Report

	contigs_no_error_ont_hq_50x.fastq	contigs_no_error_reads_hiseq_5k.fastq	contigs_ont_hq_50x.fastq	contigs_reads_hiseq_5k.fastq
# contigs (>= 0 bp)	1	1	1	1
# contigs (>= 1000 bp)	1	1	1	1
# contigs (>= 5000 bp)	1	1	1	1
# contigs (>= 10000 bp)	1	1	1	1
# contigs (>= 25000 bp)	1	1	1	1
# contigs (>= 50000 bp)	1	0	1	1
Total length (>= 0 bp)	258446	30215	1505388	102372
Total length (>= 1000 bp)	258446	30215	1505388	102372
Total length (>= 5000 bp)	258446	30215	1505388	102372
Total length (>= 10000 bp)	258446	30215	1505388	102372
Total length (>= 25000 bp)	258446	30215	1505388	102372
Total length (>= 50000 bp)	258446	0	1505388	102372
# contigs	1	1	1	1
Largest contig	258446	30215	1505388	102372
Total length	258446	30215	1505388	102372
Reference length	30119	30119	30119	30119
GC (%)	40.97	41.30	40.84	41.16
Reference GC (%)	41.24	41.24	41.24	41.24
N50	258446	30215	1505388	102372
NG50	258446	30215	1505388	102372
N90	258446	30215	1505388	102372
NG90	258446	30215	1505388	102372
auN	258446.0	30215.0	1505388.0	102372.0
auNG	2217681.0	30311.3	75241310.5	347954.0
L50	1	1	1	1
LG50	1	1	1	1
L90	1	1	1	1
LG90	1	1	1	1
# misassemblies	17	4	118	0
# misassembled contigs	1	1	1	0
Misassembled contigs length	258446	30215	1505388	0
# local misassemblies	0	3	3	0
# scaffold gap ext. mis.	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0
# unaligned mis. contigs	0	0	0	1
# unaligned contigs	0 + 0 part	0 + 0 part	0 + 1 part	0 + 1 part
Unaligned length	0	0	388167	57449
Genome fraction (%)	98.768	97.892	98.655	88.452
Duplication ratio	8.687	1.024	37.599	1.692
# N's per 100 kbp	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	0.00	0.00	493.38	423.66
# indels per 100 kbp	0.00	0.00	1463.03	15.53
Largest alignment	25603	19101	20561	1270
Total aligned length	258424	30196	1117202	45083
NA50	16920	19101	8755	-
NGA50	25603	19101	20561	526
NA90	9605	2419	-	-
NGA90	25582	2419	20434	349
auNA	17495.5	14265.2	7382.5	204.5
auNGA	150125.9	14310.7	368988.2	695.2
LA50	6	1	74	-
LGA50	1	1	1	21
LA90	15	3	-	-
LGA90	2	3	2	50

All statistics are based on contigs of size >= 500 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).
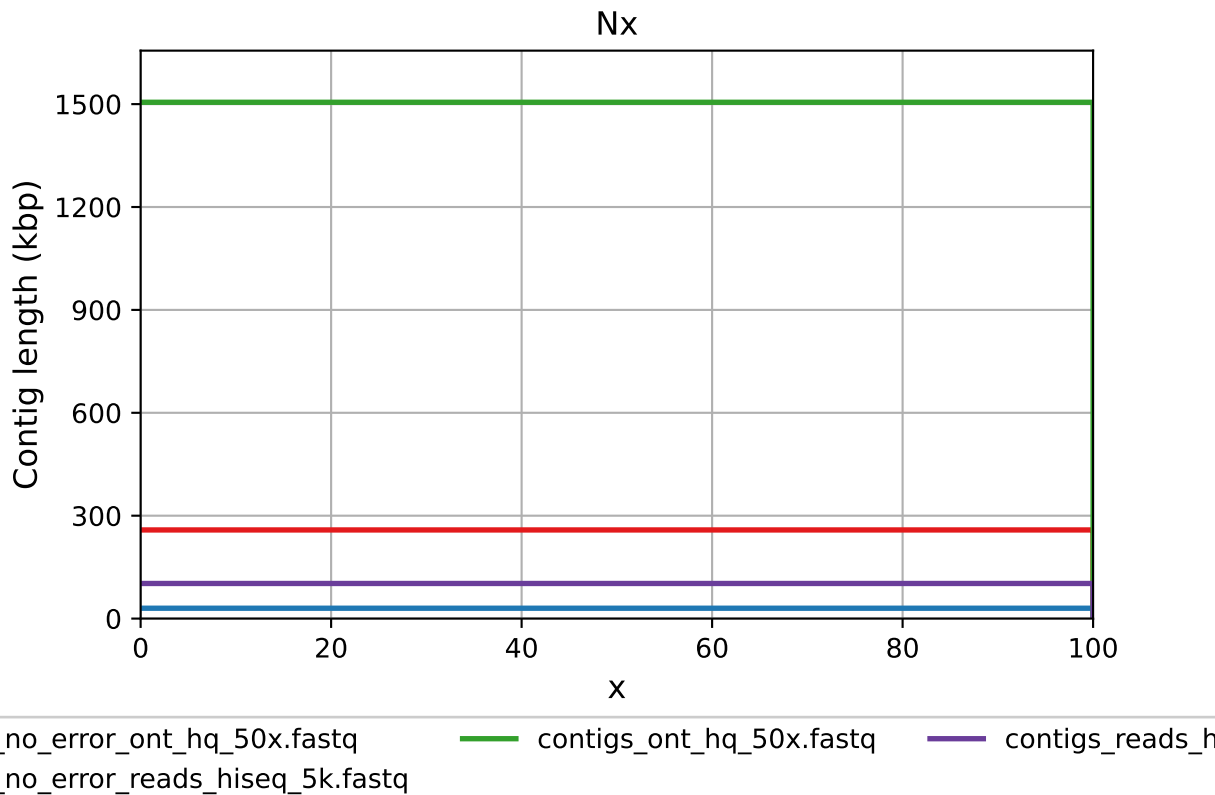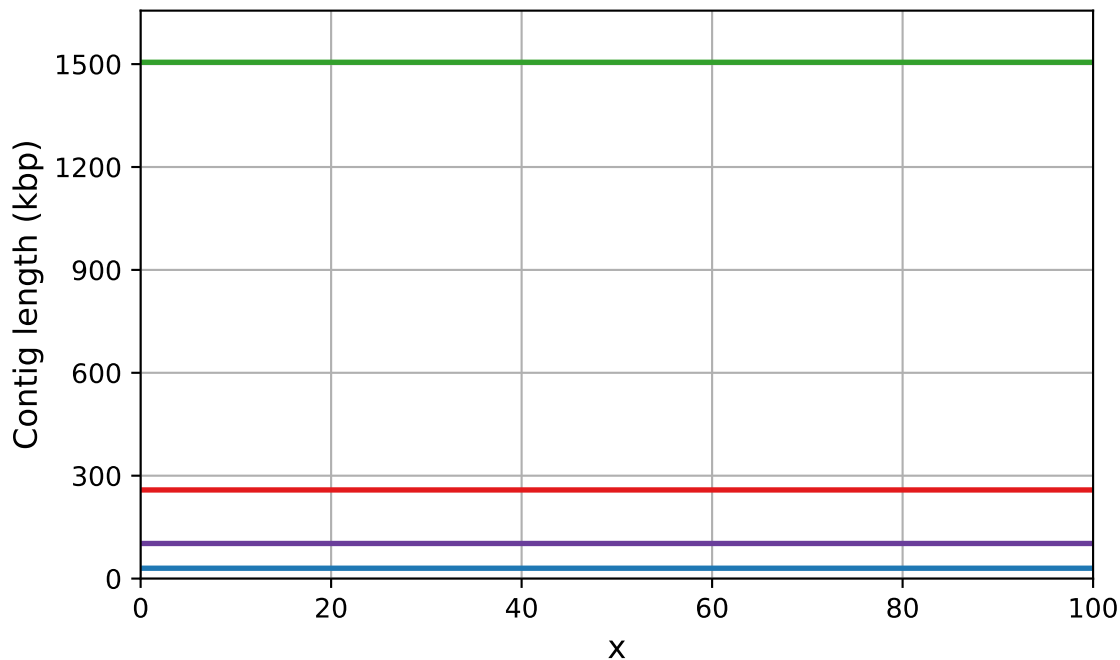
Misassemblies report

	contigs_no_error_ont_hq_50x.fastq	contigs_no_error_reads_hiseq_5k.fastq	contigs_ont_hq_50x.fastq	contigs_reads_hiseq_5k.fastq
# misassemblies	17	4	118	0
# contig misassemblies	17	4	118	0
# c. relocations	17	4	113	0
# c. translocations	0	0	0	0
# c. inversions	0	0	5	0
# scaffold misassemblies	0	0	0	0
# s. relocations	0	0	0	0
# s. translocations	0	0	0	0
# s. inversions	0	0	0	0
# misassembled contigs	1	1	1	0
Misassembled contigs length	258446	30215	1505388	0
# local misassemblies	0	3	3	0
# scaffold gap ext. mis.	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0
# unaligned mis. contigs	0	0	0	1
# mismatches	0	0	5512	191
# indels	0	0	16345	7
# indels (<= 5 bp)	0	0	16322	5
# indels (> 5 bp)	0	0	23	2
Indels length	0	0	19742	41

All statistics are based on contigs of size >= 500 bp, unless otherwise noted
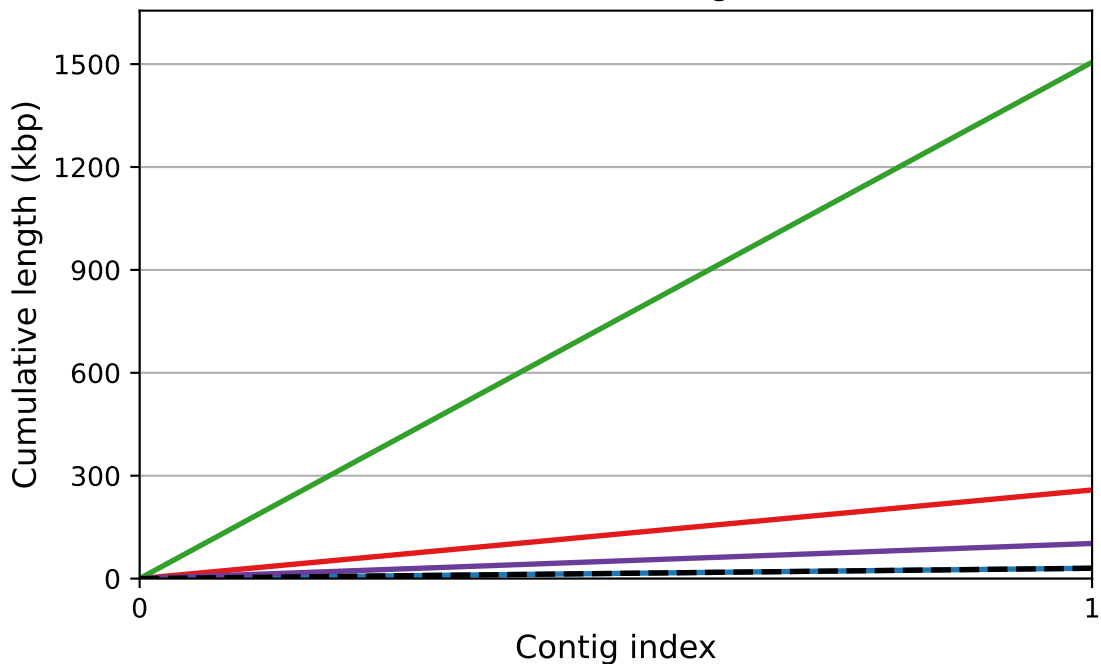(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Unaligned report

	contigs_no_error_ont_hq_50x.fastq	contigs_no_error_reads_hiseq_5k.fastq	contigs_ont_hq_50x.fastq	contigs_reads_hiseq_5k.fastq
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	0	0	1	1
Partially unaligned length	0	0	388167	57449
# N's	0	0	0	0

All statistics are based on contigs of size >= 500 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Nx

Contig length (kbp)

- s_no_error_ont_hq_50x.fastq
- contigs_ont_hq_50x.fastq
- contigs_reads_h
- s_no_error_reads_hiseq_5k.fastq

NGx

Contig length (kbp)

x

s_no_error_ont_hq_50x.fastq ▬▬ contigs_ont_hq_50x.fastq ▬▬ contigs_reads_h
s_no_error_reads_hiseq_5k.fastq

Cumulative length

contigs_no_error_ont_hq_50x.fastq   contigs_ont_hq_50x.fastq   Refe
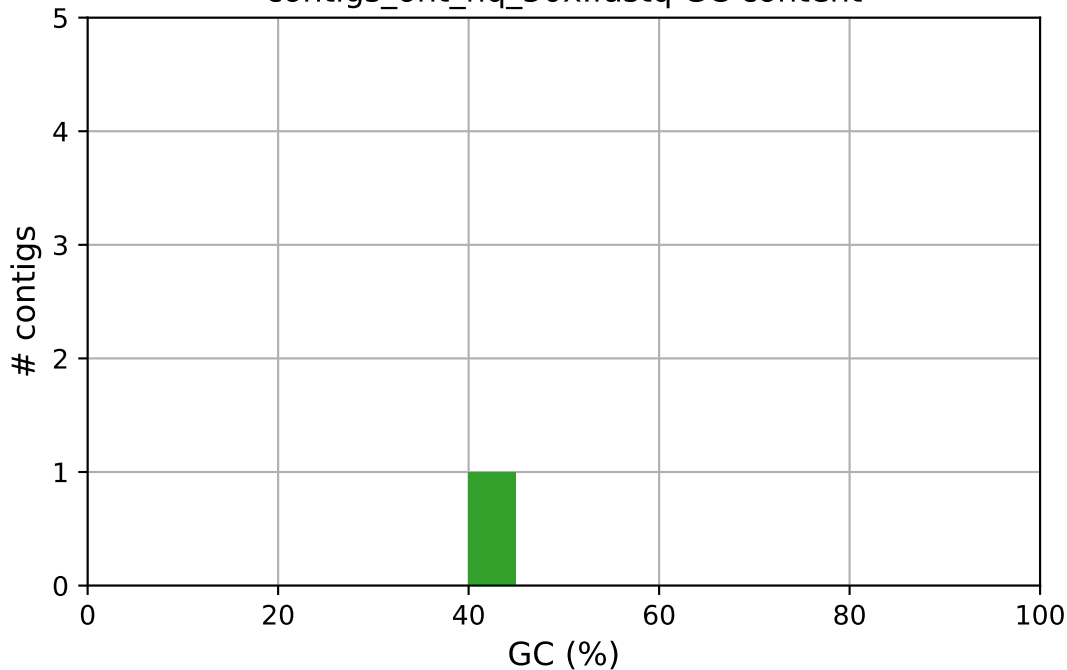
contigs_no_error_reads_hiseq_5k.fastq   contigs_reads_hiseq_5k.fastq
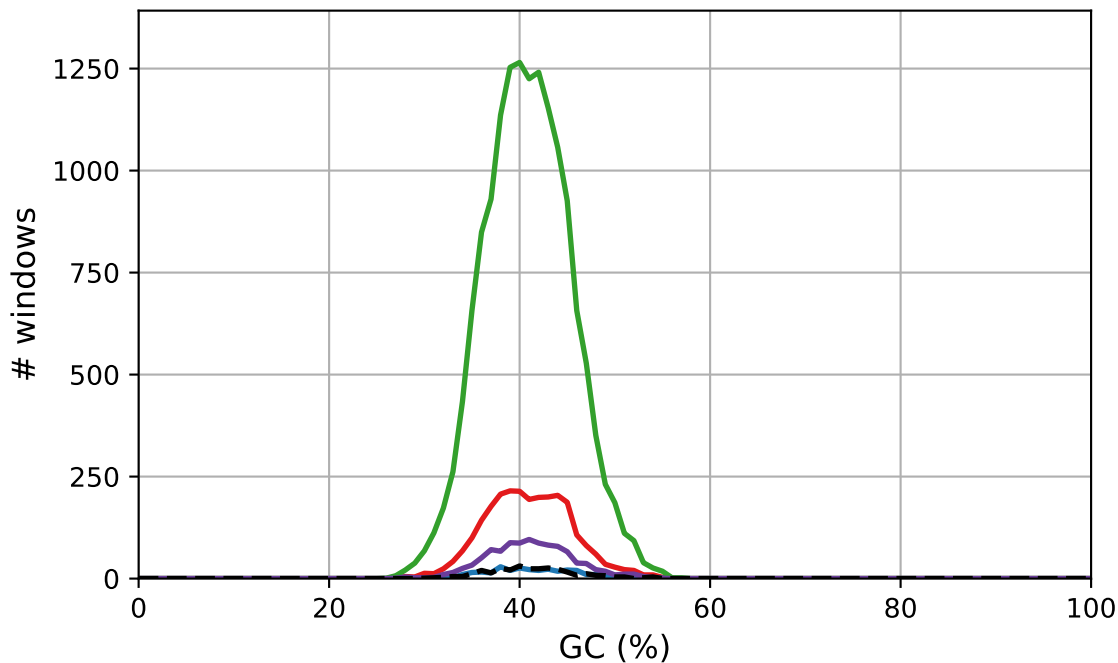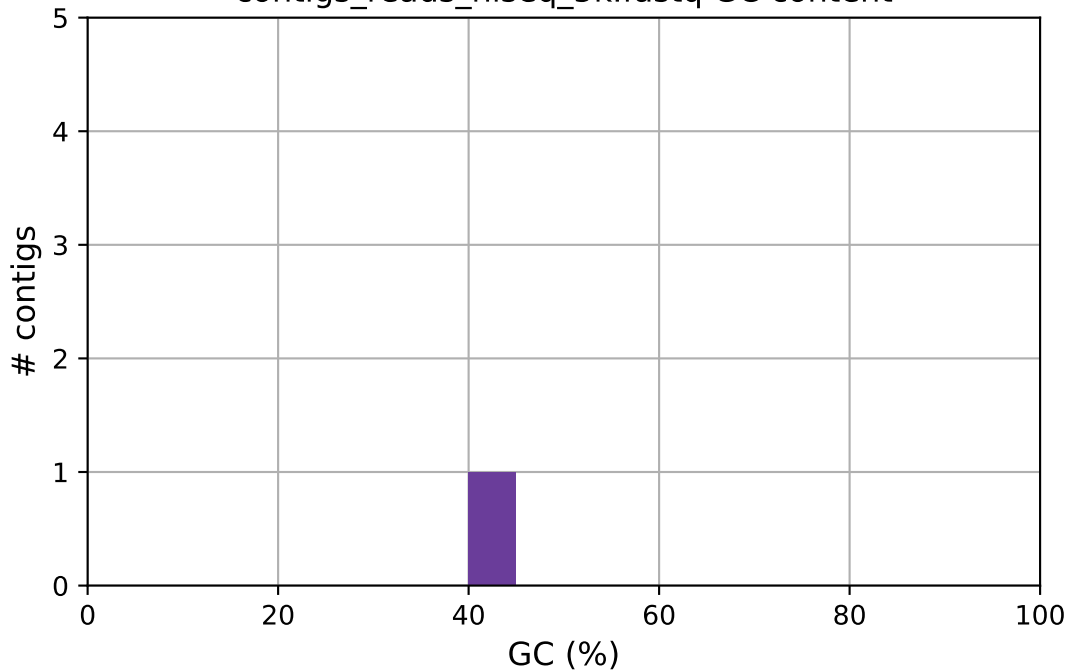
GC content

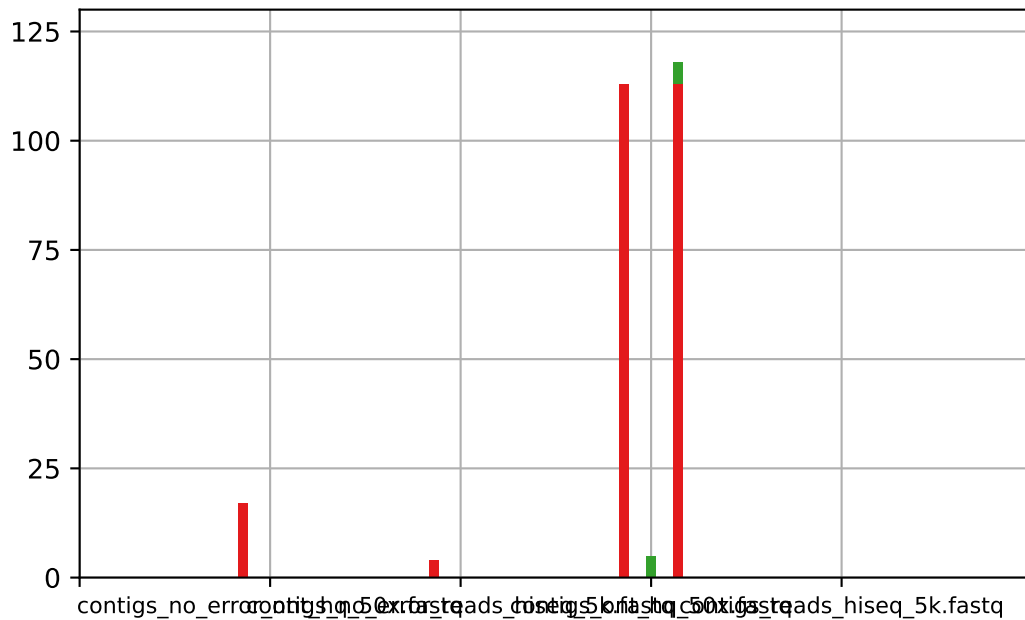contigs_no_error_ont_hq_50x.fastq
contigs_ont_hq_50x.fastq
Refe...
contigs_no_error_reads_hiseq_5k.fastq
contigs_reads_hiseq_5k.fastq

contigs_no_error_ont_hq_50x.fastq GC content
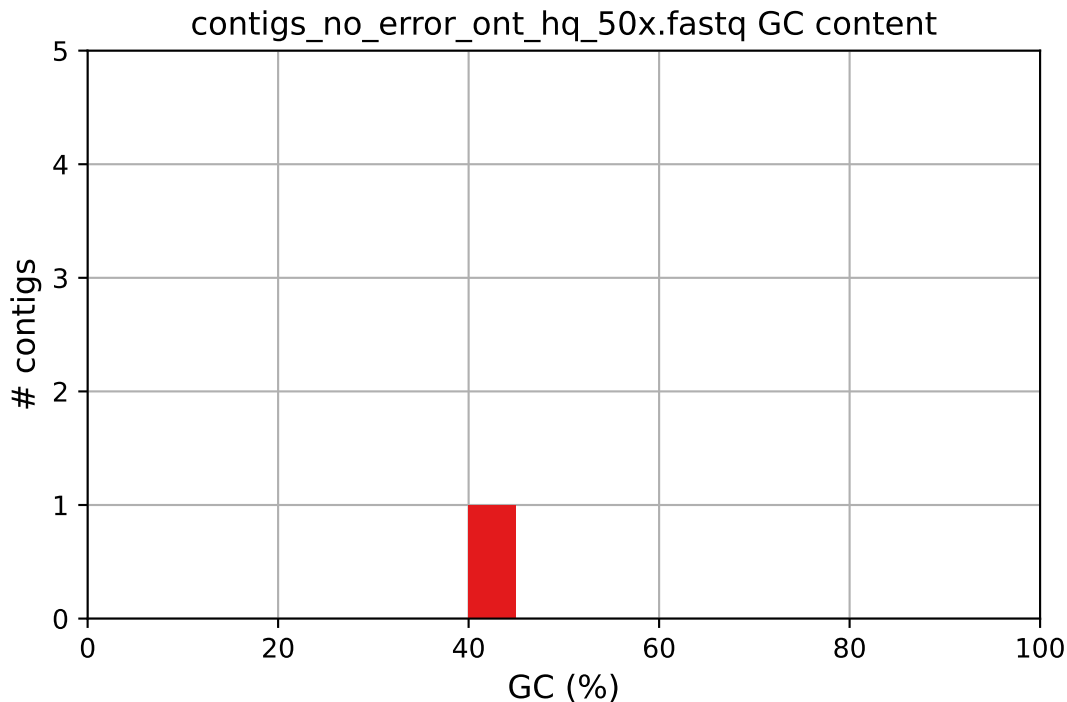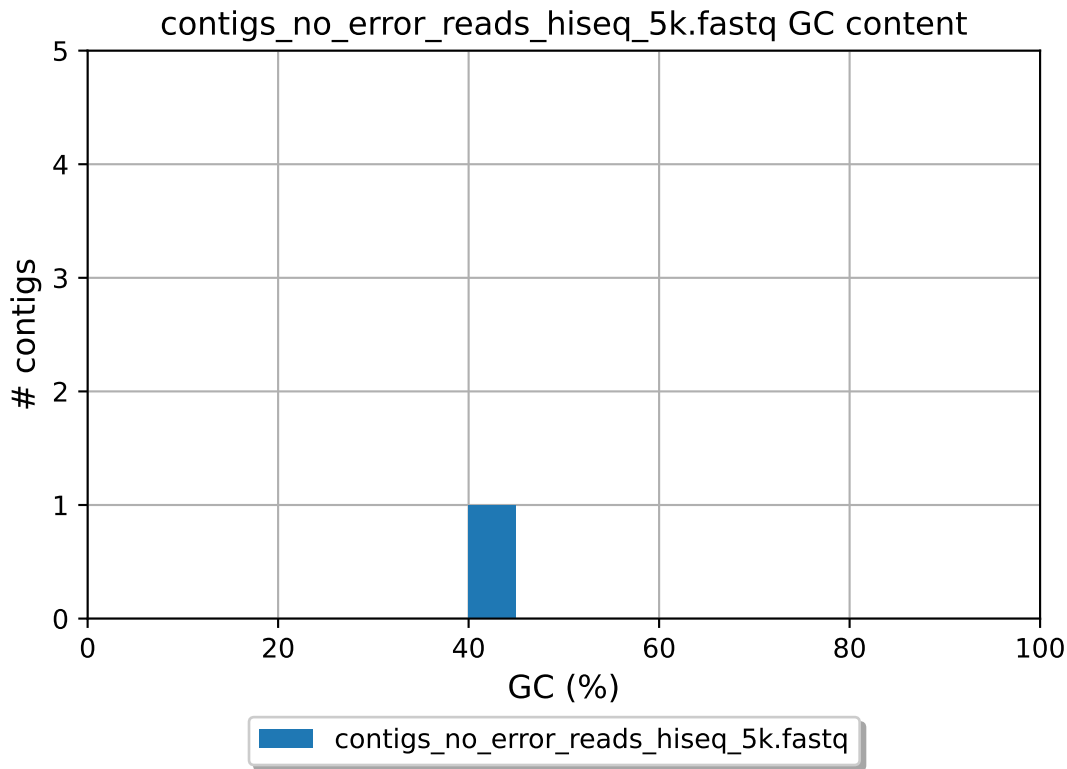
contigs_no_error_reads_hiseq_5k.fastq GC content

contigs_ont_hq_50x.fastq GC content

contigs_reads_hiseq_5k.fastq GC content

Misassemblies

Legend: ■ # relocations ■ # inversions

X-axis labels: contigs_no_error, contigs_no_50x.fastq, reads_hiseq_5k.fastq, contigs_no_50x.fastq, reads_hiseq_5k.fastq

FRCurve (misassemblies)

Genome coverage (%) vs Feature space

Legend:
- _no_error_ont_hq_50x.fastq
- contigs_ont_hq_50x.fastq
- contigs_reads_h
- _no_error_reads_hiseq_5k.fastq
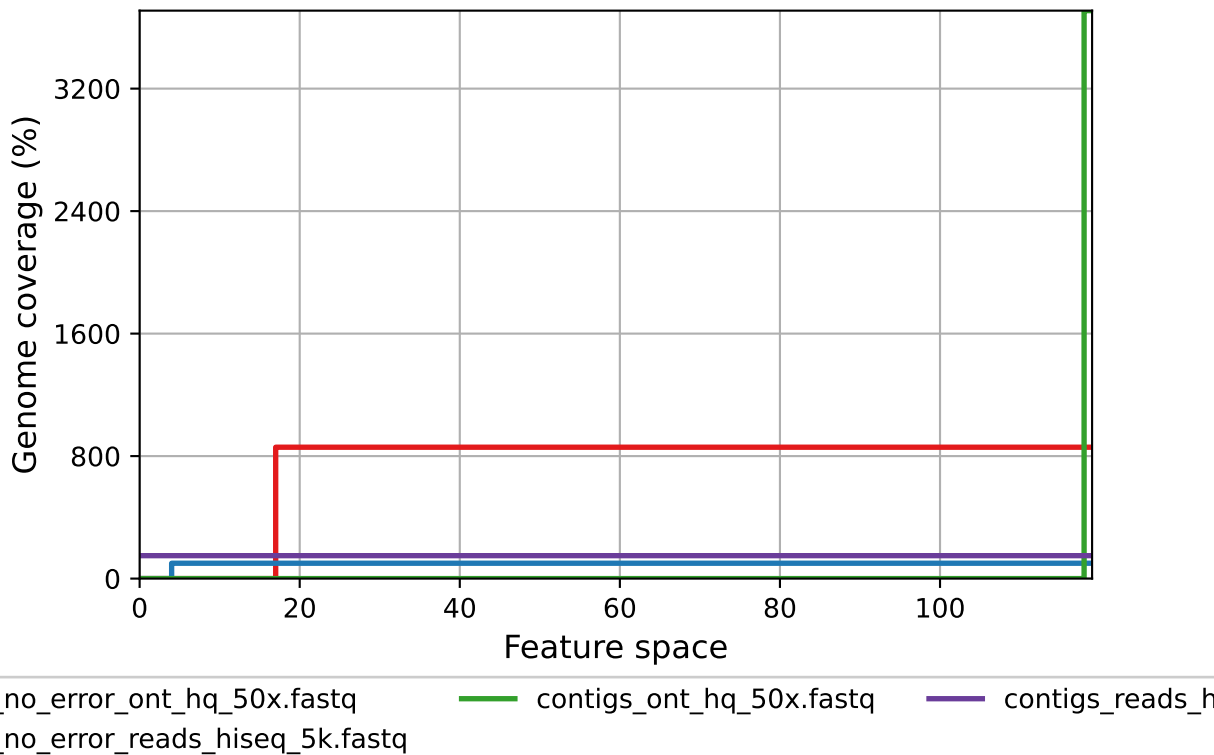
Cumulative length (aligned contigs)
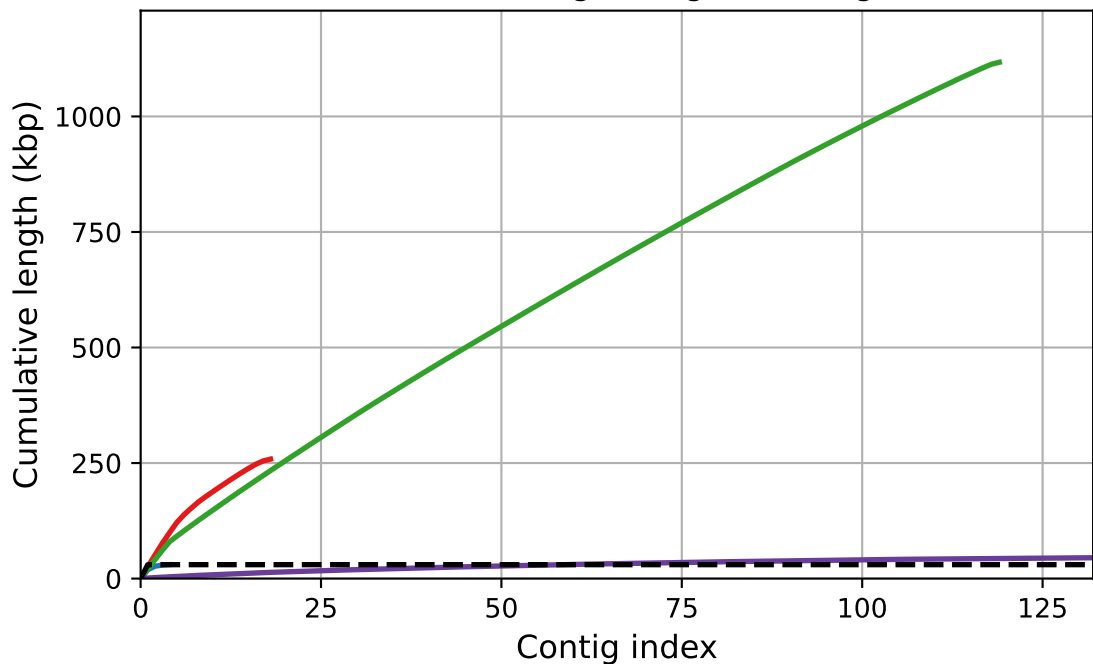
NAx

Contig length (kbp) vs x
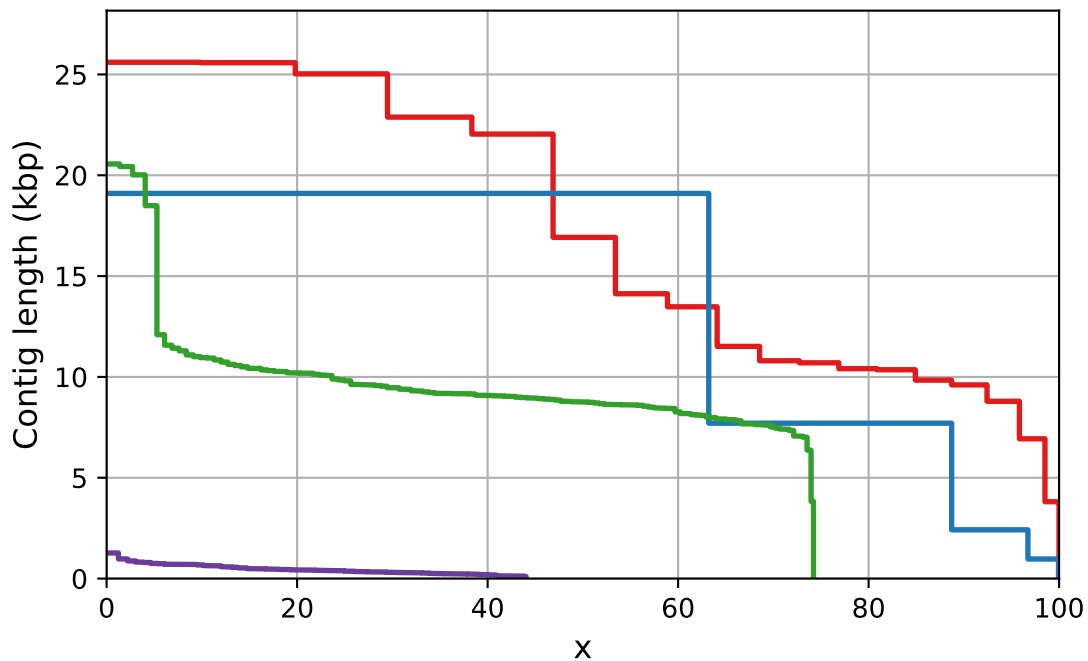
Legend: s_no_error_ont_hq_50x.fastq, contigs_ont_hq_50x.fastq, contigs_reads_h..., s_no_error_reads_hiseq_5k.fastq

NGAx

Contig length (kbp)
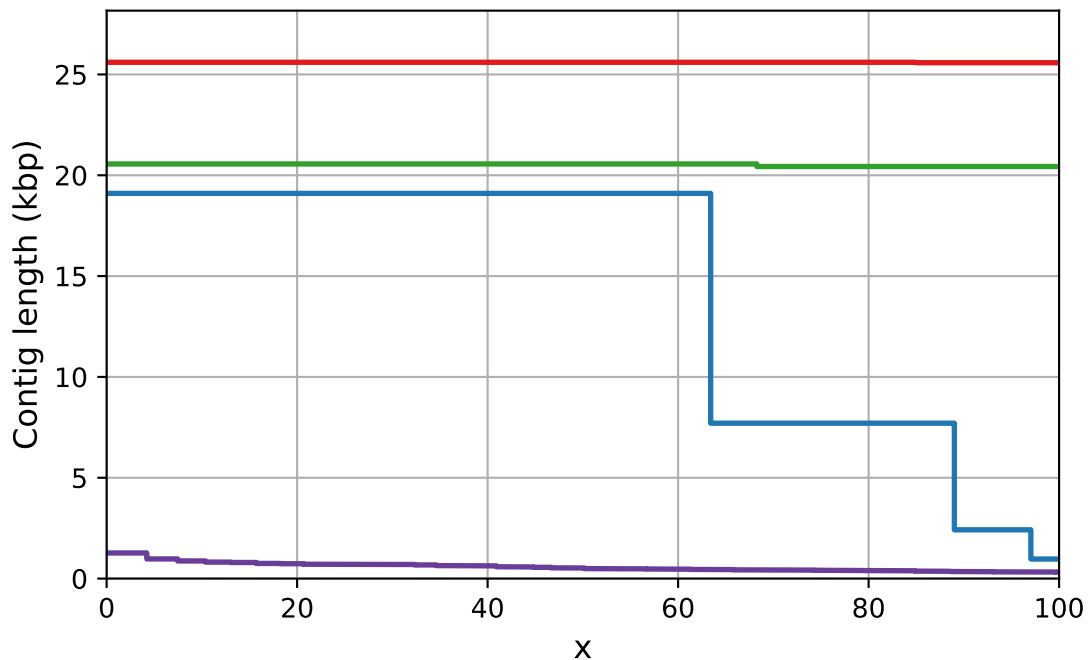
x

_no_error_ont_hq_50x.fastq   contigs_ont_hq_50x.fastq   contigs_reads_h

_no_error_reads_hiseq_5k.fastq

Genome fraction, %

s_no_error_ont_hq_50x.fastq   contigs_ont_hq_50x.fastq   contigs_reads_h
s_no_error_reads_hiseq_5k.fastq