Sequence: SEQ10012052_B1_F12_0

Samples:	27048
Bases:	314
Average spacing:	87.0
Average quality >=	10: 6, 20: 21, 30: 283

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

09.08.2022

TCCCTGGTTCGCTCCCCACGCTTTTCGTGCATCAGCGTCAGTATAAGTCCAGAAAGTCGCCTTCGCCACTGGTGTTCCTCCTA

ATATCTACGCATTTCACCGCTACACTAGGAATTCCACTTTCCTCTCCTTAACTCAAGCCTTCCAGTTTCAAATGCTTACCACGG

TTGAGCCGTGATCTTTCACATCTGACTTAAAAGRCCGCCTACGCACCCTTTACGCCCAATAAATCCGGACAACGCTCGCCCCC

TACGTATTACCGCGGCKGCTGRCACCTGTCTCTTATACACATCTGACGCTGGCCGACRAAACA

Sequence: SEQ10012052_B1_F12_0

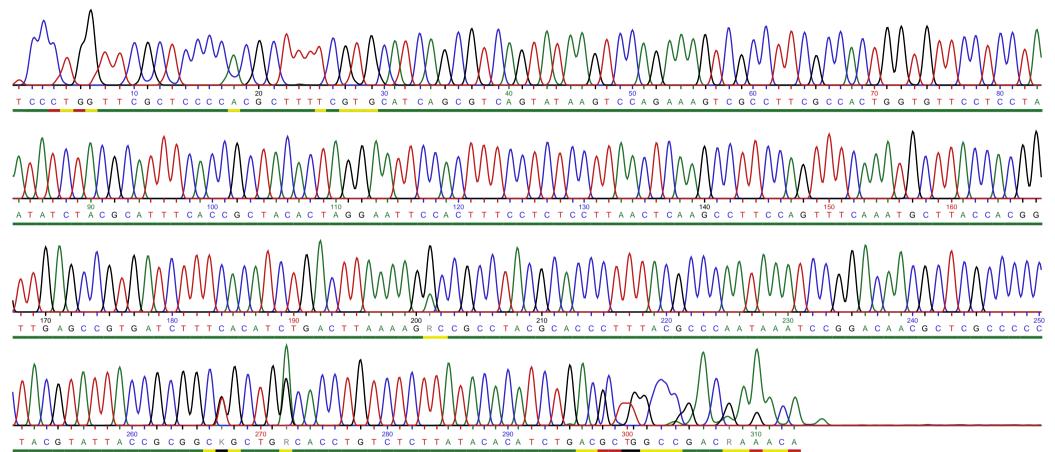|	
Samples:	27048
Bases:	314
Average spacing:	87.0
Average quality >=	10: 6, 20: 21, 30: 283

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

Sequence: SEQ10012052_B1_F12_0

Samples: 27048
Bases: 314
Average spacing: 87.0
Average quality >= 10: 6, 20: 21, 30: 283

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

Page: 5 / 5
09.08.2022