Table SI. Primer sets related to the experimental procedures: Reverse transcription-quantitative PCR primers for gene expression quantification.

Gene	Primer	Sequence (5'-3')
GAPDH	Forward	GGTCGGAGTCAACGGATTTG
	Reverse	GGAAGATGGTGATGGGATTTC
Pum2	Forward	ATTGATGAGGTCTGCTGTC
	Reverse	GCGAAGAGTAGTGATGTGA
Adm	Forward	CTTGCCCGCTCATAAACT
	Reverse	ACCTCTTGACATCAACAAAC
Plpp3	Forward	GAAATAACTGCGACTAGAGG
	Reverse	TGTATGCCACAGAAGTGTT
Itga8	Forward	ATCTGCTCATTTCCCTGTG
	Reverse	CTGACTCTTGTGACCCATT
Itga11	Forward	CAGAGGCAGATAGGCATC
	Reverse	CAACAAAGGGTTAAGGCATA
Ndrg4	Forward	AGAGAAGACAACCATCAATG
	Reverse	CCTTACTGTAGATAGCACTTC
Rgs2	Forward	GTGGTGATCTGTGGCTTT
	Reverse	TATCCAAGAGGCTACAAGTG
Cdh11	Forward	ACTATGGACACTCTATCTGTAG
	Reverse	CAAGAATCAGCAGTAACAAG
Tgfbi	Forward	ATGGACTGCTTGGTTCAC
	Reverse	ATCTGGCGGTCGTATCTT
Tpm1	M/AS forward	AGAGCCTCGGAGTATTTGTC
	AS reverse	CGCCGCCAAGCTGGAAGATG
	M reverse	GAGCAAGCAGCTGGAAGATG
Actn1	M/AS forward	CCGTCTTCTTCCGGTCAAAG
	AS reverse	CGGAGTGATCCCGGTCAAAG
	M reverse	AGCCAGGAACAGATGAACGA
Ppfibp1	M/AS forward	CTCGATCGAGACATTGAAGT
	AS reverse	AAAGAGAAAAACATTGAAGT
	M reverse	TTTTCCTCGTTTGCTGCCAT

The boundary-spanning primer of the alternative exon was designed according to the 'model exon' to detect model splicing or according to the 'altered exon' to detect altered splicing. M, model splicing; AS, altered splicing; Pum2, pumilio RNA-binding family member 2; Adm, adrenomedullin; Plpp3, phospholipid phosphatase 3; Itga8, integrin subunit α 8; Itga11, integrin subunit α 11; Ndrg4, NDRG family member 4; Rgs2, regulator of G protein signaling 2; Cdh11, cadherin 11; Tgfbi, transforming growth factor β-induced; Tpm1, tropomyosin 1; Actn1, actinin α 1; Ppfibp1, PPFIA binding protein 1.

Table SII. Classification of all regulated alternative splicing events between siPUM2 and NC samples.

Sample	siPUM2 vs. NC	siPUM2 vs. NC
Type	Up	Down
3pMXE	3	3
5pMXE	5	7
A3SS	59	70
A3SS&ES	5	9
A5SS	50	50
A5SS&ES	4	3
ES	15	26
IntronR	101	82
MXE	4	3
cassetteExon	17	14
Total	263	267

si, small interfering RNA; PUM2, pumilio RNA-binding family member 2; NC, negative control; MXE, mutually exclusive exons; 3pMXE, mutually exclusive 3'UTRs; 5pMXE, mutually exclusive 5'UTRs; A3SS, alternative 3' splice sites; ES, exon skipping; A5SS, alternative 5' splice sites; intronR, intron retention.