Sequence: SEQ10013680_B2_B11_0

Samples:	12787	Quality:	0 - 9
Bases:	445		10 - 19
Average spacing:	29.0		20 - 29
Average quality >=	10: 20, 20: 29, 30: 383		>= 30

TTTGYYTTTYSGRTGGTARCCTTCATCATTTCTGATGGAGAATACGTTAGCTGCACCACATTGATCTTGTAAATCGTAACCGWAGAAT

CCTAATCTGGAATGTTGWTCTTTGTGTAAGTACATAGCTAAGTACCATGCGCTTAAACCAGTTTGAGCATTACCAGTAGCGAAT

GCRRTAGATGCACCAGCTGCTGCGGAAATTACGGAAKCTCTTTGAGATCCACCGAAGTGAGTTTCRAGTARTGCTGGGTATTC

TTCGTATTGTTCTAATGCGTAKAATGCAACTTCAGAACCTACATCAAGAACAGTGTCCATGTTGTTAGGTGCTTCAGTTAATCC

ACCATATTTGTCTTCTACATARTCTTTACCATAGWAAGTAAAGTCATCTAATACATCATCAGTATATGCTGCAKTAGCATAYT

GHGTRAAHCCDACHCCDCCAAG

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