

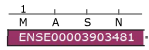
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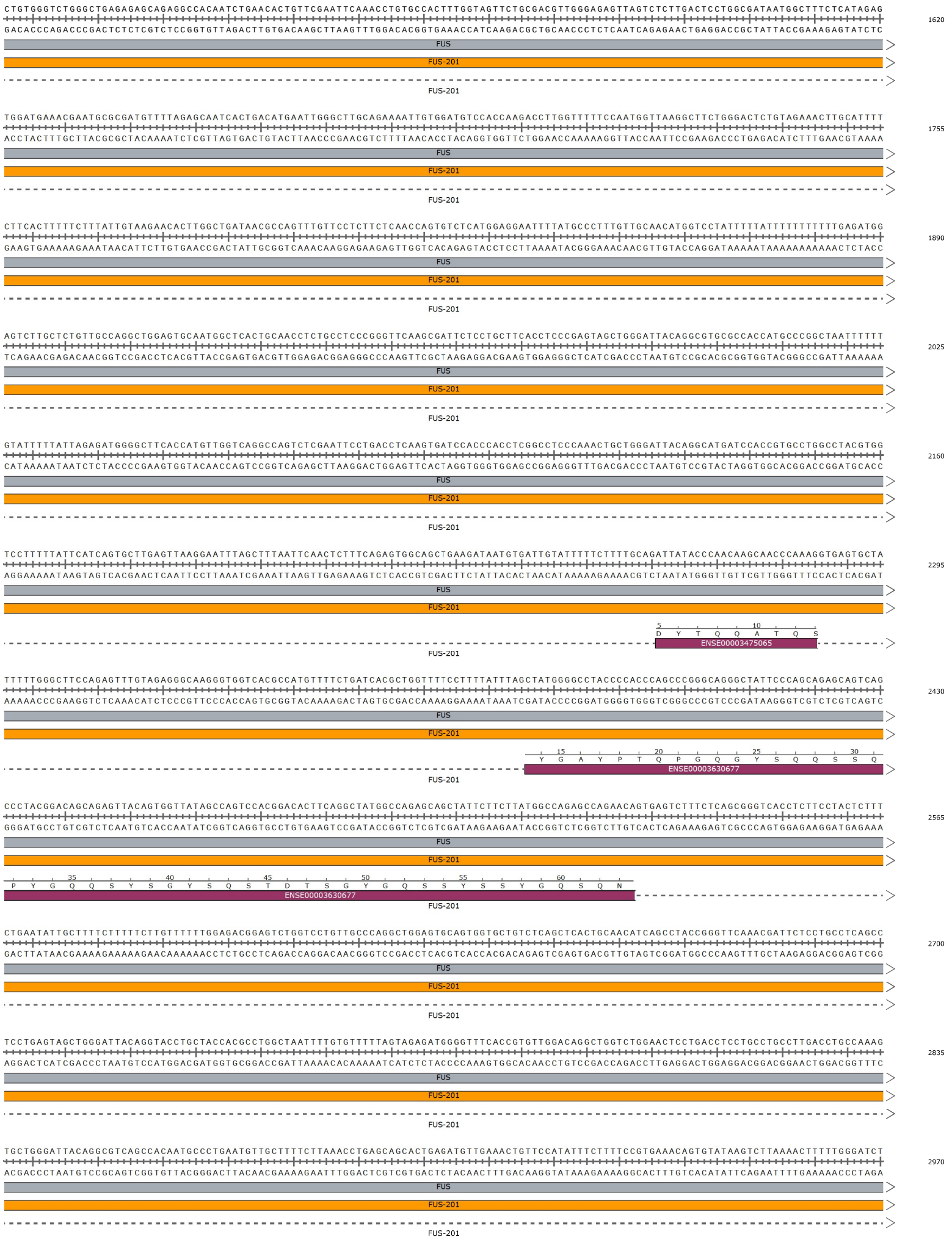
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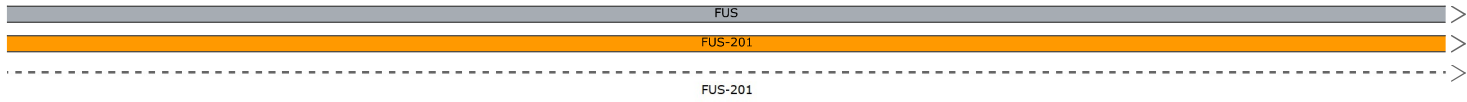
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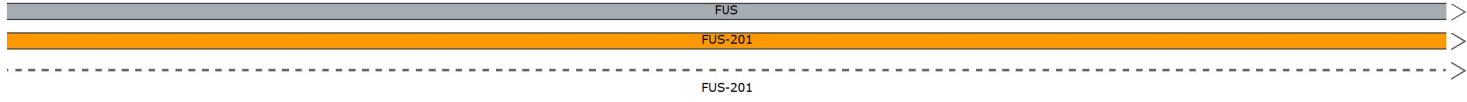
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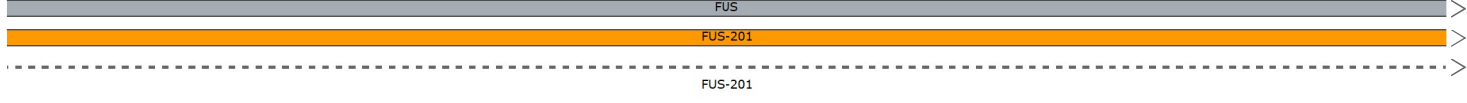
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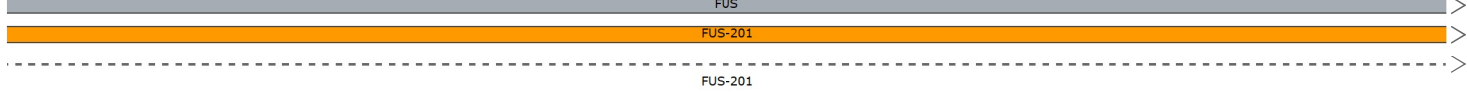
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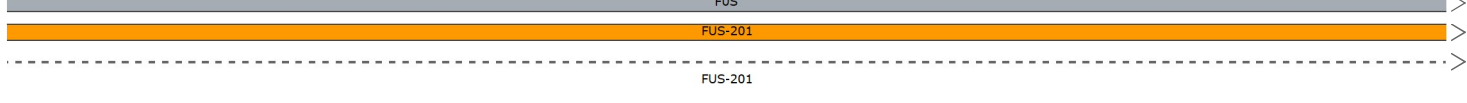
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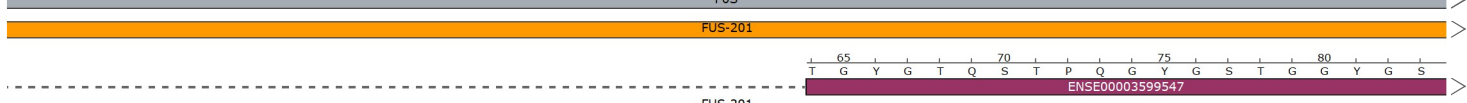
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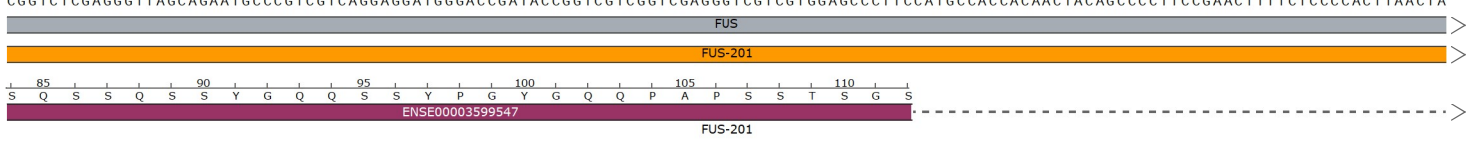
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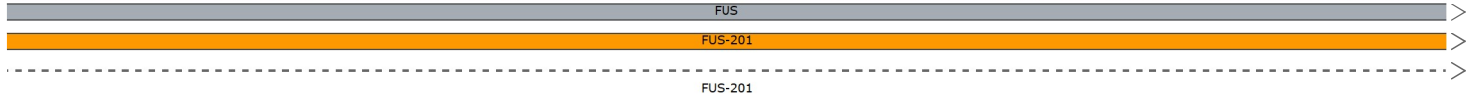
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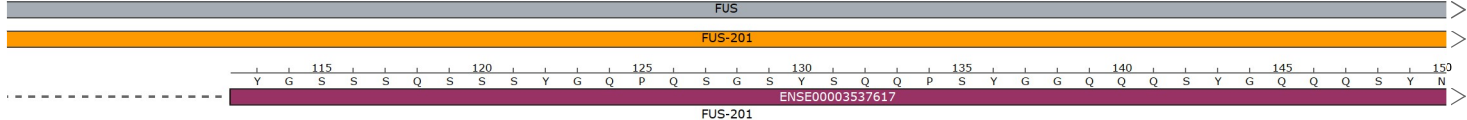
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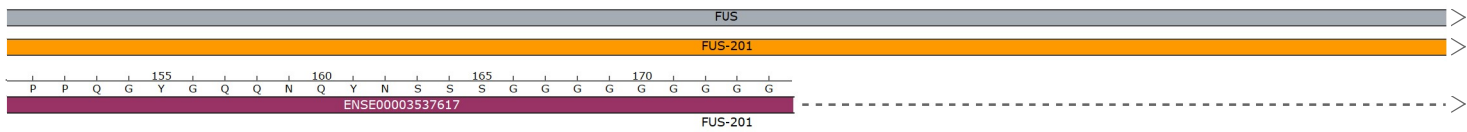
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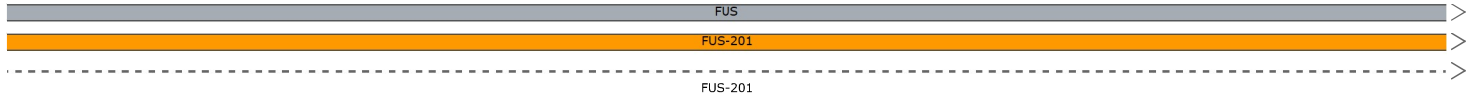
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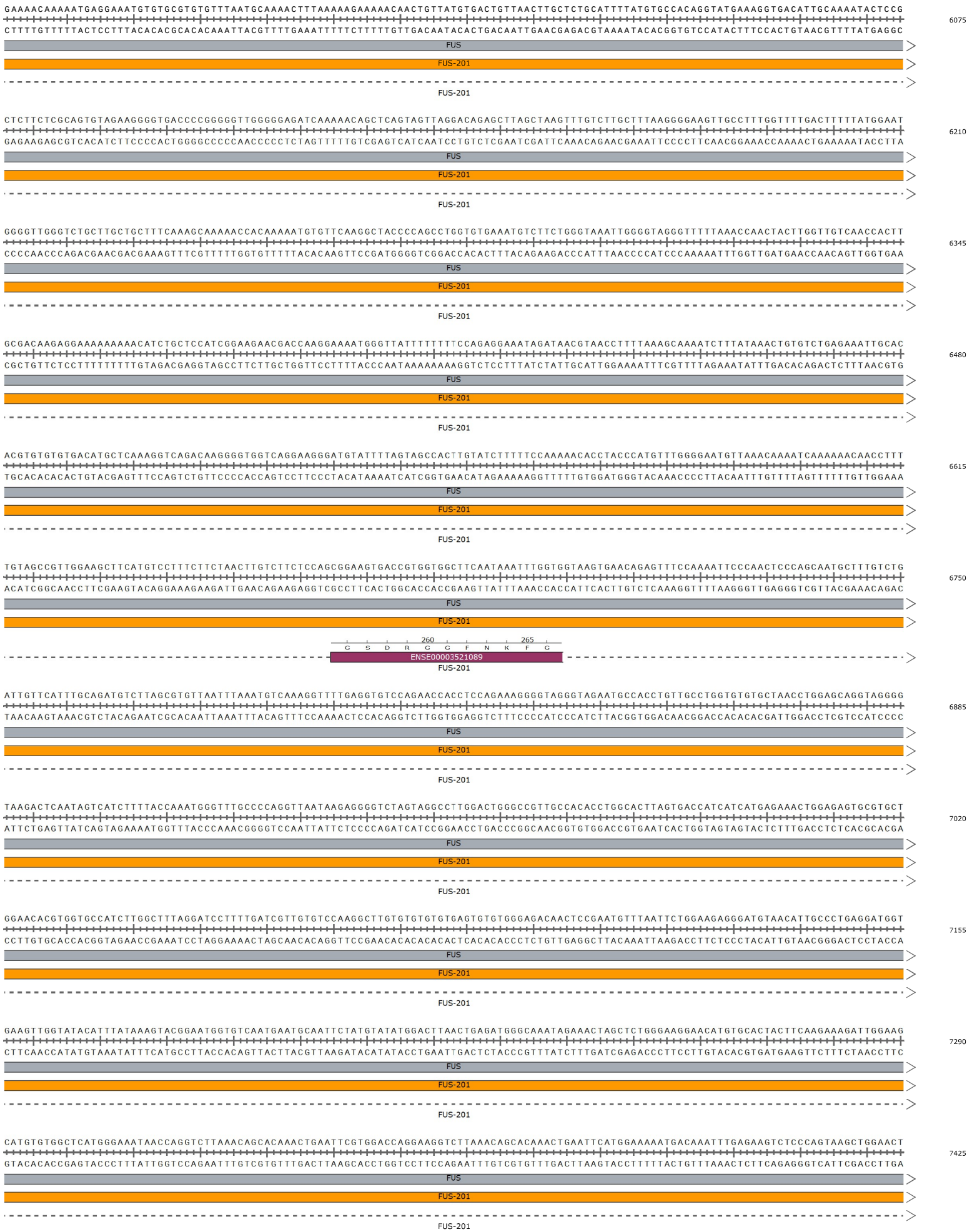
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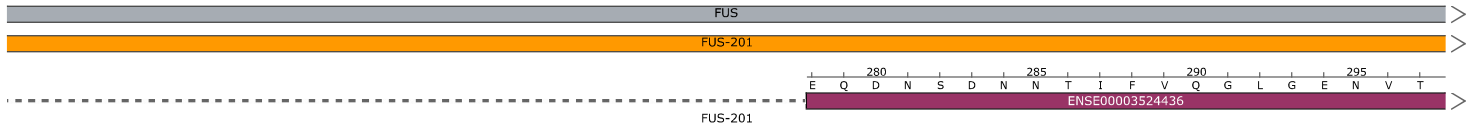
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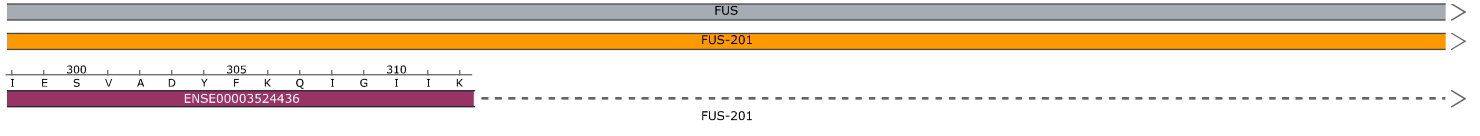
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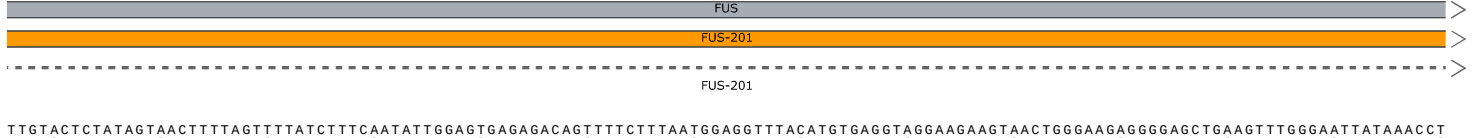
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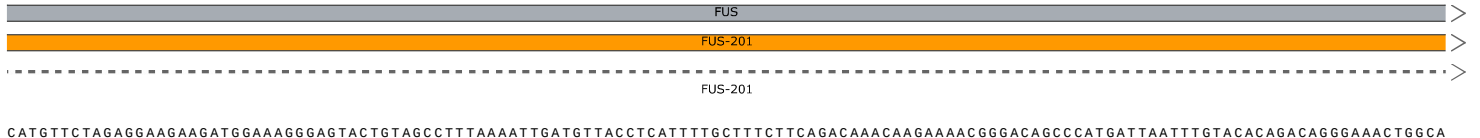
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9315



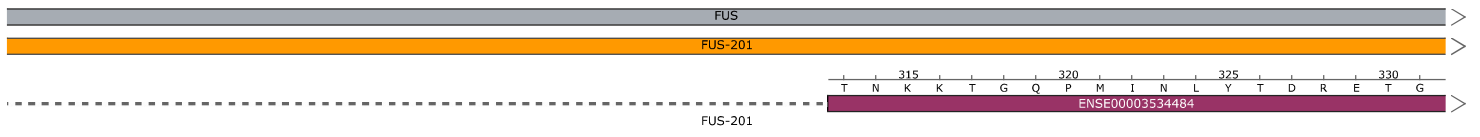
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9450



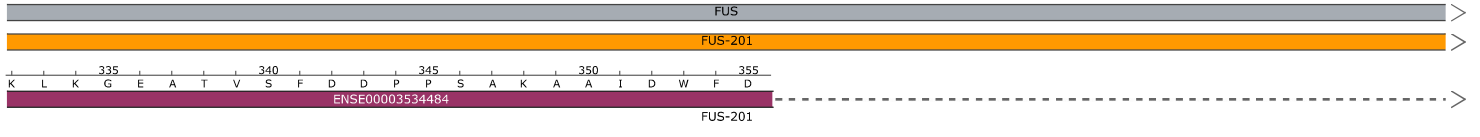
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9585



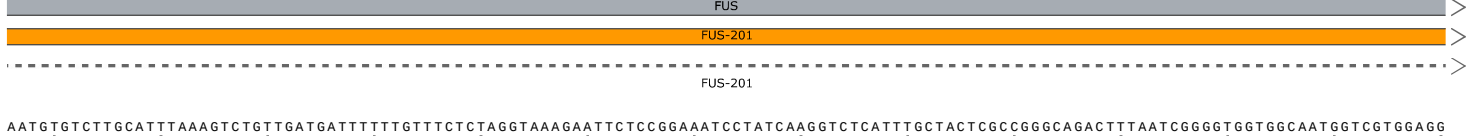
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TCGACTTCCCTCTCCGTTGCCAGAGAAAACCTACTGGGTGGAAGTCGATTTGTCGATAAAGTACGACAAACTACCATACATACTCTTCCGACCGTCTCCACCCGACCCCTATATCCCGTCTGTCGGAATCCTTTGT

9720



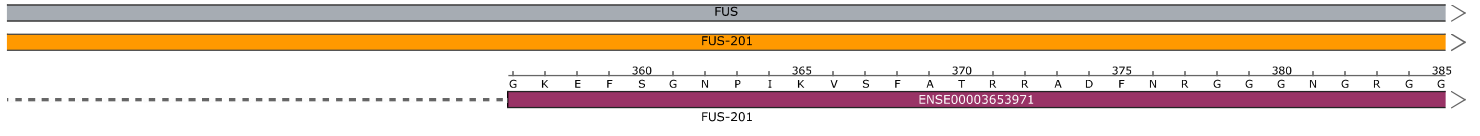
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9855



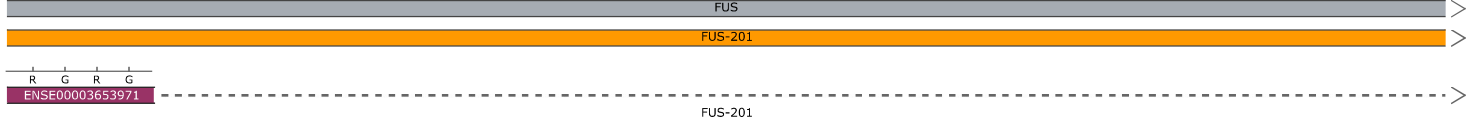
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9990



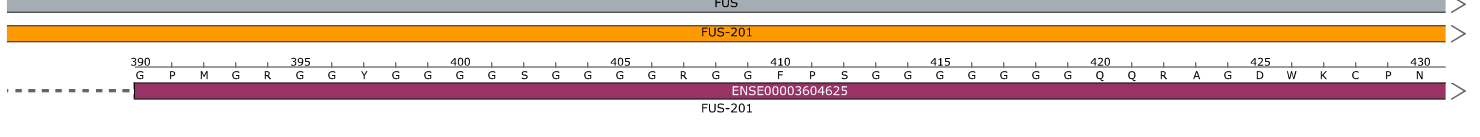
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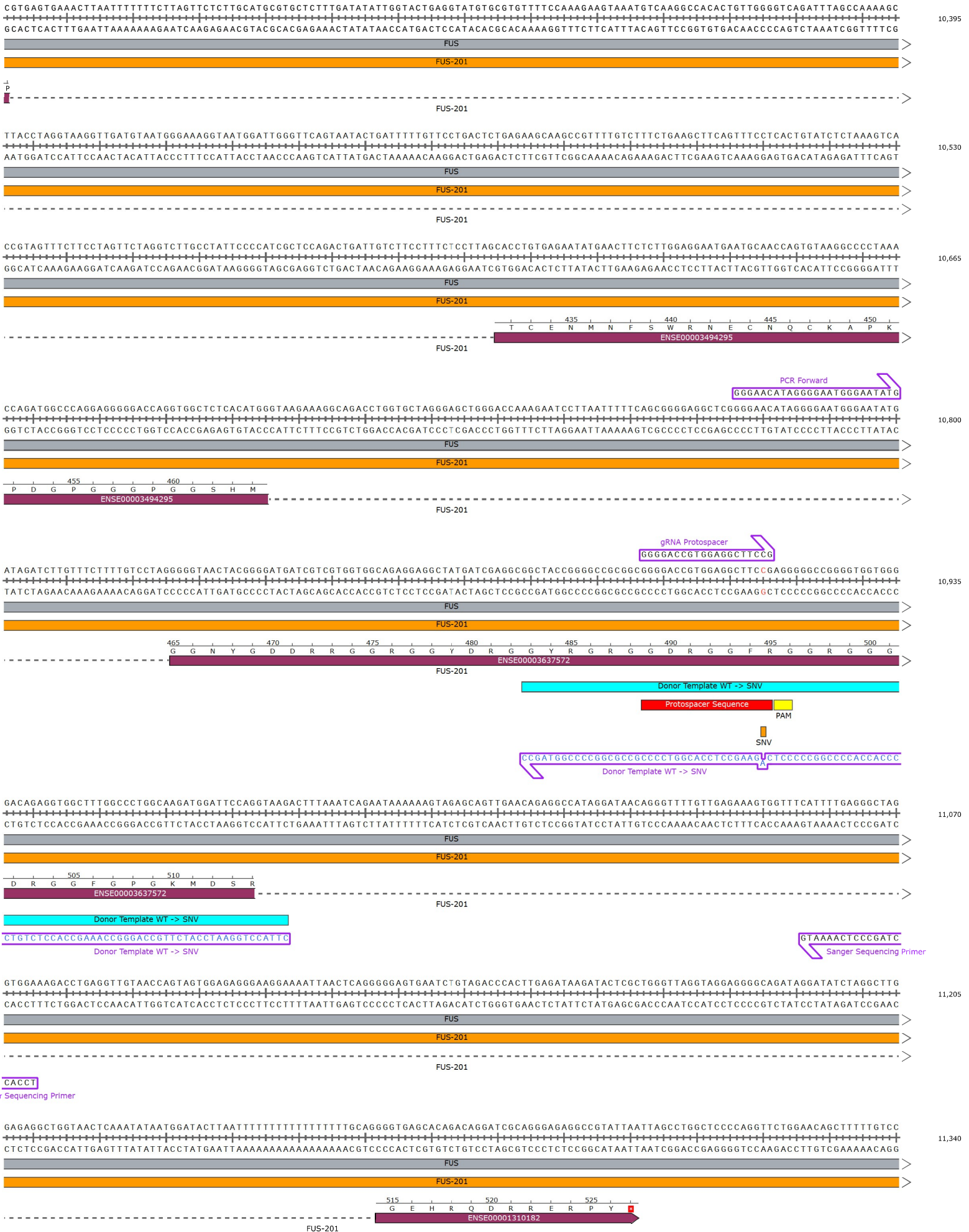
10,125



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10,260





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ACATGGGTCACAATGGGAGCAATAAACATTGGAAGGTTAAGGACTAGTGGGTTCCCAAAAAACACAGCCTGATACATTAACTTGATATGGAGACCAAGGGTAATTTCACTGGTAAATCAATTT

3'
11,468
5'

FUS

FUS-201

GAGACCAAGGGTAATTTCACTGGT

PCR Reverse

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,,YGAYPTQPGQGYSSQSSQPYGQQSYSGYSQSTDTSGYGQSSYSSYGQSQN,,TGYGTQSTPQGYGSTGGYGSSQSSQSSYGYGQQPAPSSSTSGS,,YGSSSQSSSYGQPQSGSYSQQPSYGGQQQSYGQQQSYNPPQGYGQQNQYNSSSGGGGGGGG,,GNYGQDQSSMSSGGSGGGYGNQDQSGGGSGGYGQDRGGRGRGSGGGGGGGGGGYNRSSGGYEPGRGGGRGGGGMG,,GSDRGGFNKFG,,GPRDQGSRHDS,,EQDNSDNTIFVQGLGENVTIESVADYFKQIGIIK,,TNKKTGQPMINLYTDRETGKLGKGEATVSFDDPPSAKAAIDWFD,,GKEFSGNPIKVSFATRRADFNRRGGNGRGGGRG,,GPMGRGGYGGGSGGGGRGFPSSGGGGGQQRAGDWKCPNP,,TCENMNFWRNECNQCKAPKPDGPGGGPGGSHM,,GGNYGDDRRRGGGYDRGGYRGGDRGGFRGGGGDRGGFGPKMDSR,,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,,YGAYPTQPGQGYSSQSSQPYGQQSYSGYSQSTDTSGYGQSSYSSYGQSQN,,SYGTQSTPQGYGSTGGYGSSQSSQSSYGYGQQPAPSSSTSGS,,YGSSSQSSSYGQPQSGSYSQQPSYGGQQQSYGQQQSYNPPQGYGQQNQYNSSSGGGGGGGG,,GNYGQDQSSMSSGGSGGGYGNQDQSGGGSGGYGQDRGGRGRGSGGGGGGGGGGYNRSSGGYEPGRGGGRGGGGMG,,GSDRGGFNKFG,,GPRDQGSRHDS,,EQDNSDNTIFVQGLGENVTIESVADYFKQIGIIK,,TNKKTGQPMINLYTDRETGKLGKGEATVSFDDPPSAKAAIDWFD,,GKEFSGNPIKVSFATRRADFNRRGGNGRGGGRG,,GPMGRGGYGGGSGGGGRGFPSSGGGGGQQRAGDWKCPNP,,TCENMNFWRNECNQCKAPKPDGPGGGPGGSHM,,GGNYGDDRRRGGGYDRGGYRGGDRGGFRGGGGDRGGFGPKMDSR,,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,,YGAYPTQPGQGYSSQSSQPYGQQSYSGYSQSTDTSGYGQSSYSSYGQSQN,,TGYGTQSTPQGYGSTGGYGSSQSSQSSYGYGQQPAPSSSTSGS,,YGSSSQSSSYGQPQSGSYSQQPSYGGQQQSYGQQQSYNPPQGYGQQNQYNSSSGGGGGGGG,,GNYGQDQSSMSSGGSGGGYGNQDQSGGGSGGYGQDRGGRGRGSGGGGGGGGGGYNRSSGGYEPGRGGGRGGGGMG,,GSDRGGFNKFG,,GPRDQGSRHDS,,AEQDNSDNTIFVQGLGENVTIESVADYFKQIGIIK,,TNKKTGQPMINLYTDRETGKLGKGEATVSFDDPPSAKAAIDWFD,,GKEFSGNPIKVSFATRRADFNRRGGNGRGGGRG,,GPMGRGGYGGGSGGGGRGFPSSGGGGGQQRAGDWKCPNP,,TCENMNFWRNECNQCKAPKPDGPGGGPGGSHM,,GGNYGDDRRRGGGYDRGGYRGGDRGGFRGGGGDRGGFGPKMDSR,,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		
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		
Donor Template WT -> SNV	10,879 .. 10,978	100 bp	misc_feature
Protospacer Sequence	10,897 .. 10,916	20 bp	misc_feature
SNV	10,915 .. 10,915	1 bp	misc_feature
/note	= WT = C SNV = T		
PAM	10,917 .. 10,919	3 bp	misc_feature

Primer	Length	Binding Sites	Tm	Date Added
✓ PCR Forward /sequence = GGGAACATAGGGGAATGGGAATATG 48% GC / 7884.2 Da	25-mer	10,776 .. 10,800	→ 58°C	Jun 14, 2022
✓ Donor Template WT -> SNV /sequence = CTTACCTGGAATCCATCTTGCCAGGGCCAAAGCCACCTCTGTCCCCACACCCCGGCCCTCAGAAGCCTCCACGGTCCCGCCGCGGCCCGGTAGCC 70% GC / 30,291.4 Da	100-mer	10,879 .. 10,978	← 86°C	Jun 14, 2022
✓ gRNA Protospacer /sequence = GGGGACCCTGGAGGCTTCCG 75% GC / 6215.1 Da	20-mer	10,897 .. 10,916	→ 65°C	Jun 14, 2022
✓ Sanger Sequencing Primer /sequence = TCCACCTAGCCCTCAAATG 50% GC / 6006.0 Da	20-mer	11,056 .. 11,075	← 56°C	Jun 14, 2022
✓ PCR Reverse /sequence = TGGTCACTTTTAATGGGAACCCAGAG 44% GC / 7721.1 Da	25-mer	11,433 .. 11,457	← 59°C	Jun 14, 2022