FastQC Report

Summary

✅ Basic Statistics

✅ Per base sequence quality

✅ Per sequence quality scores
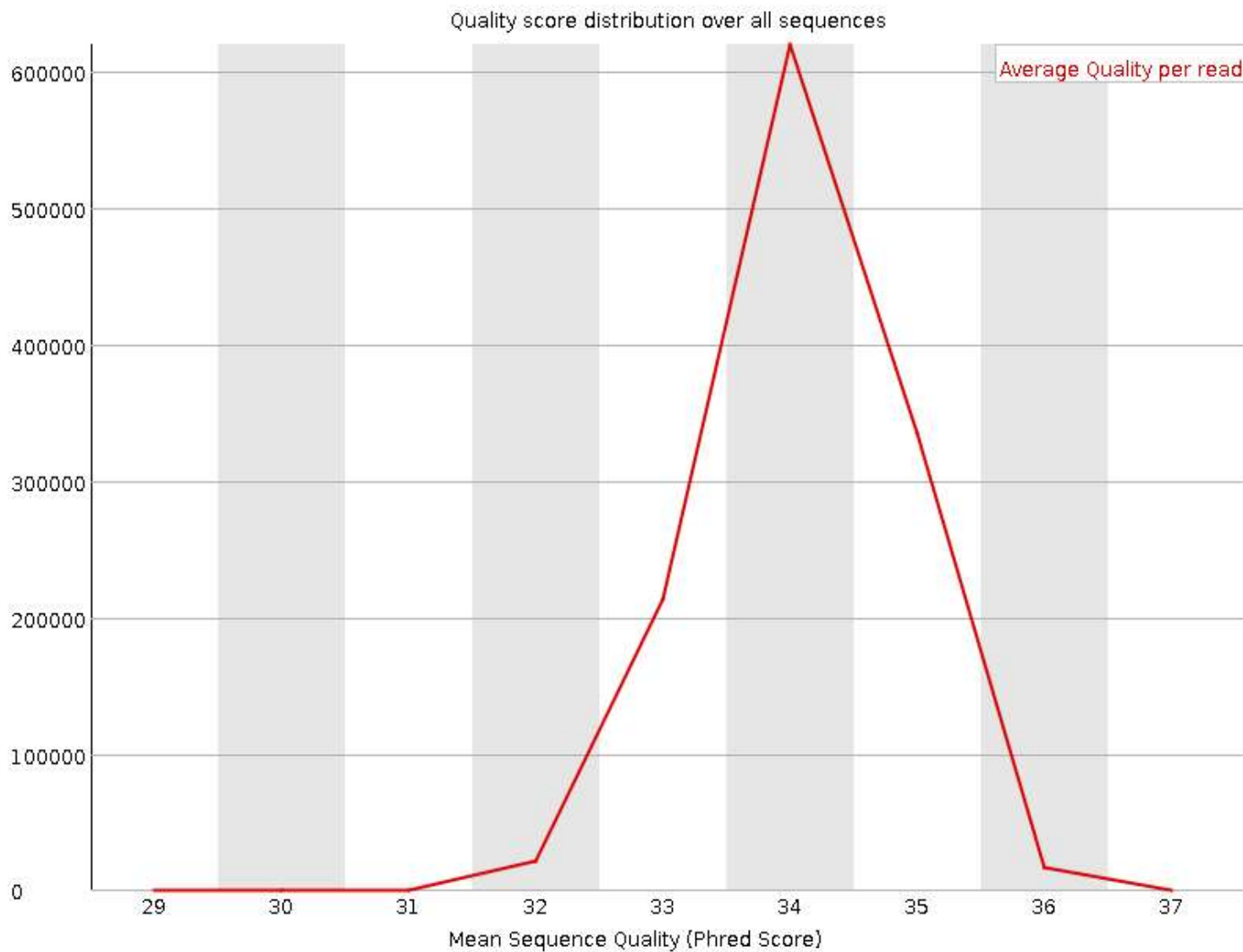
✅ Per base sequence content

✅ Per sequence GC content
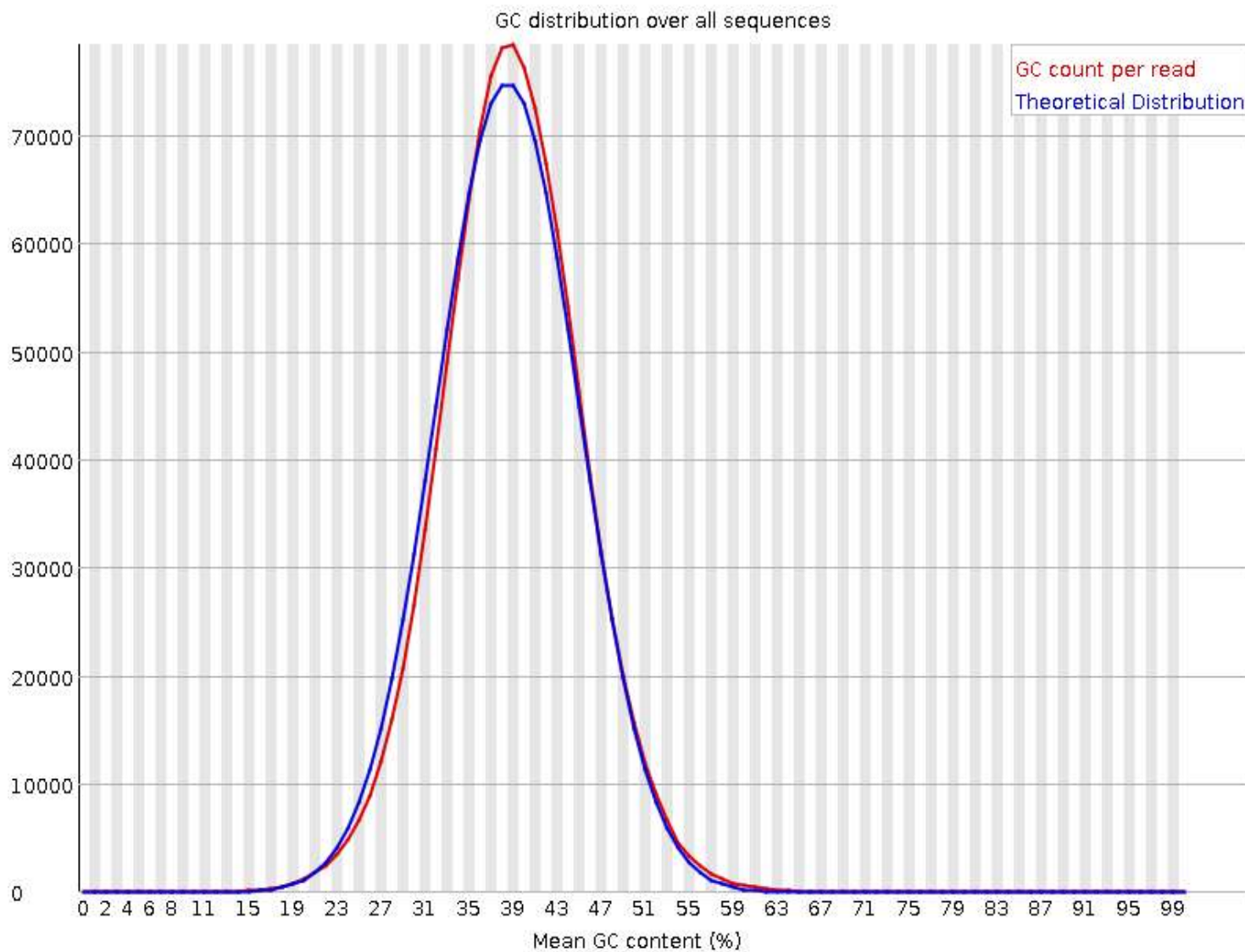
✅ Per base N content
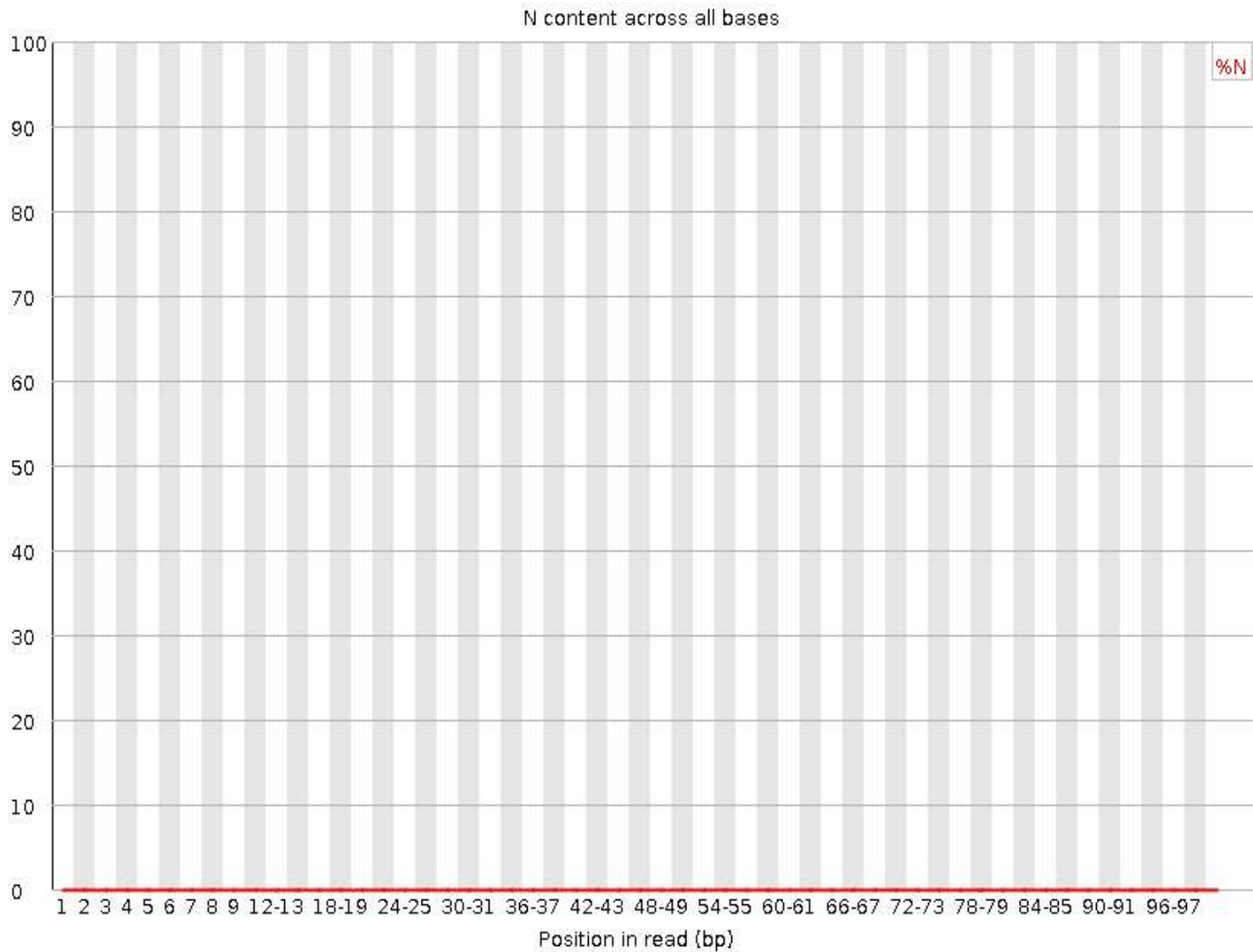
✅ Sequence Length Distribution
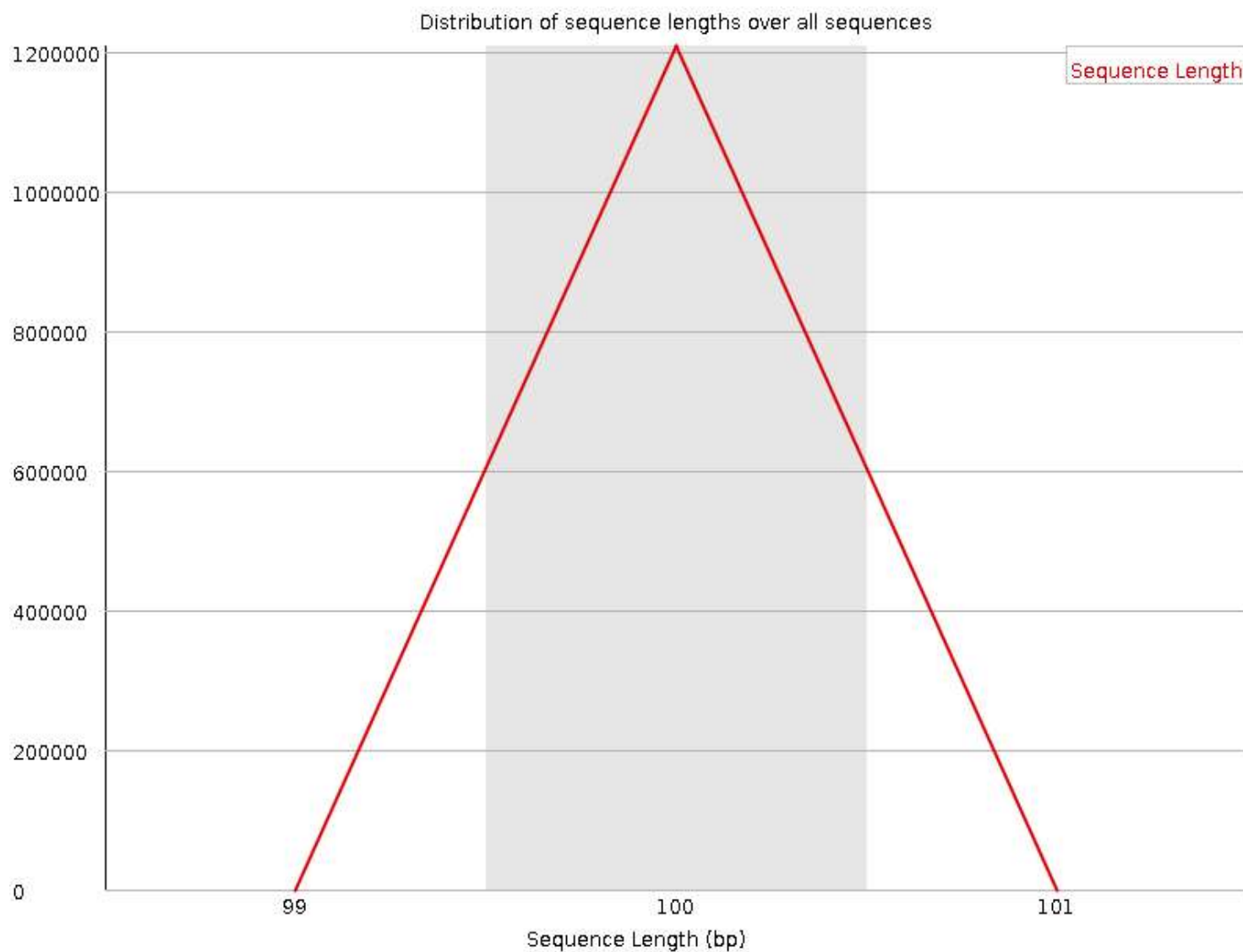
✅ Sequence Duplication Levels

✅ Overrepresented sequences

✅ Adapter Content

⚠️ Kmer Content

✅ Basic Statistics

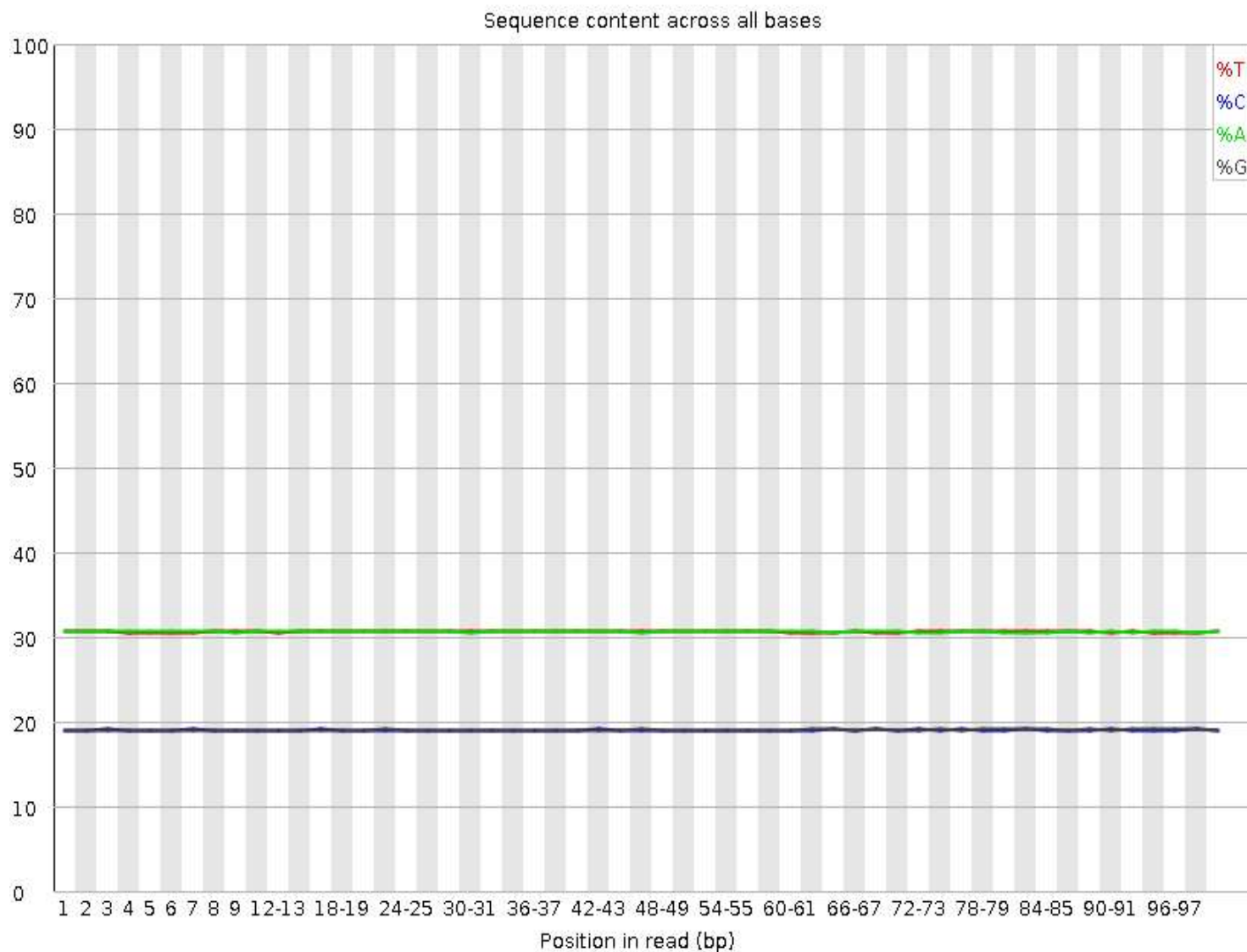| Measure	Value
Filename	A0167658L_1.fq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	1208670
Sequences flagged as poor quality	0
Sequence length	100
%GC	38

✅ Per base sequence quality

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

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

✅Per base N content

✅ Sequence Length Distribution

Distribution of sequence lengths over all sequences

Sequence Duplication Levels

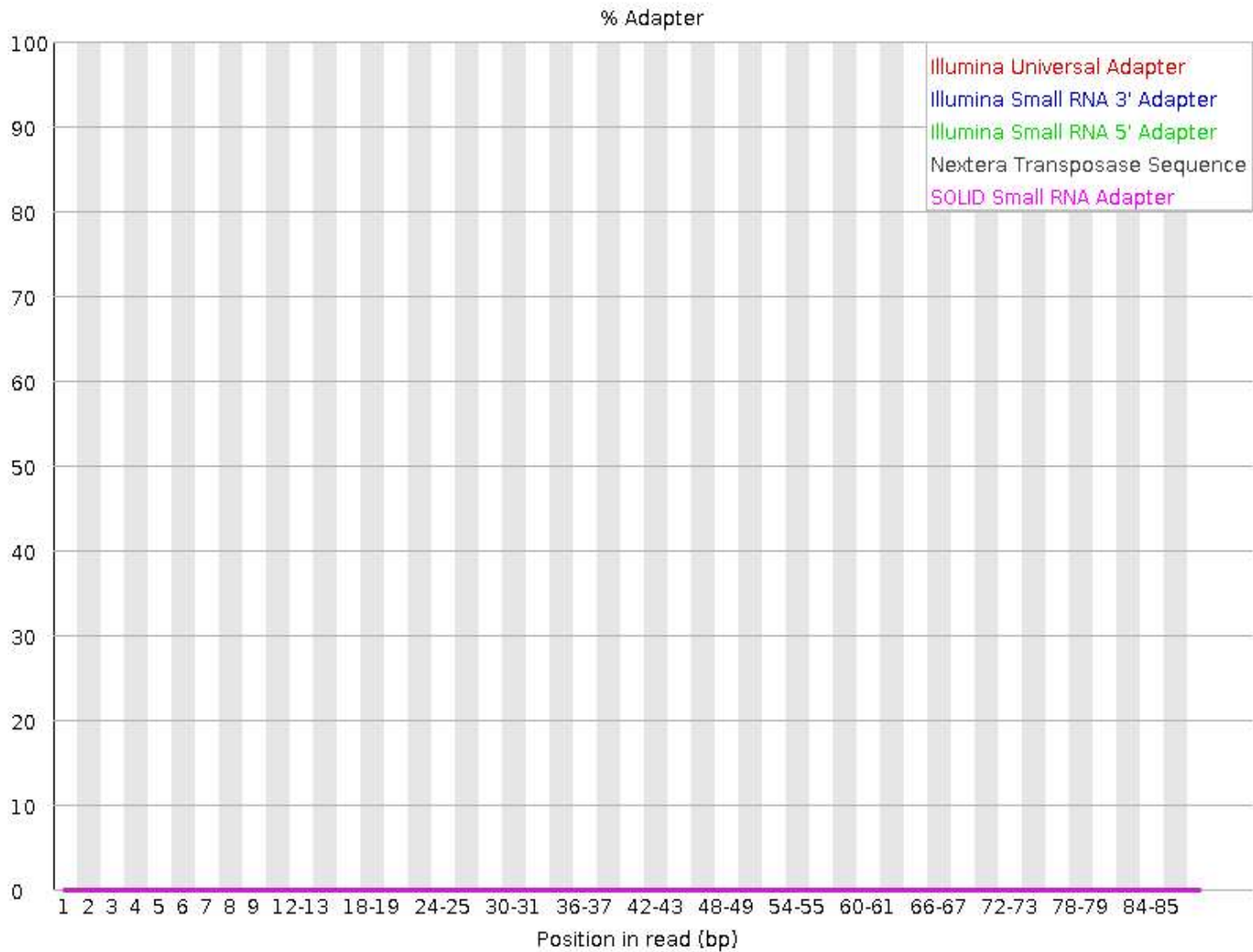Percent of seqs remaining if deduplicated 98.62%

Overrepresented sequences

No overrepresented sequences

Adapter Content

⚠️Kmer Content
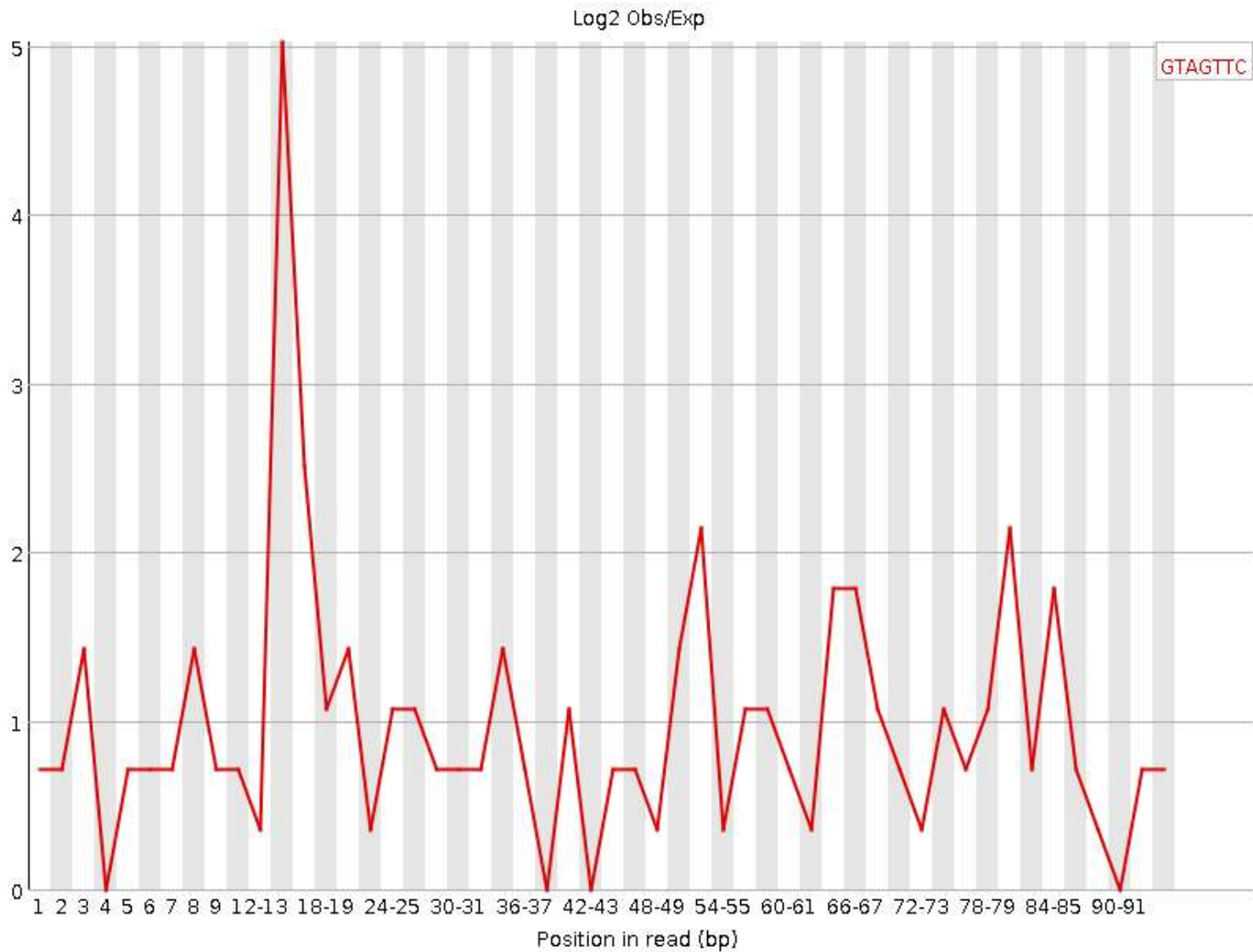
Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
GTAGTTC	655	0.0044305855	5.0229006	14-15

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