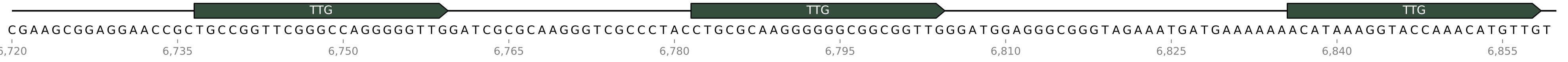
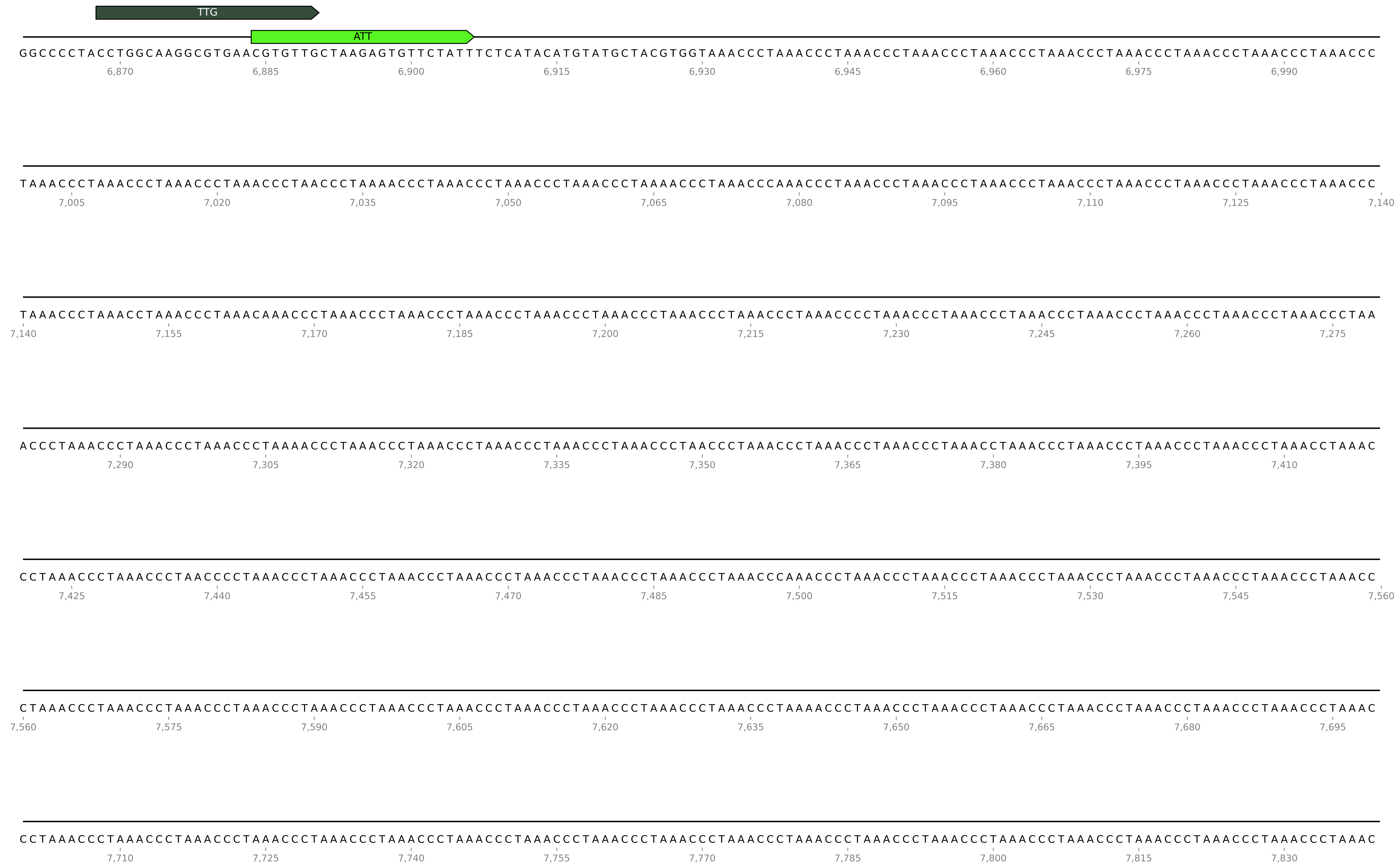


TTG









[illegible][illegible][illegible]

C T A A A C C C T

8,265                  8,280                  8,295                  8,310                  8,325                  8,340                  8,355                  8,370                  8,385                  8,400

[illegible]

AACCCCTAAACCCTAA

8,550                8,565                8,580                8,595                8,610                8,625                8,640                8,655                8,670

[illegible]



[illegible]

A A C C C T C A A C C C T C A A C C C T C A A C C C T C A A C C C T C A C C C T C A A C C C T C A A C C C T C A A C C C T C A A C C C T C A A C C C T C A A C C C T C A A C C C T C A A C C C T C A A C C C T C A A C C C T C A A C C C T C A A C C C T C A A C C C T C A A C C C C T A A C C C C T A A C C C C T A A

9,945 9,960 9,975 9,990 10,005 10,020 10,035 10,050 10,065 10,080

[illegible]

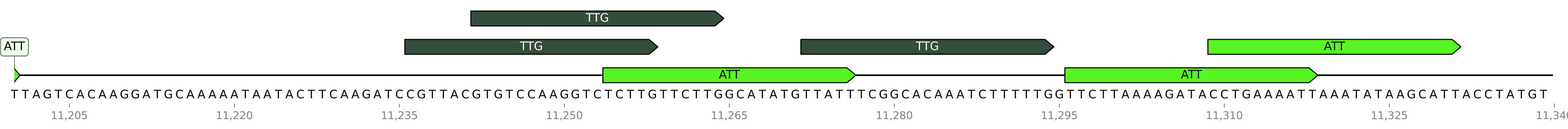
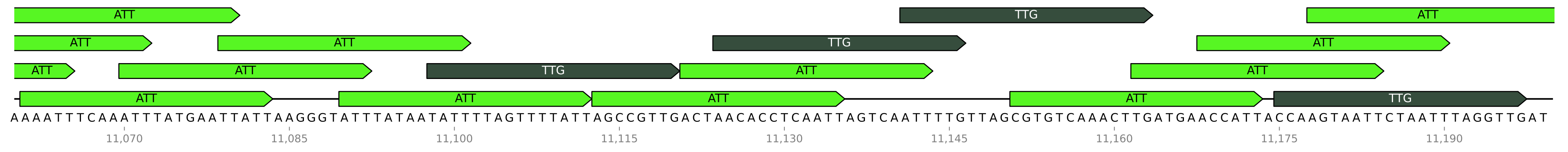
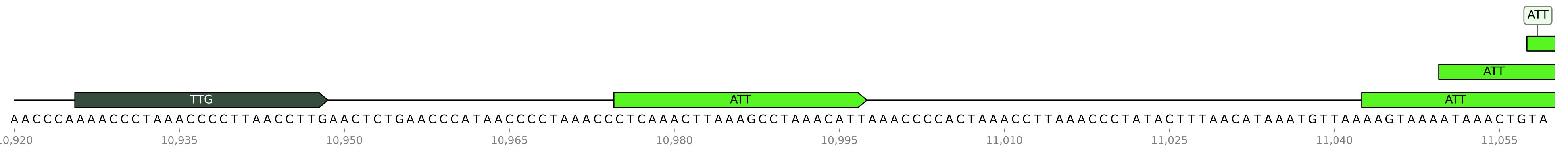
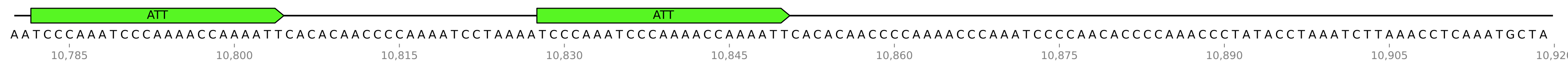
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10,230                      10,245                      10,260                      10,275                      10,290                      10,305                      10,320                      10,335                      10,350

ACCCCAAACCTCCAAACCCTGAACCCTCAACCCCTAACCCCAACCCCTAACCCCTAACCCCTCAACCCCTTAACCCCTGTACCCTGAACCCCAACCCCTAACCCCTAACCCCAACCCCTAATCTTAAAC

Genomic map of the TIGR10000 region on chromosome 10. The map shows a linear sequence of DNA with a scale from 10,500 to 10,635. A green arrow labeled 'TTG' indicates a transcription start site at approximately 10,545. The DNA sequence is displayed below the scale: CCAAACCTTAAACCTCAACCCGAACCCCTAATCCCTAACCCCAACCCCTAAACCTAAGACCTTGACCTTAGACCCTAAACCTTAAACCCAAACCTAATCCATAAACCTAACCCCTAAACCCCTCAACCC.

Genomic map of the TIGR1222 gene. The gene is represented by a dark green arrow pointing right, labeled 'TIGR1222'. Below the gene, a horizontal line represents the DNA sequence. The sequence is: TAATCCCTTGACCCTTAACCCCTAAACTTGACCTAACCTTAAACTTAAAACCCCTAAACCCTAACCCCTAACCCCTGACCCTTAATCCCTGACCCCAAACCCAAAACCTGAAAACCTAAAACCCCTAAACCTAAAATCCTAA. Below the sequence, a scale bar shows positions from 10,650 to 10,770 in increments of 5.



11,760	11,775	11,790	11,805	11,820	11,835	11,850	11,865	11,880	11,895
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11,910	11,925	11,940	11,955	11,970	11,985	12,000	12,015	12,030
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12,045	12,060	12,075	12,090	12,105	12,120	12,135	12,150	12,165	12,180
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12,180	12,195	12,210	12,225	12,240	12,255	12,270	12,285	12,300	12,315
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12,330	12,345	12,360	12,375	12,390	12,405	12,420	12,435	12,450
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12,465	12,480	12,495	12,510	12,525	12,540	12,555	12,570	12,585	12,600
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12,600	12,615	12,630	12,645	12,660	12,675	12,690	12,705	12,720	12,735
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CCTCAACCCTCAACCCTCAACCCTAAACCCTCAACCCTCAACCCTCAACCCTCAACCCTCAACCCTCAACCCTCAACCCTCAACCCTCAACCCTTAACCCCTAACCCCTAACCCCTAACCCCTAACCCCTA

12,750                  12,765                  12,780                  12,795                  12,810                  12,825                  12,840                  12,855                  12,870

CCTAACCCCTAACCCCTAACCCCTAACCCCAAACCCCAAAACCCCAAAACCCCTCAACCCCAAAACCCCTAAACCCCTAAACCCCTAAACCCCAACCCCAACCCCAACCCCAAAACCCCAAAACCCC

12,885                  12,900                  12,915                  12,930                  12,945                  12,960                  12,975                  12,990                  13,005                  13,020

AAACCCCCAACCCCAACCCCAAAACCCCAAACCCCAAAACCCCAAAACCCCTAACCCTTAACCCCTAAACCCCTAACCCCTACACCCTACACCCTCAACCCTCAACCCCGAACCCCAAAACTCCAAA

3,020                      13,035                      13,050                      13,065                      13,080                      13,095                      13,110                      13,125                      13,140                      13,155

CCCTGAACCCCTCAACCCCTAACCCCAACCCCTAACCCCTAAACCCCTAACCCCTCAACCCCTTAACCCCTGTACCCTGAACCCCAACCCCTAACCCCTAAACCCCAACCCCTAATCTTAAACCCCAACCCCTTAACCCCT

CAACCCCGAACCCCTAATCCCTAACCCCAACCCCTAAACCCCTAAGACCCTTGACCTTAGACCCTAAACCTTAAACCCCAAACCCCTAATCCATAAACCCCTAACCCCTAAACCCCTCAACCCCTAATCCCTTGACCCCTTA

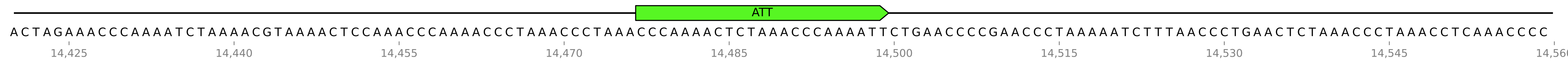
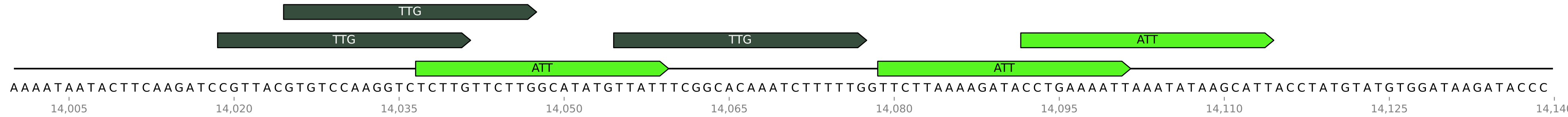
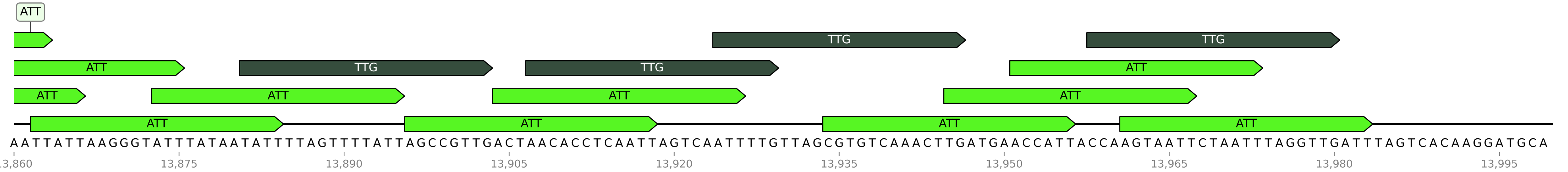
TTG

ATT

ACCCCTAAACTTGACCTAACCTTAACTTAAACCCCTAACCCCTAACCCCTGACCCTTAATCCCTGACCCCAAACCCAAAACCTGAAAACCTAAAACCTAAACCTAAAATCCTAAAATCCCAAATCCCAAAA

3,440 13,455 13,470 13,485 13,500 13,515 13,530 13,545 13,560 13,575

Genomic map of the 13,600 bp region. The top track shows the gene structure with exons in green and introns in black. The bottom track shows the DNA sequence with positions 13,590 to 13,710 marked. The sequence is: CCAAAATTACACACACCCCAAAATCCTAAAATCCCAAATCCCAAAACCAAAATTCACACAACCCCAAAACCCAAATCCCAACACCCCAAAACCCTATACCTAAATCTTAAACCTCAAATGCTAAACCCAAACCCCTAAAC.





CTCCAACCTCAACTCCCAACCCCAAACCCCTAAACCCCTAACCCCTGAACCTAAGAACCCCGAACCCCTCAAACCCCTCAATCCTAAACCAAAAACCCCTGAACCCCATAAACCCCTAAACCCCTAAAACCCCTCAACCCCTAGACCCCT

AGACCTAGATCACATACCCTATATGCTAGCCCATAGACCCAAAACCCAAAACCCCAAATCTCAAACCTAAACCCTGGACCATGGACTCTTAACCCTAAACCCCGAACCCCAAACCCGAAACCCAAACTCTGAACCCTA

AATCCCAAACCTAGACTTGAAACCCTAAACCCTAAACCCTAAACCCTAAACCCTAAACCCTAAACCCTAAACCCTAAACCCTAAACCCTCAACCCTCAACCCTCAACCCTCAACCCTCAACCCTC

4,980 14,995 15,010 15,025 15,040 15,055 15,070 15,085 15,100 15,115

AACCCCTCAACCCTCAACCCTCAACCCTCAACCCTCAACCCTCAACCCTCAACCCTAAACCCTAAACCCTAAACCCTCAACCCTCAACCCTCAACCCTCAACCCTCAACCCTCAACCCTCAACCCTCAACCCTCAACCCTCAACCCTC

15,130      15,145      15,160      15,175      15,190      15,205      15,220      15,235      15,250

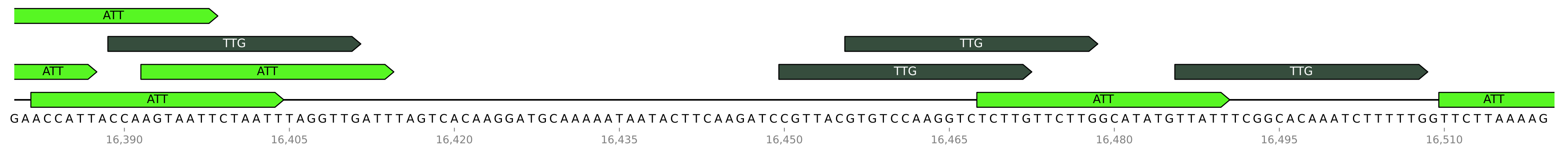
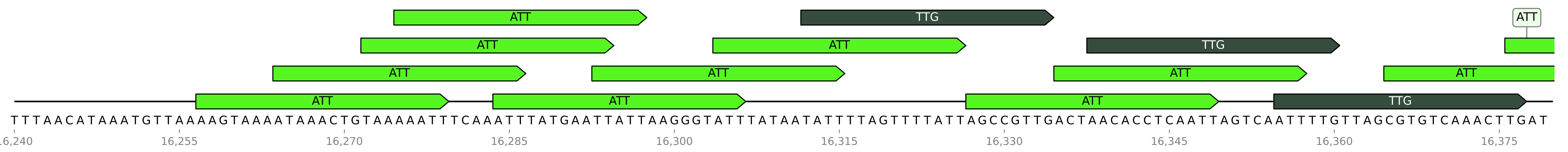
AACCTCAACCCTAACCCCTAACCCCTAACCCCTAACCCCTAAACCCTAACCCCTAACCCCTAACCCCAAACCCCAAACCCCAAACCCCAAACCCCTCAACCCCAAACCTAAACCCC

15,265 15,280 15,295 15,310 15,325 15,340 15,355 15,370 15,385 15,400

TAAACCCTAACCCCTAACCCCAACCCCAACCCCAAAACCCAACCCCAAAACCCCAACCCCAACCCCAAAACCCCAAAACCCCAACCCCAAAACCCCAAAACCCCTAACCCCTAACCCCTAAACCCCTAAA

5,400 15,415 15,430 15,445 15,460 15,475 15,490 15,505 15,520 15,535

CCCTACACCCTACACCCTCAACCCTCAACCCCGAACCCCAAACTCCAAACCCTGAACCCTCAACCCCTAACCCCAACCCCTAACCCCTAAACCCCTAACCCCTCAACCCTTAACCCTGTACCCTGAACCCCAAAACCCT



AAGCCCAAATCCCAAAGCCCTGAGCCCTAAACCCTGAGCCCTGAACCCTGAACCCTAAACCCTGAACCCTGAACCCTGACCCCTGACCCCTGACCCCTCAACCCTCAACCCTCAACCCTAAACCCTCAACCCTCAACCCCA  
16,660 16,675 16,690 16,705 16,720 16,735 16,750 16,765 16,780 16,795

TTG ATT

AACCTTGAACCTCAAATTTTAAACCCTGAATCCTAAACCCTAAACTAGAAACCCAAAATCTAAACGTAAAACTCCAAACCCAAAACCCCTAAACCCTAAACCCAAAACCTCTAAACCCAAAATTCTGAACCCCGAACCCCTA  
16,810 16,825 16,840 16,855 16,870 16,885 16,900 16,915 16,930

TTG ATT ATT

AAAATCTTTAACCCCTGAACTCTAAACCCTAAACCCTCAAACCCCTAAACCCTAAACCCTAACCCGAACCCCGAACCCAAAACCCCTTAACCCTCAACCCCAAACCCCTGAACCCCAAACCCAAAACCCCTCAACCCTCAACCTGG  
16,945 16,960 16,975 16,990 17,005 17,020 17,035 17,050 17,065 17,080

AACCCCGAACCCGGAACCCTGAACCCTCAACCCTAAACCCCAACCTCCAACCCTCAACTCCCAACCCCAAACCCCTAAACCCCTAACCCCTGAACCTAAGAACCCCGAACCCCTCAAACCCTCAATCCTAAACCAAAAACCCCT  
17,080 17,095 17,110 17,125 17,140 17,155 17,170 17,185 17,200 17,215

GAACCCCATAAACCCTAAACCCTAAAACCCTCAACCCTAGACCCTAGACCCTAGATCACATACCCTATATGCTAGCCCCTAGACCCAAAACCCAAAACCCCAAATCTCAAACCCTAAACCCTGGACCATGGACTCTTAACC  
17,230 17,245 17,260 17,275 17,290 17,305 17,320 17,335 17,350

CTAAACCCCGAACCCCAAACCCGAAACCCAAACTCTGAACCCTAAATCCCAAACCCTAGACTTGAAACCCCAAACCCCATAAACCCTAACCCCAAACCTTGAAACCTTATACTCGAAACTTGAAACCCCAAACCCCTAAACC  
17,365 17,380 17,395 17,410 17,425 17,440 17,455 17,470 17,485 17,500

TTG TTG TTG

TGAAGCCCCAAACTCTTAACCCCTAAACCCGAAACCCTAACCCCGAACCTAAAAAAATCCTAAACCCCAAACCTTAAATCCCAAACCCCAAGCCCTAACCCCTAAACTCTGAACCCCAAACCCCTGAAATCCCAAACA  
17,500 17,515 17,530 17,545 17,560 17,575 17,590 17,605 17,620 17,635

