












# FastQC Report

## Summary

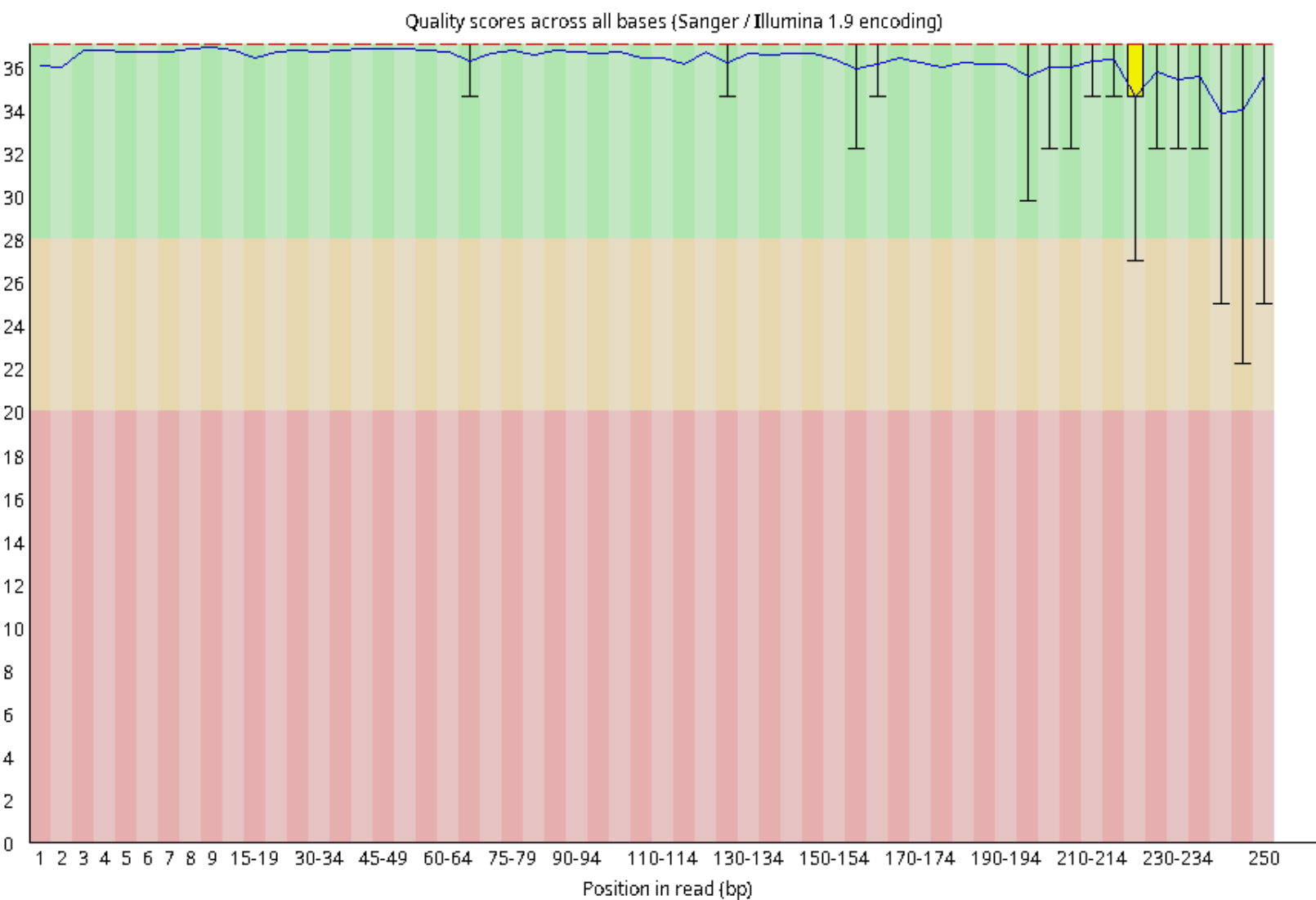
Mon 3 Mar 2025  
SRR32313970\_1\_paired.fastq

-  [Basic Statistics](#)
-  [Per base sequence quality](#)
-  [Per tile 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](#)

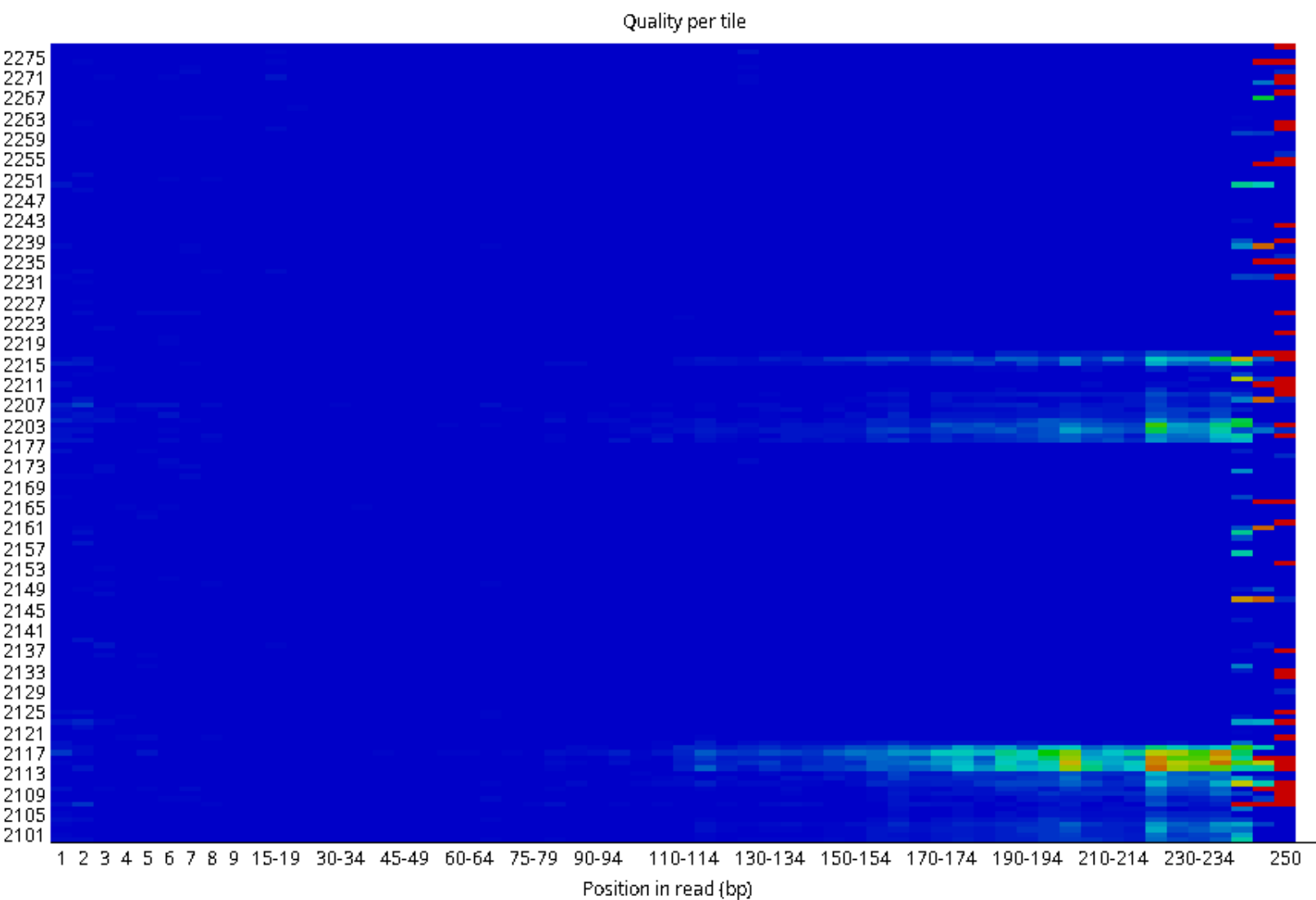
## Basic Statistics

Measure	Value
Filename	SRR32313970_1_paired.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	232649
Total Bases	54.1 Mbp
Sequences flagged as poor quality	0
Sequence length	50-250
%GC	48

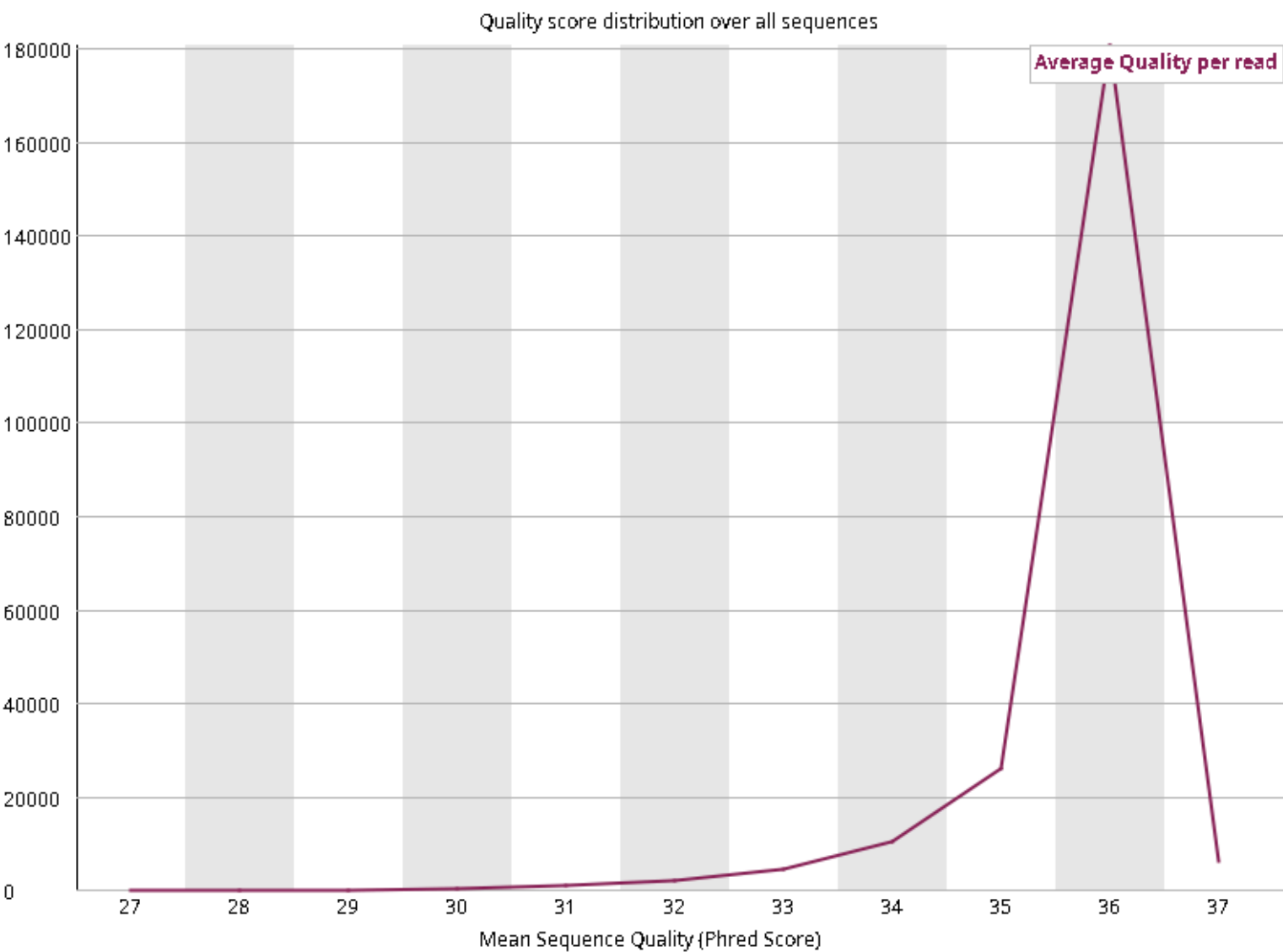
## ✔ Per base sequence quality



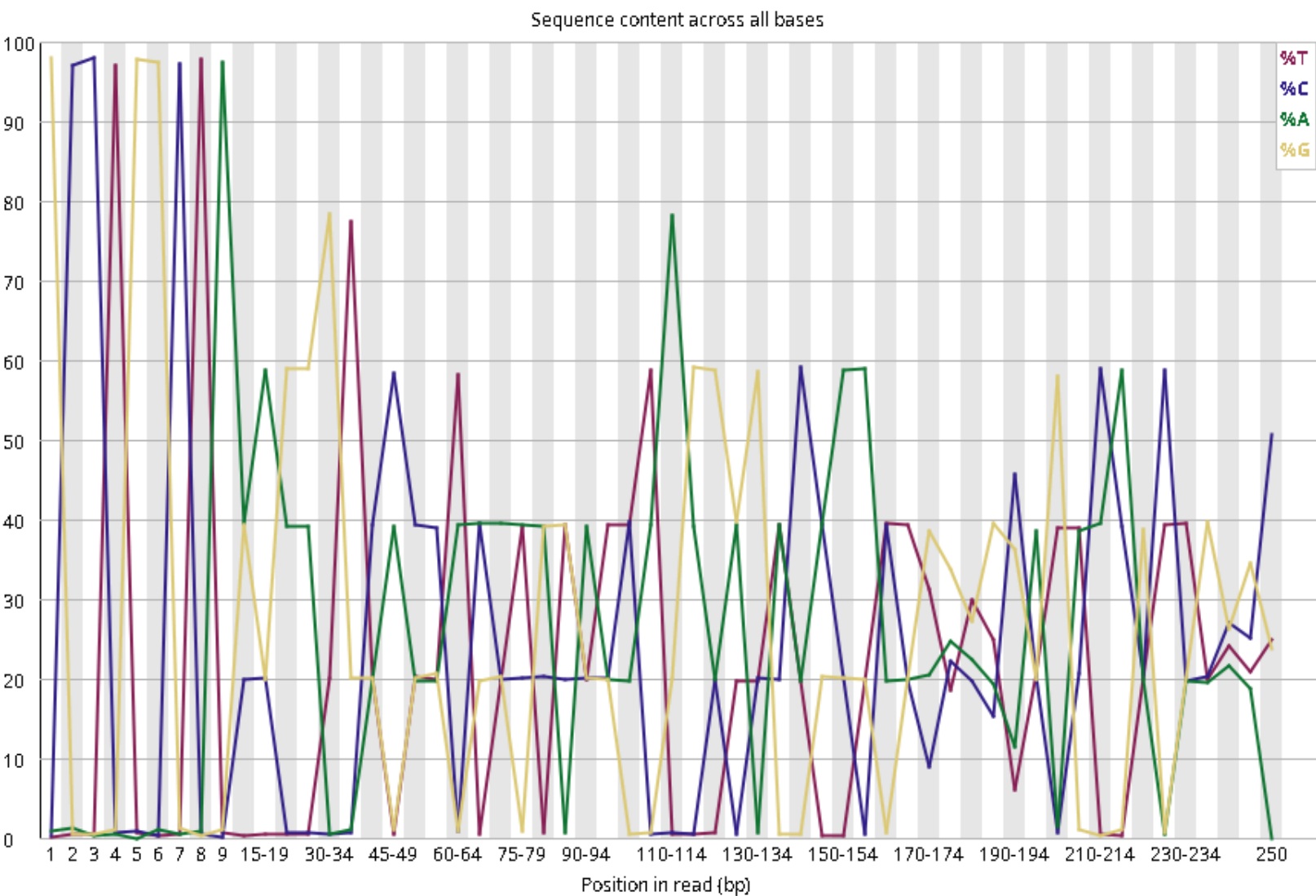
# ✖ Per tile sequence quality



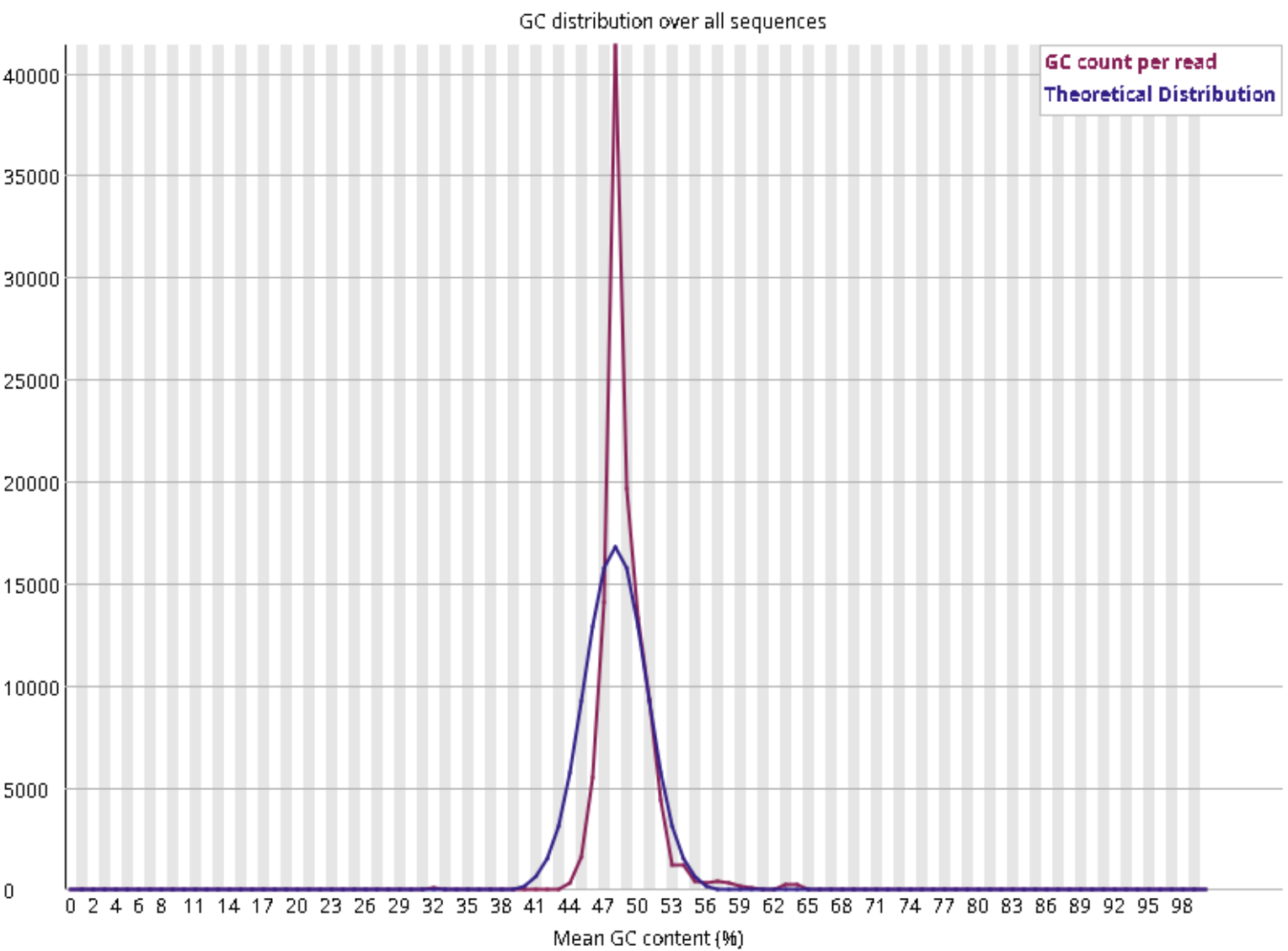
## ✔ Per sequence quality scores



# ❌ Per base sequence content

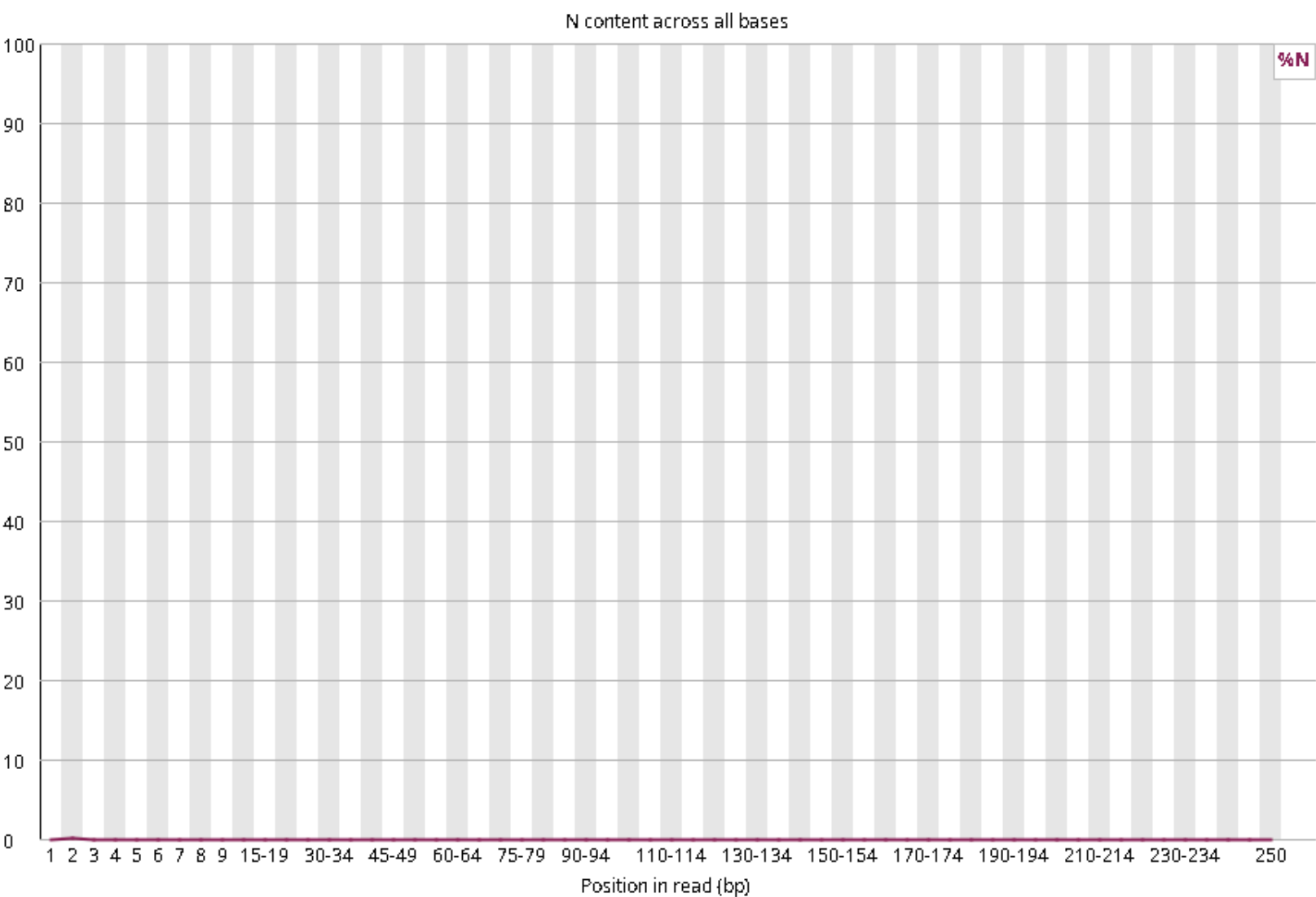


## ❌ Per sequence GC content

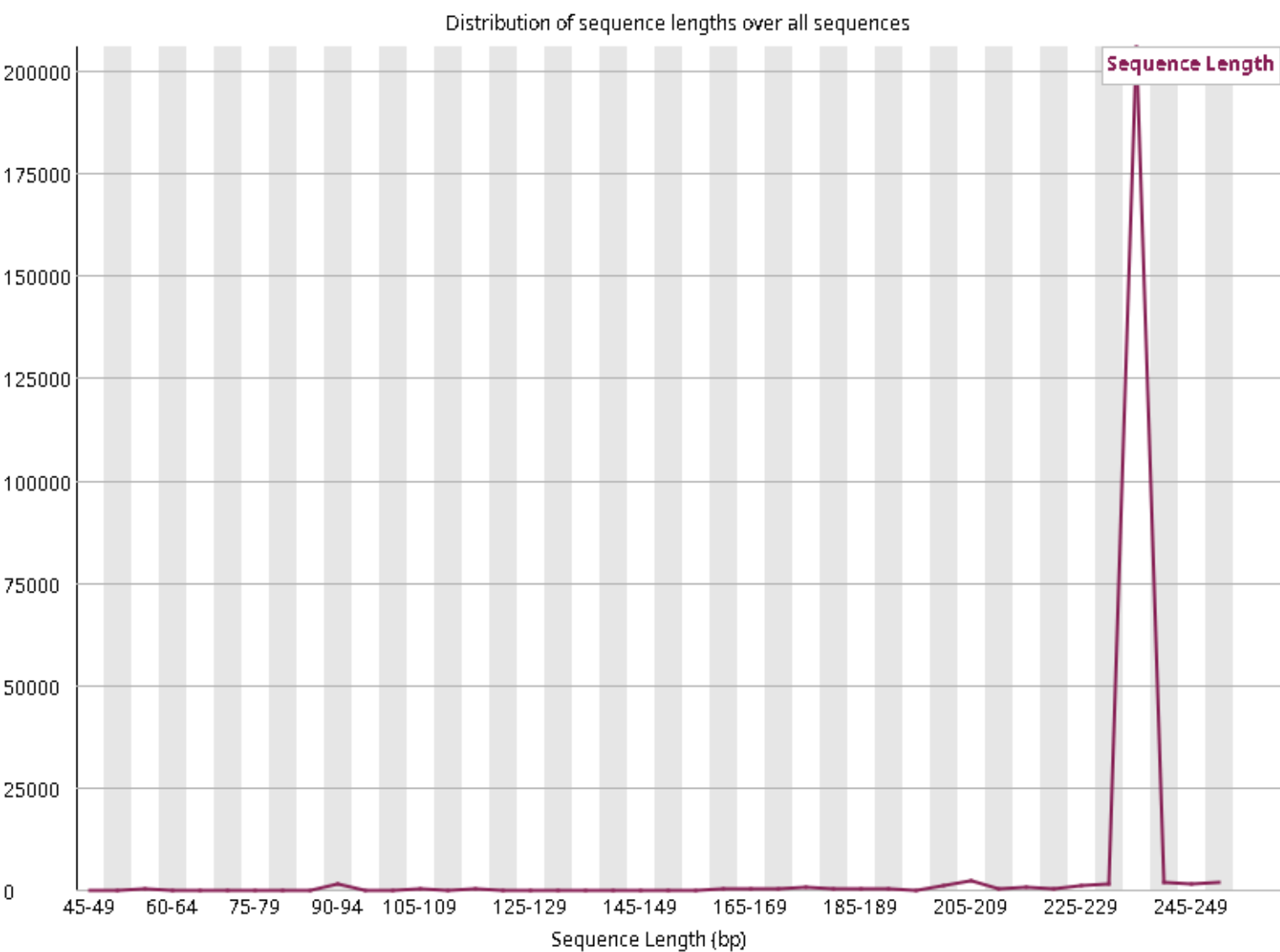




## Per base N content

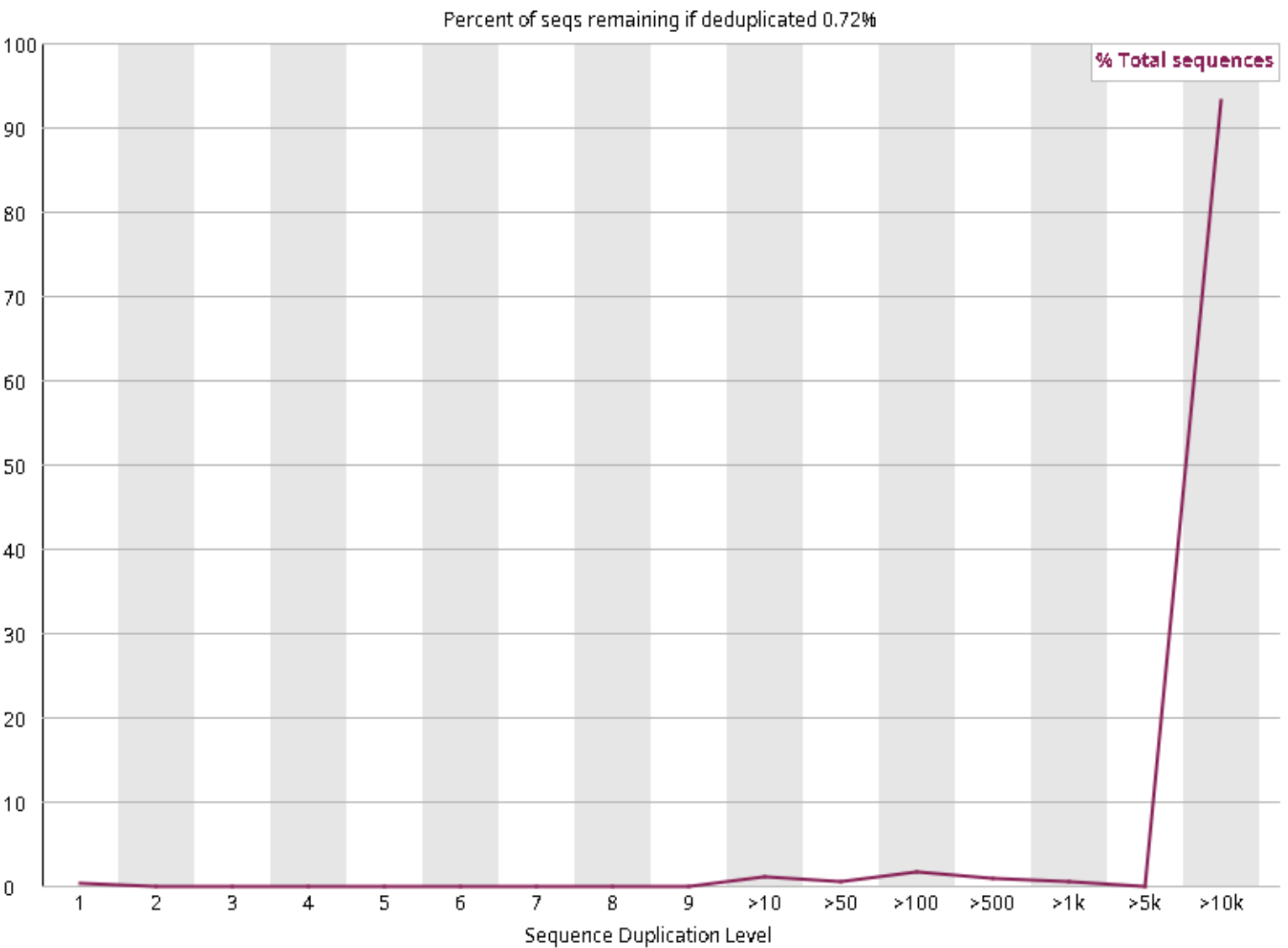


# Sequence Length Distribution





## Sequence Duplication Levels



## Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GCCTGGCTAGAAAGCACAAGAGGAGGAGGAGGTGGGTTTTCCAGTCACACC	217422	93.45494715214767	No Hit
GCCTGGCTAGAAAGCACAAGAGGAGGAGGAGGTGTGAAATTGCGCAGCCAT	1597	0.6864418071859325	No Hit
GNCTGGCTAGAAAGCACAAGAGGAGGAGGAGGTGGGTTTTCCAGTCACACC	670	0.2879874832902785	No Hit
GATGCAGTACCAAGCCCGCTGGAGCAGAGTGAGAAGCGCTTGAGACAGC	657	0.2823996664503179	No Hit
AGCCCATTTCCATCATCGACCTCATCGTGGTCGTGGCCTCCATGGTGGTC	651	0.2798206740626437	No Hit
GCCTGGCTAGAAAGCACAAGAGGAGGAGGAGGTGGGTTTTCTGTTCACACC	606	0.2604782311550877	No Hit
CTAGTGGTGGAGGAGGCTCTGGTGGAGGCGGTAGCGGAGGCGGAGGGTCG	475	0.20417023069086906	No Hit
GACATCGAGCTTGCTACAAGGGACTTTCCGCTGGGGACTTTCCAGGGAGG	365	0.15688870358350993	No Hit
GCCTGGCTAGAAAGCACAAGAGCACACGTCTGAACTGGCTACTTCCCTGAT	362	0.15559920738967287	No Hit

Sequence	Count	Percentage	Possible Source
GCCTGGCTAGAAGCACAAAGAGGAGGAGGAGGTGGGTTTTTCAGTCACACC	305	0.1310987797067686	No Hit
CAAGGGCATCGGTCGAGATCCCGGTGCCTAATGAGTGAGCTAACTTACAT	245	0.1053088558300272	No Hit
GCGCGAACATGTAAGTGGTGGGATCTGCGGCGGCTCCCAGATGATGGTCG	236	0.10144036724851602	No Hit



## Adapter Content

