

Report

	final.contigs
# contigs (>= 1000 bp)	2
# contigs (>= 5000 bp)	2
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	23006
Total length (>= 5000 bp)	23006
Total length (>= 10000 bp)	13115
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	3
Largest contig	13115
Total length	23992
Reference length	7777997
GC (%)	62.55
Reference GC (%)	50.45
N50	13115
N75	9891
L50	1
L75	2
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 3 part
Unaligned length	23759
Genome fraction (%)	0.002
Duplication ratio	1.494
# N's per 100 kbp	0.00
# mismatches per 100 kbp	641.03
# indels per 100 kbp	0.00
Largest alignment	78
Total aligned length	233
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

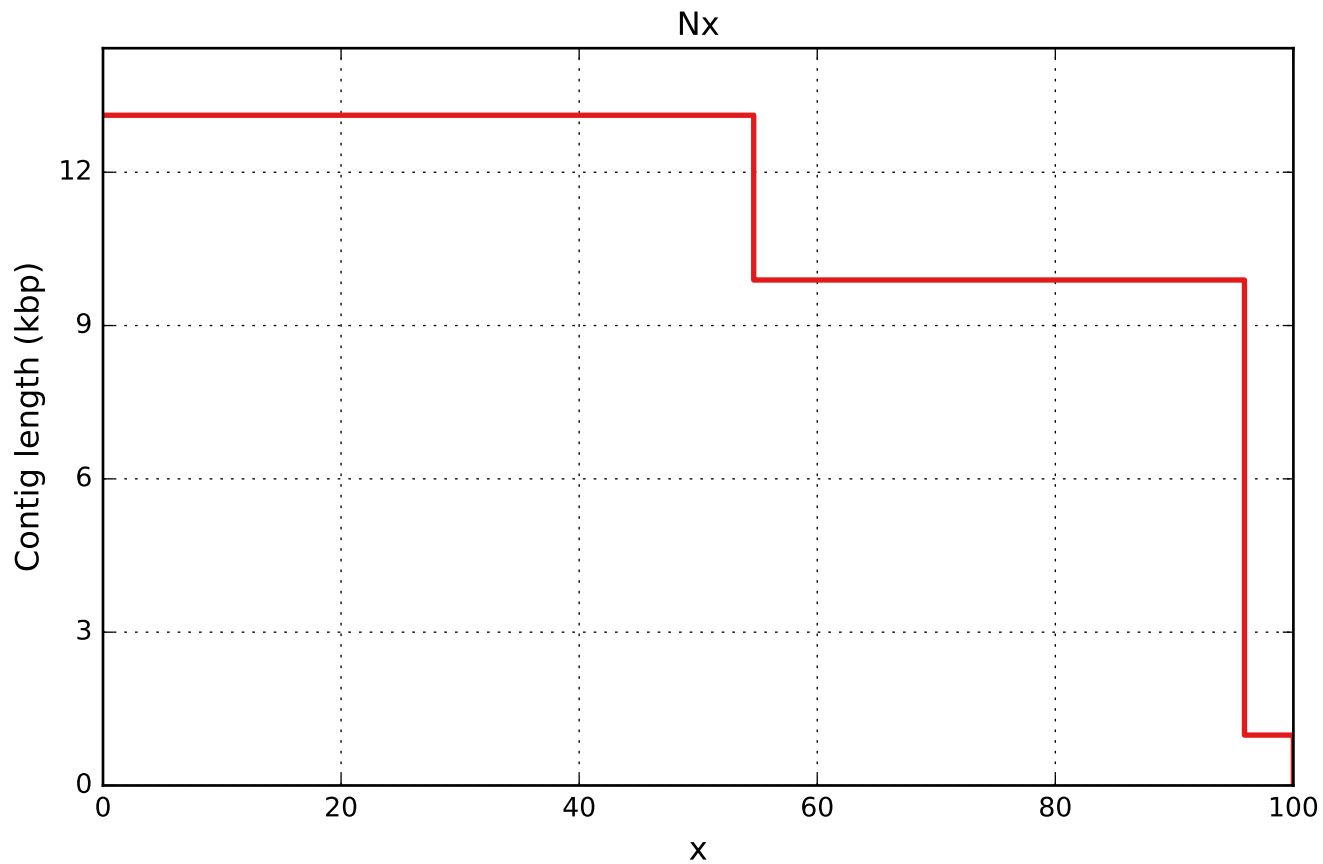
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	1
# indels	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

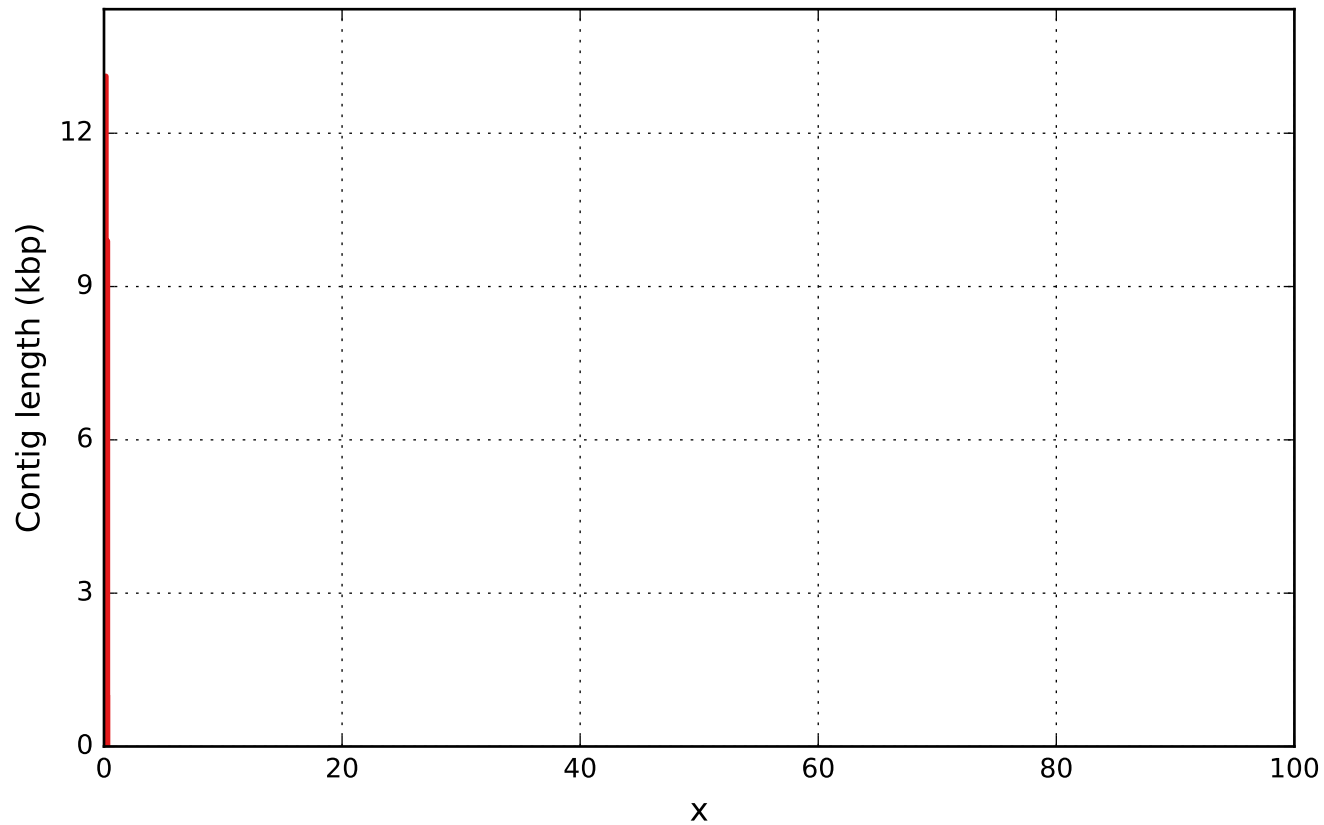
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	3
Partially unaligned length	23759
# N's	0

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).

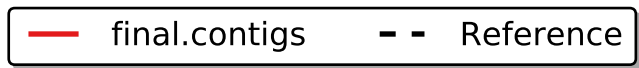
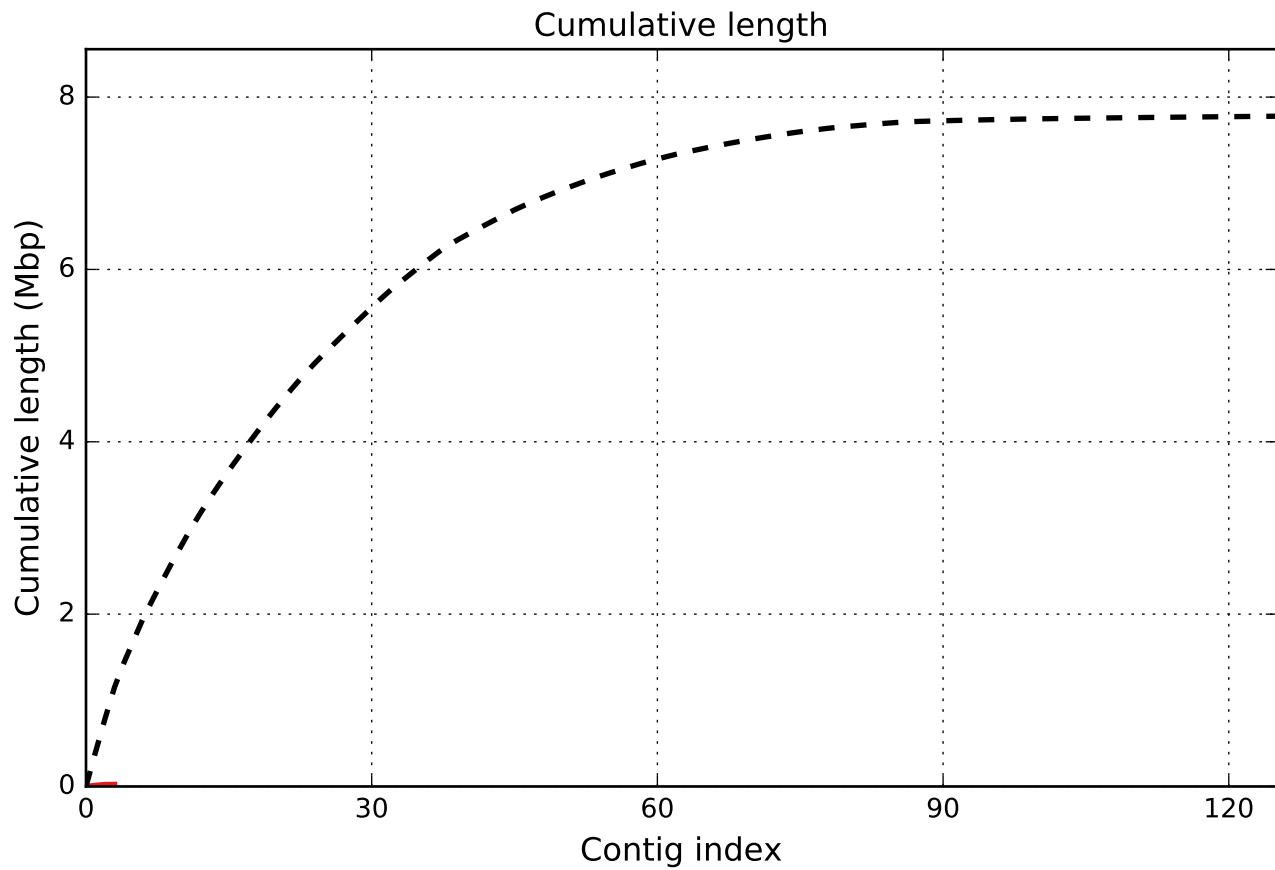


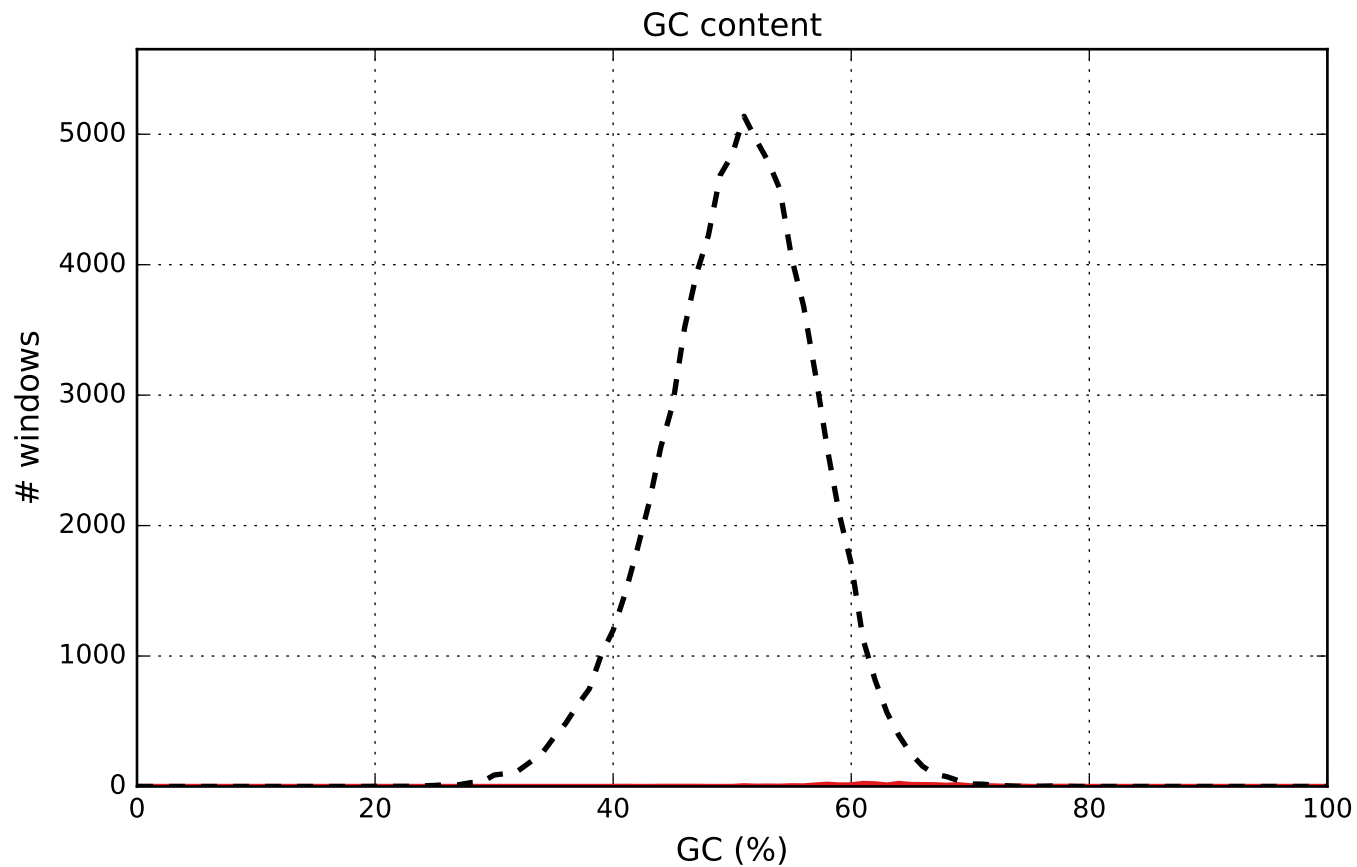
— final.contigs

NGx

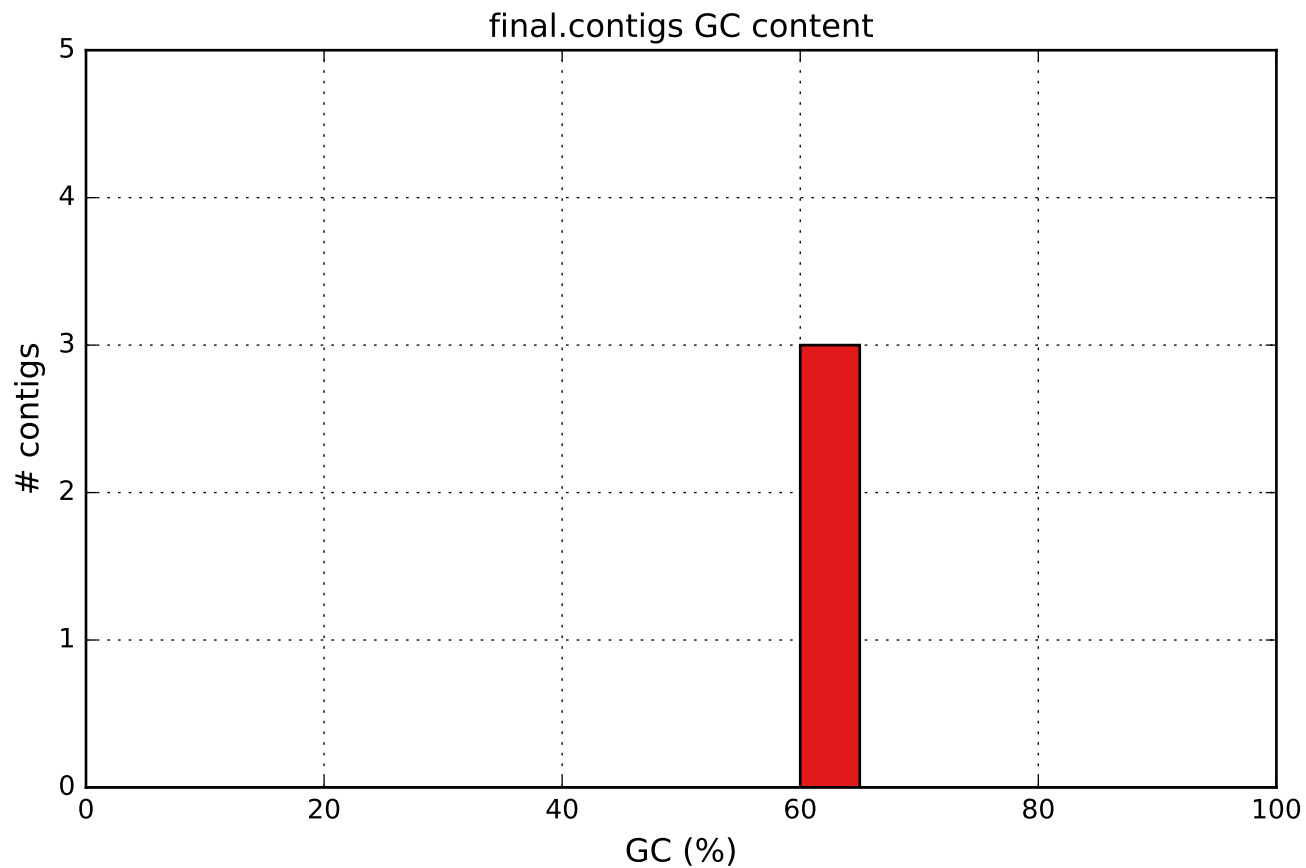


— final.contigs





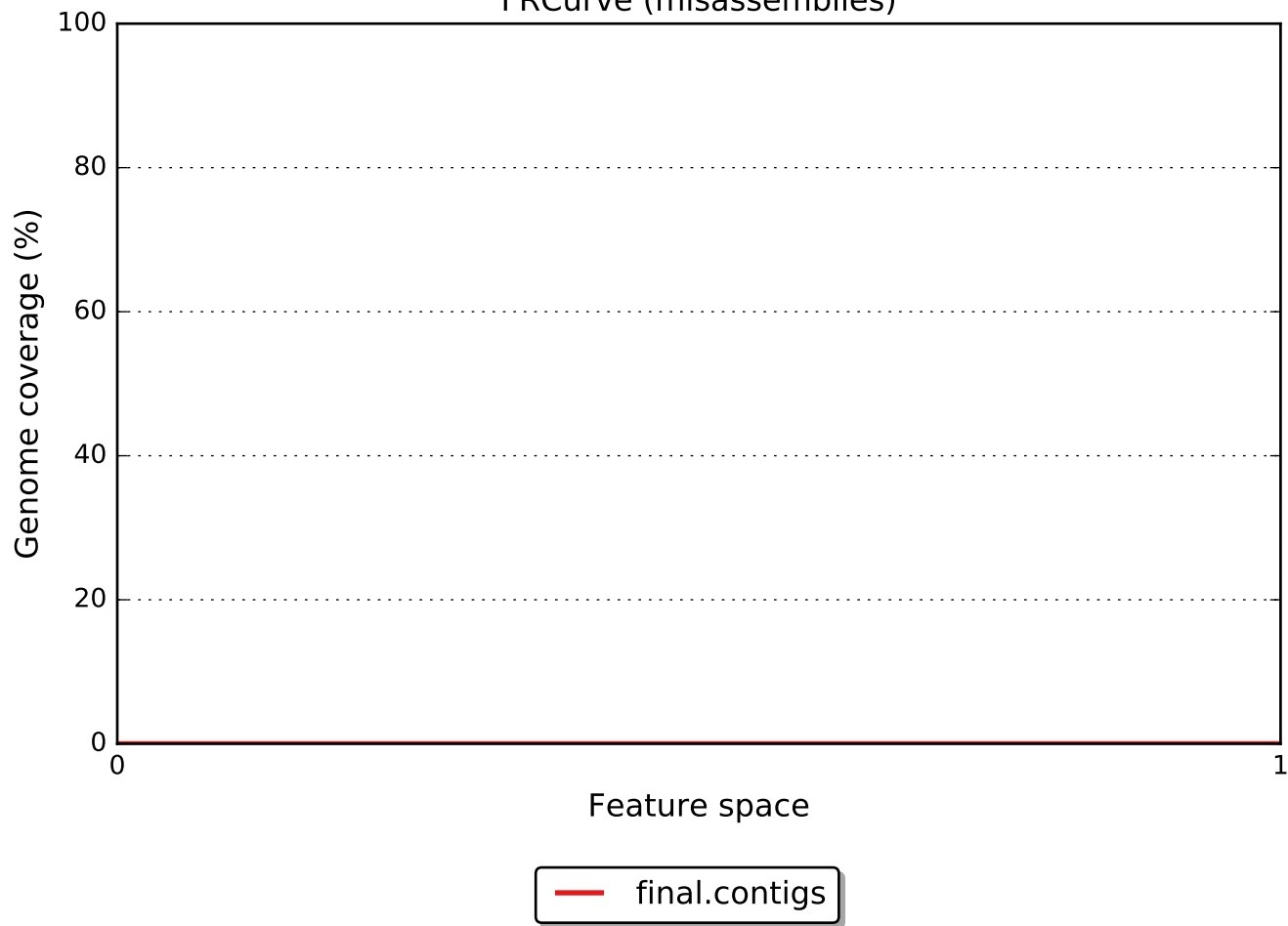
— final.contigs - - Reference

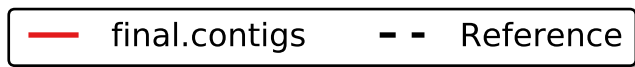
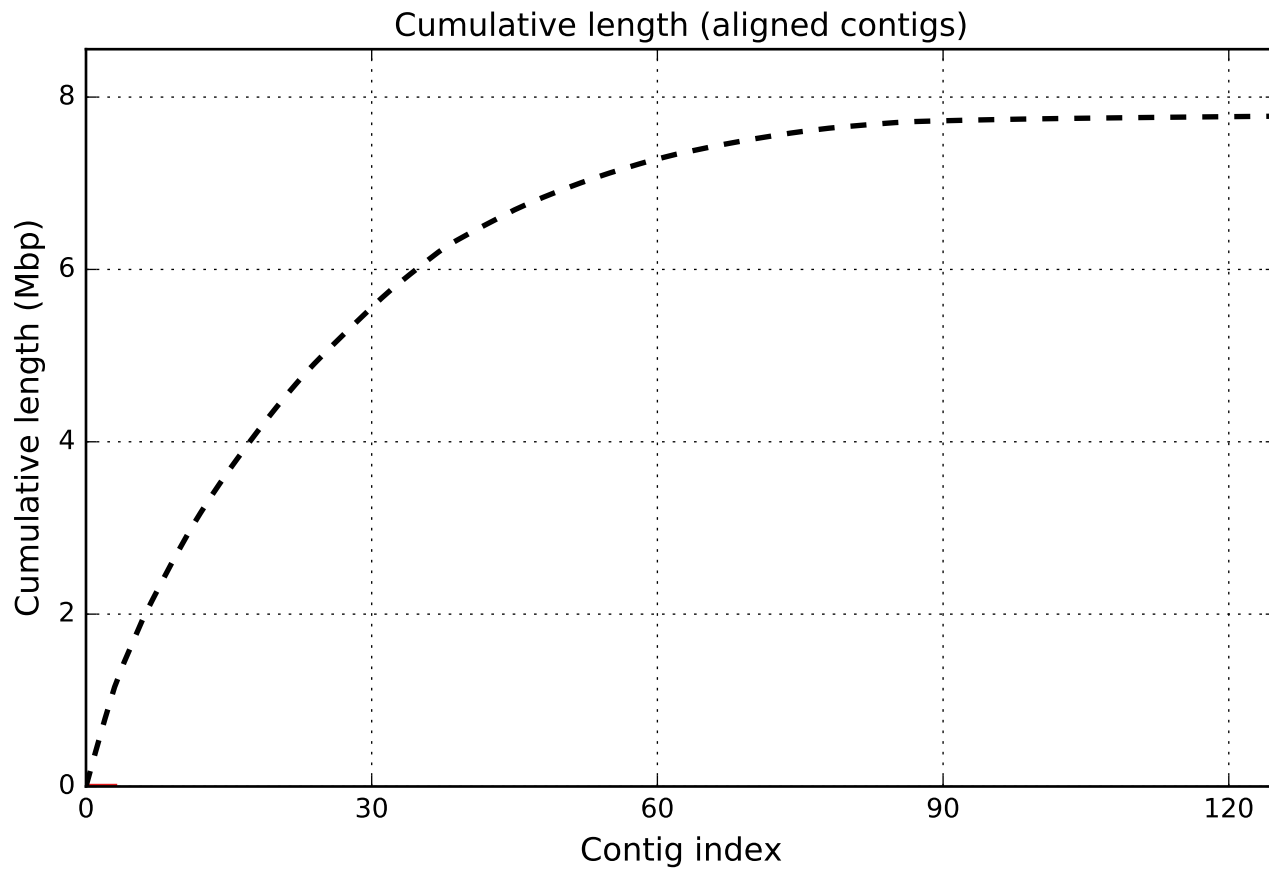


final.contigs

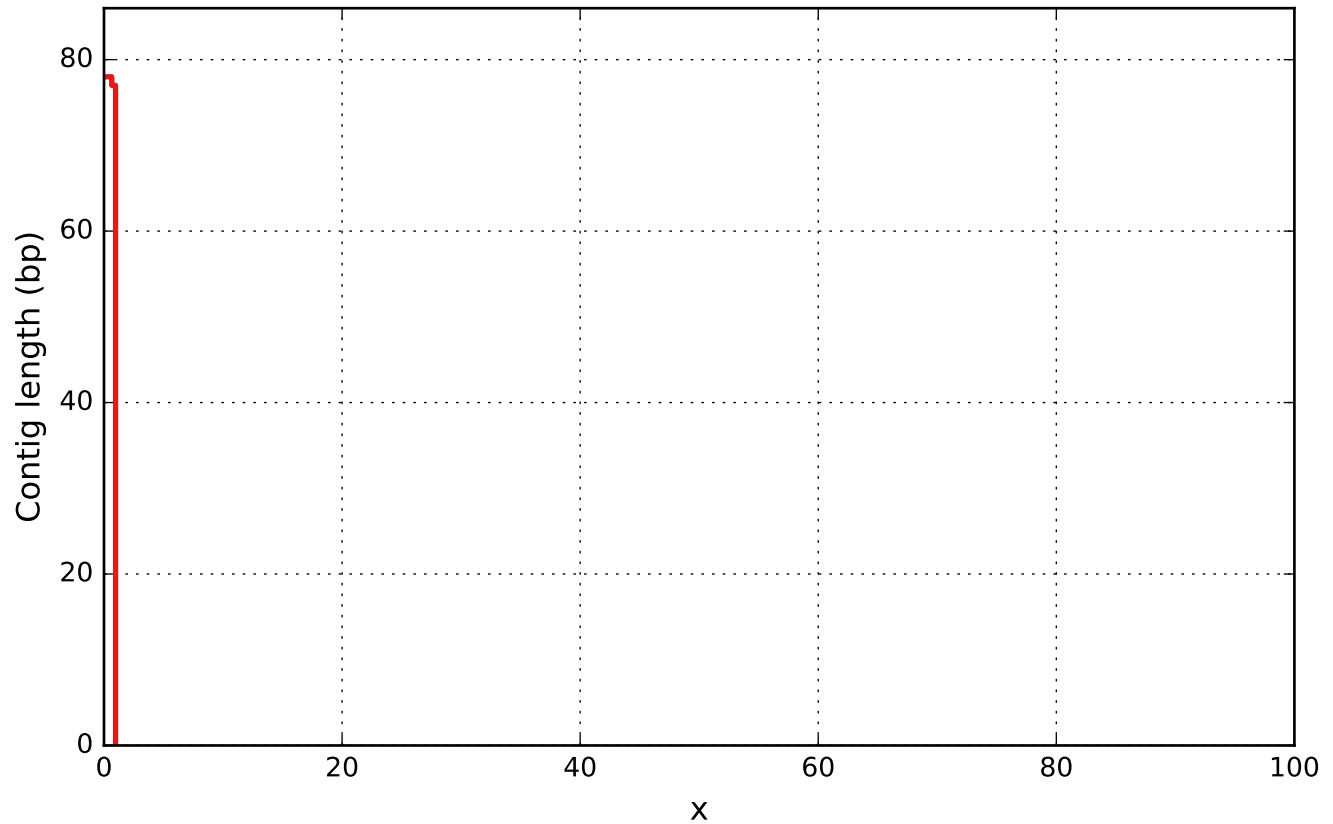


FRCurve (misassemblies)



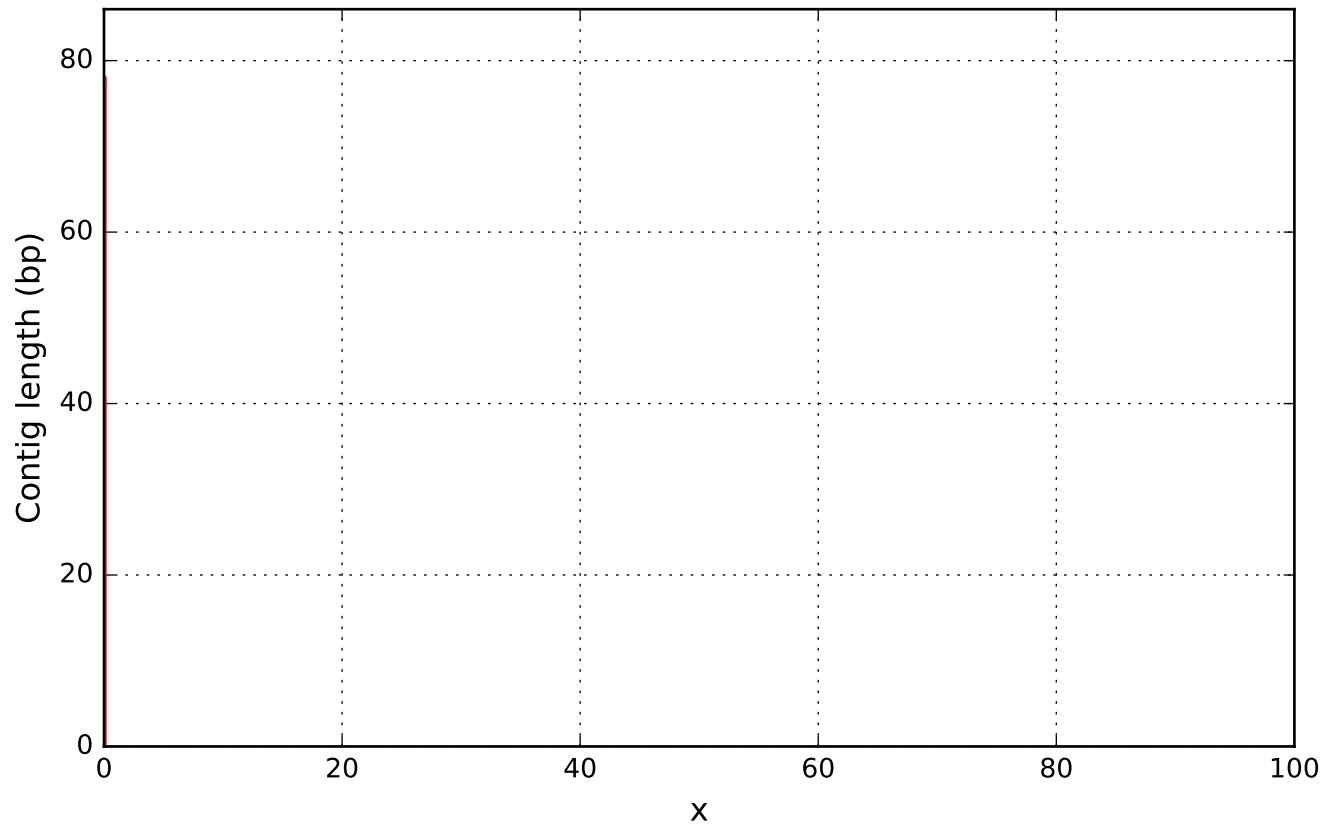


NAx



— final.contigs

NGAx



— final.contigs