

Report

	final.contigs
# contigs (>= 1000 bp)	11
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	28186
Total length (>= 5000 bp)	5625
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	15
Largest contig	5625
Total length	30838
Reference length	3712900
GC (%)	36.67
Reference GC (%)	31.25
N50	3043
N75	1805
L50	4
L75	7
# 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 + 9 part
Unaligned length	27433
Genome fraction (%)	0.054
Duplication ratio	1.707
# N's per 100 kbp	0.00
# mismatches per 100 kbp	3909.77
# indels per 100 kbp	50.13
Largest alignment	619
Total aligned length	2243
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	6
# possible misassemblies	10
# local misassemblies	1
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# mismatches	78
# indels	1
# indels (<= 5 bp)	1
# indels (> 5 bp)	0
Indels length	2

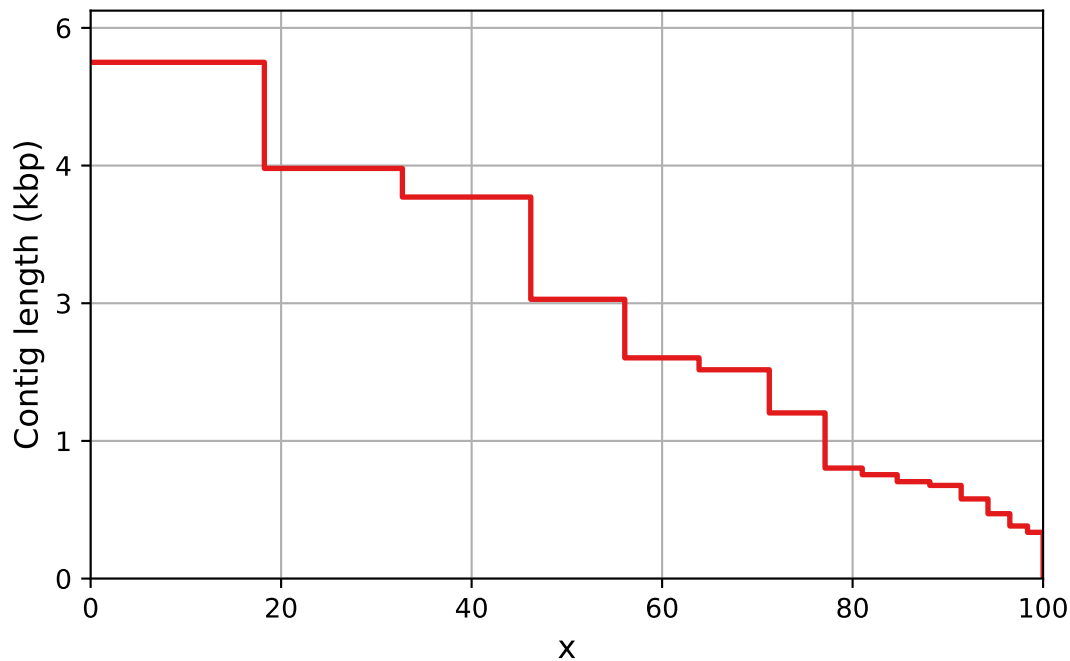
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	final.contigs
# fully unaligned contigs	3
Fully unaligned length	3965
# partially unaligned contigs	9
Partially unaligned length	23468
# N's	0

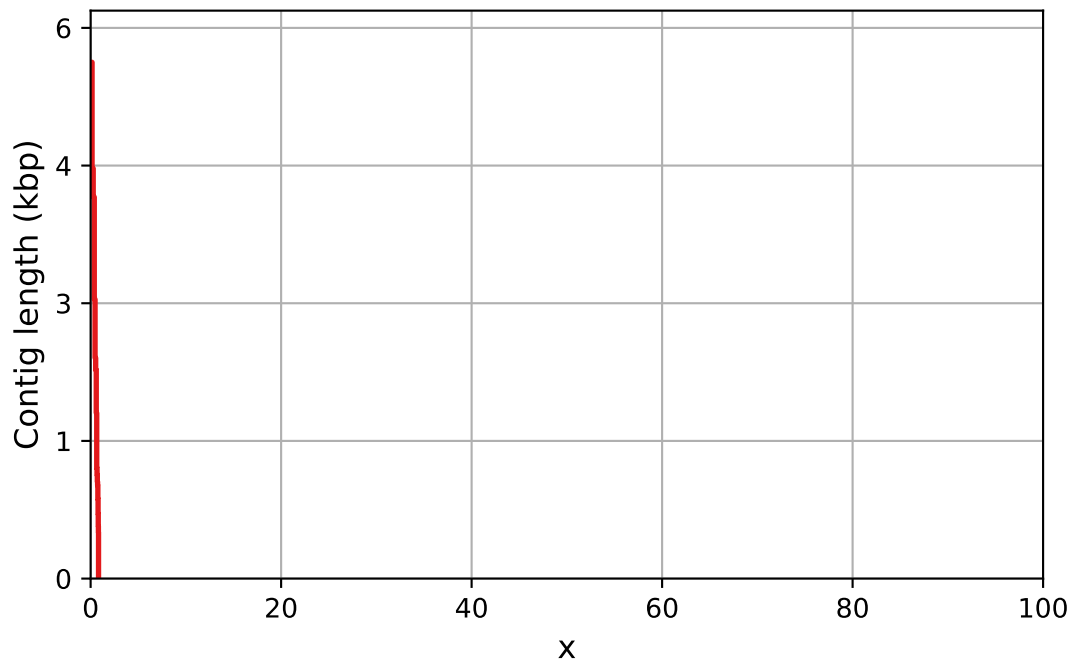
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

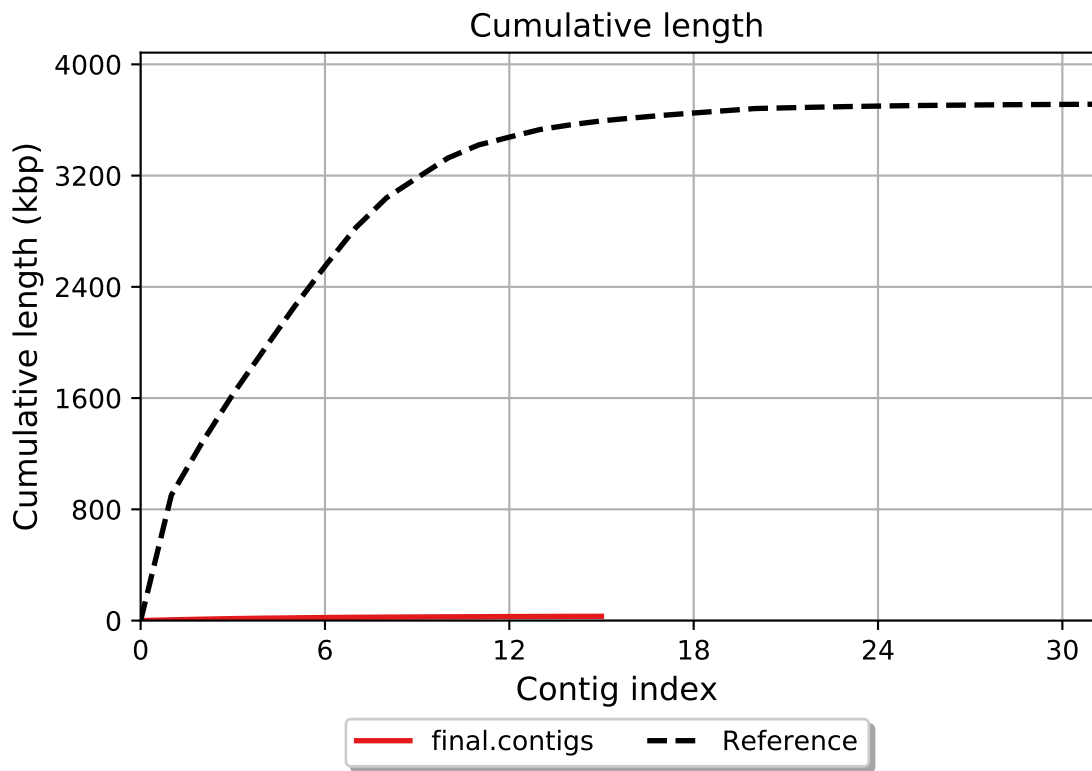


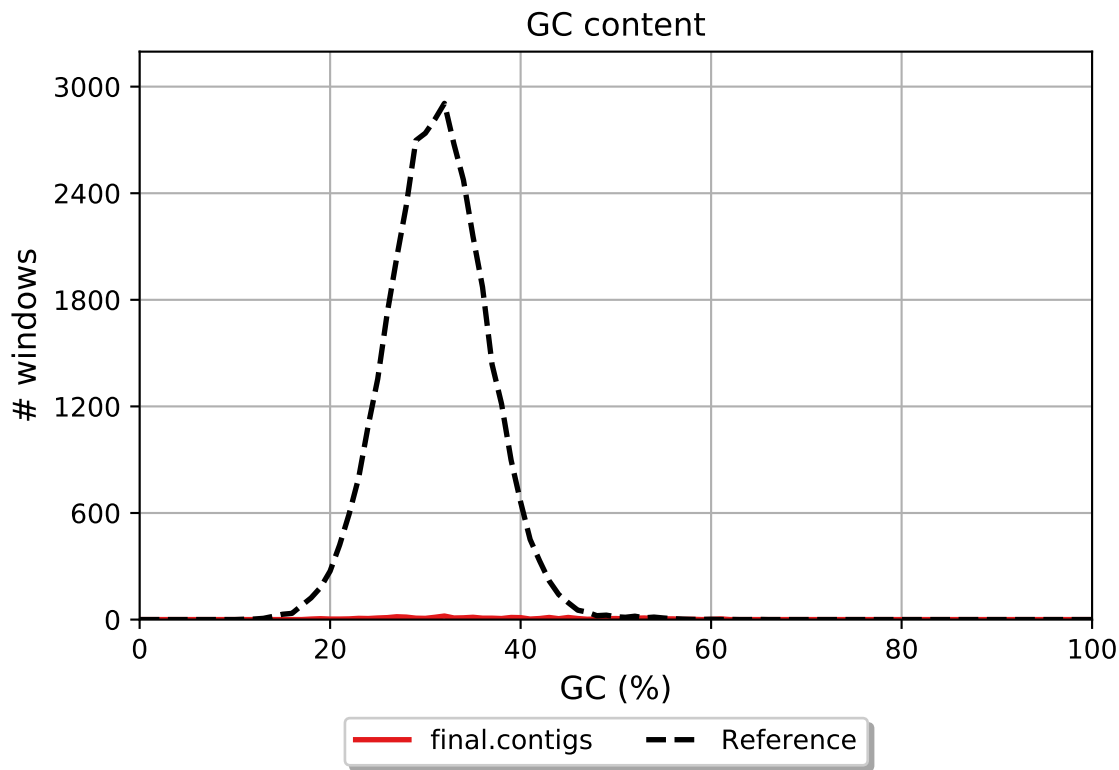
— final.contigs

NGx

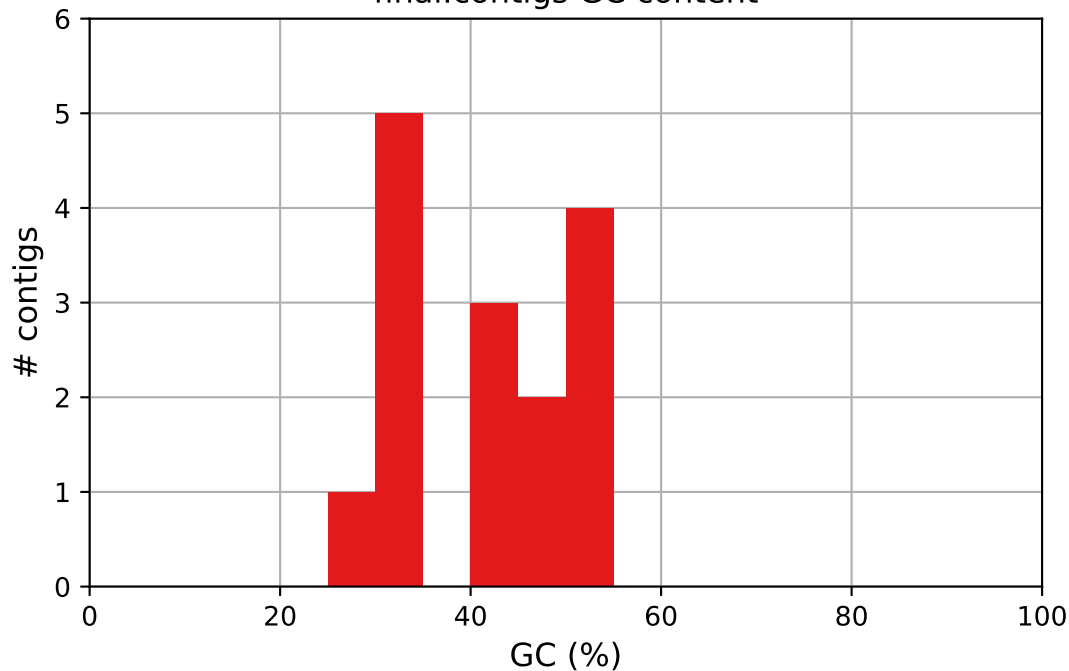


— final.contigs



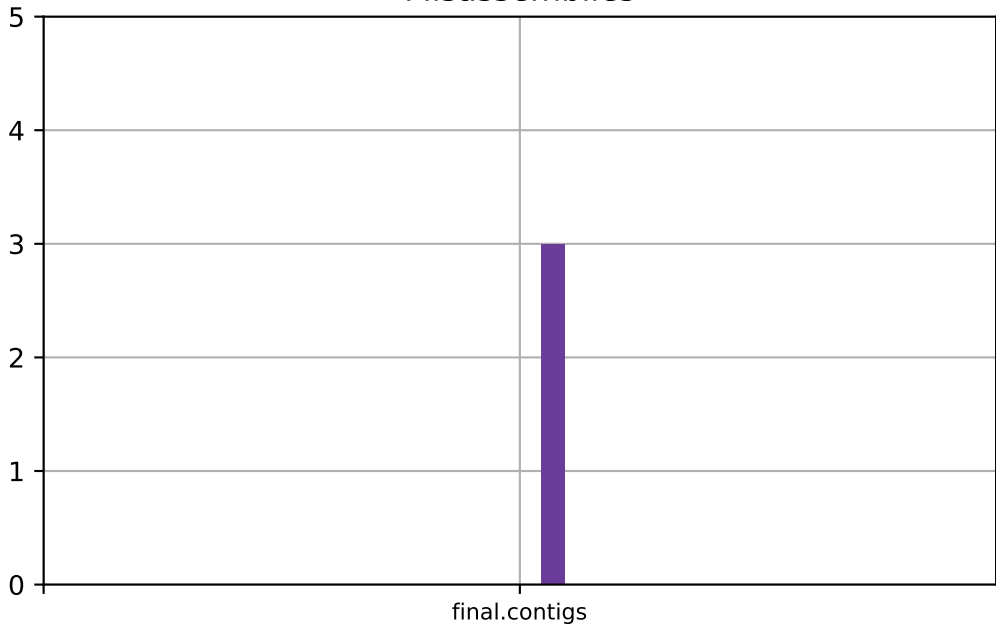


final.contigs GC content



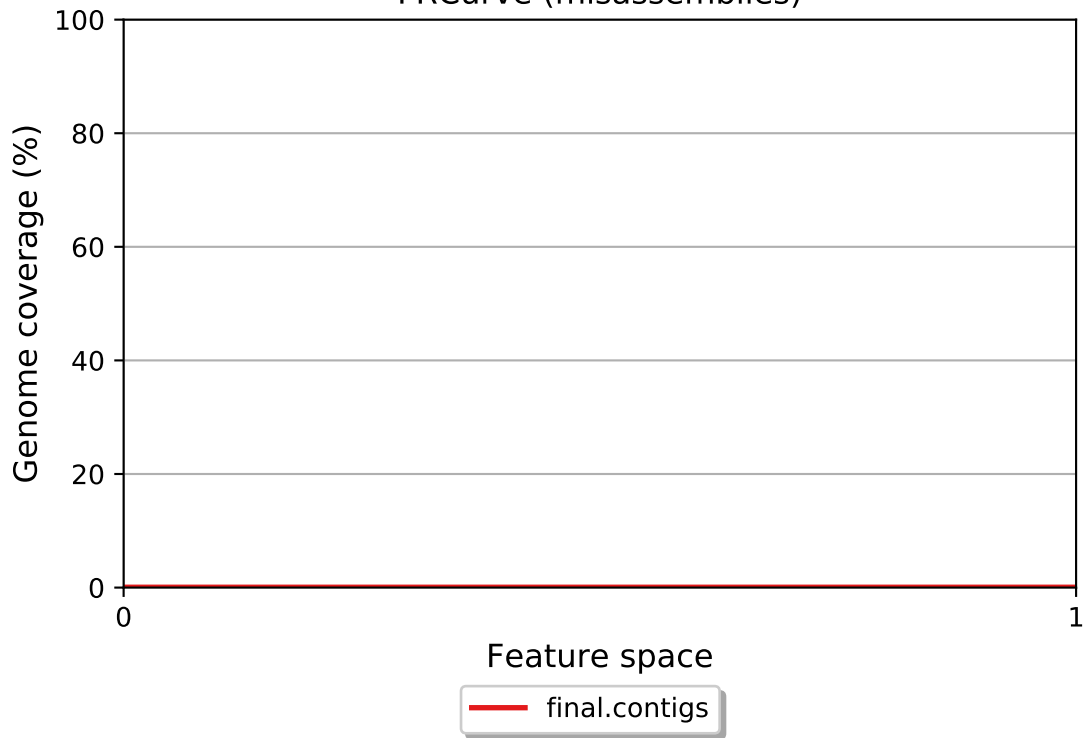
final.contigs

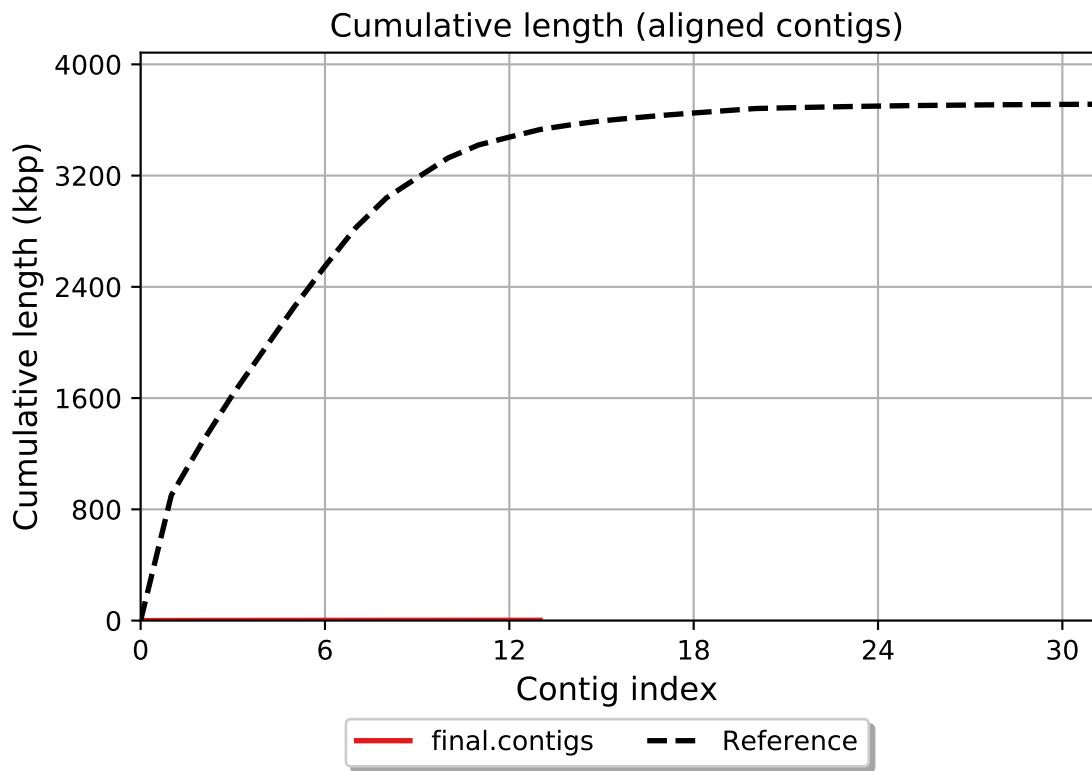
Misassemblies



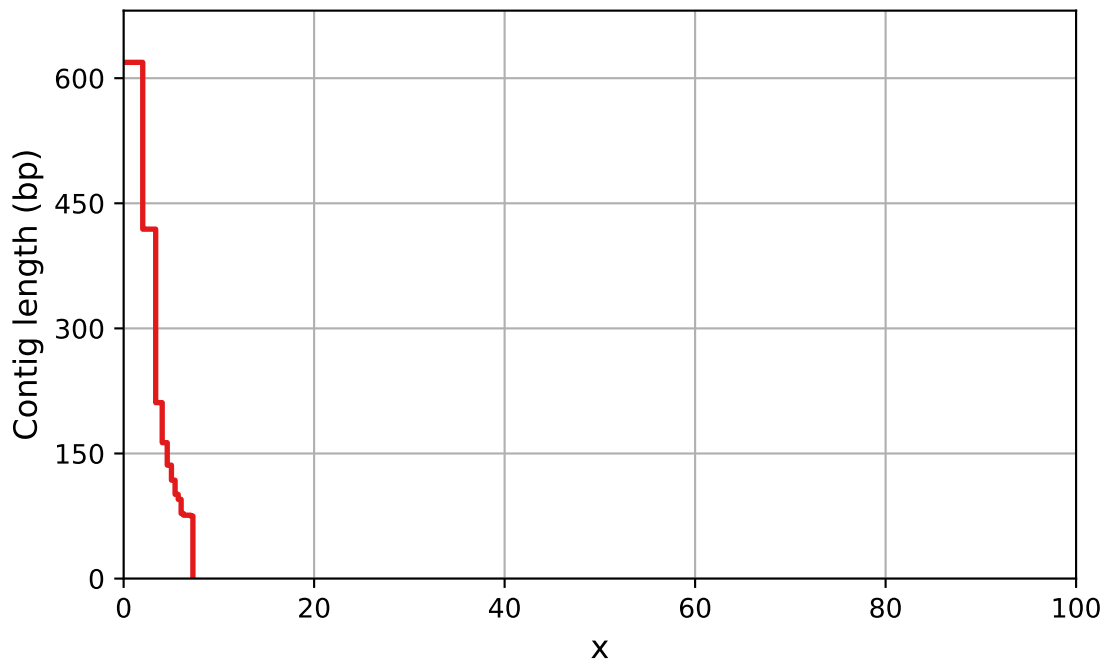
interspecies translocations

FRCurve (misassemblies)



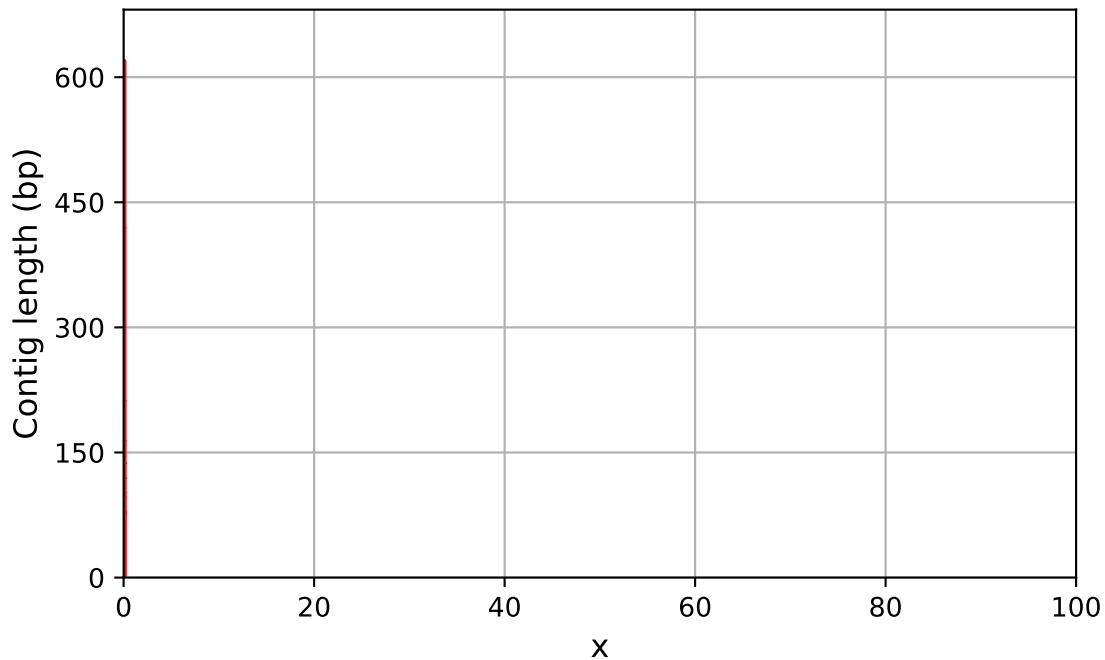


NAx



— final.contigs

NGAx



— final.contigs