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

The above plot is a boxplot which shows the quality scores across the fastq file.

Percent of seqs remaining if deduplicated 97.49%
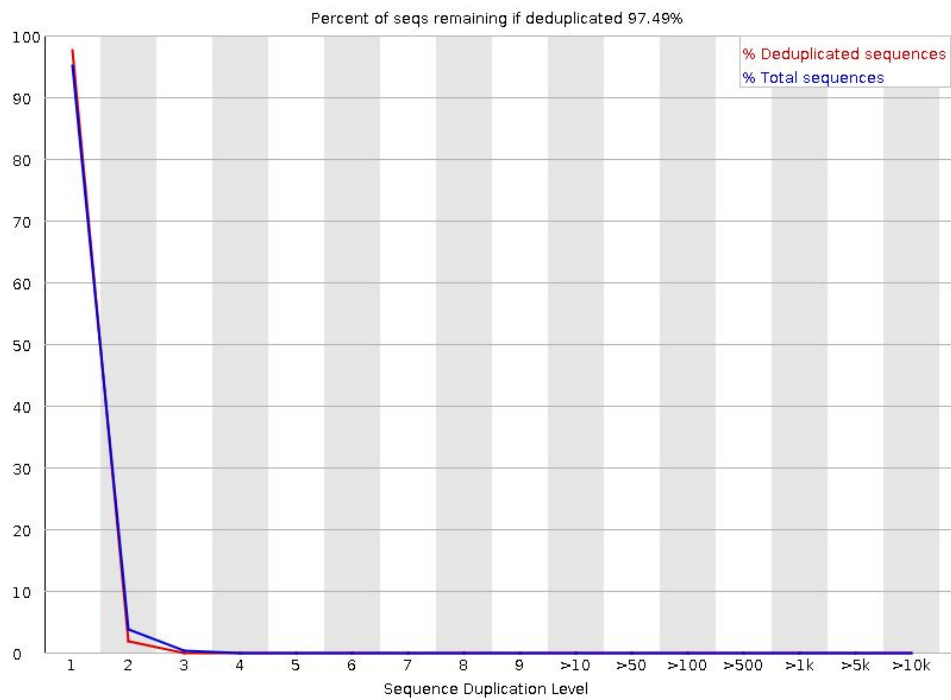
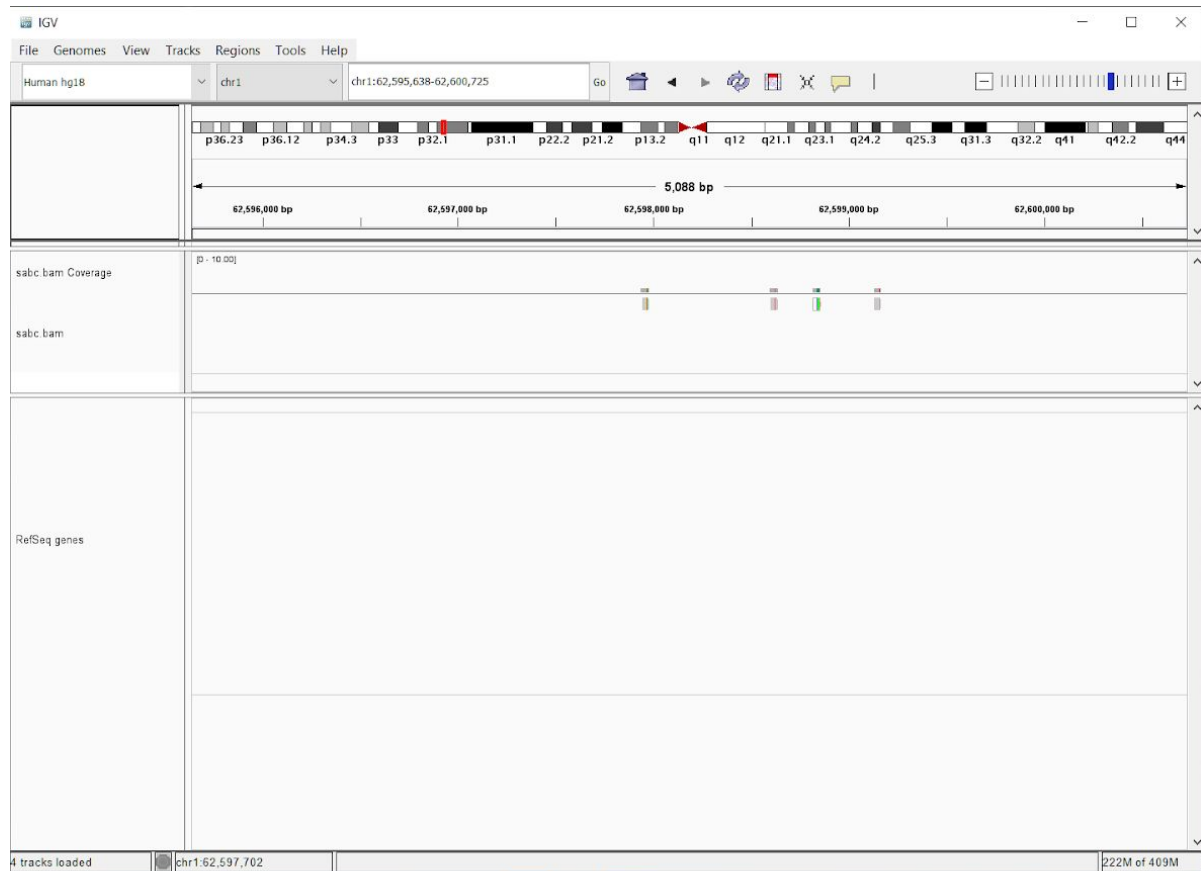This plot shows the relative number of sequences with different degrees of duplication.
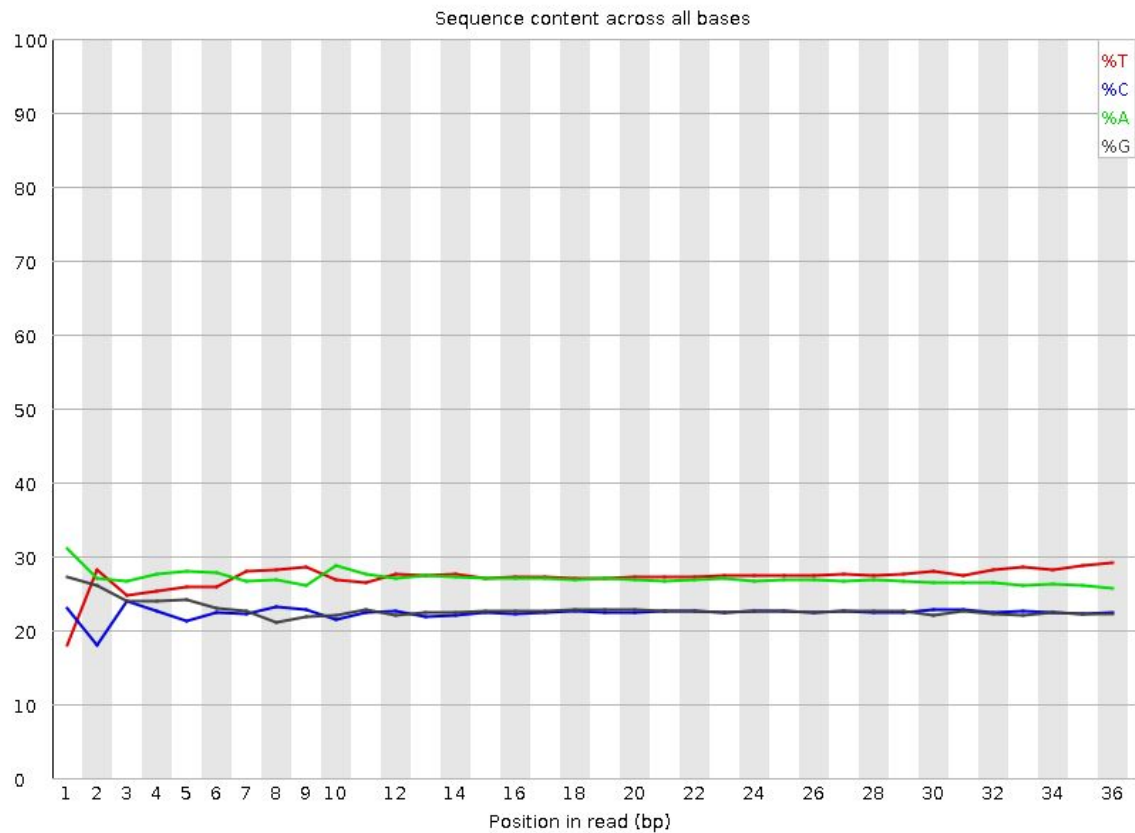
Sequence content across the fastq file.
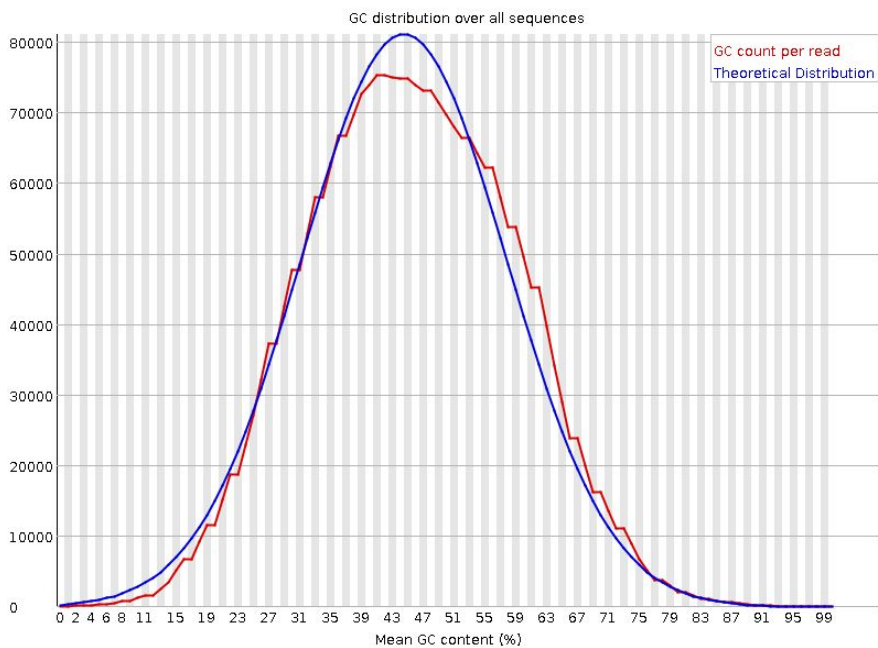
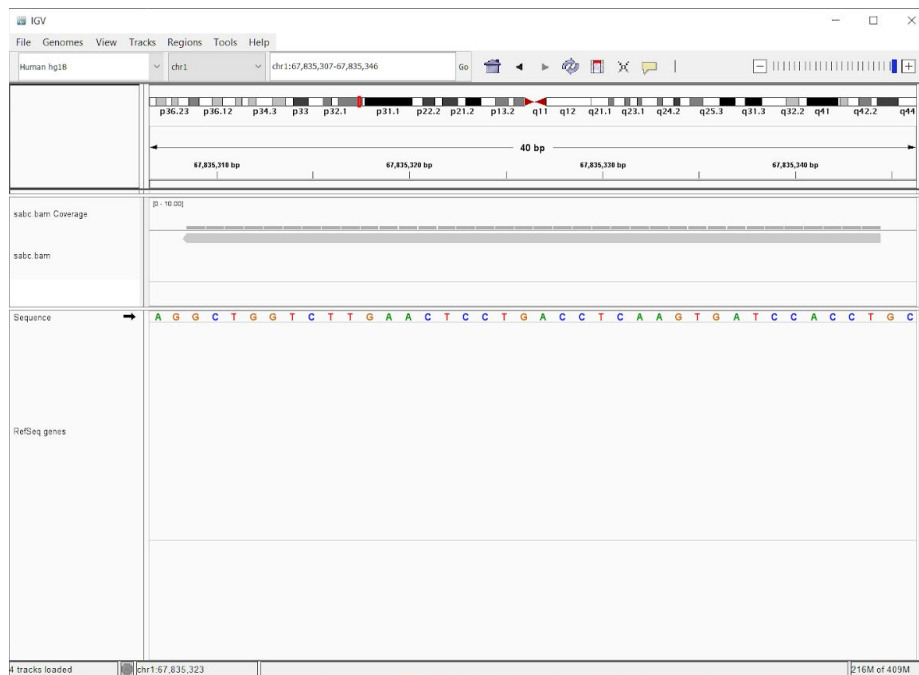

This plot shows the GC content across the whole length of each sequence in a file and compares it to a modelled normal distribution of GC content.
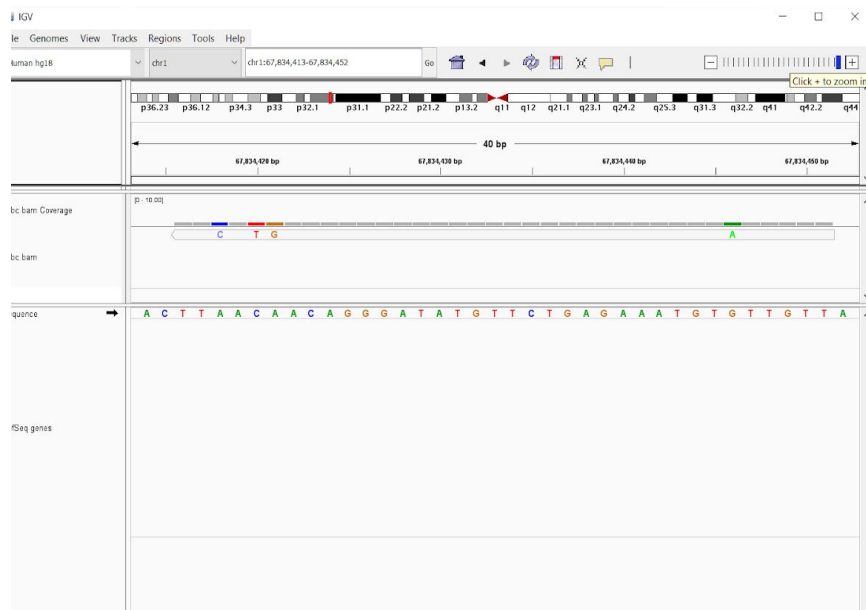
IGV

The reads have grey fill which means that the quality score is non zero.

This alignment has no insertion or deletion.

Colored bases are mismatched bases.