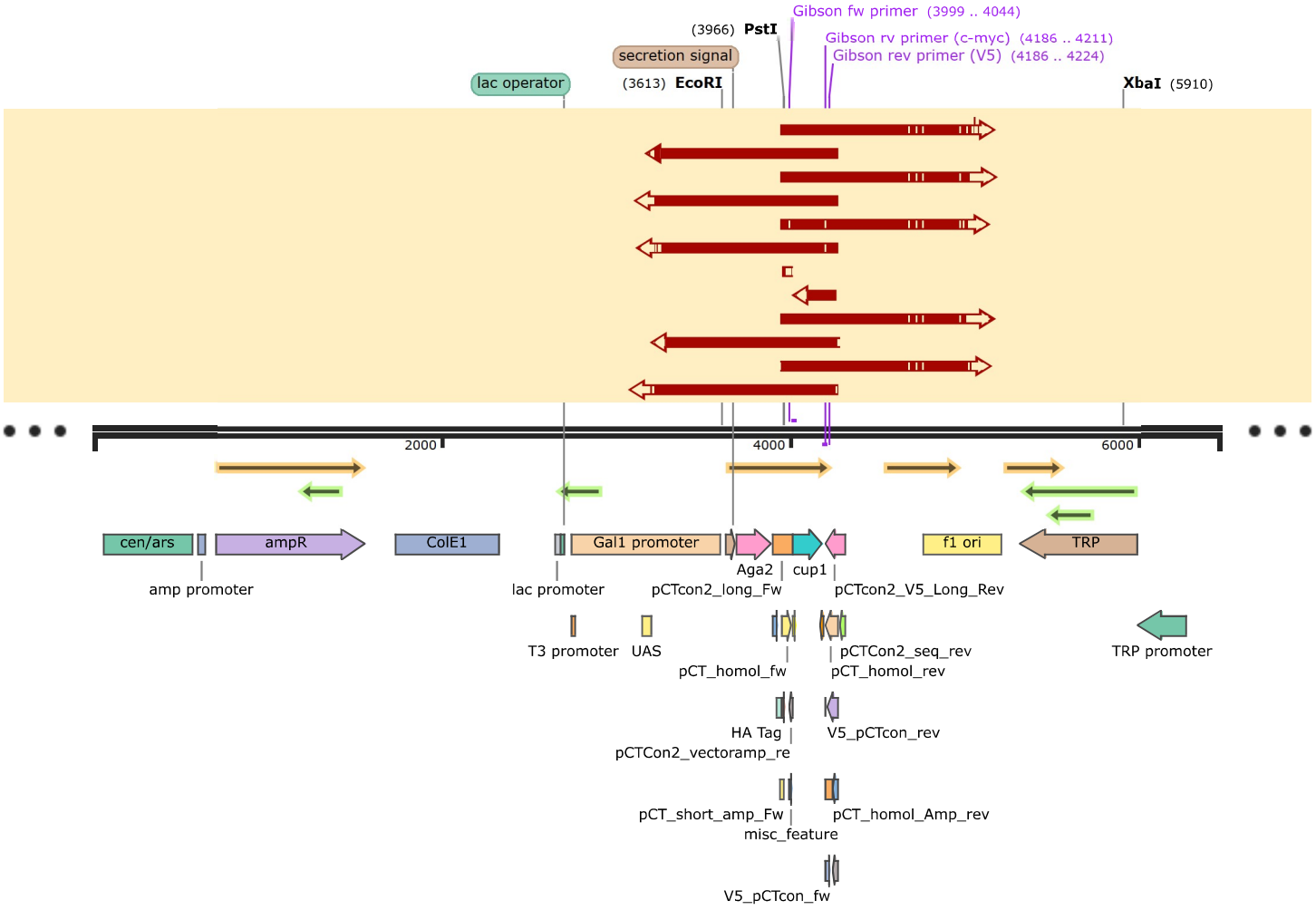

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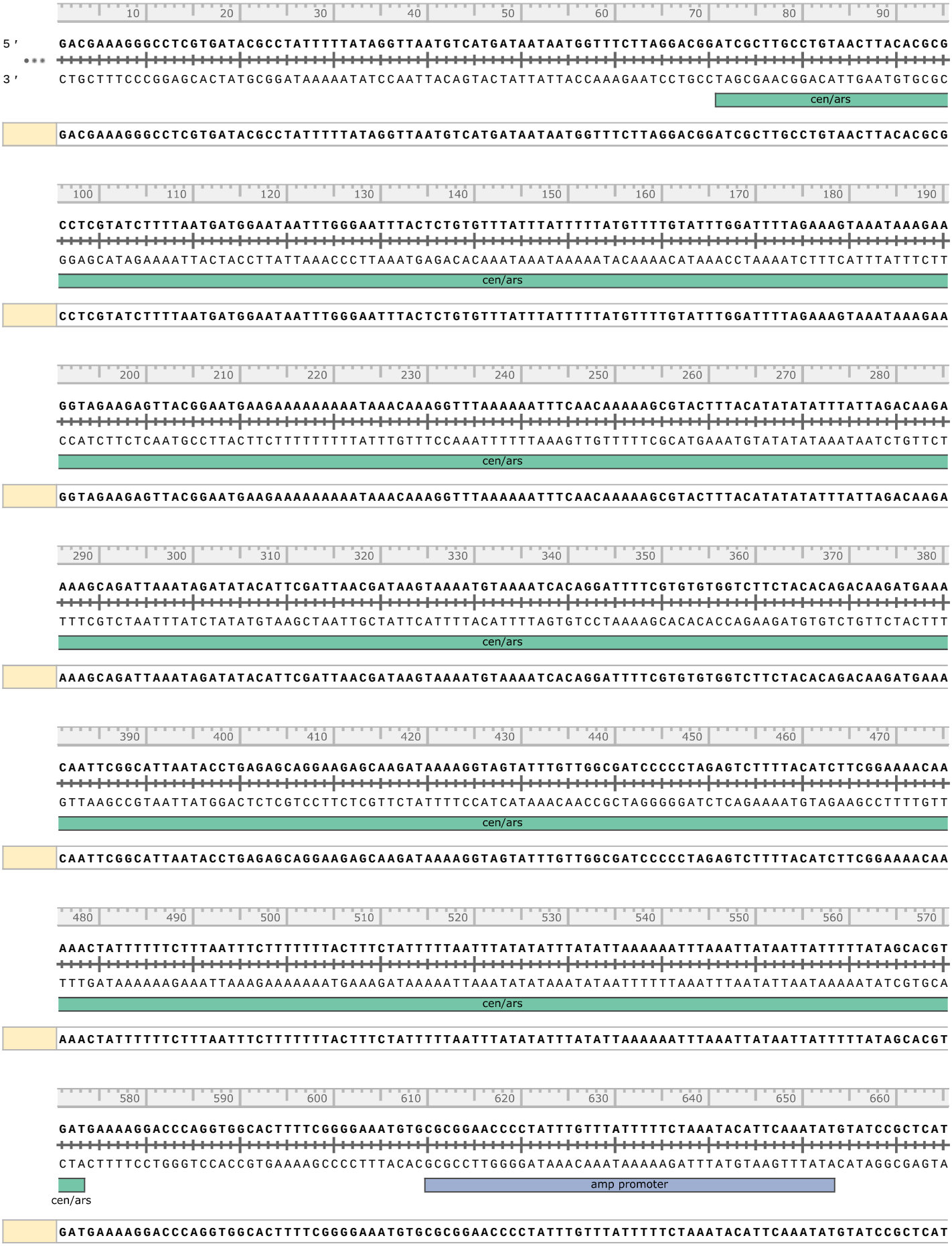
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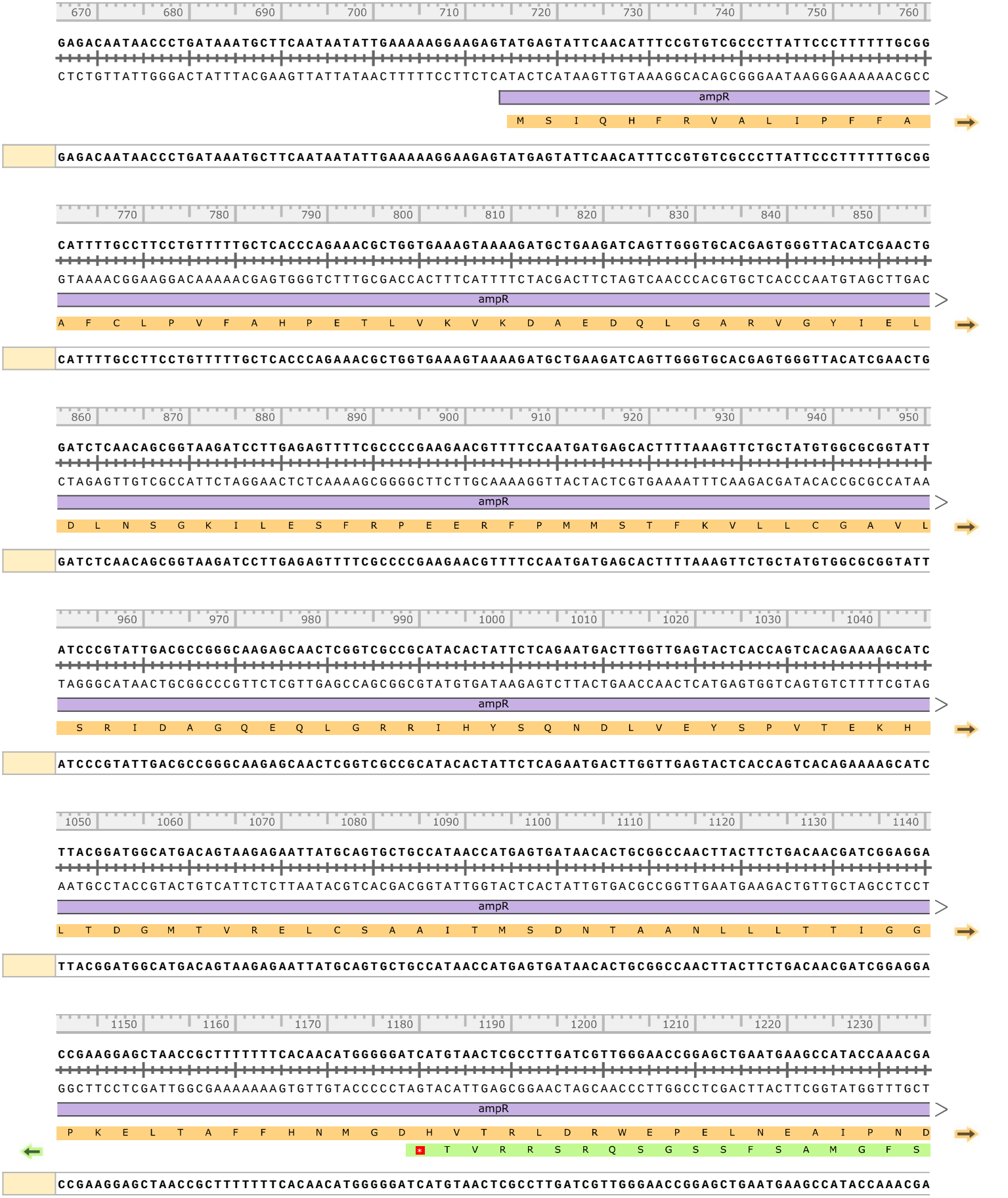
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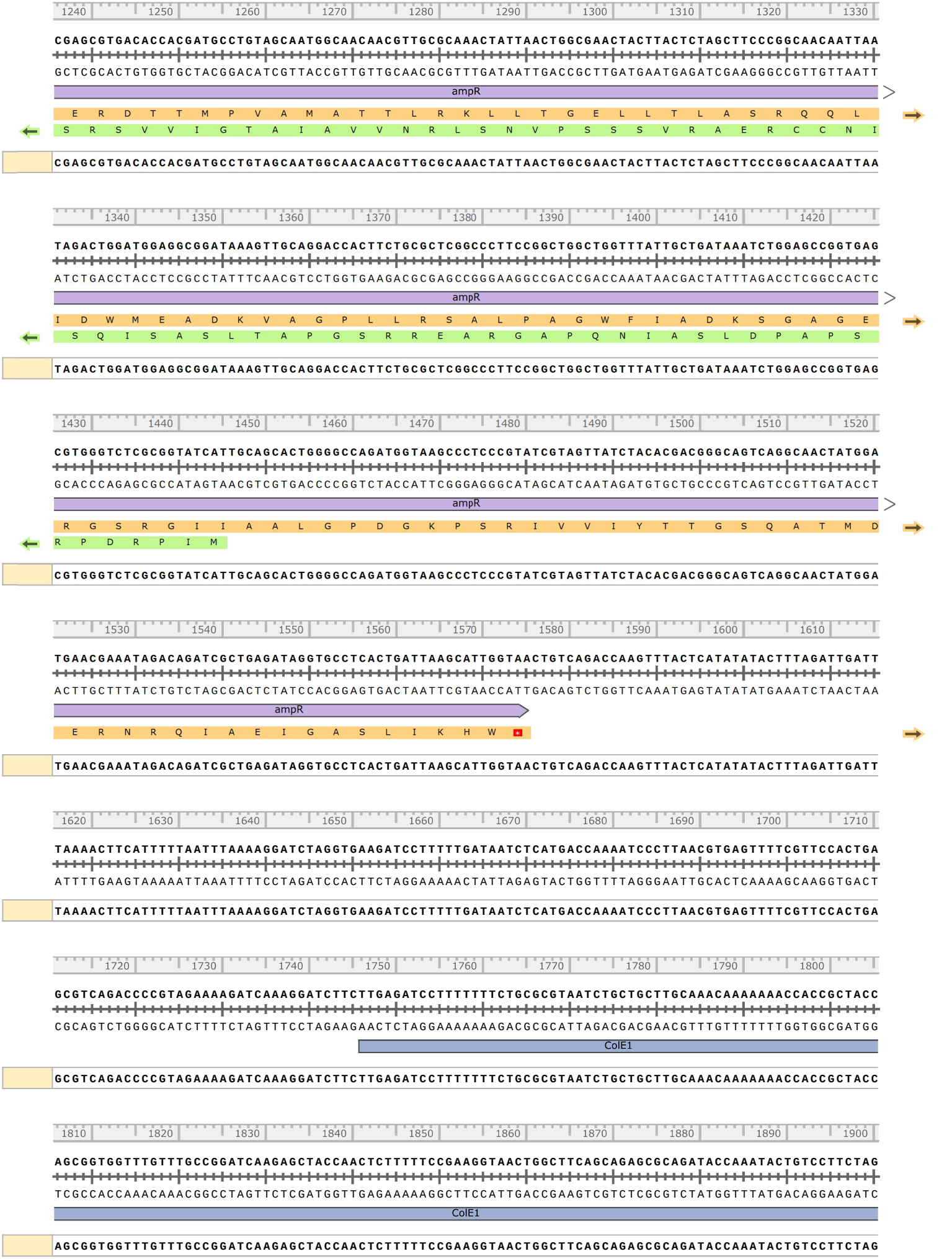
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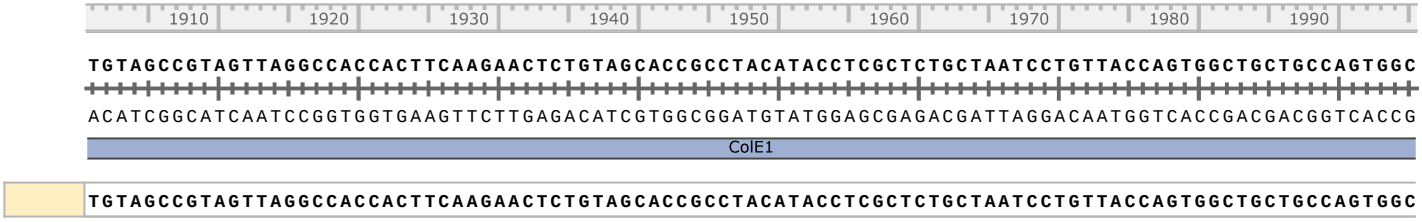
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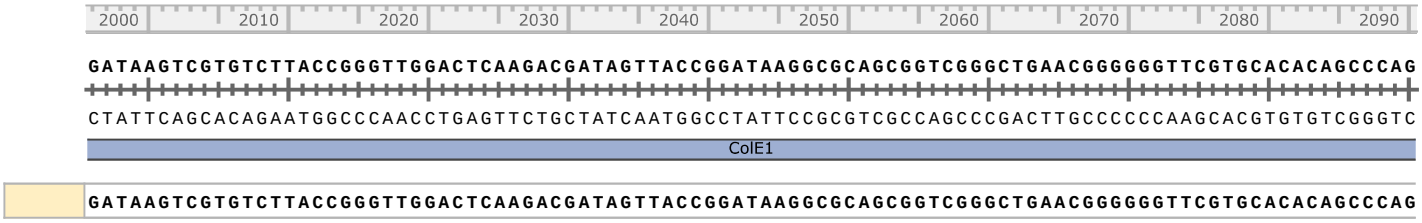
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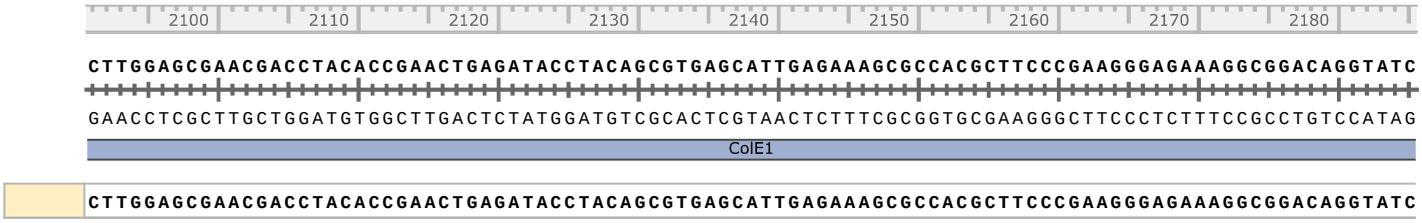
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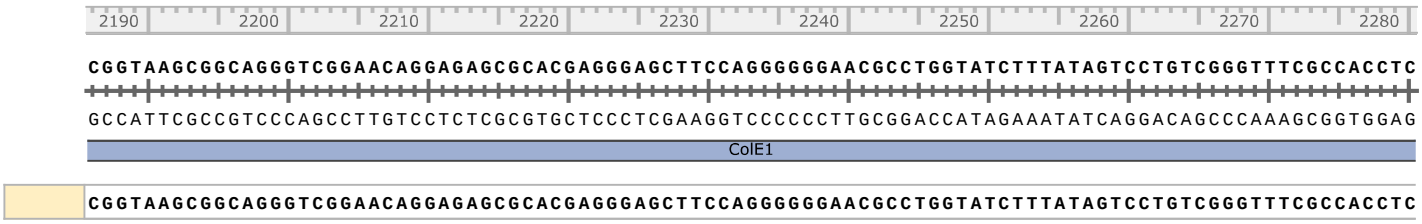
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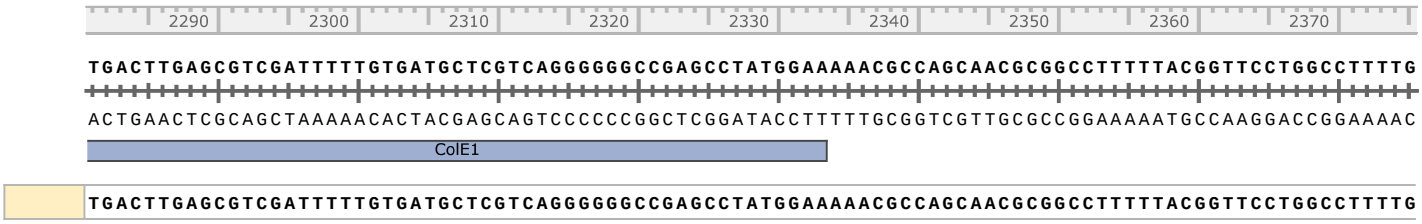
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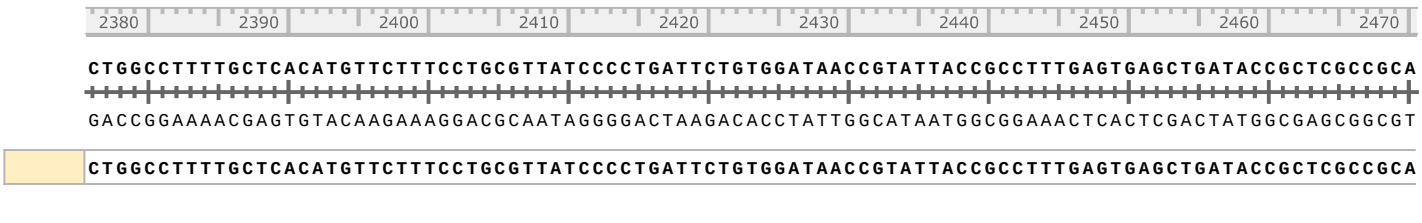
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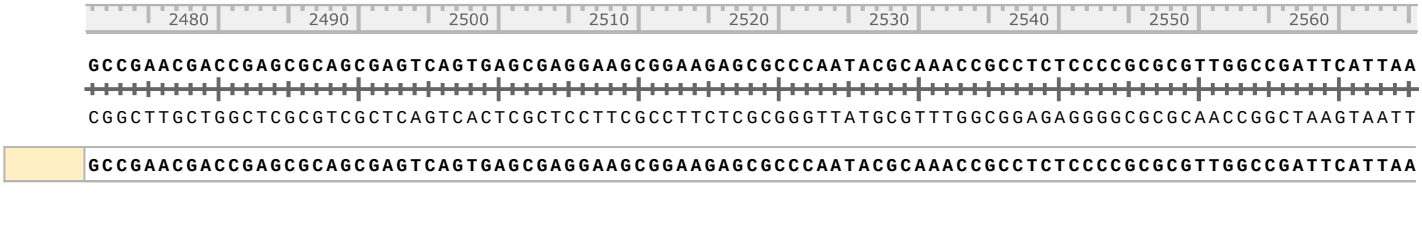
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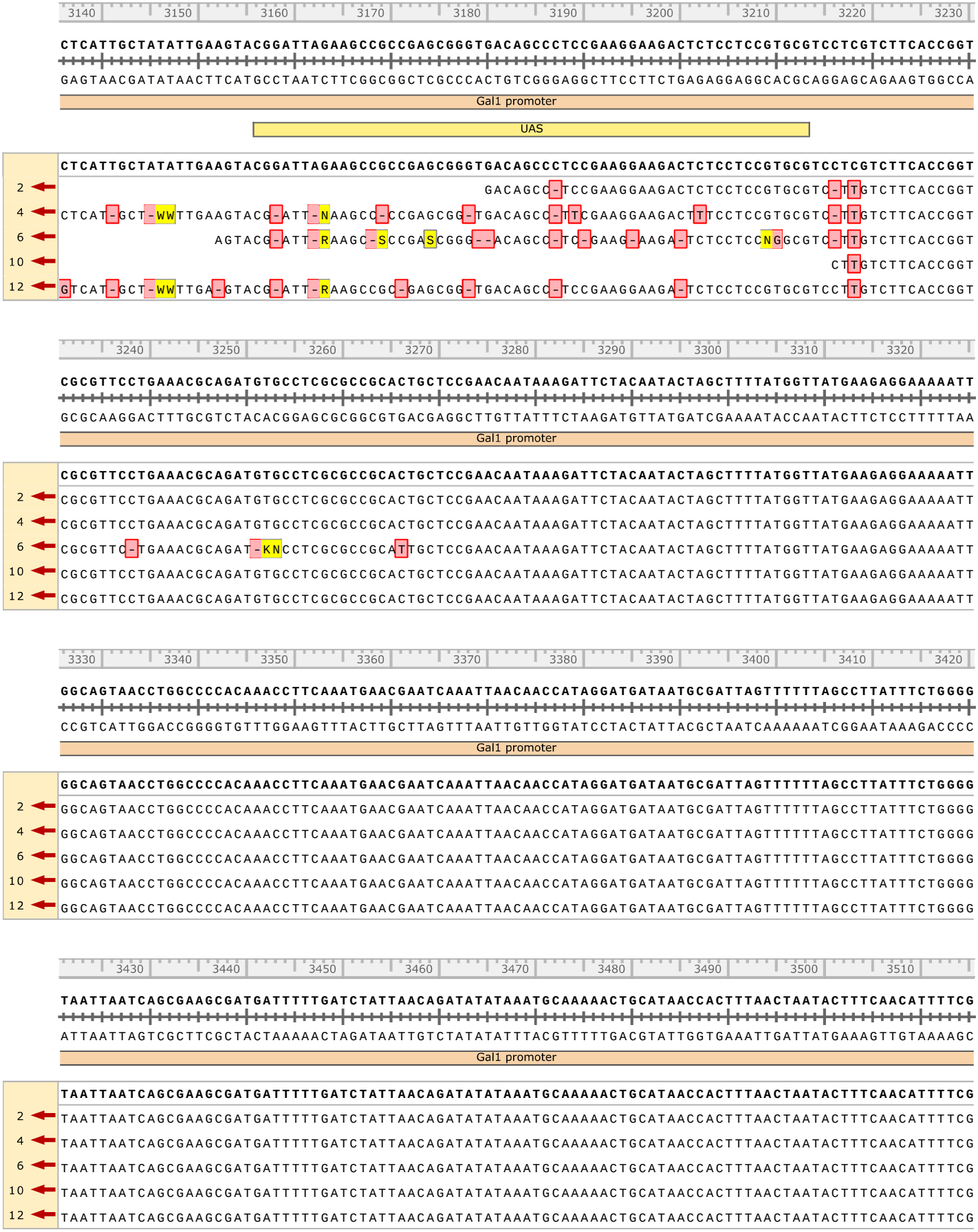
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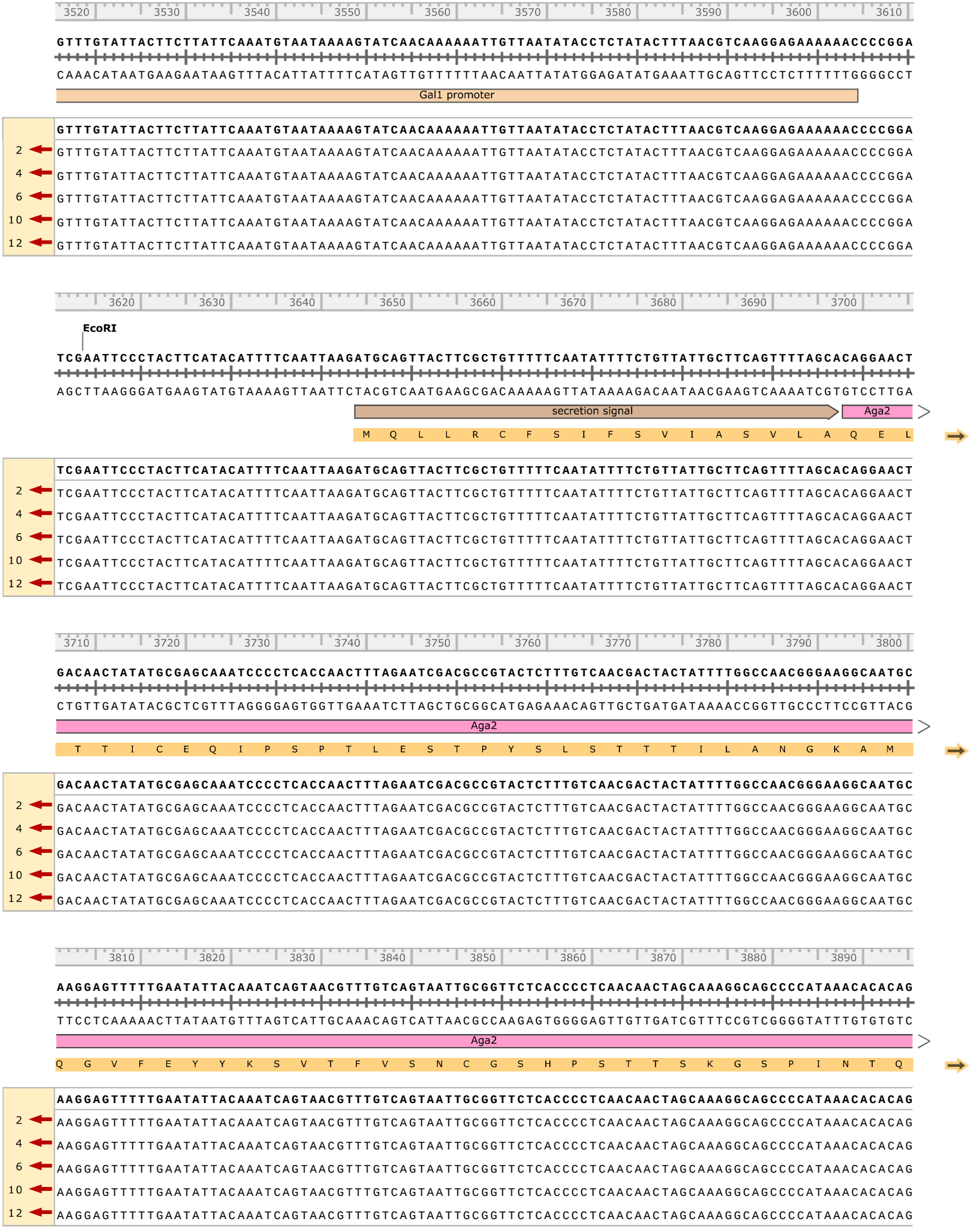
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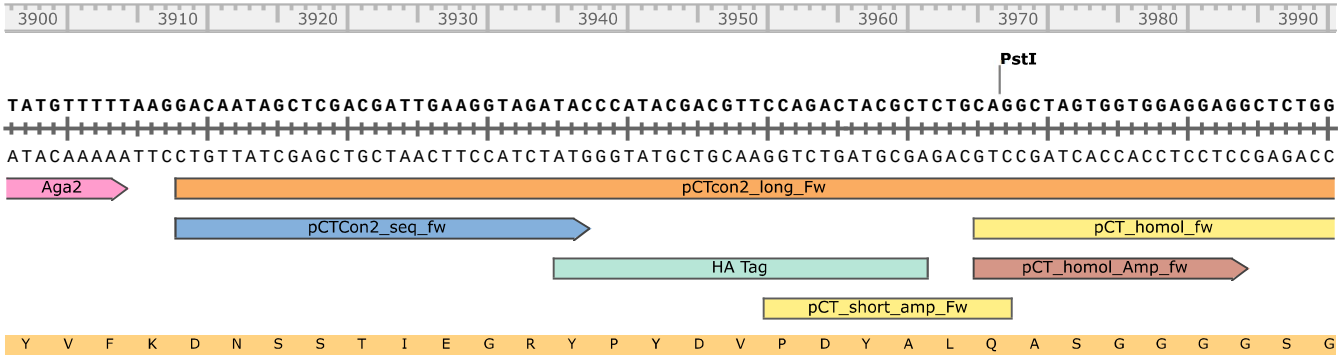
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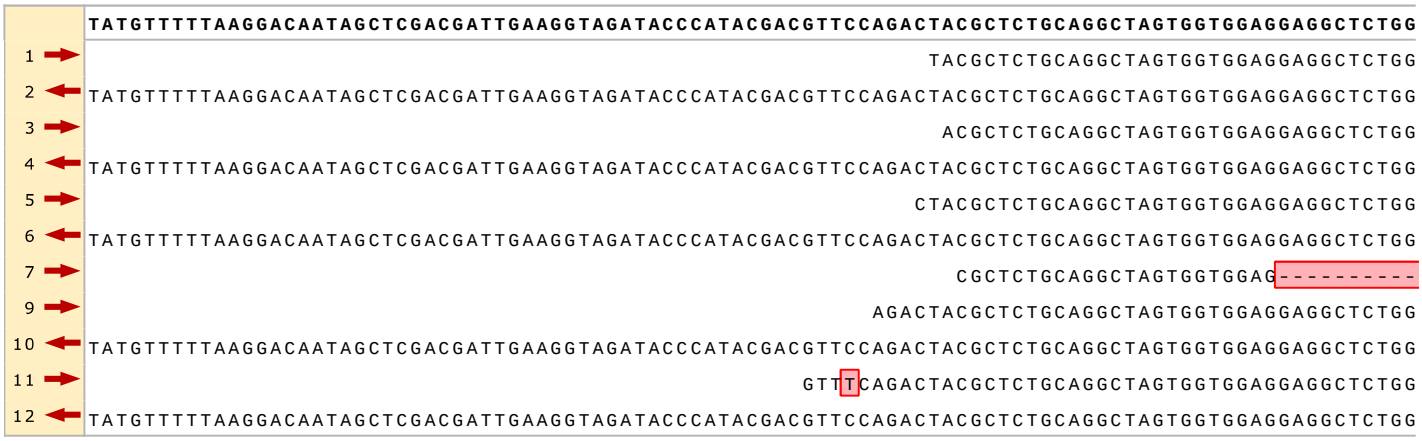
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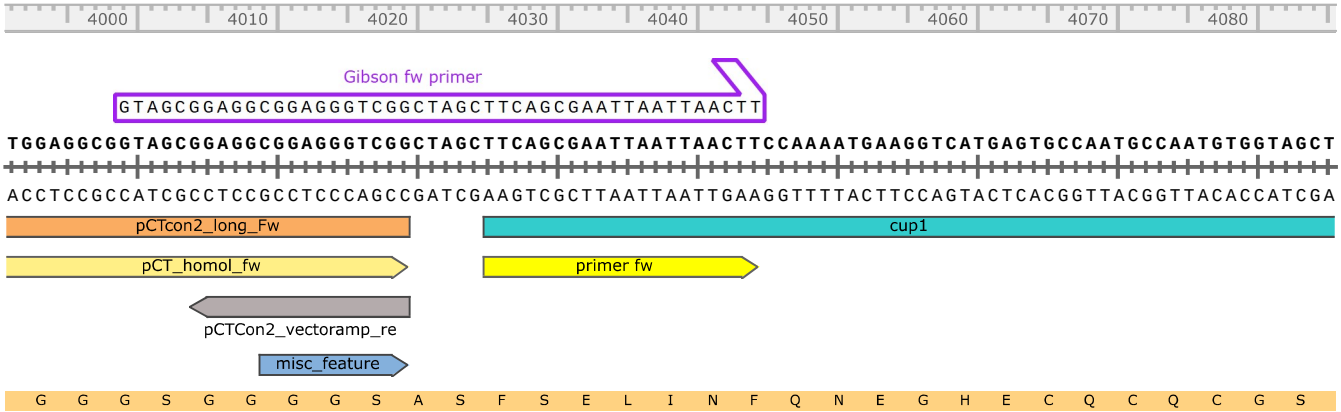
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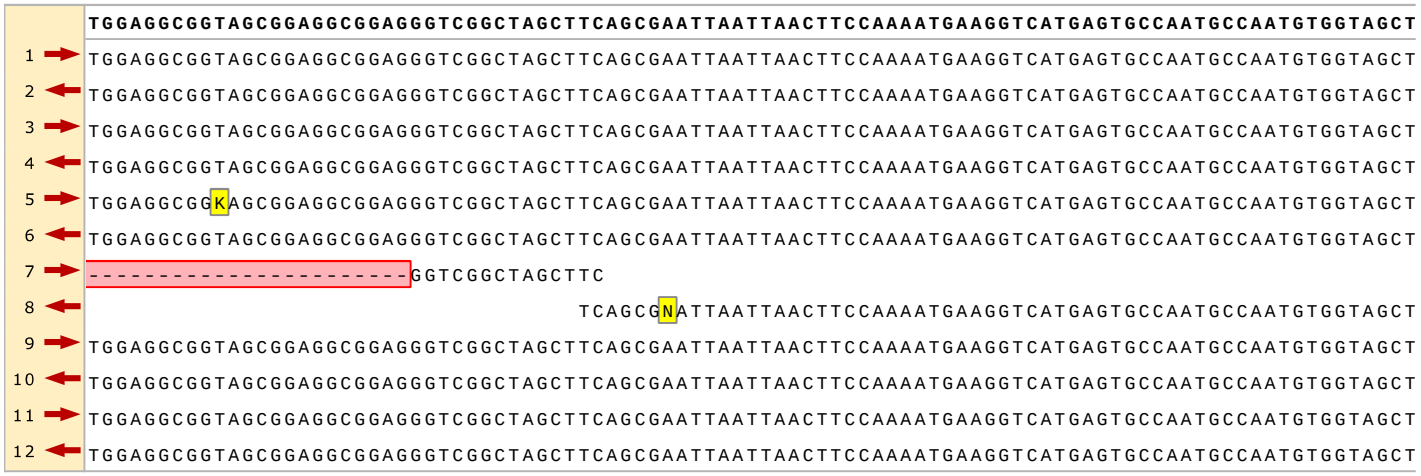
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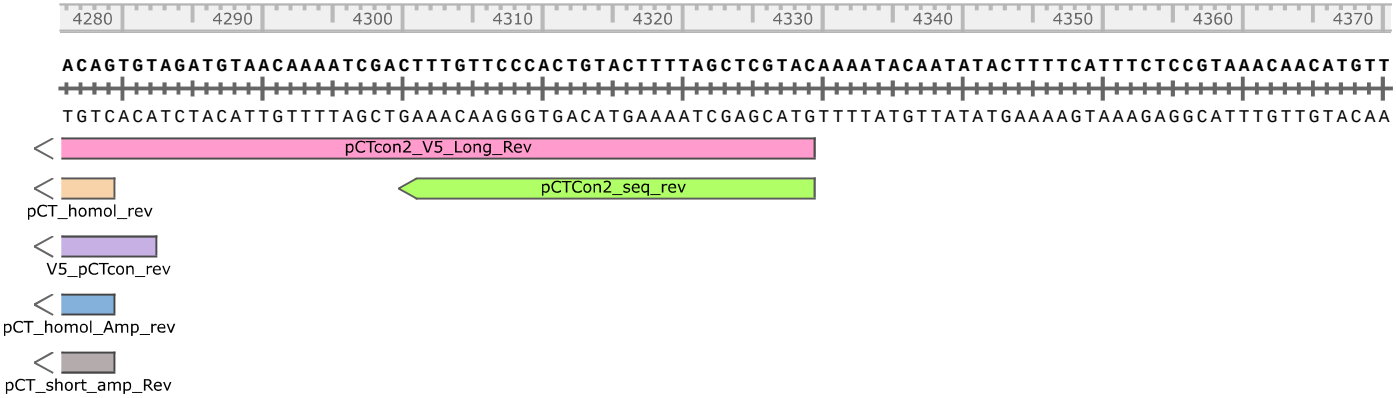

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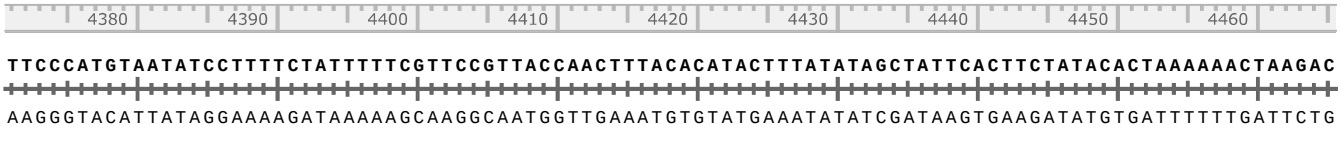

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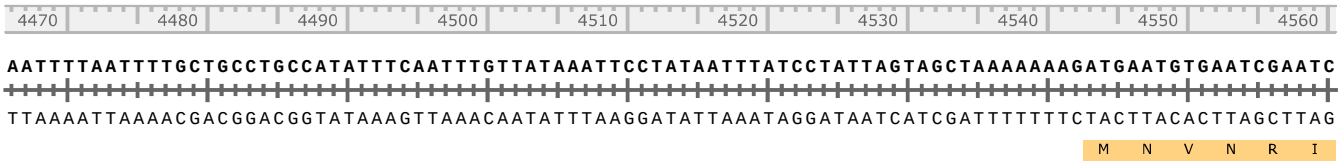

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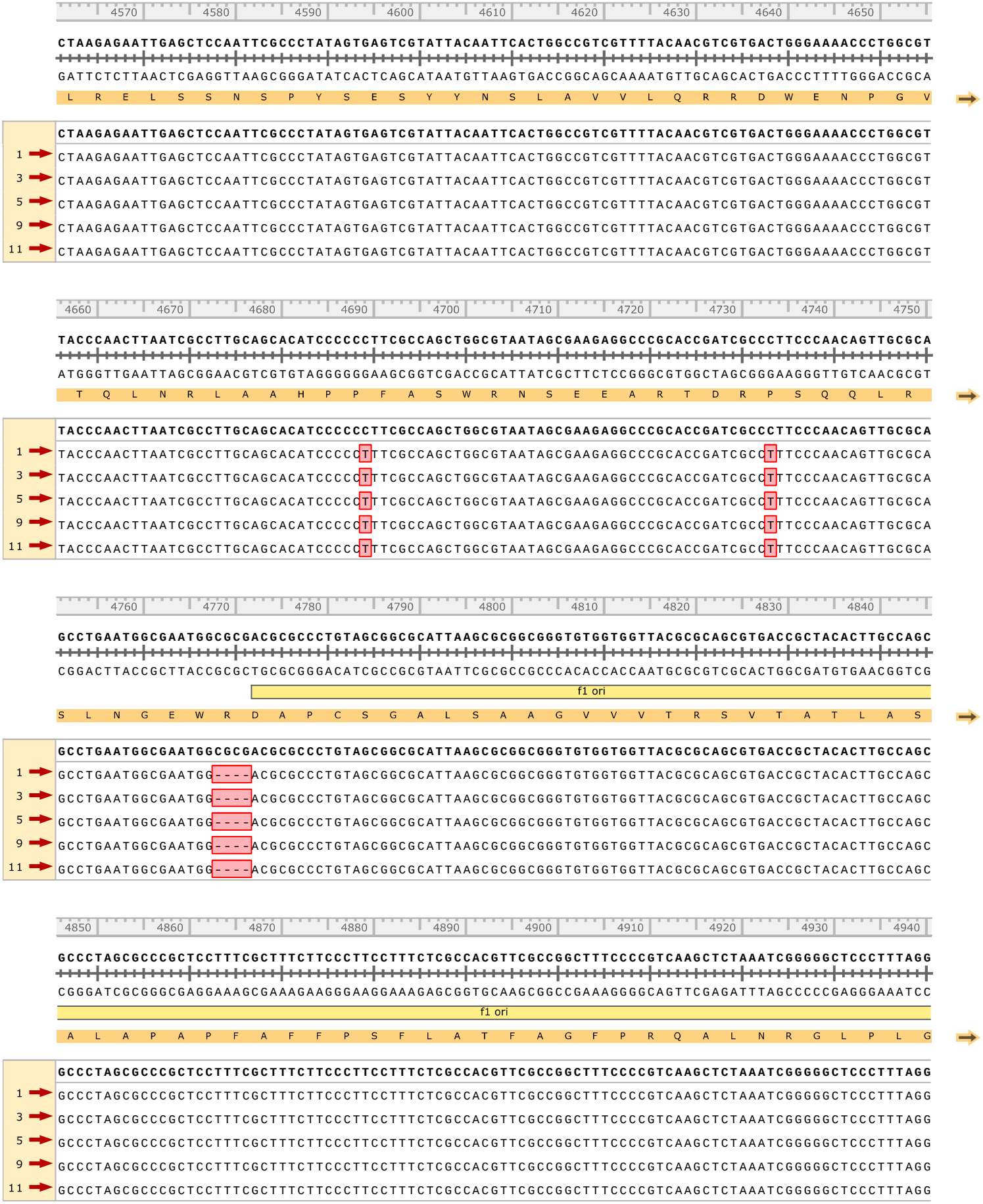
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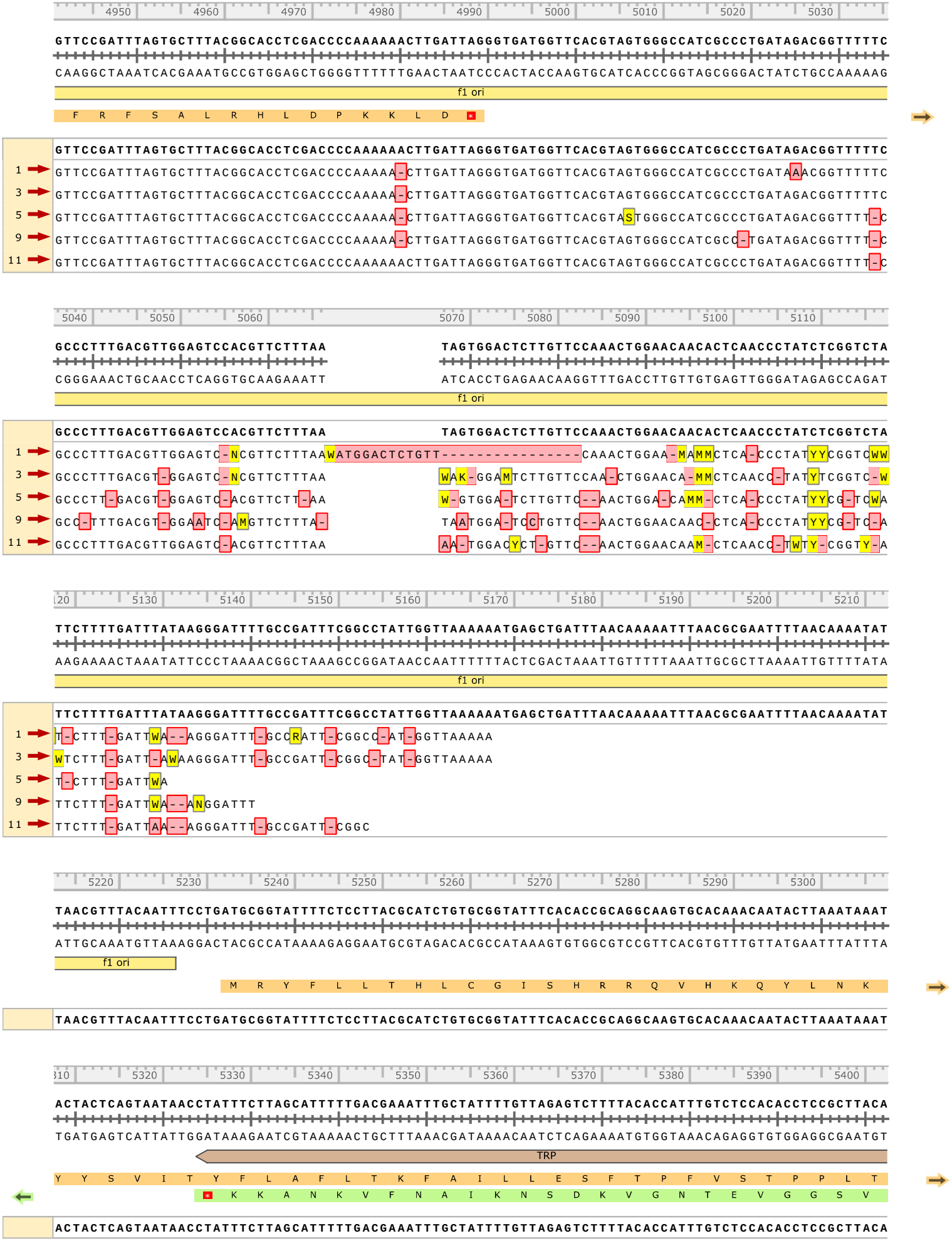
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TRP promoter
TTTTTCAATAAAGAATATCTTCCACTACTGCCATCTGGCGTCATAACTGCAAAGTACACATATATTACGATGCTGTCTATTAAATGCTTCCTATA
260
6270
6280
6290
6300
6310
6320
6330
6340
6350
TTATATATATAGTAATGTCGTTTATGGTGCACTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCGCCAACACCCGC
AATATATATATCATTACAGCAAATACCACGTGAGAGTCATGTTAGACGAGACTACGGCGTATCAATTCGGTCGGGGCTGTGGGCGGTTGTGGGCG
TRP promoter
TTATATATATAGTAATGTCGTTTATGGTGCACTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACCCGCCAACACCCGC
6360
6370
6380
6390
6400
6410
6420
6430
6440
TGACGCGCCCTGACGGGCTTGTCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGTCTCCGGGAGCTGCATGTGTCAGAGGTTTTCACCGT
ACTGCGCGGGACTGCCCGAACAGACGAGGGCCGTAGGCGAATGTCTGTTCGACACTGGCAGAGGCCCTCGACGTACACAGTCTCCAAAAGTGGCA
TGACGCGCCCTGACGGGCTTGTCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGTCTCCGGGAGCTGCATGTGTCAGAGGTTTTCACCGT
450
6460
CATCACCGAAACGCGCGA 3′
GTAGTGGCTTTGCGCGCT 5′
CATCACCGAAACGCGCGA

Original Sequence: Assembled_genomic_CUP1_pCTcon2_V5.dna

1: Y1-C1_P-Fwd →
1196 bases
1 .. 1193 (13 mismatches, 13 gaps)

2: Y1-C1_P-Rev ←
1099 bases
1 .. 1099 (1 mismatch, 2 gaps)

3: Y1-C2_P-Fwd →
1212 bases
1 .. 1193 (12 mismatches, 15 gaps)

4: Y1-C2_P-Rev ←
1154 bases
1 .. 1148 (6 mismatches, 10 gaps)

5: Y2-C1_P-Fwd →
1171 bases
1 .. 1156 (12 mismatches, 16 gaps)

6: Y2-C1_P-Rev ←
1140 bases
1 .. 1121 (10 mismatches, 11 gaps)

7: Y2-C2_P-Fwd →
38 bases
1 .. 37 (1 gap)

8: Y2-C2_P-Rev ←
254 bases
1 .. 253 (1 mismatch)

9: Y3-C1_P-Fwd →
1208 bases
1 .. 1168 (10 mismatches, 16 gaps)

10: Y3-C1_P-Rev ←
1077 bases
3 .. 1076 (1 mismatch, 1 gap)

11: Y3-C2_P-Fwd →
1199 bases
1 .. 1188 (10 mismatches, 14 gaps)

12: Y3-C2_P-Rev ←
1176 bases
4 .. 1170 (7 mismatches, 14 gaps)