# **PastQC Report**Summary

Wed 30 Aug 2017 Sample1\_reverse\_paired.fq.gz



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 Sample1\_reverse\_paired.fq.gz
File type Conventional base calls
Encoding Sanger / Illumina 1.9

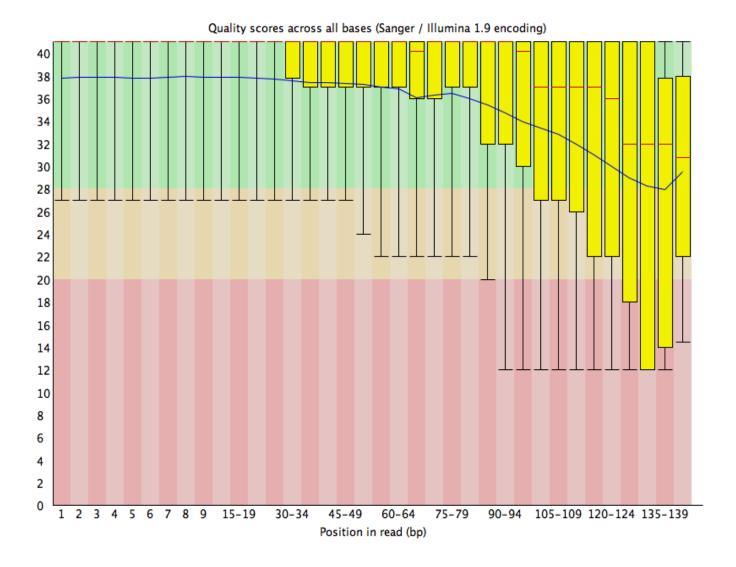
Total Sequences 34626514

Sequences flagged as poor quality  $\,\,0\,\,$ 

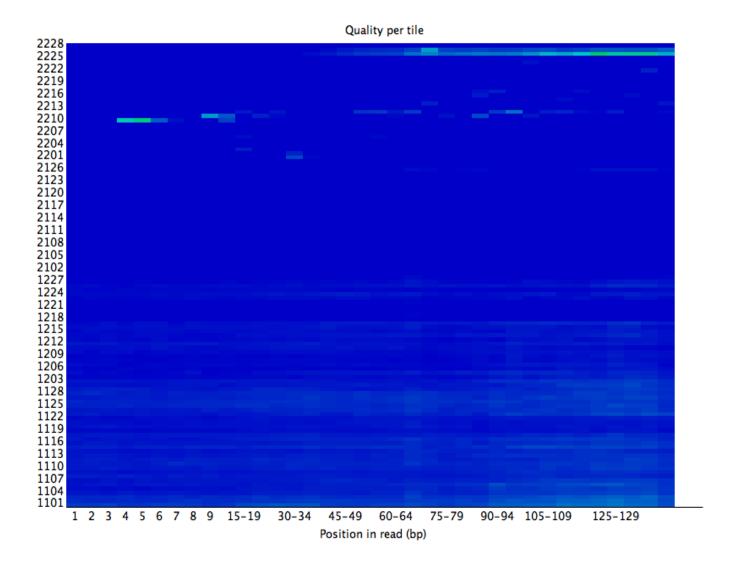
Sequence length 14-143

%GC 5!

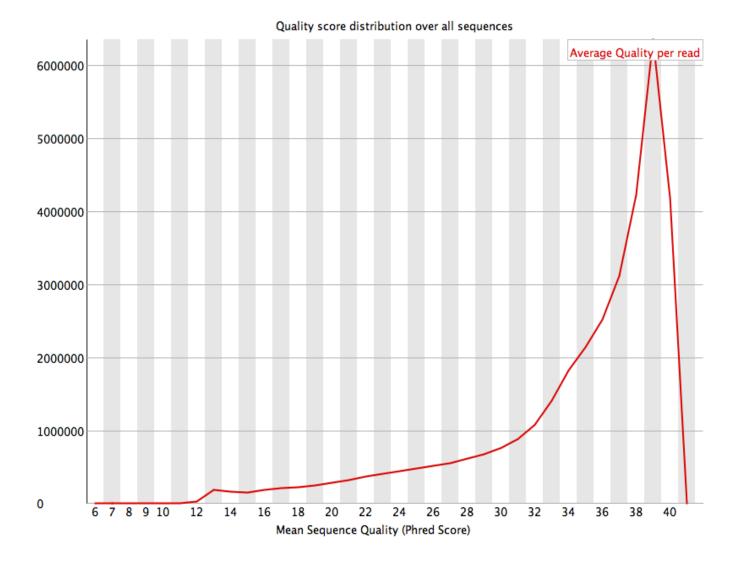
## Per base sequence quality



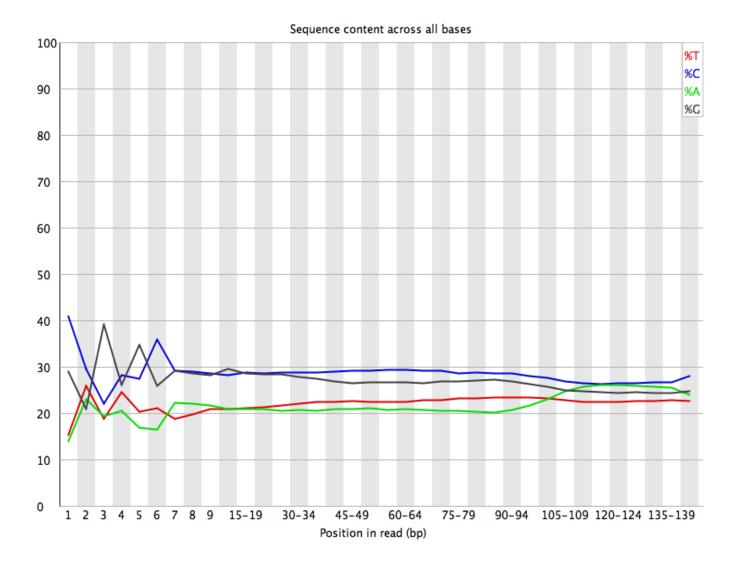
# Per tile sequence quality



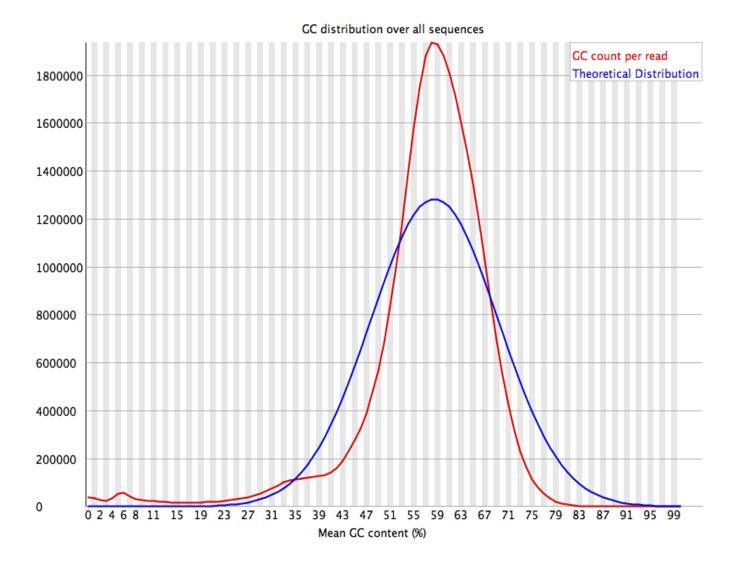
# Per sequence quality scores



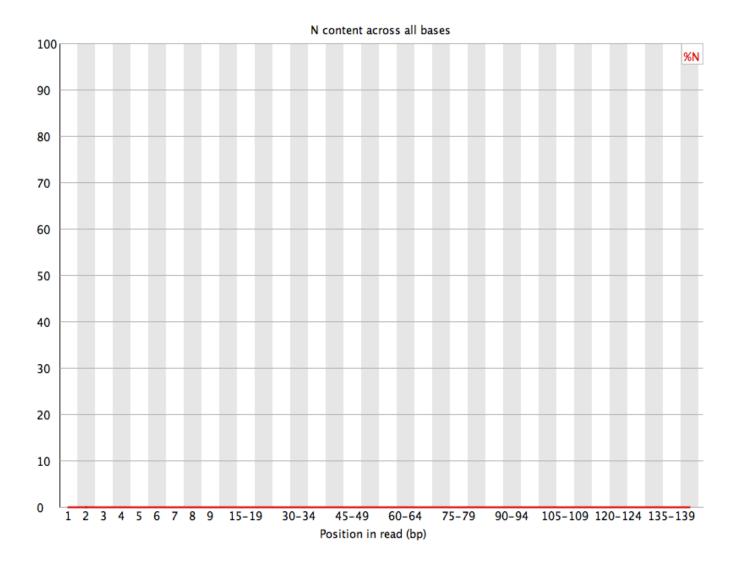
#### Per base sequence content



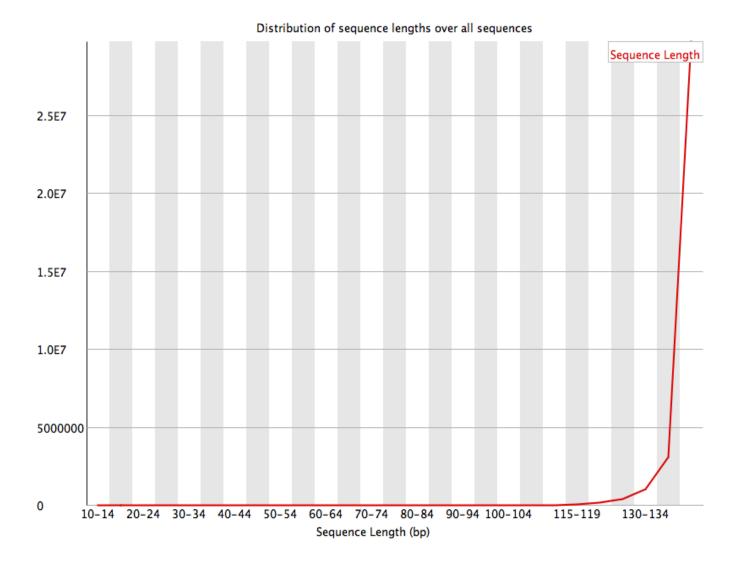
# Per sequence GC content



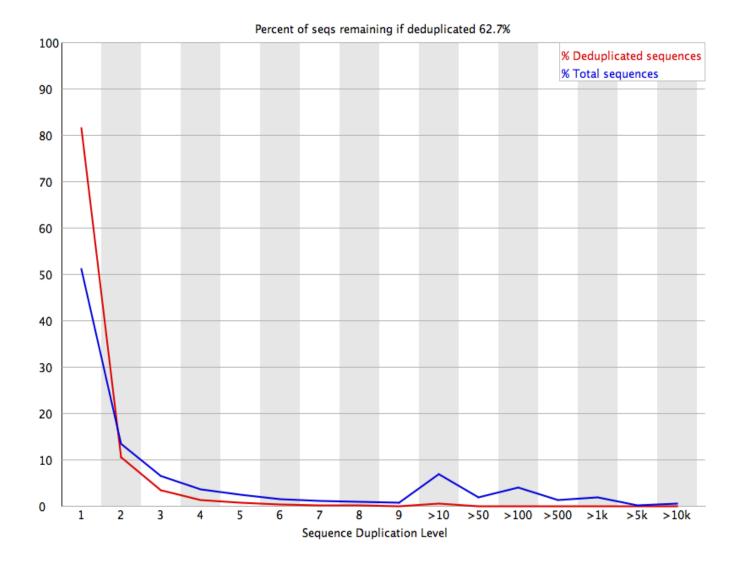




### Sequence Length Distribution



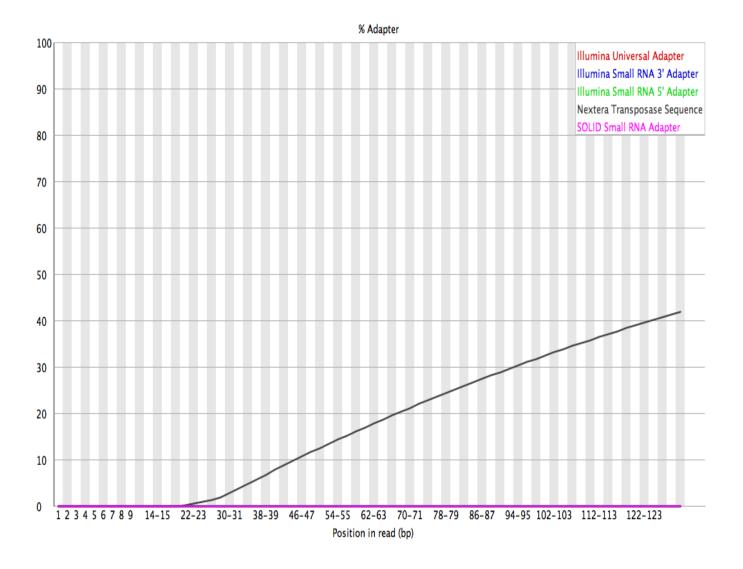
#### Sequence Duplication Levels



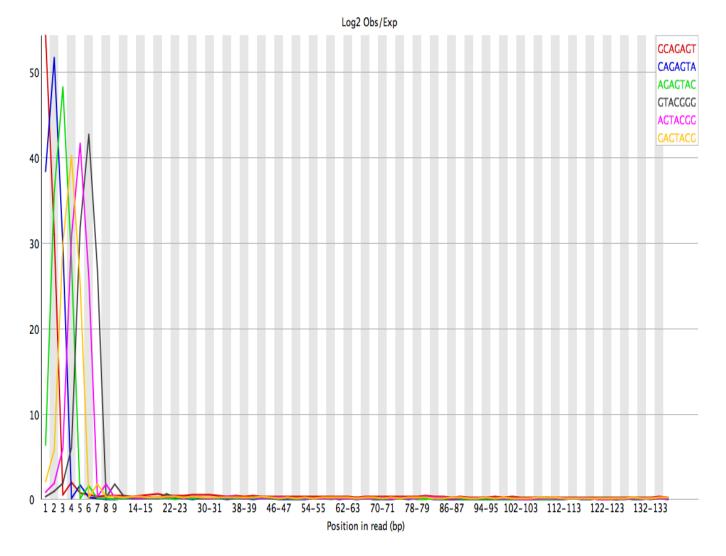
# Overrepresented sequences

| Sequence                                       | Count | Percentage          | Possible<br>Source |
|--|-------|---------------------|--------------------|
| ${\tt GCAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT$ | 72638 | 0.20977566497164568 | No Hit             |
| ${\tt CAGAGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT$ | 55215 | 0.15945873153734158 | No Hit             |
| ${\tt TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT$    | 45612 | 0.1317256481550525  | No Hit             |





#### **W**Kmer Content



| Sequence | Count | PValue | Obs/Exp Max | Max Obs/Exp Position |
|----------|-------|--------|-------------|----------------------|
| GCAGAGT  | 81595 | 0.0    | 54.228992   | 1                    |
| CAGAGTA  | 85300 | 0.0    | 51.660637   | 2                    |
| AGAGTAC  | 91215 | 0.0    | 48.22171    | 3                    |
| GTACGGG  | 72840 | 0.0    | 42.70363    | 6                    |
| AGTACGG  | 74800 | 0.0    | 41.65135    | 5                    |
| GAGTACG  | 77820 | 0.0    | 40.1801     | 4                    |
| GTACTTT  | 31765 | 0.0    | 39.960857   | 6                    |
| TACGGGG  | 46765 | 0.0    | 39.41968    | 7                    |
| TACTTTT  | 33155 | 0.0    | 38.229725   | 7                    |
| ACTTTTT  | 38200 | 0.0    | 34.02025    | 8                    |
| AGTACTT  | 39020 | 0.0    | 32.699753   | 5                    |
| CGCAGAG  | 79540 | 0.0    | 32.368744   | 1                    |
| GAGTACT  | 40600 | 0.0    | 31.441895   | 4                    |
|          |       |        |             |                      |

| Sequence | Count | <b>PValue</b> | Obs/Exp Max | Max Obs/Exp Position |
|----------|-------|---------------|-------------|----------------------|
| TACGGGA  | 13960 | 0.0           | 31.088411   | 7                    |
| TACGGGT  | 12565 | 0.0           | 29.106077   | 7                    |
| TACGGGC  | 16955 | 0.0           | 28.826336   | 7                    |
| ACGGGGG  | 37820 | 0.0           | 25.530195   | 8                    |
| ACTAGGT  | 3370  | 0.0           | 19.250591   | 4                    |
| TATGTAT  | 6575  | 0.0           | 17.574654   | 1                    |
| ACGGGGA  | 24610 | 0.0           | 17.006952   | 8                    |

Produced by FastQC (version 0.11.5)