

Name		Nucleotide sequence (5'→3')	Used in the	
PGK1	Forward	GTTCGACAGCAAGATCCAGCTC	quantification of mRNA expression	
	Reverse	GAAGTGGCAATCTCCATGTGTG		
CHERP	Forward	CCAATGTGCTACTCTCGAT	quantification of mRNA expression	
	Reverse	TGTACTCGTGATCTTCCAGCTT		
Forward	Forward	TGACAAAGCTTGATGATCGAGATGCCGCTGC	construction of expression vector wild-type	
	Reverse	GCCACTGTGCTGGATCTACTTACACTGTCCTCTGG		
tRNA	Forward	GTAGCTGCGCAGGATTGGAAC	confirmation of the fractionation	
	Reverse	GTAGTCTGCGCAGGATTGGAAC		
U6 snRNA	Forward	GTGCTCCCTCGGCAAGCACTACACTAAA	confirmation of the fractionation	
	Reverse	CTCAAAAGGAATGCTCACAATTGCGCT		
E2F8	Forward	CGGGGAGGAGAAATAAGTACG	confirmation of the fractionation	
	Reverse	CTTGCTTTTGGGGCTGTTTA		
CANT1	Forward	CCTTCTCACTACGCTTCC	quantification of increased intron inclusion	
	Reverse	GGTCAGGTAGCCCTTTTCA		
RPGR	Forward	GACGCAAGTACAGCTCTTA	quantification of increased intron inclusion	
	Reverse	TTGAATCCTCTGCTCCTTCC		
	Forward	CGCGGATCCAAACAACAACAATTGGGGAACCTGA	construction of minigene wild-type	
	Reverse	ATATCCGCTCGAGCTCTGCTTTTCTGTAAAGTCATCTGATA		
	Forward	AGATGAGGAAGCAGGTAAAGCACAGGCCA	construction of minigene mutant for 5' splice site	1st PCR
	Reverse	TGGCCTGTGCTCTTACCTGCTTCTCTCATC		
	Forward	CGCGGATCCAAACAACAACAATTGGGGAACCTGA	construction of minigene mutant for 3' splice site	1st PCR
	Reverse	ATATCCGCTCGAGCTCTGCTTTTCTGTAAAGTCATCTGATA		
	Forward	GTGATCTCTTTTACAGTATCCAGAGGAGAGAAAGG	construction of minigene mutant for 3' splice site	2nd PCR
	Reverse	CCCTTCTCTCTCTGCGGATACCTGAAAAGAGATCAC		
	Forward	CGCGGATCCAAACAACAACAATTGGGGAACCTGA	construction of minigene mutant for 3' splice site	2nd PCR
	Reverse	ATATCCGCTCGAGCTCTGCTTTTCTGTAAAGTCATCTGATA		
RSRP1	Forward	GAACAACCAACATTGACTTGC	quantification of increased intron inclusion	
	Reverse	CTTTGCTGGGTAGGTTTTC		
DVL3	Forward	TGAGCAGTGAGCTGGAGACC	quantification of decreased intron inclusion	
	Reverse	CGCGCTTGTGCTTCTCATC		
PODXL	Forward	ACCTACCTGCCAGAGACCA	quantification of decreased intron inclusion	
	Reverse	AGGACGAGCTGCTTCTCACTC		
SUPT7L	Forward	TTTGACCGACACAGATGCCCTG	quantification of decreased intron inclusion	
	Reverse	AGTGTACGAAAAGTGTAGGACCA		
ARAP2	Forward	TGGCCTTGTGCTTTTCATCC	quantification of exon inclusion	
	Reverse	CAGTCGGGTTCTCTCTTTC		
ATG16L1	Forward	TTGAGGTGATTGTGATGAAAC	quantification of exon inclusion	
	Reverse	ACTGGGAAGGAGAGACAGA		
	Forward	CGCGGATCCGATGATGACATTGAGGTCATTGTGGA	construction of minigene wild-type	
	Reverse	CCGCTCGAGGAAGACACACAAGGCAGTAG		
	Forward	CCTTCTCCCTCCCTTTTATGTAAGCGACTCTCGC	construction of minigene mutant for 3' splice site	1st PCR
	Reverse	GCGAGAGTCGCTTACTATAAAGGAGGGAGGAAAGG		
	Forward	CCATTCTCGCCTCTCTTTAGTAAGCGACTCTCG	construction of minigene mutant for 3' splice site	2nd PCR
	Reverse	CGAGAGTCGCTTACTAAAGAGGAGGGGAGGATAGG		
	Forward	CGCGGATCCGATGATGACATTGAGGTCATTGTGGA	construction of minigene mutant for 3' splice site	2nd PCR
	Reverse	CCGCTCGAGGAAGACACACAAGGCAGTAG		
	Forward	TTCTGATTTCTATCACTAATATCTTTGGGTAAAGTTAGAAGACCTTCTCTTTTAAAT	construction of minigene mutant for 5' splice site	1st PCR
	Reverse	CACATTAAAGAGAAAGGCTCTTCTAACTACCGAAGATATTAGTAGAATCG		
	Forward	TTCTGATTTCTATCACTAATATCTTTGGGTAAAGTTAGAAGACCTTCTCTTTTAAAT	construction of minigene mutant for 5' splice site	2nd PCR
	Reverse	TACACATTTAAAGAGAAAGGCTCTTACCCTACCCAAGATATTAGTAGAATCG		
	Forward	CGCGGATCCGATGATGACATTGAGGTCATTGTGGA	construction of minigene mutant for 5' splice site	2nd PCR
	Reverse	CCGCTCGAGGAAGACACACAAGGCAGTAG		
CLASP1	Forward	TGCCATGAGAATTCTGAGC	quantification of exon inclusion	
	Reverse	AACTAGCACAAGTGGTTGAGA		
EFCAB14	Forward	ATCATTCGCTCACCTTCAGC	quantification of exon inclusion	
	Reverse	ACTGCTTTTTCAGAGTGGCAG		
INTS13	Forward	GAACAACCAAGCAAGTCAGG	quantification of exon inclusion	
	Reverse	CCCTTTGTACCAACTGTGGA		
MAP4K2	Forward	TGACTTTGGGGTGTCAGG	quantification of exon inclusion	
	Reverse	CTTATCTCTCAGTTTGGGCG		
MON2	Forward	GCCATTGTGTAGGACACAG	quantification of exon inclusion	
	Reverse	AATTCAAGGCTACCCATTCC		
SNX14	Forward	CAGAATCACCAACACGCAA	quantification of exon inclusion	
	Reverse	TCATCTTCACTTCAGCTACA		
ZNF207	Forward	CCTCCAATGACTCAAGCACA	quantification of exon inclusion	
	Reverse	AATGTAGCTTTGGGGGTTT		
ZFAND1	Forward	GTGTGTGATGATTGTCAGG	quantification of exon inclusion	
	Reverse	TAACTGCCACAAGTTCTCTC		
AURKB	Forward	GGCGTGGCAGATTCAATTG	quantification of exon skipping	
	Reverse	TGAGGACAAGTCAGATGGG		
CDA7L	Forward	CTTCCGAGATGATGTTCCCA	quantification of exon skipping	
	Reverse	GAAAGGCTACTCGAAGACCA		
CHFR	Forward	AAAGCAAGGCATGACACAAG	quantification of exon skipping	
	Reverse	AGACTTCATCACTTGCACACA		
FN1	Forward	TACCACAACCCCTACAAACG	quantification of exon skipping	
	Reverse	ACTGCATTGTCTGAAGGAGA		
KTN1	Forward	GAAAAGGCAGAGATGGAACG	quantification of exon skipping	
	Reverse	ATCACCAAGCTACCTTCTGTC		
MYO1B	Forward	CATCAAAAGCGGTGAAGGA	quantification of exon skipping	
	Reverse	CAAGCGTTTCAATTCCCTTC		
NUP50	Forward	AAGAAATGCCGAGAAGGAAC	quantification of exon skipping	
	Reverse	GCGCTTTGCTTCTTTATGG		
NUP62	Forward	AAGAAAGAGGTGGGAGCGG	quantification of exon skipping	
	Reverse	AGTGAAGCCTGTGCTGTG		
OGT	Forward	AGGCAAGCATTTTGGACAG	quantification of exon skipping	
	Reverse	GCGAAGCTGCTTCTCAATG		
PPP1R12A	Forward	AGCTCAGTTAATGAAGGATCAACG	quantification of exon skipping	
	Reverse	TCCCTGACCTCTGTGTGGA		
RPP40	Forward	ACTTCAGGCTATCCATCTC	quantification of exon skipping	
	Reverse	CTACTTTGGCTGATGCTCC		
SIK3	Forward	GACATGGGACTGGACAAGA	quantification of exon skipping	
	Reverse	ACAATTGTGTTCTCTGGGTTG		
	Forward	TACCGAGCTGCTAGTTAATAGCTGAATGCCAACACTAAGGAAG	construction of minigene wild-type	
	Reverse	CTGGACTAGTGTAGCTCCACAATTTGGTCTCTGGGTTG		
	Forward	GTTTTGTACTCTTTTCCCCTCTCTTGTAGTCATTAAATC	construction of minigene mutant for 3' splice site	1st PCR
	Reverse	GATCTTAATGACTACAAGAGAGAGGGGAAAGAGTACAAAAC		
	Forward	CAGGGTTTTGTACTCTTTTCACTCTCTCTGTAGTCATTAAATC	construction of minigene mutant for 3' splice site	2nd PCR
	Reverse	GATCTTAATGACTACAAGAGAGAGGAAAGAGTACAAAACCTG		
	Forward	TACCGAGCTGCTAGTTAATAGCTGAATGCCAACACTAAGGAAG	construction of minigene mutant for 5' splice site	1st PCR
	Reverse	CTGGACTAGTGTAGCTCCACAATTTGGTCTCTGGGTTG		
	Forward	CACCACTCAATATCCAGGTAGGAATAACTCCAGTGACCTAG	construction of minigene mutant for 5' splice site	2nd PCR
	Reverse	CTAGTCACTGGAGTTATTACCACTGGATATTGACTGGTG		
SKA3	Forward	GCACCACTCAATATCCAGGTGGCAATAACTCCAGTGACCTAG	quantification of exon skipping	
	Reverse	CTAGTCACTGGAGTTATTACCACTGGATATTGACTGGTG		
TBL1X	Forward	GTCTTATGACCGATGCTGGG	quantification of exon skipping	
	Reverse	ATGCTCATCTTAGCCTCAC		
pcDNA5 (-specific)	Forward	GTTTTGACCTCCATAGAAGACA	quantification of minigene reporter assay	
	Reverse	TAGAAGGCACAGTCGAGG		
BIRC5	Forward	TTGGCCAGTGTTTCTCTGC	quantification of mRNA expression	
	Reverse	TGACAGAAAGGAAGCGCAACC		
AURKB	Forward	AGAAGCAATTGCAGGCAACCAG	quantification of mRNA expression	
	Reverse	GTTTTGATGCCAGTTCTCTCTAG		
CENPA	Forward	AAGCTTCAGAGAGCACACACC	quantification of mRNA expression	
	Reverse	TGCCAATTGAAGTCCACACCAC		
BRCA1	Forward	GTCCCATCTGTCTGGAGTTG	quantification of mRNA expression	
	Reverse	GCCCTTTCTCTGGTTGAGA		