









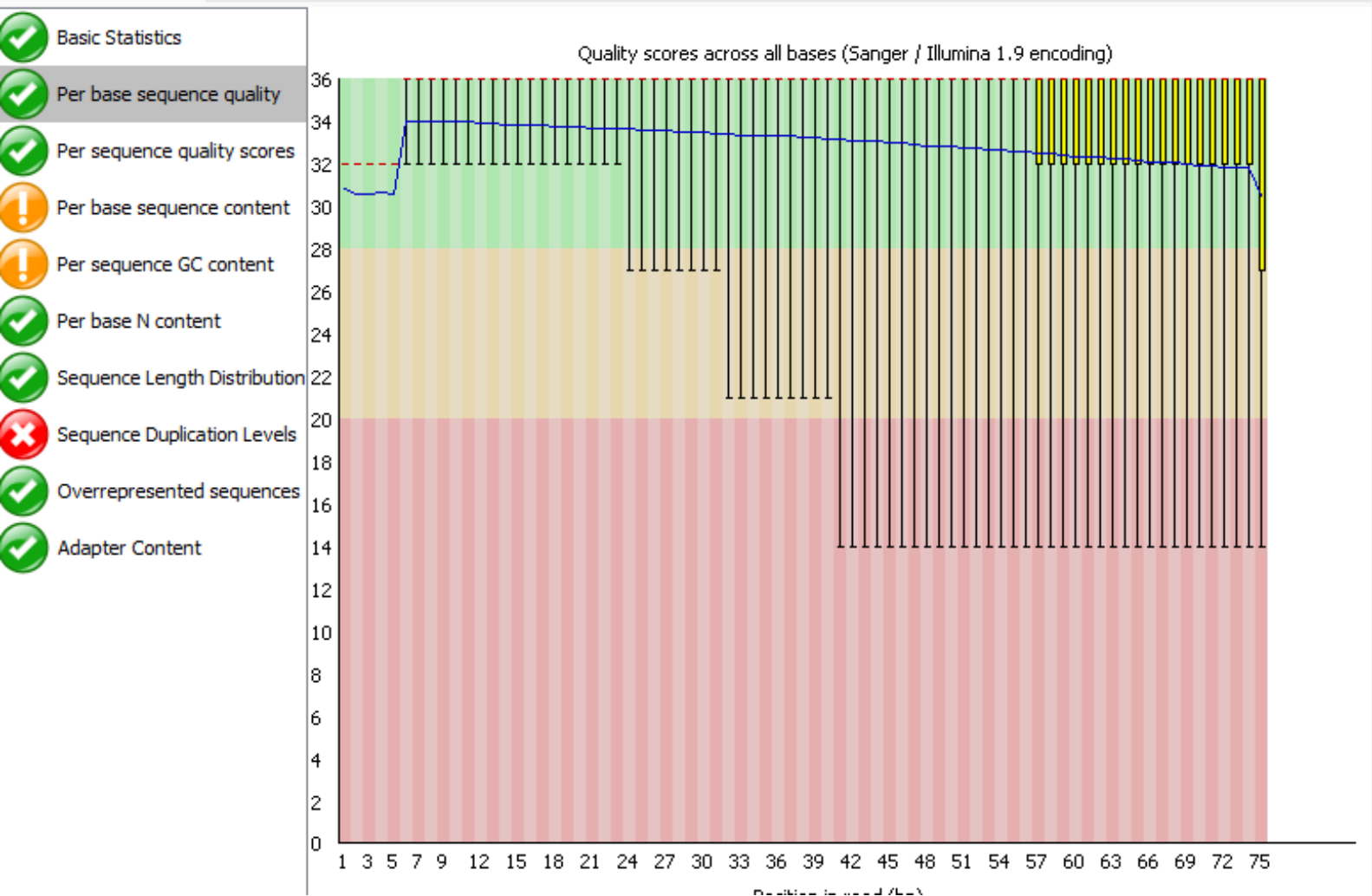


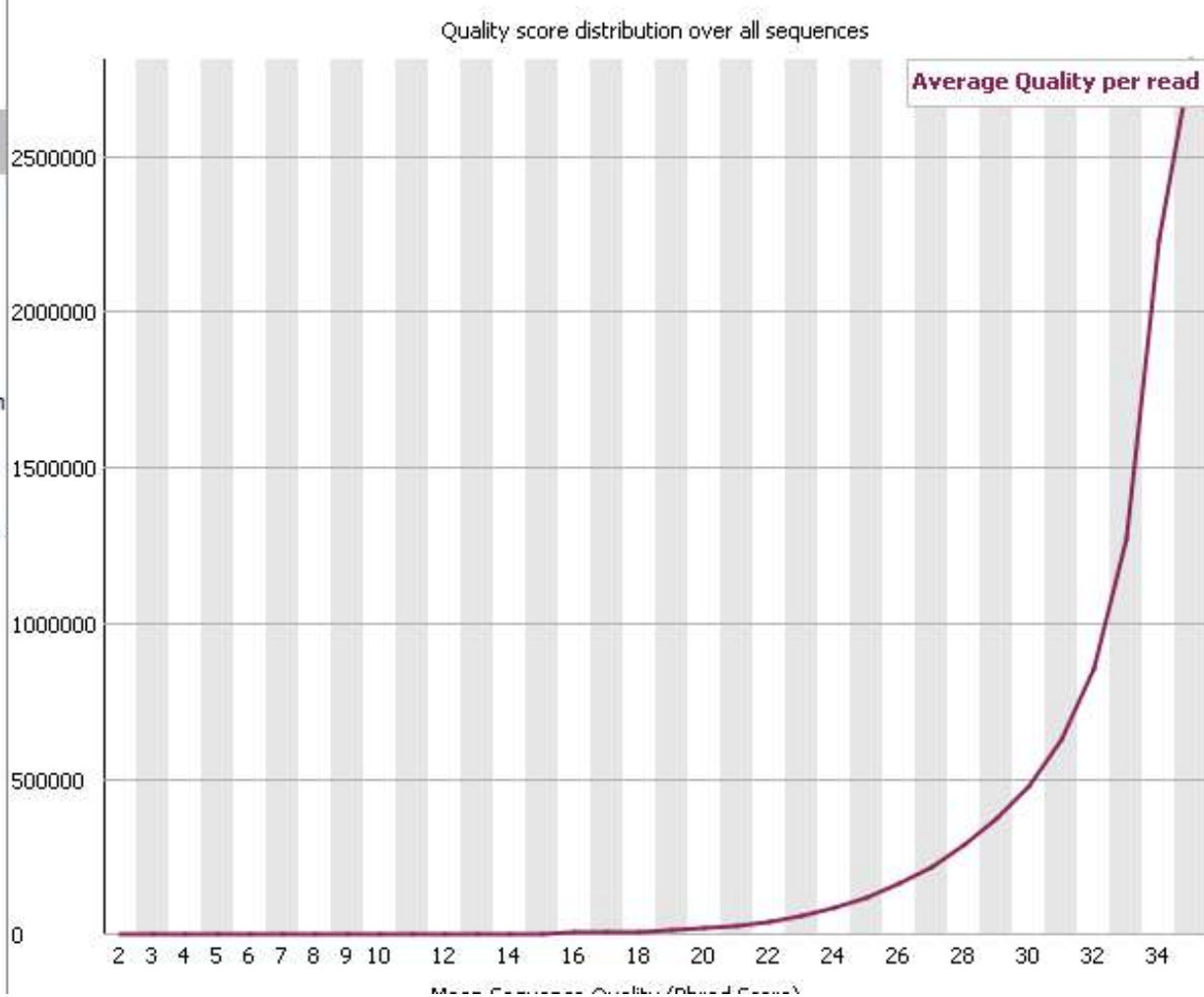
SRR15718926_2.fastq

Basic sequence stats		
Measure		Value
 Basic Statistics	Filename	SRR15718926_2.fastq
 Per base sequence quality	File type	Conventional base calls
 Per sequence quality scores	Encoding	Sanger / Illumina 1.9
 Per base sequence content	Total Sequences	9739476
 Per sequence GC content	Total Bases	730.4 Mbp
 Per base N content	Sequences flagged as poor quality	0
 Sequence Length Distribution	Sequence length	75
 Sequence Duplication Levels	%GC	45
 Overrepresented sequences		
 Adapter Content		



SRR15718926_2.fastq

- Basic Statistics
- 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
- Adapter Content



- ✓

Basic Statistics
- ✓

Per base sequence quality
- ✓

Per sequence quality scores
- !

Per base sequence content
- !

Per sequence GC content
- ✓

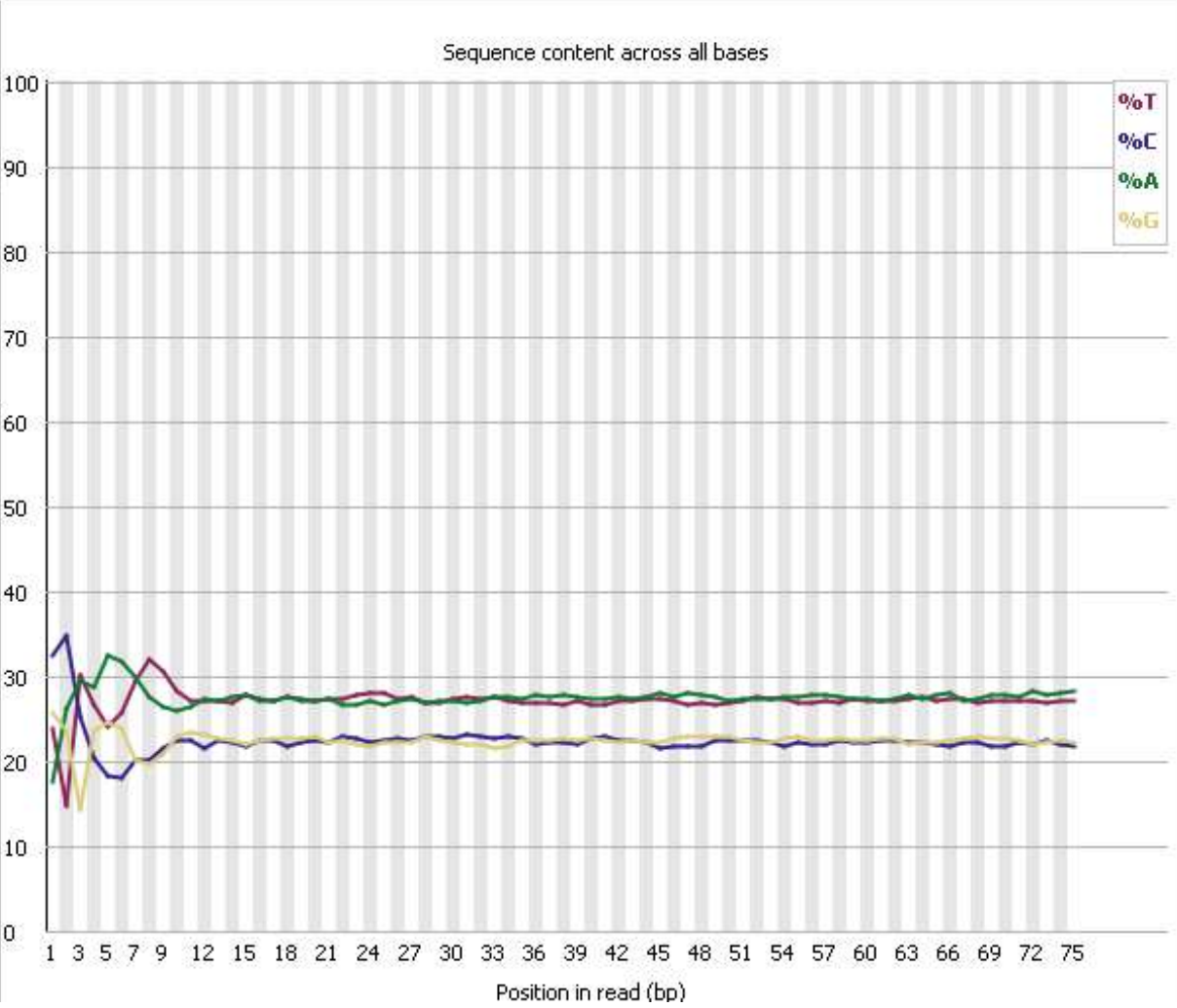
Per base N content
- ✓

Sequence Length Distribution
- ✗

Sequence Duplication Levels
- ✓

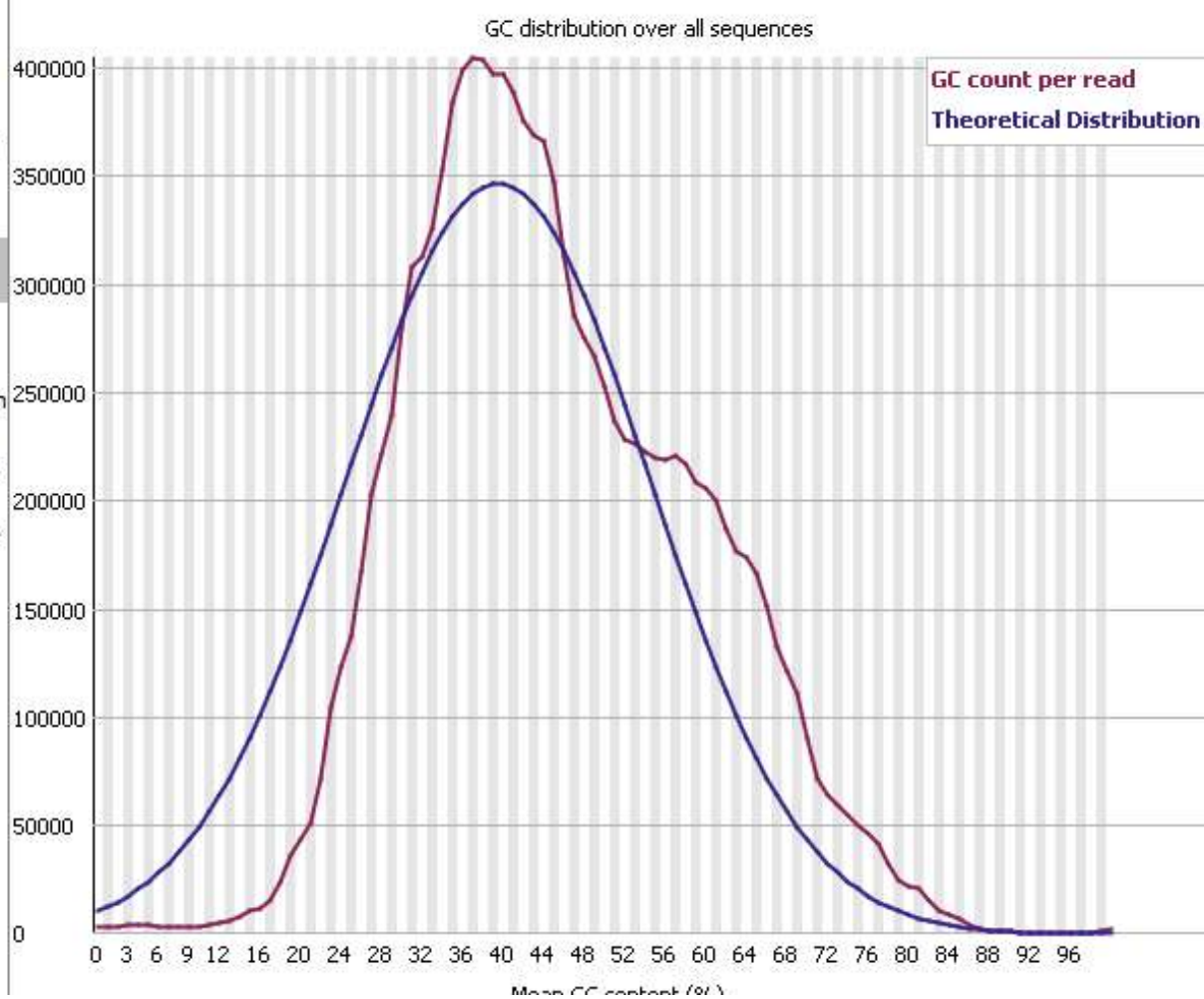
Overrepresented sequences
- ✓

Adapter Content

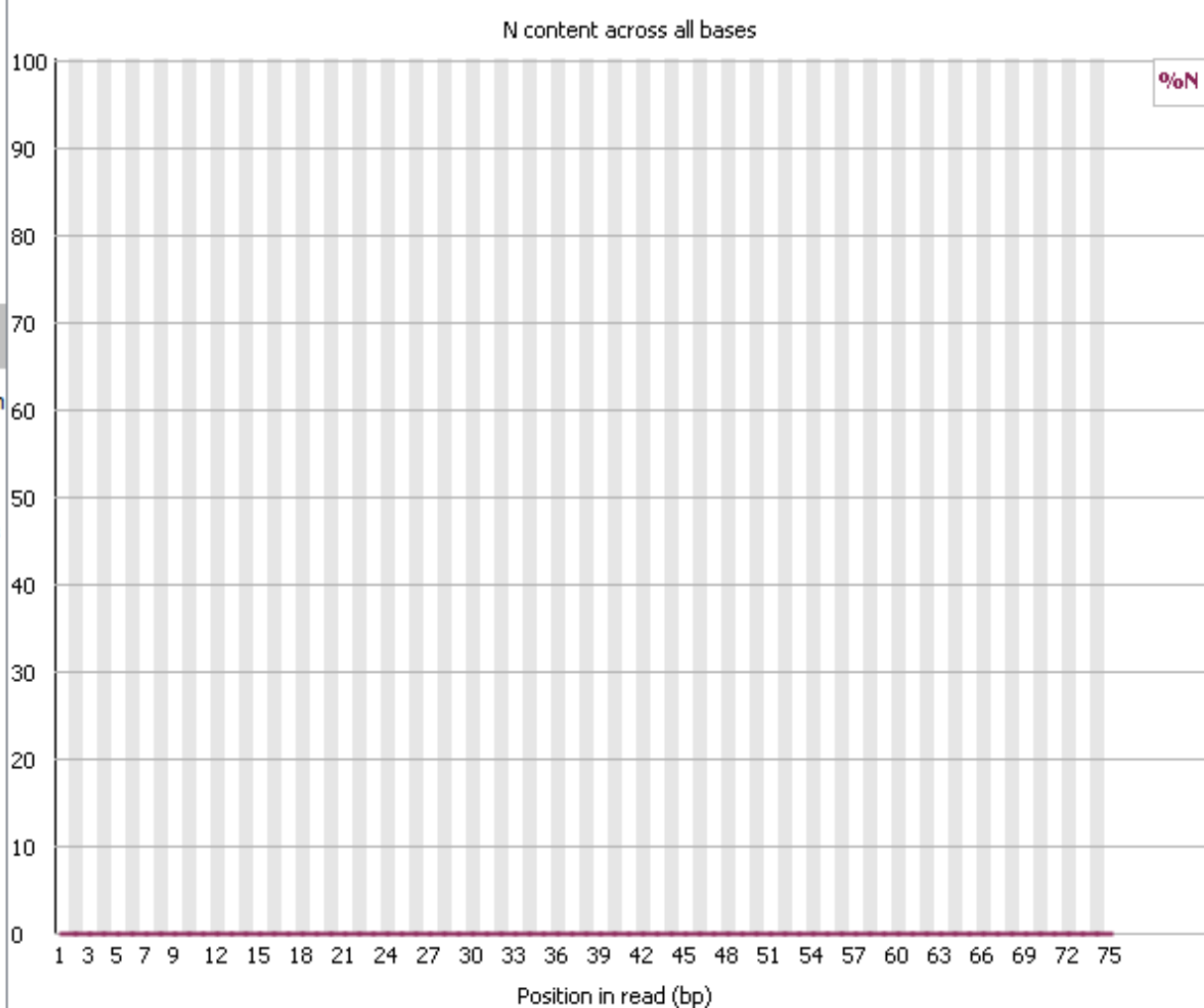


SRR15718926_2.fastq

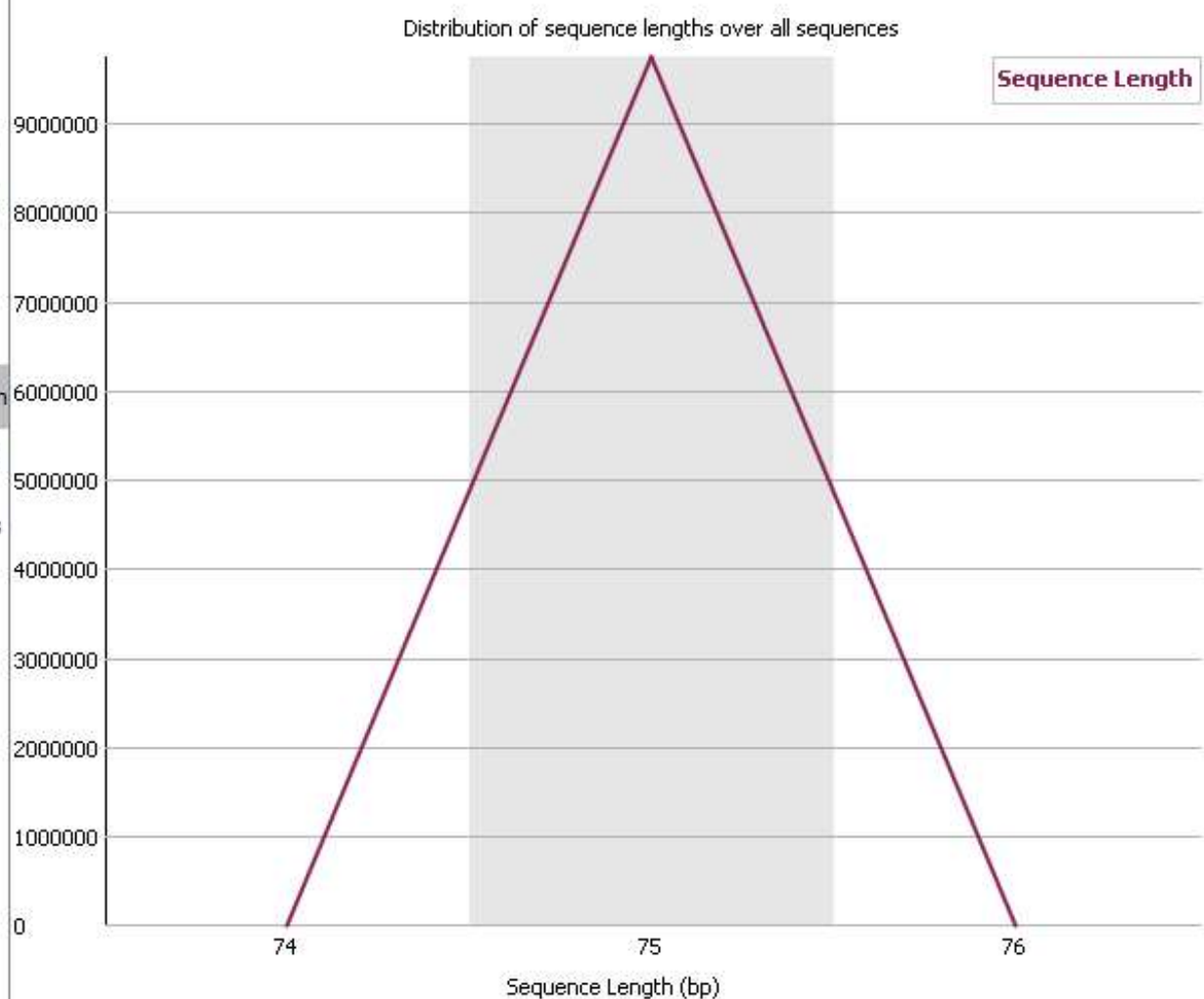
- Basic Statistics
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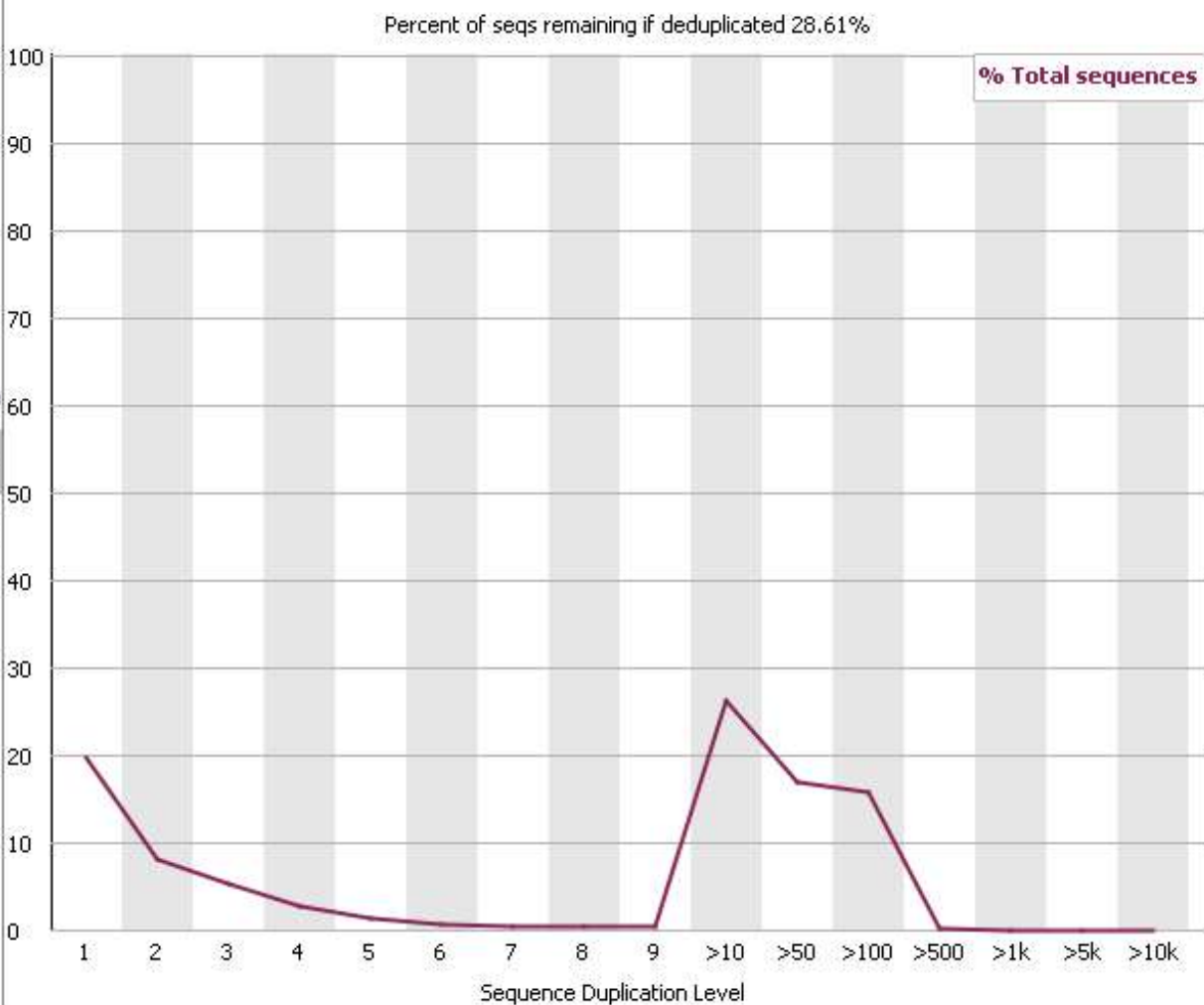



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FastQC


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□


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FileHelp


SRR15718926_2.fastq


Basic Statistics


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

Adapter Content

Overrepresented sequences

There are no overrepresented sequences

SRR15718926_2.fastq

