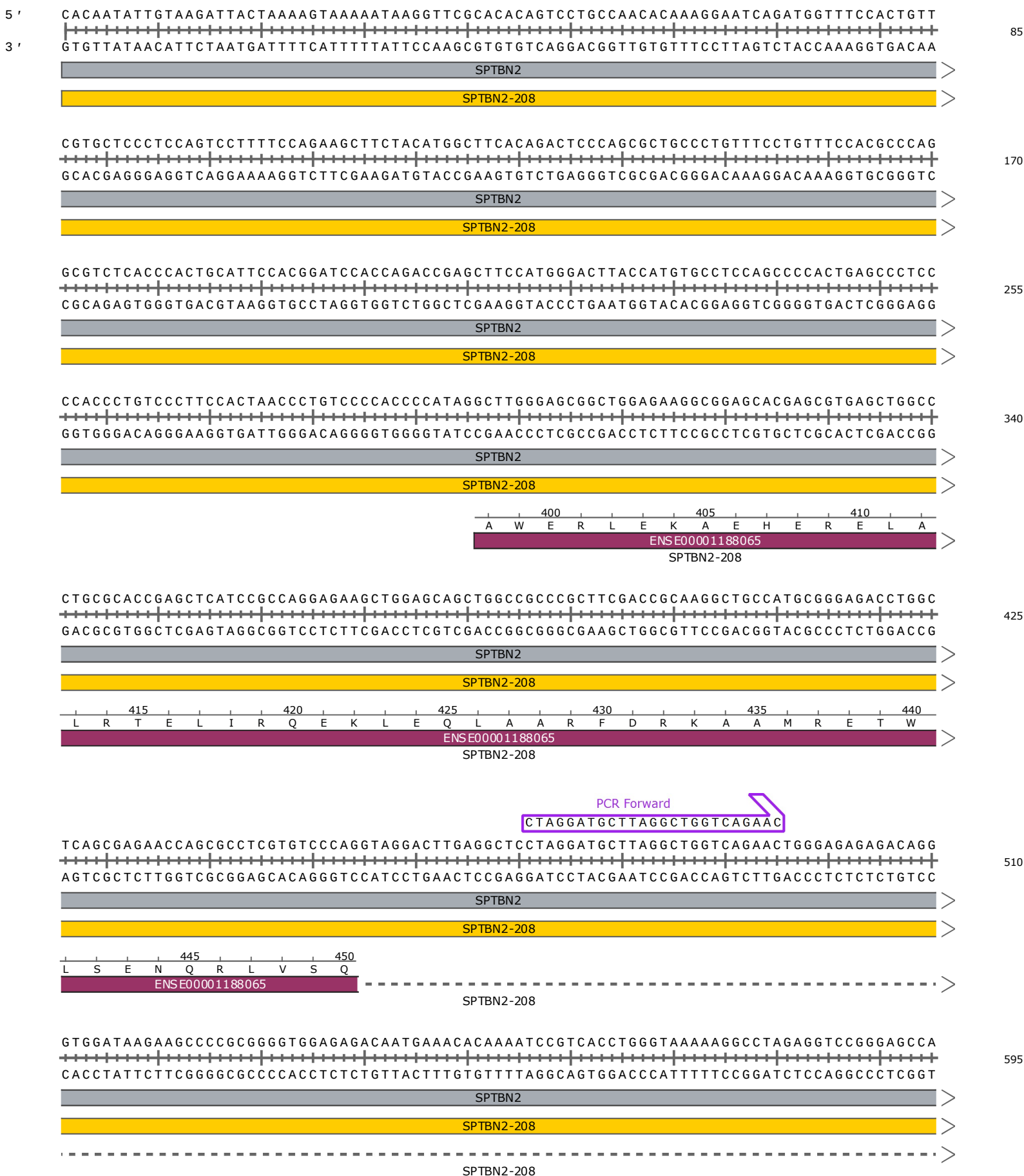
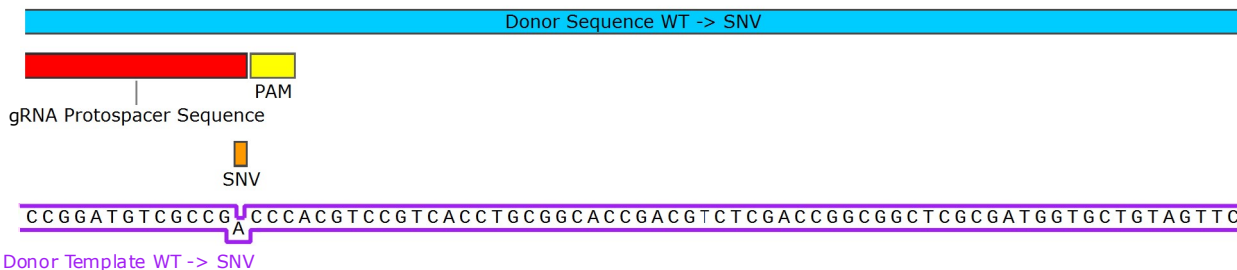
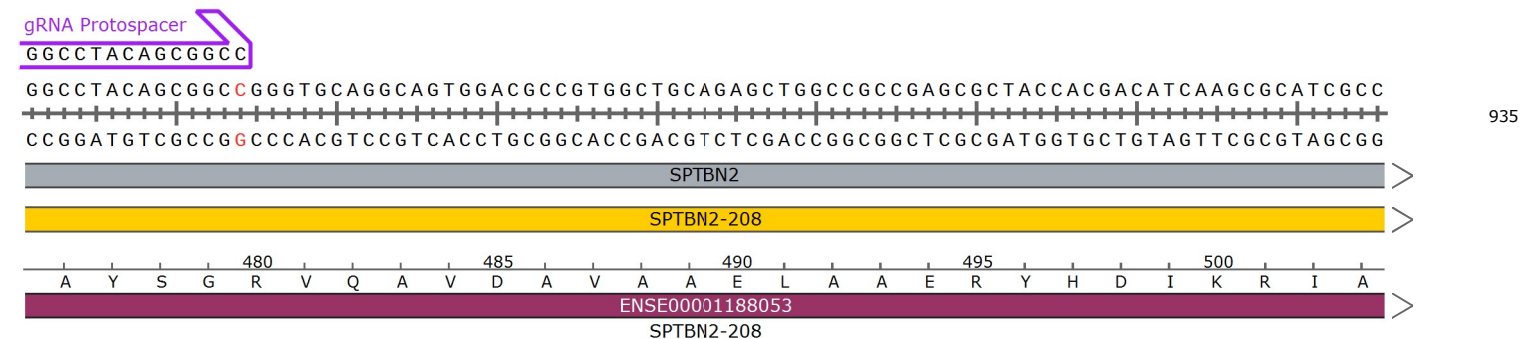
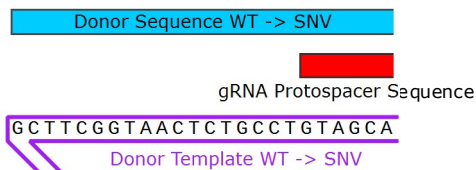
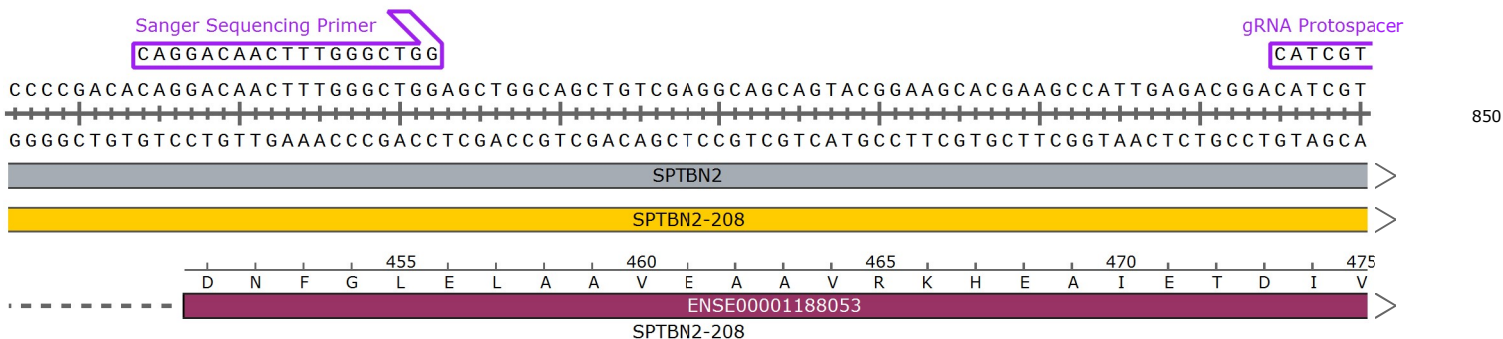
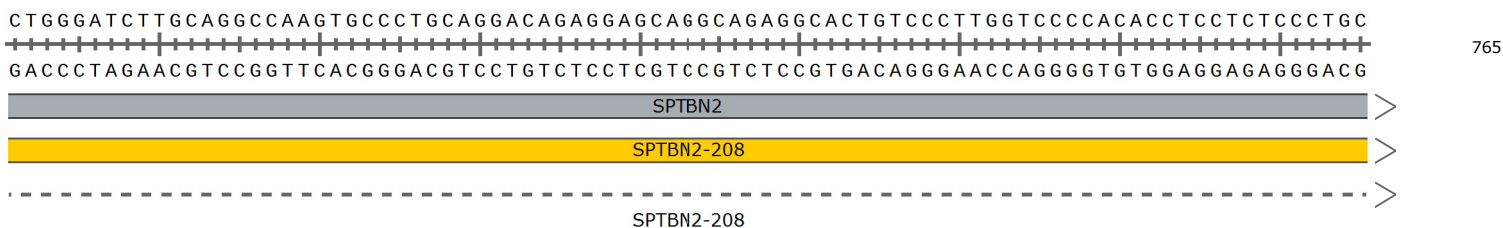
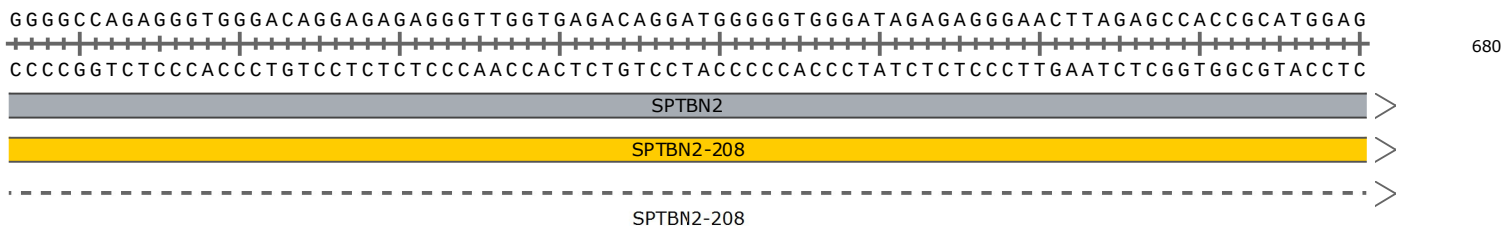


INK2J00076_SPTBN2_R480W_A12_BB
1771 bp





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 CGAGCCGTCGTGTTGCACCGTGCCGAGACCCTGAAGAACGCCGCTACCACCAGCCGGCCGCCCTCGCCGAGGAGGAGTTGGACC

SPTBN2
 SPTBN2-208

505 510 515 520 525 530
 A R Q H N V A R L W D F L R Q M V A A R R E R L L L N L

ENSE00001188053
 SPTBN2-208

AGCTGCAGAAGGTGTTCCAGGACCTGCTCTACCTCATGGACTGGATGGAAGAGATGAAGGTACCAGTGAGGCGTGCTGGGTGGGG
 TCGACGCTTCCACAAGGTCTGGACGAGATGGAGTACCTGACCTACCTTCTCTACTTCCATGGTCACTCCGCACGACCCACCCC

SPTBN2
 SPTBN2-208

535 540 545 550
 E L Q K V F Q D L L Y L M D W M E E M K V P V R R A G W G

ENSE00001188053
 SPTBN2-208 (in frame with SPTBN2-208)

TAAGAGTGATCAAGAGTCGAGGGGGCCCCACAGTGGGTGCGTCCGCCCGTCTGCTCGGCCGATCTCTGTGGAGTGTGAACCAGCA
 ATTCTCACTAGTTCTCAGCTCCCCCGGGGTGTCACCCACGCAGGCGGGCAGACGAGCCGGCTAGAGACACCTCACACTTGGTCTGT

SPTBN2
 SPTBN2-208

K S D Q E S R G P H S G C V R P S A R P I S V E C E P A
 (in frame with SPTBN2-208)

CAGGGCCCTGTCCCCAGTTGCAGGGAACAAAGTAAACAGGGCCCTGTCCACATGGGGTTTCGTGTCCACATGGAGGAGGCTGATGA
 GTCCCGGGACAGGGGTCAACGTCCTTGTTCATTTGTCCCGGACAGGTGTACCCCAAGCACAGGTGTACCTCCTCCGACTACT

SPTBN2
 SPTBN2-208

Q G P V P S C R E Q S K Q G P V H M G F V S T W R R L M
 (in frame with SPTBN2-208)

CAAAACCCACGGACCTTCCGTAACAAAAGAGCAGGGGCCATAAAACCACTGATGAAACTGGAACAGGGTGGTGTGAGGGGCTG
 GTTTTGGGTGCTGGAAGGCATTTGTTTTCTCGTCCCGGATTTTGGTGACTACTTTGACCTTGTCCCACCACACTCCCCGAC

SPTBN2
 SPTBN2-208

T K P T D L S V N K R A G A I K P L M K L E Q G G V R G W
 (in frame with SPTBN2-208)

GTCAGACAAGGCCTCTGAGAAAATACCATTTAAGCCGAGACCAGAATAGTGCCAGGAGCCAGCACAGAGAGCTCTCAGGAGAGAA
 CAGTCTGTTCCGGAGACTCTTTTATGGTAAATTCGGCTCTGGTCTTATCACGGTCCTCGGTCTGTCTCTCGAGAGTCTCTCTT

SPTBN2
 SPTBN2-208

S D K A S E K I P F K P R P E
 (in frame with SPTBN2-208)

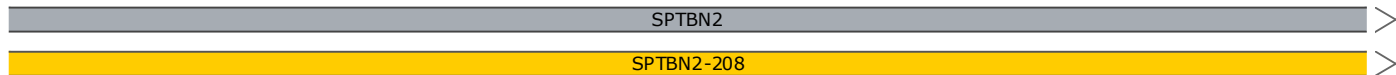
CTCTTTTATGGTAAATTCGGCTCTG
 PCR Reverse

TGTTCCGGGCAGAAGGAACAGCCGGCACAGGCCCTCGGCCGATCAGCATGGTGTGTTTCAGGATCAGAAGGAAGGCCGGTGGGG
 ACAAGGCCCGTCTTCTTGTCCGGCCGTGTCCGGGAGCCGGACCTAGTCGTACCACACAAGTCTAGTCTTCTTCCGGCCACCCG

SPTBN2
 SPTBN2-208

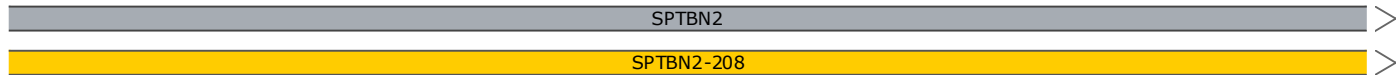
TGTGAGCATGAGGAGTGGGGGCCATGGACTGAGATTTGGGAGGGGCACGGCCAGCCCACTAGGGCCTTACAGGCCTGGTCAGGGAG
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 AACTCGTACTCCTCACCCCGGTACCTGACTCTAAACCTCCCGTGCCGGTCGGGTGATCCCGGAATGTCCGGACCAGTCCCTC

1615

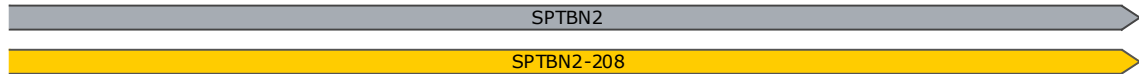


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 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 AAACCTAAAATAAGTTTCATTGTACCTAGGAAATTTCACTAAACTTCCCGGTCCGCGTCACCGAGTACGGACATTAGGGTCGAG

1700



TTTGGGAGGCCAAGGCAGGCAGATCACTTGAGGTCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGA AAC 3'
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1771
 AAACCTCCGGTTCCGTCCGTCTAGTGA ACTCCAGTCCTCAAGTTCTGGTCCGACC GGTTGTACCACTTTG 5'



Feature	Location	Size	Start	End	Type
✓ SPTBN2	1 .. 1771	1771 bp	■	→	gene
/note = gene ENSG00000173898 Protein coding					
C11orf80-216	1 .. 1771	1771 bp	■	←	prim_transcript
/note = primary transcript ENST00000534325 Protein coding					
SPTBN2-201	1 .. 1771	1771 bp	■	→	prim_transcript
/note = primary transcript ENST00000309996					
SPTBN2-203	1 .. 1771	1771 bp	■	→	prim_transcript
/note = primary transcript ENST00000529997					
✓ SPTBN2-208	1 .. 1771	1771 bp	■	→	prim_transcript
/note = primary transcript ENST00000533211					
SPTBN2-209	1 .. 1771	1771 bp	■	→	prim_transcript
/note = primary transcript ENST00000611817					
SPTBN2-210	1 .. 1771	1771 bp	■	→	prim_transcript
/note = primary transcript ENST00000617502					
SPTBN2-211	1 .. 1771	1771 bp	■	→	prim_transcript
/note = primary transcript ENST00000647510 Nonsense mediated decay					
SPTBN2-201	296 .. 1079	784 bp	■	→	CDS
▶ 2 segments = 462 bp					
/note = coding sequence ENSP00000311489					
/translation = AWERLEKAEHERELALRTELIRQEKLEQLAARFDRKAAMRETWLSENQRLVSQ, ,DNFGLELAAVEAAVRKHEAIETDIVAYSGRVQAVDAVAELAERYHDIKRIAARQHN VARLWDFLRQMVAARRERLLLNLLELQKVFQDLLYLMDWMEEMK 154 amino acids = 18.2 kDa					
SPTBN2-203	296 .. 1079	784 bp	■	→	CDS
▶ 2 segments = 462 bp					
/note = coding sequence ENSP00000433593					
/translation = AWERLEKAEHERELALRTELIRQEKLEQLAARFDRKAAMRETWLSENQRLVSQ, ,DNFGLELAAVEAAVRKHEAIETDIVAYSGRVQAVDAVAELAERYHDIKRIAARQHN VARLWDFLRQMVAARRERLLLNLLELQKVFQDLLYLMDWMEEMK 154 amino acids = 18.2 kDa					
✓ SPTBN2-208	296 .. 1079	784 bp	■	→	CDS
▶ 2 segments = 462 bp					
/note = coding sequence ENSP00000432568					
/translation = AWERLEKAEHERELALRTELIRQEKLEQLAARFDRKAAMRETWLSENQRLVSQ, ,DNFGLELAAVEAAVRKHEAIETDIVAYSGRVQAVDAVAELAERYHDIKRIAARQHN VARLWDFLRQMVAARRERLLLNLLELQKVFQDLLYLMDWMEEMK 154 amino acids = 18.2 kDa					
SPTBN2-209	296 .. 1079	784 bp	■	→	CDS
▶ 2 segments = 462 bp					
/note = coding sequence ENSP00000480692					
/translation = AWERLEKAEHERELALRTELIRQEKLEQLAARFDRKAAMRETWLSENQRLVSQ, ,DNFGLELAAVEAAVRKHEAIETDIVAYSGRVQAVDAVAELAERYHDIKRIAARQHN VARLWDFLRQMVAARRERLLLNLLELQKVFQDLLYLMDWMEEMK 154 amino acids = 18.2 kDa					
SPTBN2-210	296 .. 1079	784 bp	■	→	CDS
▶ 2 segments = 462 bp					
/note = coding sequence ENSP00000482000					
/translation = AWERLEKAEHERELALRTELIRQEKLEQLAARFDRKAAMRETWLSENQRLVSQ, ,DNFGLELAAVEAAVRKHEAIETDIVAYSGRVQAVDAVAELAERYHDIKRIAARQHN VARLWDFLRQMVAARRERLLLNLLELQKVFQDLLYLMDWMEEMK 154 amino acids = 18.2 kDa					
✓ Donor Sequence WT -> SNV	827 .. 926	100 bp	■		misc_feature
✓ gRNA Protospacer Sequence	845 .. 864	20 bp	■		misc_feature
✓ SNV	864 .. 864	1 bp	■		misc_feature
/note = WT = A SNV = T					
✓ PAM	865 .. 867	3 bp	■		misc_feature

Feature	Location	Size		Type
C11orf80	38,442 .. 17294,932,397 bp		 ←	gene

/note = gene [ENSG00000173715](#)
 Protein coding

Primer	Length	Binding Sites	Tm	Date Added
✓ PCR Forward /sequence = CTAGGATGCTTAGGCTGGTCAGAAC 52% GC / 7722.1 Da	25-mer	471 .. 495 →	60°C	Aug 18, 2023
✓ Sanger Sequencing Primer /sequence = CAGGACAACCTTTGGGCTGG 58% GC / 5868.9 Da	19-mer	774 .. 792 →	57°C	Aug 18, 2023
✓ Donor Template WT -> SNV /sequence = CTTGATGTCGTGGTAGCGCTCGGCGGCCAGCTCTGCAGCCACGGCGTCCACTGCCTGCACCCAGCCGCTGTAGGCCACGATGCCGTCTCAATGGCTTCG 66% GC / 30,684.8 Da	100-mer	827 .. 926 ←	84°C	Aug 18, 2023
✓ gRNA Protospacer /sequence = CATCGTGGCCTACAGCGGCC 70% GC / 6079.0 Da	20-mer	845 .. 864 →	64°C	Aug 18, 2023
✓ PCR Reverse /sequence = GTCTCGGCTTAAATGGTATTTTCTC 40% GC / 7629.0 Da	25-mer	1377 .. 1401 ←	56°C	Aug 18, 2023