FastQC Report

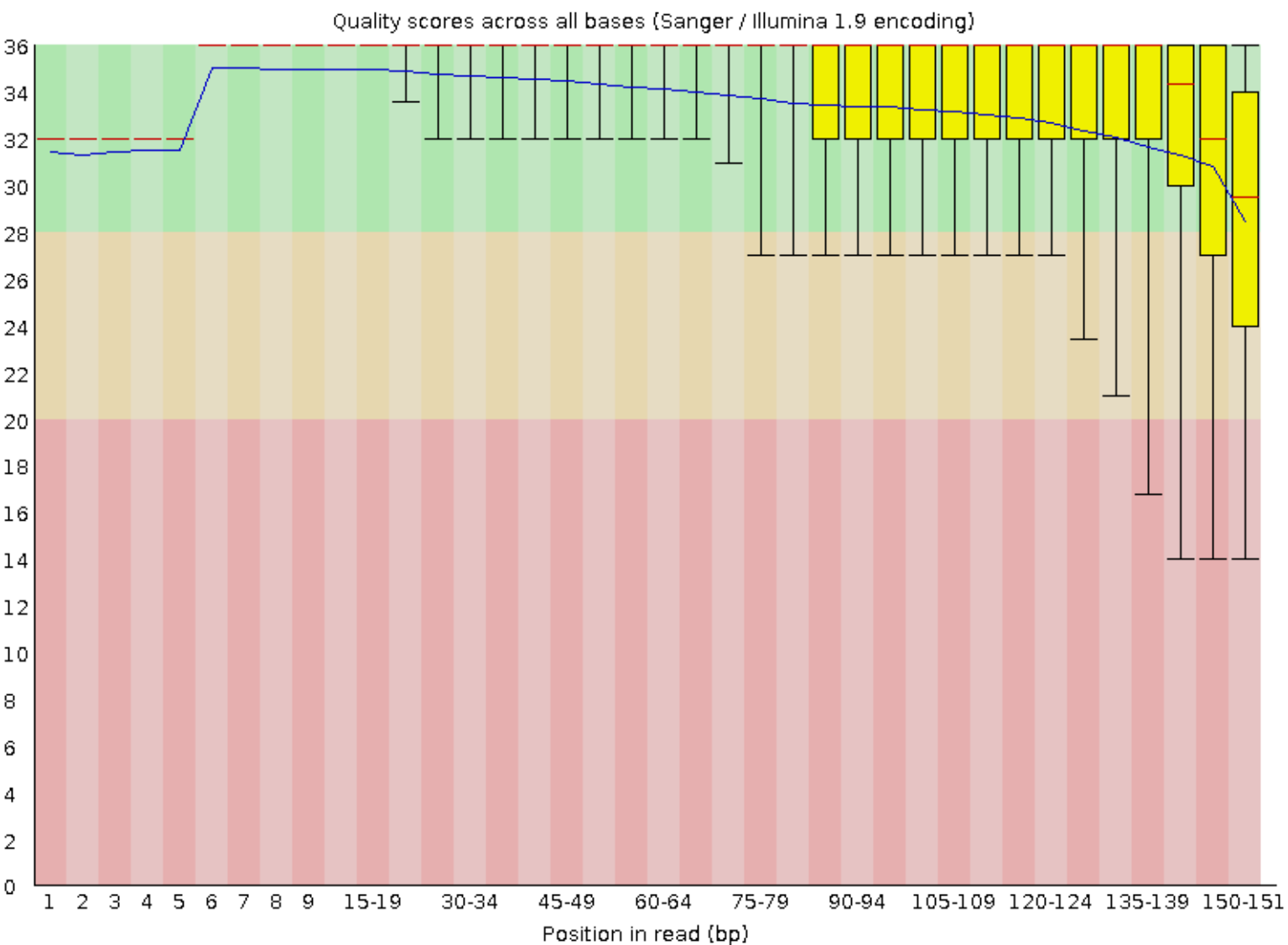# Summary

✅ [Basic Statistics](#)

✅ [Per base sequence quality](#)

✅ [Per sequence quality scores](#)

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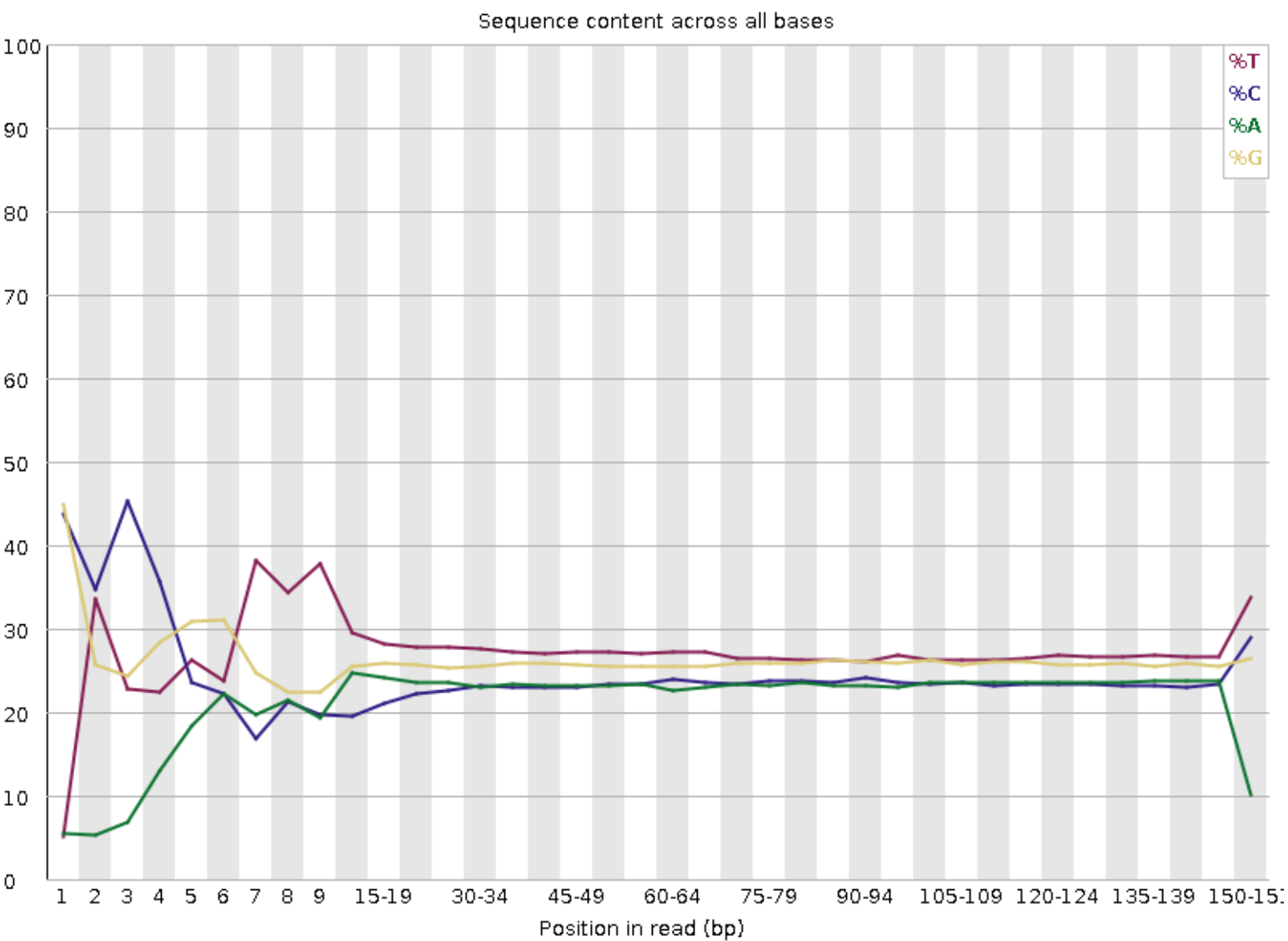
⚠️ [Per sequence GC content](#)
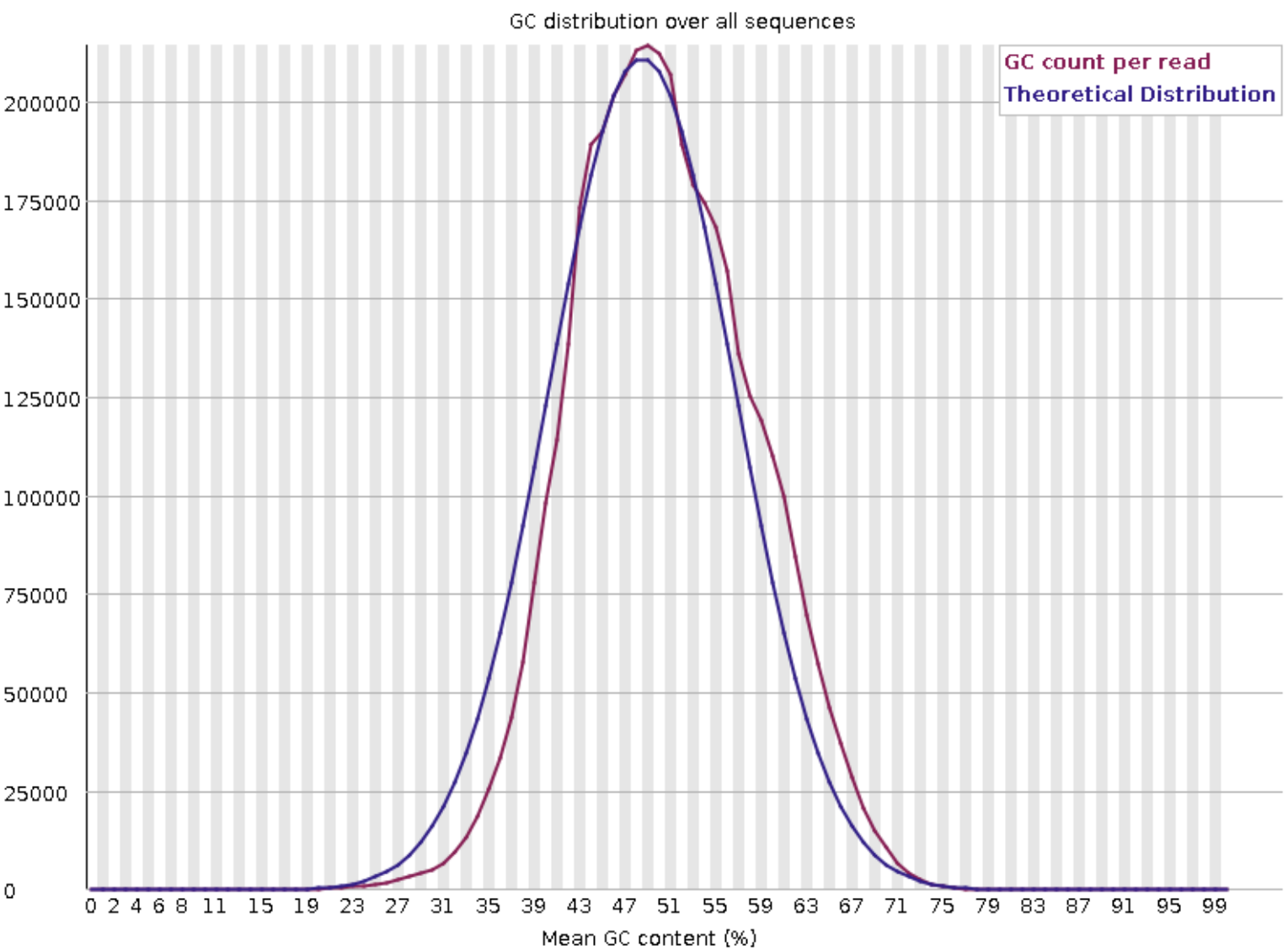
✅ [Per base N content](#)
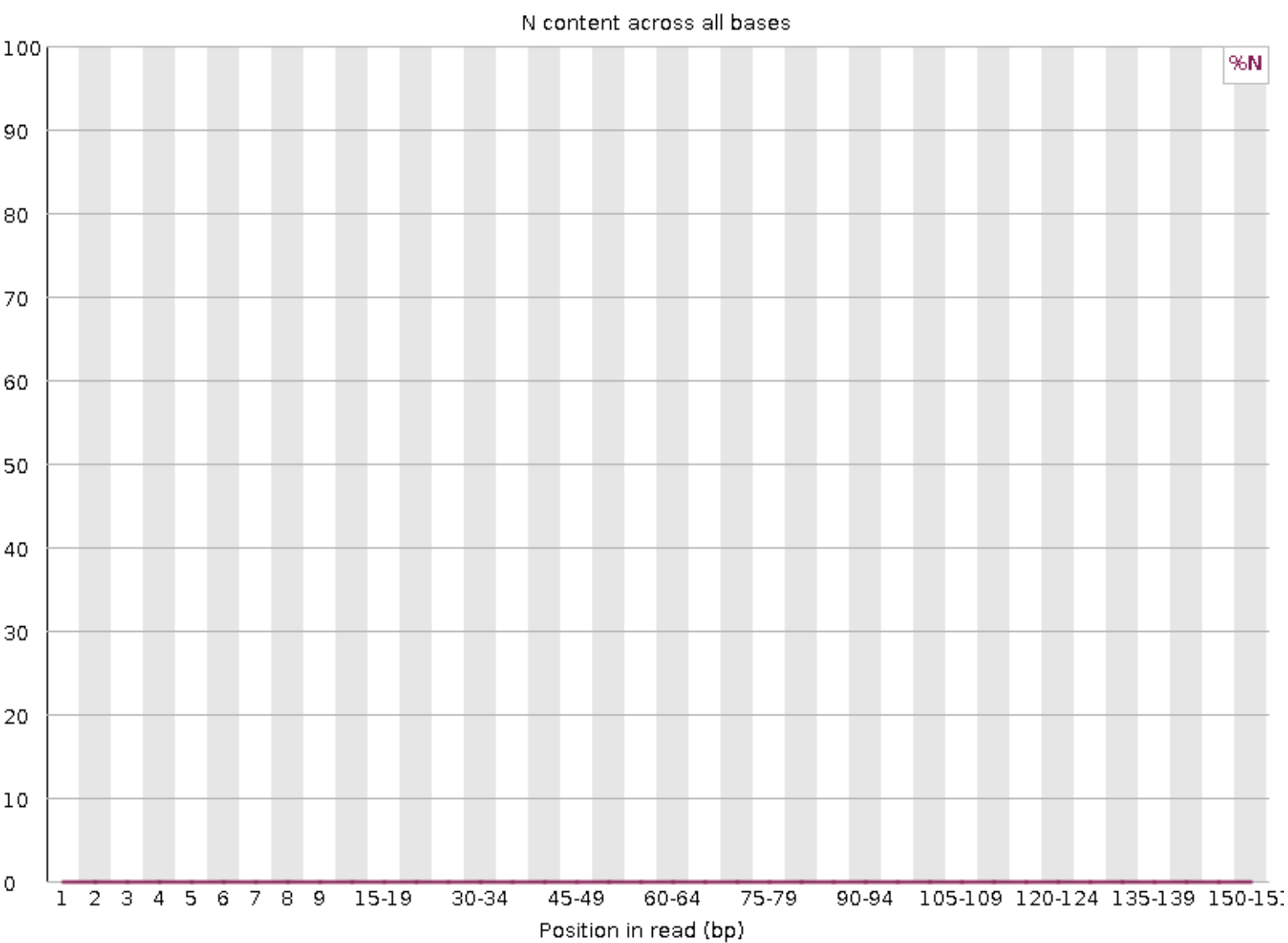
⚠️ [Sequence Length Distribution](#)
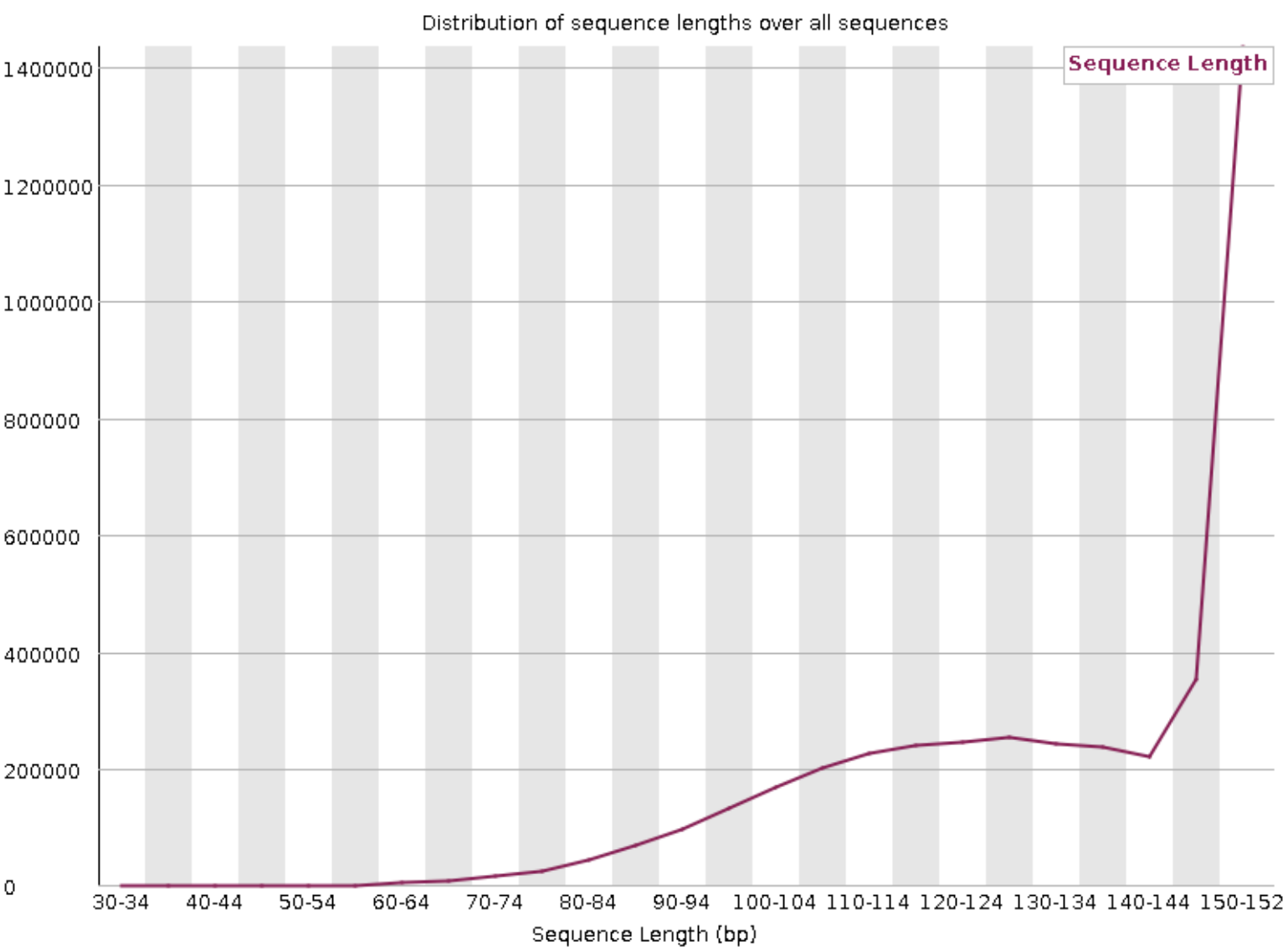
❌ [Sequence Duplication Levels](#)
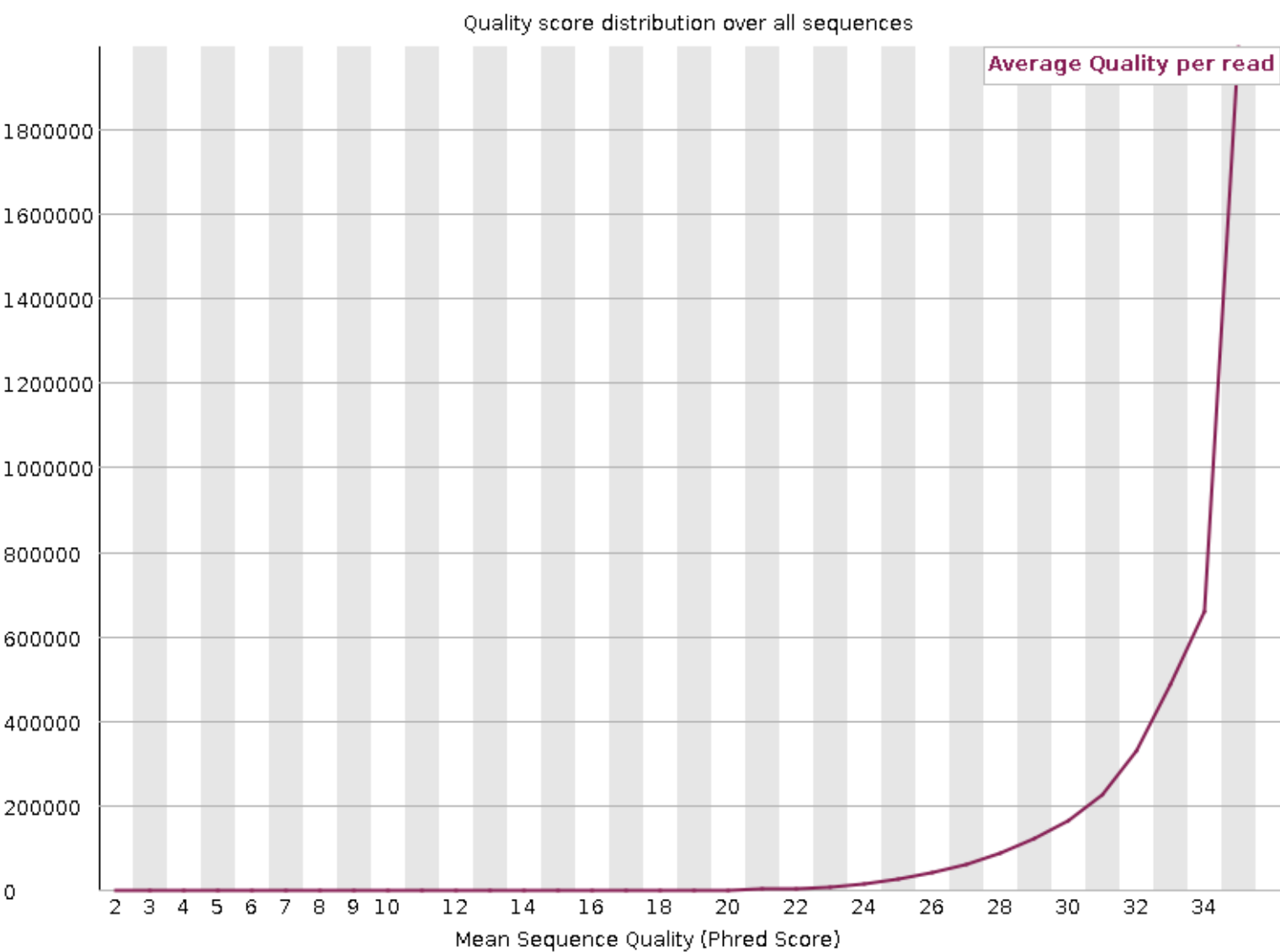
⚠️ [Overrepresented sequences](#)

✅ [Adapter Content](#)

✅ Basic Statistics

Measure	Value
Filename	SRR11412215_pass.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	4260400
Total Bases	558.2 Mbp
Sequences flagged as poor quality	0
Sequence length	35-151
%GC	49

Per base sequence quality

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

Per sequence quality scores

Quality score distribution over all sequences

Per base sequence content

Sequence content across all bases

Per sequence GC content

GC distribution over all sequences

Per base N content

N content across all bases

Sequence Length Distribution

Distribution of sequence lengths over all sequences

Sequence Duplication Levels

Percent of seqs remaining if deduplicated 39.43%

Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GGGCAGGATAGTTCAGACGGTTTCTATTTCCTGAGCGTCTGAGATGTTAG	12710	0.29832879541827056	No Hit
GTCTGTTAGTAGTATAGTGATGCCAGCAGCTAGGACTGGGAGAGATAGGA	10302	0.24180828091259038	No Hit
CCCCTTACTCAGCTTGAACTTGTCGCCCTCTTGGCAGGAGTACTTGTGGA	5090	0.1194723500140832	No Hit
GGGAGGGCGATGAGGACTAGGATGATGGCGGGCAGGATAGTTCAGACGGT	4824	0.11322880480706037	No Hit
CCCGTATCGAAGGCCTTTTTGGACAGGTGGTGTGTGGTGGCCTTGGTATG	4794	0.11252464557318562	No Hit
GCCTGGTTCTAGGAATAATGGGGGAAGTATGTAGGAGTTGAAGATTAGTC	4649	0.10912120927612431	No Hit
GTGGTGATTAGTCGGTTGTTGATGAGATATTTGGAGGTGGGGATCAATAG	4613	0.10827621819547462	No Hit
GGGGCAATGAATGAAGCGAACAGATTTTCGTTCATTTTGGTTCTCAGGGT	4498	0.10557694113228805	No Hit

Sequence	Count	Percentage	Possible Source
CCCCCTTACTCAGCTTGAACTTGTCGCCCTCTTGGCAGGAGTACTTGTGG	4314	0.10125809783118955	No Hit

✅ Adapter Content