FastQC Report

Tue 19 May 2015
skewer_SW042-trimmed-pair2.fastq

Summary

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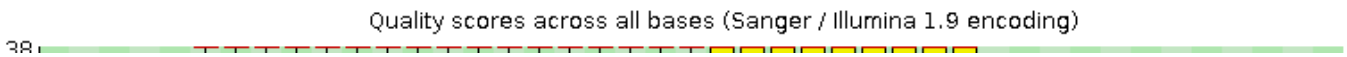
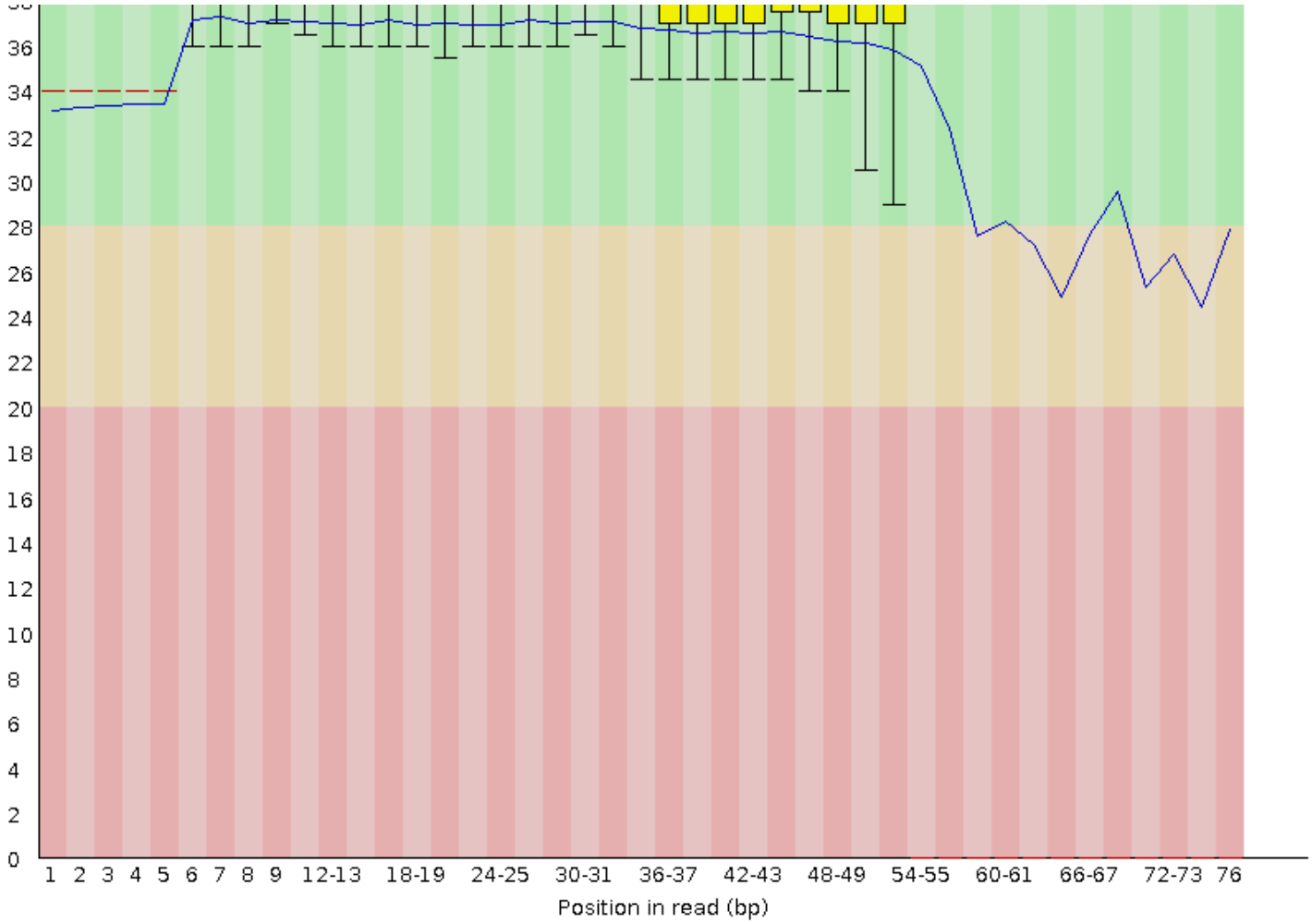
Basic Statistics

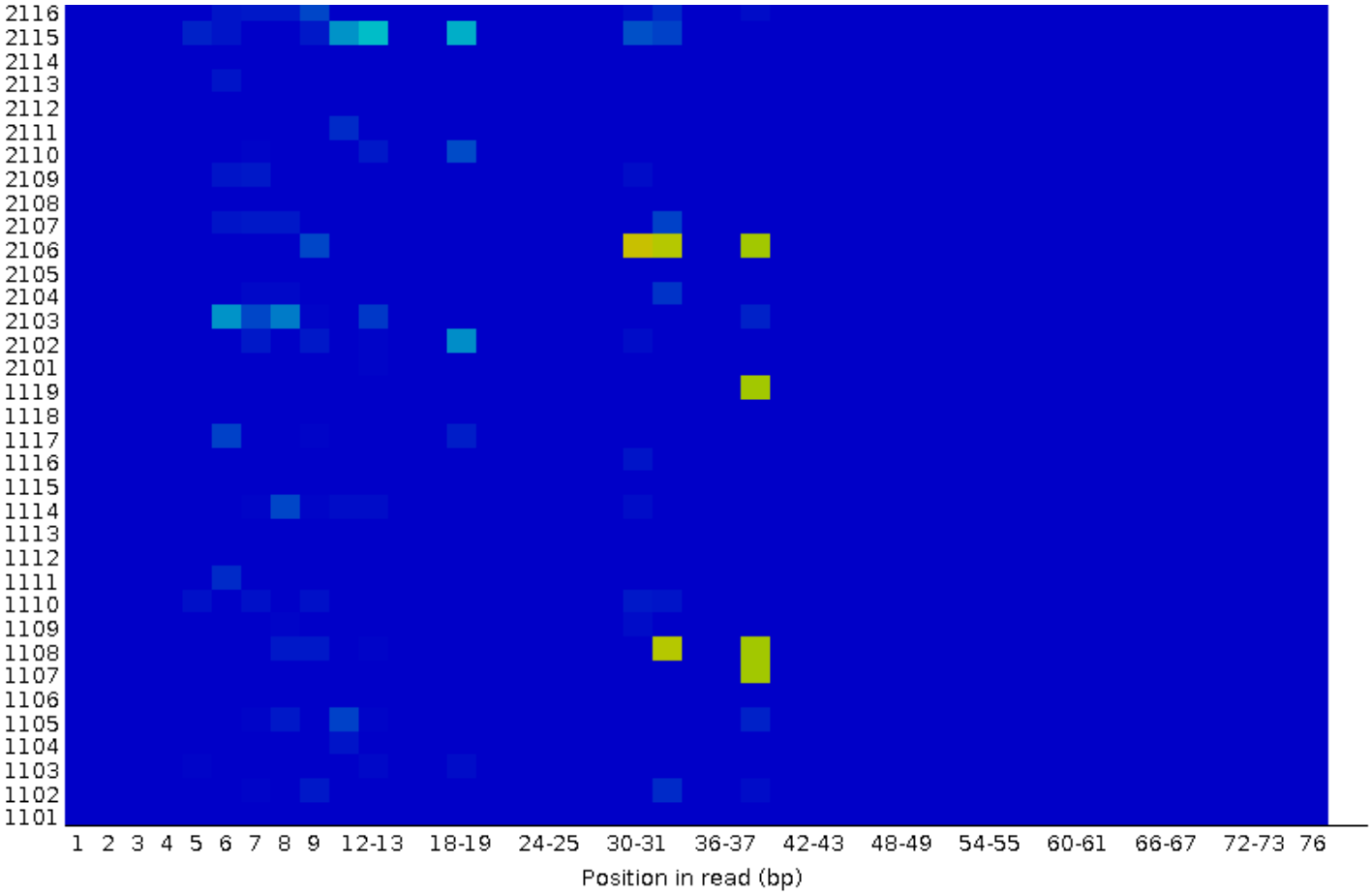
Measure	Value
Filename	skewer_SW042-trimmed-pair2.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	730
Sequences flagged as poor quality	0
Sequence length	29-76
%GC	42

Per base sequence quality

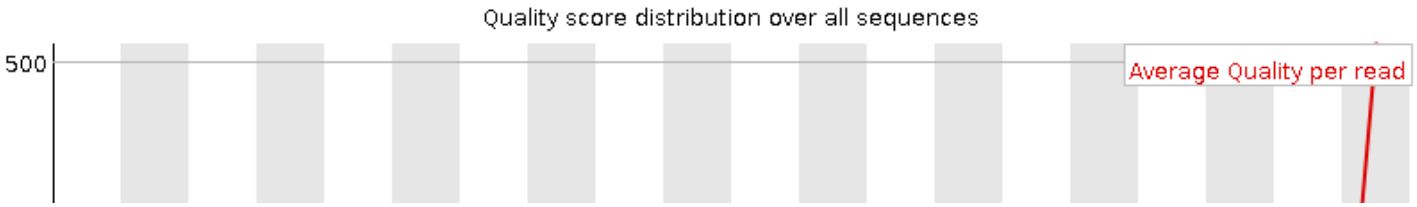


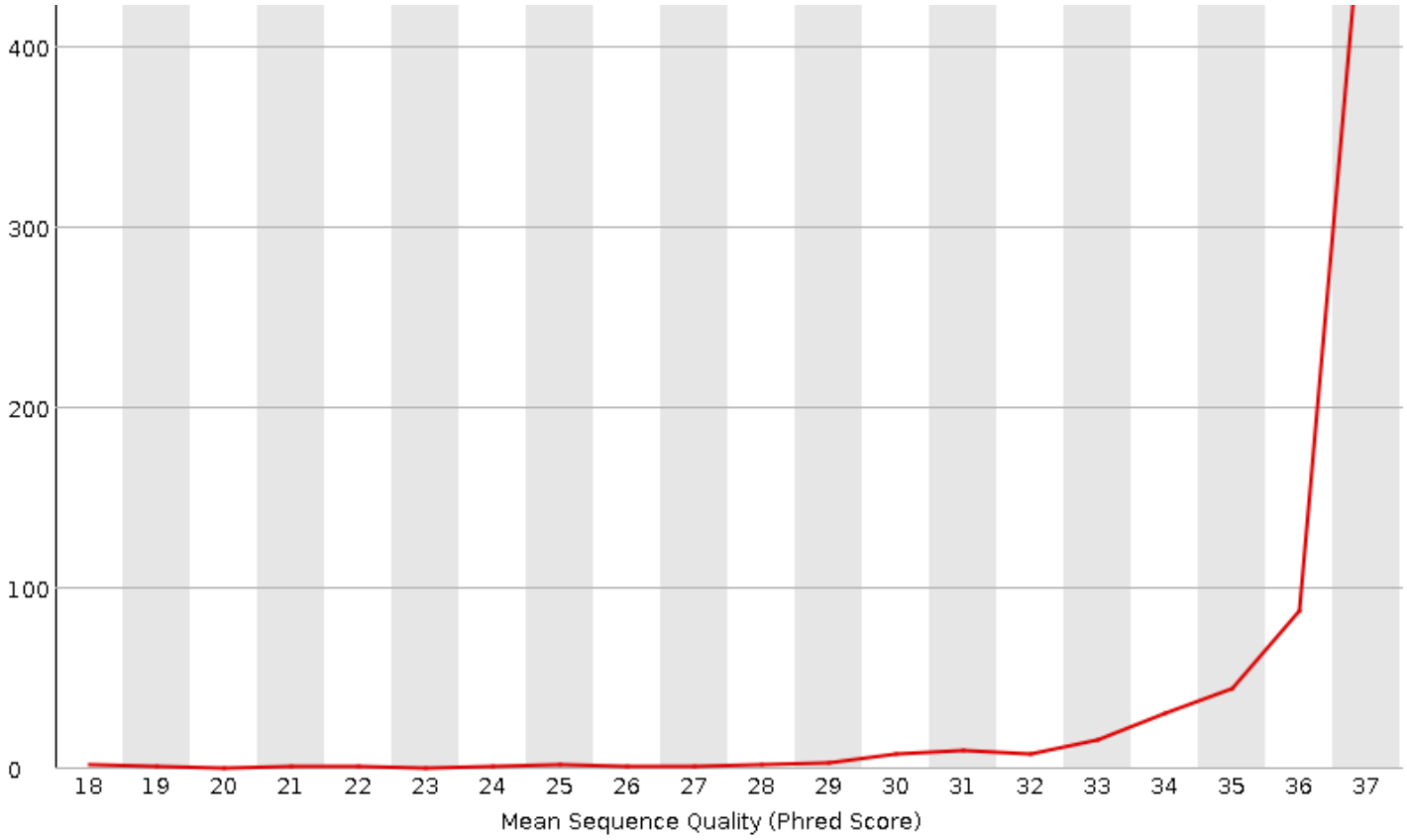


Per tile sequence quality

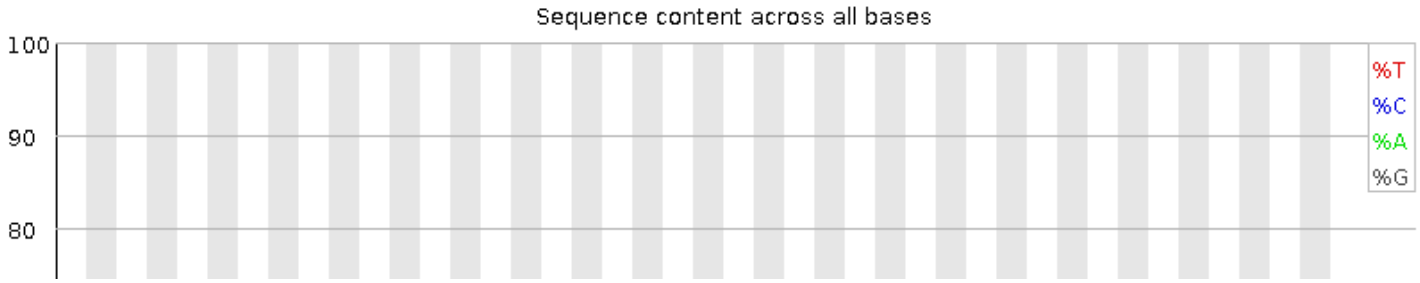


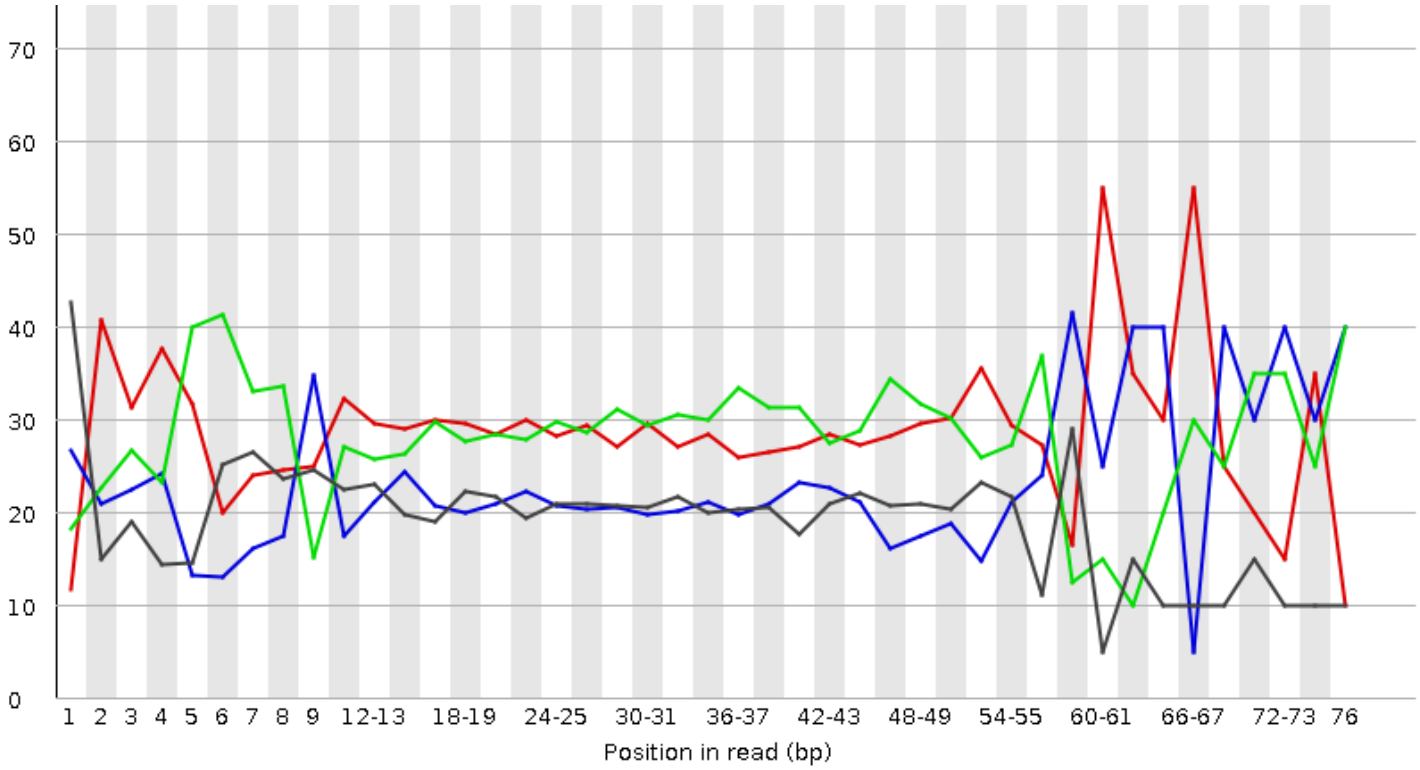
Per sequence quality scores



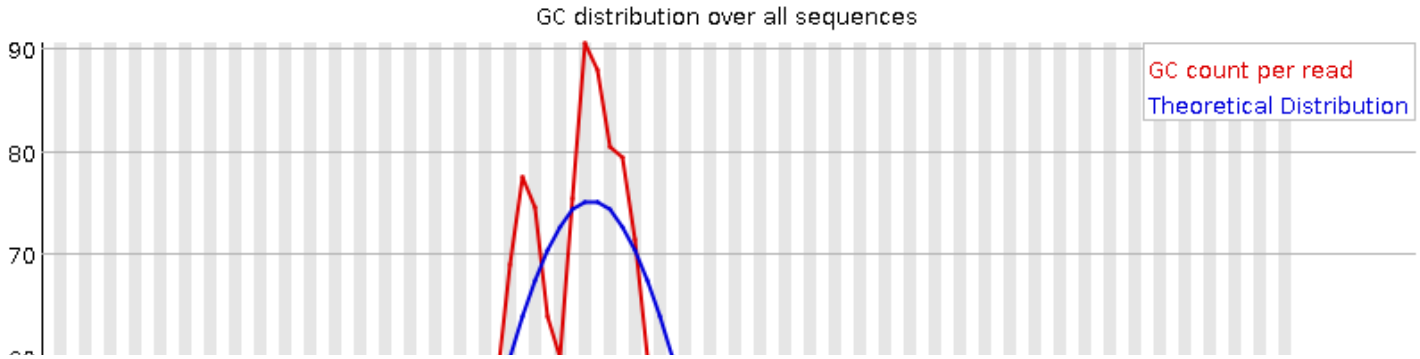


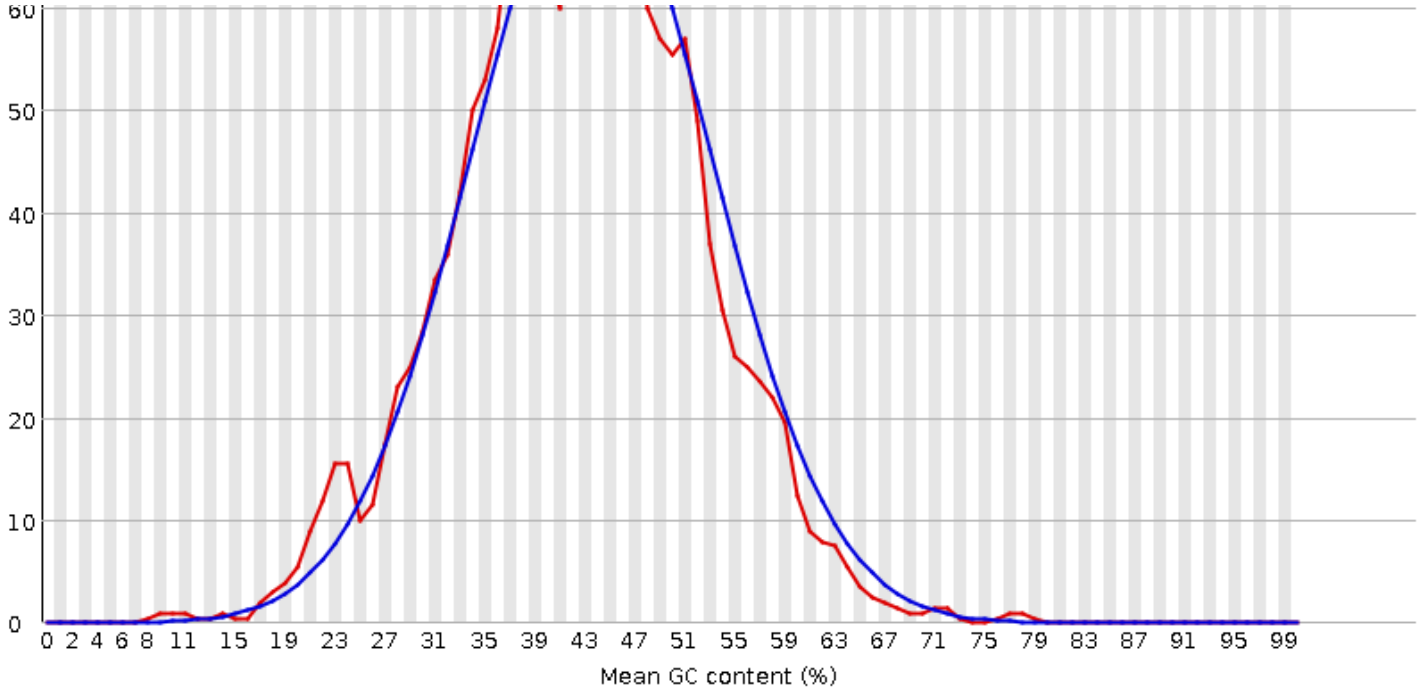
Per base sequence content



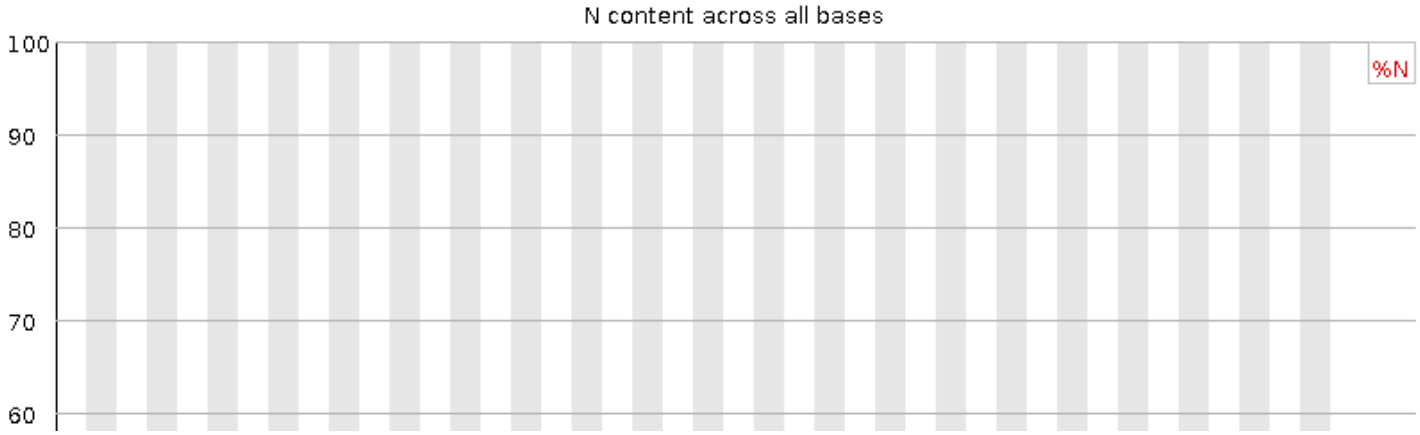


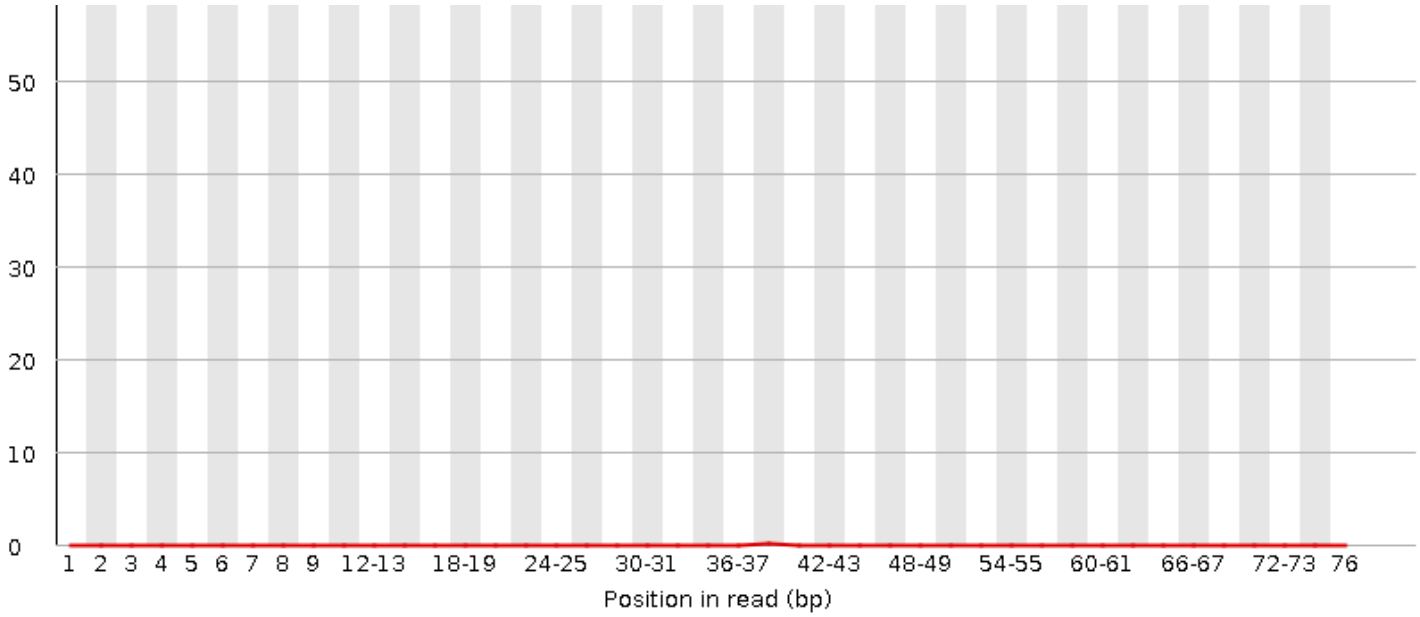
Per sequence GC content



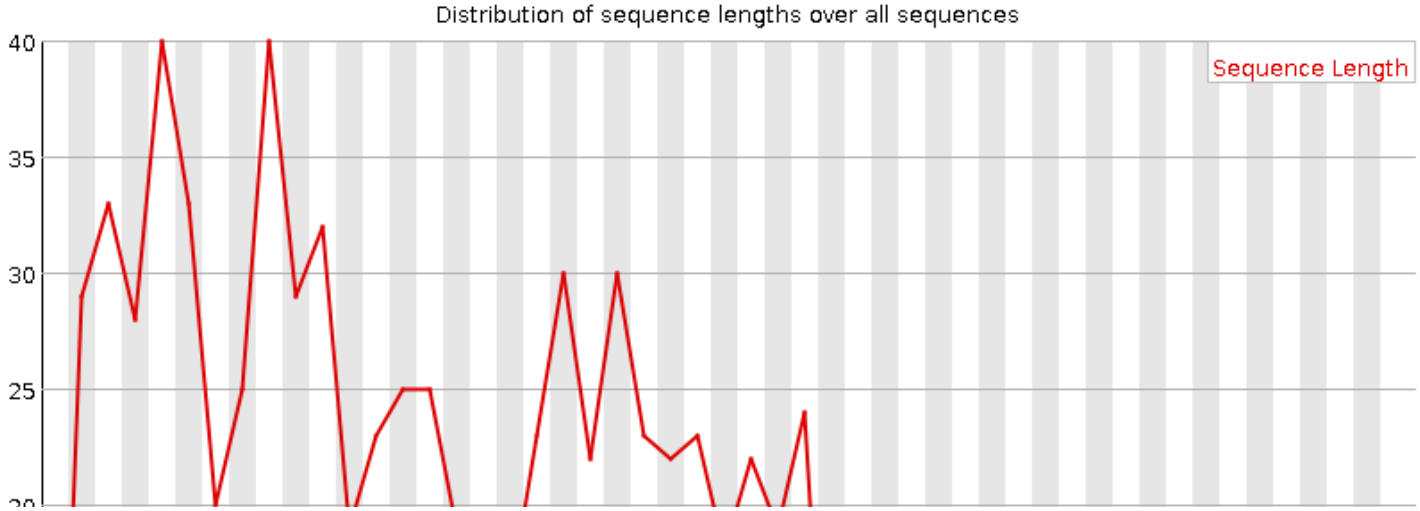


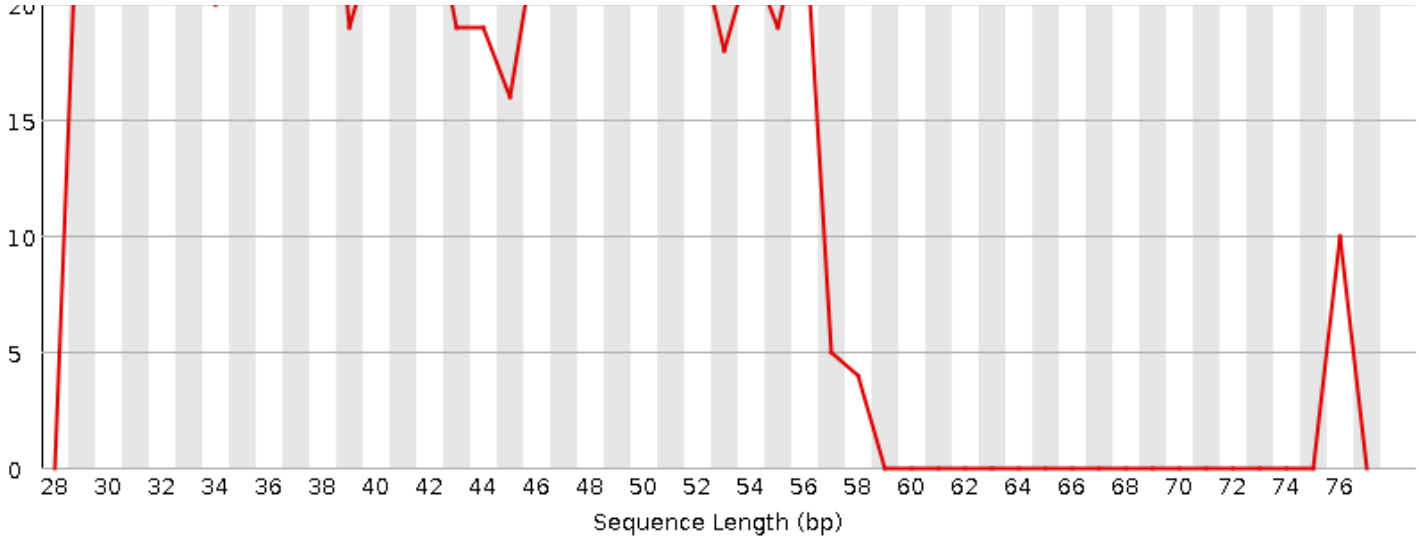
Per base N content



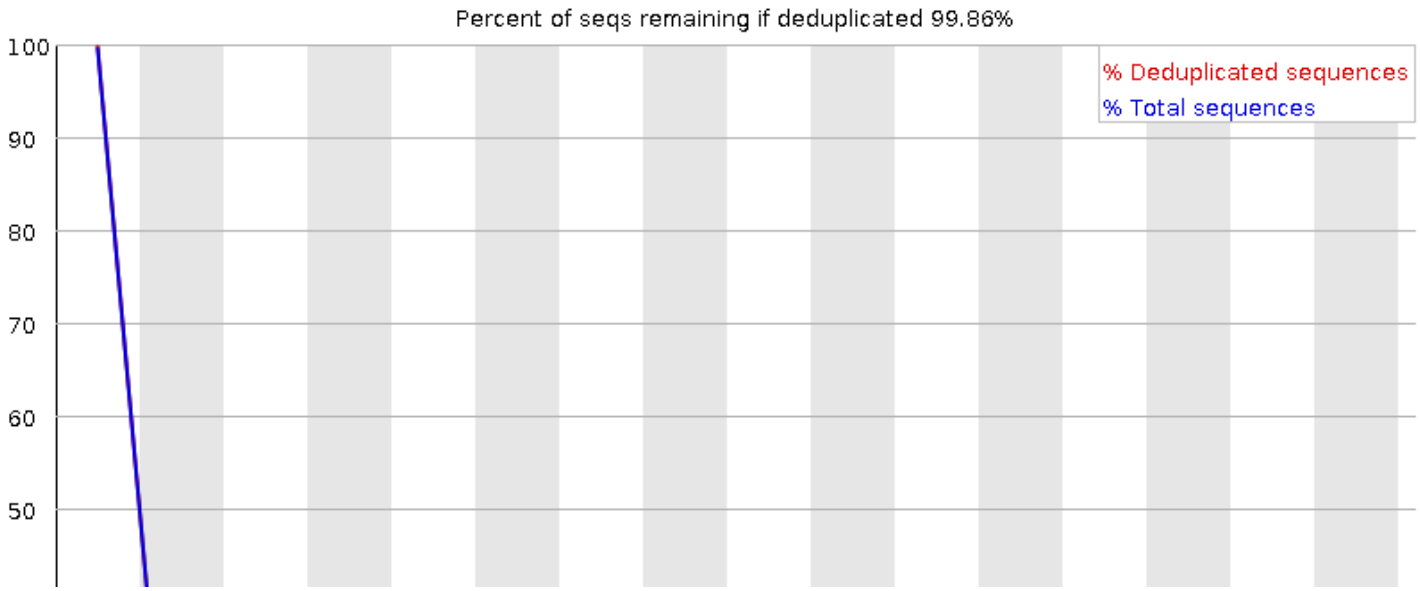


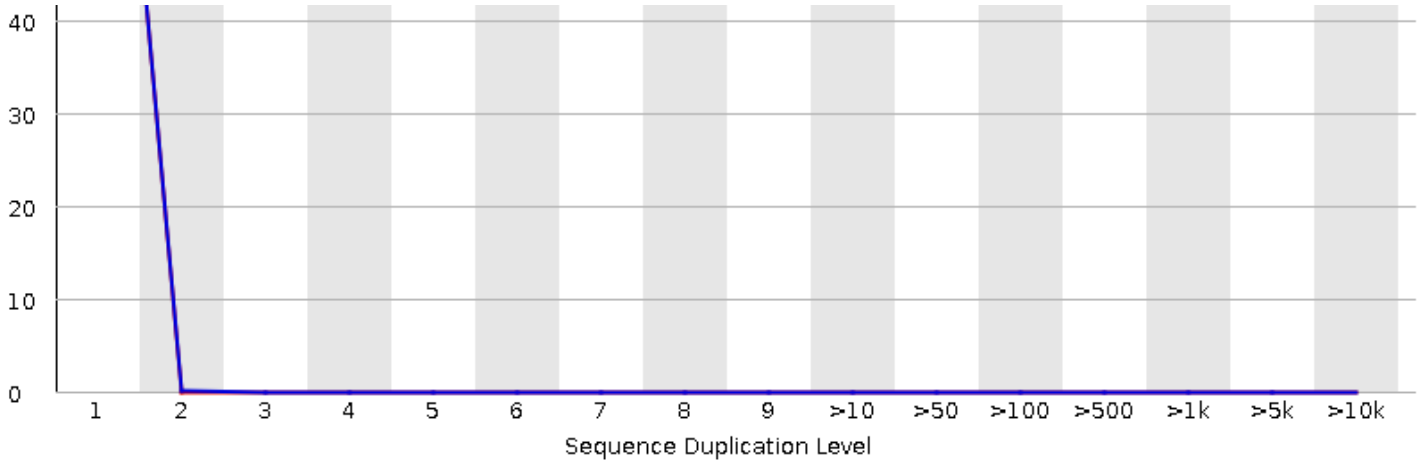
Sequence Length Distribution





Sequence Duplication Levels





Overrepresented sequences

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GTATCAATCCTGAATTCTTCAAAACAGTC	1	0.136986301369863	No Hit
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ACTAAGTGGAGAGGGTAATACAAATGGTGCTTTAGCATACA	1	0.136986301369863	No Hit
CATGAGTTCAACTAAATCATATTGCTCTTTAACGGGTCCATG	1	0.136986301369863	No Hit
CCAAATGACTTTGCGTATAAATAGCATTAGAGATTTCTTGGCAGA	1	0.136986301369863	No Hit
CTGTAGTGTTGACCCTATACTCCGAATGGAGTG	1	0.136986301369863	No Hit
GGGATATAGCCAACTGGACAGAAGAGAAAACAGCCACCCCCAAGGTTGGGA	1	0.136986301369863	No Hit
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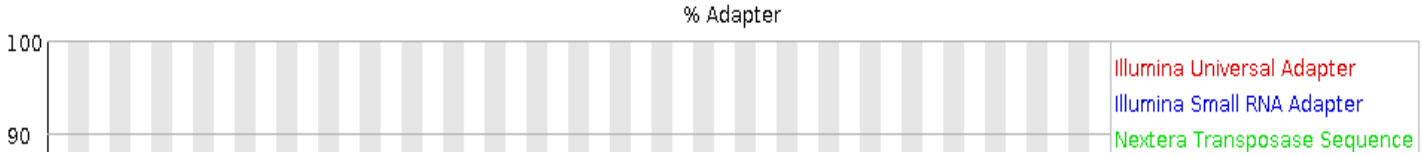

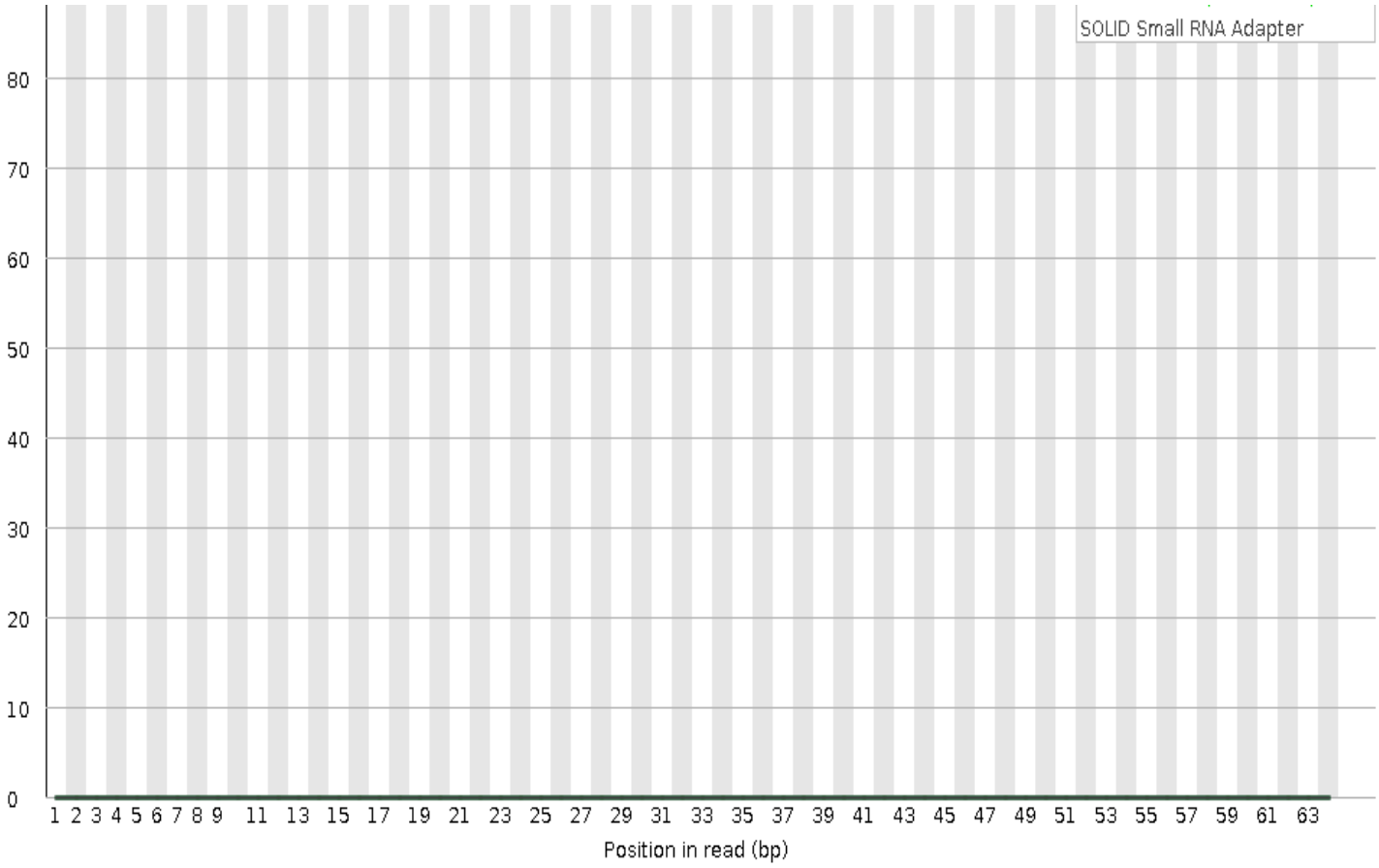

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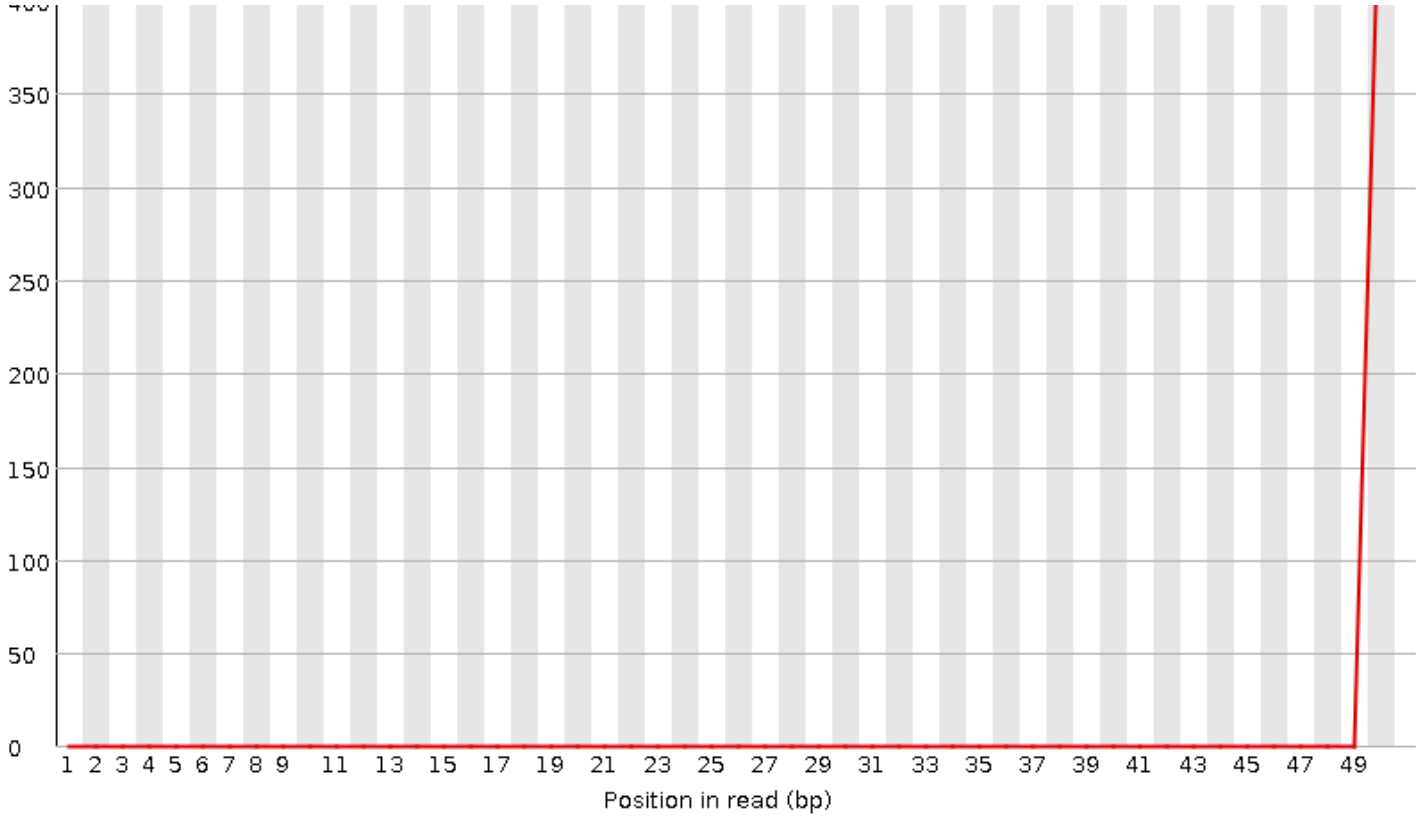

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Produced by FastQC (version 0.11.3)