

Report

	assembly_canu.contigs
# contigs (>= 0 bp)	2
# contigs (>= 1000 bp)	2
# contigs (>= 5000 bp)	2
# contigs (>= 10000 bp)	2
# contigs (>= 25000 bp)	2
# contigs (>= 50000 bp)	1
Total length (>= 0 bp)	2614415
Total length (>= 1000 bp)	2614415
Total length (>= 5000 bp)	2614415
Total length (>= 10000 bp)	2614415
Total length (>= 25000 bp)	2614415
Total length (>= 50000 bp)	2565741
# contigs	2
Largest contig	2565741
Total length	2614415
Reference length	2610531
GC (%)	54.14
Reference GC (%)	54.14
N50	2565741
NG50	2565741
N75	2565741
NG75	2565741
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	2565741
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	1 + 0 part
Unaligned length	48674
Genome fraction (%)	97.567
Duplication ratio	1.007
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.12
# indels per 100 kbp	10.84
Largest alignment	1797172
Total aligned length	2565741
NA50	1797172
NGA50	1797172
NA75	768569
NGA75	768569
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).

Misassemblies report

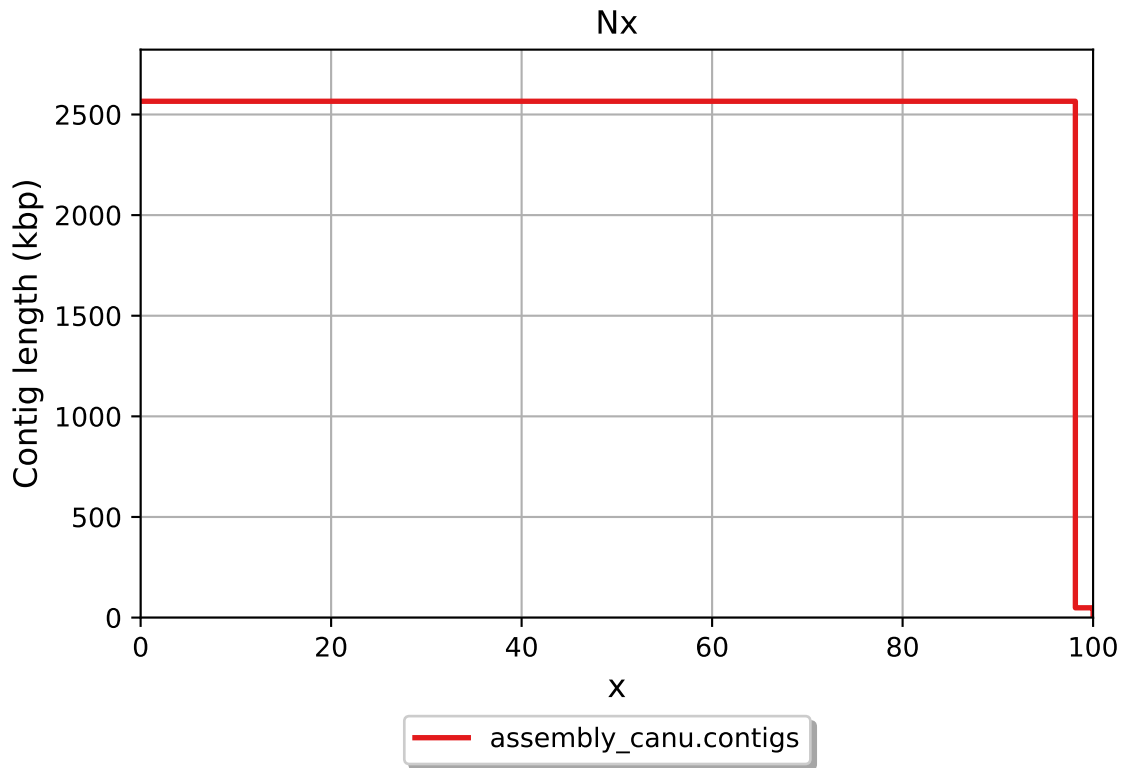
	assembly_canu.contigs
# misassemblies	1
# contig misassemblies	1
# c. relocations	1
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	1
Misassembled contigs length	2565741
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	3
# indels	276
# indels (<= 5 bp)	276
# indels (> 5 bp)	0
Indels length	278

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).

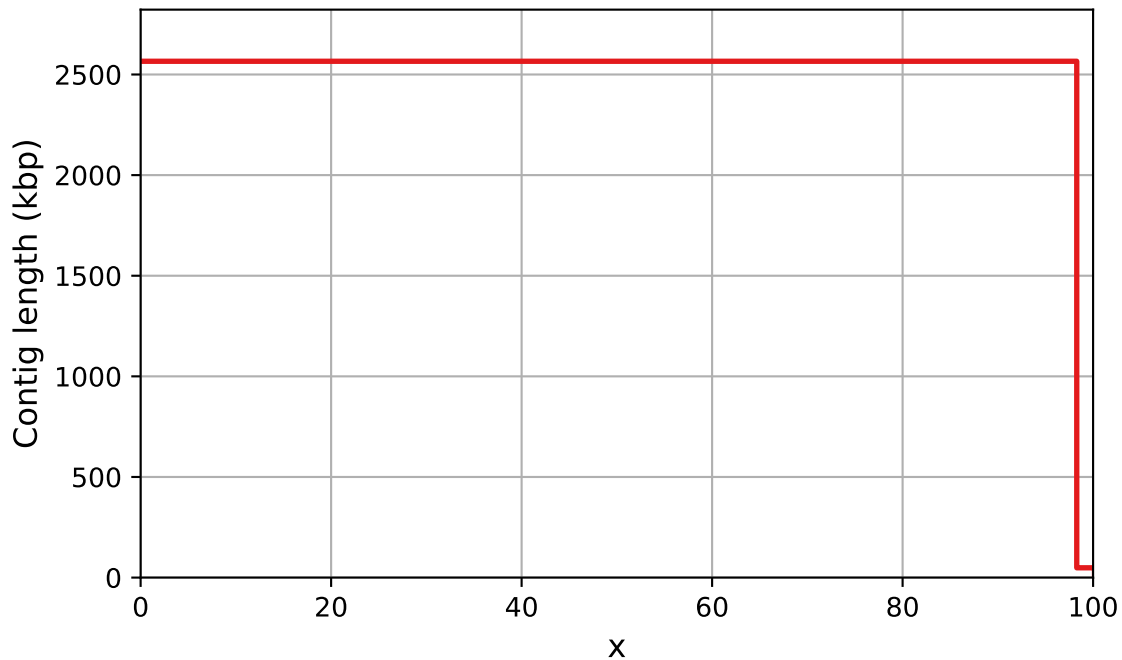
Unaligned report

	assembly_canu.contigs
# fully unaligned contigs	1
Fully unaligned length	48674
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

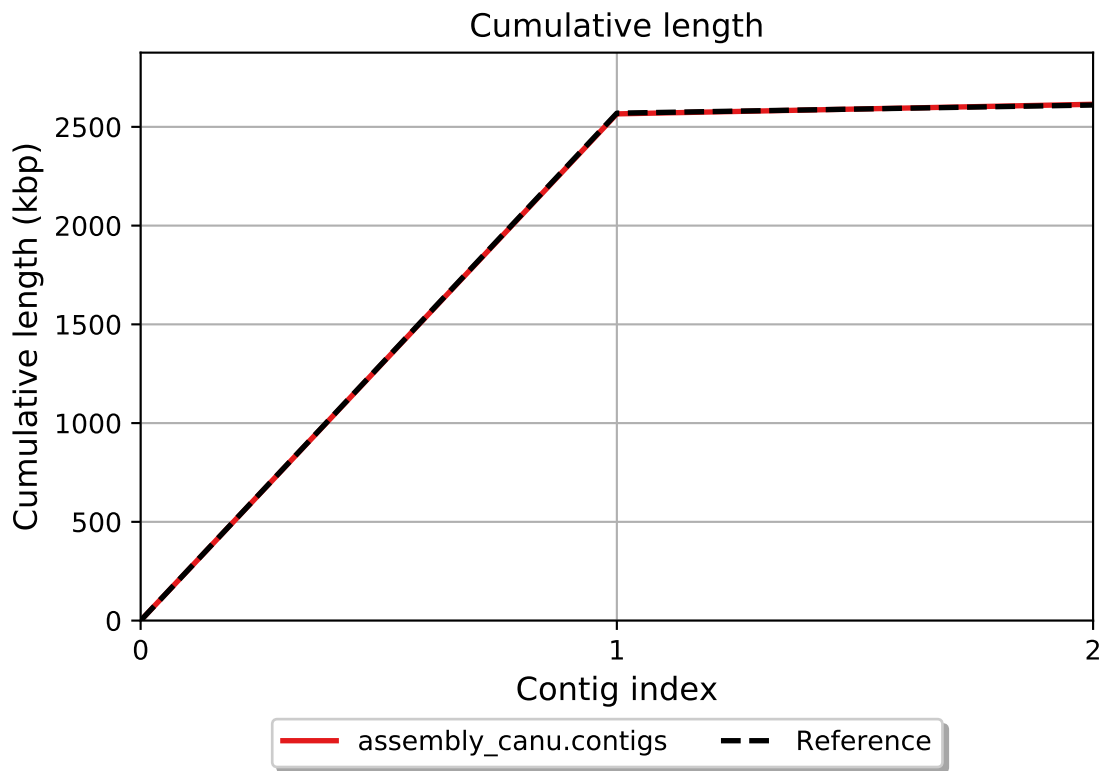
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



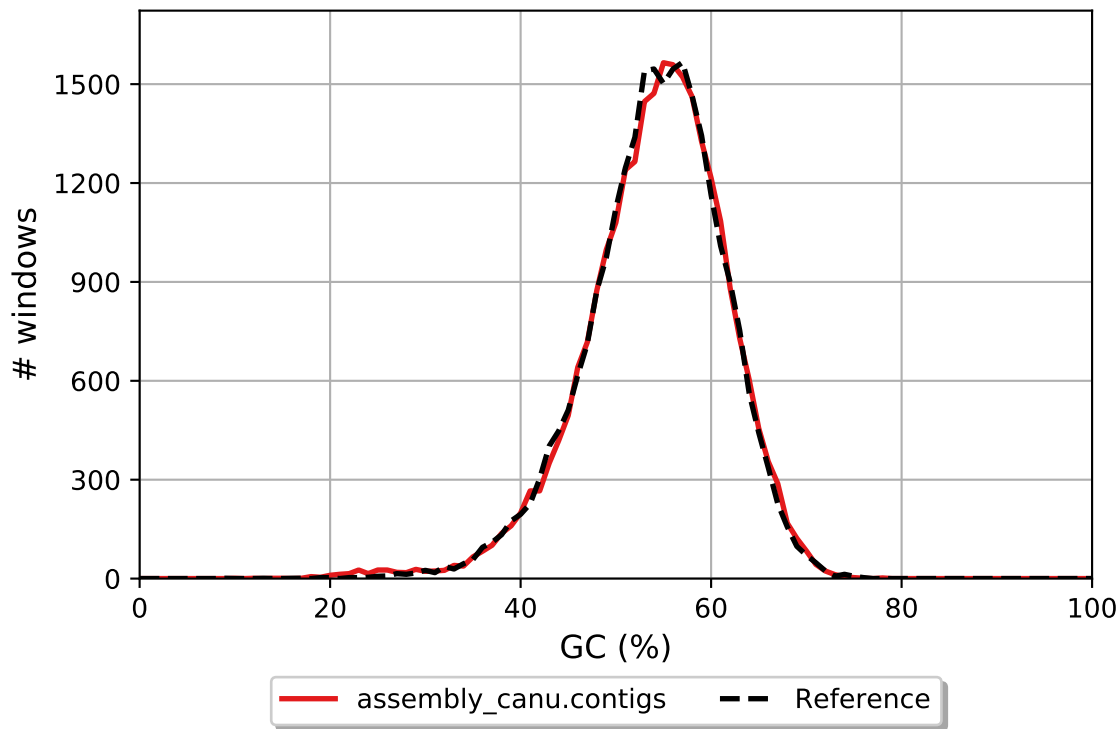
NGx



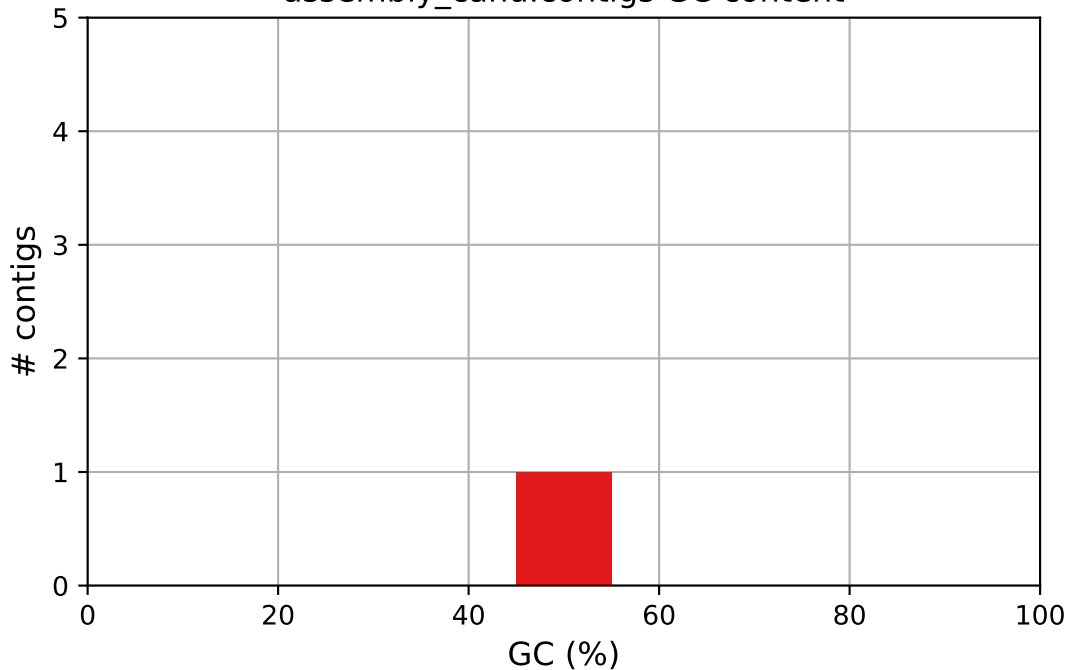
— assembly_canu.contigs



GC content

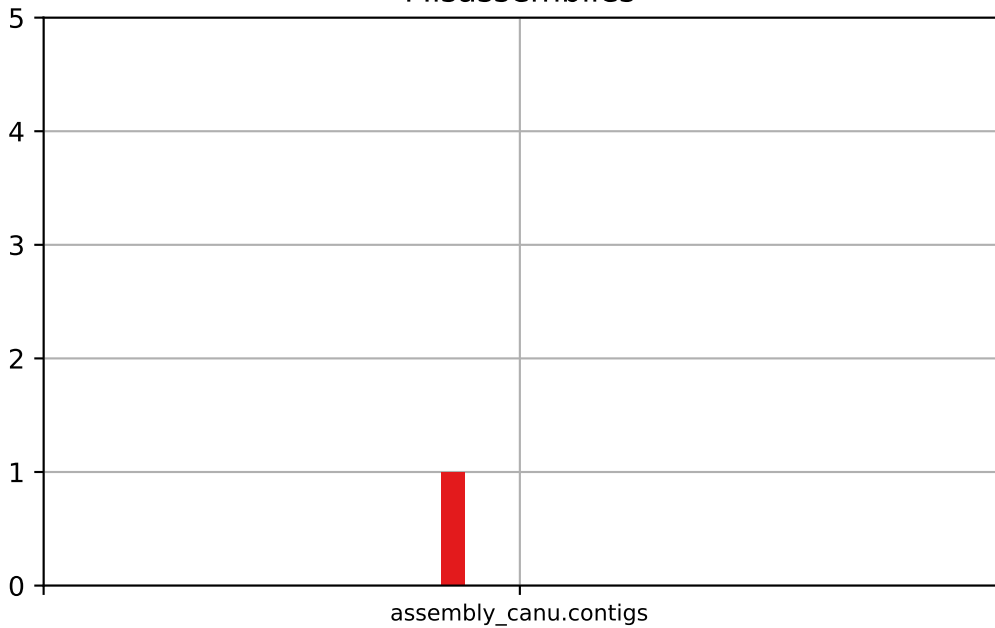


assembly_canu.contigs GC content

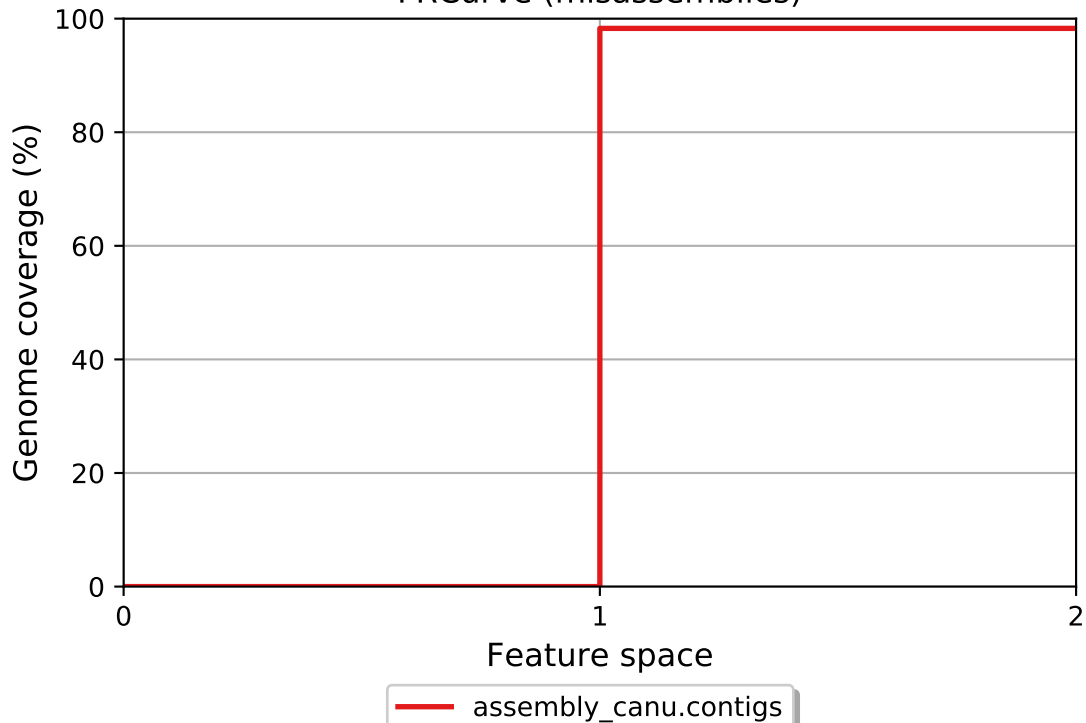


assembly_canu.contigs

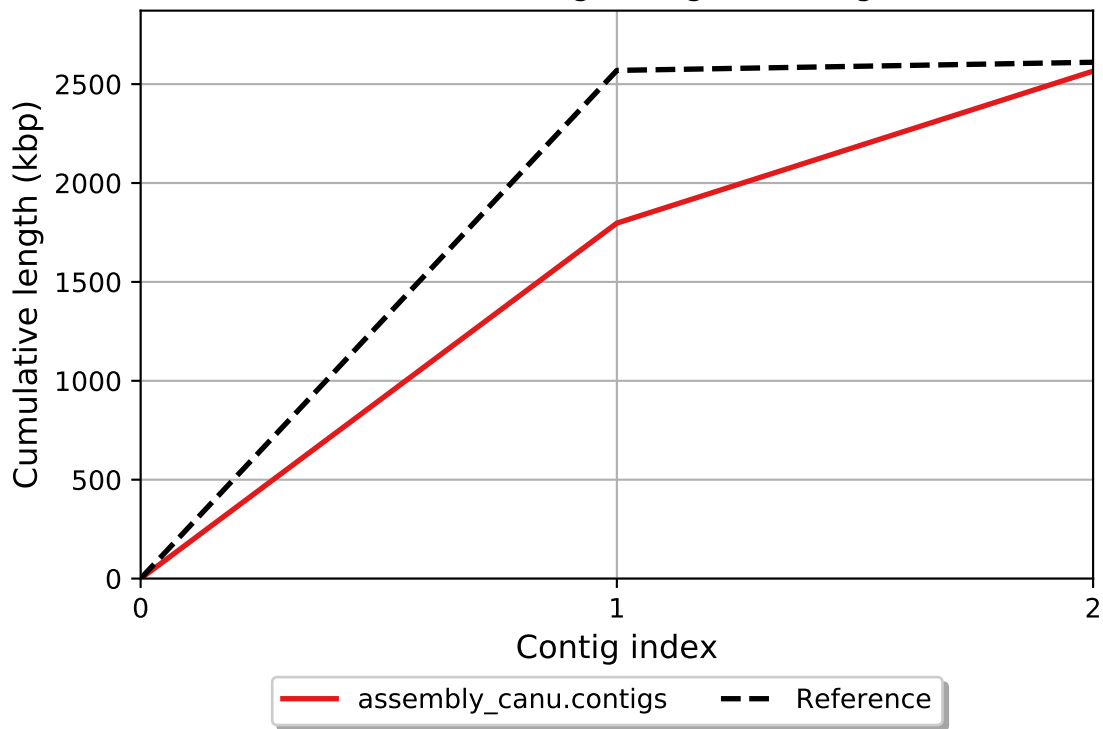
Misassemblies



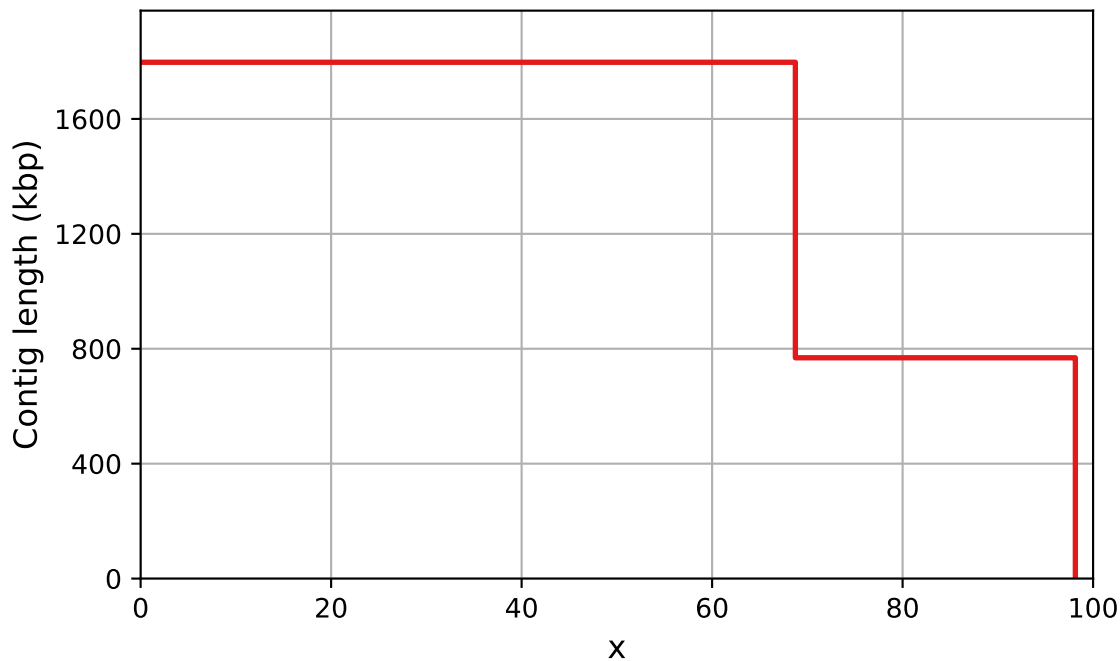
FRCurve (misassemblies)



Cumulative length (aligned contigs)

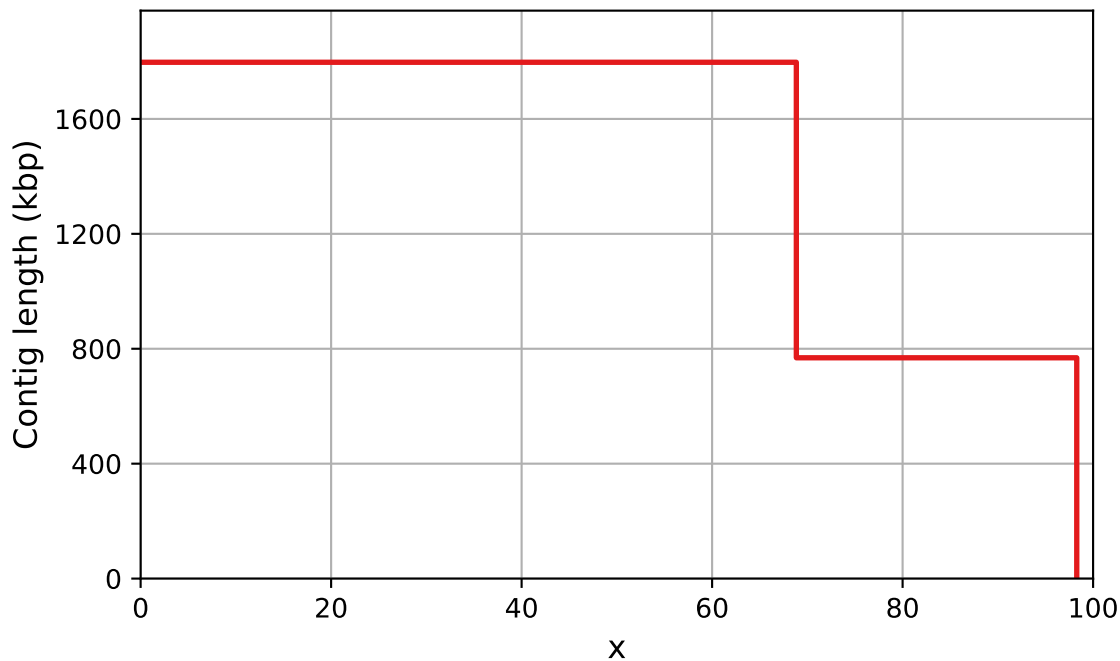


NAx



— assembly_canu.contigs

NGAx



— assembly_canu.contigs