

Report

	contigs
# contigs (>= 0 bp)	16044
# contigs (>= 1000 bp)	417
# contigs (>= 5000 bp)	52
# contigs (>= 10000 bp)	43
# contigs (>= 25000 bp)	38
# contigs (>= 50000 bp)	26
Total length (>= 0 bp)	8694945
Total length (>= 1000 bp)	3966879
Total length (>= 5000 bp)	3418006
Total length (>= 10000 bp)	3344438
Total length (>= 25000 bp)	3270701
Total length (>= 50000 bp)	2885063
# contigs	1735
Largest contig	271548
Total length	4855457
Reference length	68998803
N50	73211
N90	703
auN	88238.6
L50	19
L90	907
# misassemblies	38
# misassembled contigs	33
Misassembled contigs length	40915
# local misassemblies	7
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# unaligned contigs	334 + 18 part
Unaligned length	3700200
Genome fraction (%)	4.488
Duplication ratio	1.002
# N's per 100 kbp	0.00
# mismatches per 100 kbp	5002.02
# indels per 100 kbp	113.40
Largest alignment	3900
Total aligned length	1139379
NA50	-
NA90	-
auNA	222.9
LA50	-
LA90	-

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

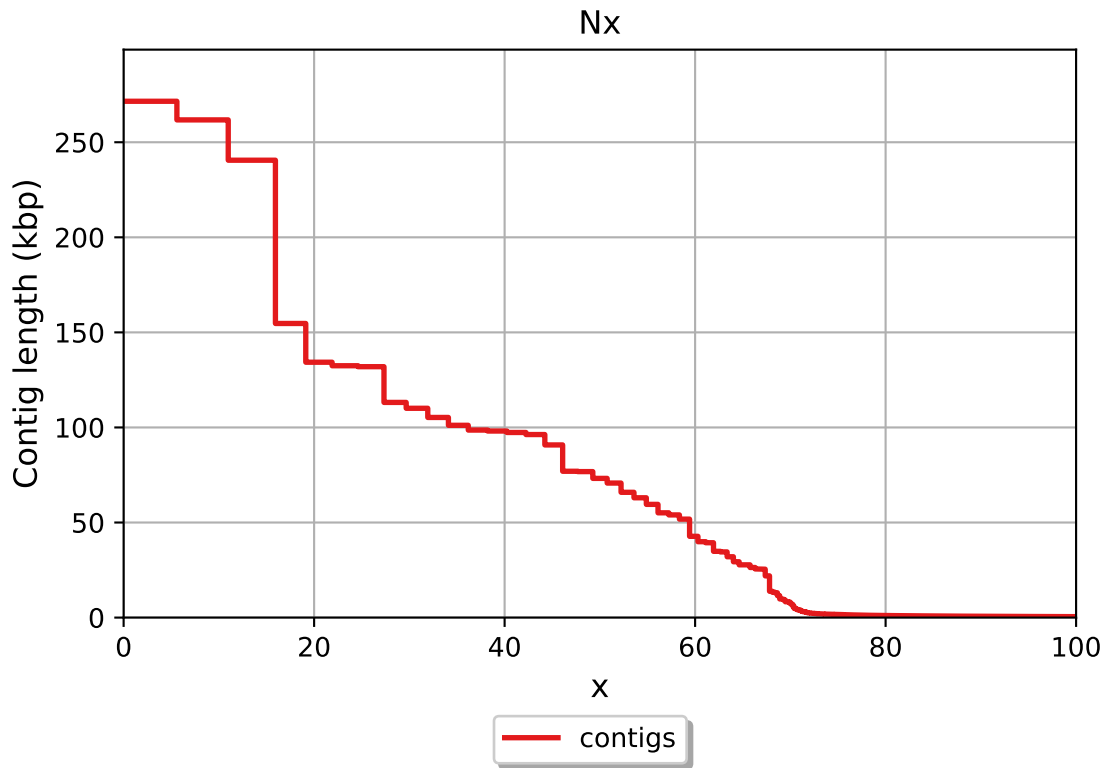
	contigs
# misassemblies	38
# contig misassemblies	38
# c. relocations	1
# c. translocations	16
# c. inversions	0
# c. interspecies translocations	21
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# s. interspecies translocations	0
# misassembled contigs	33
Misassembled contigs length	40915
# possibly misassembled contigs	17
# possible misassemblies	22
# local misassemblies	7
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# mismatches	56992
# indels	1292
# indels (<= 5 bp)	1157
# indels (> 5 bp)	135
Indels length	5236

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).

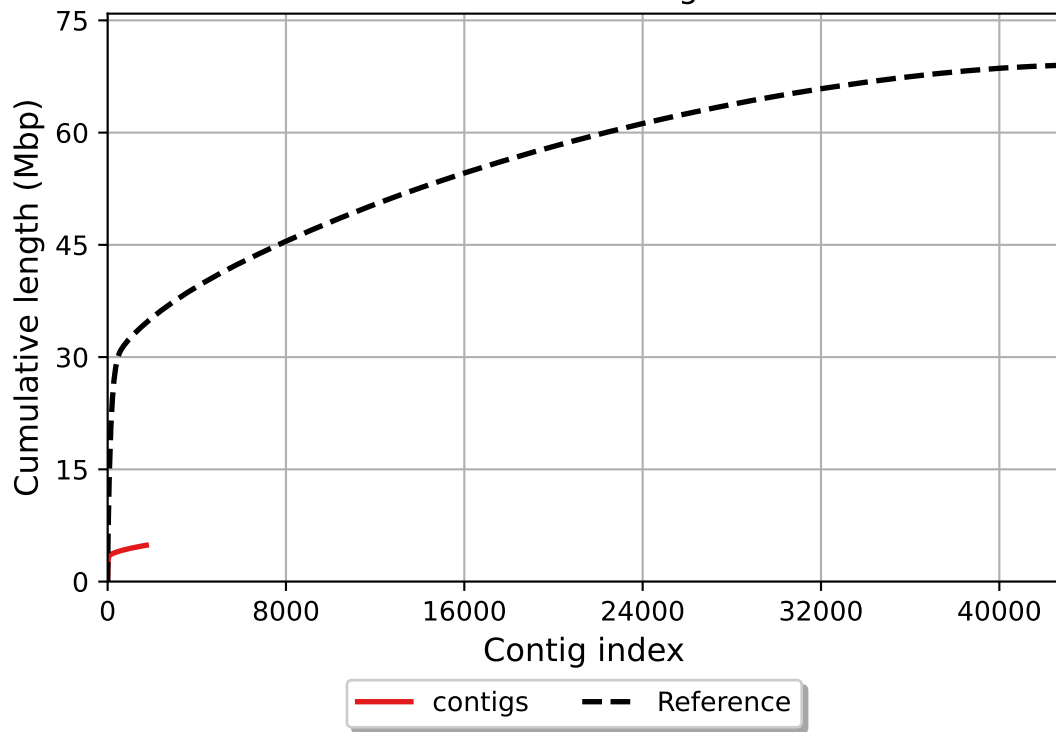
Unaligned report

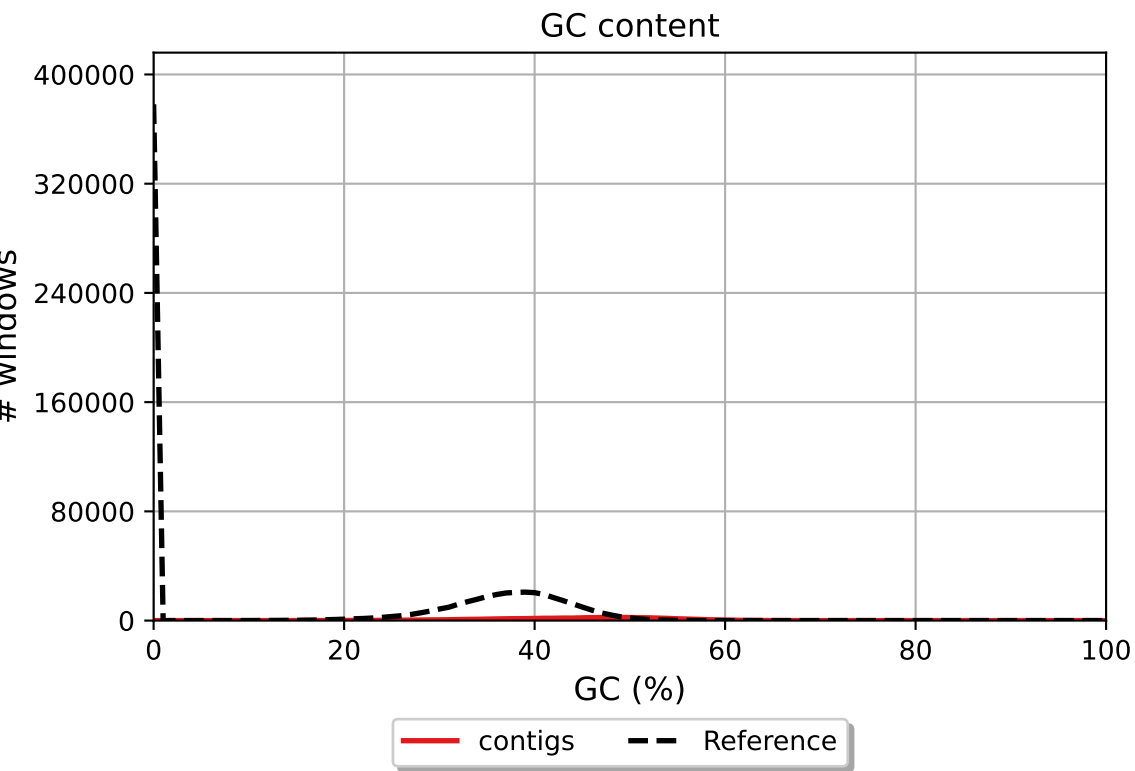
	contigs
# fully unaligned contigs	334
Fully unaligned length	3459874
# partially unaligned contigs	18
Partially unaligned length	240326
# N's	0

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).

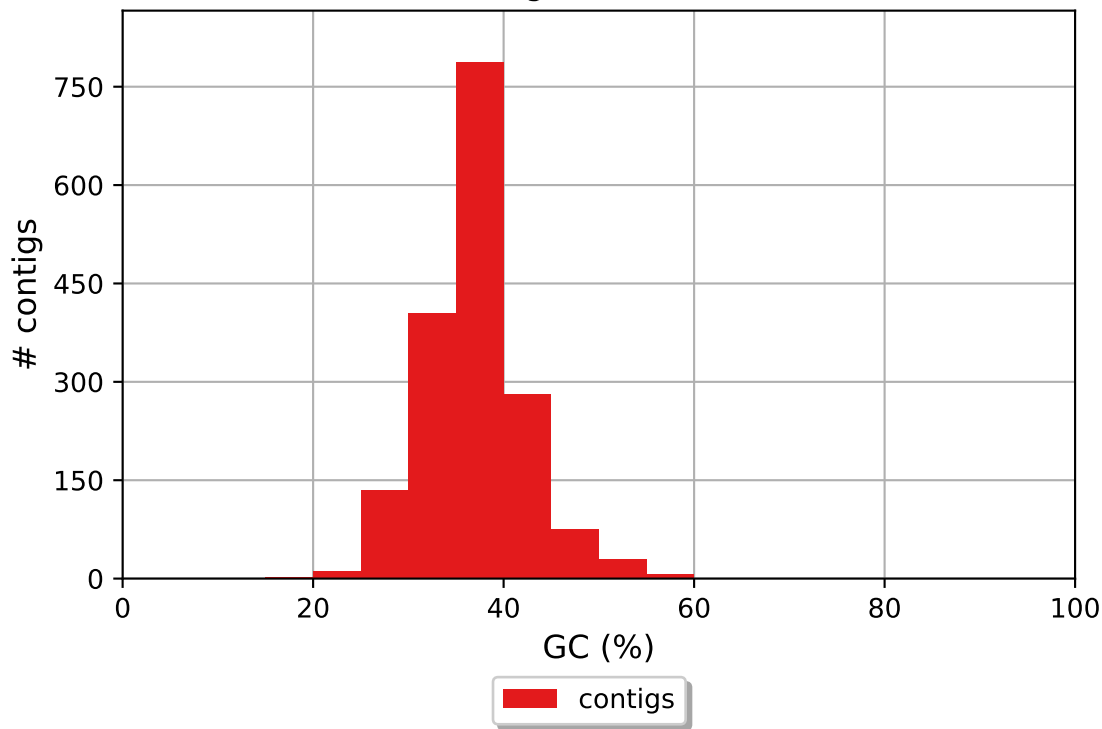


Cumulative length

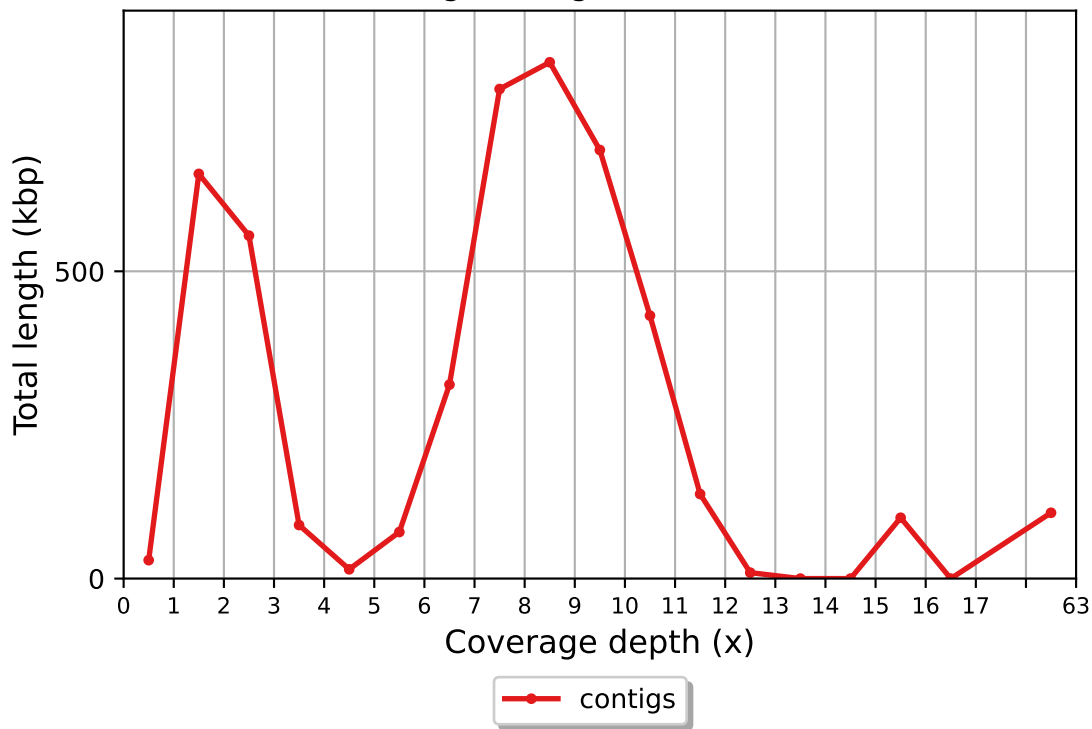




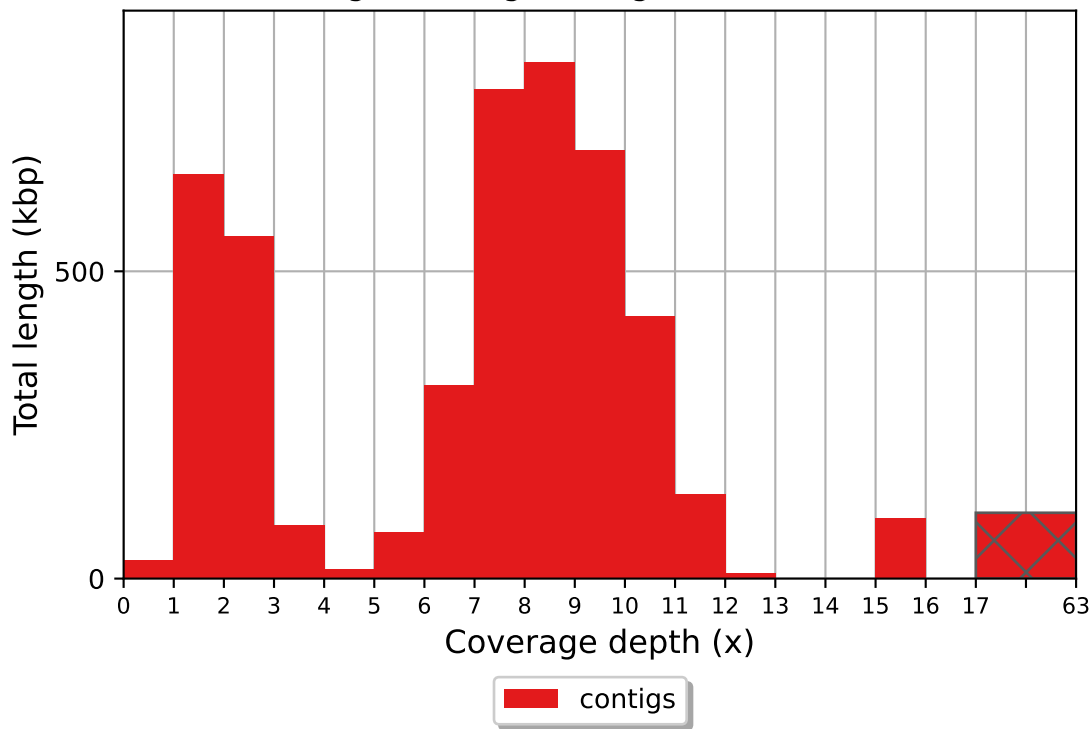
contigs GC content



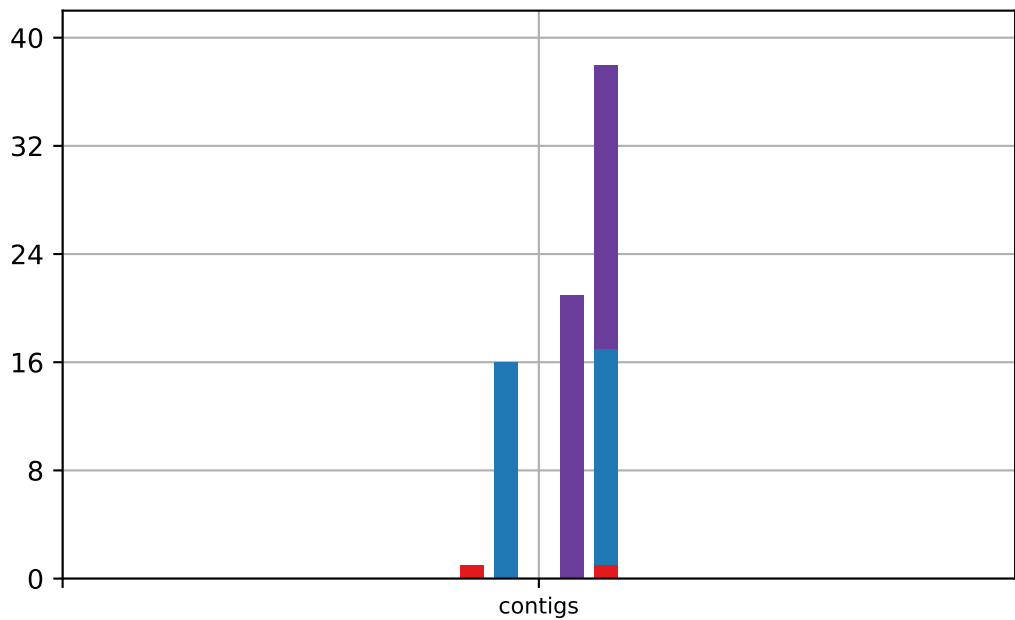
Coverage histogram (bin size: 1x)



contigs coverage histogram (bin size: 1x)

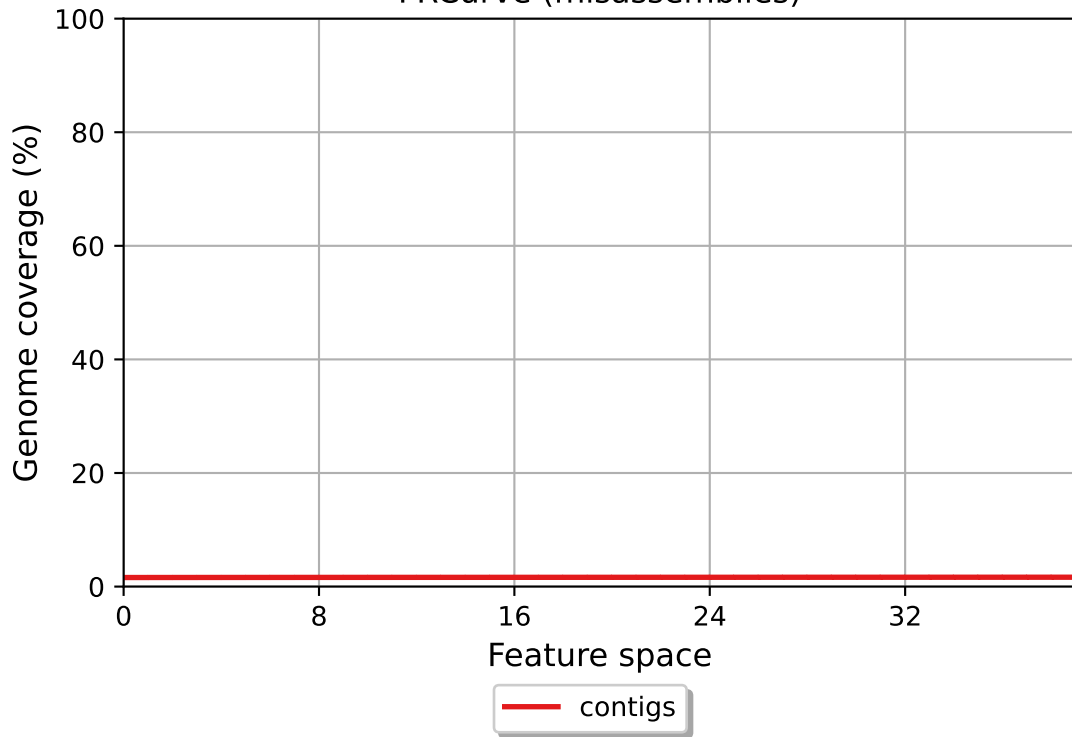


Misassemblies

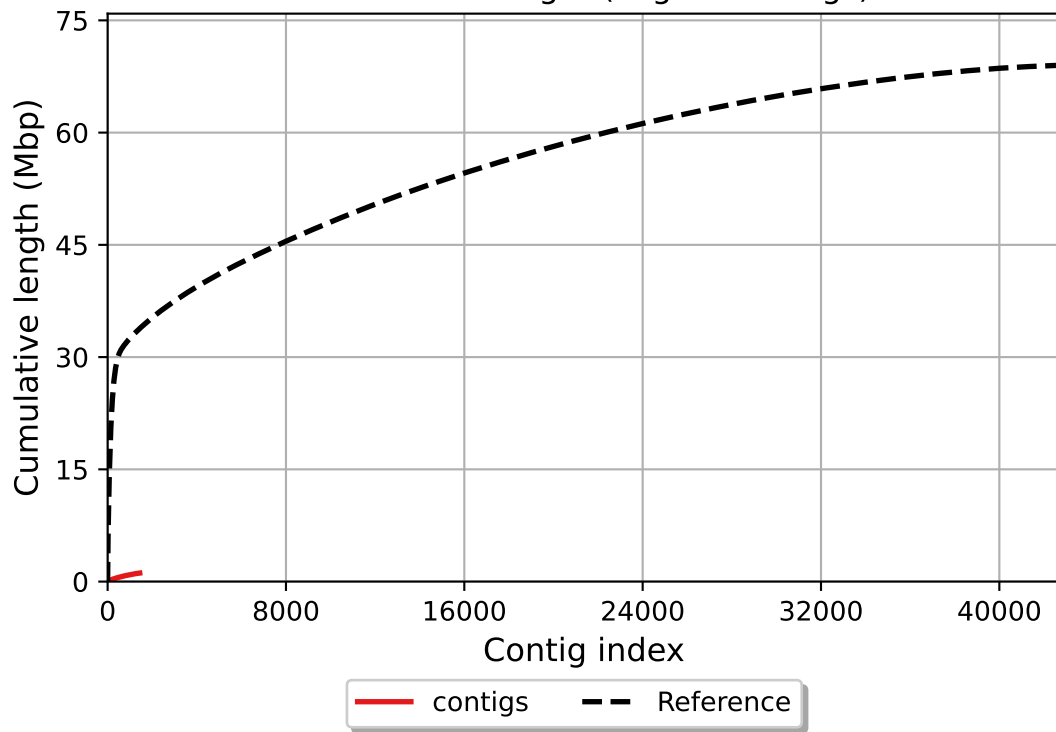


relocations # translocations # interspecies translocations

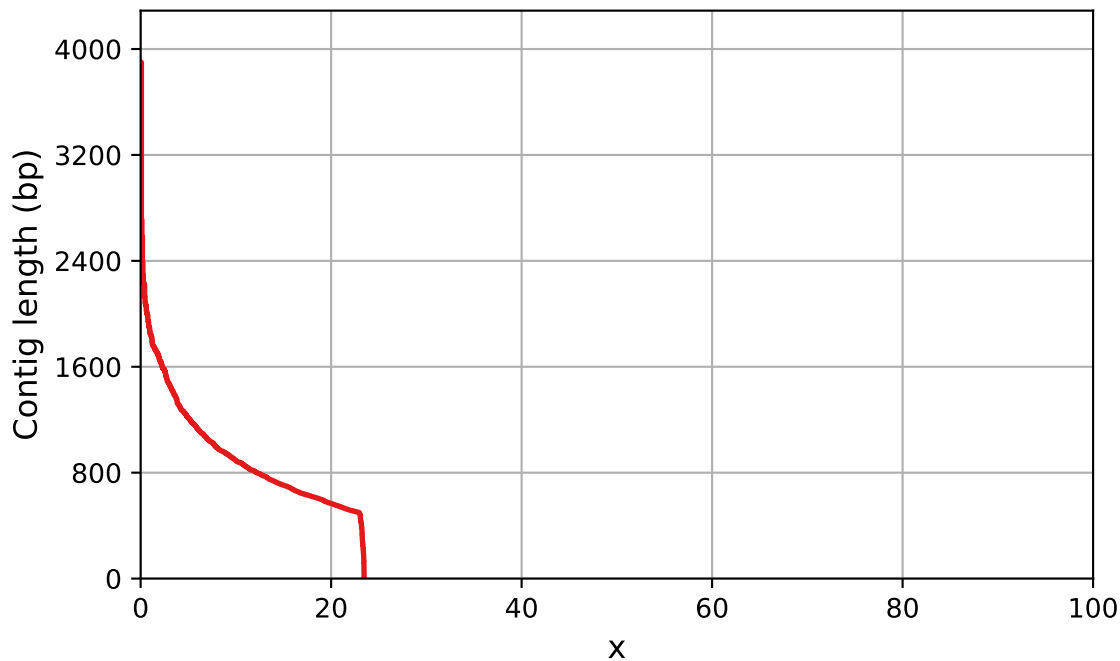
FRCurve (misassemblies)



Cumulative length (aligned contigs)



NAx



contigs