FastQC Report

Summary

✅ [Basic Statistics](#)

✅ [Per base sequence quality](#)

✅ [Per tile sequence quality](#)
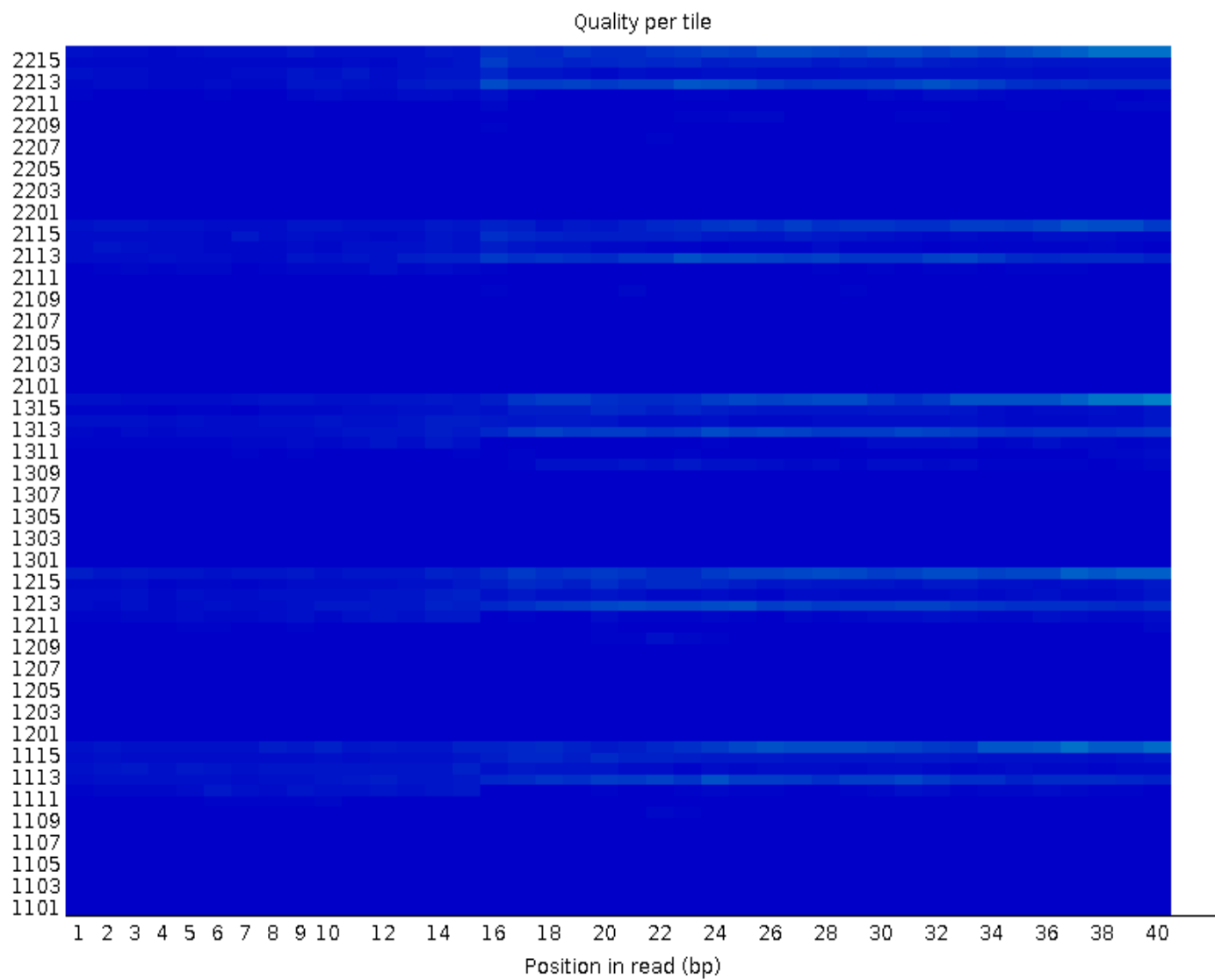
✅ [Per sequence quality scores](#)

❌ [Per base sequence content](#)
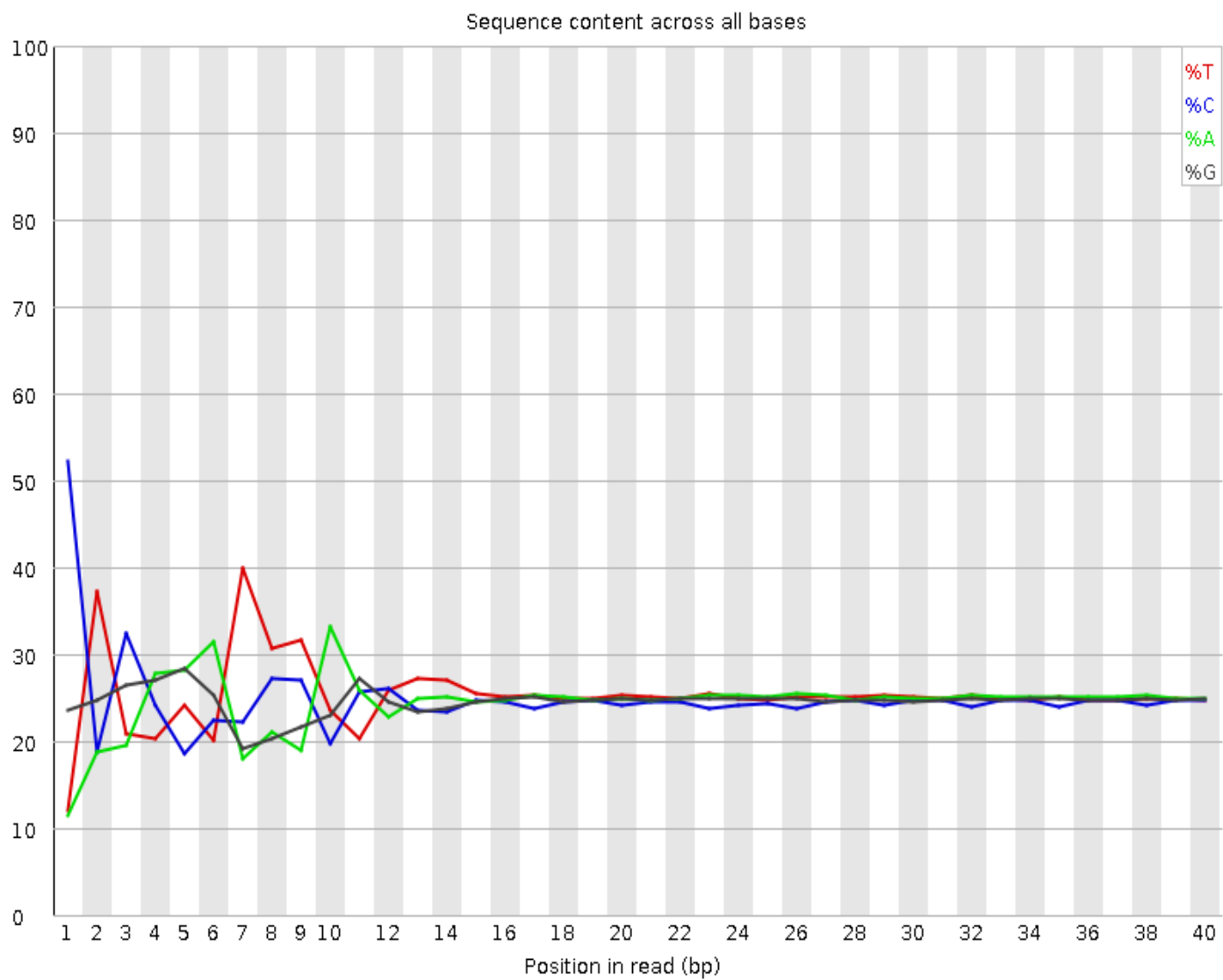
✅ [Per sequence GC content](#)
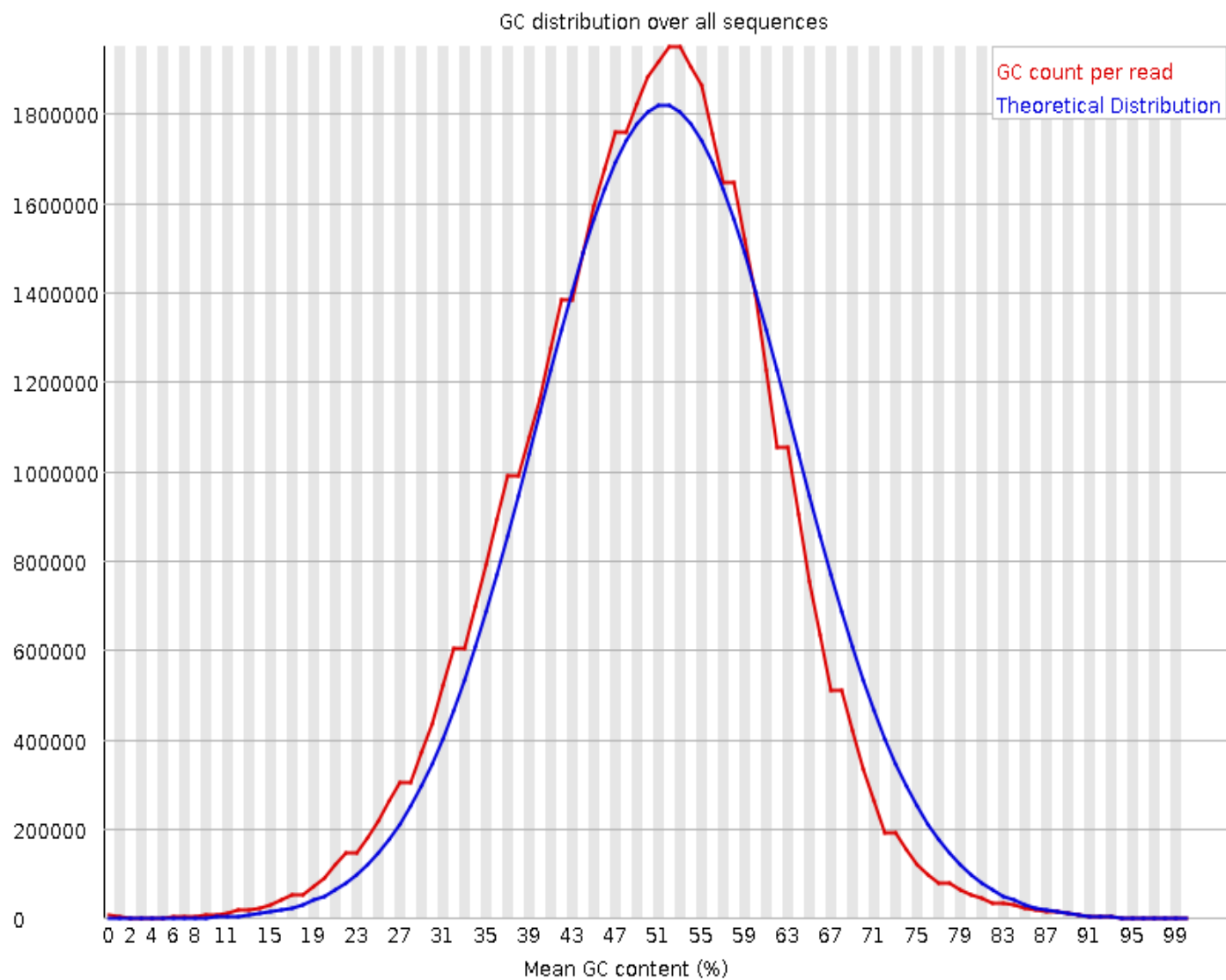
✅ [Per base N content](#)
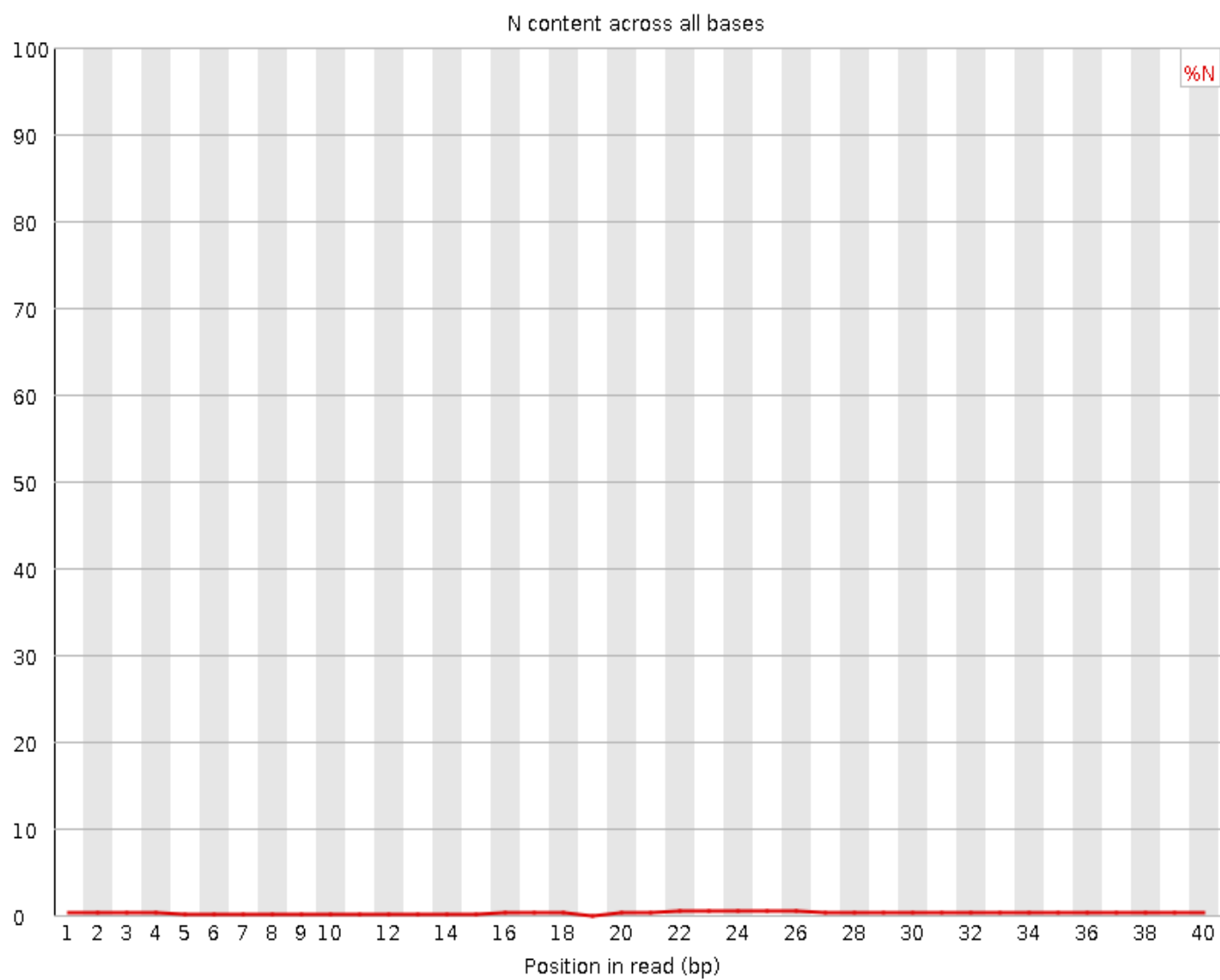
✅ [Sequence Length Distribution](#)
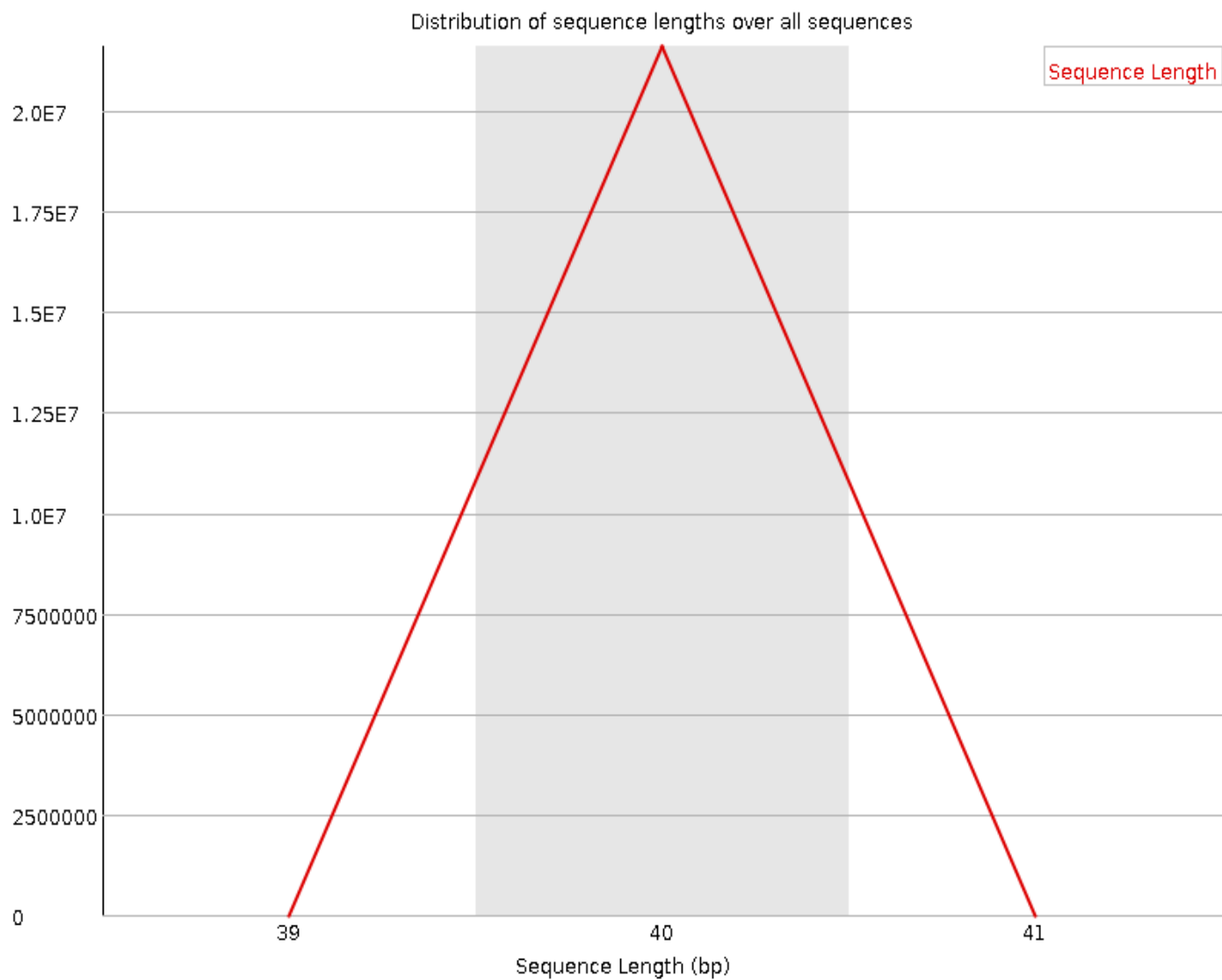
⚠️ [Sequence Duplication Levels](#)

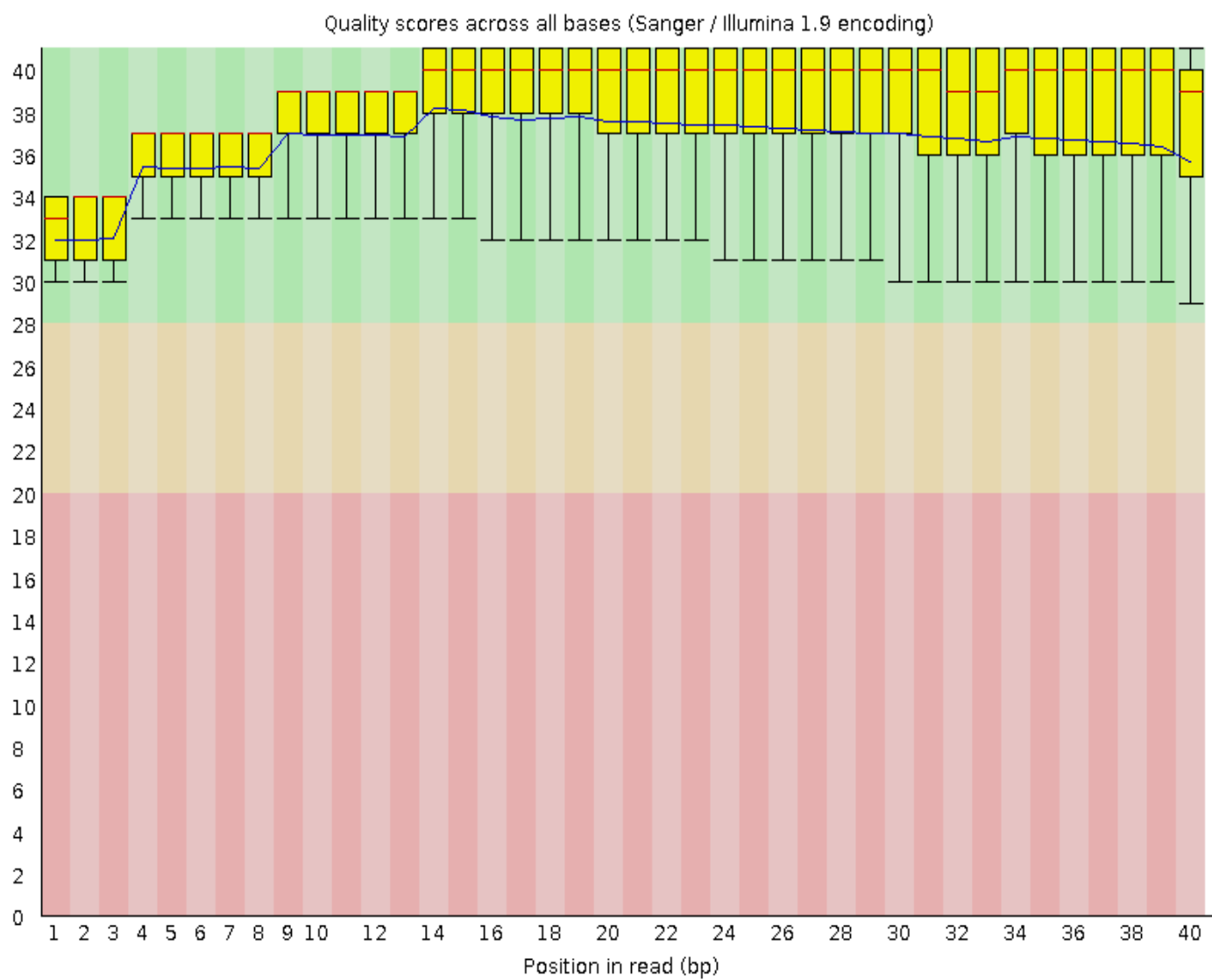✅ [Overrepresented sequences](#)

✅ [Adapter Content](#)

✅ Basic Statistics

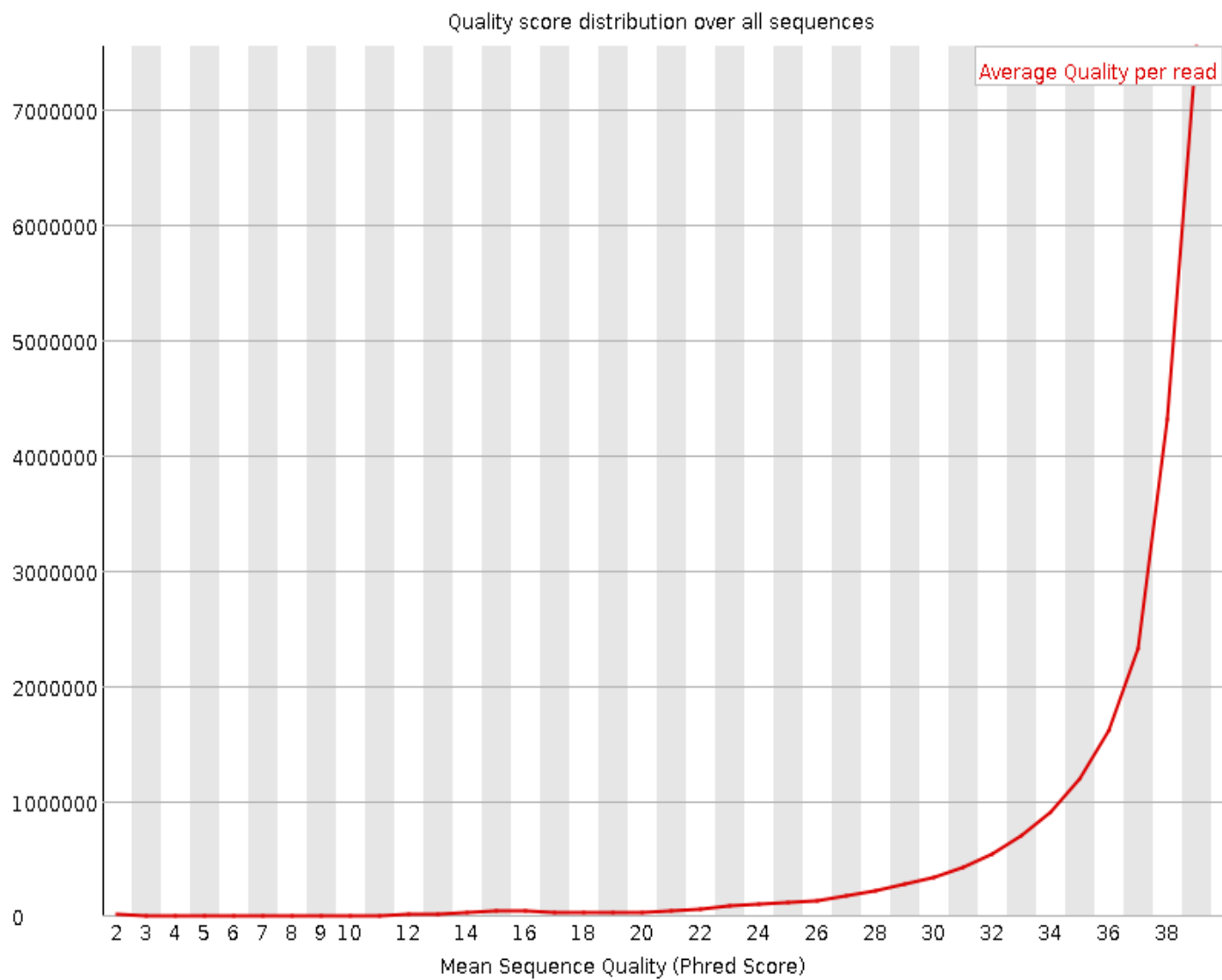| Measure	Value
Filename	P0_1_2.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	21577562
Sequences flagged as poor quality	0
Sequence length	40
%GC	49

✅ 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

❌Per base sequence content

✅ Per sequence GC content

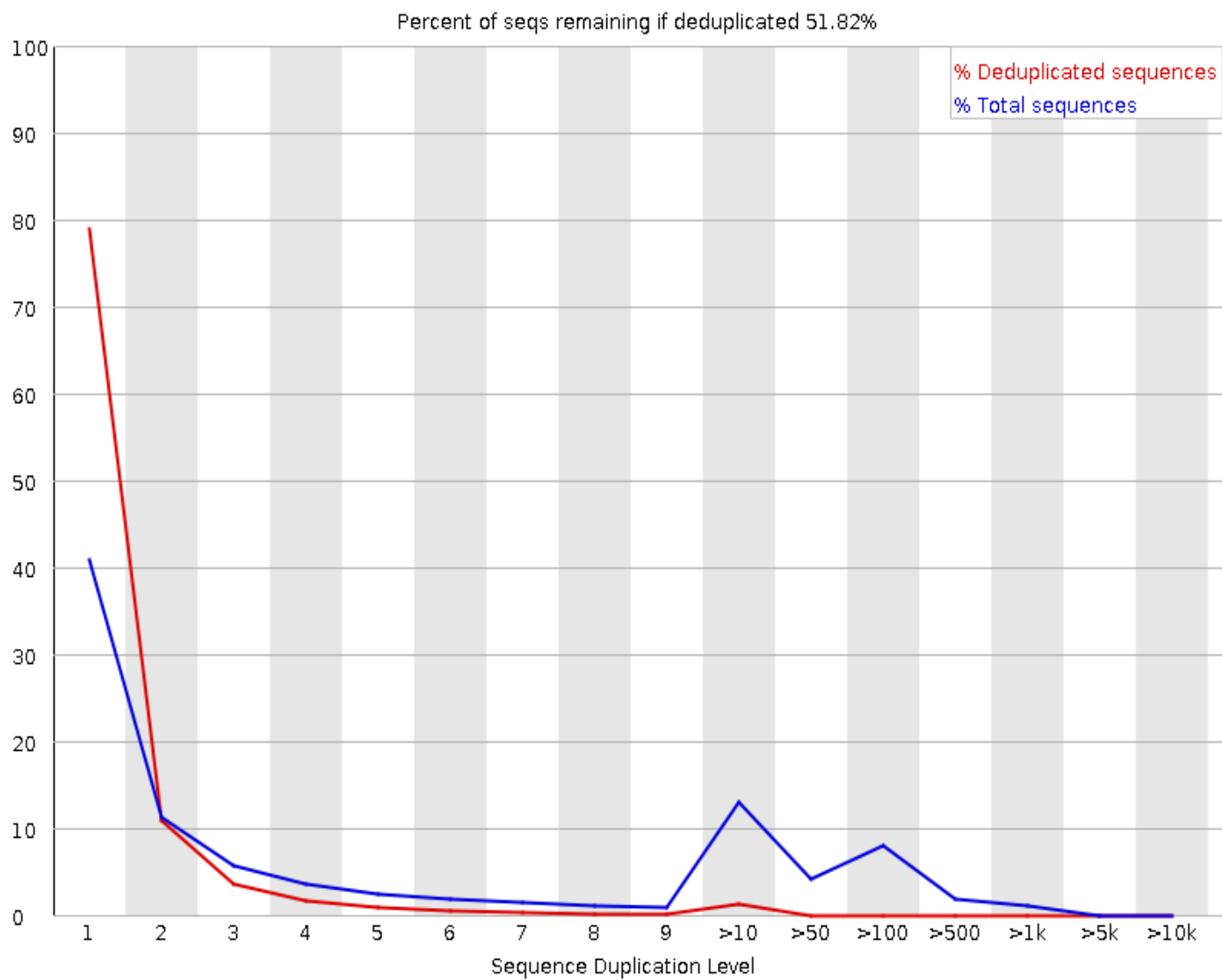# ✅Per base N content

✅ Sequence Length Distribution

Distribution of sequence lengths over all sequences

⚠️ Sequence Duplication Levels

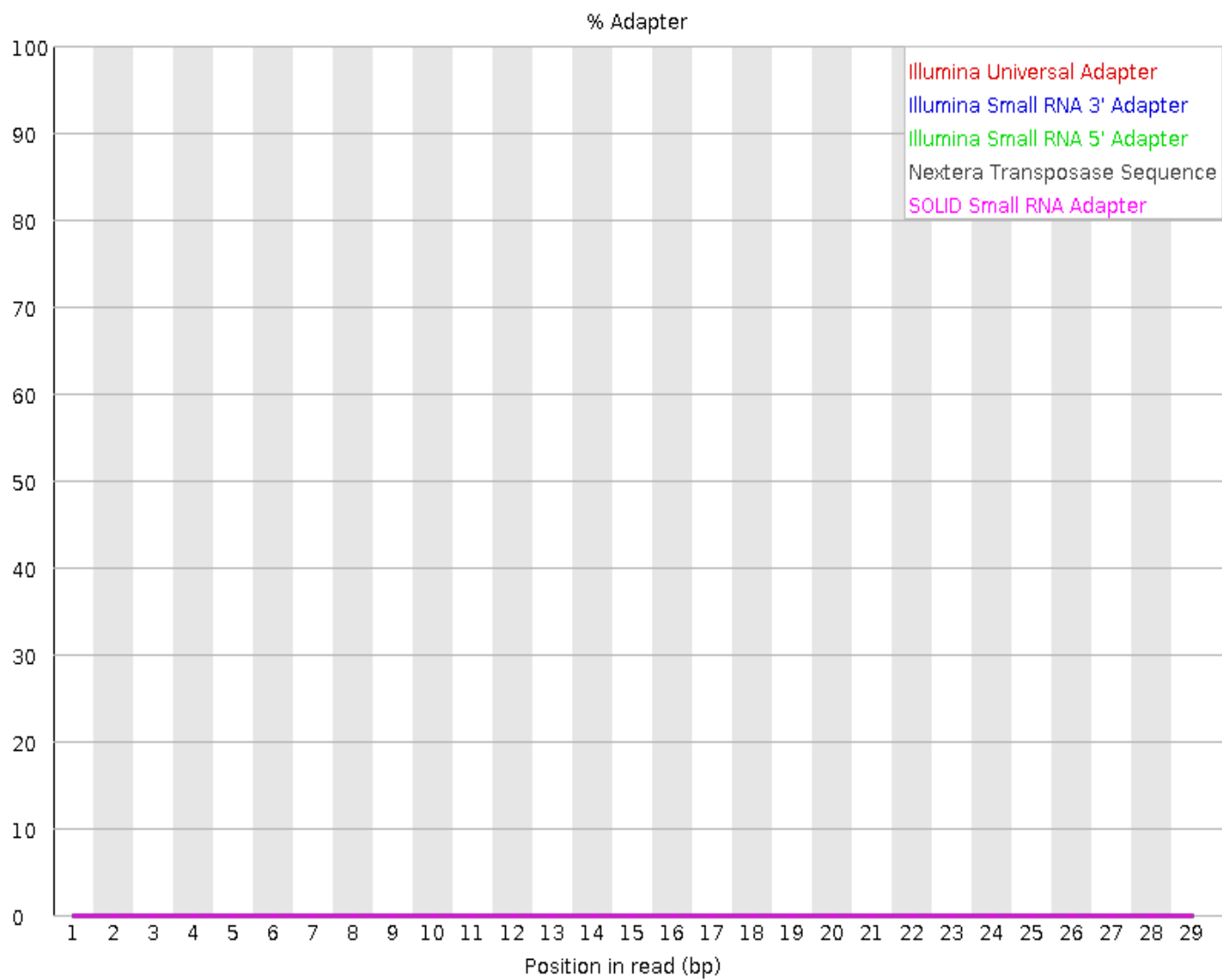Percent of seqs remaining if deduplicated 51.82%

✅ Overrepresented sequences

No overrepresented sequences

✅ Adapter Content

Produced by [FastQC](#) (version 0.11.7)