

fastp report

Summary

General

fastp version:	0.23.2 (https://github.com/OpenGene/fastp)
sequencing:	paired end (101 cycles + 101 cycles)
mean length before filtering:	101bp, 101bp
mean length after filtering:	100bp, 100bp
duplication rate:	0.492627%
Insert size peak:	171

Before filtering

total reads:	67.671844 M
total bases:	6.834856 G
Q20 bases:	6.212100 G (90.888522%)
Q30 bases:	5.657187 G (82.769655%)
GC content:	45.621445%

After filtering

total reads:	60.743926 M
total bases:	6.103671 G
Q20 bases:	5.795487 G (94.950852%)
Q30 bases:	5.333758 G (87.386072%)
GC content:	45.052993%

Filtering result

reads passed filters:	60.743926 M (89.762481%)
reads with low quality:	6.895254 M (10.189251%)
reads with too many N:	32.664000 K (0.048268%)
reads too short:	0 (0.000000%)

Adapters

Adapter or bad ligation of read1

The input has little adapter percentage (~0.467199%), probably it's trimmed before.

Sequence	Occurrences
all adapter sequences	410428

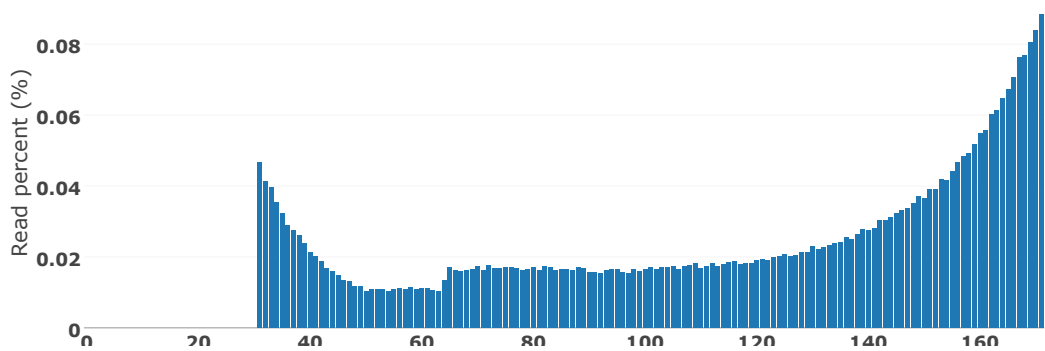
Adapter or bad ligation of read2

The input has little adapter percentage (~0.467199%), probably it's trimmed before.

Sequence	Occurrences
all adapter sequences	410428

Insert size estimation

Insert size distribution (96.407660% reads are with unknown length)



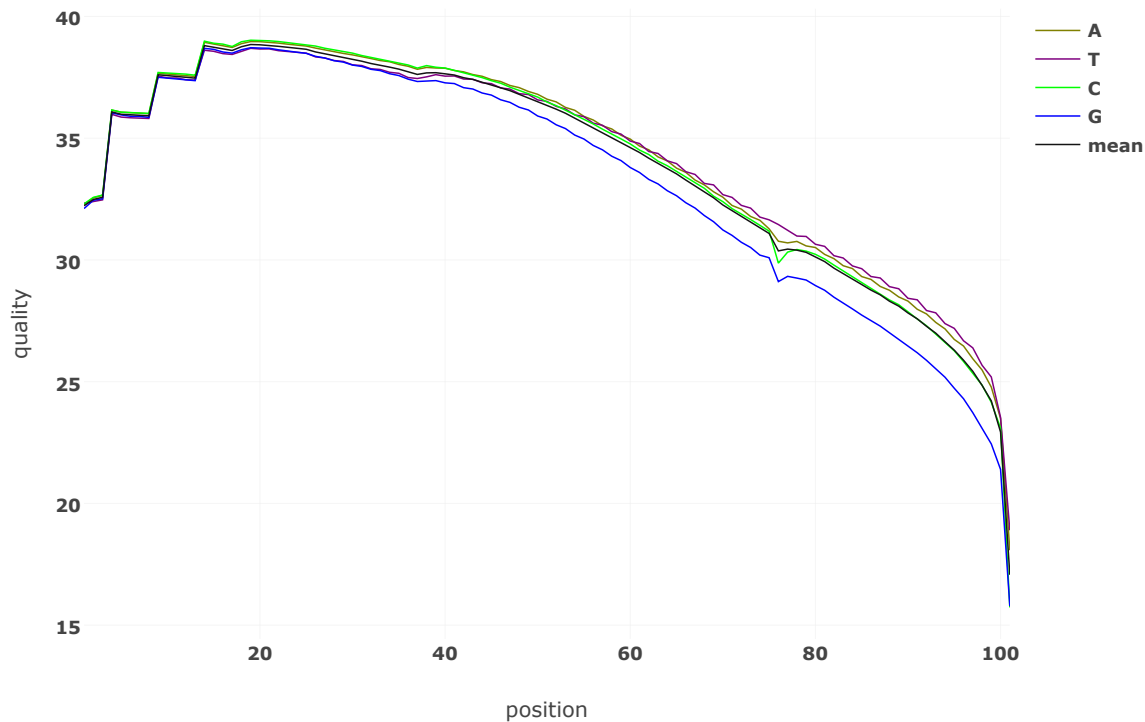
Insert size

This estimation is based on paired-end overlap analysis, and there are 96.407660% reads found not overlapped.
The nonoverlapped read pairs may have insert size <30 or >172, or contain too much sequencing errors to be detected as overlapped.

Before filtering

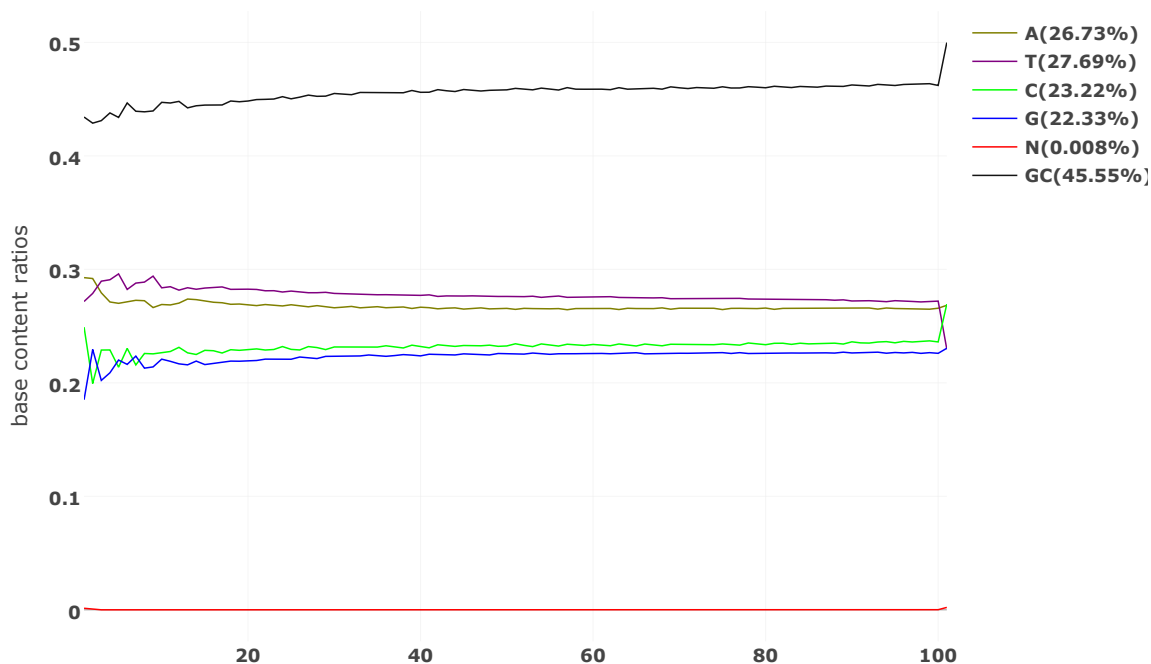
Before filtering: read1: quality

Value of each position will be shown on mouse over.



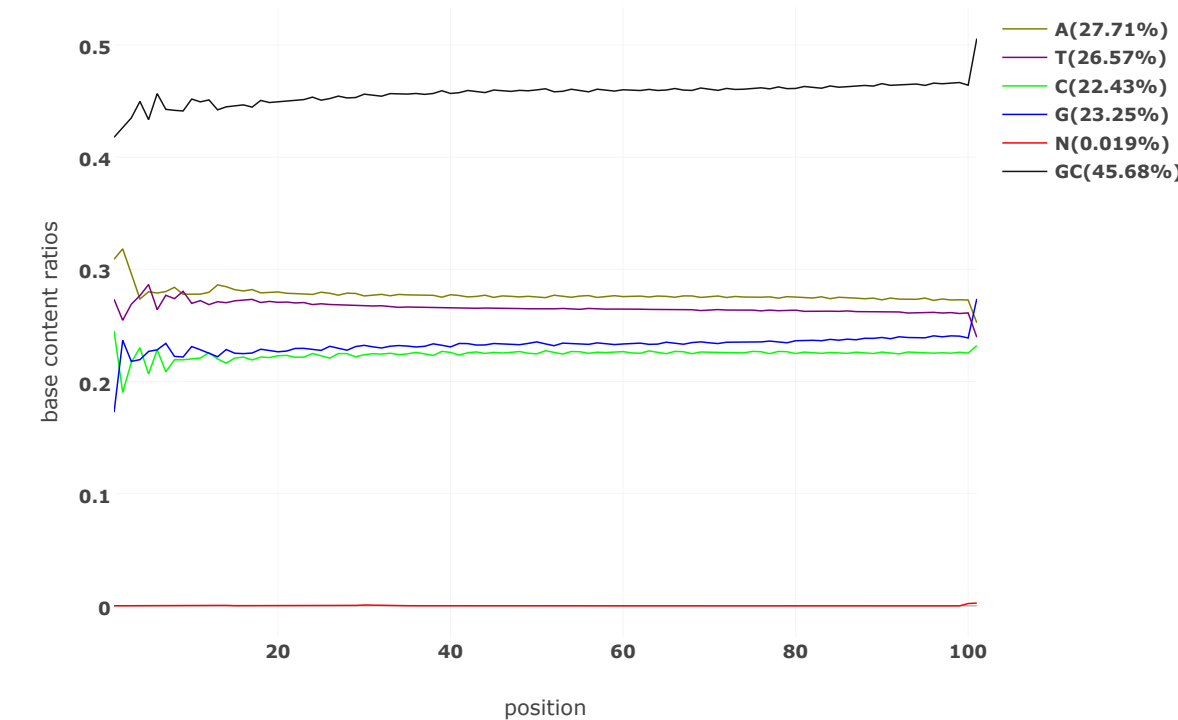
Before filtering: read1: base contents

Value of each position will be shown on mouse over.



Before filtering: read2: base contents

Value of each position will be shown on mouse over.



Before filtering: read2: KMER counting

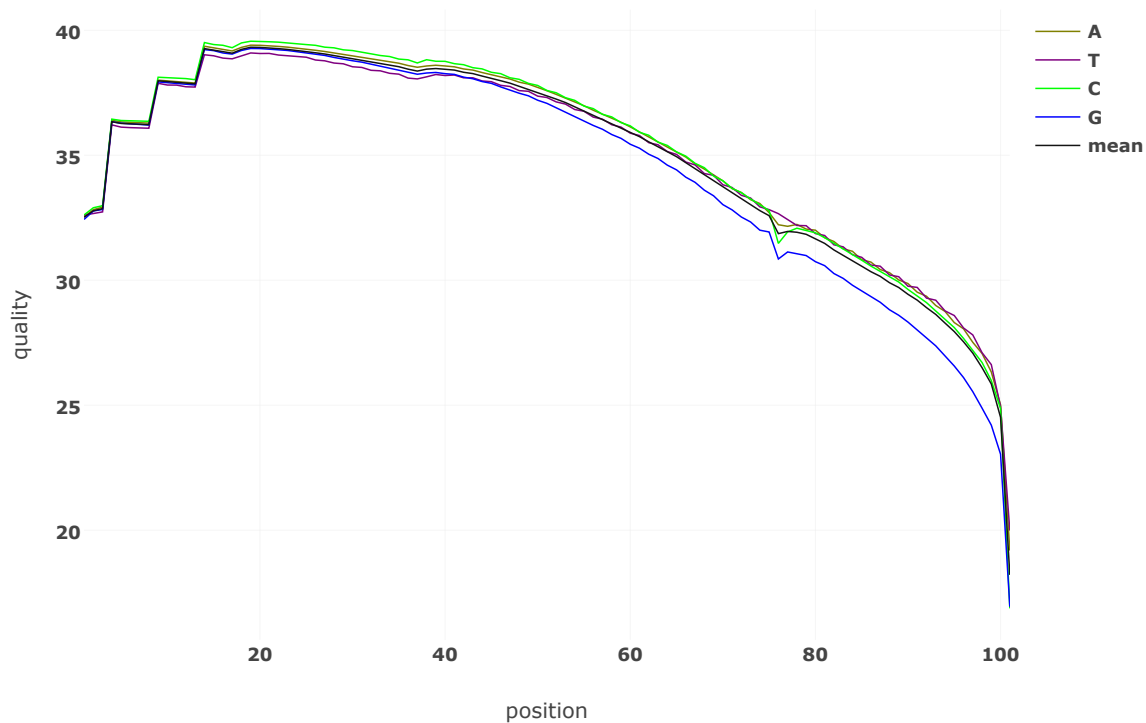
Darker background means larger counts. The count will be shown on mouse over.

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After filtering

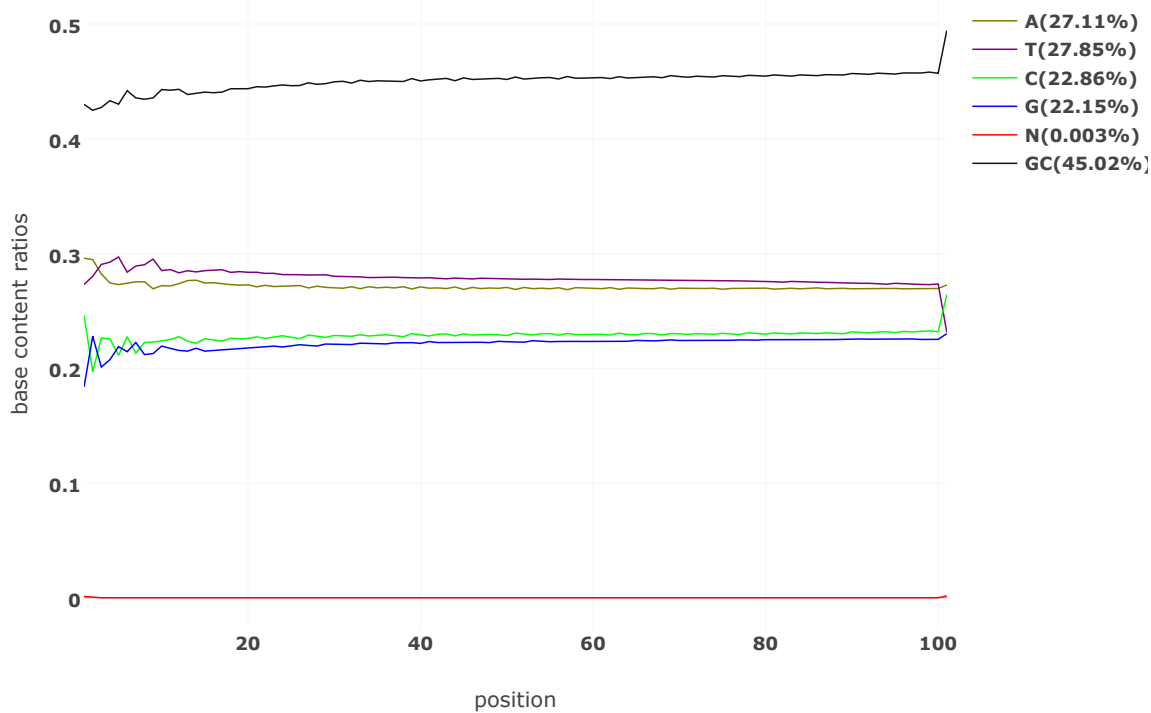
After filtering: read1: quality

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.



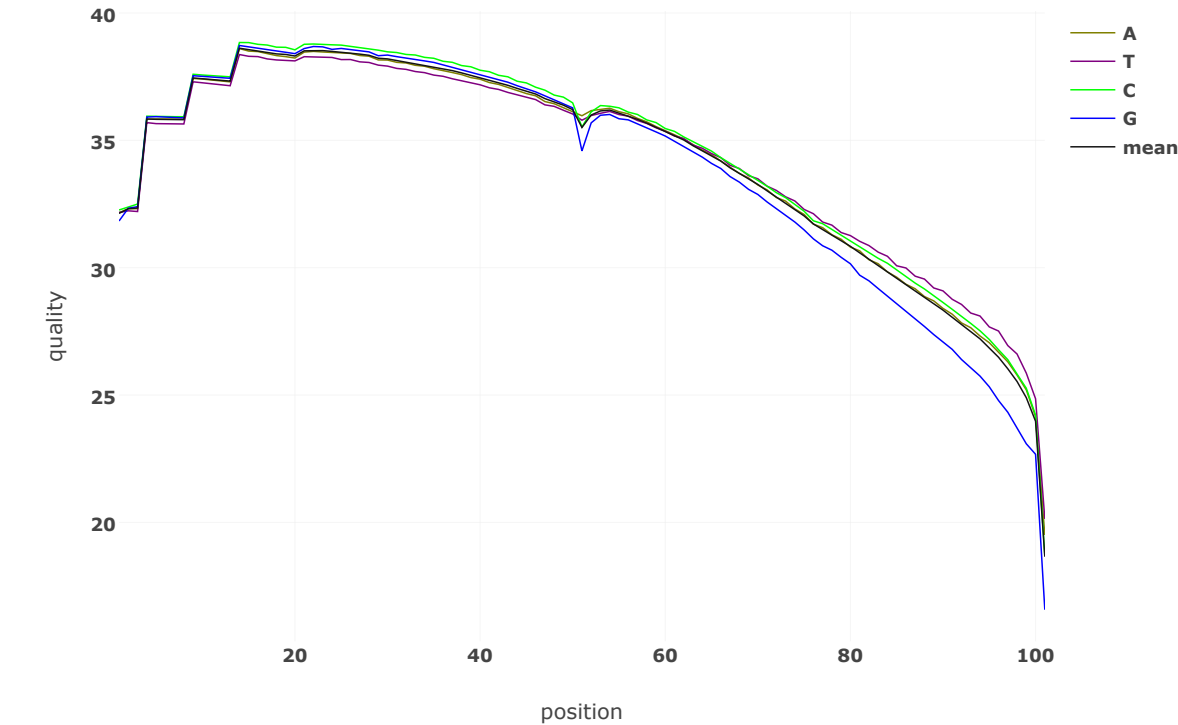
After filtering: read1: KMER counting

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
AAA	AAAAA	AAAT	AAAC	AAAG	AAATA	AAATT	AAATC	AAATG	AAACA	AAACT	AAACC	AAACG	AAAGA	AAAGT	AAAGC	AAAGG
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GAT	GATAA	GATAT	GATAC	GATAG	GATTA	GATTT	GATTC	GATTG	GATCA	GATCT	GATCC	GATCG	GATGA	GATGT	GATGC	GATGG
GAC	GACAA	GACAT	GACAC	GACAG	GACTA	GACTT	GACTC	GACTG	GACCA	GACCT	GACCC	GACCG	GACGA	GACGT	GACGC	GACGG
GAG	GAGAA	GAGAT	GAGAC	GAGAG	GAGTA	GAGTT	GAGTC	GAGTG	GAGCA	GAGCT	GAGCC	GAGCG	GAGGA	GAGGT	GAGGC	GAGGG
GTA	GTAATA	GTAAT	GTAAC	GTAAG	GTATA	GTATT	GTATC	GTAATG	GTACA	GTACT	GTACC	GTACG	GTAGA	GTAGT	GTAGC	GTAGG
GTT	GTTAA	GTTAT	GTTAC	GTTAG	GTTTA	GTTTT	GTTTC	GTTTG	GTTCA	GTTCT	GTTCC	GTTCG	GTTGA	GTTGT	GTTGC	GTTGG
GTC	GTCAA	GTCAT	GTCA	GTCAG	GICTA	GICTT	GICTC	GICTG	GTCCA	GTCCT	GTC	GTCG	GTCGA	GTCGT	GTCGC	GTCGG
GTG	GTGAA	GTGAT	GTGAC	GTGAG	GICTA	GICTT	GICTC	GTGTG	GTGCA	GTGCT	GTGCC	GTGCG	GTGGA	GTGGT	GTGGC	GTGGG
GCA	GCAAA	GCAAT	GCAAC	GCAAG	GCATA	GCATT	GCATC	GCAATG	GCACA	GCACT	GCA	GCA	GCA	GCA	GCA	GCA
GCT	GCTAA	GCTAT	GCTAC	GCTAG	GCTTA	GCTTT	GCTTC	GCTTG	GCTCA	GCTCT	GCTCC	GCTCG	GCTGA	GCTGT	GCTGC	GCTGG
GCC	GCCAA	GCCAT	GCCAC	GCCAG	GCCTA	GCCTT	GCCTC	GCCTG	GCCCA	GCCCT	GCC	GCC	GCC	GCC	GCC	GCC
GCG	GCGAA	GCGAT	GCGAC	GCGAG	GCGTA	GCGTT	GCGTC	GCGTG	GCGCA	GCGCT	GCGCC	GCGCG	GCGGA	GCGGT	GCGGC	GCGGG
GGA	GGAATA	GGAAT	GGAAC	GGAAG	GGATA	GGATT	GGATC	GGAATG	GGACA	GGACT	GGACC	GGACG	GGAGA	GGAGT	GGAGC	GGAGG
GGT	GGTAA	GGTAT	GGTAC	GGTAG	GGTTA	GGTTT	GGTTC	GGTTG	GGTCA	GGTCT	GGTCC	GGTCG	GGTGA	GGTGT	GGTGC	GGTGG
GGC	GGCAA	GGCAT	GGCAC	GGCAG	GGCTA	GGCTT	GGCTC	GGCTG	GGCCA	GGCCT	GGCCC	GGCCG	GGCGA	GGCGT	GGCGC	GGCGG
GGG	GGGAA	GGGAT	GGGAC	GGGAG	GGGTA	GGGTT	GGGTC	GGGTG	GGGCA	GGGCT	GGGCC	GGGCG	GGGGA	GGGGT	GGGGC	GGGGG

After filtering: read2: quality

Value of each position will be shown on mouse over.



After filtering: read2: base contents

Value of each position will be shown on mouse over.

