

RTastp Report

Summary

General

sequencin
mean leng

mean length after filtering:	72bp
duplication rate:	27.222037% (may be overestimated since this is SE data)
Detected read1 adapter:	AGATCGGAAGAGCACACGTCTGAACTCCAGTCA
Before filtering	
total reads:	113.279191 M
total bases:	8.609219 G
Q20 bases:	7.699522 G (89.433457%)
Q30 bases:	7.358279 G (85.469769%)

After filtering

total reads:	98.927226 M
total bases:	7.129650 G
Q20 bases:	6.768725 G (94.896138%)
Q30 bases:	6.491600 G (91.850748%)
GC content:	58.381298%
Filtering result	
reads passed filters:	98.927226 M (87.330449%)

reads with too many

Sequence	Occurrences
AGATC	882681
AGATCG	814367
AGATCGG	835186
AGATCGGA	835048

AGATCGGAAG
+ + + + + + + + + +

AGATCGGAAGAGC

AGATCGGAAGAGCA	829188
AGATCGGAAGAGCAC	879511
AGATCGGAAGAGCACAC	785345
AGATCGGAAGAGCACAC	892209
AGATCGGAAGAGCACACG	761078
AGATCGGAAGAGCACACGT	753720
AGATCGGAAGAGCACACGTC	740841
AGATCGGAAGAGCACACGCTCT	667123
AGATCGGAAGAGCACACGCTCTG	687653
AGATCGGAAGAGCACACGCTCTGA	580108
AGATCGGAAGAGCACACGCTCTGAAC	623554
AGATCGGAAGAGCACACGCTCTGAAC	630484
AGATCGGAAGAGCACACGCTCTGAACCT	524587
AGATCGGAAGAGCACACGCTCTGAACCTC	482769
AGATCGGAAGAGCACACGCTCTGAACCTCC	423976
AGATCGGAAGAGCACACGCTCTGAACCTCCA	356249
AGATCGGAAGAGCACACGCTCTGAACCTCCAG	397511
AGATCGGAAGAGCACACGCTCTGAACCTCCAGT	299837
AGATCGGAAGAGCACACGCTCTGAACCTCCAGTC	3595843
AGATCGGAAGAGCACACGCTCTGAACCTCCAGTCA	258543
other adapter sequences	2152188

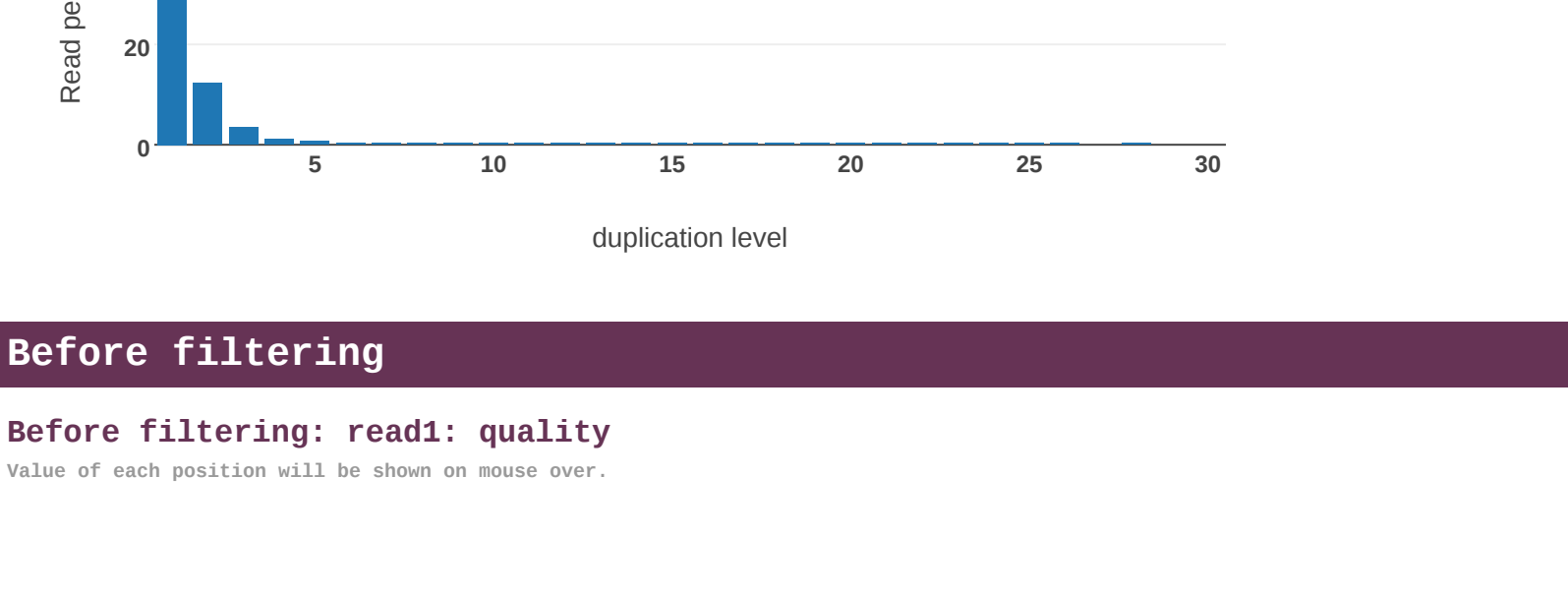
Duplication

duplication rate (27.222037%)

Category	% GC ratio
Read percent (%)	~80
Mean GC ratio (%)	~65

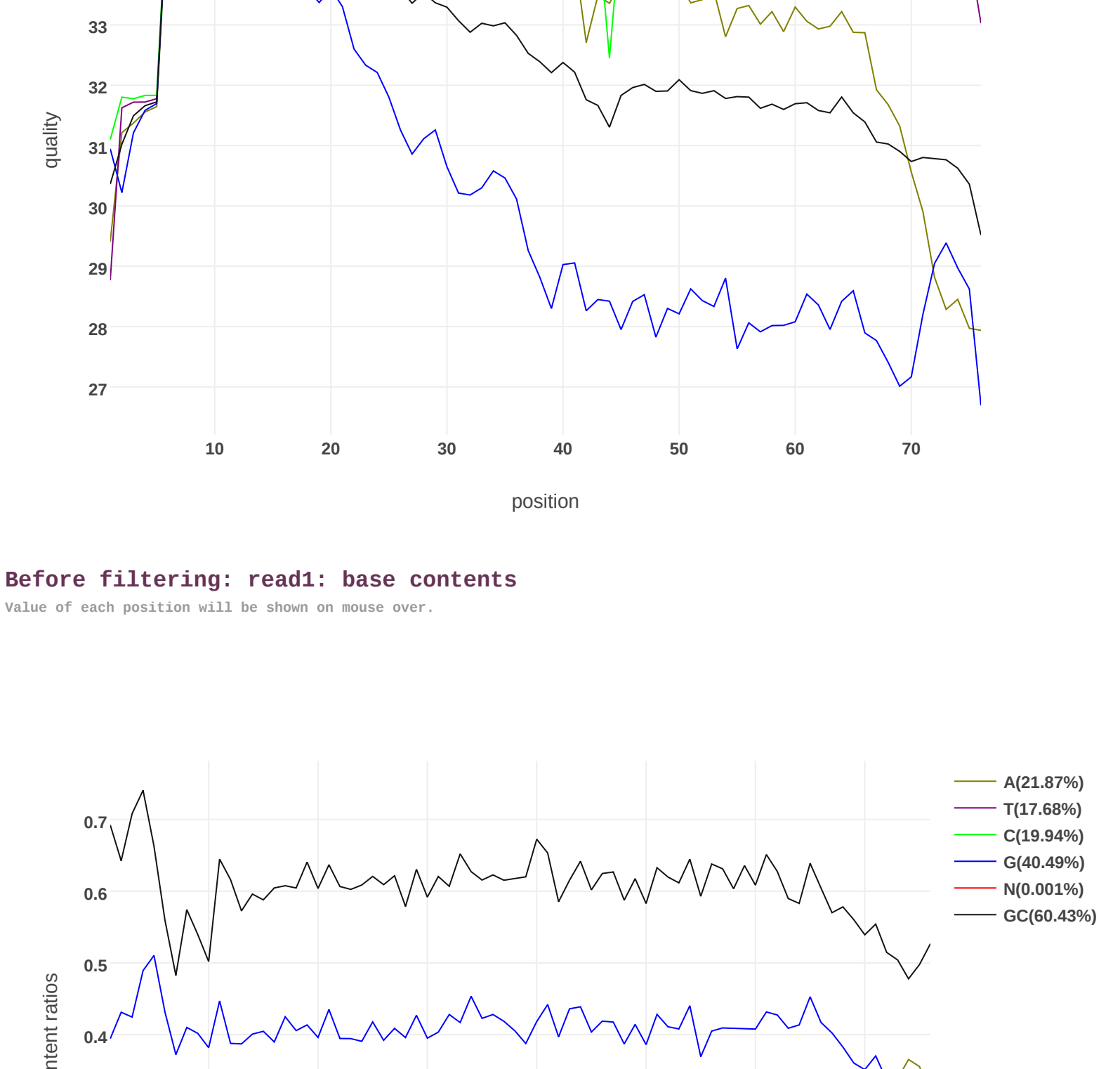
cent

40



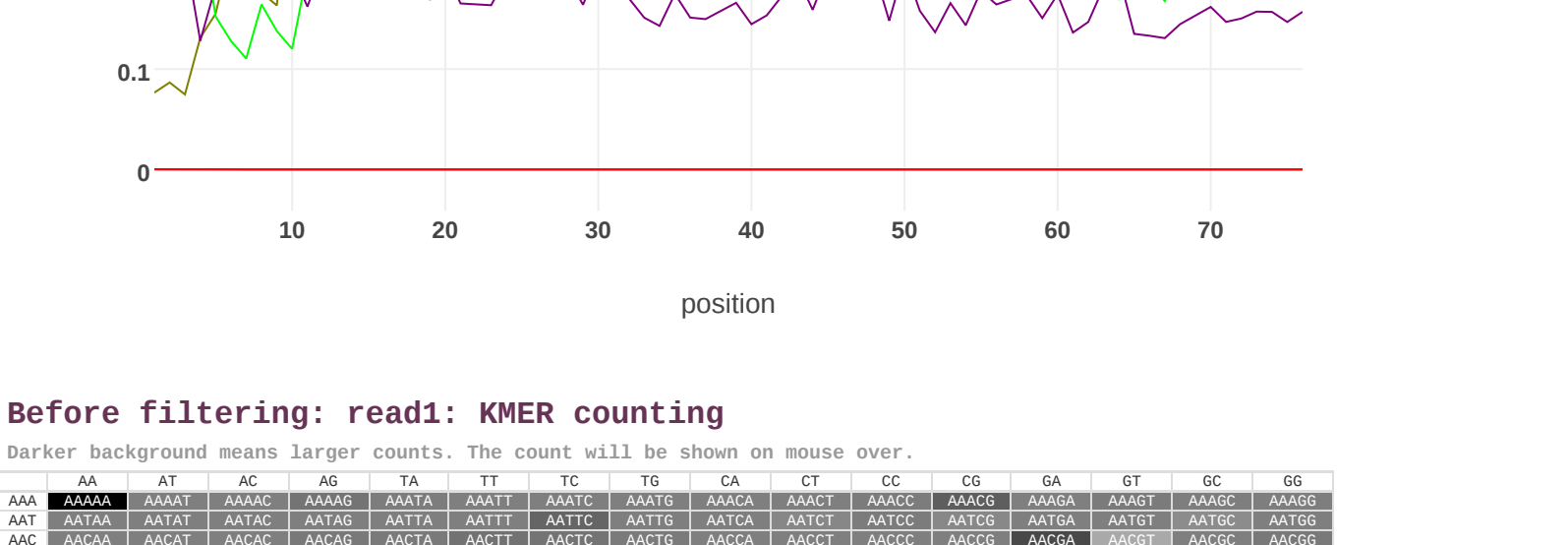
Year	Total (thousands)	Male (thousands)	Female (thousands)
1990	28.5	18.5	10.0
1995	30.0	20.0	11.0
2000	29.5	19.5	10.0
2005	29.0	19.0	10.0
2010	30.0	20.0	10.0

34

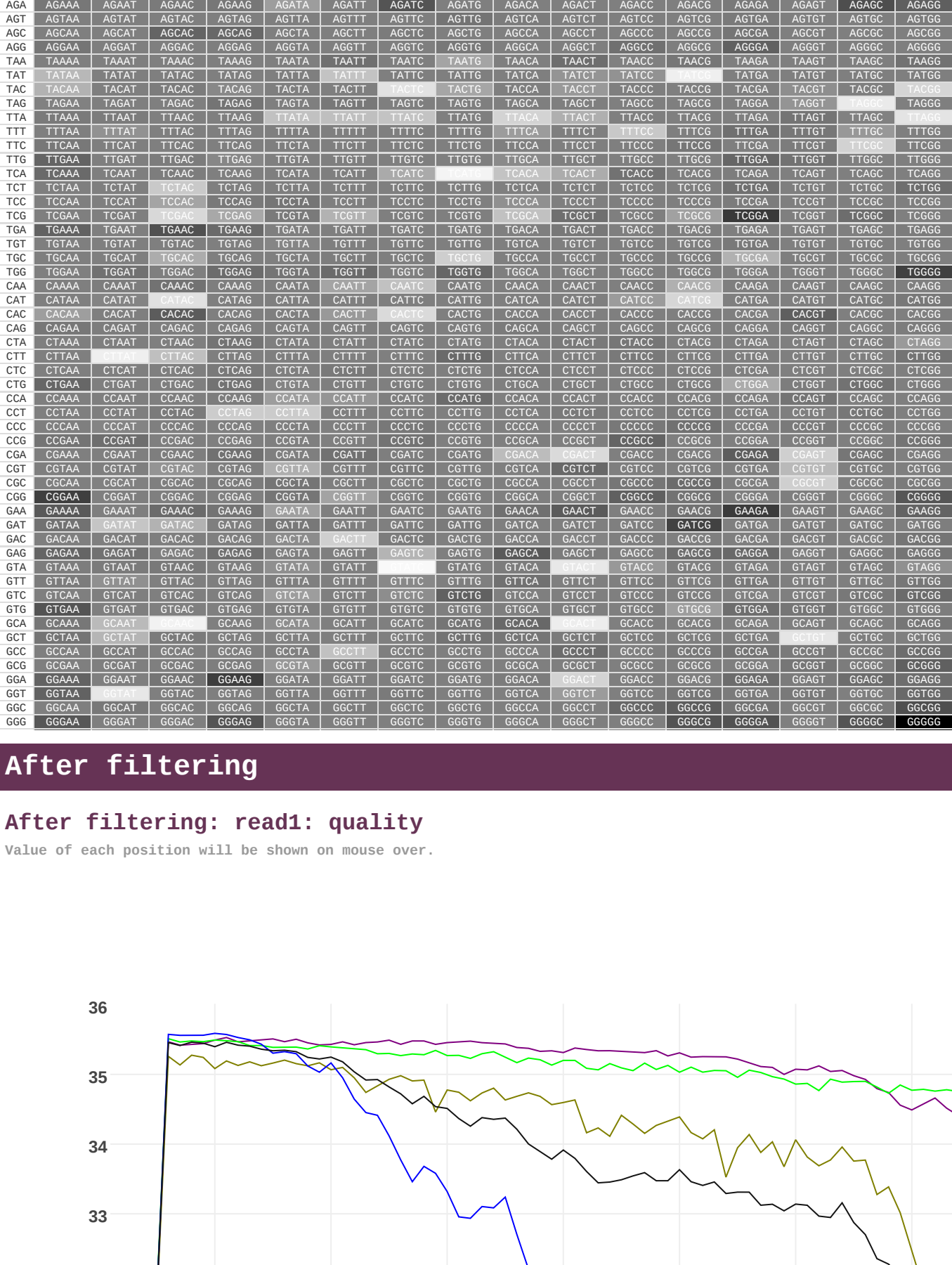


bas 0.3

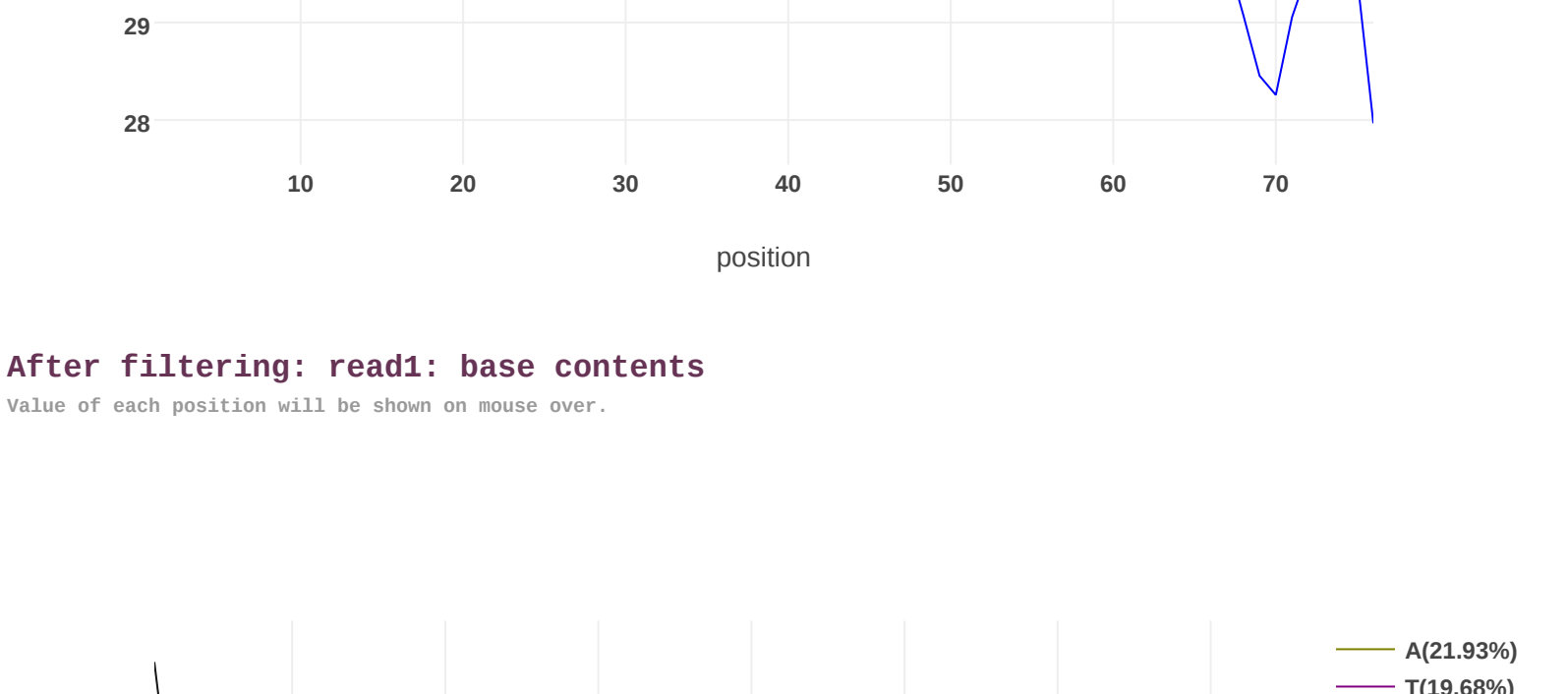
0.2

[illegible]

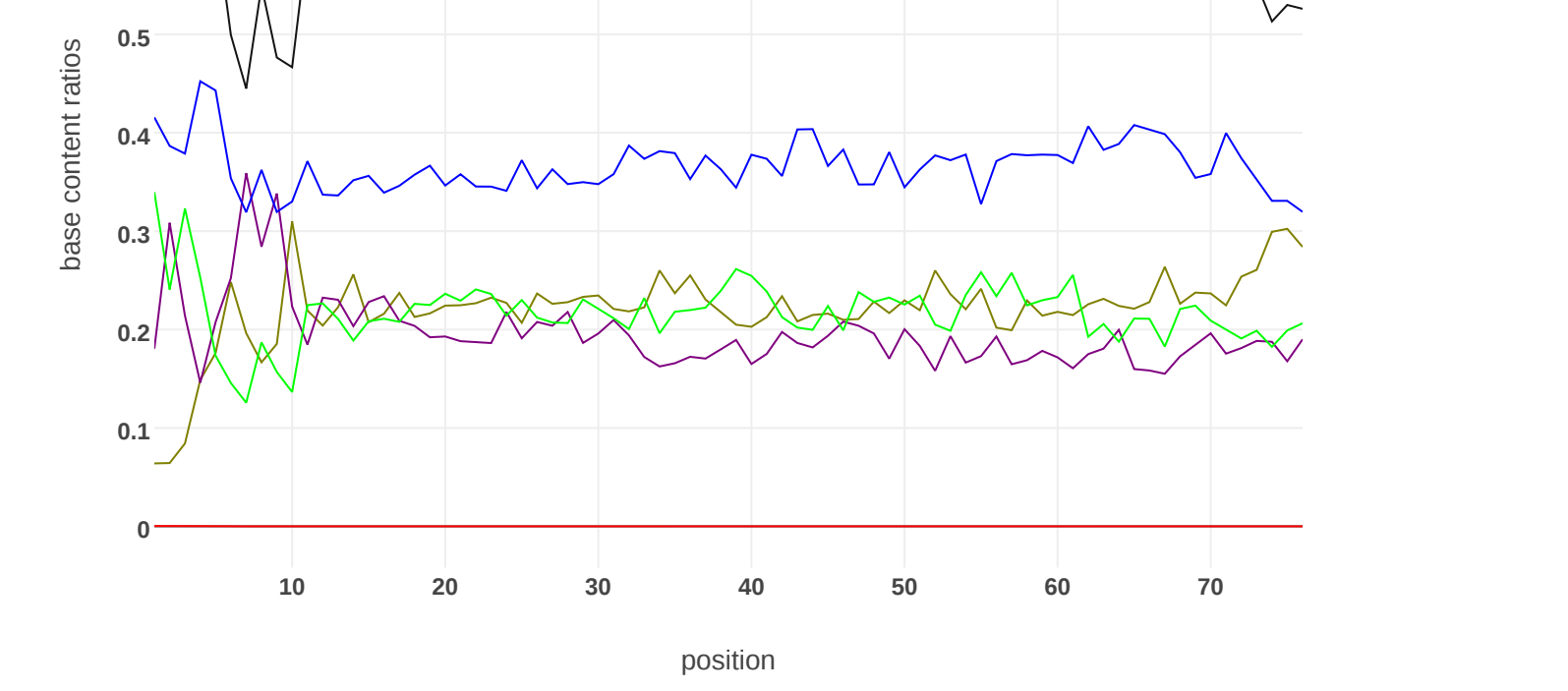
ACT	ACTAA	ACTAT	ACTAC	ACTAG	ACTTA	ACTTT	ACTTC	ACTTG	ACTCA	ACTCT	ACTCC
ACC	ACCAA	ACCAT	ACCAC	ACCAG	ACCTA	ACCTT	ACCTC	ACCTG	ACCCA	ACCCCT	ACCCC
ACG	ACGAA	ACGAT	ACGAC	ACGAG	ACGTA	ACGTT	ACGTC	ACGTG	ACGCA	ACGCT	ACGCC



22

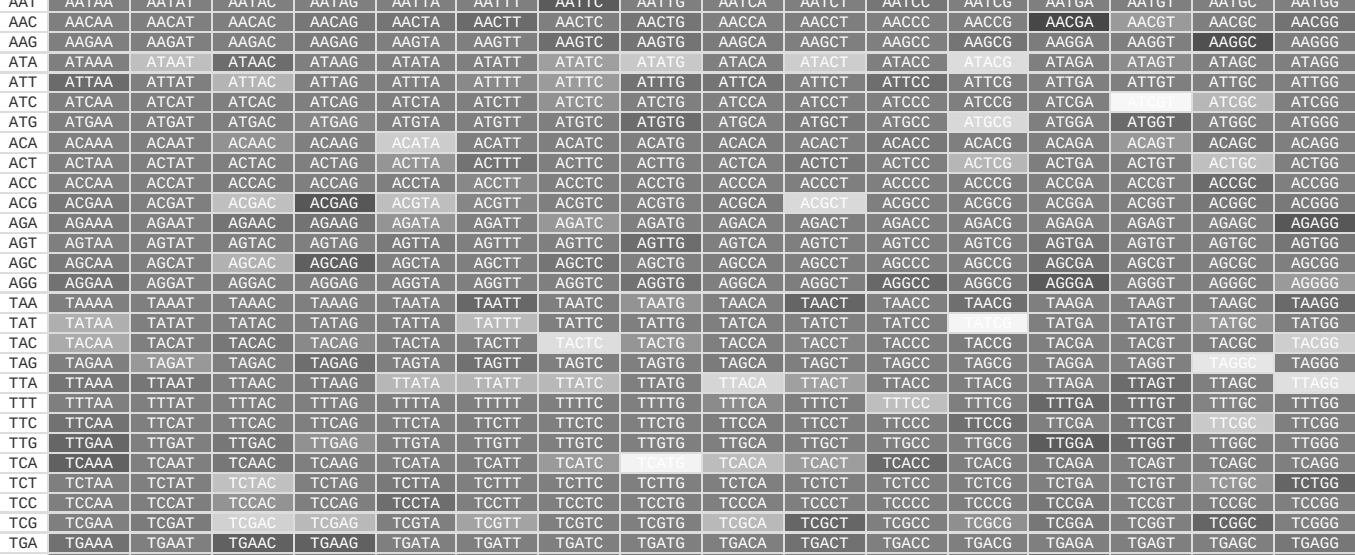


1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
---	---	---	---	---	---	---	---	---	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	-----



After filtering: read1: KMER counting

	AA	AT	AC	AG	TA	TT	TC	TG	CA	CT	CC
AAA	AAAAA	AAAAT	AAAAC	AAAAG	AAATA	AAATT	AAATC	AAATG	AAACA	AAACT	AAACC



CAA	CAAA
CAT	CATA