

Report

	final.contigs
# contigs (>= 1000 bp)	14
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	43559
Total length (>= 5000 bp)	12656
Total length (>= 10000 bp)	12656
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	21
Largest contig	12656
Total length	48451
Reference length	3712900
GC (%)	36.61
Reference GC (%)	31.25
N50	4157
N75	1924
L50	4
L75	9
# 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	3 + 15 part
Unaligned length	43938
Genome fraction (%)	0.059
Duplication ratio	2.046
# N's per 100 kbp	0.00
# mismatches per 100 kbp	4986.40
# indels per 100 kbp	0.00
Largest alignment	619
Total aligned length	3505
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	10
# possible misassemblies	16
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# mismatches	110
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

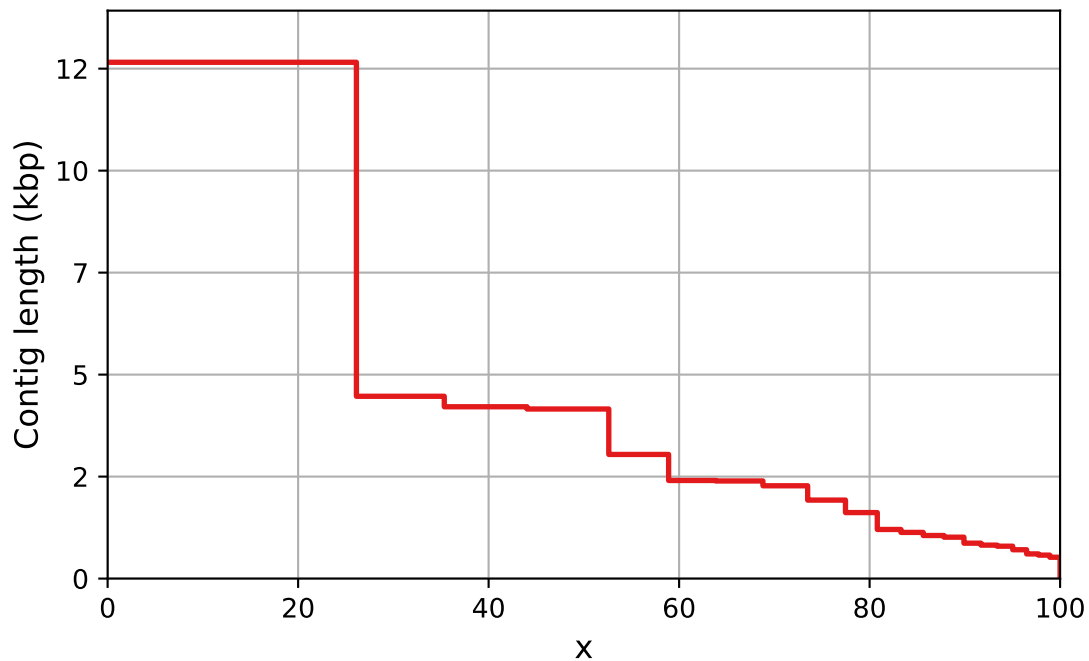
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	final.contigs
# fully unaligned contigs	3
Fully unaligned length	4036
# partially unaligned contigs	15
Partially unaligned length	39902
# N's	0

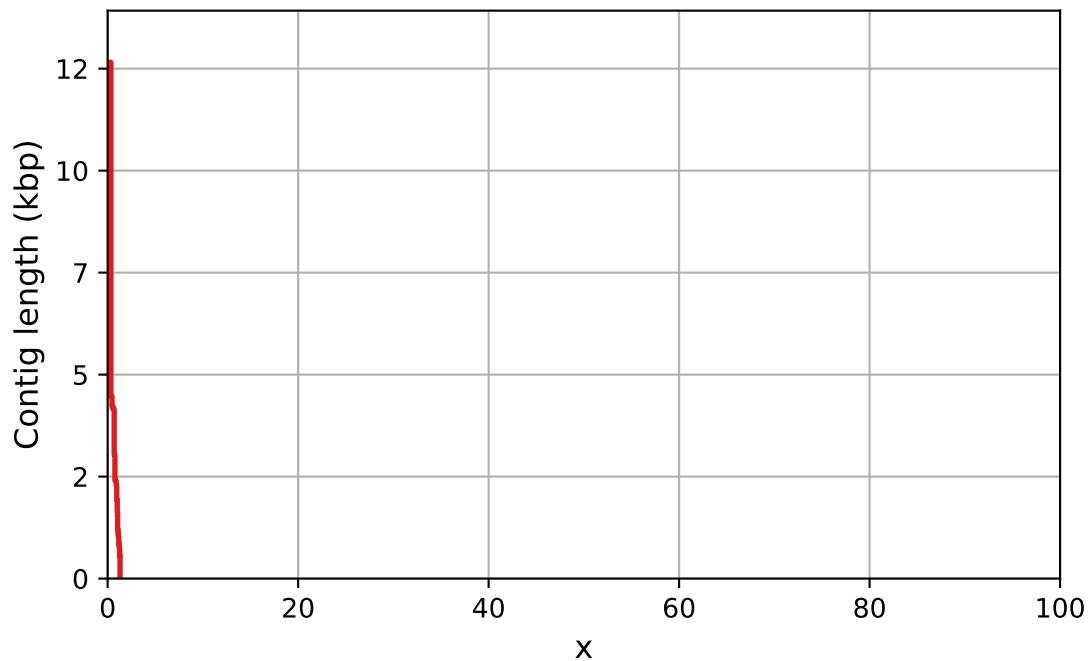
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

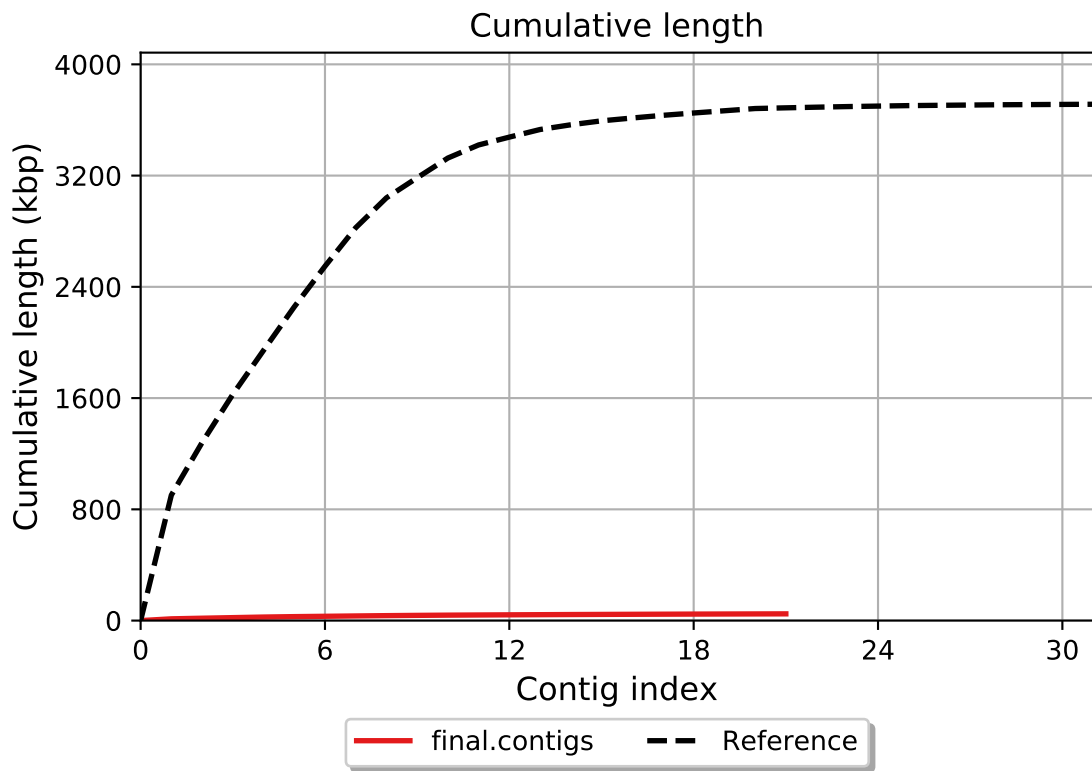


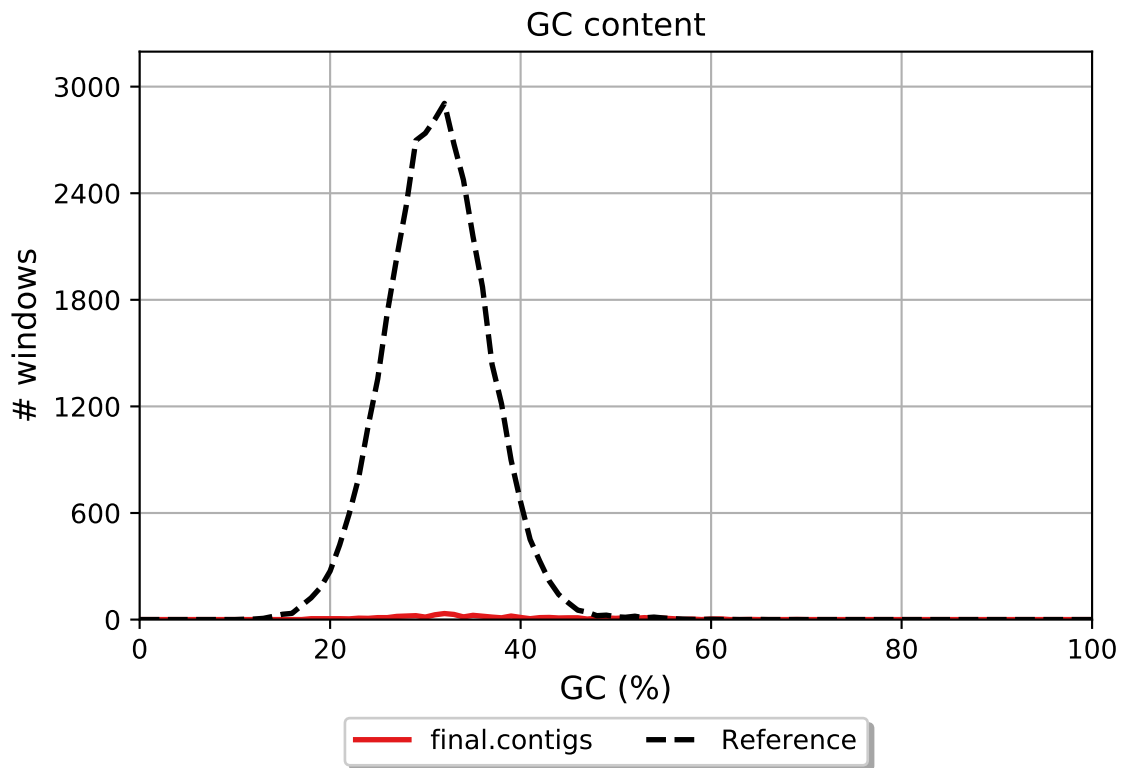
— final.contigs

NGx

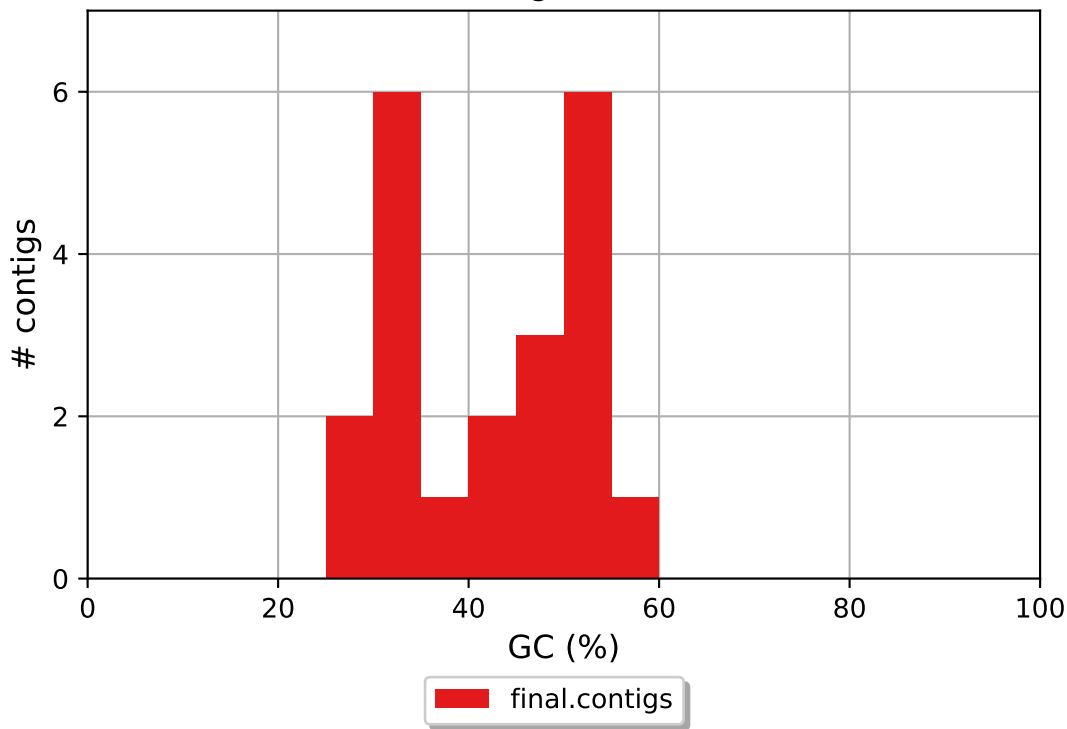


— final.contigs





final.contigs GC content

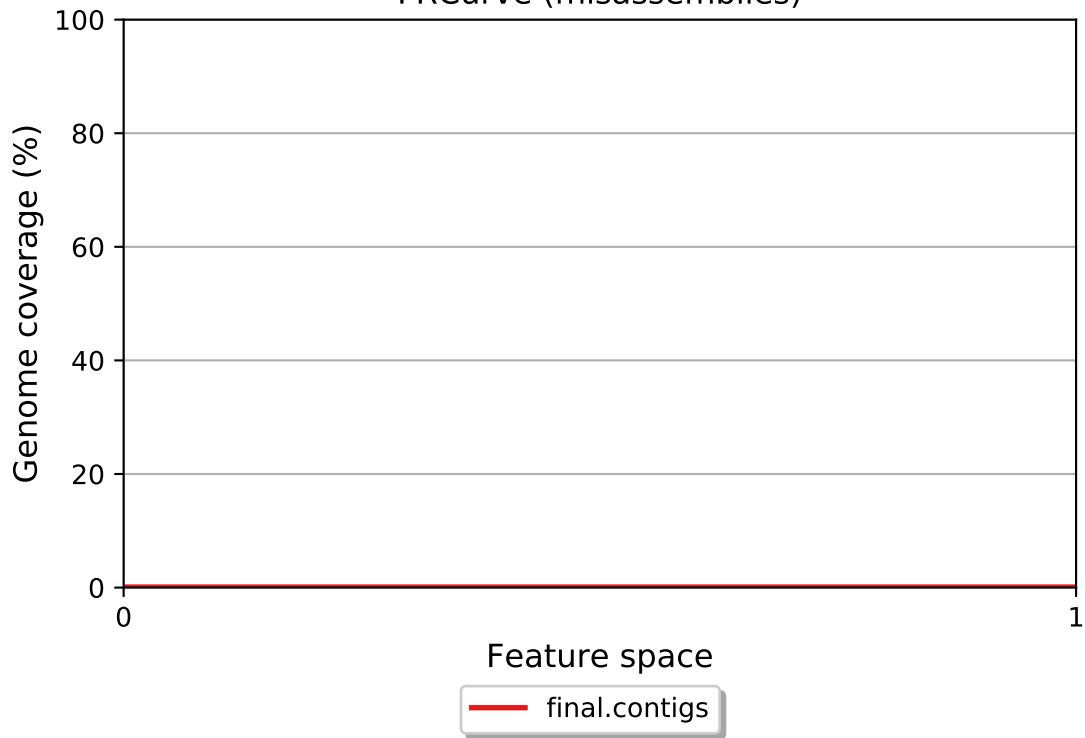


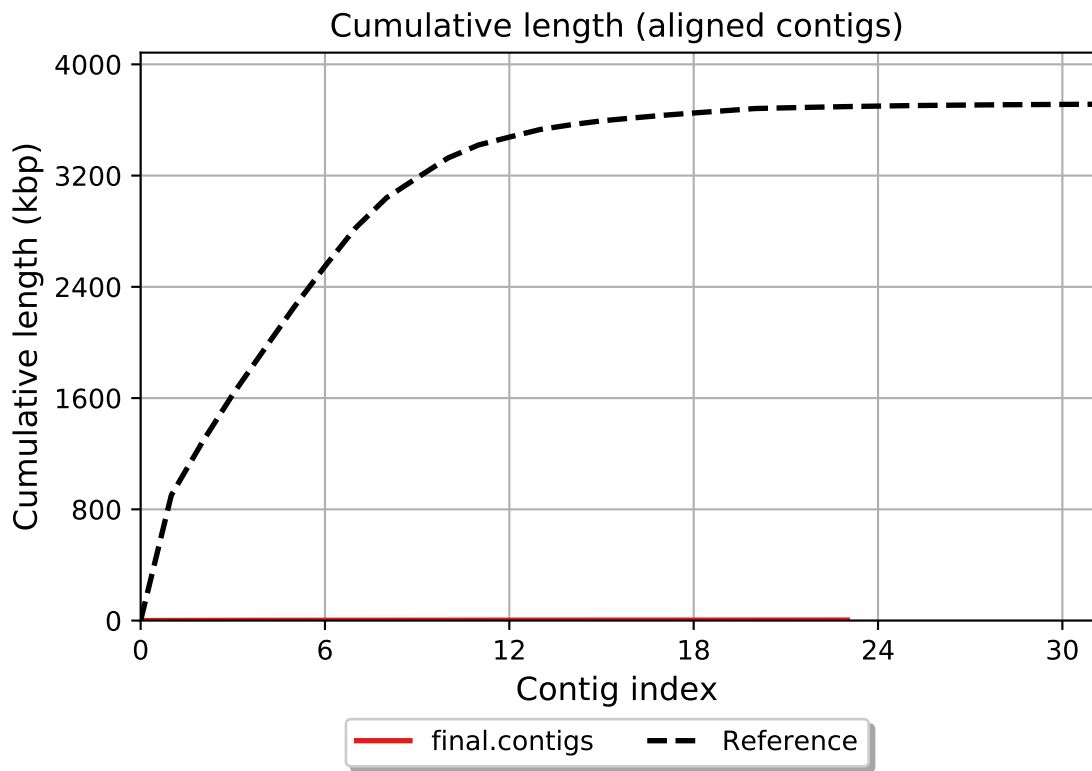
Misassemblies



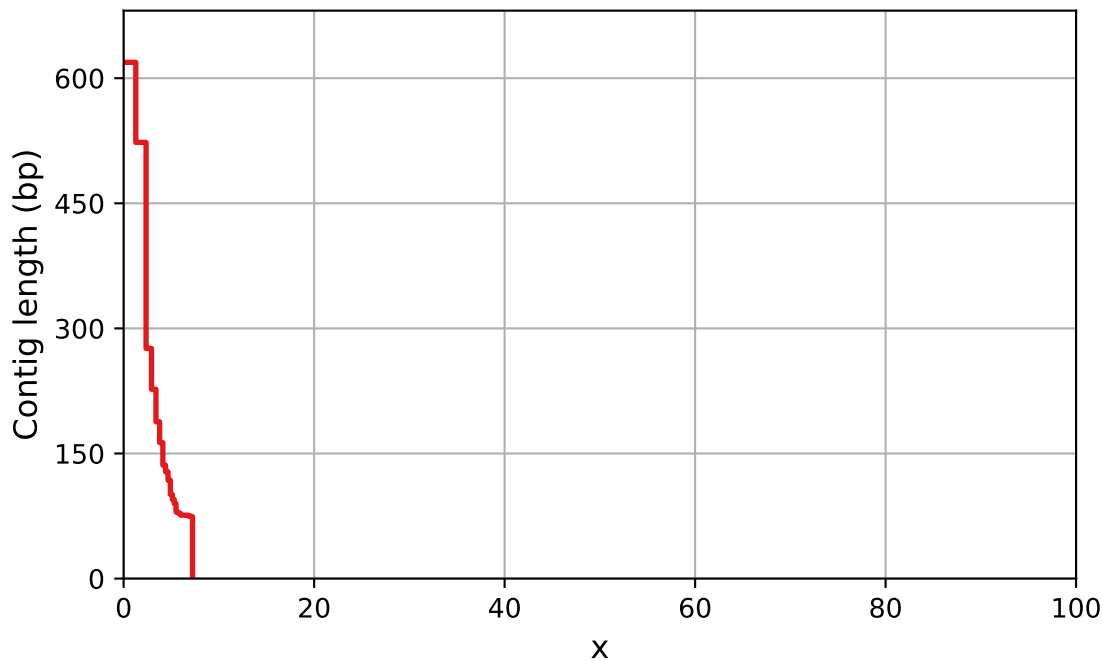
interspecies translocations

FRCurve (misassemblies)



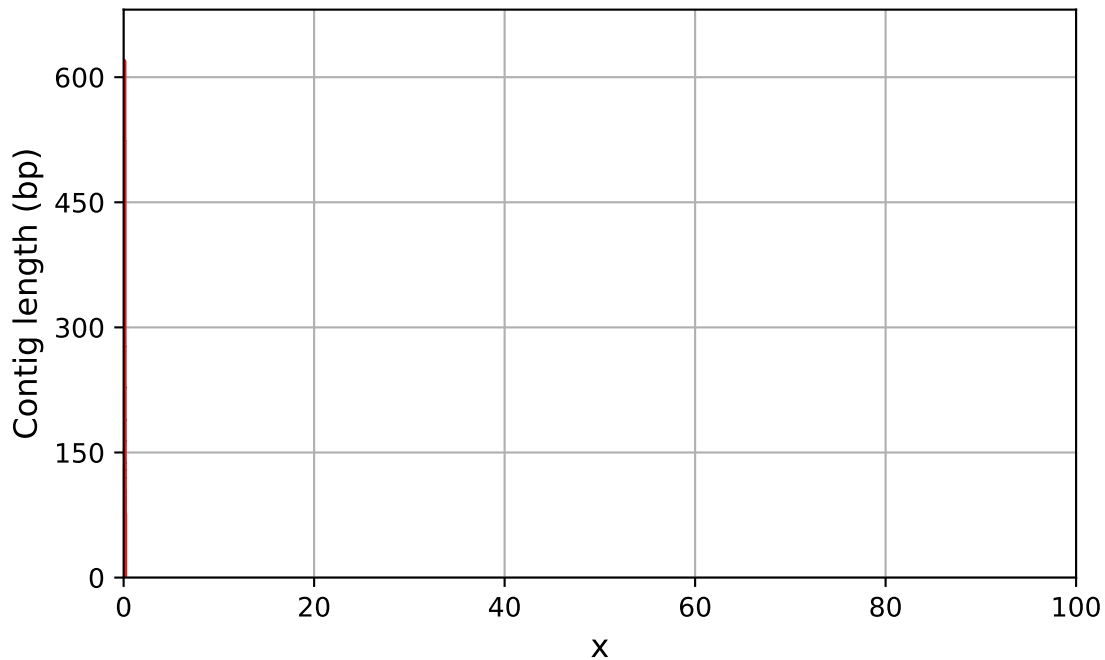


NAx



— final.contigs

NGAx



— final.contigs