

Report

	assembly
# contigs (>= 0 bp)	26
# contigs (>= 1000 bp)	26
# contigs (>= 5000 bp)	25
# contigs (>= 10000 bp)	24
# contigs (>= 25000 bp)	22
# contigs (>= 50000 bp)	19
Total length (>= 0 bp)	4653613
Total length (>= 1000 bp)	4653613
Total length (>= 5000 bp)	4649137
Total length (>= 10000 bp)	4643514
Total length (>= 25000 bp)	4606570
Total length (>= 50000 bp)	4506314
# contigs	26
Largest contig	627349
Total length	4653613
Reference length	4639675
GC (%)	50.75
Reference GC (%)	50.79
N50	303962
NG50	303962
N75	187853
NG75	187853
L50	6
LG50	6
L75	10
LG75	10
# misassemblies	11
# misassembled contigs	5
Misassembled contigs length	1253321
# local misassemblies	5
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 10 part
Unaligned length	25731
Genome fraction (%)	99.026
Duplication ratio	1.007
# N's per 100 kbp	0.00
# mismatches per 100 kbp	3.81
# indels per 100 kbp	73.96
Largest alignment	625460
Total aligned length	4623882
NA50	302627
NGA50	302627
NA75	145967
NGA75	145967
LA50	6
LGA50	6
LA75	12
LGA75	12

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	11
# contig misassemblies	11
# c. relocations	9
# c. translocations	0
# c. inversions	2
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	5
Misassembled contigs length	1253321
# local misassemblies	5
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	175
# indels	3398
# indels (<= 5 bp)	3395
# indels (> 5 bp)	3
Indels length	3550

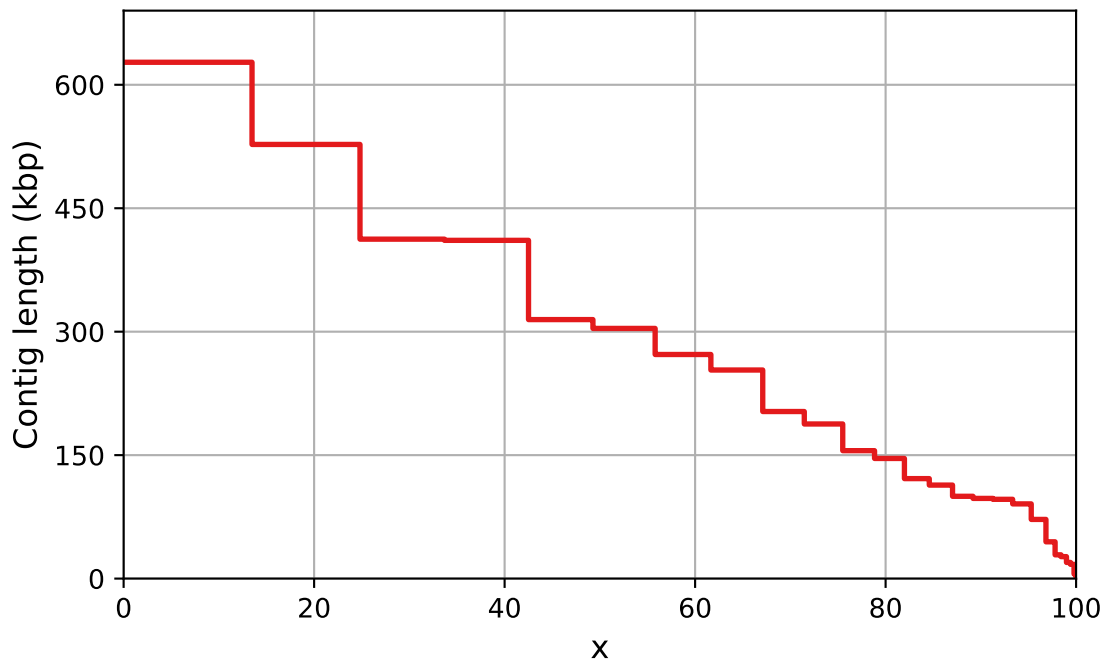
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	assembly
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	10
Partially unaligned length	25731
# N's	0

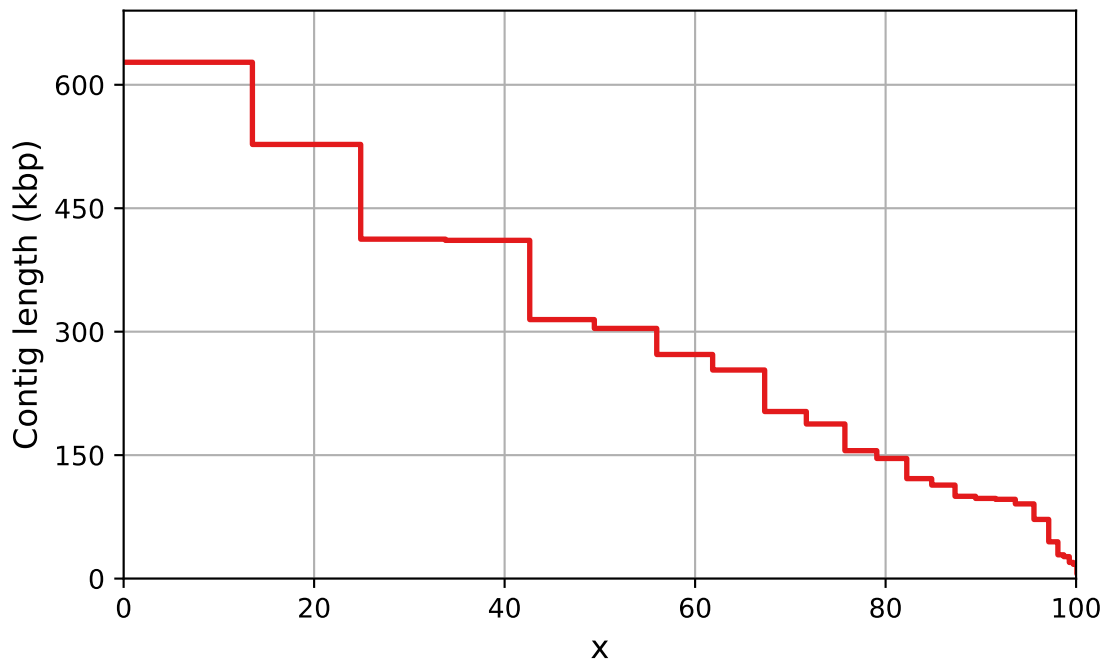
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

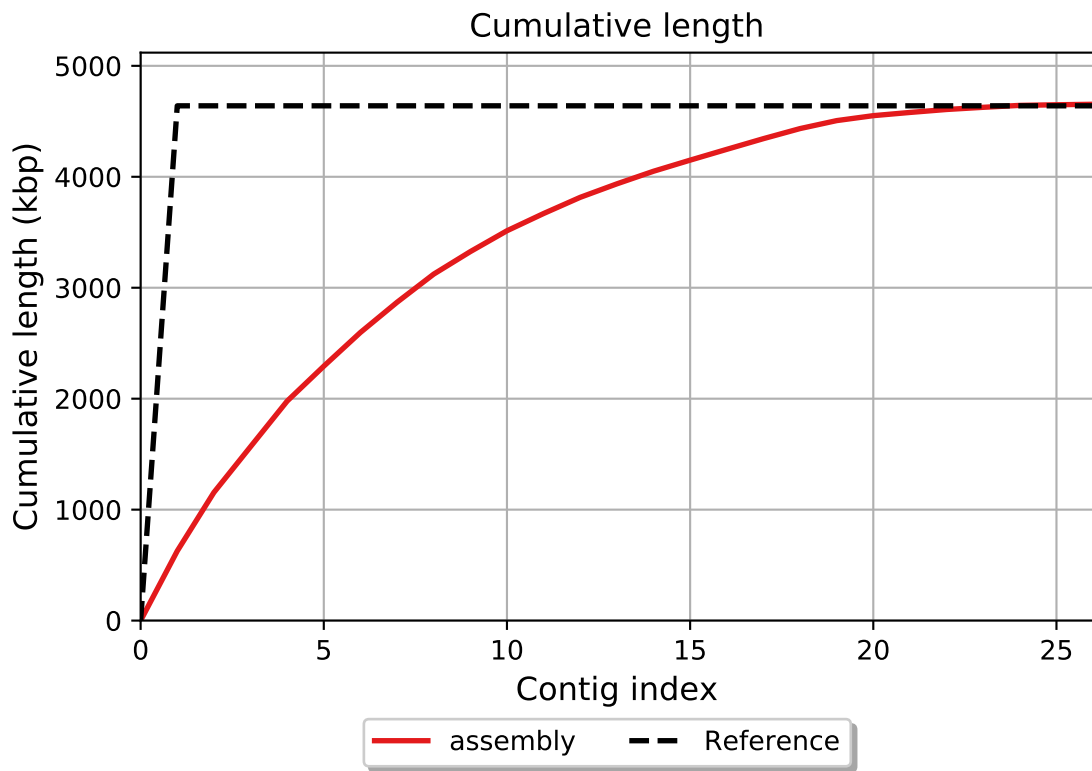


— assembly

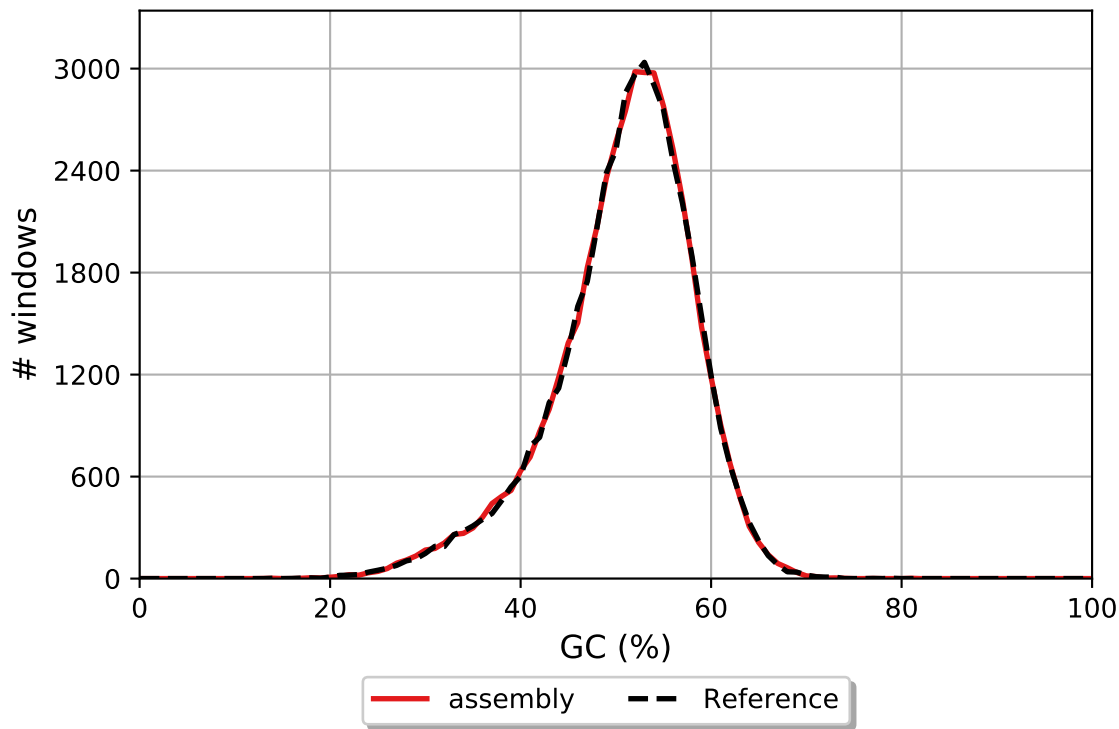
NGx



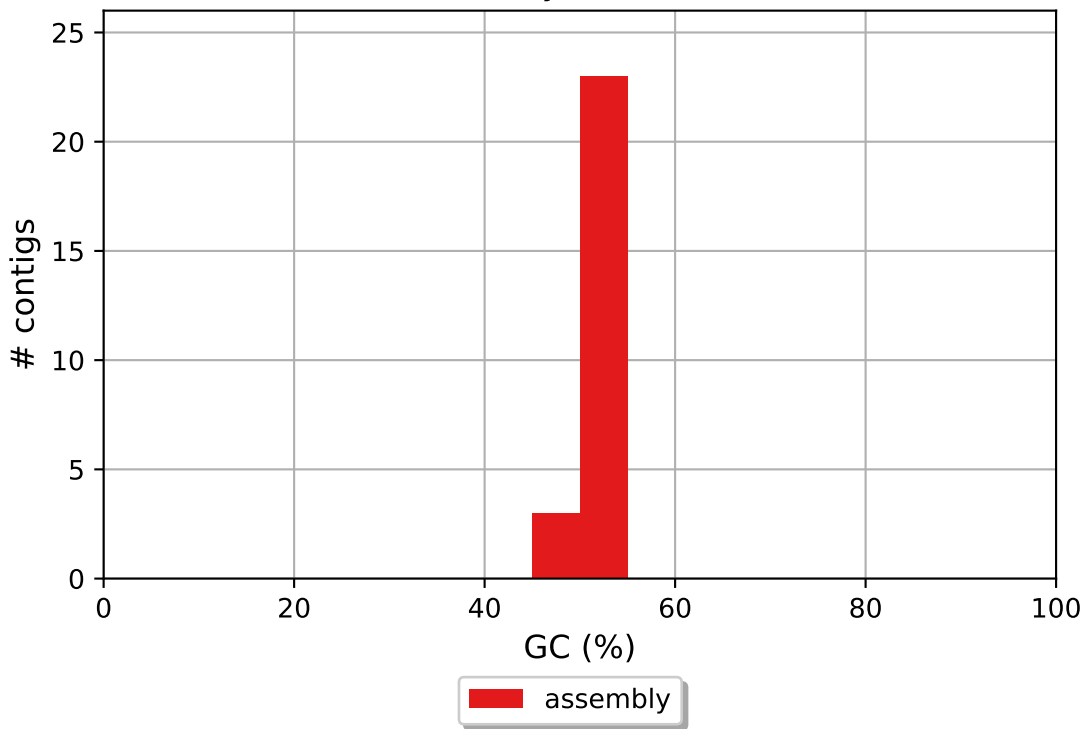
— assembly



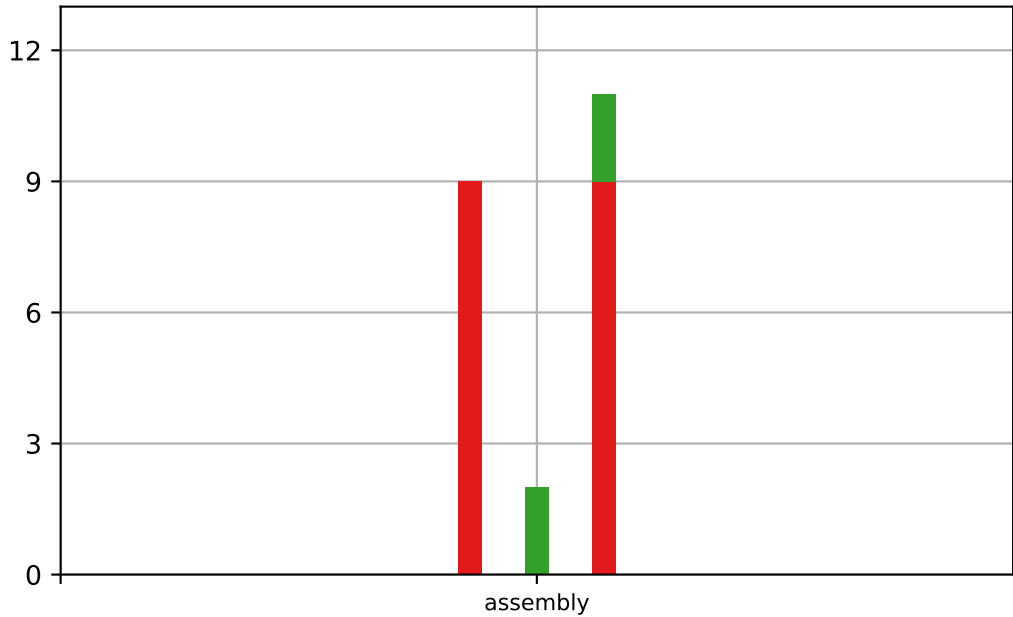
GC content



assembly GC content



Misassemblies

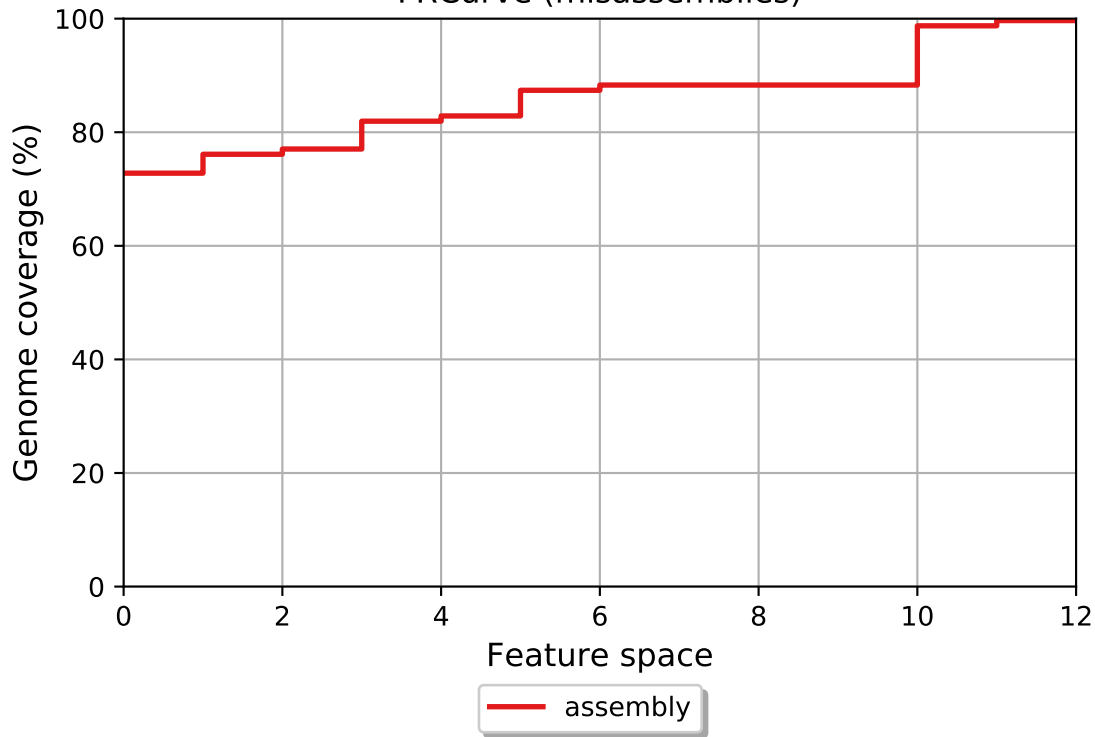


relocations

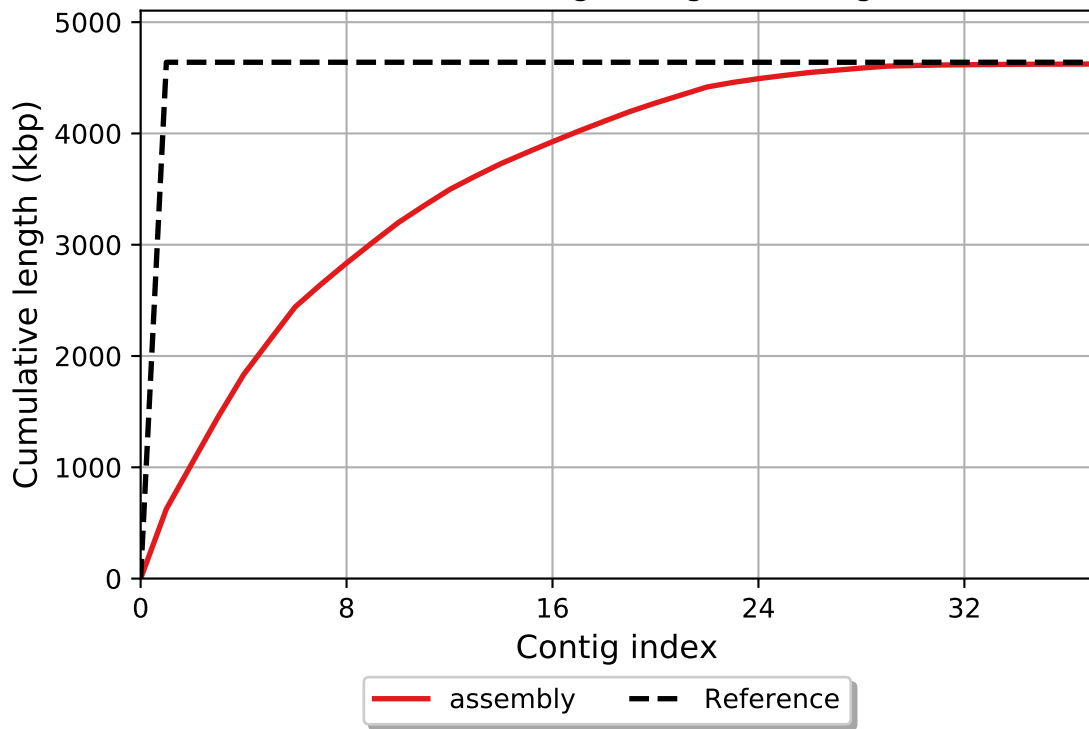


inversions

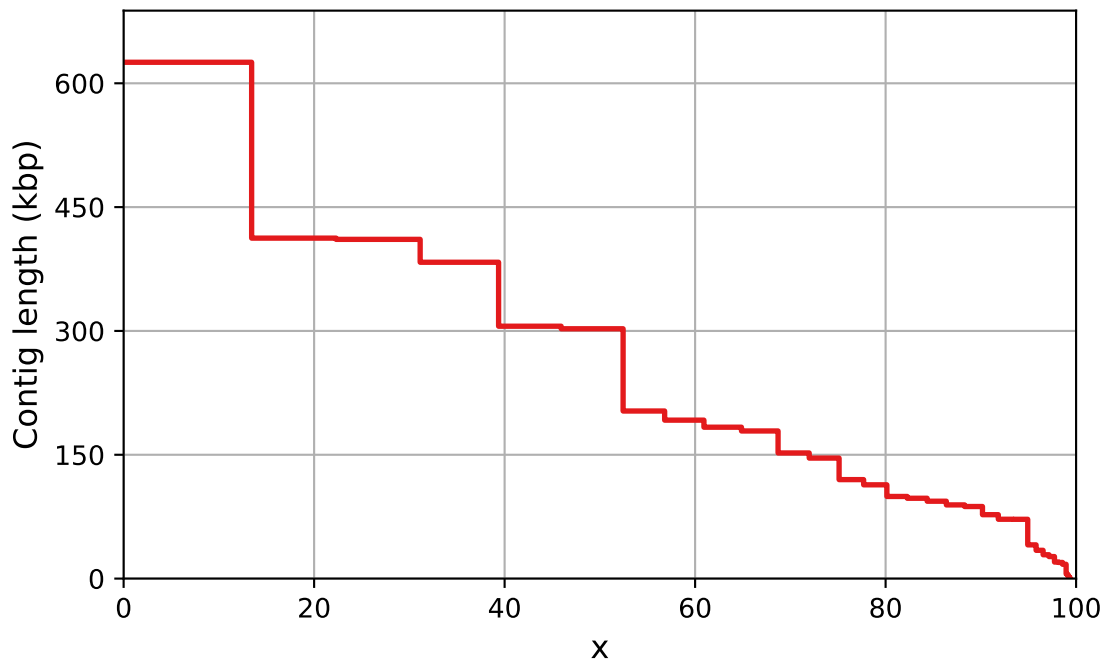
FRCurve (misassemblies)



Cumulative length (aligned contigs)



NAx



— assembly

NGAx

