Sequence: SEQ10012873_A1_G12_0

Samples:	20150
Bases:	459
Average spacing:	44.0
Average quality >=	10: 131, 20: 128, 30: 153

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

TTTGYYTTTYRRAAKKWAACCTTTMMTCAMTTTCTAGWWGGDAAWGAATTARGGMKRRMMCGACACYTGGATCTTGCAAGTCATATCCAKWRAA

TCCTAATCTTGGATGGCCTTCCTTAKKKWAARKACTACTCWAAKWMCMRTGMWCTWMAMCMRSWTTGRRMWTTGCCWGTTGC

ARAAKSYGTKGRAMMWCCTGCMTGYKSMKRWAWWAMYGATGCCCTTTGTAGACCTCCGAAATGAGTTTCAAGAGAGCTGG

TATATTCTAYTGTTGTATCTAATGCAGAGWATGCTTCTKCWGAAATATCCCTWACAACTGYGTACATGTTATCAGCCTGCTT

CTAATTAATCCAYYATMYTYGTCTTCTACCAAATCTTTATAAAMAAAATCGTCTAAAATATCATACATCATAAGTTGTATG

YTGCATATTGCATAGAABCBKAAAWCOWCACACCCDC

Sequence: SEQ10012873_A1_G12_0

Samples: 20150
Bases: 459
Average spacing: 44.0
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