

# FastQC Report

## Summary

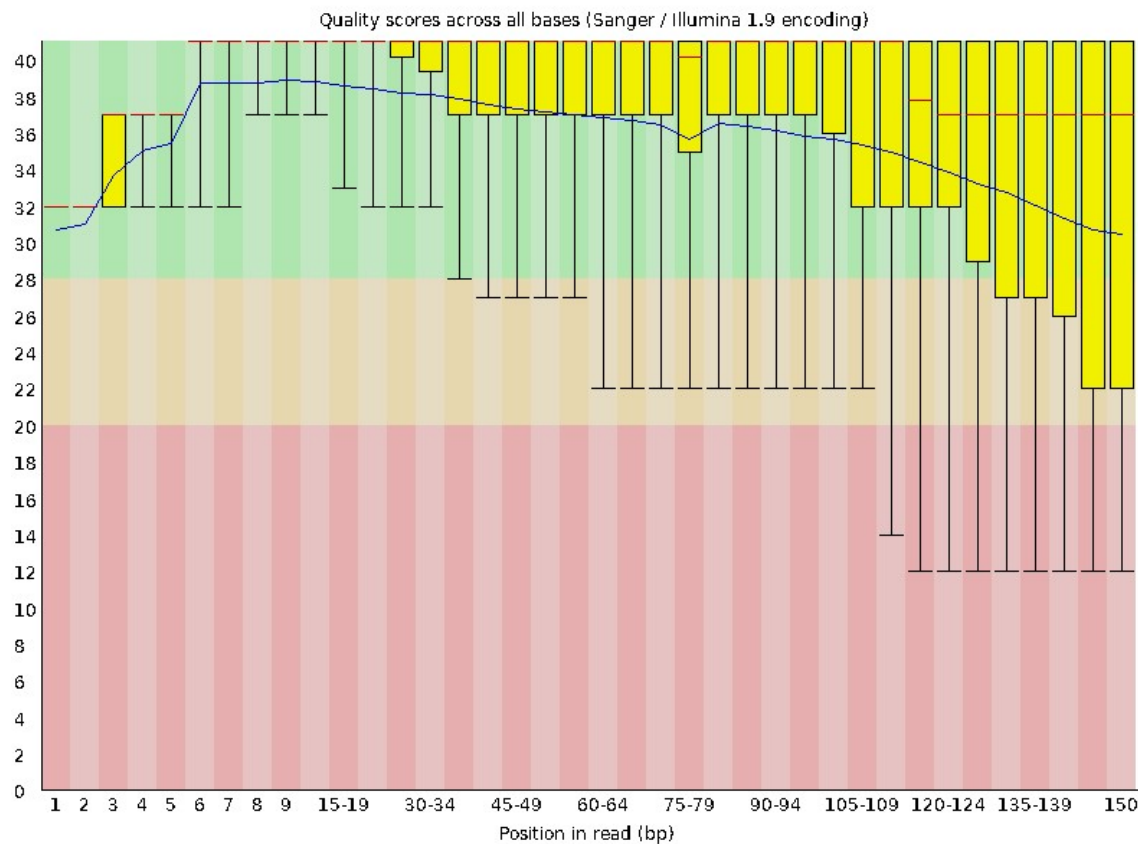
Mon 25 Jun 2018  
9IRM1\_HWC3LBBXX\_CGCTCATT-TAAGATTA\_L001\_R2.fastq.gz

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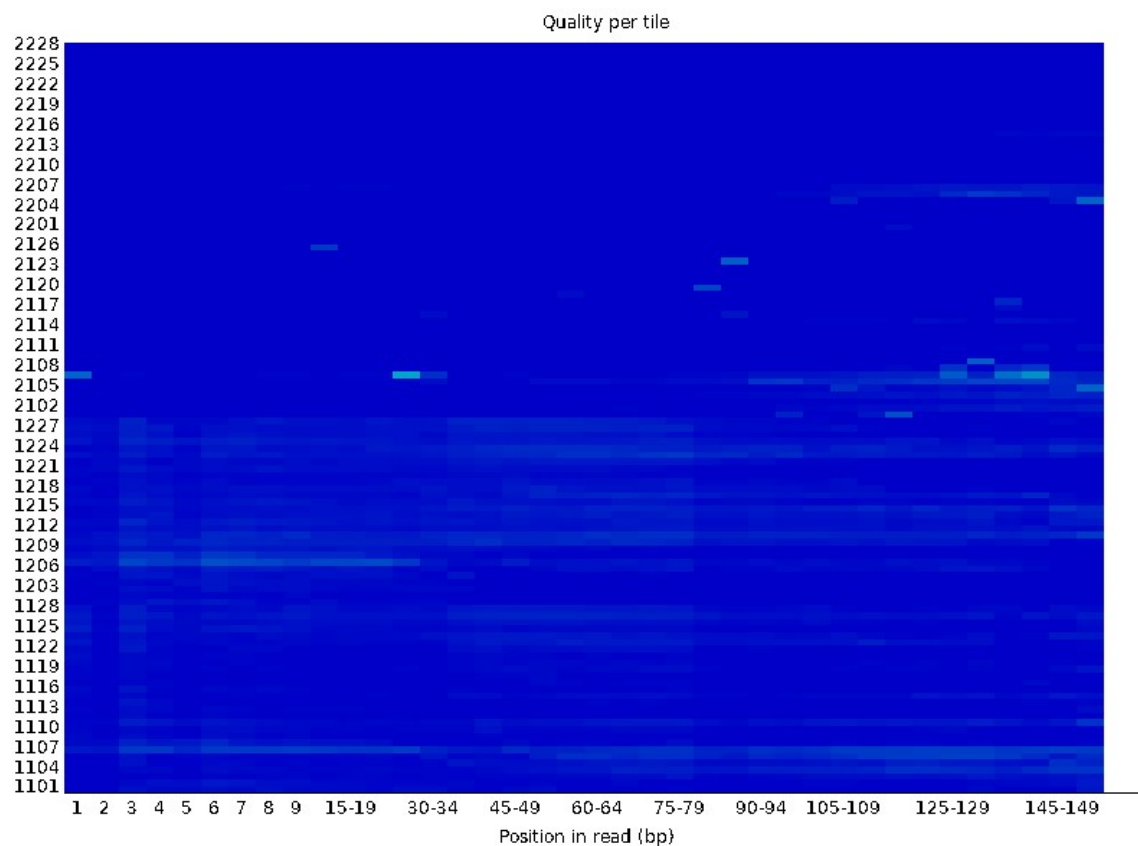
## Basic Statistics

| Measure                           | Value                                              |
|-----------------------------------|----------------------------------------------------|
| Filename                          | 9IRM1_HWC3LBBXX_CGCTCATT-TAAGATTA_L001_R2.fastq.gz |
| File type                         | Conventional base calls                            |
| Encoding                          | Sanger / Illumina 1.9                              |
| Total Sequences                   | 94005512                                           |
| Sequences flagged as poor quality | 0                                                  |
| Sequence length                   | 150                                                |
| %GC                               | 37                                                 |

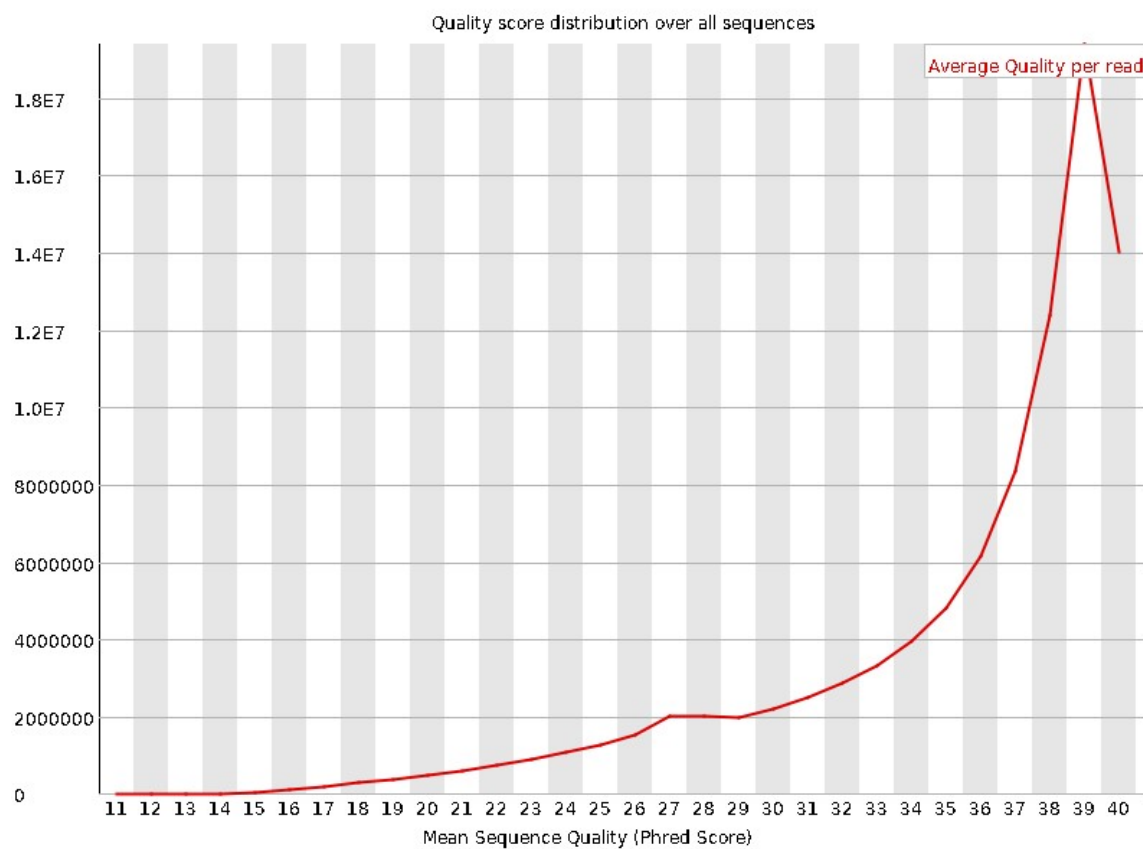
## Per base sequence quality



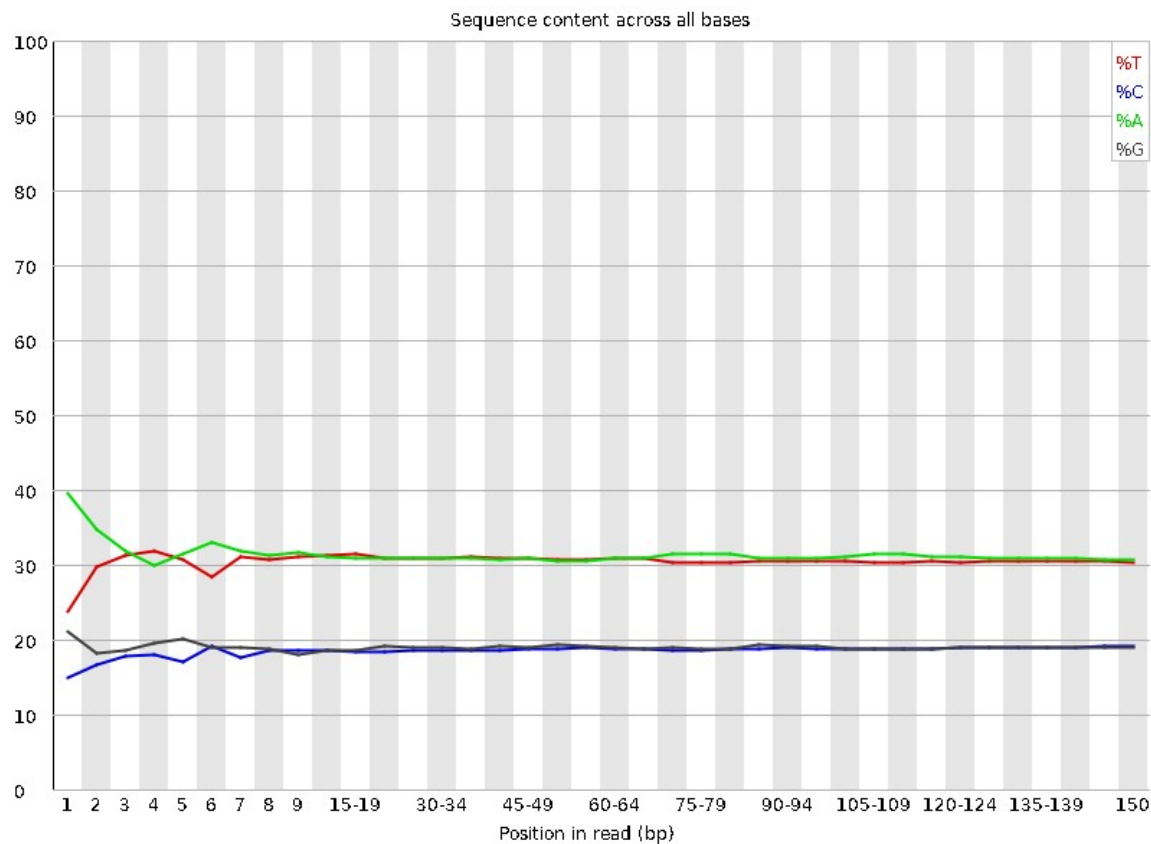
### ✓ Per tile sequence quality



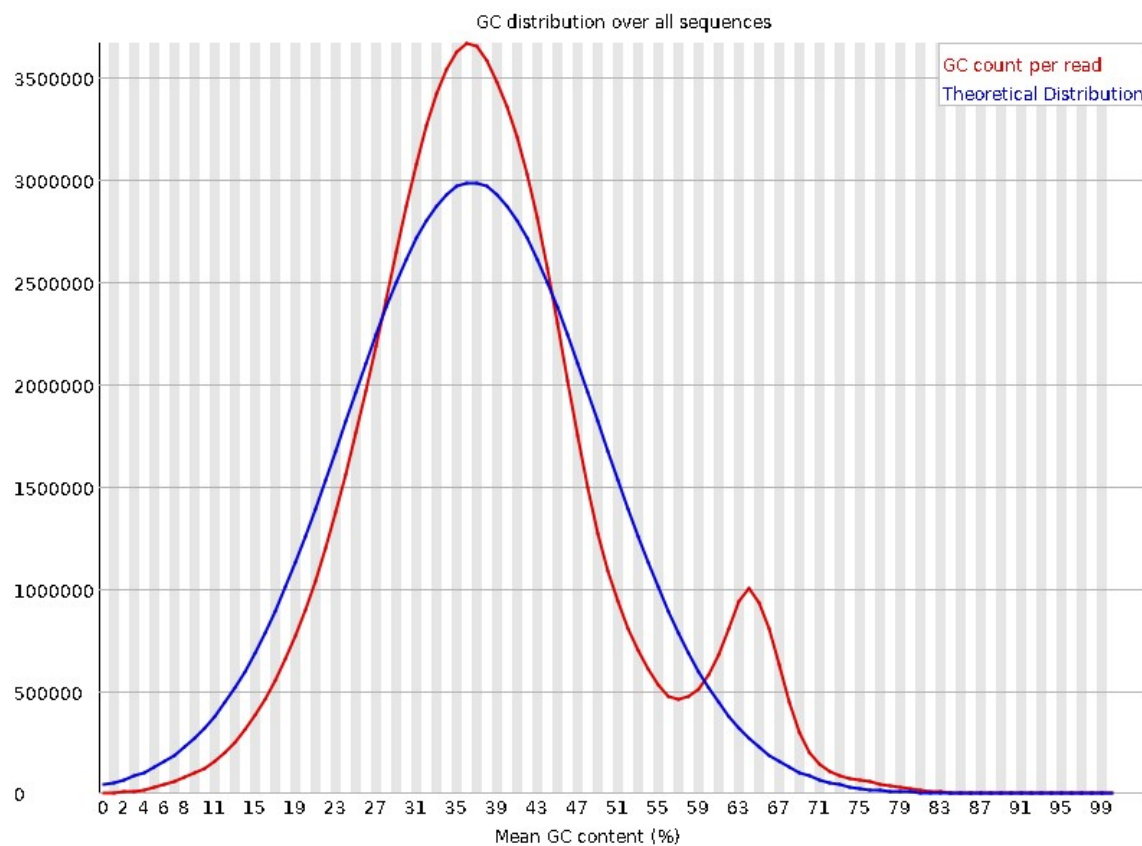
## ✓ Per sequence quality scores



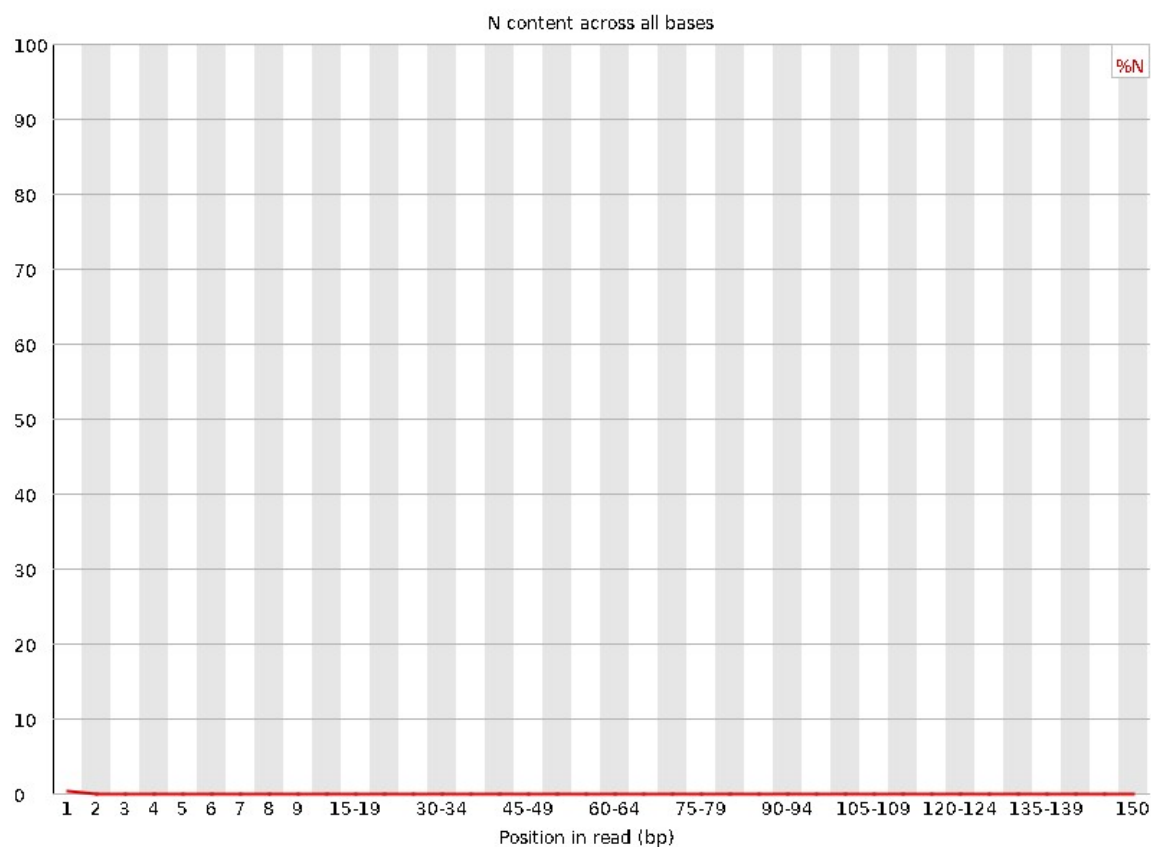
## ! Per base sequence content



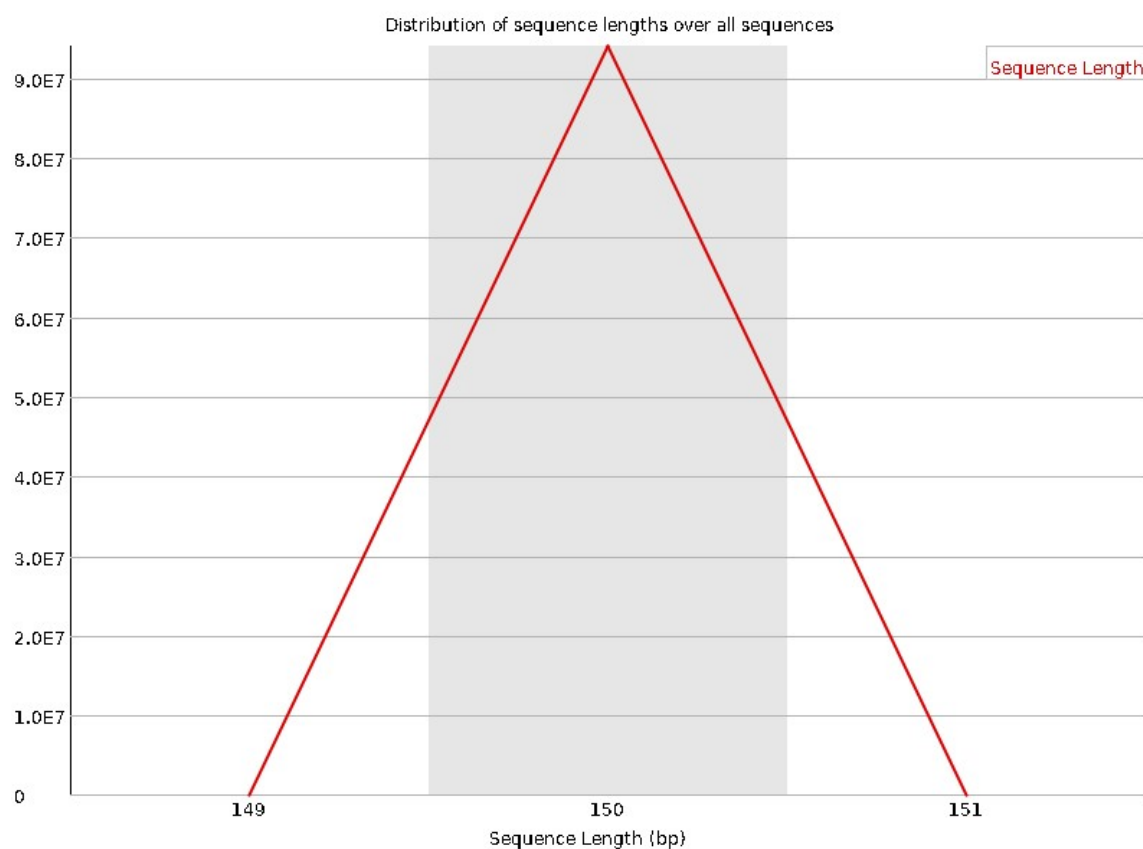
### ! Per sequence GC content



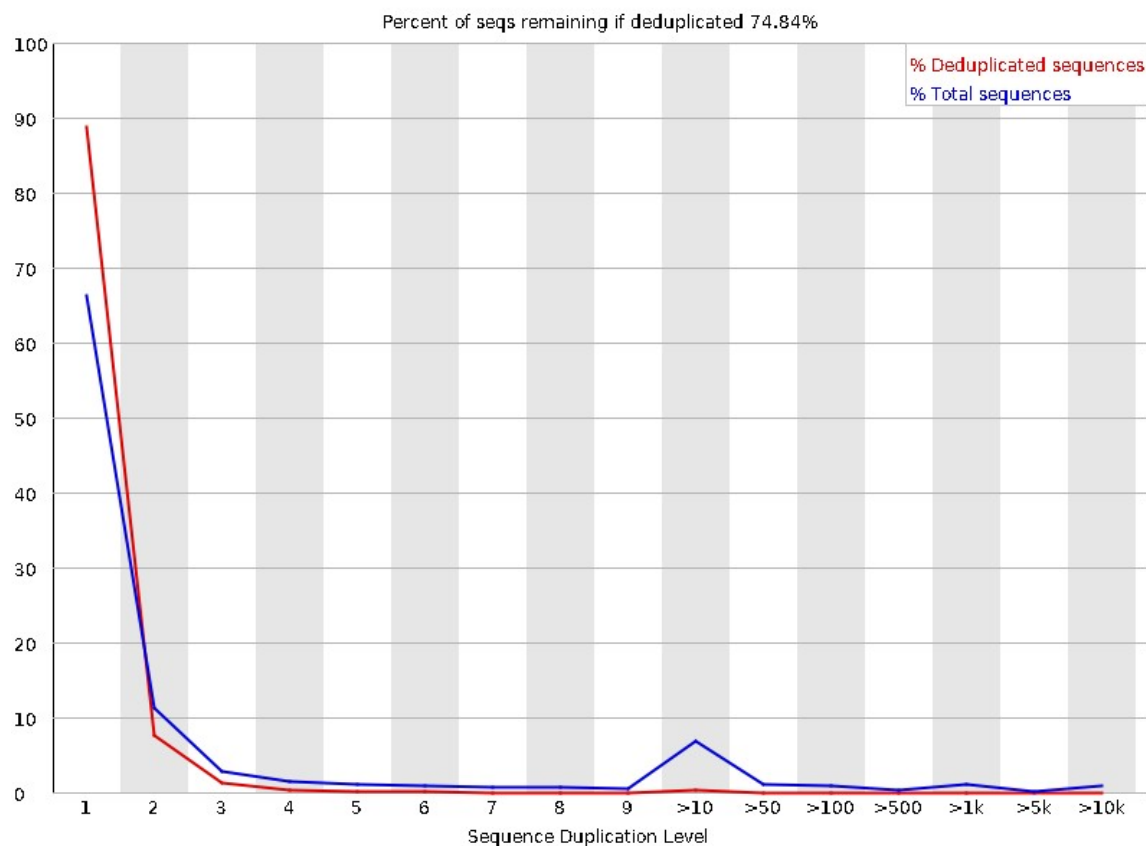
## ✔ Per base N content



## ✔ Sequence Length Distribution



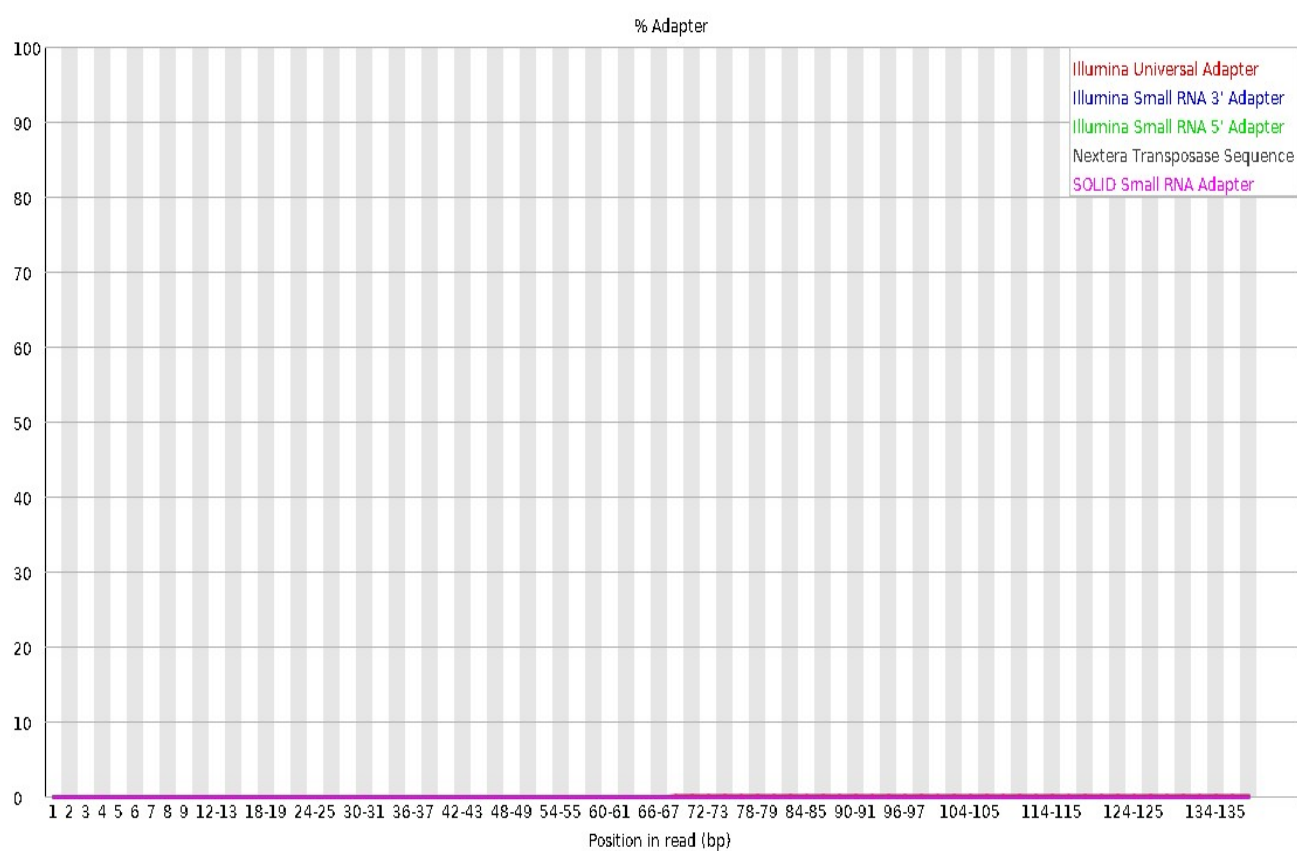
## Sequence Duplication Levels



## ✖ Overrepresented sequences

| Sequence                                           | Count  | Percentage         | Possible Source                                                    |
|----------------------------------------------------|--------|--------------------|--------------------------------------------------------------------|
| ATCGGAAGAGCGTCGTGTAGGGAAAGAGTGTAAAGATTAGTGTAGATCTC | 999769 | 1.0635216794521583 | Illumina<br>Single<br>End PCR<br>Primer 1<br>(96%<br>over<br>31bp) |

## ✔ Adapter Content



Produced by [FastQC](#) (version 0.11.7)