Sequence: SEQ10013680_B2_A12_0

GGG T GAAAT CC G CA T GACG CG CATG T GGAT G G AAAAAG S R TCCCAS Y T TCGTGGACCG G GT TGCAC ACTCC

AKYCCGAAYGG AA AG AGG TTTT GGGG ATTGG C WTCCACTCGC G KG TT M GCGG CCCTCT G TACCCC ACCATT G WAMM ACTGGG G WA

S CCCS G AACTTAA GGG C CATG ATGATTGAC K TCT TCCCCCC TTCCTCAAATTTT GTCCCTGG S TCTTGGCA TAS TCC CCCAM

C TAAACTT G TT GGAAACAAAAA A W A GGG TTG GCC CTCGTA W GGCAM TTAA ACCCAACATCC CACG ACACA AGTG G GACACACCA

T GG CACCACTT G TTTT CTT GTCCCC GAATT GAAATTTTTATC TCTATTCC G CGAAT CTTT GTCCC GGG TTGGGG TCCTTCTTC

A CG TTGCAAAATAAA AACCCATGG T CCTCCG ACTGG TTGG G CCCCC CCCCA W TTC TTTK ATTGA RT CGKTCCC TG CGTAATCCC

Sequence: SEQ10013680_B2_A12_0

		Quality:	0 - 9	
Samples:	13116		10 - 19	
Bases:	1087		20 - 29	
Average spacing:	13.0		>= 30	
Average quality >=	10: 690, 20: 92, 30: 0			

11.10.2022

CARGGGGAAAAATTTCTTATTGCGTTGGTCCGTTGCAGAATGGGTCGACCCTCCTACTTATTTATTAATCTGGAGGAAGAAC

MAGGTACCTAATCCTGGTTTAAACCCCCMCTACCCTGGCTTTCGCATCTCATGGTCARACACAGGGCAGCTTGGCMACTTCGAC

TCTGGTGTAWCTCCAATATTTACCCSTTTCACCSTAAATTCGSCATGCCCCATTGCTCTCCAGATATCCAGTATAAATTSTA

TTTTGCCGTTGGGGCGTGAACCTTSCAMTYTGACKTTAAAMTTCMTAMKCCCCCCCCTTGCACCTTACACACYCKGATTACGGACR

ACWCCCSCCAAATACCKSKTACCGCGGCWGCGGGYTMASASATYCCTRTGTMTTAMKCRYATACWAACGGGTWTGCAATGCMSTGT

TTAYTCYCTGYAWAAAMRTSWTAAAAACAGAGSKGTASASAYYCATMMCSYTATYRSKCRGGYGMGYTSCTCCCCATASWCT
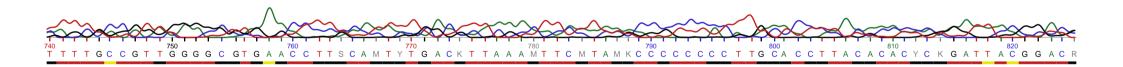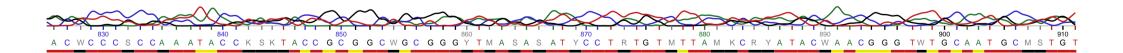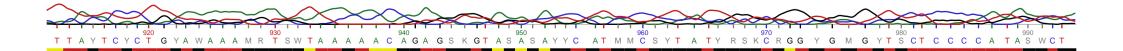
Sequence: SEQ10013680_B2_A12_0

Samples: 13116
Bases: 1087
Average spacing: 13.0
Average quality >= 10: 690, 20: 92, 30: 0

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

11.10.2022

CRTACACTGCGTACKATTCYCCMGTRSWRYTSSAYRKGAYTYAGTTCCGAKKSKGRGKCAMCATSCTSCTCARWCCTCCTACTCA

TMSGAGAT