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)	6276
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	6
Largest contig	4055
Total length	8554
Reference length	2688239
GC (%)	35.60
Reference GC (%)	37.49
N50	1181
NG50	-
N90	704
NG90	-
auN	2421.8
auNG	7.7
L50	2
LG50	-
L90	5
LG90	-
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 2 part
Unaligned length	1909
Genome fraction (%)	0.235
Duplication ratio	1.003
# N's per 100 kbp	0.00
# mismatches per 100 kbp	4235.15
# indels per 100 kbp	63.21
Largest alignment	2709
Total aligned length	6328
NA50	891
NGA50	-
NA90	-
NGA90	-
auNA	1193.4
auNGA	3.8
LA50	3
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).
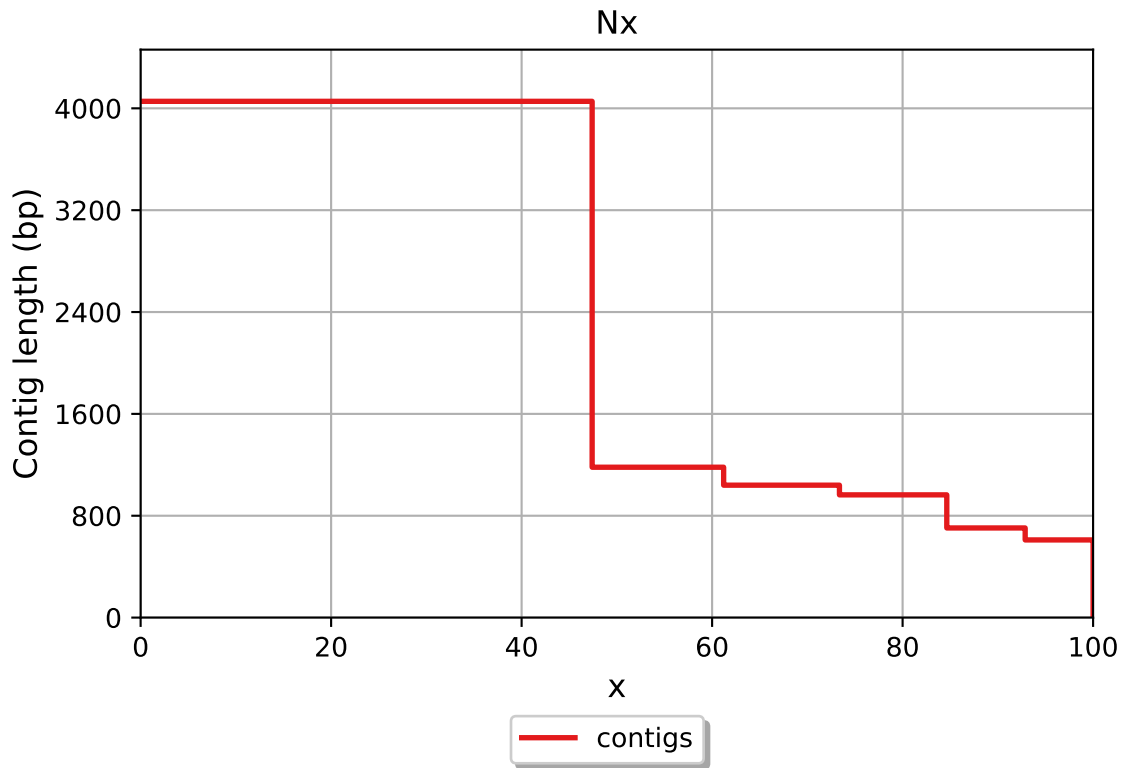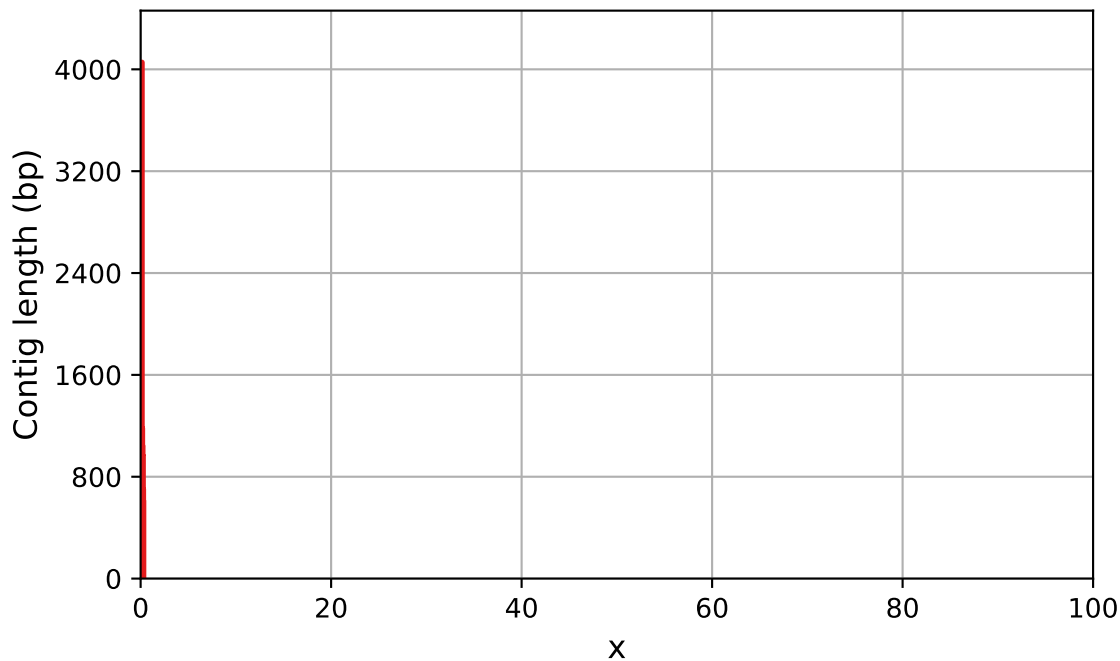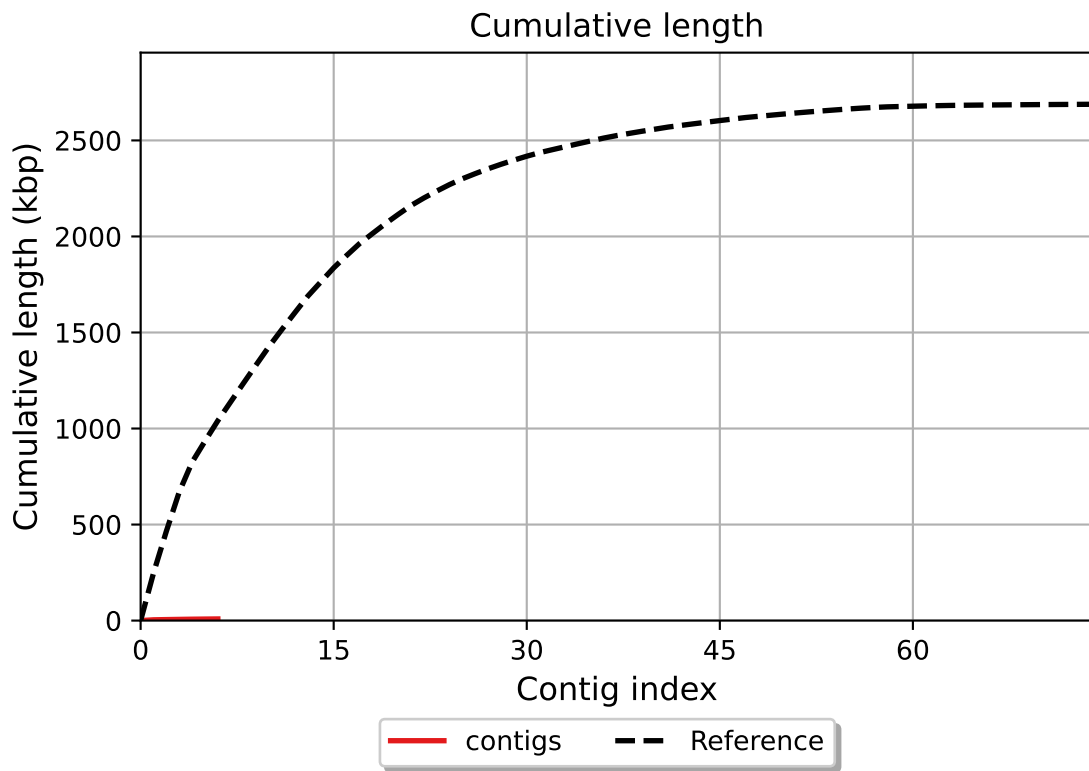
Misassemblies report

	contigs
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	1
# possible misassemblies	1
# local misassemblies	1
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	268
# indels	4
# indels (<= 5 bp)	2
# indels (> 5 bp)	2
Indels length	218

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
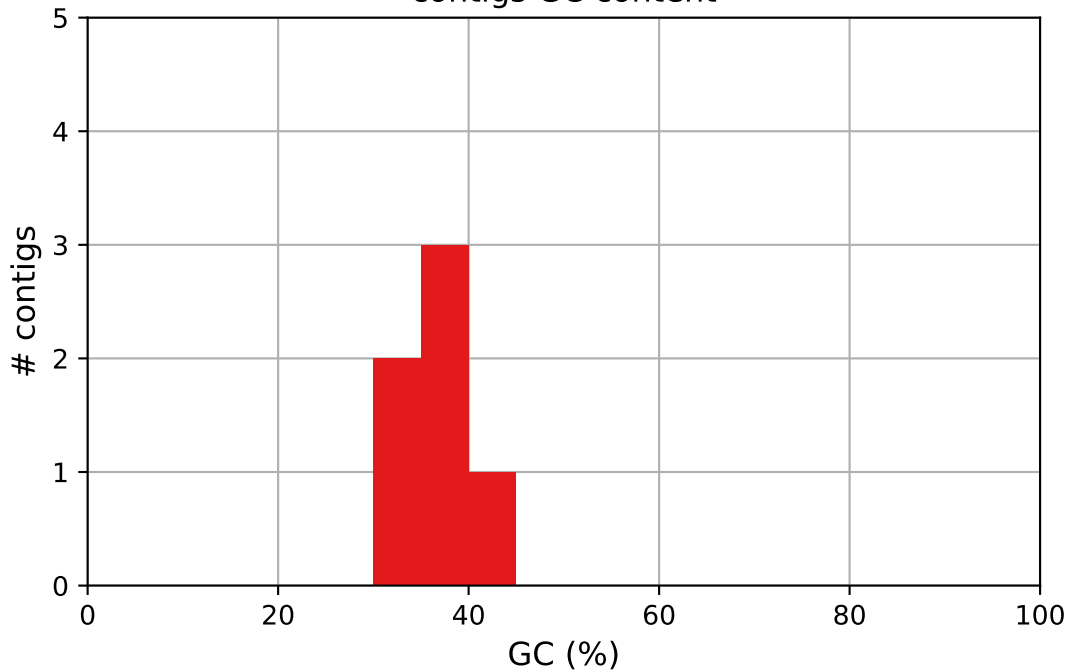
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
Partially unaligned length	1909
# N's	0

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

Cumulative length (kbp)

Contig index

contigs — — Reference
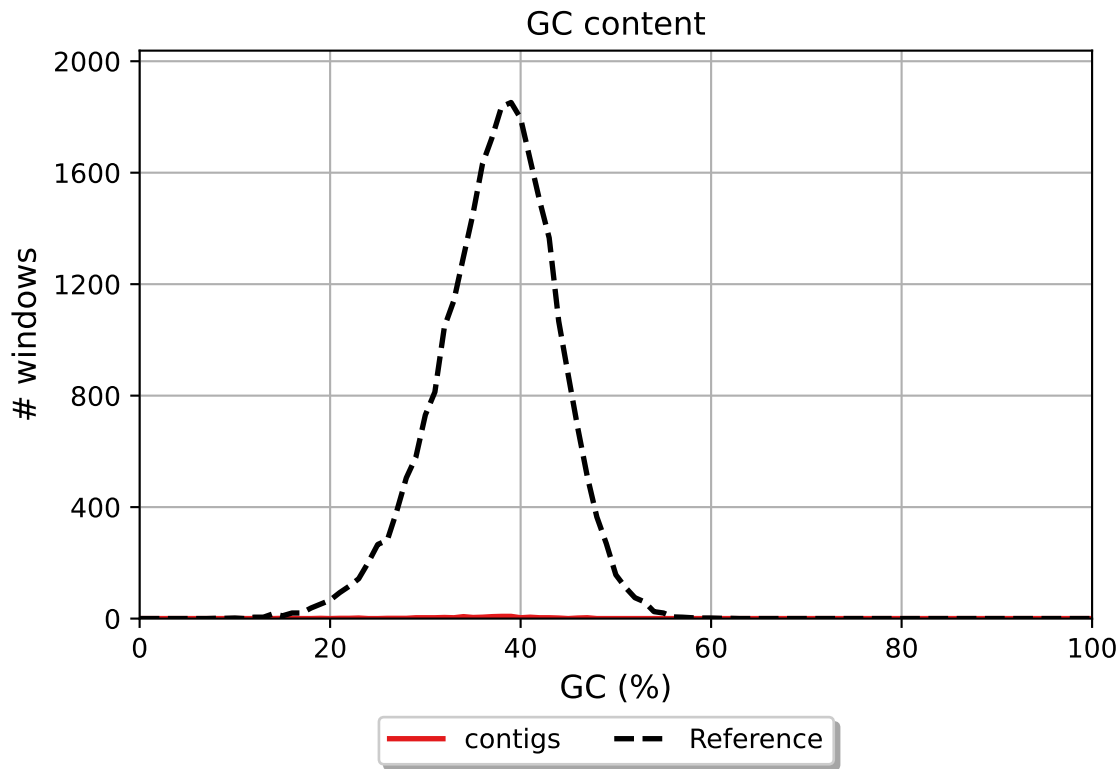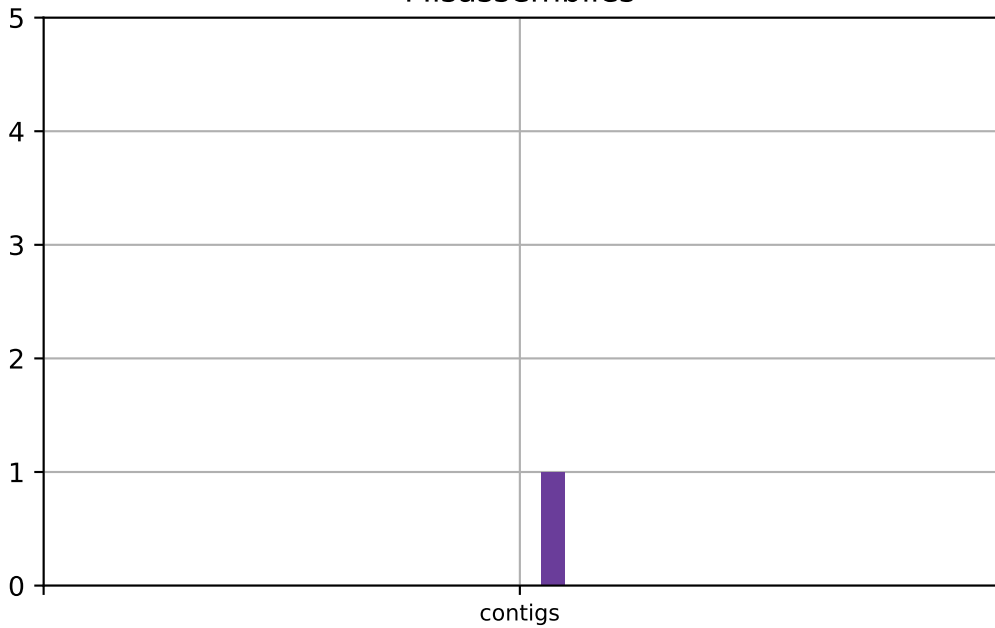
GC content

contigs GC content

Coverage histogram (bin size: 1x)
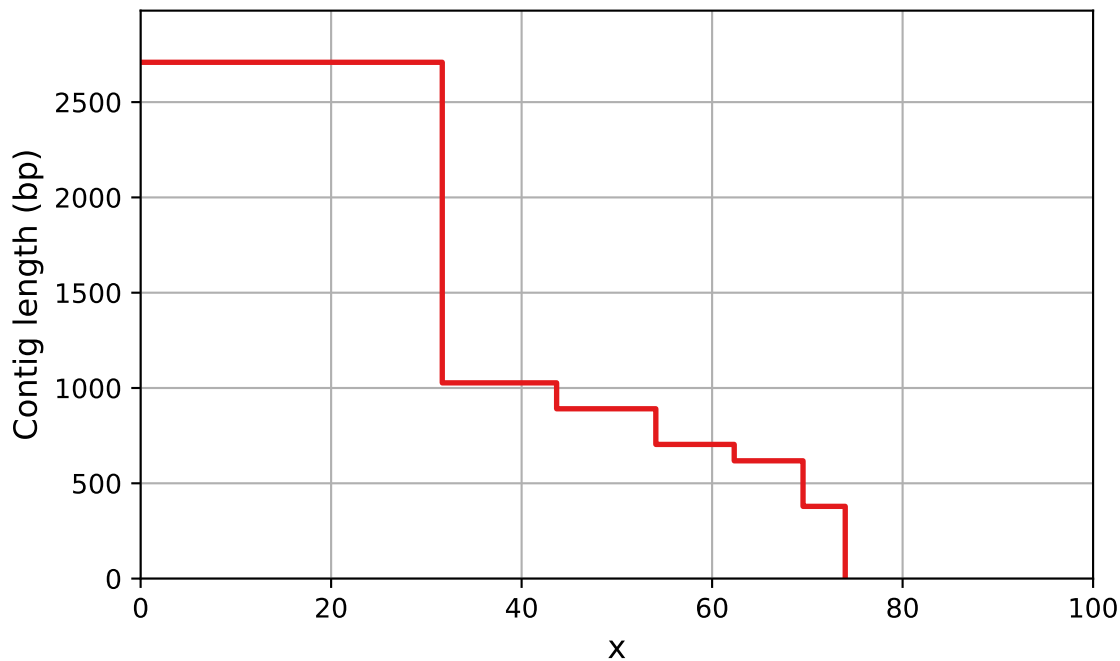
contigs coverage histogram (bin size: 1x)
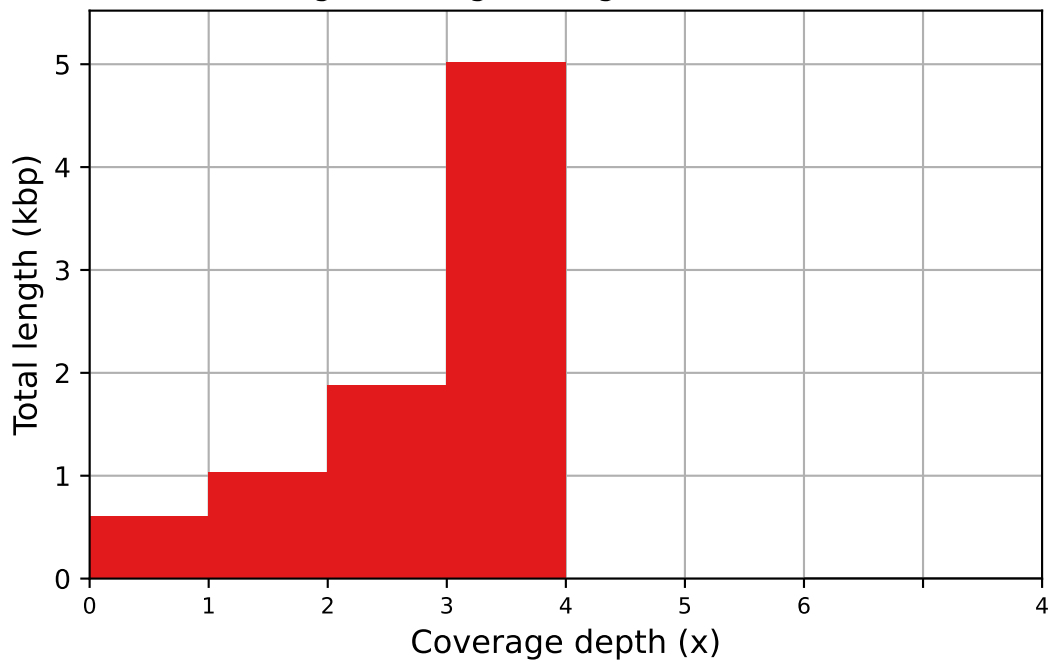
Misassemblies

FRCurve (misassemblies)
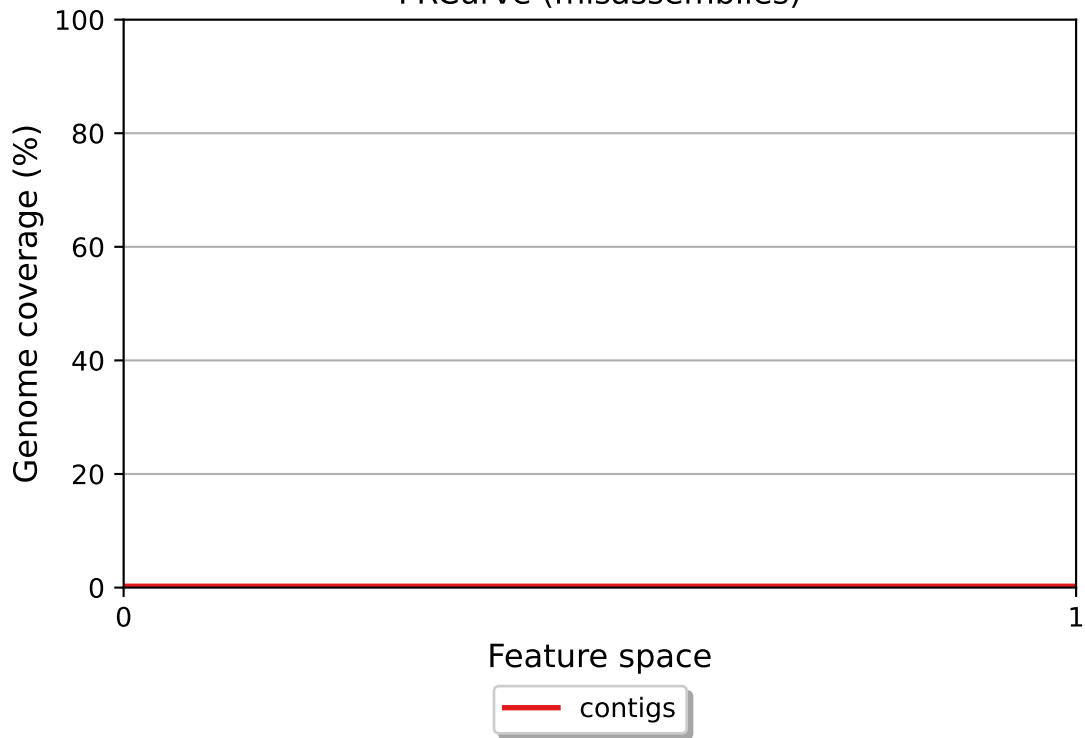
Cumulative length (aligned contigs)

NAx

NGAx