











FastQC Report

Summary

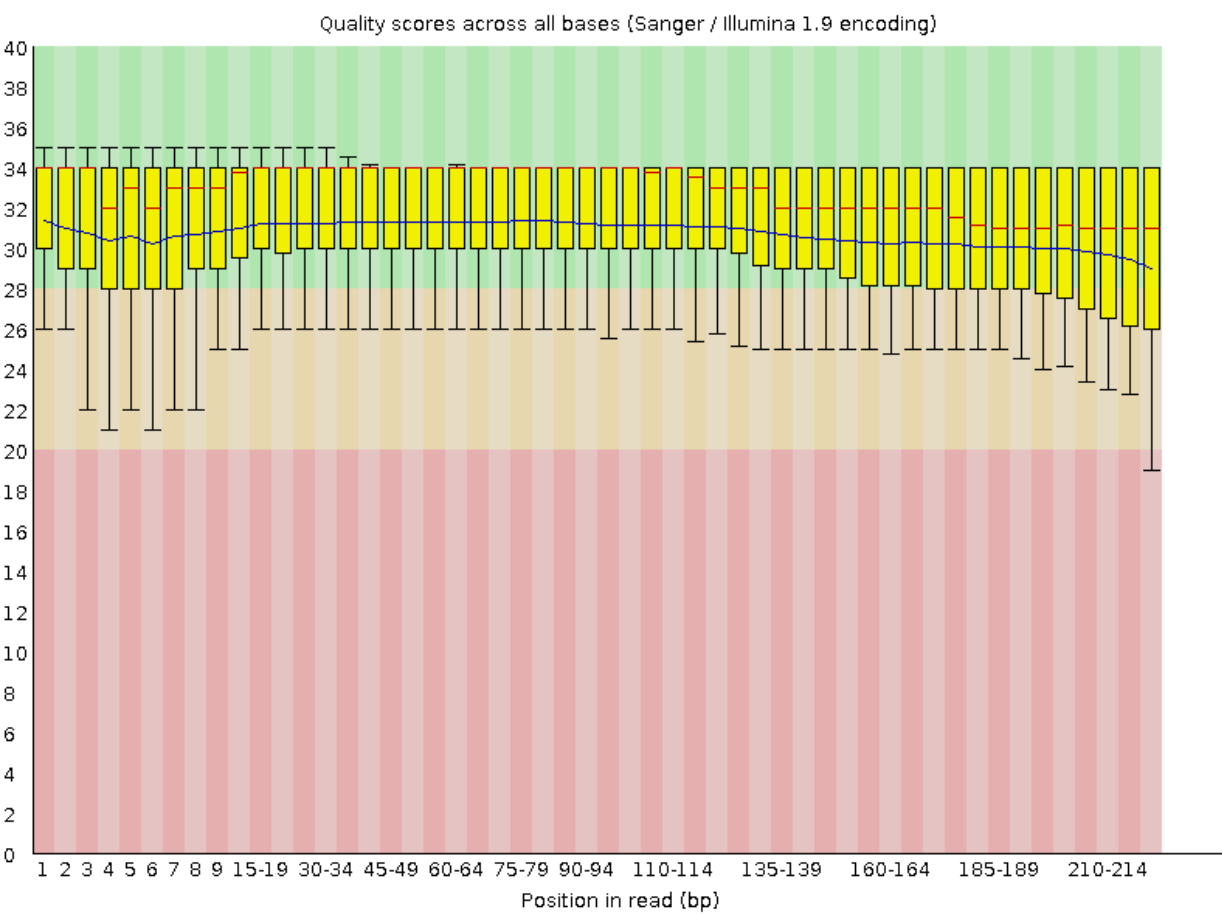
Wed 7 Oct 2020
single_end_data_trimmed_fastp.fastq

-  [Basic Statistics](#)
-  [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](#)
-  [Adapter Content](#)

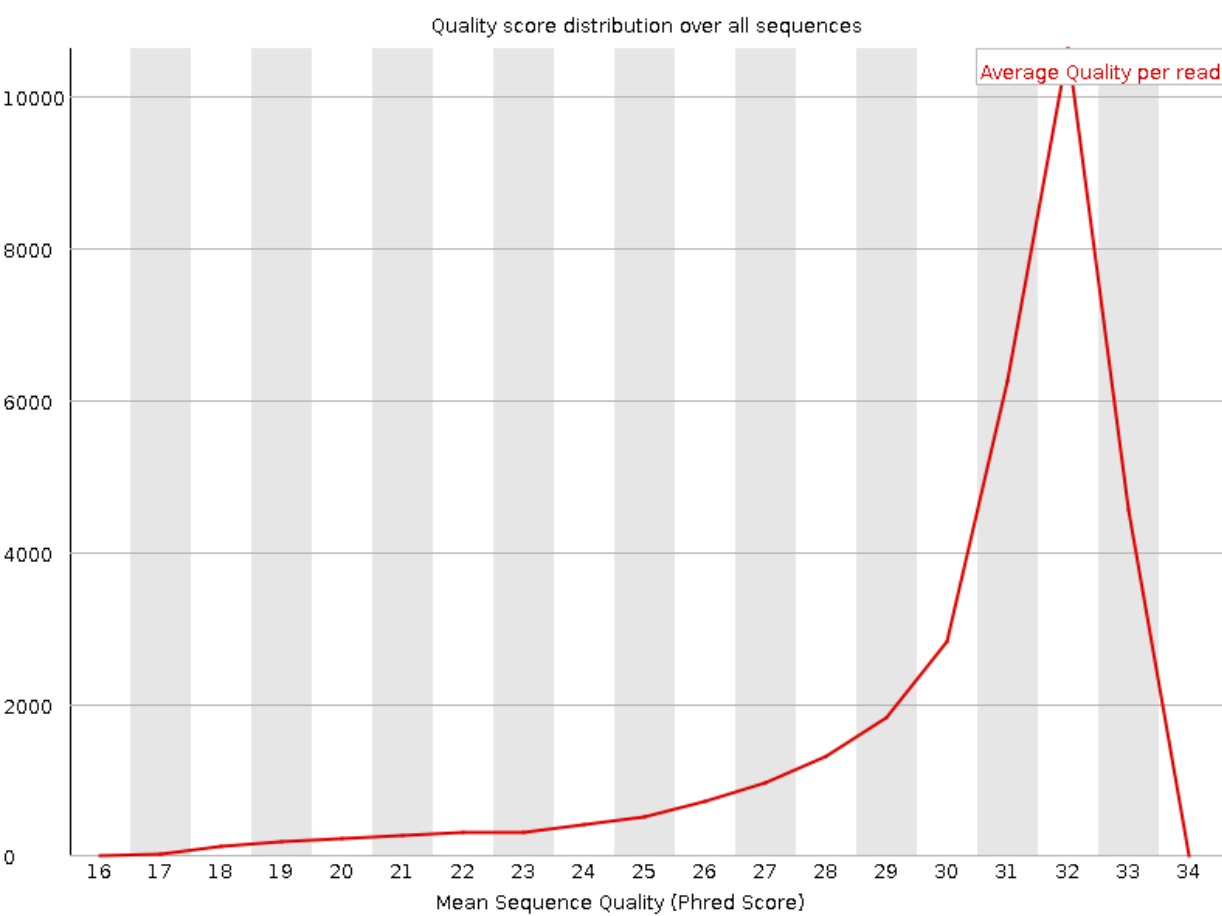
Basic Statistics

Measure	Value
Filename	single_end_data_trimmed_fastp.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	31622
Sequences flagged as poor quality	0
Sequence length	25-220
%GC	43

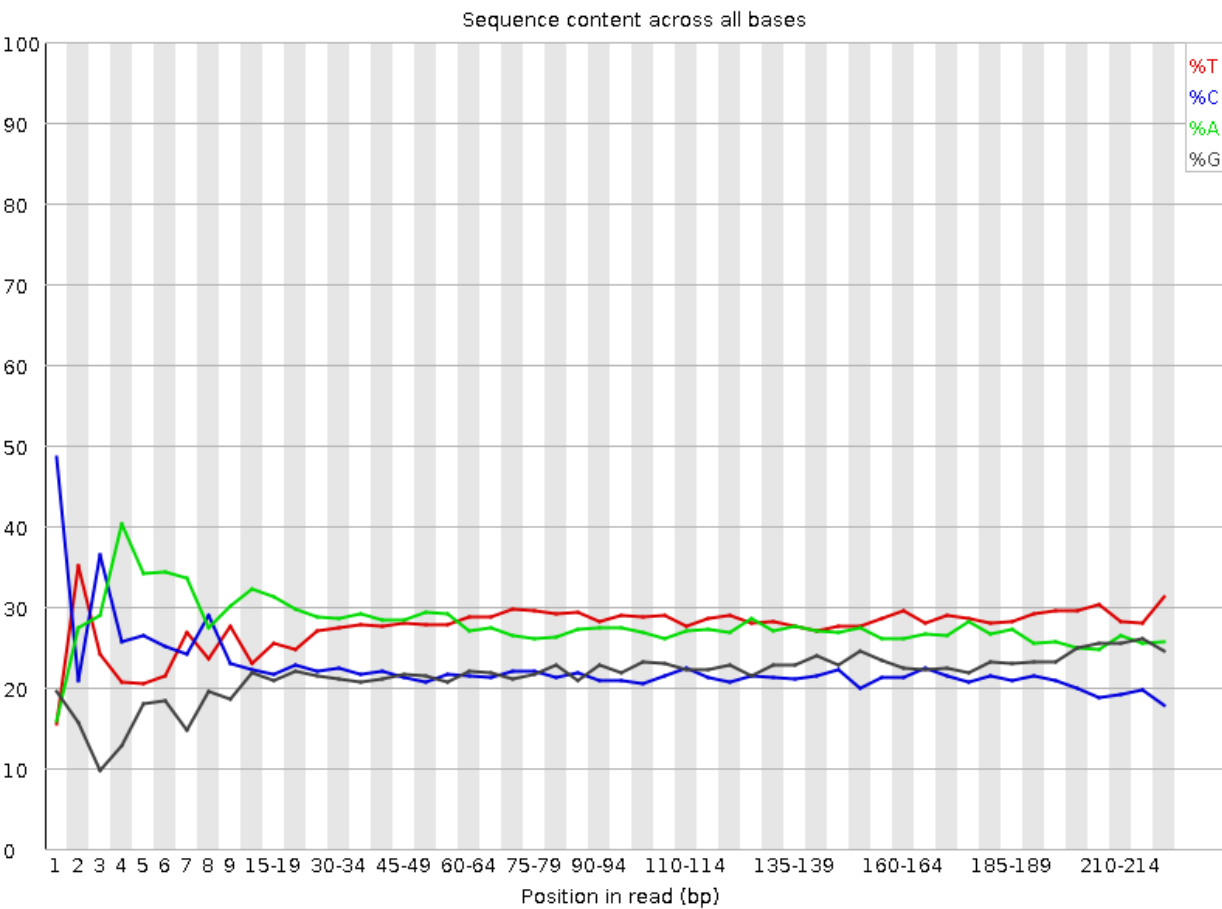
Per base sequence quality



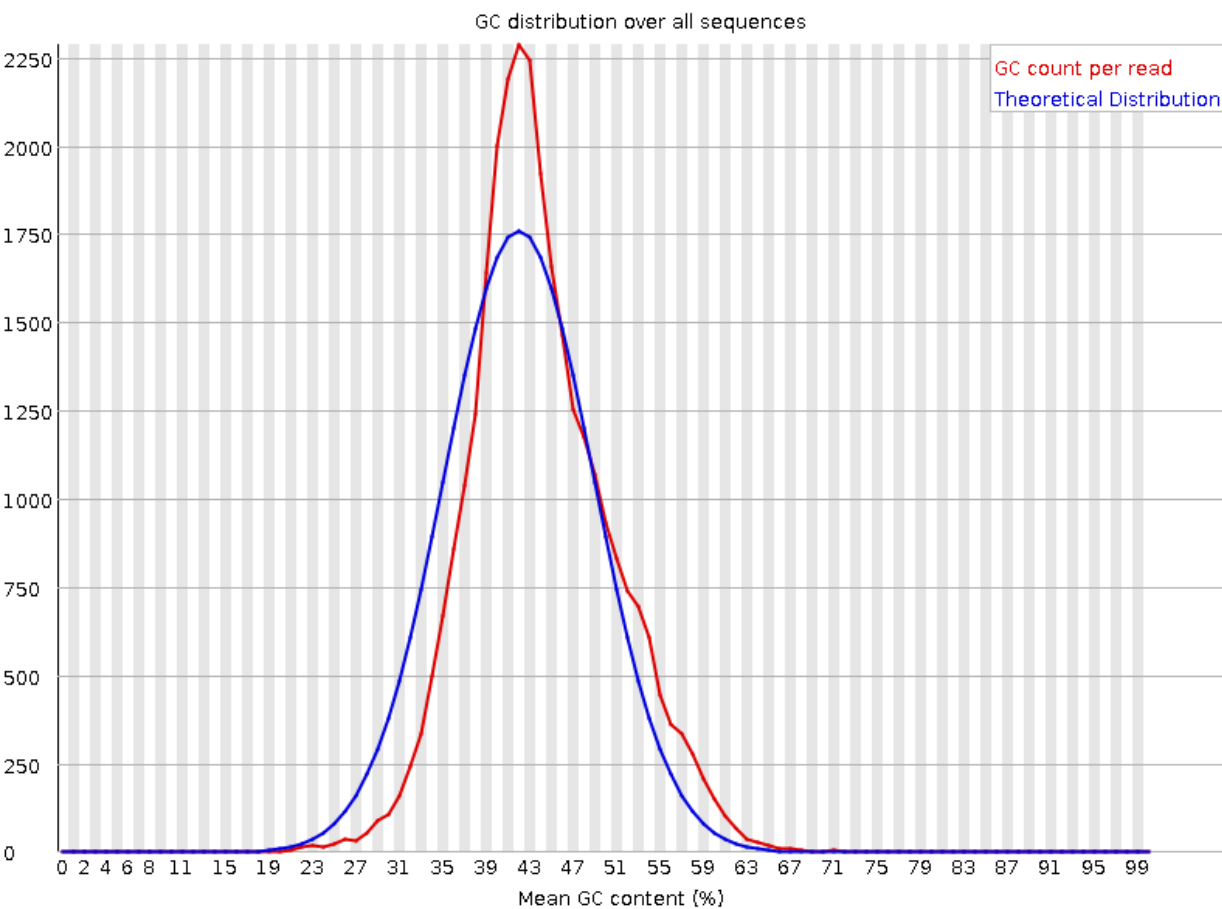
Per sequence quality scores



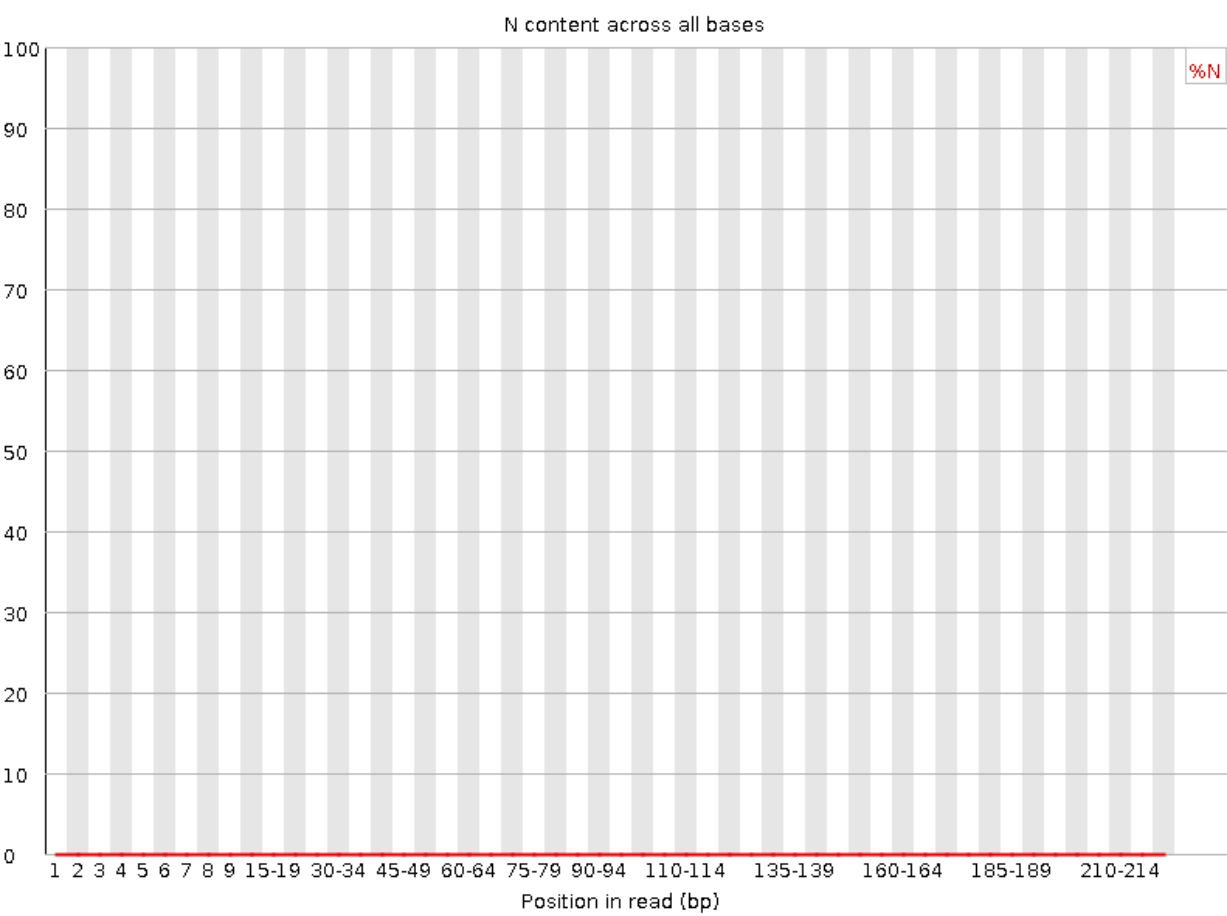
✖ Per base sequence content



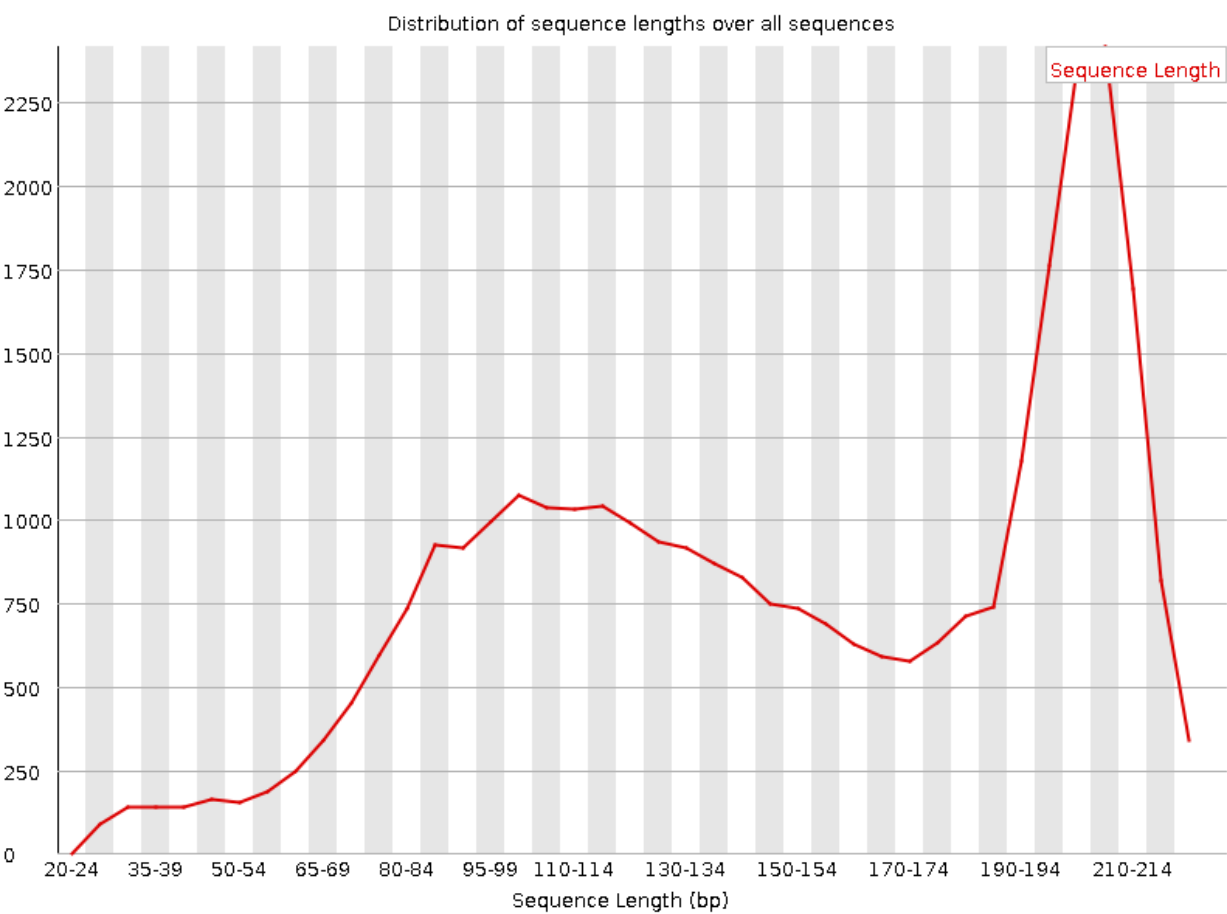
! Per sequence GC content



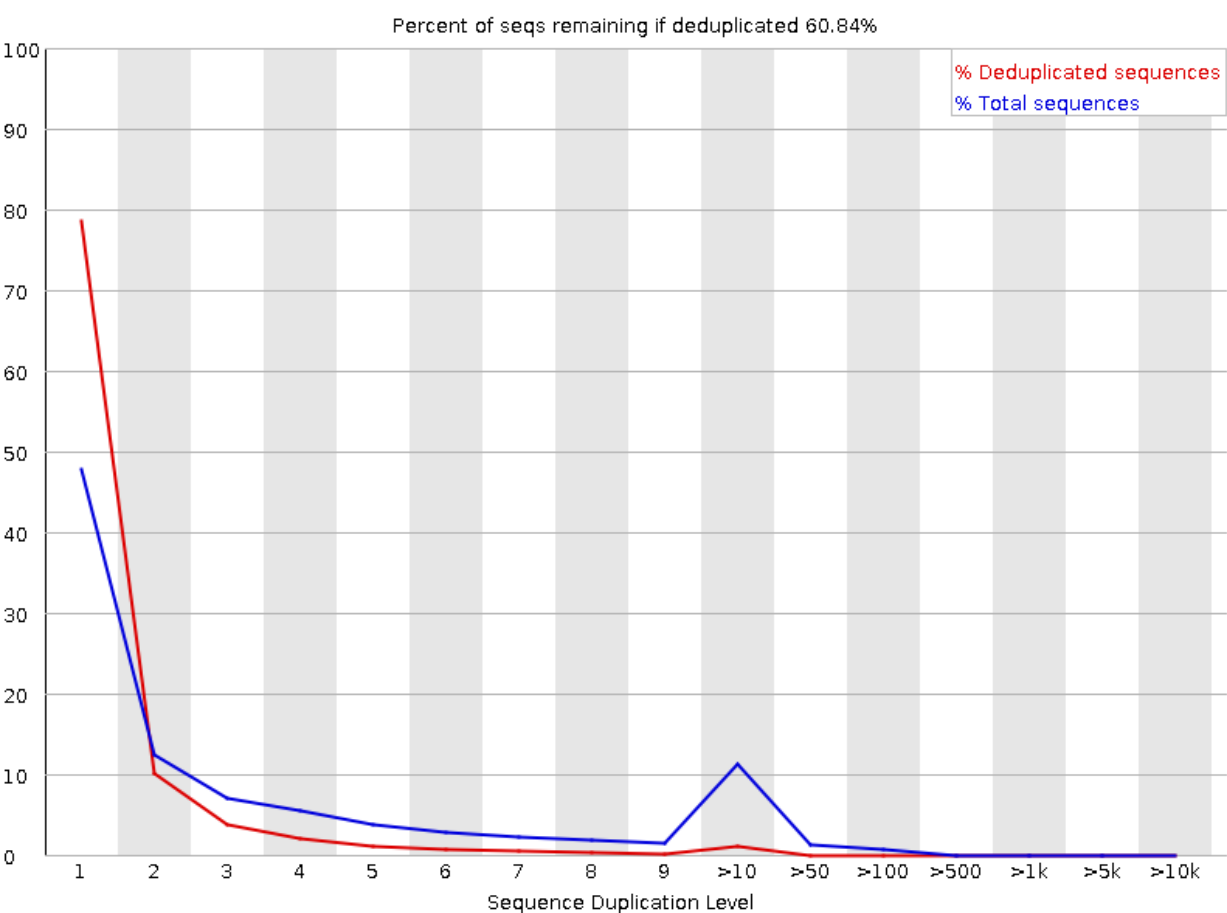
✔ Per base N content



⚠ Sequence Length Distribution



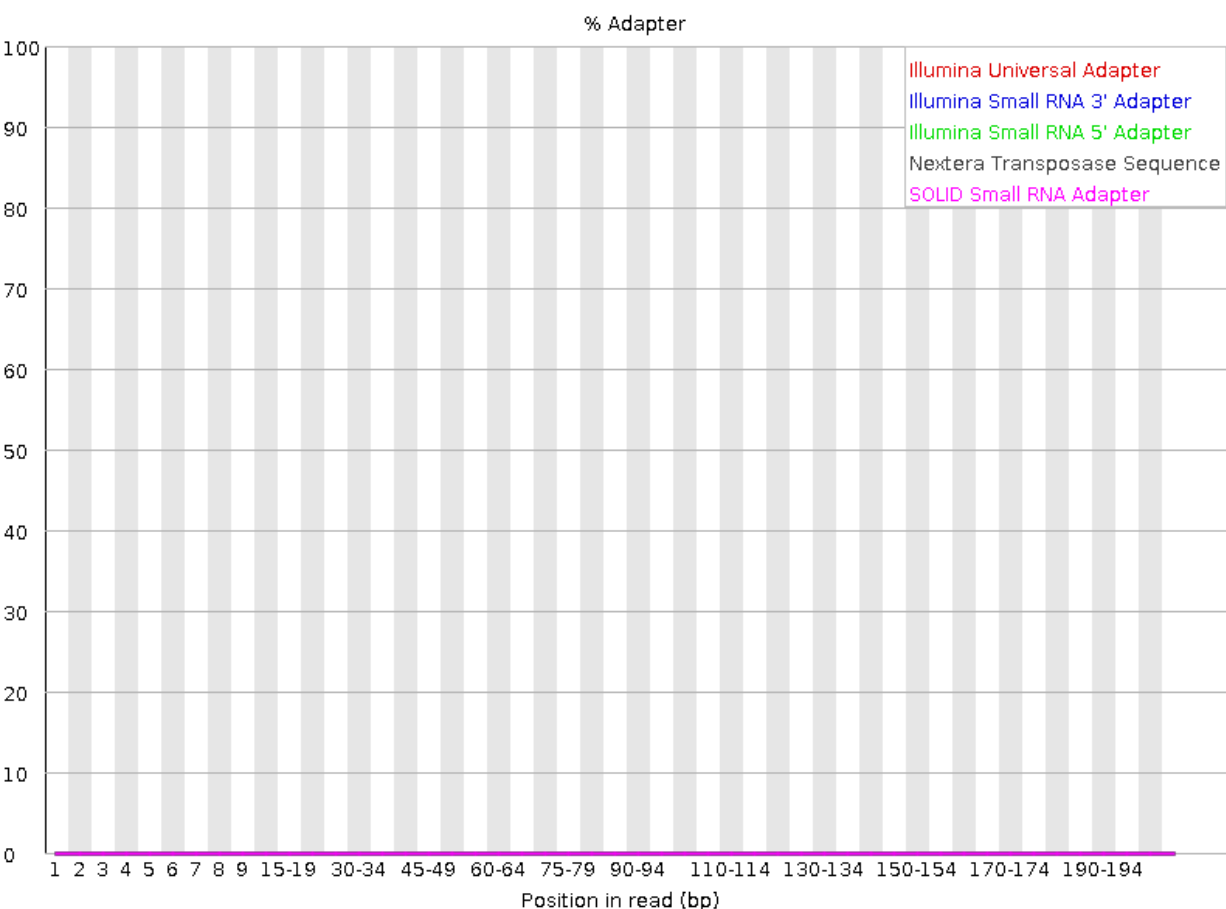
Sequence Duplication Levels



! Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GTCACCACAAACAGAGACTAAAGCAAGTGTGGATTCAAAGCTGGTGTTA	172	0.5439251154259692	No Hit
GTCACCACAAACAGAGACTAAAGCATGTCAACCACAAACAGAGACTAAAGC	132	0.41743090253620896	No Hit
GTCACCACAAACAGAGACTAAAGCTAGTGTGCGATTCAAAGCTGGTGTTA	80	0.2529884257795206	No Hit
GTCACCACAAACAGAGACTAAAGCCGATGTGCAATCTATTACTACAGTA	73	0.23085193852381256	No Hit
CTCCAACGCATGAAACGGTCTCTCCAACGCATGAAACGGTCTCTCCAACG	73	0.23085193852381256	No Hit
CAAAAACCTTTCCAAGGTCCGCCTCACGGTATCCAAGTTGAAAGGGATAAG	68	0.2150401619125925	No Hit
CTAAAACCTTTCCAAGGTCCGCCTCATGGCATCCAAGTTGAGAGGGATAAA	58	0.18341660869015244	No Hit
GTCACCACAAACAGAGACTAAAGCAAGTGTGGATTAAAGCTGGTGTTA	53	0.16760483207893237	No Hit
CAAAACCTTTTCAGGGTCCACCTCATGGTATCCAAGTTGAAAGAGATAAAT	53	0.16760483207893237	No Hit
CCACAAACAGAGACTAAAGCAAGTGTGGATTCAAAGCTGGTGTTAAAGA	49	0.15495541078995634	No Hit
GTCACCACAAACAGAGACTAAAGCATAAAAGGAAGTAATCGATCGACGAA	43	0.1359812788564923	No Hit
CCAAAACCTTTTCAGGGTCCACCTCATGGTATCCAAGTTGAAAGAGATAAA	36	0.11384479160078426	No Hit
CTCCAACGCATAAATGGTTGTGAGTTTACGTTTTTCATCATCTTTGGTAAA	36	0.11384479160078426	No Hit
GTCTCTCCAACGCATGAAACGGTCTCTCCAACGCATGAAACGGTCTCTCC	33	0.10435772563405224	No Hit
GTCACCACAAACAGAGACTAAAGTATGTCAACCACAAACAGAGACTAAAGC	32	0.10119537031180822	No Hit

✓ Adapter Content



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