

Report

	final.contigs
# contigs (>= 1000 bp)	17
# contigs (>= 5000 bp)	5
# contigs (>= 10000 bp)	3
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	92992
Total length (>= 5000 bp)	66155
Total length (>= 10000 bp)	54194
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	23
Largest contig	24092
Total length	97395
Reference length	4775416
GC (%)	62.26
Reference GC (%)	68.59
N50	10027
N75	3311
L50	3
L75	7
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 20 part
Unaligned length	93638
Genome fraction (%)	0.032
Duplication ratio	2.448
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2214.98
# indels per 100 kbp	325.73
Largest alignment	248
Total aligned length	2354
NGA50	-

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

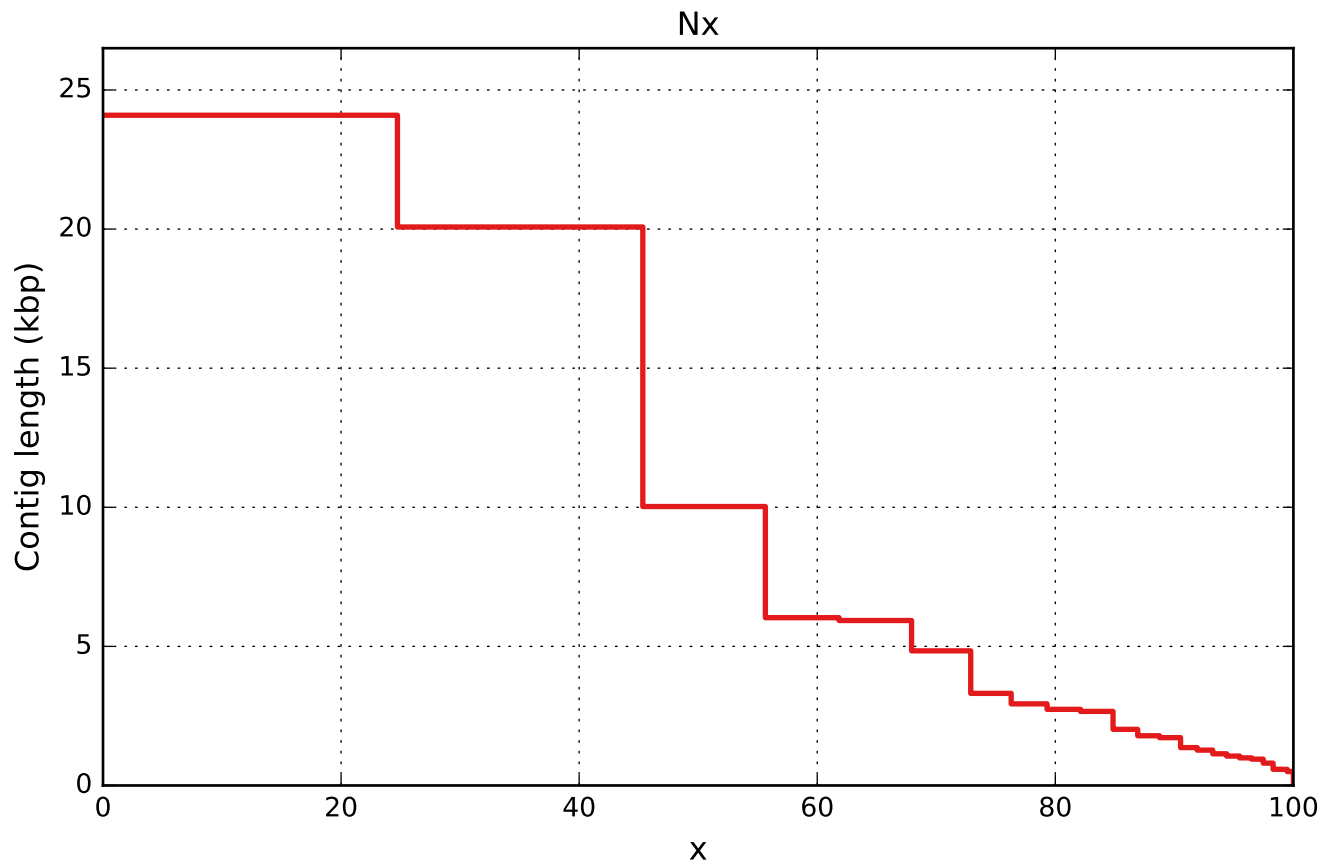
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	34
# indels	5
# indels (≤ 5 bp)	5
# indels (> 5 bp)	0
Indels length	5

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

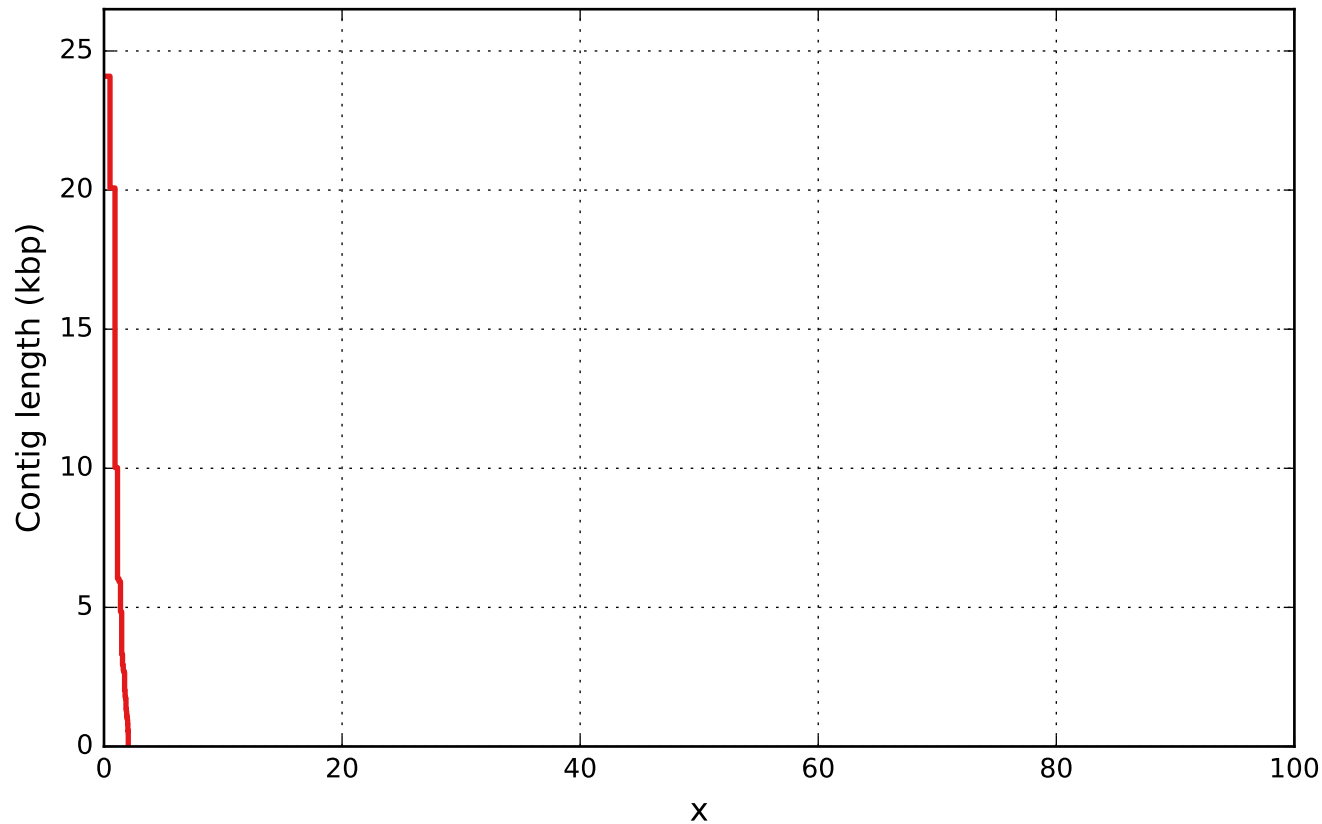
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	20
Partially unaligned length	93638
# N's	0

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).

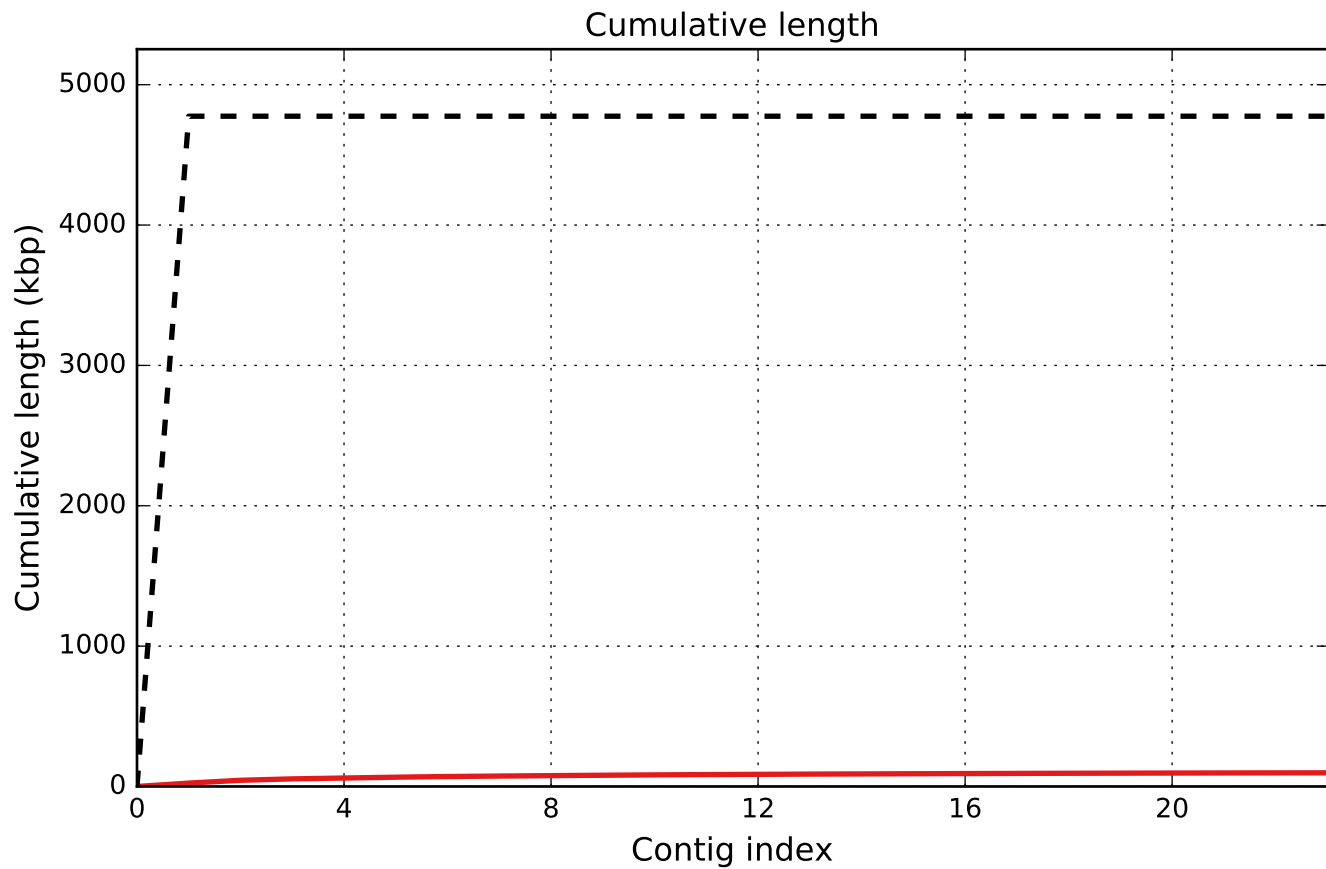


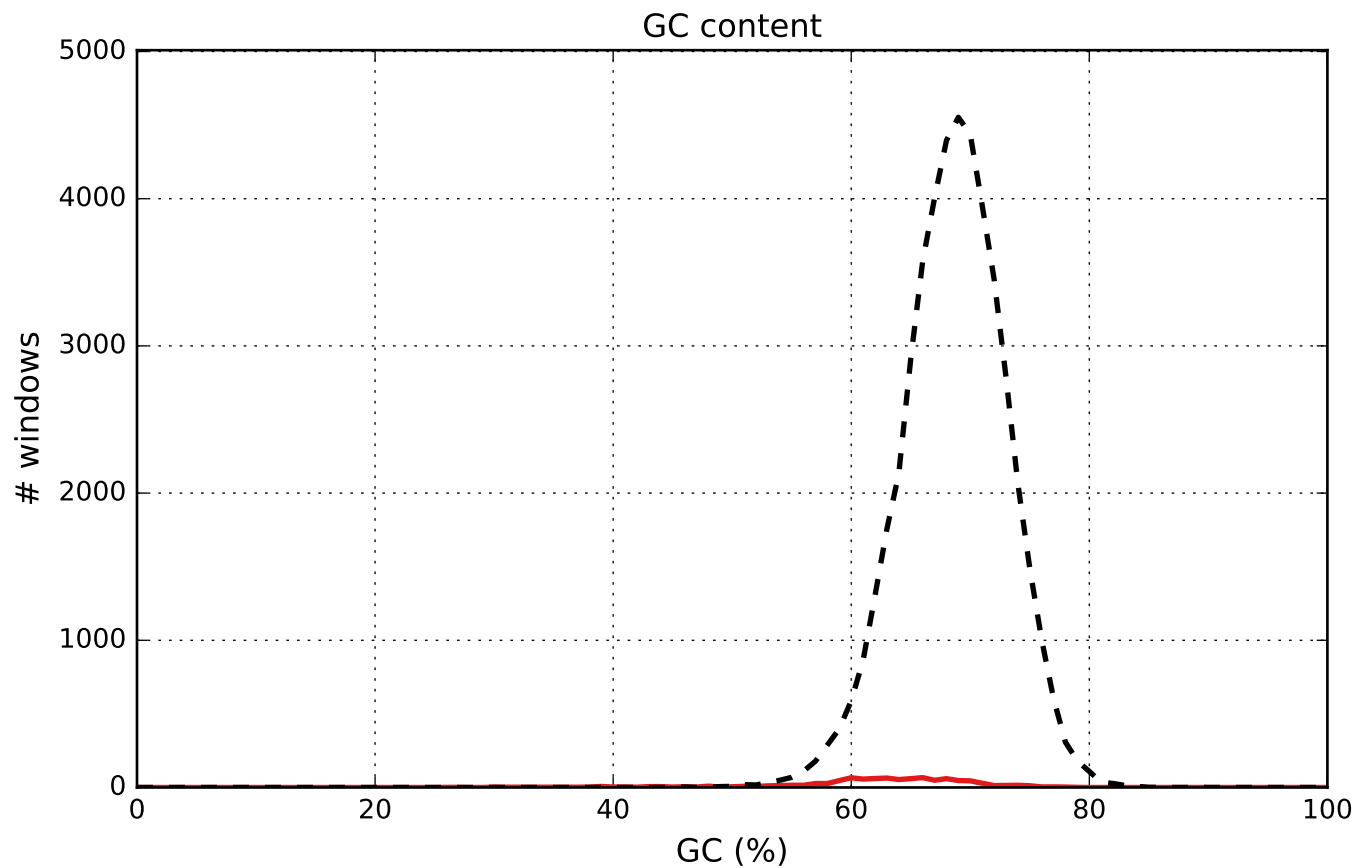
— final.contigs

NGx



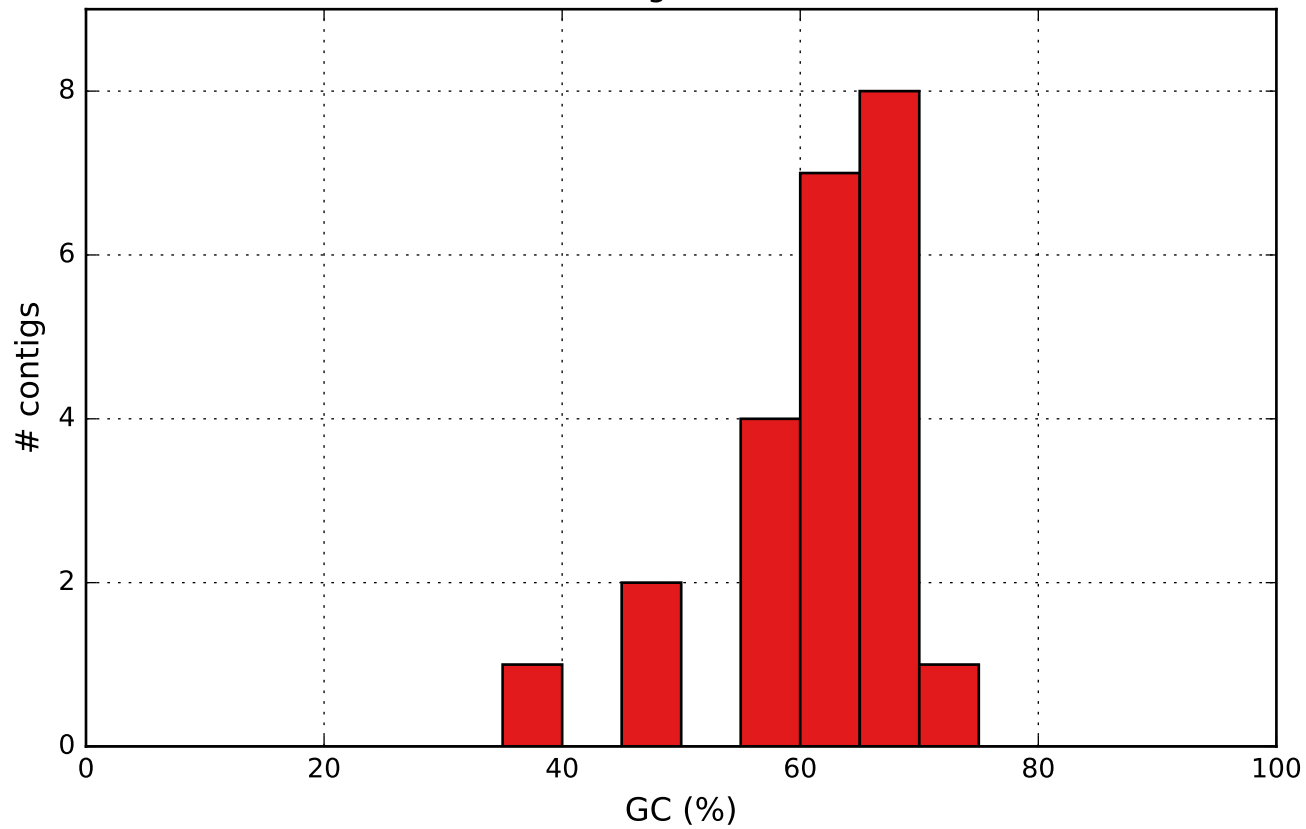
— final.contigs





— final.contigs - - Reference

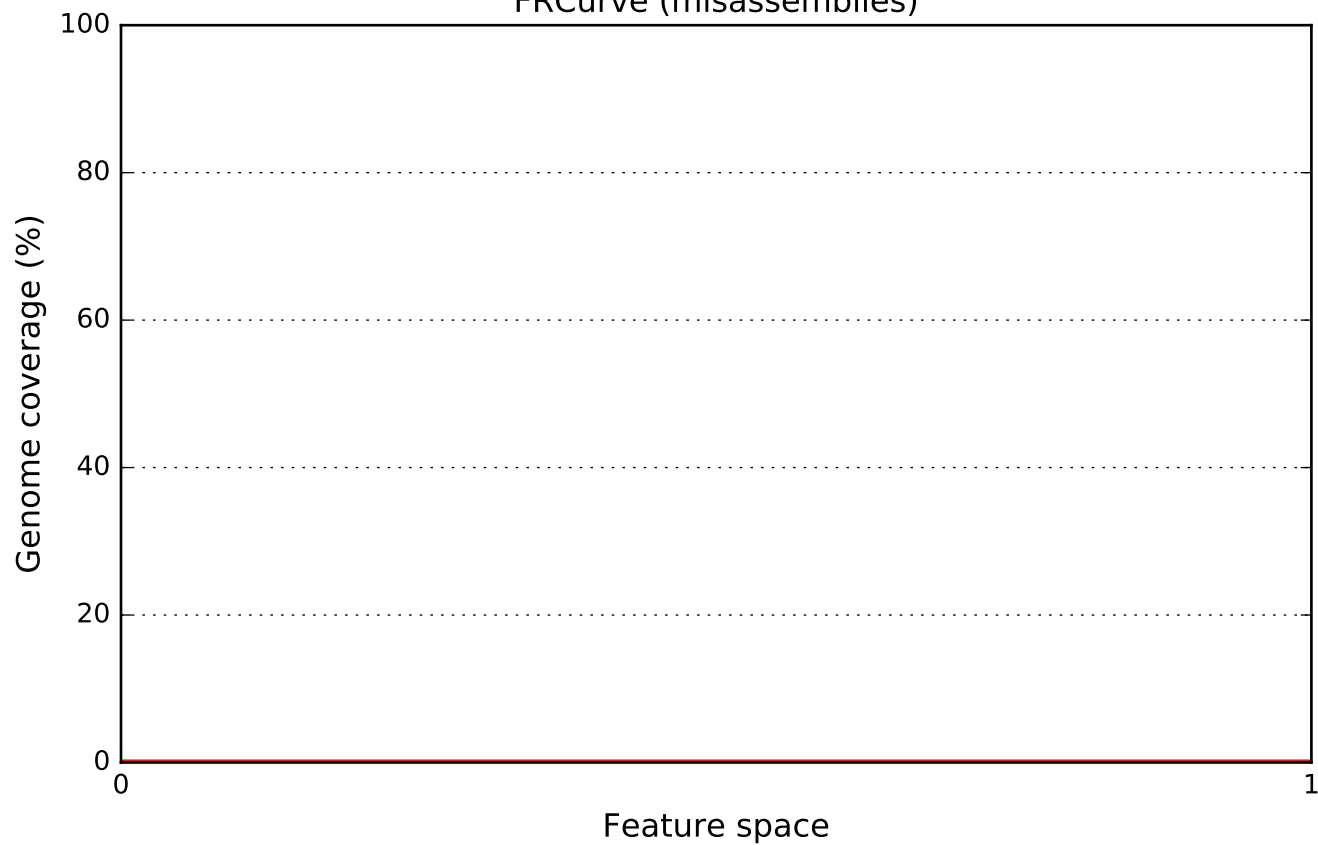
final.contigs GC content



final.contigs

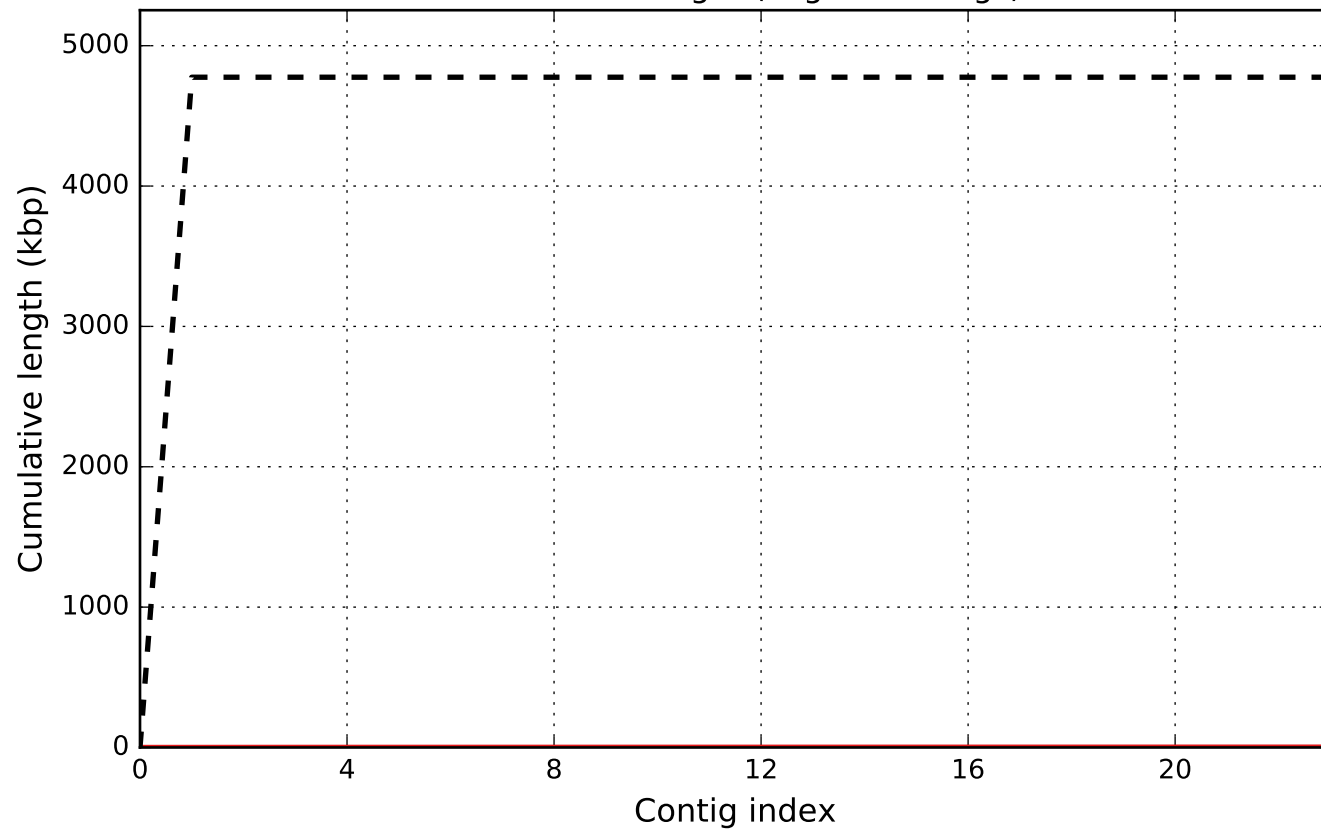


FRCurve (misassemblies)



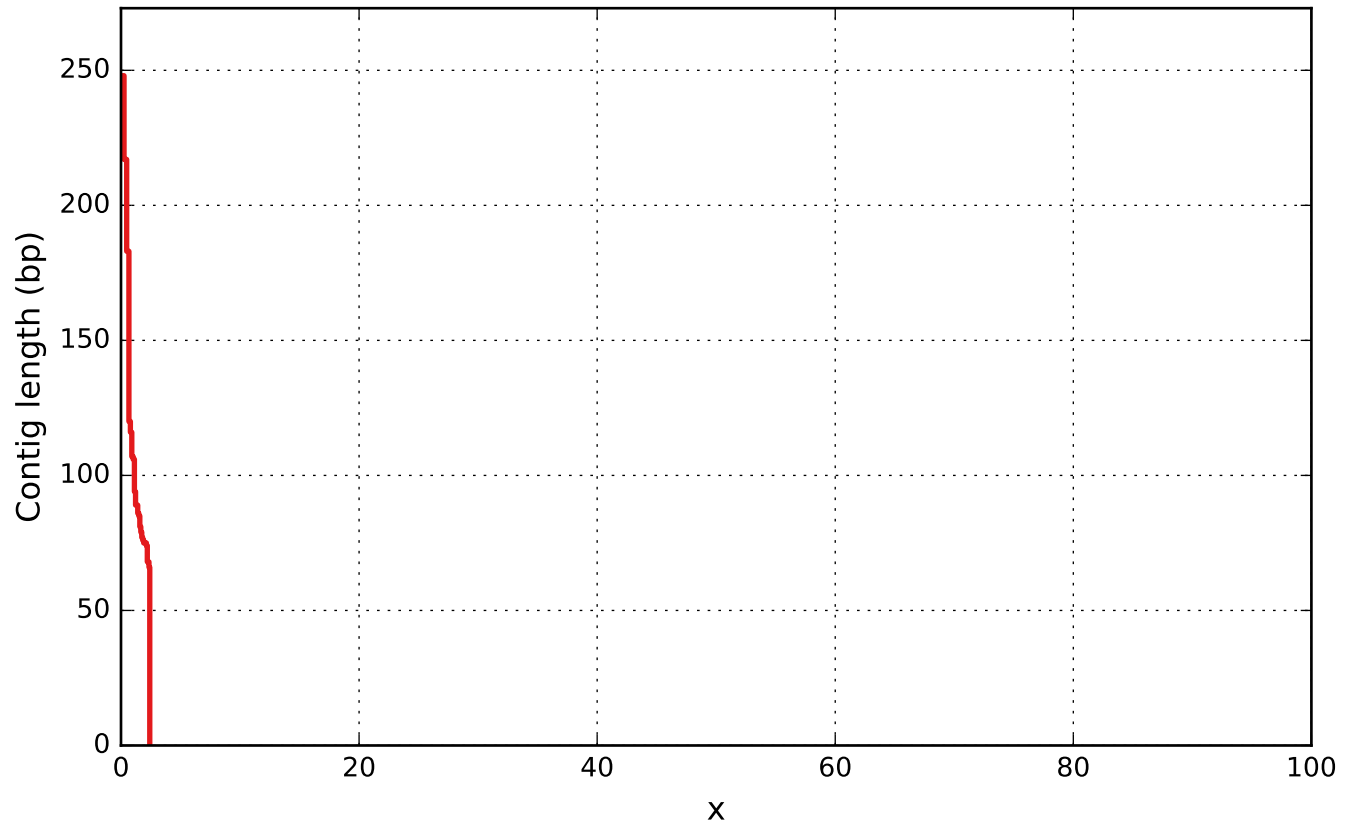
— final.contigs

Cumulative length (aligned contigs)



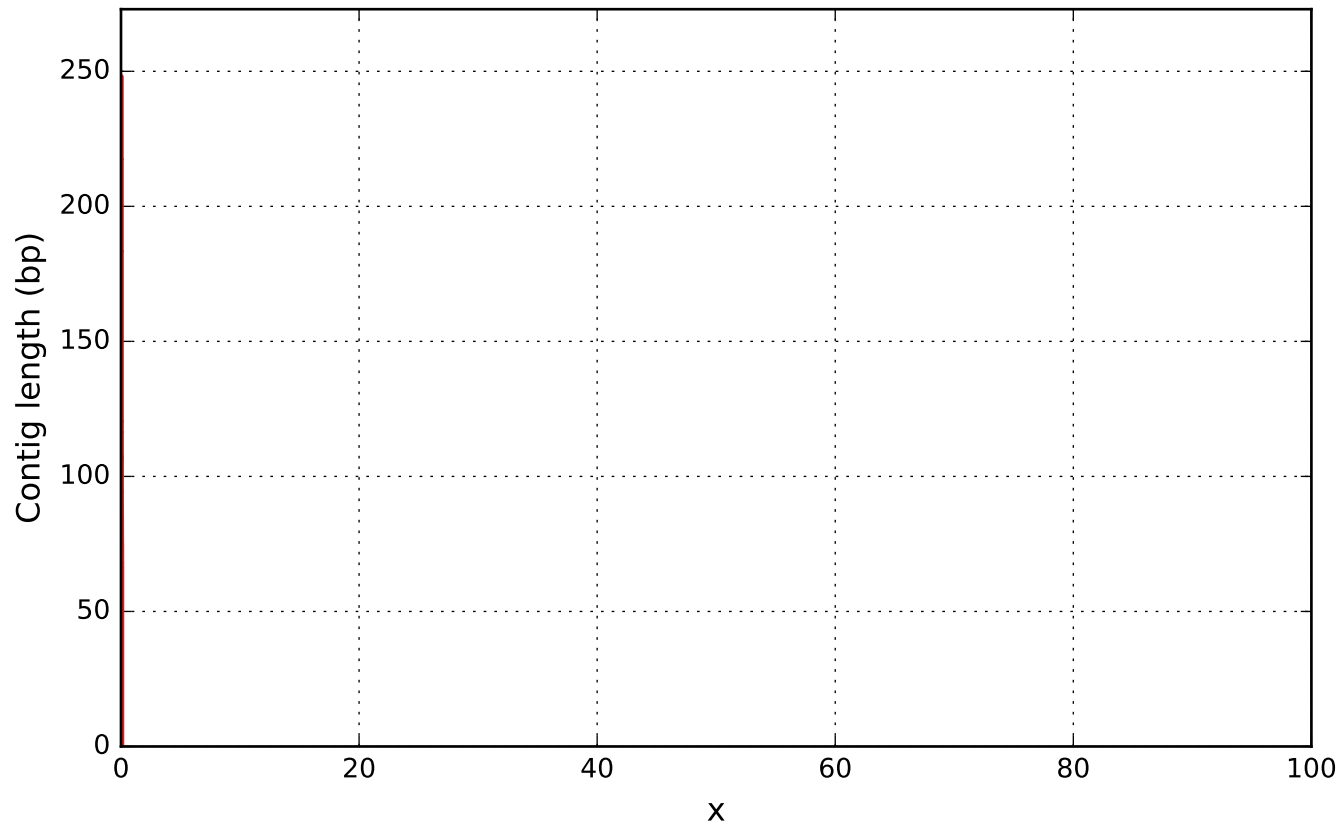
— final.contigs - - Reference

NAx



— final.contigs

NGAx



— final.contigs