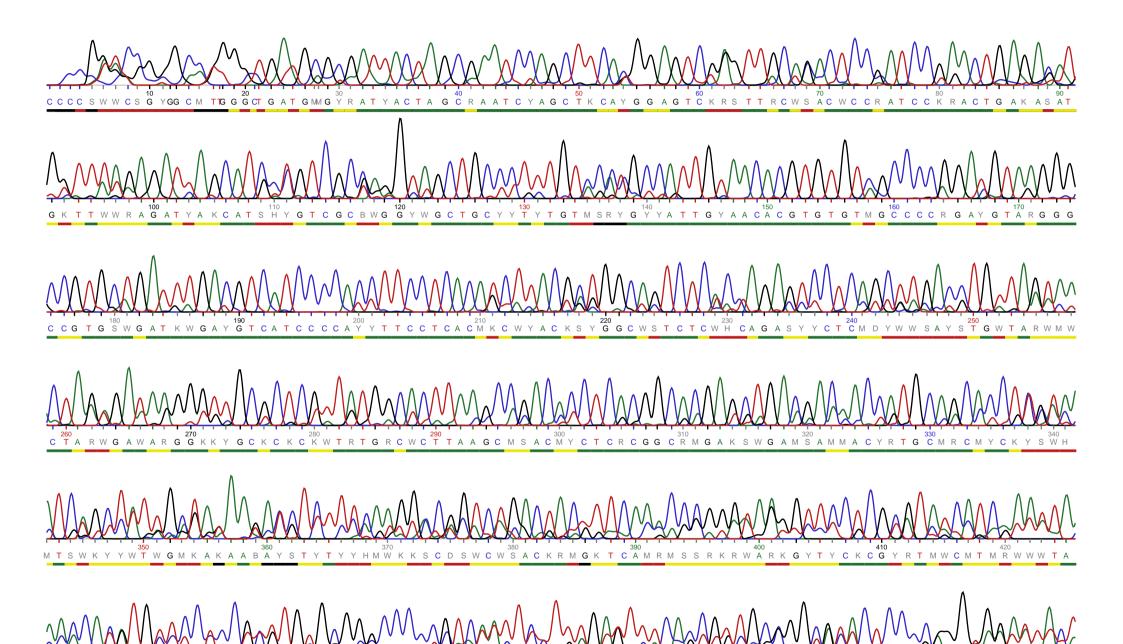
Quality: 0 - 9 10 - 19 20 - 29 >= 30

G S S G G Y R Y W C T C C M S R K G T R R W W Y W Y W





Samples:

Average spacing:

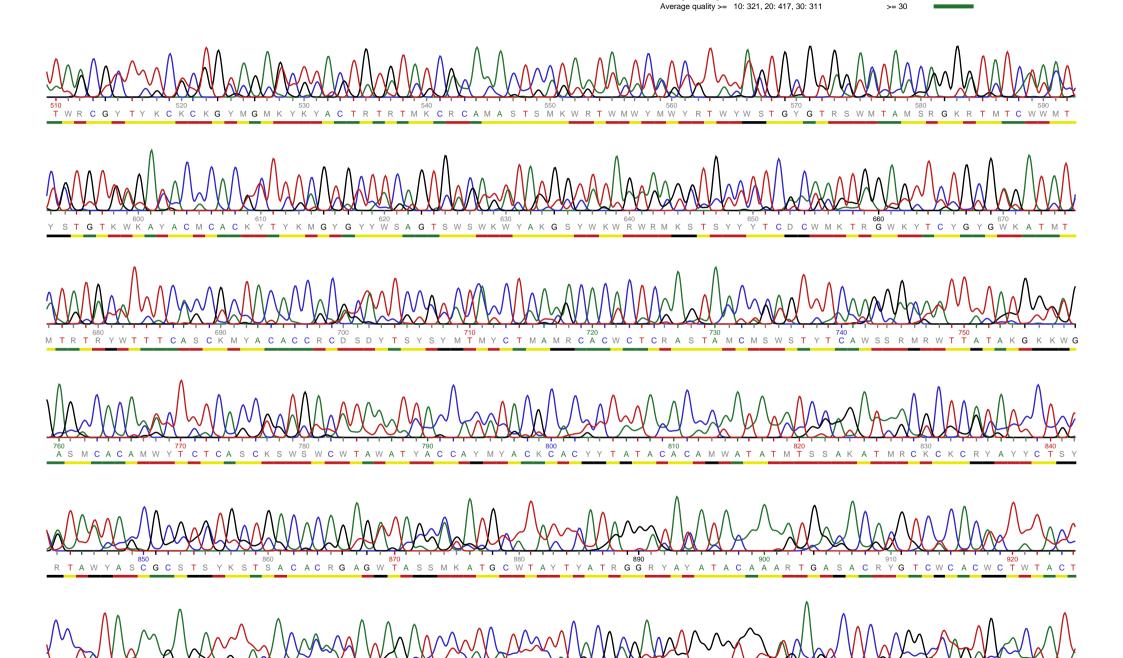
Bases:

13806

1159

12.0

Average quality >= 10: 321, 20: 417, 30: 311



CCTMTATAAGAGAGATGTAYACAMMCYAKAGATCYTWCMTYYYWCRCGMGWCGTGTGGTGKCWCASTCTCKCSSMYAKWGMMCTAT

Samples:

Average spacing:

1159

12.0

Bases:

Sequence: SEQ10013680 B2 C11 0

Samples: 13806 Bases: 1159 Average spacing: 12.0

Average quality >= 10: 321, 20: 417, 30: 311

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



