












FastQC Report

Summary

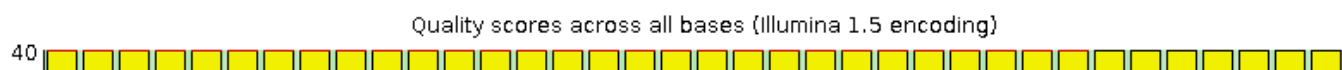
P'C, 29 PëCTП» 2014
K562_IFNg30_IRF1_rep1.fastq

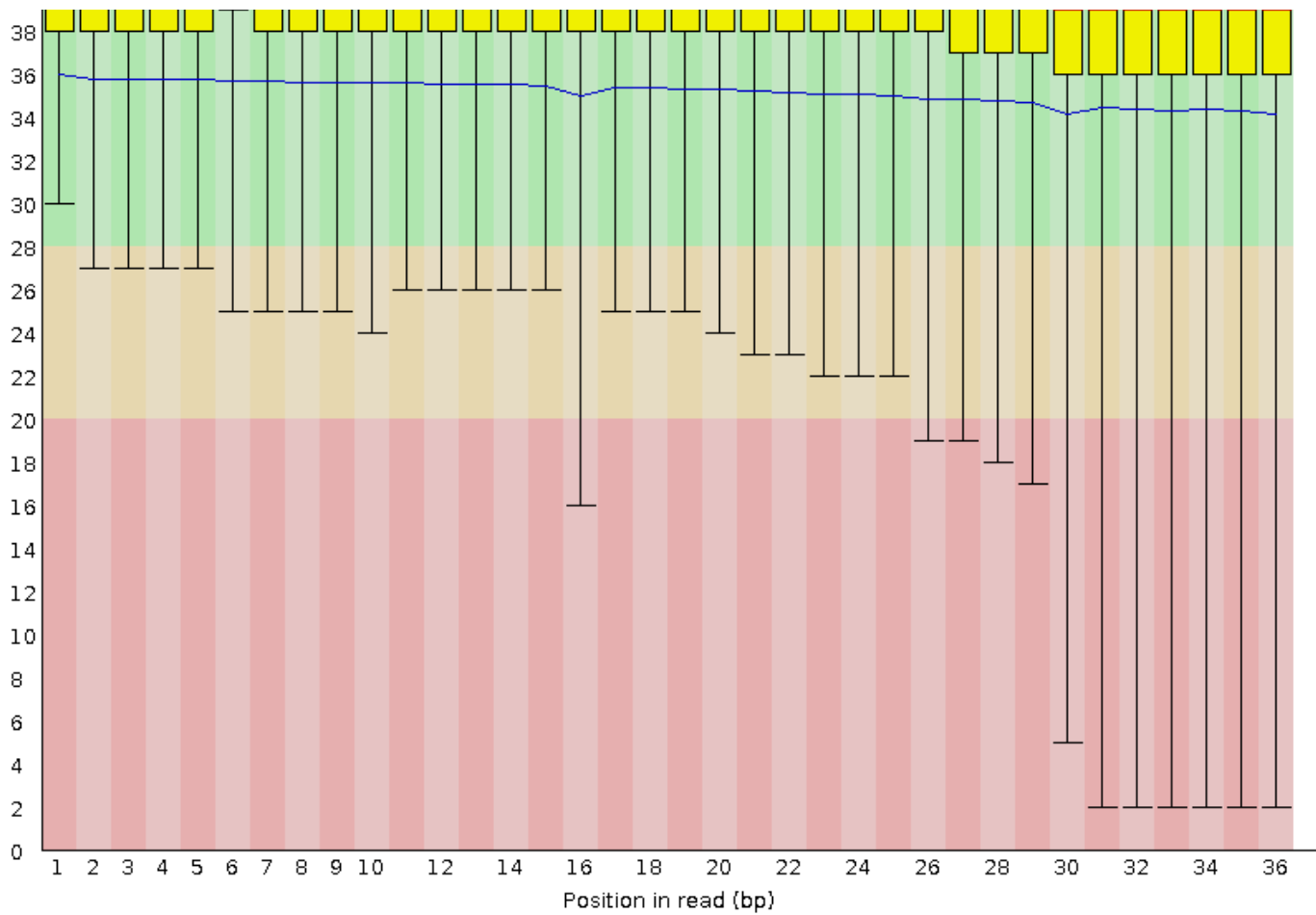
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Basic Statistics

Measure	Value
Filename	K562_IFNg30_IRF1_rep1.fastq
File type	Conventional base calls
Encoding	Illumina 1.5
Total Sequences	28678433
Filtered Sequences	0
Sequence length	36
%GC	41

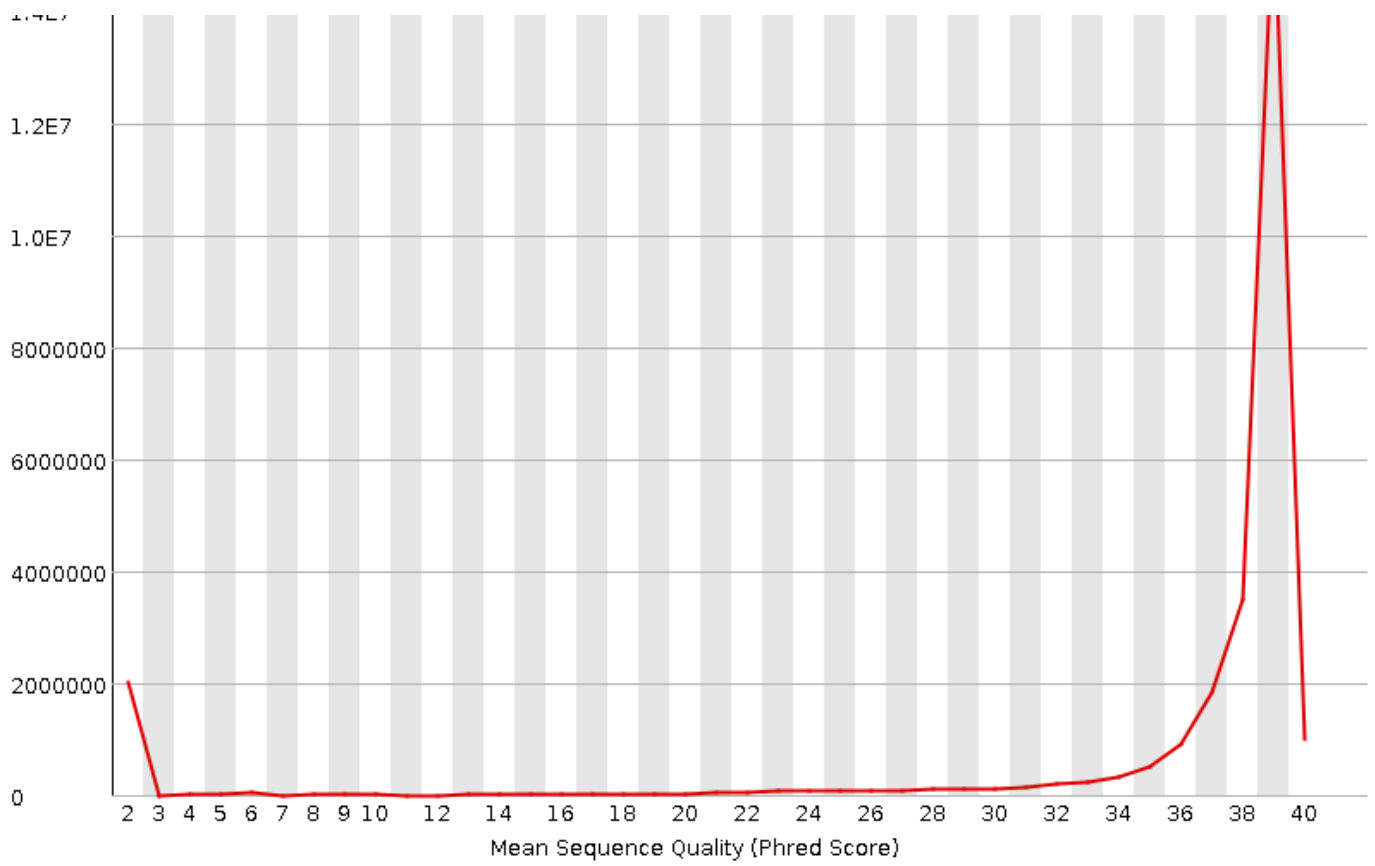
Per base sequence quality



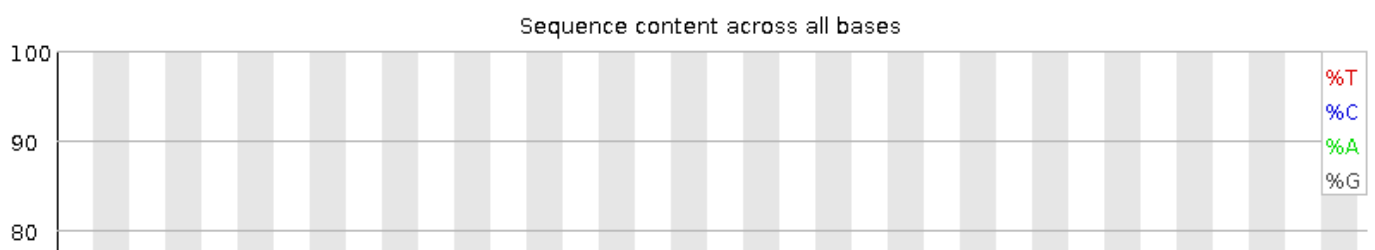


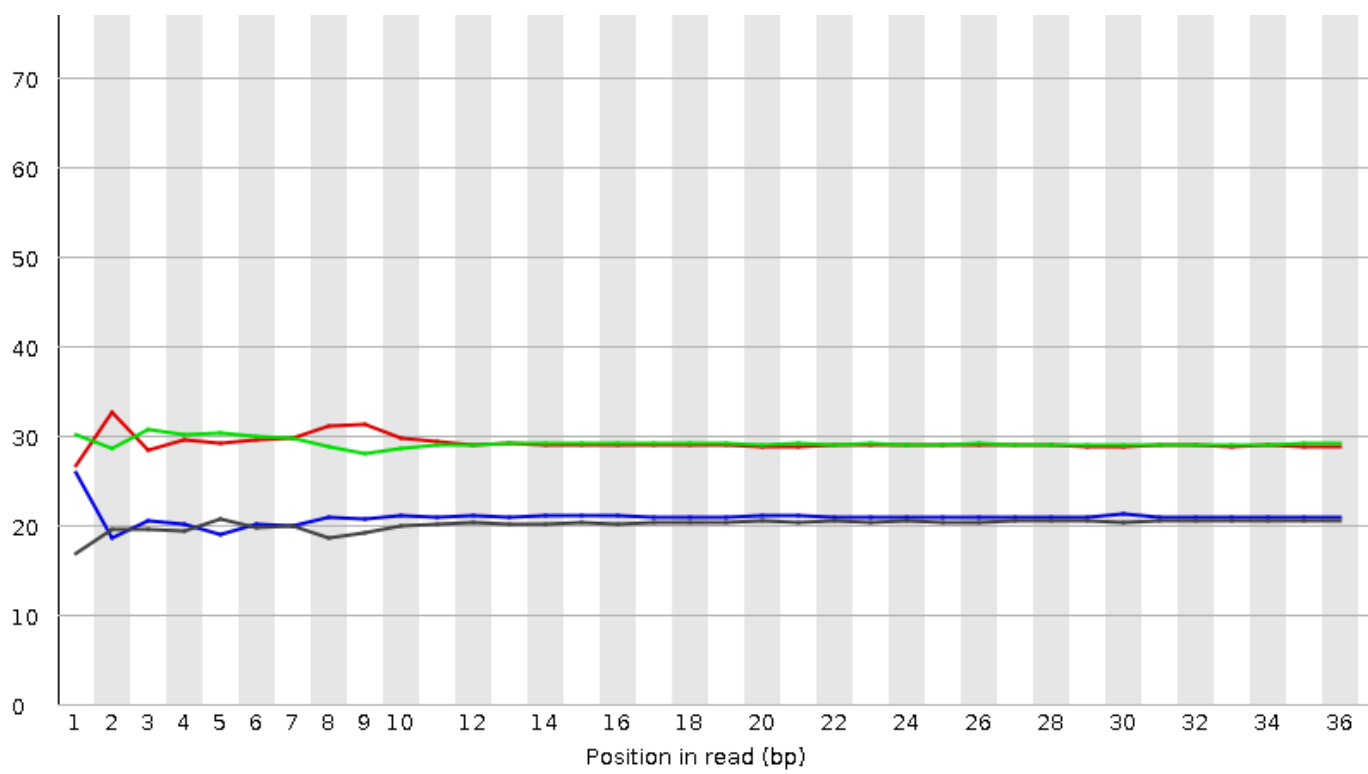
Per sequence quality scores



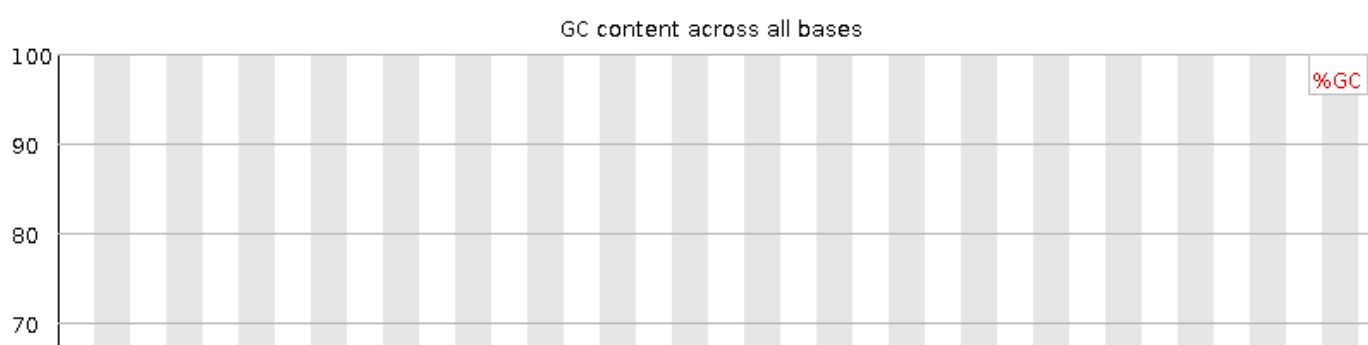


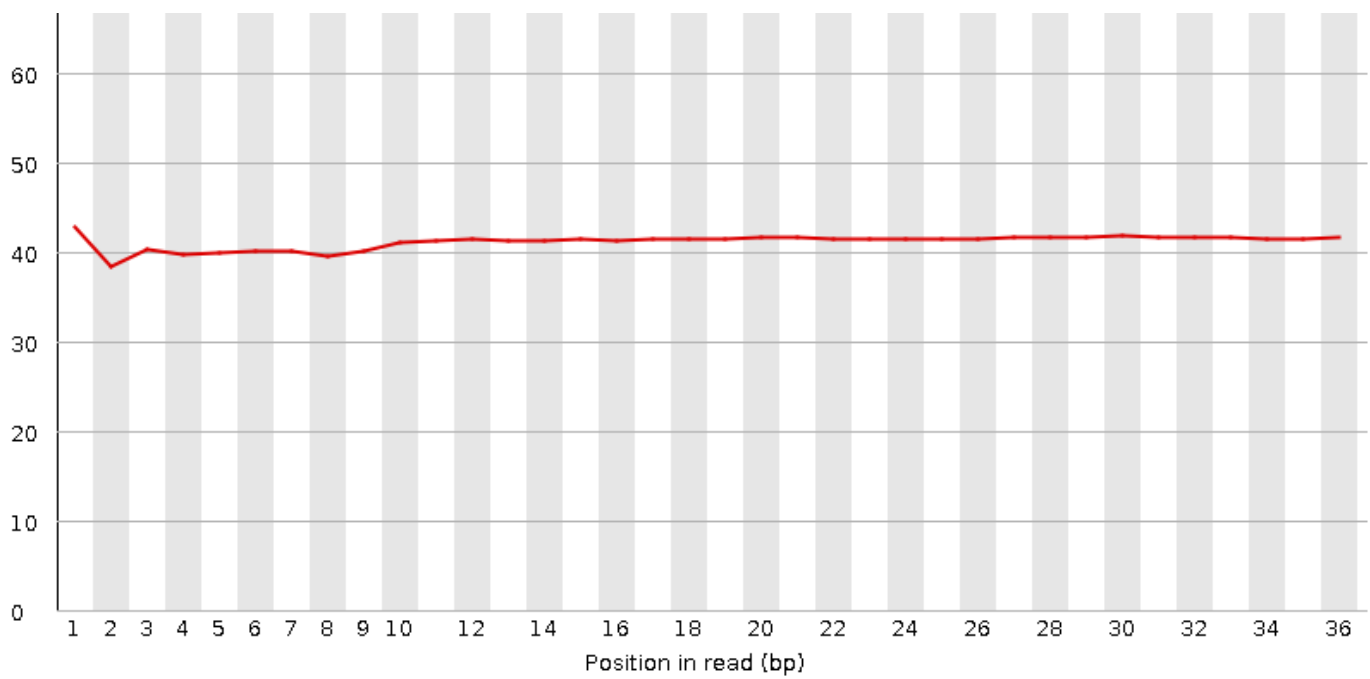
! Per base sequence content



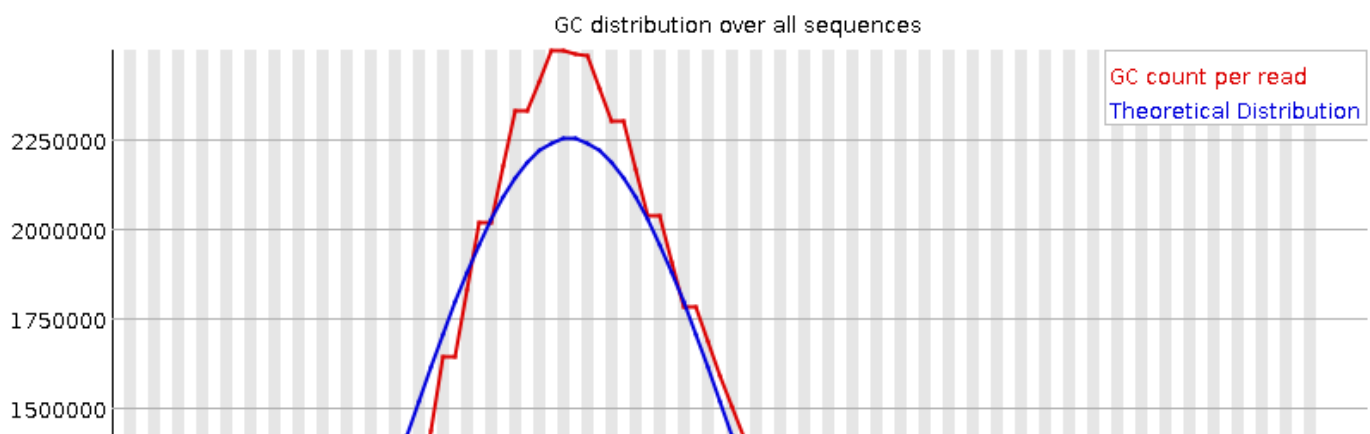


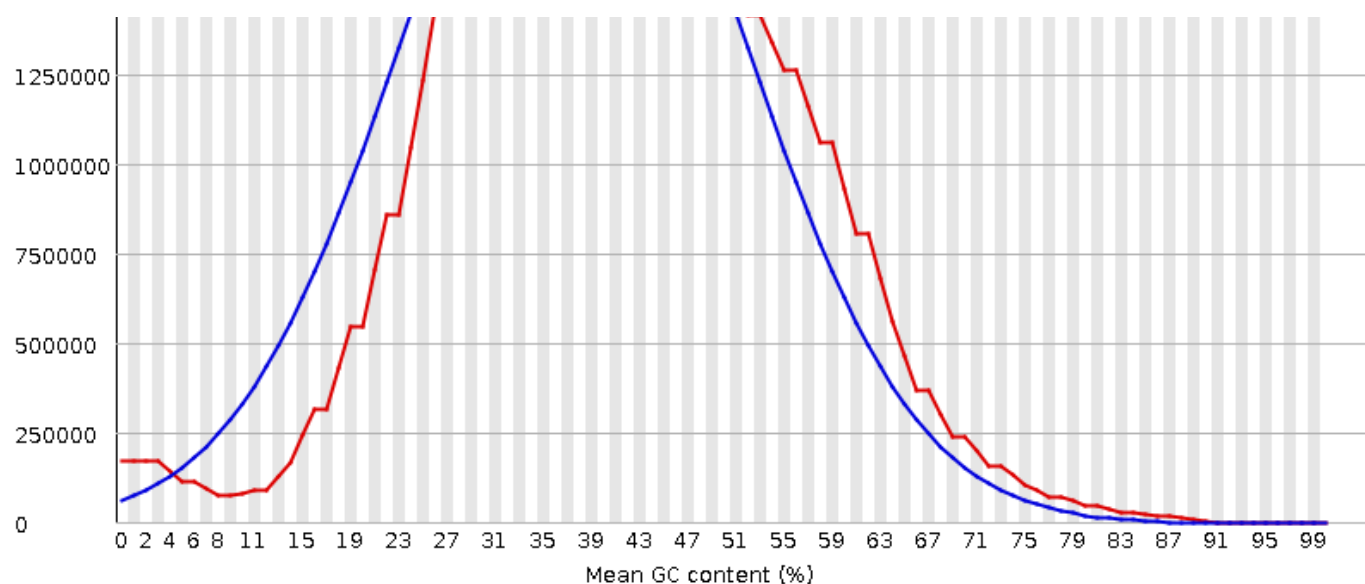
✅ Per base GC content



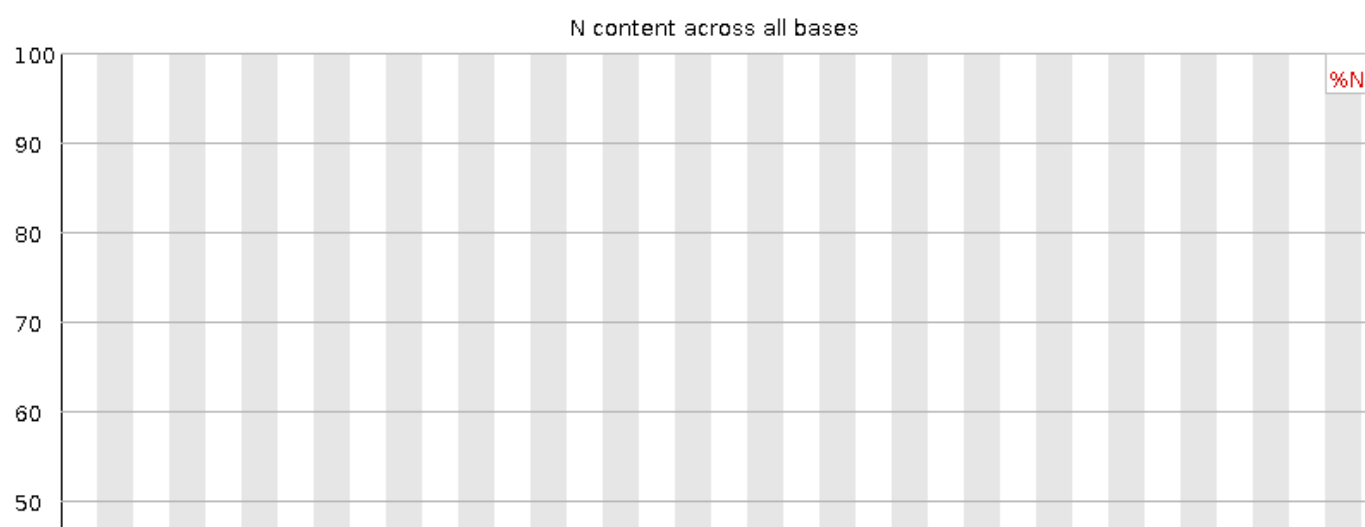


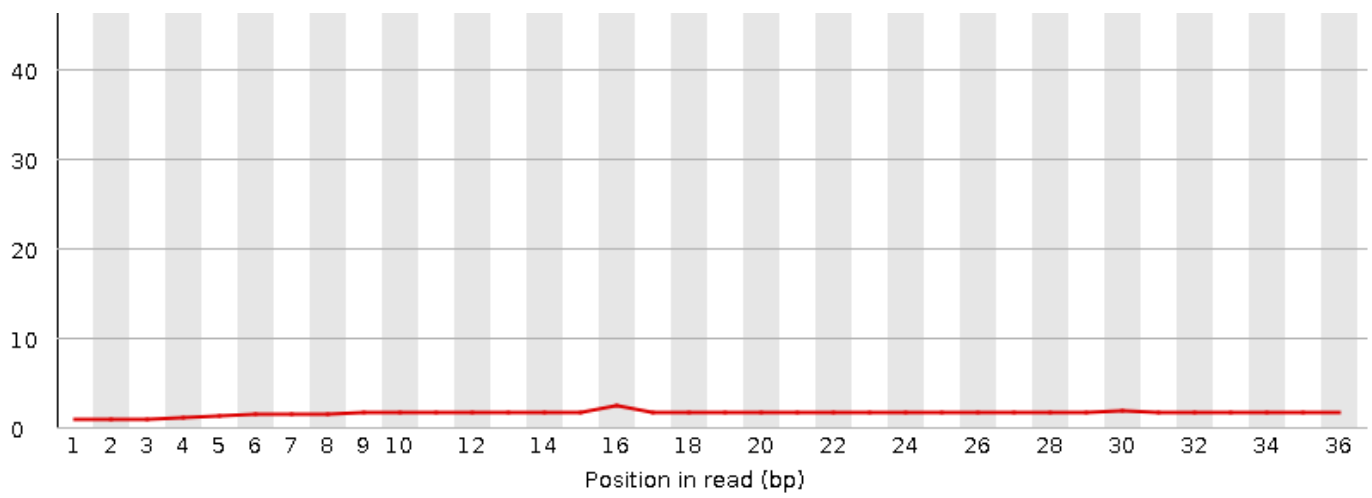
! Per sequence GC content



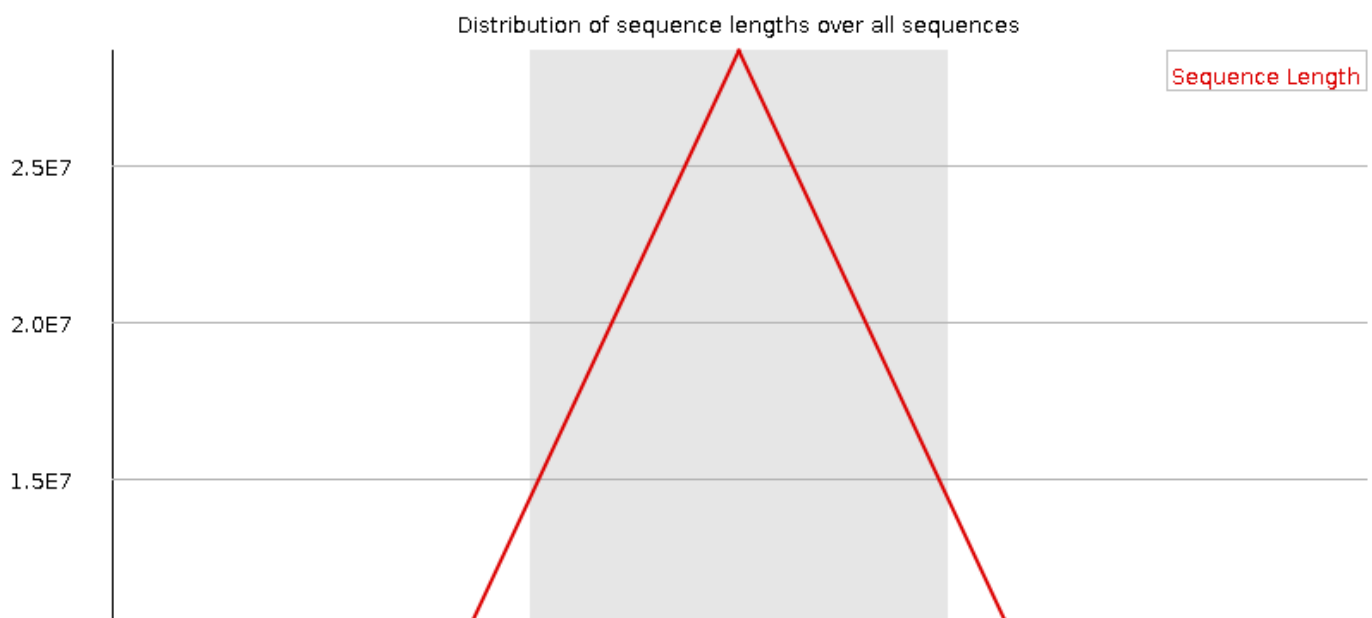


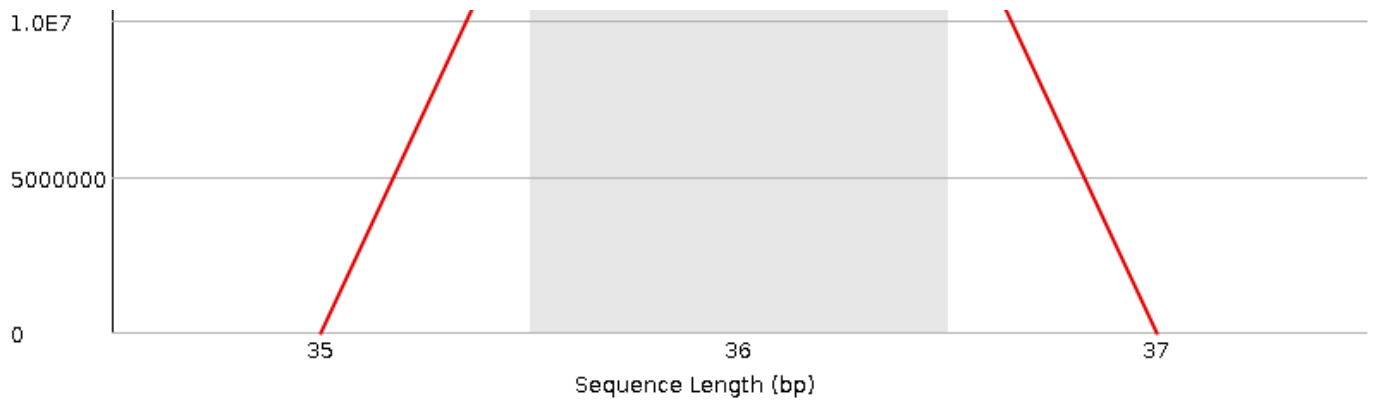
Per base N content



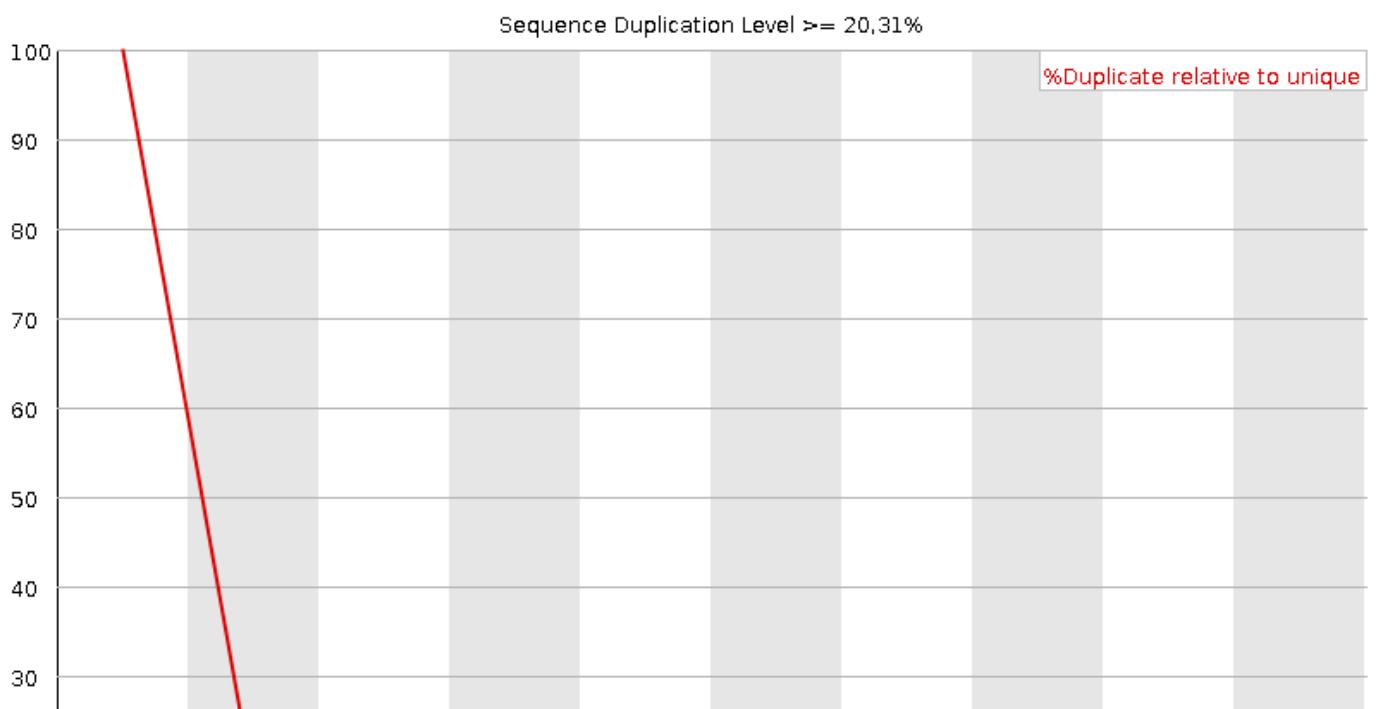


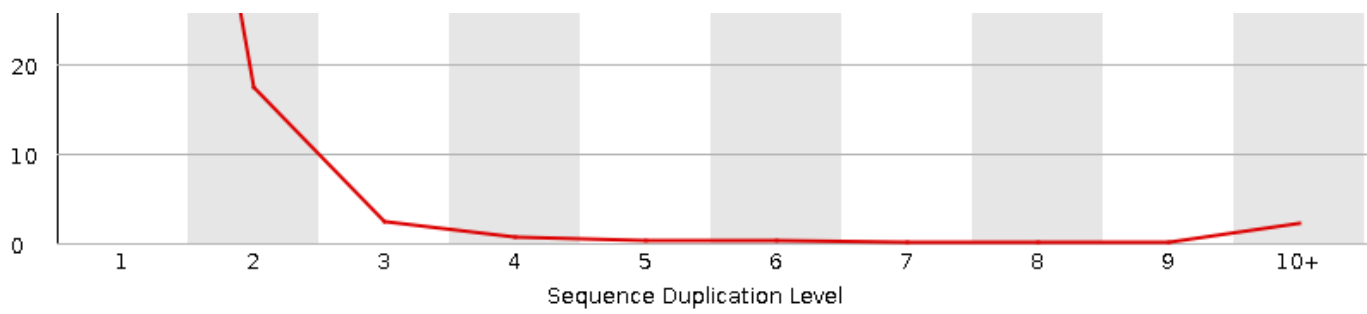
✔ Sequence Length Distribution





! Sequence Duplication Levels



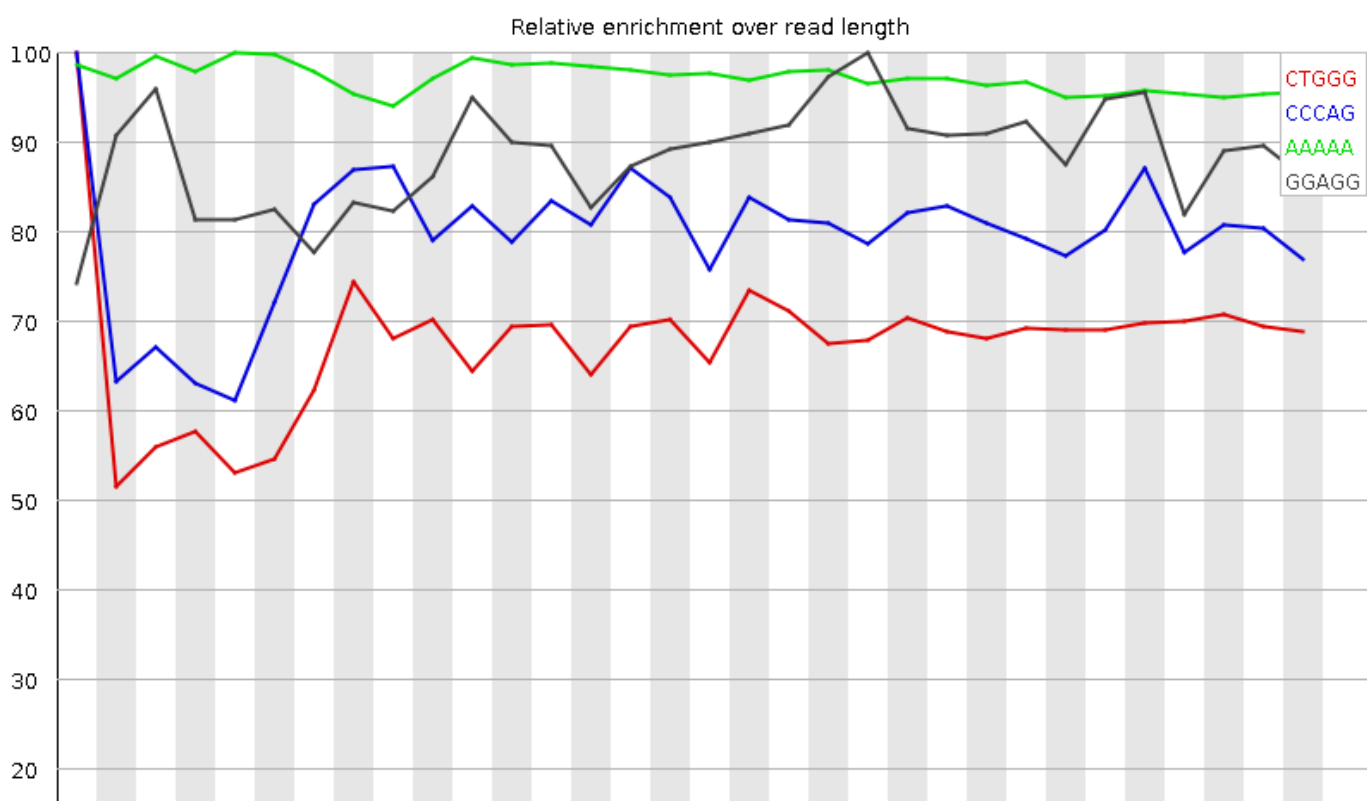


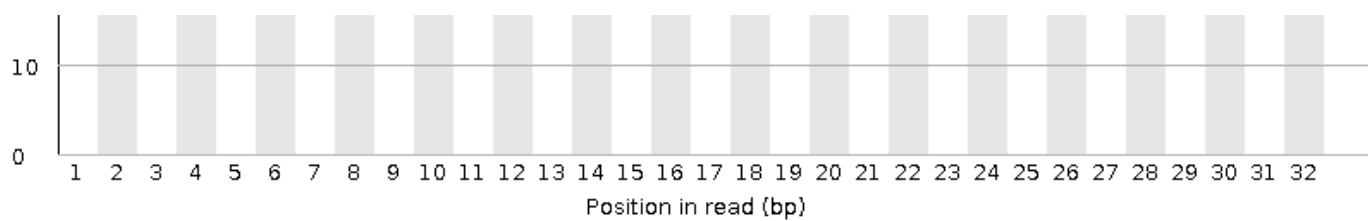
Overrepresented sequences

No overrepresented sequences



Kmer Content





Sequence	Count	Obs/Exp Overall	Obs/Exp Max	Max Obs/Exp Position
CTGGG	1578765	3.4161193	5.0453887	1
CCCAG	1578275	3.1595964	3.967051	1
AAAAA	6067145	3.1116526	3.1989884	5
GGAGG	1354990	3.050023	3.445545	21

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