

Summary

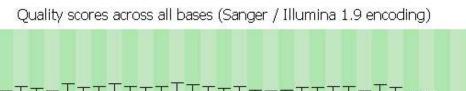


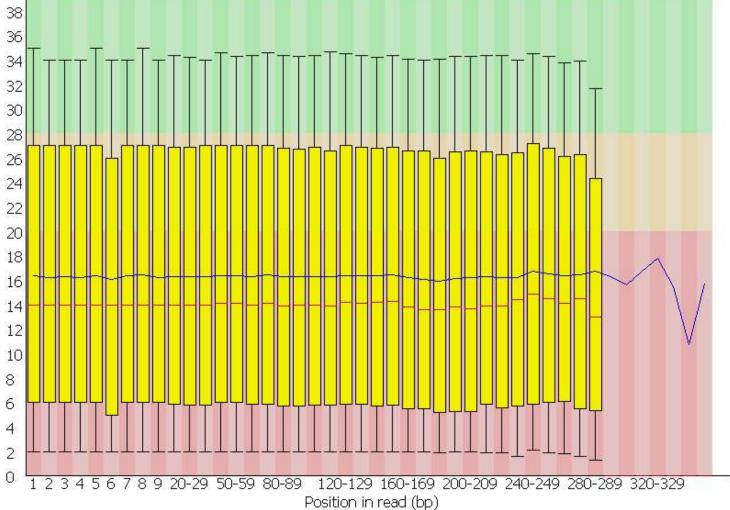
- Per base sequence quality
- Per sequence quality scores
- Per base sequence content
- Per sequence GC content
- Per base N content
- Sequence Length Distribution
- Sequence Duplication Levels
- Overrepresented sequences
- Adapter Content

Basic Statistics

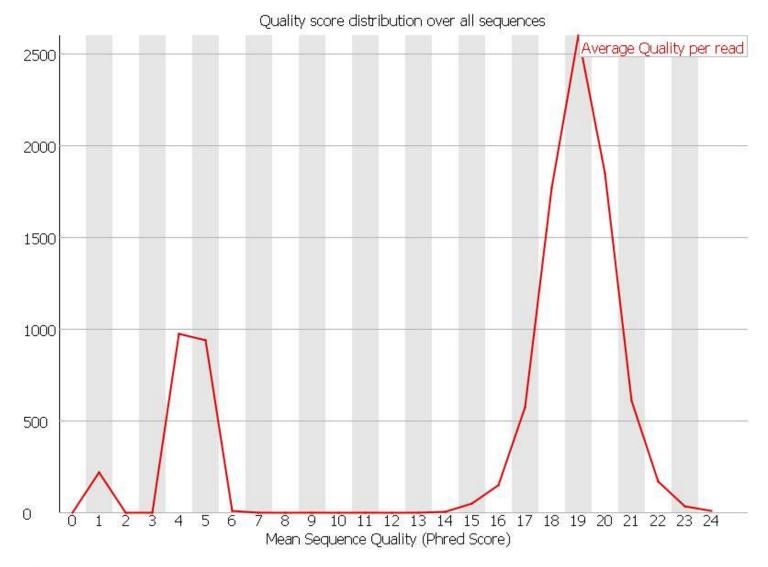
MeasureValueFilenamereads_1.fqFile typeConventional base callsEncodingSanger / Illumina 1.9Total Sequences10000Sequences flagged as poor quality0Sequence length40-354%GC49

OPer base sequence quality

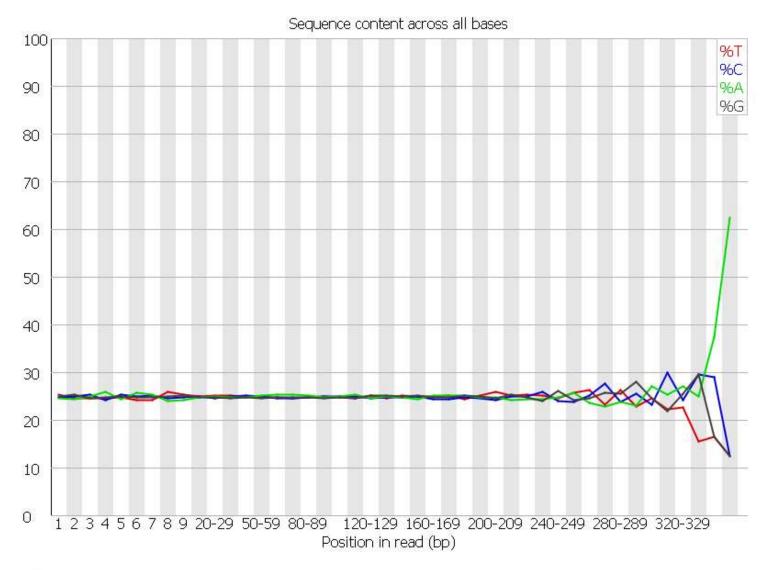




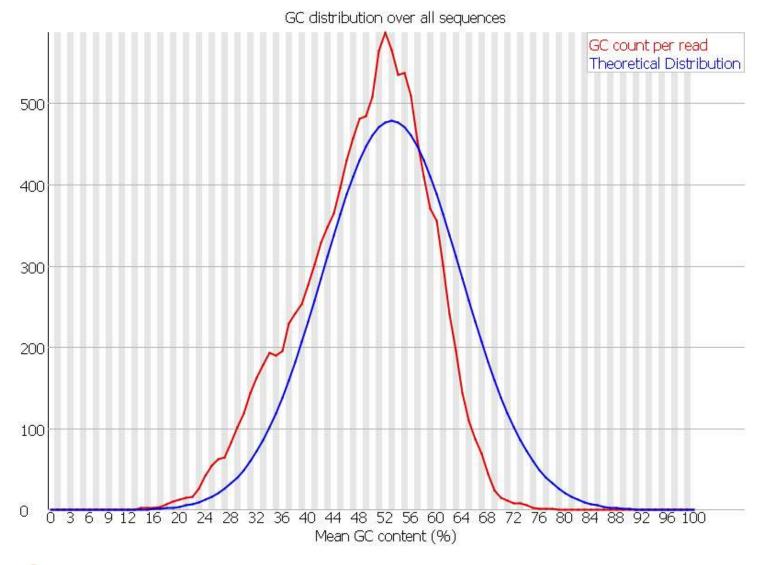
Per sequence quality scores



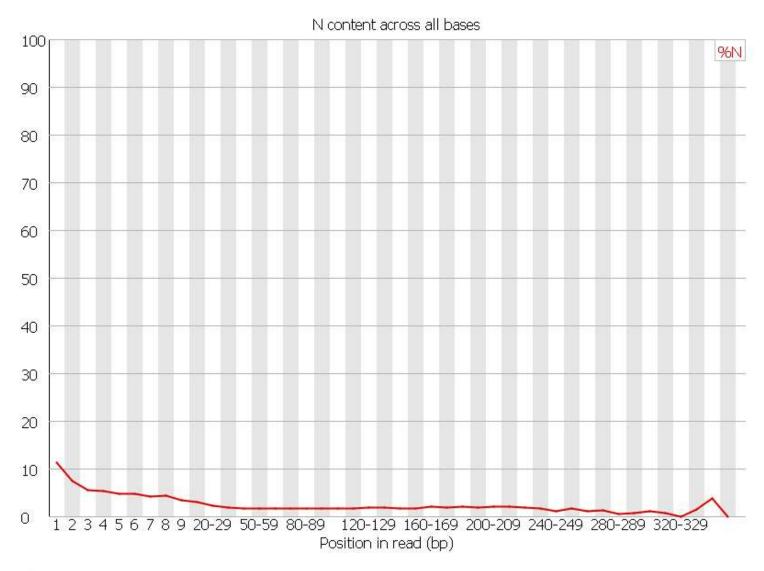
OPER Per base sequence content



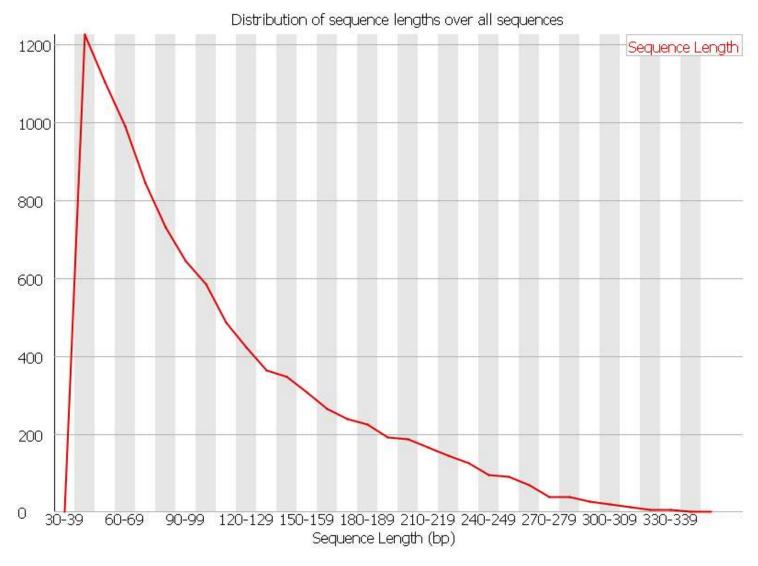
Per sequence GC content



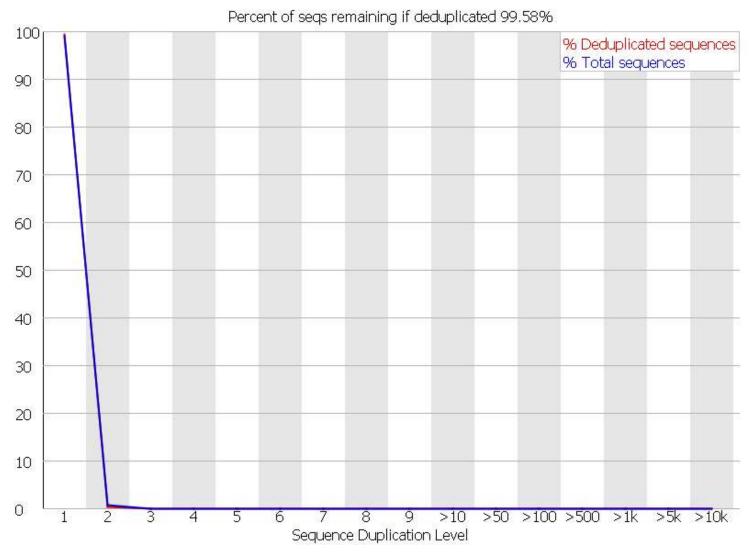
OutputPer base N content



Sequence Length Distribution



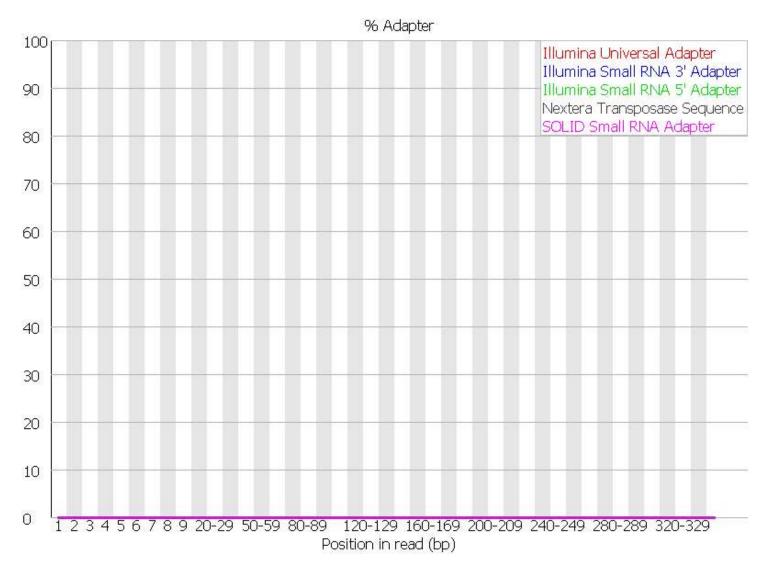
Sequence Duplication Levels



Overrepresented sequences

No overrepresented sequences





Produced by <u>FastQC</u> (version 0.11.7)