

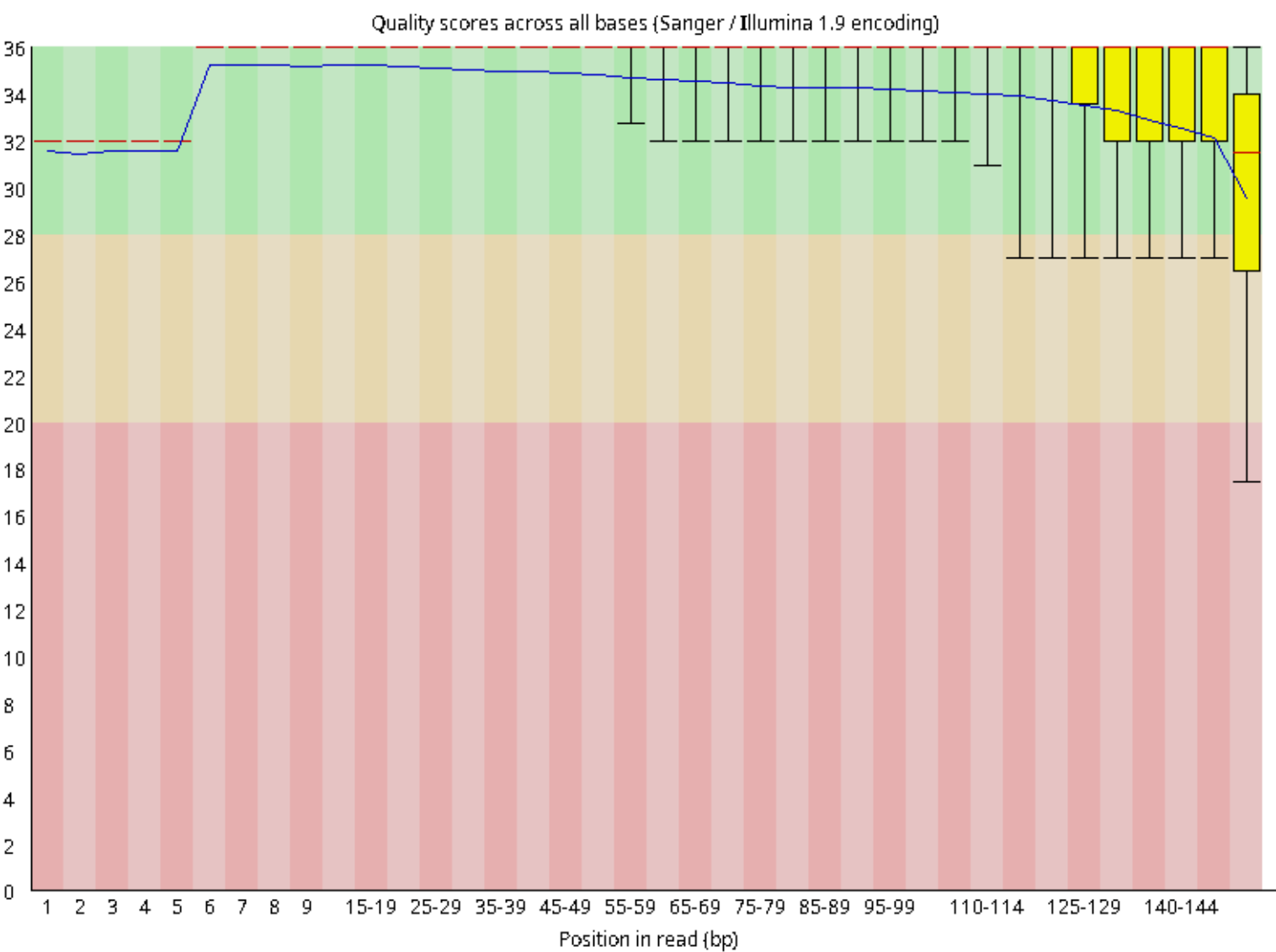
## Summary

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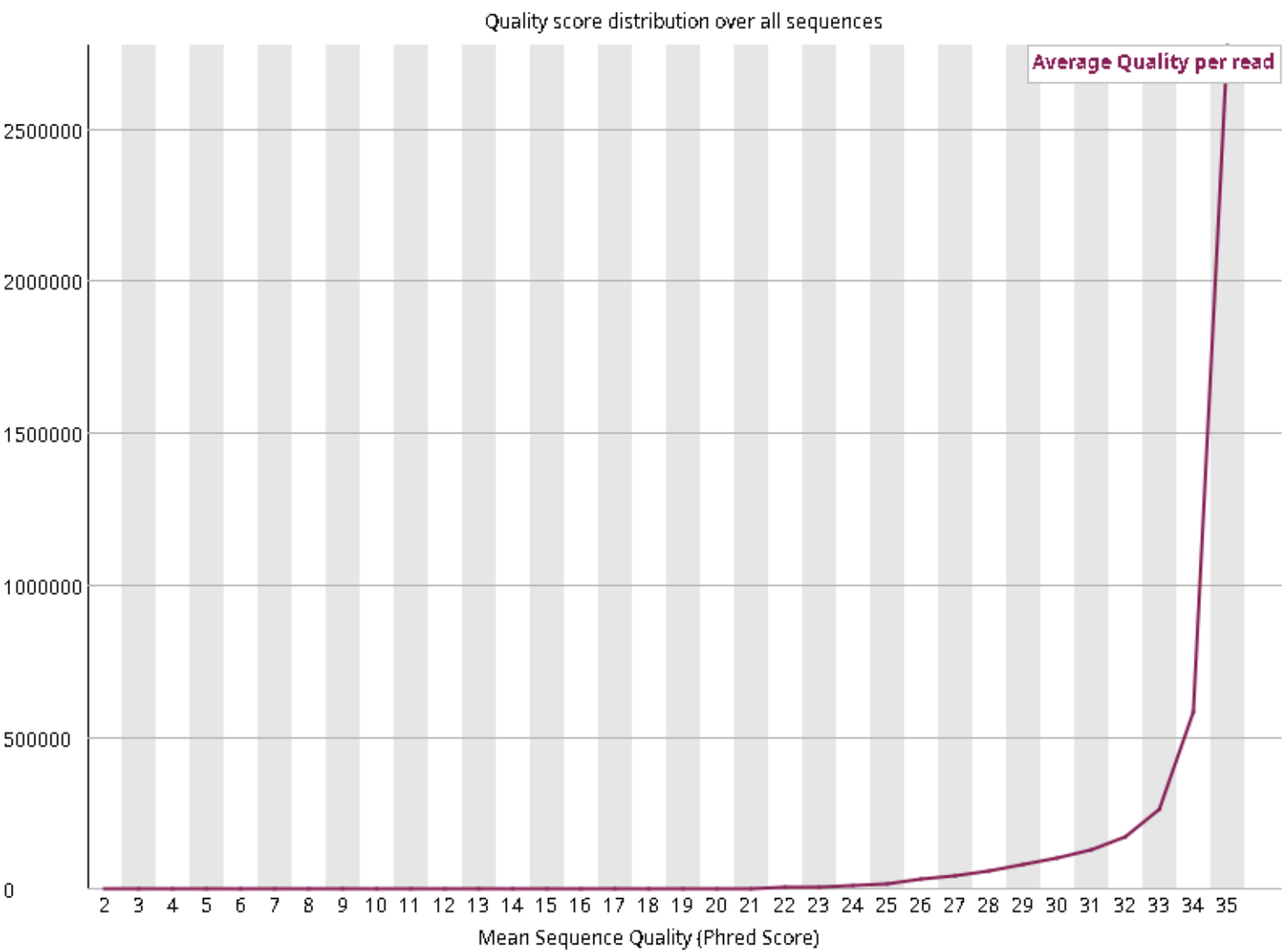
## ✓ Basic Statistics

| Measure                           | Value                     |
|-----------------------------------|---------------------------|
| Filename                          | SRR11412217_pass.fastq.gz |
| File type                         | Conventional base calls   |
| Encoding                          | Sanger / Illumina 1.9     |
| Total Sequences                   | 4322242                   |
| Total Bases                       | 566 Mbp                   |
| Sequences flagged as poor quality | 0                         |
| Sequence length                   | 35-151                    |
| %GC                               | 49                        |

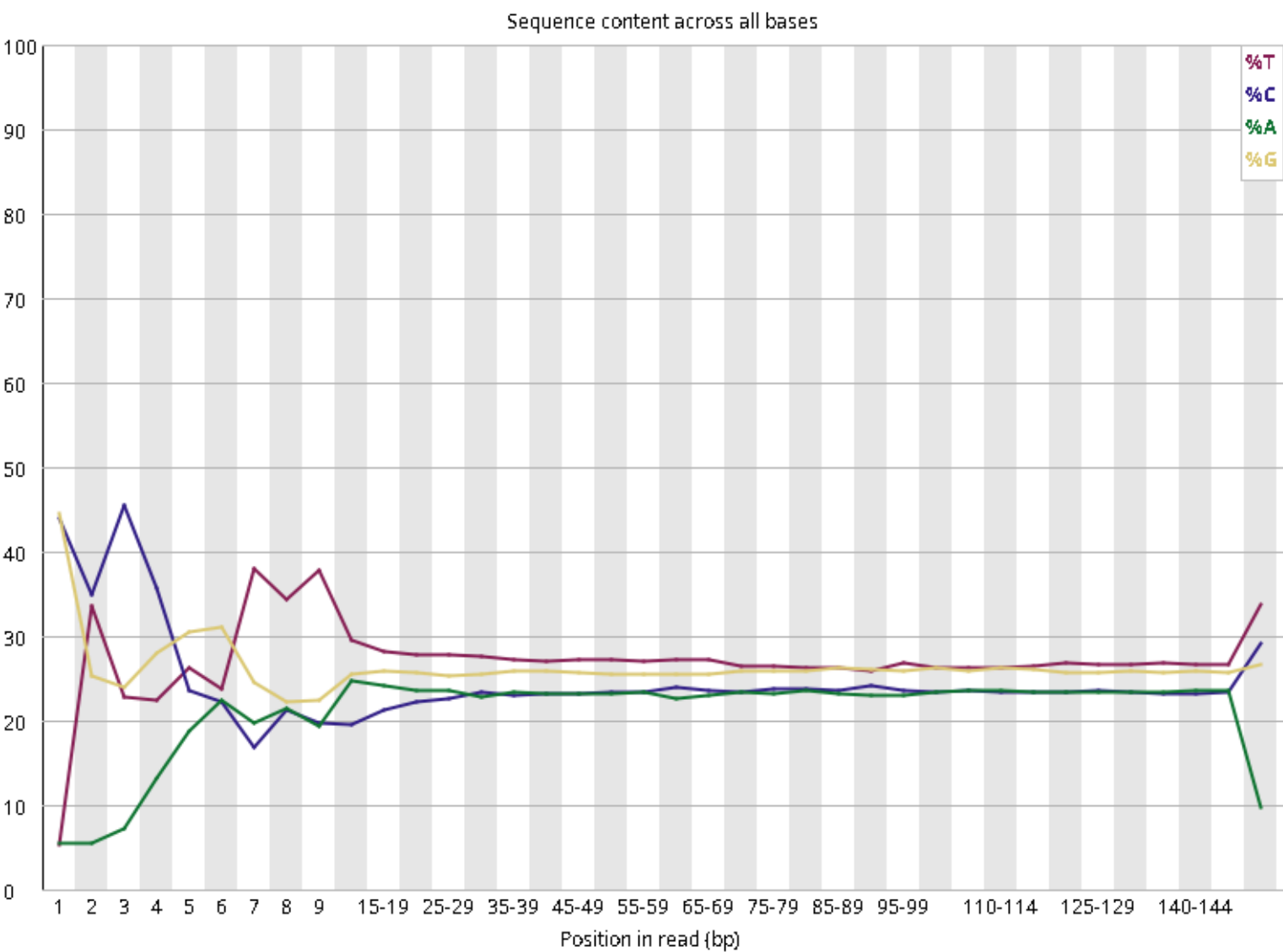
## ✔ Per base sequence quality



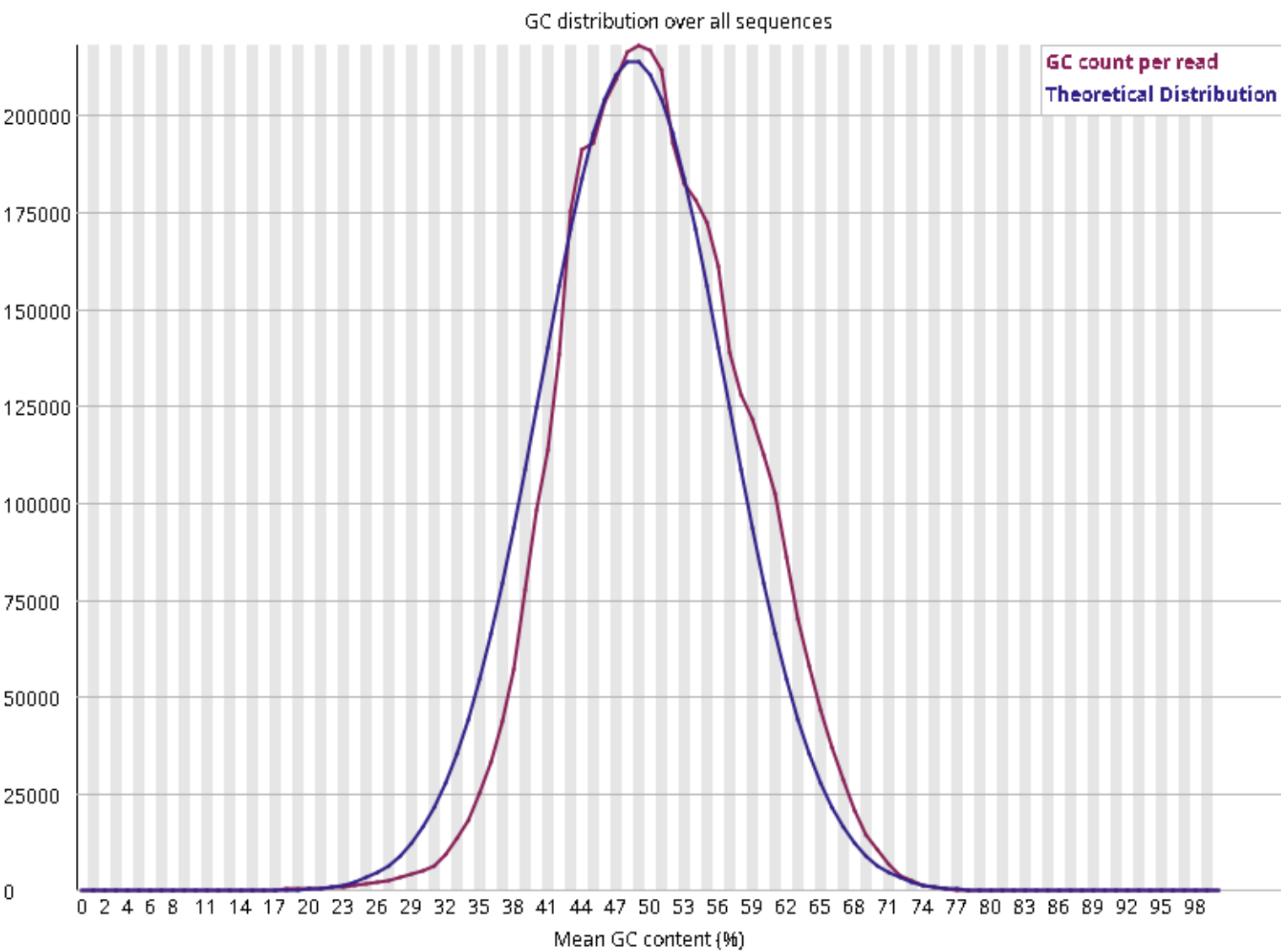
## ✔ Per sequence quality scores



## ❌ Per base sequence content

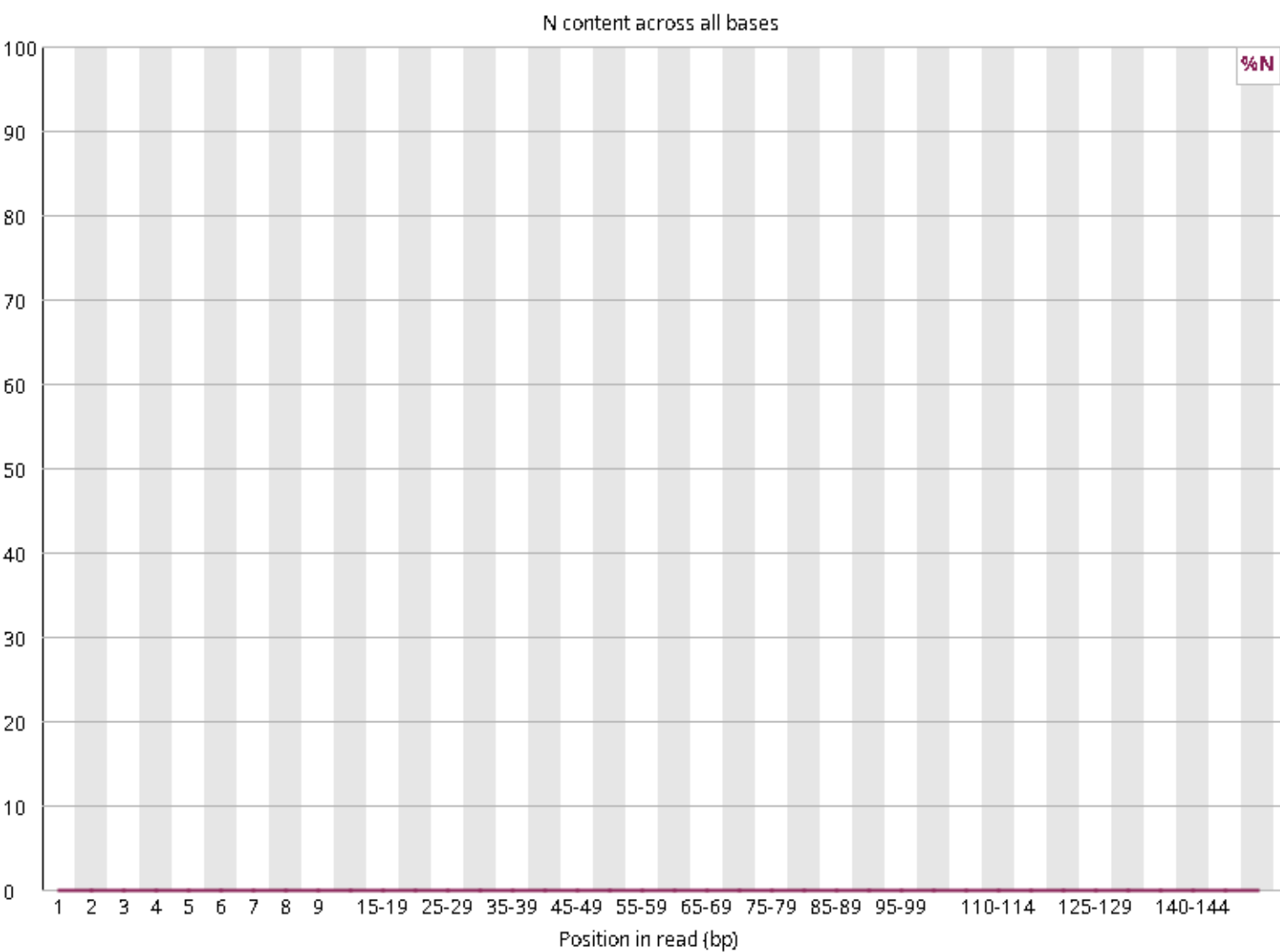


## ! Per sequence GC content

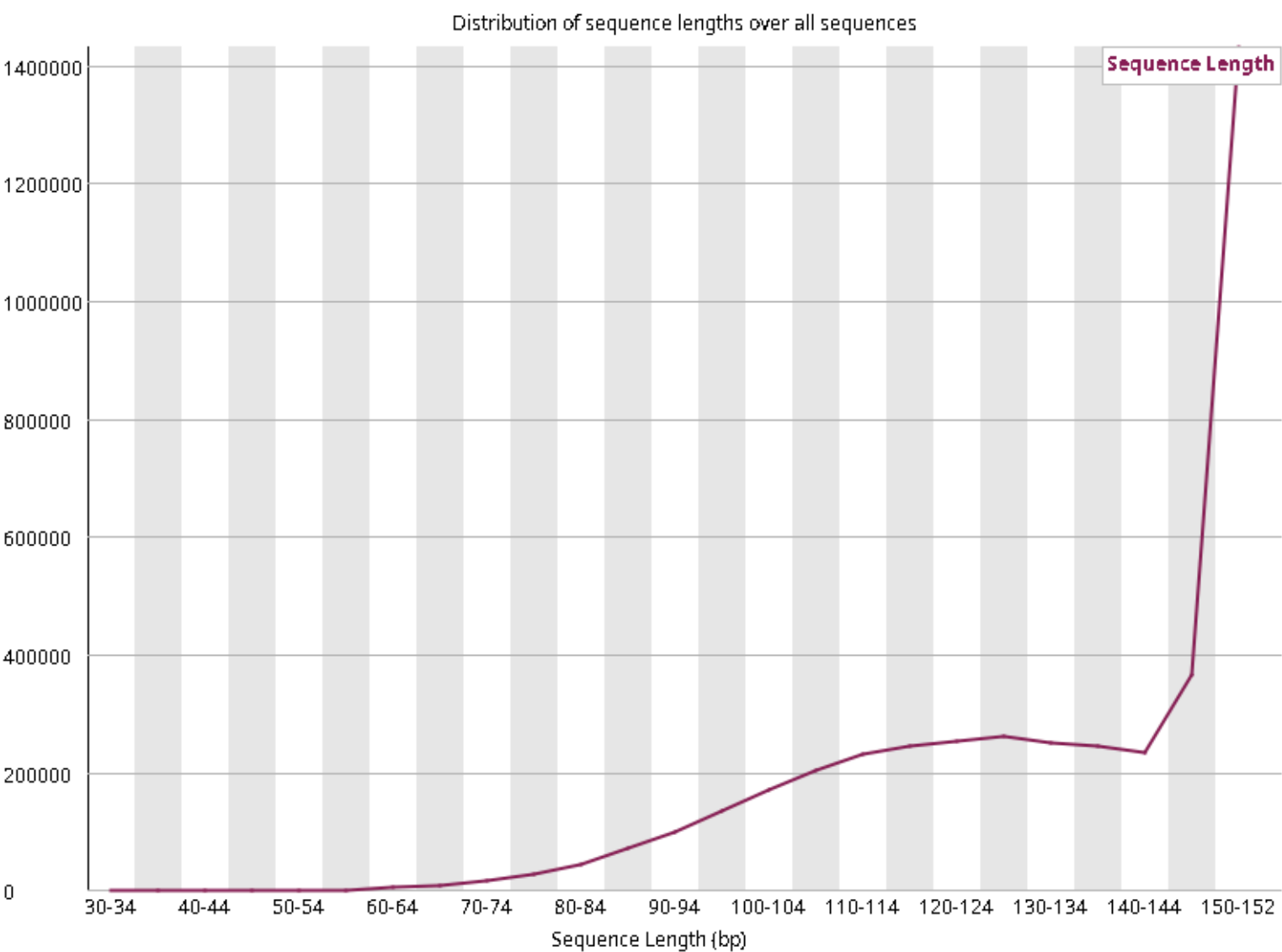




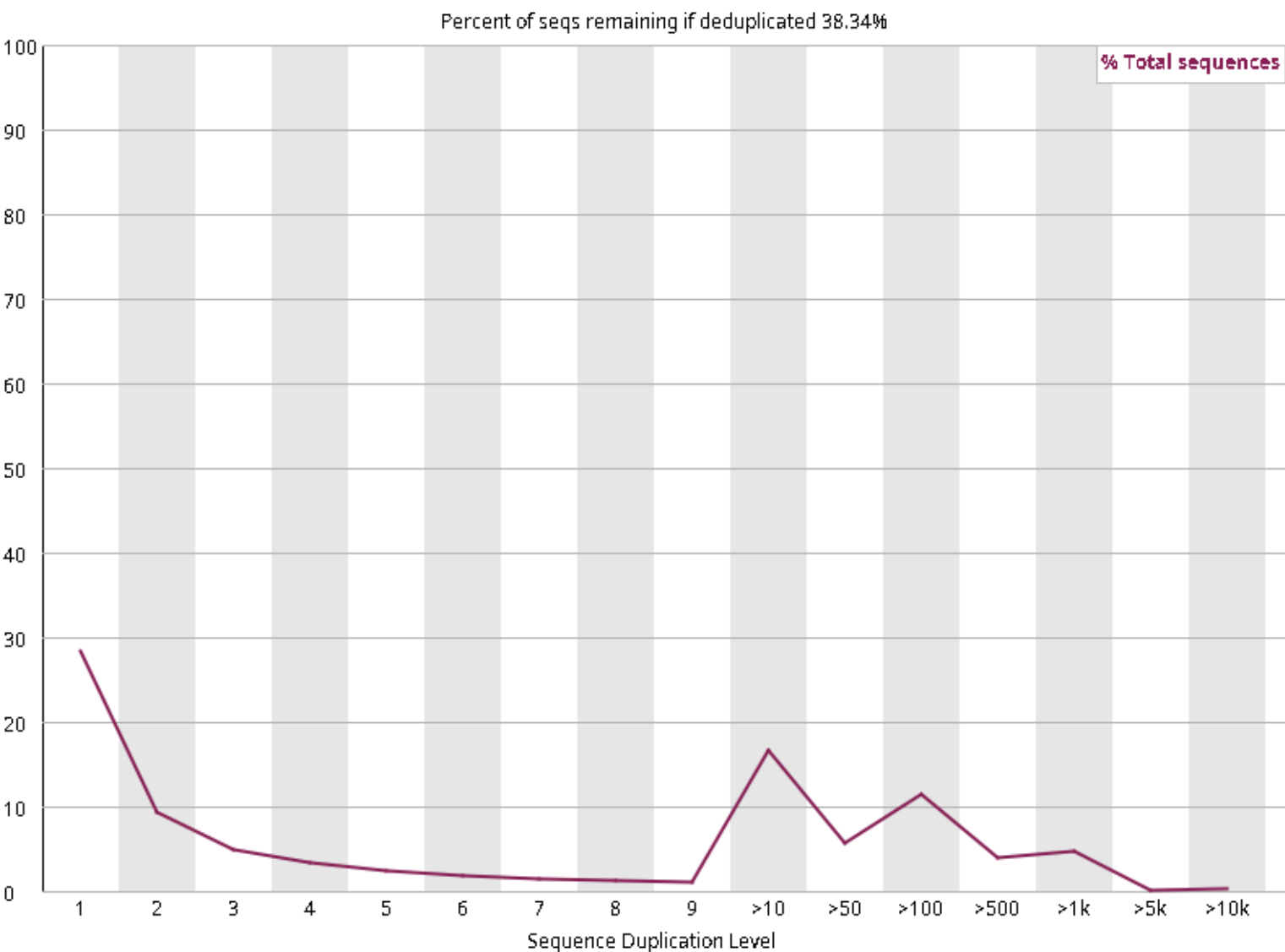
## Per base N content



# Sequence Length Distribution



## Sequence Duplication Levels



## Overrepresented sequences

| Sequence  | Count | Percentage          | Possible Source |
|---|-------|---------------------|-----------------|
| GGGCAGGATAGTTCAGACGGTTTCTATTTCTGAGCGTCTGAGATGTTAG   | 13286 | 0.30738676825591904 | No Hit          |
| GTCTGTTAGTAGTATAGTGATGCCAGCAGCTAGGACTGGGAGAGATAGGA  | 10727 | 0.248181383643026   | No Hit          |
| CCCCTTACTCAGCTTGAACCTGTGCGCCCTCTTGGCAGGAGTACTTGTGGA | 5354  | 0.12387089848277814 | No Hit          |
| CCCGTATCGAAGGCCTTTTTGGACAGGTGGTGTGTGGTGGCCTTGGTATG  | 5317  | 0.1230148612687582  | No Hit          |
| GGGAGGGCGATGAGGACTAGGATGATGGCGGGCAGGATAGTTCAGACGGT  | 5046  | 0.11674496707958508 | No Hit          |
| GTGGTGATTAGTCGTTTGTGATGAGATATTTGGAGGTGGGGATCAATAG   | 5000  | 0.11568070459729002 | No Hit          |
| GGGGCAATGAATGAAGCGAACAGATTTTCGTTTCATTTGGTTCTCAGGGT  | 4815  | 0.11140051852719028 | No Hit          |
| GCCTGGTTCTAGGAATAATGGGGGAAGTATGTAGGAGTTGAAGATTAGTC  | 4773  | 0.11042880060857306 | No Hit          |
| CCCCCTTACTCAGCTTGAACCTGTGCGCCCTCTTGGCAGGAGTACTTGTGG | 4528  | 0.10476044608330586 | No Hit          |



| Sequence   | Count | Percentage          | Possible Source |
|--|-------|---------------------|-----------------|
| CCCTTACTCAGCTTGAACCTGTCGCCCTCTTGGCAGGAGTACTTGTGGAA | 4371  | 0.10112807195895093 | No Hit          |



## Adapter Content

