

fastp report

Summary

General	
fastp version:	1.0.1 (https://github.com/OpenGene/fastp)
sequencing:	paired end (151 cycles + 151 cycles)
mean length before filtering:	147bp, 147bp
mean length after filtering:	147bp, 146bp
duplication rate:	0.661239%
Insert size peak:	261

Before filtering	
total reads:	557.438990 K
total bases:	82.387931 M
Q28 bases:	80.784361 M (98.054786%)
Q38 bases:	80.372733 M (97.555979%)
Q48 bases:	126.976000 K (0.154121%)
GC content:	40.821670%

After filtering	
total reads:	553.084000 K
total bases:	81.261373 M
Q28 bases:	80.064519 M (98.527155%)
Q38 bases:	79.773441 M (98.168955%)
Q48 bases:	126.778900 K (0.156013%)
GC content:	40.770512%

Filtering result	
reads passed filters:	553.084000 K (99.218927%)
reads with low quality:	98 (0.017580%)
reads with too many N:	0 (0.000000%)
reads too short:	4.256000 K (0.763493%)

Adapters

Adapter or bad ligation of read1	
The input has little adapter percentage (-0.358558%), probably it's trimmed before.	
Sequence	Occurrences
all adapter sequences	1758

Adapter or bad ligation of read2	
The input has little adapter percentage (-0.347955%), probably it's trimmed before.	
Sequence	Occurrences
TT	22
other adapter sequences	1852

Insert size estimation



Filtering statistics

