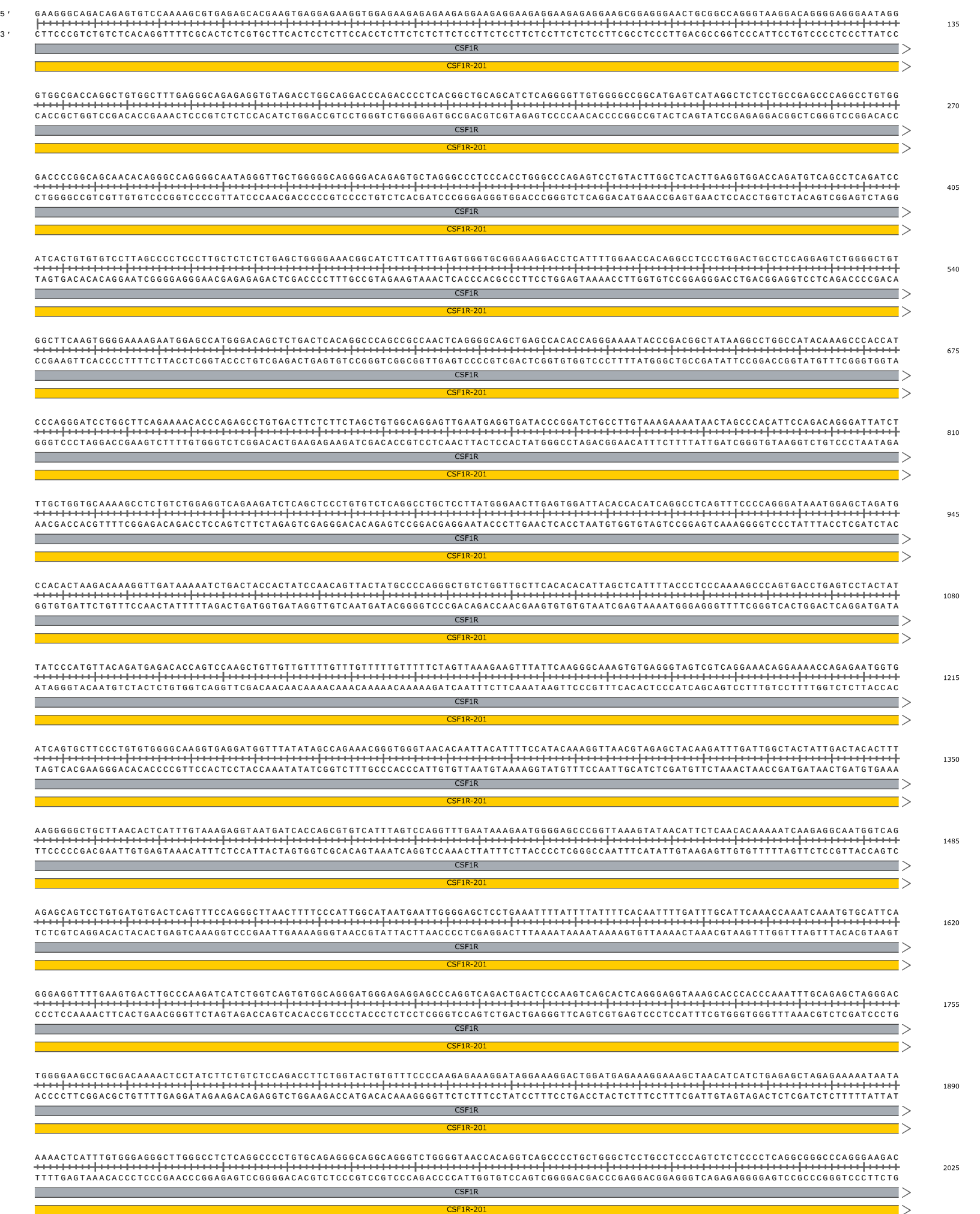
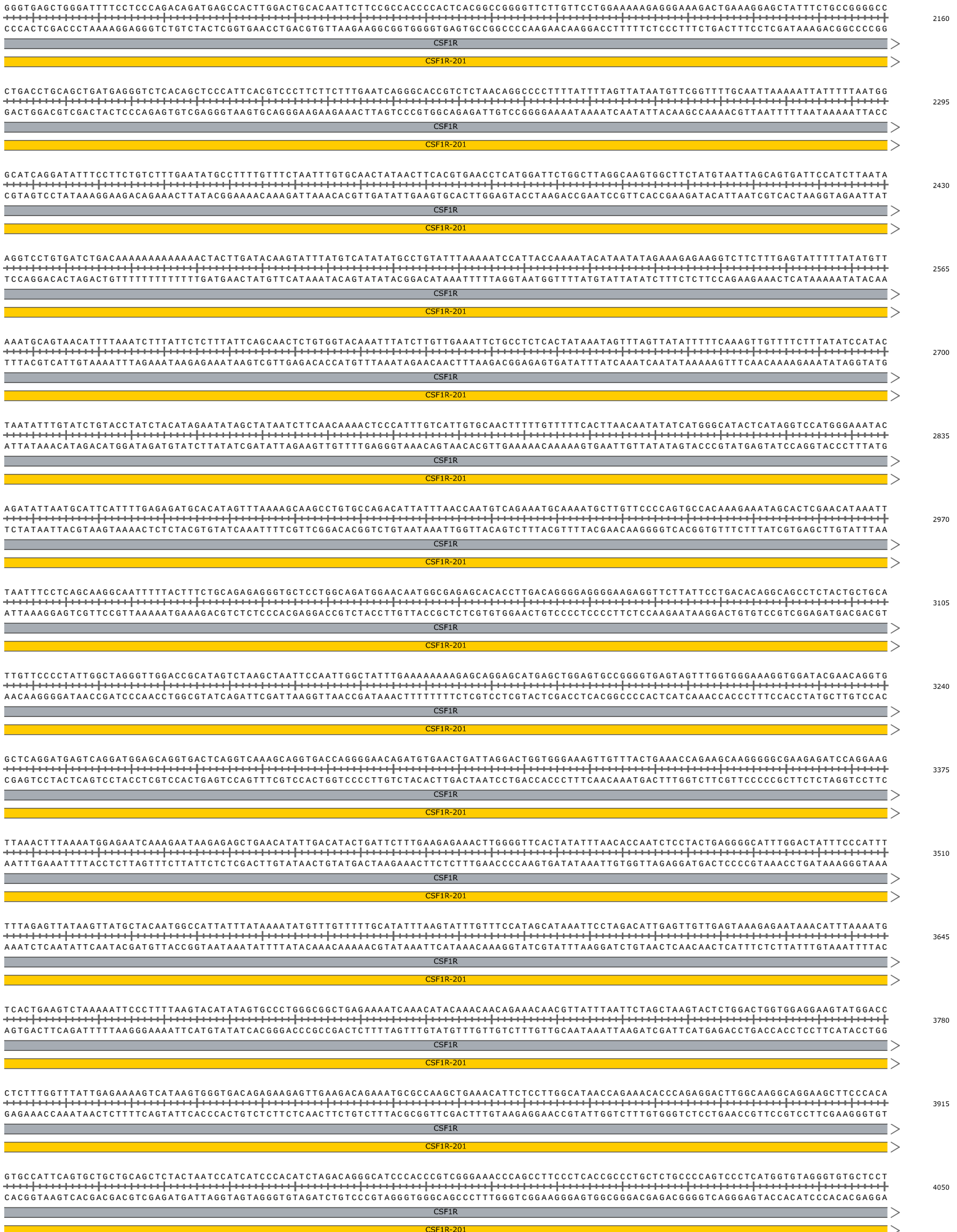


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CSF1R-201

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CSF1R-201

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CSF1R-201

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CSF1R-201

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CSF1R-201

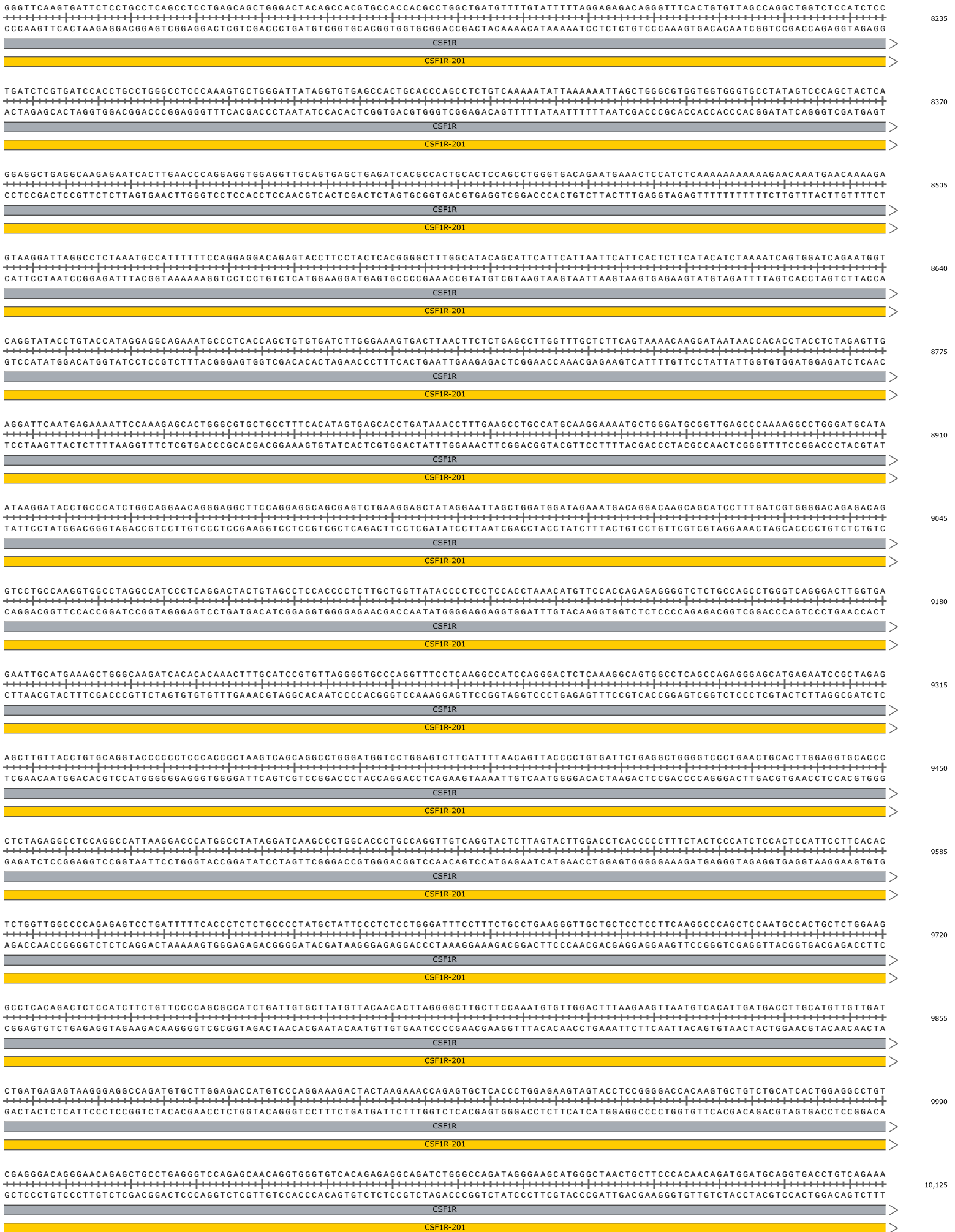
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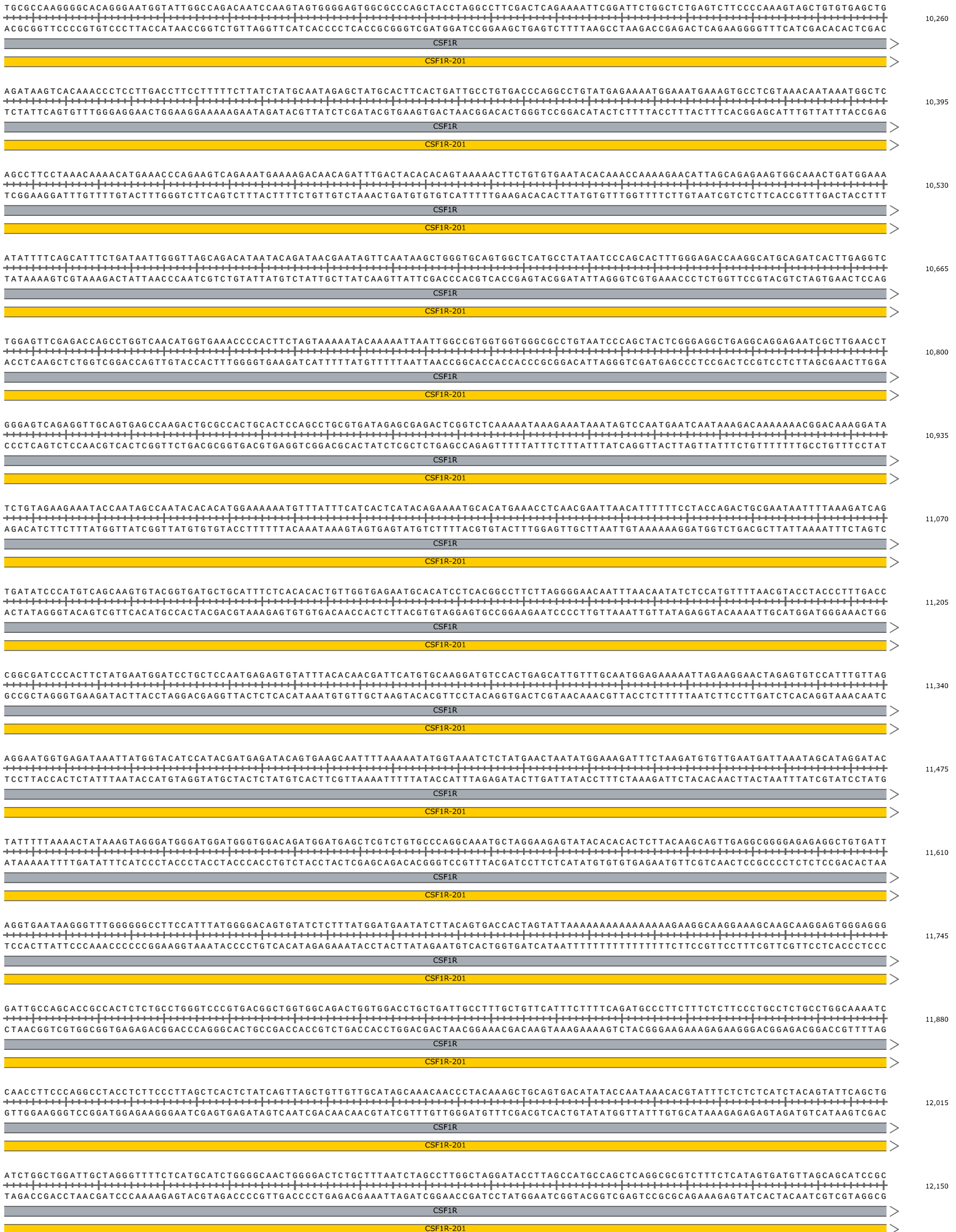
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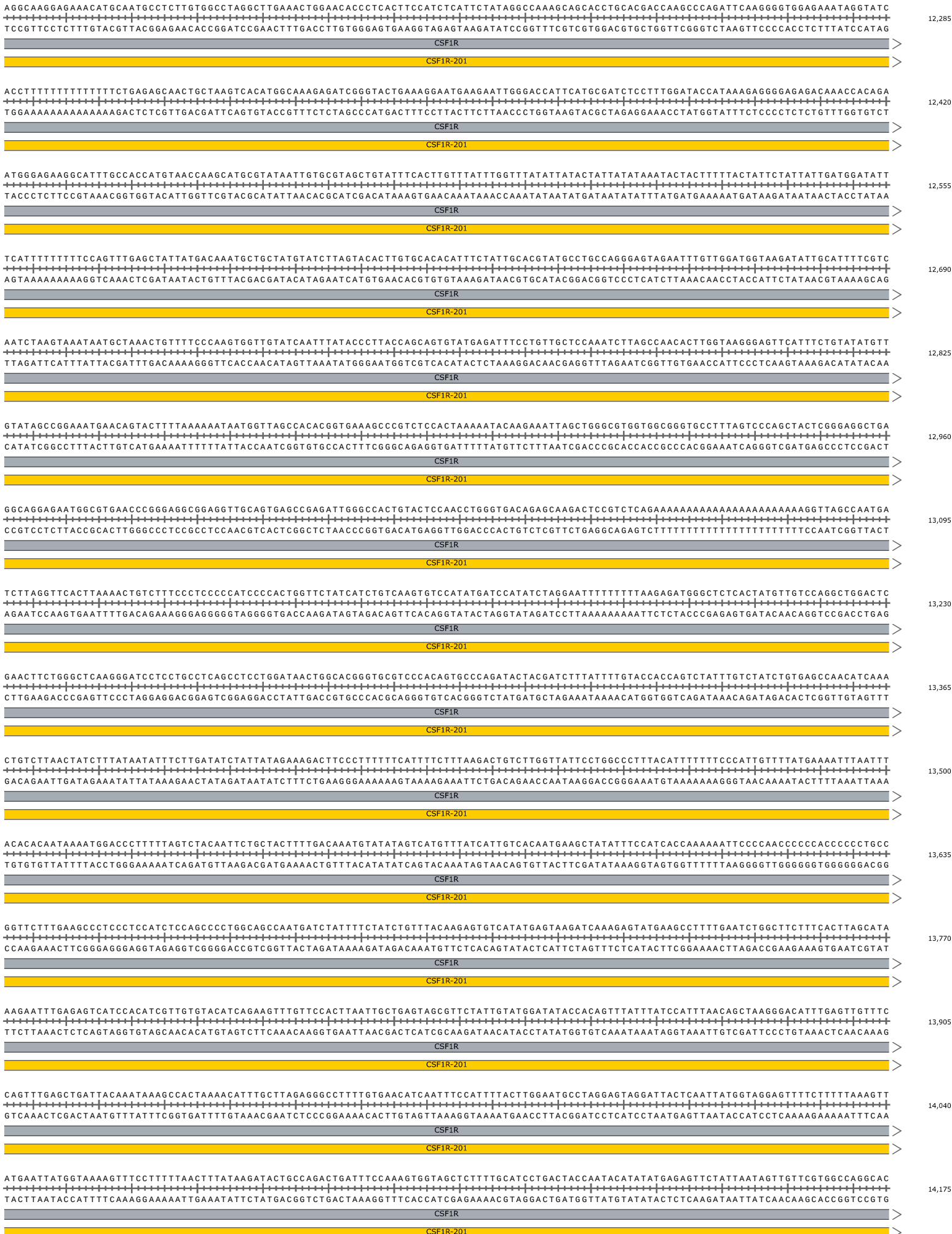
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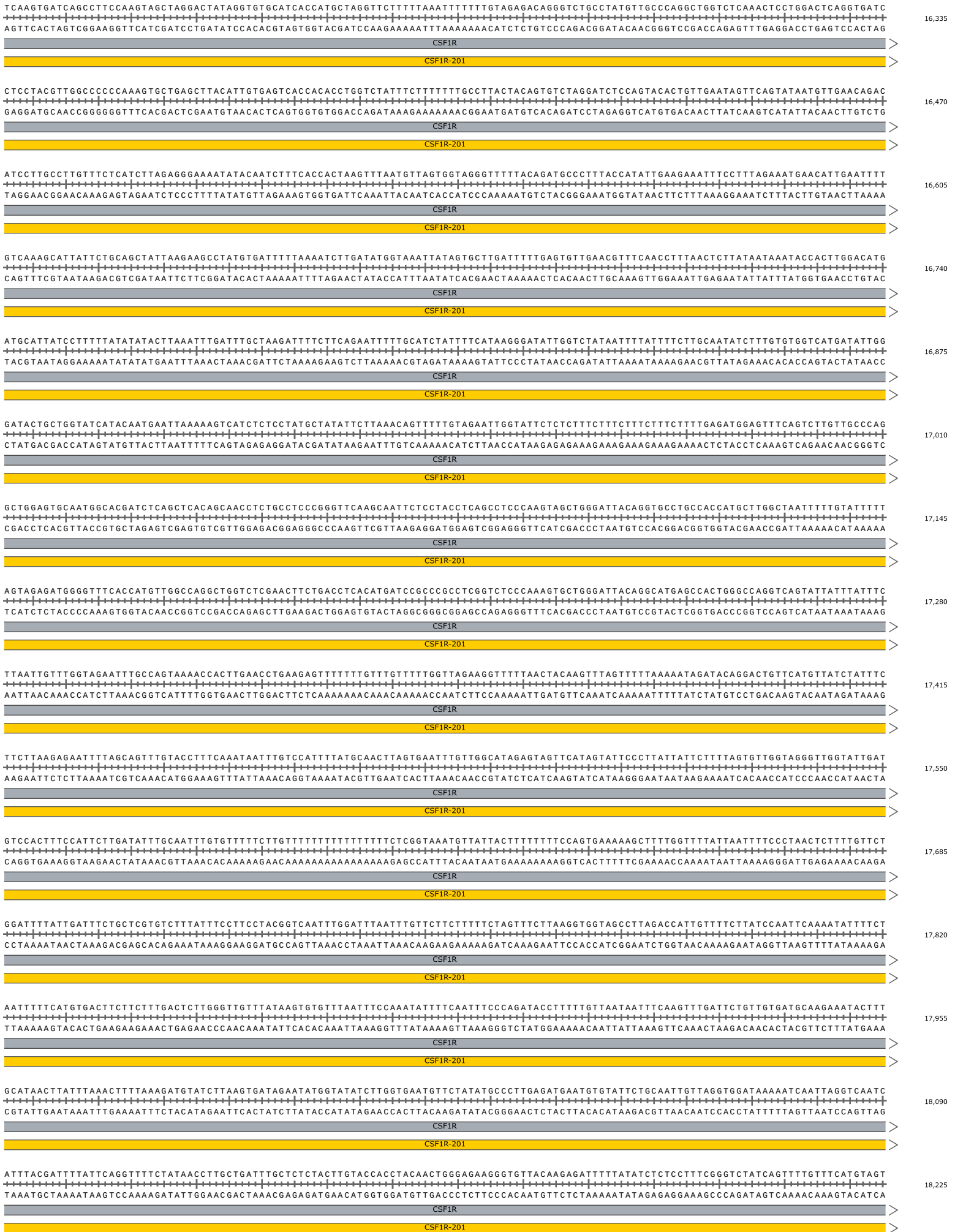


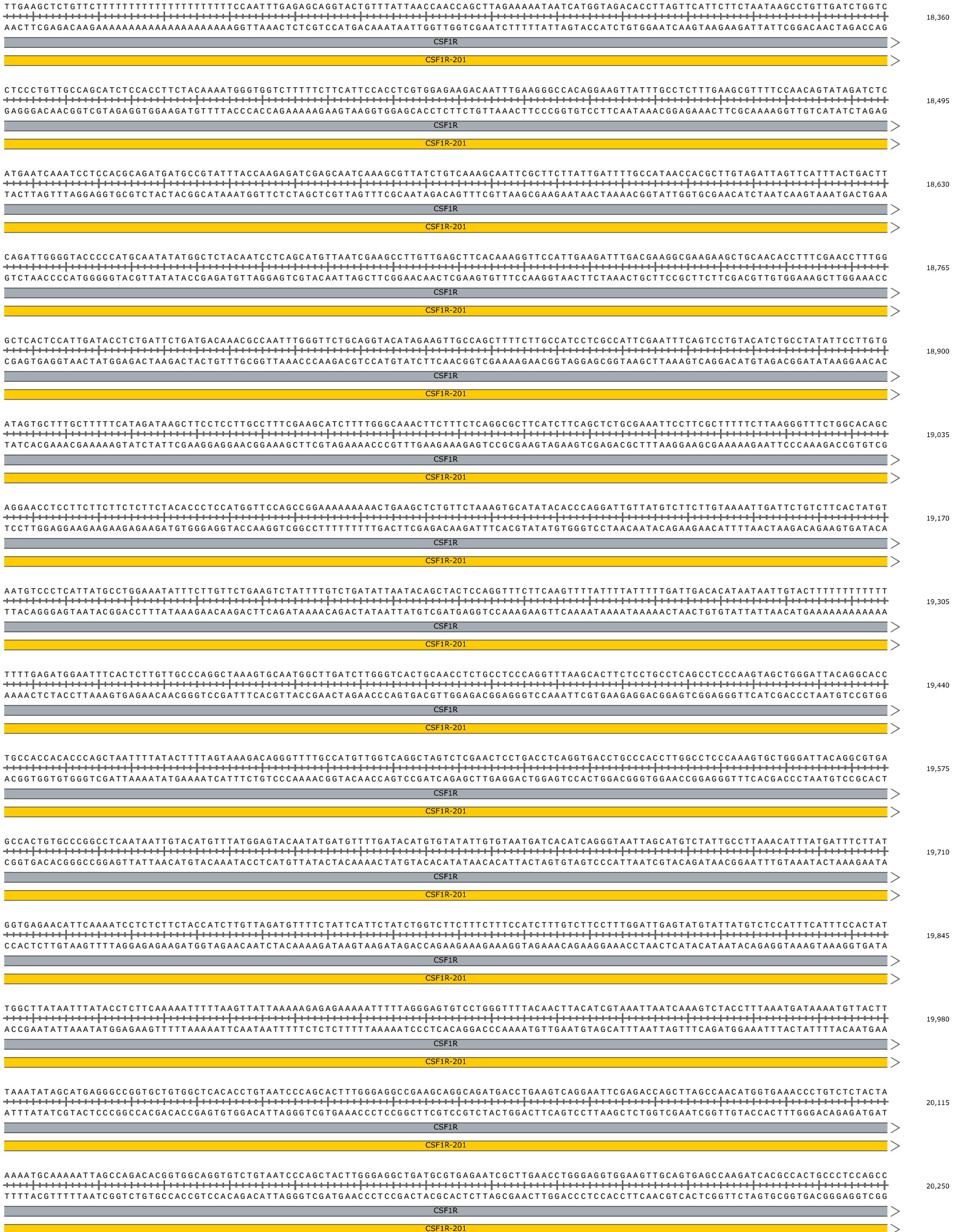




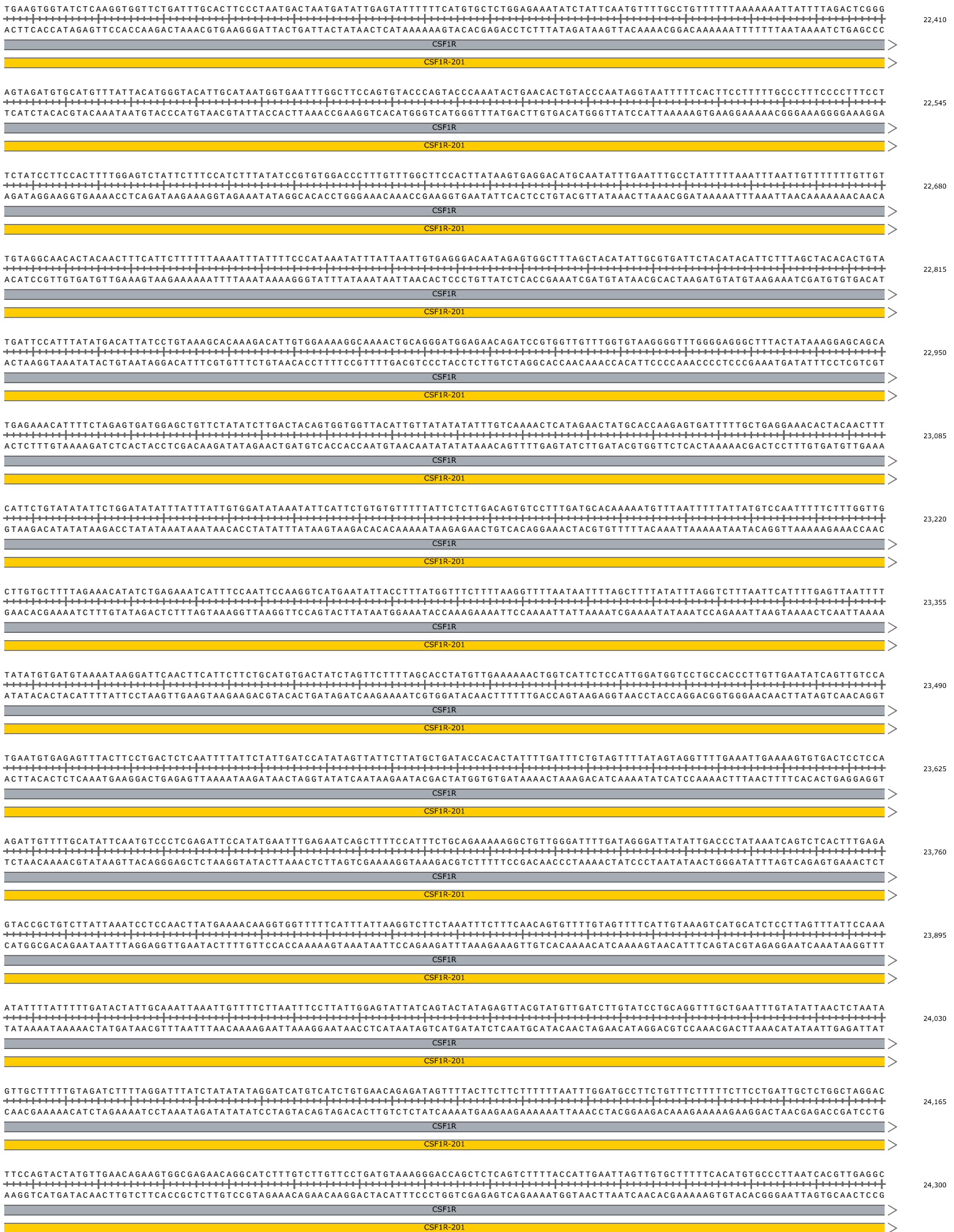


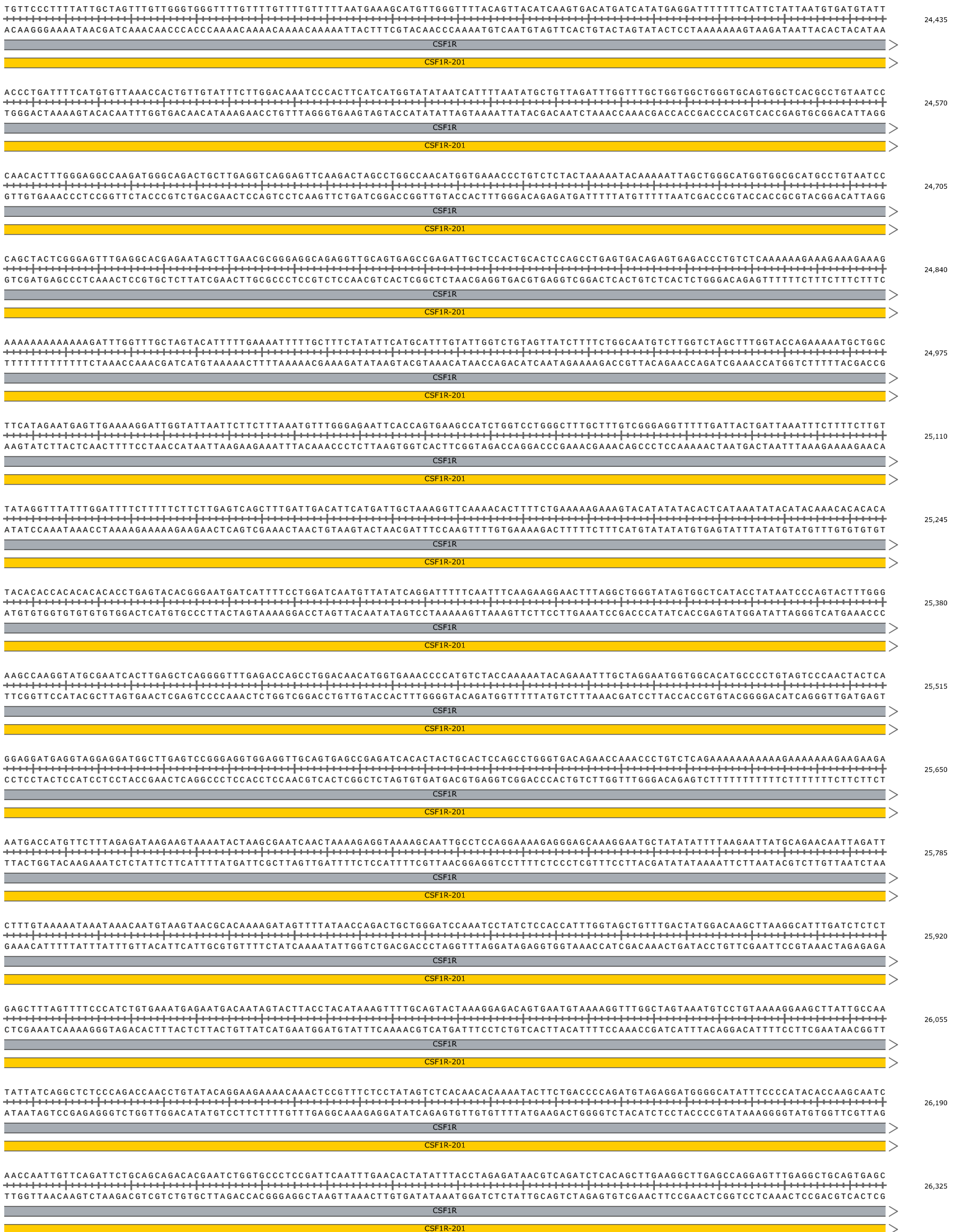




















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31,050

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CSF1R-201

CSF1R-201

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31,185

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31,320

CSF1R

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31,455

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CSF1R-201

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31,590

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CSF1R-201

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31,725

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31,860

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31,995

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CSF1R-201

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32,130

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32,265

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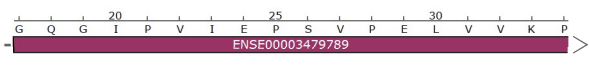
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32,400

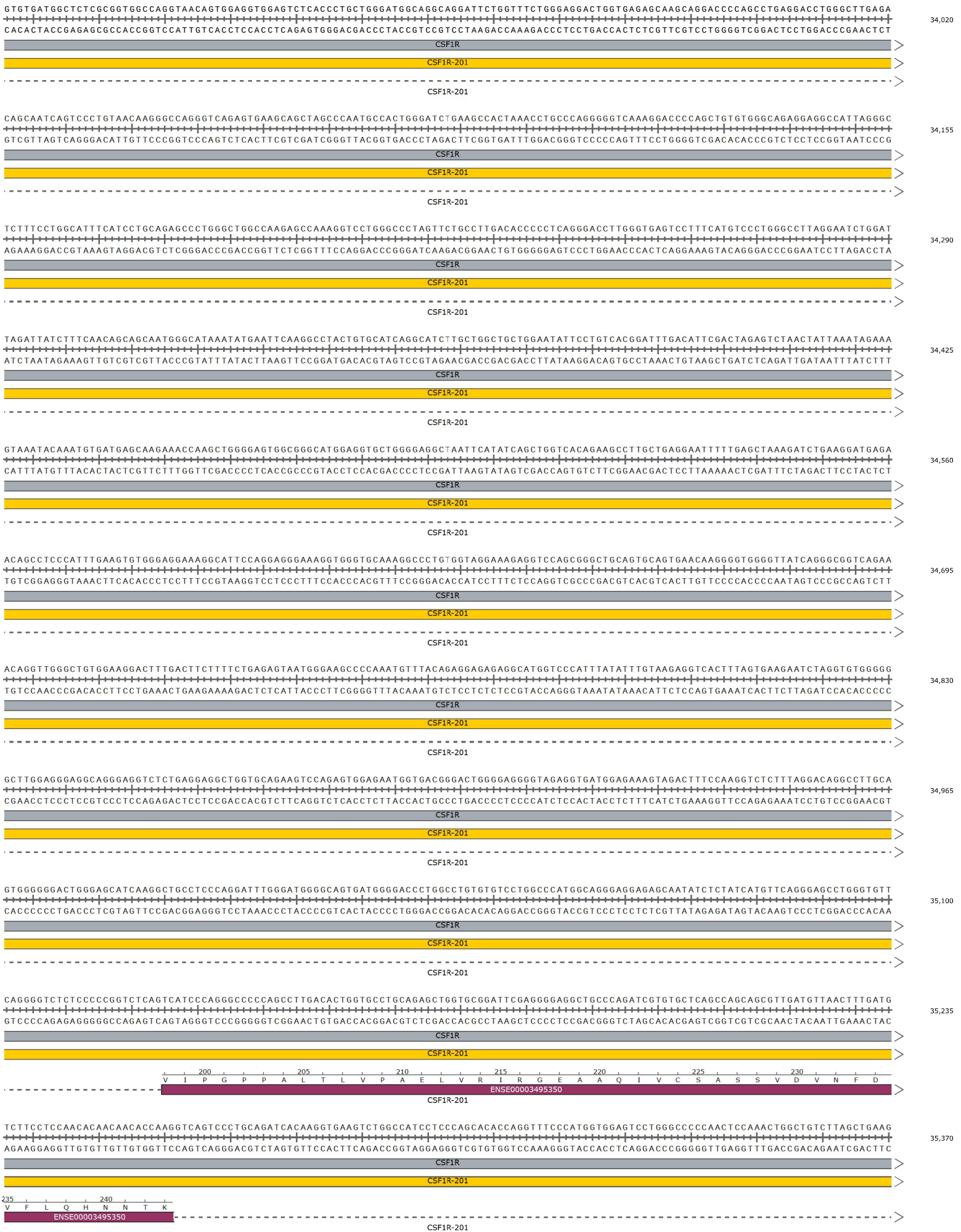
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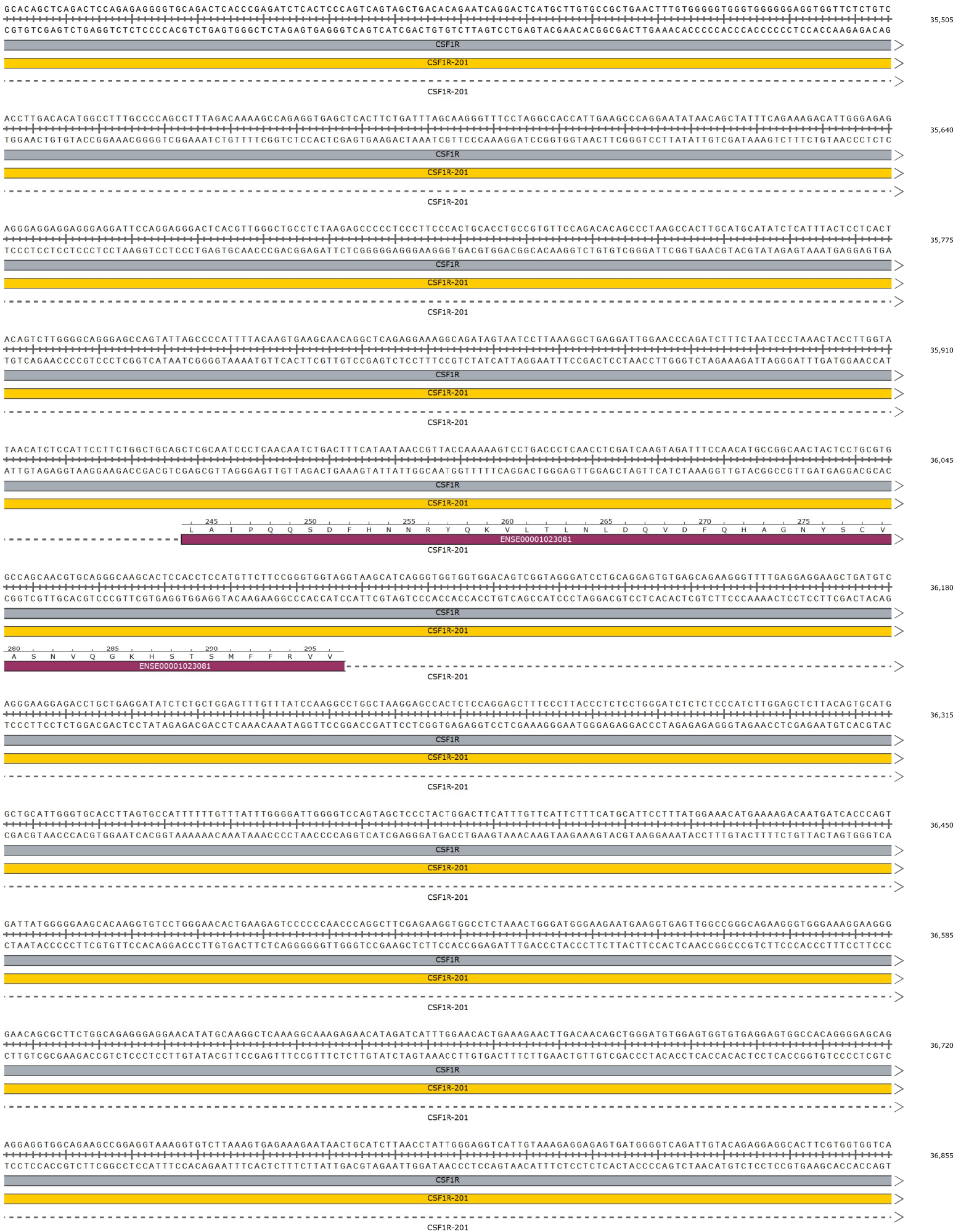
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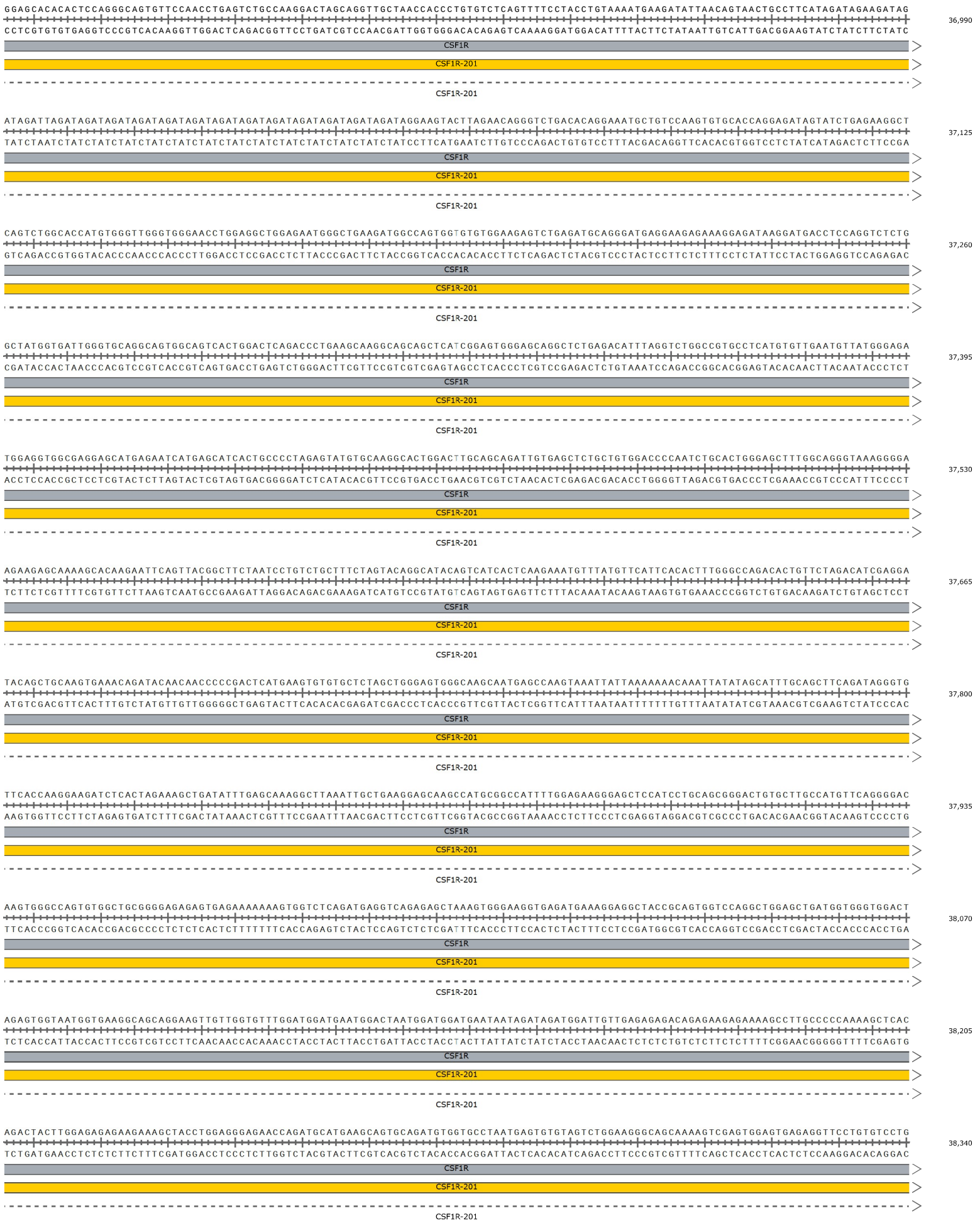
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38,475

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38,610

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38,745

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38,880

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39,015

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CSF1R-201

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39,150

CSF1R

CSF1R-201

CSF1R-201

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39,285

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39,420

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39,555

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CSF1R

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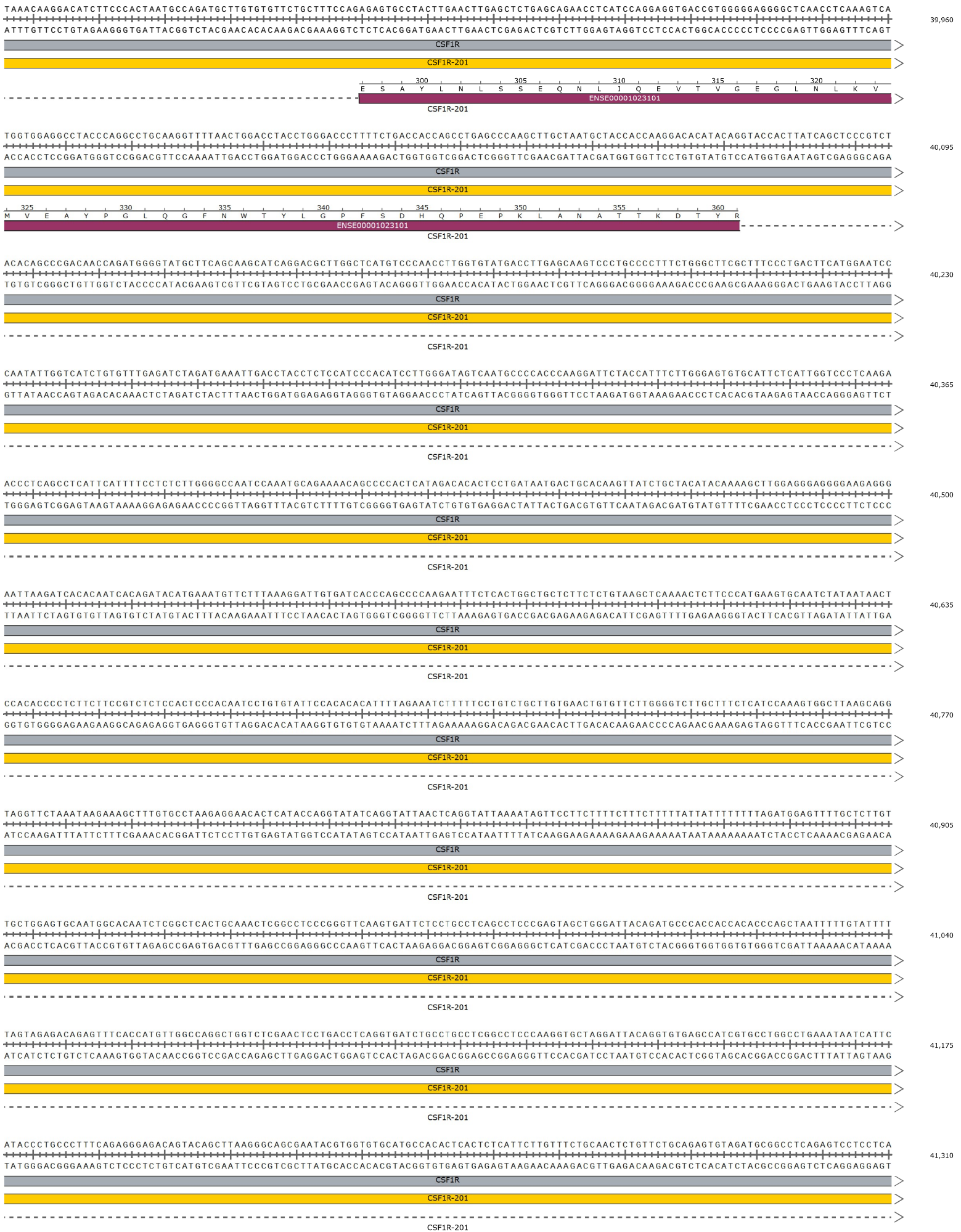
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39,825

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CSF1R

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CSF1R-201

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41,580

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41,850

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41,985

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42,120

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CSF1R-201

CSF1R-201

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42,255

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42,390

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42,525

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CSF1R-201

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42,660

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CSF1R-201

CSF1R-201

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42,795

CSF1R

CSF1R-201

CSF1R-201

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42,930

CSF1R

CSF1R-201

H T F 365 L S L P R L K P S E A G R Y S F L A R N P G G W R A L T F 395 E L T L R

ENSE00001023092

CSF1R-201

CCGAGCGCCACCTGGGGCGGAGGCCCTGGGACTGCCTGGAGGGATGGGGTTGACTGGGGCAGGGACAGGAAAGTAGGACTGGGAGATTGGGAGTGGCGGGAAAGTGTACTGGGGCCTCCTCTTCTTC  
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43,065

CSF1R

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CTCAGACCCCAAGAGGTAAGCGTCATATGGACATTCATCAACGGCTCTGGCACCTTTTGTGTGCTGCTCTGGTACCCCAAGCCCAAGTACAGTGGCTCGAGTGCAGTGGCCACACTGATAGGTAAGTGGG  
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43,200

CSF1R

CSF1R-201

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ENSE00001023097

CSF1R-201

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43,335

CSF1R

CSF1R-201

C D E A 445 V L Q

ENSE00001023094

CSF1R-201

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43,470

CSF1R

CSF1R-201

V W D D P Y 450 P E V L S Q E P F H K V T V Q 470 S L L T V 475 E T L E H 480 Q T Y E C R A H N S V G S 490

ENSE00001023094

CSF1R-201

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43,605

CSF1R

CSF1R-201

G S W A F I 495 P I S A 500

ENSE00001023094

CSF1R-201

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43,740

CSF1R

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CSF1R-201

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43,875

CSF1R

CSF1R-201

CSF1R-201

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44,010

CSF1R

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44,145

CSF1R

CSF1R-201

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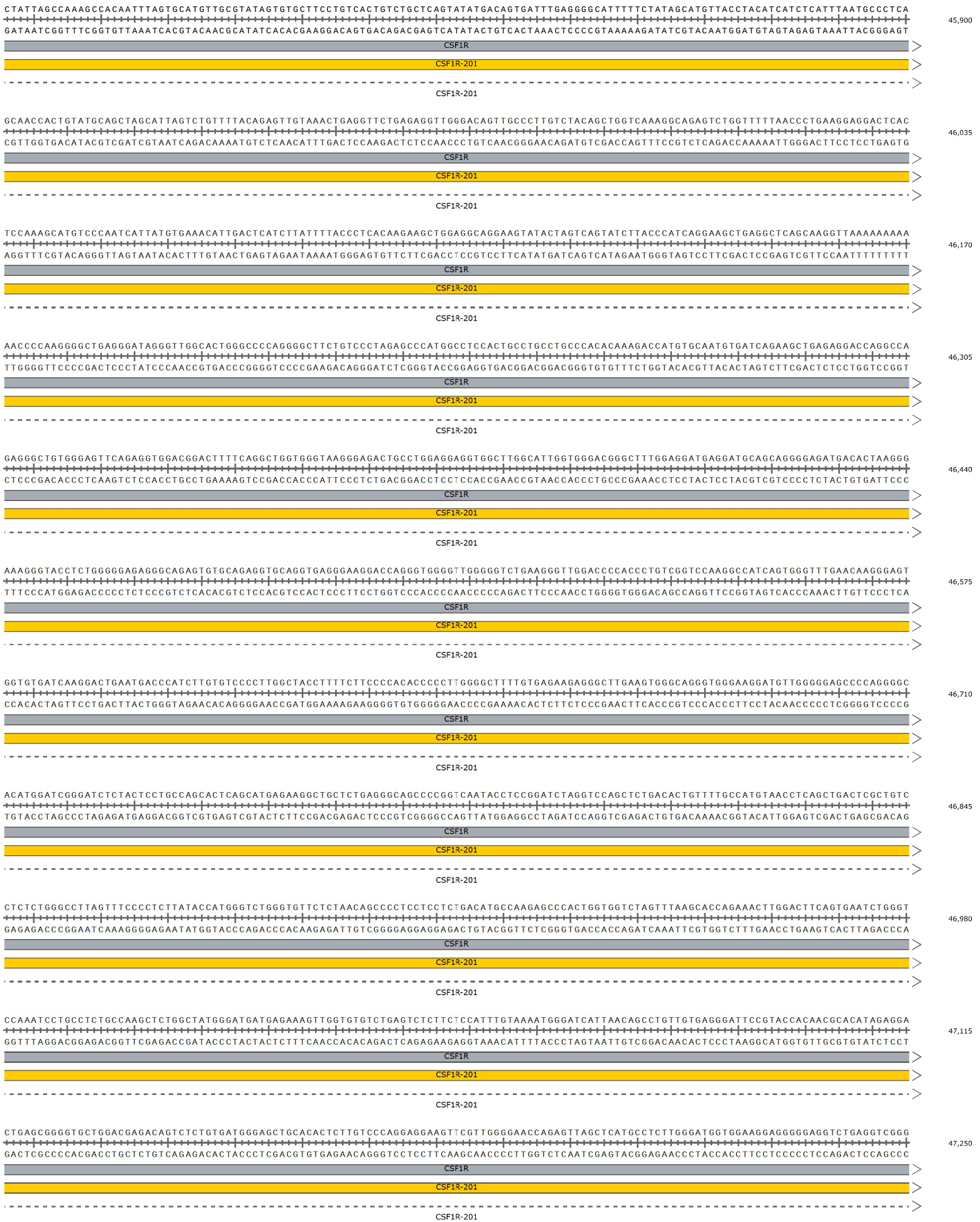
44,280

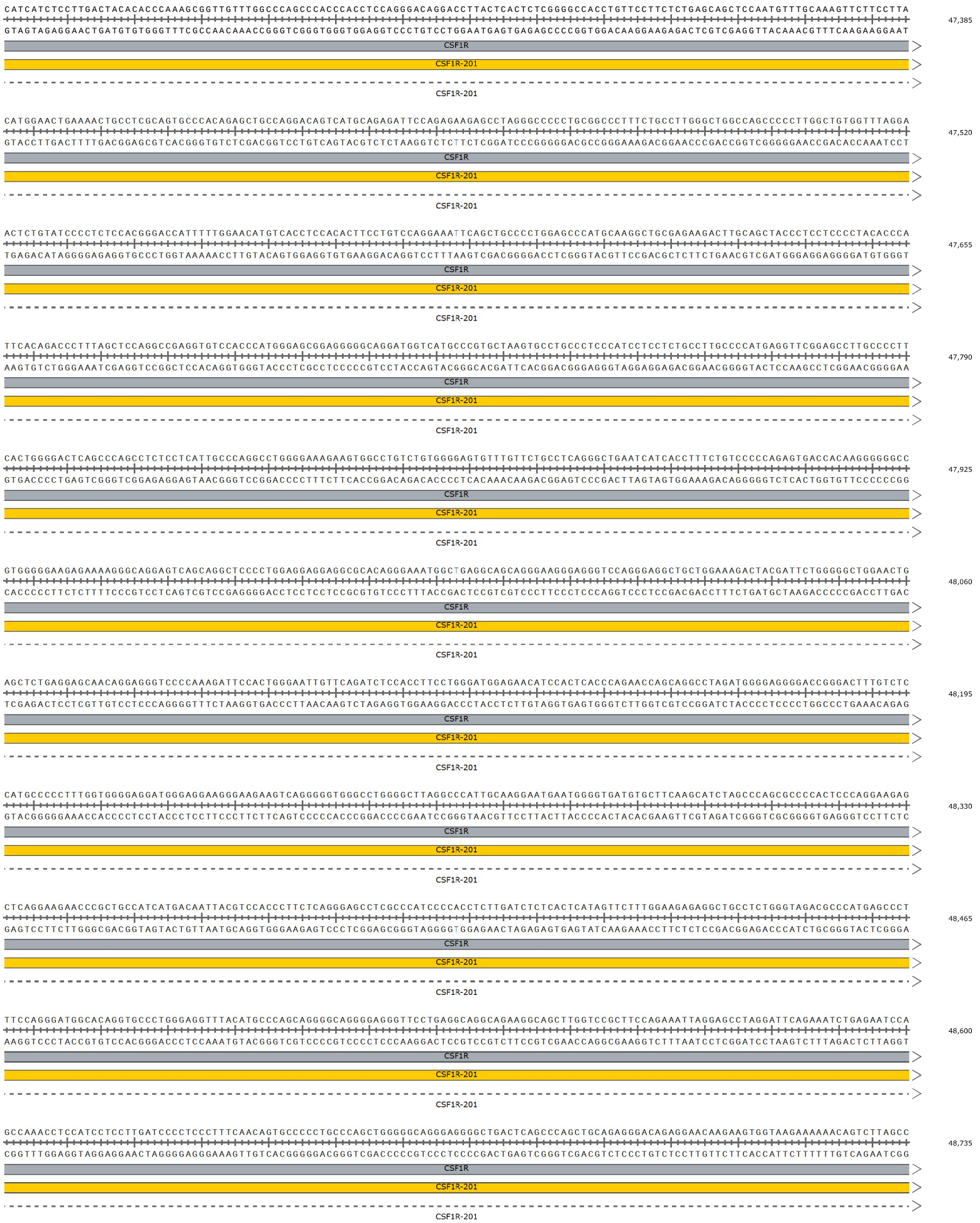
CSF1R

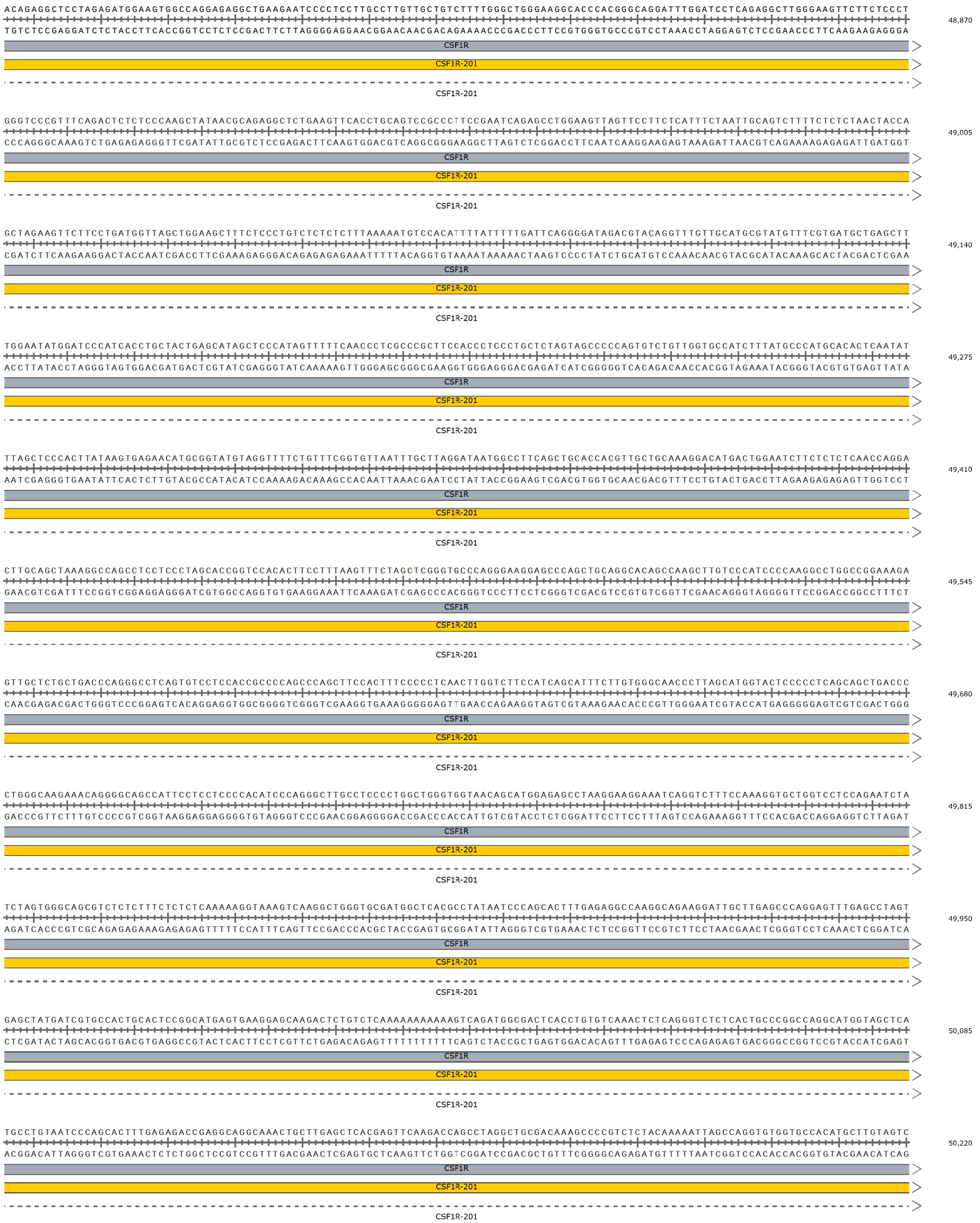
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C C G G C T G C T T G G G A G A C T G A G G T G G G A G G A T T G C T T G A A C C T C G G G G G T C G A G G C T G T A G T G A G C C A A G A C T G C C C C C A C T G C A T G C C A G T C T G G G G G A C A G A G A T C C T G T C T T G G A A A A A A A A A A A T C C C A A A A  
G G C C G A C G A A C C C T G A C T C C A C C C T C T A A C G A A C T T G G A G C C C C A G C T C C G A C A T C A C T C G G T T C T G A C G G G G T G A C G T A C G G T C A G A C C C C C T G T C T A G G A C A A C C T T T T T T T T T T A G G G T T T T

50,355

CSF1R

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G G G A A C C C A C T C A C T T A T C A T A G C C C T C A A G G C C T T C C T G T T T C T G G A A T C T G C C C C C A C T T C C C T C A A G C C A T G A T G G C T G C C T T C C T A T A G C T C A A A C T T G C C A G G A T C A T T C C C A T G T C A A G C A T A C A G C  
C C C T T G G G T G A G T G G A A T A G T A T C G G G A G T T C C G G A A G G A C A A A G A C C T T A G A C G G G G G T G A A G G G A G T T C G G T A C T A C C G A C G G A A G G A T A T C G A G T T T G A A C G G T C C T A G T A A G G G T A C A G T T C G T A T G T C G

50,490

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A T T C C A T G C A C T G T T C C T G G A A A A T T C T T C C T C T G A T G G T C A C A T G G T G G G C T C T T A G G G G C C T T C C T G A C T T A T C T T A C T T A T T T T T C T T C A T A G C A C C A C T T G A G A A T C C T C T A G A T A C A T G T T T A T T G  
T A A A G T A C G T G A C A A G A C C T T T A A G A A G G A G A C T A C C A G T G T A C C A C C G A G A A A T C C C G G A A G G A C T G A A T A G A A T G A A T A A A A A G A T A T C G T G G T G A A C T C T T A G A G G A T C A T G T A C A A A A A A C

50,625

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G T T T A A T G C C T C T C T A G C C A C T A G A A T G C A A A C C C A T G G A G G G C A G G G A C T T T G T C C T G T T A A C T C T G A A T C A G C G G G T G C C T G A C A C A A T A G A T G T T C A A G A A A G T A T G G G A T G G G T A C T A T T A T T C  
G C A A A T T A C G G A G A G T C G G T G A T C T T A C G T T T G A G G T A C C T C C C G T C C C T G A A A C A G G A C A A G T T G A G A C T A G T C G C C A C G G A C T G T G T T A T C T A C A A G T T C T T T C A T A C A C C T A C C C G A T G A T A A T A A G

50,760

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A G C C T T A A A A G G A A G G G A A T T C T G A C C T G T G C T G C A G C A T G A A T G A A C C T T G A A G A C A T T A T G C T G G G T G A A A T A A G G C A A T C T C A A T A G A C A C A T G C T G T G T G A G T C C A C T G A G G T G C A G T G C C T A G A G C A G T  
T C G G A A T T T T C C T T C C C T T A A G A C T G G A C A C G A C G T C G T A C T T A C T T G G A A C T T C T G A A T A C G A C C C A C T T T A T T C C G T T A G A G T T A T C T G T G T A C G A C A C A C T A G G T G A C T C C A C G T C A C G G A T C T C G T C A

50,895

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G C A A T T C A C A G A G A C A G C A G A A T C A T G G T T G C C A G G G C T G G A G G A G G G A A A G G G A G T T G C T T T T A A C A G G A A C A G A A T T T C A G T T T T G C A A G A T G A A A A G A G C T C T G G A A A C T G G T T G C A C A A G G T A G A A T G  
C G T T A A G T G T C T G T C G T C T T A G T A C C A C G G T C C C G A C C T C C C T T T C C C C T C A A C G A A A A A T G T C C T T G T C T T A A A G T C A A A A C G T T C T A C T T T T C T G A G A C C T T G A C C A A C G T T T C C A T C T T A C

51,030

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T A A T T A C T T A A T A C T A C T G A A C C A T A C A C T T A A A A T G G T T G A A A T G G T A A T T T C A T G T A T G T T T A T C A C A A T T A A A A T A T A T A T A T A T T T G G A T G G G A G G T T G G G T G G G T G G A T G G A T G G G T A G A T G G A  
A T T A A A T G A A T T A G A T A C T T G G T A T G T A A T T T T A C C A A C T T T A C C A T T A A A G T A C A T A C A A A A T A G T G T T A A T T T A T A T A T A T A T A A A C C T A C C T C C A A C C C A C C C A C C T A C C T A C C A T C T A C C T

51,165

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T G G A C A G A T G A A C G G A T G G A T A A G A T C T C A A G T T C C A C C C T C C C T C C T G G C T C A G G A A T T A C C A G A T T A C A G A G A T A C A G G G C C C T C A G A G G T T G T C T T G T C C A A G G T C T T C A A T A C A C A A A T A G T G A A A C A G  
A C C T G T C A C T T G C C T A C C T A T T C T A G A G T T C A A G G T G G G A G G G A G G A C C G A G T C C T T A A T G G T C T A A T A G T C T A T A G T C C C G G G A G T C T C C A C A G A A C A G G T T C C A G A A G T T A T G T G T T A T C A C T T T G T C

51,300

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G C T T G G A G A A G G G A A G G T C A C A C A A A A G G C A G A G T C A A G C A G G A A C A T G C T C T C A G T G C T A T G T T C A T G A G A C A C C T C T C T C A G C C A G A G C A G G C C T T G C C C T G C C T T C T C C A C T G G G C G C C T T G G G A C T G  
G A A C C T C T T C C C T C C A G T G T G T T G T C C G T C A G T T C G T C C T T G T A C G A G A G T C A C G A T A C A A G T A C T C T G C T G G A G A G A G T C G G G T C T G T C C G A A C G G G A C G G A A G A G G G T G A C C C G G A A C C C T G A C

51,435

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C C C A C A C C C T G C T C T T G G G G G T C A G A A A C A A G G T C C A G G A A C T G C C T G C C A G C C C G A C T G C C A C G T G C C C T T C C C T T T C T G C A G A A G C C A A G T A C C A G G T C C G C T G G A A G A T C A T C G A G A G C A T A G A G G  
G G G T G T G G G A C G A G A A C C C C A G T C T T G T T C C A G G T C C T T G A C G G A C G G T C G G G G C T G A C G G T G C A C A G G G A A G G A A G A C G T C T T C G G G T C A T G G T C C A G G C G A C C T C T A G T A G C T C T C G A T A C T C C C

51,570

CSF1R

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545 K P K Y Q V R W K I I E S Y E G  
ENSE00003547588

C A A C A G T T A C T T T C A T C G A C C C C A C G C A G C T G C C T T A C A A C G A G A A G T G G G A G T T C C C C G G A A C A A C C T G C A G T T T G G T G A G A T G G C A G C T A T C A C T C C A C A G C T T C C A T C A C A G G G C C T G T G G G G T T G  
G T T G T C A A T A G A A G T A G C T G G G G T G C T C G A C G G A A T G T T G C T T C A C C C T C A A G G G G C C T G T T G G A C G T C A A A C A C T C A C C G T C G A G T A G T A G G T G T C G A A G G A T A G T G T C C C G A C A C C C C A A C

51,705

CSF1R

CSF1R-201

560 N S Y T F I D P T Q L P Y N E K W E F P R N N L Q F  
ENSE00003547588

CSF1R-201

CAAGGAGCCCATGGGCCCTTGGACAGAGGCCCTTGGTGCACAGGGACTTAAGGGACCTGTGTCGTGGCAGGTAAGACCCCTCGGAGCTGGAGCCCTTGGGAAGGTGGTGGAGGCCACGGCCCTTGGTCTGGGCA  
GTCCCTCGGGTACCCGGGAACCTGTCTCCGGGAAACCACGGGTCCCTGAATTCCTGGACACACGCCAGTCCATCTCTGGAGCTCGACCTCGGAAACCTTCCACCACCTCCGGTCCGGGAAACCAGACCCGT

51,840

CSF1R

CSF1R-201

585 G K T L G A G A F G K V V E A 600 605  
ENSE00003595569

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PCR Forward

ACATTT

AGGAGGATGCTGTCCGAAGGTGGCTGTGAAGATGCTGAAGTGTGAGTGAAGGGAGGGGATGAGGGAAAGGGATGGGGGGTGGTAGATGCTGGGGGTGGCTGGCCCTGGTGTACAAAGAGGCATCACACACATTT  
TCCTCCTACGACAGGACTTCCACCAGACTTCTACGACTTCACACTCACTCCCTCCCTACTCCCTTCCCTACCCCCACCATCTACGACCCCAACCAGCCGGGACCACAGTGTCTCCGTAGTGTGTGATAA

51,975

CSF1R

CSF1R-201

610 K E D A V L K V A V K M L K 615  
ENSE00003595569

CSF1R-201

PCR Forward

CAACCTGTTGAAGCCTGGG

CAACCTGTTGAAGCCTGGGGGACAGAGCTCAGGGGTGAGGACTTGGGTTTTCTGTGAGCTCCAGGCACCCCTCTGACTCCCGGCTCCAAAGAGGTCTAGGTACCCTTTAGTTGTGAAGGGGCTCCTGACTGAGC  
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52,110

CSF1R

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52,245

CSF1R

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CSF1R-201

Donor Template WT -> SNV

CTGTCTTTGGG

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52,380

CSF1R

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Donor Template WT -> SNV

Donor Template WT -> SNV

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52,515

CSF1R

CSF1R-201

620 S T A H A D E K E A L M S E L K I M S H L G Q H E N I V N L L G A C T H G 655  
ENSE00003586812

CSF1R-201

Donor Template WT -> SNV

PAM Protospacer Sequence

SNV

GTACAGGCTCGACTTCTAGT  
gRNA Protospacer

CTCGGACATGGGTACCTCCA  
Sanger Sequencing Primer

GGCCCTTGGGGTCTCCTGGGGCCAAAGTCTTGGGGCTCTGGGGAATCTCAGGGCCCAAGGGCTACCTTGTTCCTCTCTCCTTCTCAGGATCCTACTGCTCCAAGTGTAGGGGGATCCCGGTACAGCATCCC  
CCCGGAACCCAAAGACCCCGGTTCCAGAACCCCGAGACCCCTTAGAGTCCCGGGTCCCGATGGAACAAGGCAAGAGGAAAGAGTCTAGGATGACGAGGTTCCAGTCCCCCTAGGGCCAGTGTCTGATGGG

52,650

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52,785

CSF1R

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CSF1R-201





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TGGGGCAGAGATAATTTATATGTTTAAATCGGCCGACCACCAGCGTACGGATATTAGGGTCGATGAGCCCTCCGACTCCGCCCTCTAACGAACCTTGGGTCTCCGTCTCCAACGACACTCGACTCTAGTGTGG

54,270

CSF1R

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TAACGTGAGGTGGACCCGTTGTTCTTACTTTGAGGCAGAGTTTTTTTTTCTCTCTACCGAGACAACAGGACAACGACACTAAGGACCTTCGGTAGGCTTTGCTCGGTAGGTTGCTGTCTCGGTGATCCCTT

54,405

CSF1R

CSF1R-201

CSF1R-201

CCAAAGAGAGGAAGTGGGAGATTTCATGTACACATGAGTCAGGGTTAGAGGTGGAGCCTGGACTAGAATCTGCTCTCTTGACTTCCAGTCCAGGAGTCAACCAAGCCACACTGCTGTCTGGAGGTCTCTGTC  
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54,540

CSF1R

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CSF1R-201

TCAGGGGCTTGTGGGTCAGGACAGGATCAGAAACAAGAGGGTGTACACTGCGCCCTCATCTAGATACTGTGAGTCCACGCTGGGGAAGCAAAAGAGAAGGAGGCCATCTCTTACCCAGGGCCTTAAAAA  
AGTCCCAGAACCCAGTCTGTCTAGTCTTGTCTTCCACATGTGACGCGGAGTAGGATCTATGACAGTCCAGGTCGGGACCCCTCCGTTTTCTCTTCCCGGTAGAGAAGTGGGTCGGAAATTTT

54,675

CSF1R

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CSF1R-201

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54,810

CSF1R

CSF1R-201

CSF1R-201

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54,945

CSF1R

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CSF1R-201

GAACACTAGAATATGGACATTGTCAAGGTACACATCTCTAGCGCAGAGGGGACAGGAGGGAGAGAAAATCTATCTGGCTGGAACGTTAGGAGCAGTAGTGCTTCAGTCTACAGTAGTGCTTCAAATCTCT  
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55,080

CSF1R

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55,215

CSF1R

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55,350

CSF1R

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CSF1R-201

AAAGCTCCCGAAGTATTTTAAATGTGAAGCCAGGGGTGTGAGGCACTGTCCAGAGAAGAGAGGGCAACAAGGGGCCCTAGAATATGCCCAATCTAGTAGGGCTGTTATGGGGAAGAGACTCCAACCTCTCTGT  
TTTCGAGGGCTTCACTAAAATTACACTTCGGTCCCACACTCCGTGACAGGTCCTCTCTCCCGTGTTCGCCGGGATCTTACGGGGTTAAGATCATCCCGACAATACCCCTTCTCCTGAGGTTGAAGAGACA

55,485

CSF1R

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GGCCCTTGAAGGTAGAGCAGGGGCTAGGAGGAAAATCTCAGGGGTAGATTGGCATTAGGAACAGTGAAGAACCTTCTCACAGGCAGAGCTGCCAAAACAGAAATGGGTTGTAAGTCCCTCACCGGGGACAGCC  
CCGGAACTCCCATCTCGTCCCGATCCTCCTTTAGAGTCCCATCTAACCGTAATCTTGTCACTTCTTGAAGAGTGTCCGCTCGACGGGTTTTGGTCTTACCAACATTCGAGGGAGTGGCCCTGTGCGG

55,620

CSF1R

CSF1R-201

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GAGCAGAGACCAATGCTCACTCAGATGGAGTGTGGCAGGAGGGTTTCTTATCAGAAAAGGGAGTCCACAGTTGACCATGGGGTGGTGGGTGGTCAAGGCCCTGAGCTGACAGTGCAGTGTATGATGAGTGACCTCTGCTCGTCTCTGGTTACGAGTGTGAGTCTACCTCACACCGTCTCCCAAAGATAAGTCTTTCCCTCCAAGGTCAACTGGTACCCACCACCCAGTTCGGACTCGACTGTCACGTCACTACTACTACTGAGAC

55,755

CSF1R

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CCCCCAACCCCTCTCCTATGTAGGGACAGTGGCTTCTCCAGCCAGGGTGTGGACACCTATGTGGAGATGAGGCCTGTCTCCACTTCTTCAAATGACTCCTTCTCTGAGCAAGGTGAGGAGGTCCCAAGGCCAGGGGGTGGGAGAGAGGATACATCCCTGTACCAGAAAGGTCGGTCCACACCTGTGGATACACCTCTACTCCGGACAGAGGTGAAGAAGTTTACTGAGGAAGAGACTCGTTCCACTCTCCAGGGTCCCGGTC

55,890

CSF1R

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715 720 725 730 735 740  
D S G F S S Q G V D T Y V E M R P V S T S S N D S F S E Q  
ENSE00003582642  
CSF1R-201

GCCCCATTTGCTTGATAACAAGGGAAAAGGAGAAGGGCTGCTGGGGTGAAGGGTGGGGAGTGTGGCAGGGCTGCCCTGACGCCTTCTCCACCCCTAGACCTGGACAAGGAGGATGGACGGCCCTGGAGCTCCGCGGGTAAACGAAGTATTGTTCCCTTTTCCCTTCCCGACGACCCCACTCCCAACCCCTCACACCGTCCGACGGACTGCGGAGAAGGGTGGGATCTGGACCTGTTCTCTACCTGCGGGGACCTCGAGGC

56,025

CSF1R

CSF1R-201

745 750  
D L D K E D G R P L E L R  
ENSE00003499486

GGACCTGCTTCACTTCTCCAGCCAAGTAGCCAGGGCATGGCCTTCTCGCTTCCAAGAAATGTGAGTAGGAACCTGGCCCTGGCTCATAGCCACCCAGGTTCTGTCTCCGGGAGGCTGGATGAGTGACGATGGCCTGGACGAAGTGAAGAGGTCGGTTCATCGGGTCCCGTACCAGGAGGAGCAAGGTTCTTACACTCATCCTTGGACCGGGACCGAGTATCGGTGGTCCAGACAGAGGCCCTCCGACCTACTACTGCTACCC

56,160

CSF1R

CSF1R-201

755 760 765 770  
D L L H F S S Q V A Q G M A F L A S K N  
ENSE00003499486

CSF1R-201

GAGGAGGAAACGGGAGCCTGTGAGGGGTAGGGGAGGAGACAGATGAGAGAGTCAATTTGGGCAGCAGCTGCAAGGATGAGTGGGAGAAGCTGTGCCAGGGCTGGAGCTCTGGGGCTGGGACCTGTGTCCCTCCTTTGCCCTCGGACACTCCCCATCCCTCCTGTCTCATACTCTCTCAGTAAACCGTCTCGACGTTCTACTCACCCCTTTTCGACACGGGTCCCGACCTCGAGACCCCGACCCGTGGACACAGG

56,295

CSF1R

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CSF1R-201

CCAGCGTGAAGATGAGGAAGGGTACCAGGCTTCTCATTCTGTTTTACTAAATAGTGTATGAGAGACAACAGTTGTCTCTCATAAAGCACGGCTCTGGTGGGATGATAACGGAAAGCTTCTCAGAATTTGGTGCACCTTCTACTCCTTCCCATGGTCCGAAAGAAAGTAAAGCAAAATGATTTATCACATACTCTCTGTGTCAACAGAGACGAGTATTTCTGTCGCGACACCCCTACTATTGCTTGAAGGAGTCTTAAA

56,430

CSF1R

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TGGGATATTAGATAACGTATAAAGTGCCTCGGCCCTAGGAAAGGATGCCAGGGAATGGGAGCTTGTGCATCTTCTTAGAACAGATTCCGGAGTCAGTGGTTTATTGTTGGCTCTGCCACCTGCTCCGTGACACCCCTATAATCTATTGCATATTTACGCGAGCCGGATCCTTCTCACGGTCCCTTACCCTCGAGAACGGTAGAAGGAATCTGTCTAAGCCCTCAGTCACAACTAACAACCGAGACGGTGGACGAGGCACTG

56,565

CSF1R

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CSF1R-201

TTTAAGCAACTATTTAAATTCGTGCCTCAGTTTCTACACCTATAAAAATGGGCATAACGATGTTGAAAAGAAAAGGGTTCAATGTGTGCAGAGTTTAGGGAAAGGGCTGGCAGATAGCAGCTGCTATGATCAAATTCGTTGATAAATTAAGACACGGAGTCAAAGATGTGGATATTTTACCCTGATTGCTAACAACTTTCTTTTCCCAAGTTACACACGCTCAAATCCCTCCCGGACCGTCTATCGTCGACGATACTAGT

56,700

CSF1R

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CSF1R-201

GAAGTAACGGTAGGGTTGGAGACTGCTCTCTGCACGGAAGCCCTTCGCTTCTGGGGCTGAGCAGACCAAGTCAAGAGCAAAAGGGTGAAGAAGGCCATGGCTGCTCAGGGTAATGGGGTTTCTAAGCATTAAACCTTCATGCCATCCCAACCTCTGACGAGAGACGTGCCCTTCGGGAAGCGAAGACCCGGACTGCTGTTGTCAGTCTCTGTTTCCCACTCTTCCCGTACCGACGAGTCCCATTACCCCAAGGATTCGTAATTT

56,835

CSF1R

CSF1R-201

CSF1R-201

TGATCAGATCACGATACACATTCTCAGATCCTGGGCCCTGGTAGAAGGTATAGACAAGGGTTTGGTAAAGGACCAAACCTGTTGTTCACTCCAGCAGGGACTCCAAAGCCATGTGGGGCCCTCCCTGCCATCCACTAGTCTAGTCTATGTGAAGAGTCTAGGACCCGGGACCATCTCCATATCTGTTCCCAAACACCATTTCTGGTTTGAACAAGTGAAGTCTGCTGAGGTTTCGGTACACCCGGGAGGGACGGTAAAG

56,970

CSF1R

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CSF1R-201

TCTCACCTCAGGCTCAGGTAGGAGAAAGCCAAAGACTAACCTGCAAGTCTTCCCTCAGTGCATCCACCGGGACGTGGCAGCGGTAACGTGCTGTTGACCAATGGTTCATGTGGCCAAGATTGGGGACTTCGGAGGAGTGGAGTCCGAGTCCATCCTCTCCGGGTTCTGATTGGGACGTCACGAAAGGGAGTCAAGTAGGTTGGCCCTGCACCGTCGCGCATTGCACGACAACTGGTTACCAGTACACCGGTTCTAACCCCTGAAGCC

57,105

CSF1R

CSF1R-201

775 780 785 790 795  
C I H R D V A A R N V L T N G H V A K I G D F G  
ENSE00003511616  
CSF1R-201





Feature	Location	Size	Type
<b>CSF1R</b>	1 .. 60,082	60,082 bp	gene
/note	= gene <a href="#">ENSG00000182578</a>		Protein coding
<b>CSF1R-201</b>	1 .. 60,082	60,082 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000286301</a>		
<b>CSF1R-205</b>	1 .. 33,321	33,321 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000511344</a>		
<b>Y_RNA</b>	14,867 .. 14,967	101 bp	gene
/note	= gene <a href="#">ENSG00000199409</a>		misc_RNA
<b>Y_RNA.26-201</b>	14,867 .. 14,967	101 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000362539</a>		misc_RNA
<b>RPL7P1</b>	18,325 .. 19,071	747 bp	gene
/note	= gene <a href="#">ENSG00000214485</a>		processed_pseudogene
<b>RPL7P1-201</b>	18,325 .. 19,071	747 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000468161</a>		processed_pseudogene
<b>CSF1R-203</b>	26,783 .. 60,082	33,300 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000504875</a>		Nonsense mediated decay
<b>CSF1R-210</b>	26,819 .. 60,078	33,260 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000675795</a>		
<b>CSF1R-202</b>	26,819 .. 36,469	9651 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000502660</a>		Retained intron
<b>CSF1R-201</b>	26,946 .. 59,304	32,359 bp	CDS
▶ 21 segments = 2919 bp			
/note	= coding sequence <a href="#">ENSP00000286301</a>		
/translation	<pre> MGPVGLLLLLVATAWH,,GQGIPVIEPSVPELVVKPGATVTLRCVGNVSVEWDGPPSPHWLTYSDGSSSILSTNNATFQNTGTYRCTEPGDP LGGSSAAIHLVVK,,DPA RPNVWLAQEVVVFEDQDALLPCLLTD PVL EAGVSLV RVRGRPLMRHTNYSFSPWHGFTIHRAKFIQSQDYQCSALMGGRKVMMSISIRLKVQK,,VIPGPPALTLVPAELVRIRGEAAQIVCSASSVDVNFDFLQHNNTK,,LAIPQSDFHNNRYQKVLTLNLDQVDFQHAGNYSCVAS NVQ GK HST MFFRVV,,ESAYLNLSEQLIQEVTVGEGLNKVMVEAYPLQGFNWTYLGPFSDHQPEPKLANATTKD TYR,,HTFTLSLRLK PSEA GRYSFLARNP GGWRALT FELTLR,,Y P EV SVI WTF INGS GTLLCAA SG YPQPNVTLWQCSGHTDR,,CDEAQLVQVWDDPYPEVLSQEPFHKVTVQSLTLETLEHNQTYECRAHNSVGGSGWAFIPISA,,GAHTHPDEFELFTPVVACMSIMALLLLLLLLLLLYKYK,,KPKYQVRWKIIESYEGNSYTFI DPTQLPYNEKWEFPRNNLQF,,GKTLGAGAFGKVVEATAFGLGKEDAVLKVAVKMLK,,STAHADEKEALMSELKIMSHLGQHENIVNLLGACTHG,,GPVLVITEYCCYGDLLNFLRRKAEAMLGP SLSPGQDPEGGVDYKNIHL EKKYVRR,,DSGFSSQGVDTYVEMRPVSTSSNDSFSEQ,,DLDKEDGRPLELRDLLHFSSQVAQGMFLASKN,,CIHRDVAARNVLLTNGHVAKIGDFGLARDIMNDSNYIVKGN,,ARLPVKWMAPE SIFDCVYTVQSDVWSYG DZVHRJAGUYPQKVMDFYKLVKDGQYMAQPAFA PKNI,,YSIMQACWALEP THRPTFQIC SFLQEQAE DR RER,,DYTNLPSSRSRSGSGSSSSEEEEESSHELTCC EQGDIAQPLLQPNNYQFC* </pre>		
<b>CSF1R-210</b>	26,946 .. 59,304	32,359 bp	CDS
▶ 21 segments = 2919 bp			
/note	= coding sequence <a href="#">ENSP00000501699</a>		
/translation	<pre> MGPVGLLLLLVATAWH,,GQGIPVIEPSVPELVVKPGATVTLRCVGNVSVEWDGPPSPHWLTYSDGSSSILSTNNATFQNTGTYRCTEPGDP LGGSSAAIHLVVK,,DPA RPNVWLAQEVVVFEDQDALLPCLLTD PVL EAGVSLV RVRGRPLMRHTNYSFSPWHGFTIHRAKFIQSQDYQCSALMGGRKVMMSISIRLKVQK,,VIPGPPALTLVPAELVRIRGEAAQIVCSASSVDVNFDFLQHNNTK,,LAIPQSDFHNNRYQKVLTLNLDQVDFQHAGNYSCVAS NVQ GK HST MFFRVV,,ESAYLNLSEQLIQEVTVGEGLNKVMVEAYPLQGFNWTYLGPFSDHQPEPKLANATTKD TYR,,HTFTLSLRLK PSEA GRYSFLARNP GGWRALT FELTLR,,Y P EV SVI WTF INGS GTLLCAA SG YPQPNVTLWQCSGHTDR,,CDEAQLVQVWDDPYPEVLSQEPFHKVTVQSLTLETLEHNQTYECRAHNSVGGSGWAFIPISA,,GAHTHPDEFELFTPVVACMSIMALLLLLLLLLLLYKYK,,KPKYQVRWKIIESYEGNSYTFI DPTQLPYNEKWEFPRNNLQF,,GKTLGAGAFGKVVEATAFGLGKEDAVLKVAVKMLK,,STAHADEKEALMSELKIMSHLGQHENIVNLLGACTHG,,GPVLVITEYCCYGDLLNFLRRKAEAMLGP SLSPGQDPEGGVDYKNIHL EKKYVRR,,DSGFSSQGVDTYVEMRPVSTSSNDSFSEQ,,DLDKEDGRPLELRDLLHFSSQVAQGMFLASKN,,CIHRDVAARNVLLTNGHVAKIGDFGLARDIMNDSNYIVKGN,,ARLPVKWMAPE SIFDCVYTVQSDVWSYG DZVHRJAGUYPQKVMDFYKLVKDGQYMAQPAFA PKNI,,YSIMQACWALEP THRPTFQIC SFLQEQAE DR RER,,DYTNLPSSRSRSGSGSSSSEEEEESSHELTCC EQGDIAQPLLQPNNYQFC* </pre>		
<b>CSF1R-209</b>	26,946 .. 42,833	15,888 bp	CDS
▶ 6 segments = 921 bp			
/note	= coding sequence <a href="#">ENSP00000445282</a>		
/translation	<pre> MGPVGLLLLLVATAWH,,GQGIPVIEPSVPELVVKPGATVTLRCVGNVSVEWDGPPSPHWLTYSDGSSSILSTNNATFQNTGTYRCTEPGDP LGGSSAAIHLVVK,,DPA RPNVWLAQEVVVFEDQDALLPCLLTD PVL EAGVSLV RVRGRPLMRHTNYSFSPWHGFTIHRAKFIQSQDYQCSALMGGRKVMMSISIRLKVQK,,VIPGPPALTLVPAELVRIRGEAAQIVCSASSVDVNFDFLQHNNTK,,LAIPQSDFHNNRYQKVLTLNLDQVDFQHAGNYSCVAS NVQ GK HST MFFRVV,,ESAYLNLSEQLIQEVTVGEGLNKVMVEAYPLQGFNWTYLGPFSDHQPEPKLANATTKD TYR,,HTFTLSLRLK PSEA GRYSFLARNP GGWRALT FELTLR,,Y P EV SVI WTF INGS GTLLCAA SG YPQPNVTLWQCSGHTDR,,CDEAQLVQVWDDPYPEVLSQEPFHKVTVQSLTLETLEHNQTYECRAHNSVGGSGWAFIPISA,,GAHTHPDEFELFTPVVACMSIMALLLLLLLLLLLYKYK,,KPKYQVRWKIIESYEGNSYTFI DPTQLPYNEKWEFPRNNLQF,,GKTLGAGAFGKVVEATAFGLGKEDAVLKVAVKMLK,,STAHADEKEALMSELKIMSHLGQHENIVNLLGACTHG,,GPVLVITEYCCYGDLLNFLRRKAEAMLGP SLSPGQDPEGGVDYKNIHL EKKYVRR,,DSGFSSQGVDTYVEMRPVSTSSNDSFSEQ,,DLDKEDGRPLELRDLLHFSSQVAQGMFLASKN,,CIHRDVAARNVLLTNGHVAKIGDFGLARDIMNDSNYIVKGN,,ARLPVKWMAPE SIFDCVYTVQSDVWSYG DZVHRJAGUYPQKVMDFYKLVKDGQYMAQPAFA PKNI,,YSIMQACWALEP THRPTFQIC SFLQEQAE DR RER,,DYTNLPSSRSRSGSGSSSSEEEEESSHELTCC EQGDIAQPLLQPNNYQFC* </pre>		
<b>CSF1R-209</b>	26,946 .. 42,833	15,888 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000543093</a>		
<b>CSF1R-205</b>	33,174 .. 33,321	148 bp	CDS
/note	= coding sequence <a href="#">ENSP00000421174</a>		
/translation	<pre> MRHTNYSFSPWHGFTIHRAKFIQSQDYQCSALMGGRKVMMSISIRLKVQK 49 amino acids = 5.8 kDa </pre>		
<b>CSF1R-206</b>	46,192 .. 53,595	7404 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000513609</a>		Retained intron
<b>CSF1R-208</b>	46,192 .. 53,595	7404 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000515239</a>		
<b>CSF1R-207</b>	51,705 .. 57,347	5643 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000515068</a>		Nonsense mediated decay
<b>Donor Template WT -&gt; SNV</b>	52,370 .. 52,469	100 bp	misc_feature
<b>PAM</b>	52,429 .. 52,431	3 bp	misc_feature
<b>Protospacer Sequence</b>	52,432 .. 52,451	20 bp	misc_feature
<b>SNV</b>	52,439 .. 52,439	1 bp	misc_feature
/note	= WT=G SNV=A		
<b>CSF1R-204</b>	58,553 .. 59,535	983 bp	prim_transcript
/note	= primary transcript <a href="#">ENST00000509861</a>		Retained intron

Primer	Length	Binding Sites	Tm	Date Added
✓ <b>PCR Forward</b> /sequence = ACATTTCAACCTGTTGAAGCCTGGG 48% GC / 7657.0 Da	25-mer	51,970 .. 51,994	→ 61°C	Jun 14, 2022
✓ <b>Donor Template WT -&gt; SNV</b> /sequence = CTGTCTTTGGGACTGTGGTTCTTCTCCAGCCACGGCCCATGCTGATGAGAAAGGAGGCCCTCATGTCCAAGCTGAAGATCATGAGCCACCTGGGCCAGC 59% GC / 30,763.9 Da	100-mer	52,370 .. 52,469	→ 80°C	Jun 14, 2022
✓ <b>gRNA Protospacer</b> /sequence = TGATCTTCAGCTCGGACATG 50% GC / 6108.0 Da	20-mer	52,432 .. 52,451	← 57°C	Jun 14, 2022
✓ <b>Sanger Sequencing Primer</b> /sequence = ACCTCCATGGGTACAGGCTC 60% GC / 6078.0 Da	20-mer	52,494 .. 52,513	← 60°C	Jun 14, 2022
✓ <b>PCR Reverse</b> /sequence = CAGTGAAGAGGATGTGGGGCACTTG 56% GC / 7827.2 Da	25-mer	52,908 .. 52,932	← 64°C	Jun 14, 2022