

Report

	WGS_assembly.contigs
# contigs (>= 0 bp)	3
# contigs (>= 1000 bp)	3
# contigs (>= 5000 bp)	2
# contigs (>= 10000 bp)	2
# contigs (>= 25000 bp)	2
# contigs (>= 50000 bp)	1
Total length (>= 0 bp)	2625141
Total length (>= 1000 bp)	2625141
Total length (>= 5000 bp)	2622390
Total length (>= 10000 bp)	2622390
Total length (>= 25000 bp)	2622390
Total length (>= 50000 bp)	2575927
# contigs	3
Largest contig	2575927
Total length	2625141
Reference length	2610531
GC (%)	54.06
Reference GC (%)	54.14
N50	2575927
NG50	2575927
N75	2575927
NG75	2575927
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	2
# misassembled contigs	1
Misassembled contigs length	2575927
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	2 + 0 part
Unaligned length	49214
Genome fraction (%)	97.567
Duplication ratio	1.011
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.24
# indels per 100 kbp	16.22
Largest alignment	2452183
Total aligned length	2575885
NA50	2452183
NGA50	2452183
NA75	2452183
NGA75	2452183
LA50	1
LGA50	1
LA75	1
LGA75	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

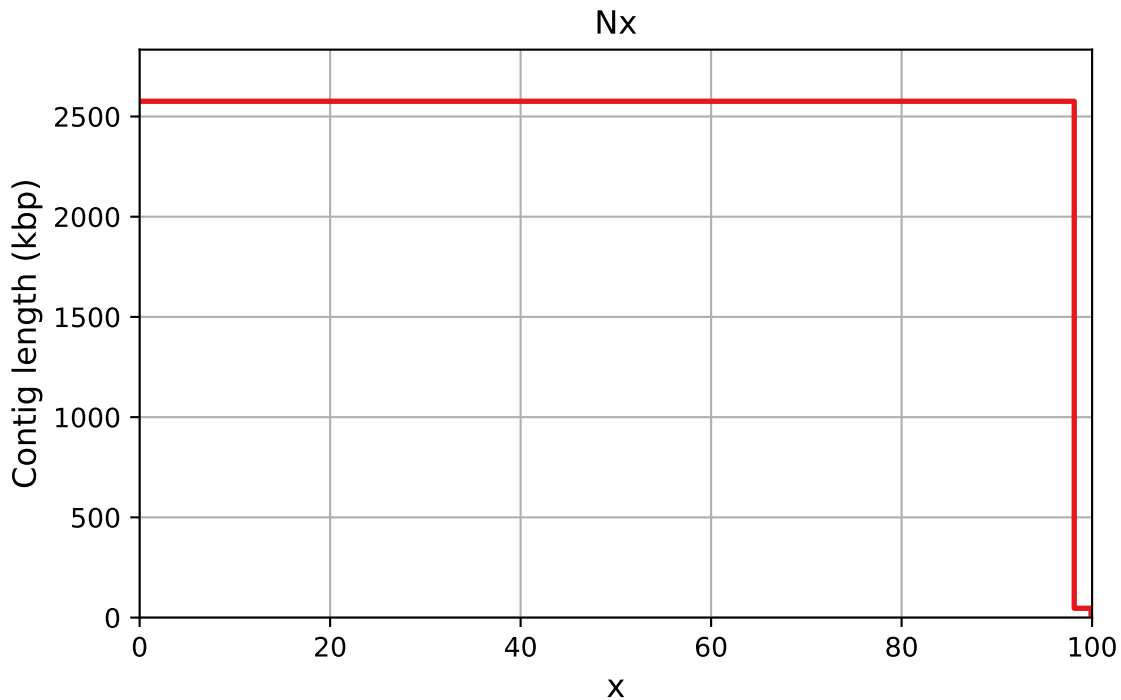
	WGS_assembly.contigs
# misassemblies	2
# contig misassemblies	2
# c. relocations	2
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	1
Misassembled contigs length	2575927
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	6
# indels	413
# indels (<= 5 bp)	413
# indels (> 5 bp)	0
Indels length	446

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

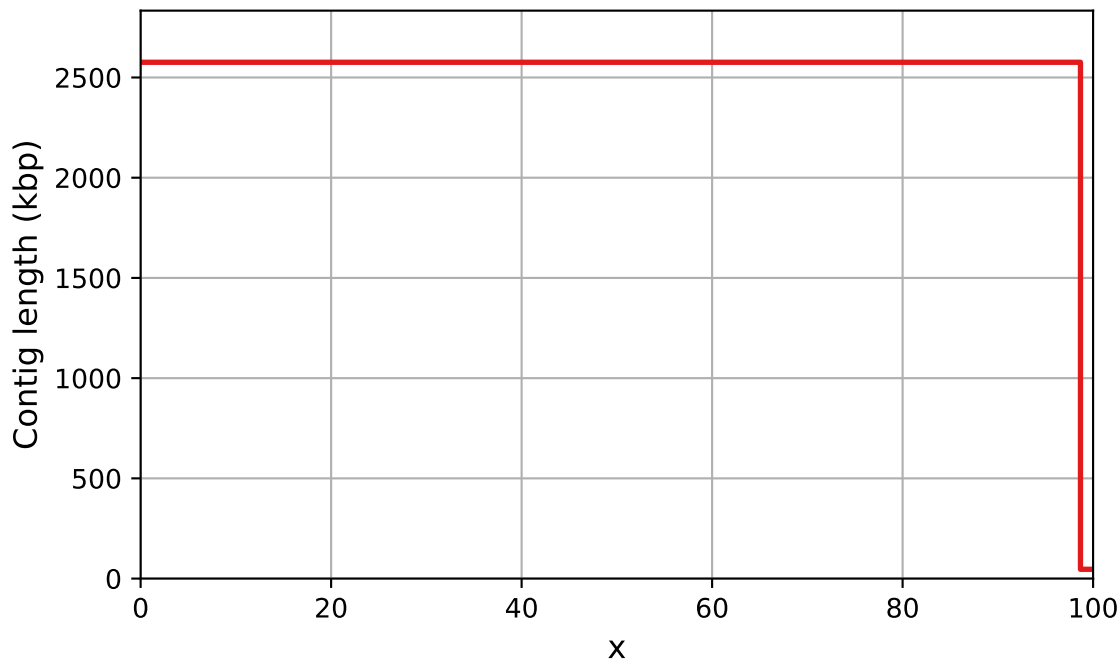
	WGS_assembly.contigs
# fully unaligned contigs	2
Fully unaligned length	49214
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

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).

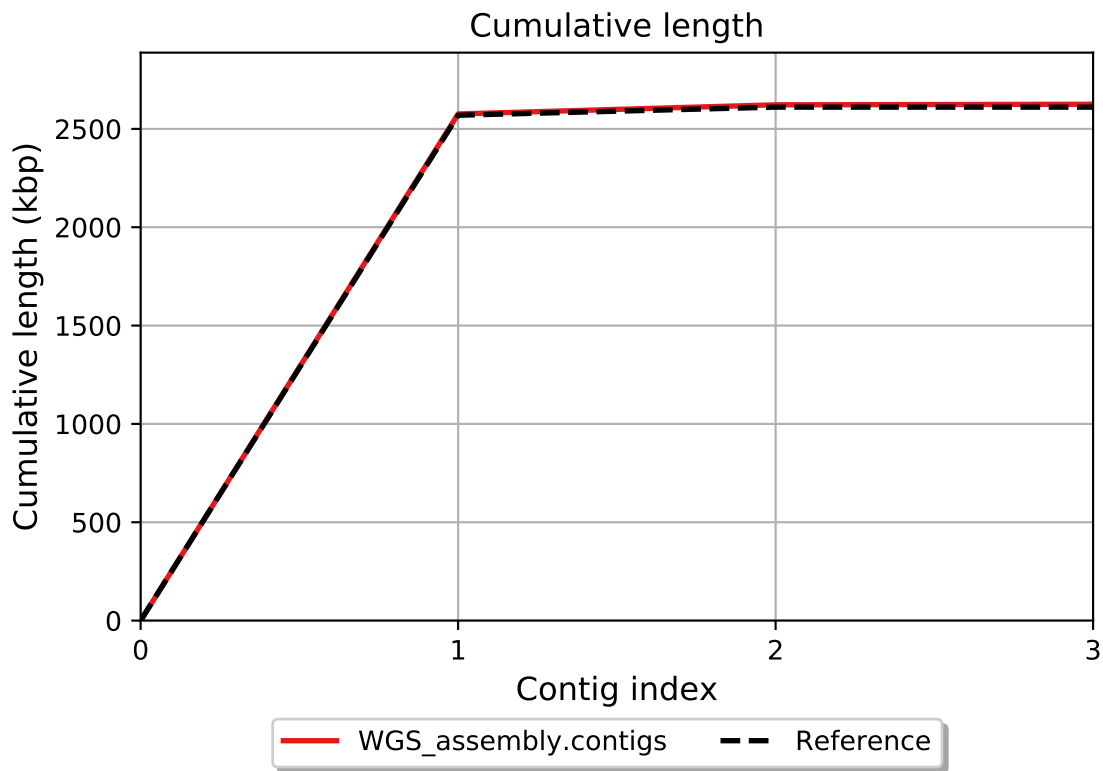


— WGS_assembly.contigs

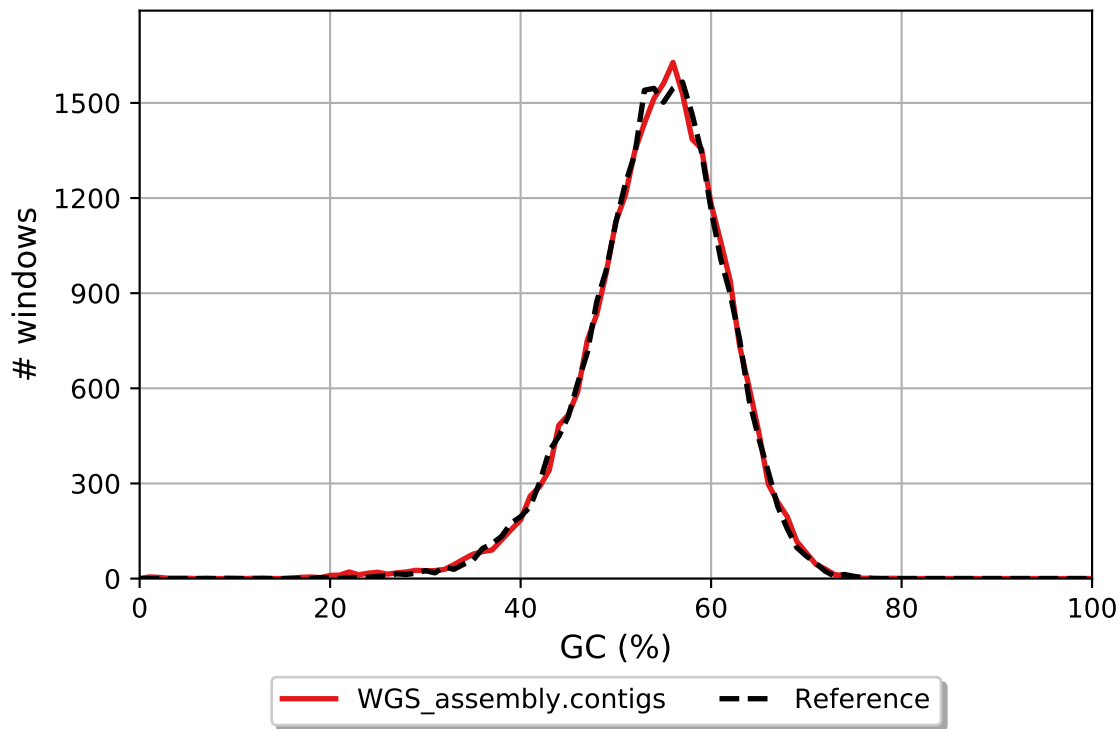
NGx



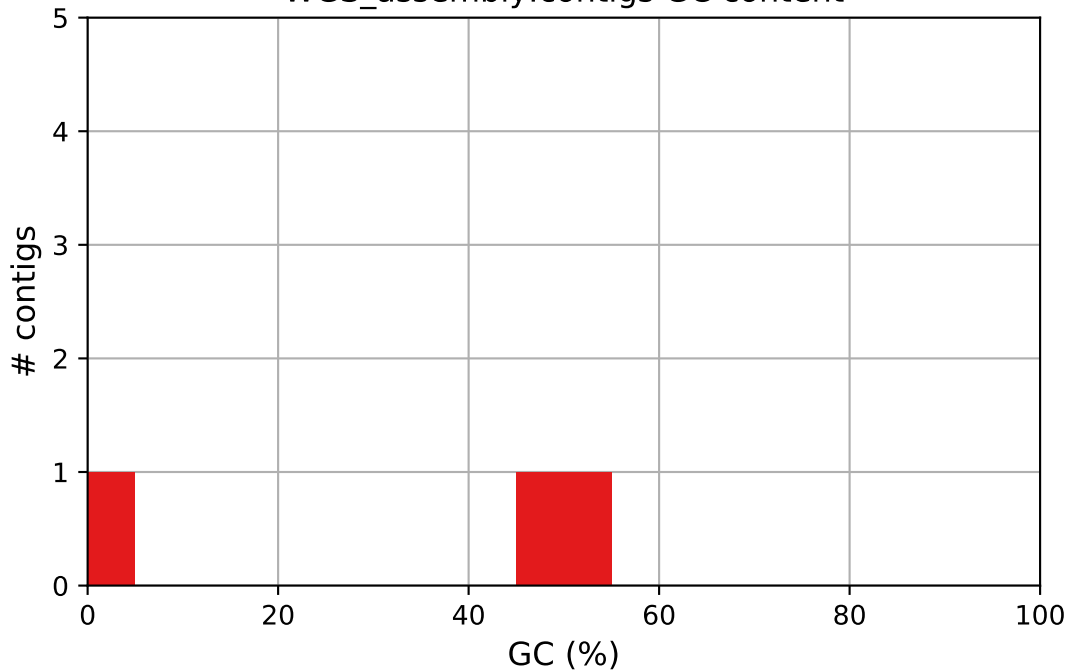
WGS_assembly.contigs



GC content

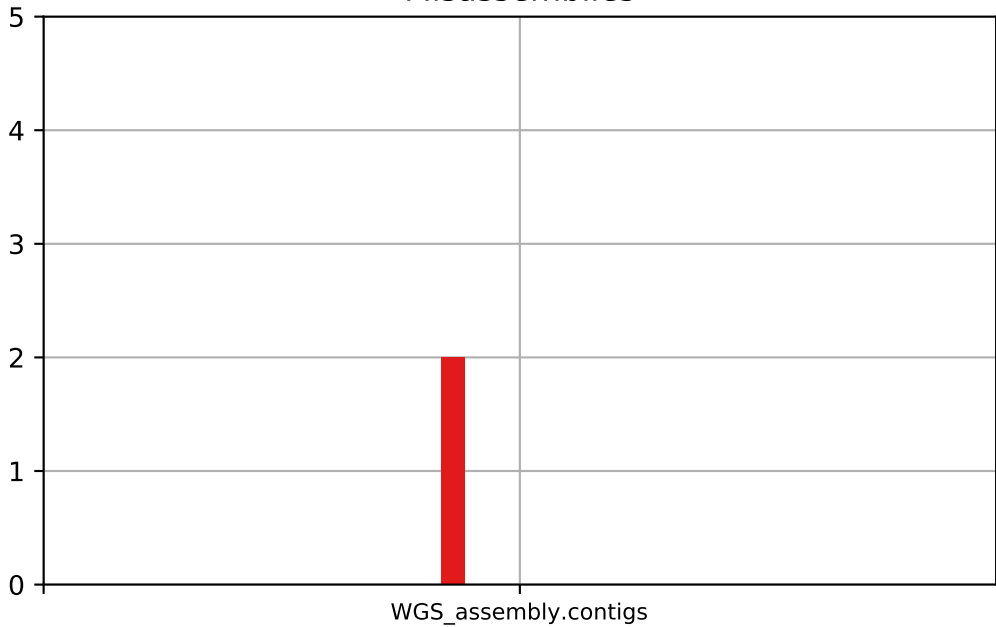


WGS_assembly.contigs GC content

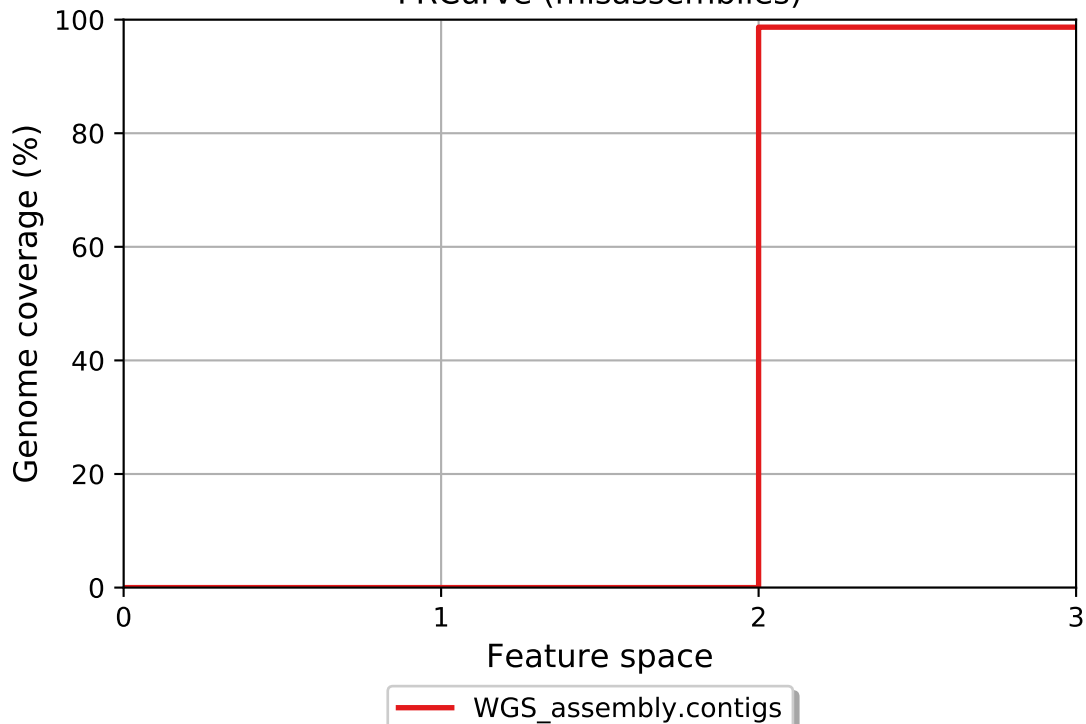


WGS_assembly.contigs

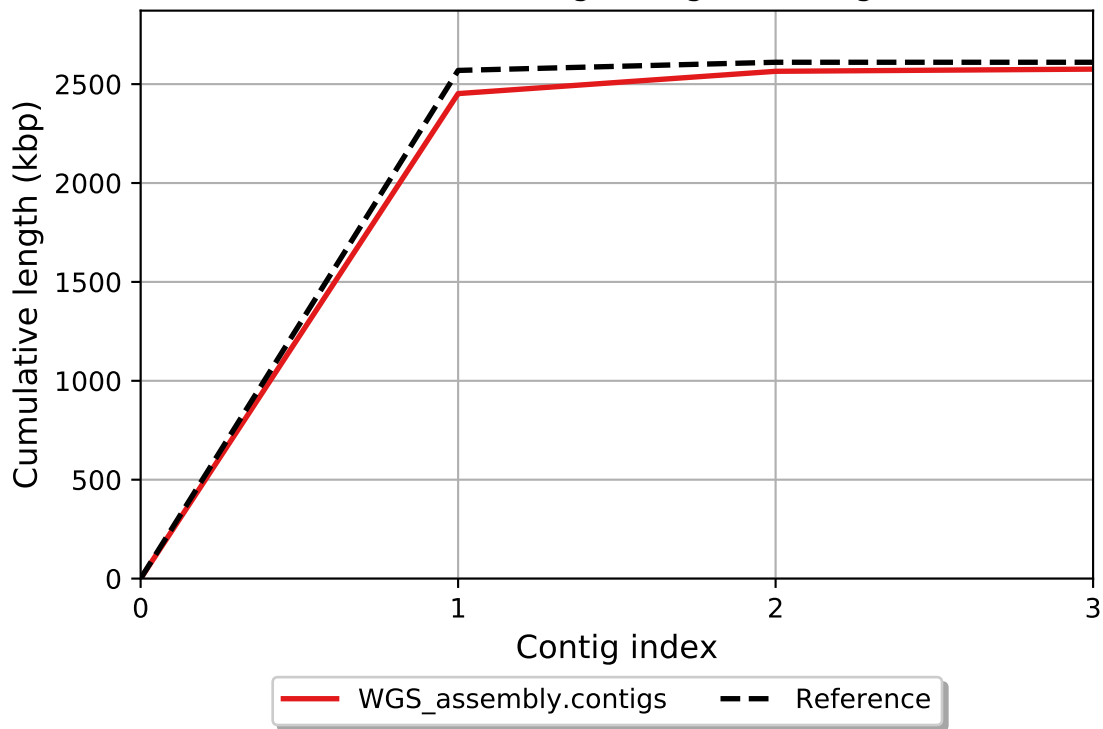
Misassemblies



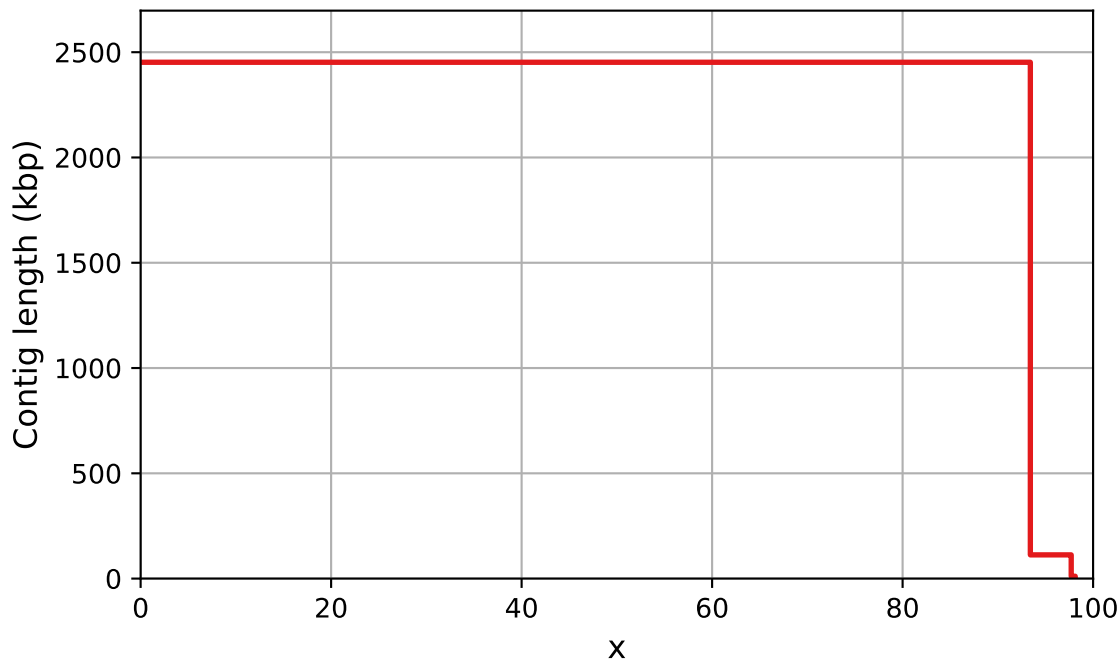
FRCurve (misassemblies)



Cumulative length (aligned contigs)

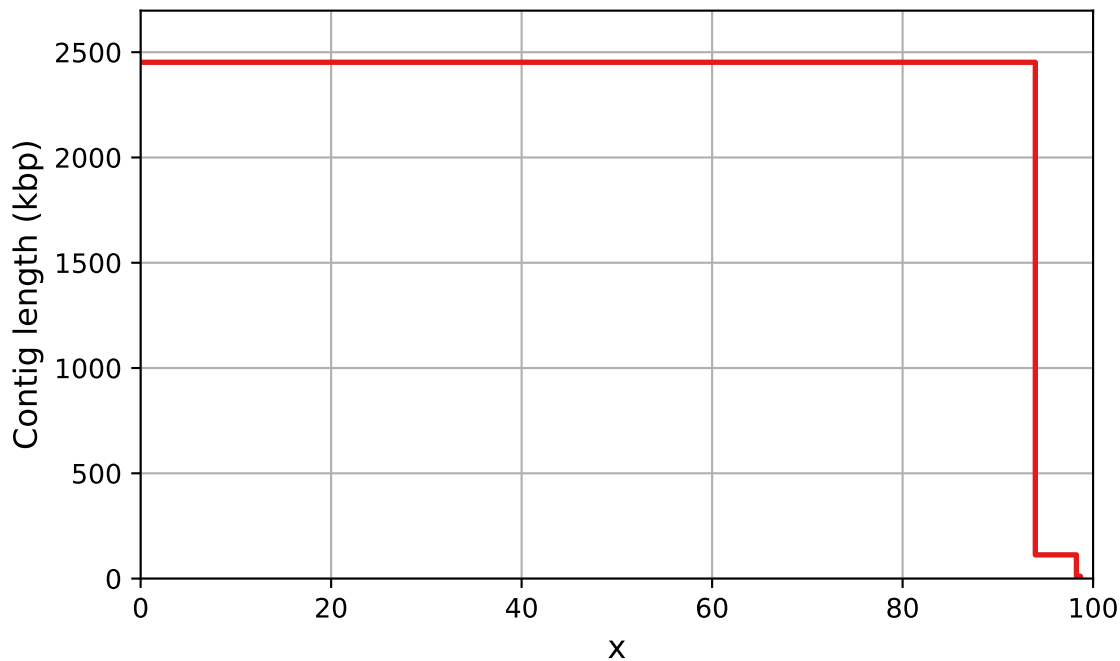


NAx



WGS_assembly.contigs

NGAx



— WGS_assembly.contigs