Summary
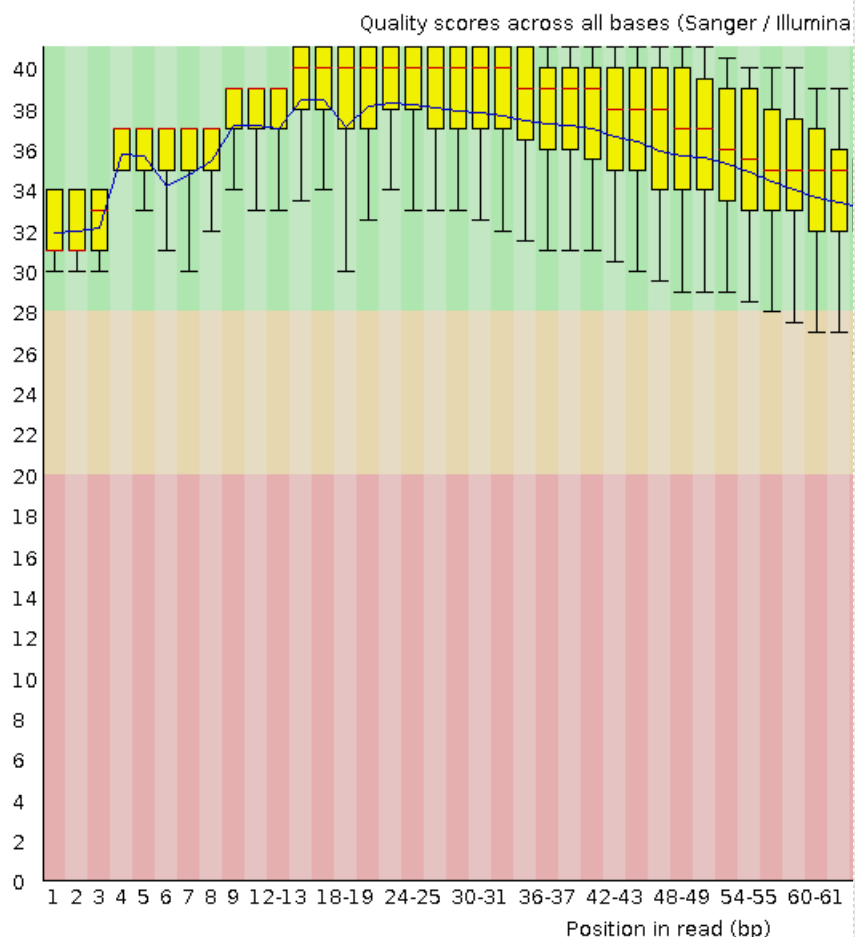
✅ [Basic Statistics](#)

✅ [Per base sequence quality](#)

❌ [Per tile sequence quality](#)

✅ [Per sequence quality scores](#)

⚠️ [Per base sequence content](#)

⚠️ [Per sequence GC content](#)

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⚠️ [Sequence Length Distribution](#)

✅ [Sequence Duplication Levels](#)

✅ [Overrepresented sequences](#)

✅ [Adapter Content](#)

⚠️ [Kmer Content](#)

✅ Basic Statistics

Measure	Value
Filename	_1P.fq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	446259
Sequences flagged as poor quality	0
Sequence length	20-101
%GC	50

✅ Per base sequence quality

Quality scores across all bases (Sanger / Illumina

Position in read (bp)

❌ Per tile sequence quality

Quality per tile

2316