Sequence: SEQ10013680_B2_B12_0

		Quality:	0 - 9	
Samples:	12141		10 - 19	
Bases:	447		20 - 29	
Average spacing:	28.0		>= 30	
Average quality >=	10: 16, 20: 27, 30: 394			

CTTGCCYTTYSRRTGKTAACCTTMMTCATTTCTGATGGAGAATACGTTAGCTGCACCACATTGATCTTGTAAATCGTAACCGTAGAATC

CTAATCTGGAATGTTGTTCTTTGTGTAAGTACATAGCTAAGTACCATGCGCTTAAACCAGTTTGAGCATTACCAGTAGCGAATG

CAGTAGATGCACCAGCTGCTGCGGAAATTACGGAAGCTCTTTGAGATCCACCGAAGTGAGTTTCAAGTAATGCTGGGTATTCTT

CGTATTGTTCTAATGCGTAGAATGCAACTTCAGAACCTACATCAAGAACAGTGTCCATGTTGTTAGGTGCTTCAGTTAATCCA

CCATATTTGTCTTCTACATARTCTTTACCATAGTAAGTAAAGTCATCTAATACATCATCAGTATATGCTGCAGTAGCATAYTGH

GTRAAHCCAACVCCDCCAAAGA

Sequence: SEQ10013680_B2_B12_0

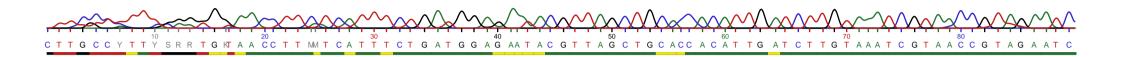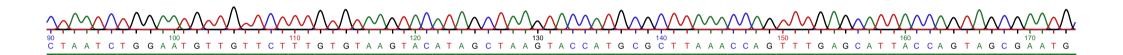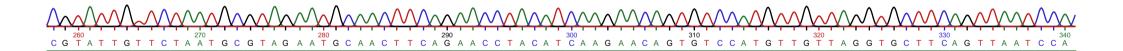| Samples:	12141	Quality:	0 - 9
Bases:	447		10 - 19
Average spacing:	28.0		20 - 29
Average quality >=	10: 16, 20: 27, 30: 394		>= 30

Samples: 12141
Bases: 447
Average spacing: 28.0
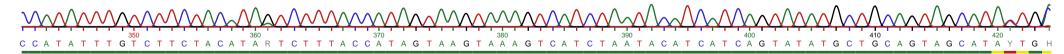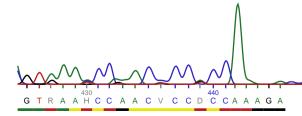Average quality >= 10: 16, 20: 27, 30: 394

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