Report

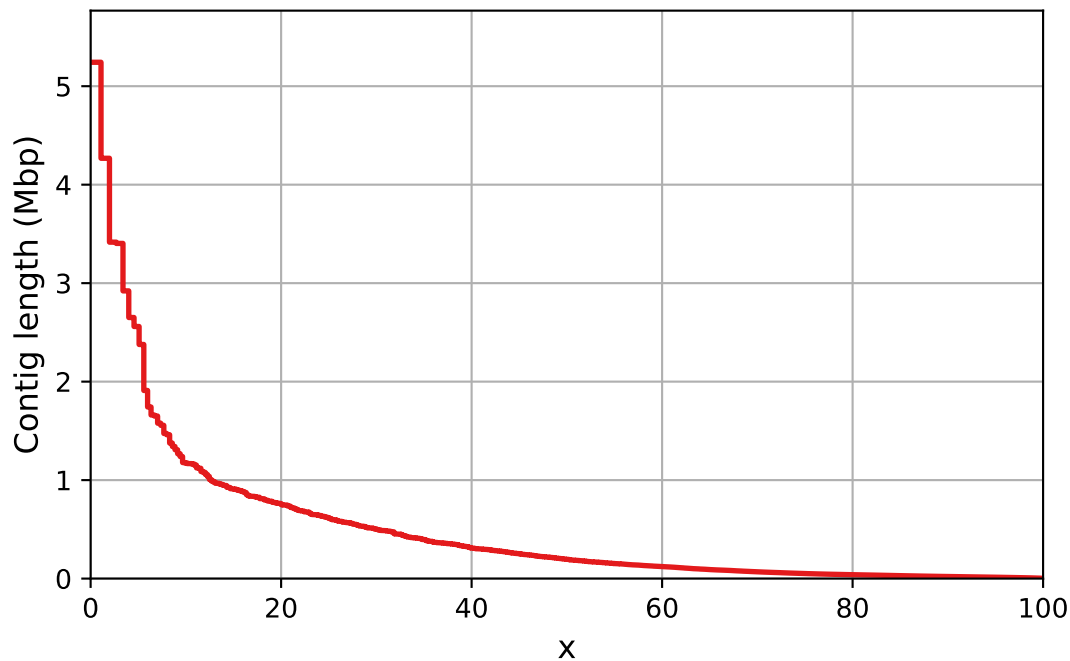|	assembly
# contigs (>= 0 bp)	8489
# contigs (>= 1000 bp)	8391
# contigs (>= 5000 bp)	7612
# contigs (>= 10000 bp)	6237
# contigs (>= 25000 bp)	3396
# contigs (>= 50000 bp)	1761
Total length (>= 0 bp)	480682550
Total length (>= 1000 bp)	480614334
Total length (>= 5000 bp)	477965686
Total length (>= 10000 bp)	467654033
Total length (>= 25000 bp)	420580563
Total length (>= 50000 bp)	362624021
# contigs	8484
Largest contig	5242943
Total length	480680666
Reference length	15710962
N50	195279
N90	21219
auN	522529.6
L50	470
L90	3920
# misassemblies	502
# misassembled contigs	55
Misassembled contigs length	9764040
# local misassemblies	218
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	251
# unaligned contigs	7604 + 830 part
Unaligned length	469795488
Genome fraction (%)	54.608
Duplication ratio	1.434
# N's per 100 kbp	0.00
# mismatches per 100 kbp	4245.94
# indels per 100 kbp	675.03
Largest alignment	164422
Total aligned length	10874893
NA50	-
NA90	-
auNA	715.1
LA50	-
LA90	-

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

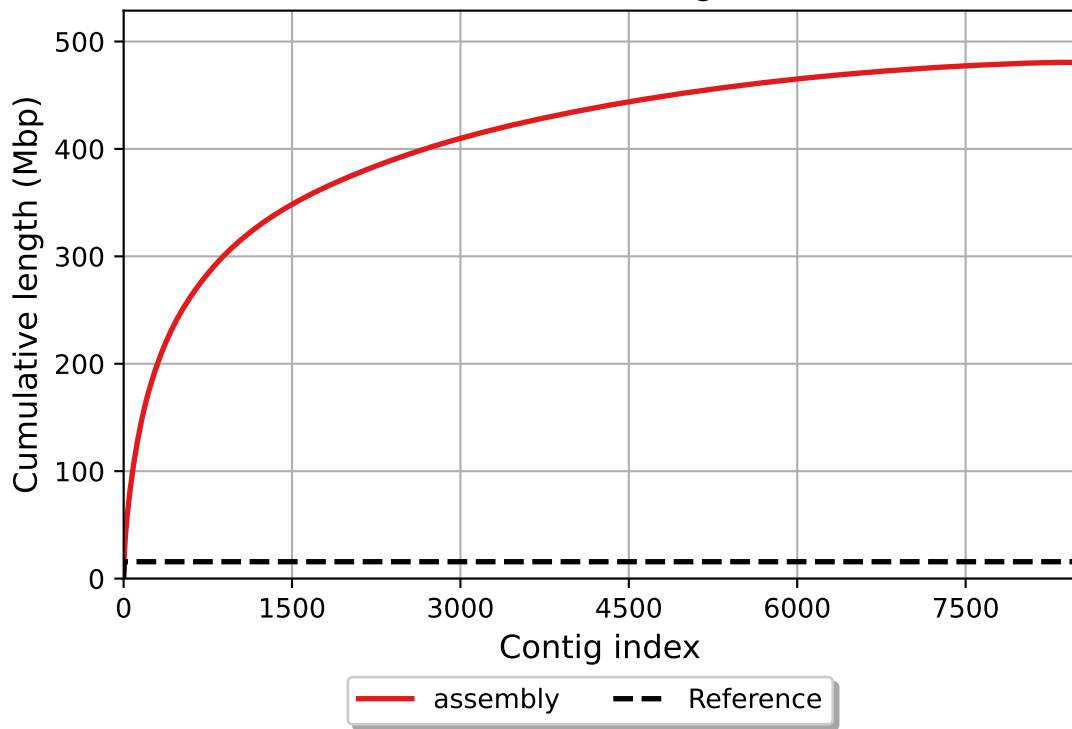|	assembly
# misassemblies	502
# contig misassemblies	502
# c. relocations	494
# c. translocations	7
# c. inversions	1
# c. interspecies translocations	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# s. interspecies translocations	0
# misassembled contigs	55
Misassembled contigs length	9764040
# possibly misassembled contigs	579
# possible misassemblies	1542
# local misassemblies	218
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	251
# mismatches	461741
# indels	73409
# indels (<= 5 bp)	71964
# indels (> 5 bp)	1445
Indels length	134409

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).
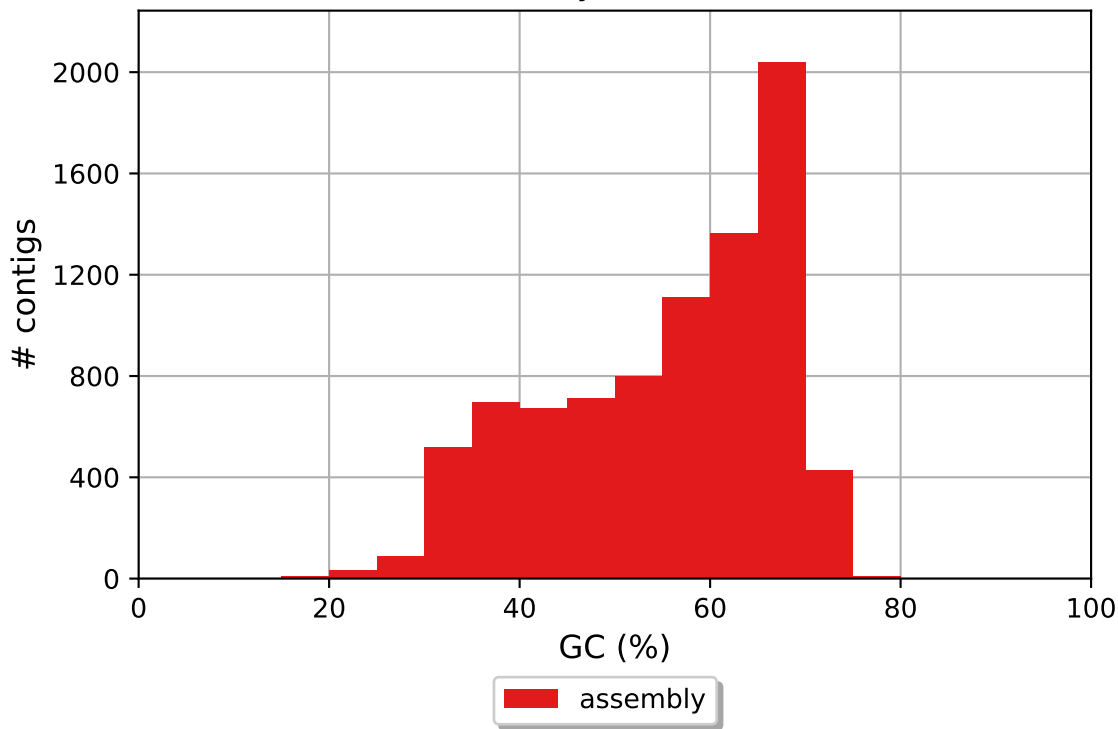
Unaligned report

	assembly
# fully unaligned contigs	7604
Fully unaligned length	297741966
# partially unaligned contigs	830
Partially unaligned length	172053522
# 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).
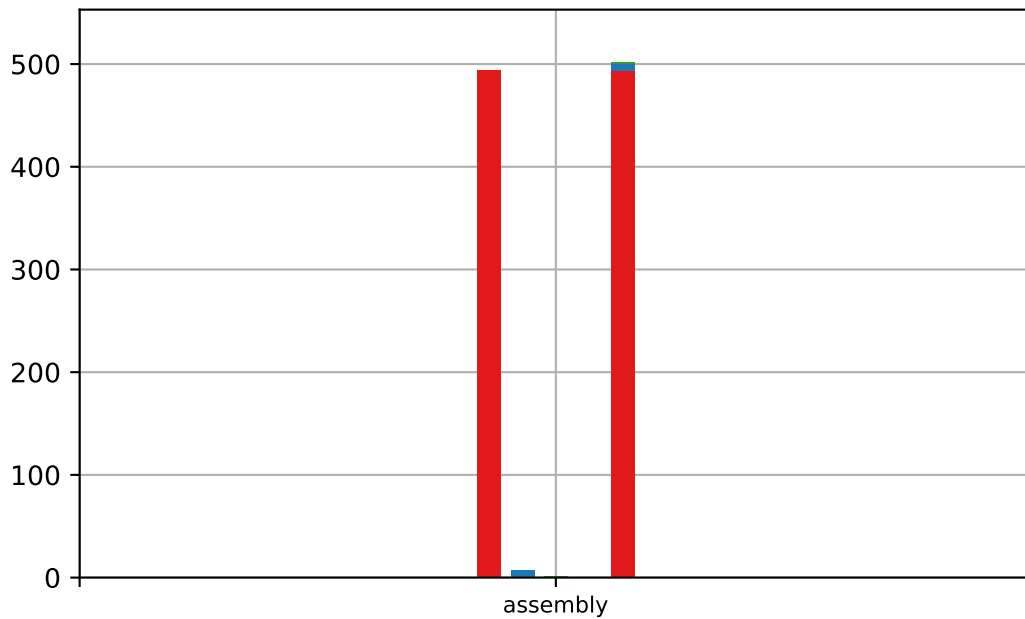
Nx

Cumulative length

Contig index (x-axis), **Cumulative length (Mbp)** (y-axis)

Legend: assembly, Reference
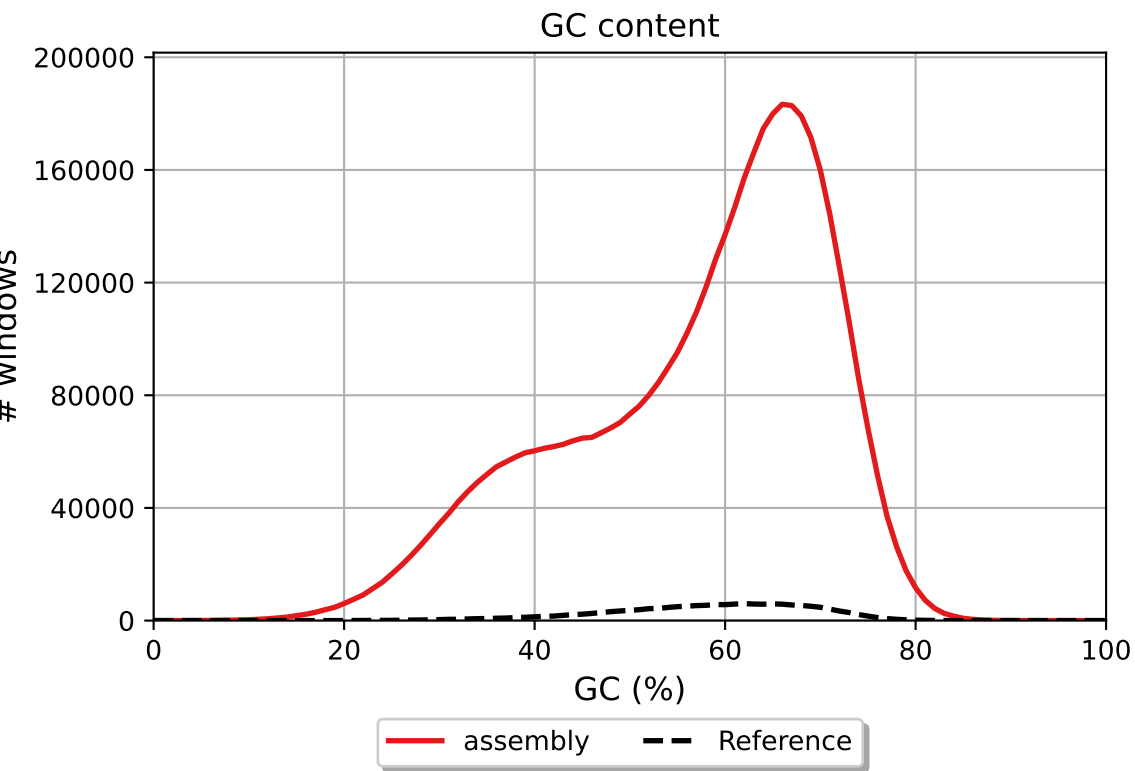
GC content

assembly GC content

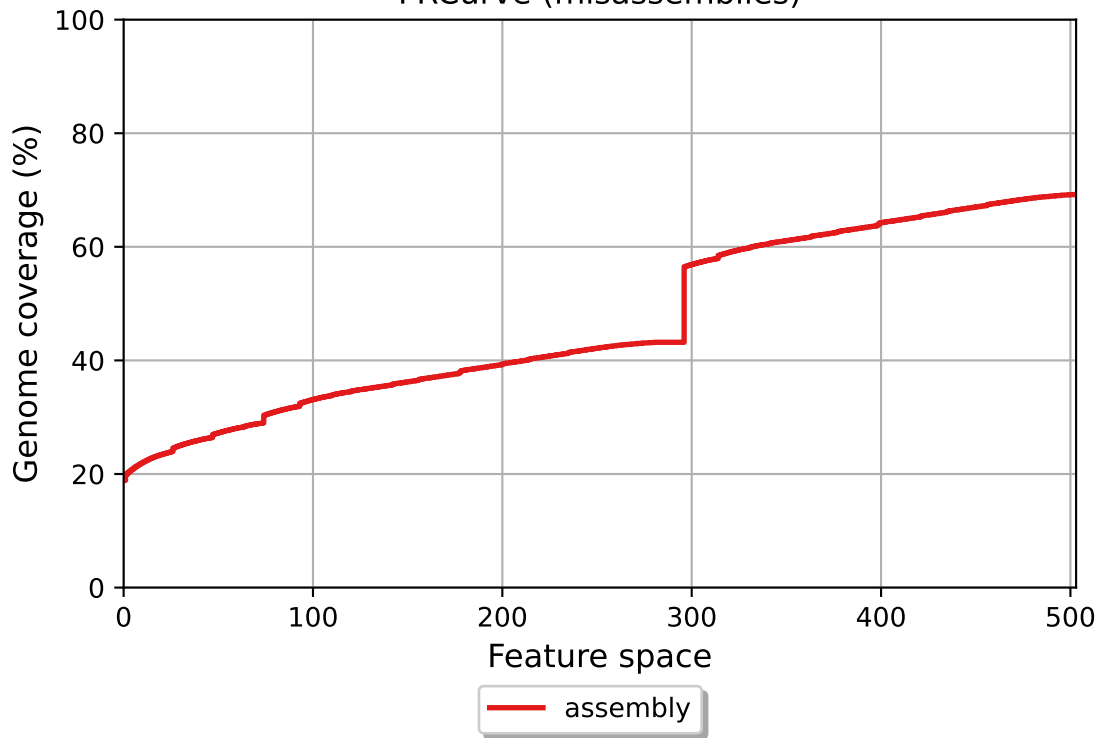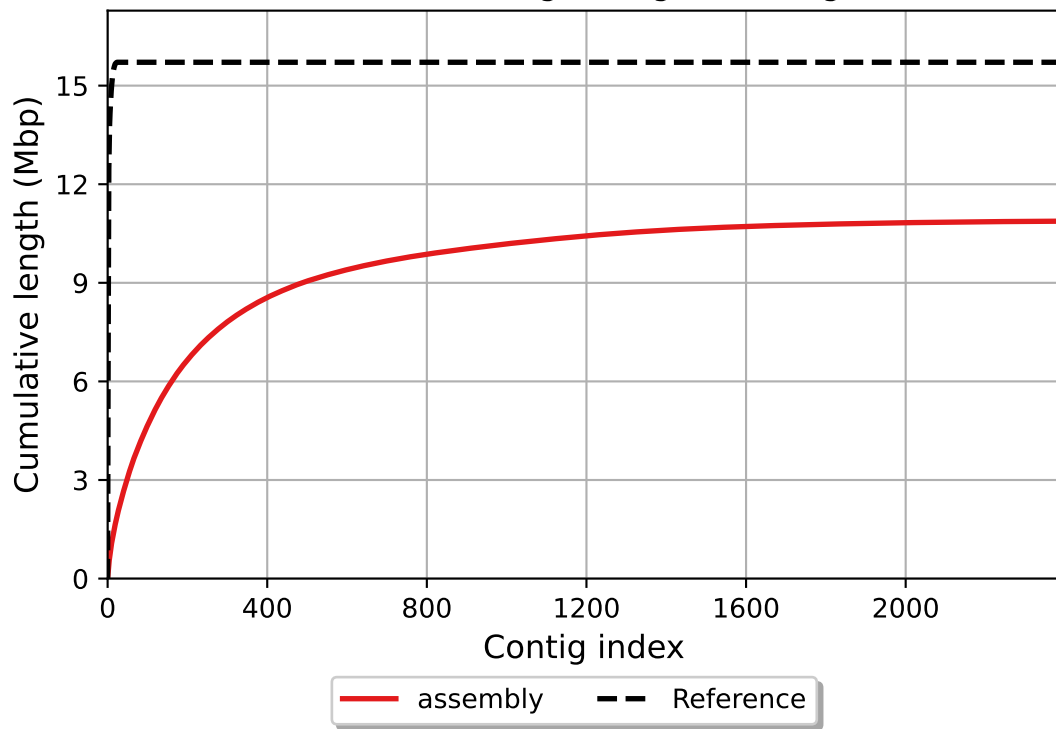Misassemblies

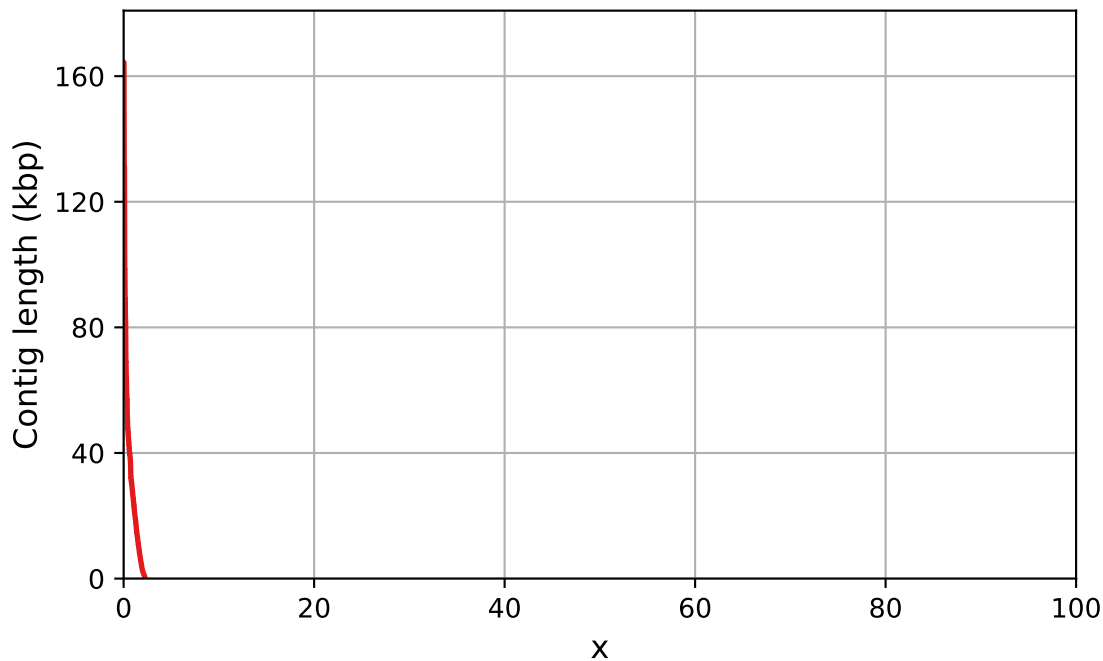- █ # relocations
- █ # translocations
- █ # inversions

FRCurve (misassemblies)

Cumulative length (aligned contigs)

NAx