

# FastQC Report

## Summary

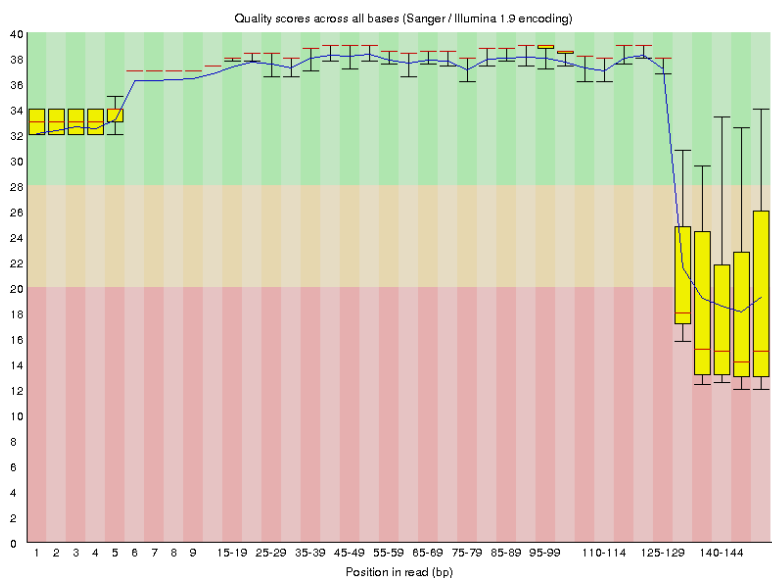
Sat 24 Mar 2018  
GOOD\_AMPLICON-2\_S2\_L001\_R2\_001\_fastq

- 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

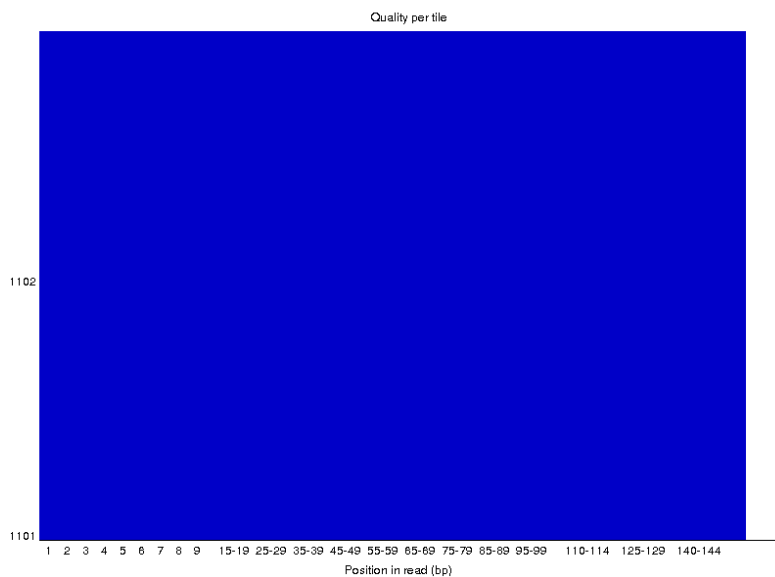
## Basic Statistics

| Measure                           | Value                                |
|-----------------------------------|--------------------------------------|
| Filename                          | GOOD_AMPLICON-2_S2_L001_R2_001_fastq |
| File type                         | Conventional base calls              |
| Encoding                          | Sanger / Illumina 1.9                |
| Total Sequences                   | 51199                                |
| Sequences flagged as poor quality | 0                                    |
| Sequence length                   | 151                                  |
| %GC                               | 43                                   |

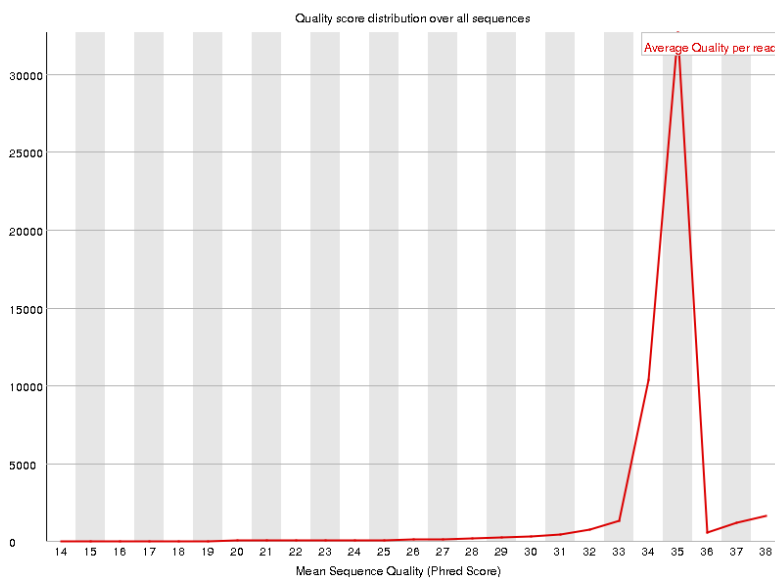
## Per base sequence quality



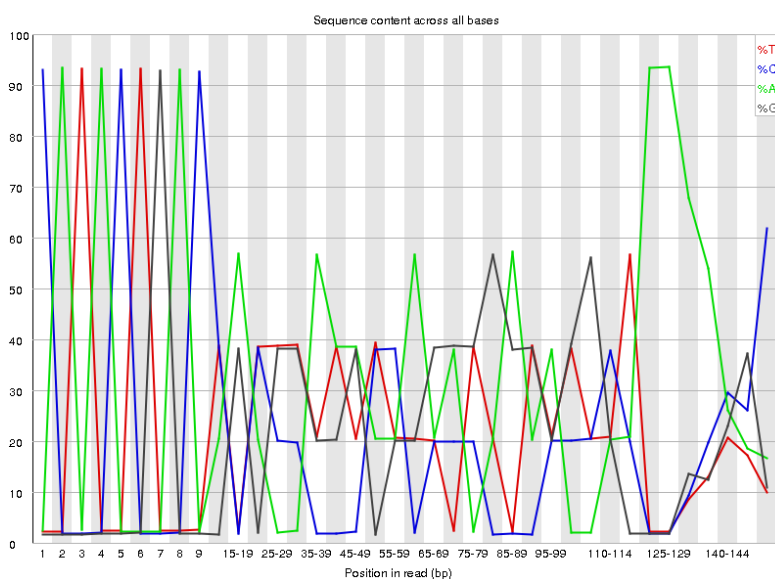
## Per tile sequence quality



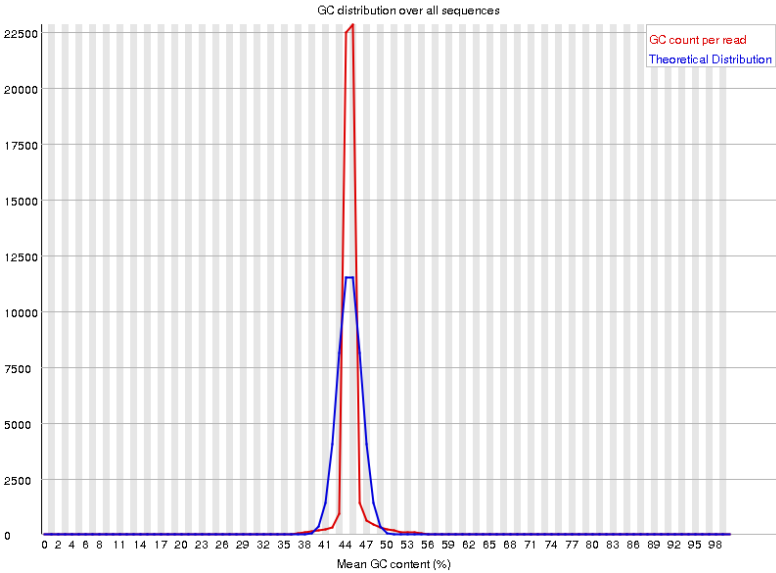
### ✔ Per sequence quality scores



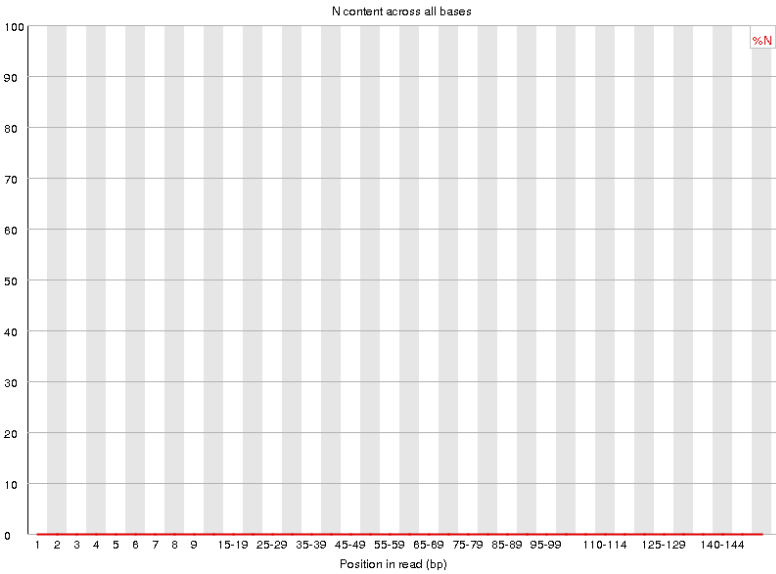
### ✖ Per base sequence content



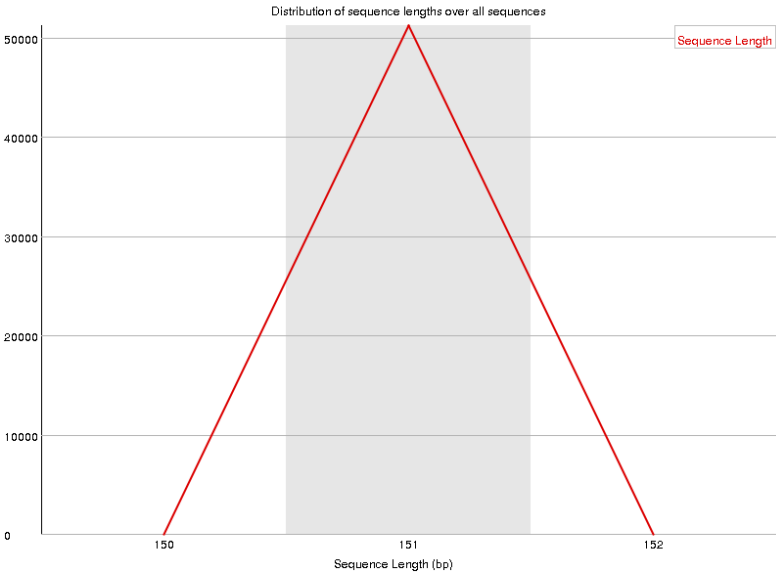
✖ Per sequence GC content



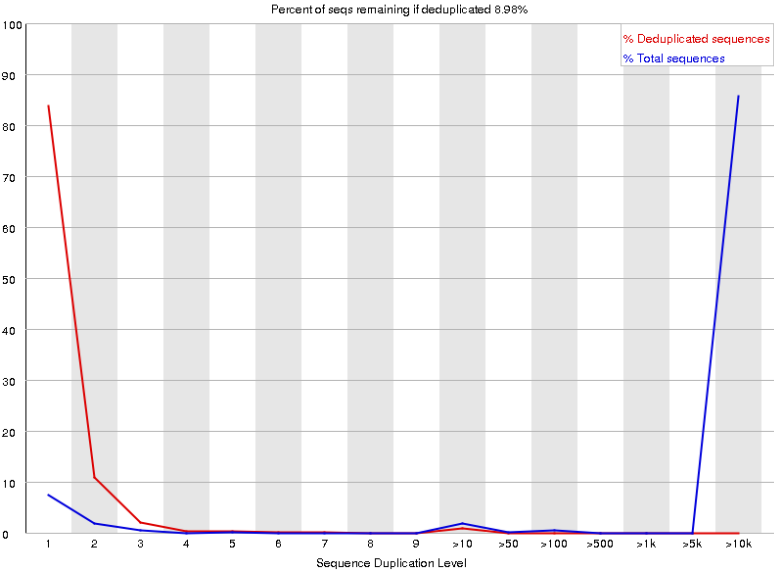
✔ Per base N content



✔ Sequence Length Distribution



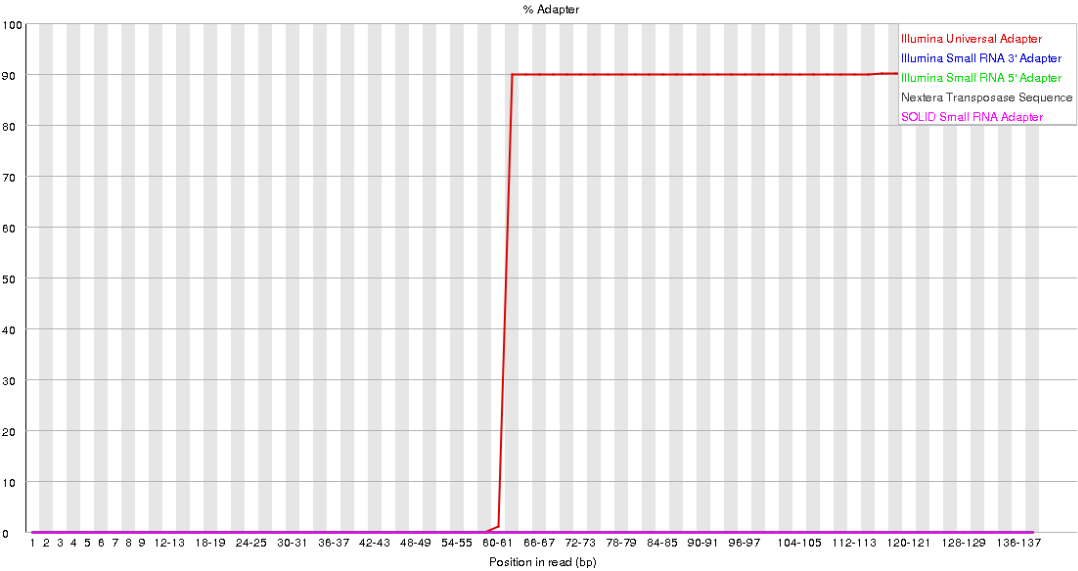
Sequence Duplication Levels



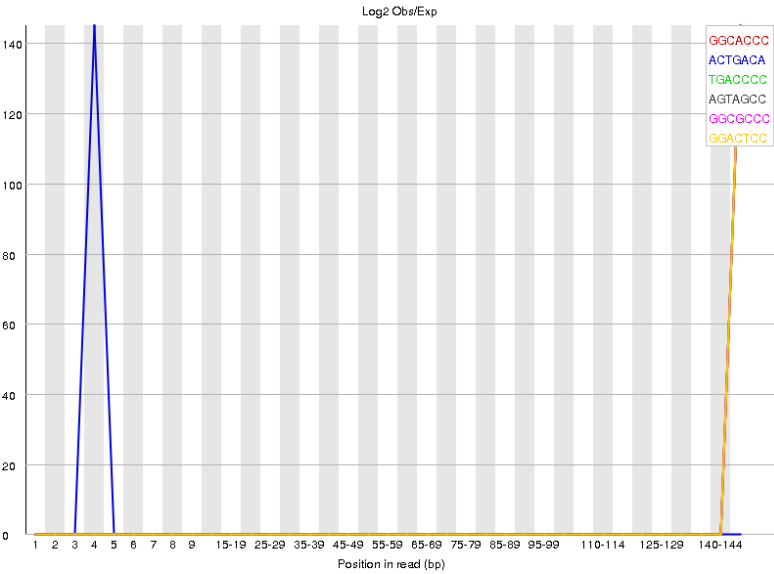
Overrepresented sequences

| Sequence                                            | Count | Percentage          | Possible Source |
|-----------------------------------------------------|-------|---------------------|-----------------|
| CATACTGACTCATCAGAAGTCTCAGCGTTCGGTTAAAGTTTAAGGAAGTC  | 44003 | 85.94503798902322   | No Hit          |
| CATACTGACTCATCAGAAGTCTCAGCGTTAGGTTAAAGTTTAAGGAAGTC  | 123   | 0.24023906716928062 | No Hit          |
| CATACTGACTCATCAGAAGTCTCAGCGTTCGGTTAAAGTTTAAGGAAGTT  | 116   | 0.22656692513525656 | No Hit          |
| CATACTGACTCATCAGAAGTCTCGGCGTTCGGTTAAAGTTTAAGGAAGTC  | 107   | 0.20898845680579697 | No Hit          |
| CATACTGACTCATCAGAAGTCTCAGCGTTCGGTTAAAGTTTAAGGAAGTCC | 81    | 0.15820621496513604 | No Hit          |
| CATACTGACTCATCAGAAGTCTCAGCGTTCGGTTAAAGTTAAGGAAGTCC  | 53    | 0.10351764682903963 | No Hit          |
| CATACTGACTCATCGAAGTCTCAGCGTTCGGTTAAAGTTTAAGGAAGTCC  | 52    | 0.1015644836813219  | No Hit          |

Adapter Content



Kmer Content



| Sequence | Count | PValue       | Obs/Exp Max | Max Obs/Exp Position |
|----------|-------|--------------|-------------|----------------------|
| GGCACCC  | 10    | 0.0070713446 | 145.0       | 145                  |
| ACTGACA  | 10    | 0.0070713446 | 145.0       | 4                    |
| TGACCCC  | 15    | 1.2232459E-4 | 145.0       | 145                  |
| AGTAGCC  | 10    | 0.0070713446 | 145.0       | 145                  |
| GGCGCCC  | 15    | 1.2232459E-4 | 145.0       | 145                  |
| GGACTCC  | 15    | 1.2232459E-4 | 145.0       | 145                  |
| GGACTAC  | 10    | 0.0070713446 | 145.0       | 145                  |
| GGTCCCC  | 40    | 0.0          | 145.0       | 145                  |
| GGTCCAC  | 10    | 0.0070713446 | 145.0       | 145                  |
| GGACAGC  | 10    | 0.0070713446 | 145.0       | 145                  |
| CGTAGCC  | 10    | 0.0070713446 | 145.0       | 145                  |
| TATGACT  | 10    | 0.0070713446 | 145.0       | 3                    |
| GGGAGCC  | 15    | 1.2232459E-4 | 145.0       | 145                  |
| GGCCCCC  | 10    | 0.0070713446 | 145.0       | 145                  |
| AGACGCC  | 10    | 0.0070713446 | 145.0       | 145                  |
| GACCGCA  | 10    | 0.0070713446 | 145.0       | 145                  |
| AGGCTCC  | 10    | 0.0070713446 | 145.0       | 145                  |
| CGTACAT  | 10    | 0.0070713446 | 145.0       | 145                  |
| AGATGTG  | 10    | 0.0070713446 | 145.0       | 145                  |
| GGCCACC  | 15    | 1.2232459E-4 | 145.0       | 145                  |