Rfastp Report

Summary

General		
fastp version:	0.21.0 (https://github.com/0penGene/fastp)	
sequencing:	single end (148 cycles)	
mean length before filtering:	148bp	
mean length after filtering:	97bp	
duplication rate:	9.846651% (may be overestimated since this is SE data)	
Detected read1 adapter:	AGATCGGAAGACCACGTCTGAACTCCAGTCA	

Before filtering	
total reads:	25.004969 M
total bases:	3.700735 G
Q20 bases:	3.382553 G (91.402172%)
Q30 bases:	3.203913 G (86.575036%)

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Q30 bases:	3.203913 G (86.575036%)
GC content:	53.916375%
After filtering	

total reads:	24.408531 M
total bases:	2.377710 G
Q20 bases:	2.263740 G (95.206721%)
Q30 bases:	2.191686 G (92.176299%)
GC content:	55.104335%

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Q30 bases:	2.191686 G (92.176299%)
GC content:	55.104335%
Filtering result	

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reads passed filters:	24.408531 M (97.614722%)
reads with low quality:	558.815000 K (2.234816%)
reads with too many N:	4.633000 K (0.018528%)

32.990000 K (0.131934%)

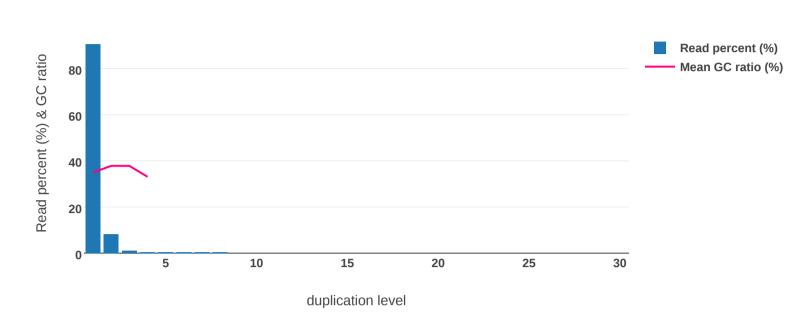
Adapters

reads too short:

Adapter or bad ligation of read1				
Sequence	Occurrences			
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACACAGTGATCTCGTATGCCGTCTTCTGCTTGAAAAA	201799			
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACACAGTGATCTCGTATGCCGTCTTCTGCTTGAAAAAAAA	202477			
other adapter sequences	19621711			

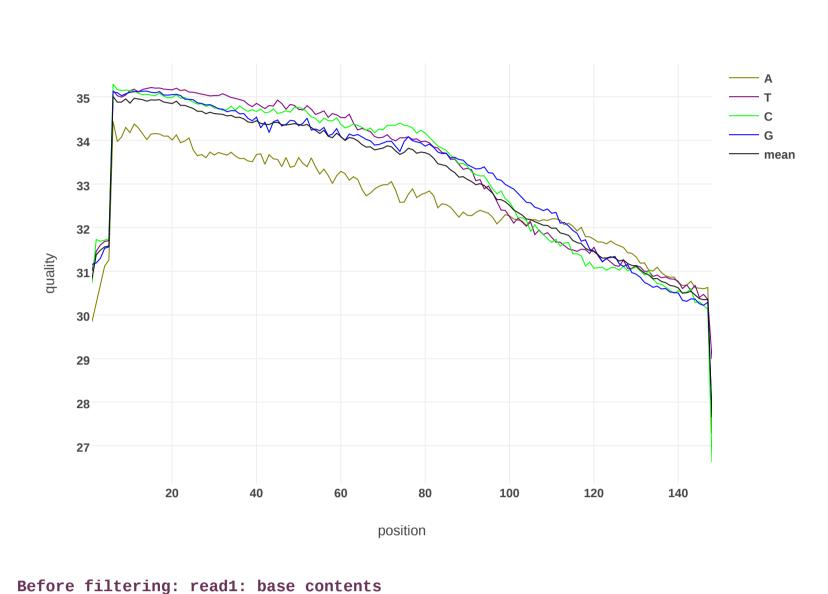
other adapter sequences **Duplication**

duplication rate (9.846651%)

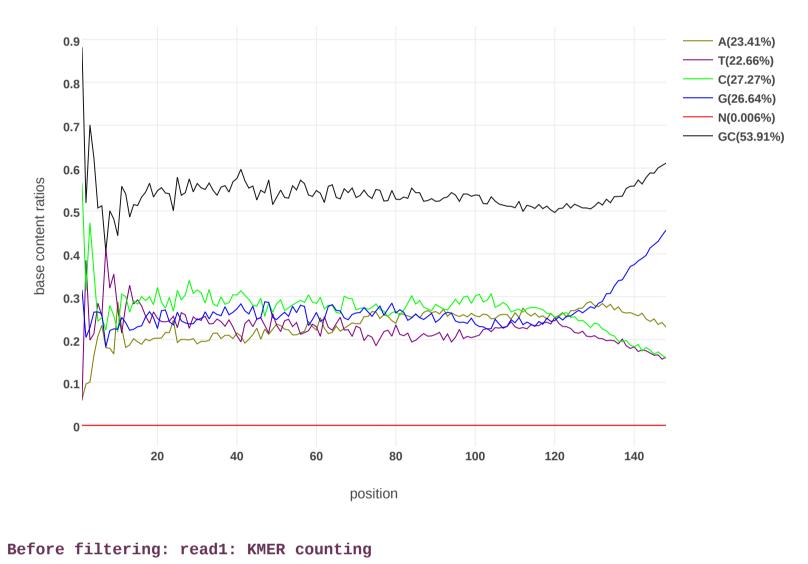


Before filtering

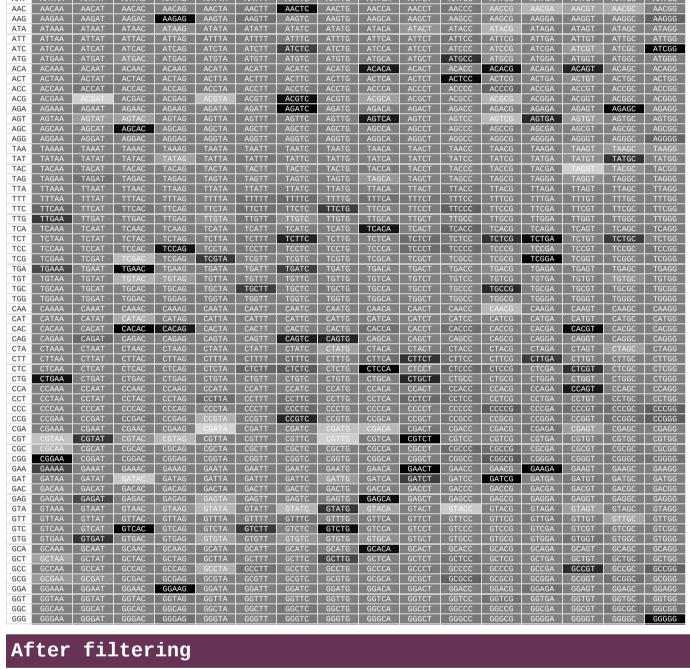
Before filtering: read1: quality Value of each position will be shown on mouse over.



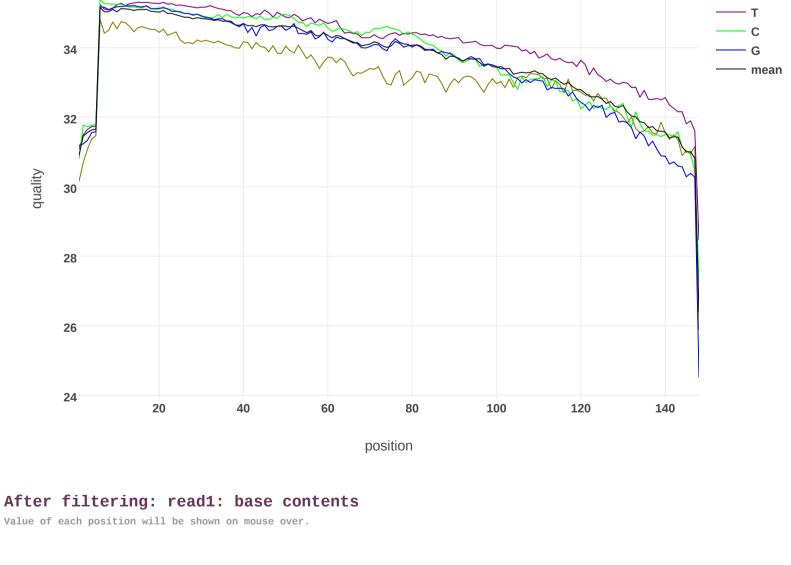
Value of each position will be shown on mouse over.



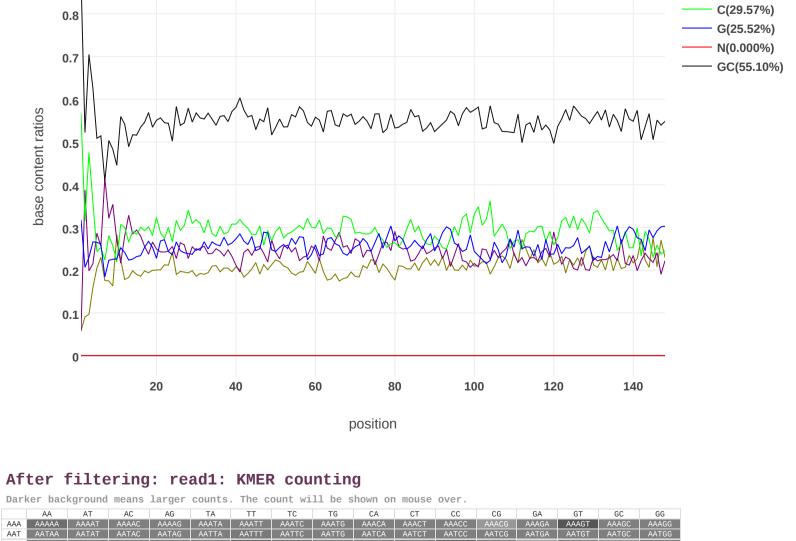
Darker background means larger counts. The count will be shown on mouse over. AA AT AC AG TA TT TC TG CA CT CC CG GA GT GC GG AAA AAAAA AAAAT AAAAC AAAAG AAATA AAATT AAATC AAATG AAACA AAACT AAACC AAAAG AAAGT AAAGC AAAGG AAT AATAA AATAT AATAC AATAG AATTA AATTT AATTC AATTG AATCA AATCT AATCC AATCG AATCG AATGA AATGT AATGC AATGG AAC AACAA AACAT AACAC AACAG AACTA AACTT AACTC AACTG AACCG AACCG AACCG AACGG AACGA AACGT AACGC AACGG AACAA AACAT AACAC AACAG AACTA AACTT AACTC AACTG AACTG AACCG AACCG AACCG AACGG AACGA AACGT AACGC AACGG



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



0.9



A(20.07%) — T(24.82%)

