FastQC Report

Tue 19 May 2015
skewer_SW042-trimmed-pair1.fastq

Summary

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- Per tile sequence quality
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- Per base sequence content
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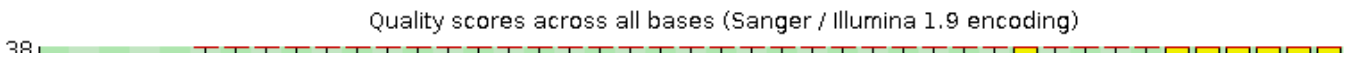
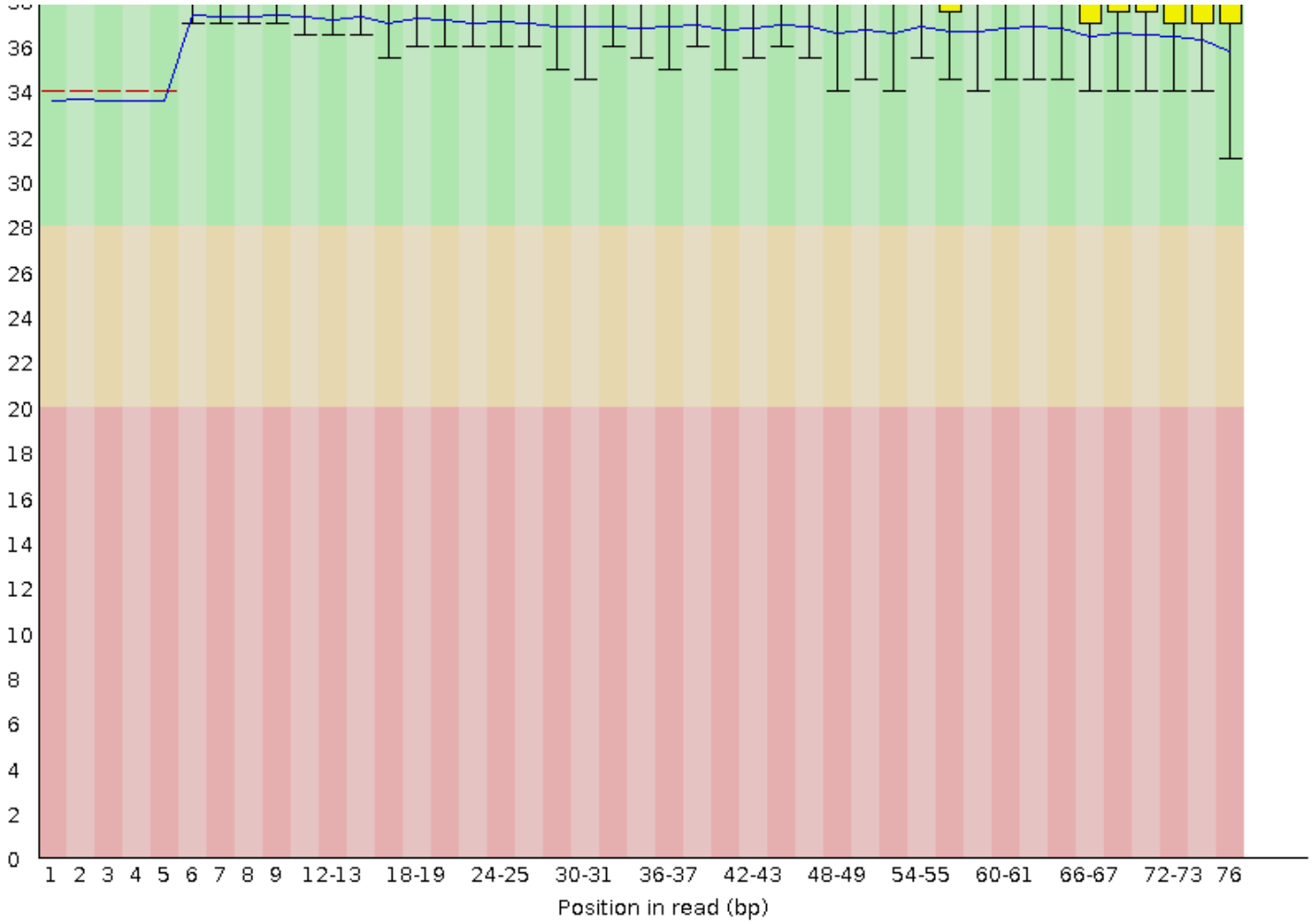
Basic Statistics

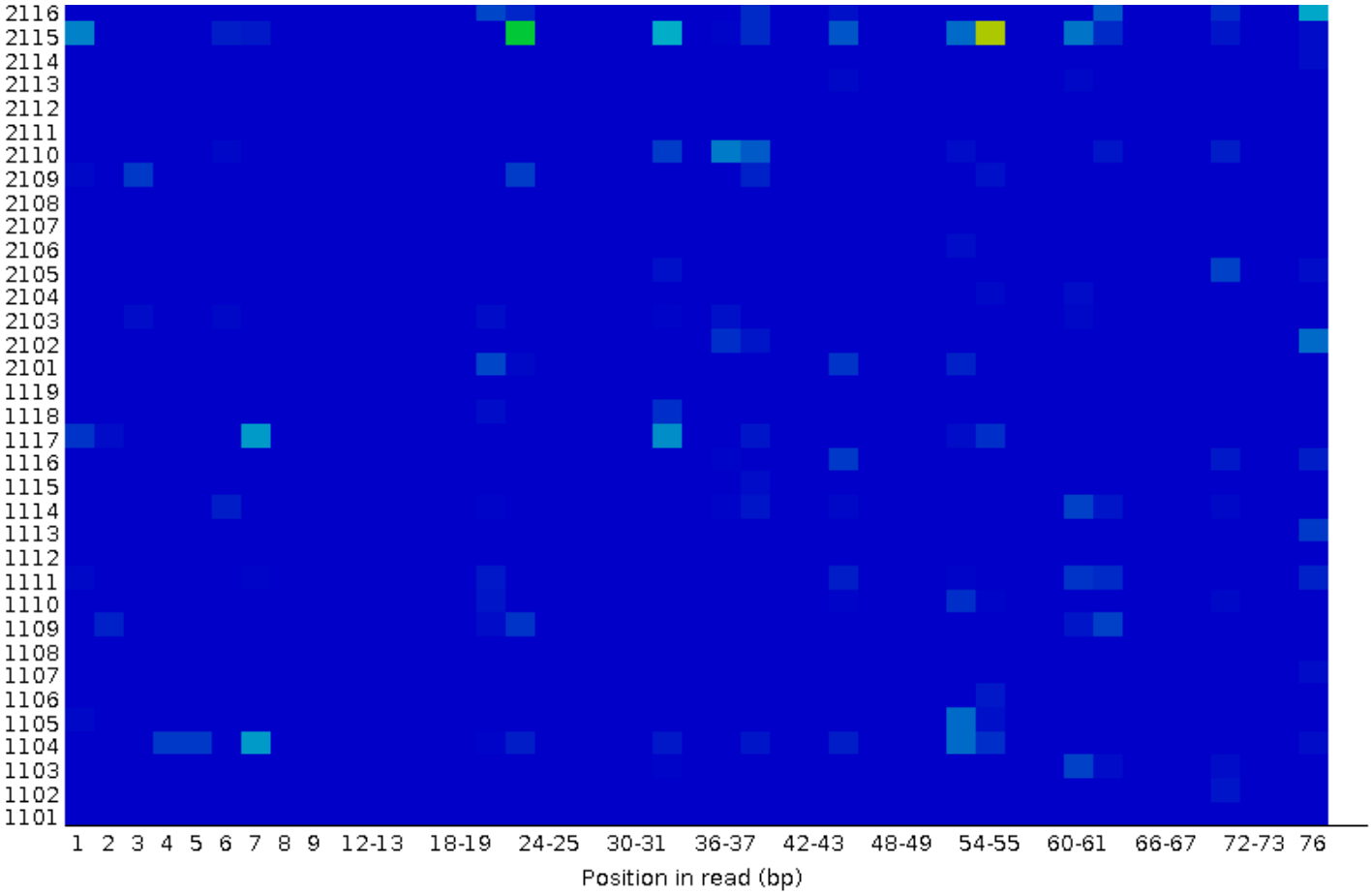
Measure	Value
Filename	skewer_SW042-trimmed-pair1.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	730
Sequences flagged as poor quality	0
Sequence length	56-76
%GC	42

Per base sequence quality

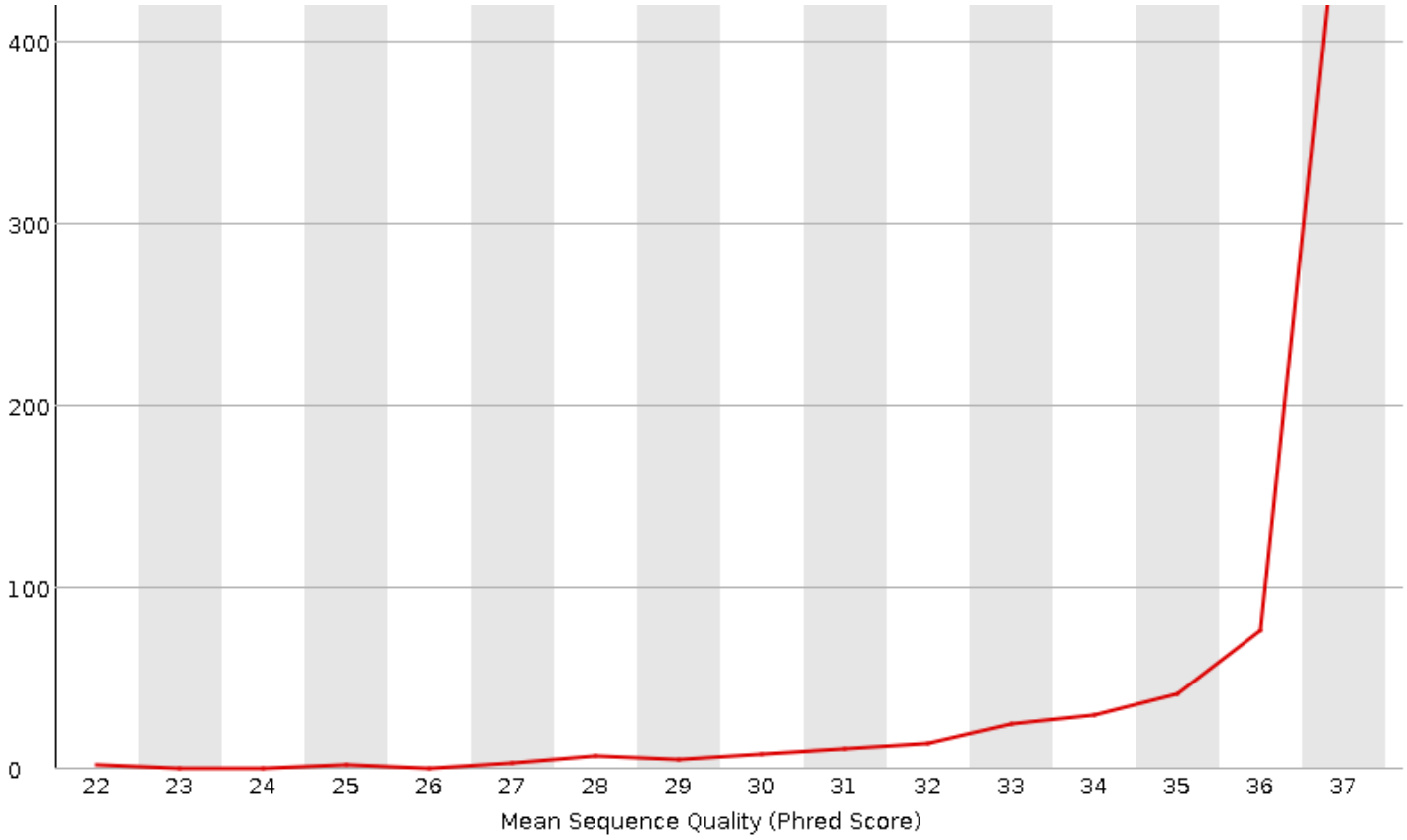




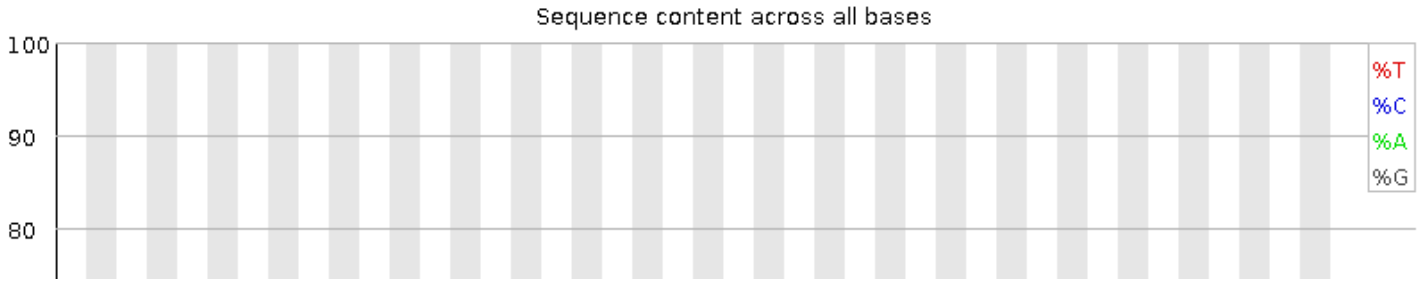
Per tile sequence quality

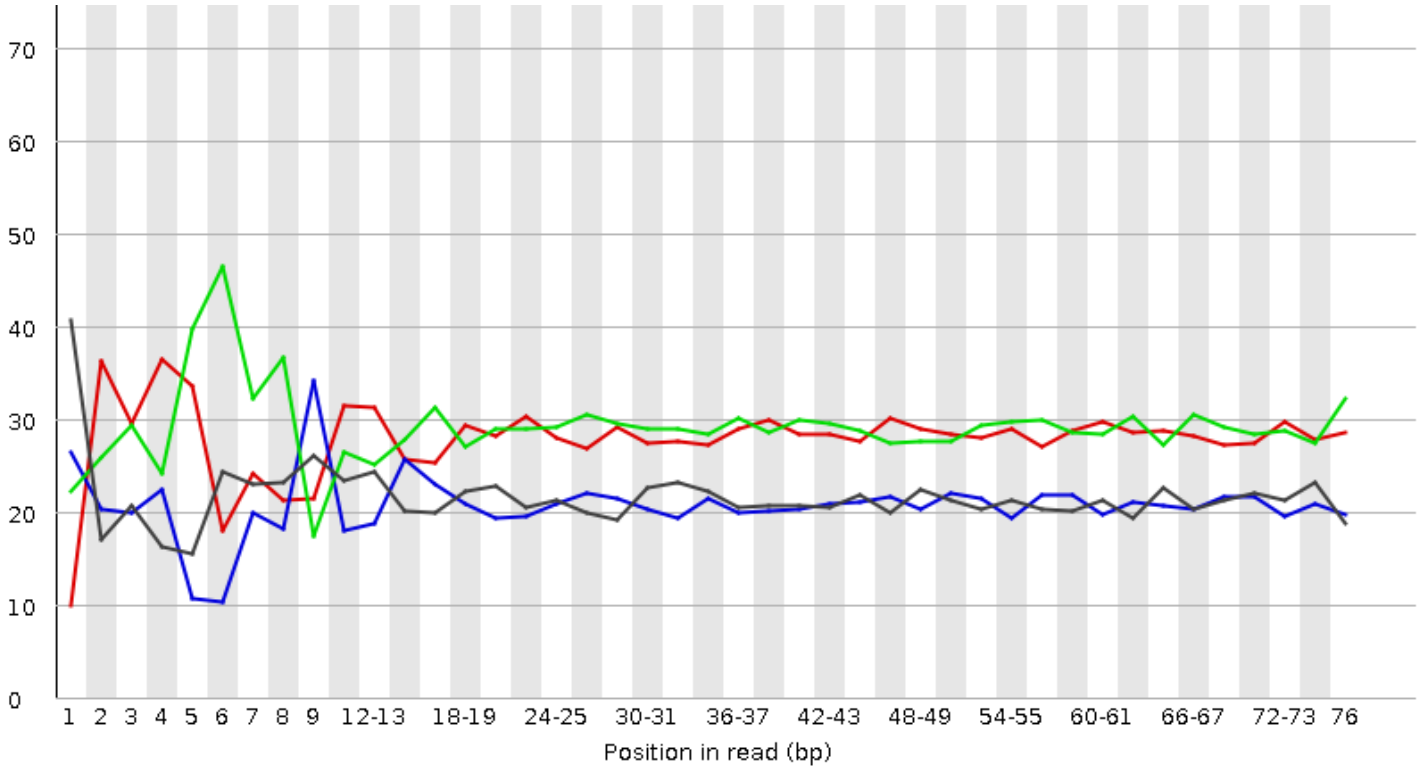


Per sequence quality scores

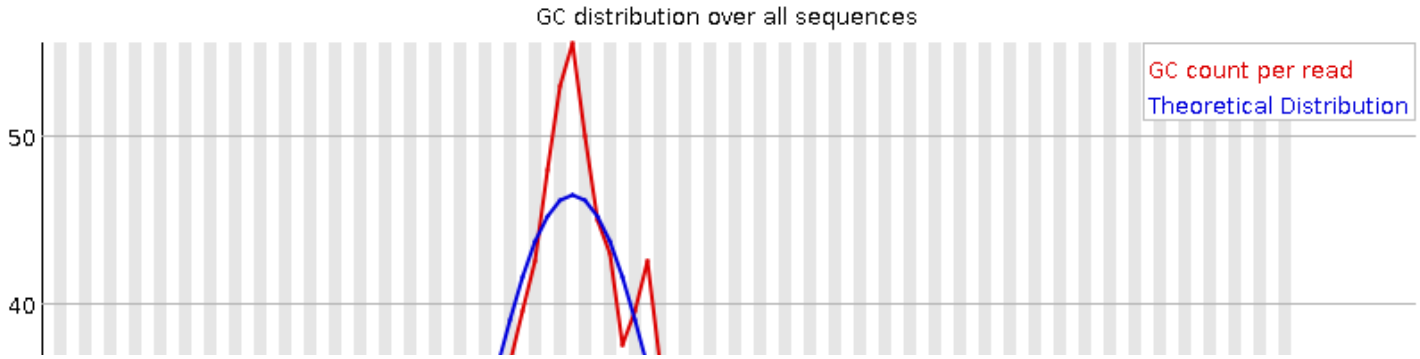


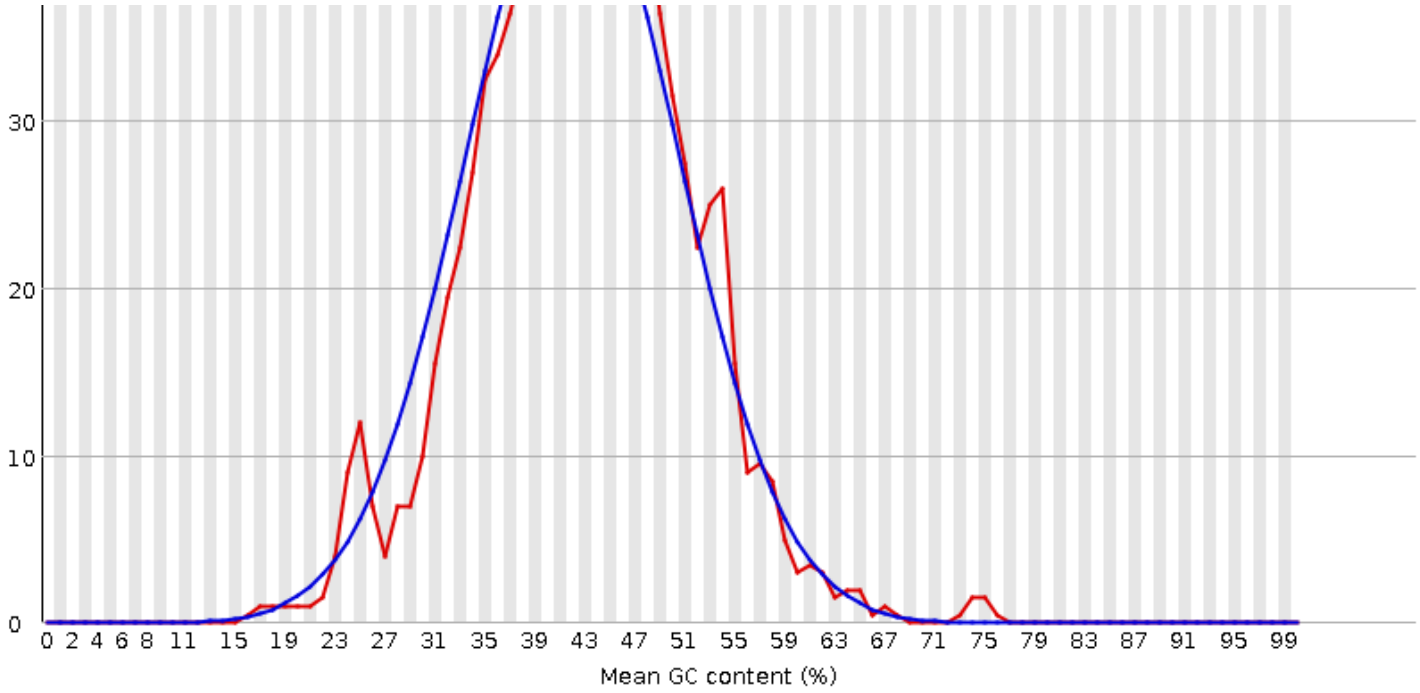
Per base sequence content



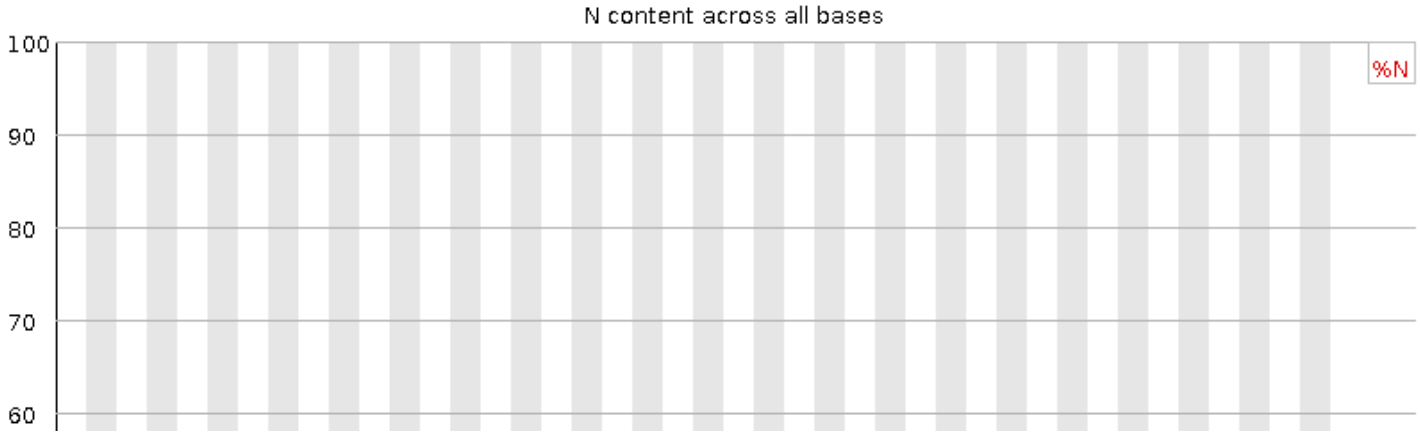


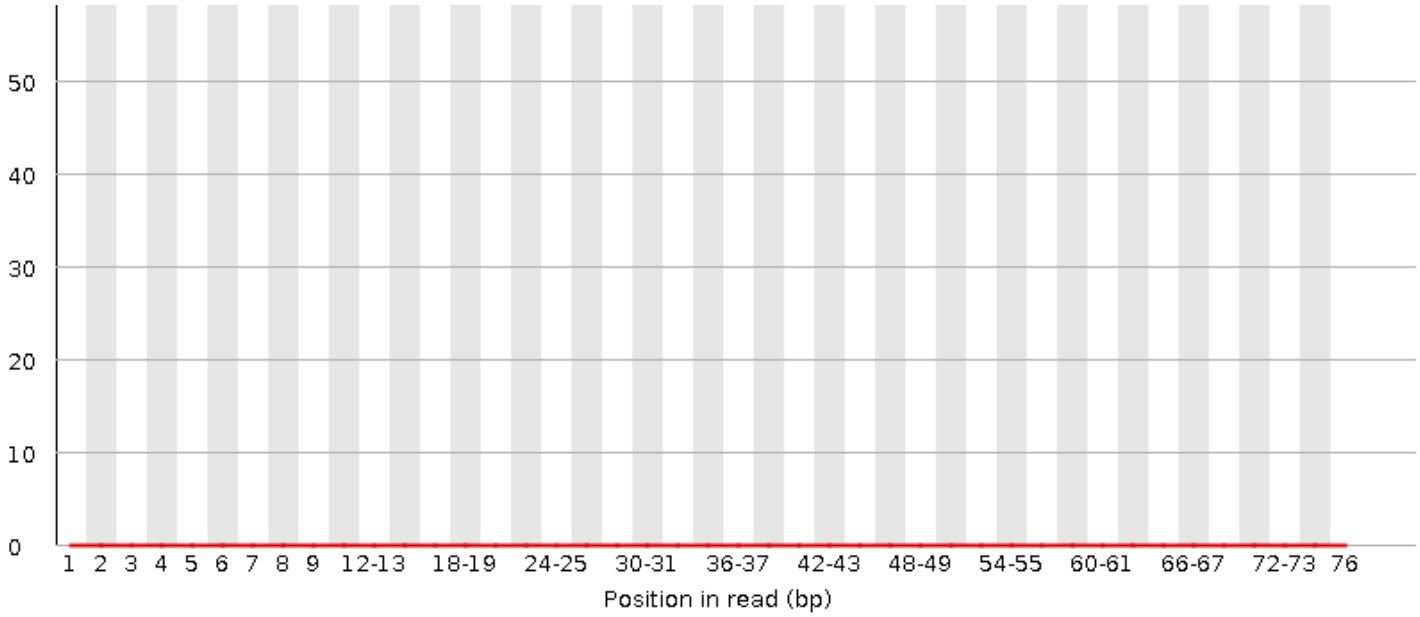
Per sequence GC content



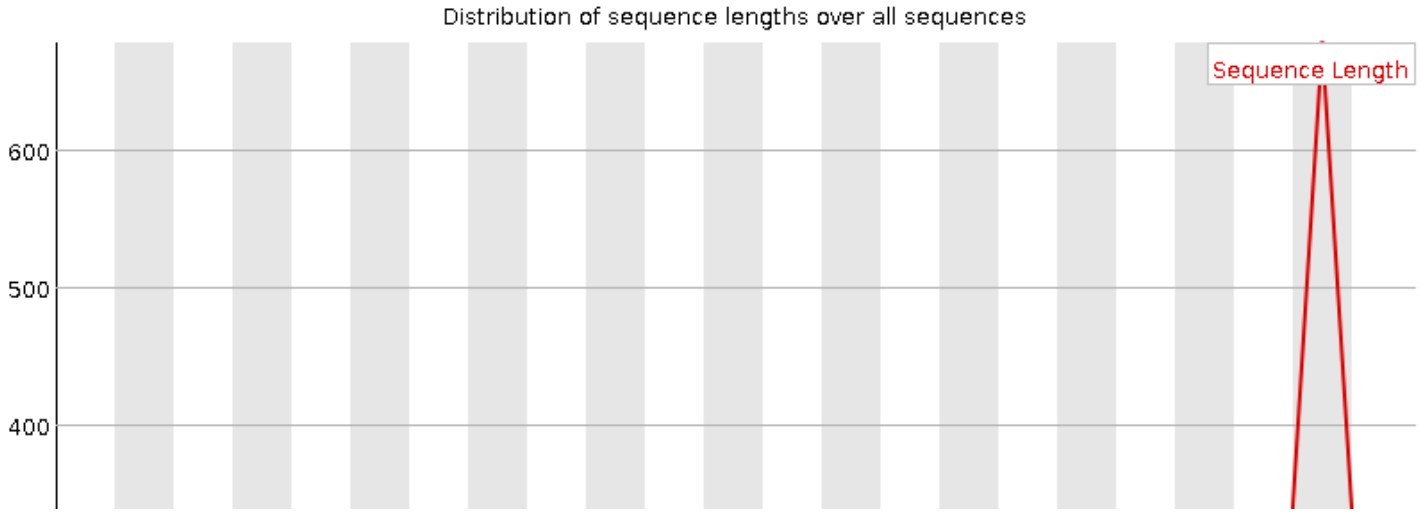


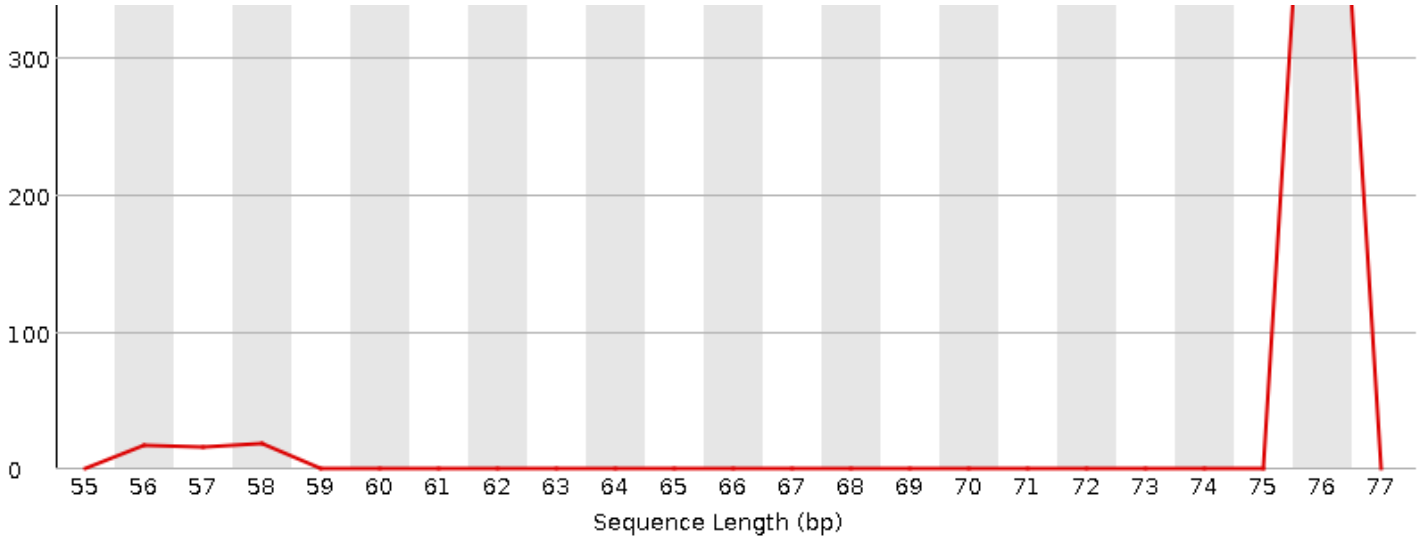
Per base N content



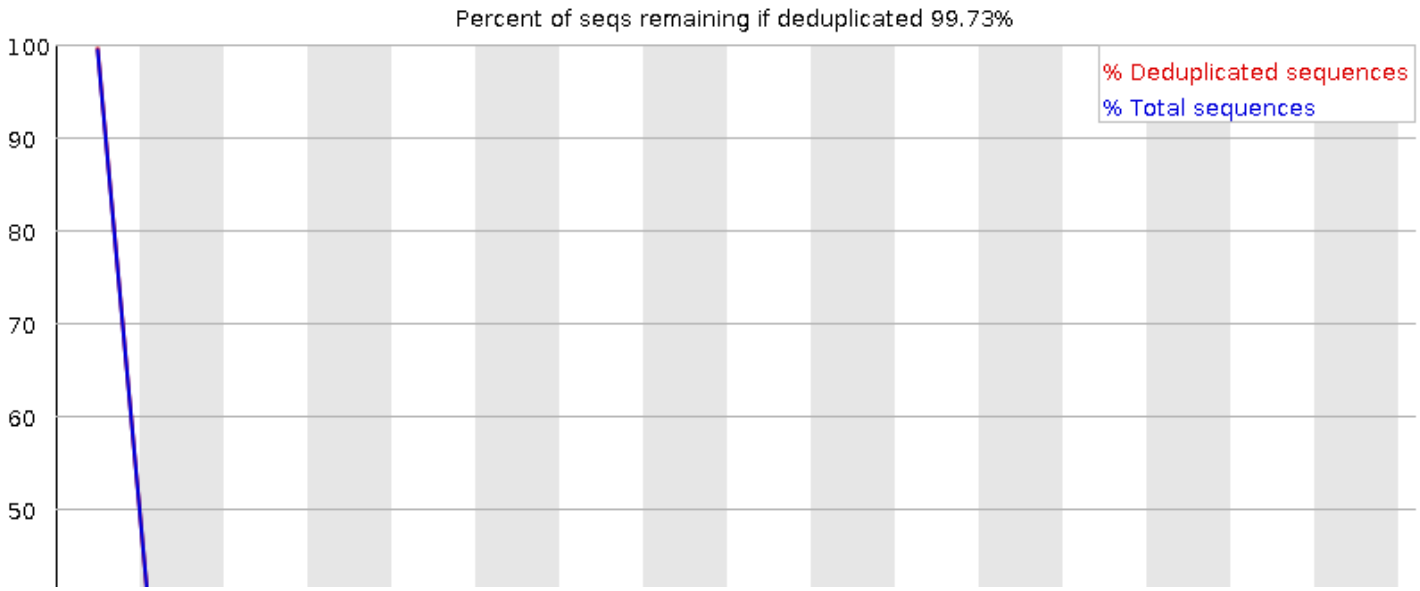


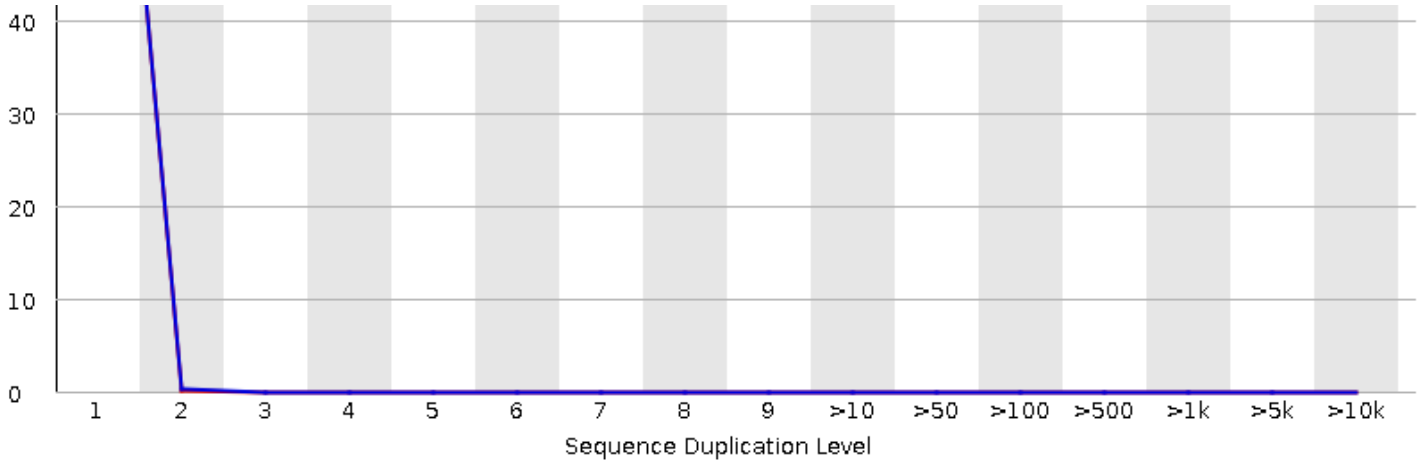
Sequence Length Distribution





Sequence Duplication Levels





Overrepresented sequences

Sequence	Count	Percentage	Possible Source
CTTATAGAGAATACACACAGGATAAAGAGGTTTAACATTGTCAATGTAGC	2	0.273972602739726	No Hit
GCAAACCAAAGAGAGCCAGTCTGGTCCGCTTAGCGACCATACTAGGGATAACAGGGT	2	0.273972602739726	No Hit
CTGAGGAATGACTTGTGTTGTATCTTGTGGGCCGGGGTTTTCTGGCCCAG	1	0.136986301369863	No Hit
ACATAGTAGTCATTAATTTAACATAGTATTGAATTATGACATGCATATCC	1	0.136986301369863	No Hit
GGAGAGTGTGAACCAGTTCTTCTACATGTCAACTATTGTCGAATGTCTGT	1	0.136986301369863	No Hit
CATCAGTCTGATCCTATCTCCTCAGTCTGCTACTATCTCATTAGTCTGAT	1	0.136986301369863	No Hit
TATAAATGTTATGTGCATCCAATTGTCACAGGCAATAAGCATTTGTAAAT	1	0.136986301369863	No Hit
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ATTATTAAGTTTAGAAATTCTTTGGTTTTTGTTGATATTGTTGATATTGT	1	0.136986301369863	No Hit
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CTATTACCCTGTTATTCCTATCTTCTACTACGAAACTTTTTACTCTTGCCTCACTC	1	0.136986301369863	No Hit
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GTAAAAATCCATAGACACAATTACACAAACCTGCTTGACAGTAATTACGT	1	0.136986301369863	No Hit
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GCCAGTGTCCTTCCACGAGAAGCTGTACGGAAGCGTACAGCGCCTTGAGT	1	0.136986301369863	No Hit
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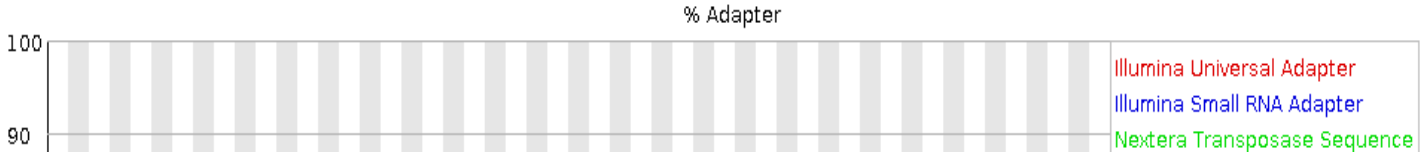

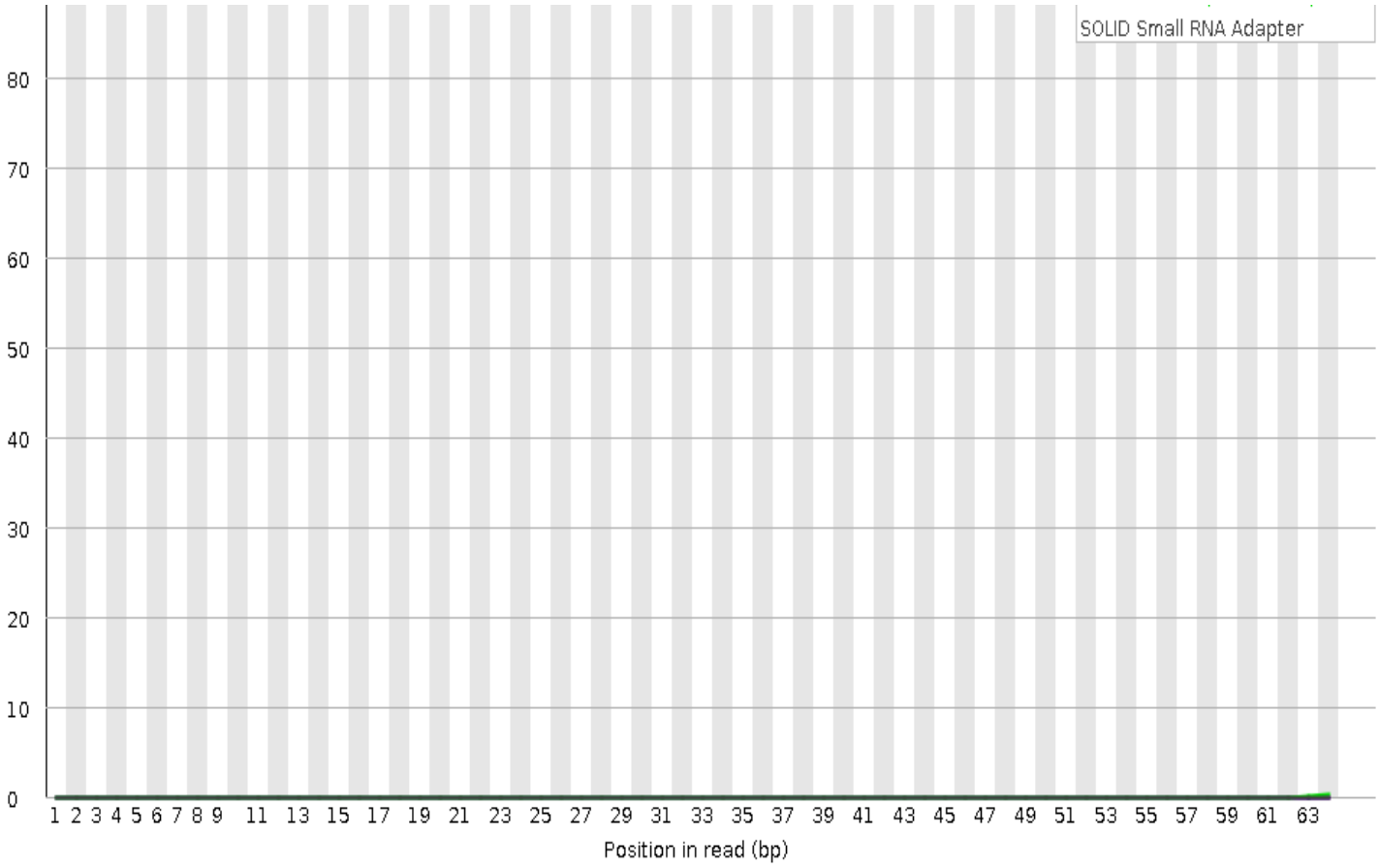

Kmer Content

No overrepresented Kmers

Produced by FastQC (version 0.11.3)