

## Report

	final.contigs
# contigs (>= 1000 bp)	5
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	38466
Total length (>= 5000 bp)	32249
Total length (>= 10000 bp)	32249
Total length (>= 25000 bp)	32249
Total length (>= 50000 bp)	0
# contigs	10
Largest contig	32249
Total length	41692
Reference length	4984172
GC (%)	56.32
Reference GC (%)	64.67
N50	32249
N75	32249
L50	1
L75	1
# 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	3 + 3 part
Unaligned length	39100
Genome fraction (%)	0.012
Duplication ratio	4.423
# N's per 100 kbp	0.00
# mismatches per 100 kbp	3242.32
# indels per 100 kbp	0.00
Largest alignment	102
Total aligned length	586
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	3
# possible misassemblies	3
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	19
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

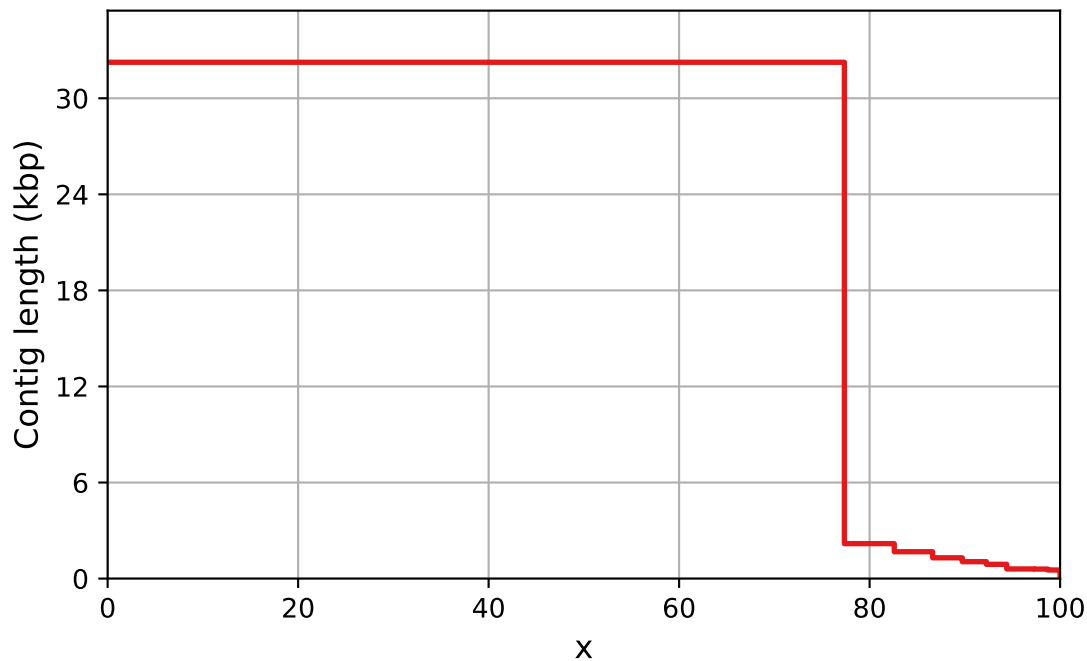
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	final.contigs
# fully unaligned contigs	3
Fully unaligned length	4033
# partially unaligned contigs	3
Partially unaligned length	35067
# N's	0

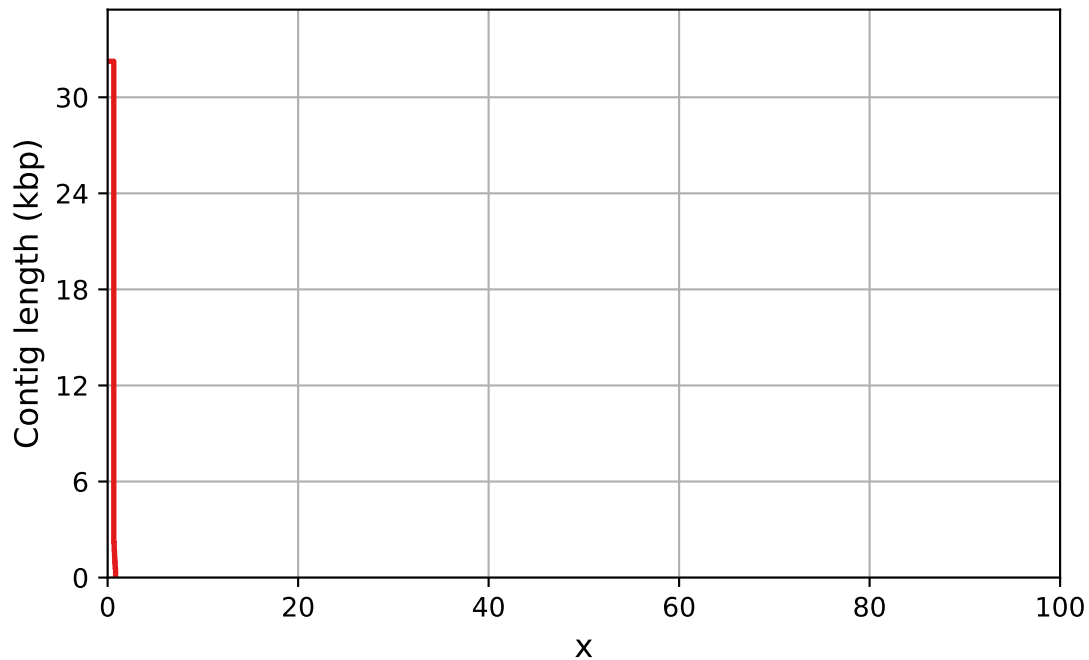
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

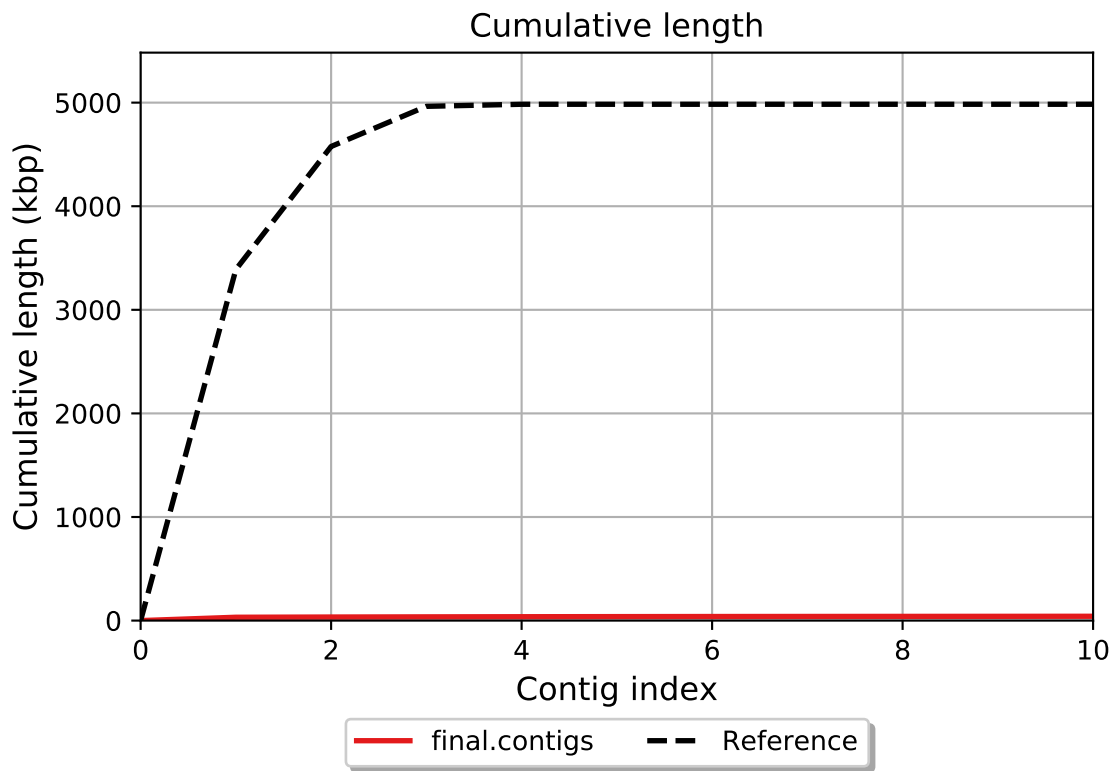


— final.contigs

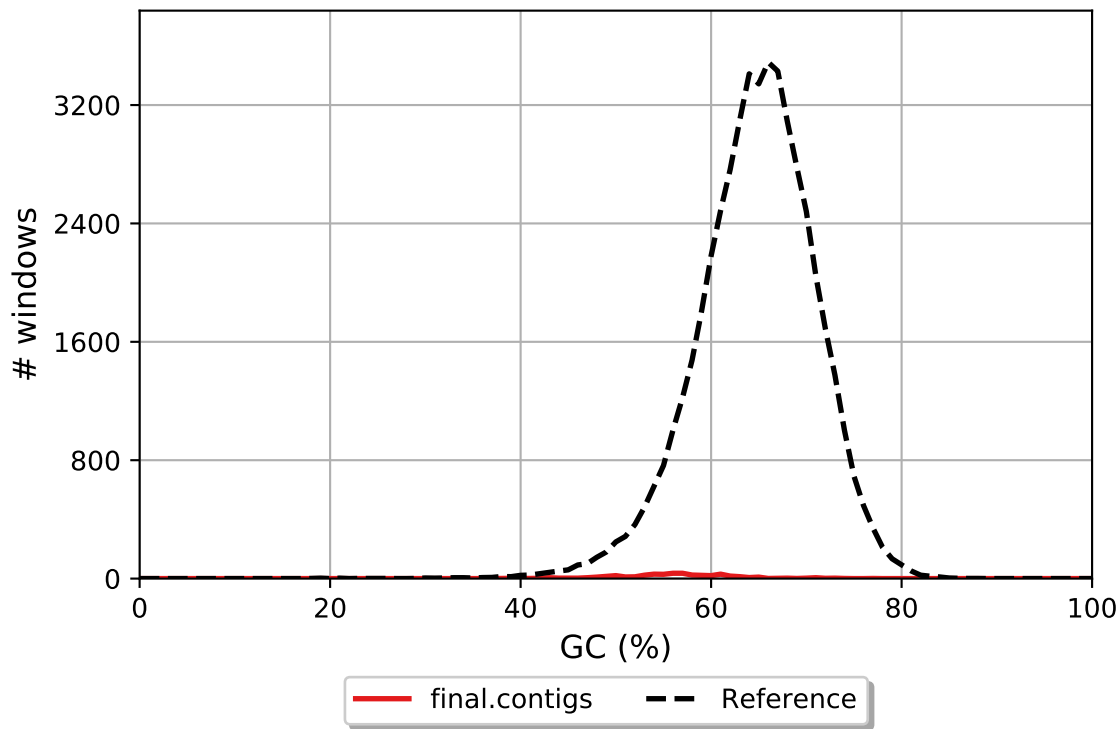
NGx



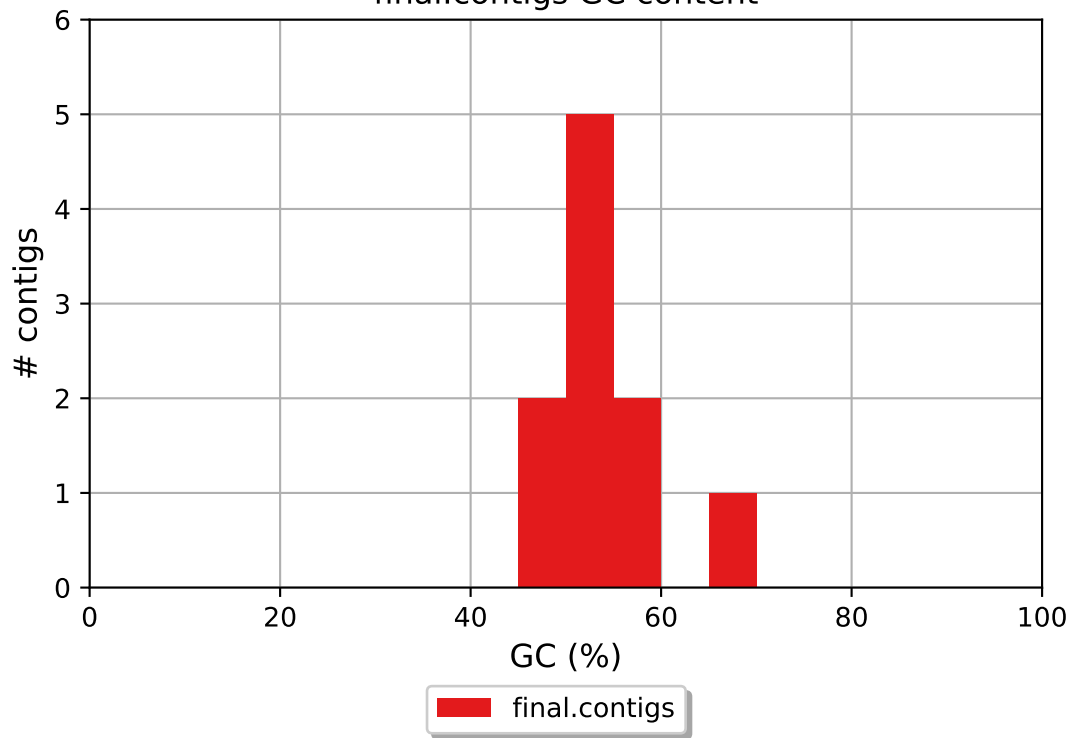
— final.contigs



## GC content



final.contigs GC content



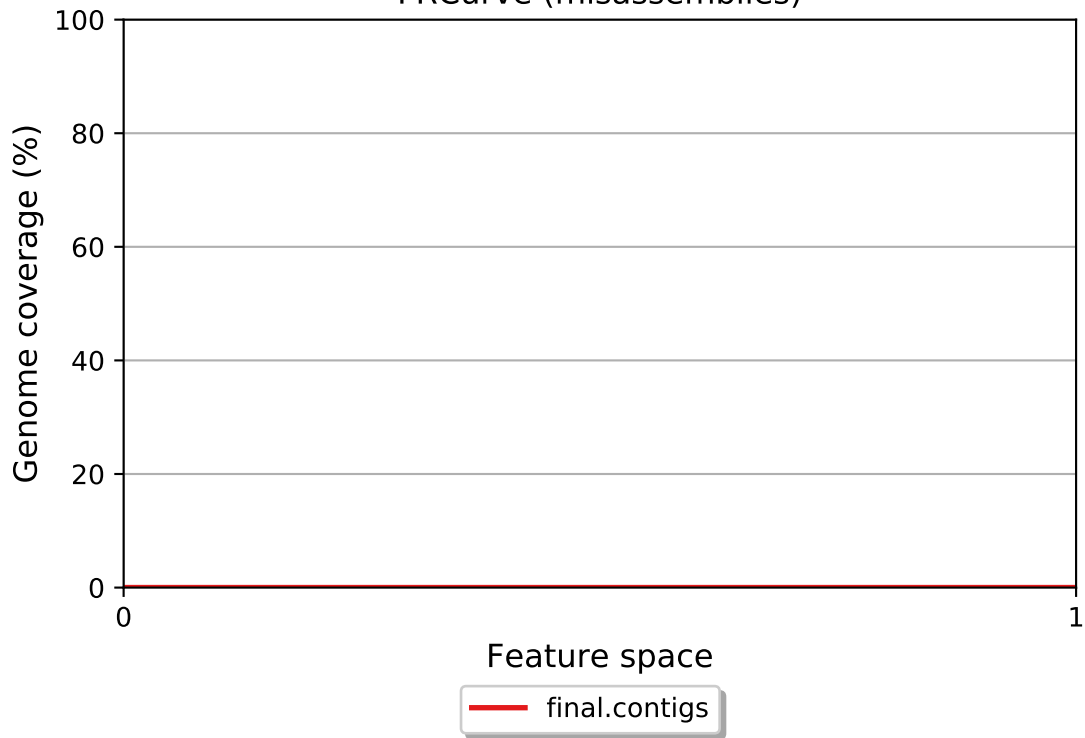


## Misassemblies

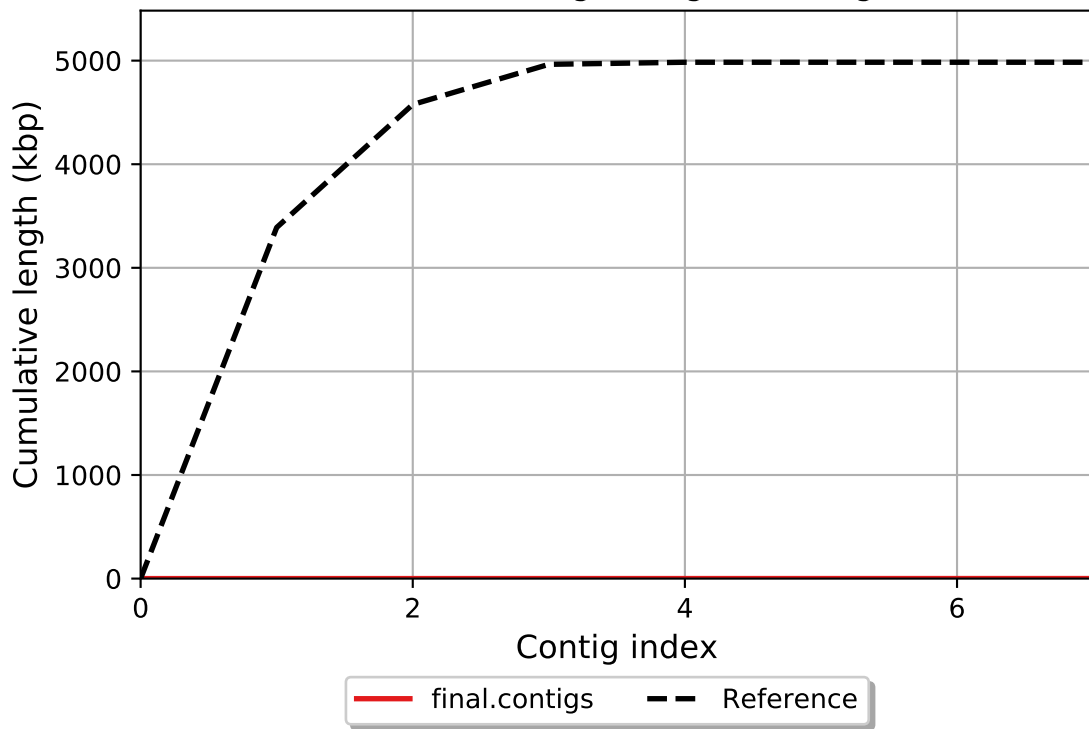


# interspecies translocations

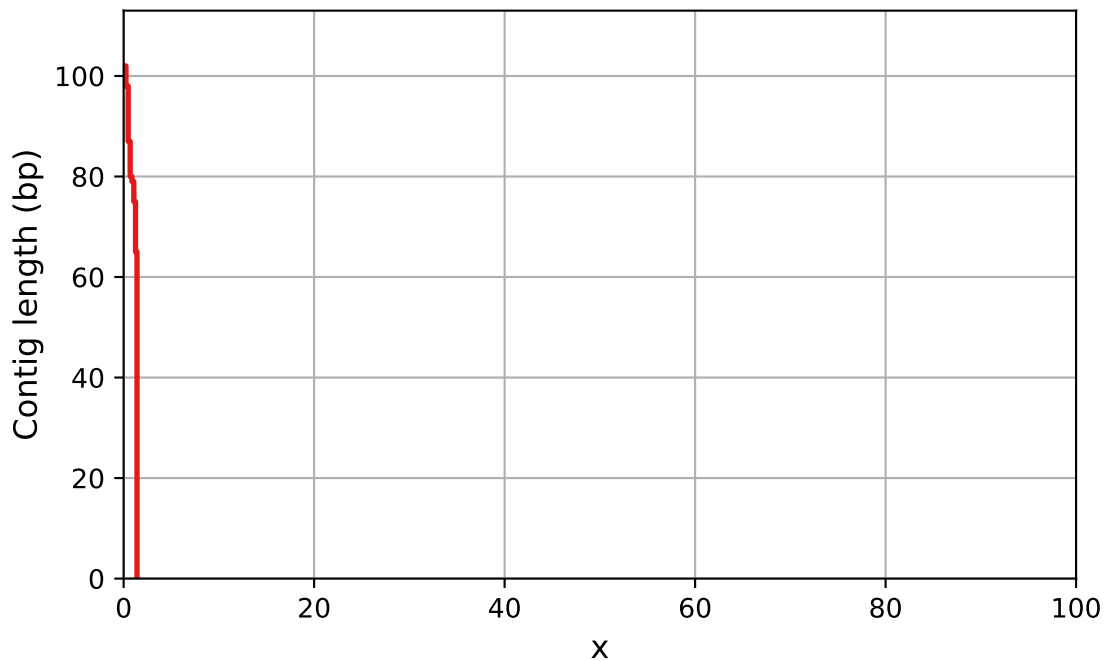
FRCurve (misassemblies)



Cumulative length (aligned contigs)

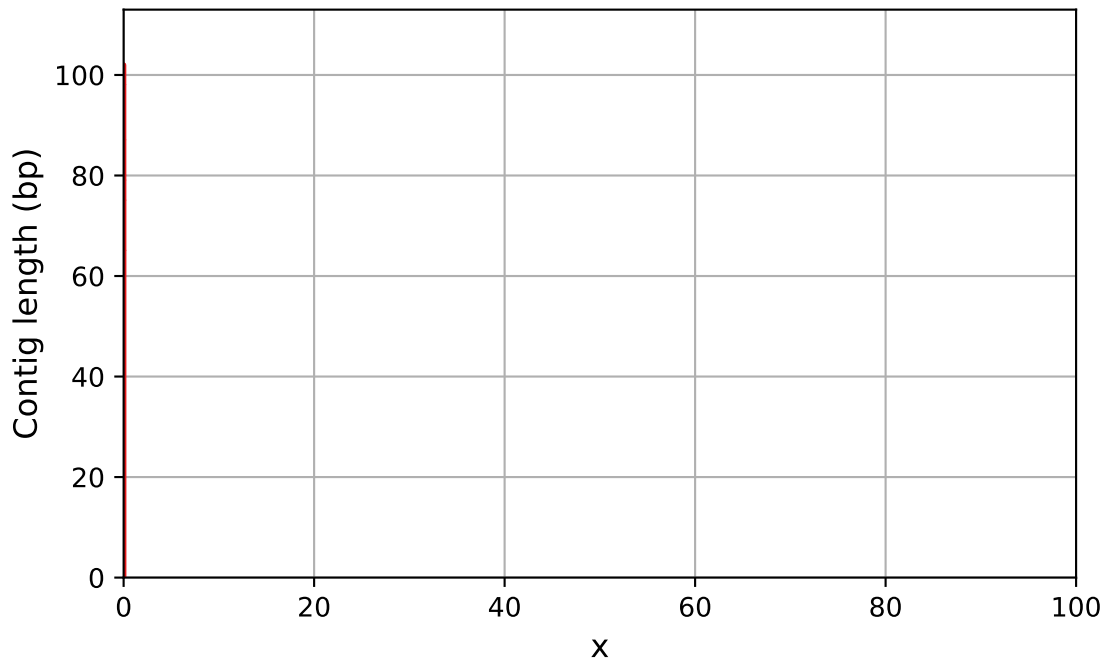


NAx



— final.contigs

# NGAx



— final.contigs