












# FastQC Report Sun 10 May 2015 R1\_IJS8\_mates\_ICC5\_SW023\_S60\_L001\_R1\_001.fastq.200

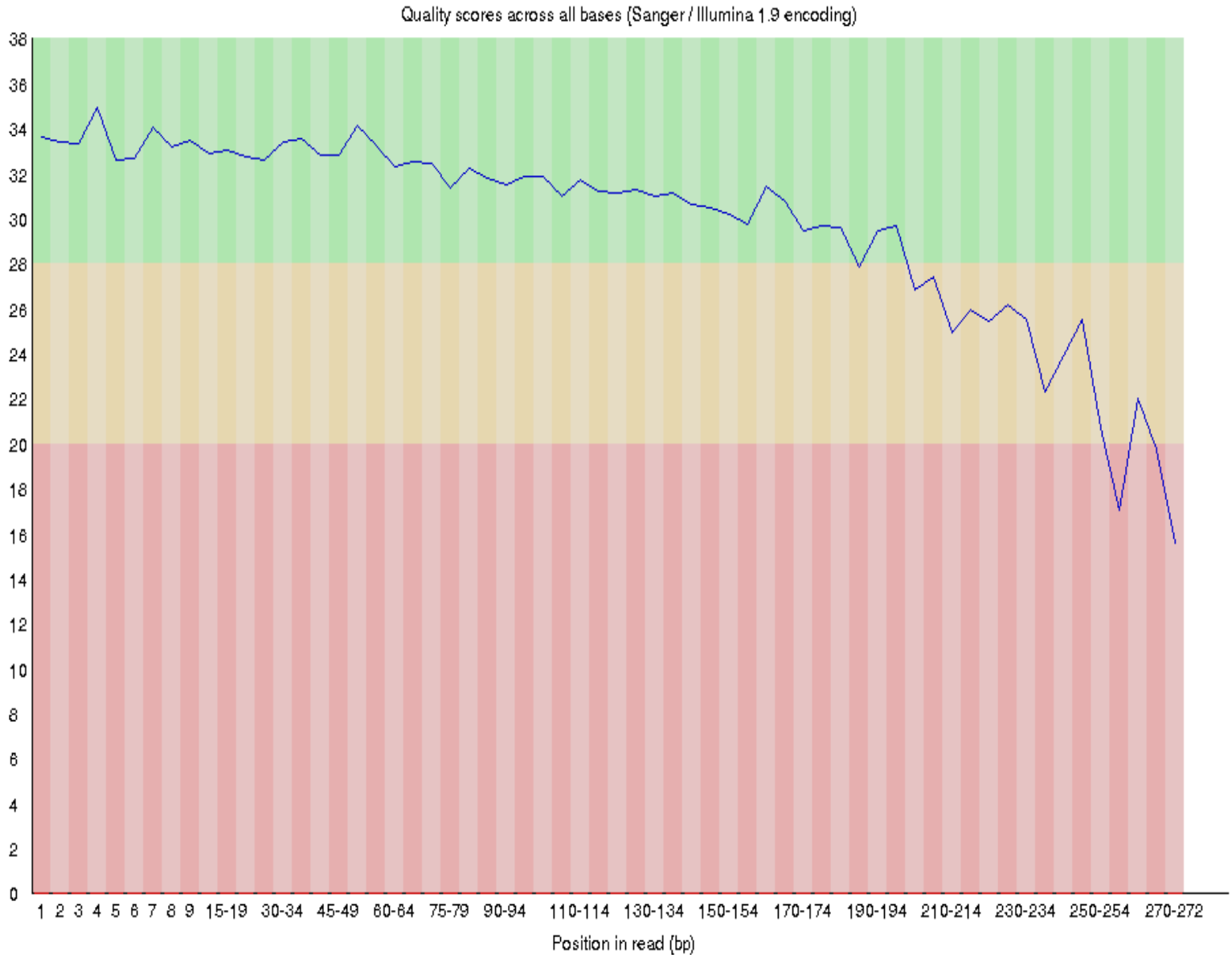
## Summary

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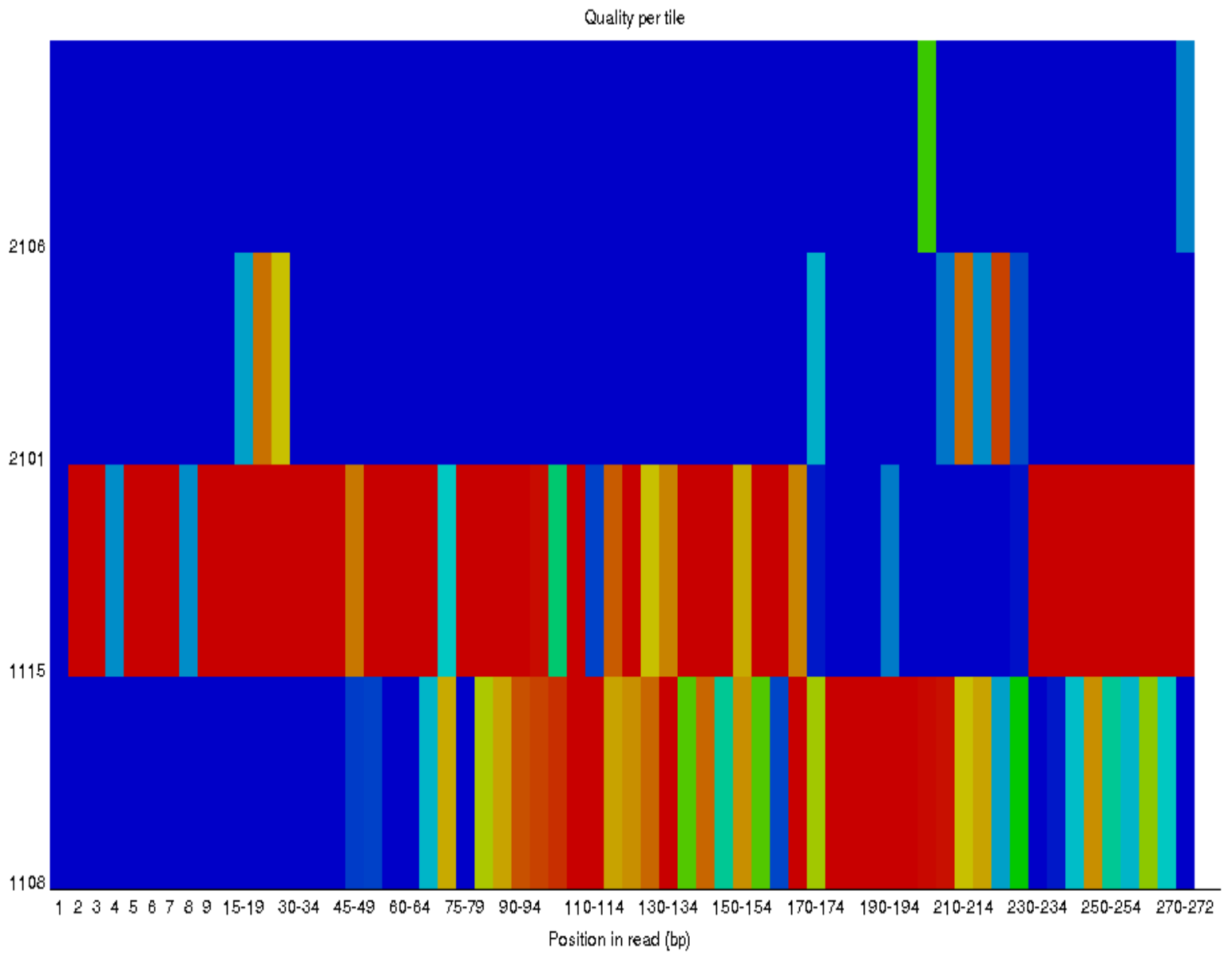
## Basic Statistics

Measure	Value
Filename	R1_IJS8_mates_ICC5_SW023_S60_L001_R1_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	40

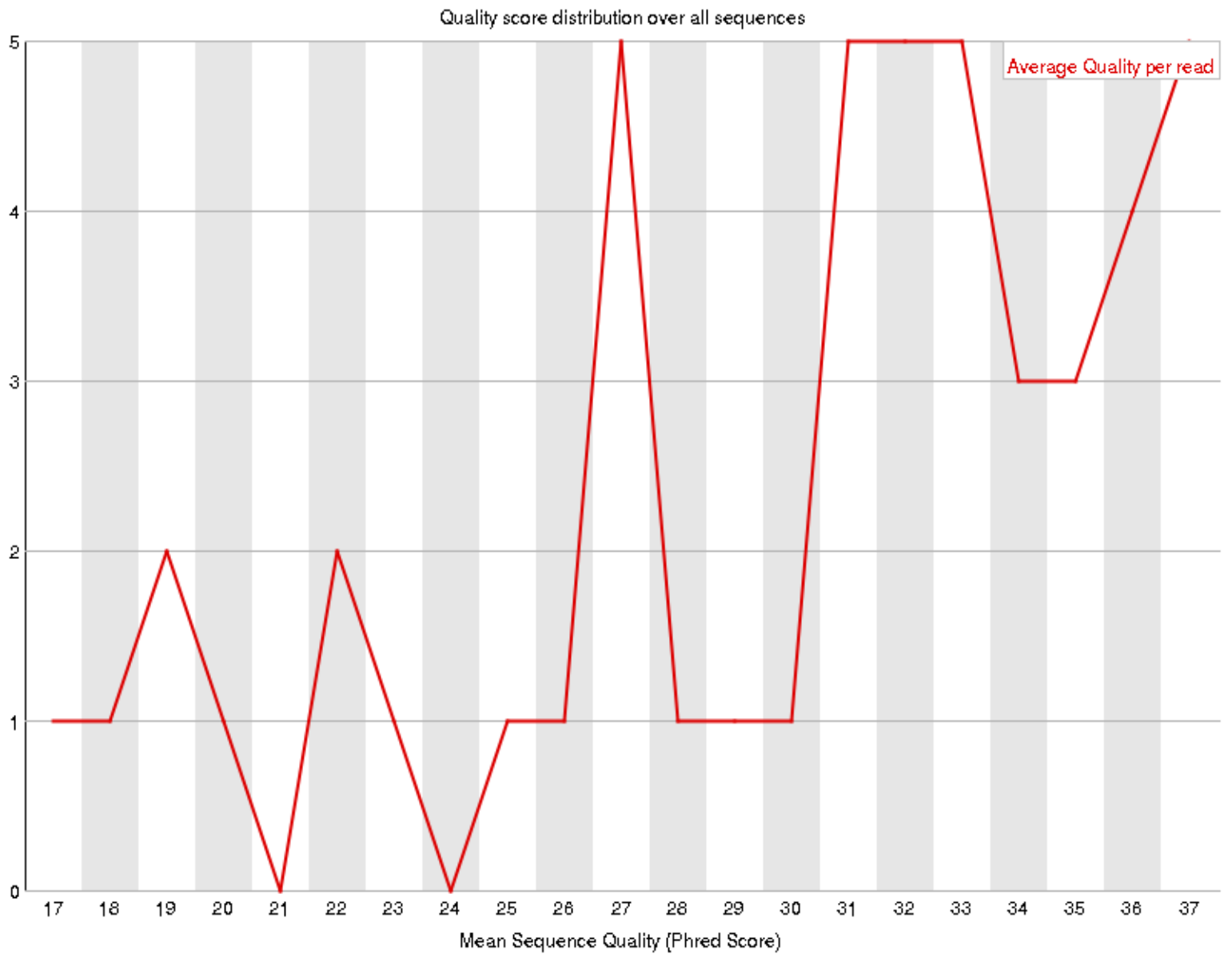
## Per base sequence quality



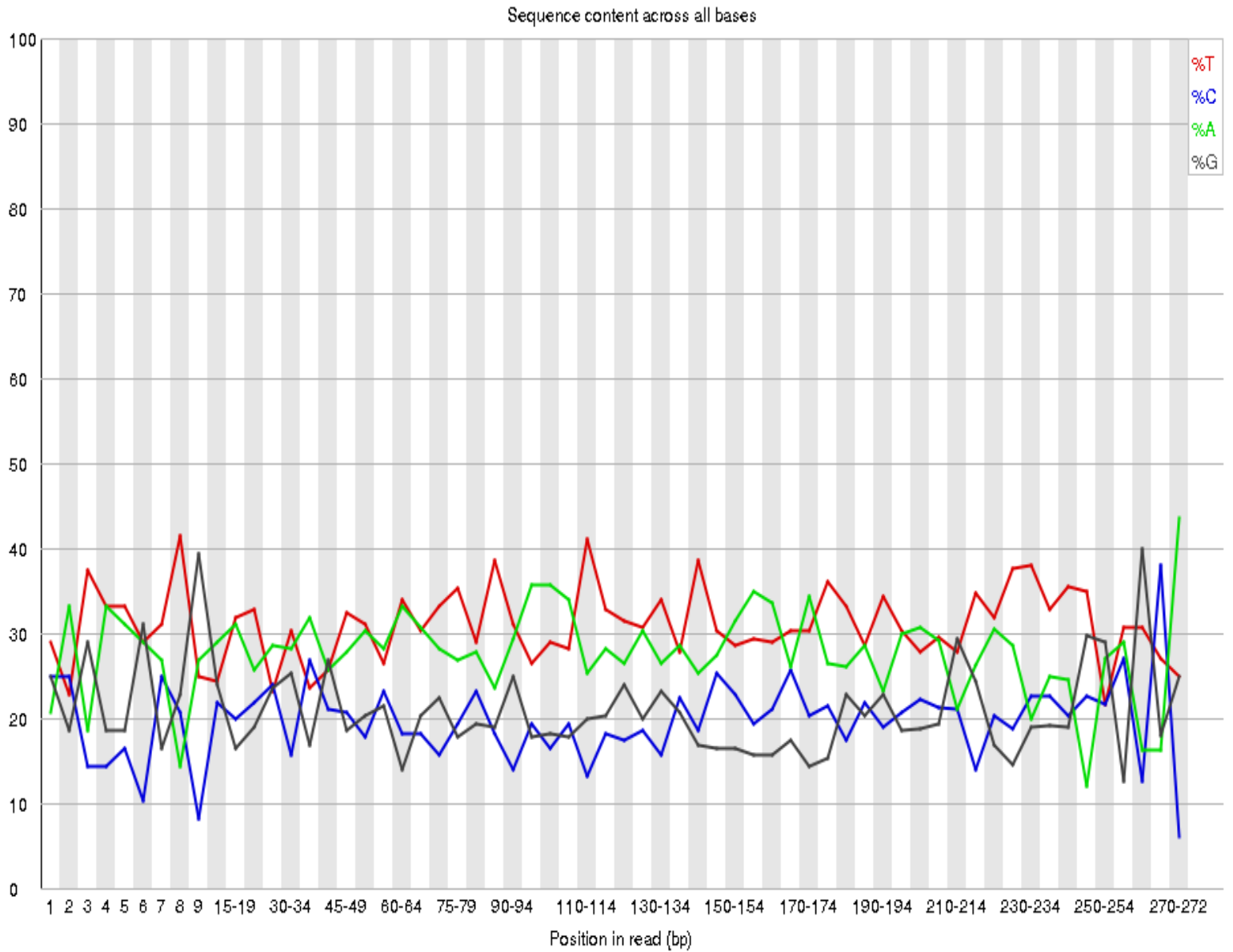
## Per tile sequence quality



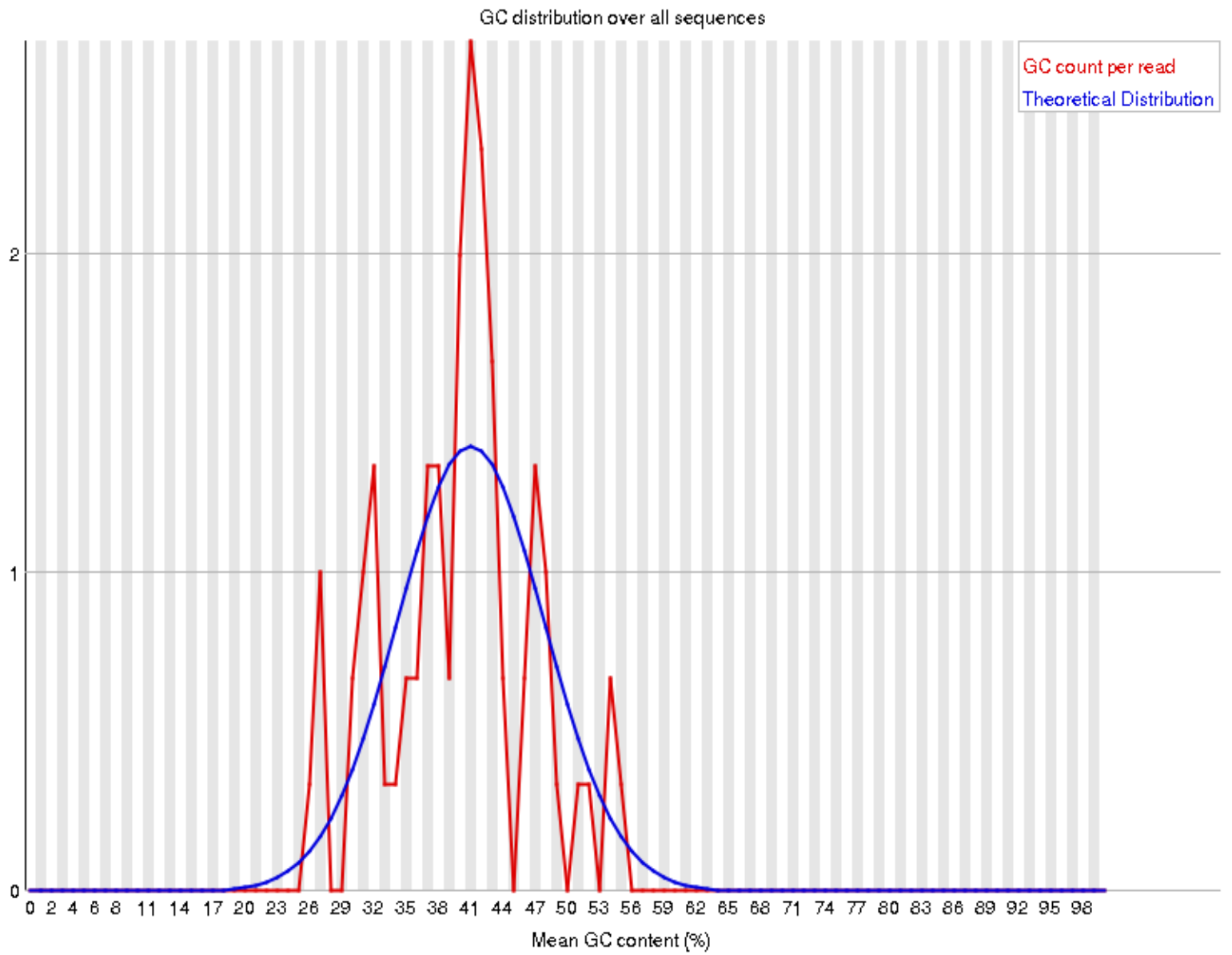
## Per sequence quality scores



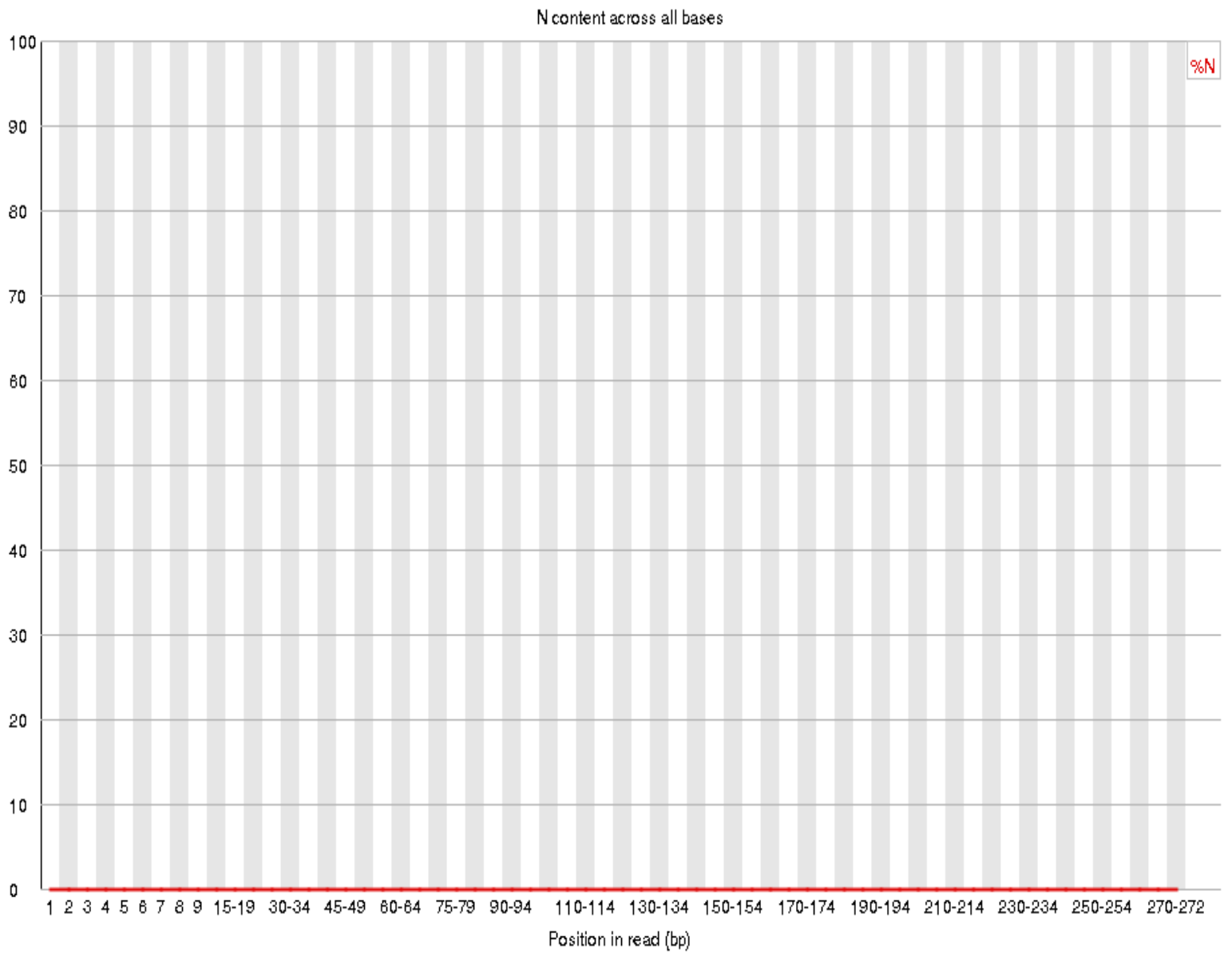
## Per base sequence content



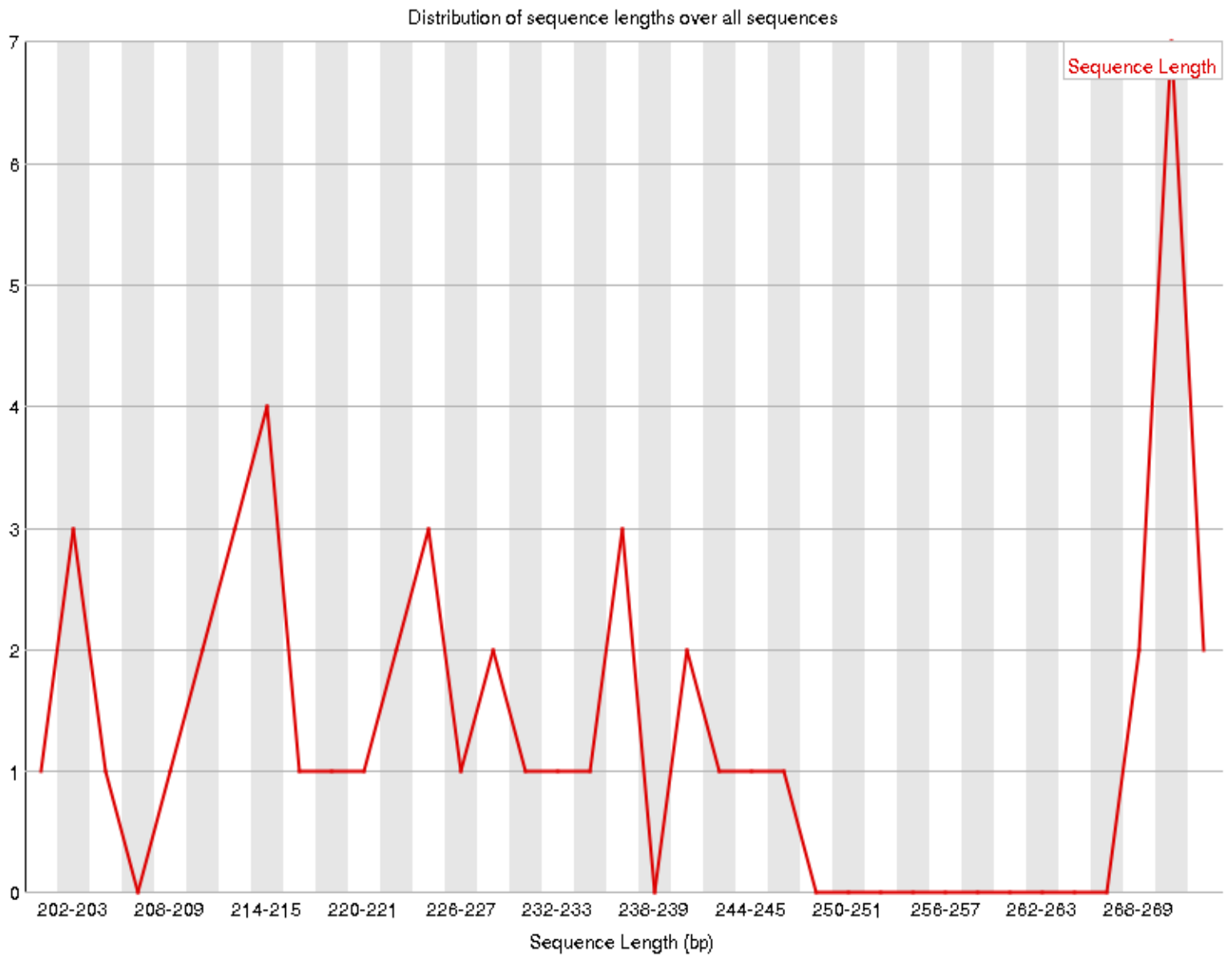
 **Per sequence GC content**



 **Per base N content**

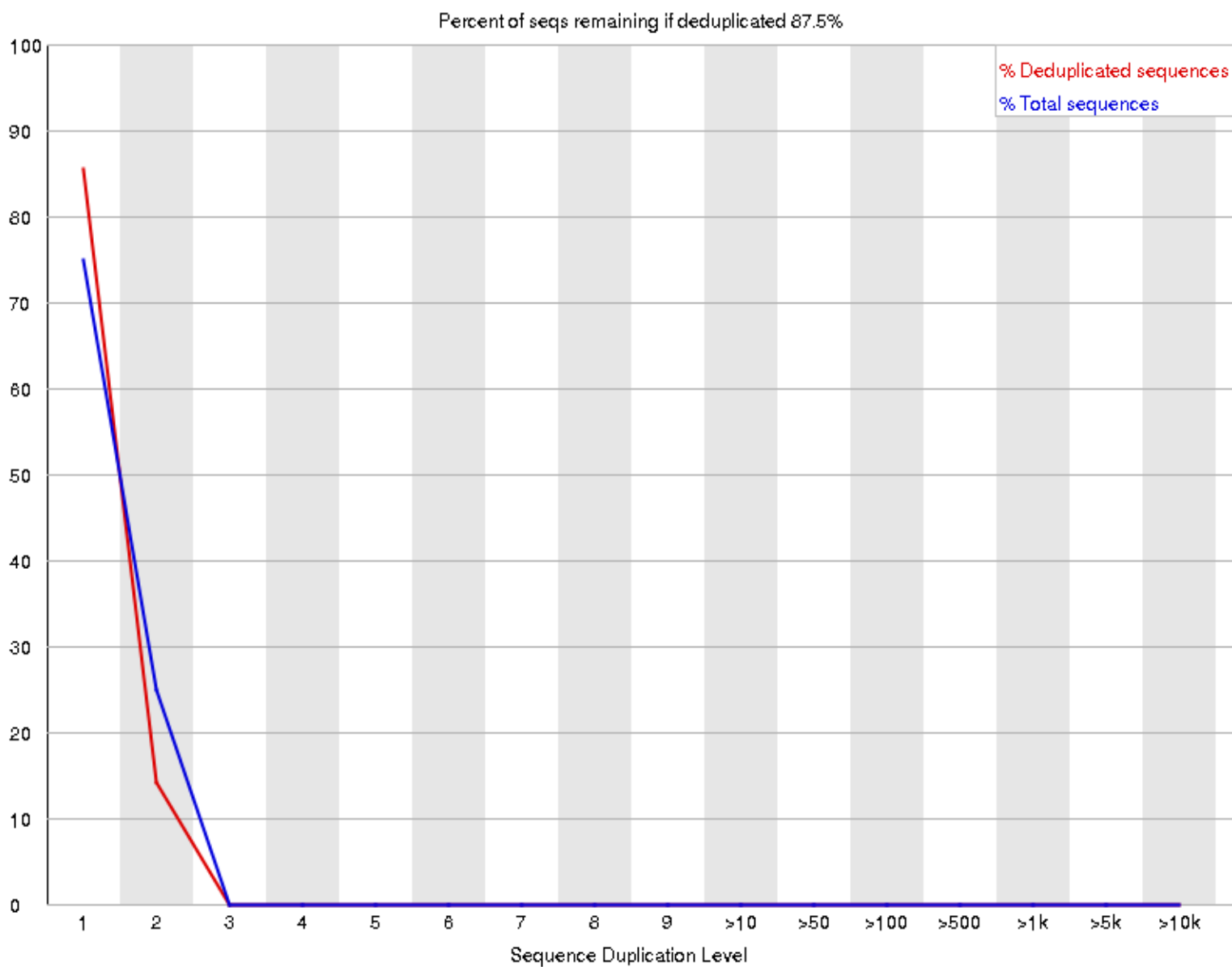


## Sequence Length Distribution



 **Sequence Duplication Levels**





## Overrepresented sequences

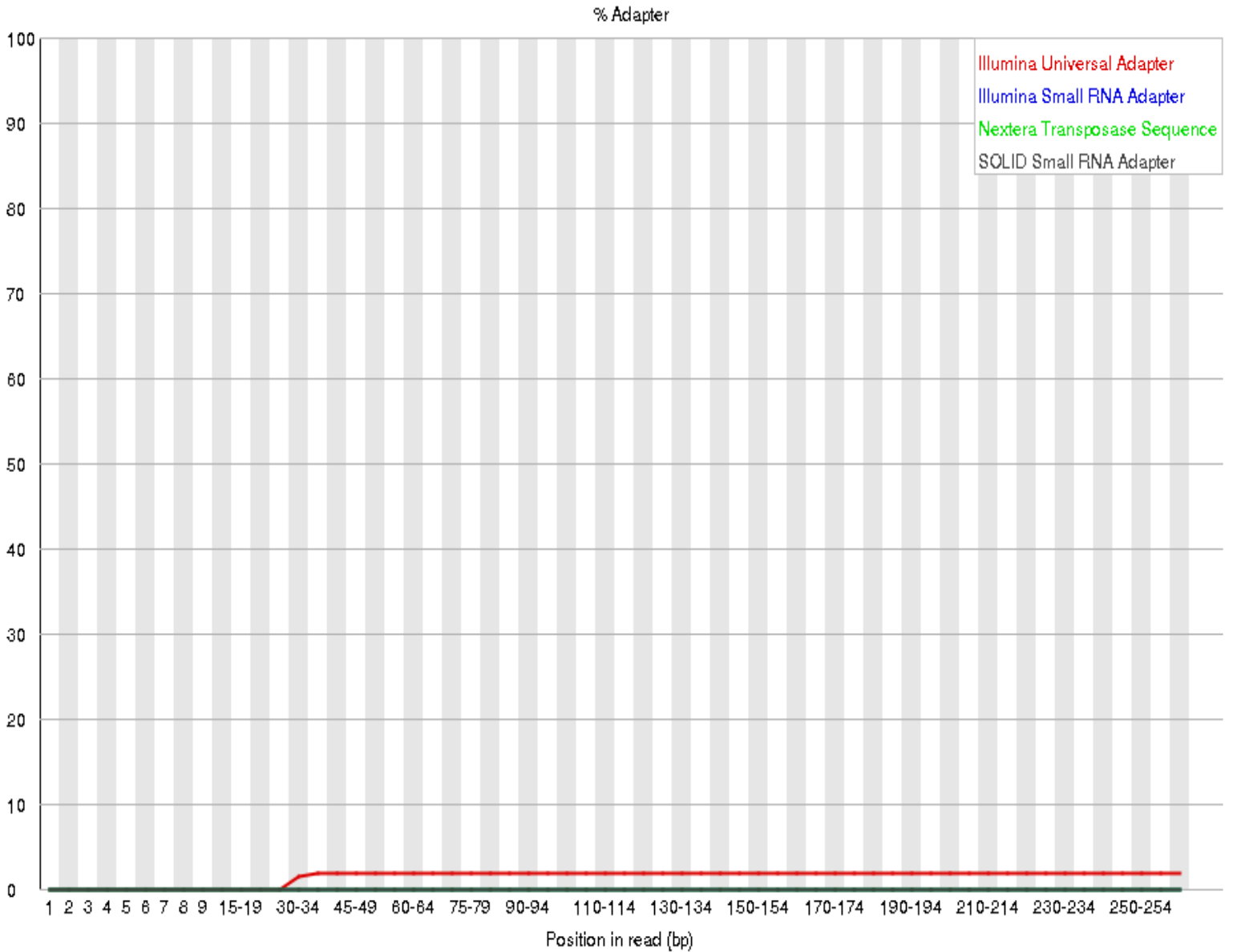
Sequence	Count	Percentage	Possible Source
GTGTTTTTTAGGATCTTTAGTTATAGTGCCTTGTGGTAGTGACATGTATA	2	4.166666666666666	No Hit
CTGACGATGAACCCTTTTTTTTTGAGAATTTTGAACAATGACCCTTTCAA	2	4.166666666666666	No Hit
TCAGGCCTGACGATGAACCCAGGCAGTGTATGGTGACAAAAGTGGGTCTGA	2	4.166666666666666	No Hit
TGGATGATGGACATGACAACATGGATGATGGACATGACAACATGGGTGAT	2	4.166666666666666	No Hit

AAGTCTCGTCTGAGAACACACAATGACATTGATGTATCGGAACTGAAGTC	2	4.1666666666666666	No Hit
TGTAATTGGAGTTTTACTACTTTTACAGCTGTCCGCAAGTTTTTTTTTAA	2	4.1666666666666666	No Hit
TACATAAGCACTACGGCAATGAGAGAGAGGAAAAATTCATCCATCAACA	1	2.0833333333333333	No Hit
TTTATACAGGACAGTCTATTCCCTTCGTTGTTCACTTGGTCGTACAATATG	1	2.0833333333333333	No Hit
GCTTGTCTGTCTATCTATTCATCTATCAATATATCTATCTATATAAGTAT	1	2.0833333333333333	No Hit
GTTGACTTAATACAGGTTTATAAGATGAGTTGACTTAATACAGGTTTATA	1	2.0833333333333333	No Hit
TATGACCAGGACTTCAAATTACACTGAACACAGAAAGCAGACGTAATGAC	1	2.0833333333333333	No Hit
CGCTTGACGGACACATTGGGAGTCTGACTGAGATCGGAAGAGCACACGTC	1	2.0833333333333333	No Hit
TAGAGGTTTGTTACAAATGCTAAAAATCAAGATGAACTATTGGGGGACGG	1	2.0833333333333333	No Hit
GCCATAAGGGGGTTCGTAATTTATCTAGGCGAAGAACCCAAAAGCACAAG	1	2.0833333333333333	No Hit
CCACTACTATGGGGATCACATCGATCCACATCTTGTCAGCCGGGCTGGCT	1	2.0833333333333333	No Hit
CACTGGCTTACCCGGCCTTTTTCCACTTCTACCGCCCTCTGACCATTTA	1	2.0833333333333333	No Hit
CTATAATCCTCATAACAGCGCACATCACATTATTAAGATAAGAGTGAGATT	1	2.0833333333333333	No Hit
GCTCTTGTGGTTCATTGCCACTTAACAATCAAATGTTTAGTGATGCCTGA	1	2.0833333333333333	No Hit
ACTACCACTACGTCTTCTACTATTCCCTACAACCACATCTAATCATCACAC	1	2.0833333333333333	No Hit
AACATTCCGTCAATCAAACATCTGTGACGAGCCTTGAACCATCTCATCCT	1	2.0833333333333333	No Hit
TAGAGGTTTGTTACAAATGCTAAAAATCAAGATGAACTATTGGGGGACTG	1	2.0833333333333333	No Hit
AGTGGGCGAGGTGTCTTTGTGCTAGTCTAGTCTGACCAGAGCTGTTGAA	1	2.0833333333333333	No Hit
CAGATAAATAACCTTATCTAGATGCATCGTATGGCCTAGCGATAAACACA	1	2.0833333333333333	No Hit
AAAGAATGGACCAGTCTCCGACCAGAAGAGTCACAGGCAGCGGCATCTGA	1	2.0833333333333333	No Hit
CCCTCAGTAAGATCTATTGTGACGAGCCACCAAAAAACCACATCAAGAG	1	2.0833333333333333	No Hit
AGATGATCTAGCCCTTCCGCACTTCTTGATAGTATCACTGTGTCATCTAC	1	2.0833333333333333	No Hit
CTTTTGGGGGAGAAGAGGAAGGGGGGAAGAGGAACCCACCTCAATAATTC	1	2.0833333333333333	No Hit
GGTGAGGCTCTTGTTTCCAGCATGTTGTGCCGACCAGCCGTTTCGTCTTCCT	1	2.0833333333333333	No Hit
CATCCTGTAGAGACTTCAAGCCCCCCCCCTTCCCTCCTCCCCCTTTT	1	2.0833333333333333	No Hit
AATGAATGGGAGATATTTATCACAGGCTTCCCTGTAAGATGACGGACAAC	1	2.0833333333333333	No Hit
CATTCTACCTGATACACTGGGCAGCAAATATTGCGCATTCTGTTCTCCAG	1	2.0833333333333333	No Hit
TTATGGTTTGCCCCAAATATATCAACCTCTGTACTTGTGGATTATTTCT	1	2.0833333333333333	No Hit
GTGTAACTACTGGCGAAGACGACCGTGTGTGAAAGCCAGAGCCGACTC	1	2.0833333333333333	No Hit
GAGAAAGAATGACAATCATGAGGAACCTTGCTGGCACAAGCTGGGAAGCA	1	2.0833333333333333	No Hit
GGTCTTTAAAATTTGCGTTTTCCAGGTGAGACGTTGTCTAAGGAACATCC	1	2.0833333333333333	No Hit
GAAAATGTTGAGAACCTGTGTTTTCCCGCTGGGGTCATCGGCCGGCCTGA	1	2.0833333333333333	No Hit
GCTCTGTCCTCTTTTGTGGGGGAGAGAGACAGGCCTGACGATGAACCCAC	1	2.0833333333333333	No Hit

```

AAGGAGAAGGGAACAGCGGGAGGAGGGACGATGAACCCTTTGTCAGTTAT 1 2.0833333333333333 No Hit
TCTTTTAGAAGCTACCATACTTAACTCCATAGGATTGATGTCTACTTGCT 1 2.0833333333333333 No Hit
CCCTAAGCTGTGGTCTAGTAGTTTGGATGAAATAGAACATGTCATAATAT 1 2.0833333333333333 No Hit
ACACAAAAAAAAAAAAAAAAAATGCTTTTGTATTCTGCTAGCTATTTTTT 1 2.0833333333333333 No Hit
TTTCAGTCATGCTATAGTAGCCTCTTTCAGTCATGCCTGACTATAGTAGC 1 2.0833333333333333 No Hit
    
```

## Adapter Content



 **Kmer Content**  
No overrepresented Kmers

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