

## 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)	503230
Total length (>= 5000 bp)	481269
Total length (>= 10000 bp)	481269
Total length (>= 25000 bp)	481269
Total length (>= 50000 bp)	481269
# contigs	27
Largest contig	172953
Total length	512739
Reference length	3299615
GC (%)	59.74
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 + 19 part
Unaligned length	505393
Genome fraction (%)	0.073
Duplication ratio	3.043
# N's per 100 kbp	0.00
# mismatches per 100 kbp	4722.45
# indels per 100 kbp	82.85
Largest alignment	284
Total aligned length	3621
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

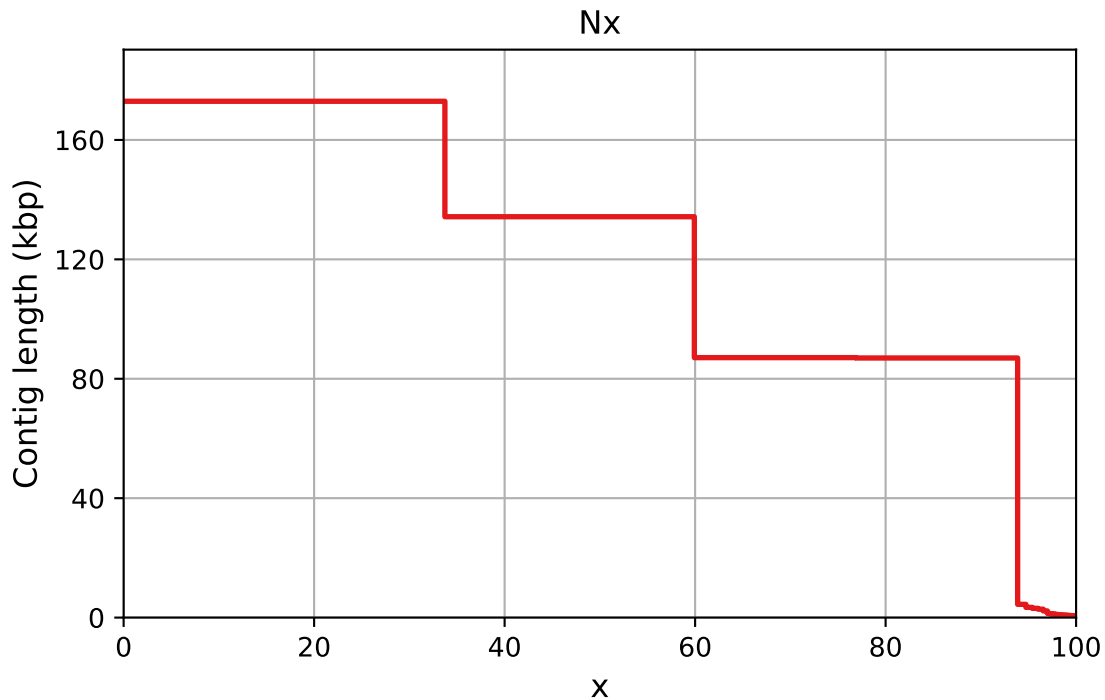
	final.contigs
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	7
# possible misassemblies	11
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	4
# mismatches	114
# indels	2
# indels (<= 5 bp)	2
# indels (> 5 bp)	0
Indels length	2

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

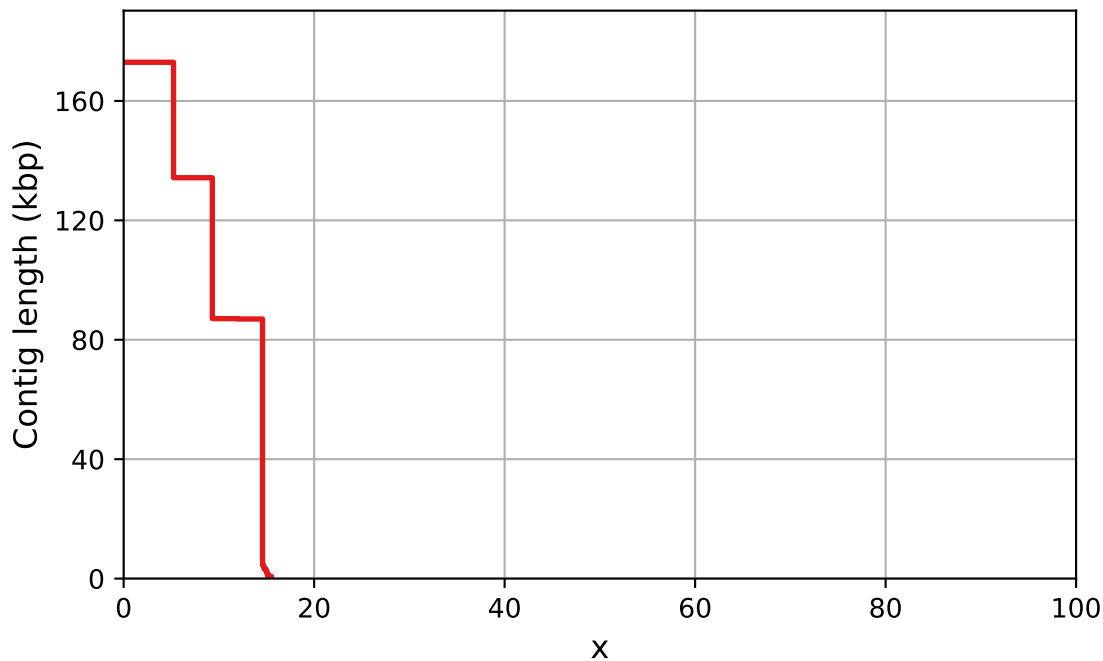
	final.contigs
# fully unaligned contigs	1
Fully unaligned length	691
# partially unaligned contigs	19
Partially unaligned length	504702
# N's	0

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).

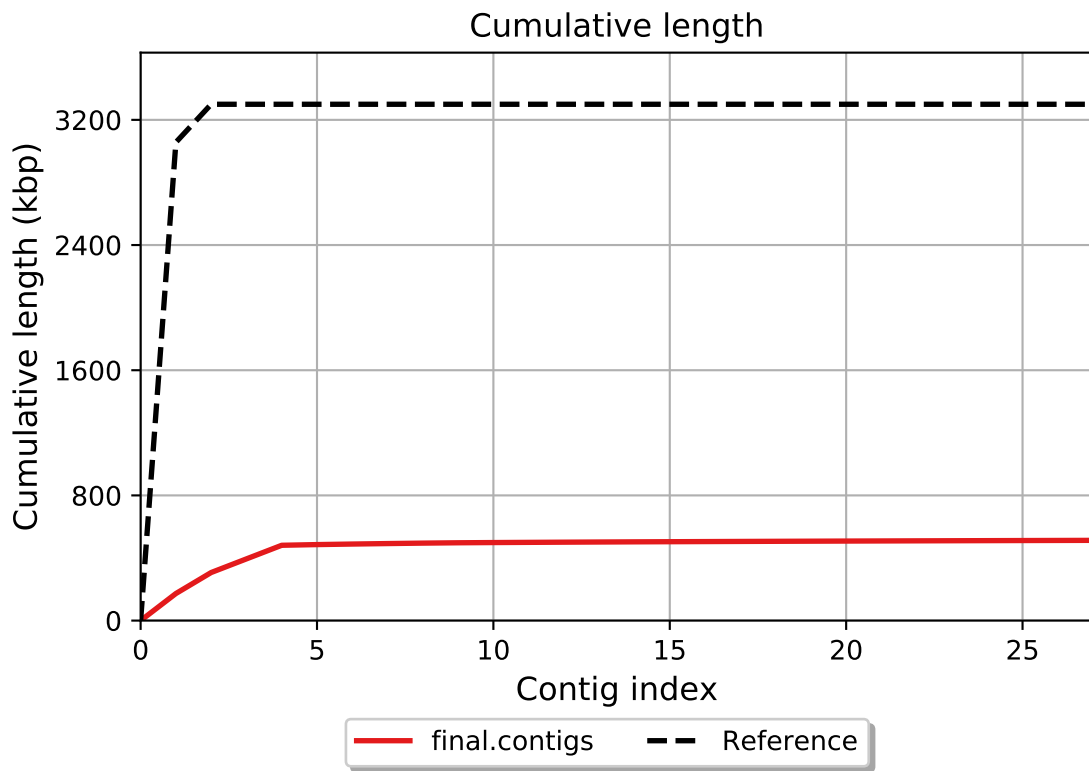


— final.contigs

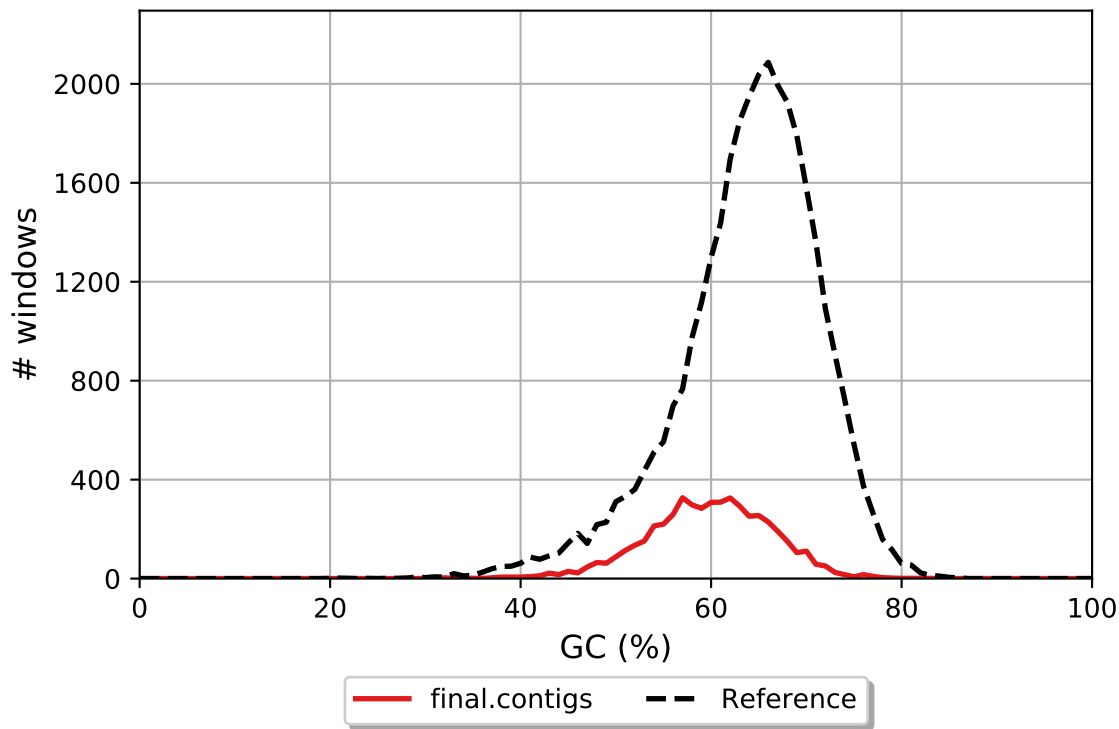
NGx



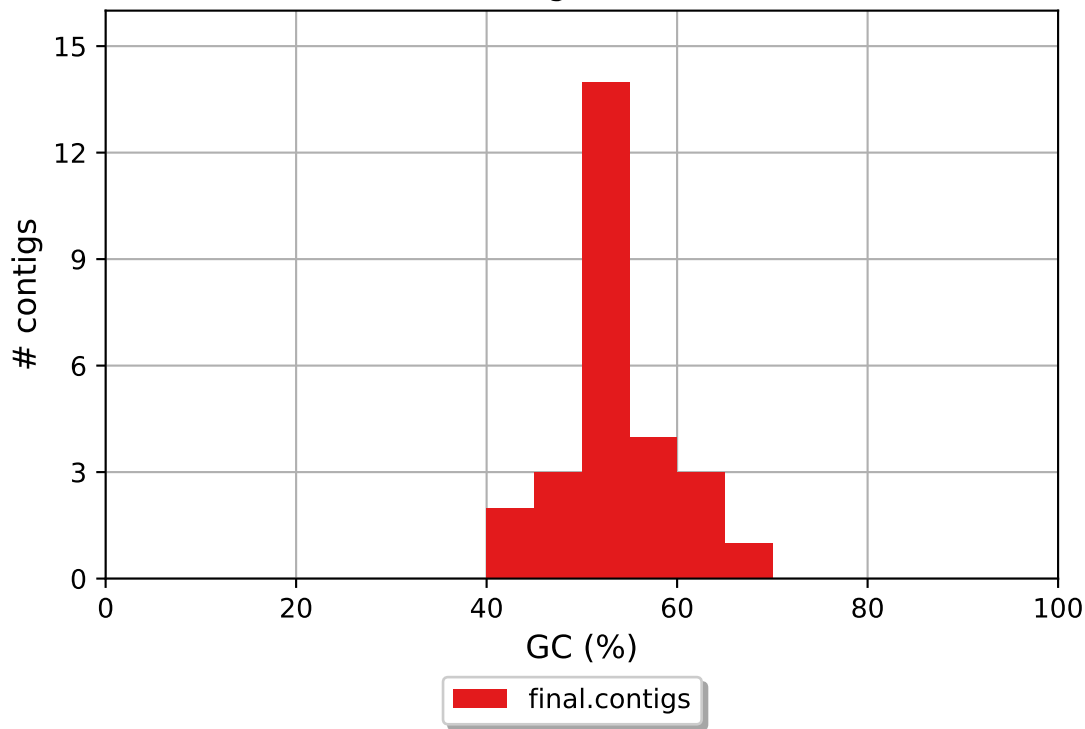
— final.contigs



GC content

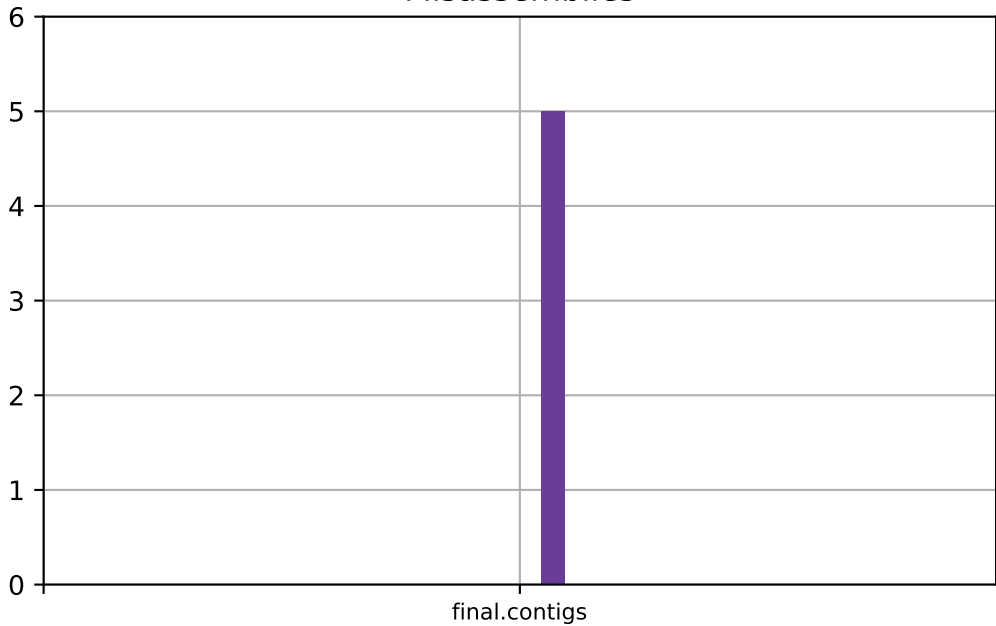


final.contigs GC content



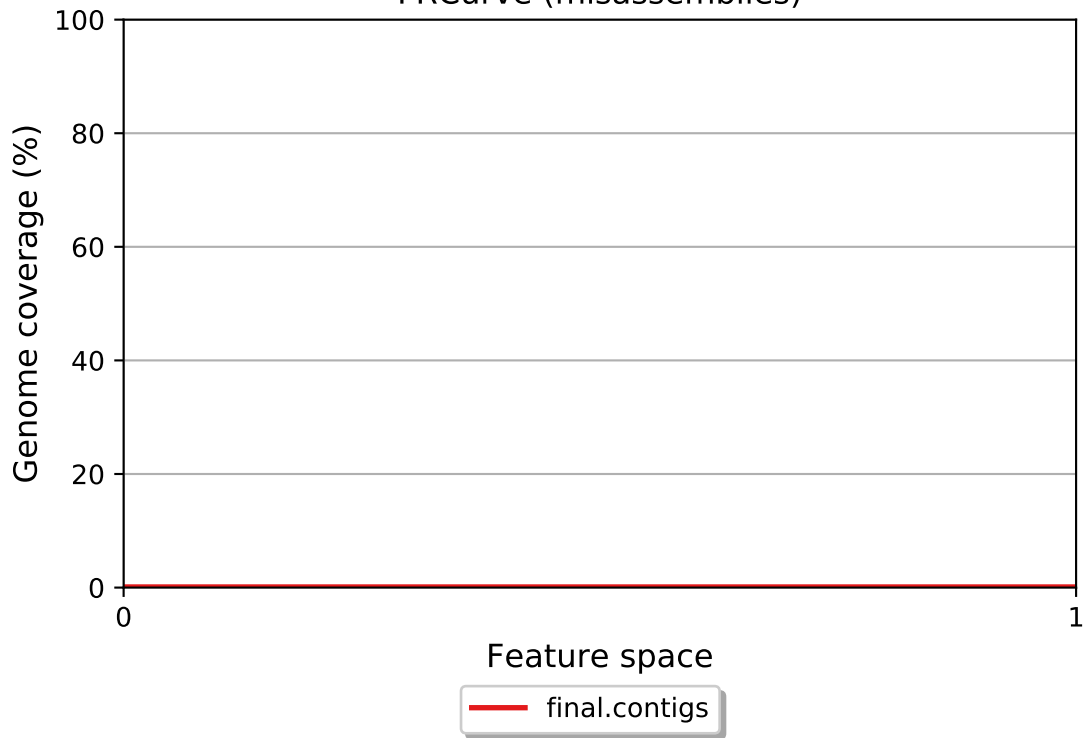


## Misassemblies

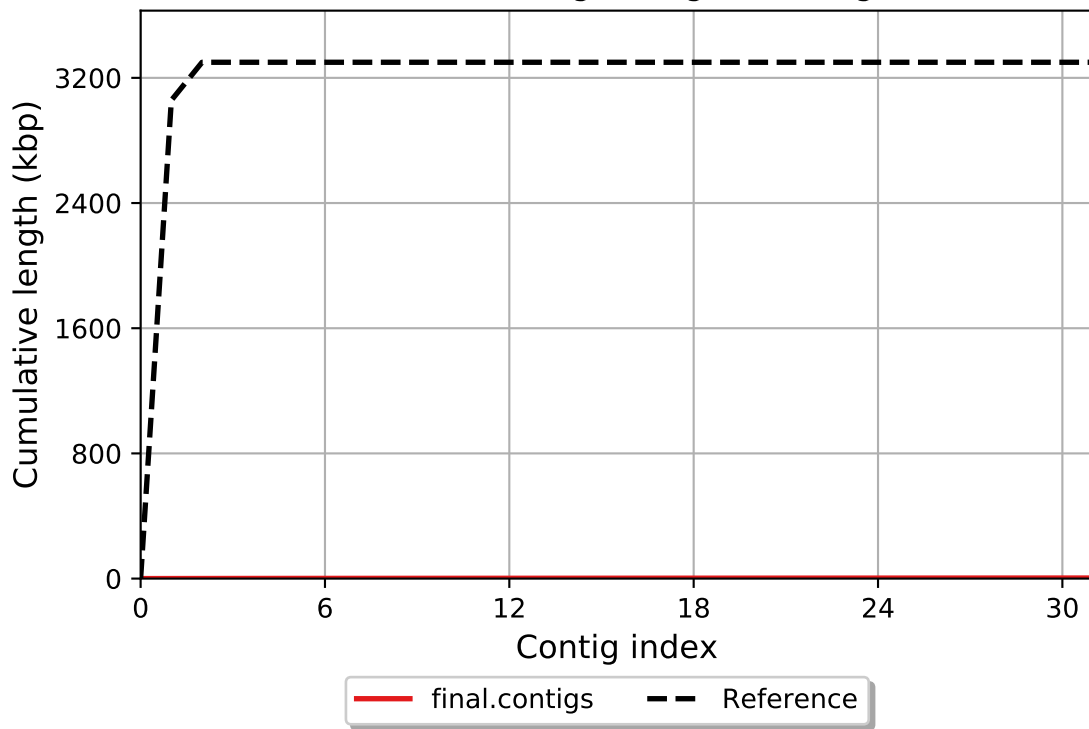


# interspecies translocations

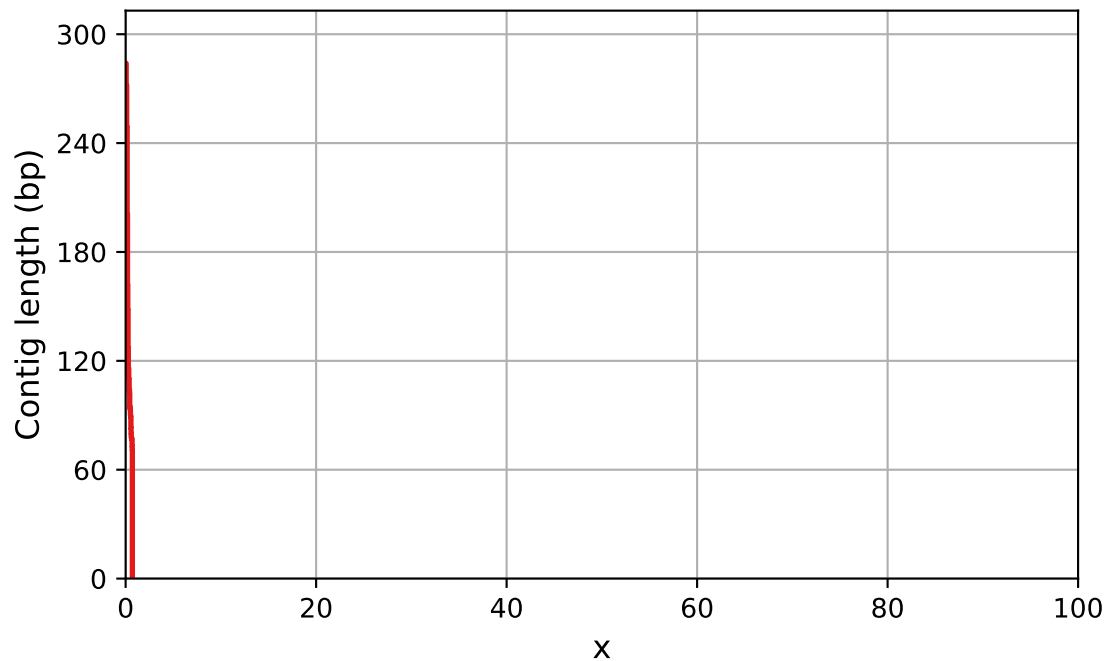
FRCurve (misassemblies)



Cumulative length (aligned contigs)

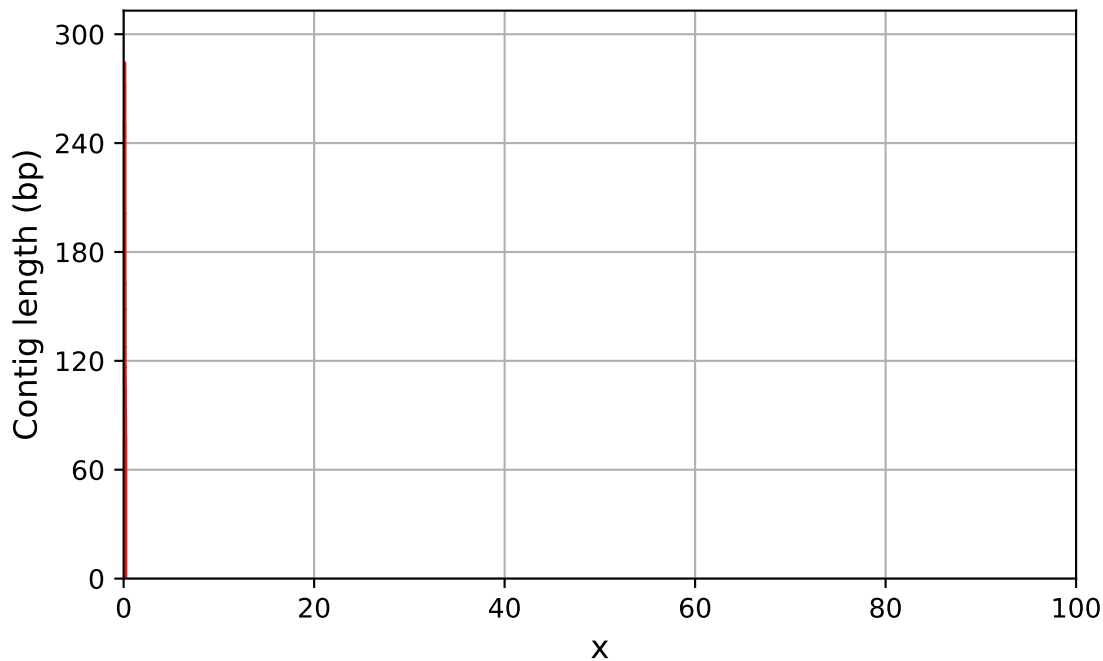


NAx



— final.contigs

# NGAx



— final.contigs