

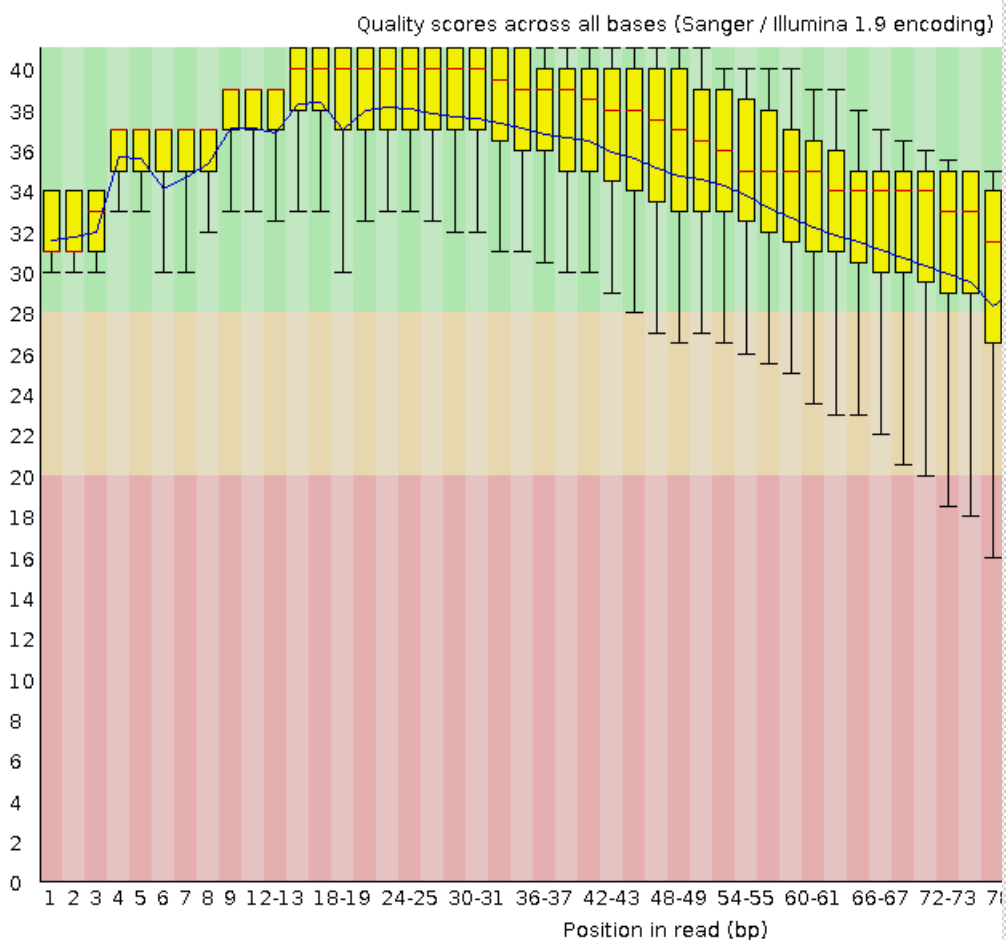
Summary

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✔ Basic Statistics

Measure	Value
Filename	amp_res_1.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	455876
Sequences flagged as poor quality	0
Sequence length	101
%GC	50

✘ Per base sequence quality



✘ Per tile sequence quality

