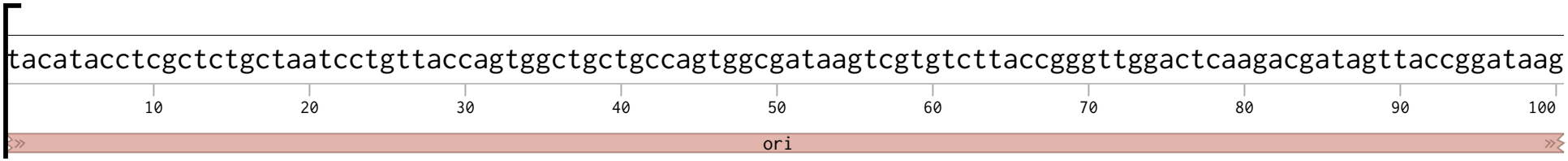
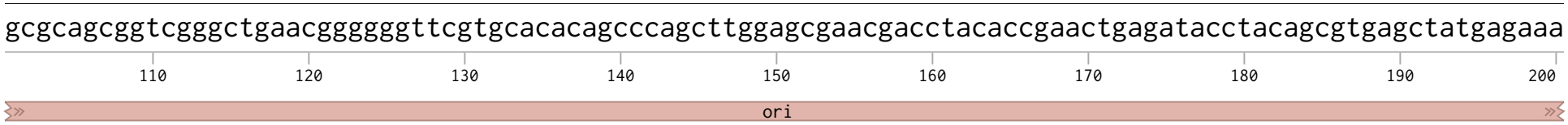
Template Alignment: 2020-11-13_H01_ASAS012ASP1



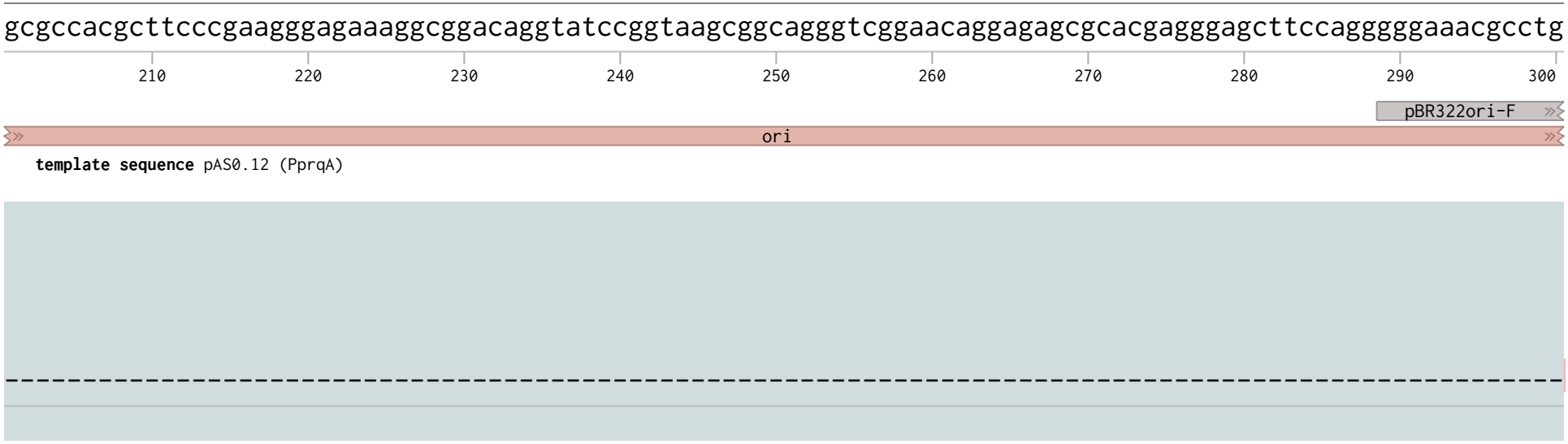
template sequence pAS0.12 (PprqA)

aligned sequence 2020-11-13_H01_ASAS012ASP1



template sequence pAS0.12 (PprqA)

aligned sequence 2020-11-13_H01_ASAS012ASP1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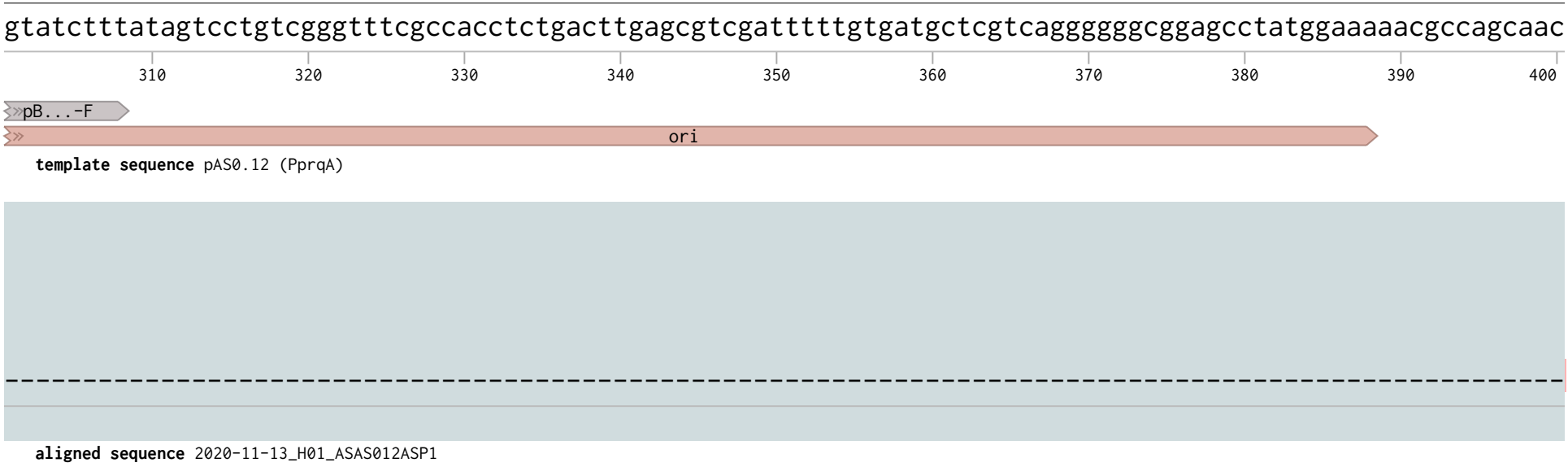
210
220
230
240
250
260
270
280
290
300
pBR322ori-F
ori
template sequence pAS0.12 (PprqA)
aligned sequence 2020-11-13_H01_ASAS012ASP1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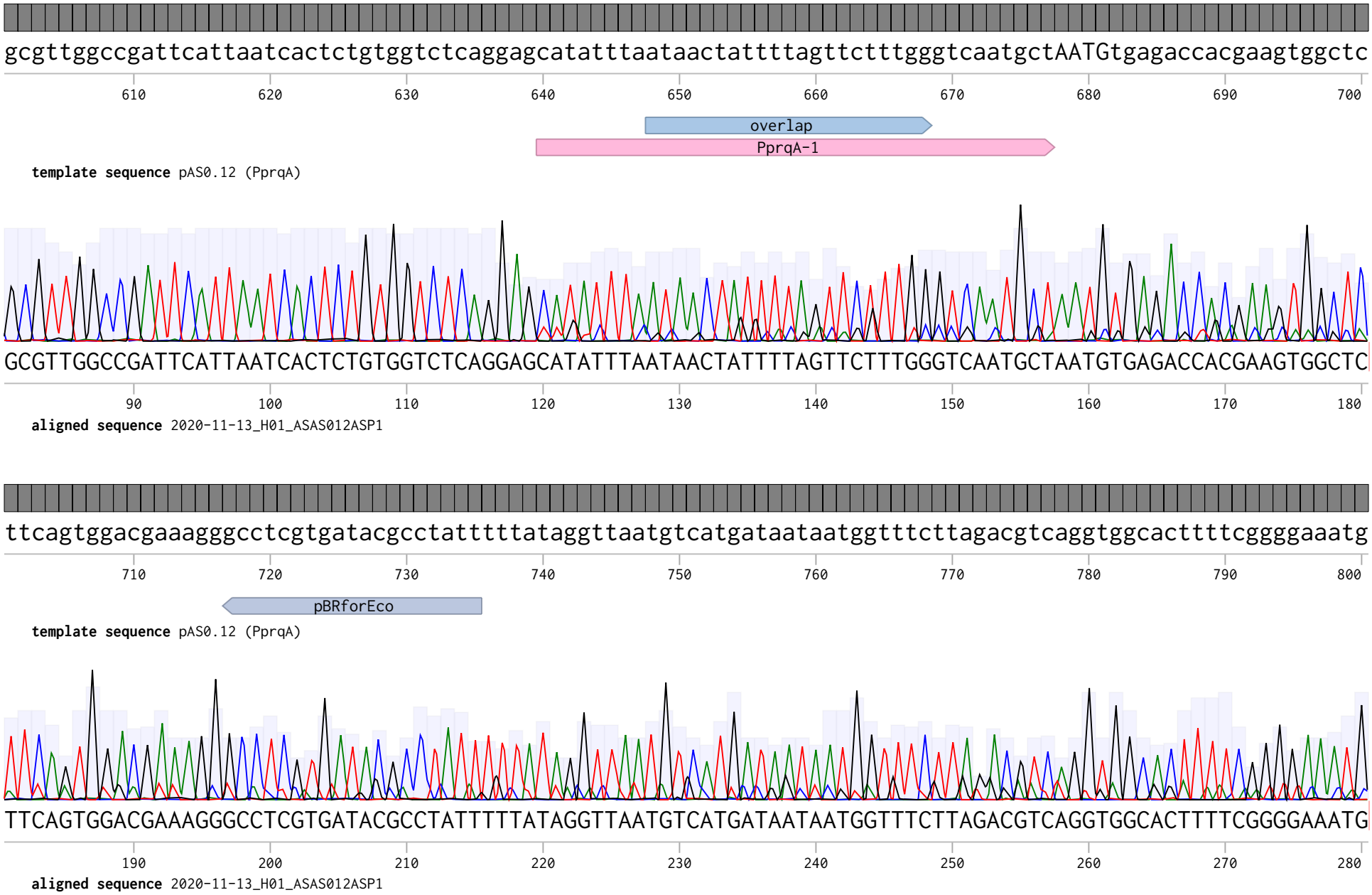
310
320
330
340
350
360
370
380
390
400
pB...-F
ori
template sequence pAS0.12 (PprqA)
aligned sequence 2020-11-13_H01_ASAS012ASP1

gcggccttttacggttcctggcctttgctggcctttgctcacatgttctttcctgcgttatcccctgattctgtggataaccgtattaccgcctttg
410
420
430
440
450
460
470
480
490
500
template sequence pAS0.12 (PprqA)
aligned sequence 2020-11-13_H01_ASAS012ASP1
agtgagctgataccgctcgccgcagccgaacgaccgagcgcagcgagtcagtgagcgaggaagcggaagagcgcccaatacgcaaaccgcctctccccgc
510
520
530
540
550
560
570
580
590
600
L4440
template sequence pAS0.12 (PprqA)
TATCCTGGCAGAGACGAGCGCAGCGAGTCAGTGAGCGAGGAAGCGGAAGAGCGCCCAATACGCAAACCGCCTCTCCCCGC
10
20
30
40
50
60
70
80
aligned sequence 2020-11-13_H01_ASAS012ASP1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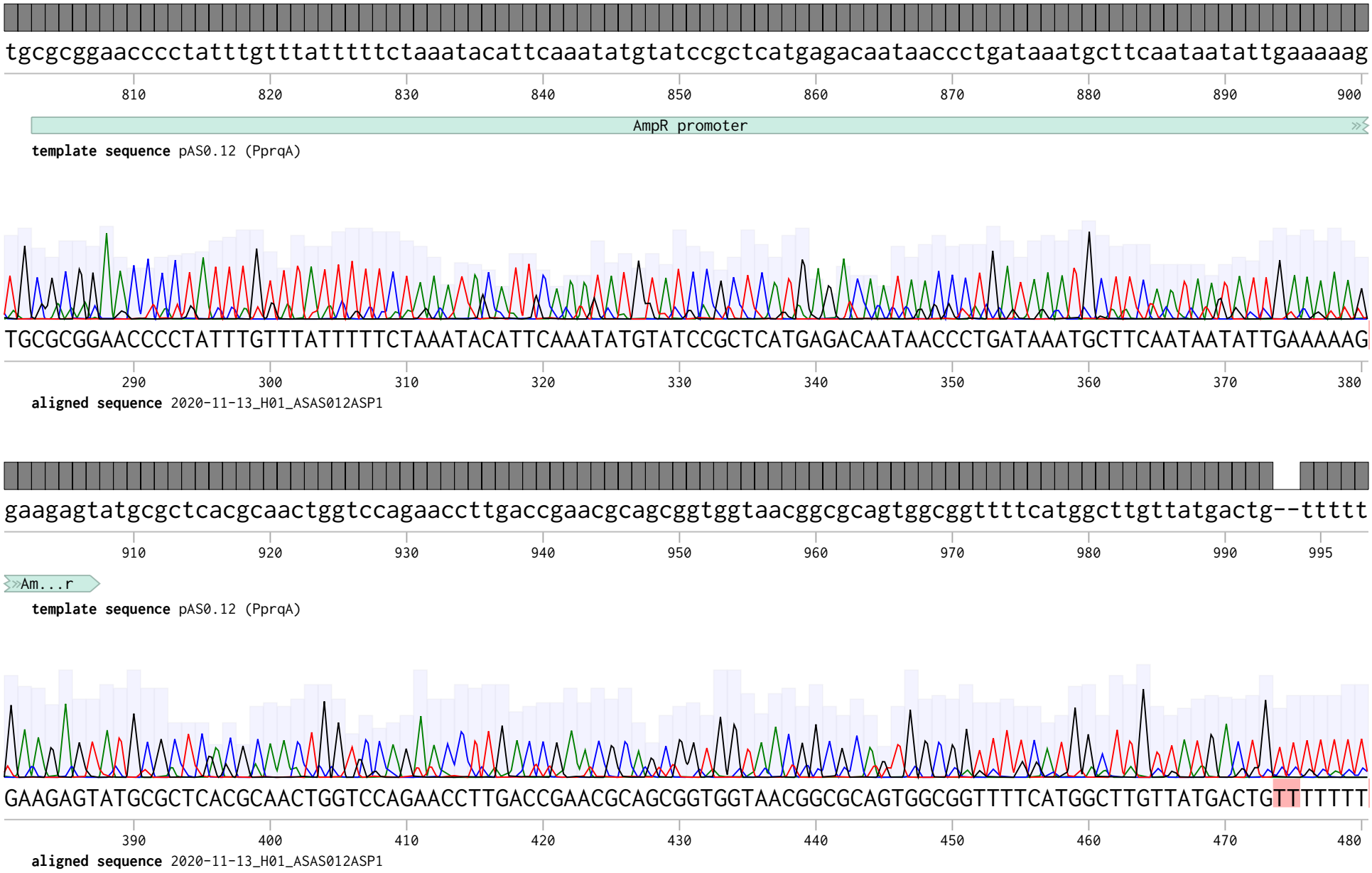
610
620
630
640
650
660
670
680
690
700
overlap
PprqA-1
template sequence pAS0.12 (PprqA)
GCGTTGGCCGATTCATTAATCACTCTGTGGTCTCAGGAGCATATTTAATAACTATTTTAGTTCTTTGGGTCAATGCTAATGTGAGACCACGAAGTGGCTC
90
100
110
120
130
140
150
160
170
180
aligned sequence 2020-11-13_H01_ASAS012ASP1
ttcagtggacgaaagggcctcgtgatacgcctatttttataggttaatgtcatgataataatggtttcttagacgtcaggtggcacttttcggggaaatg
710
720
730
740
750
760
770
780
790
800
pBRforEco
template sequence pAS0.12 (PprqA)
TTCAGTGGACGAAAGGGCCTCGTGATACGCCTATTTTTATAGGTTAATGTCATGATAATAATGGTTTCTTAGACGTCAGGTGGCACTTTTCGGGGAAATG
190
200
210
220
230
240
250
260
270
280
aligned sequence 2020-11-13_H01_ASAS012ASP1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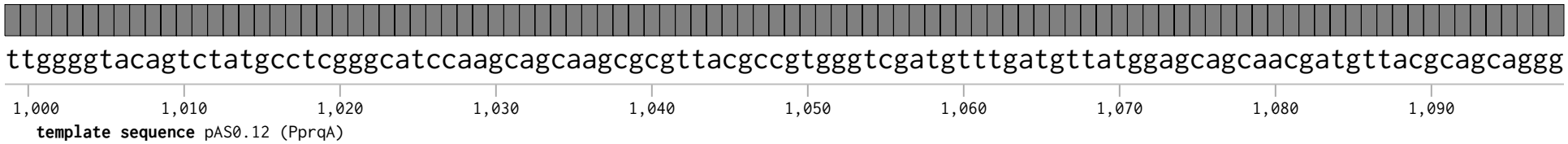
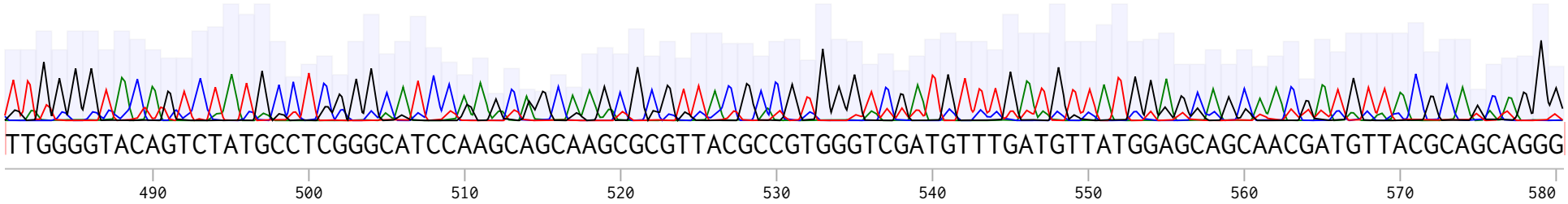
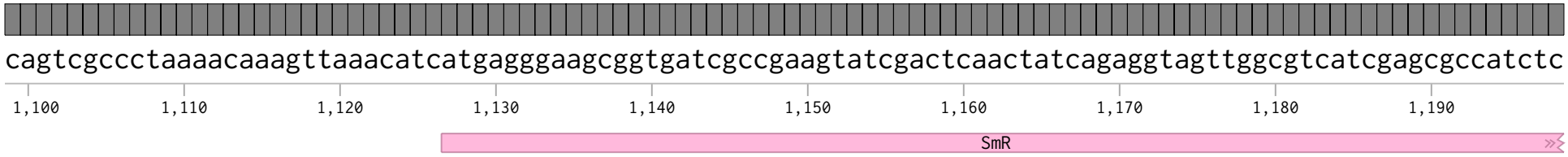
810 820 830 840 850 860 870 880 890 900
AmpR promoter
template sequence pAS0.12 (PprqA)
TGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAATATTGAAAAAG
290 300 310 320 330 340 350 360 370 380
aligned sequence 2020-11-13_H01_ASAS012ASP1
gaagagtatgcgctcacgcaactggtccagaaccttgaccgaacgcagcggtggtaacggcgcagtggcggttttcatggcttgttatgactg--ttttt
910 920 930 940 950 960 970 980 990 995
Am...r
template sequence pAS0.12 (PprqA)
GAAGAGTATGCGCTCACGCAACTGGTCCAGAACCTTGACCGAACGCAGCGGTGGTAACGGCGCAGTGGCGGTTTTCATGGCTTGTTATGACTGTTTTTTT
390 400 410 420 430 440 450 460 470 480
aligned sequence 2020-11-13_H01_ASAS012ASP1



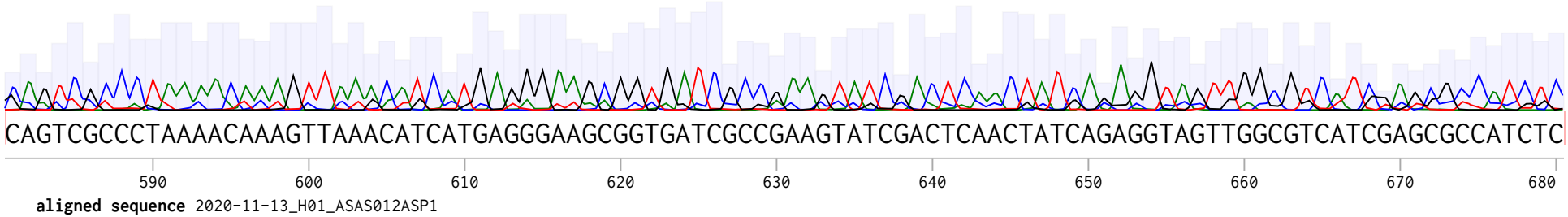
template sequence pAS0.12 (PprqA)



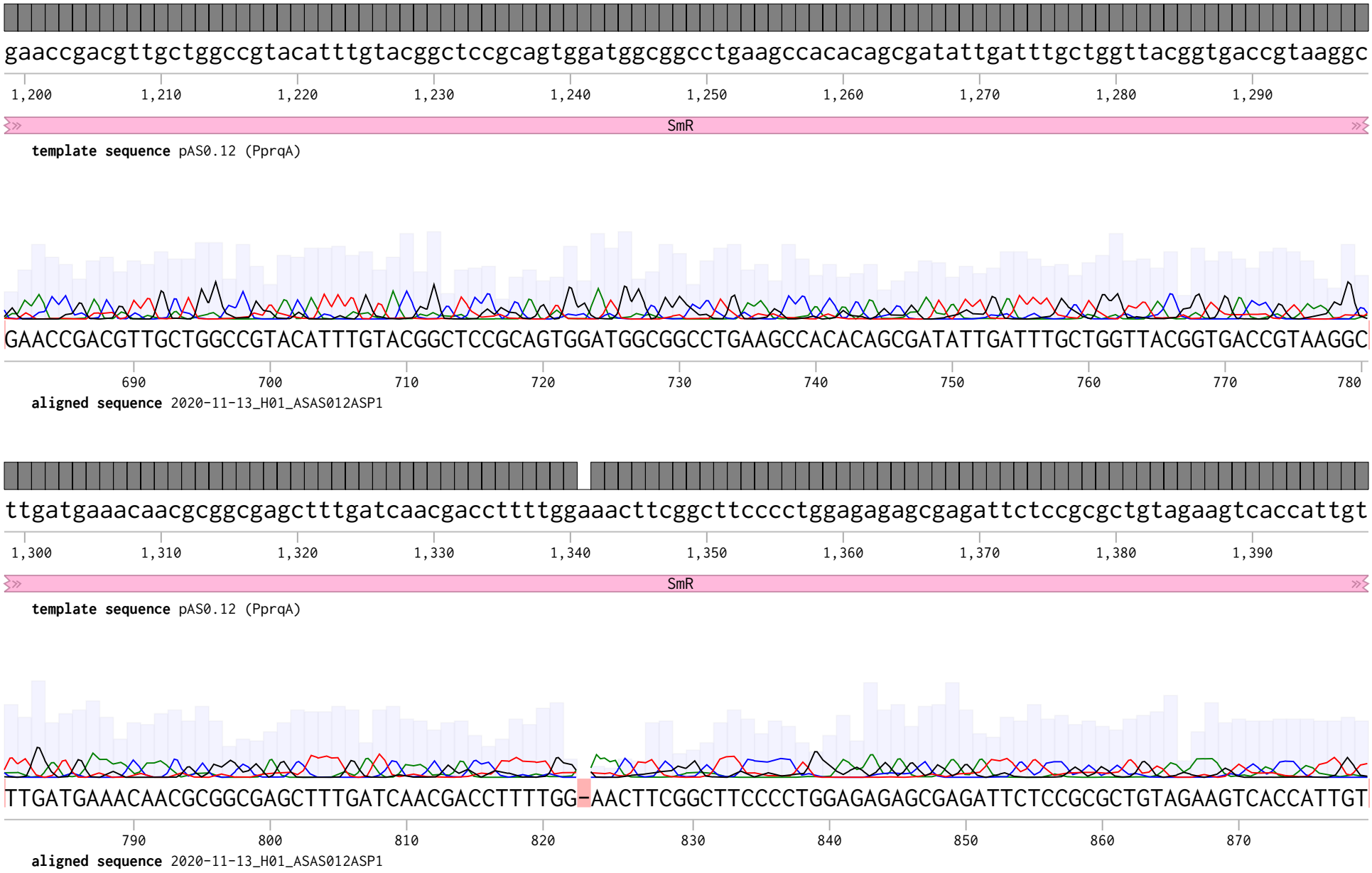
aligned sequence 2020-11-13_H01_ASAS012ASP1



template sequence pAS0.12 (PprqA)



aligned sequence 2020-11-13_H01_ASAS012ASP1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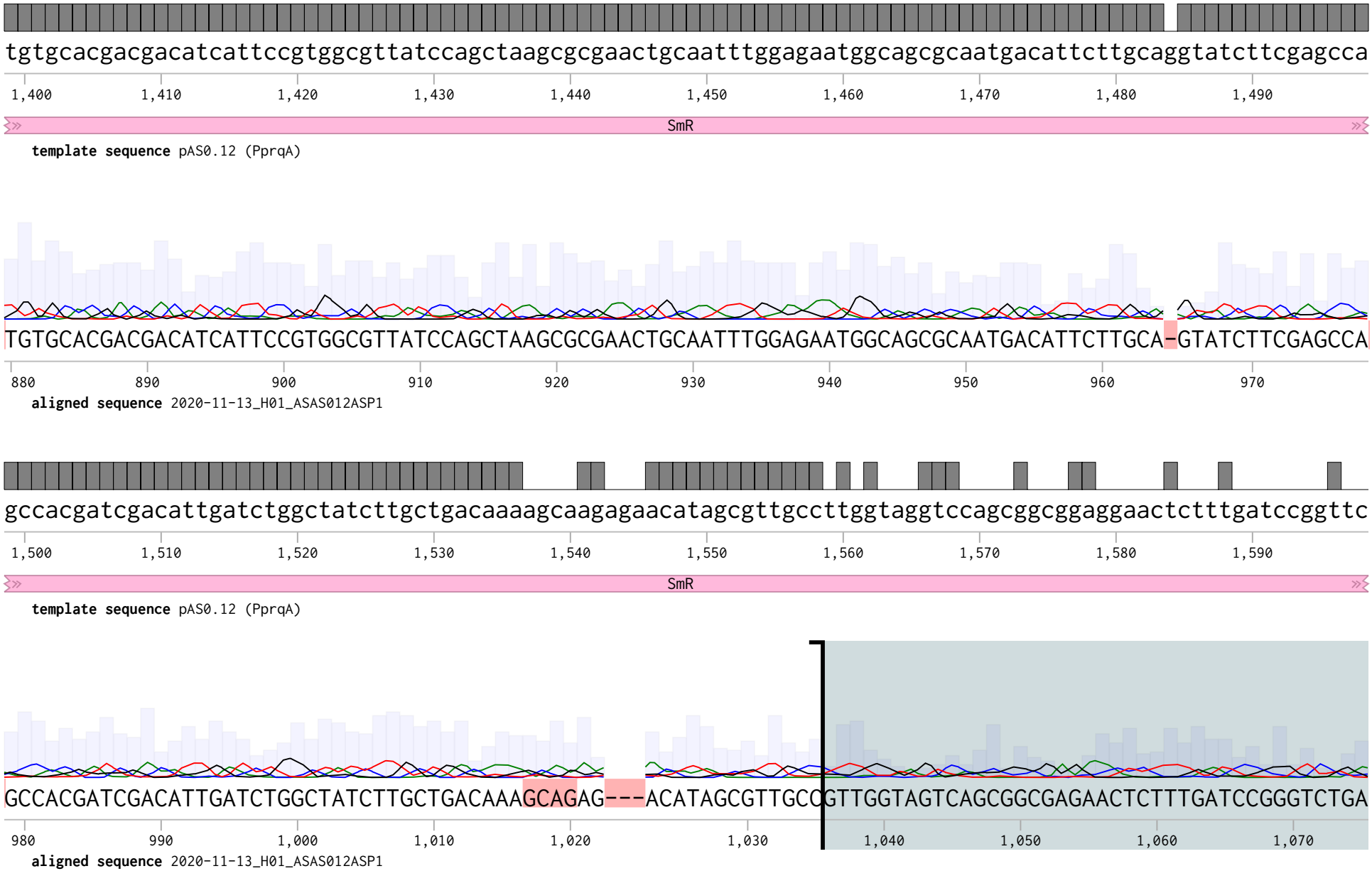
1,200
1,210
1,220
1,230
1,240
1,250
1,260
1,270
1,280
1,290
SmR
template sequence pAS0.12 (PprqA)
GAACCGACGTTGCTGGCCGTACATTTGTACGGCTCCGCAGTGGATGGCGGCCTGAAGCCACACAGCGATATTGATTTGCTGGTTACGGTGACCGTAAGGC
690
700
710
720
730
740
750
760
770
780
aligned sequence 2020-11-13_H01_ASAS012ASP1
ttgatgaaacaacgcggcgagctttgatcaacgacctttggaaacttcggcttcccctggagagagcgagattctccgcgctgtagaagtcaccattgt
1,300
1,310
1,320
1,330
1,340
1,350
1,360
1,370
1,380
1,390
SmR
template sequence pAS0.12 (PprqA)
TTGATGAAACAACGCGGCGAGCTTTGATCAACGACCTTTTGG-AACTTCGGCTTCCCCTGGAGAGAGCGAGATTCTCCGCGCTGTAGAAGTCACCATTGT
790
800
810
820
830
840
850
860
870
aligned sequence 2020-11-13_H01_ASAS012ASP1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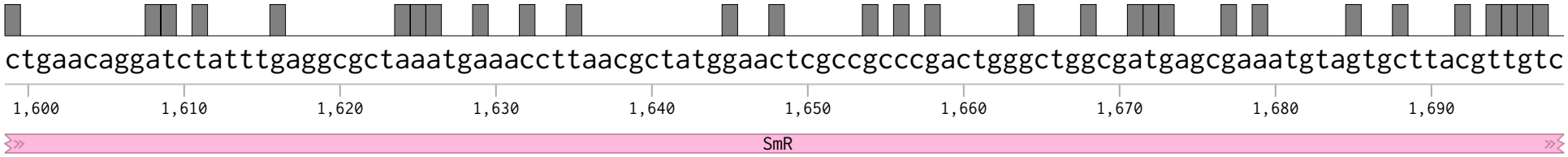
1,400
1,410
1,420
1,430
1,440
1,450
1,460
1,470
1,480
1,490
SmR
template sequence pAS0.12 (PprqA)
TGTGCACGACGACATCATTCCGTGGCGTTATCCAGCTAAGCGCGAACTGCAATTTGGAGAATGGCAGCGCAATGACATTCTTGCA-GTATCTTCGAGCCA
880
890
900
910
920
930
940
950
960
970
aligned sequence 2020-11-13_H01_ASAS012ASP1
gccacgatcgacattgatctggctatcttgctgacaaaagcaagagaacatagcgttgccttggtaggtccagcggcggaggaactctttgatccggttc
1,500
1,510
1,520
1,530
1,540
1,550
1,560
1,570
1,580
1,590
SmR
template sequence pAS0.12 (PprqA)
GCCACGATCGACATTGATCTGGCTATCTTGCTGACAAAGCAGAG---ACATAGCGTTGCCGTTGGTAGTCAGCGGCGAGAACTCTTTGATCCGGGTCTGA
980
990
1,000
1,010
1,020
1,030
1,040
1,050
1,060
1,070
aligned sequence 2020-11-13_H01_ASAS012ASP1



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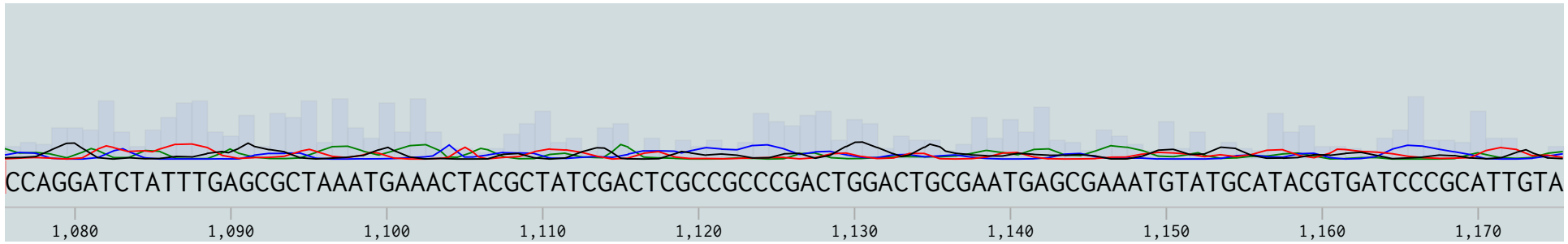
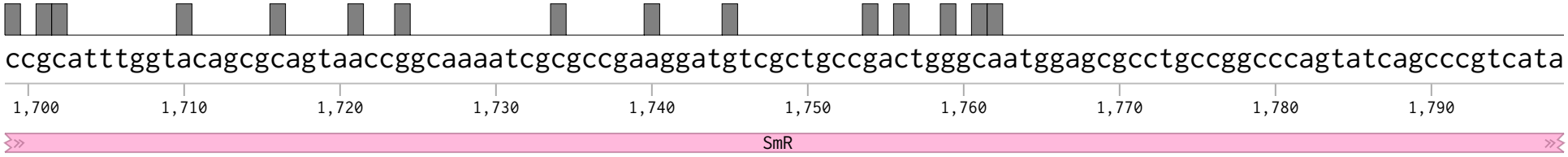
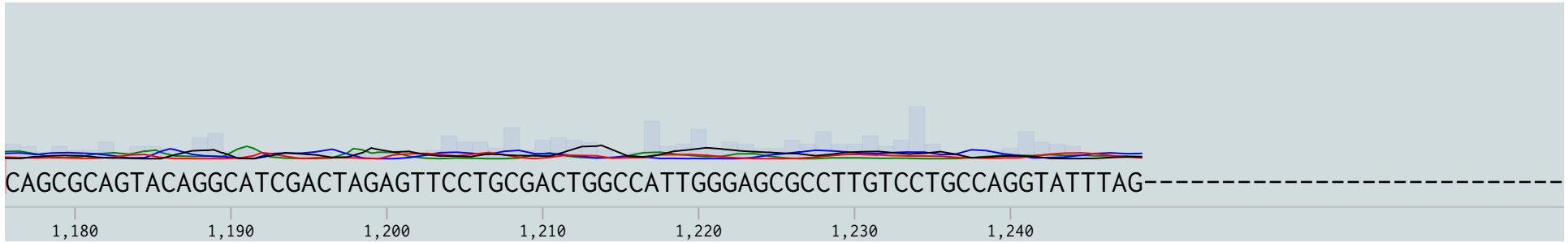


aligned sequence 2020-11-13_H01_ASAS012ASP1



template sequence pAS0.12 (PprqA)



aligned sequence 2020-11-13_H01_ASAS012ASP1

cttgaagctagacaggcttatcttggacaagaagaagatcgcttggcctcgcgcgcagatcagttggaagaatttgtccattacgtaaaaggcgagatca

1,800 1,810 1,820 1,830 1,840 1,850 1,860 1,870 1,880 1,890

SmR

template sequence pAS0.12 (PprqA)

aligned sequence 2020-11-13_H01_ASAS012ASP1

ccaaggtagtcggcaaataactgtcagaccaagtttactcatatatactttagattgatttaaaacttcatttttaatttaaaaggatctaggtgaagat

1,900 1,910 1,920 1,930 1,940 1,950 1,960 1,970 1,980 1,990

SmR

template sequence pAS0.12 (PprqA)

aligned sequence 2020-11-13_H01_ASAS012ASP1

cctttttgataatctcatgaccaaaatcccttaacgtgagttttcgttccactgagcgtcagaccccgtagaaaagatcaaaggatcttcttgagatcct

2,000 2,010 2,020 2,030 2,040 2,050 2,060 2,070 2,080 2,090

ori

template sequence pAS0.12 (PprqA)

aligned sequence 2020-11-13_H01_ASAS012ASP1

ttttttctgcgcgtaatctgctgcttgcaaacaaaaaaaccaccgctaccagcggtggtttgtttgccggatcaagagctaccaactctttttccgaagg

2,100 2,110 2,120 2,130 2,140 2,150 2,160 2,170 2,180 2,190

ori

template sequence pAS0.12 (PprqA)

aligned sequence 2020-11-13_H01_ASAS012ASP1

template sequence pAS0.12 (PprqA)

aligned sequence 2020-11-13_H01_ASAS012ASP1