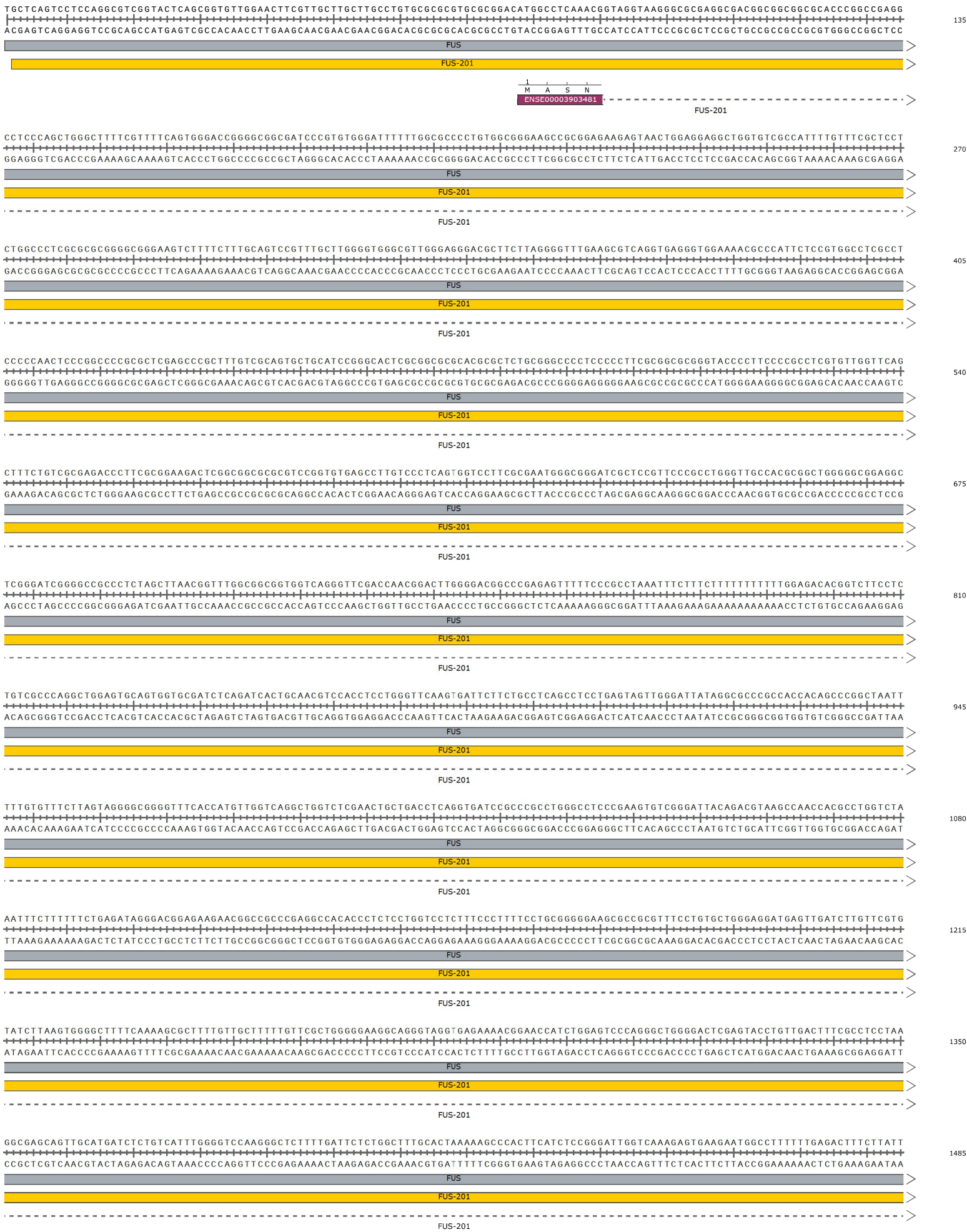
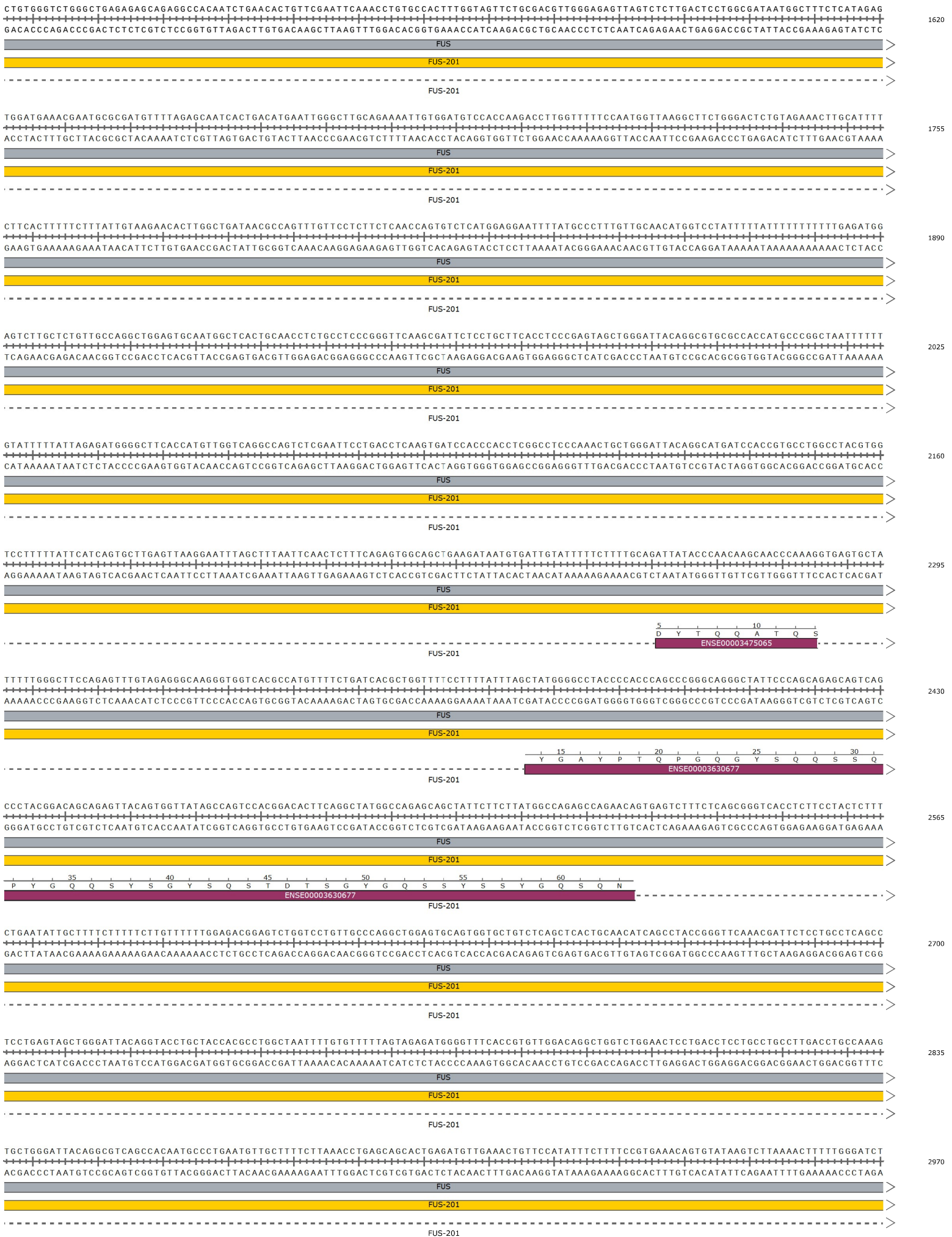


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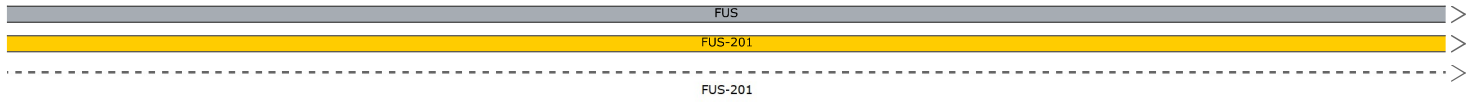






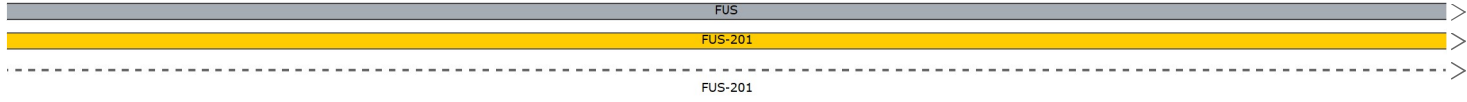
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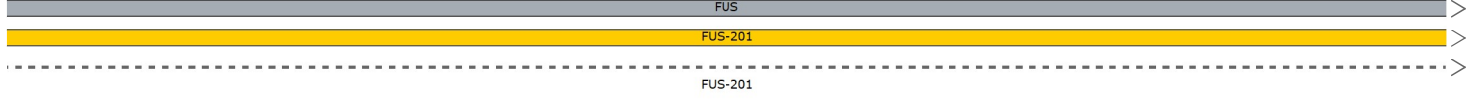
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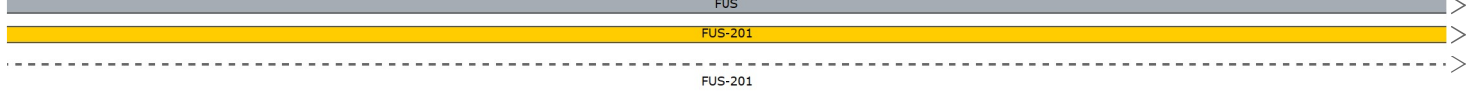
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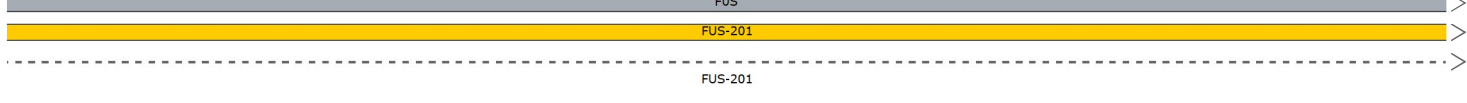
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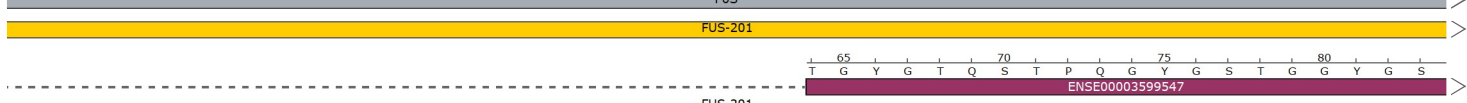
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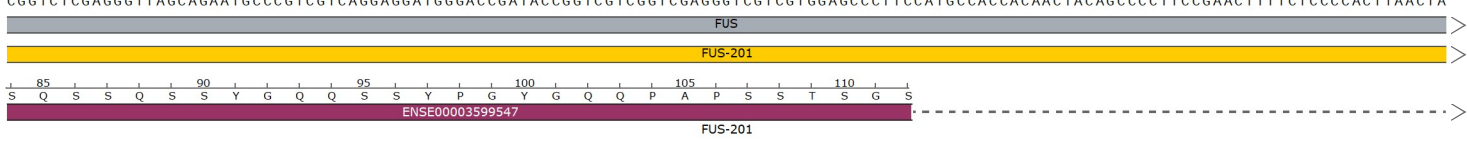
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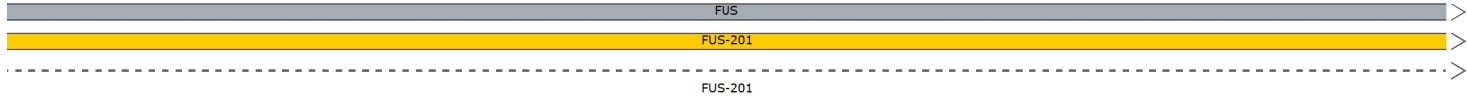
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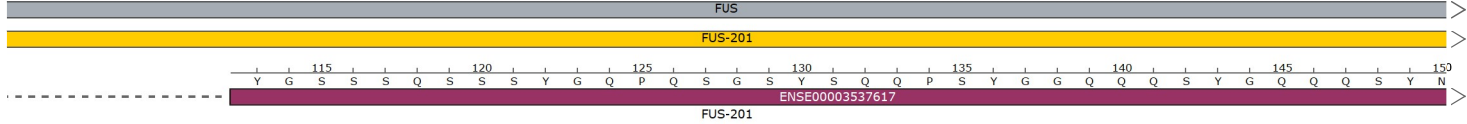
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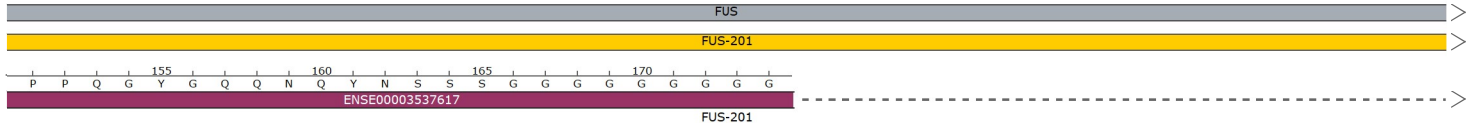
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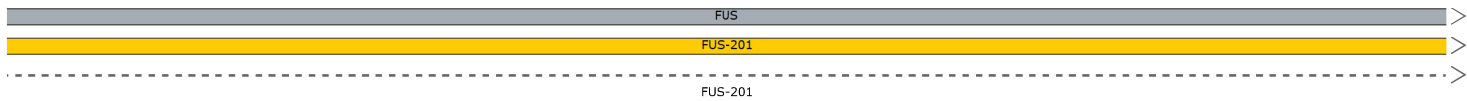
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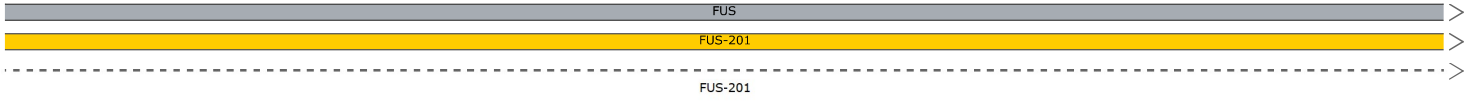
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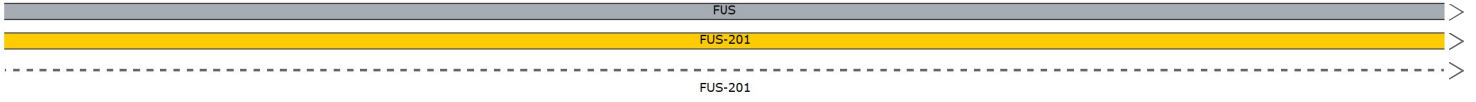
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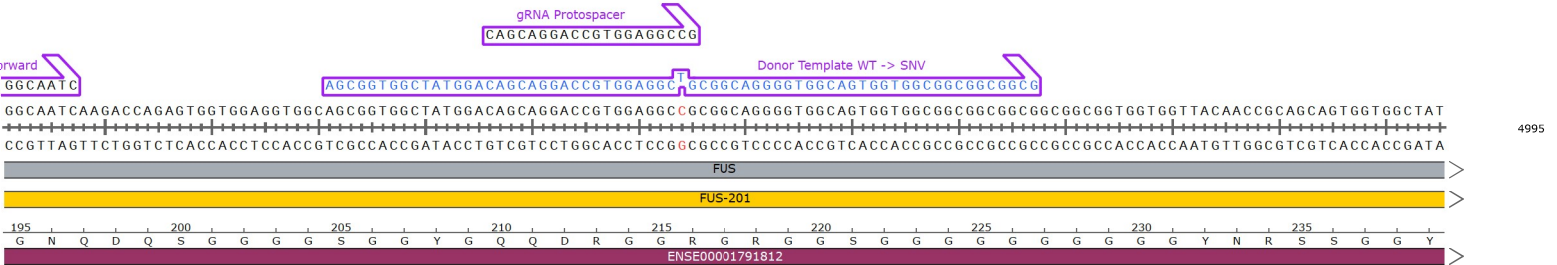
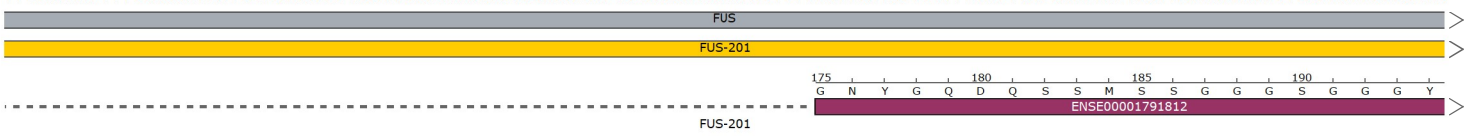
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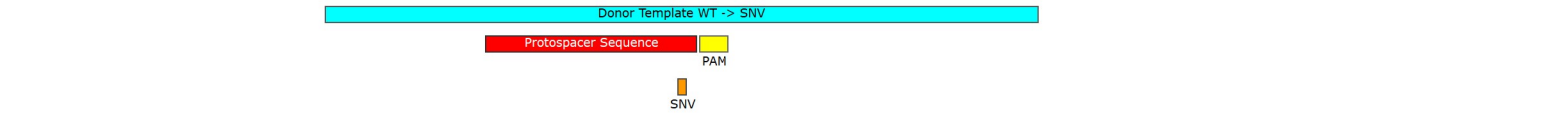


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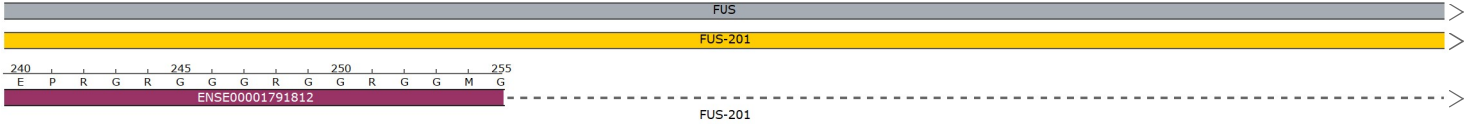


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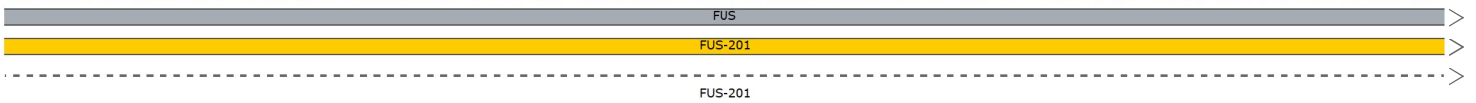
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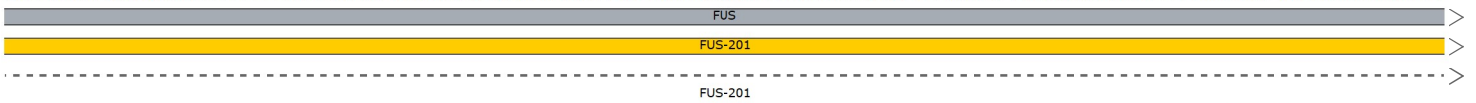
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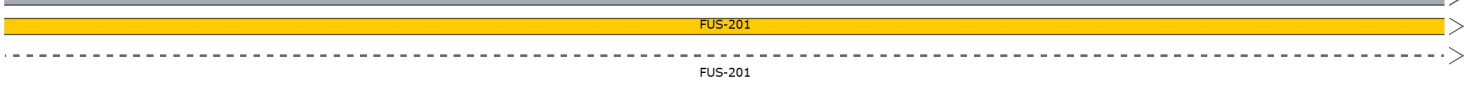
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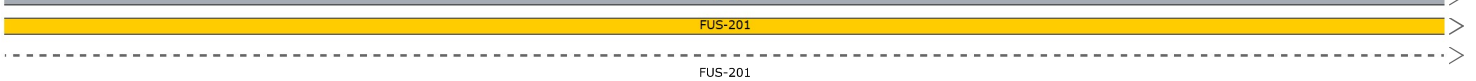
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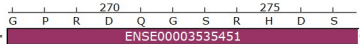
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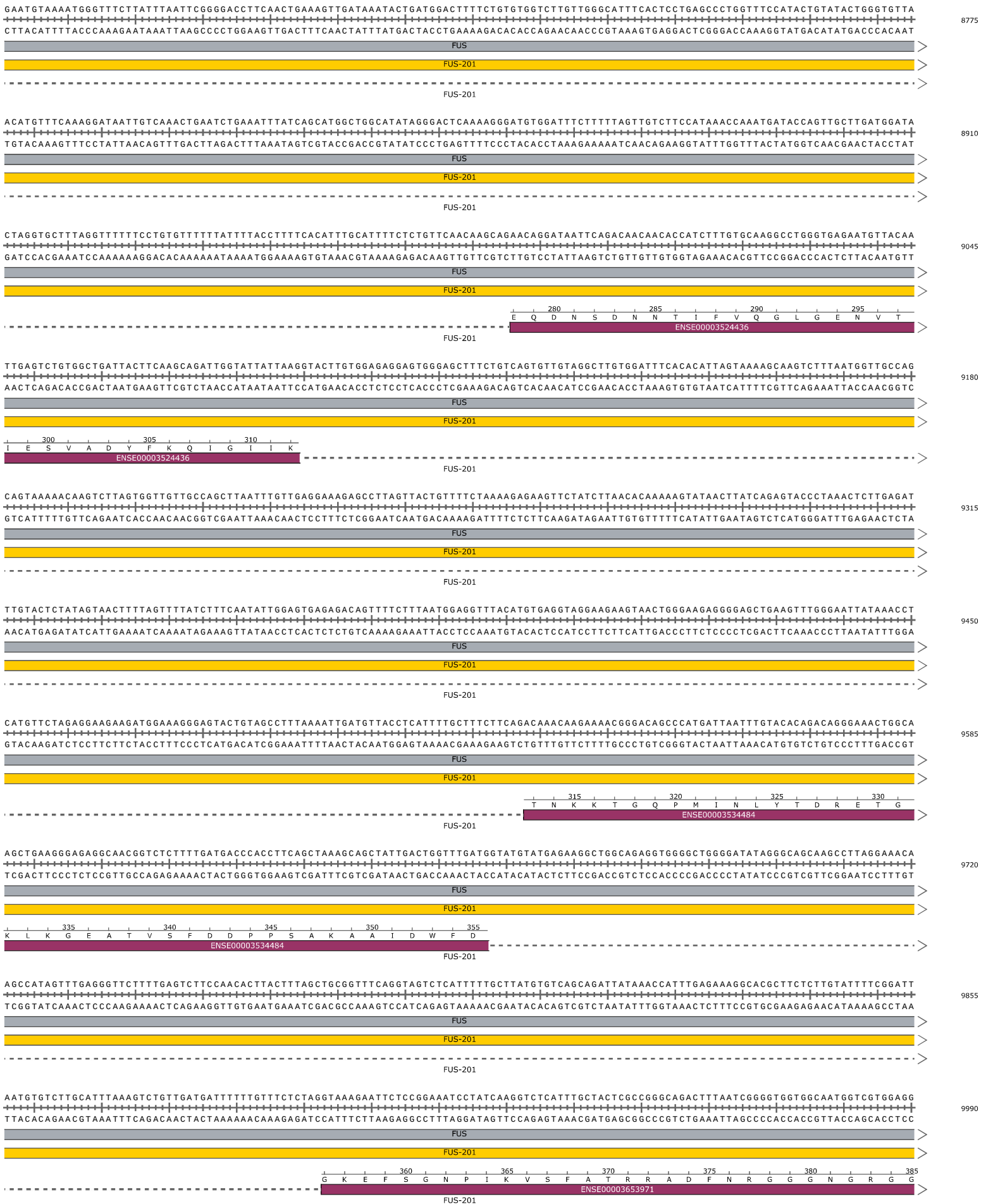
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CGTGAGTGAACCTAAATTTTCTTAGTCTCTTGCATCGTGTCTTTGTATATATTGGTACTGAGGTATGTCGTGTTTTCCAAAAGTAAATGTCAAGGCCACACTGTGGGGTTCAGATTTAGCCAAAAGC  
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10,395

FUS

FUS-201

I P

FUS-201

TTACCTAGGTAAGGTTGATGTAATGGAAAAGTAATGGATTGGGTTTCAGTAATACTGATTTTTGTTCTGACTCTGAGAAGCAAGCCGTTTGTCTTCTGAAGCTTCAAGTTCCTCACTGTATCTCAAAGTCA  
AATGGATCCATCCAACACTACATTACCTTTCCATTACCTAACCAAGTCAATATGACTAAAACAAGGACTGAGACTCTTCCTGTTGGCAAACGAAAGACTTCGAAGTCAAAGGAGTGACATAGAGATTTCAAT

10,530

FUS

FUS-201

FUS-201

CCGTAGTTTCTTCTAGTTCTAGGTCCTGCCTATTCCCCATCGCTCCAGACTGATTGTCTTCTCTTCTAGCACCTGTGAGAATATGAACCTCTTGGAGGAATGAATGCAACCACTGTAAGGCCCTAAA  
GGCATCAAGAAGGATCAAGATCCAGAACGGATAAGGGGTAGCGAGGTCTGACTAACAGAAGGAAAGGAAATCGTGGACACTCTTATACTTGAAGAGAACCCTTACTTACGTTGGTACATTCCGGGGATTT

10,665

FUS

FUS-201

435 440 445 450  
T C E N M N F S W R N E C N Q C K A P K  
ENSE00003494295

FUS-201

CCAGATGGCCAGGAGGGGACAGGTTGGCTCTCACATGGGTAAGAAAAGGCAGACCTGGTGTCTAGGAGCTGGGACCAAAGAATCCTTAATTTTTACGCGGGGAGGCTCGGGAAACATAGGGGAATGGGAATAG  
GGTCTACCGGGTCTCCCTGGTCCACCGAGAGGTACCATTCTTTCCGTCTGGACACGATCCCTCGACCTGTTTCTTAGGAATAAAAGTCCGCCCTCCGAGCCCTTGATACCCCTTACCCTTATAC

10,800

FUS

FUS-201

455 460  
P D G P G G G P G G S H M  
ENSE00003494295

FUS-201

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10,935

FUS

FUS-201

465 470 475 480 485 490 495 500  
G G N Y G D D R R G G R G G Y D R R G G Y R R G R G G D R R G G F R R G G R G G G  
ENSE00003637572

FUS-201

GACAGAGGTGGCTTTGGCCCTGGCAAGATGGATTCCAGGTAAGACTTTAAATCAGAATAAAAAGTAGAGCAGTTGACAGAGGCCATAGGATAACAGGGTTTTGTTGAGAAAAGTGGTTTCATTTGAGGGCTAG  
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11,070

FUS

FUS-201

505 510  
D R G G F G P G K M D S R  
ENSE00003637572

FUS-201

GTGAAAAGACCTGAGGTTGTAACCAAGTAGTGGAGAGGGAAGGAAAATTAACTCAGGGGAGTGAATCTGTAGACCCACTTGAGATAAGATACTCGCTGGGTTAGGTAAGGAGGGGACAGATAGGATATCTAGGCTTG  
CACCTTTCTGGACTCCAACATTGGTCACTACCTCTCCCTTCTTTAATTAAGTCCCTCCTACTAGACACTGTTGGTGAACCTATTCTATAGCGACCAACCTCACTCCCGGCTATCTTATAGATCCGAAAC

11,205

FUS

FUS-201

FUS-201

GAGAGGCTGGTAACTCAAATATAATGGATACTTAATTTTTTTTTTTTTTTCAGGGGTGAGCACAGACAGGATCGCAGGGAGAGGCGGTATTAATTAGCTGGCTCCCCAGGTTCTGGAACAGCTTTTTGTCC  
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11,340

FUS

FUS-201

515 520 525  
G E H R Q D R R E R P Y  
ENSE00001310182

FUS-201

TGTACCCAGTGTTACCCCTCGTTATTTTGTAACTTCCAATTCCTGATCACCCAAGGGTTTTTTTGTGTCGGACTATGTAATTGTAACCTATACCTCTGGTCCCATTAAAAGTGACCATTTTGTAA  
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3'  
11,468  
5'

FUS

FUS-201



Feature	Location	Size	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,,DYTQATQS,,YGAYPTQPGQYSQSSQPYGQQSYSGYSQSTDTSGYGQSSYSSYGQSQN,,TGYGTQSTPQGYGSTGGYGSSQSSQSSYGYGQQPAPSSTSGS,,YGSSSQSSSYGQPQSGSYSQQPSYGGQQQSYGQQQSYNPPQGYGQQNQYNSSSGGGGGGGG,,GNYGQQDQSSMSSGGGSGGGYGNQDQSGGGSGGYGQQDRGGRGRGSGGGGGGGGGGYNRSGGYEPRGRGGRRGGMG,,GSDRGGFNKFG,,GPRDQGSRHDS,,EQDNSDNNTIFVQGLGENVTIESVADYFKQIGIIK,,TNKKTGQPMINLYTDRETGKLGKGEATVSFDDPPSAKAAIDWFD,,GKEFSGNPIKVSFATRRADFNRGGNGRGGRRG,,GPMGRGGYGGGGSGGGRRGFPSSGGGGGQQRAGDWKCPNP,,TCENMNFWRNECNQC KAPKPDGPGGGPGGSHM,,GGNYGDDRRGGRGGYDRGGYRGRGGDRGGFRGGGGDRGGFGPKMDSR,,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,,DYTQATQS,,YGAYPTQPGQYSQSSQPYGQQSYSGYSQSTDTSGYGQSSYSSYGQSQN,,SYGTQSTPQGYGSTGGYGSSQSSQSSYGYGQQPAPSSTSGS,,YGSSSQSSSYGQPQSGSYSQQPSYGGQQQSYGQQQSYNPPQGYGQQNQYNSSSGGGGGGGG,,GNYGQQDQSSMSSGGGSGGGYGNQDQSGGGSGGYGQQDRGGRGRGSGGGGGGGGGGYNRSGGYEPRGRGGRRGGMG,,GSDRGGFNKFG,,GPRDQGSRHDS,,EQDNSDNNTIFVQGLGENVTIESVADYFKQIGIIK,,TNKKTGQPMINLYTDRETGKLGKGEATVSFDDPPSAKAAIDWFD,,GKEFSGNPIKVSFATRRADFNRGGNGRGGRRG,,GPMGRGGYGGGGSGGGRRGFPSSGGGGGQQRAGDWKCPNP,,TCENMNFWRNECNQC KAPKPDGPGGGPGGSHM,,GGNYGDDRRGGRGGYDRGGYRGRGGDRGGFRGGGGDRGGFGPKMDSR,,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,,DYTQATQS,,YGAYPTQPGQYSQSSQPYGQQSYSGYSQSTDTSGYGQSSYSSYGQSQN,,TGYGTQSTPQGYGSTGGYGSSQSSQSSYGYGQQPAPSSTSGS,,YGSSSQSSSYGQPQSGSYSQQPSYGGQQQSYGQQQSYNPPQGYGQQNQYNSSSGGGGGGGG,,GNYGQQDQSSMSSGGGSGGGYGNQDQSGGGSGGYGQQDRGGRGRGSGGGGGGGGGGYNRSGGYEPRGRGGRRGGMG,,GSDRGGFNKFG,,GPRDQGSRHDS,,AEQDNSDNNTIFVQGLGENVTIESVADYFKQIGIIK,,TNKKTGQPMINLYTDRETGKLGKGEATVSFDDPPSAKAAIDWFD,,GKEFSGNPIKVSFATRRADFNRGGNGRGGRRG,,GPMGRGGYGGGGSGGGRRGFPSSGGGGGQQRAGDWKCPNP,,TCENMNFWRNECNQC KAPKPDGPGGGPGGSHM,,GGNYGDDRRGGRGGYDRGGYRGRGGDRGGFRGGGGDRGGFGPKMDSR,,GEHRQDRRERPY* 527 amino acids = 53.5 kDa		
/note	= gene <a href="#">ENSG00000260304</a> lncRNA	2374 .. 3148	775 bp
/note	= primary transcript <a href="#">ENST00000564743</a> lncRNA	2374 .. 3148	775 bp
<b>FUS-207</b>	3413 .. 4261	849 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000487974</a> Retained intron		
<b>Donor Template WT -&gt; SNV</b>	4891 .. 4957	67 bp	misc_feature
<b>Protospacer Sequence</b>	4906 .. 4925	20 bp	misc_feature
<b>SNV</b>	4924 .. 4924	1 bp	misc_feature
/note	= WT=C SNV=T		
<b>PAM</b>	4926 .. 4928	3 bp	misc_feature
<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		

Primer	Length	Binding Sites	Tm	Date Added
✓ <b>PCR Forward</b>	20-mer	4848 .. 4867 →	60°C	Jun 16, 2022
/sequence = TGGTGGCGGTTATGGCAATC 55% GC / 6204.1 Da				
✓ <b>Donor Template WT -&gt; SNV</b>	67-mer	4891 .. 4957 →	86°C	Jun 16, 2022
/sequence = AGCGGTGGCTATGGACAGCAGGACCGTGGAGGCTGCGGCAGGGGTGGCAGTGGTGGCGGCGGCGGCG 75% GC / 21,090.6 Da				
✓ <b>gRNA Protospacer</b>	20-mer	4906 .. 4925 →	66°C	Jun 16, 2022
/sequence = CAGCAGGACCGTGGAGGCCG 75% GC / 6193.1 Da				
✓ <b>PCR Reverse</b>	20-mer	5381 .. 5400 ←	60°C	Jun 16, 2022
/sequence = CCAGGAGTGGGATCATCGGT 60% GC / 6198.1 Da				
✓ <b>Sanger Sequencing Primer</b>	20-mer	5381 .. 5400 ←	60°C	Jun 16, 2022
/sequence = CCAGGAGTGGGATCATCGGT 60% GC / 6198.1 Da				