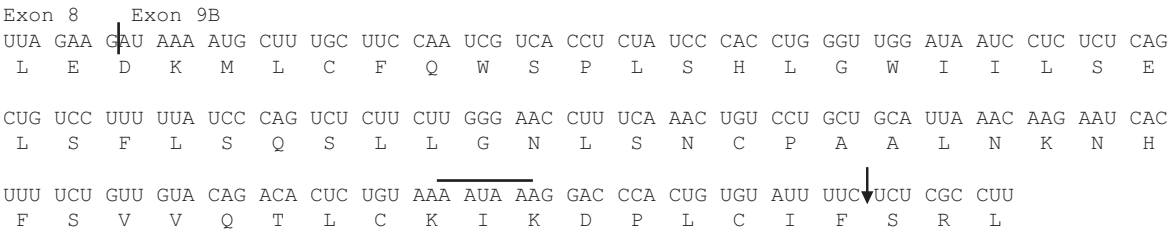
SUPPLEMENTAL DATA

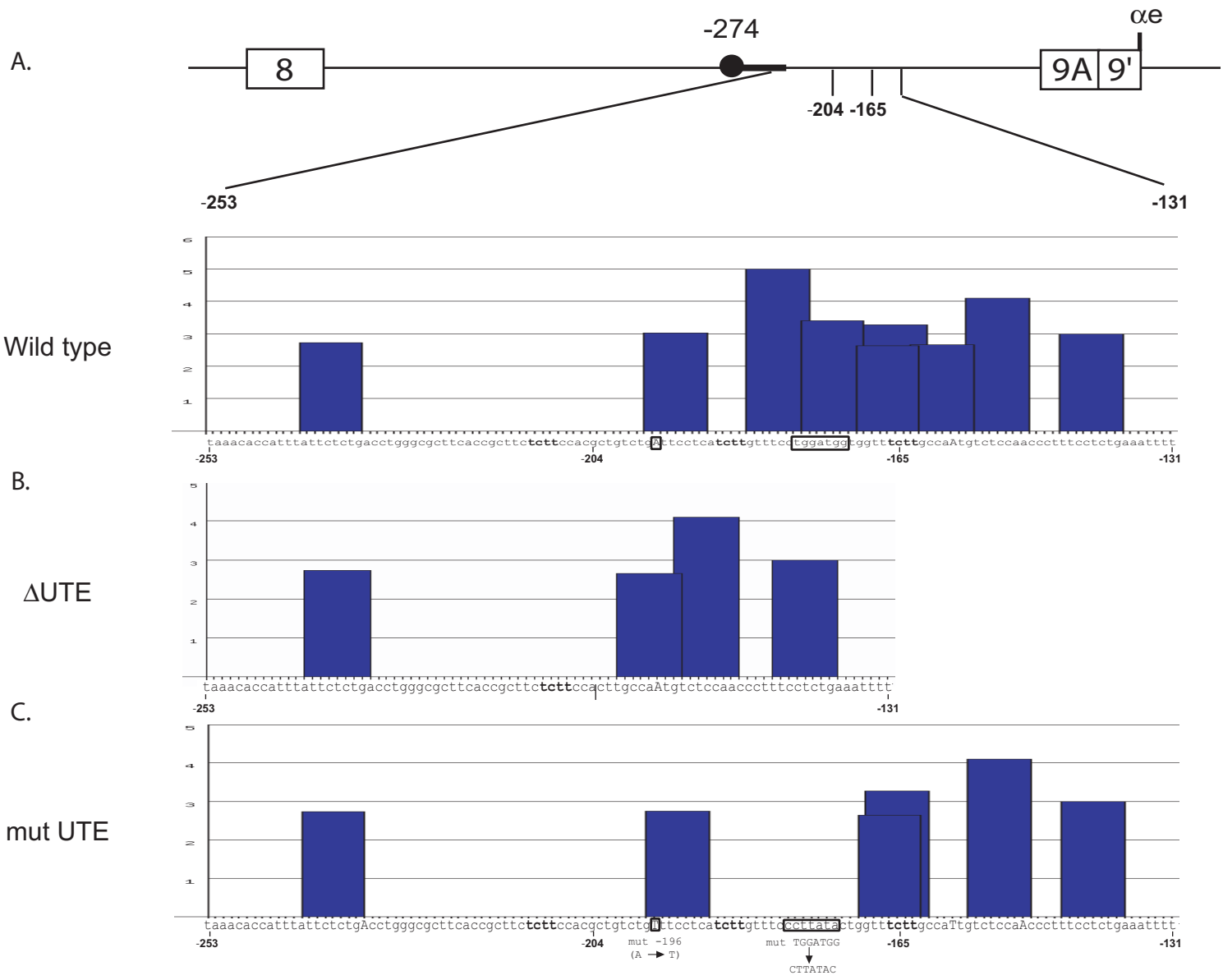
Table S1 : Sequences of the forward and reverse oligonucleotides used to generate the different minigene mutants and PCR amplify the open reading frame of the different SR proteins.

Figure S1. The splicing product α2Δ9A is a potential substrate for non sense decay (NSD). Nucleotide and derived amino acid sequences of the open reading frame encompassing exon 8 to exon 9B. The end of exon 8 and the beginning of exon 9B are written and the exon junction is indicated by the symbol (/). The hexanucleotide and the cleavage site of the αe poly(A) site are underlined and indicated by an arrow respectively.

Figure S2. Localization of candidate SC35 binding sites in the intronic region encompassing UTE using ESE finder 3. **A.** The organisation of the wild-type pre-mRNA region spanning exon 8 to exon 9A9' is diagrammed at the top. The position of UTE from -204 to -165 is given and the distant -274 branch site and its associated polypyrimidine tract are represented by a black circle and a black rectangle respectively. The intronic sequence from -253 to -131 upstream of exon 9A is written below and the predicted SC35 binding sites are diagrammed with bars. The height of the bars indicates the strength of the potential SC35 binding sites as calculated by the ESE finder software. **B.** Effects of UTE deletion upon candidate SC35 binding sites. **C.** Effects of UTE mutation upon candidate SC35 binding sites. The mutations are indicated related to the wild type sequence.

name		sequence 5' - 3'
pActin.7-9B Δ -204-165	forward	GTCCATTGATGATTTAGAAGG
	reverse	AGGGTTGGAGACATTGGCAAGTGGAAGAGAAGCGGTGAAG
	forward	TTGCCAATGTCTCCAACCCT
	reverse	TGGAAAGGGTACGGAGGTAAGC
pActin.7-9B mut UGGAUGG	forward	GTCCATTGATGATTTAGAAGG
	reverse	GAAACCAGTATAAGGGAAACAAGATGAGGATCAG
	forward	CTTGTTTCCCTTATACTGGTTTCTTGCCAATGTCTC
	reverse	TGGAAAGGGTACGGAGGTAAGC
pActin.7-9B mut UGGAUGG +mut-196	forward	GTCCATTGATGATTTAGAAGG
	reverse	GATGAGGAAACAGACAGCGAGGAAGAGAAG
	forward	CGCTGTCTGTTTCCTCATCTTGTTTCCCT
	reverse	TGGAAAGGGTACGGAGGTAAGC
pActin.7-9B mut BS + 3'cons	forward	GTCCATTGATGATTTAGAAGG
	reverse	GGAAAAAAAAATAGAAGGAGAAAGGTAGAAG
	forward	CTCCTTCTATTTTTTTTTCCTCTCTCTCTT
	reverse	CATGTGGTACCAGACTAGAG
pActin.7-9B mut BS	forward	GTCCATTGATGATTTAGAAGG
	reverse	GGAAAAAAAAATAGAAGGAGAAAGGTAGAAG
	forward	CTCCTTCTATTTTTTTTTCCTCTCTCTCTT
	reverse	GGAGGGGTAGGACAAAGAAATG
pActin.7-9B SPA	forward	GCAGCACCCAGCCAATTC
	reverse	CCAACACACAGATCTAATGAAAATAAAGATCTTTTATTAAGTGGAAAGGGTACGG
	forward	TTCATTAGATCTGTGTGTTGGTTTTTTGTGTGCTTTTGGGTGTTTTTTACCCCTG
	reverse	CATGTGGTACCAGACTAGAG
xASF/SF2	forward	GGATCCATGGATACGTCAGCGGGC
	reverse	GCGGCCGCTGTACGAGAGCGAGATCTG
xSC35	forward	GATATCTGAGCTACGGTCGGCCT
	reverse	GCGGCCGCTGAAGACACTGCTCCCTC
xSRp20	forward	GATATCATGCATCGTGACTCCTGT
	reverse	GCGGCCGCCTTTCGCTCATTGGACC
x9G8	forward	GATATCATGTCGCGTTACGGGCGA
	reverse	GCGGCCGCCATTTCTTTCTGGGC
hSRp30c	forward	GGATCCACCATGTCGGGCTGGGCGGACG
	reverse	GCGGCCGCGTAGGGCCTGAAAGGAGAG
hSRp40	forward	GATATCCACCATGAGTGGCTGTCGGGTAT
	reverse	GCGGCCGCATTGCCACTGTCAACTGATCT
hSRp55	forward	GGATCCACCATGCCGCGCGTCTACATAG
	reverse	GCGGCCGCATCTCTGGAACTCGACCTG


Exon 8
Exon 9B
UUA GAA GAU AAA AUG CUU UGC UUC CAA UCG UCA CCU CUA UCC CAC CUG GGU UGG AUA AUC CUC UCU CAG
L E D K M L C F Q W S P L S H L G W I I L S E
CUG UCC UUU UUA UCC CAG UCU CUU CUU GGG AAC CUU UCA AAC UGU CCU GCU GCA UUA AAC AAG AAU CAC
L S F L S Q S L L G N L S N C P A A L N K N H
UUU UCU GUU GUA CAG ACA CUC UGU AAA AUA AAG GAC CCA CUG UGU AUU UUC UCU CGC CUU
F S V V Q T L C K I K D P L C I F S R L


A.
8
-274
αe
9A
9'
-204
-165
-253
-131
Wild type
B.
ΔUTE
C.
mut UTE
-253
-204
-165
-131
mut -196
(A → T)
mut TGGATGG
CTTATAC