

Report

	final.contigs
# contigs (>= 1000 bp)	112
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	152479
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	627
Largest contig	4705
Total length	500379
Reference length	2518737
GC (%)	35.72
Reference GC (%)	35.13
N50	784
NG50	-
N90	542
NG90	-
auN	961.4
auNG	191.0
L50	224
LG50	-
L90	531
LG90	-
# misassemblies	9
# misassembled contigs	9
Misassembled contigs length	8308
# local misassemblies	1
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# unaligned contigs	1 + 10 part
Unaligned length	14610
Genome fraction (%)	18.697
Duplication ratio	1.006
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1245.27
# indels per 100 kbp	43.92
Largest alignment	4705
Total aligned length	473551
NA50	738
NGA50	-
NA90	502
NGA90	-
auNA	851.0
auNGA	169.1
LA50	240
LGA50	-
LA90	569
LGA90	-

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

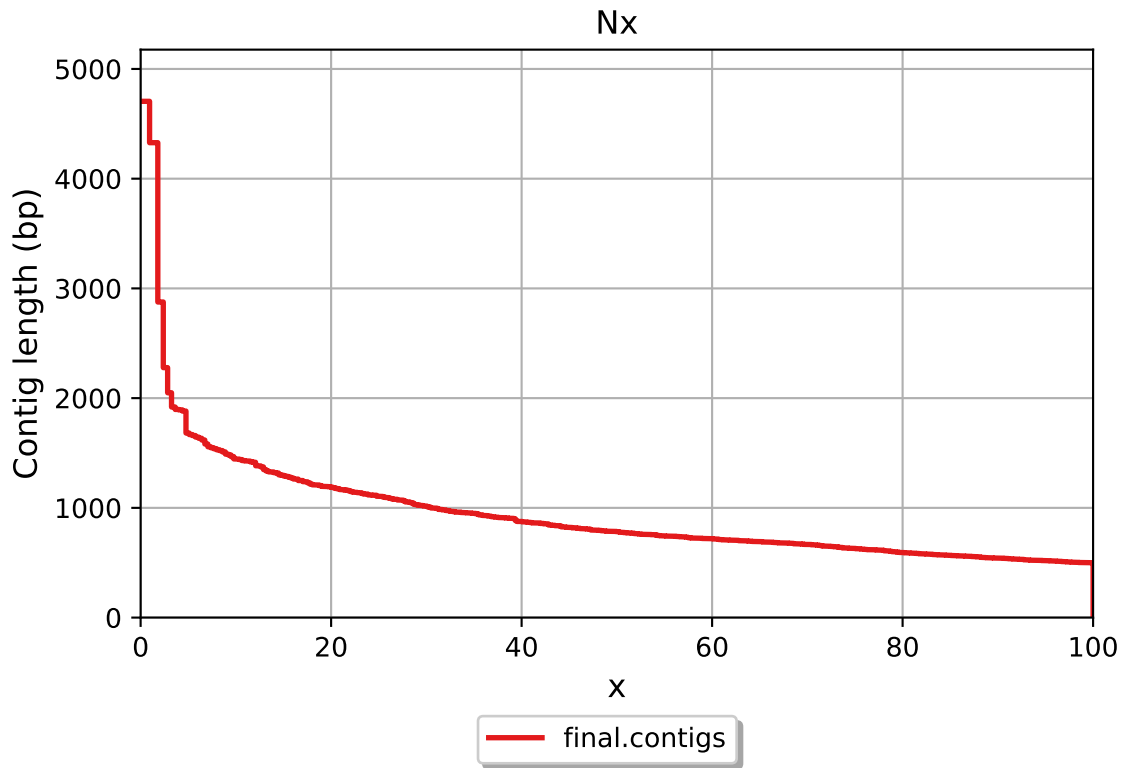
	final.contigs
# misassemblies	9
# contig misassemblies	9
# c. relocations	9
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	9
Misassembled contigs length	8308
# possibly misassembled contigs	9
# possible misassemblies	9
# local misassemblies	1
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# mismatches	5897
# indels	208
# indels (<= 5 bp)	190
# indels (> 5 bp)	18
Indels length	838

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).

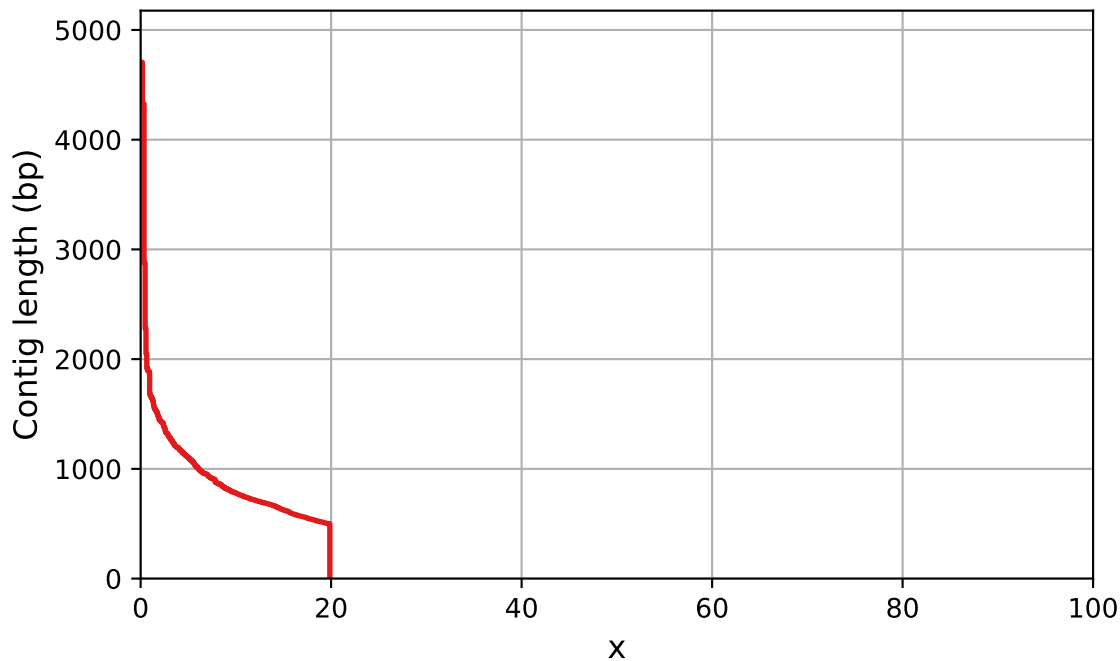
Unaligned report

	final.contigs
# fully unaligned contigs	1
Fully unaligned length	855
# partially unaligned contigs	10
Partially unaligned length	13755
# 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).

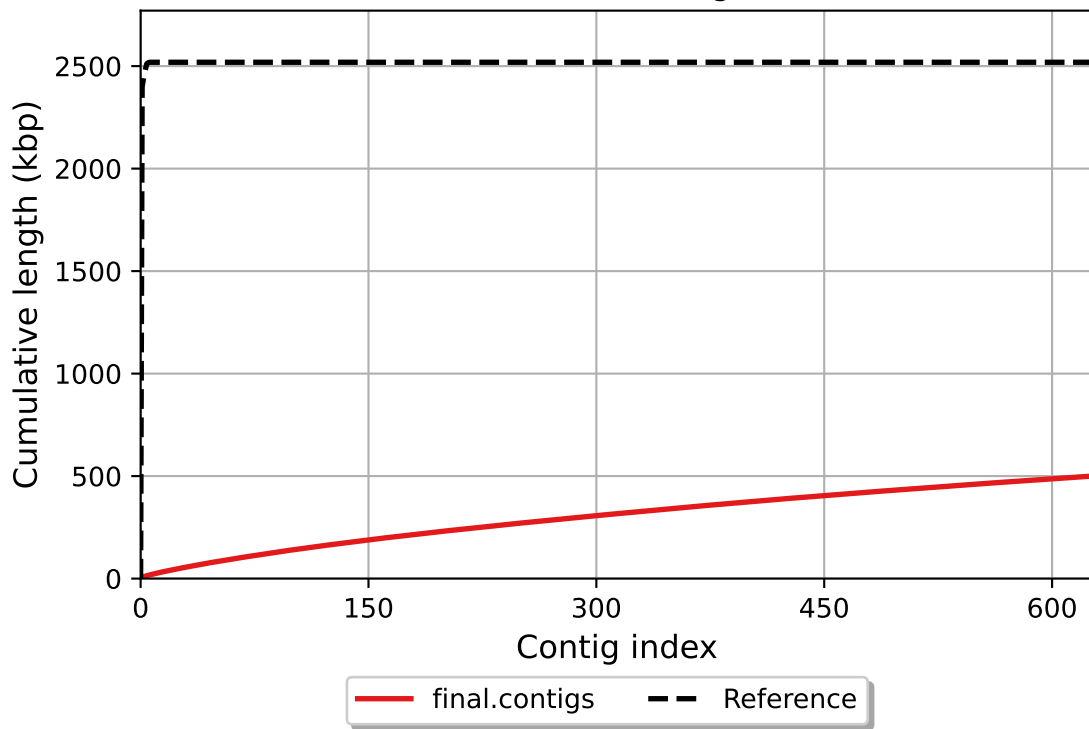


NGx

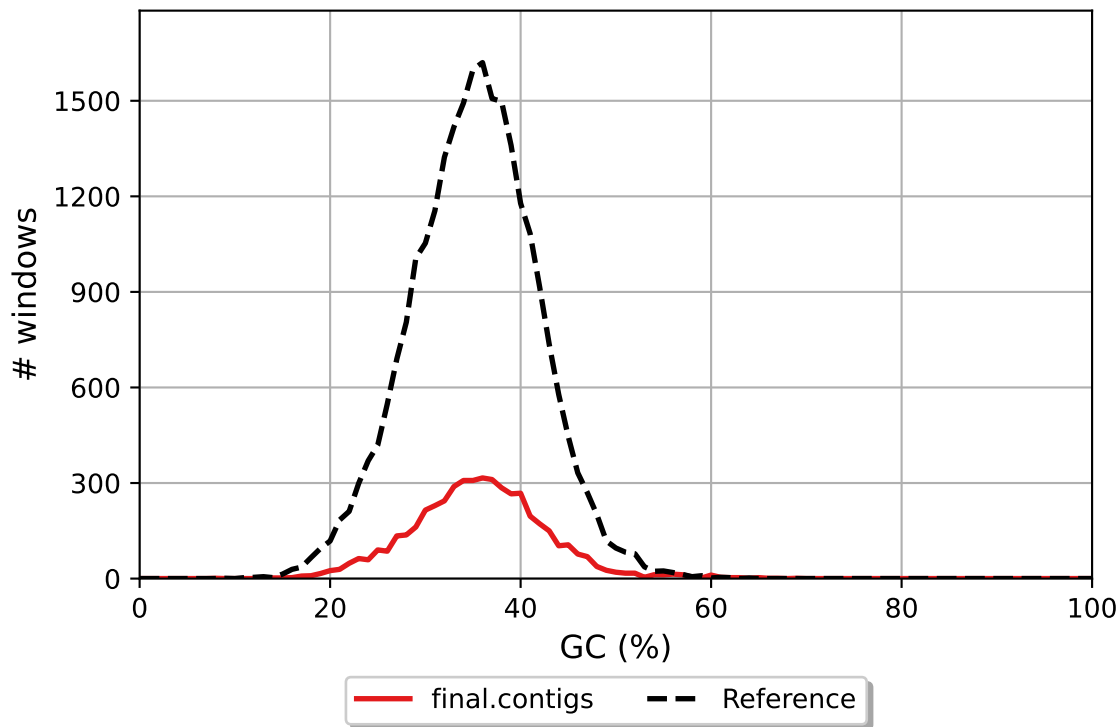


— final.contigs

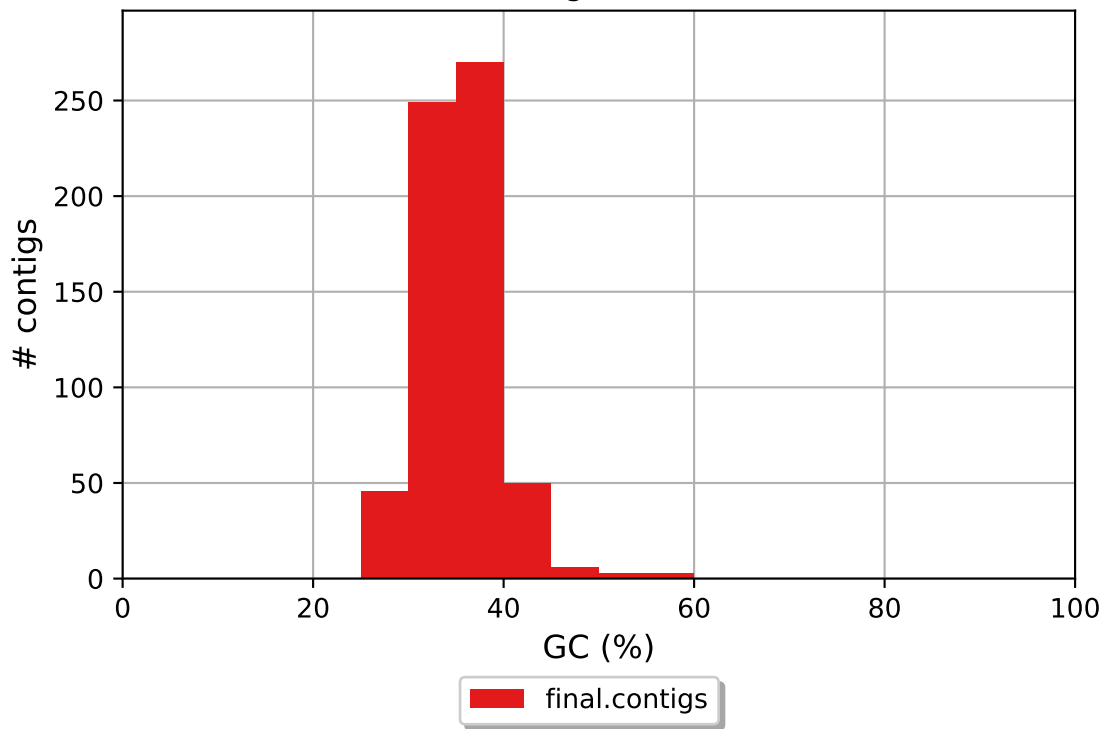
Cumulative length



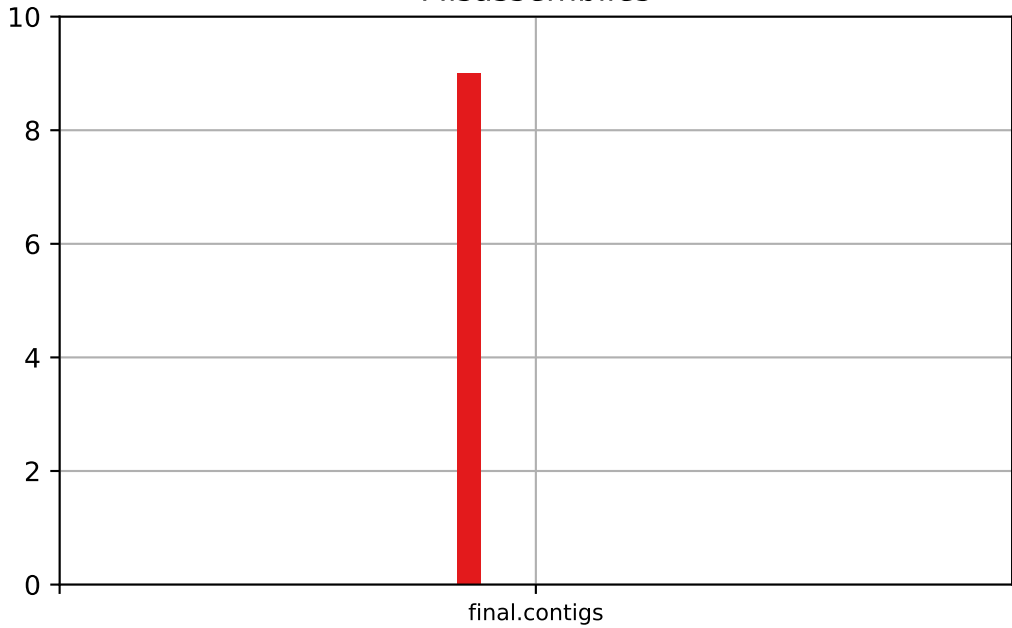
GC content



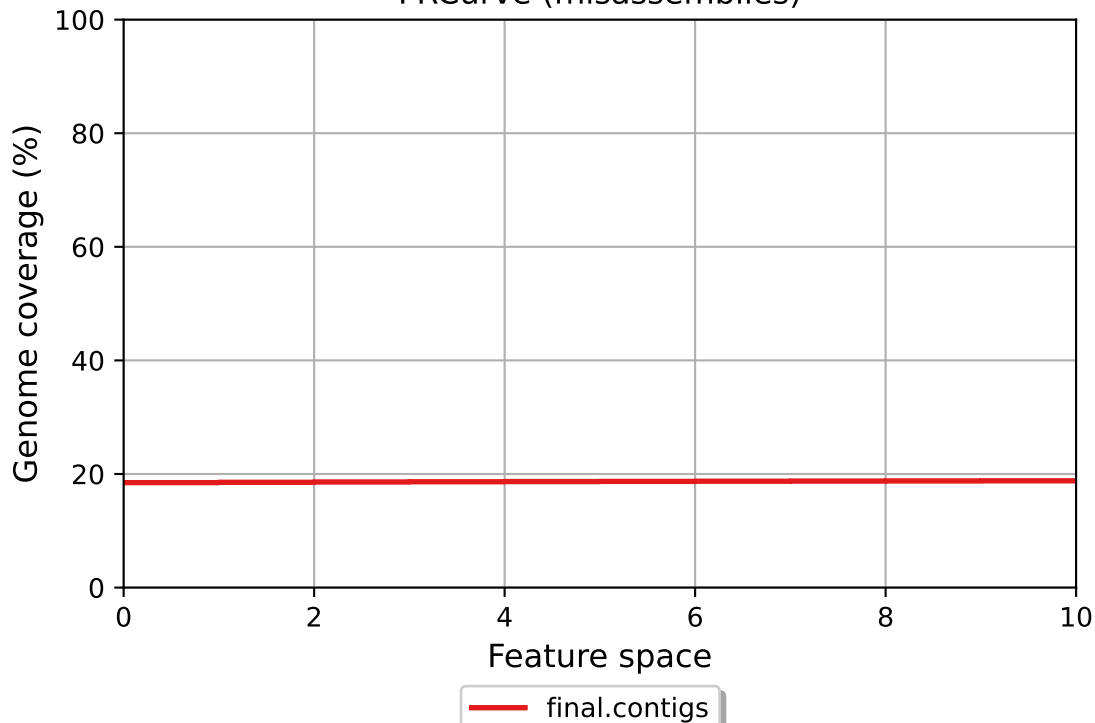
final.contigs GC content



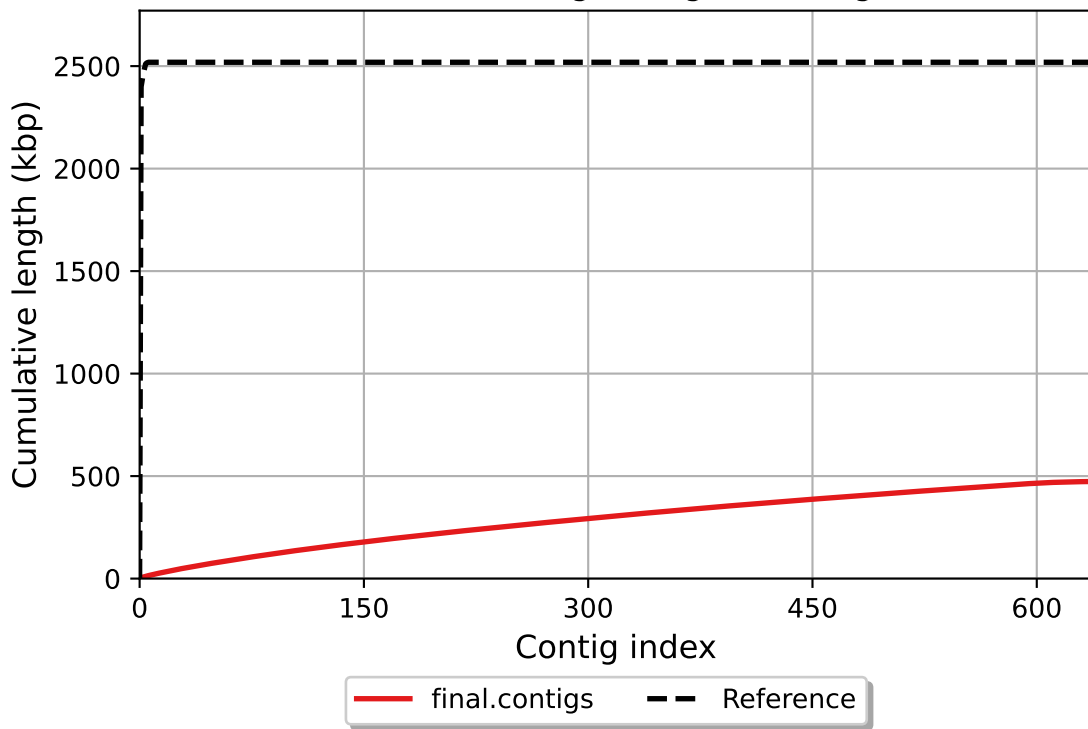
Misassemblies



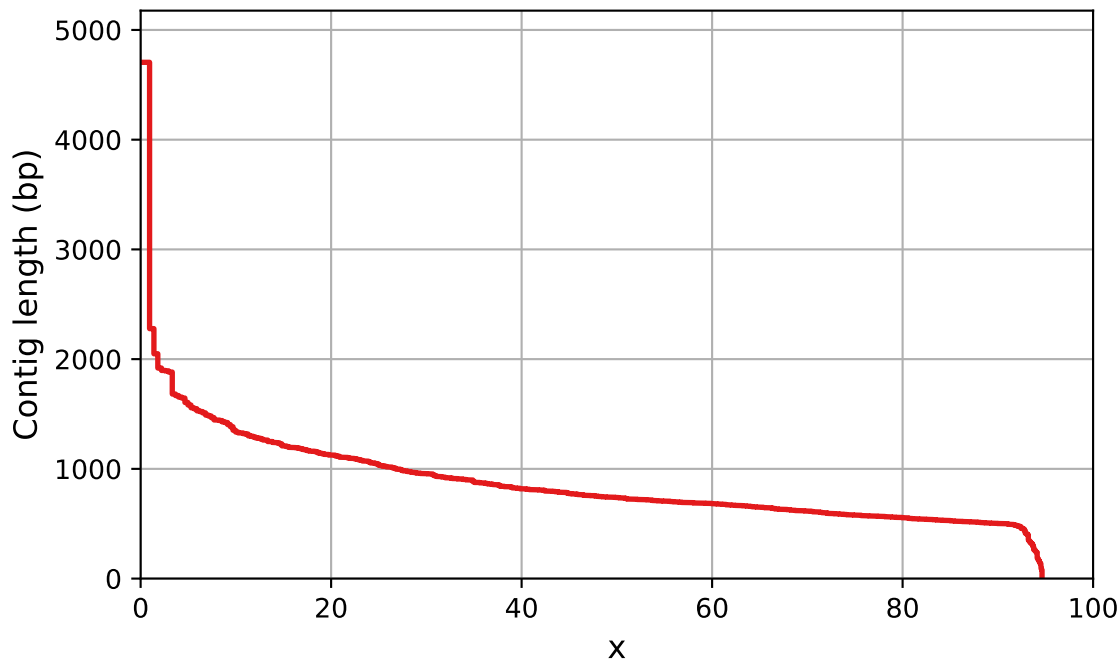
FRCurve (misassemblies)



Cumulative length (aligned contigs)

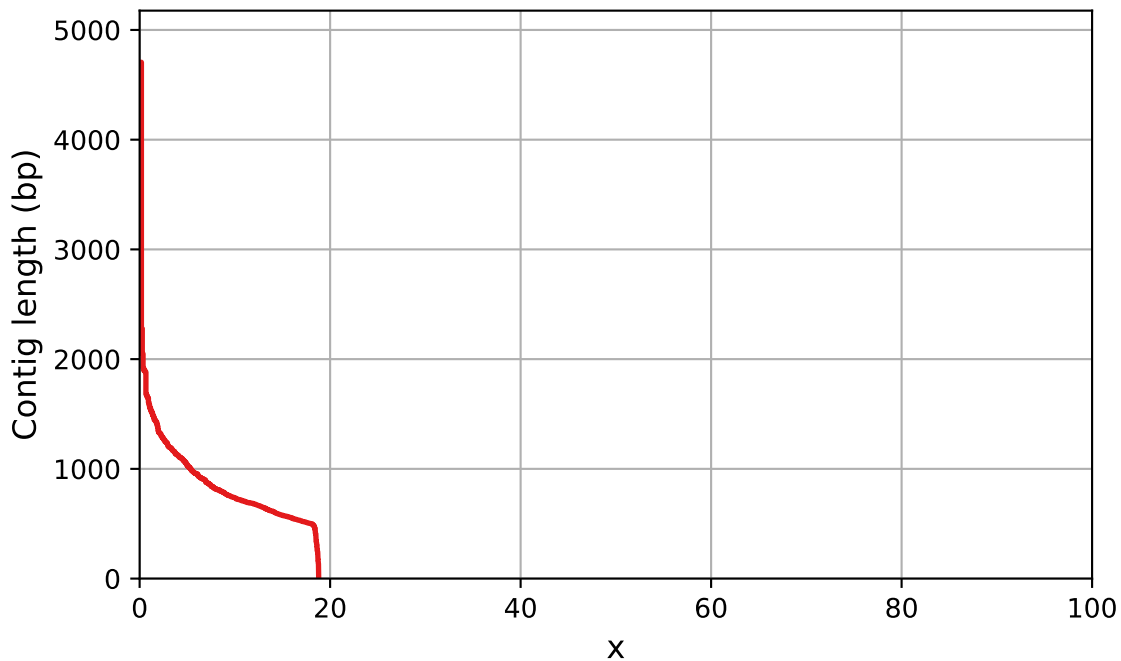


NAx



— final.contigs

NGAx



— final.contigs