

## Report

	final.contigs
# contigs (>= 1000 bp)	14
# contigs (>= 5000 bp)	4
# contigs (>= 10000 bp)	4
# contigs (>= 25000 bp)	4
# contigs (>= 50000 bp)	4
Total length (>= 1000 bp)	504732
Total length (>= 5000 bp)	481269
Total length (>= 10000 bp)	481269
Total length (>= 25000 bp)	481269
Total length (>= 50000 bp)	481269
# contigs	28
Largest contig	172953
Total length	515083
Reference length	3299615
GC (%)	59.69
Reference GC (%)	63.89
N50	134279
N75	87077
L50	2
L75	3
# 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	1 + 20 part
Unaligned length	507719
Genome fraction (%)	0.069
Duplication ratio	3.257
# N's per 100 kbp	0.00
# mismatches per 100 kbp	5218.93
# indels per 100 kbp	0.00
Largest alignment	284
Total aligned length	3662
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

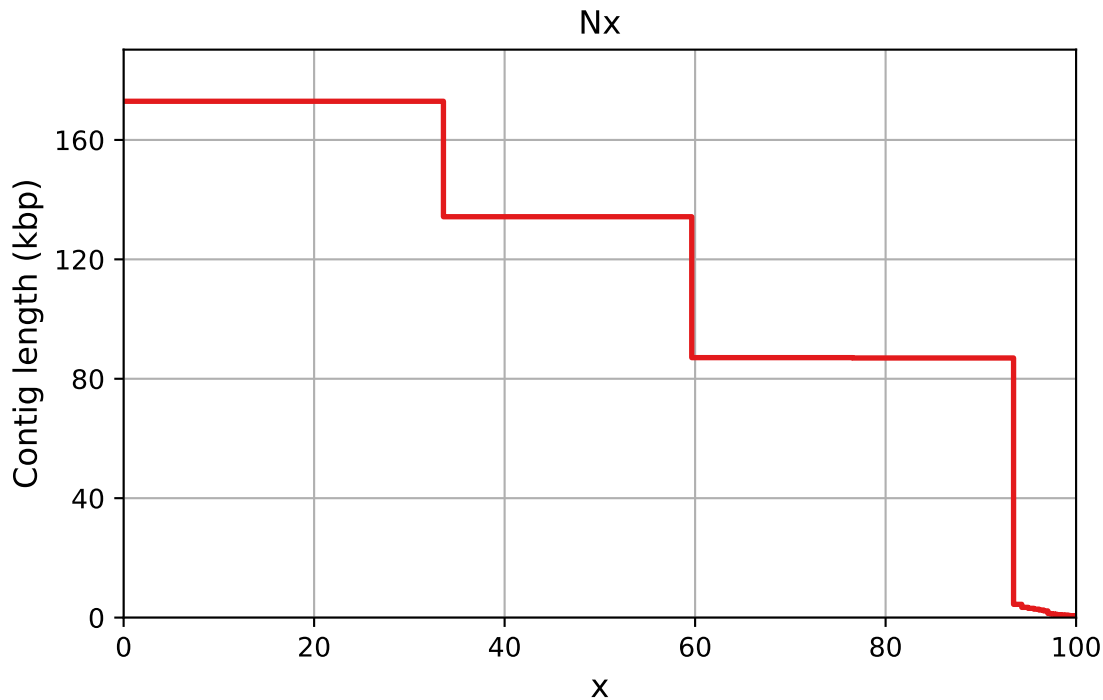
	final.contigs
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	11
# possible misassemblies	17
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	4
# mismatches	118
# 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

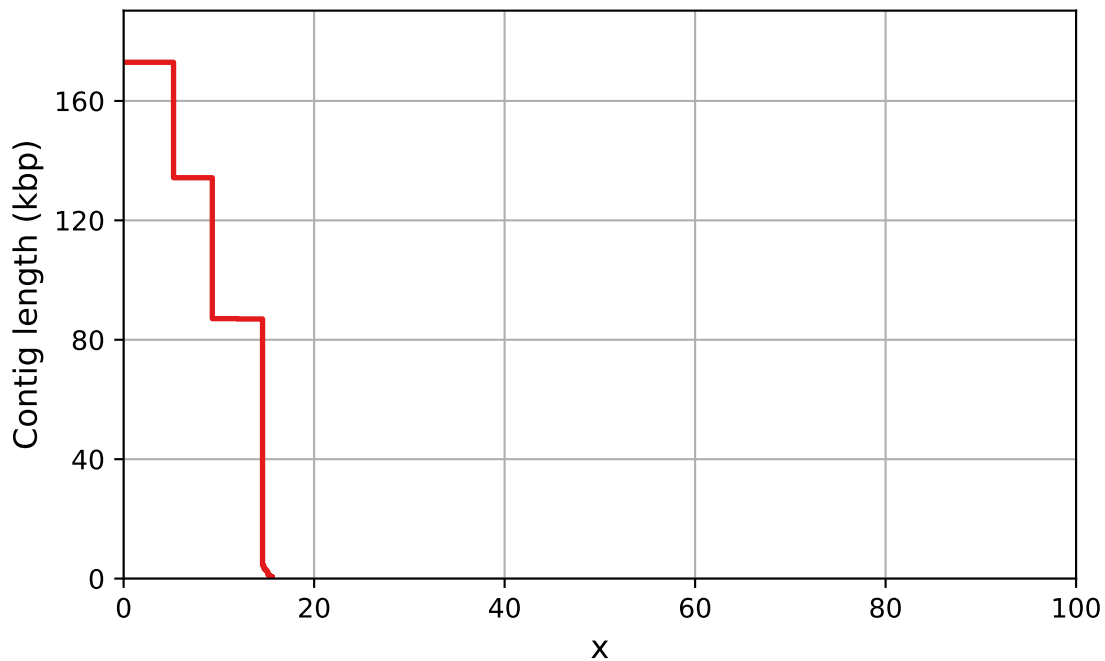
	final.contigs
# fully unaligned contigs	1
Fully unaligned length	597
# partially unaligned contigs	20
Partially unaligned length	507122
# N's	0

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).

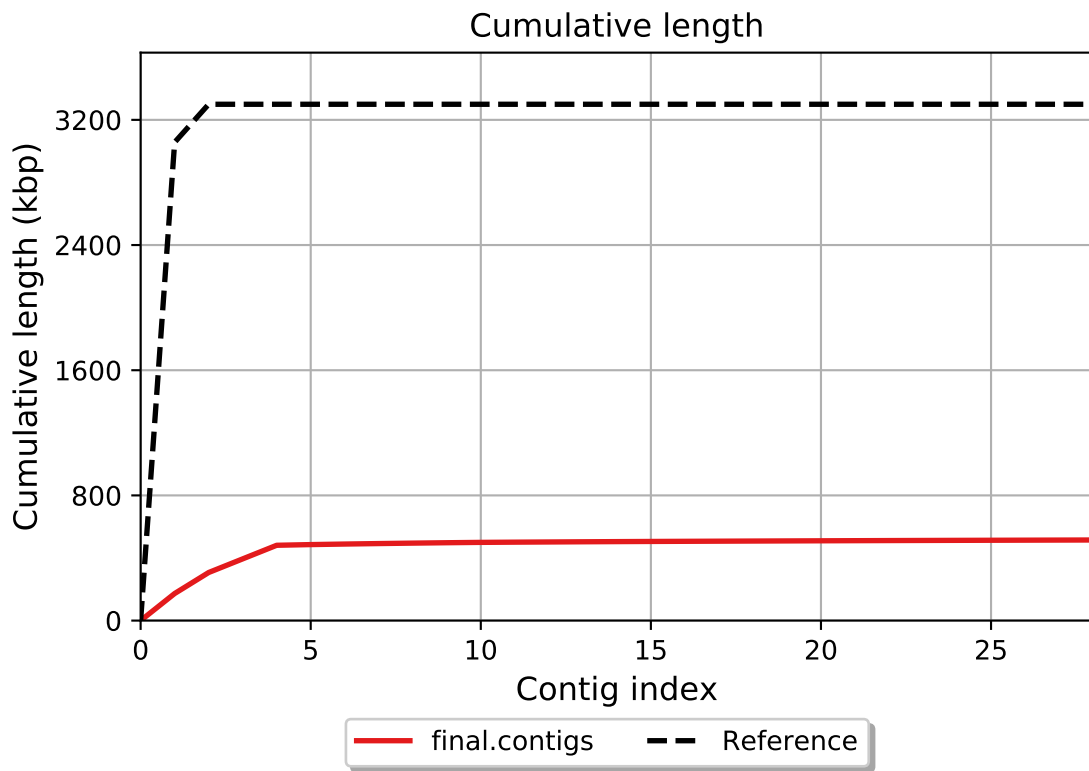


— final.contigs

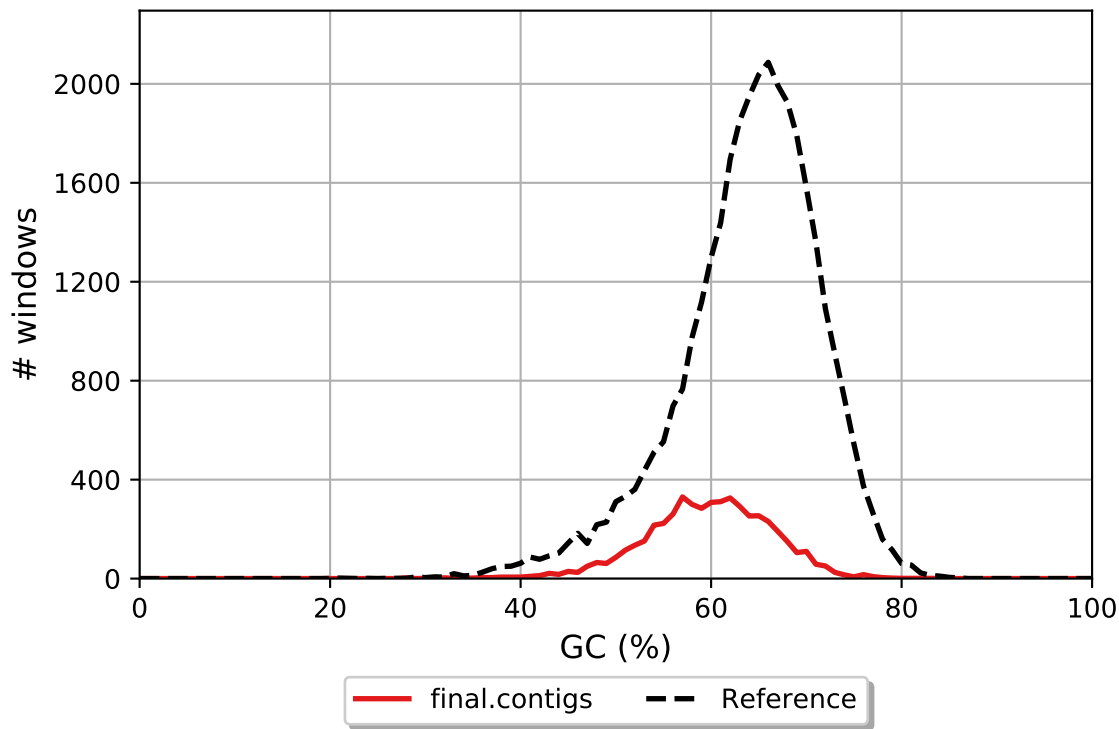
NGx



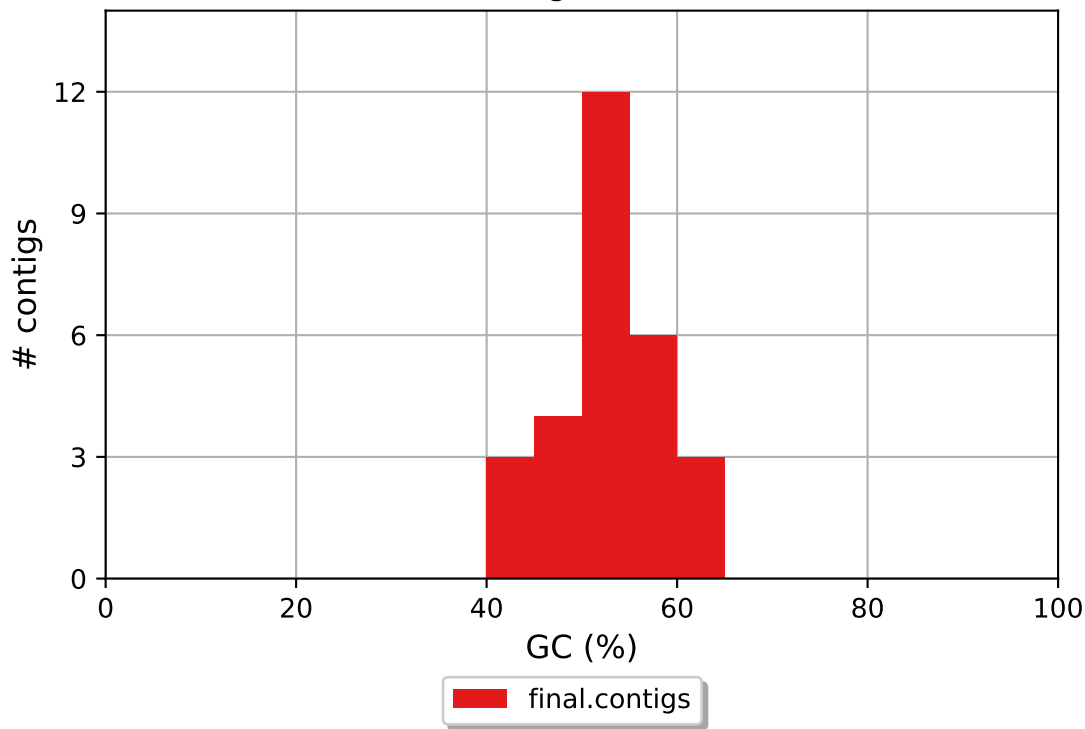
— final.contigs



# GC content

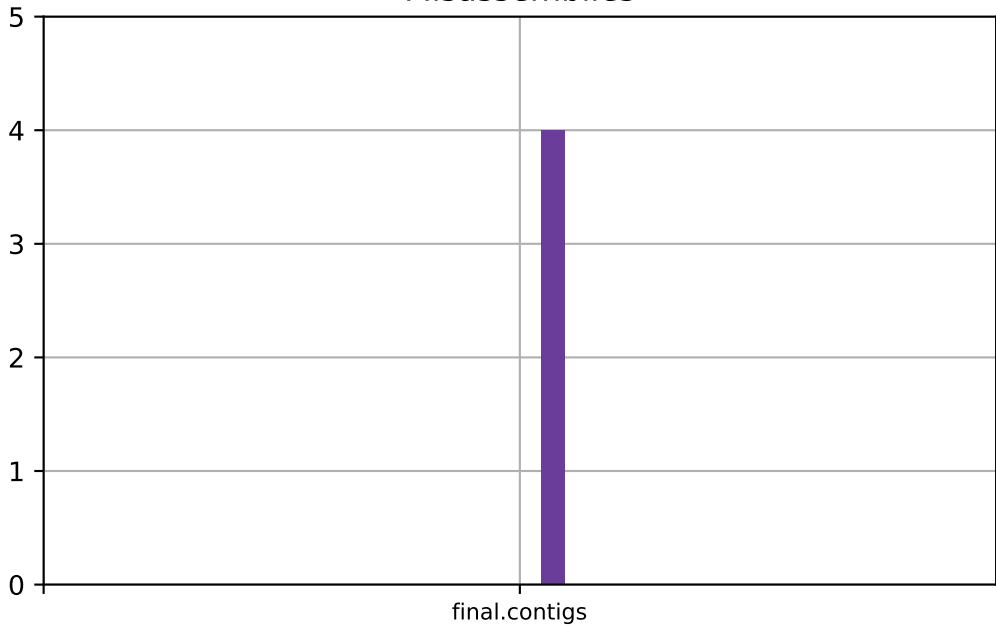


final.contigs GC content



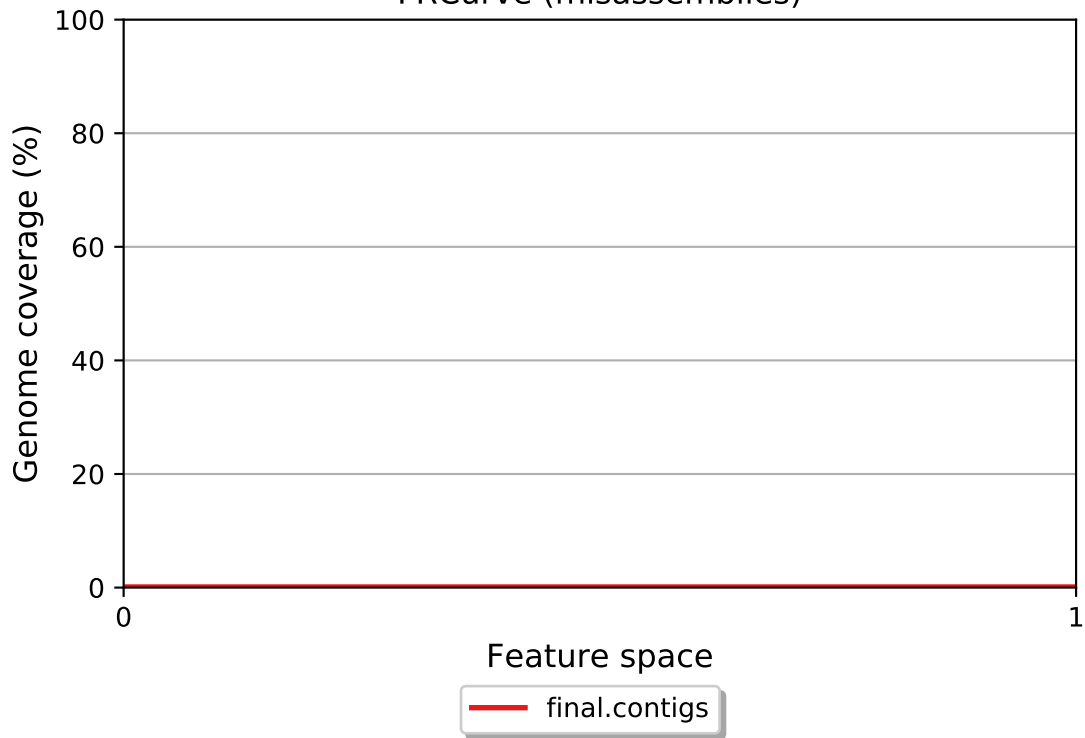


## Misassemblies

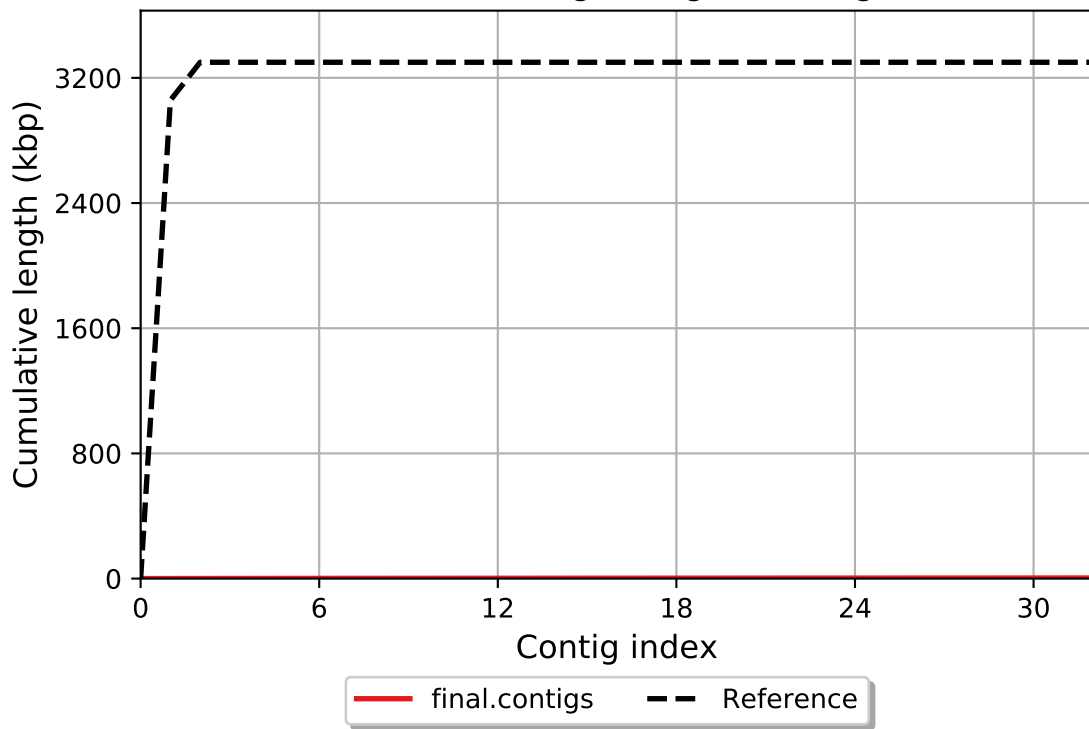


# interspecies translocations

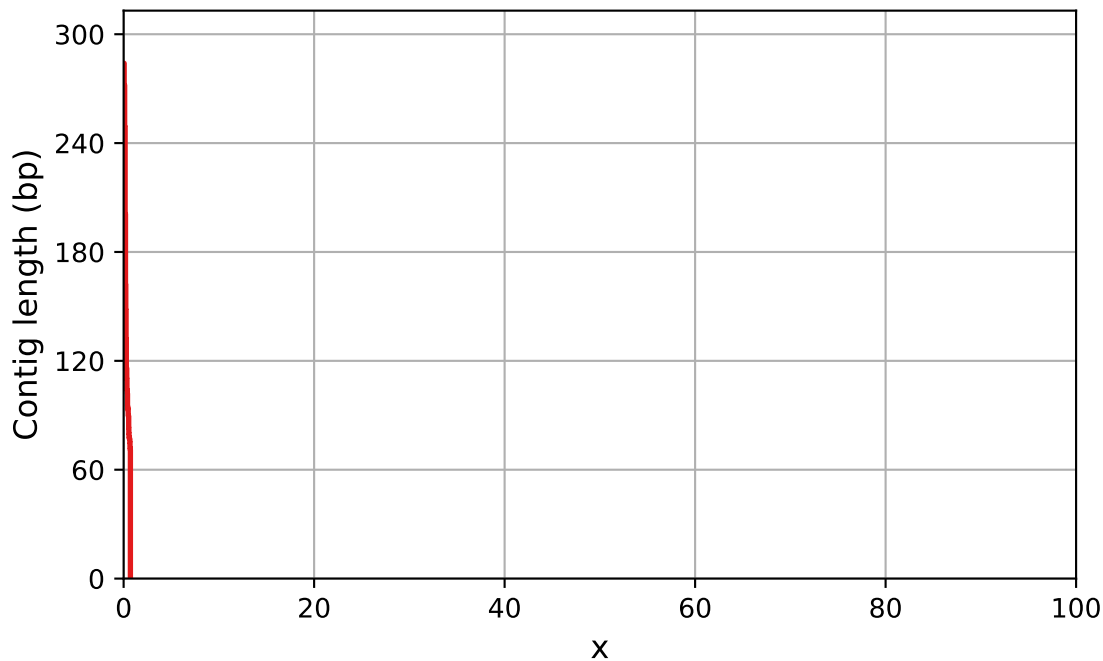
FRCurve (misassemblies)



Cumulative length (aligned contigs)

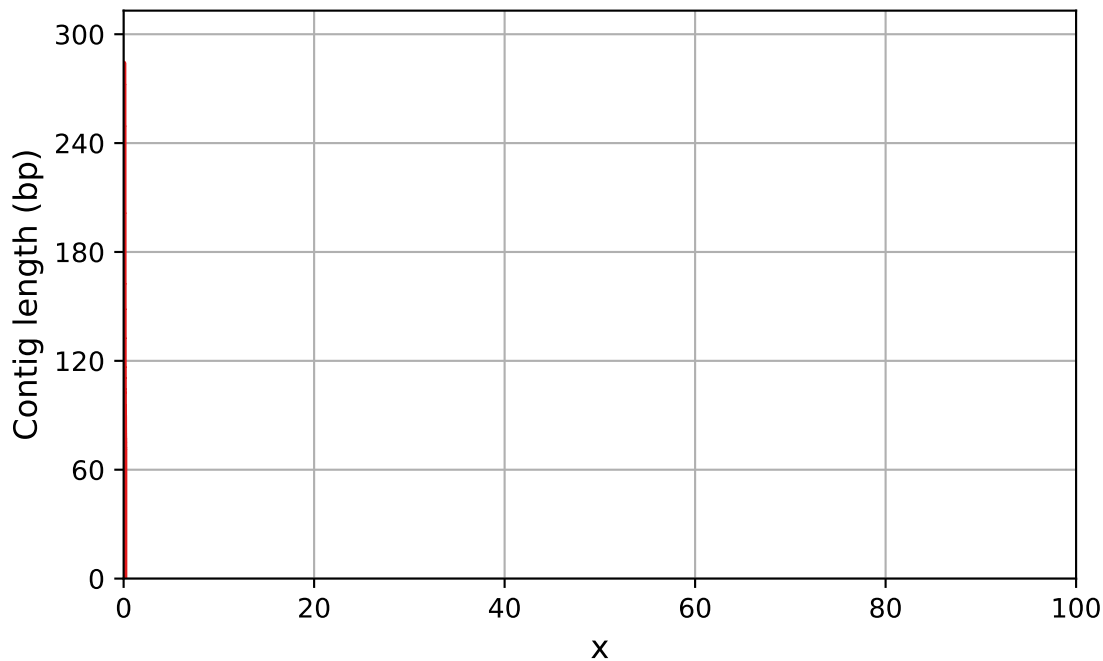


NAx



— final.contigs

# NGAx



— final.contigs