FastQC Report

Thu 21 May 2015
myskewer_41_seqprep_dupRemoved_R2.fastq

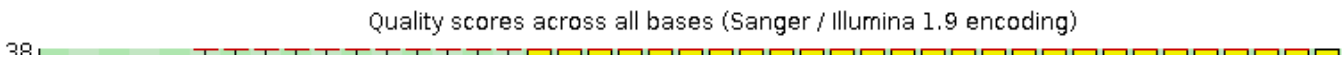
Summary

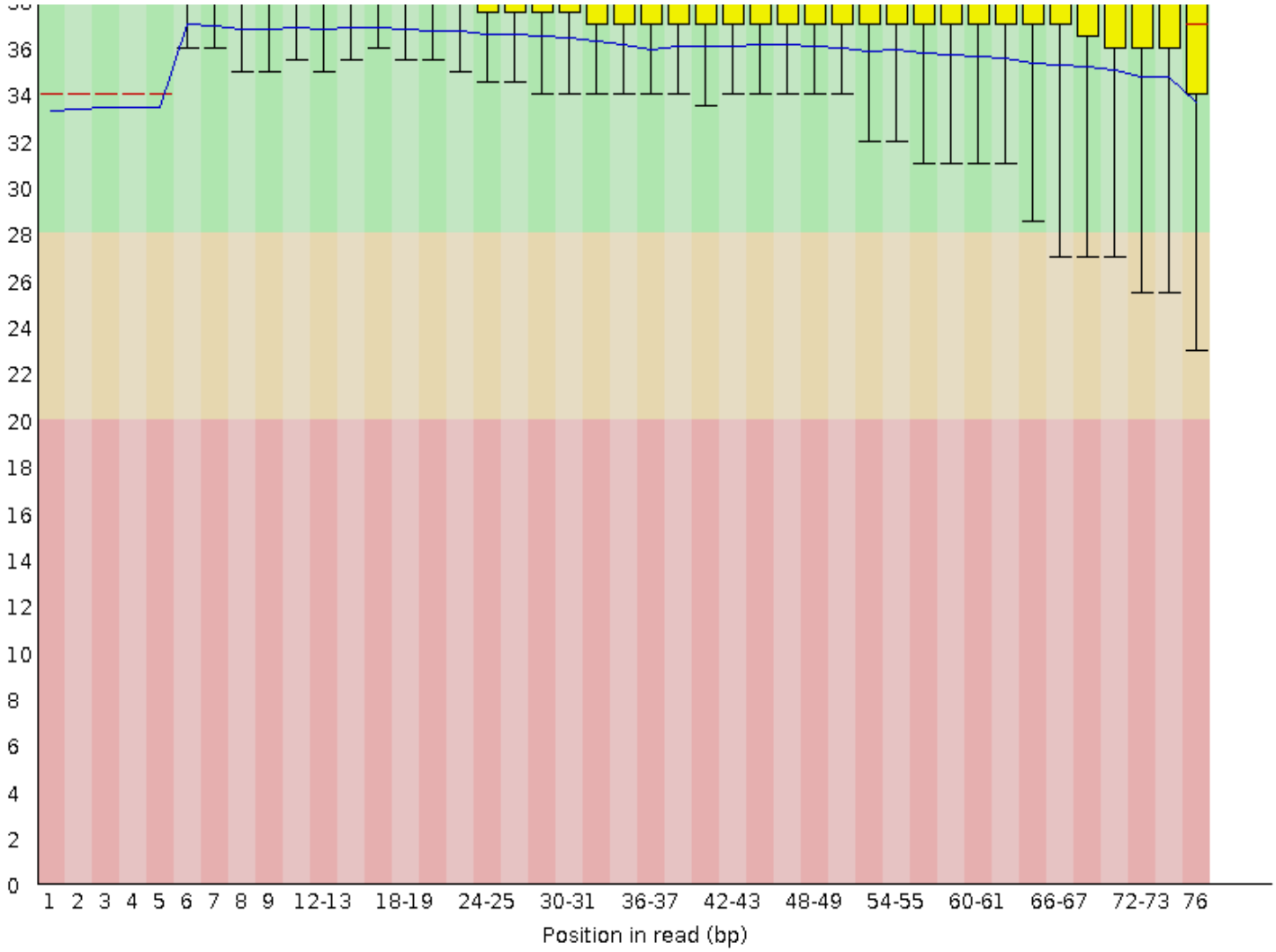
- Basic Statistics
- Per base sequence quality
- Per tile sequence quality
- Per sequence quality scores
- Per base sequence content
- Per sequence GC content
- Per base N content
- Sequence Length Distribution
- Sequence Duplication Levels
- Overrepresented sequences
- Adapter Content
- Kmer Content

Basic Statistics

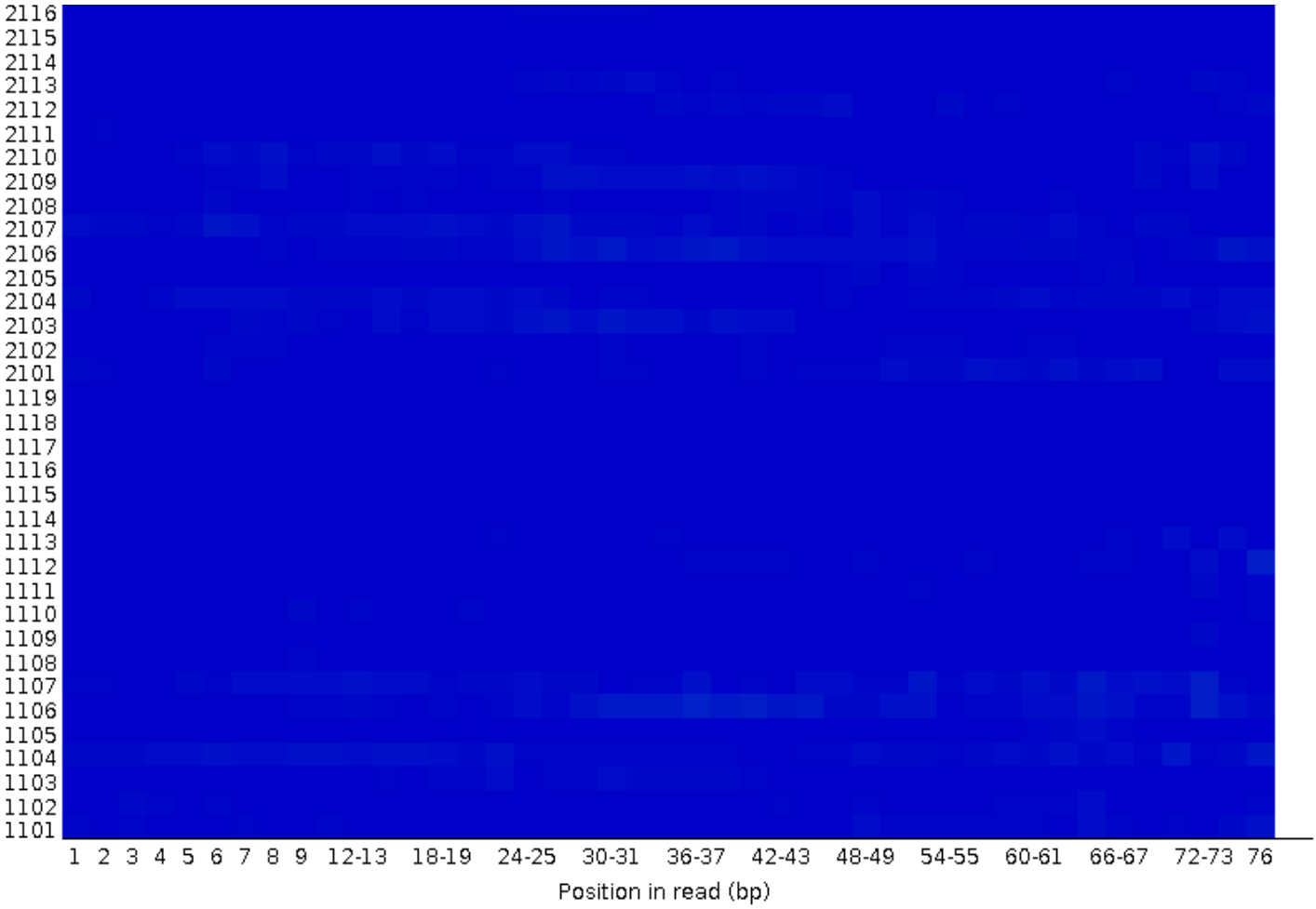
Measure	Value
Filename	myskewer_41_seqprep_dupRemoved_R2.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	1237731
Sequences flagged as poor quality	0
Sequence length	28-76
%GC	44

Per base sequence quality

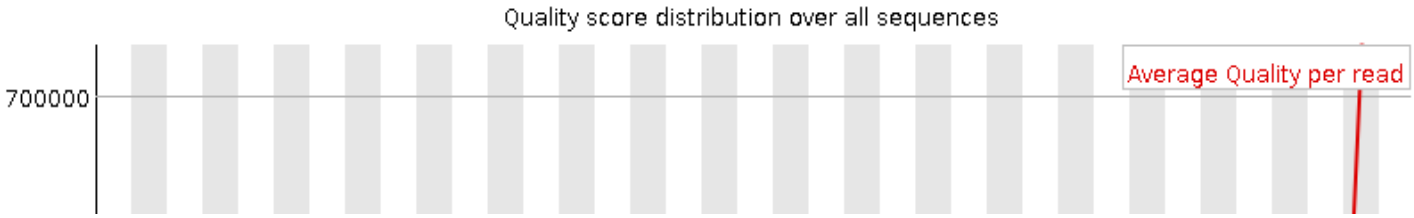


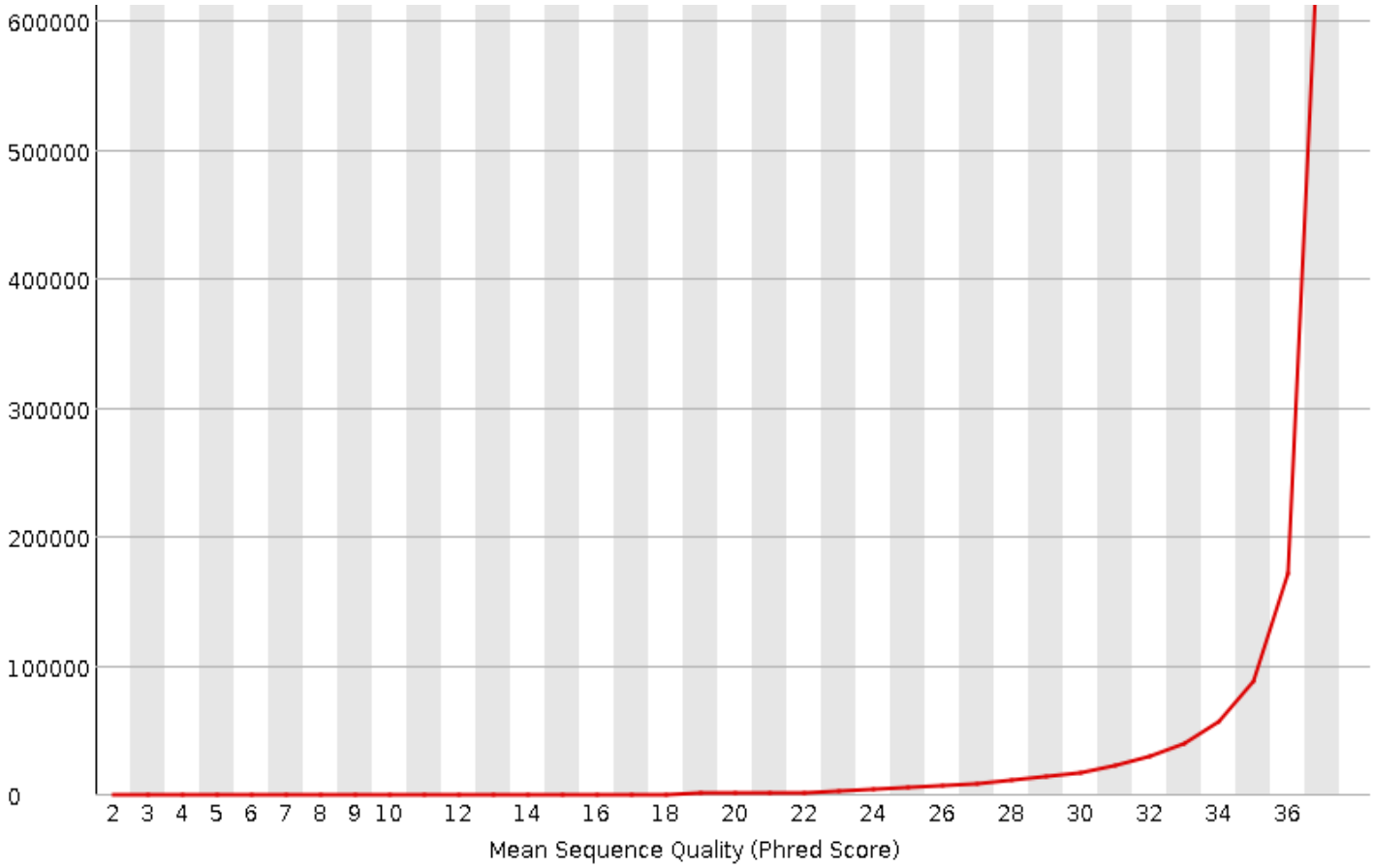


Per tile sequence quality

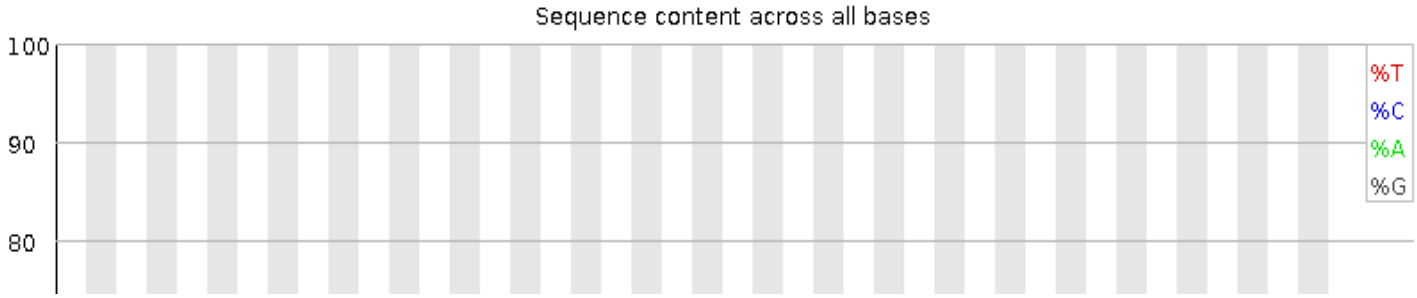


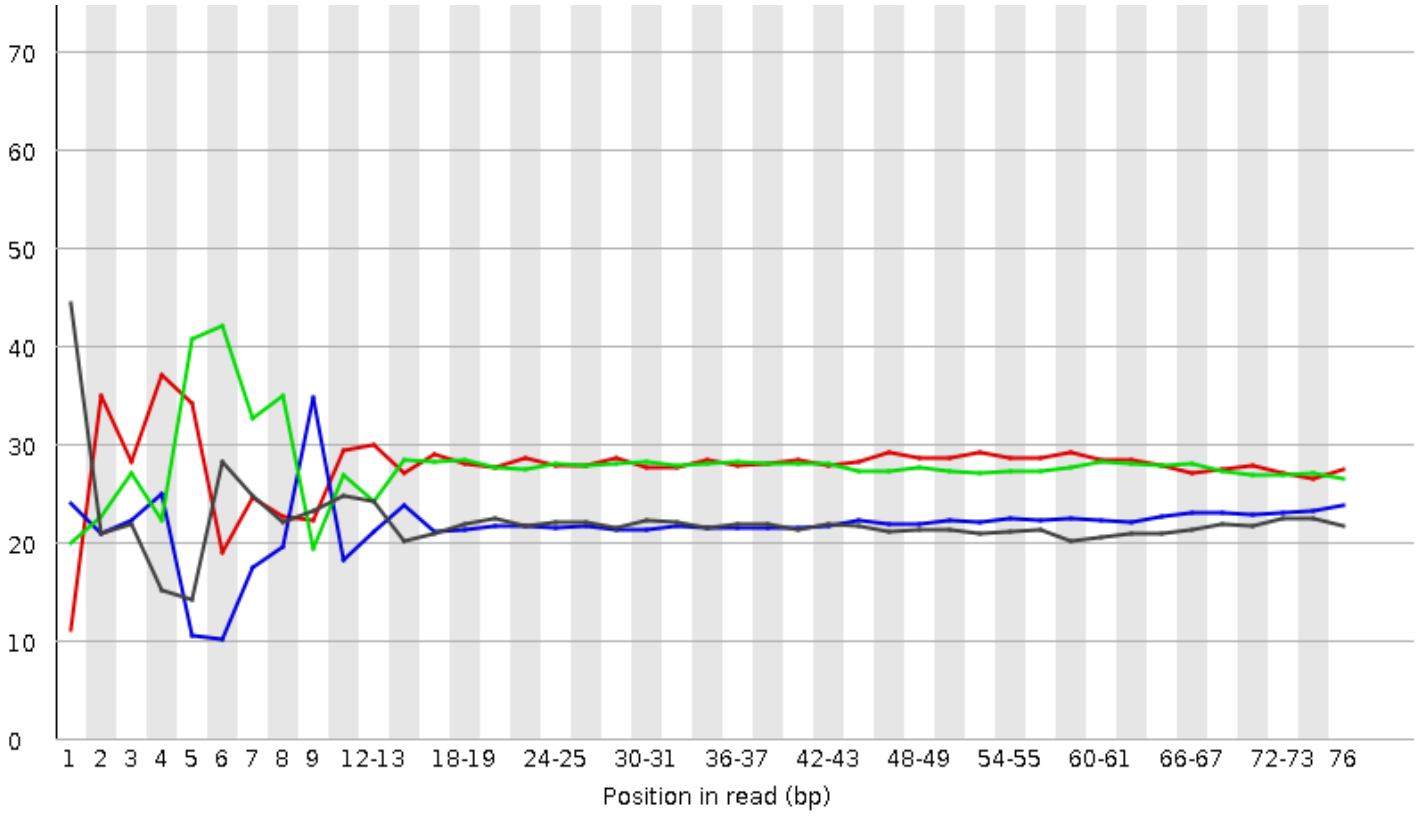
Per sequence quality scores



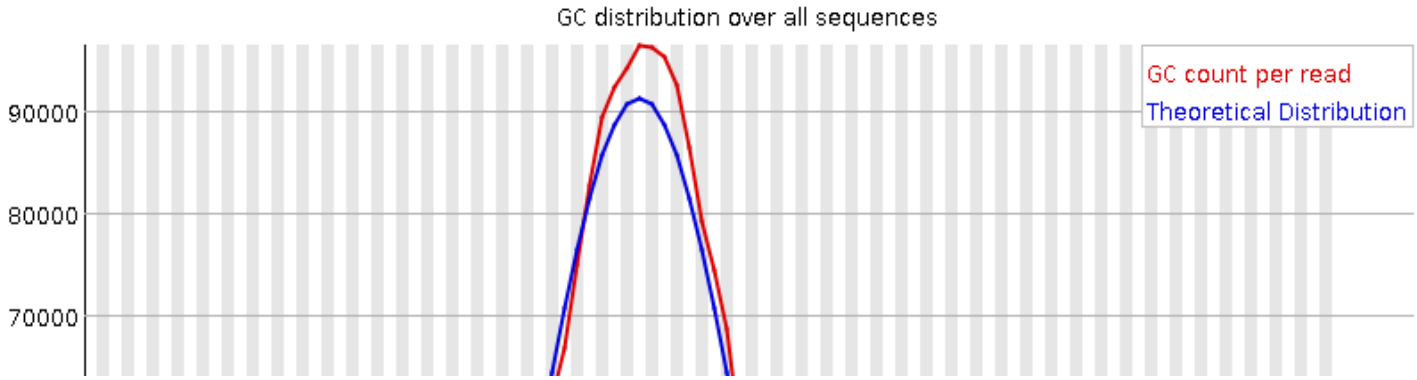


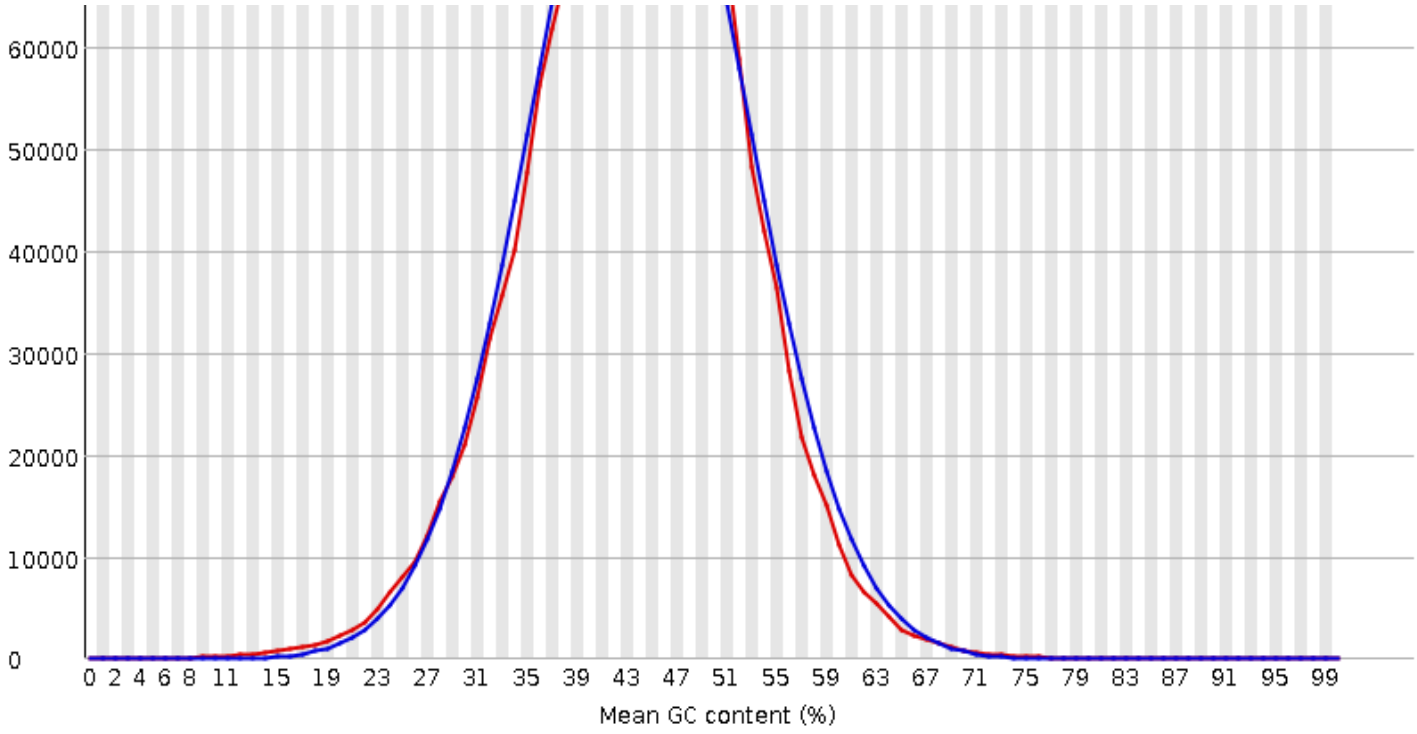
Per base sequence content



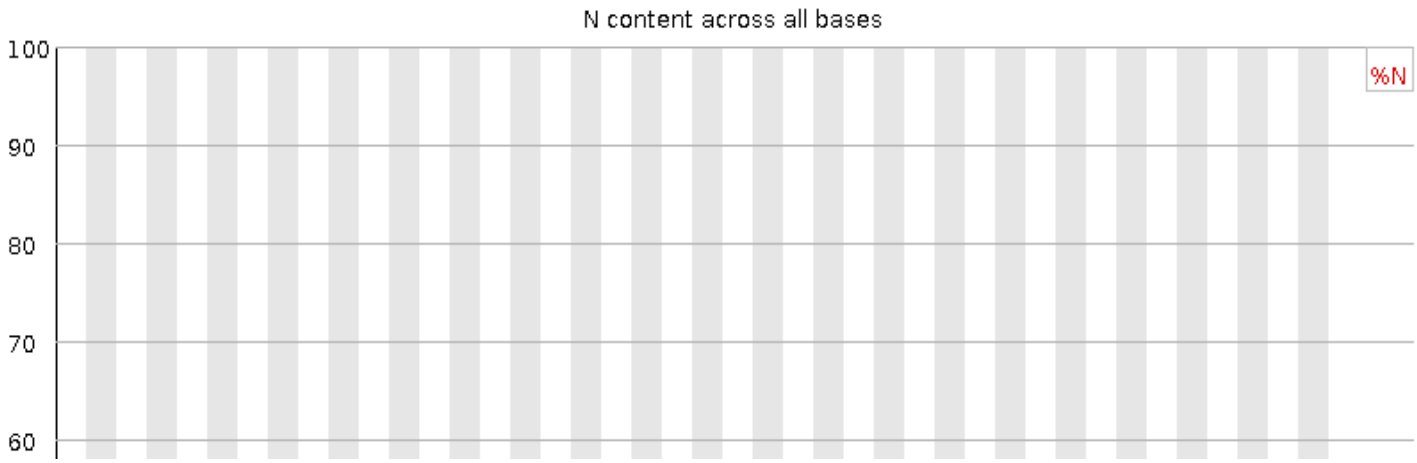


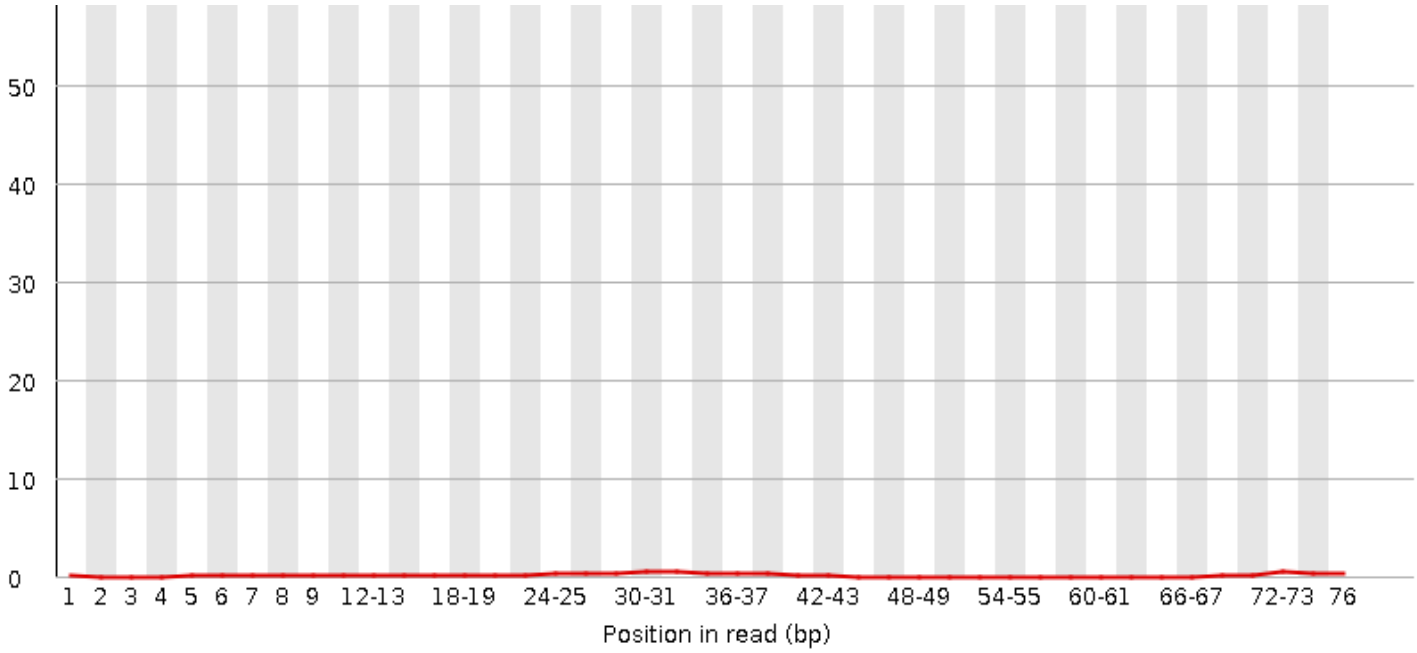
Per sequence GC content



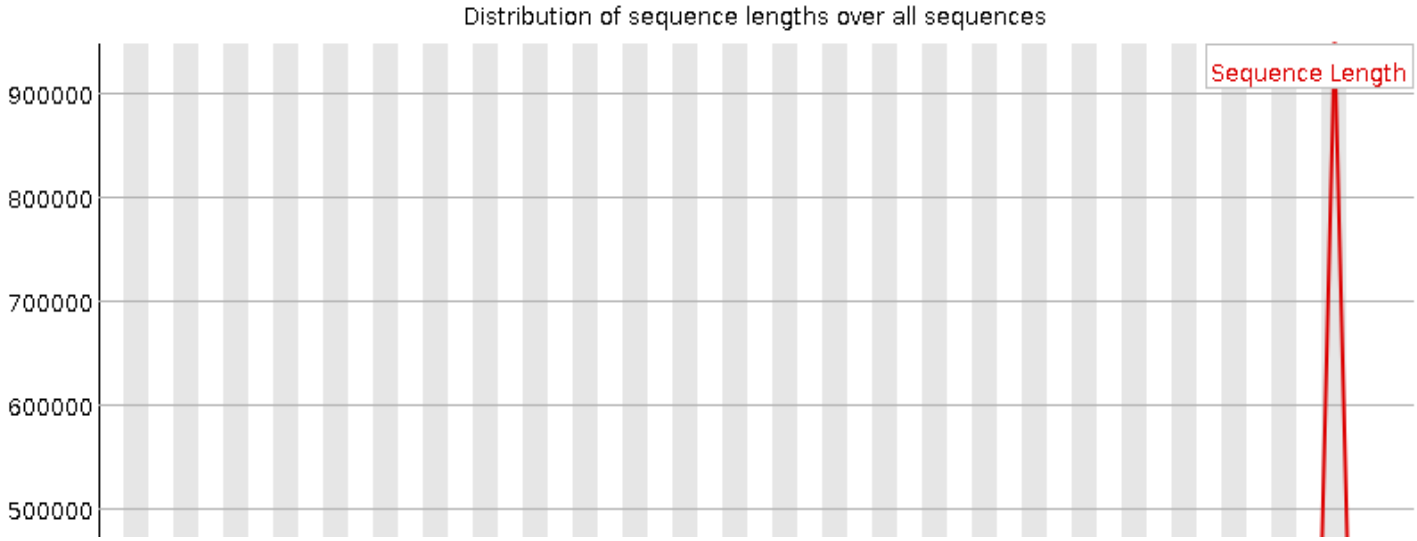


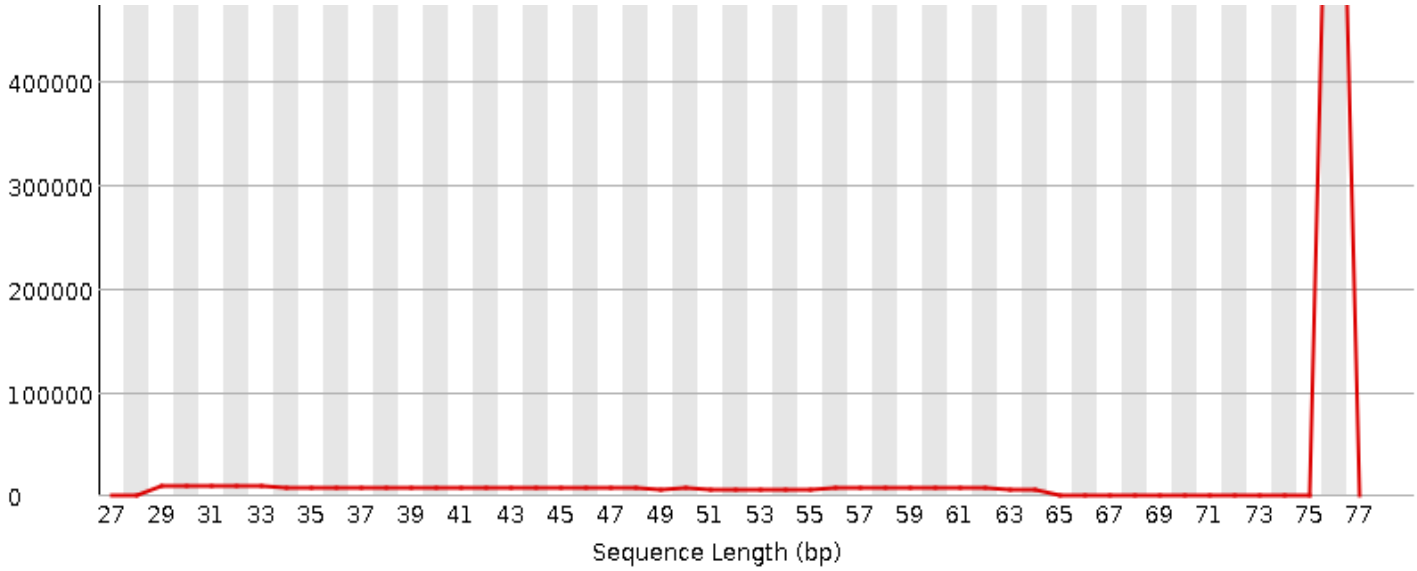
Per base N content



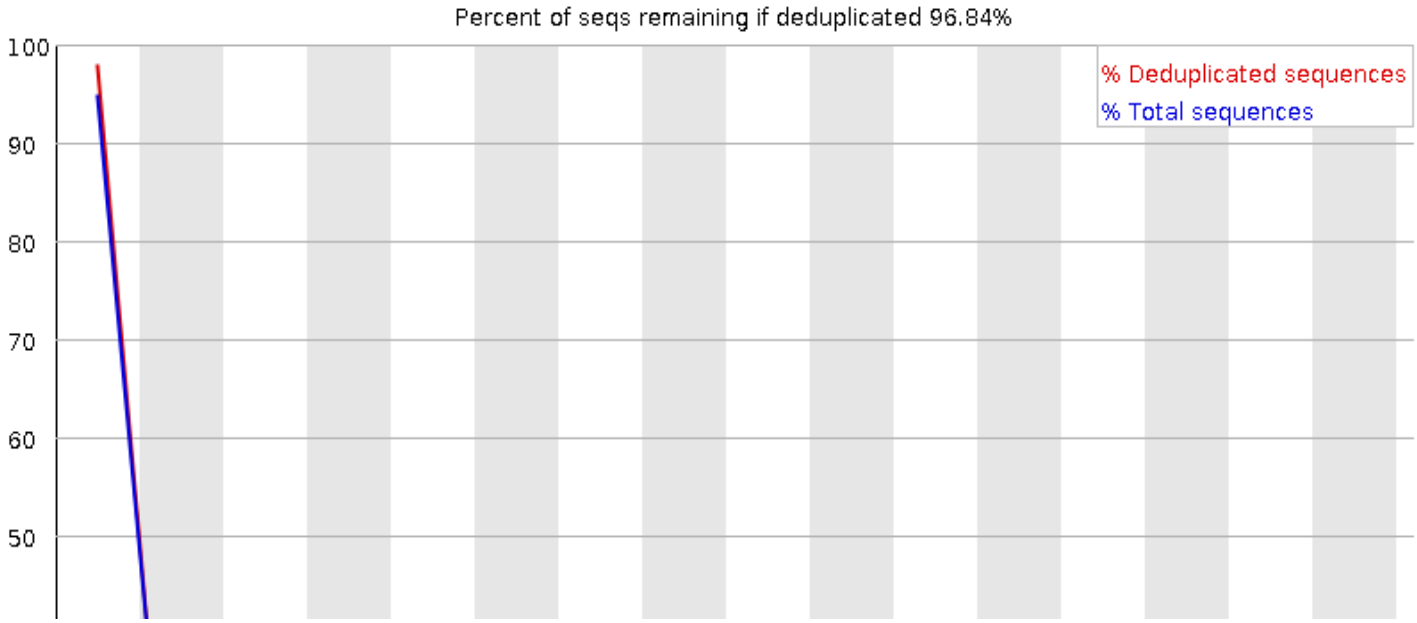


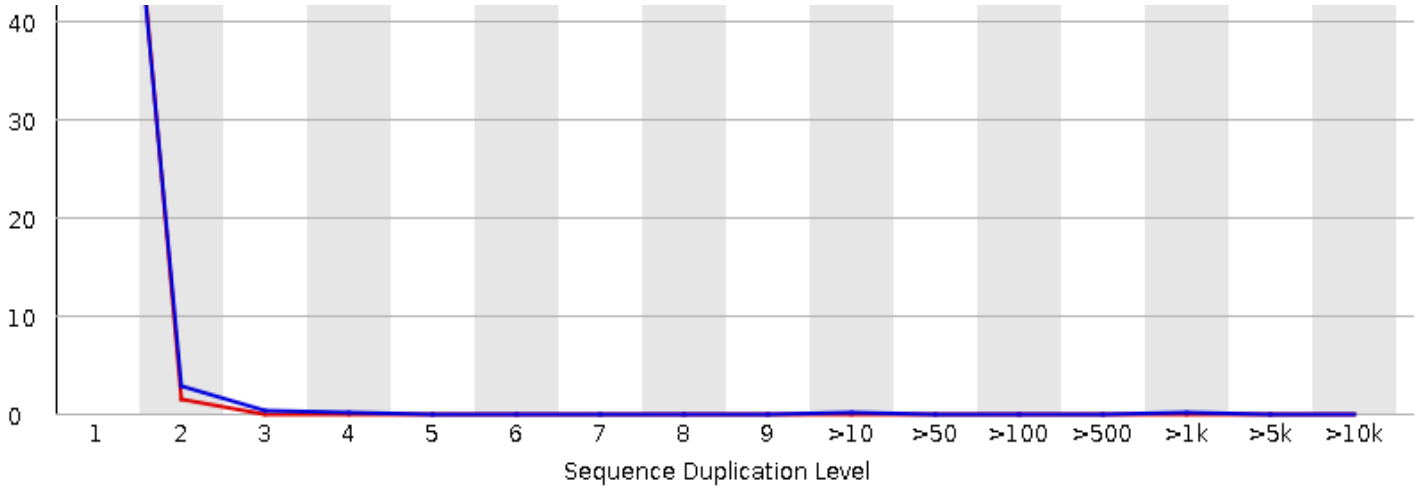
Sequence Length Distribution





Sequence Duplication Levels

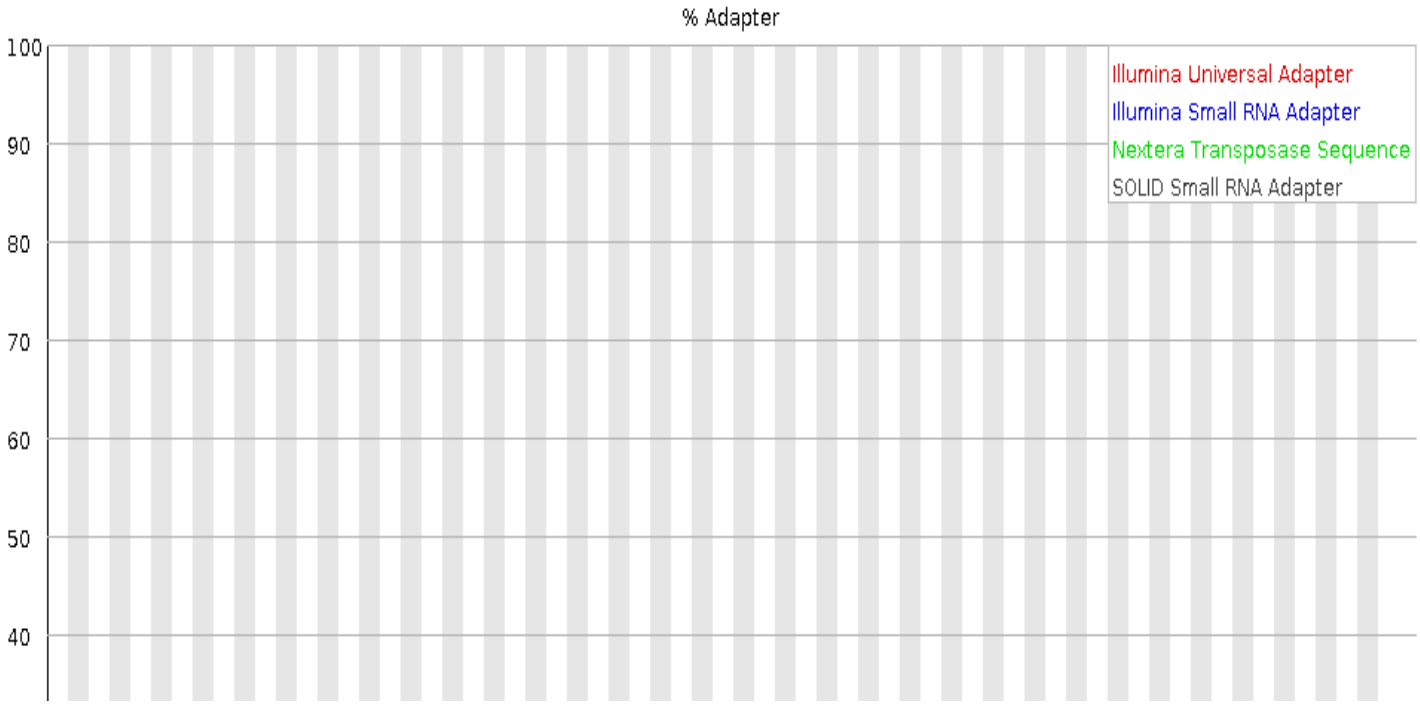


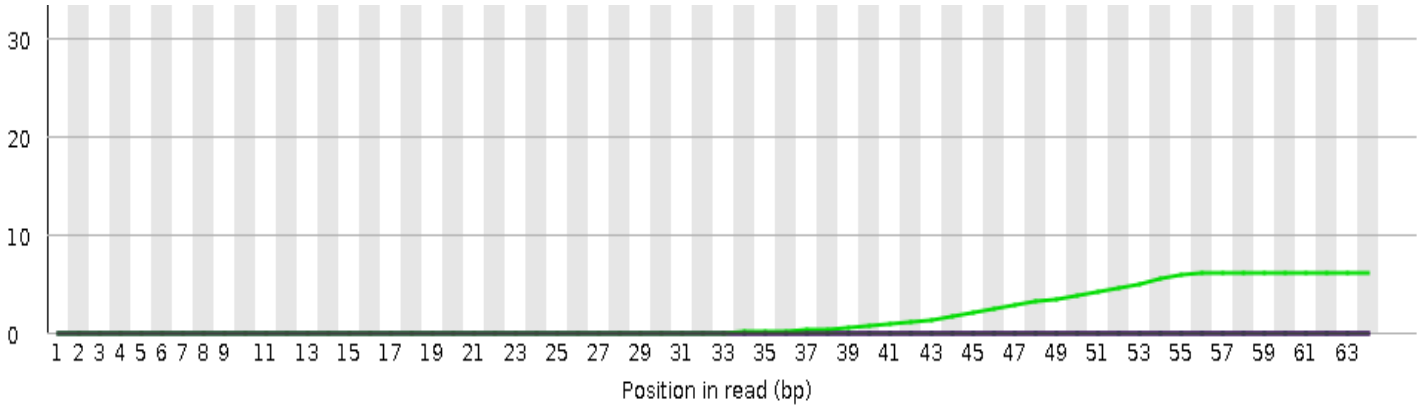


Overrepresented sequences

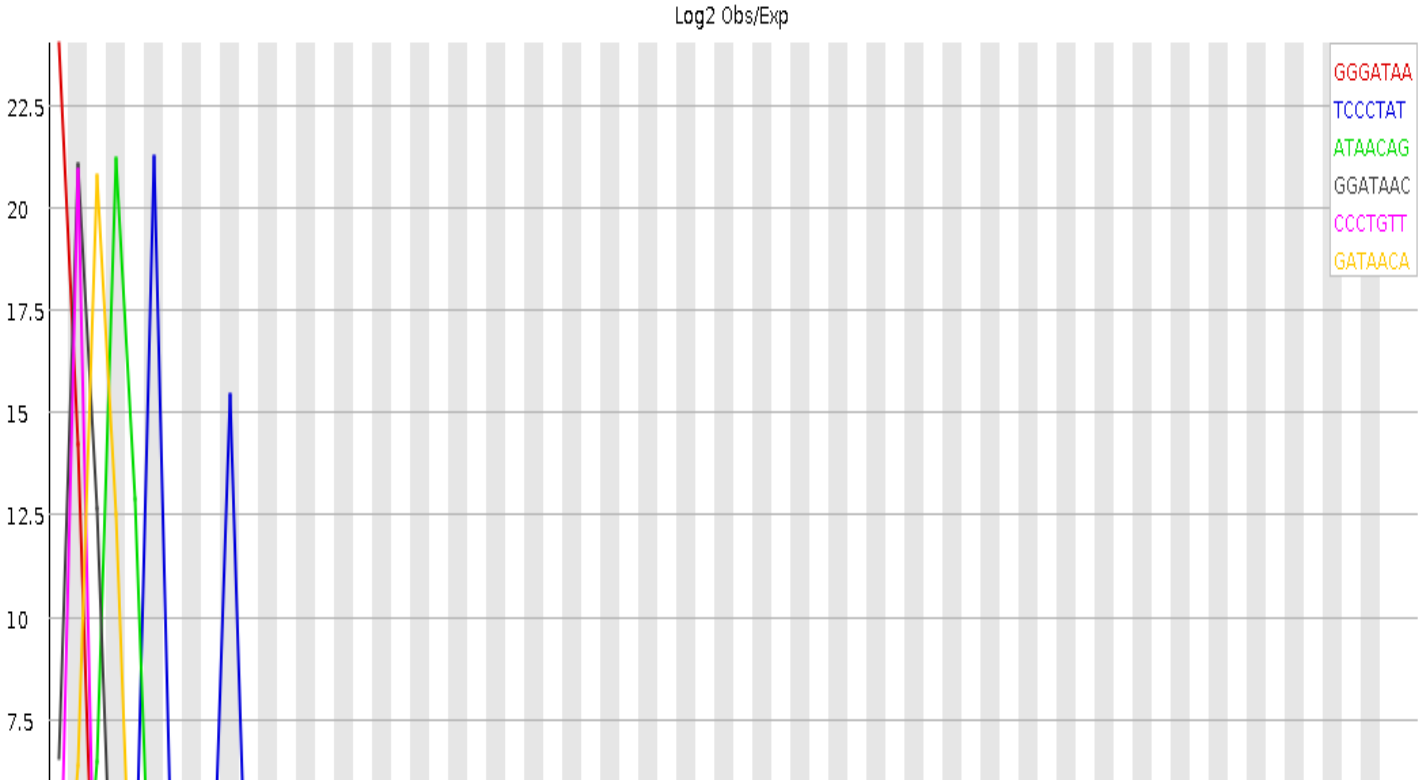
Sequence	Count	Percentage	Possible Source
CCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACC	1682	0.13589382507184516	No Hit
GGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGG	1444	0.11666509120317743	No Hit

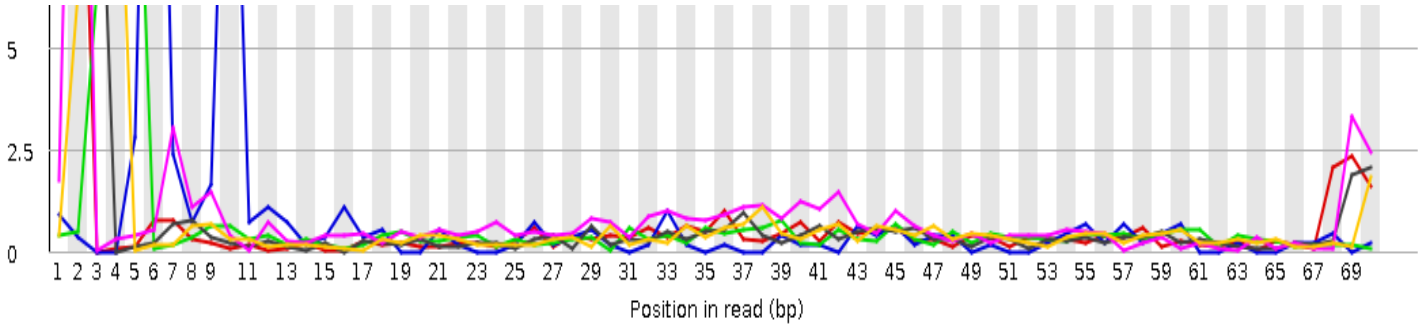
Adapter Content





Kmer Content





Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
GGGATAA	7190	0.0	23.982878	1
TCCCTAT	1675	0.0	21.220467	6
ATAACAG	8225	0.0	21.188507	4
GGATAAC	8210	0.0	21.031376	2
CCCTGTT	5970	0.0	20.914848	2
GATAACA	8350	0.0	20.795965	3
AGGGATA	4645	0.0	20.729334	1
CCTGTTA	5910	0.0	20.545956	3
ATCCCTA	5805	0.0	20.501505	9
ACCCTGT	6035	0.0	20.491083	1
CCCTATG	650	0.0	20.327314	7
TCCCTAG	1915	0.0	20.057978	10
AGGGTAA	8620	0.0	20.015638	9
CTGTTAT	6130	0.0	19.859896	4
CAGGGTA	8750	0.0	19.643908	8
GGTAATT	2455	0.0	19.493427	11
ACAGGGT	9055	0.0	19.142878	7
GGGTAAT	8715	0.0	18.785904	10
AACAGGG	9445	0.0	18.383509	6
TACCGGC	95	0.007712162	18.207466	35

Produced by FastQC (version 0.11.3)