Sequence: SEQ10013680_B2_H11_0

		Quality:	0 - 9		Page: 1 / 3
Samples:	13882		10 - 19		11.10.2022
Bases:	1149		20 - 29		
Average spacing:	13.0		>= 30		
Average quality >=	10: 105, 20: 223, 30: 799				

```
CCCGWHCGGSGMMTGGGYGATGMGGYGATTACTAAGCGAKAYCBAGCTYCWSGAAGTCKGGTTRCWKACTTCSAYCCDAMYKGAGASAG

GCTKKWRGGATTRGCATSCYKYCACSWRGYWGCBWYCYKCTGYRCCCCYCATTGYAACACGTGTGTAGCCCSRGACRTARGG

GSCGTGSWGAYKWGAYGTCRTCCCCAYYTTCCTCAYATCWYAMGASGGCWSTCTCTMYAGASYYCWCAGYRTGAYSTGWKAGWM

WCTRAAKATMRGGKKYGCKCKCGWTATGGCDHTTAMGCMGACAYCTCRSGGCRMGAKSTGAMSACARMYRTGSMSCAYCTKCA

YATTTGYCWTAMSRMTATACYGTTTCCAATATAYTCAWATGCRATTTAAGCCCGGGTAAGGTTCCTCGCGTRWCMTCGAATTA

AACCAYATGTTCSTCCGCKTGTGCGGGCCCCCGTCAATTCCTTTGAGTTTCACCGTTGCCGGCGTACTCCCCAGGTGGAATA
```

Sequence: SEQ10013680_B2_H11_0

Samples:	13882		Quality:	0 - 9			Page: 2 / 3
Bases:	1149			10 - 19			11.10.2022
Average spacing:	13.0			20 - 29			
Average quality >=	10: 105, 20: 223, 30: 799			>= 30			

CTTAATGCTTWCGCTTGGCCGSTTACTGTATATCGCAAACASCGAGTRTTCATCGTTTACTGTGWGGACTACCAGGGTATCT

AATCCTGTTYGATACCCACRCTTTCGAKCATCAGYGTCAGTTRYRGTCCAGWGAGCYGCCTTCGCMAYCGGWGTTCTTCSTG

ATATCTRMGYATTYCACCGCTACACYACGAATTCCRCCYWCCTCTACTGTACTCAAGASWGCCRGTATCAAMWGCRRWTTKA

CGGTTGAGCCGCRRACTTWCAYAACTGACTTAACTGWCCACCTACGMTCGCTTTACACCCAATRAATCCGGATAACGCTCG

SATCMTMCRTATTACCGCGGCTGCTGGCACRKAGTTAGCCGATCCTTATTCAKATGGTACATACAAAWAKCCACACGTGGA

YCRCTTTATTCCBATATAAAASAAGTTTACAWYCYATAGGGCAGTCATCYTTCACGCTACKTGGCTSGCTCAGACTCTMGT

Sequence: SEQ10013680_B2_H11_0

Samples:	13882
Bases:	1149
Average spacing:	13.0
Average quality >=	10: 105, 20: 223, 30: 799

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

11.10.2022

C Y A Y T G A C C R A T A T Y C C T C A S T R S T R Y C T C S C G T A G G A T T T T R G A C C G W G T C T S A C Y T C C A R T G T G G G R G A A C C T T C C T C T C A

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