FastQC Report

Mon 3 Mar 2025
SRR32313970_2_unpaired.fastq

Summary

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- Per base sequence content
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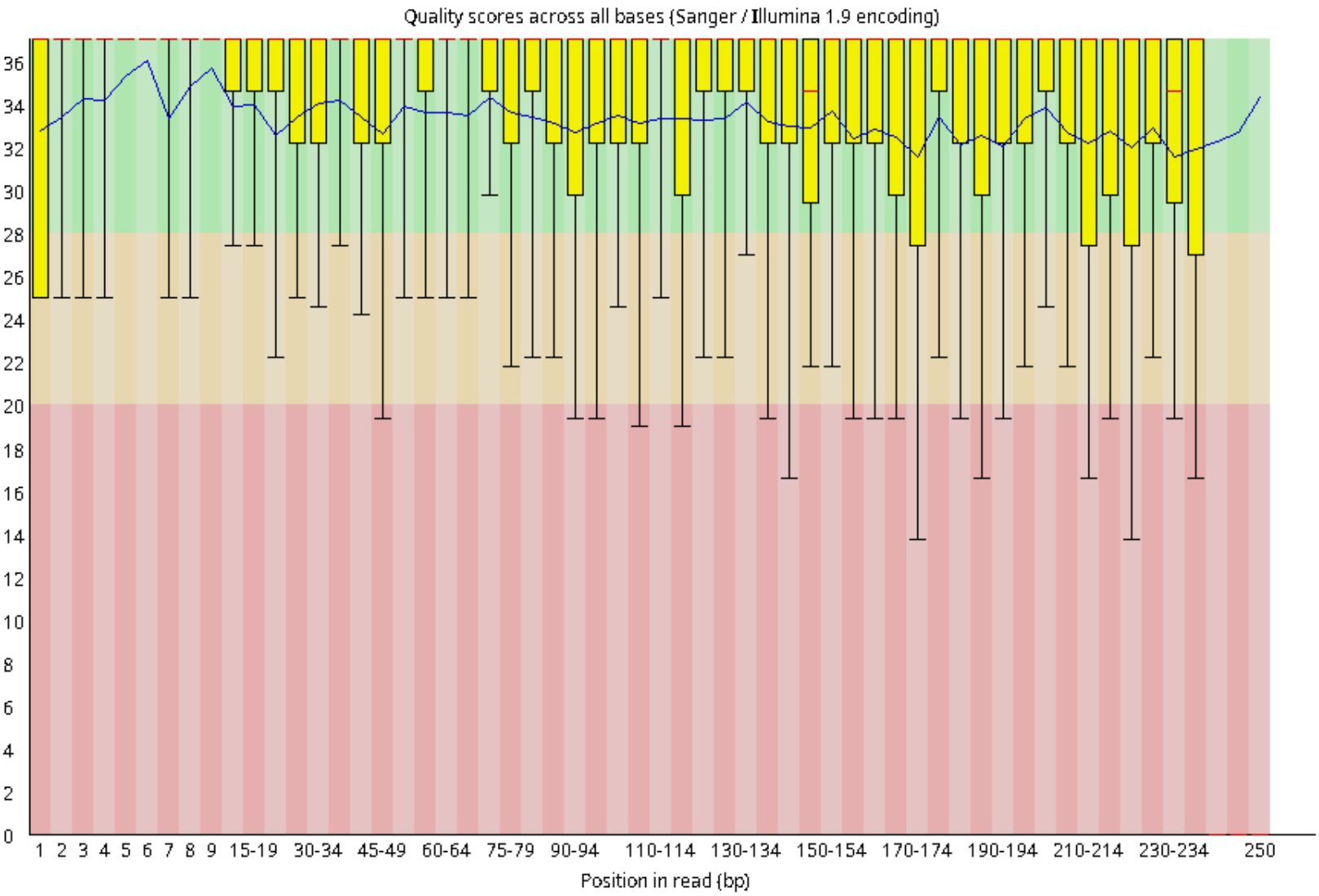
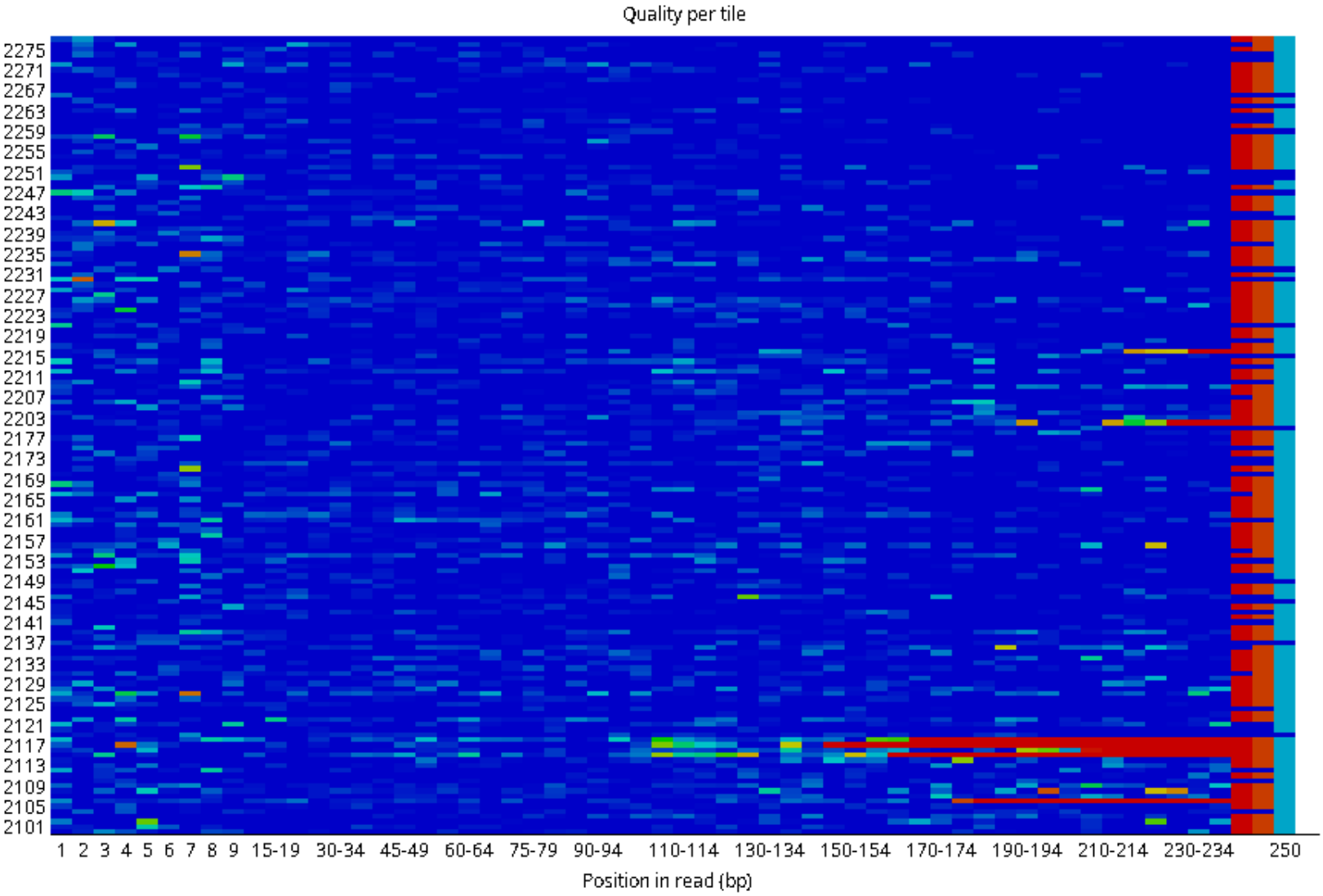
Basic Statistics

Measure	Value
Filename	SRR32313970_2_unpaired.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	2325
Total Bases	404.2 kbp
Sequences flagged as poor quality	0
Sequence length	50-250
%GC	48

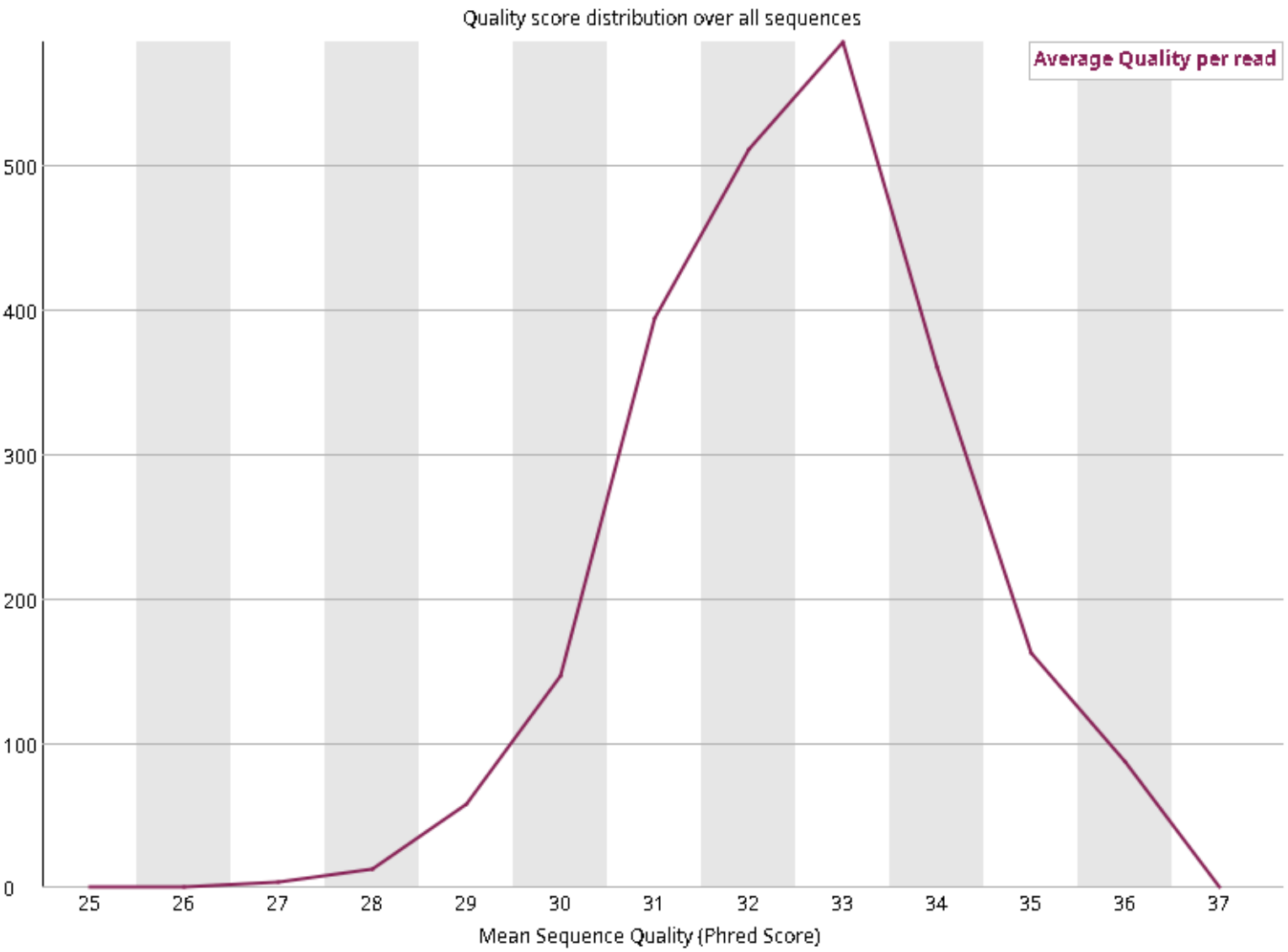
Per base sequence quality



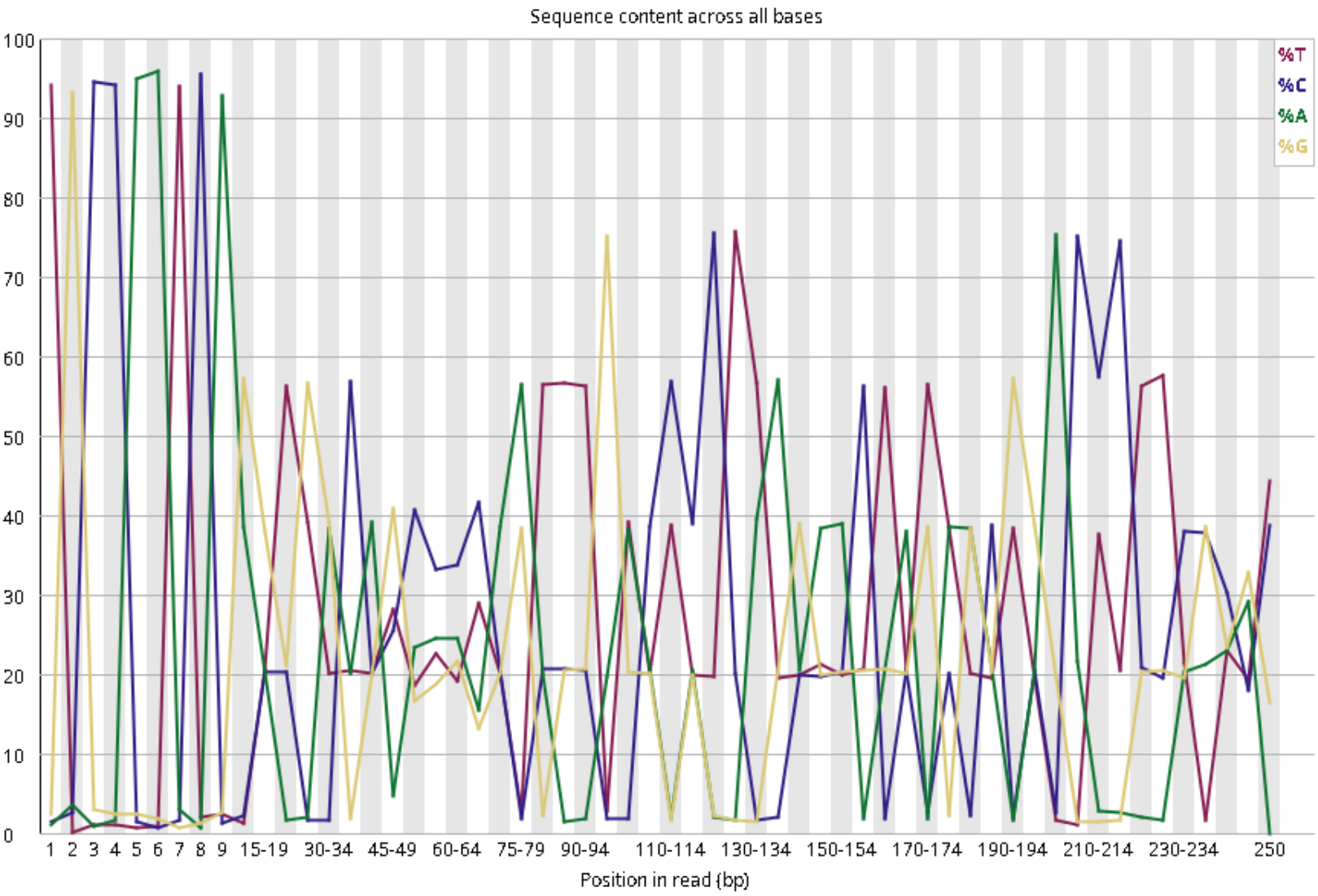
Per tile sequence quality



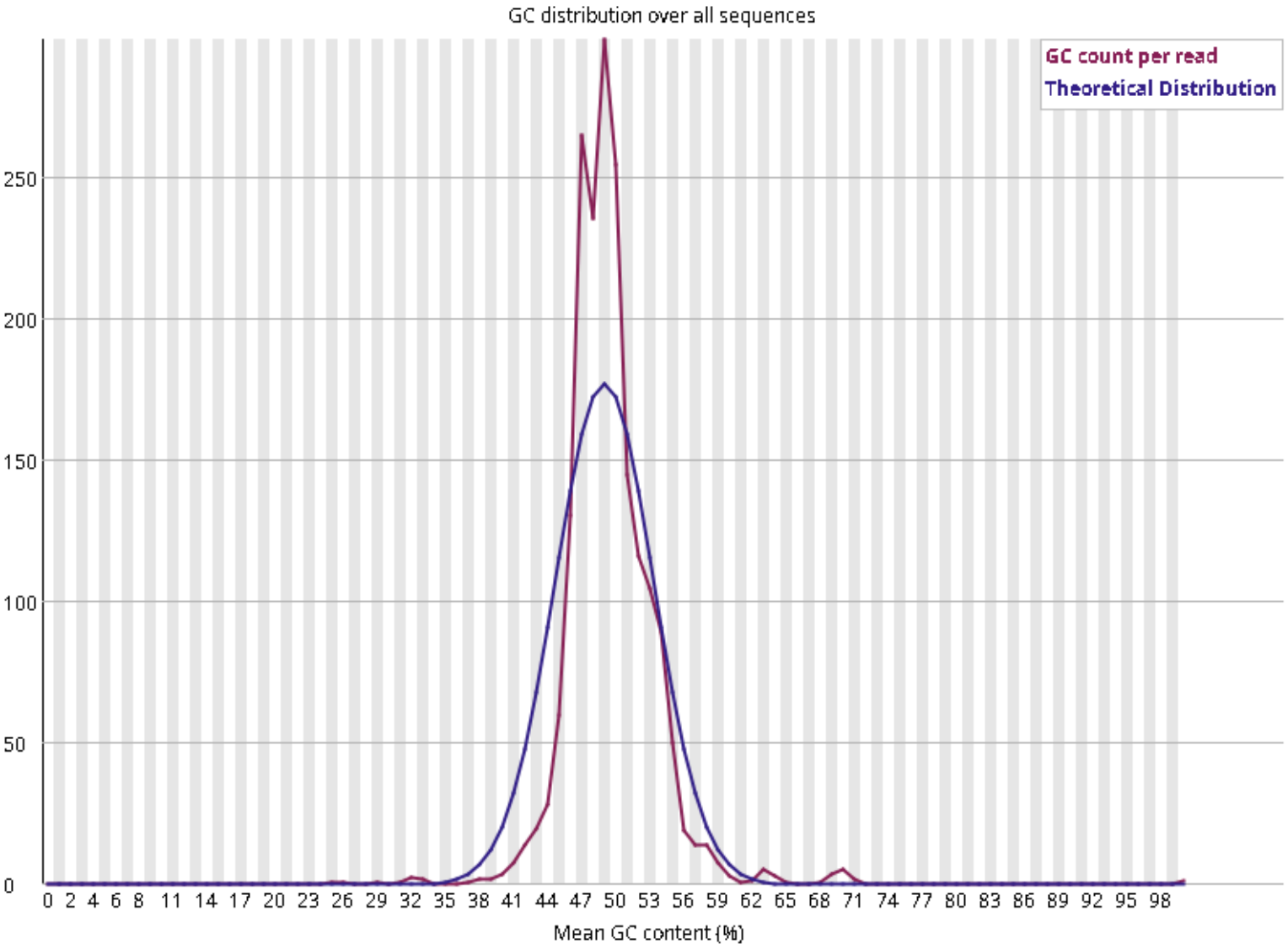
Per sequence quality scores



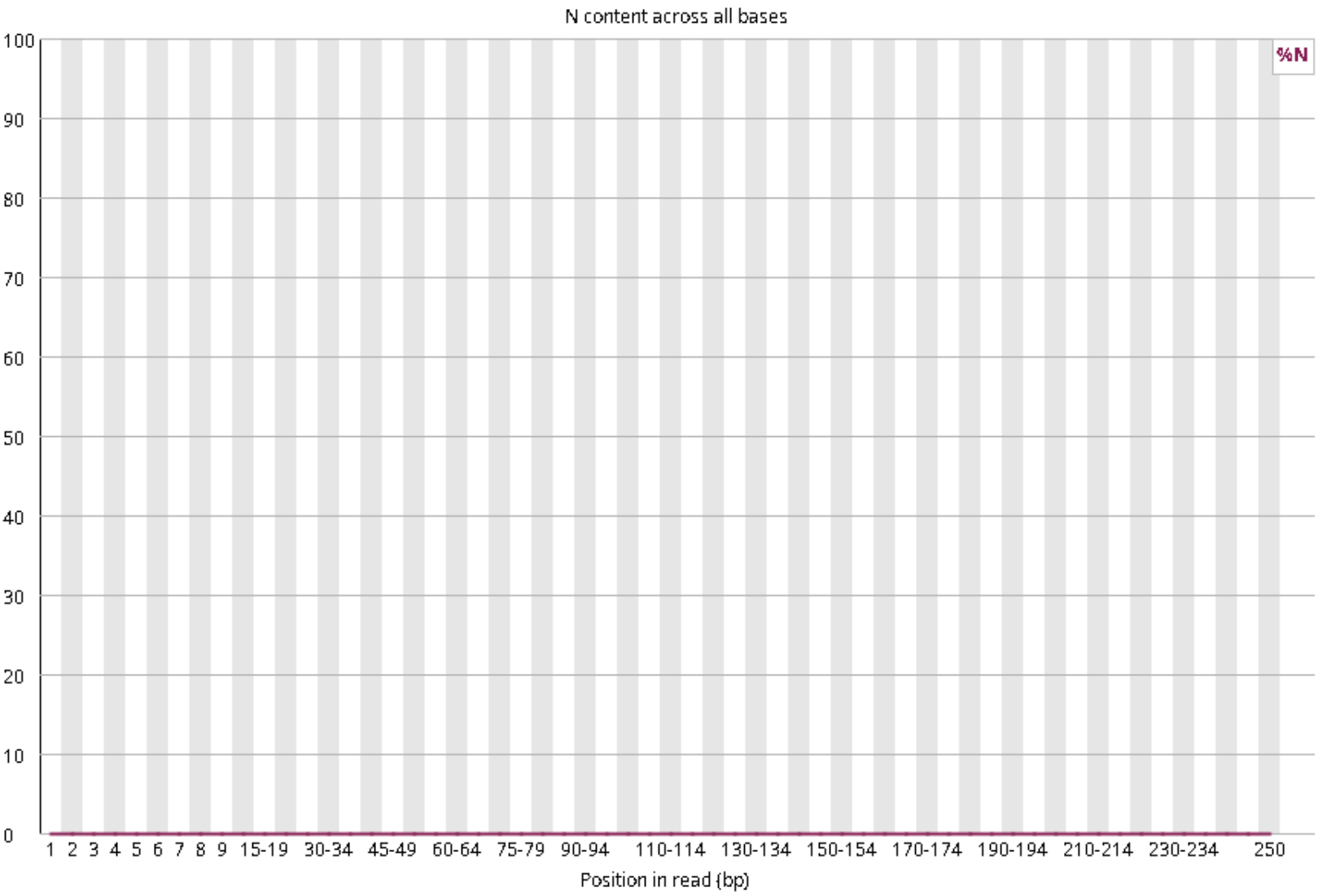
Per base sequence content



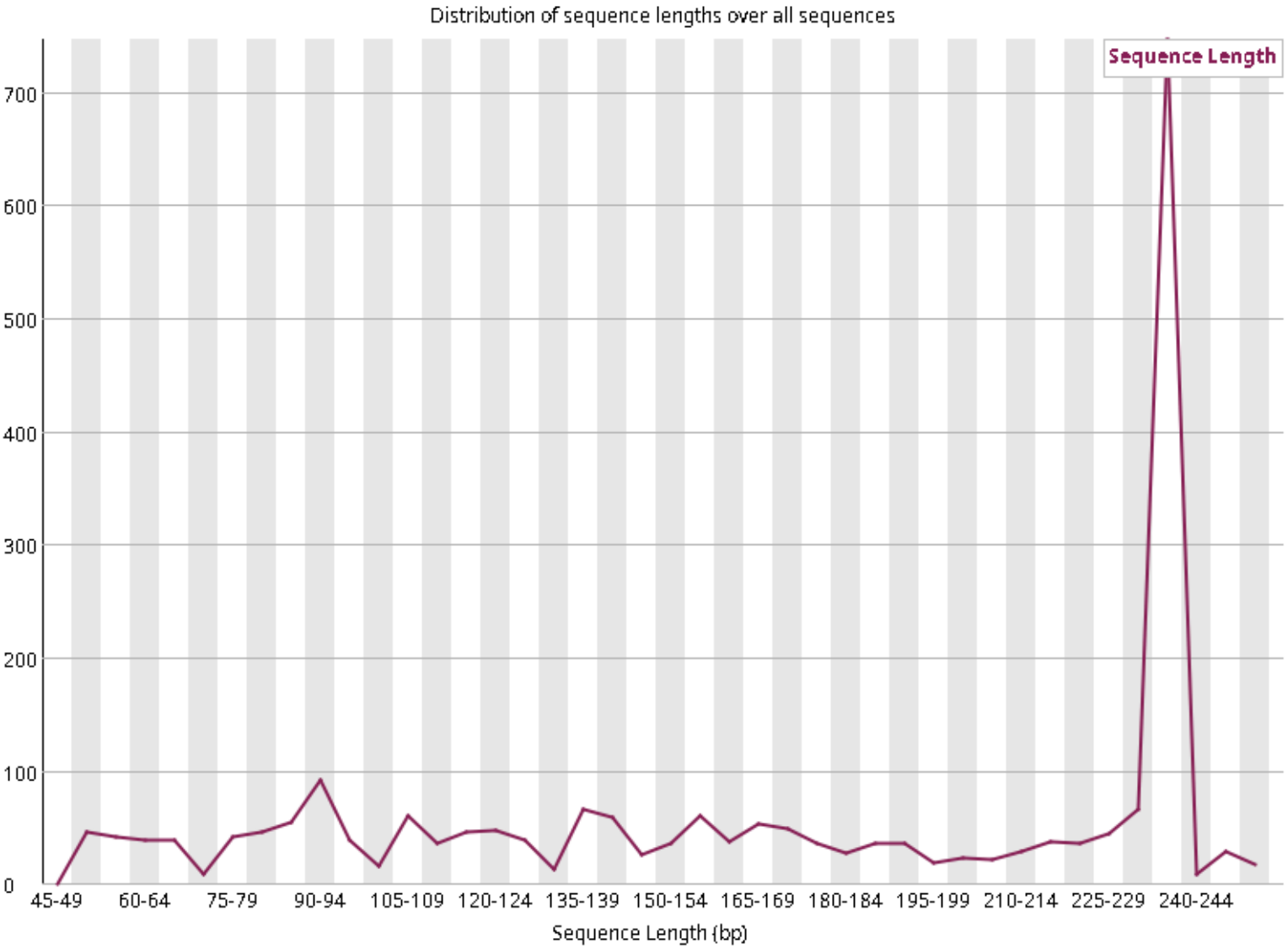
Per sequence GC content



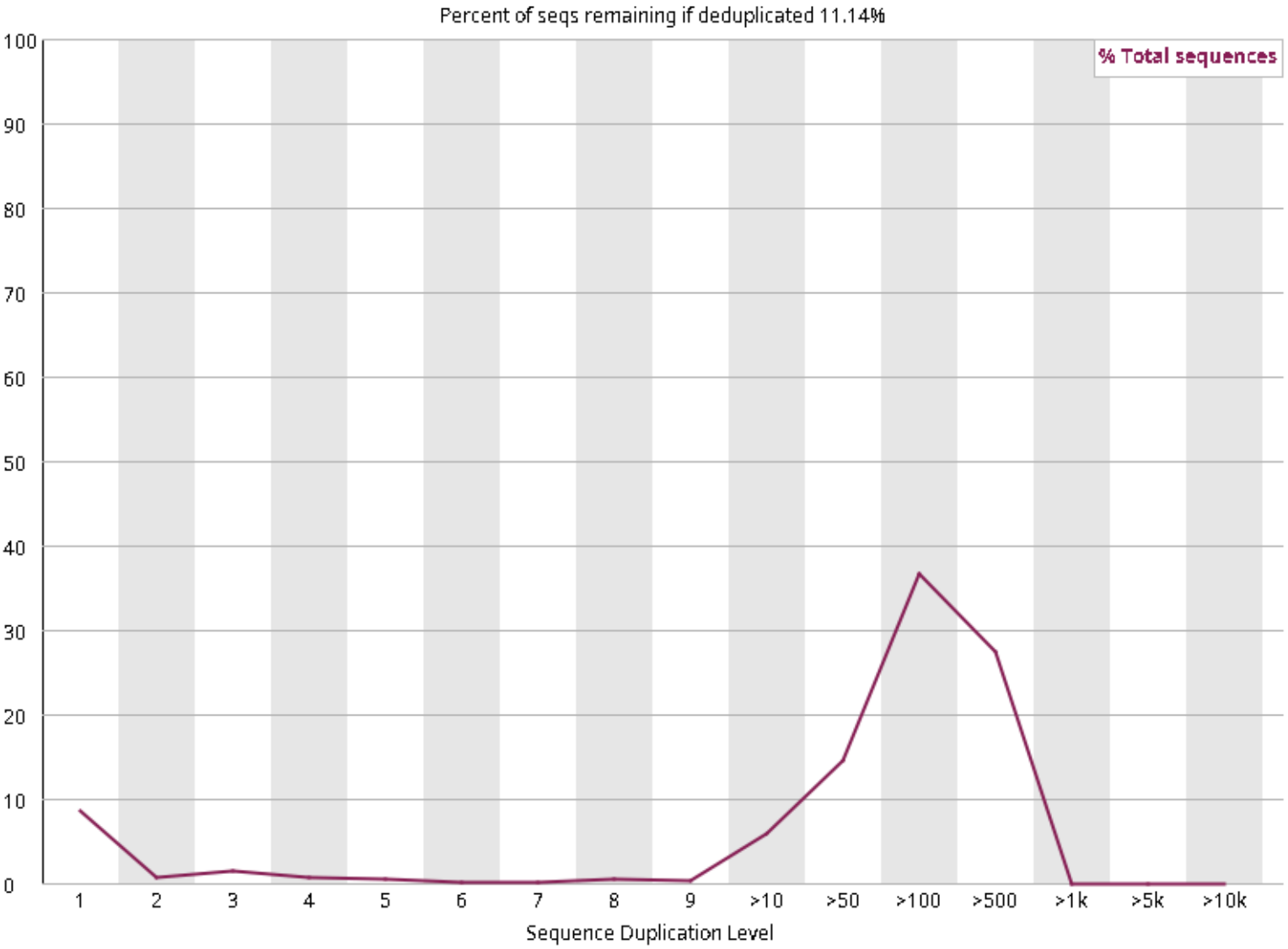
Per base N content



Sequence Length Distribution

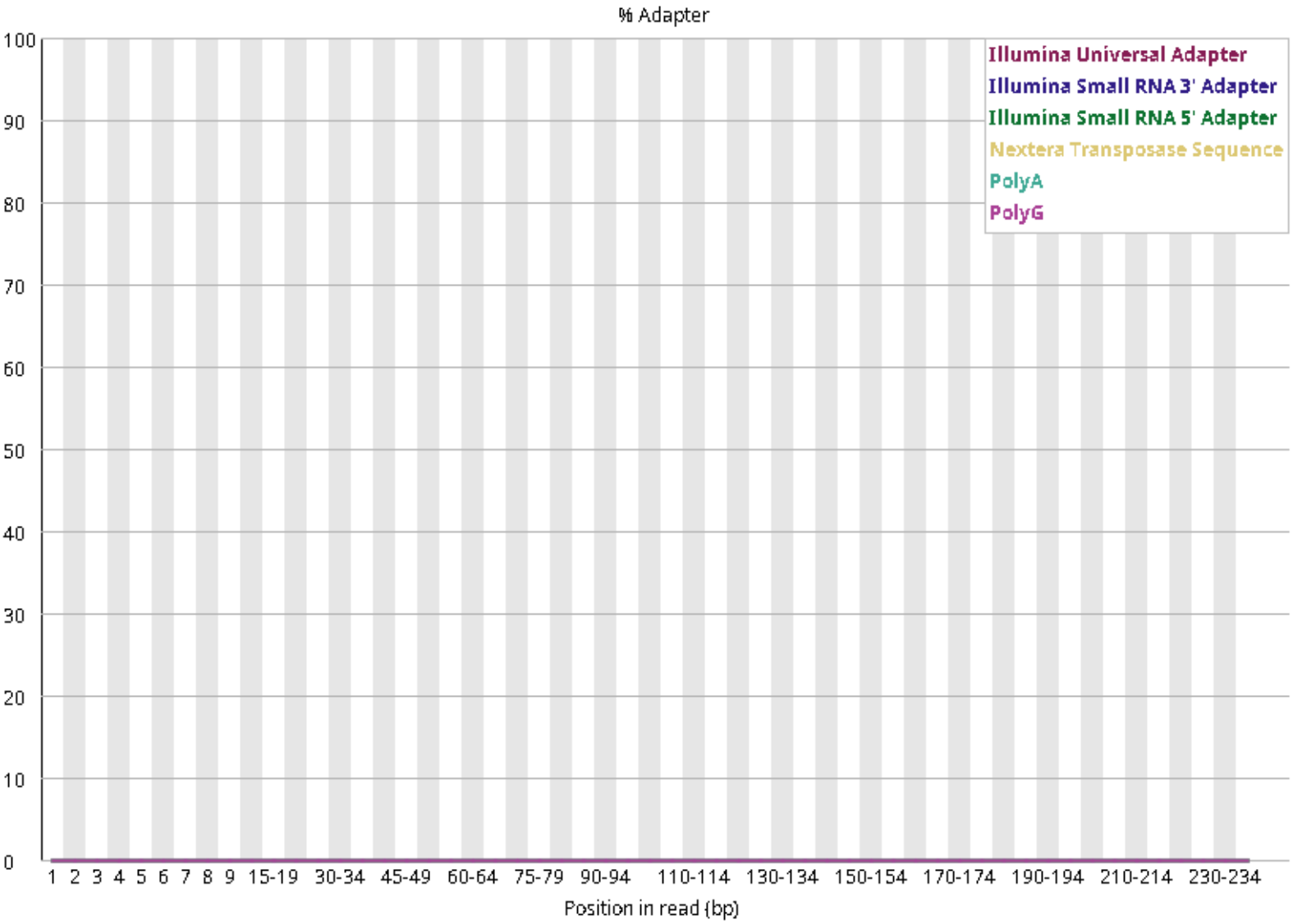


Sequence Duplication Levels



Overrepresented sequences

Sequence	Count	Percentage	Possible Source
TGCCAATCAGGGAAGTAGCCTTGTGTGTGGTAGATCCACATCGATGGCTC	643	27.655913978494624	No Hit
TGCCAATCAGGGAAGTAGCCTTGTGTGTGGTAGATCCACATCGATGGCCC	222	9.548387096774194	No Hit
TGCCAATCAGGGAAGTAGCCTTGTGTGTGGTAGATCCACATCGATGGCCT	158	6.795698924731183	No Hit
TGCCAATCAGGGAAGTAGCCTTGTGTGTGGTAGATCCACATCGATGGCAC	147	6.322580645161291	No Hit
TGCCAATCAGGGAAGTAGCCTTGTGTGTGGTAGATCCACATCGATGGCGC	115	4.946236559139785	No Hit
TGCCAATCAGGGAAGTAGCCTTGTGTGTGGTAGATCCACATCGATGGCGG	114	4.903225806451613	No Hit
TGCCAATCAGGGAAGTAGCCTTGTGTGTGGTAGATCCACATCGATGGCTG	101	4.344086021505376	No Hit
TGCCAATCAGGGAAGTAGCCTTGTGTGTGGTAGATCCACATCGATGGCCA	91	3.913978494623656	No Hit
TGCCAATCAGGGAAGTAGCCTTGTGTGTGGTAGATCCACATCGATGGCCG	83	3.5698924731182795	No Hit

Sequence	Count	Percentage	Possible Source
TGCCAATCAGGGAAGTAGCCTTGTGTGTGGTAGATCCACATCGATGGCAA	59	2.5376344086021505	No Hit
TGCCAATCAGGGAAGTAGCCTTGTGTGTGGTAGATCCACATCGATGGCAG	58	2.4946236559139785	No Hit
TGCCAATCAGGGAAGTAGCCTTGTGTGTGGTAGATCCACATCGATGGCAT	53	2.2795698924731185	No Hit
TGCCAATCAGGGAAGTAGCCTTGTGTGTGGTAGATCCACATCGATGGCTT	46	1.9784946236559142	No Hit
TGCCAATCAGGGAAGTAGCCTTGTGTGTGGTAGATCCACATCGATGGCTA	28	1.2043010752688172	No Hit
TGCCAATCAGGGAAGTAGCCTTGTGTGTGGTAGATCCACATCGATGGCGA	25	1.0752688172043012	No Hit
GAGAAGATGAGGCCCAGGAAGCCGATGTACAGGGTGGTTATCAGCTCCTG	19	0.8172043010752689	No Hit
TGCCAATCAGGGAAGTAGCCTTGTGTGTGGTAGATCCACATCGATGGCGT	15	0.6451612903225806	No Hit
GAGGGATCTCTAGTTACCAGAGTCACACAACAGACGGGCACACACTACTT	10	0.43010752688172044	No Hit
GACCGAAGGTTTCCCAGACTGGGCGTCTGTCGCCCCCAACAGCATCGCCG	9	0.3870967741935484	No Hit
TATCAGATCTCGAGCTATTACAAGTCCTCTTCAGAAATAAGCTTTTGTTC	8	0.34408602150537637	No Hit
TGCCAATCAGGGAAGTAGCCTTGTGTGTGGTAGATCCACAGATCAAGGAT	8	0.34408602150537637	No Hit
TGCCAATCAGGGAAGTAGCCAGTTCAGACGTGTGCTCTTGTGCTTCTAGC	7	0.3010752688172043	No Hit
TAGCGAGGGAAGCAAGTTGGACCCACAGCAGGCTTTGGAGTCAAGGAAAG	6	0.25806451612903225	No Hit
AAGTGGACTTCGGTGCTTACCTGGTTTTCCACTACCCGAAAAAAATCCAG	5	0.21505376344086022	No Hit
CCCTCATAGTTAGCGTAACGATCTAAAGTTTTGTCGTCTTTCCAGACGTT	5	0.21505376344086022	No Hit
TCCGGAACTCGCCGTTCTCTGTGATCTGCAGCCGGGGTGGGGGGGGTGGG	5	0.21505376344086022	No Hit
GCTCTTCCTCTATCTTATCTAAGGCTTCCTTGGTGTCTTTTACATCTATC	4	0.17204301075268819	No Hit
TGAGATCCTTGTGATCATCAAAGGAGAGCTTACGGTTCTTCTGTCTTTCC	4	0.17204301075268819	No Hit
TGCCAATCAGGGAAGTAGCCGTGTGTGTGGTAGATCCACATCGATGGCGG	4	0.17204301075268819	No Hit
CCCGCAATTTGACGGTCTTGCCTTTTAAACCGATGCAATCTATTGGTTTA	4	0.17204301075268819	No Hit
TGCCAATCAGGGAAGTAGCCGTGTGTGTGGTAGATCCACATCGATGGCCC	4	0.17204301075268819	No Hit
TGCCAATCAGGGAAGTAGCCTTGTGTGTGGTAGATCCACATCGATGTCCC	3	0.12903225806451613	No Hit
GATCCCCGGTCGAACTCGCGTGCAGTGTTCCCCAGTTGAACGTGCGGGTA	3	0.12903225806451613	No Hit
TGCCAATCAGGGAAGTAGCCTTGTGTGTGGTAGATCCACATAGATGGCTC	3	0.12903225806451613	No Hit
ACGTCATCCCCACCTTCCTCCGGTTTGTCACCGGCAGTCTCATTAGAGTG	3	0.12903225806451613	No Hit
TGCCAATCAGGGAAGTAGCCTTGTGTGTGGTAGATCCACATCGATGGATC	3	0.12903225806451613	No Hit
CCAGAATCTCCCAATCATAAGGAATGAGTCTATGTCCATGAGCAATGGAA	3	0.12903225806451613	No Hit
TGCCAATCAGGGACGTAGCCTTGTGTGTGGTAGATCCACATCGATGGCTC	3	0.12903225806451613	No Hit
TGCCAATCAGGGAAGTAGCCGTGTGTGTGGTAGATCCACATCGATGGCTC	3	0.12903225806451613	No Hit
TGCCAATCAGGGAAGTAGCCGTGTGTGTGGTAGATCCACATCGATGGCTG	3	0.12903225806451613	No Hit
GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	3	0.12903225806451613	No Hit
CAGACGCTGGAAGGGAAGTTTGCGAATCAGAAGTTCAGTGGACTTCTGAT	3	0.12903225806451613	No Hit
GGGTGCCCTAATACCTGACGACCATTCATTGATGGGCAGTCAGACCCCTC	3	0.12903225806451613	No Hit
CCAATTCCCACTCCTTTCAAGACCTAGCTAGCGAATTCAAAAAAGCACCG	3	0.12903225806451613	No Hit

Adapter Content