FastQC Report

Sat 13 Dec 2025
LNCAP_Hypoxia_S1.fastq.gz

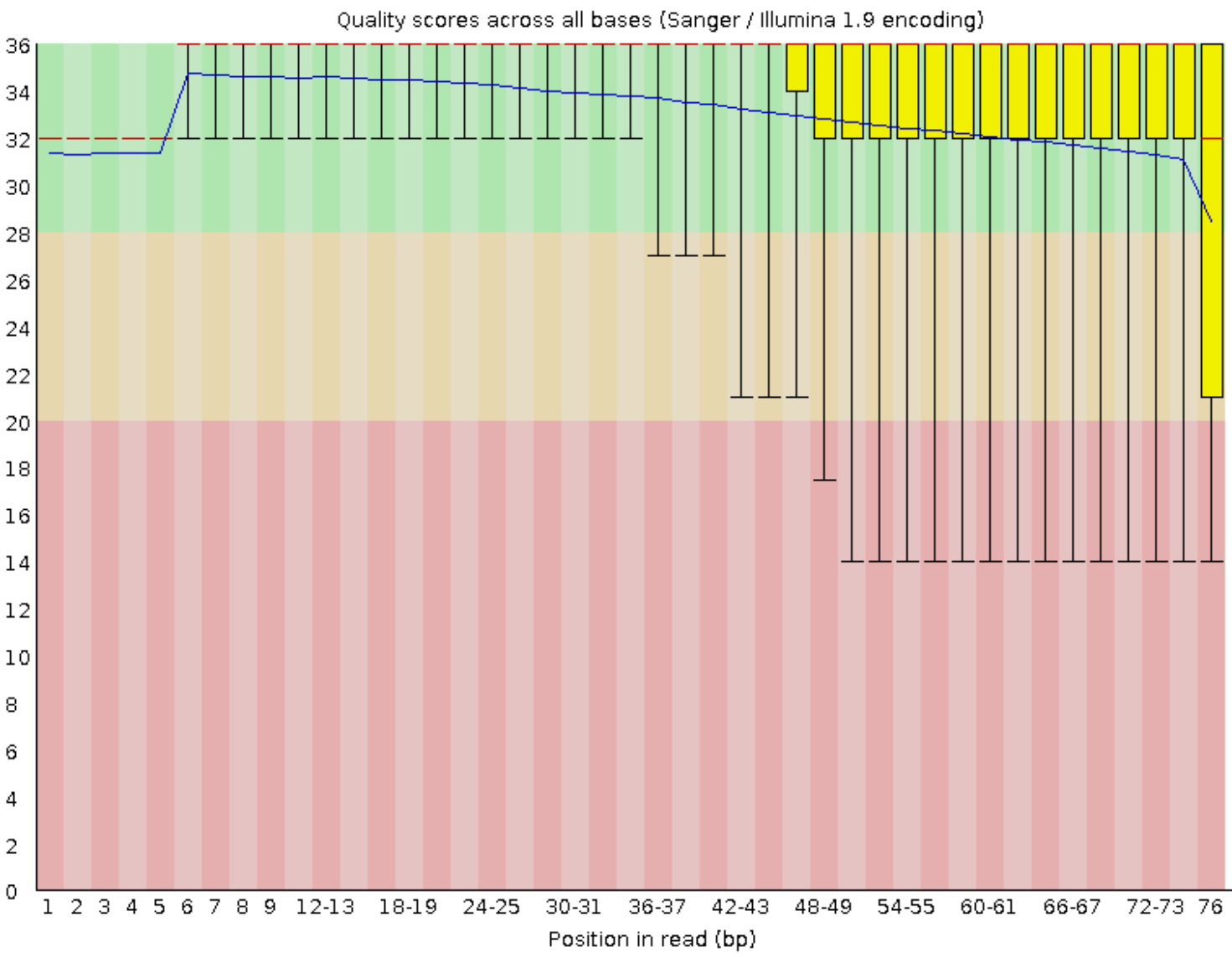
Summary

- 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

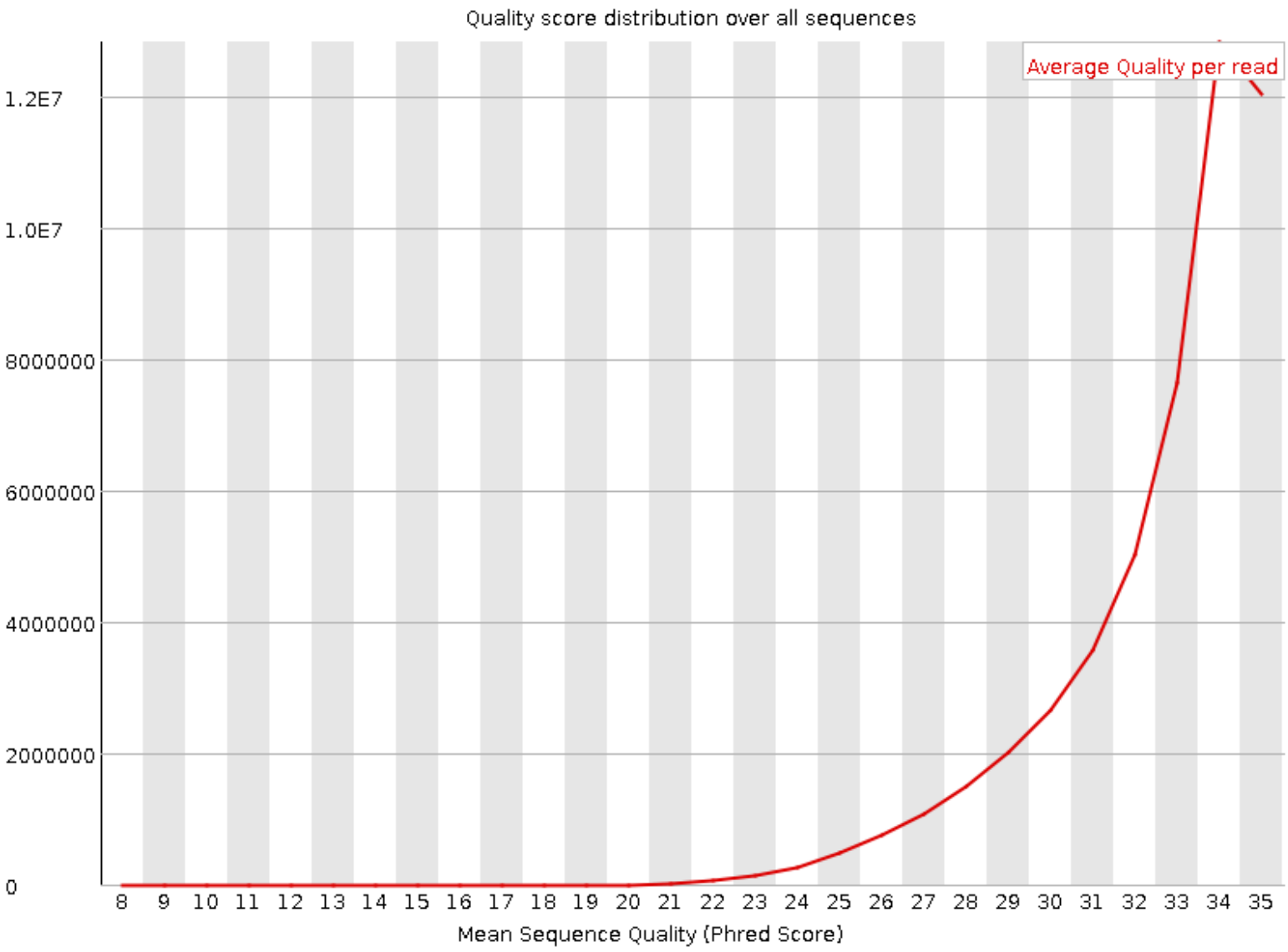
Basic Statistics

Measure	Value
Filename	LNCAP_Hypoxia_S1.fastq.gz
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	50364498
Sequences flagged as poor quality	0
Sequence length	76
%GC	46

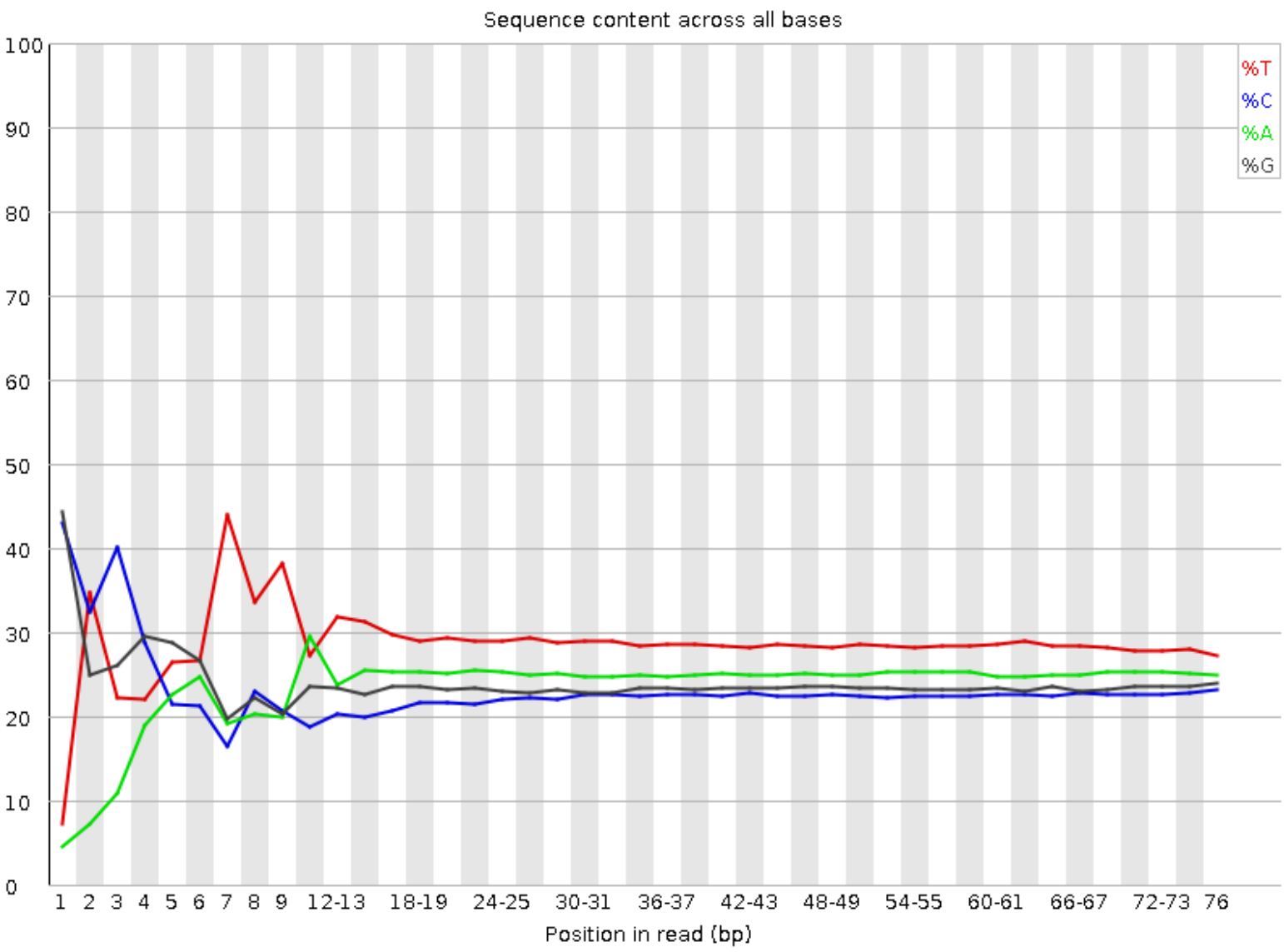
Per base sequence quality



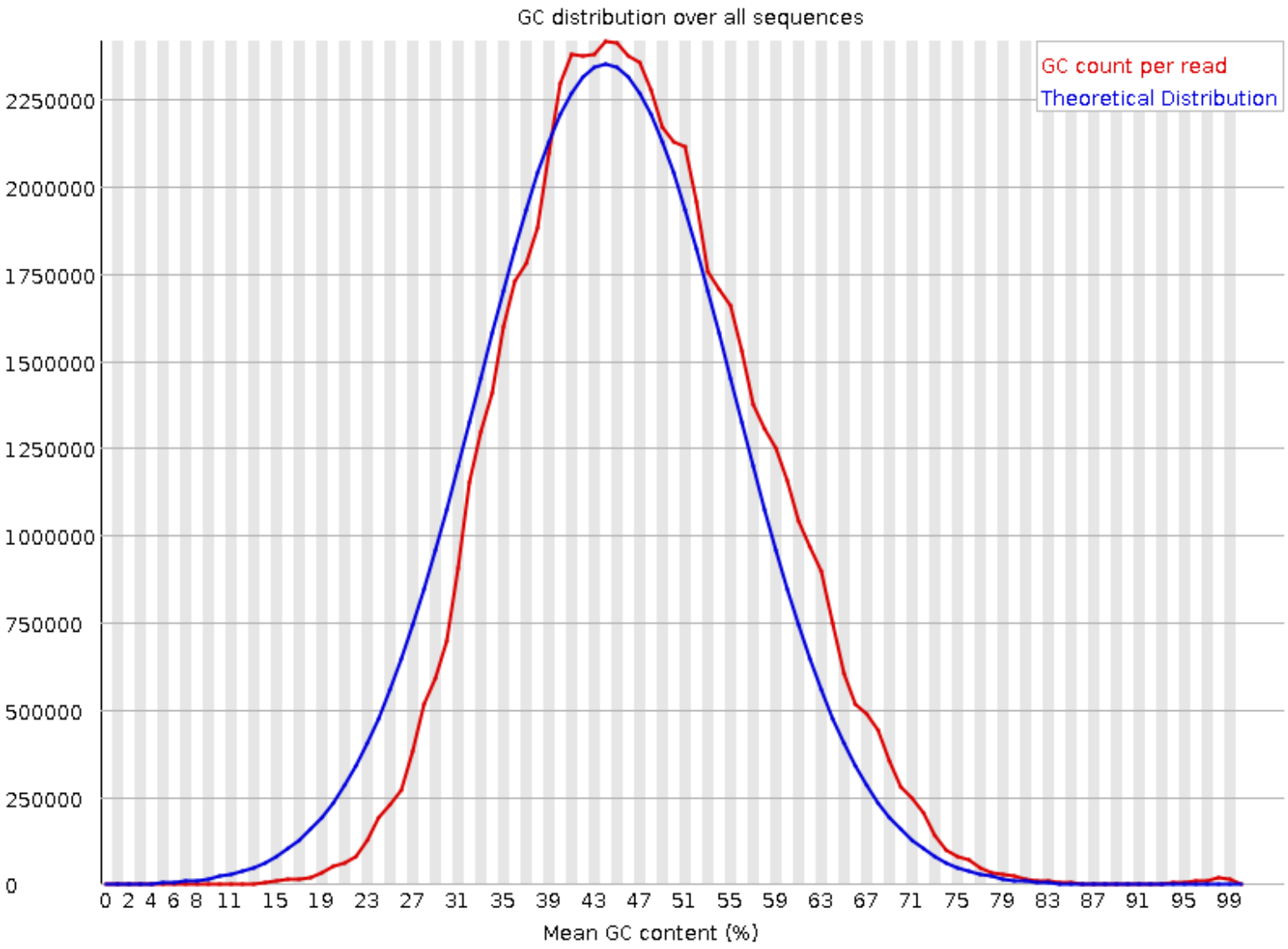
Per sequence quality scores



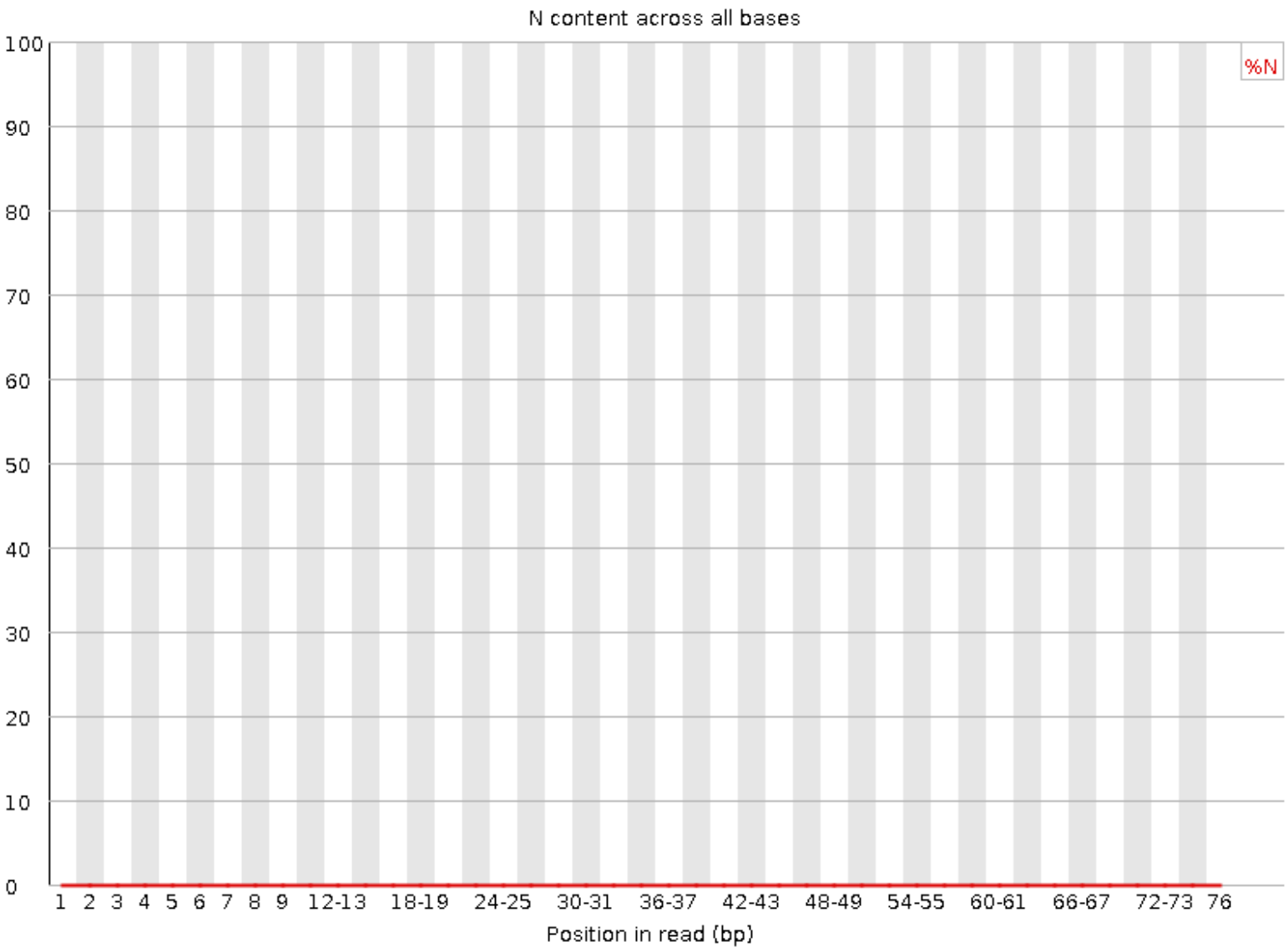
Per base sequence content



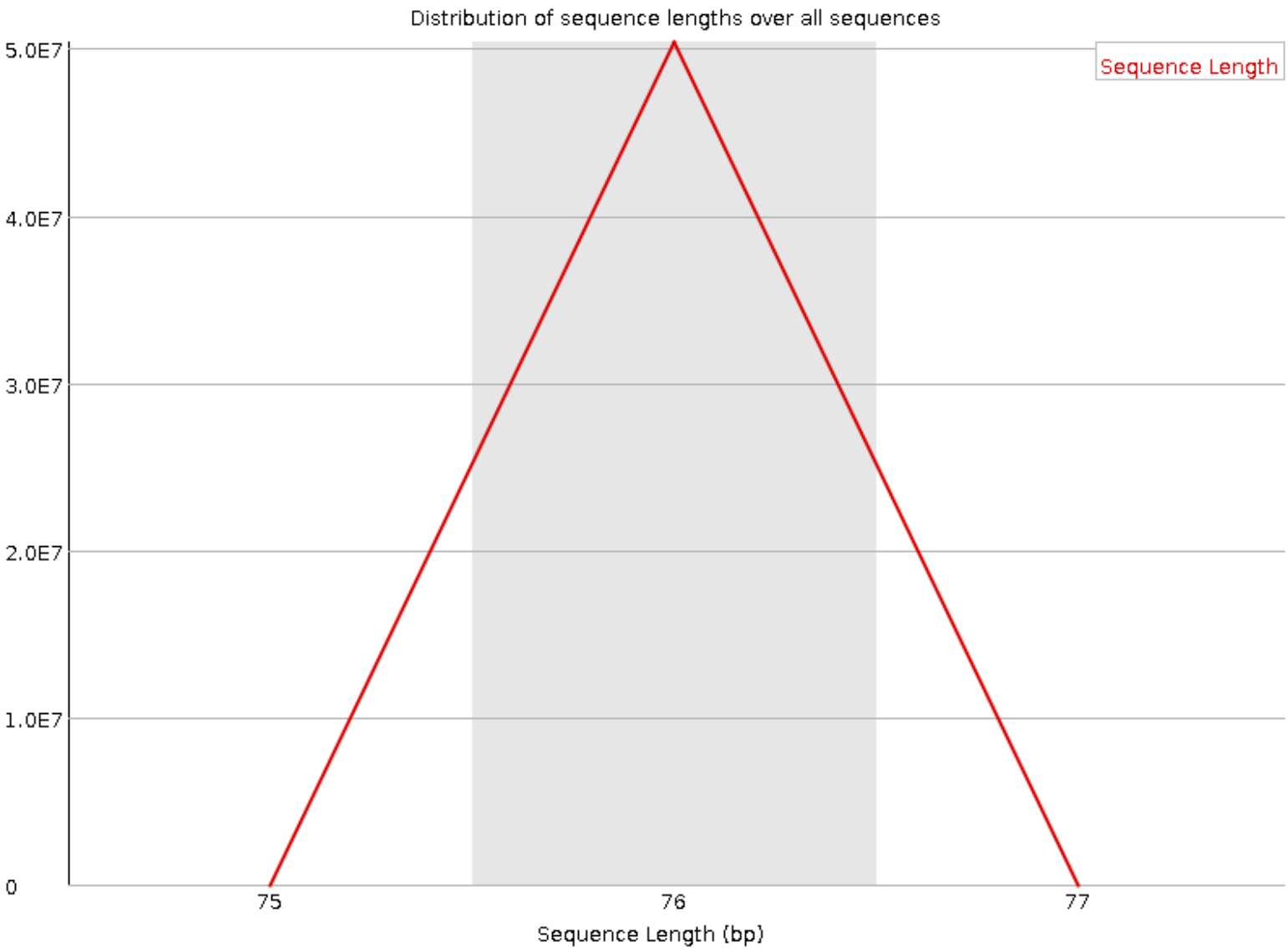
Per sequence GC content



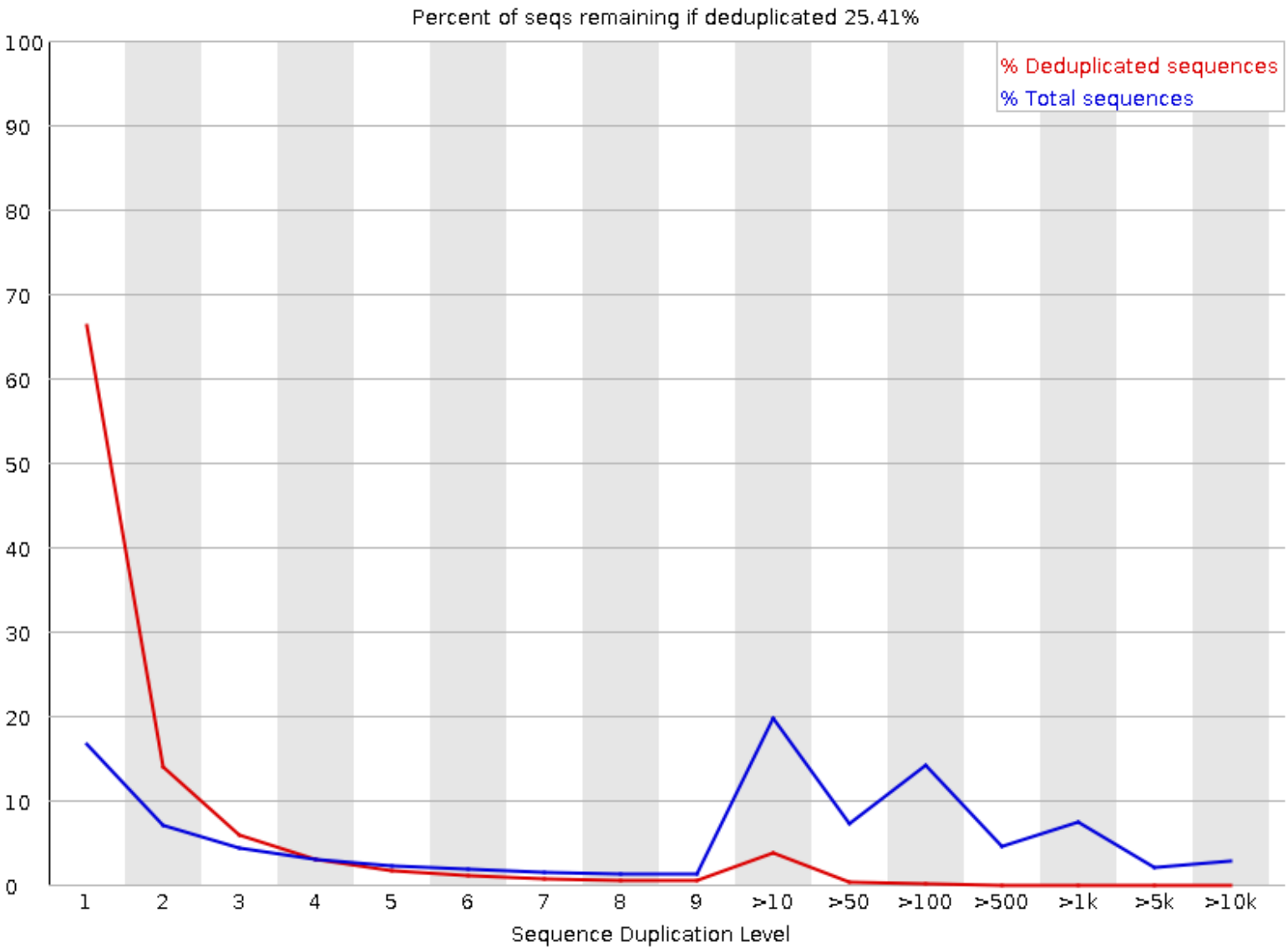
Per base N content



Sequence Length Distribution



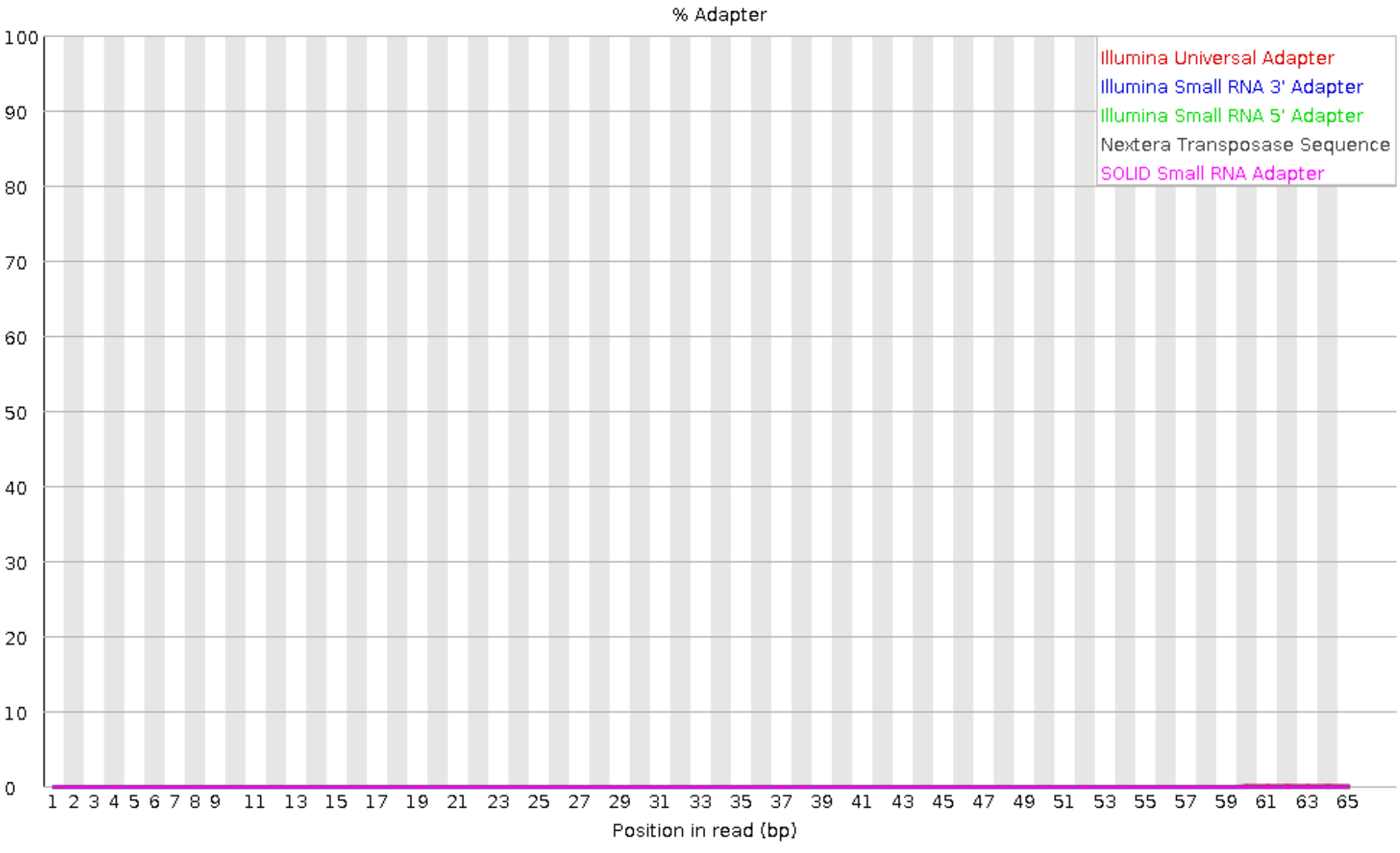
Sequence Duplication Levels



Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GGCGGATCTTGAAGTTGGCCTTGATGCCGTTCTTCTGCTTGTCGGCGGTG	82343	0.1634941343007132	No Hit
GGTAAGGCGAGGTTAGCGAGGCTTGCTAGAAGTCATCAAAAAGCTATTAG	53367	0.10596154457848464	No Hit
GCCCTCTTGAACTCTCTCTTCAAAGTTCTTTTCAACTTTCCCTTACGGTA	51259	0.10177605661829489	No Hit

Adapter Content



Produced by FastQC (version 0.11.9)