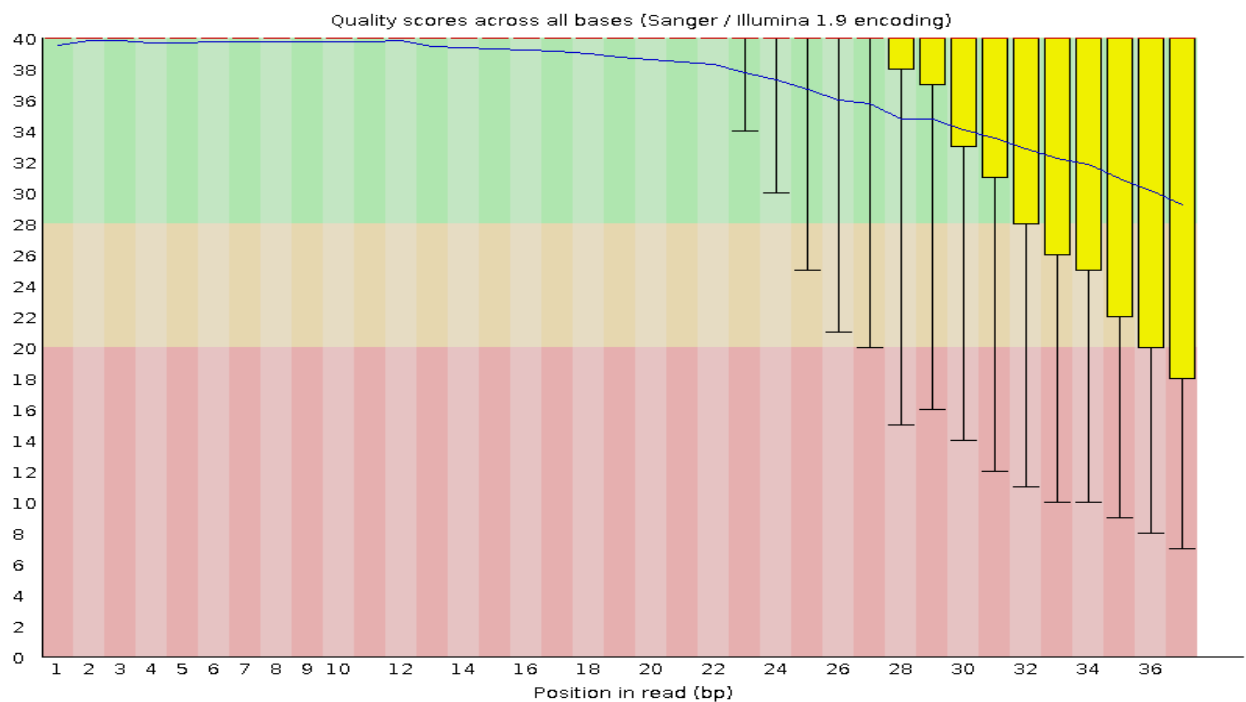
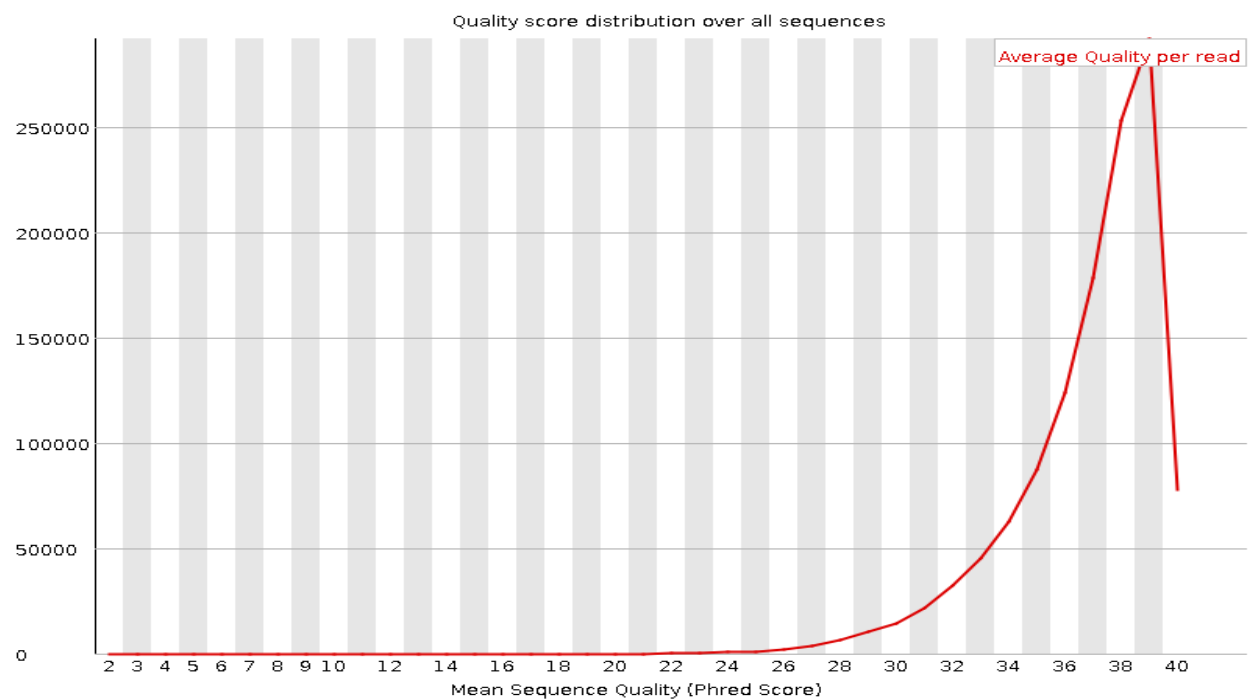
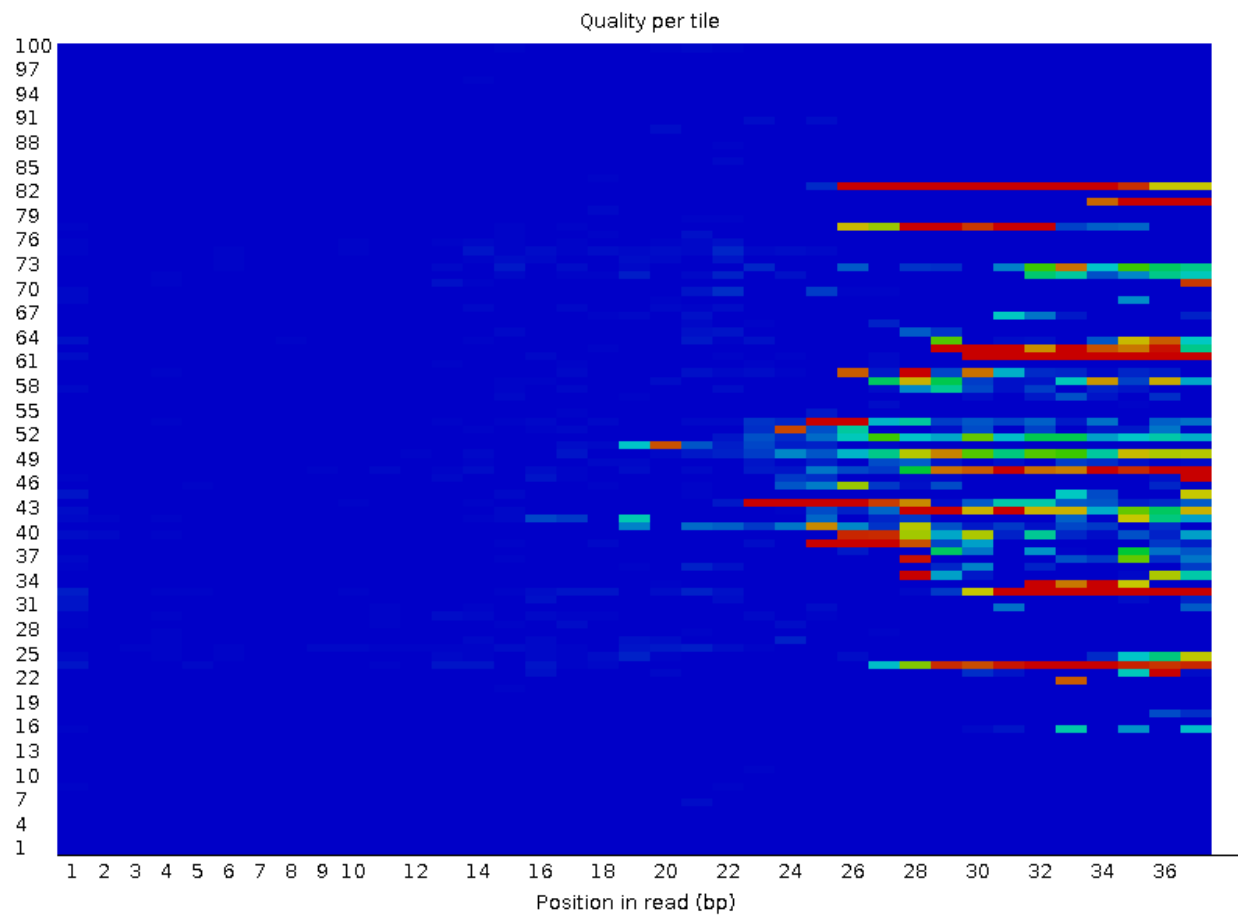
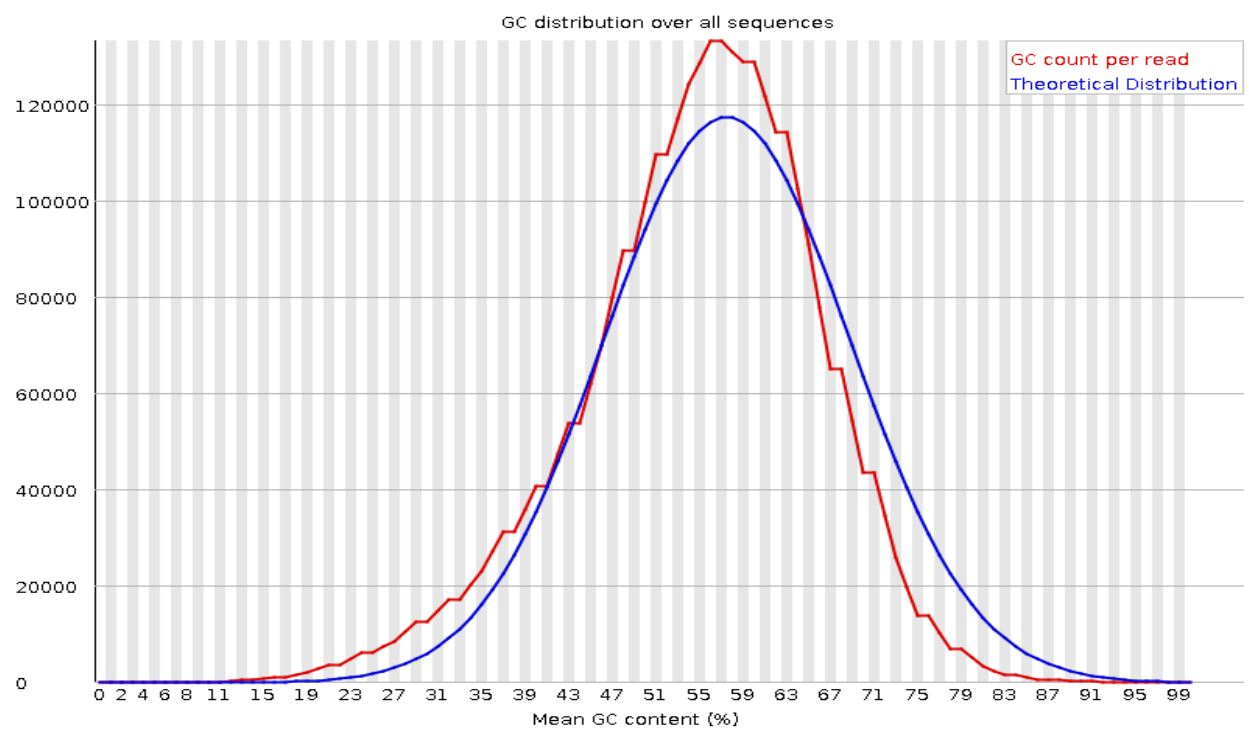
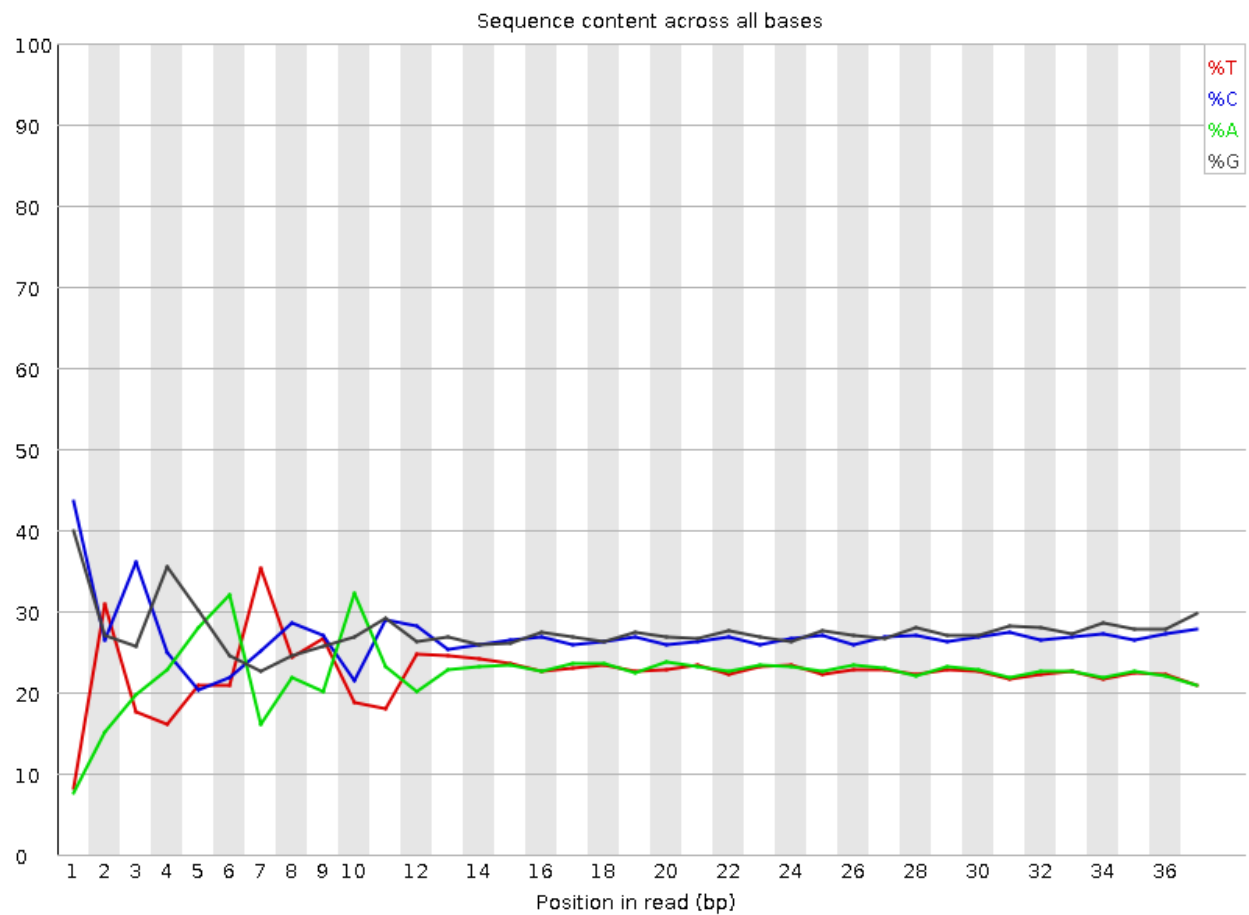


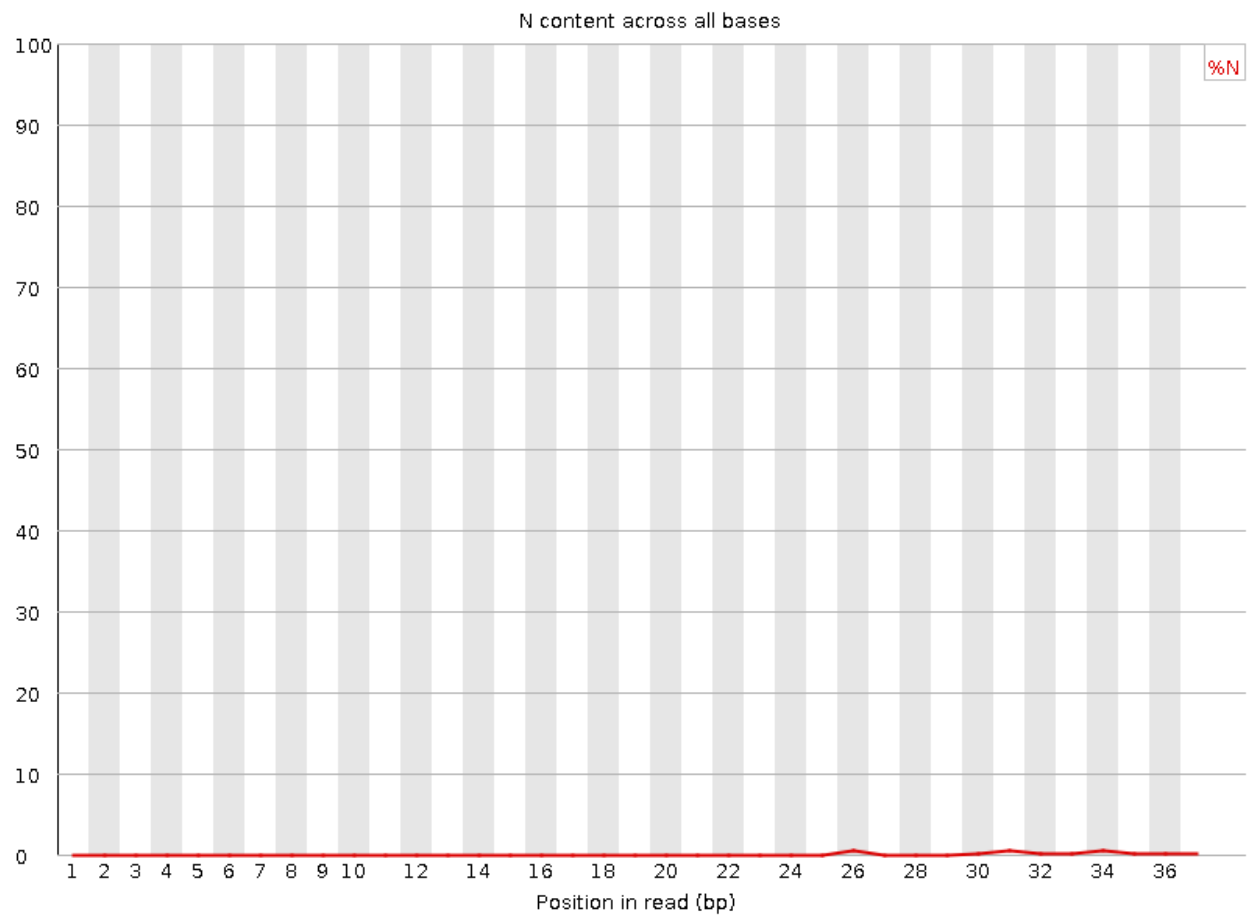
GSM461180_1_subsampled_fastqsanger

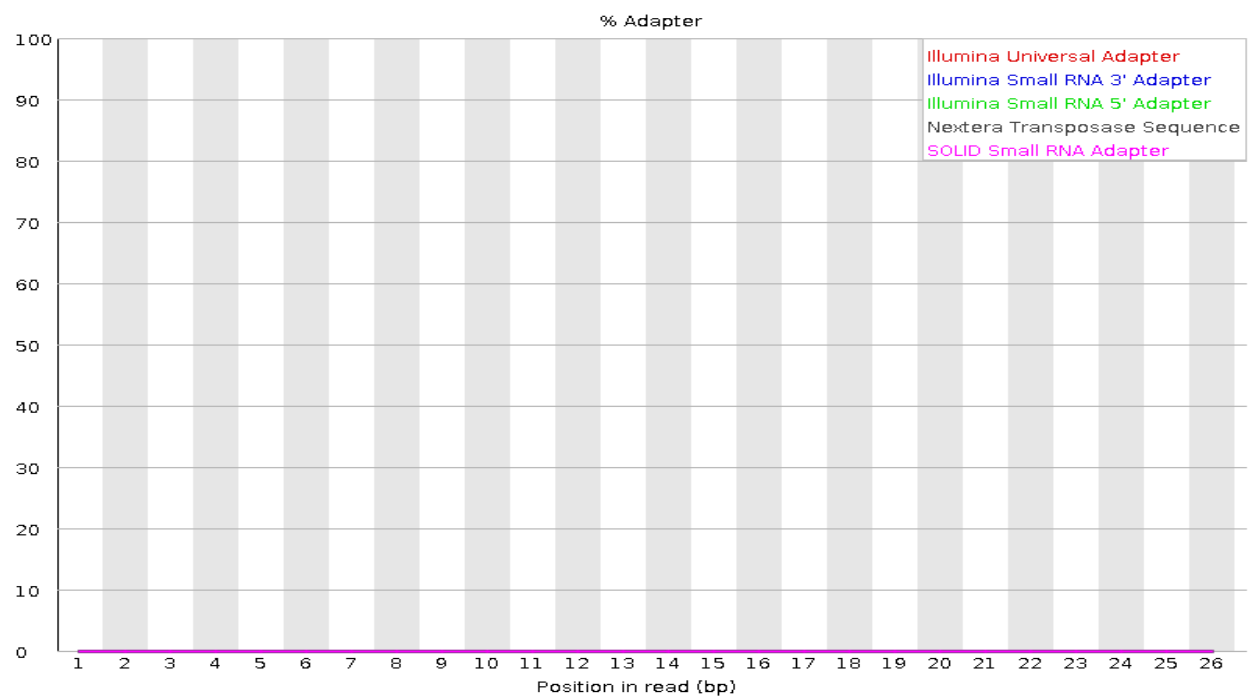
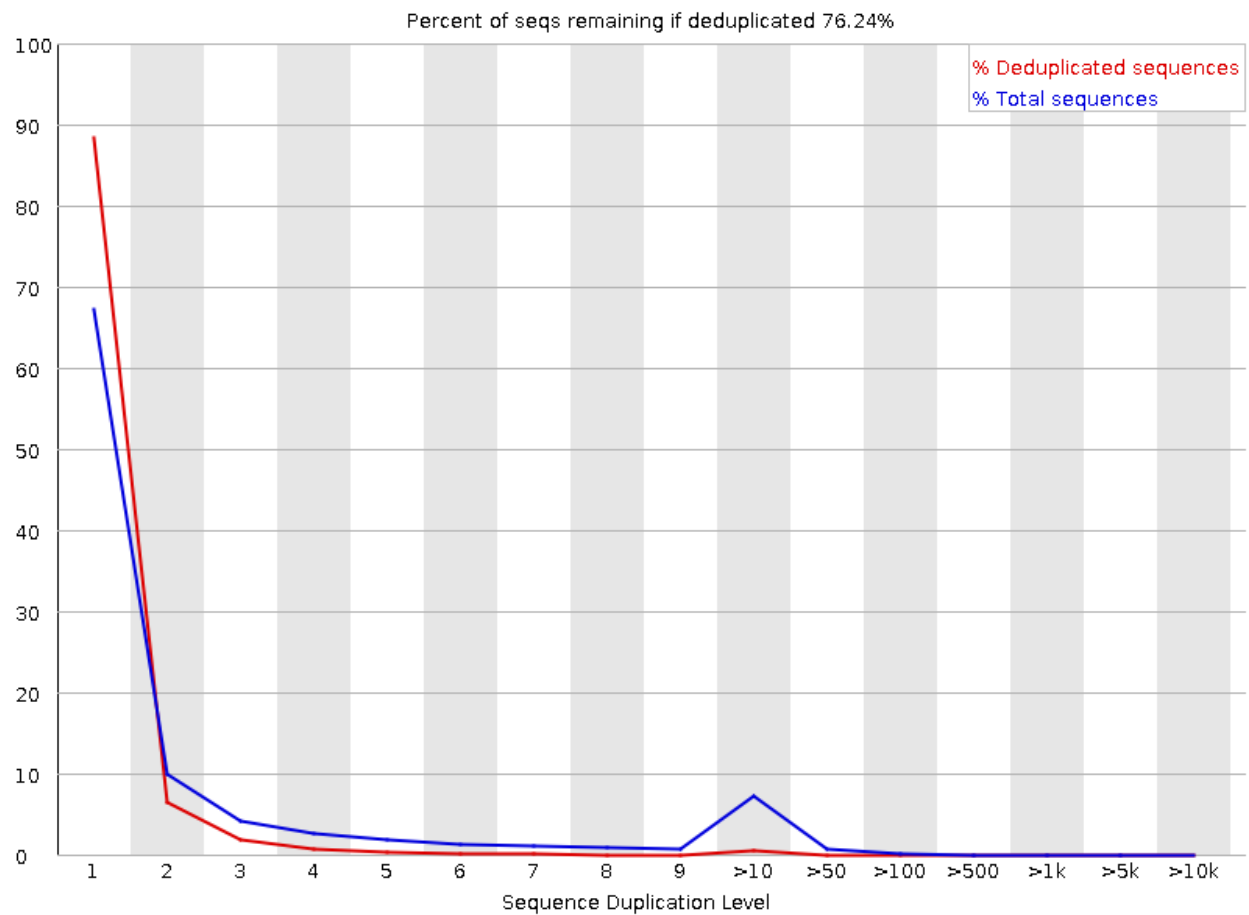
Measure	Value
Filename	GSM461180_1_subsampled_fastqsanger
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	1226483
Sequences flagged as poor quality	0
Sequence length	37
%GC	54











GSM461180_2_subsampled_fastqsanger

Basic Statistics

Measure	Value
Filename	GSM461180_2_subsampled_fastqsanger
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	1226483
Sequences flagged as poor quality	0
Sequence length	37
%GC	55

