Sequence: SEQ10013680_B2_F05_0

Samples: 20966
Bases: 1754
Average spacing: 12.0
Average quality >= 10: 609, 20: 430, 30: 230

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

Page: 1 / 4
11.10.2022

Sequence reads:

```
  10        20        30        40        50        60        70        80        90
T G G G G C A T T T C C C G G C G A G G C A W W C C G G C S A S K K W Y K G A C T S G Y G K A T T A C T A C G G S A T Y Y Y A C G Y T T C R T G M K M A R Y K A G T T A C A K T C M T C M M T Y

       100       110       120       130       140       150       160       170       180
C G G A R S T A C R A H T A A K A T T W A W G A G R A W T A Y S K C C S A Y B Y T S K C G C K C G C T C W G C A M M Y M T T K T M T C A R Y C A T T G T A G C C C G Y G T

       190       200       210       220       230       240       250       260
G T T G C C C A G G A A T Y A T T S A G G G G C R T A C R T G A C S T A C C G T C G A T C C A C T C Y T T C C T C M K A T G T T M T C A T R K G C K S Y C C Y Y W C T

       270       280       290       300       310       320       330       340
W G T G T G C S S G G Y A T M C A A A A R R R G M T M C D S A K G G A T M W C W G D T G V G C G T G C S T C G C G R C T A G T T G A Y S T G M W Y W T A C A C M G M

       350       360       370       380       390       400       410       420       430
G A C G C C T C W C T G A C A C A A G S T R W S C R S C R C C R K G T C A Y C T C T C C K C W C A K C T A G K C A A G R C A G A A Y S W C M T C A C A C C S T G G T M T

       440       450       460       470       480       490       500       510
A T A T A T A S T G T C T G G A C C C G C T G G T G A G R T G T C G C G G T T G T S T G M A T A A C A T A T T A C A C M W S A Y Y C W C C R C G K T G T K G G G
```
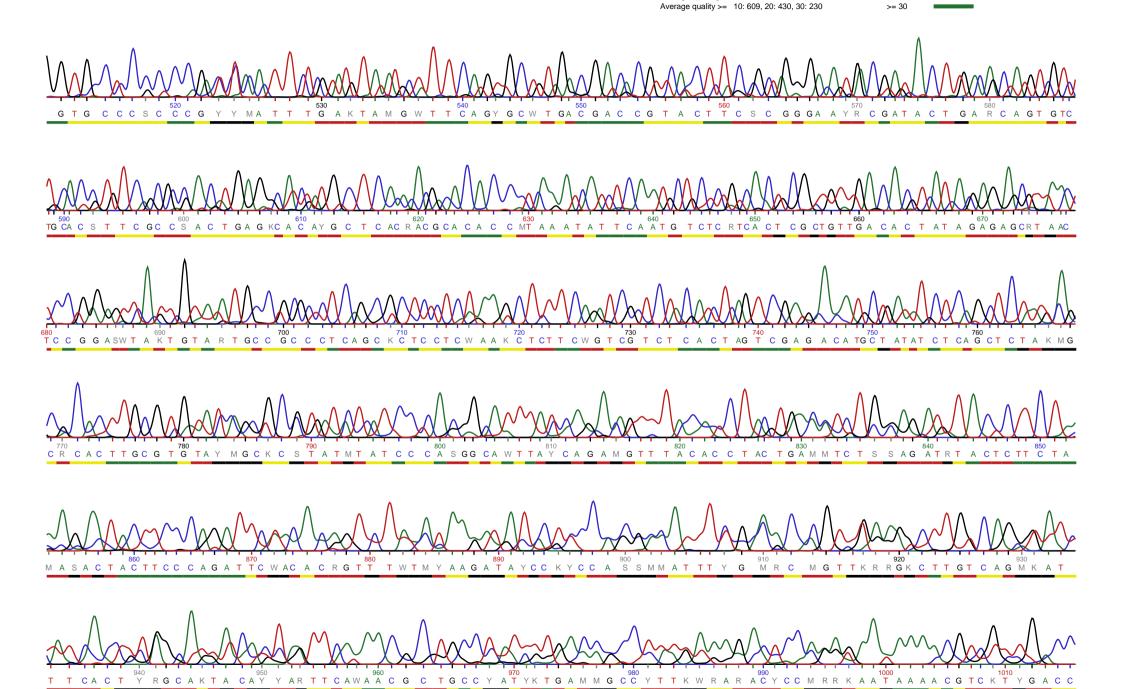
Samples: 20966
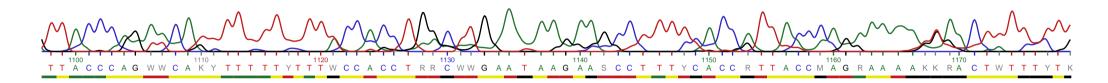Bases: 1754
Average spacing: 12.0
Average quality >= 10: 609, 20: 430, 30: 230

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

GTGCCCSCCCGYYMATTTGAKTAMGWTTCAGYGCWTGACGACCGTACTTCSCGGGAYRCGATACTGARCAGTGTC

TGCACSTTCGCCSACTGAGKCACAYGCTCACRACGCACACCMTAAATATTCAATGTCTCRTCACTCGCTGTTGACACTATAGAGAGCRTAAC

TCCGGASWTAKTGTARTGCCGCCCTCAGCKCTCCTCWAAKCTCTTCWGTCGTCTCACTAGTCGAGACATGCTATATCTCAGCTCTAKMG

CRCACTTGCGTGTAYMGCKCSTATMTATCCCASGGCAWTTAYCAGAMGTTTACACCTACTGAMMTCTSSAGATRTACTCTTCTA

MASACTTCCCAGATTCWACACRGTTTWTMYAAGATAYCCKYCCASSMMATTTYGMRCMGTTKRRGKCTTGTCAGMKAT

TTCACTYRGCAKTACAYYARTTCAWAACGCTGCCYATYKTGAMMGCCYTTKWRARACYCCMRRKAATAAAACGTCKTYGACC

Sequence: SEQ10013680_B2_F05_0

Samples:	20966
Bases:	1754
Average spacing:	12.0
Average quality >=	10: 609, 20: 430, 30: 230

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

CCACMTAACRGTMTGTACSCGGYGGKTCAYGCCTSGGCCACGYTWGGKTTAGCCSGGKGGKTCGYYCCWWKACTTCWWKRG

TTACCCAGWWCAKYTTTTTYTTTWCCACCTRRCWWGAATAAGAASCCTTTYCACCRTTACCMAGRAAAAKKRACTWTTTYTK

GCAWMMTCCACCGSCSGGGYCSGTCCKGMTTGTCAATCCARGGGTTTGTTTCSGCMCSCTATTTTGGYCGGCCACATTRATT

TCCCCCCCACSGGGGCGTGGGGCCCCCCCCGATAAAAGGAATTTTTTGGGGAGGSCCGTGTGGTTYYTCYWTSTCTCC

CCCWAAAYTTGGGTGGCCCCCCGGSWMCCCCCCCCCTTCTTCCAARGGGGTTGCGGGGGCTTAGCCTTGGARTTCCCT

TTCCCCCCCTTTTTGGRGTAAAAMSCCCCSGTTTTTTCCCCTTTTTTACCCCMCARAASCTTTRAAGMGCWTAAAAATC

Sequence: SEQ10013680_B2_F05_0

Samples:	20966
Bases:	1754
Average spacing:	12.0
Average quality >=	10: 609, 20: 430, 30: 230

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

11.10.2022

CCCASAGAAGGSSCGGGGGGGGGGCMCCCAATMTRTTTWTAGWTTAACMCMCMCCRMGAGAAAAT TTTTT TTTTTCCATCCC

CRTCWGGGGTGATATTATTATRKGWGGMAMMAYYAMWGTGGGGGGGGCCSMTYTTAAYGTGGCGCGGRTTATTTATTRGRSMRG

AGGSTKTTMTTTTTCCYAAAAMGTTGKGTTTGGGBGCCCCCCTCAAGTATAAAABAAGGGGGGWGGGGTTTACCMCMCA