

Report

	final.contigs
# contigs (>= 1000 bp)	624
# contigs (>= 5000 bp)	73
# contigs (>= 10000 bp)	16
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	1
Total length (>= 1000 bp)	1864719
Total length (>= 5000 bp)	640547
Total length (>= 10000 bp)	271730
Total length (>= 25000 bp)	63871
Total length (>= 50000 bp)	63871
# contigs	1098
Largest contig	63871
Total length	2194628
Reference length	2095808
GC (%)	38.75
Reference GC (%)	38.91
N50	3036
NG50	3346
N90	801
NG90	964
auN	5967.4
auNG	6248.8
L50	189
LG50	173
L90	748
LG90	646
# misassemblies	32
# misassembled contigs	30
Misassembled contigs length	73049
# local misassemblies	21
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	17
# unaligned contigs	1 + 138 part
Unaligned length	241462
Genome fraction (%)	84.157
Duplication ratio	1.081
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2295.34
# indels per 100 kbp	53.29
Largest alignment	18493
Total aligned length	1906693
NA50	2495
NGA50	2698
NA90	-
NGA90	258
auNA	3621.9
auNGA	3792.6
LA50	232
LGA50	213
LA90	-
LGA90	1016

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	32
# contig misassemblies	32
# c. relocations	16
# c. translocations	16
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	30
Misassembled contigs length	73049
# possibly misassembled contigs	124
# possible misassemblies	138
# local misassemblies	21
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	17
# mismatches	43765
# indels	1016
# indels (<= 5 bp)	968
# indels (> 5 bp)	48
Indels length	2289

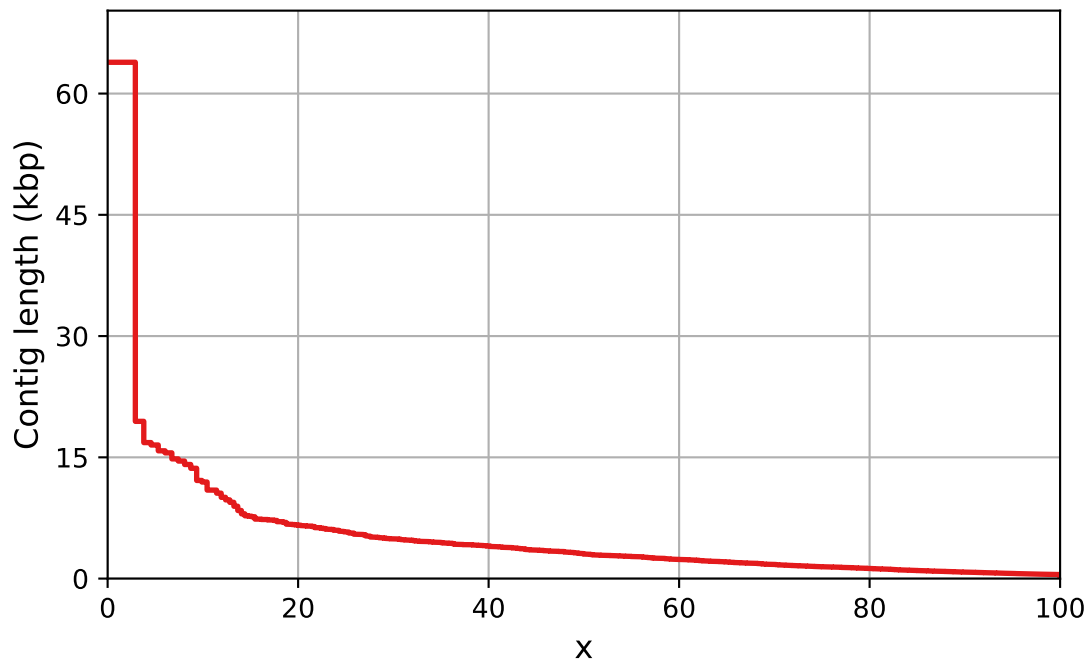
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	final.contigs
# fully unaligned contigs	1
Fully unaligned length	1163
# partially unaligned contigs	138
Partially unaligned length	240299
# N's	0

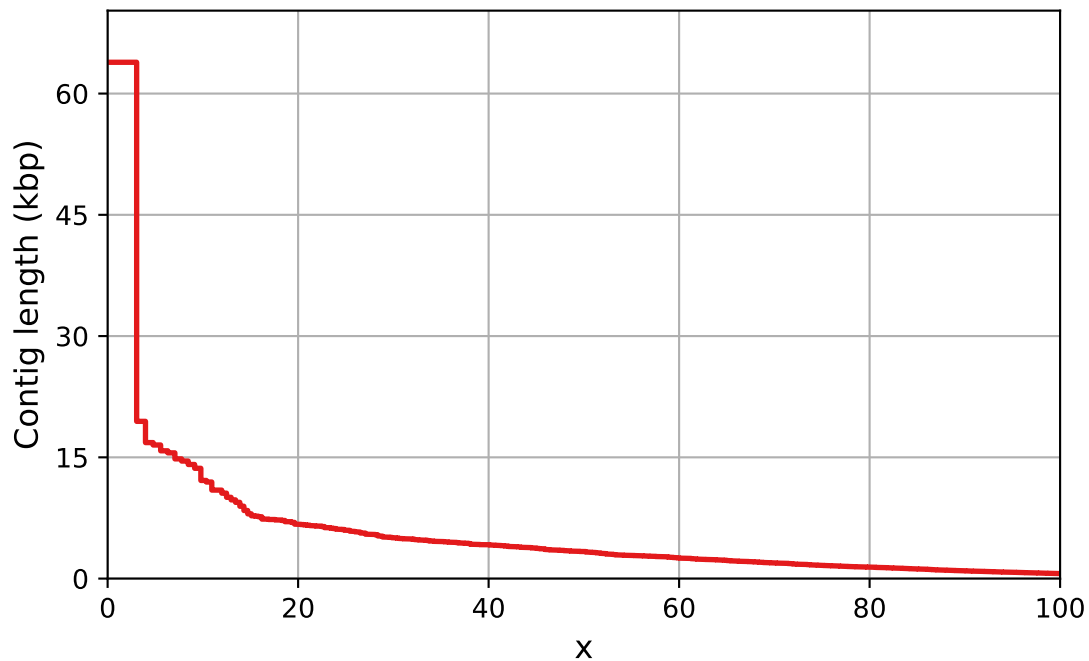
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



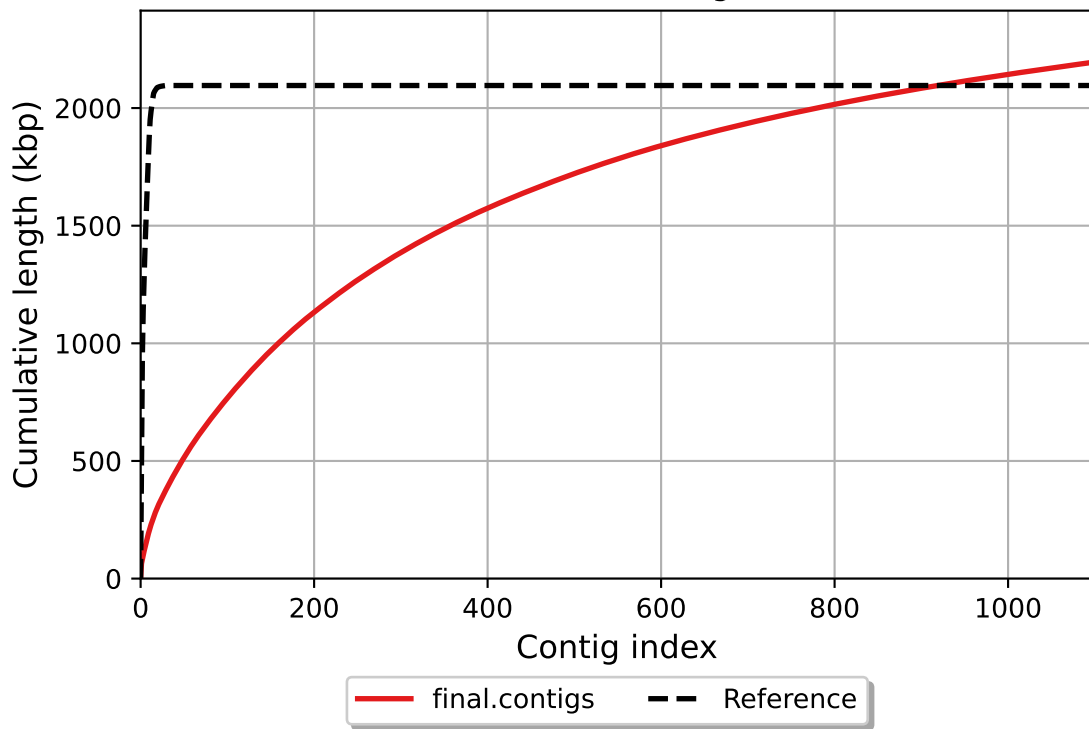
— final.contigs

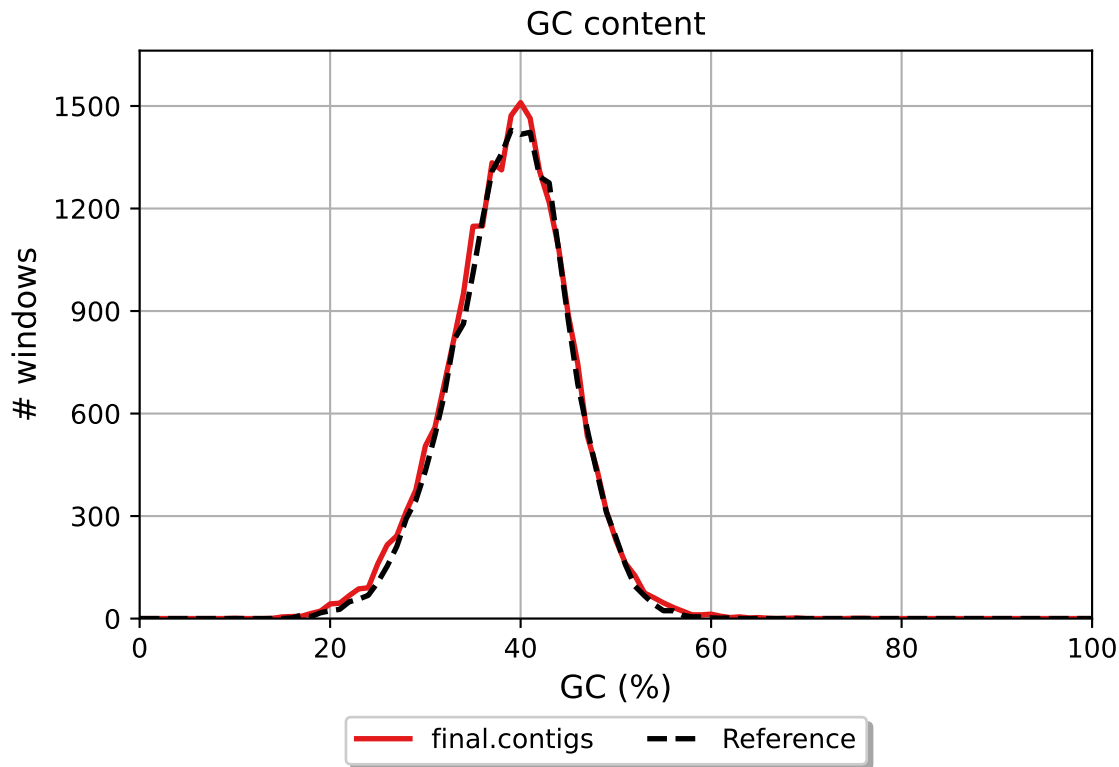
NGx



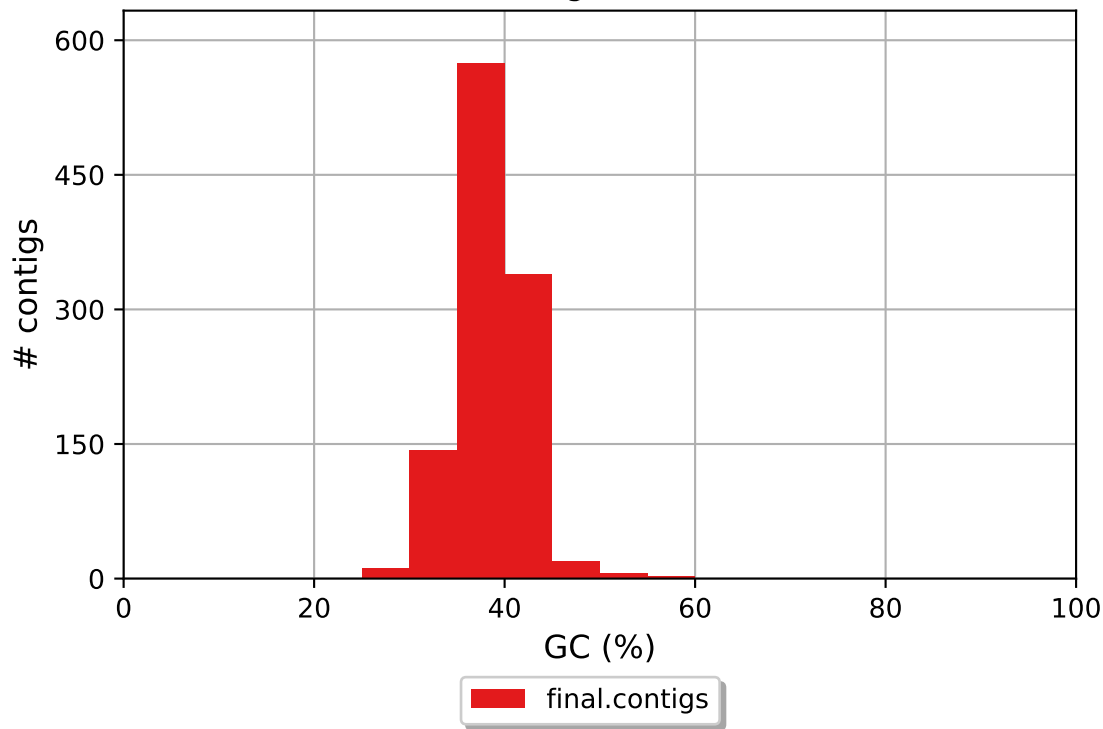
— final.contigs

Cumulative length

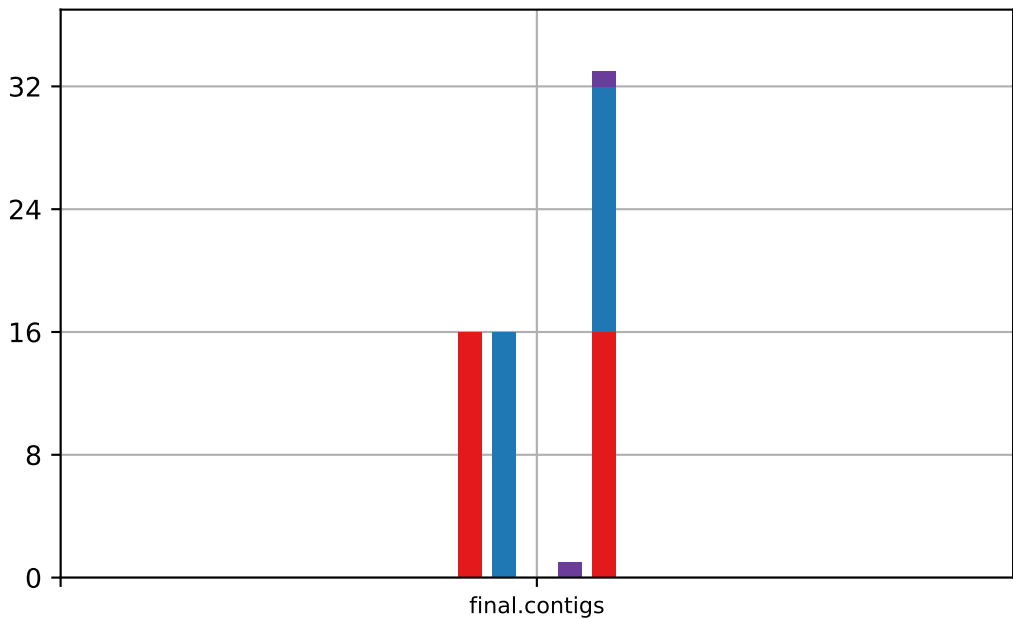




final.contigs GC content

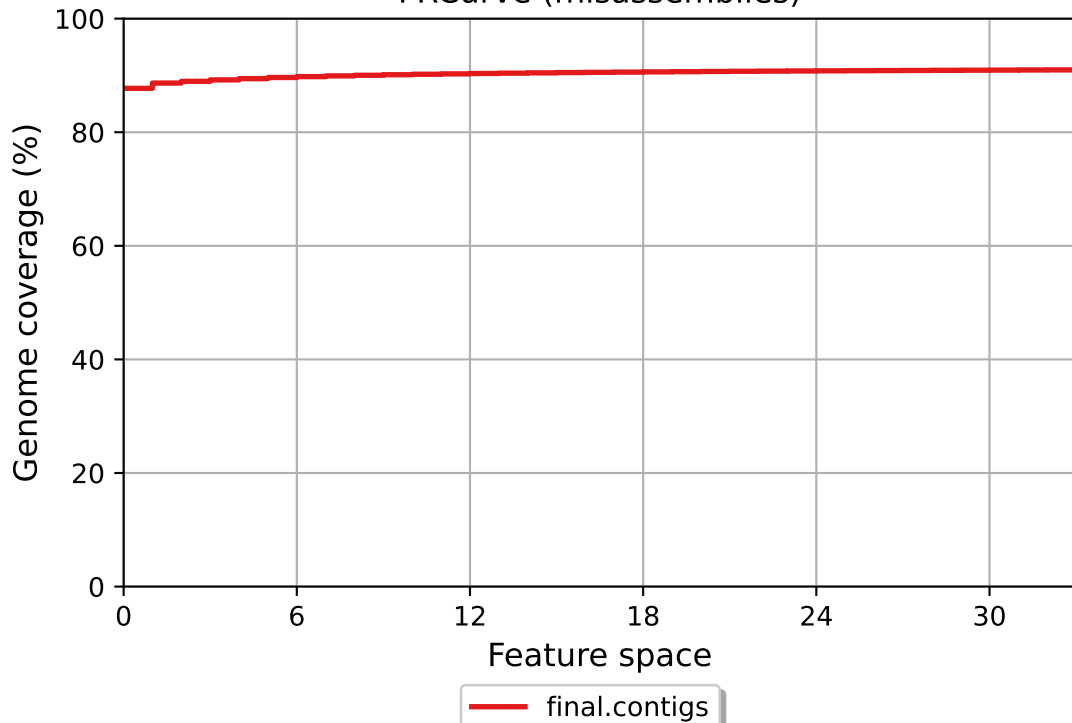


Misassemblies

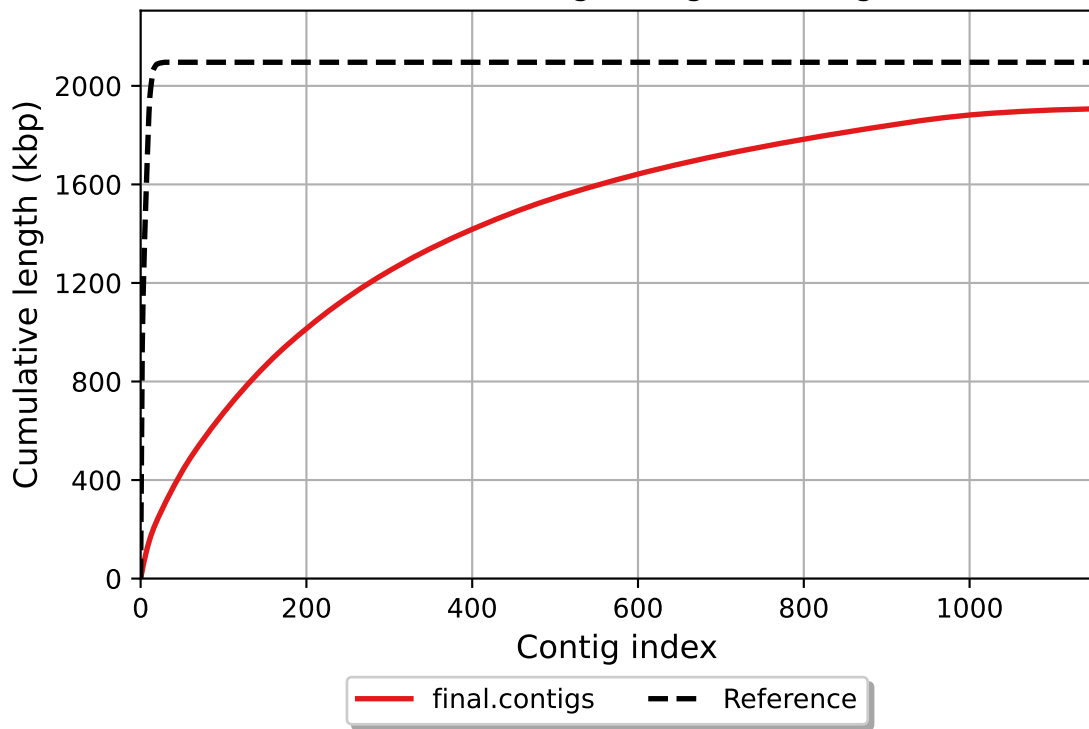


relocations # translocations # interspecies translocations

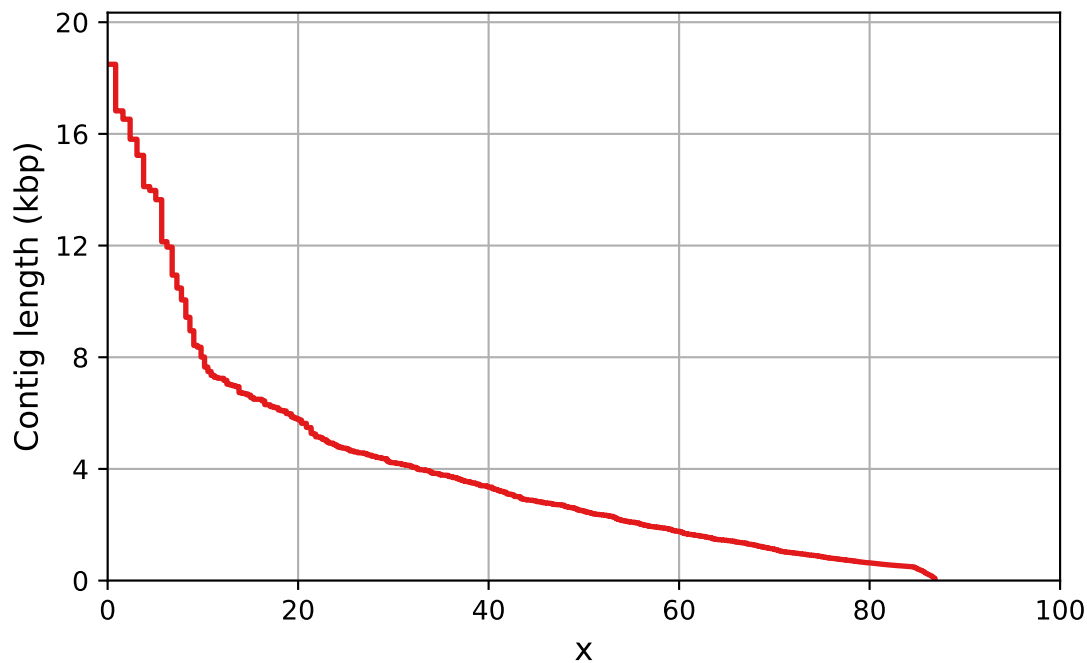
FRCurve (misassemblies)



Cumulative length (aligned contigs)

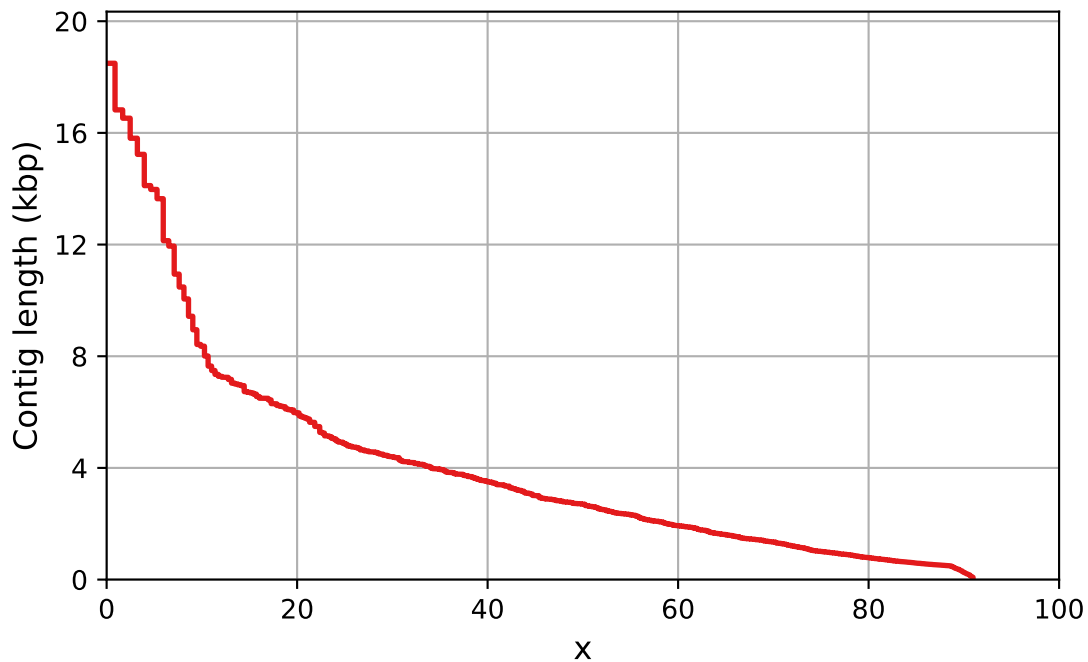


NAx



— final.contigs

NGAx



— final.contigs