

## Report

	final.contigs
# contigs (>= 1000 bp)	8
# contigs (>= 5000 bp)	2
# contigs (>= 10000 bp)	2
# contigs (>= 25000 bp)	2
# contigs (>= 50000 bp)	2
Total length (>= 1000 bp)	117721
Total length (>= 5000 bp)	109736
Total length (>= 10000 bp)	109736
Total length (>= 25000 bp)	109736
Total length (>= 50000 bp)	109736
# contigs	19
Largest contig	56925
Total length	125231
Reference length	3691014
GC (%)	58.43
Reference GC (%)	66.65
N50	52811
N75	52811
L50	2
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	3
# unaligned contigs	4 + 10 part
Unaligned length	120652
Genome fraction (%)	0.066
Duplication ratio	1.866
# N's per 100 kbp	0.00
# mismatches per 100 kbp	3341.48
# indels per 100 kbp	0.00
Largest alignment	513
Total aligned length	3175
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	5
# possible misassemblies	5
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# mismatches	82
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

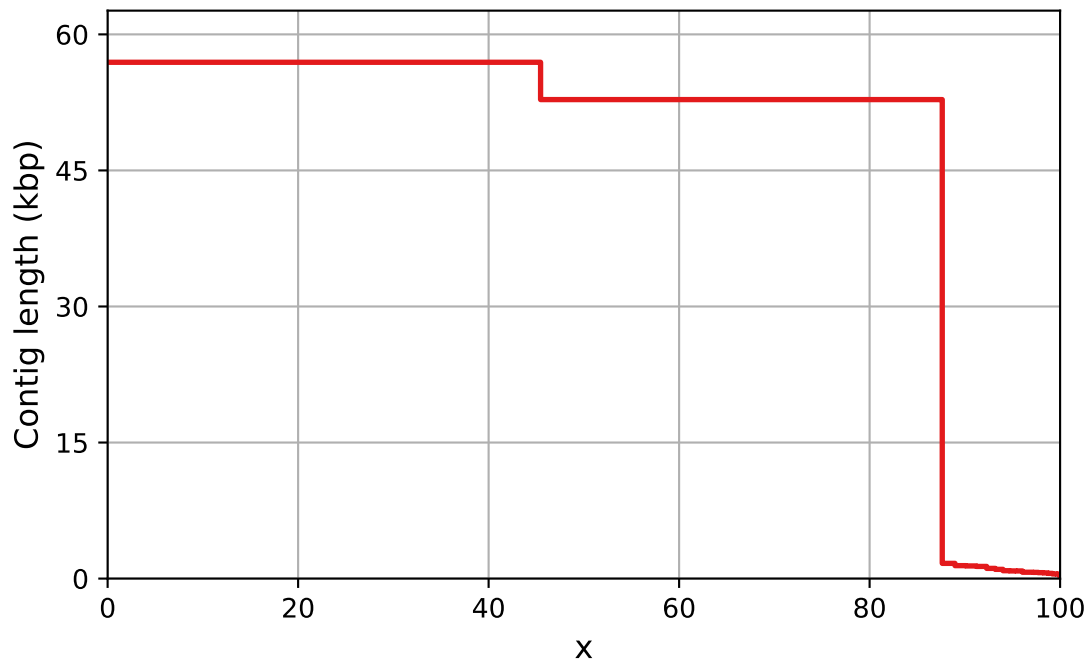
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	final.contigs
# fully unaligned contigs	4
Fully unaligned length	3739
# partially unaligned contigs	10
Partially unaligned length	116913
# N's	0

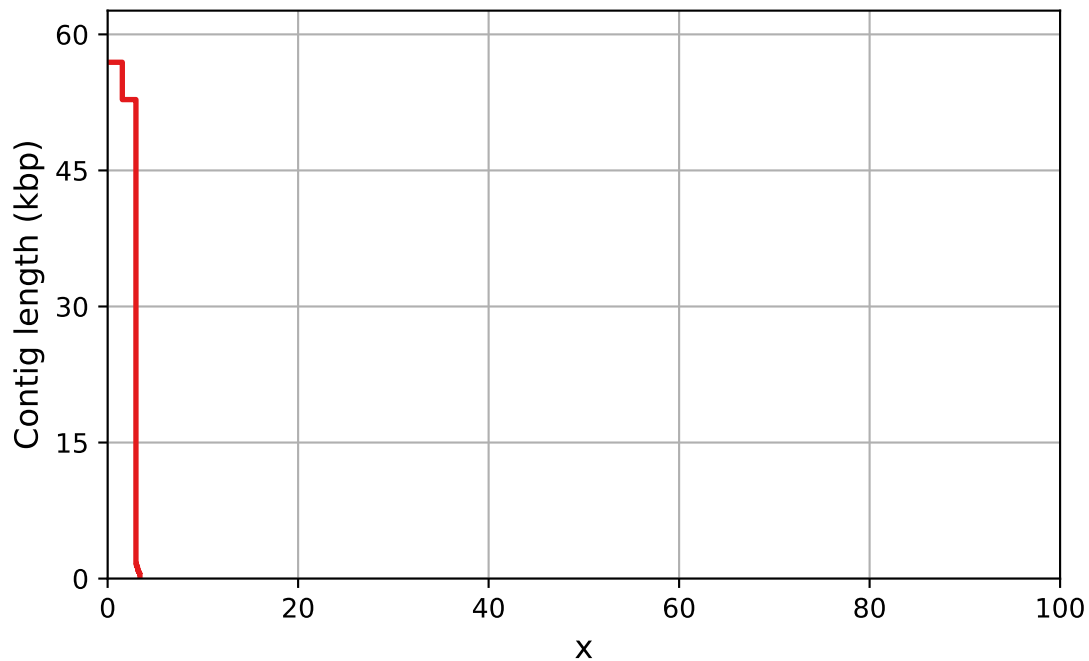
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

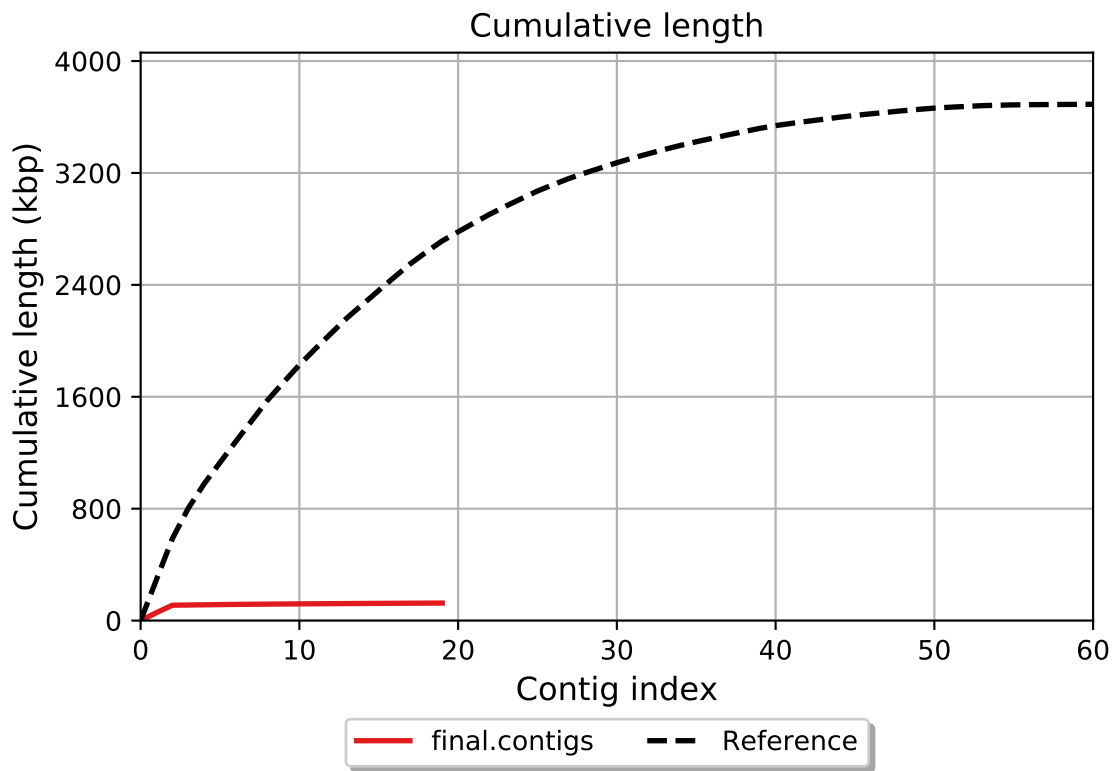


— final.contigs

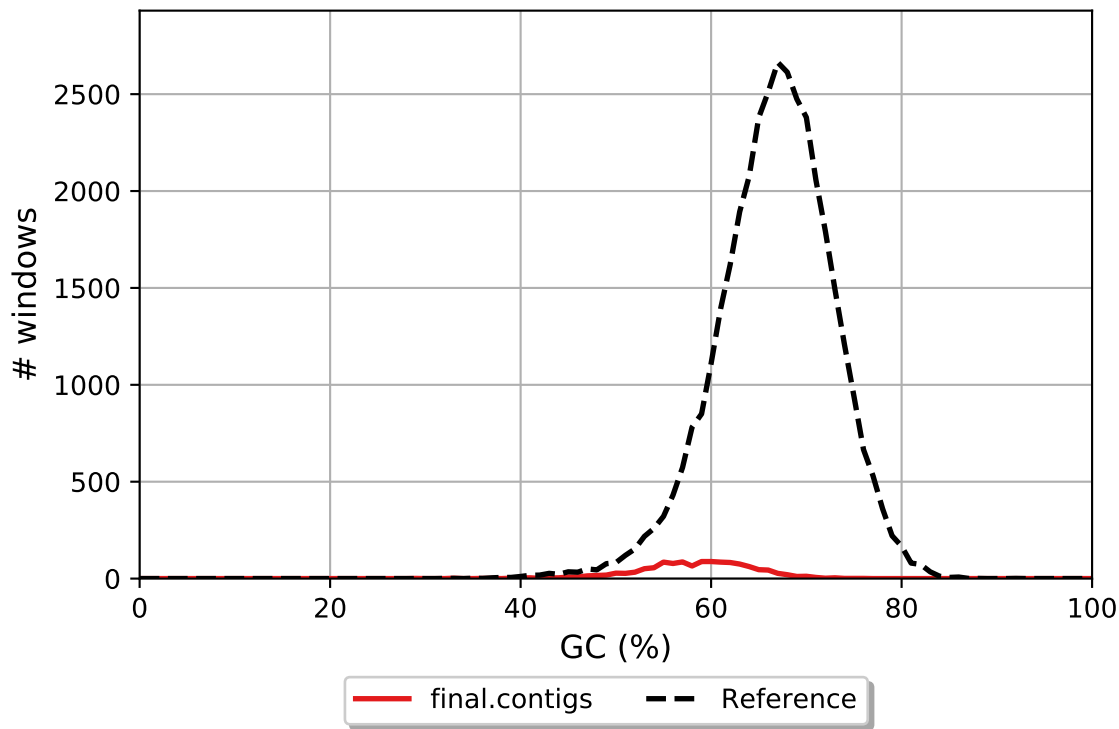
NGx



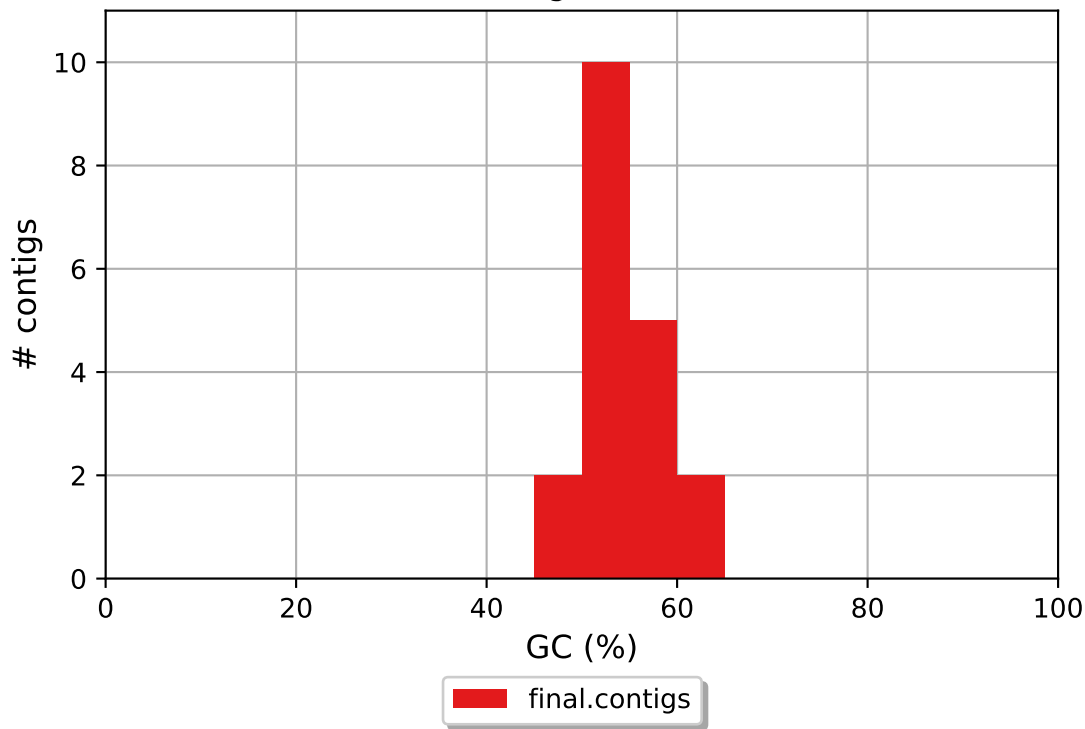
— final.contigs



## GC content



final.contigs GC content



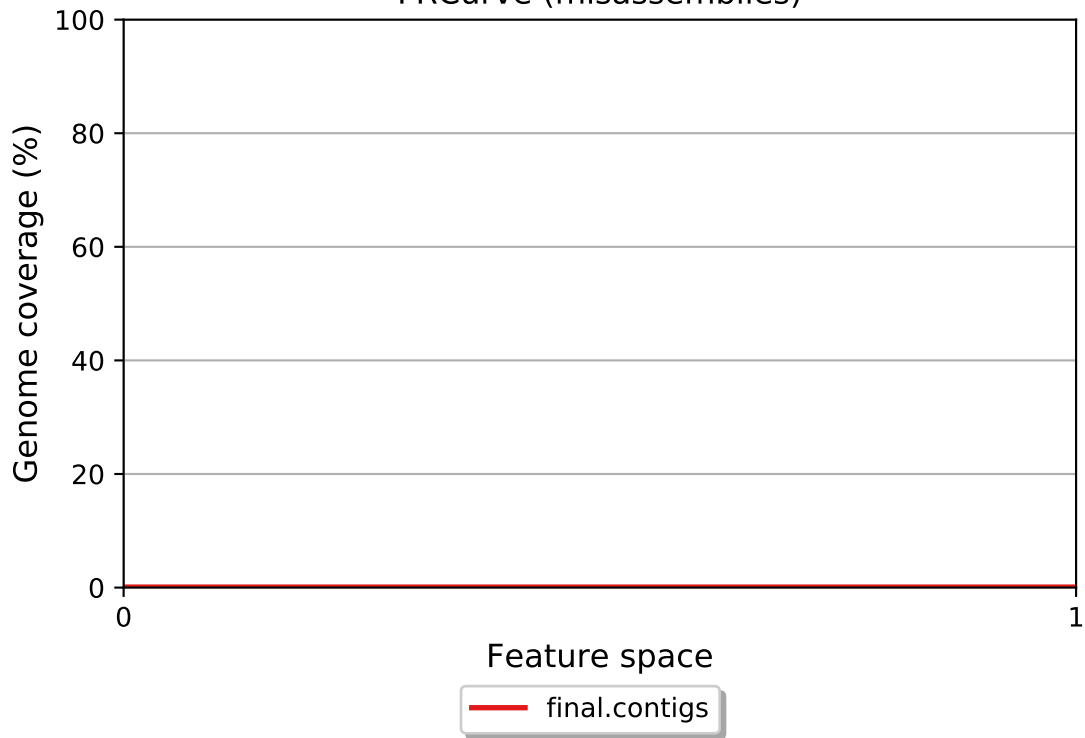


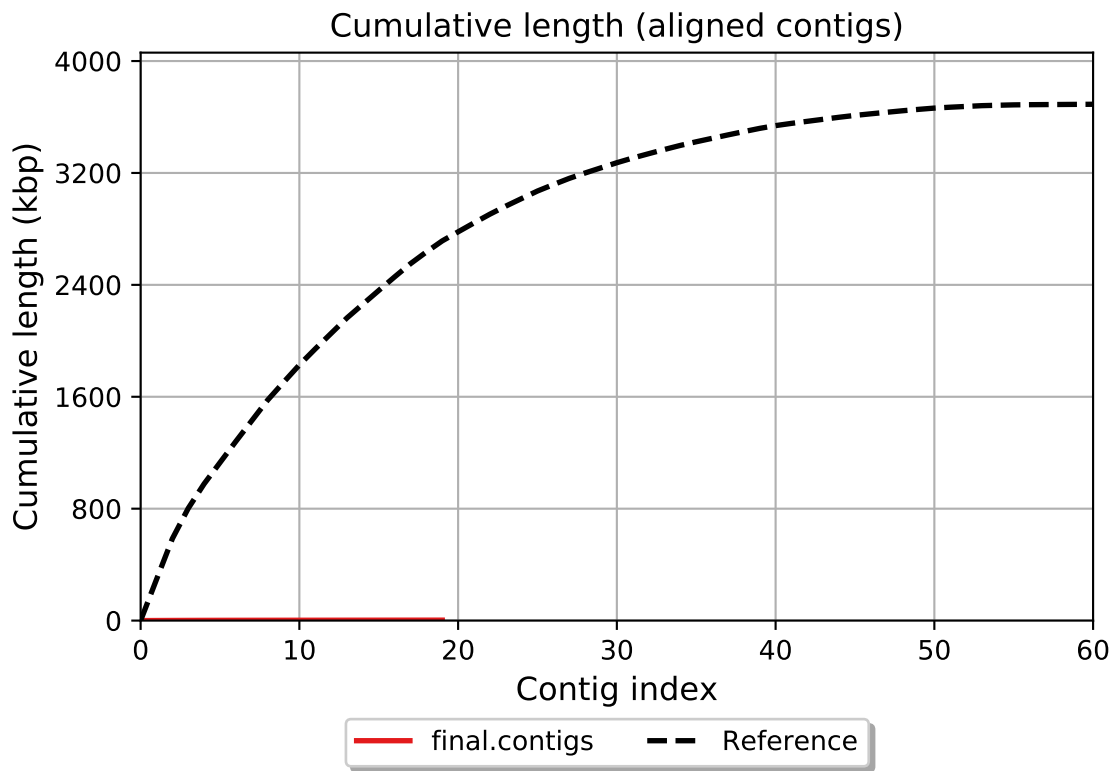
## Misassemblies



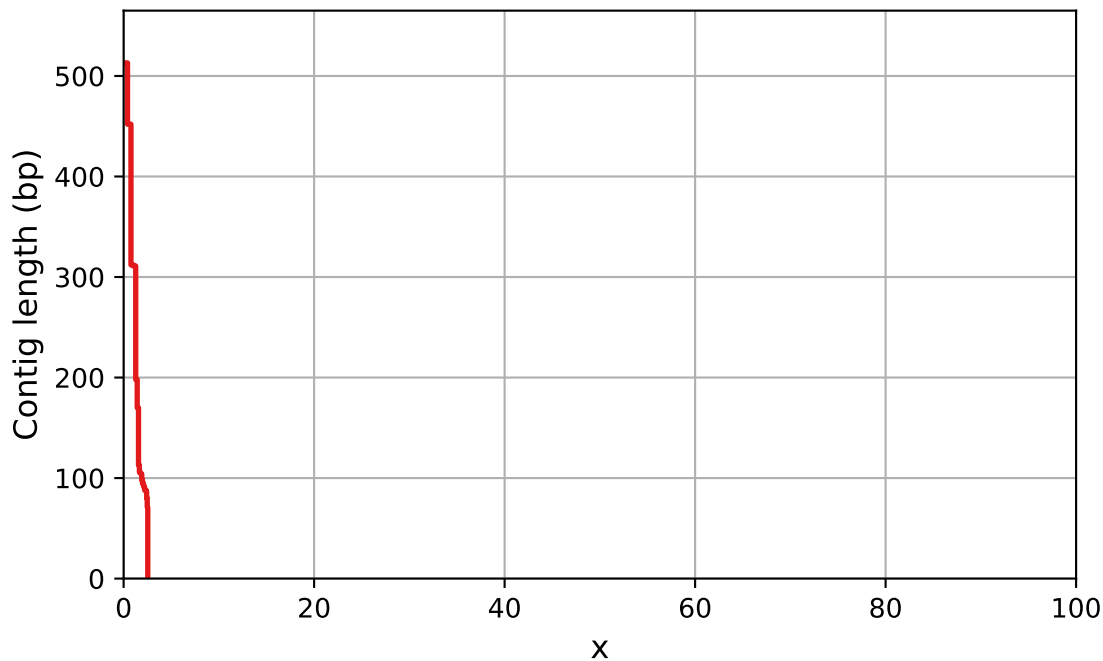
# interspecies translocations

FRCurve (misassemblies)



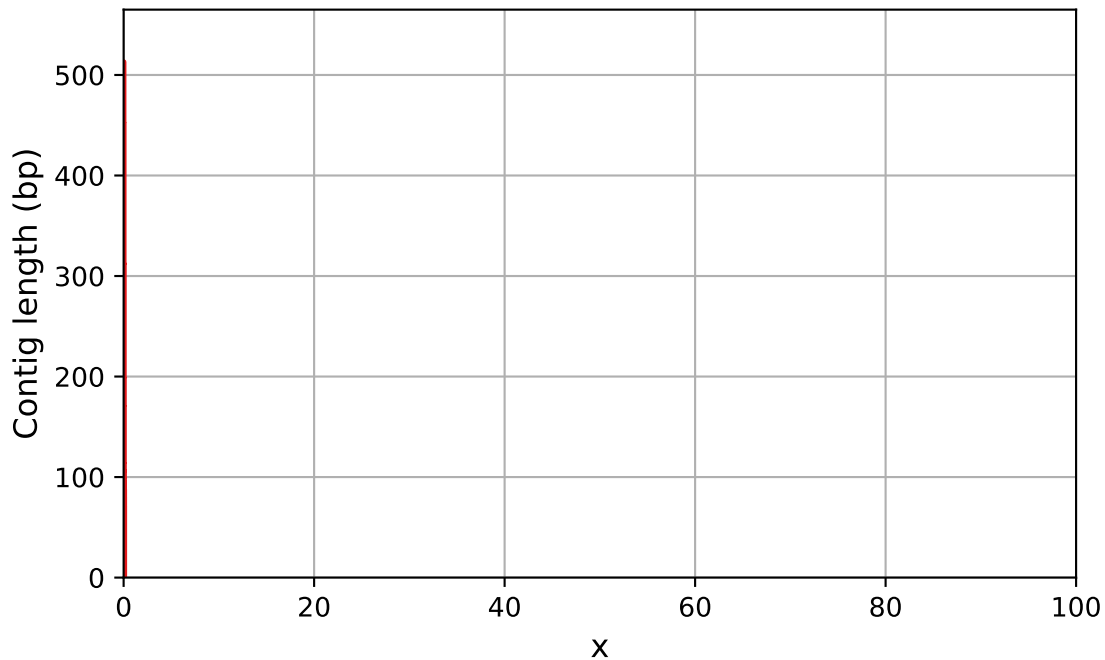


NAx



— final.contigs

# NGAx



— final.contigs