













Sun 21 Sep 2014  
SRR1033799.fastq

# FastQC Report

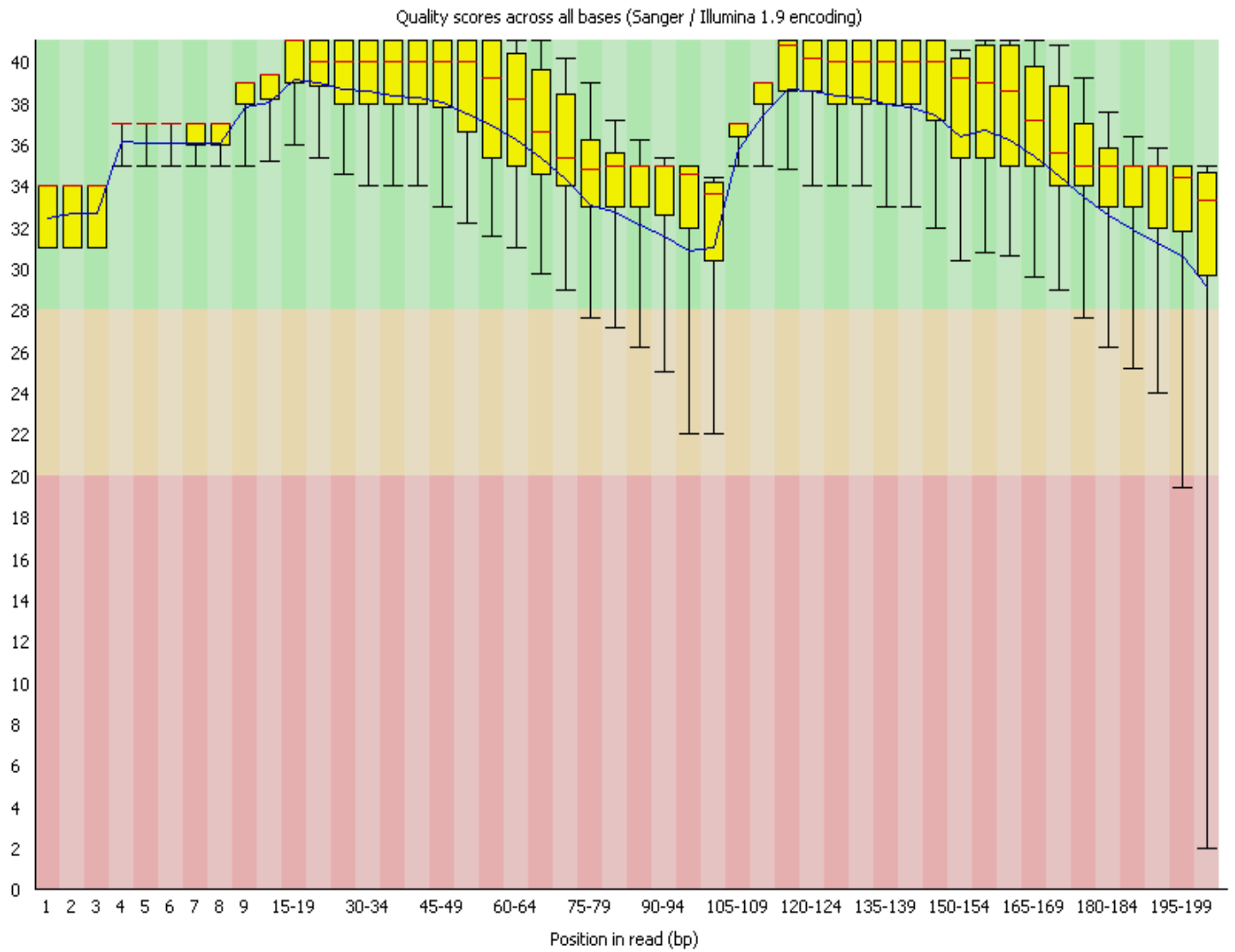
## Summary

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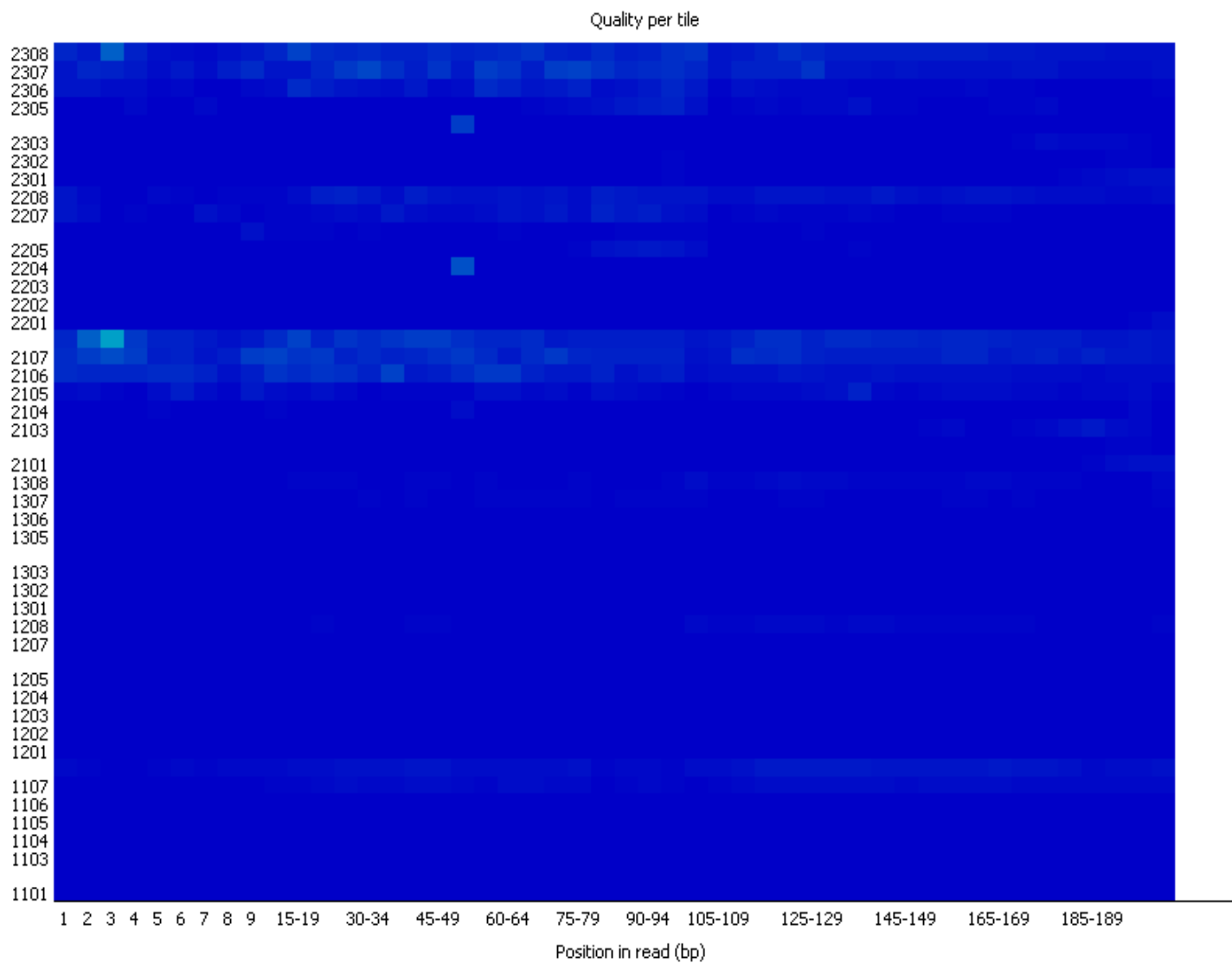
## Basic Statistics

| Measure                           | Value                   |
|-----------------------------------|-------------------------|
| Filename                          | SRR1033799.fastq        |
| File type                         | Conventional base calls |
| Encoding                          | Sanger / Illumina 1.9   |
| Total Sequences                   | 30172824                |
| Sequences flagged as poor quality | 0                       |
| Sequence length                   | 202                     |
| %GC                               | 48                      |

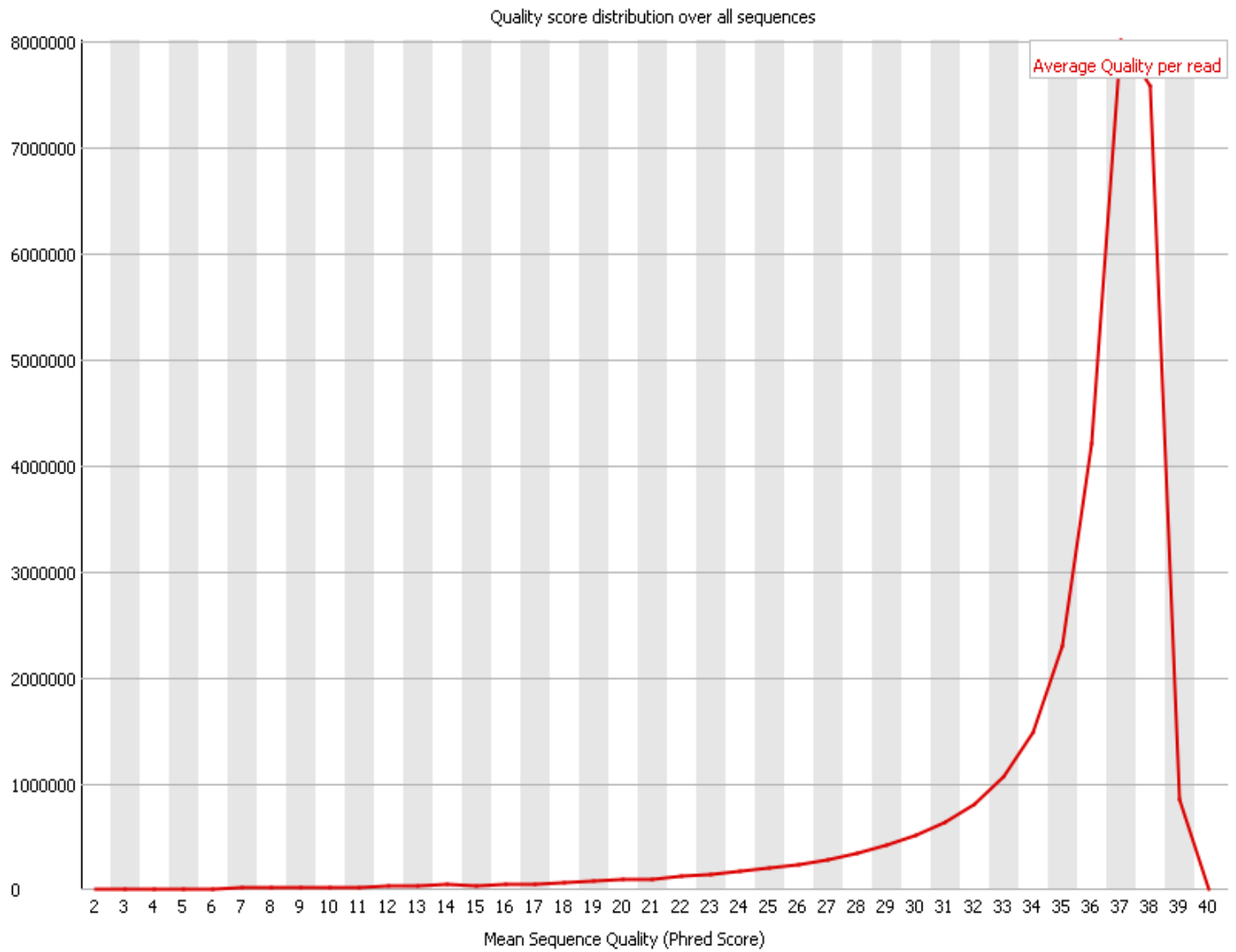
## Per base sequence quality



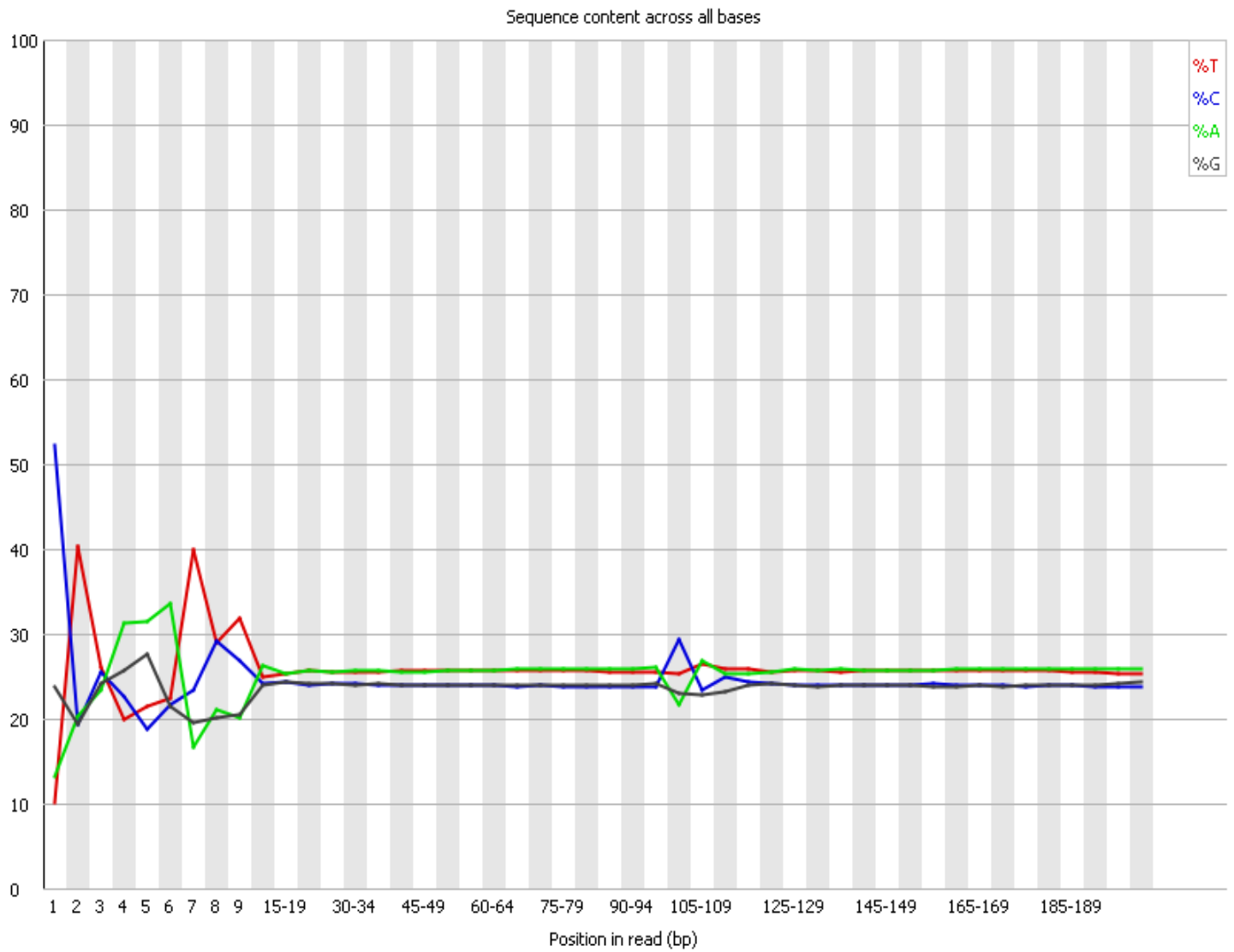
**Per tile sequence quality**



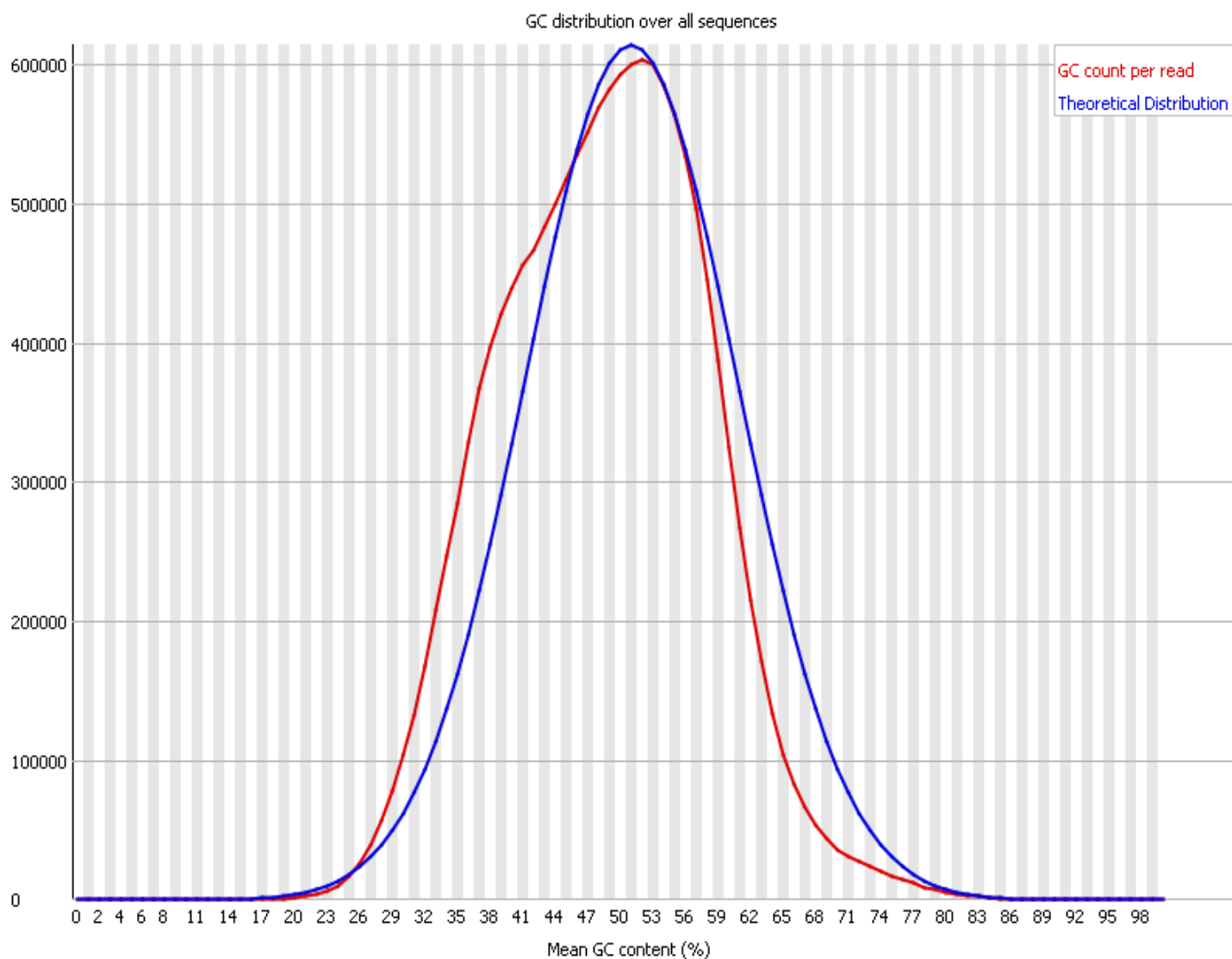
## Per sequence quality scores



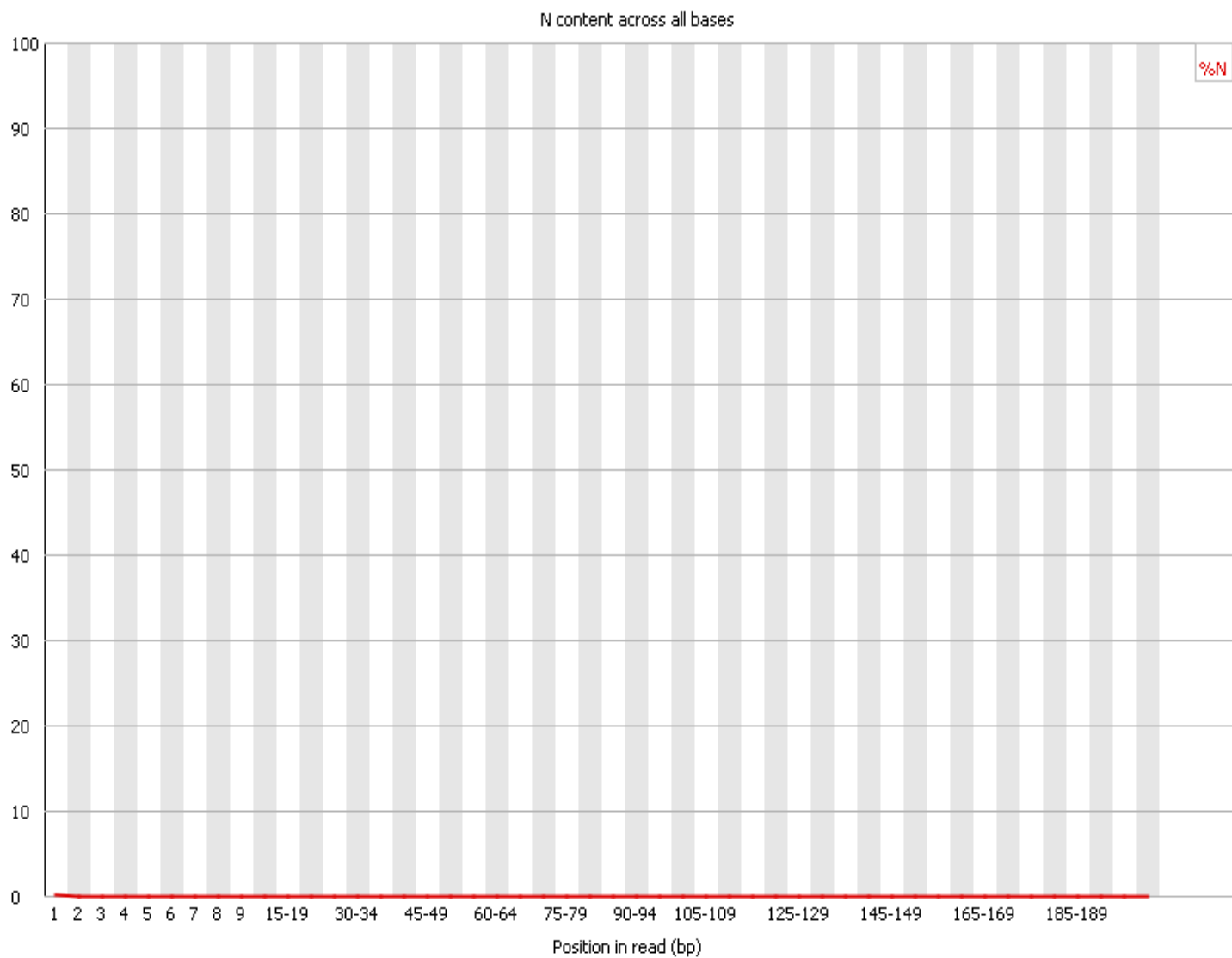
## ❌ Per base sequence content



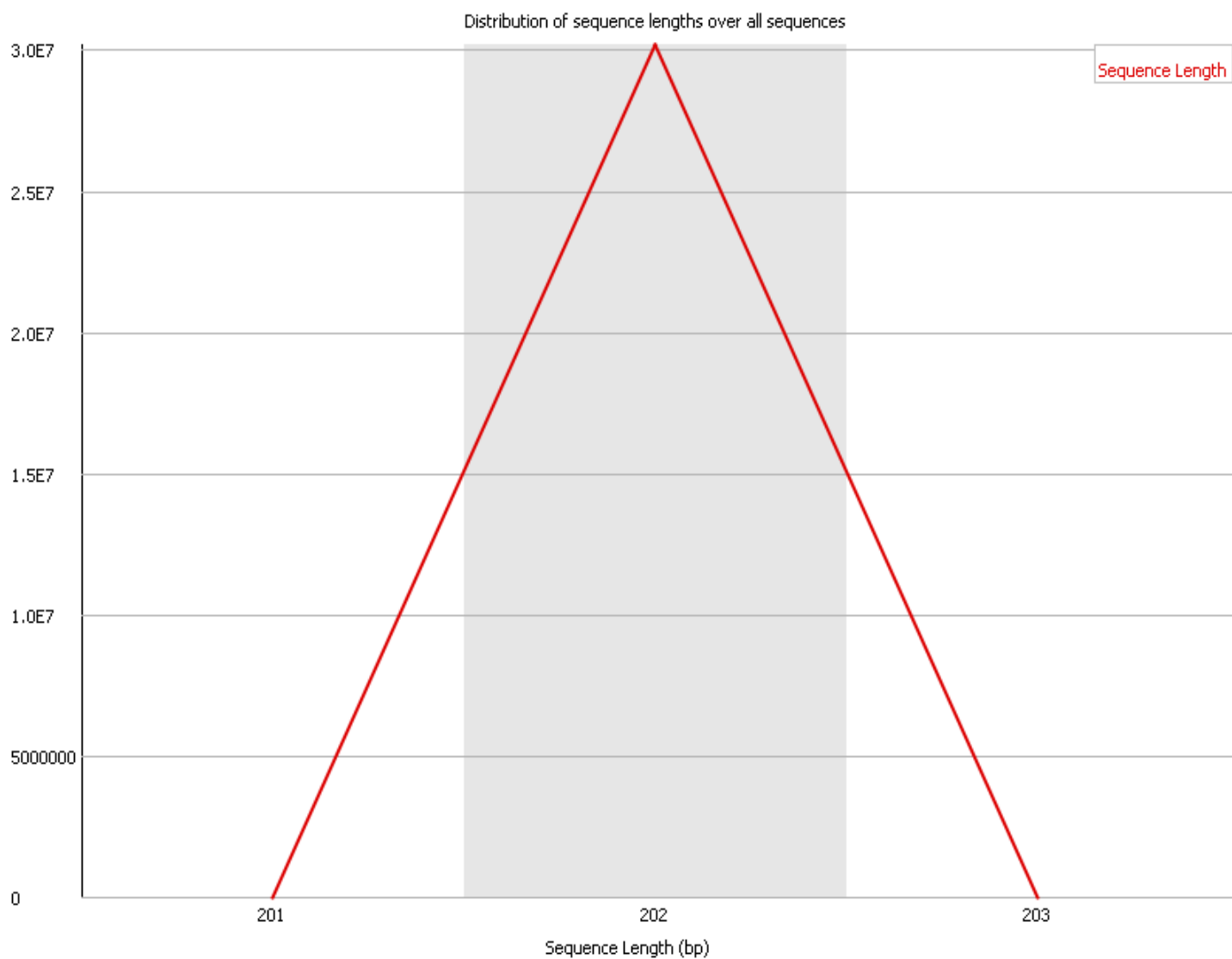
## ! Per sequence GC content



## Per base N content

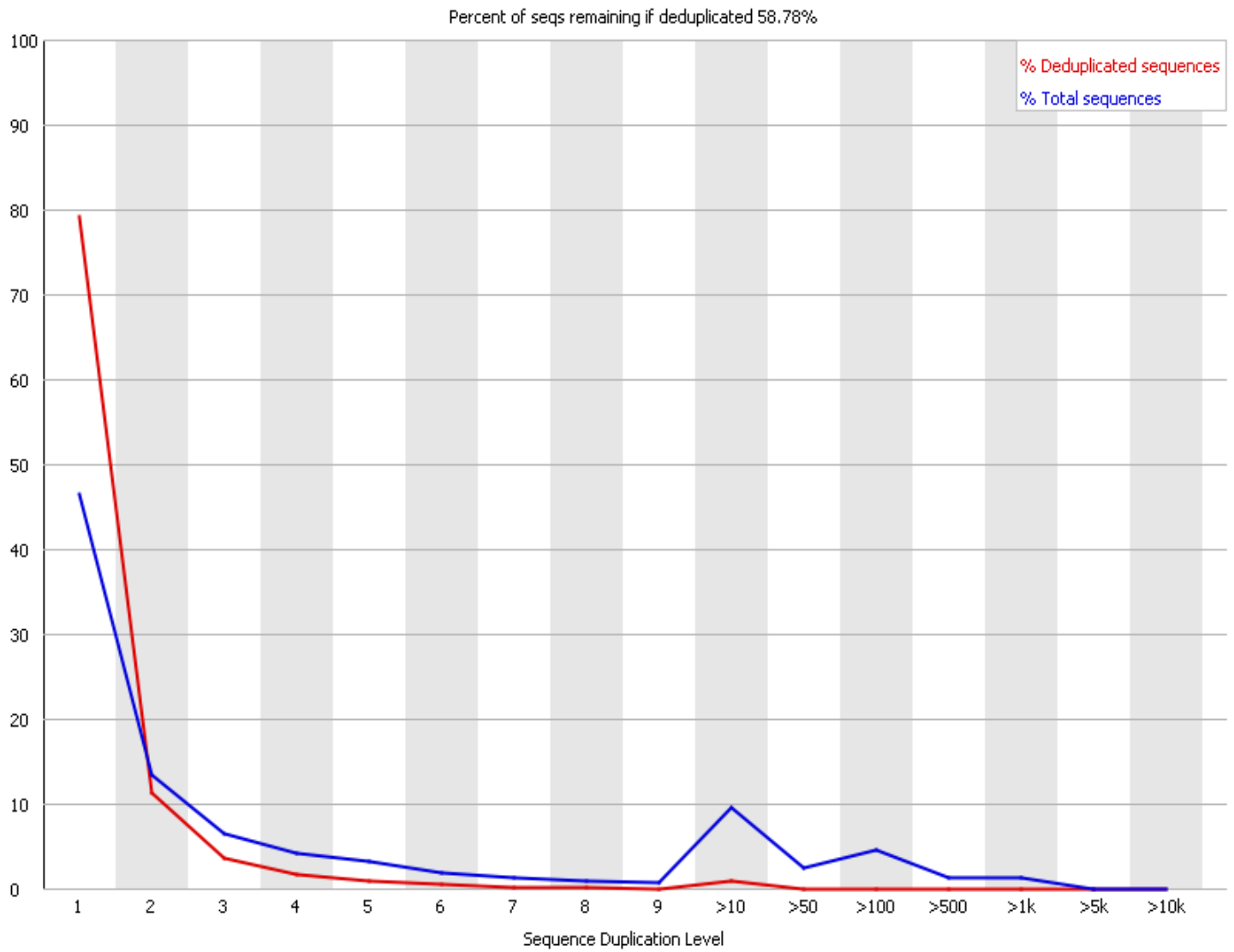


## Sequence Length Distribution



## ⚠ Sequence Duplication Levels



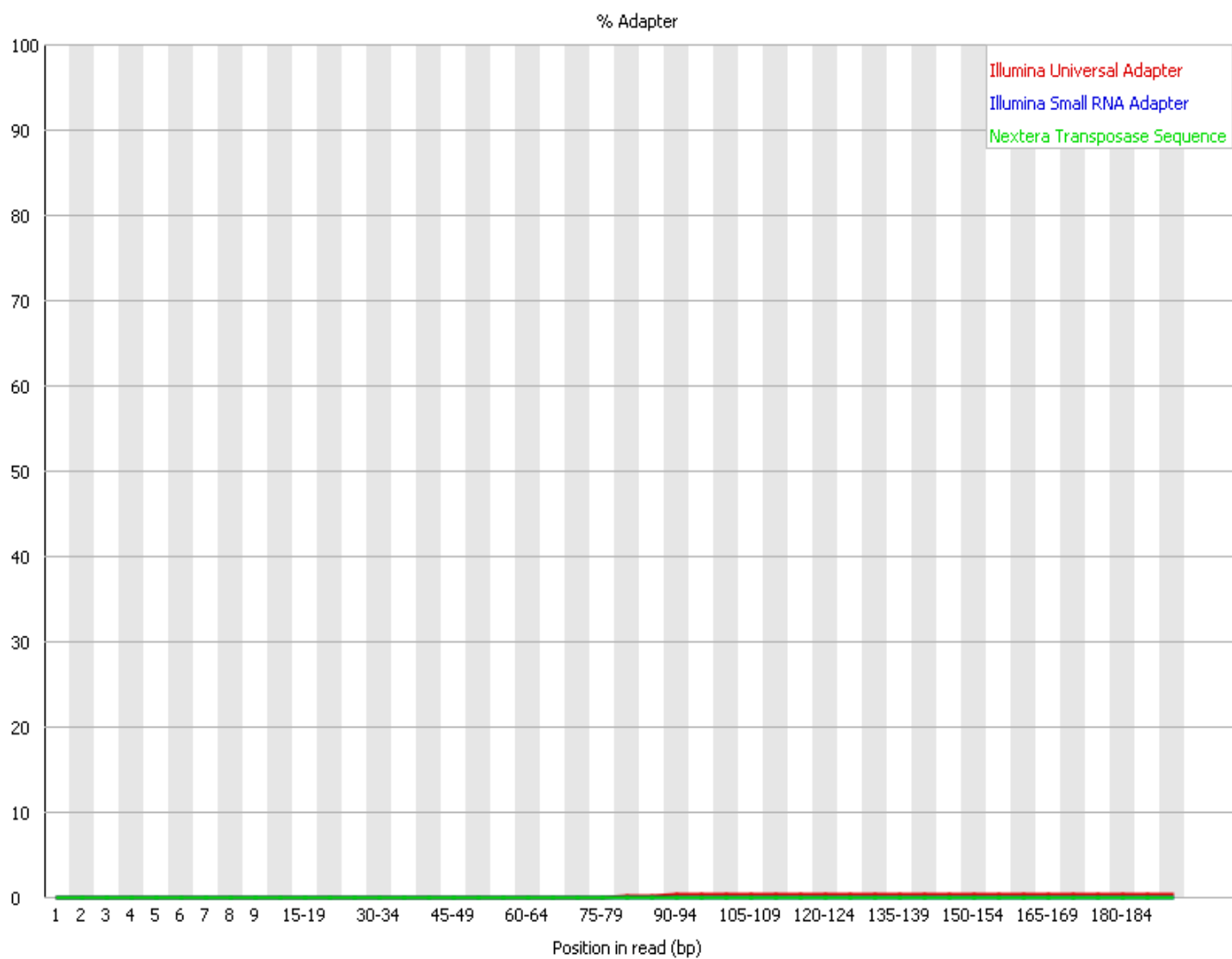


## Overrepresented sequences

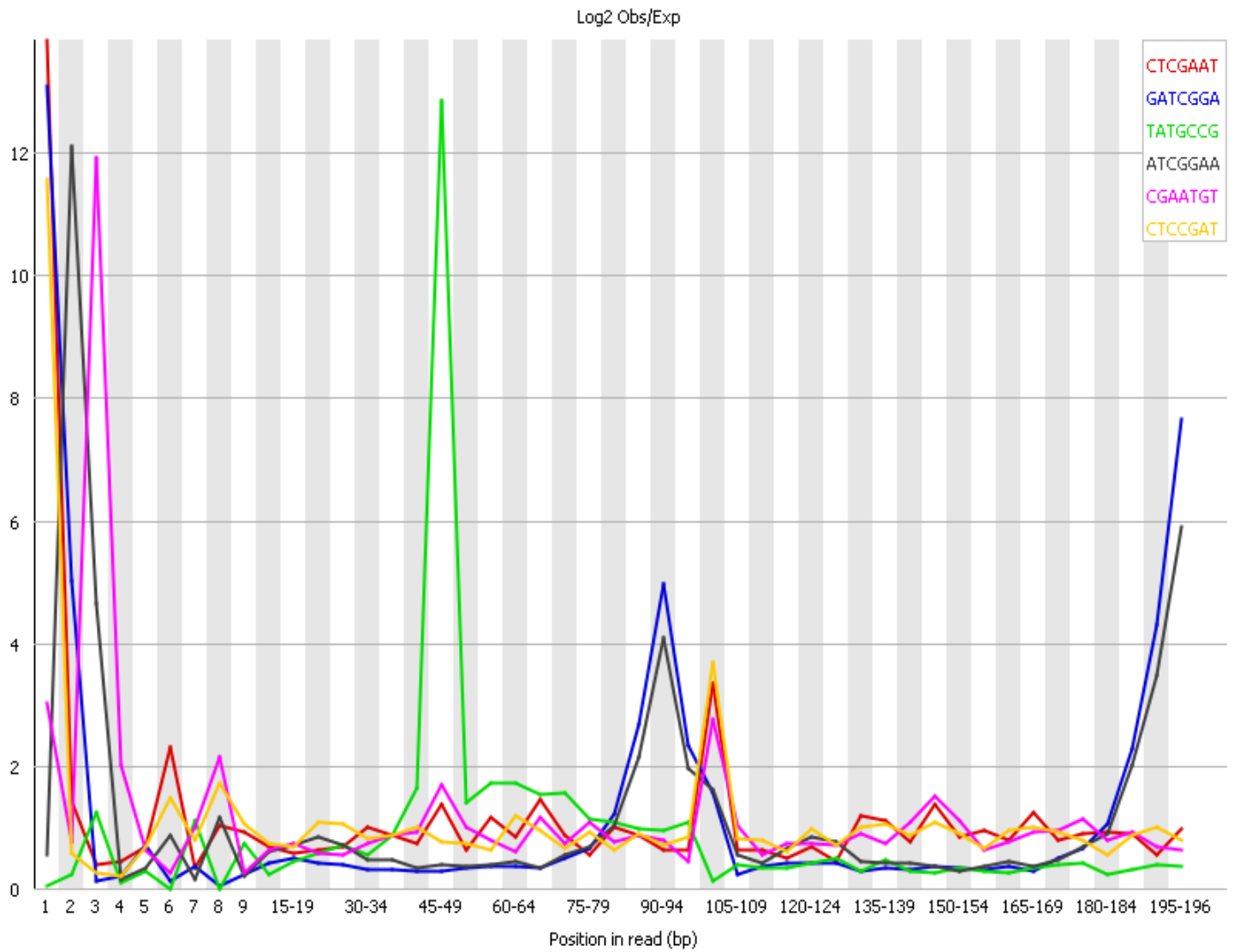
No overrepresented sequences



## Adapter Content



 **Kmer Content**



| Sequence | Count | PValue | Obs/Exp Max | Max Obs/Exp Position |
|----------|-------|--------|-------------|----------------------|
| CTCGAAT  | 16840 | 0.0    | 13.818129   | 1                    |
| GATCGGA  | 49685 | 0.0    | 13.082045   | 1                    |
| TATGCCG  | 15450 | 0.0    | 12.837652   | 45-49                |
| ATCGGAA  | 53480 | 0.0    | 12.11168    | 2                    |
| CGAATGT  | 13575 | 0.0    | 11.910732   | 3                    |
| CTCCGAT  | 18140 | 0.0    | 11.582957   | 1                    |
| CGGAAGA  | 61590 | 0.0    | 11.089626   | 4                    |
| CTCGTTT  | 21215 | 0.0    | 11.061089   | 1                    |
| CGATTAG  | 12780 | 0.0    | 11.041448   | 4                    |
| AGAGCAC  | 65285 | 0.0    | 11.0029745  | 8                    |
| CCGATTA  | 12750 | 0.0    | 10.9137125  | 3                    |
| TCGTATG  | 18830 | 0.0    | 10.772619   | 40-44                |

| Sequence | Count | PValue        | Obs/Exp Max | Max Obs/Exp Position |
|----------|-------|---------------|-------------|----------------------|
| CTCGTAT  | 18450 | 0.0           | 10.527094   | 40-44                |
| GAGCACA  | 69730 | 0.0           | 10.5264435  | 9                    |
| CTCGGAT  | 21580 | 0.0           | 10.282529   | 1                    |
| CGCGTAA  | 1935  | 7.6397555E-11 | 10.148269   | 1                    |
| CTCAAAT  | 43315 | 0.0           | 10.087061   | 1                    |
| TCCGATT  | 15910 | 0.0           | 10.039493   | 2                    |
| TCTCGTA  | 19590 | 0.0           | 10.024542   | 40-44                |
| CGACGAT  | 7005  | 0.0           | 9.951606    | 1                    |

Produced by [FastQC](#) (version 0.11.2)