

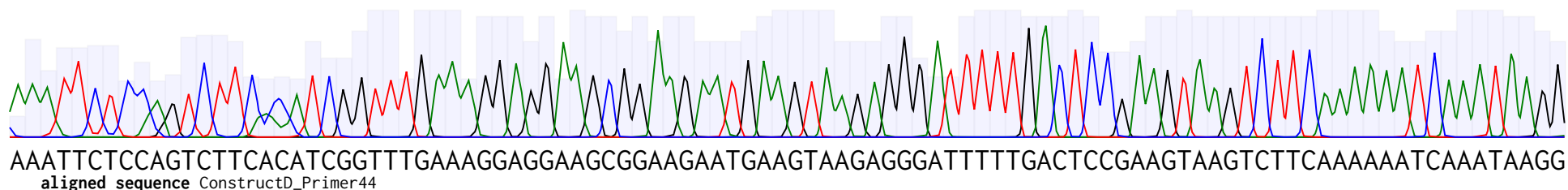
Template Alignment: ConstructD_Primer44

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template sequence ConstructD_Primer44

aaattctccagtcttcacatcggtttgaaaggaggaagcggaagaatgaagtaagagggatttttgactccgaagtaagtcttcaaaaaatcaaataagg

Chromosome 2

aligned sequence ch168 + D



AGTGTCAAGAATGTTTGCAAAACGATTCAAACCTCTTTACTGCCGTTATTGCTGGATTTTATTGCTGTTTCATTGGTTCTGGCAGGACCGGCGGCT
template sequence ConstructD_Primer44

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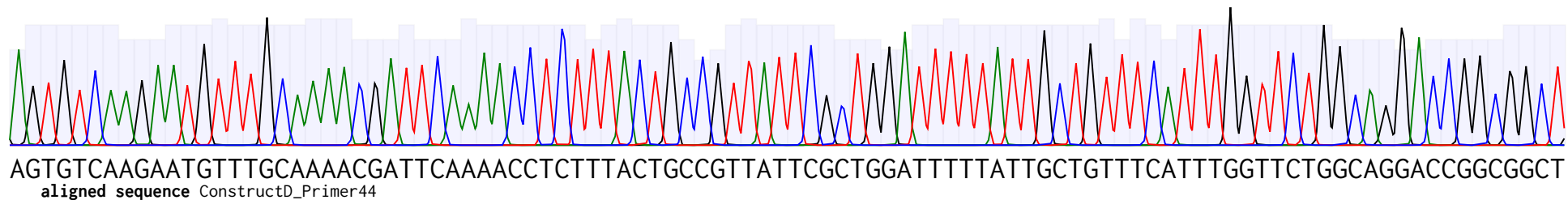
pDG3661

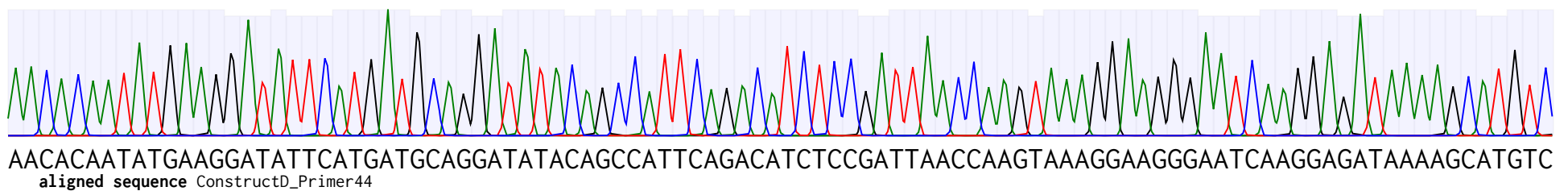
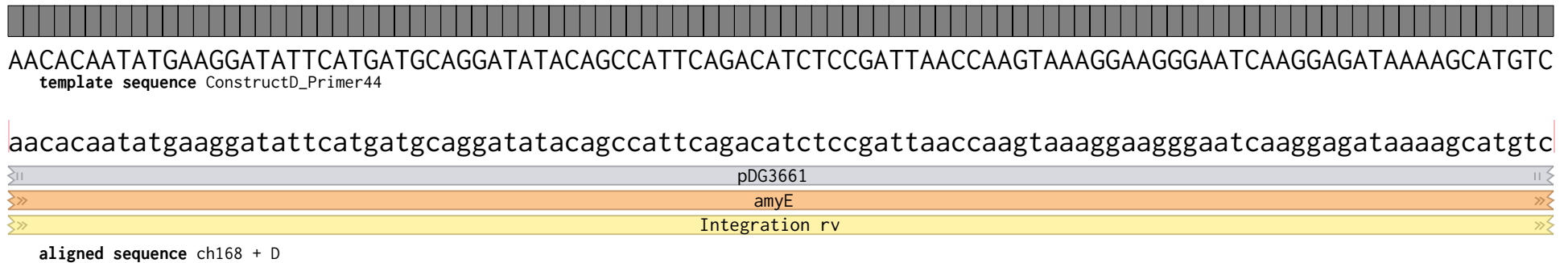
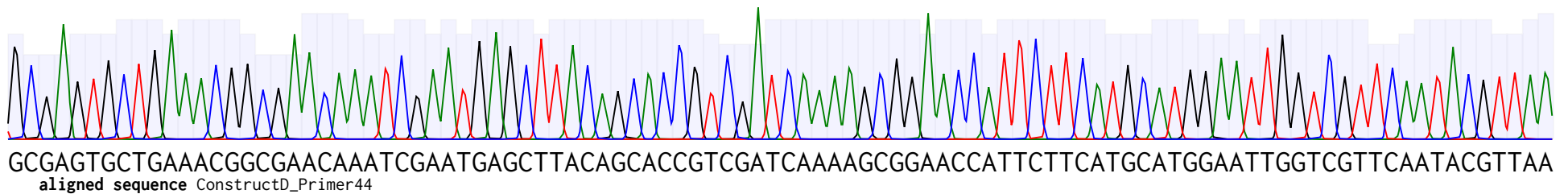
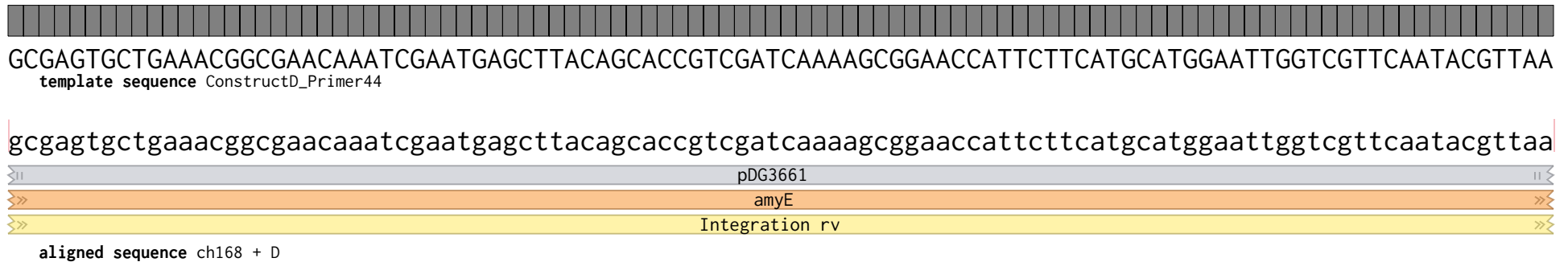
amyE

Chro...e 2

Integration rv

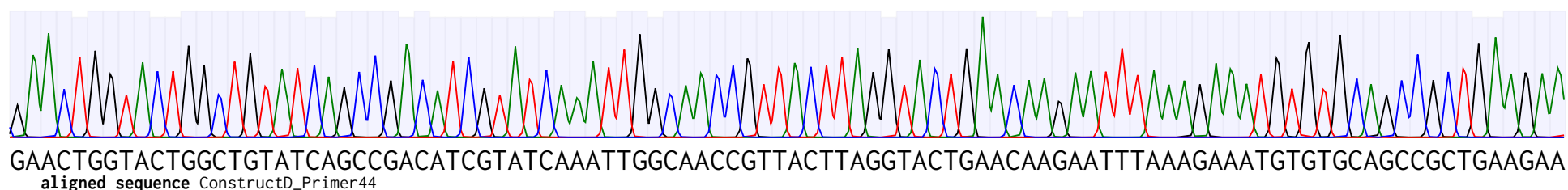
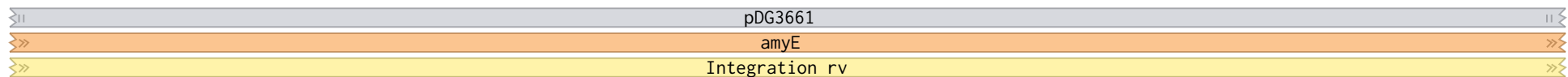
aligned sequence ch168 + D





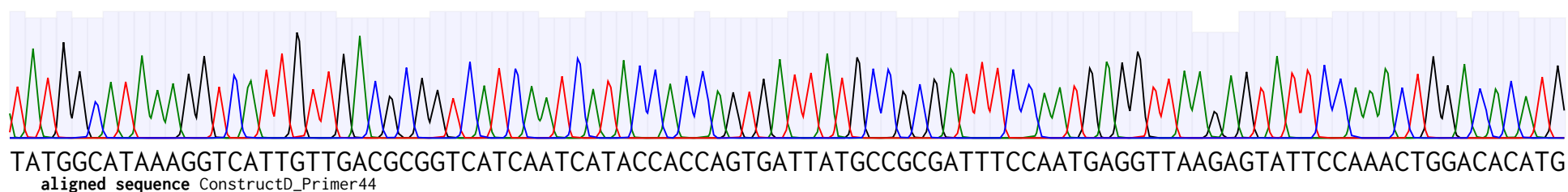
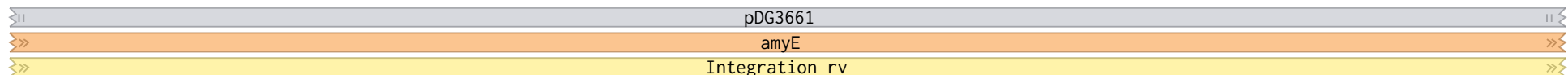
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template sequence ConstructD_Primer44

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TATGGCATAAAGGTCATTGTTGACGCGGTCATCAATCATACCACCAGTGATTATGCCGCGATTTCCAATGAGGTTAAGAGTATTCCAAACTGGACACATG
template sequence ConstructD_Primer44

tatggcataaaggctcattgttgacgcggtcatcaatcataccaccagtgattatgccgcgattttccaatgaggttaagagtattccaaactggacacatg



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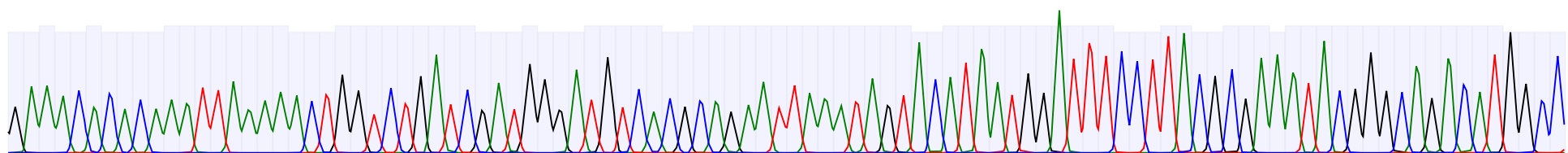
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pDG3661

amyE

Integration rv

aligned sequence ch168 + D



GAAACACACAAATTA AAAA ACTGGTCTGATCGATGGGATGTCACGCAGAATTAAATAGTACATAATGGATTTCTTACGCGAAATACGGGCAGACATGGCC
aligned sequence ConstructD_Primer44

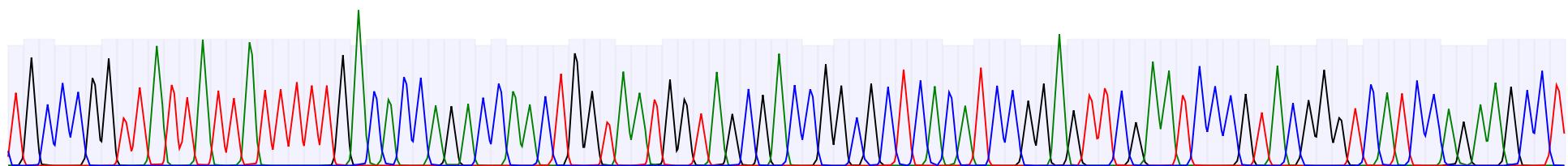
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template sequence ConstructD_Primer44

tgcccggttattattatttttgacaccagaccaactggtaatggtagcgaccggcgctcacatccggagttcgaatcccgtaggggtcatccagaagcct

pDG3661

derived from Bacillu...ion from amyE front

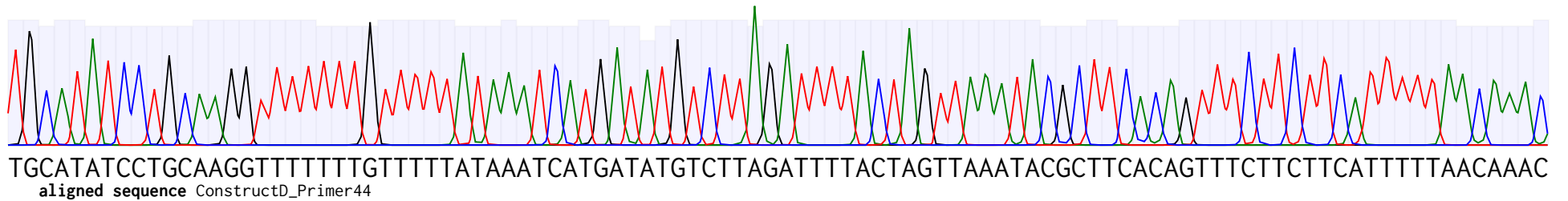
aligned sequence ch168 + D



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aligned sequence ConstructD_Primer44

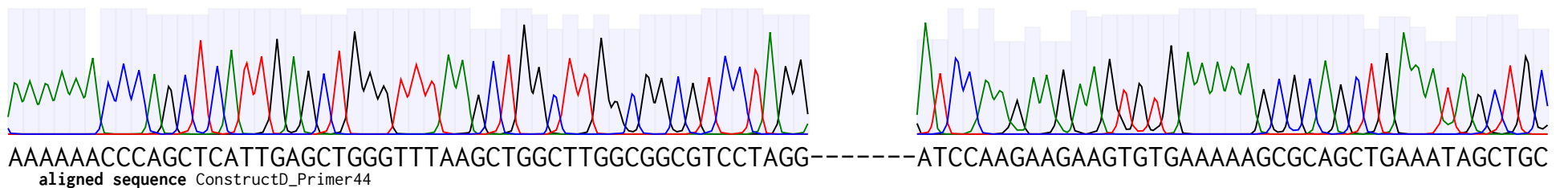
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template sequence ConstructD_Primer44

tgcataatcctgcaagggttttttgtttttataaatcatgatatgtcttagatTTTactagTTAAATACGCTTCACAGTTTCTTCTTCATTTTTTAACAAAC
pDG3661
derived from Bacillus subtilis rrnB;...nates transcription from amyE front derived from Bacillus sub...inates lacZtranscription
aligned sequence ch168 + D



AAAAAACCAGCTCATTGAGCTGGGTTTAAGCTGGCTTGGCGGCGTCCTAGG-----ATCCAAGAAGAAGTGTGAAAAAGCGCAGCTGAAATAGCTGC
template sequence ConstructD_Primer44

aaaaaaccagctcattgagctgggtttaagctggcttggcggcgctcctagaaaaaGGATCCaagaagaagtgtgaaaaagcgcagctgaaatagctgc
pDG3661
derived from Bacillus subtilis rrn0; terminates lacZtranscription Reverse terminator - BBa_K780000
aligned sequence ch168 + D





GCTTTTTTGTGTCATAAAGGCA
template sequence ConstructD_Primer44

gcttttttgtgtcataaAGGCA
Reverse t..._K780000
aligned sequence ch168 + D

