

Report

	final.contigs
# contigs (>= 1000 bp)	7
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	17362
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	12
Largest contig	4213
Total length	20843
Reference length	4053139
GC (%)	49.24
Reference GC (%)	70.41
N50	2628
N75	1687
L50	4
L75	6
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 9 part
Unaligned length	18345
Genome fraction (%)	0.021
Duplication ratio	2.878
# N's per 100 kbp	0.00
# mismatches per 100 kbp	806.45
# indels per 100 kbp	230.41
Largest alignment	102
Total aligned length	1024
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

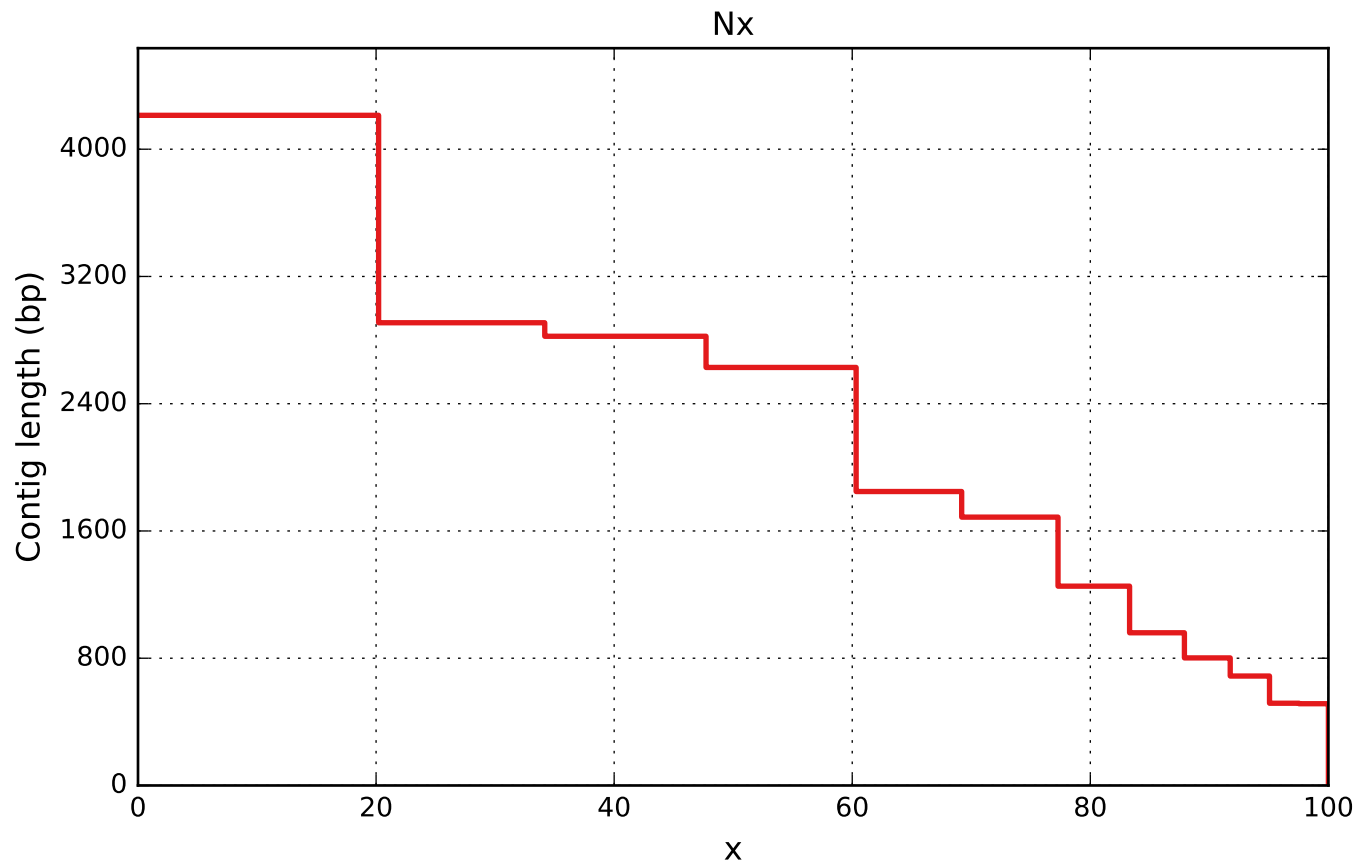
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	7
# indels	2
# indels (<= 5 bp)	2
# indels (> 5 bp)	0
Indels length	3

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).

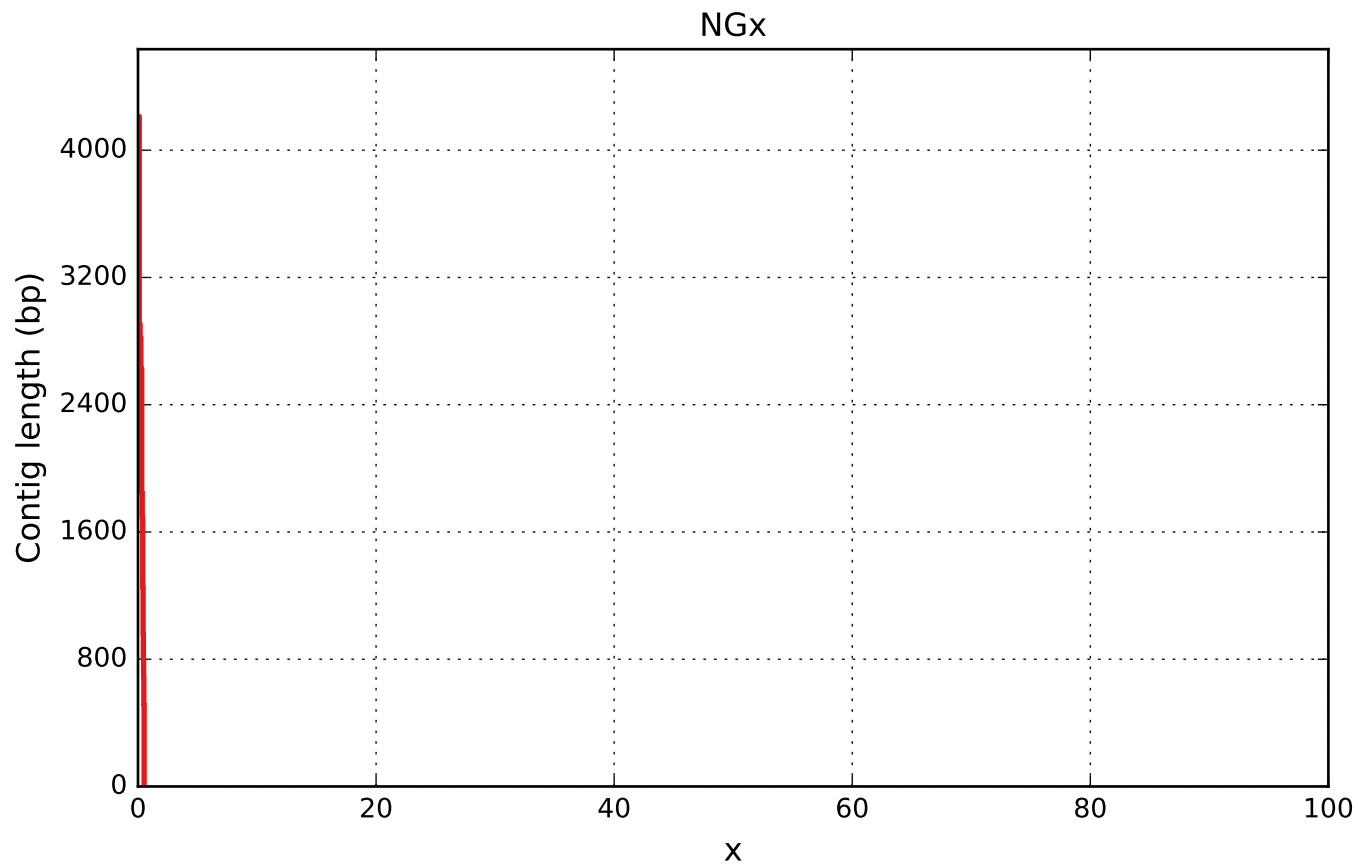
Unaligned report

	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	9
Partially unaligned length	18345
# N's	0

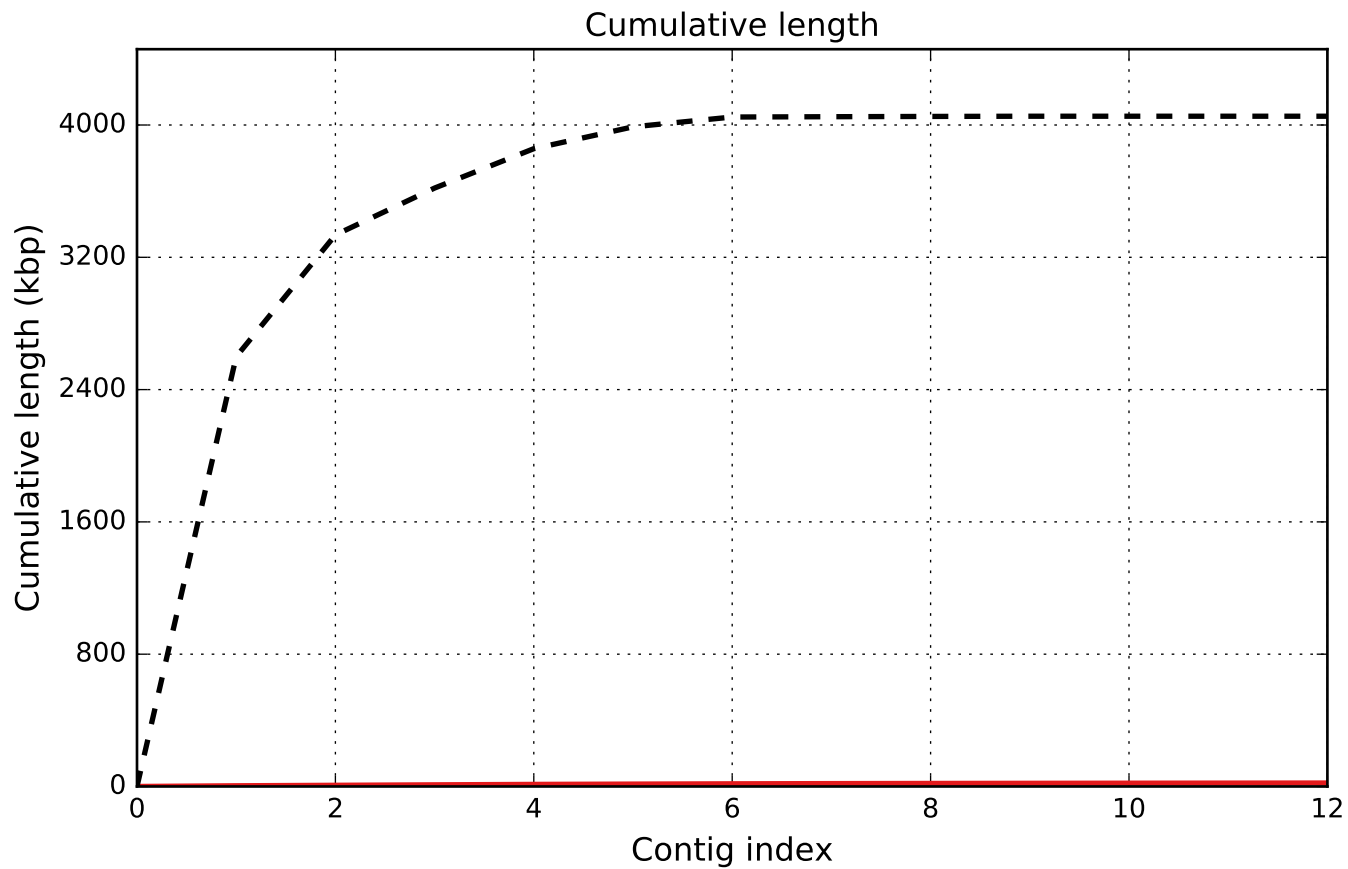
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



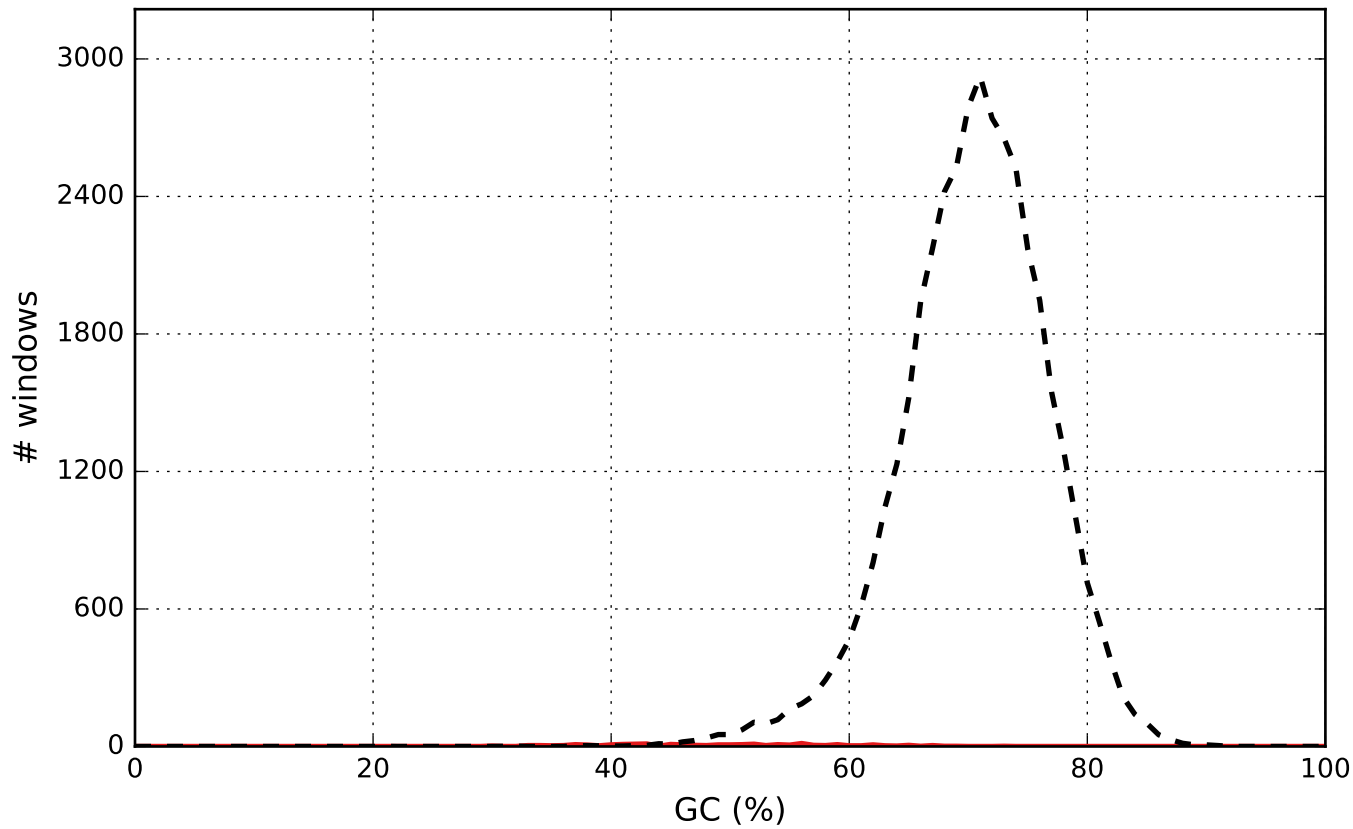
— final.contigs



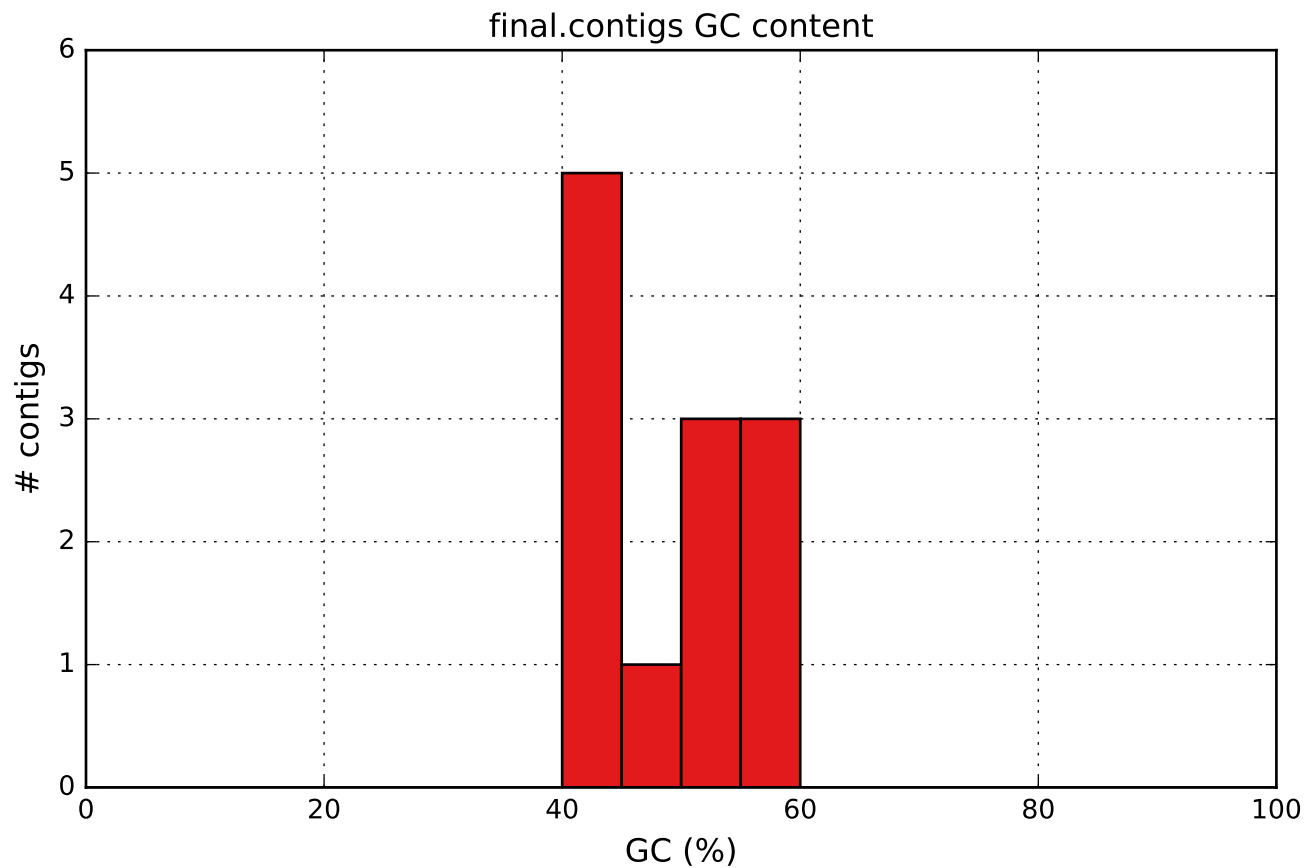
— final.contigs



GC content



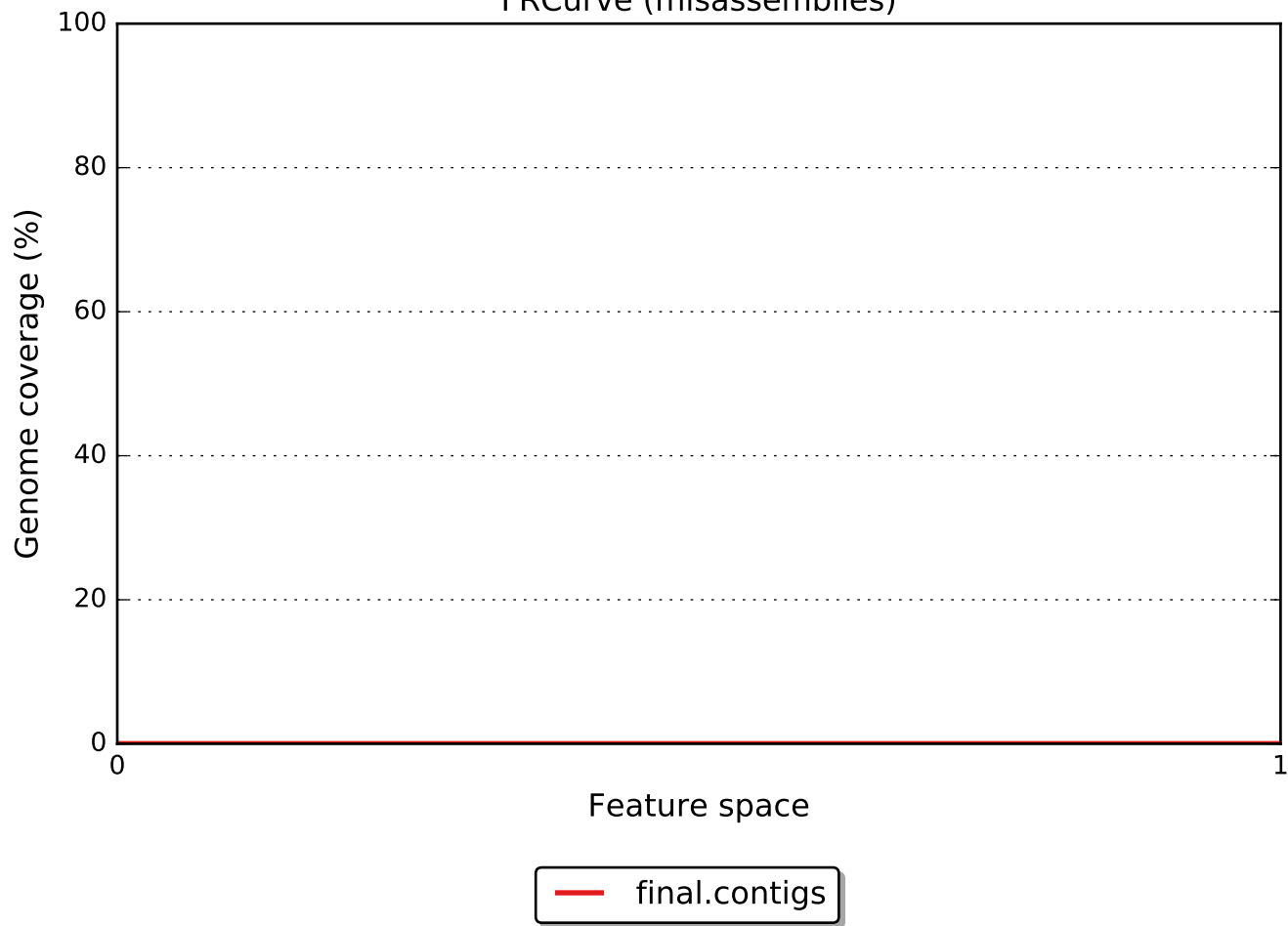
— final.contigs - - Reference



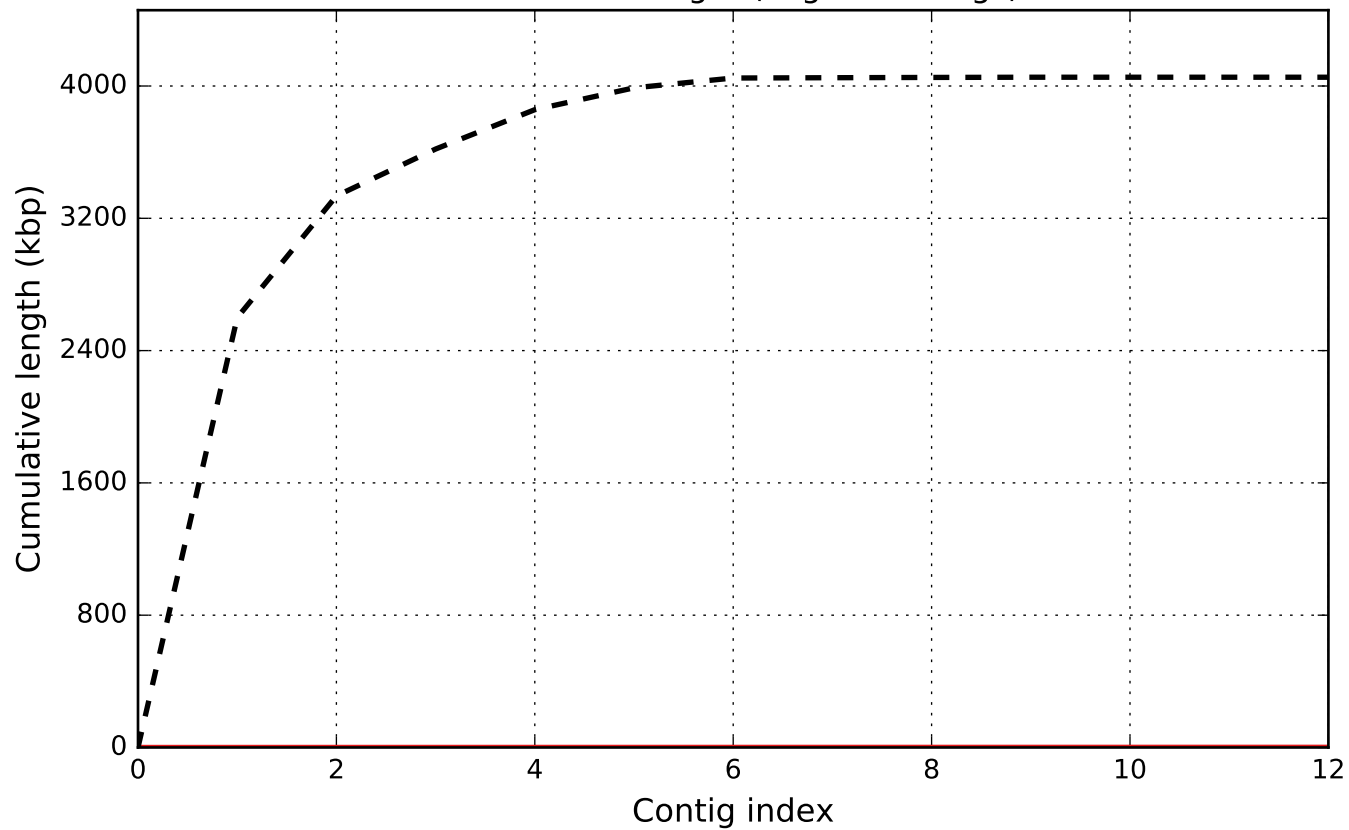
 final.contigs



FRCurve (misassemblies)

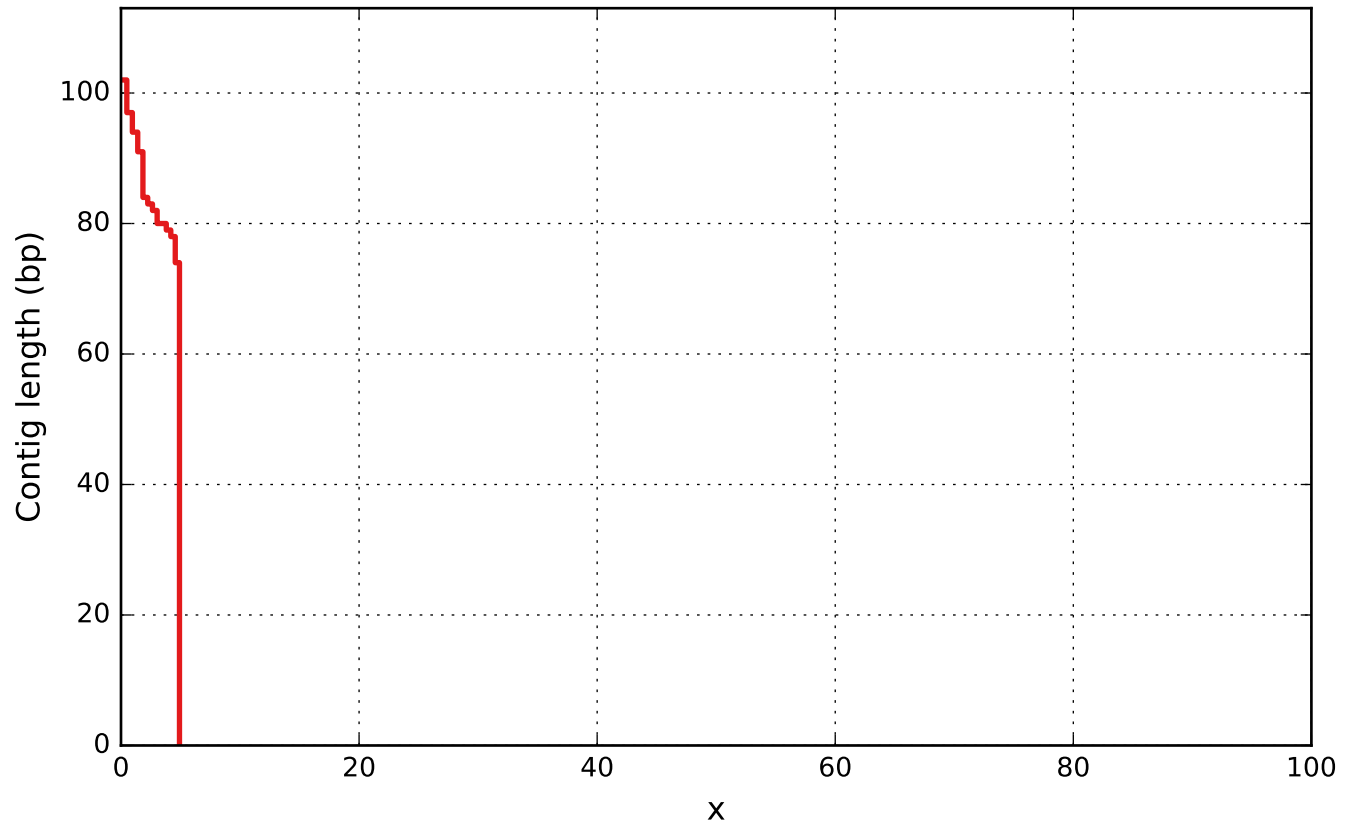


Cumulative length (aligned contigs)



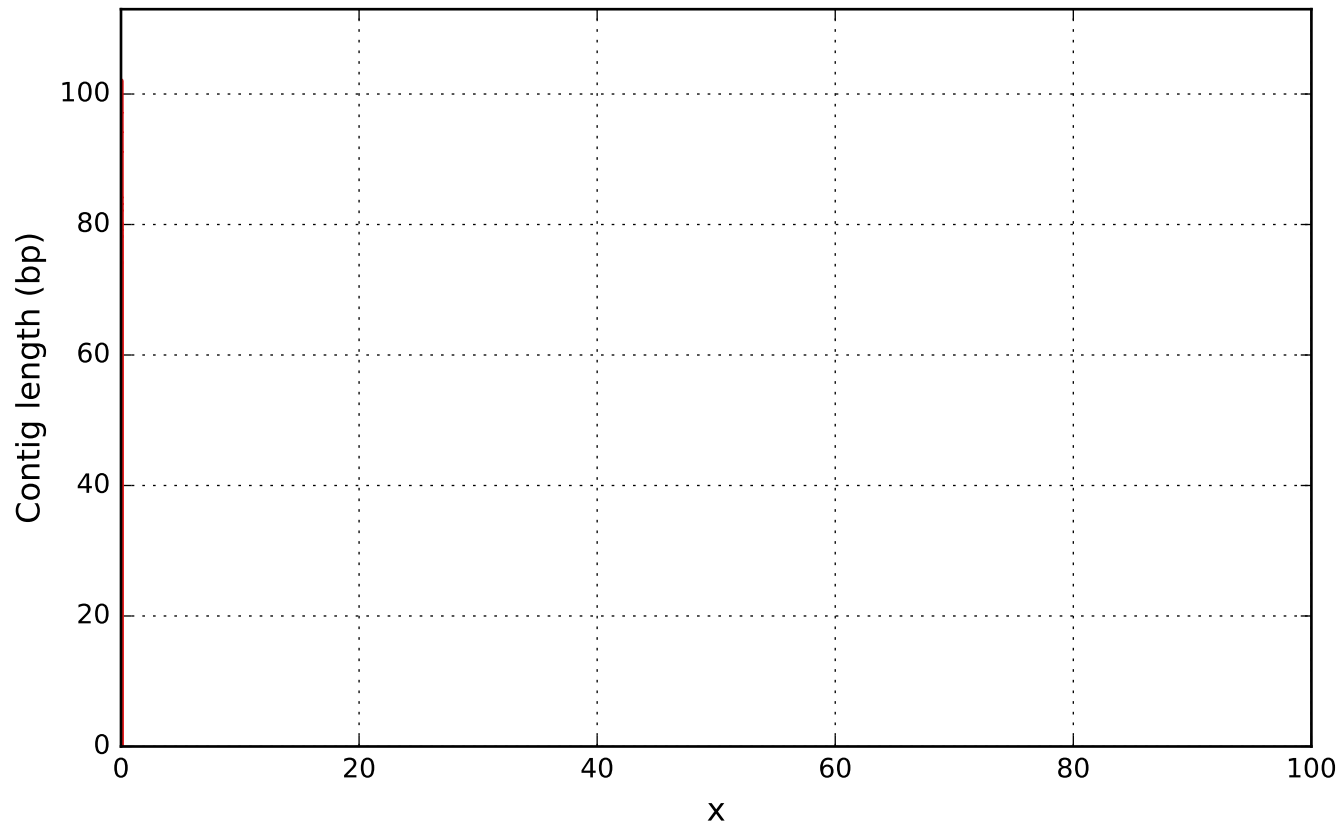
— final.contigs - - Reference

NAx



— final.contigs

NGAx



— final.contigs