

Report

	final.contigs
# contigs (>= 1000 bp)	13
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	36872
Total length (>= 5000 bp)	12656
Total length (>= 10000 bp)	12656
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	29
Largest contig	12656
Total length	47952
Reference length	3821926
GC (%)	42.25
Reference GC (%)	35.84
N50	2056
N75	1187
L50	5
L75	13
# 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	4
# unaligned contigs	3 + 19 part
Unaligned length	40598
Genome fraction (%)	0.066
Duplication ratio	2.916
# N's per 100 kbp	0.00
# mismatches per 100 kbp	6225.22
# indels per 100 kbp	79.30
Largest alignment	411
Total aligned length	4516
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	10
# possible misassemblies	12
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	4
# mismatches	157
# indels	2
# indels (<= 5 bp)	1
# indels (> 5 bp)	1
Indels length	84

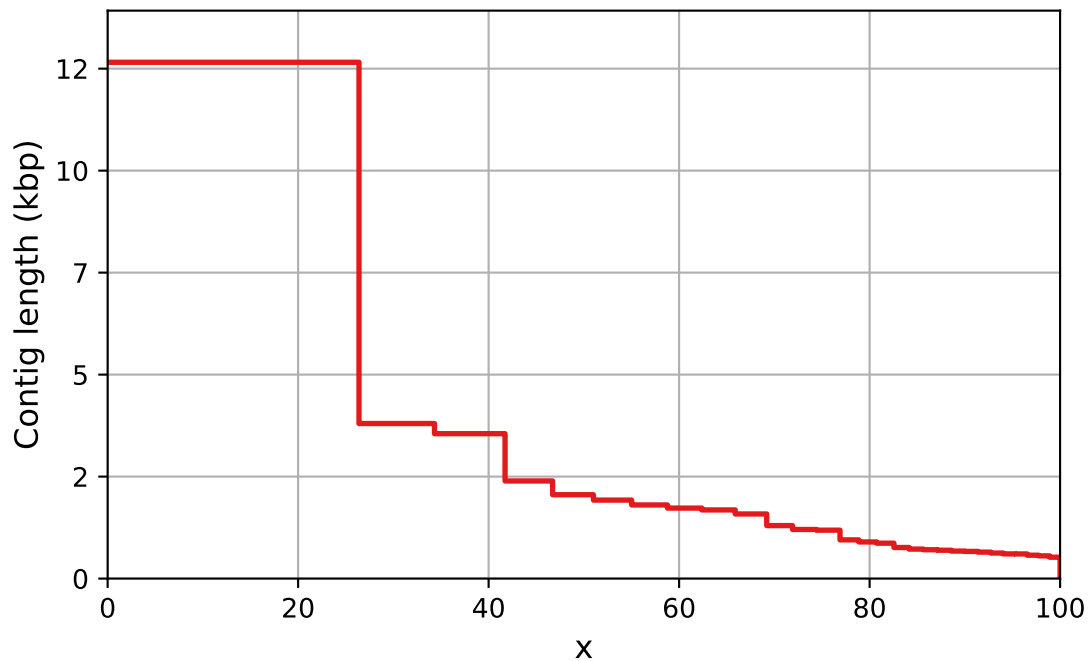
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	final.contigs
# fully unaligned contigs	3
Fully unaligned length	3321
# partially unaligned contigs	19
Partially unaligned length	37277
# N's	0

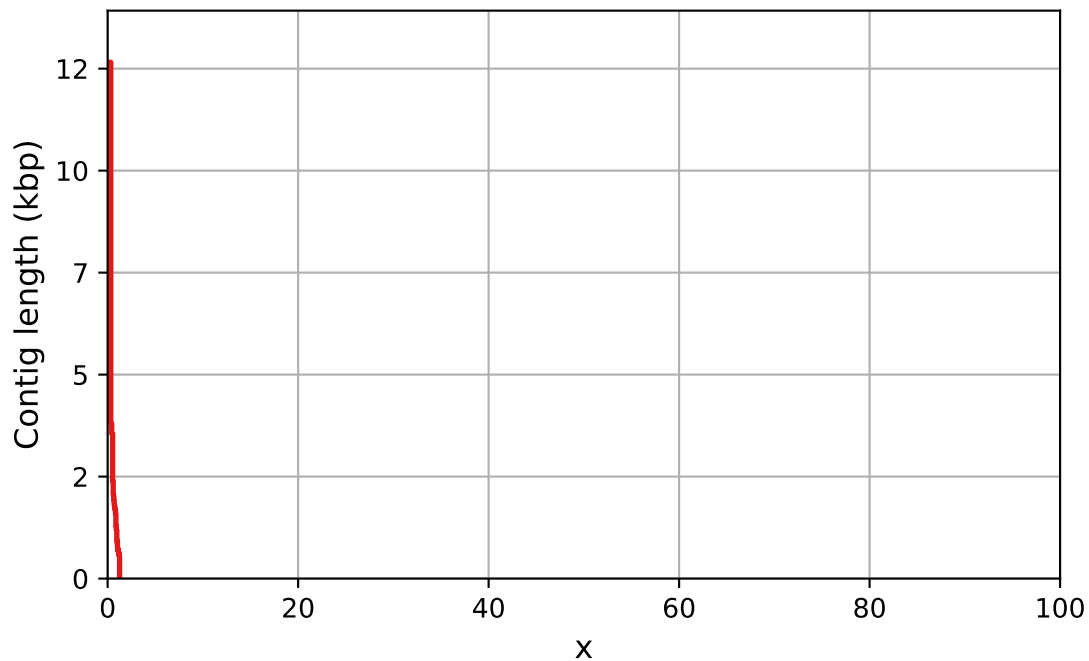
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

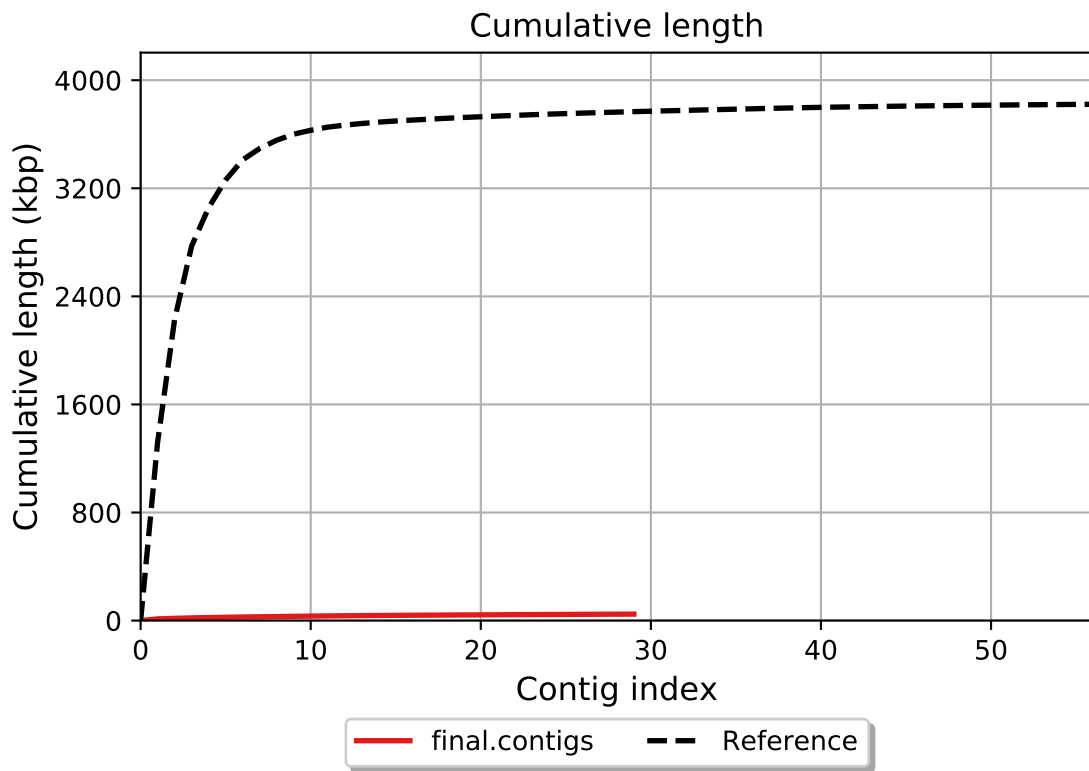


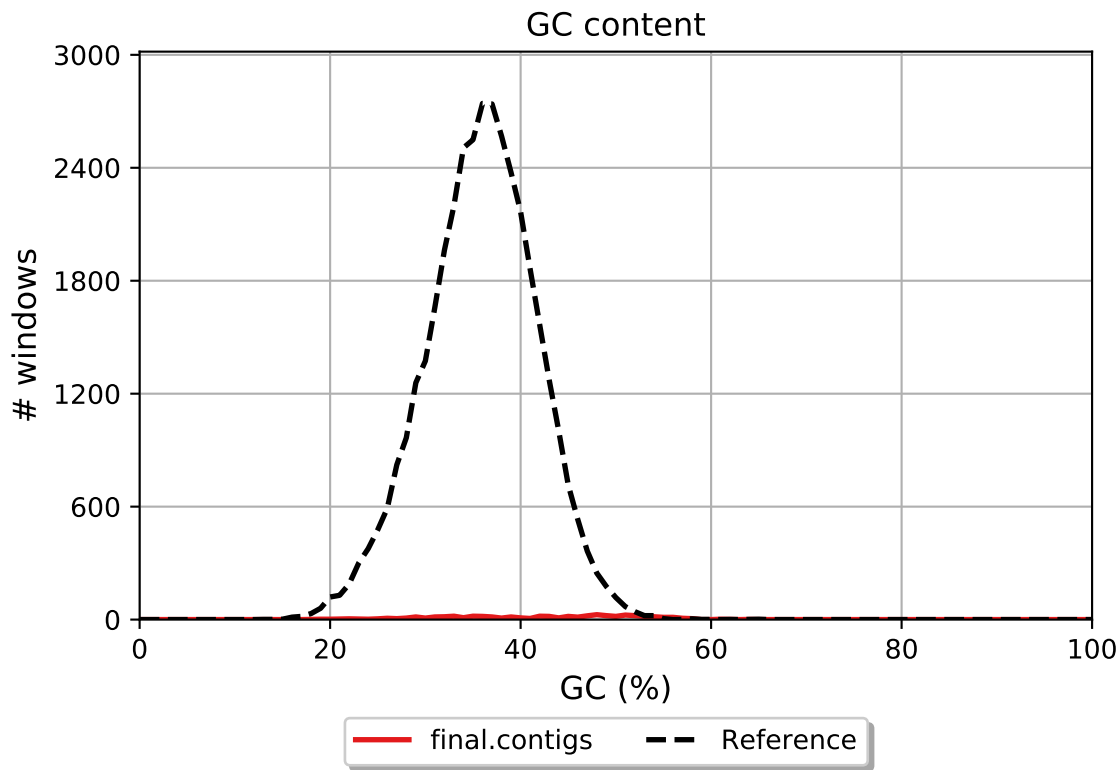
final.contigs

NGx

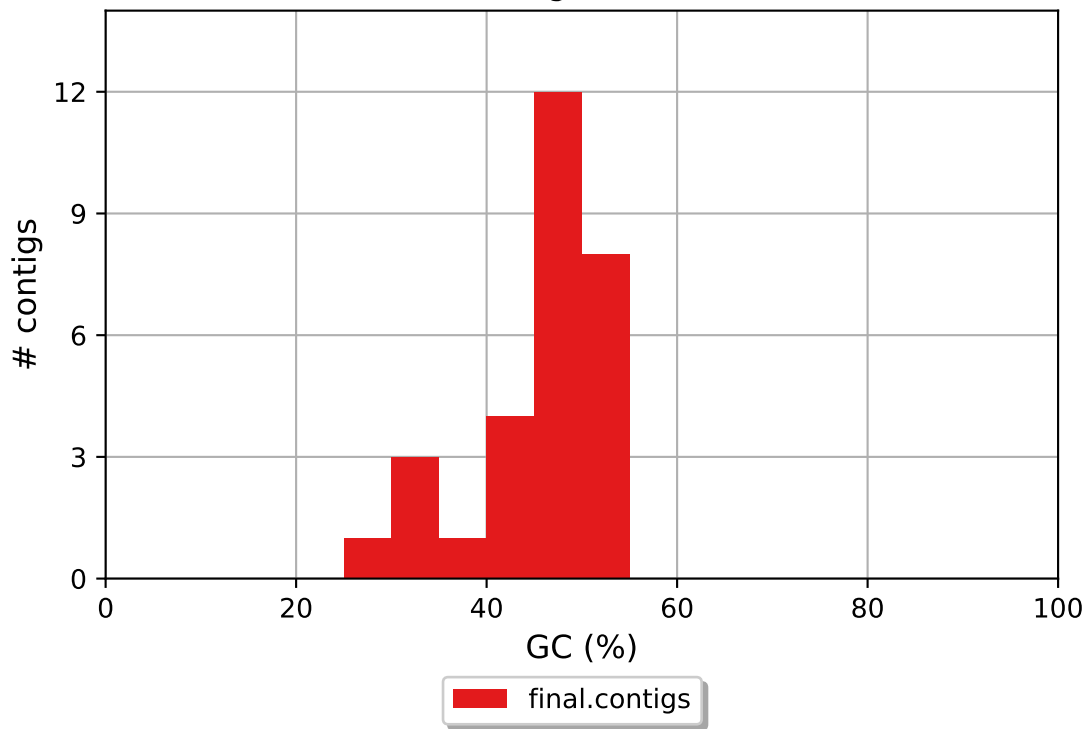


— final.contigs

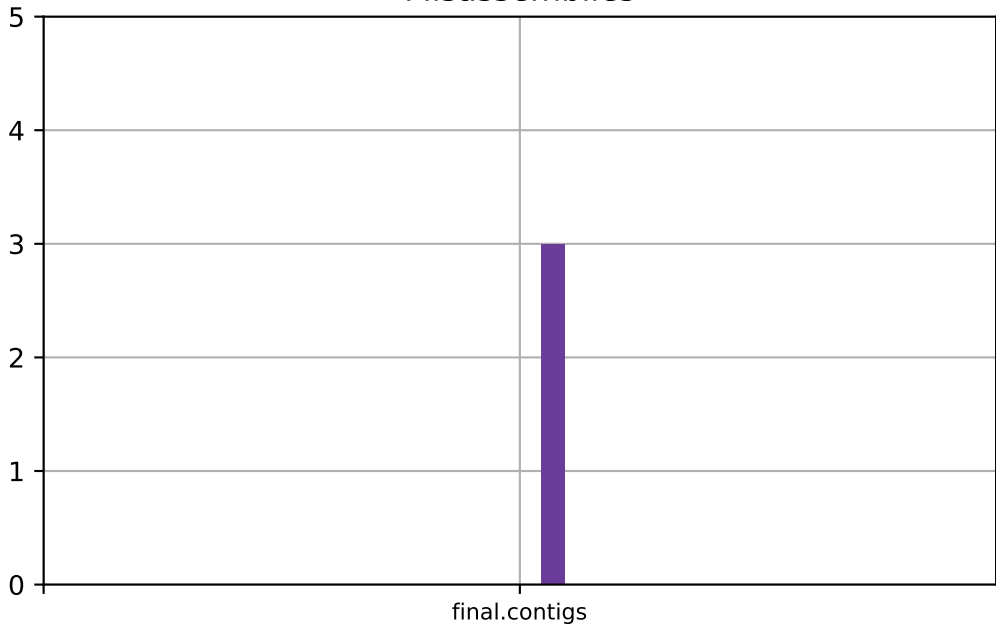




final.contigs GC content

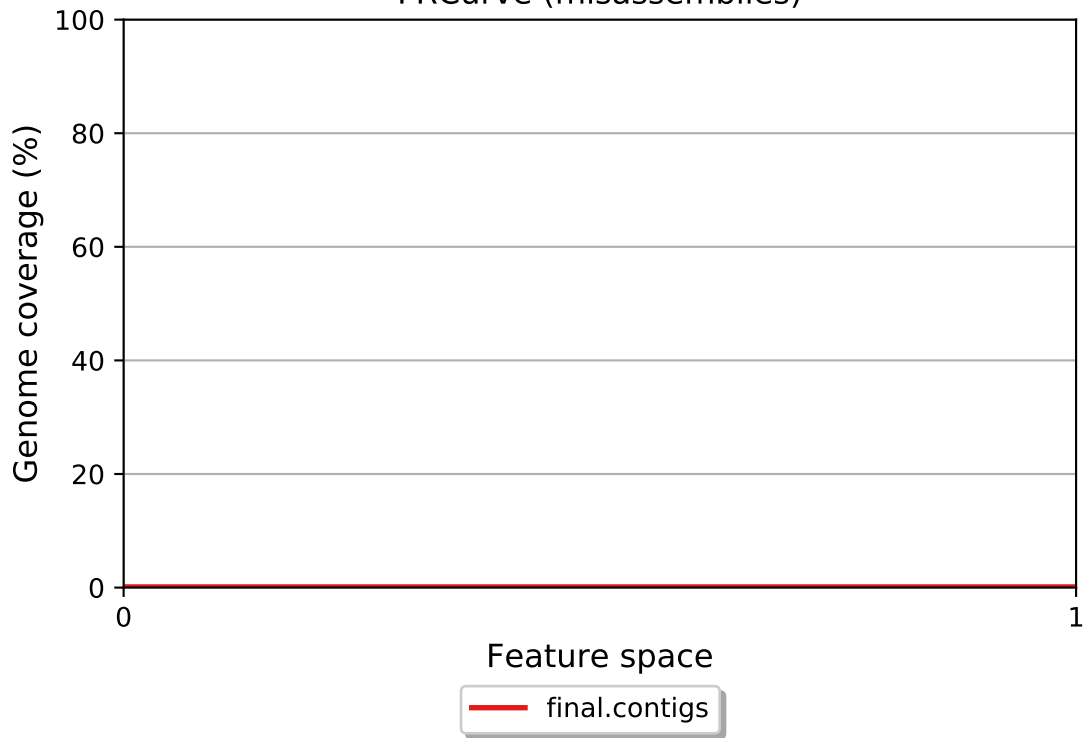


Misassemblies

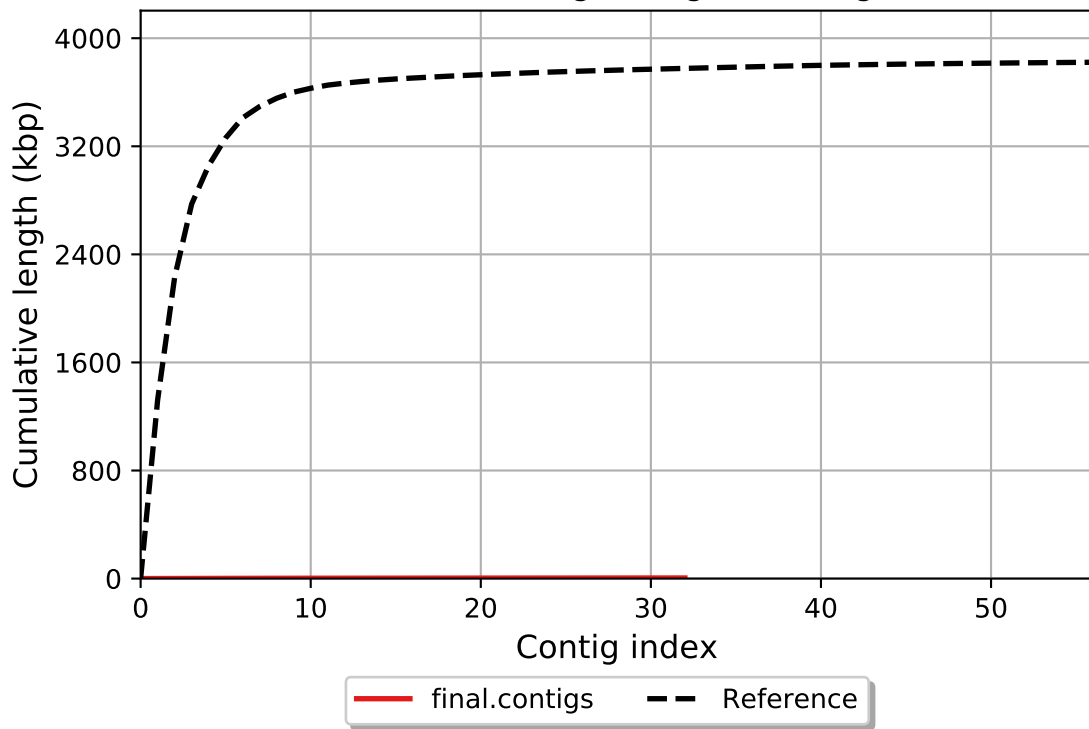


interspecies translocations

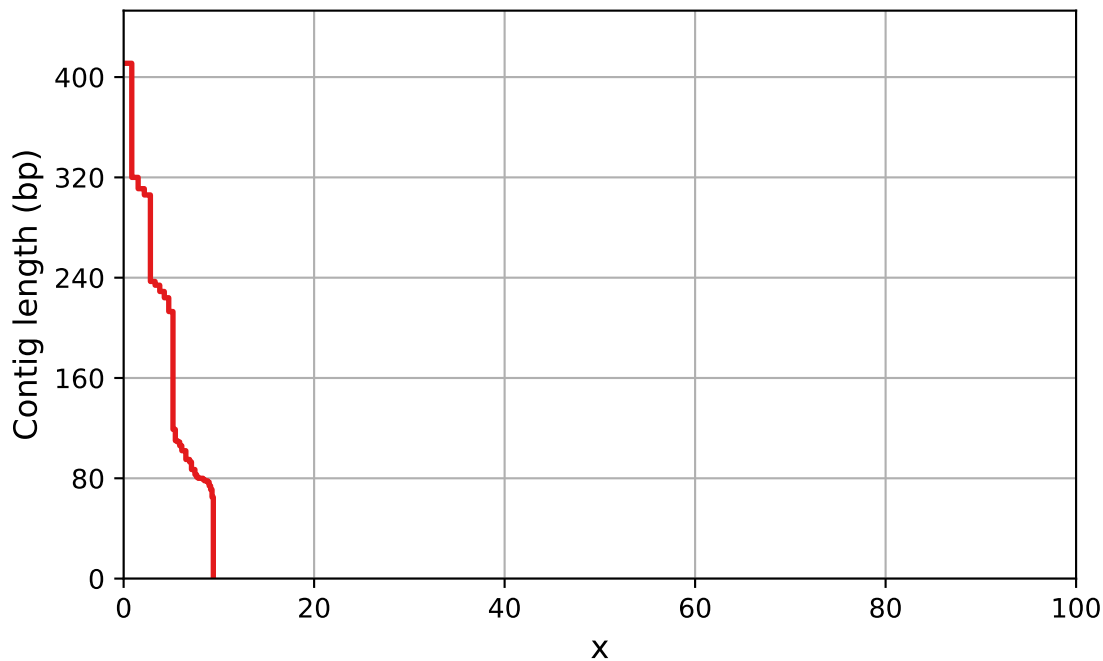
FRCurve (misassemblies)



Cumulative length (aligned contigs)

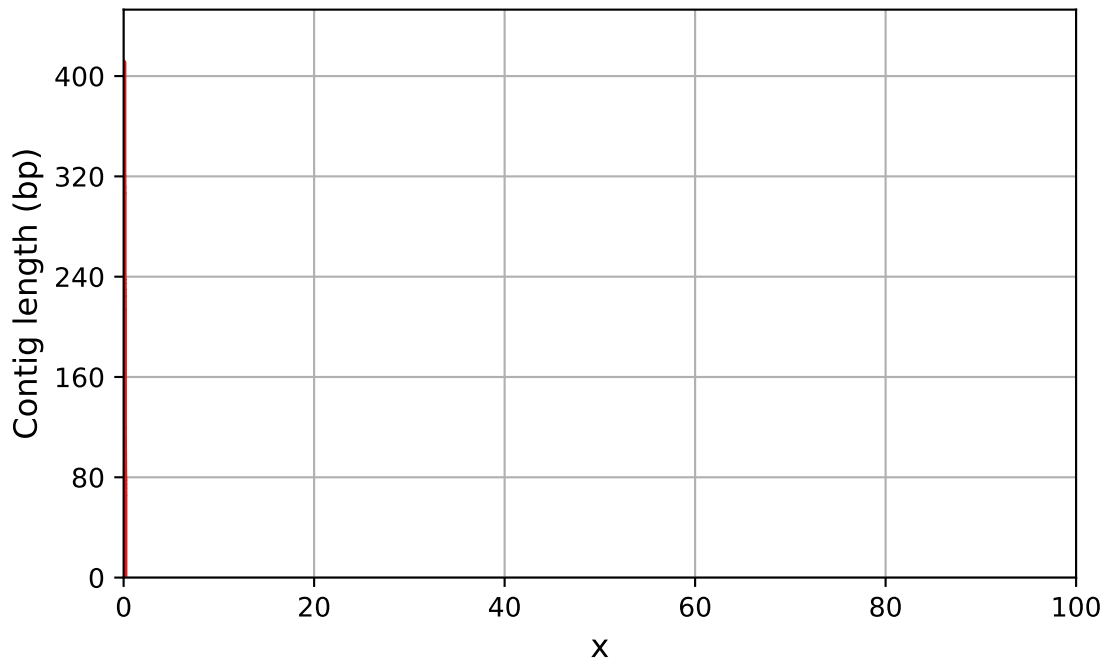


NAx



— final.contigs

NGAx



— final.contigs