FastQC Report

Summary

✅ [Basic Statistics](#)

✅ [Per base sequence quality](#)

❌ [Per tile sequence quality](#)

✅ [Per sequence quality scores](#)
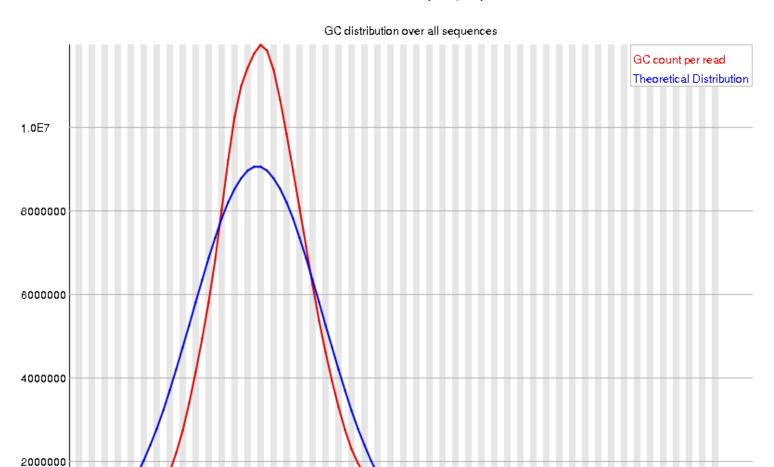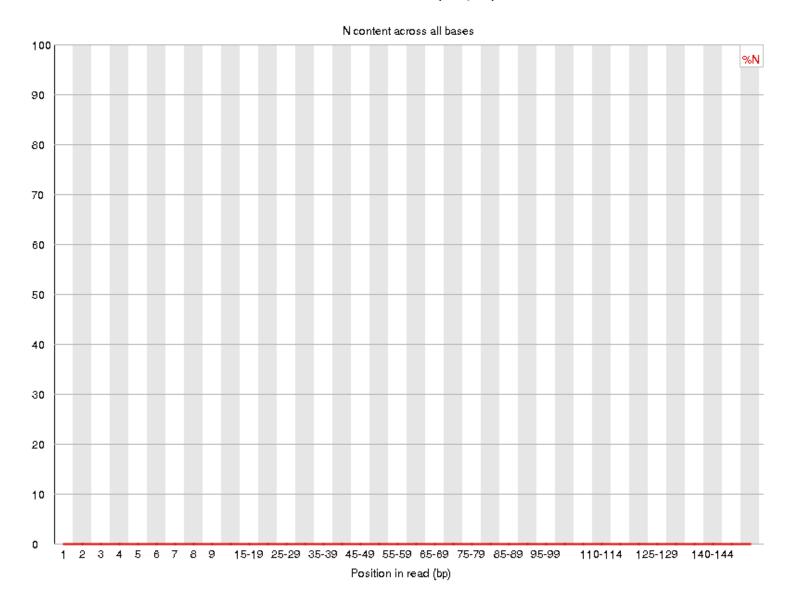
✅ [Per base sequence content](#)
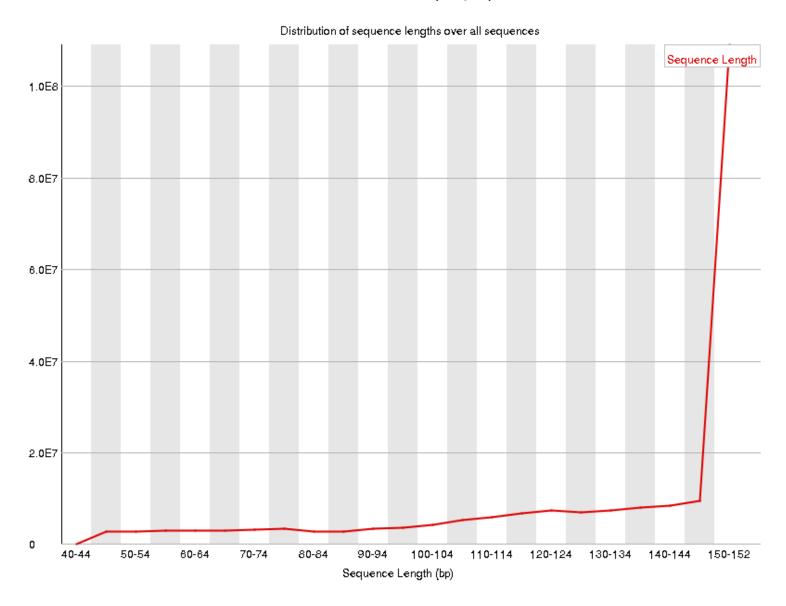
⚠️ [Per sequence GC content](#)

✅ [Per base N content](#)
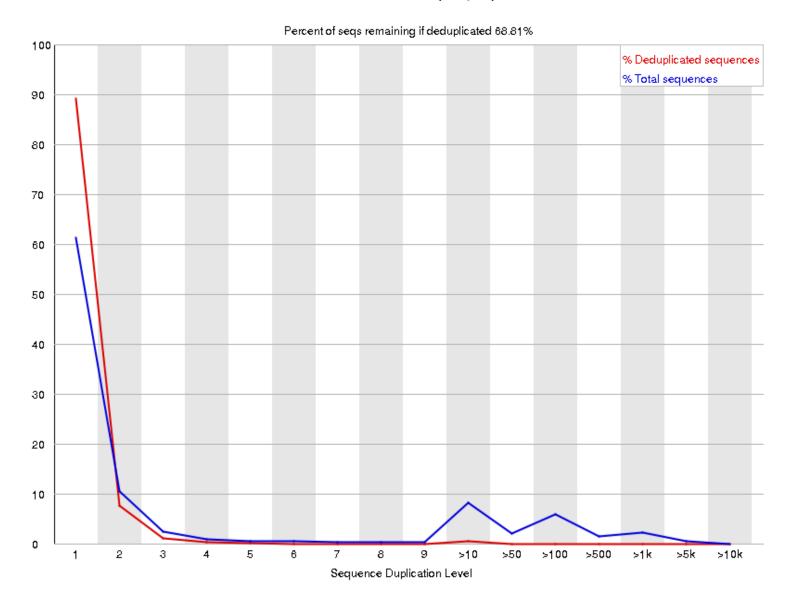
⚠️ [Sequence Length Distribution](#)

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✅ Basic Statistics

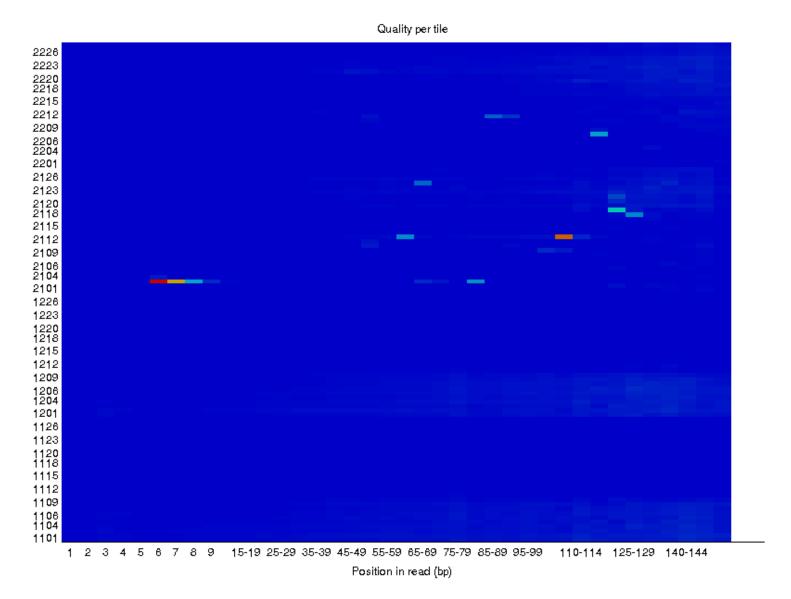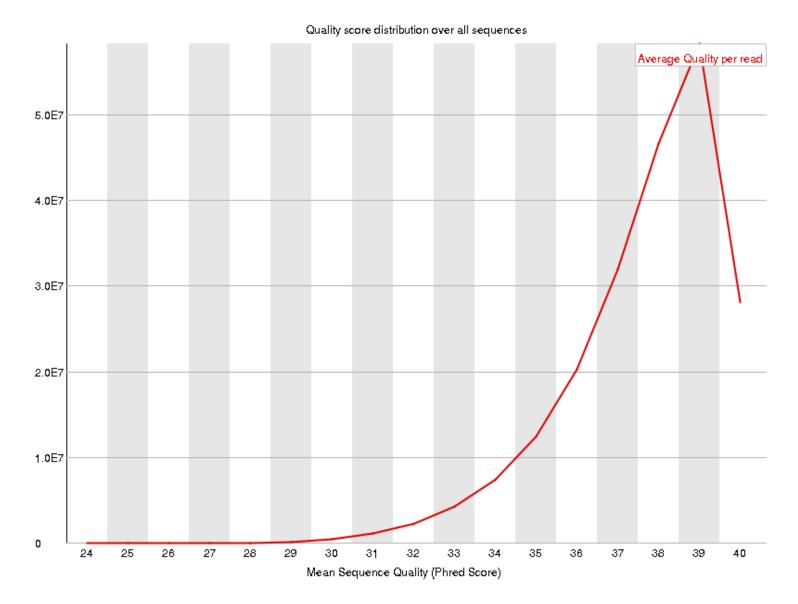| Measure	Value
Filename	carnea_2_filtered.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	213735465
Sequences flagged as poor quality	0
Sequence length	45-151
%GC	30

✅ Per base sequence quality

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

Position in read (bp)

❌Per tile sequence quality

Quality per tile

✅ Per sequence quality scores

Quality score distribution over all sequences

Per base sequence content

⚠️Per sequence GC content

GC distribution over all sequences

✅ Per base N content

Sequence Length Distribution

Distribution of sequence lengths over all sequences

⚠ Sequence Duplication Levels

Percent of seqs remaining if deduplicated 68.81%

✅ Overrepresented sequences

No overrepresented sequences

✅ Adapter Content

✅ Kmer Content

No overrepresented Kmers

Produced by FastQC (version 0.11.5)