

Report

	final.contigs
# contigs (>= 0 bp)	393172
# contigs (>= 1000 bp)	58991
# contigs (>= 5000 bp)	4560
# contigs (>= 10000 bp)	1518
# contigs (>= 25000 bp)	375
# contigs (>= 50000 bp)	115
Total length (>= 0 bp)	316557061
Total length (>= 1000 bp)	152732973
Total length (>= 5000 bp)	56357286
Total length (>= 10000 bp)	35725630
Total length (>= 25000 bp)	18963180
Total length (>= 50000 bp)	10035074
# contigs	182483
Largest contig	343433
Total length	236413144
Reference length	100726002
N50	1501
N75	792
L50	30336
L75	86764
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# unaligned mis. contigs	5
# unaligned contigs	182338 + 117 part
Unaligned length	236383363
Genome fraction (%)	0.018
Duplication ratio	2.127
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2079.24
# indels per 100 kbp	141.89
Largest alignment	869
Total aligned length	15594

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	0
# possible misassemblies	0
# local misassemblies	2
# unaligned mis. contigs	5
# mismatches	381
# indels	26
# indels (≤ 5 bp)	26
# indels (> 5 bp)	0
Indels length	26

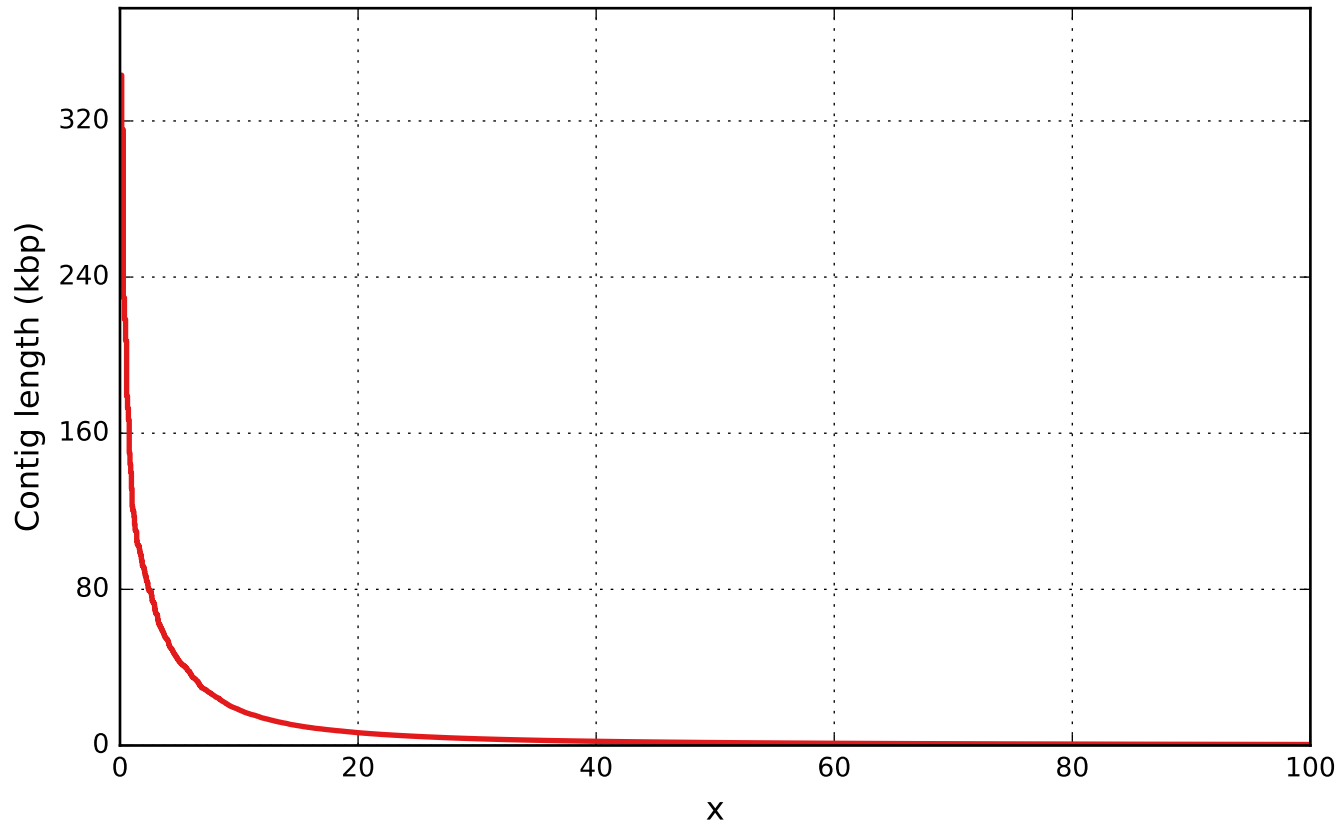
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	final.contigs
# fully unaligned contigs	182338
Fully unaligned length	235384305
# partially unaligned contigs	117
Partially unaligned length	999058
# N's	0

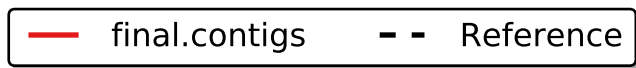
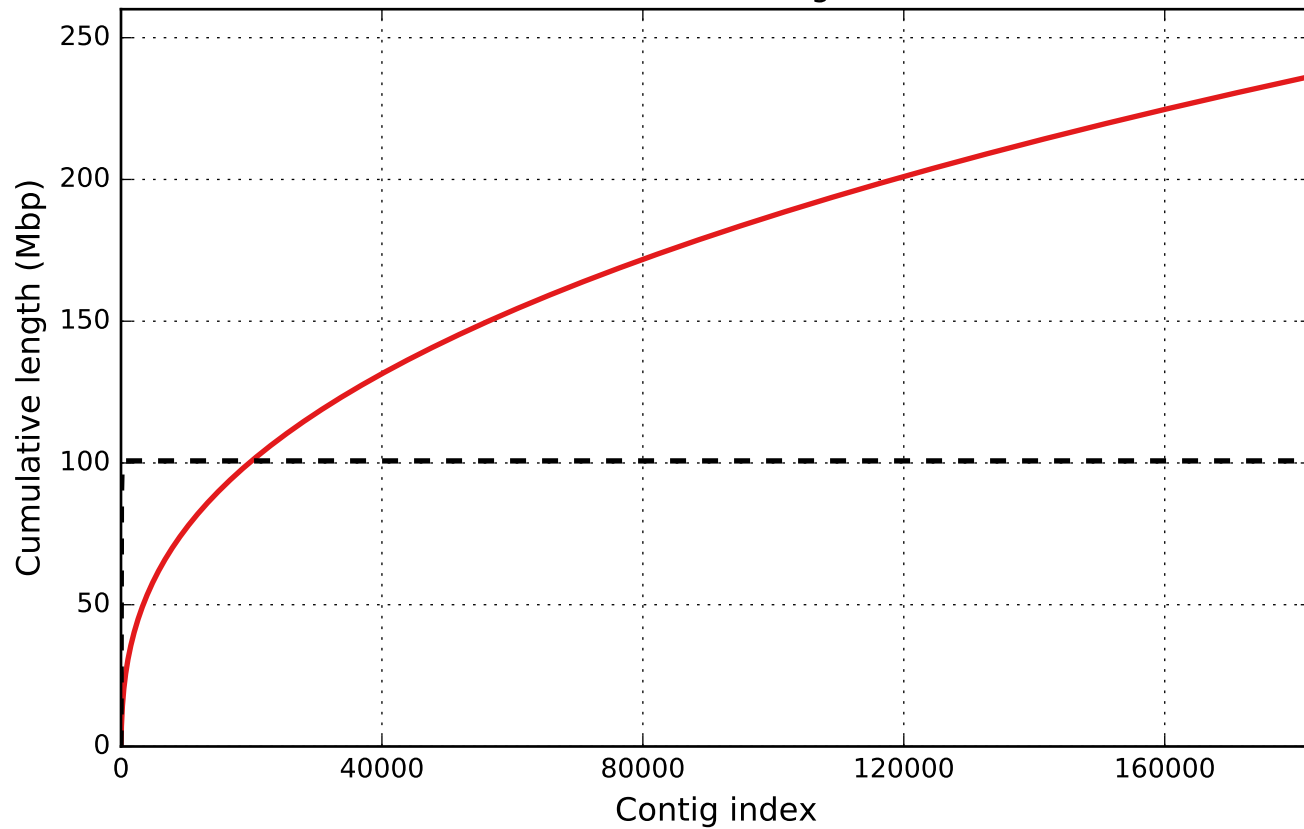
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

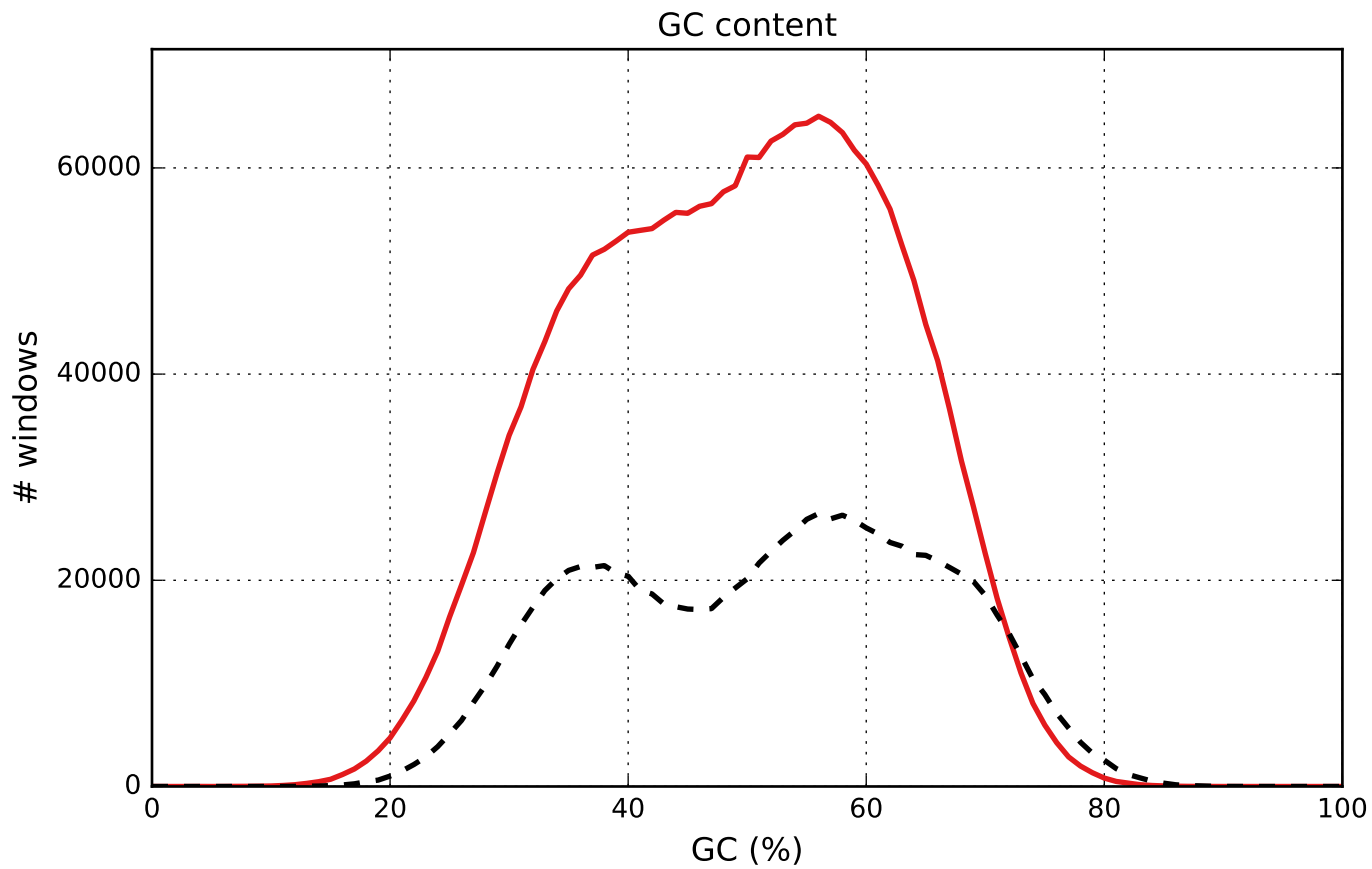
Nx



— final.contigs

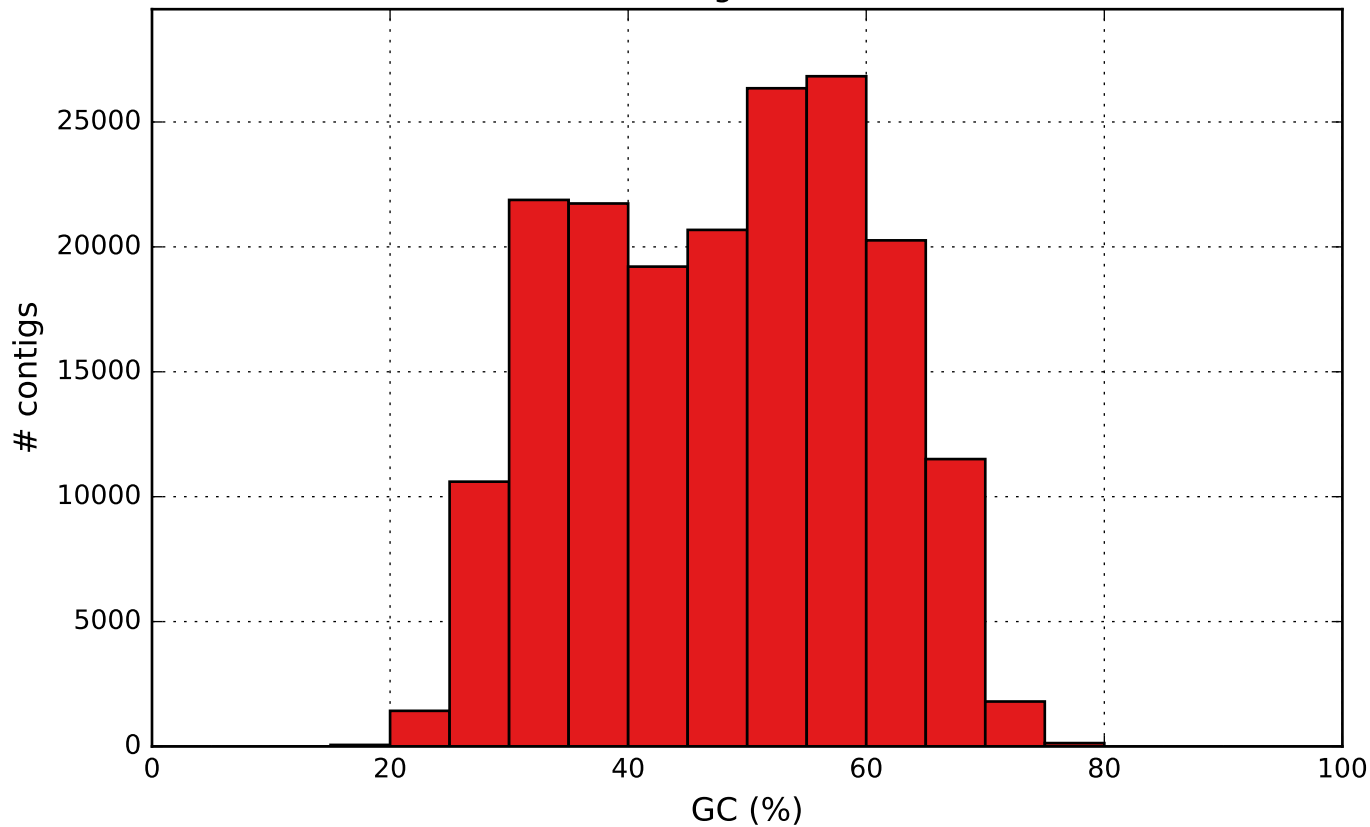
Cumulative length



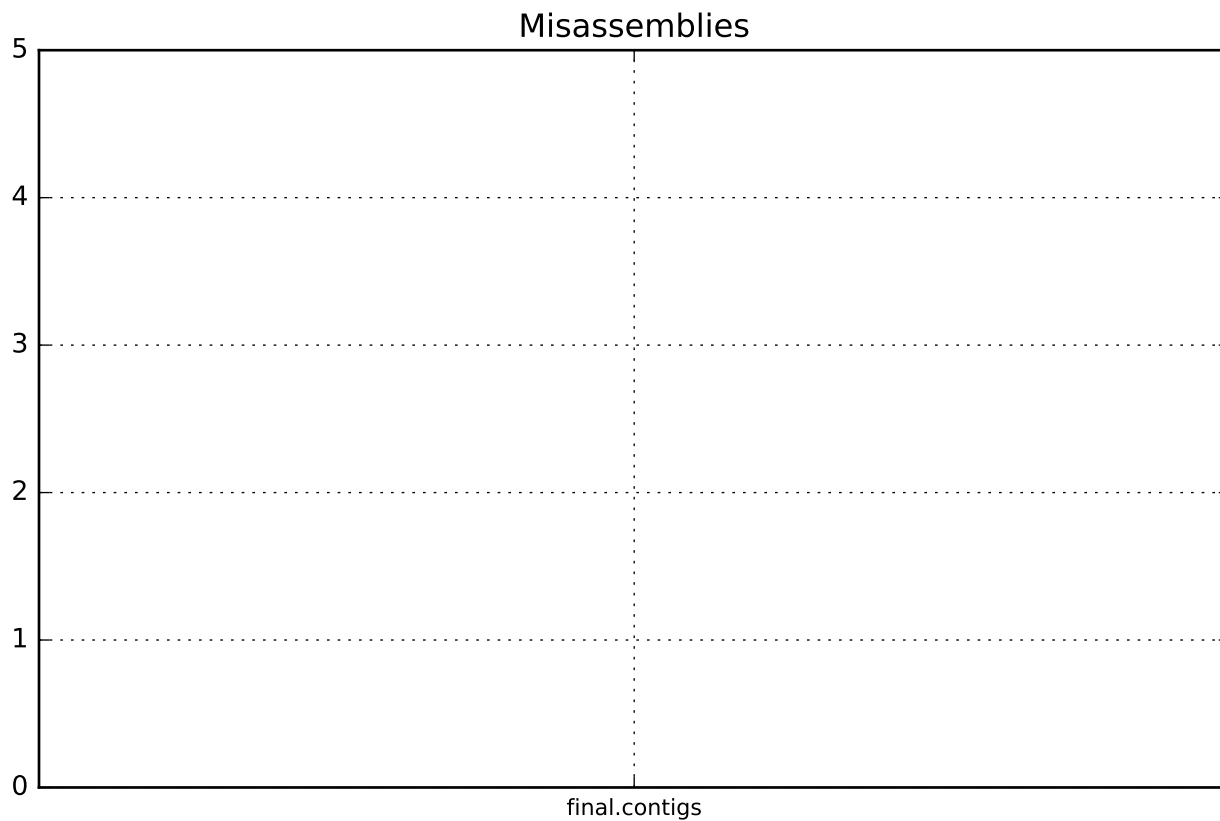


— final.contigs - - Reference

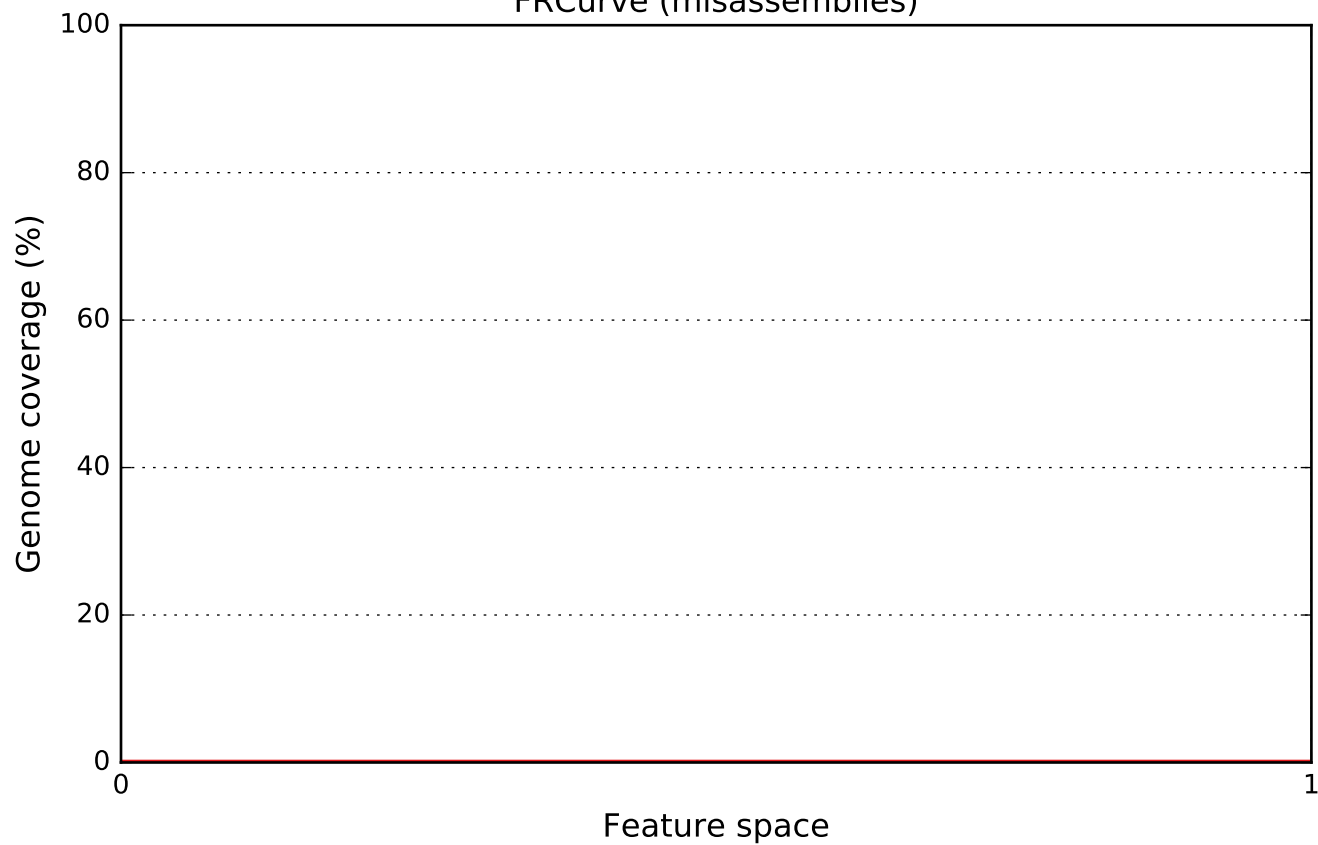
final.contigs GC content



final.contigs

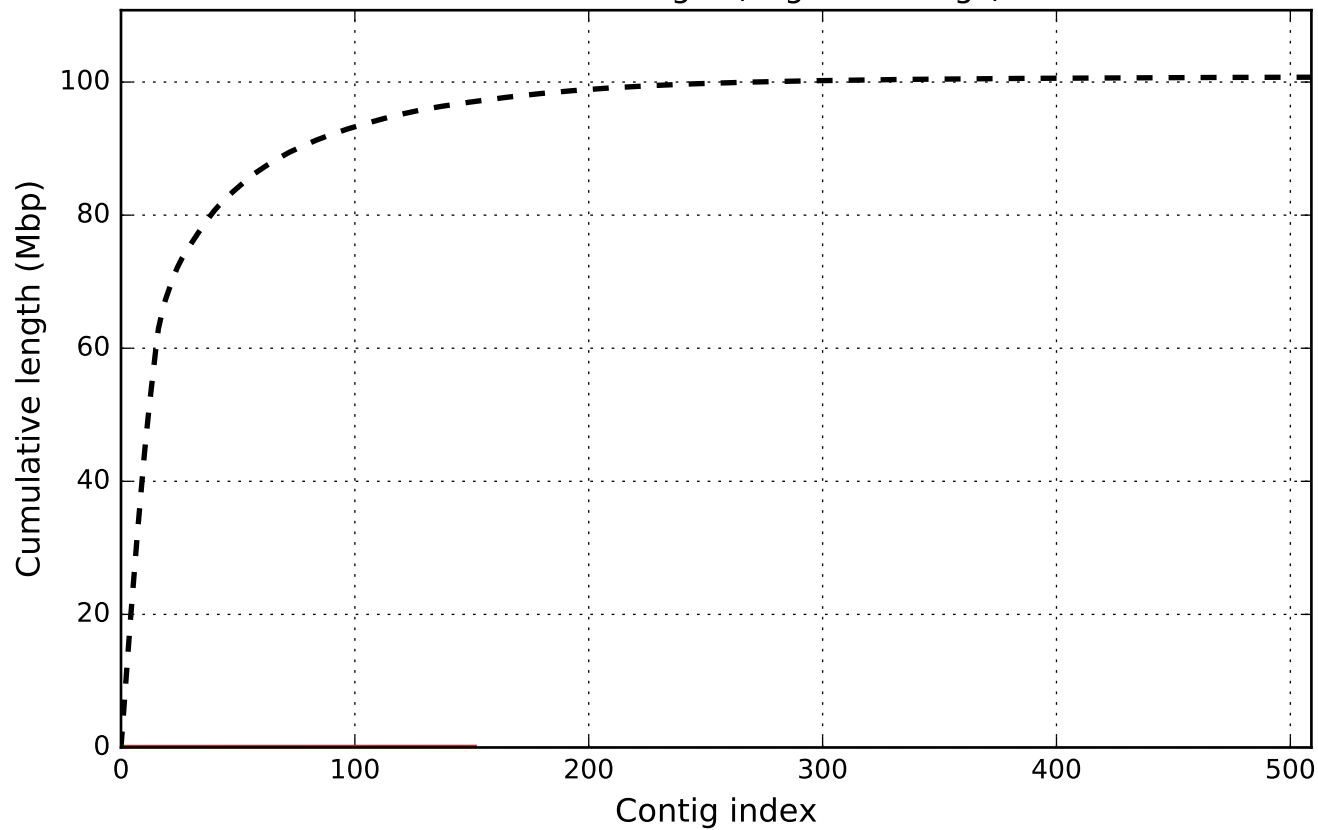


FRCurve (misassemblies)



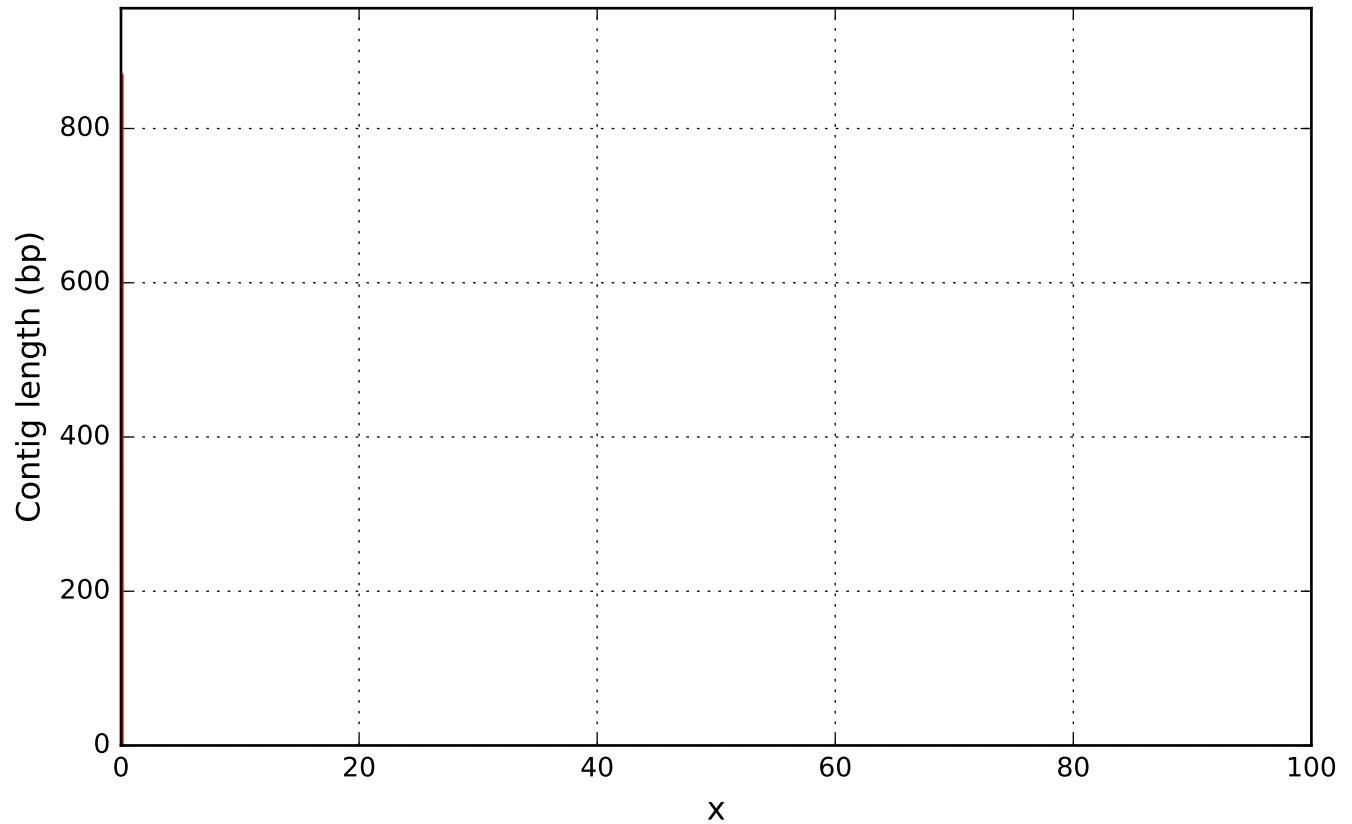
— final.contigs

Cumulative length (aligned contigs)



— final.contigs - - Reference

NAx



— final.contigs