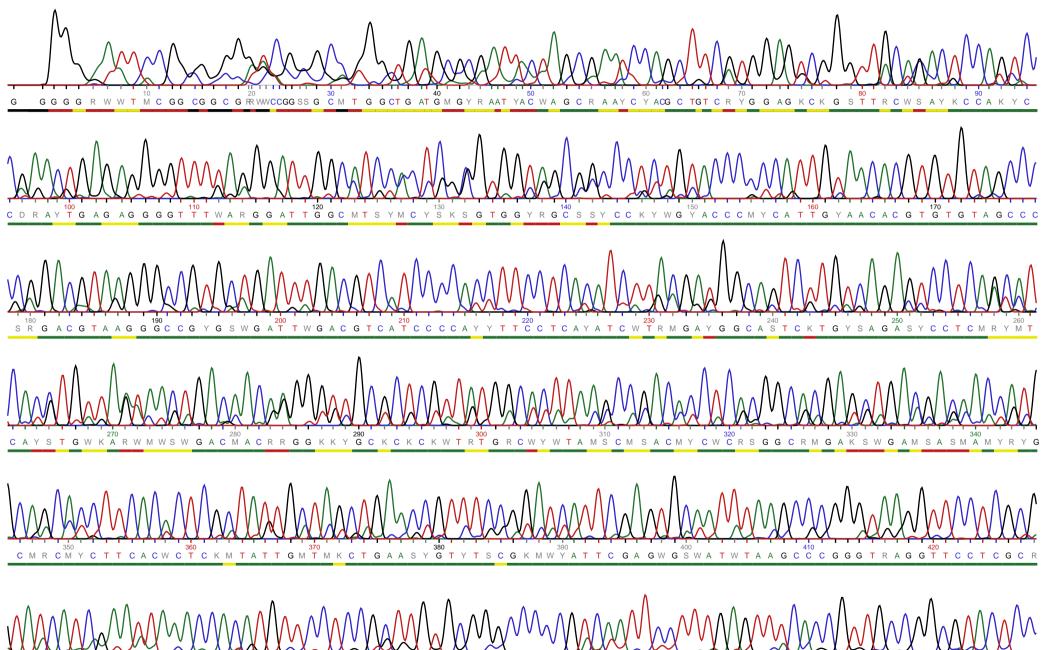
Samples: 13324 Bases: 1110

Average spacing: 13.0 Average quality >= 10: 69, 20: 154, 30: 875 Quality: 0 - 9 10 - 19 20 - 29 >= 30



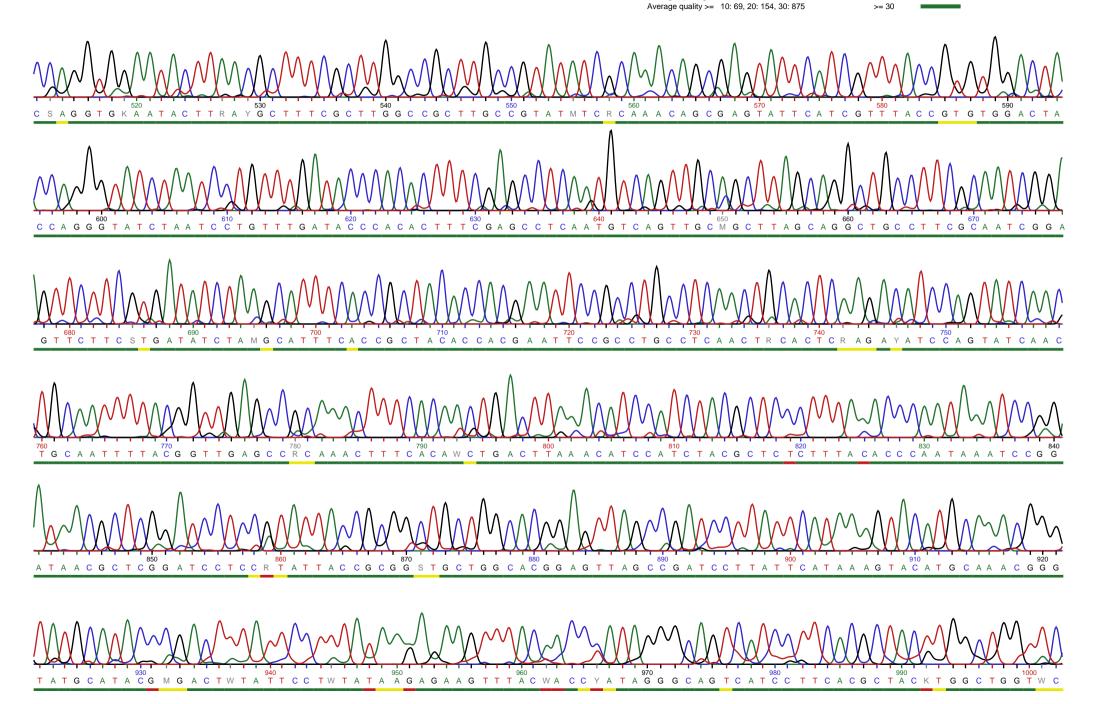
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430 440 440 500 500 500 TAWCATCGWAWTAAACCACATGTTCCTCCGSTTGTGCGGGCCCCCGWCWATTCCTTTGAGTTWCACCGTTGCCGGMGTACTCC

Quality: 0 - 9 10 - 19 20 - 29





Samples:

Average spacing:

Bases:

13324

1110

13.0

Sequence: SEQ10013680 B2 H12 0

 Samples:
 13324

 Bases:
 1110

 Average spacing:
 13.0

 Average quality >=
 10: 69, 20: 154, 30: 875

Quality: 0 - 9 10 - 19 20 - 29 >= 30



