

Report

	Unicycler_hybrid
# contigs (>= 0 bp)	1
# contigs (>= 1000 bp)	1
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	1
Total length (>= 0 bp)	5236984
Total length (>= 1000 bp)	5236984
Total length (>= 5000 bp)	5236984
Total length (>= 10000 bp)	5236984
Total length (>= 25000 bp)	5236984
Total length (>= 50000 bp)	5236984
# contigs	1
Largest contig	5236984
Total length	5236984
Reference length	5231428
GC (%)	50.48
Reference GC (%)	50.48
N50	5236984
NG50	5236984
N75	5236984
NG75	5236984
L50	1
LG50	1
L75	1
LG75	1
# total reads	3293261
# left	1564704
# right	1563050
Mapped (%)	99.64
Reference mapped (%)	99.64
Properly paired (%)	94.34
Reference properly paired (%)	94.29
Avg. coverage depth	397
Reference avg. coverage depth	398
Coverage >= 1x (%)	100.0
Reference coverage >= 1x (%)	100.0
# misassemblies	3
# misassembled contigs	1
Misassembled contigs length	5236984
# local misassemblies	8
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 1 part
Unaligned length	2907
Genome fraction (%)	99.982
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	8.91
# indels per 100 kbp	5.07
Largest alignment	2720115
Total aligned length	5228567
NA50	2720115
NGA50	2720115
NA75	1323766
NGA75	1323766
LA50	1
LGA50	1
LA75	2
LGA75	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).

Reads report

	Unicycler_hybrid
# total reads	3293261
# left	1564704
# right	1563050
# mapped	3281541
Mapped (%)	99.64
# properly paired	3106814
Properly paired (%)	94.34
# singletons	5481
Singletons (%)	0.17
# misjoint mates	0
Misjoint mates (%)	0.0
Avg. coverage depth	397
Coverage >= 1x (%)	100.0
Coverage >= 5x (%)	100.0
Coverage >= 10x (%)	100.0
# reference mapped	3281829
Reference mapped (%)	99.64
# reference properly paired	3105484
Reference properly paired (%)	94.29
# reference singletons	5479
Reference singletons (%)	0.17
# reference misjoint mates	0
Reference misjoint mates (%)	0.0
Reference avg. coverage depth	398
Reference coverage >= 1x (%)	100.0
Reference coverage >= 5x (%)	100.0
Reference coverage >= 10x (%)	100.0

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).

Misassemblies report

	Unicycler_hybrid
# misassemblies	3
# contig misassemblies	3
# c. relocations	3
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	1
Misassembled contigs length	5236984
# local misassemblies	8
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	466
# indels	265
# indels (<= 5 bp)	257
# indels (> 5 bp)	8
Indels length	630

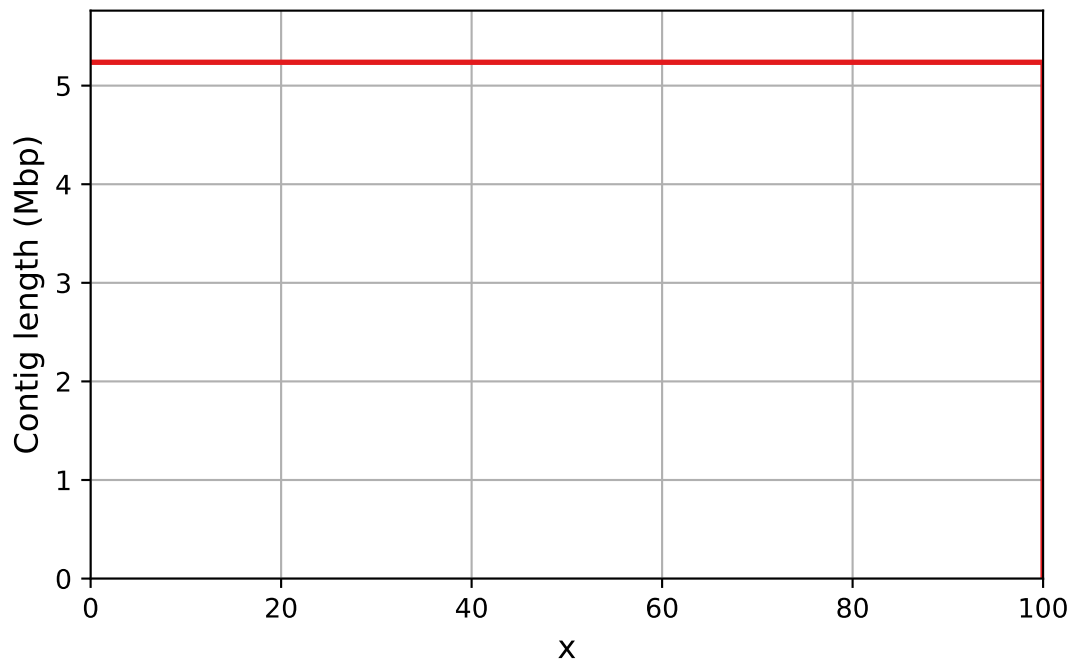
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	Unicycler_hybrid
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
Partially unaligned length	2907
# N's	0

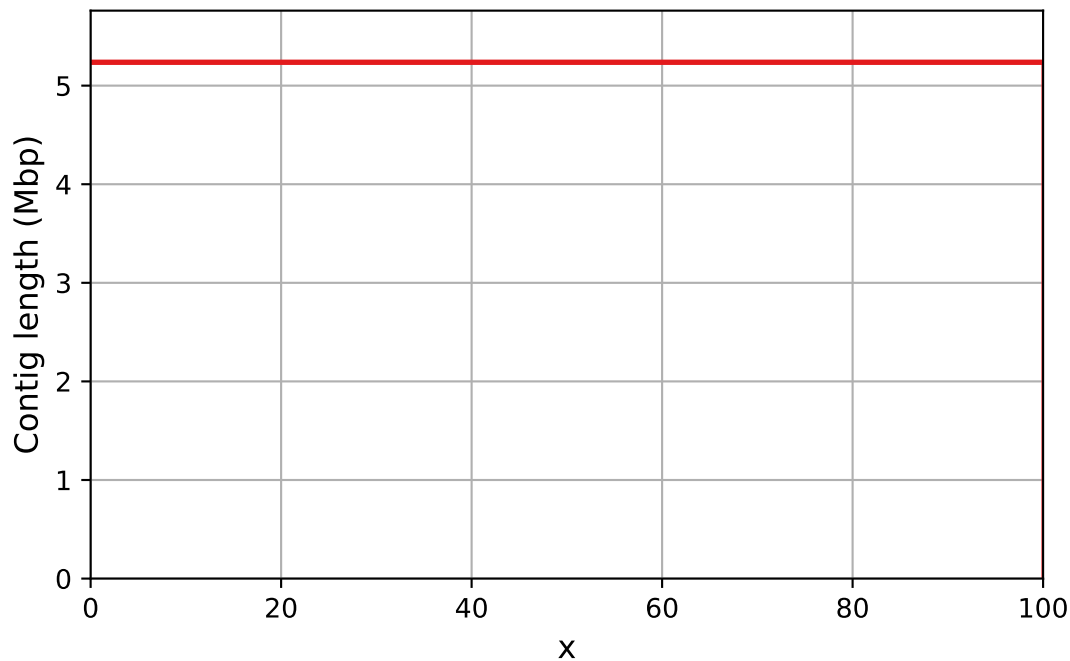
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



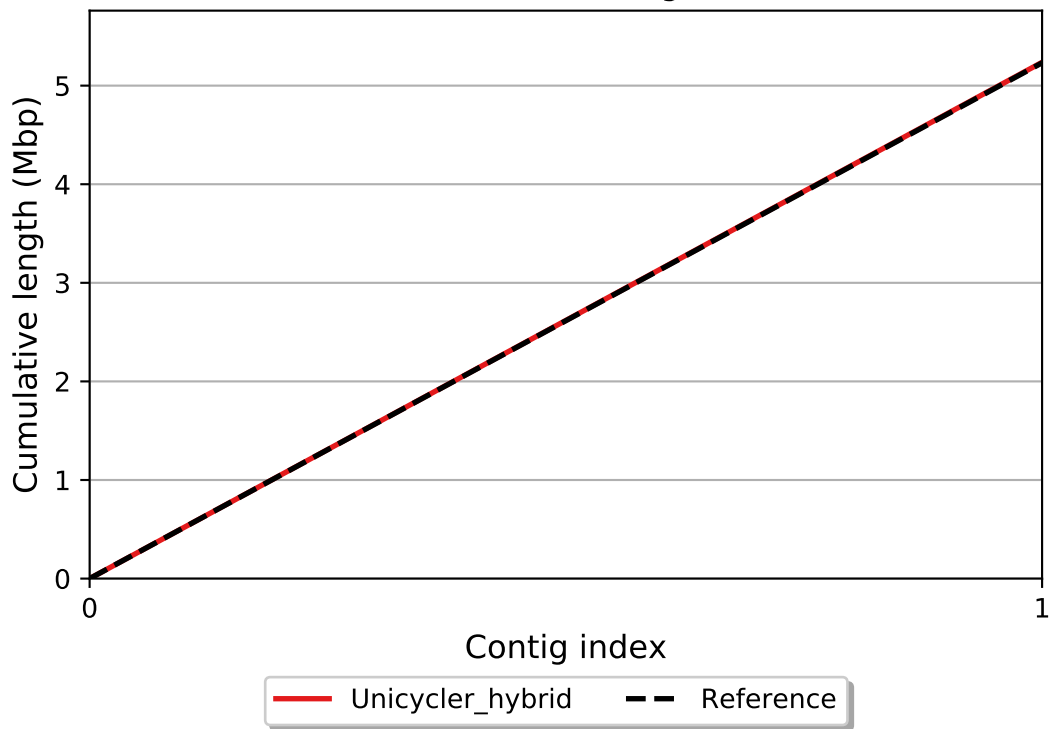
Unicycler_hybrid

NGx

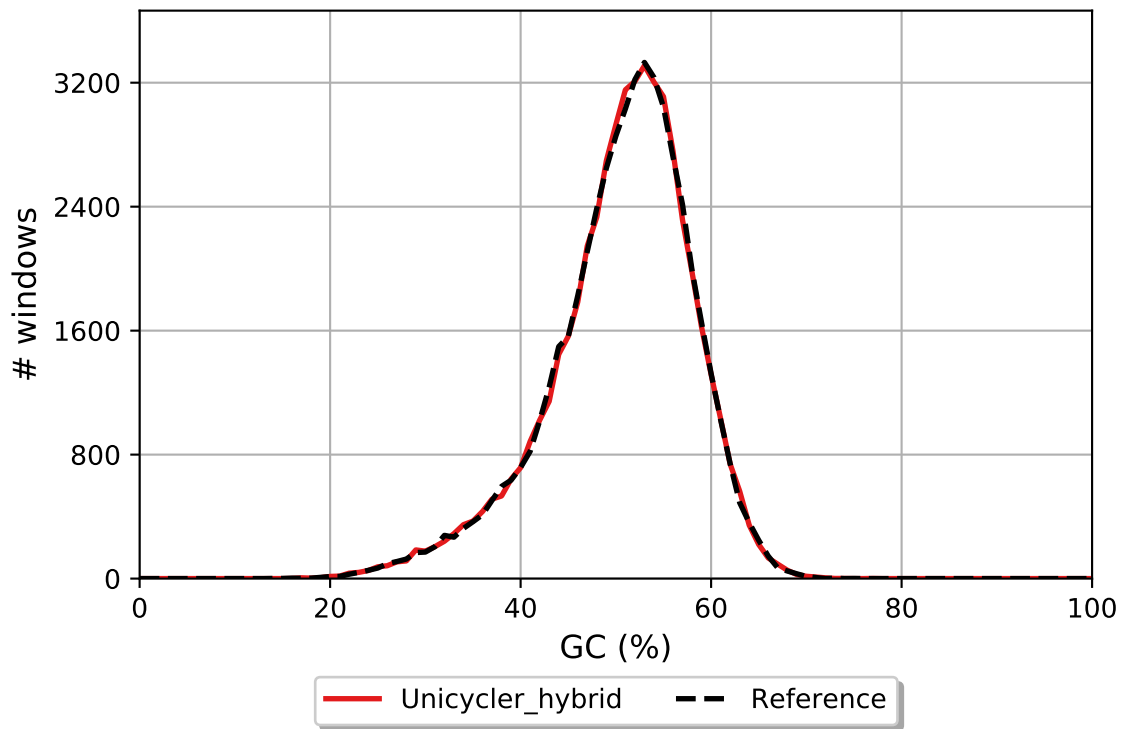


Unicycler_hybrid

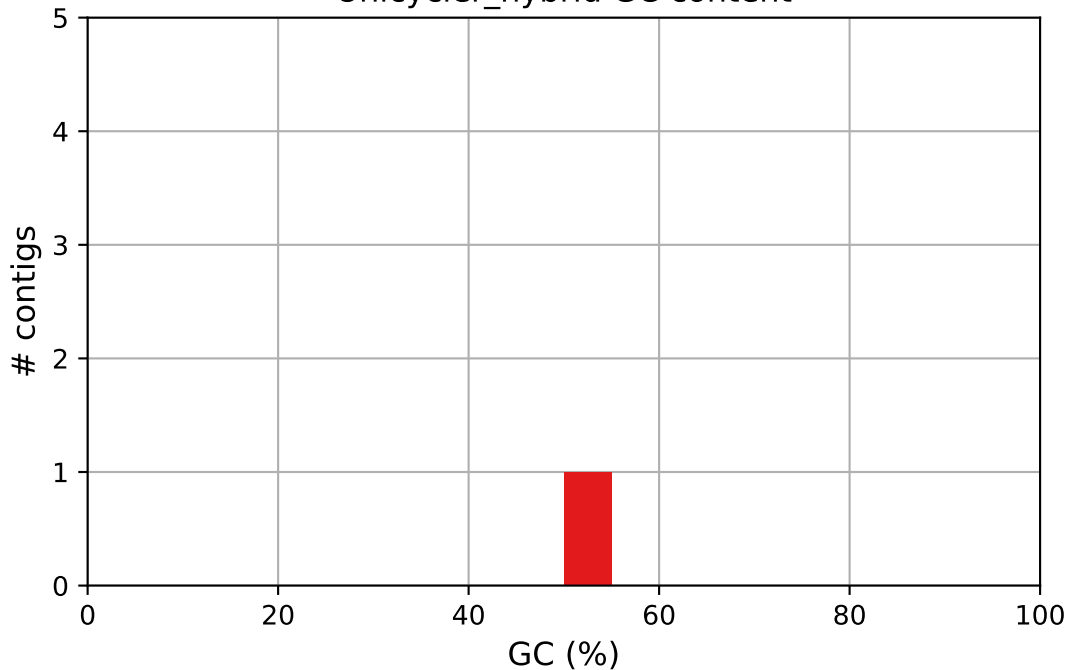
Cumulative length



GC content

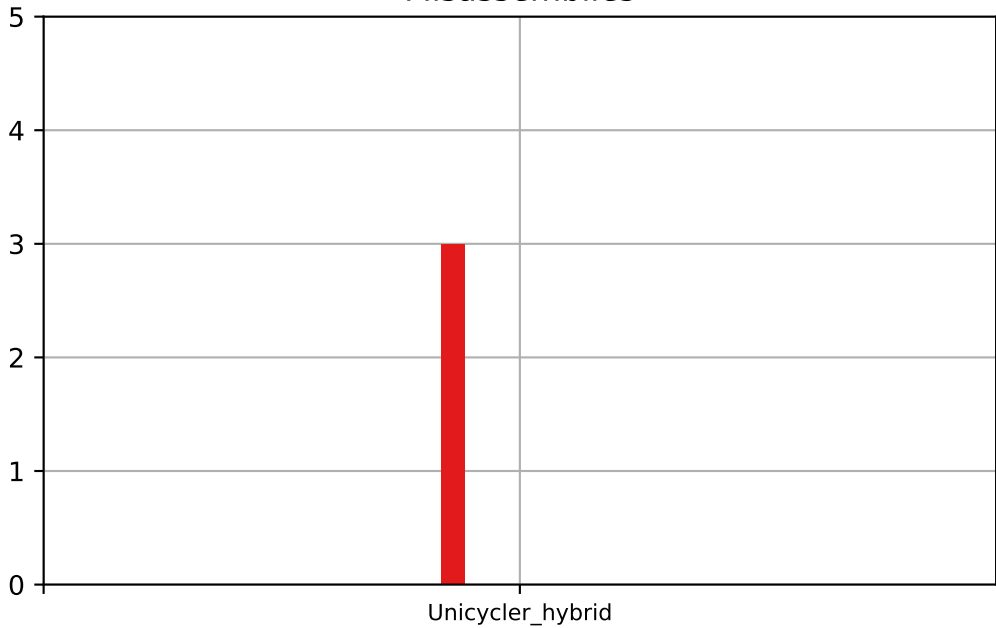


Unicycler_hybrid GC content

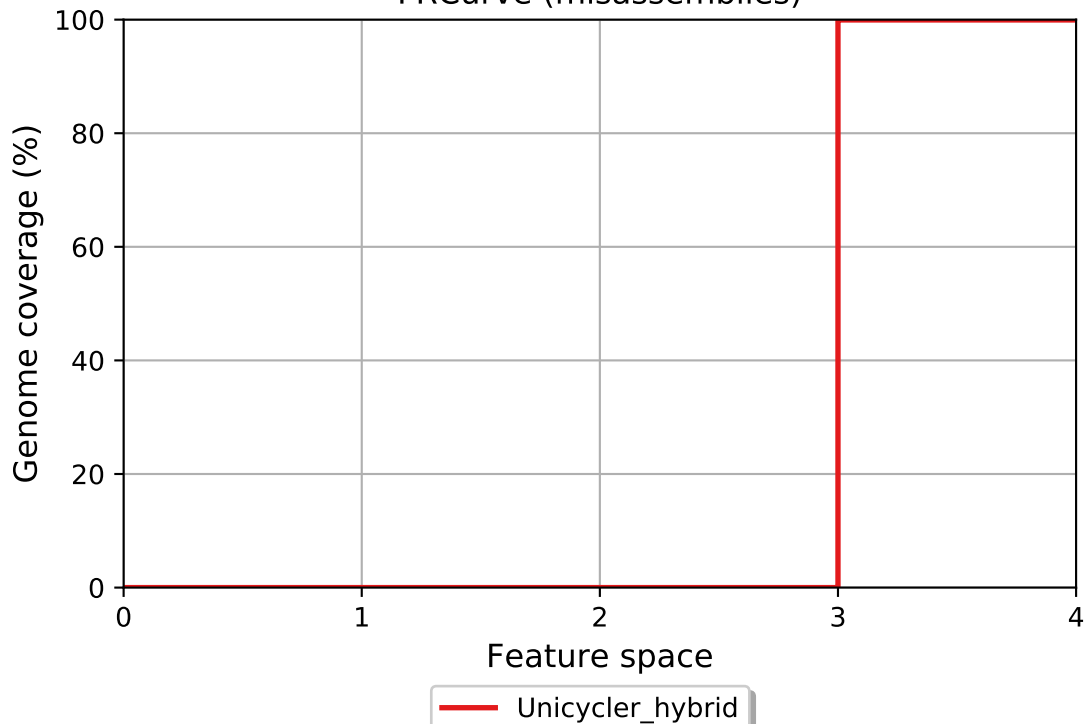


Unicycler_hybrid

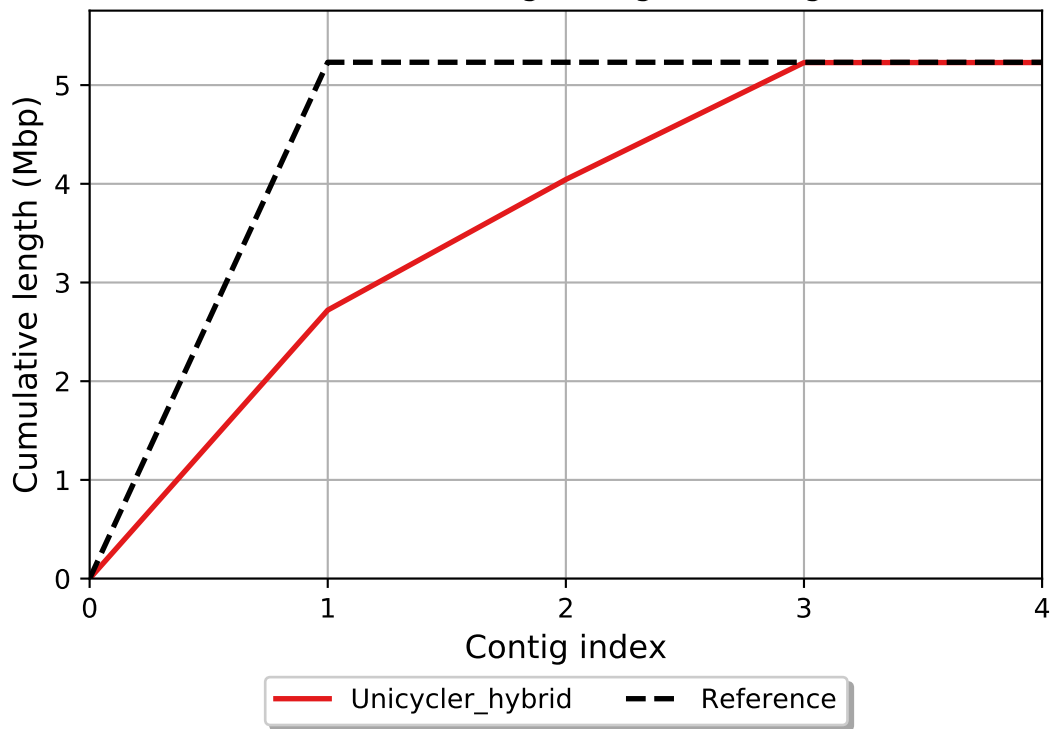
Misassemblies



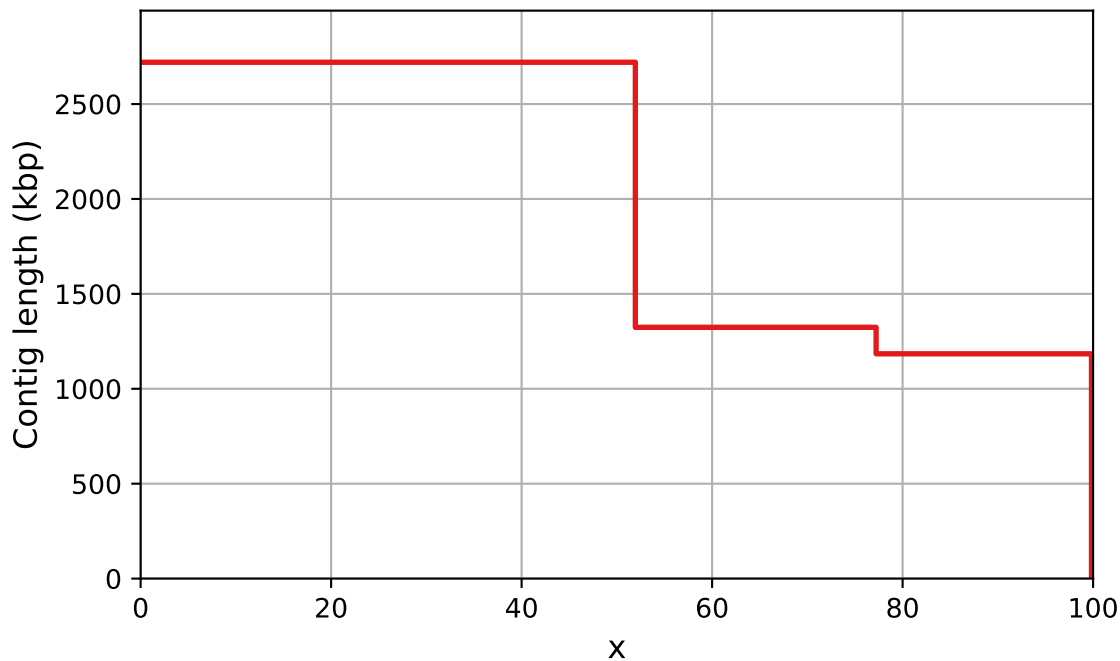
FRCurve (misassemblies)



Cumulative length (aligned contigs)

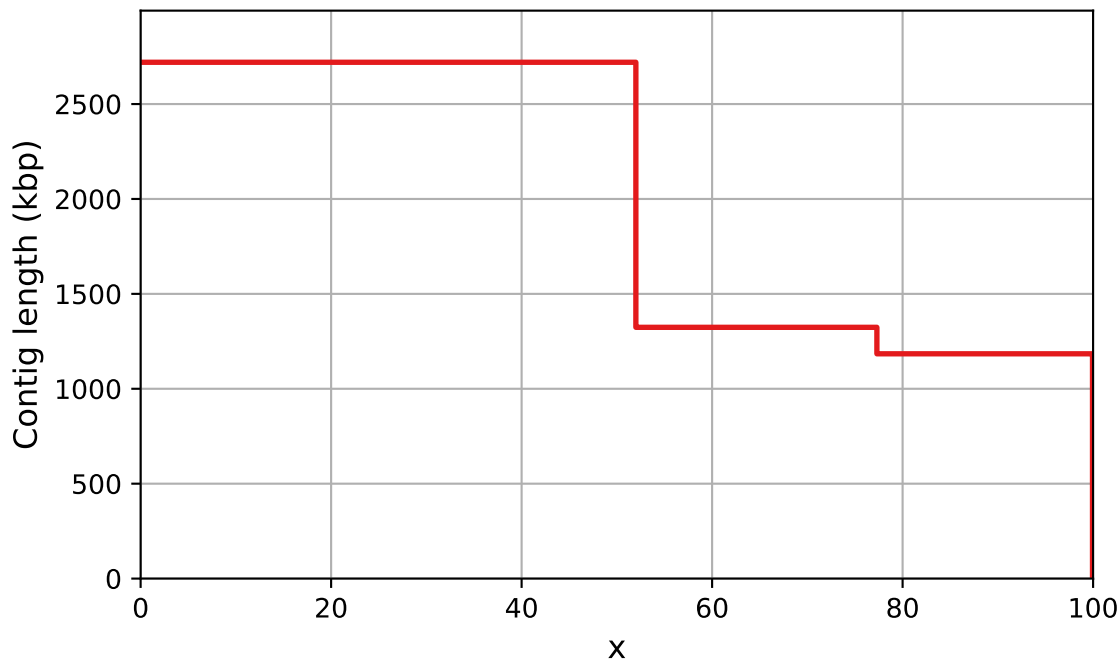


NAx



Unicycler_hybrid

NGAx



— Unicycler_hybrid