

Report

	final.contigs
# contigs (≥ 1000 bp)	2
# contigs (≥ 5000 bp)	1
# contigs (≥ 10000 bp)	1
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 1000 bp)	18428
Total length (≥ 5000 bp)	16005
Total length (≥ 10000 bp)	16005
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	4
Largest contig	16005
Total length	19602
Reference length	5722743
GC (%)	56.17
Reference GC (%)	46.67
N50	16005
N75	16005
L50	1
L75	1
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# structural variations	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 2 part
Unaligned length	18276
Genome fraction (%)	0.005
Duplication ratio	4.510
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2721.09
# indels per 100 kbp	0.00
Largest alignment	215
Total aligned length	446
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

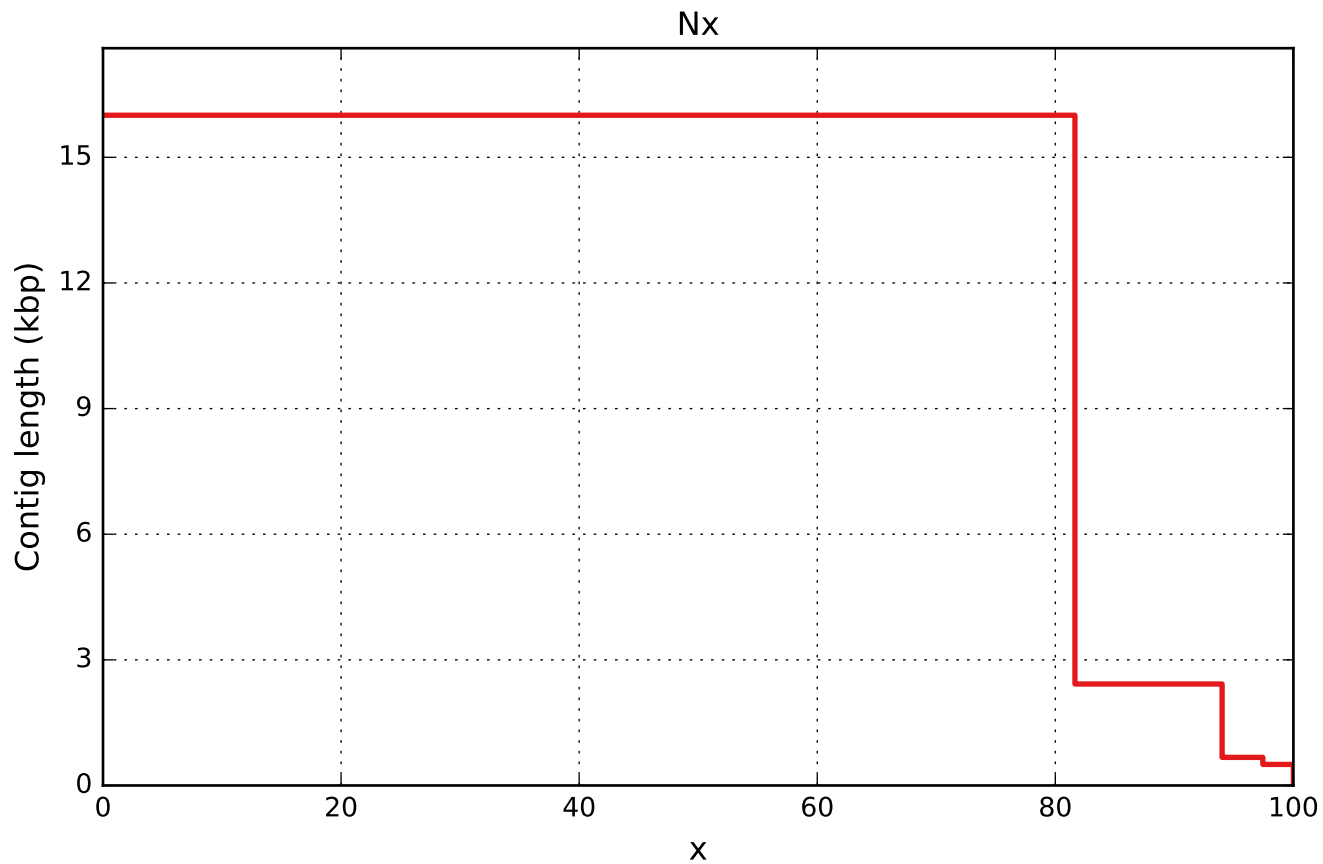
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# structural variations	0
# unaligned mis. contigs	0
# mismatches	8
# 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

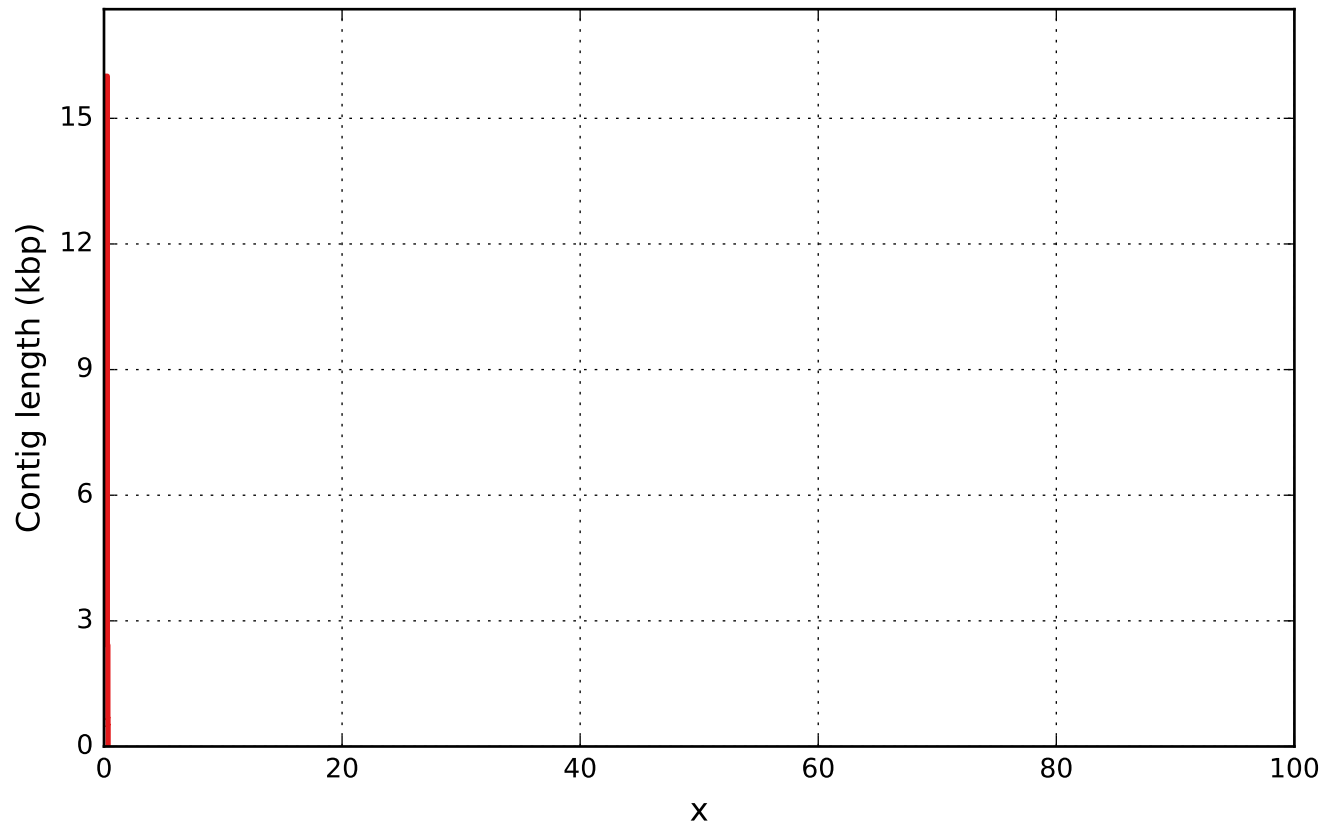
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
Partially unaligned length	18276
# N's	0

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).

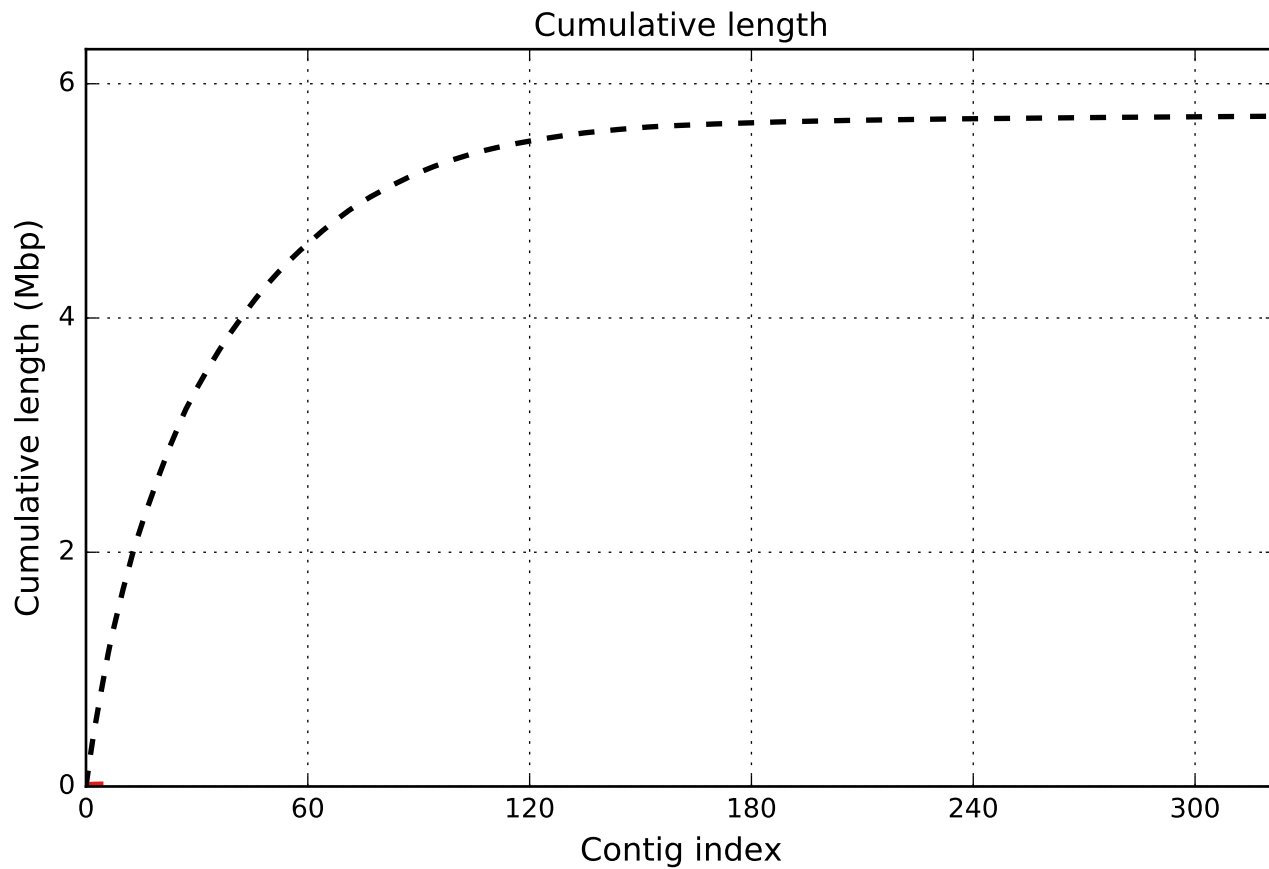


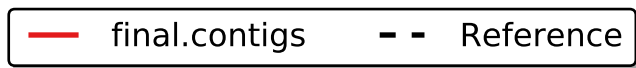
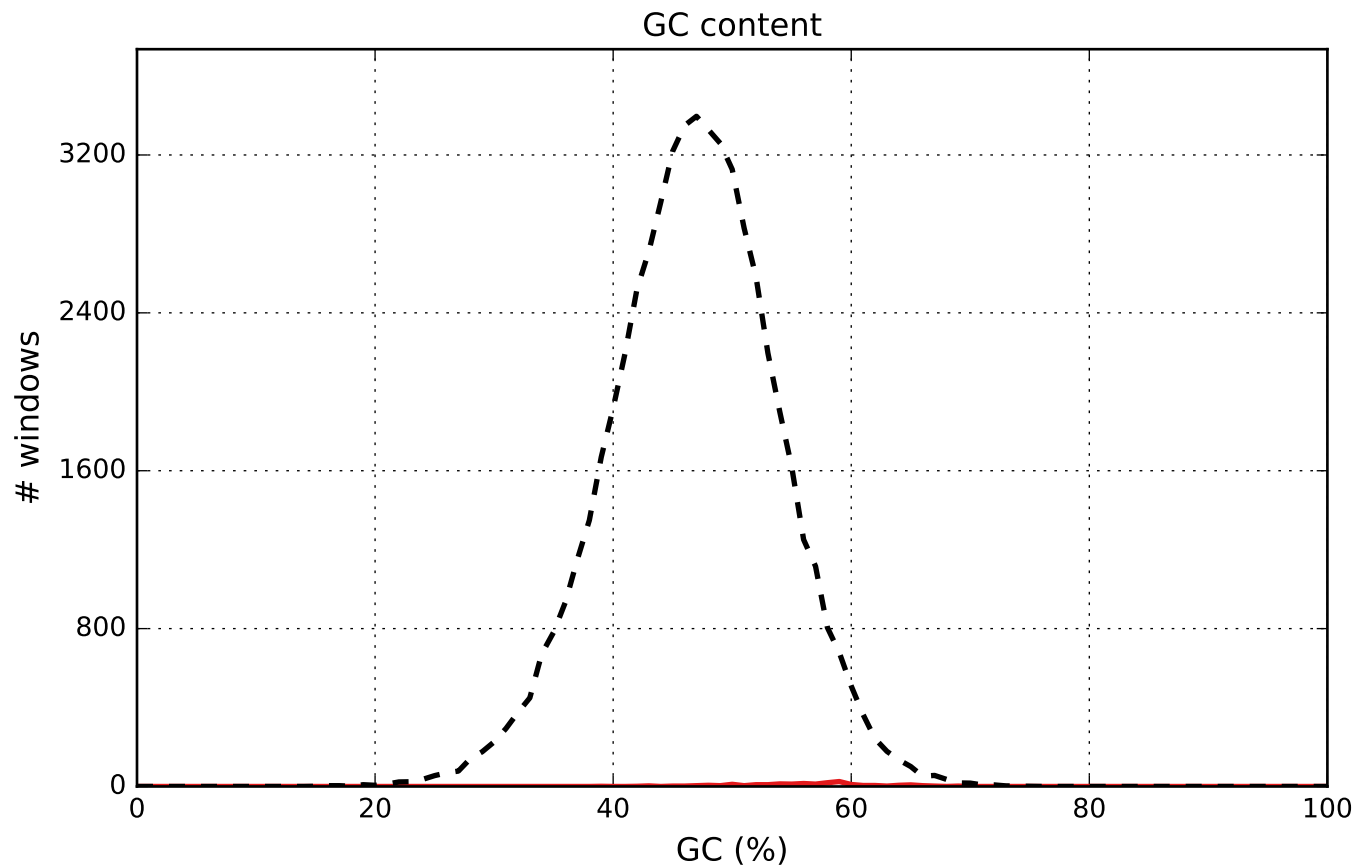
— final.contigs

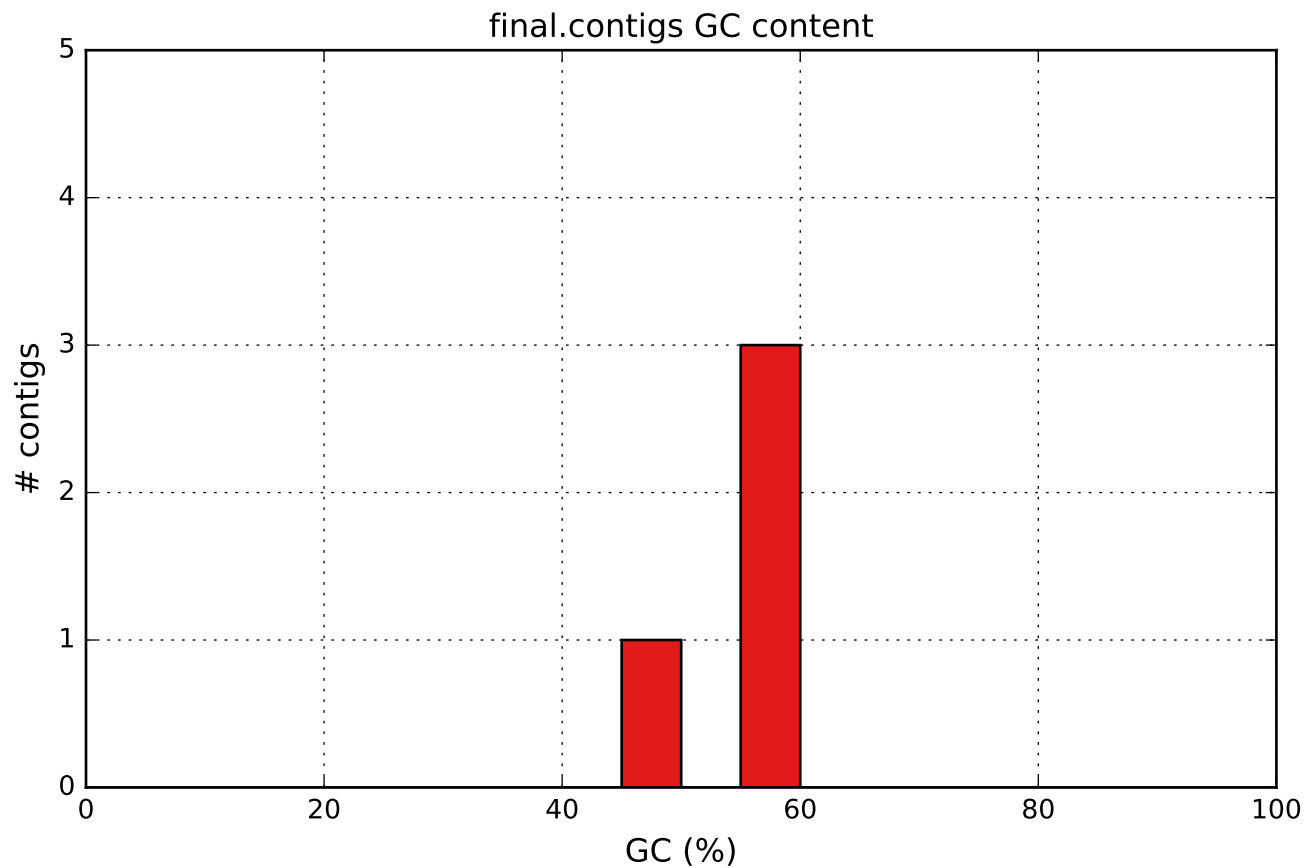
NGx



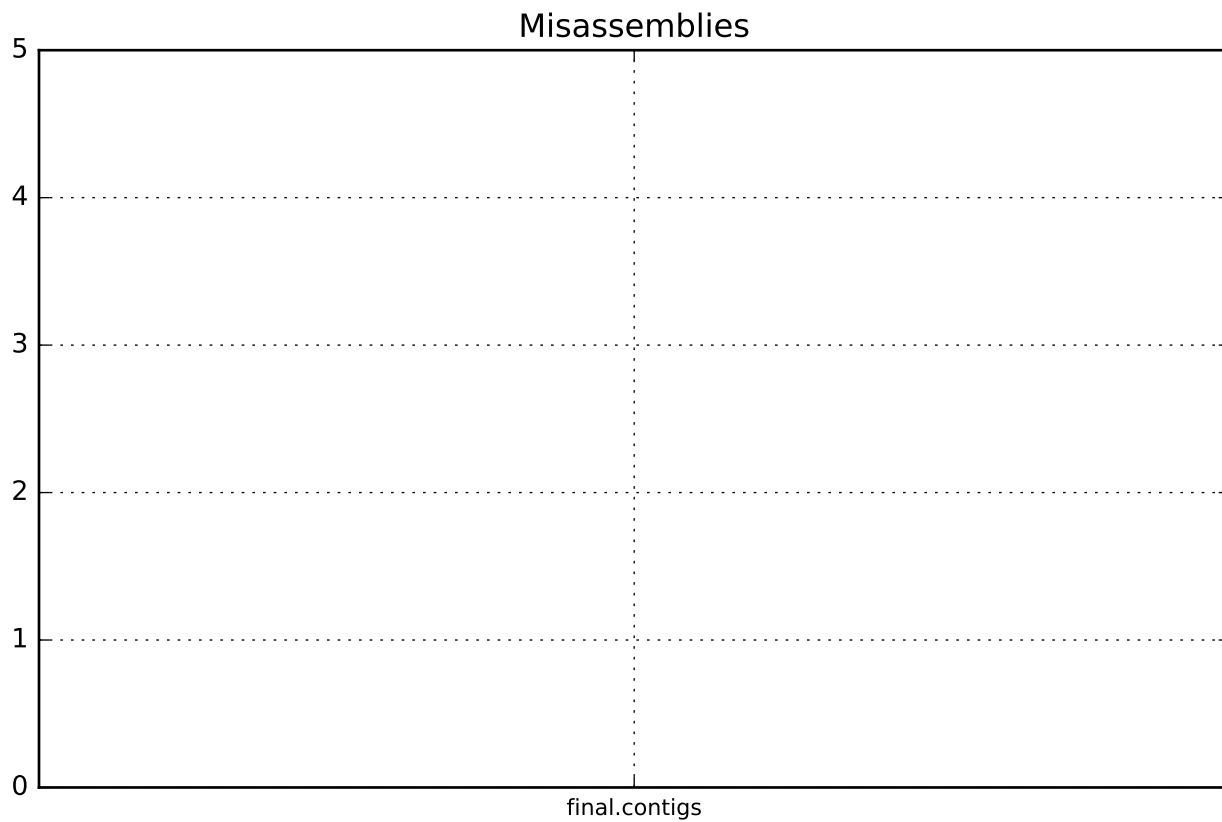
— final.contigs



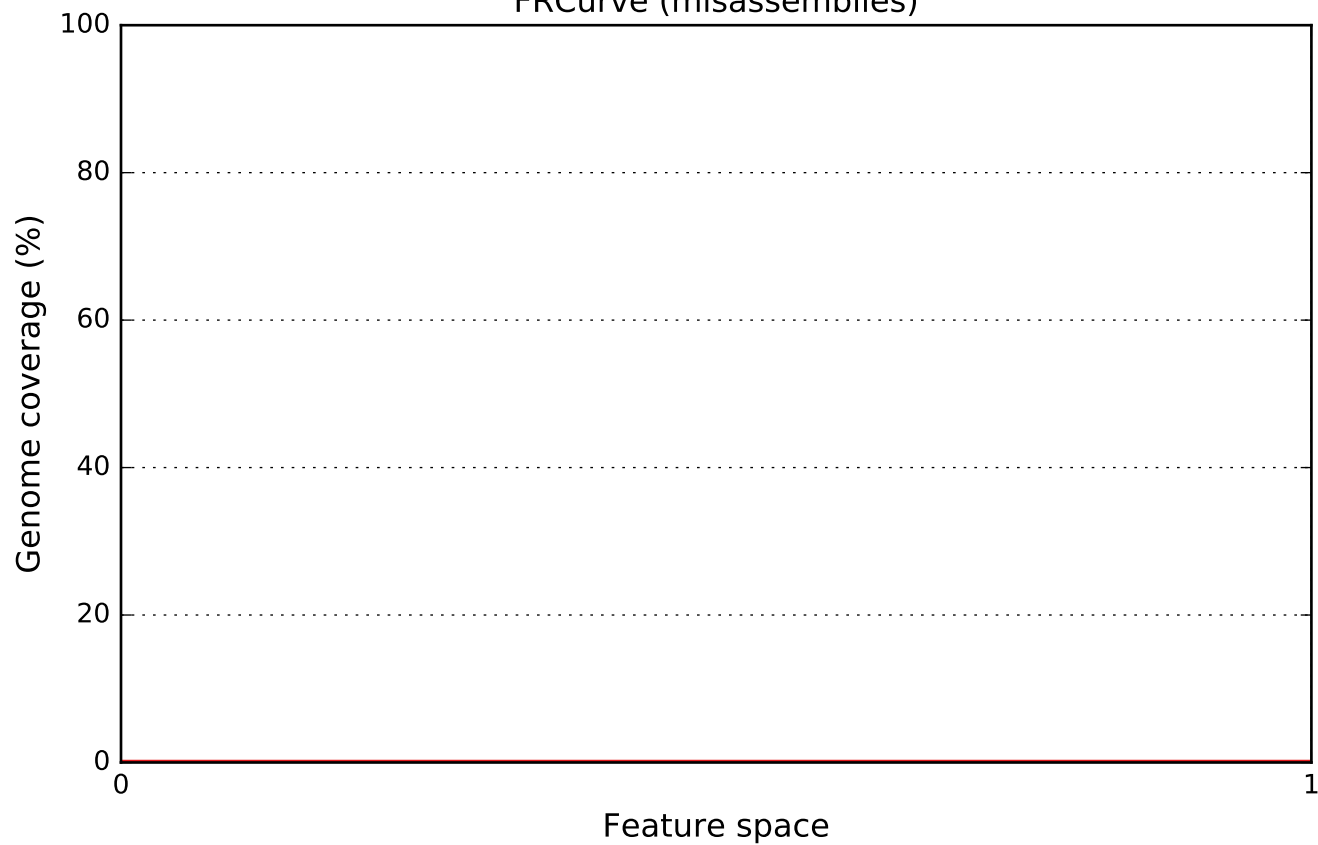




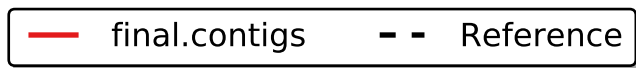
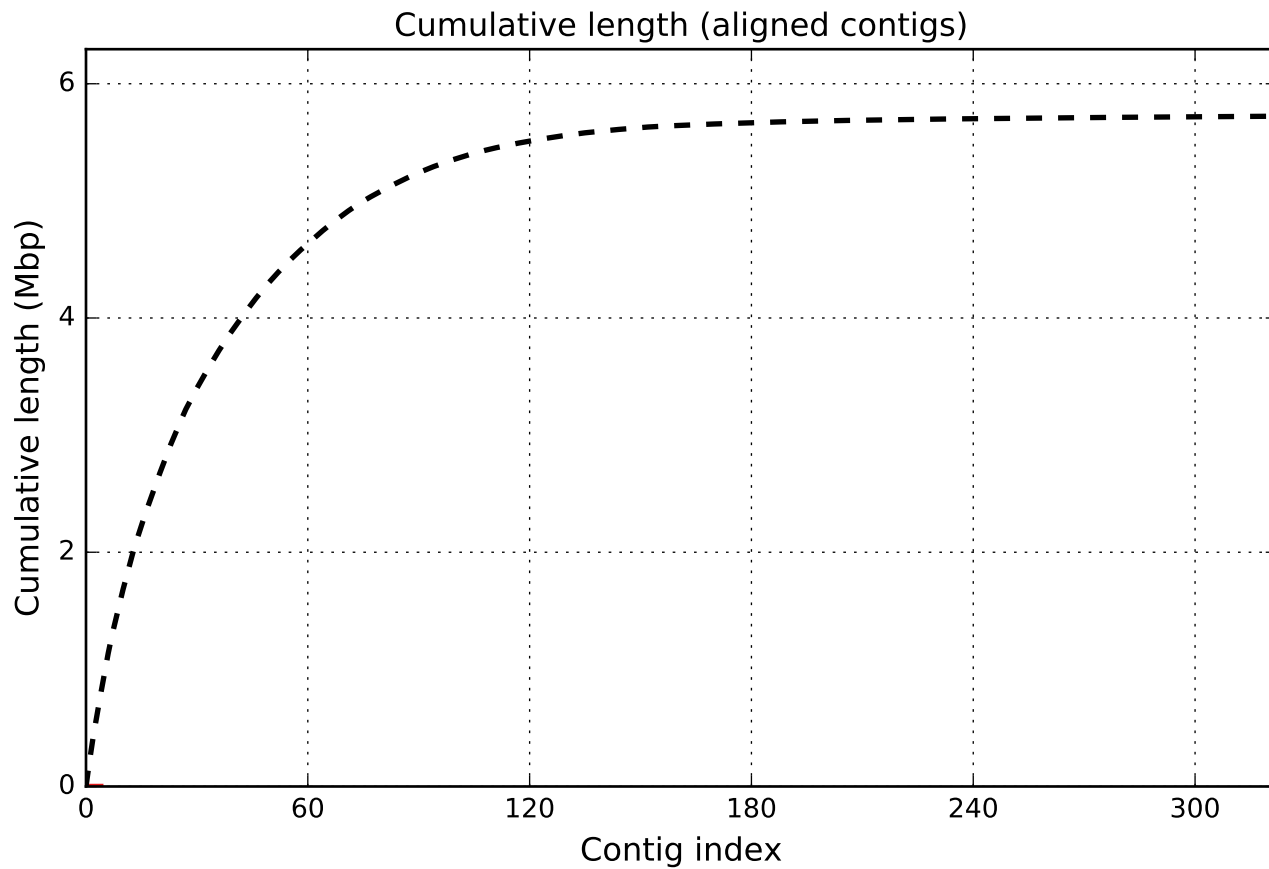
final.contigs



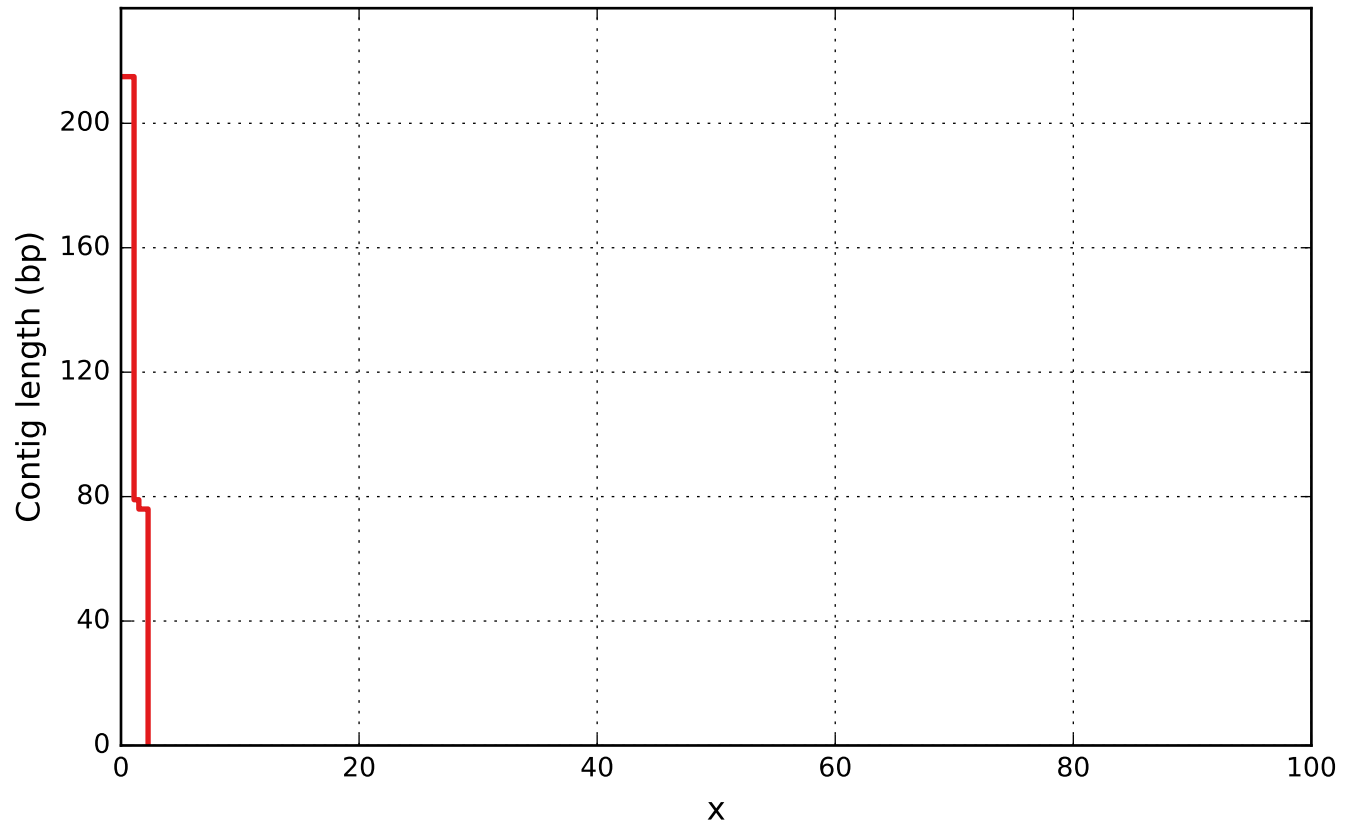
FRCurve (misassemblies)



— final.contigs

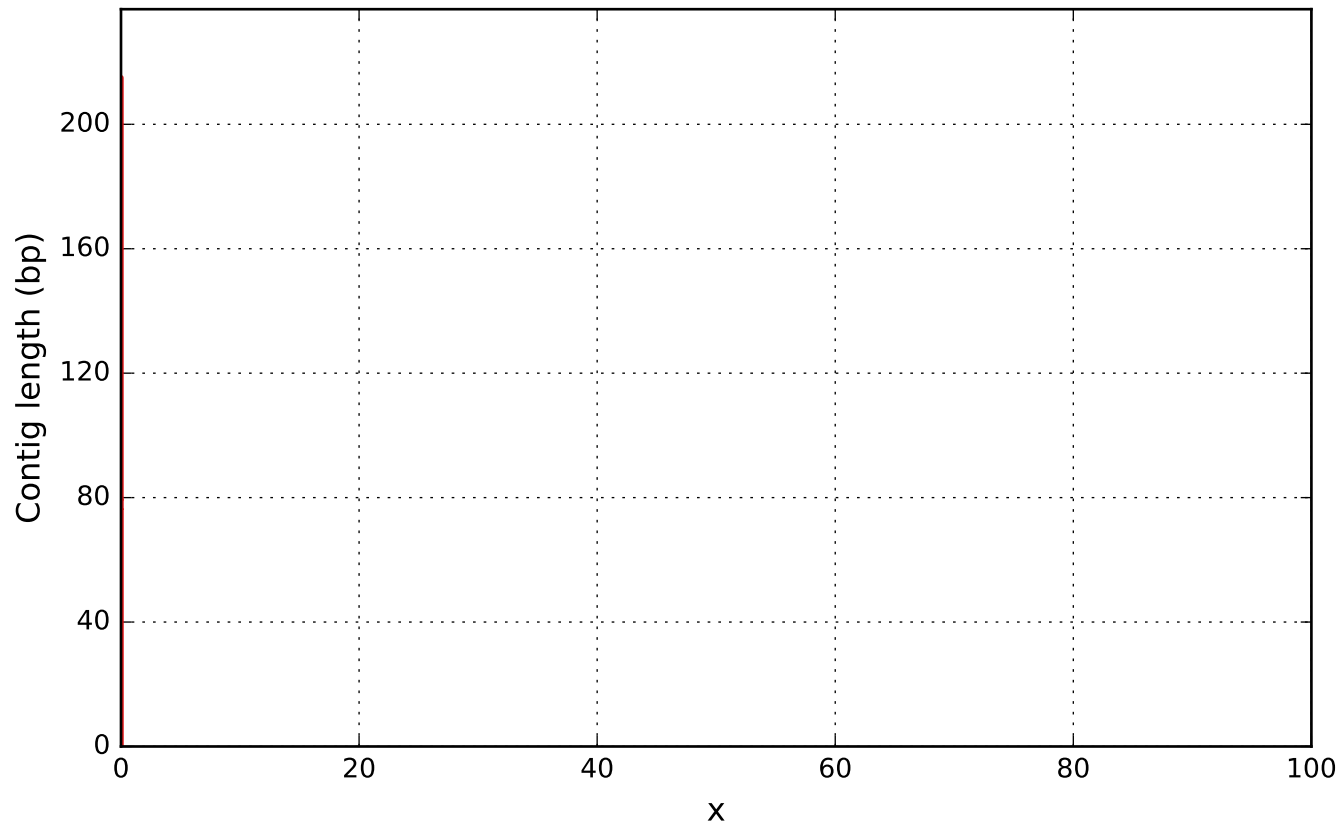


NAx



— final.contigs

NGAx



— final.contigs