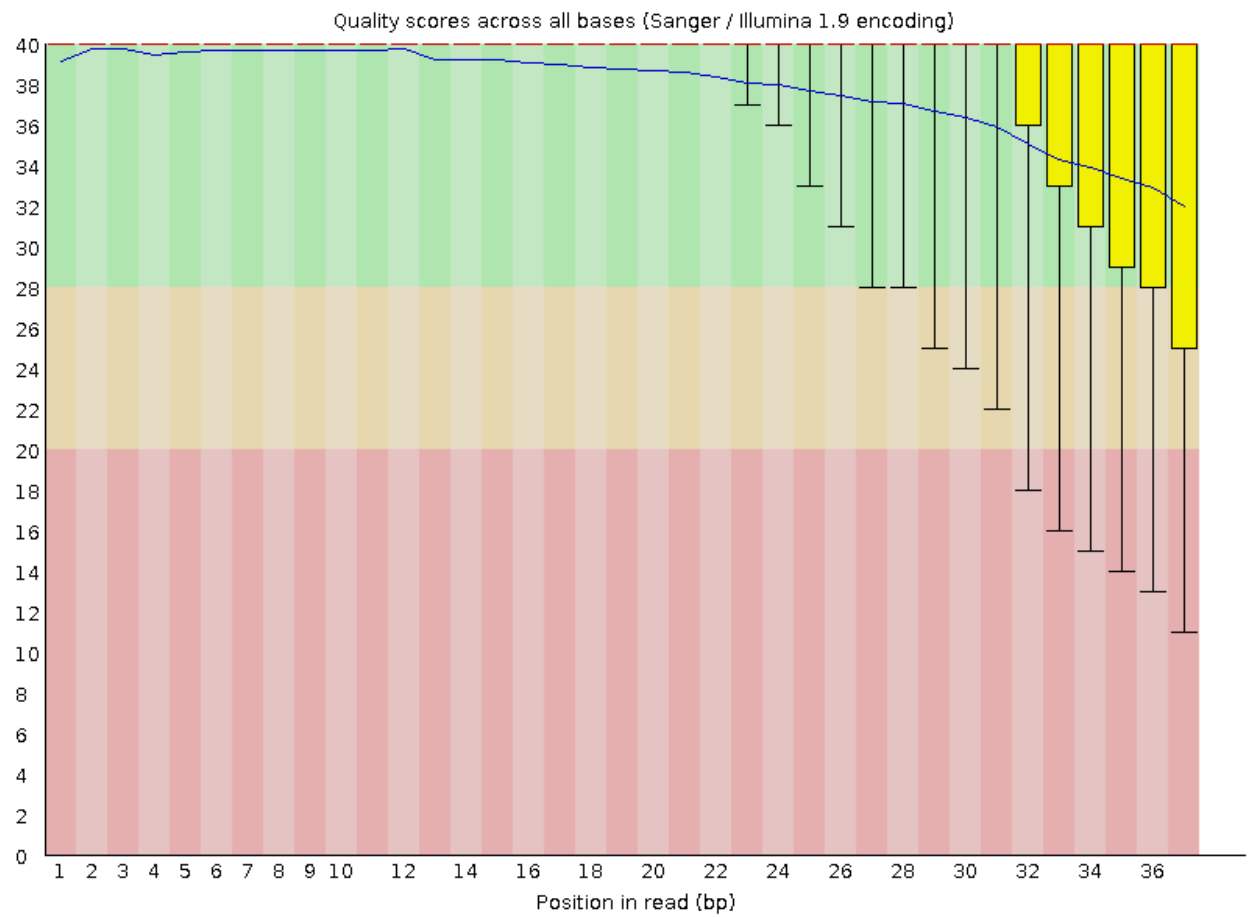# GSM461177_1_subsampled_fastqsanger

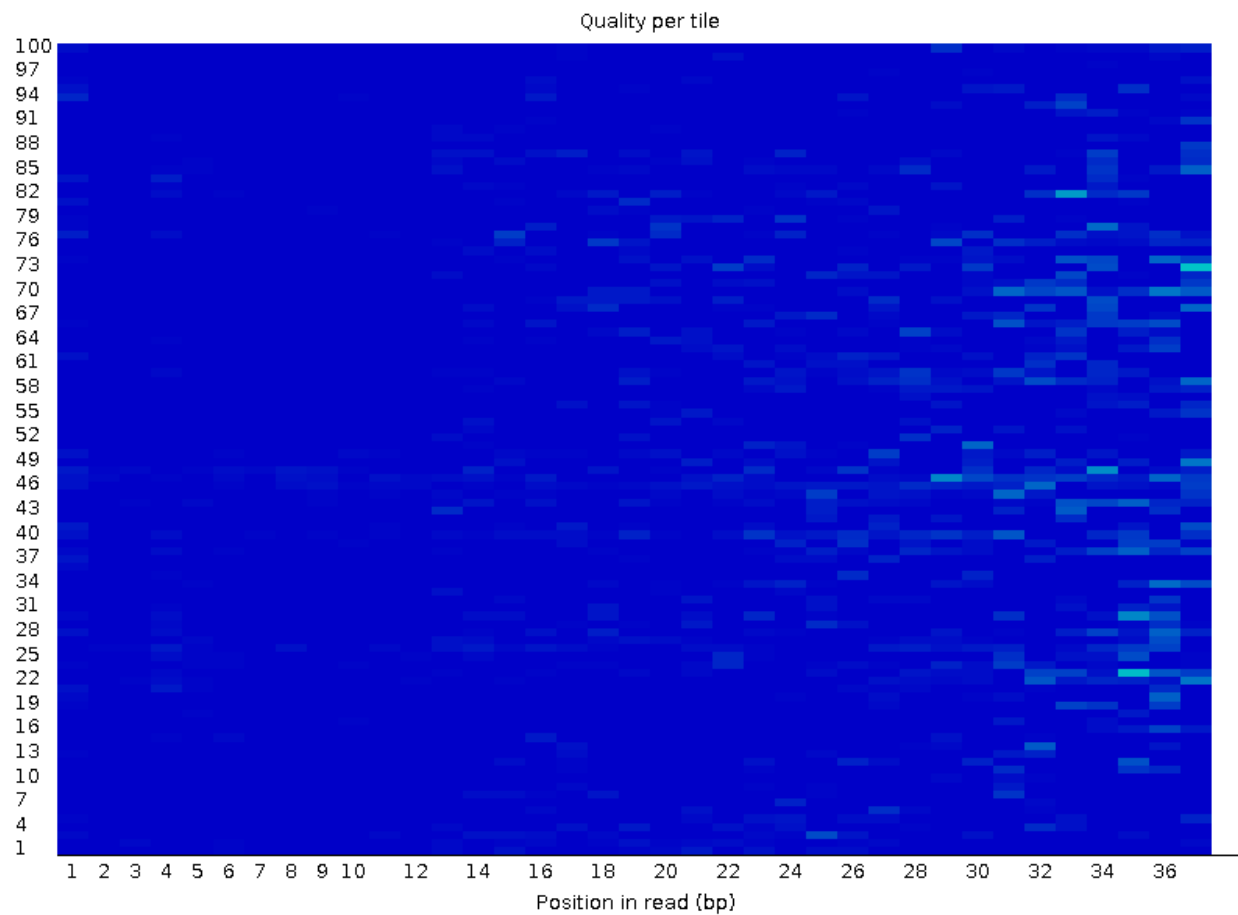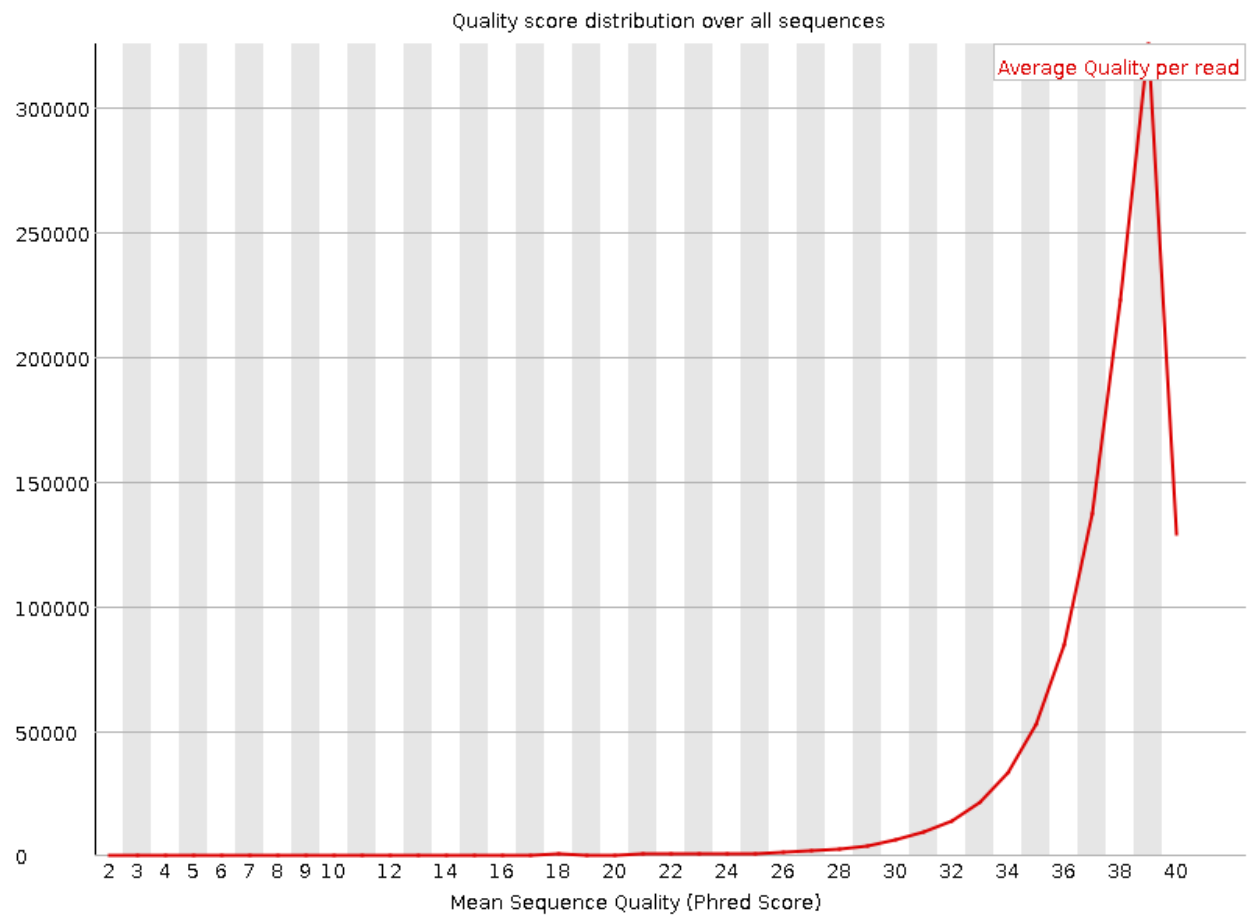## Basic Statistics

Measure	Value
Filename	GSM461177_1_subsampled_fastqsanger
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	1057657
Sequences flagged as poor quality	0
Sequence length	37
%GC	53

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

Quality per tile

Quality score distribution over all sequences

Sequence content across all bases

GC distribution over all sequences

N content across all bases

Distribution of sequence lengths over all sequences
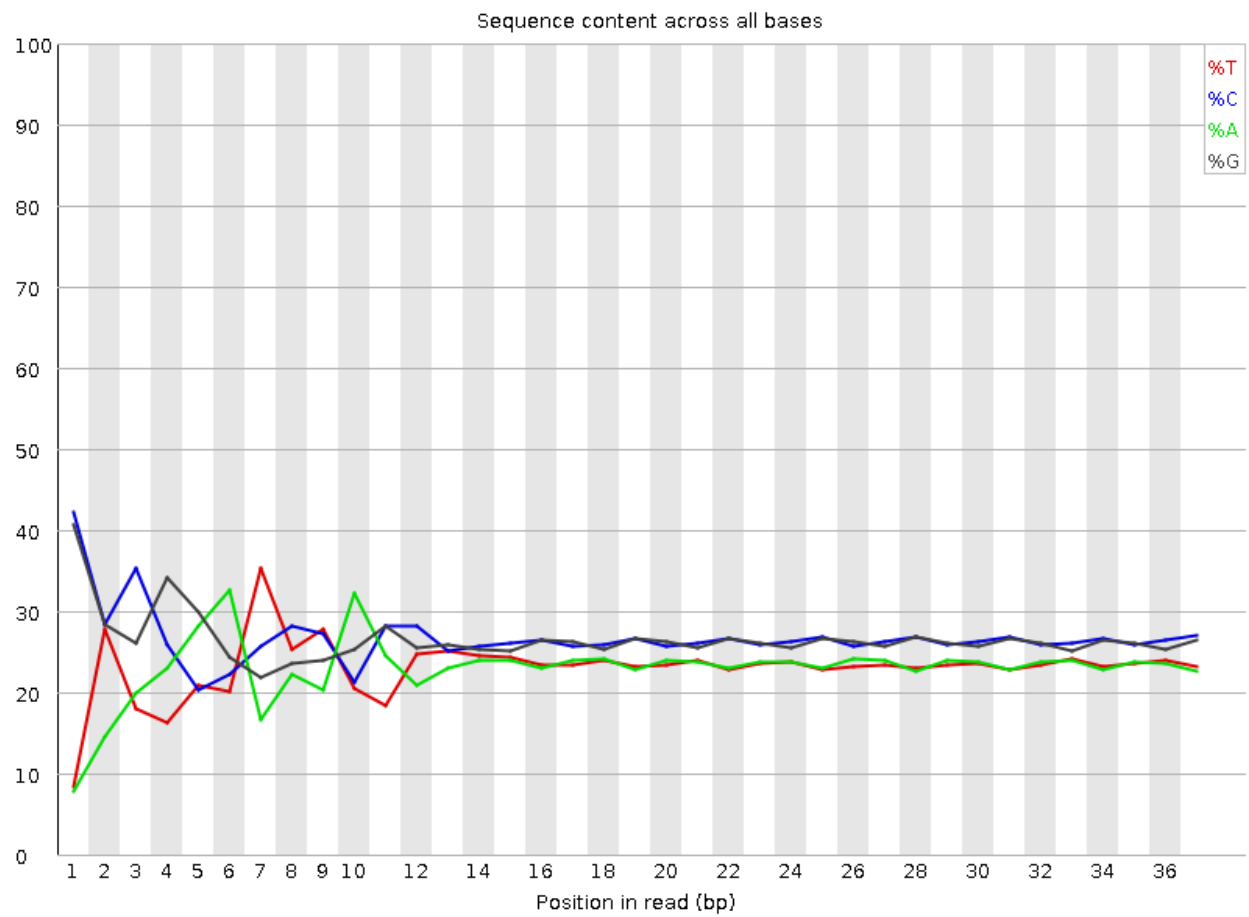

Sequence Length

Sequence Length (bp)
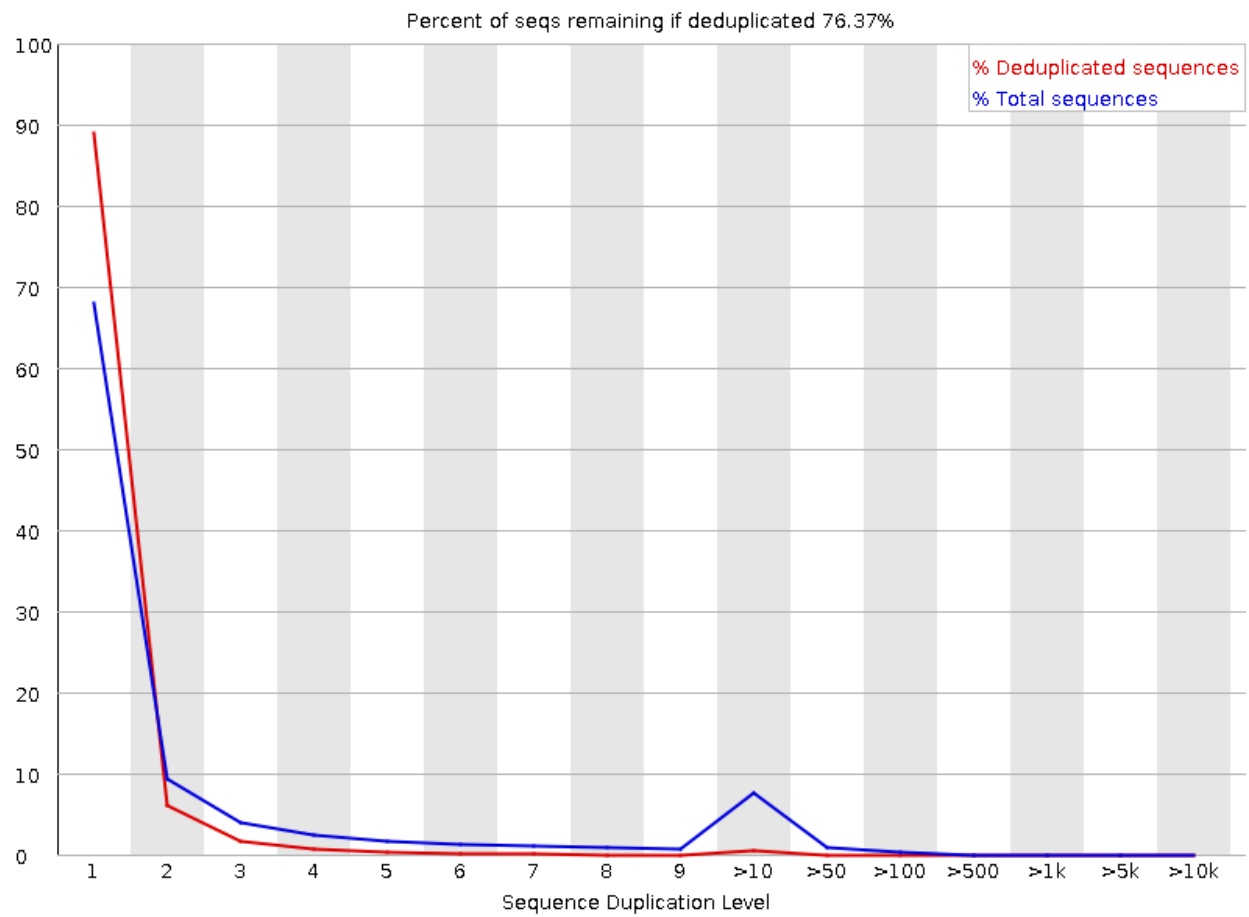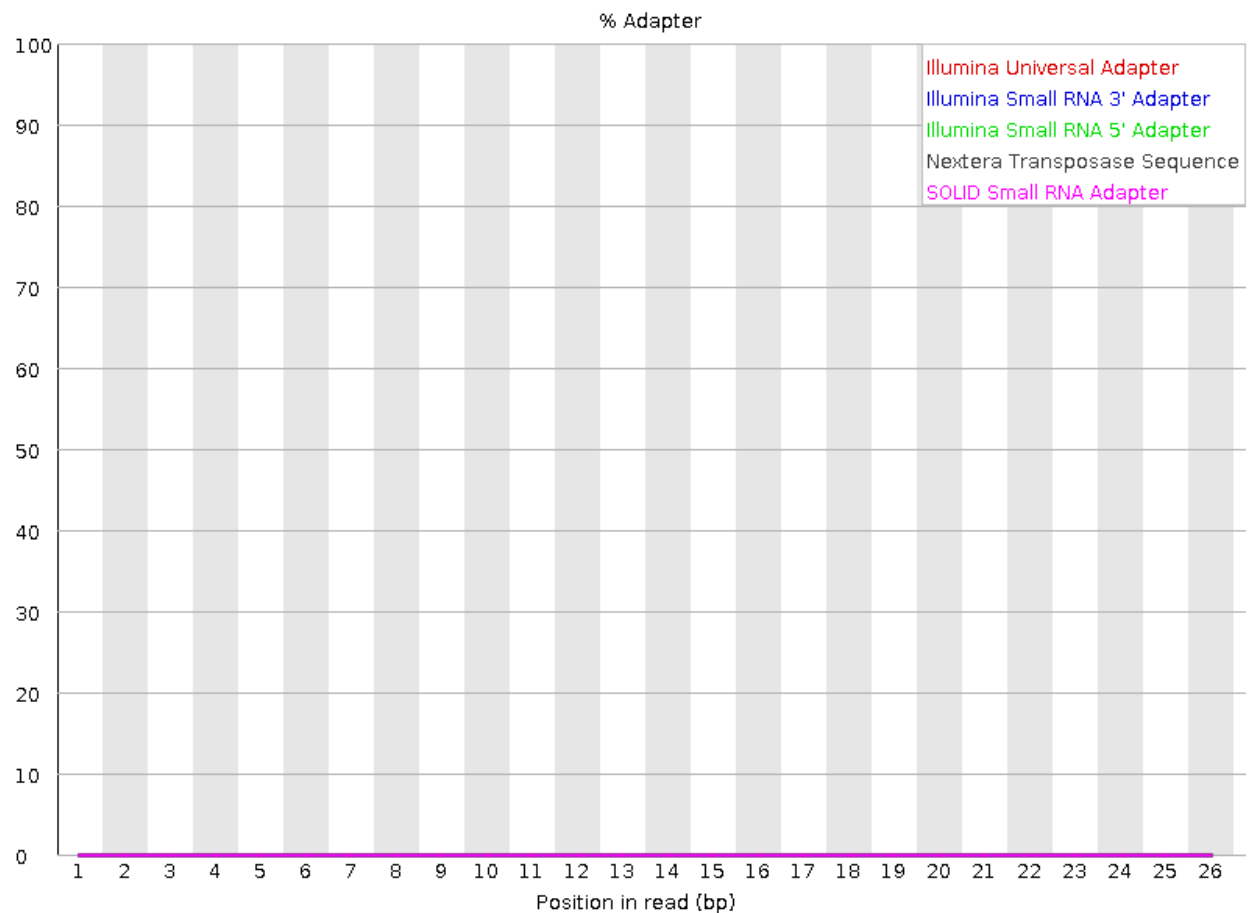
GSM461177_2_subsampled_fastqsanger
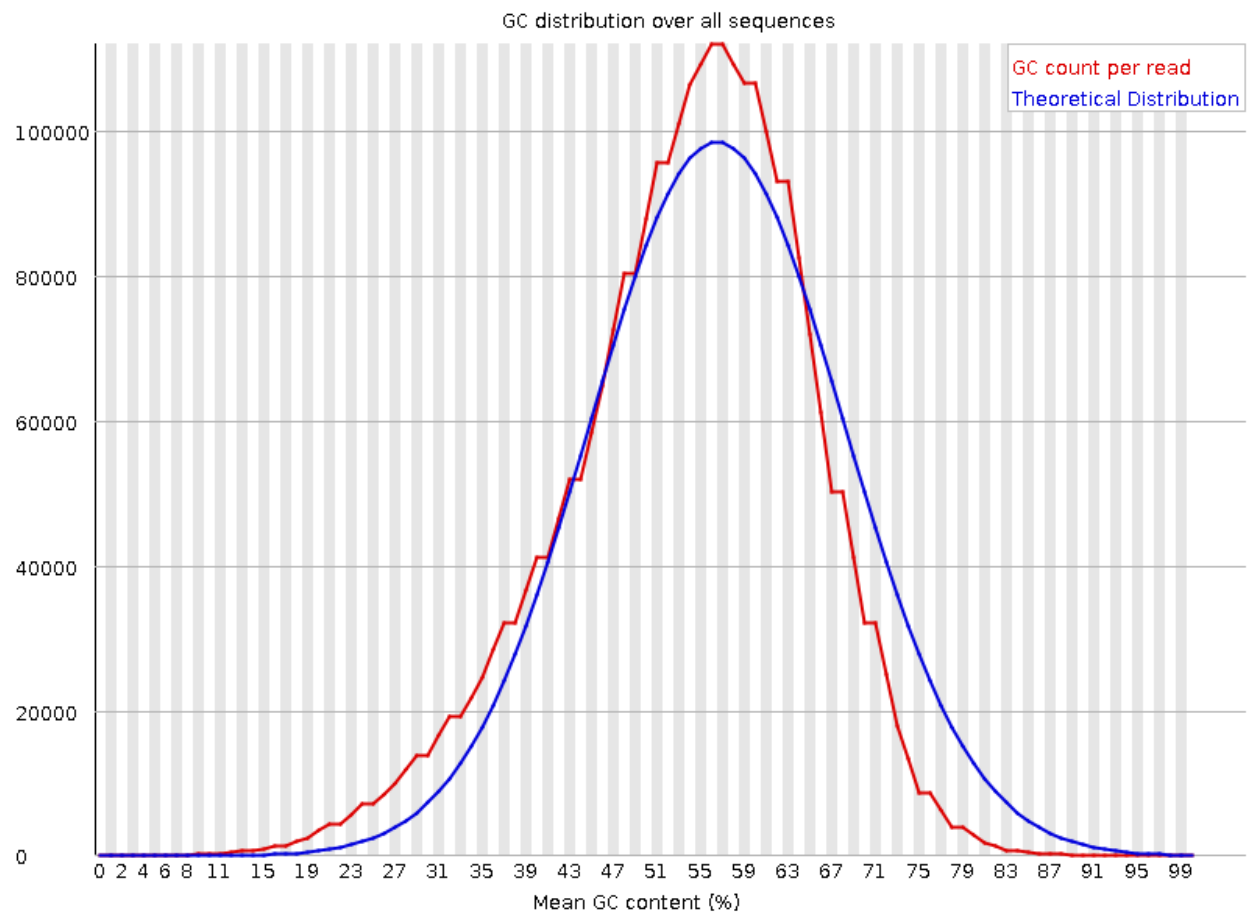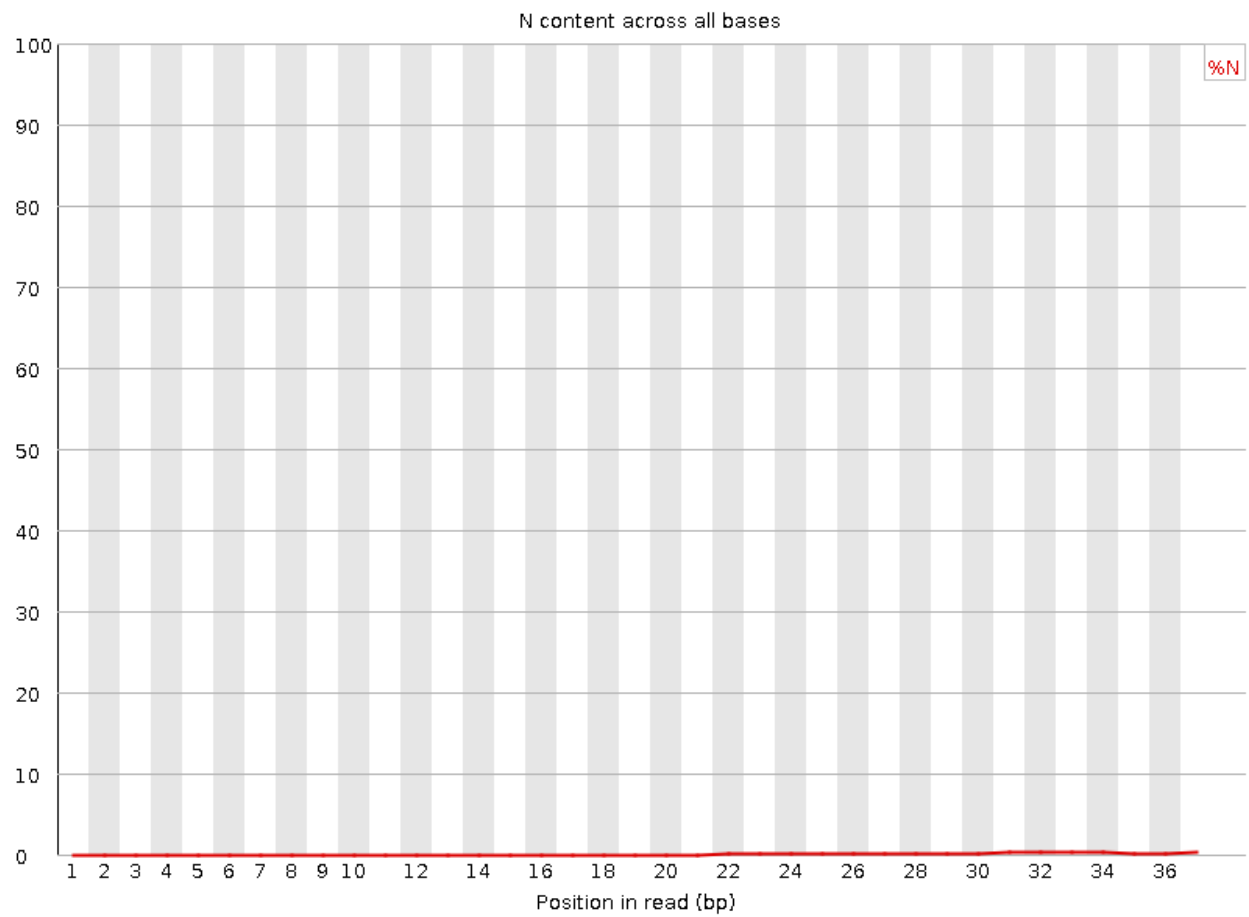
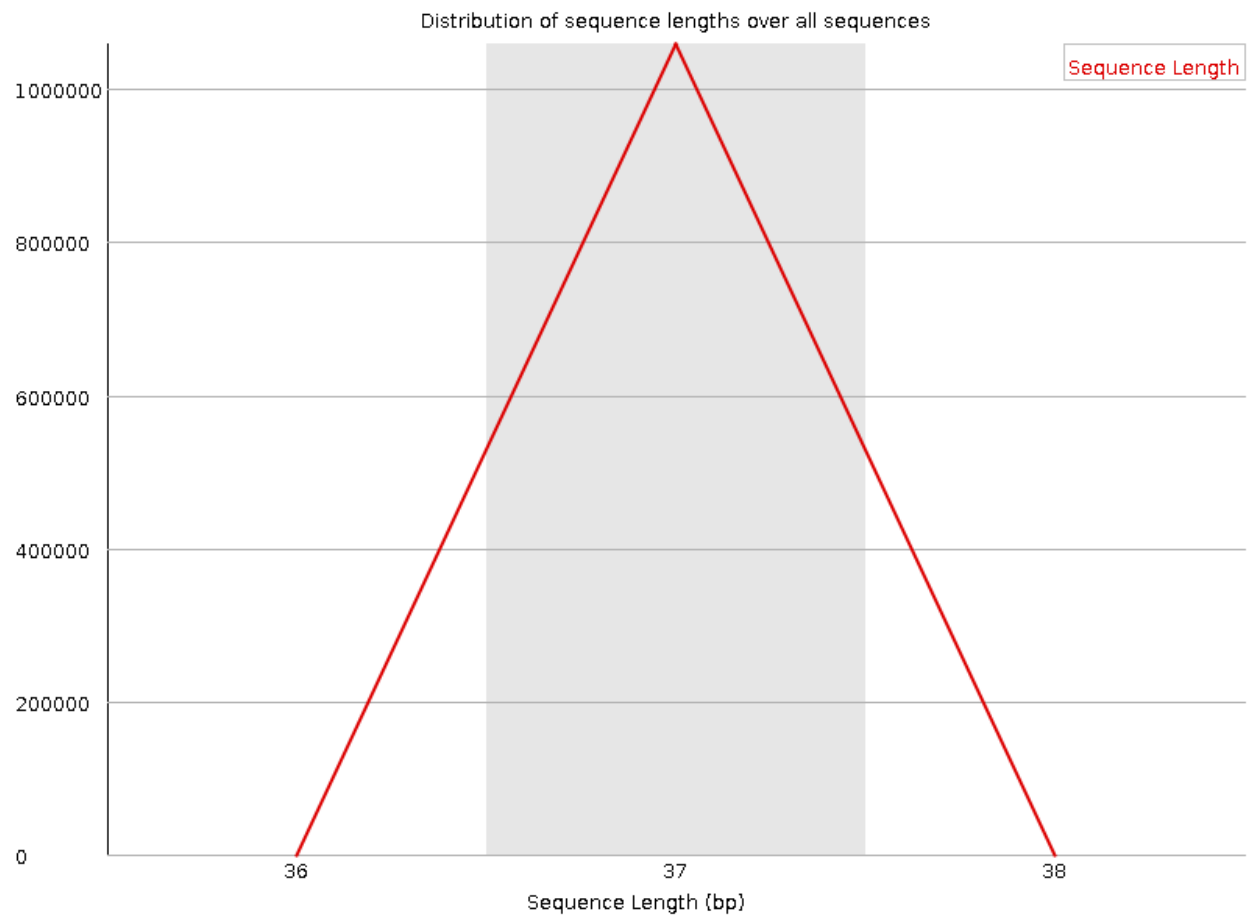| Measure	Value
Filename	GSM461177_2_subsampled_fastqsanger
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	1057657
Sequences flagged as poor quality	0

Measure	Value
Sequence length	37
%GC	53

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

Quality per tile

Position in read (bp)

Quality score distribution over all sequences

Average Quality per read

Mean Sequence Quality (Phred Score)

Sequence content across all bases

GC distribution over all sequences

N content across all bases

Position in read (bp)

Distribution of sequence lengths over all sequences

Sequence Length (bp)

Percent of seqs remaining if deduplicated 74.8%

Legend:
- % Deduplicated sequences (red)
- % Total sequences (blue)

X-axis: Sequence Duplication Level (1, 2, 3, 4, 5, 6, 7, 8, 9, >10, >50, >100, >500, >1k, >5k, >10k)

% Adapter

Legend:
- Illumina Universal Adapter (red)
- Illumina Small RNA 3' Adapter (blue)
- Illumina Small RNA 5' Adapter (green)
- Nextera Transposase Sequence (black)
- SOLID Small RNA Adapter (magenta)

X-axis: Position in read (bp) (1–26)