












FastQC Report

Summary

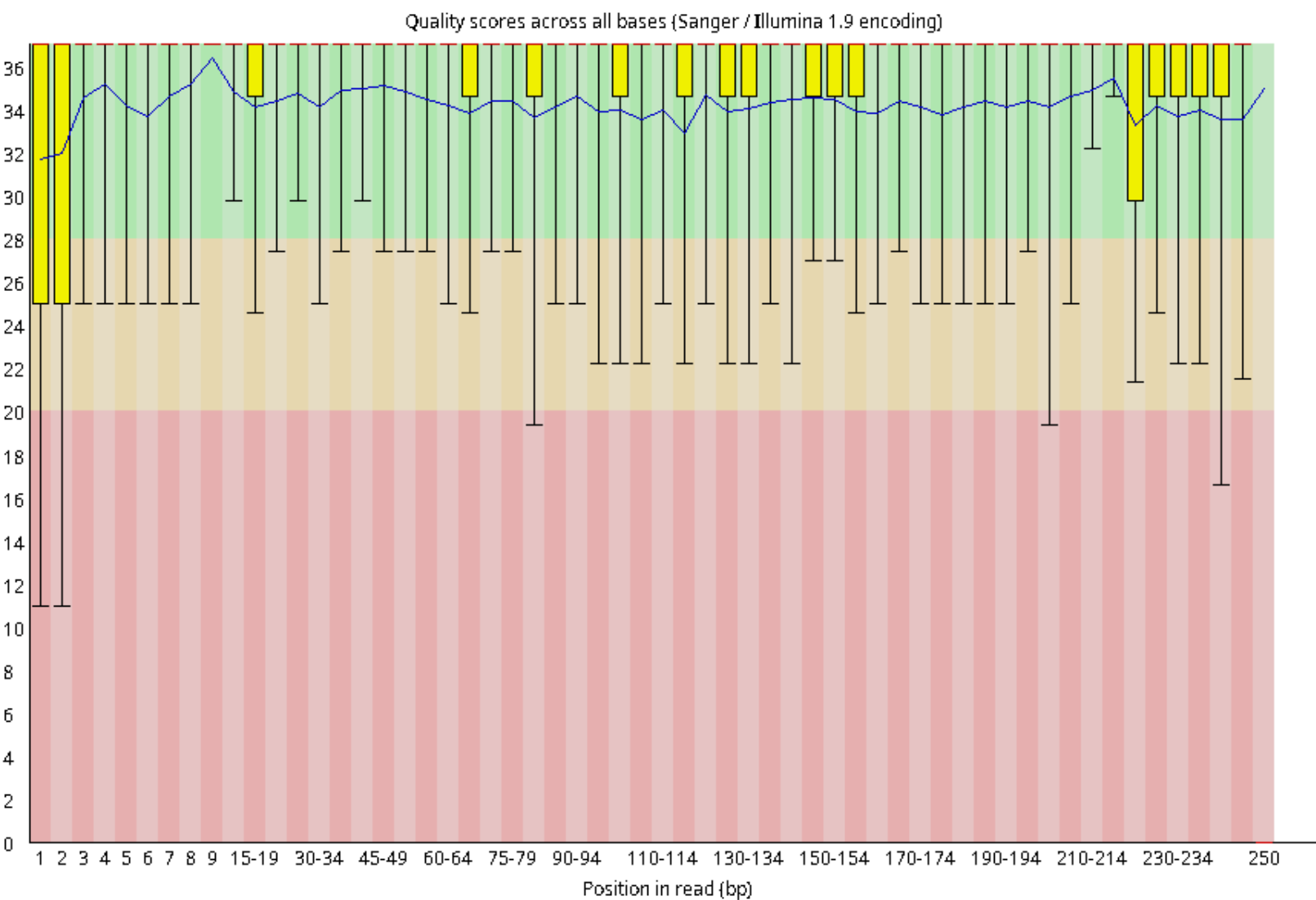
Mon 3 Mar 2025
SRR32313970_1_unpaired.fastq

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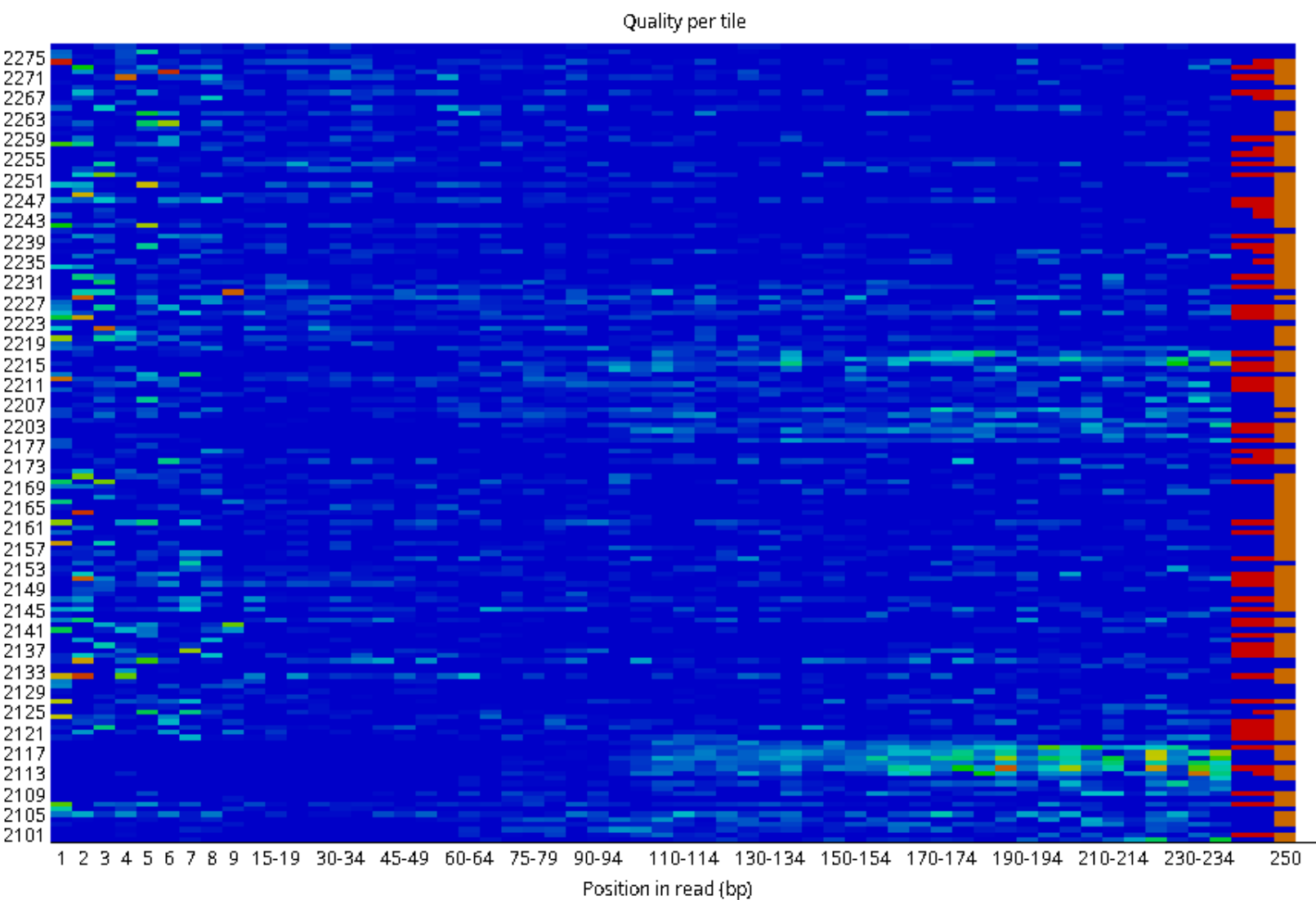
Basic Statistics

Measure	Value
Filename	SRR32313970_1_unpaired.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	2998
Total Bases	506.3 kbp
Sequences flagged as poor quality	0
Sequence length	50-250
%GC	49

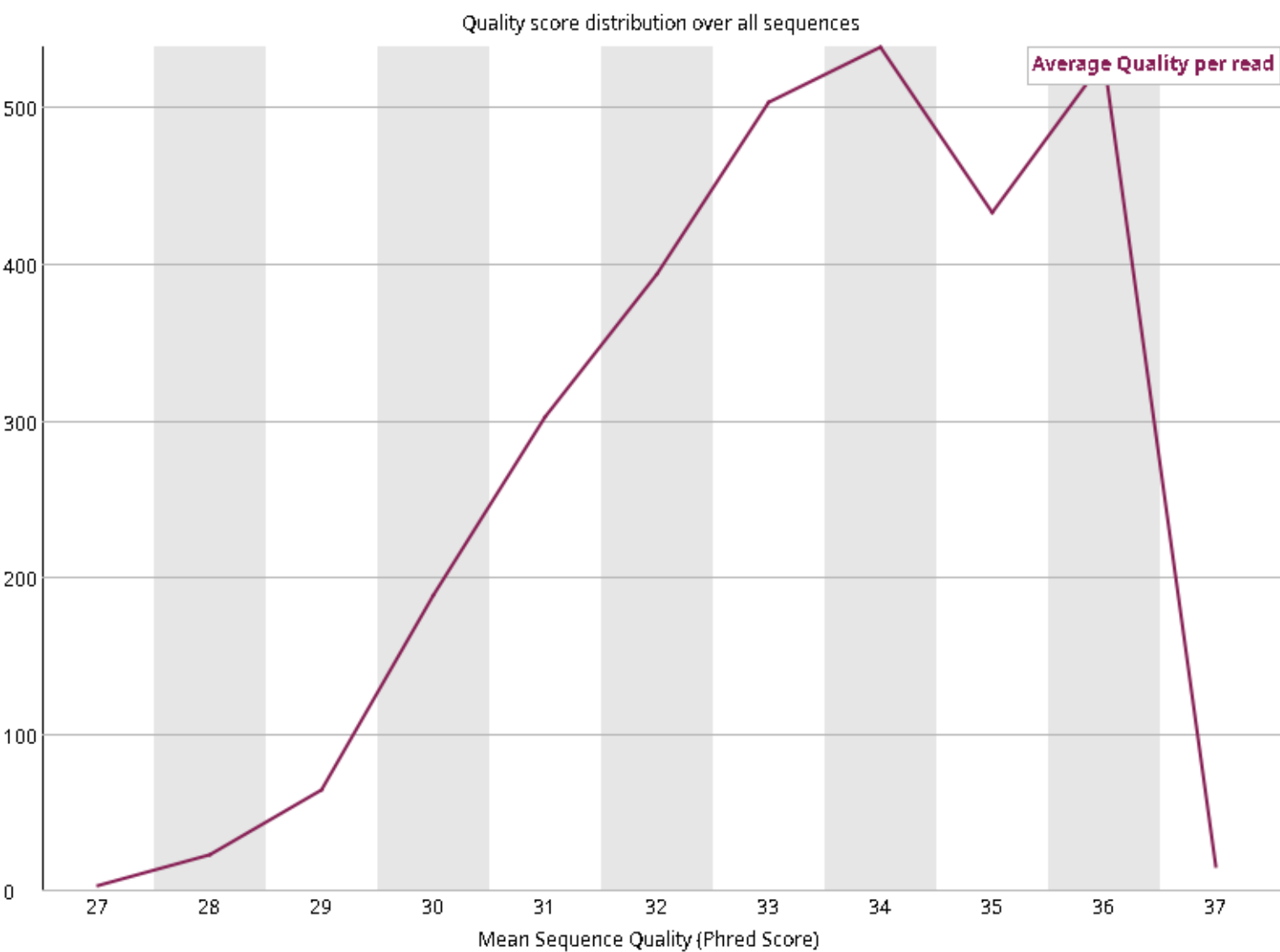
✔ Per base sequence quality



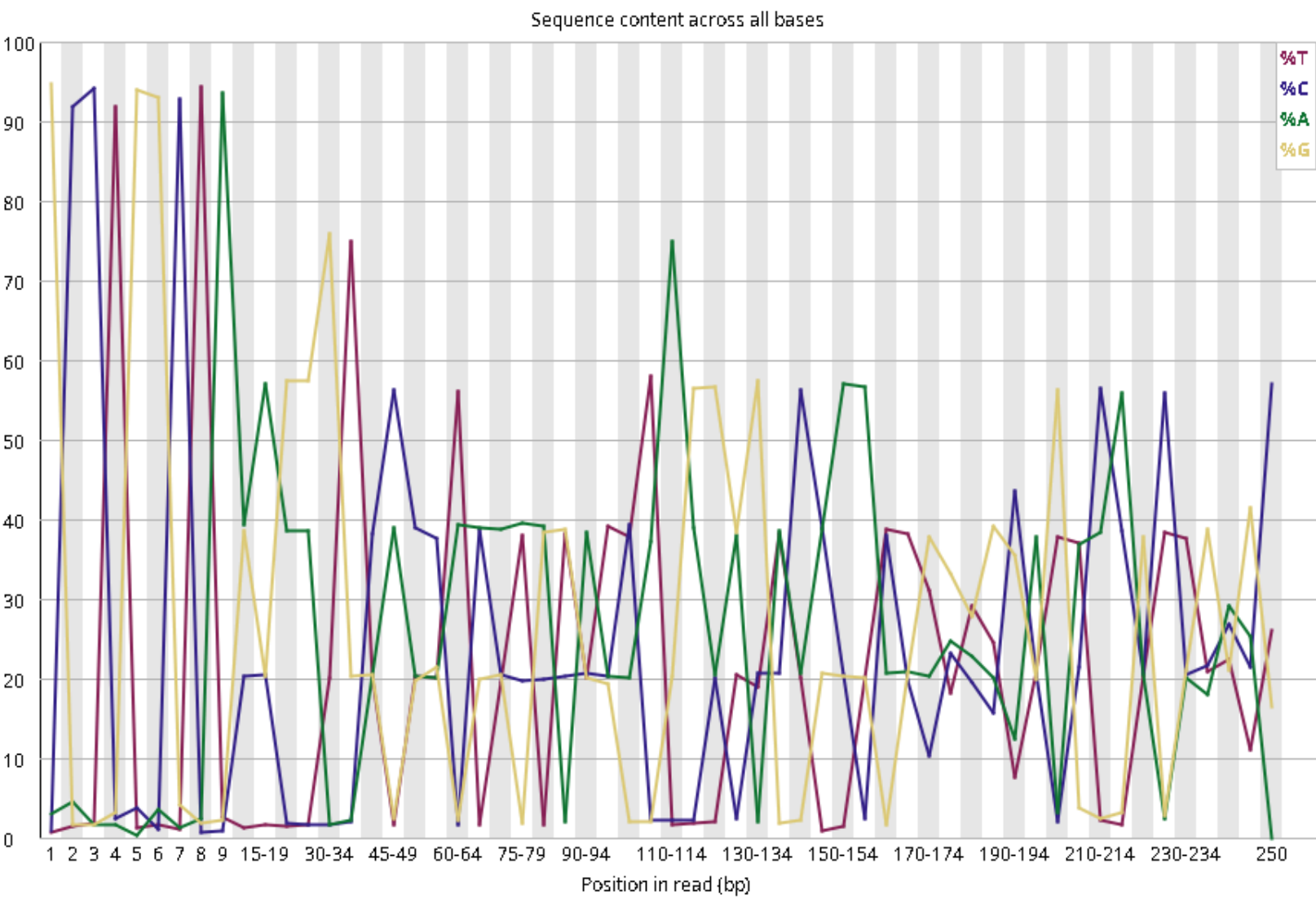
✖ Per tile sequence quality



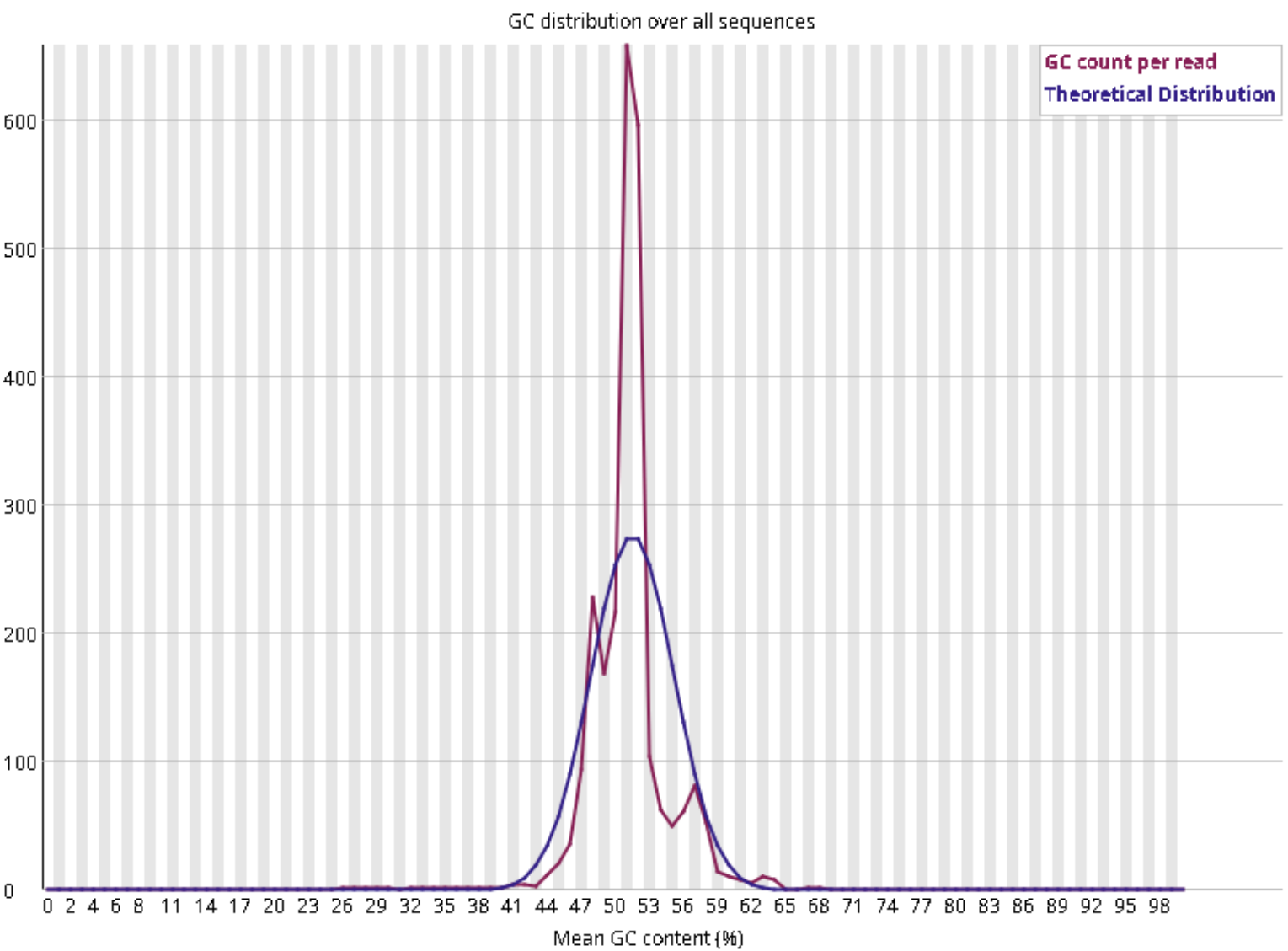
✔ Per sequence quality scores



❌ Per base sequence content

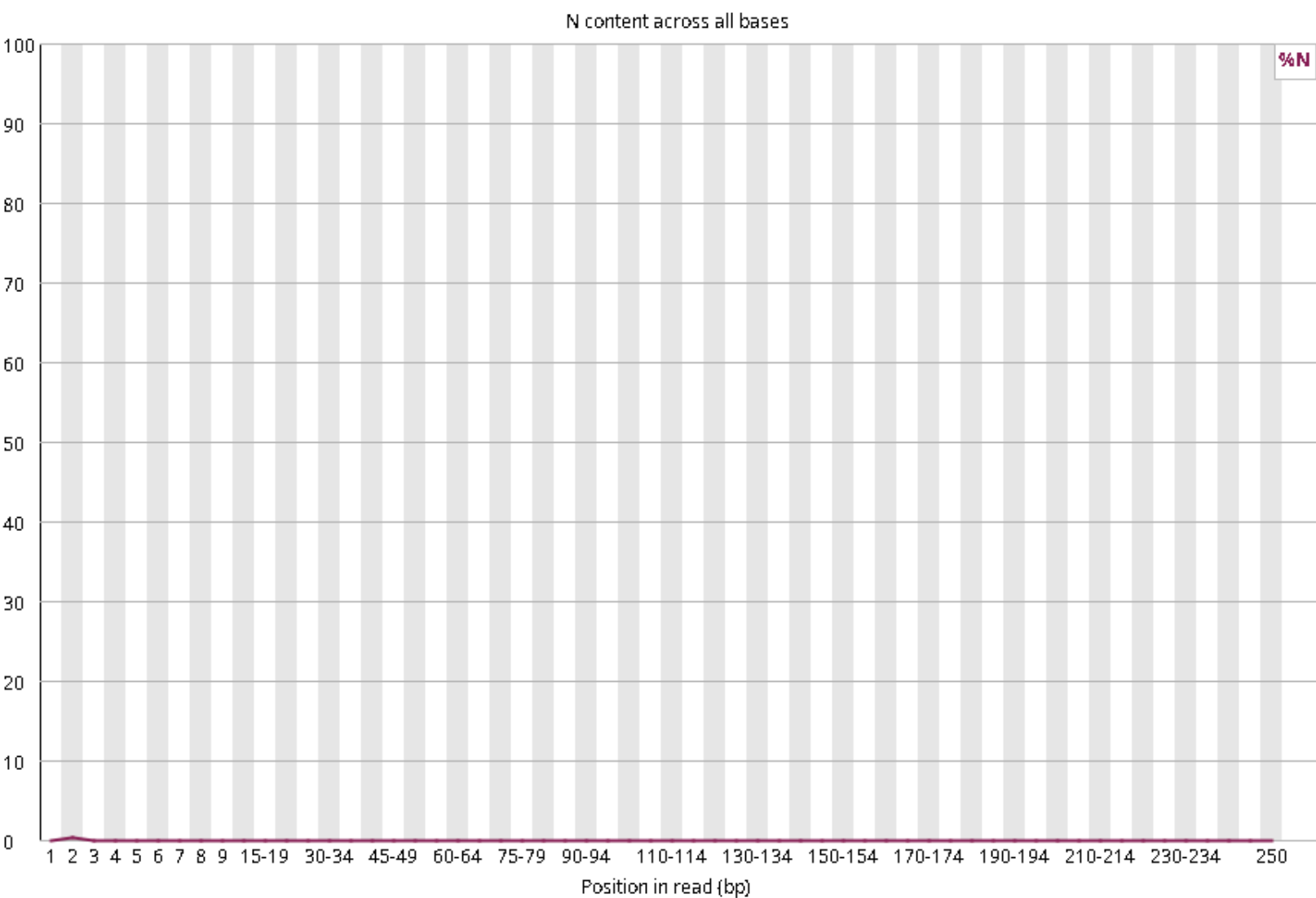


✖ Per sequence GC content

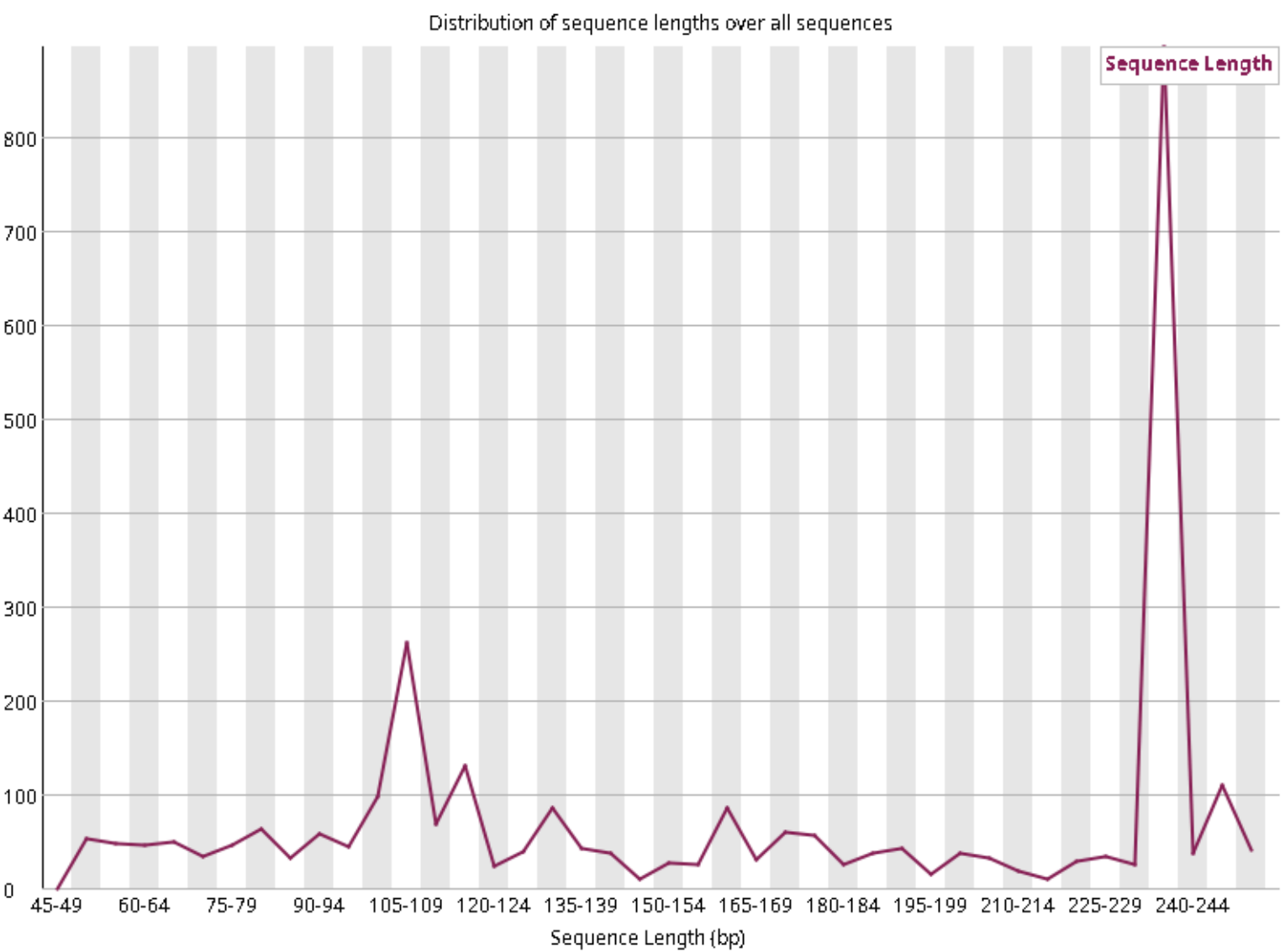




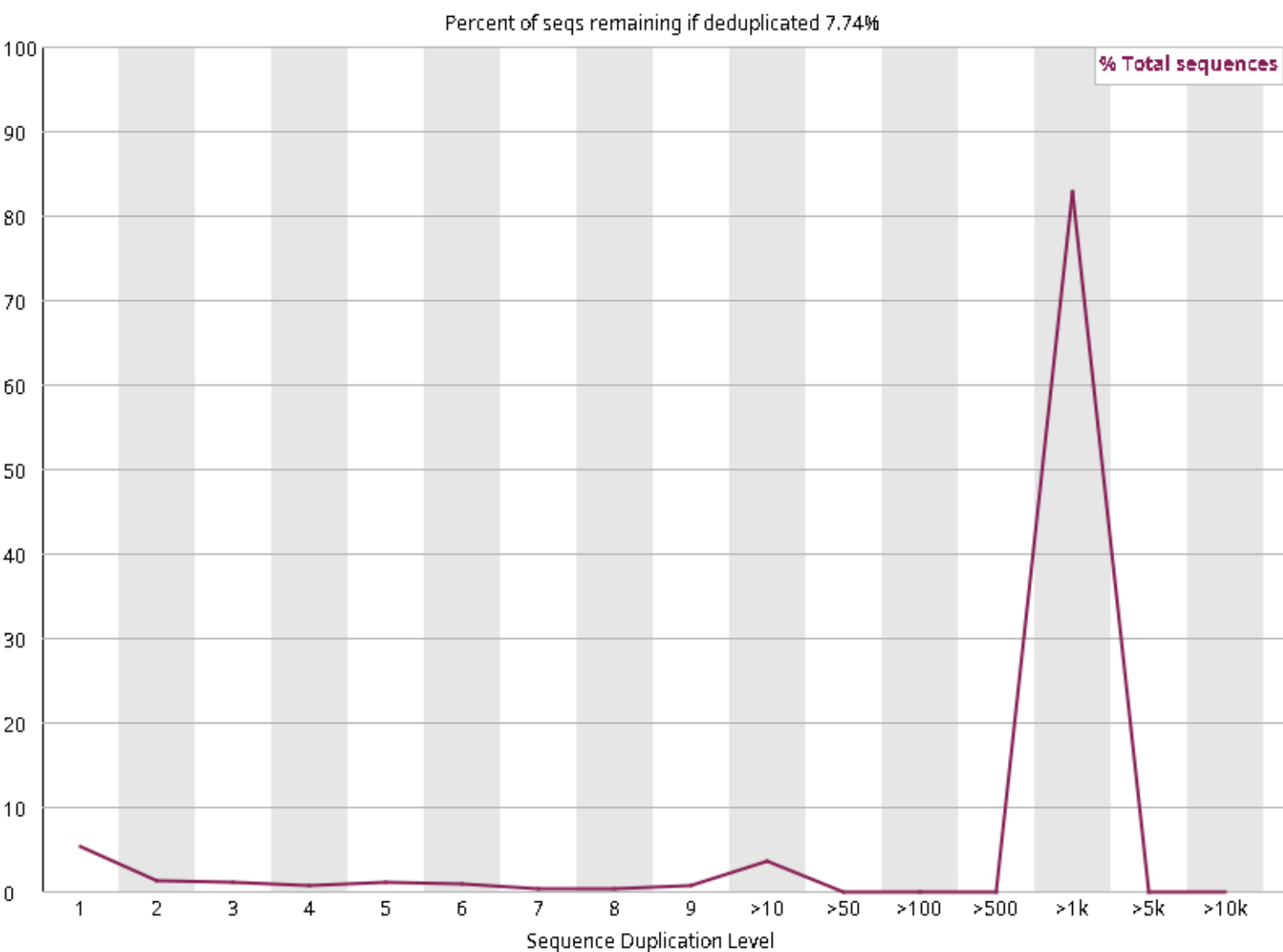
Per base N content



Sequence Length Distribution



Sequence Duplication Levels



Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GCCTGGCTAGAAGCACAAGAGGAGGAGGAGGTGGGTTTTCCAGTCACACC	2488	82.98865910607071	No Hit
GACTGGCTAGAAGCACAAGAGGAGGAGGAGGTGGGTTTTCCAGTCACACC	23	0.7671781187458305	No Hit
GCCCCAGGTGTGCATAAGTAAGAGCAGATAGCTGATTCCAGTGCAAAGTC	22	0.733822548365577	No Hit
GATGCAGTACCAAGCCCGCCTGGAGCAGAGTGAGAAGCGCTTGAGACAGC	20	0.66711140760507	No Hit
AGCCCATTTCCATCATCGACCTCATCGTGGTCGTGGCCTCCATGGTGGTC	16	0.5336891260840559	No Hit
CTAGTGGTGGAGGAGGCTCTGGTGGAGGCGGTAGCGGAGGCGGAGGGTCG	12	0.40026684456304207	No Hit
GCCTGGCTAGAAGCACAATAGGAGGAGGAGGTGGGTTTTCCAGTCACACC	10	0.333555703802535	No Hit
GCCTGGCTAGAAGCACAAGAGGAGGAGGAGGTGTGAAATTGCGCAGCCAT	10	0.333555703802535	No Hit
GCATGGCTAGAAGCACAAGAGGAGGAGGAGGTGGGTTTTCCAGTCACACC	9	0.3002001334222815	No Hit

Sequence	Count	Percentage	Possible Source
AATACTGGCCTCCGGCTGAACTTCAGTATCGGCCACCCCAGAAAGTCAG	9	0.3002001334222815	No Hit
GACATCGAGCTTGCTACAAGGGACTTTCCGCTGGGGACTTTCCAGGGAGG	9	0.3002001334222815	No Hit
GCCTGGCTAGAAGCACAAAGAGGAGGAGGAGGTGGGTTTTCCAGTCACAAC	8	0.26684456304202797	No Hit
GNCTGGCTAGAAGCACAAAGAGGAGGAGGAGGTGGGTTTTCCAGTCACACC	8	0.26684456304202797	No Hit
ATGGACGAGGGCTTGTCAGGCTTTTGCATTAGATCATCATCAGGAAGTGT	7	0.23348899266177453	No Hit
TAGCGAGGGAAGCAAGTTGGACCCACAGCAGGCTTTGGAGTCAAGGAAAG	7	0.23348899266177453	No Hit
CAAGGGCATCGGTGAGATCCCGGTGCCTAATGAGTGAGCTAACTTACAT	6	0.20013342228152103	No Hit
AACCGATACAATTAAGGCTCCTTTTGGAGCCTTTTTTTTGGAGATTTTC	6	0.20013342228152103	No Hit
GCCTGGCTAGAAGCACAAAGAGGAGGAGGAGGTGGGTTTTCTGTACACACC	6	0.20013342228152103	No Hit
GCCTGGCTAGAAGAACAAGAGGAGGAGGAGGTGGGTTTTCCAGTCACACC	6	0.20013342228152103	No Hit
GCCTGGATAGAAGCACAAAGAGGAGGAGGAGGTGGGTTTTCCAGTCACACC	6	0.20013342228152103	No Hit
GCCTGGCTAGAAGCACAAAGAGGAGGAGGAGGTGGTTTTTCCAGTCACACC	5	0.1667778519012675	No Hit
GGCTGGCTAGAAGCACAAAGAGGAGGAGGAGGTGGGTTTTCCAGTCACACC	5	0.1667778519012675	No Hit
GCCTGGCTAGAAGCACAAAGAGGAGGAGGAGTTGGGTTTTCCAGTCACACC	5	0.1667778519012675	No Hit
GCCTGGCTAGAAGCACAAAGAGGAGGAGGAGGTGGGTTTTCCAGTCACACA	5	0.1667778519012675	No Hit
GCCTGGCTAGAAGCACAAAGAGGAGGAGGAGGAGGTTTTTCCAGTCACACC	5	0.1667778519012675	No Hit
GTGCGAGAGCGTCGGTATTAAGCGGGGGAGAATTAGATAAATGGGAAAAA	5	0.1667778519012675	No Hit
GCCTGGCTAGAAGCACAAAGAGGAGGAGGAGGTGGGTTTTCCAGTAACACC	5	0.1667778519012675	No Hit
GTAGTGCTGGGGCTTAGACGCAGGTGTTCTGATTATAGTTCAAAACCTC	4	0.13342228152101399	No Hit
AATCGACCGGTGGTAAAGCACCCAGGAAGCAACTGGCTACAAAAGCCGCT	4	0.13342228152101399	No Hit
GCCTGGCTAGAAGCACAAAGAGGAGGAGGAGGTGGGTATCCAGTCACACC	4	0.13342228152101399	No Hit
GCCTGGCTAGAAGCACAAAGAGGAGGAGGAGGTGGGTTTTCCAGTCATACC	4	0.13342228152101399	No Hit
GCCTGGCTAGAGCACAAAGAGGAGGAGGAGGTGGGTTTTCCAGTCACACCT	4	0.13342228152101399	No Hit
GGGTGCCCTAATACCTGACGACCATTCAATTGATGGGCAGTCAGACCCCTC	4	0.13342228152101399	No Hit
GCCTGGCTAGAAGCACAAAGATGAGGAGGAGGTGGGTTTTCCAGTCACACC	4	0.13342228152101399	No Hit
TCCACTAACGAAAGAGGTCAAGAGCGCTCGGGCAGATCTGATCGTCGGAT	3	0.10006671114076052	No Hit
GCTGGCTAGAAGCACAAAGAGGAGGAGGAGGTGGGTTTTCCAGTCACACCT	3	0.10006671114076052	No Hit
GCCTGGCTAGAAGCACAAAGAGGAGGAGGAGGTGTGTTTTCCAGTCACACC	3	0.10006671114076052	No Hit
GCCTGGTAGAAGCACAAAGAGGAGGAGGAGGTGGGTTTTCCAGTCACACCT	3	0.10006671114076052	No Hit
AATACTGGCCTCCGGCTGAACTTCAGTATCGGCCACCCCTAGAAAGTCAG	3	0.10006671114076052	No Hit
GCCTGGCTAGAAGCACAAAGAGGAGGAGGAGGGGGGTTTTCCAGTCACACC	3	0.10006671114076052	No Hit
GCCTGGCTAGAAGCACAAAGAGGAGGAGGAGGTGGGTATTCCAGTCACACC	3	0.10006671114076052	No Hit
GCCTGGCTAGAAGCACAAAGAGGATGAGGAGGTGGGTTTTCCAGTCACACC	3	0.10006671114076052	No Hit
GCCTGGCTAGAAGCACAAAGAGGAGGAGGAGGTGGGTTTTCCAGACACACC	3	0.10006671114076052	No Hit
AGCGTTAAAGGCAGATTCAACCATAAGTCGAGACAATTCTAAAAATACGGT	3	0.10006671114076052	No Hit
GCCTGGCTAGAAGCACAAAGAGGAGGAGGAGGTGGGTTTTCCAGTCAAACC	3	0.10006671114076052	No Hit
GCCTGGCTAGAAGCACAAAGAGGAGGAGGAGGTGGGTTTTCAAGTCACACC	3	0.10006671114076052	No Hit
GAGGGAAGAGACGGTGGAAGCGAGCGGGTTCTGGGCTCCTGGGTCTCTGG	3	0.10006671114076052	No Hit



Adapter Content

