Report

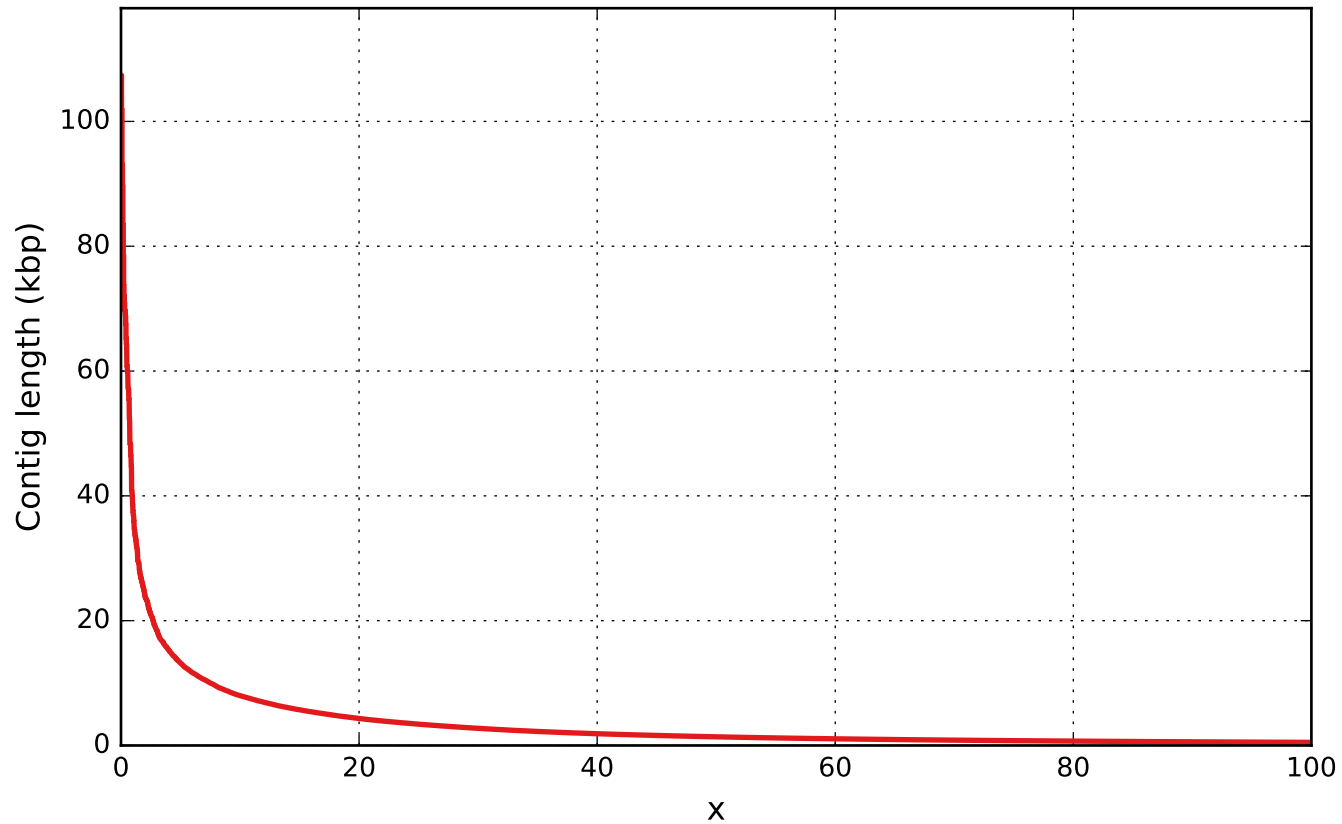|	final.contigs
# contigs (>= 0 bp)	440792
# contigs (>= 1000 bp)	67804
# contigs (>= 5000 bp)	4787
# contigs (>= 10000 bp)	1125
# contigs (>= 25000 bp)	119
# contigs (>= 50000 bp)	27
Total length (>= 0 bp)	339514356
Total length (>= 1000 bp)	156998240
Total length (>= 5000 bp)	43307574
Total length (>= 10000 bp)	18769569
Total length (>= 25000 bp)	4791641
Total length (>= 50000 bp)	1860260
# contigs	204876
Largest contig	107401
Total length	249816090
Reference length	98017596
N50	1388
N75	771
L50	40279
L75	102606
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned mis. contigs	5
# unaligned contigs	204653 + 135 part
Unaligned length	249738212
Genome fraction (%)	0.063
Duplication ratio	1.537
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2679.24
# indels per 100 kbp	98.81
Largest alignment	3271
Total aligned length	53269

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

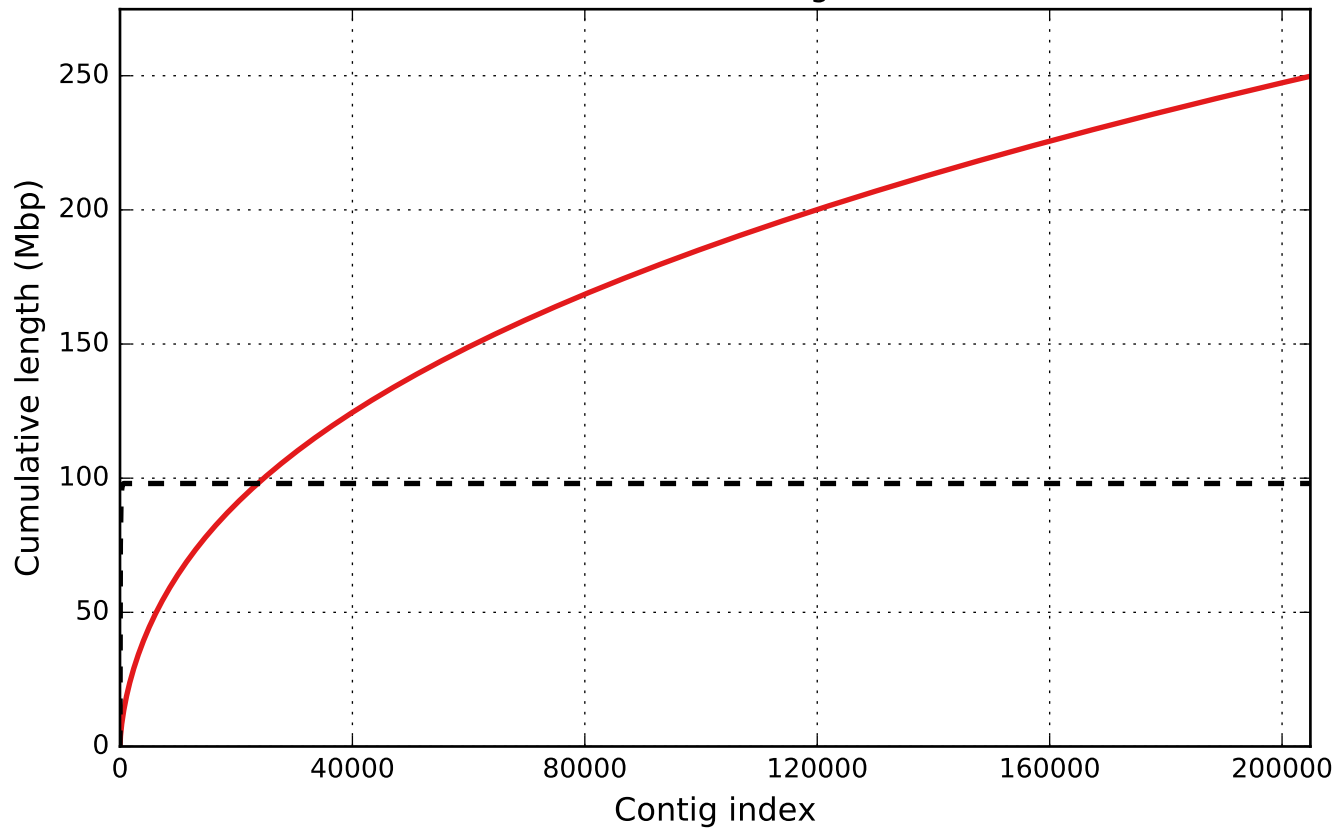|	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	2
# possible misassemblies	3
# local misassemblies	1
# unaligned mis. contigs	5
# mismatches	1654
# indels	61
# indels (<= 5 bp)	61
# indels (> 5 bp)	0
Indels length	69

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

	final.contigs
# fully unaligned contigs	204653
Fully unaligned length	249342516
# partially unaligned contigs	135
Partially unaligned length	395696
# 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

GC content
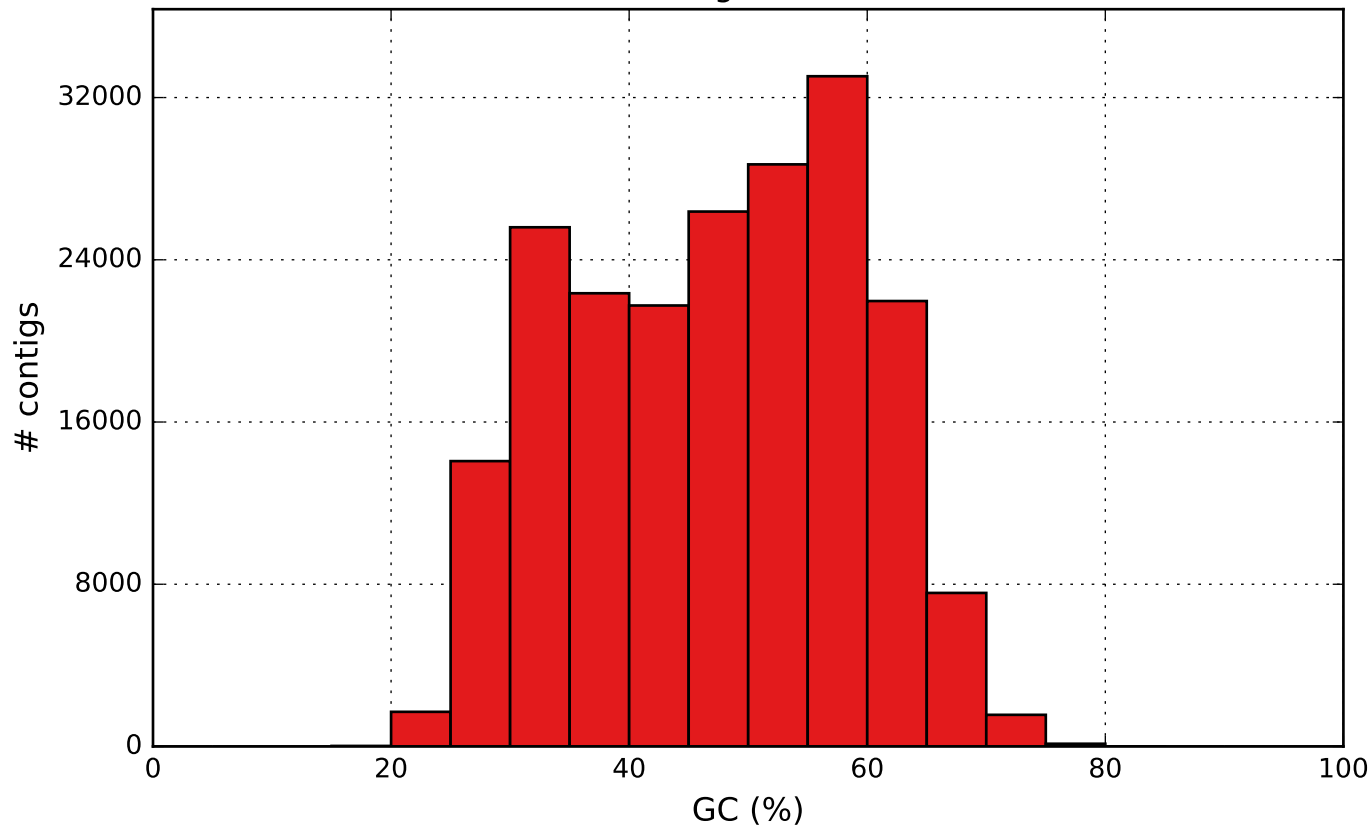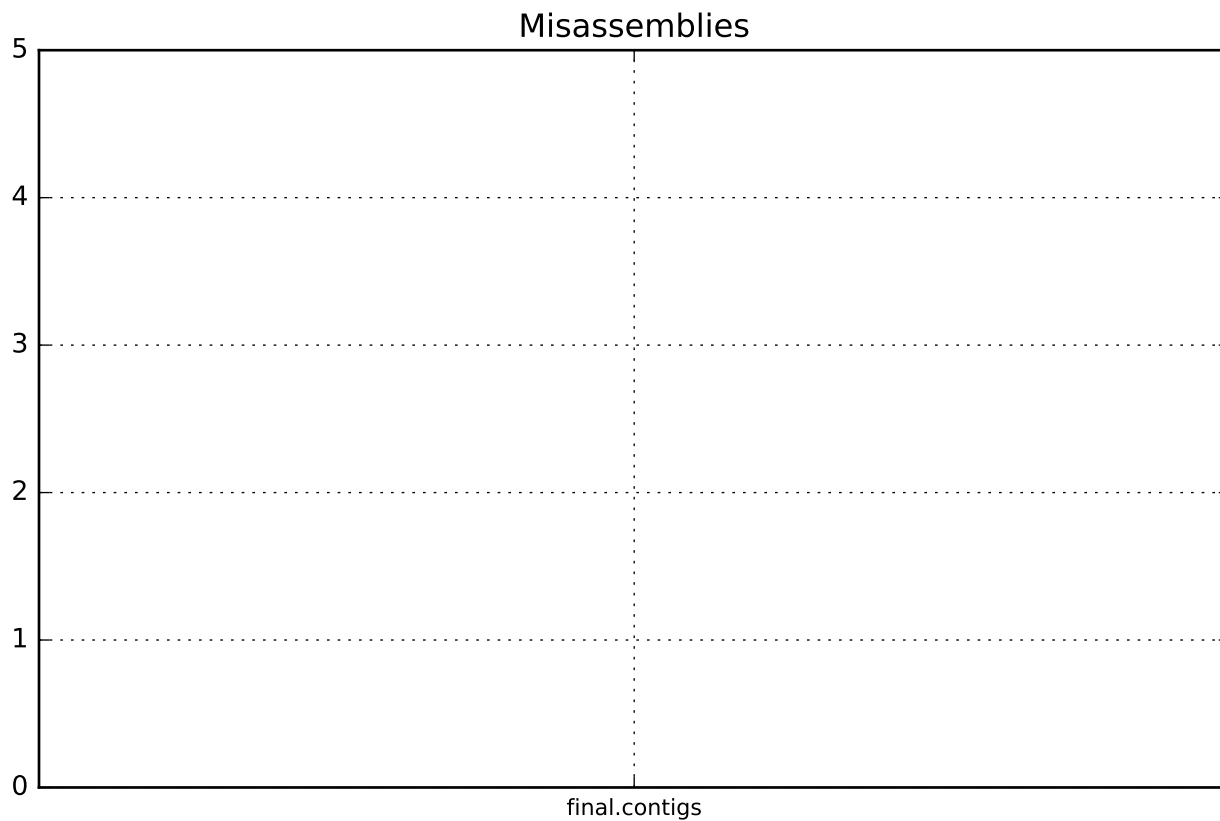
windows vs GC (%)
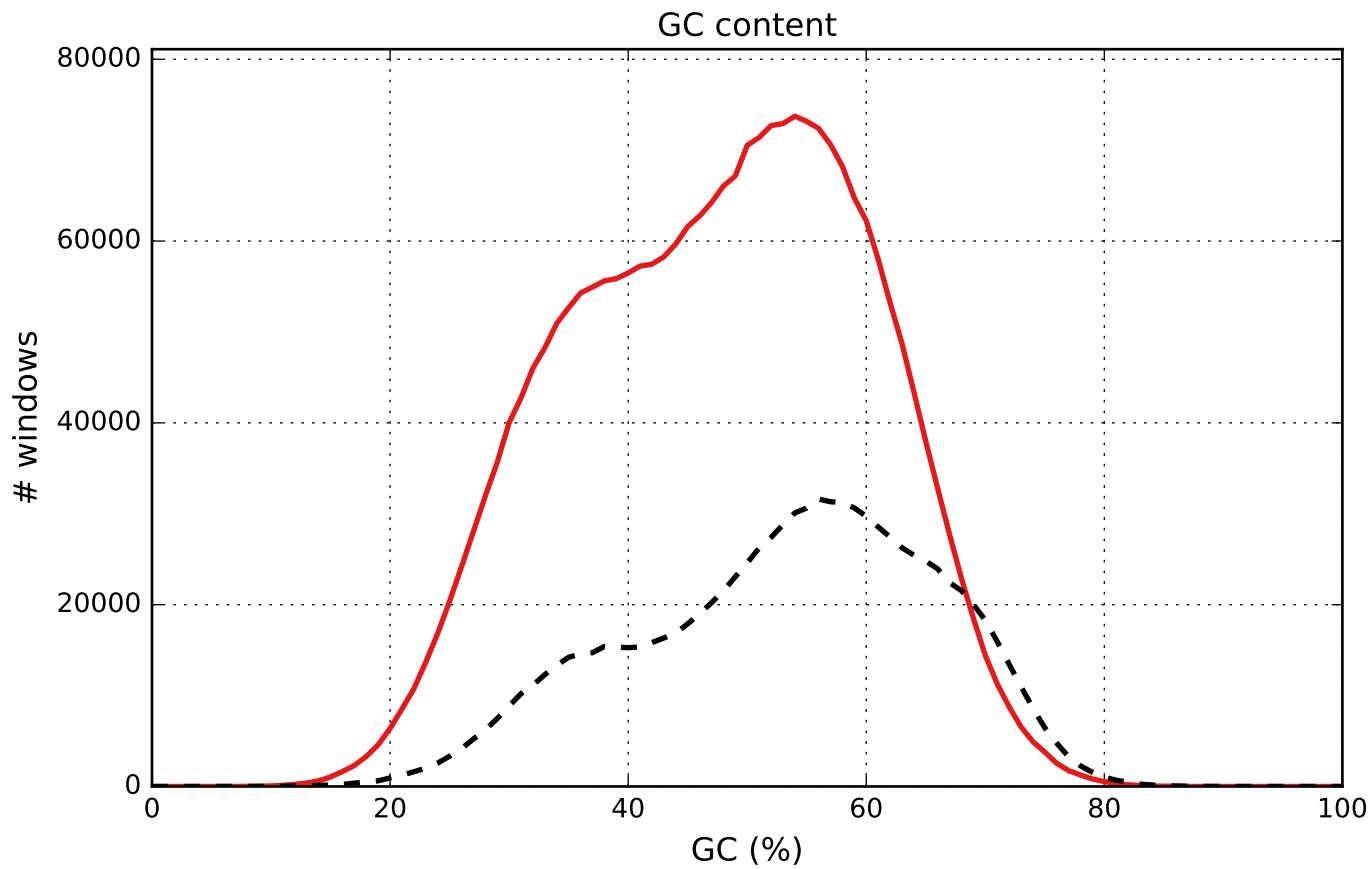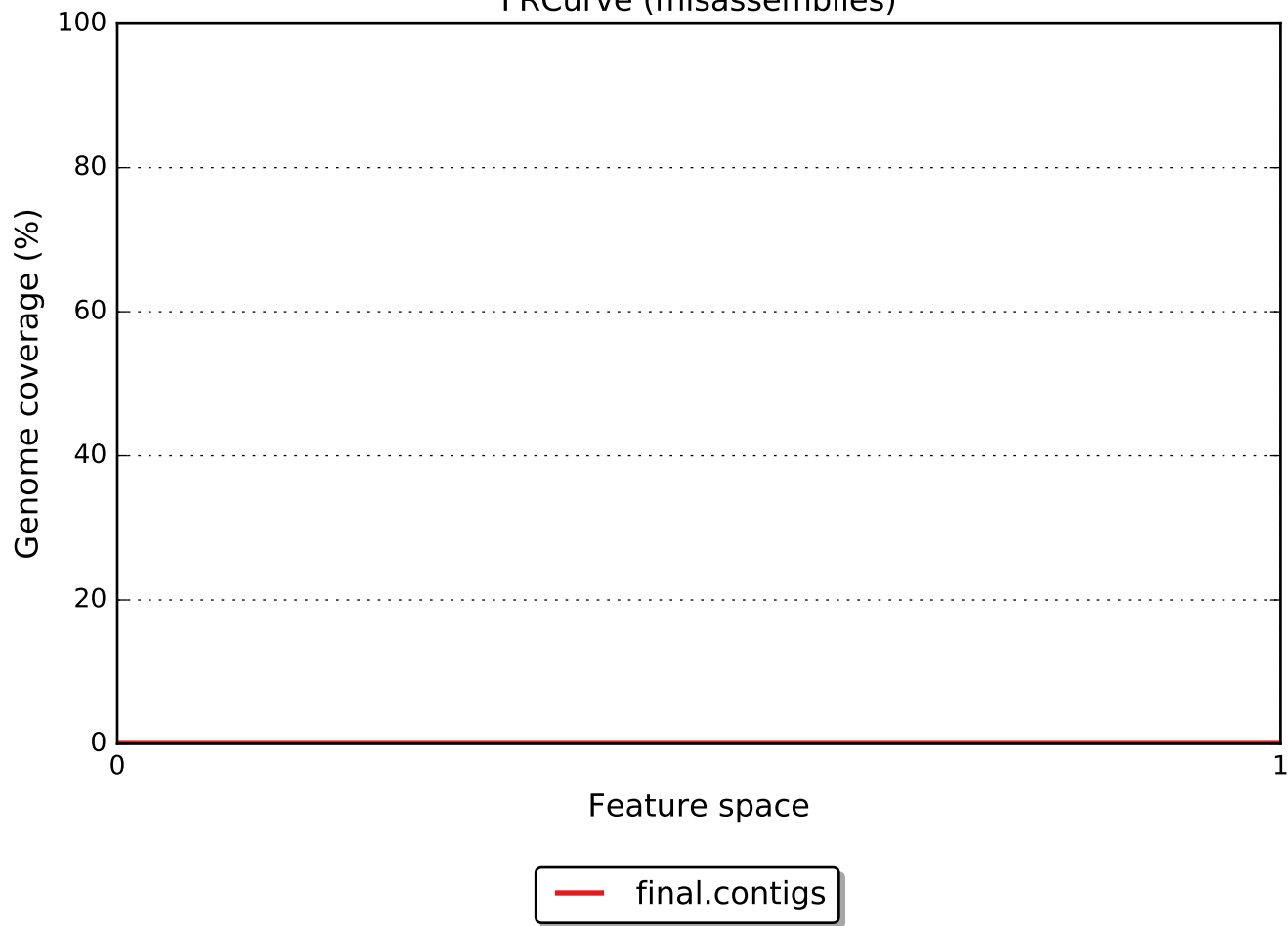
final.contigs — Reference

final.contigs GC content

Misassemblies

final.contigs

FRCurve (misassemblies)

Cumulative length (aligned contigs)

Contig index — Cumulative length (Mbp)

Legend: final.contigs, Reference

NAx

final.contigs