FastQC Report

Wed 20 May 2015
skewer_run2_SW042_1-trimmed-pair2.fastq

Summary

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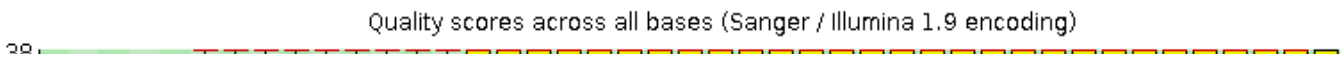
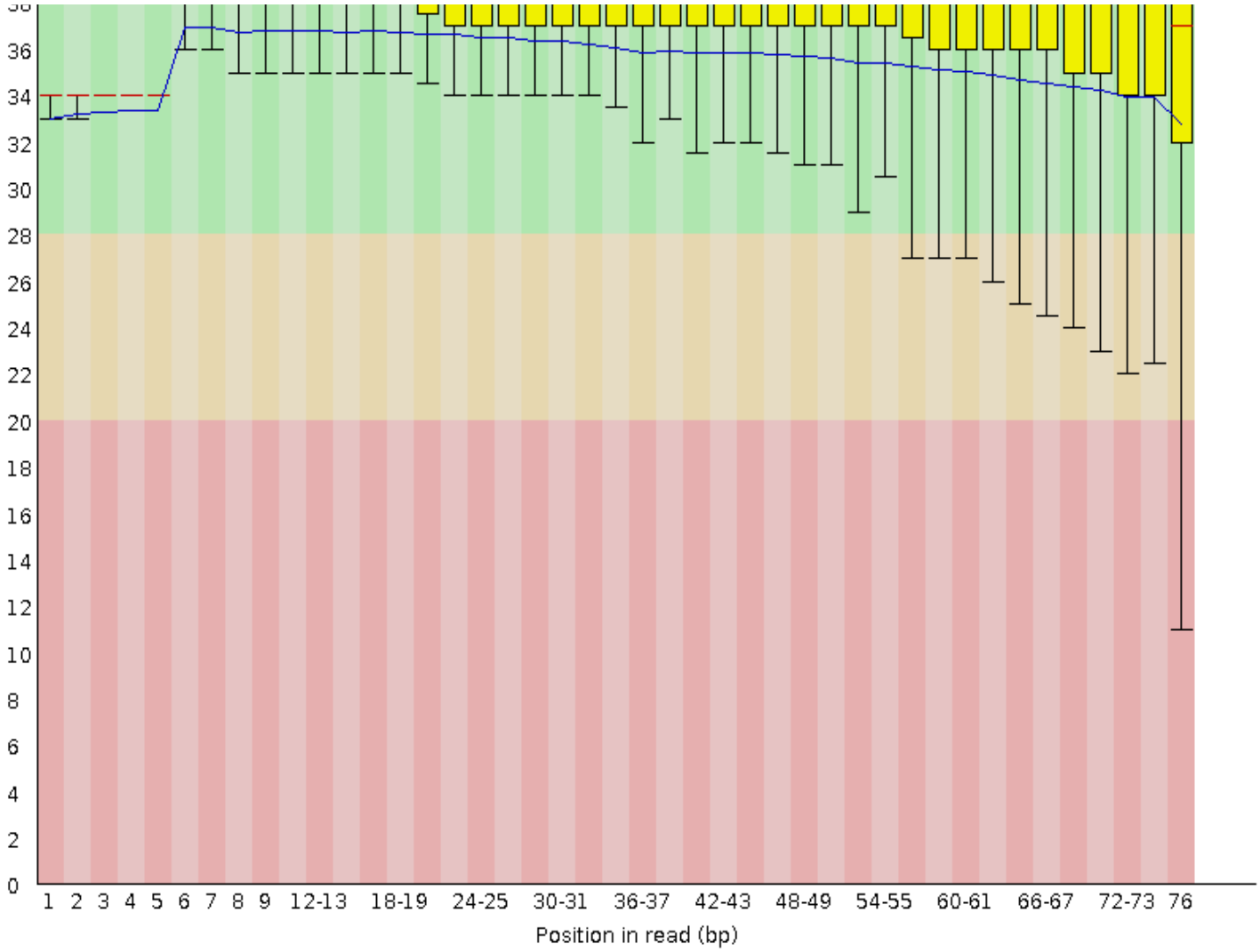
Basic Statistics

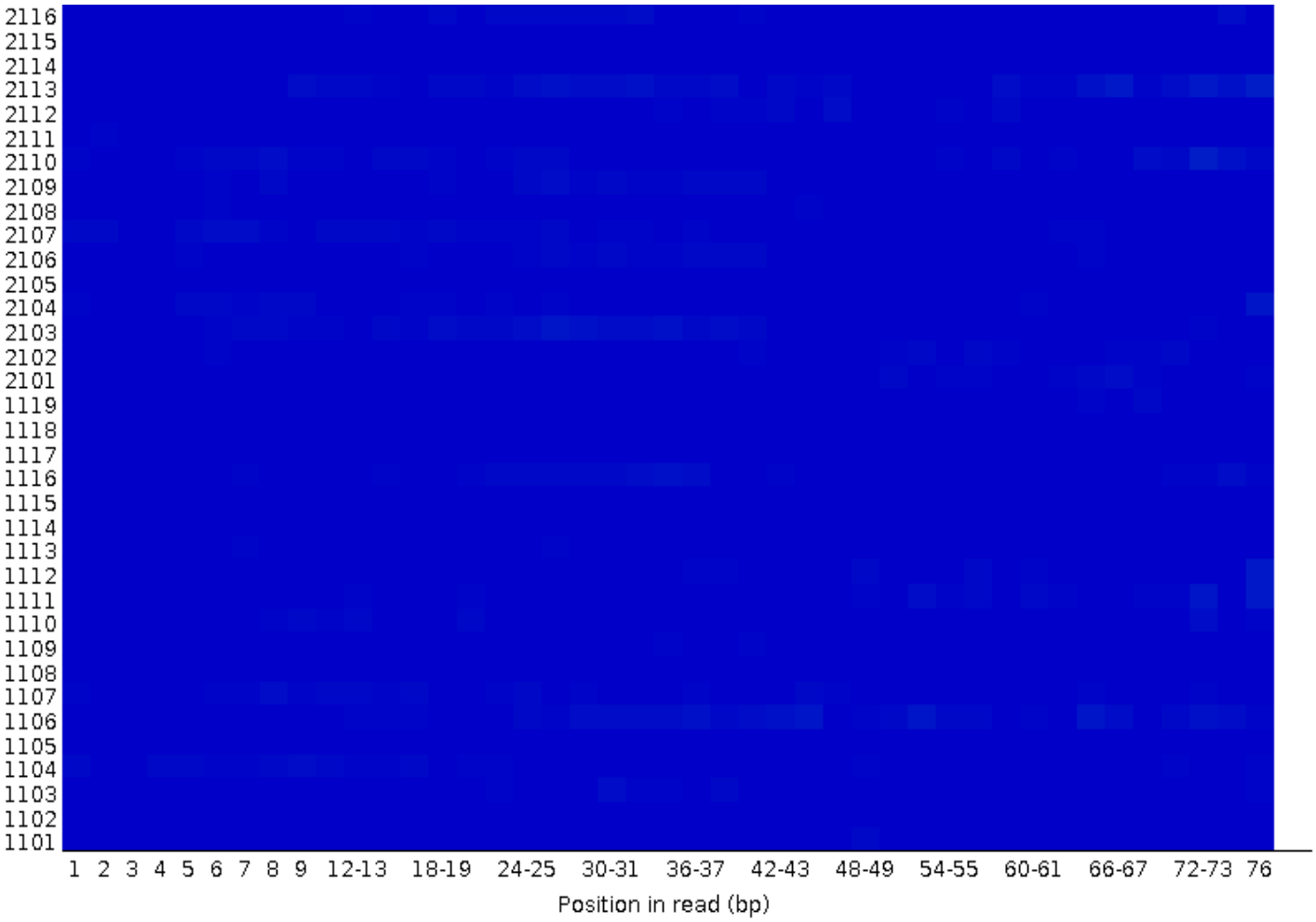
Measure	Value
Filename	skewer_run2_SW042_1-trimmed-pair2.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	735906
Sequences flagged as poor quality	0
Sequence length	29-76
%GC	43

Per base sequence quality

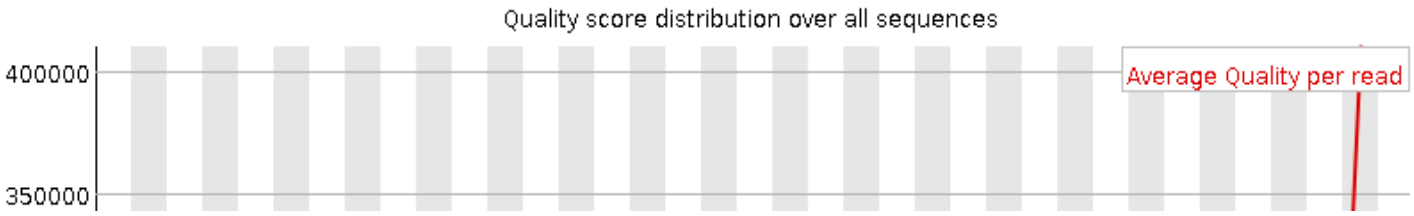


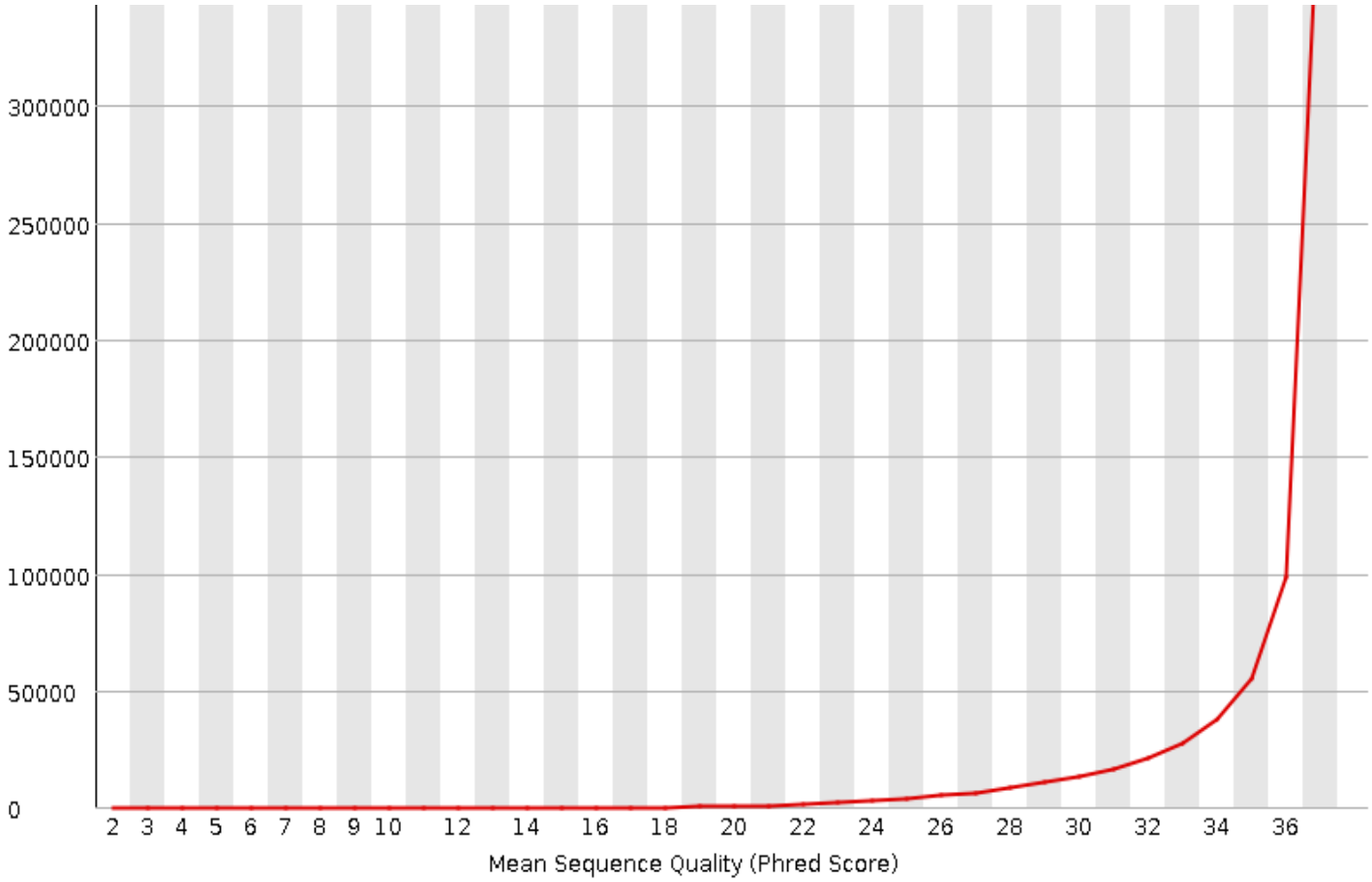


Per tile sequence quality

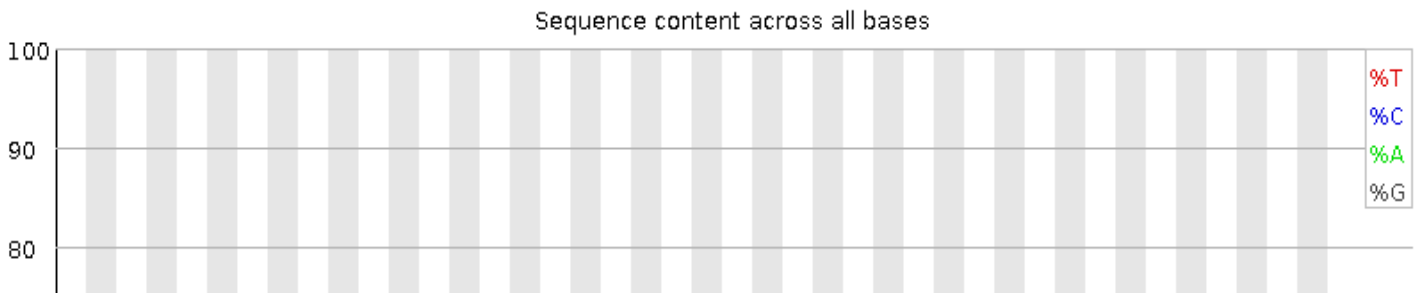


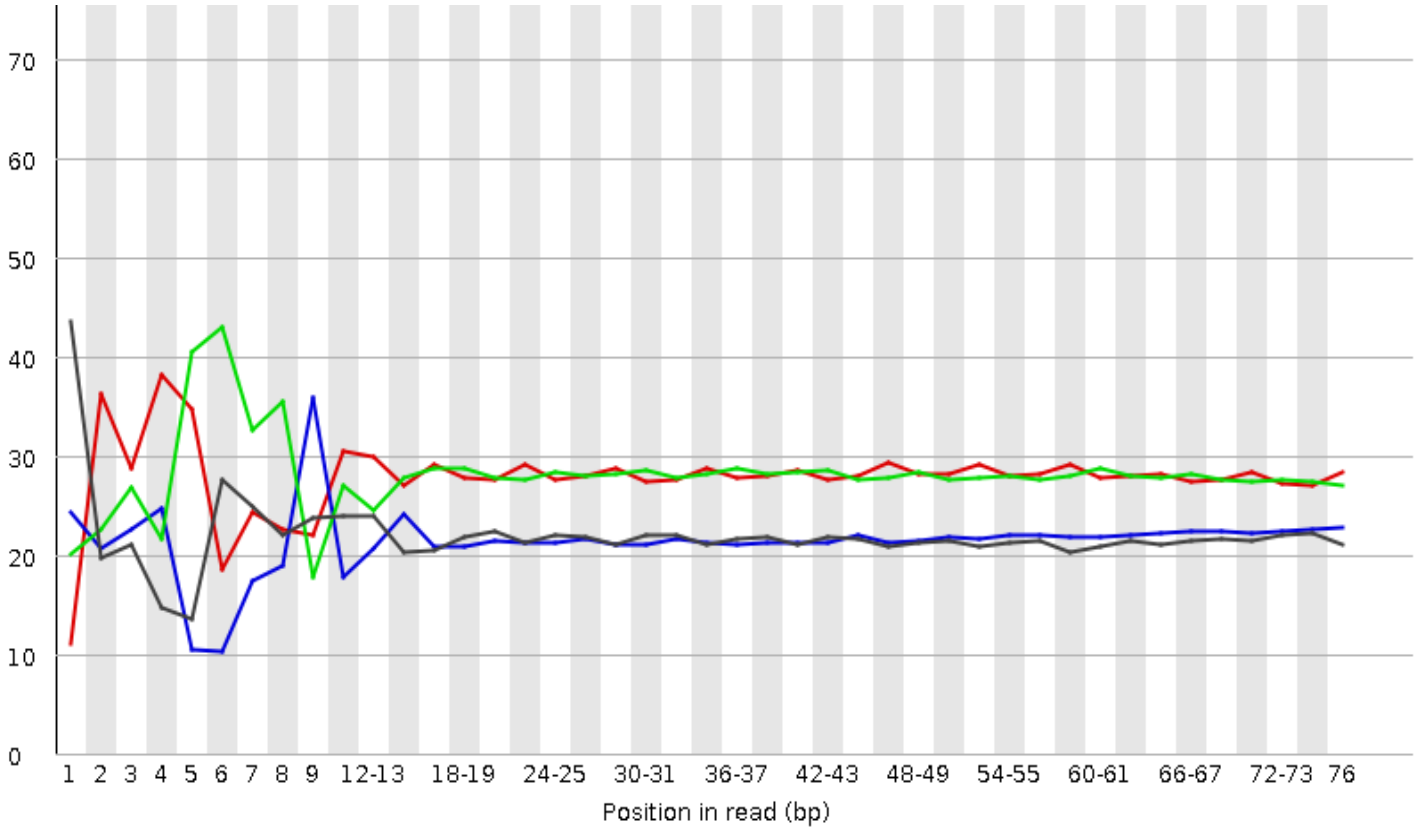
Per sequence quality scores



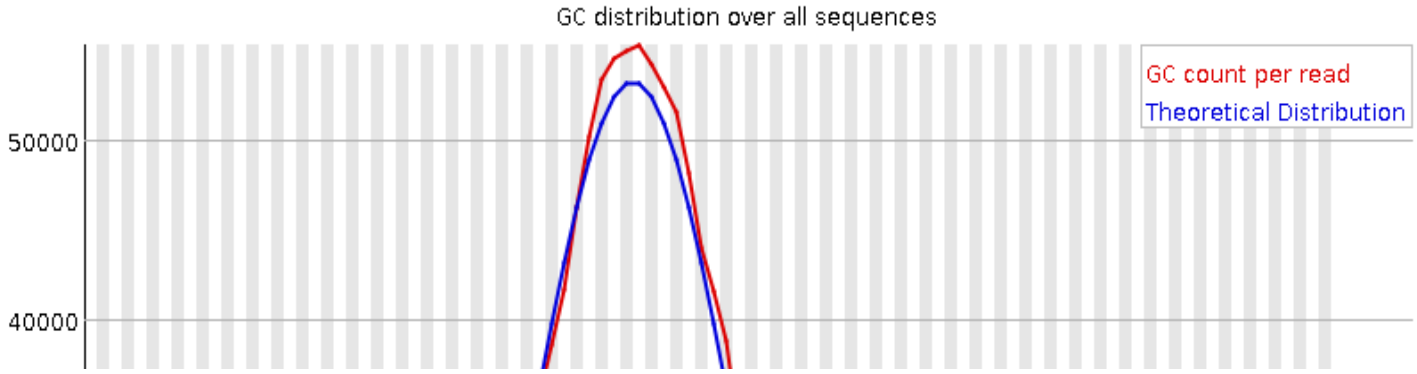


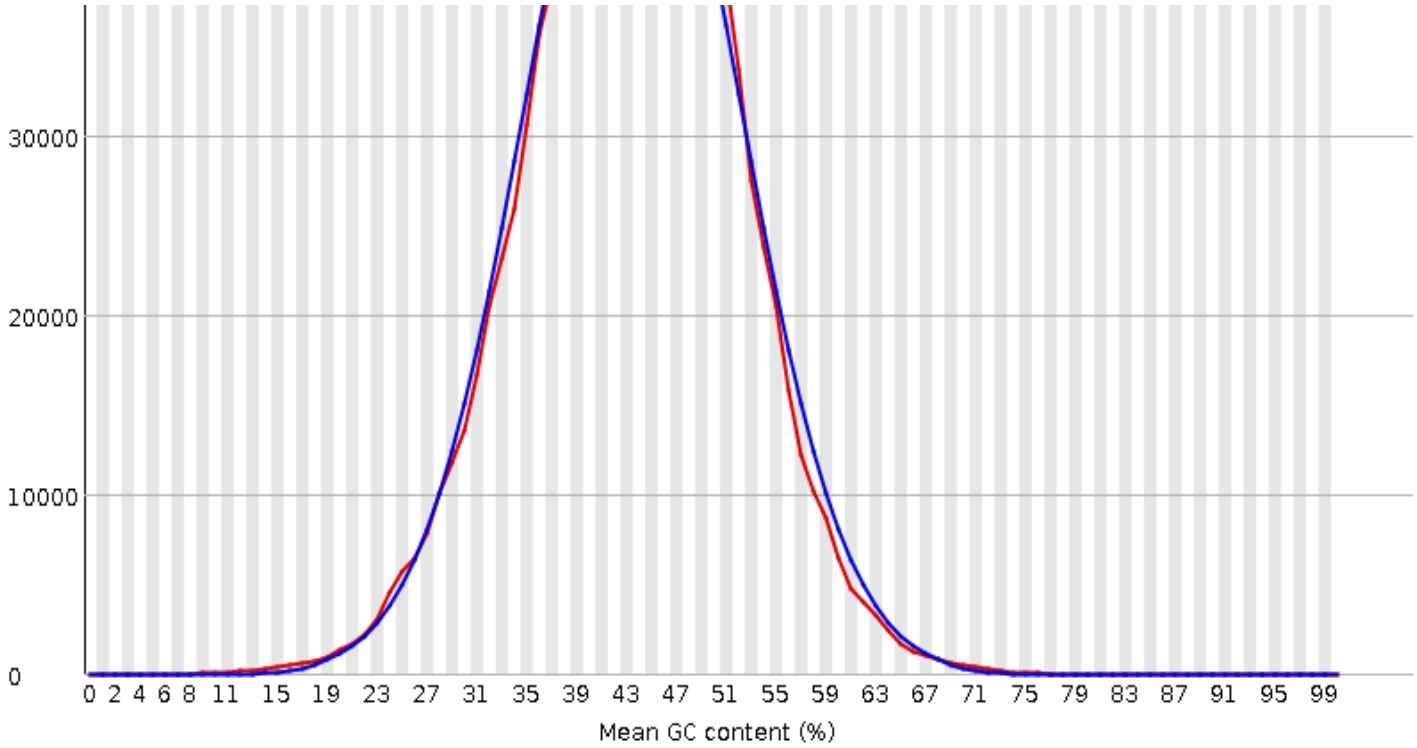
Per base sequence content



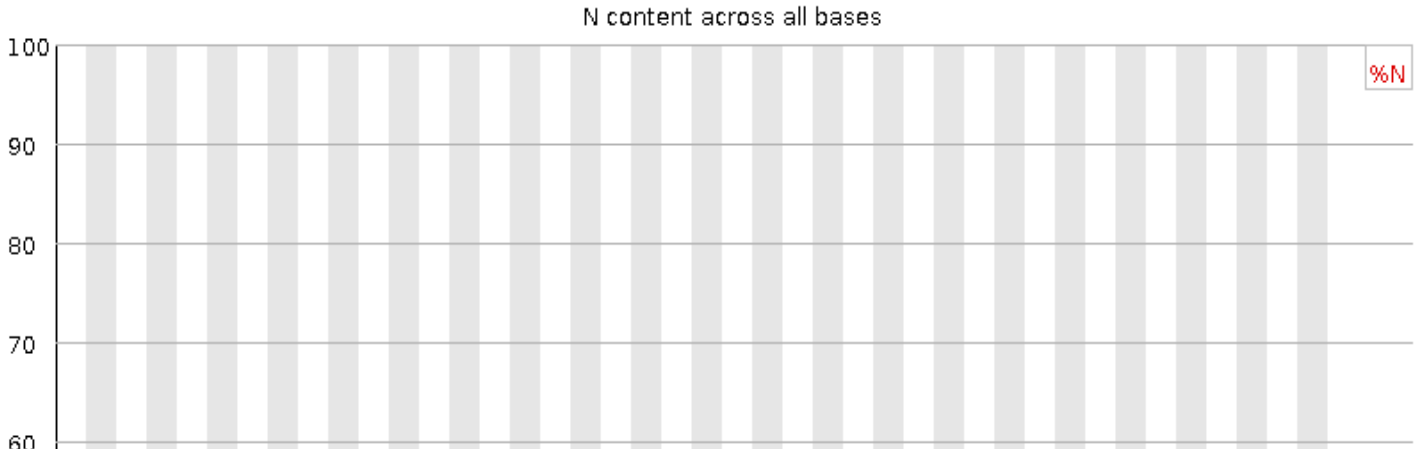


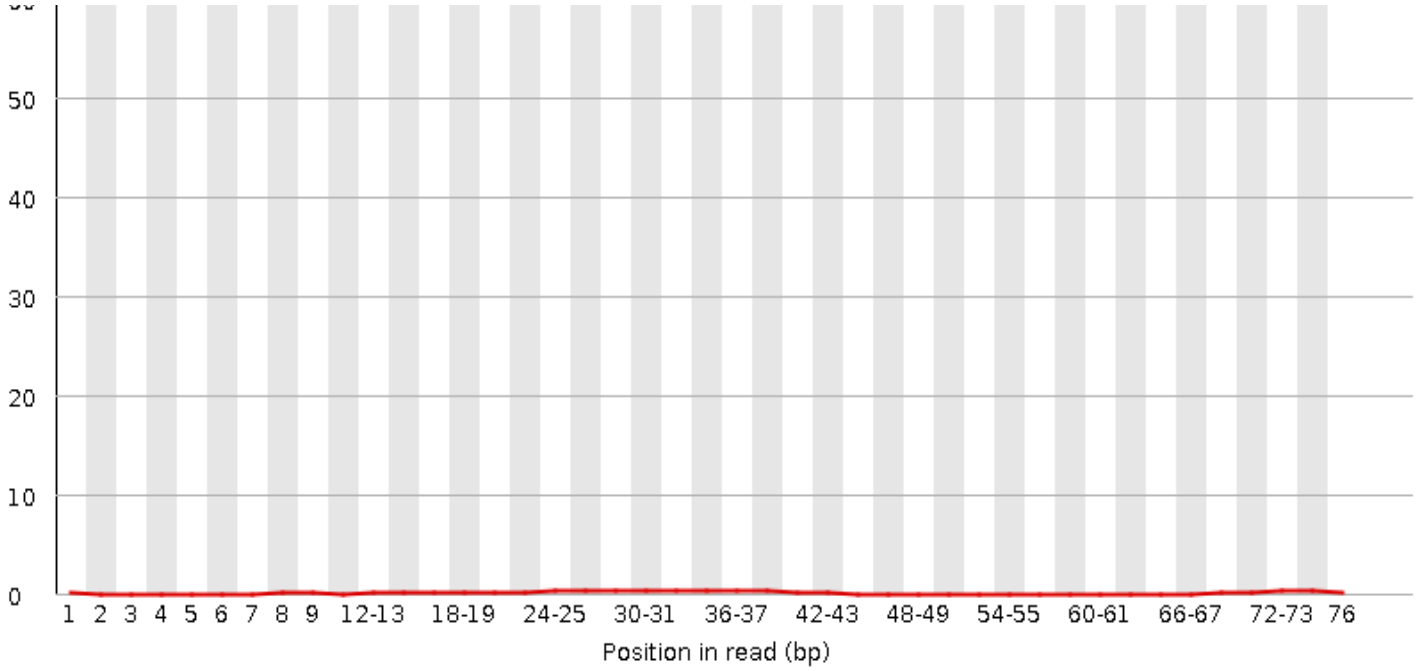
Per sequence GC content



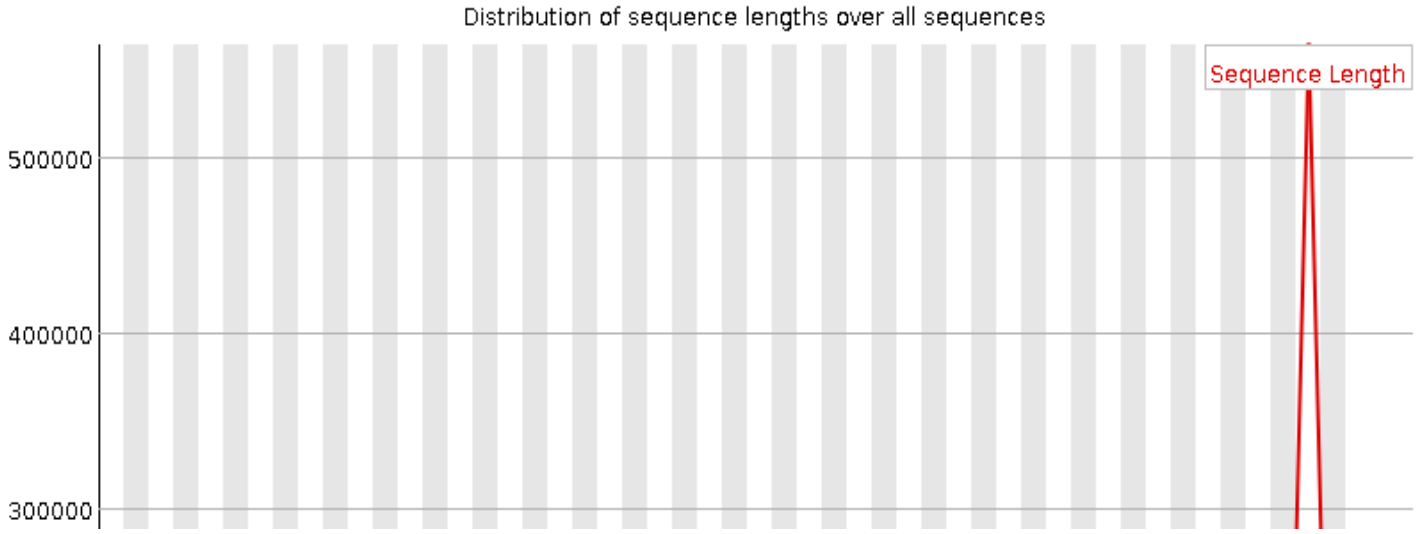


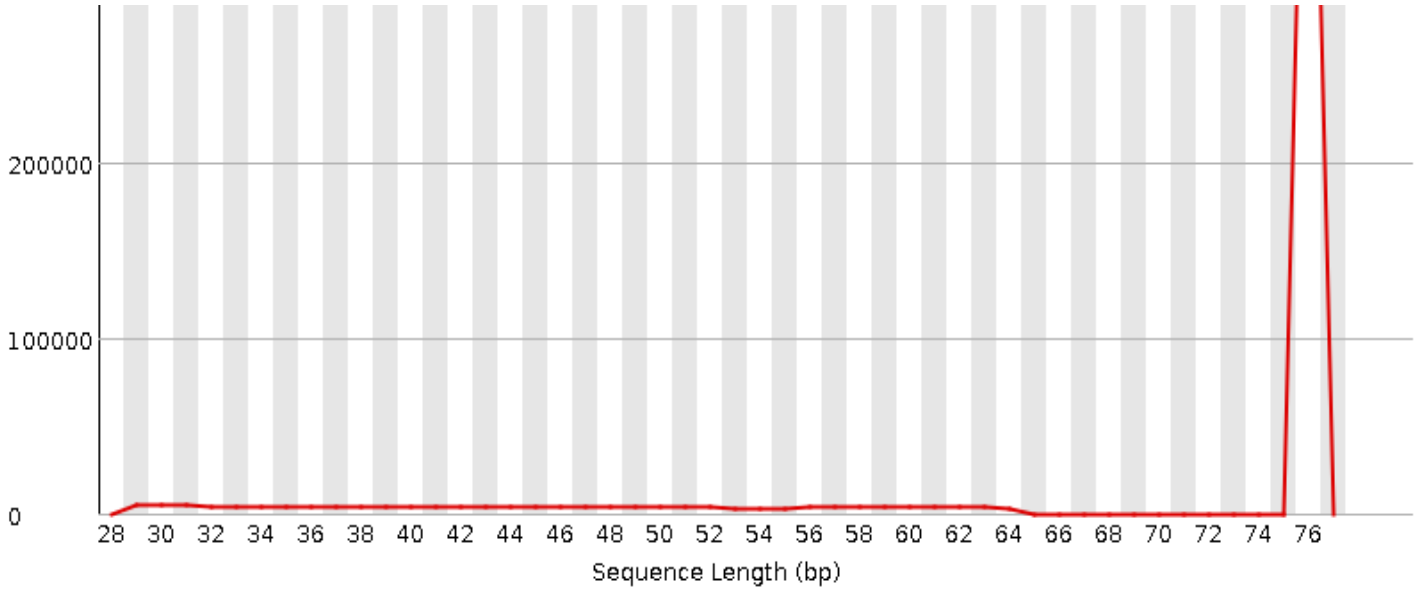
Per base N content



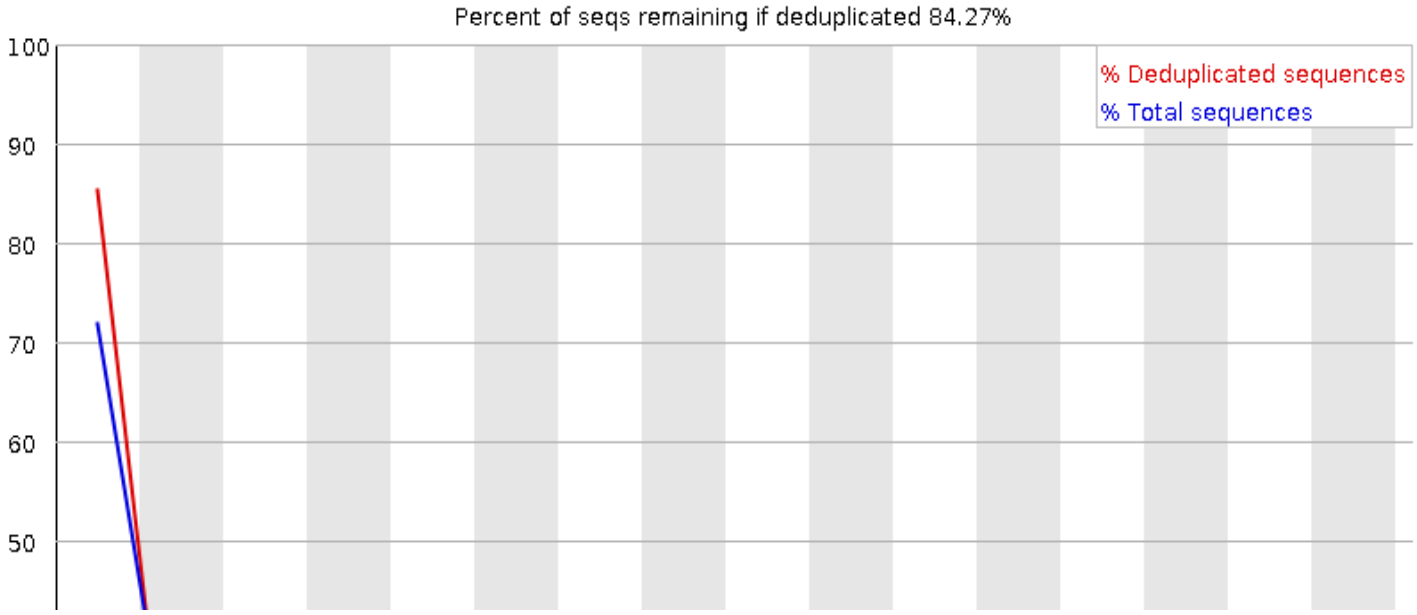


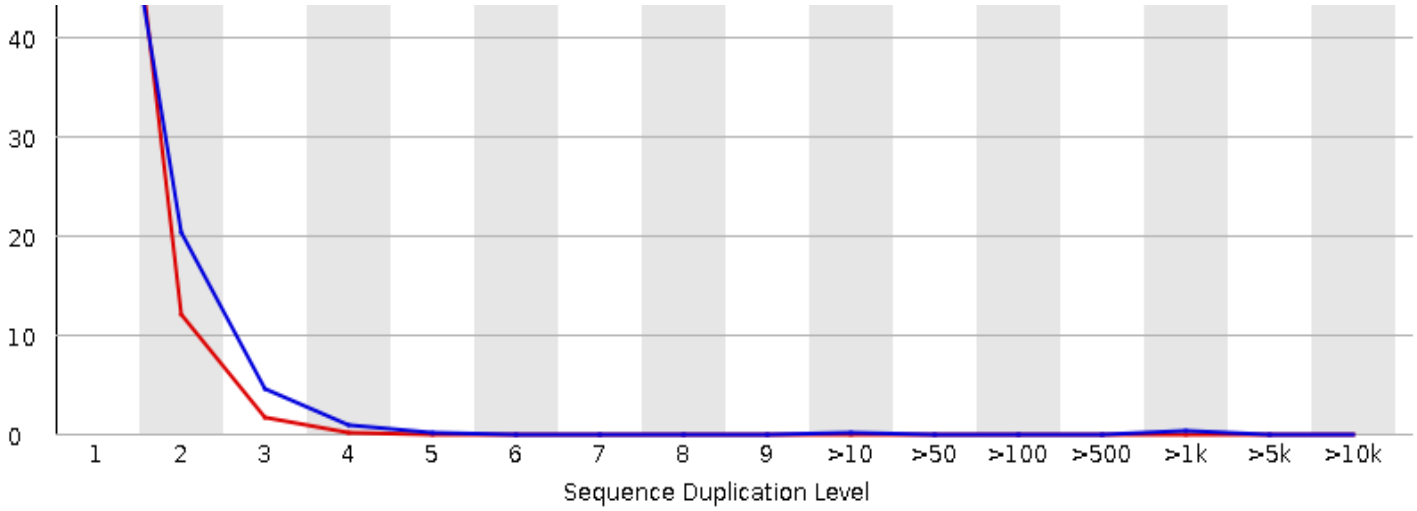
Sequence Length Distribution





Sequence Duplication Levels

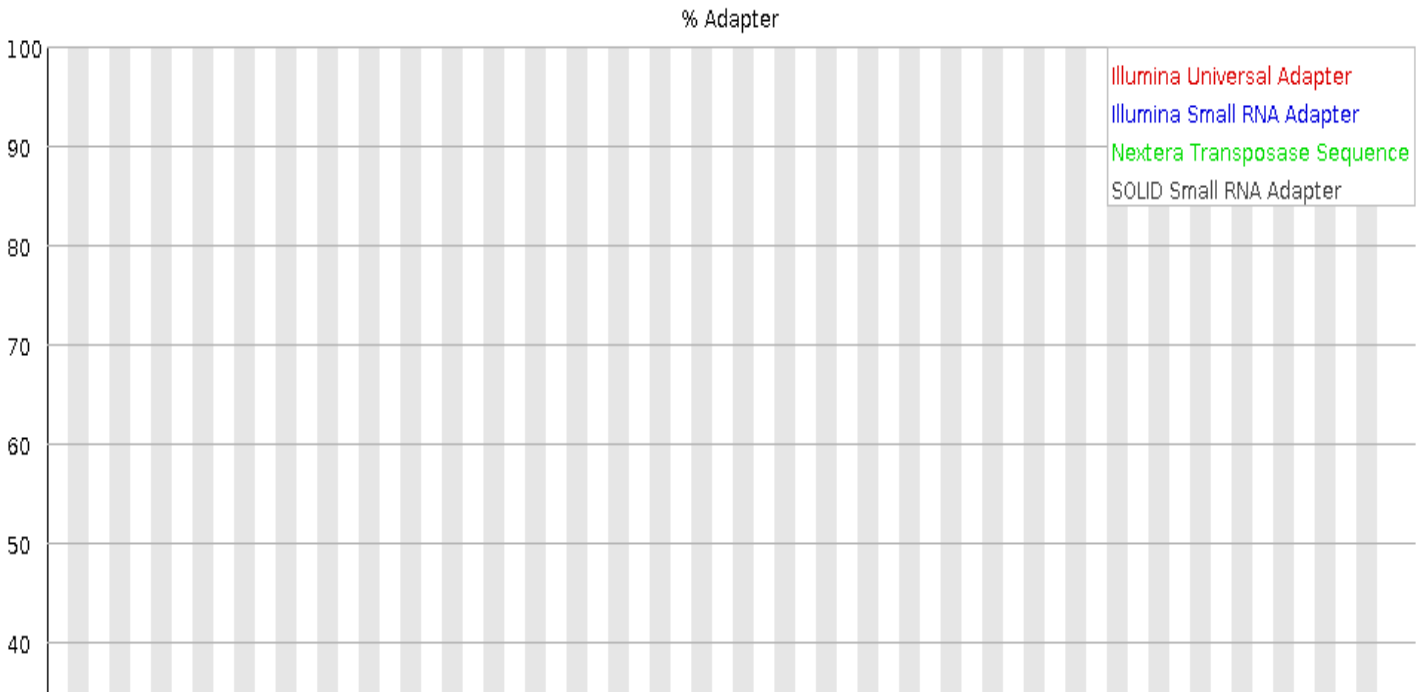


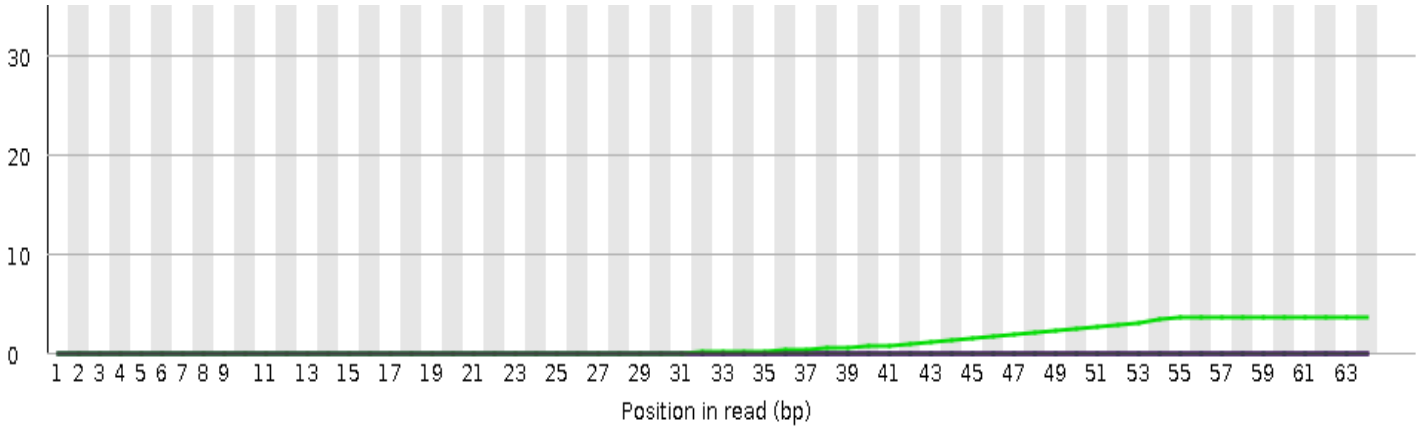


Overrepresented sequences

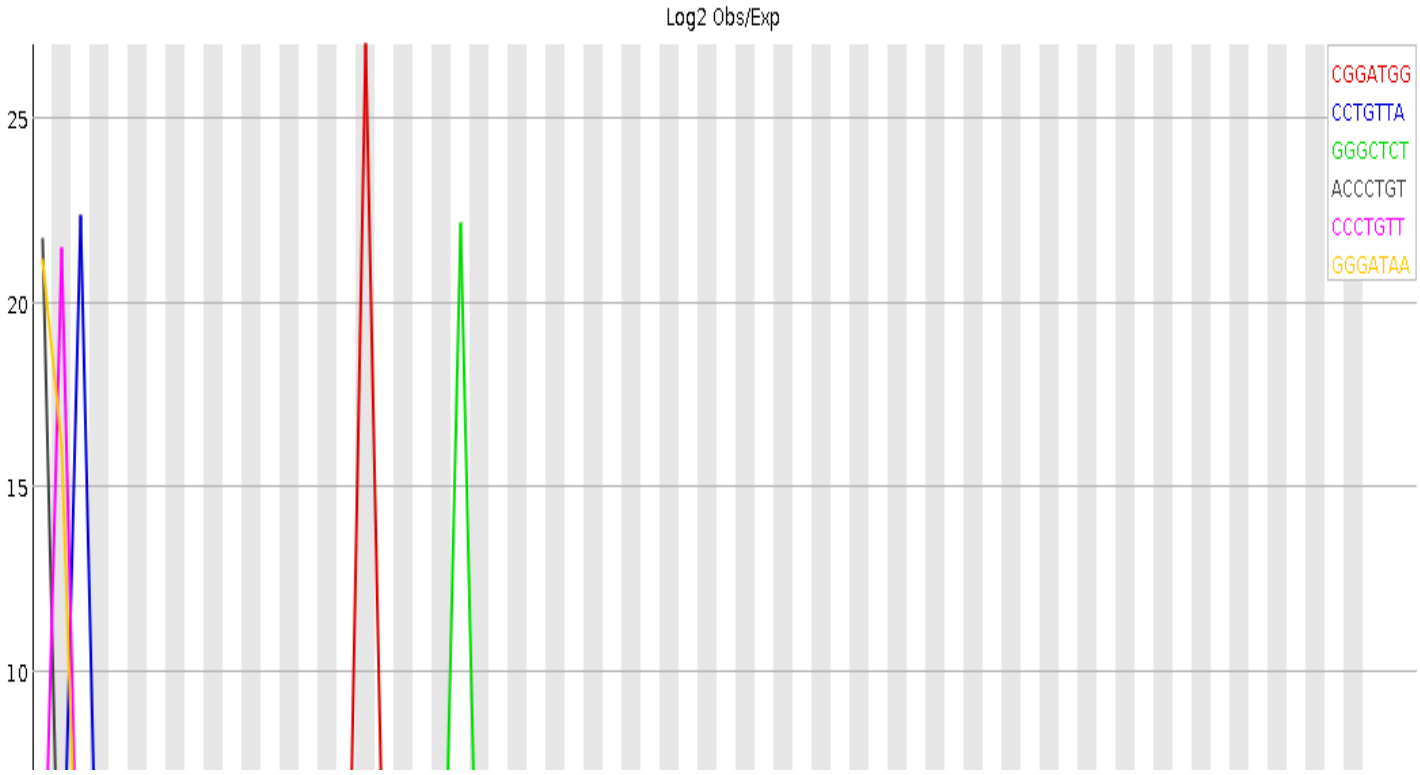
Sequence	Count	Percentage	Possible Source
CCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACC	1840	0.25003193342628	No Hit
GGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGG	1471	0.1998896598206836	No Hit

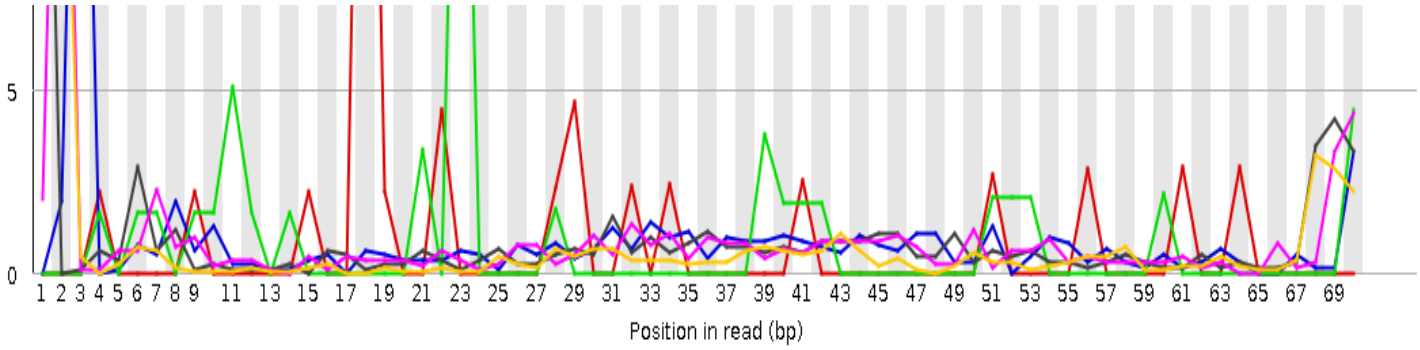
Adapter Content





Kmer Content





Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
CGGATGG	140	4.7293724E-11	26.945515	18
CCTGTTA	2365	0.0	22.299229	3
GGGCTCT	185	6.366463E-11	22.123663	23
ACCCTGT	2360	0.0	21.694696	1
CCCTGTT	2460	0.0	21.43808	2
GGGATAA	3335	0.0	21.09746	1
TGGGCTC	195	1.2914825E-10	20.987684	22
AGGACCG	90	4.0244413E-4	20.92765	5
AGGGATA	2465	0.0	20.898008	1
CTGTTAT	2655	0.0	19.86353	4
CGTGTAG	355	0.0	19.795761	68
TCCCTAG	860	0.0	19.727047	10
AGTCGTG	320	7.2759576E-12	19.318377	65
ATCCCTA	2675	0.0	19.261354	9
GACGGAT	170	2.8989416E-7	18.483196	16
GGATAAC	3800	0.0	18.174011	2
ATAACAG	3890	0.0	17.914928	4
TATCCCT	2955	0.0	17.855442	8
ATGGGCT	215	9.815267E-9	17.565084	21
TCGTGTA	380	5.456968E-12	17.400879	67

Produced by FastQC (version 0.11.3)