

Report

	final.contigs
# contigs (>= 1000 bp)	6
# contigs (>= 5000 bp)	2
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	29131
Total length (>= 5000 bp)	23126
Total length (>= 10000 bp)	16005
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	18
Largest contig	16005
Total length	37114
Reference length	5846582
GC (%)	51.07
Reference GC (%)	46.79
N50	7121
N75	1193
L50	2
L75	5
# 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	4 + 6 part
Unaligned length	30733
Genome fraction (%)	0.041
Duplication ratio	2.648
# N's per 100 kbp	0.00
# mismatches per 100 kbp	5726.14
# indels per 100 kbp	41.49
Largest alignment	744
Total aligned length	2815
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	5
# possible misassemblies	5
# local misassemblies	1
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# mismatches	138
# indels	1
# indels (<= 5 bp)	1
# indels (> 5 bp)	0
Indels length	2

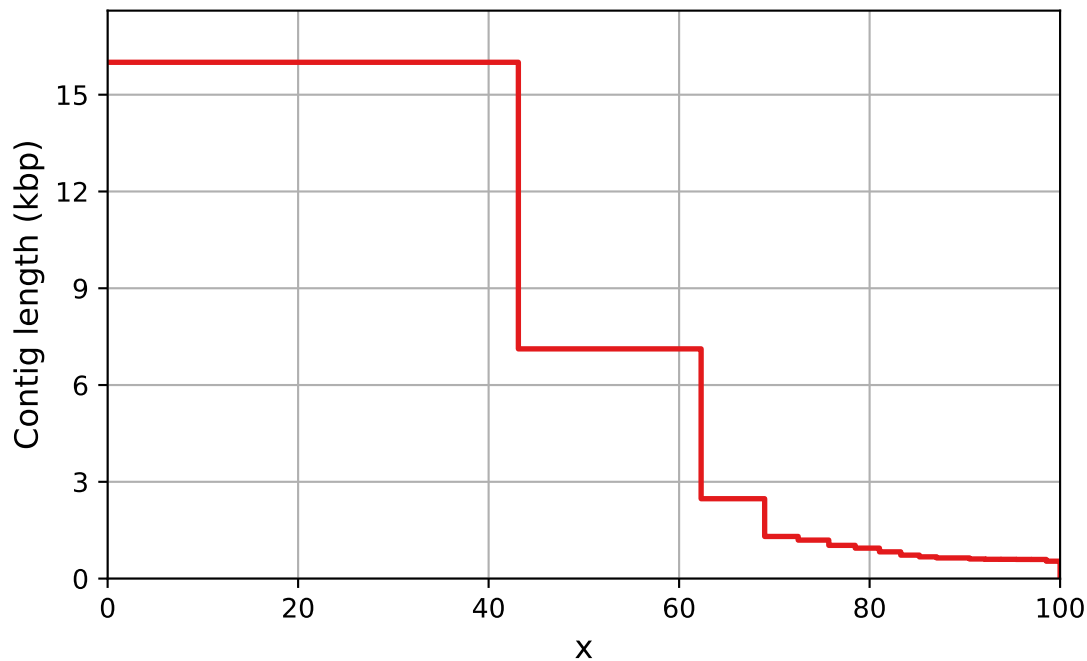
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	final.contigs
# fully unaligned contigs	4
Fully unaligned length	2808
# partially unaligned contigs	6
Partially unaligned length	27925
# N's	0

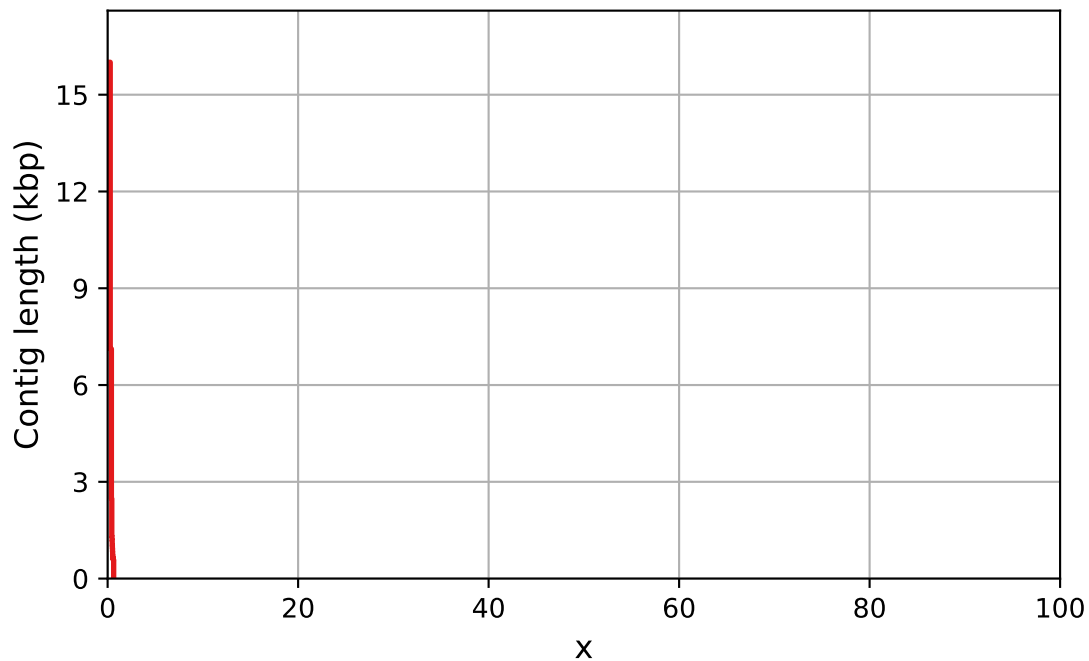
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



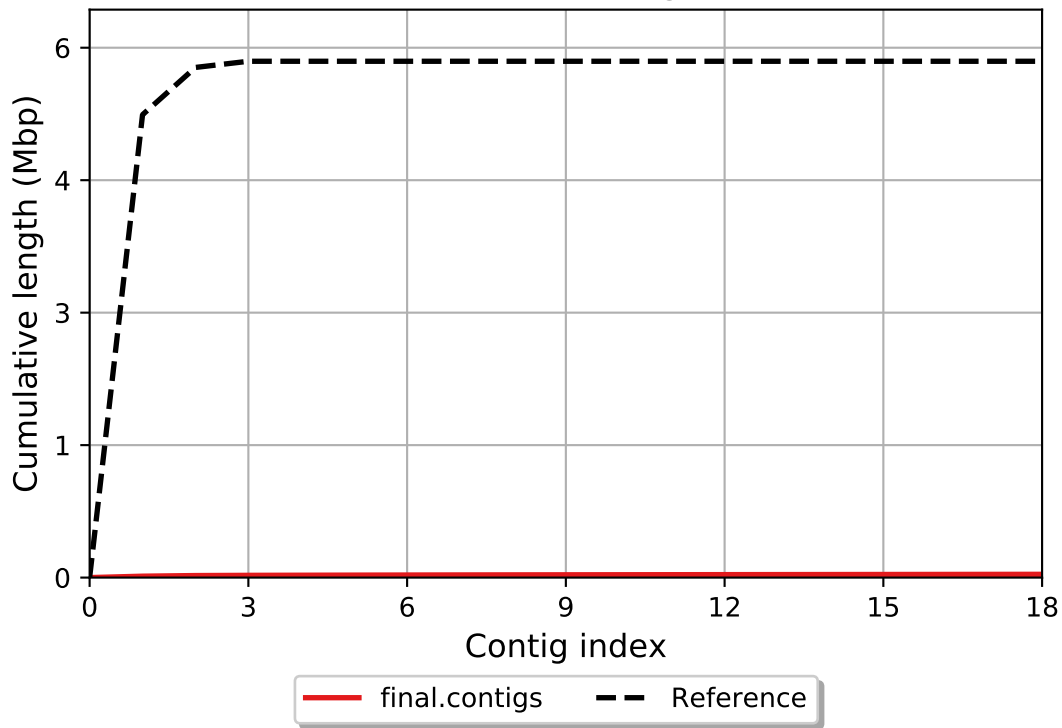
— final.contigs

NGx

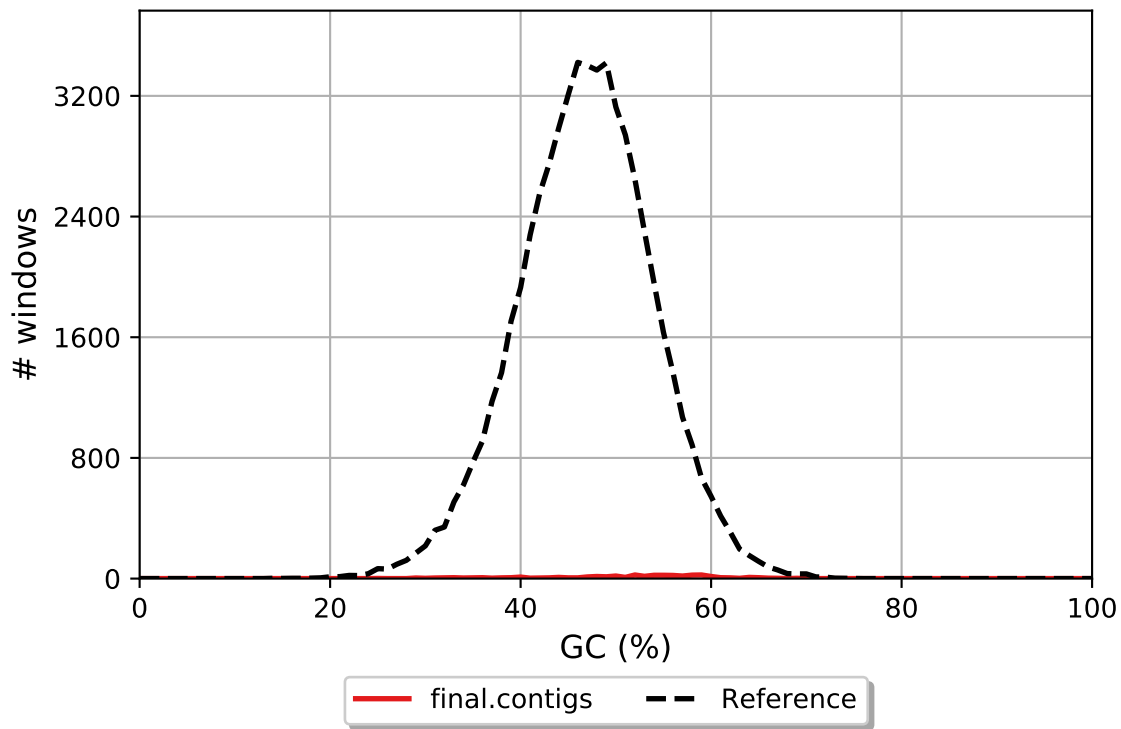


— final.contigs

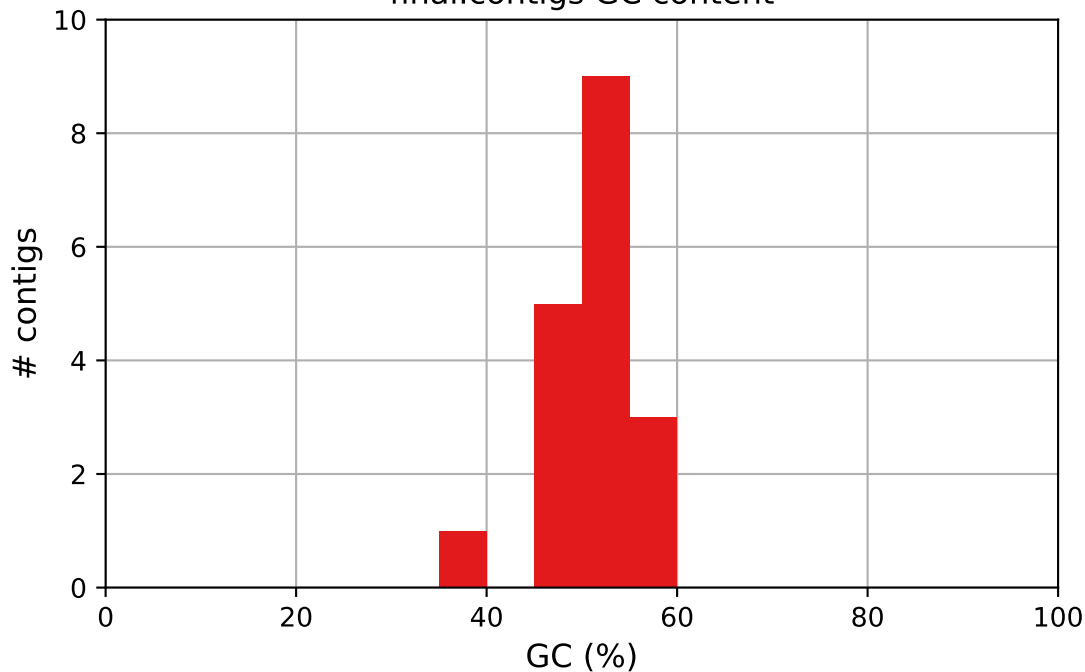
Cumulative length



GC content

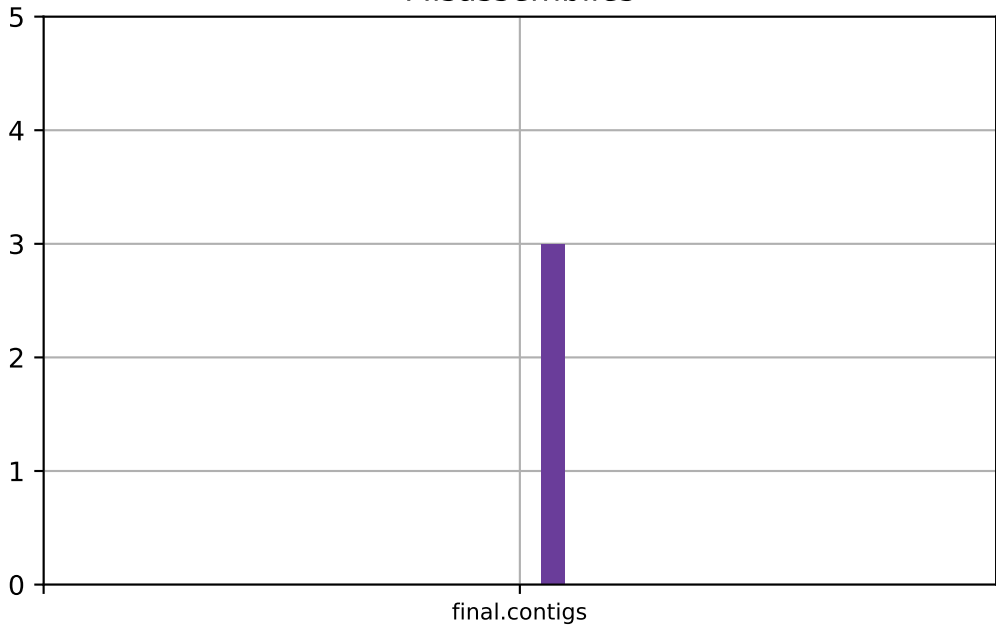


final.contigs GC content



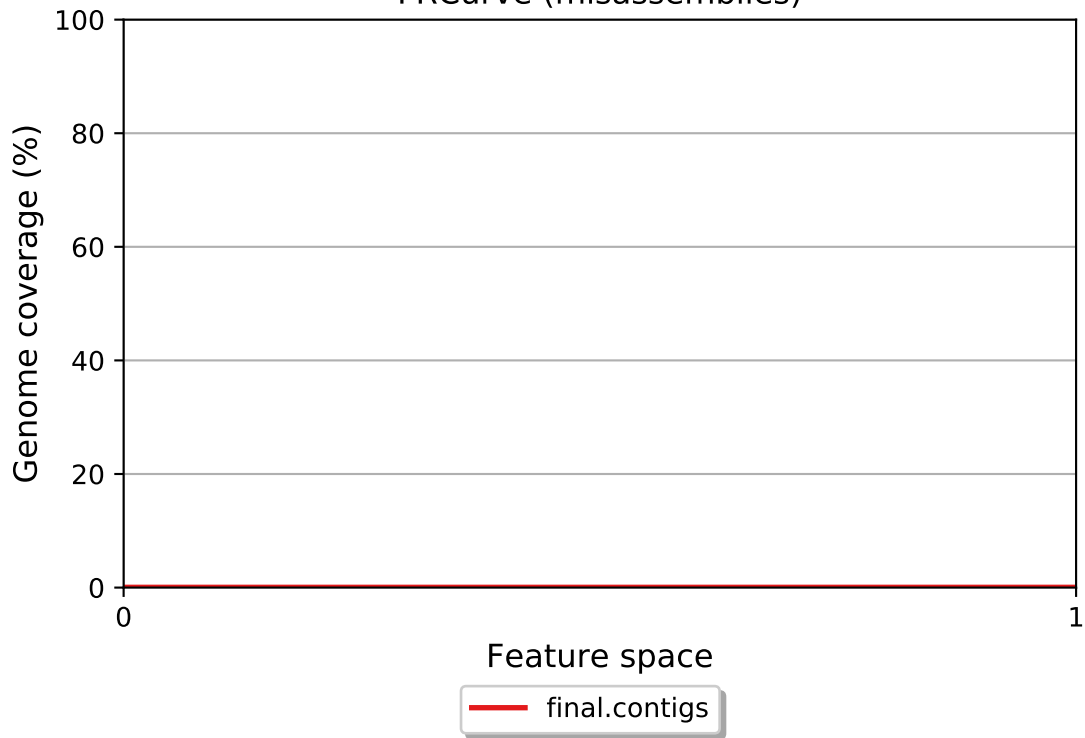
final.contigs

Misassemblies

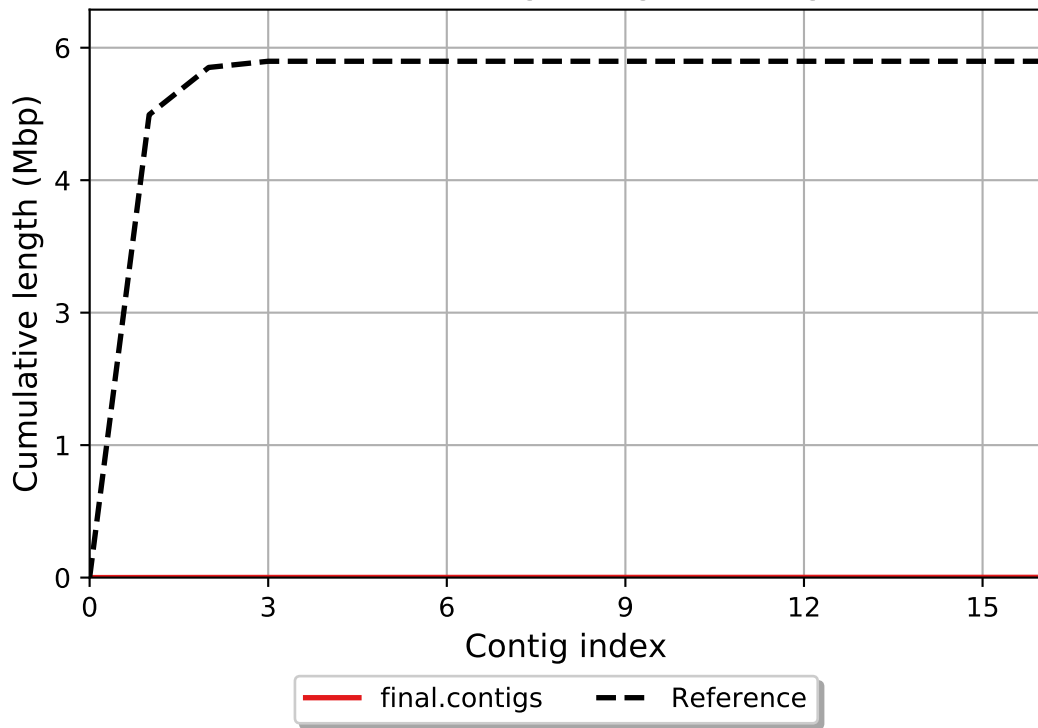


interspecies translocations

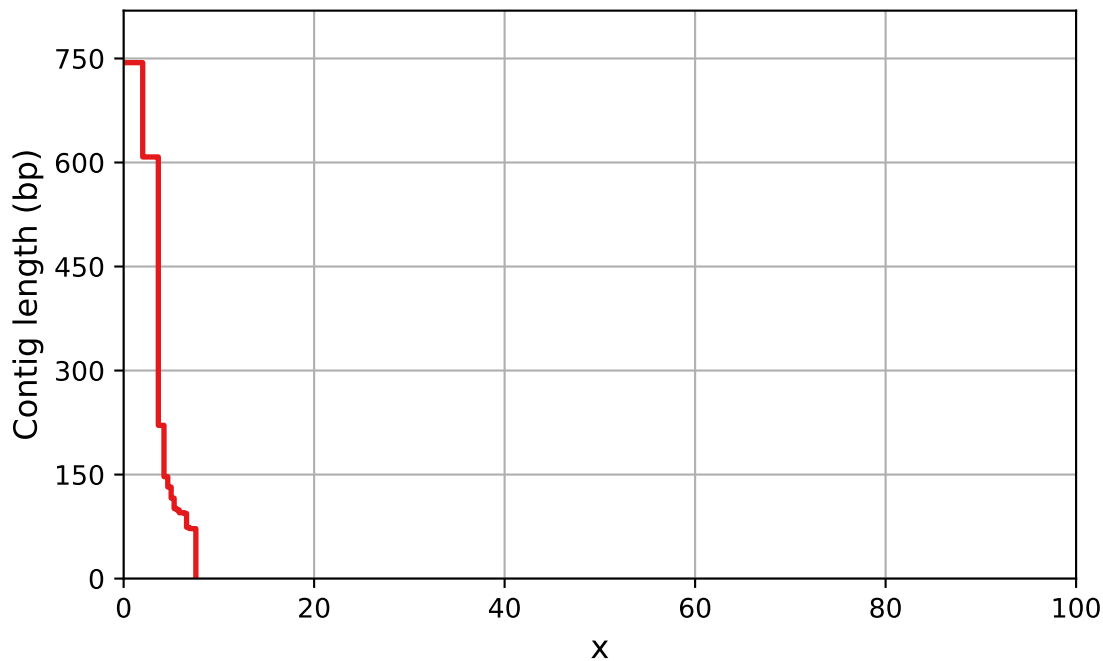
FRCurve (misassemblies)



Cumulative length (aligned contigs)

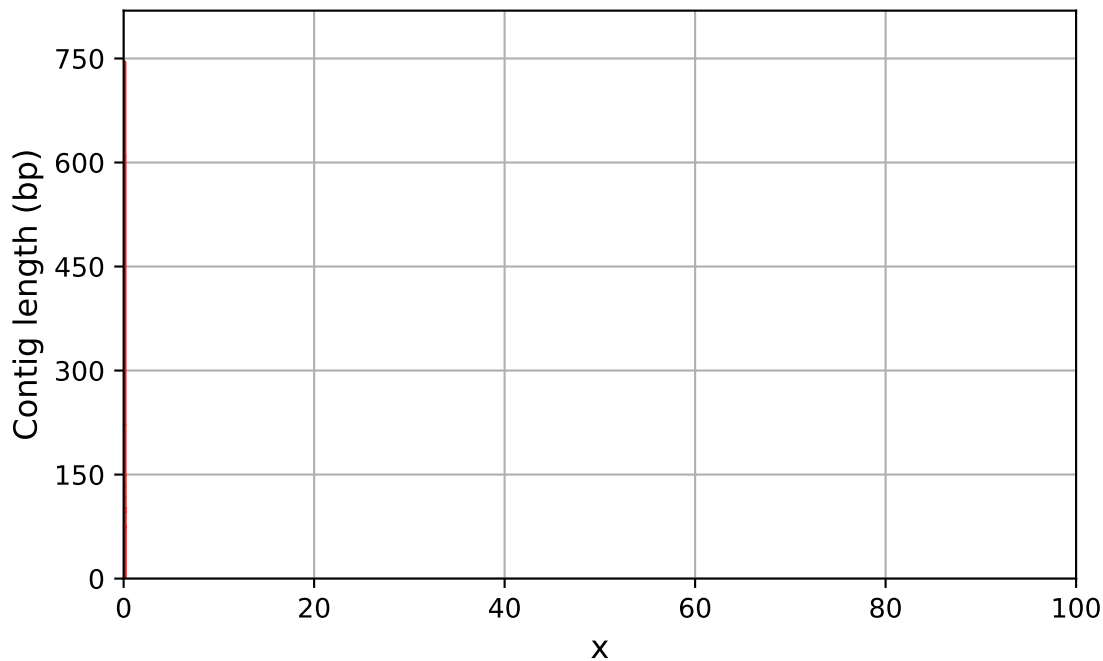


NAx



— final.contigs

NGAx



final.contigs