












FastQC Report Sun 10 May 2015 R2_IJS8_mates_ICC5_SW023_S60_L001_R2_001.fastq.200

Summary

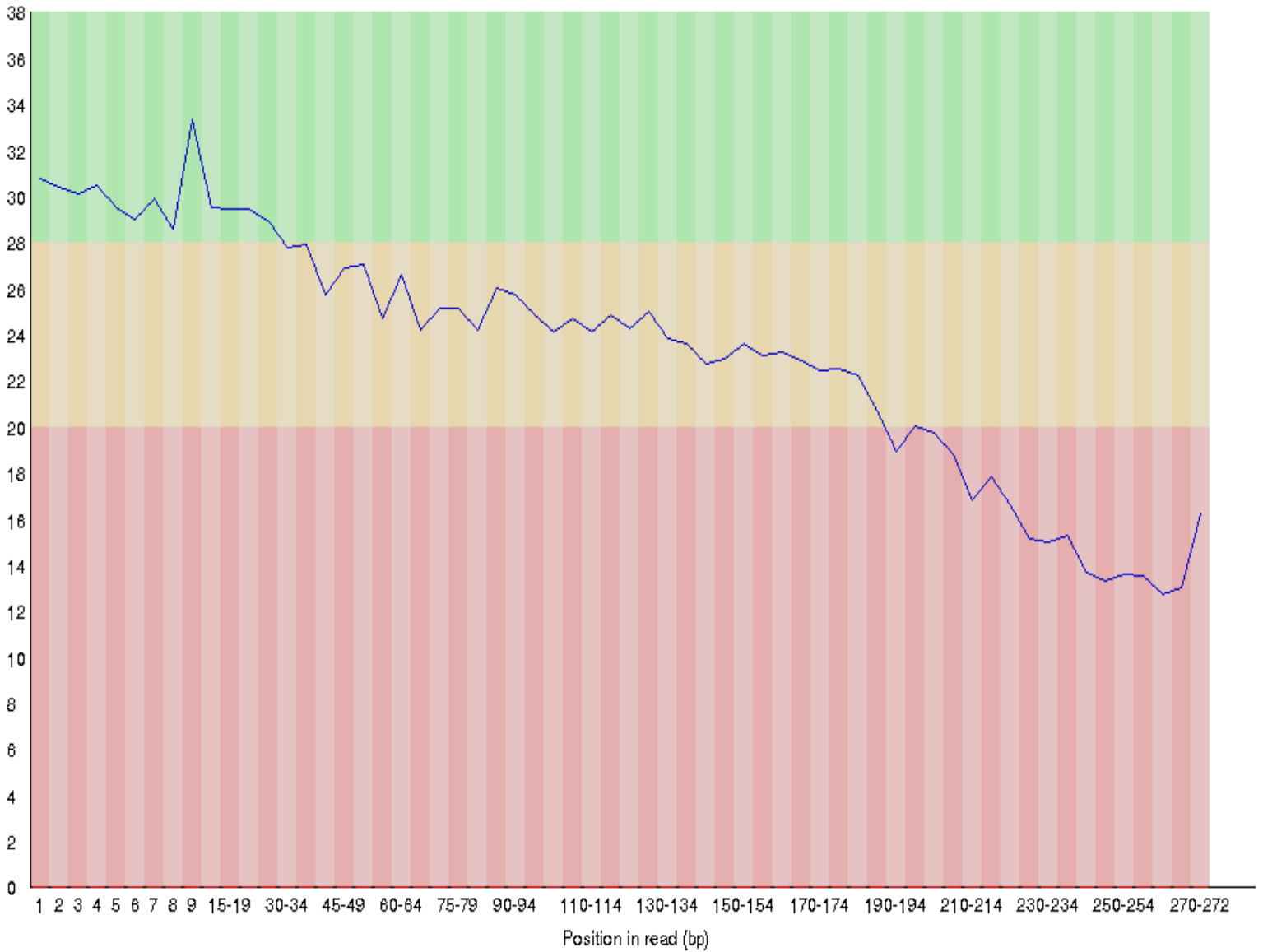
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Basic Statistics

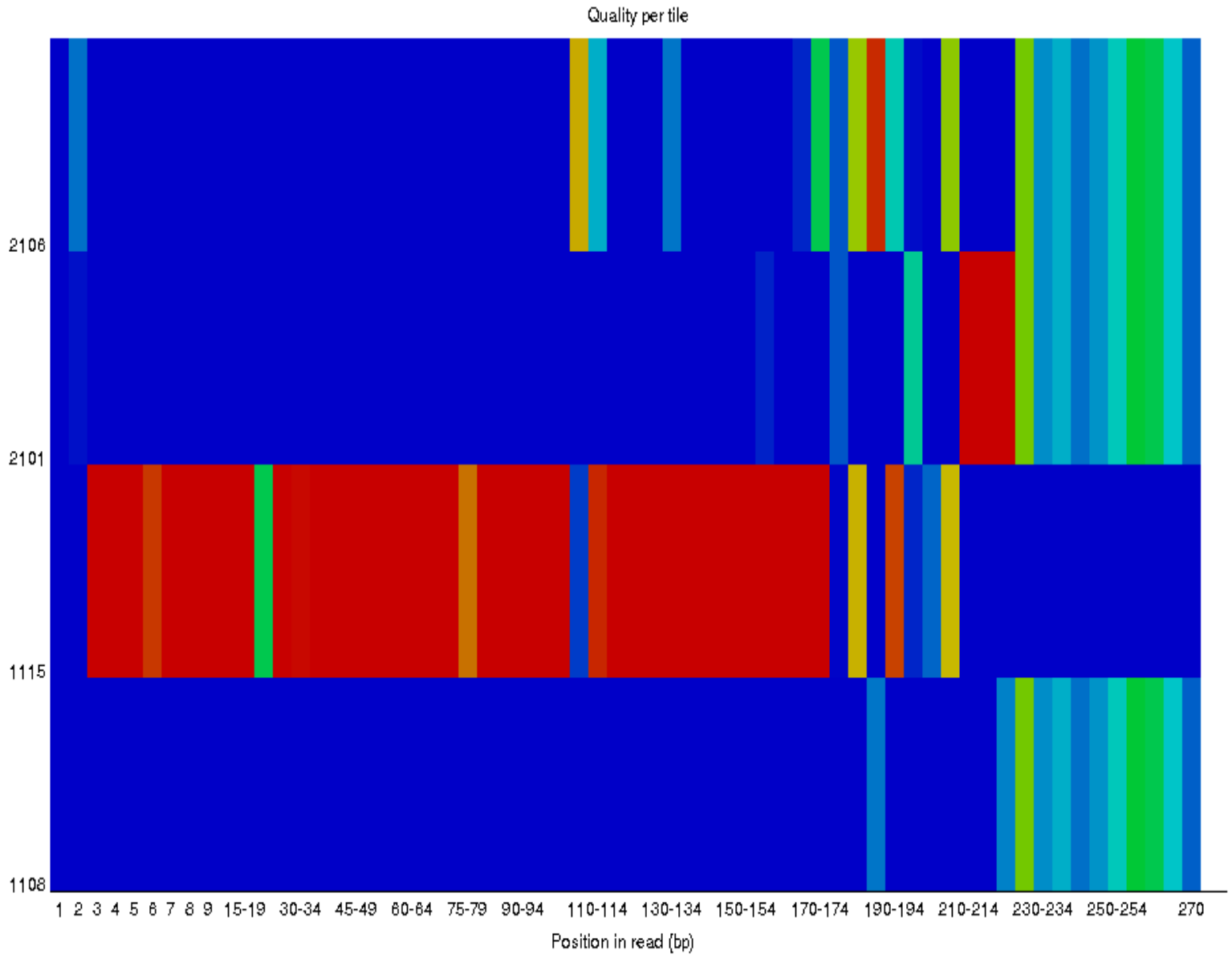
Measure	Value
Filename	R2_IJS8_mates_ICC5_SW023_S60_L001_R2_001.fastq.200
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	48
Sequences flagged as poor quality	0
Sequence length	201-272
%GC	42

Per base sequence quality

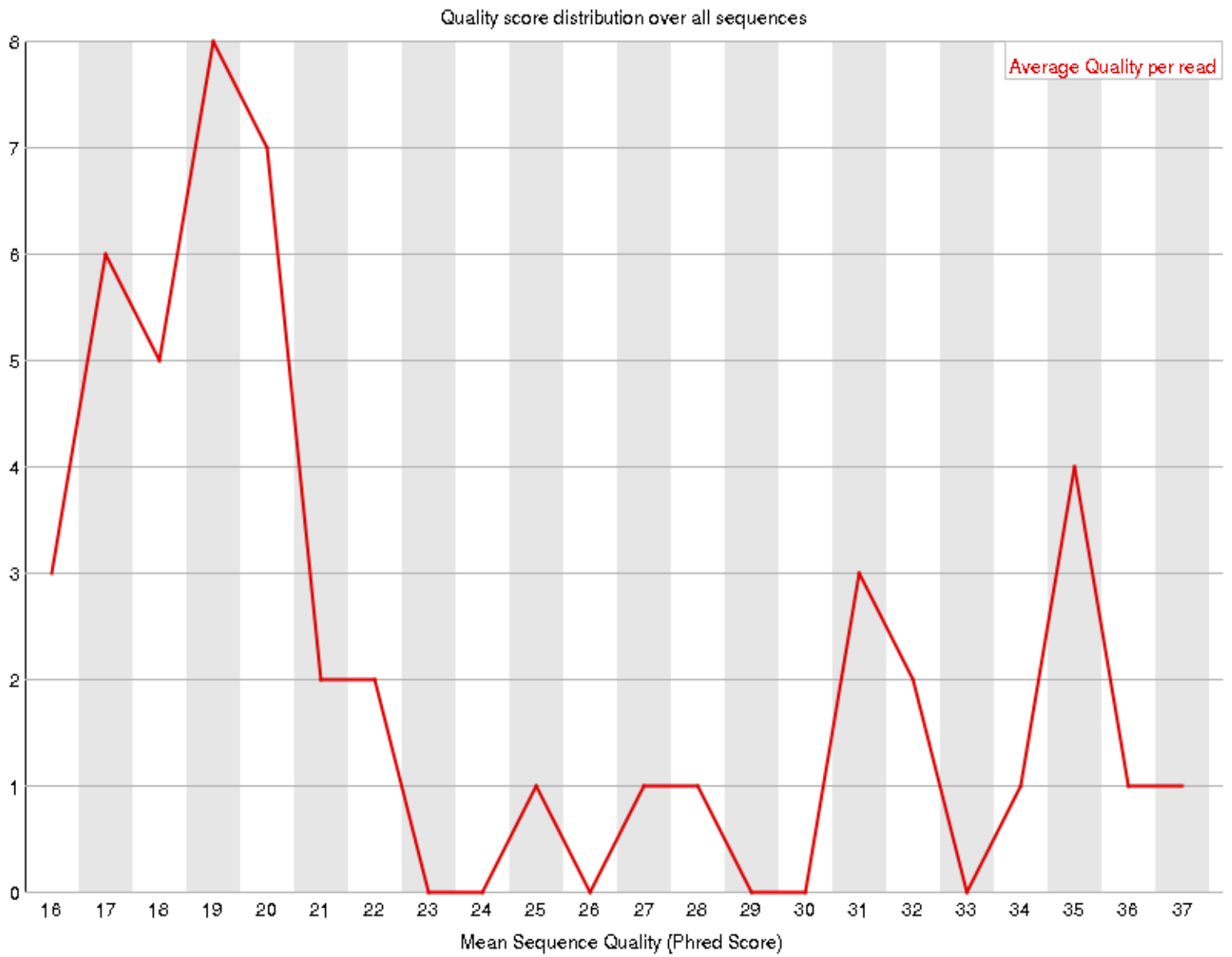
Quality scores across all bases (Sanger / Illumina 1.9 encoding)



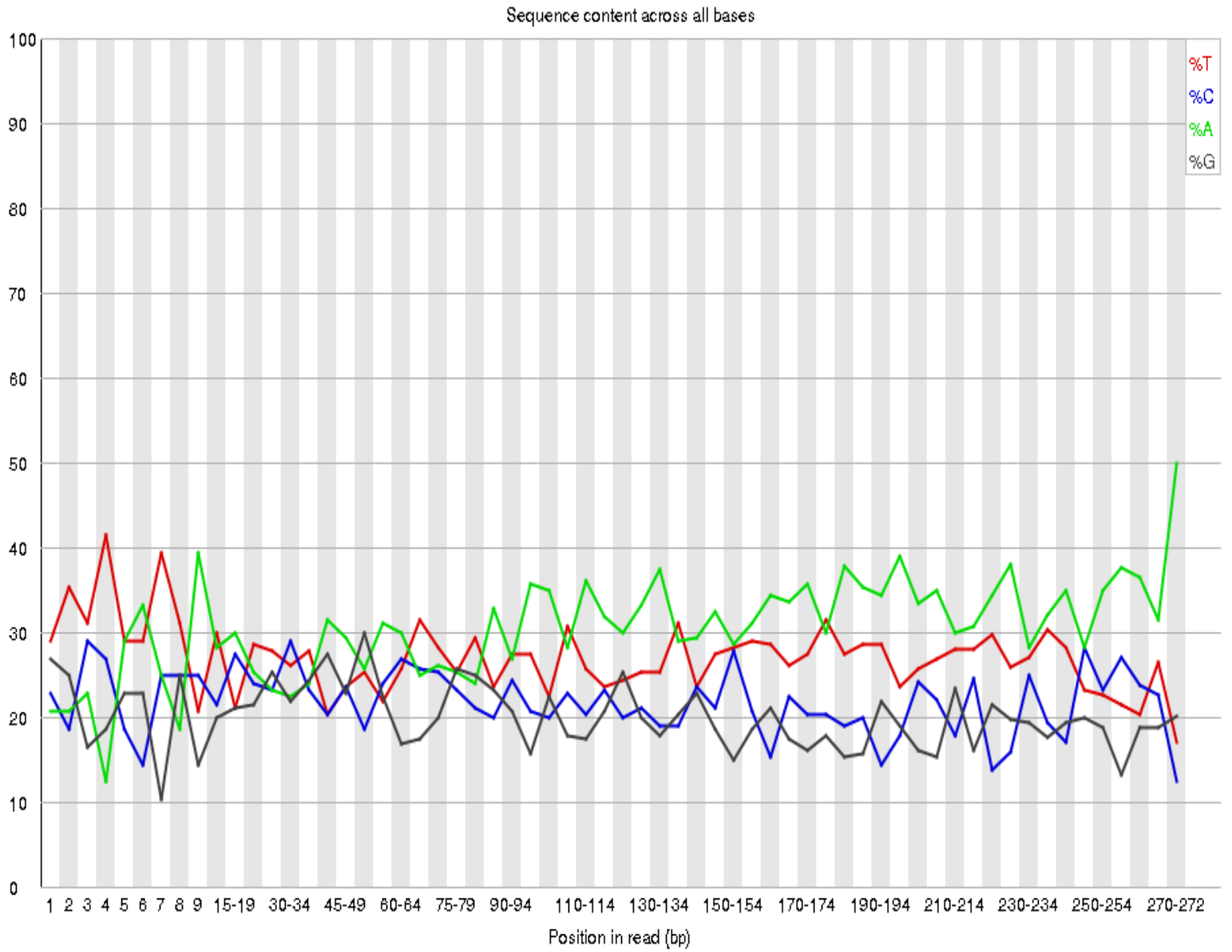
Per tile sequence quality



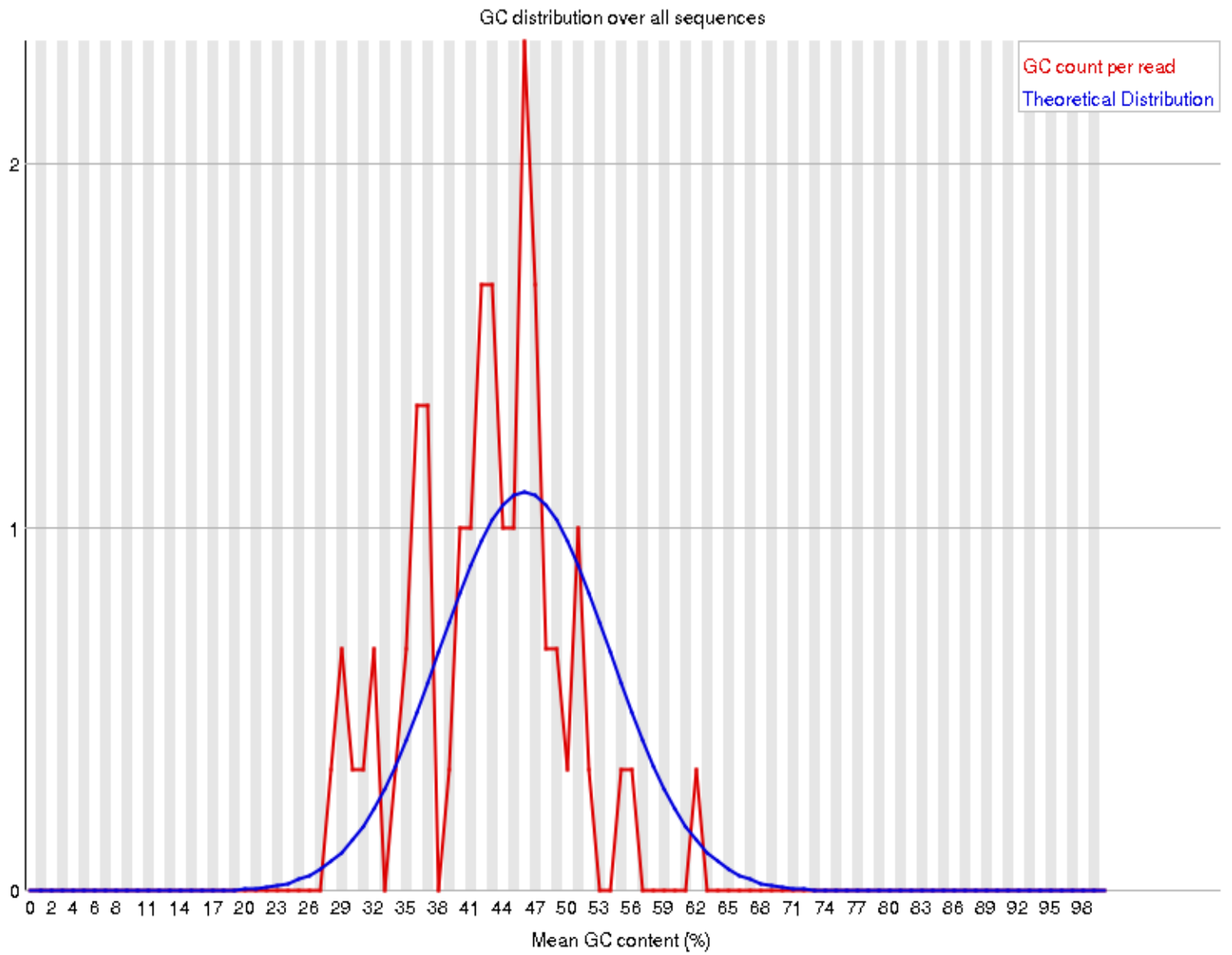
 **Per sequence quality scores**



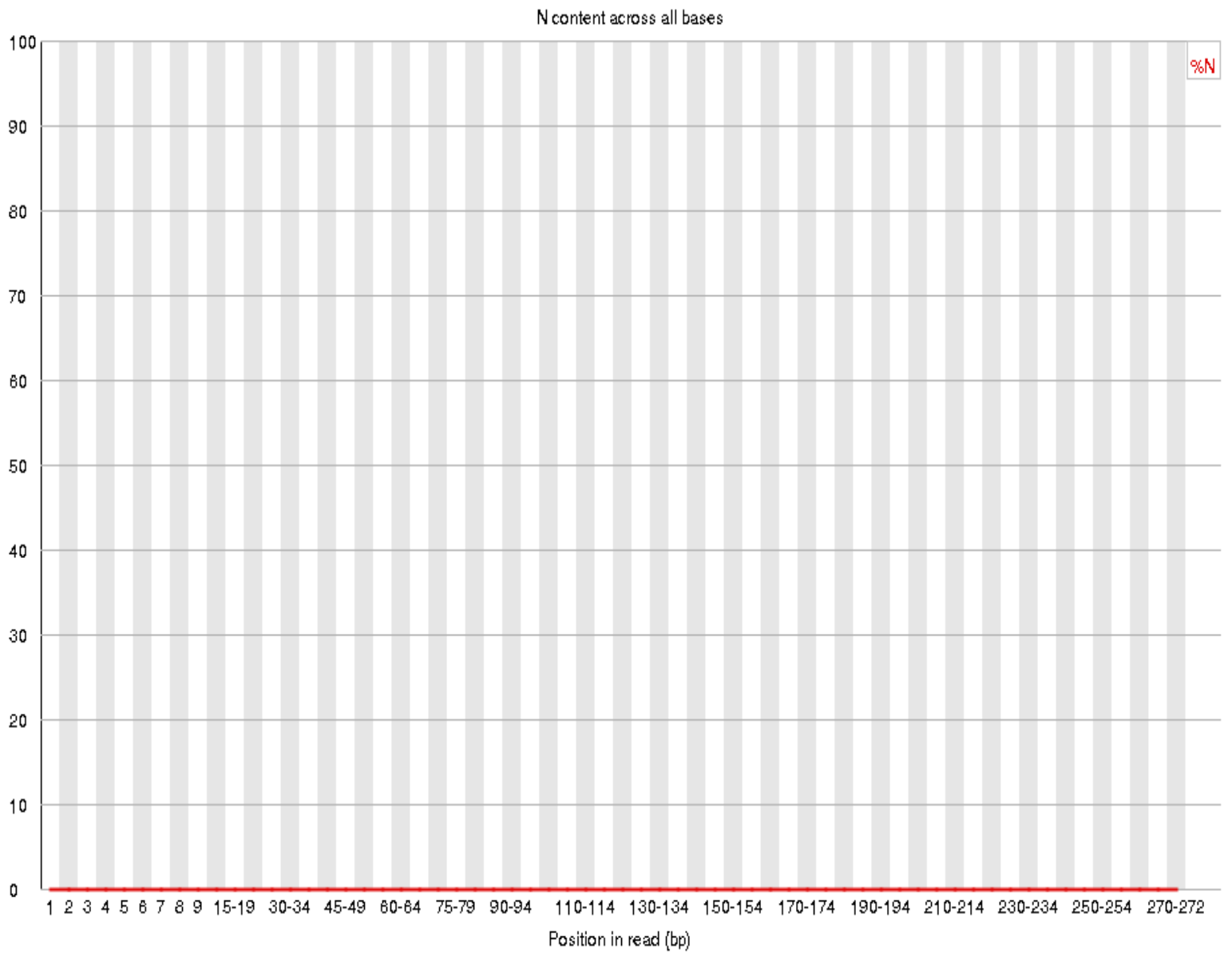
 **Per base sequence content**



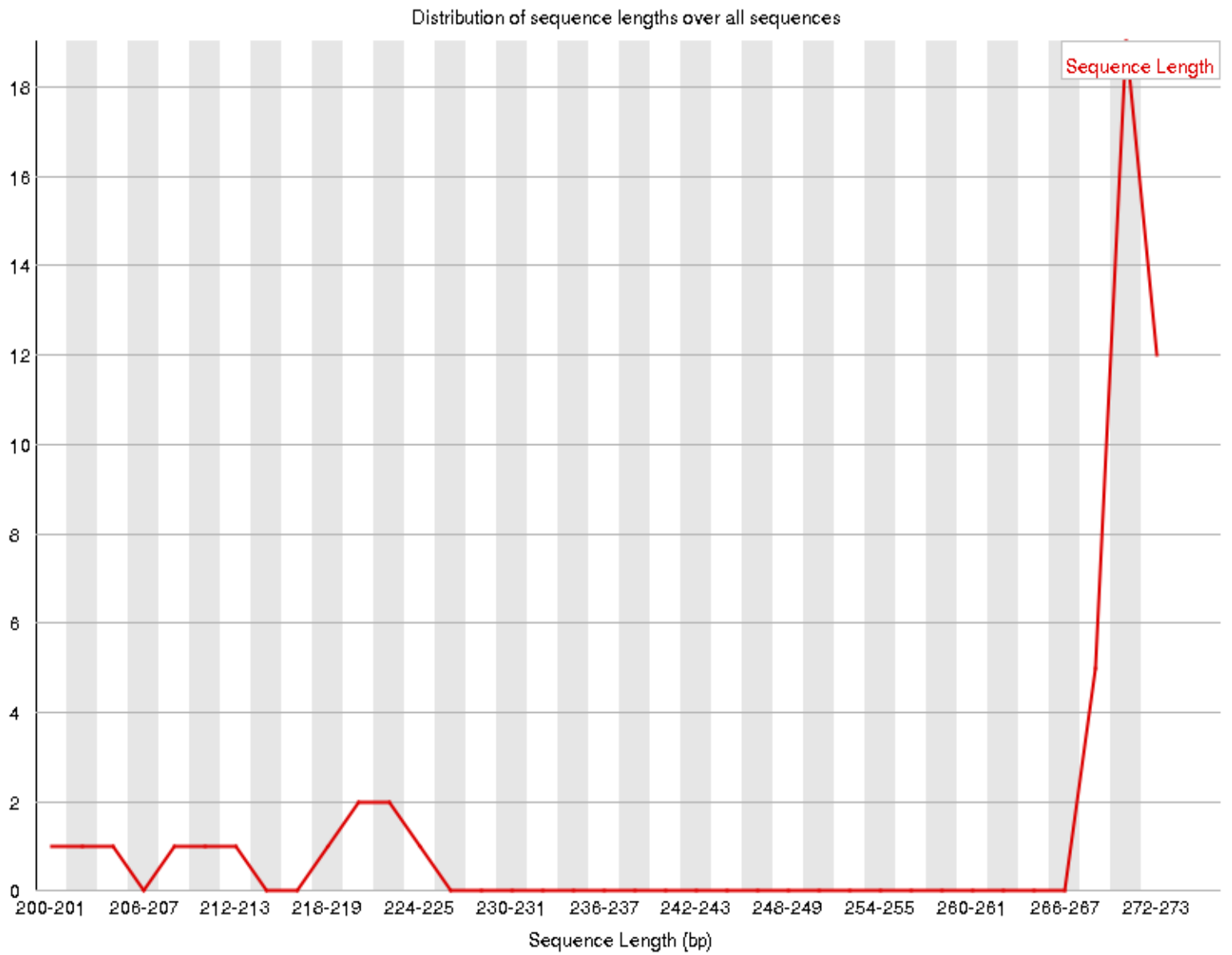
Per sequence GC content



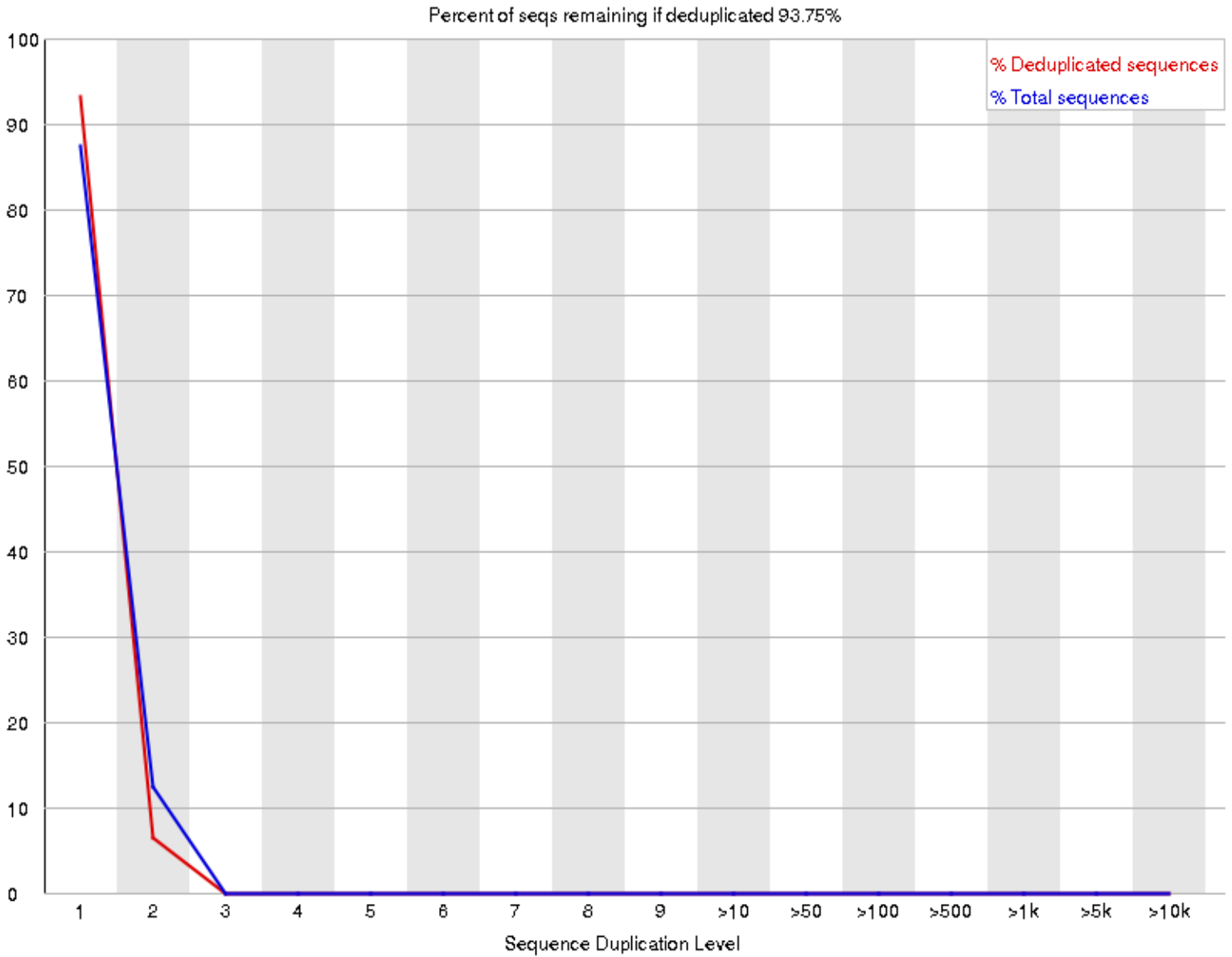
 **Per base N content**



Sequence Length Distribution



 **Sequence Duplication Levels**



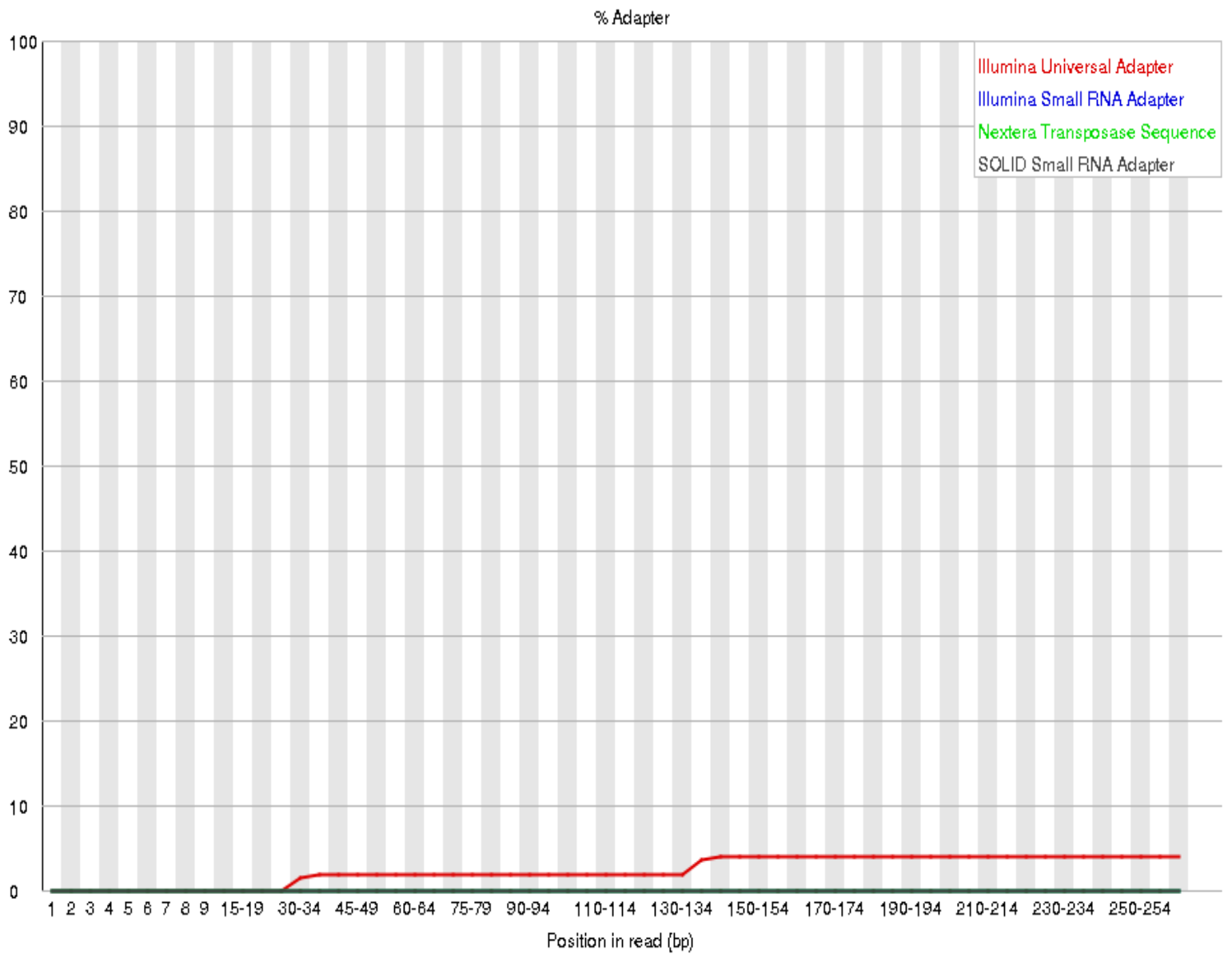
Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GCCTGACGATGAACCCACCAATATCAGTTAACGTAGTTGGGGTTTCAAAT	2	4.166666666666666	No Hit
AGTCAGTCAAGACAAACATACTGATCAAACATATGTTAGTCAAGGTGAAAC	2	4.166666666666666	No Hit
GTCTTGGACGTGAGTTAACTCAACAATATGCGCCTGACCTGGTCTTGGGC	2	4.166666666666666	No Hit
TACAATTGTTTCATCCTAAGGCCTGACGGGGACCCCGACCACAGCGACAAA	1	2.083333333333333	No Hit

TTCTGTCTCTATCCCCAAATCGCCGTGTGTTTCTCCATCCCCAGACCTG	1	2.0833333333333333	No Hit
TGACCAACCTTGAAAGACTCATCGCGTCGCATAATCAGCGGGGACATCGT	1	2.0833333333333333	No Hit
TGATCACTACTTAAGGGCCTTATTGCTTGGACTGAAGGACACATCGTCAG	1	2.0833333333333333	No Hit
GTTAAAATCACATGGAATAGGTGGGGAAGTTGCCAAATGGATAGAAAATT	1	2.0833333333333333	No Hit
TGGTGTCTGTCGACAGTCTGACGCTGAACCAGCGAATGTCAATCATATGC	1	2.0833333333333333	No Hit
ATGAACCCCCCAGGGAAGCGAAAGAGCGGAAAACCTTAAAATGCGCCCA	1	2.0833333333333333	No Hit
CTGGAATTAGGTTTTCTAAAAGATAGTTAGTGTAAGCCAAATACAGCGT	1	2.0833333333333333	No Hit
CCATGTCCACACTTCTATCATCGTCATGCCTGCCGCTGAACCCAAATGT	1	2.0833333333333333	No Hit
CAATCCCCCACCACCCCCCCCCCCCCCAACCGGGGCCATCTTCAGTC	1	2.0833333333333333	No Hit
AGGCTGCTATAGTCAGGCATGACTGAAAGAGGCTACTGTGATCAGGCATG	1	2.0833333333333333	No Hit
GAGTAATGGGGTGTCTCAAACGCCTGAGGATAGAACCCTGGATAATACTC	1	2.0833333333333333	No Hit
TTCCCTTTCTCATTGACAAGGCTGTCTGGGGTTCTTCATCAGTGCTTATGG	1	2.0833333333333333	No Hit
TTTTCGTGGACTAAAAGTTGTTTCATCTTCAGCCCTGAGGAGAAACCCACC	1	2.0833333333333333	No Hit
TTCCATTTAGGGTAAAGGGGATTACAGGTCGGTATAATTTTATTTCAAAT	1	2.0833333333333333	No Hit
CATCAATGTCATTGTGTGTTCTCAGATGAGACTTCAGTTCCGATGGCTCC	1	2.0833333333333333	No Hit
ATCTTACTCATTGTAGACATTCAACAACAATTCCAAACATCATAATACGA	1	2.0833333333333333	No Hit
CGCTTGACGGACACAGTGGAGGTGACTGACAGATCGGAAGAGCGTCGTGT	1	2.0833333333333333	No Hit
TCCAAGTAATTGTGTCATAATGCCAACCTTCATAGAGAATAGTAAGAAG	1	2.0833333333333333	No Hit
GAGTAACTCACTCTTTTATCCCAGCCCCAACATTTTGTGAGGGGACATCG	1	2.0833333333333333	No Hit
ACTTGTAGTTATACTGAGTTGTGGCGCTTGCTTTGGATTAAATCGCACTT	1	2.0833333333333333	No Hit
TGATCAAATTTTACACTGACATTCATATATCCATAACATGATGTAATTCAG	1	2.0833333333333333	No Hit
GTTGTCATGTCCATCACCCATGTTGTCATGTCCATCATCGACAGTCTGA	1	2.0833333333333333	No Hit
CCAGGAGCGGATGGGTTACCTTCAGGCCCGAACACAATCGCAAAGGGCA	1	2.0833333333333333	No Hit
TGACCAACATTGAAACACTCATCGCTTCGCATAATCAGTGGGGTCATCGT	1	2.0833333333333333	No Hit
ACCATCTATGCCTGCTGCCTTATTTTTTTTTGCTGTCTCGCAGGGGGTTCA	1	2.0833333333333333	No Hit
CTCTGTCTACTATGTCAGCAGTCTGGGCACGTCCACCGGCCTGACGATGG	1	2.0833333333333333	No Hit
CAAAATTACAACCTAGCCCGGCTGCATCGTCAGCCCTGTCATTGAACCGG	1	2.0833333333333333	No Hit
TATGTTTAAAATCTGAAGCTGTAGTTGGTTCATCGCCCCCACGACGAAG	1	2.0833333333333333	No Hit
CATCAATGTCATTGTGTGTTCTCAGACGAGACTTCAGTTCCGATGGATCA	1	2.0833333333333333	No Hit
CCCTCTGCATTCAACTGTGGTATTTTGAGGGGCTTGAGGTTTTACGATCA	1	2.0833333333333333	No Hit
GTGCCCTGAATCGTGTGTTGACCGCATCCTTATTAGGGCTCATCGTGCG	1	2.0833333333333333	No Hit
GGTCAGACTAGACTAGCGACAAAGACACCTCGCTTACTACAACAGCAATG	1	2.0833333333333333	No Hit
GAATTGAATACTGGGACAATGTGTACTTTGTTTTCTTTCAAAGTGCTTG	1	2.0833333333333333	No Hit

TTAGTTTAAAATCTGAACATGTAGTTGGTTCATCGCCAGGCATAACGATG	1	2.0833333333333333	No Hit
ACTGTATGAAAGATGGTGGCACACCTAGCCAAGTGGAGGGACTTTGCTCA	1	2.0833333333333333	No Hit
AATCTCACTCTTATCTTAATAATGTGATGTGAGCTGTATGAGGATTATAG	1	2.0833333333333333	No Hit
TTTGGTTTGAGGCAAAGGATGACATGGTTCAAGGCTCGTCACAGATGTTT	1	2.0833333333333333	No Hit
AGATGTGTAGTGAATACAAGGCACGAACCTCCATTATGAGACATGACATC	1	2.0833333333333333	No Hit
GGTGTGATACTGGCATTTCAGAGTTGTAGTGGCAGTCCTAGCGGTGGAAGT	1	2.0833333333333333	No Hit
CTGCGATGCTGATTTGGTGTATCCCCGTCAGGCCCCACGGTGAAACACGA	1	2.0833333333333333	No Hit
GTTGTCATGTCCATCACCCATGTTGTCATGTGCATCATCGTCATTCTGA	1	2.0833333333333333	No Hit

Adapter Content



Kmer Content

No overrepresented Kmers

Produced by [FastQC](#) (version 0.11.3)