# Rfastp Report

## Summary

### General

| | |
|---|---|
| **fastp version:** | 0.21.0 (https://github.com/OpenGene/fastp) |
| **sequencing:** | single end (50 cycles) |
| **mean length before filtering:** | 50bp |
| **mean length after filtering:** | 49bp |
| **duplication rate:** | 32.6193225% (may be overestimated since this is SE data) |
| **Detected read1 adapter:** | CGAAAGCAGGTCAATTATATTCAATATGGAAAAGATAAAAAGAACTAAGGAATCTAATGTC |

### Before filtering

| | |
|---|---|
| **total reads:** | 23.379546 M |
| **total bases:** | 1.168977 G |
| **Q20 bases:** | 1.150622 G (98.429834%) |
| **Q30 bases:** | 1.081053 G (92.478555%) |
| **GC content:** | 46.123001% |

### After filtering

| | |
|---|---|
| **total reads:** | 23.325007 M |
| **total bases:** | 1.166046 G |
| **Q20 bases:** | 1.147887 G (98.442700%) |
| **Q30 bases:** | 1.078491 G (92.491327%) |
| **GC content:** | 46.155371% |

### Filtering result

| | |
|---|---|
| **reads passed filter:** | 23.325007 M (99.746723%) |
| **reads with low quality:** | 6.241000 K (0.026694%) |
| **reads with too many N:** | 0 (0.000000%) |
| **reads too short:** | 48.298000 K (0.206582%) |

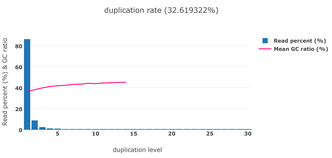
## Adapters

### Adapter or bad ligation of read1

The input has little adapter percentage (~0.230334%), probably it's trimmed before.

| SEQUENCE | OCCURRENCES |
|---|---|
| CGAAA | 14851 |
| CGAAAG | 4280 |
| AGAAAGCA | 1403 |
| GGAAAGCA | 1316 |
| CGAAAGCAT | 802 |
| CGAAAGCAGGTCAATTATATTCAATATGGAAAAGATAAAAAGAACTAAG | 6738 |
| CGAAAGCAGGTCAATTATATTCAATATGGAAAAGATAAAAAGAACTAAGG | 10086 |
| CGAAAGCAGGTCAATTATATTCAATATGGAAAAGATAAAAAGAACTAAGGA | 14176 |
| CGAAAGCAGGTCAATTATATTCAATATGGAAAAGATAAAAAGAACTAAGGAA | 5543 |
| CGAAAGCAGGTCAATTATATTCAATATGGAAAAGATAAAAAGAACTAAGGAATCTAAT | 4722 |
| CGAAAGCAGGTCAATTATATTCAATATGGAAAAGATAAAAAGAACTAAGGAATCTAATG | 1606 |
| CGAAAGCAGGTCAATTATATTCAATATGGAAAAGATAAAAAGAACTAAGGAATCTAATGT | 2085 |
| other adapter sequences | 11906 |

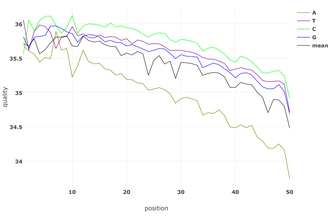
## Duplication




## Before filtering

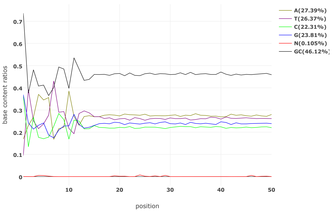
### Before filtering: read1: quality

Value of each position will be shown on mouse over.



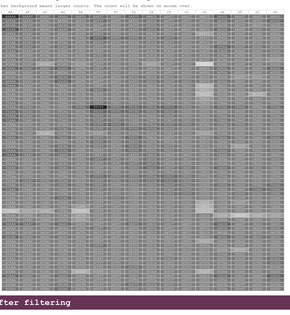

### Before filtering: read1: base contents

Value of each position will be shown on mouse over.




### Before filtering: read1: KMER counting

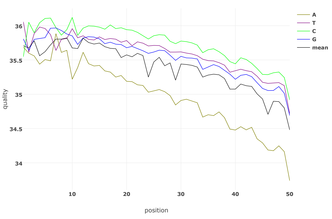
Darker background means larger counts. The count will be shown on mouse over.



## After filtering

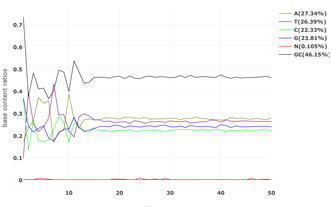
### After filtering: read1: quality

Value of each position will be shown on mouse over.




### After filtering: read1: base contents

Value of each position will be shown on mouse over.




### After filtering: read1: KMER counting

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