon inclusion	
	Reverse	CAGTCGGGTTCTTCTTTC		
ATG16L1	Forward	TTGAGGCTATTGGATGAAAC	quantification of exon inclusion	
	Reverse	ACTGGGAAGGAGAGACAGA		
ATG16L1	Forward	CGCGGATCCGAGTATGACATTGAGGTCATTGTGGA	construction of minigene wild-type	
	Reverse	CCGCTCGAGGAAGACACAAAGCGAGTAG		
ATG16L1	Forward	CGCGGATCCGAGTATGACATTGAGGTCATTGTGGA	construction of minigene mutant for 3' splice site	1st PCR
	Reverse	CCGCTCGAGGAAGACACAAAGCGAGTAG		2nd PCR
ATG16L1	Forward	CGCGGATCCGAGTATGACATTGAGGTCATTGTGGA	construction of minigene mutant for 5' splice site	1st PCR
	Reverse	CCGCTCGAGGAAGACACAAAGCGAGTAG		2nd PCR
CLASP1	Forward	TTCTGSAATCTATCACTAATCTTTGSGTAAAGTGAAGACCTTTTCTTTTAAAT	quantification of exon inclusion	
	Reverse	CAACATTTAAAGSAAAGGCTGTOTAACTACCGAAAGATTAAGTATAGTAAATC		
EF CAB14	Forward	TTCTGSAATCTATCACTAATCTTTGSGTAAAGTGAAGACCTTTTCTTTTAAAT	quantification of exon inclusion	
	Reverse	CAACATTTAAAGSAAAGGCTGTOTAACTACCGAAAGATTAAGTATAGTAAATC		
INTS13	Forward	TACACATTTAAAGSAAAGGCTGTOTAACTACCGAAAGATTAAGTATAGTAAATC	quantification of exon inclusion	
	Reverse	CGCGGATCCGAGTATGACATTGAGGTCATTGTGGA		
MAP4K2	Forward	CGCGGATCCGAGTATGACATTGAGGTCATTGTGGA	quantification of exon inclusion	
	Reverse	CCGCTCGAGGAAGACACAAAGCGAGTAG		
MON2	Forward	TGCCATGAGATTCTGAGC	quantification of exon inclusion	
	Reverse	AACAGCAGTGGTGGAGA		
SNX14	Forward	ATCATTCCTCACCTTCAGC	quantification of exon inclusion	
	Reverse	ACTGCTTTTTCAGAGTGGCAG		
ZNF207	Forward	GAACAACCCAAAGTCAAG	quantification of exon inclusion	
	Reverse	CCTCTTGTCCAATGTGGA		
ZFAND1	Forward	TGACTTTGGGGTGTCAAG	quantification of exon inclusion	
	Reverse	CTTATCTCTCAGTTGGGGCG		
AURKB	Forward	GCCATTGTGTAGGACCAG	quantification of exon inclusion	
	Reverse	AATTCAAGGTACCCATTCC		
CDCA7L	Forward	CAGAATCACCAACACGCAA	quantification of exon inclusion	
	Reverse	TCATCTCACCTTCAGCTACA		
CHFR	Forward	CCTCCAACTCAAGCACA	quantification of exon inclusion	
	Reverse	AAGTAGCTTTGGGGTTC		
NUP50	Forward	GTGTGTGATGATTTCAGG	quantification of exon inclusion	
	Reverse	TAAGTCCACAAAGTCTCTC		
NUP82	Forward	GGCGTGGCAGATTGAGTTG	quantification of exon skipping	
	Reverse	TGAGGACAAGTGCAGATGGG		
OGT	Forward	CTCCGAGATGATTTCCCA	quantification of exon skipping	
	Reverse	GAAAGGCTACTCGAAGACCA		
PPP1R12A	Forward	AAAGCAAGGCATGACACAAG	quantification of exon skipping	
	Reverse	AGACTTATCACTTGCACACA		
RPP40	Forward	TACCACAACCCCTACAAACG	quantification of exon skipping	
	Reverse	ACTGCATTGTCTGAAGGAGA		
MYO1B	Forward	GAAAAGGCAGATGGAACG	quantification of exon skipping	
	Reverse	ATCACCAAGCTACCTCTCTGTC		
NUP50	Forward	CATCAAAGCGCTGTAAGGA	quantification of exon skipping	
	Reverse	CAAGCCTTCAATTCCTCTC		
NUP82	Forward	AAGAATGCCGAGGAAGAAC	quantification of exon skipping	
	Reverse	GCGCTTGTCTTCTTATGAG		
OGT	Forward	AAGAAGAGGTGGGAGCGG	quantification of exon skipping	
	Reverse	AGTGAAGCCTGTGCTCTGTG		
PPP1R12A	Forward	AGGCAAGCATTGACAG	quantification of exon skipping	
	Reverse	GCGAAGCCTCTCAATG		
RPP40	Forward	AGCTCAGTTAATGAAGGATCAACG	quantification of exon skipping	
	Reverse	TCCCTGACCTCTGTGTGGA		
RPP40	Forward	ACTTCAAGGTCATCCATCTC	quantification of exon skipping	
	Reverse	CTACTTTGGCTGATGCTCC		
RPP40	Forward	GACATTGGGACTGGACAAGA	quantification of exon skipping	
	Reverse	ACAATTTGTTCTCTGGGTTG		
RPP40	Forward	TACCGAGTGGCTAGTTAATGCTGAATGCCAACAACTAAAGGAAG	construction of minigene wild-type	
	Reverse	CTGGACTAGTGTAGCTCCACAATTTGGTCTCTGGGTTG		
SIK3	Forward	GATTTTACTCTTTTCCCTCTCTTGTAGTCAATTAAGATC	construction of minigene mutant for 3' splice site	1st PCR
	Reverse	GATCTTAATGACTACAAGAGAGAGSAGSAAAGAGTACAAAAC		2nd PCR
SIK3	Forward	CAGGCTTTGTAAGTCTTTTCACTCTCTCTGTAGTCAATTAAGATC	construction of minigene mutant for 5' splice site	1st PCR
	Reverse	GATCTTAATGACTACAAGAGAGAGSAGSAAAGAGTACAAAAC		2nd PCR
SIK3	Forward	TACCGAGTGGCTAGTTAATGCTGAATGCCAACAACTAAAGGAAG	construction of minigene mutant for 5' splice site	1st PCR
	Reverse	CTGGACTAGTGTAGCTCCACAATTTGGTCTCTGGGTTG		2nd PCR
SIK3	Forward	CACCAGTCAATATCCAGGTAAGAACTCACTGACCTAG	construction of minigene mutant for 5' splice site	1st PCR
	Reverse	CTAGTCACTGGAGTTATTACCACCTGGATATTGACTGGTG		2nd PCR
SIK3	Forward	GCACCAGTCAATATCCAGGTAAGAACTCACTGACCTAG	construction of minigene mutant for 5' splice site	1st PCR
	Reverse	CTAGTCACTGGAGTTATTACCACCTGGATATTGACTGGTG		2nd PCR
SIK3	Forward	TACCGAGTGGCTAGTTAATGCTGAATGCCAACAACTAAAGGAAG	construction of minigene mutant for 5' splice site	1st PCR
	Reverse	CTGGACTAGTGTAGCTCCACAATTTGGTCTCTGGGTTG		2nd PCR
SKA3	Forward	GCGCCGAGATTCAAATA	quantification of exon skipping	
	Reverse	TTTTCTTGACACGTGGACTA		
TBL1X	Forward	TTTTATGACCGGATGCTGGG	quantification of exon skipping	
	Reverse	ATGCTCATCTTAGCCTCAC		
pcDNA5 (-specific)	Forward	GTTTTGACCTCCATAAGAGACA	quantification of minigene reporter assay	
	Reverse	TAGAAGGCACAGTCGAGG		
BIRC5	Forward	TTGGCCAGTGTCTTCTCTGC	quantification of mRNA expression	
	Reverse	TGACAGAAAGGAAAGCGCAACC		
AURKB	Forward	AGAAGCAATTCAGGCAACCAG	quantification of mRNA expression	
	Reverse	GTTTTGATCCAGTCTCTCTCAG		
CENPA	Forward	AAGCTCAGAAGAGCACACACC	quantification of mRNA expression	
	Reverse	TGCCAATGAAGTCCACACCAC		
BRCA1	Forward	GTCCCATCTGTGGAGTTG	quantification of mRNA expression	
	Reverse	GCCCTTTCTCTGGTTGAGA		