

Report

	final.contigs
# contigs (>= 1000 bp)	0
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	0
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	4
Largest contig	752
Total length	2562
Reference length	3764053
GC (%)	57.38
Reference GC (%)	46.60
N50	639
N75	622
L50	2
L75	3
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	2
# unaligned contigs	0 + 1 part
Unaligned length	676
Genome fraction (%)	0.006
Duplication ratio	8.165
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1731.60
# indels per 100 kbp	0.00
Largest alignment	77
Total aligned length	460
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	2
# mismatches	4
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

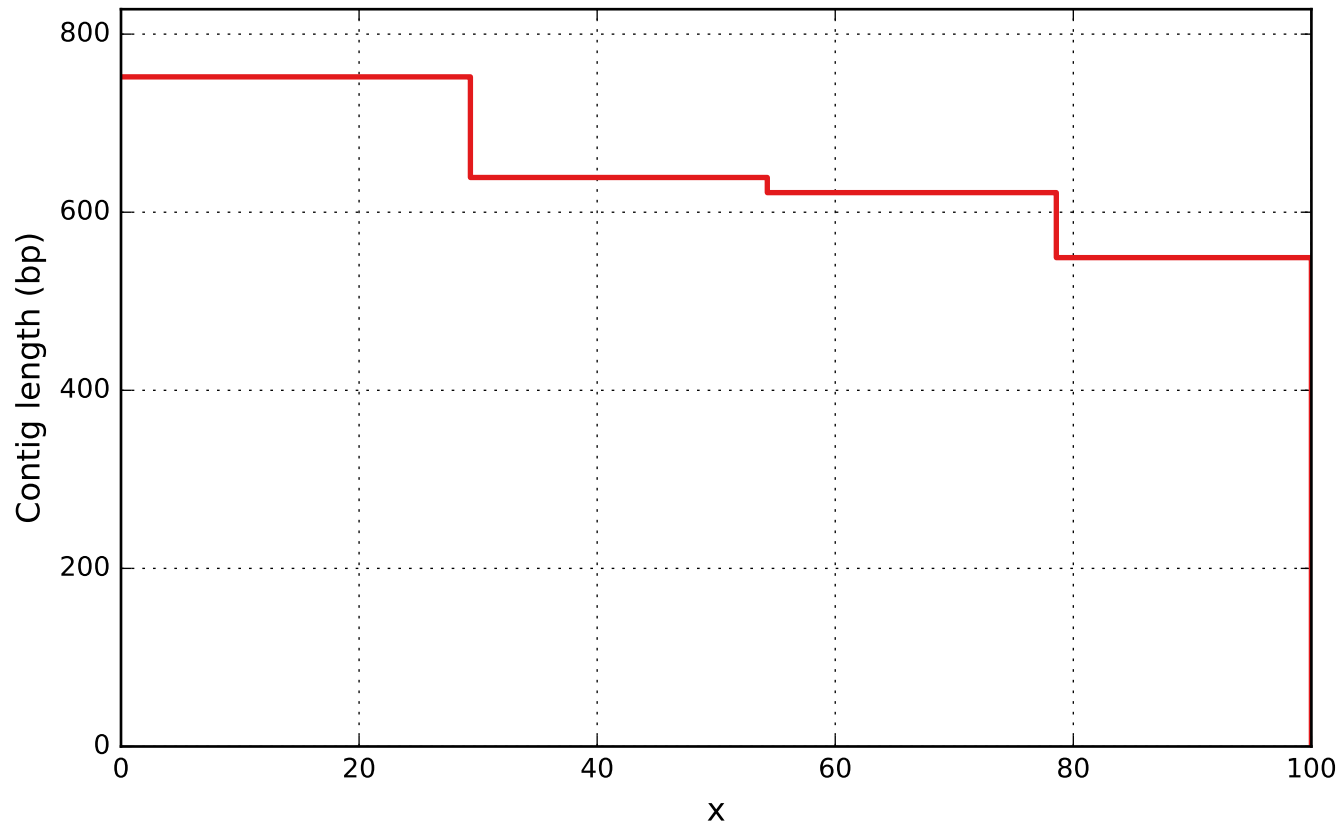
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
Partially unaligned length	676
# N's	0

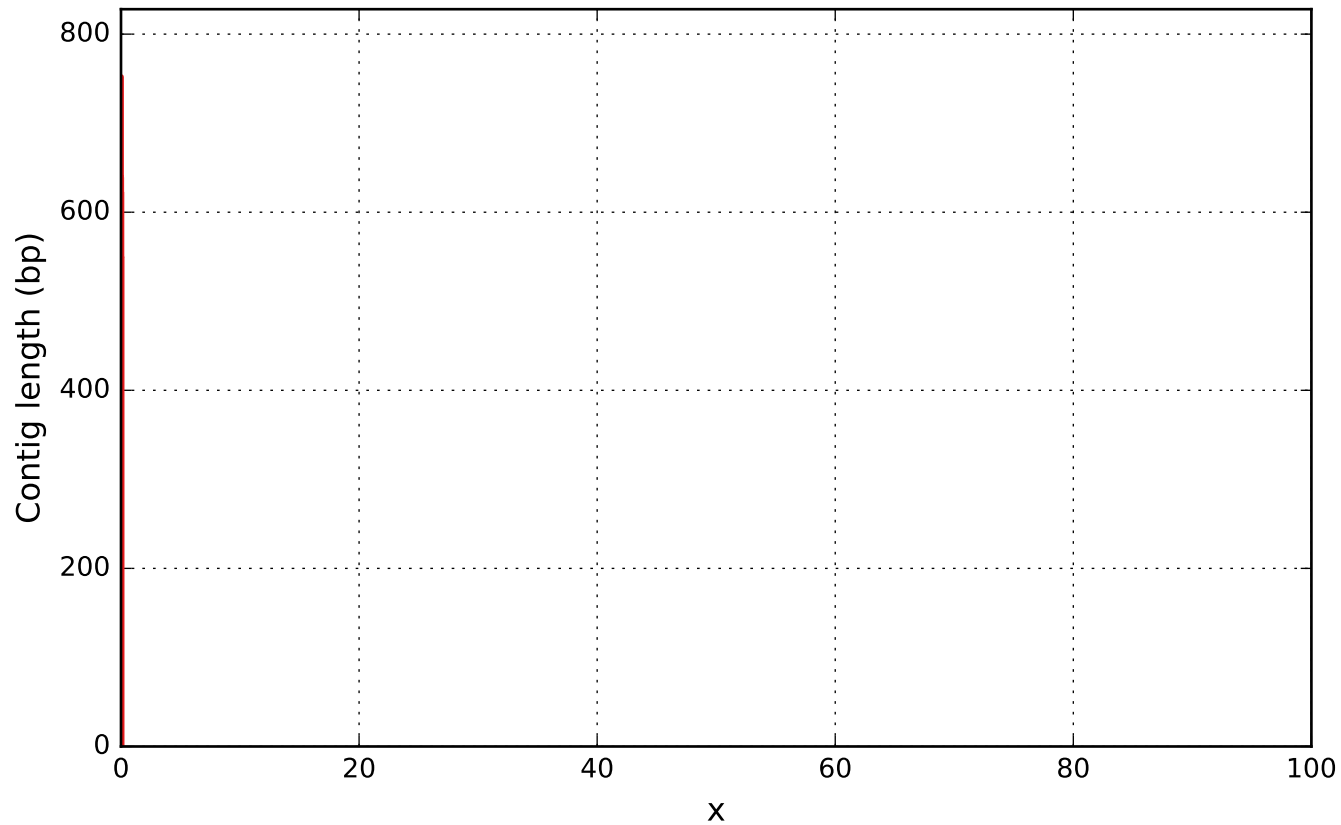
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

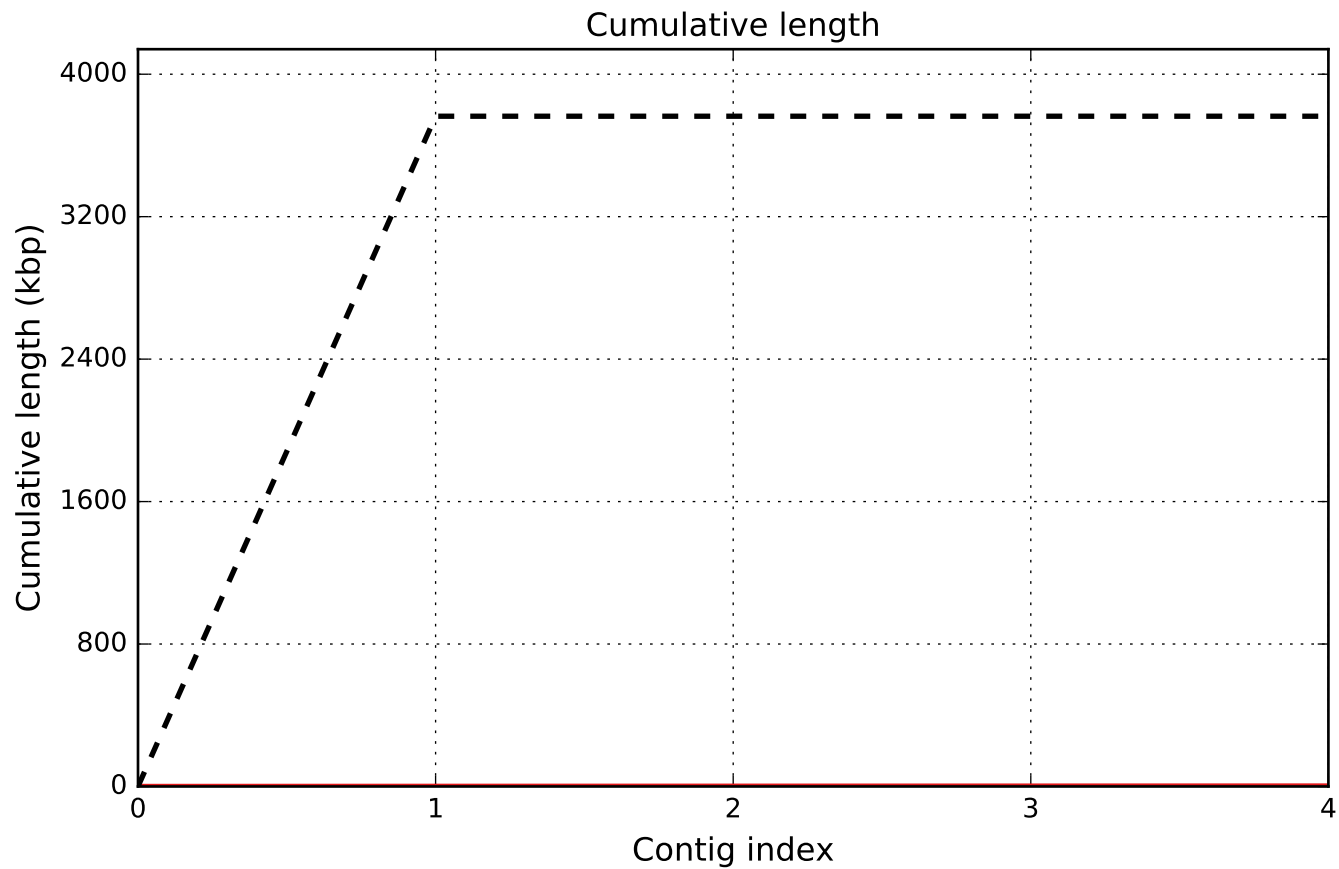


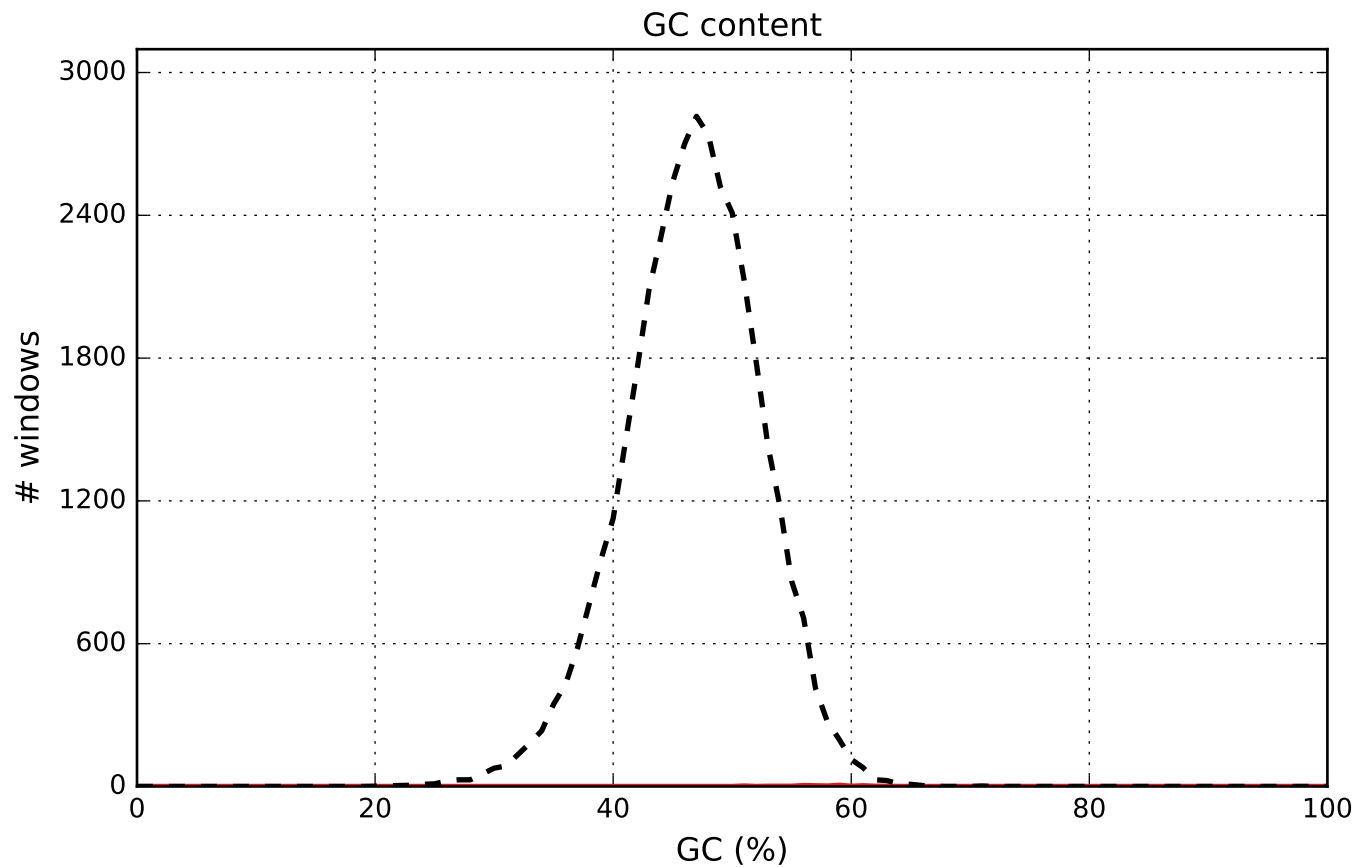
— final.contigs

NGx

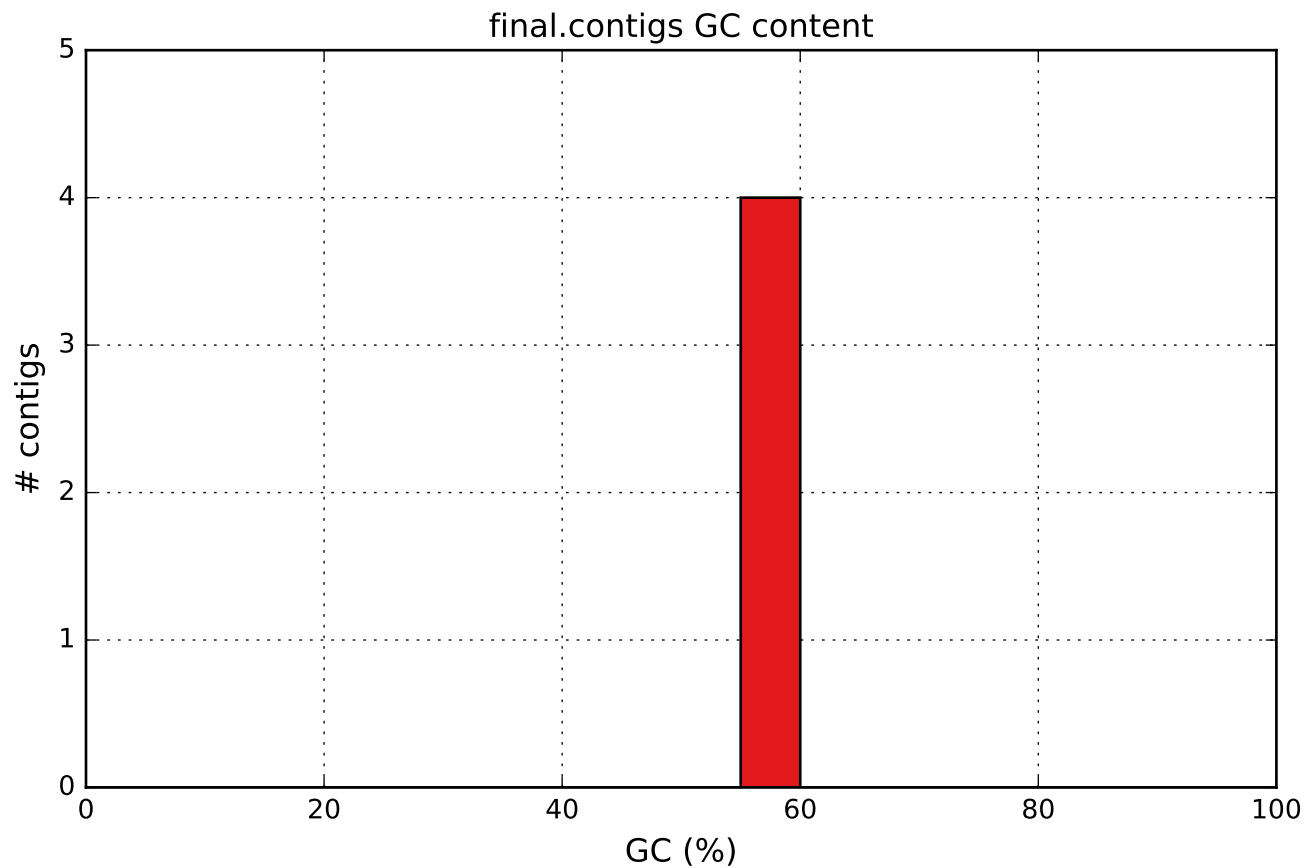


— final.contigs





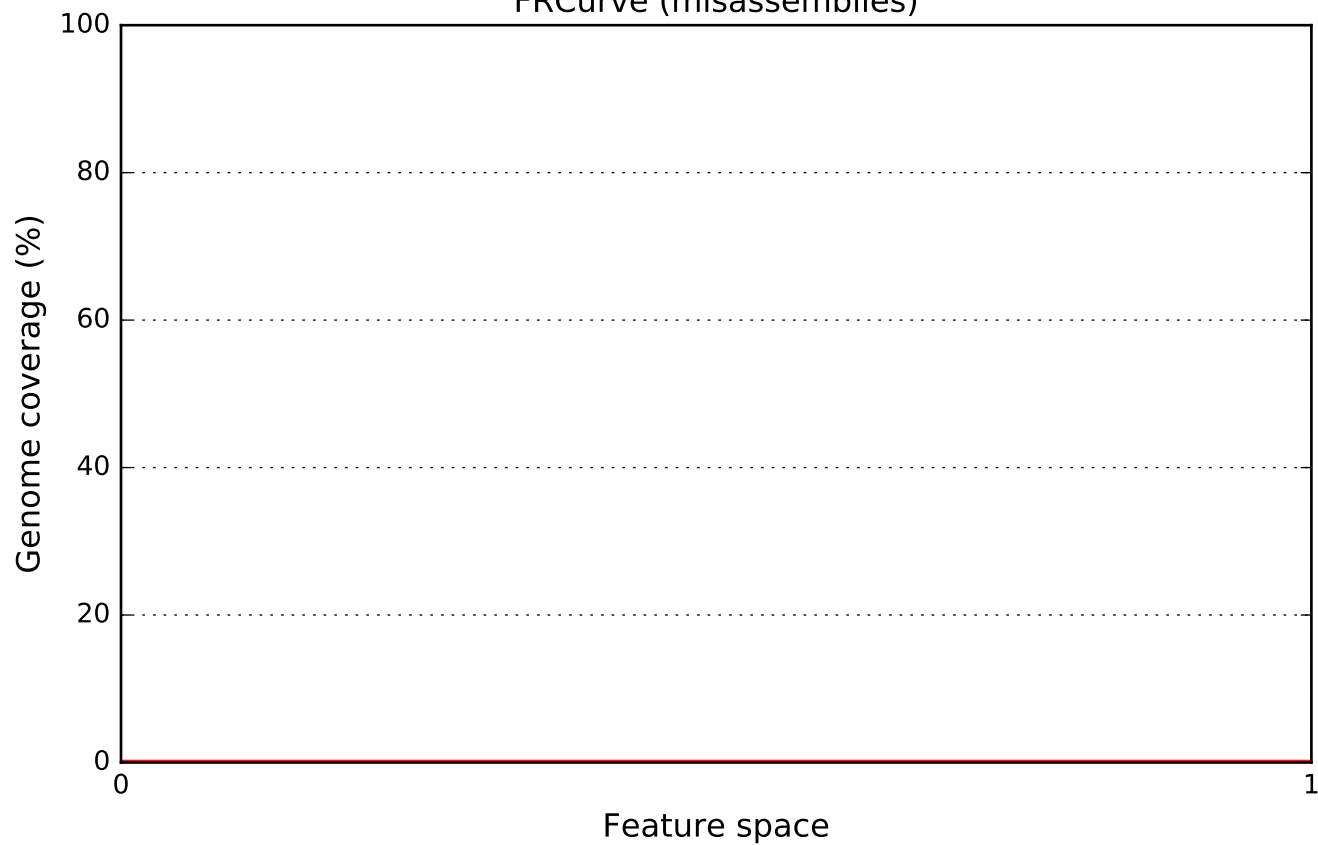
— final.contigs - - Reference



final.contigs

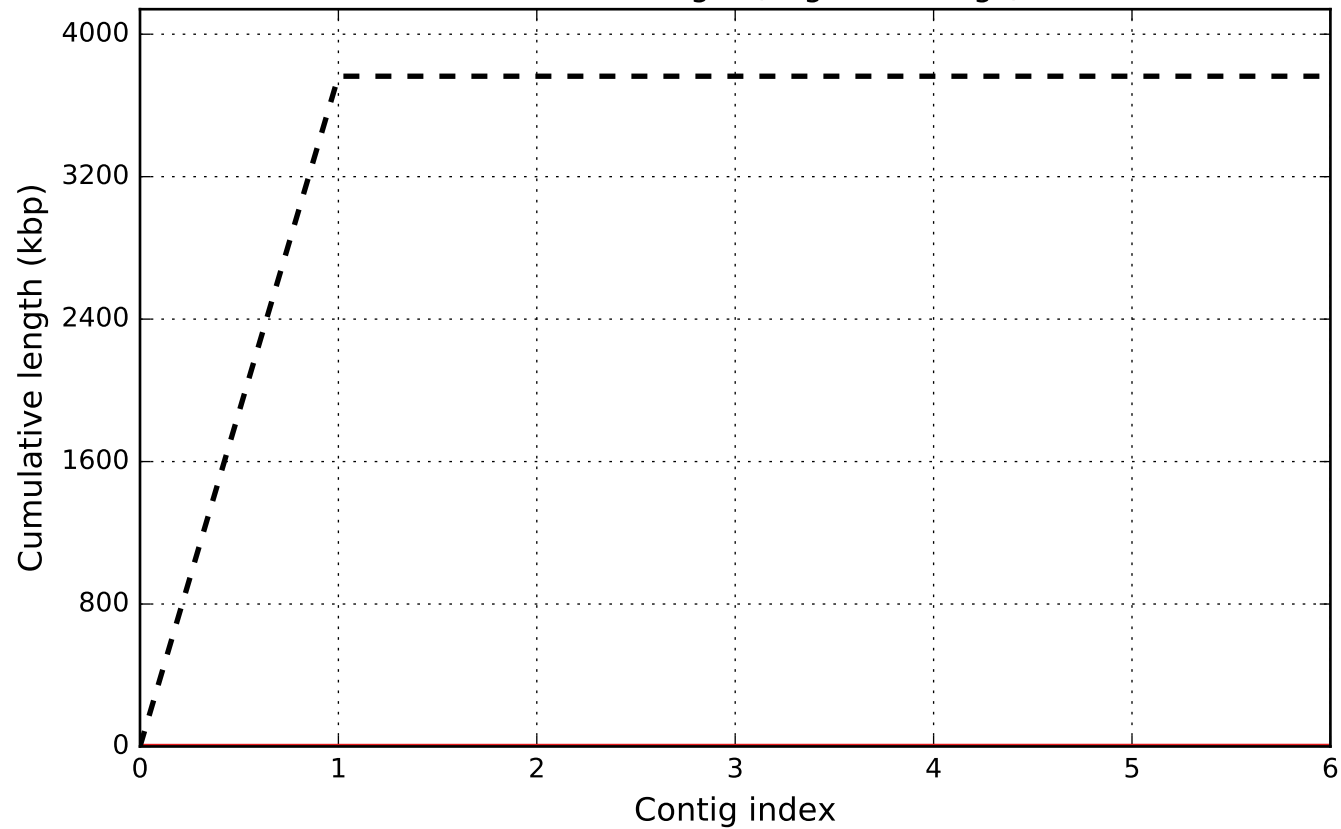


FRCurve (misassemblies)



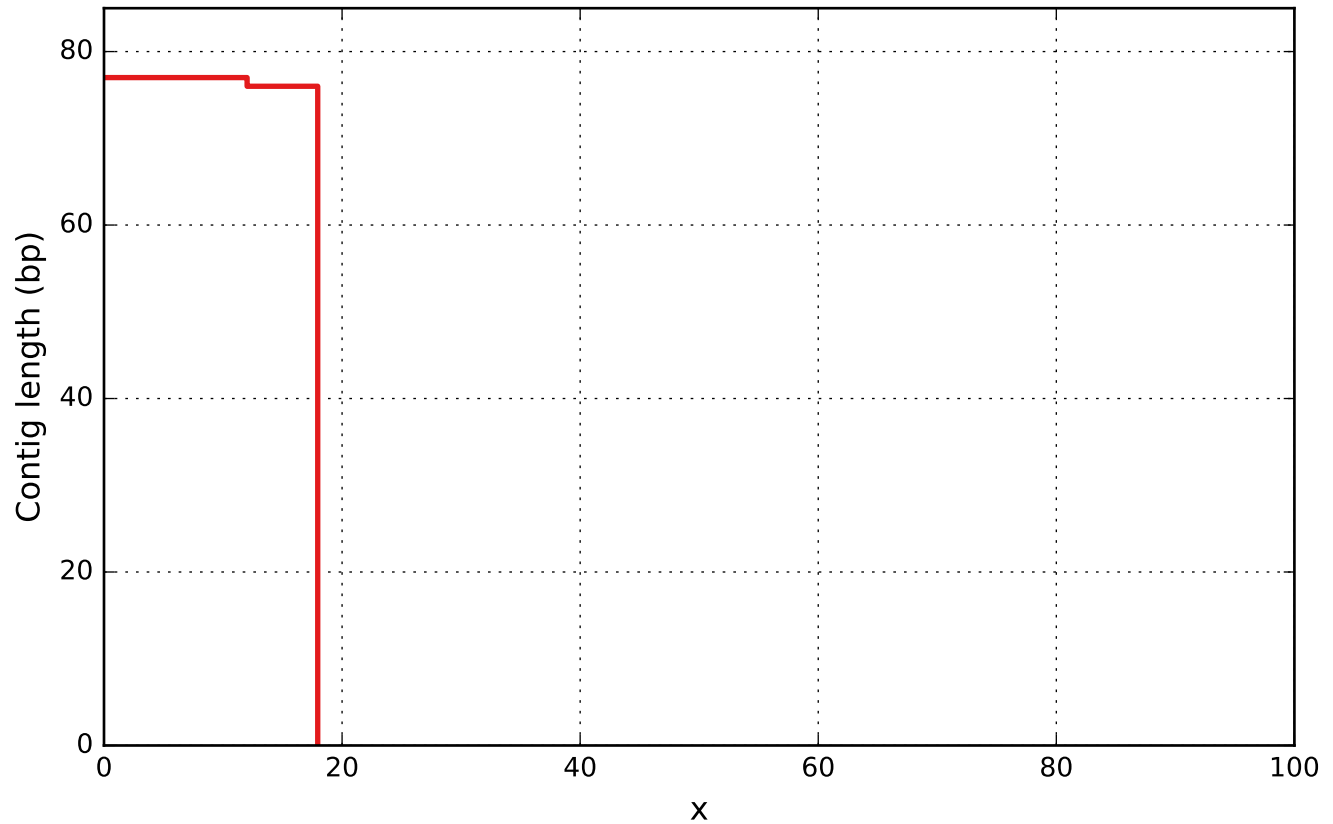
— final.contigs

Cumulative length (aligned contigs)



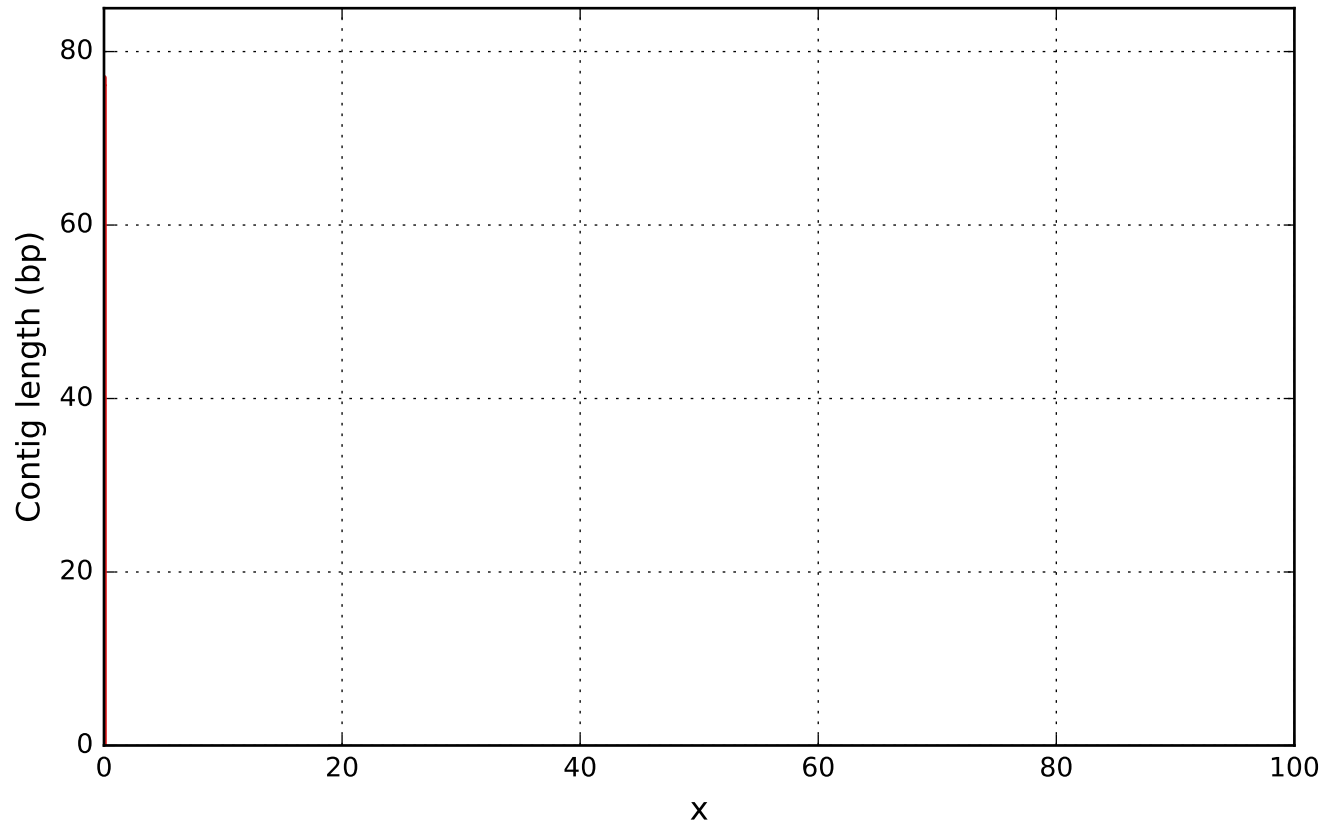
— final.contigs - - Reference

NAx



— final.contigs

NGAx



— final.contigs