Mon 25 Mar 2019 JATA_Pur_1_trimmed.fq

№FastQC Report **Summary**





Per tile sequence quality

<u>Per sequence quality scores</u>

Per base sequence content

Per sequence GC content

Per base N content

Sequence Length Distribution

Sequence Duplication Levels

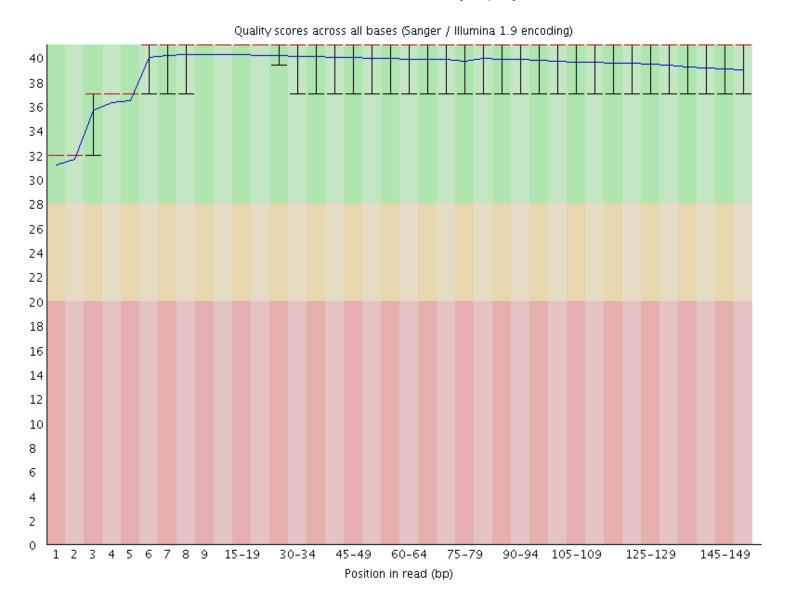
Overrepresented sequences

Adapter Content

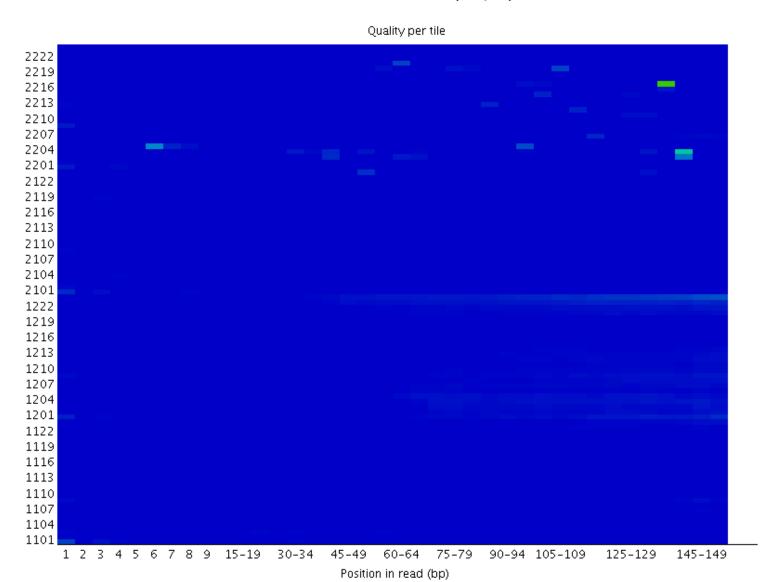
Basic Statistics

Measure	Value
Filename	JATA_Pur_1_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

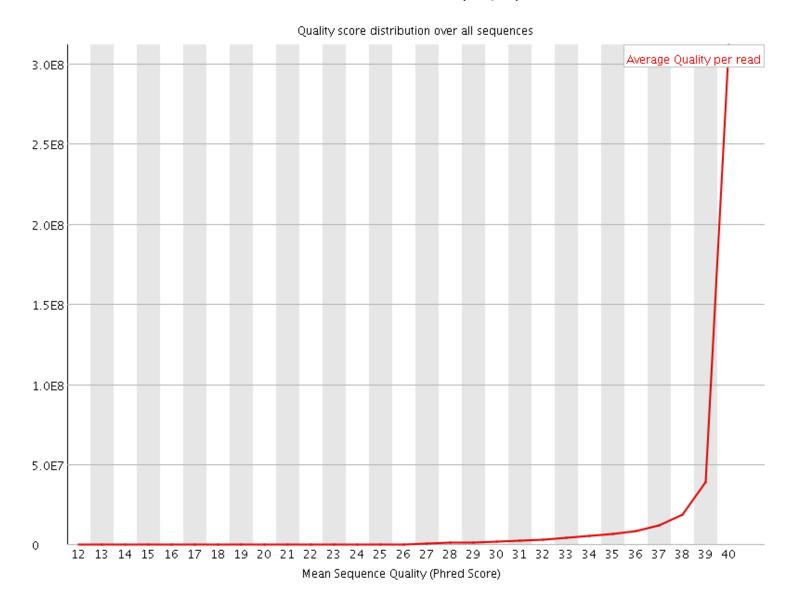
Per base sequence quality



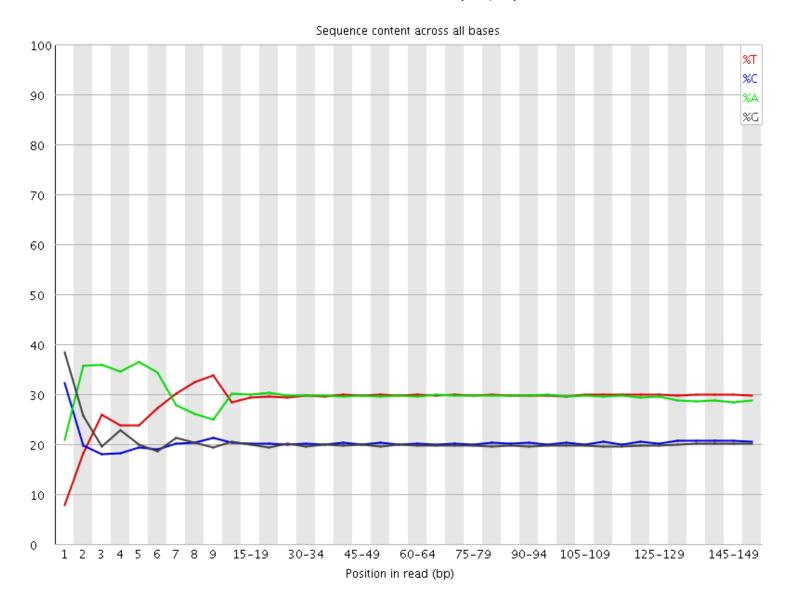
Per tile sequence quality



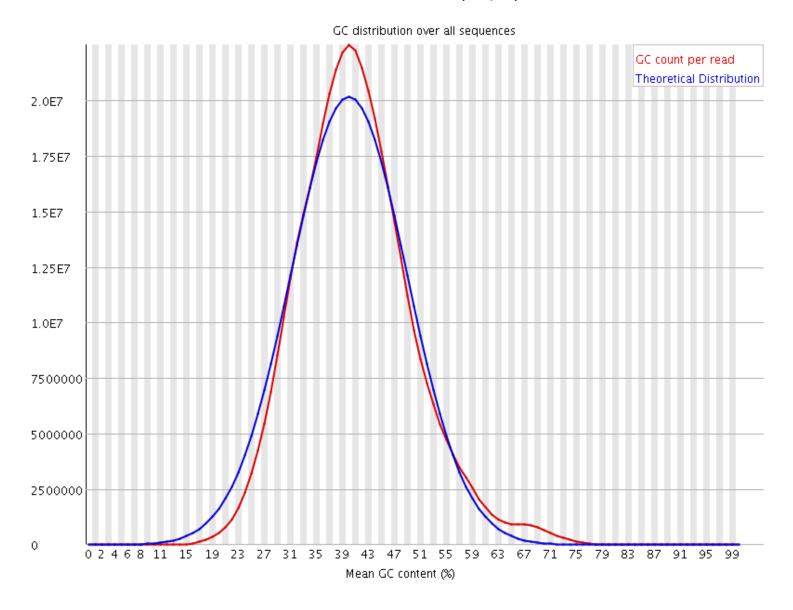
Per sequence quality scores



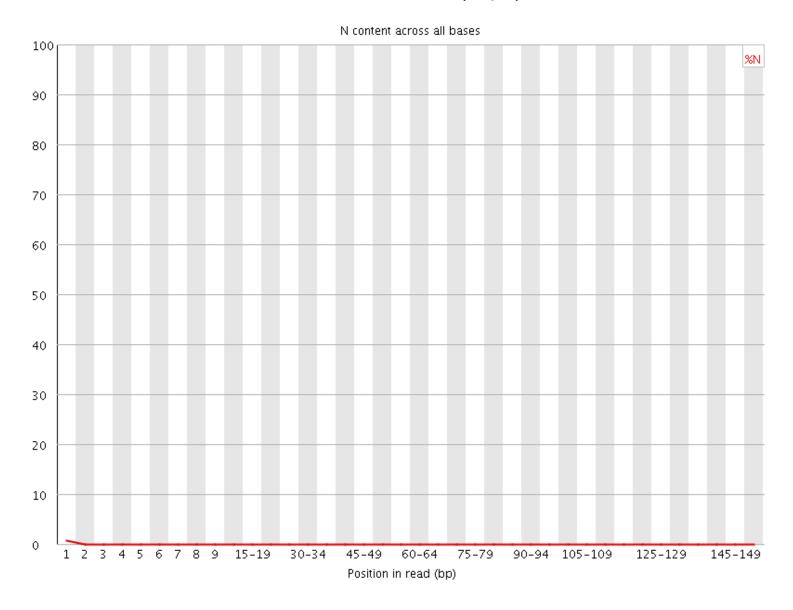
Per base sequence content



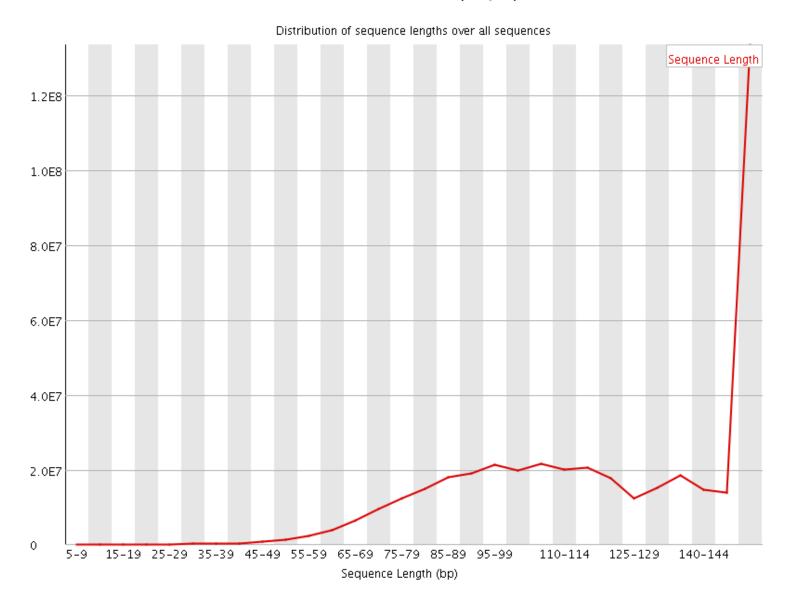






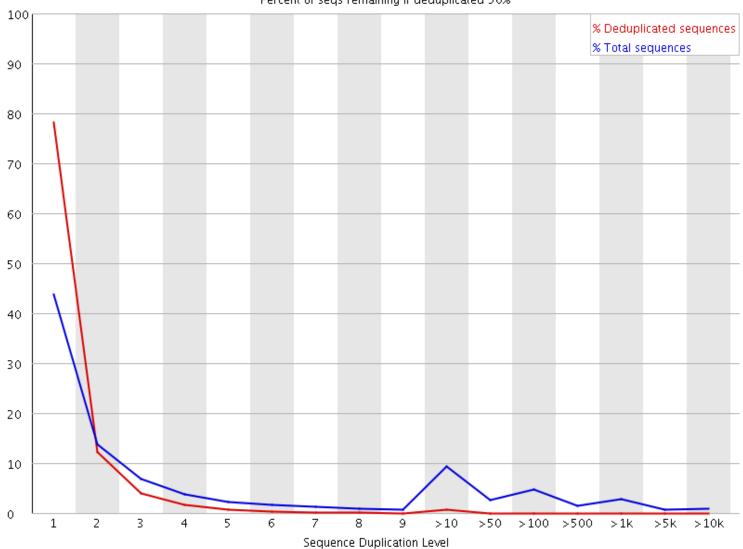


Sequence Length Distribution



Sequence Duplication Levels

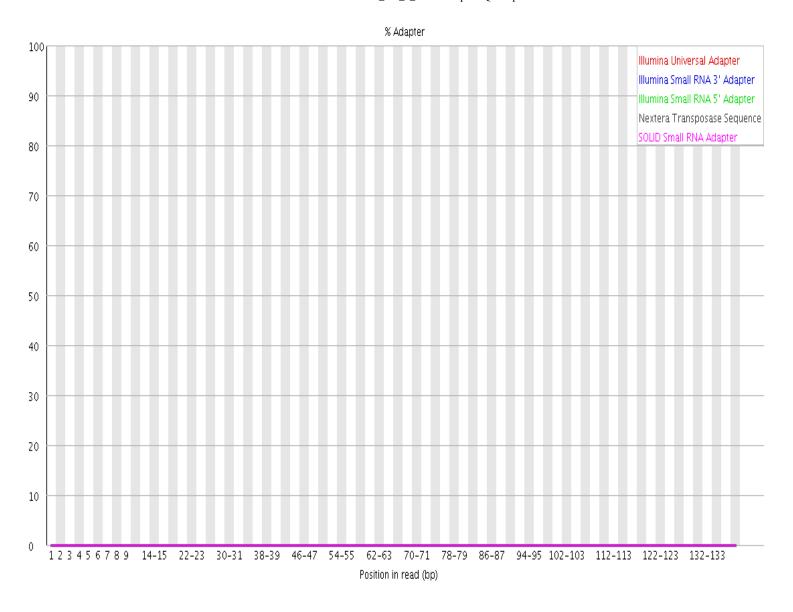






No overrepresented sequences





Produced by FastQC (version 0.11.7)