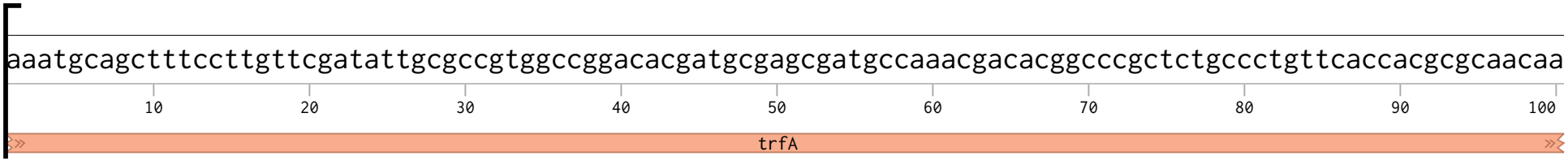
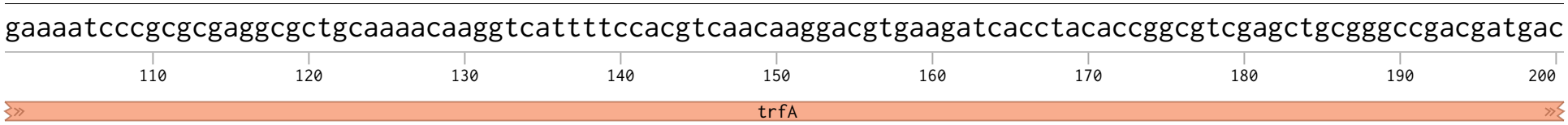
Template Alignment: 2020-11-19_B09_ASAS16BSP3



template sequence pAS1.6 (prqA-HRT + L1P3)

aligned sequence 2020-11-19_B09_ASAS16BSP3



template sequence pAS1.6 (prqA-HRT + L1P3)

aligned sequence 2020-11-19_B09_ASAS16BSP3

gaactggtgtggcagcaggtgttggagtacgcgaagcgcacccctatcggcgagccgatcaccttcacgttctacgagctttgccaggacctgggctggt

210 220 230 240 250 260 270 280 290 300

trfA

template sequence pAS1.6 (prqA-HRT + L1P3)

aligned sequence 2020-11-19_B09_ASAS16BSP3

cgatcaatggccggtattacacgaaggccgaggaatgcctgtcgcgcctacaggcgacggcgatgggcttcacgtccgaccgcgttgggcacctggaatc

310 320 330 340 350 360 370 380 390 400

trfA

template sequence pAS1.6 (prqA-HRT + L1P3)

aligned sequence 2020-11-19_B09_ASAS16BSP3

ggtgtcgctgctgcaccgcttccgcgtcctggaccgtggcaagaaaacgtcccgttgccaggtcctgatcgacgaggaaatcgtcgtgctgtttgctggc

410 420 430 440 450 460 470 480 490 500

trfA

template sequence pAS1.6 (prqA-HRT + L1P3)

aligned sequence 2020-11-19_B09_ASAS16BSP3

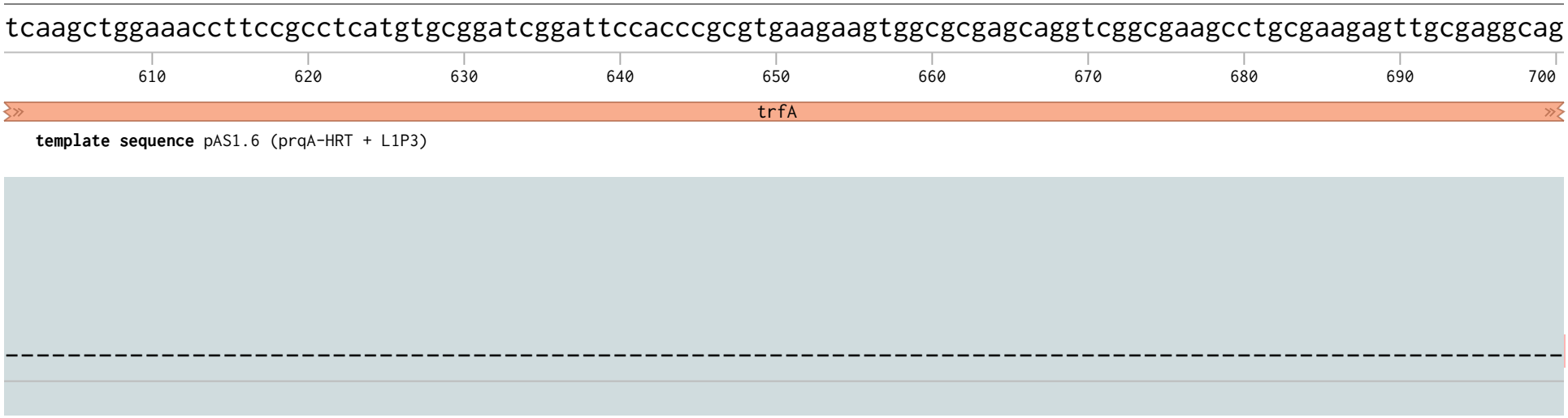
gaccactacacgaaattcatatgggagaagtaccgcaagctgtcgccgacggcccgacggatgttcgactatttcagctcgcaccgggagccgtacccgc

510 520 530 540 550 560 570 580 590 600

trfA

template sequence pAS1.6 (prqA-HRT + L1P3)

aligned sequence 2020-11-19_B09_ASAS16BSP3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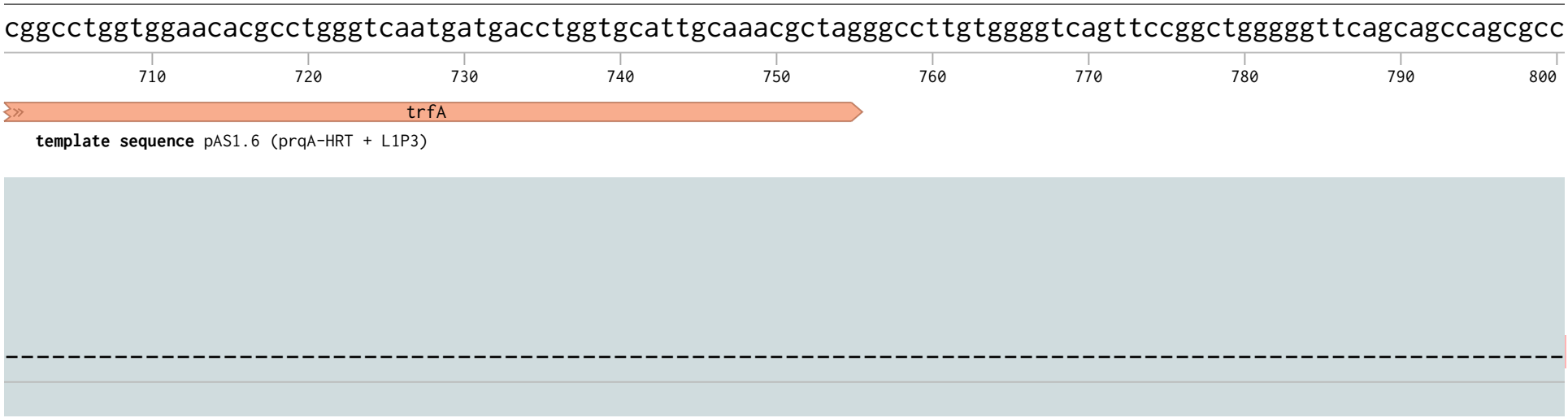
610
620
630
640
650
660
670
680
690
700
trfA
template sequence pAS1.6 (prqA-HRT + L1P3)
aligned sequence 2020-11-19_B09_ASAS16BSP3


cggcctggtggaacacgcctgggtcaatgatgacctggtgcattgcaaacgctagggccttgtggggtcagttccggctgggggttcagcagccagcgcc
710
720
730
740
750
760
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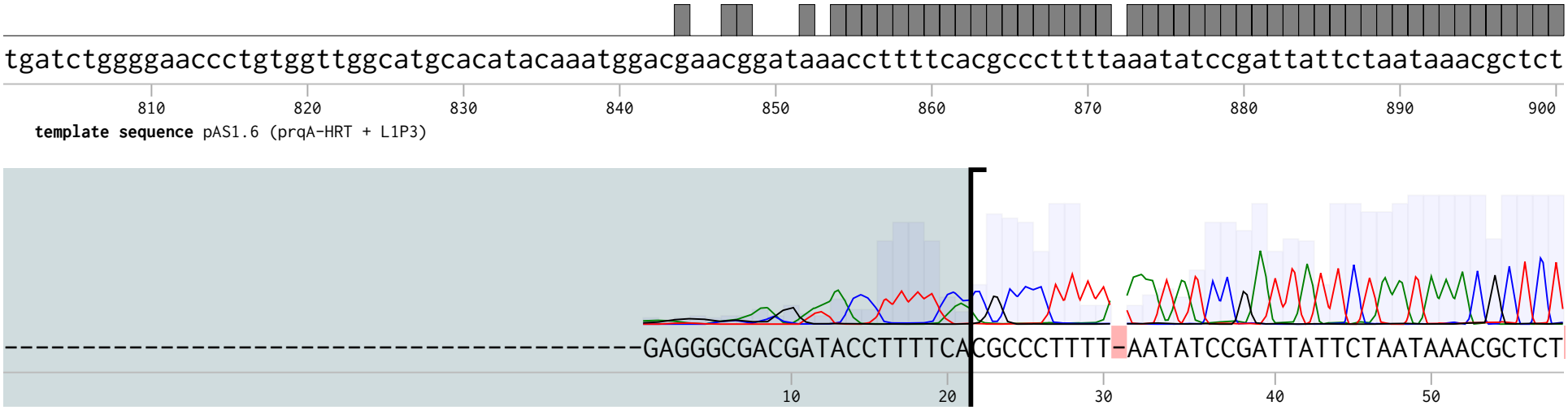
800
trfA
template sequence pAS1.6 (prqA-HRT + L1P3)
aligned sequence 2020-11-19_B09_ASAS16BSP3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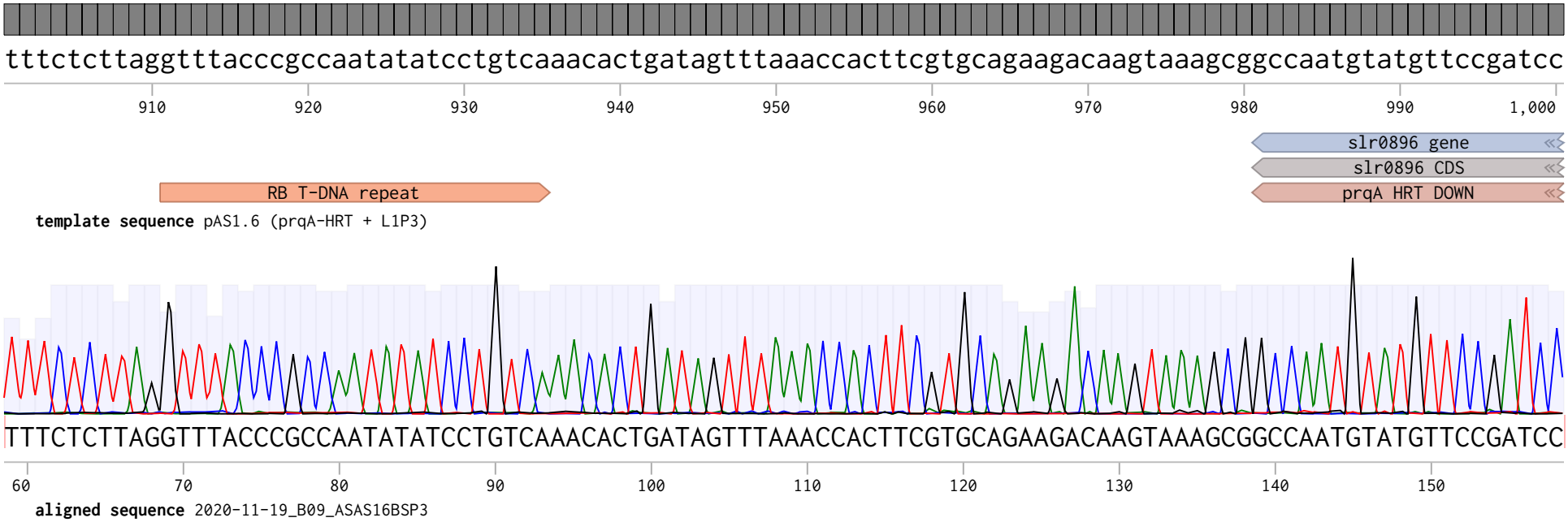
810
820
830
840
850
860
870
880
890
900
template sequence pAS1.6 (prqA-HRT + L1P3)
GAGGGCGACGATACCTTTTCACGCCCTTTT-AATATCCGATTATTCTAATAAACGCTCT
10
20
30
40
50
aligned sequence 2020-11-19_B09_ASAS16BSP3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910
920
930
940
950
960
970
980
990
1,000
slr0896 gene
slr0896 CDS
prqA HRT DOWN
RB T-DNA repeat
template sequence pAS1.6 (prqA-HRT + L1P3)
TTTCTCTTAGGTTTACCCGCCAATATATCCTGTCAAACACTGATAGTTTAAACCACTTCGTGCAGAAGACAAGTAAAGCGGCCAATGTATGTTCCGATCC
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70
80
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100
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120
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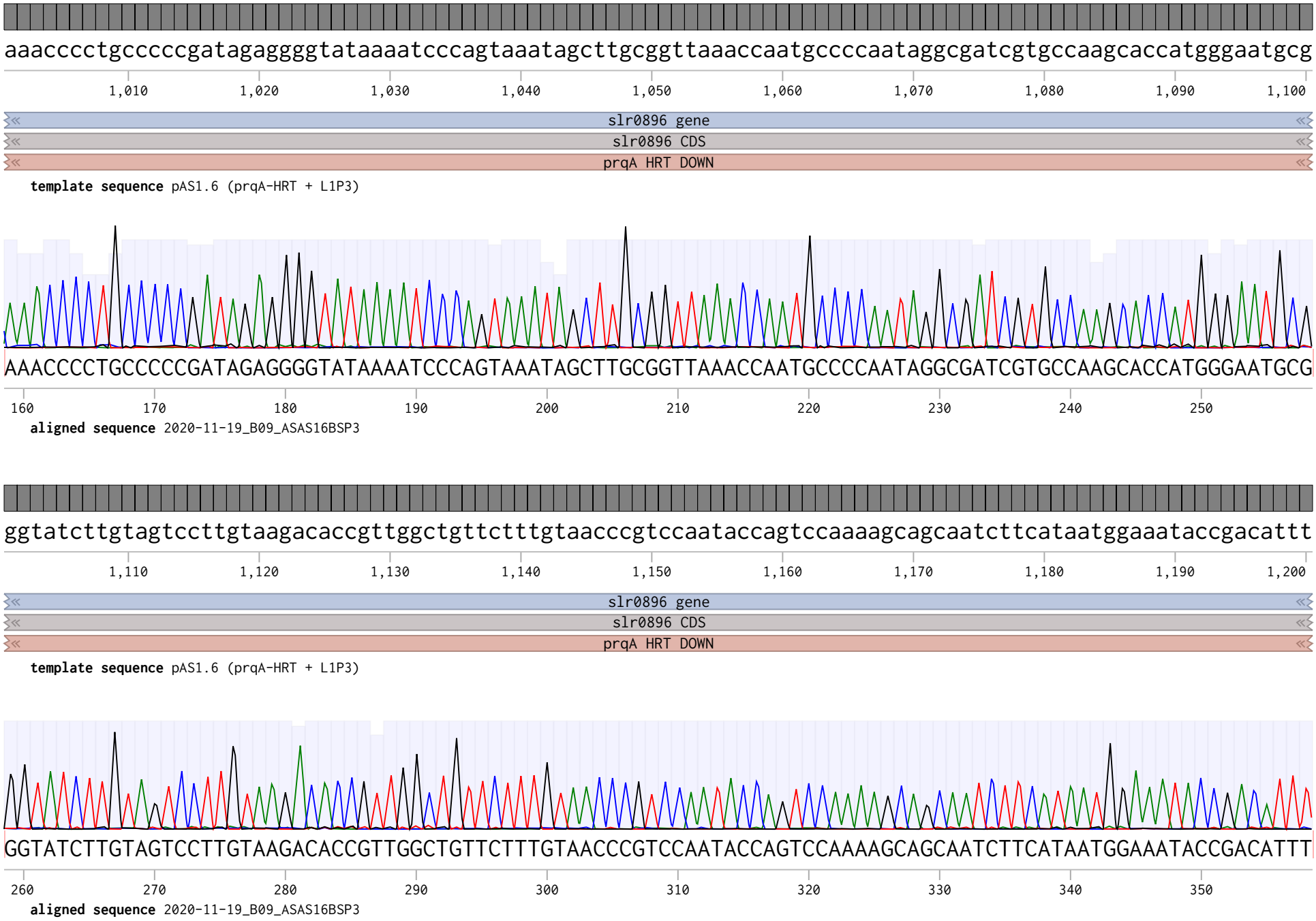
140
150
aligned sequence 2020-11-19_B09_ASAS16BSP3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1,020
1,030
1,040
1,050
1,060
1,070
1,080
1,090
1,100
slr0896 gene
slr0896 CDS
prqA HRT DOWN
template sequence pAS1.6 (prqA-HRT + L1P3)
AAACCCCTGCCCCCGATAGAGGGGTATAAAATCCCAGTAAATAGCTTGCGGTTAAACCAATGCCCCAATAGGCGATCGTGCCAAGCACCATGGGAATGCG
160
170
180
190
200
210
220
230
240
250
aligned sequence 2020-11-19_B09_ASAS16BSP3
ggtatcttgtagtccttgtaagacaccgttggctgttctttgtaacccgtccaataccagtccaaaagcagcaatcttcataatggaaataccgacattt
1,110
1,120
1,130
1,140
1,150
1,160
1,170
1,180
1,190
1,200
slr0896 gene
slr0896 CDS
prqA HRT DOWN
template sequence pAS1.6 (prqA-HRT + L1P3)
GGTATCTTGTAGTCCTTGTAAGACACCGTTGGCTGTTCTTTGTAACCCGTCCAATACCAGTCCAAAAGCAGCAATCTTCATAATGGAAATACCGACATTT
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300
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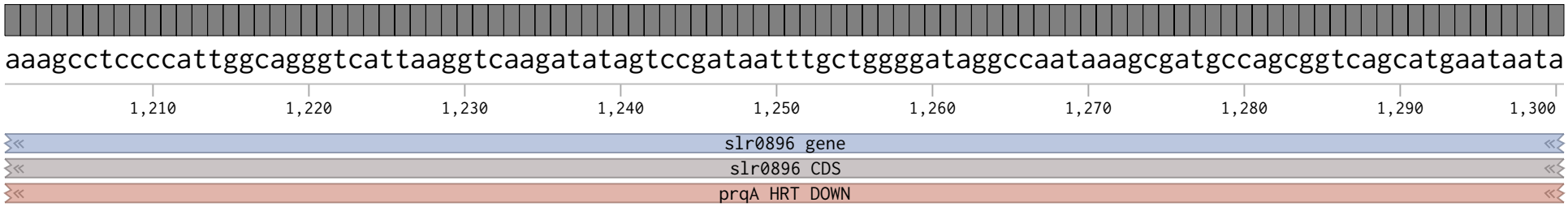
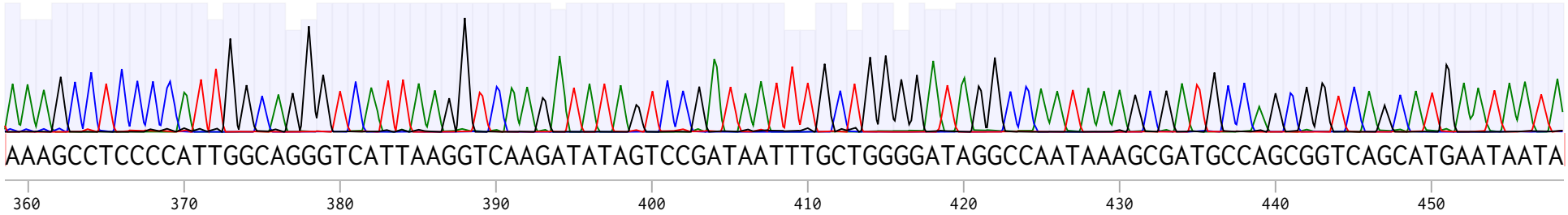
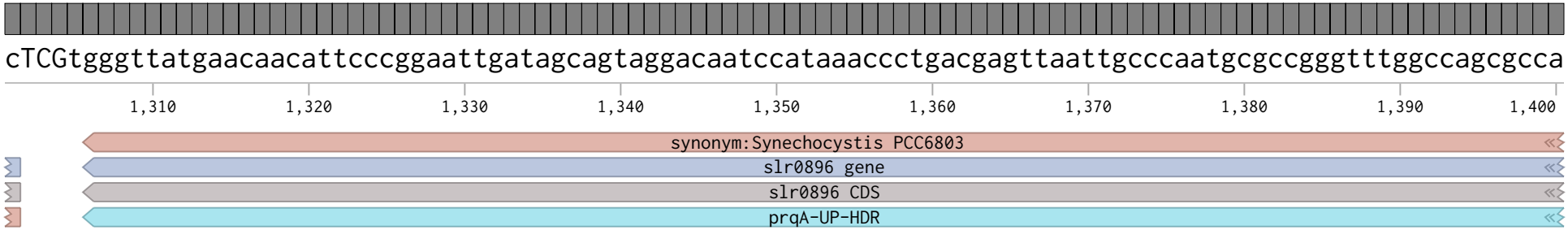
340
350
aligned sequence 2020-11-19_B09_ASAS16BSP3



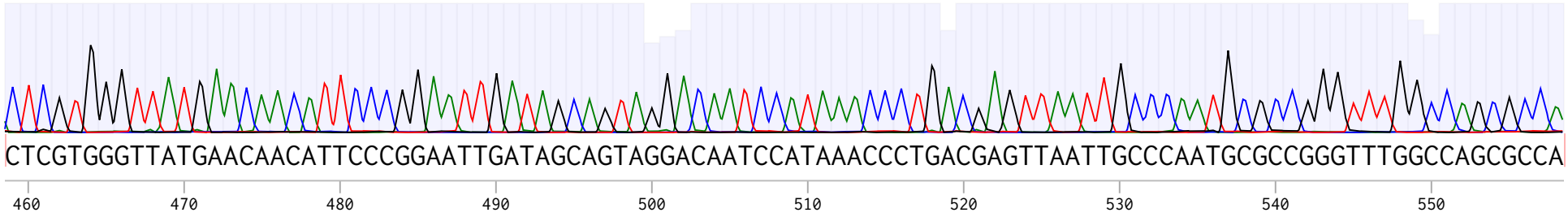
template sequence pAS1.6 (prqA-HRT + L1P3)



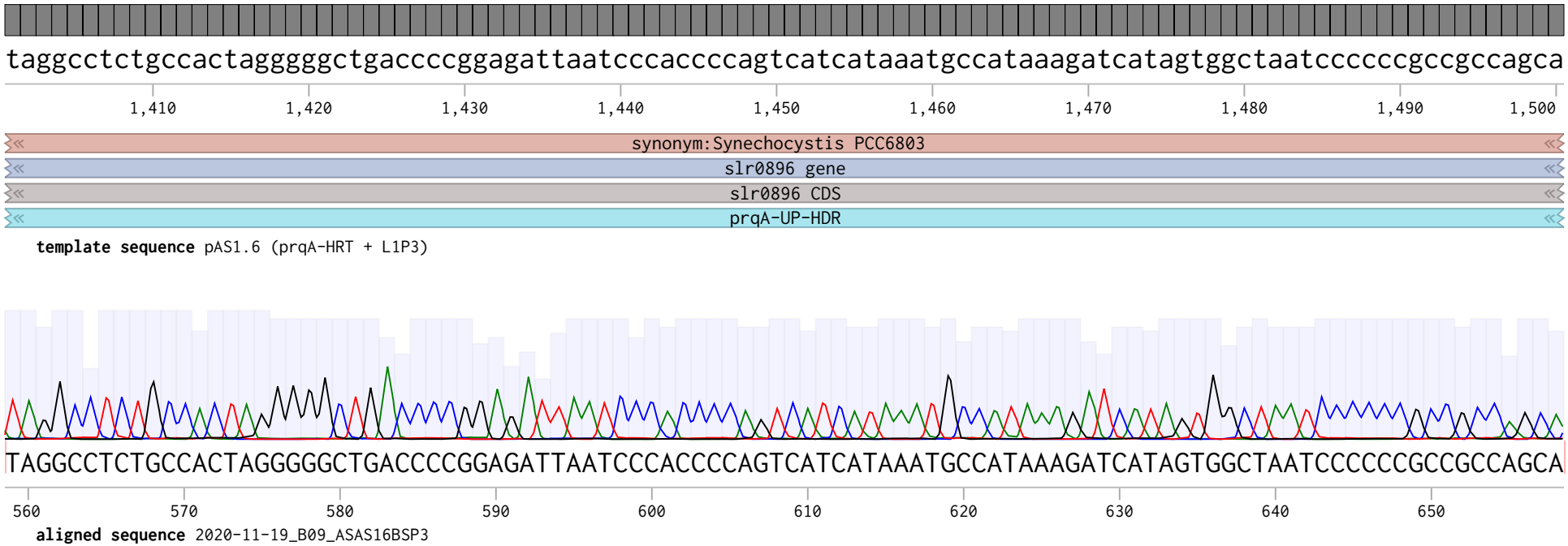
aligned sequence 2020-11-19_B09_ASAS16BSP3



template sequence pAS1.6 (prqA-HRT + L1P3)



aligned sequence 2020-11-19_B09_ASAS16BSP3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1,420
1,430
1,440
1,450
1,460
1,470
1,480
1,490
1,500
synonym:Synechocystis PCC6803
slr0896 gene
slr0896 CDS
prqA-UP-HDR
template sequence pAS1.6 (prqA-HRT + L1P3)
TAGGCCTCTGCCACTAGGGGGCTGACCCCGGAGATTAATCCCACCCCAGTCATCATAAATGCCATAAAGATCATAGTGGCTAATCCCCCCGCCGCCAGCA
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570
580
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600
610
620
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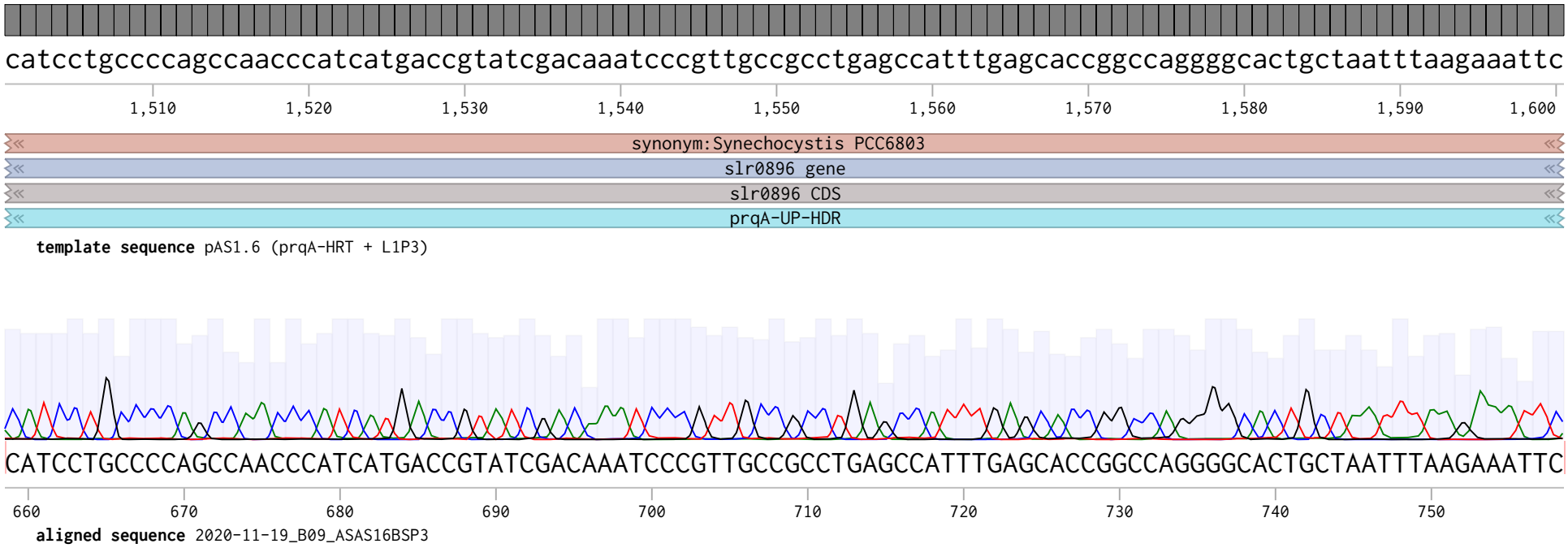
640
650
aligned sequence 2020-11-19_B09_ASAS16BSP3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1,510
1,520
1,530
1,540
1,550
1,560
1,570
1,580
1,590
1,600
synonym:Synechocystis PCC6803
slr0896 gene
slr0896 CDS
prqA-UP-HDR
template sequence pAS1.6 (prqA-HRT + L1P3)
CATCCTGCCCCAGCCAACCCATCATGACCGTATCGACAAATCCCGTTGCCGCCTGAGCCATTTGAGCACCGGCCAGGGGCACTGCTAATTTAAGAAATTC
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670
680
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700
710
720
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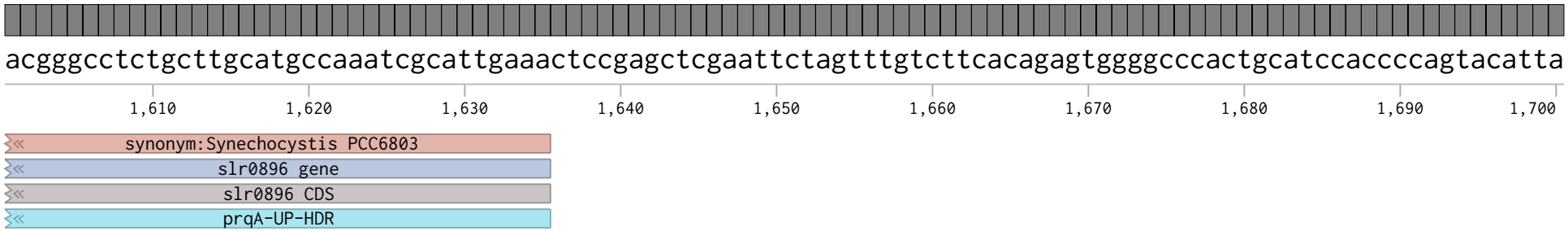
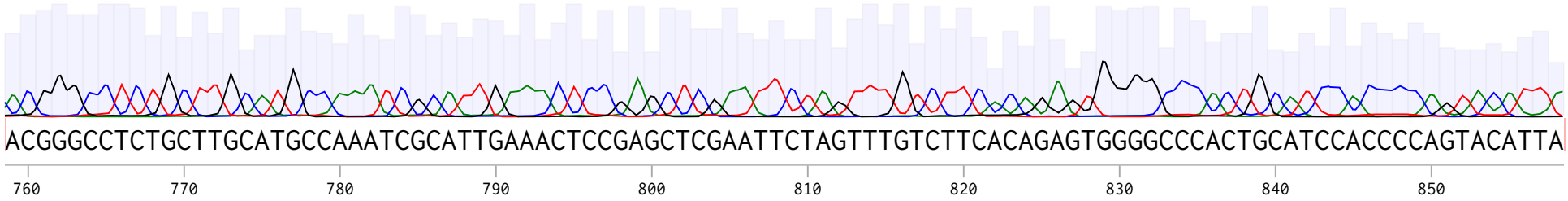
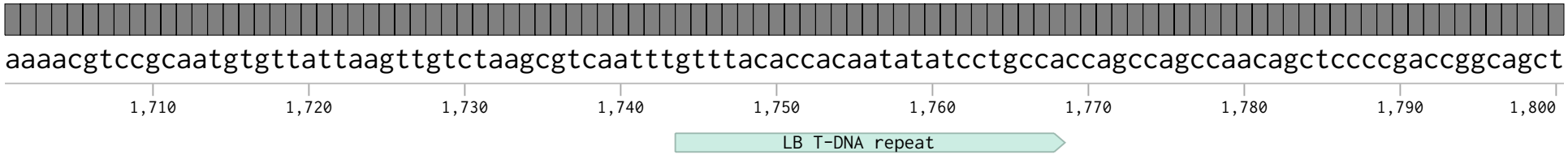
740
750
aligned sequence 2020-11-19_B09_ASAS16BSP3



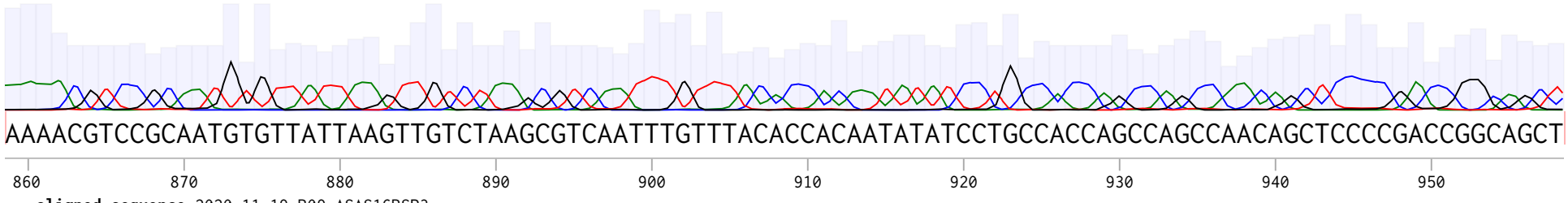
template sequence pAS1.6 (prqA-HRT + L1P3)



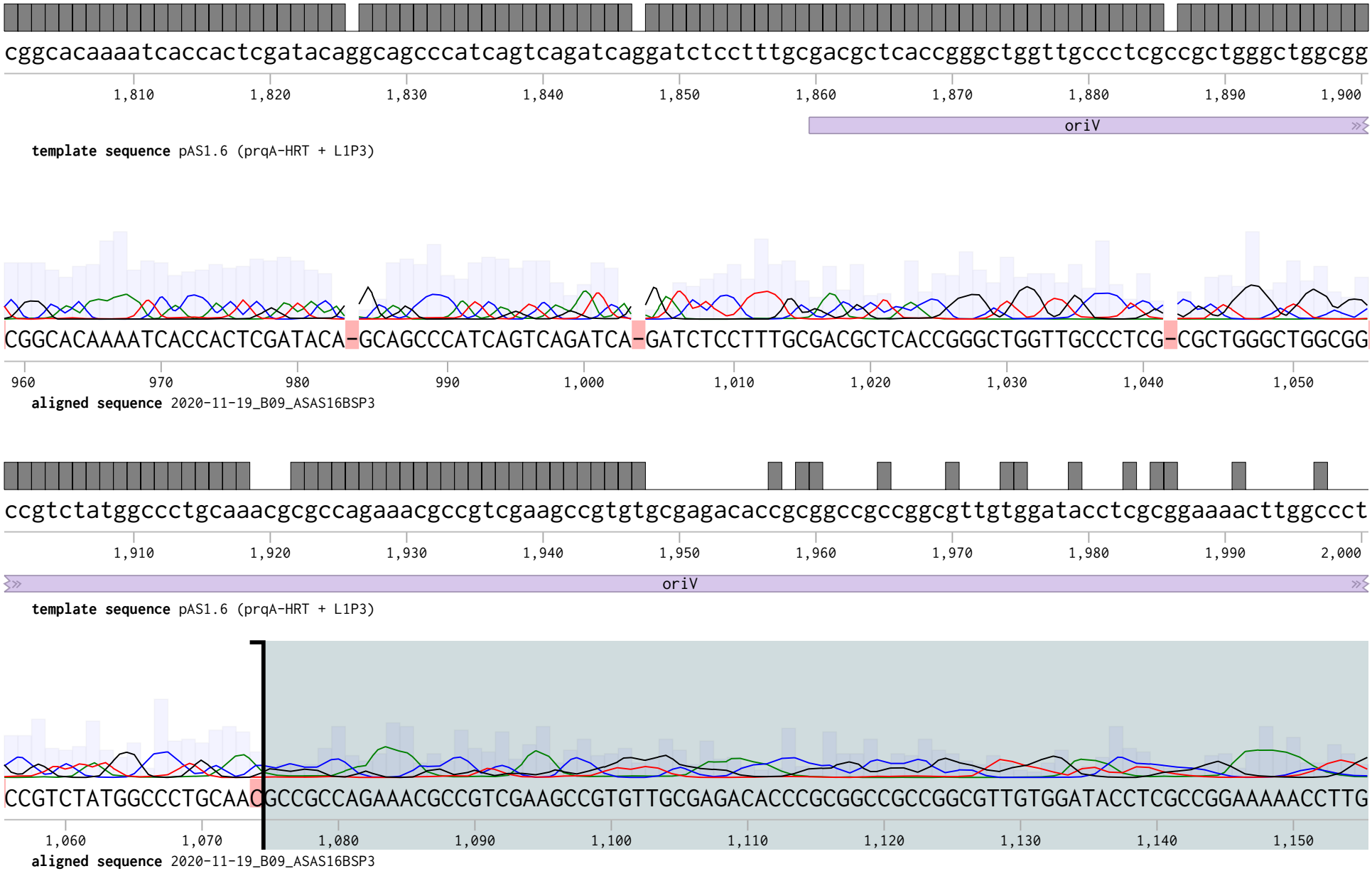
aligned sequence 2020-11-19_B09_ASAS16BSP3



template sequence pAS1.6 (prqA-HRT + L1P3)



aligned sequence 2020-11-19_B09_ASAS16BSP3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1,810
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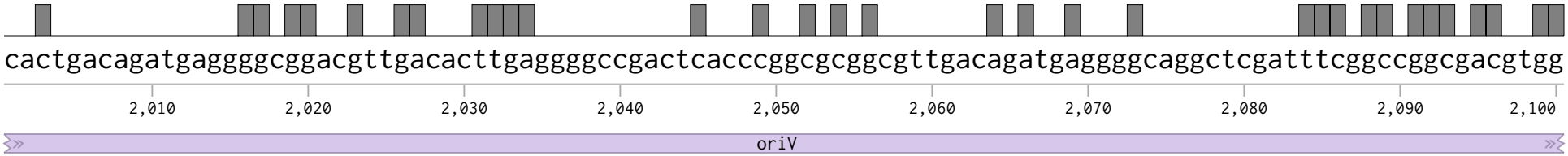
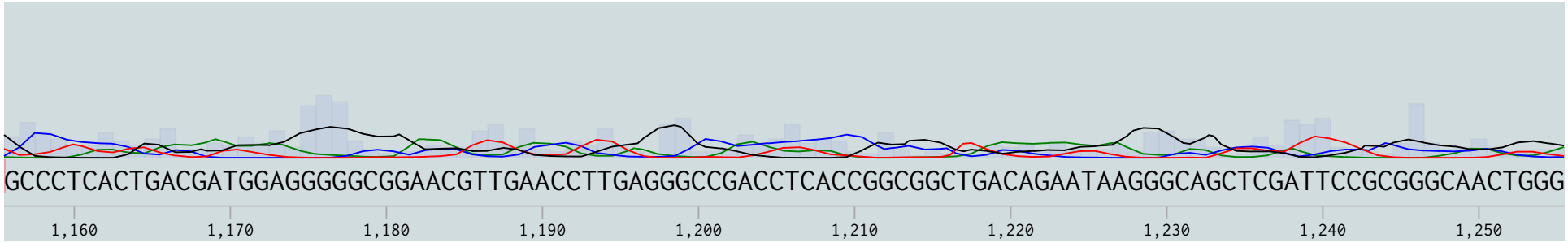
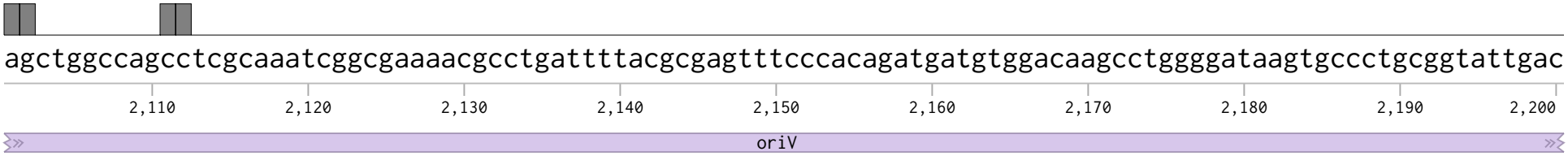
1,840
1,850
1,860
1,870
1,880
1,890
1,900
oriV
template sequence pAS1.6 (prqA-HRT + L1P3)
CGGCACAAAATCACCACTCGATACA-GCAGCCCATCAGTCAGATCA-GATCTCCTTTGCGACGCTCACCGGGCTGGTTGCCCTCG-CGCTGGGCTGGCGG
960
970
980
990
1,000
1,010
1,020
1,030
1,040
1,050
aligned sequence 2020-11-19_B09_ASAS16BSP3
ccgtctatggccctgcaaacgcgccagaaacgccgtcgaagccgtgtgcgagacaccgcggccgccggcgttgtggatacctcgcggaaaacttggccct
1,910
1,920
1,930
1,940
1,950
1,960
1,970
1,980
1,990
2,000
oriV
template sequence pAS1.6 (prqA-HRT + L1P3)
CCGTCTATGGCCCTGCAACGCCGCCAGAAACGCCGTCGAAGCCGTGTTGCGAGACACCCGCGGCCGCCGGCGTTGTGGATACCTCGCCGGAAAAACCTTG
1,060
1,070
1,080
1,090
1,100
1,110
1,120
1,130
1,140
1,150
aligned sequence 2020-11-19_B09_ASAS16BSP3



template sequence pAS1.6 (prqA-HRT + L1P3)



aligned sequence 2020-11-19_B09_ASAS16BSP3



template sequence pAS1.6 (prqA-HRT + L1P3)

aligned sequence 2020-11-19_B09_ASAS16BSP3

acttgaggggcgcgactactgacagatgaggggcgcgatccttgacacttgaggggcagagtgctgacagatgaggggcgcacctattgacatttgaggg

2,210 2,220 2,230 2,240 2,250 2,260 2,270 2,280 2,290 2,300

oriV

template sequence pAS1.6 (prqA-HRT + L1P3)

aligned sequence 2020-11-19_B09_ASAS16BSP3

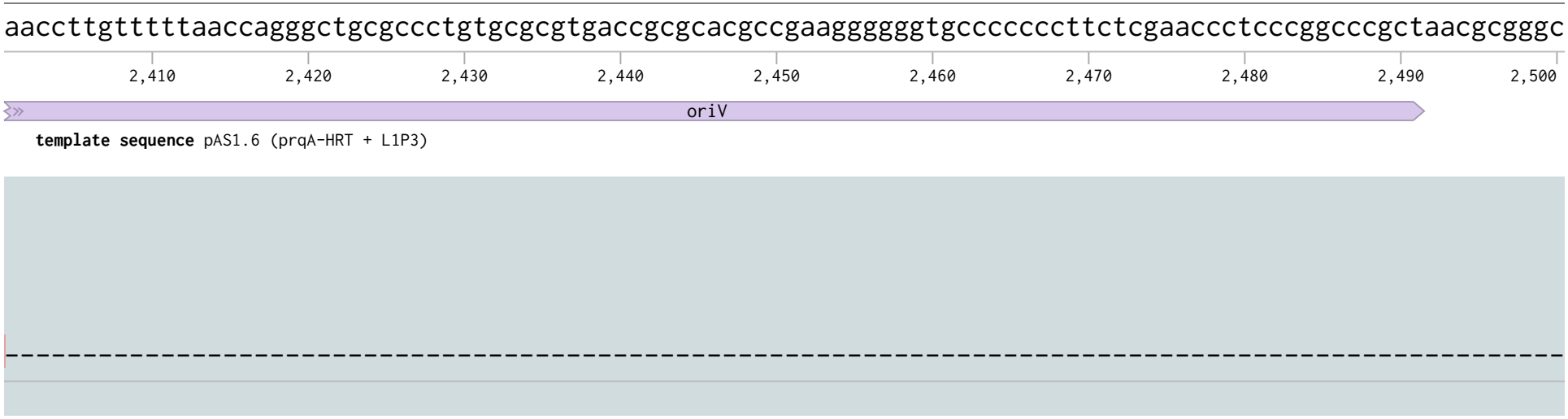
gctgtccacaggcagaaaatccagcatttgcaagggtttccgcccgttttcggccaccgctaacctgtcttttaacctgcttttaaaccaatatttata

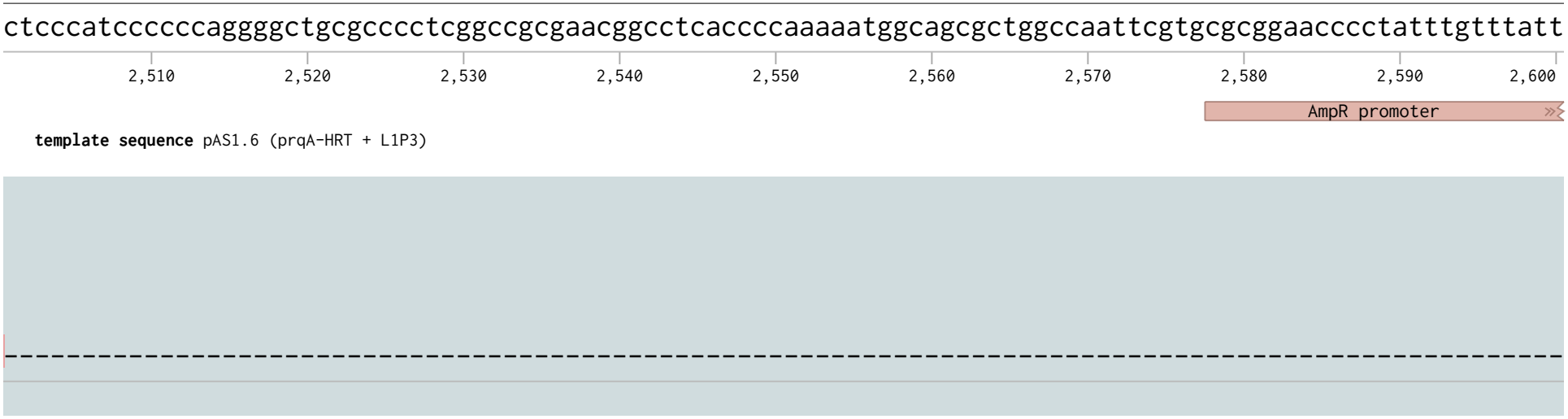
2,310 2,320 2,330 2,340 2,350 2,360 2,370 2,380 2,390 2,400

oriV

template sequence pAS1.6 (prqA-HRT + L1P3)

aligned sequence 2020-11-19_B09_ASAS16BSP3


aaccttgtttttaaccagggctgcgccctgtgcgcgtgaccgcgcacgccgaaggggggtgccccccccttctcgaaccctcccggcccgctaacgcgggc
2,410
2,420
2,430
2,440
2,450
2,460
2,470
2,480
2,490
2,500
oriV
template sequence pAS1.6 (prqA-HRT + L1P3)
aligned sequence 2020-11-19_B09_ASAS16BSP3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2,510
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2,530
2,540
2,550
2,560
2,570
2,580
2,590
2,600
AmpR promoter
template sequence pAS1.6 (prqA-HRT + L1P3)
aligned sequence 2020-11-19_B09_ASAS16BSP3

tttctaaatacattcaaatatgtatccgctcatgagacaataaccctgataaatgcttcaataatattgaaaaaggaagagtatgagtattcaacatttc

2,610 2,620 2,630 2,640 2,650 2,660 2,670 2,680 2,690 2,700

AmpR promoter AmpR

template sequence pAS1.6 (prqA-HRT + L1P3)

aligned sequence 2020-11-19_B09_ASAS16BSP3

cgtgtcgcccttattccctttttgcggcattttgccttcctgttttgctcacccagaaacgctggtgaaagtaaaagatgctgaagatcagttgggtg

2,710 2,720 2,730 2,740 2,750 2,760 2,770 2,780 2,790 2,800

AmpR

template sequence pAS1.6 (prqA-HRT + L1P3)

aligned sequence 2020-11-19_B09_ASAS16BSP3

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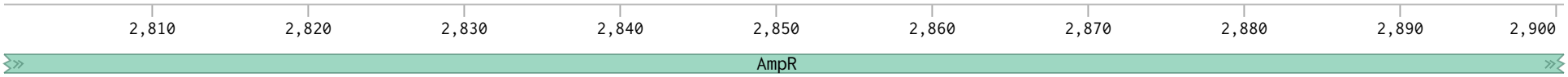

template sequence pAS1.6 (prqA-HRT + L1P3)

aligned sequence 2020-11-19_B09_ASAS16BSP3

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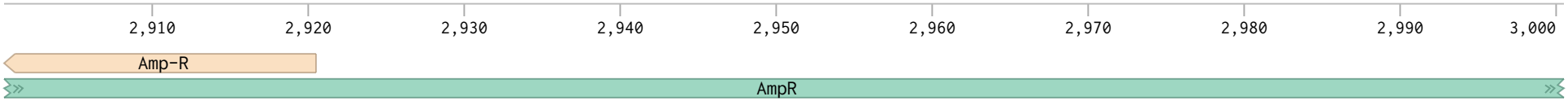


template sequence pAS1.6 (prqA-HRT + L1P3)

aligned sequence 2020-11-19_B09_ASAS16BSP3

acagaaaagcatcttacggatggcatgacagtaagagaattatgcagtgctgccataaccatgagtgataacactgcggccaacttacttctgacaacga

3,010 3,020 3,030 3,040 3,050 3,060 3,070 3,080 3,090 3,100

AmpR

template sequence pAS1.6 (prqA-HRT + L1P3)

aligned sequence 2020-11-19_B09_ASAS16BSP3

tcggaggaccgaaggagctaaccgcttttttgcacaacatgggggatcatgtaactcgccttgatcgttgggaaccggagctgaatgaagccataccaaa

3,110 3,120 3,130 3,140 3,150 3,160 3,170 3,180 3,190 3,200

AmpR

template sequence pAS1.6 (prqA-HRT + L1P3)

aligned sequence 2020-11-19_B09_ASAS16BSP3

cgacgagcgtgacaccacgatgcctgtagcaatggcaacaacgttgcgcaaactattaactggcgaactacttactctagcttcccggcaacaattaata

3,210 3,220 3,230 3,240 3,250 3,260 3,270 3,280 3,290 3,300

AmpR

template sequence pAS1.6 (prqA-HRT + L1P3)

aligned sequence 2020-11-19_B09_ASAS16BSP3

gactggatggaggcggataaagttgcaggaccacttctgcgctcggcccttccggctggctggtttattgctgataaatctggagccggtgagcgtggtt

3,310 3,320 3,330 3,340 3,350 3,360 3,370 3,380 3,390 3,400

AmpR

template sequence pAS1.6 (prqA-HRT + L1P3)

aligned sequence 2020-11-19_B09_ASAS16BSP3

ctcgcggtatcattgcagcactggggccagatggtaagccctcccgtatcgtagttatctacacgacggggagtcaggcaactatggatgaacgaaatag

3,410 3,420 3,430 3,440 3,450 3,460 3,470 3,480 3,490 3,500

AmpR

template sequence pAS1.6 (prqA-HRT + L1P3)

aligned sequence 2020-11-19_B09_ASAS16BSP3

acagatcgctgagataggtgcctcactgattaagcattggtaactgtcagaccaagtttactcatatatactttagattgatttaaaacttcatttttaa

3,510 3,520 3,530 3,540 3,550 3,560 3,570 3,580 3,590 3,600

AmpR

template sequence pAS1.6 (prqA-HRT + L1P3)

aligned sequence 2020-11-19_B09_ASAS16BSP3

tttaaaaggatctaggtgaagatccttttgataatctcatgaccaaaatcccttaacgtgagttttcgttccactgagcgtcagaccccgtagaaaaga

3,610 3,620 3,630 3,640 3,650 3,660 3,670 3,680 3,690 3,700

template sequence pAS1.6 (prqA-HRT + L1P3)

aligned sequence 2020-11-19_B09_ASAS16BSP3

tcaaaggatcttcttgagatccttttttttctgcgcgtaatctgctgcttgcaaacaaaaaaaccaccgctaccagcggtggtttgtttgccggatcaaga

3,710 3,720 3,730 3,740 3,750 3,760 3,770 3,780 3,790 3,800

ori

template sequence pAS1.6 (prqA-HRT + L1P3)

aligned sequence 2020-11-19_B09_ASAS16BSP3

gctaccaactctttttccgaaggtaactggcttcagcagagcgcagataccaaatactgtccttctagtgtagccgtagttaggccaccacttcaagaac

3,810 3,820 3,830 3,840 3,850 3,860 3,870 3,880 3,890 3,900

ori

template sequence pAS1.6 (prqA-HRT + L1P3)

aligned sequence 2020-11-19_B09_ASAS16BSP3

tctgtagcaccgcctacatacctcgctctgctaatcctgttaccagtggctgctgccagtggcgataagtcgtgtcttaccgggttggactcaagacgat

3,910 3,920 3,930 3,940 3,950 3,960 3,970 3,980 3,990 4,000

ori

template sequence pAS1.6 (prqA-HRT + L1P3)

aligned sequence 2020-11-19_B09_ASAS16BSP3

agttaccggataaggcgcagcggtcgggctgaacgggggttcgtgcacacagcccagcttggagcgaacgacctacaccgaactgagatacctacagcg

4,010 4,020 4,030 4,040 4,050 4,060 4,070 4,080 4,090 4,100

ori

template sequence pAS1.6 (prqA-HRT + L1P3)

aligned sequence 2020-11-19_B09_ASAS16BSP3

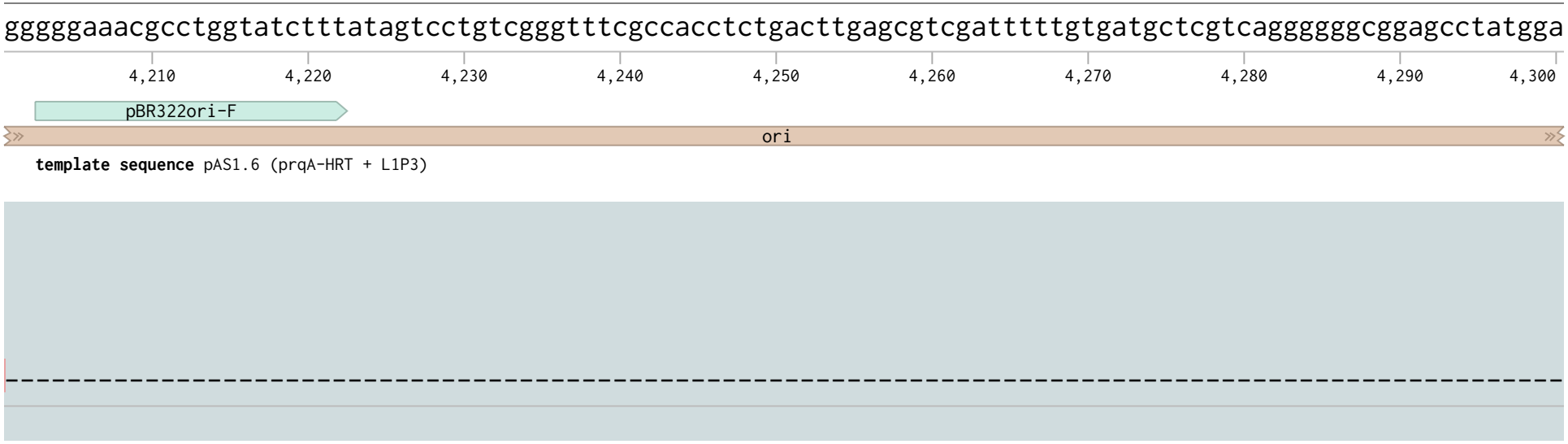
tgagctatgagaaagcgccacgcttcccgaagggagaaaggcggacaggtatccggtaagcggcagggtcggaacaggagagcgcacgagggagcttcca

4,110 4,120 4,130 4,140 4,150 4,160 4,170 4,180 4,190 4,200

ori

template sequence pAS1.6 (prqA-HRT + L1P3)

aligned sequence 2020-11-19_B09_ASAS16BSP3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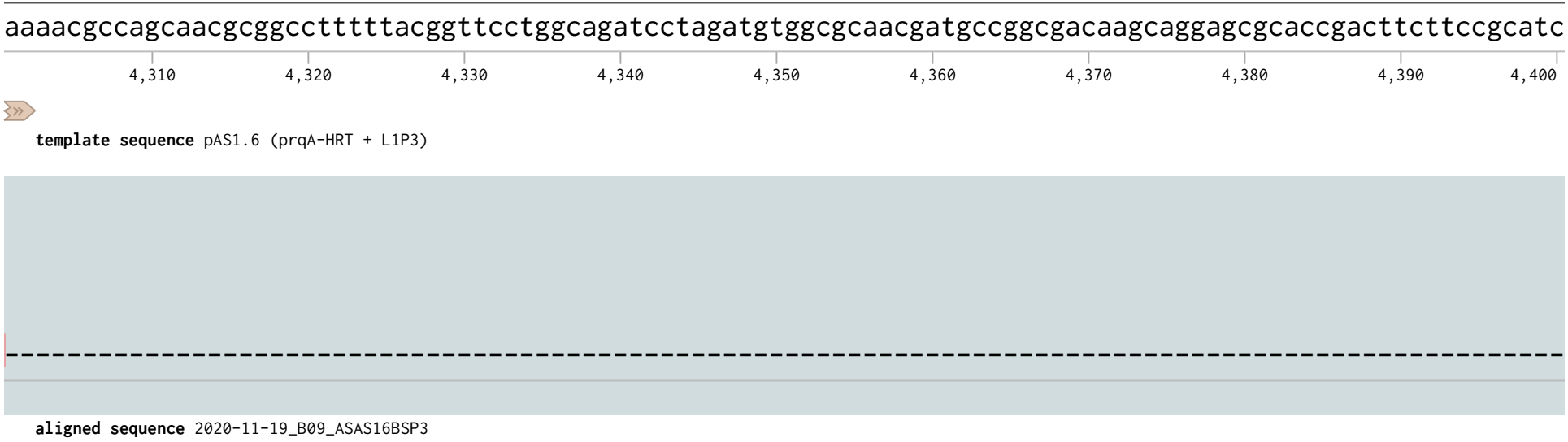
4,210
4,220
4,230
4,240
4,250
4,260
4,270
4,280
4,290
4,300
pBR322ori-F
ori
template sequence pAS1.6 (prqA-HRT + L1P3)
aligned sequence 2020-11-19_B09_ASAS16BSP3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4,310
4,320
4,330
4,340
4,350
4,360
4,370
4,380
4,390
4,400
template sequence pAS1.6 (prqA-HRT + L1P3)
aligned sequence 2020-11-19_B09_ASAS16BSP3

aagtgttttggctctcaggccgaggcccacggcaagtatttgggcaaggggtcgctggtattcgtgcagggcaagattcggaataccaagtacgagaagg

4,410 4,420 4,430 4,440 4,450 4,460 4,470 4,480 4,490 4,500

template sequence pAS1.6 (prqA-HRT + L1P3)

aligned sequence 2020-11-19_B09_ASAS16BSP3

acggccagacggtctacgggaccgacttcattgccgataaggtggattatctggacaccaaggcaccaggcgggtcaaatcaggaataagggcacattgc

4,510 4,520 4,530 4,540 4,550 4,560 4,570 4,580 4,590 4,600

template sequence pAS1.6 (prqA-HRT + L1P3)

aligned sequence 2020-11-19_B09_ASAS16BSP3

cccggcgtgagtcggggcaatcccgcaaggagggtgaatgaatcggacgtttgaccggaaggcatacaggcaagaactgatcgacgcggggttttccgcc

4,610 4,620 4,630 4,640 4,650 4,660 4,670 4,680 4,690 4,700

trfA

template sequence pAS1.6 (prqA-HRT + L1P3)

aligned sequence 2020-11-19_B09_ASAS16BSP3

gaggatgccgaaaccatcgcaagccgcaccgtcatgcgtgcgccccgcgaaaccttccagtccgtcggctcgatggtccagcaagctacggccaagatcg

4,710 4,720 4,730 4,740 4,750 4,760 4,770 4,780 4,790 4,800

trfA

template sequence pAS1.6 (prqA-HRT + L1P3)

aligned sequence 2020-11-19_B09_ASAS16BSP3

agcgcgacagcgtgcaactggctccccctgccctgcccgcgccatcggccgccgtggagcgttcgcgtcgtcttgaacaggaggcggcaggtttggcgaa

4,810 4,820 4,830 4,840 4,850 4,860 4,870 4,880 4,890 4,900

trfA

template sequence pAS1.6 (prqA-HRT + L1P3)

aligned sequence 2020-11-19_B09_ASAS16BSP3

gtcgatgaccatcgacacgcgaggaactatgacgaccaagaagcgaaaaaccgccggcgaggacctggcaaaacaggtcagcgaggccaagcaggccgcg

4,910 4,920 4,930 4,940 4,950 4,960 4,970 4,980 4,990 5,000

trfA

template sequence pAS1.6 (prqA-HRT + L1P3)

aligned sequence 2020-11-19_B09_ASAS16BSP3

template sequence pAS1.6 (prqA-HRT + L1P3)

aligned sequence 2020-11-19_B09_ASAS16BSP3