

## Report

	final.contigs
# contigs (>= 1000 bp)	12
# contigs (>= 5000 bp)	2
# contigs (>= 10000 bp)	2
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	76748
Total length (>= 5000 bp)	53127
Total length (>= 10000 bp)	53127
Total length (>= 25000 bp)	39648
Total length (>= 50000 bp)	0
# contigs	27
Largest contig	39648
Total length	87043
Reference length	3069626
GC (%)	47.71
Reference GC (%)	57.43
N50	13479
N75	2304
L50	2
L75	6
# 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	2
# unaligned contigs	2 + 15 part
Unaligned length	78361
Genome fraction (%)	0.079
Duplication ratio	3.598
# N's per 100 kbp	0.00
# mismatches per 100 kbp	5346.04
# indels per 100 kbp	0.00
Largest alignment	506
Total aligned length	3787
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	8
# possible misassemblies	12
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# mismatches	129
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

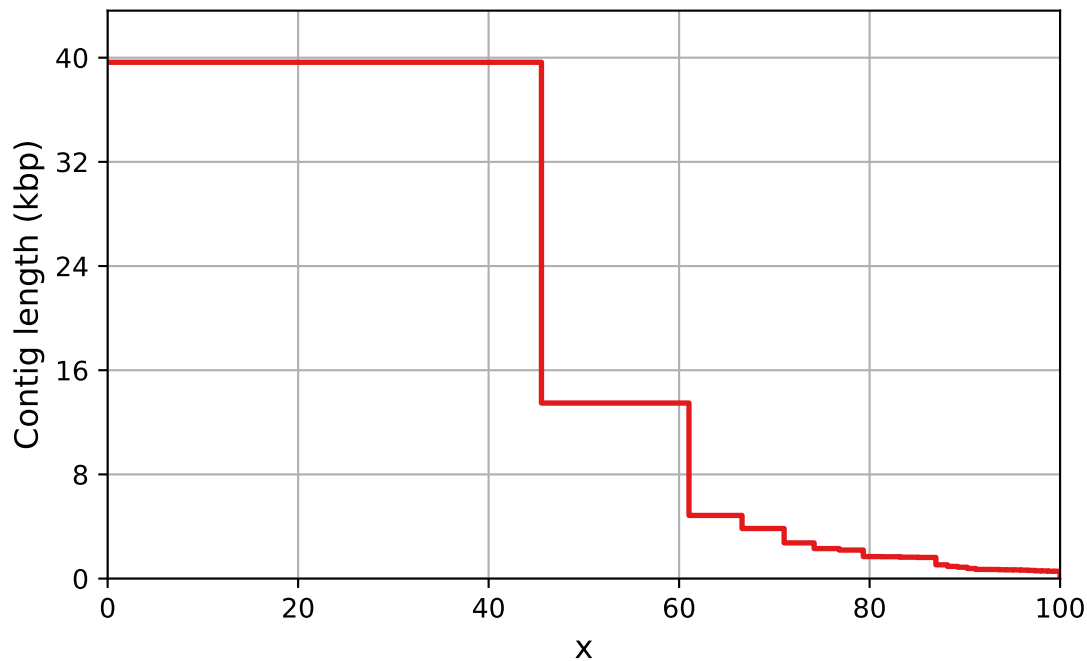
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	final.contigs
# fully unaligned contigs	2
Fully unaligned length	1735
# partially unaligned contigs	15
Partially unaligned length	76626
# N's	0

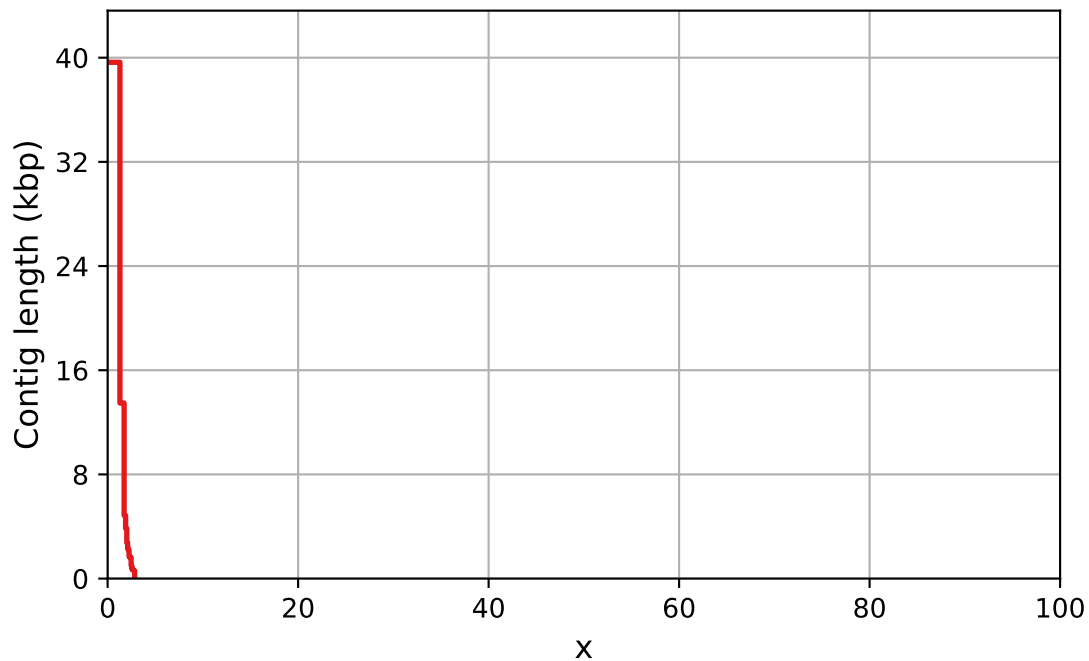
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

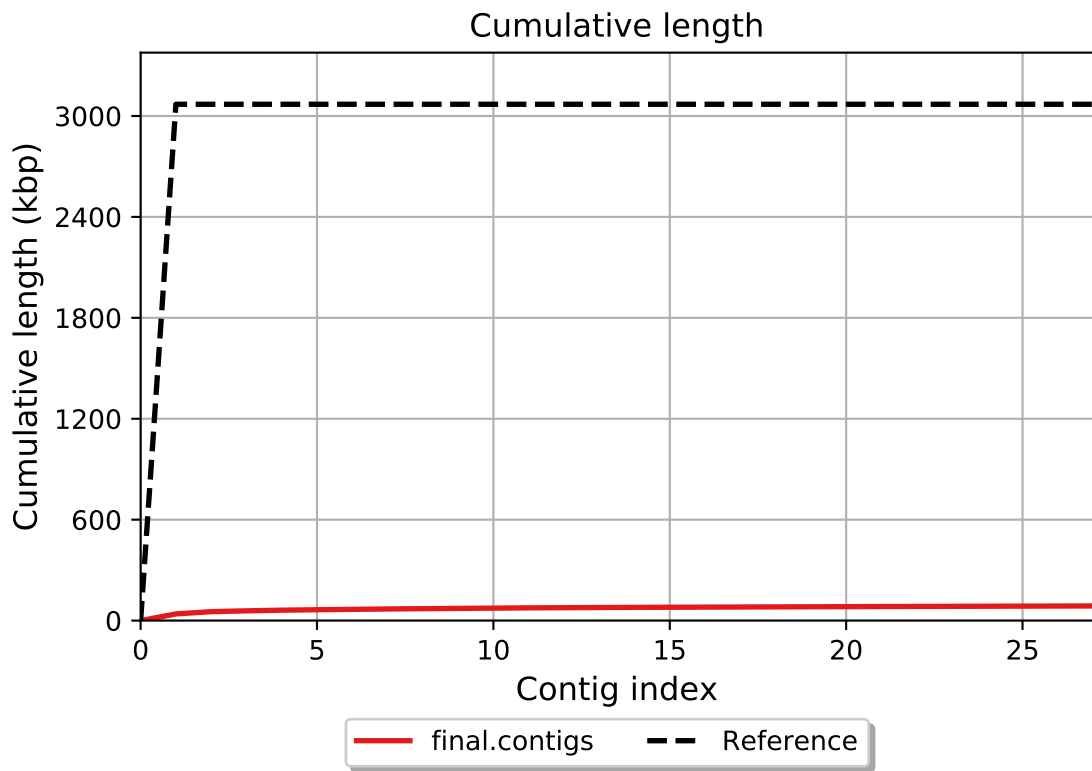


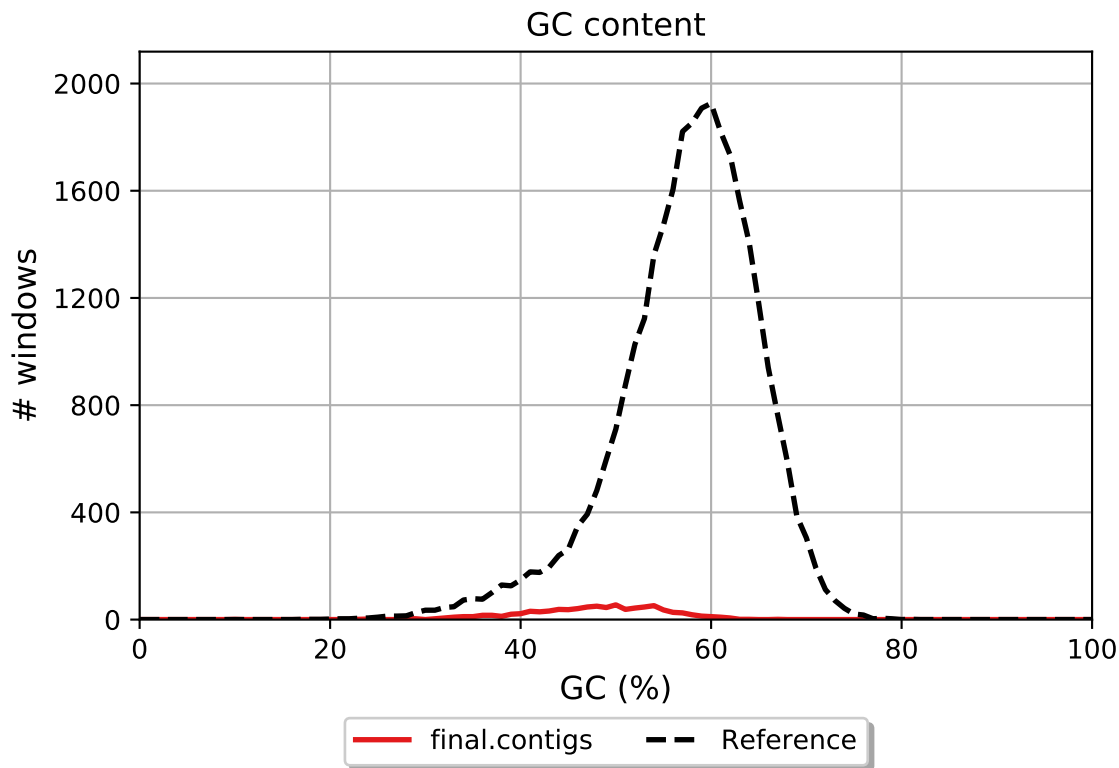
final.contigs

NGx

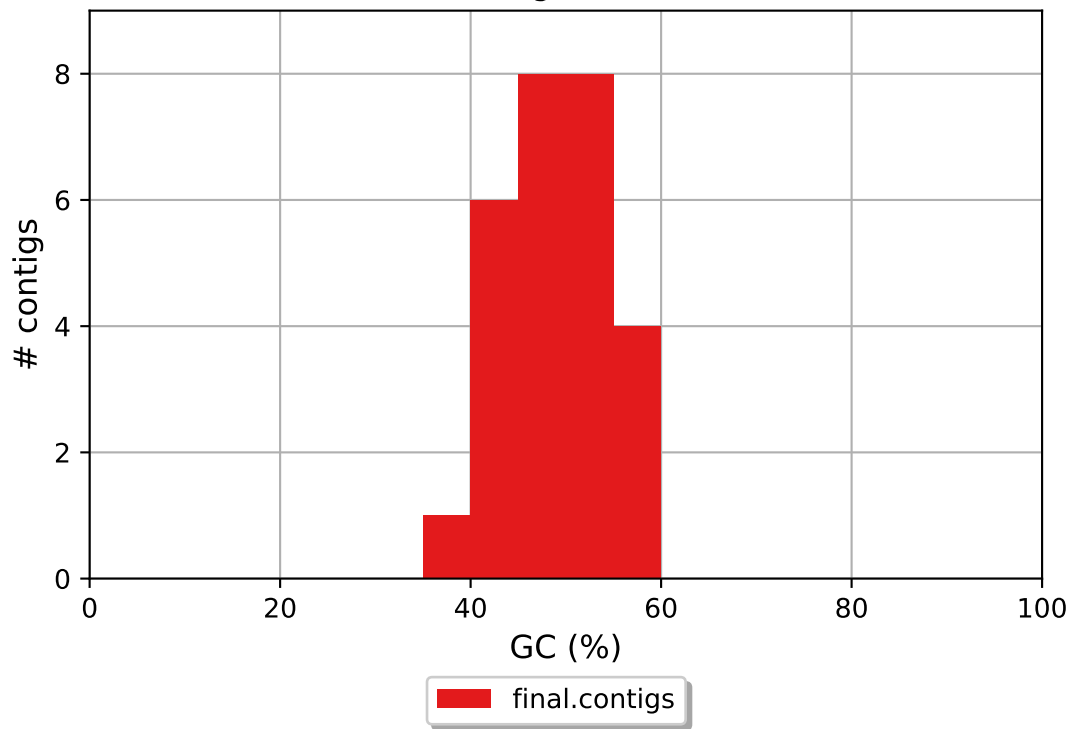


— final.contigs





final.contigs GC content



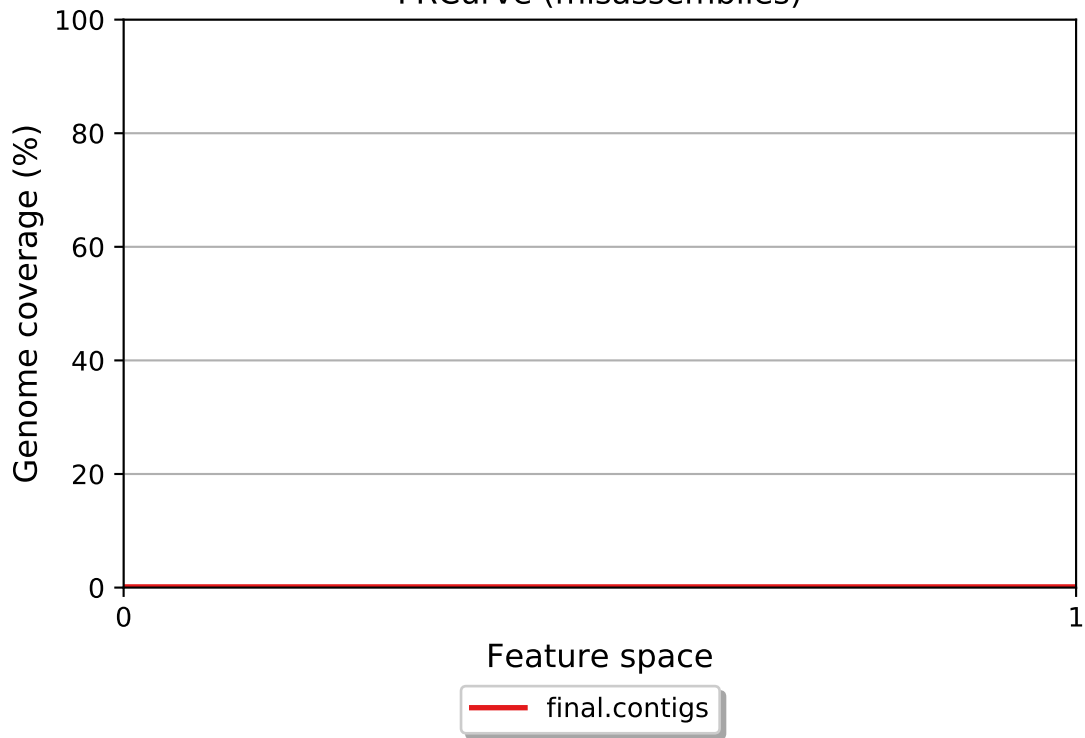


## Misassemblies

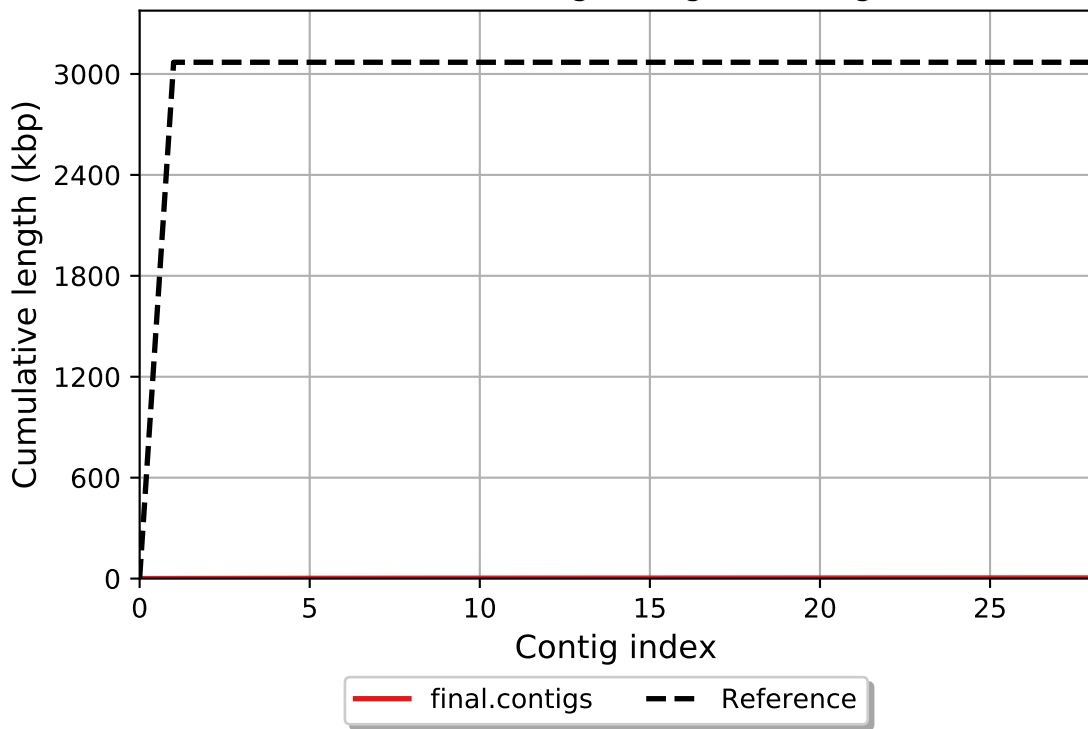


# interspecies translocations

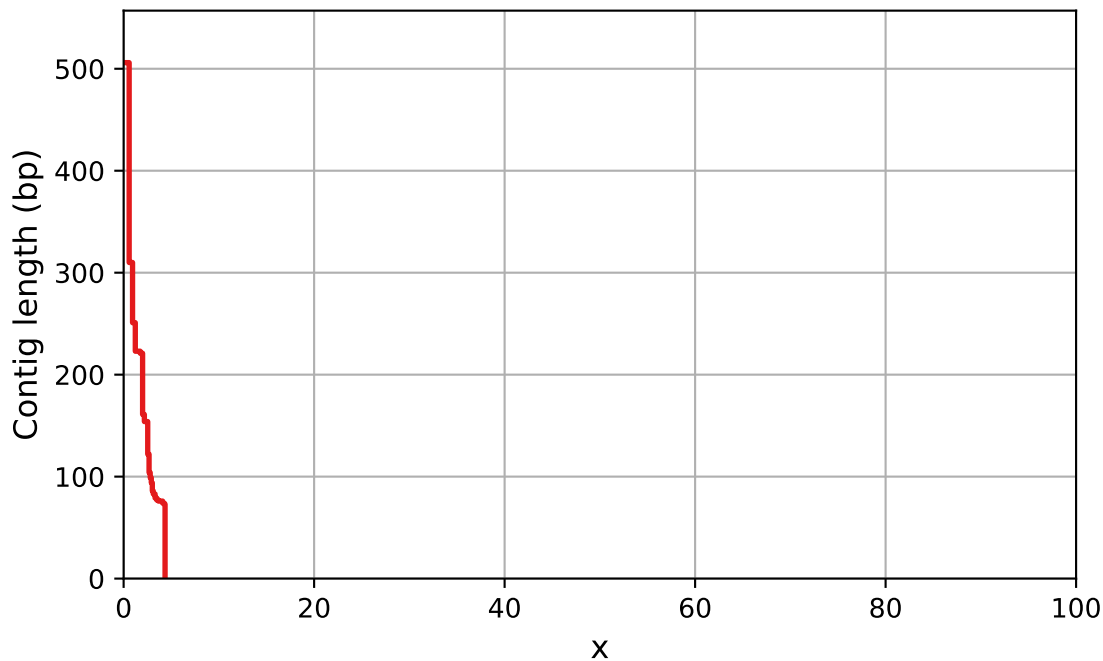
FRCurve (misassemblies)



Cumulative length (aligned contigs)

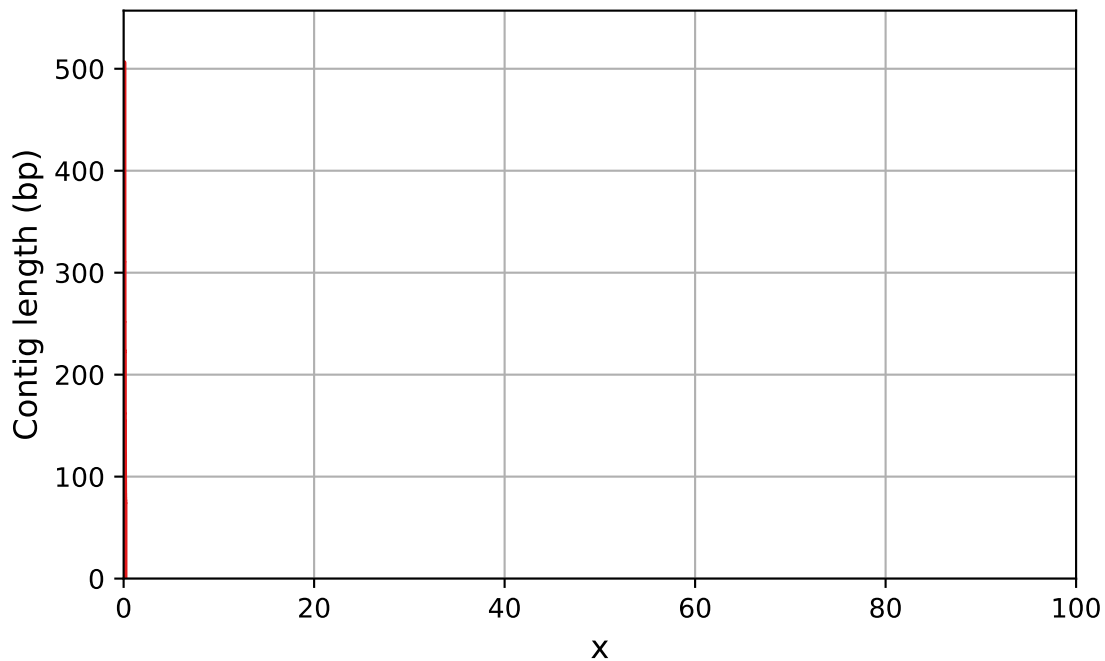


NAx



— final.contigs

# NGAx



— final.contigs