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fastq version: 0.24.0 (https://www.broadinstitute.org/genepipe/faq/)
sequencing: single end (76 cycles)
mean length before filtering: 76bp
mean length after filtering: 70bp
duplication rate: 22.239563% (may be overestimated since this is SE data)
Detected read1 adapter: AGATCGGAAGAGCACACGTCTGAACTCAGTCA

Before filtering
total reads: 288.151295 M
total bases: 15.819498 G
Q30 bases: 15.207285 G (95.509555%)

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GC content:	51.406345%
After filtering	
total reads:	205.072192 M
total bases:	14.573207 G
Q20 bases:	14.159007 G (97.157799%)
Q30 bases:	13.975074 G (95.895665%)
GC content:	51.413660%

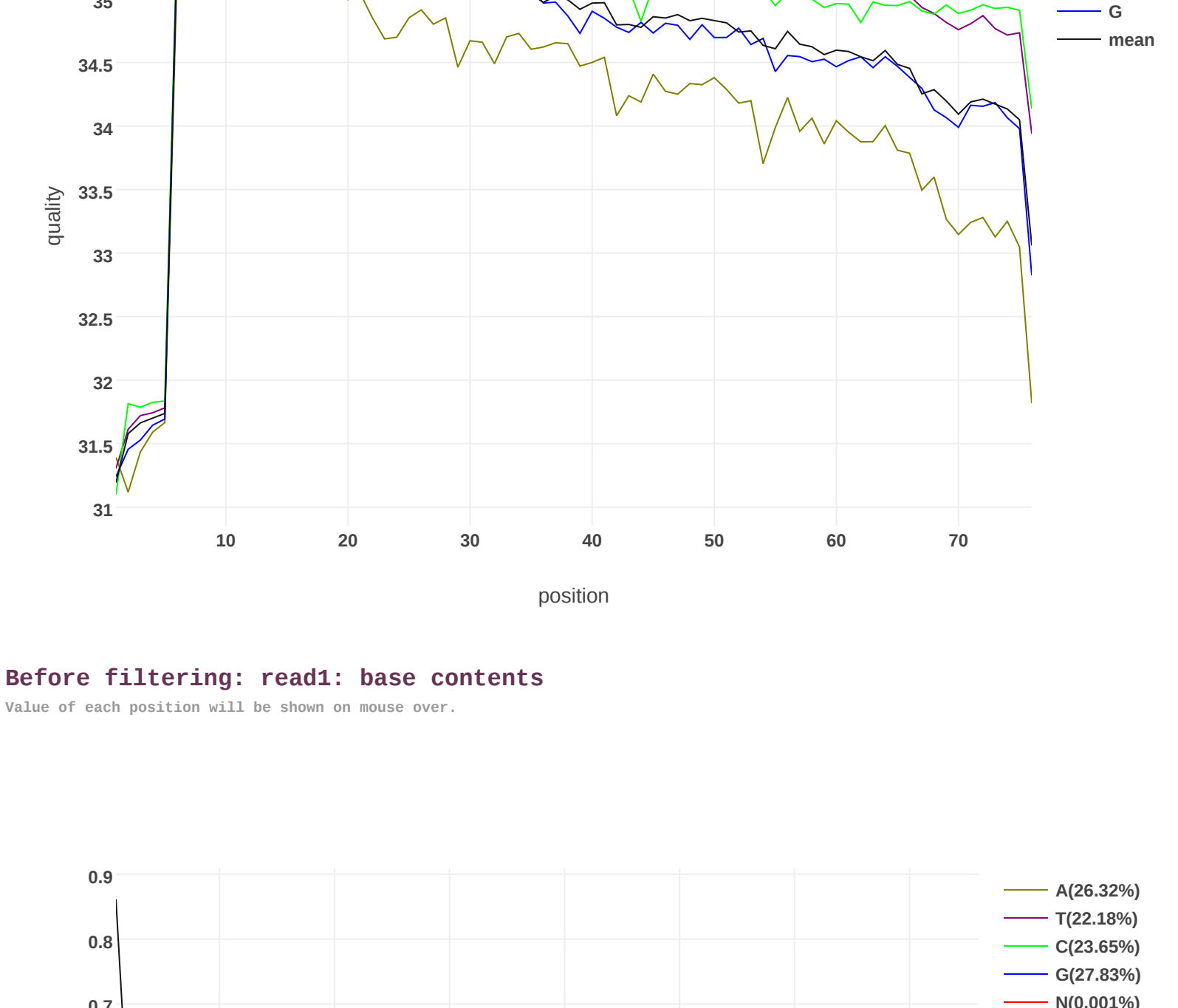
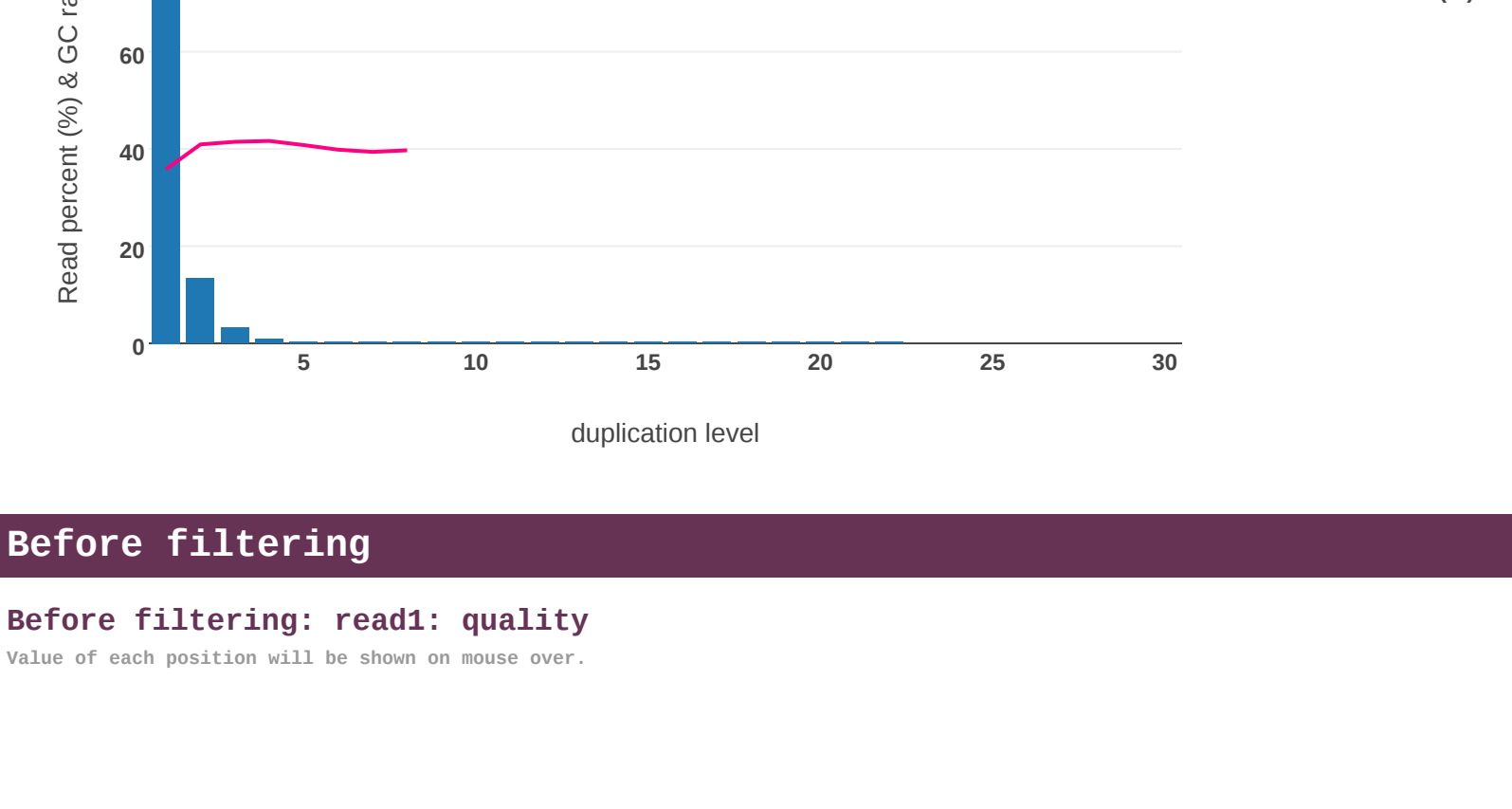
reads passed filters:	285.872192 M (98.9958974%)
reads with low quality:	1.311499 M (0.6388978%)
reads with too many N:	6.324000 K (0.003038%)
reads too short:	961.280000 K (0.461818%)

Adapters

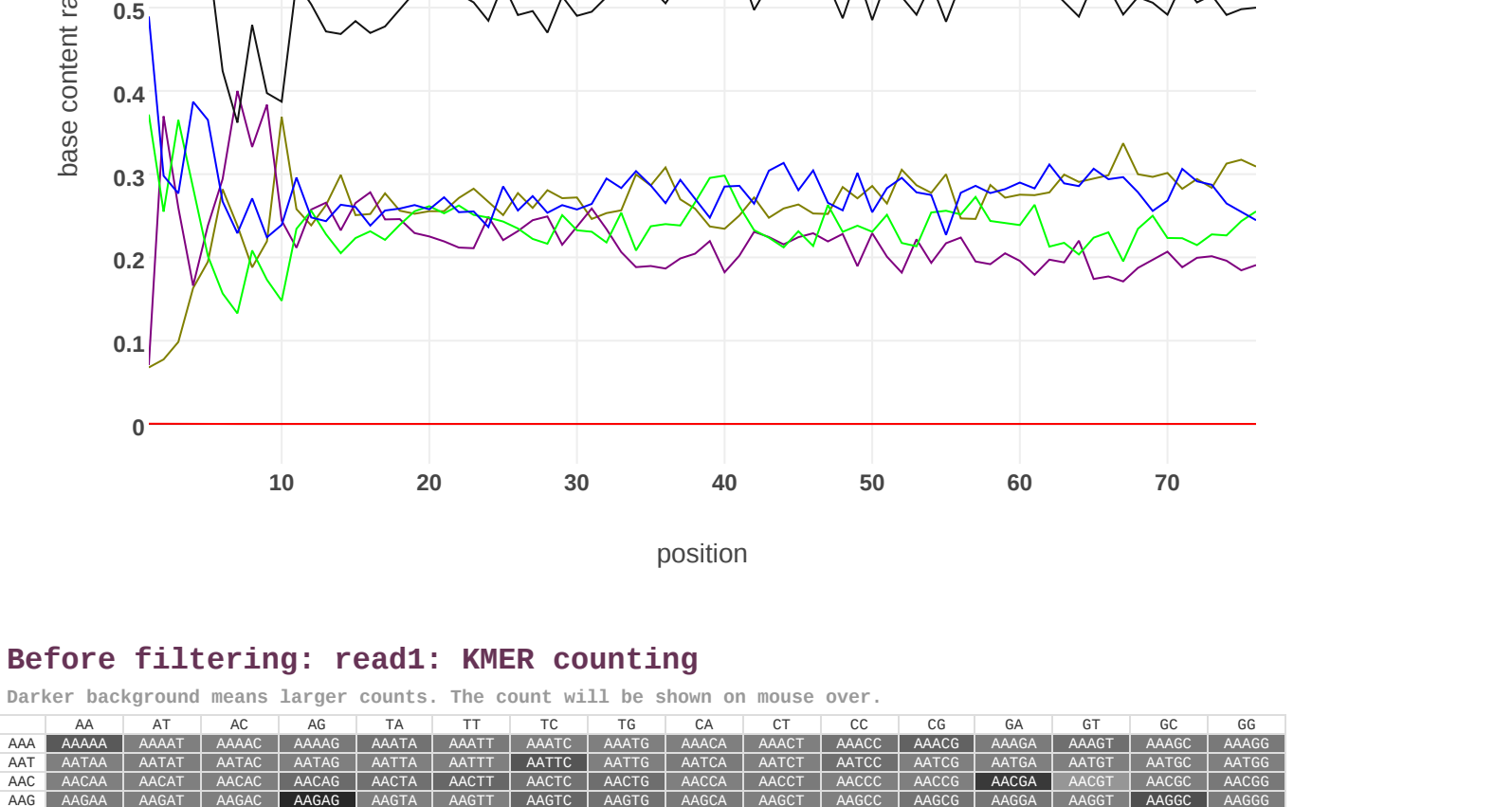
Adapter or bad ligation of read1

AGATCG	2519449
AGATCGG	2637186
AGATCGGA	2443510
AGATCGGAA	2523484
AGATCGGAAG	2373797
AGATCGGAAGA	2508759

AGATCGGAAGAGCA	2554447
AGATCGGAAGAGCAC	2740322
AGATCGGAAGAGCACGA	2468810
AGATCGGAAGAGCACAC	2814089
AGATCGGAAGAGCACACG	2362591
AGATCGGAAGAGCACACGT	2255324
AGATCGGAAGAGCACACGTC	2229486
AGATCGGAAGAGCACACGCT	1974452
AGATCGGAAGAGCACACGCTG	1986940
AGATCGGAAGAGCACACGCTGA	1659241
AGATCGGAAGAGCACACGCTGAA	1810306
AGATCGGAAGAGCACACGCTGGAAC	1832729
AGATCGGAAGAGCACACGCTGGAAGT	1437280
AGATCGGAAGAGCACACGCTGGAAGTC	1367821
AGATCGGAAGAGCACACGCTGGAAGTCC	1170389
AGATCGGAAGAGCACACGCTGGAAGTCCA	959282
AGATCGGAAGAGCACACGCTGGAAGTCCAG	787943
AGATCGGAAGAGCACACGCTGGAAGTCCAGT	696202
AGATCGGAAGAGCACACGCTGGAAGTCCAGTC	1634057
other adapter sequences	5116290



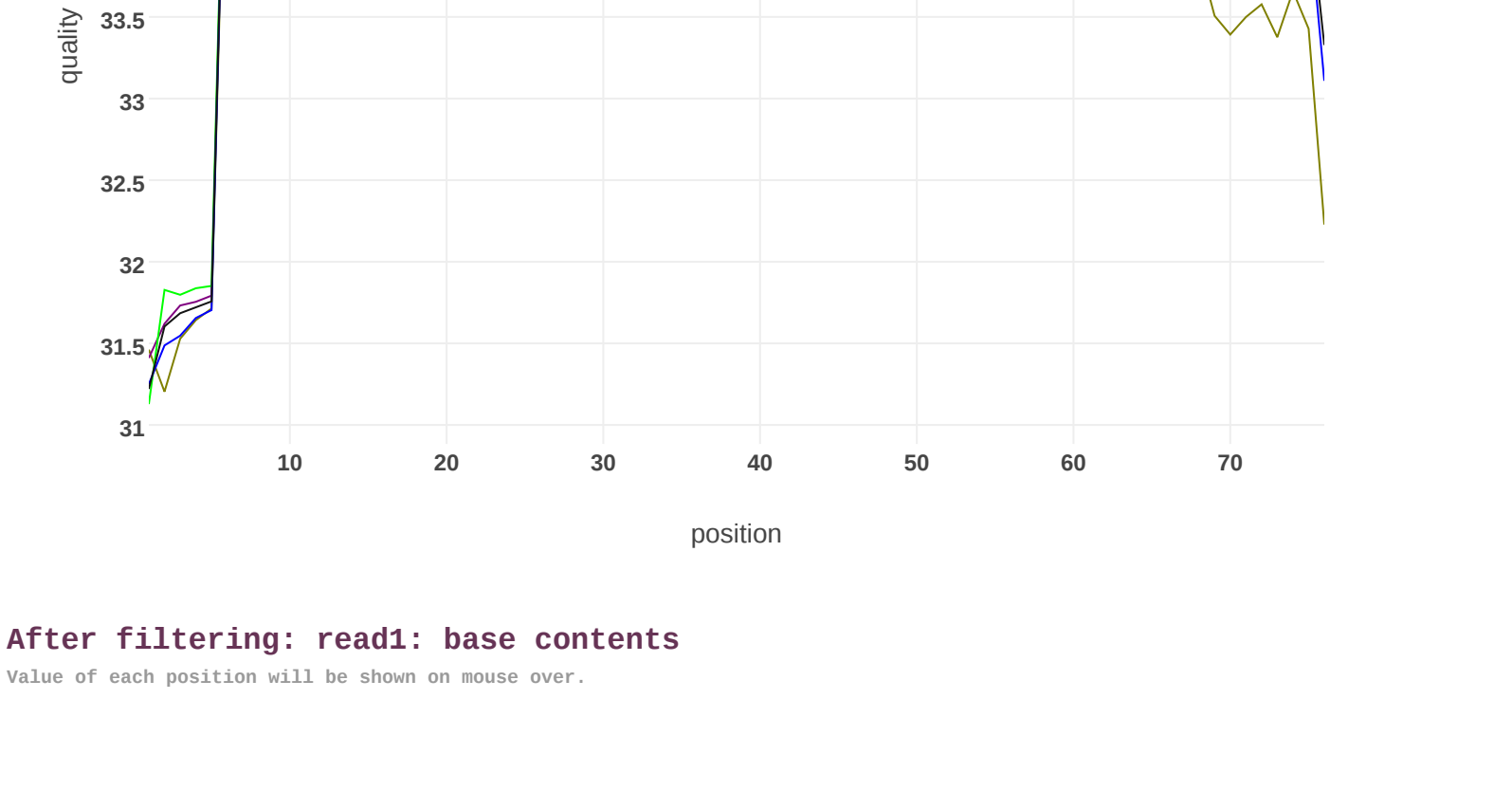
ios



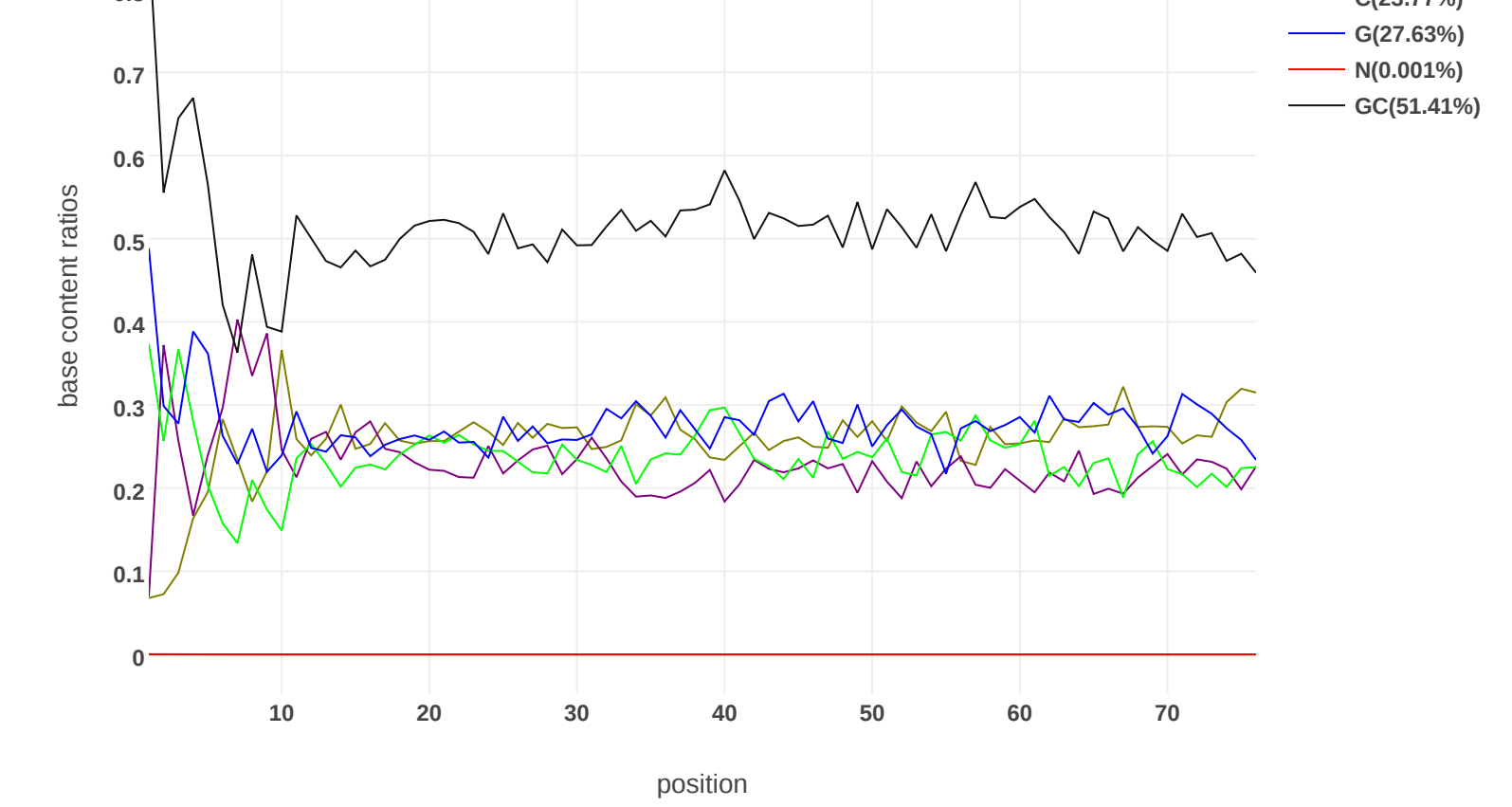
ACC	ACCA	ACCAT	ACCAC	ACCAG	ACCAG	ACCTA	ACCTT	ACCTC	ACCTG	ACCTA	ACCTT	ACCTC	ACCTG
ACG	ACGAA	ACGAT	ACGAC	ACGAG	ACGAG	ACGTA	ACGTT	ACGTC	ACGTG	ACGCA	ACGCT	ACGTC	ACGTG
AGA	AGAAA	AGAAAT	AGAAC	AGAAE	AGAAE	AGATA	AGATT	AGATC	AGATG	AGACA	AGACT	AGATC	AGATG



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20			
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Darker background means larger counts. The count will be shown on mouse over

	AA	AT	AC	AG	TA	TT	TC	TG	CA	CT	CC
AAA	AAAA	AAT	AAC	AAG	ATA	ATT	ATC	ATG	CAT	CTT	CCA

