

Report

	assembly.contigs
# contigs (>= 0 bp)	5
# contigs (>= 1000 bp)	5
# contigs (>= 5000 bp)	3
# contigs (>= 10000 bp)	3
# contigs (>= 25000 bp)	3
# contigs (>= 50000 bp)	1
Total length (>= 0 bp)	2664083
Total length (>= 1000 bp)	2664083
Total length (>= 5000 bp)	2660794
Total length (>= 10000 bp)	2660794
Total length (>= 25000 bp)	2660794
Total length (>= 50000 bp)	2572340
# contigs	5
Largest contig	2572340
Total length	2664083
Reference length	2610531
GC (%)	53.95
Reference GC (%)	54.14
N50	2572340
NG50	2572340
N75	2572340
NG75	2572340
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	2572340
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	4 + 0 part
Unaligned length	91743
Genome fraction (%)	97.566
Duplication ratio	1.010
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.35
# indels per 100 kbp	10.29
Largest alignment	2033778
Total aligned length	2572340
NA50	2033778
NGA50	2033778
NA75	2033778
NGA75	2033778
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

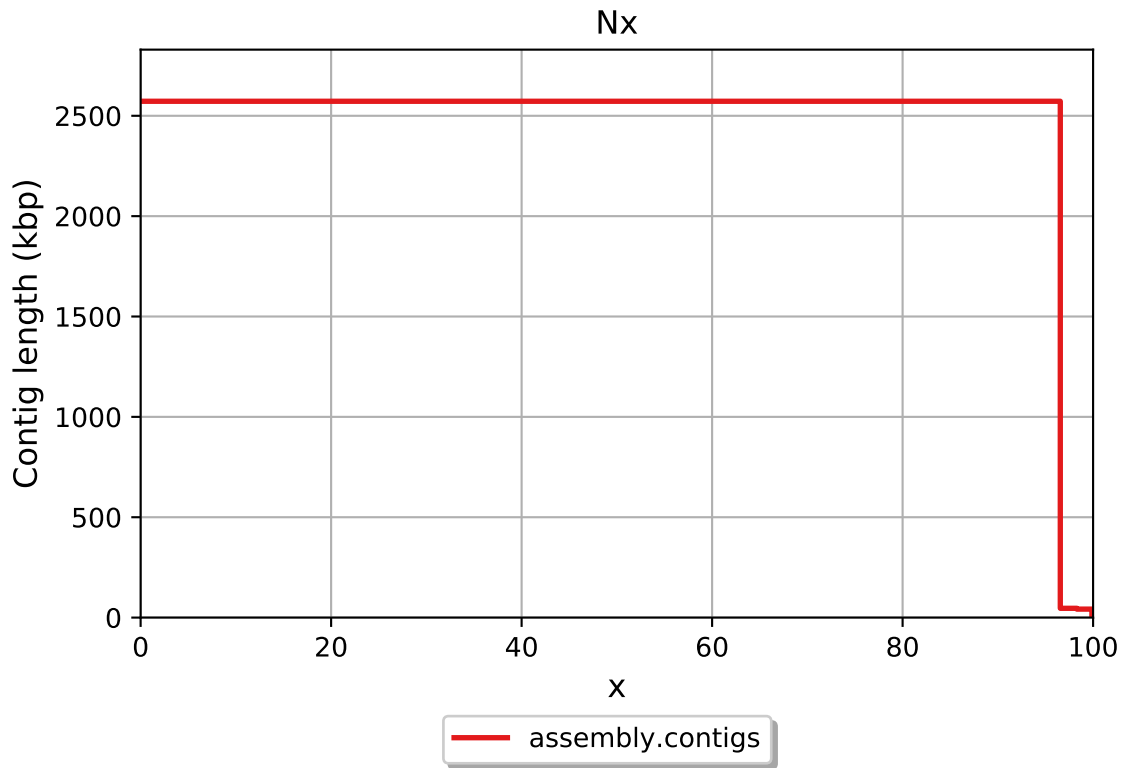
	assembly.contigs
# misassemblies	1
# contig misassemblies	1
# c. relocations	1
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	1
Misassembled contigs length	2572340
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	9
# indels	262
# indels (<= 5 bp)	262
# indels (> 5 bp)	0
Indels length	269

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).

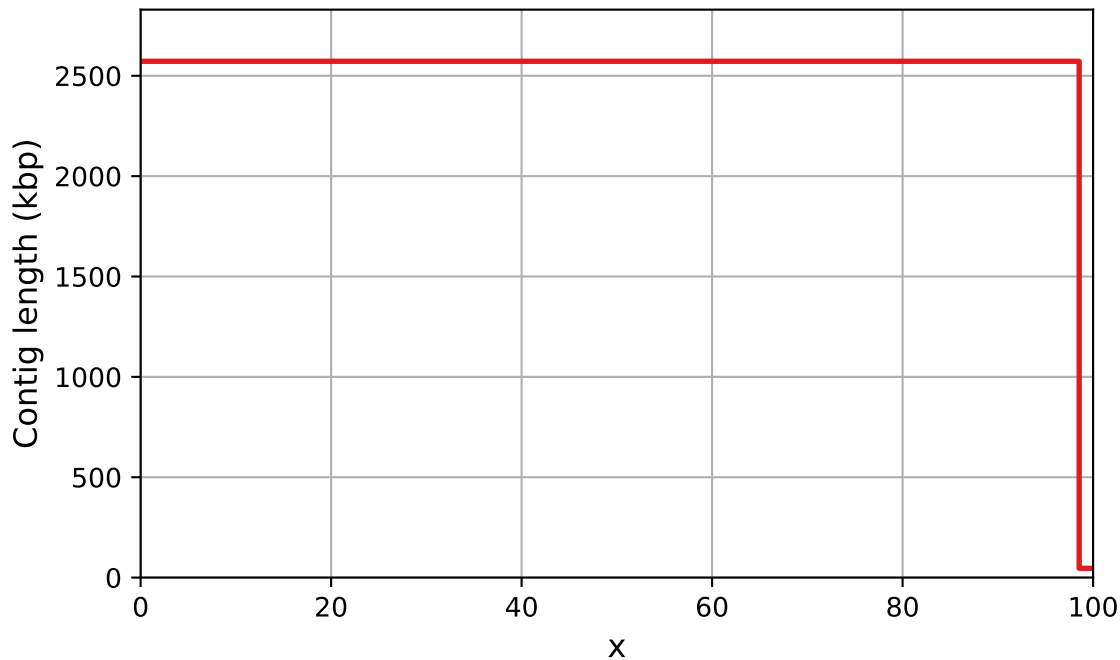
Unaligned report

	assembly.contigs
# fully unaligned contigs	4
Fully unaligned length	91743
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

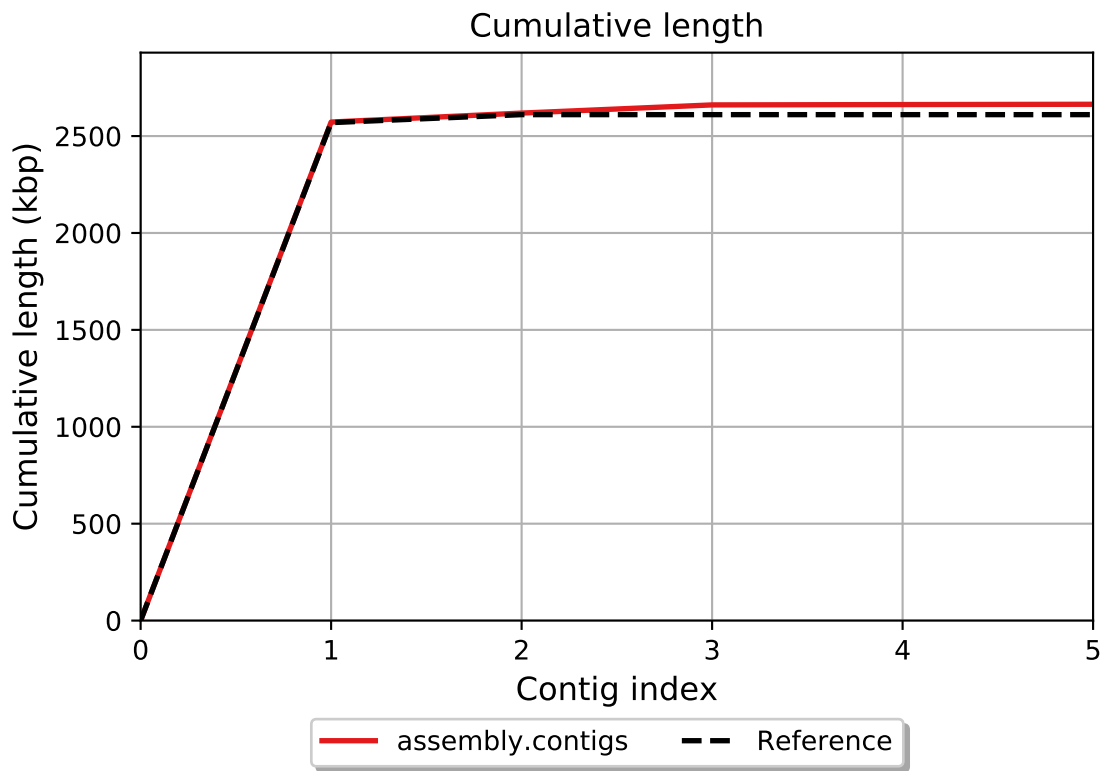
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



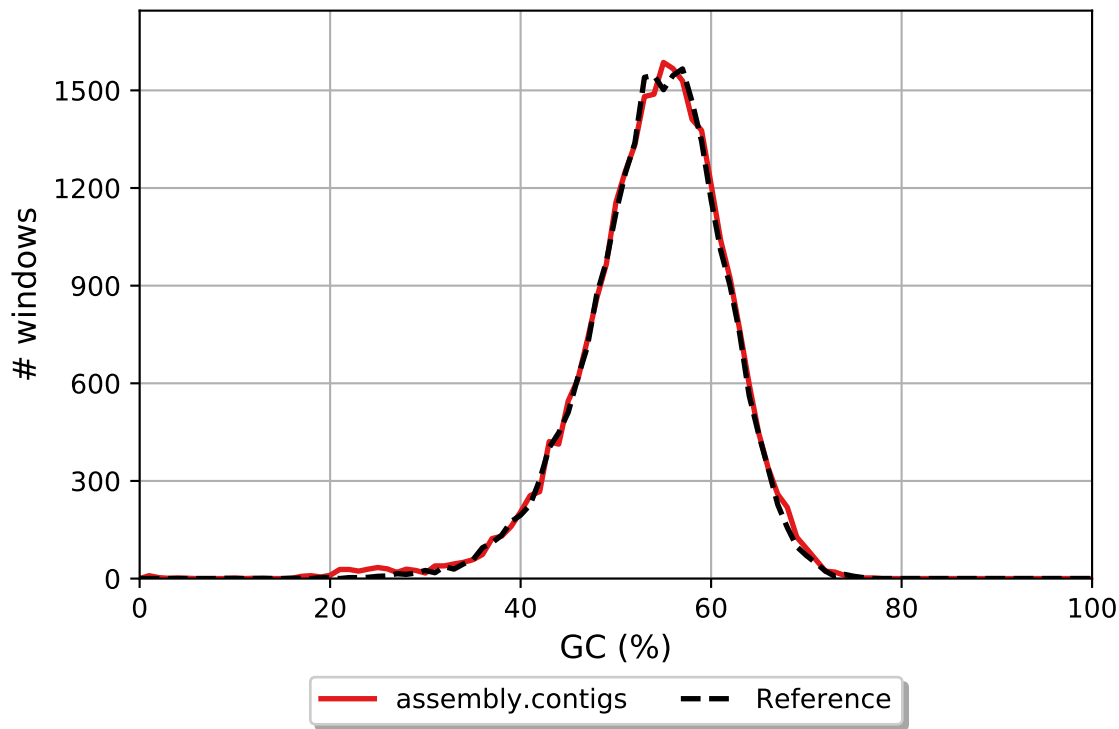
NGx



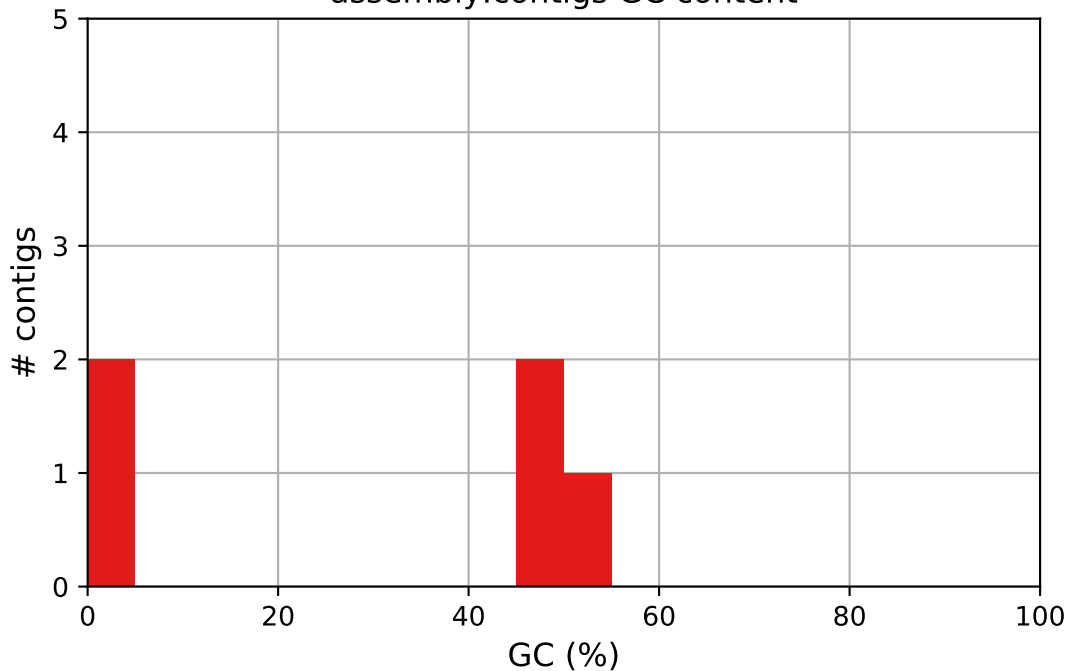
— assembly.contigs



GC content

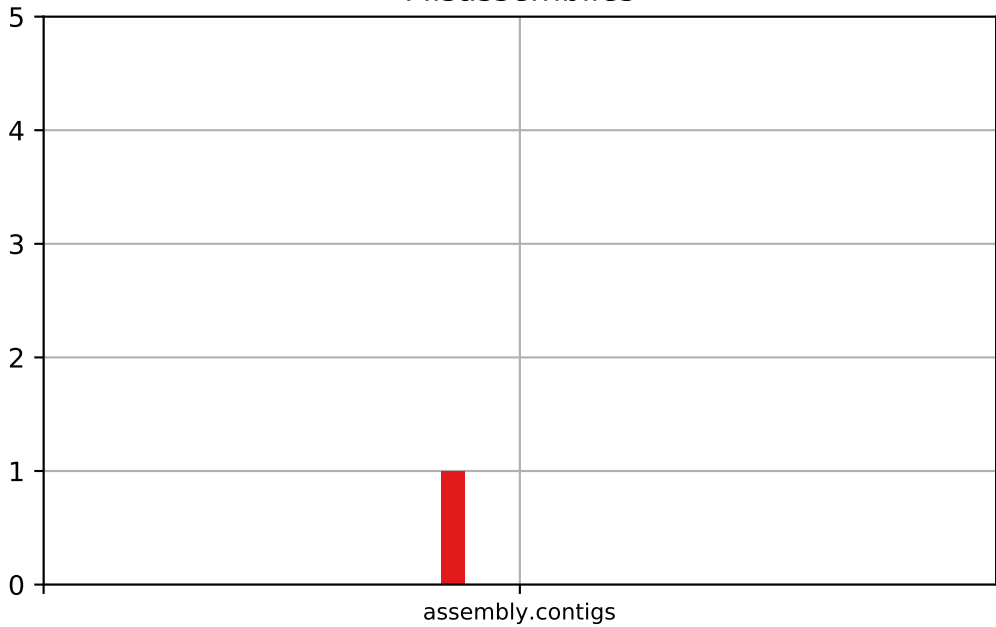


assembly.contigs GC content

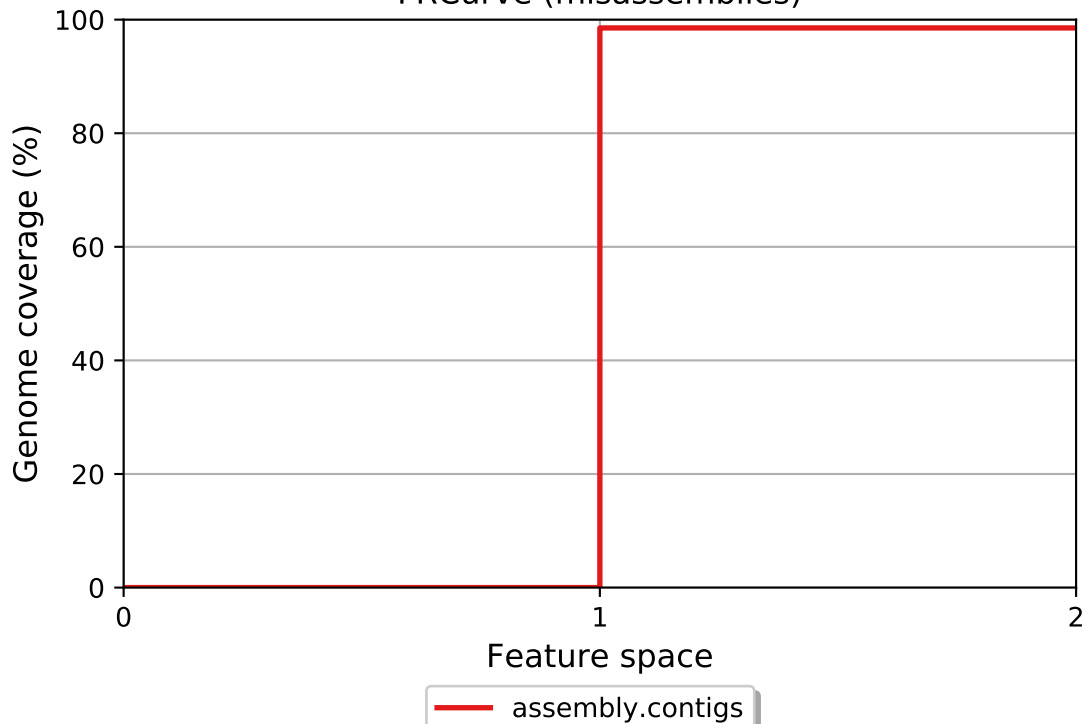


assembly.contigs

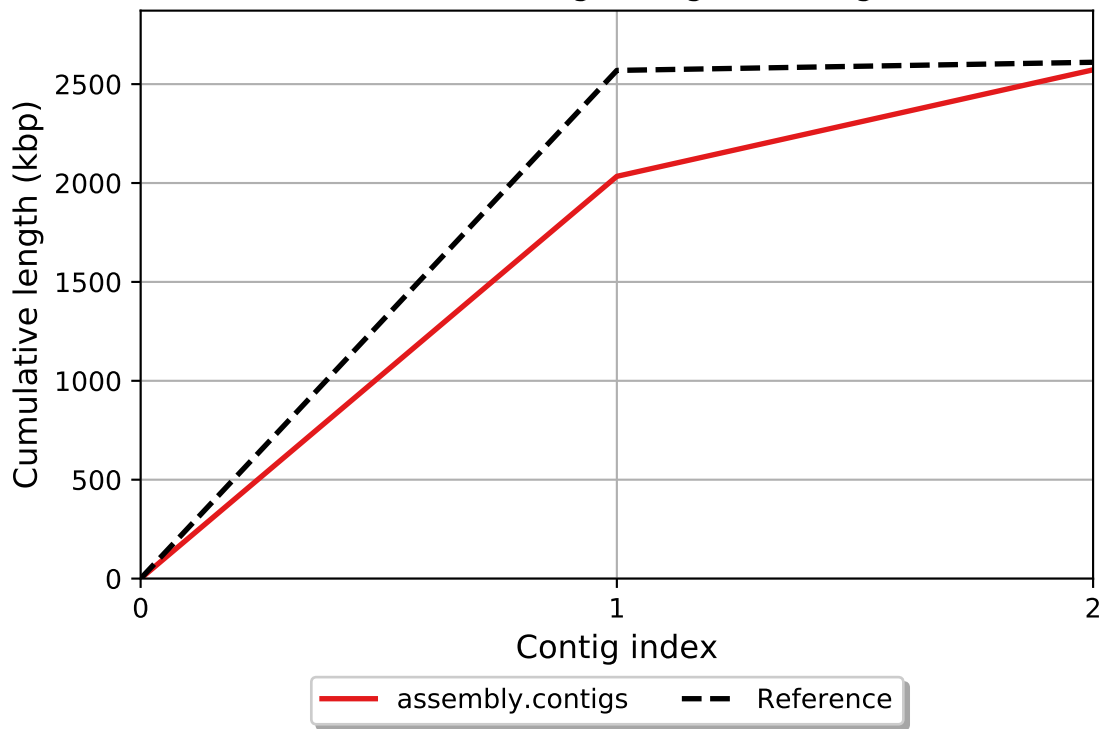
Misassemblies



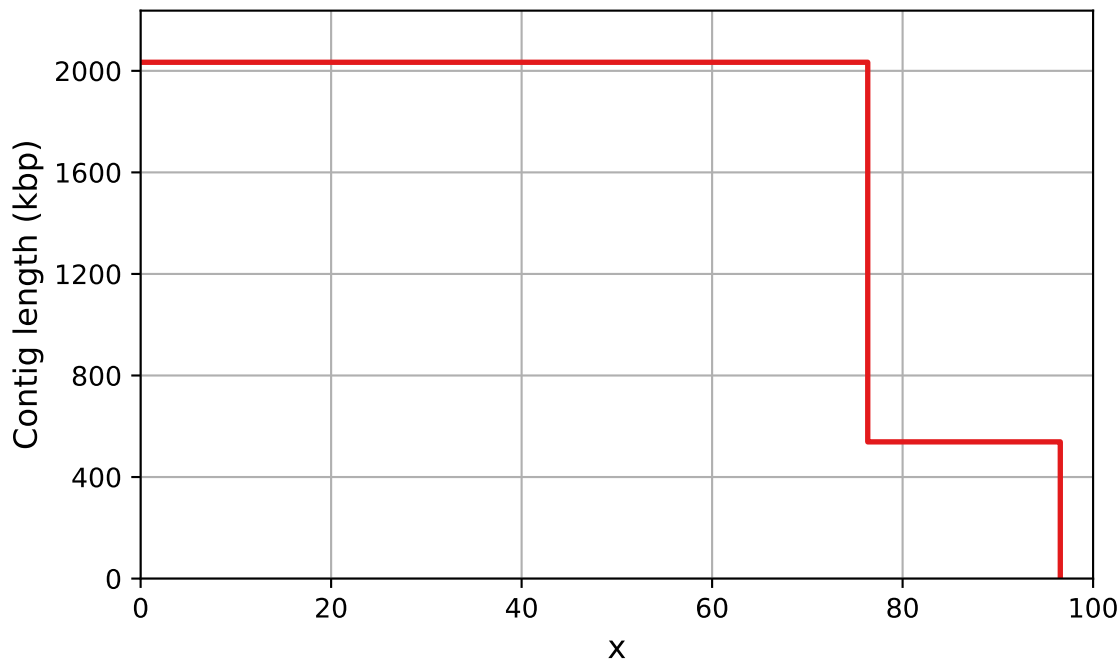
FRCurve (misassemblies)



Cumulative length (aligned contigs)

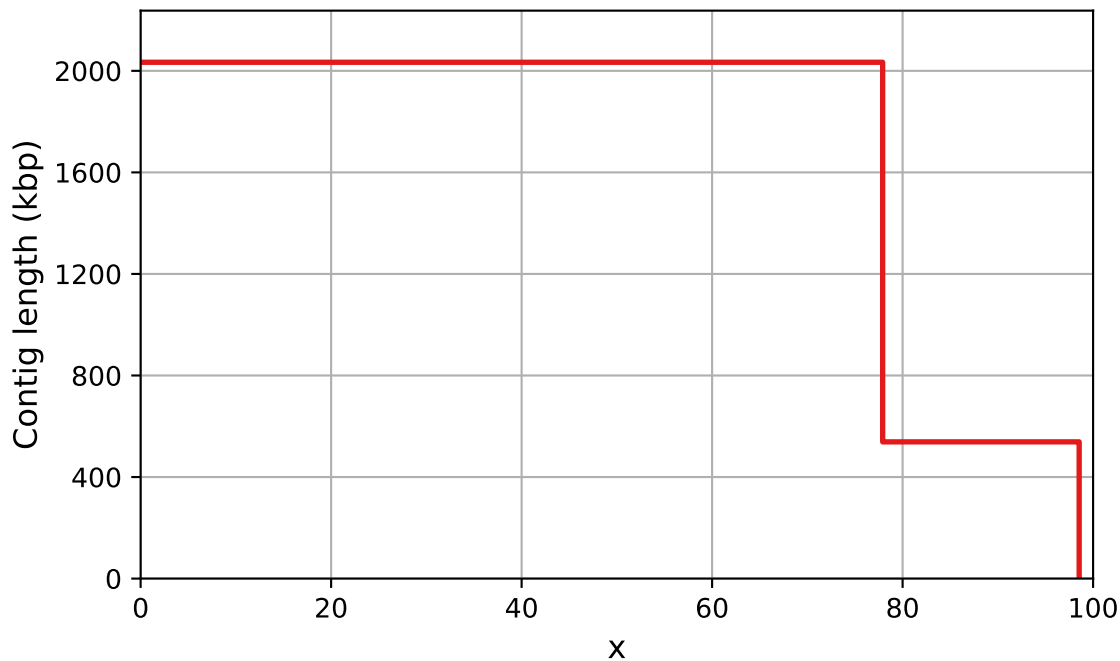


NAx



— assembly.contigs

NGAx



— assembly.contigs