FastQC Report

Summary

✅ [Basic Statistics](#)

✅ [Per base sequence quality](#)

❌ [Per tile sequence quality](#)

✅ [Per sequence quality scores](#)
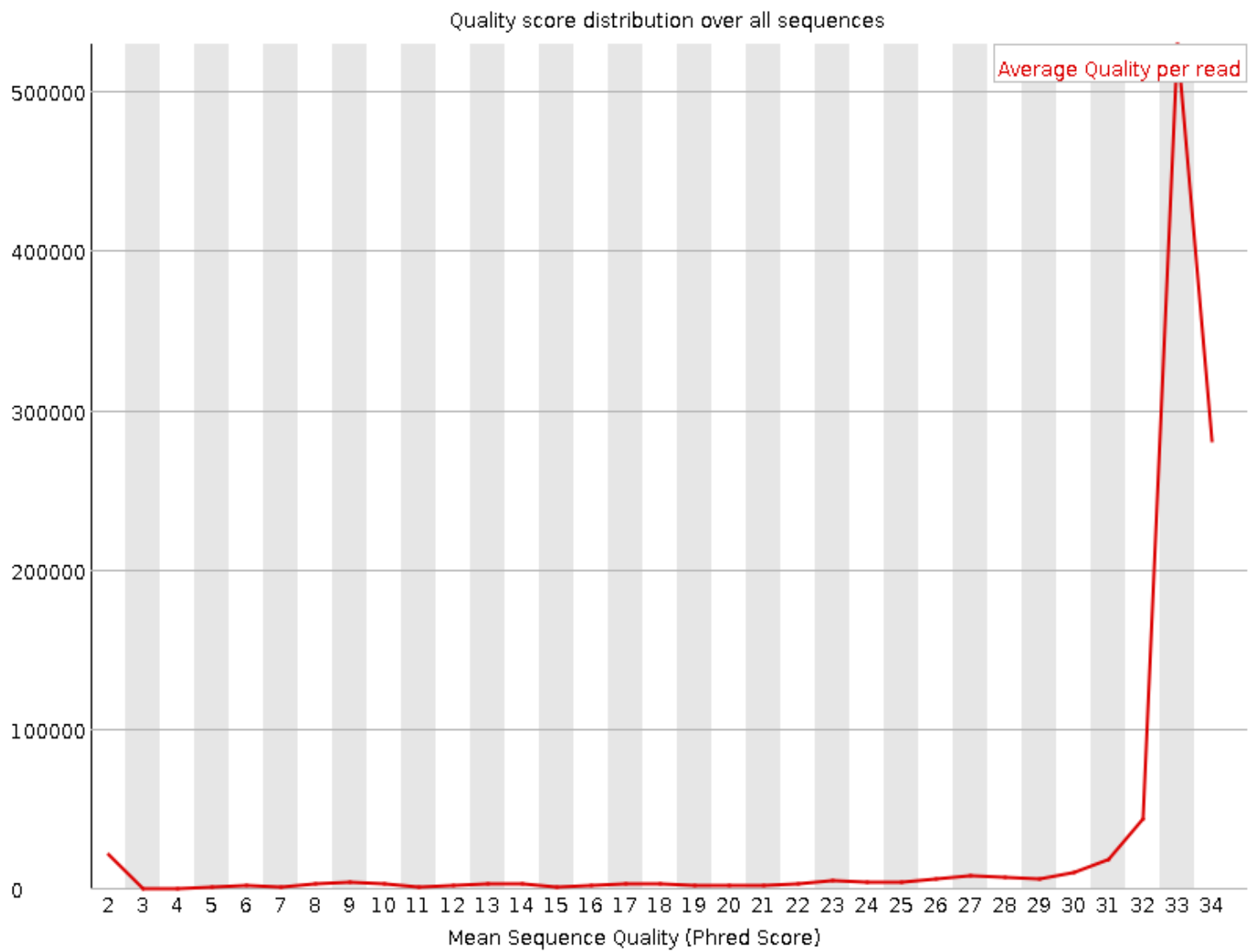
❌ [Per base sequence content](#)
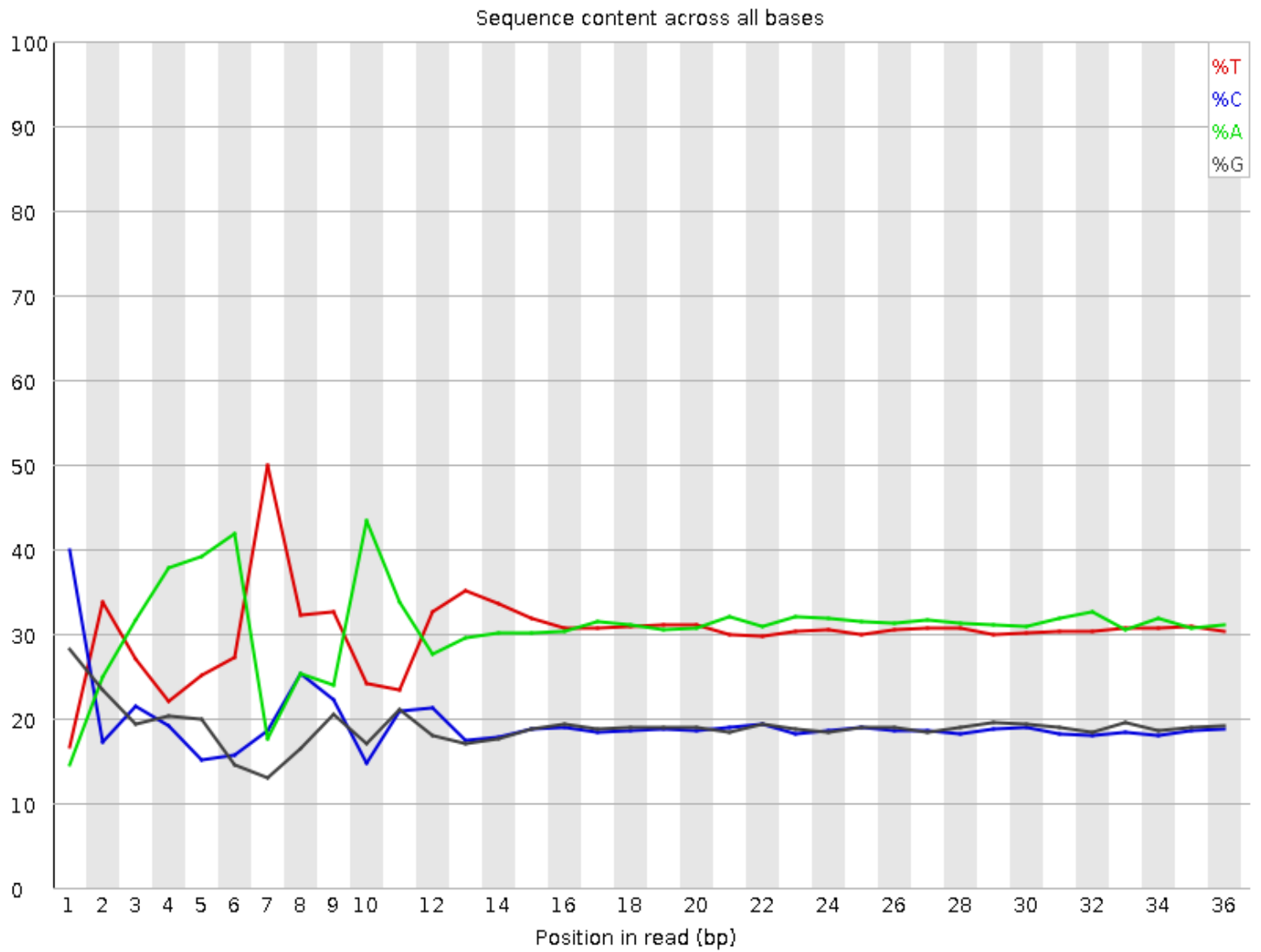
✅ [Per sequence GC content](#)

✅ [Per base N content](#)

✅ [Sequence Length Distribution](#)

⚠️ [Sequence Duplication Levels](#)

⚠️ [Overrepresented sequences](#)

✅ [Adapter Content](#)

✅ Basic Statistics

Measure	Value
Filename	ERR032068_2_REP2.fq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	1000000
Sequences flagged as poor quality	0
Sequence length	36
%GC	38

✅ Per base sequence quality

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

Position in read (bp)

❌ **Per tile sequence quality**

Quality per tile

Position in read (bp)

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 62%

Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GGGATATAGAATCTTGGAGGACATATCGAAGATTTT	3248	0.3248	No Hit
GGCCTCTACACCTATCTTTAACTACAATTCAACATC	2882	0.2882	No Hit
TCTACACCTATCTTTAACTACAATTCAACATCGAGG	2657	0.2657	No Hit
CTTAGGGATAACAGGGATATAGAATCTTGGAGGACA	2076	0.2076	No Hit
CAAGATTCTATATCCCTGTTATCCCTAAGGAAGTTC	1918	0.1918	No Hit
CAGGGATATAGAATCTTGGAGGACATATCGAAGATT	1719	0.1719	No Hit
CAAATAACTAAAGTAAGAAACACCACTAAGTTAAAA	1457	0.1457	No Hit
CTCAAATCACGAATAATATTATTAGTCGAACAGACT	1401	0.1401	No Hit
CTAAACTCAAATCACGAATAATATTATTAGTCGAAC	1368	0.1368	No Hit

Sequence	Count	Percentage	Possible Source
GTTGAATTGTAGTTAAAGATAGGTGTAGAGGCCTTT	1339	0.1339	No Hit
CCAAGATTCTATATCCCTGTTATCCCTAAGGAAGTT	1177	0.11770000000000001	No Hit
CTTTAACTACAATTCAACATCGAGGTAGAAAACAAA	1120	0.11199999999999999	No Hit
CTACACCTATCTTTAACTACAATTCAACATCGAGGT	1101	0.1101	No Hit
CTTCCTTAGGGATAACAGGGATATAGAATCTTGGAG	1033	0.1033	No Hit
CAATTCTAGAATTAGTAGACAAGTAATTATGCTACC	1013	0.1013	No Hit

Adapter Content

Produced by FastQC (version 0.11.7)