

Report

	final.contigs
# contigs (>= 1000 bp)	7
# contigs (>= 5000 bp)	2
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	31799
Total length (>= 5000 bp)	23126
Total length (>= 10000 bp)	16005
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	19
Largest contig	16005
Total length	39884
Reference length	5846582
GC (%)	51.46
Reference GC (%)	46.79
N50	7121
N75	1214
L50	2
L75	6
# 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 + 8 part
Unaligned length	33562
Genome fraction (%)	0.043
Duplication ratio	2.506
# N's per 100 kbp	0.00
# mismatches per 100 kbp	4320.25
# indels per 100 kbp	0.00
Largest alignment	608
Total aligned length	2927
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	7
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# mismatches	109
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

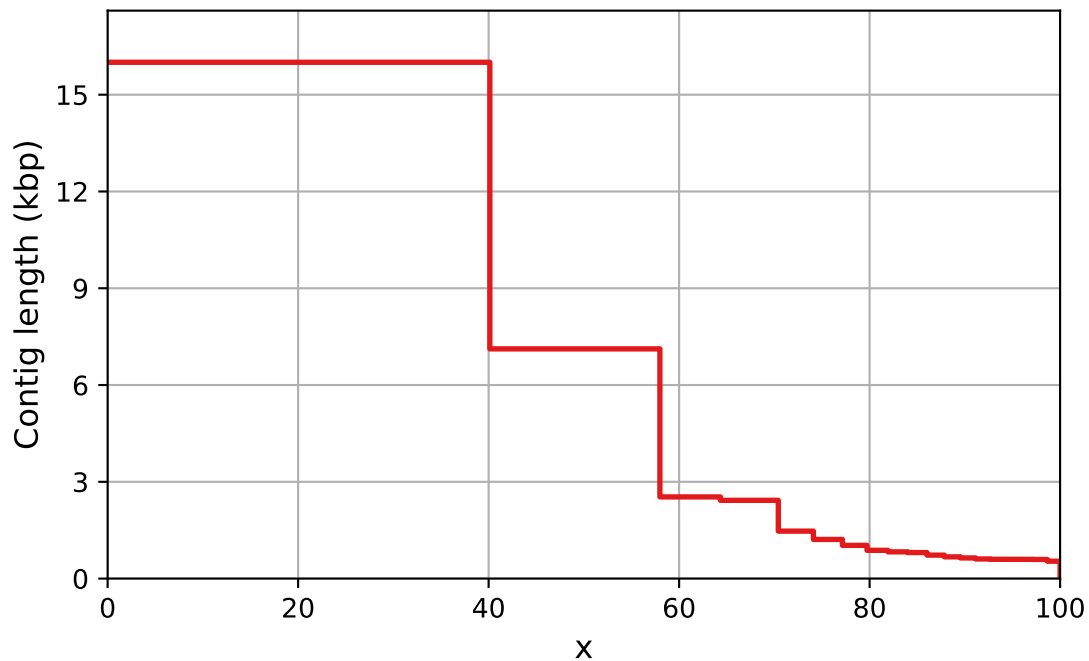
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	final.contigs
# fully unaligned contigs	4
Fully unaligned length	2671
# partially unaligned contigs	8
Partially unaligned length	30891
# N's	0

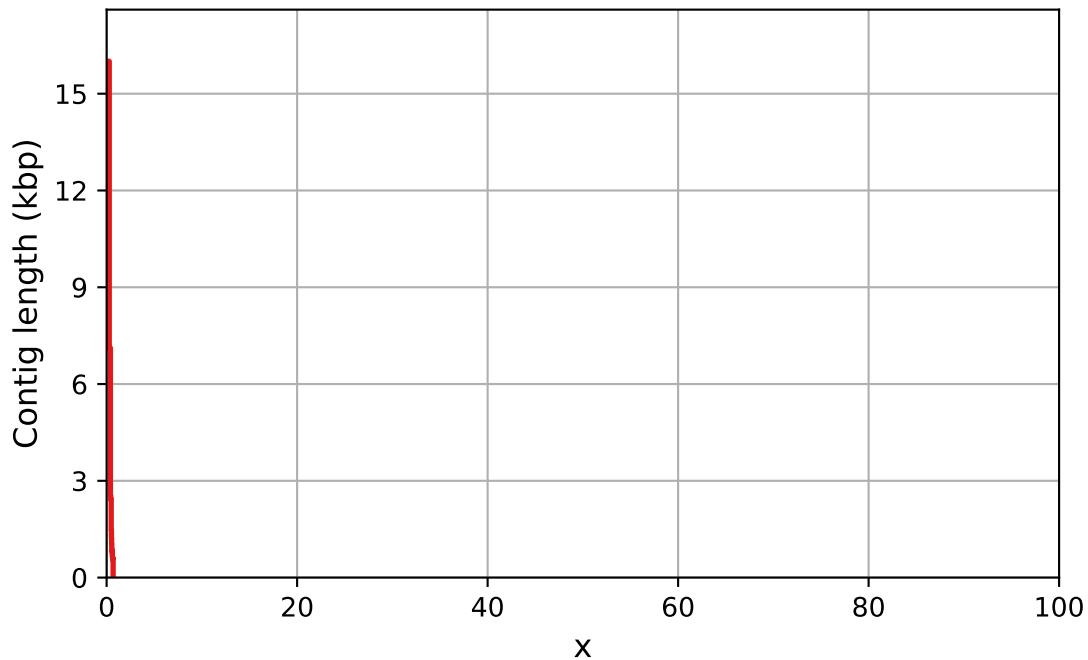
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



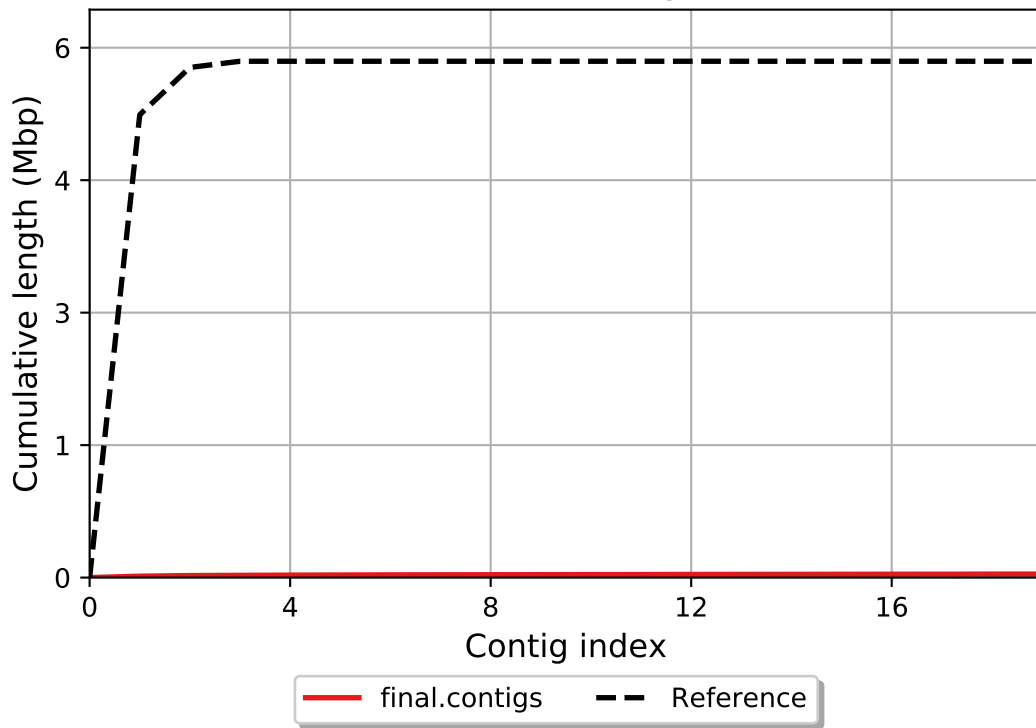
— final.contigs

NGx

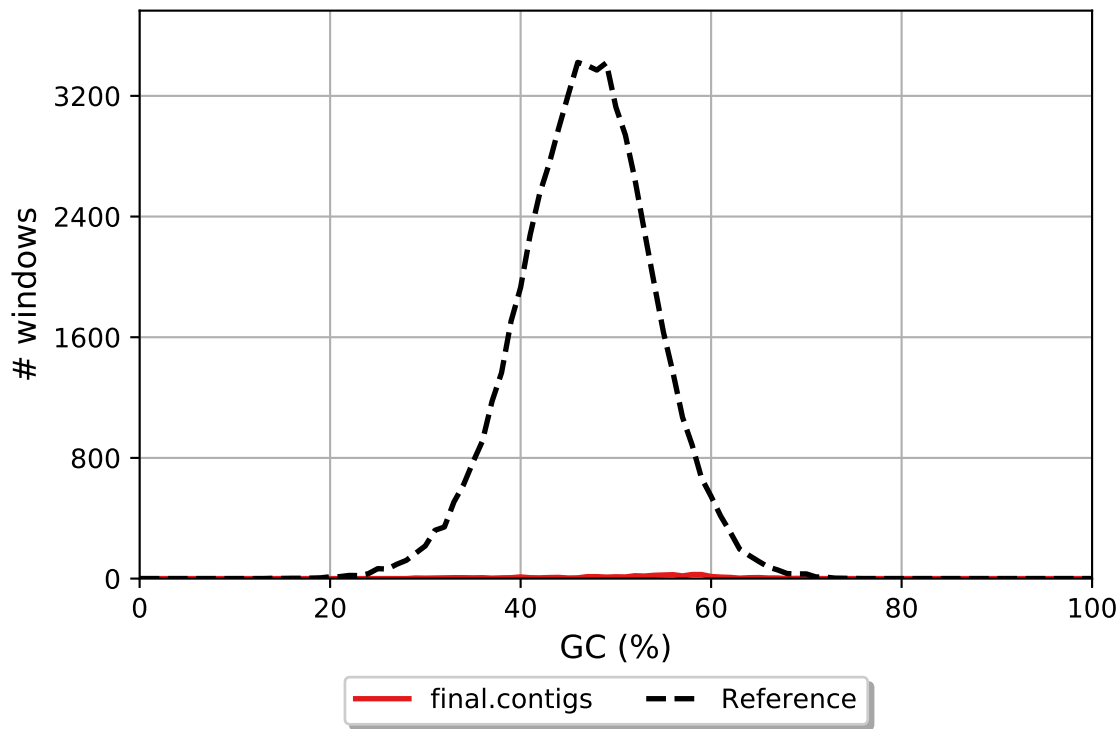


— final.contigs

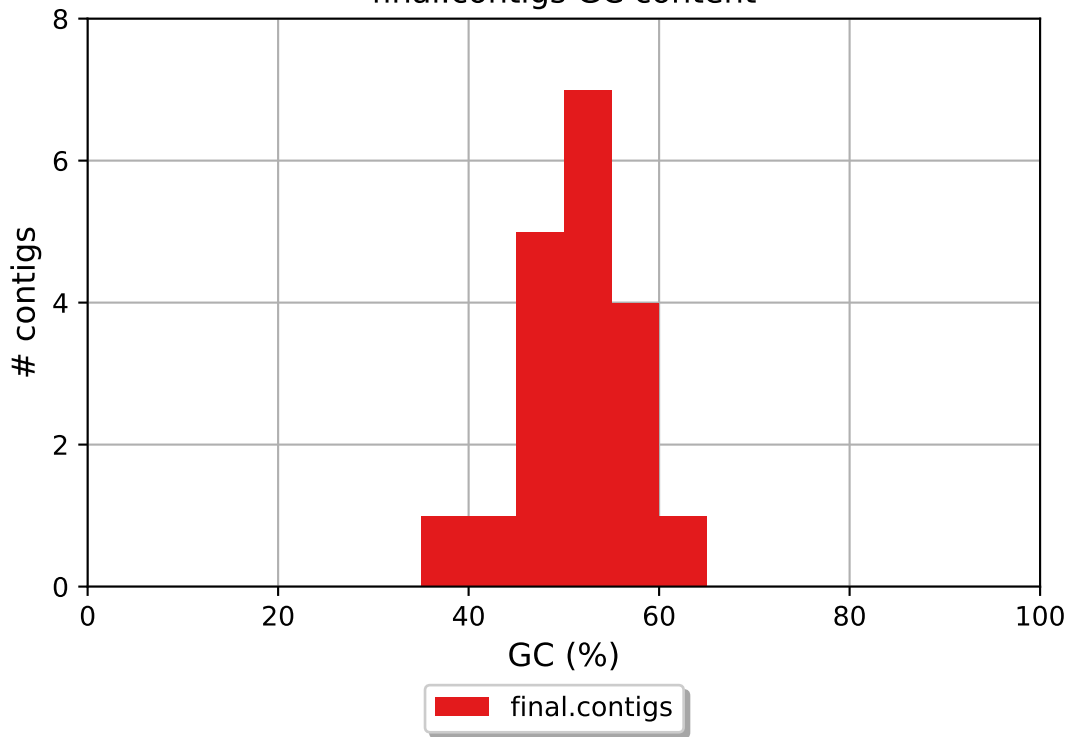
Cumulative length



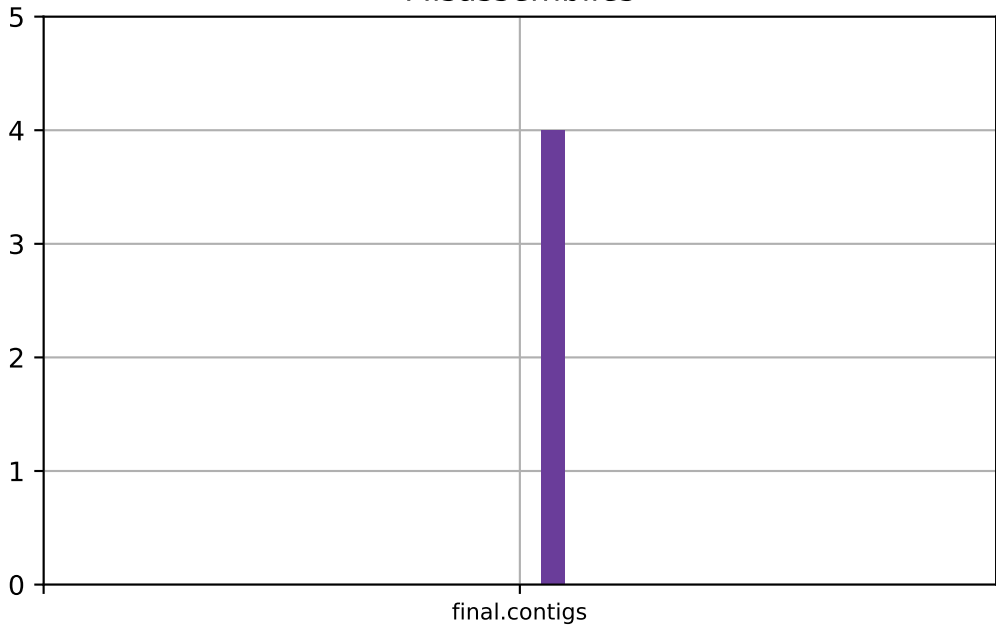
GC content



final.contigs GC content

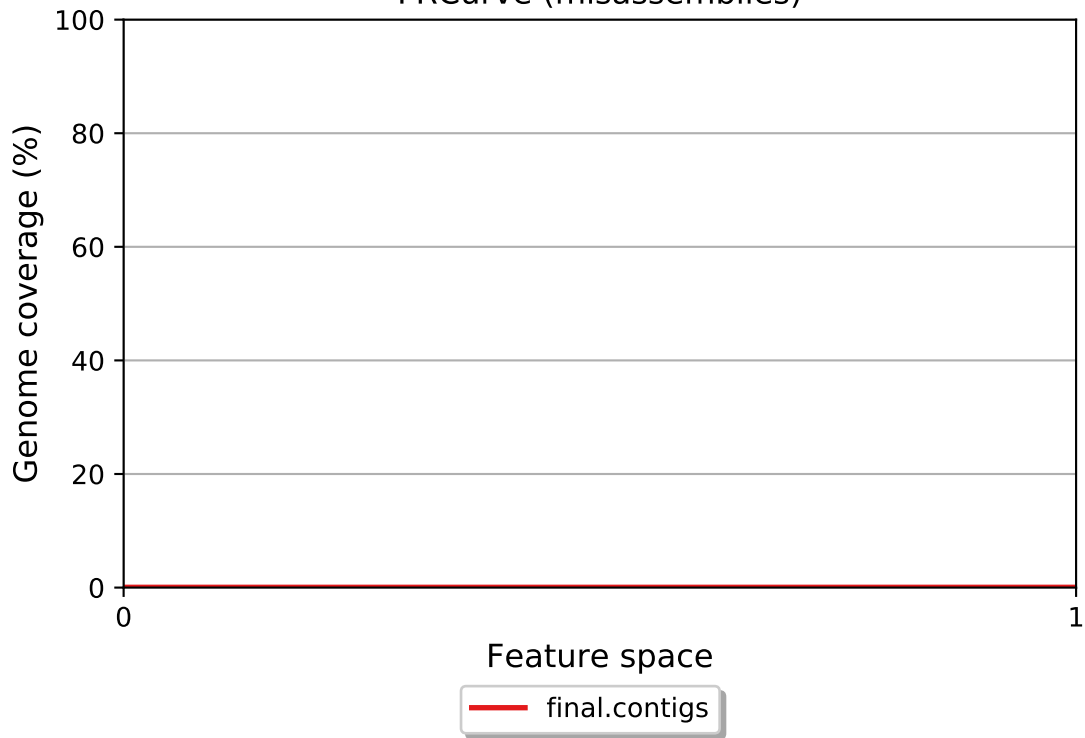


Misassemblies

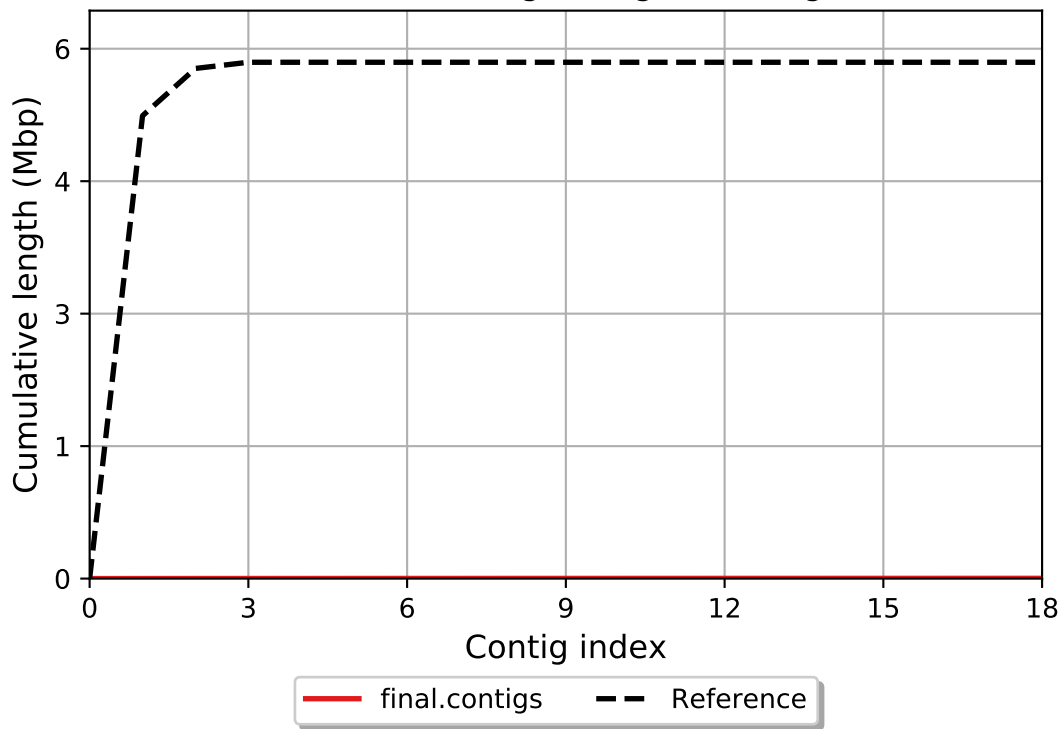


interspecies translocations

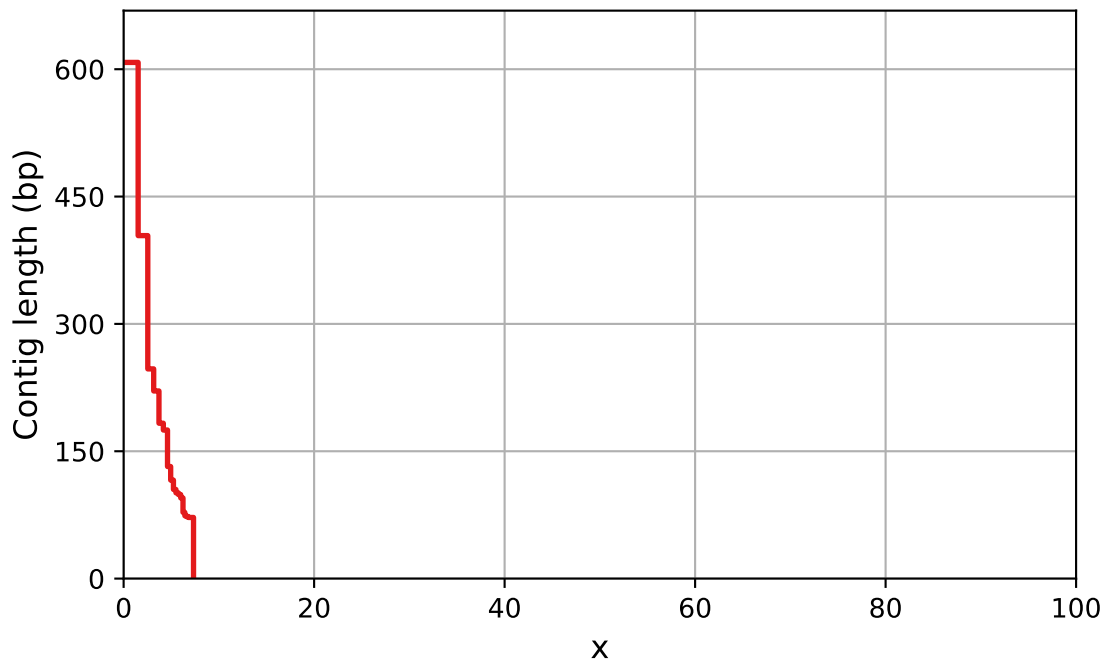
FRCurve (misassemblies)



Cumulative length (aligned contigs)

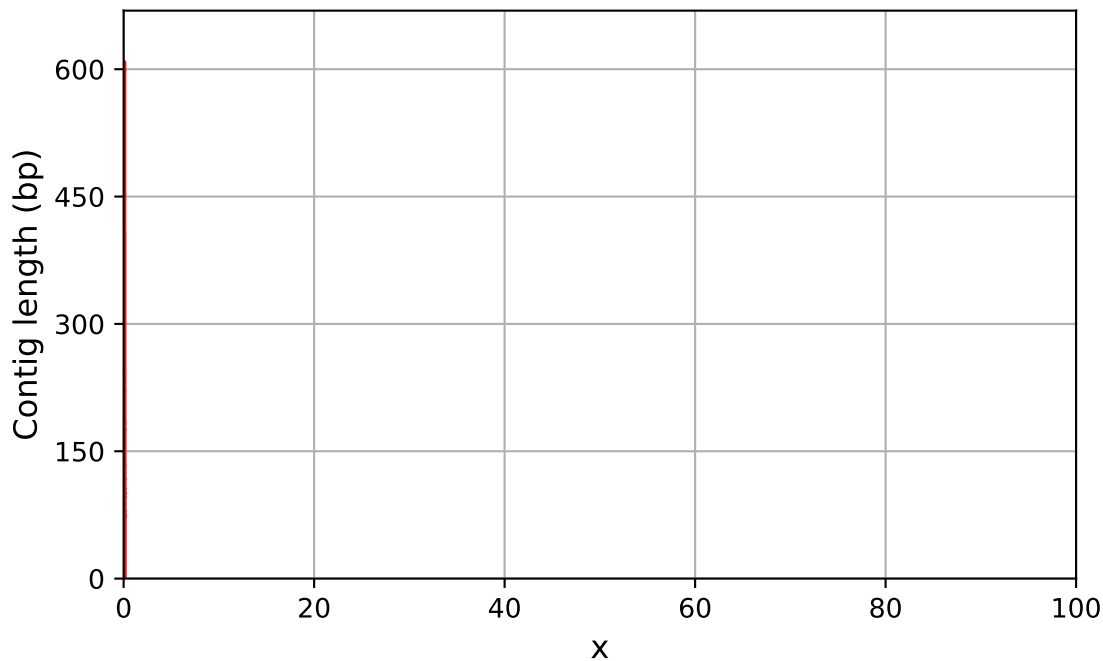


NAx



final.contigs

NGAx



— final.contigs