

sequencing:	single end (120 cycles)
mean length before filtering:	126bp
mean length after filtering:	95bp
duplication rate:	42.000587% (may be overestimated since this is SE data)
Detected read1 adapter:	AGATCGGAAGAGCACACGTCTGAACTCCAGTCA

Before filtering

total reads:	31.984509 M
total bases:	4.830056 G

GC content:	60.681488%
After filtering	
total reads:	31.747571 M
total bases:	3.036475 G
Q20 bases:	2.978715 G (98.097790%)
Q30 bases:	2.871628 G (94.571102%)

reads passed filters:	31.747571 M (99.259824%)
reads with low quality:	79.380000 K (0.248182%)
reads with too many N:	11.520000 K (0.036017%)
reads too short:	146.098000 K (0.456777%)

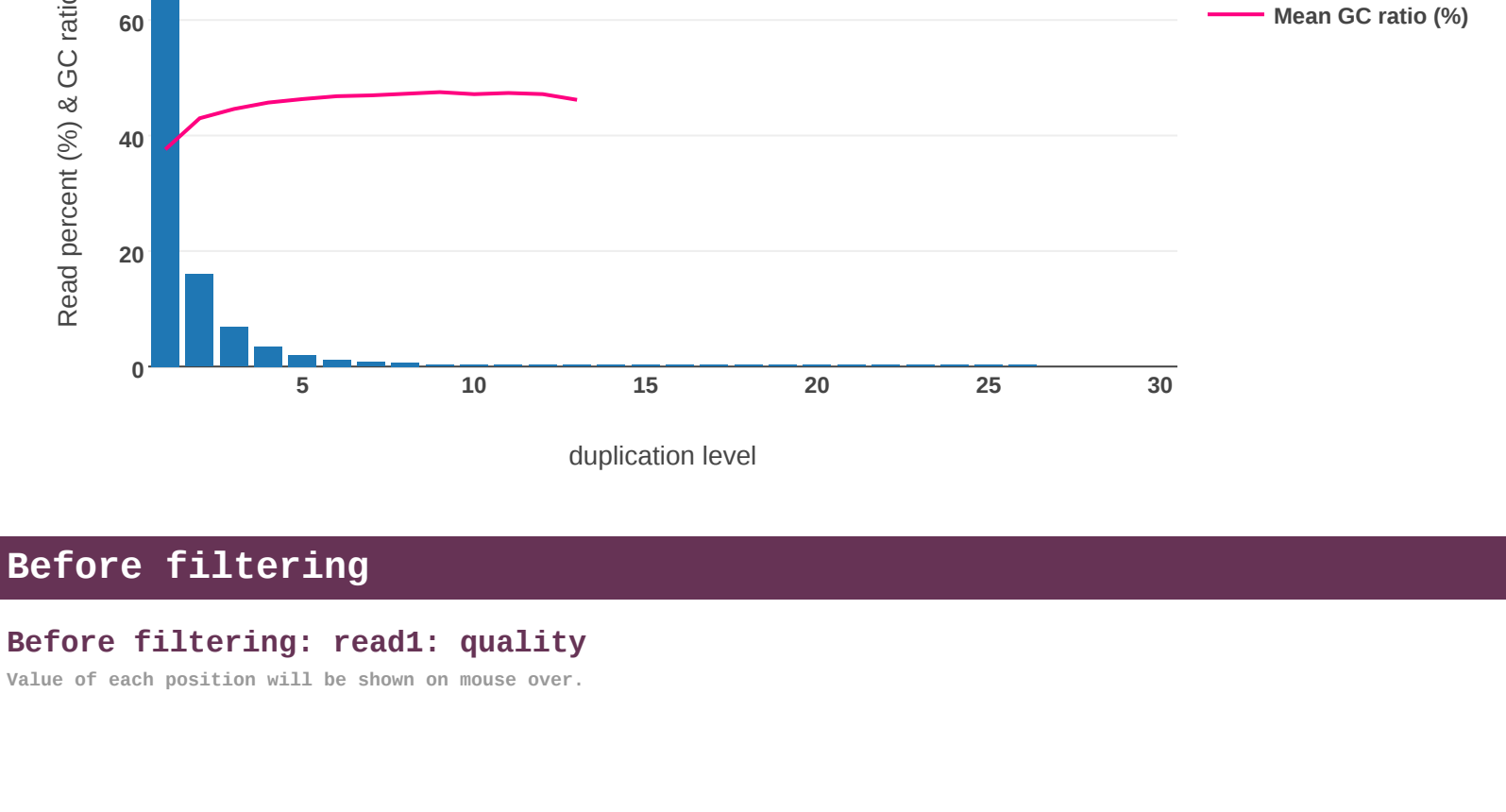
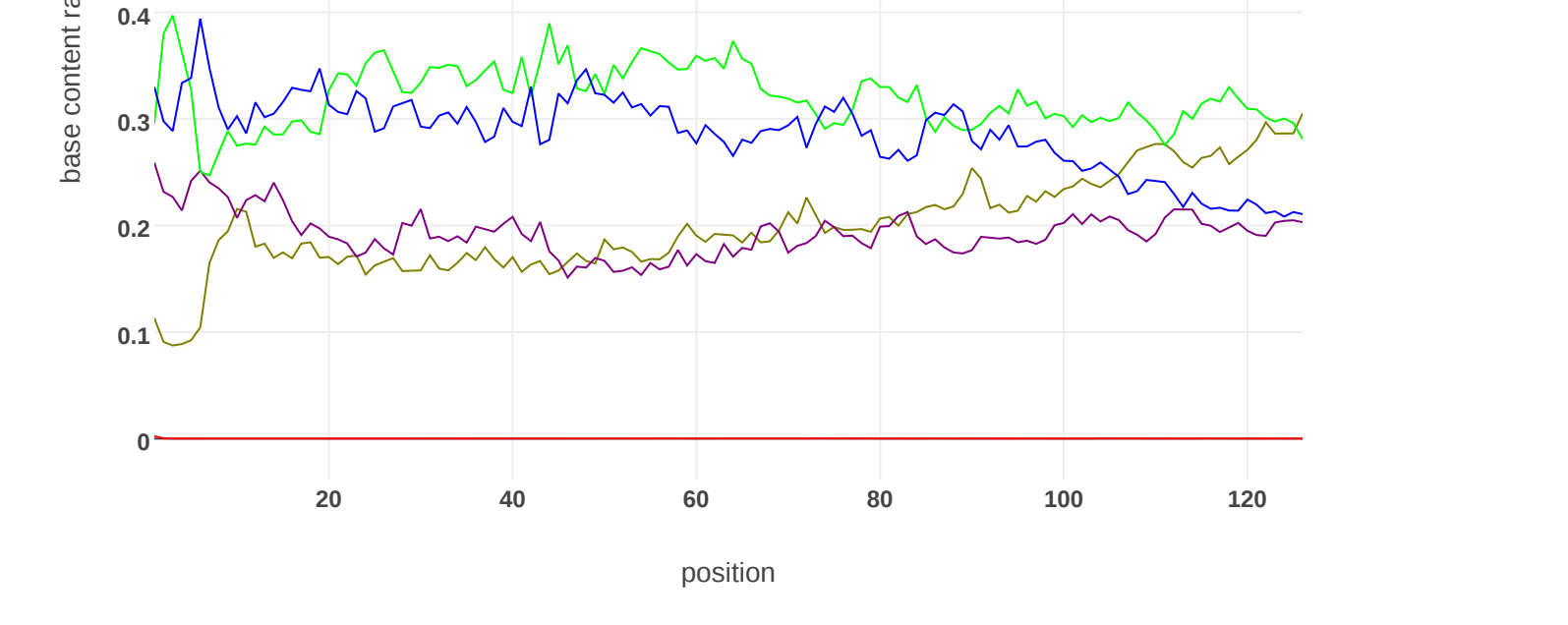
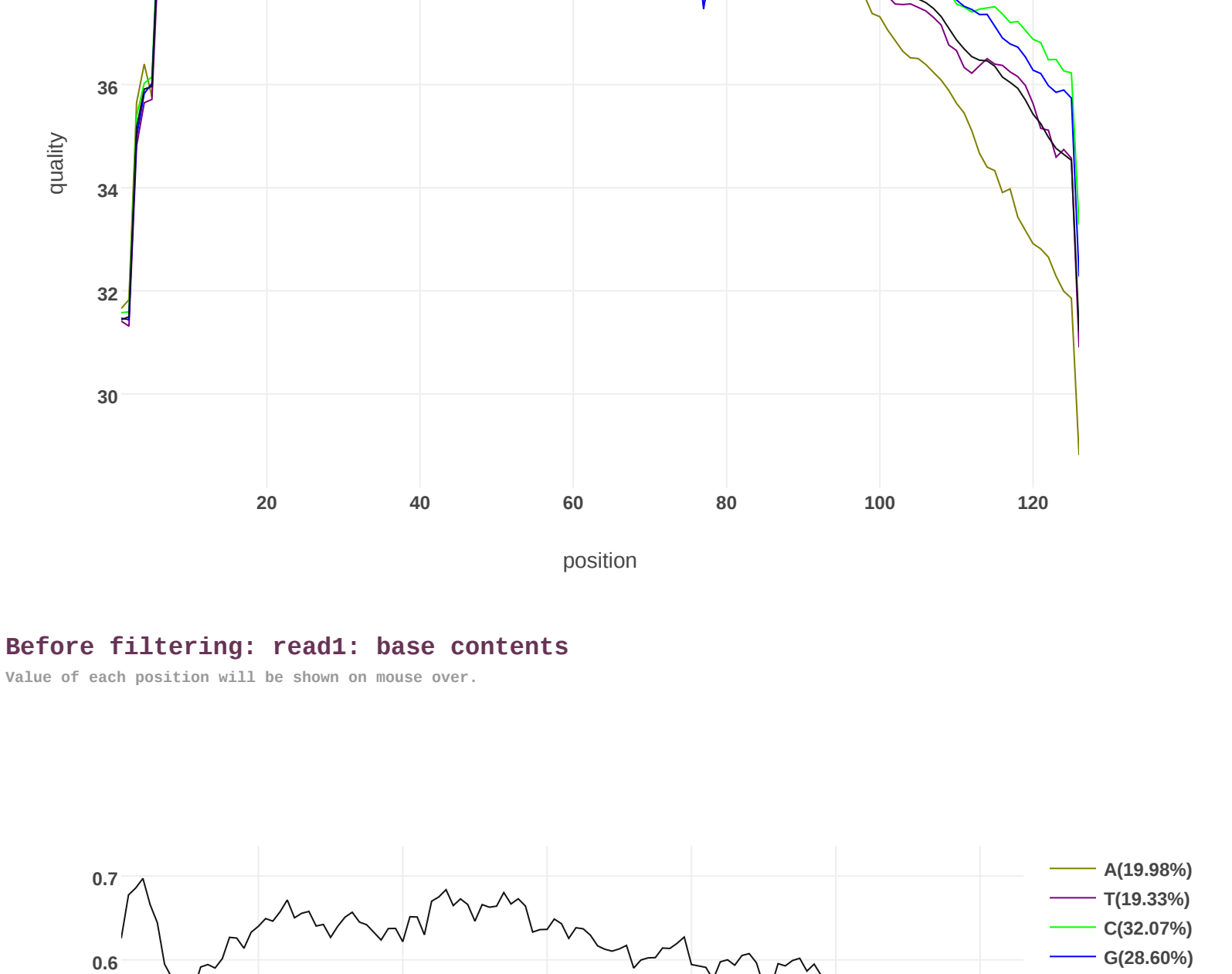
Adapters

AGATC	224321
AGATCG	238764
AGATCGG	254793
AGATCGGAAGAGCACACA	212831
AGATCGGAAGAGCACAC	229219

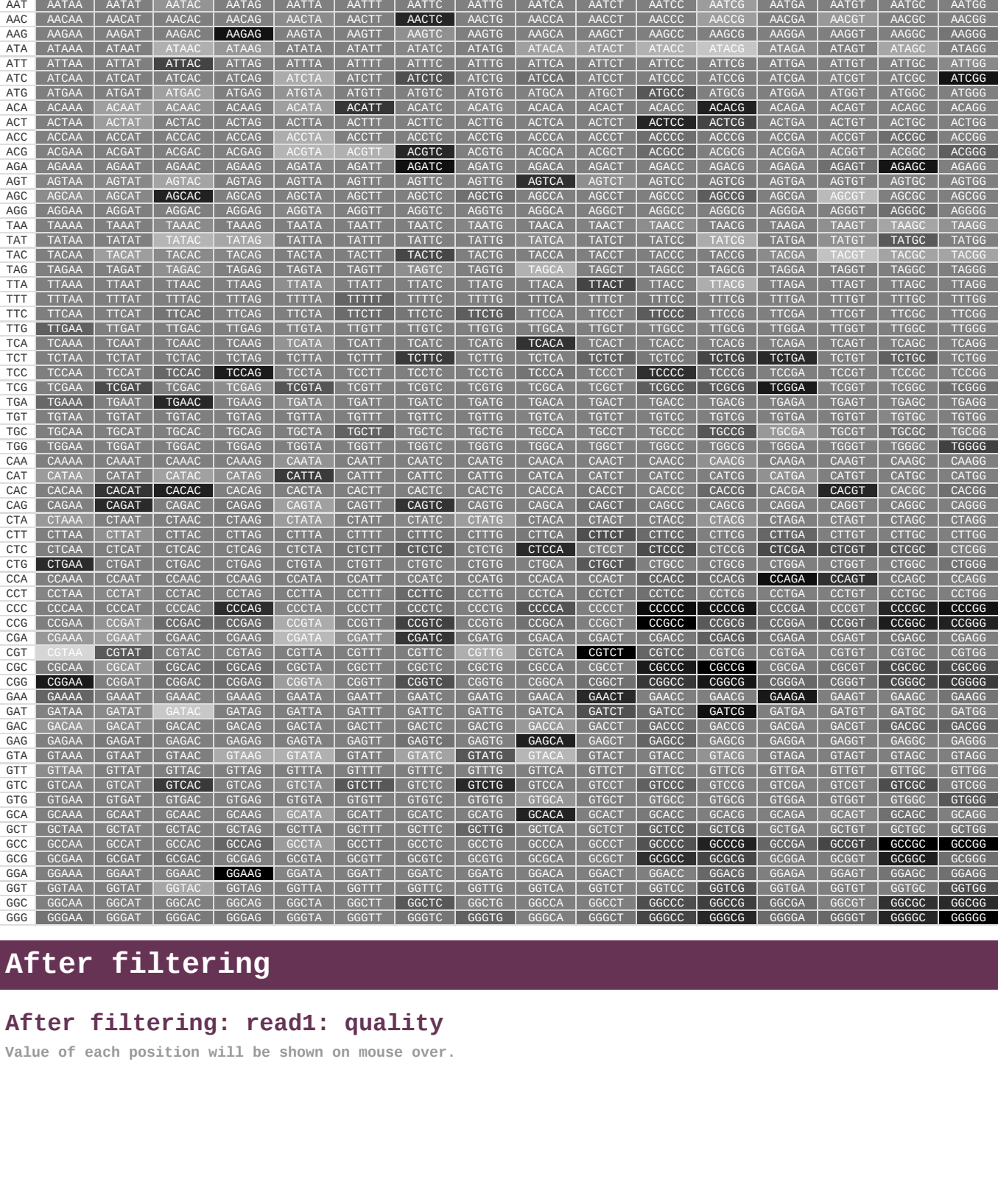
AGATCGGAAGAGCACACGTCTGAACTCCAGTC	216695
AGATCGGAAGAGCACACGTCTGAACTCCAGTC	2055129
AGATCGGAAGAGCACACGTCTGAACTCCAGTCAC	264036
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACATTA	259948
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACATTAC	1215242
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACACTTACT	205114
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACACTTACTC	215071
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACACTTCTG	246768
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACACTTCTGGA	237457
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACACTTCTGAT	288689
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACACTTCTGATCT	206811
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACACTTCTGATCTC	266800
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACACTTCTGATCTCGT	235571
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACACTTCTGATCTCGTATGCCGCTT	253109
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACACTTCTGATCTCGTATGCCGCTTCTC	222209
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACACTTCTGATCTCGTATGCCGCTTCTCT	259869
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACACTTCTGATCTCGTATGCCGCTTCTCTG	216265
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACACTTCTGATCTCGTATGCCGCTTCTCTGAAAA	205287
other adapter sequences	12946979

Duplication

duplication rate (42.000587%)

[illegible]

	AA	AT	AC	AG	TA	TT	TC	TG	CA	CT	CC	CG	GA	GT	GC	GG
AAA	AAAA	AAAT	AAAC	AAAG	AAATA	AAATT	AAATC	AAATG	AAACA	AAACT	AAACC	AAACG	AAAGA	AAAGT	AAAGC	AAAGG



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