#### Sun 3 Nov 2024 WTC2\_2\_trPE.fq

# **Report**

Summary





Per tile 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

Measure Value

Filename WTC2\_2\_trPE.fq

File type Conventional base calls

Encoding Sanger / Illumina 1.9

Total Sequences 19434301

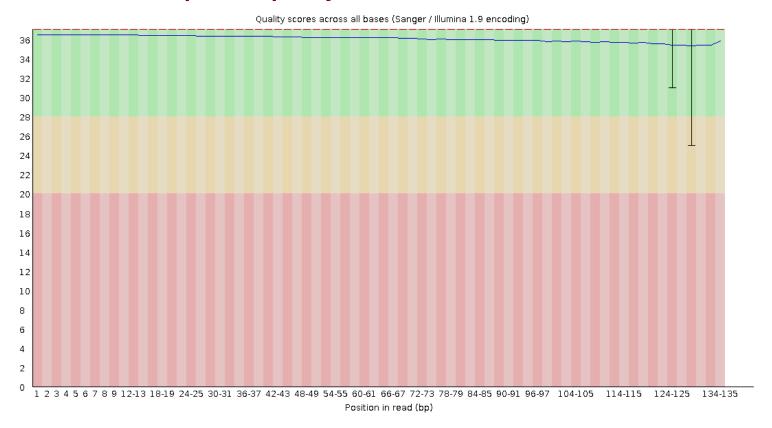
Total Bases 2.6 Gbp

Sequences flagged as poor quality 0

Sequence length 75–135

%GC 37

## Per base sequence quality

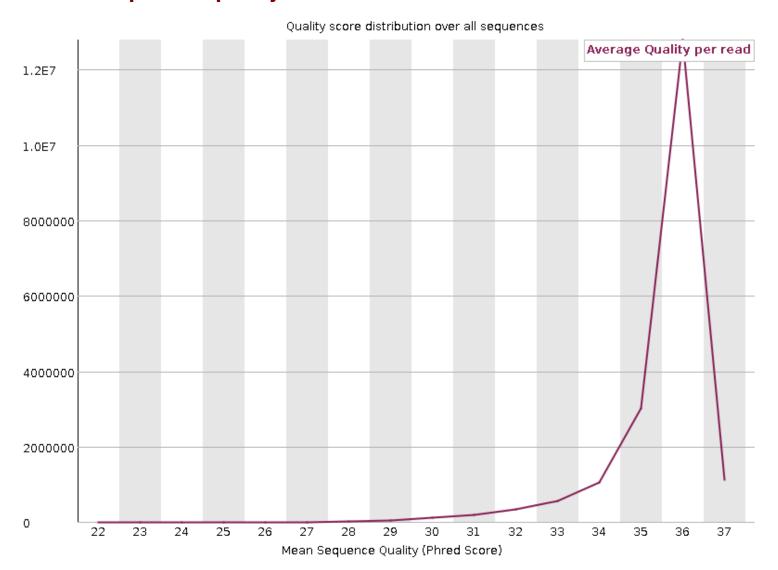


#### Per tile sequence quality

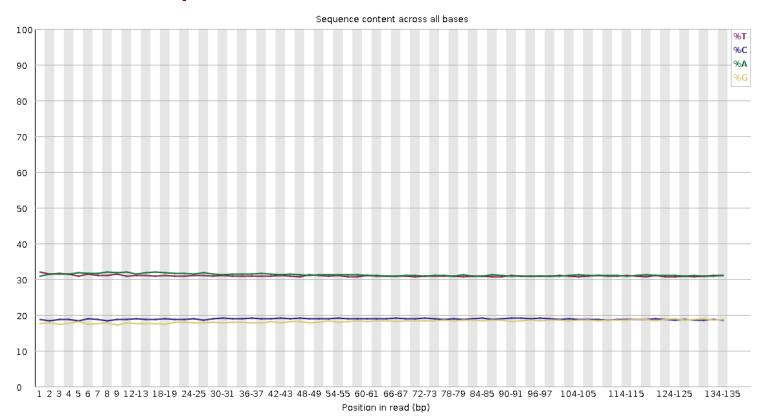


1 2 3 4 5 6 7 8 9 12-13 18-19 24-25 30-31 36-37 42-43 48-49 54-55 60-61 66-67 72-73 78-79 84-85 90-91 96-97 104-105 114-115 124-125 134-135 Position in read (bp)

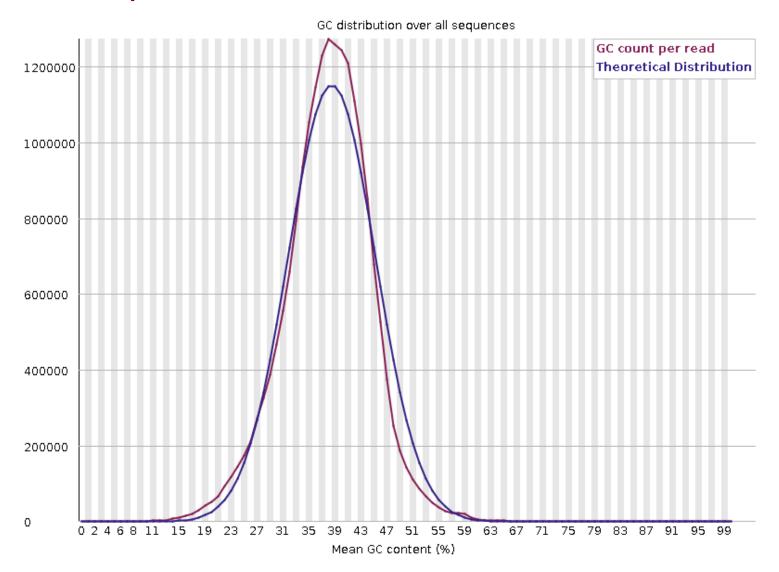
### Per sequence quality scores



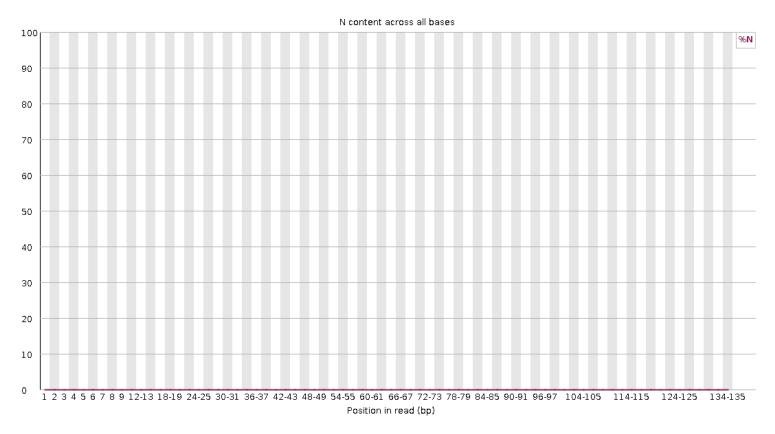
## Per base sequence content



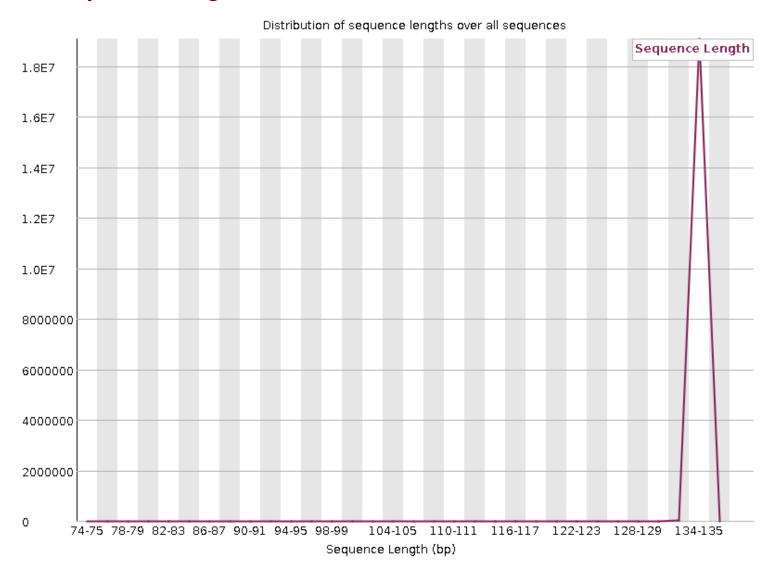
## Per sequence GC content



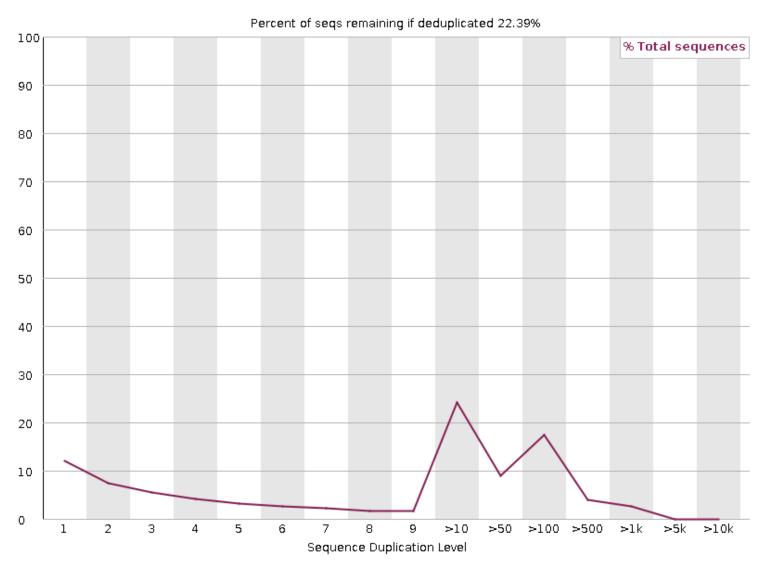
#### Per base N content



#### Sequence Length Distribution



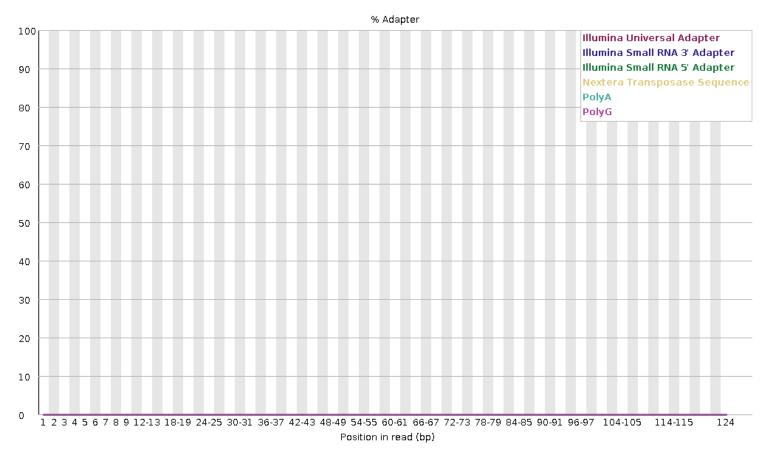
#### Sequence Duplication Levels





No overrepresented sequences

## Adapter Content



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