

Summary

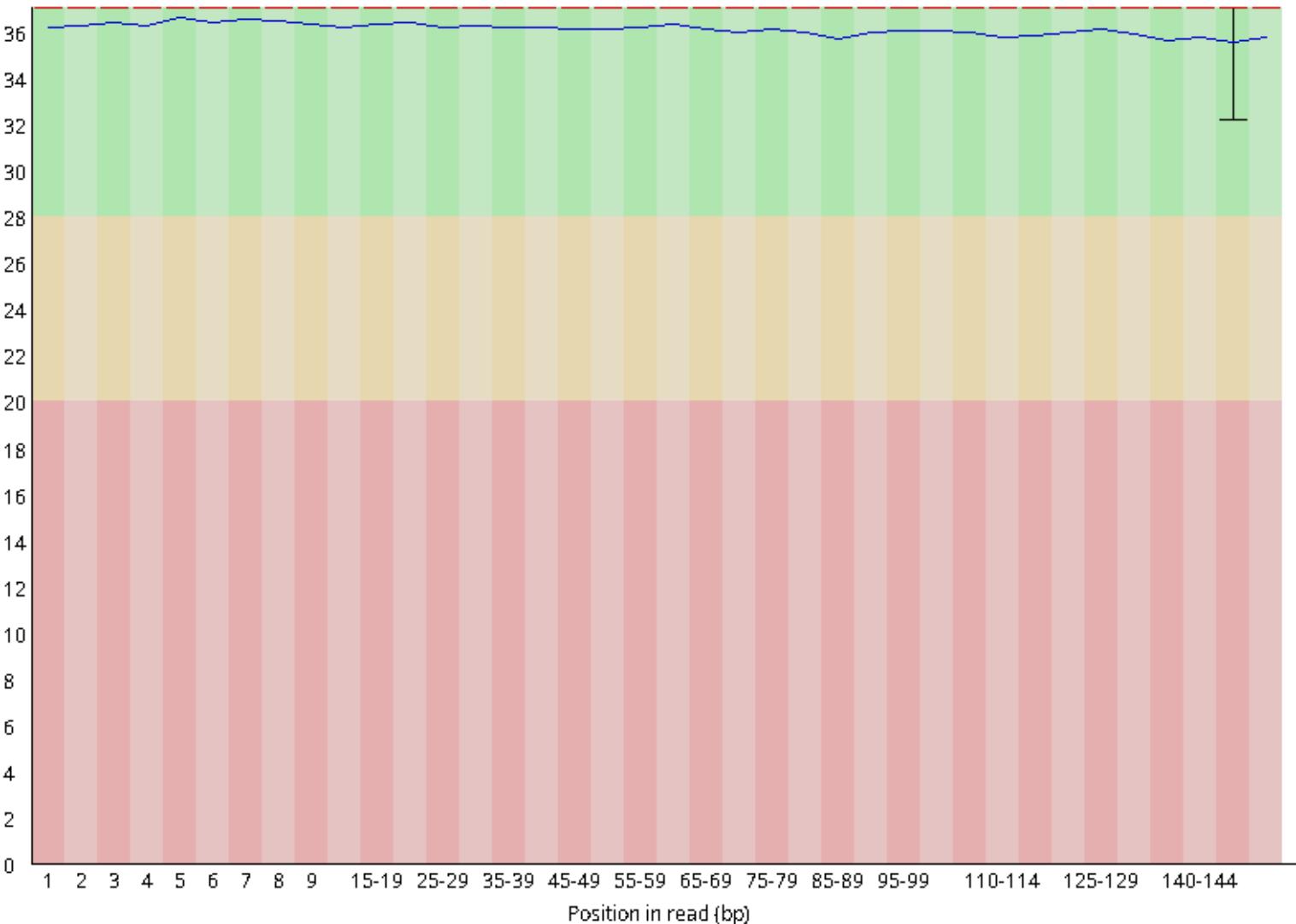
-  [Basic Statistics](#)
-  [Per base sequence quality](#)
-  [Per sequence quality scores](#)
-  [Per base sequence content](#)
-  [Per sequence GC content](#)
-  [Per base N content](#)
-  [Sequence Length Distribution](#)
-  [Sequence Duplication Levels](#)
-  [Overrepresented sequences](#)
-  [Adapter Content](#)

Basic Statistics

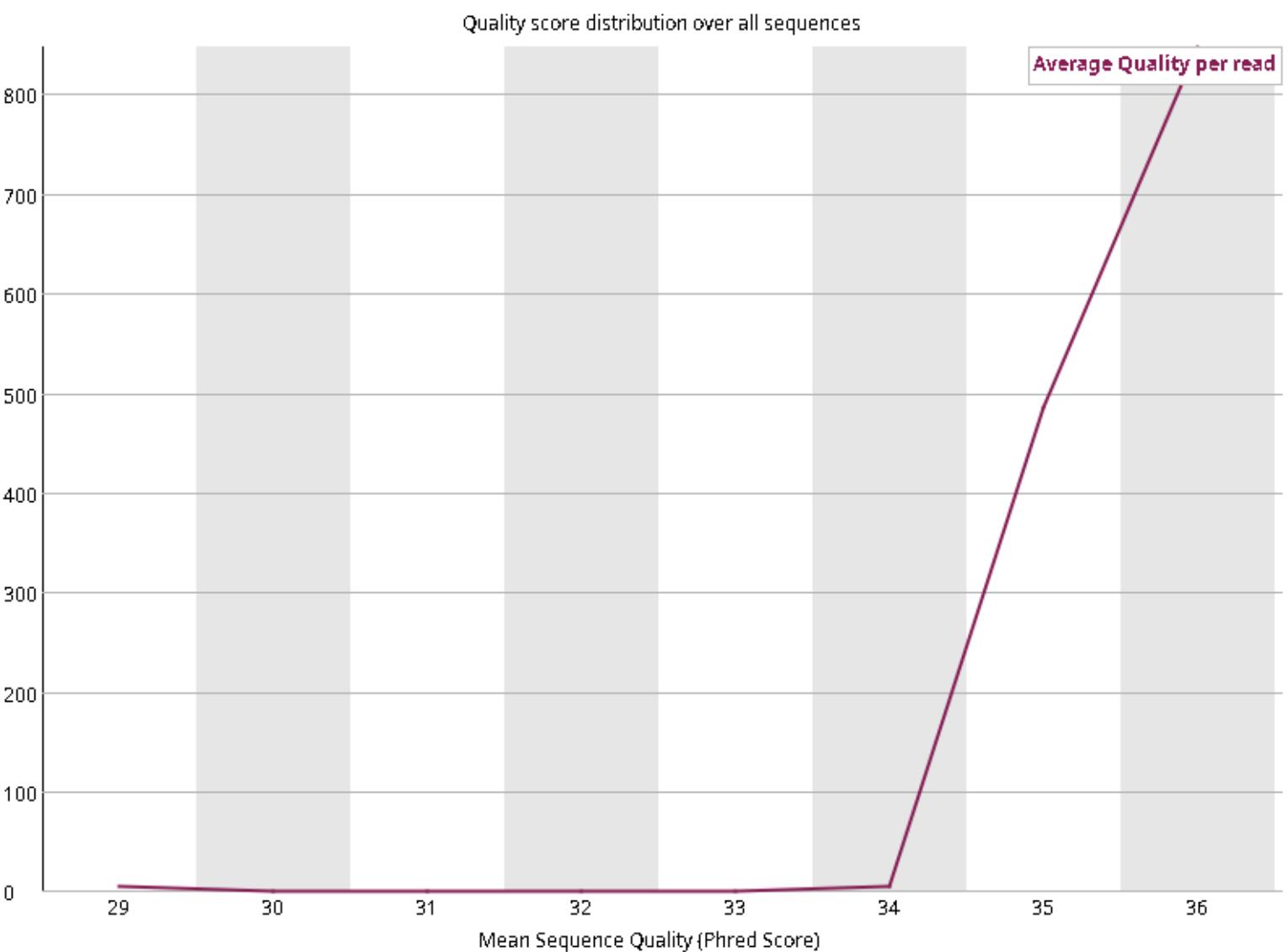
| Measure | Value |
|-----------------------------------|-------------------------|
| Filename | PattyBouvier_R2.fastq |
| File type | Conventional base calls |
| Encoding | Sanger / Illumina 1.9 |
| Total Sequences | 1344 |
| Total Bases | 202.9 kbp |
| Sequences flagged as poor quality | 0 |
| Sequence length | 151 |
| %GC | 46 |



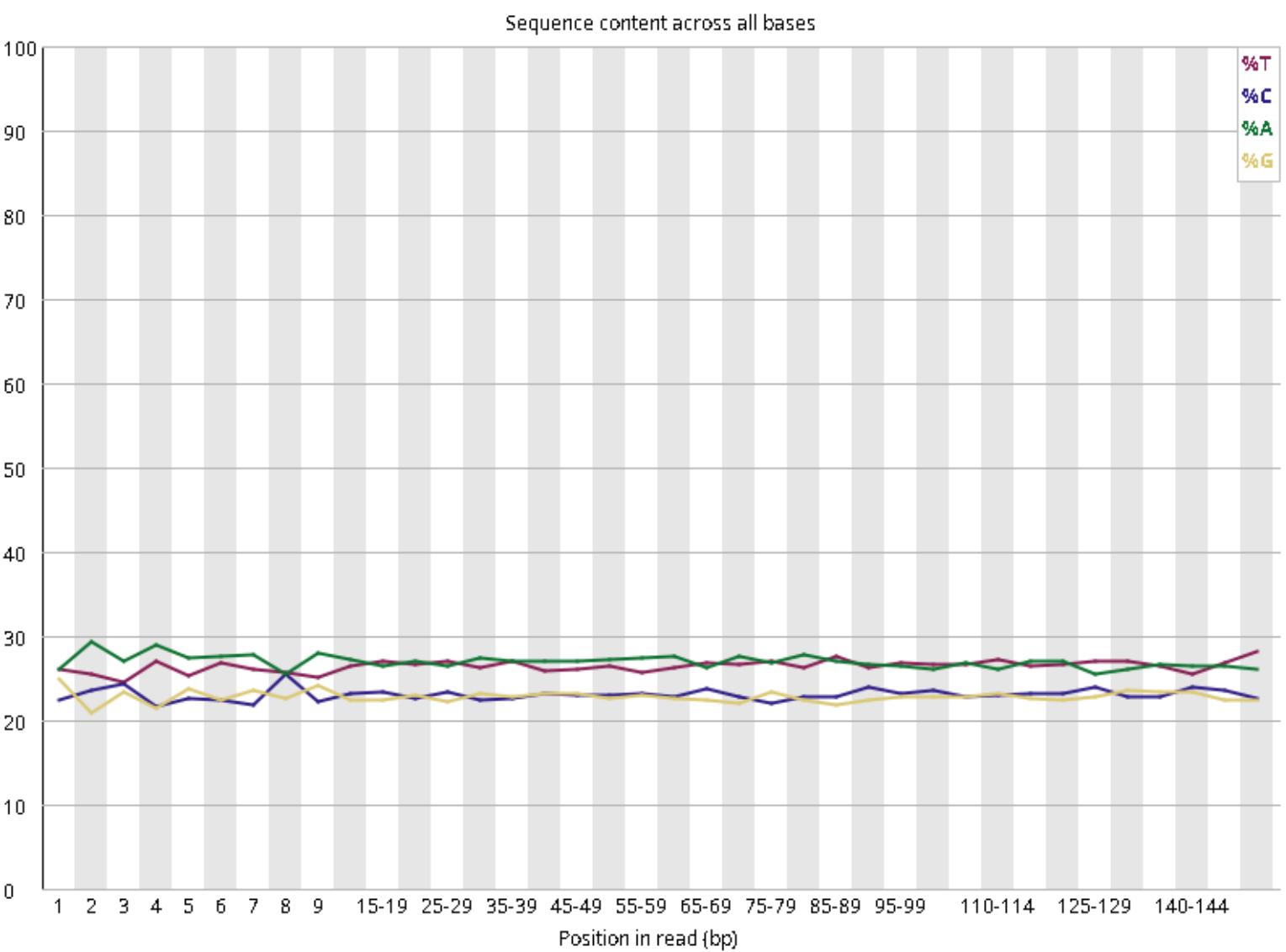
Quality scores across all bases (Sanger / Illumina 1.9 encoding)



Per sequence quality scores

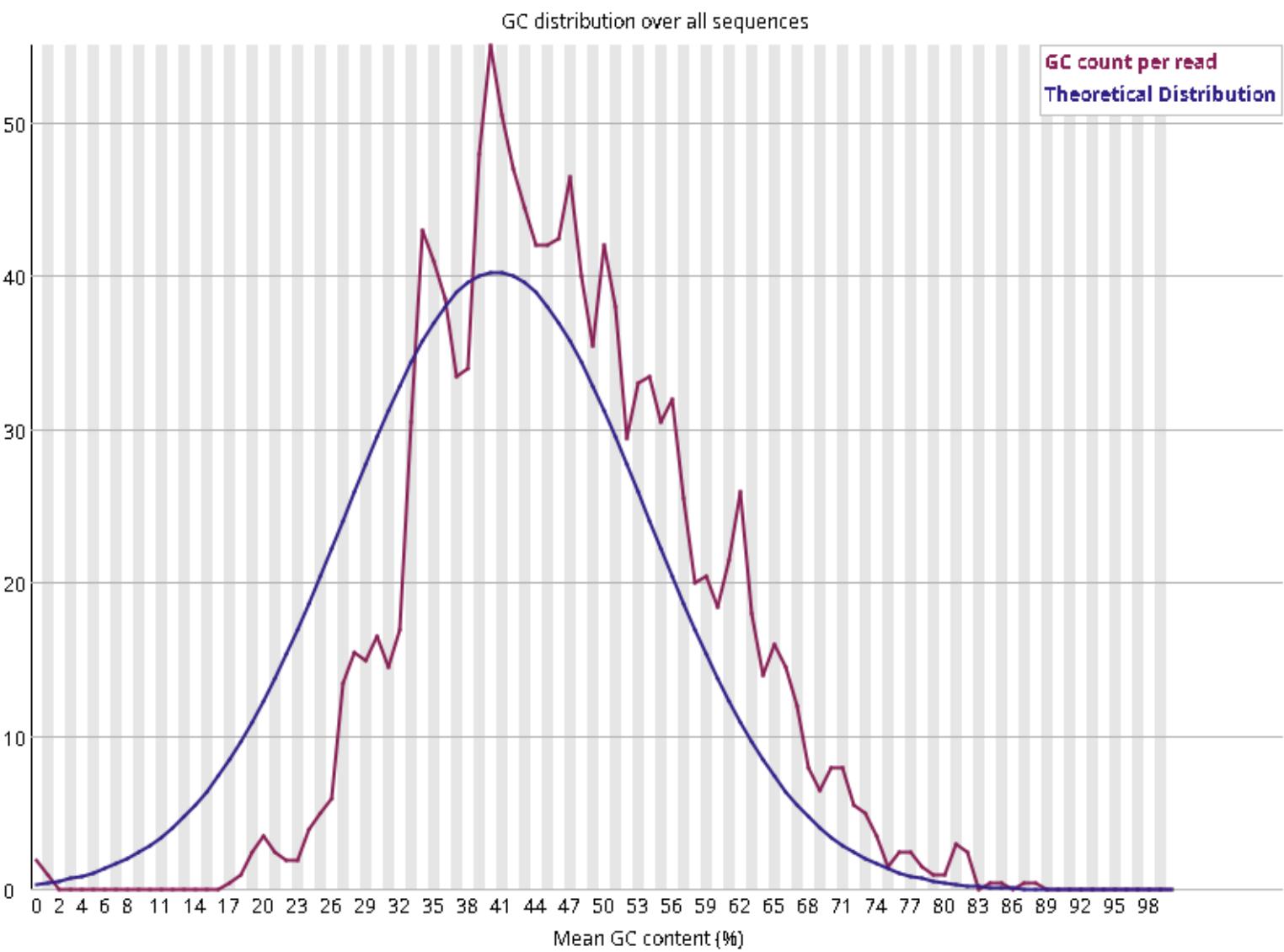


Per base sequence content





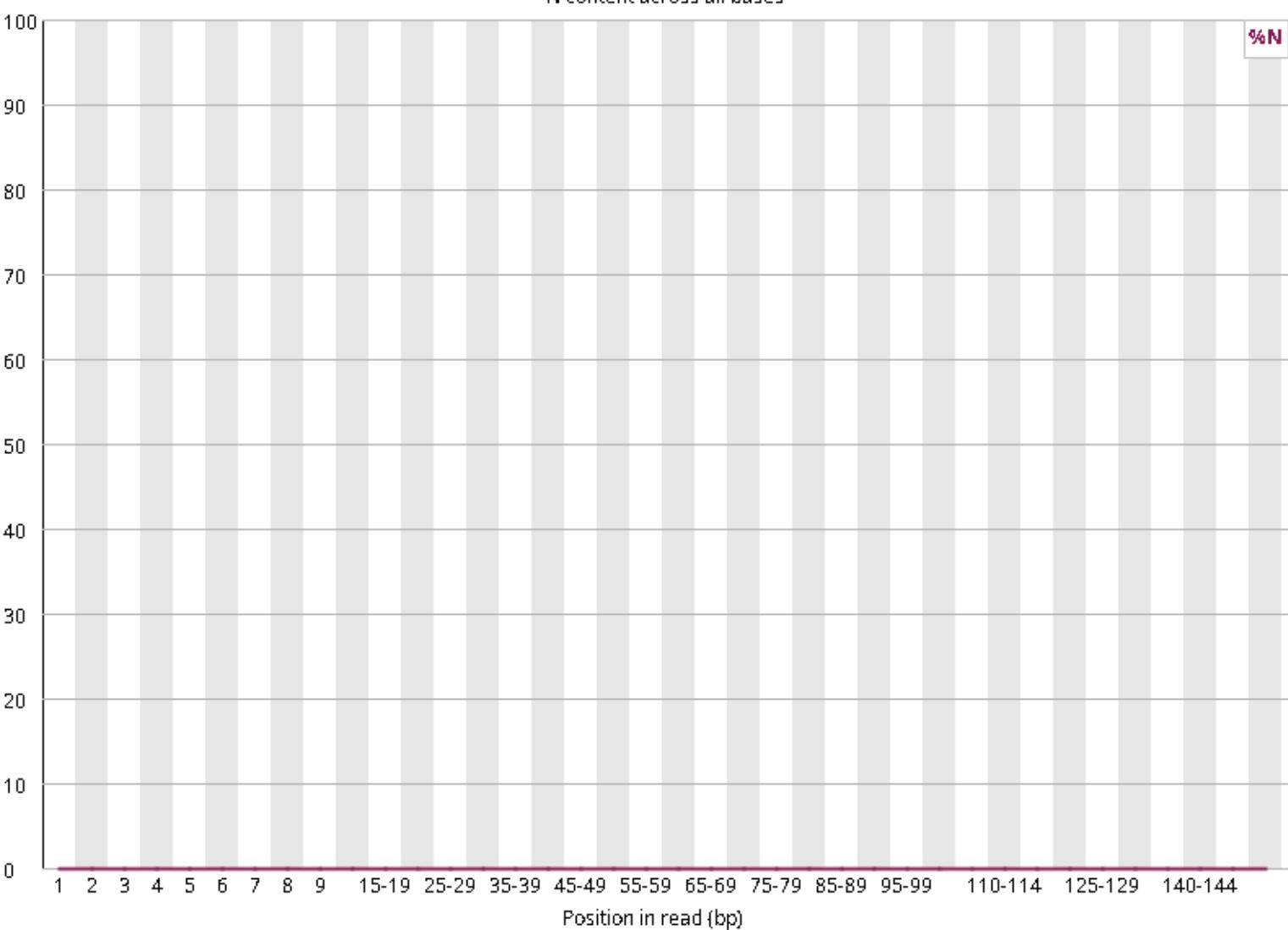
Per sequence GC content





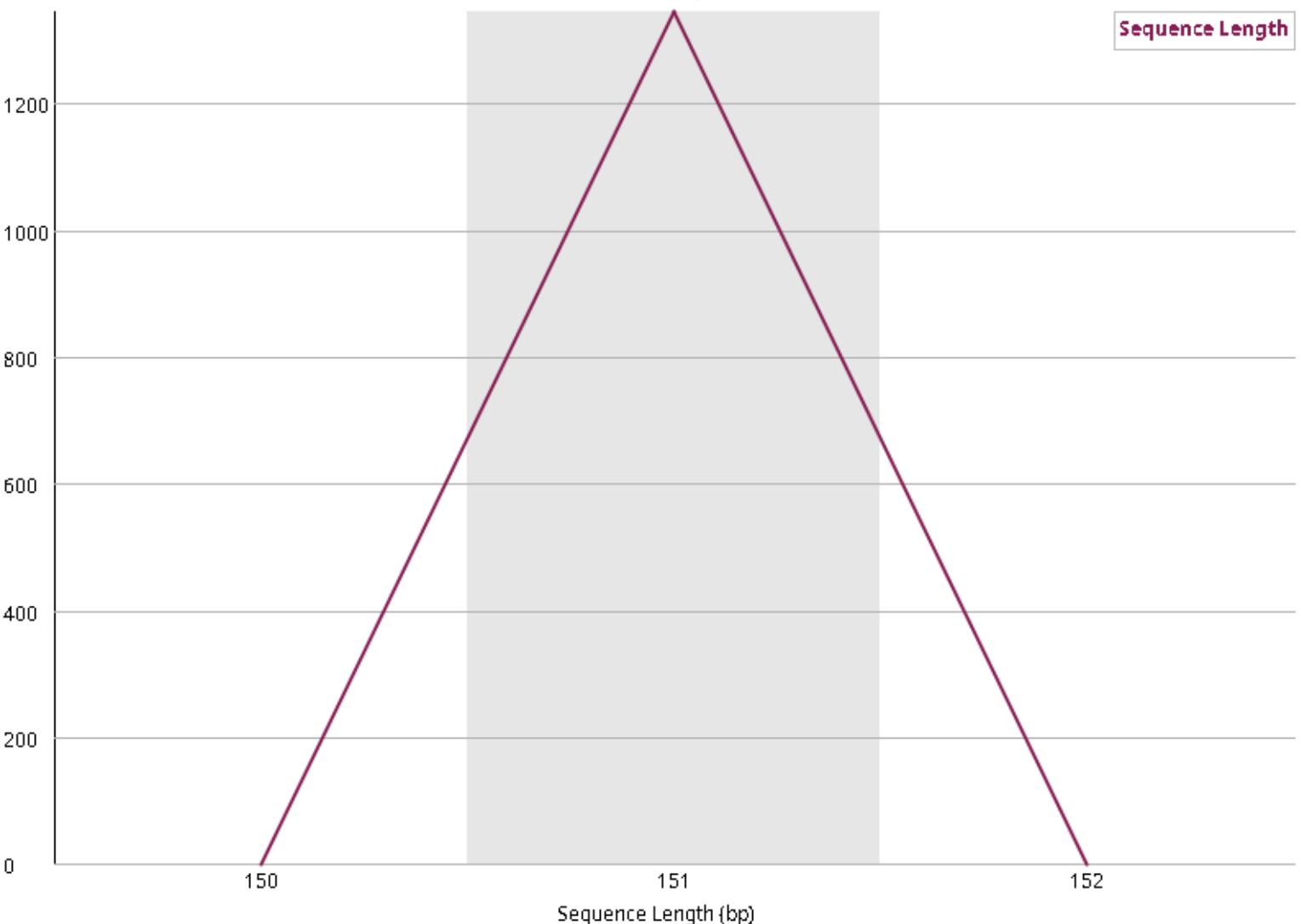
Per base N content

N content across all bases



Sequence Length Distribution

Distribution of sequence lengths over all sequences

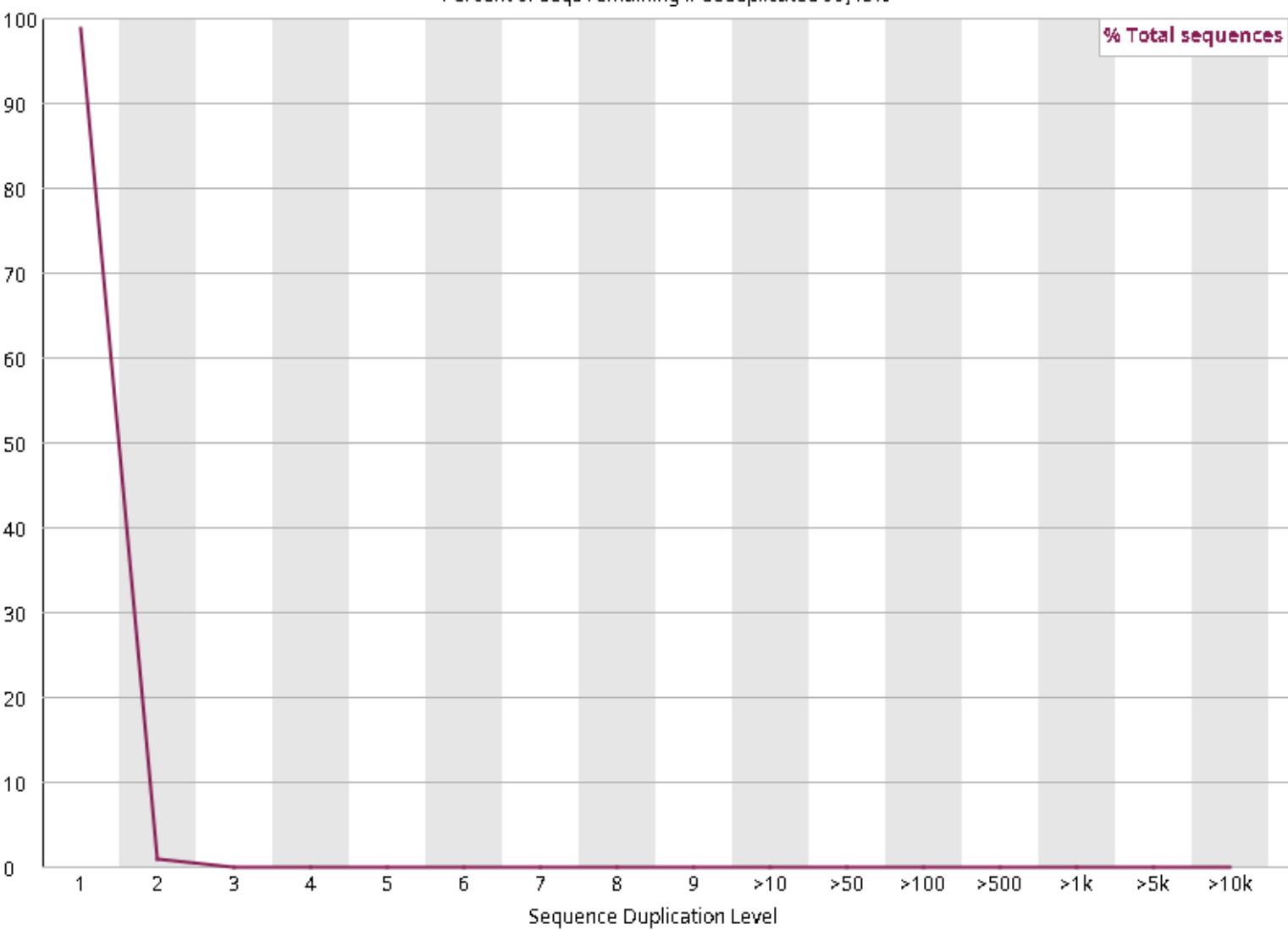


Sequence Length



Sequence Duplication Levels

Percent of seqs remaining if deduplicated 99,48%

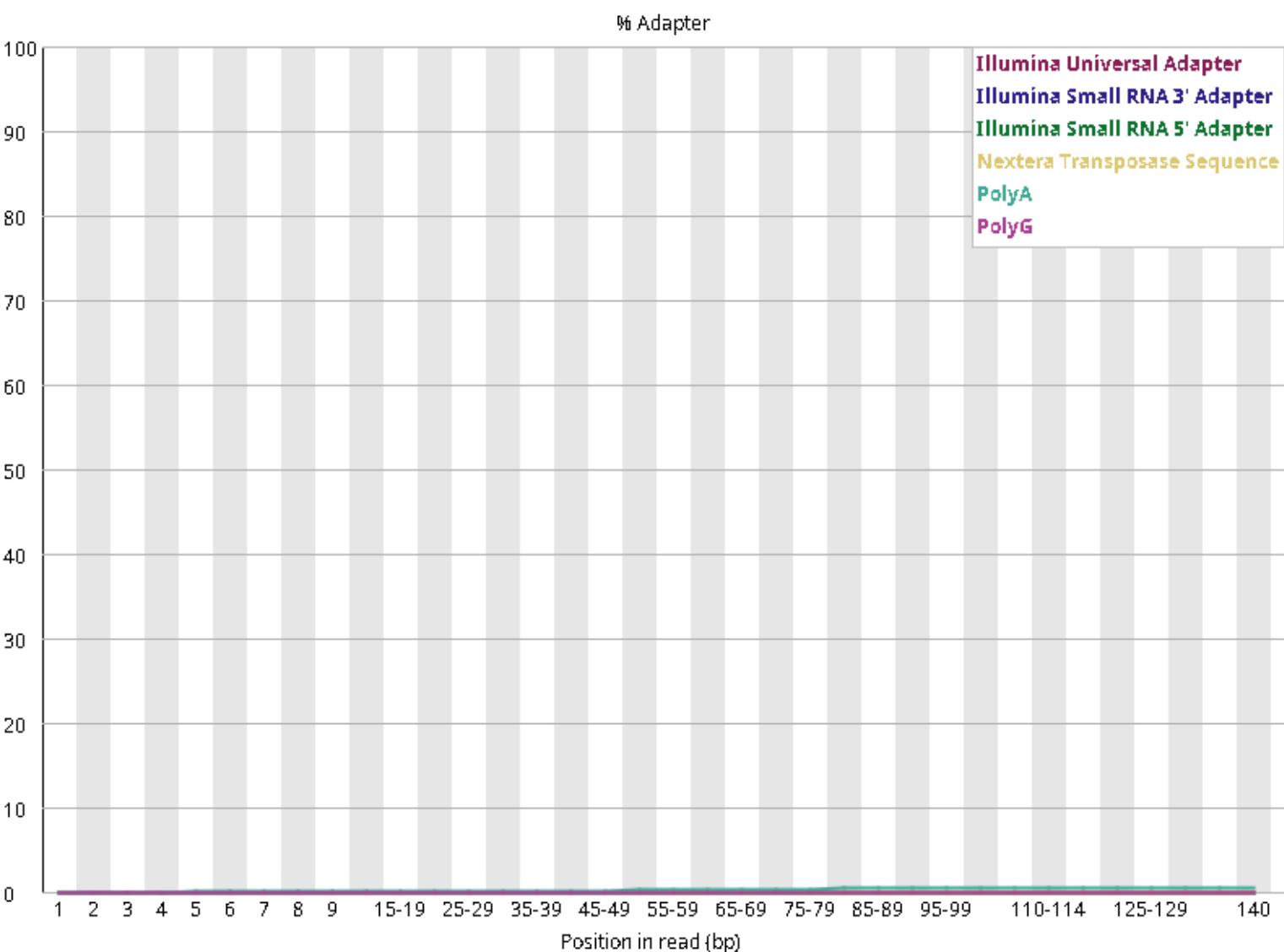


Overrepresented sequences

| Sequence | Count | Percentage | Possible Source |
|---|-------|--------------------|-----------------|
| AATGCAGGATAAACAGTATTAGAAGATGCAATCGAACATTGCTGACTTC | 2 | 0.1488095238095238 | No Hit |
| TTCTCACAGTCATCGCAGAAGCAGAGAGGGTGACACATCTTGGACGGT | 2 | 0.1488095238095238 | No Hit |
| TTGTAGACGTGCACGCAGGGCGGCGTGCACGCTGCTGTAGTGGCTGAC | 2 | 0.1488095238095238 | No Hit |
| AAAGTGAATCTAACTAGTTAACCTTTAAATGAAGGTTGTATAACA | 2 | 0.1488095238095238 | No Hit |
| GAGCAAACCCCTATTGGCAATGACCACACTCTCACTTTGAGTTAACG | 2 | 0.1488095238095238 | No Hit |
| AAACCCAGAAAATTTGGACTTTATACTATCATATGTGACTCAATCTAA | 2 | 0.1488095238095238 | No Hit |
| AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA | 2 | 0.1488095238095238 | No Hit |



Adapter Content



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