

Report

	contigs
# contigs (>= 1000 bp)	179
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	250916
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	716
Largest contig	2698
Total length	622128
Reference length	2421479
GC (%)	36.53
Reference GC (%)	36.71
N50	882
NG50	-
N90	561
NG90	-
auN	1031.7
auNG	265.1
L50	243
LG50	-
L90	598
LG90	-
# misassemblies	5
# misassembled contigs	5
Misassembled contigs length	7261
# local misassemblies	2
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# unaligned contigs	0 + 6 part
Unaligned length	7567
Genome fraction (%)	25.225
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1931.65
# indels per 100 kbp	45.28
Largest alignment	2584
Total aligned length	611704
NA50	864
NGA50	-
NA90	543
NGA90	-
auNA	979.5
auNGA	251.7
LA50	254
LGA50	-
LA90	619
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

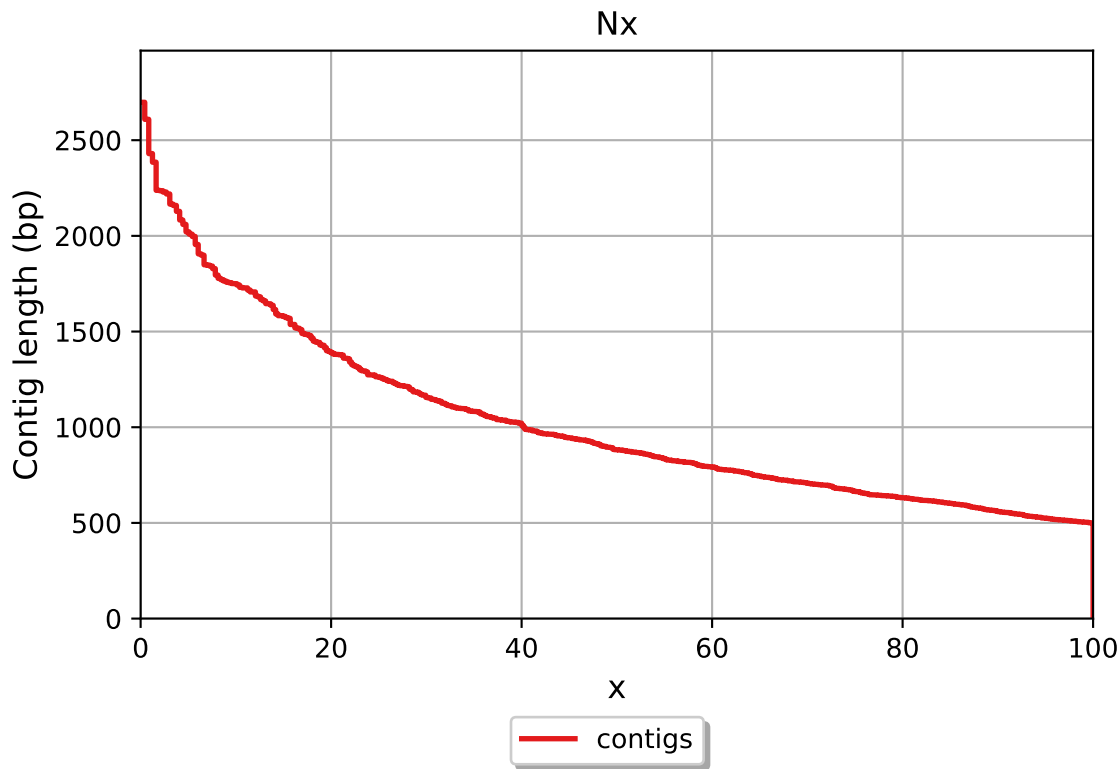
	contigs
# misassemblies	5
# contig misassemblies	5
# c. relocations	1
# c. translocations	4
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	5
Misassembled contigs length	7261
# possibly misassembled contigs	2
# possible misassemblies	2
# local misassemblies	2
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# mismatches	11816
# indels	277
# indels (<= 5 bp)	248
# indels (> 5 bp)	29
Indels length	1116

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).

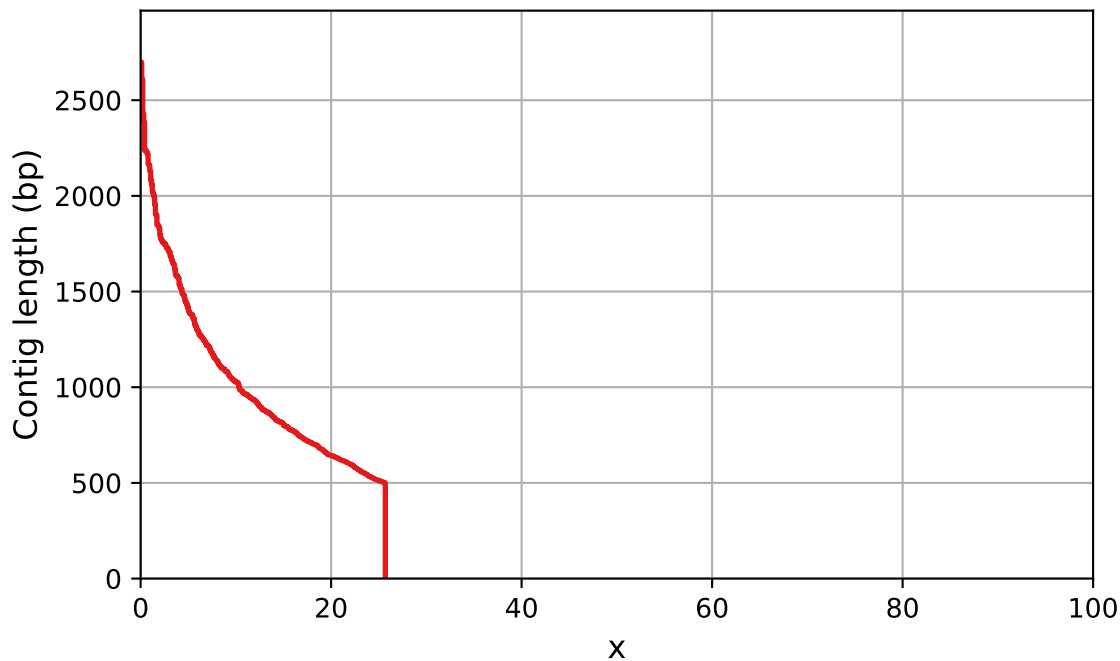
Unaligned report

	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	6
Partially unaligned length	7567
# N's	0

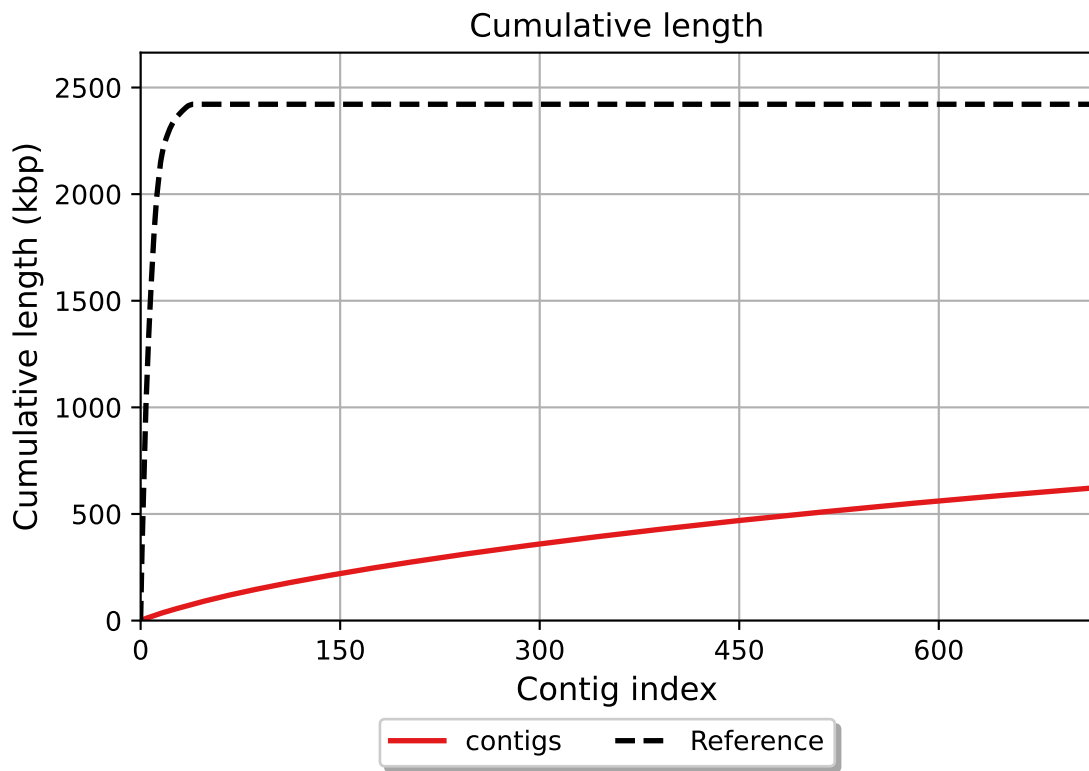
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



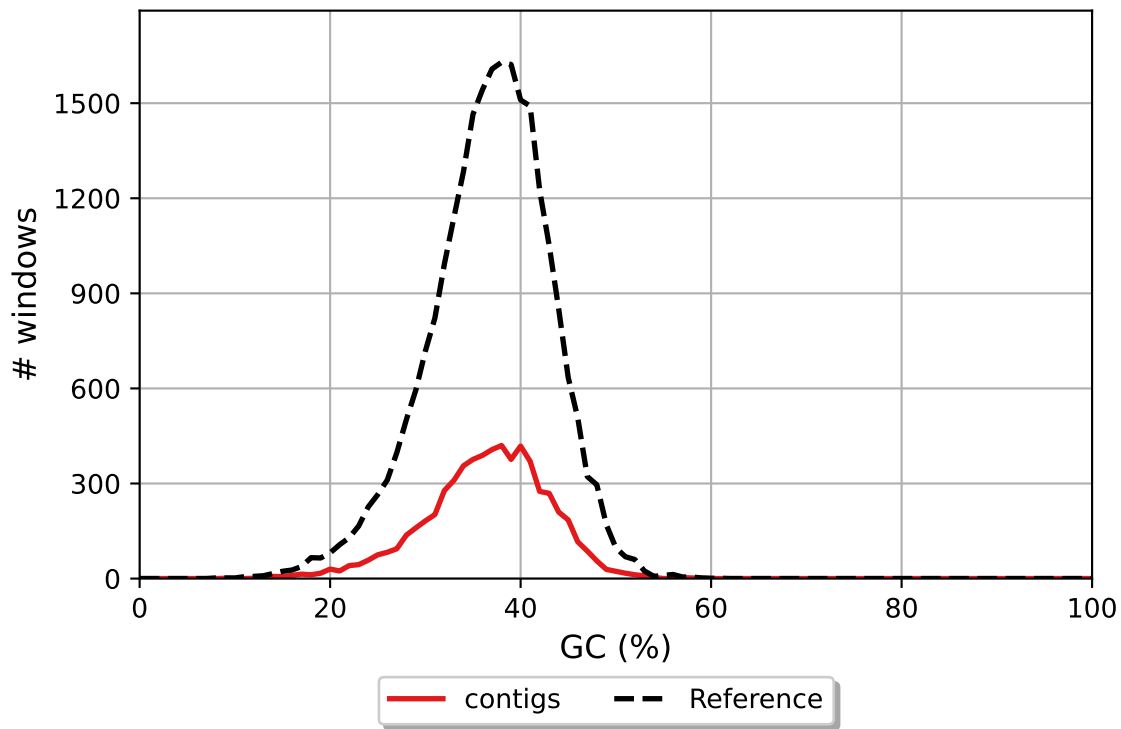
NGx



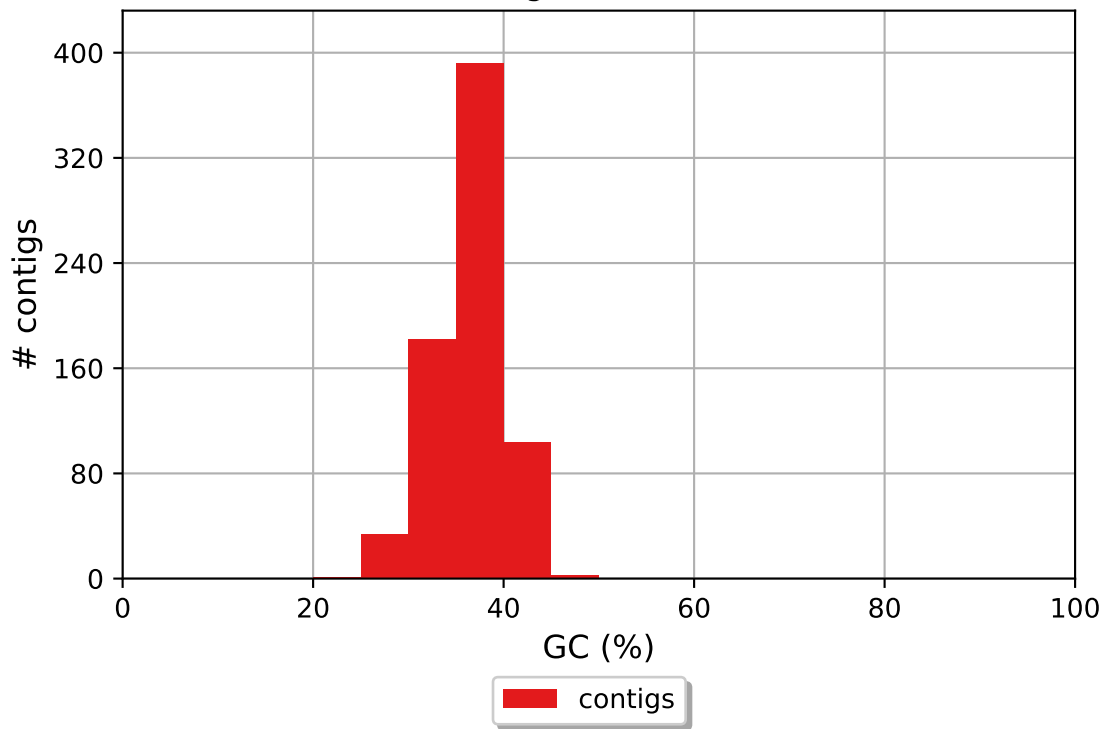
contigs



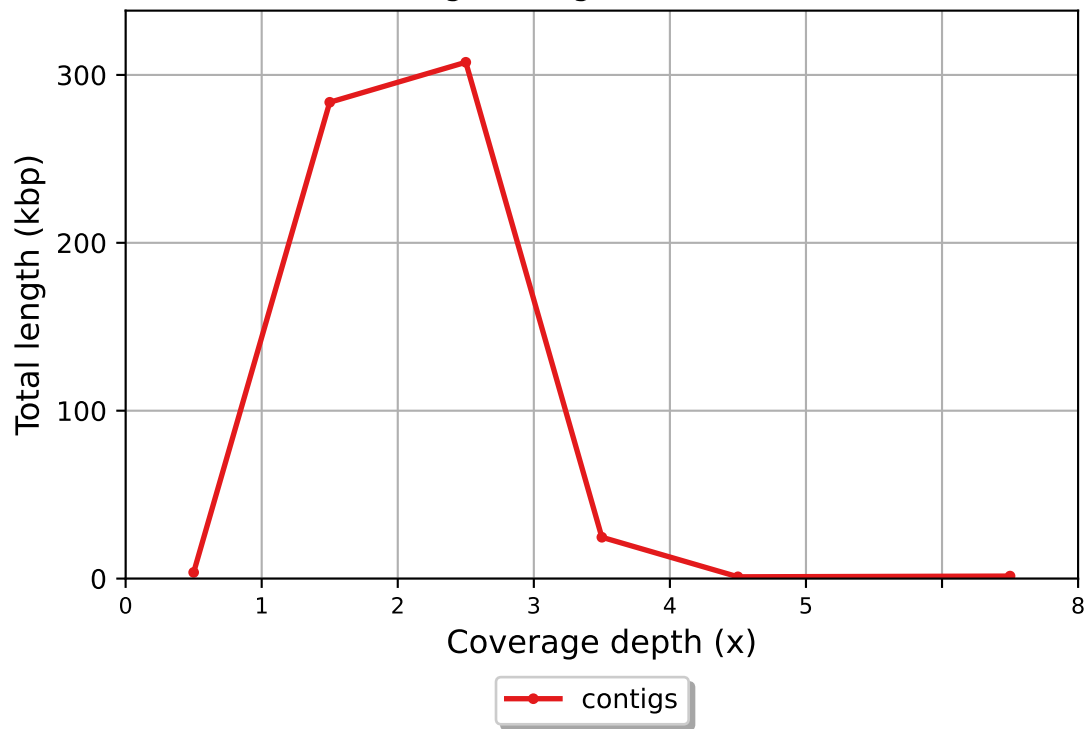
GC content



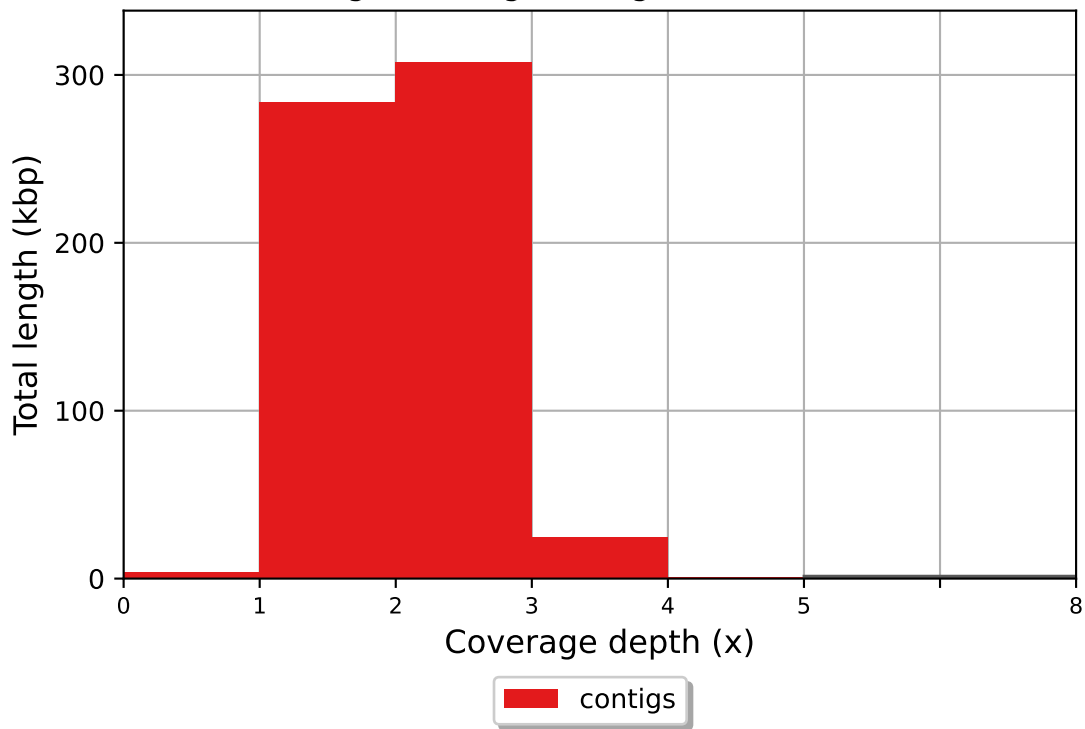
contigs GC content



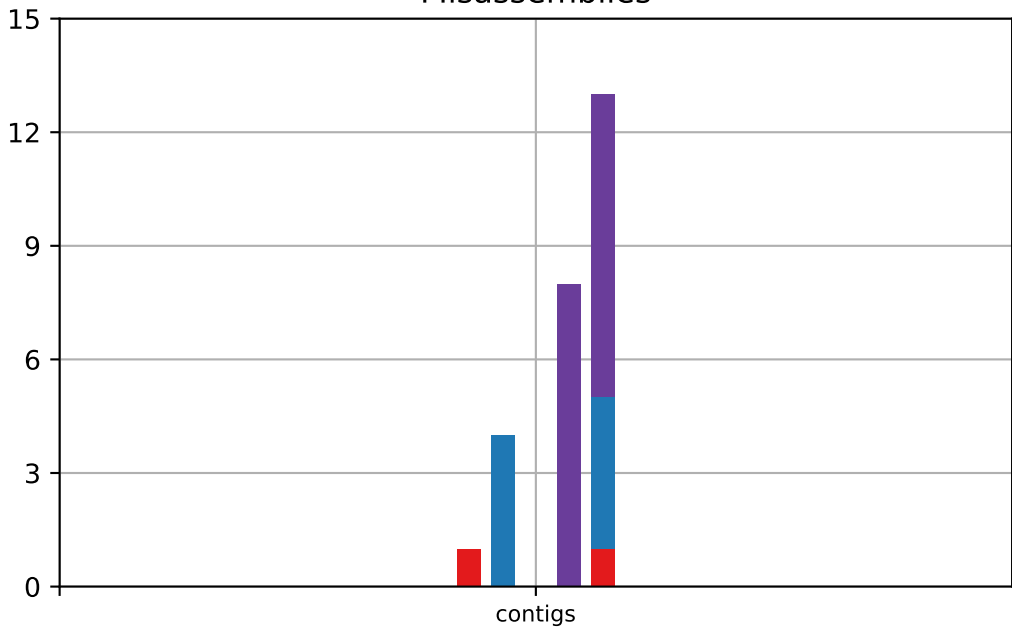
Coverage histogram (bin size: 1x)



contigs coverage histogram (bin size: 1x)

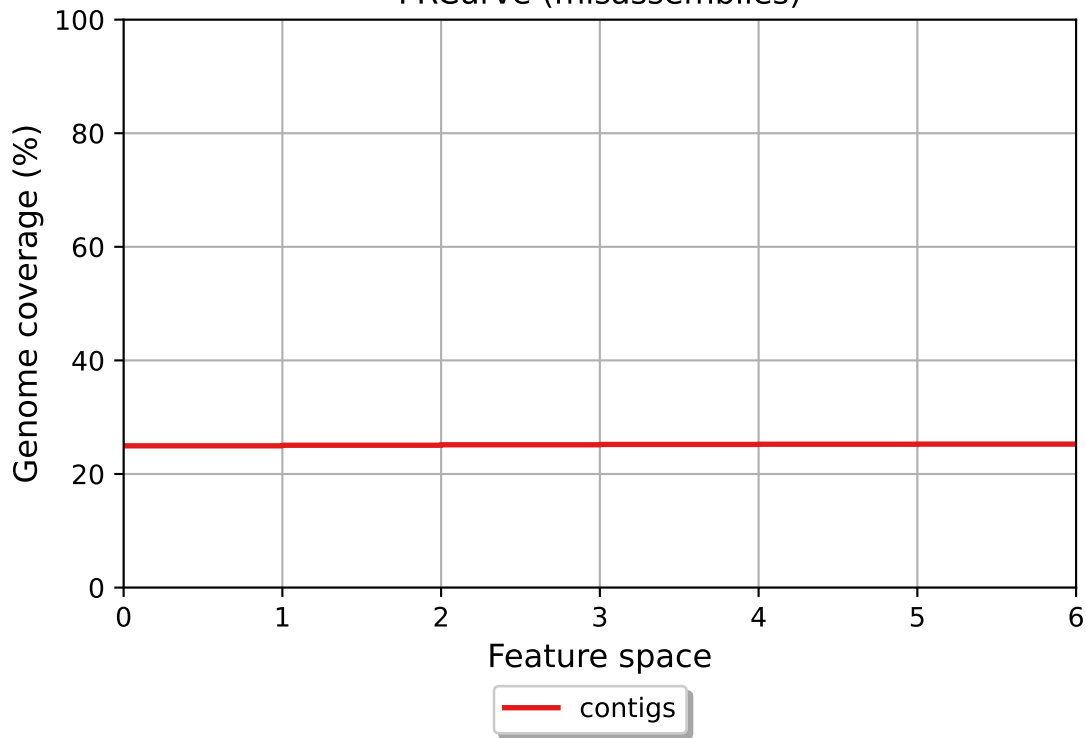


Misassemblies

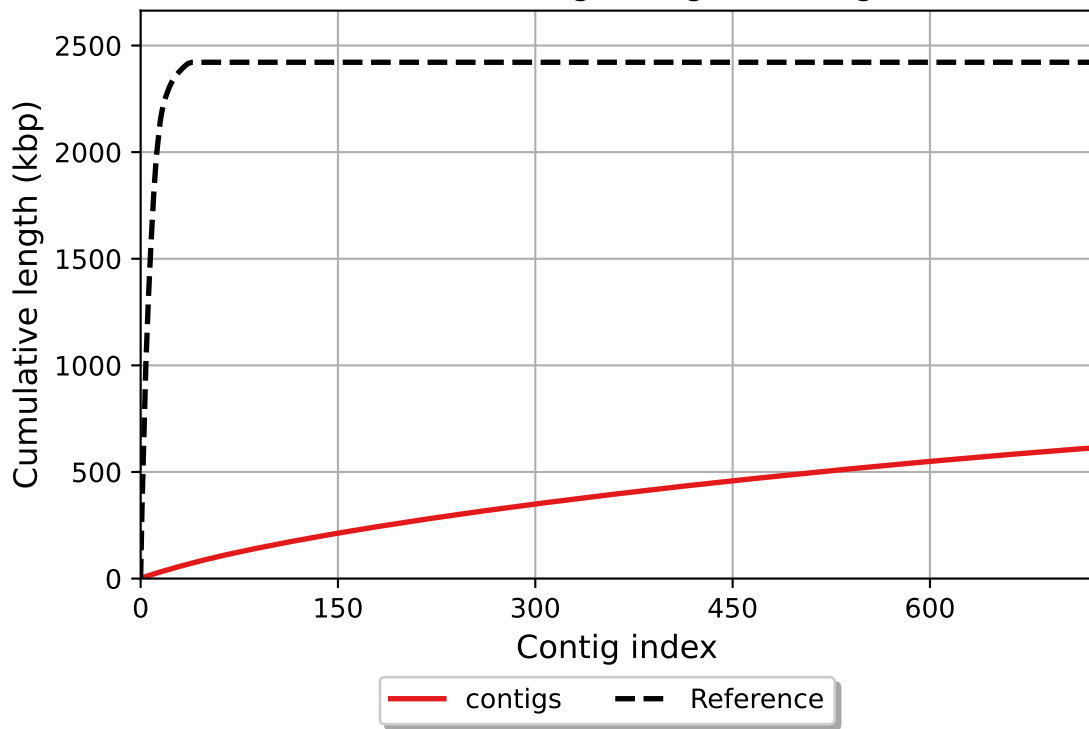


relocations # translocations # interspecies translocations

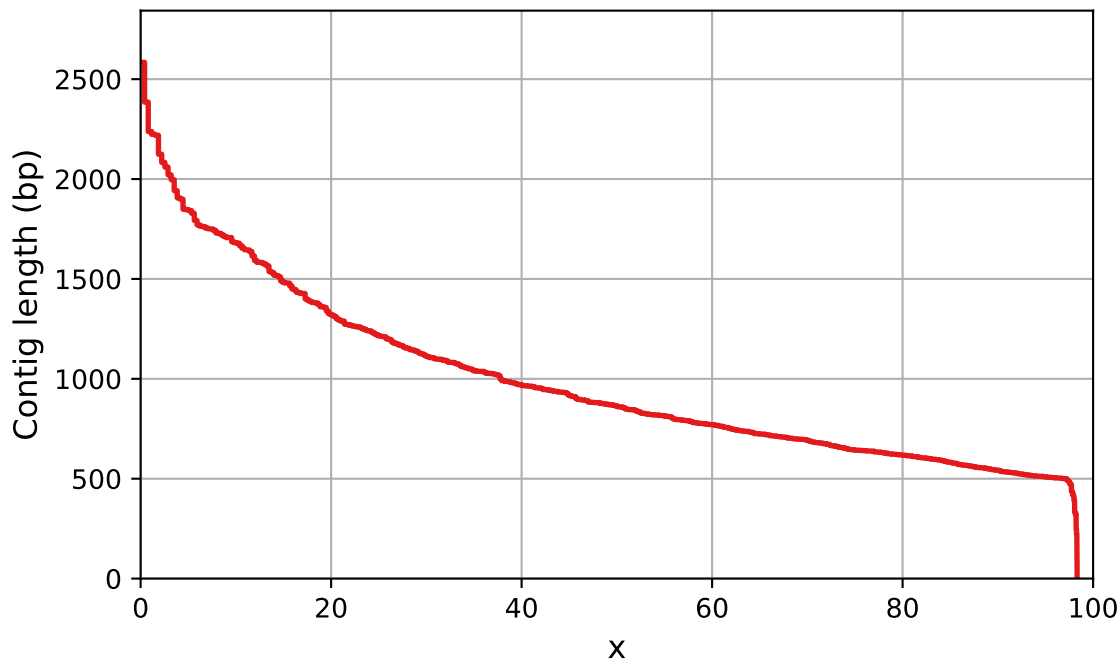
FRCurve (misassemblies)



Cumulative length (aligned contigs)

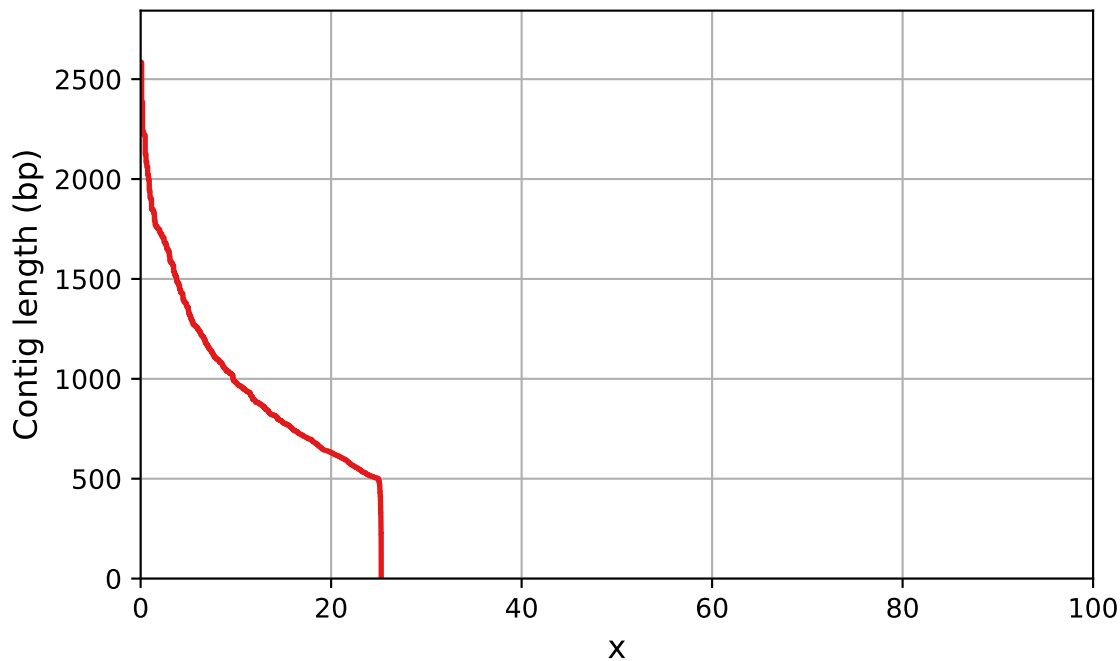


NAx



contigs

NGAx



— contigs