FastQC Report

Summary

✅ 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

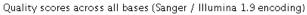✅ Overrepresented sequences
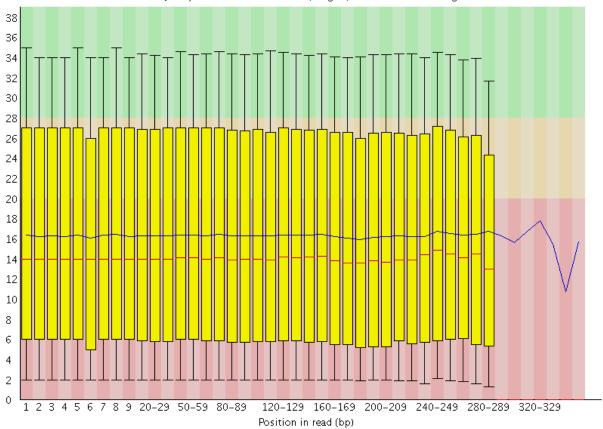
✅ Adapter Content

✅ Basic Statistics

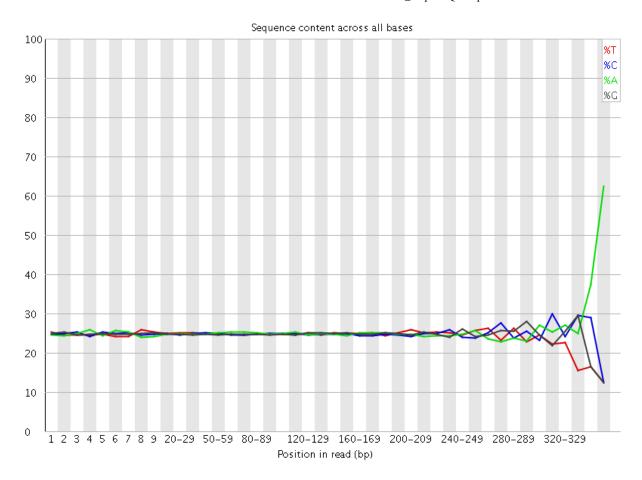| Measure	Value
Filename	reads_1.fq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	10000
Sequences flagged as poor quality	0
Sequence length	40-354
%GC	49
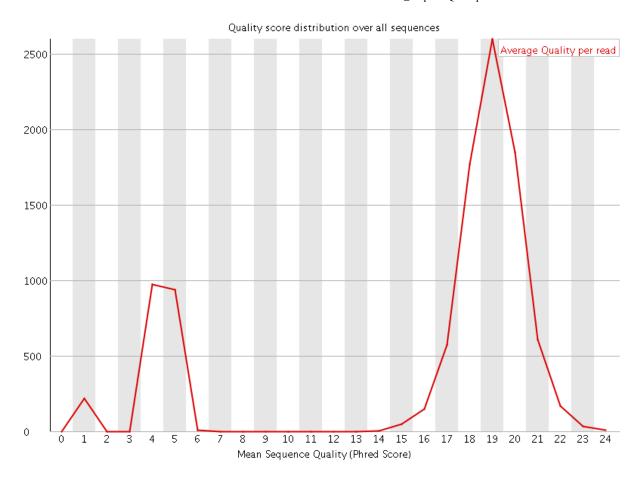
❌ Per base sequence quality

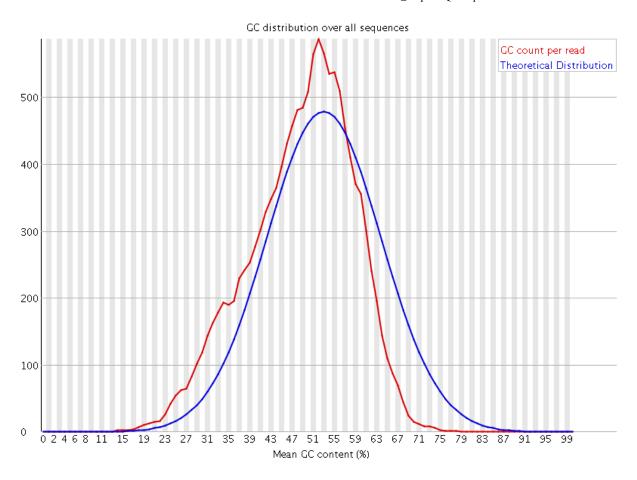Quality scores across all bases (Sanger / Illumina 1.9 encoding)

Position in read (bp)

❌Per sequence quality scores

❌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 99.58%

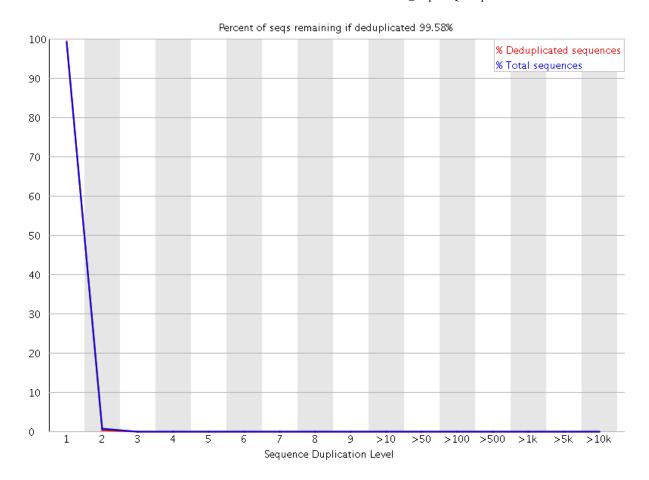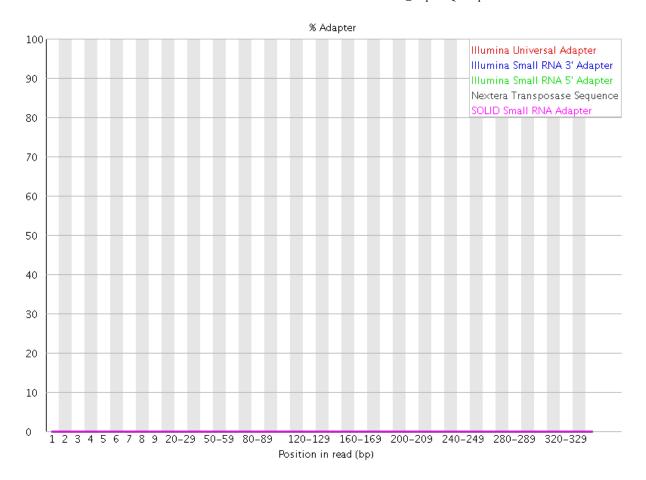## ✅Overrepresented sequences

No overrepresented sequences

✅Adapter Content

Produced by [FastQC](#) (version 0.11.7)