FastQC Report

Wed 23 Dec 2020
SRR9738569.fastq

Summary

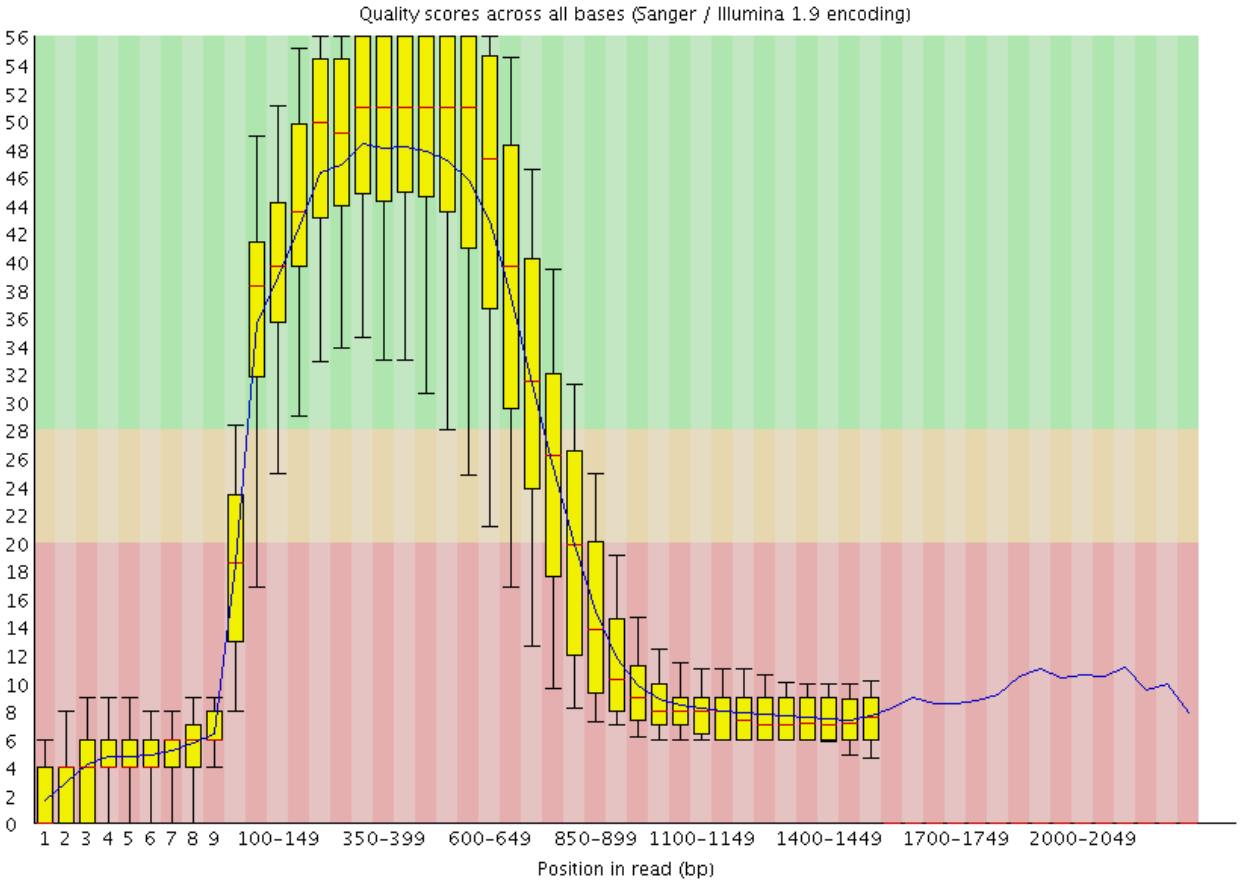
- Basic Statistics
- Per base sequence quality
- Per sequence quality scores
- Per base sequence content
- Per sequence GC content
- Per base N content
- Sequence Length Distribution
- Sequence Duplication Levels
- Overrepresented sequences
- Adapter Content

Basic Statistics

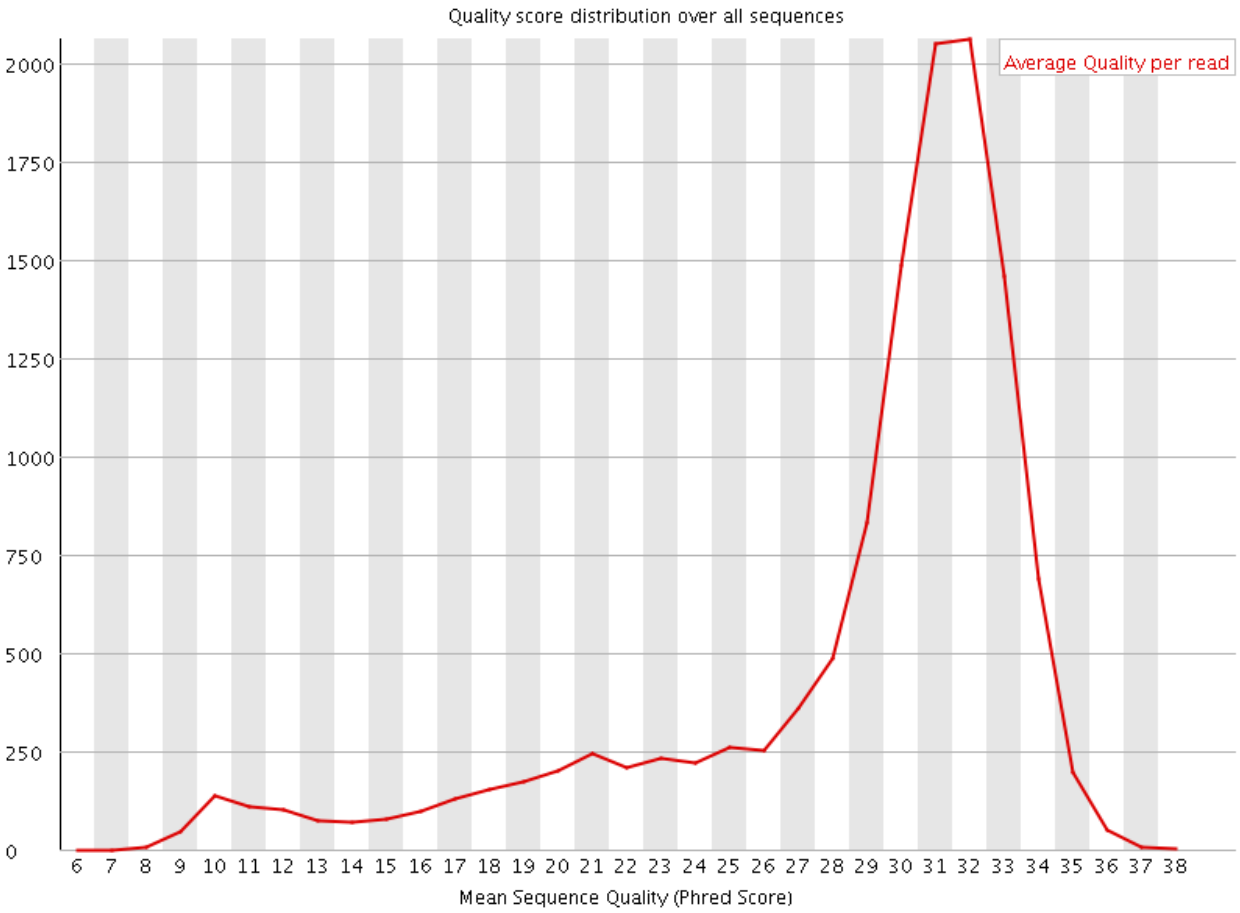
Filename	SRR9738569.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	12574

Sequences flagged as poor quality	0
Sequence length	772-2263
%GC	39

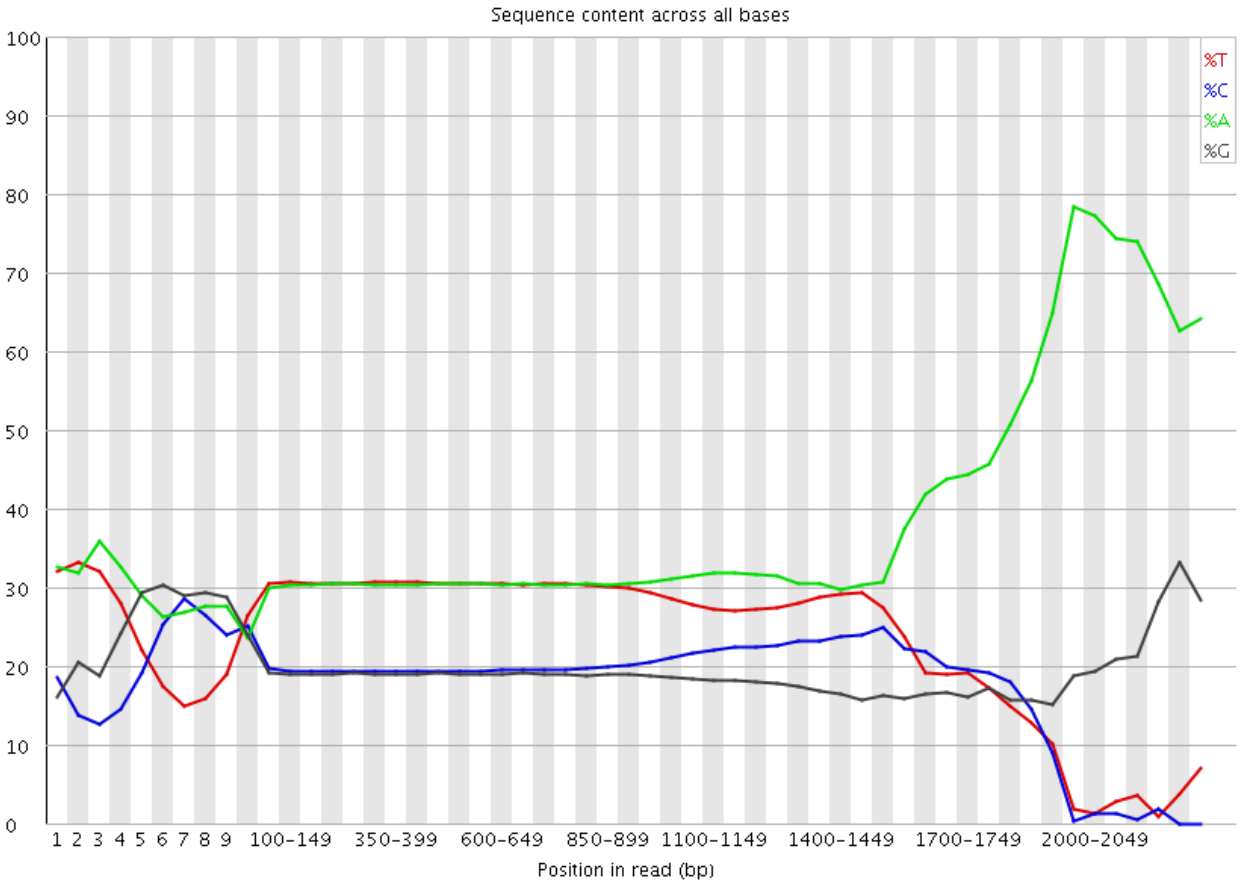
Per base sequence quality



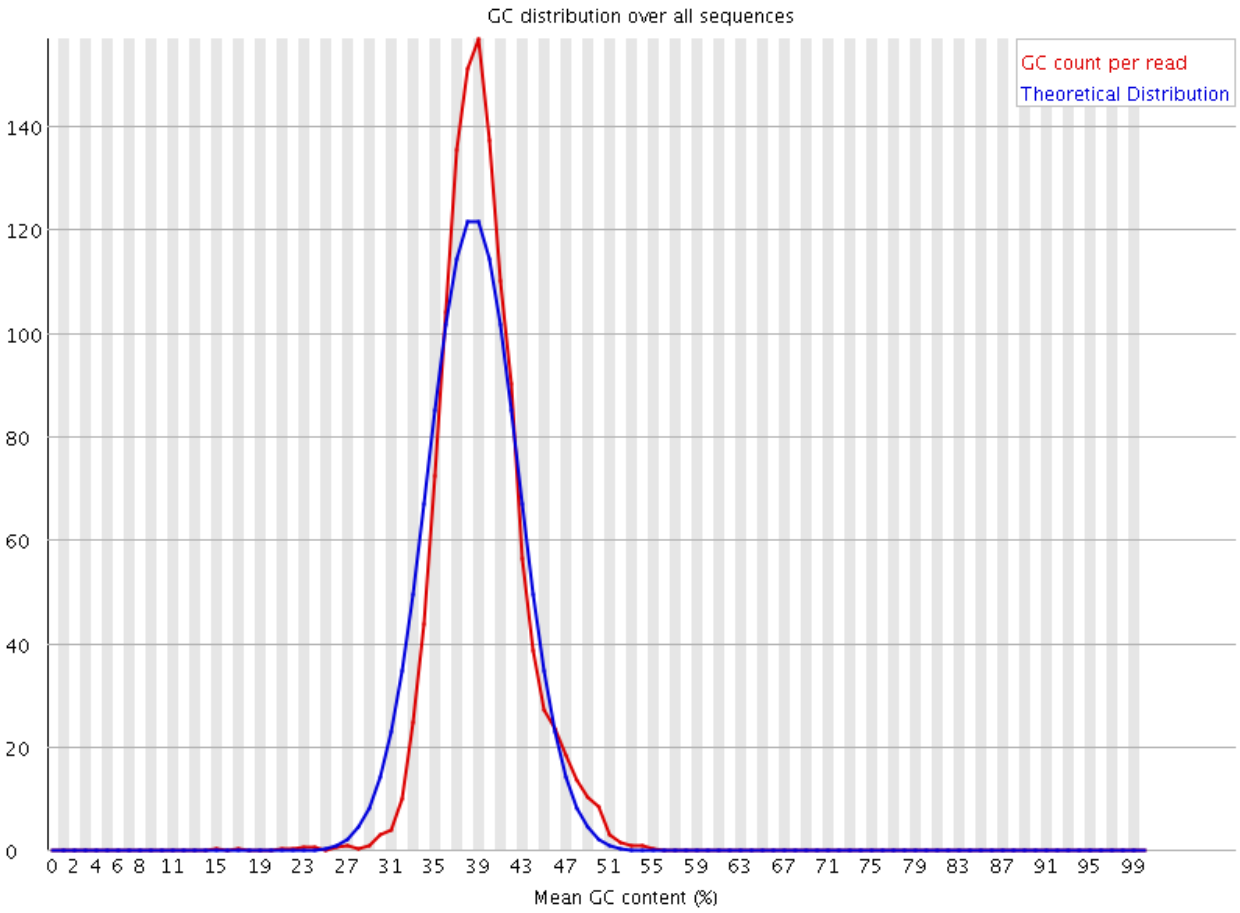
Per sequence quality scores



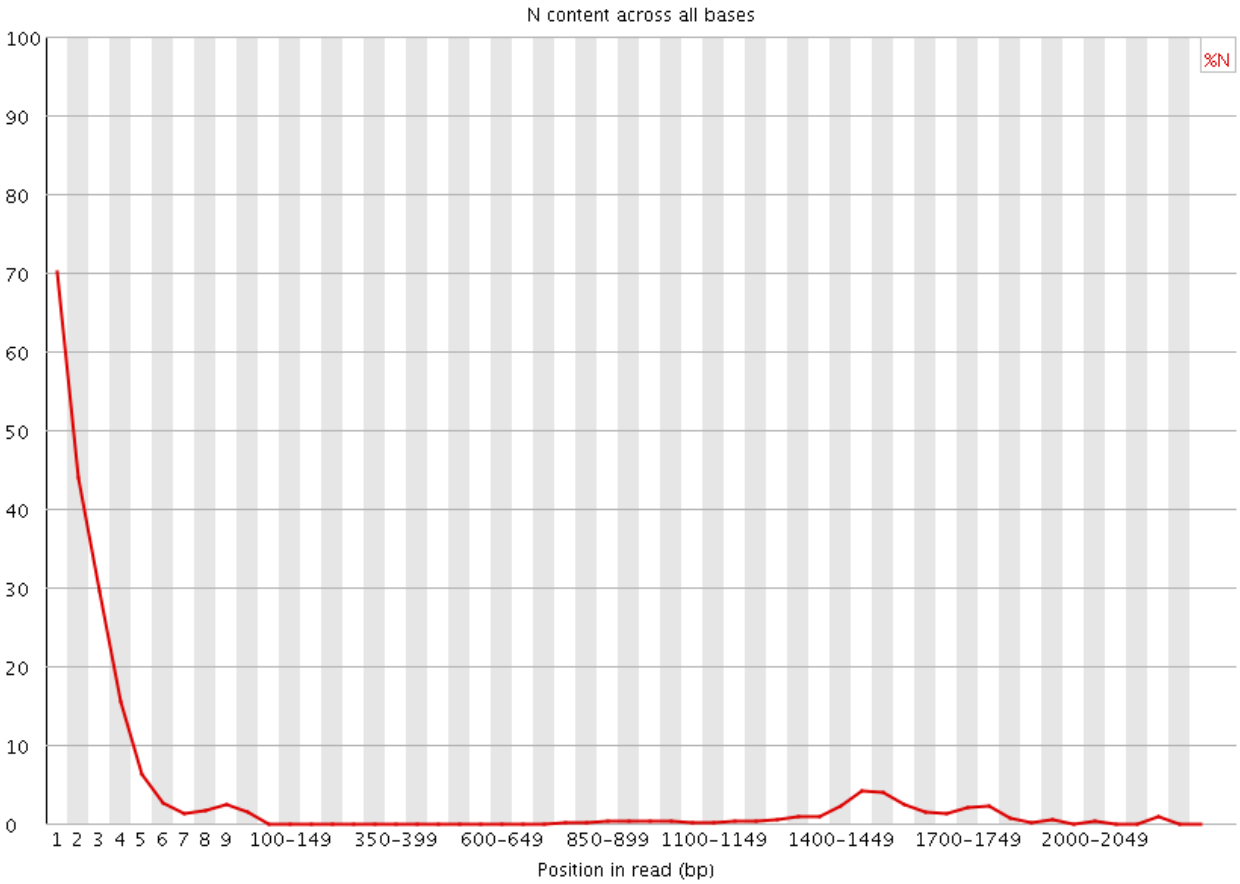
Per base sequence content



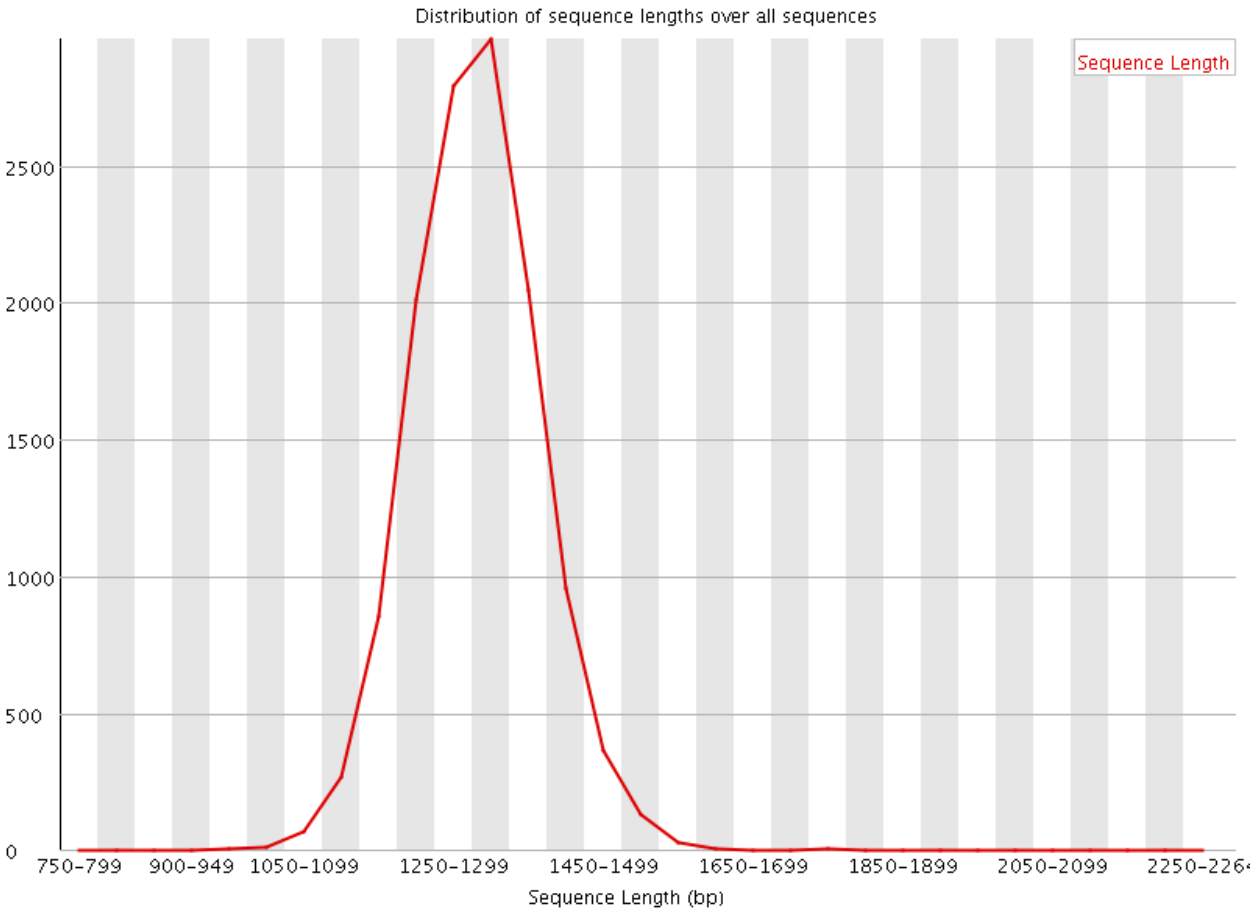
Per sequence GC content



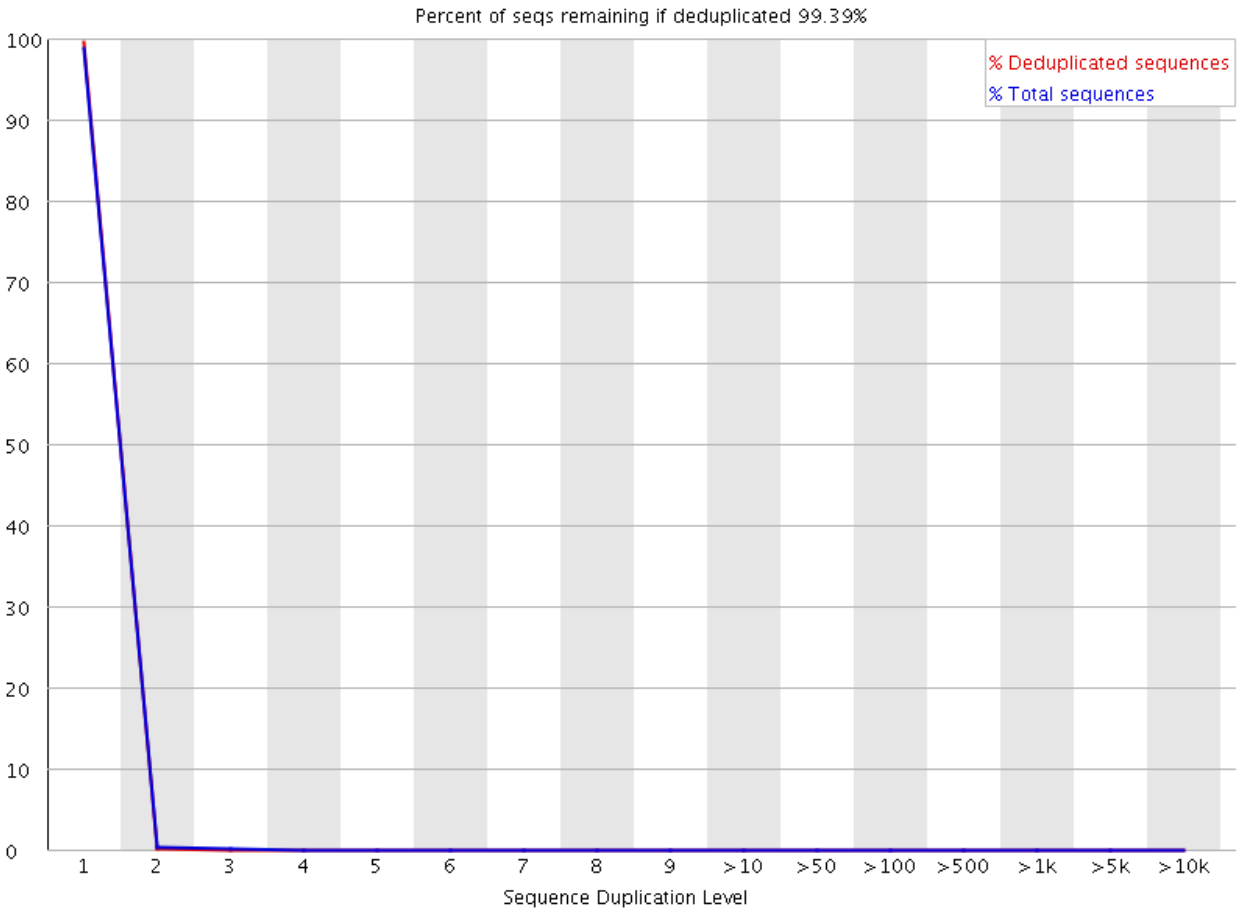
Per base N content



Sequence Length Distribution



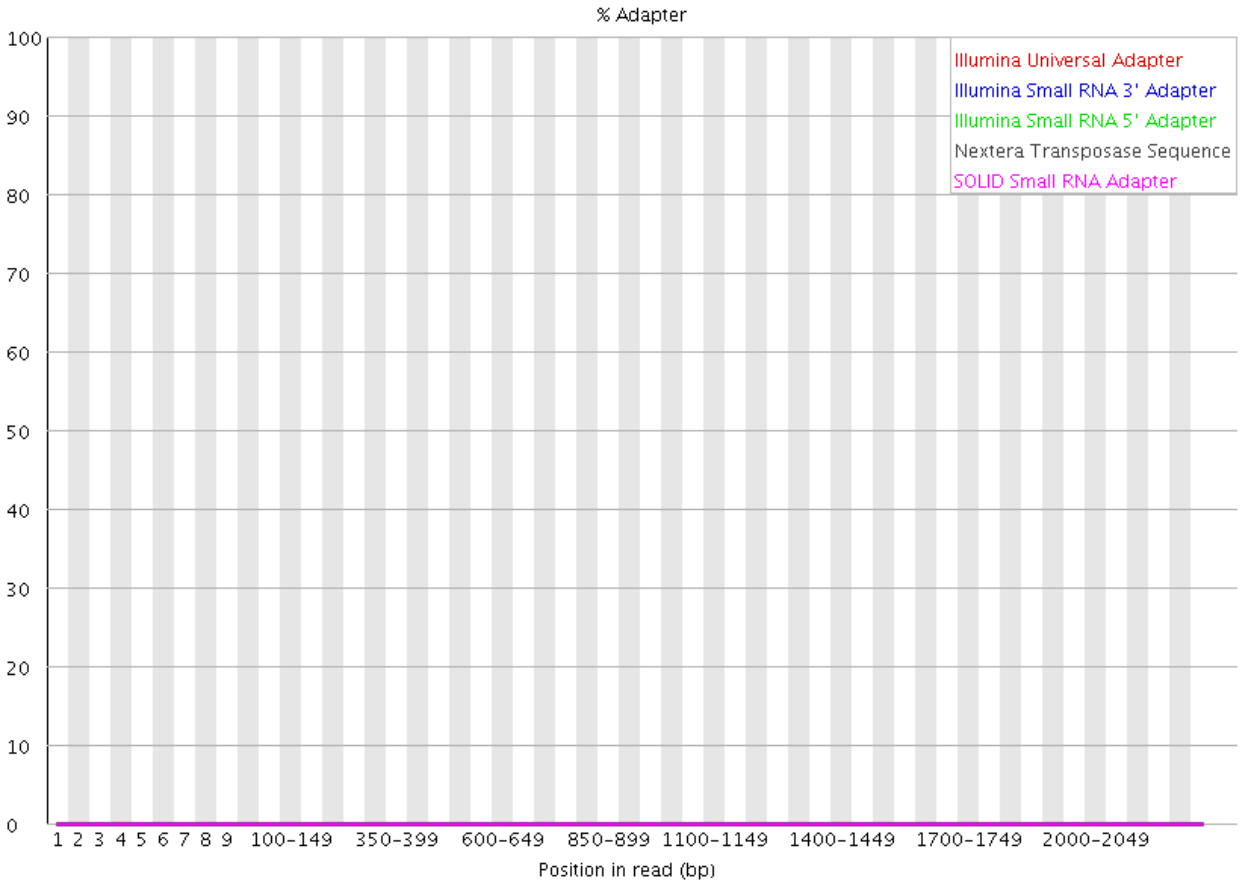
Sequence Duplication Levels



Overrepresented sequences

No overrepresented sequences

Adapter Content



Produced by FastQC (version 0.11.7)