Rfastp Report

Summary	
General	
fastp version:	0.21.0 (https://github.com/OpenGene/fastp)
sequencing:	single end (76 cycles)
mean length before filtering:	76bp
mean length after filtering:	70bp
duplication rate:	31.114805% (may be overestimated since this is SE data)
Detected read1 adapter:	AGATCGGAAGAGCACACGTCTGAACTCCAGTCA
Before filtering	
total reads:	16.324992 M
total bases:	1.240699 G
Q20 bases:	1.167735 G (94.119059%)
Q30 bases:	1.141835 G (92.031565%)
GC content:	61.405470%

total reads:

15.709643 M total bases: 1.106473 G Q20 bases: 1.059826 G (95.784156%) Q30 bases: 1.040847 G (94.068962%) GC content: 61.639523%

Filtering result

reads passed filters: 15.709643 M (96.230632%) reads with low quality: 454.888000 K (2.786452%) reads with too many N: 471 (0.002885%)

Occurrences

178997 180665

183847

192670

214375

191573

192968

188612

170447

195993

165937

153268

179136 149519

147668

145571

117070 122029

106803

101520

94607 84988

78837

78952

71453 64641

58932

212761

51358 50829

652247

Read percent (%)

70

70

70

- A(18.35%) - T(20.00%)

C(29.38%) G(32.25%)

- N(0.001%) — GC(61.63%)

A(19.55%)

T(19.04%) C(28.29%) G(33.10%)

N(0.001%) - GC(61.40%)

Mean GC ratio (%)

duplication rate (31.114805%)

duplication level

position

position

ATCAG ATCTA ATCTT ATCTC ATCTG ATCCA ATCCT ATCCC ATCCG ATCGA ATCGT ATGAG ATGTA ATGTT ATGTC ATGTG ATGCA ATGCT ATGCC ATGCG ATGGA ATGGT ACAAG ACATA ACATT ACATC ACATG ACACA ACACT ACACC ACACG ACAGA ACAGT

159.990000 K (0.980031%)

Adapters

reads too short:

Adapter or bad ligation of read1

Sequence AGATC AGATCG

AGATCGG

AGATCGGA AGATCGGAA

AGATCGGAAGA

AGATCGGAAG ${\sf AGATCGGAAGAG}$ AGATCGGAAGAGC AGATCGGAAGAGCA AGATCGGAAGAGCAC AGATCGGAAGAGCACA AGATCGGAAGAGCACAC AGATCGGAAGAGCACACG

AGATCGGAAGAGCACACGT AGATCGGAAGAGCACACGTC AGATCGGAAGAGCACACGTCT AGATCGGAAGAGCACACGTCTG AGATCGGAAGAGCACACGTCTGA AGATCGGAAGAGCACACGTCTGAA AGATCGGAAGAGCACACGTCTGAAC AGATCGGAAGAGCACACGTCTGAACT

AGATCGGAAGAGCACACGTCTGAACTC

 ${\tt AGATCGGAAGAGCACACGTCTGAACTCC}$

AGATCGGAAGAGCACACGTCTGAACTCCA AGATCGGAAGAGCACACGTCTGAACTCCAG AGATCGGAAGAGCACACGTCTGAACTCCAGT ${\tt AGATCGGAAGAGCACACGTCTGAACTCCAGTC}$ AGATCGGAAGAGCACACGTCTGAACTCCAGTCA AGATCGGAAGAGCACACGTCTGAACTCCAGTCAC other adapter sequences **Duplication**

Read percent (%) & GC ratio 40 20

60

Before filtering Before filtering: read1: quality Value of each position will be shown on mouse over.

31

30

Before filtering: read1: base contents Value of each position will be shown on mouse over.

0.8 0.7 0.6 base content ratios 0.5

0.2 Before filtering: read1: KMER counting

0.3

10

AAGTA AAGTT AAGTC
ATATA ATATT ATATC

Darker background means larger counts. The count will be shown on mouse over
 AA
 AT
 AC
 AG
 TA
 TT
 TC
 TG
 CA
 CT
 CC
 CG
 GA
 GT
 GC
 GG

 AAAAA
 AAAAT
 AAAAC
 AAAAG
 AAAAG
 AAATT
 AAATT
 AAATC
 AAACA
 AAACT
 AAACC
 AAAGC
 AAAGA
 AAAGT
 AAAGC
 AAAGC
 AATAA AATAT AATAC AATAG AATTA AATTT AATTC AATTG AATCA AATCT AATCC AATCG AATGA
AACAA AACAT AACAC AACAG AACAA AACAT AACAC AACAG AACAA AACAT AACAC AACAG AACAG AACAC ACC ACCAA ACCAT ACCAC ACCAG ACCTA ACCTT ACCTC ACCTG ACCCA ACCCT ACCCC ACCCG ACCGA ACCGT ACCGC ACCGG ACG ACGAA ACGAT ACGAC ACGAC ACGTA ACGTT ACGTC ACGTC ACGTC ACGTC ACGCC ACGCG ACGCA ACGCT ACGCC ACGCG ACGCA ACGCC ACGCG ACGCA ACGCT ACGCC ACGCG ACGCA ACGCC ACGCG ACGCA ACGCC ACGCG ACGCA ACGCC AC

TAT TATAA TAGAT TAGAC TAGAG TAGTA TAGTT TAGTC TAGTG TAGCA TAGCT TAGCG TAGGA TAGGT TAGGC TAGGG
TAC TACAA TAGAT TAGAC TACAC TACAC TACTA TACTT TACTC TACTG TACCA TACCT TACCC TACCG TACGA TAGGT TAGGC TAGGG
TAGA TAGAT TAGAC TAGAC TAGAC TACTA TACTT TACTC TACTG TACCA TACCT TACCC TACCG TAGGA TAGGT TAGGC TAGGG
TAGA TAGAT TAGAC TAGAG TAGTA TAGTT TAGTC TAGTG TAGCA TAGCT TAGCC TAGGG TAGGA TAGGT TAGGC TAGGG
TAGAA TAGAT TAGAC TAGAG TAGTA TAGTT TAGTC TAGTG TAGCA TAGCT TAGCC TAGGG TAGGA TAGGT TAGGC TAGGG
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TAGAG TAGGT TAGGC TAGGG TAGGA TAGGT TAGGC TAGGA TAGGT TAGGC TAGGA TAGGT TAGGC TAGGG TAGGA TAGGT TAGGC TAGGA TAGGT TAGGT TAGGA TAGGT TAGGT TAGGC TAGGA TAGGT TAGGC TAGGA TAGGT TAGGC TAGGA TAGGT TAGGA TITAA TITAT TITAC TITAG TITTA TITTI TITTC TITTG TITCA TITCT TITCC TITCG TITGA TITGA TITGC TITGC TITGG TTC TTCAA TTCAT TTCAC TTCAG TTCTA TTCTT TTCTC TTCTG TTCCA TTCCT TTCCC TTCCG TTCGA TTCGT TTCGC TTCGG
TTG TTGAA TTGAT TTGAC TTGAG TTGTA TTGTT TTGTC TTGTG TTGCA TTGCT TTGCC TTGCG TTGGA TTGGT TTGGC TTGGG
TCA TCAAA TCAAT TCAAC TCAAG TCATA TCATT TCATC TCATG TCACA TCACA TCACG TCA
TCAAA TCAAT TCAAC TCAAG TCATA TCATT TCATC TCATG TCACA TCACA TCACT TCACC TCACG TCAGA TCAGT TCAGC TCAGG
TCT TCTAA TCTAT TCTAC TCTAG TCTTA TCTTT TCTTC TCTTG TCTCA TCTCT TCTCC TCTCG TCCCA TCCCT TCCCG TCCGA TCCTT TCACC TCAGG
TCC TCCAA TCCAT TCCAC TCCAG TCCTA TCCTT TCCTC TCCTG TCCCA TCCCT TCCCC TCCCG TCCGA TCCGT TCCGC TCCGG
TCGA TCGAT TCCAC TCCAG TCCTA TCCTT TCCTC TCCTG TCCCA TCCCT TCCCC TCCCG TCCGA TCCGT TCCGC TCCGG TCGGA
TCGAT TCGAC TCGAG TCGAT TCGAC TCGAG TCGTA TCCTT TCCTC TCCTG TCCAC TCCCG TCCGG TCGGA TCGGT TCGGC TCGGG
TGA TGAAA TGAAT TGAAC TGAAG TGATA TGATT TGATC TGATG TGACA TGACT TGACC TGACG TGAGA TGAGT TGAGC TGAGG
TGT TGTAA TGTAT TGTAC TGTAG TGTTA TGTTT TGTTC TGTTG TGTCA TGTCT TGCCC TCCCG TCCGA TGGGT TGGGC TGGGG
TGC TGCAA TGCAT TGCAC TGCAG TGCTA TGCTT TGCTC TGCTG TGCCA TGCCT TGCCC TGCCG TGCGA TGCGT TGCGC TGCGG
TGGAA TGGAT TGCAC TGCAG TGCTA TGCTT TGCTC TGCTG TGCCA TGCCT TGCCC TGCCG TGCGA TGCGT TGCGC TGCGG
CAA CAAAA CAA

CCA CCAAA CCAAT CCAAC CCAAG CCATA CCATT CCATC CCATG CCACA CCACT CCACC CCACG CCACAG CCAGA CCAGT CCAGT CCAGT CCACT CCTCAC CCACAGT CCAGT CCCAGT CCCCAGT CCAGT C

GGG GGGAA GGGAT GGGAC GGGAG GGGTA GGGTT GGGTC GGGTG GGGCA GGGCT GGGCC GGGCG GGGGA GGGGT GGGCC After filtering

After filtering: read1: quality Value of each position will be shown on mouse over.

testcommand

After filtering: read1: base contents Value of each position will be shown on mouse over.

8.0

0.7 0.6 base content ratios 0.5 0.3 0.2

After filtering: read1: KMER counting

fastp 0.21.0, at 2023-02-26 22:44:21

10 20 60 30 position

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

position

CCC CCCAA CCCAT CCCAC CCCAG CCCTA CCCTT CCCTC CCCTG CCCCA CCCCT CCCCC CCCGA CCCGT CCCGC CCCGG
CCGAA CCGAT CCCAC CCCAG CCCTA CCCTT CCGTC CCGTG CCGCA CCGCT CCGCC CCGCG CCGGA CCGGT CCGGC
CGAA CGAAA CGAAA CGAAA CGAAA CGAAA CGAAT CGATT CGATC CGATC CGATC CGATC CGACA CGACA CGACC CGACG CGAGA CGAGT CGAGC
CGT CGTAA CGTAT CGTAC CGTAG CGTTA CGTTT CGTTC CGTTG CGTCA CGTCT CGTCC CGCGG CGCGA CGGGT CGGCC
CGCAA CGCAT CGCAC CGCAG CGCTA CGCTT CGCTC CGCTG CGCCA CGCCT CGCCG CGCGA CGGGT CGCGC CGCGG
CGGAA CGCAT CGCAC CGCAG CGCTA CGCTT CGCTC CGCTG CGCCA CGCCT CGCCC CGCCG CGCGA CGGGT CGCGC CGCGG
CGGAA CGCAT CGCAC CGCAG CGCTA CGCTT CGCTC CGCTG CGCCA CGCCT CGCCC CGCCG CGCGA CGGGT CGCGC CGGGG
CAA GAAAA GAAAT GAAAC GAAAG GAATA GAATT GAATC GAATG GAACA GAACT GAACC GAACG GAAGA GAAGT GAAGC GAAGG
GAT GATAA GATAT GATAC GATAG GATTA GATTT GATTC GATTC GATCA GATCT GACCC GACCG GACGA GACGT GACGC
GACG GACAA GACAT GACAC GACAG GACTA GACTT GACTC GACTG GACCA GACCT GACCC GACCG GACGA GACGT GACGC GACGG
GAG GACAA GACAT GACAC GACAG GACTA GACTT GACTC GACTG GACCA GACCT GACCC GACCG GACGA GACGT GACGC GACGG
GAGAA GACAA GACAT GACAC GACAG GACTA GACTT GACTC GACTG GACCA GACCT GACCC GACCG GACGA GACGT GACGC GACGG
GAGAA GACAA GACAT GACAC GACAG GACTA GACTT GACTC GACTG GACCA GACCT GACCC GACCG GACGA GACGT GACGC GACGG
GAGAA GACAA GACAT GACAC GACAG GACTA GACTT GACTC GACTG GACCA GACCT GACCC GACCG GACGA GACGT GACGC GACGG
GAGAA GACAA GACAT GACAC GACAG GACTA GACTT GACTC GACTC GACCC GACCG GACGA GACGT GACGC GACGG
GAGAA GACAA GACAT GACAC GACAG GACTA GACTT GACTC GACTC GACCC GACCG GACGA GACGT GACGC GACGG
GACAA GACAA GACAT GACAC GACAG GACTA GACTT GACTC GACCC GACCG GACGA GACGT GACGC GACGG
GACAA GACAA GACAT GACAC GACAC GACAT GACTT GACTC GACCC GACCG GACGA GACGT GACGC GACGG
GACAA GACAT GACAC GACAC GACAT GACTT GACCC GACCG GACCA GACCT GACCC GACGA GACGT GACCC GACGA GACGT GACGC GACGA GACGT GACGC GACGA GACGT GACCC GACGA GACGT GACCC GACGA GACGT GACCC GACGA GACGT GACCC GACGA GACGT GACGC GACGA GACGT GACCC GACGA

GTT GTTAA GTTAT GTTAC GTTAG GTTTA GTTTT GTTTC GTTG GTTCA GTTCT GTTCC GTTCG GTTCA GTTCT GTTCC GTTCG GTTCA GTTCT GTTCC GTTCG GTTCA GTTCT GTTCC GTTCG GTTCA GTTCT GTTCC GTTCC GTCCA GTCCT GTCCC GTCCA GTCCA GTCCT GTCCC GTCCA GTCCA GTCCT GTCCC GTCCA GTC GGC GGCAA GGCAT GGCAC GGCAG GGCTA GGCTT GGCTC GGCTG GGCCA GGCCC GGCCG GGCGA GGCGT GGCCC GGCGG
GGG GGGAA GGGAT GGGAC GGGAA GGGTT GGGTT GGGTC GGGTG GGGCA GGGCT GGGCC GGGGA GGGGT GGGCC GGGGG