












FastQC Report

Summary

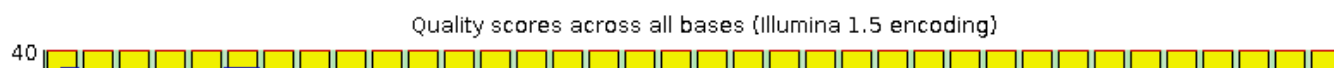
РҮСТ 30 РѢСТР» 2014
K562.trimmed1.fastq

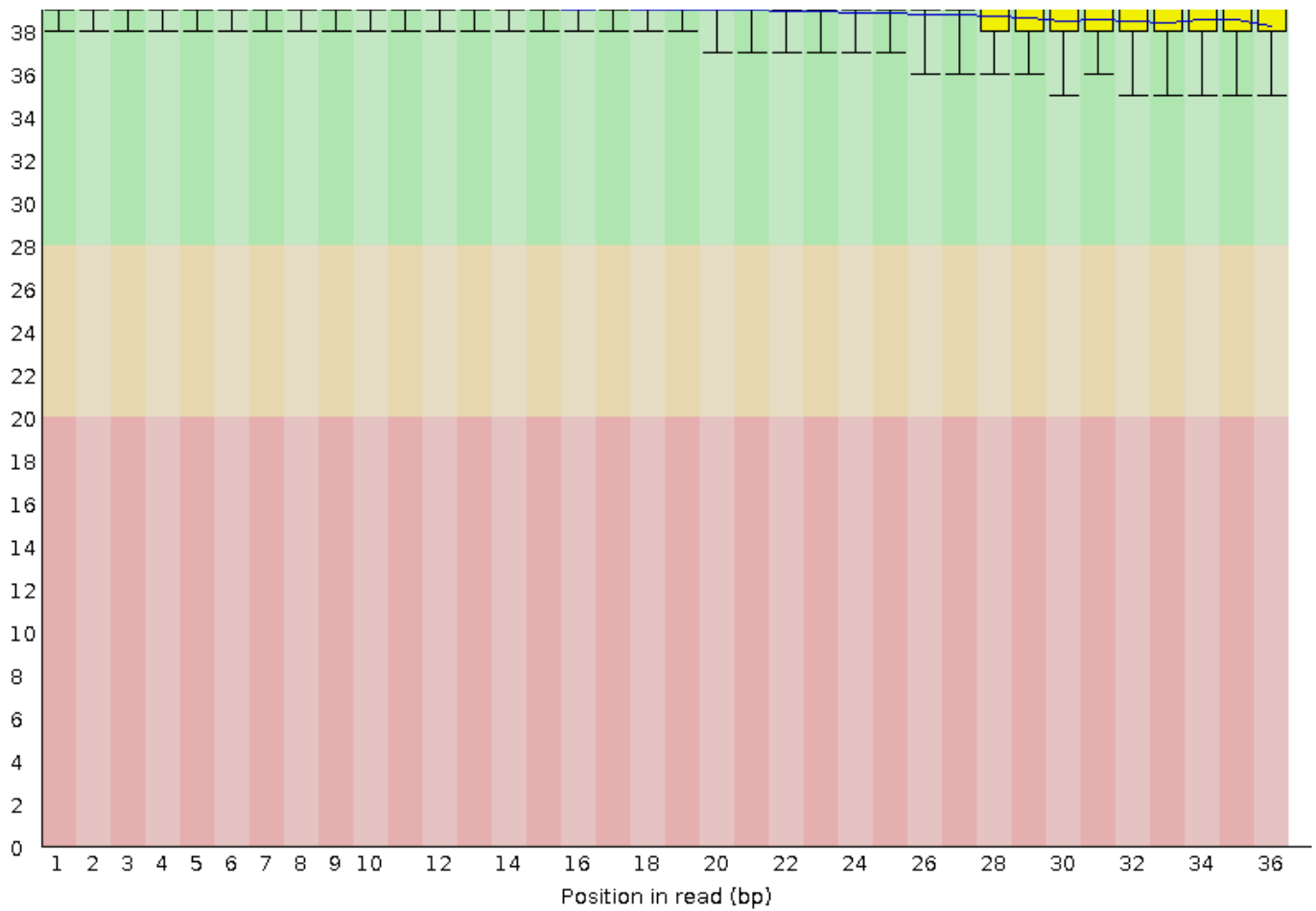
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Basic Statistics

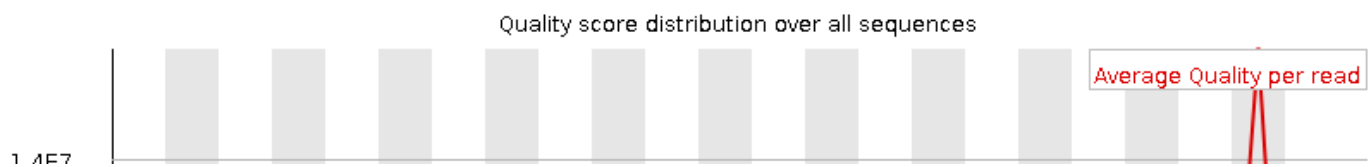
Measure	Value
Filename	K562.trimmed1.fastq
File type	Conventional base calls
Encoding	Illumina 1.5
Total Sequences	24041407
Filtered Sequences	0
Sequence length	36
%GC	40

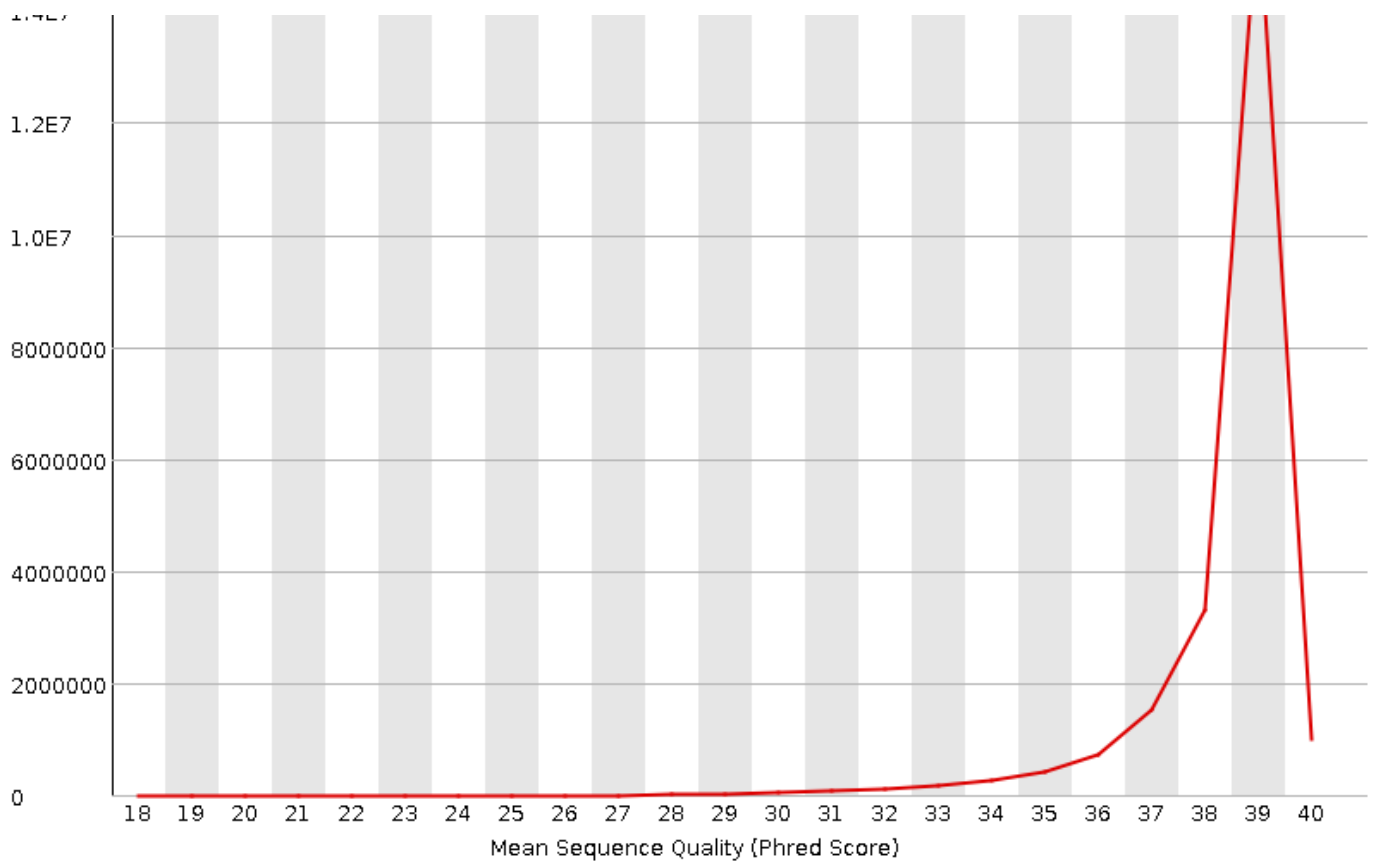
Per base sequence quality



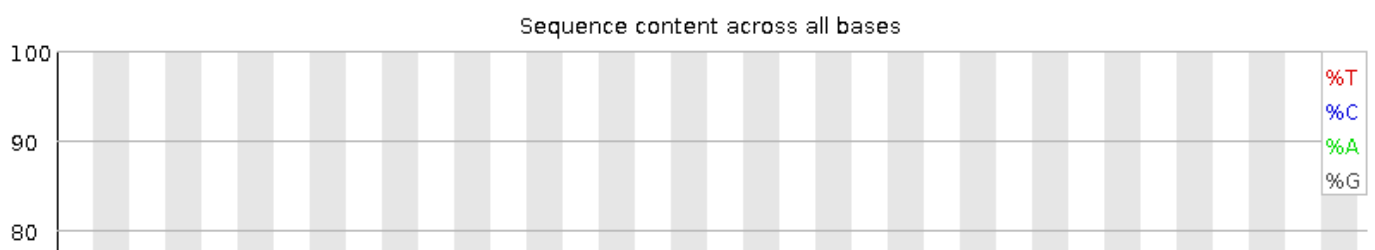


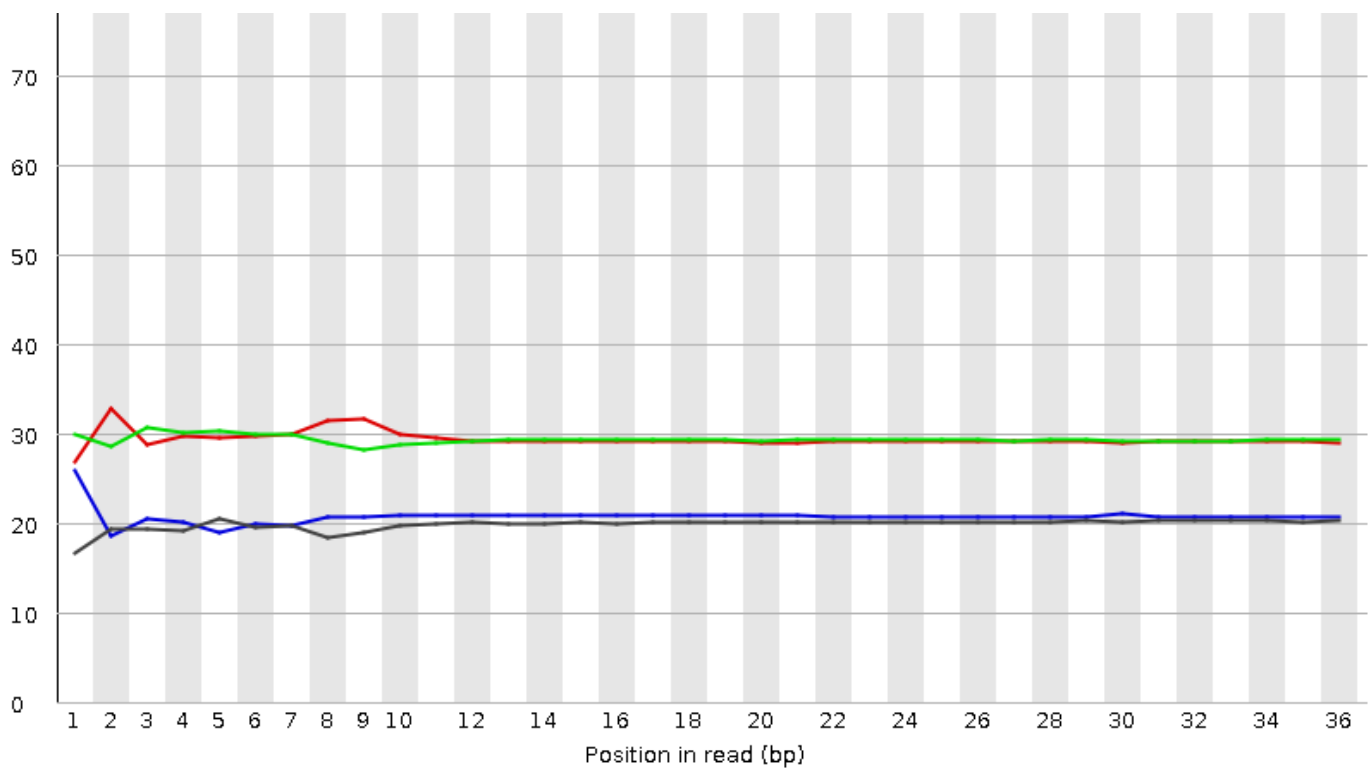
✔ Per sequence quality scores



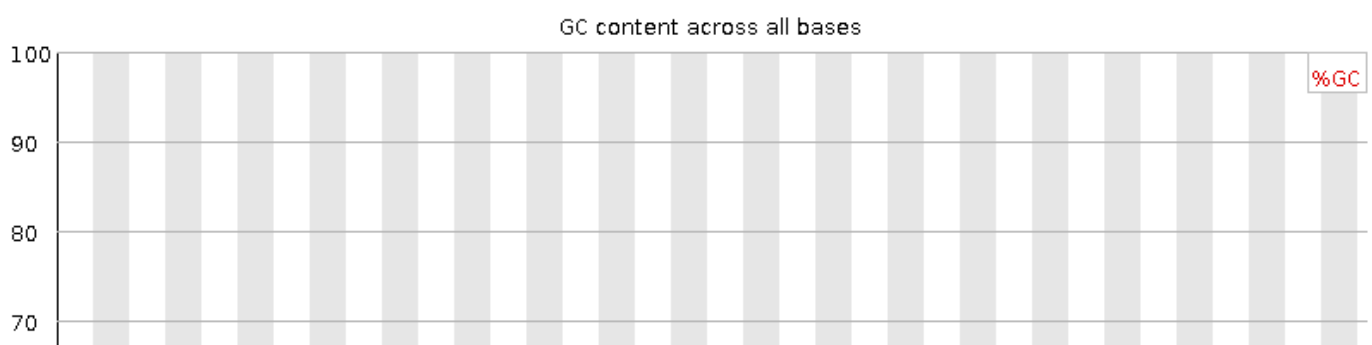


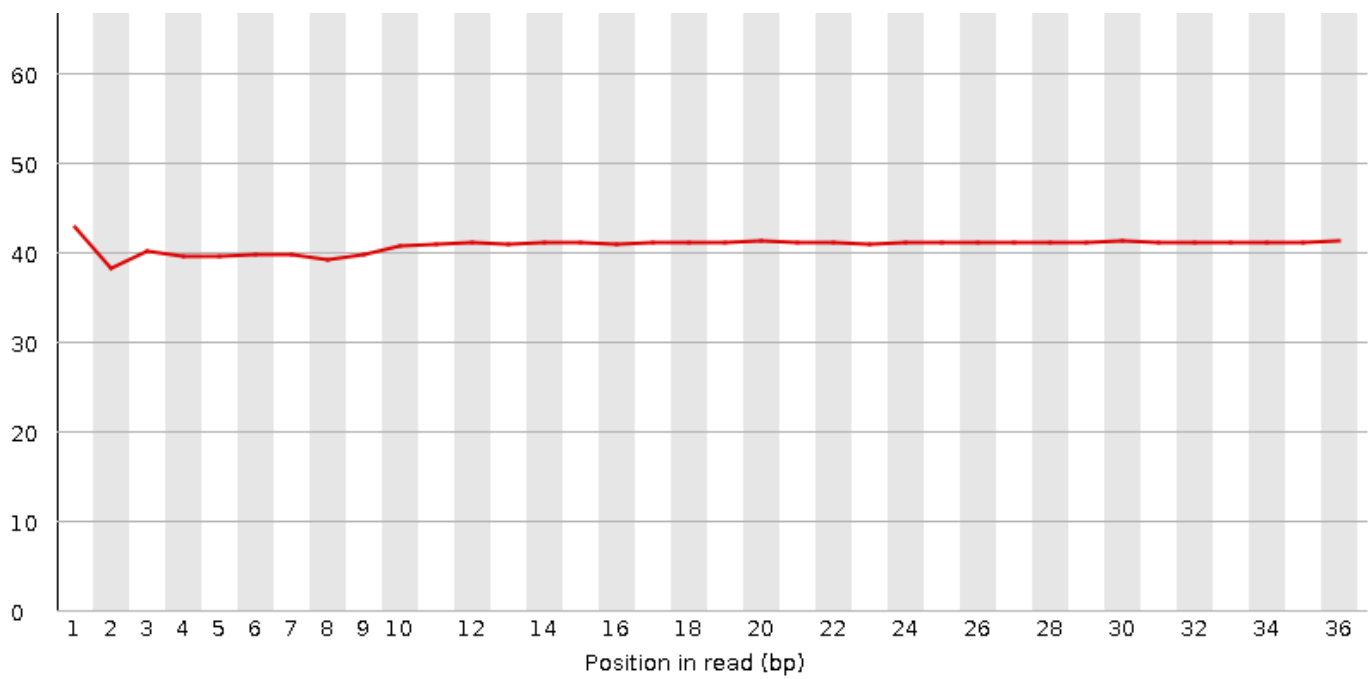
! Per base sequence content



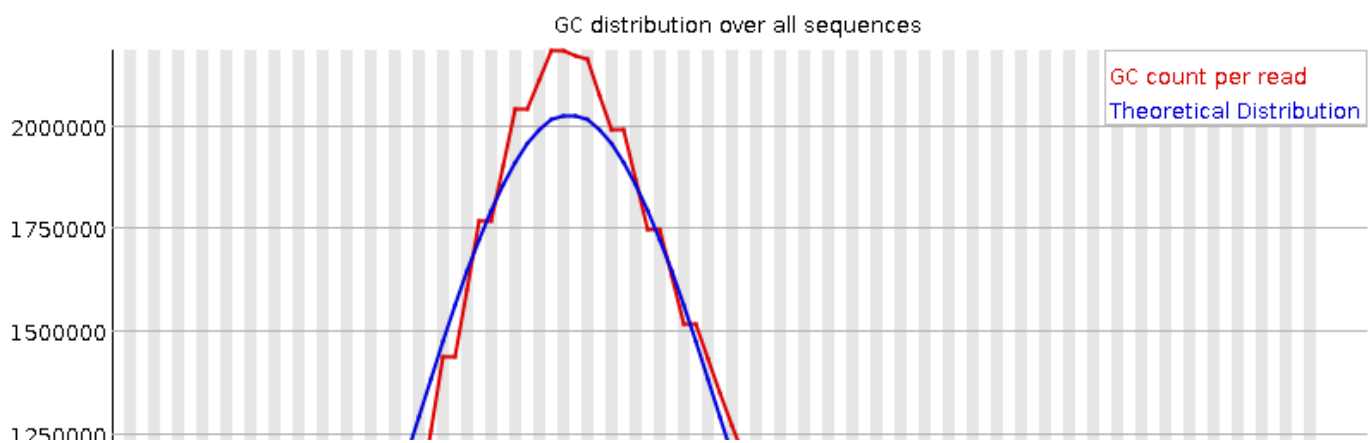


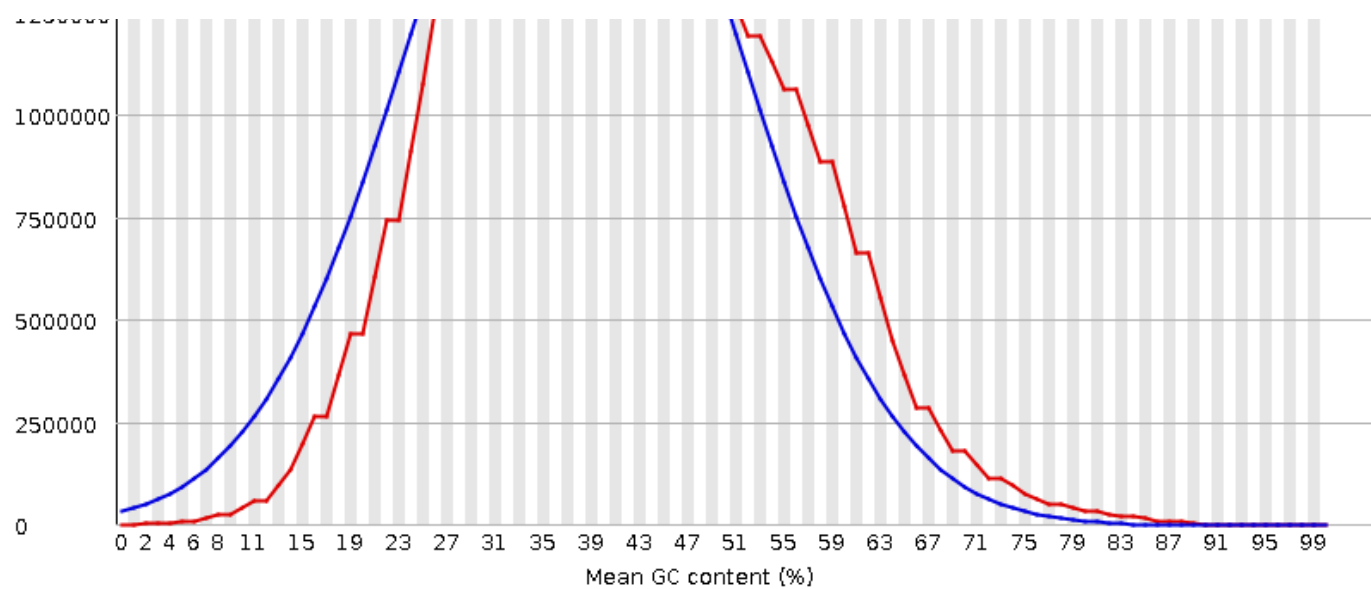
✅ Per base GC content



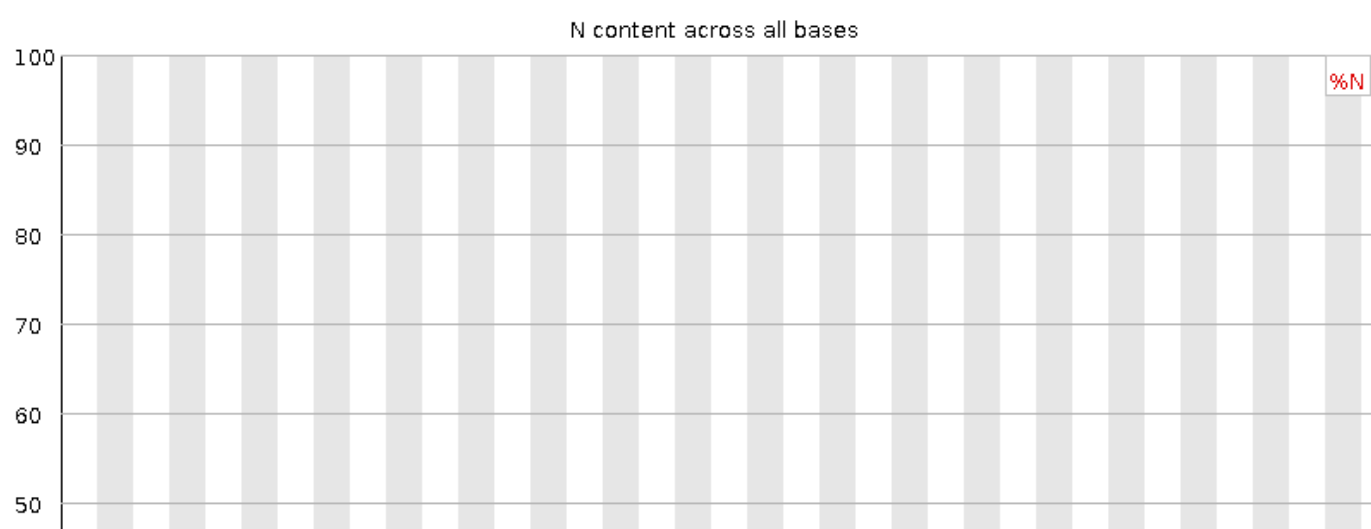


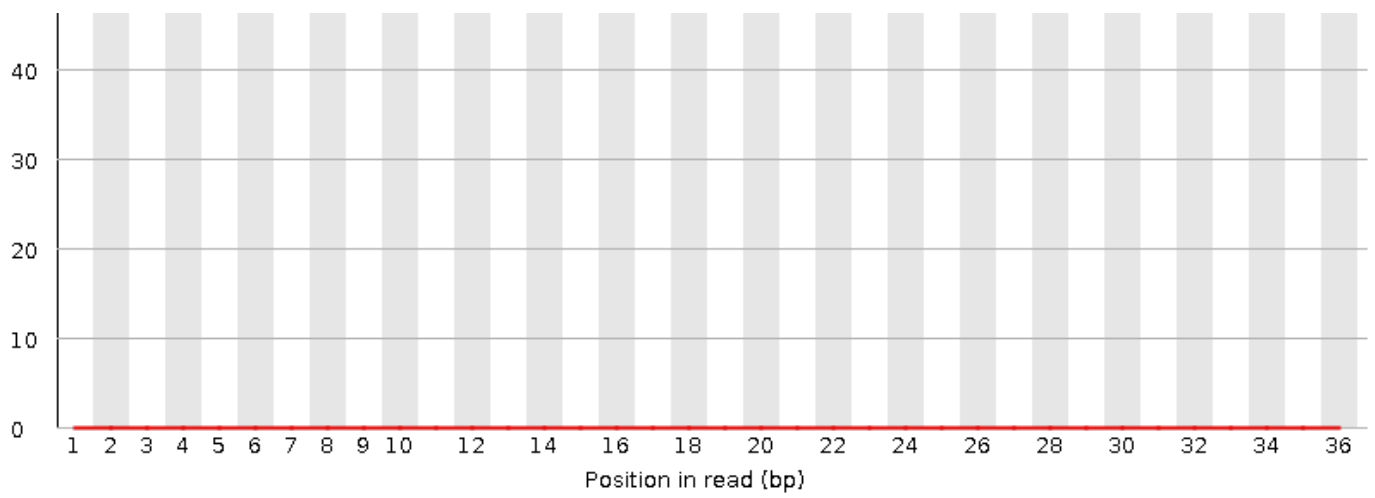
! Per sequence GC content



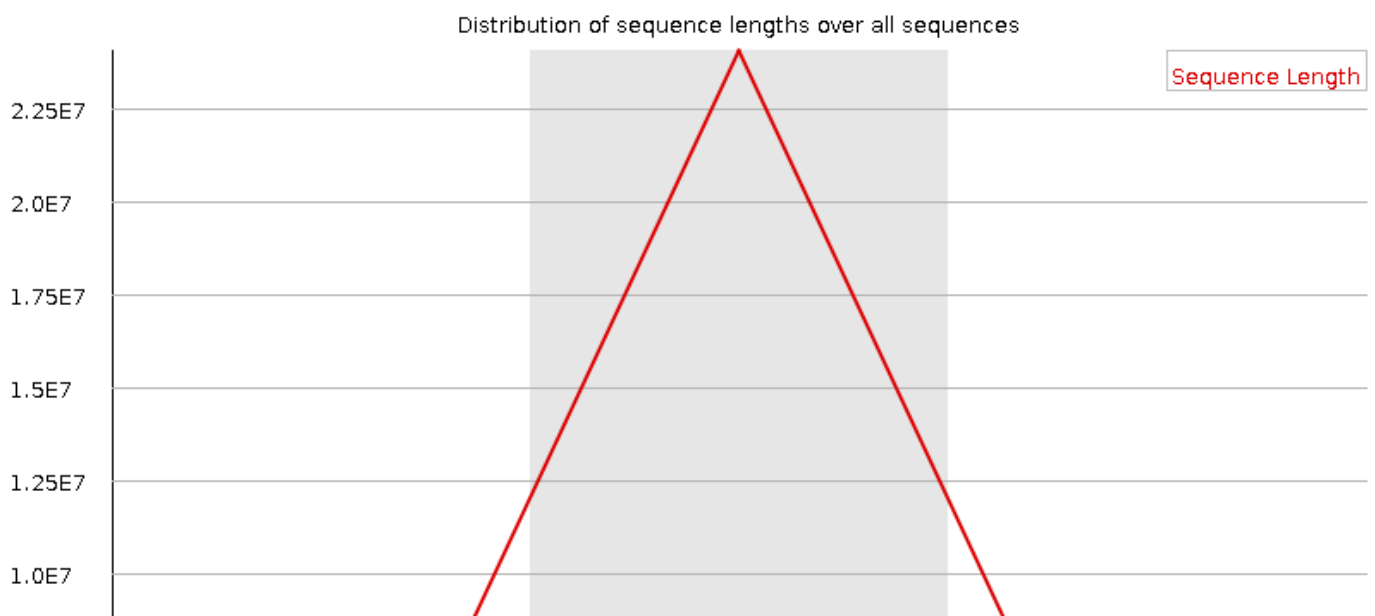


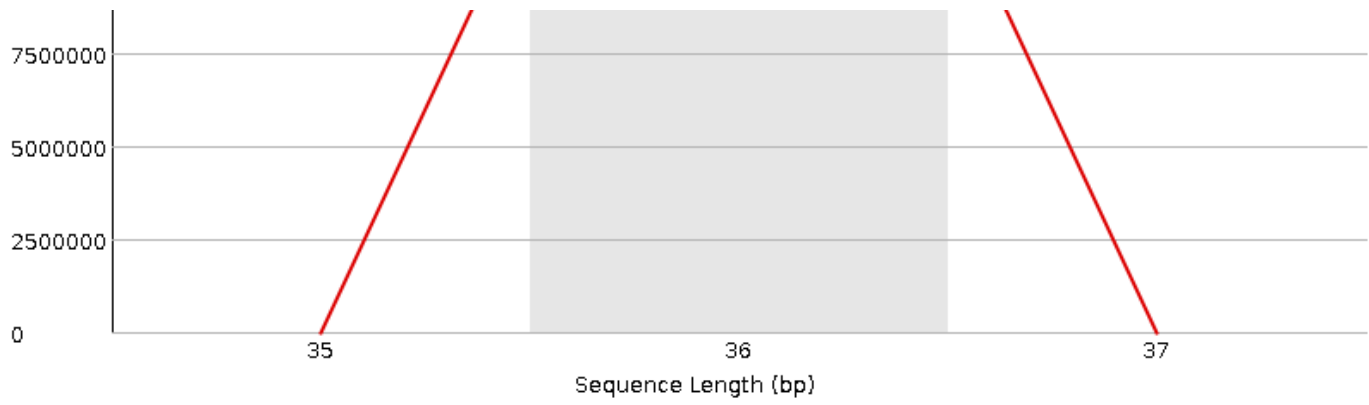
Per base N content



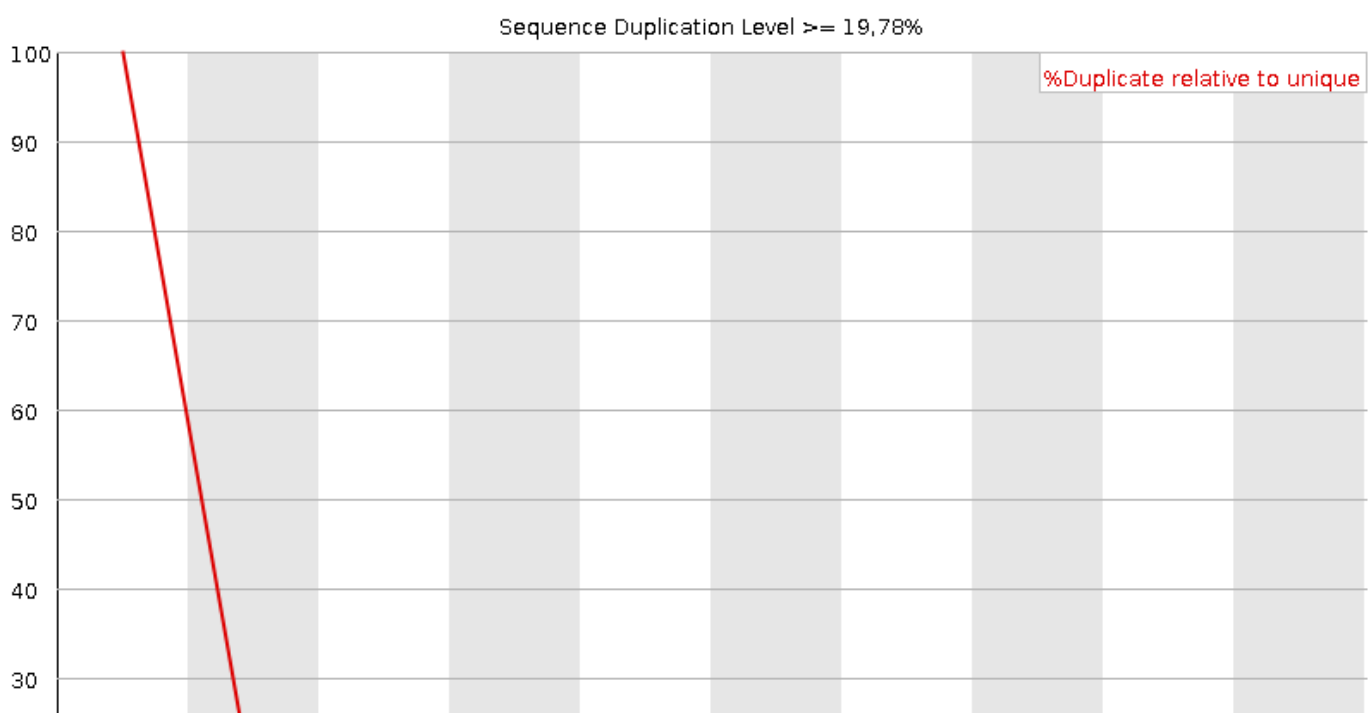


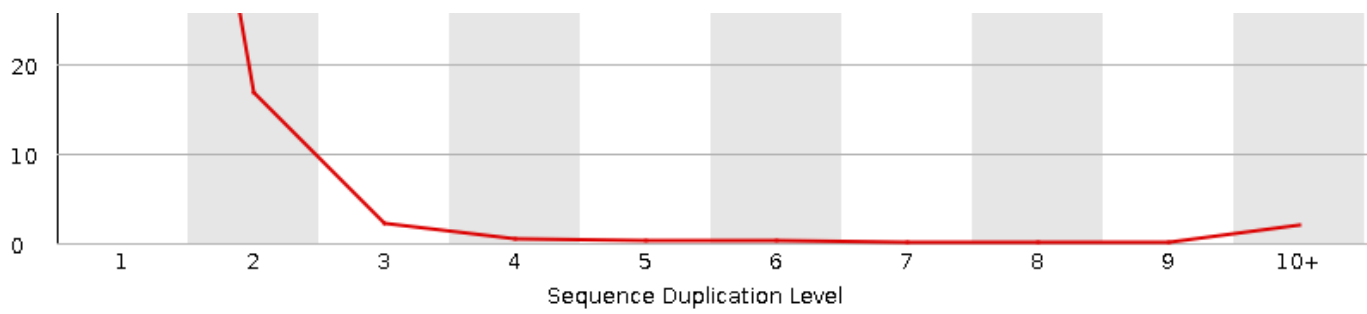
✔ Sequence Length Distribution





Sequence Duplication Levels



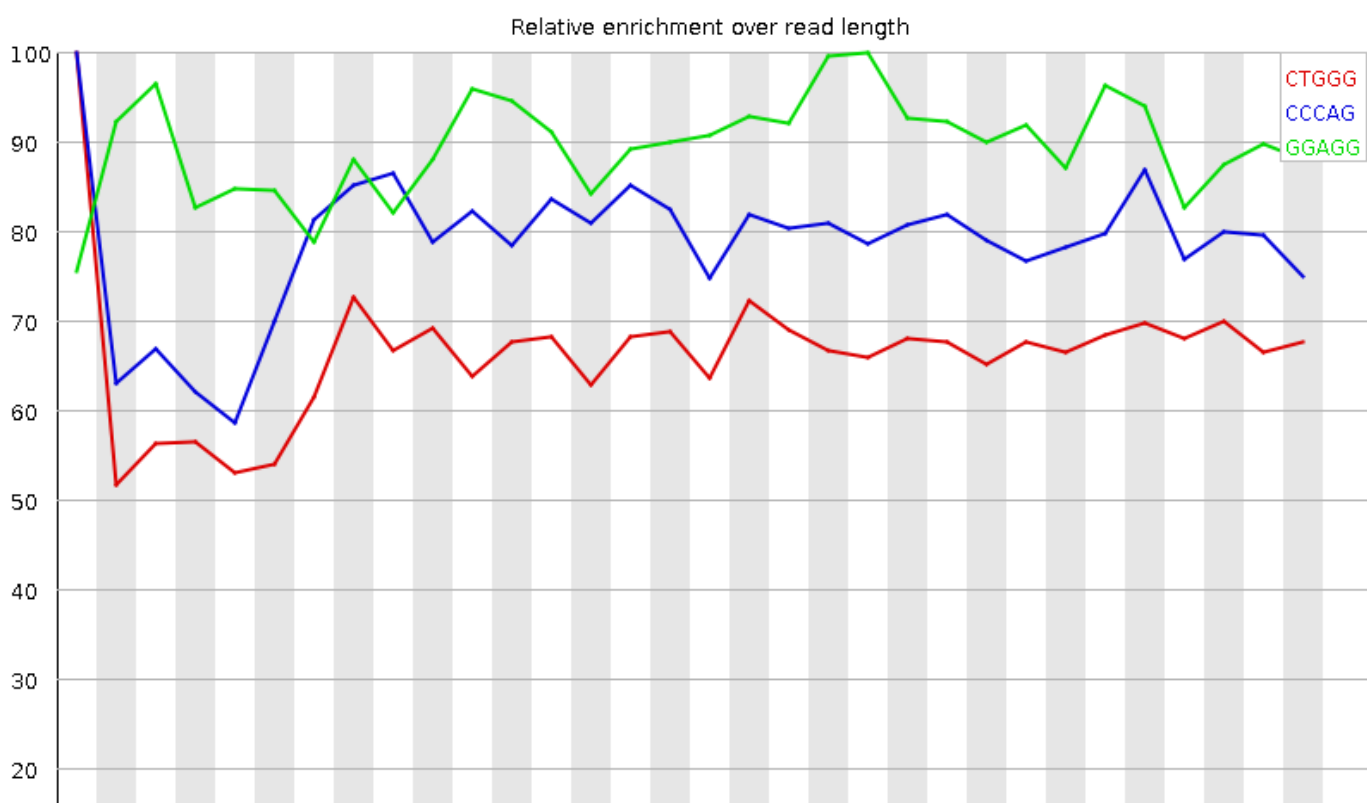


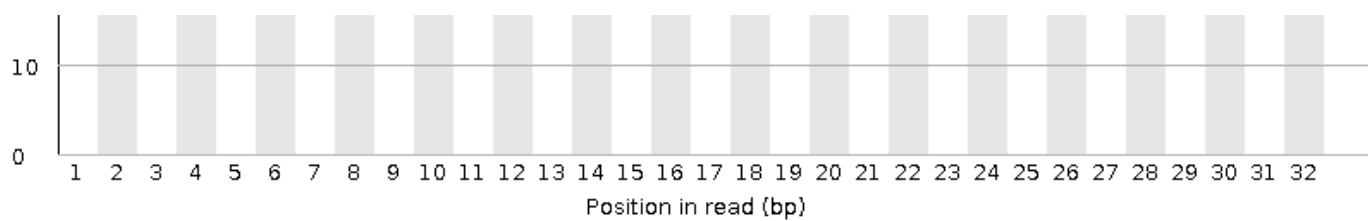
Overrepresented sequences

No overrepresented sequences



Kmer Content





Sequence	Count	Obs/Exp Overall	Obs/Exp Max	Max Obs/Exp Position
CTGGG	1326845	3.475149	5.225642	1
CCCAG	1336350	3.2171552	4.0845246	1
GGAGG	1105295	3.0264652	3.3751552	21

Produced by [FastQC](#) (version 0.10.1)