Sequence: SEQ10013680_B2_C10_0

Samples:	14407
Bases:	1201
Average spacing:	12.0
Average quality >=	10: 26, 20: 121, 30: 1046

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

CC CCR TCCG SRK CAT TCT GATCCA GYG ATTACTWG CAACTCYAACKTCATGCRRGYKASTTGCWGCCTGCARTCCKRACTGGSS ATCTG

TTTTRRRGG AK TTGCTYCWCCT CGCKKCTYCGCSGYCCKCTGWTCMSAYYATTGTAGCACGTGTGTAGCCCAKGTCATARGG

GGCATGATGATKWGAYSTCATCCCCAYYTTCCYCCRTAKTGTMTASGGSWSYCYCTCTAGAGYGCCMMWYTTWRYGGSKGGMMWM

TARRGGSRGGKKKTGCKCTCKKTGSGRGWYTTMMCCCMAYMTCTCAMSACAMGAKSWGAMSACMAMYRTGCMMCAYSTGTCTC

TSTGYTCCMRARRGAMWCTTYMTMTCTMTAGKCTCGWCAGAGKRTGTCRAGACCTGGTRAGGTTCTTCGCGKTGCTTCGWATT

AAAMCAYRTGCTCCGSTGCTTGTGCGGGTCCCCGTCAATTCCTTTGAGTTWCAACCTTGCGGTCGYACTCCCCAGGCGGARTG
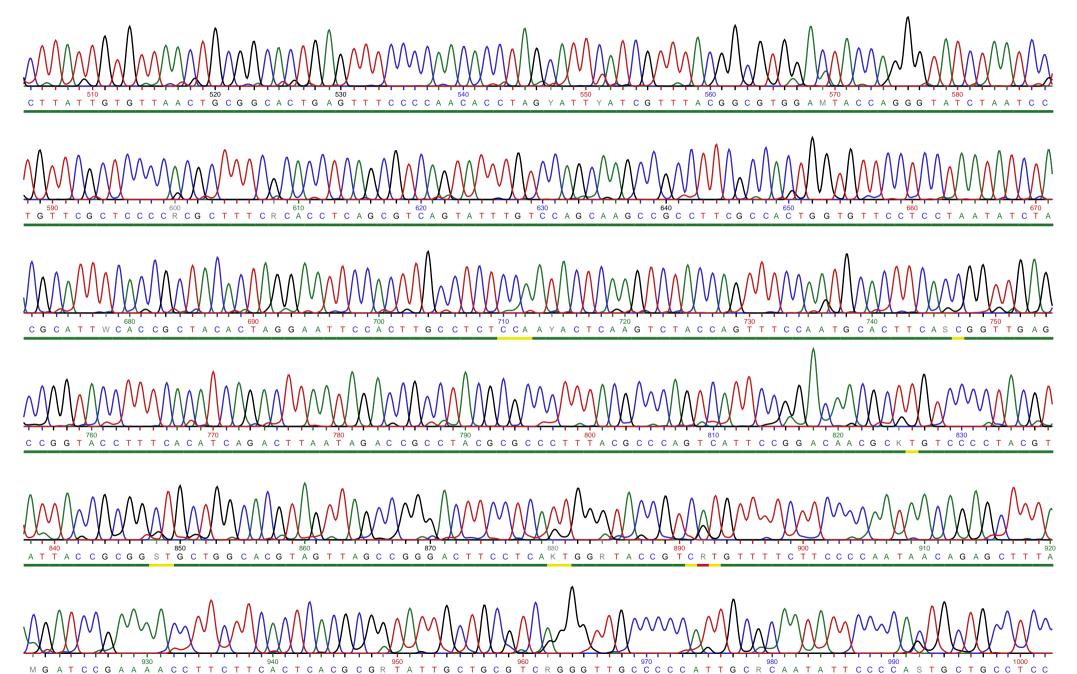
Sequence: SEQ10013680_B2_C10_0

Samples: 14407
Bases: 1201
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Quality: 0 - 9
10 - 19
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CTTATTGTGTTAACTGCGGCACTGAGTTTCCCCAACACCTAGYATTYATCGTTTACGGCGTGGAMTACCAGGGTATCTAATCC

TGTTCGCTCCCCRCGCTTTCRCACCTCAGCGTCAGTATTTGTCCAGCAAGCCGCCTTCGCCACTGGTGTTCCTCCTAATATCTA

CGCATTWCACCGCTACACTAGGAATTCCACTTGCCTCTCCAYACTCAAGTCTACCAGTTTCCAATGCACTTCASCGGTTGAG

CCGGTACCTTTCACATCAGACTTAATAGACCGCCTACGCGCCCTTTACGCCCAGTCATTCCGGACAACGCKTGTCCCTACGT

ATTACCGCGGSTGCTGGCACGTAGTTAGCCGGGACTTCCTCAKTGGRTACCGTCRTGTTTTCTTCCCCAATAACAGAGCTTTA

MGATCCGAAAACCTTCTTCACTCACGCGRTATTGCTGCGTCRGGGTTGCCCCCATTGCRCAATATTCCCCASTGCTGCCTCC

Sequence: SEQ10013680_B2_C10_0

Samples:	14407	Quality:	0 - 9
Bases:	1201		10 - 19
Average spacing:	12.0		20 - 29
Average quality >=	10: 26, 20: 121, 30: 1046		>= 30

11.10.2022

CGTAAGAGTCTGGACCGTGTCTCAGYTCCAGTGTGACCGTTCGCYCTCTCAGACCGGWTACCCATCGTCGCCTTGGTGGGCTG

TTATCTCACCAACTAGCTAATGGGACGCGGGTCCATCCTATGGCACCGGAGTTTTCATGATCTCGYCATGCGACAAAACCA

TAATATRAGGCTTTACTCCCAGTTTCCCGAAGGC