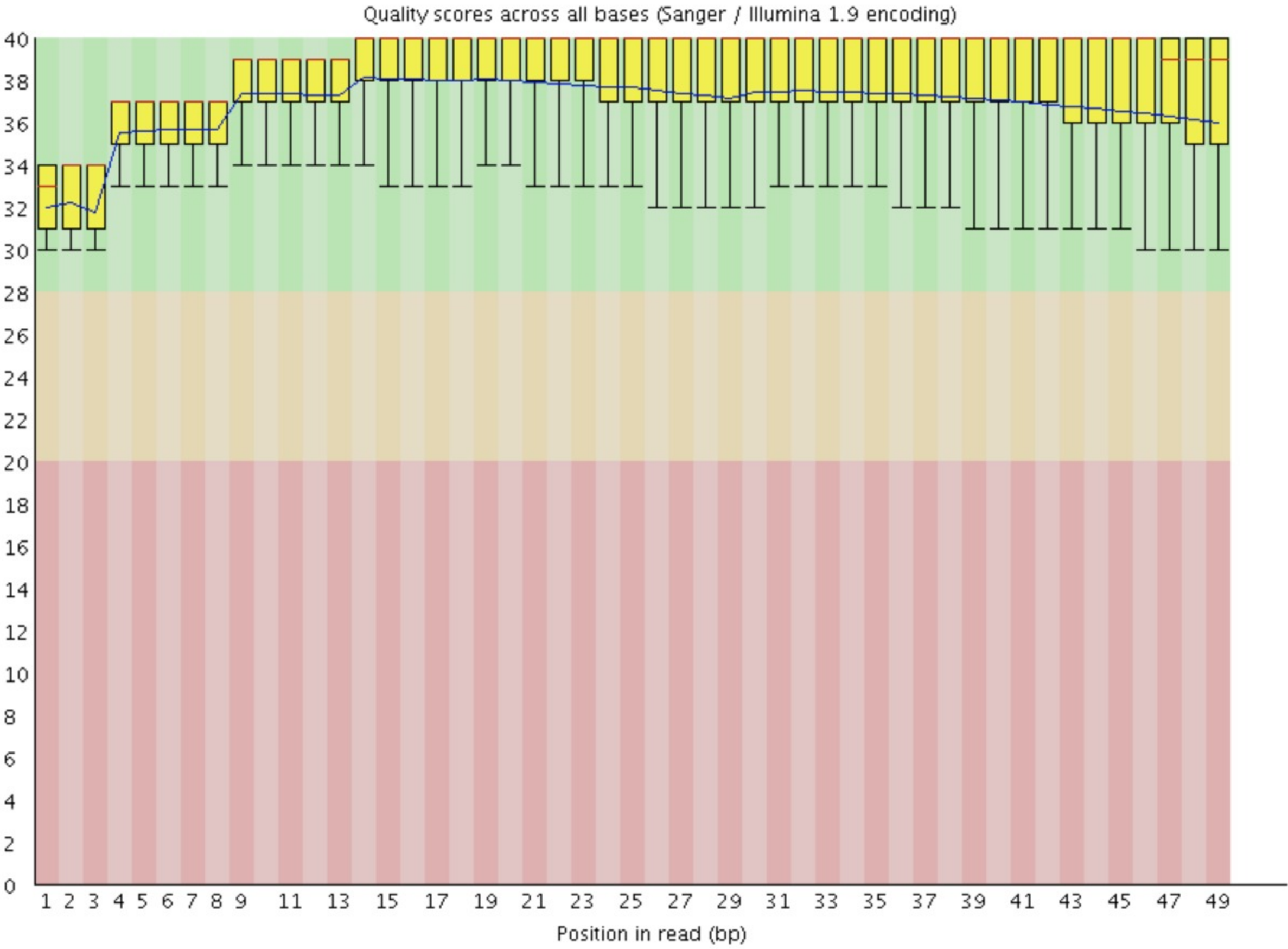## Summary

- ✅ Basic Statistics
- ✅ Per base 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 | KO01.test.fastq.gz |
| File type | Conventional base calls |
| Encoding | Sanger / Illumina 1.9 |
| Total Sequences | 239866 |
| Sequences flagged as poor quality | 0 |
| Sequence length | 49 |
| %GC | 49 |

## ✅ Per base sequence quality

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



Position in read (bp)

## ✅ Per sequence quality scores

Quality score distribution over all sequences



Average Quality per read

Mean Sequence Quality (Phred Score)