# **<b>᠙**FastQC Report

Tue 12 Dec 2017 m54115\_170810\_231757.fastq

#### Summary





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 m54115 170810 231757.fastq

Conventional base calls File type

Sanger / Illumina 1.9 Encoding

Total Sequences 83027

Sequences flagged as poor quality 0

Sequence length 50-62974

%GC 38

#### Per base sequence quality

0



Position in read (bp)

13000-13999 19000-19999 25000-25999 31000-31999 37000-37999 43000-43999 49000-49999 55000-55999 61000-61999

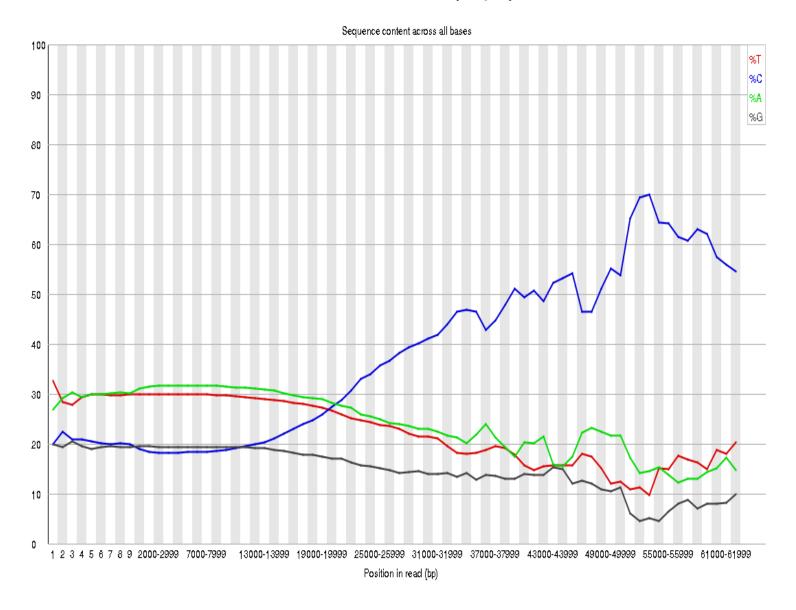
### Per sequence quality scores

1 2 3 4 5 6 7 8 9 2000-2999 7000-7999

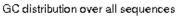
#### Quality score distribution over all sequences

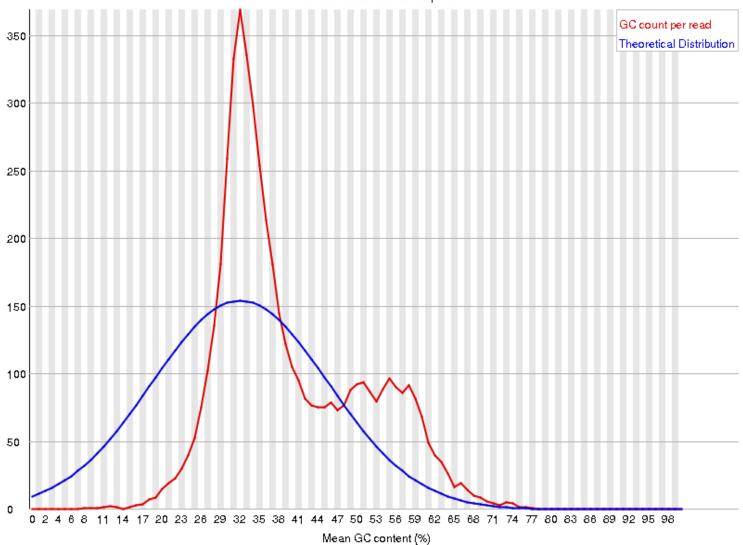


#### Per base sequence content

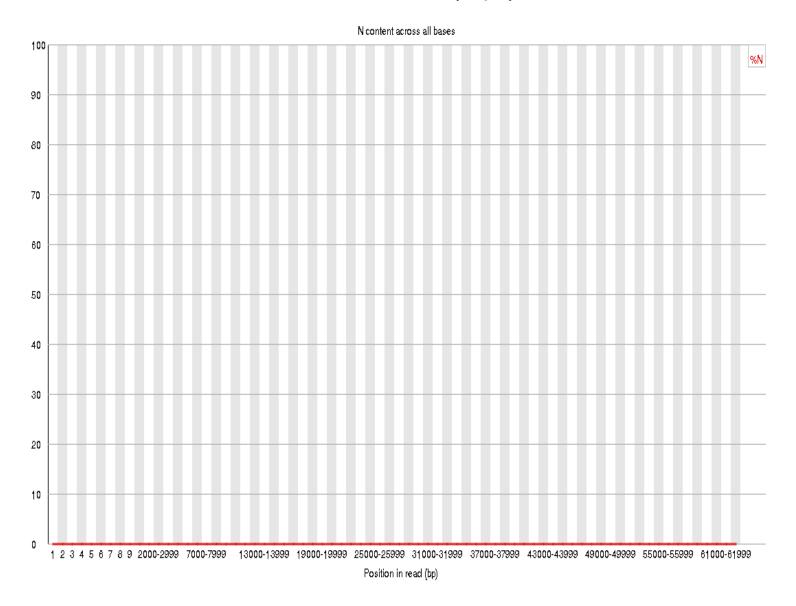


## Per sequence GC content

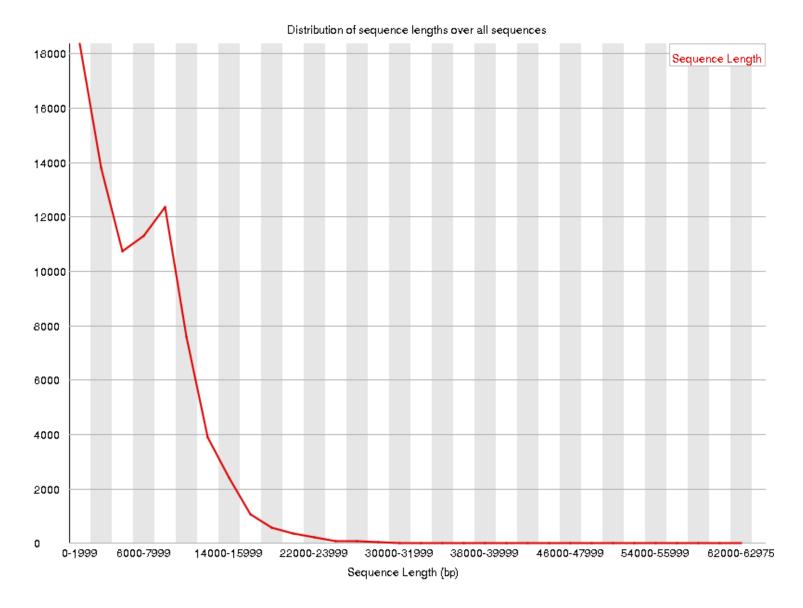




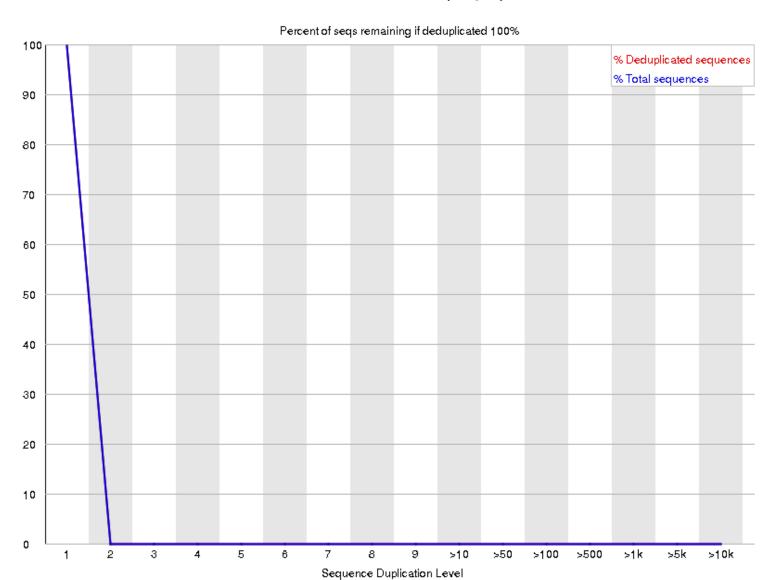




### Sequence Length Distribution

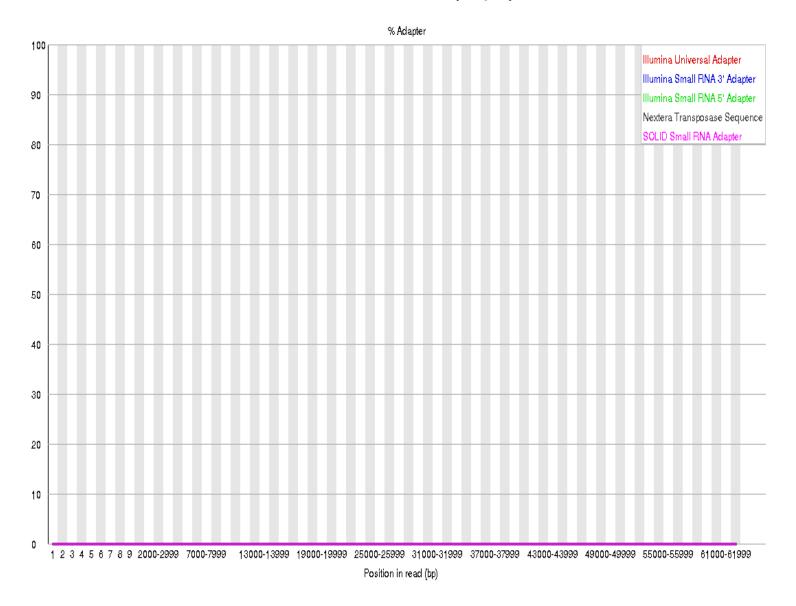


## Sequence Duplication Levels

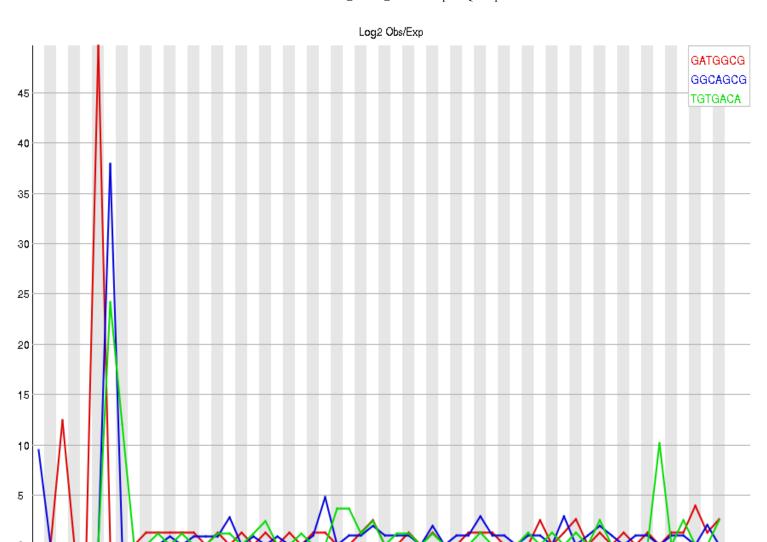












1 2 3 4 5 6 7 8 9 20-29 50-59 80-89 120-129 160-169 200-209 240-249 280-289 320-329 360-369 400-409 440-449 480-489

Position in read (bp)

| Sequence | Count | PValue       | Obs/Exp Max | Max Obs/Exp Position |
|----------|-------|--------------|-------------|----------------------|
| GATGGCG  | 195   | 4.3293153E-4 | 49.60049    | 6                    |
| GGCAGCG  | 255   | 0.0016218591 | 37.92979    | 7                    |
| TGTGACA  | 200   | 0.0025842101 | 24.180243   | 7                    |

#### Produced by FastQC (version 0.11.5)