

Report

	final.contigs
# contigs (>= 1000 bp)	0
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	0
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	12
Largest contig	742
Total length	7151
Reference length	1739927
GC (%)	33.97
Reference GC (%)	31.29
N50	593
NG50	-
N90	519
NG90	-
auN	601.9
auNG	2.5
L50	6
LG50	-
L90	11
LG90	-
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	570
# 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 (%)	0.410
Duplication ratio	1.003
# N's per 100 kbp	0.00
# mismatches per 100 kbp	615.30
# indels per 100 kbp	69.92
Largest alignment	742
Total aligned length	7151
NA50	593
NGA50	-
NA90	511
NGA90	-
auNA	588.4
auNGA	2.4
LA50	6
LGA50	-
LA90	11
LGA90	-

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

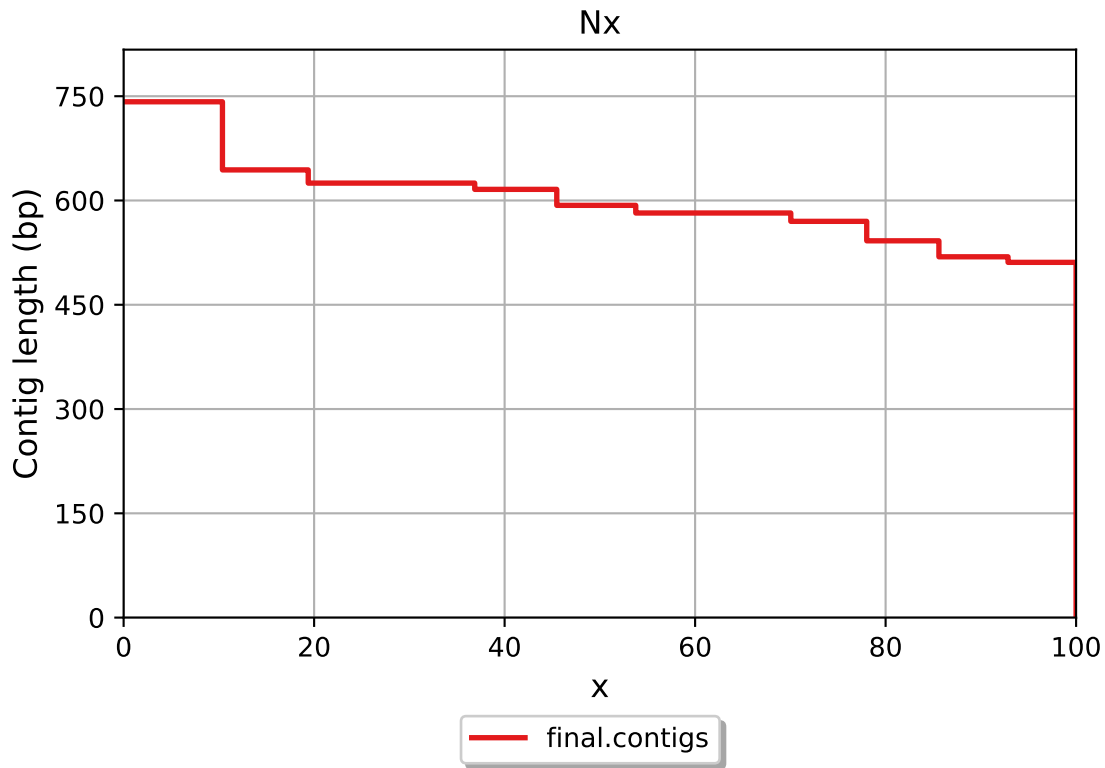
	final.contigs
# misassemblies	1
# contig misassemblies	1
# c. relocations	0
# c. translocations	0
# c. inversions	1
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	1
Misassembled contigs length	570
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	44
# indels	5
# indels (<= 5 bp)	3
# indels (> 5 bp)	2
Indels length	32

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).

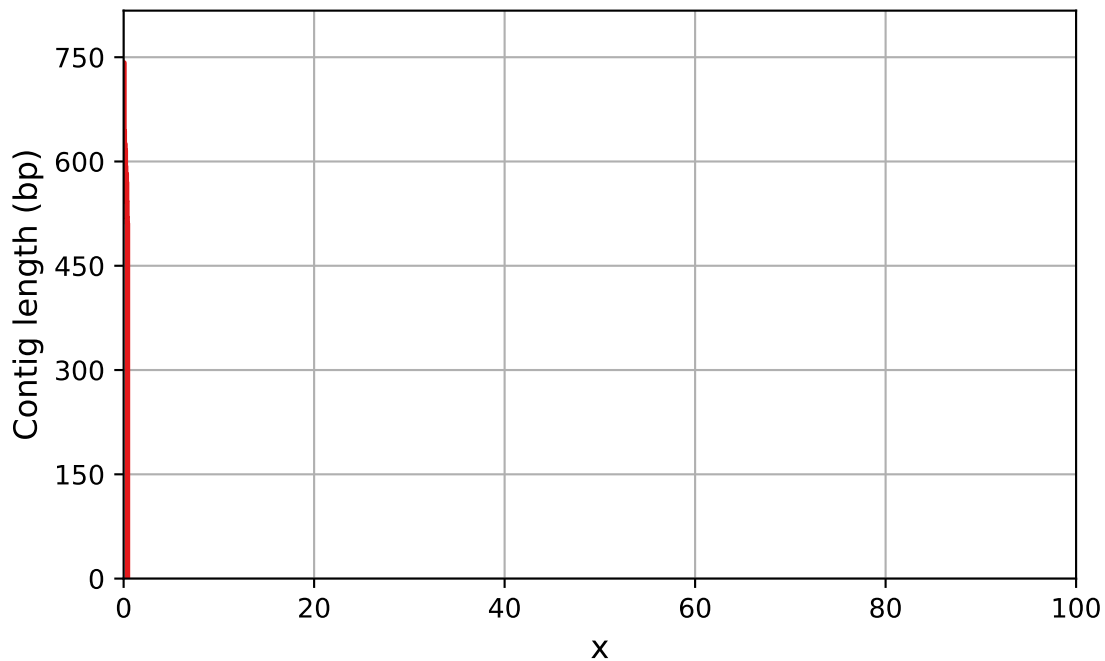
Unaligned report

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

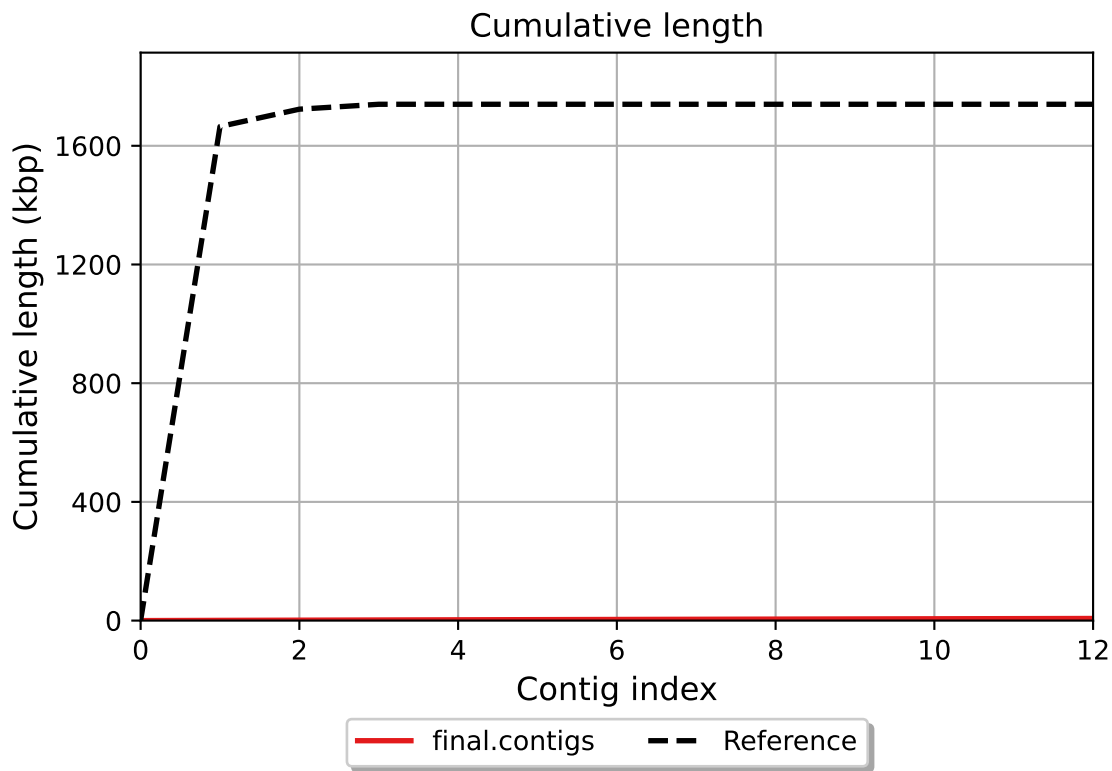
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



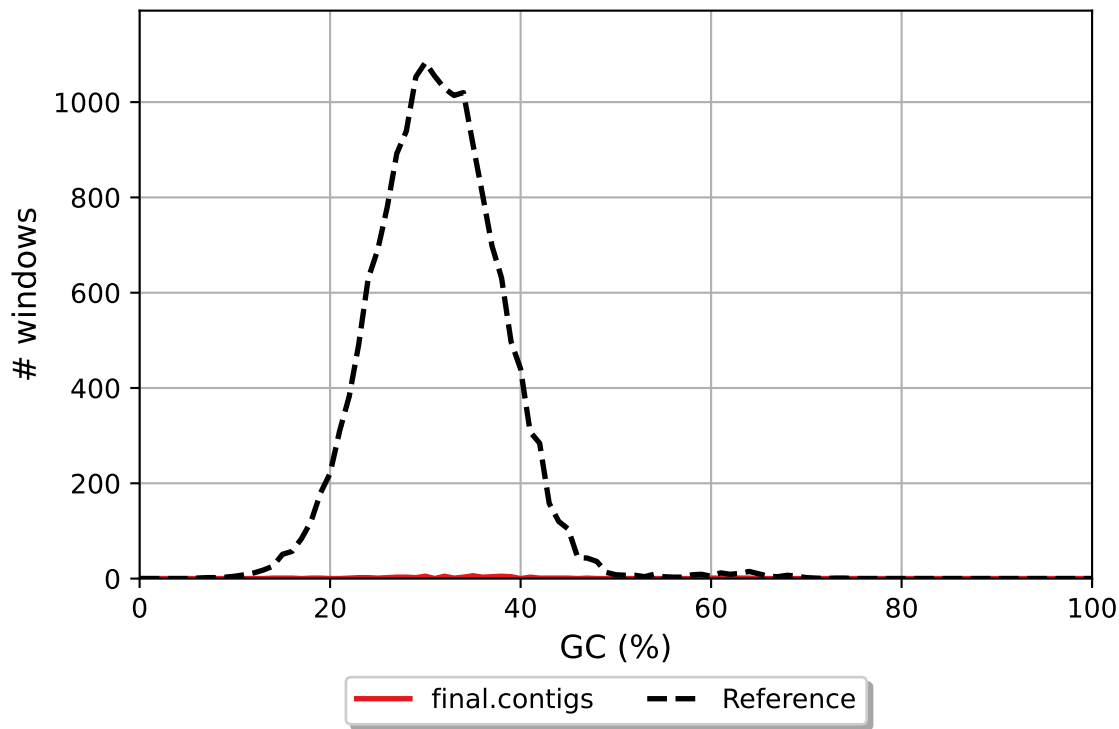
NGx



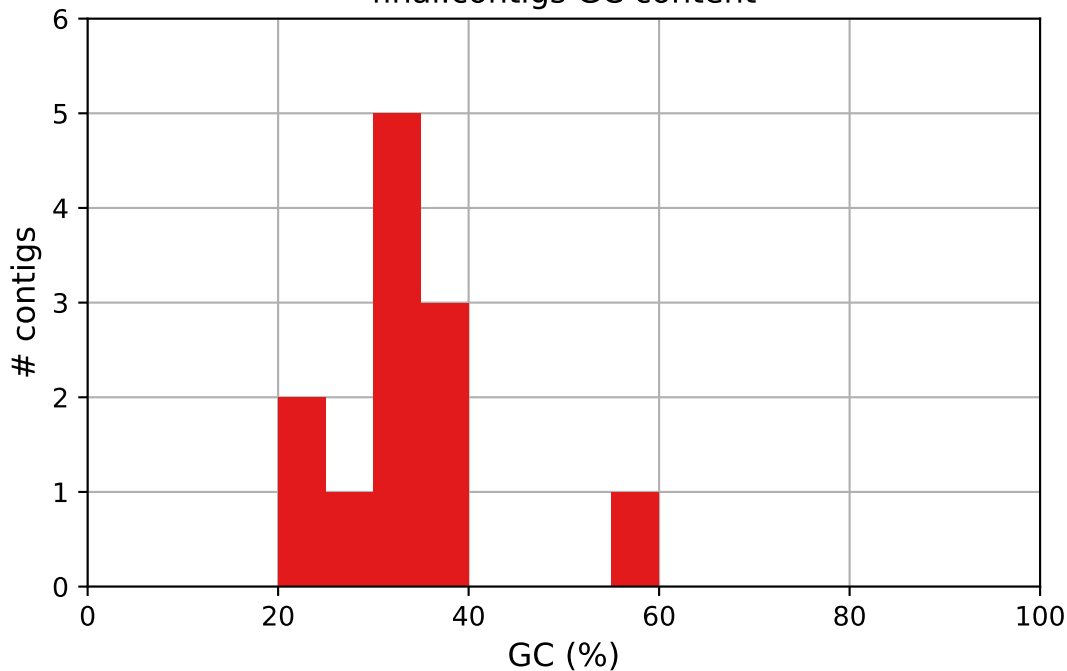
— final.contigs



GC content

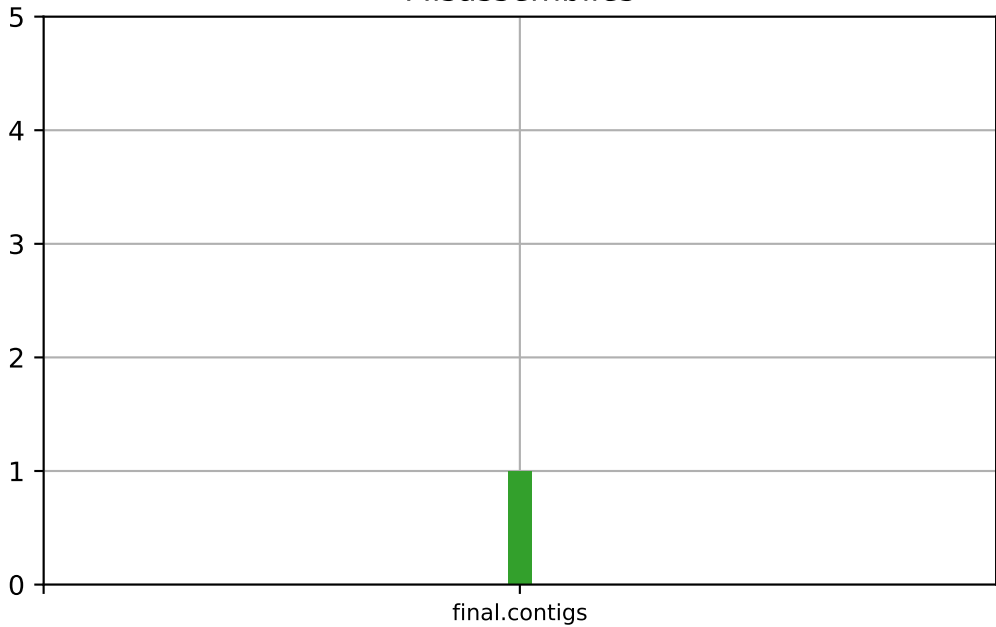


final.contigs GC content



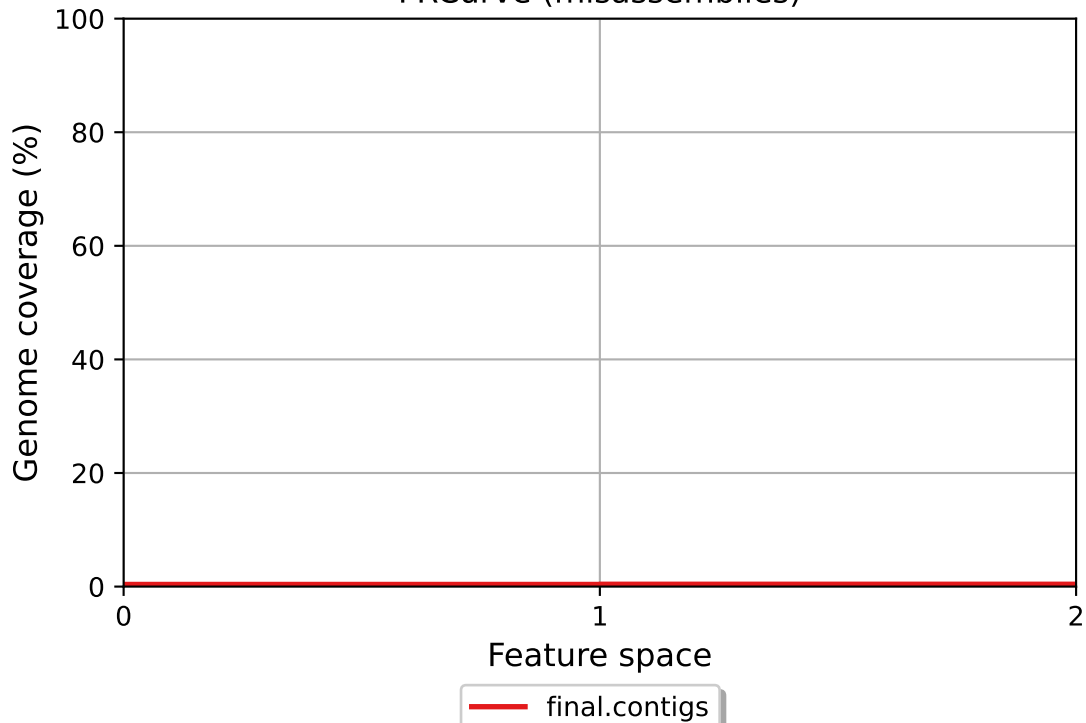
final.contigs

Misassemblies

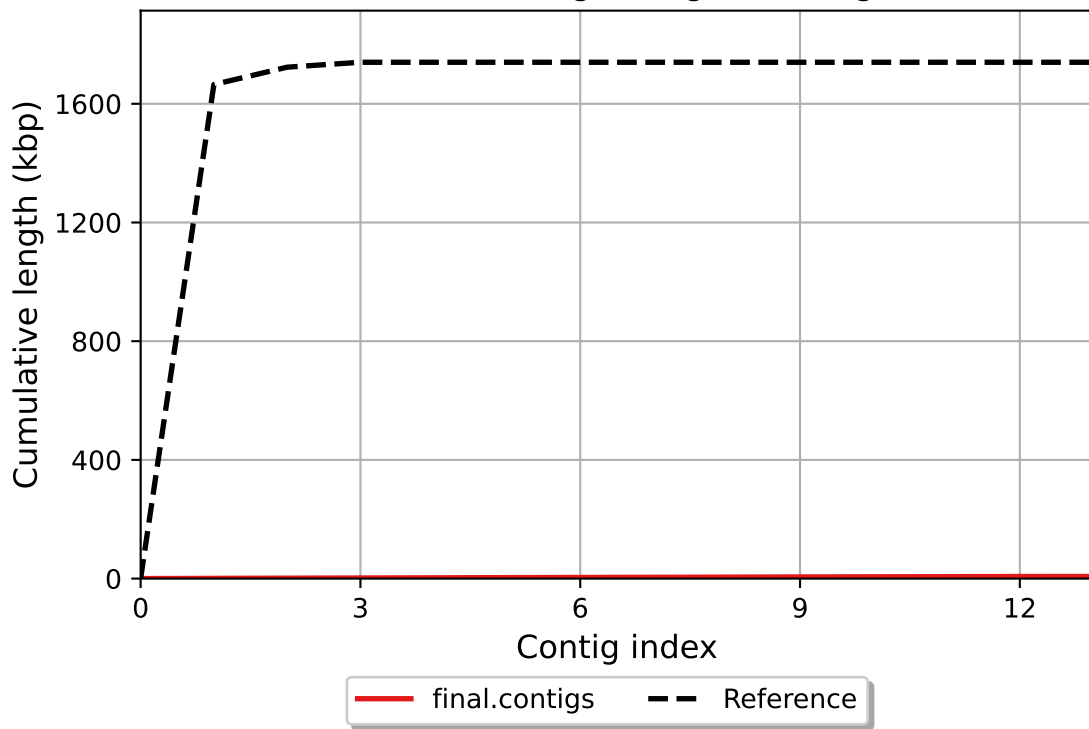


inversions

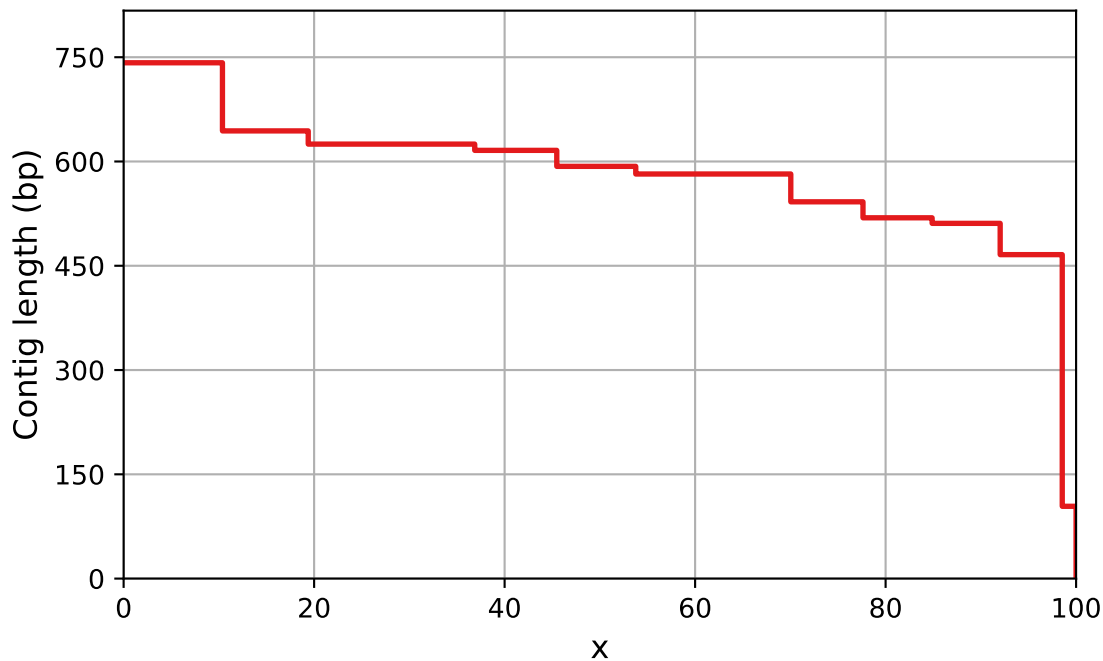
FRCurve (misassemblies)



Cumulative length (aligned contigs)

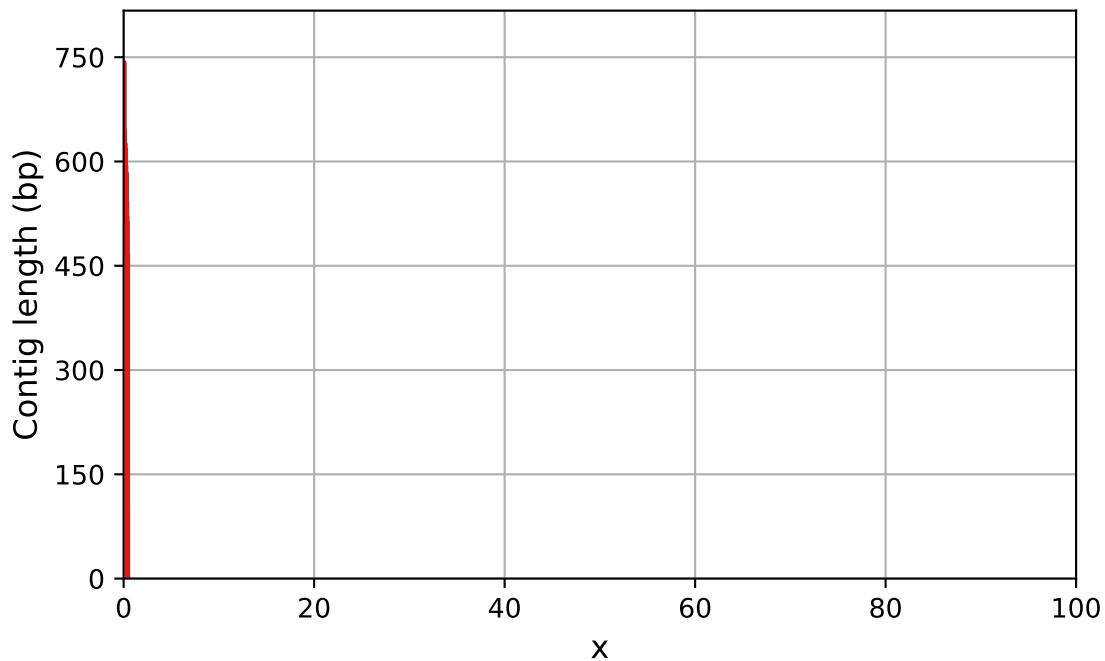


NAx



— final.contigs

NGAx



— final.contigs