













FastQC Report

Summary

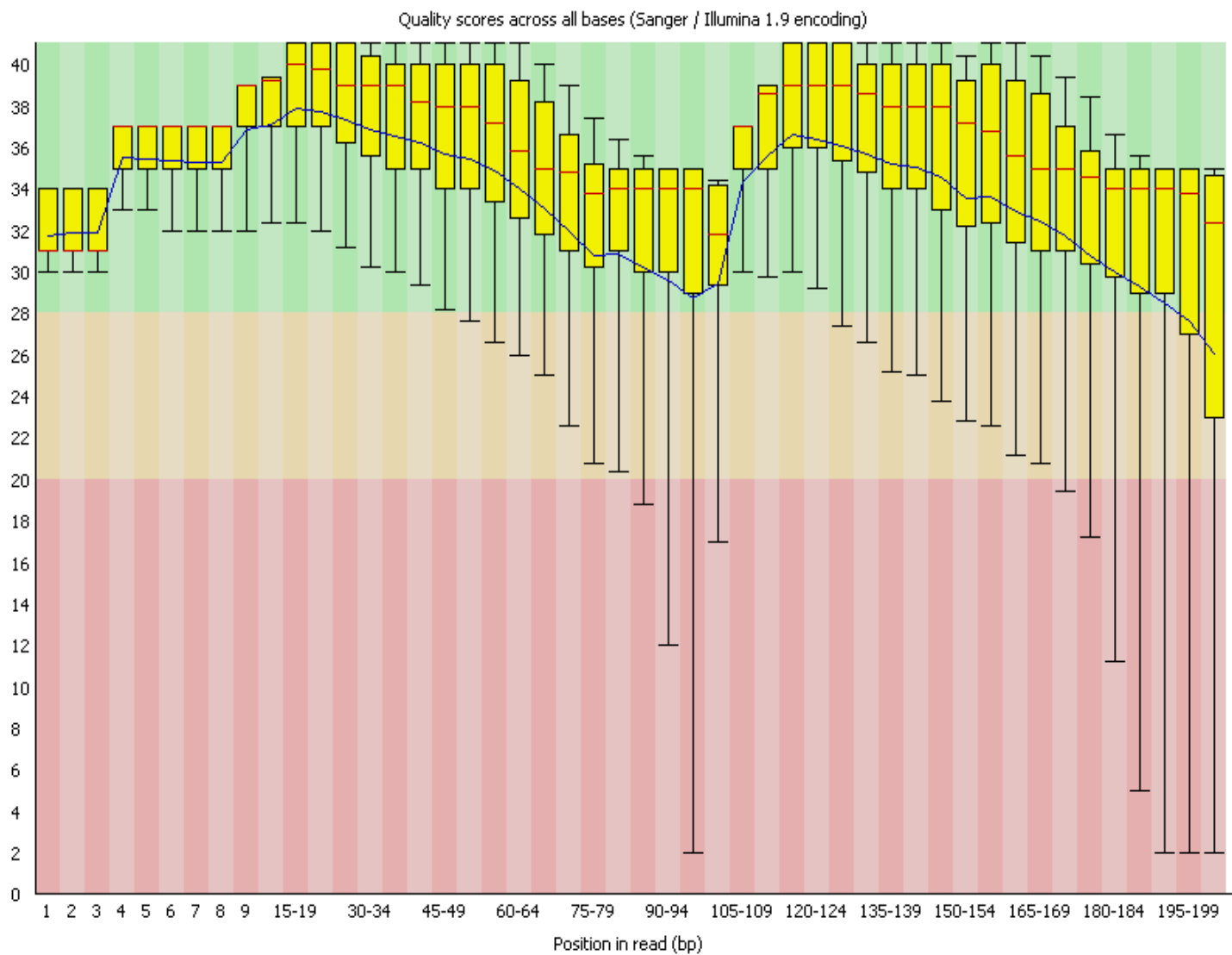
Sun 21 Sep 2014
SRR1033795.fastq

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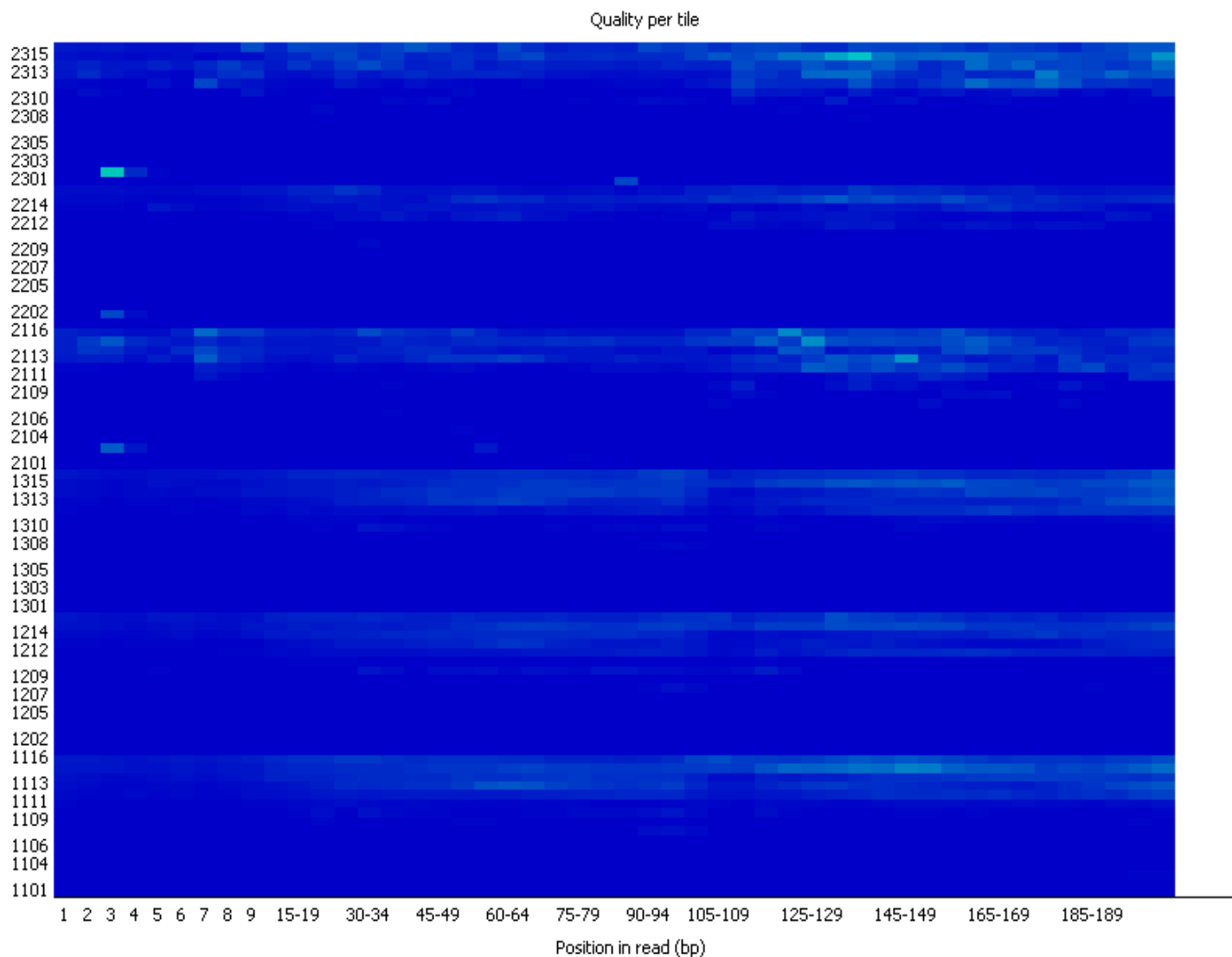
Basic Statistics

| Measure | Value |
|-----------------------------------|-------------------------|
| Filename | SRR1033795.fastq |
| File type | Conventional base calls |
| Encoding | Sanger / Illumina 1.9 |
| Total Sequences | 36538349 |
| Sequences flagged as poor quality | 0 |
| Sequence length | 202 |
| %GC | 50 |

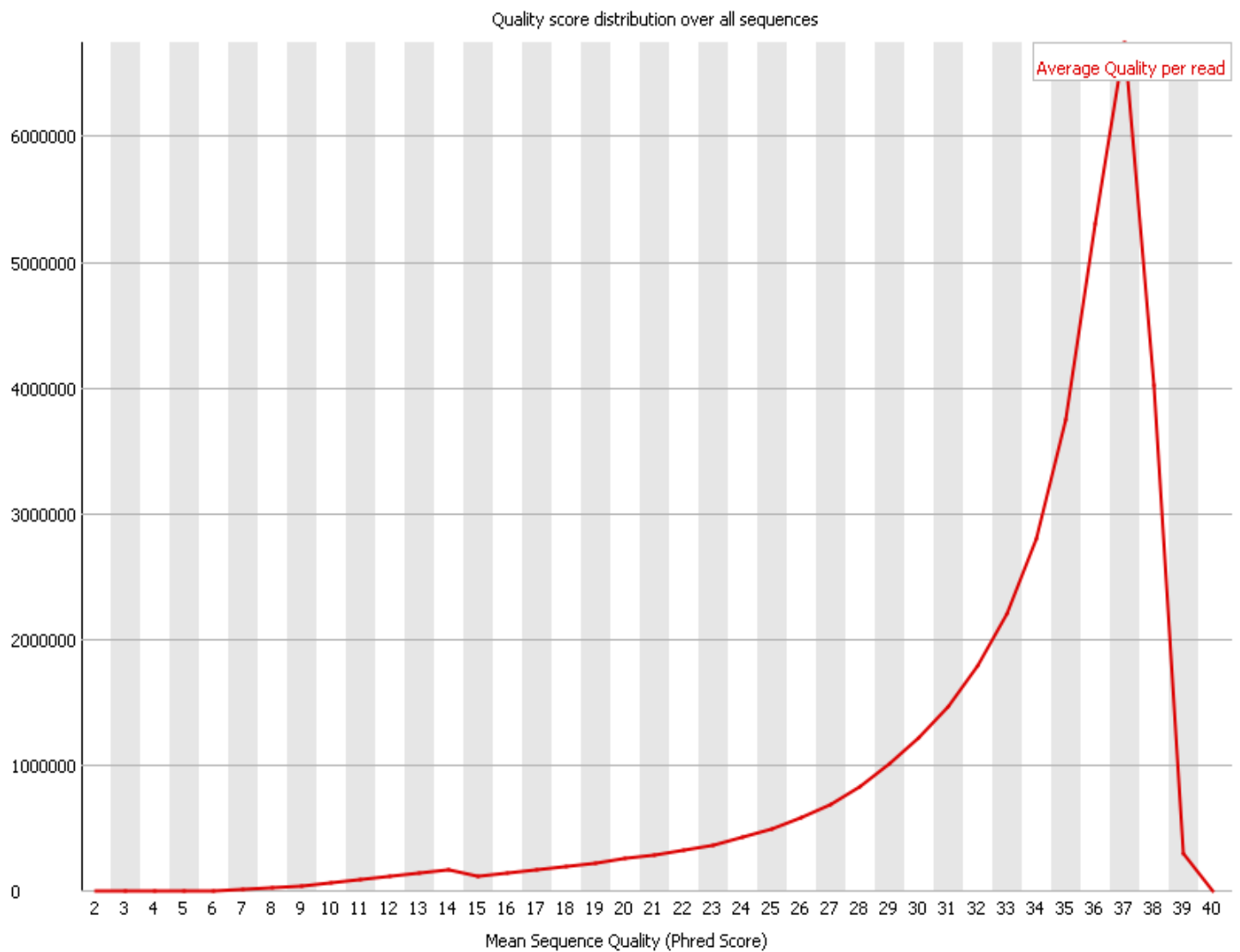
Per base sequence quality



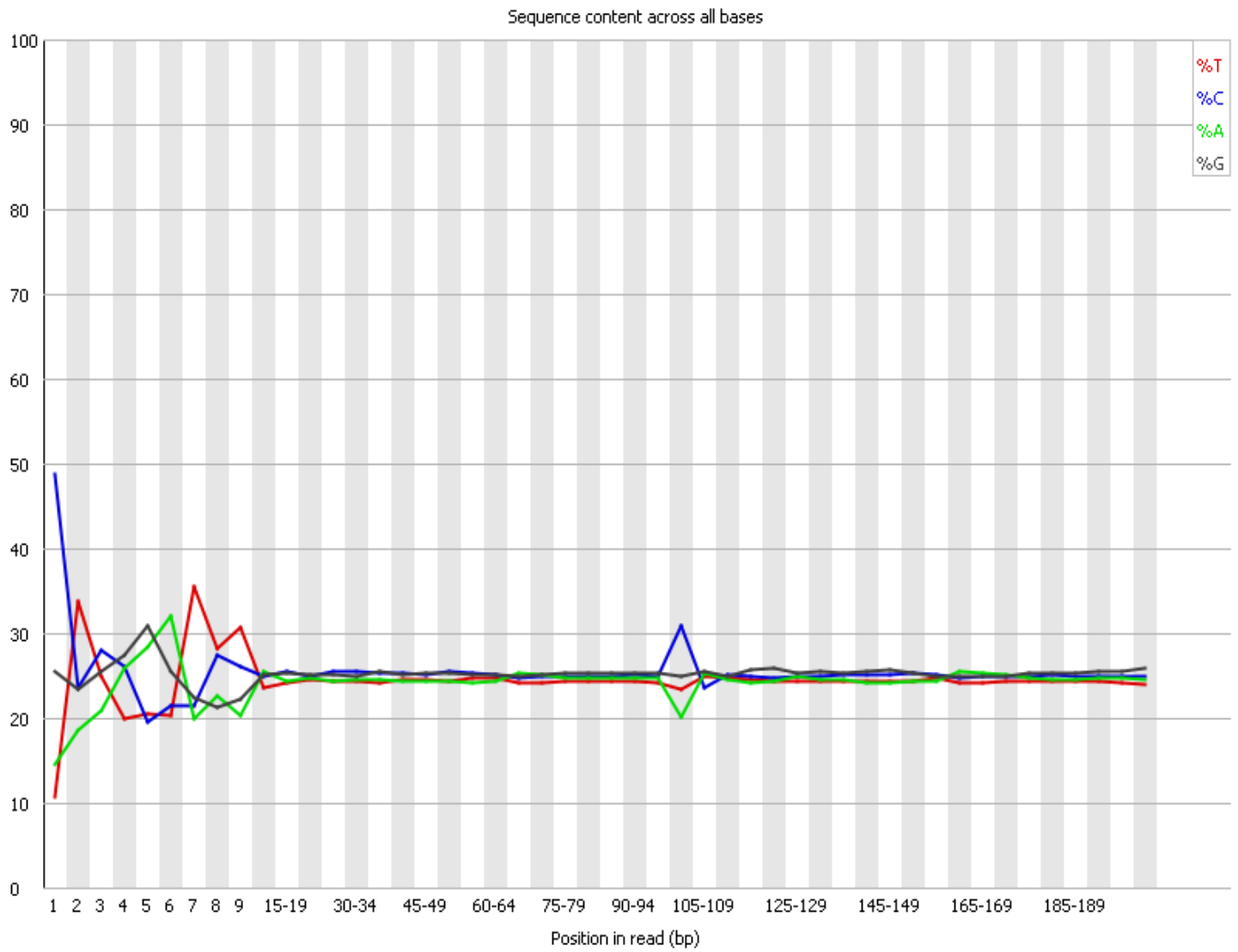
Per tile sequence quality



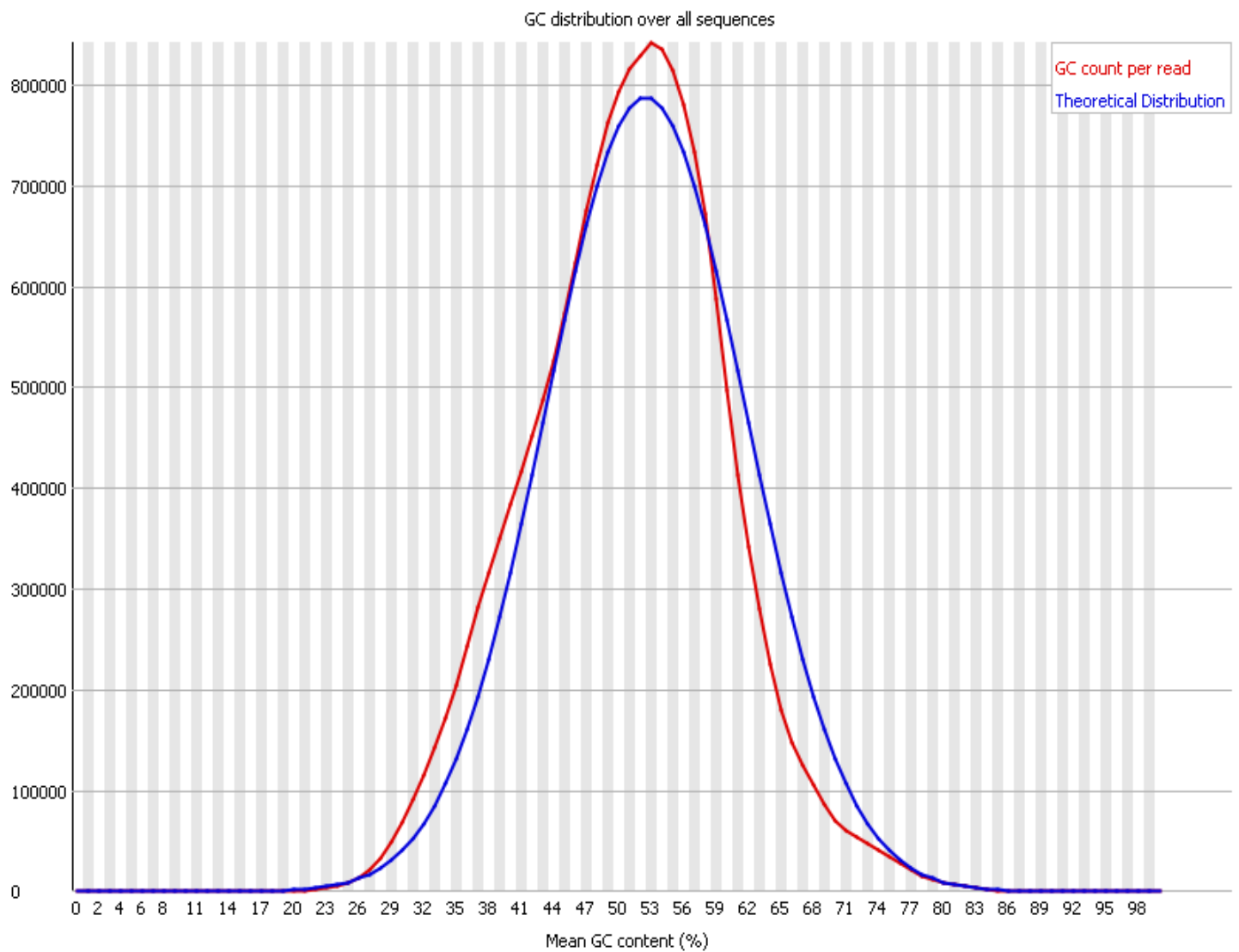
Per sequence quality scores



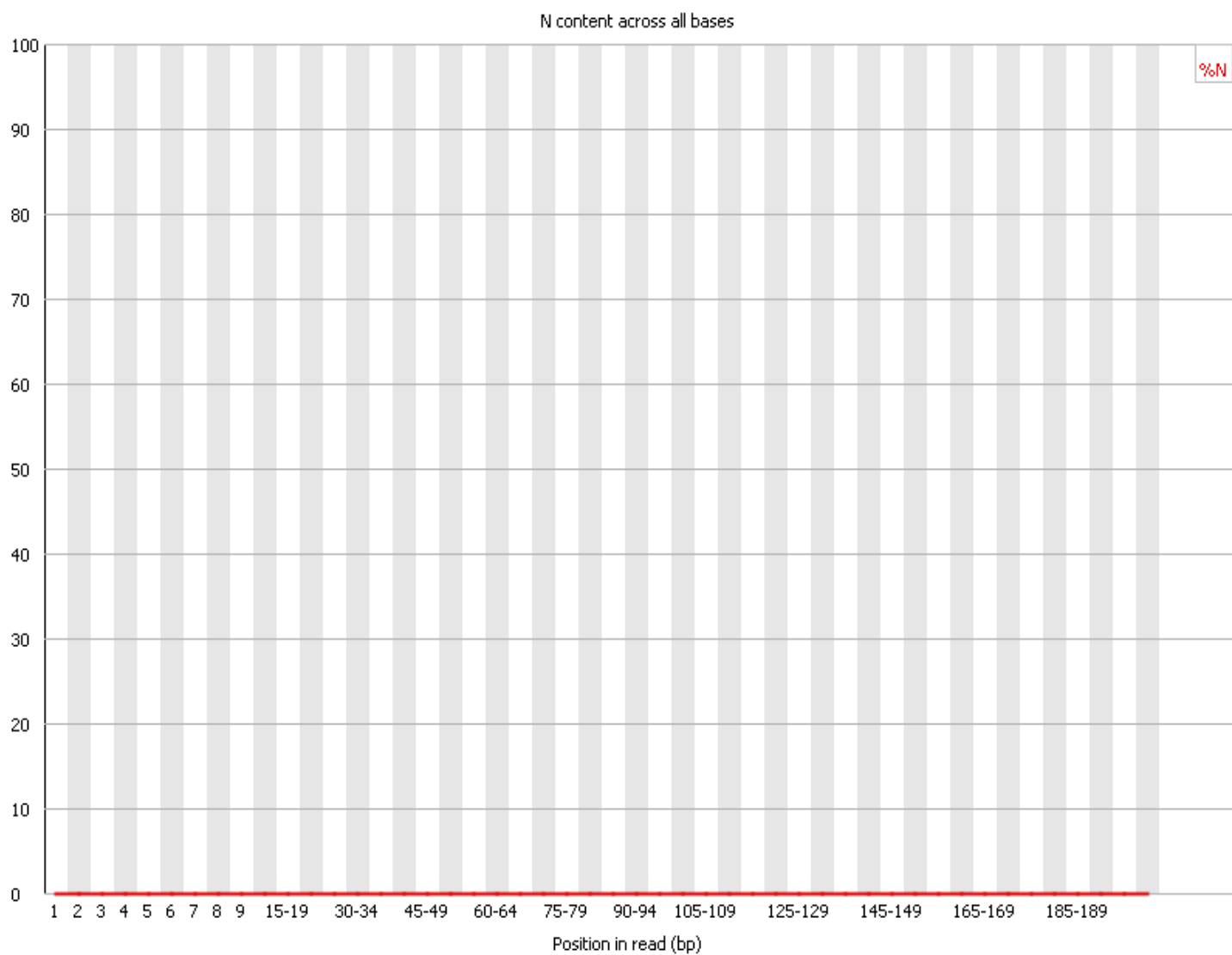
❌ Per base sequence content



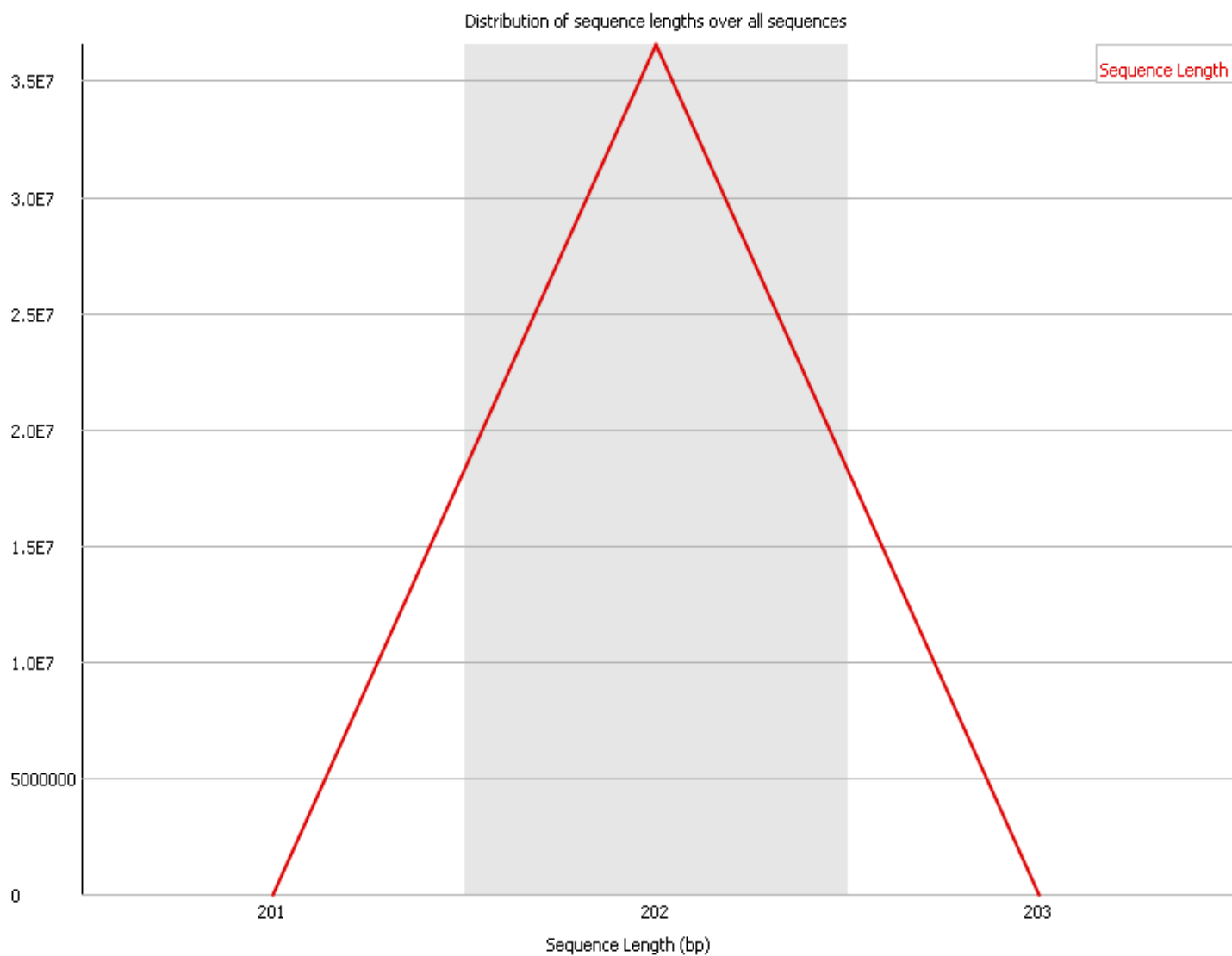
Per sequence GC content



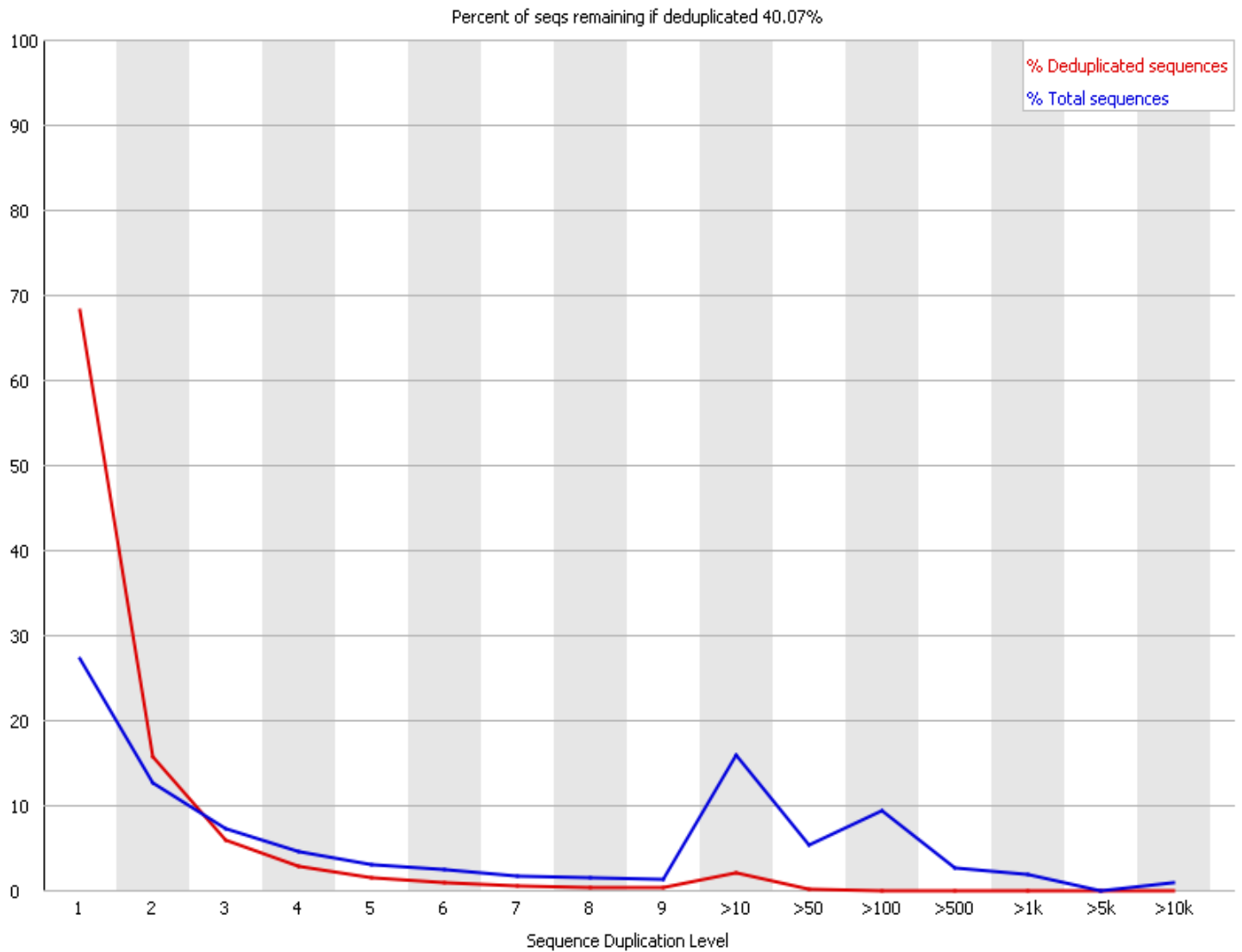
Per base N content



Sequence Length Distribution



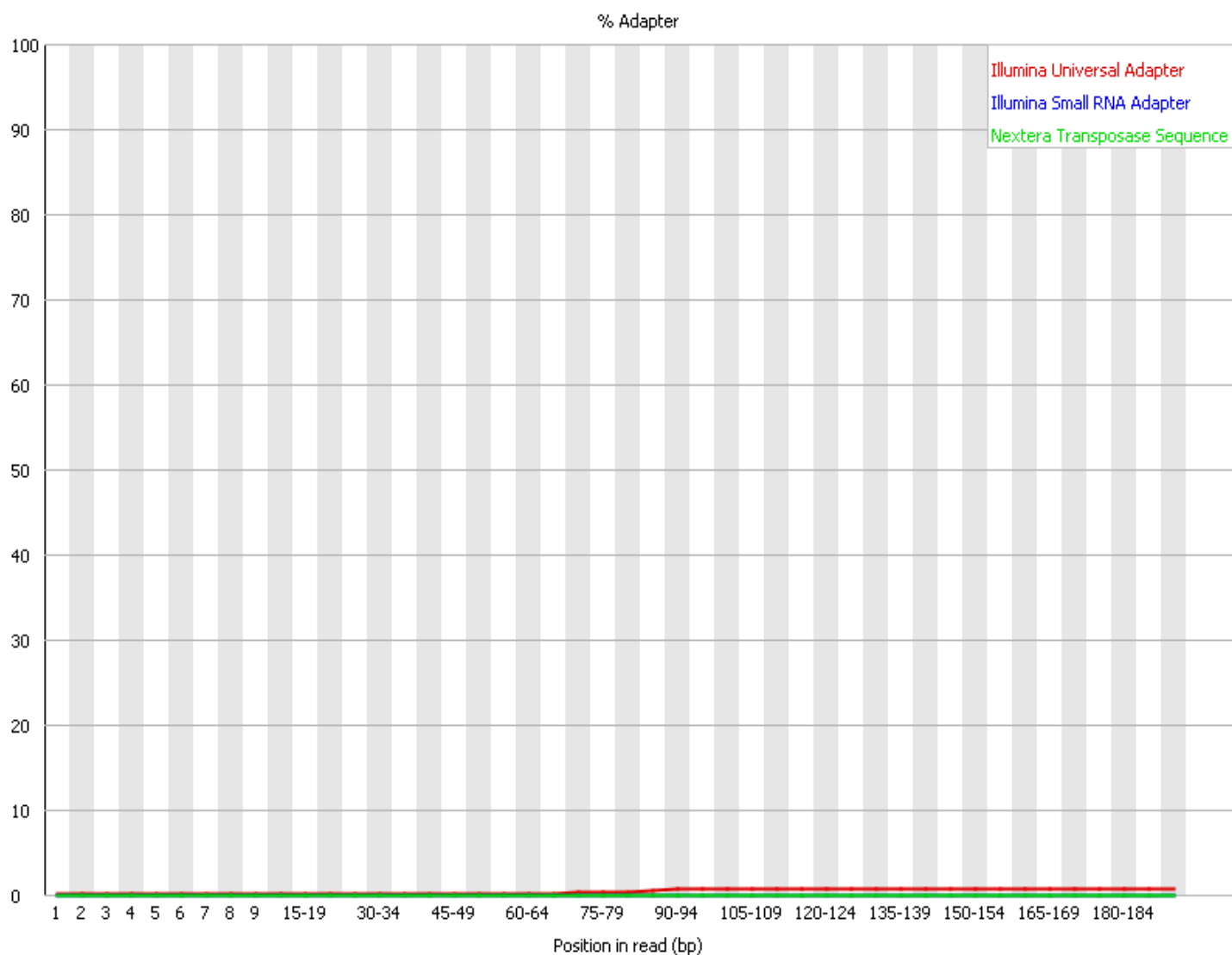
❌ Sequence Duplication Levels



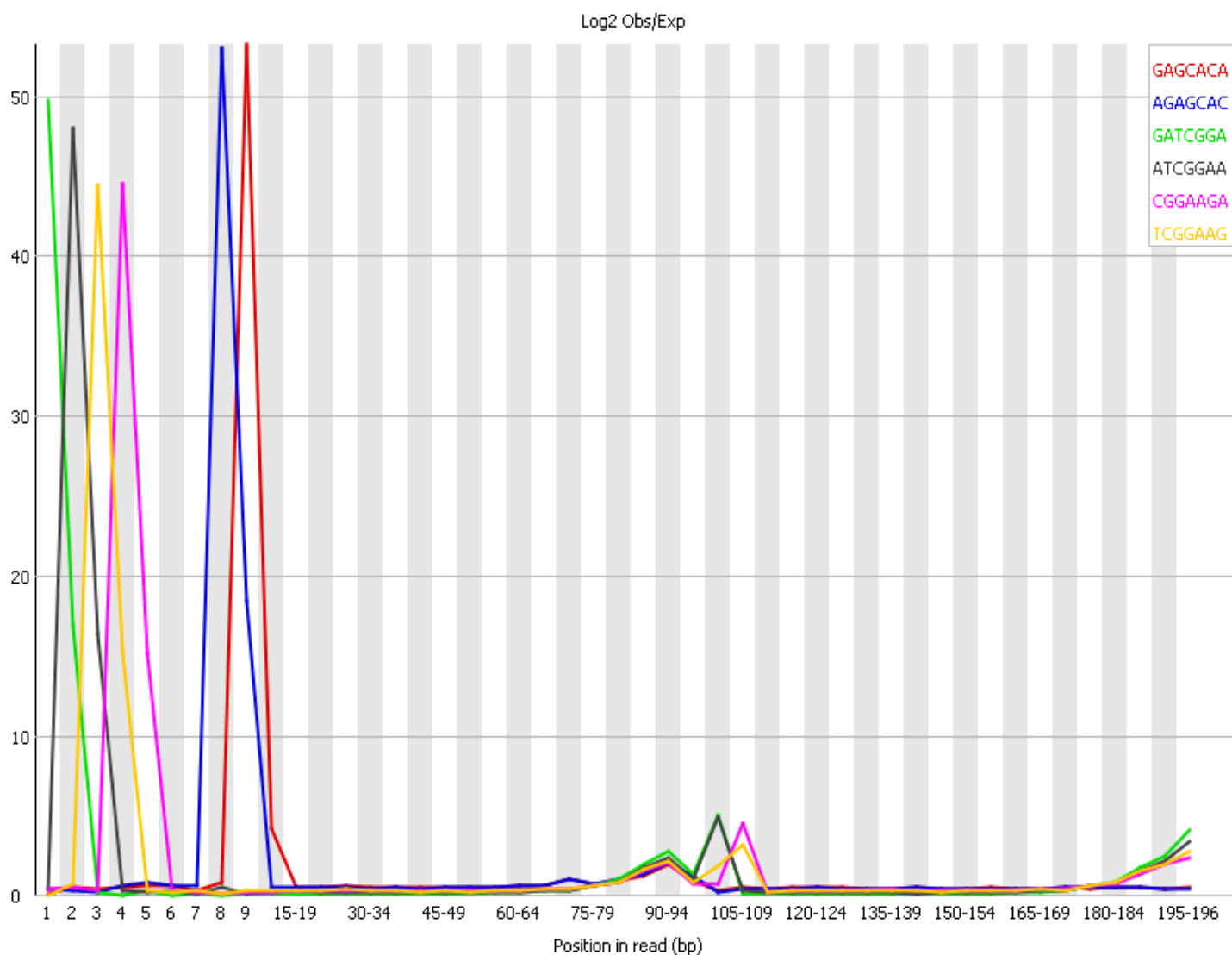
! Overrepresented sequences

| Sequence | Count | Percentage | Possible Source |
|--|--------|---------------------|--|
| GATCGGAAGAGCACACGTCTGAACTCCAGTCACACAGTGATCTCGTATGC | 272623 | 0.7461284033386402 | TruSeq Adapter, Index 5 (100% over 50bp) |
| AGATCGGAAGAGCACACGTCTGAACTCCAGTCACACAGTGATCTCGTATG | 90032 | 0.24640412734576486 | TruSeq Adapter, Index 5 (100% over 49bp) |

✓ Adapter Content



✗ Kmer Content



| Sequence | Count | PValue | Obs/Exp Max | Max Obs/Exp Position |
|----------|--------|--------|-------------|----------------------|
| GAGCACA | 122035 | 0.0 | 53.17276 | 9 |
| AGAGCAC | 122725 | 0.0 | 52.969604 | 8 |
| GATCGGA | 129795 | 0.0 | 49.73614 | 1 |
| ATCGGAA | 134095 | 0.0 | 48.02819 | 2 |
| CGGAAGA | 145675 | 0.0 | 44.533184 | 4 |
| TCGGAAG | 144910 | 0.0 | 44.47728 | 3 |
| AAGAGCA | 156840 | 0.0 | 41.497852 | 7 |
| TATGCCG | 56490 | 0.0 | 30.831665 | 45-49 |
| GAAGAGC | 217515 | 0.0 | 30.141985 | 6 |
| CTCGTAT | 59400 | 0.0 | 28.87183 | 40-44 |
| TCGTATG | 61910 | 0.0 | 28.144407 | 40-44 |
| GGAAGAG | 252965 | 0.0 | 26.09327 | 5 |

| Sequence | Count | PValue | Obs/Exp Max | Max Obs/Exp Position |
|----------|-------|--------|-------------|----------------------|
| ATGCCGT | 67140 | 0.0 | 25.882658 | 45-49 |
| CGTATCA | 19715 | 0.0 | 25.748611 | 150-154 |
| TCTCGTA | 65795 | 0.0 | 25.586111 | 40-44 |
| ACACGTC | 71025 | 0.0 | 24.777672 | 10-14 |
| TGCCGTC | 72010 | 0.0 | 24.007048 | 45-49 |
| ATCTCGT | 69470 | 0.0 | 23.930779 | 40-44 |
| CGTCTGA | 74920 | 0.0 | 23.544344 | 15-19 |
| GTATGCC | 74475 | 0.0 | 23.33612 | 45-49 |

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