

Report

	final.contigs
# contigs (≥ 1000 bp)	3
# contigs (≥ 5000 bp)	0
# contigs (≥ 10000 bp)	0
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 1000 bp)	5058
Total length (≥ 5000 bp)	0
Total length (≥ 10000 bp)	0
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	55
Largest contig	2468
Total length	37445
Reference length	2441632
GC (%)	30.58
Reference GC (%)	26.82
N50	633
N75	562
L50	22
L75	38
# misassemblies	2
# misassembled contigs	2
Misassembled contigs length	1426
# local misassemblies	2
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	1 + 2 part
Unaligned length	3274
Genome fraction (%)	1.261
Duplication ratio	1.111
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2873.49
# indels per 100 kbp	126.77
Largest alignment	1369
Total aligned length	31022
NA50	562
NGA50	-
NA75	431
LA50	27
LA75	45

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	2
# contig misassemblies	2
# c. relocations	2
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	2
Misassembled contigs length	1426
# possibly misassembled contigs	3
# possible misassemblies	3
# local misassemblies	2
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	884
# indels	39
# indels (<= 5 bp)	35
# indels (> 5 bp)	4
Indels length	100

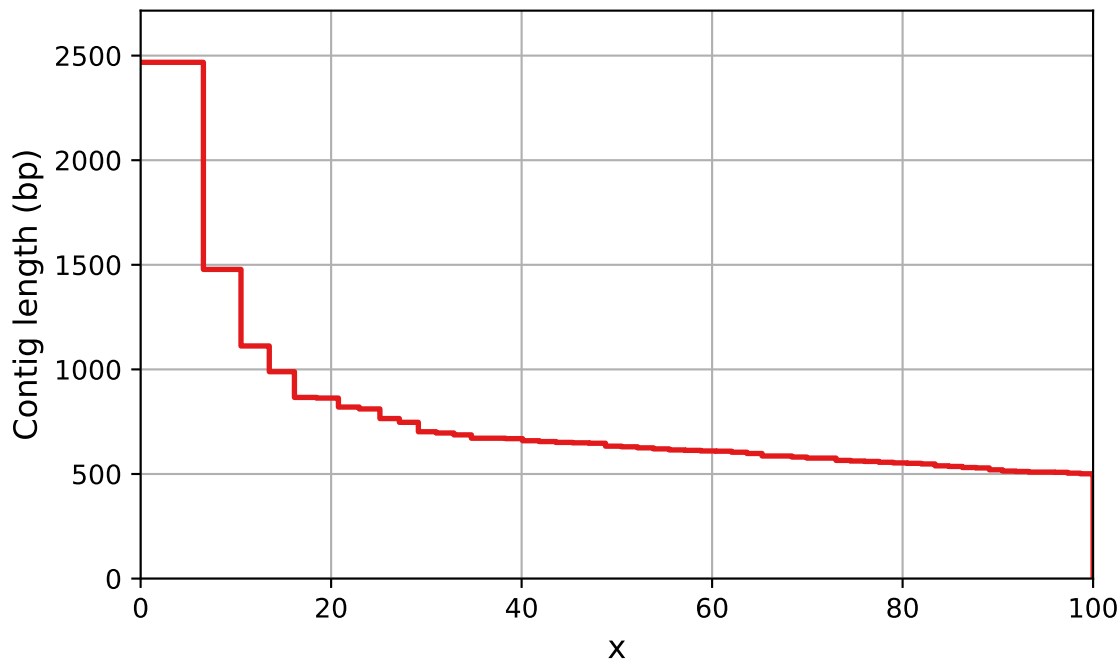
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	final.contigs
# fully unaligned contigs	1
Fully unaligned length	671
# partially unaligned contigs	2
Partially unaligned length	2603
# N's	0

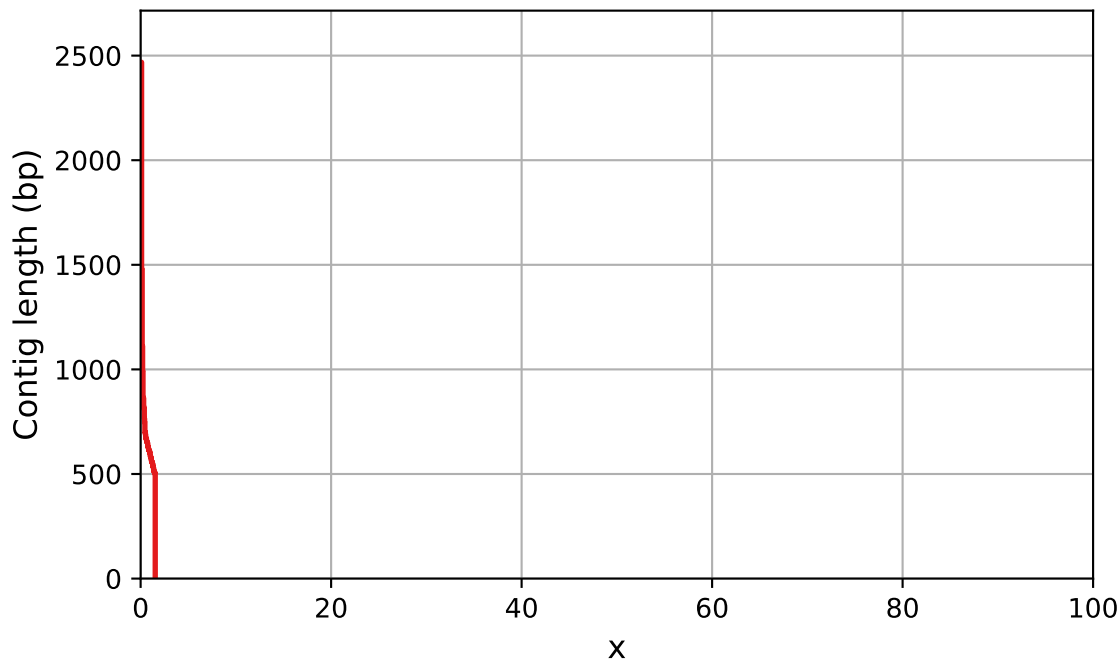
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

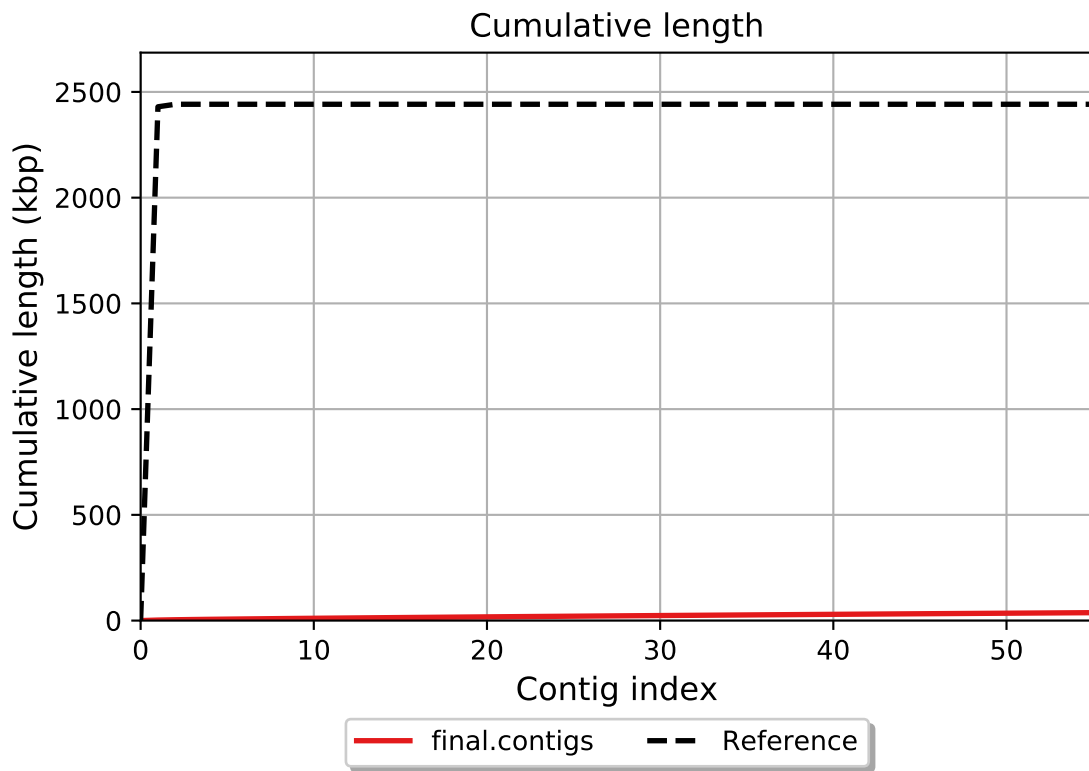


— final.contigs

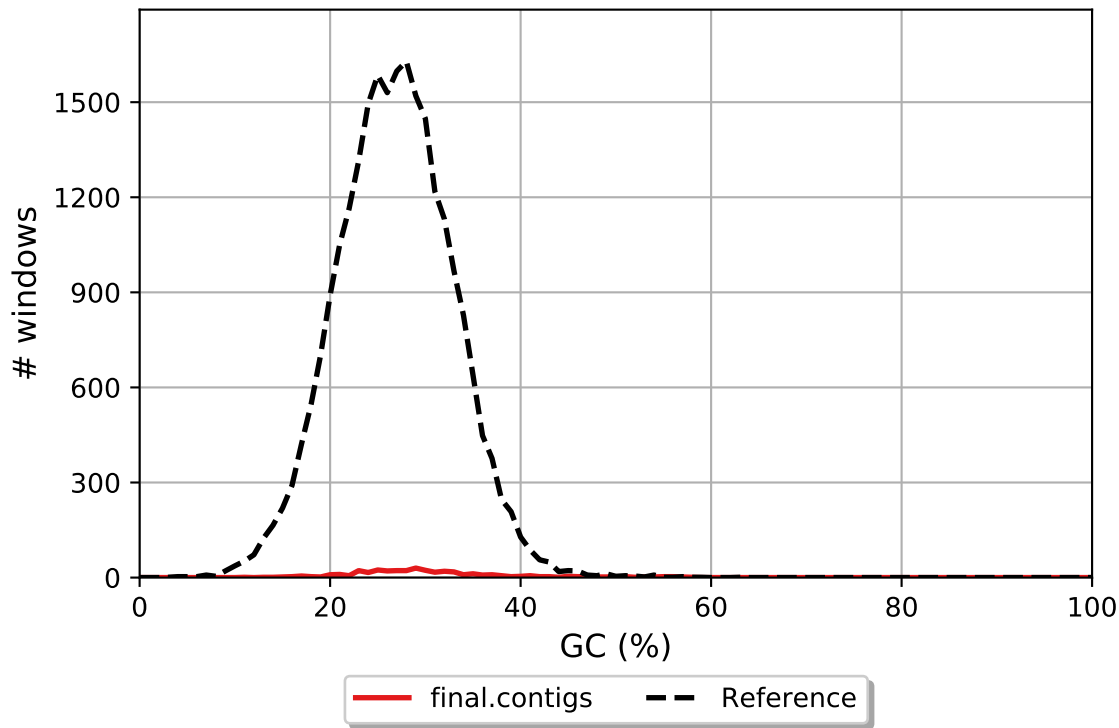
NGx



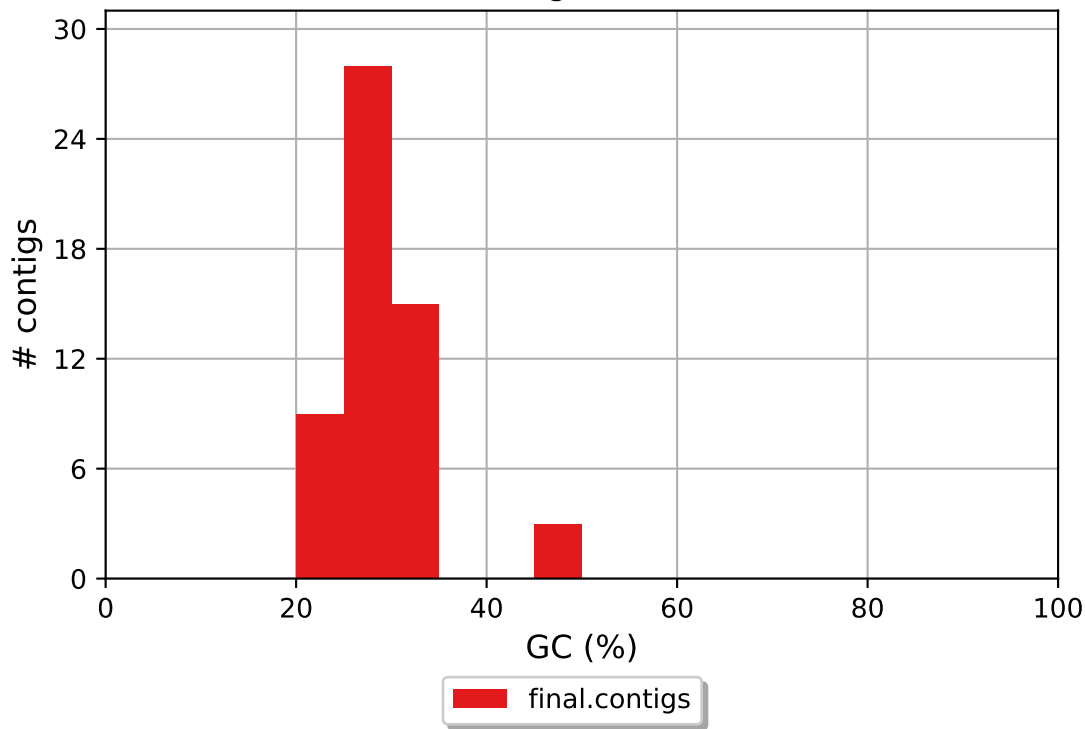
— final.contigs



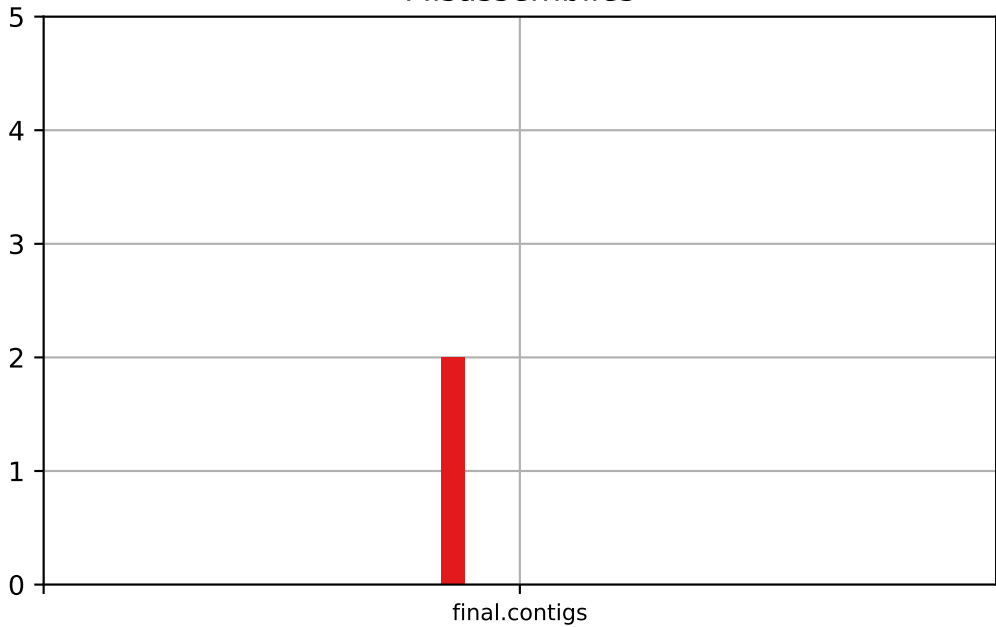
GC content



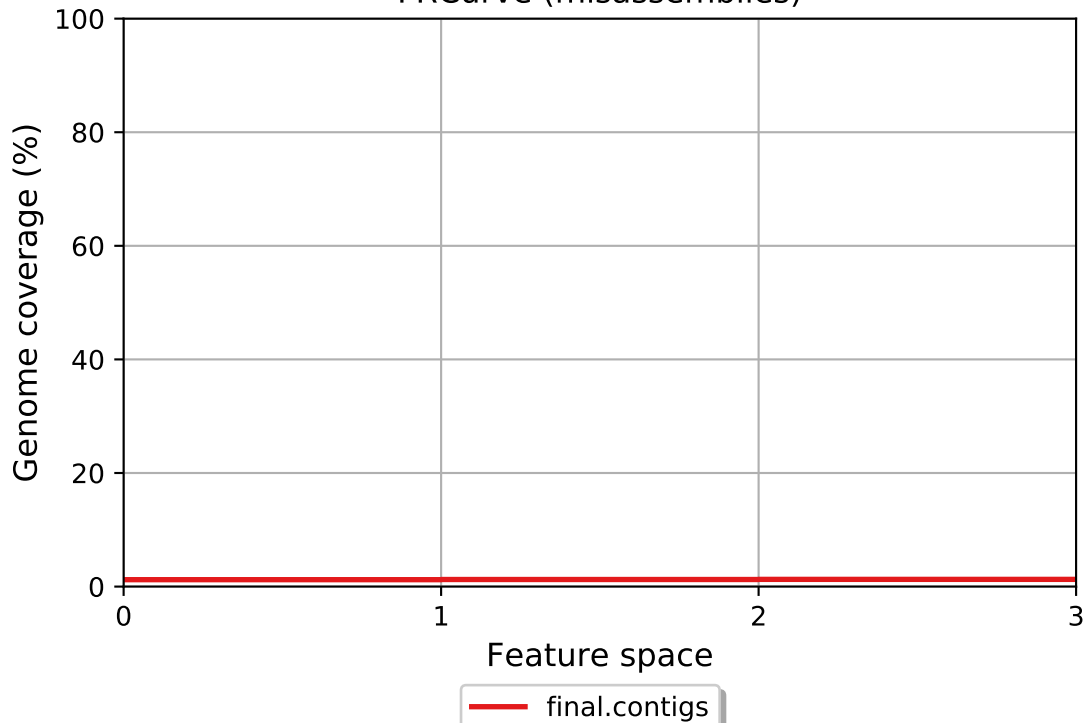
final.contigs GC content



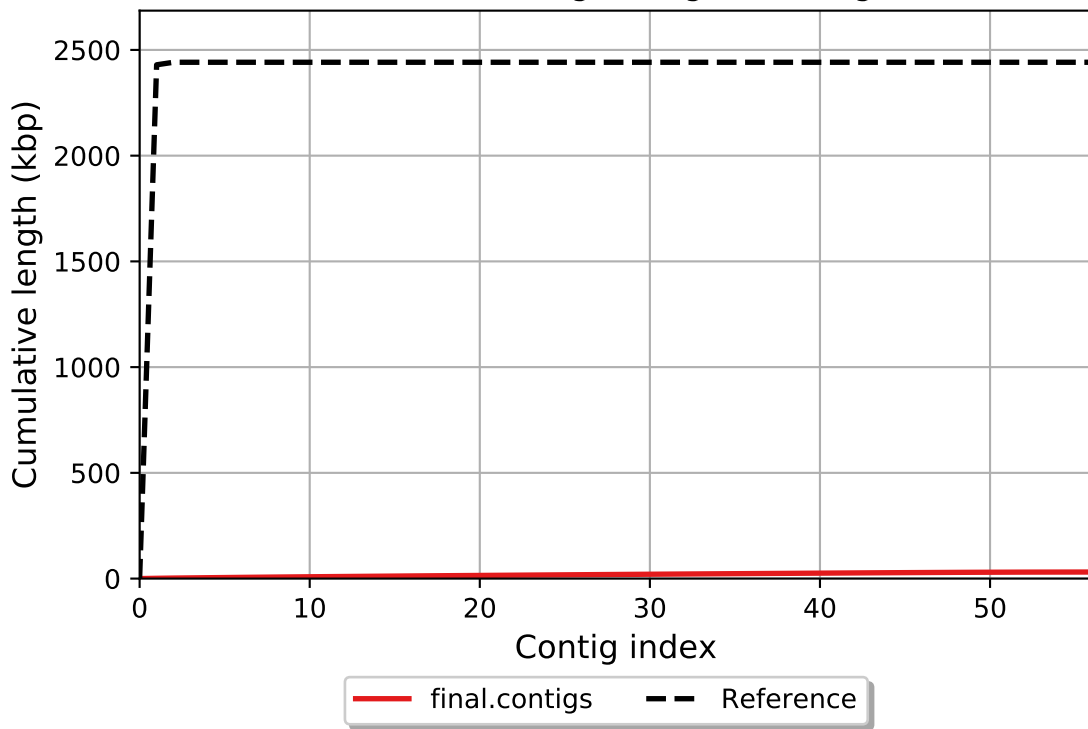
Misassemblies



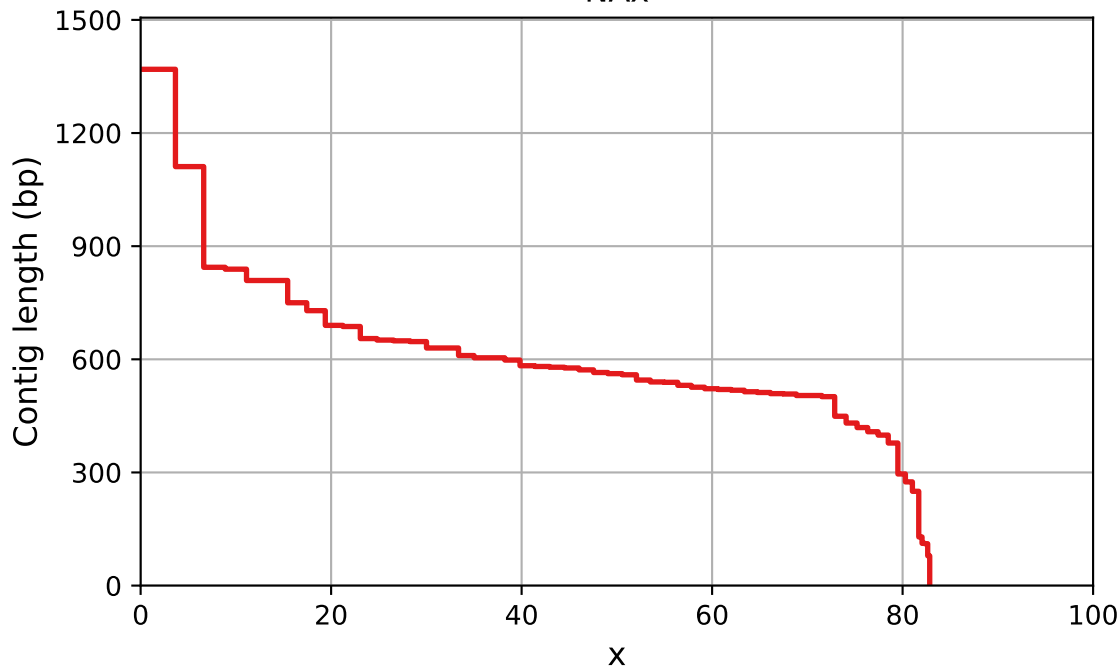
FRCurve (misassemblies)



Cumulative length (aligned contigs)

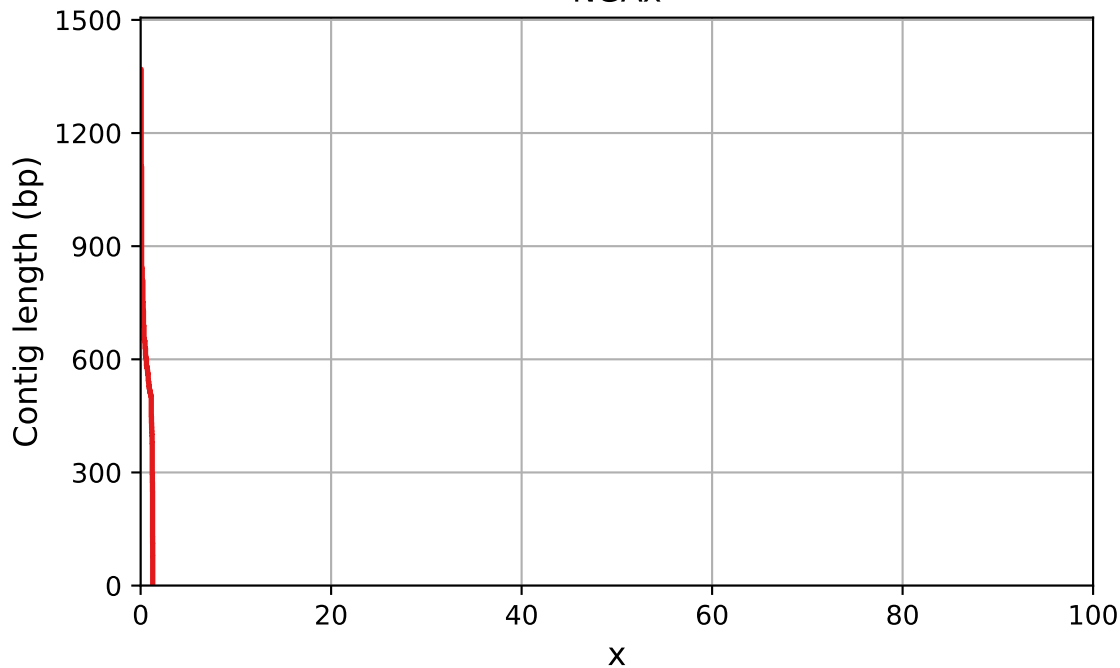


NAx



— final.contigs

NGAx



— final.contigs