3.8M Forward reads for index AR001

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

Sequence content across all bases

N content across all bases
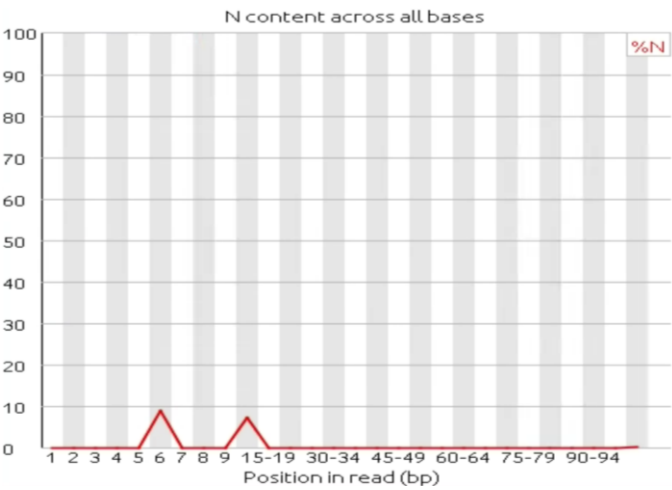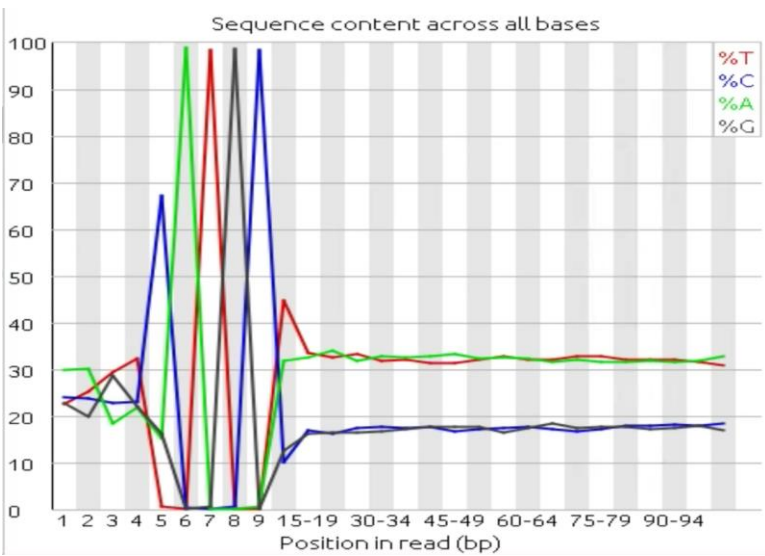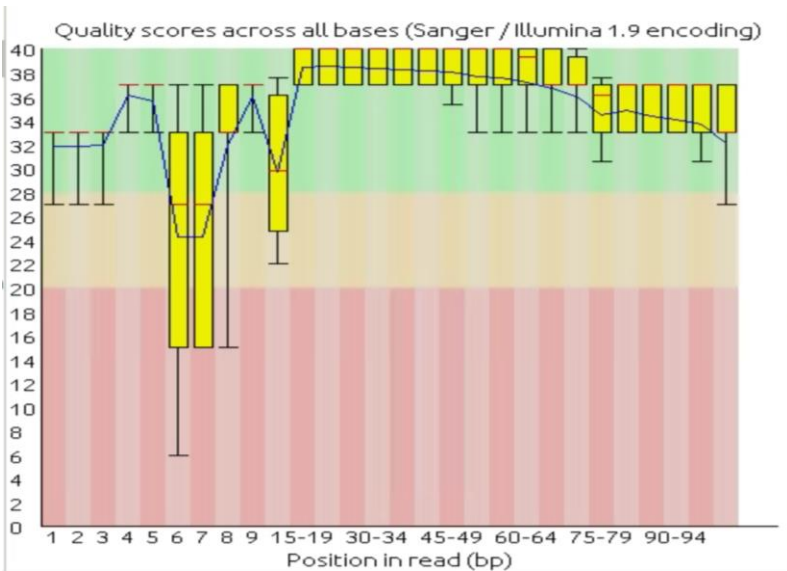
3.8 M Reverse reads for index AR001

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

Sequence content across all bases

N content across all bases