



Per base sequence quality

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

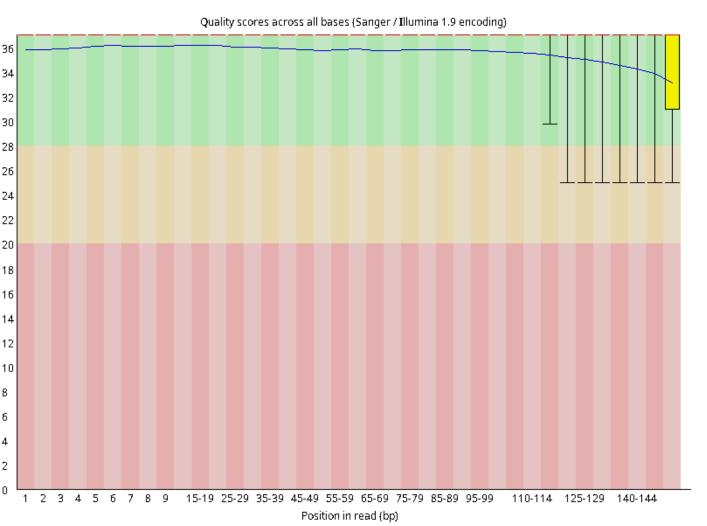
Overrepresented sequences

Adapter Content

Basic Statistics

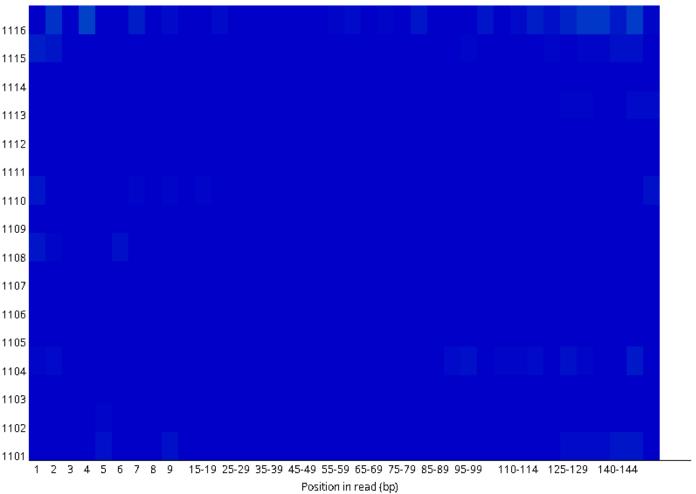
Measure	Value	
Filename	SRR33784444_2_paired.fastq	
File type	Conventional base calls	
Encoding	Sanger / Illumina 1.9	
Total Sequences	49186	
Sequences flagged as poor quality	0	
Sequence length	50-151	
%GC	45	

Per base sequence quality

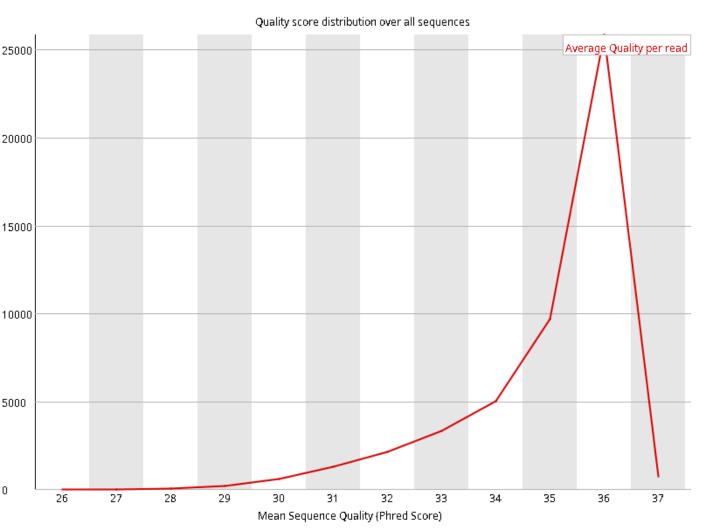


Per tile sequence quality

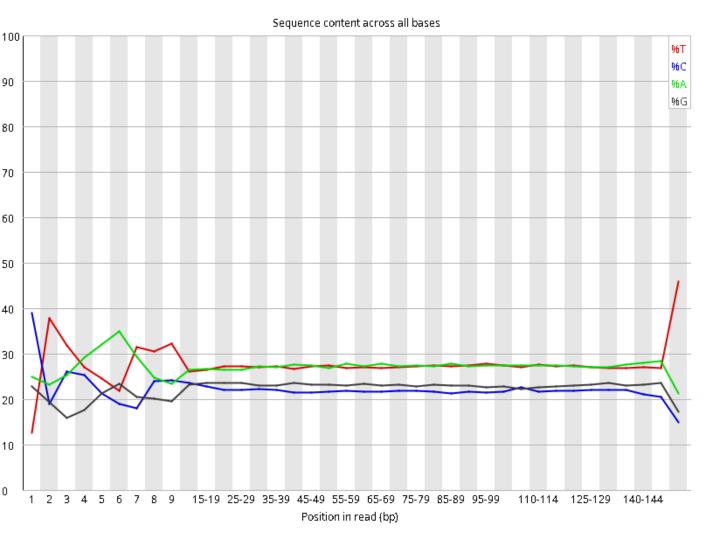




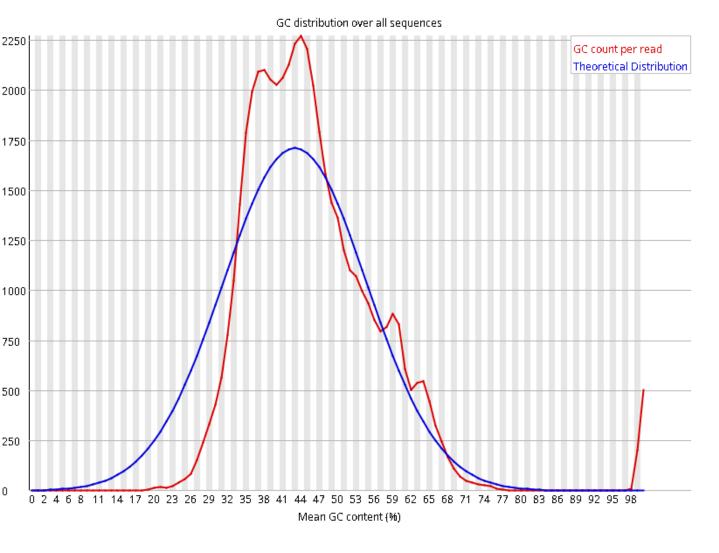
Per sequence quality scores



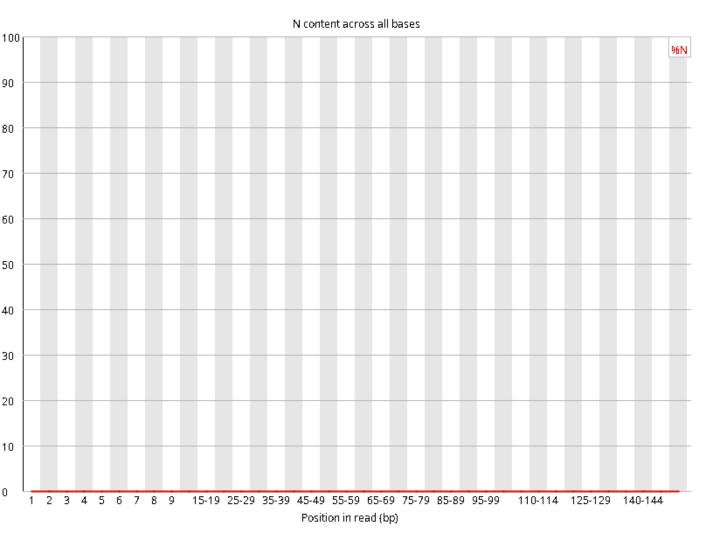
Per base sequence content



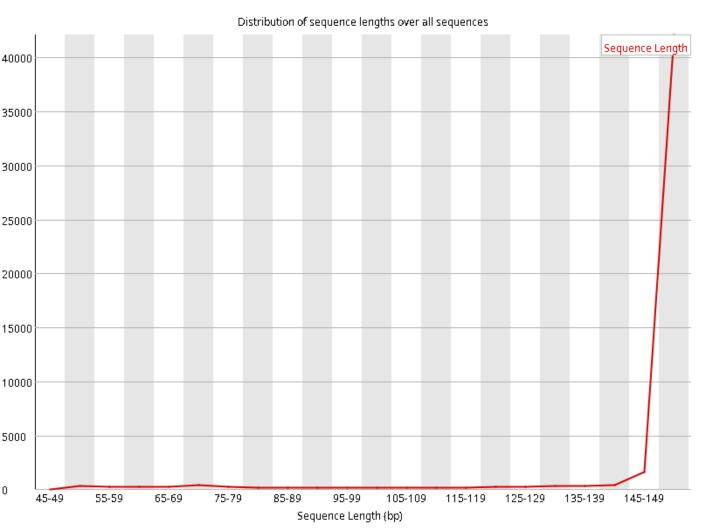
Per sequence GC content



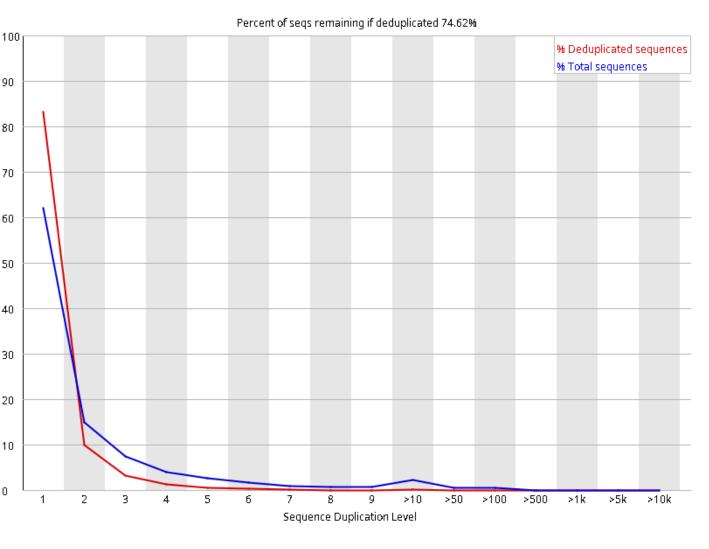




Sequence Length Distribution



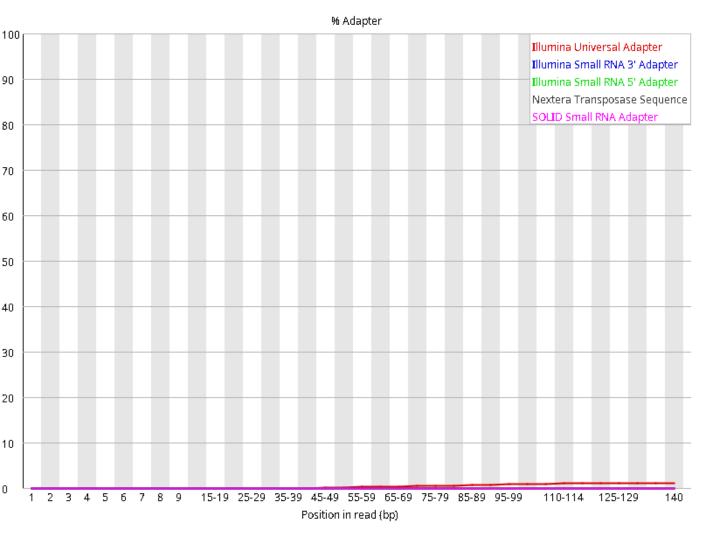
Sequence Duplication Levels



Overrepresented sequences

Sequence	Count	Percentage	Possible Source
699999999999999999999999999999999999999	351	0.713617696092384	No Hit
CCTCCAATTCCTCCTATCATTTTTGGTTTCCATTTTCCTGGTAAATTTAT	94	0.19111129183100883	No Hit
CCTCCAATTCCCCCTATCATTTTTGGTTTCCATTTTCCTGGTAAATTTAT	89	0.18094579758467857	No Hit
000000000000000000000000000000000000000	71	0.14435001829788965	No Hit
CTCCAATTCCCCCTATCATTTTTGGTTTCCATTTTCCTGGTAAATTTATT	70	0.1423169194486236	No Hit





Produced by FastQC (version 0.11.7)