

Report

	spades_no_error_hybrid_output_contigs	spades_no_error_hiseq_output_contigs	spades_no_error_ont_output_contigs	spades_hybrid_output_contigs	spades_reads_hiseq_5k_output_contigs	spades_ont_hq_50x_output_contigs
# contigs (>= 0 bp)	1	1	1	1	1	1
# contigs (>= 1000 bp)	1	1	1	1	1	1
# contigs (>= 5000 bp)	1	1	1	1	1	1
# contigs (>= 10000 bp)	1	1	1	1	1	1
# contigs (>= 25000 bp)	1	1	1	1	1	1
# contigs (>= 50000 bp)	0	0	0	0	0	0
Total length (>= 0 bp)	29482	29482	29748	29482	29482	29754
Total length (>= 1000 bp)	29482	29482	29748	29482	29482	29754
Total length (>= 5000 bp)	29482	29482	29748	29482	29482	29754
Total length (>= 10000 bp)	29482	29482	29748	29482	29482	29754
Total length (>= 25000 bp)	29482	29482	29748	29482	29482	29754
Total length (>= 50000 bp)	0	0	0	0	0	0
# contigs	1	1	1	1	1	1
Largest contig	29482	29482	29748	29482	29482	29754
Total length	29482	29482	29748	29482	29482	29754
Reference length	30119	30119	30119	30119	30119	30119
GC (%)	41.26	41.26	41.27	41.26	41.26	41.27
Reference GC (%)	41.24	41.24	41.24	41.24	41.24	41.24
N50	29482	29482	29748	29482	29482	29754
NG50	29482	29482	29748	29482	29482	29754
N90	29482	29482	29748	29482	29482	29754
NG90	29482	29482	29748	29482	29482	29754
auN	29482.0	29482.0	29748.0	29482.0	29482.0	29754.0
auNG	28858.5	28858.5	29381.6	28858.5	28858.5	29393.4
L50	1	1	1	1	1	1
LG50	1	1	1	1	1	1
L90	1	1	1	1	1	1
LG90	1	1	1	1	1	1
# misassemblies	0	0	0	0	0	0
# misassembled contigs	0	0	0	0	0	0
Misassembled contigs length	0	0	0	0	0	0
# local misassemblies	0	0	0	0	0	0
# scaffold gap ext. mis.	0	0	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0	0	0
# unaligned mis. contigs	0	0	0	0	0	0
# unaligned contigs	0 + 0 part	0 + 0 part	0 + 0 part	0 + 0 part	0 + 0 part	0 + 0 part
Unaligned length	0	0	0	0	0	0
Genome fraction (%)	97.885	97.885	98.768	97.885	97.885	98.738
Duplication ratio	1.000	1.000	1.000	1.000	1.000	1.000
# N's per 100 kbp	0.00	0.00	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	0.00	0.00	0.00	0.00	0.00	26.90
# indels per 100 kbp	0.00	0.00	0.00	0.00	0.00	73.96
Largest alignment	29482	29482	29748	29482	29482	29744
Total aligned length	29482	29482	29748	29482	29482	29744
NA50	29482	29482	29748	29482	29482	29744
NGA50	29482	29482	29748	29482	29482	29744
NA90	29482	29482	29748	29482	29482	29744
NGA90	29482	29482	29748	29482	29482	29744
auNA	29482.0	29482.0	29748.0	29482.0	29482.0	29734.0
auNGA	28858.5	28858.5	29381.6	28858.5	28858.5	29373.7
LA50	1	1	1	1	1	1
LGA50	1	1	1	1	1	1
LA90	1	1	1	1	1	1
LGA90	1	1	1	1	1	1

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

	spades_no_error_hybrid_output_contigs	spades_no_error_hiseq_output_contigs	spades_no_error_ont_output_contigs	spades_hybrid_output_contigs	spades_reads_hiseq_5k_output_contigs	spades_ont_hq_50x_output_contigs
# misassemblies	0	0	0	0	0	0
# contig misassemblies	0	0	0	0	0	0
# c. relocations	0	0	0	0	0	0
# c. translocations	0	0	0	0	0	0
# c. inversions	0	0	0	0	0	0
# scaffold misassemblies	0	0	0	0	0	0
# s. relocations	0	0	0	0	0	0
# s. translocations	0	0	0	0	0	0
# s. inversions	0	0	0	0	0	0
# misassembled contigs	0	0	0	0	0	0
Misassembled contigs length	0	0	0	0	0	0
# local misassemblies	0	0	0	0	0	0
# scaffold gap ext. mis.	0	0	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0	0	0
# unaligned mis. contigs	0	0	0	0	0	0
# mismatches	0	0	0	0	0	8
# indels	0	0	0	0	0	22
# indels (<= 5 bp)	0	0	0	0	0	22
# indels (> 5 bp)	0	0	0	0	0	0
Indels length	0	0	0	0	0	31

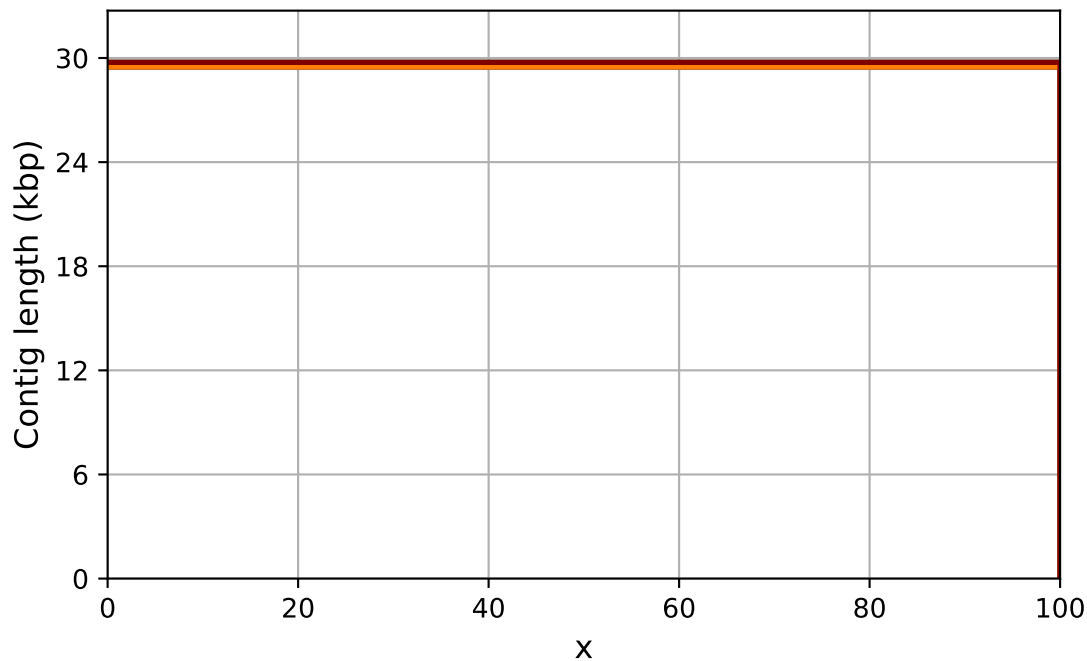
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Unaligned report

	spades_no_error_hybrid_output_contigs	spades_no_error_hiseq_output_contigs	spades_no_error_ont_output_contigs	spades_hybrid_output_contigs	spades_reads_hiseq_5k_output_contigs	spades_ont_hq_50x_output_contigs
# fully unaligned contigs	0	0	0	0	0	0
Fully unaligned length	0	0	0	0	0	0
# partially unaligned contigs	0	0	0	0	0	0
Partially unaligned length	0	0	0	0	0	0
# N's	0	0	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



hybrid_output_contigs

spades_no_error_ont_output_contigs

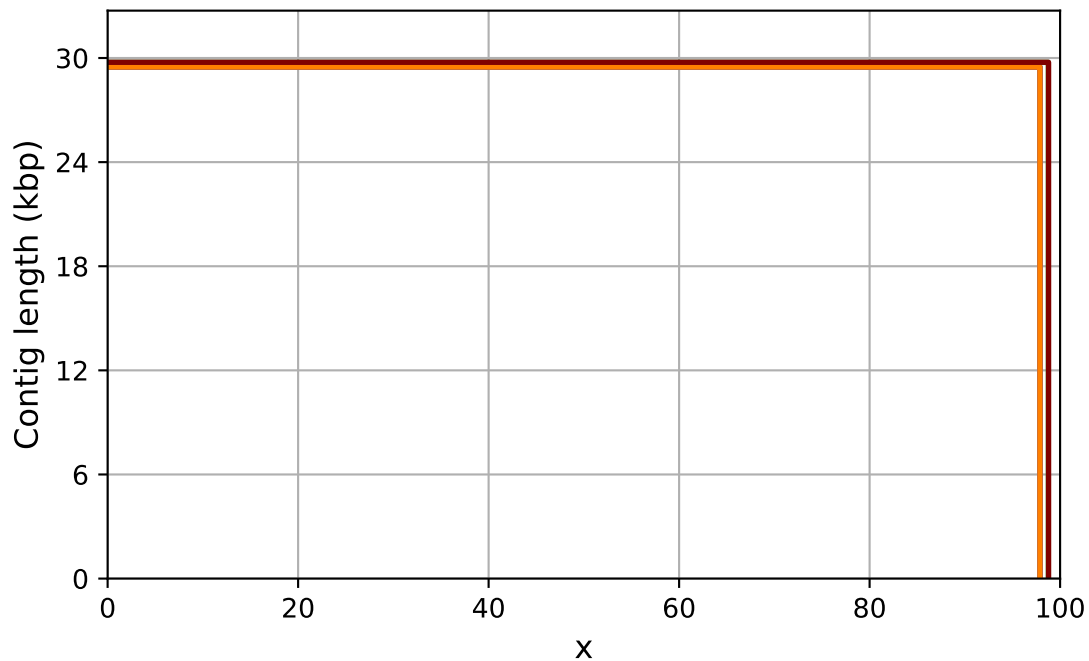
spades_reads_

iseq_output_contigs

spades_hybrid_output_contigs

spades_ont_hq

NGx



hybrid_output_contigs

spades_no_error_ont_output_contigs

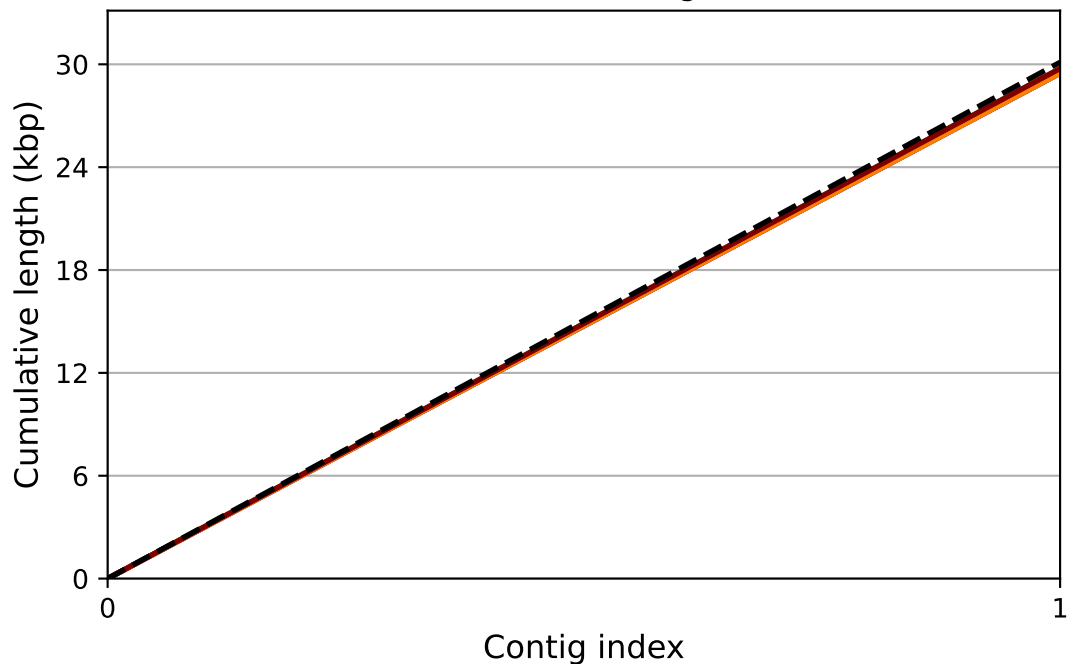
spades_reads_hq

naniseq_output_contigs

spades_hybrid_output_contigs

spades_ont_hq

Cumulative length

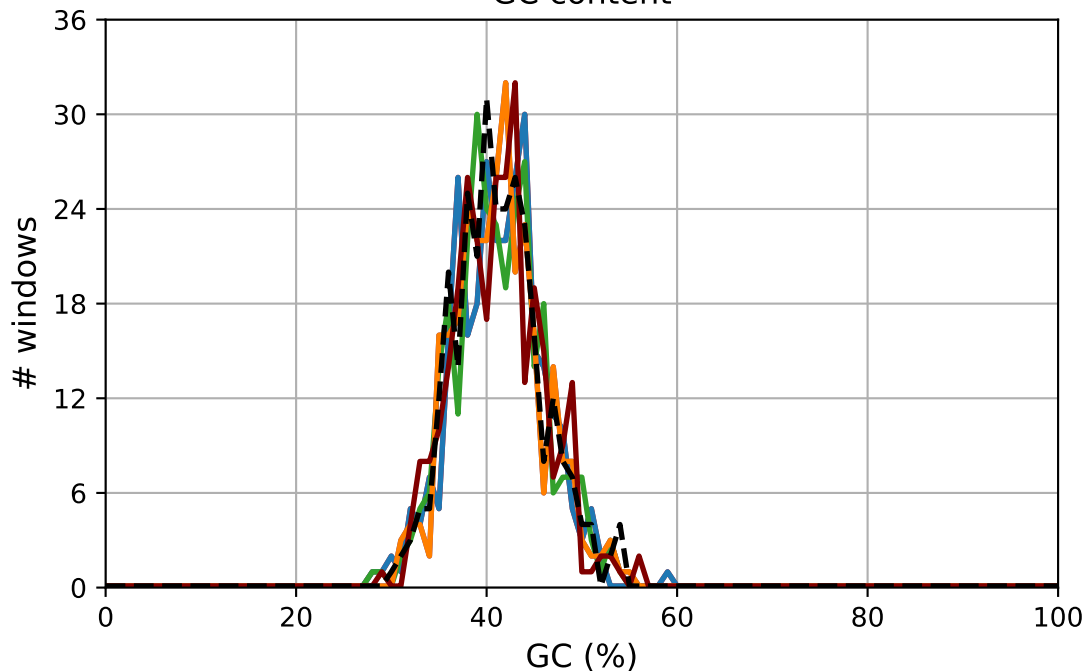


hybrid_output_contigs
hiseq_output_contigs
ont_output_contigs

spades_hybrid_output_contigs
spades_reads_hiseq_5k_output_contigs

spades_ont_output_contigs
Reference

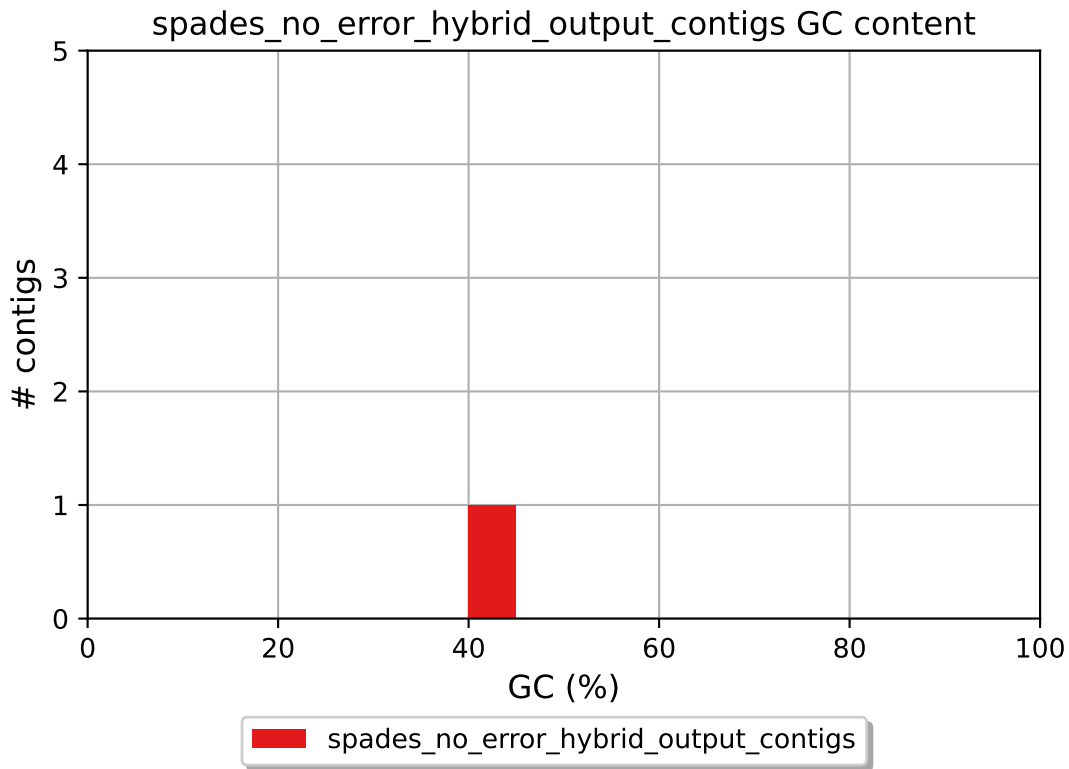
GC content

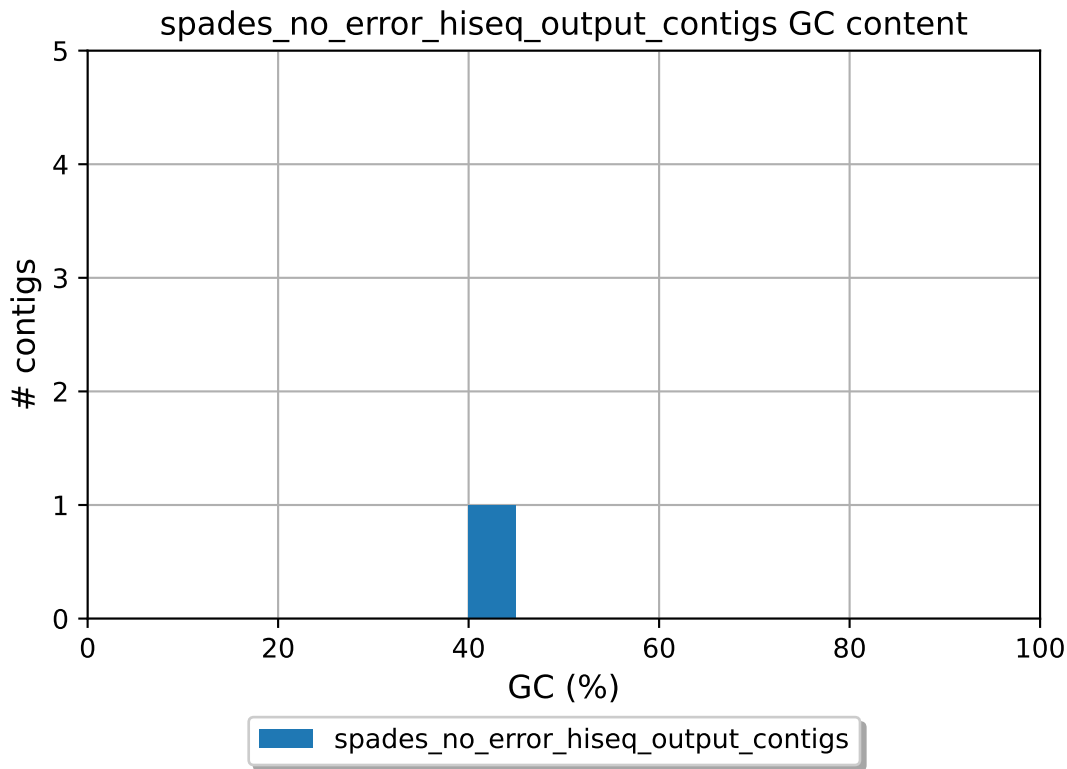


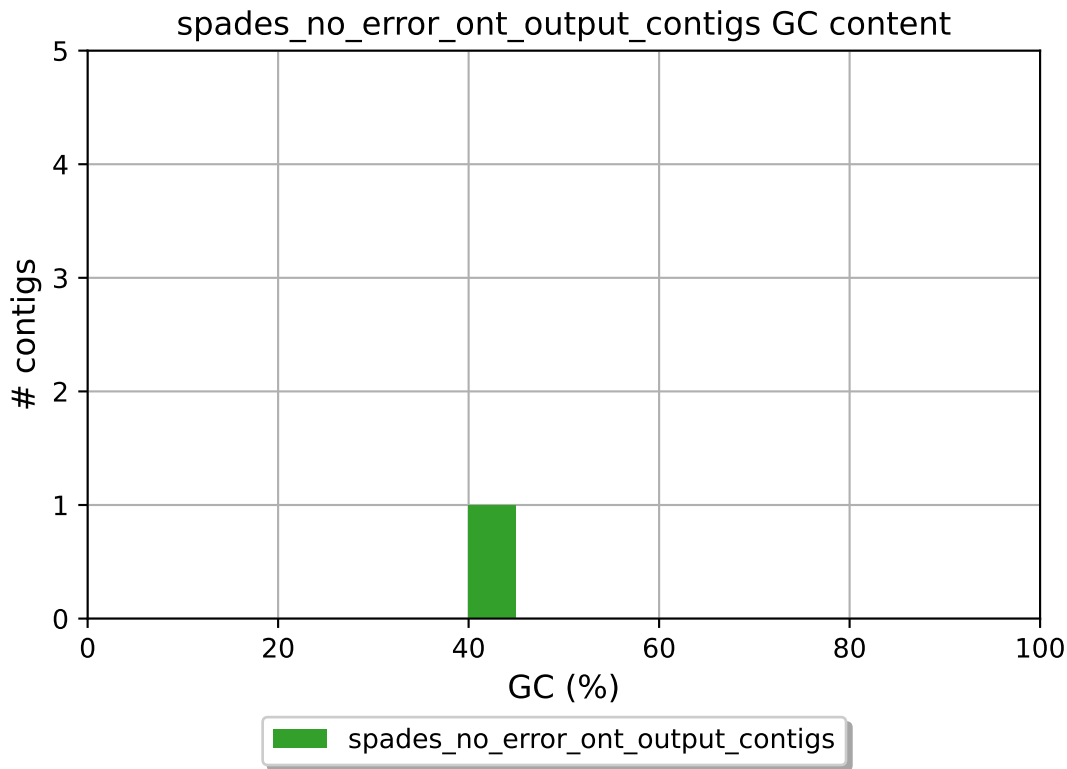
hybrid_output_contigs
hiseq_output_contigs
ont_output_contigs

spades_hybrid_output_contigs
spades_reads_hiseq_5k_output_contigs

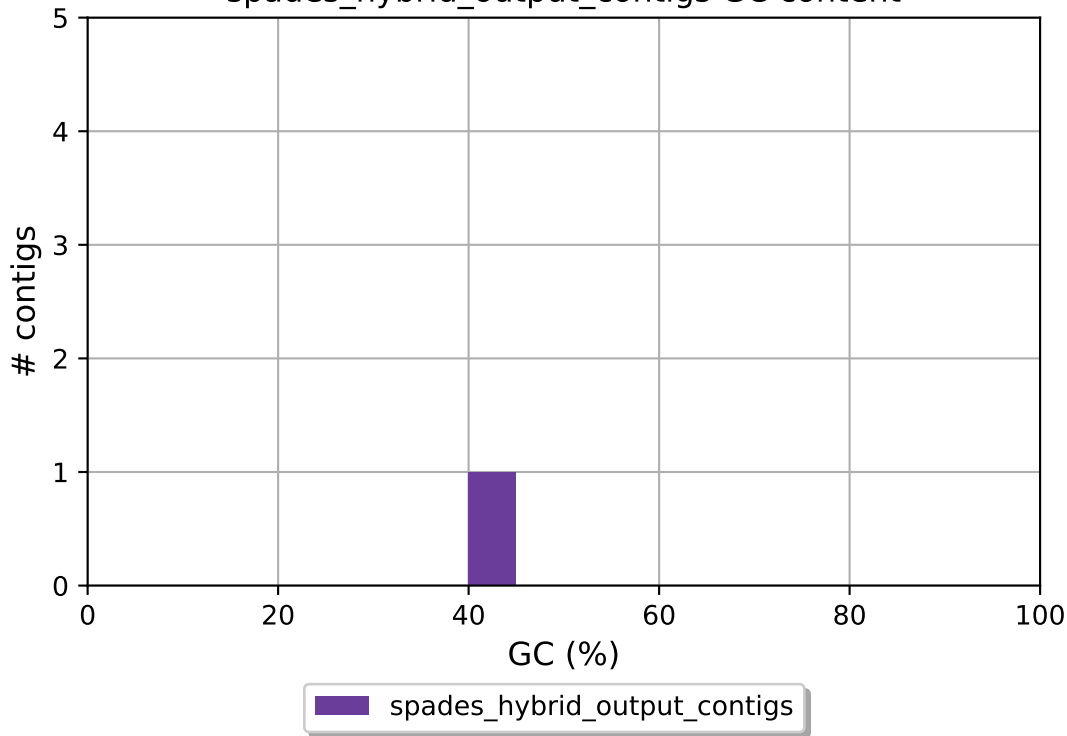
spades_ont_output_contigs
Reference



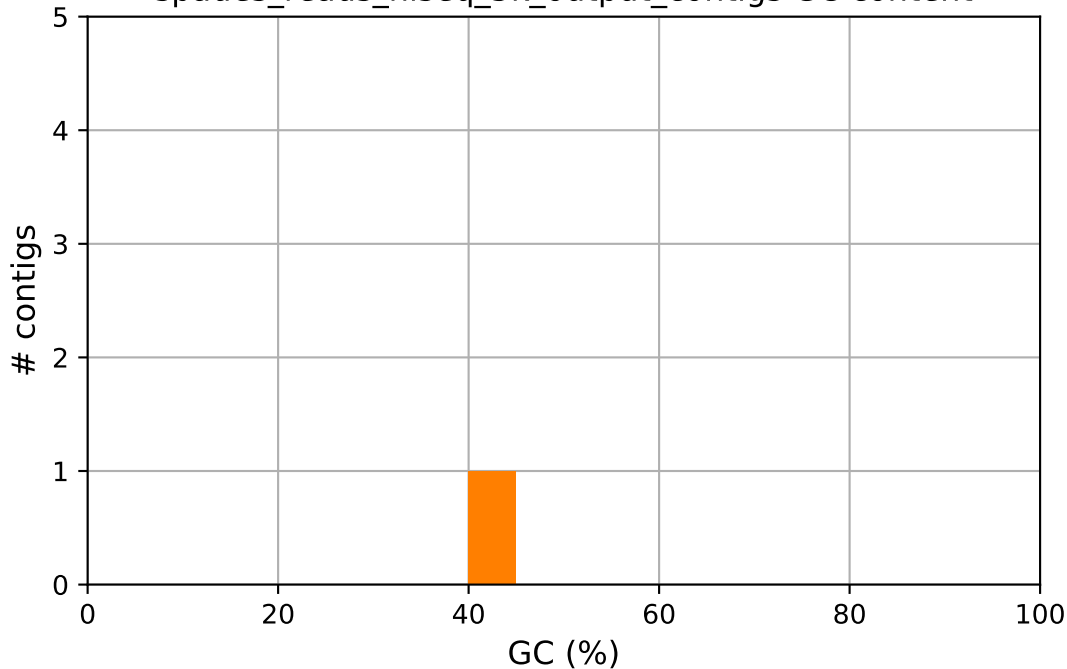




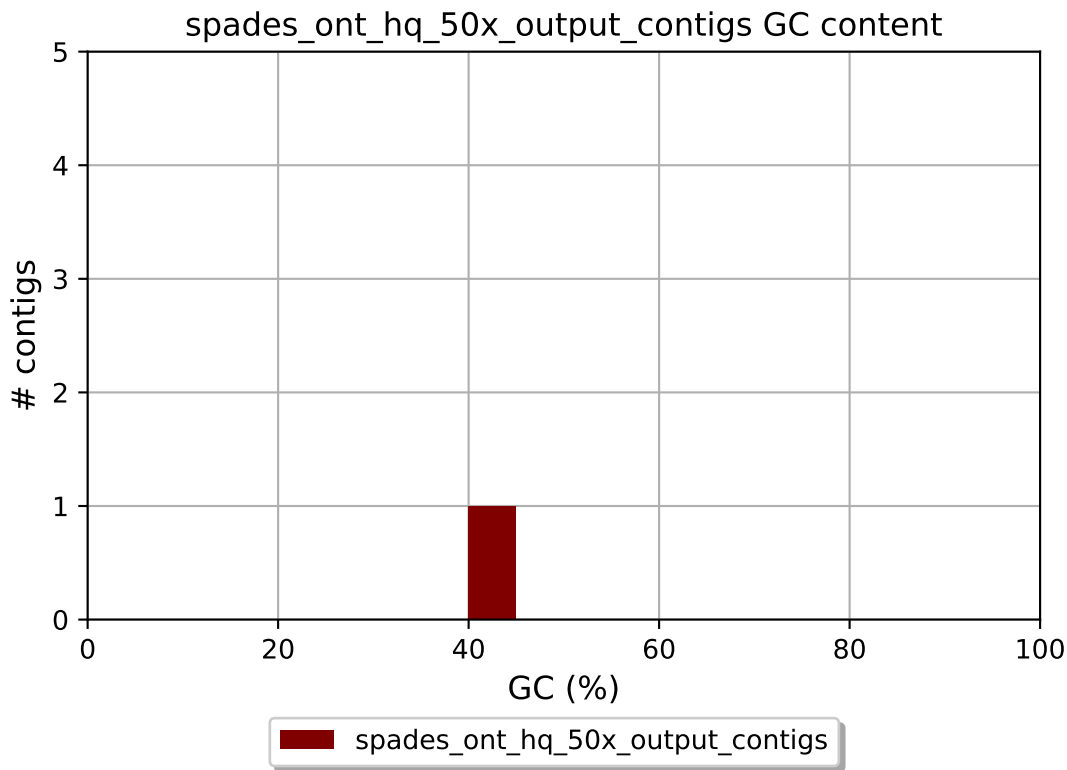
spades_hybrid_output_contigs GC content



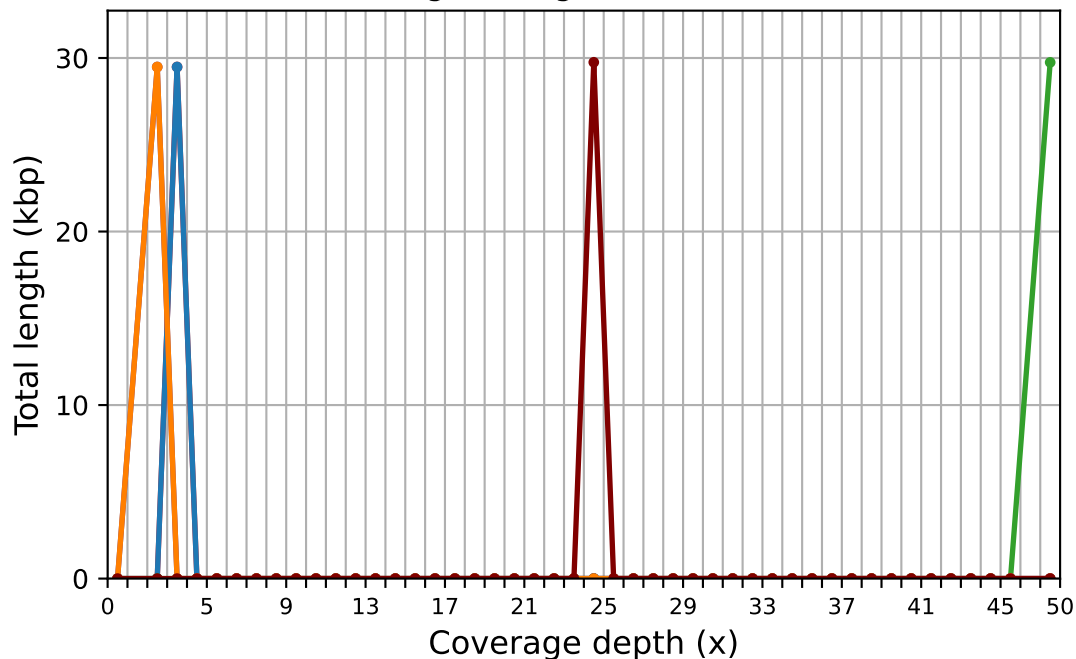
spades_reads_hiseq_5k_output_contigs GC content



spades_reads_hiseq_5k_output_contigs



Coverage histogram (bin size: 1x)



hybrid_output_contigs

spades_no_error_ont_output_contigs

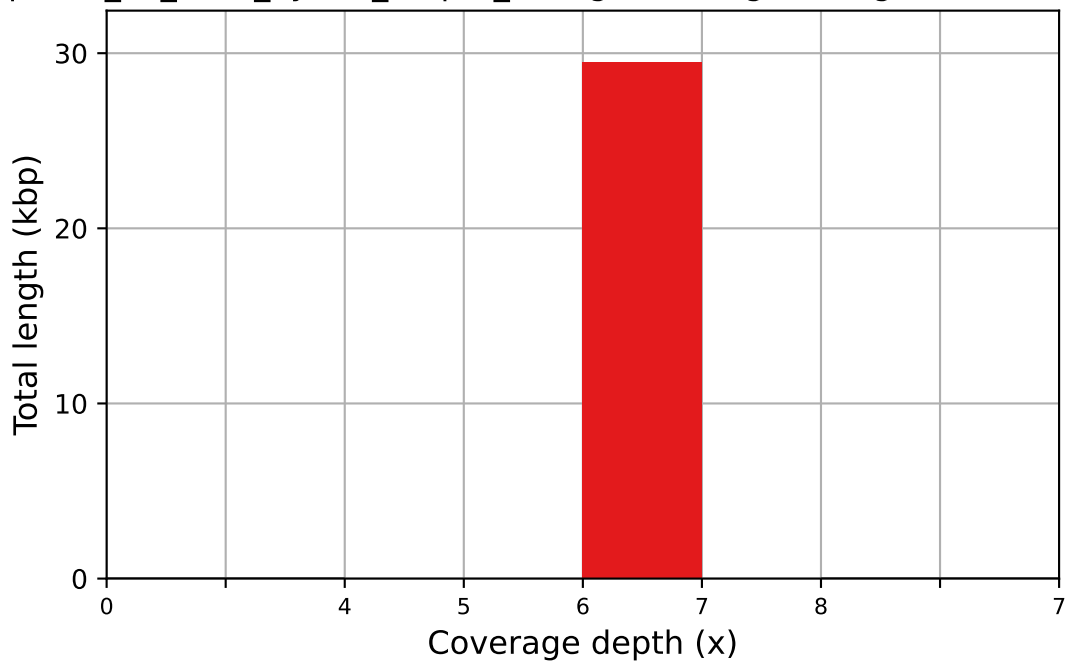
spades_reads_ont_output_contigs

spades_hybrid_output_contigs

spades_hybrid_output_contigs

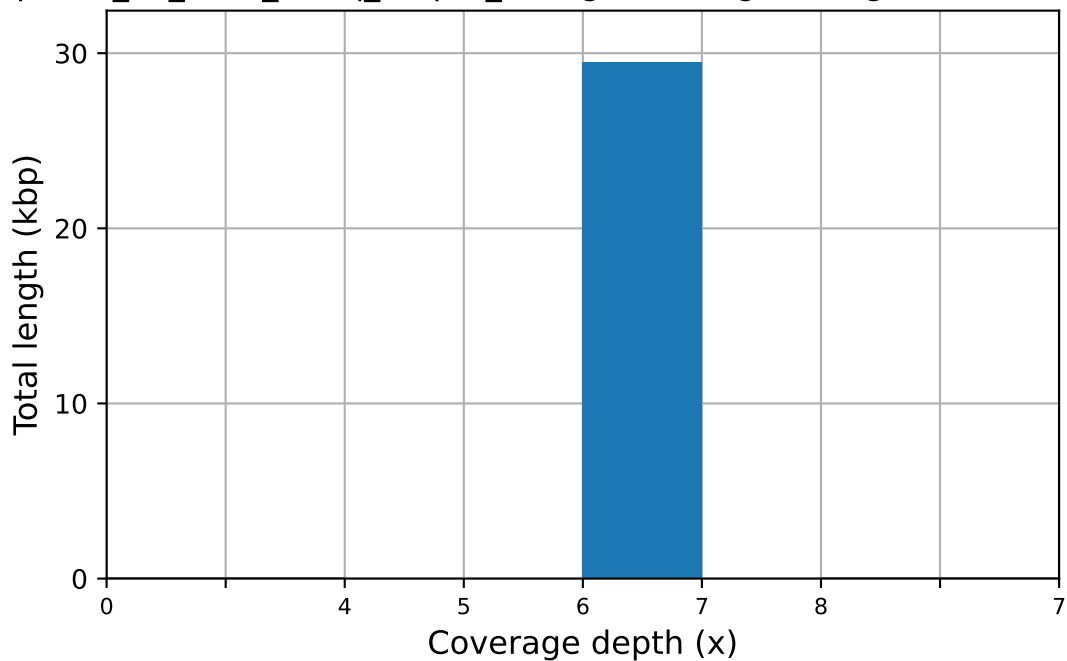
spades_ont_hq

spades_no_error_hybrid_output_contigs coverage histogram (bin size: 1x)



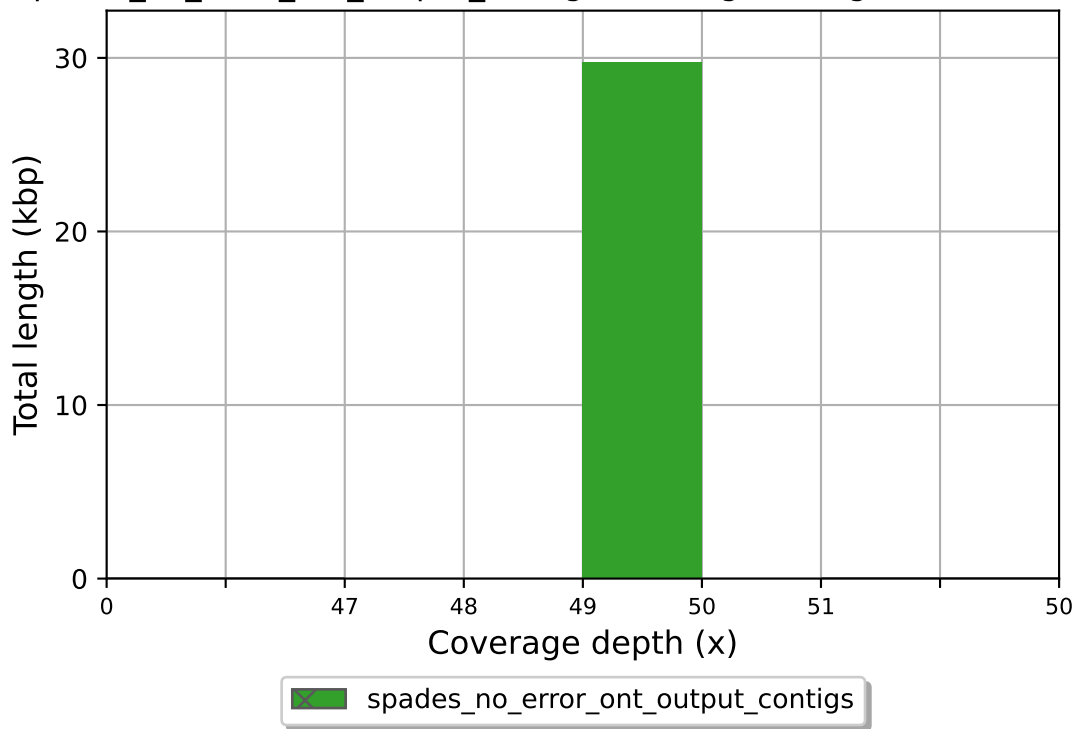
spades_no_error_hybrid_output_contigs

spades_no_error_hiseq_output_contigs coverage histogram (bin size: 1x)

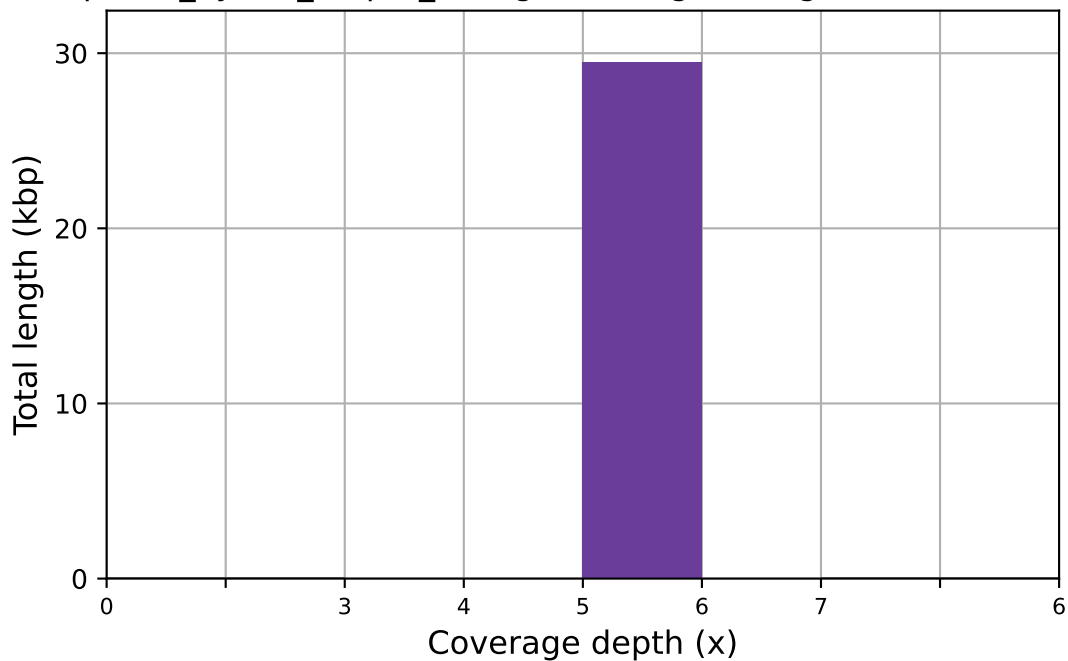


spades_no_error_hiseq_output_contigs

spades_no_error_ont_output_contigs coverage histogram (bin size: 1x)

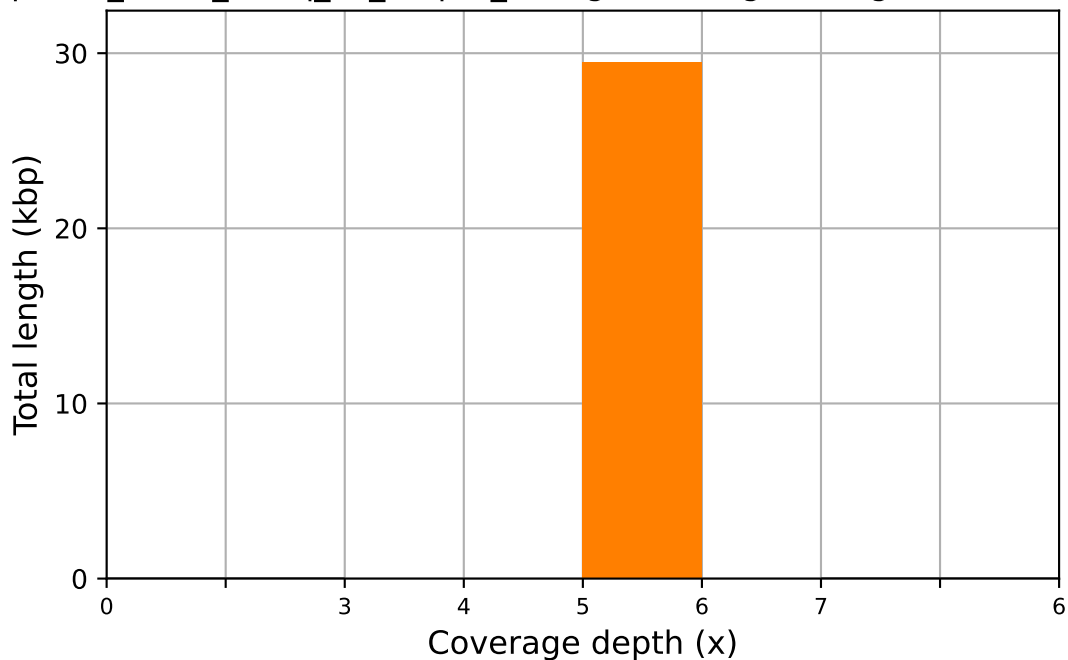


spades_hybrid_output_contigs coverage histogram (bin size: 1x)



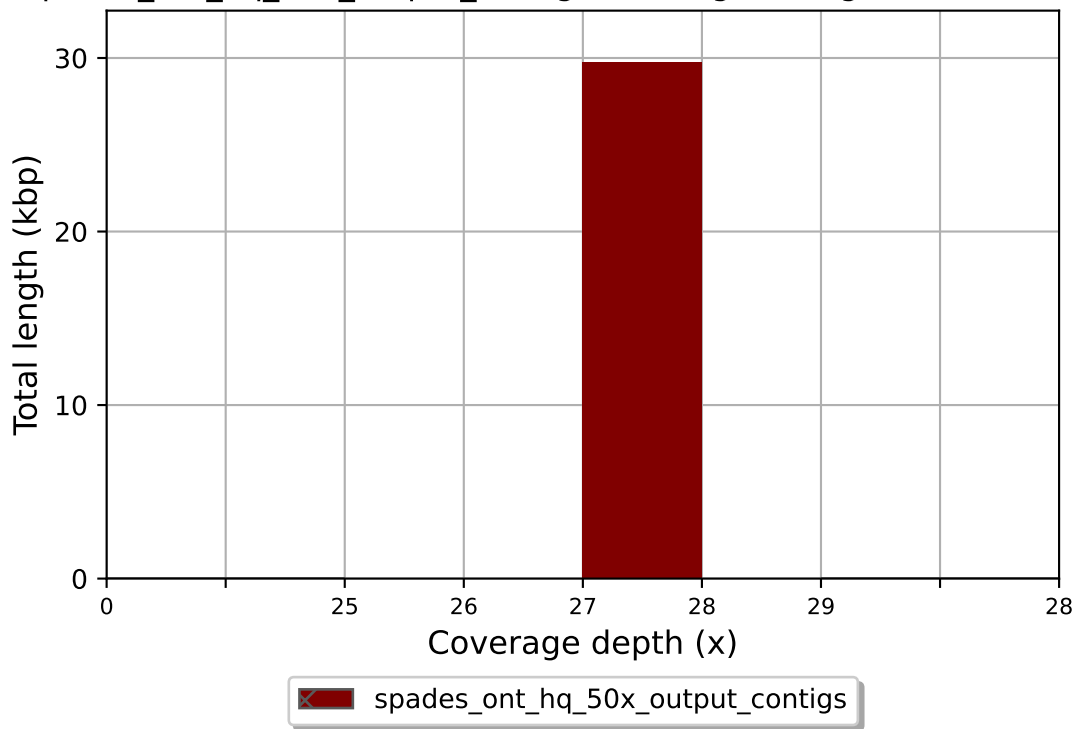
spades_hybrid_output_contigs

spades_reads_hiseq_5k_output_contigs coverage histogram (bin size: 1x)

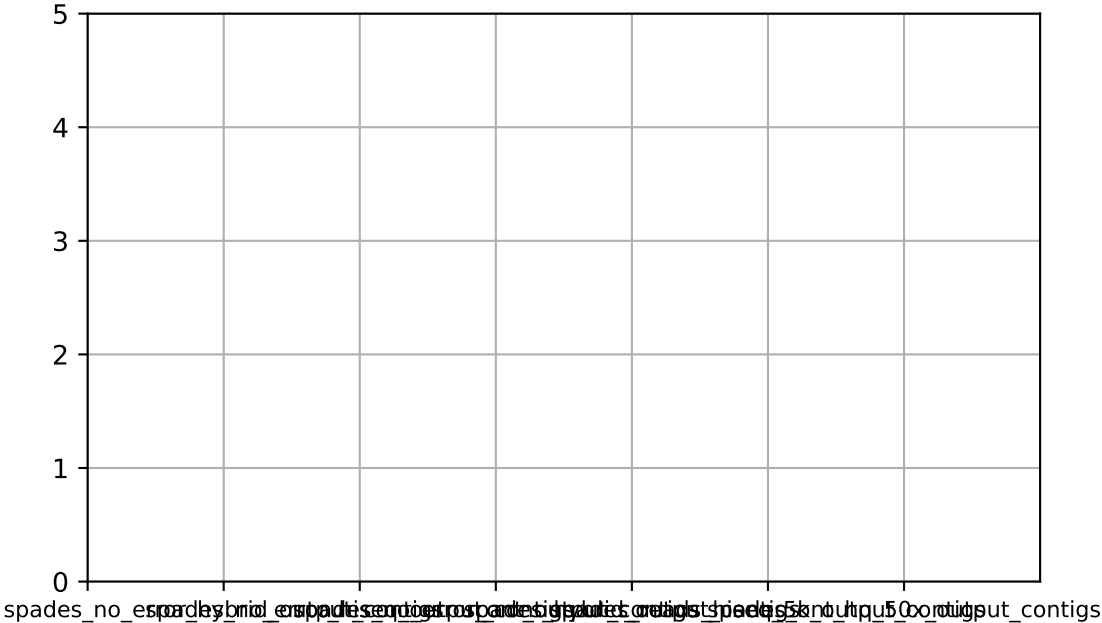


spades_reads_hiseq_5k_output_contigs

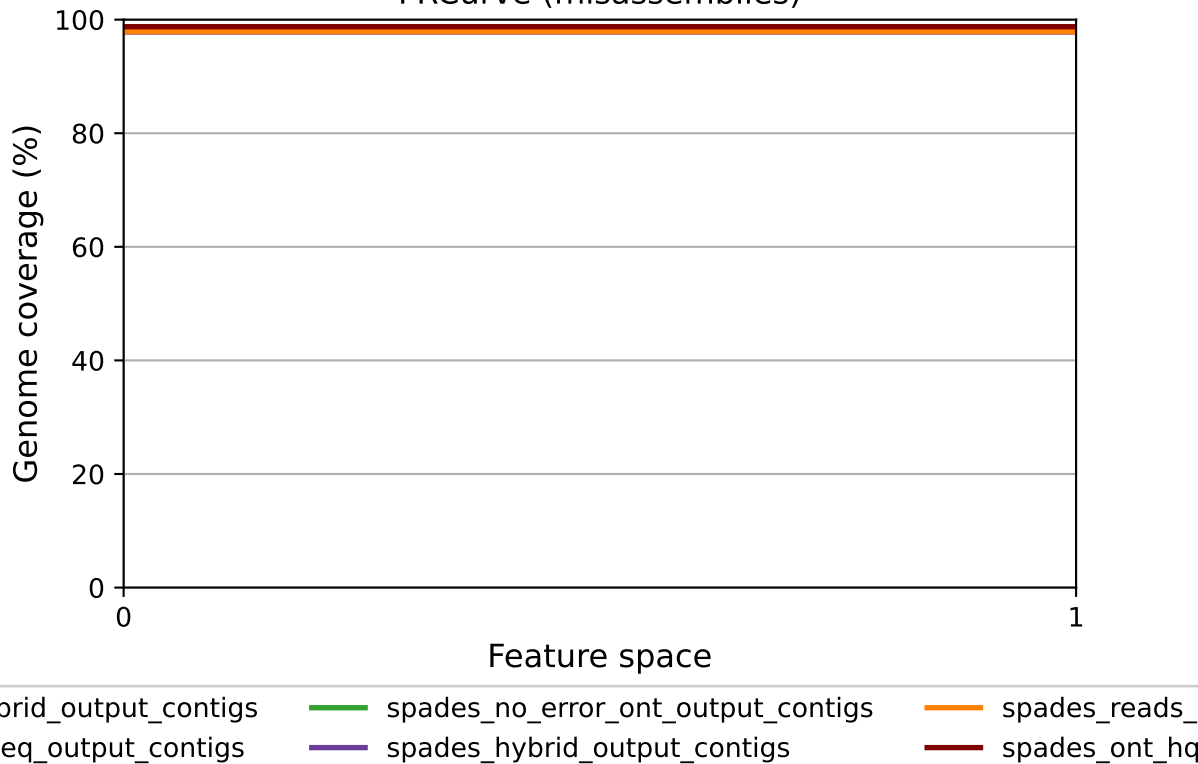
spades_ont_hq_50x_output_contigs coverage histogram (bin size: 1x)



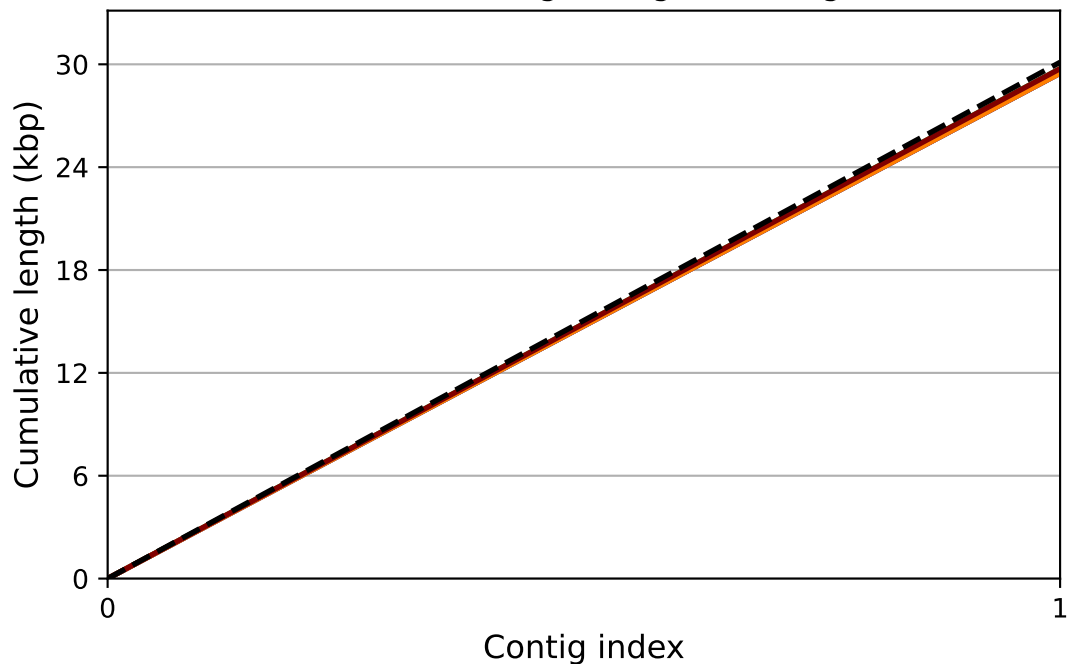
Misassemblies



FRCurve (misassemblies)



Cumulative length (aligned contigs)

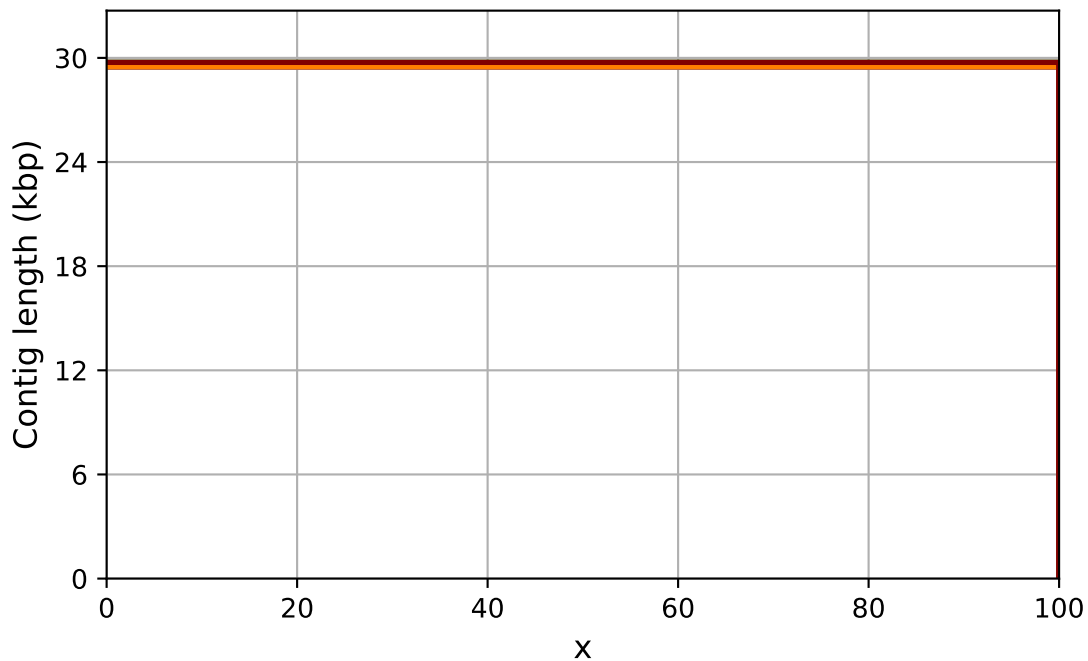


hybrid_output_contigs
hiseq_output_contigs
ont_output_contigs

spades_hybrid_output_contigs
spades_reads_hiseq_5k_output_contigs

spades_ont
Reference

NAX



hybrid_output_contigs

spades_no_error_ont_output_contigs

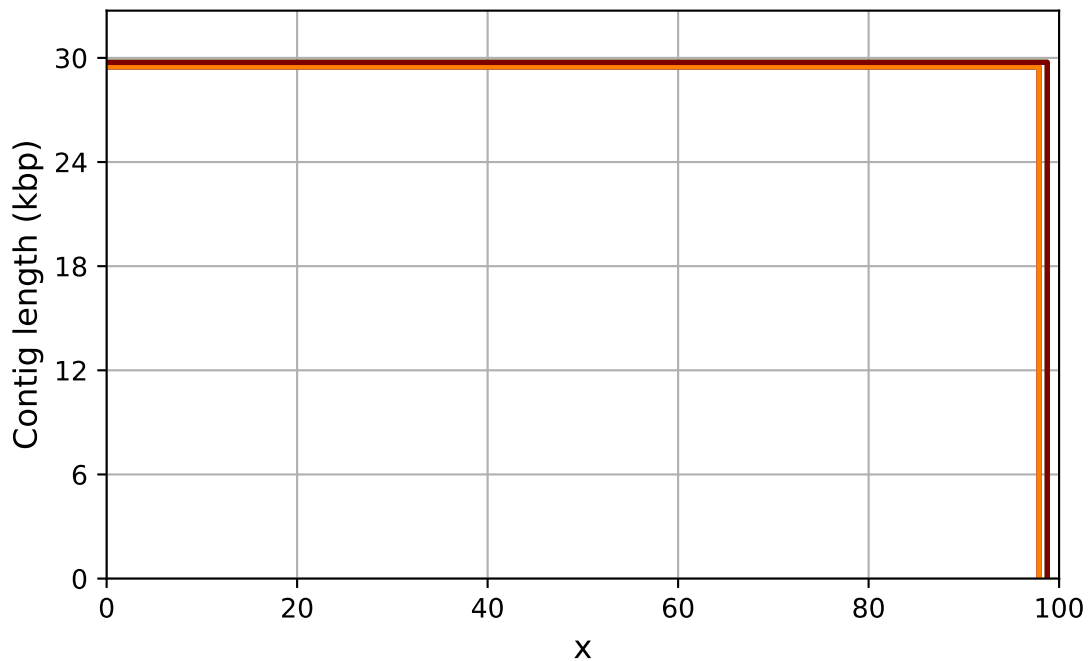
spades_reads_

iseq_output_contigs

spades_hybrid_output_contigs

spades_ont_hq

NGAx



hybrid_output_contigs

spades_no_error_ont_output_contigs

spades_reads_hq

naniseq_output_contigs

spades_hybrid_output_contigs

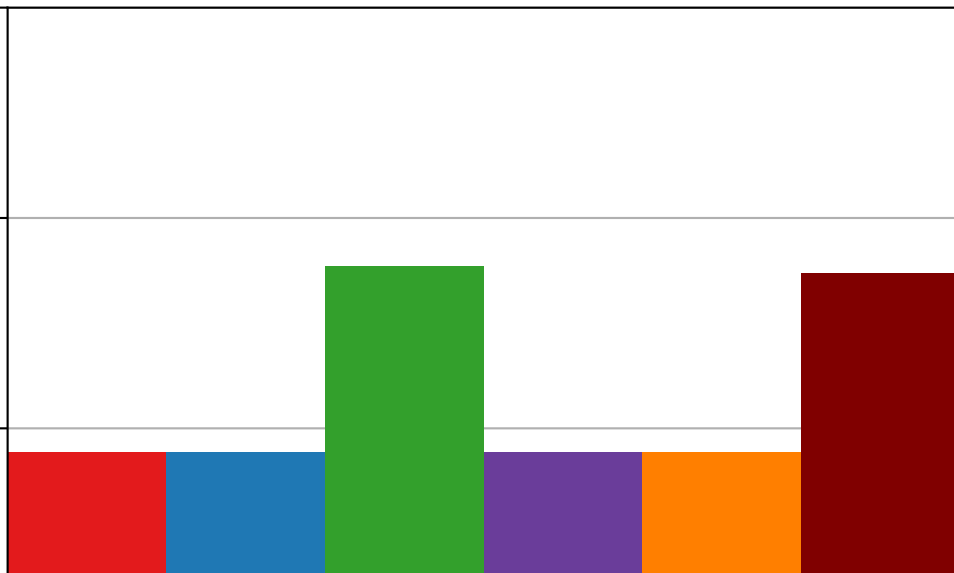
spades_ont_hq

Genome fraction, %

100

99

98



hybrid_output_contigs



spades_no_error_ont_output_contigs



spades_reads_hq

niseq_output_contigs



spades_hybrid_output_contigs



spades_ont_hq