Sequence: SEQ10012873_A1_A04_0

Samples: 18768
Bases: 447
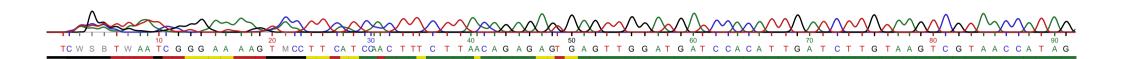Average spacing: 42.0
Average quality >= 10: 20, 20: 24, 30: 393

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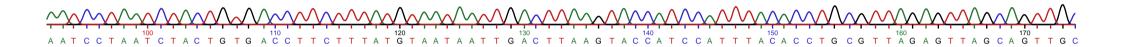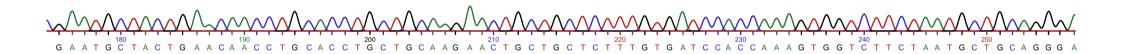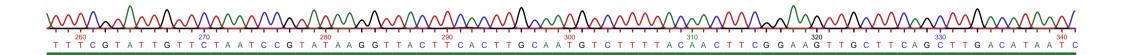10 - 19
20 - 29
>= 30

TCWSBTWAATCGGGAAAAGTMCCTTCATCCAACTTTCTTAACAGAGAGTGAGTTGGATGATCCACATTGATCTTGTAAGTCGTAACCATAG

AATCCTAATCTACTGTGACCTTCTTTATGTAATAATTGACTTAAGTACCATCCATTTACACCTGCGTTAGAGTTAGCAGTTGC

GAATGCTACTGAACAACCTGCACCTGCTGCAAGAACTGCTGCTCTTTGTGATCCACCAAAGTGGTCTTCTAATGCTGCAGGGA

TTTCGTATTGTTTCTAATCCGTATAAGGTTACTTCACTTGCAATGTCTTTTACAACTTCGGAAGTTGCTTCAGCTTGACATAATC

CACCATATTTACCTTCTACGTARTCTTTACCATAGTAAATGAAGTCATCTAATATTTCATCTGTGTATGCTGCTGTAGCATAY

TGHGTRAAHCCAWACTCCDCCA

Sequence: SEQ10012873_A1_A04_0

Samples:	18768
Bases:	447
Average spacing:	42.0
Average quality >=	10: 20, 20: 24, 30: 393

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

Samples: 18768
Bases: 447
Average spacing: 42.0
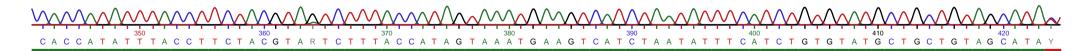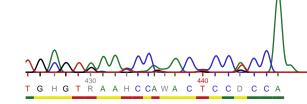Average quality >= 10: 20, 20: 24, 30: 393

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

Sequence: SEQ10012873_A1_A04_0

Samples: 18768
Bases: 447
Average spacing: 42.0
Average quality >= 10: 20, 20: 24, 30: 393

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

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