Sat 2 Nov 2024 SRR14866429_2.fastq

ReportSummary





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 SRR14866429_2.fastq

File type Conventional base calls

Encoding Sanger / Illumina 1.9

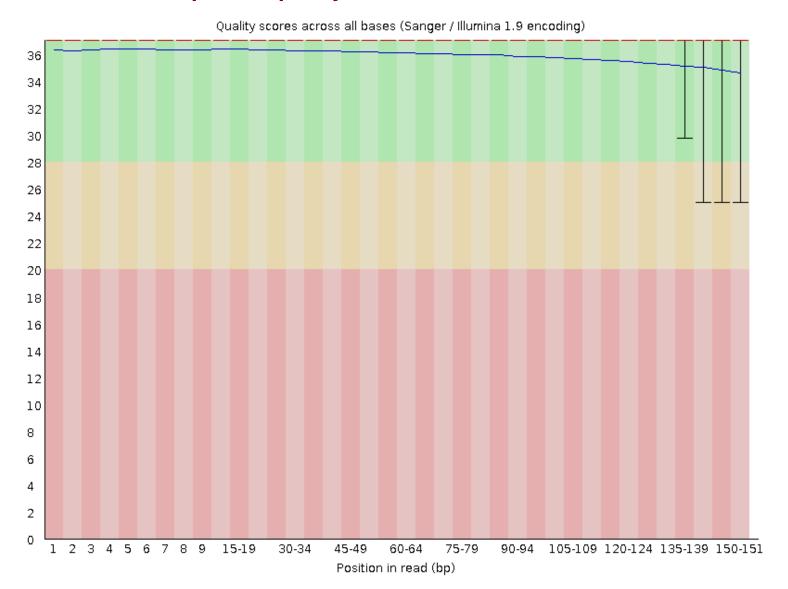
Total Sequences 21908548

Sequences flagged as poor quality 0

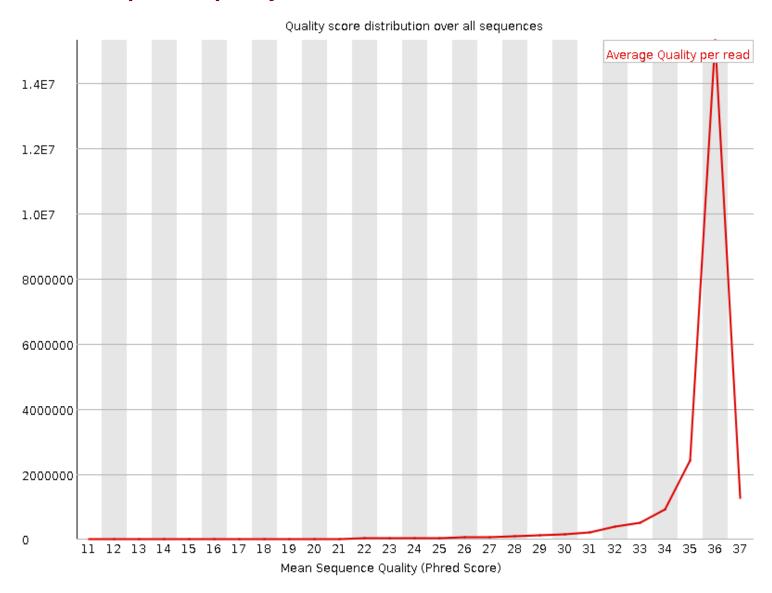
Sequence length 151

%GC 51

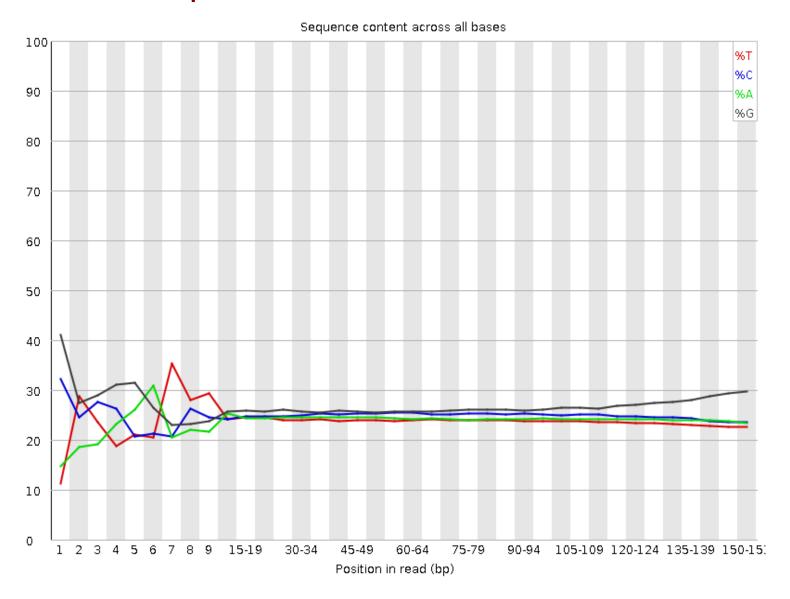
Per base sequence quality



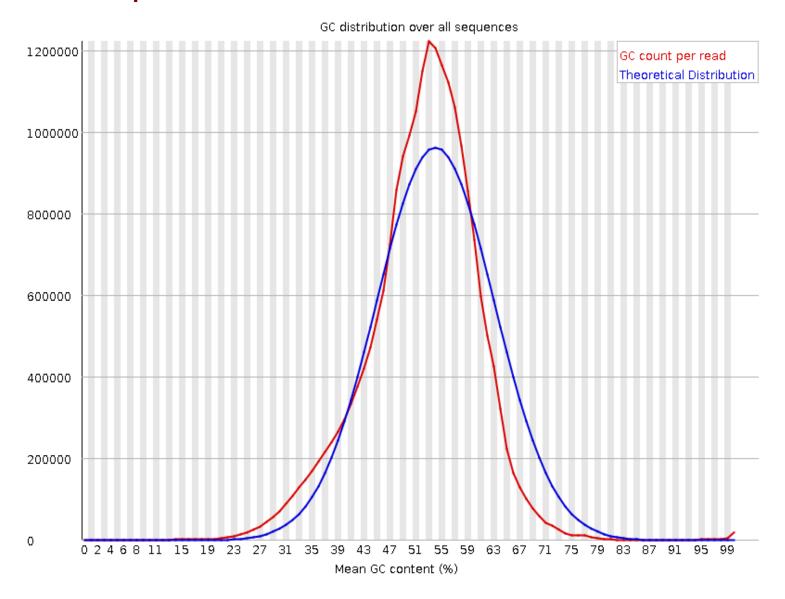
Per sequence quality scores



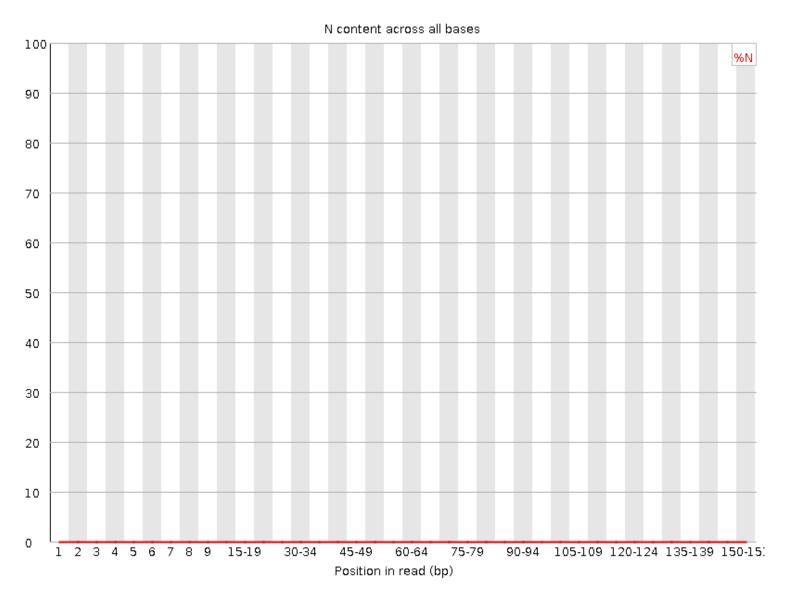
Per base sequence content



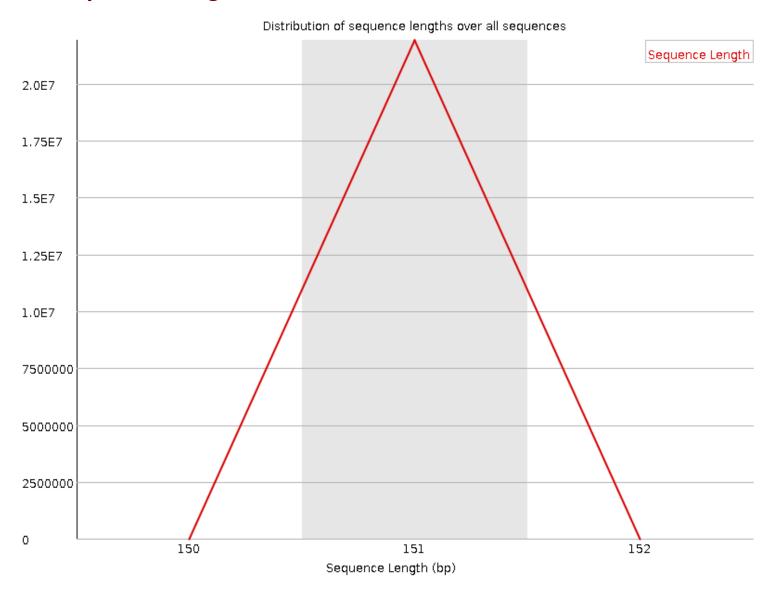
Per sequence GC content



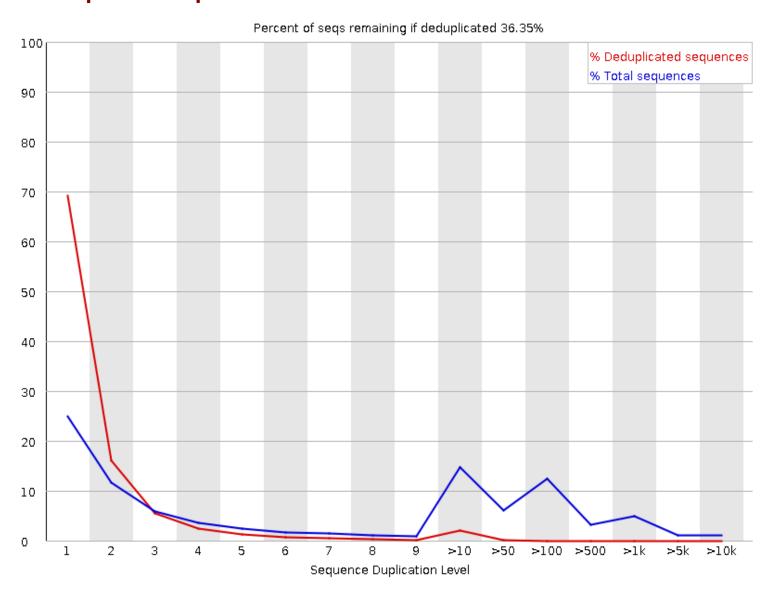
Per base N content



Sequence Length Distribution



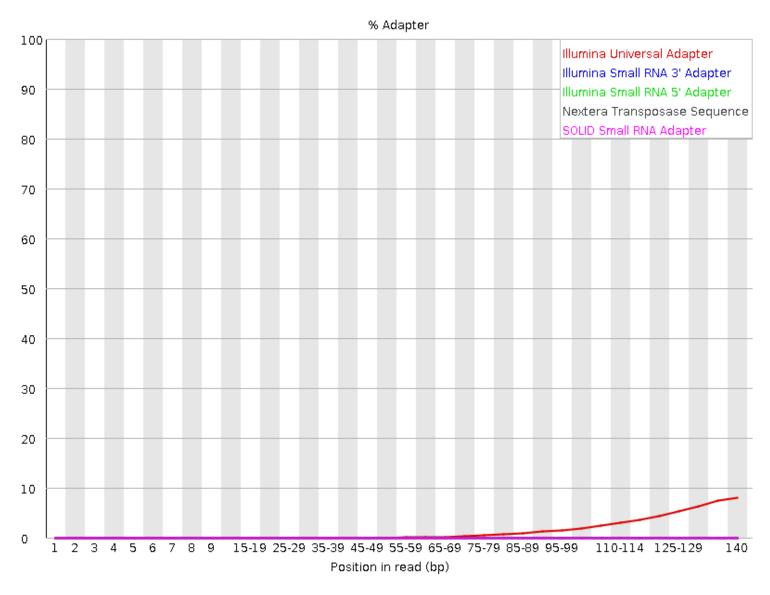
Sequence Duplication Levels



Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	36730	0.16765145732158973	No Hit
${\tt GTCTCTTTCTGCTGACGACAAGAAGTGGTCAAGGCCTTCTGGGGCAAGG}$	25886	0.1181547951055451	No Hit
${\tt CGACAAGAAAGTGGTCAAGGCCTTCTGGGGCAAGGTGTCCACCAAGGCTG}$	25353	0.11572195473657132	No Hit
${\tt AAGAAAGTGGTCAAGGCCTTCTGGGGCAAGGTGTCCACCAAGGCTGATGC}$	24674	0.11262270781249402	No Hit
CGCAAACTAAACAAGAGTCACCATGGTTGAGTGGACTGATCAAGAGCGCA	24223	0.11056415057720849	No Hit

Adapter Content



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