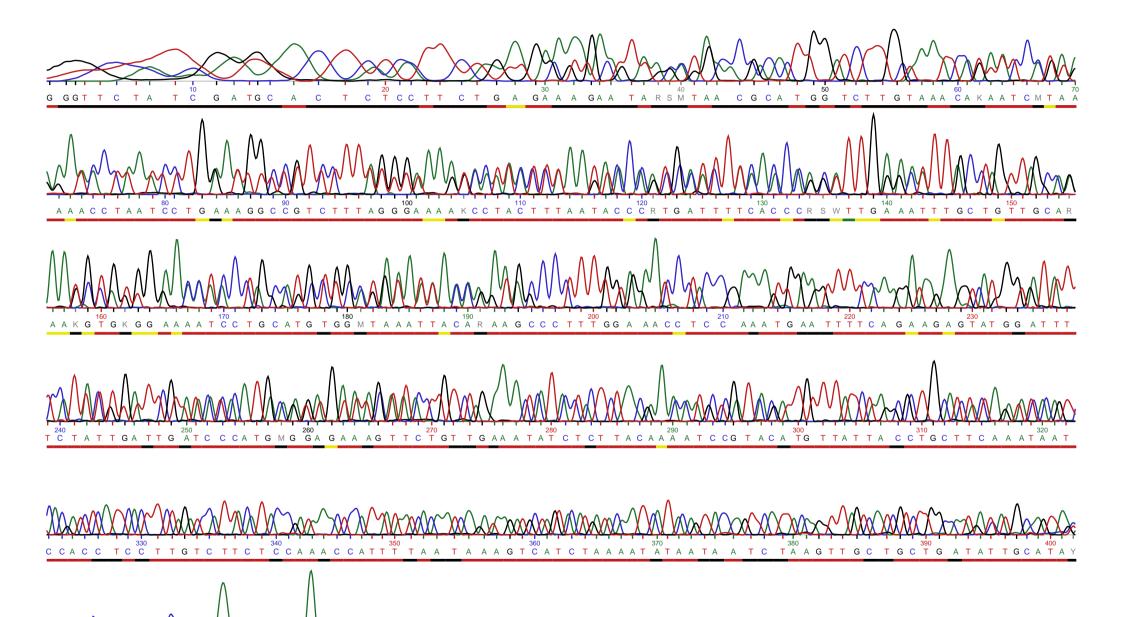
СС

C C W C C A A



440

T C C A G T G

Samples:

Average spacing:

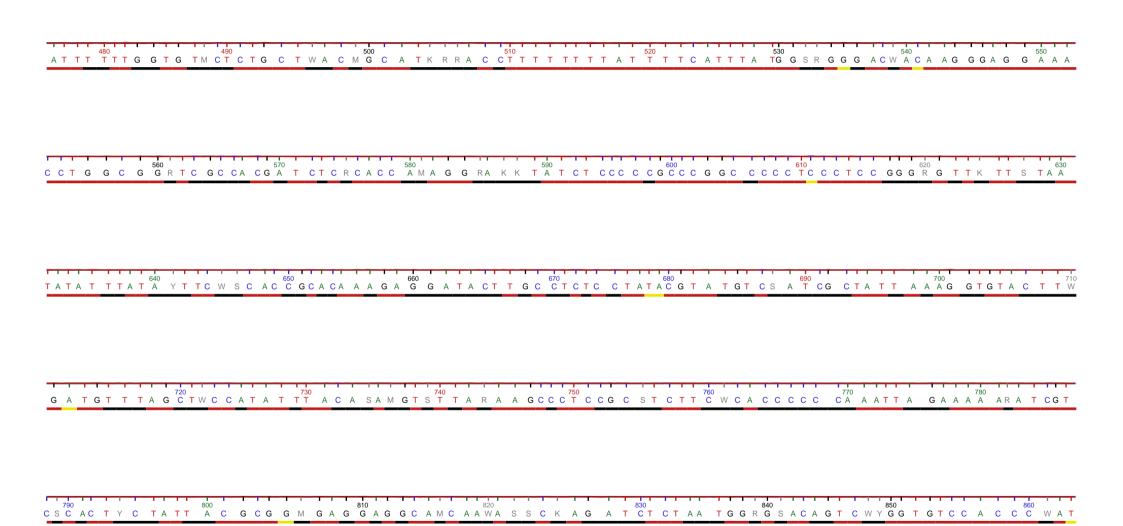
1150

W C C C C G G C C G G C C C A C

14.0

Average quality >= 10: 653, 20: 87, 30: 7

Bases:



ARCAYAGCTAACG ACCCCAAAACKCACTTRC MM TKAC ASGC WAT GC CTG C TT S GG TK T M C C C S Y K T G G RW AAWAWAC

Sequence: SEQ10012873 A1 B04 0 Samples: 16045 1150

Bases: Average spacing: 14.0

Average quality >= 10: 653, 20: 87, 30: 7

10 - 19 20 - 29

Quality: 0 - 9

>= 30

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