

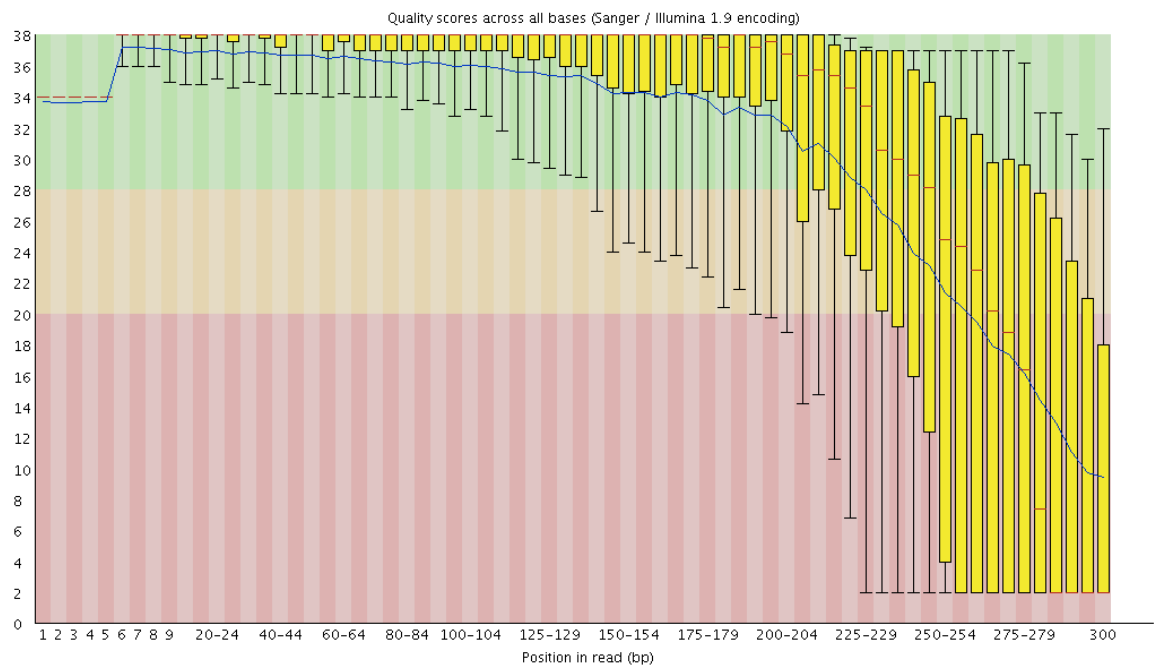
## ***Streptomyces* Quality Control**

FASTQC (v0.11.2) was used for the analysis on CSC

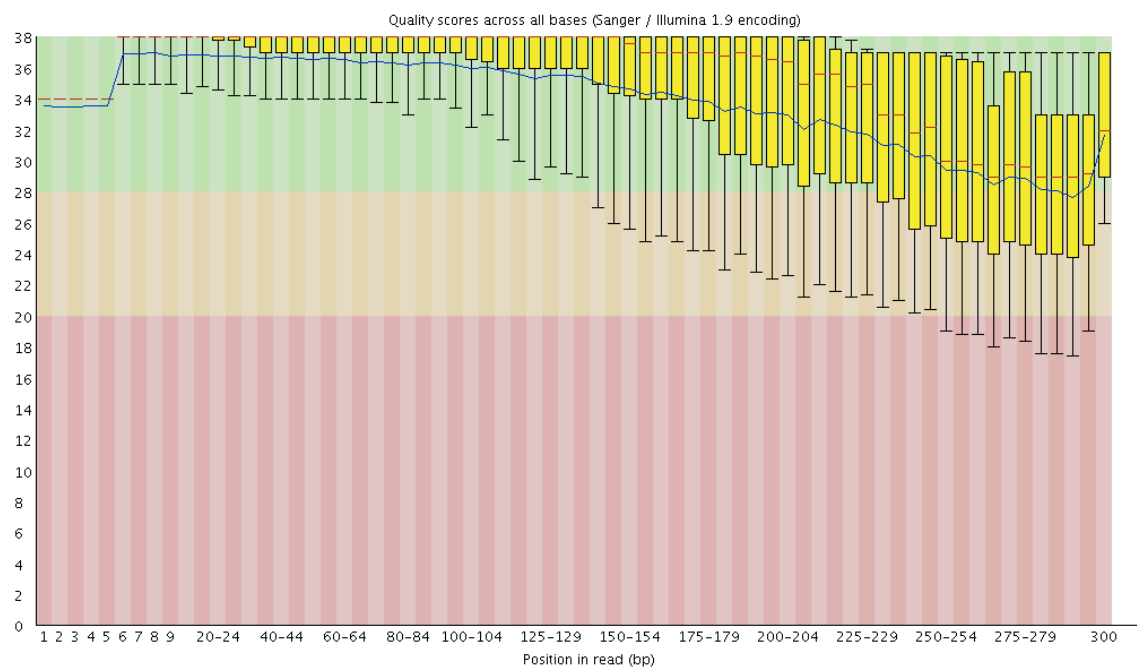
The quality of the reads was manually inspected even though a5 does it automatically.

### **Quality Scores (based on position in the read)**

- The average quality dropped dramatically after ~200bp probably due to the high GC content

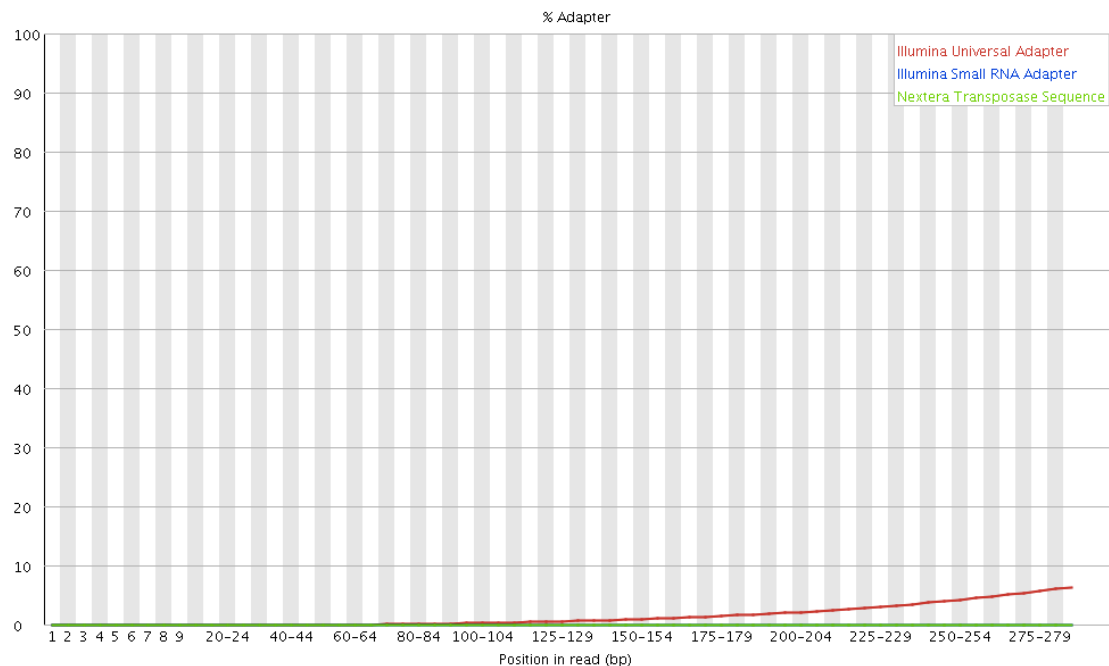


- These low quality regions were trimmed away (a5/TRIMMOMATIC)

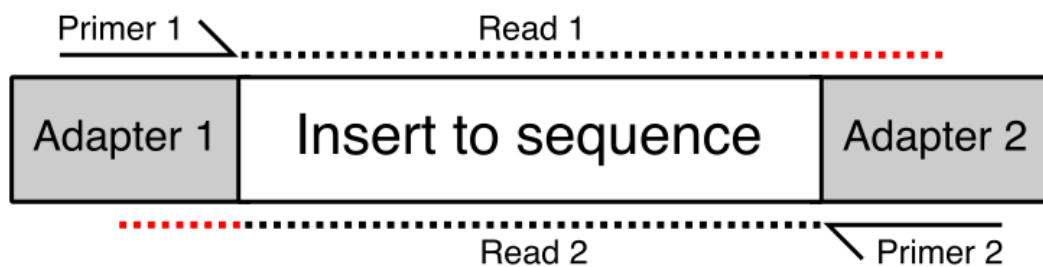


## Adapter Content

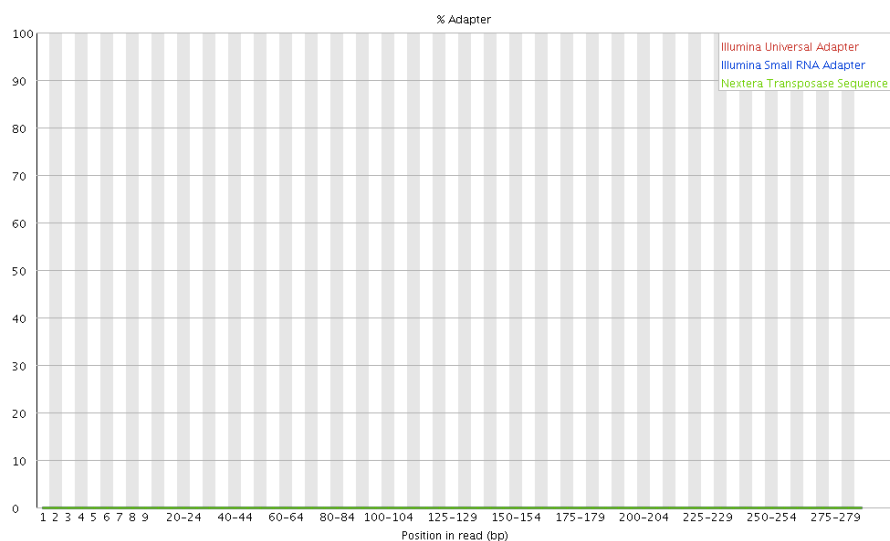
- Adapter sequences were found towards the end of up to ~10% of the reads



- This is probably because some of the inserts were shorter than the read length causing the sequencer to read through the insert into the adapter sequence



- The adapter sequences were trimmed away



All other modules in FASTQC were acceptable.

All FASTQC reports were very similar; ATCC\_31615 is shown above as an example.

The statistics for the number of reads/bases passing QC are shown in a separate file (strep\_assembly\_stats).