FastQC Report

Summary

✅ [Basic Statistics](#)

✅ [Per base sequence quality](#)

✅ [Per tile sequence quality](#)
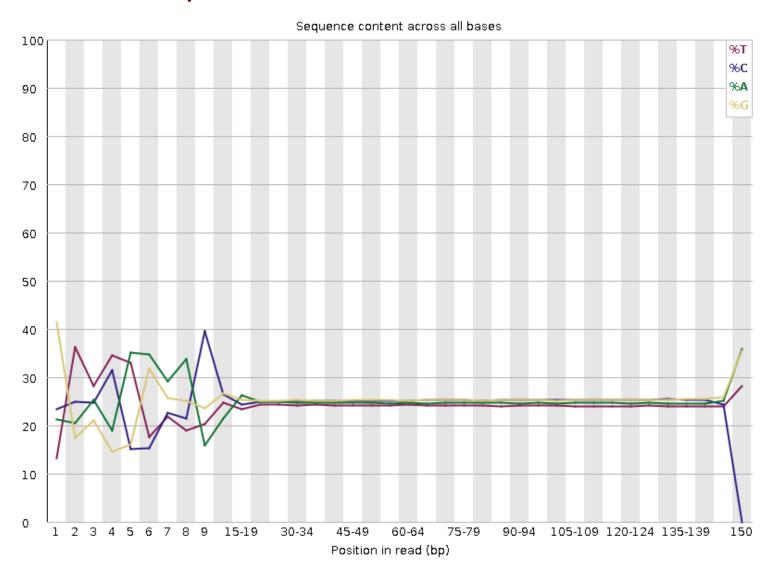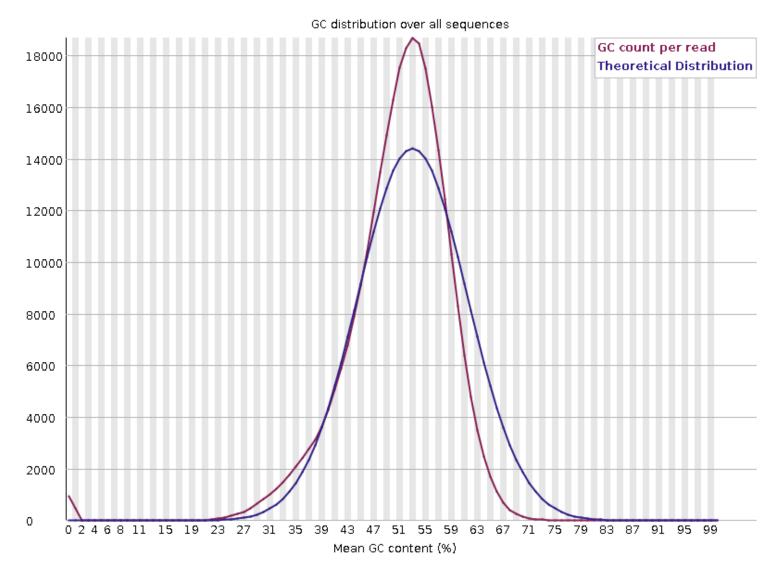
✅ [Per sequence quality scores](#)

❌ [Per base sequence content](#)
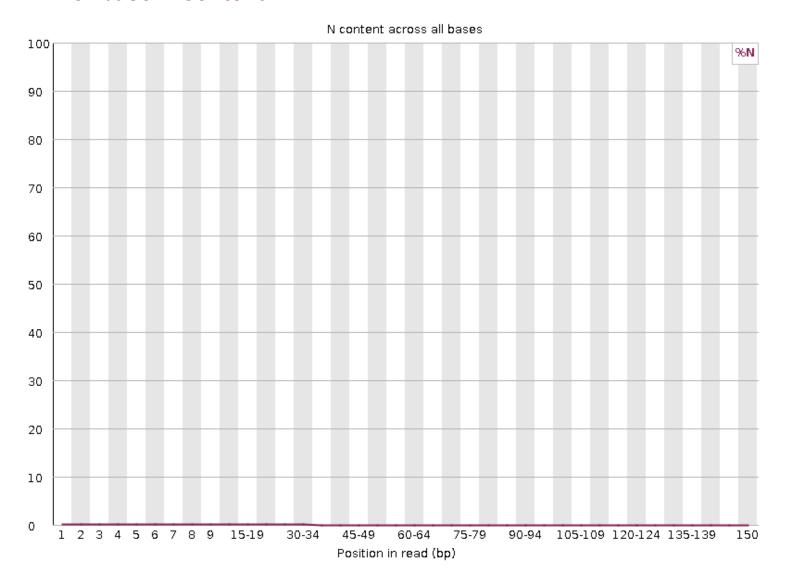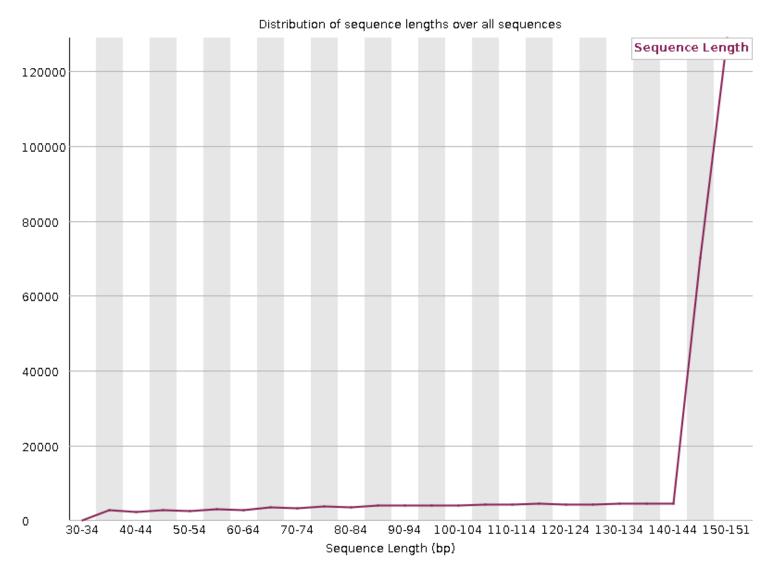
⚠️ [Per sequence GC content](#)
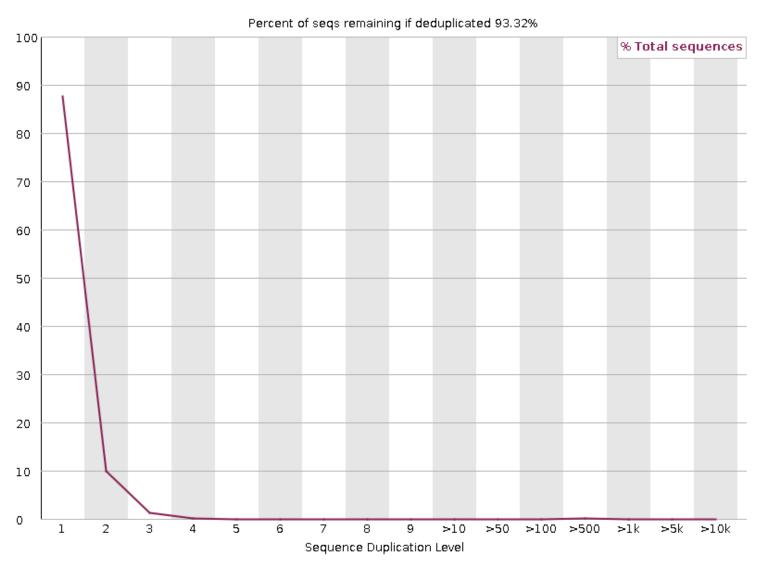
✅ [Per base N content](#)

⚠️ [Sequence Length Distribution](#)
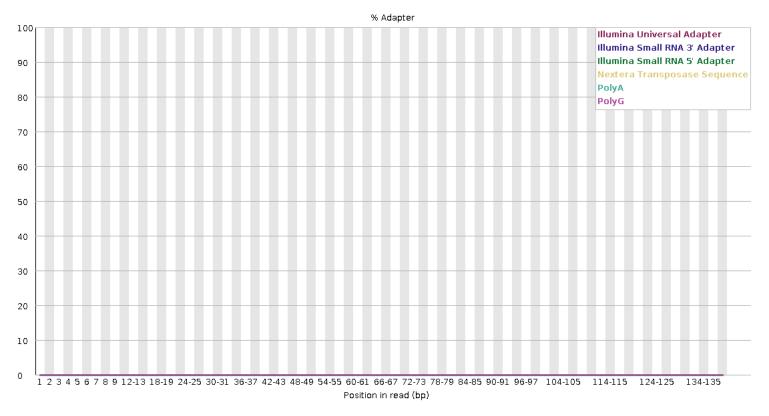
✅ [Sequence Duplication Levels](#)

⚠️ [Overrepresented sequences](#)

✅ [Adapter Content](#)

✅ Basic Statistics

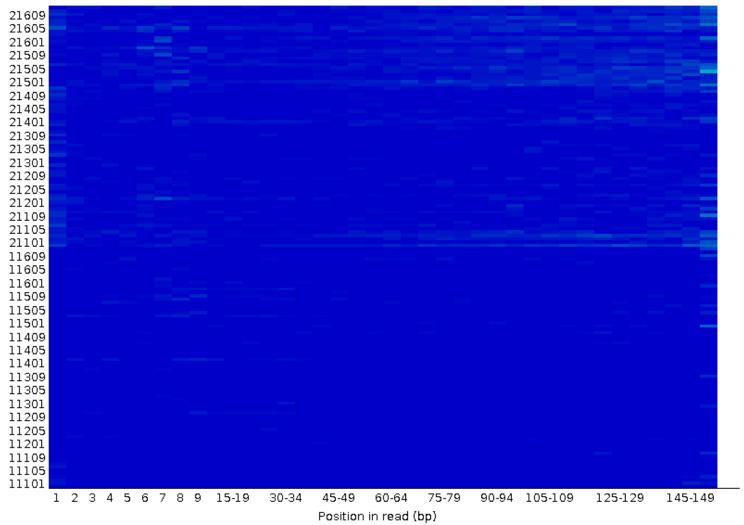| Measure	Value
Filename	anc_R1.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	281748
Total Bases	37.6 Mbp
Sequences flagged as poor quality	0
Sequence length	35-150
%GC	50

✅Per base sequence quality

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

✅ Per tile sequence quality

Quality per tile

Position in read (bp)

✅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

N content across all bases

⚠ Sequence Length Distribution

Distribution of sequence lengths over all sequences

✅ Sequence Duplication Levels

Percent of seqs remaining if deduplicated 93.32%

⚠️ Overrepresented sequences

Sequence	Count	Percentage	Possible Source
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	942	0.3343413262915797	No Hit

✅ Adapter Content

Produced by [FastQC](#) (version 0.12.1)