

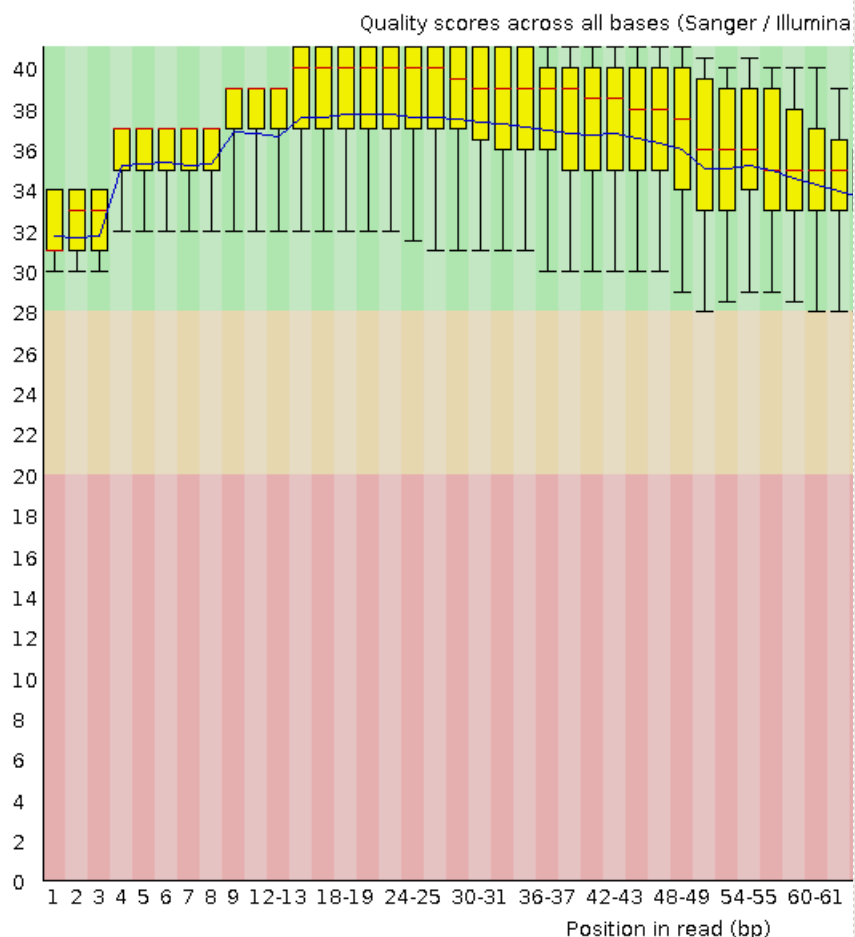
## Summary

- ✔ [Basic Statistics](#)
- ✔ [Per base sequence quality](#)
- ! [Per tile sequence quality](#)
- ✔ [Per sequence quality scores](#)
- ! [Per base sequence content](#)
- ! [Per sequence GC content](#)
- ✔ [Per base N content](#)
- ! [Sequence Length Distribution](#)
- ✔ [Sequence Duplication Levels](#)
- ✔ [Overrepresented sequences](#)
- ✔ [Adapter Content](#)
- ! [Kmer Content](#)

## ✔ Basic Statistics

Measure	Value
Filename	_2P.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



## ! Per tile sequence quality

