FastQC Report

Tue 19 May 2015
skewer_SW042_2-trimmed-pair1.fastq

Summary

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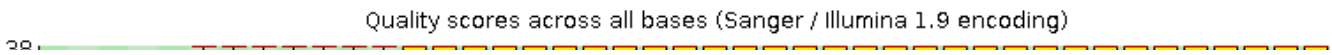
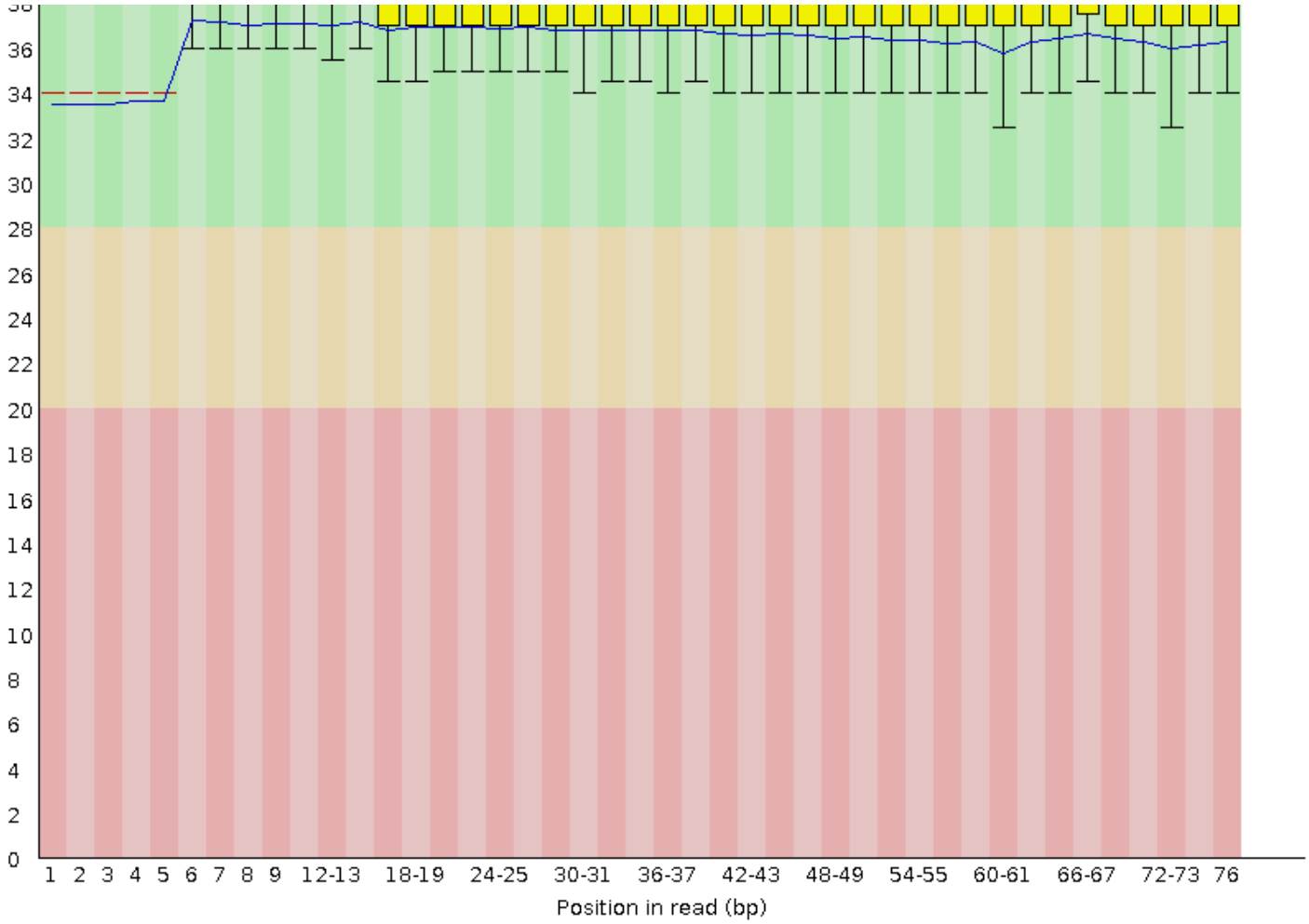
Basic Statistics

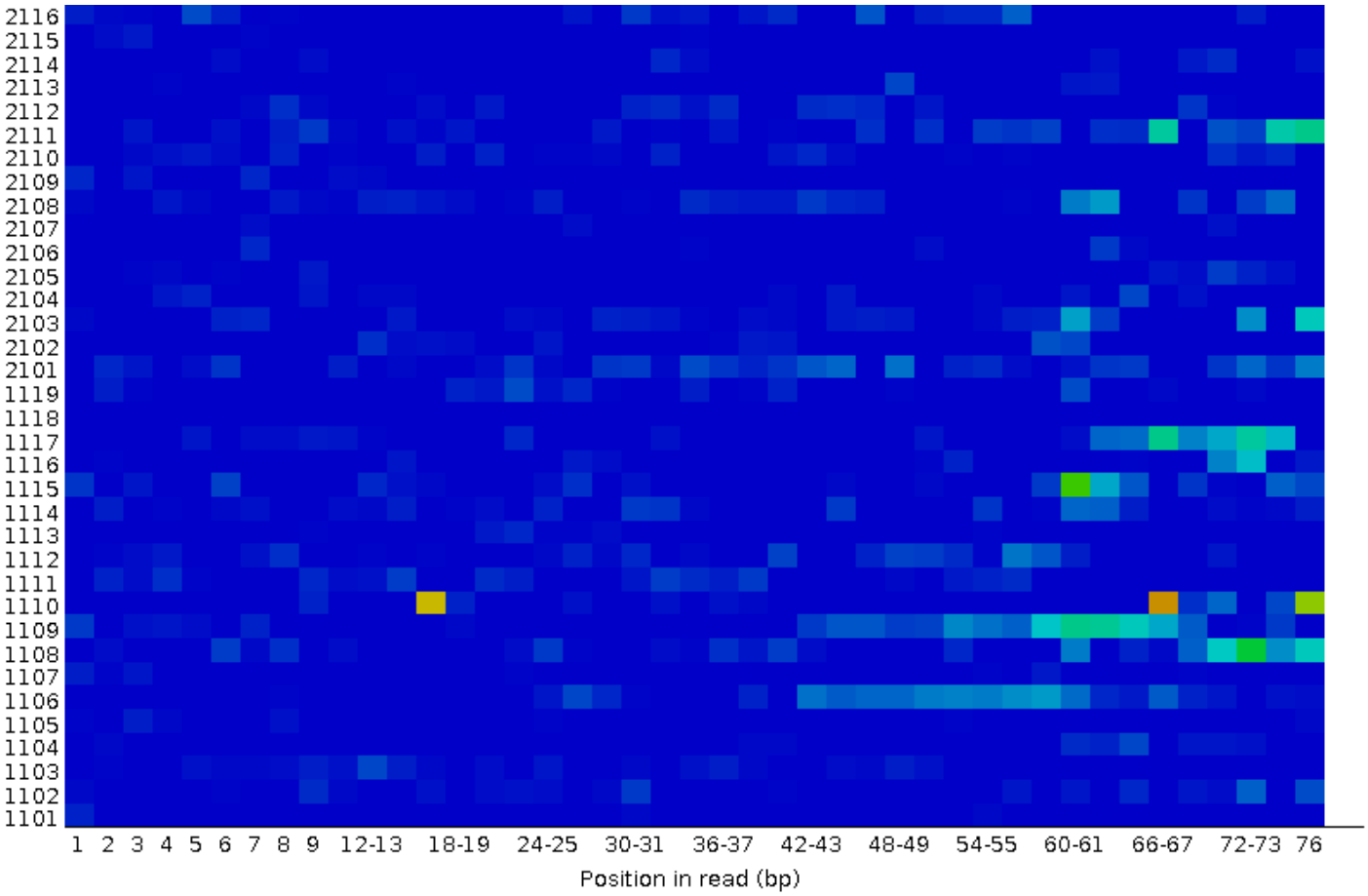
Measure	Value
Filename	skewer_SW042_2-trimmed-pair1.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	7900
Sequences flagged as poor quality	0
Sequence length	53-76
%GC	43

Per base sequence quality

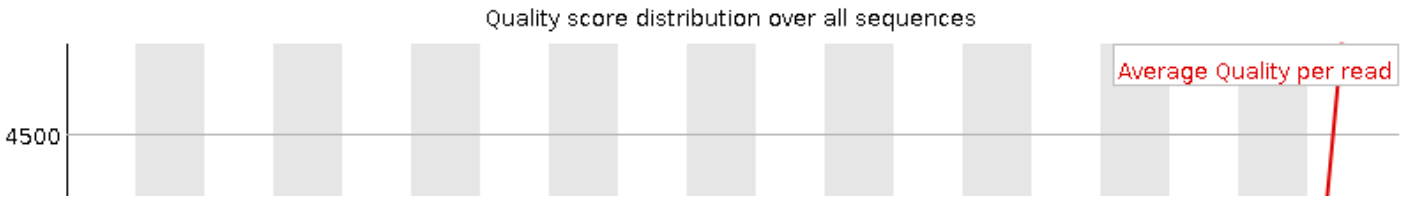


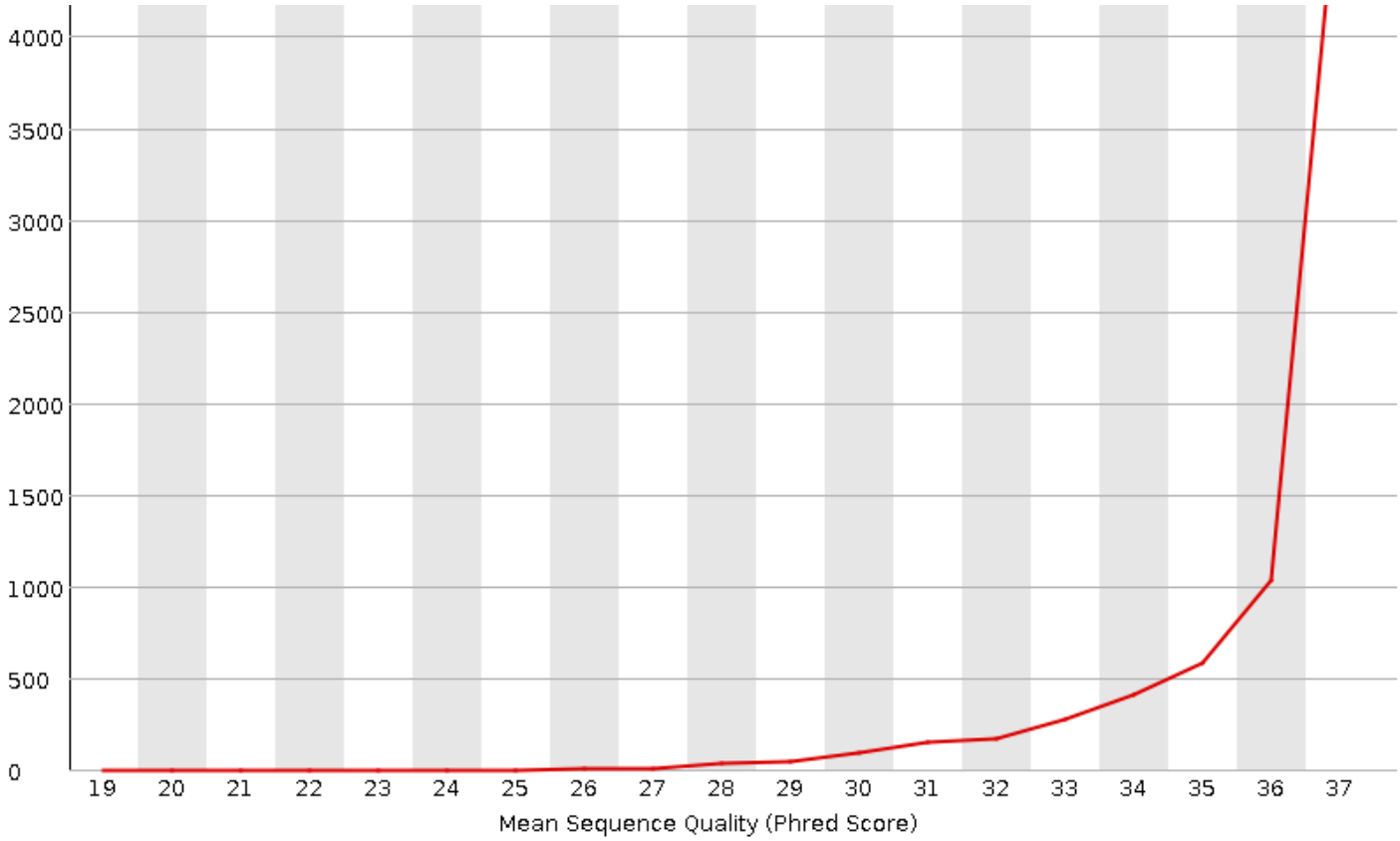


Per tile sequence quality

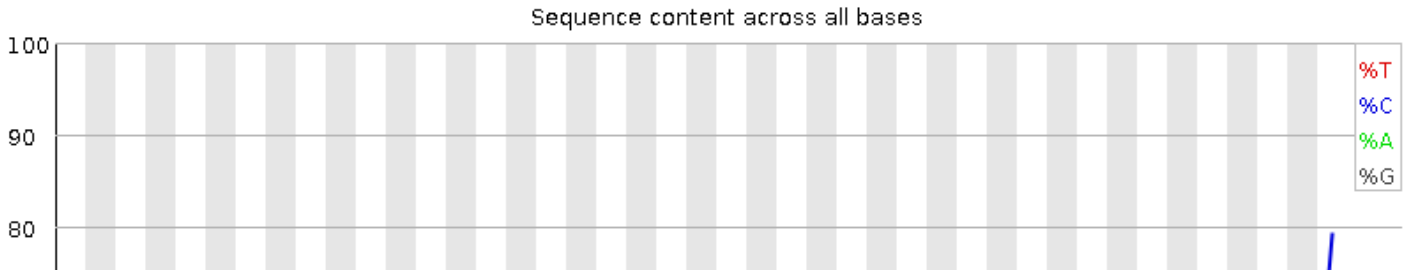


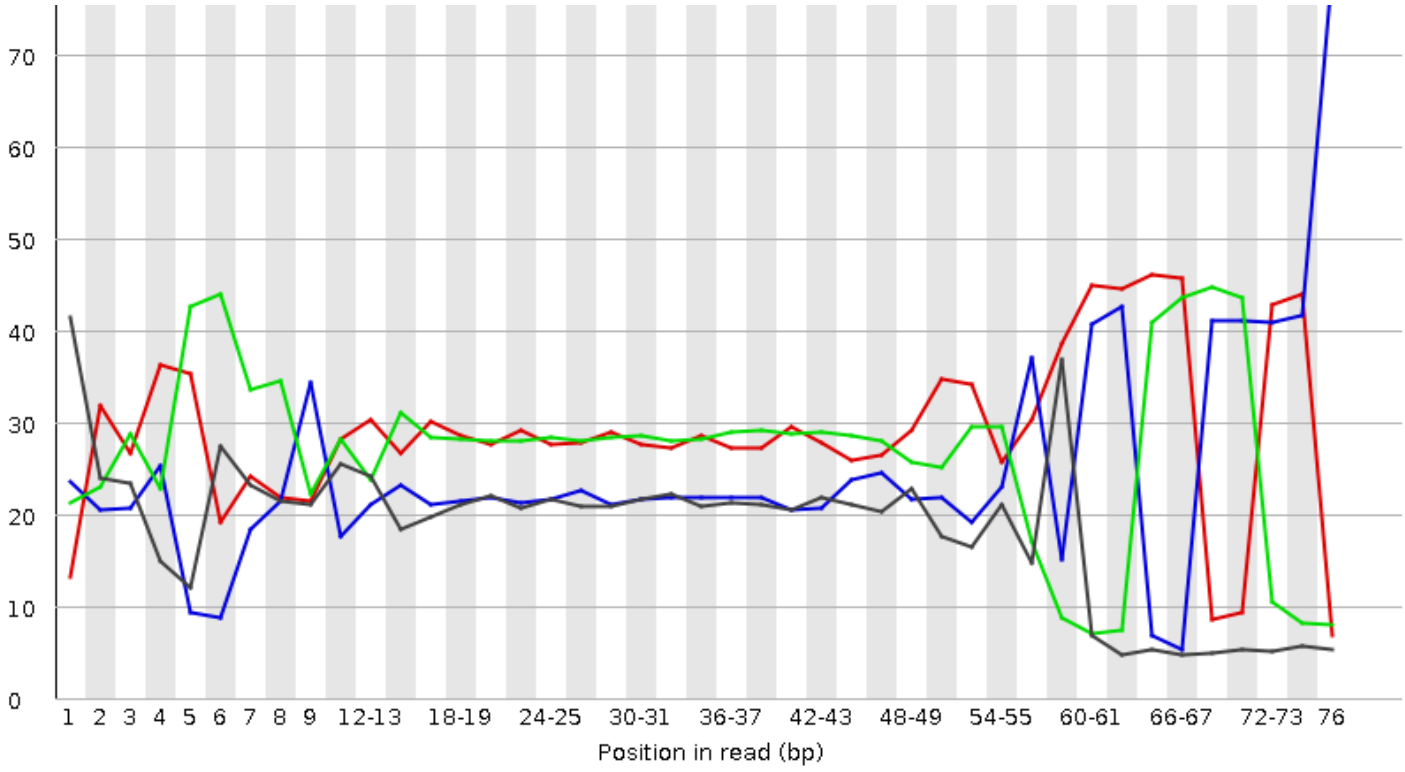
Per sequence quality scores



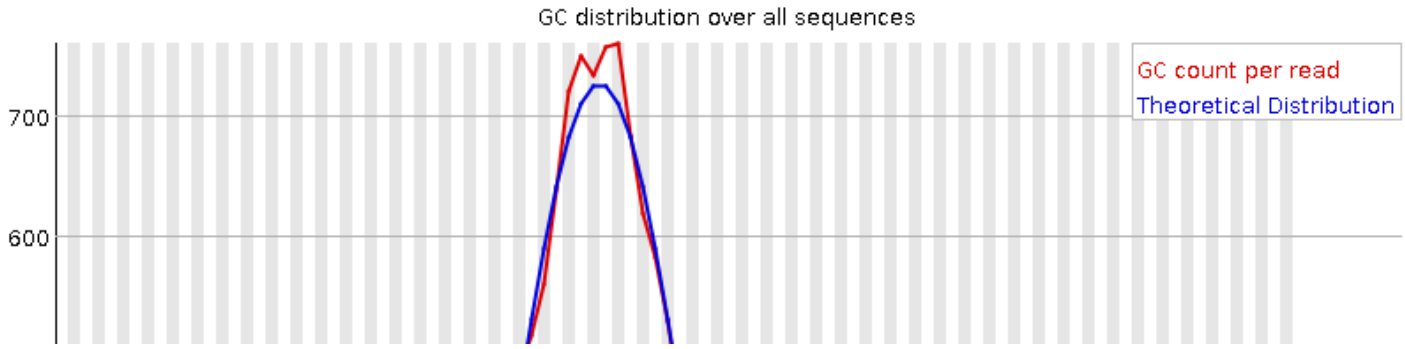


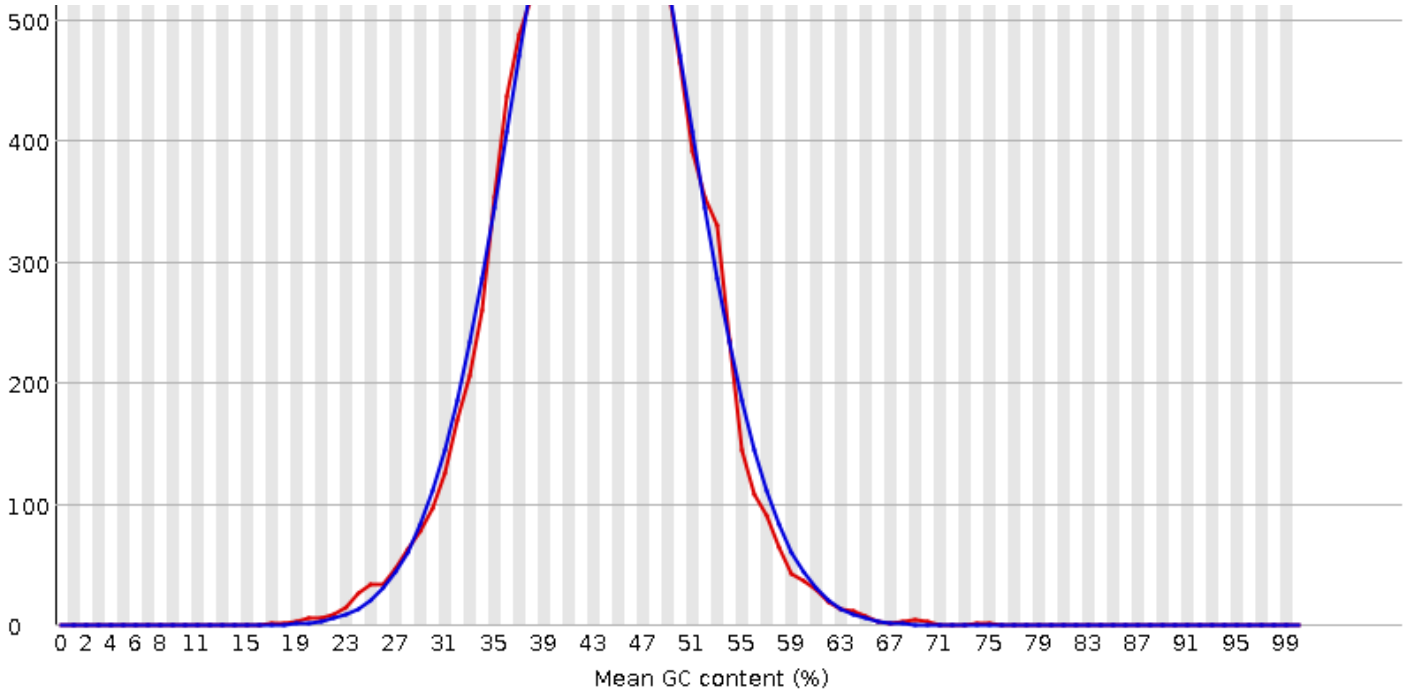
Per base sequence content



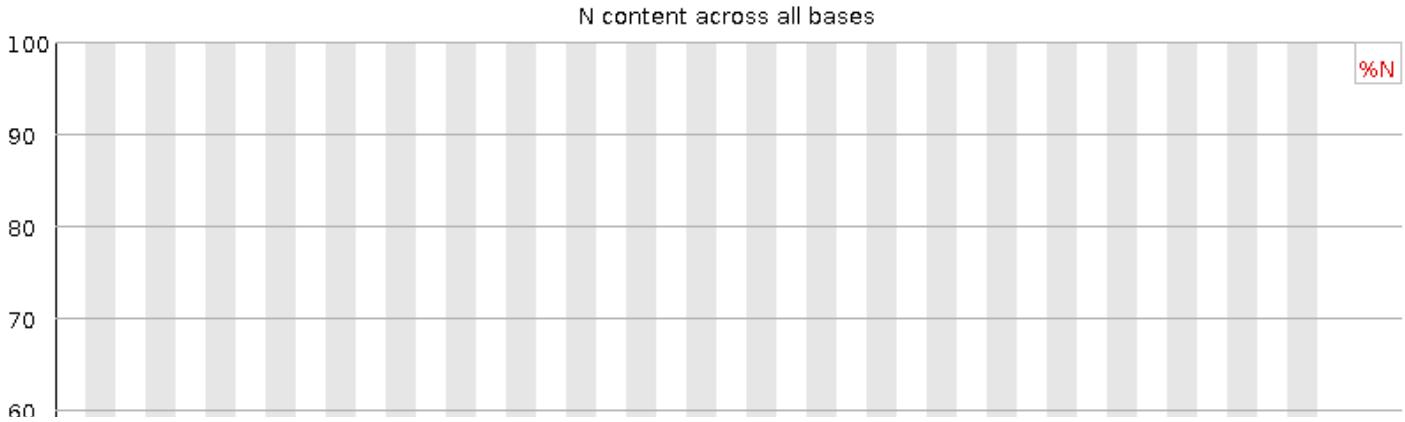


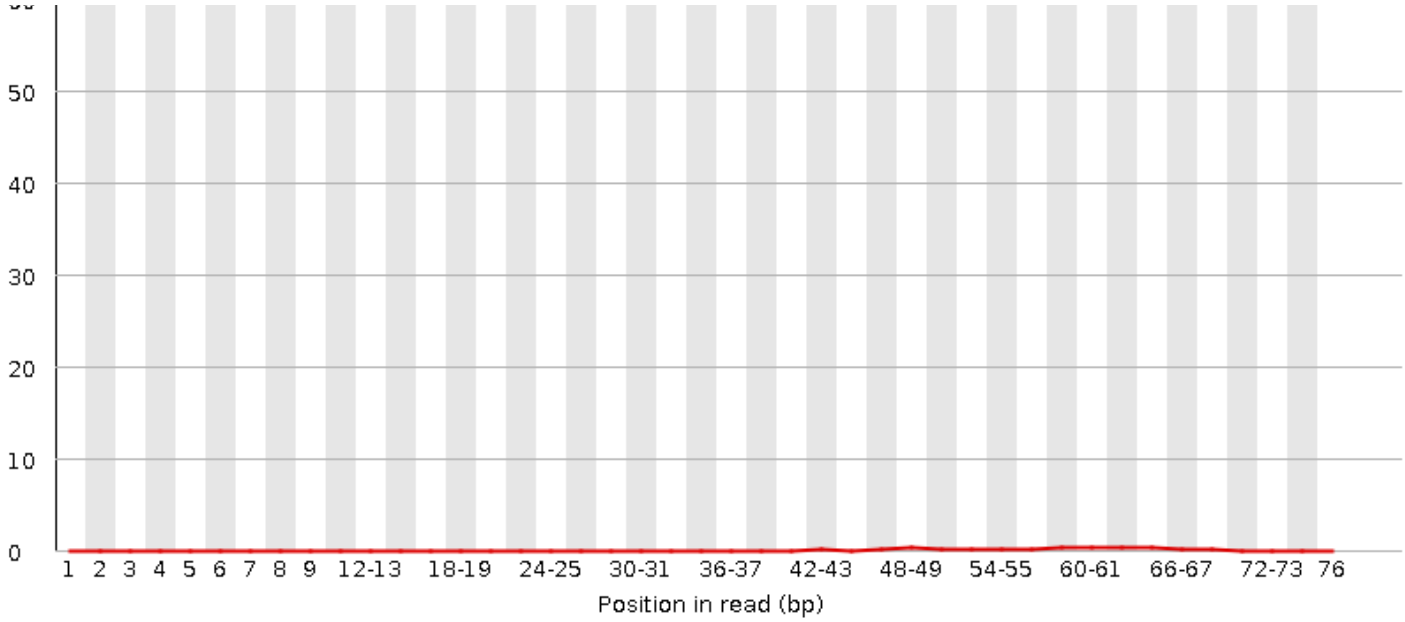
Per sequence GC content



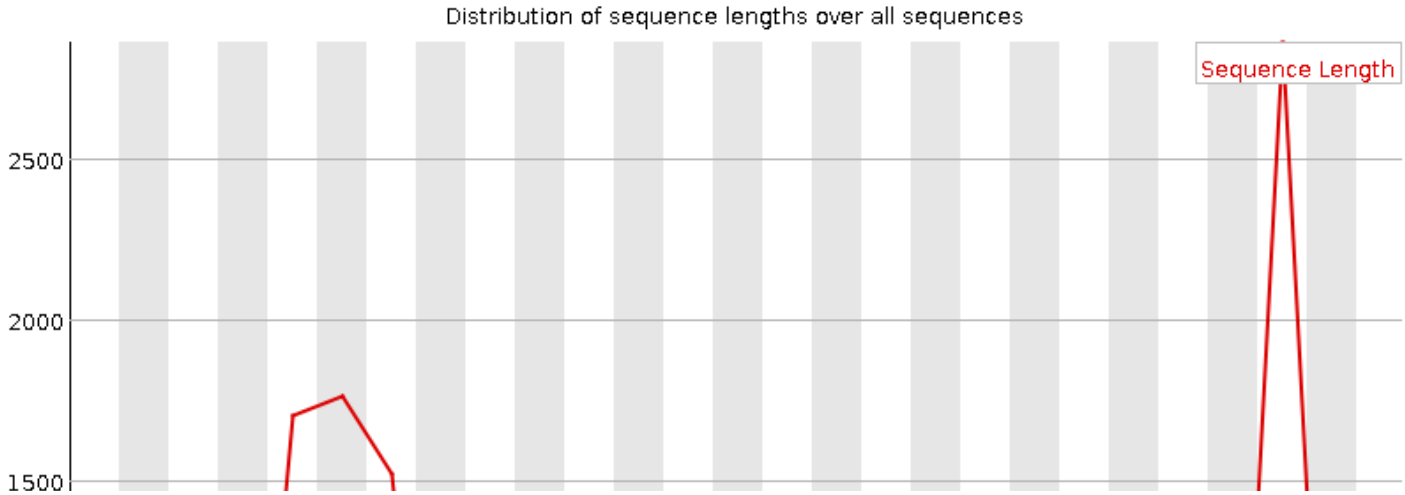


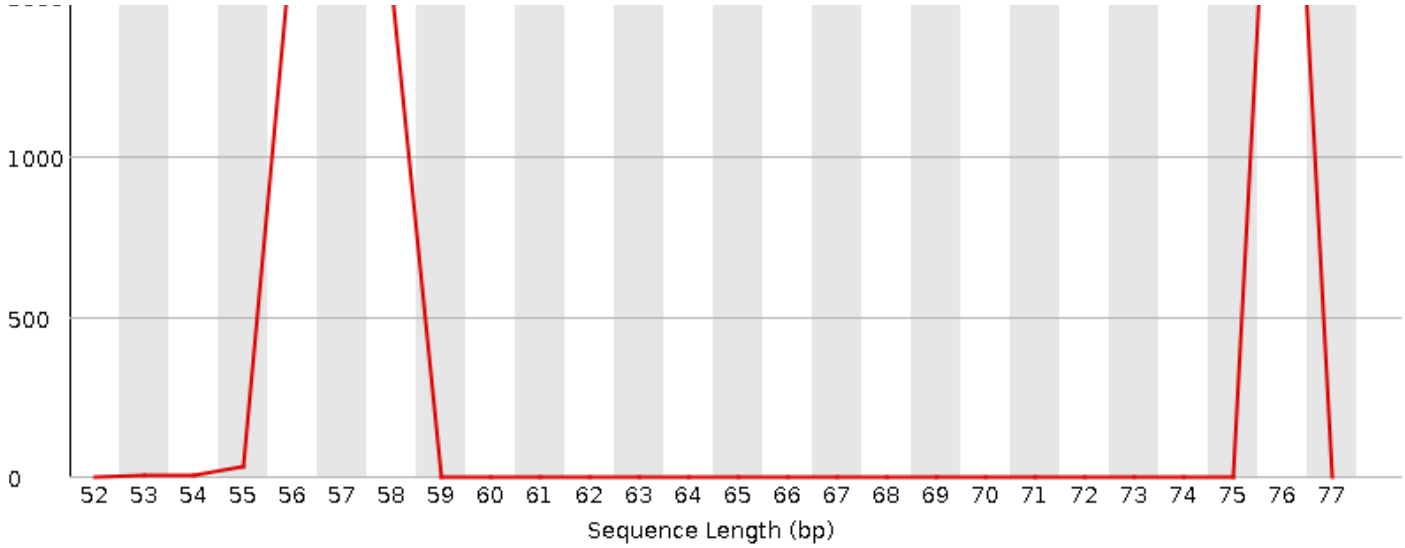
Per base N content



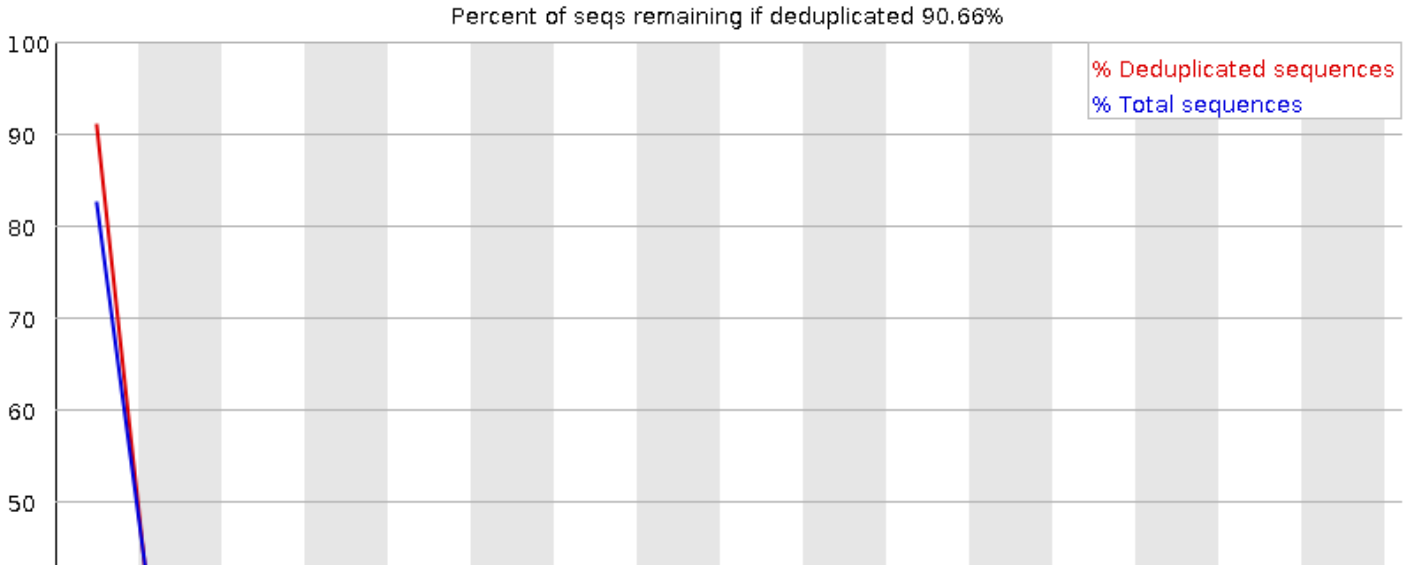


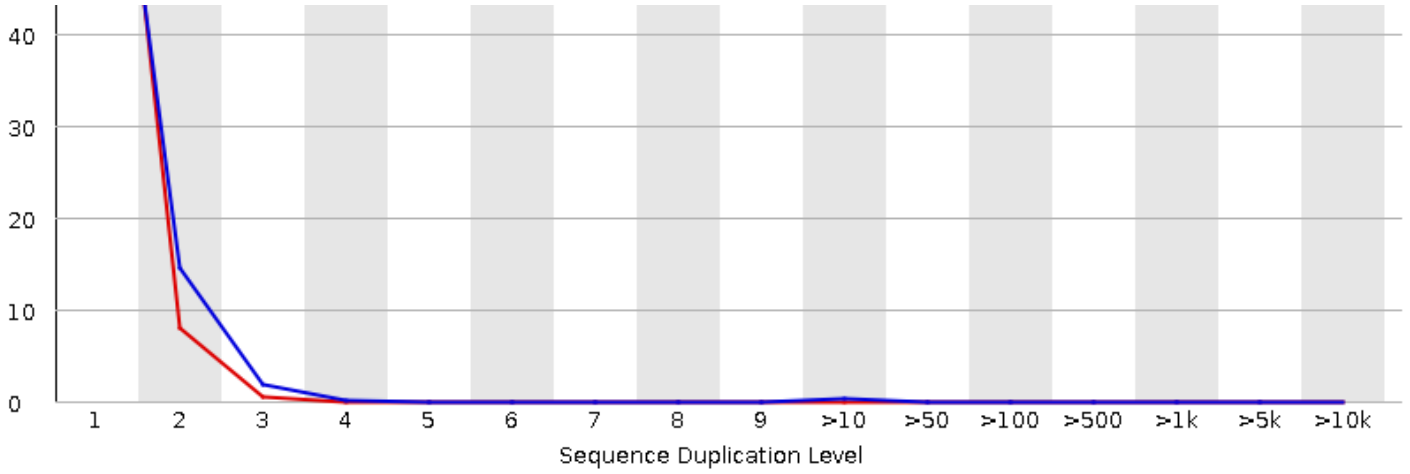
Sequence Length Distribution





Sequence Duplication Levels

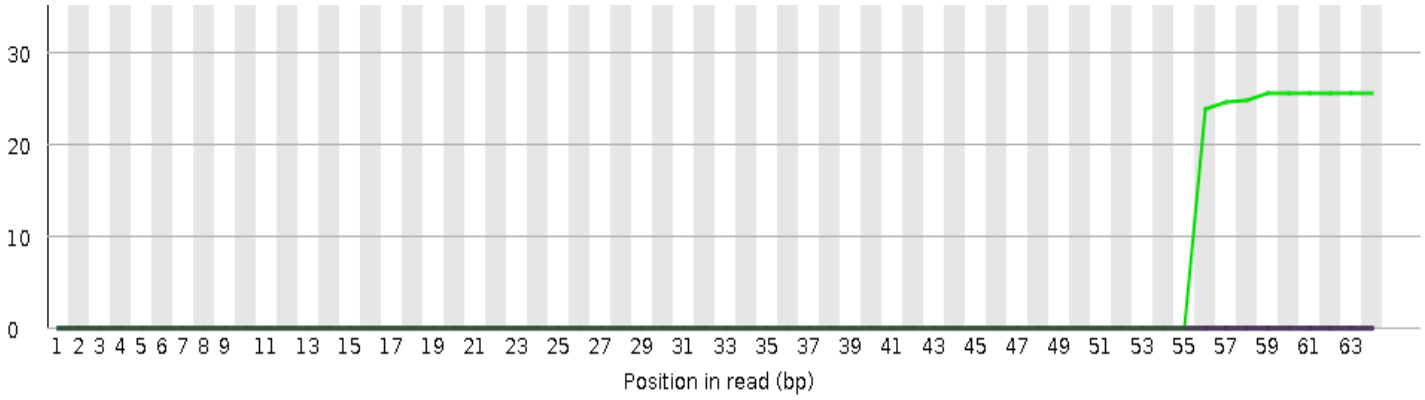




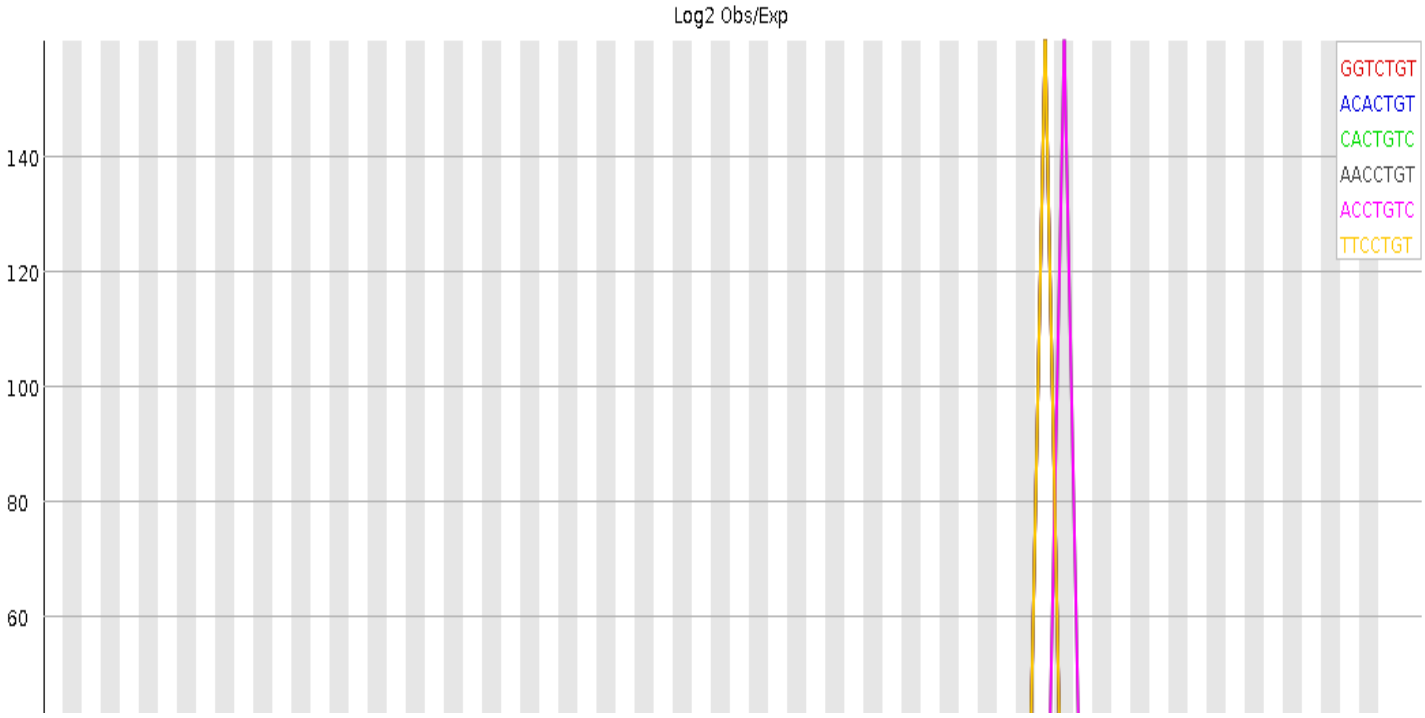
Overrepresented sequences

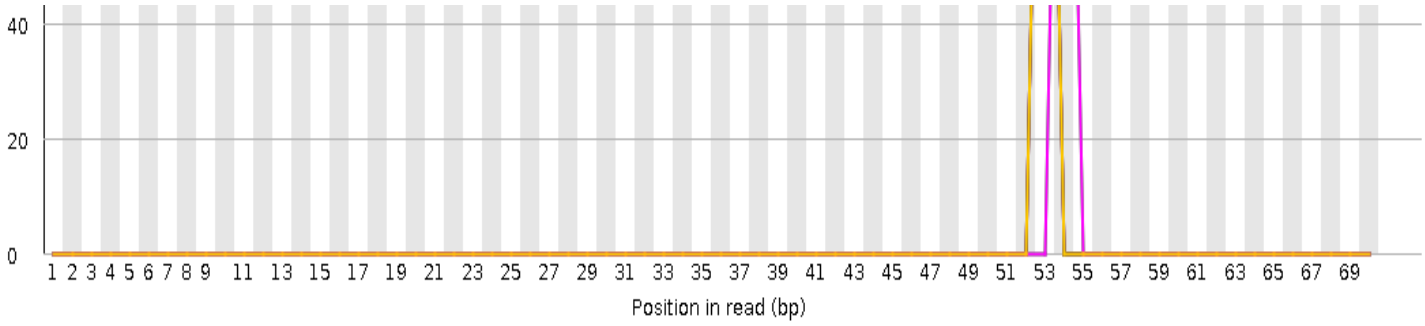
Sequence	Count	Percentage	Possible Source
CCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACCC	20	0.25316455696202533	No Hit
GGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGG	17	0.21518987341772153	No Hit

Adapter Content



Kmer Content





Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
GGTCTGT	10	0.0050425758	159.66667	53
ACACTGT	10	0.0050425758	159.66667	53
CACTGTC	20	1.1038683E-6	159.66667	54
AACCTGT	10	0.0050425758	159.66667	53
ACCTGTC	35	3.6379788E-12	159.66667	54
TTCCTGT	10	0.0050425758	159.66667	53
CCCTGTC	35	3.6379788E-12	159.66667	54
GACTGTC	10	0.0050425758	159.66667	54
TTGCTGT	10	0.0050425758	159.66667	53
CCTGTCT	95	0.0	159.66666	55
TATACAA	10	0.005316749	156.9138	64
CTCTTAT	245	0.0	156.40816	60
CTTATAC	245	0.0	156.40816	62
TCTCTTA	245	0.0	156.40816	59
ACACATC	235	0.0	153.5752	67
CACATCT	230	0.0	153.50262	68
TGTCTCT	250	0.0	153.28	57
GTCTCTT	250	0.0	153.28	58
CTGTCTC	250	0.0	153.28	56
TTATACA	255	0.0	150.76031	63

Produced by FastQC (version 0.11.3)