

Report

	final.contigs
# contigs (>= 1000 bp)	560
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	738442
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	2432
Largest contig	3425
Total length	2036305
Reference length	4327607
GC (%)	53.60
Reference GC (%)	53.93
N50	848
NG50	-
N90	562
NG90	-
auN	967.1
auNG	455.1
L50	865
LG50	-
L90	2048
LG90	-
# misassemblies	11
# misassembled contigs	11
Misassembled contigs length	11711
# local misassemblies	5
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# unaligned contigs	1 + 105 part
Unaligned length	78187
Genome fraction (%)	38.366
Duplication ratio	1.073
# N's per 100 kbp	0.00
# mismatches per 100 kbp	6492.52
# indels per 100 kbp	127.92
Largest alignment	3144
Total aligned length	1780803
NA50	731
NGA50	-
NA90	-
NGA90	-
auNA	784.1
auNGA	368.9
LA50	970
LGA50	-
LA90	-
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

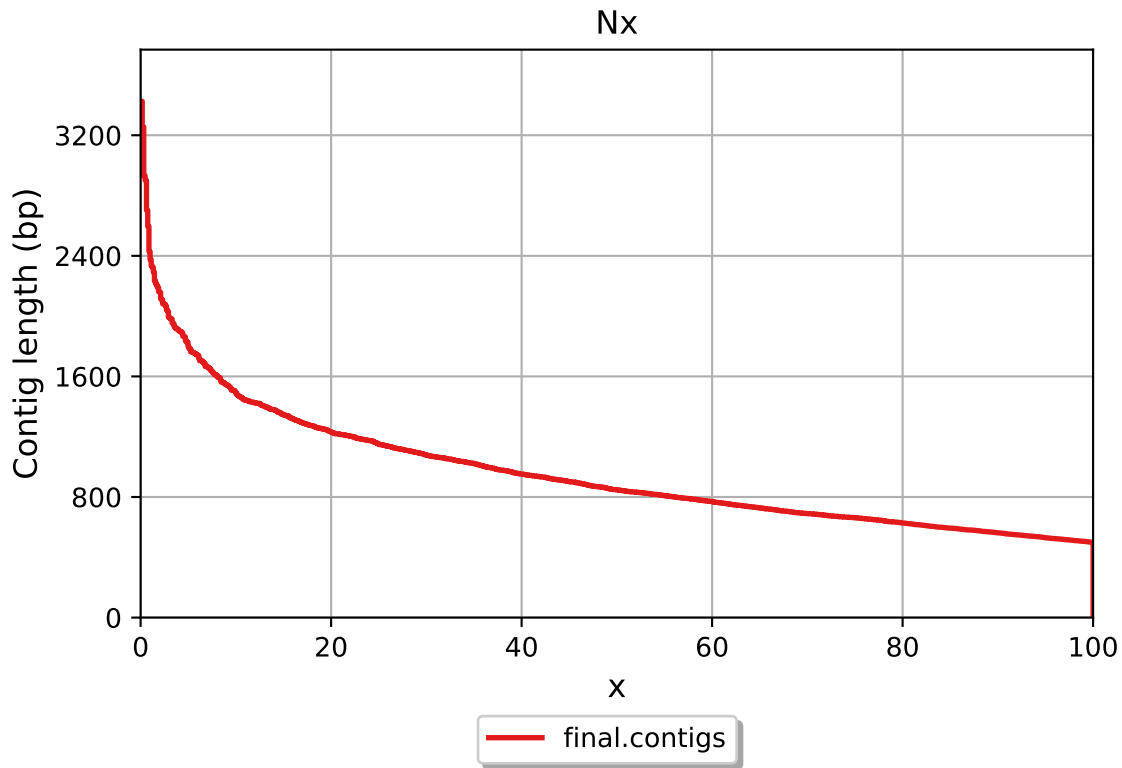
	final.contigs
# misassemblies	11
# contig misassemblies	11
# c. relocations	11
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	11
Misassembled contigs length	11711
# possibly misassembled contigs	84
# possible misassemblies	85
# local misassemblies	5
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# mismatches	115619
# indels	2278
# indels (<= 5 bp)	2234
# indels (> 5 bp)	44
Indels length	4966

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).

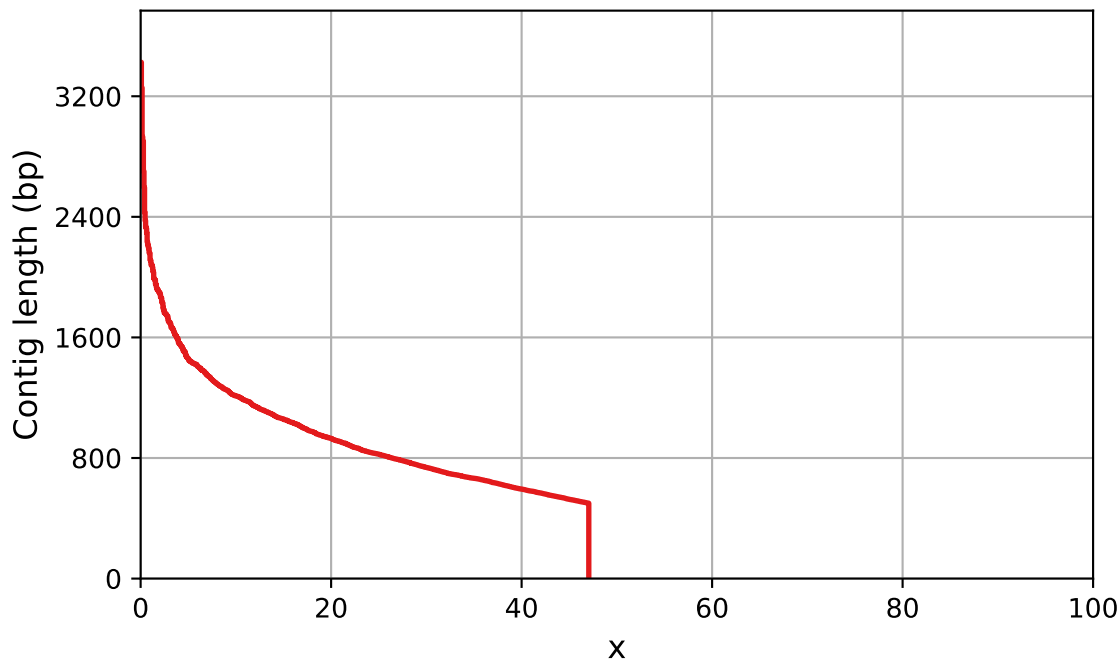
Unaligned report

	final.contigs
# fully unaligned contigs	1
Fully unaligned length	745
# partially unaligned contigs	105
Partially unaligned length	77442
# 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).

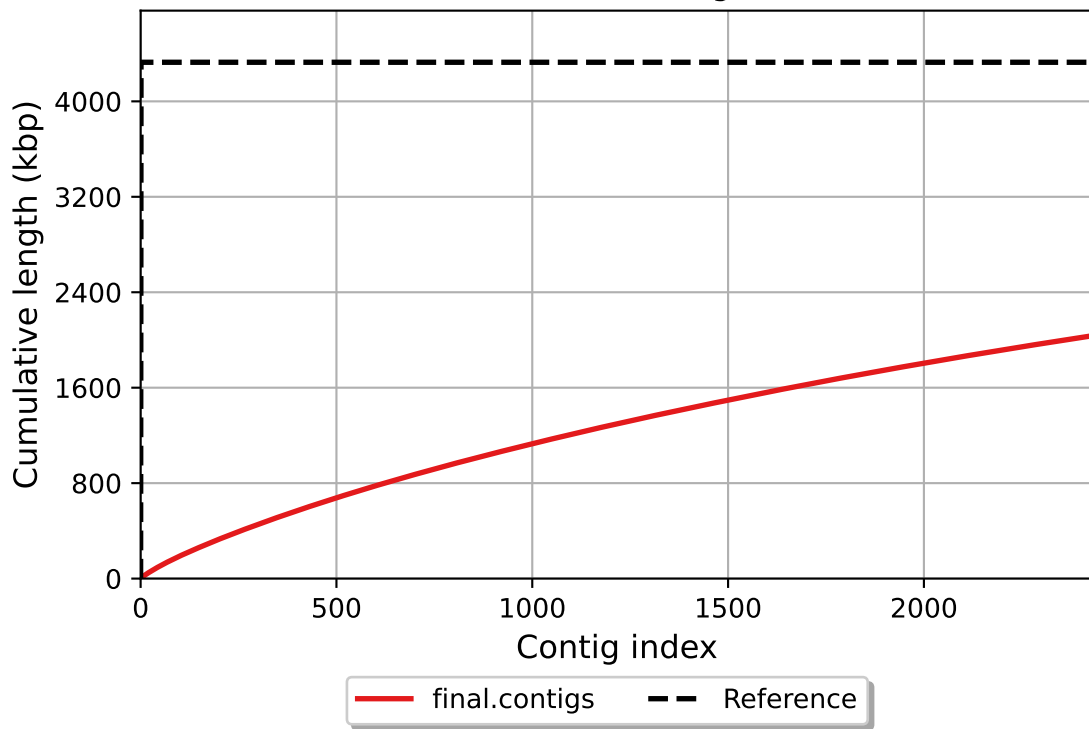


NGx

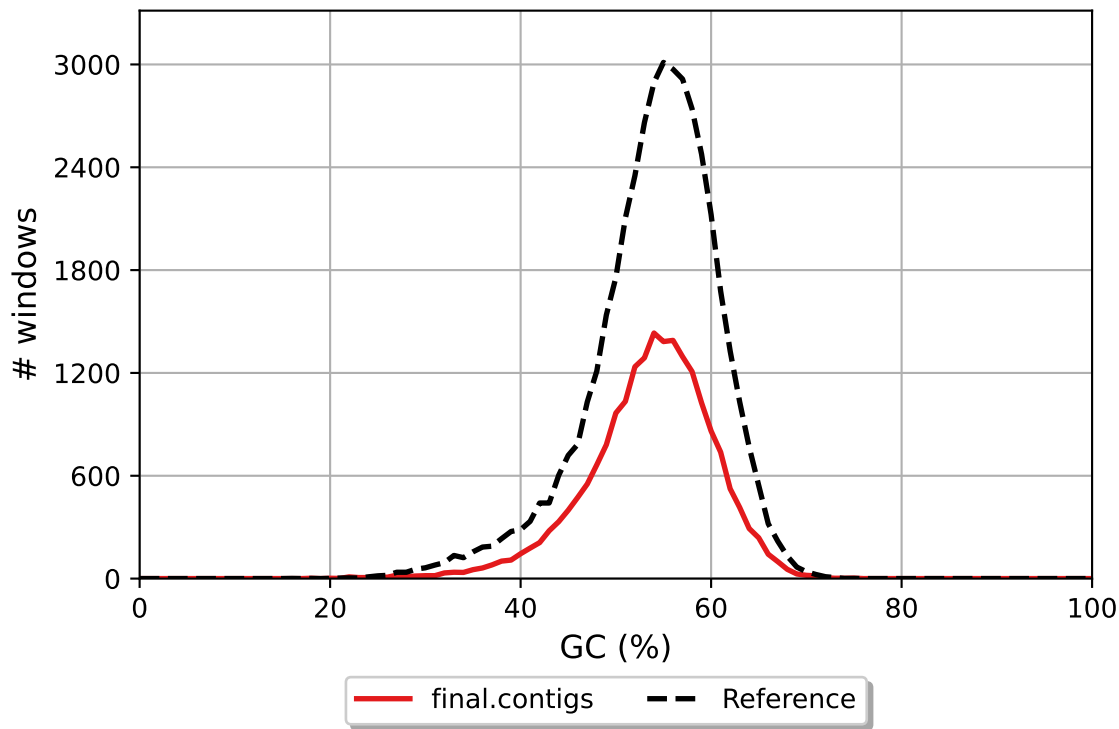


— final.contigs

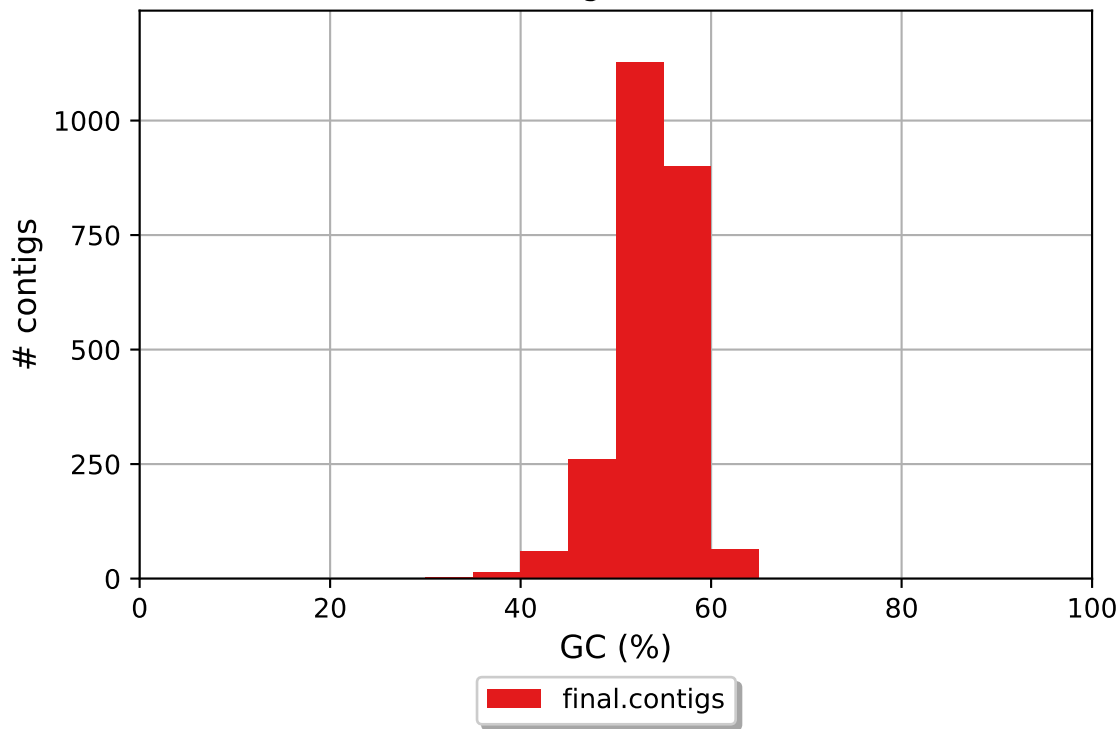
Cumulative length



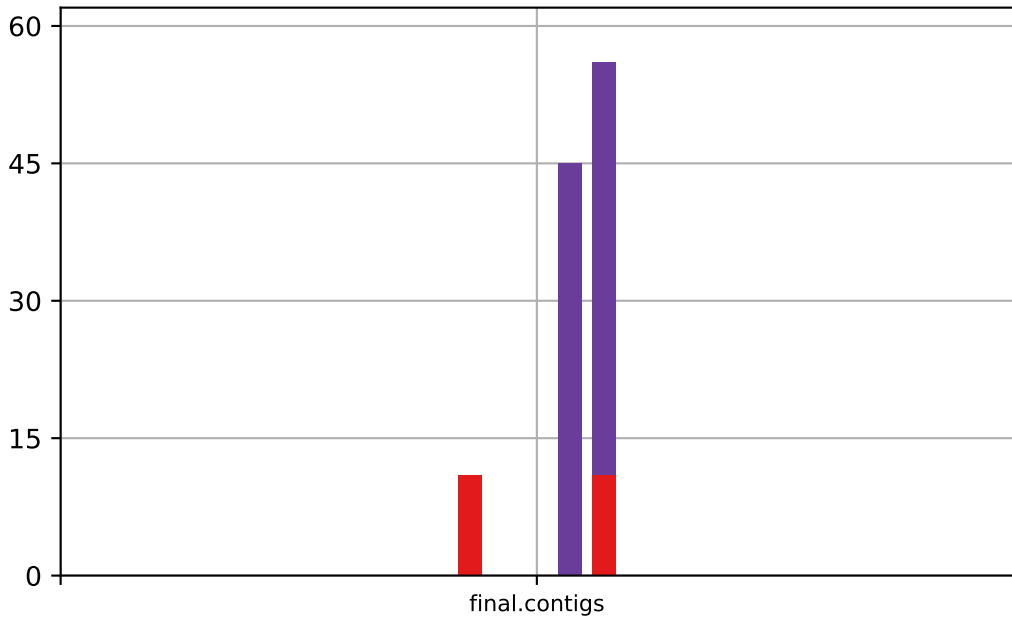
GC content



final.contigs GC content



Misassemblies

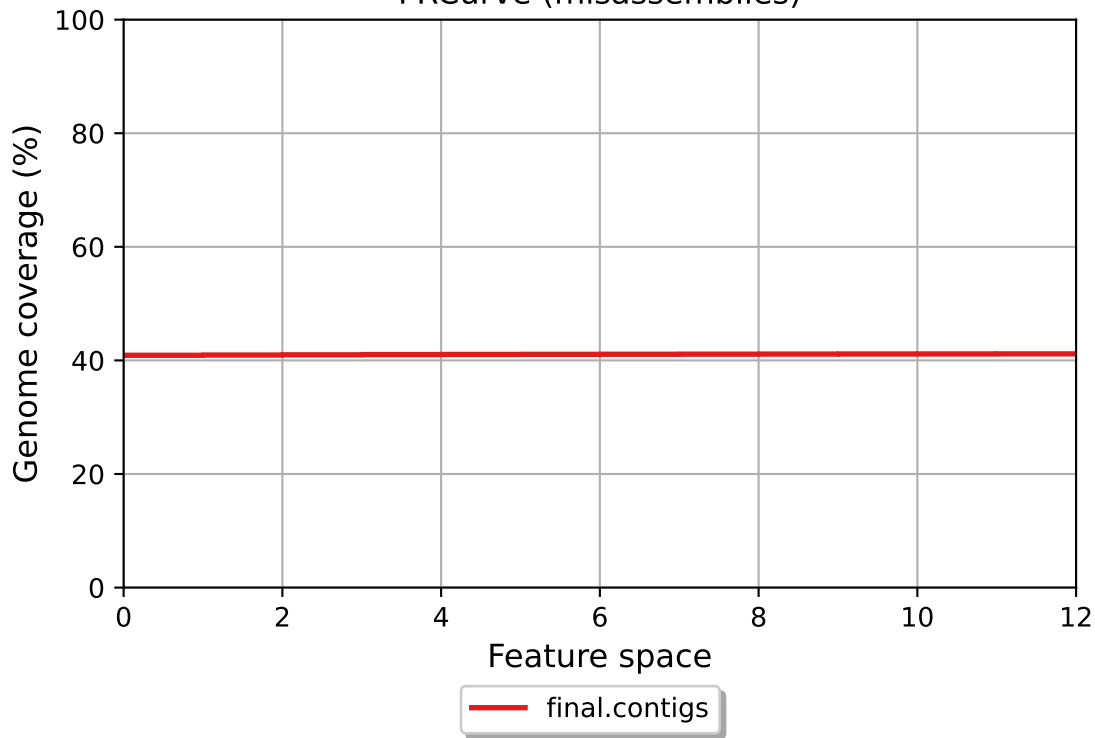


relocations

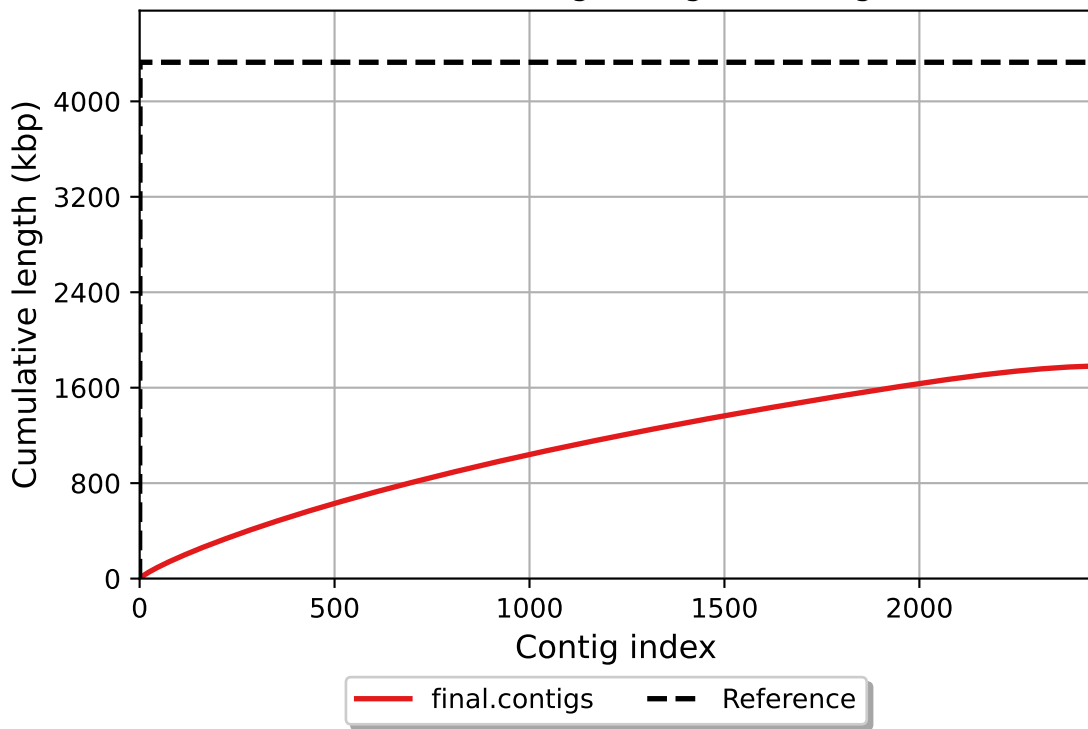


interspecies translocations

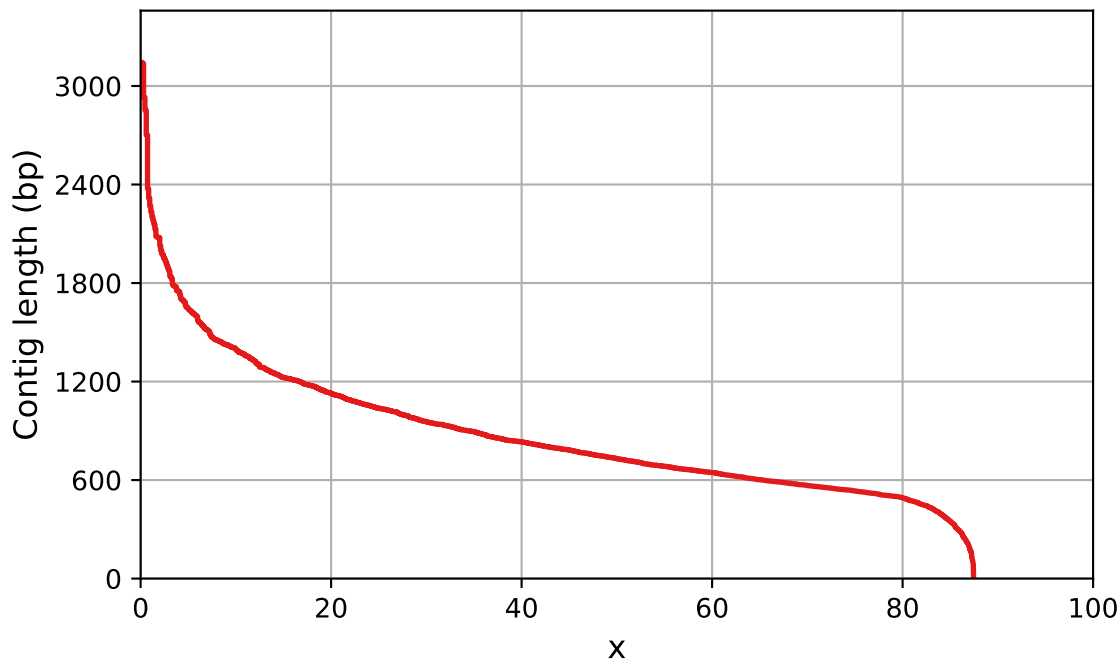
FRCurve (misassemblies)



Cumulative length (aligned contigs)

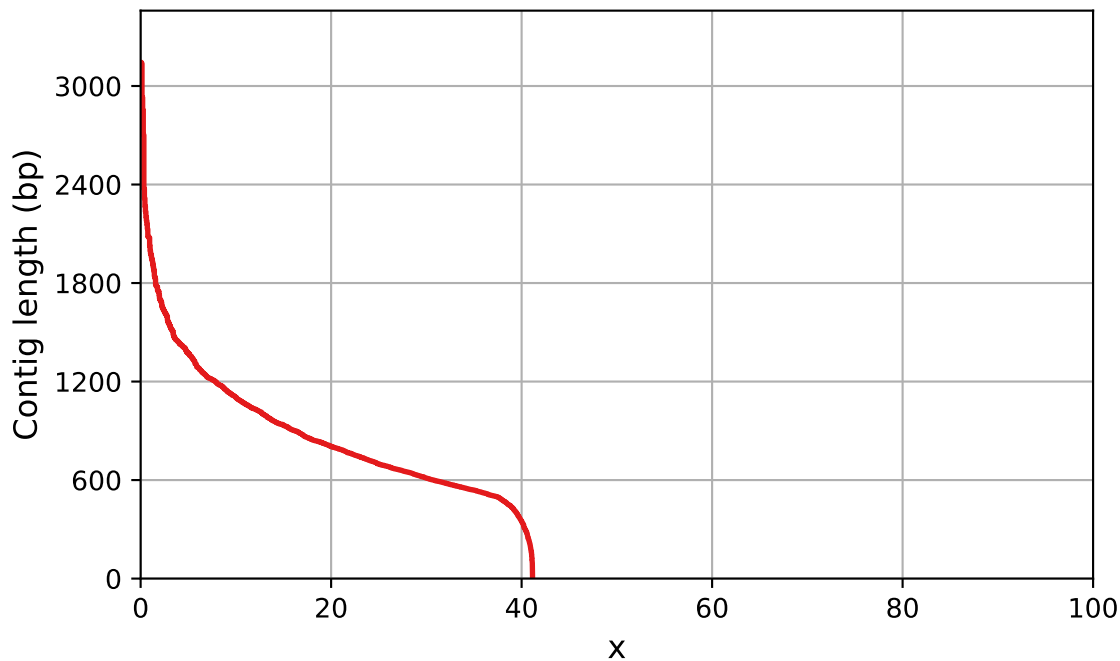


NAx



— final.contigs

NGAx



— final.contigs