

Report

	final.contigs
# contigs (>= 1000 bp)	11
# contigs (>= 5000 bp)	3
# contigs (>= 10000 bp)	3
# contigs (>= 25000 bp)	3
# contigs (>= 50000 bp)	1
Total length (>= 1000 bp)	354585
Total length (>= 5000 bp)	343370
Total length (>= 10000 bp)	343370
Total length (>= 25000 bp)	343370
Total length (>= 50000 bp)	266140
# contigs	24
Largest contig	266140
Total length	363954
Reference length	3464554
GC (%)	59.25
Reference GC (%)	65.06
N50	266140
N75	43547
L50	1
L75	2
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	1 + 14 part
Unaligned length	356426
Genome fraction (%)	0.065
Duplication ratio	3.325
# N's per 100 kbp	0.00
# mismatches per 100 kbp	3621.91
# indels per 100 kbp	132.51
Largest alignment	573
Total aligned length	2690
NGA50	-

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

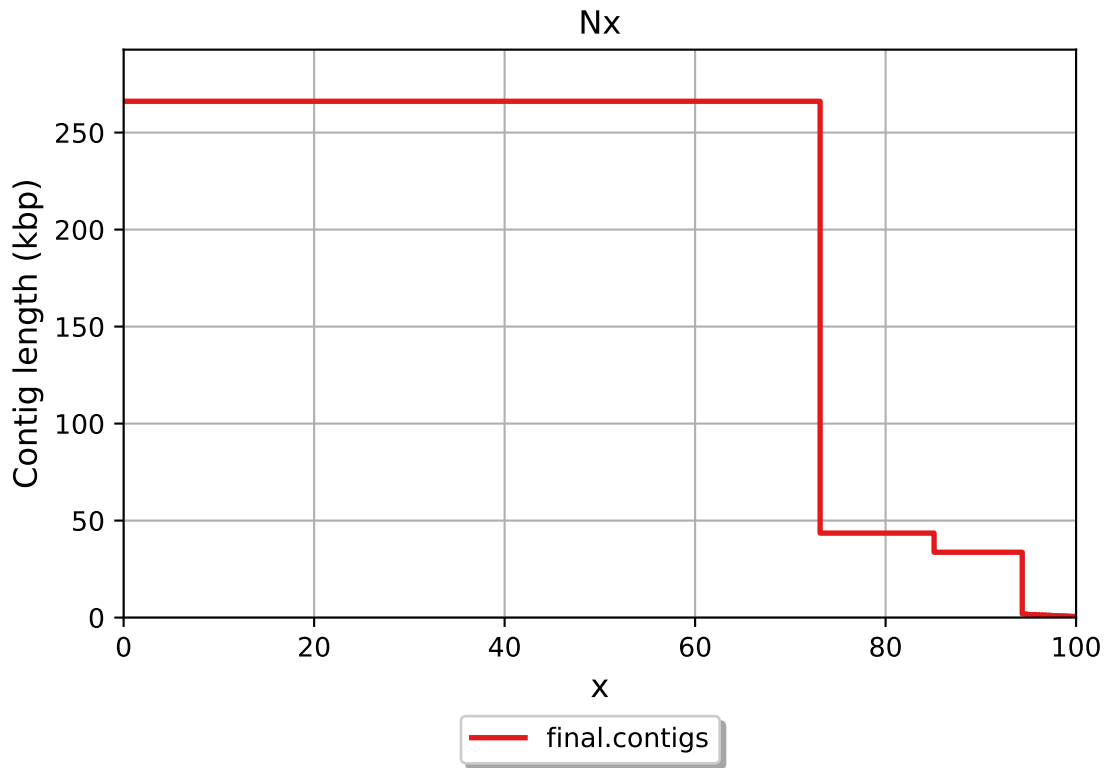
	final.contigs
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	6
# possible misassemblies	10
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	82
# indels	3
# indels (<= 5 bp)	3
# indels (> 5 bp)	0
Indels length	4

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).

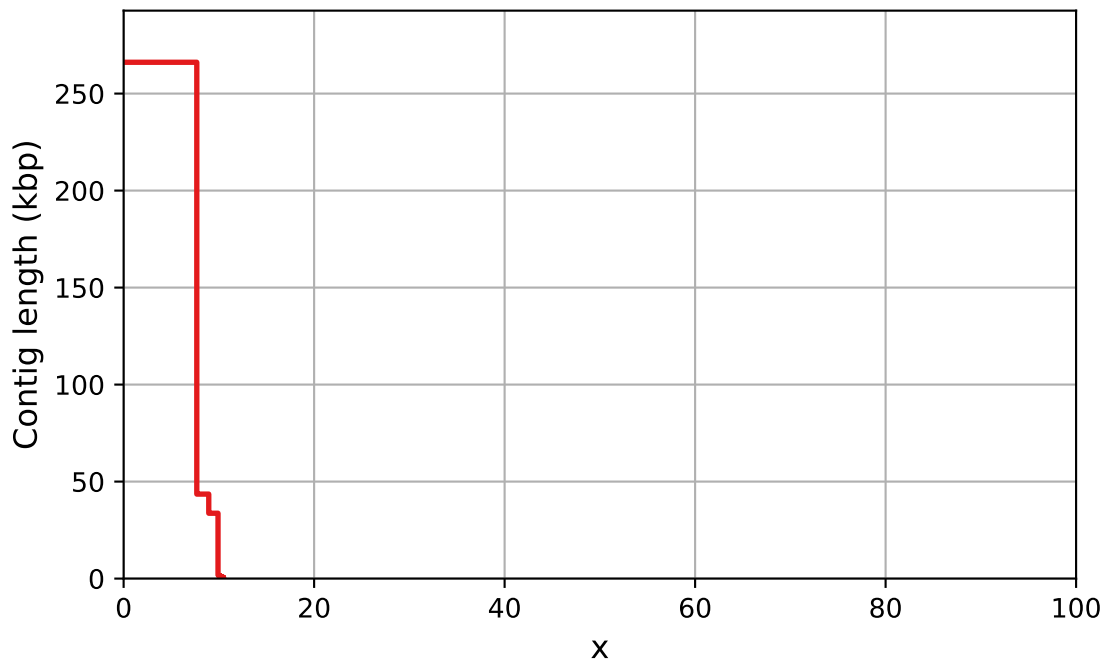
Unaligned report

	final.contigs
# fully unaligned contigs	1
Fully unaligned length	679
# partially unaligned contigs	14
Partially unaligned length	355747
# N's	0

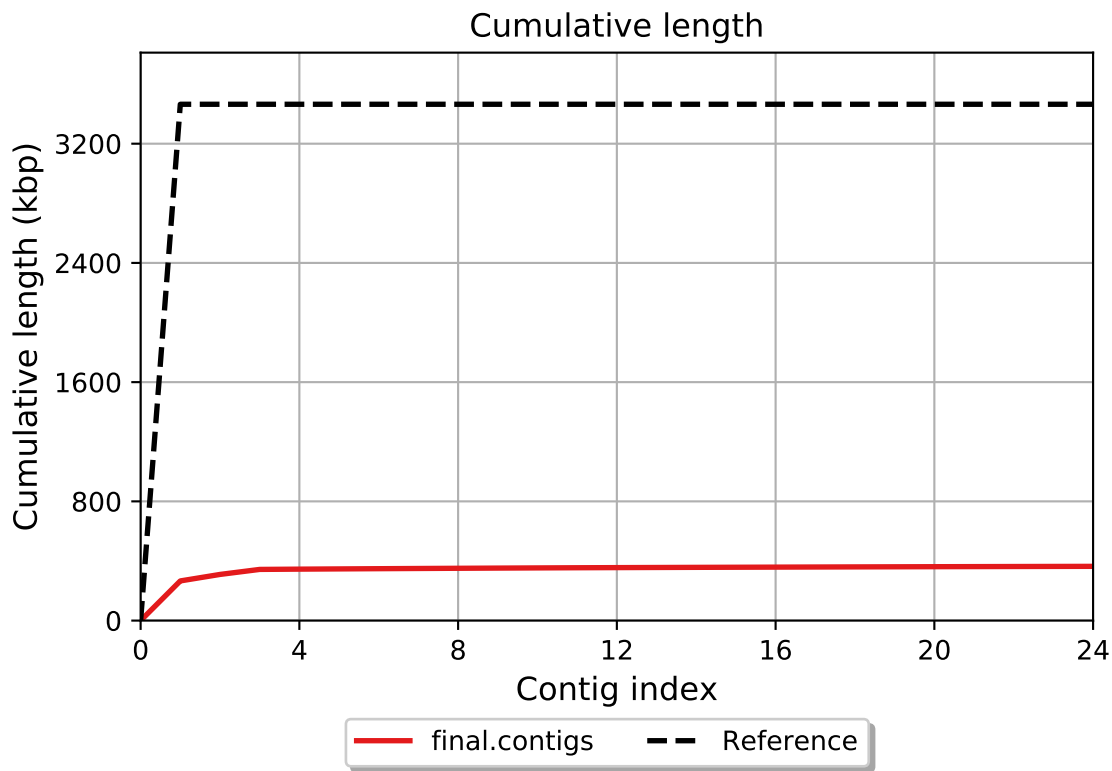
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



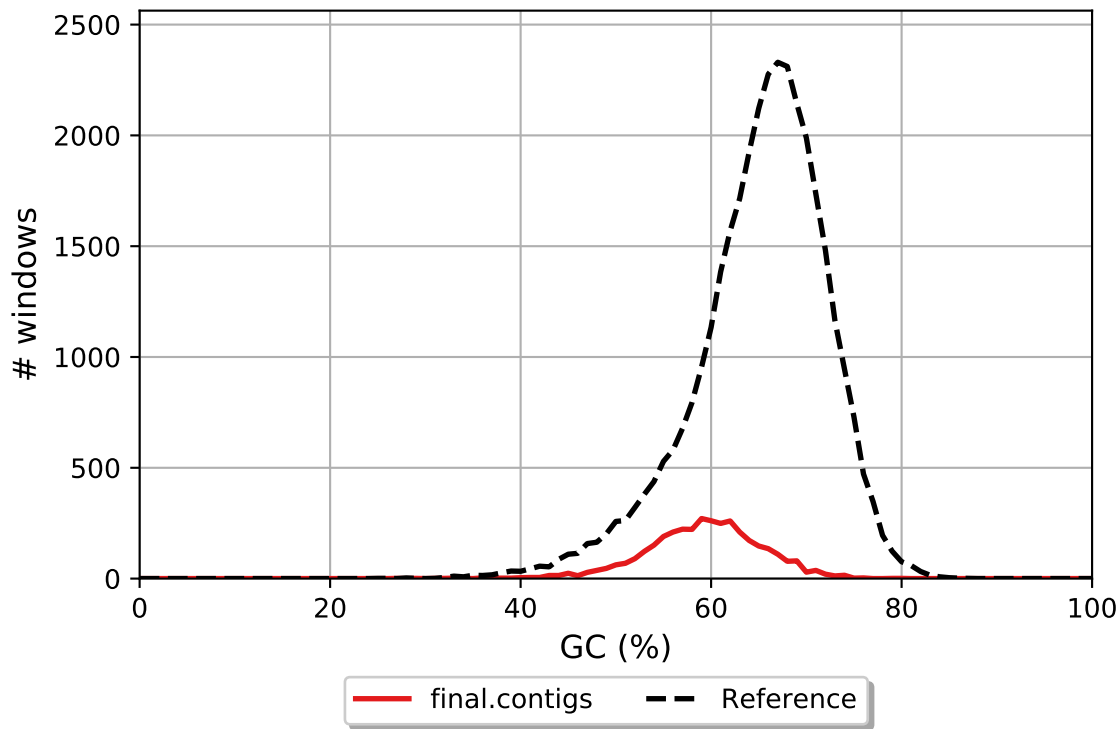
NGx



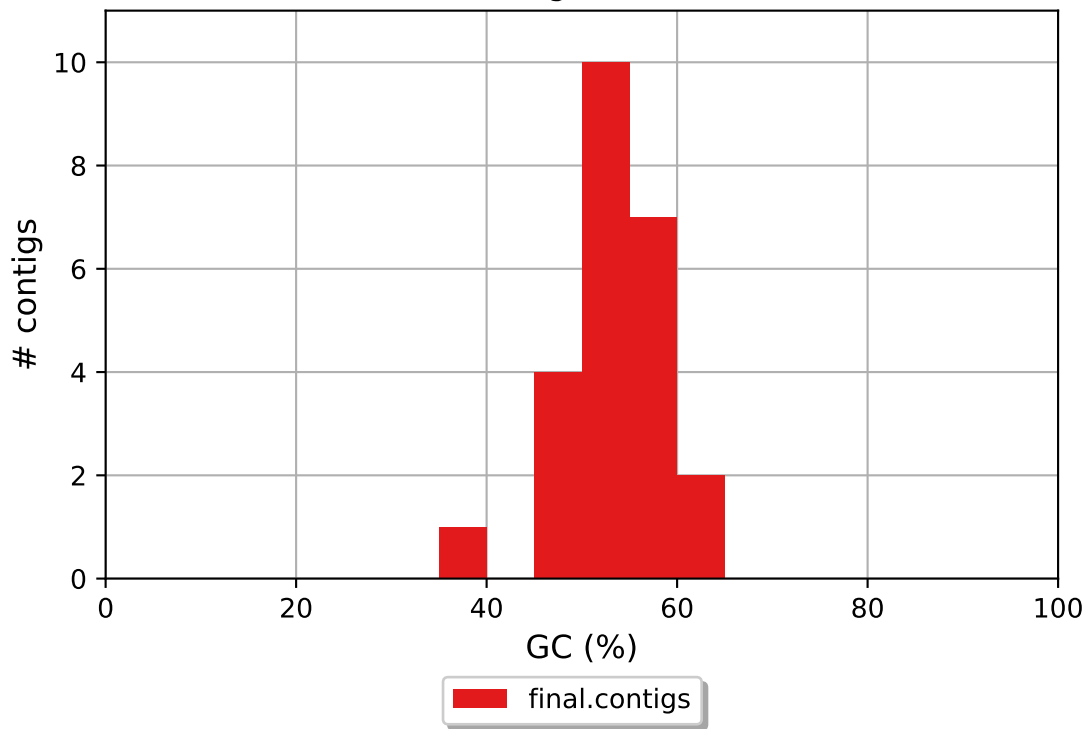
— final.contigs



GC content



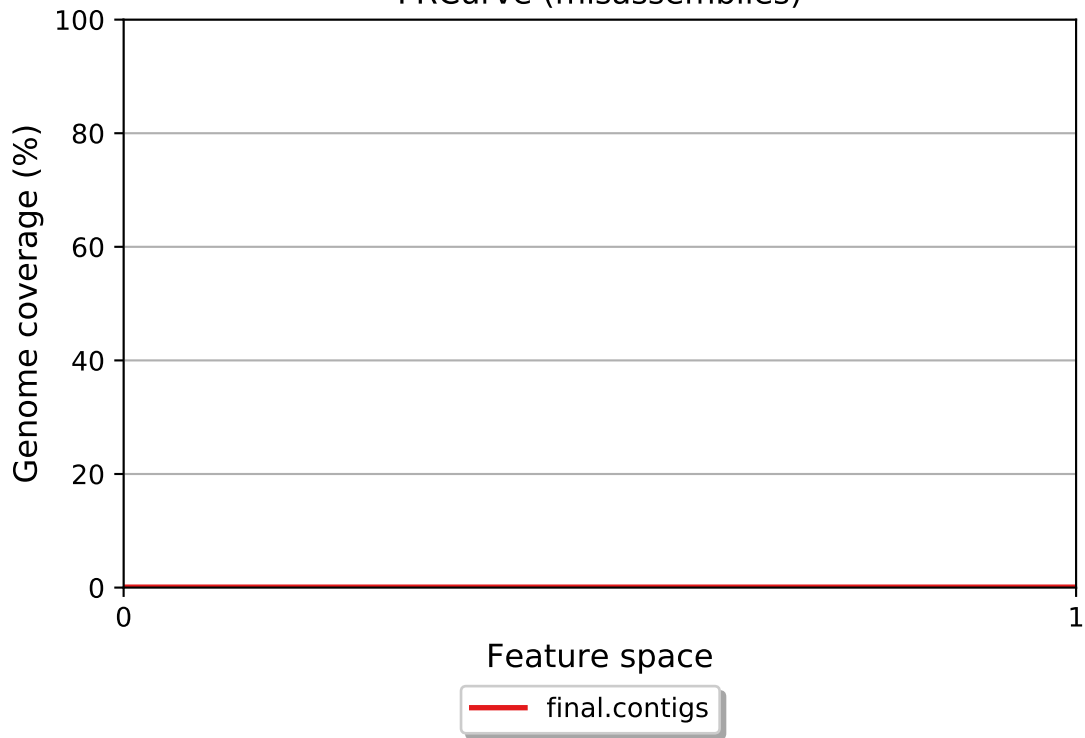
final.contigs GC content



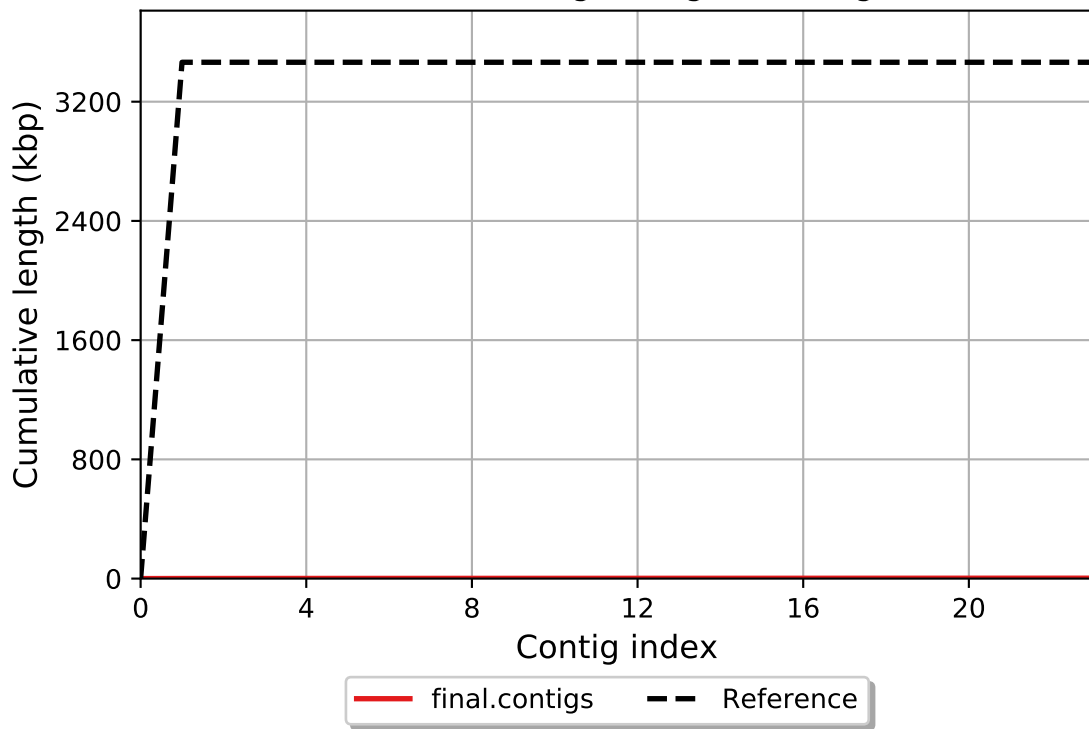
Misassemblies



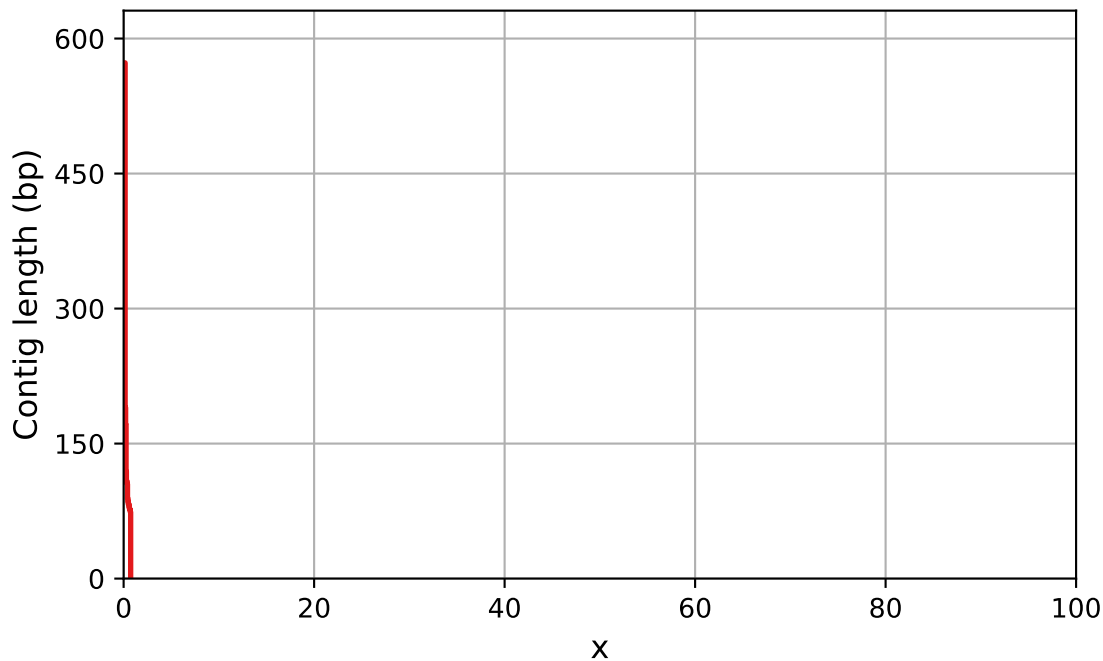
FRCurve (misassemblies)



Cumulative length (aligned contigs)

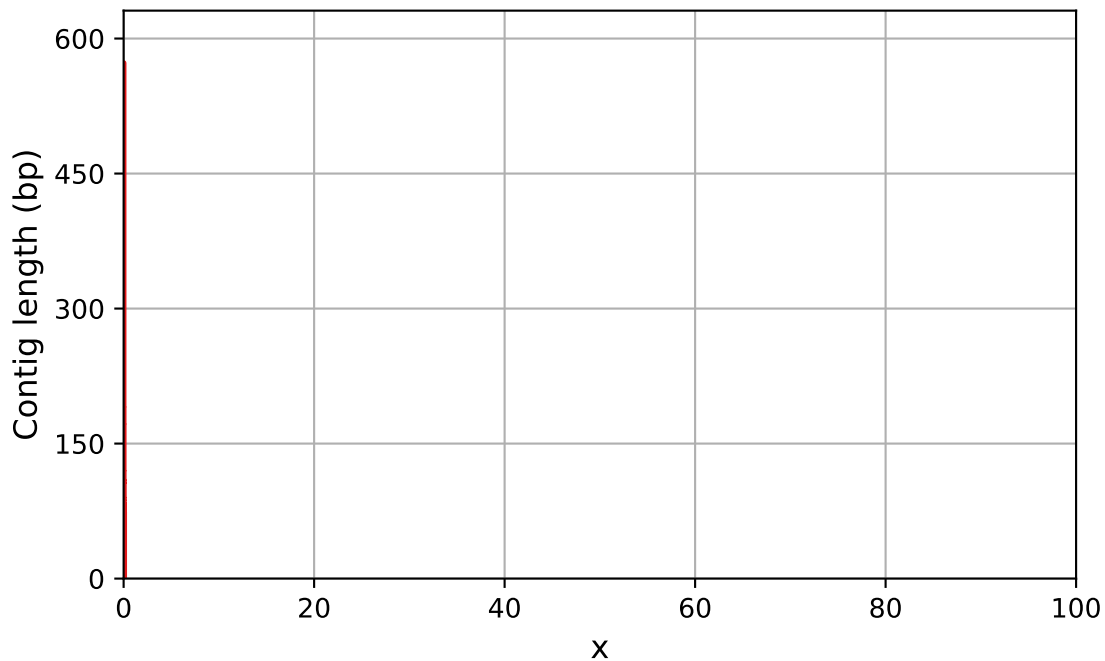


NAx



— final.contigs

NGAx



— final.contigs