

## Report

	final.contigs
# contigs (>= 1000 bp)	7
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	31076
Total length (>= 5000 bp)	23416
Total length (>= 10000 bp)	23416
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	20
Largest contig	23416
Total length	39743
Reference length	4053139
GC (%)	61.95
Reference GC (%)	70.41
N50	23416
N75	1125
L50	1
L75	6
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# unaligned contigs	3 + 8 part
Unaligned length	33202
Genome fraction (%)	0.065
Duplication ratio	2.478
# N's per 100 kbp	0.00
# mismatches per 100 kbp	3068.18
# indels per 100 kbp	75.76
Largest alignment	456
Total aligned length	2846
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	4
# possible misassemblies	6
# local misassemblies	1
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# mismatches	81
# indels	2
# indels (<= 5 bp)	2
# indels (> 5 bp)	0
Indels length	2

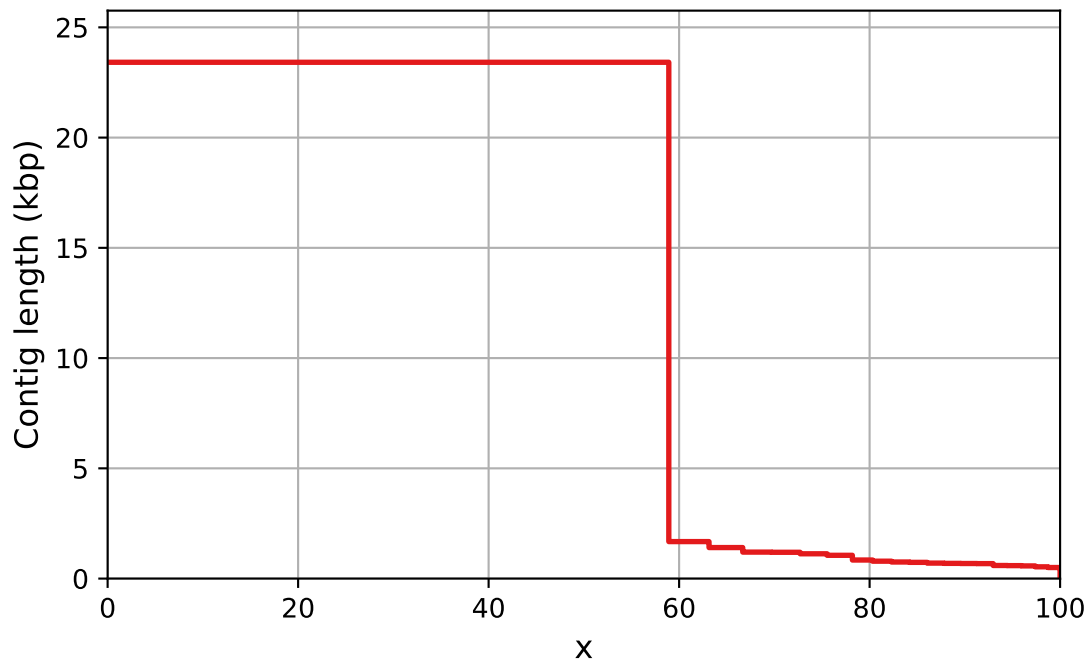
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	final.contigs
# fully unaligned contigs	3
Fully unaligned length	25277
# partially unaligned contigs	8
Partially unaligned length	7925
# N's	0

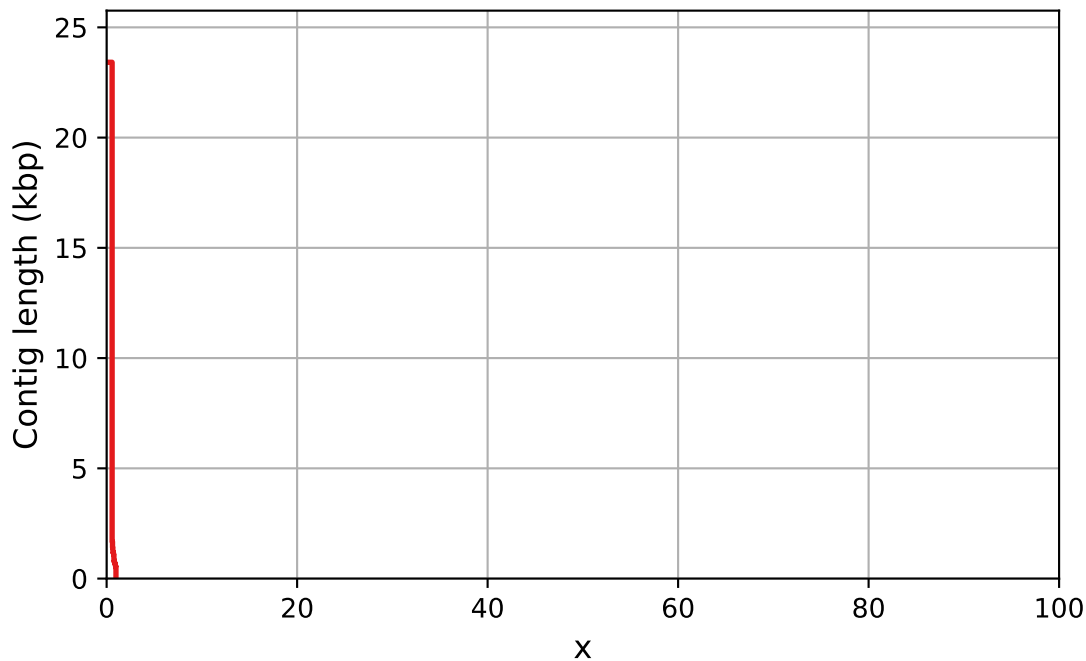
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

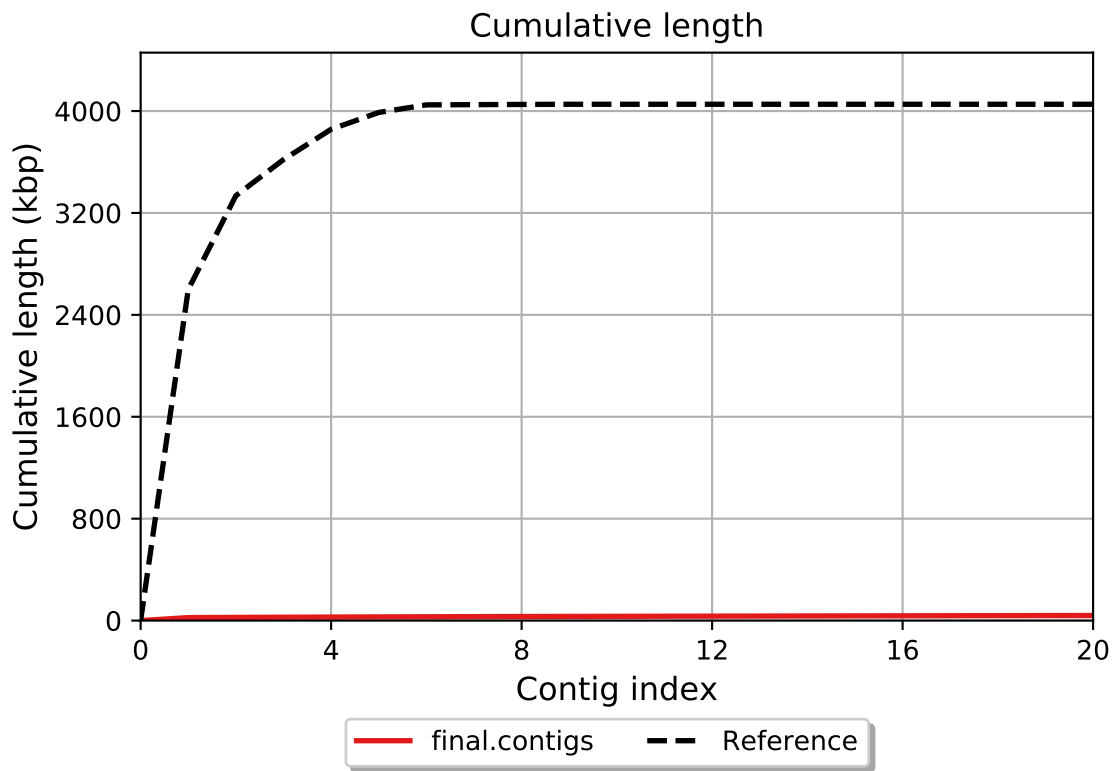


— final.contigs

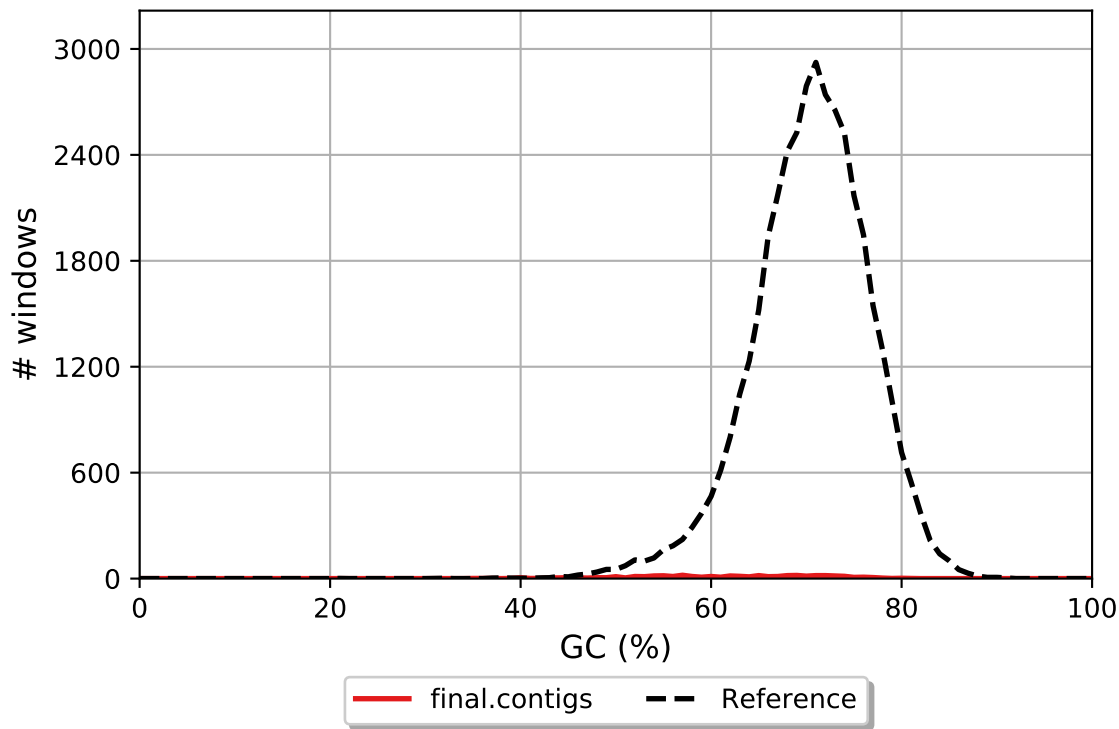
NGx



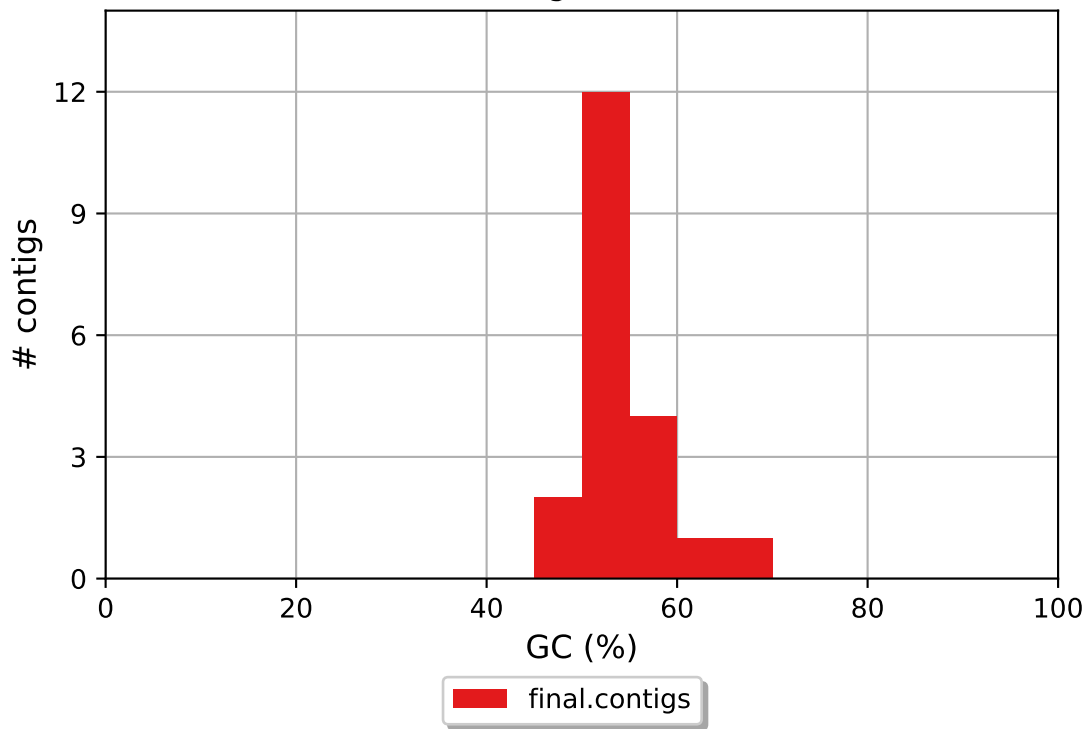
— final.contigs



## GC content



final.contigs GC content



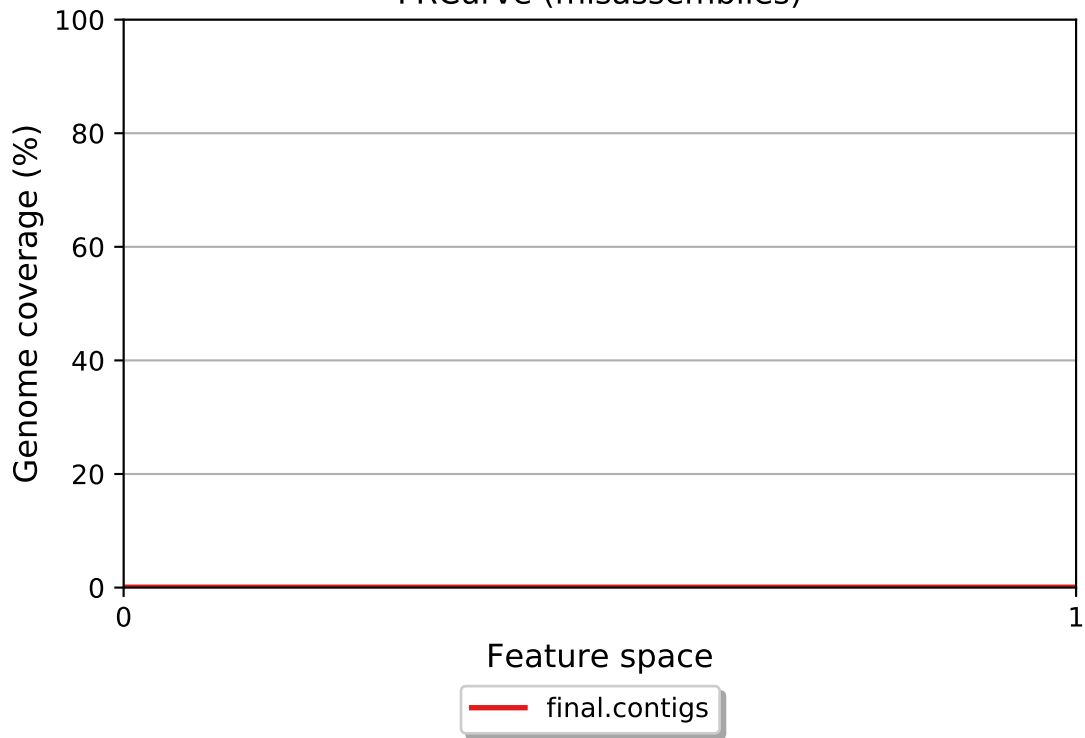


## Misassemblies

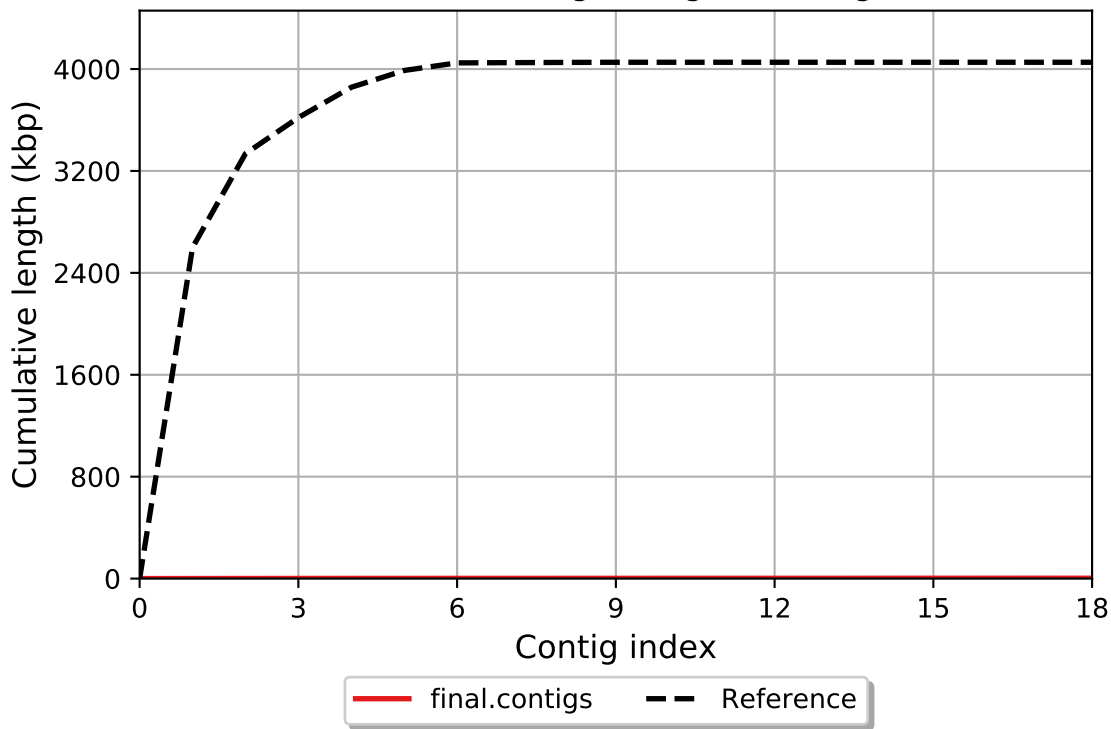


# interspecies translocations

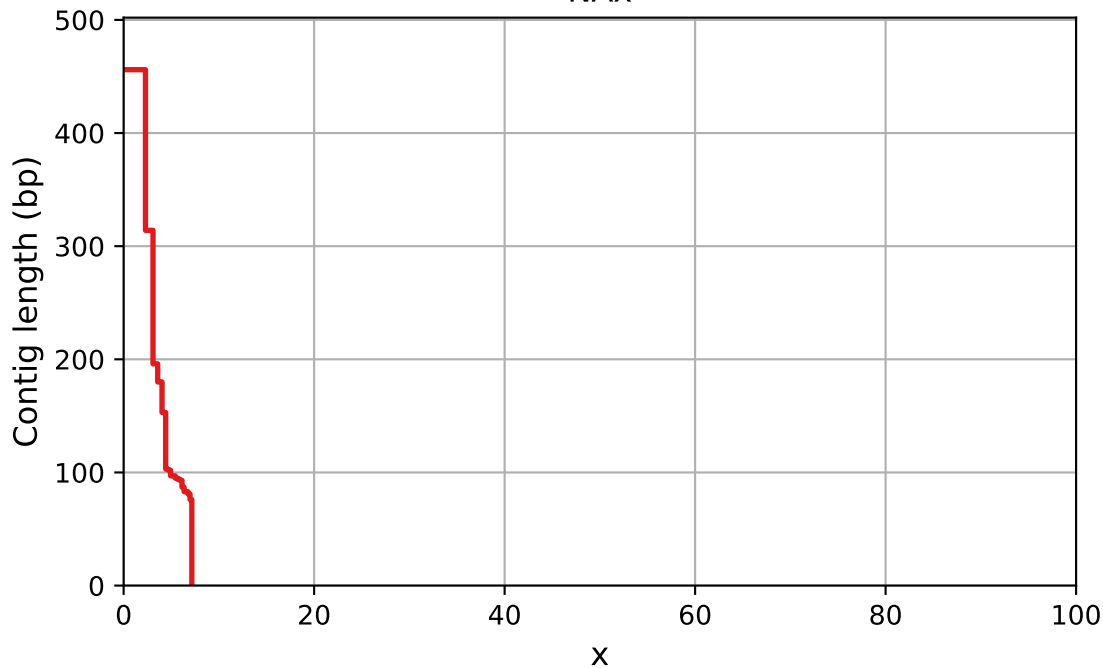
FRCurve (misassemblies)



Cumulative length (aligned contigs)

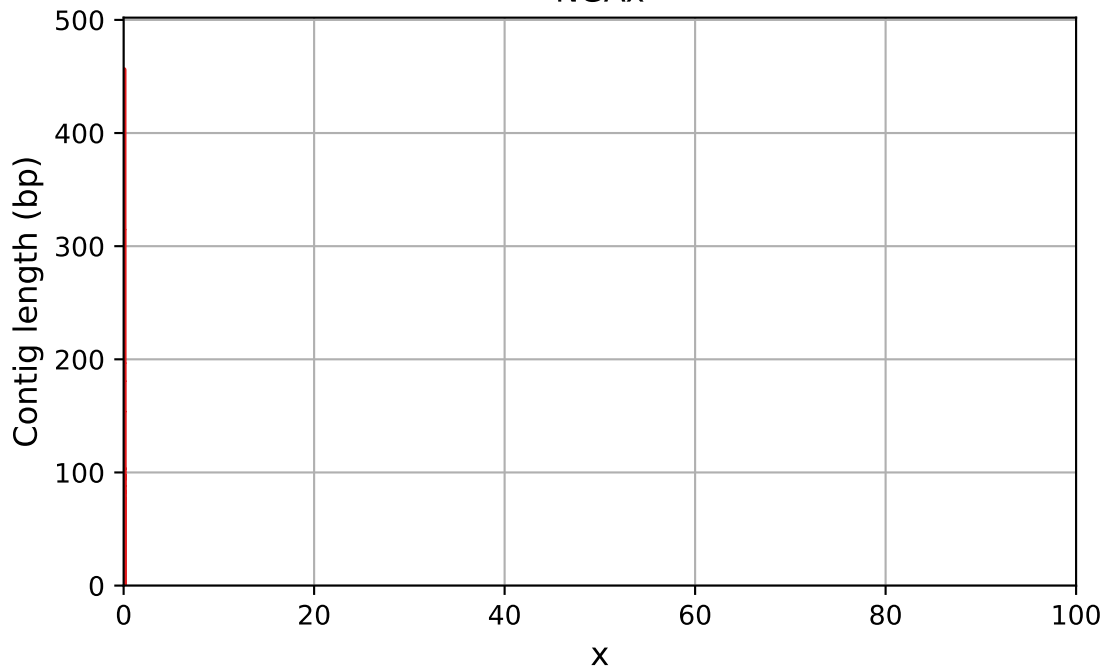


NAx



— final.contigs

# NGAx



— final.contigs