Table SI. Sequences table for DEGs and RASEs in reverse transcription-quantitative PCR.

Name	Sequence
hum-GAPDH-F	GGTCGGAGTCAACGGATTTG
hum-GAPDH-R	GGAAGATGGTGATGGGATTTC
IL1A-F	CGGACCAATTACTGGCTCAA
IL1A-R	TCCAAGTTGTGCTTATCCCATA
EGR1-F	GCTTCGGTTCTCCAGAATGTA
EGR1-R	AATCGCCGCCTACTCAGT
RPPH1-F	GCCGTGAGTCTGTTCCAAG
RPPH1-R	GGAGGTGAGTTCCCAGAGAA
USP48-AS-F	AAATCCATCGCCCTTTACTG
USP48-M-F	TCCATCGCTGCCCTTTACTG
USP48-M/AS-R	CGTCTGAAGAACCAACTAAA
UBE2I-M-F	GGCTGGAGAGGGACTTTGAA
UBE2I-AS-F	CGAGTGCCAGGGACTTTGAA
UBE2I-M/AS-R	CTGGGCGAGTCTGCTGAGGG
PLEC-AS-F	TCTTCATGGCCTCCTCCTCC
PLEC-M-F	CCGTCTGCATCTCCTCCTCC
PLEC-M/AS-R	GAGCCAGTACATCAAGTTCATCAG
STXBP1-F	GTGTGAGCCTGAATGAGAT
STXBP1-R	AGTGTGTCCAGCAGTTTC

The boundary-spanning primer of the alternative exon was designed according to the “model exon” to detect model splicing or according to “altered exon” to detect altered splicing. F, forward; R, reverse; M, model; AS, alternative spliced; DEGs, differentially expressed genes; RASE, regulated ASEs.