

Report

	contigs
# contigs (>= 1000 bp)	209
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	284618
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	908
Largest contig	2609
Total length	767584
Reference length	2576508
GC (%)	36.56
Reference GC (%)	36.68
N50	864
NG50	-
N90	559
NG90	-
auN	985.0
auNG	293.5
L50	317
LG50	-
L90	763
LG90	-
# misassemblies	6
# misassembled contigs	6
Misassembled contigs length	8110
# local misassemblies	5
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# unaligned contigs	0 + 5 part
Unaligned length	4117
Genome fraction (%)	29.373
Duplication ratio	1.003
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1780.73
# indels per 100 kbp	44.28
Largest alignment	2584
Total aligned length	758847
NA50	844
NGA50	-
NA90	545
NGA90	-
auNA	955.9
auNGA	284.8
LA50	324
LGA50	-
LA90	779
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

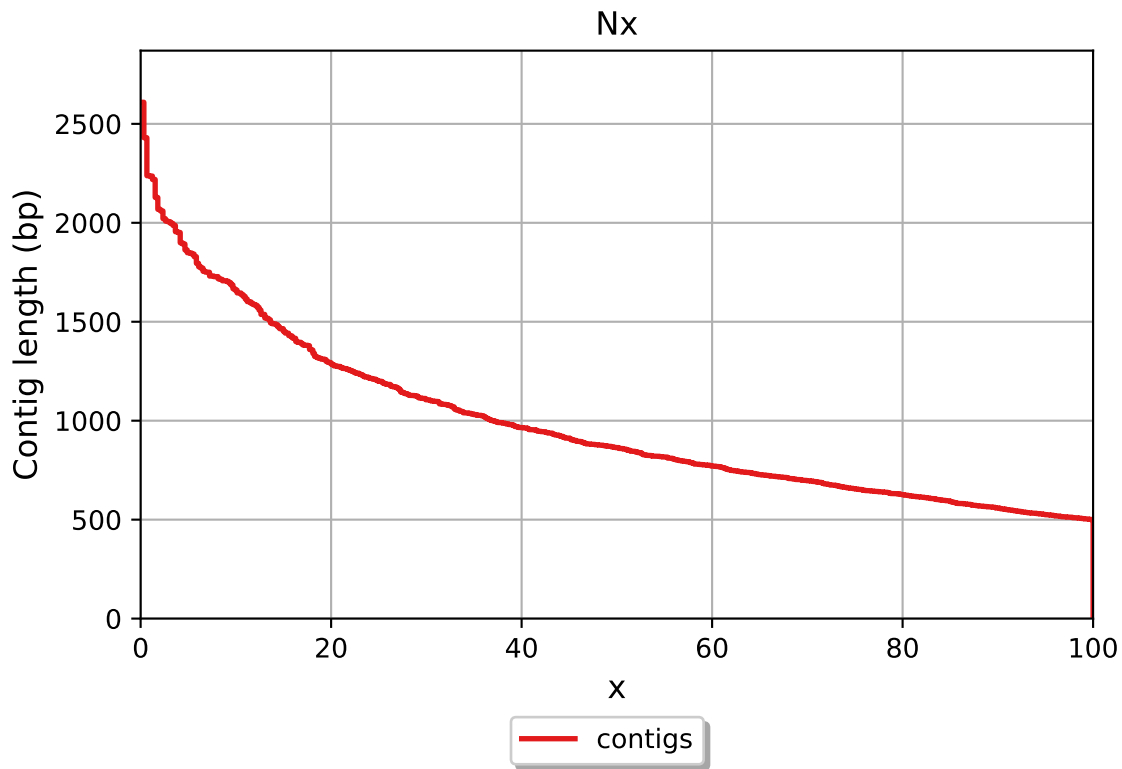
	contigs
# misassemblies	6
# contig misassemblies	6
# c. relocations	1
# c. translocations	5
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	6
Misassembled contigs length	8110
# possibly misassembled contigs	2
# possible misassemblies	2
# local misassemblies	5
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# mismatches	13513
# indels	336
# indels (<= 5 bp)	296
# indels (> 5 bp)	40
Indels length	1617

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).

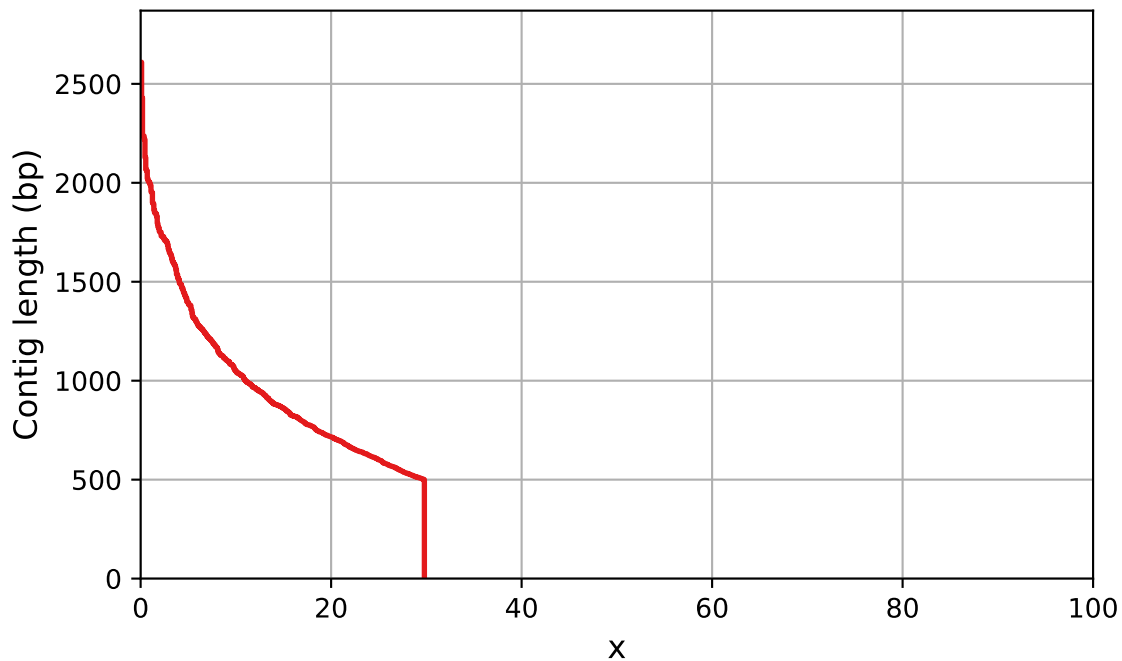
Unaligned report

	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	5
Partially unaligned length	4117
# 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).

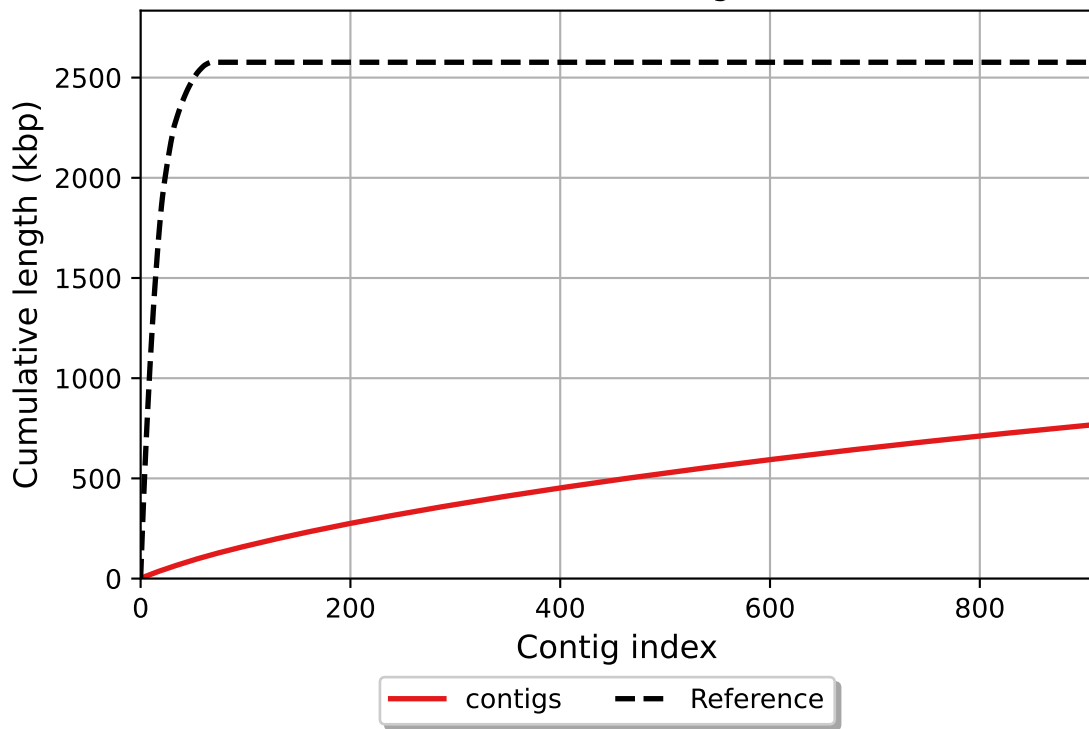


NGx

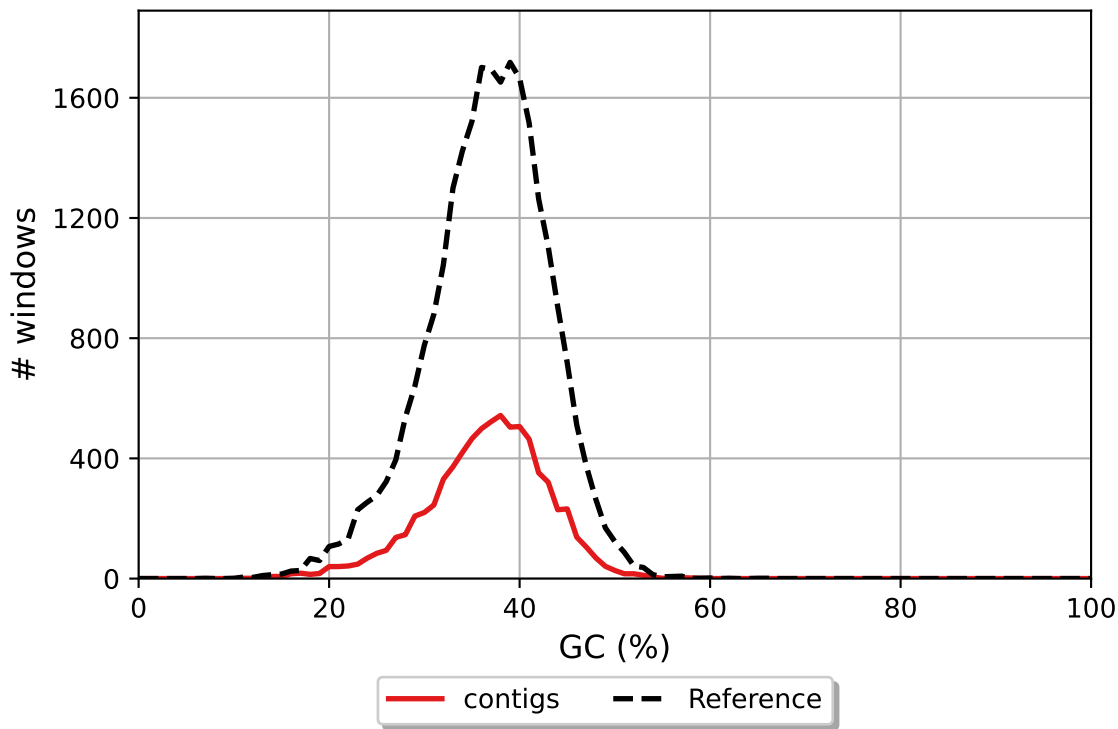


— contigs

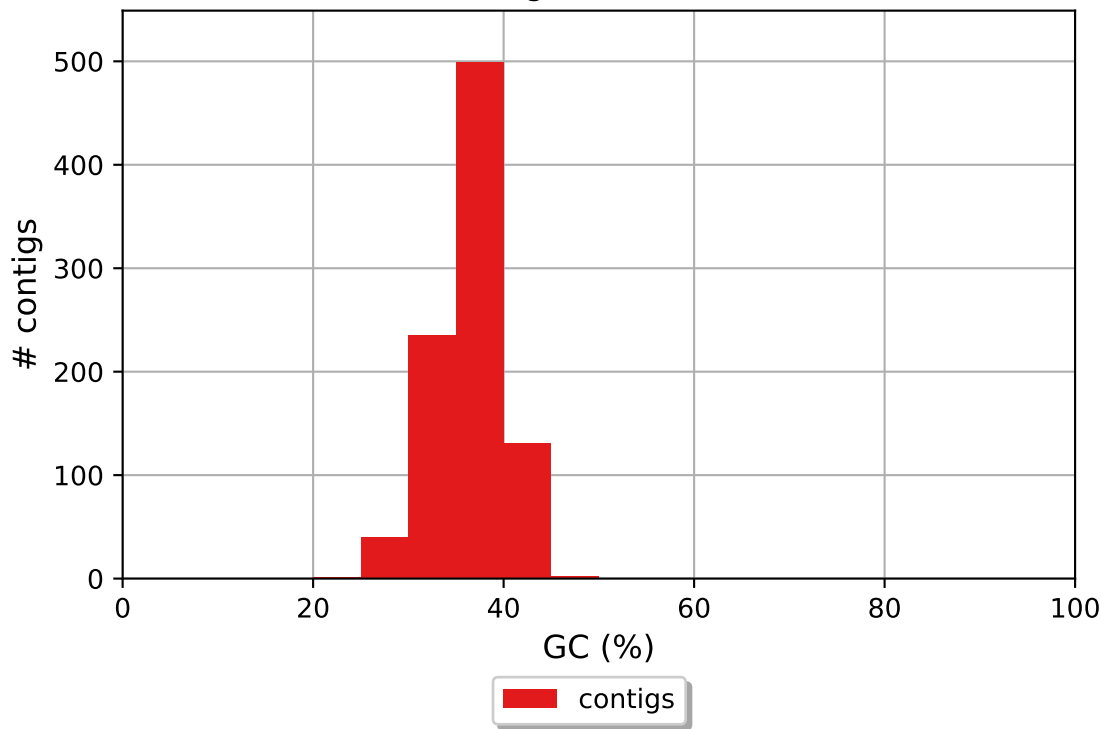
Cumulative length



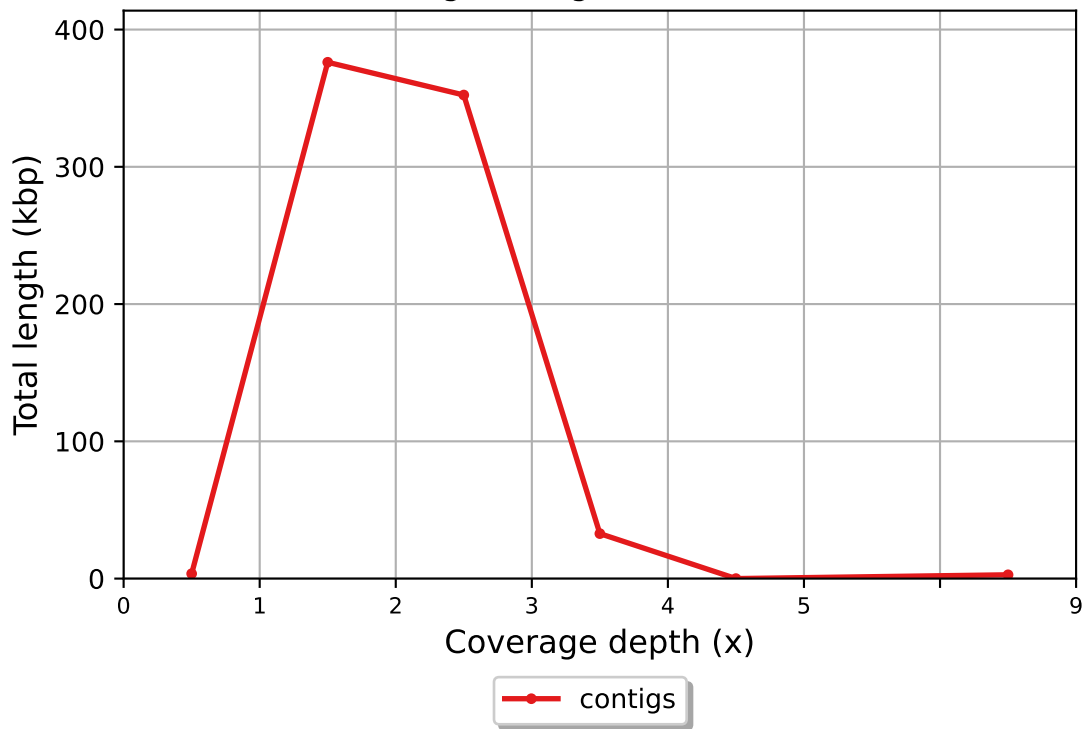
GC content



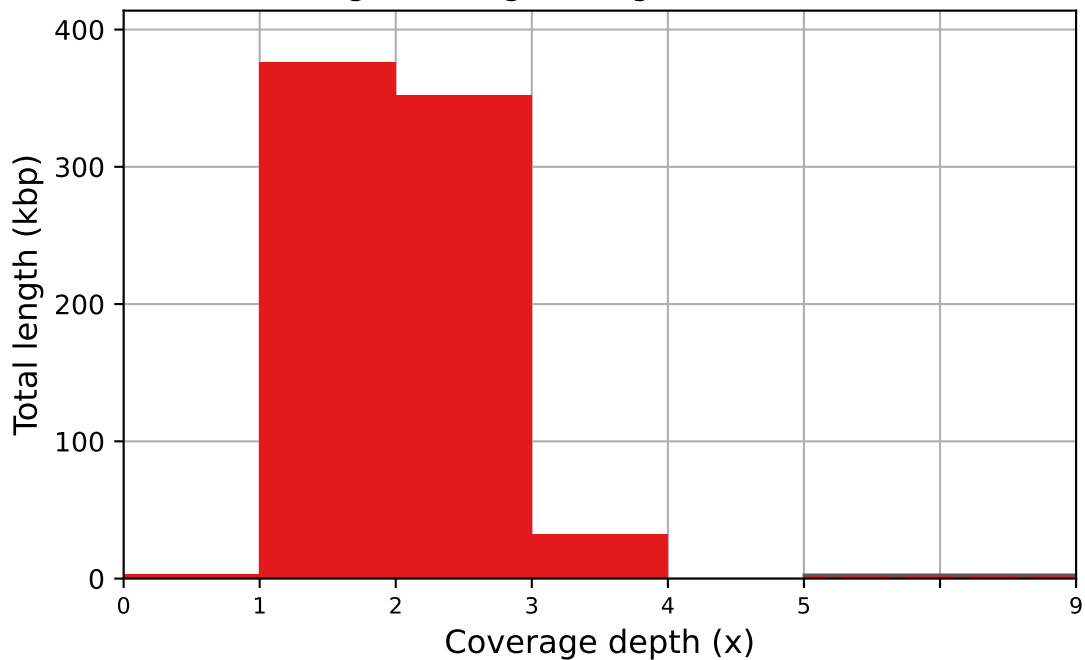
contigs GC content



Coverage histogram (bin size: 1x)

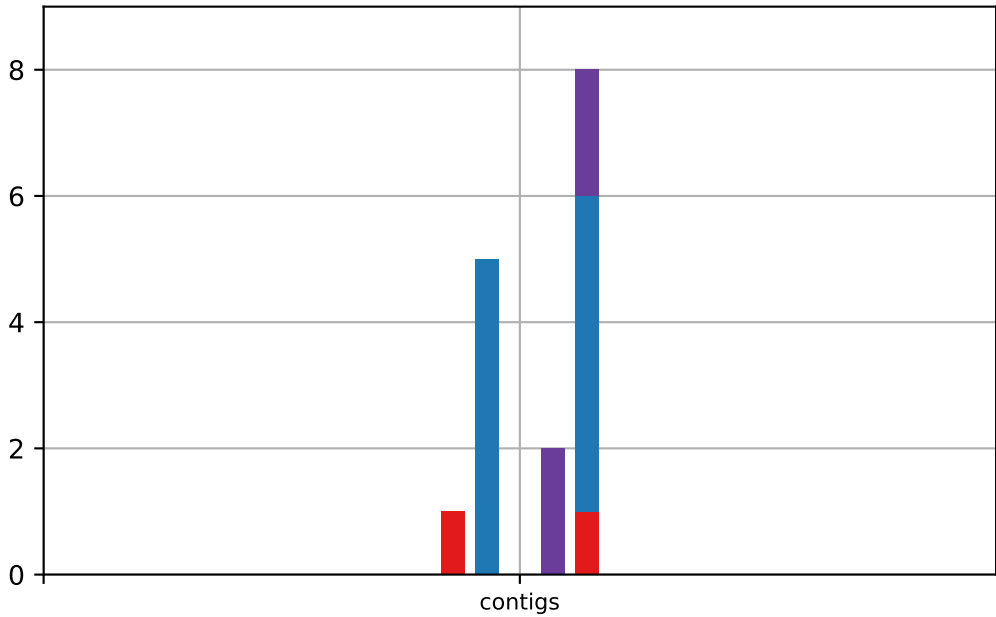


contigs coverage histogram (bin size: 1x)



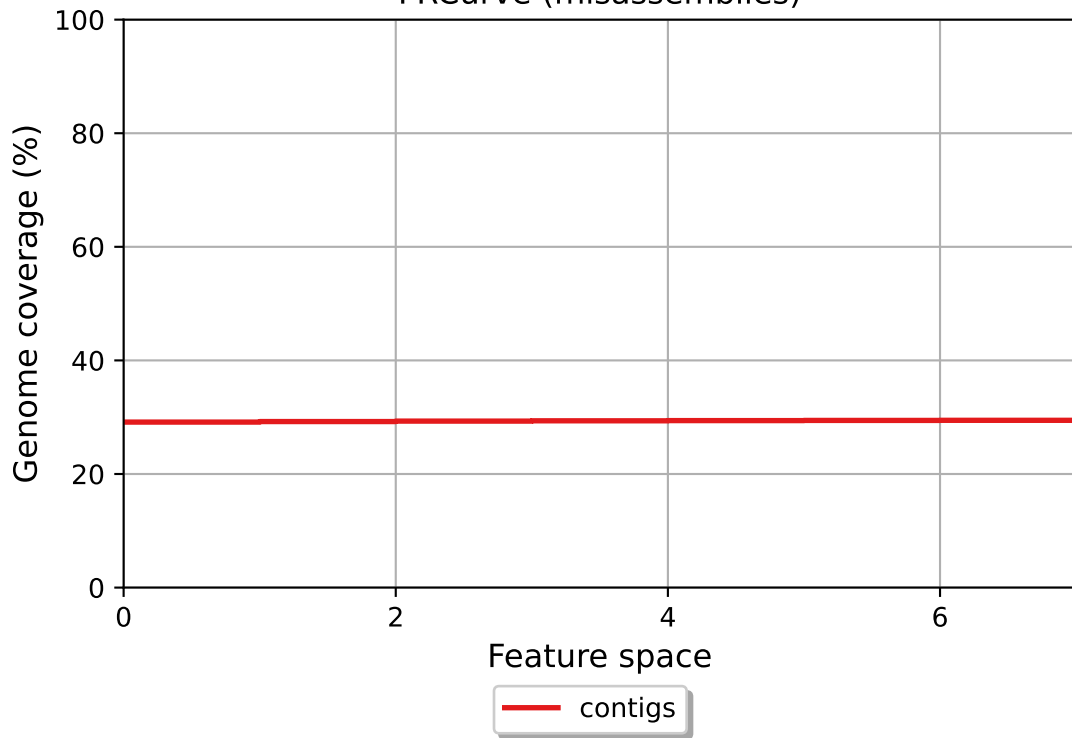
contigs

Misassemblies

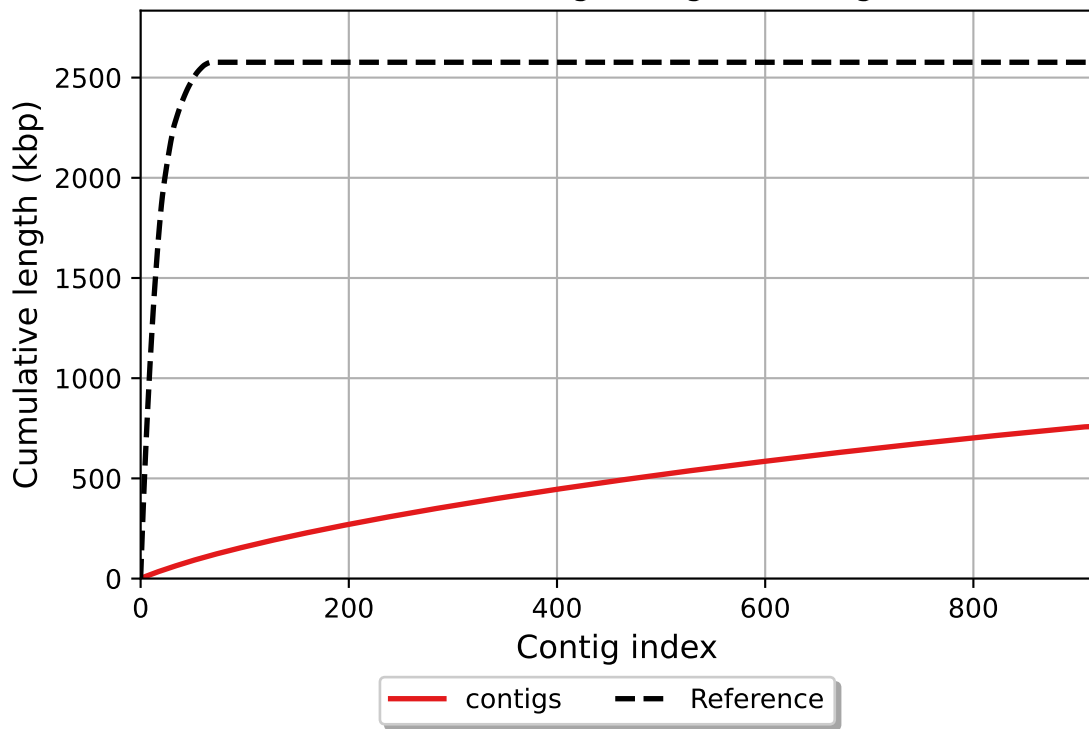


relocations # translocations # interspecies translocations

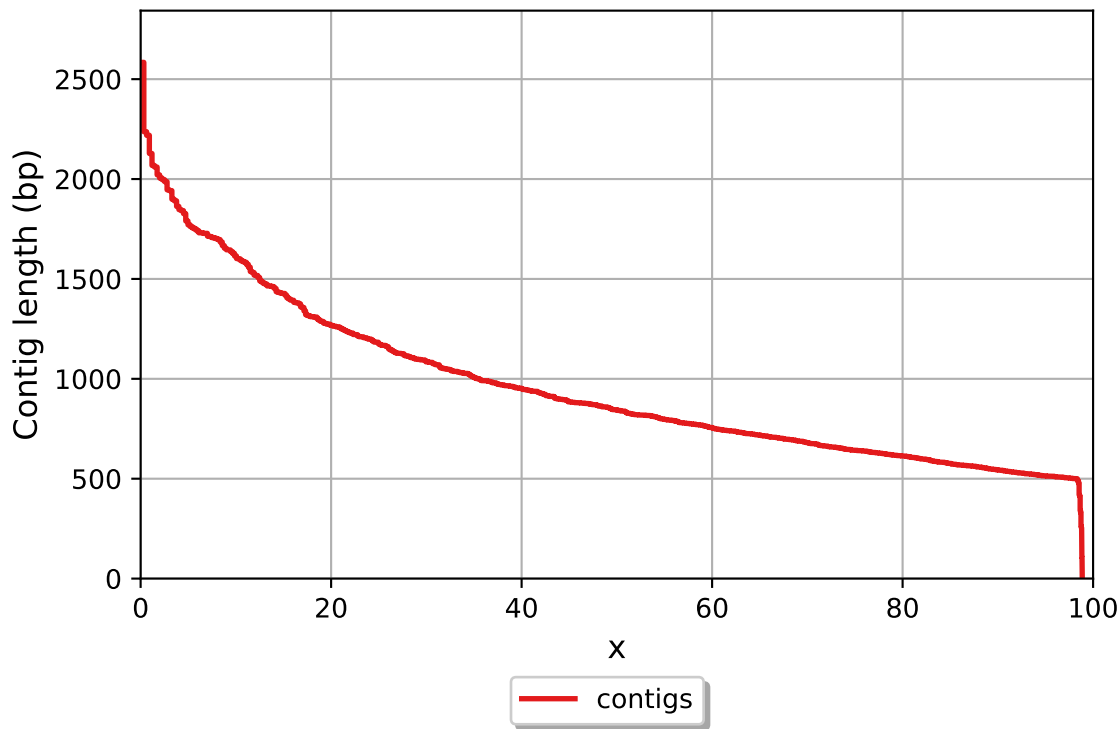
FRCurve (misassemblies)



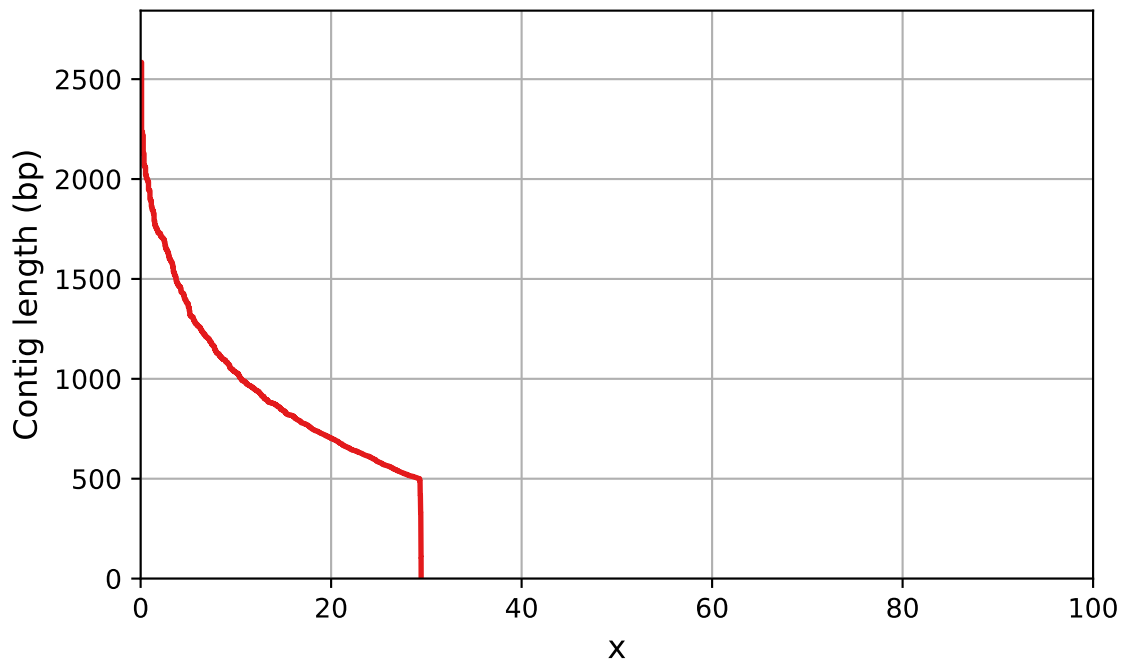
Cumulative length (aligned contigs)



NAx



NGAx



— contigs