Template Alignment: 2020-12-04_G02_ASAST15BSPTF

ctcaagaagatcctttgatcttttctacggcgcgcccagctgtctagggcggcggatttgtcctactcaggagagcgttcaccgacaaacaacagataaa

10	20	30	40	50	60	70	80	90	100

rrnB T1 terminator

template sequence pAST.010 (ΔprqRA Cas12a KO 1)

aligned sequence 2020-12-04_G02_ASAST15BSPTF

acgaaaggcccagtctttcgactgagcctttcgttttatttgatgccttgccgaattcggatccggagtttacggctagctcagtcctaggtactatgct

110	120	130	140	150	160	170	180	190	200

rrnB T1 terminator

Bba_J23105

template sequence pAST.010 (ΔprqRA Cas12a KO 1)

aligned sequence 2020-12-04_G02_ASAST15BSPTF

agctattgtgagcggataacaatttcacacatactagagaaagaggagaaatactaaATGAGCAAGCTGGAGAAGTTTACAAACTGCTACTCCCTGTCTA

| 210 | 220 | 230 | 240 | 250 | 260 | 270 | 280 | 290 | 300 |

lac operator

stron...000)

synthetic parts

LB cpf 1

template sequence pAST.010 (ΔprqRA Cas12a KO 1)

aligned sequence 2020-12-04_G02_ASAST15BSPTF

AGACCCTGAGGTTCAAGGCCATCCCTGTGGGCAAGACCCAGGAGAACATCGACAATAAGCGGCTGCTGGTGGAGGACGAGAAGAGAGCCGAGGATTATAA

| 310 | 320 | 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |

LB cpf 1

template sequence pAST.010 (ΔprqRA Cas12a KO 1)

aligned sequence 2020-12-04_G02_ASAST15BSPTF

GGGCGTGAAGAAGCTGCTGGATCGCTACTATCTGTCTTTTATCAACGACGTGCTGCACAGCATCAAGCTGAAGAATCTGAACAATTACATCAGCCTGTTC
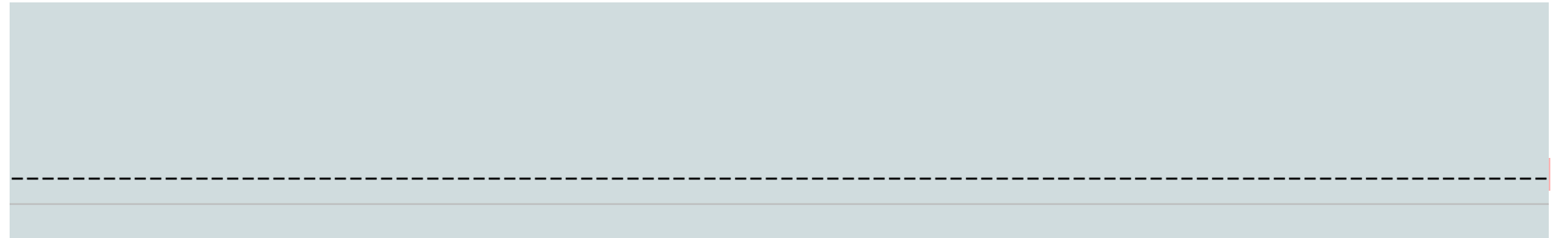
410	420	430	440	450	460	470	480	490	500

LB cpf 1

template sequence pAST.010 (ΔprqRA Cas12a KO 1)

----

aligned sequence 2020-12-04_G02_ASAST15BSPTF

CGGAAGAAAACCAGAACCGAGAAGGAGAATAAGGAGCTGGAGAACCTGGAGATCAATCTGCGGAAGGAGATCGCCAAGGCCTTCAAGGGCAACGAGGGCT

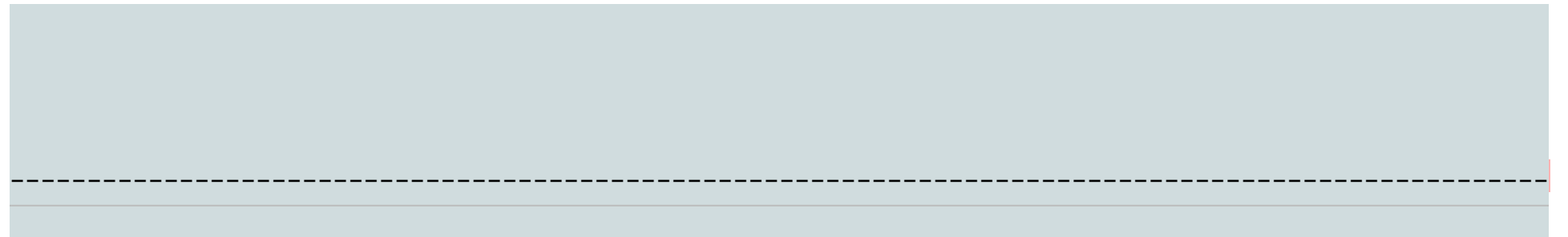|									
510	520	530	540	550	560	570	580	590	600

LB cpf 1

template sequence pAST.010 (ΔprqRA Cas12a KO 1)

----

aligned sequence 2020-12-04_G02_ASAST15BSPTF

ACAAGTCCCTGTTTAAGAAGGATATCATCGAGACAATCCTGCCAGAGTTCCTGGACGATAAGGACGAGATCGCCCTGGTGAACAGCTTCAATGGCTTTAC
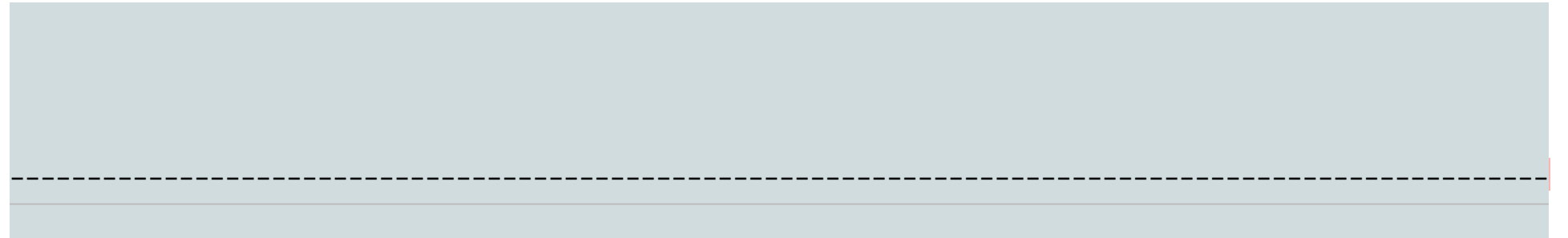
| 610 | 620 | 630 | 640 | 650 | 660 | 670 | 680 | 690 | 700 |

LB cpf 1

template sequence pAST.010 (ΔprqRA Cas12a KO 1)

----

aligned sequence 2020-12-04_G02_ASAST15BSPTF

CACAGCCTTCACCGGCTTCTTTGATAACAGAGAGAATATGTTTTCCGAGGAGGCCAAGAGCACATCCATCGCCTTCAGGTGTATCAACGAGAATCTGACC
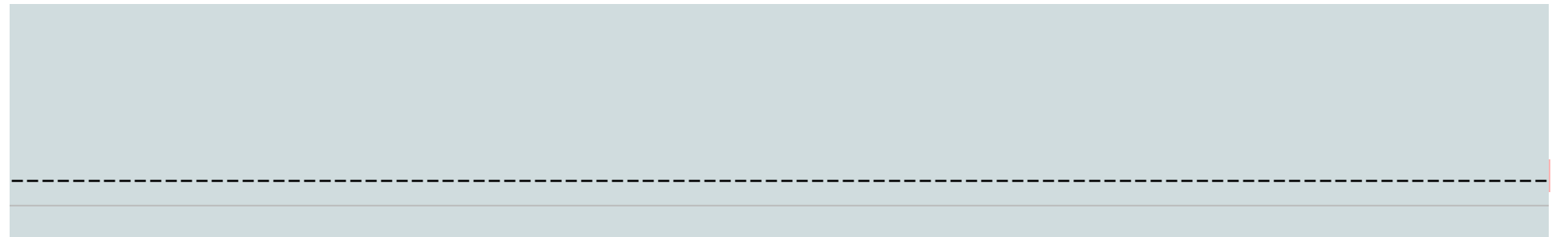
| 710 | 720 | 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 |

LB cpf 1

template sequence pAST.010 (ΔprqRA Cas12a KO 1)

----

aligned sequence 2020-12-04_G02_ASAST15BSPTF

CGCTACATCTCTAATATGGACATCTTCGAGAAGGTGGACGCCATCTTTGATAAGCACGAGGTGCAGGAGATCAAGGAGAAGATCCTGAACAGCGACTATG
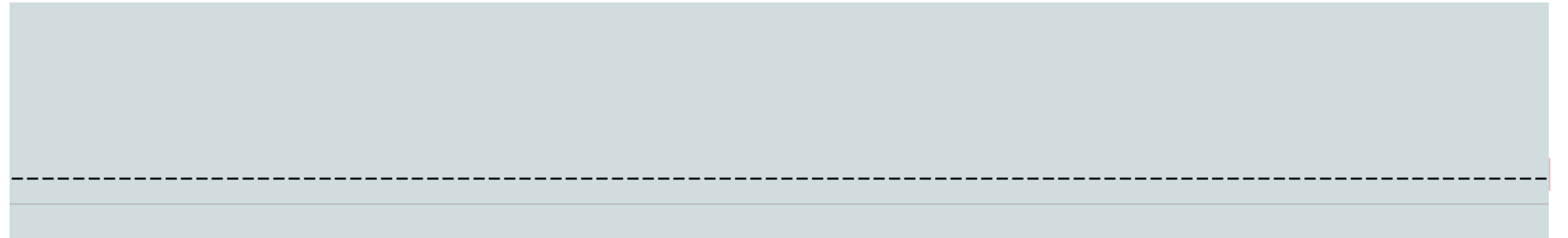
810 820 830 840 850 860 870 880 890 900

LB cpf 1

template sequence pAST.010 (ΔprqRA Cas12a KO 1)

aligned sequence 2020-12-04_G02_ASAST15BSPTF

ATGTGGAGGATTTCTTTGAGGGCGAGTTCTTTAACTTTGTGCTGACACAGGAGGGCATCGACGTGTATAACGCCATCATCGGCGGCTTCGTGACCGAGAG
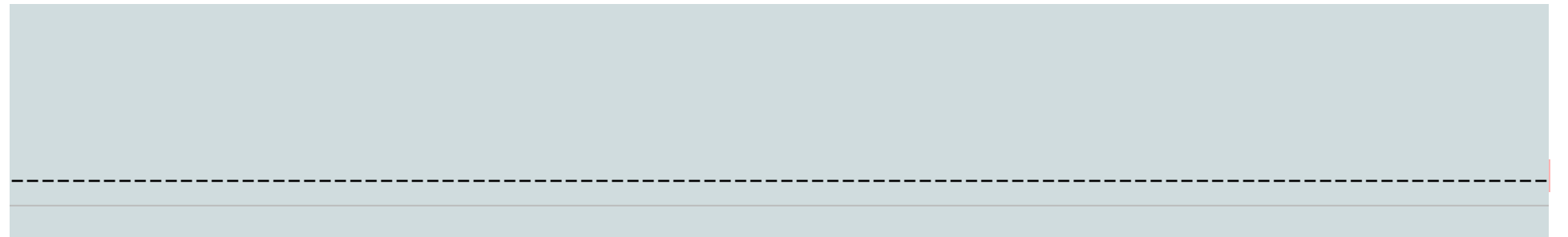
910 920 930 940 950 960 970 980 990 1,000

LB cpf 1

template sequence pAST.010 (ΔprqRA Cas12a KO 1)

aligned sequence 2020-12-04_G02_ASAST15BSPTF

CGGCGAGAAGATCAAGGGCCTGAACGAGTACATCAACCTGTATAATCAGAAAACCAAGCAGAAGCTGCCTAAGTTTAAGCCACTGTATAAGCAGGTGCTG

| 1,010 | 1,020 | 1,030 | 1,040 | 1,050 | 1,060 | 1,070 | 1,080 | 1,090 | 1,100 |

LB cpf 1

template sequence pAST.010 (ΔprqRA Cas12a KO 1)

aligned sequence 2020-12-04_G02_ASAST15BSPTF

AGCGATCGGGAGTCTCTGAGCTTCTACGGCGAGGGCTATACATCCGATGAGGAGGTGCTGGAGGTGTTTAGAAACACCCTGAACAAGAACAGCGAGATCT

| 1,110 | 1,120 | 1,130 | 1,140 | 1,150 | 1,160 | 1,170 | 1,180 | 1,190 | 1,200 |

LB cpf 1

template sequence pAST.010 (ΔprqRA Cas12a KO 1)

aligned sequence 2020-12-04_G02_ASAST15BSPTF

TCAGCTCCATCAAGAAGCTGGAGAAGCTGTTCAAGAATTTTGACGAGTACTCTAGCGCCGGCATCTTTGTGAAGAACGGCCCCGCCATCAGCACAATCTC

| 1,210 | 1,220 | 1,230 | 1,240 | 1,250 | 1,260 | 1,270 | 1,280 | 1,290 | 1,300 |

LB cpf 1

template sequence pAST.010 (ΔprqRA Cas12a KO 1)

aligned sequence 2020-12-04_G02_ASAST15BSPTF

CAAGGATATCTTCGGCGAGTGGAACGTGATCCGGGACAAGTGGAATGCCGAGTATGACGATATCCACCTGAAGAAGAAGGCCGTGGTGACCGAGAAGTAC

| 1,310 | 1,320 | 1,330 | 1,340 | 1,350 | 1,360 | 1,370 | 1,380 | 1,390 | 1,400 |

LB cpf 1

template sequence pAST.010 (ΔprqRA Cas12a KO 1)

aligned sequence 2020-12-04_G02_ASAST15BSPTF

GAGGACGATCGGAGAAAGTCCTTCAAGAAGATCGGCTCCTTTTCTCTGGAGCAGCTGCAGGAGTACGCCGACGCCGATCTGTCTGTGGTGGAGAAGCTGA

| 1,410 | 1,420 | 1,430 | 1,440 | 1,450 | 1,460 | 1,470 | 1,480 | 1,490 | 1,500 |

LB cpf 1

template sequence pAST.010 (ΔprqRA Cas12a KO 1)

aligned sequence 2020-12-04_G02_ASAST15BSPTF

AGGAGATCATCATCCAGAAGGTGGATGAGATCTACAAGGTGTATGGCTCCTCTGAGAAGCTGTTCGACGCCGATTTTGTGCTGGAGAAGAGCCTGAAGAA

| 1,510 | 1,520 | 1,530 | 1,540 | 1,550 | 1,560 | 1,570 | 1,580 | 1,590 | 1,600 |

LB cpf 1

template sequence pAST.010 (ΔprqRA Cas12a KO 1)

aligned sequence 2020-12-04_G02_ASAST15BSPTF

GAACGACGCCGTGGTGGCCATCATGAAGGACCTGCTGGATTCTGTGAAGAGCTTCGAGAATTACATCAAGGCCTTCTTTGGCGAGGGCAAGGAGACAAAC

| 1,610 | 1,620 | 1,630 | 1,640 | 1,650 | 1,660 | 1,670 | 1,680 | 1,690 | 1,700 |

LB cpf 1

template sequence pAST.010 (ΔprqRA Cas12a KO 1)

aligned sequence 2020-12-04_G02_ASAST15BSPTF

AGGGACGAGTCCTTCTATGGCGATTTTGTGCTGGCCTACGACATCCTGCTGAAGGTGGACCACATCTACGATGCCATCCGCAATTATGTGACCCAGAAGC

| 1,710 | 1,720 | 1,730 | 1,740 | 1,750 | 1,760 | 1,770 | 1,780 | 1,790 | 1,800 |

LB cpf 1

template sequence pAST.010 (ΔprqRA Cas12a KO 1)

aligned sequence 2020-12-04_G02_ASAST15BSPTF

CCTACTCTAAGGATAAGTTCAAGCTGTATTTTCAGAACCCTCAGTTCATGGGCGGCTGGGACAAGGATAAGGAGACAGACTATCGGGCCACCATCCTGAG

| | | | | | | | | | |
|1,810|1,820|1,830|1,840|1,850|1,860|1,870|1,880|1,890|1,900|

LB cpf 1

template sequence pAST.010 (ΔprqRA Cas12a KO 1)

aligned sequence 2020-12-04_G02_ASAST15BSPTF

ATACGGCTCCAAGTACTATCTGGCCATCATGGATAAGAAGTACGCCAAGTGCCTGCAGAAGATCGACAAGGACGATGTGAACGGCAATTACGAGAAGATC

| | | | | | | | | | |
|1,910|1,920|1,930|1,940|1,950|1,960|1,970|1,980|1,990|2,000|

LB cpf 1

template sequence pAST.010 (ΔprqRA Cas12a KO 1)

aligned sequence 2020-12-04_G02_ASAST15BSPTF

AACTATAAGCTGCTGCCCGGCCCTAATAAGATGCTGCCAAAGGTGTTCTTTTCTAAGAAGTGGATGGCCTACTATAACCCCAGCGAGGACATCCAGAAGA

| 2,010 | 2,020 | 2,030 | 2,040 | 2,050 | 2,060 | 2,070 | 2,080 | 2,090 | 2,100 |

LB cpf 1

template sequence pAST.010 (ΔprqRA Cas12a KO 1)

aligned sequence 2020-12-04_G02_ASAST15BSPTF

TCTACAAGAATGGCACATTCAAGAAGGGCGATATGTTTAACCTGAATGACTGTCACAAGCTGATCGACTTCTTTAAGGATAGCATCTCCCGGTATCCAAA

| 2,110 | 2,120 | 2,130 | 2,140 | 2,150 | 2,160 | 2,170 | 2,180 | 2,190 | 2,200 |

LB cpf 1

template sequence pAST.010 (ΔprqRA Cas12a KO 1)

aligned sequence 2020-12-04_G02_ASAST15BSPTF

GTGGTCCAATGCCTACGATTTCAACTTTTCTGAGACAGAGAAGTATAAGGACATCGCCGGCTTTTACAGAGAGGTGGAGGAGCAGGGCTATAAGGTGAGC

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

LB cpf 1

template sequence pAST.010 (ΔprqRA Cas12a KO 1)

aligned sequence 2020-12-04_G02_ASAST15BSPTF

TTCGAGTCTGCCAGCAAGAAGGAGGTGGATAAGCTGGTGGAGGAGGGCAAGCTGTATATGTTCCAGATCTATAACAAGGACTTTTCCGATAAGTCTCACG

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

LB cpf 1

template sequence pAST.010 (ΔprqRA Cas12a KO 1)

aligned sequence 2020-12-04_G02_ASAST15BSPTF

GCACACCCAATCTGCACACCATGTACTTCAAGCTGCTGTTTGACGAGAACAATCACGGACAGATCAGGCTGAGCGGAGGAGCAGAGCTGTTCATGAGGCG

| 2,410 | 2,420 | 2,430 | 2,440 | 2,450 | 2,460 | 2,470 | 2,480 | 2,490 | 2,500 |

LB cpf 1

template sequence pAST.010 (ΔprqRA Cas12a KO 1)

aligned sequence 2020-12-04_G02_ASAST15BSPTF

CGCCTCCCTGAAGAAGGAGGAGCTGGTGGTGCACCCAGCCAACTCCCCTATCGCCAACAAGAATCCAGATAATCCCAAGAAAACCACAACCCTGTCCTAC

| 2,510 | 2,520 | 2,530 | 2,540 | 2,550 | 2,560 | 2,570 | 2,580 | 2,590 | 2,600 |

LB cpf 1

template sequence pAST.010 (ΔprqRA Cas12a KO 1)

aligned sequence 2020-12-04_G02_ASAST15BSPTF

GACGTGTATAAGGATAAGAGGTTTTCTGAGGACCAGTACGAGCTGCACATCCCAATCGCCATCAATAAGTGCCCCAAGAACATCTTCAAGATCAATACAG

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

LB cpf 1

template sequence pAST.010 (ΔprqRA Cas12a KO 1)

aligned sequence 2020-12-04_G02_ASAST15BSPTF

AGGTGCGCGTGCTGCTGAAGCACGACGATAACCCCTATGTGATCGGCATCGATAGGGGCGAGCGCAATCTGCTGTATATCGTGGTGGTGGACGGCAAGGG

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

LB cpf 1

template sequence pAST.010 (ΔprqRA Cas12a KO 1)

aligned sequence 2020-12-04_G02_ASAST15BSPTF

CAACATCGTGGAGCAGTATTCCCTGAACGAGATCATCAACAACTTCAACGGCATCAGGATCAAGACAGATTACCACTCTCTGCTGGACAAGAAGGAGAAG

| 2,810 | 2,820 | 2,830 | 2,840 | 2,850 | 2,860 | 2,870 | 2,880 | 2,890 | 2,900 |

LB cpf 1

template sequence pAST.010 (ΔprqRA Cas12a KO 1)

----
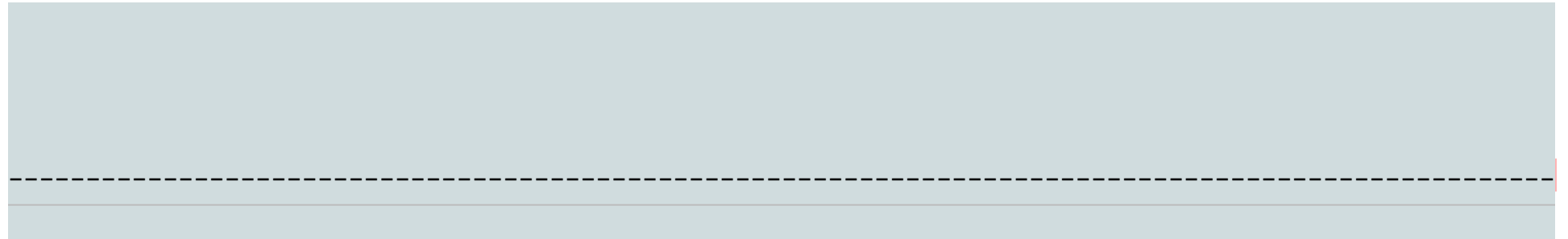
aligned sequence 2020-12-04_G02_ASAST15BSPTF

GAGAGGTTCGAGGCCCGCCAGAACTGGACCTCCATCGAGAATATCAAGGAGCTGAAGGCCGGCTATATCTCTCAGGTGGTGCACAAGATCTGCGAGCTGG

| 2,910 | 2,920 | 2,930 | 2,940 | 2,950 | 2,960 | 2,970 | 2,980 | 2,990 | 3,000 |

LB cpf 1

template sequence pAST.010 (ΔprqRA Cas12a KO 1)

----
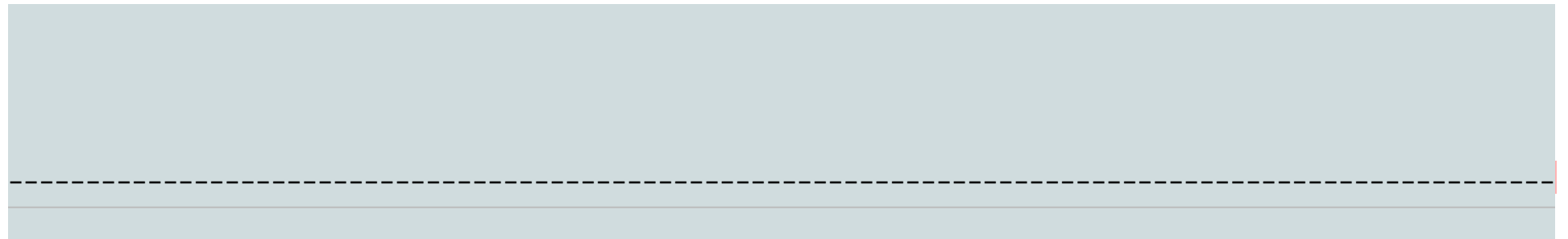
aligned sequence 2020-12-04_G02_ASAST15BSPTF

TGGAGAAGTACGATGCCGTGATCGCCCTGGAGGACCTGAACTCTGGCTTTAAGAATAGCCGCGTGAAGGTGGAGAAGCAGGTGTATCAGAAGTTCGAGAA

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

LB cpf 1

template sequence pAST.010 (ΔprqRA Cas12a KO 1)

aligned sequence 2020-12-04_G02_ASAST15BSPTF

GATGCTGATCGATAAGCTGAACTACATGGTGGACAAGAAGTCTAATCCTTGTGCAACAGGCGGCGCCCTGAAGGGCTATCAGATCACCAATAAGTTCGAG

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

LB cpf 1

template sequence pAST.010 (ΔprqRA Cas12a KO 1)

aligned sequence 2020-12-04_G02_ASAST15BSPTF

AGCTTTAAGTCCATGTCTACCCAGAACGGCTTCATCTTTTACATCCCTGCCTGGCTGACATCCAAGATCGATCCATCTACCGGCTTTGTGAACCTGCTGA

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

LB cpf 1

template sequence pAST.010 (ΔprqRA Cas12a KO 1)
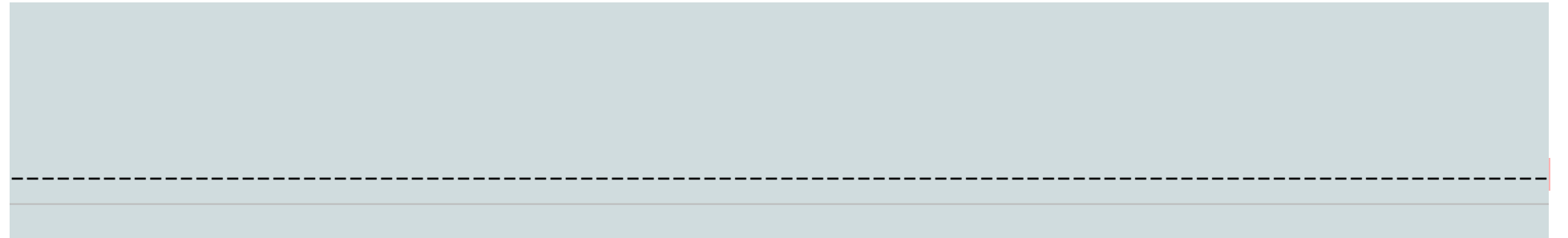
aligned sequence 2020-12-04_G02_ASAST15BSPTF

AAACCAAGTATACCAGCATCGCCGATTCCAAGAAGTTCATCAGCTCCTTTGACAGGATCATGTACGTGCCCGAGGAGGATCTGTTCGAGTTTGCCCTGGA

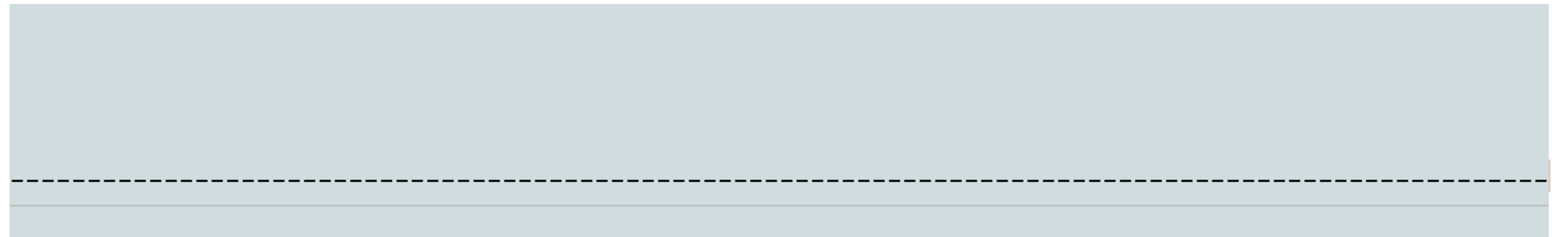| 3,310 | 3,320 | 3,330 | 3,340 | 3,350 | 3,360 | 3,370 | 3,380 | 3,390 | 3,400 |

LB cpf 1

template sequence pAST.010 (ΔprqRA Cas12a KO 1)

aligned sequence 2020-12-04_G02_ASAST15BSPTF

CTATAAGAACTTCTCTCGCACAGACGCCGATTACATCAAGAAGTGGAAGCTGTACTCCTACGGCAACCGGATCAGAATCTTCCGGAATCCTAAGAAGAAC

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

LB cpf 1
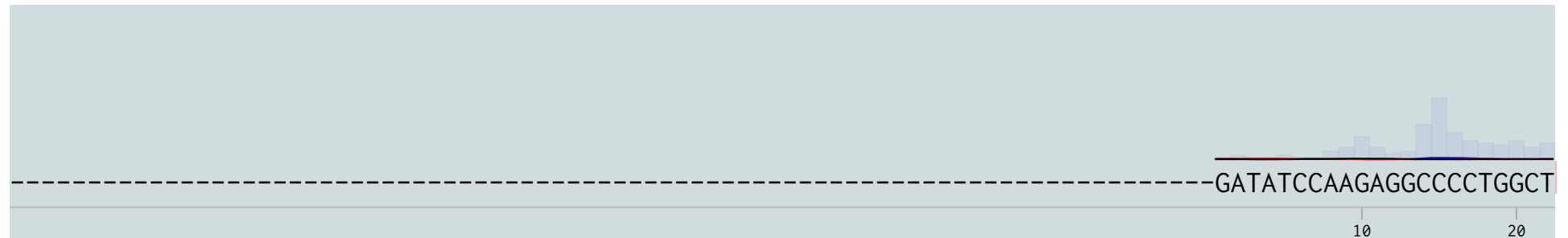
template sequence pAST.010 (ΔprqRA Cas12a KO 1)
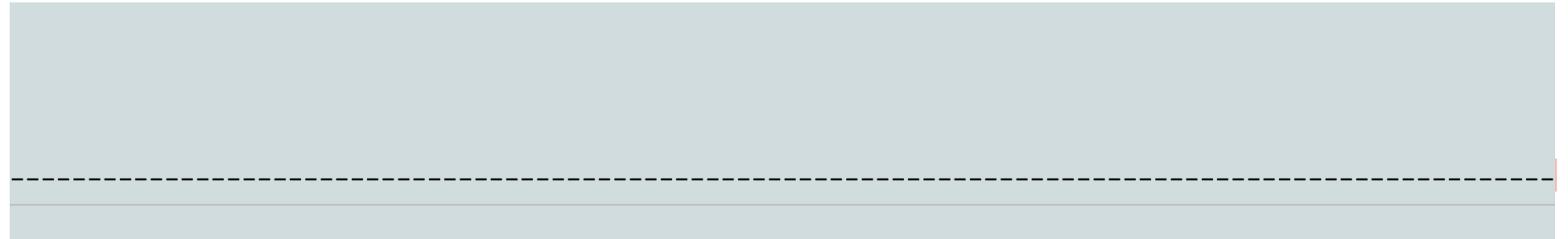
aligned sequence 2020-12-04_G02_ASAST15BSPTF

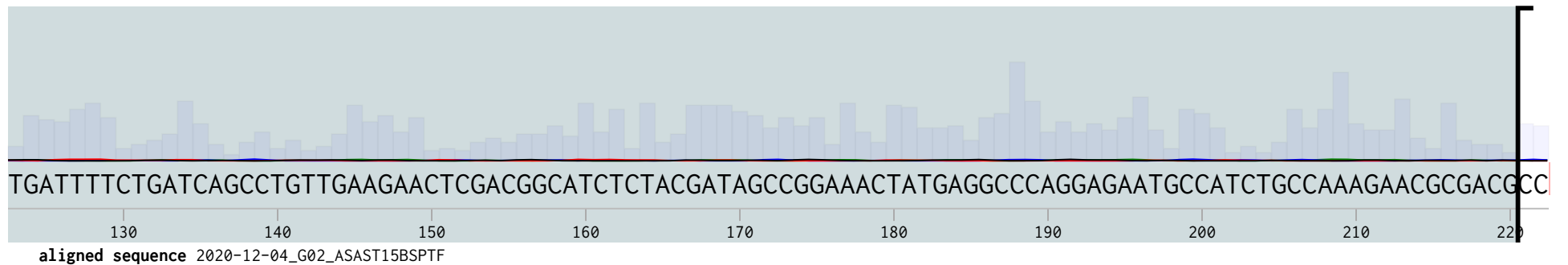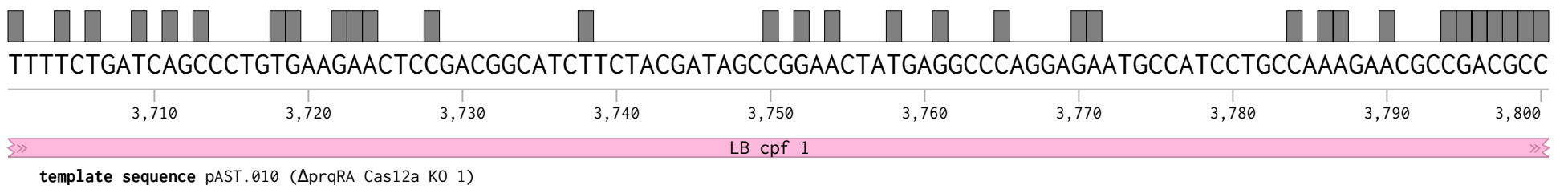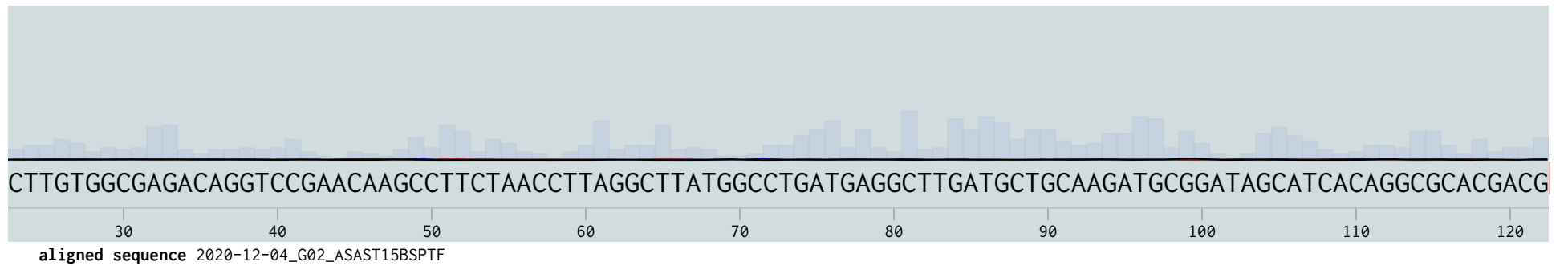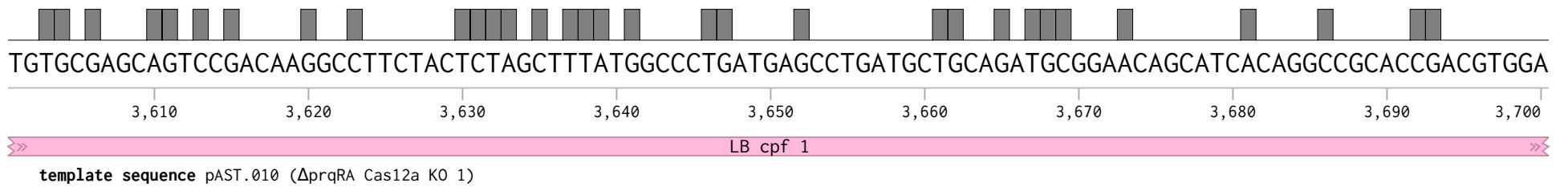AACGTGTTCGACTGGGAGGAGGTGTGCCTGACCAGCGCCTATAAGGAGCTGTTCAACAAGTACGGCATCAATTATCAGCAGGGCGATATCAGAGCCCTGC

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

LB cpf 1

template sequence pAST.010 (ΔprqRA Cas12a KO 1)

GATATCCAAGAGGCCCCTGGCT

| 10 | 20 |

aligned sequence 2020-12-04_G02_ASAST15BSPTF

TGTGCGAGCAGTCCGACAAGGCCTTCTACTCTAGCTTTATGGCCCTGATGAGCCTGATGCTGCAGATGCGGAACAGCATCACAGGCCGCACCGACGTGGA

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

LB cpf 1

template sequence pAST.010 (ΔprqRA Cas12a KO 1)

CTTGTGGCGAGACAGGTCCGAACAAGCCTTCTAACCTTAGGCTTATGGCCTGATGAGGCTTGATGCTGCAAGATGCGGATAGCATCACAGGCGCACGACG
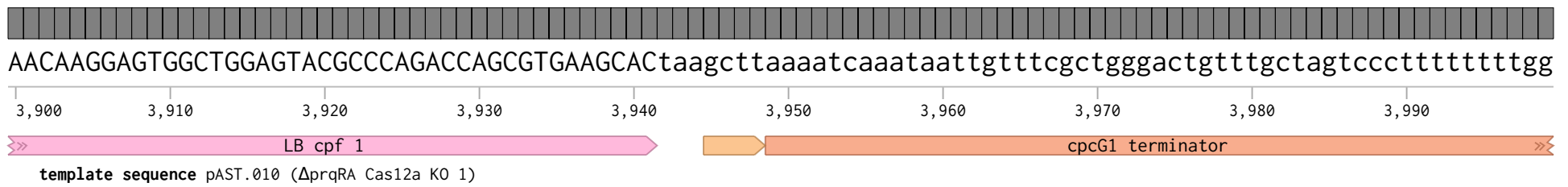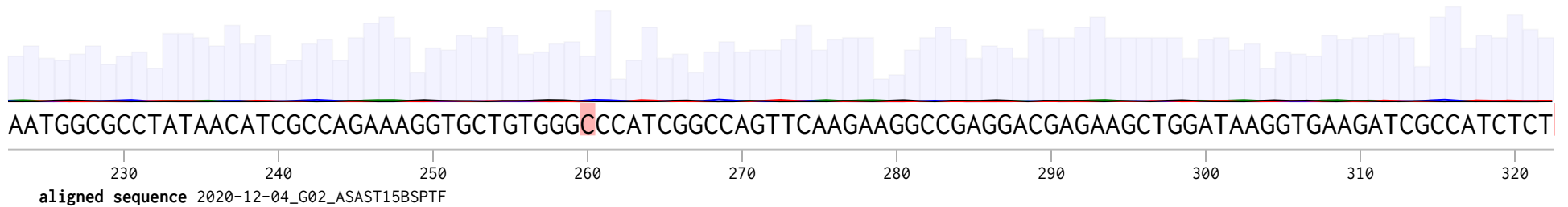
30   40   50   60   70   80   90   100   110   120

aligned sequence 2020-12-04_G02_ASAST15BSPTF

TTTTCTGATCAGCCCTGTGAAGAACTCCGACGGCATCTTCTACGATAGCCGGAACTATGAGGCCCAGGAGAATGCCATCCTGCCAAAGAACGCCGACGCC

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

LB cpf 1

template sequence pAST.010 (ΔprqRA Cas12a KO 1)

TGATTTTCTGATCAGCCTGTTGAAGAACTCGACGGCATCTCTACGATAGCCGGAAACTATGAGGCCCAGGAGAATGCCATCTGCCAAAGAACGCGACGCC
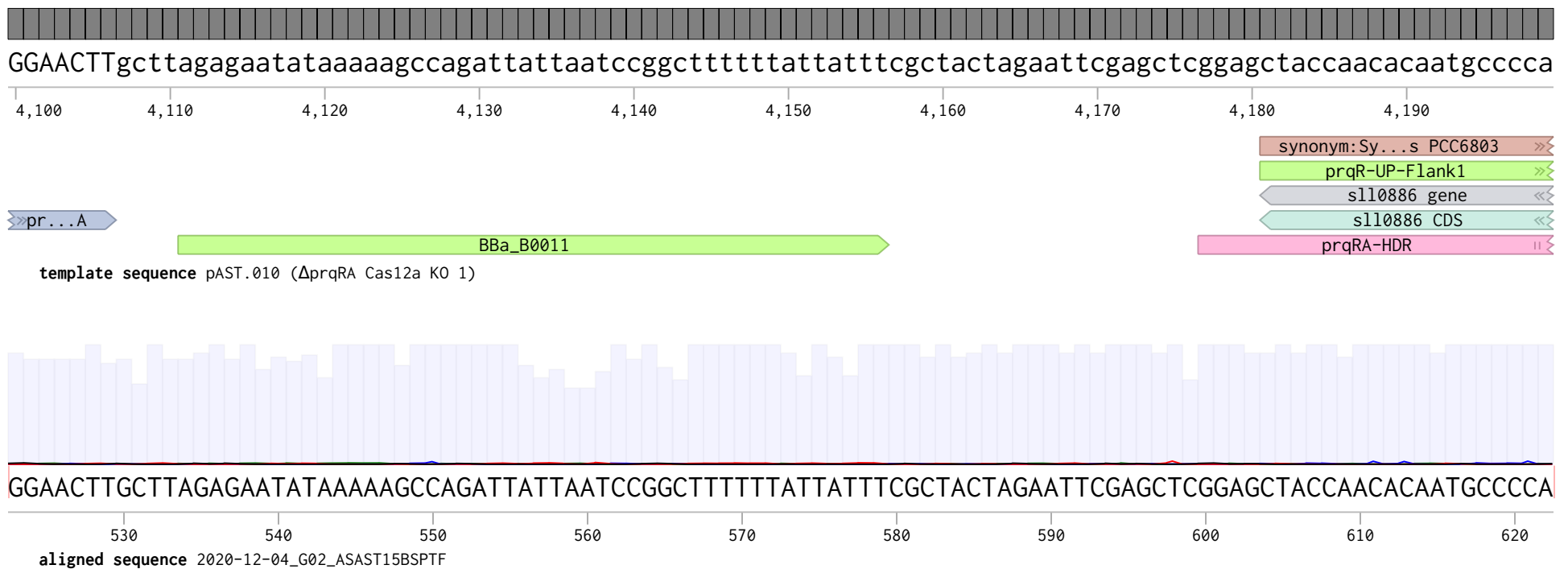
130   140   150   160   170   180   190   200   210   220

aligned sequence 2020-12-04_G02_ASAST15BSPTF

AATGGCGCCTATAACATCGCCAGAAAGGTGCTGTGGG-CCATCGGCCAGTTCAAGAAGGCCGAGGACGAGAAGCTGGATAAGGTGAAGATCGCCATCTCT

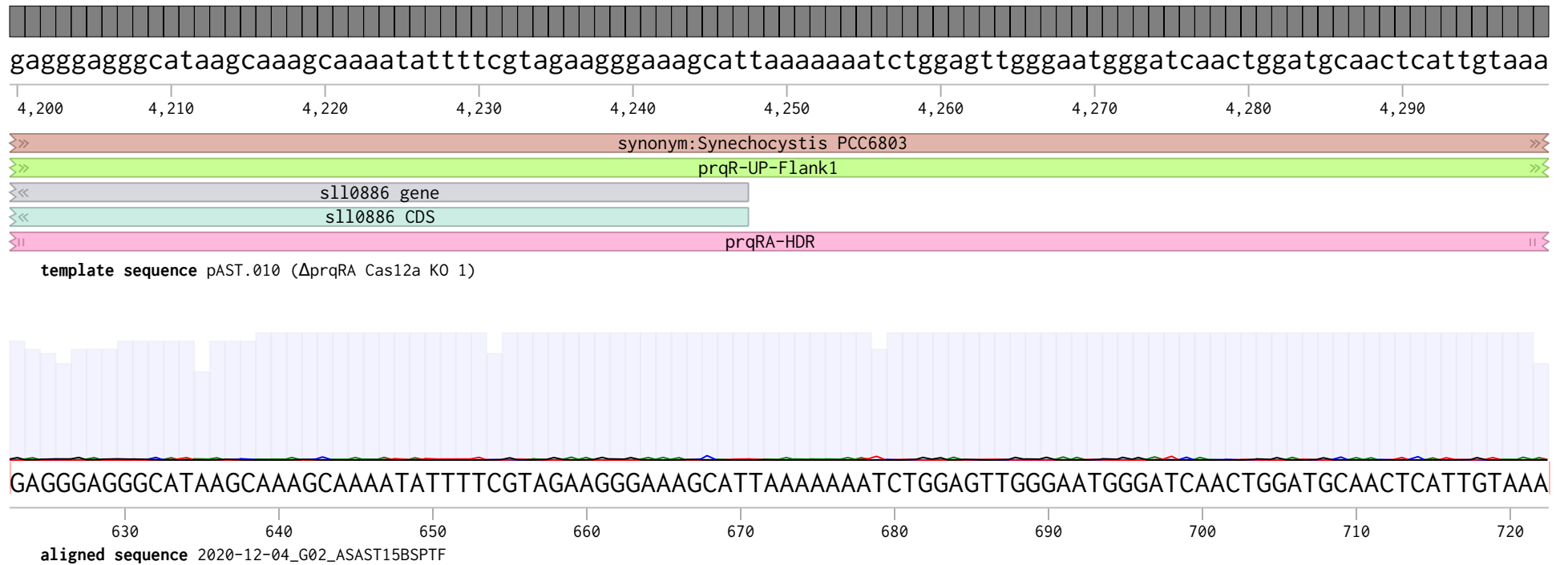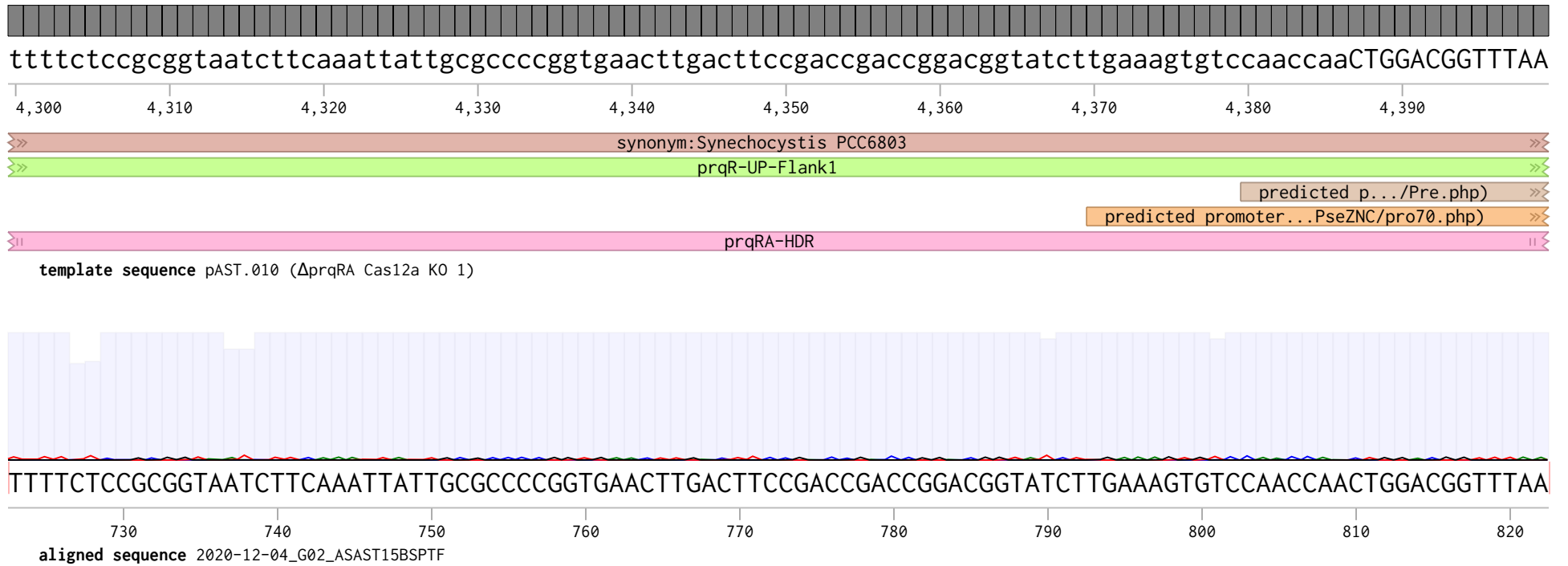3,810   3,820   3,830   3,840   3,850   3,860   3,870   3,880   3,890

LB cpf 1

template sequence pAST.010 (ΔprqRA Cas12a KO 1)

AATGGCGCCTATAACATCGCCAGAAAGGTGCTGTGGGCCCATCGGCCAGTTCAAGAAGGCCGAGGACGAGAAGCTGGATAAGGTGAAGATCGCCATCTCT

230   240   250   260   270   280   290   300   310   320

aligned sequence 2020-12-04_G02_ASAST15BSPTF

AACAAGGAGTGGCTGGAGTACGCCCAGACCAGCGTGAAGCACtaagcttaaaatcaaataattgtttcgctgggactgtttgctagtccctttttttgg

3,900   3,910   3,920   3,930   3,940   3,950   3,960   3,970   3,980   3,990
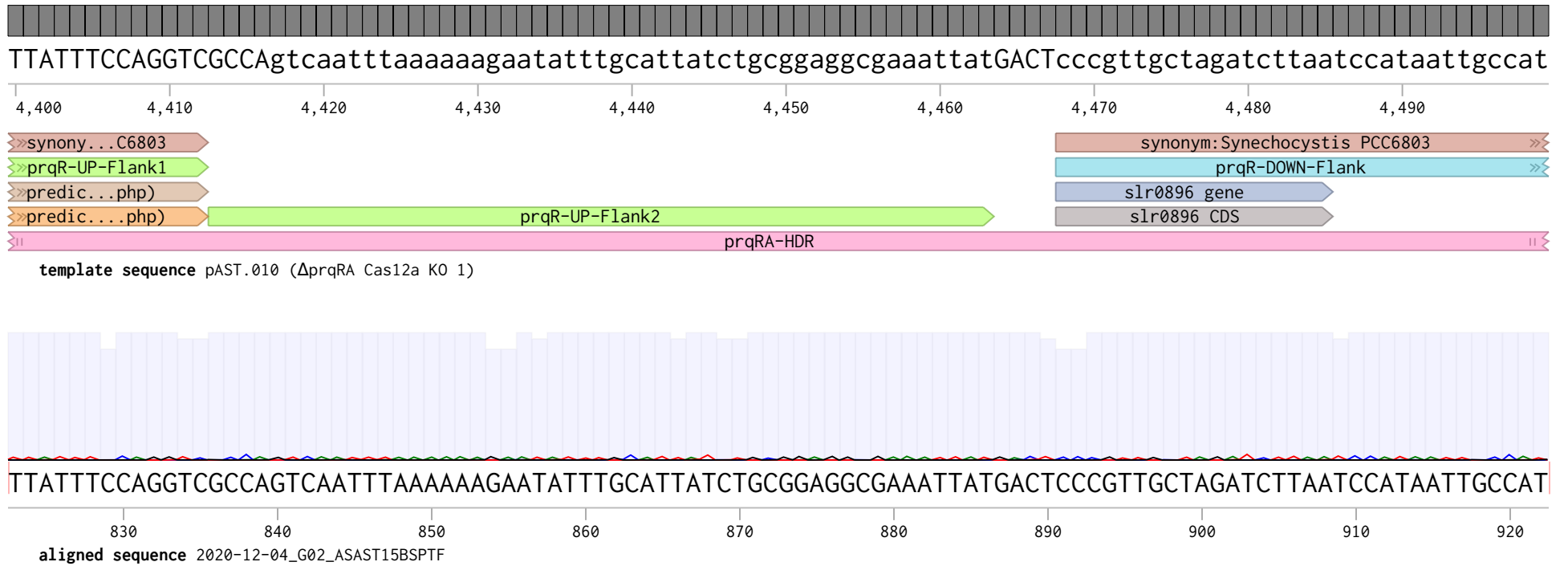
LB cpf 1   cpcG1 terminator

template sequence pAST.010 (ΔprqRA Cas12a KO 1)

AACAAGGAGTGGCTGGAGTACGCCCAGACCAGCGTGAAGCACTAAGCTTAAAATCAAATAATTGTTTCGCTGGGACTGTTTGCTAGTCCCTTTTTTTTGG

330   340   350   360   370   380   390   400   410   420

aligned sequence 2020-12-04_G02_ASAST15BSPTF

ctatcgctgcaagaattcaagcttggagctgacagctagctcagtcctaggtataatgcTAGCTAATTTCTACTAAGTGTAGATTGGAAACATTGCATCA

4,000   4,010   4,020   4,030   4,040   4,050   4,060   4,070   4,080   4,090

prqR gRNA

Bba_J23108

template sequence pAST.010 (ΔprqRA Cas12a KO 1)

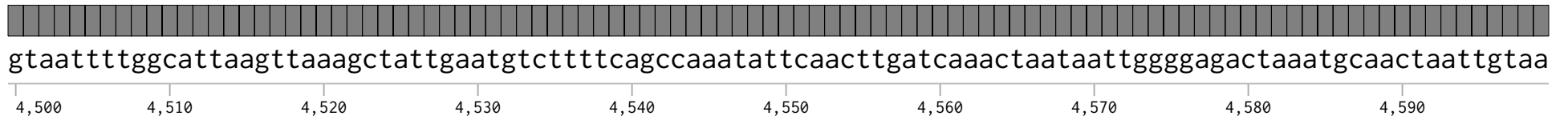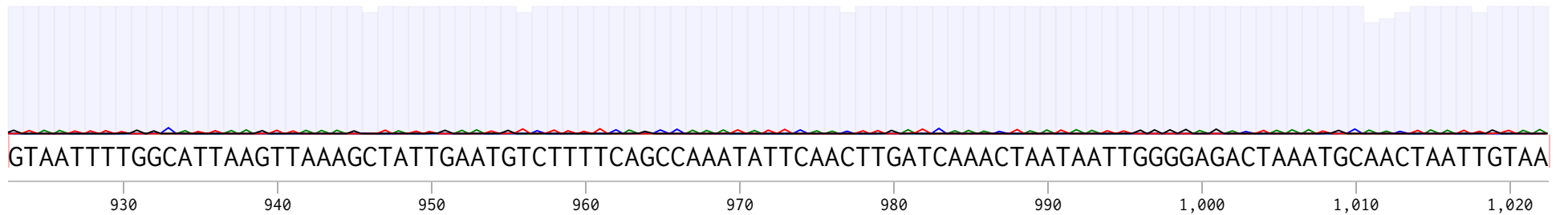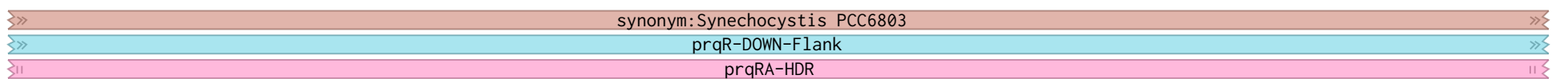CTATCGCTGCAAGAATTCAAGCTTGGAGCTGACAGCTAGCTCAGTCCTAGGTATAATGCTAGCTAATTTCTACTAAGTGTAGATTGGAAACATTGCATCA

430   440   450   460   470   480   490   500   510   520

aligned sequence 2020-12-04_G02_ASAST15BSPTF

GGAACTTgcttagagaatataaaaagccagattattaatccggcttttttattatttcgctactagaattcgagctcggagctaccaacacaatgcccca

4,100   4,110   4,120   4,130   4,140   4,150   4,160   4,170   4,180   4,190

synonym:Sy...s PCC6803

prqR-UP-Flank1

sll0886 gene

pr...A   sll0886 CDS

BBa_B0011   prqRA-HDR

template sequence pAST.010 (ΔprqRA Cas12a KO 1)

GGAACTTGCTTAGAGAATATAAAAAGCCAGATTATTAATCCGGCTTTTTTATTATTTCGCTACTAGAATTCGAGCTCGGAGCTACCAACACAATGCCCCA

530   540   550   560   570   580   590   600   610   620

aligned sequence 2020-12-04_G02_ASAST15BSPTF

gagggagggcataagcaaagcaaaatattttcgtagaagggaaagcattaaaaaaatctggagttgggaatgggatcaactggatgcaactcattgtaaa

4,200   4,210   4,220   4,230   4,240   4,250   4,260   4,270   4,280   4,290

synonym:Synechocystis PCC6803

prqR-UP-Flank1

sll0886 gene

sll0886 CDS

prqRA-HDR

template sequence pAST.010 (ΔprqRA Cas12a KO 1)

GAGGGAGGGCATAAGCAAAGCAAAATATTTTCGTAGAAGGGAAAGCATTAAAAAAATCTGGAGTTGGGAATGGGATCAACTGGATGCAACTCATTGTAAA

630   640   650   660   670   680   690   700   710   720

aligned sequence 2020-12-04_G02_ASAST15BSPTF

ttttctccgcggtaatcttcaaattattgcgccccggtgaacttgacttccgaccgaccggacggtatcttgaaagtgtccaaccaaCTGGACGGTTTAA

| 4,300 | 4,310 | 4,320 | 4,330 | 4,340 | 4,350 | 4,360 | 4,370 | 4,380 | 4,390 |

synonym:Synechocystis PCC6803

prqR-UP-Flank1

predicted p.../Pre.php)

predicted promoter...PseZNC/pro70.php)

prqRA-HDR

template sequence pAST.010 (ΔprqRA Cas12a KO 1)

TTTTCTCCGCGGTAATCTTCAAATTATTGCGCCCCGGTGAACTTGACTTCCGACCGACCGGACGGTATCTTGAAAGTGTCCAACCAACTGGACGGTTTAA

| 730 | 740 | 750 | 760 | 770 | 780 | 790 | 800 | 810 | 820 |

aligned sequence 2020-12-04_G02_ASAST15BSPTF

TTATTTCCAGGTCGCCAgtcaatttaaaaaagaatatttgcattatctgcggaggcgaaattatGACTcccgttgctagatcttaatccataattgccat

4,400   4,410   4,420   4,430   4,440   4,450   4,460   4,470   4,480   4,490

synony...C6803
prqR-UP-Flank1
predic...php)
predic....php)   prqR-UP-Flank2
prqRA-HDR

synonym:Synechocystis PCC6803
prqR-DOWN-Flank
slr0896 gene
slr0896 CDS

template sequence pAST.010 (ΔprqRA Cas12a KO 1)

TTATTTCCAGGTCGCCAGTCAATTTAAAAAAGAATATTTGCATTATCTGCGGAGGCGAAATTATGACTCCCGTTGCTAGATCTTAATCCATAATTGCCAT

830   840   850   860   870   880   890   900   910   920

aligned sequence 2020-12-04_G02_ASAST15BSPTF

gtaattttggcattaagttaaagctattgaatgtctttttcagccaaatattcaacttgatcaaactaataattggggagactaaatgcaactaattgtaa

4,500   4,510   4,520   4,530   4,540   4,550   4,560   4,570   4,580   4,590

synonym:Synechocystis PCC6803

prqR-DOWN-Flank

prqRA-HDR

template sequence pAST.010 (ΔprqRA Cas12a KO 1)

GTAATTTTGGCATTAAGTTAAAGCTATTGAATGTCTTTTCAGCCAAATATTCAACTTGATCAAACTAATAATTGGGGAGACTAAATGCAACTAATTGTAA

930   940   950   960   970   980   990   1,000   1,010   1,020

aligned sequence 2020-12-04_G02_ASAST15BSPTF

attttctctggggaaatattcccattactgtctgccaacaaggaacaacttaggagtatttacctataggcgatcgccaacgagggggggaggatggcaat

4,600   4,610   4,620   4,630   4,640   4,650   4,660   4,670   4,680   4,690

synonym:Synechocystis PCC6803

prqR-DOWN-Flank

prqRA-HDR

template sequence pAST.010 (ΔprqRA Cas12a KO 1)

ATTTTCTCTGGGGAAATATTCCCATTACTGTCTGCCAACAAGGAACAACTTAGGAGTATTTACCTATAGGCGATCGCCAACGAGGGGGGGAGGATGGCAAT

1,030   1,040   1,050   1,060   1,070   1,080   1,090   1,100   1,110   1,120

aligned sequence 2020-12-04_G02_ASAST15BSPTF

gaccagtaaaaaccctccacttgaagggtttaggtttccagaaattgttgcttaagttataaaagttccctttaacgctcctccctcgctttactgaga

4,700   4,710   4,720   4,730   4,740   4,750   4,760   4,770   4,780   4,790

synonym:Synechocystis PCC6803
prqR-DOWN-Flank
prqRA-HDR

template sequence pAST.010 (ΔprqRA Cas12a KO 1)

GACCAGTAAAAAACCCTCCACTTGAAGGGTTTAGGTTTCCAGAAATTGTTGCTTAAGTTATAAAAGTTCCCTTTAACGCTCCTCCCTCGCTTTAC-----

1,130   1,140   1,150   1,160   1,170   1,180   1,190   1,200   1,210

aligned sequence 2020-12-04_G02_ASAST15BSPTF

ccgaggatgcacatgtgaccgagggagactcctgttgatagatccagtaatgacctcagaactccatctggatttgttcagaacgctcggttgccgccgg

4,800   4,810   4,820   4,830   4,840   4,850   4,860   4,870   4,880   4,890

lambda t0 terminator

template sequence pAST.010 (ΔprqRA Cas12a KO 1)

------------------ATGCGGGAGACTCCTGTTGATAGATAAAGTATAGTCTAAAGTTGACTGACGTTAACTT----------------------

1,220   1,230   1,240   1,250   1,260   1,270

aligned sequence 2020-12-04_G02_ASAST15BSPTF

gcgttttttattggtgagaatccaggggtccccaataattacgatttacgtatttaaatgaaccttgaccgaacgcagcggtggtaacggcgcagtggcg

| | | | | | | | | | |
4,900   4,910   4,920   4,930   4,940   4,950   4,960   4,970   4,980   4,990

lambda t0 terminator

template sequence pAST.010 (ΔprqRA Cas12a KO 1)
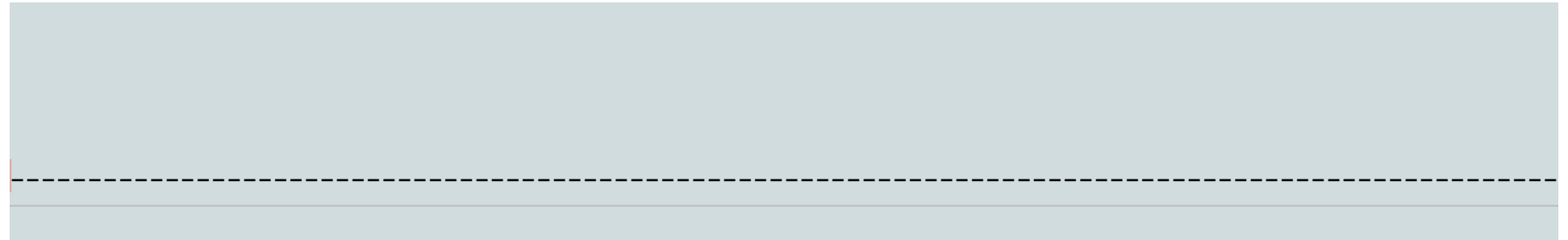
aligned sequence 2020-12-04_G02_ASAST15BSPTF

gttttcatggcttgttatgactgtttttttggggtacagtctatgcctcgggcatccaagcagcaagcgcgttacgccgtgggtcgatgtttgatgttat

| | | | | | | | | | |
5,000   5,010   5,020   5,030   5,040   5,050   5,060   5,070   5,080   5,090

template sequence pAST.010 (ΔprqRA Cas12a KO 1)
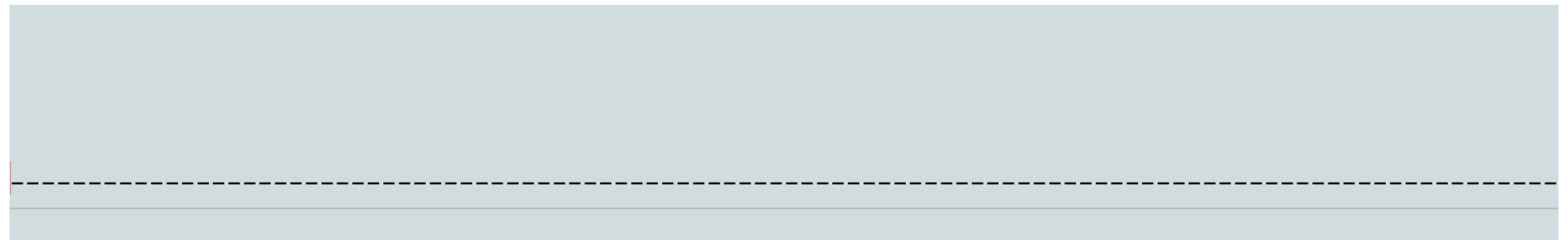
aligned sequence 2020-12-04_G02_ASAST15BSPTF

ggagcagcaacgatgttacgcagcagggcagtcgccctaaaacaaagttaaacatcatgagggaagcggtgatcgccgaagtatcgactcaactatcaga

5,100	5,110	5,120	5,130	5,140	5,150	5,160	5,170	5,180	5,190

SmR

template sequence pAST.010 (ΔprqRA Cas12a KO 1)
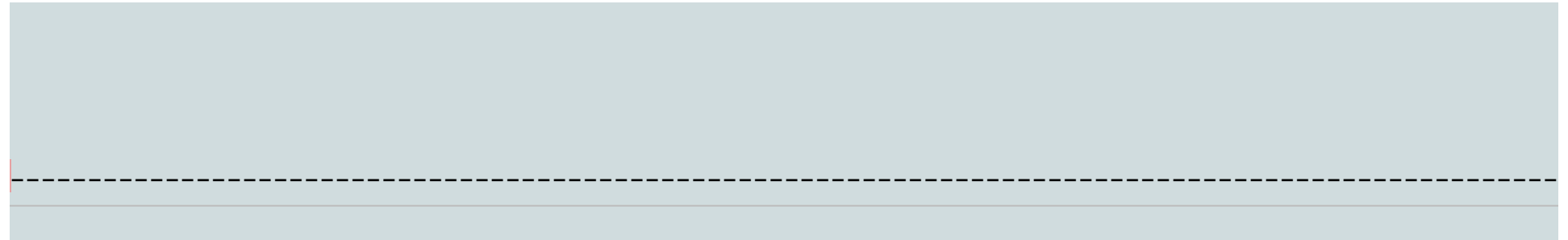
aligned sequence 2020-12-04_G02_ASAST15BSPTF

ggtagttggcgtcatcgagcgccatctcgaaccgacgttgctggccgtacatttgtacggctccgcagtggatggcggcctgaagccacacagtgatatt

5,200	5,210	5,220	5,230	5,240	5,250	5,260	5,270	5,280	5,290

SmR

template sequence pAST.010 (ΔprqRA Cas12a KO 1)
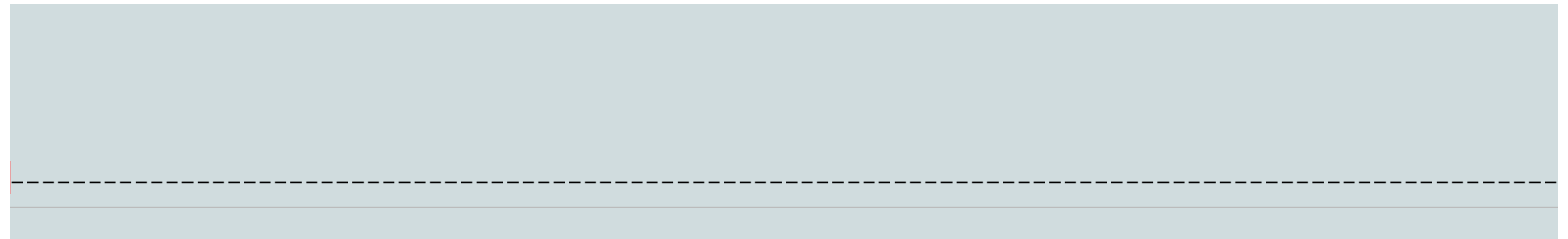
aligned sequence 2020-12-04_G02_ASAST15BSPTF

gatttgctggttacggtgaccgtaaggcttgatgaaacaacgcggcgagctttgatcaacgacctttttggaaacttcggcttcccctggagagagcgaga

| 5,300 | 5,310 | 5,320 | 5,330 | 5,340 | 5,350 | 5,360 | 5,370 | 5,380 | 5,390 |

SmR

template sequence pAST.010 (ΔprqRA Cas12a KO 1)
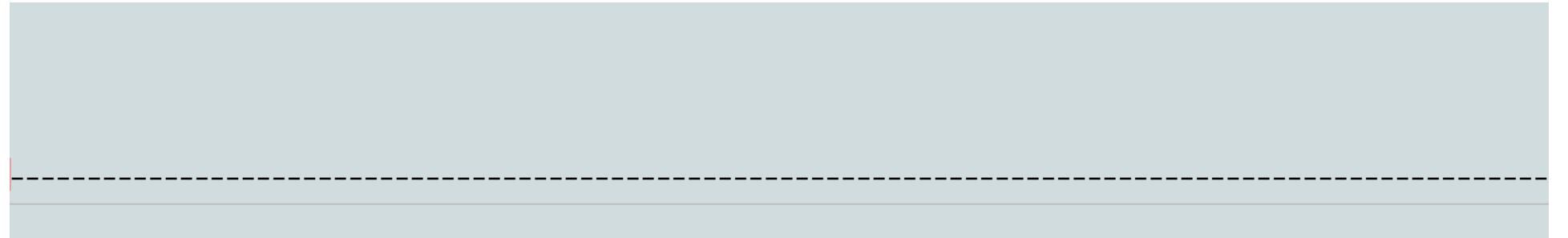
aligned sequence 2020-12-04_G02_ASAST15BSPTF

ttctccgcgctgtagaagtcaccattgttgtgcacgacgacatcattccgtggcgttatccagctaagcgcgaactgcaatttggagaatggcagcgcaa

| 5,400 | 5,410 | 5,420 | 5,430 | 5,440 | 5,450 | 5,460 | 5,470 | 5,480 | 5,490 |

SmR

template sequence pAST.010 (ΔprqRA Cas12a KO 1)
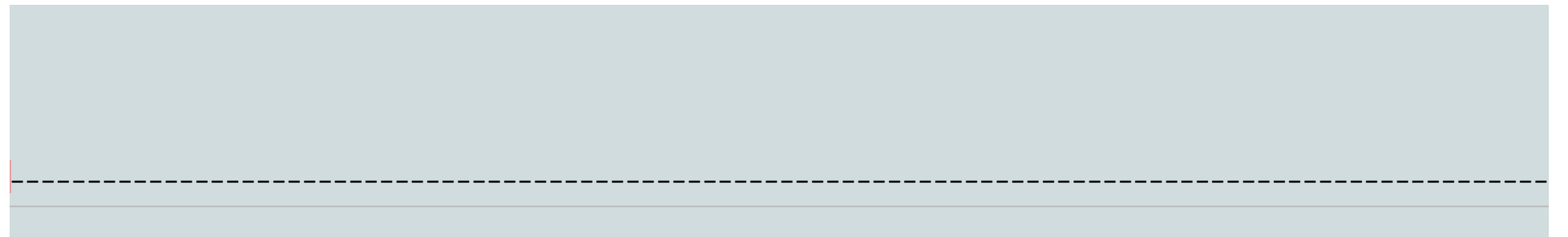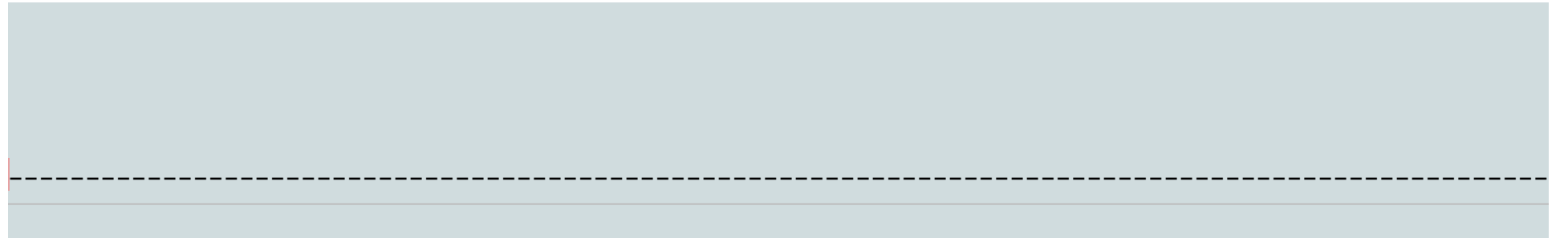
aligned sequence 2020-12-04_G02_ASAST15BSPTF

tgacattcttgcaggtatcttcgagccagccacgatcgacattgatctggctatcttgctgacaaaagcaagagaacatagcgttgccttggtaggtcca

5,500   5,510   5,520   5,530   5,540   5,550   5,560   5,570   5,580   5,590

SmR

template sequence pAST.010 (ΔprqRA Cas12a KO 1)
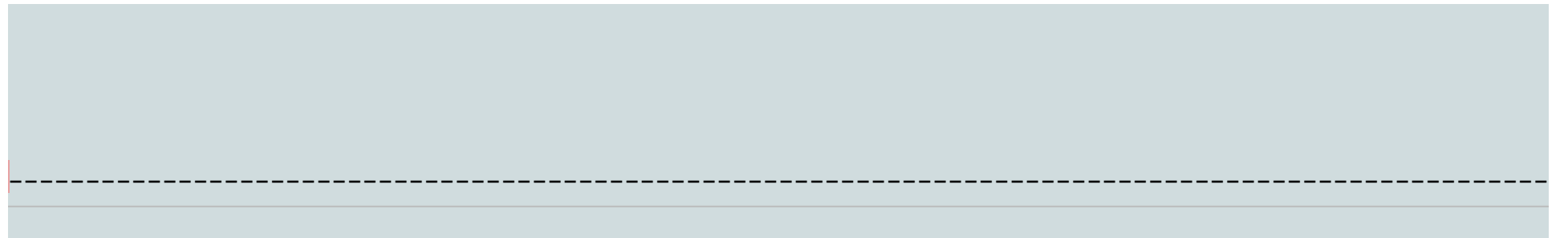
aligned sequence 2020-12-04_G02_ASAST15BSPTF

gcggcggaggaactctttgatccggttcctgaacaggatctatttgaggcgctaaatgaaaccttaacgctatggaactcgccgcccgactgggctggcg

5,600   5,610   5,620   5,630   5,640   5,650   5,660   5,670   5,680   5,690

SmR

template sequence pAST.010 (ΔprqRA Cas12a KO 1)

aligned sequence 2020-12-04_G02_ASAST15BSPTF

atgagcgaaatgtagtgcttacgttgtcccgcatttggtacagcgcagtaaccggcaaaatcgcgccgaaggatgtcgctgccgactgggcaatggagcg

| 5,700 | 5,710 | 5,720 | 5,730 | 5,740 | 5,750 | 5,760 | 5,770 | 5,780 | 5,790 |

SmR

template sequence pAST.010 (ΔprqRA Cas12a KO 1)

aligned sequence 2020-12-04_G02_ASAST15BSPTF
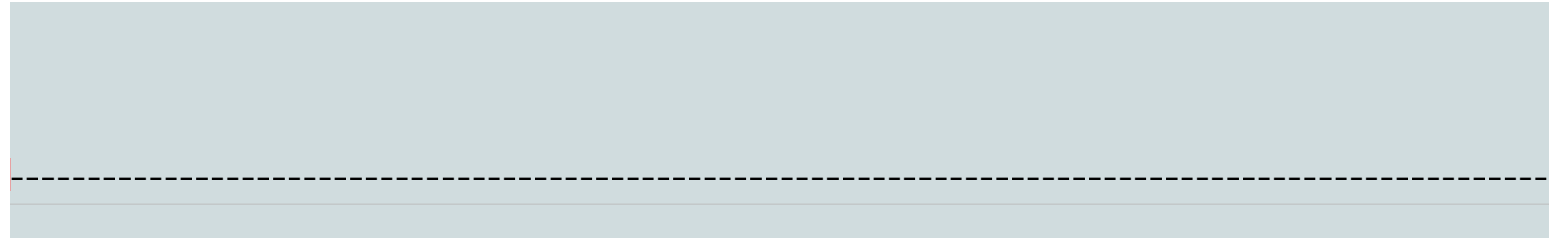
cctgccggcccagtatcagcccgtcatacttgaagctagacaggcttatcttggacaagaagaagatcgcttggcctcgcgcgcagatcagttggaagaa

| 5,800 | 5,810 | 5,820 | 5,830 | 5,840 | 5,850 | 5,860 | 5,870 | 5,880 | 5,890 |

SmR

template sequence pAST.010 (ΔprqRA Cas12a KO 1)

aligned sequence 2020-12-04_G02_ASAST15BSPTF
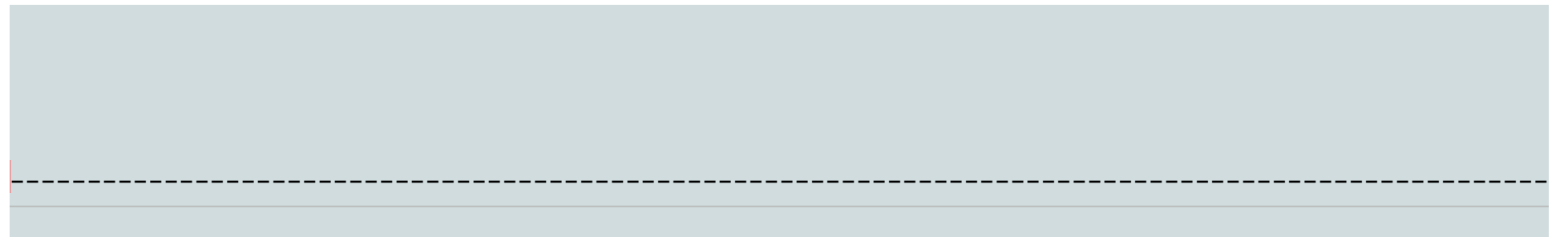
tttgtccactacgtgaaaggcgagatcaccaaggtagtcggcaaataagacaattgtccttttccgctgcataaccctgcttcggggtcattatagcgat

| | | | | | | | | | |
|5,900|5,910|5,920|5,930|5,940|5,950|5,960|5,970|5,980|5,990|
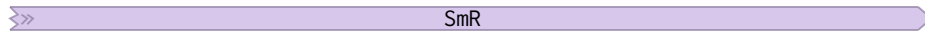
SmR

template sequence pAST.010 (ΔprqRA Cas12a KO 1)
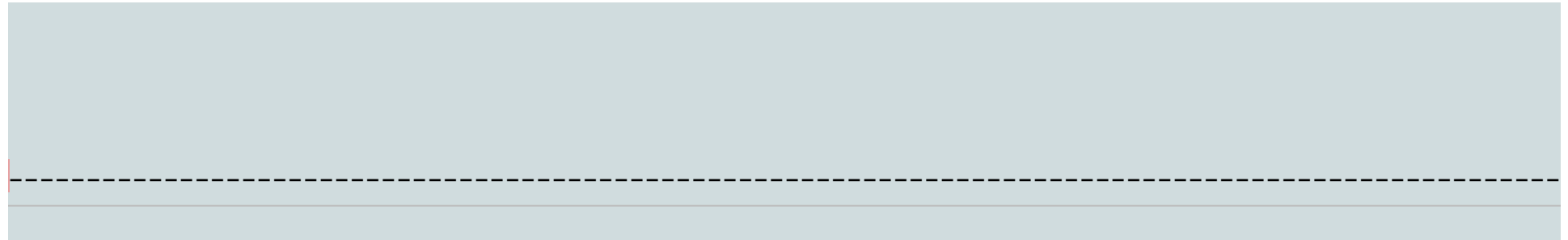
aligned sequence 2020-12-04_G02_ASAST15BSPTF

tttttcggtatatccatcctttttcgcacgatatacaggattttgccaaagggttcgtgtagactttccttggtgtatccaacggcgtcagccgggcagg

| | | | | | | | | | |
|6,000|6,010|6,020|6,030|6,040|6,050|6,060|6,070|6,080|6,090|

in...r »

template sequence pAST.010 (ΔprqRA Cas12a KO 1)
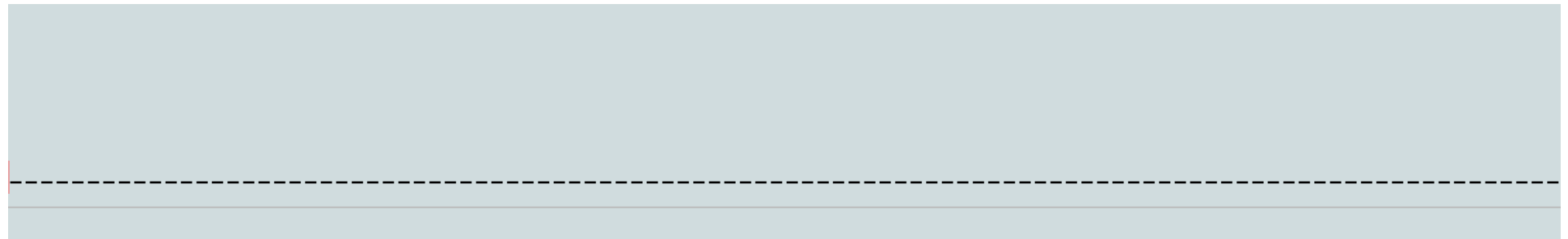
aligned sequence 2020-12-04_G02_ASAST15BSPTF

ataggtgaagtaggcccacccgcgagcgggtgttccttcttcactgtcccttattcgcacctggcggtgctcaacgggaatcctgctctgcgaggctggc

6,100   6,110   6,120   6,130   6,140   6,150   6,160   6,170   6,180   6,190

incP origin of transfer

template sequence pAST.010 (ΔprqRA Cas12a KO 1)
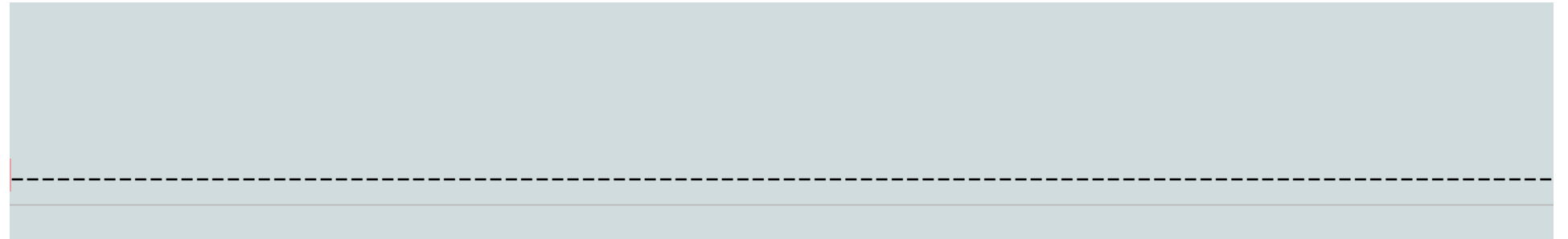
aligned sequence 2020-12-04_G02_ASAST15BSPTF

cgtaggccggccgcgatgcaggtggctgctgaacccccagccggaactgaccccacaaggccctagcgtttgcaatgcaccaggtcatcattgacccagg

6,200   6,210   6,220   6,230   6,240   6,250   6,260   6,270   6,280   6,290

trfA

template sequence pAST.010 (ΔprqRA Cas12a KO 1)
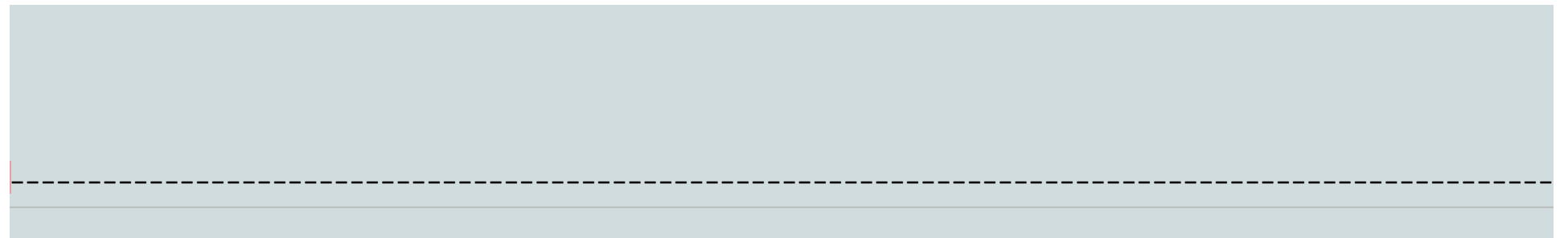
aligned sequence 2020-12-04_G02_ASAST15BSPTF

cgtgttccaccaggccgctgcctcgcaactcttcgcaggcttcgccgacctgctcgcgccacttcttcacgcgggtggaatccgatccgcacatgaggcg

| 6,300 | 6,310 | 6,320 | 6,330 | 6,340 | 6,350 | 6,360 | 6,370 | 6,380 | 6,390 |

trfA

template sequence pAST.010 (ΔprqRA Cas12a KO 1)
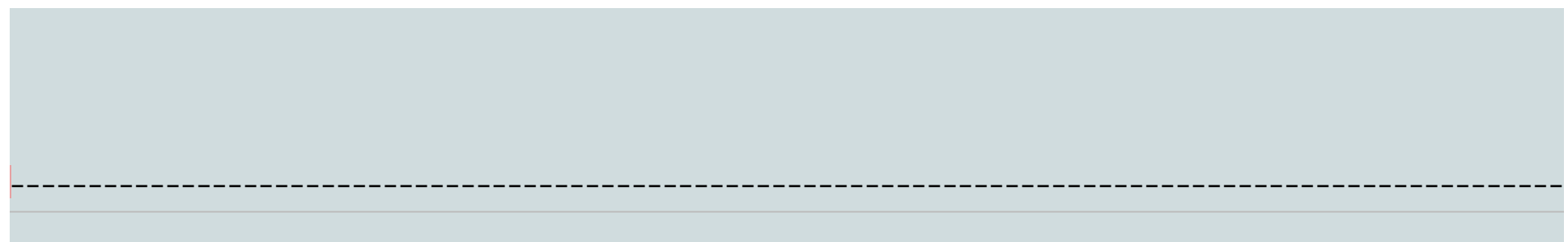
aligned sequence 2020-12-04_G02_ASAST15BSPTF

gaaggtttccagcttgagcgggtacggctcccggtgcgagctgaaatagtcgaacatccgtcgggccgtcggcgacagcttgcggtacttctcccatatg

| 6,400 | 6,410 | 6,420 | 6,430 | 6,440 | 6,450 | 6,460 | 6,470 | 6,480 | 6,490 |

trfA

template sequence pAST.010 (ΔprqRA Cas12a KO 1)
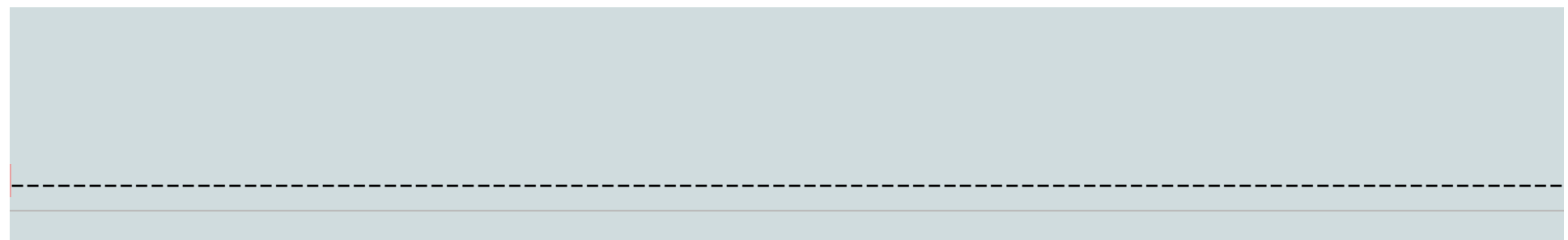
aligned sequence 2020-12-04_G02_ASAST15BSPTF

aatttcgtgtagtggtcgccagcaaacagcacgacgatttcctcgtcgatcaggacctggcaacgggacgttttcttgccacggtccaggacgcggaagc

| 6,500 | 6,510 | 6,520 | 6,530 | 6,540 | 6,550 | 6,560 | 6,570 | 6,580 | 6,590 |

≪ trfA ≪

template sequence pAST.010 (ΔprqRA Cas12a KO 1)
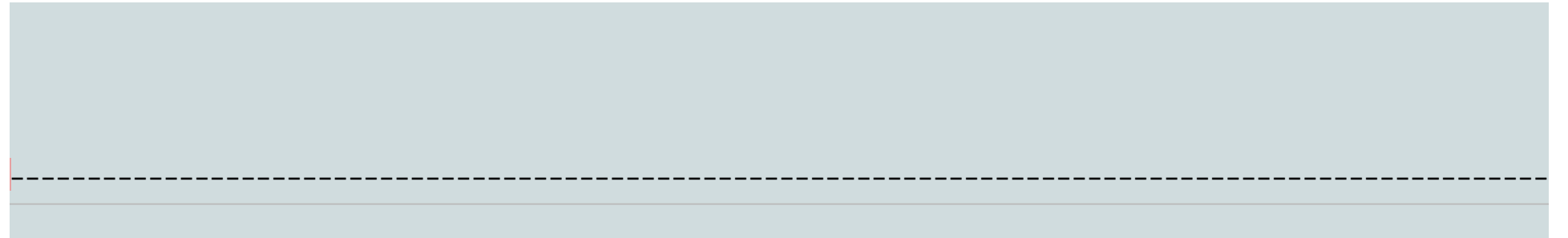
aligned sequence 2020-12-04_G02_ASAST15BSPTF

ggtgcagcagcgacaccgattccaggtgcccaacgcggtcggacgtgaagcccatcgccgtcgcctgtaggcgcgacaggcattcctcggccttcgtgta

| 6,600 | 6,610 | 6,620 | 6,630 | 6,640 | 6,650 | 6,660 | 6,670 | 6,680 | 6,690 |

≪ trfA ≪

template sequence pAST.010 (ΔprqRA Cas12a KO 1)
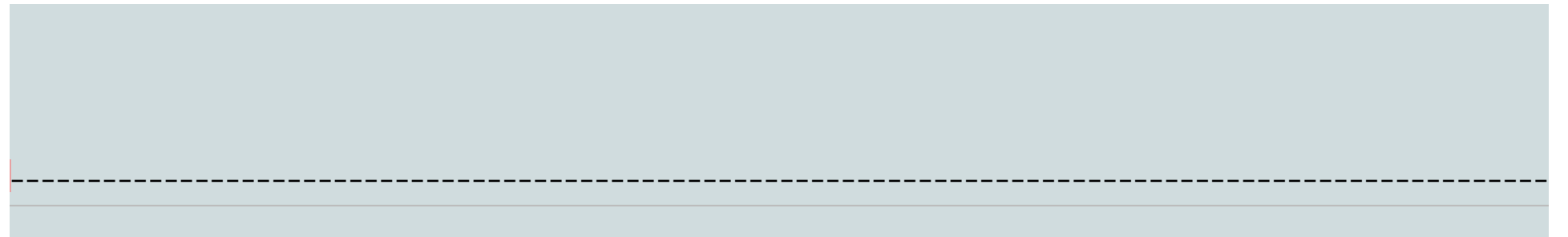
aligned sequence 2020-12-04_G02_ASAST15BSPTF

ataccggccattgatcgaccagcccaggtcctggcaaagctcgtagaacgtgaaggtgatcggctcgccgatagggggtgcgcttcgcgtactccaacacc

| | | | | | | | | | |
6,700   6,710   6,720   6,730   6,740   6,750   6,760   6,770   6,780   6,790

≫   trfA   ≪

template sequence pAST.010 (ΔprqRA Cas12a KO 1)

----
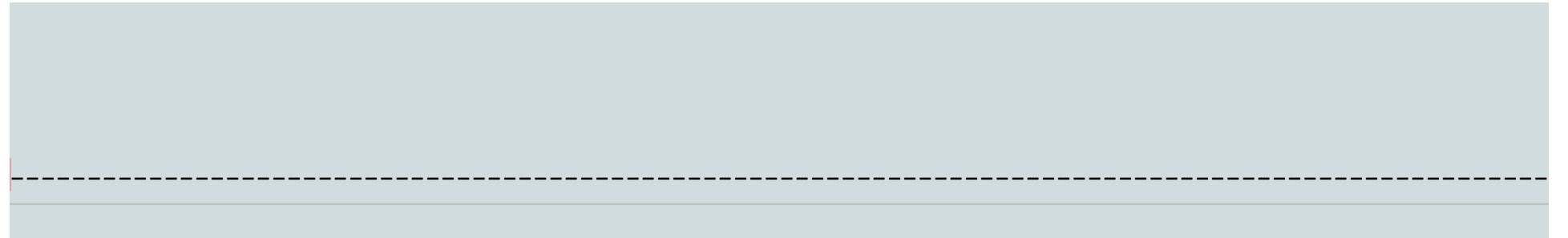
aligned sequence 2020-12-04_G02_ASAST15BSPTF

tgctgccacaccagttcgtcatcgtcggcccgcagctcgacgccggtgtaggtgatcttcacgtccttgttgacgtggaaaatgaccttgttttgcagcg

| | | | | | | | | | |
6,800   6,810   6,820   6,830   6,840   6,850   6,860   6,870   6,880   6,890

≫   trfA   ≪

template sequence pAST.010 (ΔprqRA Cas12a KO 1)

----
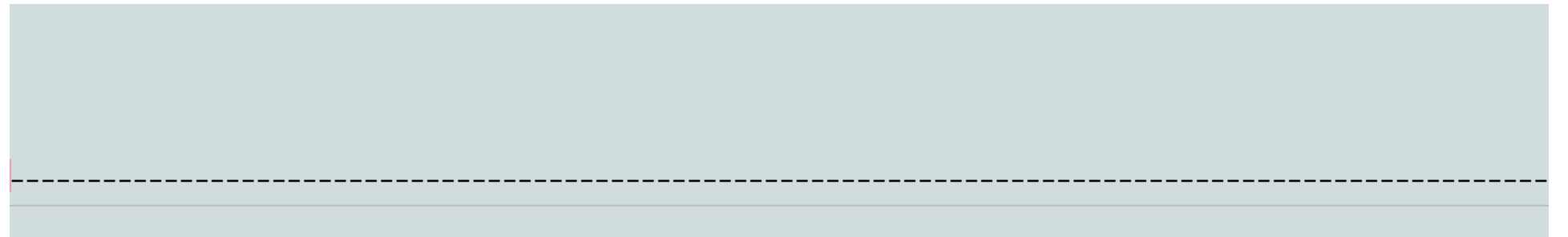
aligned sequence 2020-12-04_G02_ASAST15BSPTF

cctcgcgcgggattttcttgttgcgcgtggtgaacagggcagagcgggccgtgtcgtttggcatcgctcgcatcgtgtccggccacggcgcaatatcgaa

6,900	6,910	6,920	6,930	6,940	6,950	6,960	6,970	6,980	6,990

trfA

template sequence pAST.010 (ΔprqRA Cas12a KO 1)
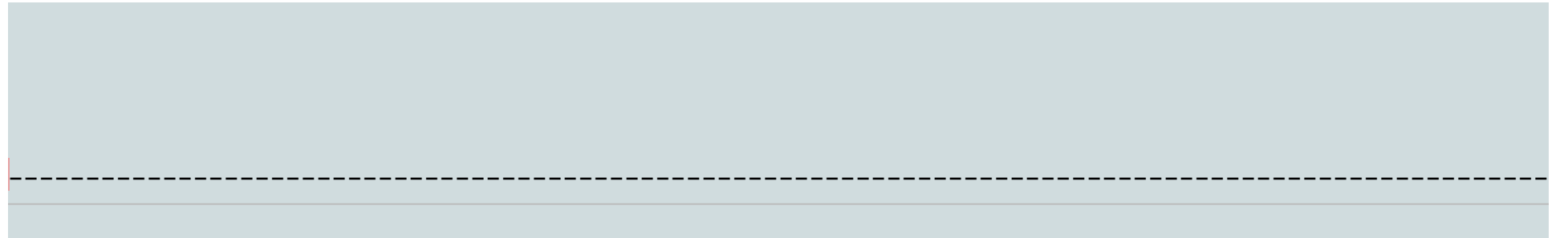
aligned sequence 2020-12-04_G02_ASAST15BSPTF

caaggaaagctgcatttccttgatctgctgcttcgtgtgtttcagcaacgcggcctgcttggcttcgctgacctgttttgccaggtcctcgccggcggtt

7,000	7,010	7,020	7,030	7,040	7,050	7,060	7,070	7,080	7,090

trfA

template sequence pAST.010 (ΔprqRA Cas12a KO 1)
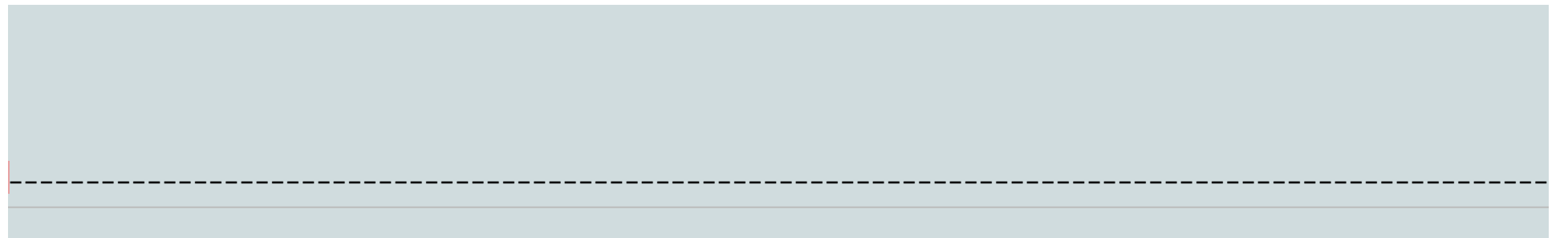
aligned sequence 2020-12-04_G02_ASAST15BSPTF

tttcgcttcttggtcgtcatagttcctcgcgtgtcgatggtcatcgacttcgccaaacctgccgcctcctgttcgagacgacgcgaacgctccacggcgg

| 7,100 | 7,110 | 7,120 | 7,130 | 7,140 | 7,150 | 7,160 | 7,170 | 7,180 | 7,190 |

trfA

template sequence pAST.010 (ΔprqRA Cas12a KO 1)

aligned sequence 2020-12-04_G02_ASAST15BSPTF

ccgatggcgcgggcagggcaggggagccagttgcacgctgtcgcgctcgatcttggccgtagcttgctggactatcgagccgacggactggaaggtttc

| 7,200 | 7,210 | 7,220 | 7,230 | 7,240 | 7,250 | 7,260 | 7,270 | 7,280 | 7,290 |

trfA

template sequence pAST.010 (ΔprqRA Cas12a KO 1)

aligned sequence 2020-12-04_G02_ASAST15BSPTF

gcggggcgcacgcatgacggtgcggcttgcgatggtttcggcatcctcggcggaaaaccccgcgtcgatcagttcttgcctgtatgccttccggtcaaac

| 7,300 | 7,310 | 7,320 | 7,330 | 7,340 | 7,350 | 7,360 | 7,370 | 7,380 | 7,390 |

trfA

template sequence pAST.010 (ΔprqRA Cas12a KO 1)
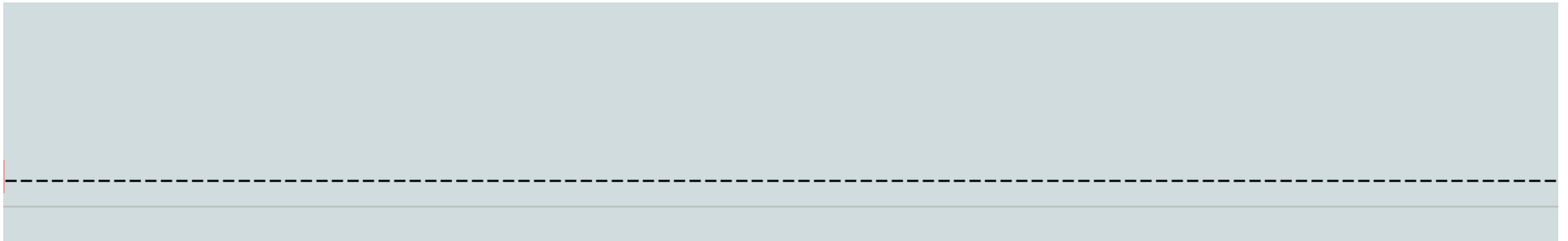
aligned sequence 2020-12-04_G02_ASAST15BSPTF

gtccgattcattcaccctccttgcgggattgccccggaattaattccccggatcgatccgtcgatcttgatcccctgcgccatcagatccttggcggcaa

| 7,400 | 7,410 | 7,420 | 7,430 | 7,440 | 7,450 | 7,460 | 7,470 | 7,480 | 7,490 |

trfA

template sequence pAST.010 (ΔprqRA Cas12a KO 1)
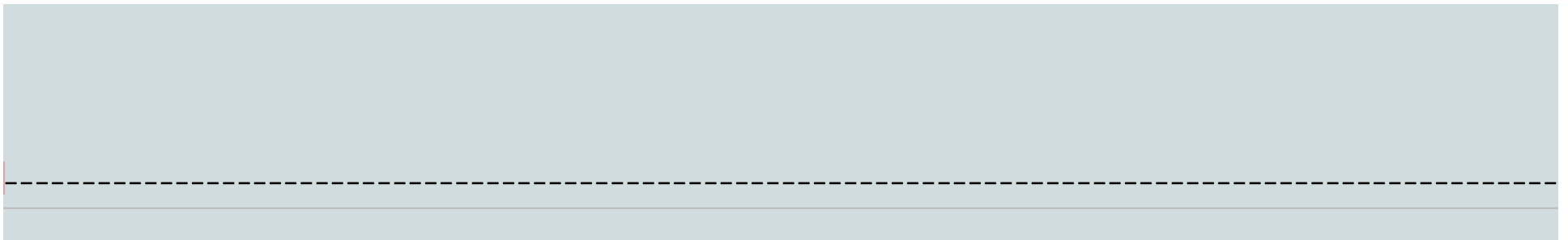
aligned sequence 2020-12-04_G02_ASAST15BSPTF

gaaagccatccagtttactttgcagggcttcccaaccttaccagagggcgccccagctggcaattccggttcgcttgctgtccataaaaccgcccagtct

| 7,500 | 7,510 | 7,520 | 7,530 | 7,540 | 7,550 | 7,560 | 7,570 | 7,580 | 7,590 |

template sequence pAST.010 (ΔprqRA Cas12a KO 1)
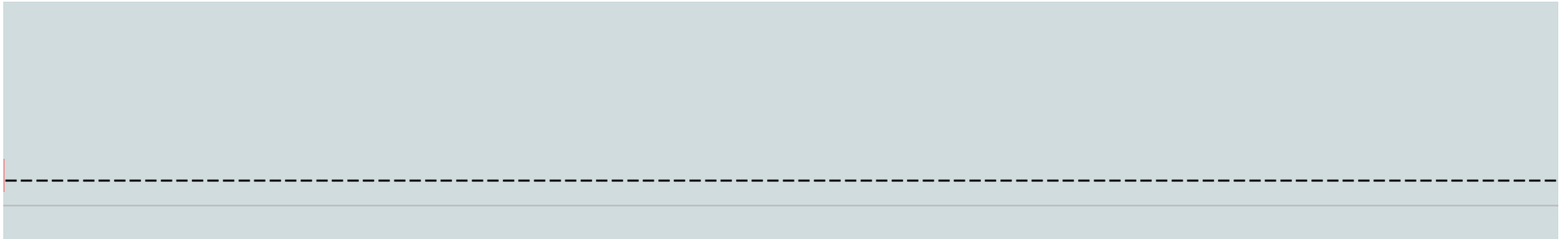
aligned sequence 2020-12-04_G02_ASAST15BSPTF

agctatcgccatgtaagcccactgcaagctacctgctttctctttgcgcttgcgttttcccttgtccagatagcccagtagctgacattcatccggggtc

| 7,600 | 7,610 | 7,620 | 7,630 | 7,640 | 7,650 | 7,660 | 7,670 | 7,680 | 7,690 |

template sequence pAST.010 (ΔprqRA Cas12a KO 1)
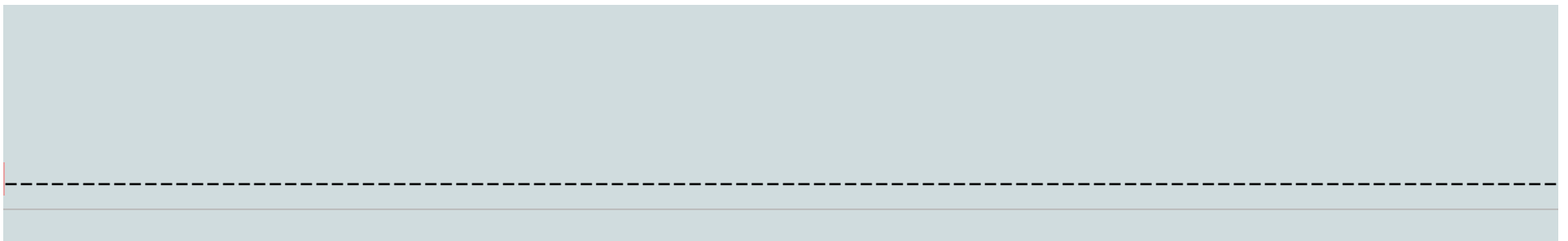
aligned sequence 2020-12-04_G02_ASAST15BSPTF

agcaccgtttctgcggactggctttctacgtggctgccattttttggggtgaggccgttcgcggccgaggggcgcagcccctggggggatgggaggcccgc

7,700   7,710   7,720   7,730   7,740   7,750   7,760   7,770   7,780   7,790

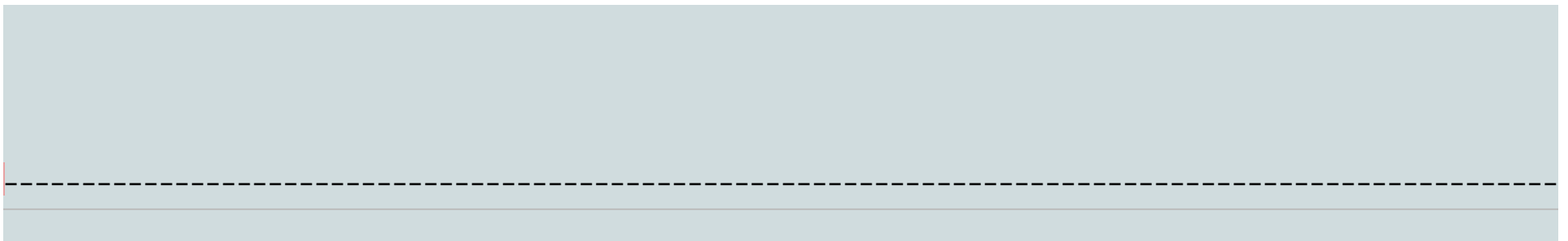**template sequence** pAST.010 (ΔprqRA Cas12a KO 1)
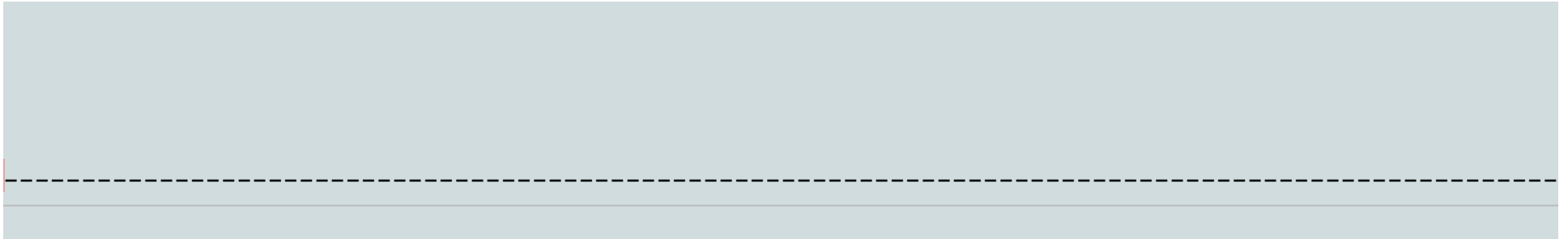
aligned sequence 2020-12-04_G02_ASAST15BSPTF

gttagcgggccgggagggttcgagaagggggggcaccccccttcggcgtgcgcggtcacgcgcacagggcgcagccctggttaaaaacaaggtttataaa

7,800   7,810   7,820   7,830   7,840   7,850   7,860   7,870   7,880   7,890

oriV

template sequence pAST.010 (ΔprqRA Cas12a KO 1)

aligned sequence 2020-12-04_G02_ASAST15BSPTF

tattggtttaaaagcaggttaaaagacaggttagcggtggccgaaaaacgggcggaaacccttgcaaatgctggattttctgcctgtggacagcccctca

7,900	7,910	7,920	7,930	7,940	7,950	7,960	7,970	7,980	7,990

oriV
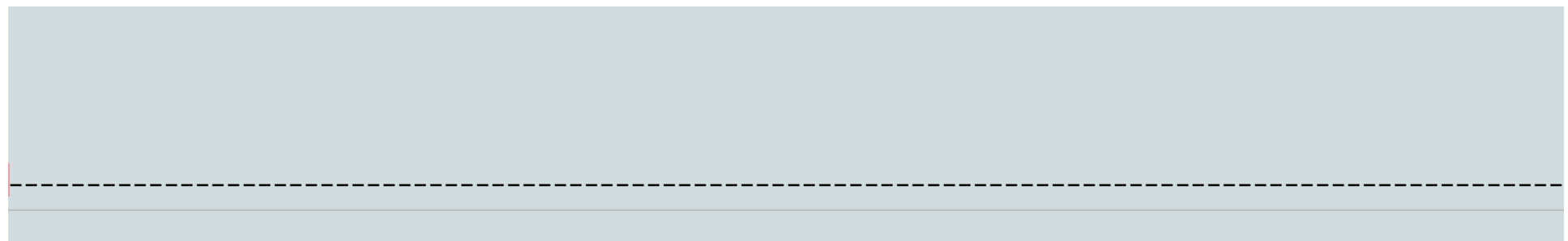
template sequence pAST.010 (ΔprqRA Cas12a KO 1)
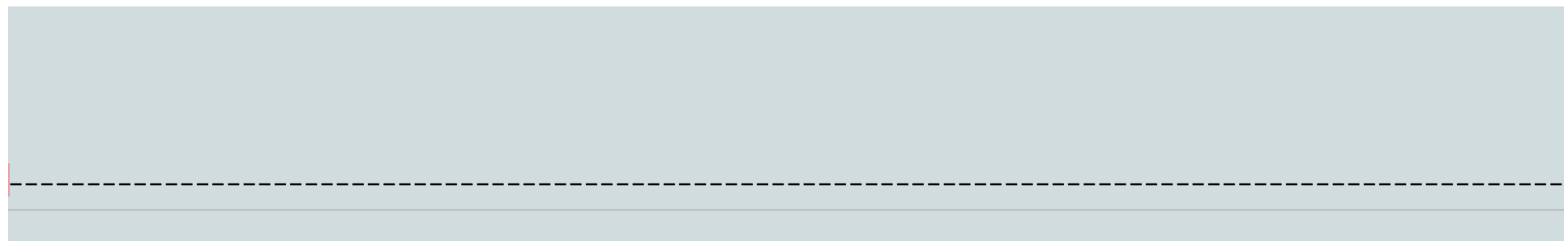
aligned sequence 2020-12-04_G02_ASAST15BSPTF

aatgtcaataggtgcgcccctcatctgtcagcactctgcccctcaagtgtcaaggatcgcgcccctcatctgtcagtagtcgcgcccctcaagtgtcaat

8,000	8,010	8,020	8,030	8,040	8,050	8,060	8,070	8,080	8,090

oriV
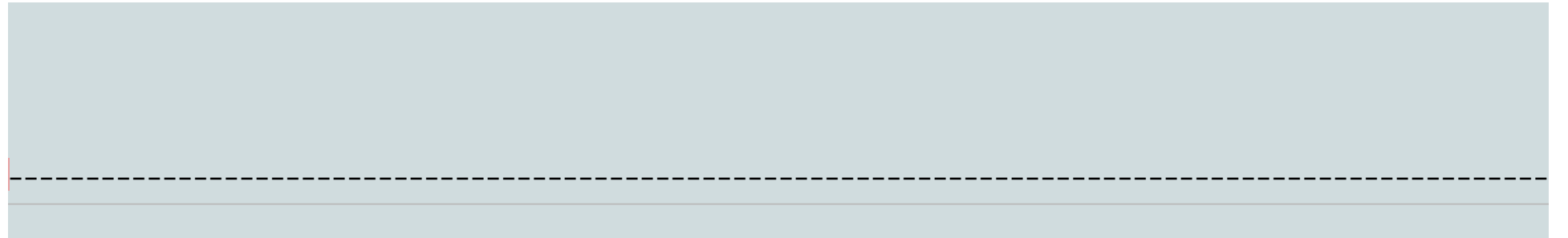
template sequence pAST.010 (ΔprqRA Cas12a KO 1)

aligned sequence 2020-12-04_G02_ASAST15BSPTF

accgcagggcacttatccccaggcttgtccacatcatctgtgggaaactcgcgtaaaatcaggcgttttcgccgatttgcgaggctggccagctccacgt

| 8,100 | 8,110 | 8,120 | 8,130 | 8,140 | 8,150 | 8,160 | 8,170 | 8,180 | 8,190 |

oriV
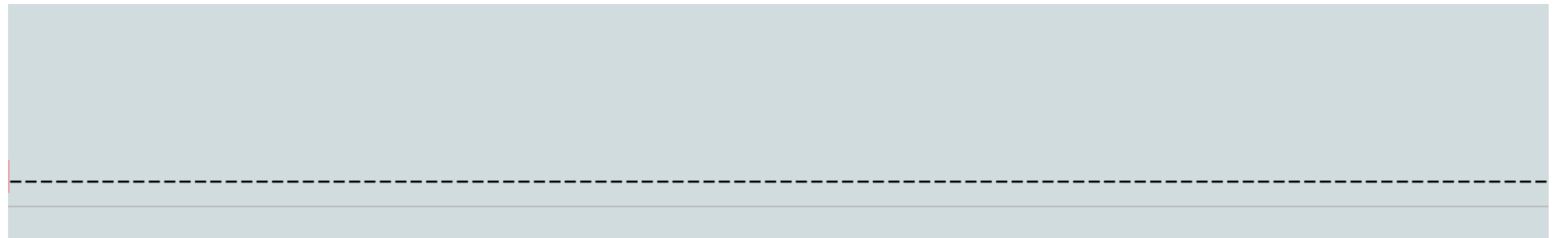
template sequence pAST.010 (ΔprqRA Cas12a KO 1)

aligned sequence 2020-12-04_G02_ASAST15BSPTF

cgccggccgaaatcgagcctgcccctcatctgtcaacgccgcgccgggtgagtcggcccctcaagtgtcaacgtccgcccctcatctgtcagtgagggcc

| 8,200 | 8,210 | 8,220 | 8,230 | 8,240 | 8,250 | 8,260 | 8,270 | 8,280 | 8,290 |

oriV
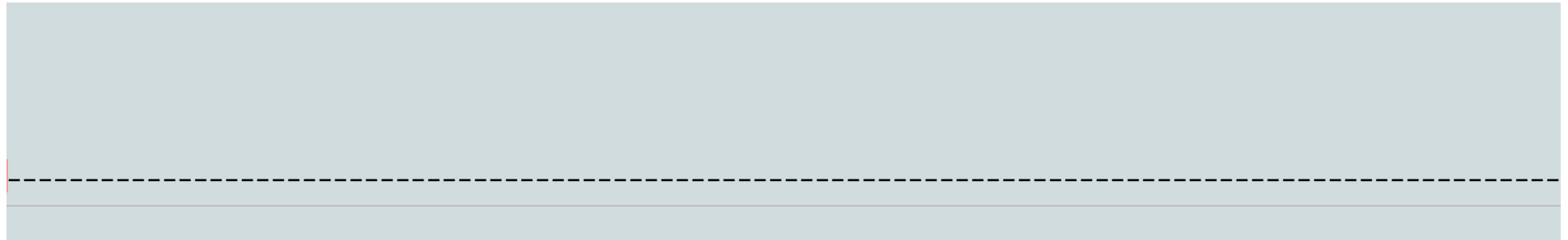
template sequence pAST.010 (ΔprqRA Cas12a KO 1)

aligned sequence 2020-12-04_G02_ASAST15BSPTF

aagttttccgcgaggtatccacaacgccggcggccctacatggctctgctgtagtgagtgggttgcgctccggcagcggtcctgatcccccgcagaaaaa

| | | | | | | | | | |
8,300   8,310   8,320   8,330   8,340   8,350   8,360   8,370   8,380   8,390

oriV

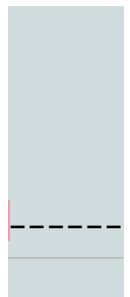**template sequence** pAST.010 (ΔprqRA Cas12a KO 1)

aligned sequence 2020-12-04_G02_ASAST15BSPTF

aaggat

8,400 8,405

template sequence pAST.010 (ΔprqRA Cas12a KO 1)

aligned sequence 2020-12-04_G02_ASAST15BSPTF