

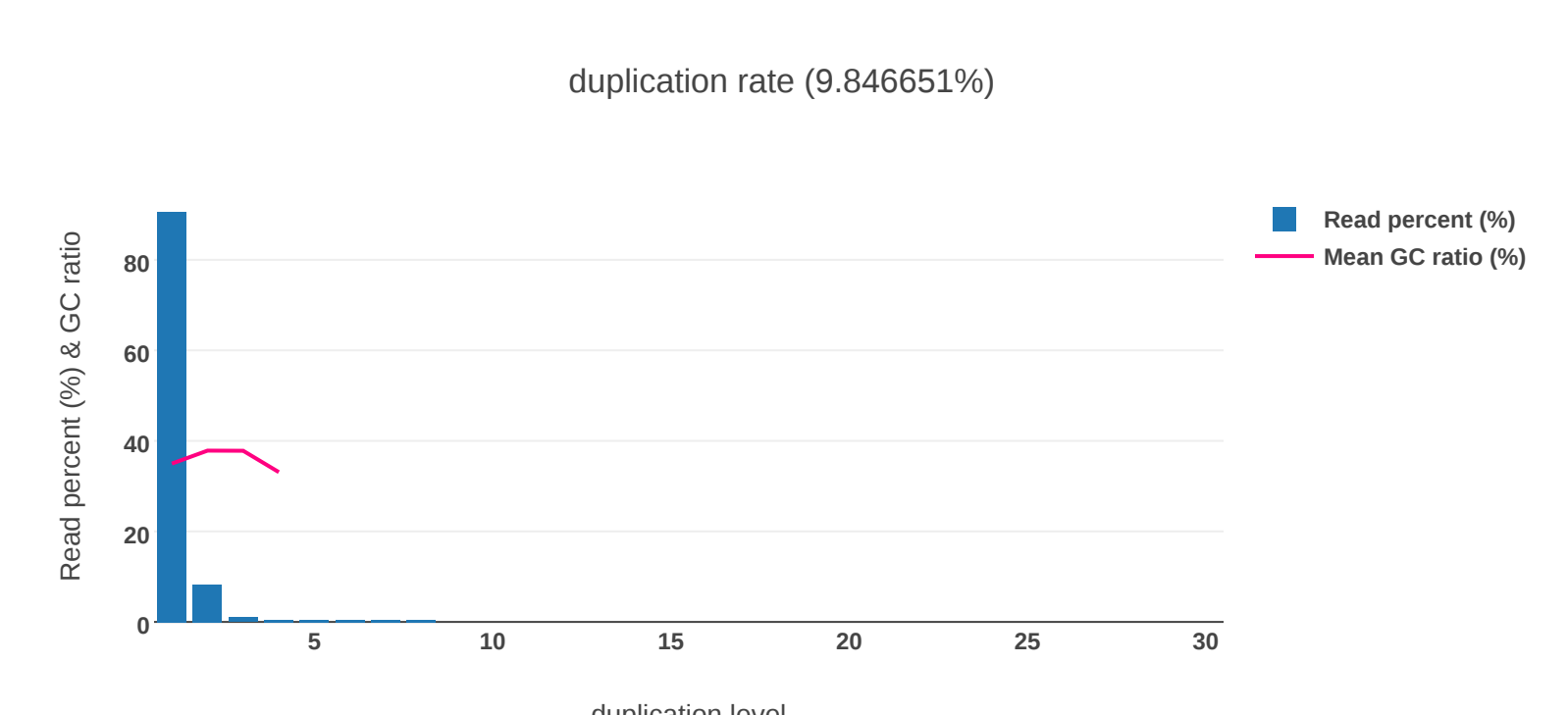
fastp version:	0.21.0 (https://github.com/OpenGenome/fastp)
sequencing:	single end (148 cycles)
mean length before filtering:	148bp
mean length after filtering:	97bp
duplication rate:	9.846651% (may be overestimated since this is SE data)
Detected read1 adapter:	AGATCGGAAGAGCACACGTCTGAACTCCAGTCA

total reads:	25.004969 M
total bases:	3.700735 G
Q20 bases:	3.382553 G (91.402172%)
Q30 bases:	3.203913 G (86.575036%)
GC content:	53.916375%

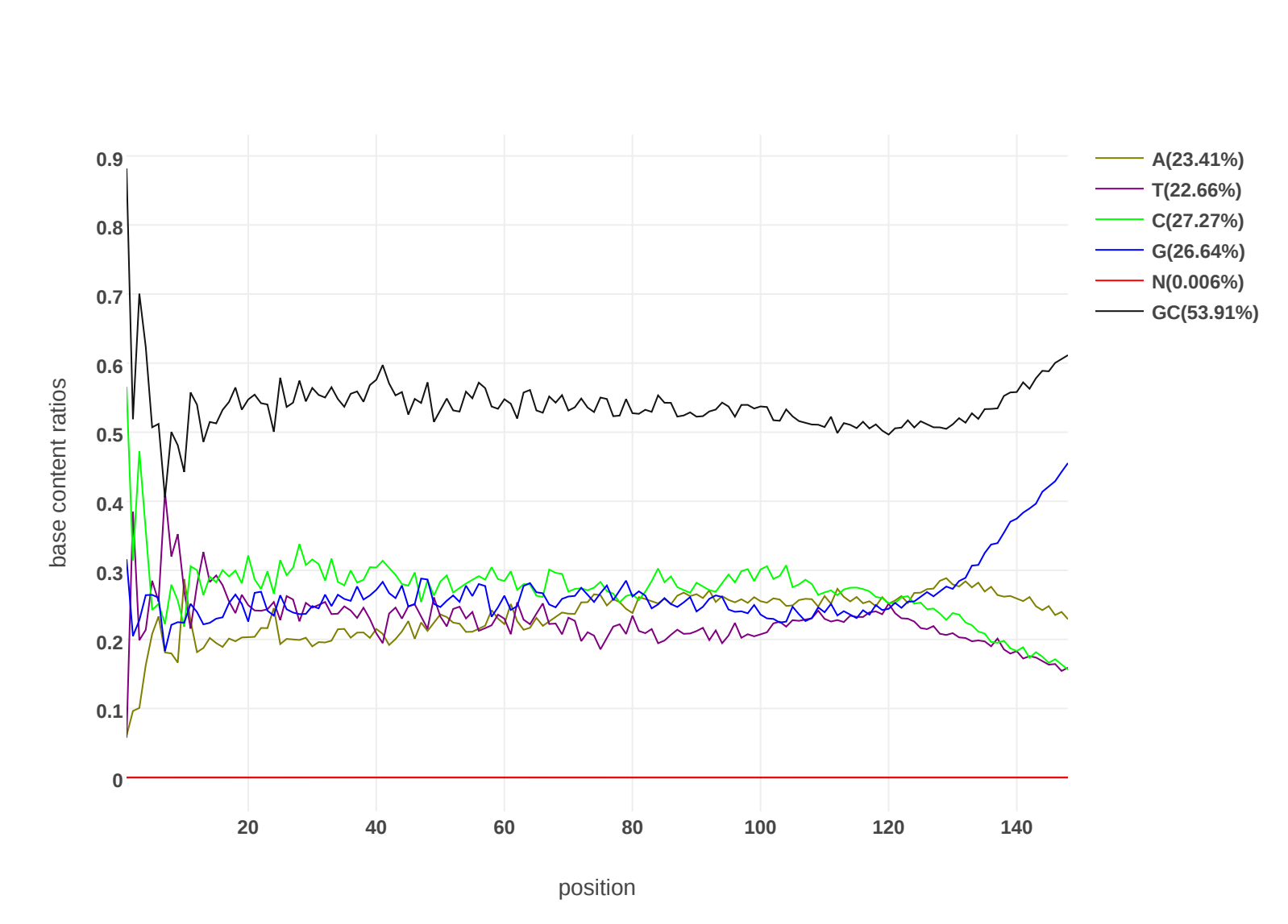
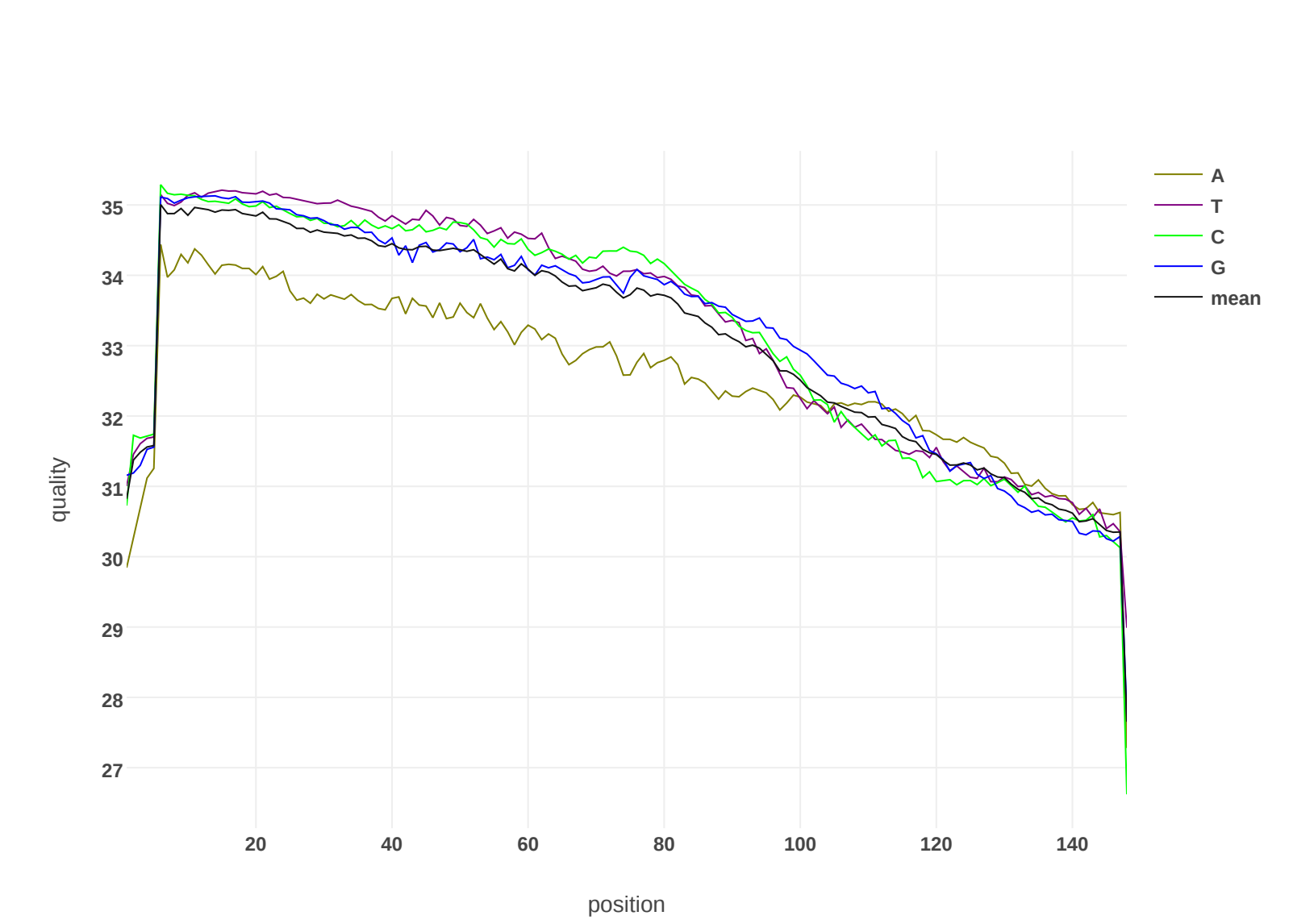
total reads:	24.408531 M
total bases:	2.377710 G
Q20 bases:	2.263740 G (95.206721%)
Q30 bases:	2.191686 G (92.176299%)
GC content:	55.104335%

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%)
reads too short:	32.990000 K (0.131934%)

Sequence	Occurrences
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACACAGTGATCTGATGCCCTCTTCGCTTGA	201799
AGATCGGAAGAGCACACGTCTGAACTCCAGTCACACAGTGATCTGATGCCCTCTTCGCTTGA	202477
other adapter sequences	19621711

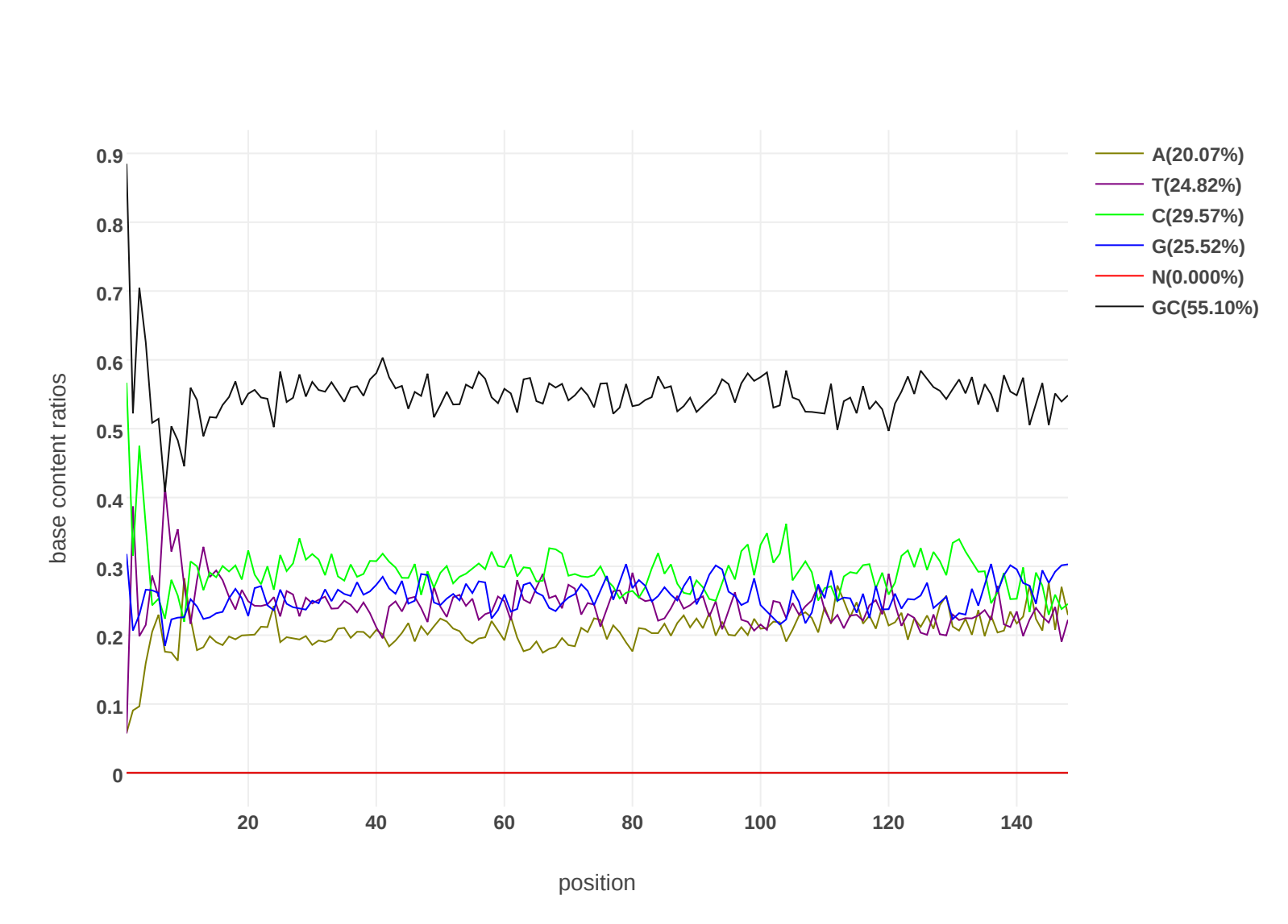
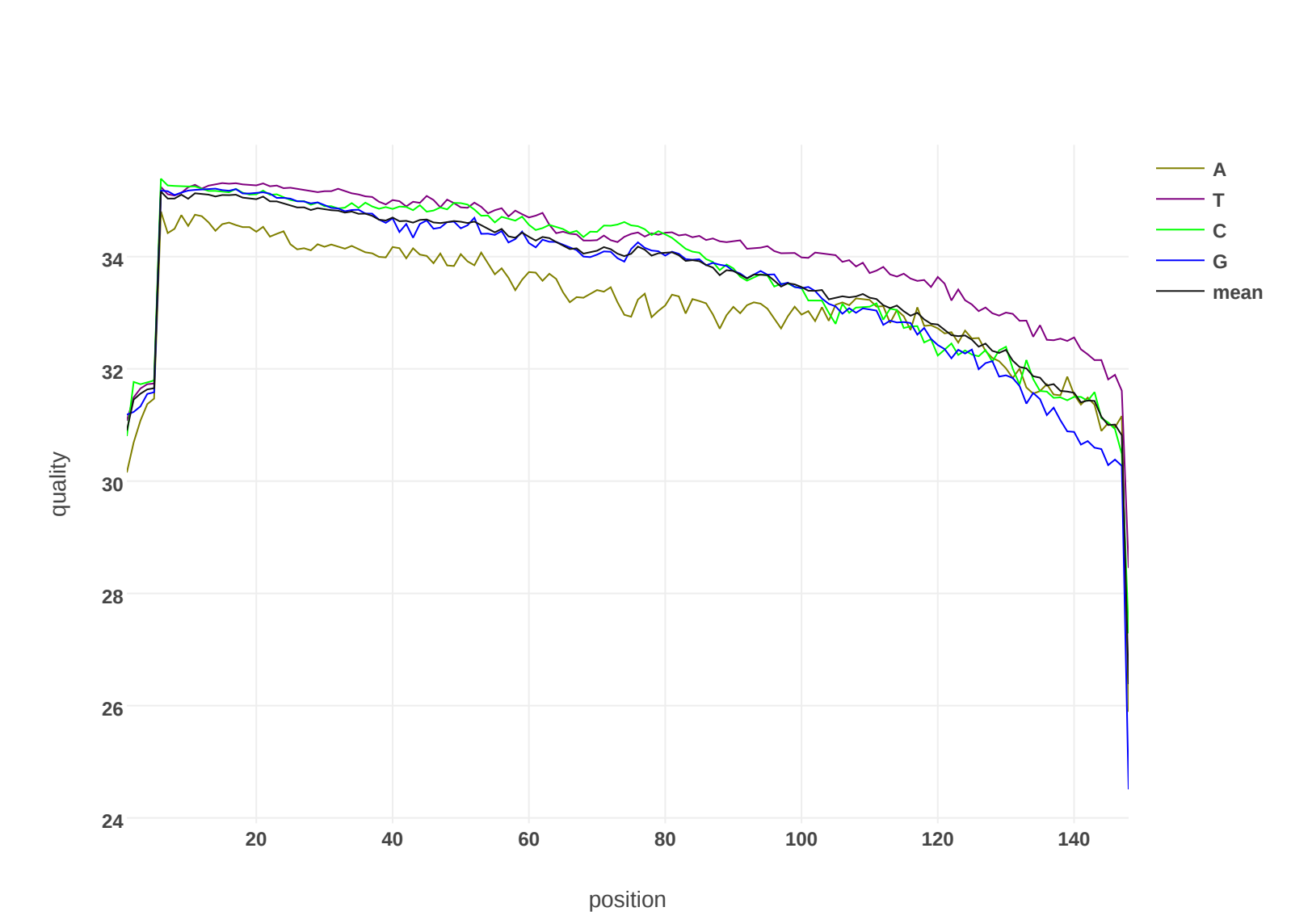


Before filtering: read1: quality



AA	AT	AC	AG	TA	TT	TC	TG	CA	CT	CC	CG	GA	GT	GC	GG
----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----

AAT	AATA	AATAT	AATAC	AATAG	AATTA	AATTT	AATTC	AATTG	AATCA	AATCT	AATCC	AATCG	AATGA	AATGT	AATGC	AATGG
-----	------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------

[illegible]

AAT	AATAA	AATAT	AATAC	AATAG	AATTA	AATTT	AATTC	AATTG	AATCA	AATCT	AATCC	AATCG	AATGA	AATGT	AATGC	AATGG
-----	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------

[illegible]