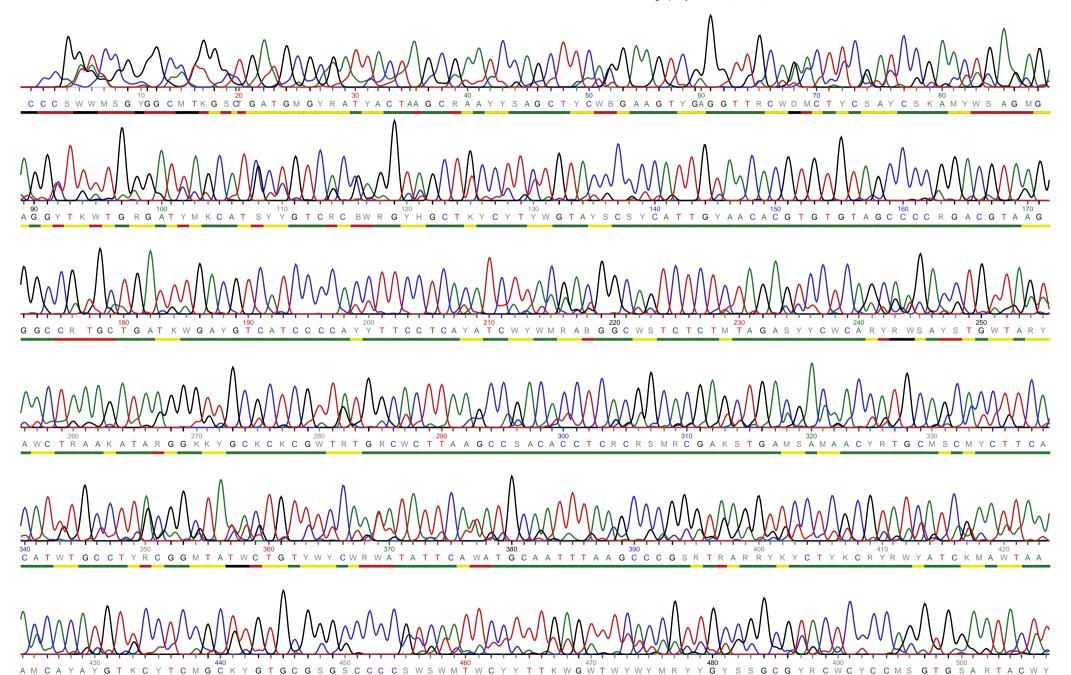Sequence: SEQ10013680_B2_G12_0

Samples:	14158
Bases:	1158
Average spacing:	13.0
Average quality >=	10: 134, 20: 298, 30: 702

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

CCCSWWMSGYGGCMTKGSCTGATGMGYRATYACTAAGCRAAYYSAGCTYCWBGAAGTYGAGGTTRCWDMCTYCSAYCSKAMYWSAGMG

AGGYTKWTGRGATYMKCATSYYGTCRCBWRGYHGCTKYCYTYWGTAYSCSYCATTGYAACACGTGTGTAGCCCCRGACGTAAG

GGCCRTGCTGATKWGAYGTCATCCCCAYYTTCCTCAYATCWYWMRABGGCWSTCTCTMTAGASYYCWCARYRWSAYSTGWTARY

AWCTRAAKATARGGKKYGCKCKCGWTRTGRCWCTTAAGCCSACACCTCRCRSMRCGAKSTGAMSAMAACYRTGCMSCMYCTTCA

CATWTGCCTYRCGGMTATWCTGTYWYCWRWATATTCAWATGCAATTTAAGCCCGSRTRARRYKYCTYKCRYRWYATCKMAWTAA

AMCAYAYGTKCYTCMGCKYGTGCGSGSCCCCSWSWMTWCYYTTKWGTWYWYMRYYGYSSGCGYRCWCYCCMSGTGSARTACWY

Sequence: SEQ10013680_B2_G12_0

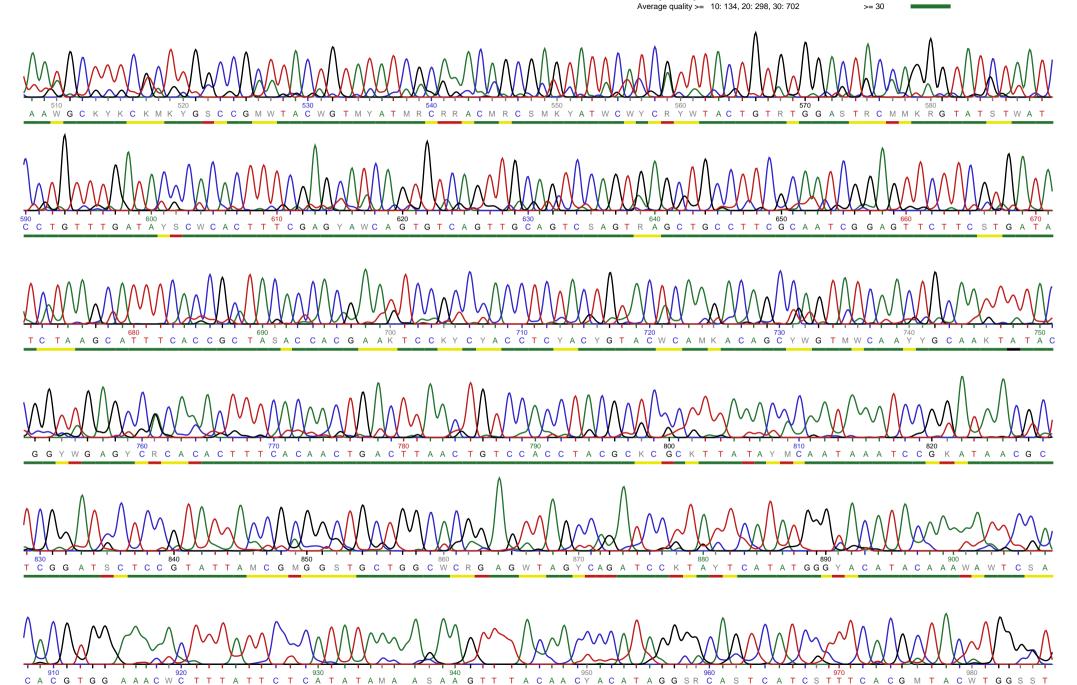| Samples: | 14158 |
Bases:	1158
Average spacing:	13.0
Average quality >=	10: 134, 20: 298, 30: 702

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

AAWGCKYKCKMKYGSCCGMWTACWGTMYATMRCRRACMRCSMKYATWCWYCRYWTACTGTRTGGASTRCMMKRGTATSTWAT

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TCTAAGCATTTCACCGCTASACCACGAAKTCCKYCYACCTCYACYGTACWCAMKACAGCYWGTMWCAAYYGCAAKTATAC

GGYWGAGYCRCACACTTTCACAACTGACTTAACTGTCCACCTACGCKCGCKTTATAYMCAATAAATCCGKATAACGC

TCGGATSCTCCGTATTAMCGMGGSTGCTGGCWCRGAGWTAGYCAGATCCKTAYTCATATGGGYACATACAAAWWTCSA

CACGTGGAAACWCTTTATTCTCATATAMAASAAGTTTACAACYACATAGGSRCASTCATCSTTTCACGMTACWTGGSST

Sequence: SEQ10013680_B2_G12_0

Samples:	14158
Bases:	1158
Average spacing:	13.0
Average quality >=	10: 134, 20: 298, 30: 702

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

11.10.2022

GG TT W C R G R C Y B Y G Y G C C C S A TT G A C C A A TA TT S C C T C A S T G C T G C C T C C C G T R R G A W Y TTT GG A A C M G T G TT C TT C A T Y

TT C C A A T G T K GGGG R G A A Y S TT K C C T C G T A A G A A C C T C C T A A T C M M A T C S R A A GG K TTT GG T G S A G C C K R TT W C C M T C C C C C

W A C Y G C C C T A