

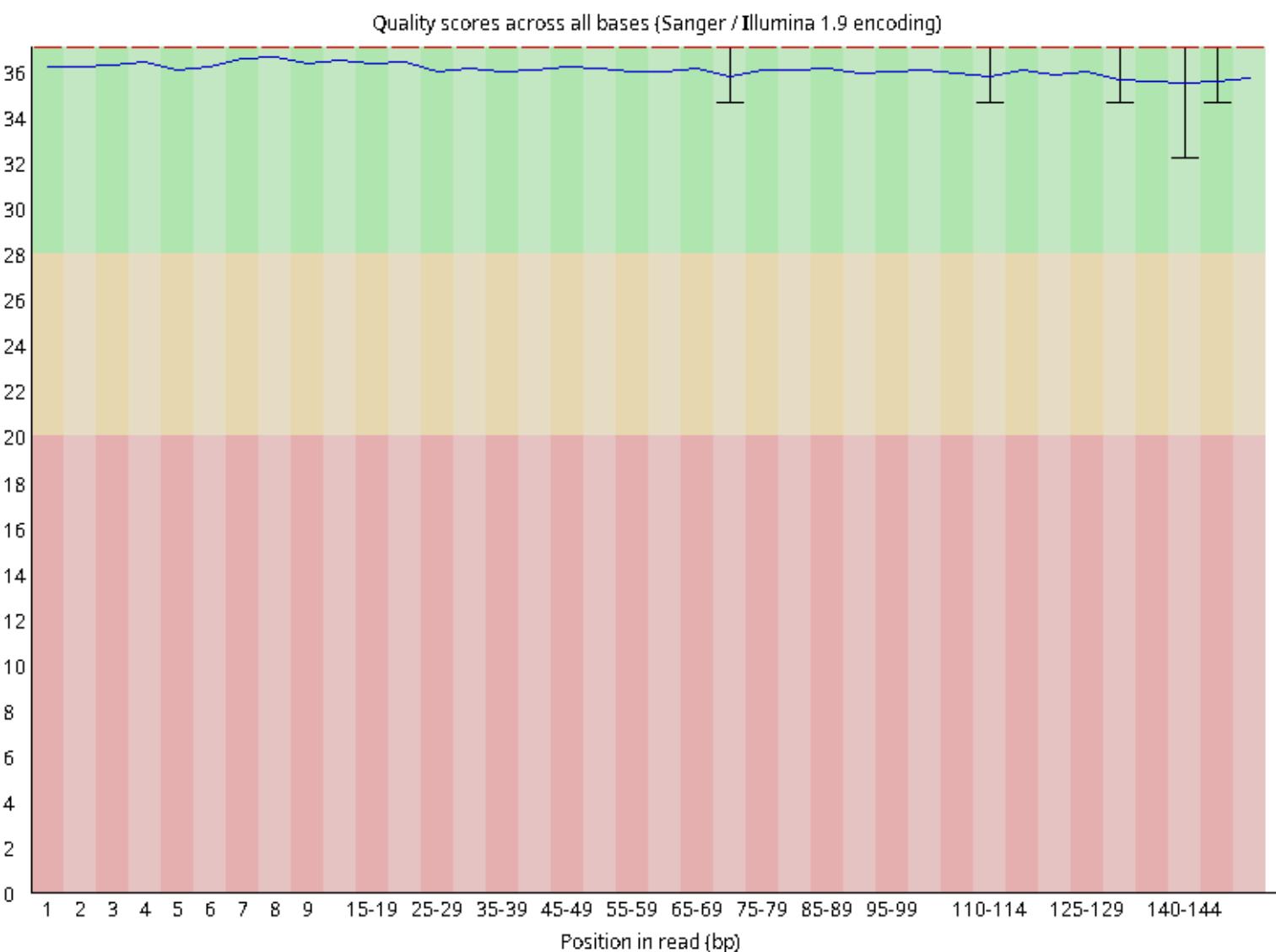
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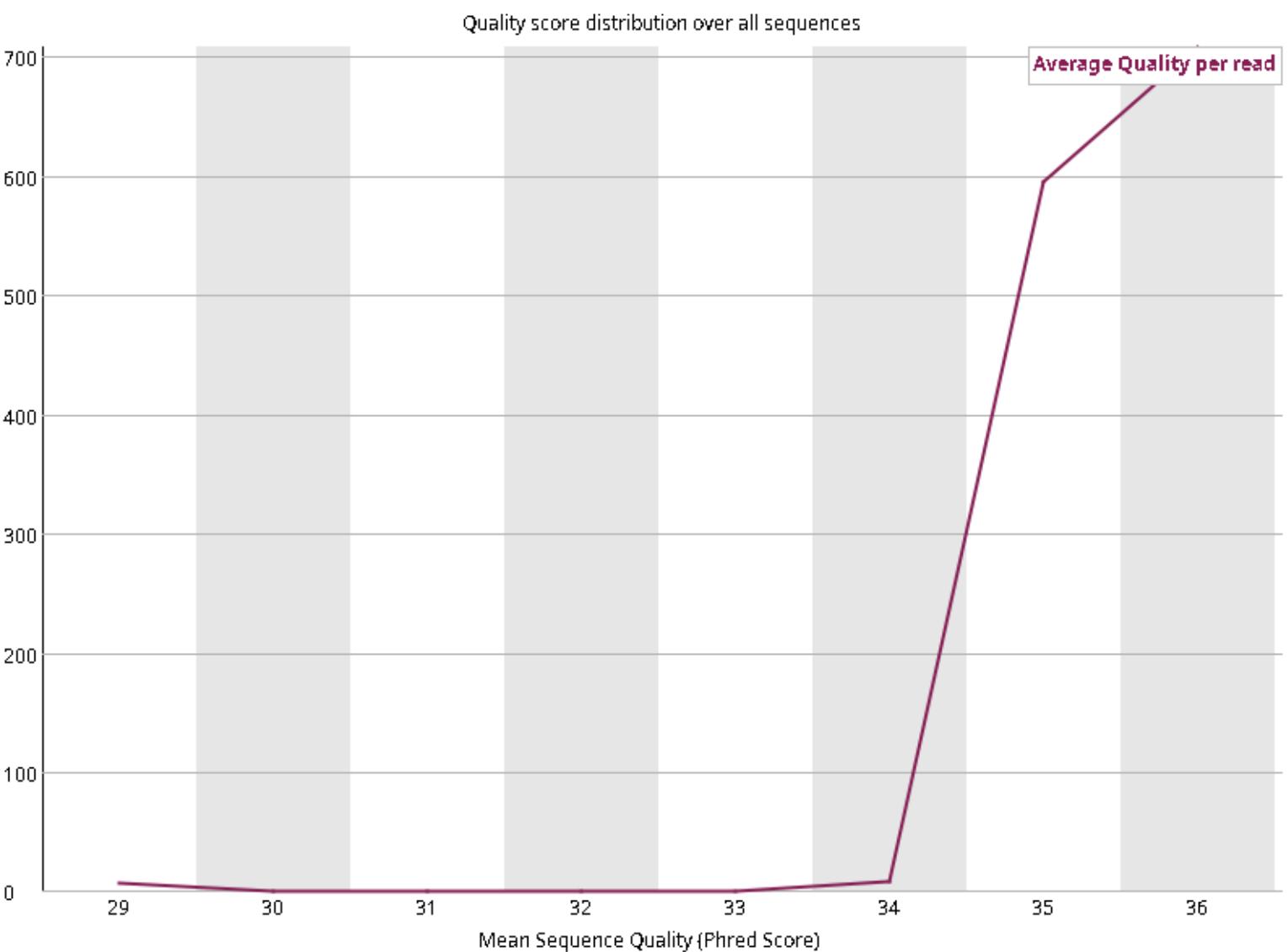
Basic Statistics

| Measure | Value |
|-----------------------------------|-------------------------|
| Filename | AbrahamSimpson_R2.fastq |
| File type | Conventional base calls |
| Encoding | Sanger / Illumina 1.9 |
| Total Sequences | 1320 |
| Total Bases | 199.3 kbp |
| Sequences flagged as poor quality | 0 |
| Sequence length | 151 |
| %GC | 46 |

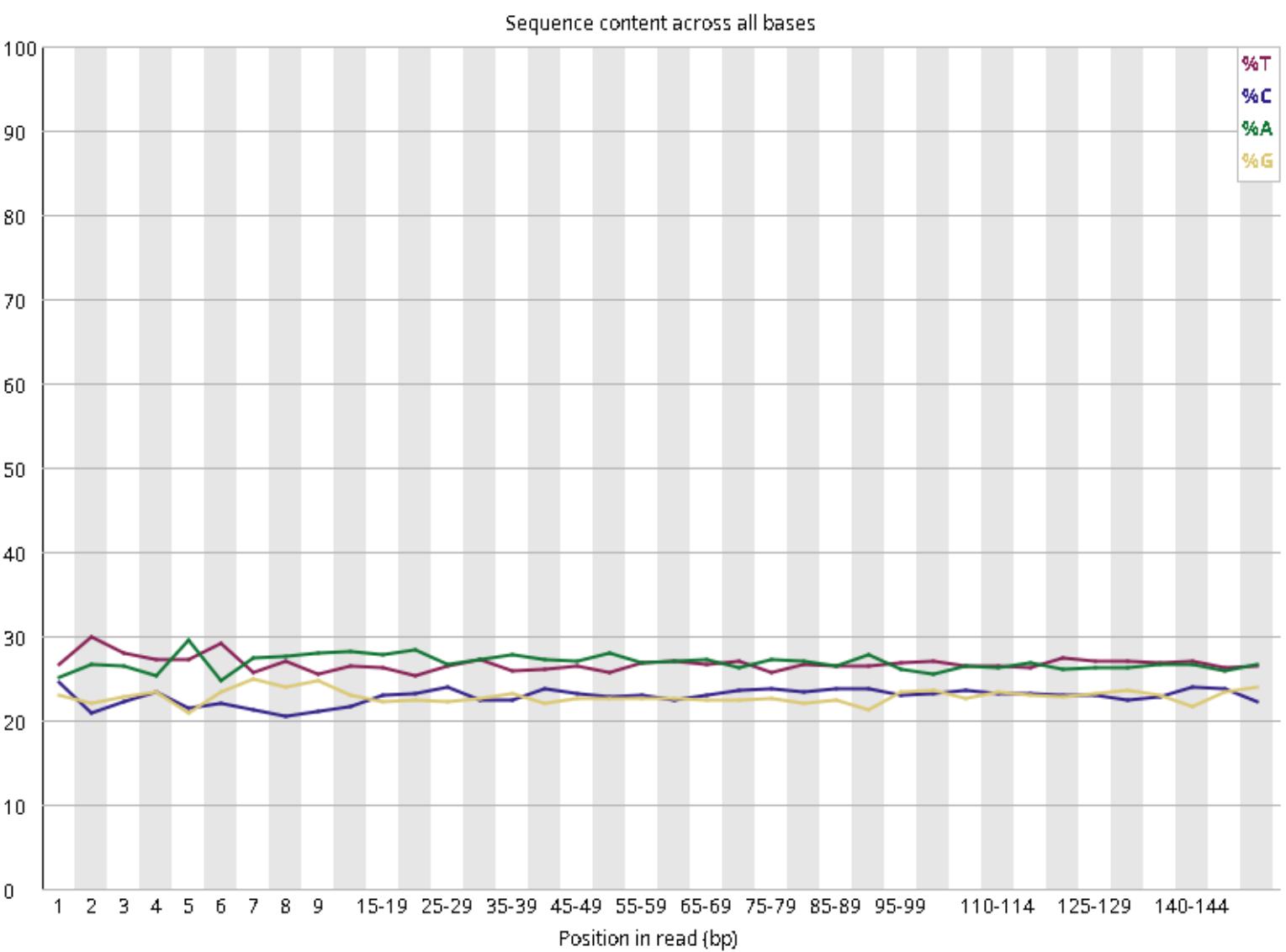
Per base sequence quality



Per sequence quality scores



Per base sequence content

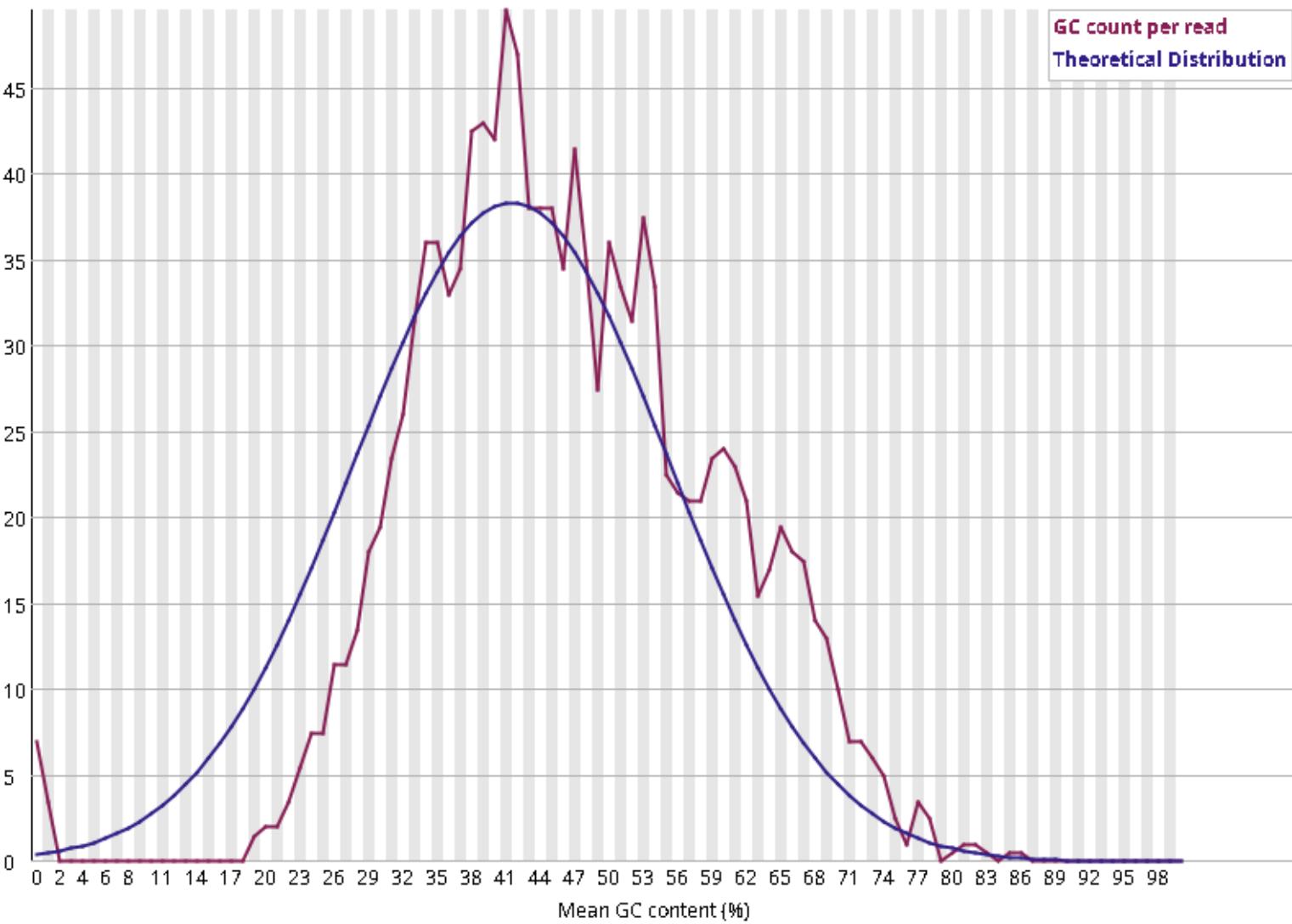




Per sequence GC content

GC distribution over all sequences

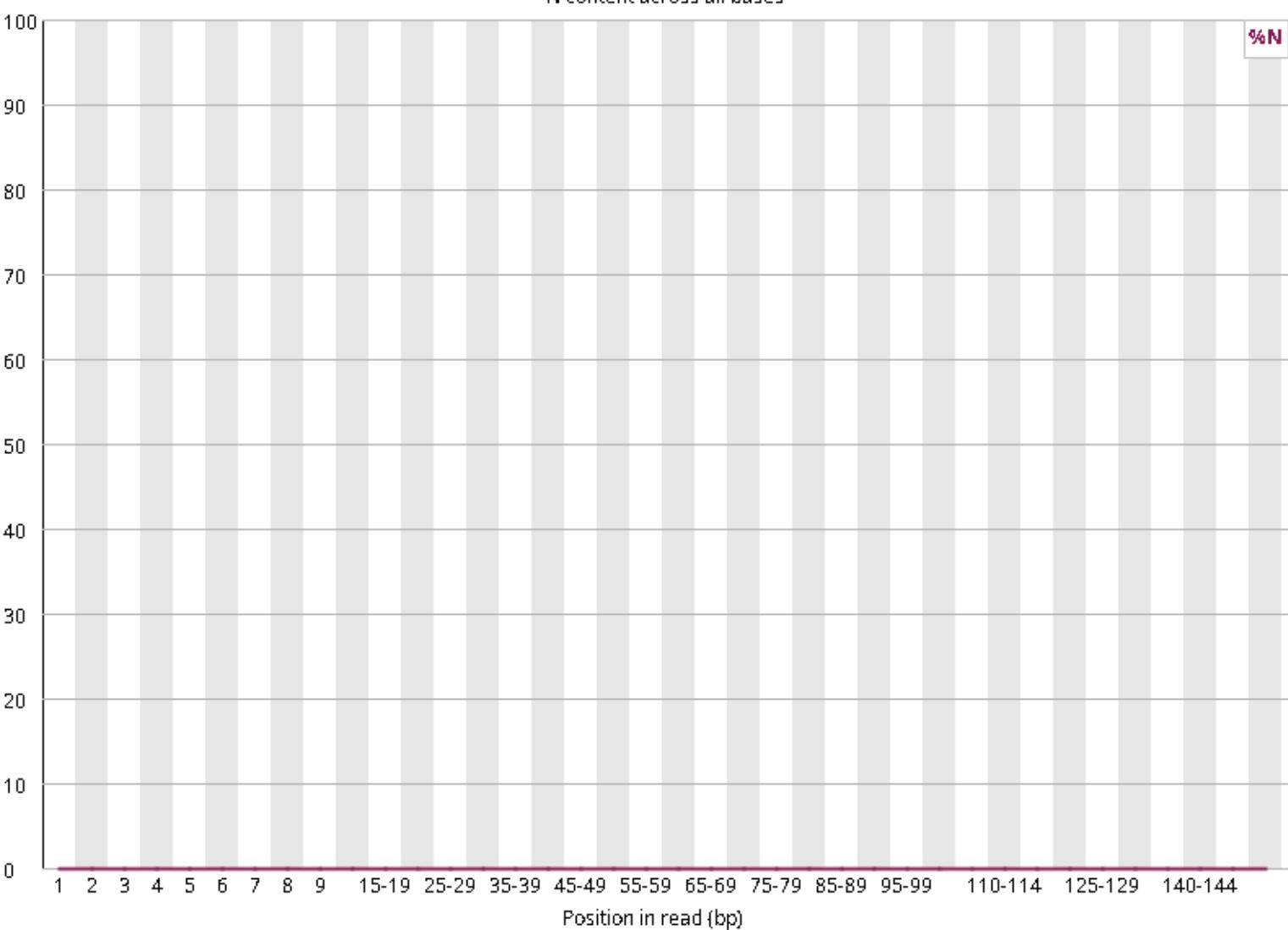
GC count per read
Theoretical Distribution





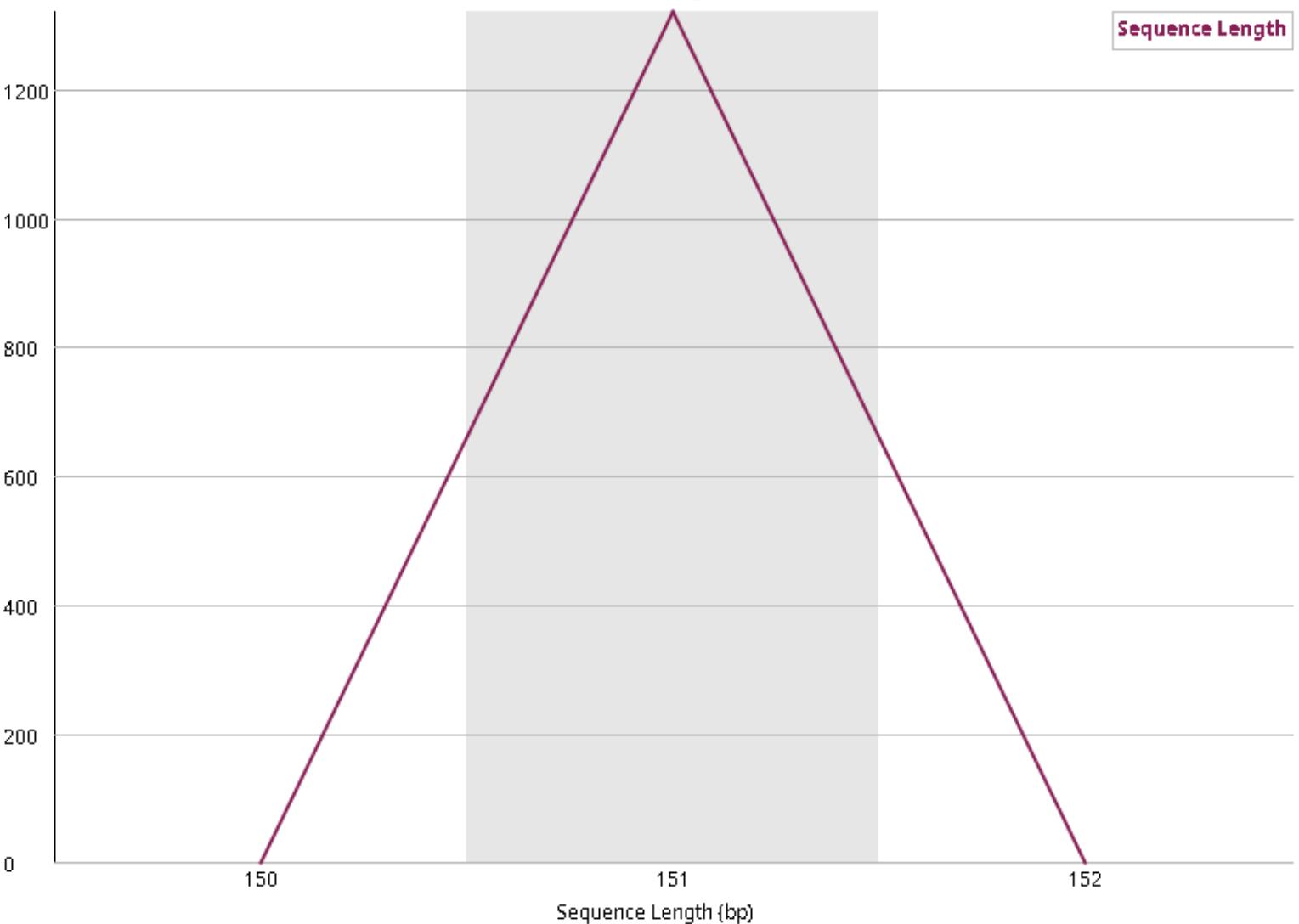
Per base N content

N content across all bases



Sequence Length Distribution

Distribution of sequence lengths over all sequences

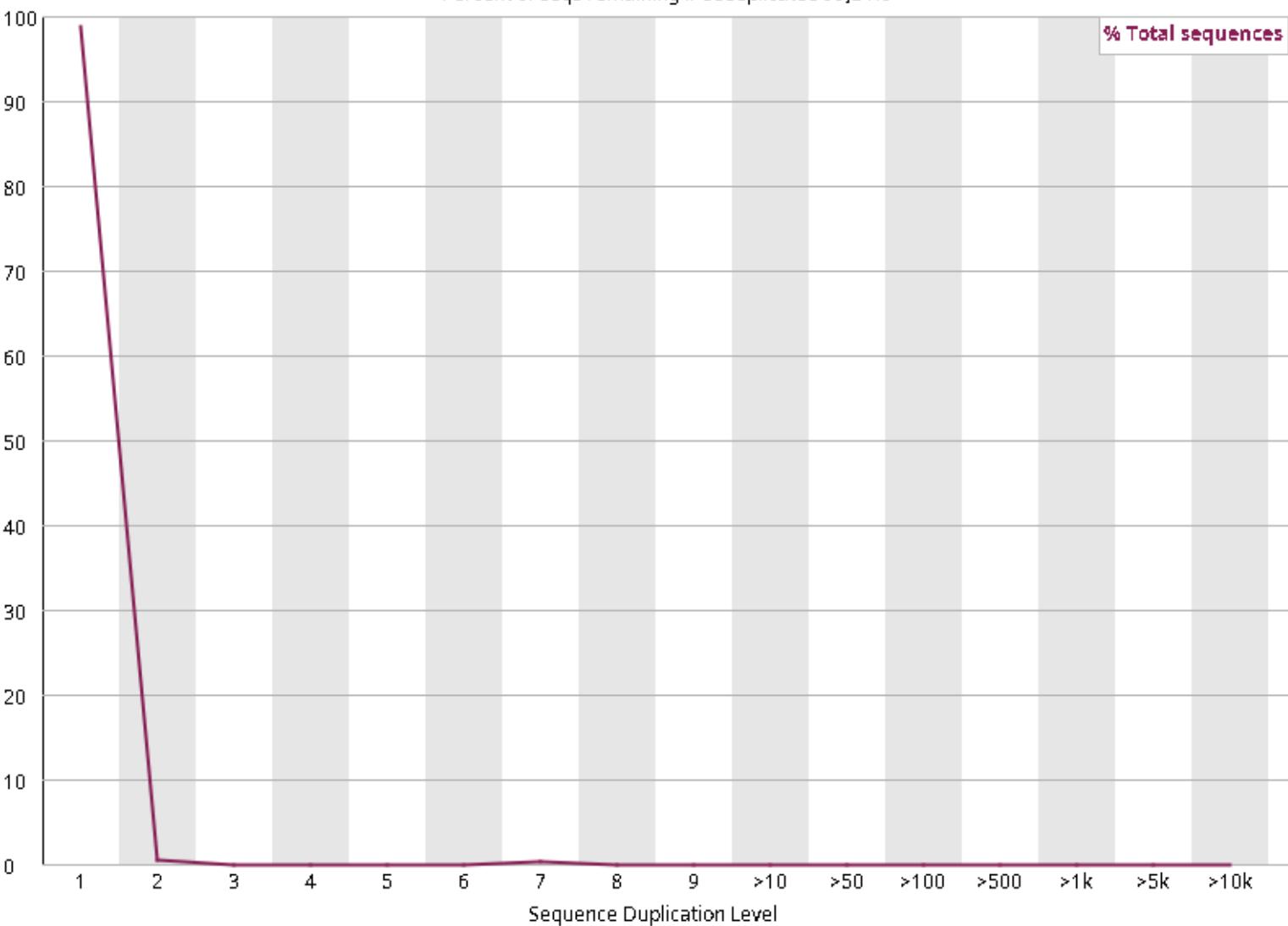


Sequence Length



Sequence Duplication Levels

Percent of seqs remaining if deduplicated 99,24%

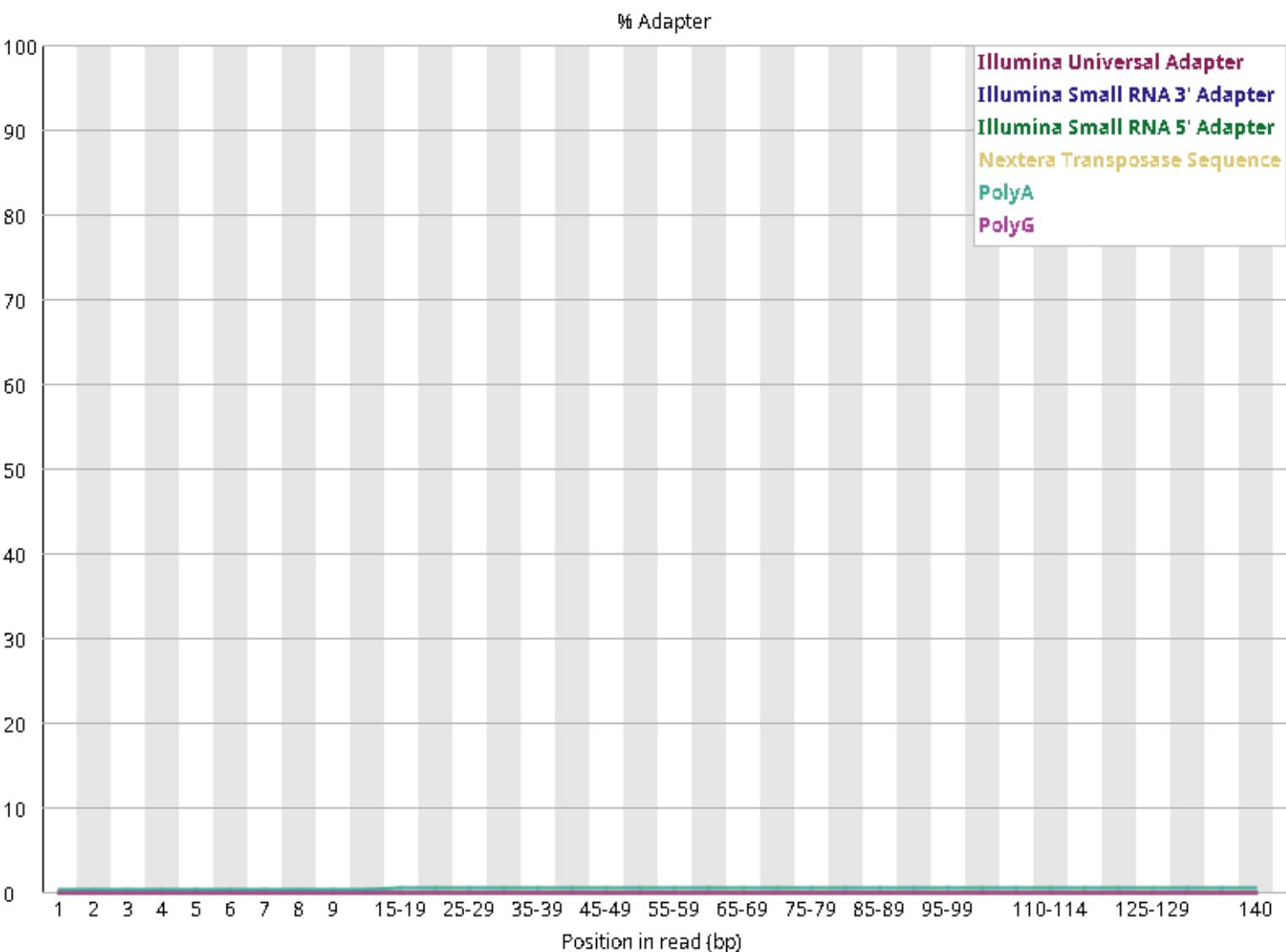


Overrepresented sequences

| Sequence | Count | Percentage | Possible Source |
|--|-------|---------------------|-----------------|
| AAAAAAAAAAAAAAAAAAAAA | 7 | 0.53030303030304 | No Hit |
| CTGTGCCCTCACTGCCCTTGTAGGC GTTCTTGATGATGGCGTTTT | 2 | 0.15151515151515152 | No Hit |
| CGGGTCTAACGTGCTGCAGTTGTTGAATTCTGGTT CCTATACAGAGC | 2 | 0.15151515151515152 | No Hit |
| GCAGGACTCATGCAGCCTTACGCAGCGACGTGAGGAGCGGGCTCGCGT | 2 | 0.15151515151515152 | No Hit |
| GGAGAGCAAGGGCTTGGGTCGACCTCTGGGGAGGGTAGCCCTGGG | 2 | 0.151515151515152 | No Hit |



Adapter Content



Produced by [FastQC](#) (version 0.12.1)