

# FastQC Report

Wed 28 Sep 2016

M\_16\_F0932\_0\_B\_MSS1\_cDNA\_pool\_BacteriaEnterobacter\_ATCACG\_L003\_R2\_001.fastq.gz

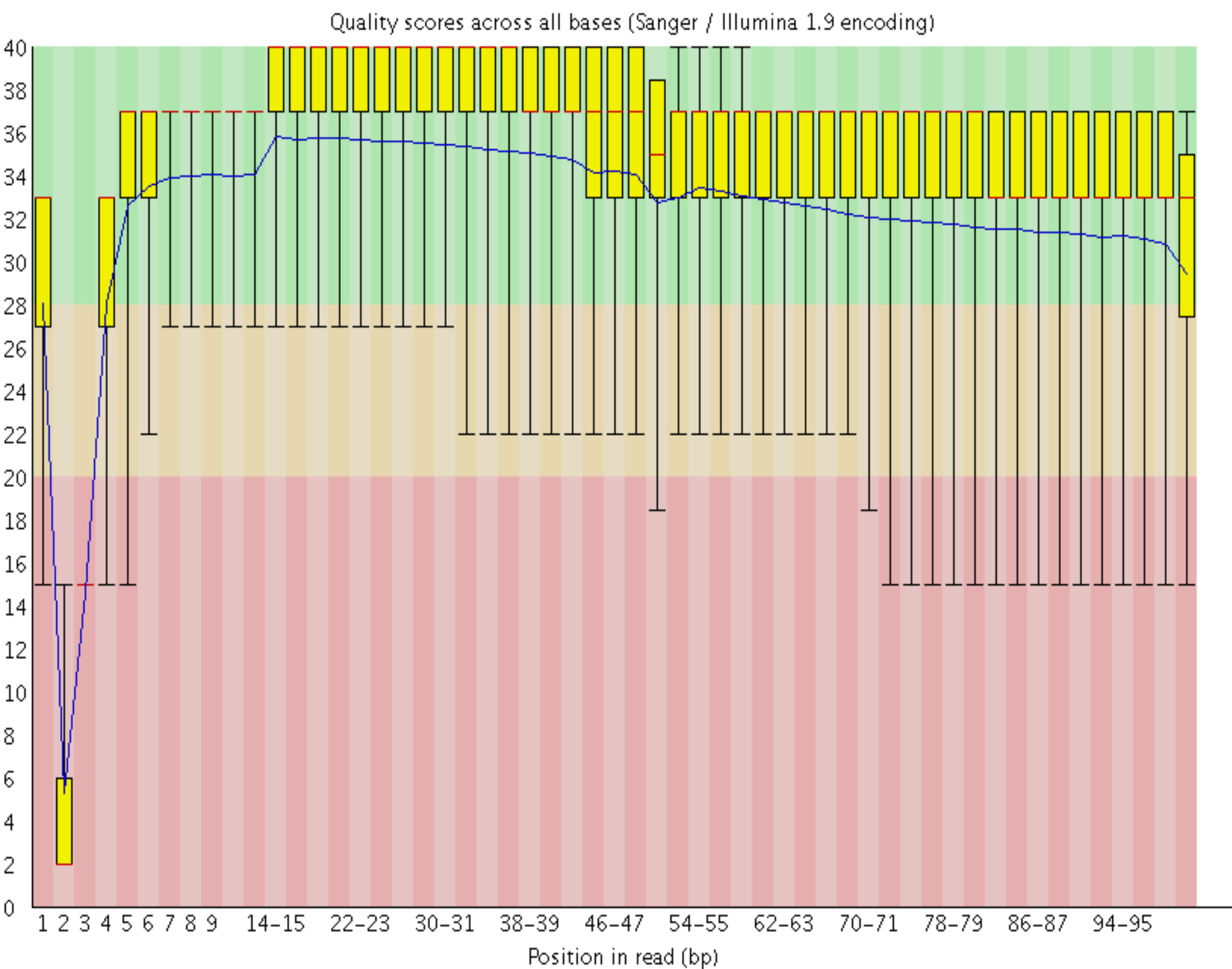
## Summary

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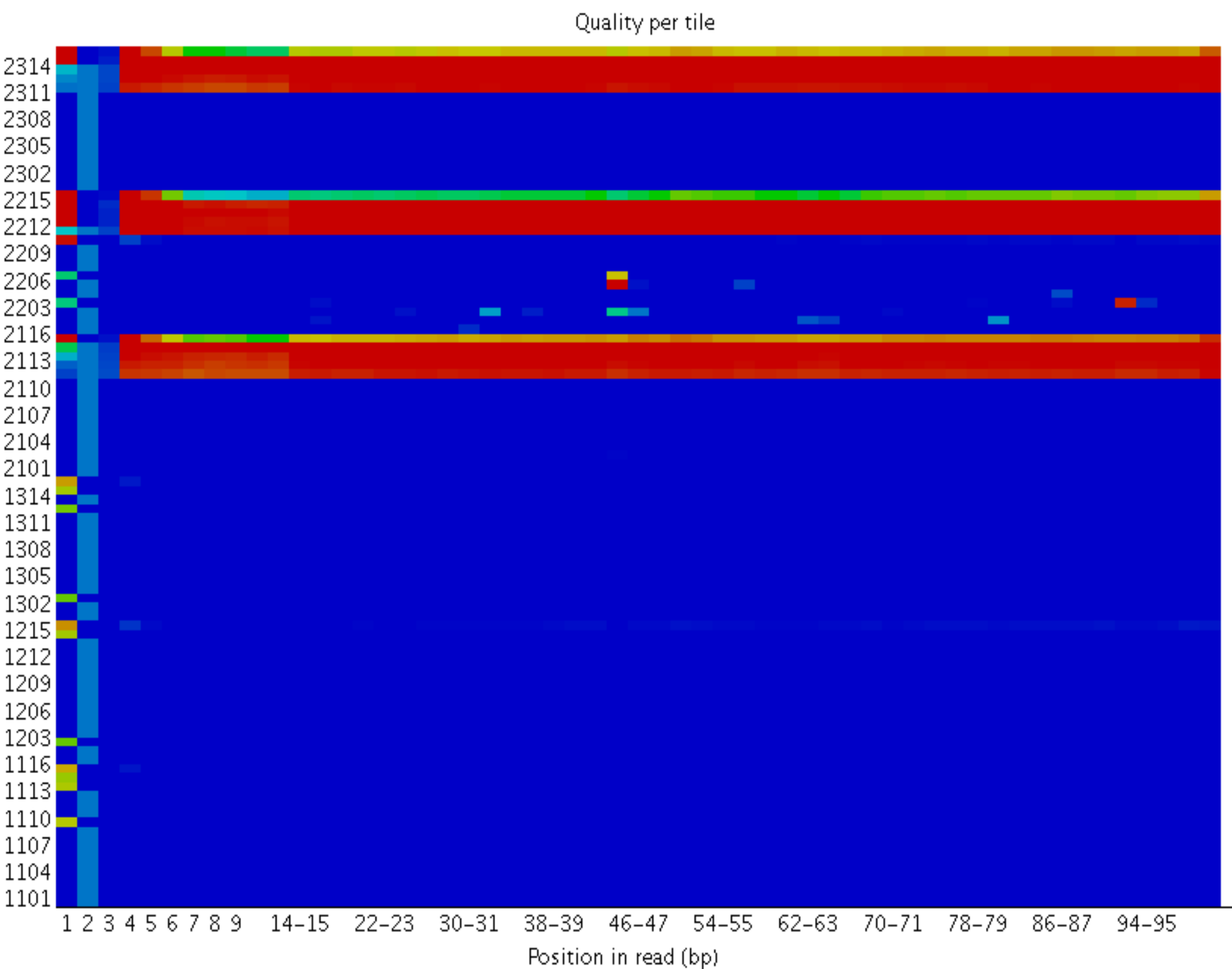
## Basic Statistics

| Measure                           | Value                                                                          |
|-----------------------------------|--------------------------------------------------------------------------------|
| Filename                          | M_16_F0932_0_B_MSS1_cDNA_pool_BacteriaEnterobacter_ATCACG_L003_R2_001.fastq.gz |
| File type                         | Conventional base calls                                                        |
| Encoding                          | Sanger / Illumina 1.9                                                          |
| Total Sequences                   | 7023308                                                                        |
| Sequences flagged as poor quality | 0                                                                              |
| Sequence length                   | 101                                                                            |
| %GC                               | 53                                                                             |

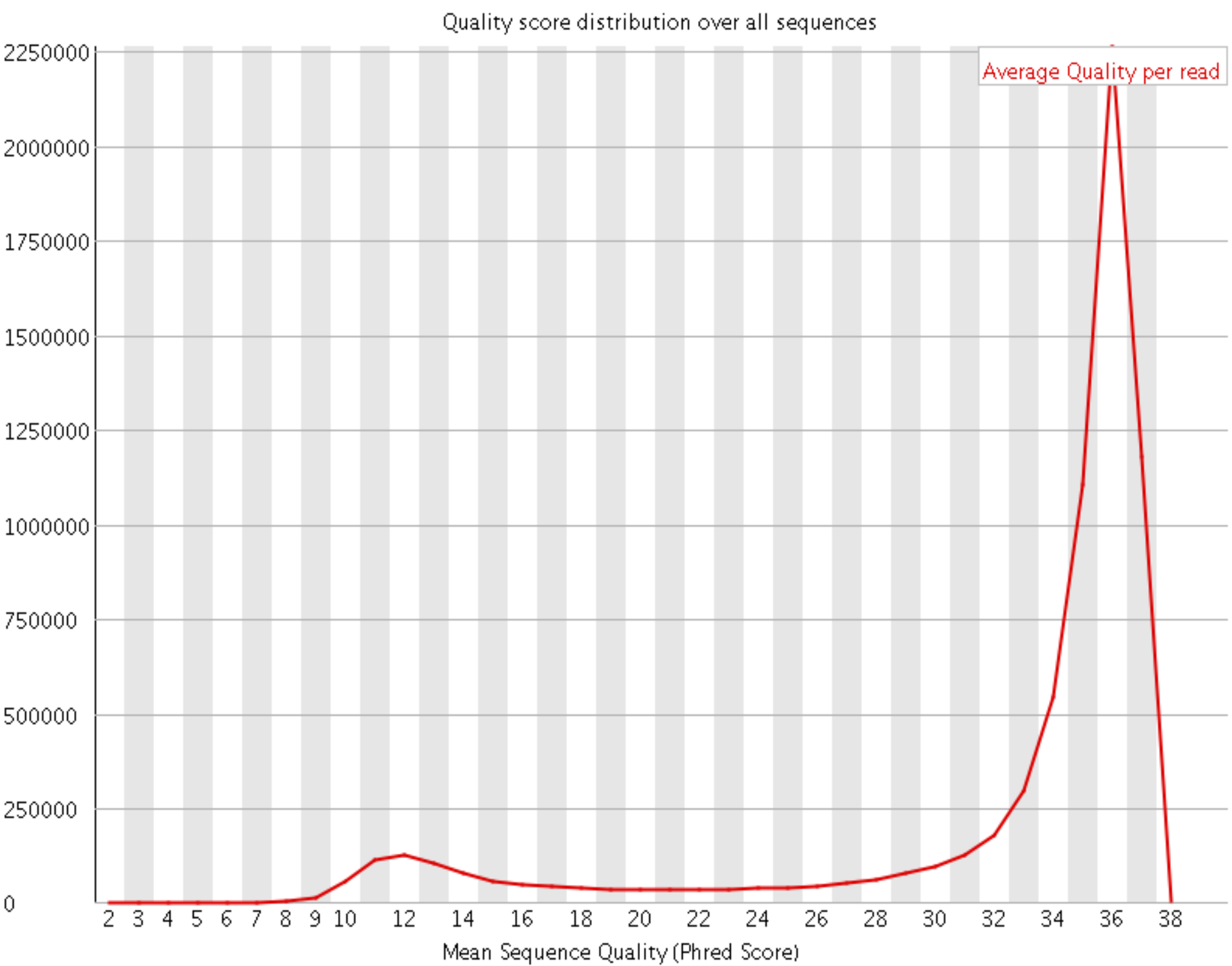
## ✖ Per base sequence quality



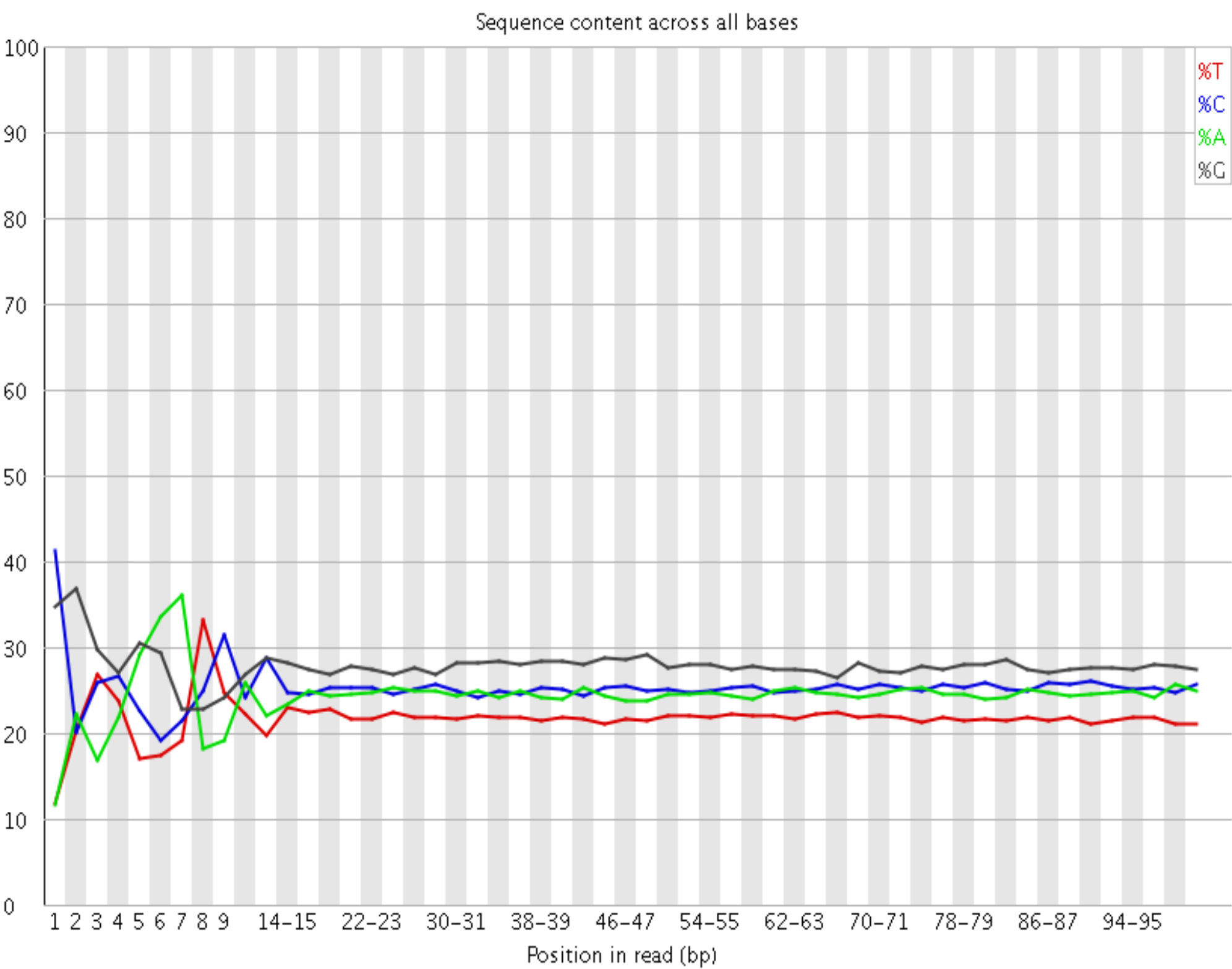
## ✖ Per tile sequence quality



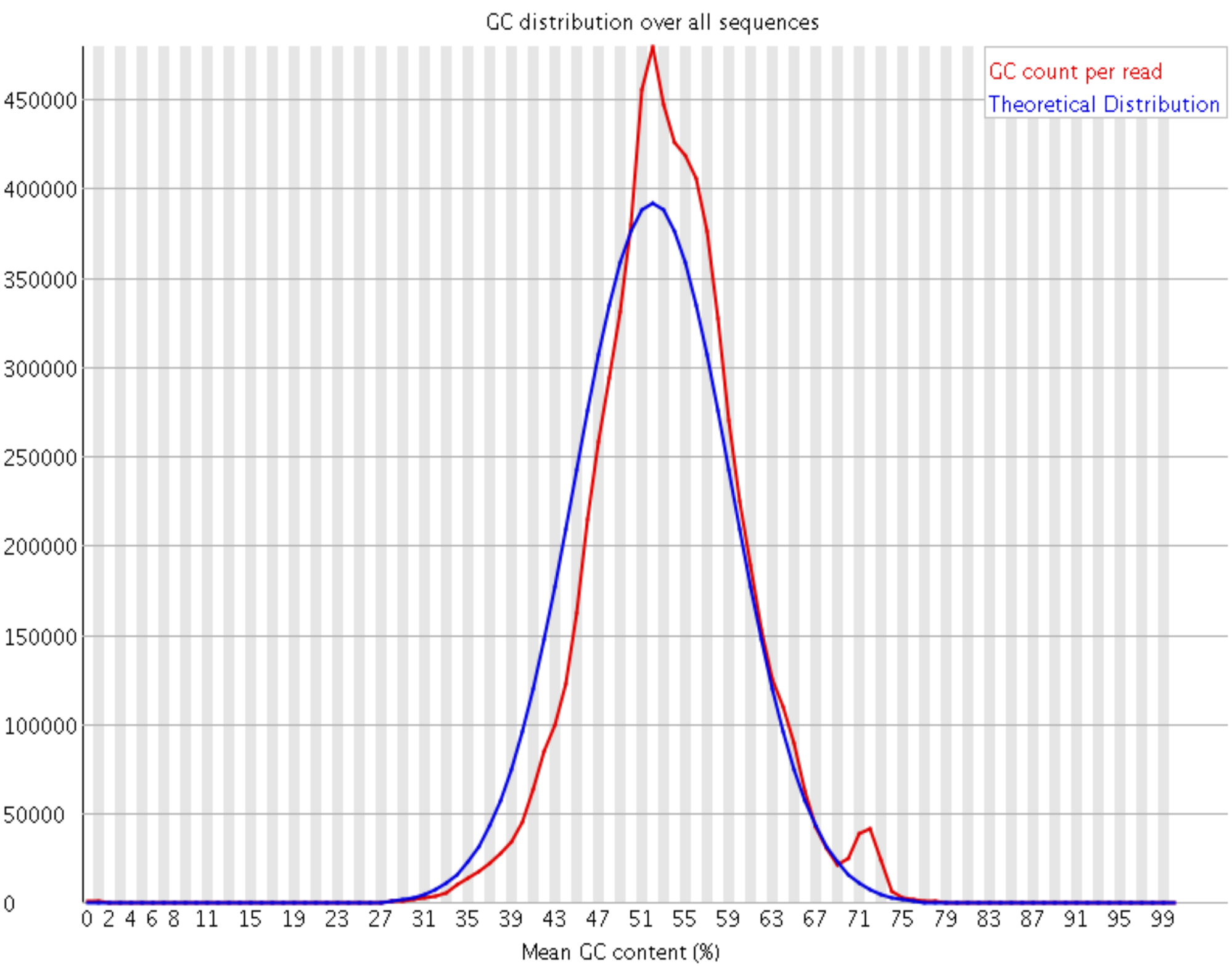
✔ Per sequence quality scores



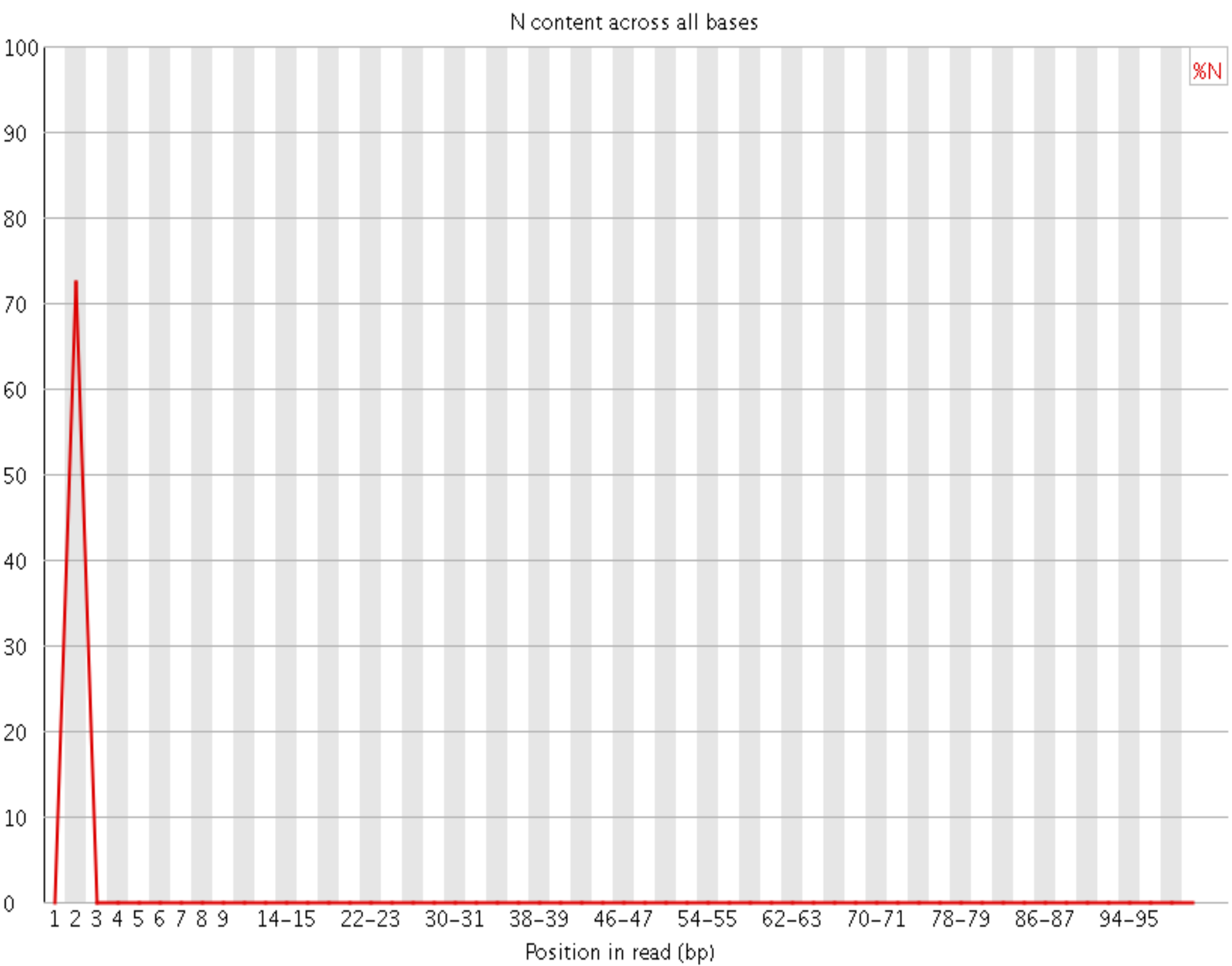
! Per base sequence content



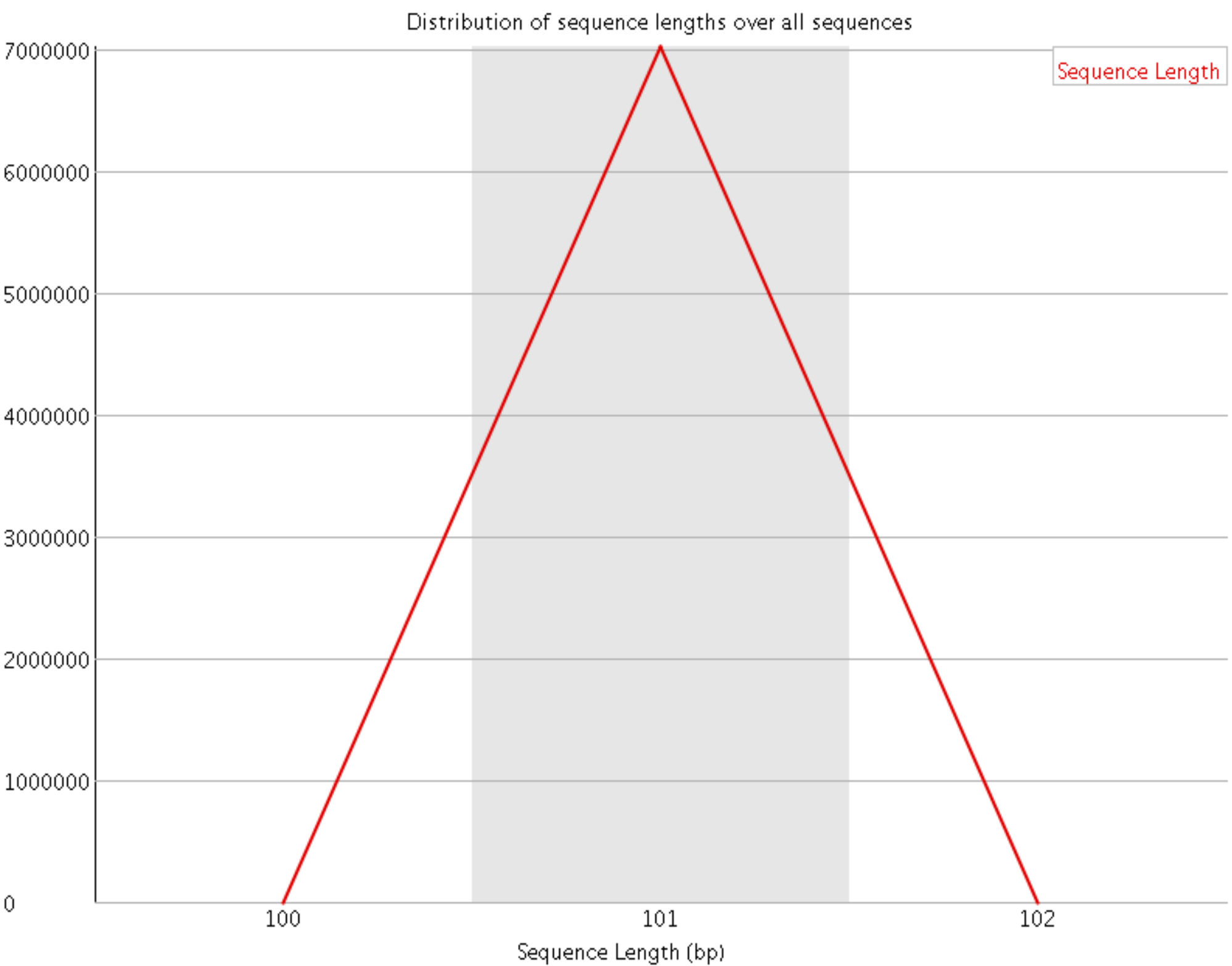
! Per sequence GC content



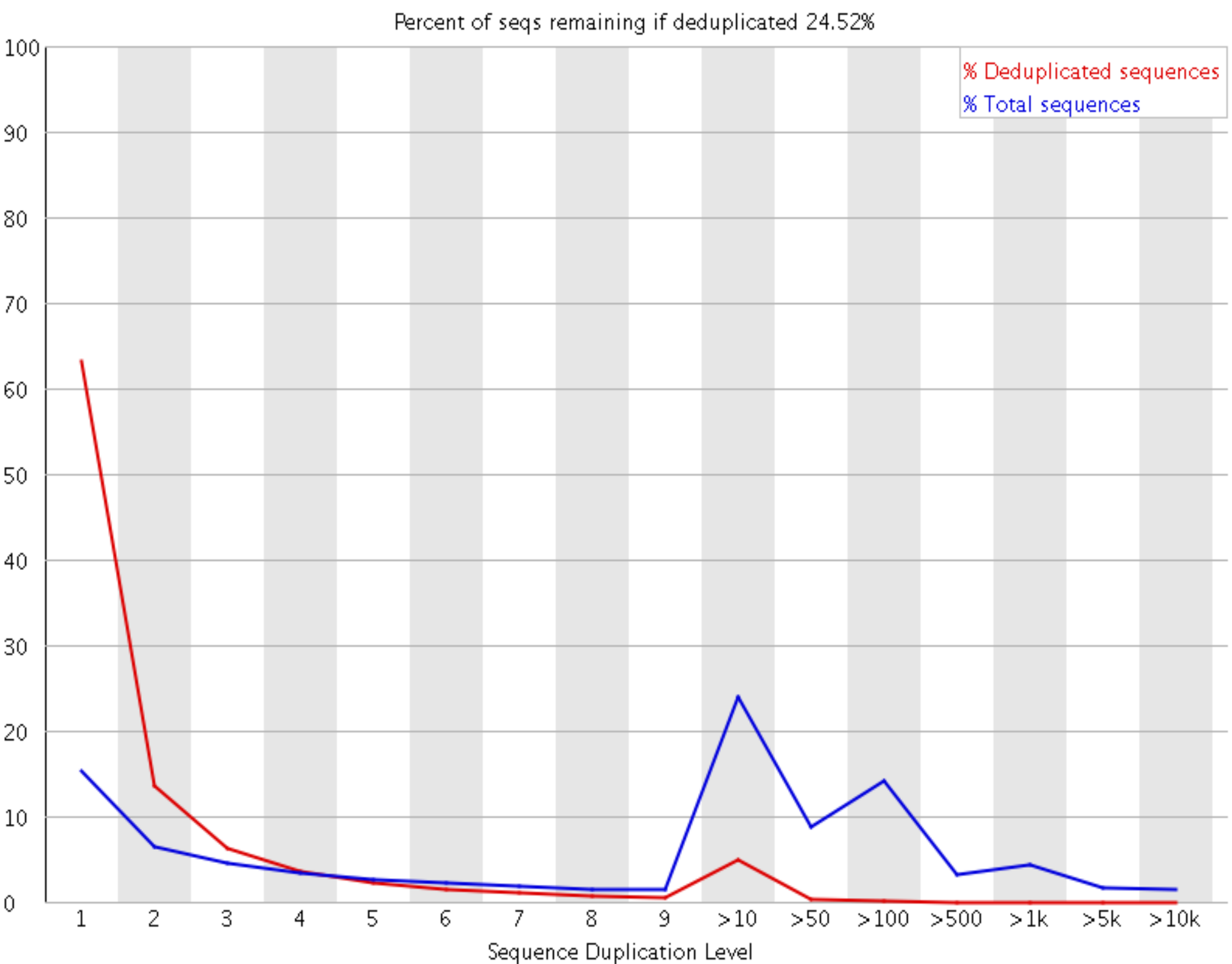
❌ Per base N content



## ✔ Sequence Length Distribution



❌ Sequence Duplication Levels



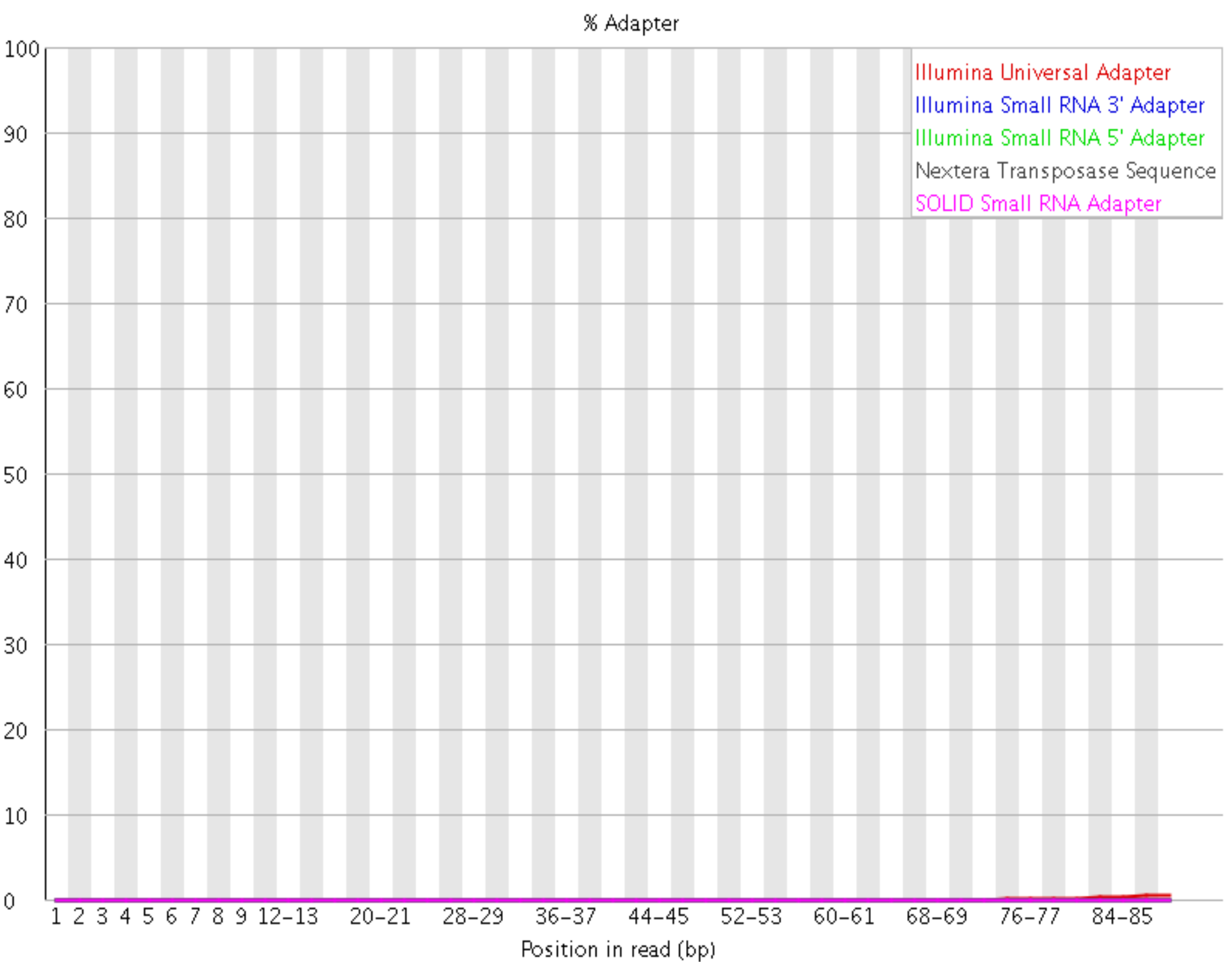
## ! Overrepresented sequences

| Sequence                                           | Count | Percentage          | Possible Source |
|----------------------------------------------------|-------|---------------------|-----------------|
| CNTGGATTTCGACGGGATTGCGAAACCCAAGGTGCATGCCGAGGGGCGGT | 34488 | 0.4910506559017489  | No Hit          |
| GNTCGCCGCTTCGTCGTCGTCCCCCTCGGGGGGAGACGGGCGGAGGGGA  | 21865 | 0.31132053442622765 | No Hit          |
| CNTCAATCTAGAGGGTATTAATAATGAATCGTACTAACTGGTACTGGGC  | 14445 | 0.2056723128189736  | No Hit          |
| CNGGGATTTGCGAAACCCAAGGTGCATGCCGAGGGGCGGTTTGCCTCGTA | 13267 | 0.18889958976596213 | No Hit          |
| ANCGGGATTTGCGAAACCCAAGGTGCATGCCGAGGGGCGGTTTGCCTCGT | 11508 | 0.16385441162483547 | No Hit          |
| CNGCCGCTTCGTCGTCGTCCCCCTCGGGGGGAGACGGGCGGAGGGGAGG  | 9732  | 0.13856718230212886 | No Hit          |
| GNAAAACCGTAGGCGGAAGCCTGAATCTGATAACTTTTTCAAAGGAATAC | 8654  | 0.1232182897289995  | No Hit          |
| GNATTA ACTCAATCTAGAGGGTATTAATAATGAATCGTACTAACTGGTA | 8298  | 0.11814945322061912 | No Hit          |
| CNGGGGATCAAGAGAGGTCAAACCCAAAAGAGATCGCGTGGATGCCCTGC | 7744  | 0.11026143236207211 | No Hit          |
| ANTTA ACTCAATCTAGAGGGTATTAATAATGAATCGTACTAACTGGTAC | 7557  | 0.10759886936469254 | No Hit          |
|                                                    |       |                     |                 |

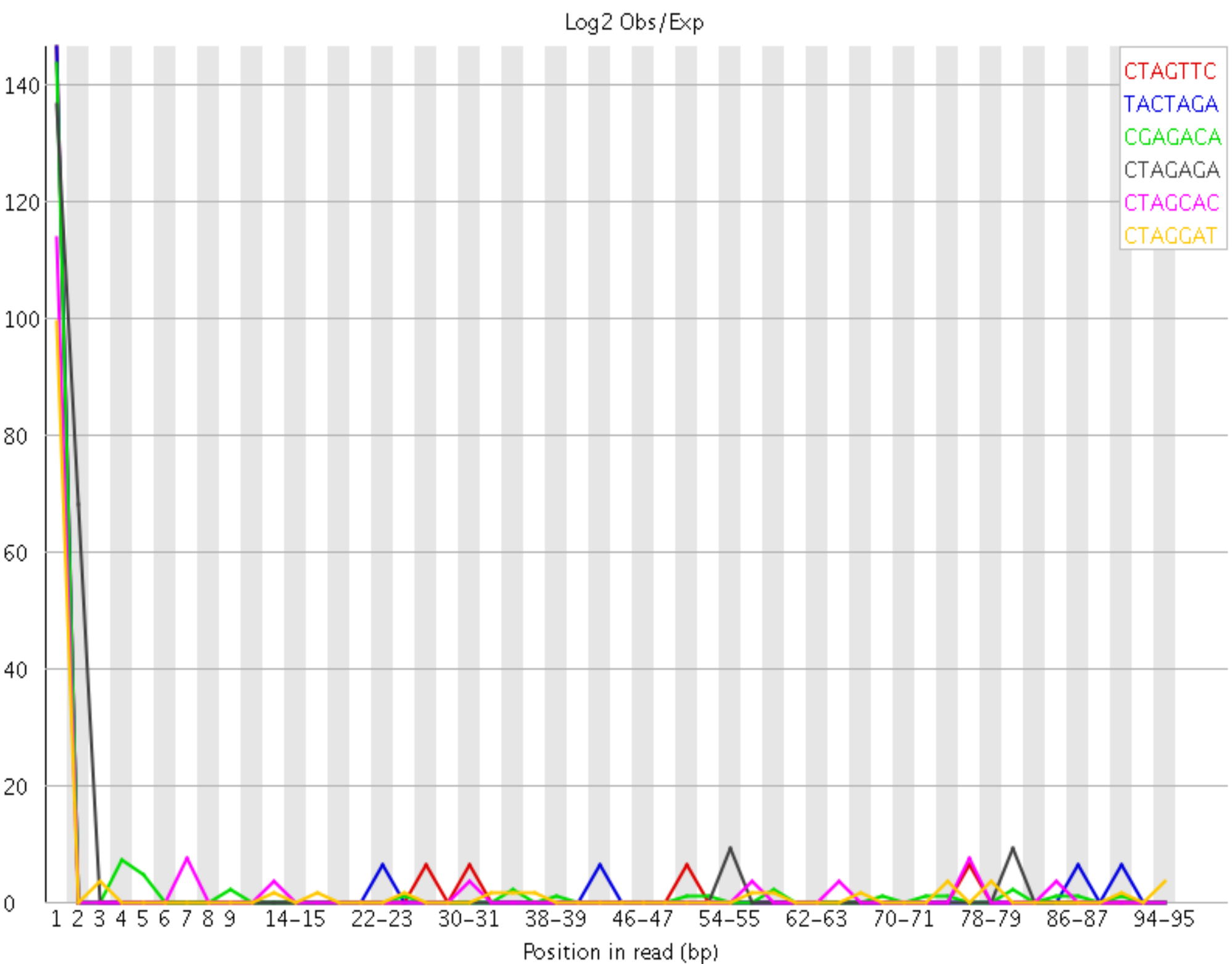
|                                                     |      |                     |        |
|-----------------------------------------------------|------|---------------------|--------|
| ANCTCAATCTAGAGGGTATTAATAATGAATCGTACTAAACTGGTACTGGG  | 7407 | 0.10546312364486934 | No Hit |
| CNGAAGAGTCTTTTTTTGGAATGCGTGTTCTGAAGGGCTTTTGGCTTGCGG | 7211 | 0.10267241590430037 | No Hit |
| GNCGAAACCCAAGGTGCATGCCGAGGGGCGGTTTGCCTCGTAAAAAGCCG  | 7098 | 0.10106348746203356 | No Hit |



## Adapter Content



## Kmer Content



| Sequence | Count | PValue        | Obs/Exp Max | Max Obs/Exp Position |
|----------|-------|---------------|-------------|----------------------|
| CTAGTTC  | 35    | 1.1896605E-4  | 146.22427   | 1                    |
| TACTAGA  | 35    | 1.1896605E-4  | 146.22427   | 1                    |
| CGAGACA  | 190   | 0.0           | 143.65894   | 1                    |
| CTAGAGA  | 25    | 0.008499334   | 136.47598   | 1                    |
| CTAGCAC  | 60    | 7.133929E-6   | 113.729996  | 1                    |
| CTAGGAT  | 120   | 2.2919266E-10 | 99.51375    | 1                    |
| ACTAGAG  | 70    | 1.5354082E-5  | 97.47018    | 2                    |
| CCTAGAG  | 95    | 6.467635E-7   | 89.786835   | 1                    |
| CTCGGGA  | 375   | 0.0           | 81.8856     | 1                    |
| CTAGAAA  | 190   | 1.8189894E-12 | 80.80815    | 1                    |
| CTAGCGA  | 115   | 2.0148036E-6  | 74.17173    | 1                    |
| CTTGGAT  | 820   | 0.0           | 70.734505   | 1                    |
| TTGGATT  | 825   | 0.0           | 68.229126   | 2                    |
| CACTAGC  | 105   | 1.1454728E-4  | 64.98856    | 1                    |
| GATTCGA  | 7095  | 0.0           | 57.525192   | 5                    |

|         |      |              |           |   |
|---------|------|--------------|-----------|---|
| CCCTCAA | 730  | 0.0          | 56.086025 | 1 |
| GTCAATC | 1135 | 0.0          | 55.605236 | 2 |
| CTAGAAG | 185  | 5.212187E-7  | 55.328106 | 1 |
| CTCGAGG | 285  | 6.548362E-11 | 53.8721   | 1 |
| CGACGGG | 8545 | 0.0          | 48.837387 | 9 |