# FastQC Report

## Summary

✅ Basic Statistics

✅ Per base sequence quality

❌ Per tile sequence quality
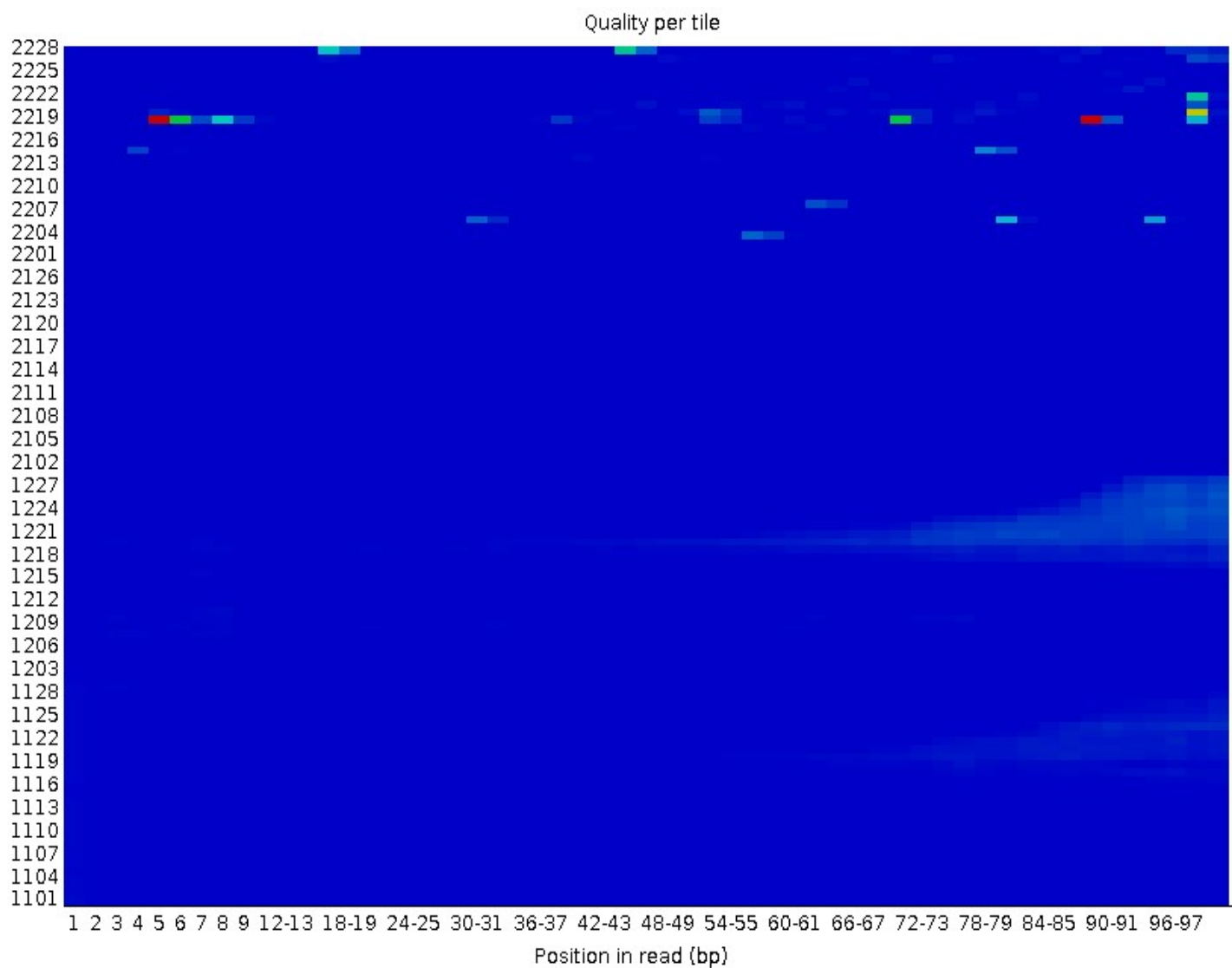
✅ Per sequence quality scores
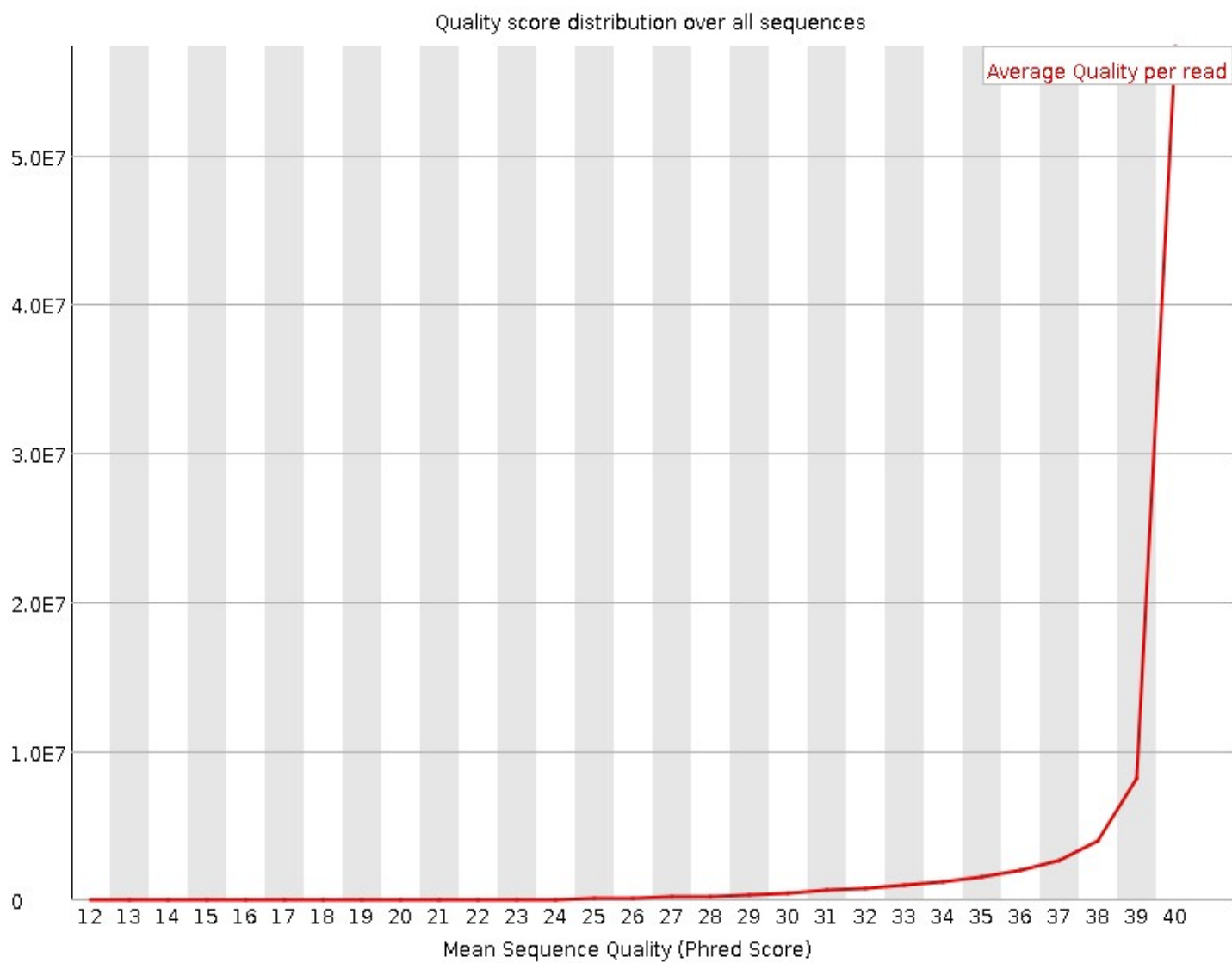
❌ Per base sequence content
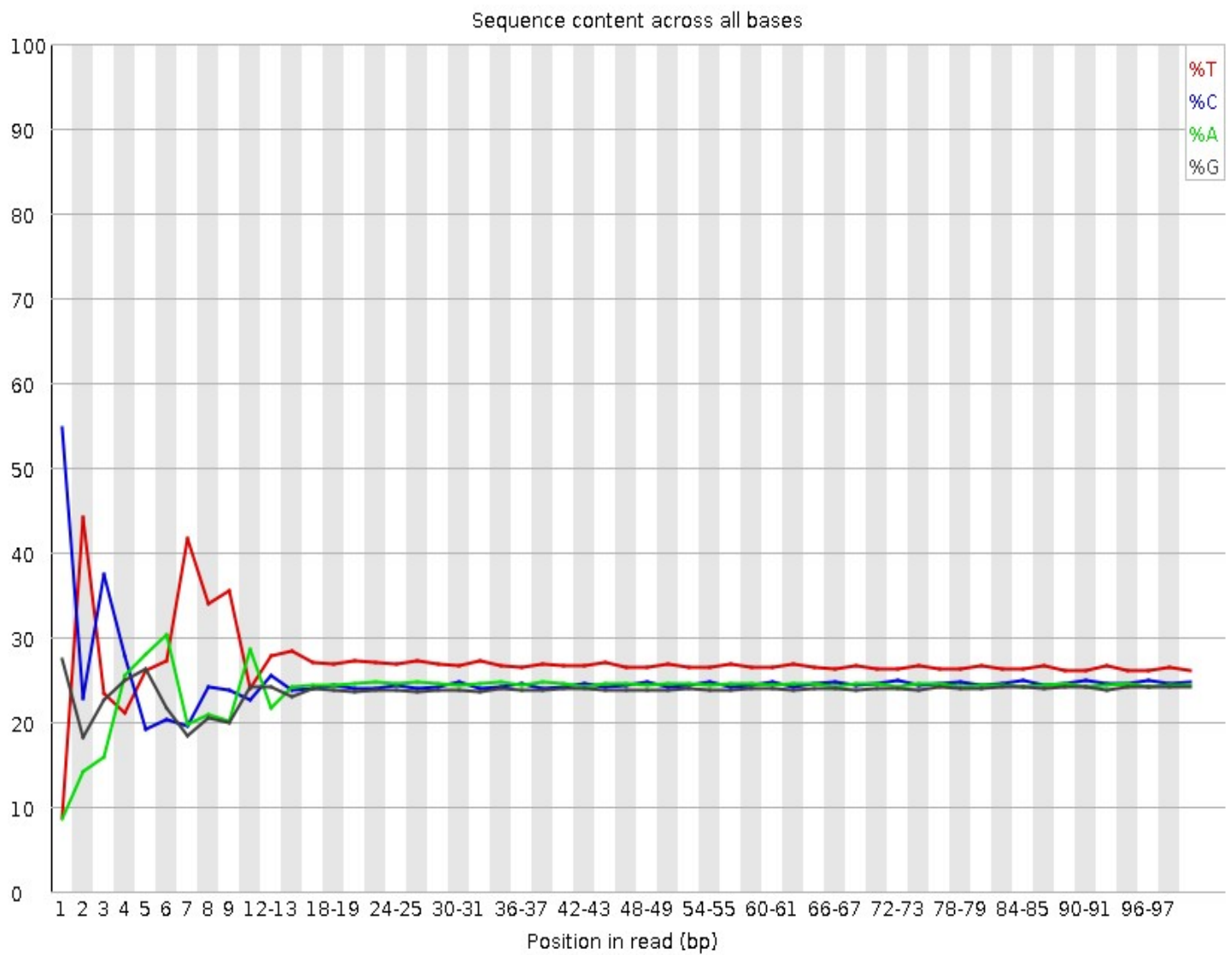
⚠️ Per sequence GC content
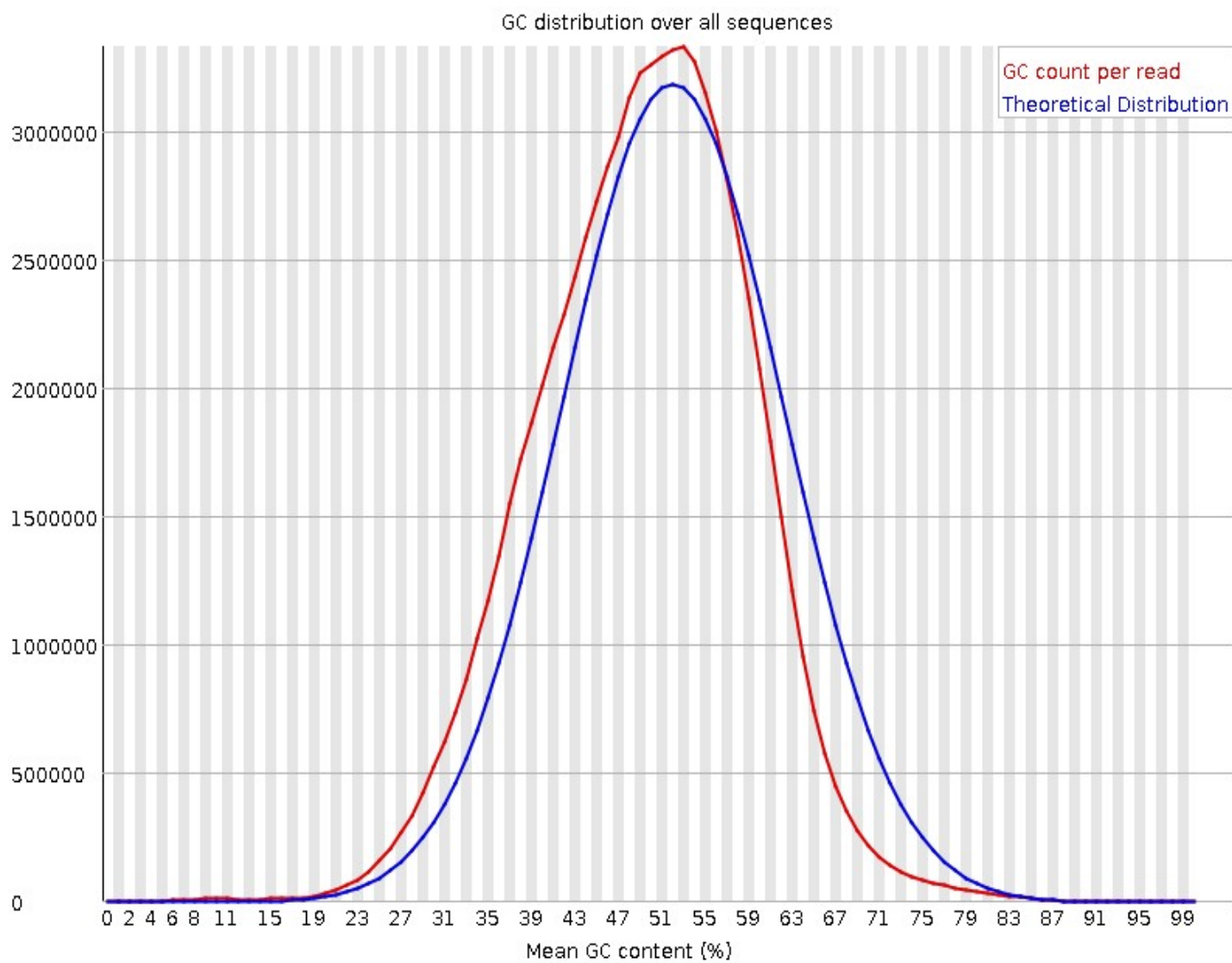
✅ Per base N content
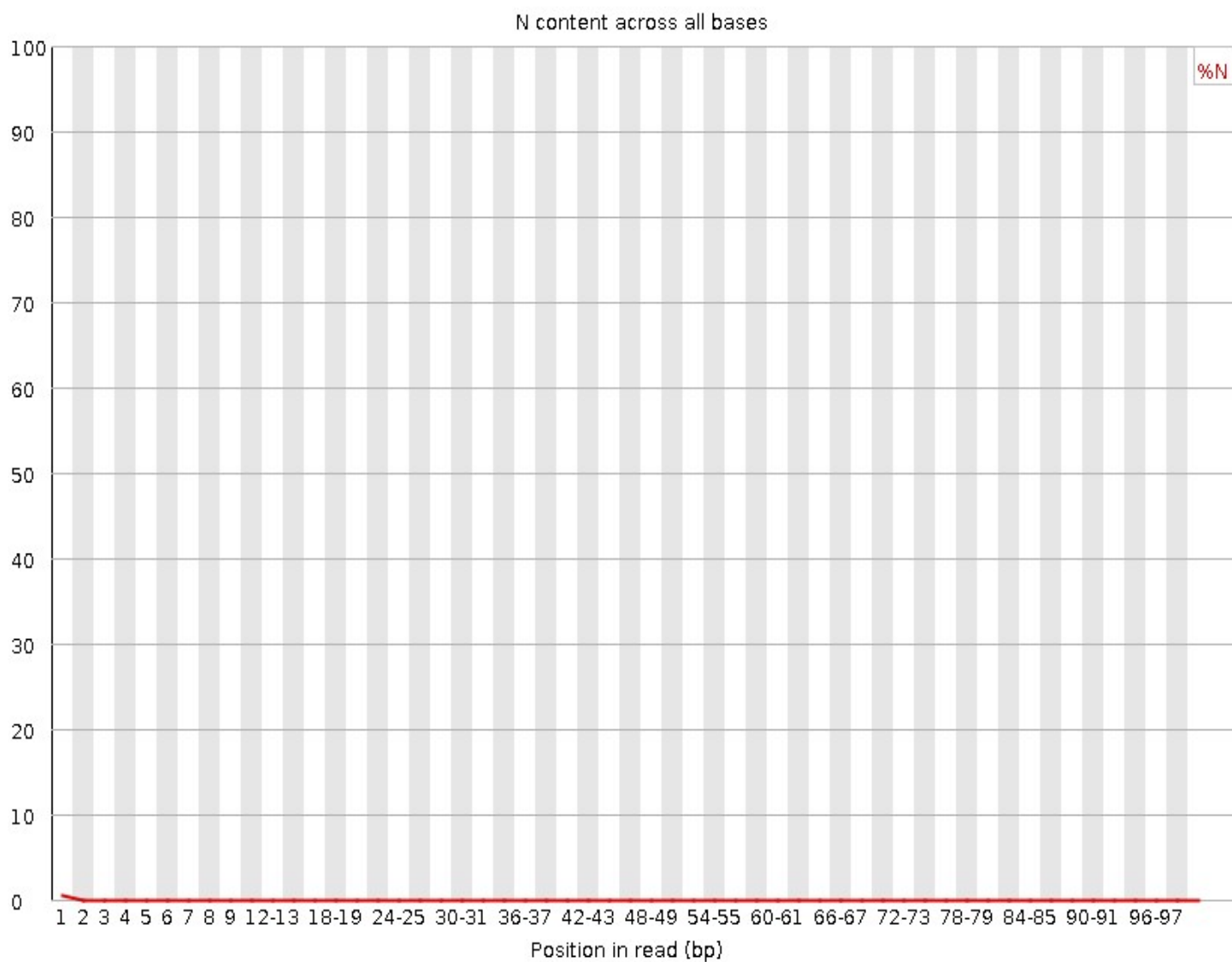
✅ Sequence Length Distribution

❌ Sequence Duplication Levels

✅ Overrepresented sequences

✅ Adapter Content

❌ Kmer Content

## ✅ Basic Statistics

| Measure | Value |
|---|---|
| Filename | 10_2G_both_S8_L008_R1_001.fastq.gz |
| File type | Conventional base calls |
| Encoding | Sanger / Illumina 1.9 |
| Total Sequences | 81477069 |
| Sequences flagged as poor quality | 0 |
| Sequence length | 101 |
| %GC | 48 |

## ✅ Per base sequence quality

Quality scores across all bases (Sanger / Illumina 1.9 encoding)

## ❌Per tile sequence quality

Quality per tile

Position in read (bp)

## ✅ Per sequence quality scores

Quality score distribution over all sequences

# ❌Per base sequence content

# ⚠️Per sequence GC content

GC distribution over all sequences

Legend:
- GC count per read
- Theoretical Distribution

X-axis: Mean GC content (%)

# ✅Per base N content

## ✅ Sequence Length Distribution

Distribution of sequence lengths over all sequences

# ⊗Sequence Duplication Levels

## ✅ Overrepresented sequences

No overrepresented sequences

## ✅ Adapter Content

# ❌Kmer Content

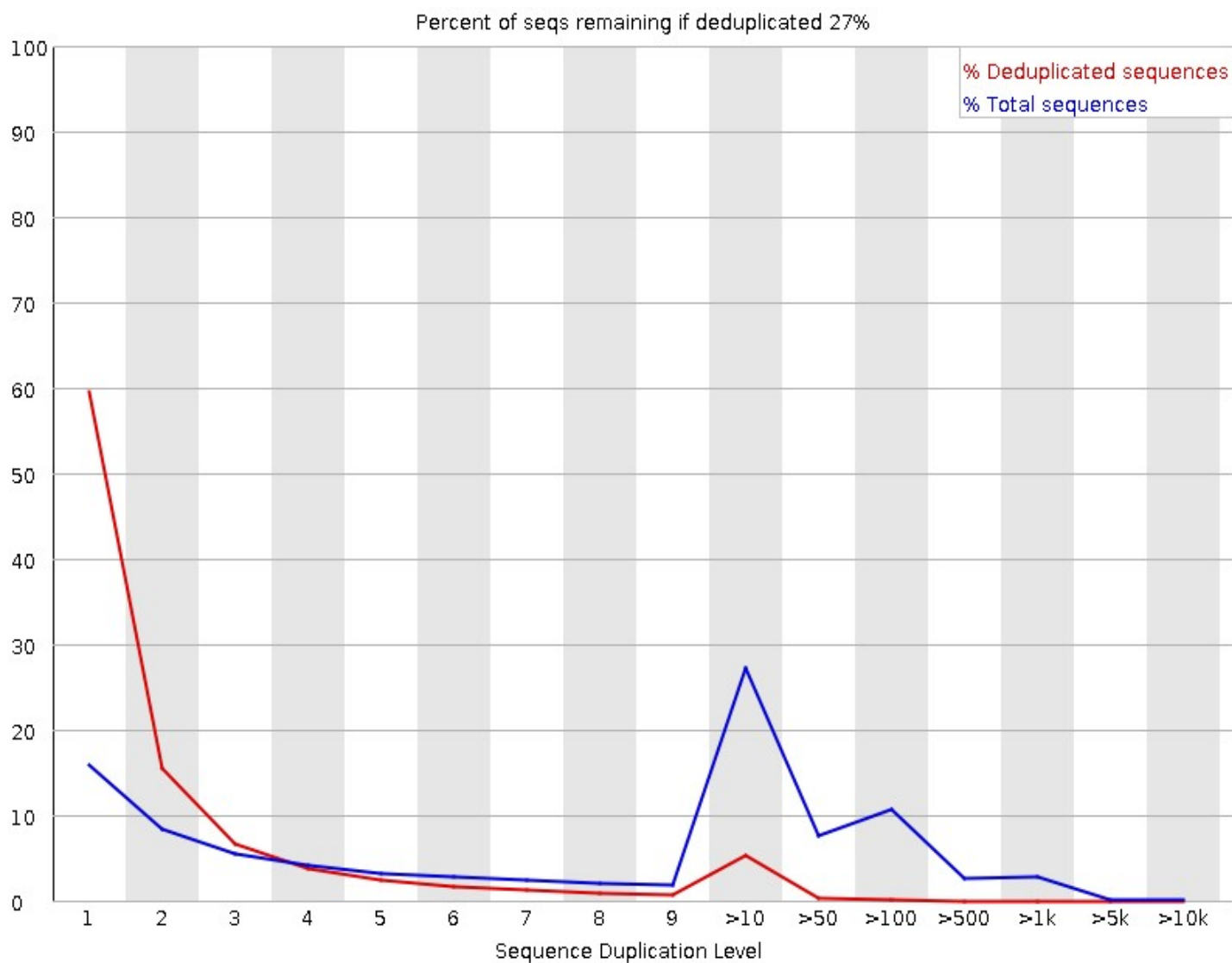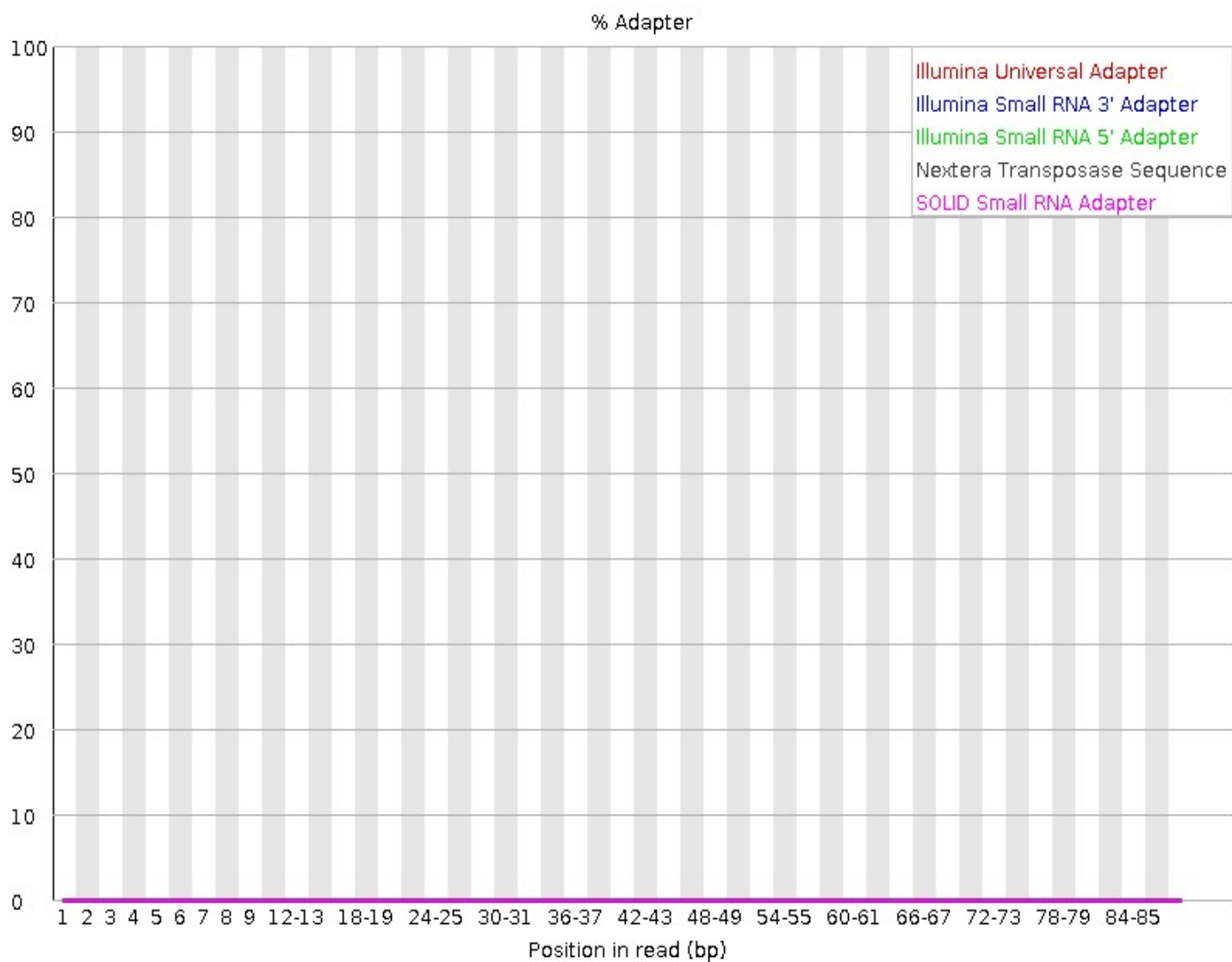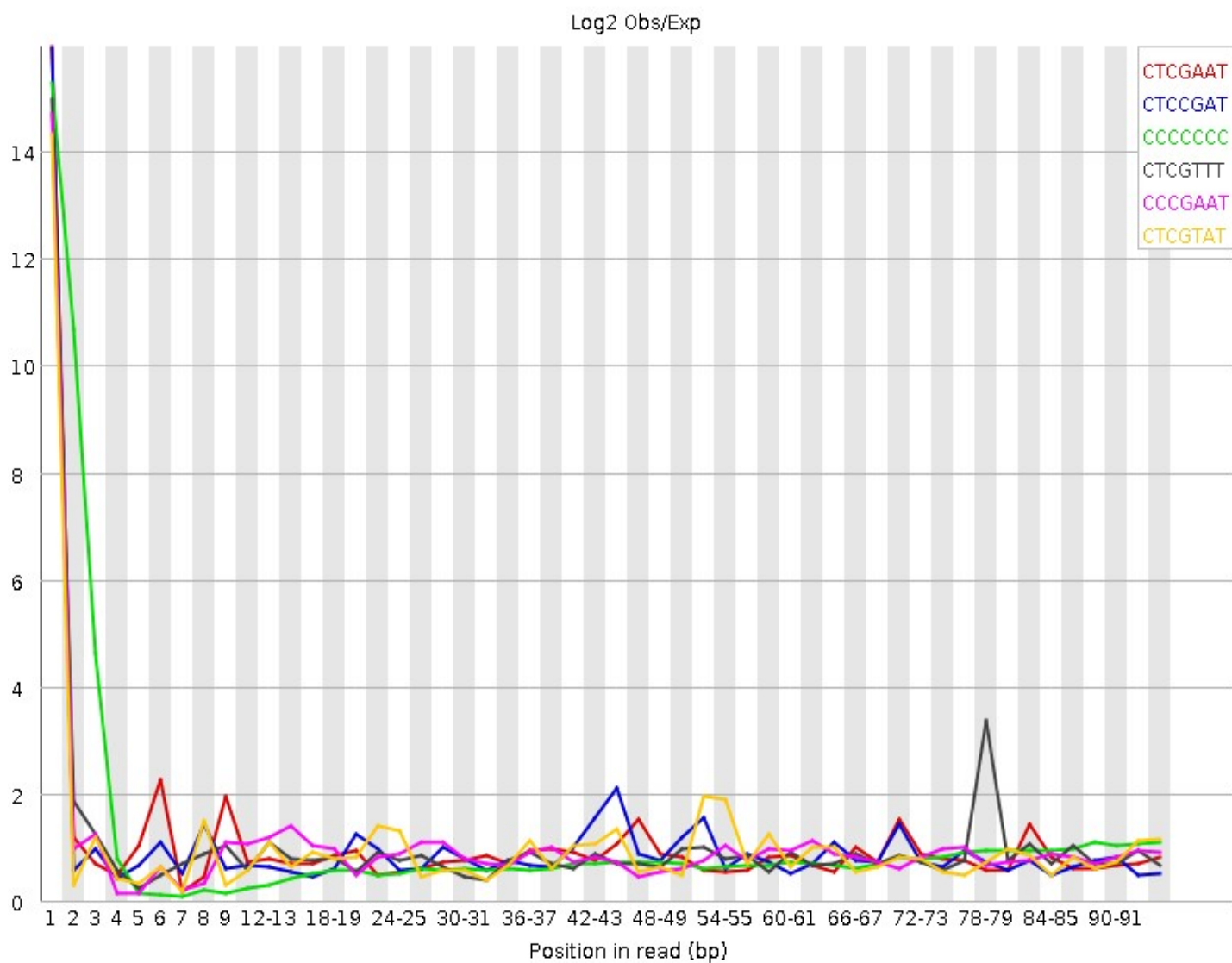| Sequence | Count | PValue | Obs/Exp Max | Max Obs/Exp Position |
|----------|-------|--------|-------------|----------------------|
| CTCGAAT  | 29340 | 0.0    | 15.948988   | 1                    |
| CTCCGAT  | 30695 | 0.0    | 15.945673   | 1                    |
| CCCCCCC  | 86515 | 0.0    | 15.287211   | 1                    |
| CTCGTTT  | 36795 | 0.0    | 14.977903   | 1                    |
| CCCGAAT  | 16090 | 0.0    | 14.704819   | 1                    |
| CTCGTAT  | 18360 | 0.0    | 14.344633   | 1                    |
| TCGAATG  | 18440 | 0.0    | 14.198977   | 2                    |
| TCCGATT  | 26235 | 0.0    | 12.6065     | 2                    |
| CCCCCCT  | 43835 | 0.0    | 12.504019   | 3                    |
| CTCCGTT  | 28060 | 0.0    | 12.452033   | 1                    |
| CGAATGT  | 20750 | 0.0    | 12.4292965  | 3                    |
| CGATTAG  | 20445 | 0.0    | 12.080392   | 4                    |

| Sequence | Count | PValue | Obs/Exp Max | Max Obs/Exp Position |
|----------|-------|--------|-------------|----------------------|
| CCCGTTT | 22980 | 0.0 | 11.876722 | 1 |
| CCGATTA | 22075 | 0.0 | 11.83387 | 3 |
| CCCGATT | 11410 | 0.0 | 11.645809 | 1 |
| GTCGGTT | 20225 | 0.0 | 11.391189 | 1 |
| CTCCTAT | 30325 | 0.0 | 11.380122 | 1 |
| CTCCGGT | 31010 | 0.0 | 11.313704 | 1 |
| CCCGGTT | 23920 | 0.0 | 11.230153 | 1 |
| CCCGTAT | 11700 | 0.0 | 11.030328 | 1 |

**Produced by [FastQC](#) (version 0.11.5)**