

Wed 30 Jun 2021 SRR1554535\_2\_fastq\_gz.gz

#### Summary





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

Measure Value

Filename SRR1554535\_2\_fastq\_gz.gz

File type Conventional base calls

Encoding Sanger / Illumina 1.9

Total Sequences 91185969

Sequences flagged as poor quality 0

Sequence length 50

%GC 47

### **OPER** Per base sequence quality

123456789



23 25 27

Position in read (bp)

29 31

33 35

37

39

41

43

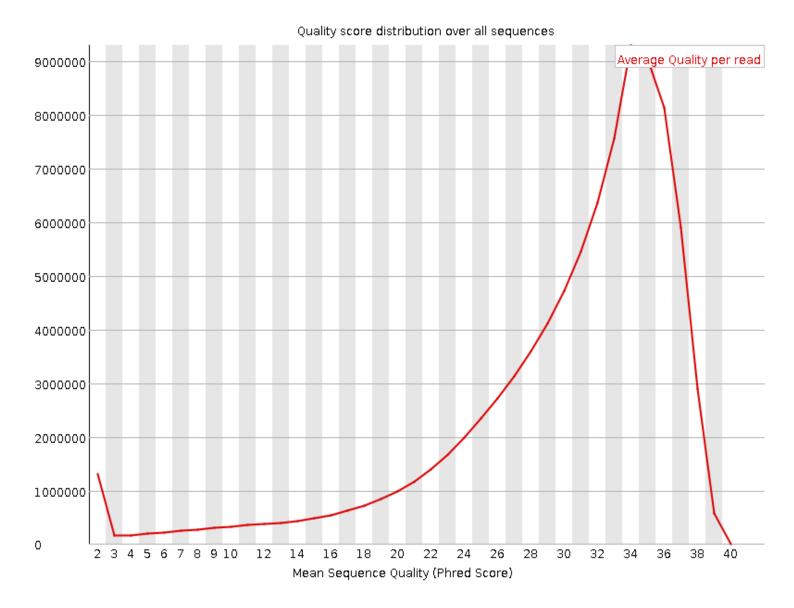
45

47

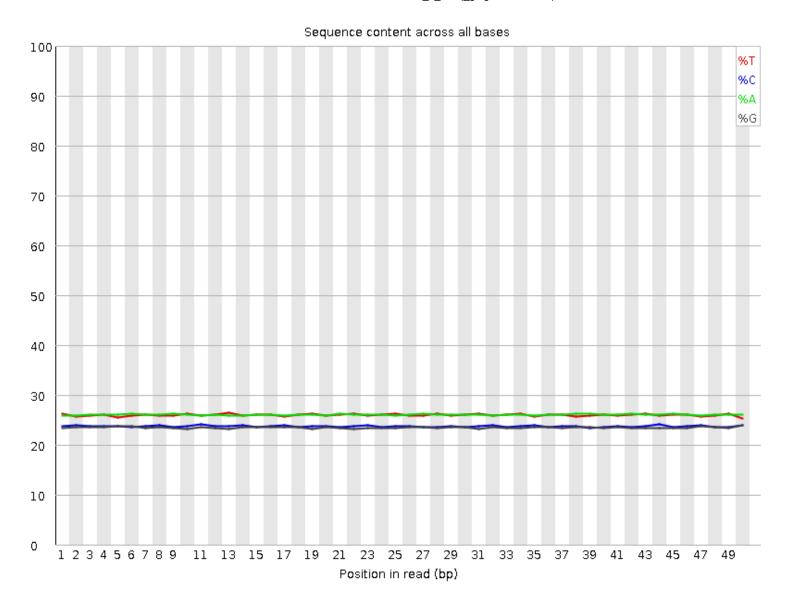
49

# Per sequence quality scores

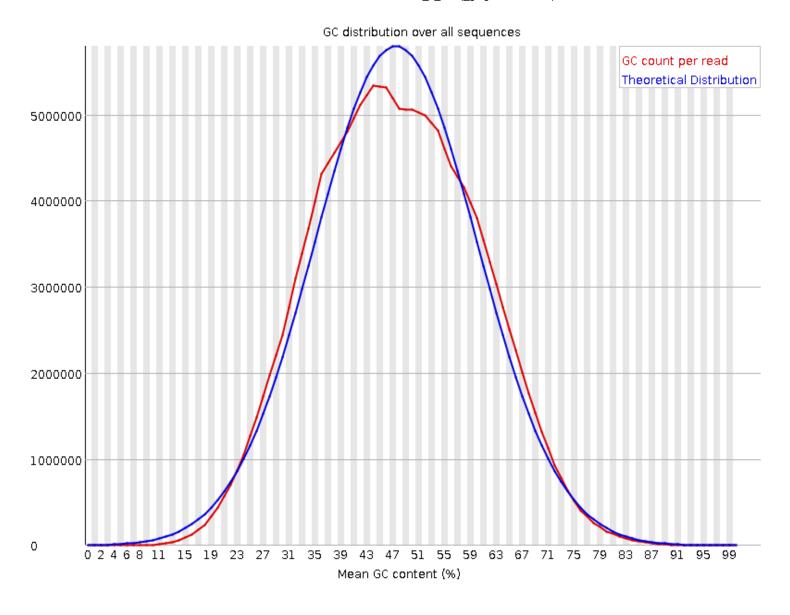
11 13 15 17 19 21



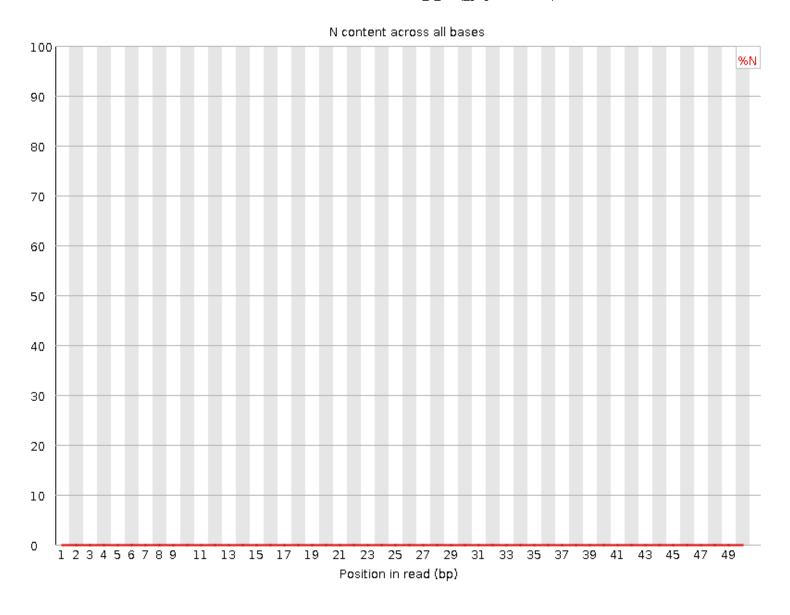




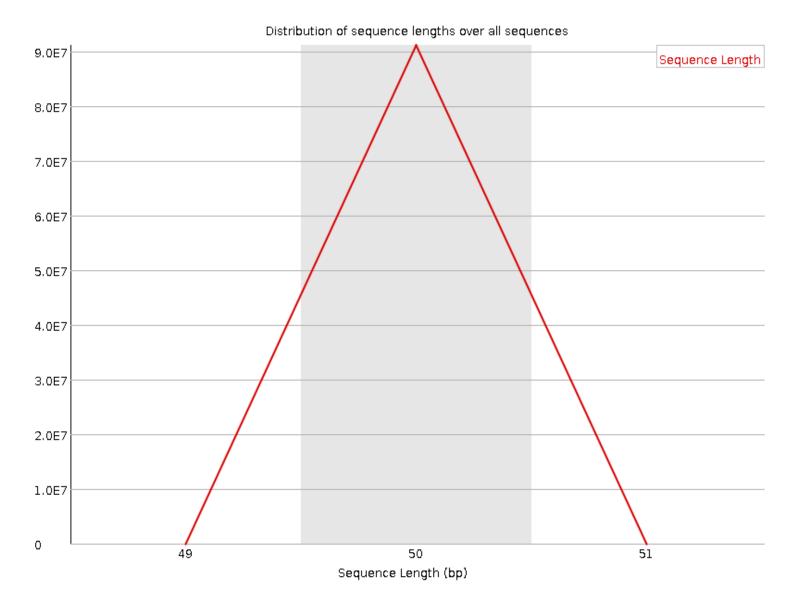
## Per sequence GC content



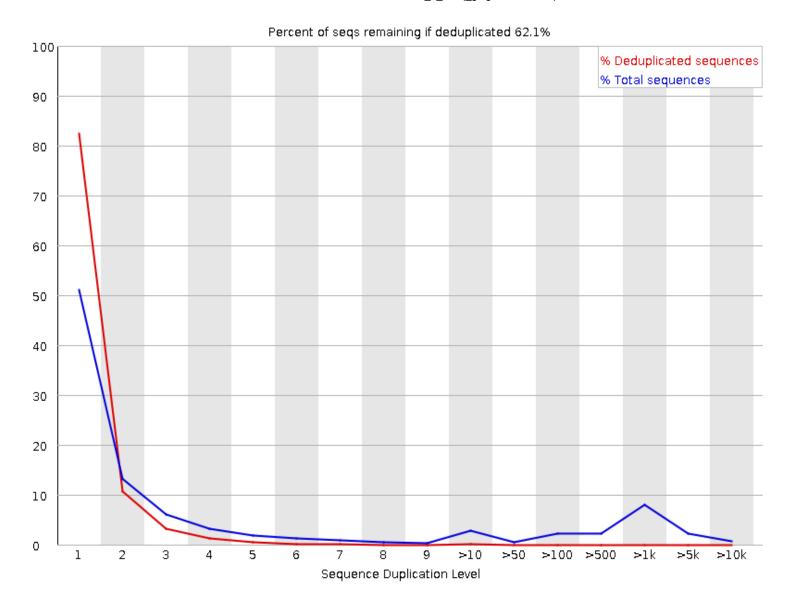




## Sequence Length Distribution

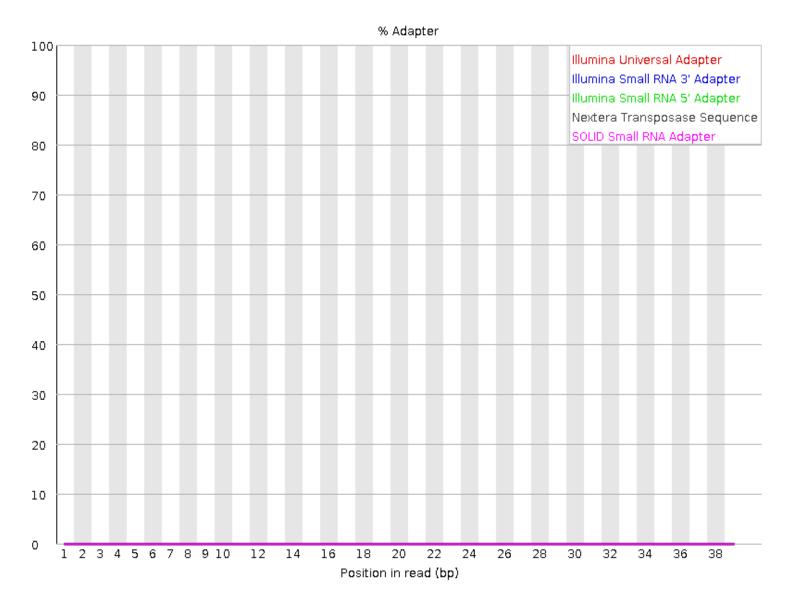


#### Sequence Duplication Levels





Adapter Content



Produced by FastQC (version 0.11.8)