Report

	pilon
# contigs (>= 0 bp)	9
# contigs (>= 1000 bp)	9
# contigs (>= 5000 bp)	9
# contigs (>= 10000 bp)	8
# contigs (>= 25000 bp)	5
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	3159597
Total length (>= 1000 bp)	3159597
Total length (>= 5000 bp)	3159597
Total length (>= 10000 bp)	3149801
Total length (>= 25000 bp)	3099716
Total length (>= 50000 bp)	3006371
# contigs	9
Largest contig	2775723
Total length	3159597
Reference length	2919198
GC (%)	37.78
Reference GC (%)	37.88
N50	2775723
NG50	2775723
N75	2775723
NG75	2775723
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	190
# misassembled contigs	1
Misassembled contigs length	2775723
# local misassemblies	36
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# unaligned contigs	3 + 6 part
Unaligned length	561711
Genome fraction (%)	85.017
Duplication ratio	1.047
# N's per 100 kbp	0.00
# mismatches per 100 kbp	391.25
# indels per 100 kbp	15.31
Largest alignment	115727
Total aligned length	2592523
NA50	24553
NGA50	30127
NA75	4951
NGA75	10362
LA50	32
LGA50	27
LA75	88
LGA75	66

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).
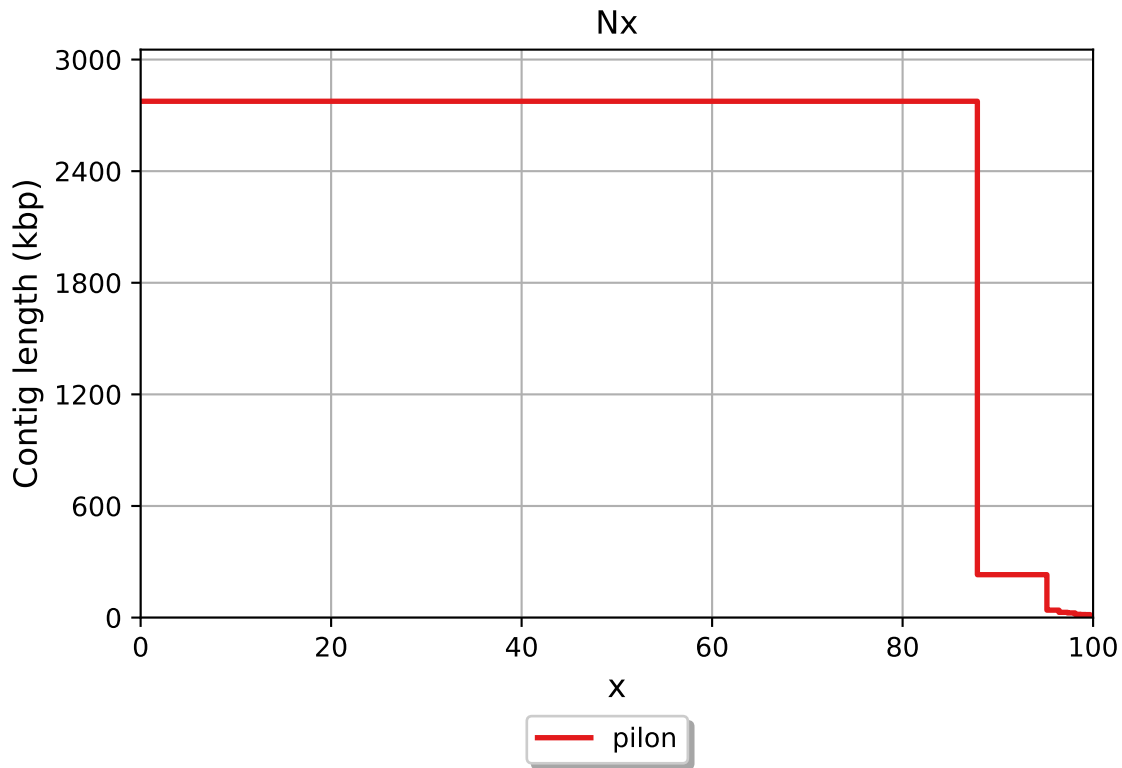
Misassemblies report
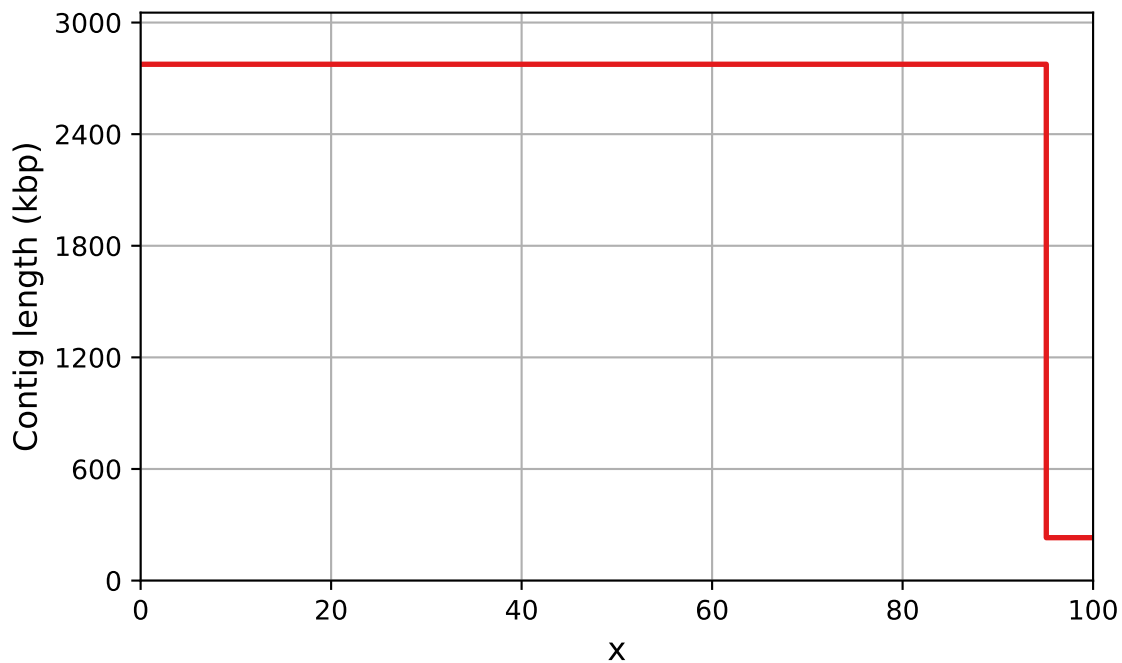
	pilon
# misassemblies	190
# contig misassemblies	190
# c. relocations	174
# c. translocations	14
# c. inversions	2
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	1
Misassembled contigs length	2775723
# local misassemblies	36
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# mismatches	9710
# indels	380
# indels (<= 5 bp)	342
# indels (> 5 bp)	38
Indels length	1563

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
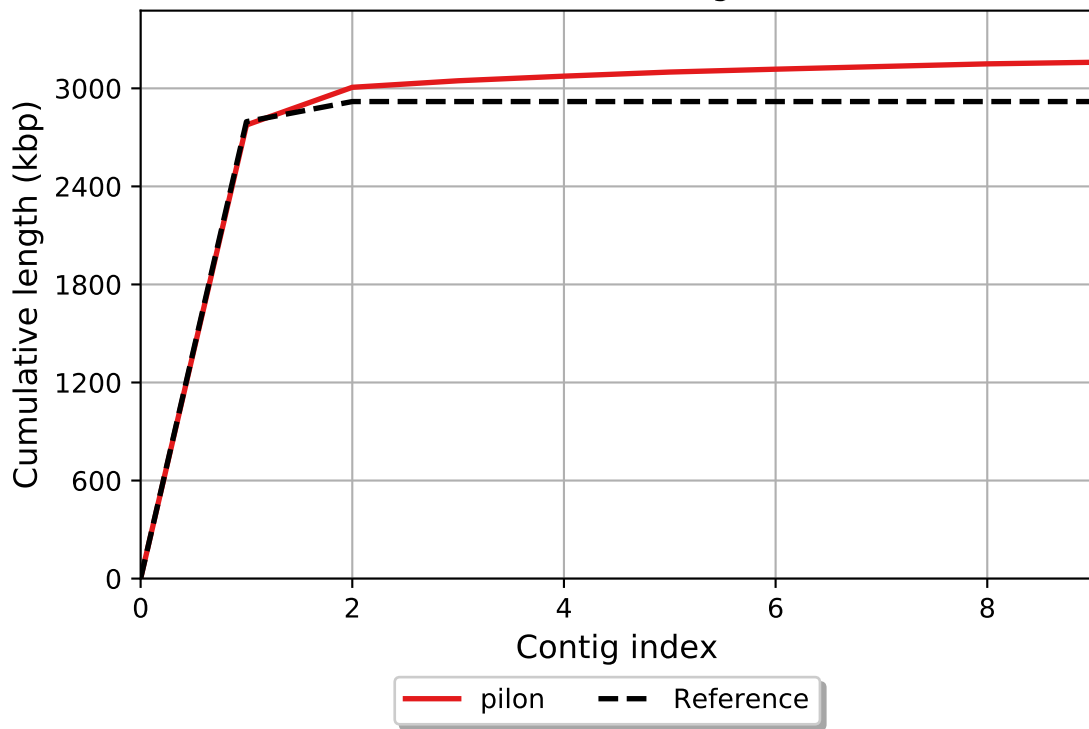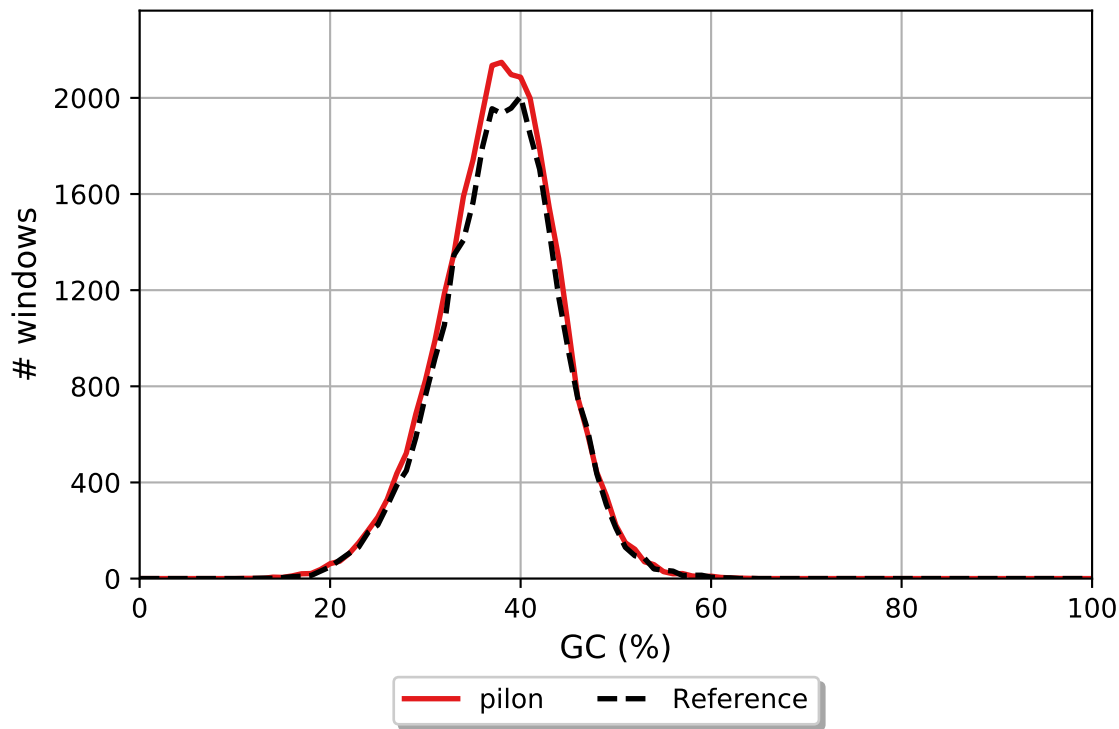
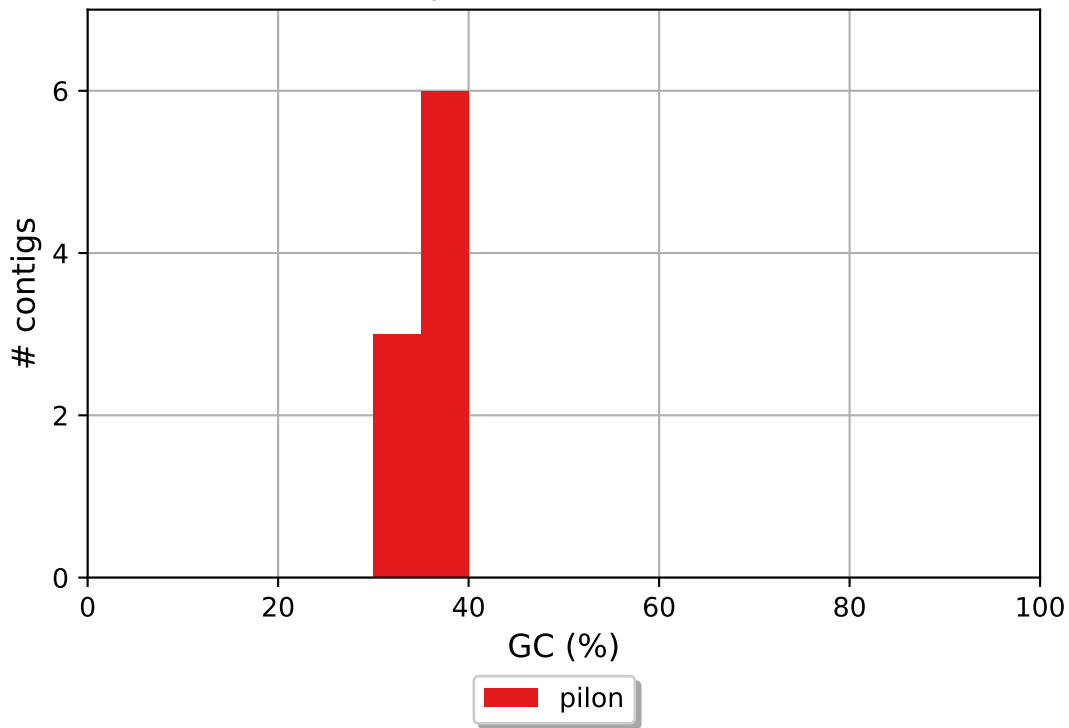|	pilon
# fully unaligned contigs	3
Fully unaligned length	58708
# partially unaligned contigs	6
Partially unaligned length	503003
# N's	0

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

Contig length (kbp) vs **x**

— pilon

Cumulative length

GC content

windows vs GC (%)

pilon — Reference

pilon GC content

Misassemblies

Legend: # relocations (red), # translocations (blue), # inversions (green)

x-axis: pilon
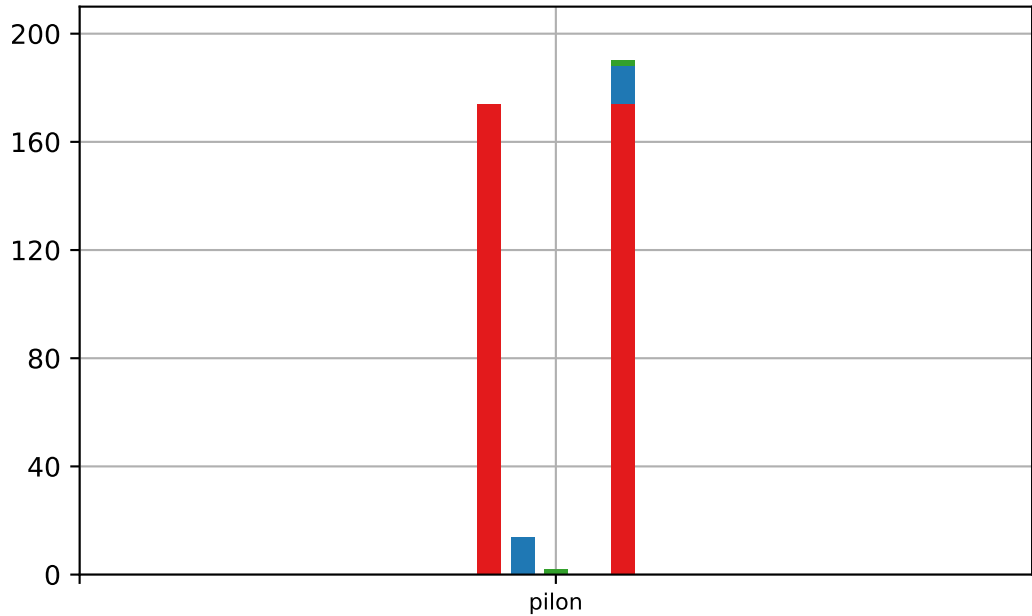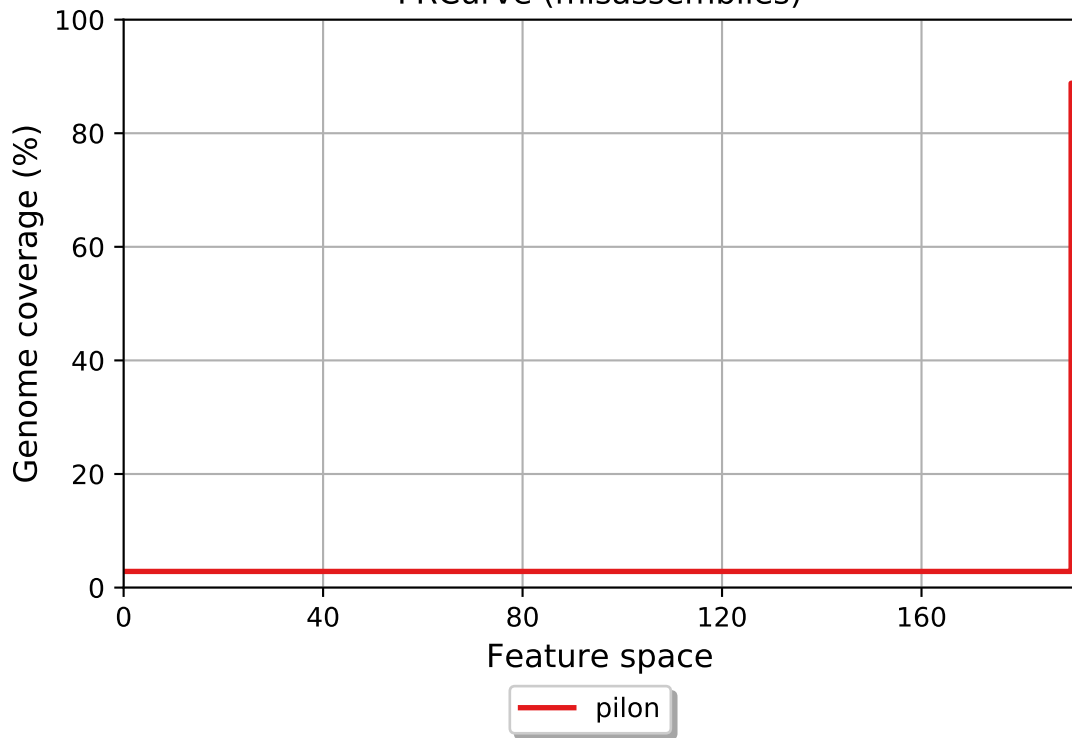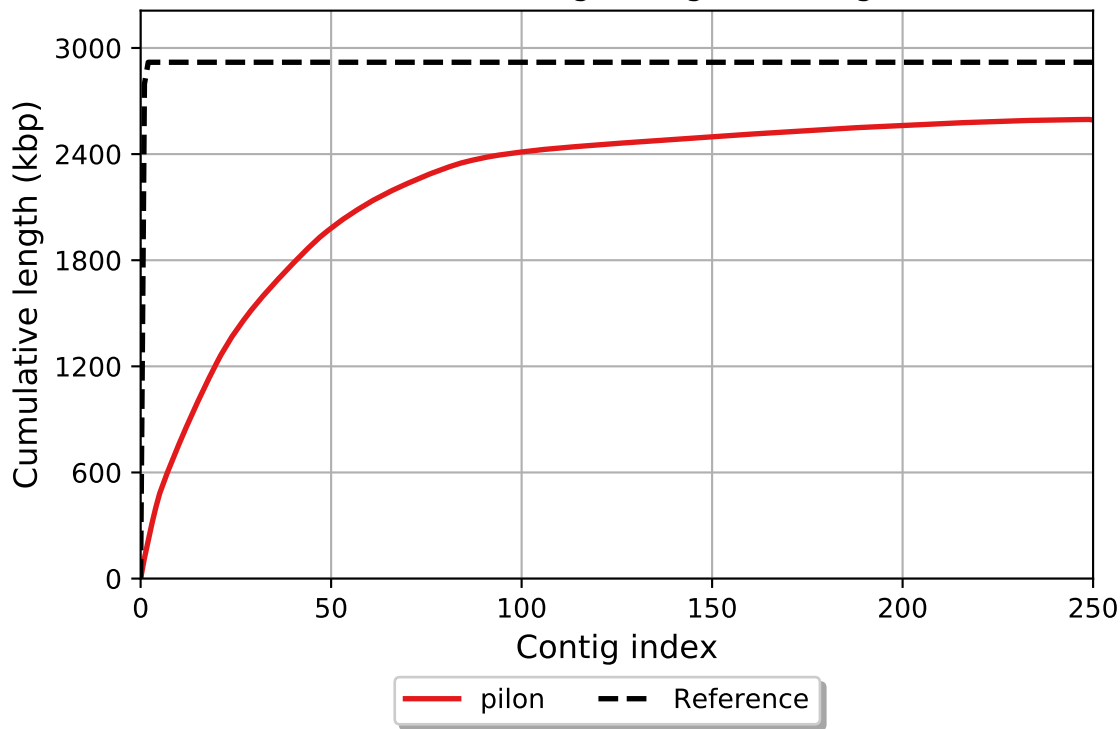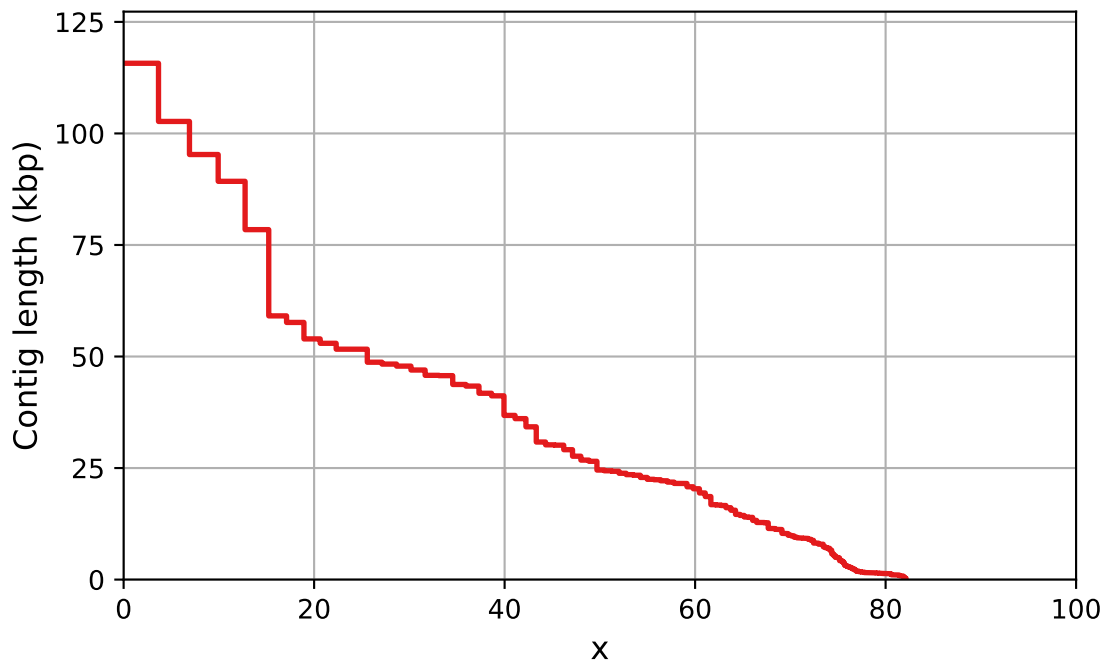
FRCurve (misassemblies)

Cumulative length (aligned contigs)

NAx

NGAx