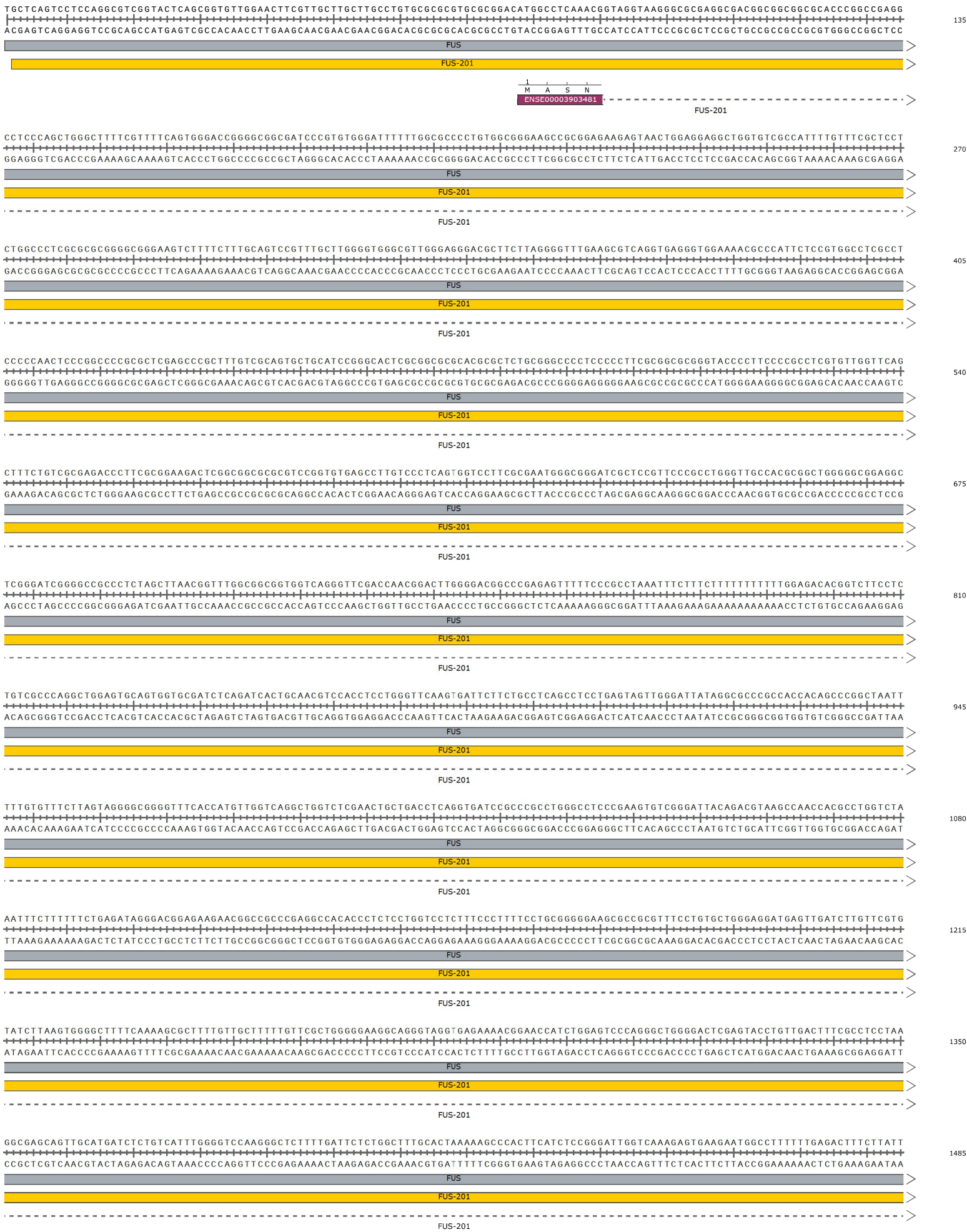
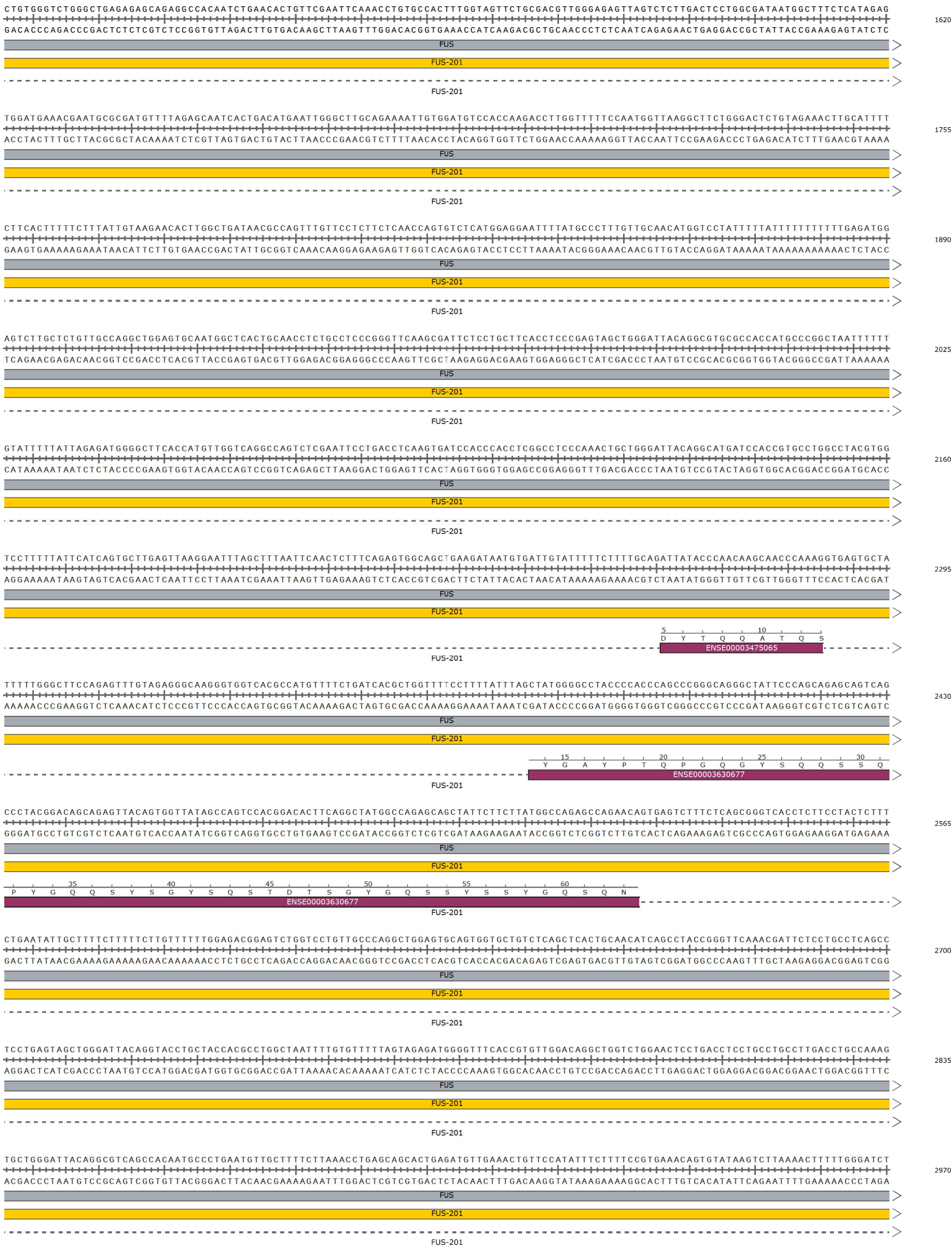


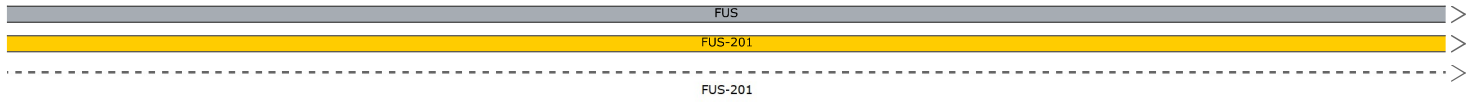
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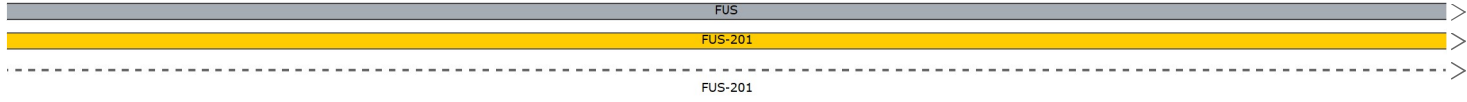
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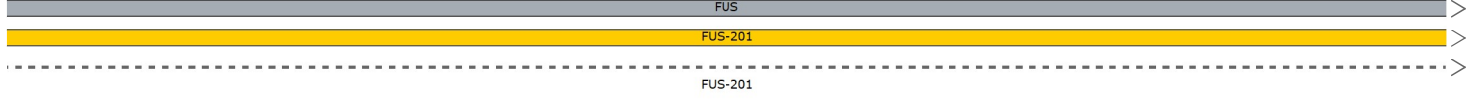
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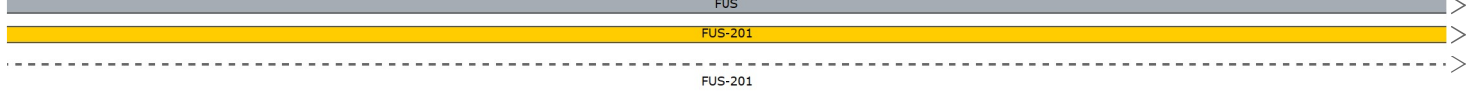
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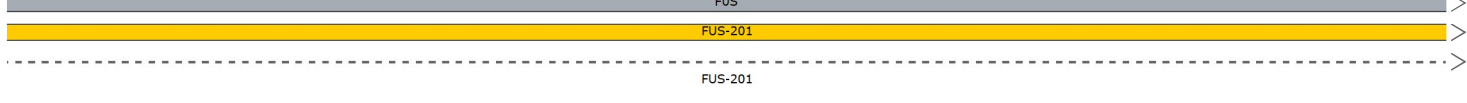
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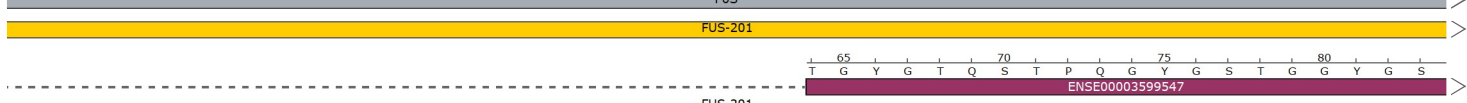
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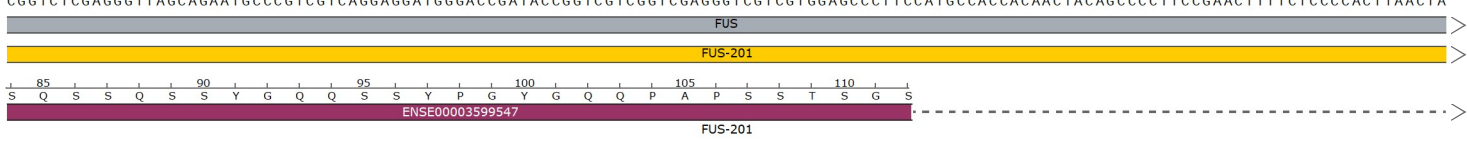
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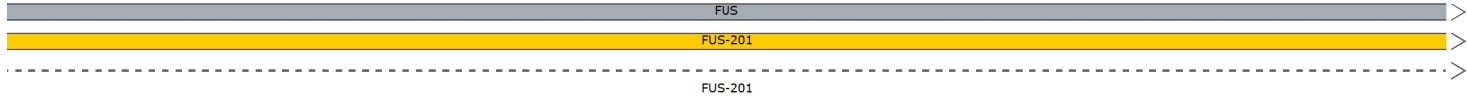
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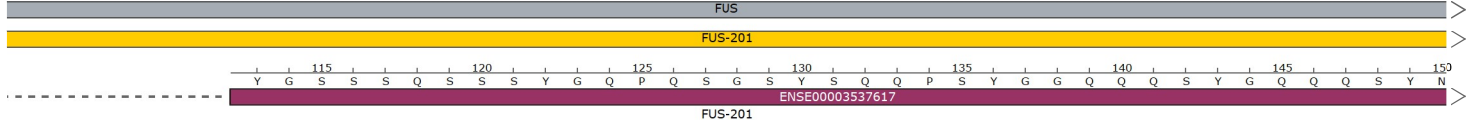
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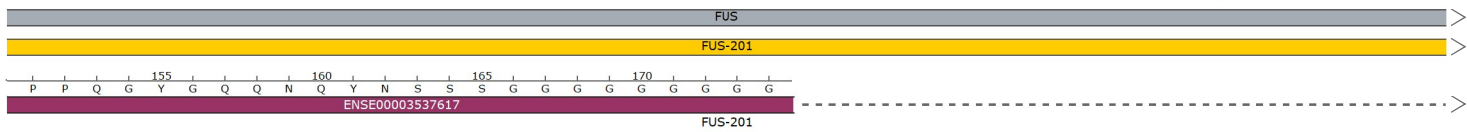
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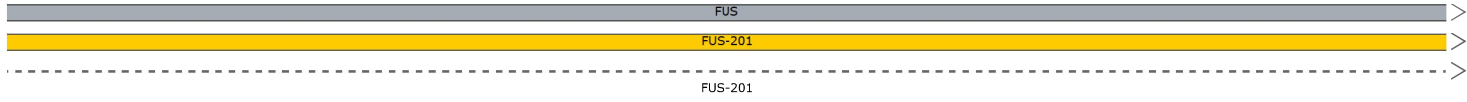
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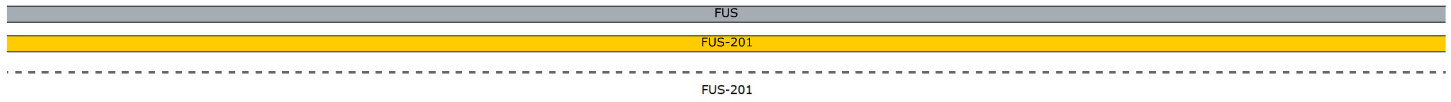
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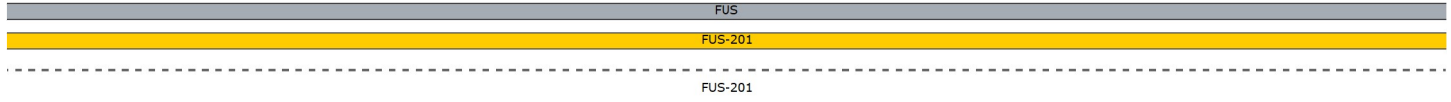
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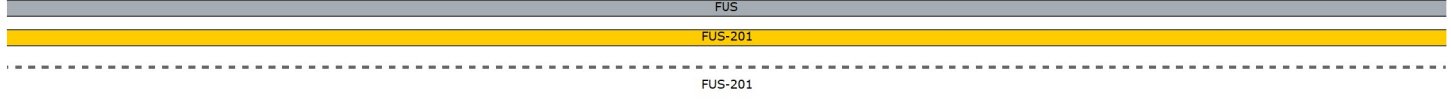
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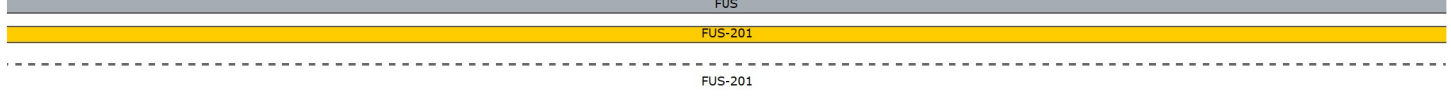
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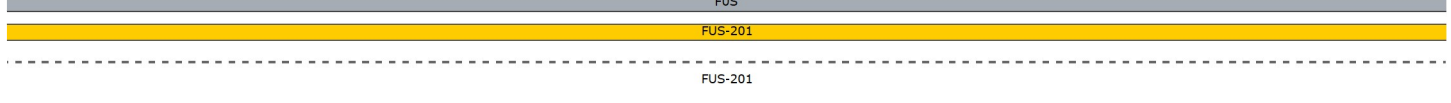
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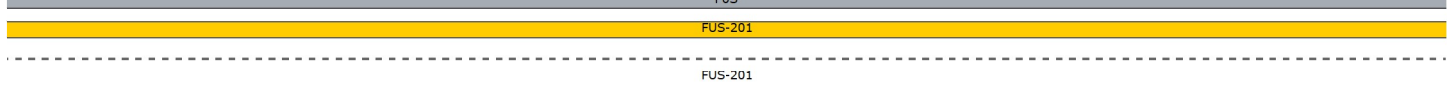
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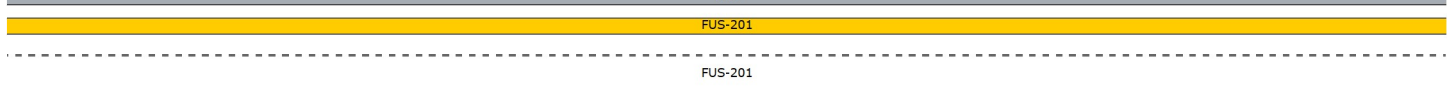
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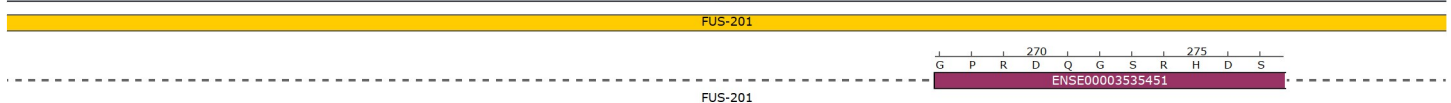
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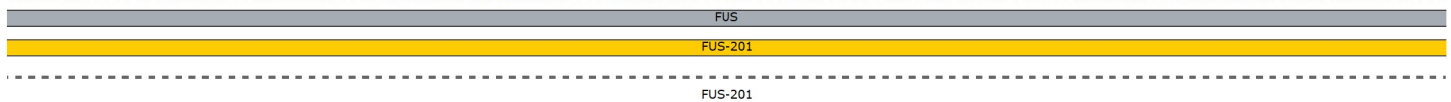
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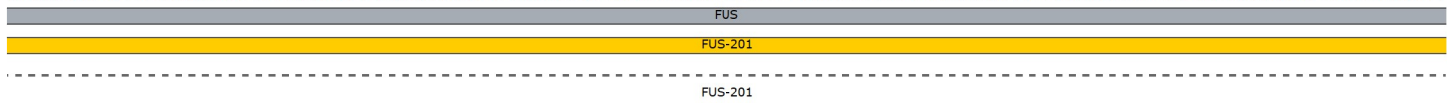
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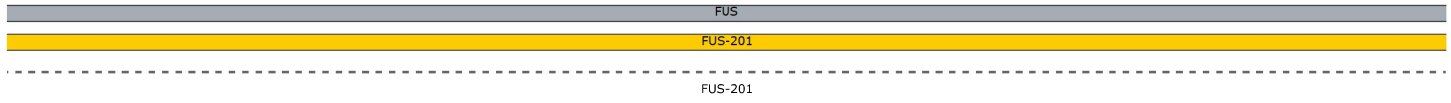
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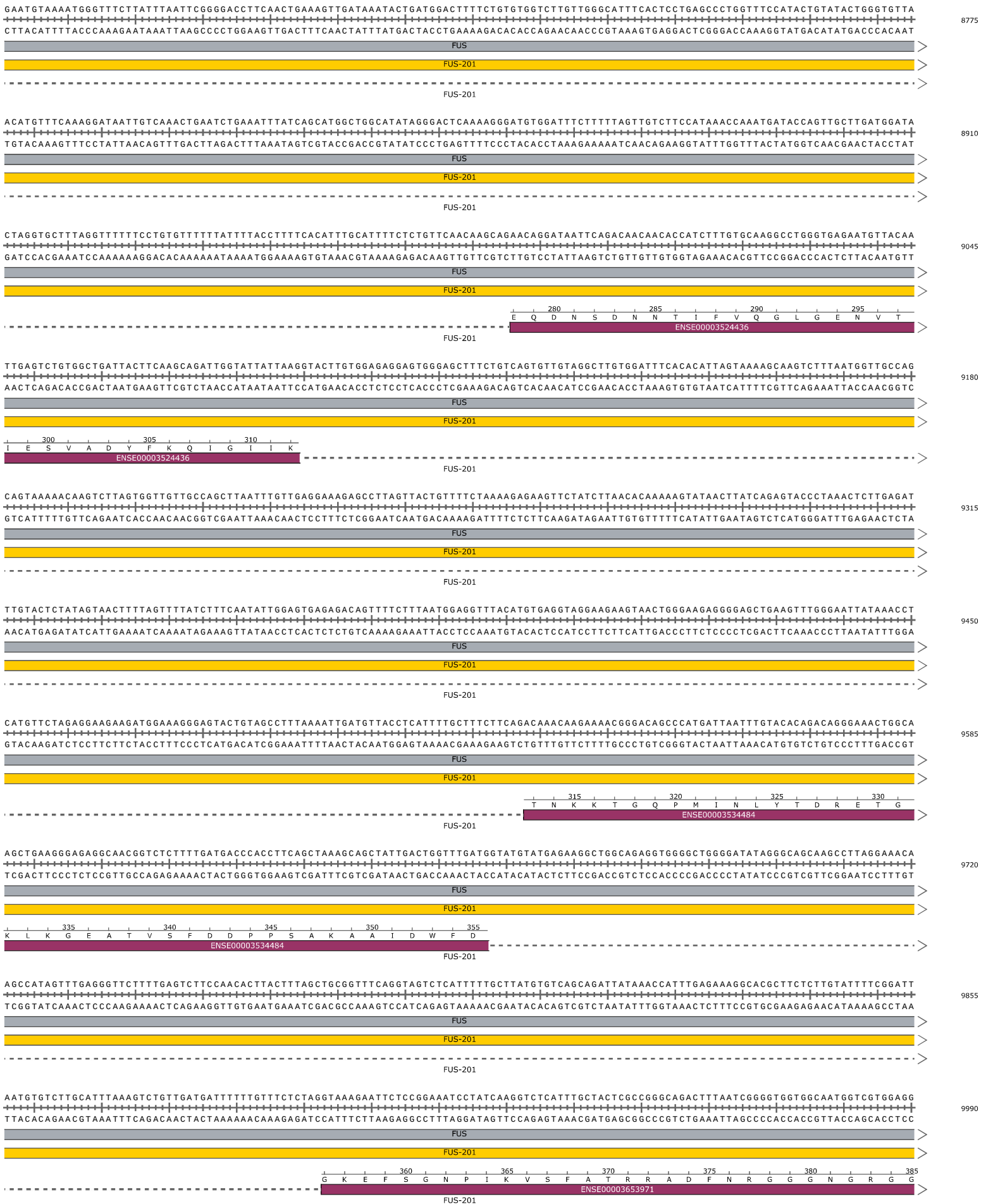
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FUS-201

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CTCTCCGACCACTTGAAGTTATATTACCTATGAATTAATAAAGAAAACAAACAGTCCCACTCGTGTCTGTCTAGCGTCCCTCTCCGGCATAATTAATCGGACCGAGGGGTCCAAGACCTTGTGAAAAACAGG

11,340

FUS

FUS-201

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

FUS-201

TGTACCCAGTGTTACCCCTCGTTATTTTGTAACTTCCAATTCCTGATCACCCAAGGGTTTTTTTGTGTCGGACTATGTAATTGTAACCTATACCTCTGGTTCCCATTAAAAGTGACCATTTTGTAA
ACATGGGTCACAATGGGAGCAATAAACATTGGAAGGTTAAGGACTAGTGGGTTCCCAAAAAACACAGCCTGATACATTAACTTGATATGGAGACCAAGGGTAATTTCACTGGTAAATCAATTT

3'
11,468
5'

FUS

FUS-201

Feature	Location	Size	Type
FUS	1 .. 11,468	11,468 bp	gene
/note	= gene ENSG00000089280 Protein coding		
FUS-209	1 .. 11,465	11,465 bp	prim_transcript
/note	= primary transcript ENST00000566605 Nonsense mediated decay		
FUS-201	2 .. 11,468	11,467 bp	prim_transcript
/note	= primary transcript ENST00000254108		
FUS-202	2 .. 11,465	11,464 bp	prim_transcript
/note	= primary transcript ENST00000380244		
FUS-205	2 .. 3213	3212 bp	prim_transcript
/note	= primary transcript ENST00000487045 Retained intron		
FUS-206	13 .. 11,465	11,453 bp	prim_transcript
/note	= primary transcript ENST00000487509 Retained intron		
FUS-210	14 .. 11,438	11,425 bp	prim_transcript
/note	= primary transcript ENST00000568685		
FUS-201	78 .. 11,301	11,224 bp	CDS
▶ 15 segments = 1581 bp			
/note	= coding sequence ENSP00000254108		
/translation	= MASN,,DYTQATQS,,YGAYPTQPGQYSQQSSQPYGQQSYSGYSQSTDTSGYGQSSYSSYGQSQN,,TGYGTQSTPQGYGSTGGYGSSQSSQSSYGYGQQPAPSSTSGS,,YGSSSQSSSYGQPQSGSYSQQPSYGGQQQSYGQQQSYNPPQGYGQQNQYNSSSGGGGGGGG,,GNYGQDQSSMSSGGSGGGYGNQDQSGGGSGGYGQQDRGGRGRGSGGGGGGGGGGYNRSGGYEPRGRGGRGRGGMG,,GSDRGGFNKFG,,GPRDQGSRHDS,,EQDNSDNTIFVQGLGENVTIESVADYFKQIGIIK,,TNKKTGQPMINLYTDRETGKLGKGEATVSFDDPPSAKAAIDWFD,,GKEFSGNPIKVSFATRRADFNRGGNGRGRGRG,,GPMGRGGYGGGSGGGGRGFPSSGGGGGQQRAGDWKCPNP,,TCENMNFWRNECNQCKAPKPDGPGGGPGGSHM,,GGNYGDDRRGRGGYDRGGYRGRGDRGGFRGGRGGDRGGFGPKMDSR,,GEHRQDRRERPY* 526 amino acids = 53.4 kDa		
FUS-202	78 .. 11,301	11,224 bp	CDS
▶ 15 segments = 1578 bp			
/note	= coding sequence ENSP00000369594		
/translation	= MASN,,DYTQATQS,,YGAYPTQPGQYSQQSSQPYGQQSYSGYSQSTDTSGYGQSSYSSYGQSQN,,SYGTQSTPQGYGSTGGYGSSQSSQSSYGYGQQPAPSSTSGS,,YGSSSQSSSYGQPQSGSYSQQPSYGGQQQSYGQQQSYNPPQGYGQQNQYNSSSGGGGGGGG,,GNYGQDQSSMSSGGSGGGYGNQDQSGGGSGGYGQQDRGGRGRGSGGGGGGGGGGYNRSGGYEPRGRGGRGRGGMG,,GSDRGGFNKFG,,GPRDQGSRHDS,,EQDNSDNTIFVQGLGENVTIESVADYFKQIGIIK,,TNKKTGQPMINLYTDRETGKLGKGEATVSFDDPPSAKAAIDWFD,,GKEFSGNPIKVSFATRRADFNRGGNGRGRGRG,,GPMGRGGYGGGSGGGGRGFPSSGGGGGQQRAGDWKCPNP,,TCENMNFWRNECNQCKAPKPDGPGGGPGGSHM,,GGNYGDDRRGRGGYDRGGYRGRGDRGGFRGGRGGDRGGFGPKMDSR,,GEHRQDRRERPY* 525 amino acids = 53.4 kDa		
FUS-210	78 .. 11,301	11,224 bp	CDS
▶ 15 segments = 1584 bp			
/note	= coding sequence ENSP00000455282		
/translation	= MASN,,DYTQATQS,,YGAYPTQPGQYSQQSSQPYGQQSYSGYSQSTDTSGYGQSSYSSYGQSQN,,TGYGTQSTPQGYGSTGGYGSSQSSQSSYGYGQQPAPSSTSGS,,YGSSSQSSSYGQPQSGSYSQQPSYGGQQQSYGQQQSYNPPQGYGQQNQYNSSSGGGGGGGG,,GNYGQDQSSMSSGGSGGGYGNQDQSGGGSGGYGQQDRGGRGRGSGGGGGGGGGGYNRSGGYEPRGRGGRGRGGMG,,GSDRGGFNKFG,,GPRDQGSRHDS,,AEQDNSDNTIFVQGLGENVTIESVADYFKQIGIIK,,TNKKTGQPMINLYTDRETGKLGKGEATVSFDDPPSAKAAIDWFD,,GKEFSGNPIKVSFATRRADFNRGGNGRGRGRG,,GPMGRGGYGGGSGGGGRGFPSSGGGGGQQRAGDWKCPNP,,TCENMNFWRNECNQCKAPKPDGPGGGPGGSHM,,GGNYGDDRRGRGGYDRGGYRGRGDRGGFRGGRGGDRGGFGPKMDSR,,GEHRQDRRERPY* 527 amino acids = 53.5 kDa		
	2374 .. 3148	775 bp	gene
/note	= gene ENSG00000260304 lncRNA		
	2374 .. 3148	775 bp	prim_transcript
/note	= primary transcript ENST00000564743 lncRNA		
FUS-207	3413 .. 4261	849 bp	prim_transcript
/note	= primary transcript ENST00000487974 Retained intron		
Donor Template WT -> SNV	4891 .. 4957	67 bp	misc_feature
Protospacer Sequence	4906 .. 4925	20 bp	misc_feature
SNV	4924 .. 4924	1 bp	misc_feature
/note	= WT=C SNV=T		
PAM	4926 .. 4928	3 bp	misc_feature
FUS-213	4943 .. 7108	2166 bp	prim_transcript
/note	= primary transcript ENST00000570090 Retained intron		
FUS-203	5362 .. 10,965	5604 bp	prim_transcript
/note	= primary transcript ENST00000474990		
FUS-211	8015 .. 9983	1969 bp	prim_transcript
/note	= primary transcript ENST00000568901 Retained intron		
FUS-208	8330 .. 9558	1229 bp	prim_transcript
/note	= primary transcript ENST00000564766 Retained intron		
FUS-212	10,079 .. 11,468	1390 bp	prim_transcript
/note	= primary transcript ENST00000569760 Retained intron		
FUS-204	10,236 .. 11,421	1186 bp	prim_transcript
/note	= primary transcript ENST00000483853 Retained intron		

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