Sequence: SEQ10013680_B2_C06_0

Samples:	14964
Bases:	1244
Average spacing:	13.0
Average quality >=	10: 107, 20: 262, 30: 856

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

Trace sequence bases:

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C CM G D W C G G Y G C M T G G G C T G A T G M G Y G A T T A C T A G C G A A Y Y Y A C G C T W C A C T G C A A G T Y K G S T T R C W B A C T T C G A T C C K R A C K G A G A G W G G

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

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

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

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

A M C A B A T G T T C C T C C G G S T T G T G C G G G C C C C C G W C W A T T Y C T T T G W G T T W C A C C G T T G C C G G C G Y A C T C C C S A G G T G G A A T A C T
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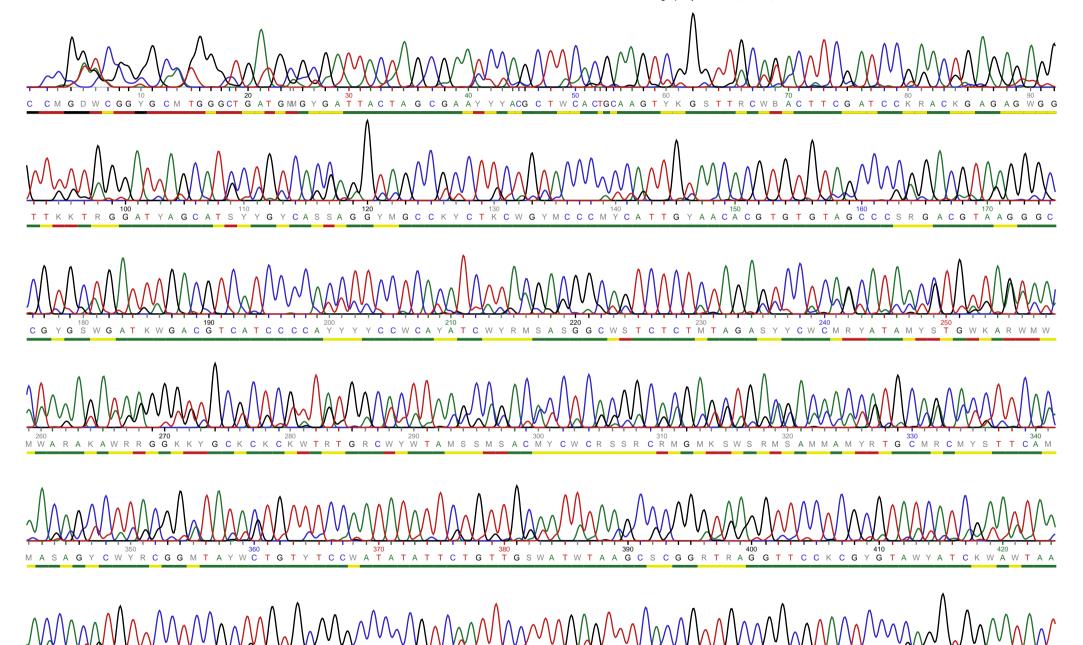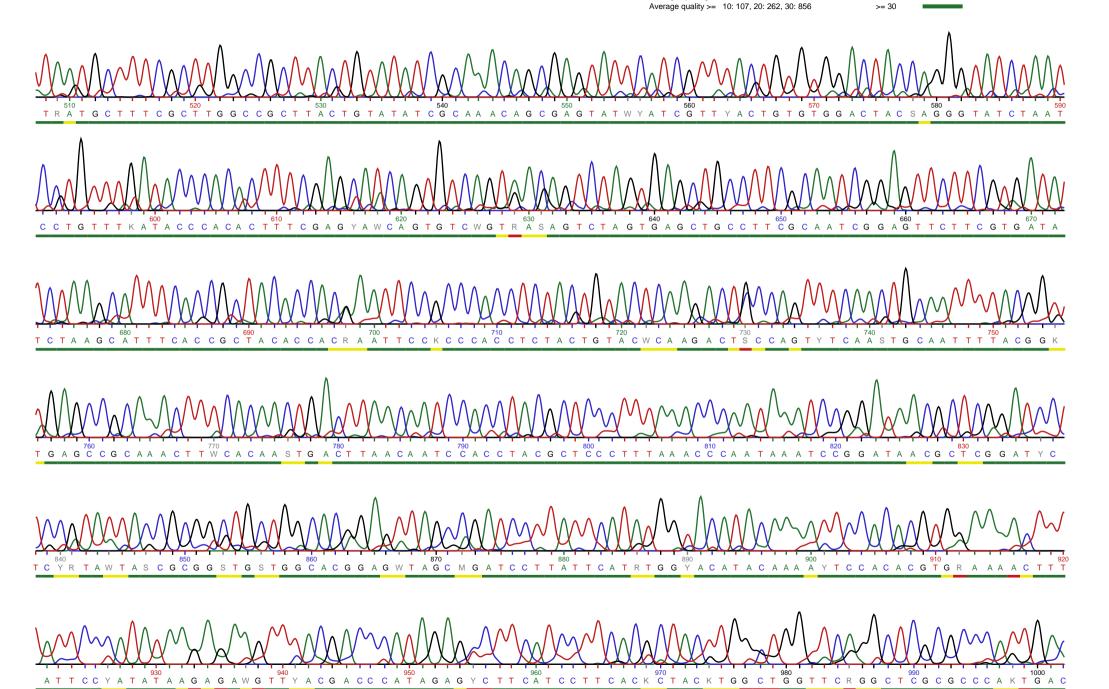
Samples: 14964
Bases: 1244
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Quality: 0 - 9
10 - 19
20 - 29
>= 30

11.10.2022

TRATGCTTTCGCTTGGCCGCTTACTGTATATCGCAAACAGCGAGTATWYATCGTTYACTGTGTGGACTACSAGGGTRATCTAAT

CCTGTTTKATACCCACACTTTCGAGYAWCAGTGTCWGTRASAGTCTAGTGAGCTGCCTTCGCAATCGGAGTTCTTCGTGATA

TCTAAGCATTTCACCGCTACACCACRAATTCCKCCCACCTCTACTGTACWCAAGACTSCCAGTYTCAASTGCAATTTTACGGK

TGAGCCGCAAACTTWCACAASTGACTTAACAATCCACCTACGCTCCCTTTAAACCCAATAAATCCGGATAACGCTCGGATYC

TCYRTAWTASCGCGGSTGSTGGCACGGAGWTAGCMGATCCTTATTCATRTGGYACATACAAAAYTCCACACGTGRAAACTTT

ATTCCYATATAAGAGAWGTTYACGACCCATAGAGYCTTCATCCTTCACKCTACKTGGCTGGTTCRGGCTCGCGCCCAKTGAC

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Samples:	14964
Bases:	1244
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CAATATTCCTCASTGCTGCCTCCCGTAAGAGTTTRSACCGTGTCTCAKTTCCARTGTGGGRGAYCTTCCTCTCAGAACCTCT

ATCCATCGTAGTCKTGGTGGGGCGTTACCCCGMCAAMAAACTARKGGAACKCATCCTCATCGATMACCGAAATTCTTTAAT

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