Rfastp Report

Summary

General

fastp version:	0.21.0 (https://github.com/OpenGene/fastp)
sequencing:	single end (148 cycles)
mean length before filtering:	148bp
mean length after filtering:	125bp
duplication rate:	8.415952% (may be overestimated since this is SE data)
Detected read1 adapter:	AGATCGGAAGAGCACACGTCTGAACTCCAGTCA

Before filtering

total reads:	53.589419 M
total bases:	7.931234 G
Q20 bases:	7.433562 G (93.725169%)
Q30 bases:	7.071094 G (89.155024%)
GC content:	51.083613%

After filtering

total reads:	52.771983 M
total bases:	6.629240 G
Q20 bases:	6.286434 G (94.828872%)
Q30 bases:	6.032528 G (90.998783%)
GC content:	50.931999%

Filtering result

reads passed filters:	52.771983 M (98.474632%)
reads with low quality:	558.239000 K (1.041696%)
reads with too many N:	11.759000 K (0.021943%)
reads too short:	247.438000 K (0.461729%)

Adapters

Adapter or bad ligation of read1

Sequence	Occurrences
AGATC	507892
AGATCG	476365
AGATCGG	477865
AGATCGGA	465868
AGATCGGAA	478521
AGATCGGAAG	442603
AGATCGGAAGA	438053
AGATCGGAAGAG	423788
AGATCGGAAGAGC	488170
AGATCGGAAGAGCA	477831
AGATCGGAAGAGCAC	503833
AGATCGGAAGAGCACA	460270
AGATCGGAAGAGCACAC	535177
AGATCGGAAGAGCACACG	549728
AGATCGGAAGAGCACACGT	618479
AGATCGGAAGAGCACACGTC	541550
AGATCGGAAGAGCACACGTCT	597706
AGATCGGAAGAGCACACGTCTG	500289
AGATCGGAAGAGCACACGTCTGA	525825
AGATCGGAAGAGCACACGTCTGAA	609425
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AGATCGGAAGAGCACACGTCTGAACT	517702
AGATCGGAAGAGCACACGTCTGAACTC	628250
AGATCGGAAGAGCACACGTCTGAACTCC	615639
AGATCGGAAGAGCACACGTCTGAACTCCA	558211
AGATCGGAAGAGCACACGTCTGAACTCCAG	582815
AGATCGGAAGAGCACACGTCTGAACTCCAGT	619184
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AGATCGGAAGAGCACACGTCTGAACTCCAGTCACTGACC	430184
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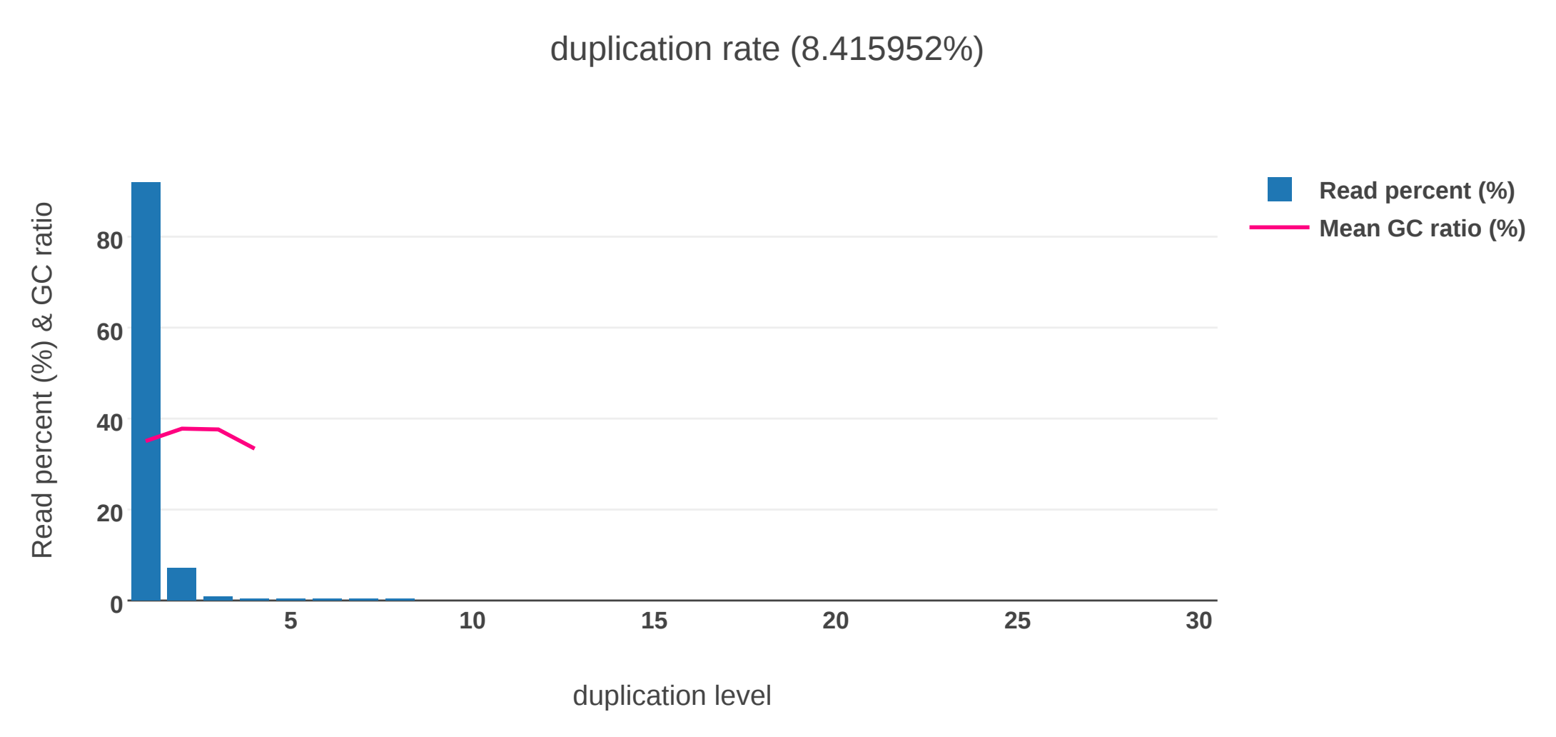
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACTGACCAAT	442971
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACTGACCAATCT	365093
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACTGACCAATCTC	359918
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACTGACCAATCTCG	345043
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACTGACCAATCTCGT	336882
other adapter sequences	11746438

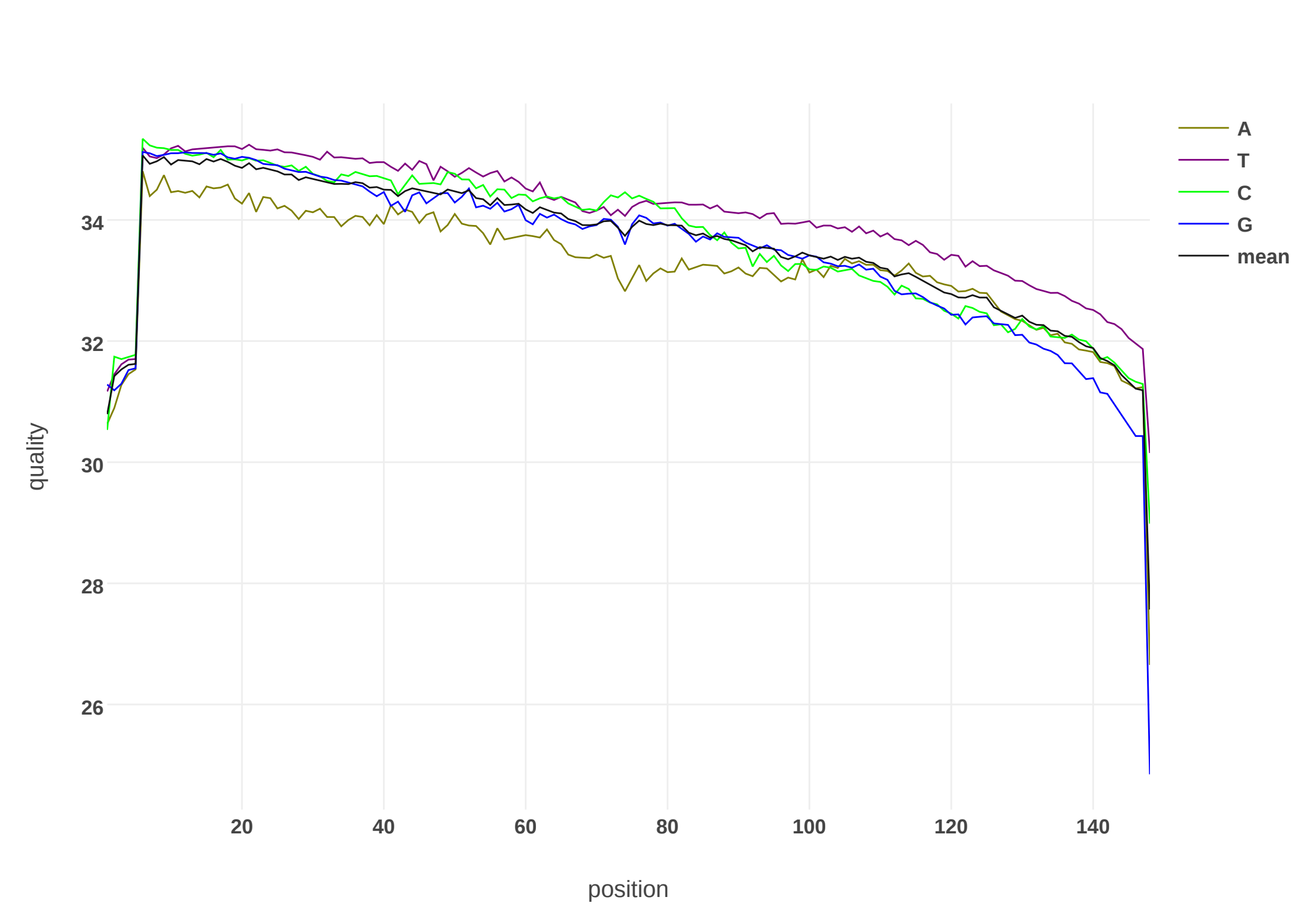
Duplication



Before filtering

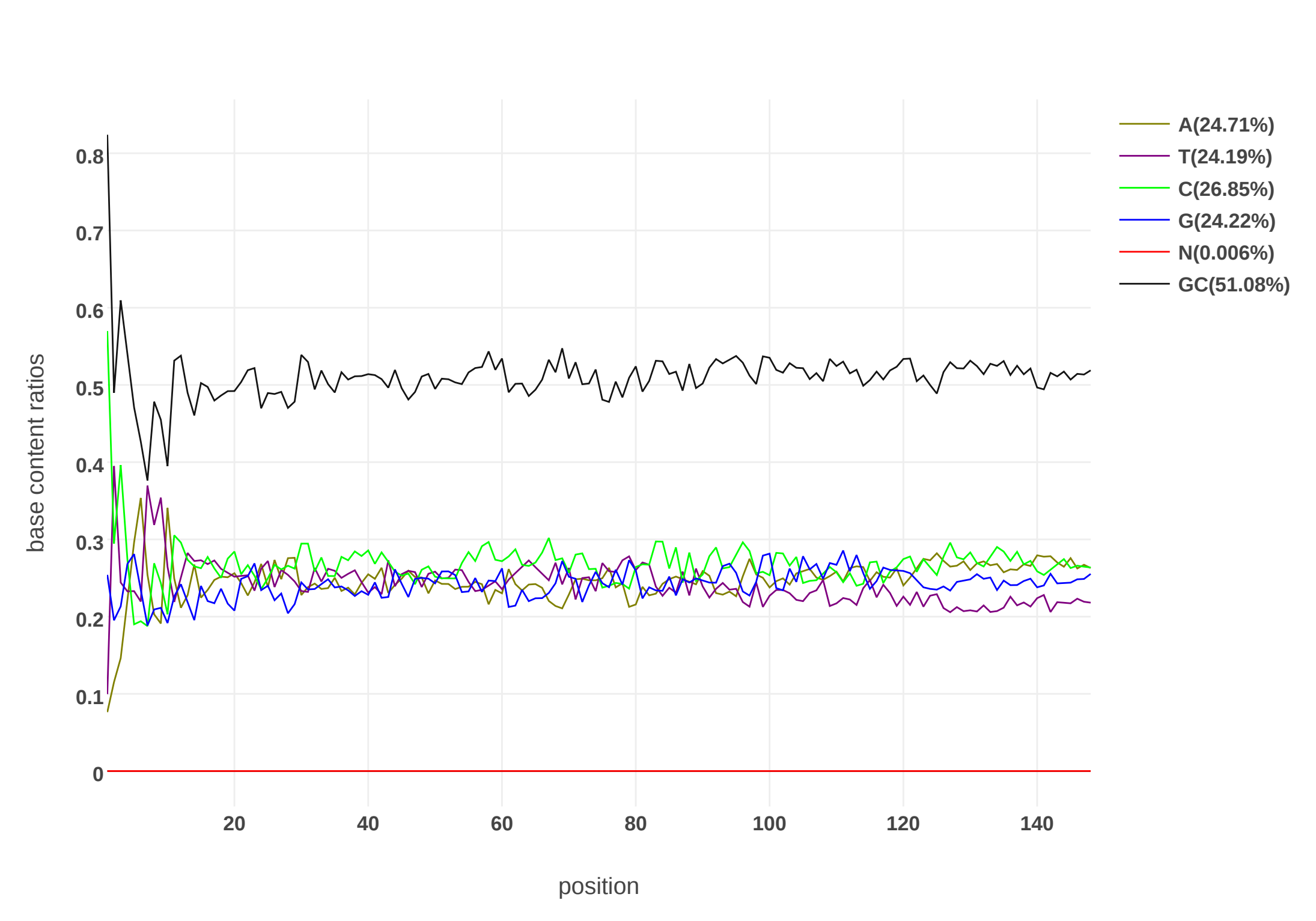
Before filtering: read1: quality

Value of each position will be shown on mouse over.



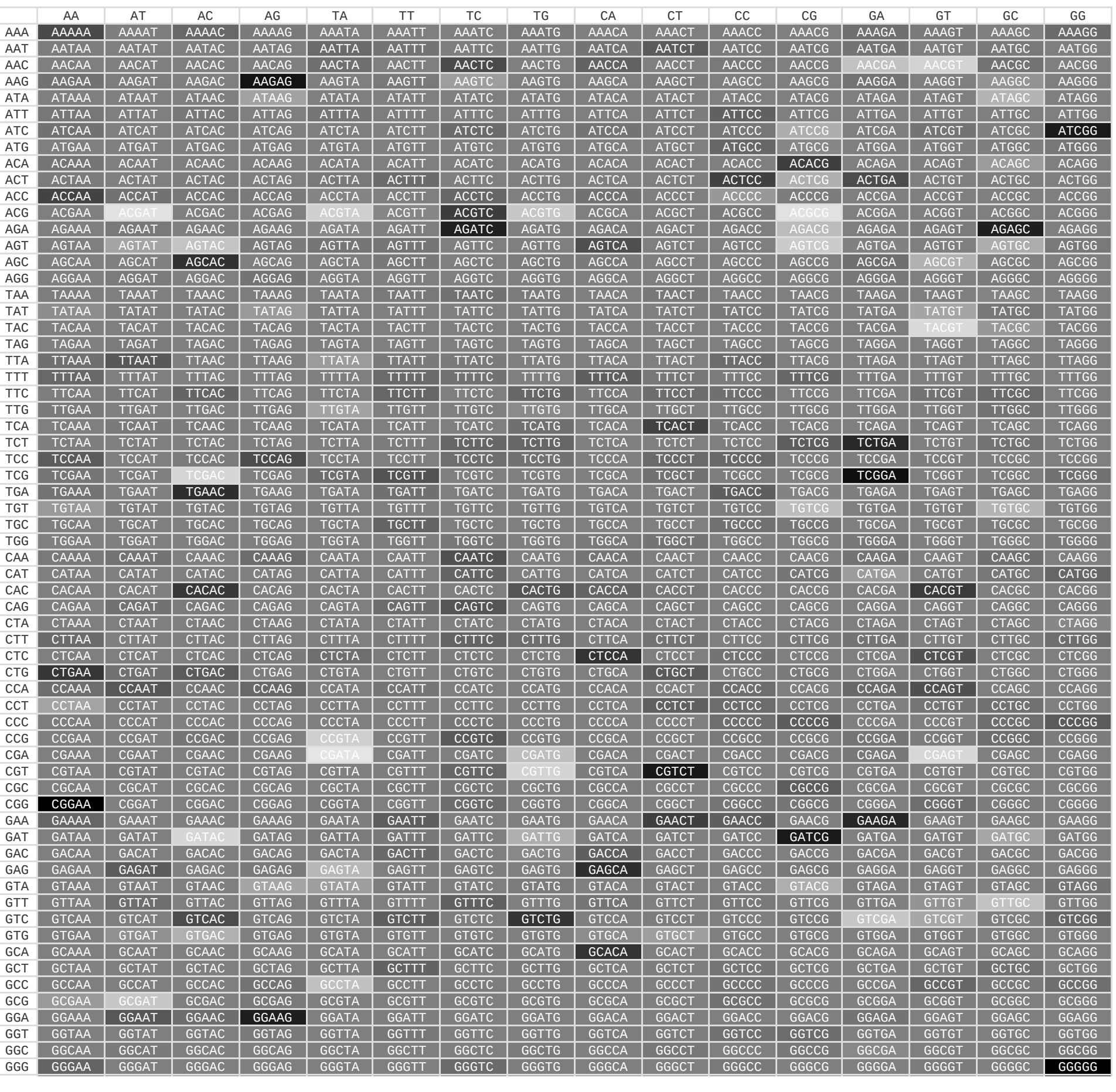
Before filtering: read1: base contents

Value of each position will be shown on mouse over.



Before filtering: read1: KMER counting

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



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ATA	ATAAA	ATAAT	ATAAC	ATAAG	ATATA	ATATT	ATATC	ATATG	ATACA	ATACT	ATACC	ATACG	ATAGA	ATAGT	ATAGC	ATAGG
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ATC	ATCAA	ATCAT	ATCAC	ATCAG	ATCTA	ATCTT	ATCTC	ATCTG	ATCCA	ATCCT	ATCCC	ATCCG	ATCGA	ATCGT	ATCGC	ATCGG
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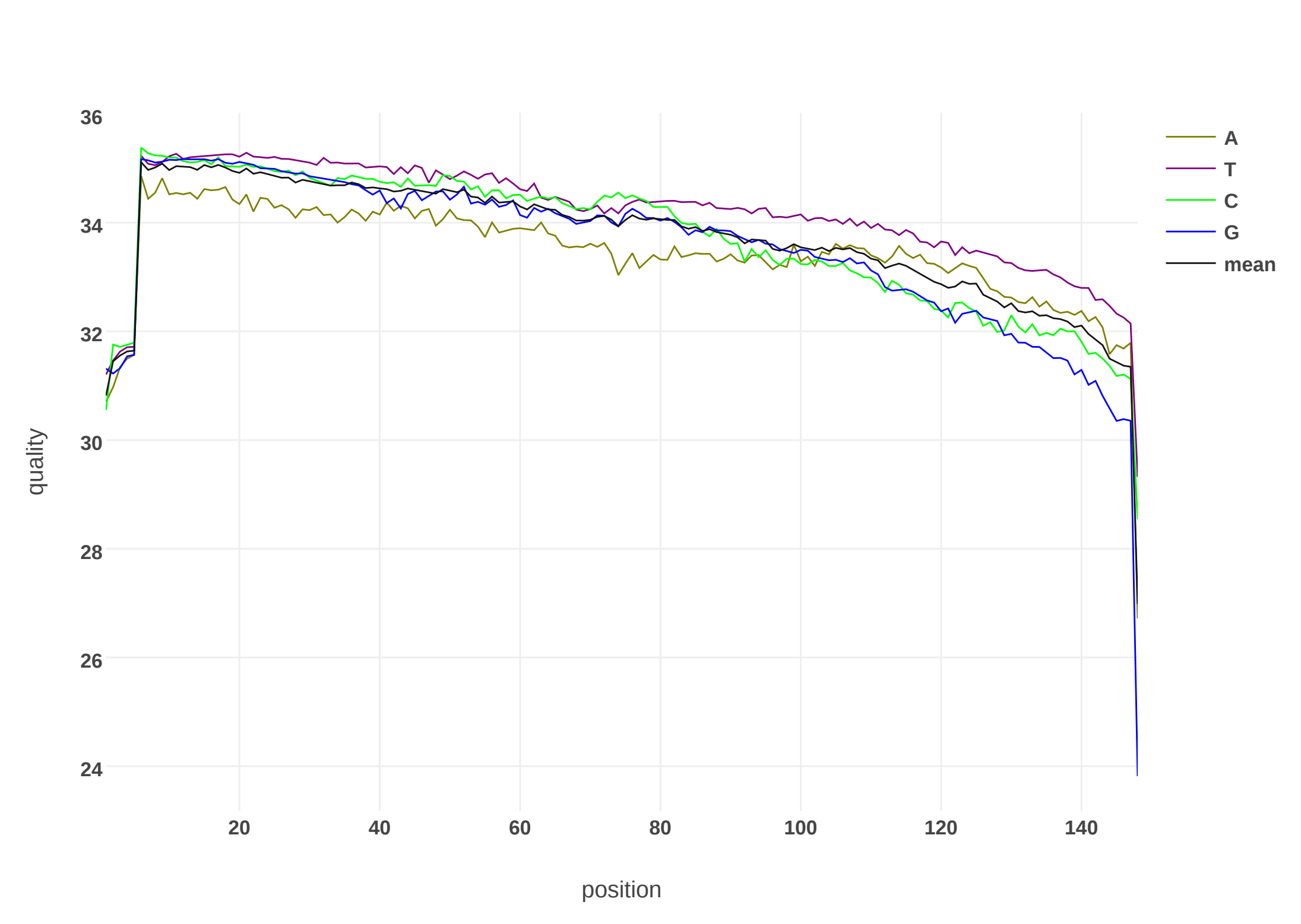
GGG	GGGAA	GGGAT	GGGAC	GGGAG	GGGTA	GGGTT	GGGTC	GGGTG	GGGCA	GGGCT	GGGCC	GGGCG	GGGGA	GGGGT	GGGGC	GGGGG

After filtering

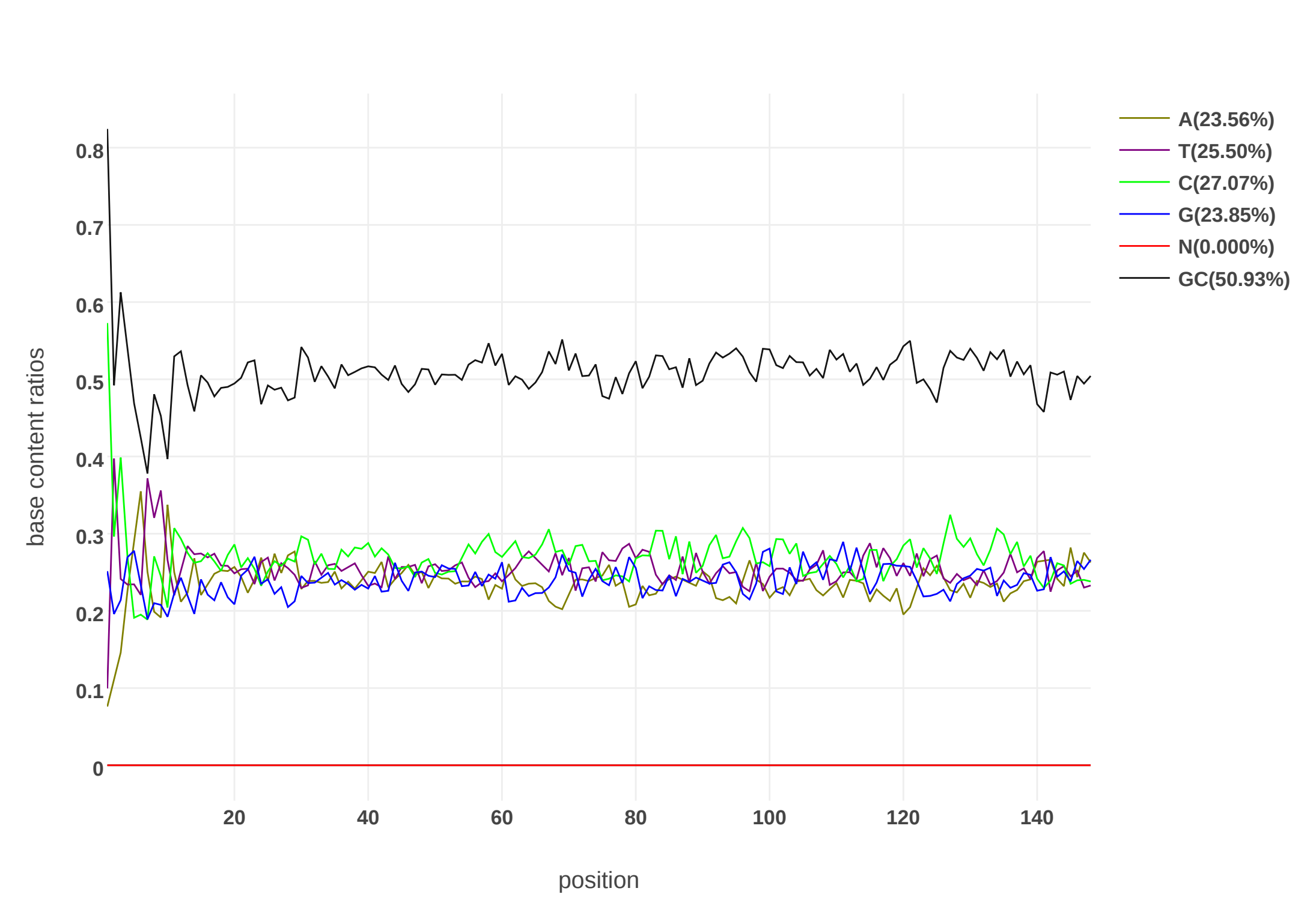
After filtering: read1: quality

Value of each position will be shown on mouse over.



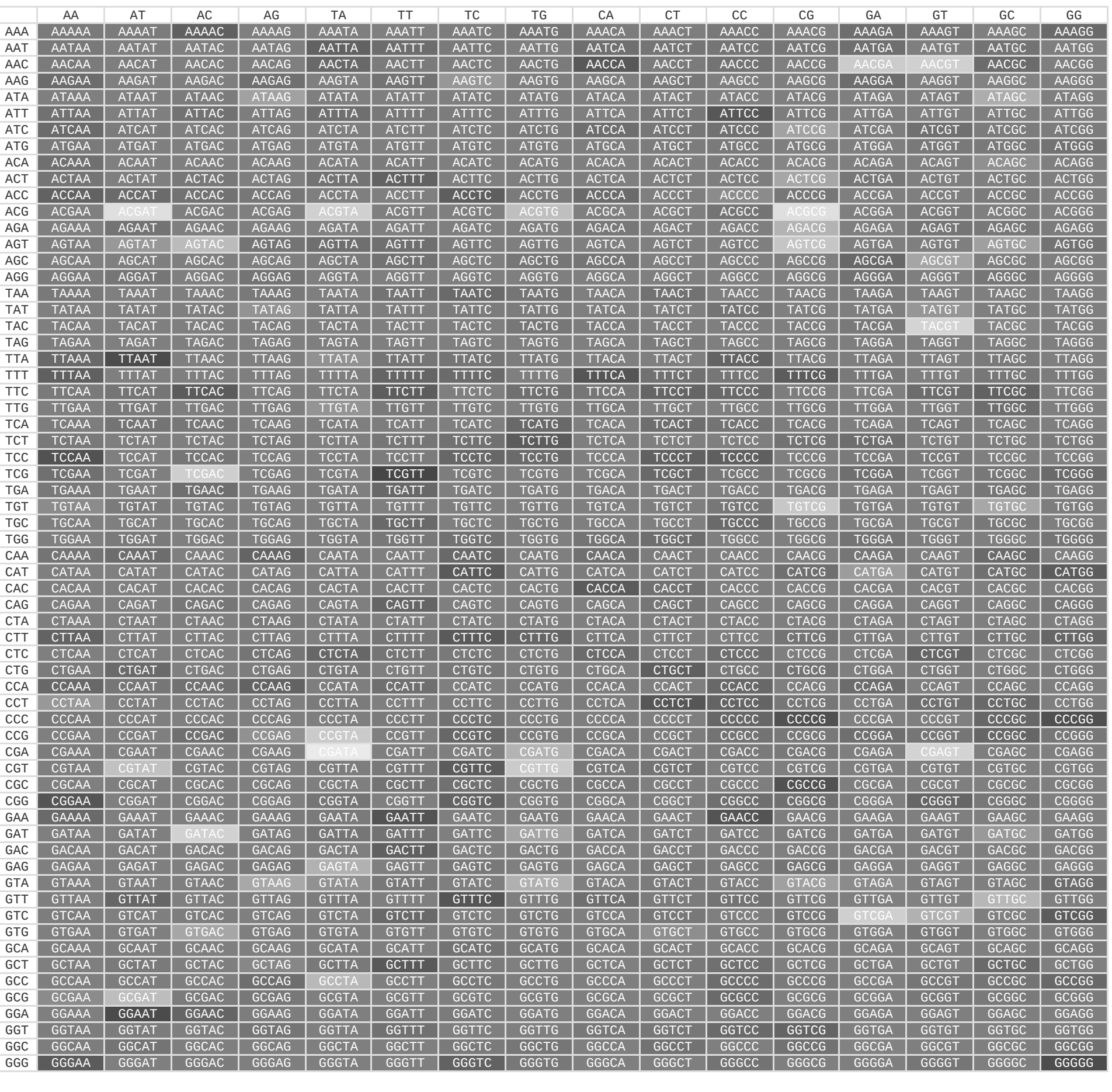
After filtering: read1: base contents

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.



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CTA	CTAAA	CTAAT	CTAAC	CTAAG	CTATA	CTATT	CTATC	CTATG	CTACA	CTACT	CTACC	CTACG	CTAGA	CTAGT	CTAGC	CTAGG
CTT	CTTAA	CTTAT	CTTAC	CTTAG	CTTTA	CTTTT	CTTTC	CTTTG	CTTCA	CTTCT	CTTCC	CTTCG	CTTGA	CTTGT	CTTGC	CTTGG
CTC	CTCAA	CTCAT	CTCAC	CTCAG	CTCTA	CTCTT	CTCTC	CTCTG	CTCCA	CTCCT	CTCCC	CTCCG	CTCGA	CTCGT	CTCGC	CTCGG
CTG	CTGAA	CTGAT	CTGAC	CTGAG	CTGTA	CTGTT	CTGTC	CTGTG	CTGCA	CTGCT	CTGCC	CTGCG	CTGGA	CTGGT	CTGGC	CTGGG
CCA	CCAAA	CCAAT	CCAAC	CCAAG	CCATA	CCATT	CCATC	CCATG	CCACA	CCACT	CCACC	CCACG	CCAGA	CCAGT	CCAGC	CCAGG
CCT	CCTAA	CCTAT	CCTAC	CCTAG	CCTTA	CCTTT	CCTTC	CCTTG	CCTCA	CCTCT	CCTCC	CCTCG	CCTGA	CCTGT	CCTGC	CCTGG
CCC	CCCAA	CCCAT	CCCAC	CCCAG	CCCTA	CCCTT	CCCTC	CCCTG	CCCCA	CCCCT	CCCCC	CCCCG	CCCGA	CCCGT	CCCGC	CCCGG
CCG	CCGAA	CCGAT	CCGAC	CCGAG	CCGTA	CCGTT	CCGTC	CCGTG	CCGCA	CCGCT	CCGCC	CCGCG	CCGGA	CCGGT	CCGGC	CCGGG
CGA	CGAAA	CGAAT	CGAAC	CGAAG	CGATA	CGATT	CGATC	CGATG	CGACA	CGACT	CGACC	CGACG	CGAGA	CGAGT	CGAGC	CGAGG
CGT	CGTAA	CGTAT	CGTAC	CGTAG	CGTTA	CGTTT	CGTTC	CGTTG	CGTCA	CGTCT	CGTCC	CGTCG	CGTGA	CGTGT	CGTGC	CGTGG
CGC	CGCAA	CGCAT	CGCAC	CGCAG	CGCTA	CGCTT	CGCTC	CGCTG	CGCCA	CGCCT	CGCCC	CGCCG	CGCGA	CGCGT	CGCGC	CGCGG
CGG	CGGAA	CGGAT	CGGAC	CGGAG	CGGTA	CGGTT	CGGTC	CGGTG	CGGCA	CGGCT	CGGCC	CGGCG	CGGGA	CGGGT	CGGGC	CGGGG
GAA	GAAAA	GAAAT	GAAAC	GAAAG	GAATA	GAATT	GAATC	GAATG	GAACA	GAACT	GAACC	GAACG	GAAGA	GAAGT	GAAGC	GAAGG
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	GTAAA	GTAAT	GTAAC	GTAAG	GTATA	GTATT	GTATC	GTATG	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	GTCAC	GTCAG	GTCTA	GTCTT	GTCTC	GTCTG	GTCCA	GTCCT	GTCCC	GTCCG	GTCGA	GTCGT	GTCGC	GTCGG
GTG	GTGAA	GTGAT	GTGAC	GTGAG	GTGTA	GTGTT	GTGTC	GTGTG	GTGCA	GTGCT	GTGCC	GTGCG	GTGGA	GTGGT	GTGGC	GTGGG
GCA	GCAAA	GCAAT	GCAAC	GCAAG	GCATA	GCATT	GCATC	GCATG	GCACA	GCACT	GCACC	GCACG	GCAGA	GCAGT	GCAGC	GCAGG
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	GCCCC	GCCCG	GCCGA	GCCGT	GCCGC	GCCGG
GCG	GCGAA	GCGAT	GCGAC	GCGAG	GCGTA	GCGTT	GCGTC	GCGTG	GCGCA	GCGCT	GCGCC	GCGCG	GCGGA	GCGGT	GCGGC	GCGGG
GGA	GGAAA	GGAAT	GGAAC	GGAAG	GGATA	GGATT	GGATC	GGATG	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

testcommand

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