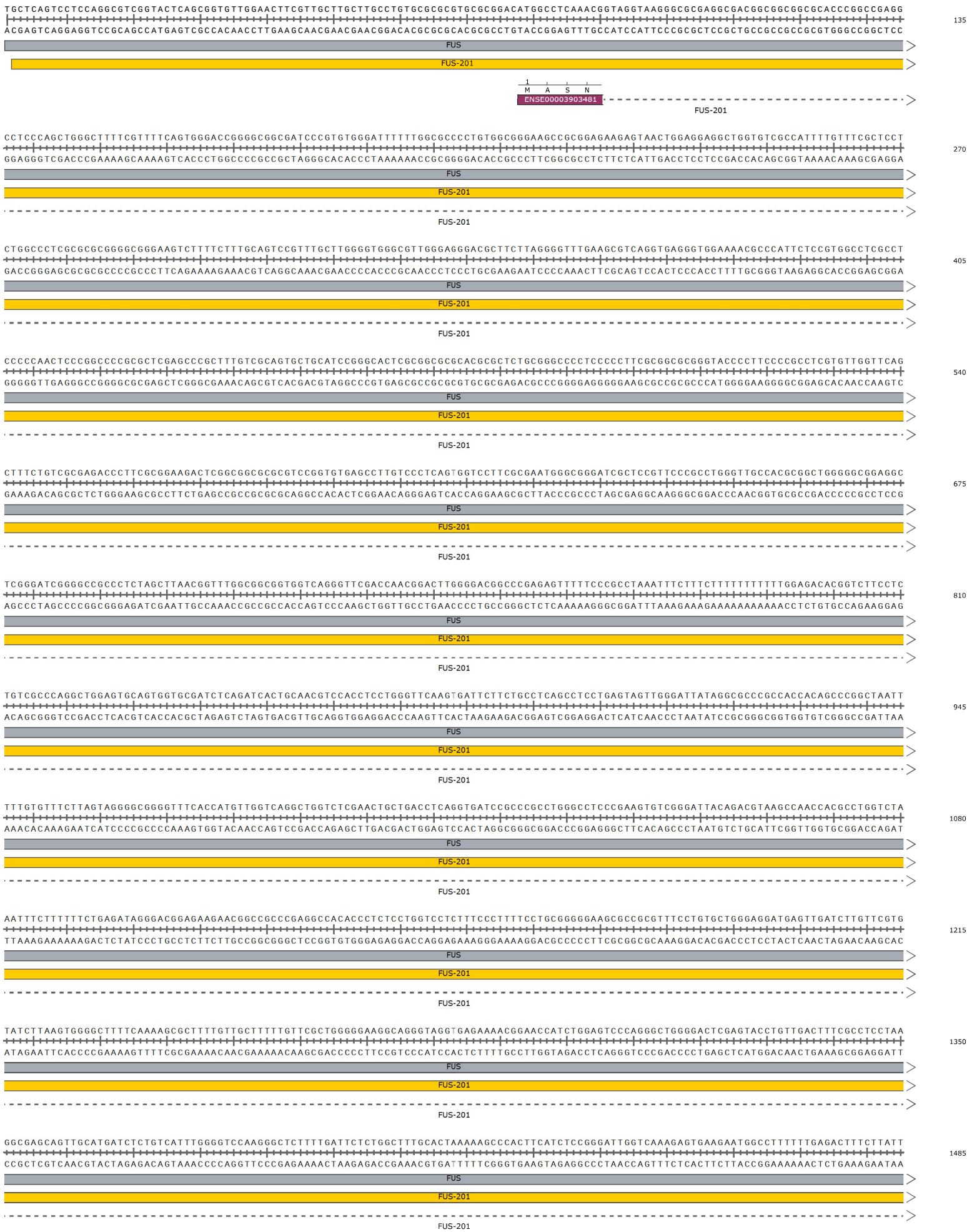


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 11,468 bp



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3105

FUS

FUS-201

FUS-201

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3240

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FUS-201

FUS-201

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3375

FUS

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FUS-201

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3510

FUS

FUS-201

FUS-201

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3645

FUS

FUS-201

FUS-201

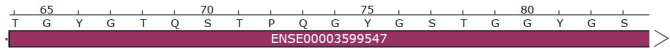
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3780

FUS

FUS-201

FUS-201



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3915

FUS

FUS-201

FUS-201

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4050

FUS

FUS-201

FUS-201

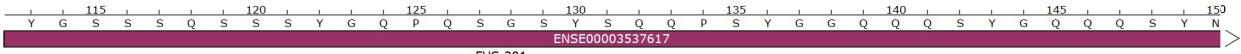
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4185

FUS

FUS-201

FUS-201



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4320

FUS

FUS-201

FUS-201

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4455

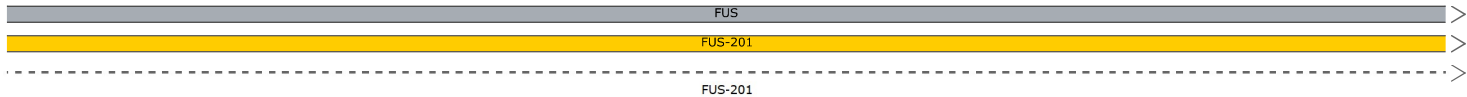
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FUS-201

FUS-201

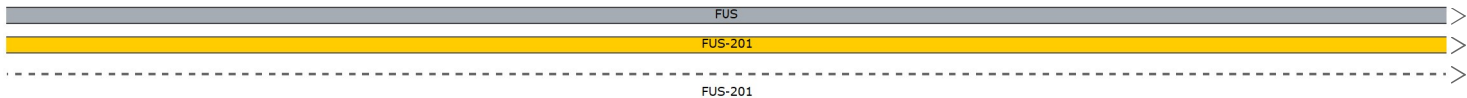
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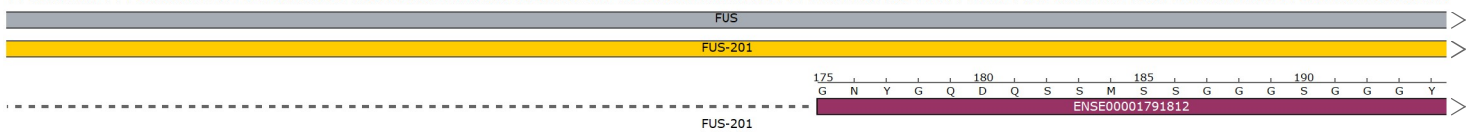
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4725



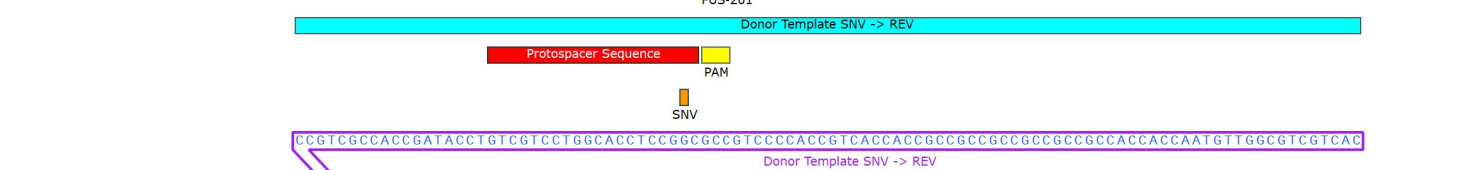
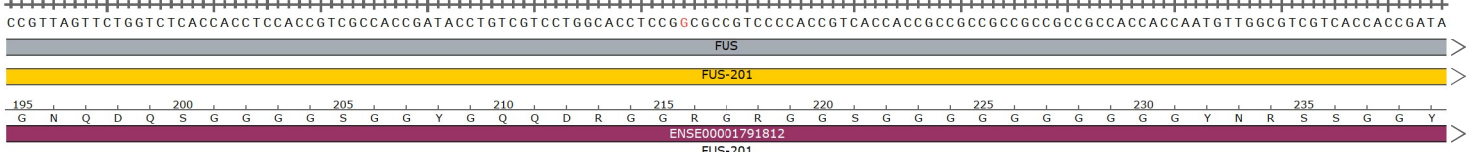
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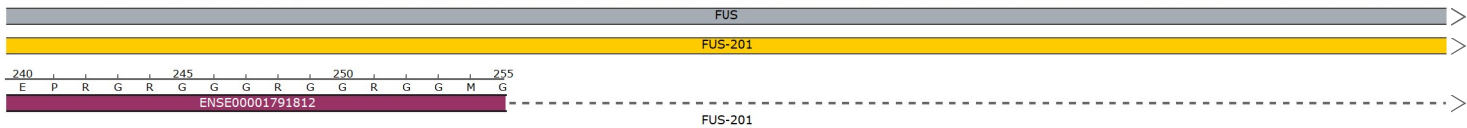
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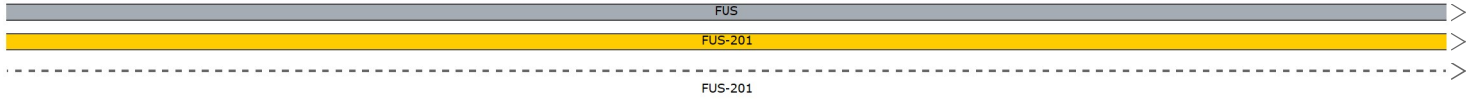
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5130



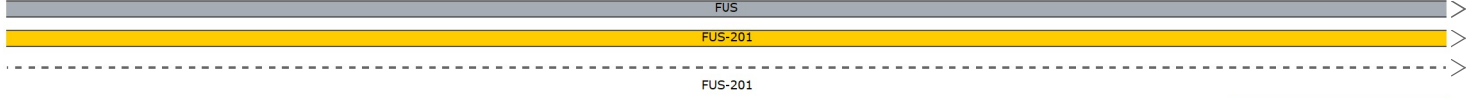
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5265



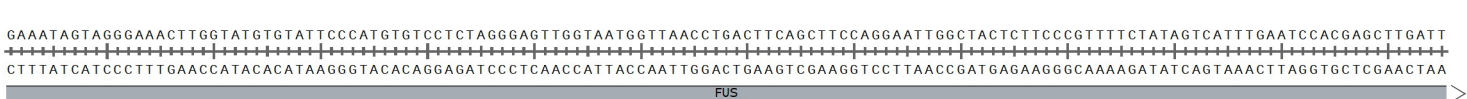
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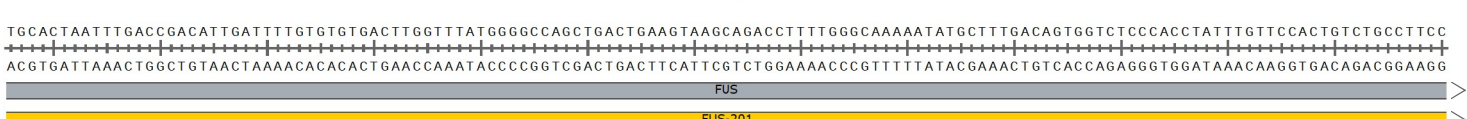
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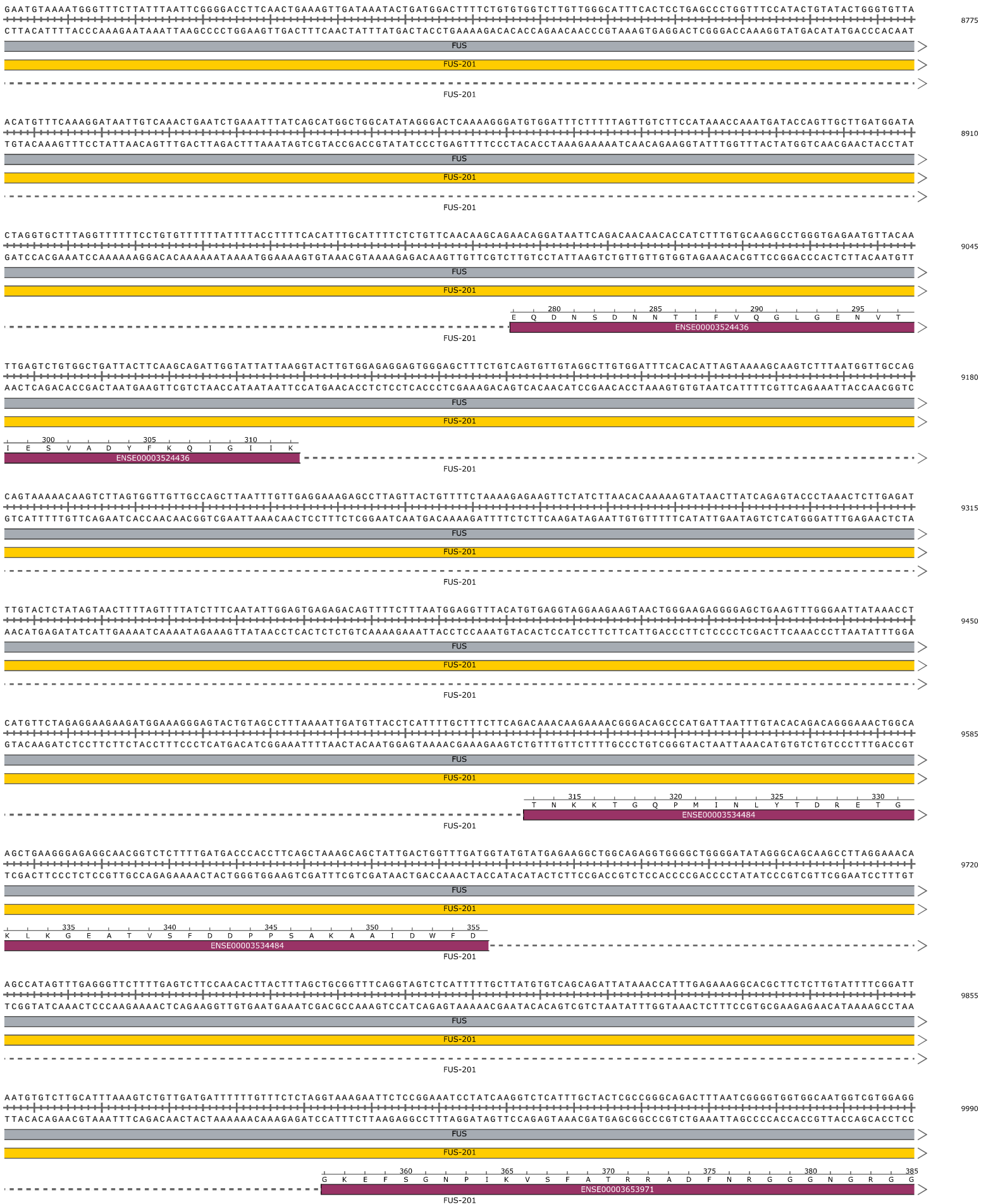
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5670








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3'
11,468
5'

FUS

FUS-201

Feature	Location	Size	Type
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/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
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FUS-206	13 .. 11,465	11,453 bp	prim_transcript
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FUS-210	14 .. 11,438	11,425 bp	prim_transcript
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FUS-201	78 .. 11,301	11,224 bp	CDS
▶ 15 segments = 1581 bp			
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▶ 15 segments = 1578 bp			
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▶ 15 segments = 1584 bp			
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/note	= primary transcript ENST00000564743 lncRNA	2374 .. 3148	775 bp
FUS-207	3413 .. 4261	849 bp	prim_transcript
/note	= primary transcript ENST00000487974 Retained intron		
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Protospacer Sequence	4906 .. 4925	20 bp	misc_feature
SNV	4924 .. 4924	1 bp	misc_feature
/note	= REV=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
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FUS-204	10,236 .. 11,421	1186 bp	prim_transcript
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Primer		Length		Binding Sites		Tm	Date Added
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/sequence	= TGGTGGCGGTTATGGCAATC 55% GC / 6204.1 Da						
✓ Donor Template SNV -> REV		100-mer		4888 .. 4987	←	89°C	Jun 16, 2022
/sequence	= CACTGCTGCGGTTGTAACCACCACCGCCGCCGCCGCCGCCGCCACCACTGCCACCCCTGCCGCGGCCTCCACGGTCCTGCTGTCCATAGCCACCGCTGCC 74% GC / 30,275.4 Da						
✓ gRNA Protospacer		20-mer		4906 .. 4923	↔	61°C	Jun 16, 2022
/sequence	= CAGCAGGACCCTGGAGGCTG 70% GC / 6208.1 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
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