

Report

	final.contigs
# contigs (>= 1000 bp)	22
# contigs (>= 5000 bp)	14
# contigs (>= 10000 bp)	11
# contigs (>= 25000 bp)	8
# contigs (>= 50000 bp)	5
Total length (>= 1000 bp)	937247
Total length (>= 5000 bp)	916507
Total length (>= 10000 bp)	893549
Total length (>= 25000 bp)	850849
Total length (>= 50000 bp)	736182
# contigs	31
Largest contig	255300
Total length	943312
Reference length	3442017
GC (%)	59.59
Reference GC (%)	58.88
N50	124997
N75	74884
L50	3
L75	5
# 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	6
# unaligned contigs	4 + 21 part
Unaligned length	935758
Genome fraction (%)	0.108
Duplication ratio	2.028
# N's per 100 kbp	0.00
# mismatches per 100 kbp	4456.38
# indels per 100 kbp	241.61
Largest alignment	608
Total aligned length	5401
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

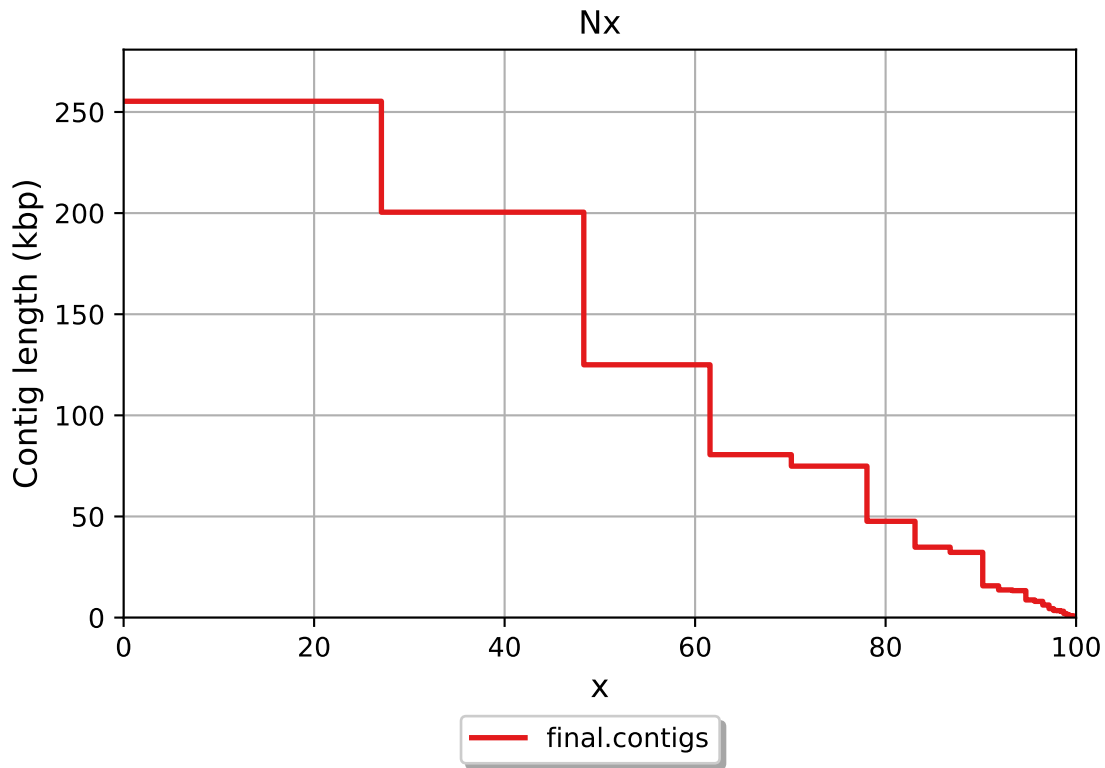
	final.contigs
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	17
# possible misassemblies	28
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	6
# mismatches	166
# indels	9
# indels (<= 5 bp)	9
# indels (> 5 bp)	0
Indels length	13

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).

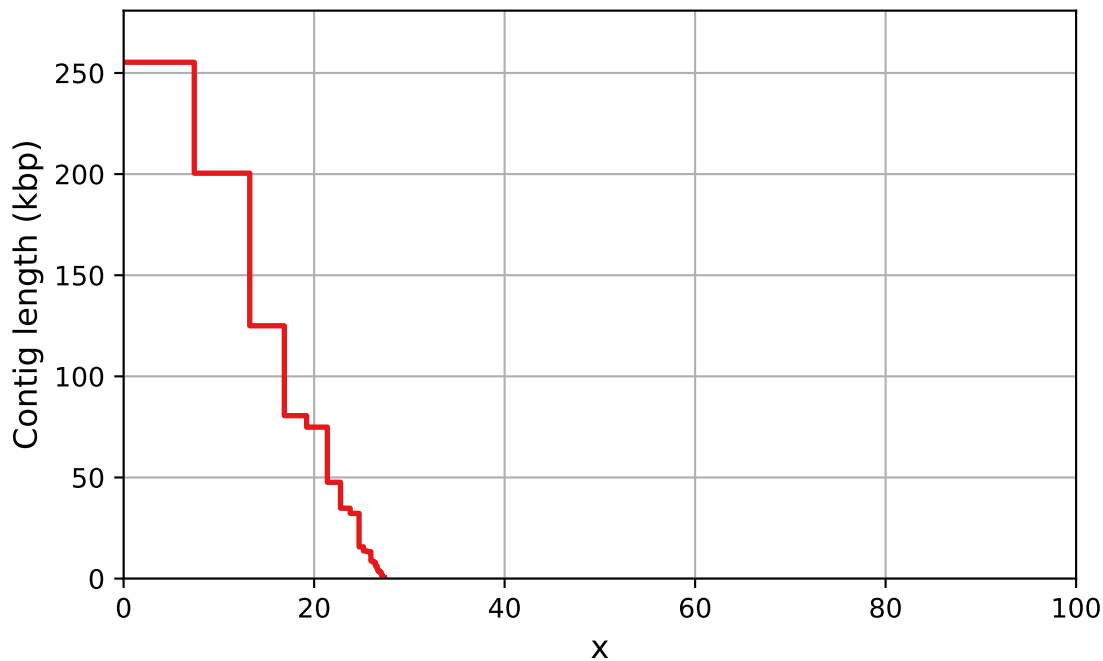
Unaligned report

	final.contigs
# fully unaligned contigs	4
Fully unaligned length	3838
# partially unaligned contigs	21
Partially unaligned length	931920
# N's	0

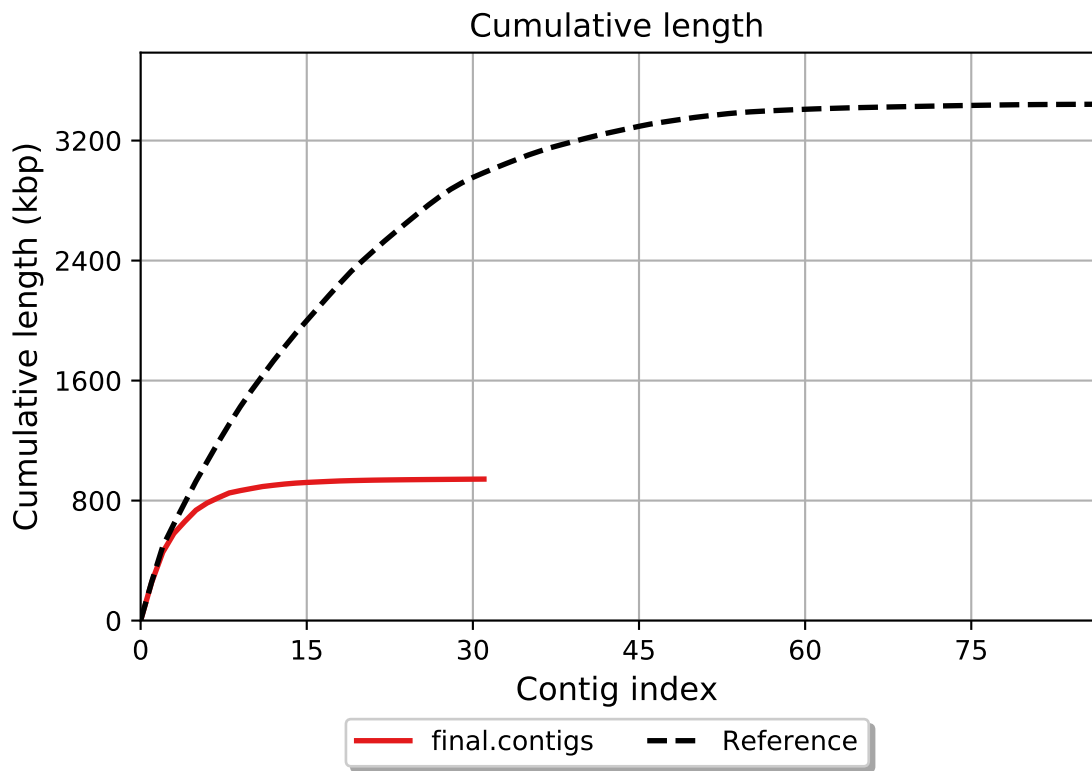
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



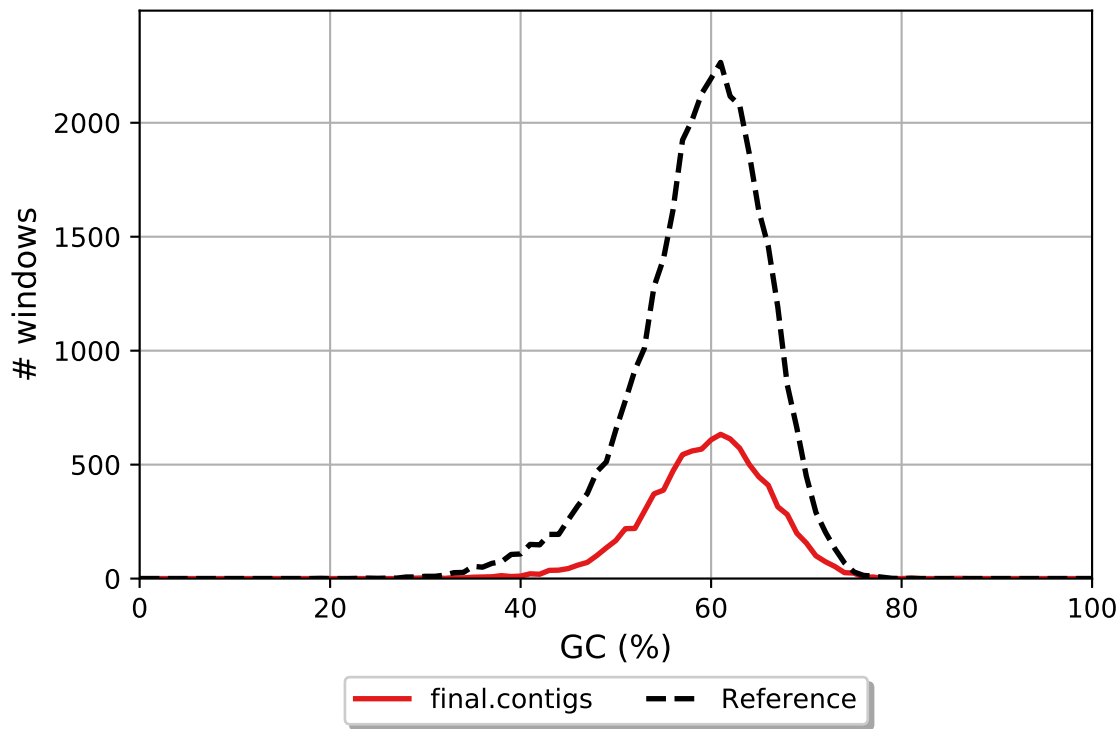
NGx



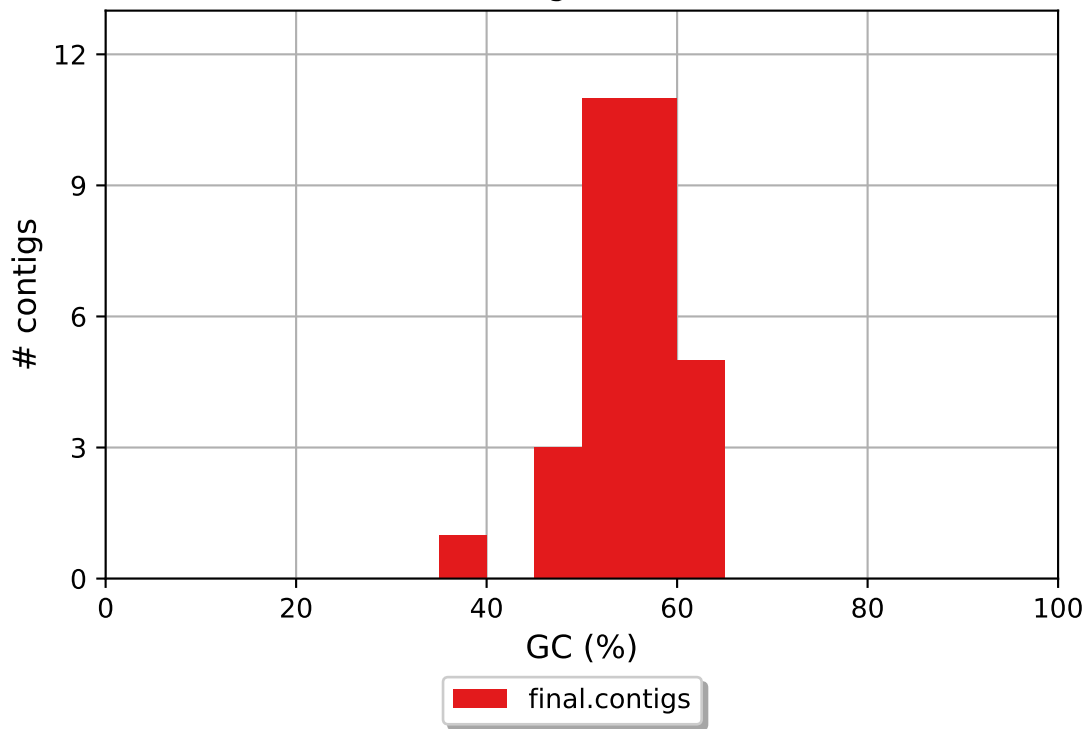
— final.contigs



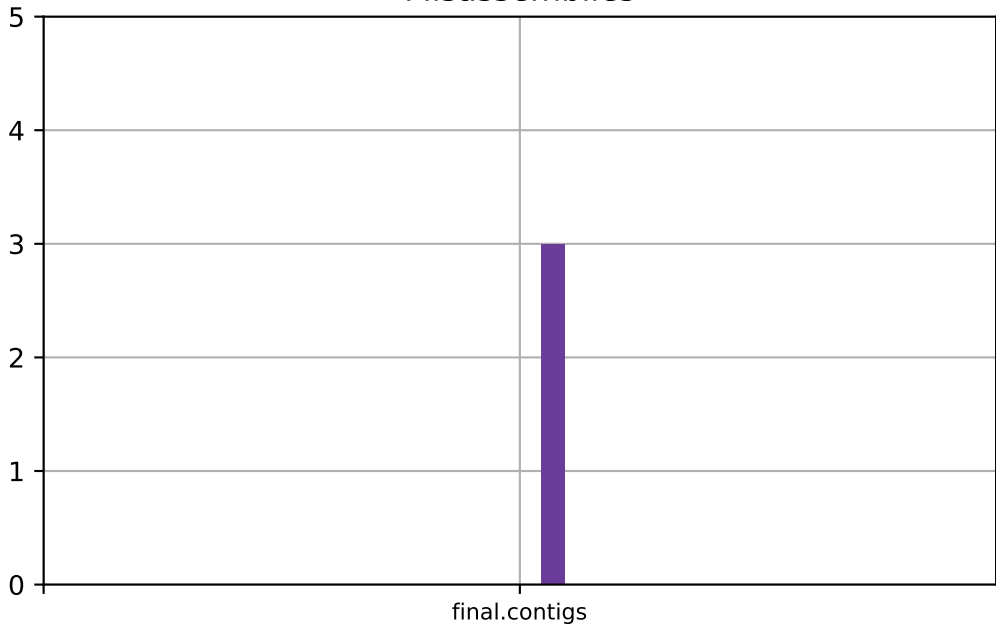
GC content



final.contigs GC content

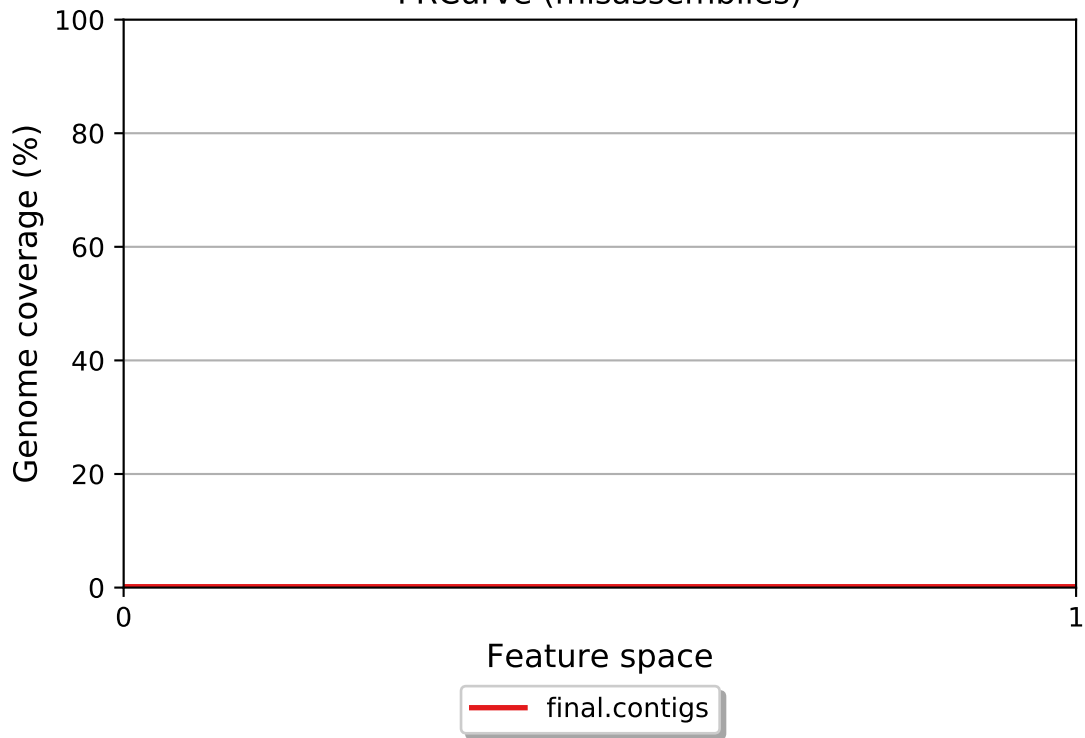


Misassemblies

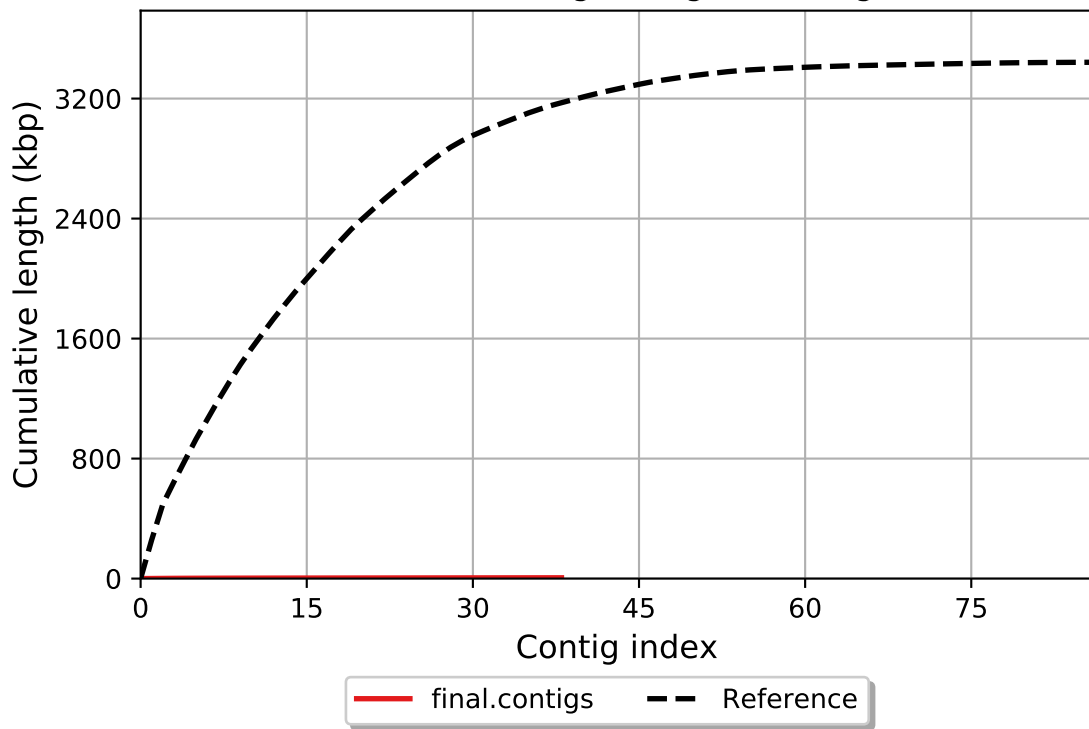


interspecies translocations

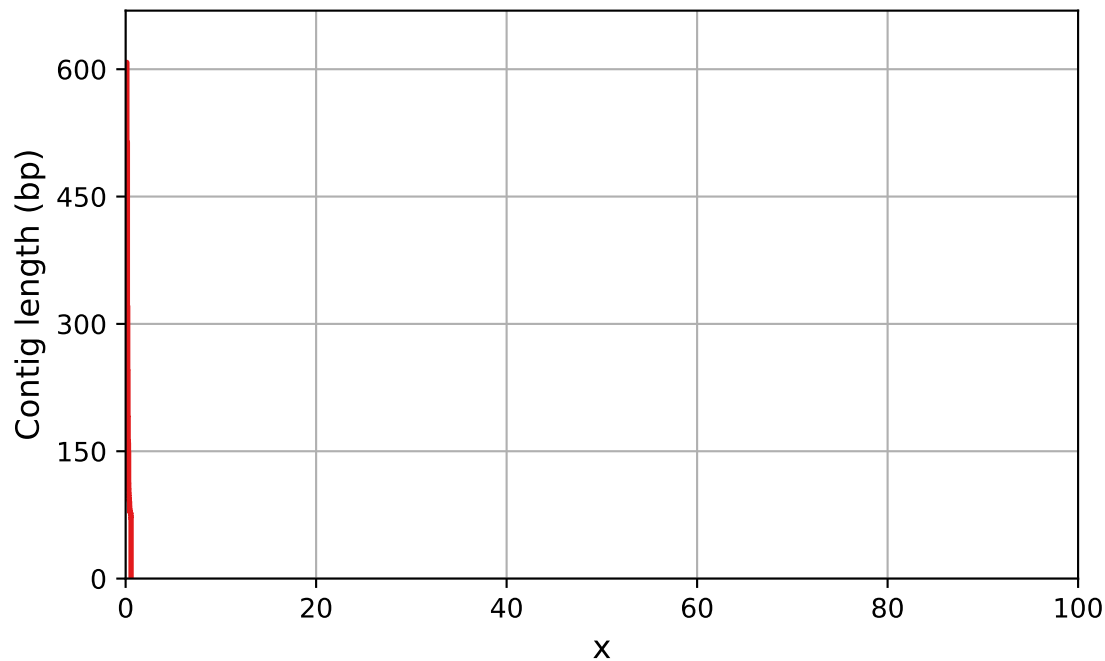
FRCurve (misassemblies)



Cumulative length (aligned contigs)

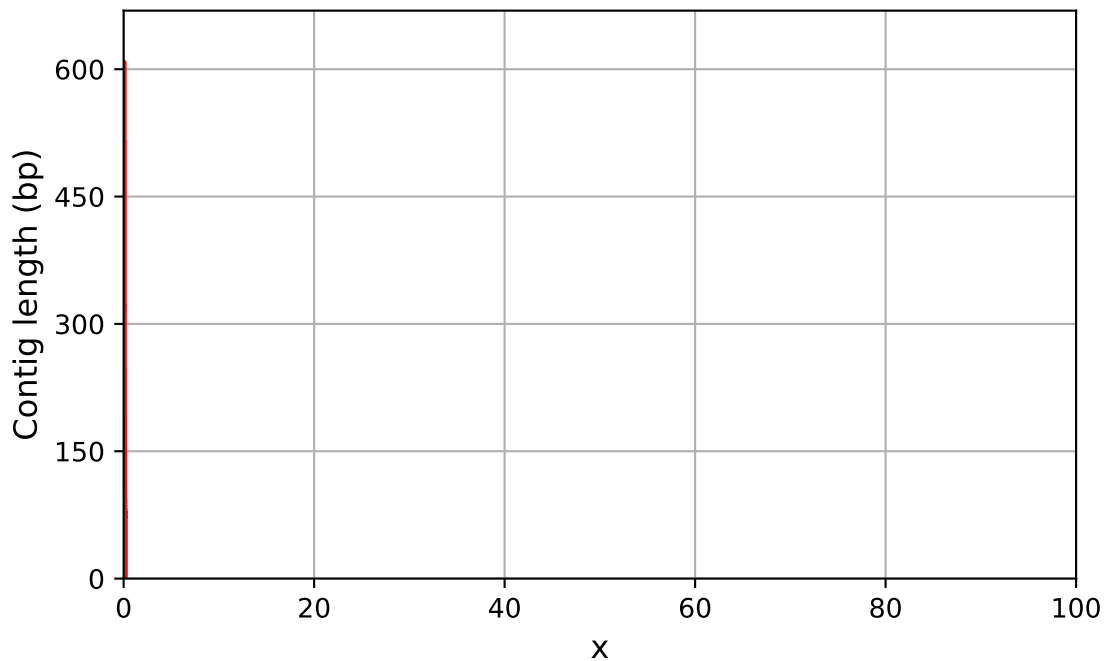


NAx



— final.contigs

NGAx



— final.contigs