

# Report

	final.contigs
# contigs (>= 0 bp)	159944
# contigs (>= 1000 bp)	23722
# contigs (>= 5000 bp)	1070
# contigs (>= 10000 bp)	226
# contigs (>= 25000 bp)	30
# contigs (>= 50000 bp)	12
Total length (>= 0 bp)	118996402
Total length (>= 1000 bp)	48247005
Total length (>= 5000 bp)	9786216
Total length (>= 10000 bp)	4144053
Total length (>= 25000 bp)	1395140
Total length (>= 50000 bp)	822203
# contigs	85351
Largest contig	128464
Total length	90052867
Reference length	86655544
N50	1078
N75	701
L50	20616
L75	47141
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# structural variations	0
# unaligned mis. contigs	0
# unaligned contigs	85246 + 49 part
Unaligned length	90003621
Genome fraction (%)	0.039
Duplication ratio	1.641
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2413.34
# indels per 100 kbp	163.81
Largest alignment	2489
Total aligned length	32641

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	2
# local misassemblies	0
# structural variations	0
# unaligned mis. contigs	0
# mismatches	825
# indels	56
# indels ( $\leq 5$ bp)	56
# indels ( $> 5$ bp)	0
Indels length	61

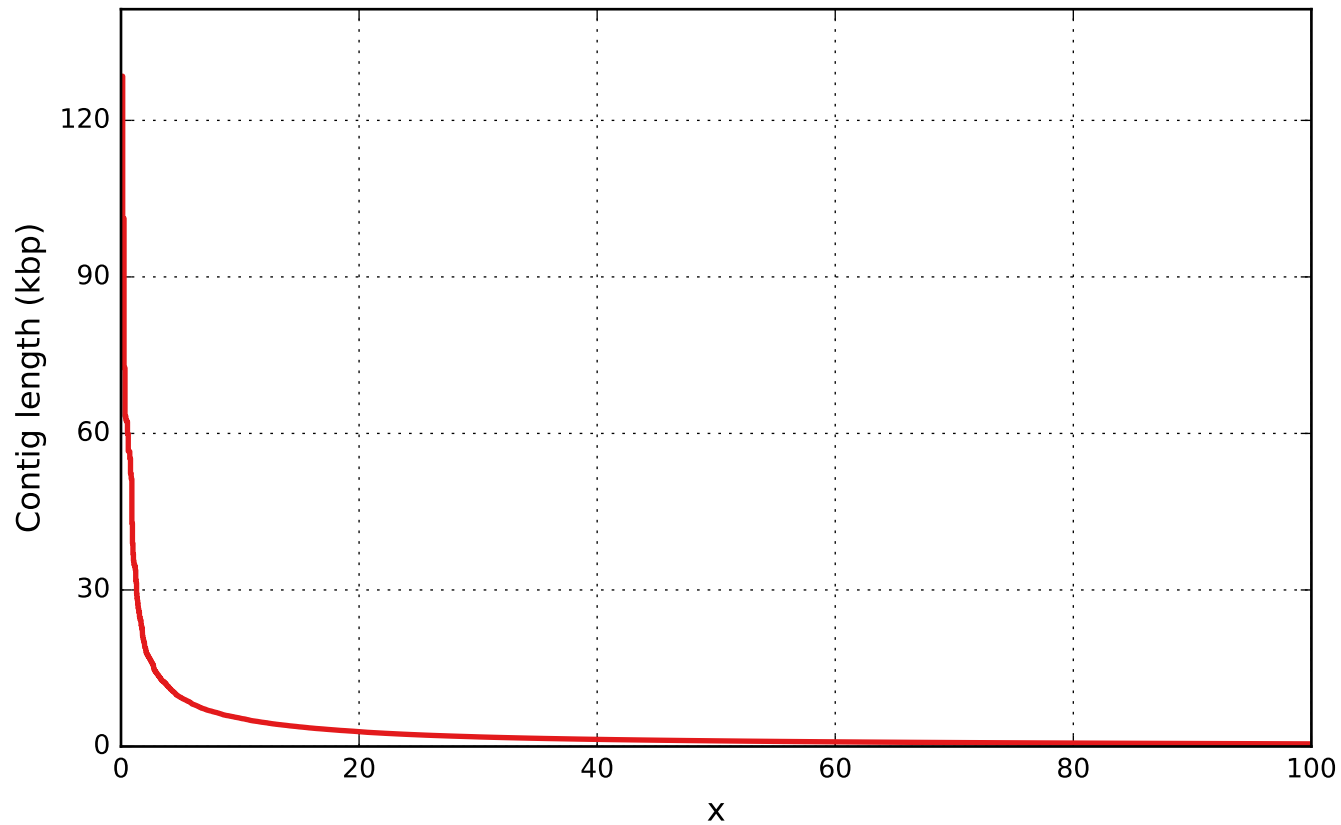
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

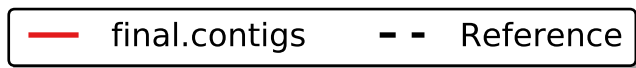
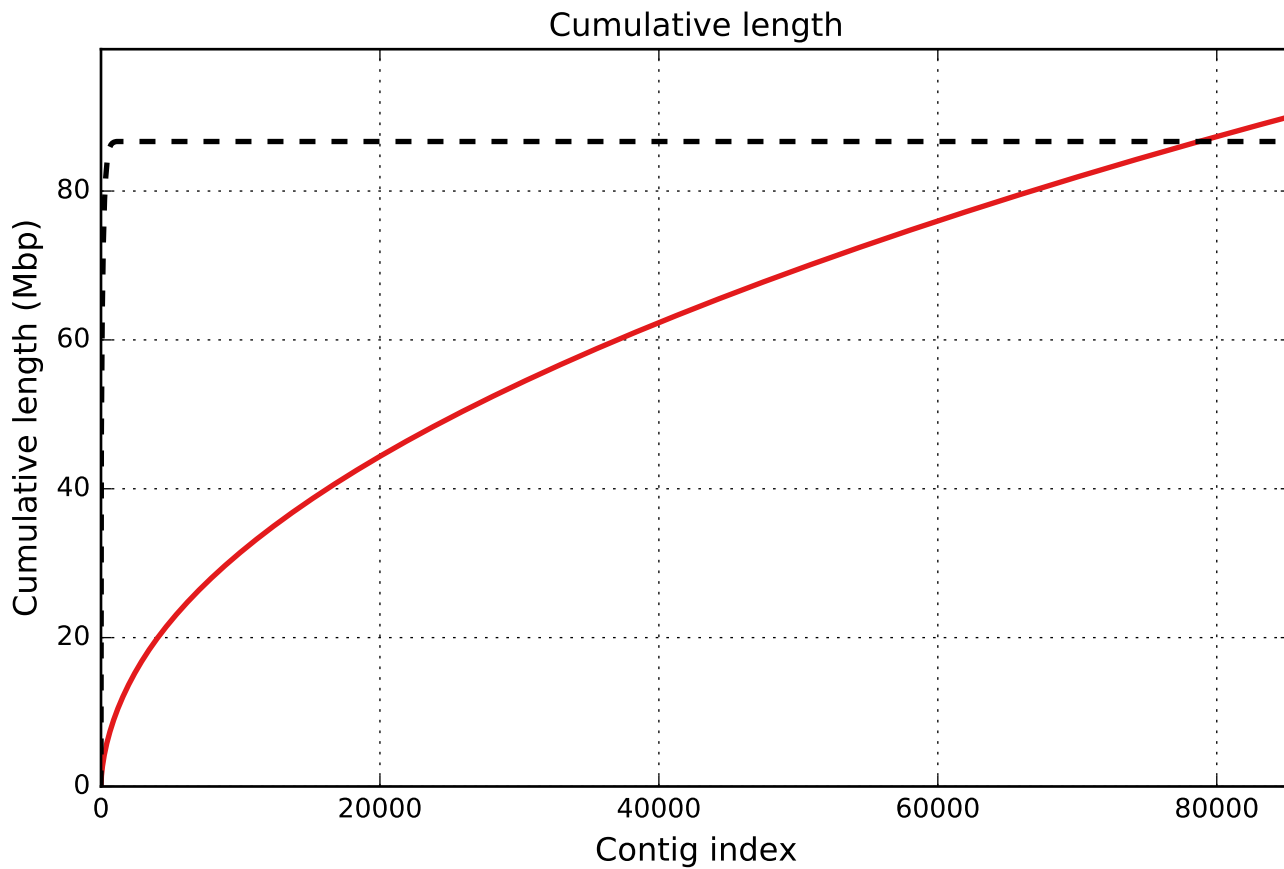
	final.contigs
# fully unaligned contigs	85246
Fully unaligned length	89931485
# partially unaligned contigs	49
Partially unaligned length	72136
# N's	0

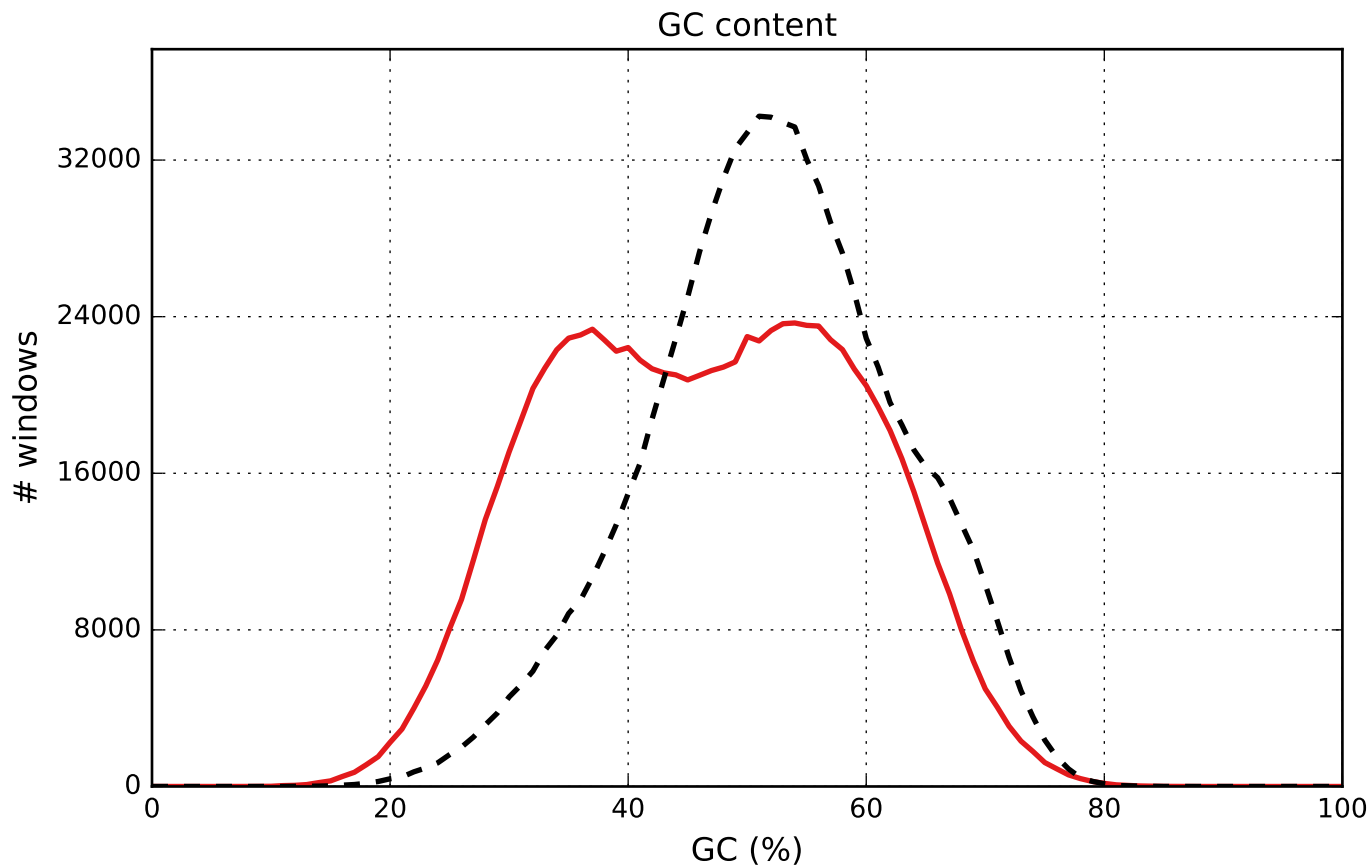
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx



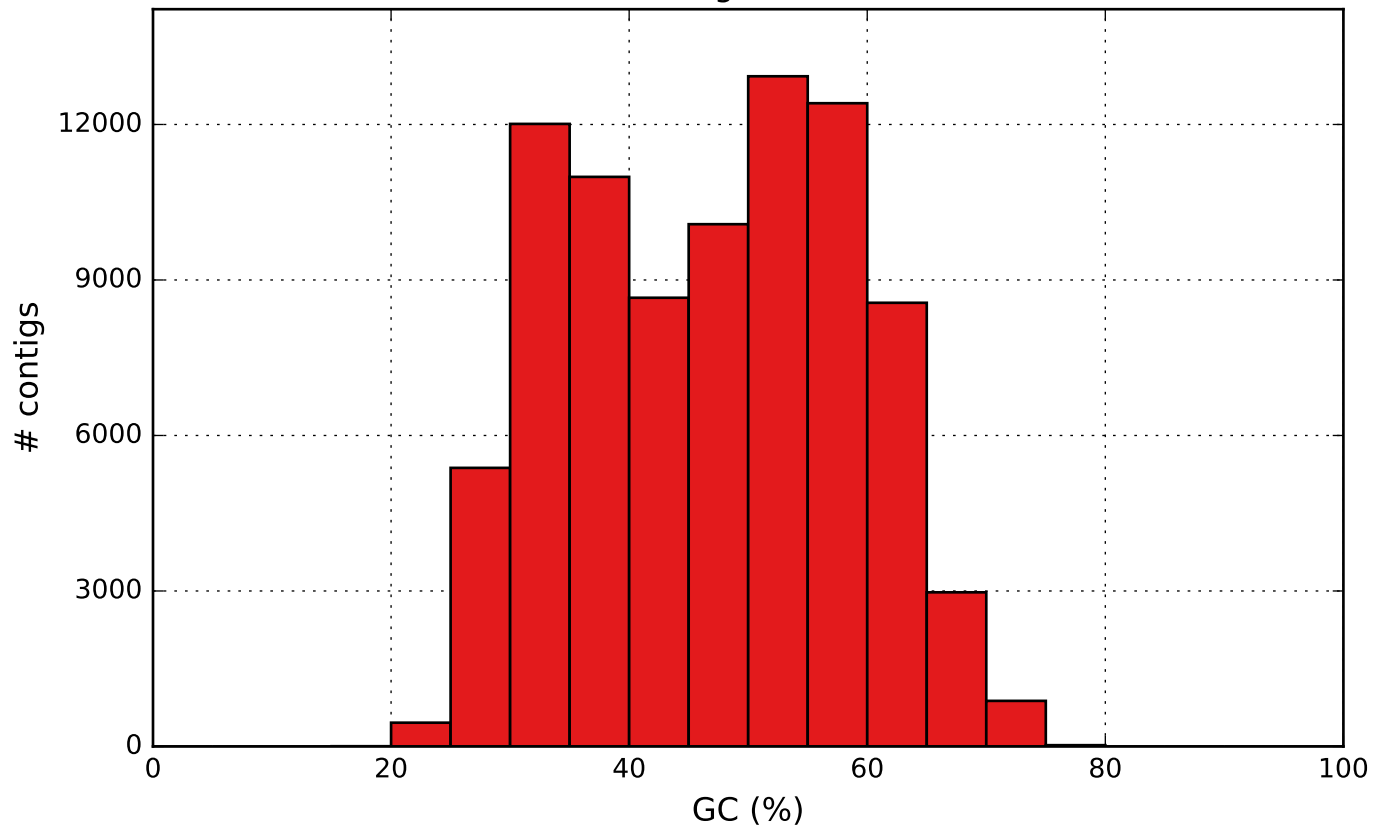
— final.contigs



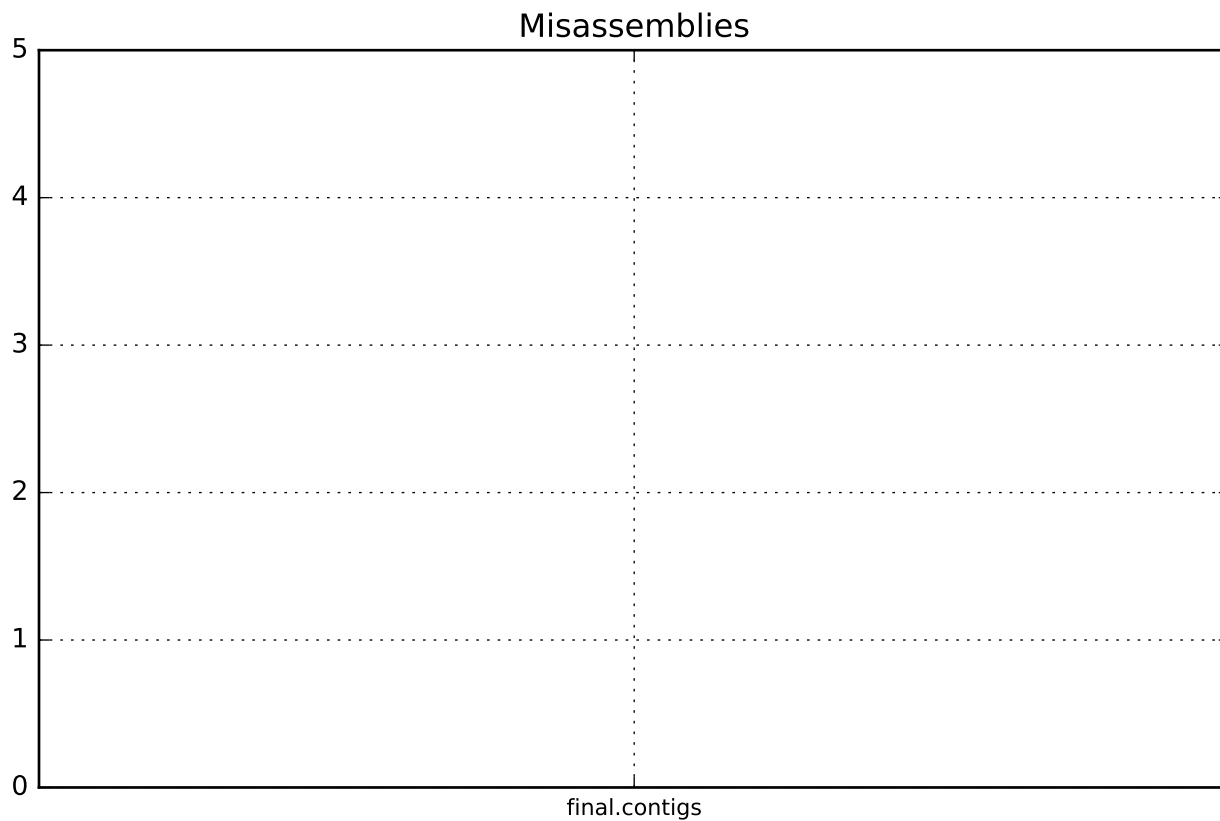


— final.contigs    - - Reference

final.contigs GC content

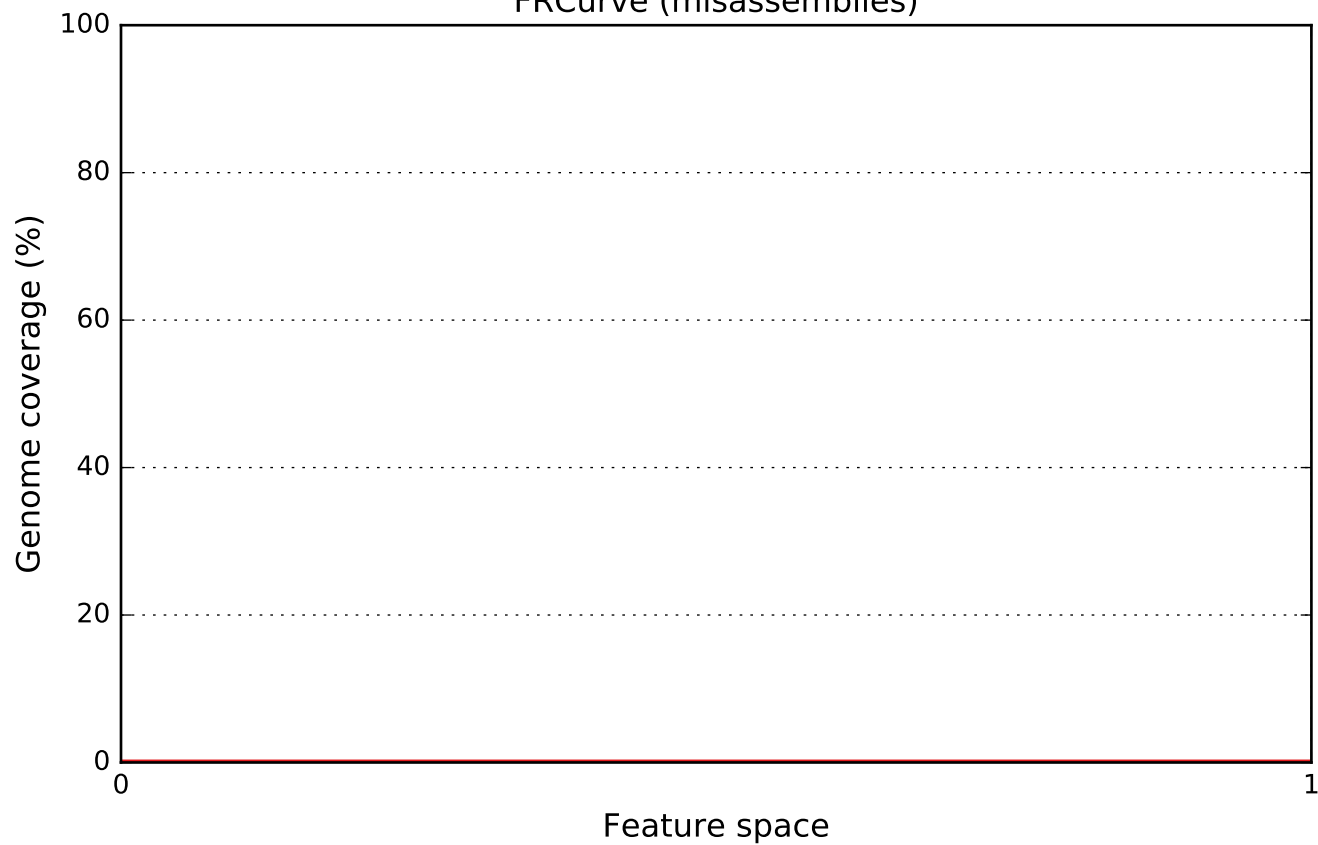


final.contigs





FRCurve (misassemblies)



— final.contigs

