

Report

	final.contigs
# contigs (>= 1000 bp)	16
# contigs (>= 5000 bp)	2
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	41831
Total length (>= 5000 bp)	16112
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	31
Largest contig	8796
Total length	52527
Reference length	3576081
GC (%)	55.74
Reference GC (%)	51.82
N50	2643
N75	1096
L50	6
L75	14
# 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	2
# unaligned contigs	2 + 18 part
Unaligned length	40252
Genome fraction (%)	0.170
Duplication ratio	2.017
# N's per 100 kbp	0.00
# mismatches per 100 kbp	3844.26
# indels per 100 kbp	98.57
Largest alignment	2013
Total aligned length	7691
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	15
# possible misassemblies	18
# local misassemblies	1
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# mismatches	234
# indels	6
# indels (<= 5 bp)	5
# indels (> 5 bp)	1
Indels length	14

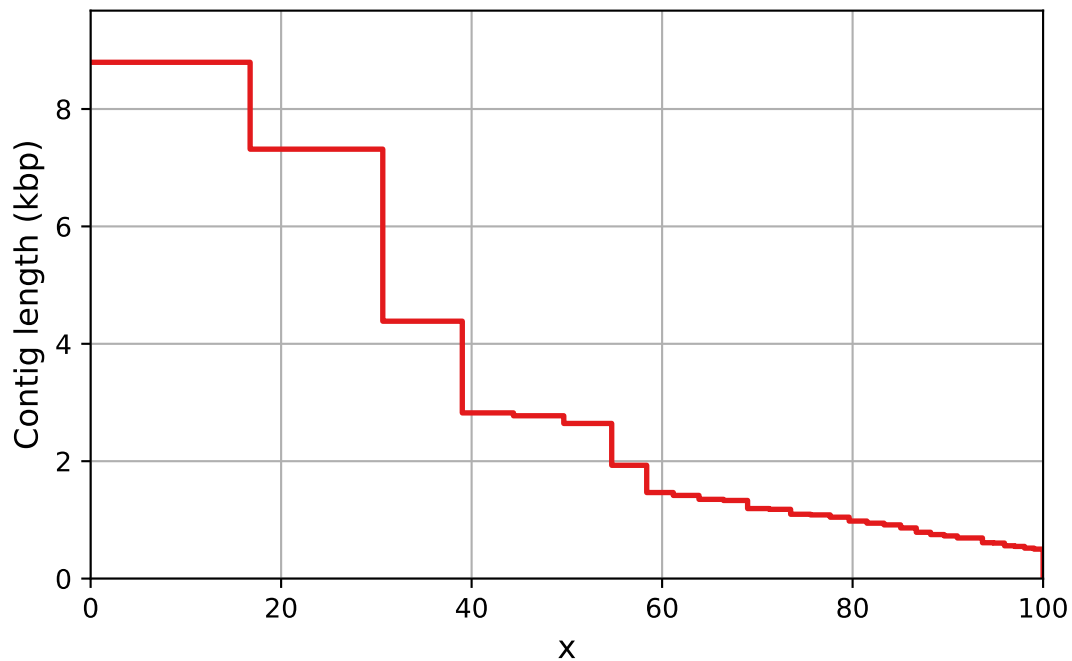
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	final.contigs
# fully unaligned contigs	2
Fully unaligned length	1859
# partially unaligned contigs	18
Partially unaligned length	38393
# N's	0

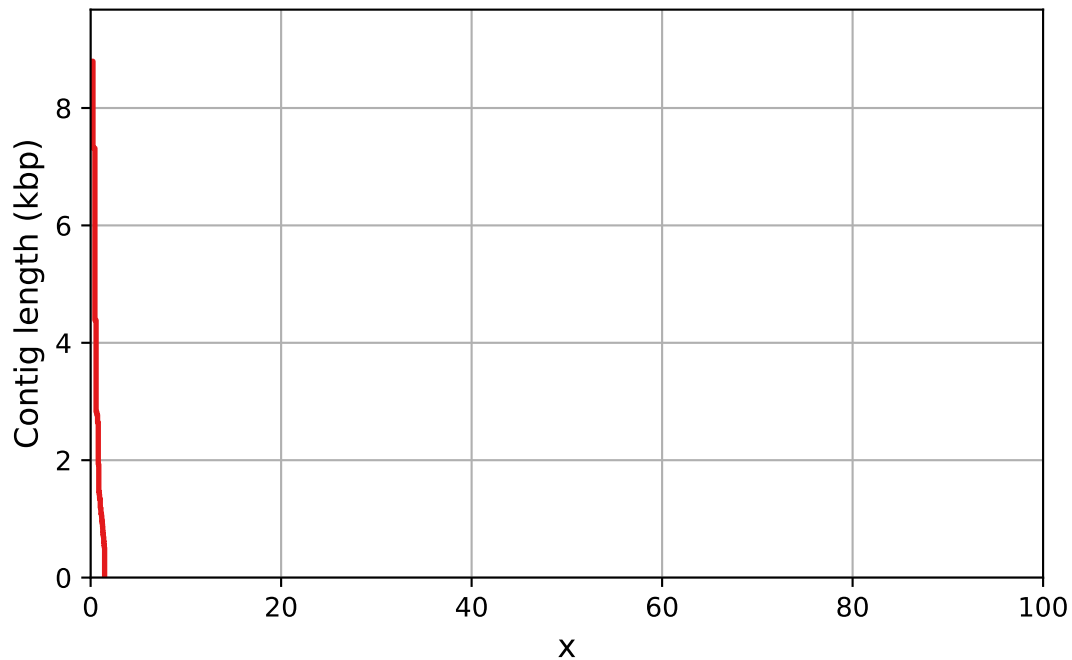
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

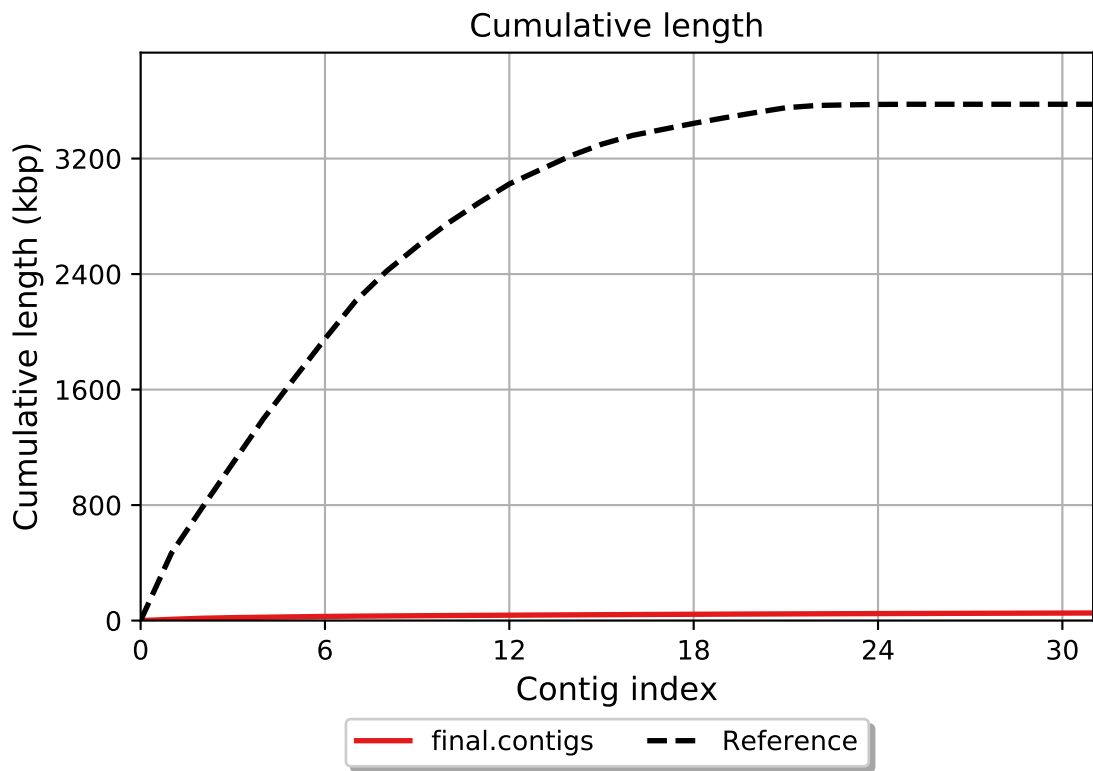


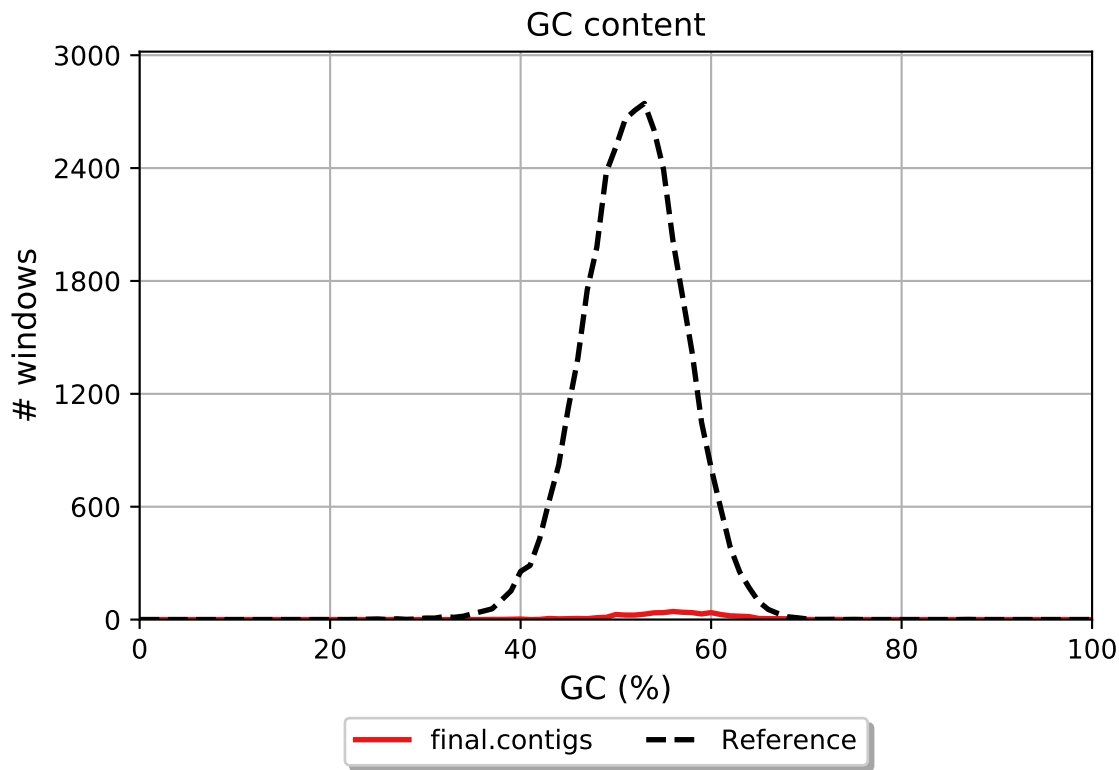
— final.contigs

NGx

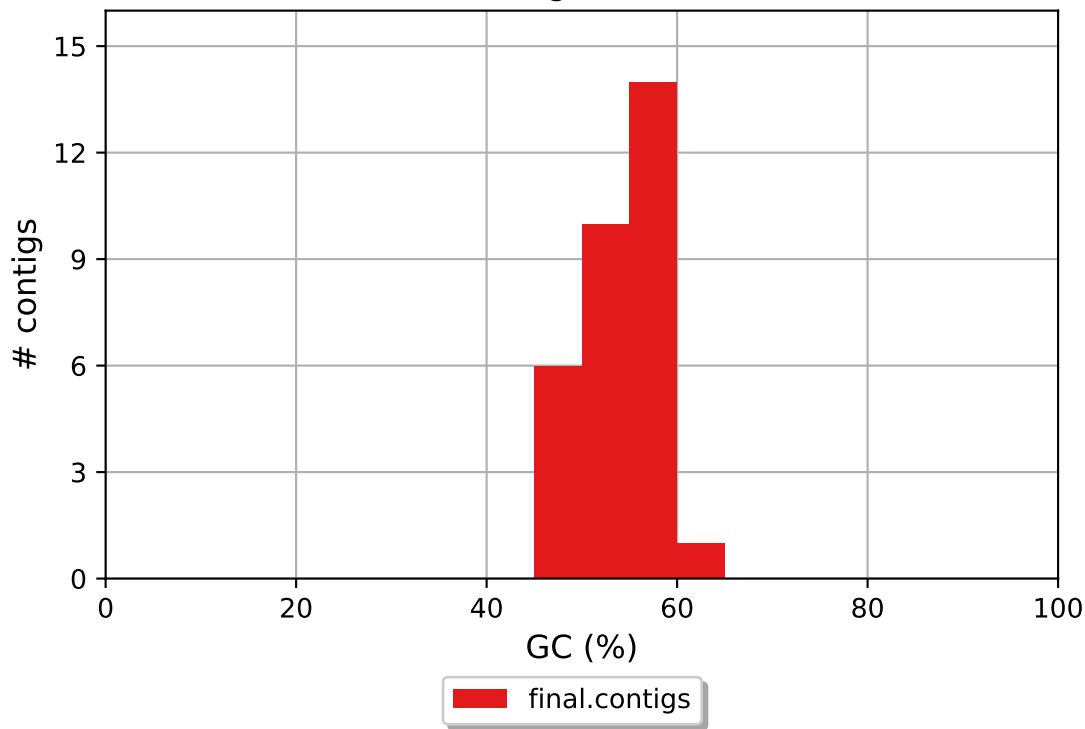


— final.contigs





final.contigs GC content

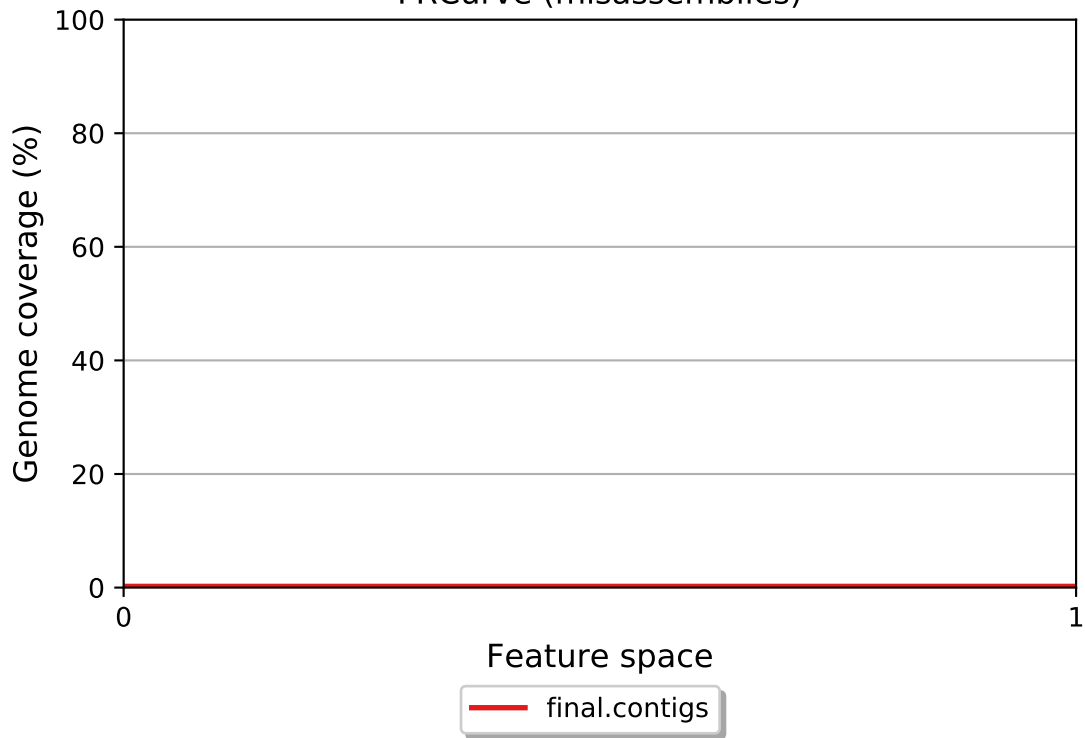


Misassemblies

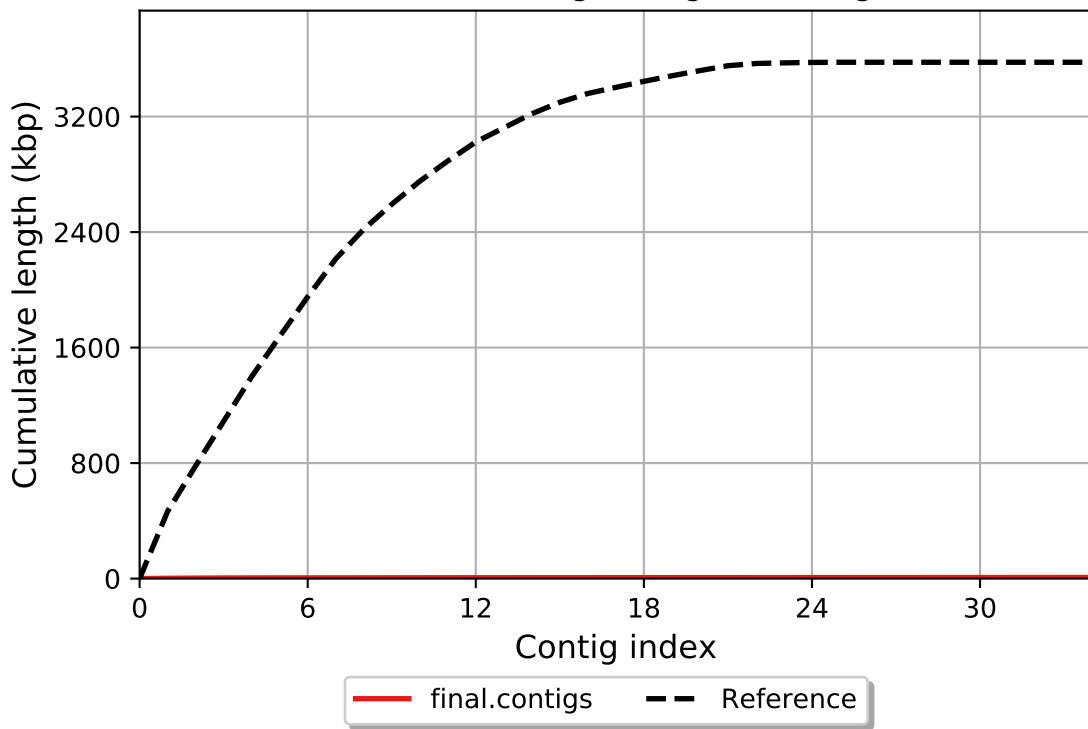


interspecies translocations

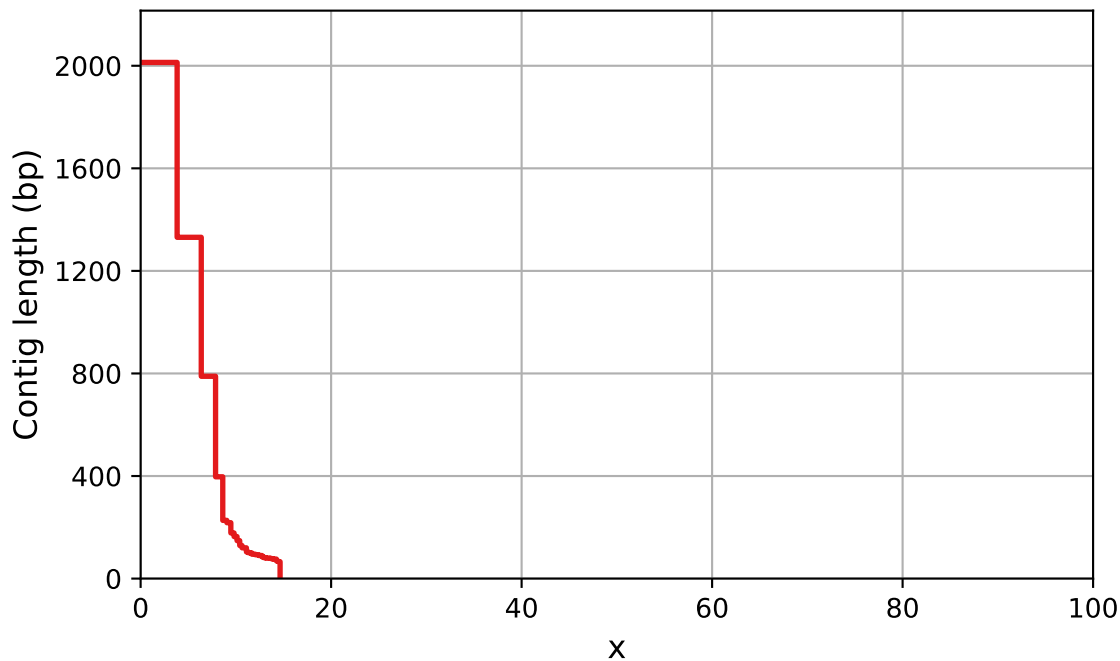
FRCurve (misassemblies)



Cumulative length (aligned contigs)

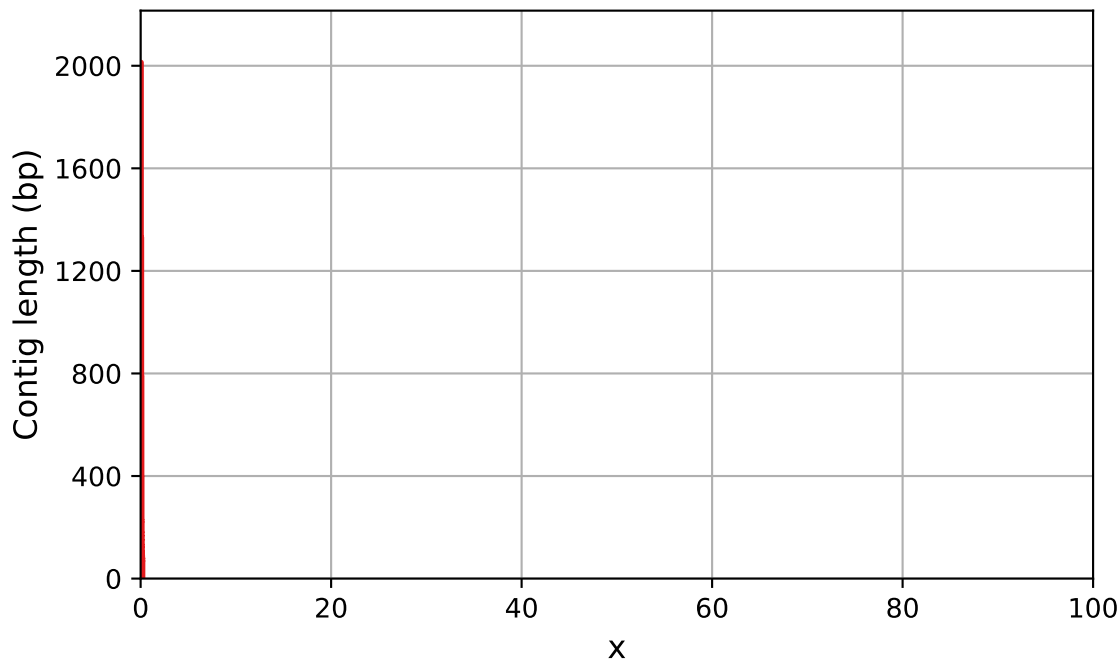


NAx



— final.contigs

NGAx



— final.contigs