

Report

	contigs_olc_min20
# contigs (>= 0 bp)	2
# contigs (>= 1000 bp)	2
# contigs (>= 5000 bp)	2
# contigs (>= 10000 bp)	2
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	37293
Total length (>= 1000 bp)	37293
Total length (>= 5000 bp)	37293
Total length (>= 10000 bp)	37293
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	2
Largest contig	20439
Total length	37293
Reference length	30119
GC (%)	40.69
Reference GC (%)	41.24
N50	20439
NG50	20439
N90	16854
NG90	16854
auN	18818.8
auNG	23301.2
L50	1
LG50	1
L90	2
LG90	2
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	86.583
Duplication ratio	1.428
# N's per 100 kbp	0.00
# mismatches per 100 kbp	343.62
# indels per 100 kbp	1251.01
Largest alignment	20434
Total aligned length	37250
NA50	20434
NGA50	20434
NA90	16816
NGA90	16816
auNA	18779.0
auNGA	23252.0
LA50	1
LGA50	1
LA90	2
LGA90	2

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_olc_min20
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	128
# indels	466
# indels (<= 5 bp)	466
# indels (> 5 bp)	0
Indels length	580

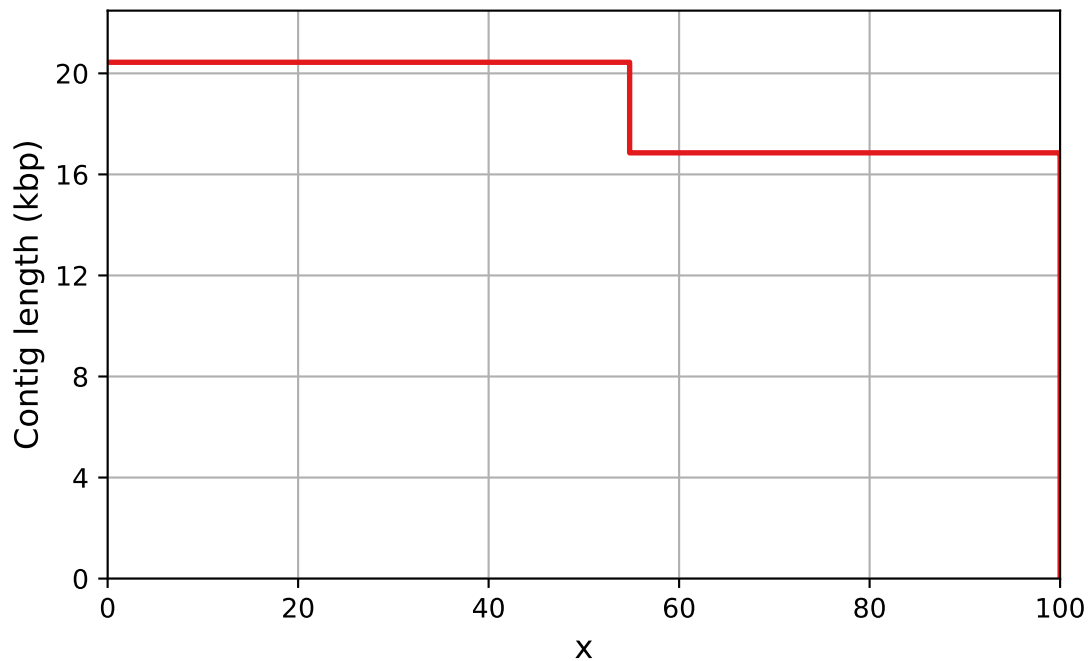
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	contigs_olc_min20
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

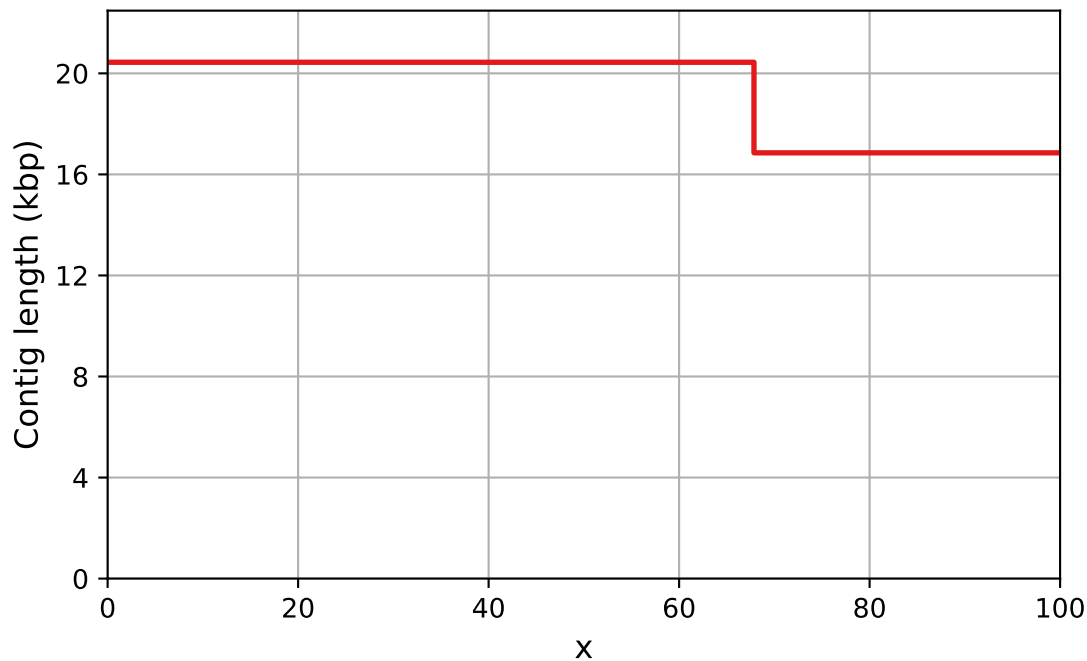
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



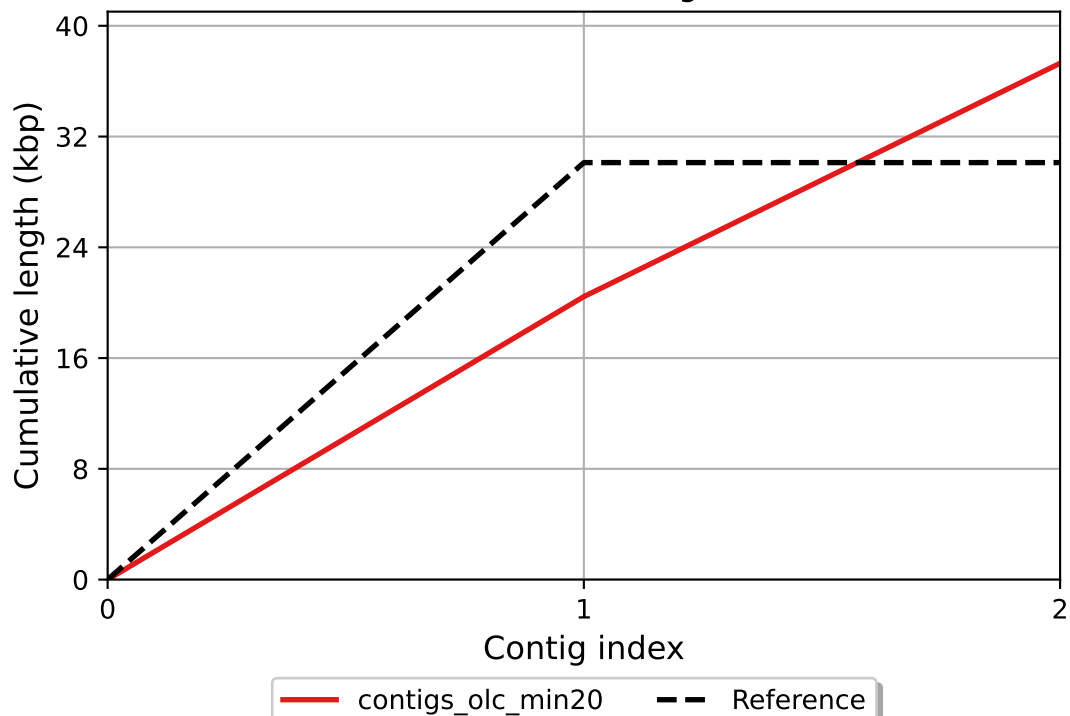
— contigs_olc_min20

NGx

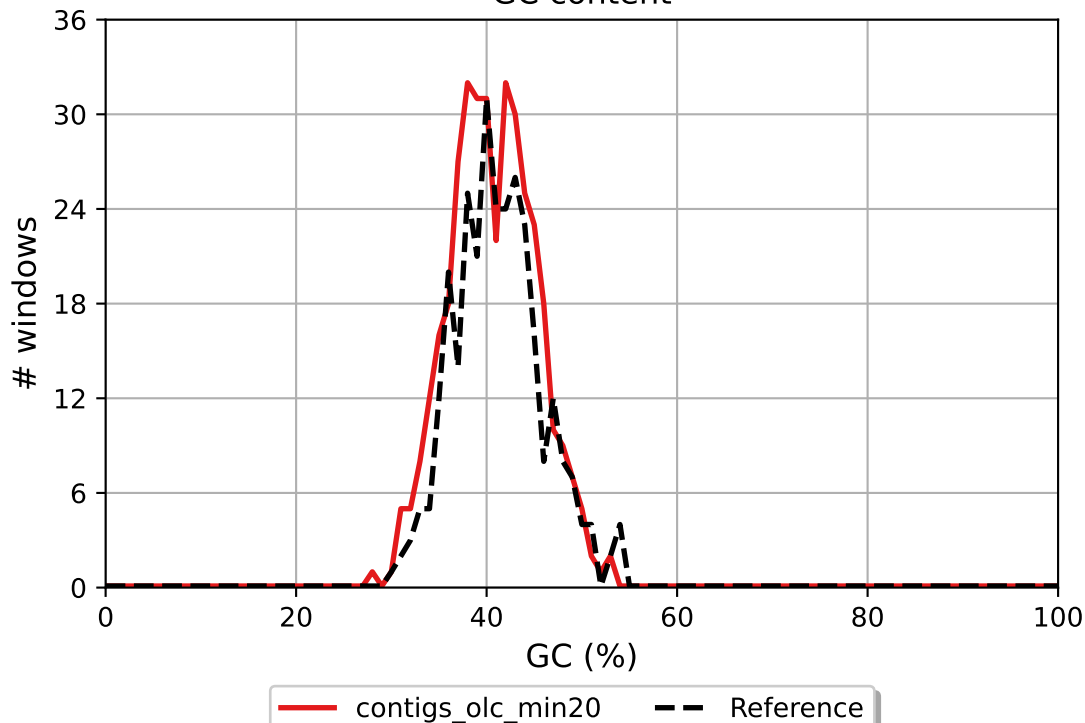


contigs_olc_min20

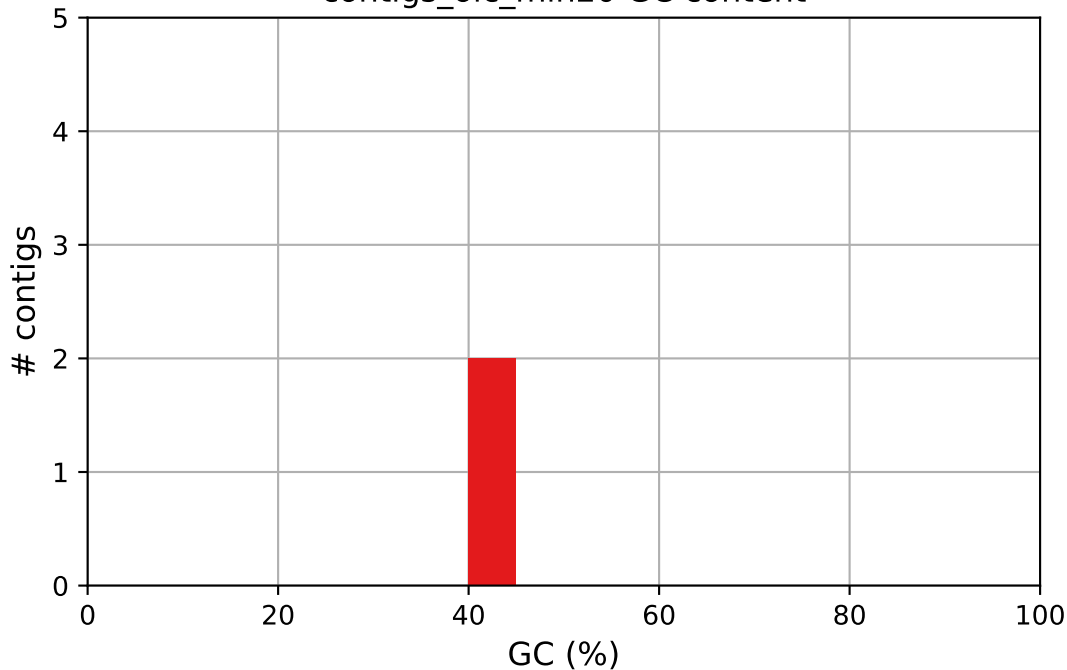
Cumulative length



GC content



contigs_olc_min20 GC content

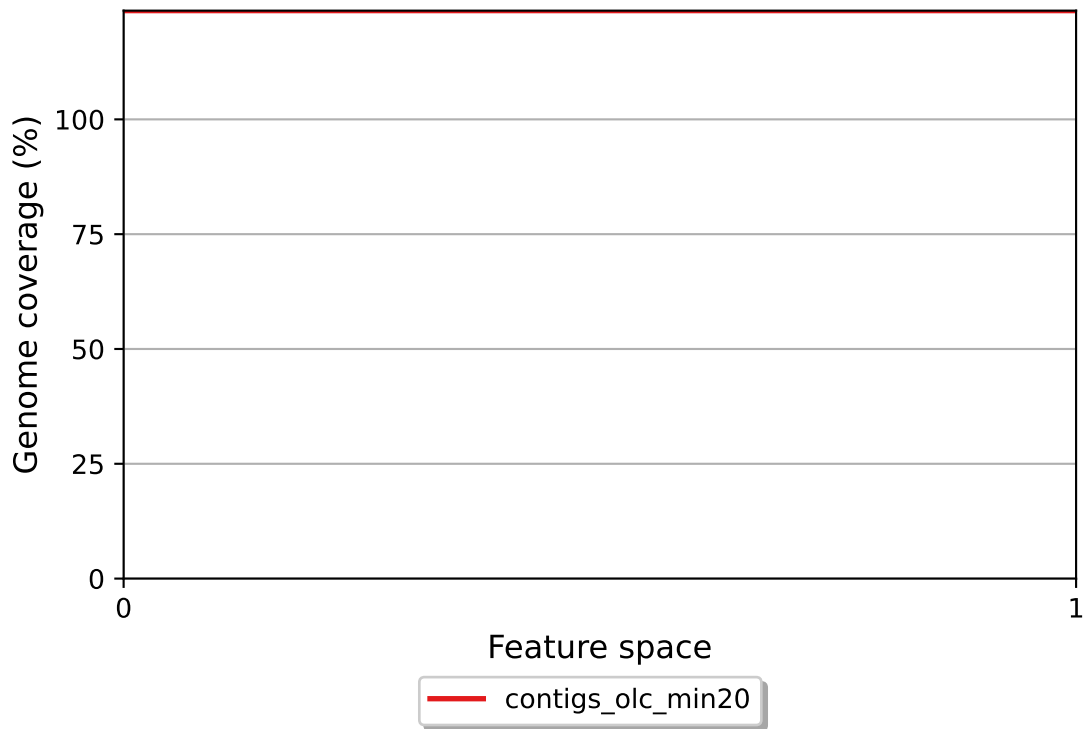


contigs_olc_min20

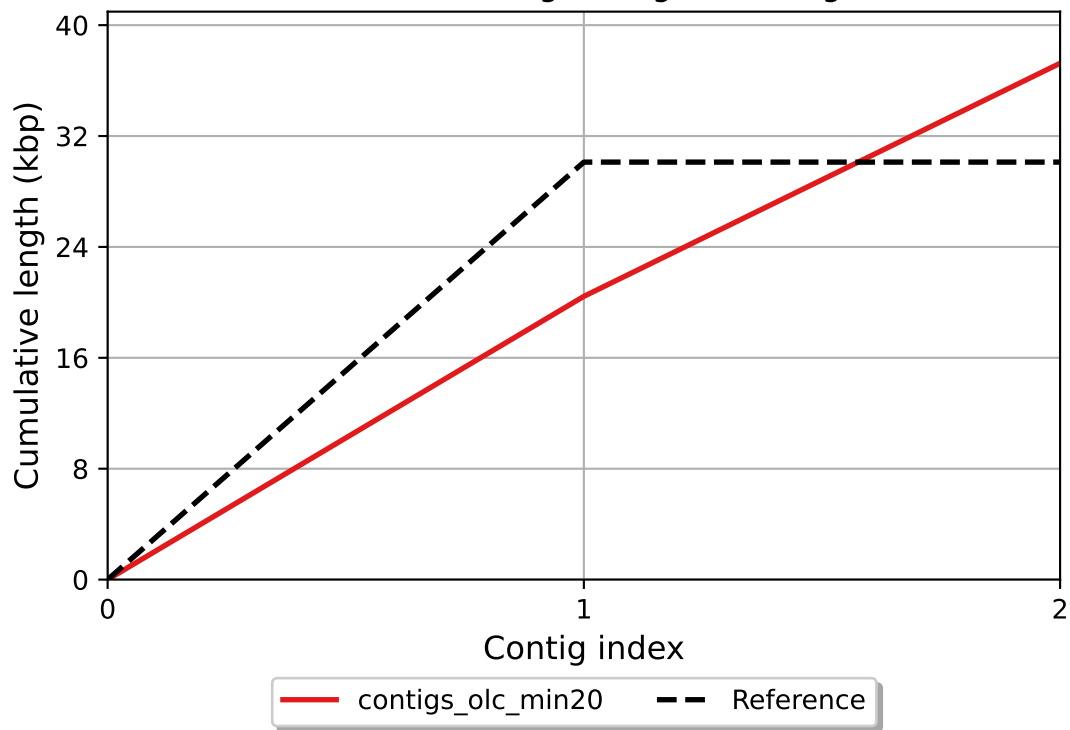
Misassemblies



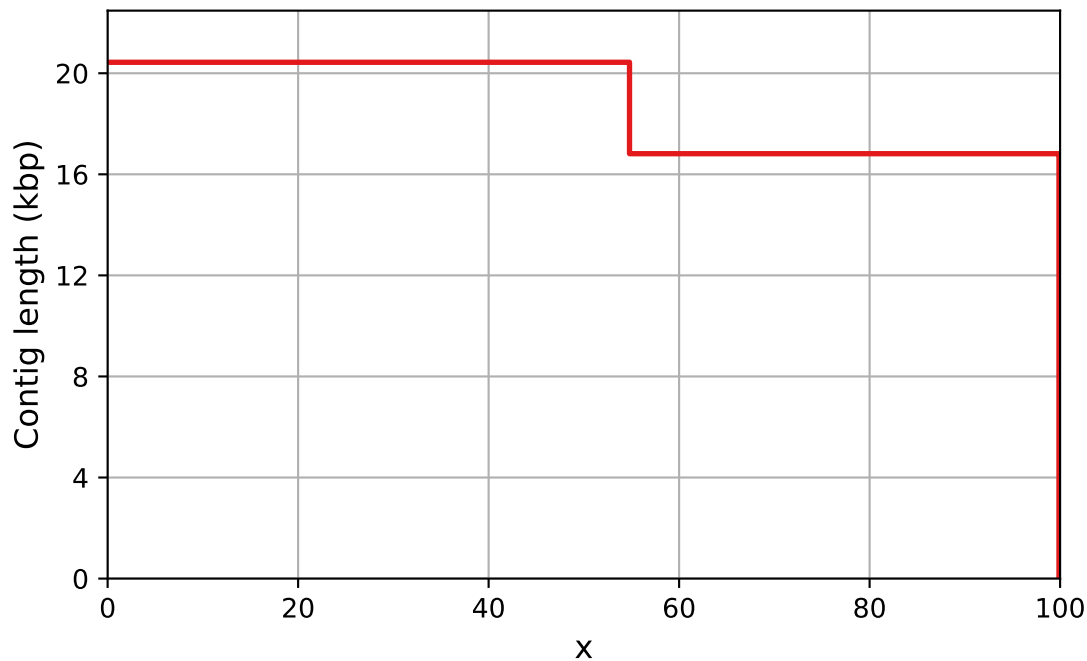
FRCurve (misassemblies)



Cumulative length (aligned contigs)

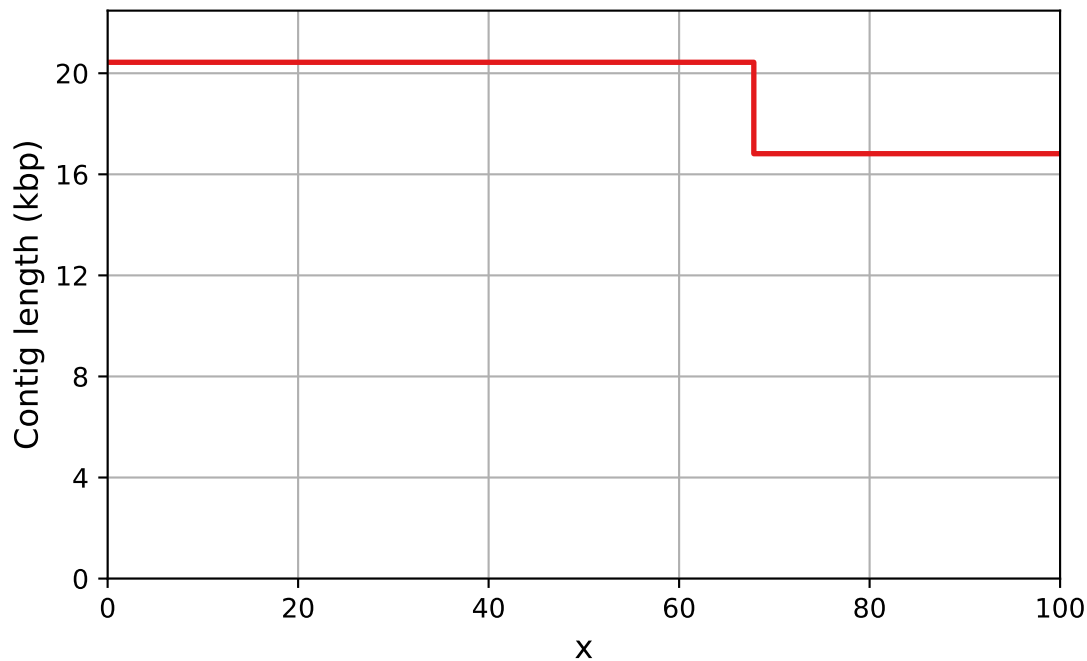


NAx



— contigs_olc_min20

NGAx



— contigs_olc_min20