

Report

	final.contigs
# contigs (>= 1000 bp)	21
# contigs (>= 5000 bp)	13
# contigs (>= 10000 bp)	10
# contigs (>= 25000 bp)	7
# contigs (>= 50000 bp)	4
Total length (>= 1000 bp)	734407
Total length (>= 5000 bp)	715168
Total length (>= 10000 bp)	693100
Total length (>= 25000 bp)	650400
Total length (>= 50000 bp)	535733
# contigs	35
Largest contig	255300
Total length	744350
Reference length	3442017
GC (%)	58.98
Reference GC (%)	58.88
N50	124997
N75	47609
L50	2
L75	5
# 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	6
# unaligned contigs	5 + 22 part
Unaligned length	735350
Genome fraction (%)	0.109
Duplication ratio	2.393
# N's per 100 kbp	0.00
# mismatches per 100 kbp	5051.85
# indels per 100 kbp	239.30
Largest alignment	608
Total aligned length	5940
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

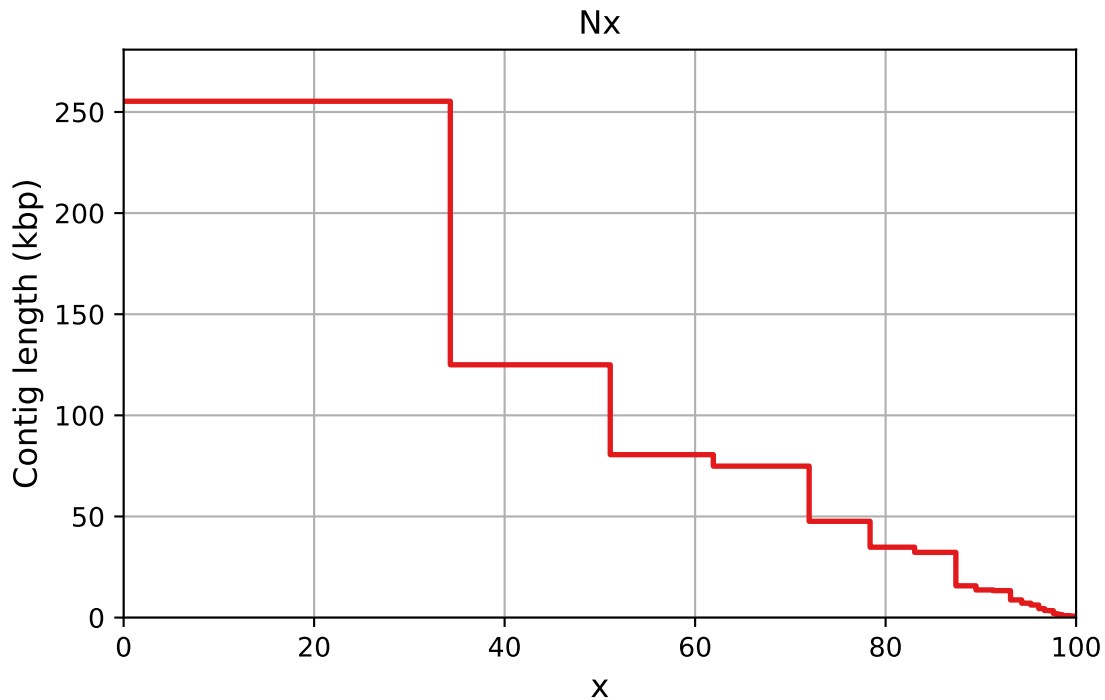
	final.contigs
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	12
# possible misassemblies	19
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	6
# mismatches	190
# indels	9
# indels (<= 5 bp)	9
# indels (> 5 bp)	0
Indels length	13

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).

Unaligned report

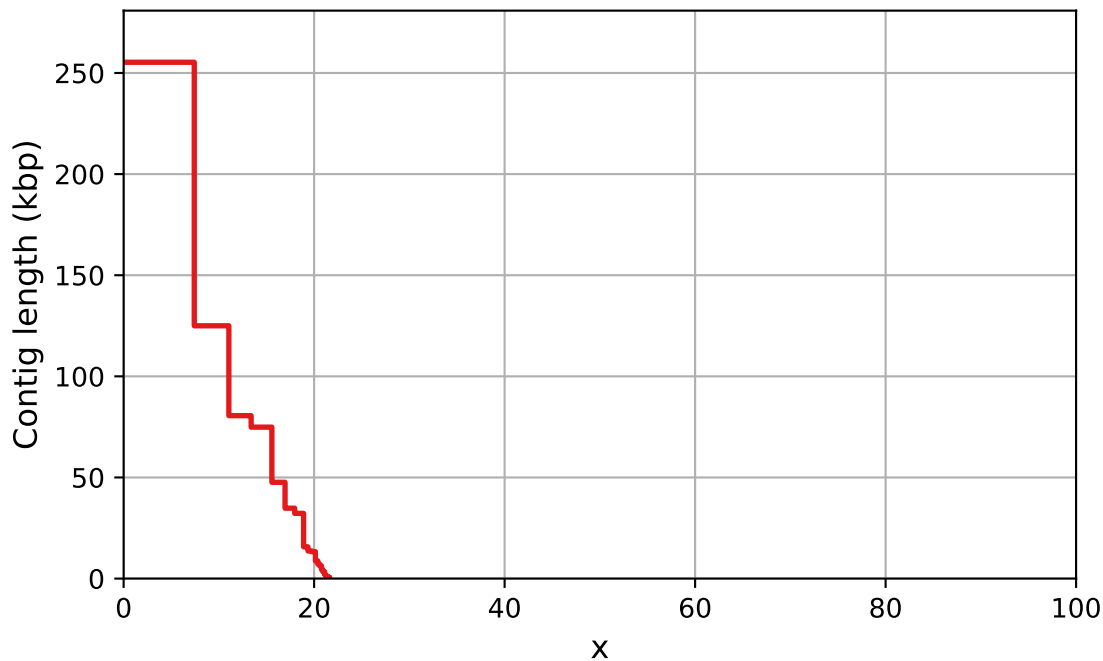
	final.contigs
# fully unaligned contigs	5
Fully unaligned length	4830
# partially unaligned contigs	22
Partially unaligned length	730520
# N's	0

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).

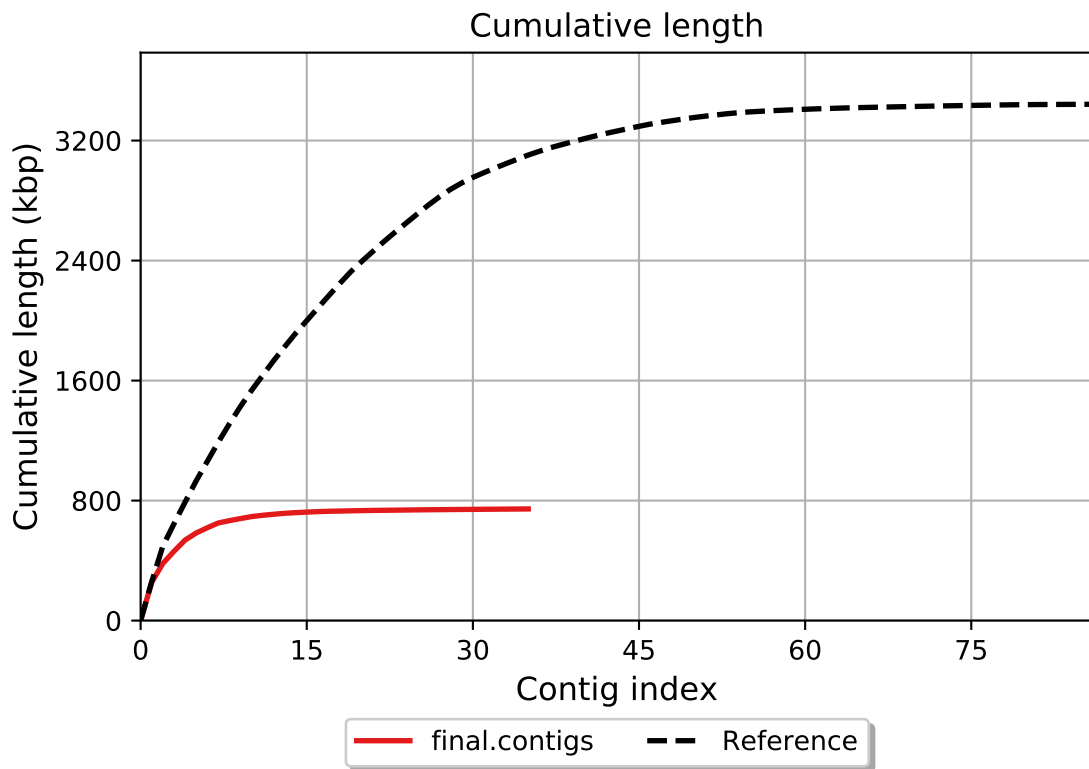


— final.contigs

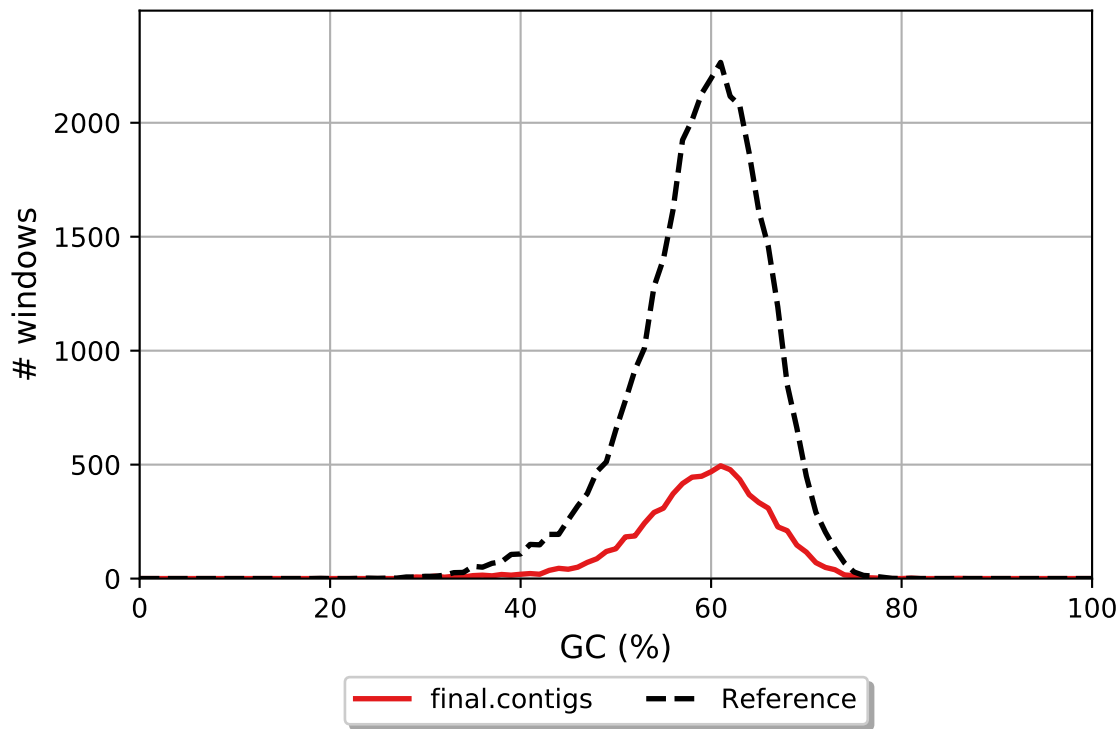
NGx



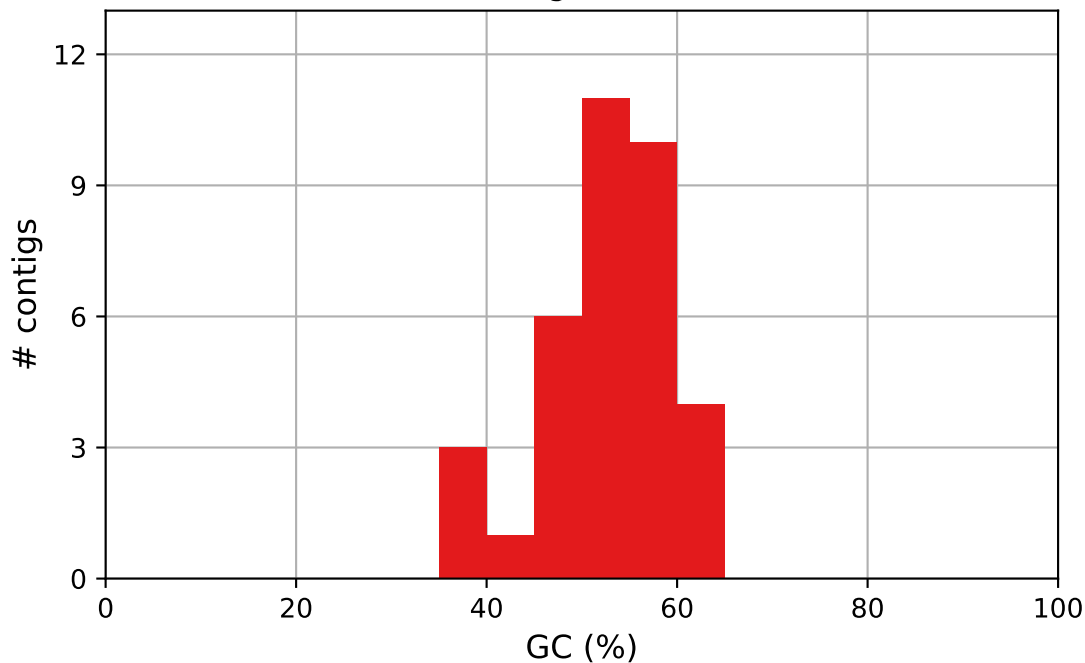
— final.contigs



GC content

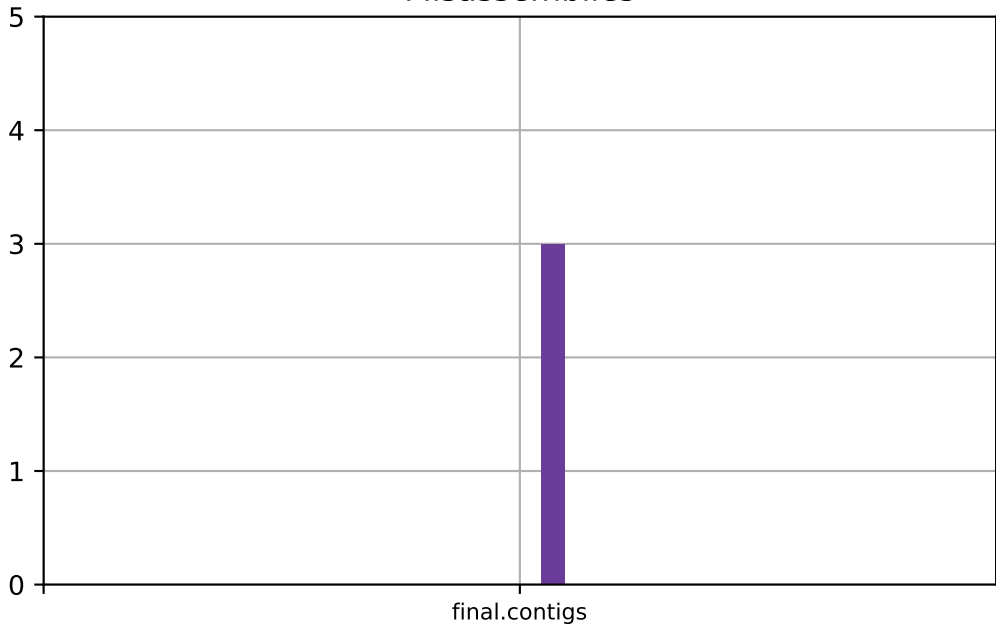


final.contigs GC content



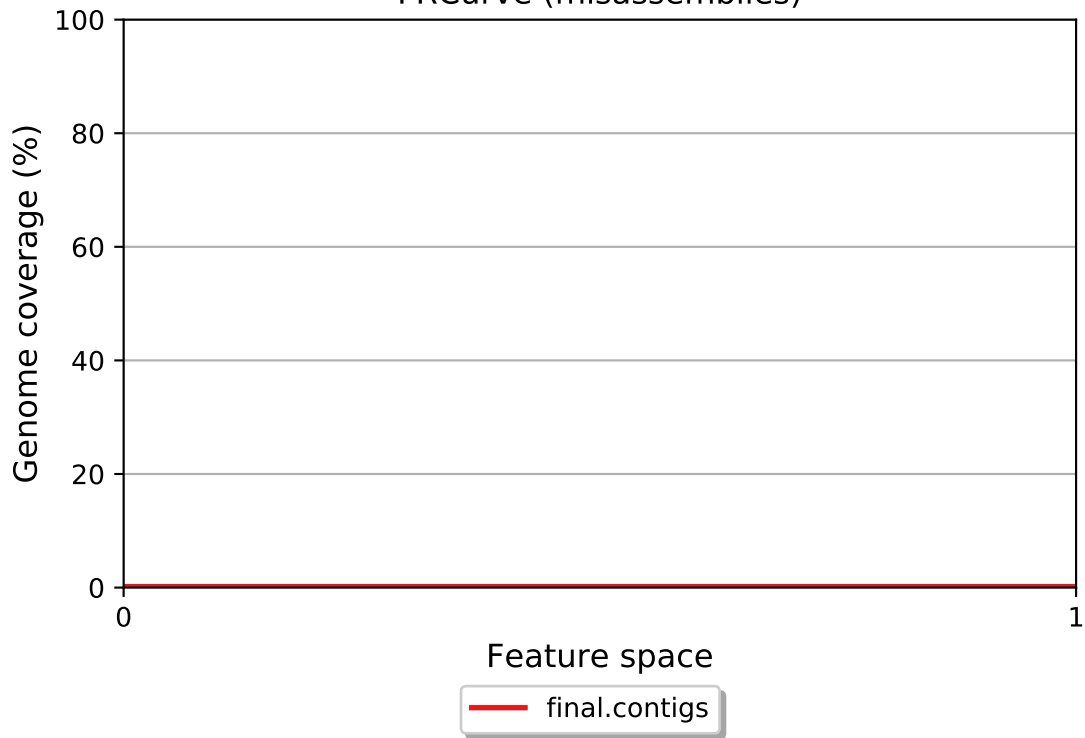
final.contigs

Misassemblies

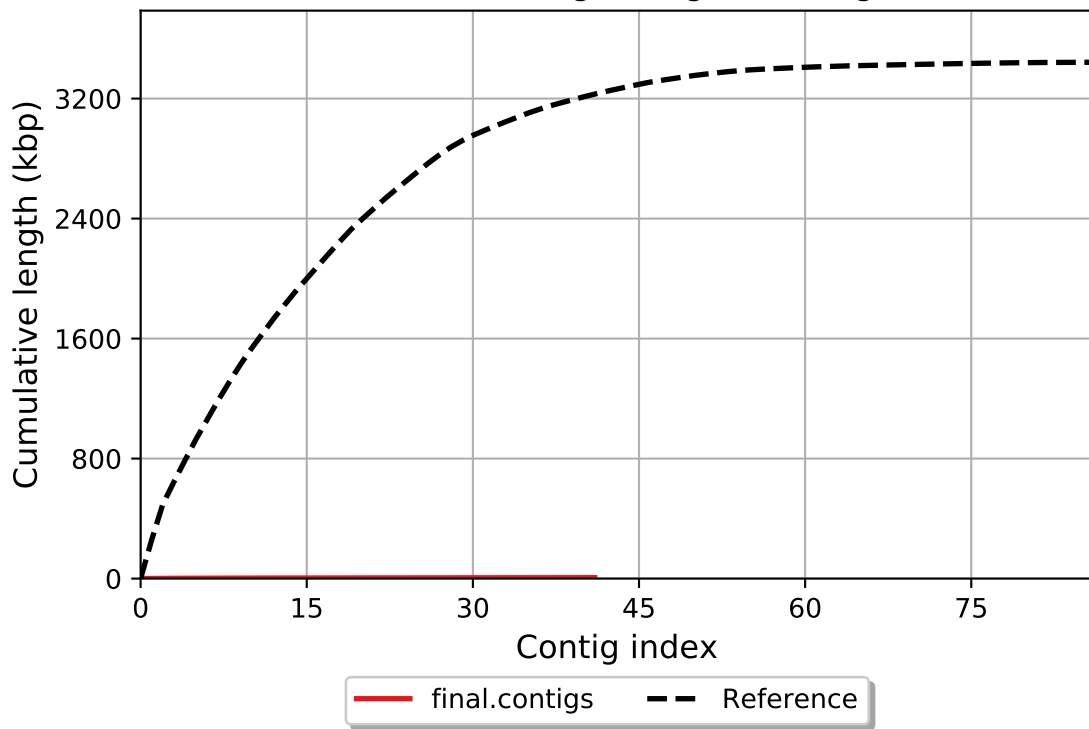


interspecies translocations

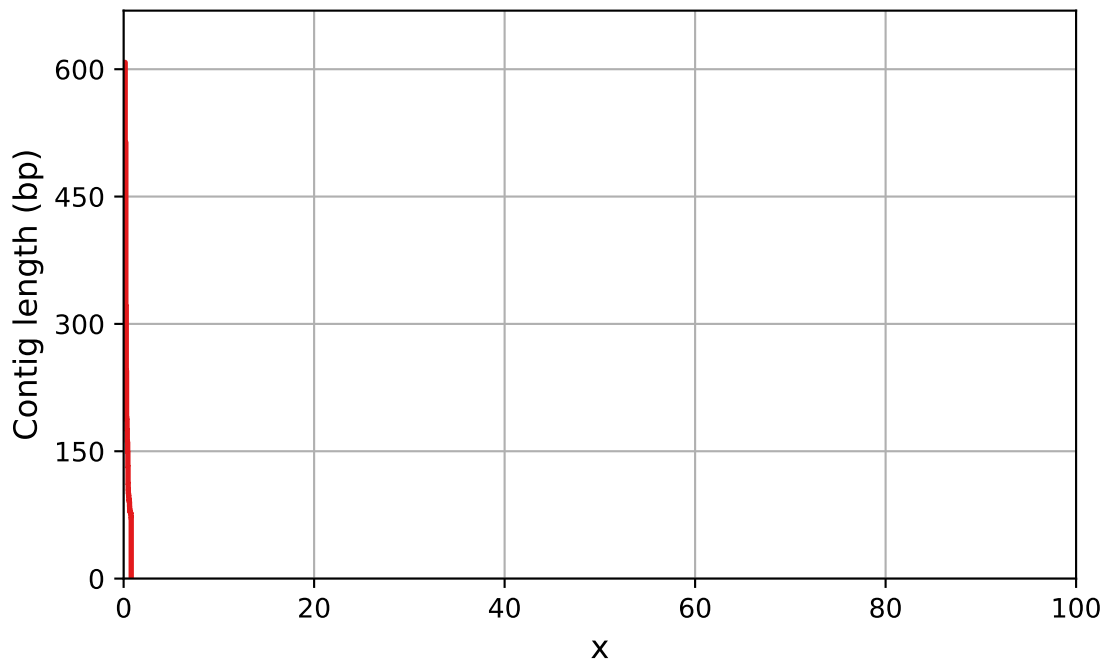
FRCurve (misassemblies)



Cumulative length (aligned contigs)

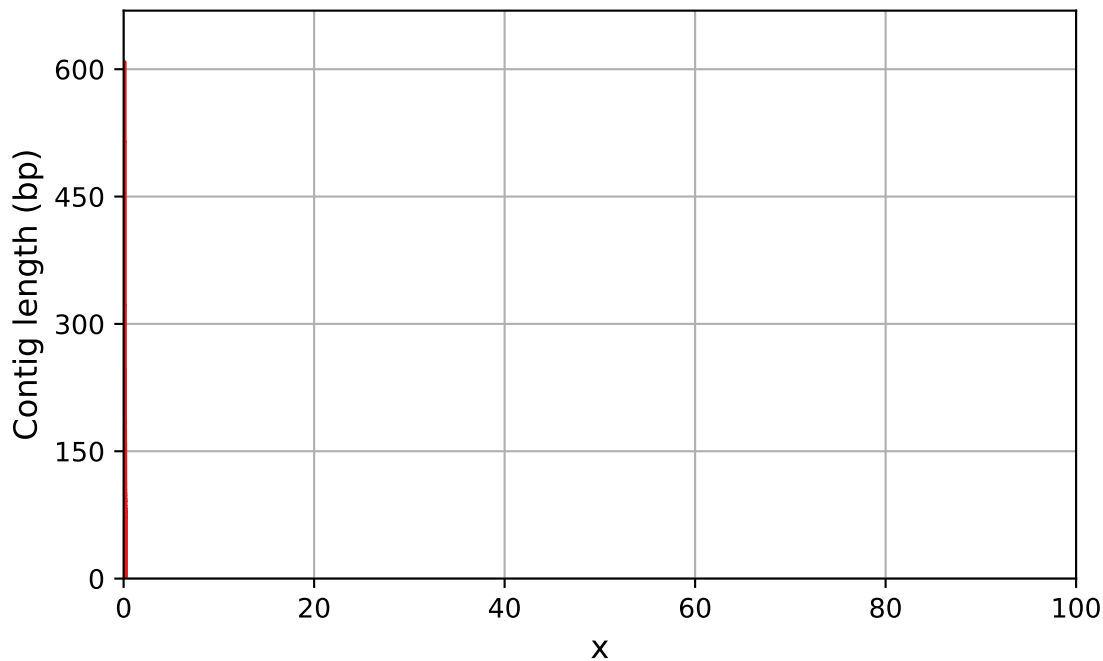


NAx



— final.contigs

NGAx



— final.contigs