

Report

	contigs
# contigs (>= 1000 bp)	37
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	44821
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	361
Largest contig	2009
Total length	257978
Reference length	2357190
GC (%)	37.99
Reference GC (%)	0.00
N50	704
NG50	-
N90	534
NG90	-
auN	780.4
auNG	85.4
L50	142
LG50	-
L90	312
LG90	-
# misassemblies	18
# misassembled contigs	15
Misassembled contigs length	13728
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# unaligned contigs	0 + 1 part
Unaligned length	541
Genome fraction (%)	10.679
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1424.23
# indels per 100 kbp	19.84
Largest alignment	1583
Total aligned length	251995
NA50	667
NGA50	-
NA90	509
NGA90	-
auNA	723.8
auNGA	79.2
LA50	148
LGA50	-
LA90	325
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

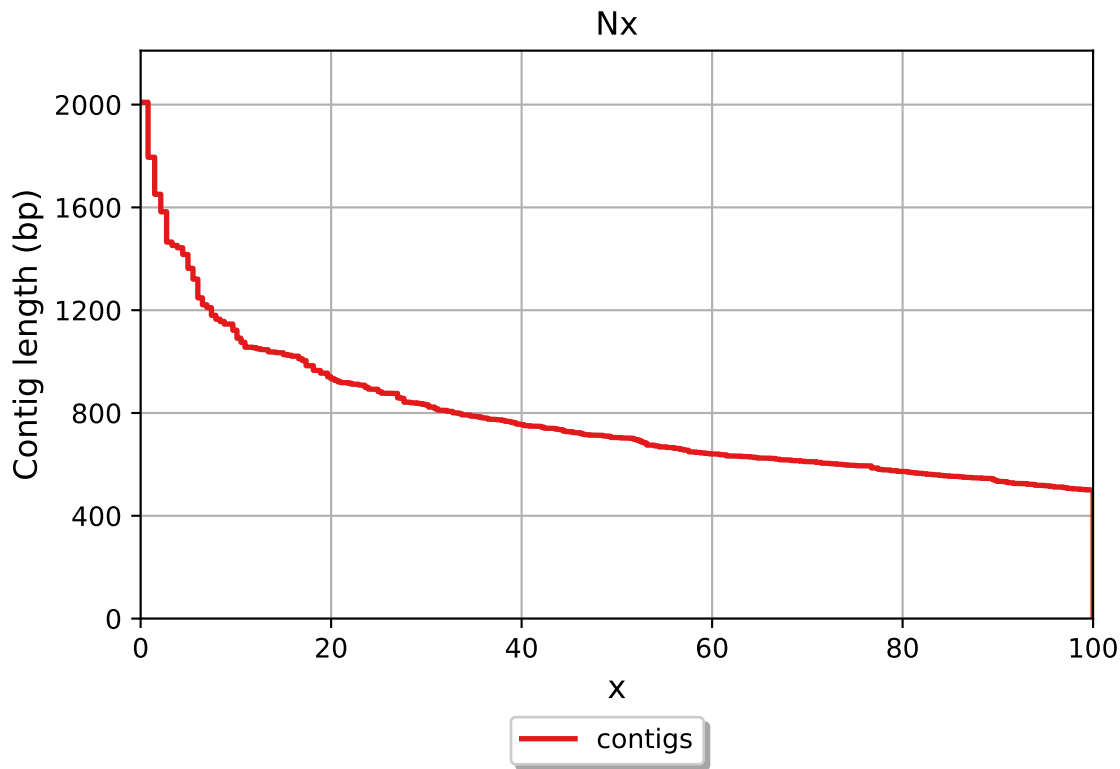
	contigs
# misassemblies	18
# contig misassemblies	18
# c. relocations	0
# c. translocations	18
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	15
Misassembled contigs length	13728
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# mismatches	3589
# indels	50
# indels (<= 5 bp)	43
# indels (> 5 bp)	7
Indels length	331

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).

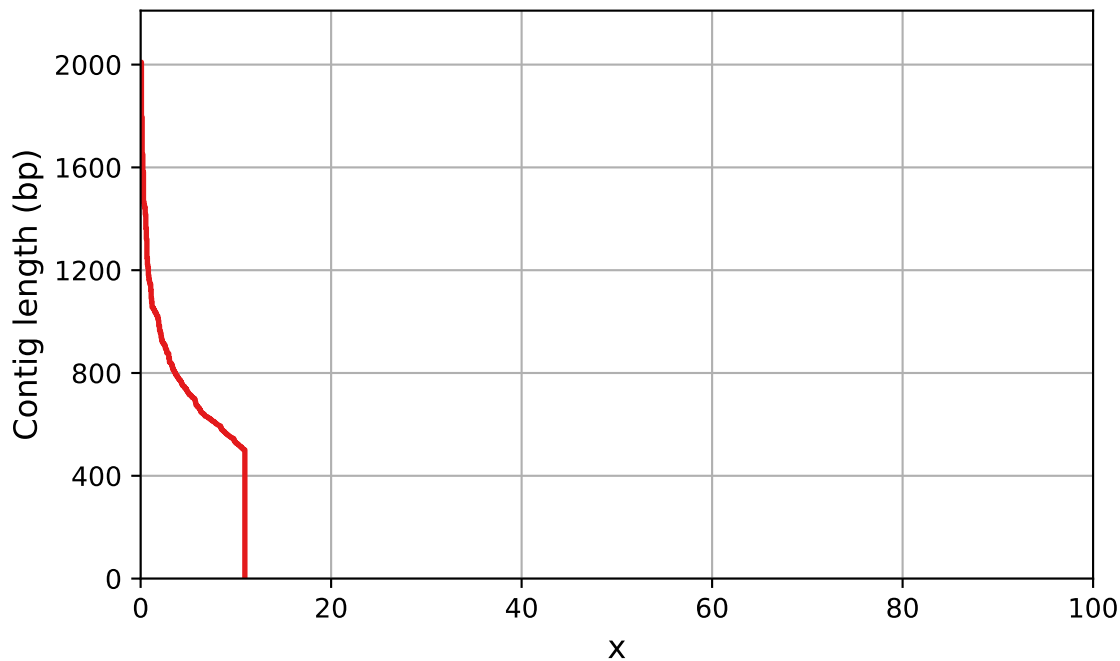
Unaligned report

	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
Partially unaligned length	541
# N's	0

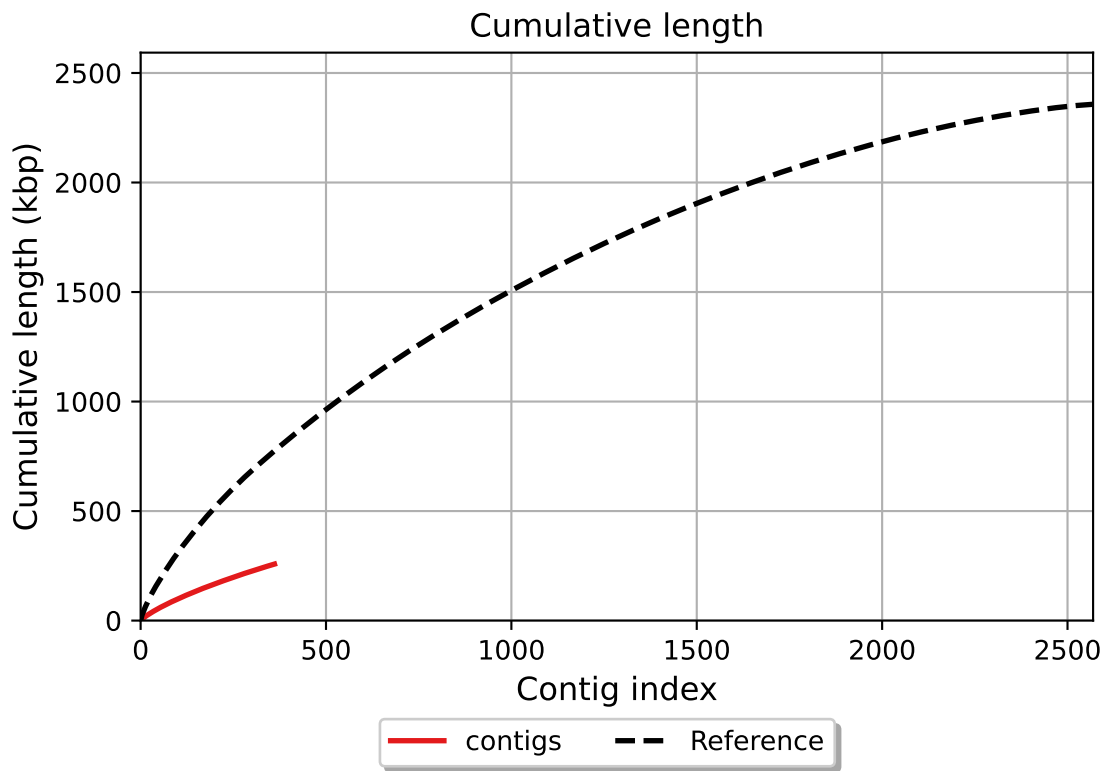
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



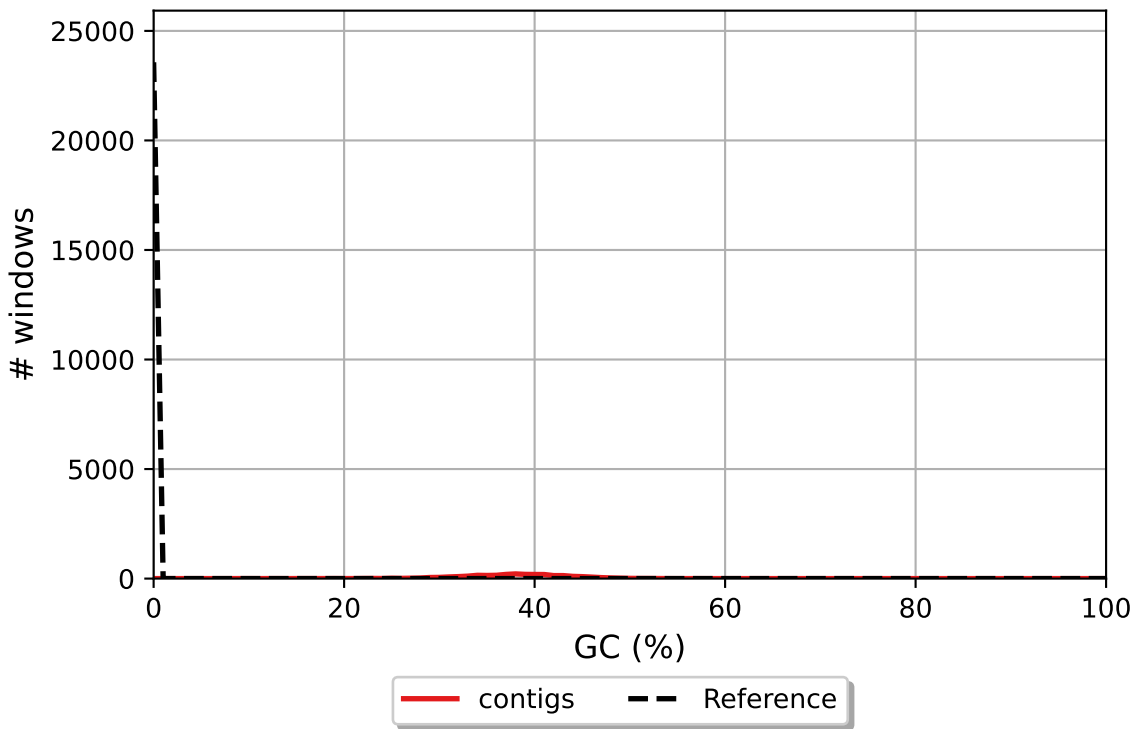
NGx



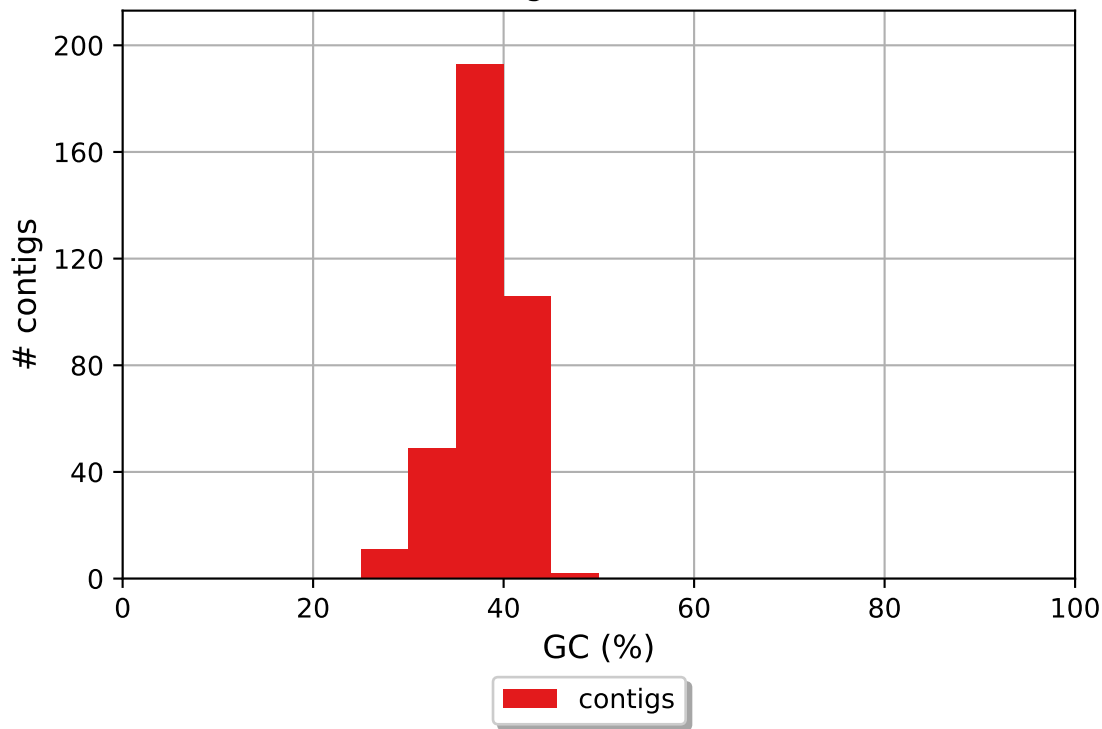
contigs



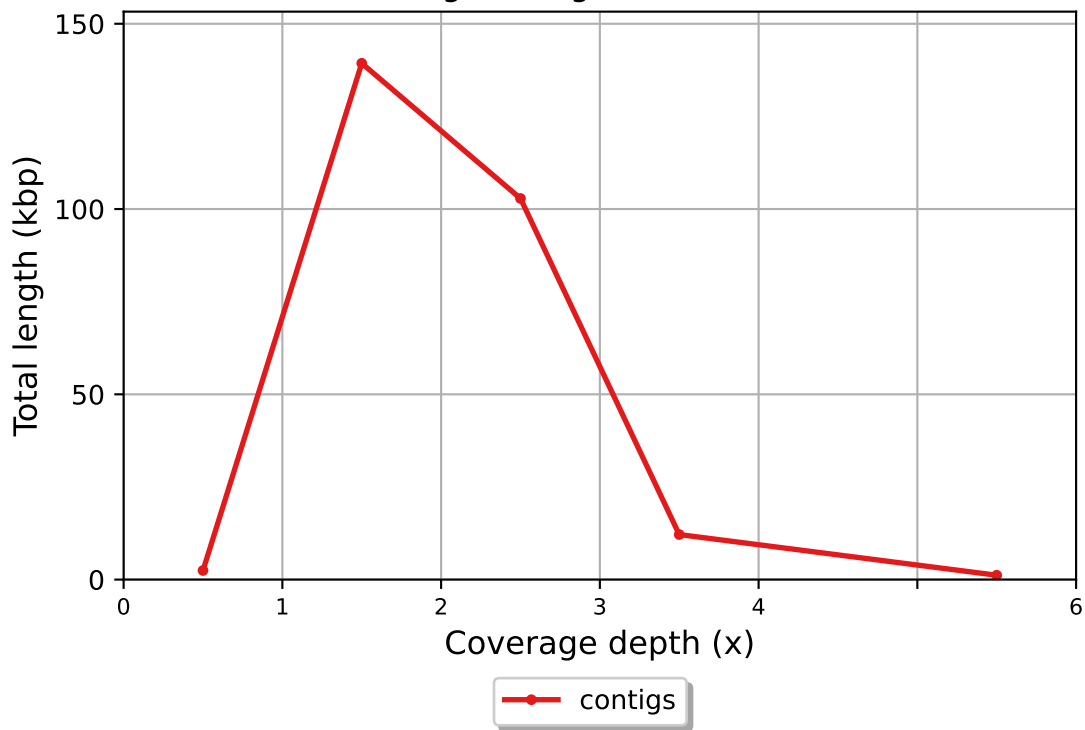
GC content



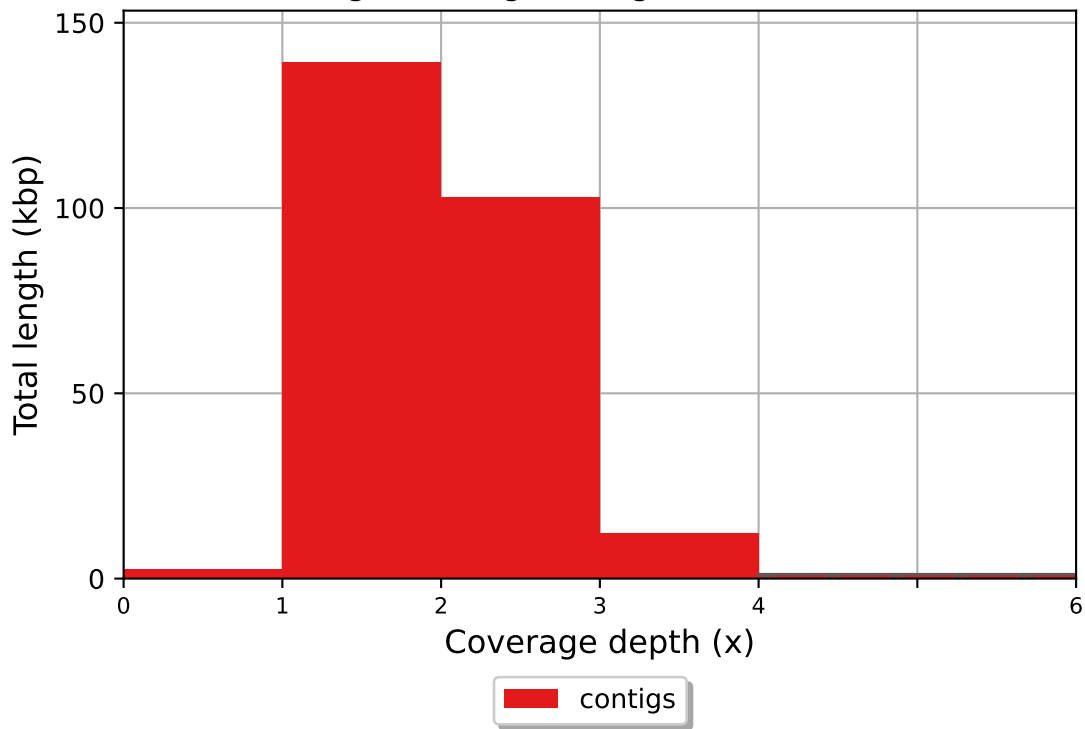
contigs GC content



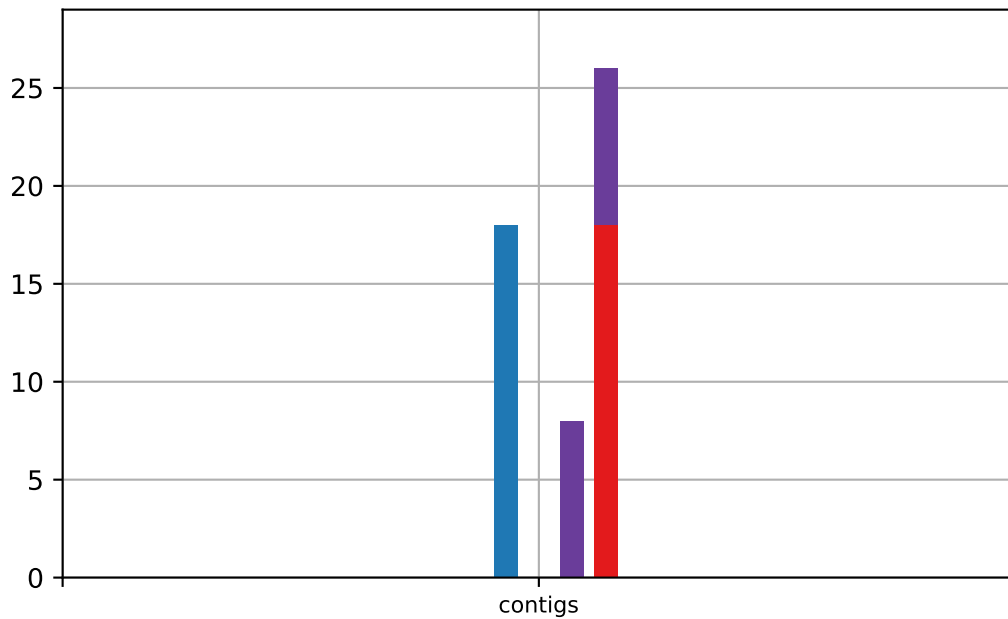
Coverage histogram (bin size: 1x)



contigs coverage histogram (bin size: 1x)



Misassemblies

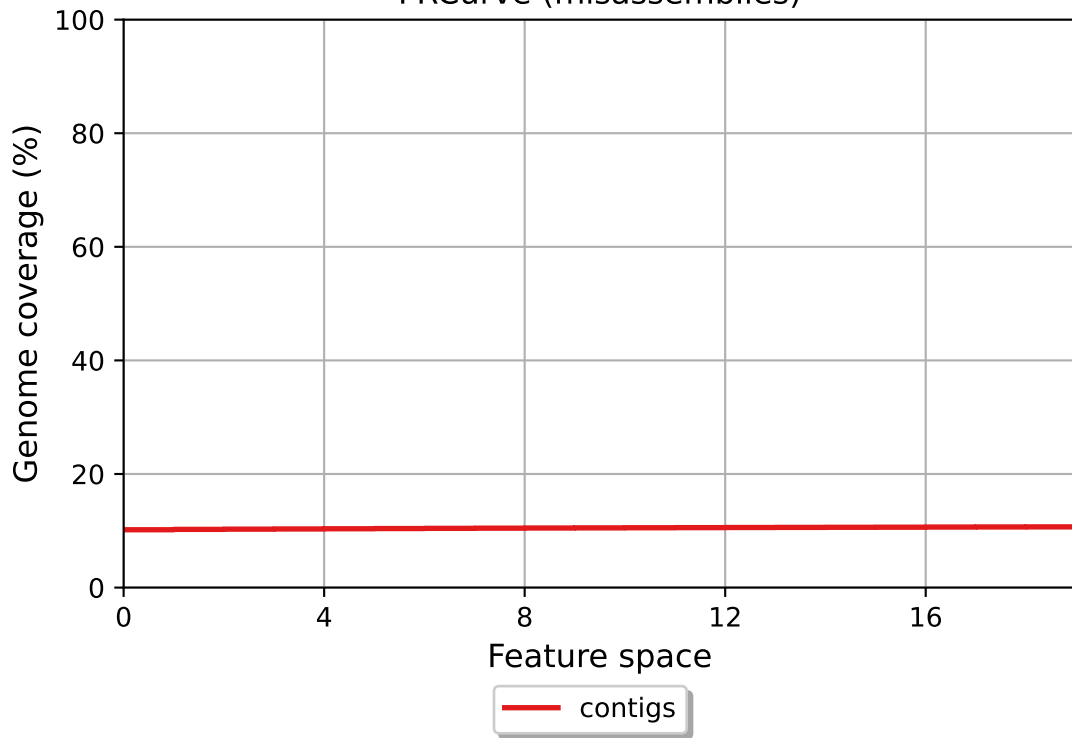


translocations

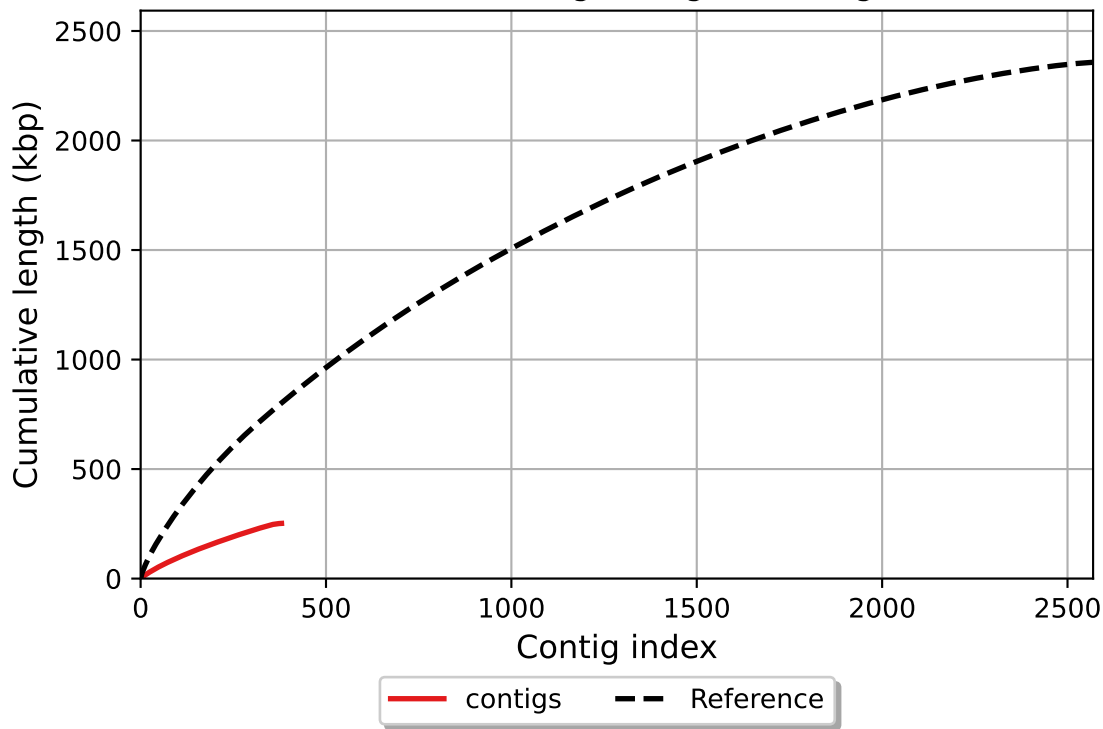


interspecies translocations

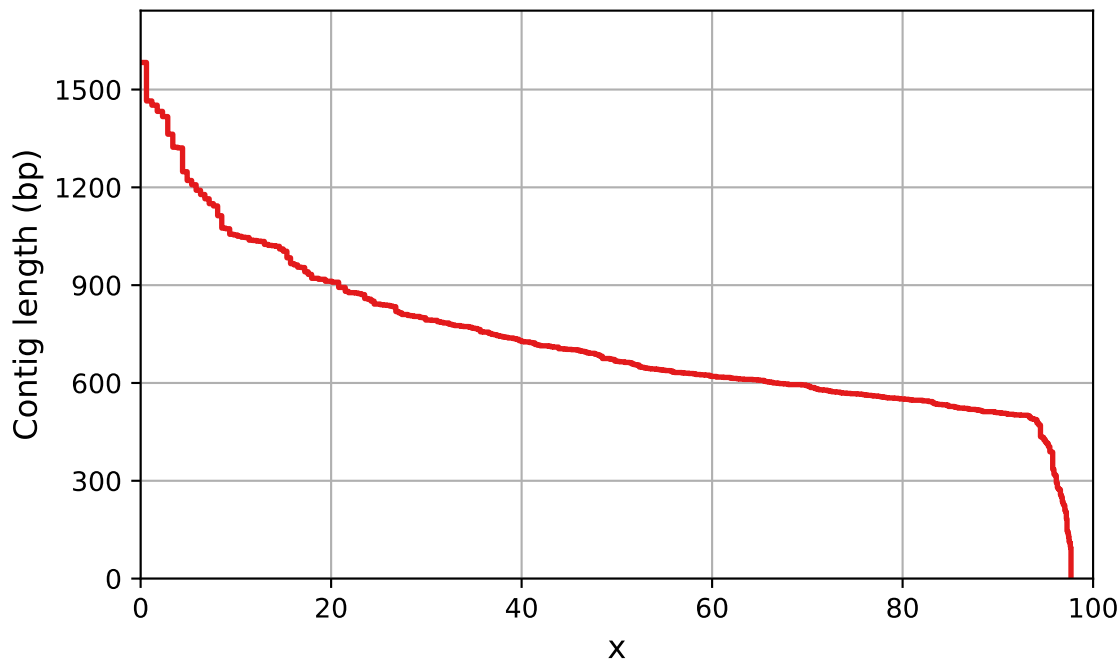
FRCurve (misassemblies)



Cumulative length (aligned contigs)



NAx



— contigs

NGAx

