Report

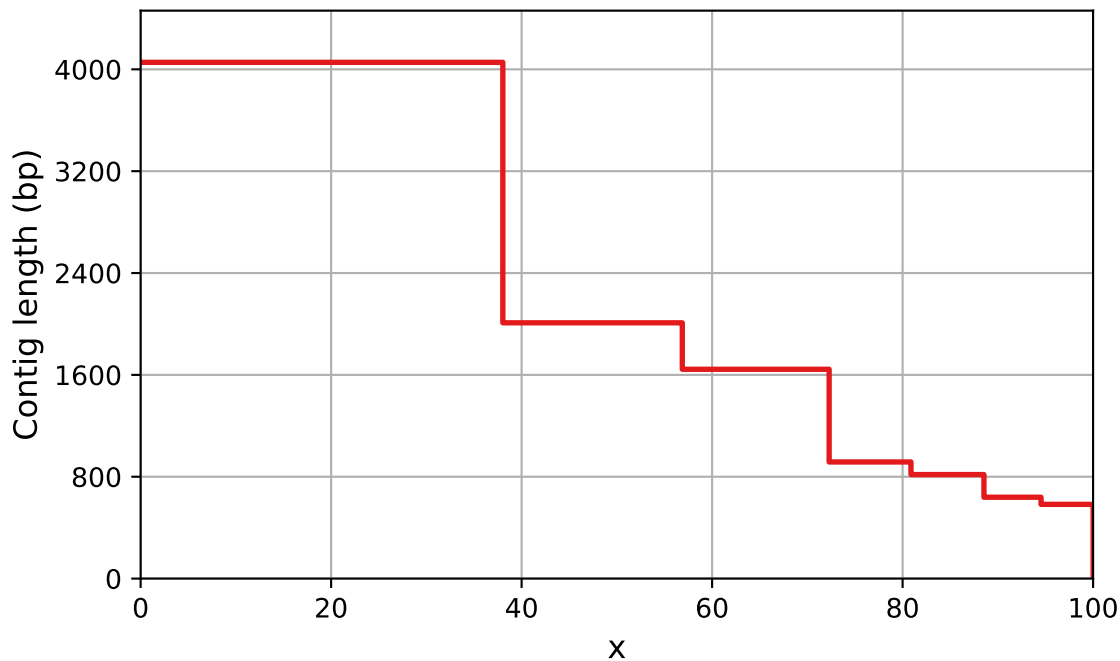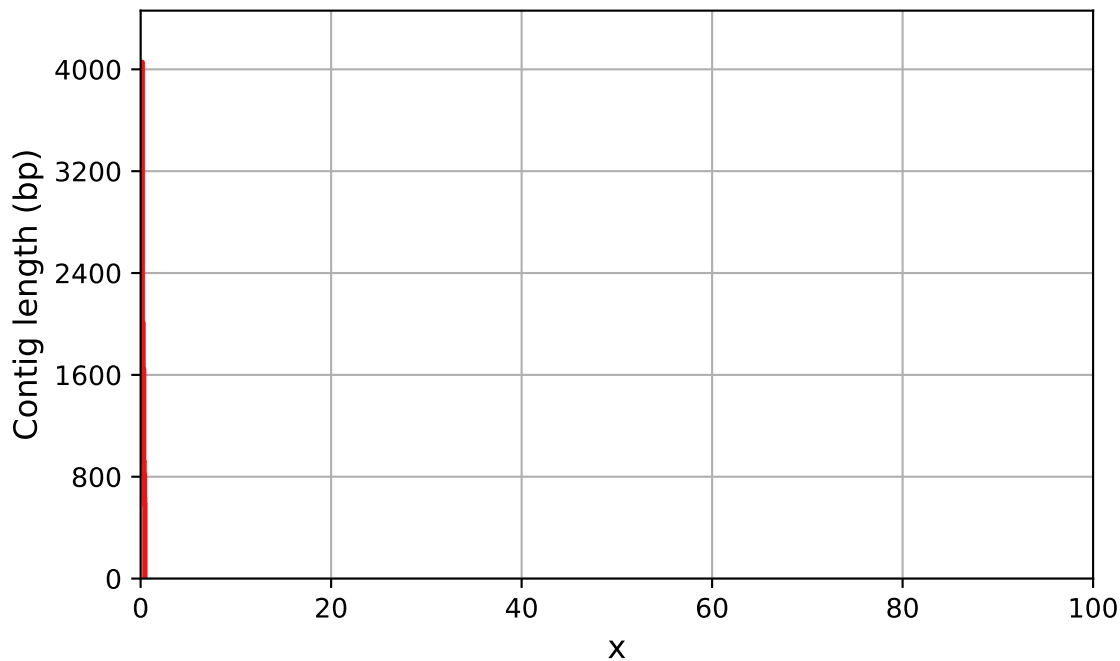|	contigs
# contigs (>= 1000 bp)	3
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	7708
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	7
Largest contig	4055
Total length	10663
Reference length	2384961
GC (%)	36.32
Reference GC (%)	0.00
N50	2009
NG50	-
N90	639
NG90	-
auN	2385.5
auNG	10.7
L50	2
LG50	-
L90	6
LG90	-
# misassemblies	4
# misassembled contigs	2
Misassembled contigs length	4971
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 3 part
Unaligned length	4101
Genome fraction (%)	0.257
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	4327.24
# indels per 100 kbp	32.66
Largest alignment	2122
Total aligned length	6124
NA50	250
NGA50	-
NA90	-
NGA90	-
auNA	609.4
auNGA	2.7
LA50	8
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).
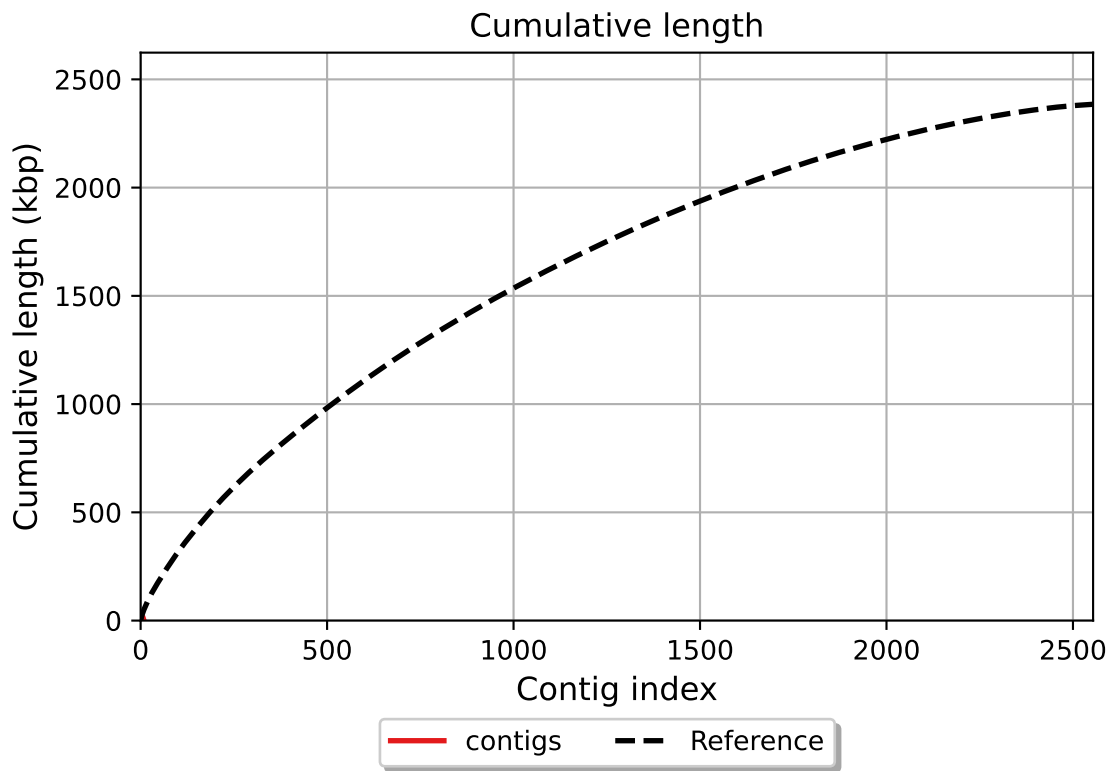
Misassemblies report

	contigs
# misassemblies	4
# contig misassemblies	4
# c. relocations	0
# c. translocations	4
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	2
Misassembled contigs length	4971
# possibly misassembled contigs	1
# possible misassemblies	2
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	265
# indels	2
# indels (<= 5 bp)	2
# indels (> 5 bp)	0
Indels length	2

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	3
Partially unaligned length	4101
# N's	0

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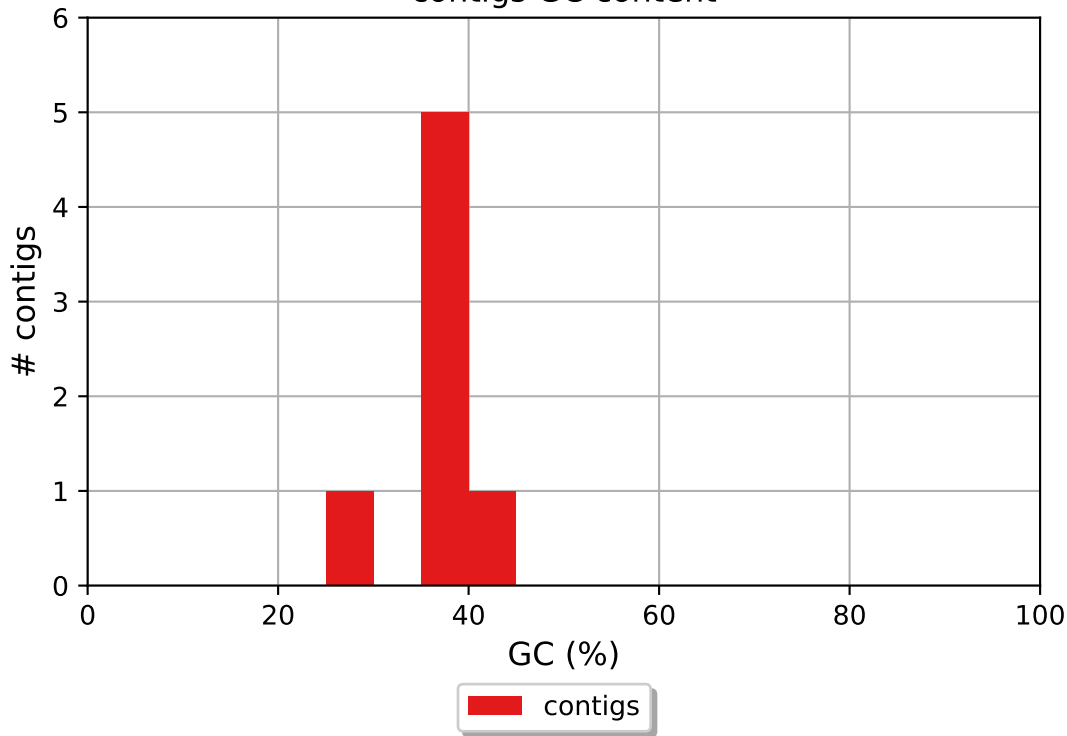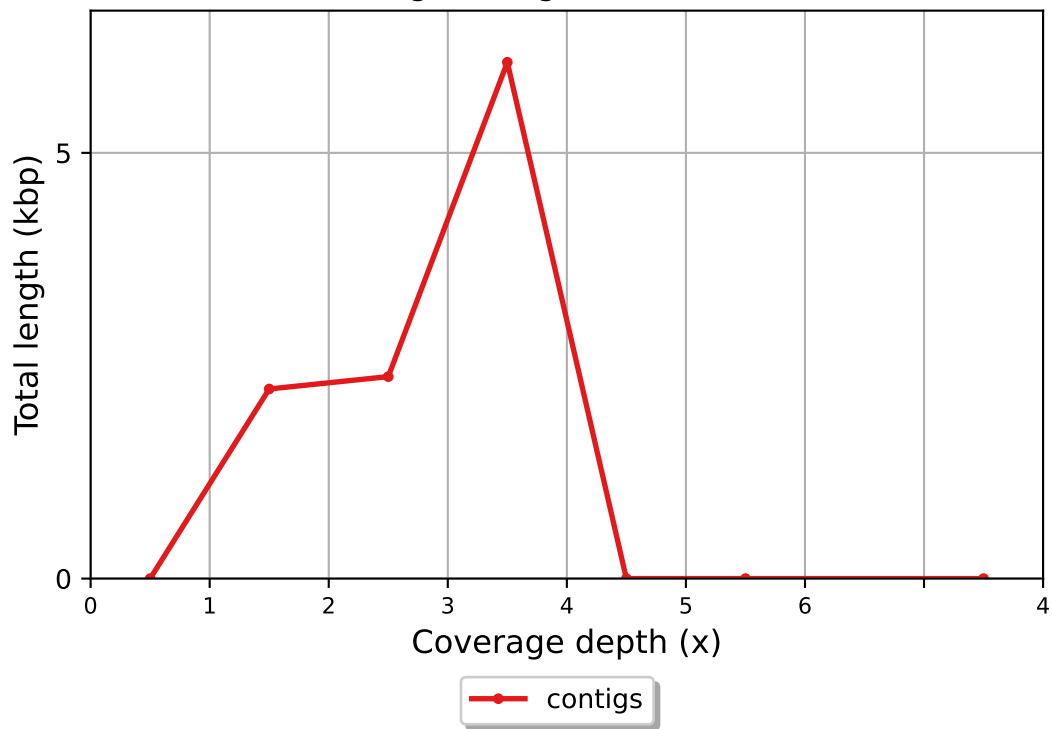(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Nx

NGx

Cumulative length
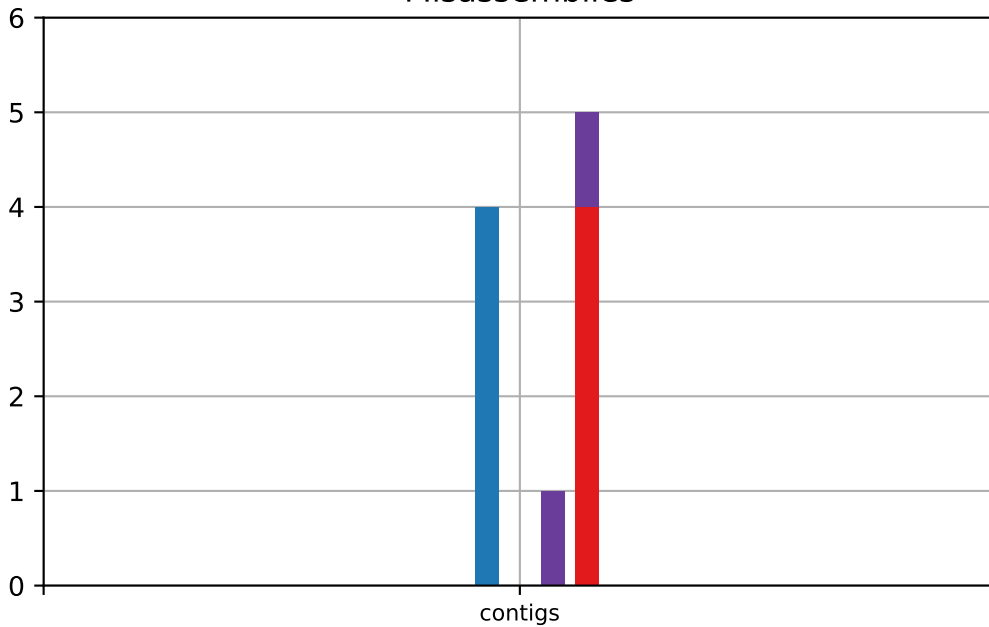
GC content
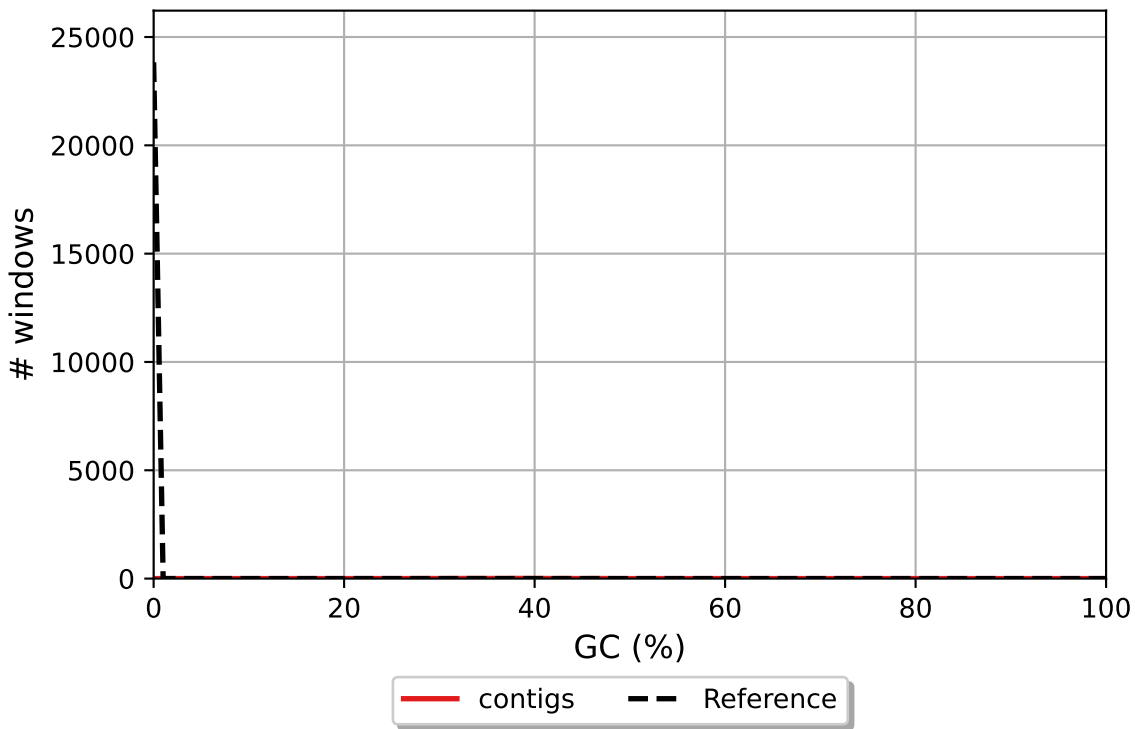
contigs GC content

Coverage histogram (bin size: 1x)

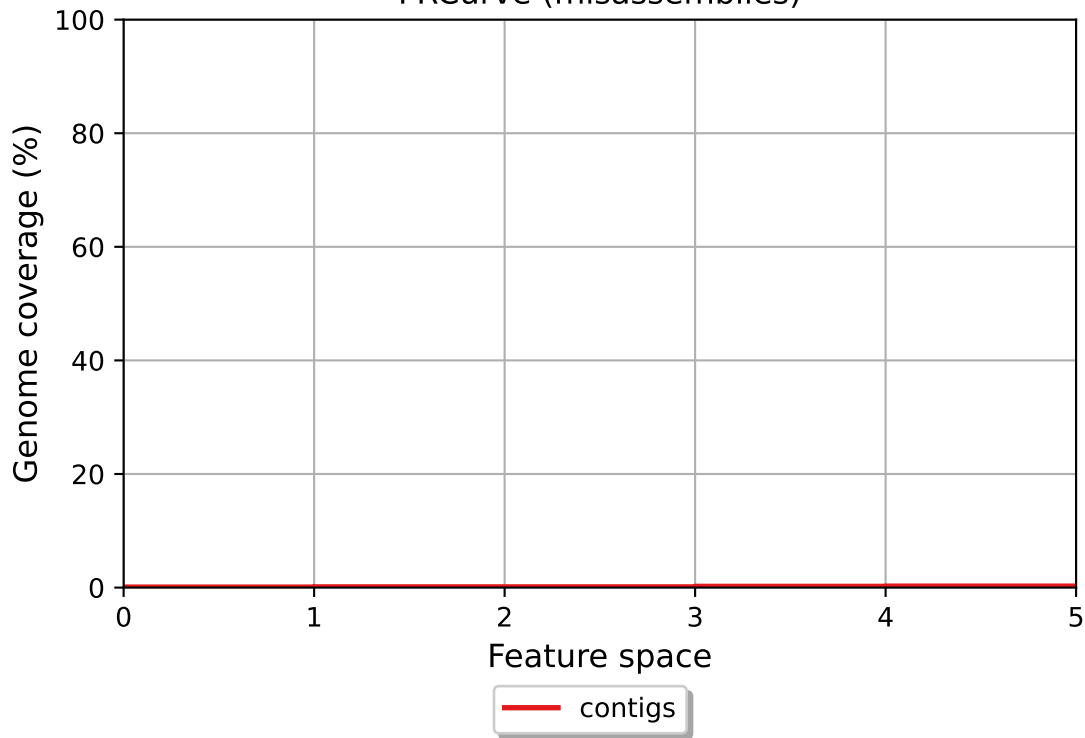contigs coverage histogram (bin size: 1x)
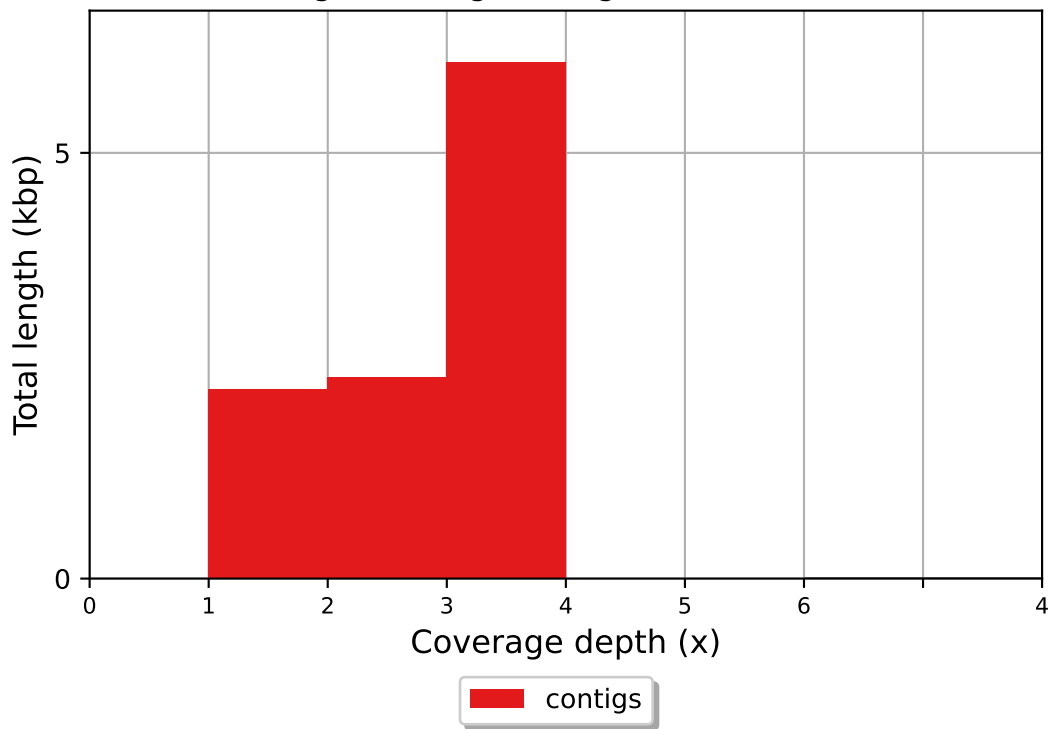
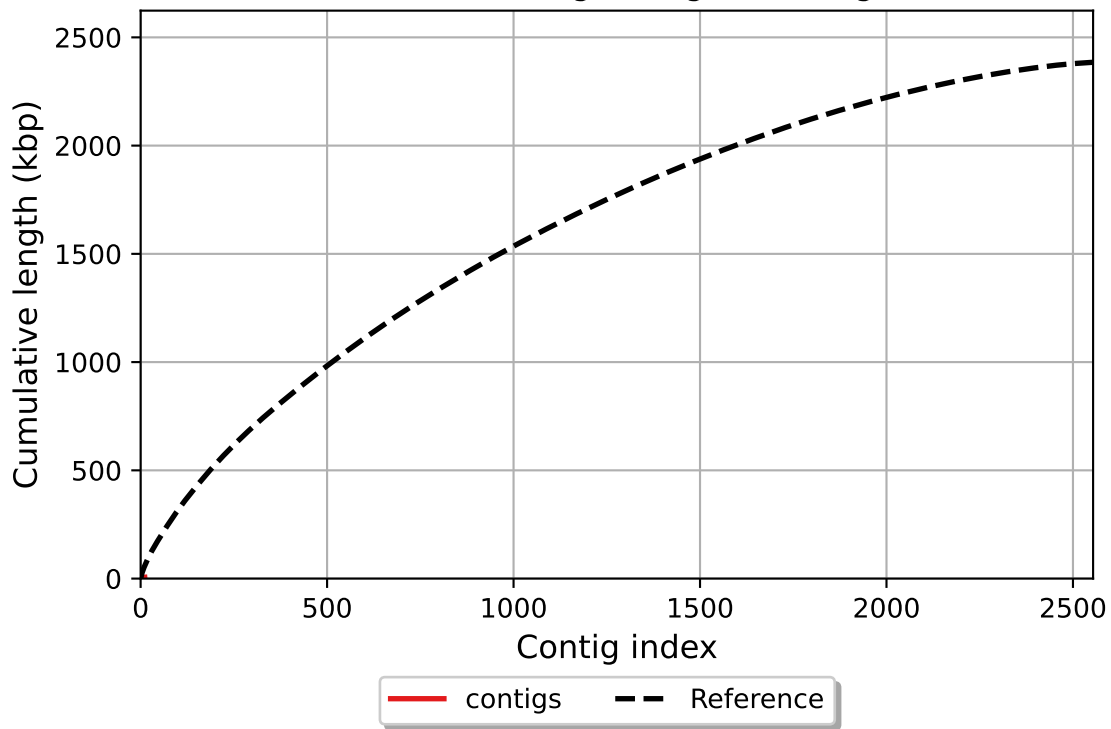Misassemblies
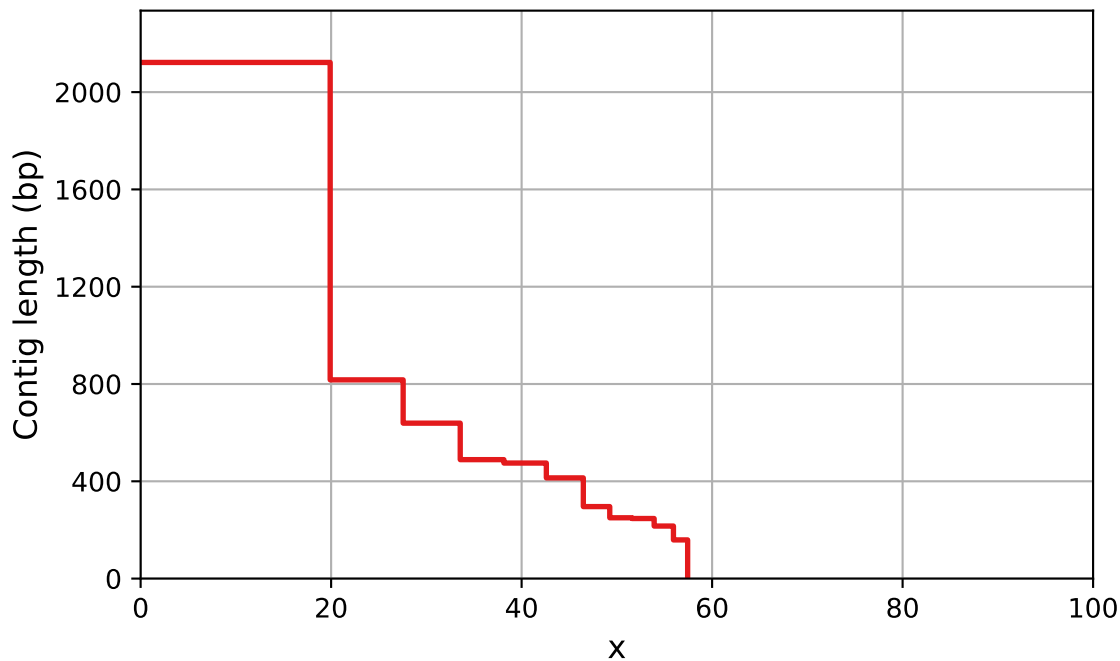
Legend:
- # translocations
- # interspecies translocations

FRCurve (misassemblies)

Cumulative length (aligned contigs)

NAx

NGAx