#### Sun 2 Jan 2022 SRR17066006.fastq

# **PastQC Report**Summary



- 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



Measure Value

Filename SRR17066006.fastq

File type Conventional base calls

Encoding Sanger / Illumina 1.9

Total Sequences 176406

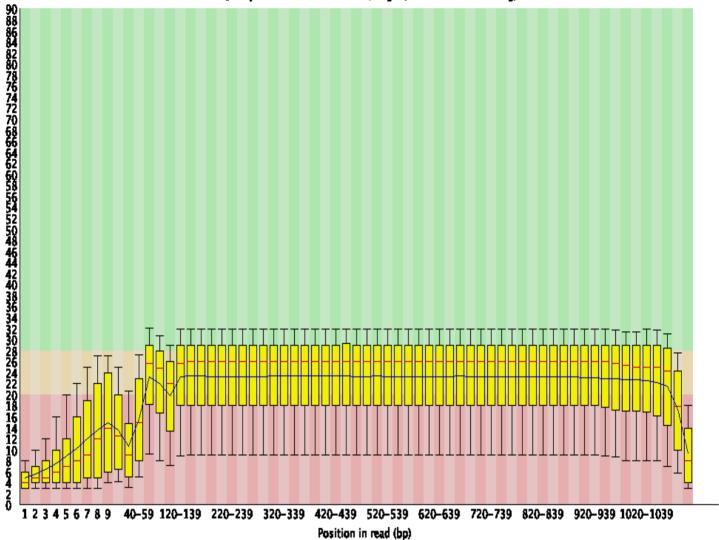
Sequences flagged as poor quality 0

Sequence length 200-1100

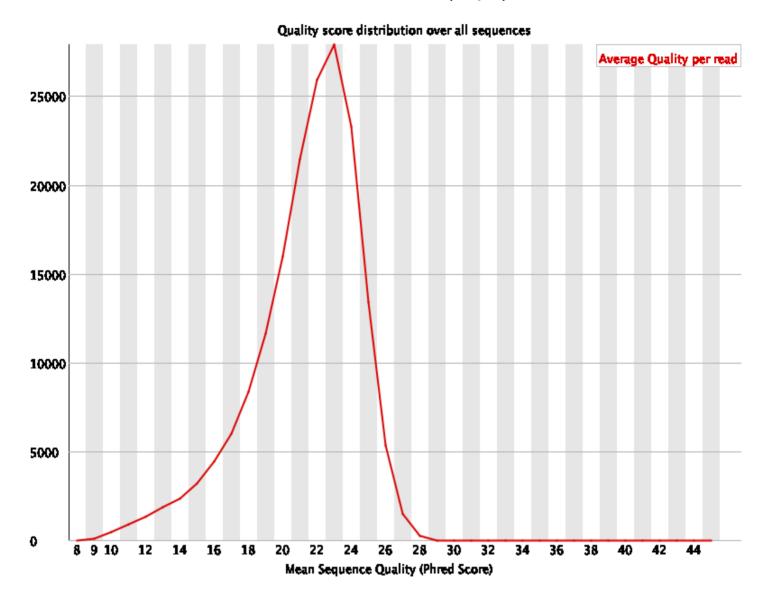
%GC 38

### **Per base sequence quality**

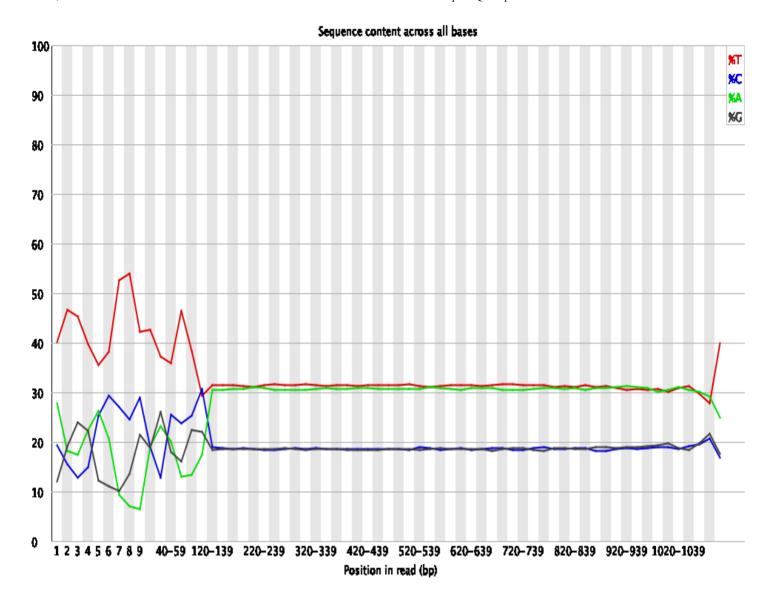
#### Quality scores across all bases (Sanger / Illumina 1.9 encoding)



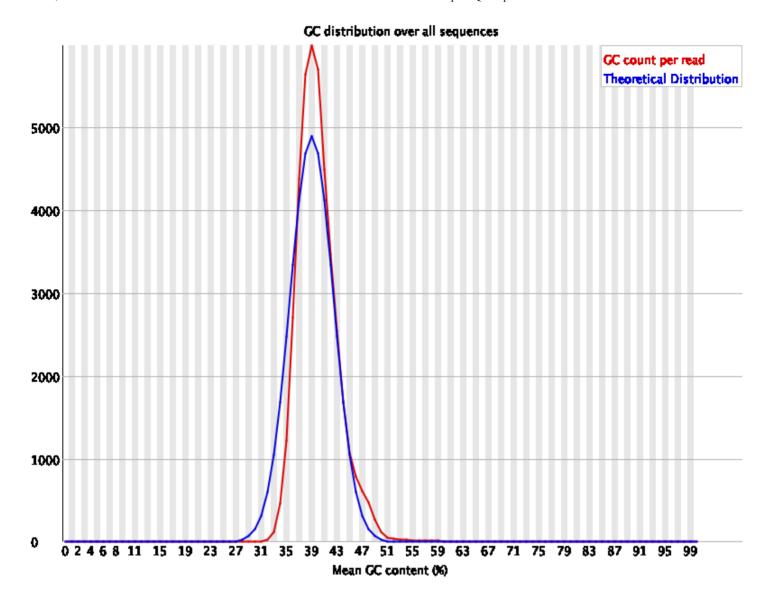
Per sequence quality scores



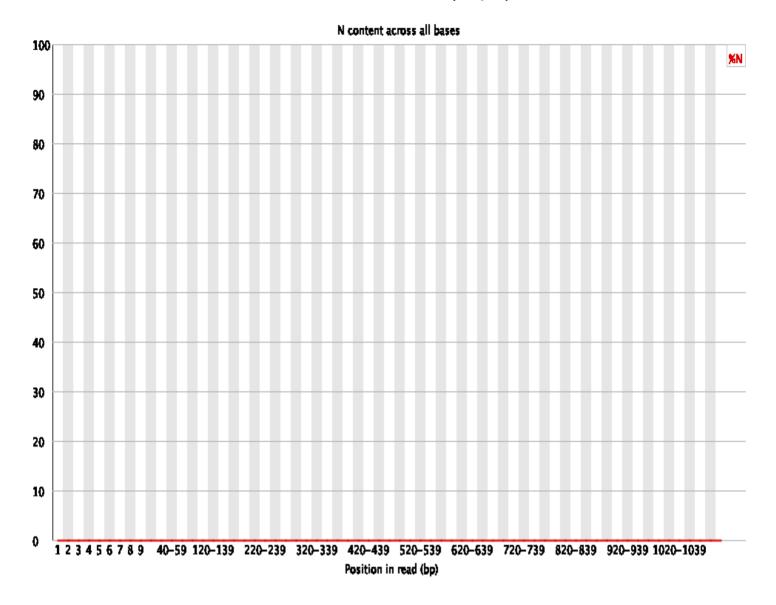
### **Per base sequence content**



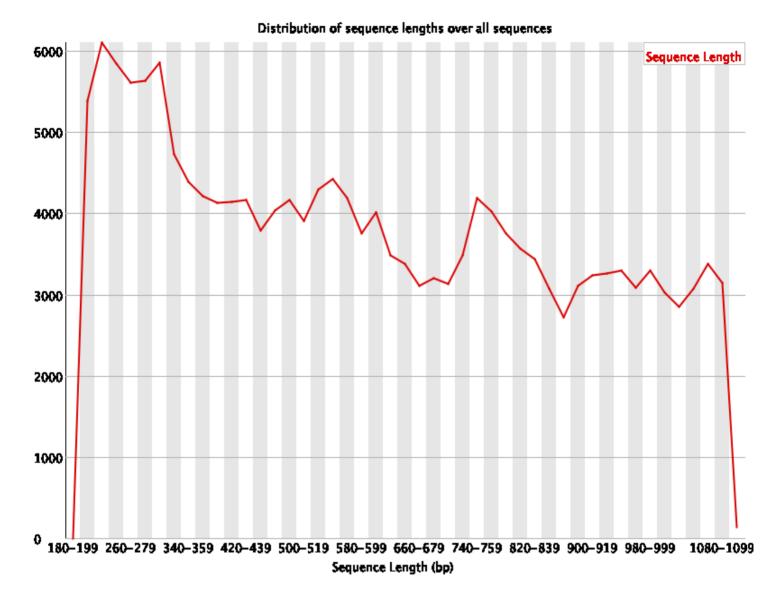
# Per sequence GC content



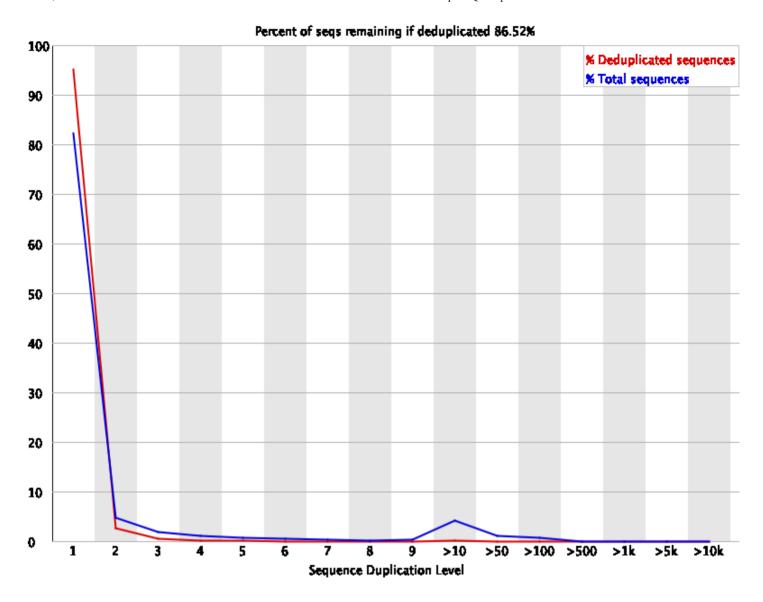




# Sequence Length Distribution



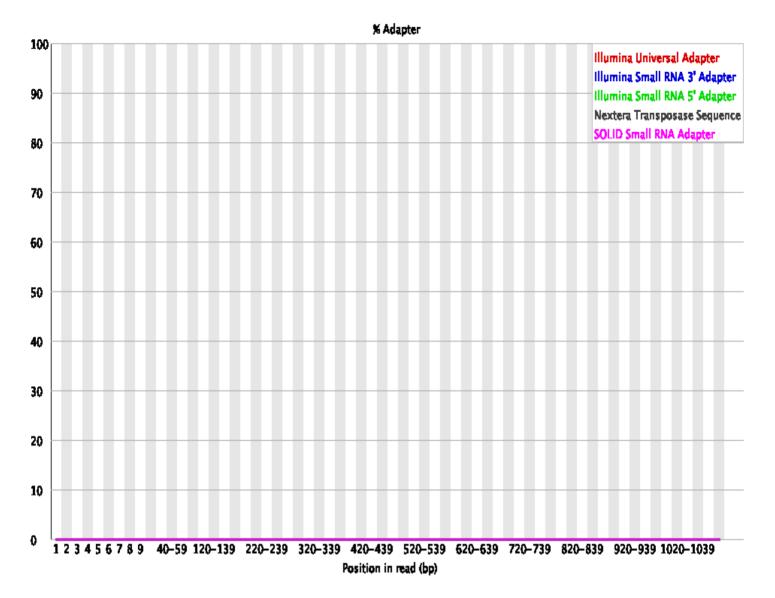




# Overrepresented sequences

Sequence	Count	Percentage	Possible Source
${\tt TTTGGGTGTTTAACCAAGCGTTGAAACCTTTGTCCTCTCGTTTTCGCATT}$	286	0.16212600478441777	No Hit
TTGGGTGTTTAACCAAGCGTTGAAACCTTTGTCCTCTCGTTTTCGCATTT	258	0.1462535287915377	No Hit





Produced by FastQC (version 0.11.9)