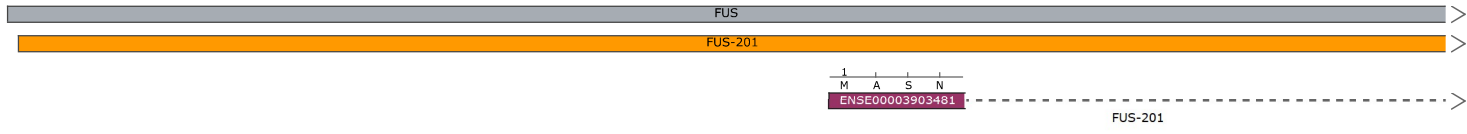


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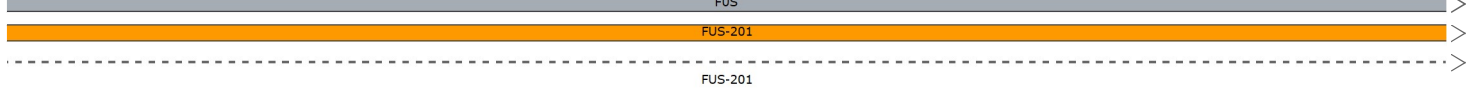
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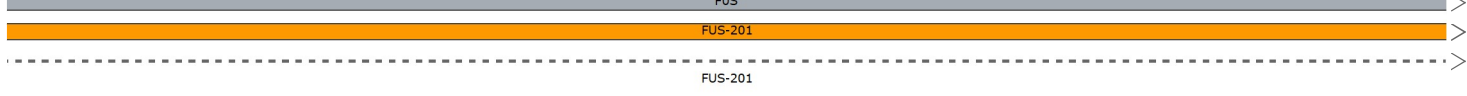
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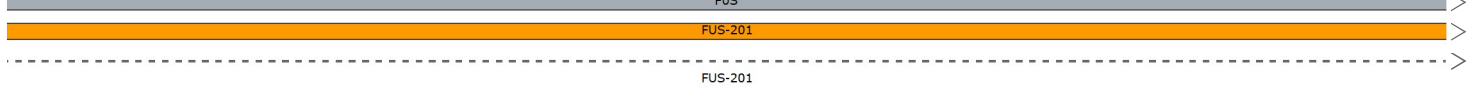
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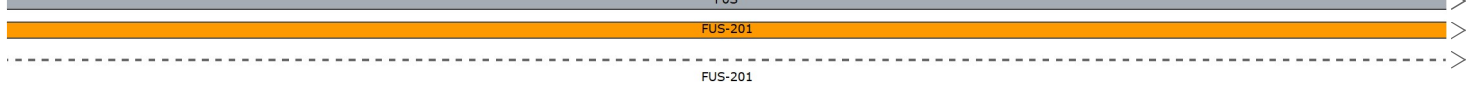
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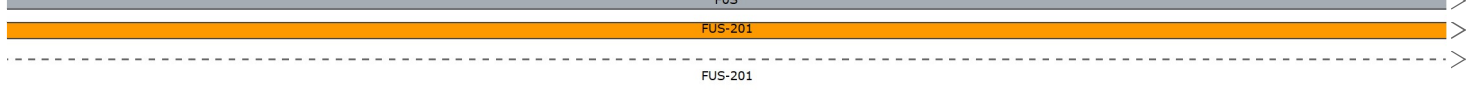
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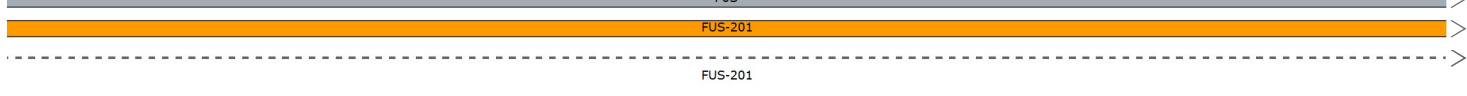
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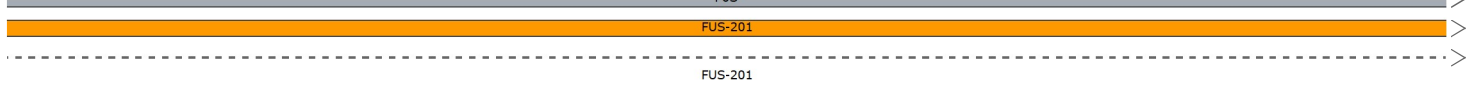
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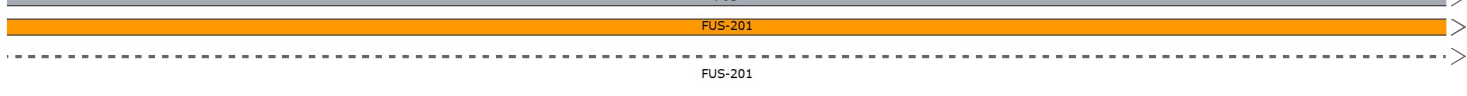
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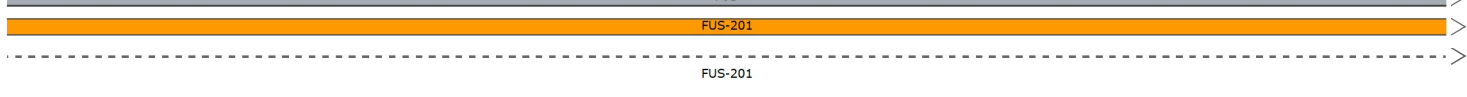
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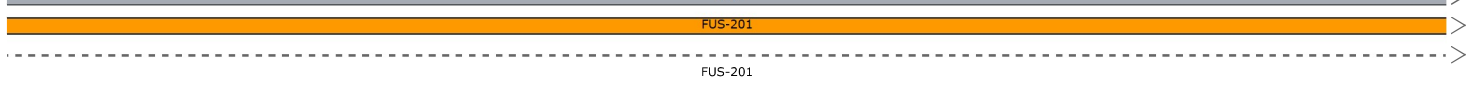
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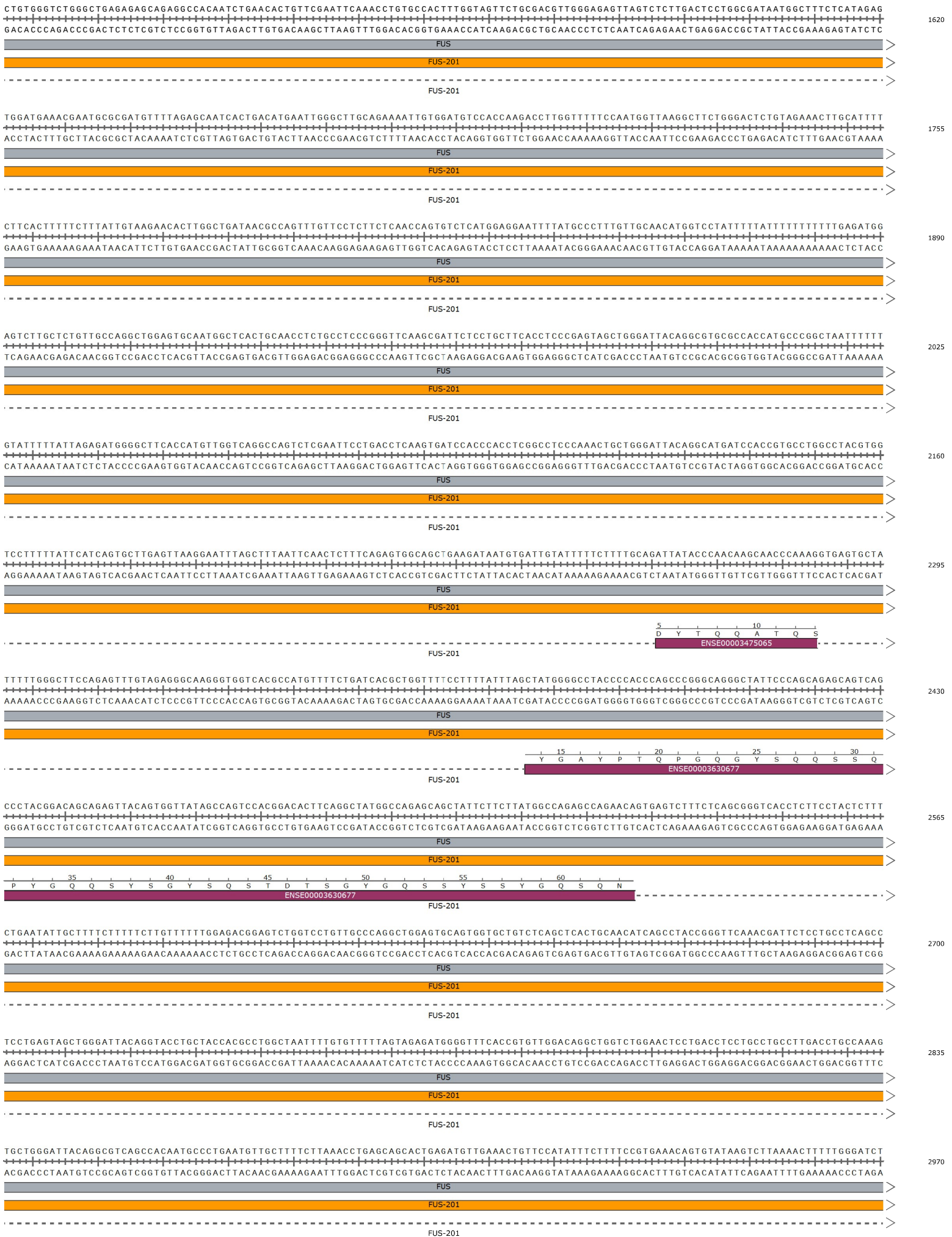


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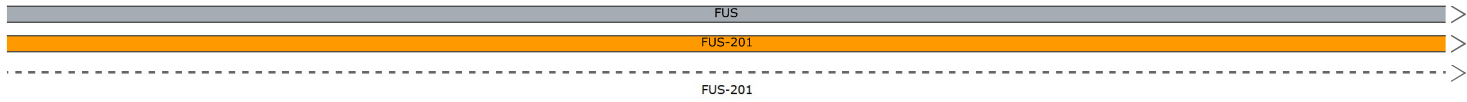


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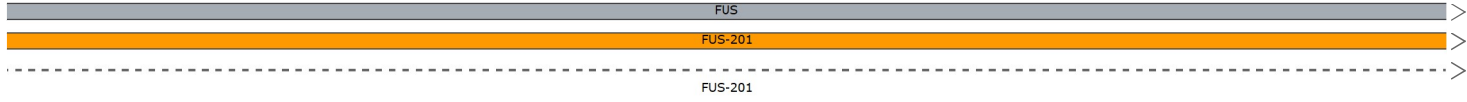
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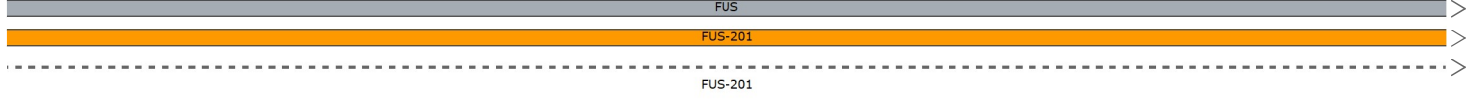
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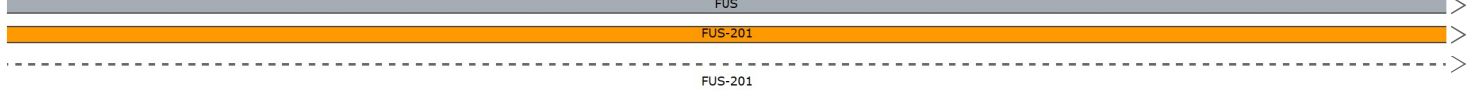
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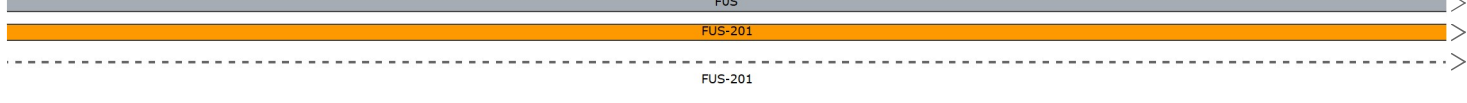
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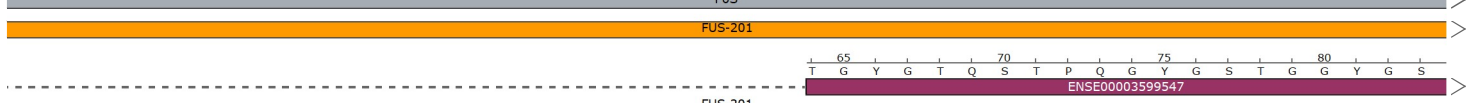
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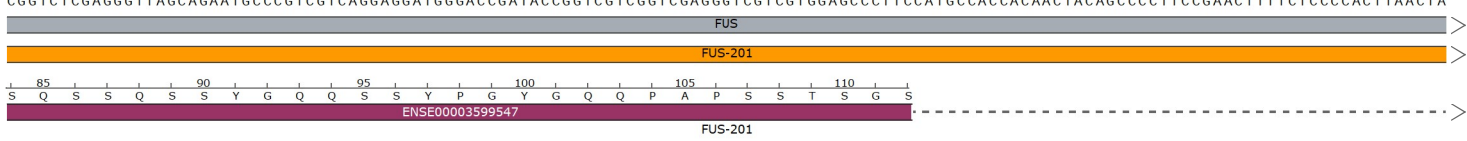
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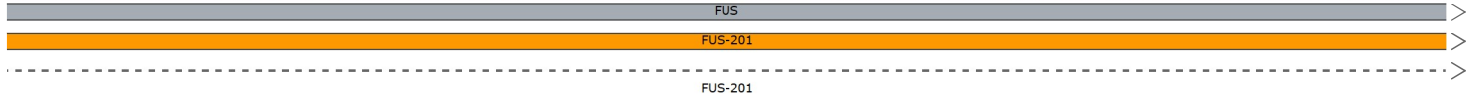
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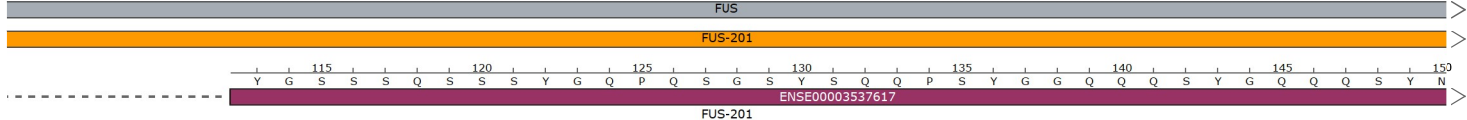
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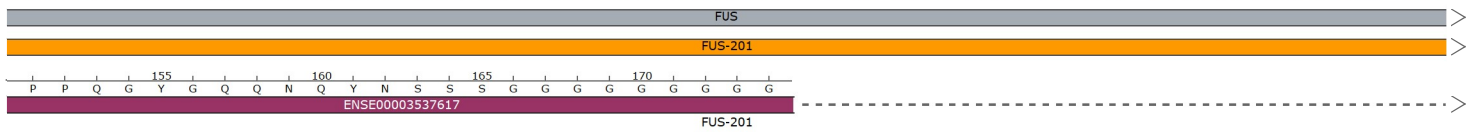
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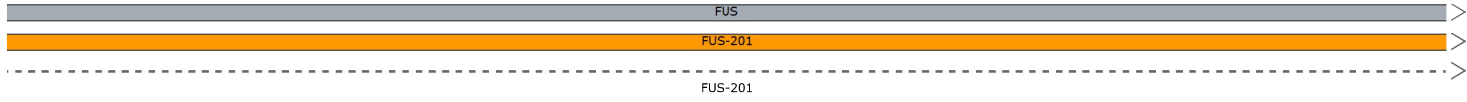
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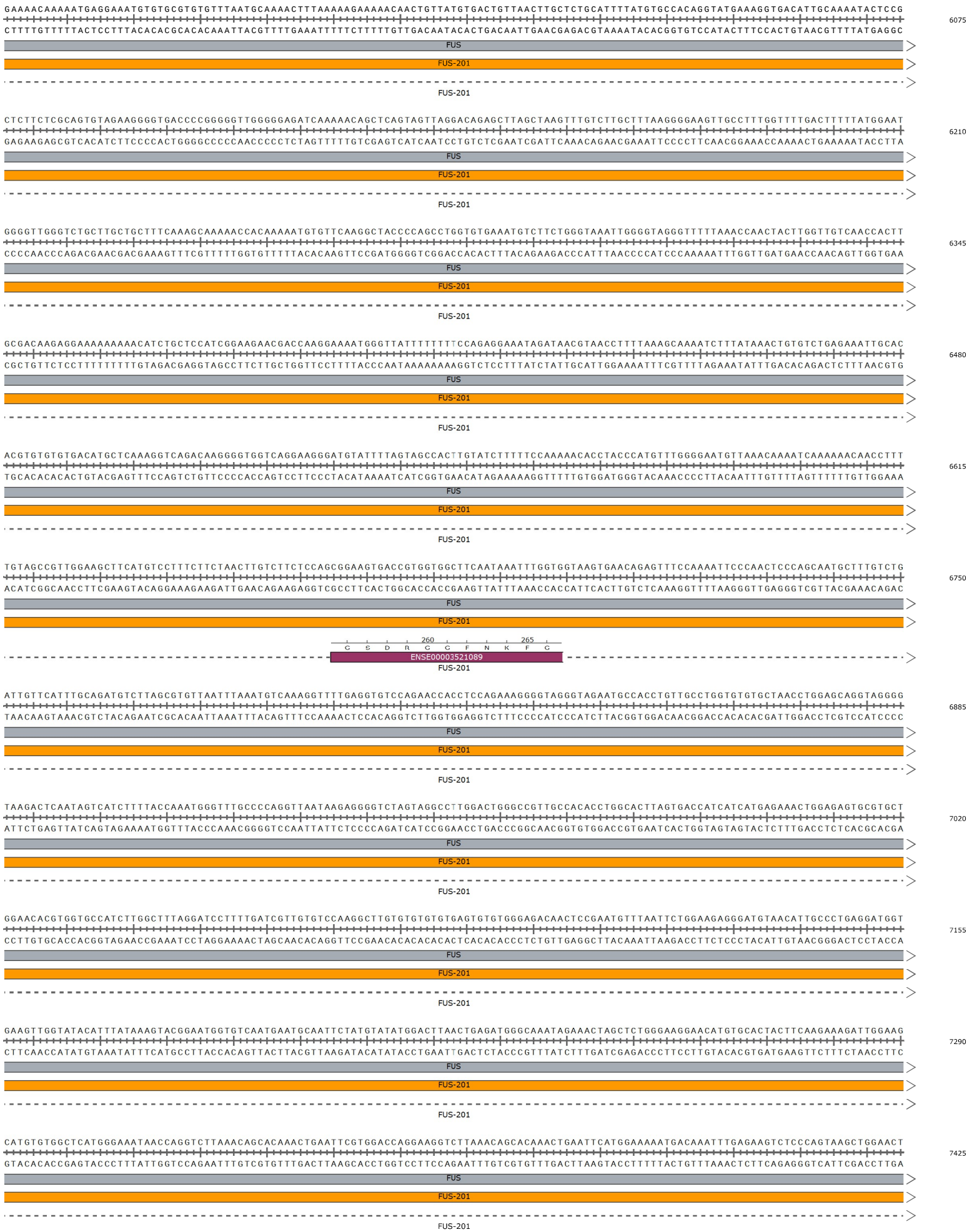
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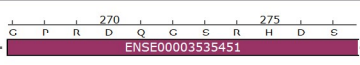
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8910

FUS

FUS-201

FUS-201

CTAGGTTGCTTTAGGTTTTTTCCTGTGTTTTTATTTTACCTTTTACATTTTGCATTTTCTGTTCACAAAGCAGAACAGGATAATTCAGACAAACACACCATCTTTGTGCAAGGCCCTGGGTGAGAAATGTTACAA  
GATCCACGAAATCCAAAAAAGGACACAAAAAATAAATGGAAAAGTGTAAACGTAAGAGACAAAGTTGTTCTGCTTGTCTTAAAGTCTGTGTGTGGTAGAAACAGTTCGGACCCACTCTTACAATGTT

9045

FUS

FUS-201

E Q D N S D N T I F V Q G L G E N V T  
ENSE00003524436

FUS-201

TTGAGTCTGTGGCTGATTACTTCAAGCAGATTGGTATTATTAAGGACTTGTGGAGAGGAGTGGGAGCTTTCTGTCAGTGTGTAGGCTTGGGATTTCACACATTAGTAAAAGCAAGTCTTTAATGGTTGCCAG  
AACTCAGACACCGACTAATGAAGTTCGCTAACCAATAAATTCATGAACACCTCTCCTCACCTCGAAAGACAGTCAACAATCCGAACACCTAAAGTGTGTAATCATTTTCGTTCCAGAAATACCAACGGTC

9180

FUS

FUS-201

I E S V A D Y F K Q I G I I K  
ENSE00003524436

FUS-201

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9315

FUS

FUS-201

FUS-201

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9450

FUS

FUS-201

FUS-201

CATGTTCTAGAGGAAGAAGATGAAAAGGGAGTACTGTAGCCTTTAAAAATGATGTTACCTCATTTTGTCTTCTCAGACAAACAAGAAAACGGGACAGCCCATGATTAATTTGTACACAGACAGGGAAACTGGCA  
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9585

FUS

FUS-201

T N K K T G Q P M I N L Y T D R E T G  
ENSE00003534484

FUS-201

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9720

FUS

FUS-201

K L K G E A T V S F D D P P S A K A A I D W F D  
ENSE00003534484

FUS-201

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9855

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FUS-201

FUS-201

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9990

FUS

FUS-201

G K E F S G N P I K V S F A T R R A D F N R G G G N G R G G  
ENSE00003653971

FUS-201

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10,125

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R G R G  
ENSE00003653971

FUS-201

TATCTGCATTAGGACCCATGGGCCGTGGAGGCTATGGAGGTGGTGGCAGTGGTGGTGGTGGCCGAGGAGGATTTCCAGTGGAGGTGGTGGCGGTGGAGGACAGCAGCGAGCTGGTGAAGTGTCTTAATC  
ATAGACGTAATCCTGGGTACCGGACCTCCGATACCTCCACCACCGTCCACCACCCACCGCTCTCTAAAGGTTCACTCCACCACCGCCACCTCTGTCGTCGCTGACCACTGACCTTCAACAGGATTAG

10,260

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G P M G R G G Y G G G G S G G G G R G G F P S G G G G G Q Q R A G D W K C P N  
ENSE00003604625

FUS-201



C GTGAGT GAAACTTAATTTTTCTTAGTTCTTGCATGCGTGCCTTTTGATATATTGGTACTGAGGTATGTGCGTGTTCCTCCAAAGGAAGTAAATGTCAAGGCCACACTGTGGGGTCAGATTTAGCCAAAAGC  
GCAC TCACTTTGAATTA AAAAAAGAATCAAGAGAACGTACGCACGAGA AACTATAAACCATGACTCCATACACGCACAAAAGTTCCTTCATTACAGTTCCGGTGTGACAACCCCACTTAATCGGTTTTCG

10,395

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-1  
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TTACCTAGGTAAAGTTGATGTAATGGGAAAGGTAATGGATTGGGTTTCAGTAATACTGATTTTTGTTCTGACTCTGAGAAGCAAGCCGTTTTGCTTTCTGAAGCTTCAGTTTCCTCACTGTATCTCTAAAGTCA  
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10,530

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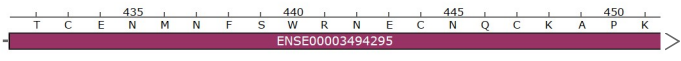
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GGCATCAAAGAAGGATCAAGATCCAGAACGGATAAGGGGTAGCGAGGTCTGACTAACAGAAGGAAAGAGGAATCTGGACACTTTATACTTGAAGAGAACCCTTACTTACGTTGGTCACATTCCGGGGATTT

10,665

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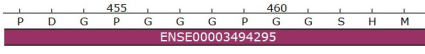
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10,800

FUS

FUS-201



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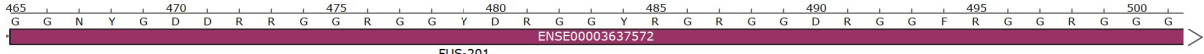
gRNA Protospacer  
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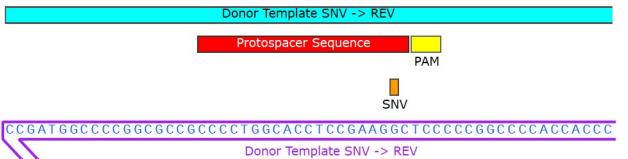
10,935

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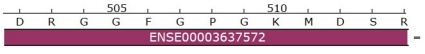


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CTGTCTCCACCGAAACCGGGACCCTTCTACCTAAGTCCATTCTGAAATTTAGTCTATTTTTTCATCTCGTCAACTTGTCTCCGGTATCCTATTGTCCAAACAACCTTTTACCAAAAGTAAAAC TCCGATC

11,070

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Donor Template SNV -> REV  
CTGTCTCCACCGAAACCGGGACCCTTCTACCTAAGTCCATTG

GTAAACTCCCGATC  
Sanger Sequencing Primer

GTGGAAGACCTGAGGTTGTAACCAAGTGTGGAGAGGGAAGGAAAATTAAC TACAGGGGAGTGAATCTGTAGACCCACTTGAGATAAGATACTCGCTGGGTTAGGTAGGAGGGGCAAGATAGGATATCTAGGCTTG  
CACCTTCTGGACTCCAACATTTGGTCATCACCTCTCCCTTCCCTTTAATTGAGTCCCCCTCACTTAGACATCTGGGTGAAC TCTATTCTATGAGCGACCAATCCATCCTCCCGTCTATCTATAGATCCGAAC

11,205

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CACCT  
Sanger Sequencing Primer

GAGAGGCTGGTAACTCAAATAATGGATACTAATTTTTTTTTTTTTTTTTTTTGCAGGGGTGAGCACAAGACAGGATCGCAGGGAGAGGCGGATTAATTAGCCTGGCTCCCAAGTTCTG6AAACAGCTTTTTGTCC  
CTCTCCGACCATTTAGTTTATATTACCTATGAATTA AAAAAA AAAAAA AAAAAAAGTCCCACTCGTGTCTGTCTAGCGTCCCTCTCCGGCATATAATTAATCGGACCGAGGGGTCCAAGACCTTGTGAAAAACAGG

11,340

FUS

FUS-201



FUS-201

TGTACCCAGTGTTACCCTCGTTATTTTGTAACTTCCAATTCCTGATCACCCAAGGGTTTTTTTGTGTCGGACTATGTAATTGTAACCTATACCTCTGGTCCCATTAAAAGTGACCATTTTAGTTAAA  
ACATGGGTCACAATGGGAGCAATAAACATTGGAAGGTTAAGGACTAGTGGGTTCCCAAAAAACACAGCCTGATACATTAACTTGATATGGAGACCAAGGGTAATTTTCACTGGTAAATCAATTT

3'  
11,468  
5'

FUS

FUS-201

GAGACCAAGGGTAATTTCACTGGT

PCR Reverse

Feature	Location	Size	Start	End	Type
<b>FUS</b>	1 .. 11,468	11,468 bp	█	→	gene
/note	= gene <a href="#">ENSG00000089280</a>				
					Protein coding
<b>FUS-209</b>	1 .. 11,465	11,465 bp	█	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000566605</a>				
					Nonsense mediated decay
<b>FUS-201</b>	2 .. 11,468	11,467 bp	█	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000254108</a>				
<b>FUS-202</b>	2 .. 11,465	11,464 bp	█	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000380244</a>				
<b>FUS-205</b>	2 .. 3213	3212 bp	█	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000487045</a>				
					Retained intron
<b>FUS-206</b>	13 .. 11,465	11,453 bp	█	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000487509</a>				
					Retained intron
<b>FUS-210</b>	14 .. 11,438	11,425 bp	█	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000568685</a>				
<b>FUS-201</b>	78 .. 11,301	11,224 bp	█	→	CDS
▶ 15 segments = 1581 bp					
/note	= coding sequence <a href="#">ENSP00000254108</a>				
/translation	MASN,,DYTQQATQS,,YGAYPTQPGQGYSSQSSQPYGQQSYSGYSQSTDTSGYGGSSYSSYGQSQN,,TGYGTQSTPQGYGSTGGYGSSQSSQSSYGGQSSYPGYGQQPAPSSTSGS,,YGSSSQSSSYGQPQSGSYSQQPSYGGQQQSYGQQQSYNPPQGYGQQNQYNSSSGGGGGGGGG,,GNYGQDQSSMSSGGGSGGGYGNQDQSGGGGSGGYGQQDRGGRGRGSSGGGGGGGGGGYNRSSGGYEPRGRGGGRGRGGMG,,GSDRGGFNKFG,,GPRDQGSRHDS,,EQDNSDNTIFVQGLGENVTIESVADYFKQIGIIK,,TNKKTGQPMINLYTDRETGKLGKGEATVSFDPPSAKAAIDWFD,,GKEFSGNPIKVSFATRRADFNRGGGNRGRGRG,,GPMGRGGYGGGSGGGGRGFPSSGGGGGGQQRAGDWKCPNP,,TCENMNFWRNECNQCKAPKPDGPGGGPGGSHM,,GGNYGDDRRRGRGGYDRGGYRGRGGDRGGFRGGGGDRGGFGPKMDSR,,GEHRQDRRERPY*				
					526 amino acids = 53.4 kDa
<b>FUS-202</b>	78 .. 11,301	11,224 bp	█	→	CDS
▶ 15 segments = 1578 bp					
/note	= coding sequence <a href="#">ENSP00000369594</a>				
/translation	MASN,,DYTQQATQS,,YGAYPTQPGQGYSSQSSQPYGQQSYSGYSQSTDTSGYGGSSYSSYGQSQN,,SYGTQSTPQGYGSTGGYGSSQSSQSSYGGQSSYPGYGQQPAPSSTSGS,,YGSSSQSSSYGQPQSGSYSQQPSYGGQQQSYGQQQSYNPPQGYGQQNQYNSSSGGGGGGGGG,,GNYGQDQSSMSSGGGSGGGYGNQDQSGGGGSGGYGQQDRGGRGRGSSGGGGGGGGGGYNRSSGGYEPRGRGGGRGRGGMG,,GSDRGGFNKFG,,GPRDQGSRHDS,,EQDNSDNTIFVQGLGENVTIESVADYFKQIGIIK,,TNKKTGQPMINLYTDRETGKLGKGEATVSFDPPSAKAAIDWFD,,GKEFSGNPIKVSFATRRADFNRGGGNRGRGRG,,GPMGRGGYGGGSGGGGRGFPSSGGGGGGQQRAGDWKCPNP,,TCENMNFWRNECNQCKAPKPDGPGGGPGGSHM,,GGNYGDDRRRGRGGYDRGGYRGRGGDRGGFRGGGGDRGGFGPKMDSR,,GEHRQDRRERPY*				
					525 amino acids = 53.4 kDa
<b>FUS-210</b>	78 .. 11,301	11,224 bp	█	→	CDS
▶ 15 segments = 1584 bp					
/note	= coding sequence <a href="#">ENSP00000455282</a>				
/translation	MASN,,DYTQQATQS,,YGAYPTQPGQGYSSQSSQPYGQQSYSGYSQSTDTSGYGGSSYSSYGQSQN,,TGYGTQSTPQGYGSTGGYGSSQSSQSSYGGQSSYPGYGQQPAPSSTSGS,,YGSSSQSSSYGQPQSGSYSQQPSYGGQQQSYGQQQSYNPPQGYGQQNQYNSSSGGGGGGGGG,,GNYGQDQSSMSSGGGSGGGYGNQDQSGGGGSGGYGQQDRGGRGRGSSGGGGGGGGGGYNRSSGGYEPRGRGGGRGRGGMG,,GSDRGGFNKFG,,GPRDQGSRHDS,,AEQDNSDNTIFVQGLGENVTIESVADYFKQIGIIK,,TNKKTGQPMINLYTDRETGKLGKGEATVSFDPPSAKAAIDWFD,,GKEFSGNPIKVSFATRRADFNRGGGNRGRGRG,,GPMGRGGYGGGSGGGGRGFPSSGGGGGGQQRAGDWKCPNP,,TCENMNFWRNECNQCKAPKPDGPGGGPGGSHM,,GGNYGDDRRRGRGGYDRGGYRGRGGDRGGFRGGGGDRGGFGPKMDSR,,GEHRQDRRERPY*				
					527 amino acids = 53.5 kDa
	2374 .. 3148	775 bp	█	←	gene
/note	= gene <a href="#">ENSG00000260304</a>				
					lncRNA
	2374 .. 3148	775 bp	█	←	prim_transcript
/note	= primary transcript <a href="#">ENST00000564743</a>				
					lncRNA
<b>FUS-207</b>	3413 .. 4261	849 bp	█	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000487974</a>				
					Retained intron
<b>FUS-213</b>	4943 .. 7108	2166 bp	█	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000570090</a>				
					Retained intron
<b>FUS-203</b>	5362 .. 10,965	5604 bp	█	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000474990</a>				
<b>FUS-211</b>	8015 .. 9983	1969 bp	█	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000568901</a>				
					Retained intron
<b>FUS-208</b>	8330 .. 9558	1229 bp	█	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000564766</a>				
					Retained intron
<b>FUS-212</b>	10,079 .. 11,468	1390 bp	█	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000569760</a>				
					Retained intron
<b>FUS-204</b>	10,236 .. 11,421	1186 bp	█	→	prim_transcript
/note	= primary transcript <a href="#">ENST00000483853</a>				
					Retained intron
<b>Donor Template SNV -&gt; REV</b>	10,879 .. 10,978	100 bp	█	↔	misc_feature
<b>Protospacer Sequence</b>	10,897 .. 10,916	20 bp	█	↔	misc_feature
<b>SNV</b>	10,915 .. 10,915	1 bp	█	↔	misc_feature
/note	= WT = C SNV = T				
<b>PAM</b>	10,917 .. 10,919	3 bp	█	↔	misc_feature

Primer	Length	Binding Sites	Tm	Date Added
✓ <b>PCR Forward</b> /sequence = GGGAACATAGGGGAATGGGAATATG 48% GC / 7884.2 Da	25-mer	10,776 .. 10,800	58°C	Jun 14, 2022
✓ <b>Donor Template SNV -&gt; REV</b> /sequence = CTTACCTGGAATCCATCTTGCCAGGGCCAAAGCCACCTCTGTCCCCACCAACCCGGCCCCCTCGGAAGCCTCCACGGTCCC GCGCGGCCCCCGGTAGCC 71% GC / 30,307.4 Da	100-mer	10,879 .. 10,978	87°C	Jun 14, 2022
✓ <b>gRNA Protospacer</b> /sequence = GGGGACC GTGGAGGCTTCTG 70% GC / 6230.1 Da	20-mer	10,897 .. 10,914	61°C	Jun 14, 2022
✓ <b>Sanger Sequencing Primer</b> /sequence = TCCACCTAGCCCTCAAATG 50% GC / 6006.0 Da	20-mer	11,056 .. 11,075	56°C	Jun 14, 2022
✓ <b>PCR Reverse</b> /sequence = TGGTCACTTTTAATGGGAACCCAGAG 44% GC / 7721.1 Da	25-mer	11,433 .. 11,457	59°C	Jun 14, 2022