











FastQC Report

Summary

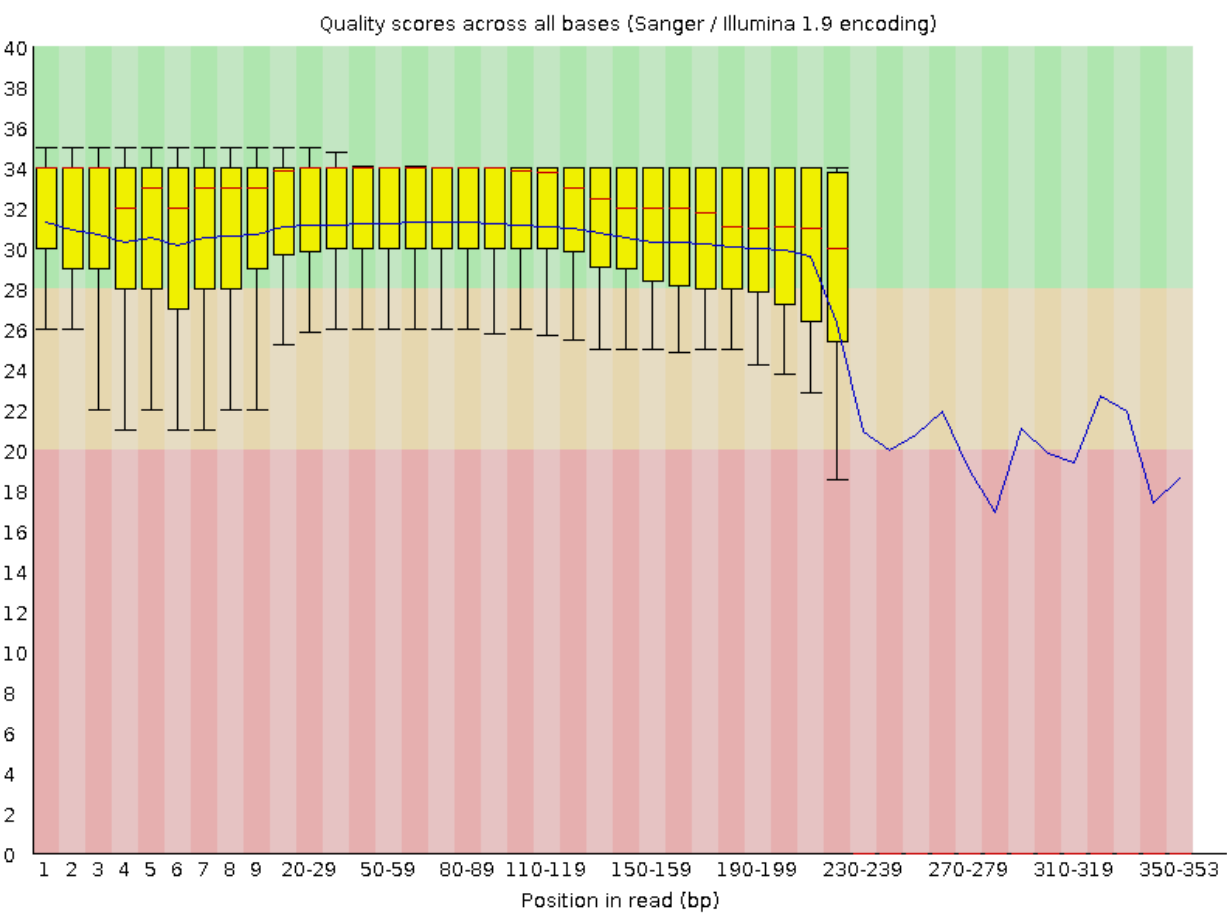
Wed 7 Oct 2020
single_end_data.fastq

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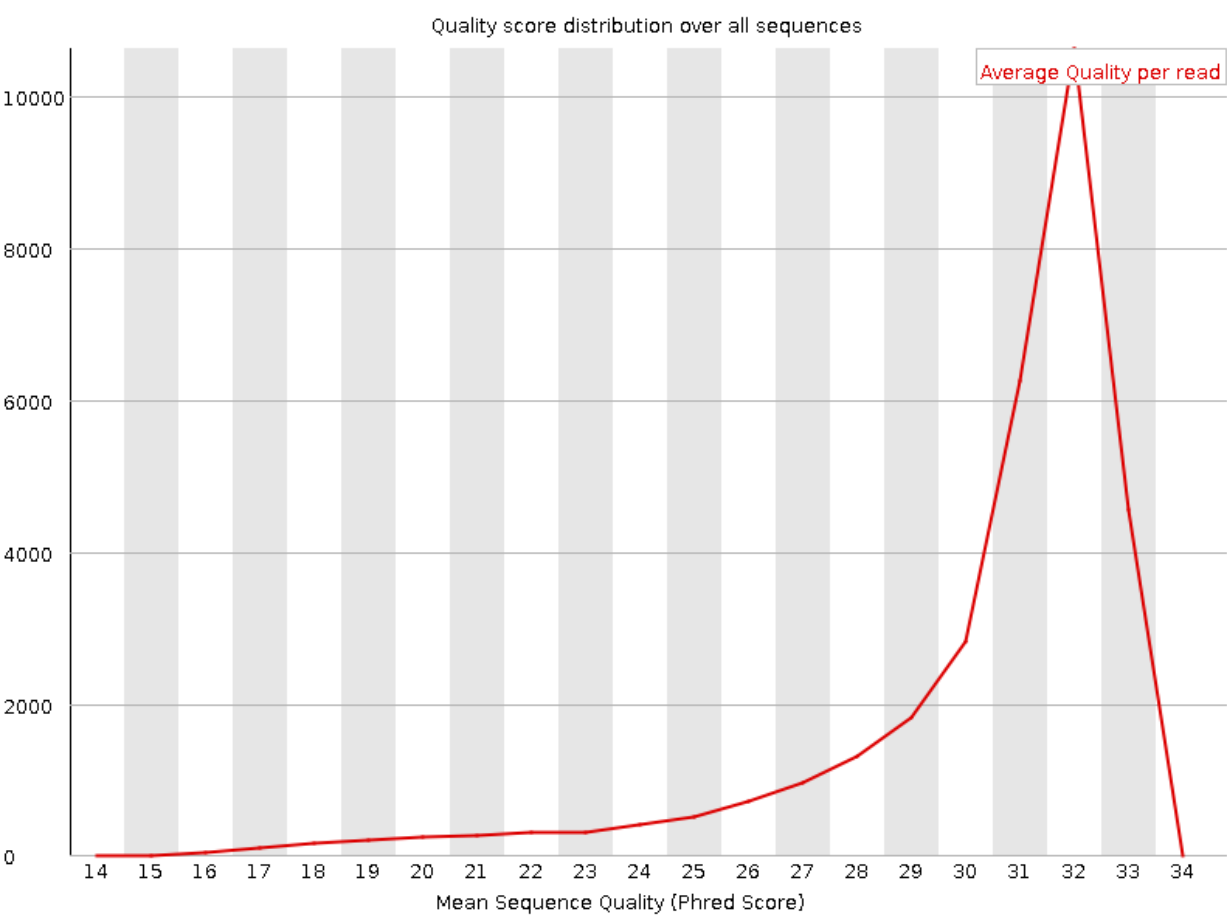
Basic Statistics

Measure	Value
Filename	single_end_data.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	31855
Sequences flagged as poor quality	0
Sequence length	25-353
%GC	43

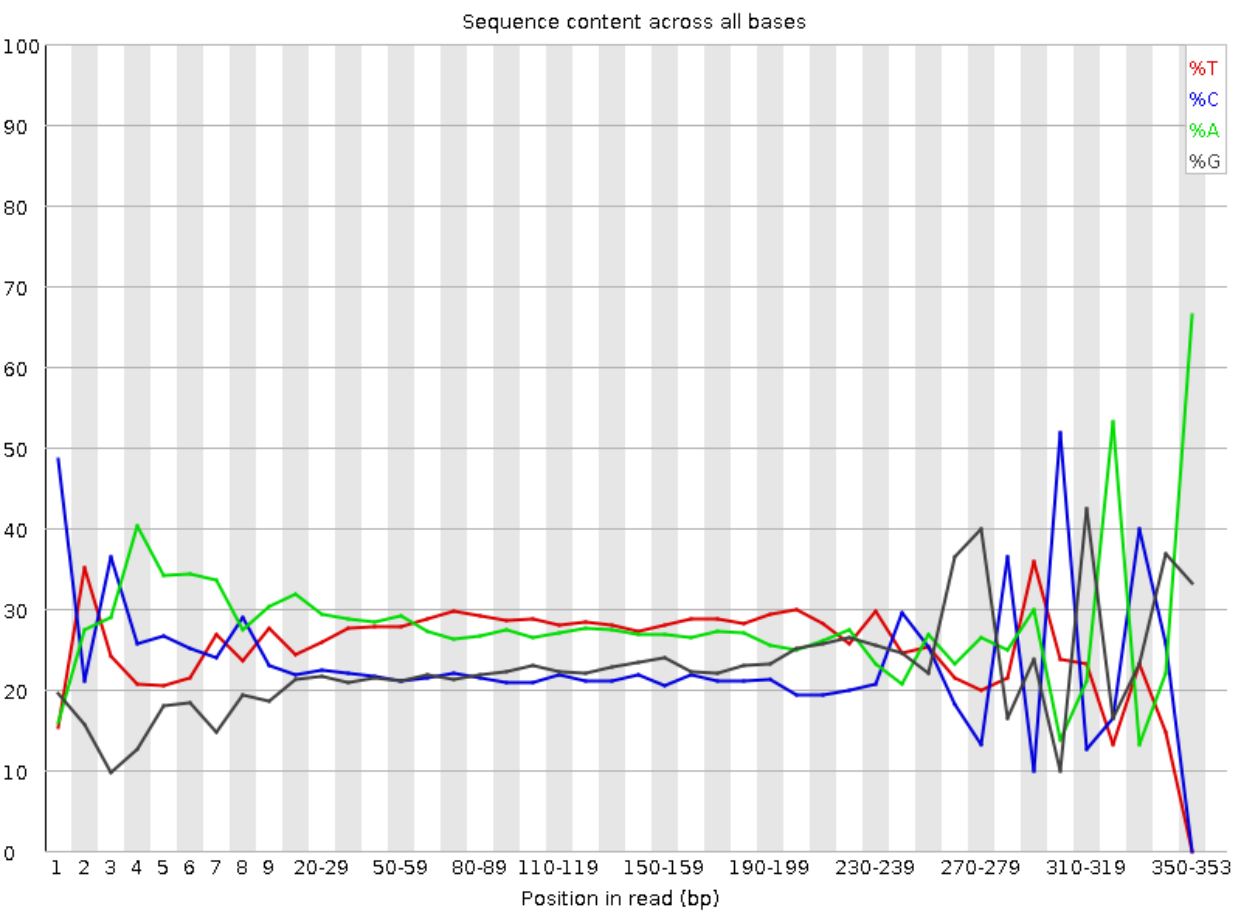
Per base sequence quality



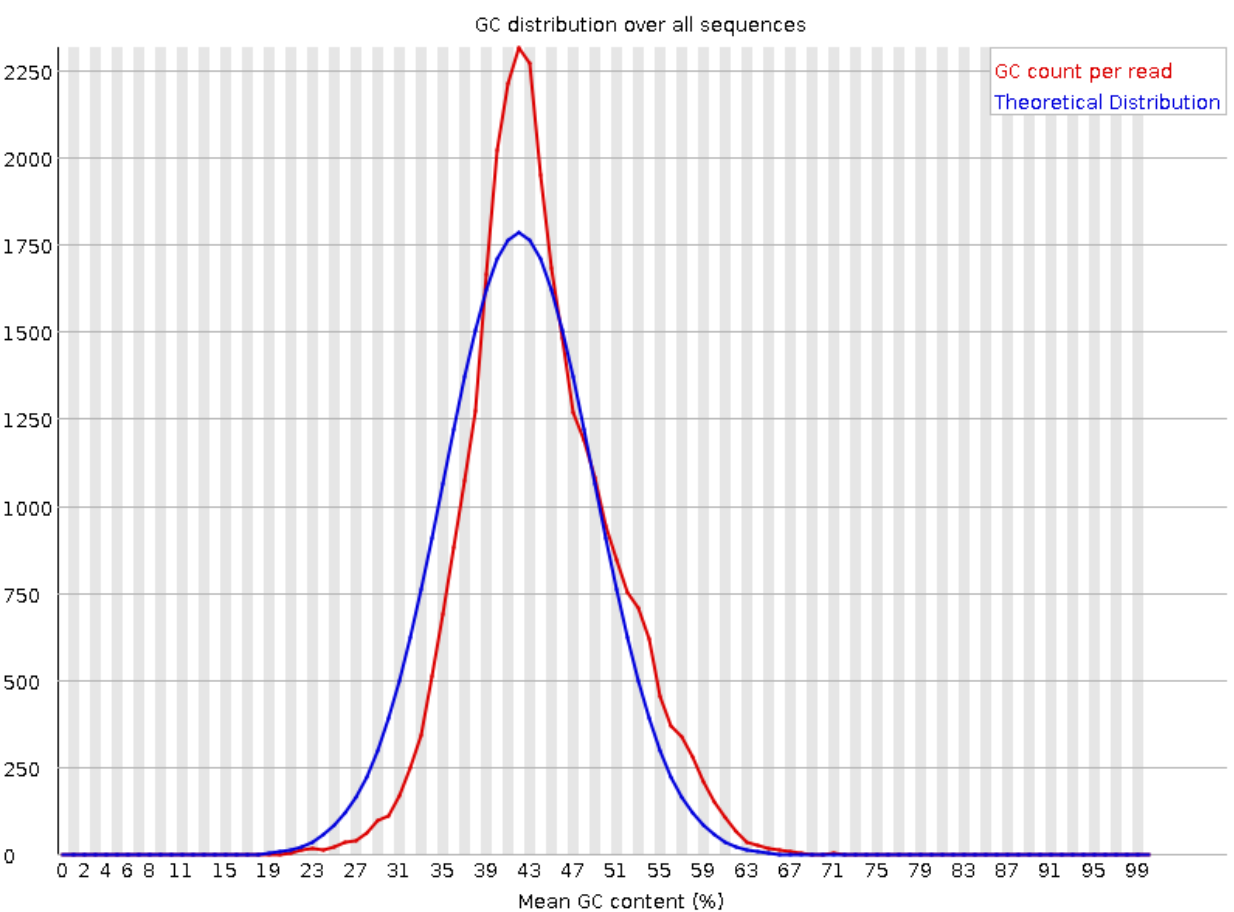
✓ Per sequence quality scores



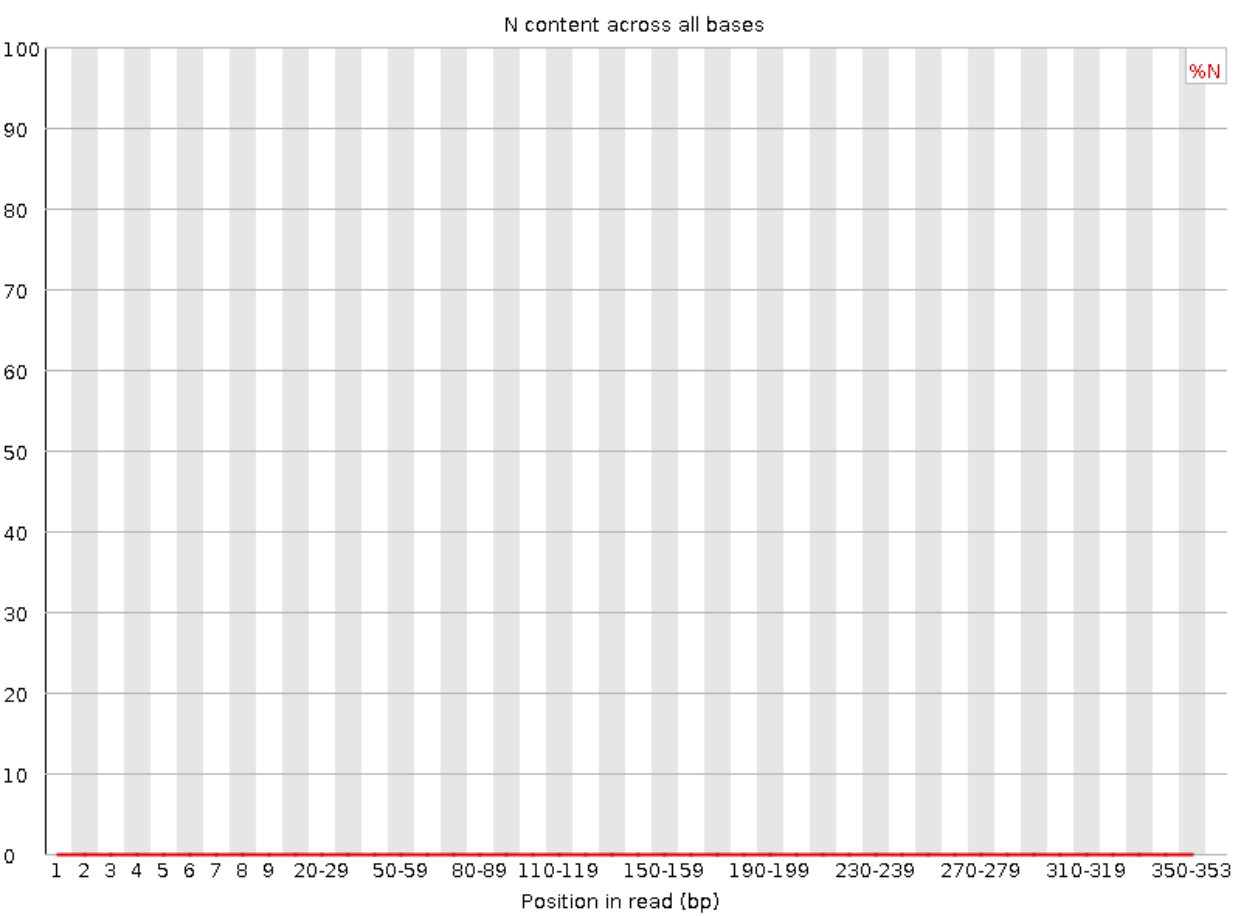
✖ Per base sequence content



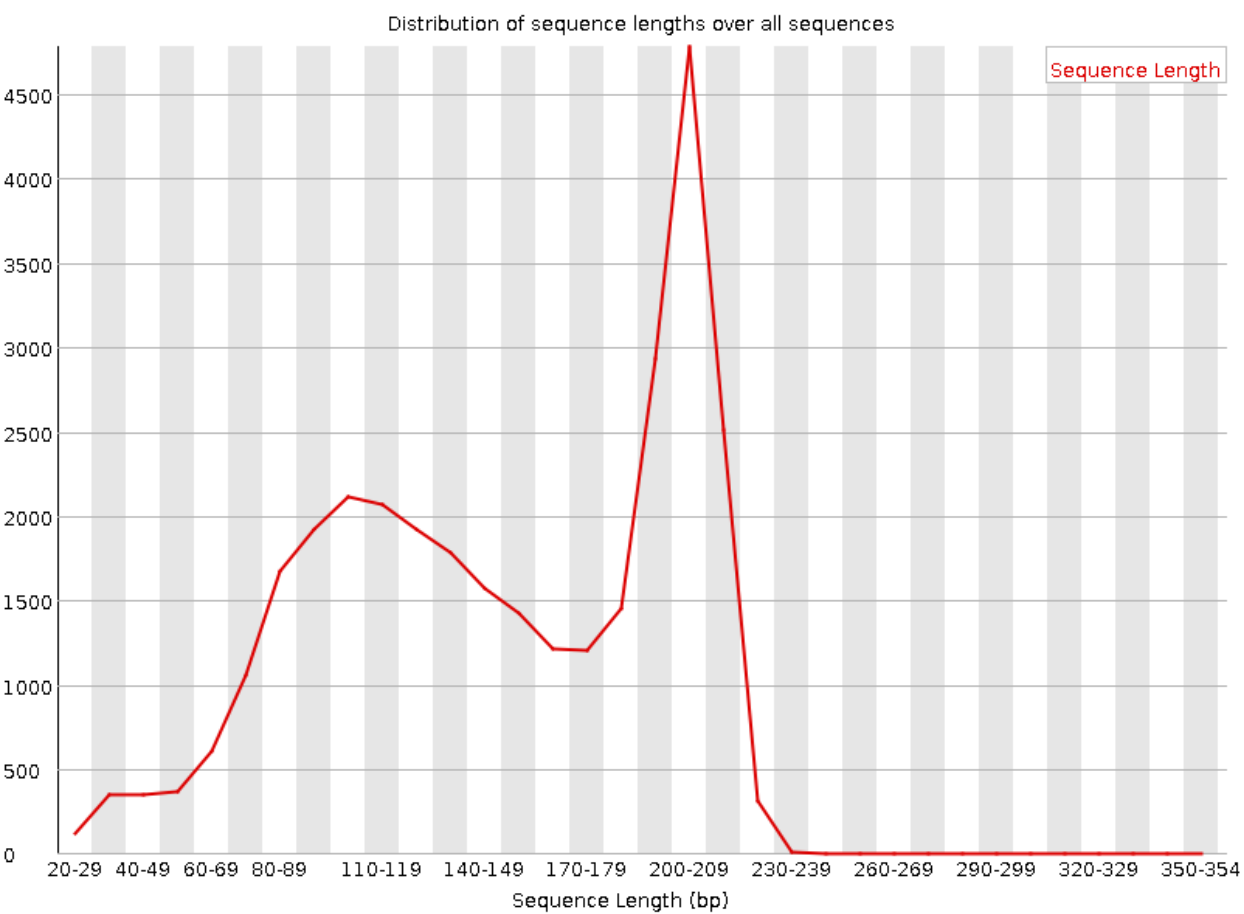
! Per sequence GC content



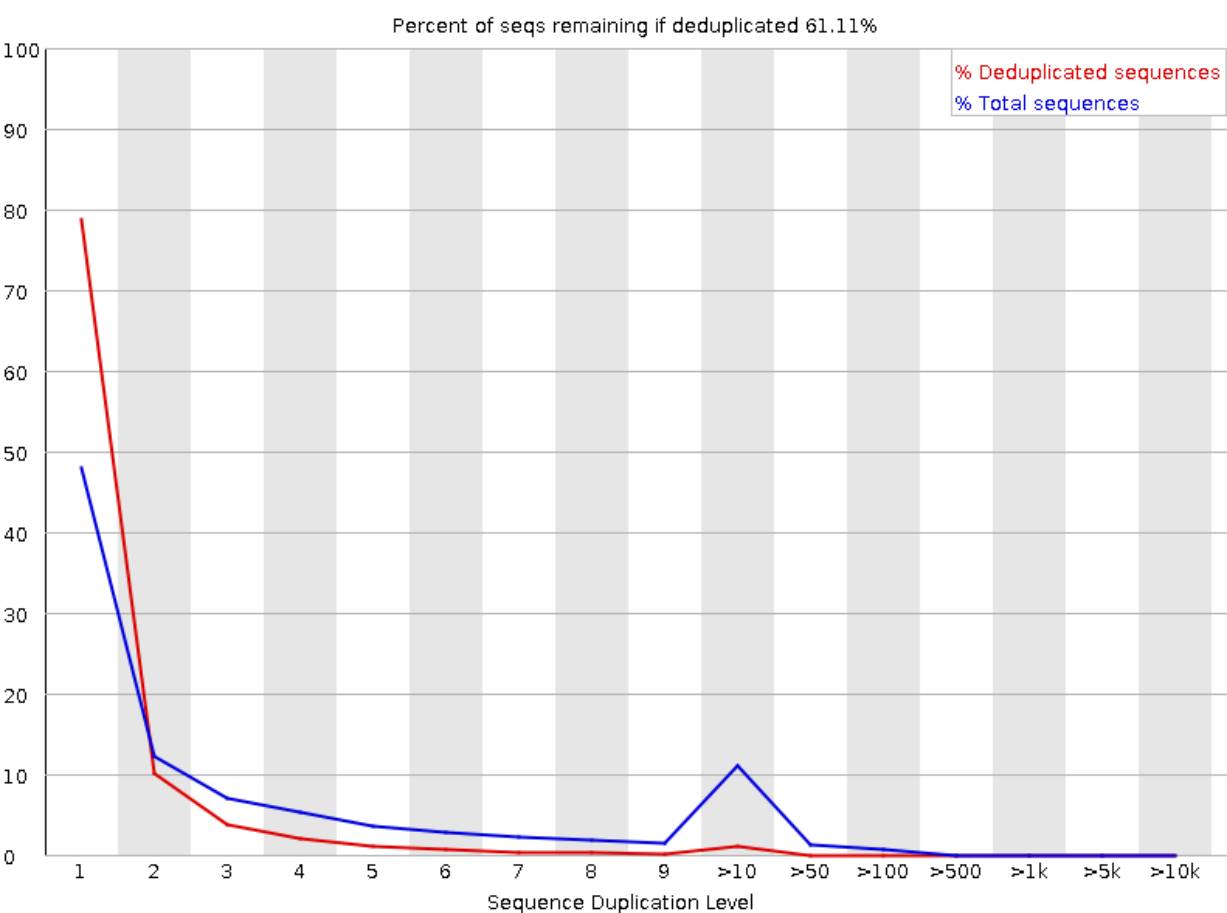
✔ Per base N content



⚠ Sequence Length Distribution



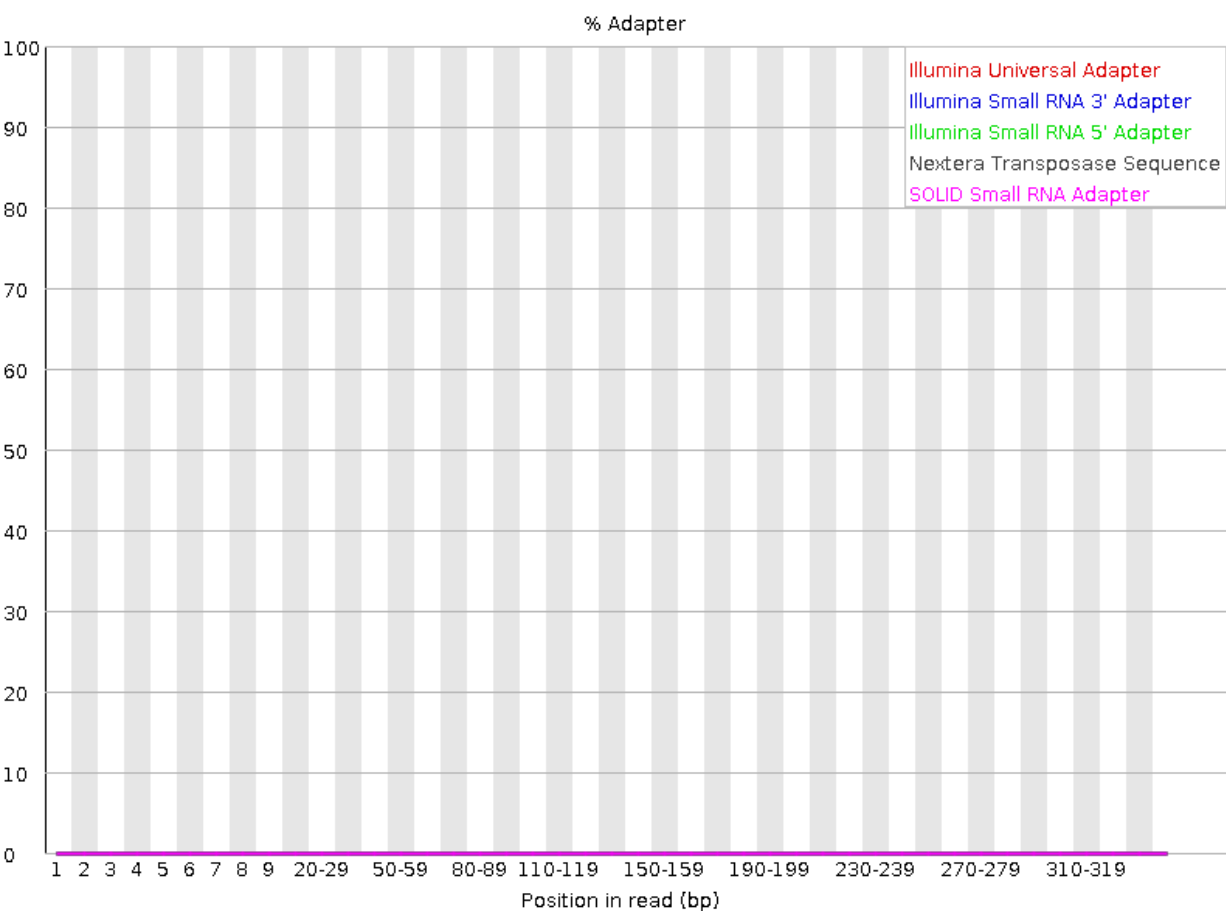
Sequence Duplication Levels



! Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GTCACCACAAACAGAGACTAAAGCAAGTGTGGATTCAAAGCTGGTGTTA	172	0.5399466331816041	No Hit
GTCACCACAAACAGAGACTAAAGCATGTCAACCACAAACAGAGACTAAAGC	132	0.414377648720766	No Hit
GTCACCACAAACAGAGACTAAAGCTAGTGTGCGATTCAAAGCTGGTGTTA	80	0.25113796892167634	No Hit
GTCACCACAAACAGAGACTAAAGCCGATGTGCCAATCTATTACTACAGTA	73	0.2291633966410297	No Hit
CTCCAACGCATGAAACGGTCTCTCCAACGCATGAAACGGTCTCTCCAACG	73	0.2291633966410297	No Hit
CAAAAACTTTCCAAGGTCCGCCTCACGGTATCCAAGTTGAAAGGGATAAG	68	0.21346727358342488	No Hit
CTAAAACTTTCCAAGGTCCGCCTCATGGCATCCAAGTTGAGAGGGATAAA	58	0.18207502746821536	No Hit
GTCACCACAAACAGAGACTAAAGCAAGTGTGGATTAAAGCTGGTGTTA	53	0.1663789044106106	No Hit
CAAAACTTTTCAGGGTCCACCTCATGGTATCCAAGTTGAAAGAGATAAAT	53	0.1663789044106106	No Hit
CCACAAACAGAGACTAAAGCAAGTGTGGATTCAAAGCTGGTGTTAAAGA	49	0.15382200596452675	No Hit
GTCACCACAAACAGAGACTAAAGCATAAAAGGAAGTAATCGATCGACGAA	43	0.13498665829540102	No Hit
CCAAAACTTTTCAGGGTCCACCTCATGGTATCCAAGTTGAAAGAGATAAA	36	0.11301208601475435	No Hit
CTCCAACGCATAAATGGTTGTGAGTTTACGTTTTTCATCATCTTTGGTAAA	36	0.11301208601475435	No Hit
GTCTCTCCAACGCATGAAACGGTCTCTCCAACGCATGAAACGGTCTCTCC	33	0.1035944121801915	No Hit
GTCACCACAAACAGAGACTAAAGTATGTCACCACAAACAGAGACTAAAGC	32	0.10045518756867054	No Hit

✓ Adapter Content



Produced by [FastQC](#) (version 0.11.9)