

Report

	final.contigs
# contigs (>= 1000 bp)	5
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	6503
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	17
Largest contig	1678
Total length	14735
Reference length	4555826
GC (%)	53.23
Reference GC (%)	57.02
N50	876
N75	725
L50	6
L75	11
# 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	3
# unaligned contigs	1 + 6 part
Unaligned length	6556
Genome fraction (%)	0.089
Duplication ratio	2.020
# N's per 100 kbp	0.00
# mismatches per 100 kbp	3333.33
# indels per 100 kbp	148.15
Largest alignment	488
Total aligned length	4054
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

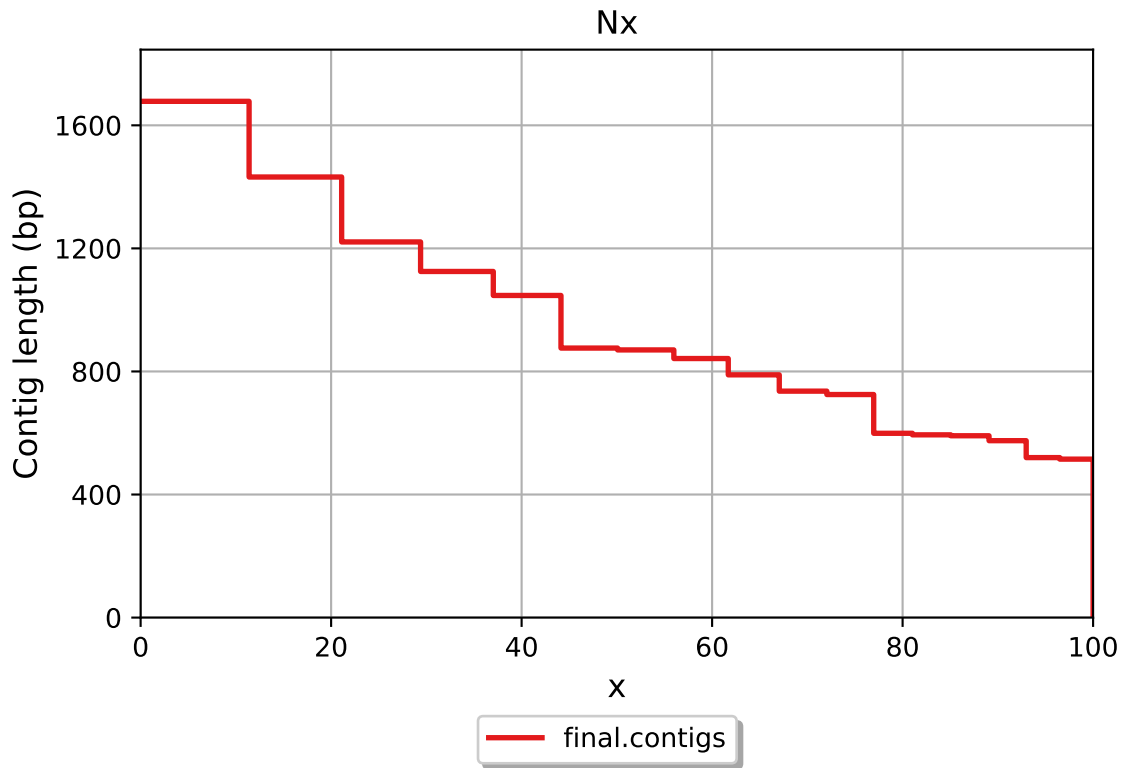
	final.contigs
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	4
# possible misassemblies	4
# local misassemblies	1
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# mismatches	135
# indels	6
# indels (<= 5 bp)	6
# indels (> 5 bp)	0
Indels length	8

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).

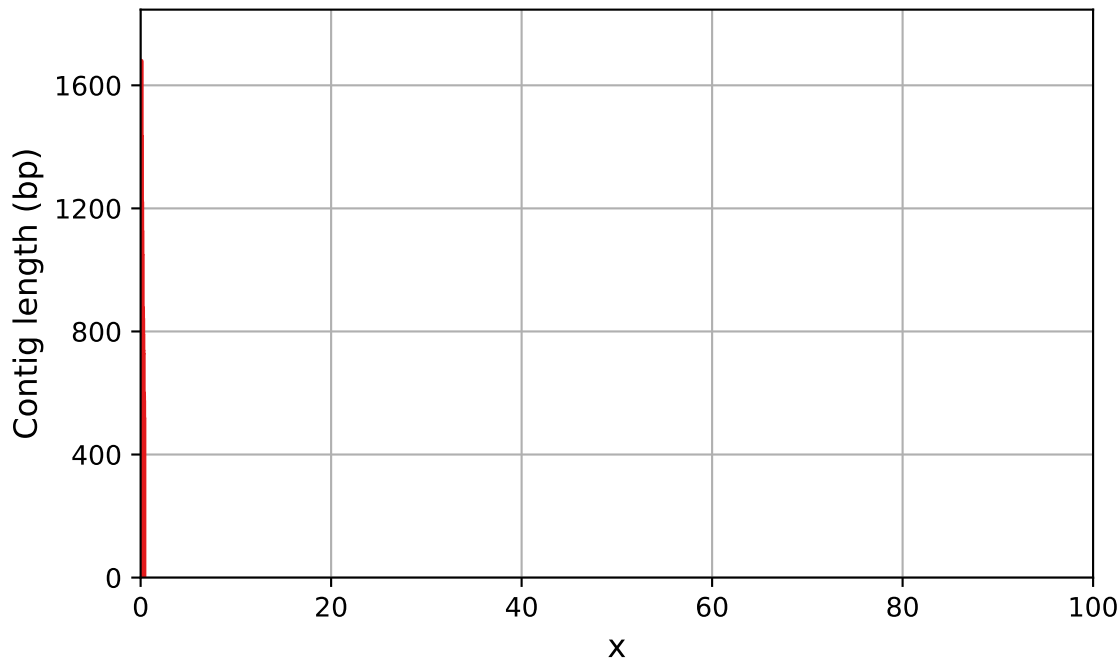
Unaligned report

	final.contigs
# fully unaligned contigs	1
Fully unaligned length	1678
# partially unaligned contigs	6
Partially unaligned length	4878
# N's	0

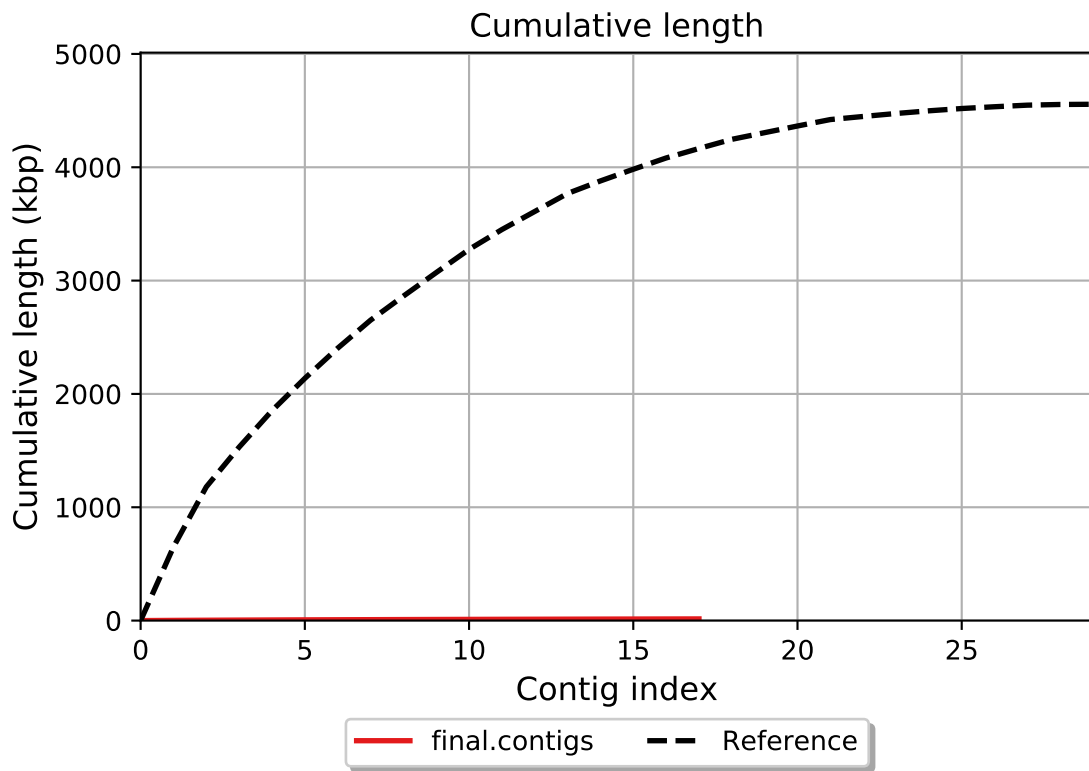
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



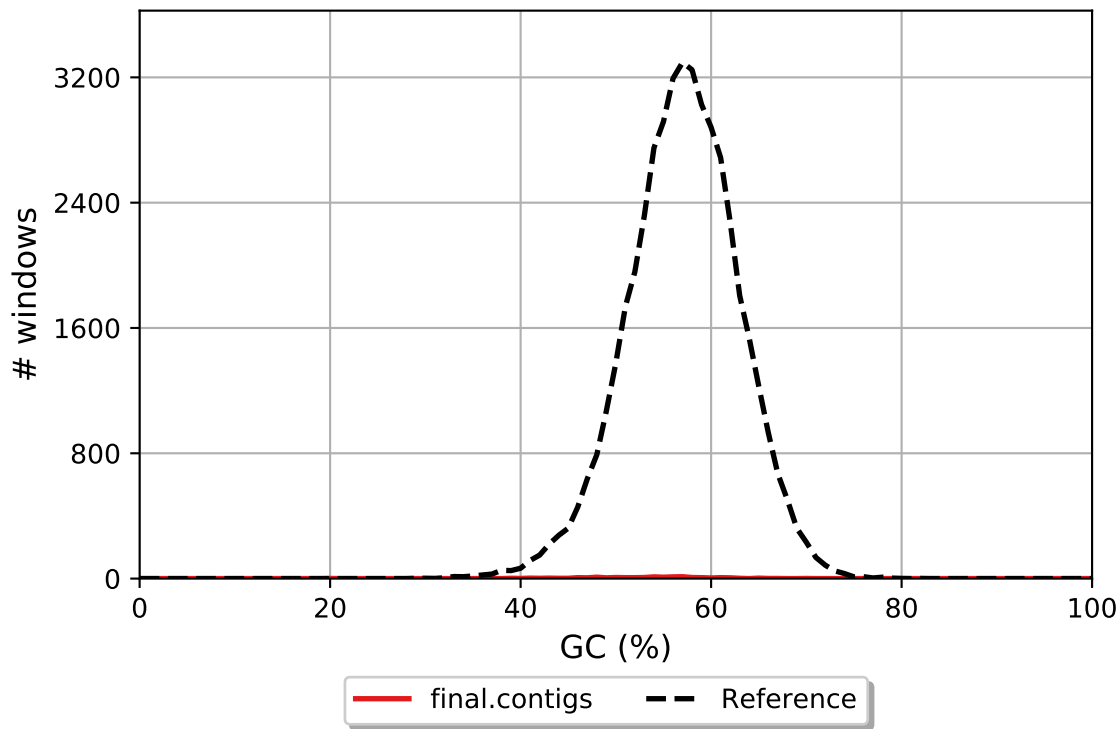
NGx



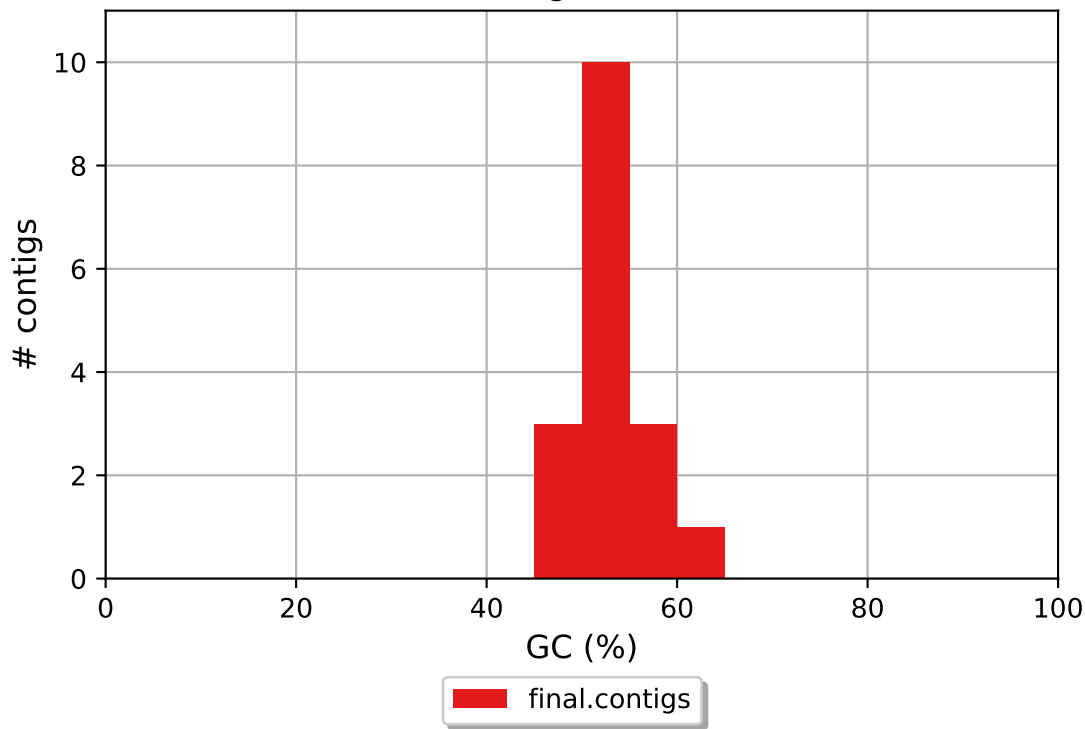
final.contigs



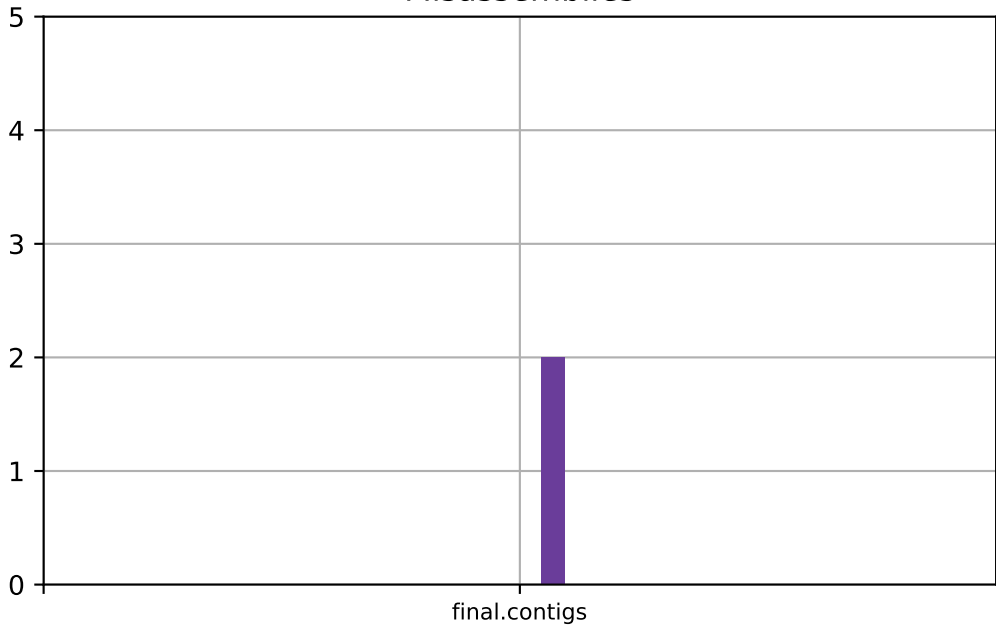
GC content



final.contigs GC content

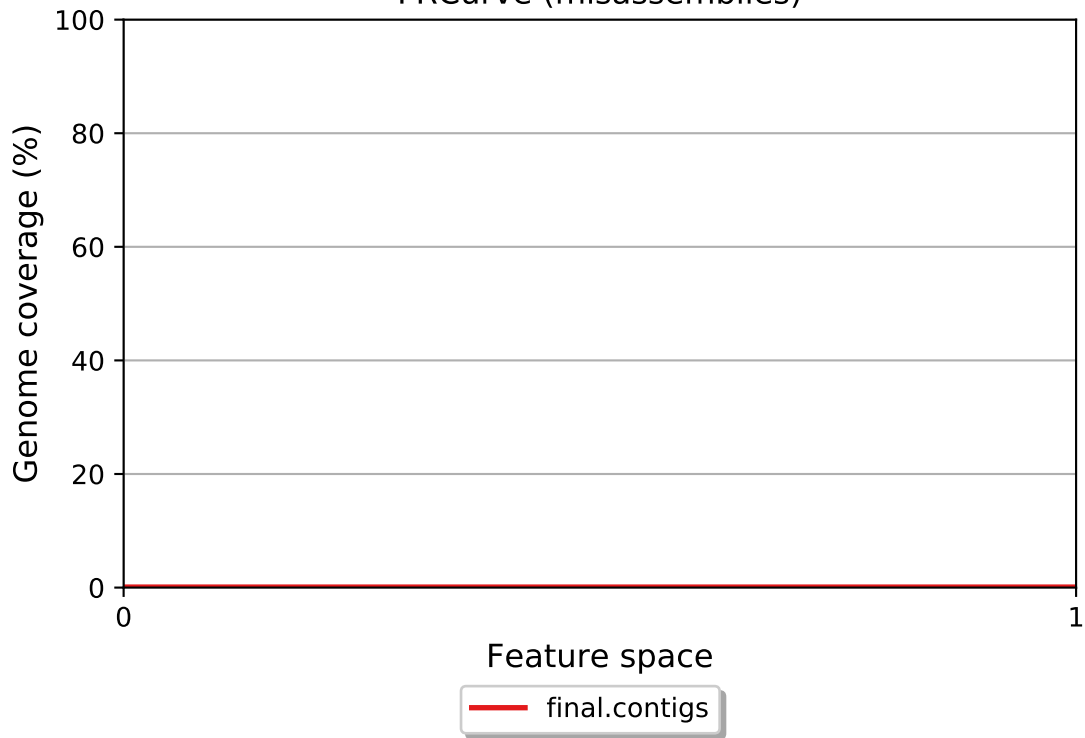


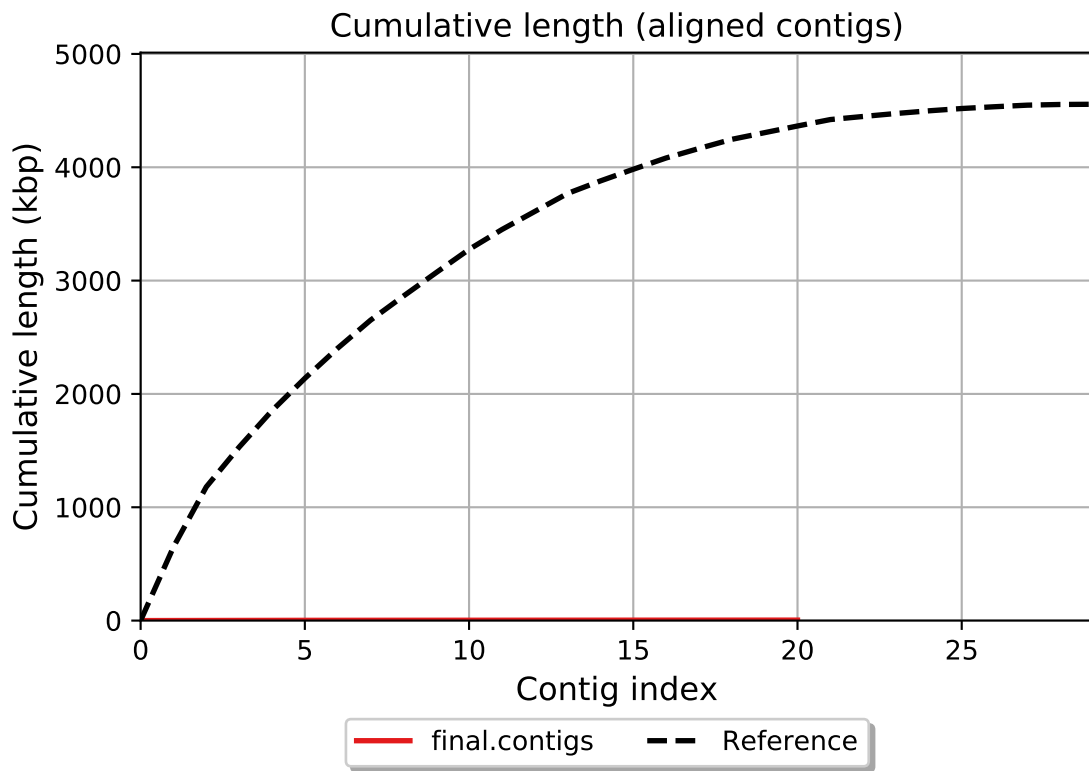
Misassemblies



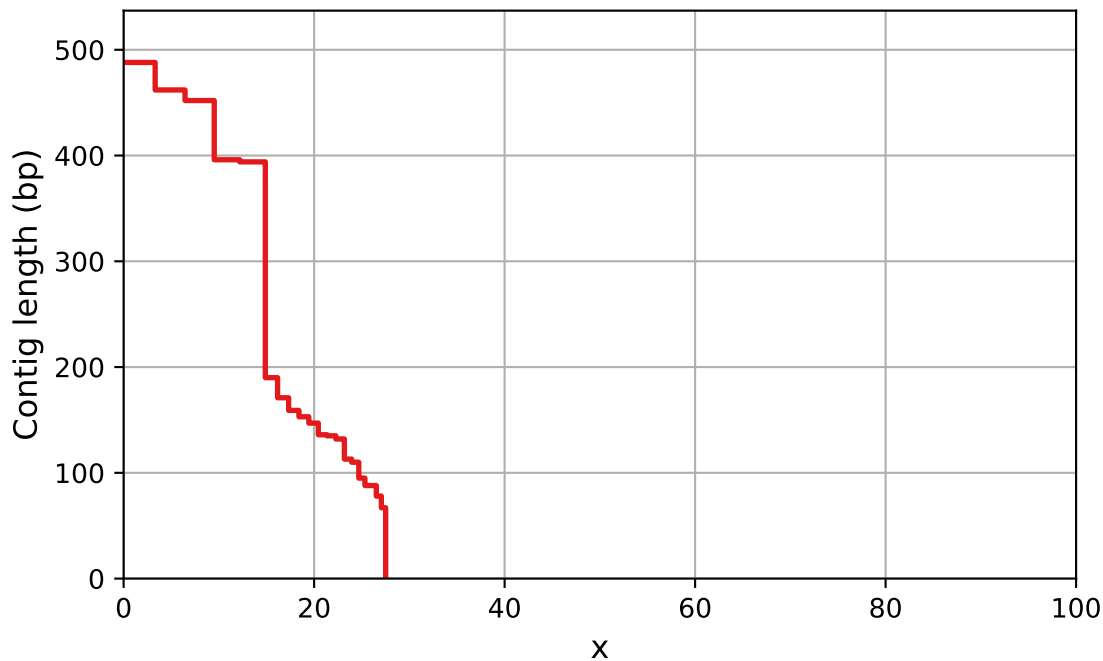
interspecies translocations

FRCurve (misassemblies)



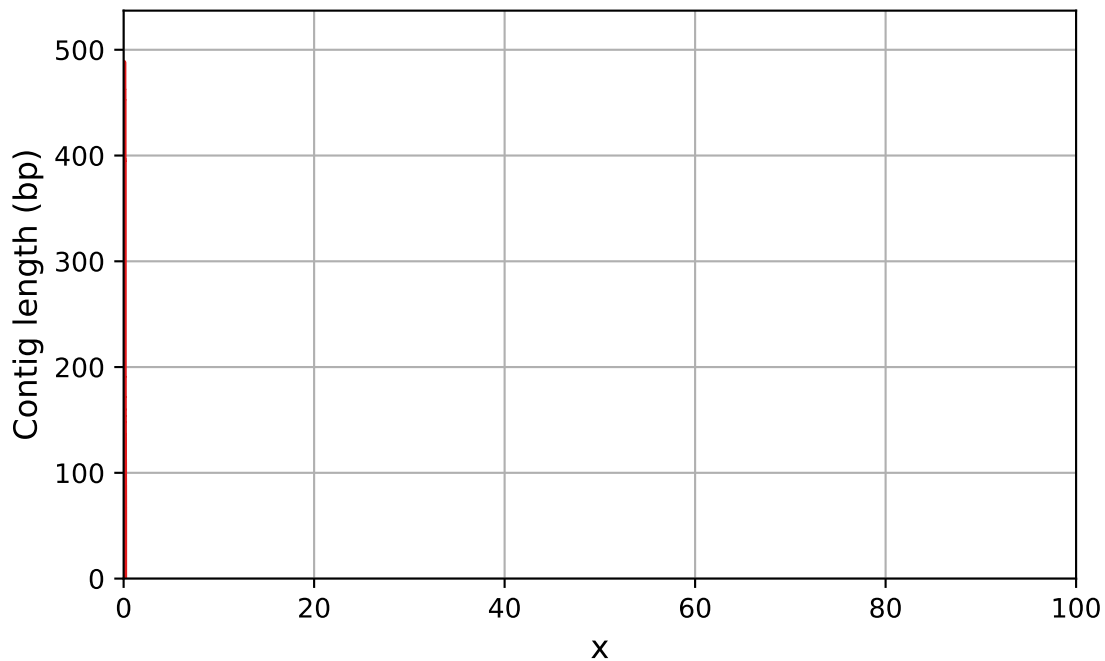


NAx



— final.contigs

NGAx



— final.contigs