Sequence: SEQ10012052_B1_A08_0

Samples: 15856
Bases: 430
Average spacing: 37.0
Average quality >= 10: 305, 20: 30, 30: 3

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

09.08.2022

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

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

R A A K G T G K G G A A C C T C C T G C A T G C T G C T A A A T A A C C R A A G C C C T T T T G A A A C C T C C G A A T G A A T T T T C A G A A G A G T A T G G A T T

T T C T A T T G A T T G A T C C C A T G C A K A G A A A C T T C T G T T G A A A T A T C T C T T A C R A A A T C C G T A C A T T T T A T T A C C T G C T T C A A A T A A T

C C A C C A T C C T T G T C T T C T C C A T A C C A T T T A C C A C A A A G T C A T C T A A A A T A T A A T A C A T C A T C R T T A T A T G C T G C T A T T G C A T A

Y T G C C A A A A C C C C A C M C C W C C A

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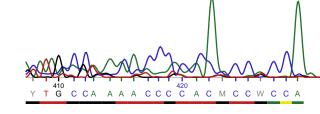Average quality >= 10: 305, 20: 30, 30: 3

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