FastQC Report

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✅ Basic Statistics

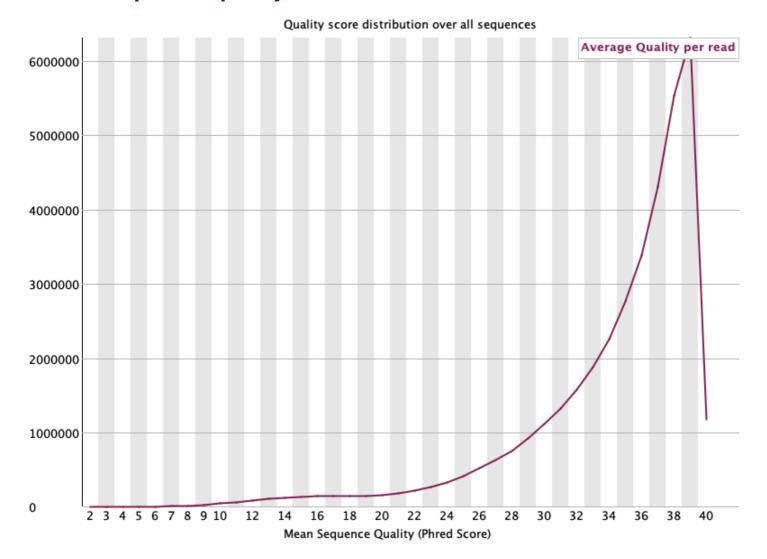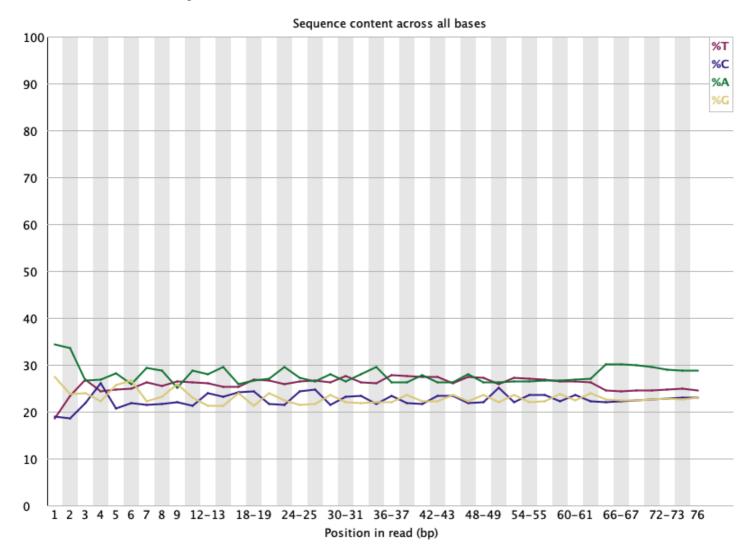| Measure	Value
Filename	SRR13380472_1.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	37454834
Total Bases	2.8 Gbp
Sequences flagged as poor quality	0
Sequence length	76
%GC	45
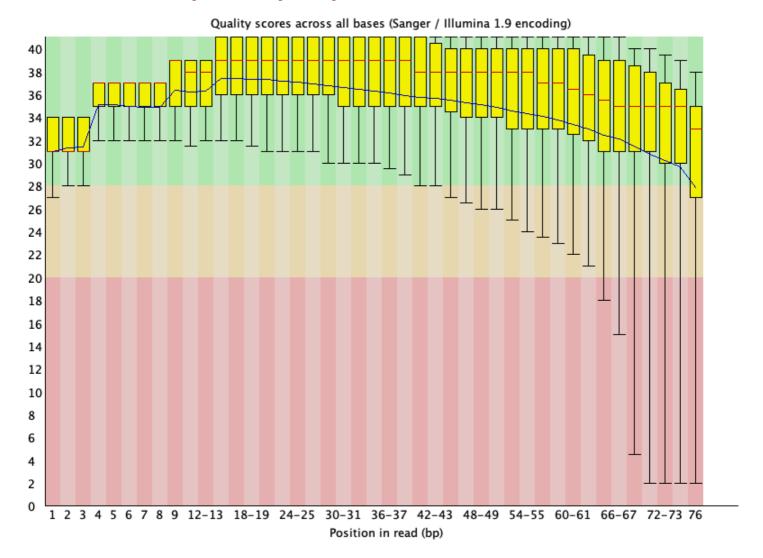
Per base sequence quality

✅Per sequence quality scores

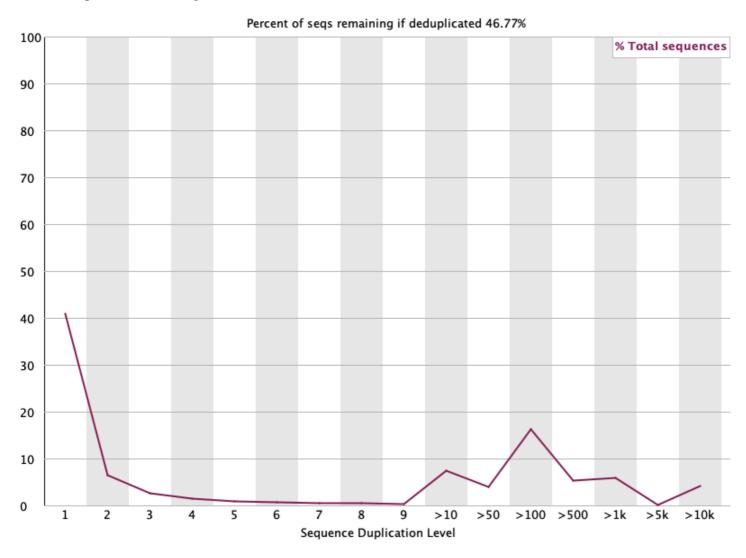# ⚠️ Per base sequence content

✅ 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

❌ Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GATCGGAAGAGCACACGTCTGAACTCCAGTCACAACTTGATCTCGTATGC	995671	2.6583244234909706	TruSeq Adapter, Index 1 (97% over 36bp)
AAGCAGTGGTATCAACGCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTT	448940	1.1986169795866668	Clontech SMART CDS Primer II A (100% over 26bp)
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	95031	0.25372158904775816	No Hit

Sequence	Count	Percentage	Possible Source
TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	73441	0.1960788292373689	No Hit

✅ Adapter Content

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