Sequence: SEQ10013680_B2_F11_0

		Quality:	0 - 9	
Samples:	15035		10 - 19	
Bases:	448		20 - 29	
Average spacing:	34.0		>= 30	
Average quality >=	10: 24, 20: 43, 30: 375			

11.10.2022

TTTGBTTTTYCRGTGGTARCCTTTCATCATTTCTGATGGGAAGAATACGTTAGGCTGYACCACATTGRTCTTGTAAATCGTAACCGWASA

ATCCTAATCTGGAATGTTGWTCTTTGTGTAAGTACATAGYTAAGTACCATGCGCTTAAMCCAGTTTGAGCATTACCAKYAKCGA

ATGCRRTAGATGCWCCAKCTGCTGCGGAAATTACRGAAKCTCTTTGAGATCCACCGAAKTGAGTTTCRAGTARTGSTGGGTATT

CTTCGTATTGWTCTAATGCGTAKAATGCAACTTCAGAACCTACATCAAGAACAGTGTCCATGTTGTTAGGTGCTTCAGTTAATC

CACCWTATTTGTCTTCTACRTARTCTTTACCATAGWAAGTAAAGTCATSTARTACATCATCAGTATAKGCTGCAKTAGCATAY

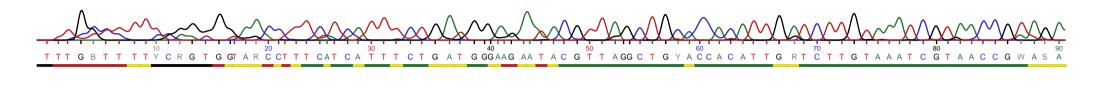TGHGTRAAHCCDACHCCDCCAA
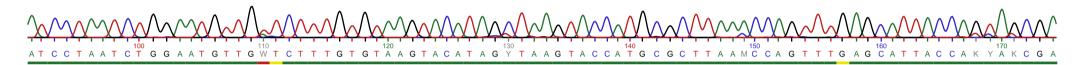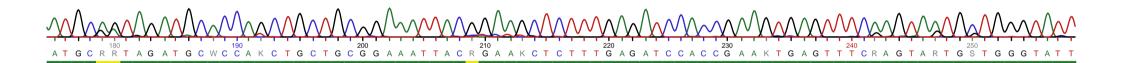
Sequence: SEQ10013680_B2_F11_0

Samples: 15035
Bases: 448
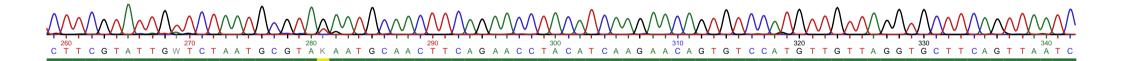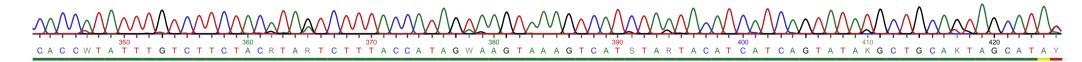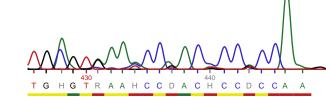Average spacing: 34.0
Average quality >= 10: 24, 20: 43, 30: 375

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

11.10.2022

Sequence: SEQ10013680_B2_F11_0

Samples:	15035
Bases:	448
Average spacing:	34.0
Average quality >=	10: 24, 20: 43, 30: 375

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