#### Mon 25 Mar 2019 JATA\_Pur\_2\_trimmed.fq

### **<b>№**FastQC 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

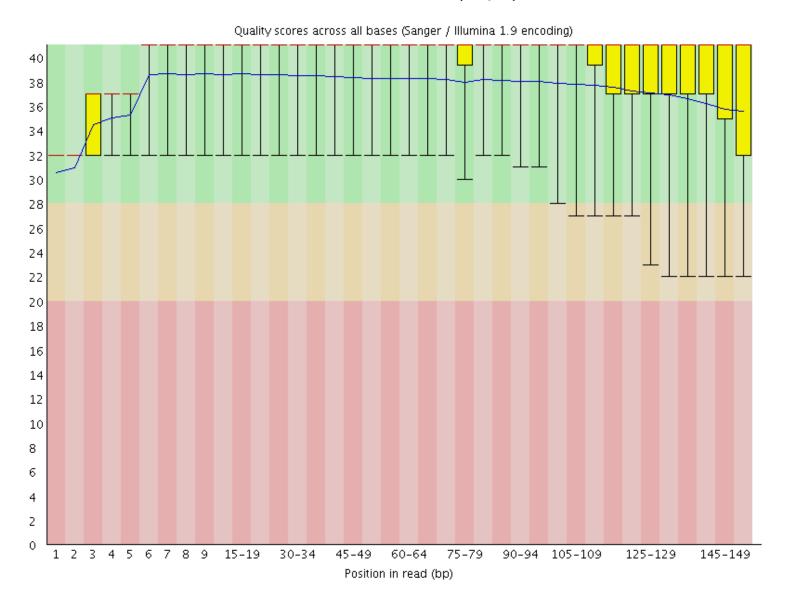
Overrepresented sequences

Adapter Content

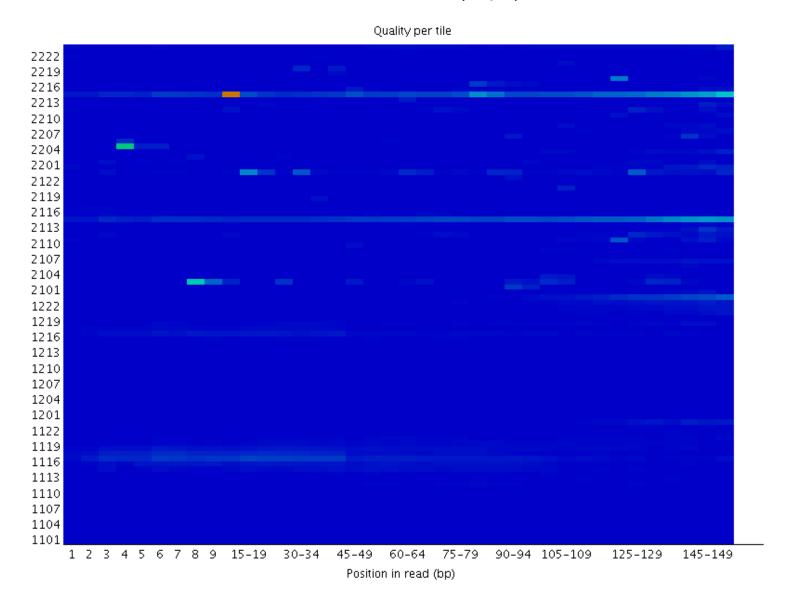
### **Basic Statistics**

Measure	Value
Filename	JATA_Pur_2_trimmed.fq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	421904422
Sequences flagged as poor quality	0
Sequence length	10-150
%GC	40

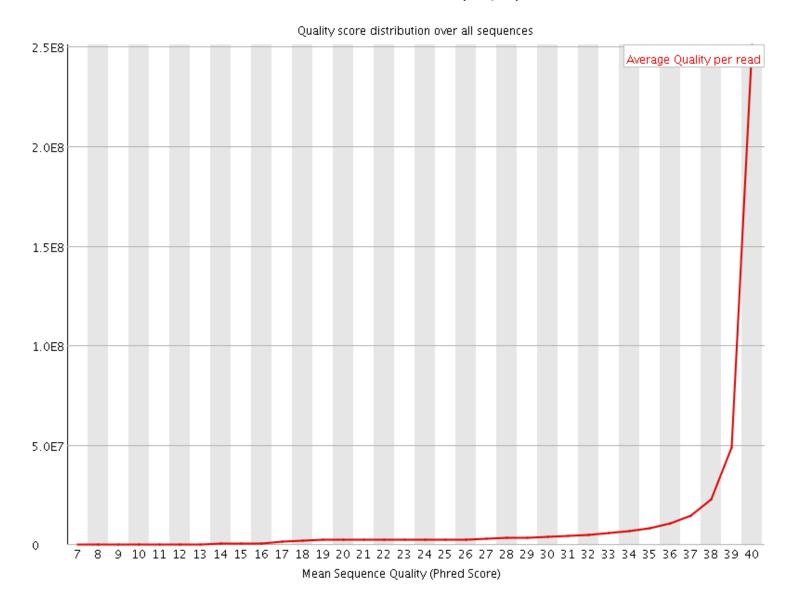
# Per base sequence quality



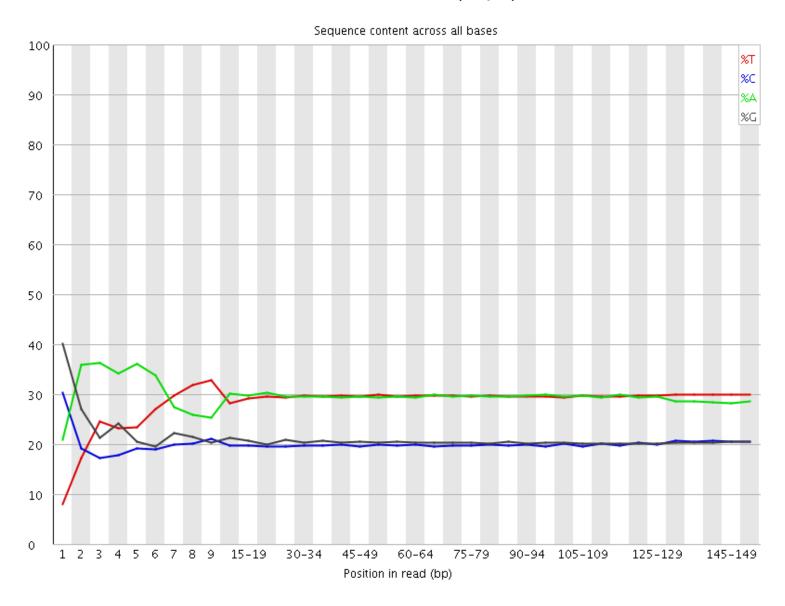
# Per tile sequence quality



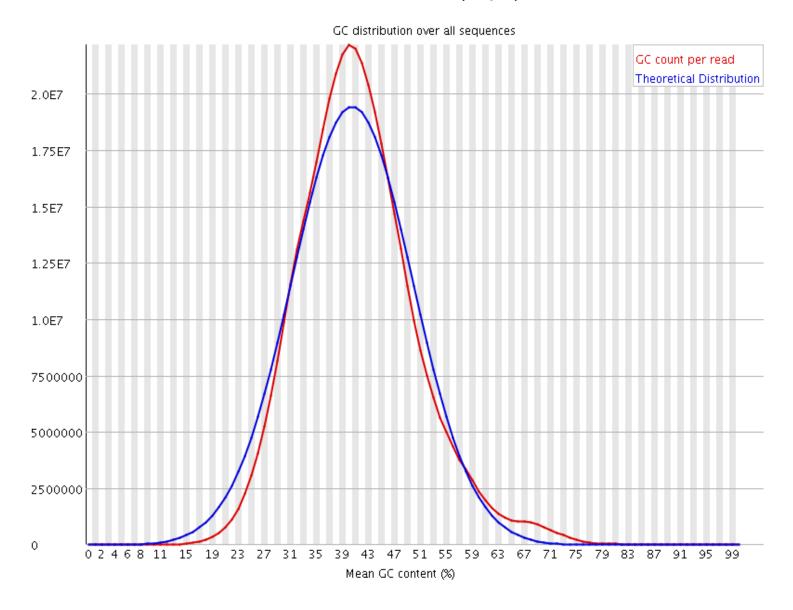
# Per sequence quality scores



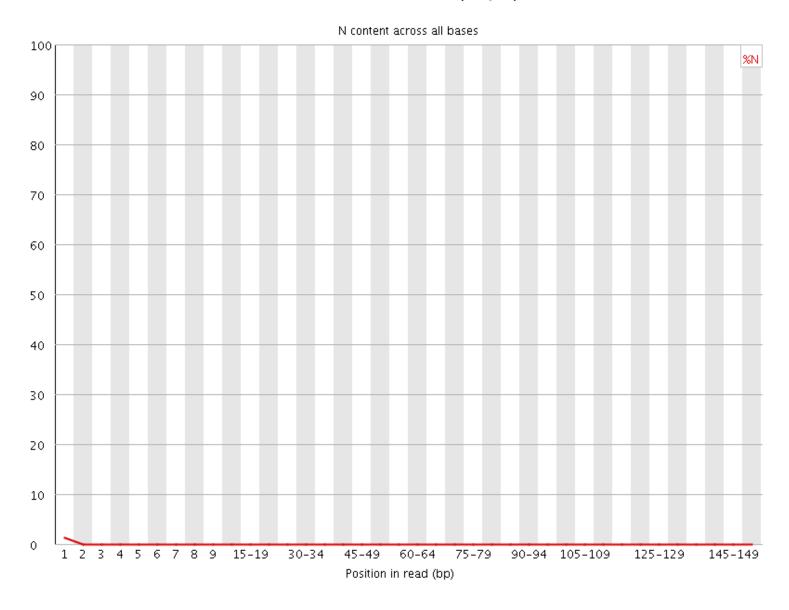
# Per base sequence content



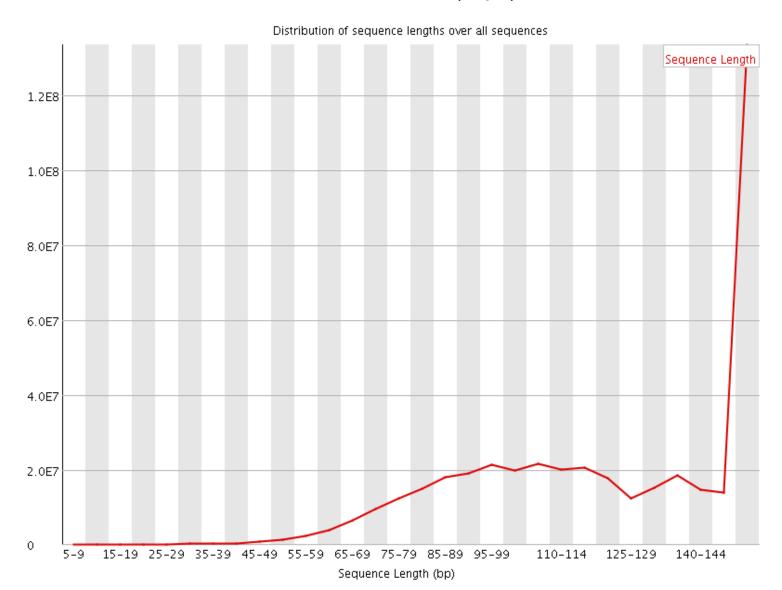




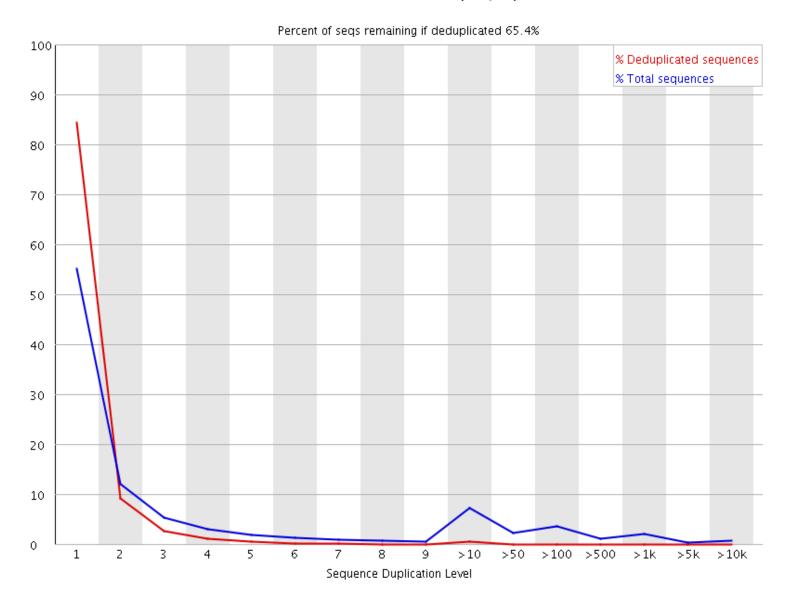




# Sequence Length Distribution

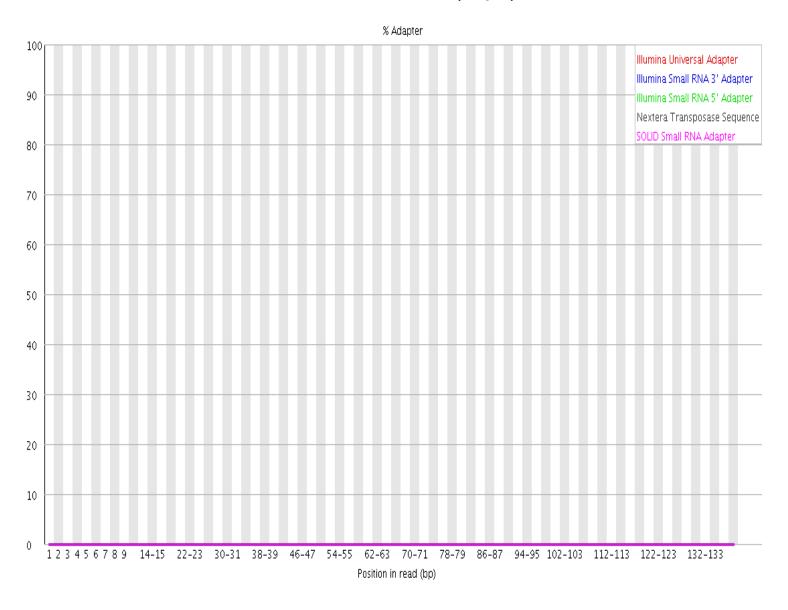


## Sequence Duplication Levels









#### Produced by FastQC (version 0.11.7)