SRR7973881

mean length before filtering:

mean length after filtering:

0.20.0 (https://github.com/OpenGene/fastp)

paired end (151 cycles + 151 cycles)

137bp, 138bp

127bp, 128bp

444.686636 M

61.493029 G

33.393754%

226.046304 M

28.973991 G

42.922805%

The input has little adapter percentage (~0.759447%), probably it's trimmed before.

The input has little adapter percentage (~0.225873%), probably it's trimmed before.

42.885807 G (69.740925%)

39.250751 G (63.829594%)

27.586558 G (95.211453%)

25.507637 G (88.036324%)

226.046304 M (50.832718%)

179.990322 M (40.475766%)

Occurrences

Occurrences

147776

139239

4872350

3324451

76919

45937

40573

43732

75471

41222

80559

145515

35093

135382

43299

duplication rate (40.522944%)

2718291

Read percent (%) Mean GC ratio (%)

10.649326 M (2.394793%)

27.997918 M (6.296101%)

2.766000 K (0.000622%)

40.522944%

151

Summary

General

fastp version:

duplication rate:

Insert size peak:

total reads:

total bases:

Q20 bases:

Q30 bases:

GC content:

total reads:

total bases:

Q20 bases:

Q30 bases:

GC content:

Before filtering

After filtering

Filtering result

reads passed filters:

reads with low quality:

reads with too many N:

reads with low complexity:

GTGACTGGAGTTCAGACGTGTGCTCTTCCGATC

Adapter or bad ligation of read1

Adapter or bad ligation of read2

reads too short:

Adapters

Sequence

Sequence

AAAAA

**AATGAT** 

AGATGT

CAAGCA

CTGTCT

TACACT

TTTTTT

CTCTCTCT

TTTTTTTTTT

CTCTCTCTCTCTCT

TTTTTTTTTTTTTTTTTTTTTTTTTT

other adapter sequences

Duplication

80

CTCTCTCTCTCTCT

other adapter sequences

CTCTCTCT

sequencing: