FastQC Report

Mon 3 Mar 2025
SRR32313970_2_paired.fastq

Summary

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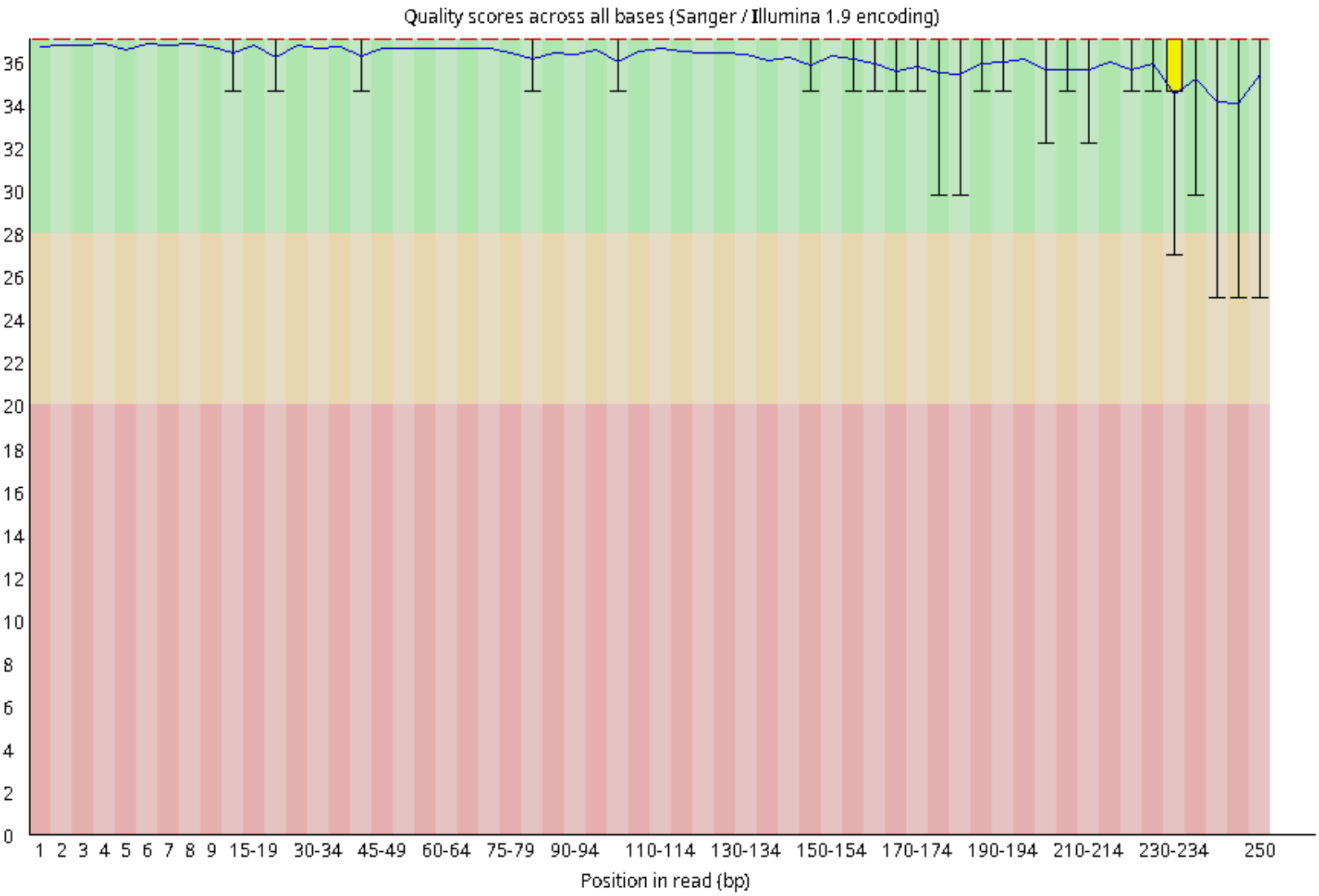
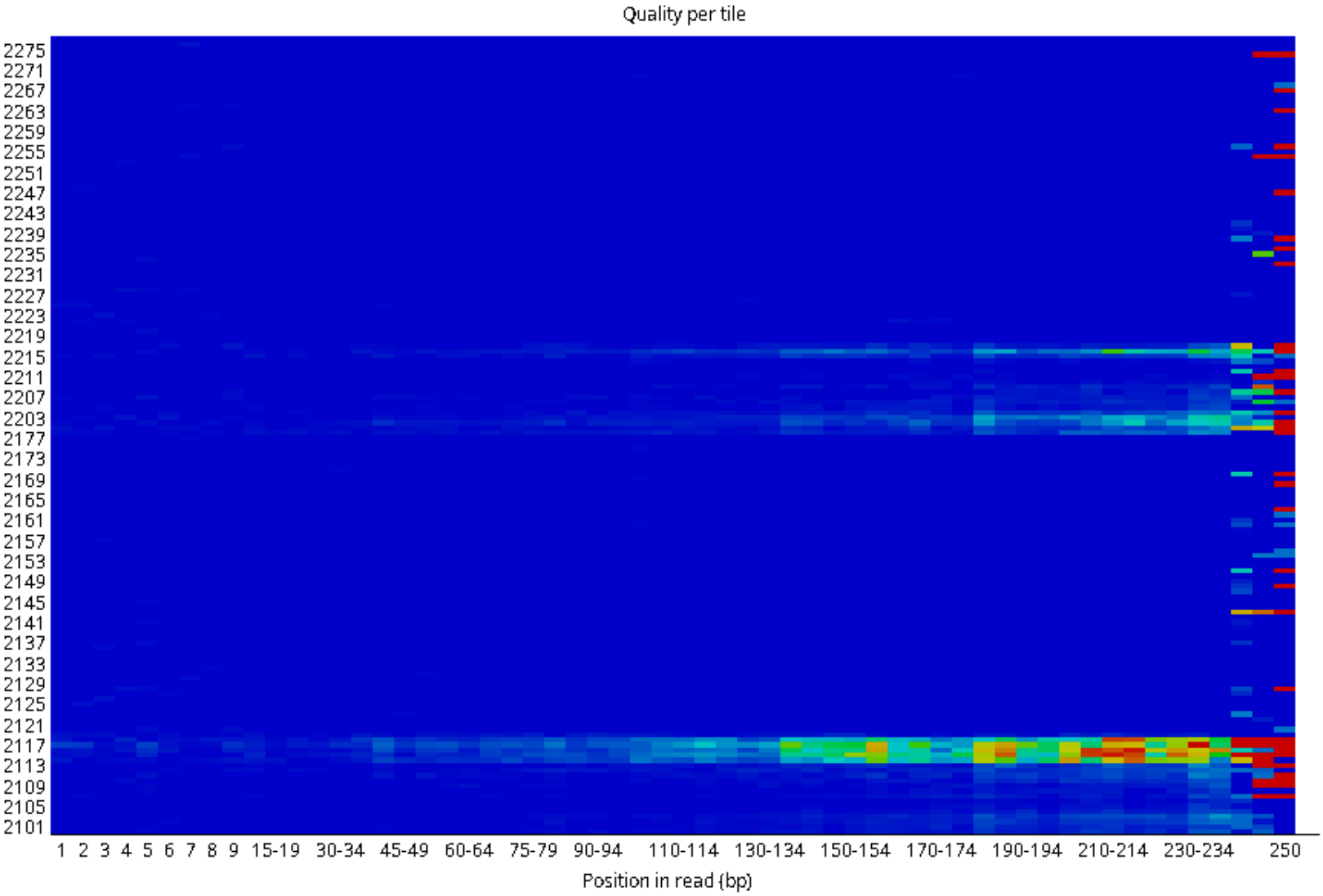
Basic Statistics

Measure	Value
Filename	SRR32313970_2_paired.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	232649
Total Bases	53.4 Mbp
Sequences flagged as poor quality	0
Sequence length	50-250
%GC	48

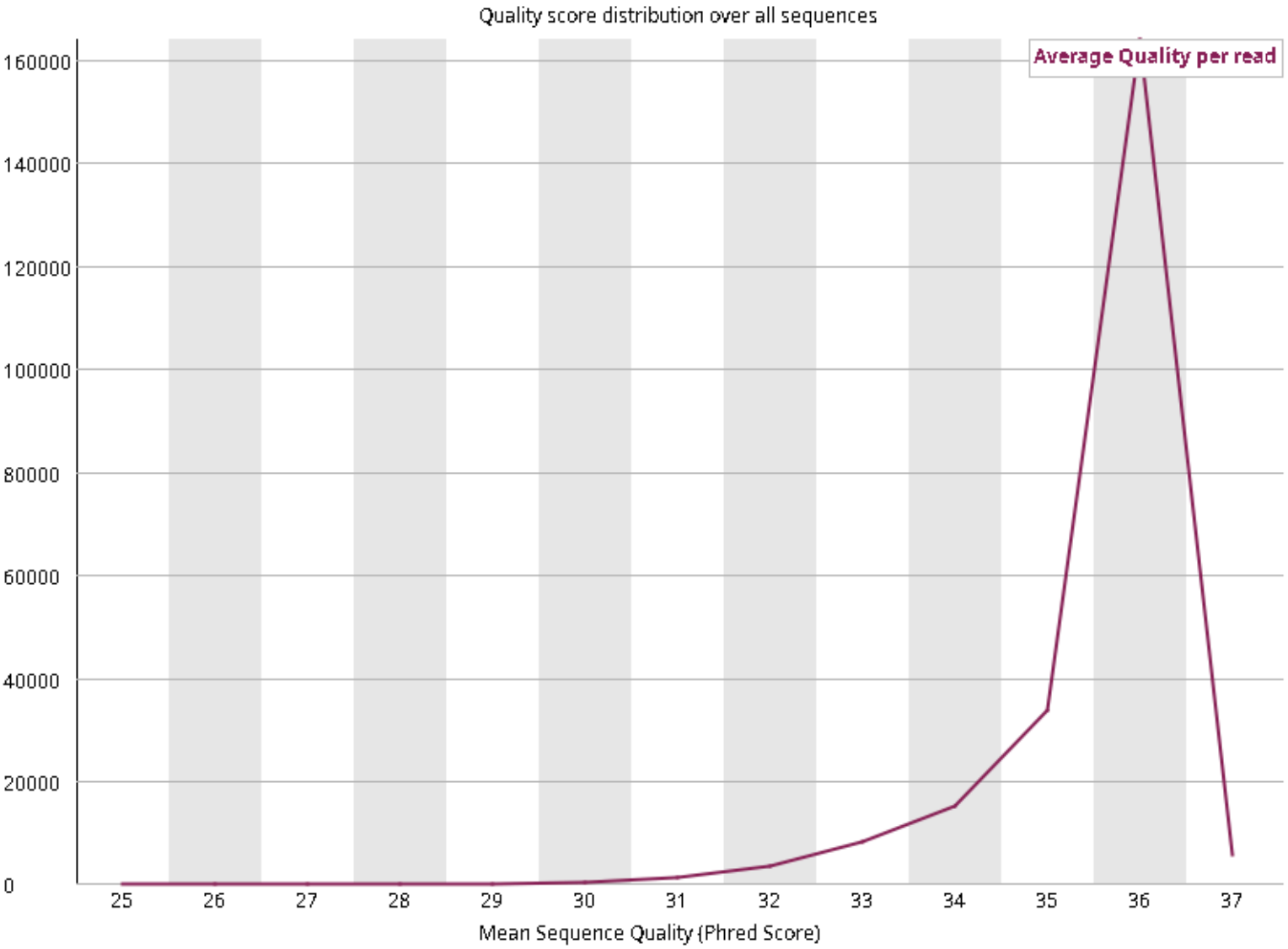
Per base sequence quality



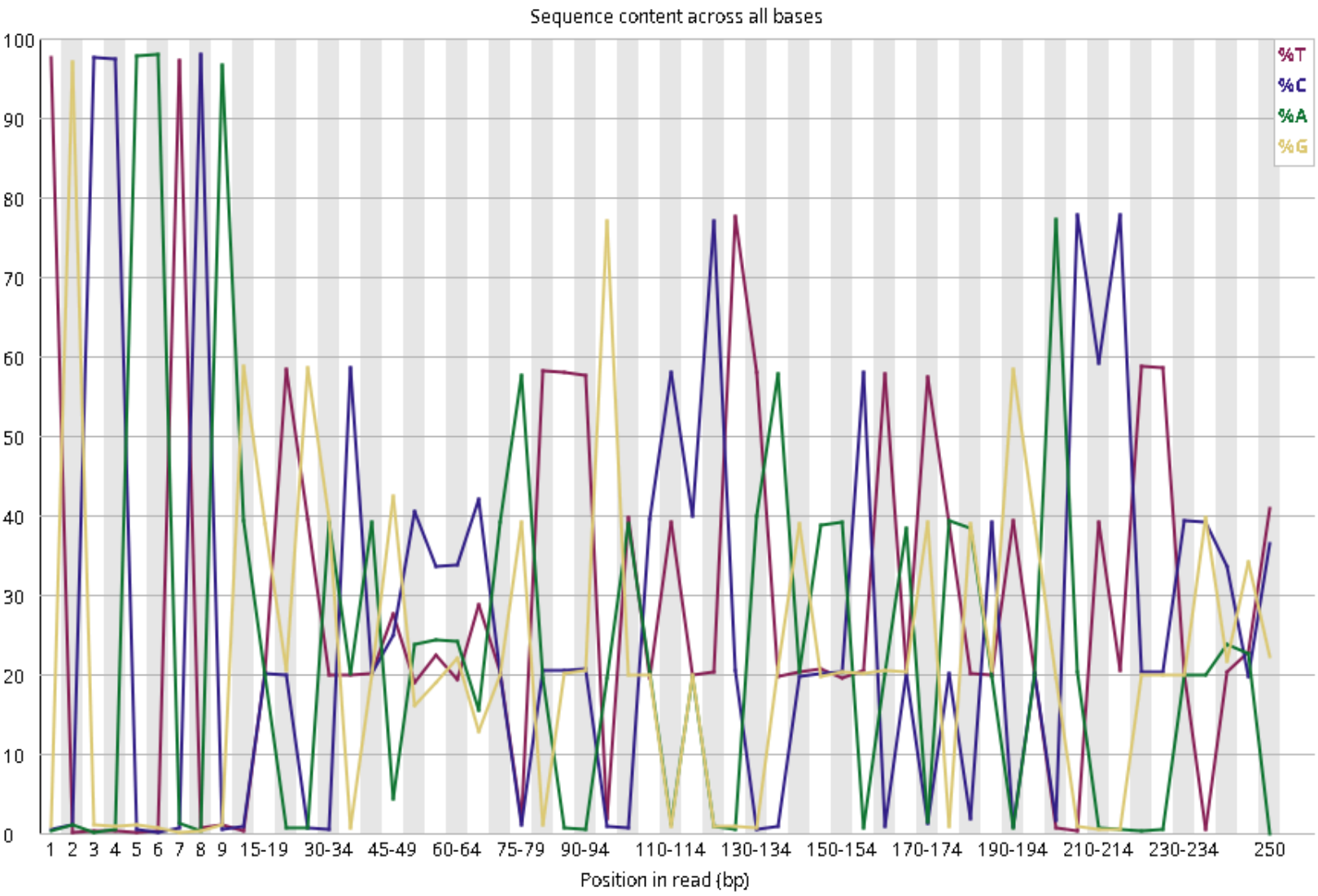
Per tile sequence quality



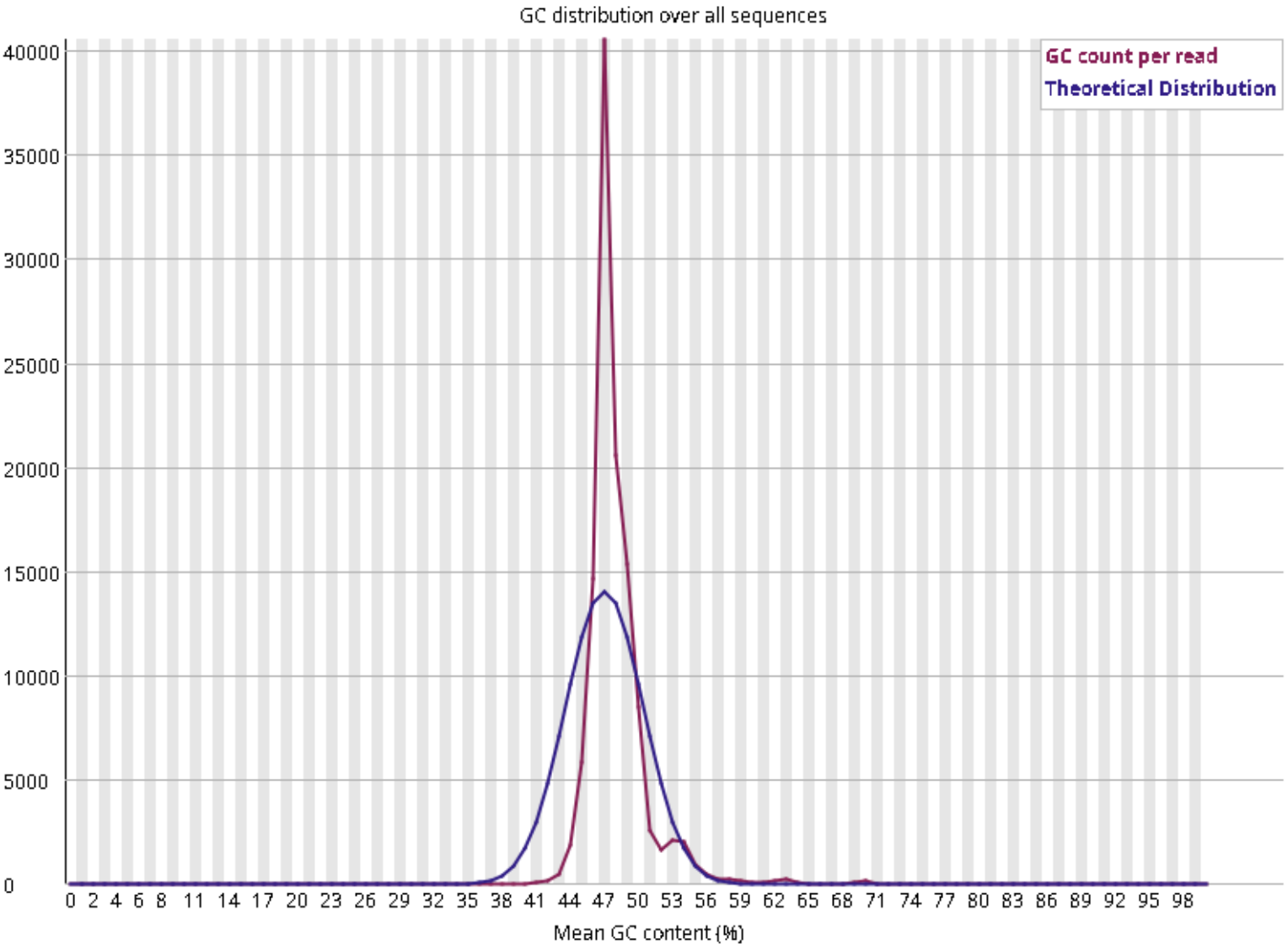
Per sequence quality scores



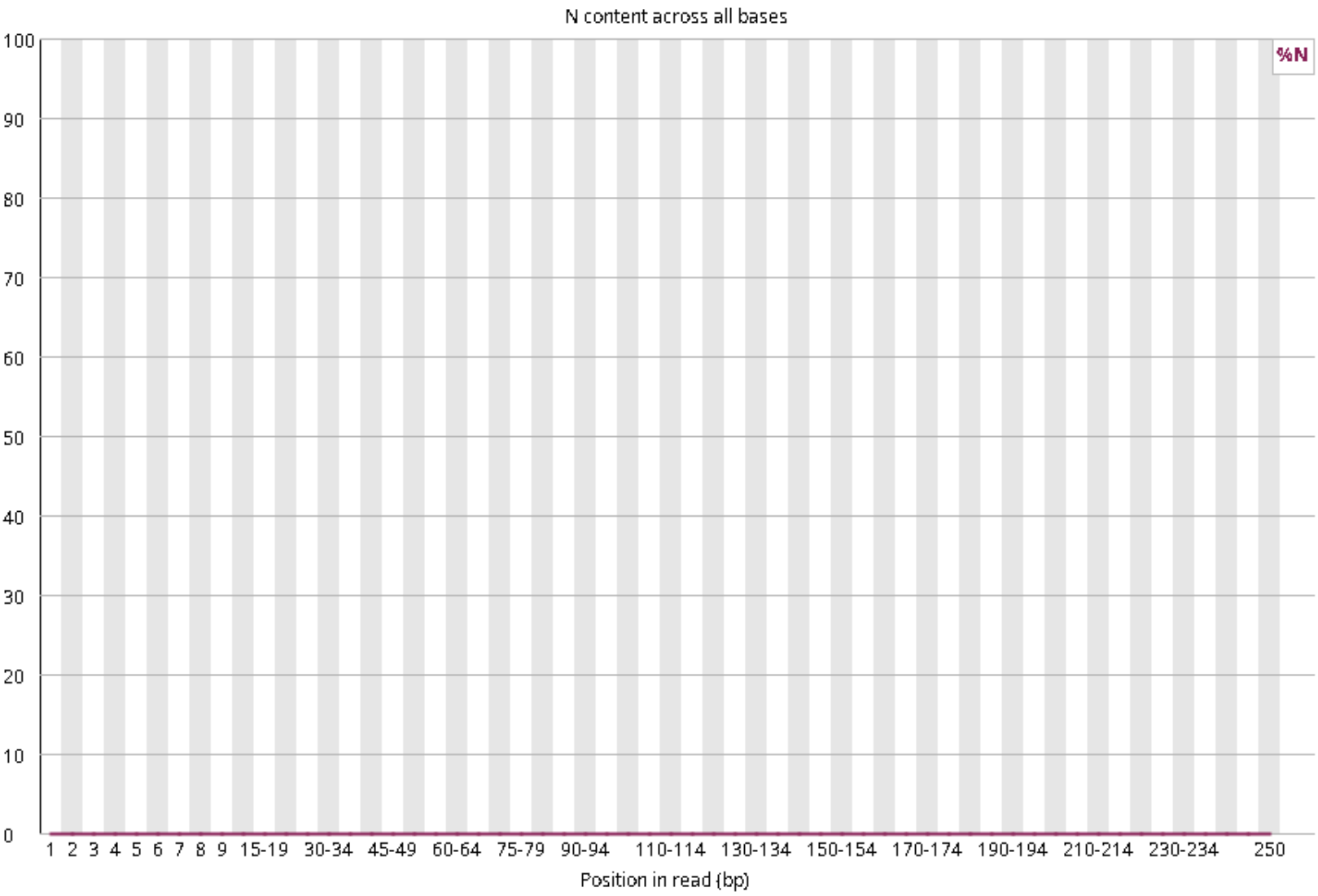
Per base sequence content



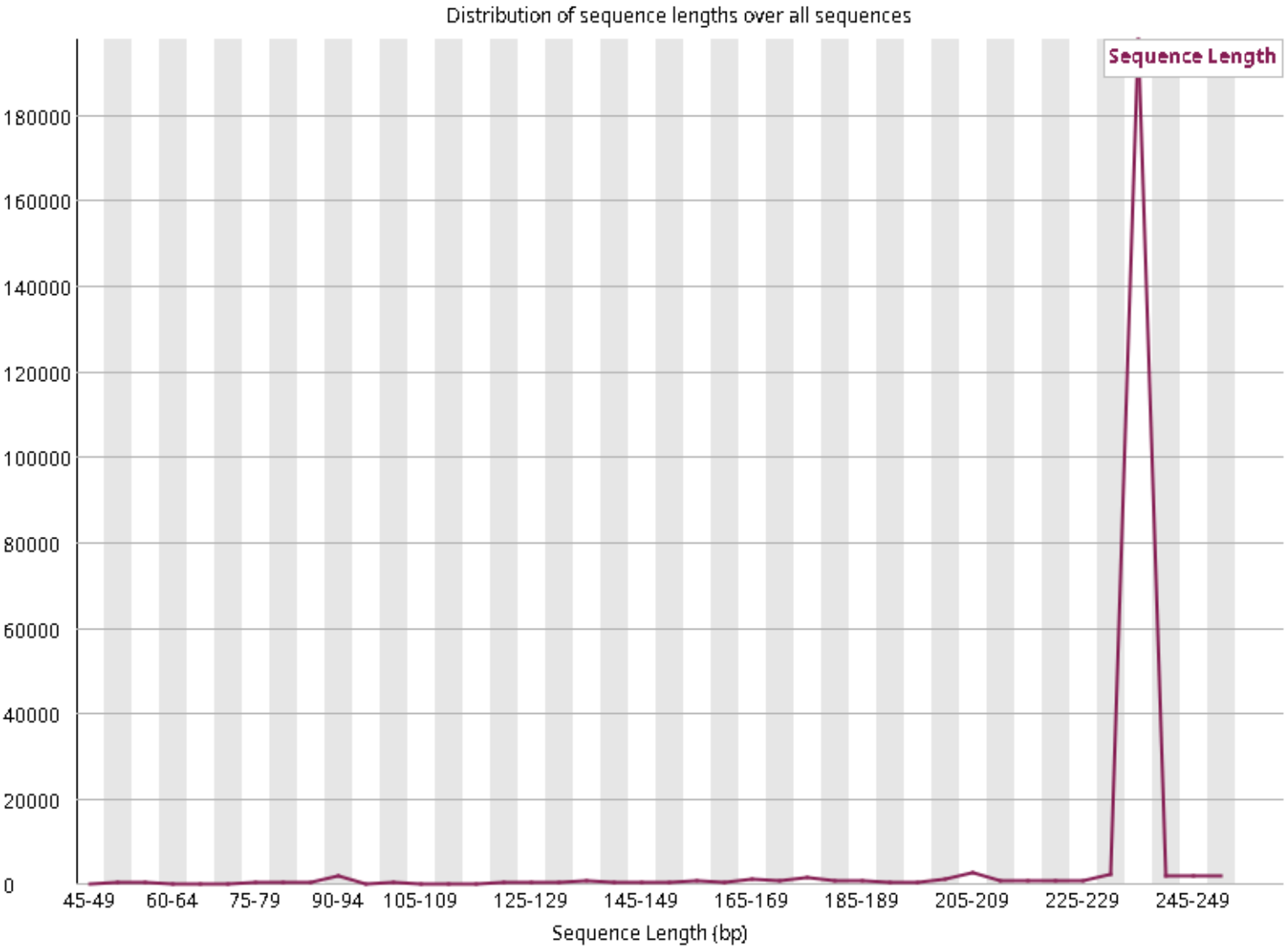
Per sequence GC content



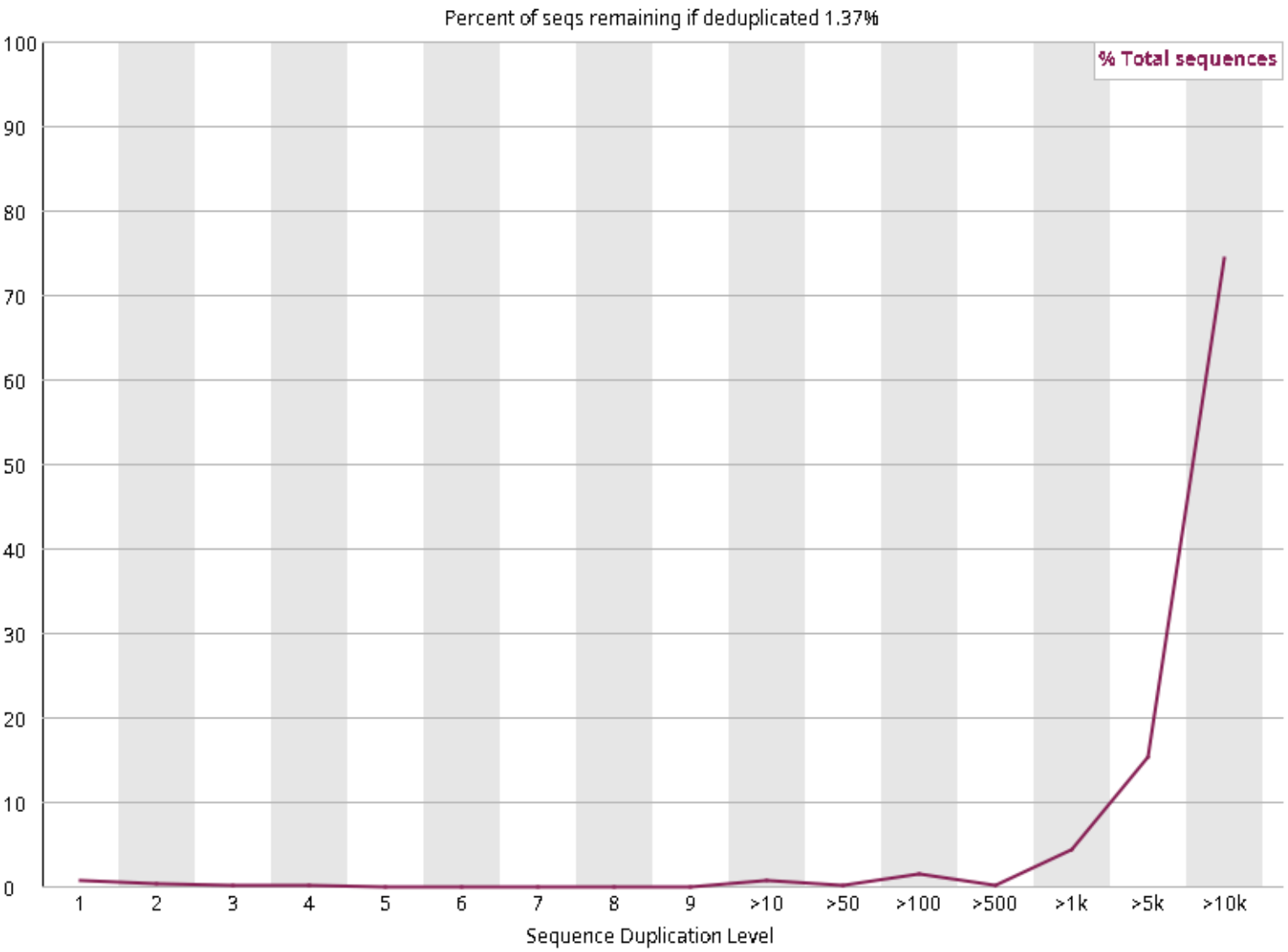
Per base N content



Sequence Length Distribution

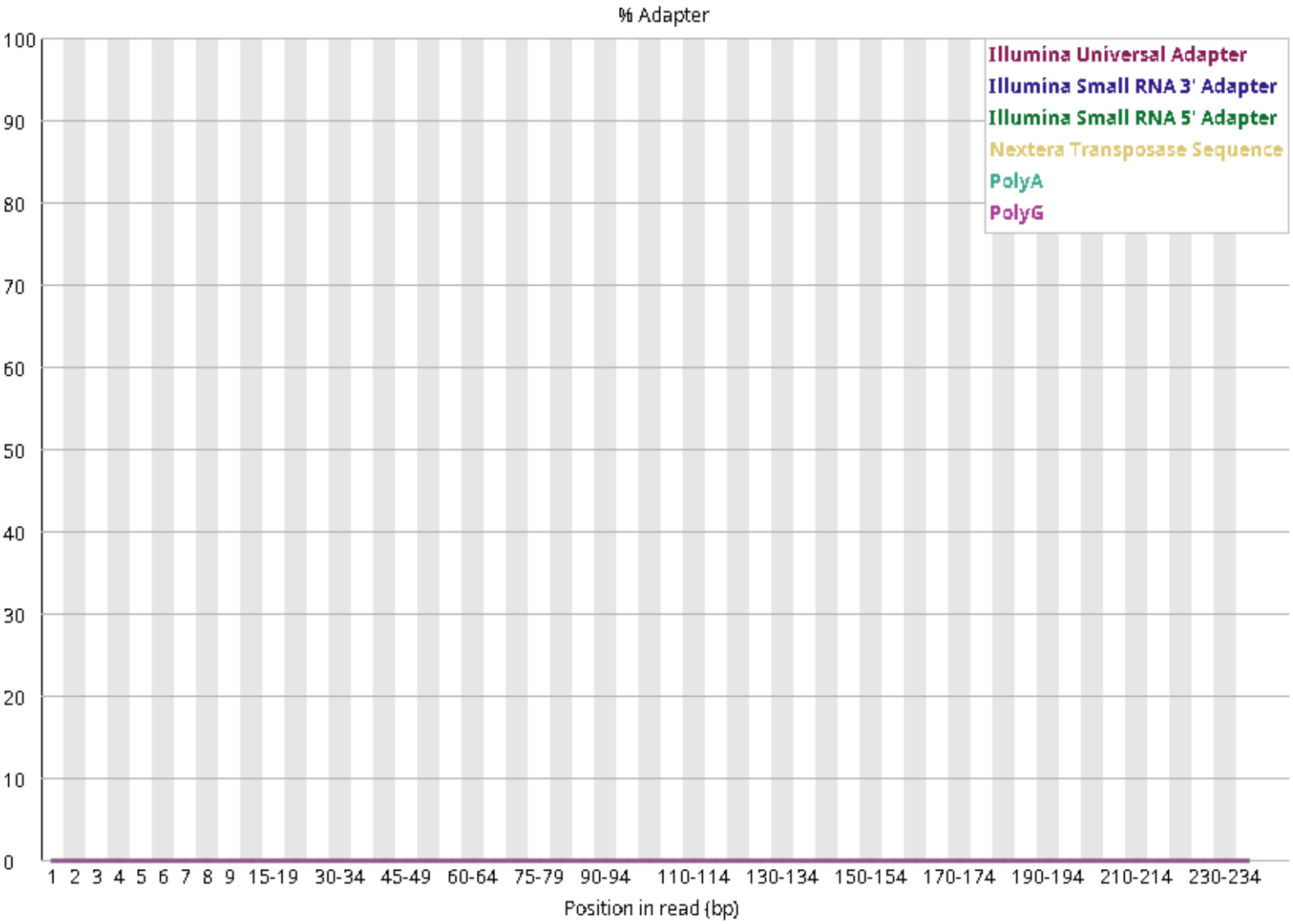


Sequence Duplication Levels



Overrepresented sequences

Sequence	Count	Percentage	Possible Source
TGCCAATCAGGGAAGTAGCCTTGTGTGTGGTAGATCCACATCGATGGCTC	69567	29.902127238887765	No Hit
TGCCAATCAGGGAAGTAGCCTTGTGTGTGGTAGATCCACATCGATGGCCC	22562	9.697871041783975	No Hit
TGCCAATCAGGGAAGTAGCCTTGTGTGTGGTAGATCCACATCGATGGCAC	15615	6.711827688921939	No Hit
TGCCAATCAGGGAAGTAGCCTTGTGTGTGGTAGATCCACATCGATGGCCT	15431	6.632738589033265	No Hit
TGCCAATCAGGGAAGTAGCCTTGTGTGTGGTAGATCCACATCGATGGCGG	15051	6.469402404480569	No Hit
TGCCAATCAGGGAAGTAGCCTTGTGTGTGGTAGATCCACATCGATGGCGC	13763	5.9157787052598545	No Hit
TGCCAATCAGGGAAGTAGCCTTGTGTGTGGTAGATCCACATCGATGGCCG	11156	4.795206512815443	No Hit
TGCCAATCAGGGAAGTAGCCTTGTGTGTGGTAGATCCACATCGATGGCCA	10160	4.3670937764615365	No Hit
TGCCAATCAGGGAAGTAGCCTTGTGTGTGGTAGATCCACATCGATGGCTG	8801	3.782952000653345	No Hit

Sequence	Count	Percentage	Possible Source
TGCCAATCAGGGAAGTAGCCTTGTGTGTGGTAGATCCACATCGATGGCAA	8563	3.6806519692756043	No Hit
TGCCAATCAGGGAAGTAGCCTTGTGTGTGGTAGATCCACATCGATGGCAG	6871	2.9533761159514977	No Hit
TGCCAATCAGGGAAGTAGCCTTGTGTGTGGTAGATCCACATCGATGGCAT	6297	2.7066525108640054	No Hit
TGCCAATCAGGGAAGTAGCCTTGTGTGTGGTAGATCCACATCGATGGCTT	5491	2.3602078667864466	No Hit
TGCCAATCAGGGAAGTAGCCTTGTGTGTGGTAGATCCACATCGATGGCGA	3389	1.4567008669712742	No Hit
TGCCAATCAGGGAAGTAGCCTTGTGTGTGGTAGATCCACATCGATGGCTA	3183	1.3681554616611291	No Hit
TGCCAATCAGGGAAGTAGCCTTGTGTGTGGTAGATCCACAGATCAAGGAT	2138	0.918980954141217	No Hit
TGCCAATCAGGGAAGTAGCCTTGTGTGTGGTAGATCCACATCGATGGCGT	1914	0.8226985716680494	No Hit
GAGAAGATGAGGCCCAGGAAGCCGATGTACAGGGTGGTTATCAGCTCCTG	697	0.2995929490348121	No Hit
TATCAGATCTCGAGCTATTACAAGTCCTCTTCAGAAATAAGCTTTTGTTC	478	0.20545972688470615	No Hit
TCCGGAACTCGCCGTTCTCTGTGATCTGCAGCCGGGGTGGGGGGGGTGGG	402	0.1727924899741671	No Hit
TGCCAATCAGGGAAGTAGCCAGTTCAGACGTGTGCTCTTGTGCTTCTAGC	368	0.15817819977734698	No Hit
GAGGGATCTCTAGTTACCAGAGTCACACAACAGACGGGCACACACTACTT	358	0.15387987913122345	No Hit
CCCGCAATTTGACGGTCTTGCCTTTTAAACCGATGCAATCTATTGGTTTA	244	0.10487902376541484	No Hit
GACCGAAGGTTTCCCAGACTGGGCGTCTGTCGCCCCCAACAGCATCGCCG	235	0.10101053518390365	No Hit

Adapter Content