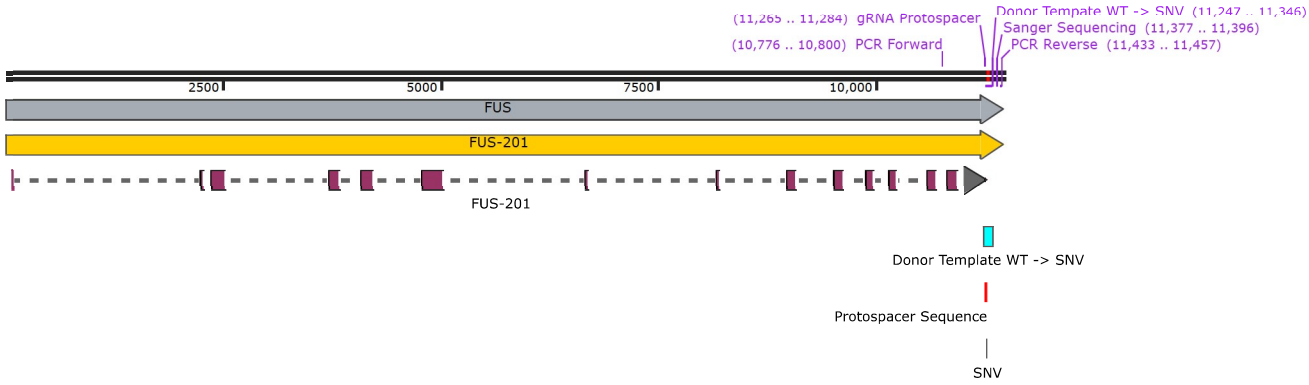
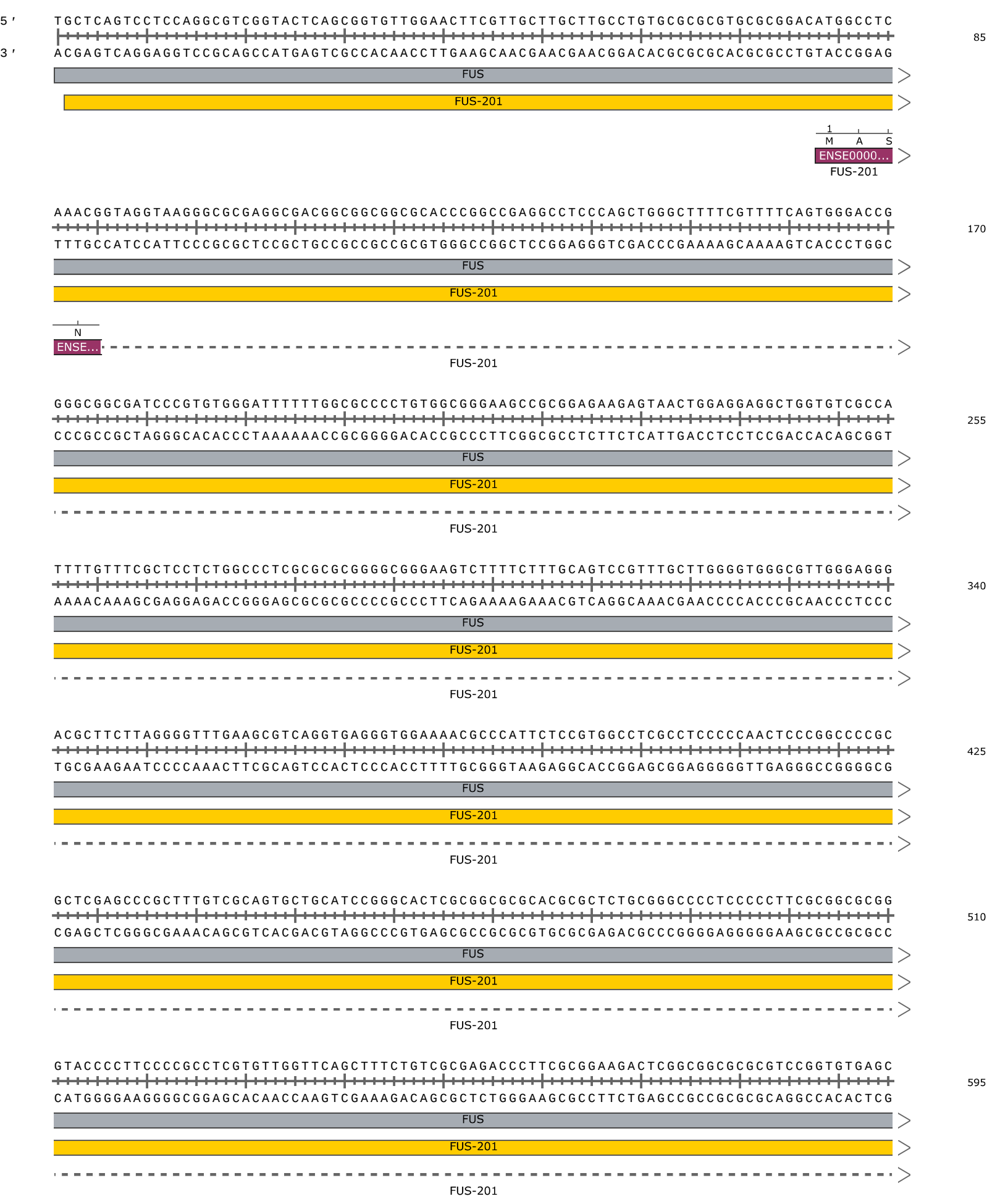
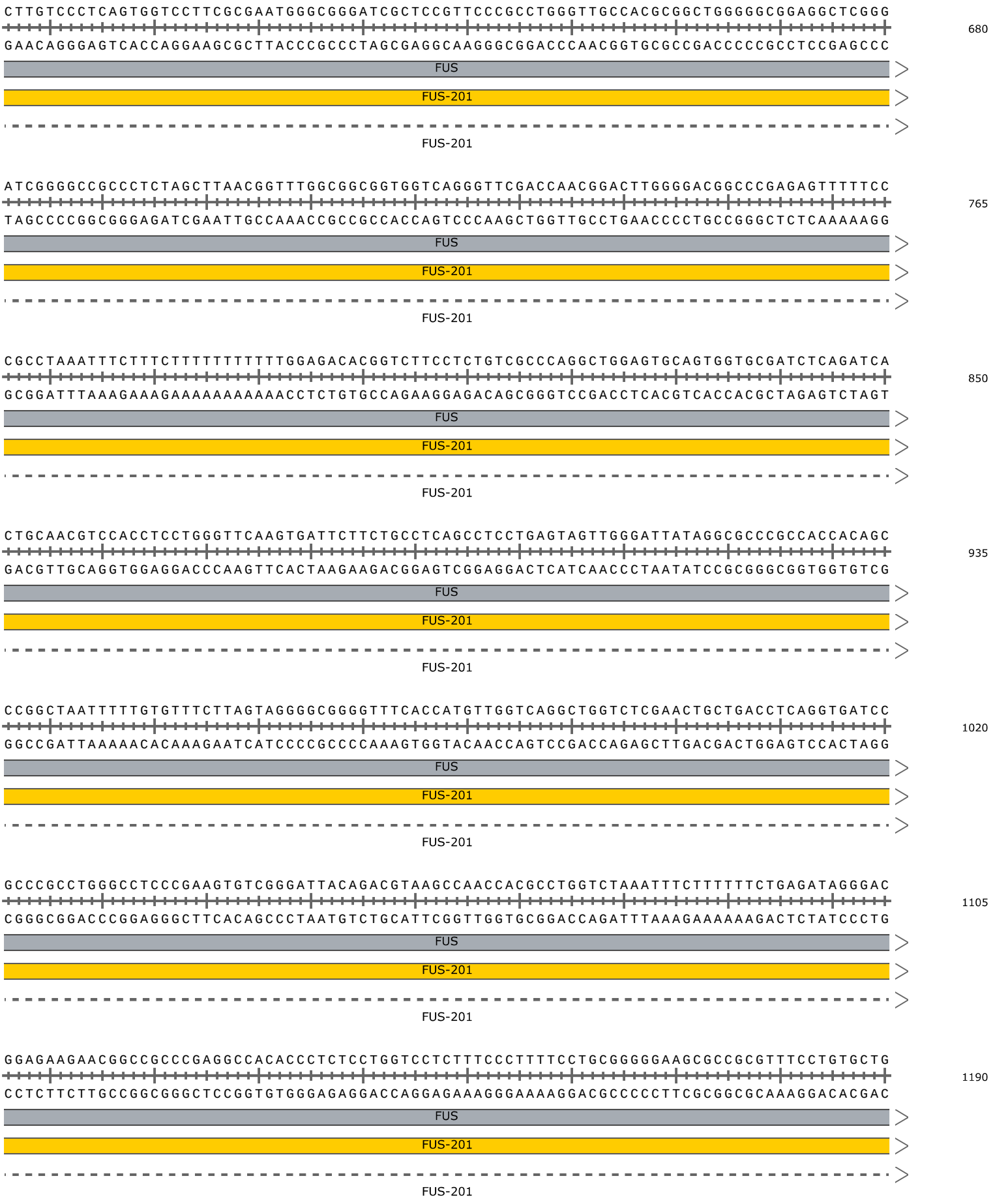
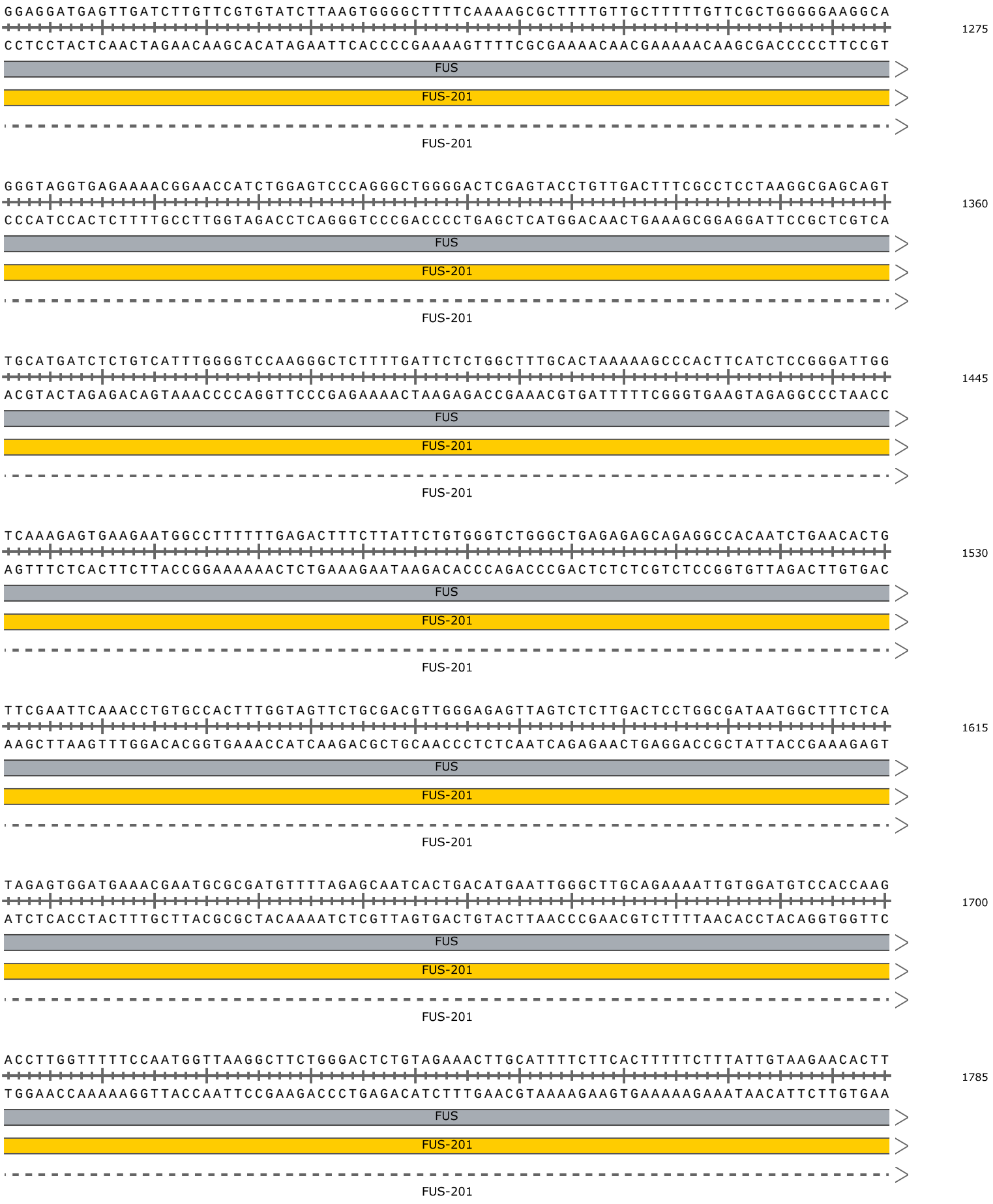


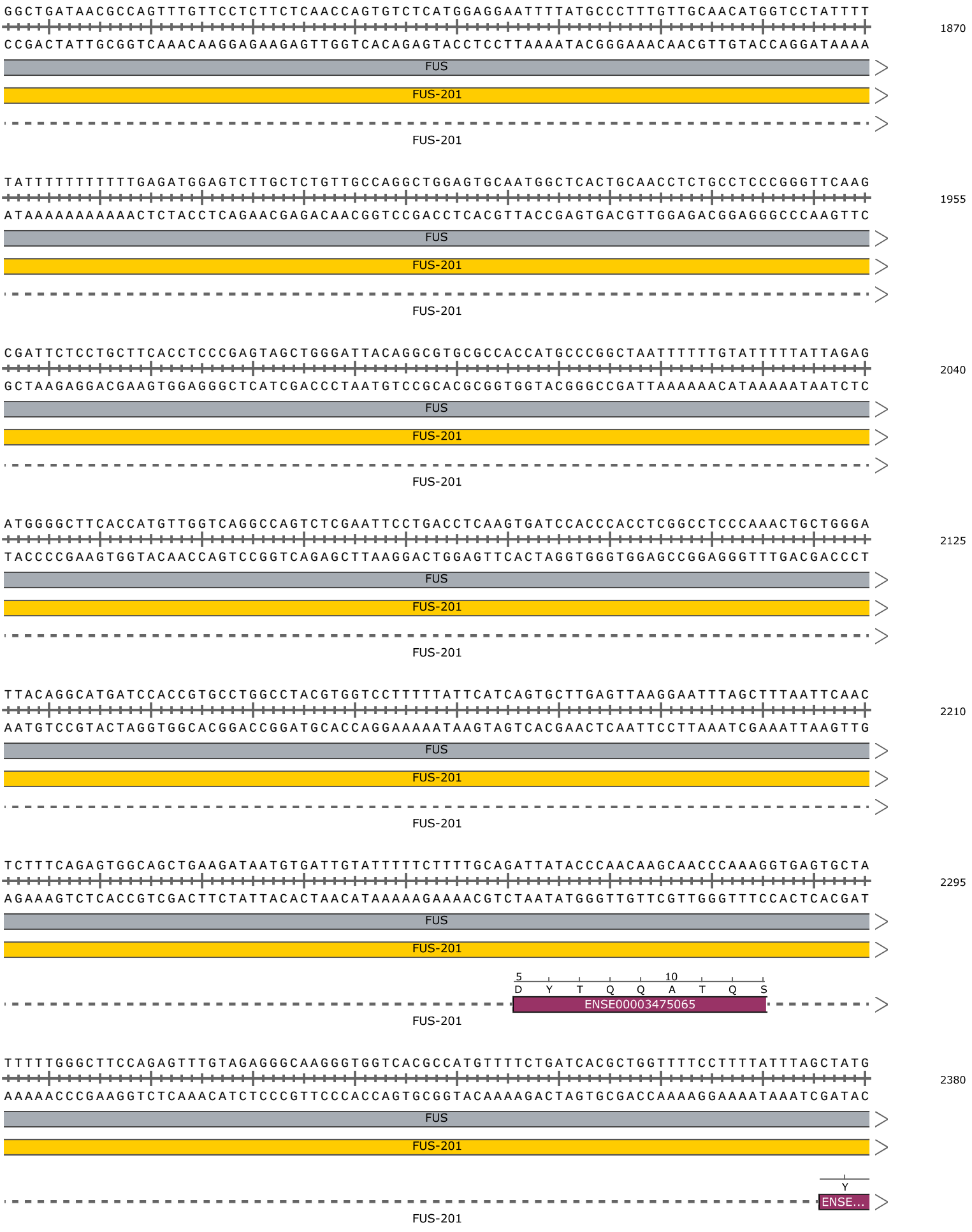

**INK2J00082_FUS_R521H_C12_AB**

11,468 bp

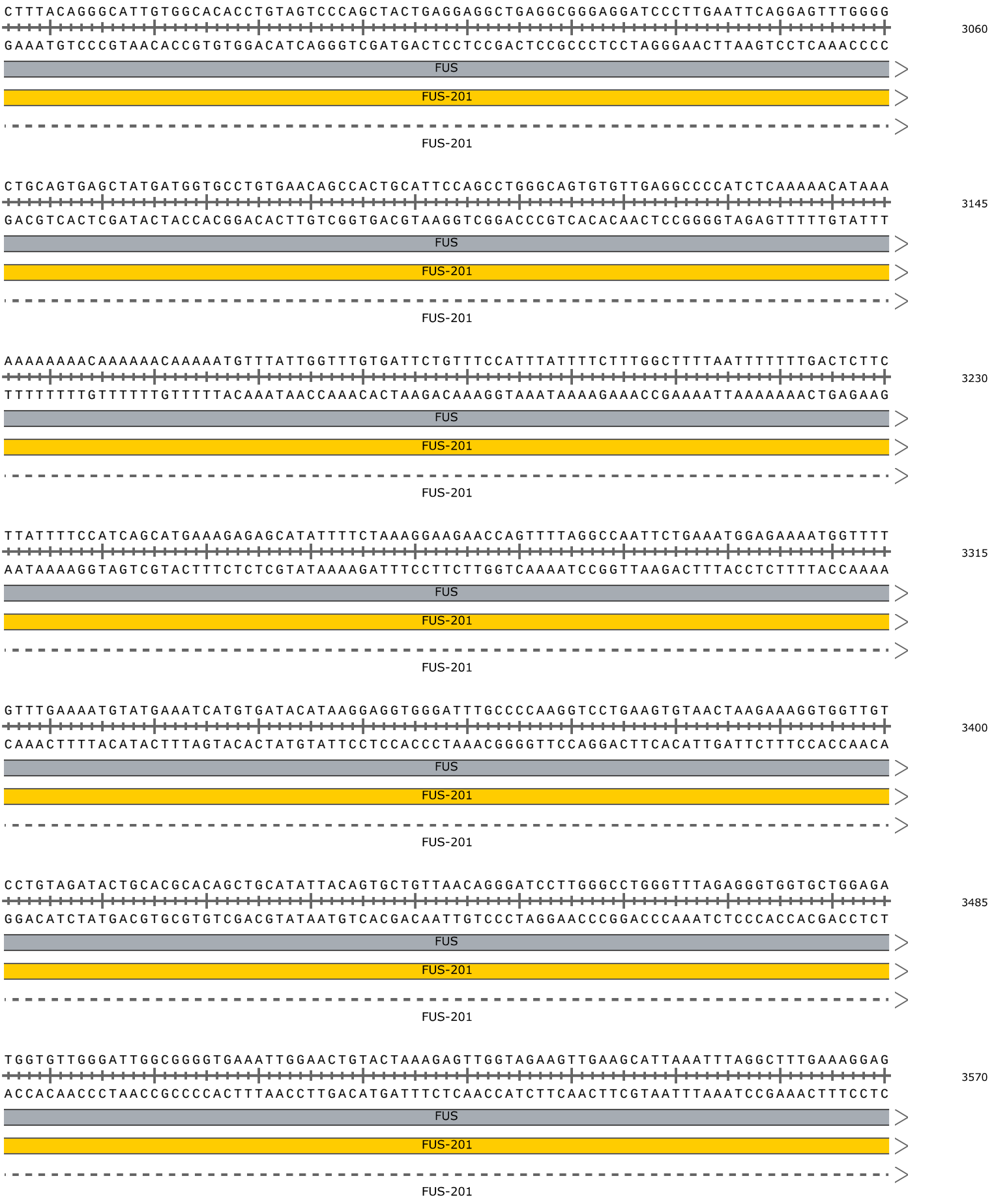

5′
TGCTCAGTCCTCCAGGCGTCGGTACTCAGCGGTGTTGGAACTTCGTTGCTTGCTTGCCTGTGCGCGCGTGCGCGGACATGGCCTC
85
3′
ACGAGTCAGGAGGTCCGCAGCCATGAGTCGCCACAACCTTGAAGCAACGAACGAACGGACACGCGCGCACGCGCCTGTACCGGAG
FUS
FUS-201
1
M
A
S
ENSE0000...
FUS-201
AAACGGTAGGTAAGGGCGCGAGGCGACGGCGGCGGCGCACCCGGCCGAGGCCTCCCAGCTGGGCTTTTCGTTTTCAGTGGGACCG
170
TTTGCCATCCATTCCCGCGCTCCGCTGCCGCCGCCGCGTGGGCCGGCTCCGGAGGGTCGACCCGAAAAGCAAAAGTCACCCTGGC
FUS
FUS-201
N
ENSE...
FUS-201
GGGCGGCGATCCCGTGTGGGATTTTTTGGCGCCCCTGTGGCGGGAAGCCGCGGAGAAGAGTAACTGGAGGAGGCTGGTGTCGCCA
255
CCCGCCGCTAGGGCACACCCTAAAAAACCGCGGGGACACCGCCCTTCGGCGCCTCTTCTCATTGACCTCCTCCGACCACAGCGGT
FUS
FUS-201
FUS-201
TTTTGTTTCGCTCCTCTGGCCCTCGCGCGCGGGGCGGGAAGTCTTTTCTTTGCAGTCCGTTTGCTTGGGGTGGGCGTTGGGAGGG
340
AAAACAAAGCGAGGAGACCGGGAGCGCGCGCCCCGCCCTTCAGAAAAGAAACGTCAGGCAAACGAACCCCACCCGCAACCCTCCC
FUS
FUS-201
FUS-201
ACGCTTCTTAGGGGTTTGAAGCGTCAGGTGAGGGTGGAAAACGCCCATTCTCCGTGGCCTCGCCTCCCCCAACTCCCGGCCCCGC
425
TGCGAAGAATCCCCAAACTTCGCAGTCCACTCCCACCTTTTGCGGGTAAGAGGCACCGGAGCGGAGGGGGTTGAGGGCCGGGGCG
FUS
FUS-201
FUS-201
GCTCGAGCCCGCTTTGTCGCAGTGCTGCATCCGGGCACTCGCGGCGCGCACGCGCTCTGCGGGCCCCTCCCCCTTCGCGGCGCGG
510
CGAGCTCGGGCGAAACAGCGTCACGACGTAGGCCCGTGAGCGCCGCGCGTGCGCGAGACGCCCGGGGAGGGGGAAGCGCCGCGCC
FUS
FUS-201
FUS-201
GTACCCCTTCCCCGCCTCGTGTTGGTTCAGCTTTCTGTCGCGAGACCCTTCGCGGAAGACTCGGCGGCGCGCGTCCGGTGTGAGC
595
CATGGGGAAGGGGCGGAGCACAACCAAGTCGAAAGACAGCGCTCTGGGAAGCGCCTTCTGAGCCGCCGCGCGCAGGCCACACTCG
FUS
FUS-201
FUS-201


CTTGTCCCTCAGTGGTCCTTCGCGAATGGGCGGGATCGCTCCGTTCCCGCCTGGGTTGCCACGCGGCTGGGGGCGGAGGCTCGGG
680
GAACAGGGAGTCACCAGGAAGCGCTTACCCGCCCTAGCGAGGCAAGGGCGGACCCAACGGTGCGCCGACCCCCGCCTCCGAGCCC
FUS
FUS-201
FUS-201
ATCGGGGCCGCCCTCTAGCTTAACGGTTTGGCGGCGGTGGTCAGGGTTCGACCAACGGACTTGGGGACGGCCCGAGAGTTTTTCC
765
TAGCCCCGGCGGGAGATCGAATTGCCAAACCGCCGCCACCAGTCCCAAGCTGGTTGCCTGAACCCCTGCCGGGCTCTCAAAAAGG
FUS
FUS-201
FUS-201
CGCCTAAATTTCTTTCTTTTTTTTTTTGGAGACACGGTCTTCCTCTGTCGCCCAGGCTGGAGTGCAGTGGTGCGATCTCAGATCA
850
GCGGATTTAAAGAAAGAAAAAAAAAAACCTCTGTGCCAGAAGGAGACAGCGGGTCCGACCTCACGTCACCACGCTAGAGTCTAGT
FUS
FUS-201
FUS-201
CTGCAACGTCCACCTCCTGGGTTCAAGTGATTCTTCTGCCTCAGCCTCCTGAGTAGTTGGGATTATAGGCGCCCGCCACCACAGC
935
GACGTTGCAGGTGGAGGACCCAAGTTCACTAAGAAGACGGAGTCGGAGGACTCATCAACCCTAATATCCGCGGGCGGTGGTGTCG
FUS
FUS-201
FUS-201
CCGGCTAATTTTTGTGTTTCTTAGTAGGGGCGGGGTTTCACCATGTTGGTCAGGCTGGTCTCGAACTGCTGACCTCAGGTGATCC
1020
GGCCGATTAAAAACACAAAGAATCATCCCCGCCCCAAAGTGGTACAACCAGTCCGACCAGAGCTTGACGACTGGAGTCCACTAGG
FUS
FUS-201
FUS-201
GCCCGCCTGGGCCTCCCGAAGTGTCGGGATTACAGACGTAAGCCAACCACGCCTGGTCTAAATTTCTTTTTTCTGAGATAGGGAC
1105
CGGGCGGACCCGGAGGGCTTCACAGCCCTAATGTCTGCATTCGGTTGGTGCGGACCAGATTTAAAGAAAAAAGACTCTATCCCTG
FUS
FUS-201
FUS-201
GGAGAAGAACGGCCGCCCGAGGCCACACCCTCTCCTGGTCCTCTTTCCCTTTTCCTGCGGGGGAAGCGCCGCGTTTCCTGTGCTG
1190
CCTCTTCTTGCCGGCGGGCTCCGGTGTGGGAGAGGACCAGGAGAAAGGGAAAAGGACGCCCCCTTCGCGGCGCAAAGGACACGAC
FUS
FUS-201
FUS-201


GGAGGATGAGTTGATCTTGTTCGTGTATCTTAAGTGGGGCTTTTCAAAAGCGCTTTTGTTGCTTTTTGTTCGCTGGGGGAAGGCA
1275
CCTCCTACTCAACTAGAACAAGCACATAGAATTCACCCCGAAAAGTTTTCGCGAAAACAACGAAAAACAAGCGACCCCCTTCCGT
FUS
FUS-201
FUS-201
GGGTAGGTGAGAAAACGGAACCATCTGGAGTCCCAGGGCTGGGGACTCGAGTACCTGTTGACTTTCGCCTCCTAAGGCGAGCAGT
1360
CCCATCCACTCTTTTGCCTTGGTAGACCTCAGGGTCCCGACCCCTGAGCTCATGGACAACTGAAAGCGGAGGATTCCGCTCGTCA
FUS
FUS-201
FUS-201
TGCATGATCTCTGTCATTTGGGGTCCAAGGGCTCTTTTGATTCTCTGGCTTTGCACTAAAAAGCCCACTTCATCTCCGGGATTGG
1445
ACGTACTAGAGACAGTAAACCCCAGGTTCCCGAGAAAACTAAGAGACCGAAACGTGATTTTTCGGGTGAAGTAGAGGCCCTAACC
FUS
FUS-201
FUS-201
TCAAAGAGTGAAGAATGGCCTTTTTTGAGACTTTCTTATTCTGTGGGTCTGGGCTGAGAGAGCAGAGGCCACAATCTGAACACTG
1530
AGTTTCTCACTTCTTACCGGAAAAAACTCTGAAAGAATAAGACACCCAGACCCGACTCTCTCGTCTCCGGTGTTAGACTTGTGAC
FUS
FUS-201
FUS-201
TTCGAATTCAAACCTGTGCCACTTTGGTAGTTCTGCGACGTTGGGAGAGTTAGTCTCTTGACTCCTGGCGATAATGGCTTTCTCA
1615
AAGCTTAAGTTTGGACACGGTGAAACCATCAAGACGCTGCAACCCTCTCAATCAGAGAACTGAGGACCGCTATTACCGAAAGAGT
FUS
FUS-201
FUS-201
TAGAGTGGATGAAACGAATGCGCGATGTTTTAGAGCAATCACTGACATGAATTGGGCTTGCAGAAAATTGTGGATGTCCACCAAG
1700
ATCTCACCTACTTTGCTTACGCGCTACAAAATCTCGTTAGTGACTGTACTTAACCCGAACGTCTTTTAACACCTACAGGTGGTTC
FUS
FUS-201
FUS-201
ACCTTGGTTTTTCCAATGGTTAAGGCTTCTGGGACTCTGTAGAAACTTGCATTTTCTTCACTTTTTCTTTATTGTAAGAACACTT
1785
TGGAACCAAAAAGGTTACCAATTCCGAAGACCCTGAGACATCTTTGAACGTAAAAGAAGTGAAAAAGAAATAACATTCTTGTGAA
FUS
FUS-201
FUS-201


GGCTGATAACGCCAGTTTGTTCCTCTTCTCAACCAGTGTCTCATGGAGGAATTTTATGCCCTTTGTTGCAACATGGTCCTATTTT
1870
CCGACTATTGCGGTCAAACAAGGAGAAGAGTTGGTCACAGAGTACCTCCTTAAAATACGGGAAACAACGTTGTACCAGGATAAAA
FUS
FUS-201
FUS-201
TATTTTTTTTTTTGAGATGGAGTCTTGCTCTGTTGCCAGGCTGGAGTGCAATGGCTCACTGCAACCTCTGCCTCCCGGGTTCAAG
1955
ATAAAAAAAAAAACTCTACCTCAGAACGAGACAACGGTCCGACCTCACGTTACCGAGTGACGTTGGAGACGGAGGGCCCAAGTTC
FUS
FUS-201
FUS-201
CGATTCTCCTGCTTCACCTCCCGAGTAGCTGGGATTACAGGCGTGCGCCACCATGCCCGGCTAATTTTTTGTATTTTTATTAGAG
2040
GCTAAGAGGACGAAGTGGAGGGCTCATCGACCCTAATGTCCGCACGCGGTGGTACGGGCCGATTAAAAAACATAAAAATAATCTC
FUS
FUS-201
FUS-201
ATGGGGCTTCACCATGTTGGTCAGGCCAGTCTCGAATTCCTGACCTCAAGTGATCCACCCACCTCGGCCTCCCAAACTGCTGGGA
2125
TACCCCGAAGTGGTACAACCAGTCCGGTCAGAGCTTAAGGACTGGAGTTCACTAGGTGGGTGGAGCCGGAGGGTTTGACGACCCT
FUS
FUS-201
FUS-201
TTACAGGCATGATCCACCGTGCCTGGCCTACGTGGTCCTTTTTTATTCATCAGTGCTTGAGTTAAGGAATTTAGCTTTAATTCAAC
2210
AATGTCCGTACTAGGTGGCACGGACCGGATGCACCAGGAAAAATAAGTAGTCACGAACTCAATTCCTTAAATCGAAATTAAGTTG
FUS
FUS-201
FUS-201
TCTTTCAGAGTGGCAGCTGAAGATAATGTGATTGTATTTTTCTTTTGCAGATTATACCCAACAAGCAACCCAAAGGTGAGTGCTA
2295
AGAAAGTCTCACCGTCGACTTCTATTACACTAACATAAAAAGAAAACGTCTAATATGGGTTGTTCGTTGGGTTTCCACTCACGAT
FUS
FUS-201
5
10
D Y T Q Q A T Q S
ENSE00003475065
FUS-201
TTTTTGGGCTTCCAGAGTTTGTAGAGGGCAAGGGTGGTCACGCCATGTTTTCTGATCACGCTGGTTTTCCTTTTATTTAGCTATG
2380
AAAAACCCGAAGGTCTCAAACATCTCCCGTTCCCACCAGTGCGGTACAAAAGACTAGTGCGACCAAAAGGAAAATAAATCGATAC
FUS
FUS-201
Y
ENSE...
FUS-201

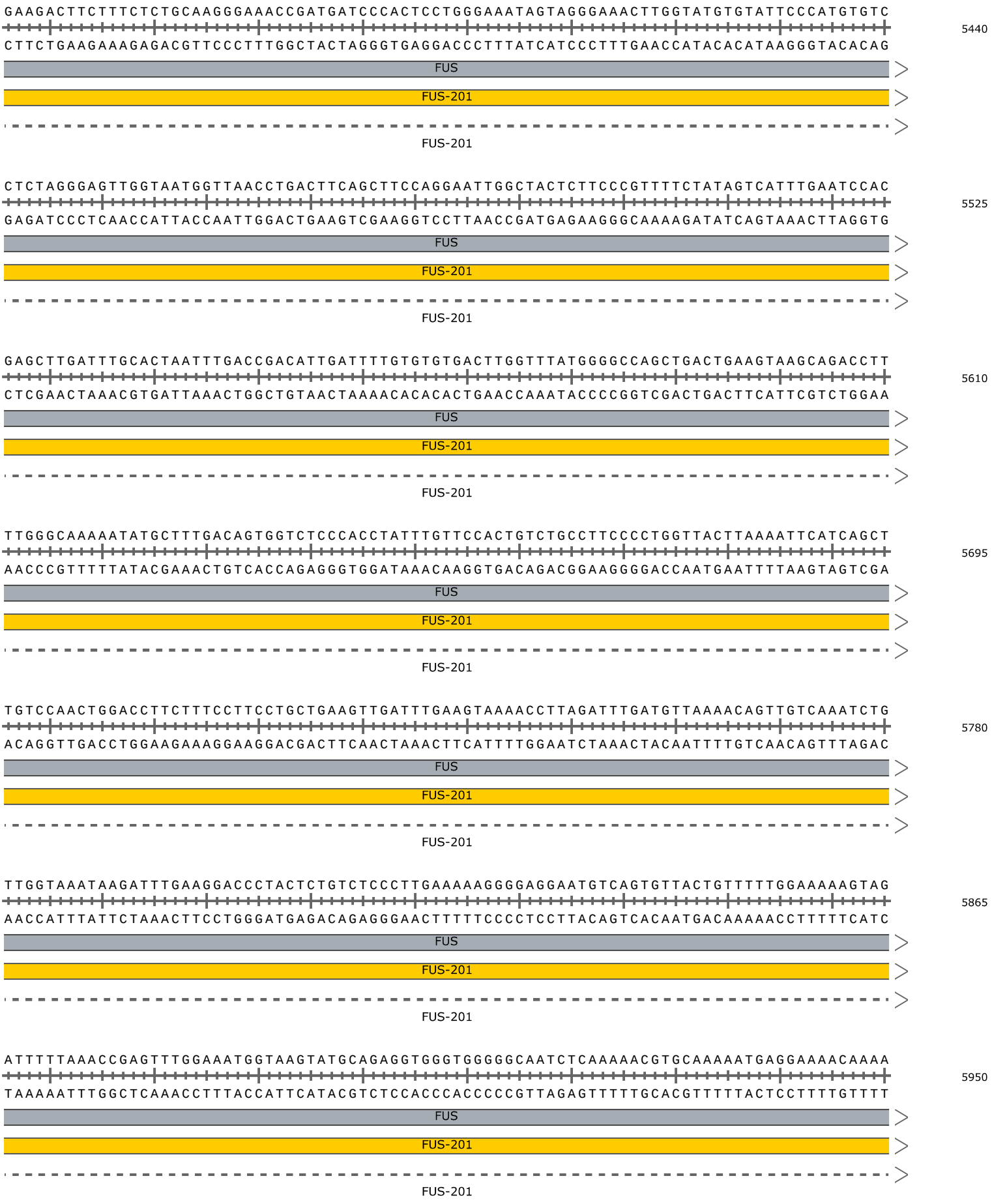

GGGCCTACCCCACCCAGCCCGGGCAGGGCTATTCCCAGCAGAGCAGTCAGCCCTACGGACAGCAGAGTTACAGTGGTTATAGCCA
2465
CCCGGATGGGGTGGGTCGGGCCCGTCCCGATAAGGGTCGTCTCGTCAGTCGGGATGCCTGTCGTCTCAATGTCACCAATATCGGT
FUS
FUS-201
15
20
25
30
35
40
G A Y P T Q P G Q G Y S Q Q S S Q P Y G Q Q S Y S G Y S Q
ENSE00003630677
FUS-201
GTCCACGGACACTTCAGGCTATGGCCAGAGCAGCTATTCTTCTTATGGCCAGAGCCAGAACAGTGAGTCTTTCTCAGCGGGTCAC
2550
CAGGTGCCTGTGAAGTCCGATACCGGTCTCGTCGATAAGAAGAATACCGGTCTCGGTCTTGTCACTCAGAAAGAGTCGCCCAGTG
FUS
FUS-201
45
50
55
60
S T D T S G Y G Q S S Y S S Y G Q S Q N
ENSE00003630677
FUS-201
CTCTTCCTACTCTTTCTGAATATTGCTTTTCTTTTTCTTGTTTTTTGGAGACGGAGTCTGGTCCTGTTGCCCAGGCTGGAGTGCA
2635
GAGAAGGATGAGAAAGACTTATAACGAAAAGAAAAAGAACAAAAAACCTCTGCCTCAGACCAGGACAACGGGTCCGACCTCACGT
FUS
FUS-201
FUS-201
GTGGTGCTGTCTCAGCTCACTGCAACATCAGCCTACCGGGTTCAAACGATTCTCCTGCCTCAGCCTCCTGAGTAGCTGGGATTAC
2720
CACCACGACAGAGTCGAGTGACGTTGTAGTCGGATGGCCCAAGTTTGCTAAGAGGACGGAGTCGGAGGACTCATCGACCCTAATG
FUS
FUS-201
FUS-201
AGGTACCTGCTACCACGCCTGGCTAATTTTGTGTTTTTAGTAGAGATGGGGTTTCACCGTGTTGGACAGGCTGGTCTGGAACTCC
2805
TCCATGGACGATGGTGCGGACCGATTAAAACACAAAAATCATCTCTACCCCAAAGTGGCACAACCTGTCCGACCAGACCTTGAGG
FUS
FUS-201
FUS-201
TGACCTCCTGCCTGCCTTGACCTGCCAAAGTGCTGGGATTACAGGCGTCAGCCACAATGCCCTGAATGTTGCTTTTCTTAAACCT
2890
ACTGGAGGACGGACGGAACTGGACGGTTTCACGACCCTAATGTCCGCAGTCGGTGTTACGGGACTTACAACGAAAAGAATTTGGA
FUS
FUS-201
FUS-201
GAGCAGCACTGAGATGTTGAAACTGTTCCATATTTCTTTTCCGTGAAACAGTGTATAAGTCTTAAAACTTTTTGGGATCTGAGTC
2975
CTCGTCGTGACTCTACAACTTTGACAAGGTATAAAGAAAAGGCACTTTGTCACATATTCAGAATTTTGAAAAACCCTAGACTCAG
FUS
FUS-201
FUS-201

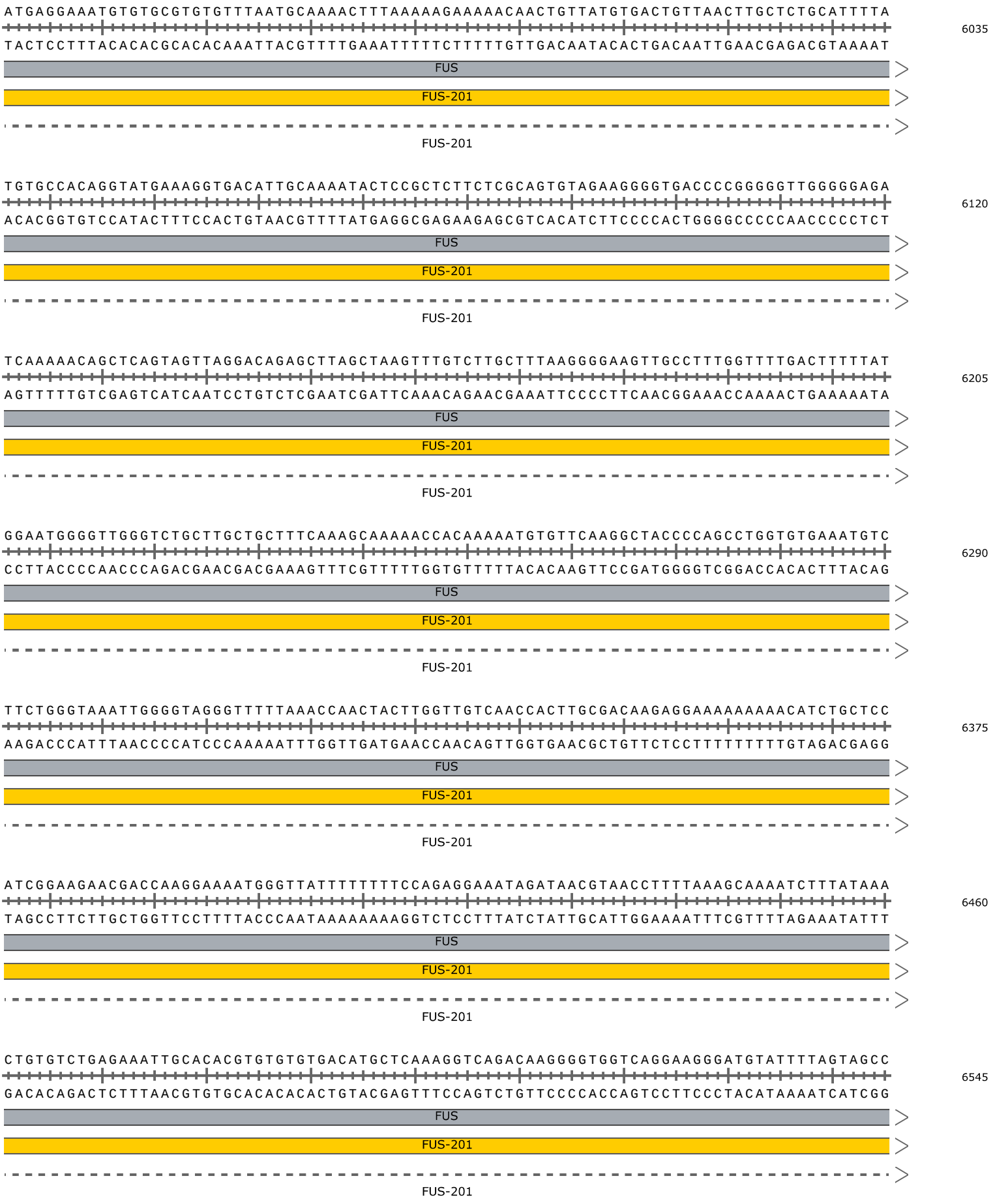

CTTTACAGGGCATTGTGGCACACCTGTAGTCCCAGCTACTGAGGAGGCTGAGGCGGGAGGATCCCTTGAATTCAGGAGTTTGGGG
3060
GAAATGTCCCGTAACACCGTGTGGACATCAGGGTCGATGACTCCTCCGACTCCGCCCTCCTAGGGAACTTAAGTCCTCAAACCCC
FUS
FUS-201
FUS-201
CTGCAGTGAGCTATGATGGTGCCTGTGAACAGCCACTGCATTCCAGCCTGGGCAGTGTGTTGAGGCCCCATCTCAAAAACATAAA
3145
GACGTCACTCGATACTACCACGGACACTTGTCGGTGACGTAAGGTCGGACCCGTCACACAACTCCGGGGTAGAGTTTTTGTATTT
FUS
FUS-201
FUS-201
AAAAAAAACAAAAAACAAAAATGTTTATTGGTTTGTGATTCTGTTTCCATTTATTTTCTTTGGCTTTTAATTTTTTTGACTCTTC
3230
TTTTTTTTGTTTTTTGTTTTTACAAATAACCAAACACTAAGACAAAGGTAAATAAAAGAAACCGAAAATTAAAAAAACTGAGAAG
FUS
FUS-201
FUS-201
TTATTTTCCATCAGCATGAAAGAGAGCATATTTTCTAAAGGAAGAACCAGTTTTAGGCCAATTCTGAAATGGAGAAAATGGTTTT
3315
AATAAAAGGTAGTCGTACTTTCTCTCGTATAAAAGATTTCCTTCTTGGTCAAAATCCGGTTAAGACTTTACCTCTTTTACCAAAA
FUS
FUS-201
FUS-201
GTTTGAAAATGTATGAAATCATGTGATACATAAGGAGGTGGGATTTGCCCCAAGGTCCTGAAGTGTAACTAAGAAAGGTGGTTGT
3400
CAAACTTTTACATACTTTAGTACACTATGTATTCCTCCACCCTAAACGGGGTTCCAGGACTTCACATTGATTCTTTCCACCAACA
FUS
FUS-201
FUS-201
CCTGTAGATACTGCACGCACAGCTGCATATTACAGTGCTGTTAACAGGGATCCTTGGGCCTGGGTTTAGAGGGTGGTGCTGGAGA
3485
GGACATCTATGACGTGCGTGTCGACGTATAATGTCACGACAATTGTCCCTAGGAACCCGGACCCAAATCTCCCACCACGACCTCT
FUS
FUS-201
FUS-201
TGGTGTTGGGATTGGCGGGGTGAAATTGGAACTGTACTAAAGAGTTGGTAGAAGTTGAAGCATTAAATTTAGGCTTTGAAAGGAG
3570
ACCACAACCCTAACCGCCCCACTTTAACCTTGACATGATTTCTCAACCATCTTCAACTTCGTAATTTAAATCCGAAACTTTCCTC
FUS
FUS-201
FUS-201


GGTAACTATCTTTGCCTATGAGTTGCAACATCACTAACAGCTTCTGAGAGGCTGGCTTTATGAGTATAGGTATTATGTTTTCTTT
3655
CCATTGATAGAAACGGATACTCAACGTTGTAGTGATTGTCGAAGACTCTCCGACCGAAATACTCATATCCATAATACAAAAGAAA
FUS
FUS-201
FUS-201
AACCCATTCCTTACATTTTCTCTTTCCTGGTGGCTTTTGTGACTCCCTTTTTCTTATCCTGGTAGCAGGCTATGGAACTCAGTCA
3740
TTGGGTAAGGAATGTAAAAGAGAAAGGACCACCGAAAACACTGAGGGAAAAAGAATAGGACCATCGTCCGATACCTTGAGTCAGT
FUS
FUS-201
65
70
T G Y G T Q S
ENSE00003599547
FUS-201
ACTCCCCAGGGATATGGCTCGACTGGCGGCTATGGCAGTAGCCAGAGCTCCCAATCGTCTTACGGGCAGCAGTCCTCCTACCCTG
3825
TGAGGGGTCCCTATACCGAGCTGACCGCCGATACCGTCATCGGTCTCGAGGGTTAGCAGAATGCCCGTCGTCAGGAGGATGGGAC
FUS
FUS-201
75
80
85
90
95
T P Q G Y G S T G G Y G S S Q S S Q S S Y G Q Q S S Y P
ENSE00003599547
FUS-201
GCTATGGCCAGCAGCCAGCTCCCAGCAGCACCTCGGGAAGGTACGGTGGTGTTGATGTCGGGGAAGGCTTGAAAAGAGGGGTGAA
3910
CGATACCGGTCGTCGGTCGAGGGTCGTCGTGGAGCCCTTCCATGCCACCACAACTACAGCCCCTTCCGAACTTTTCTCCCCACTT
FUS
FUS-201
100
105
110
G Y G Q Q P A P S S T S G S
ENSE00003599547
FUS-201
TTGATGAGGAATGATAAAGGGACCAGCAGTAGGAGCAGTTCAGAGGTGTAATTGGGGTAGGGGAGCCTGTGTTGGGTACAGAGAA
3995
AACTACTCCTTACTATTTCCCTGGTCGTCATCCTCGTCAAGTCTCCACATTAACCCCATCCCCTCGGACACAACCCATGTCTCTT
FUS
FUS-201
FUS-201
TGGACTCCACTAAAAGTGAAAGGAAATTGGGGGCTATGCTGGGATTGTGATTGTGTTTTTTGTTTGTTTTCCCTAGTTACGGTAG
4080
ACCTGAGGTGATTTTCACTTTCCTTTAACCCCCGATACGACCCTAACACTAACACAAAAAACAAACAAAAGGGATCAATGCCATC
FUS
FUS-201
115
Y G S
ENSE000035...
FUS-201
CAGTTCTCAGAGCAGCAGCTATGGGCAGCCCCAGAGTGGGAGCTACAGCCAGCAGCCTAGCTATGGTGGACAGCAGCAAAGCTAT
4165
GTCAAGAGTCTCGTCGTCGATACCCGTCGGGGTCTCACCCTCGATGTCGGTCGTCGGATCGATACCACCTGTCGTCGTTTCGATA
FUS
FUS-201
120
125
130
135
140
S S Q S S S Y G Q P Q S G S Y S Q Q P S Y G G Q Q Q S Y
ENSE00003537617
FUS-201

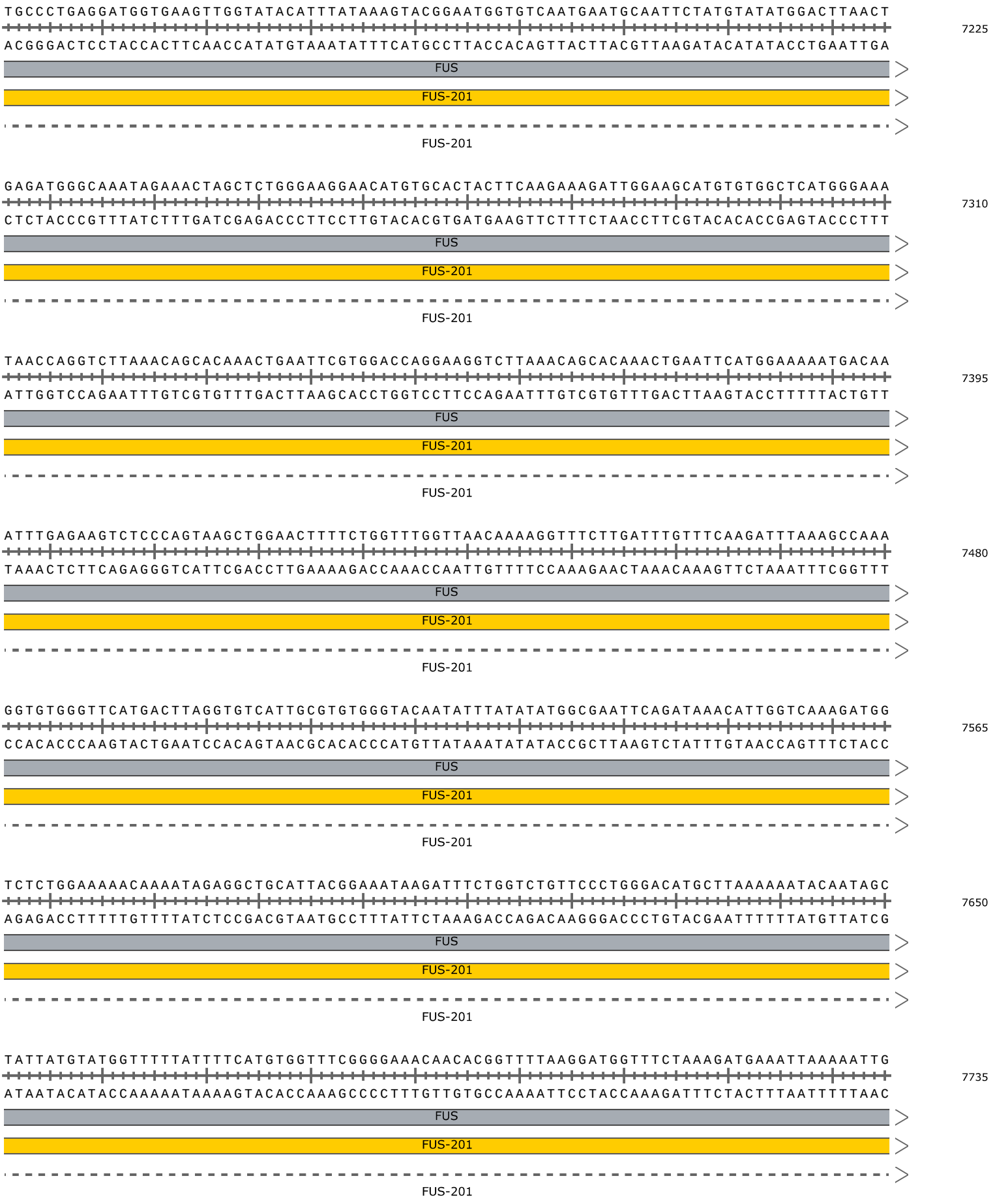

GGACAGCAGCAAAGCTATAATCCCCCTCAGGGCTATGGACAGCAGAACCAGTACAACAGCAGCAGTGGTGGTGGAGGTGGAGGTG
4250
CCTGTCGTCGTTTCGATATTAGGGGGAGTCCCGATACCTGTCGTCTTGGTCATGTTGTCGTCGTCACCACCACCTCCACCTCCAC
FUS
FUS-201
145
150
155
160
165
170
G Q Q Q S Y N P P Q G Y G Q Q N Q Y N S S S G G G G G G
ENSE00003537617
FUS-201
GAGGTGGAGGTGAGATGTCTTCAGCTTTGTCTGCAGCCCATTTTCTTTTTCTTTTTTTTTTTTTTTTTGAGACGGAGTCTTGCTC
4335
CTCCACCTCCACTCTACAGAAGTCGAAACAGACGTCGGGTAAAAGAAAAAGAAAAAAAAAAAAAAAAACTCTGCCTCAGAACGAG
FUS
FUS-201
G G G
ENSE00003...
FUS-201
TGTCTCTGTTGCTGAGGCTGGAGTGCAGTGGCACAATCTCGGCTCACTGCAAGCTCCGCCTTCCGGGTTCGCGCCAGTCTCCTGC
4420
ACAGAGACAACGACTCCGACCTCACGTCACCGTGTTAGAGCCGAGTGACGTTCGAGGCGGAAGGCCCAAGCGCGGTCAGAGGACG
FUS
FUS-201
FUS-201
CTCAGCCTCCCGAGTAGCTGGGACTACAGGCATCCGCCACCACGCCCGGCTAATTTTTTGTATTTTTAGTAGAGACGGGGTTTCA
4505
GAGTCGGAGGGCTCATCGACCCTGATGTCCGTAGGCGGTGGTGCGGGCCGATTAAAAAACATAAAAATCATCTCTGCCCCAAAGT
FUS
FUS-201
FUS-201
CCATGTTAGCCAGGATGGTTTCGATCTCCTGACCTTGTGATCCGCCCGCCTTGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAG
4590
GGTACAATCGGTCCTACCAAAGCTAGAGGACTGGAACACTAGGCGGGCGGAACCGGAGGGTTTCACGACCCTAATGTCCGCACTC
FUS
FUS-201
FUS-201
CCACTGTGCCTGGTGTCTGCAGCCCATTTTCTATAAGGATTTGTATTCTCCTGTTTTAGCTTAAAAGAGGGTTCCTGTCTTGTTT
4675
GGTGACACGGACCACAGACGTCGGGTAAAAGATATTCCTAAACATAAGAGGACAAAATCGAATTTTCTCCCAAGGACAGAACAAA
FUS
FUS-201
FUS-201
CCTAGCTGTCTTTTTACTTTCTTTTGTCCTTCATTGCCTGGCACTTGTCAAACCTTTTCAAACCTTTTAGTGCTACTTTACAATC
4760
GGATCGACAGAAAAATGAAAGAAAACAGGAAGTAACGGACCGTGAACAGTTTGGAAAAGTTTGGAAAATCACGATGAAATGTTAG
FUS
FUS-201
FUS-201

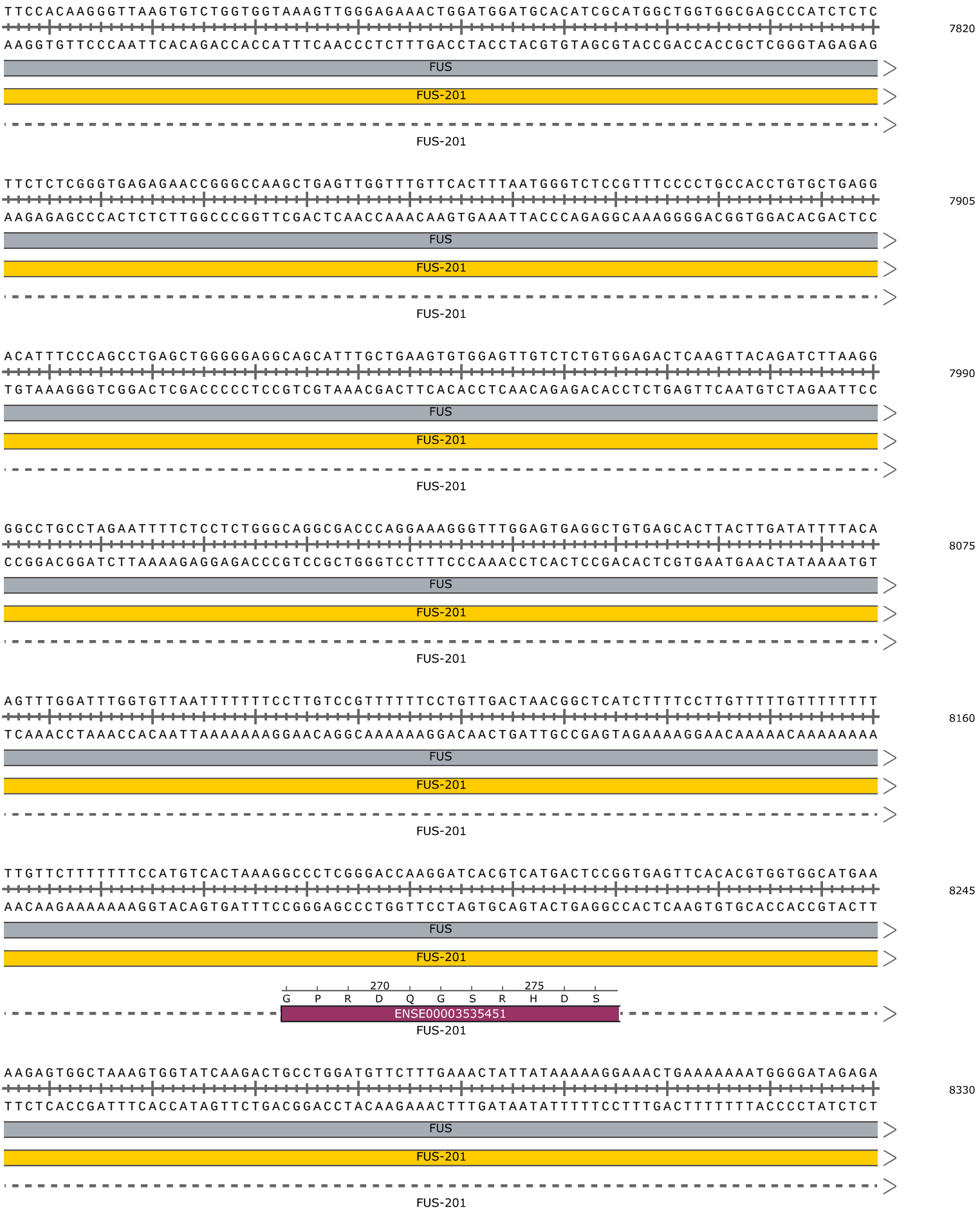

TTTTTGTTTTTTTTTTTTAATCATTCTTTCTTTTCTCACAGGTAACTATGGCCAAGATCAATCCTCCATGAGTAGTGGTGGTGGC
4845
AAAAACAAAAAAAAAAAATTAGTAAGAAAGAAAAGAGTGTCCATTGATACCGGTTCTAGTTAGGAGGTACTCATCACCACCACCG
FUS
FUS-201
175
180
185
G N Y G Q D Q S S M S S G G G
ENSE00001791812
FUS-201
AGTGGTGGCGGTTATGGCAATCAAGACCAGAGTGGTGGAGGTGGCAGCGGTGGCTATGGACAGCAGGACCGTGGAGGCCGCGGCA
4930
TCACCACCGCCAATACCGTTAGTTCTGGTCTCACCACCTCCACCGTCGCCACCGATACCTGTCGTCCTGGCACCTCCGGCGCCGT
FUS
FUS-201
190
195
200
205
210
215
S G G G Y G N Q D Q S G G G S G G Y G Q Q D R G G R G
ENSE00001791812
FUS-201
GGGGTGGCAGTGGTGGCGGCGGCGGCGGCGGCGGTGGTGGTTACAACCGCAGCAGTGGTGGCTATGAACCCAGAGGTCGTGGAGG
5015
CCCCACCGTCACCACCGCCGCCGCCGCCGCCGCCACCACCAATGTTGGCGTCGTCACCACCGATACTTGGGTCTCCAGCACCTCC
FUS
FUS-201
220
225
230
235
240
245
R G G S G G G G G G G G G Y N R S S G G Y E P R G R G G
ENSE00001791812
FUS-201
TGGCCGTGGAGGCAGAGGTGGCATGGGGTAGGTGTCTCATGAGCCAGGGAGTATCTTTGGTGGGGAGTGTGGAGGATTGCATGAA
5100
ACCGGCACCTCCGTCTCCACCGTACCCCATCCACAGAGTACTCGGTCCCTCATAGAAACCACCCCTCACACCTCCTAACGTACTT
FUS
FUS-201
250
255
G R G G R G G M G
ENSE00001791812
FUS-201
TCTCCCTGAAGCCAGTCCCTAGTGCATGGTTTAGTATTCTTGTTGTCTAGGGATCTGTGAGGGCTTTGATTTGGGGGCAGTGACT
5185
AGAGGGACTTCGGTCAGGGATCACGTACCAAATCATAAGAACAACAGATCCCTAGACACTCCCGAAACTAAACCCCCGTCACTGA
FUS
FUS-201
FUS-201
TTCTTTTTACATCCCCATTTTATTTTTGTGAGAACTTGGGAGCCTGAACTCCCATCCATACCACTGAATAGAGATTTTGAGTAAT
5270
AAGAAAAATGTAGGGGTAAAATAAAAACACTCTTGAACCCTCGGACTTGAGGGTAGGTATGGTGACTTATCTCTAAAACTCATTA
FUS
FUS-201
FUS-201
GATACTTGTTTCCAAAAAAAAAGAAACCATACATAGATACGTATGGATTGGAGTCATTAATATCCTAGGCAAGAAACATGGAAGT
5355
CTATGAACAAAGGTTTTTTTTTCTTTGGTATGTATCTATGCATACCTAACCTCAGTAATTATAGGATCCGTTCTTTGTACCTTCA
FUS
FUS-201
FUS-201

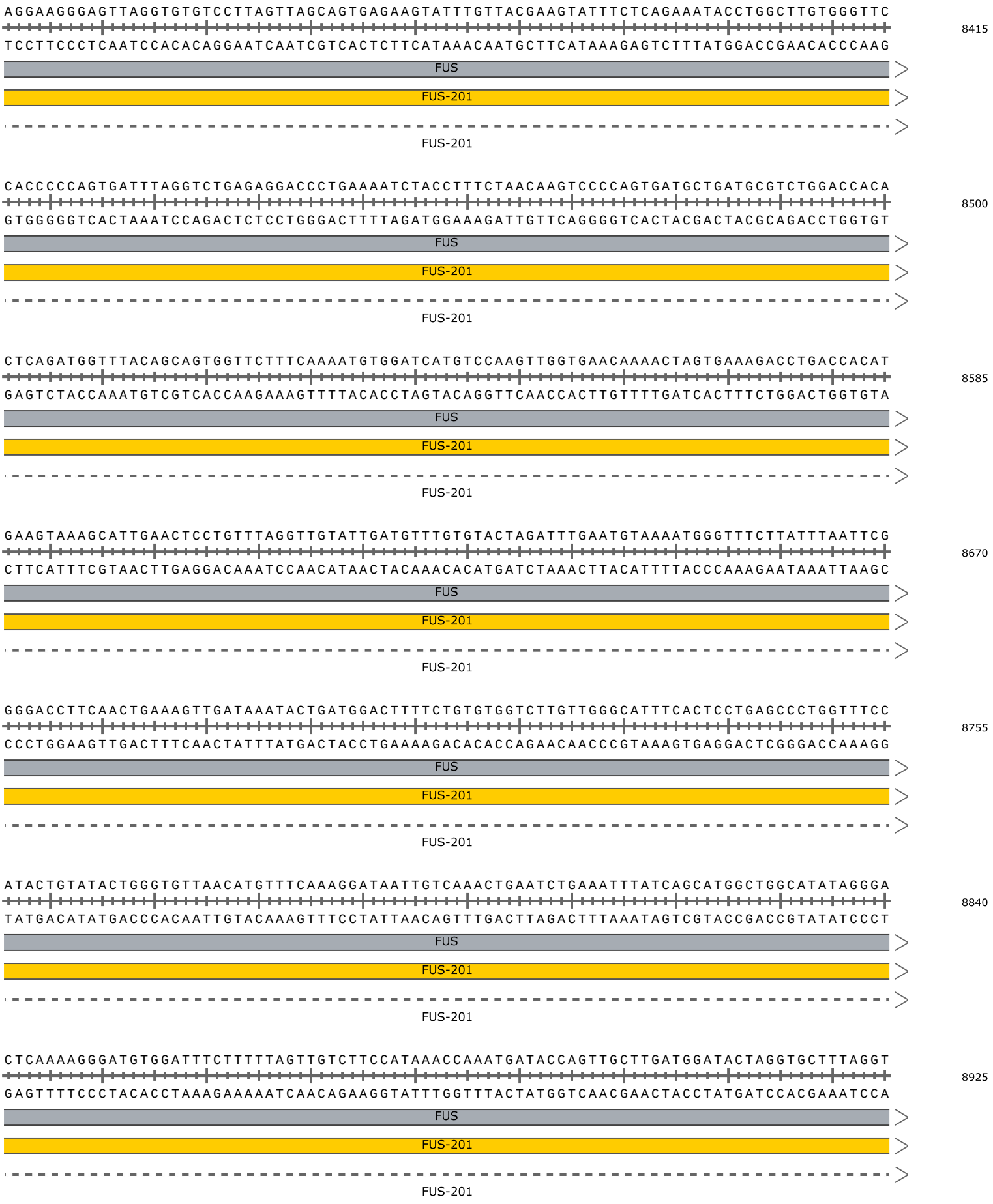

GAAGACTTCTTTCTCTGCAAGGGAAACCGATGATCCCACTCCTGGGAAATAGTAGGGAAACTTGGTATGTGTATTCCCATGTGTC
5440
CTTCTGAAGAAAGAGACGTTCCCTTTGGCTACTAGGGTGAGGACCCTTTATCATCCCTTTGAACCATACACATAAGGGTACACAG
FUS
FUS-201
FUS-201
CTCTAGGGAGTTGGTAATGGTTAACCTGACTTCAGCTTCCAGGAATTGGCTACTCTTCCCGTTTTCTATAGTCATTTGAATCCAC
5525
GAGATCCCTCAACCATTACCAATTGGACTGAAGTCGAAGGTCCTTAACCGATGAGAAGGGCAAAAGATATCAGTAAACTTAGGTG
FUS
FUS-201
FUS-201
GAGCTTGATTTGCACTAATTTGACCGACATTGATTTTGTGTGTGACTTGGTTTATGGGGCCAGCTGACTGAAGTAAGCAGACCTT
5610
CTCGAACTAAACGTGATTAAACTGGCTGTAACTAAAACACACACTGAACCAAATACCCCGGTCGACTGACTTCATTCGTCTGGAA
FUS
FUS-201
FUS-201
TTGGGCAAAAATATGCTTTGACAGTGGTCTCCCACCTATTTGTTCCACTGTCTGCCTTCCCCTGGTTACTTAAAATTCATCAGCT
5695
AACCCGTTTTTATACGAAACTGTCACCAGAGGGTGGATAAACAAGGTGACAGACGGAAGGGGACCAATGAATTTTAAGTAGTCGA
FUS
FUS-201
FUS-201
TGTCCAACTGGACCTTCTTTCCTTCCTGCTGAAGTTGATTTGAAGTAAAACCTTAGATTTGATGTTAAAACAGTTGTCAAATCTG
5780
ACAGGTTGACCTGGAAGAAAGGAAGGACGACTTCAACTAAACTTCATTTTGGAATCTAAACTACAATTTTGTCAACAGTTTAGAC
FUS
FUS-201
FUS-201
TTGGTAAATAAGATTTGAAGGACCCTACTCTGTCTCCCTTGAAAAAGGGGAGGAATGTCAGTGTTACTGTTTTTGGAAAAAGTAG
5865
AACCATTTATTCTAAACTTCCTGGGATGAGACAGAGGGAACTTTTTCCCCTCCTTACAGTCACAATGACAAAAACCTTTTTCATC
FUS
FUS-201
FUS-201
ATTTTTAAACCGAGTTTGGAAATGGTAAGTATGCAGAGGTGGGTGGGGGCAATCTCAAAAACGTGCAAAAATGAGGAAAACAAAA
5950
TAAAAATTTGGCTCAAACCTTTACCATTCATACGTCTCCACCCACCCCCGTTAGAGTTTTTGCACGTTTTTACTCCTTTTGTTTT
FUS
FUS-201
FUS-201


ATGAGGAAATGTGTGCGTGTGTTTAATGCAAAACTTTAAAAAGAAAAACAACTGTTATGTGACTGTTAACTTGCTCTGCATTTTA
6035
TACTCCTTTACACACGCACACAAATTACGTTTTGAAATTTTTCTTTTTGTTGACAATACACTGACAATTGAACGAGACGTAAAAT
FUS
FUS-201
FUS-201
TGTGCCACAGGTATGAAAGGTGACATTGCAAAATACTCCGCTCTTCTCGCAGTGTAGAAGGGGTGACCCCGGGGGTTGGGGGAGA
6120
ACACGGTGTCCATACTTTCCACTGTAACGTTTTATGAGGCGAGAAGAGCGTCACATCTTCCCCACTGGGGCCCCCAACCCCCTCT
FUS
FUS-201
FUS-201
TCAAAAACAGCTCAGTAGTTAGGACAGAGCTTAGCTAAGTTTGTCTTGCTTTAAGGGGAAGTTGCCTTTGGTTTTGACTTTTTAT
6205
AGTTTTTGTCGAGTCATCAATCCTGTCTCGAATCGATTCAAACAGAACGAAATTCCCCTTCAACGGAAACCAAAACTGAAAAATA
FUS
FUS-201
FUS-201
GGAATGGGGTTGGGTCTGCTTGCTGCTTTCAAAGCAAAAACCACAAAAATGTGTTCAAGGCTACCCCAGCCTGGTGTGAAATGTC
6290
CCTTACCCCAACCCAGACGAACGACGAAAGTTTCGTTTTTGGTGTTTTTACACAAGTTCCGATGGGGTCGGACCACACTTTACAG
FUS
FUS-201
FUS-201
TTCTGGGTAAATTGGGGTAGGGTTTTTAAACCAACTACTTGGTTGTCAACCACTTGCGACAAGAGGAAAAAAAAAACATCTGCTCC
6375
AAGACCCATTTAACCCCATCCCAAAAATTTGGTTGATGAACCAACAGTTGGTGAACGCTGTTCTCCTTTTTTTTTTGTAGACGAGG
FUS
FUS-201
FUS-201
ATCGGAAGAACGACCAAGGAAAATGGGTTATTTTTTTTTCCAGAGGAAATAGATAACGTAACCTTTTAAAGCAAAATCTTTATAAA
6460
TAGCCTTCTTGCTGGTTCCTTTTACCCAATAAAAAAAAGGTCTCCTTTATCTATTGCATTGGAAAATTTCGTTTTAGAAATATTT
FUS
FUS-201
FUS-201
CTGTGTCTGAGAAATTGCACACGTGTGTGTGACATGCTCAAAGGTCAGACAAGGGGTGGTCAGGAAGGGATGTATTTTAGTAGCC
6545
GACACAGACTCTTTAACGTGTGCACACACACTGTACGAGTTTCCAGTCTGTTCCCCACCAGTCCTTCCCTACATAAAATCATCGG
FUS
FUS-201
FUS-201

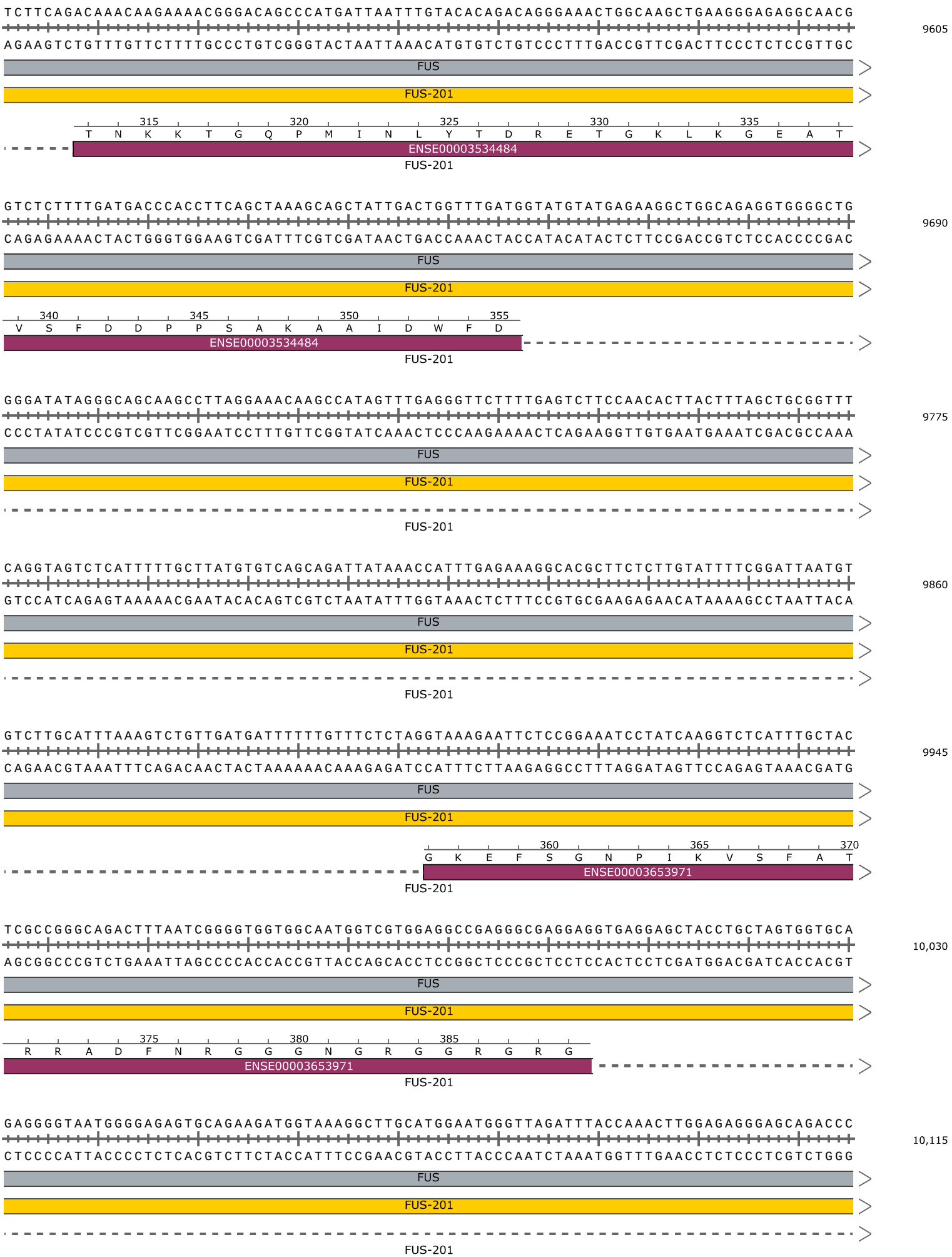

ACTTGTATCTTTTTCCAAAAACACCTACCCATGTTTGGGGAATGTTAAACAAAATCAAAAAACAACCTTTTGTAGCCGTTGGAAG
6630
TGAACATAGAAAAAGGTTTTTGTGGATGGGTACAAACCCCTTACAATTTGTTTTAGTTTTTTGTTGGAAAACATCGGCAACCTTC
FUS
FUS-201
FUS-201
CTTCATGTCCTTTCTTCTAACTTGTCTTCTCCAGCGGAAGTGACCGTGGTGGCTTCAATAAATTTGGTGGTAAGTGAACAGAGTT
6715
GAAGTACAGGAAAGAAGATTGAACAGAAGAGGTCGCCTTCACTGGCACCACCGAAGTTATTTAAACCACCATTCACTTGTCTCAA
FUS
FUS-201
260
265
G S D R G G F N K F G
ENSE00003521089
FUS-201
TCCAAAATTCCCAACTCCCAGCAATGCTTTGTCTGATTGTTCATTTGCAGATGTCTTAGCGTGTTAATTTAAATGTCAAAGGTTT
6800
AGGTTTTAAGGGTTGAGGGTCGTTACGAAACAGACTAACAAGTAAACGTCTACAGAATCGCACAATTAAATTTACAGTTTCCAAA
FUS
FUS-201
FUS-201
TGAGGTGTCCAGAACCACCTCCAGAAAGGGGTAGGGTAGAATGCCACCTGTTGCCTGGTGTGTGCTAACCTGGAGCAGGTAGGGG
6885
ACTCCACAGGTCTTGGTGGAGGTCTTTCCCCATCCCATCTTACGGTGGACAACGGACCACACACGATTGGACCTCGTCCATCCCC
FUS
FUS-201
FUS-201
TAAGACTCAATAGTCATCTTTTACCAAATGGGTTTGCCCCAGGTTAATAAGAGGGGTCTAGTAGGCCTTGGACTGGGCCGTTGCC
6970
ATTCTGAGTTATCAGTAGAAAATGGTTTACCCAAACGGGGTCCAATTATTCTCCCCAGATCATCCGGAACCTGACCCGGCAACGG
FUS
FUS-201
FUS-201
ACACCTGGCACTTAGTGACCATCATCATGAGAAACTGGAGAGTGCGTGCTGGAACACGTGGTGCCATCTTGGCTTTAGGATCCTT
7055
TGTGGACCGTGAATCACTGGTAGTAGTACTCTTTGACCTCTCACGCACGACCTTGTGCACCACGGTAGAACCGAAATCCTAGGAA
FUS
FUS-201
FUS-201
TTGATCGTTGTGTCCAAGGCTTGTGTGTGTGTGAGTGTGTGGGAGACAACTCCGAATGTTTAATTCTGGAAGAGGGATGTAACAT
7140
AACTAGCAACACAGGTTCCGAACACACACACACTCACACACCCTCTGTTGAGGCTTACAAATTAAGACCTTCTCCCTACATTGTA
FUS
FUS-201
FUS-201


TGCCCTGAGGATGGTGAAGTTGGTATACATTTATAAAGTACGGAATGGTGTCAATGAATGCAATTCTATGTATATGGACTTAACT
7225
ACGGGACTCCTACCACTTCAACCATATGTAAATATTTCATGCCTTACCACAGTTACTTACGTTAAGATACATATACCTGAATTGA
FUS
FUS-201
FUS-201
GAGATGGGCAAATAGAAACTAGCTCTGGGAAGGAACATGTGCACTACTTCAAGAAAGATTGGAAGCATGTGTGGCTCATGGGAAA
7310
CTCTACCCGTTTATCTTTGATCGAGACCCTTCCTTGTACACGTGATGAAGTTCTTTCTAACCTTCGTACACACCGAGTACCCTTT
FUS
FUS-201
FUS-201
TAACCAGGTCTTAAACAGCACAAACTGAATTCGTGGACCAGGAAGGTCTTAAACAGCACAAACTGAATTCATGGAAAAATGACAA
7395
ATTGGTCCAGAATTTGTCGTGTTTGACTTAAGCACCTGGTCCTTCCAGAATTTGTCGTGTTTGACTTAAGTACCTTTTTACTGTT
FUS
FUS-201
FUS-201
ATTTGAGAAGTCTCCCAGTAAGCTGGAACTTTTCTGGTTTGGTTAACAAAAGGTTTCTTGATTTGTTTCAAGATTTAAAGCCAAA
7480
TAAACTCTTCAGAGGGTCATTCGACCTTGAAAAGACCAAACCAATTGTTTTCCAAAGAACTAAACAAAGTTCTAAATTTCGGTTT
FUS
FUS-201
FUS-201
GGTGTGGGTTCATGACTTAGGTGTCATTGCGTGTGGGTACAATATTTATATATGGCGAATTCAGATAAACATTGGTCAAAGATGG
7565
CCACACCCAAGTACTGAATCCACAGTAACGCACACCCATGTTATAAATATATACCGCTTAAGTCTATTTGTAACCAGTTTCTACC
FUS
FUS-201
FUS-201
TCTCTGGAAAAACAAAATAGAGGCTGCATTACGGAAATAAGATTTCTGGTCTGTTCCCTGGGACATGCTTAAAAAATACAATAGC
7650
AGAGACCTTTTTGTTTTATCTCCGACGTAATGCCTTTATTCTAAAGACCAGACAAGGGACCCTGTACGAATTTTTTATGTTATCG
FUS
FUS-201
FUS-201
TATTATGTATGGTTTTTATTTTCATGTGGTTTCGGGGAAACAACACGGTTTTAAGGATGGTTTCTAAAGATGAAATTAAAAATTG
7735
ATAATACATACCAAAAATAAAAGTACACCAAAGCCCCTTTGTTGTGCCAAAATTCCTACCAAAGATTTCTACTTTAATTTTTAAC
FUS
FUS-201
FUS-201

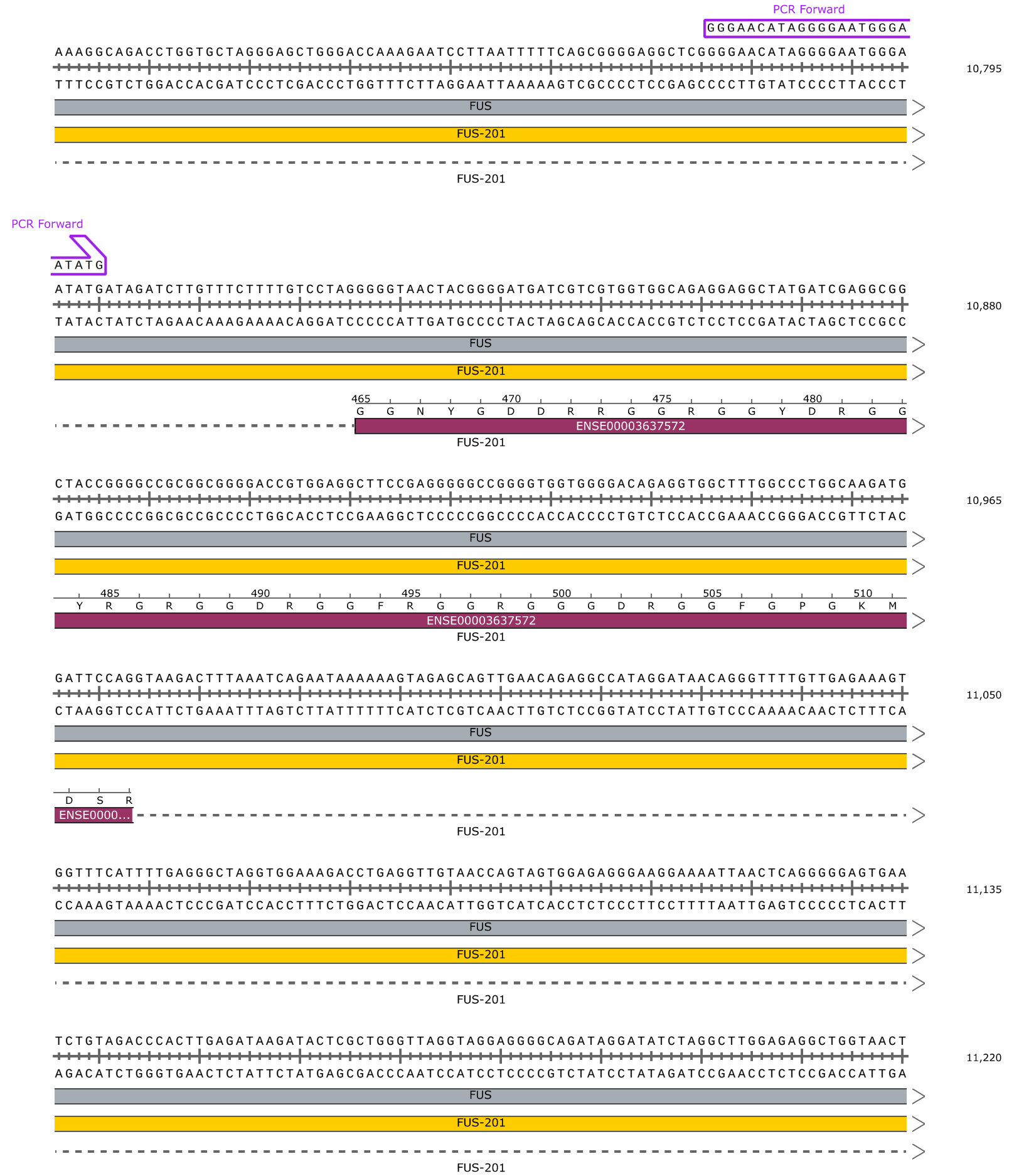

TTCCACAAGGGTTAAGTGTCTGGTGGTAAAGTTGGGAGAAACTGGATGGATGCACATCGCATGGCTGGTGGCGAGCCCATCTCTC
7820
AAGGTGTTCCCAATTCACAGACCACCATTTCAACCCTCTTTGACCTACCTACGTGTAGCGTACCGACCACCGCTCGGGTAGAGAG
FUS
FUS-201
FUS-201
TTCTCTCGGGTGAGAGAACCGGGCCAAGCTGAGTTGGTTTGTTCACTTTAATGGGTCTCCGTTTCCCCTGCCACCTGTGCTGAGG
7905
AAGAGAGCCCACTCTCTTGGCCCGGTTCGACTCAACCAAACAAGTGAAATTACCCAGAGGCAAAGGGGACGGTGGACACGACTCC
FUS
FUS-201
FUS-201
ACATTTCCCAGCCTGAGCTGGGGGAGGCAGCATTTGCTGAAGTGTGGAGTTGTCTCTGTGGAGACTCAAGTTACAGATCTTAAGG
7990
TGTAAAGGGTCGGACTCGACCCCCTCCGTCGTAAACGACTTCACACCTCAACAGAGACACCTCTGAGTTCAATGTCTAGAATTCC
FUS
FUS-201
FUS-201
GGCCTGCCTAGAATTTTCTCCTCTGGGCAGGCGACCCAGGAAAGGGTTTGGAGTGAGGCTGTGAGCACTTACTTGATATTTTACA
8075
CCGGACGGATCTTAAAAGAGGAGACCCGTCCGCTGGGTCCTTTCCCAAACCTCACTCCGACACTCGTGAATGAACTATAAAATGT
FUS
FUS-201
FUS-201
AGTTTGGATTTGGTGTTAATTTTTTTCCTTGTCCGTTTTTTCCTGTTGACTAACGGCTCATCTTTTCCTTGTTTTTGTTTTTTTT
8160
TCAAACCTAAACCACAATTAAAAAAAGGAACAGGCAAAAAAGGACAACTGATTGCCGAGTAGAAAAGGAACAAAAACAAAAAAAA
FUS
FUS-201
FUS-201
TTGTTCTTTTTTTCCATGTCACTAAAGGCCCTCGGGACCAAGGATCACGTCATGACTCCGGTGAGTTCACACGTGGTGGCATGAA
8245
AACAAGAAAAAAAGGTACAGTGATTTCCGGGAGCCCTGGTTCCTAGTGCAGTACTGAGGCCACTCAAGTGTGCACCACCGTACTT
FUS
FUS-201
270
275
G P R D Q G S R H D S
ENSE00003535451
FUS-201
AAGAGTGGCTAAAGTGGTATCAAGACTGCCTGGATGTTCTTTGAAACTATTATAAAAAGGAAACTGAAAAAAATGGGGATAGAGA
8330
TTCTCACCGATTTCACCATAGTTCTGACGGACCTACAAGAAACTTTGATAATATTTTTCCTTTGACTTTTTTTACCCCTATCTCT
FUS
FUS-201
FUS-201

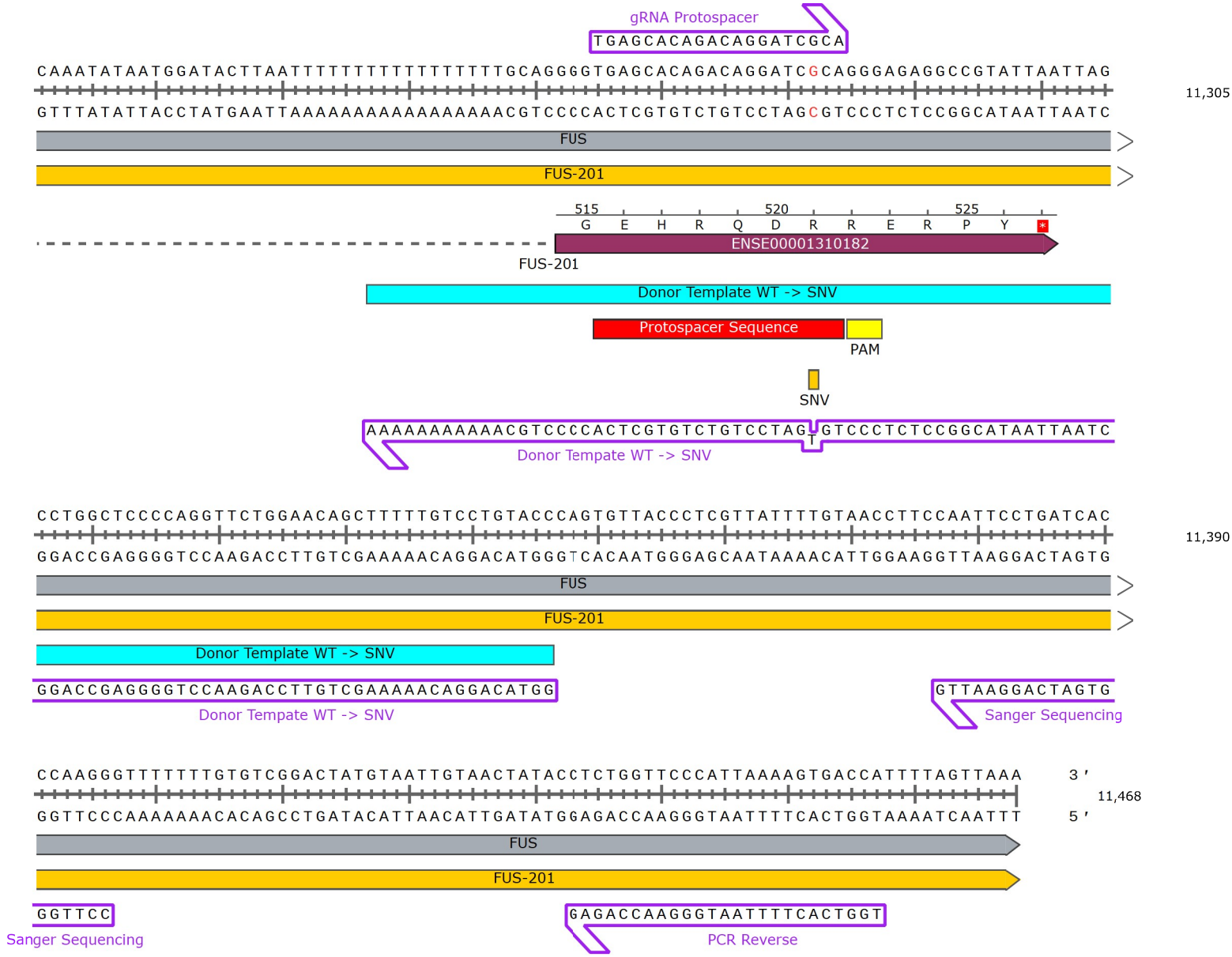

AGGAAGGGAGTTAGGTGTGTCCTTAGTTAGCAGTGAGAAGTATTTGTTACGAAGTATTTCTCAGAAATACCTGGCTTGTGGGTTC
8415
TCCTTCCCTCAATCCACACAGGAATCAATCGTCACTCTTCATAAACAATGCTTCATAAAGAGTCTTTATGGACCGAACACCCAAG
FUS
FUS-201
FUS-201
CACCCCCAGTGATTTAGGTCTGAGAGGACCCTGAAAATCTACCTTTCTAACAAGTCCCCAGTGATGCTGATGCGTCTGGACCACA
8500
GTGGGGGTCACTAAATCCAGACTCTCCTGGGACTTTTAGATGGAAAGATTGTTCAGGGGTCACTACGACTACGCAGACCTGGTGT
FUS
FUS-201
FUS-201
CTCAGATGGTTTACAGCAGTGGTTCTTTCAAAATGTGGATCATGTCCAAGTTGGTGAACAAAACTAGTGAAAGACCTGACCACAT
8585
GAGTCTACCAAATGTCGTCACCAAGAAAGTTTTACACCTAGTACAGGTTCAACCACTTGTTTTGATCACTTTCTGGACTGGTGTA
FUS
FUS-201
FUS-201
GAAGTAAAGCATTGAACTCCTGTTTAGGTTGTATTGATGTTTGTGTACTAGATTTGAATGTAAAATGGGTTTCTTATTTAATTCG
8670
CTTCATTTCGTAACTTGAGGACAAATCCAACATAACTACAAACACATGATCTAAACTTACATTTTACCCAAAGAATAAATTAAGC
FUS
FUS-201
FUS-201
GGGACCTTCAACTGAAAGTTGATAAATACTGATGGACTTTTCTGTGTGGTCTTGTTGGGCATTTCACTCCTGAGCCCTGGTTTCC
8755
CCCTGGAAGTTGACTTTCAACTATTTATGACTACCTGAAAAGACACACCAGAACAACCCGTAAAGTGAGGACTCGGGACCAAAGG
FUS
FUS-201
FUS-201
ATACTGTATACTGGGTGTTAACATGTTTCAAAGGATAATTGTCAAACTGAATCTGAAATTTATCAGCATGGCTGGCATATAGGGA
8840
TATGACATATGACCCACAATTGTACAAAGTTTCCTATTAACAGTTTGACTTAGACTTTAAATAGTCGTACCGACCGTATATCCCT
FUS
FUS-201
FUS-201
CTCAAAAGGGATGTGGATTTCTTTTTAGTTGTCTTCCATAAACCAAATGATACCAGTTGCTTGATGGATACTAGGTGCTTTAGGT
8925
GAGTTTTCCCTACACCTAAAGAAAAATCAACAGAAGGTATTTGGTTTACTATGGTCAACGAACTACCTATGATCCACGAAATCCA
FUS
FUS-201
FUS-201


TTTTTCCTGTGTTTTTTATTTTACCTTTTCACATTTGCATTTTCTCTGTTCAACAAGCAGAACAGGATAATTCAGACAACAACAC
9010
AAAAAGGACACAAAAAATAAAATGGAAAAGTGTAAACGTAAAAGAGACAAGTTGTTCGTCTTGTCCTATTAAGTCTGTTGTTGTG
FUS
FUS-201
280
285
E Q D N S D N N T
ENSE00003524436
FUS-201
CATCTTTGTGCAAGGCCTGGGTGAGAATGTTACAATTGAGTCTGTGGCTGATTACTTCAAGCAGATTGGTATTATTAAGGTACTT
9095
GTAGAAACACGTTCCGGACCCACTCTTACAATGTTAACTCAGACACCGACTAATGAAGTTCGTCTAACCATAATAATTCCATGAA
FUS
FUS-201
290
295
300
305
310
I F V Q G L G E N V T I E S V A D Y F K Q I G I I K
ENSE00003524436
FUS-201
GTGGAGAGGAGTGGGAGCTTTCTGTCAGTGTTGTAGGCTTGTGGATTTCACACATTAGTAAAAGCAAGTCTTTAATGGTTGCCAG
9180
CACCTCTCCTCACCCTCGAAAGACAGTCACAACATCCGAACACCTAAAGTGTGTAATCATTTTCGTTCAGAAATTACCAACGGTC
FUS
FUS-201
FUS-201
CAGTAAAAACAAGTCTTAGTGGTTGTTGCCAGCTTAATTTGTTGAGGAAAGAGCCTTAGTTACTGTTTTCTAAAAGAGAAGTTCT
9265
GTCATTTTTGTTCAGAATCACCAACAACGGTCGAATTAAACAACTCCTTTCTCGGAATCAATGACAAAAGATTTTCTCTTCAAGA
FUS
FUS-201
FUS-201
ATCTTAACACAAAAAGTATAACTTATCAGAGTACCCTAAACTCTTGAGATTTGTACTCTATAGTAACTTTTAGTTTTATCTTTCA
9350
TAGAATTGTGTTTTTCATATTGAATAGTCTCATGGGATTTGAGAACTCTAAACATGAGATATCATTGAAAATCAAAATAGAAAGT
FUS
FUS-201
FUS-201
ATATTGGAGTGAGAGACAGTTTTCTTTAATGGAGGTTTACATGTGAGGTAGGAAGAAGTAACTGGGAAGAGGGGAGCTGAAGTTT
9435
TATAACCTCACTCTCTGTCAAAAGAAATTACCTCCAAATGTACACTCCATCCTTCTTCATTGACCCTTCTCCCCTCGACTTCAAA
FUS
FUS-201
FUS-201
GGGAATTATAAACCTCATGTTCTAGAGGAAGAAGATGGAAAGGGAGTACTGTAGCCTTTAAAATTGATGTTACCTCATTTTGCTT
9520
CCCTTAATATTTGGAGTACAAGATCTCCTTCTTCTACCTTTCCCTCATGACATCGGAAATTTTAACTACAATGGAGTAAAACGAA
FUS
FUS-201
FUS-201


TCTTCAGACAAACAAGAAAACGGGACAGCCCATGATTAATTTGTACACAGACAGGGAAACTGGCAAGCTGAAGGGAGAGGCAACG
9605
AGAAGTCTGTTTGTTCTTTTGCCCTGTCGGGTACTAATTAAACATGTGTCTGTCCCTTTGACCGTTCGACTTCCCTCTCCGTTGC
FUS
FUS-201
315
320
325
330
335
T N K K T G Q P M I N L Y T D R E T G K L K G E A T
ENSE00003534484
FUS-201
GTCTCTTTTGATGACCCACCTTCAGCTAAAGCAGCTATTGACTGGTTTGATGGTATGTATGAGAAGGCTGGCAGAGGTGGGGCTG
9690
CAGAGAAAACTACTGGGTGGAAGTCGATTTCGTCGATAACTGACCAAACTACCATACATACTCTTCCGACCGTCTCCACCCCGAC
FUS
FUS-201
340
345
350
355
V S F D D P P S A K A A I D W F D
ENSE00003534484
FUS-201
GGGATATAGGGCAGCAAGCCTTAGGAAACAAGCCATAGTTTGAGGGTTCTTTTGAGTCTTCCAACACTTACTTTAGCTGCGGTTT
9775
CCCTATATCCCGTCGTTCGGAATCCTTTGTTCGGTATCAAACTCCCAAGAAAACTCAGAAGGTTGTGAATGAAATCGACGCCAAA
FUS
FUS-201
FUS-201
CAGGTAGTCTCATTTTTGCTTATGTGTCAGCAGATTATAAACCATTTGAGAAAGGCACGCTTCTCTTGTATTTTCGGATTAATGT
9860
GTCCATCAGAGTAAAAACGAATACACAGTCGTCTAATATTTGGTAAACTCTTTCCGTGCGAAGAGAACATAAAAGCCTAATTACA
FUS
FUS-201
FUS-201
GTCTTGCATTTAAAGTCTGTTGATGATTTTTTGTTTCTCTAGGTAAAGAATTCTCCGGAAATCCTATCAAGGTCTCATTTGCTAC
9945
CAGAACGTAAATTTCAGACAACTACTAAAAAACAAAGAGATCCATTTCTTAAGAGGCCTTTAGGATAGTTCCAGAGTAAACGATG
FUS
FUS-201
360
365
370
G K E F S G N P I K V S F A T
ENSE00003653971
FUS-201
TCGCCGGGCAGACTTTAATCGGGGTGGTGGCAATGGTCGTGGAGGCCGAGGGCGAGGAGGTGAGGAGCTACCTGCTAGTGGTGCA
10,030
AGCGGCCCGTCTGAAATTAGCCCCACCACCGTTACCAGCACCTCCGGCTCCCGCTCCTCCACTCCTCGATGGACGATCACCACGT
FUS
FUS-201
375
380
385
R R A D F N R G G G N G R G G R G R G
ENSE00003653971
FUS-201
GAGGGGTAATGGGGAGAGTGCAGAAGATGGTAAAGGCTTGCATGGAATGGGTTAGATTTACCAAACTTGGAGAGGGAGCAGACCC
10,115
CTCCCCATTACCCCTCTCACGTCTTCTACCATTTCCGAACGTACCTTACCCAATCTAAATGGTTTGAACCTCTCCCTCGTCTGGG
FUS
FUS-201
FUS-201


ATACTTGGTCTATCTGCATTAGGACCCATGGGCCGTGGAGGCTATGGAGGTGGTGGCAGTGGTGGTGGTGGCCGAGGAGGATTTC
10,200
TATGAACCAGATAGACGTAATCCTGGGTACCCGGCACCTCCGATACCTCCACCACCGTCACCACCACCACCGGCTCCTCCTAAAG
FUS
FUS-201
390
395
400
405
410
G P M G R G G Y G G G G S G G G G R G G F
ENSE00003604625
FUS-201
CCAGTGGAGGTGGTGGCGGTGGAGGACAGCAGCGAGCTGGTGACTGGAAGTGTCCTAATCCGTGAGTGAAACTTAATTTTTTTCT
10,285
GGTCACCTCCACCACCGCCACCTCCTGTCGTCGCTCGACCACTGACCTTCACAGGATTAGGCACTCACTTTGAATTAAAAAAAGA
FUS
FUS-201
415
420
425
430
P S G G G G G G G Q Q R A G D W K C P N P
ENSE00003604625
FUS-201
TAGTTCTCTTGCATGCGTGCTCTTTGATATATTGGTACTGAGGTATGTGCGTGTTTTCCAAAGAAGTAAATGTCAAGGCCACACT
10,370
ATCAAGAGAACGTACGCACGAGAAACTATATAACCATGACTCCATACACGCACAAAAGGTTTCTTCATTTACAGTTCCGGTGTGA
FUS
FUS-201
FUS-201
GTTGGGGTCAGATTTAGCCAAAAGCTTACCTAGGTAAGGTTGATGTAATGGGAAAGGTAATGGATTGGGTTCAGTAATACTGATT
10,455
CAACCCCAGTCTAAATCGGTTTTCGAATGGATCCATTCCAACTACATTACCCTTTCCATTACCTAACCCAAGTCATTATGACTAA
FUS
FUS-201
FUS-201
TTTGTTCCTGACTCTGAGAAGCAAGCCGTTTTGTCTTTCTGAAGCTTCAGTTTCCTCACTGTATCTCTAAAGTCACCGTAGTTTC
10,540
AAACAAGGACTGAGACTCTTCGTTCGGCAAAACAGAAAGACTTCGAAGTCAAAGGAGTGACATAGAGATTTCAGTGGCATCAAAG
FUS
FUS-201
FUS-201
TTCCTAGTTCTAGGTCTTGCCTATTCCCCATCGCTCCAGACTGATTGTCTTCCTTTCTCCTTAGCACCTGTGAGAATATGAACTT
10,625
AAGGATCAAGATCCAGAACGGATAAGGGGTAGCGAGGTCTGACTAACAGAAGGAAAGAGGAATCGTGGACACTCTTATACTTGAA
FUS
FUS-201
435
T C E N M N F
ENSE00003494295
FUS-201
CTCTTGGAGGAATGAATGCAACCAGTGTAAGGCCCCTAAACCAGATGGCCCAGGAGGGGGACCAGGTGGCTCTCACATGGGTAAG
10,710
GAGAACCTCCTTACTTACGTTGGTCACATTCCGGGGATTTGGTCTACCGGGTCCTCCCCCTGGTCCACCGAGAGTGTACCCATTC
FUS
FUS-201
440
445
450
455
460
S W R N E C N Q C K A P K P D G P G G G P G G S H M
ENSE00003494295
FUS-201


PCR Forward
GGGAACATAGGGGAATGGGA
AAAGGCAGACCTGGTGCTAGGGAGCTGGGACCAAAGAATCCTTAATTTTTCAGCGGGGAGGCTCGGGGAACATAGGGGAATGGGA
10,795
TTTCCGTCTGGACCACGATCCCTCGACCCTGGTTTCTTAGGAATTAAAAAGTCGCCCCTCCGAGCCCCTTGTATCCCCTTACCCT
FUS
FUS-201
FUS-201
PCR Forward
ATATG
ATATGATAGATCTTGTTTCTTTTGTCCTAGGGGGTAACTACGGGGATGATCGTCGTGGTGGCAGAGGAGGCTATGATCGAGGCGG
10,880
TATACTATCTAGAACAAAGAAAACAGGATCCCCCATTGATGCCCCTACTAGCAGCACCACCGTCTCCTCCGATACTAGCTCCGCC
FUS
FUS-201
465
470
475
480
G G N Y G D D R R G G R G G Y D R G G
ENSE00003637572
FUS-201
CTACCGGGGCCGCGGCGGGGACCGTGGAGGCTTCCGAGGGGGCCGGGGTGGTGGGGACAGAGGTGGCTTTGGCCCTGGCAAGATG
10,965
GATGGCCCCGGCGCCGCCCCTGGCACCTCCGAAGGCTCCCCCGGCCCCACCACCCCTGTCTCCACCGAAACCGGGACCGTTCTAC
FUS
FUS-201
485
490
495
500
505
510
Y R G R G G D R G G F R G G R G G G D R G G F G P G K M
ENSE00003637572
FUS-201
GATTCCAGGTAAGACTTTAAATCAGAATAAAAAAGTAGAGCAGTTGAACAGAGGCCATAGGATAACAGGGTTTTGTTGAGAAAGT
11,050
CTAAGGTCCATTCTGAAATTTAGTCTTATTTTTTCATCTCGTCAACTTGTCTCCGGTATCCTATTGTCCCAAAACAACTCTTTCA
FUS
FUS-201
D S R
ENSE0000...
FUS-201
GGTTTCATTTTGAGGGCTAGGTGGAAAGACCTGAGGTTGTAACCAGTAGTGGAGAGGGAAGGAAAATTAACTCAGGGGGAGTGAA
11,135
CCAAAGTAAAACTCCCGATCCACCTTTCTGGACTCCAACATTGGTCATCACCTCTCCCTTCCTTTTAATTGAGTCCCCCTCACTT
FUS
FUS-201
FUS-201
TCTGTAGACCCACTTGAGATAAGATACTCGCTGGGTTAGGTAGGAGGGGCAGATAGGATATCTAGGCTTGGAGAGGCTGGTAACT
11,220
AGACATCTGGGTGAACTCTATTCTATGAGCGACCCAATCCATCCTCCCCGTCTATCCTATAGATCCGAACCTCTCCGACCATTGA
FUS
FUS-201
FUS-201


gRNA Protospacer
TGAGCACAGACAGGATCGCA
CAAATATAATGGATACTTAATTTTTTTTTTTTTTTTTGCAGGGGTGAGCACAGACAGGATCGCAGGGAGAGGCCGTATTAATTAG
11,305
GTTTATATTACCTATGAATTAAAAAAAAAAAAAAAAACGTCCCCACTCGTGTCTGTCCTAGCGTCCCTCTCCGGCATAATTAATC
FUS
FUS-201
515
520
525
G E H R Q D R R E R P Y *
ENSE00001310182
FUS-201
Donor Template WT -> SNV
Protospacer Sequence
PAM
SNV
AAAAAAAAAAACGTCCCCACTCGTGTCTGTCCTAGTGTCCCTCTCCGGCATAATTAATC
Donor Tempate WT -> SNV
CCTGGCTCCCCAGGTTCTGGAACAGCTTTTTGTCCTGTACCCAGTGTTACCCTCGTTATTTTGTAACCTTCCAATTCCTGATCAC
11,390
GGACCGAGGGGTCCAAGACCTTGTCGAAAAACAGGACATGGGTCACAATGGGAGCAATAAAACATTGGAAGGTTAAGGACTAGTG
FUS
FUS-201
Donor Template WT -> SNV
GGACCGAGGGGTCCAAGACCTTGTCGAAAAACAGGACATGG
Donor Tempate WT -> SNV
GTTAAGGACTAGTG
Sanger Sequencing
CCAAGGGTTTTTTTGTGTCGGACTATGTAATTGTAACTATACCTCTGGTTCCCATTAAAAGTGACCATTTTAGTTAAA
3'
11,468
GGTTCCCAAAAAAACACAGCCTGATACATTAACATTGATATGGAGACCAAGGGTAATTTTCACTGGTAAAATCAATTT
5'
FUS
FUS-201
GGTTCC
Sanger Sequencing
GAGACCAAGGGTAATTTTCACTGGT
PCR Reverse

| | Feature | | Location | | Size | | Type |
|---|---|---|---|---|---|---|---|
| ✓ | **FUS** | | 1 .. 11,468 | | 11,468 bp | → | gene |
| | /note | = gene ENSG00000089280<br>Protein coding | | | | | |
| | **FUS-209** | | 1 .. 11,465 | | 11,465 bp | → | prim_transcript |
| | /note | = primary transcript ENST00000566605<br>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<br>Retained intron | | | | | |
| | **FUS-206** | | 13 .. 11,465 | | 11,453 bp | → | prim_transcript |
| | /note | = primary transcript ENST00000487509<br>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,,DYTQQATQS,,YGAYPTQPGQGYSQQSSQPYGQQSYSGYSQSTDTSGYGQSSYSSYGQSQN,,TGYGTQSTPQGYGSTGGYGSSQSS<br>QSSYGQQSSYPGYGQQPAPSSTSGS,,YGSSSQSSSYGQPQSGSYSQQPSYGGQQQSYGQQQSYNPPQGYGQQNQYNSSSGGGGGGGGG,<br>,GNYGQDQSSMSSGGGSGGGYGNQDQSGGGGSGGYGQQDRGGRGRGGSGGGGGGGGGGYNRSSGGYEPRGRGGGRGGRGGMG,,GSDRG<br>GFNKFG,,GPRDQGSRHDS,,EQDNSDNNTIFVQGLGENVTIESVADYFKQIGIIK,,TNKKTGQPMINLYTDRETGKLKGEATVSFDDPPSAKAAI<br>DWFD,,GKEFSGNPIKVSFATRRADFNRGGGNGRGGRGRG,,GPMGRGGYGGGGSGGGGRGGFPSGGGGGGGQQRAGDWKCPNP,,TCENMNFS<br>WRNECNQCKAPKPDGPGGGPGGSHM,,GGNYGDDRRGGRGGYDRGGYRGRGGDRGGFRGGRGGGDRGGFGPGKMDSR,,GEHRQDRRERPY*<br>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,,DYTQQATQS,,YGAYPTQPGQGYSQQSSQPYGQQSYSGYSQSTDTSGYGQSSYSSYGQSQN,,SYGTQSTPQGYGSTGGYGSSQSSQ<br>SSYGQQSSYPGYGQQPAPSSTSGS,,YGSSSQSSSYGQPQSGSYSQQPSYGGQQQSYGQQQSYNPPQGYGQQNQYNSSSGGGGGGGGG,,G<br>NYGQDQSSMSSGGGSGGGYGNQDQSGGGGSGGYGQQDRGGRGRGGSGGGGGGGGGGYNRSSGGYEPRGRGGGRGGRGGMG,,GSDRGGF<br>NKFG,,GPRDQGSRHDS,,EQDNSDNNTIFVQGLGENVTIESVADYFKQIGIIK,,TNKKTGQPMINLYTDRETGKLKGEATVSFDDPPSAKAAIDWF<br>FD,,GKEFSGNPIKVSFATRRADFNRGGGNGRGGRGRG,,GPMGRGGYGGGGSGGGGRGGFPSGGGGGGGQQRAGDWKCPNP,,TCENMNFSWR<br>NECNQCKAPKPDGPGGGPGGSHM,,GGNYGDDRRGGRGGYDRGGYRGRGGDRGGFRGGRGGGDRGGFGPGKMDSR,,GEHRQDRRERPY*<br>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,,DYTQQATQS,,YGAYPTQPGQGYSQQSSQPYGQQSYSGYSQSTDTSGYGQSSYSSYGQSQN,,TGYGTQSTPQGYGSTGGYGSSQSS<br>QSSYGQQSSYPGYGQQPAPSSTSGS,,YGSSSQSSSYGQPQSGSYSQQPSYGGQQQSYGQQQSYNPPQGYGQQNQYNSSSGGGGGGGGG,<br>,GNYGQDQSSMSSGGGSGGGYGNQDQSGGGGSGGYGQQDRGGRGRGGSGGGGGGGGGGYNRSSGGYEPRGRGGGRGGRGGMG,,GSDRG<br>GFNKFG,,GPRDQGSRHDS,,AEQDNSDNNTIFVQGLGENVTIESVADYFKQIGIIK,,TNKKTGQPMINLYTDRETGKLKGEATVSFDDPPSAKAA<br>IDWFD,,GKEFSGNPIKVSFATRRADFNRGGGNGRGGRGRG,,GPMGRGGYGGGGSGGGGRGGFPSGGGGGGGQQRAGDWKCPNP,,TCENMNF<br>SWRNECNQCKAPKPDGPGGGPGGSHM,,GGNYGDDRRGGRGGYDRGGYRGRGGDRGGFRGGRGGGDRGGFGPGKMDSR,,GEHRQDRRERPY<br>*<br>527 amino acids = 53.5 kDa | | | | | |
| | | | 2374 .. 3148 | | 775 bp | ← | gene |
| | /note | = gene ENSG00000260304<br>lncRNA | | | | | |
| | | | 2374 .. 3148 | | 775 bp | ← | prim_transcript |
| | /note | = primary transcript ENST00000564743<br>lncRNA | | | | | |
| | **FUS-207** | | 3413 .. 4261 | | 849 bp | → | prim_transcript |
| | /note | = primary transcript ENST00000487974<br>Retained intron | | | | | |
| | **FUS-213** | | 4943 .. 7108 | | 2166 bp | → | prim_transcript |
| | /note | = primary transcript ENST00000570090<br>Retained intron | | | | | |
| | **FUS-203** | | 5362 .. 10,965 | | 5604 bp | → | prim_transcript |
| | /note | = primary transcript ENST00000474990<br>protein_coding_CDS_not_defined | | | | | |

| | Feature | | | Location | | | Size | | | Type |
|---|---|---|---|---|---|---|---|---|---|---|
| | **FUS-211** | | | 8015 | .. | 9983 | 1969 bp | | → | prim_transcript |
| | /note | = | primary transcript ENST00000568901<br>Retained intron | | | | | | | |
| | **FUS-208** | | | 8330 | .. | 9558 | 1229 bp | | → | prim_transcript |
| | /note | = | primary transcript ENST00000564766<br>Retained intron | | | | | | | |
| | **FUS-212** | | | 10,079 | .. | 11,468 | 1390 bp | | → | prim_transcript |
| | /note | = | primary transcript ENST00000569760<br>Retained intron | | | | | | | |
| | **FUS-204** | | | 10,236 | .. | 11,421 | 1186 bp | | → | prim_transcript |
| | /note | = | primary transcript ENST00000483853<br>Retained intron | | | | | | | |
| ✓ | **Donor Template WT -> SNV** | | | 11,247 | .. | 11,346 | 100 bp | | ⊢ | misc_feature |
| ✓ | **Protospacer Sequence** | | | 11,265 | .. | 11,284 | 20 bp | | ⊢ | misc_feature |
| ✓ | **SNV** | | | 11,282 | .. | 11,282 | 1 bp | | ⊢ | misc_feature |
| | /note | = | WT = G<br>SNV = A | | | | | | | |
| ✓ | **PAM** | | | 11,285 | .. | 11,287 | 3 bp | | ⊢ | misc_feature |

| | Primer | Length | Binding Sites | | Tm | Date Added |
|---|---|---|---|---|---|---|
| ✓ | **PCR Forward** | 25-mer | 10,776 .. 10,800 | → | 58°C | Jan 11, 2023 |
| | /sequence = GGGAACATAGGGGAATGGGAATATG<br>48% GC / 7884.2 Da | | | | | |
| ✓ | **Donor Tempate WT -> SNV** | 100-mer | 11,247 .. 11,346 | ← | 77°C | Jan 11, 2023 |
| | /sequence = GGTACAGGACAAAAAGCTGTTCCAGAACCTGGGGAGCCAGGCTAATTAATACGGCCTCTCCCTGTGATCCTGTCTGTGCTCACCCCTG<br>61% GC / 30,782.0 Da | | | | | |
| ✓ | **gRNA Protospacer** | 20-mer | 11,265 .. 11,284 | → | 59°C | Jan 11, 2023 |
| | /sequence = TGAGCACAGACAGGATCGCA<br>55% GC / 6160.1 Da | | | | | |
| ✓ | **Sanger Sequencing** | 20-mer | 11,377 .. 11,396 | ← | 55°C | Jan 11, 2023 |
| | /sequence = CCTTGGGTGATCAGGAATTG<br>50% GC / 6188.1 Da | | | | | |
| ✓ | **PCR Reverse** | 25-mer | 11,433 .. 11,457 | ← | 59°C | Jan 11, 2023 |
| | /sequence = TGGTCACTTTTAATGGGAACCAGAG<br>44% GC / 7721.1 Da | | | | | |