

## Report

	final.contigs
# contigs (>= 1000 bp)	8
# contigs (>= 5000 bp)	2
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	30316
Total length (>= 5000 bp)	15061
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	15
Largest contig	8045
Total length	35368
Reference length	4775416
GC (%)	60.34
Reference GC (%)	68.59
N50	4673
N75	2316
L50	3
L75	6
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 8 part
Unaligned length	29534
Genome fraction (%)	0.076
Duplication ratio	1.616
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2770.08
# indels per 100 kbp	387.81
Largest alignment	715
Total aligned length	4035
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

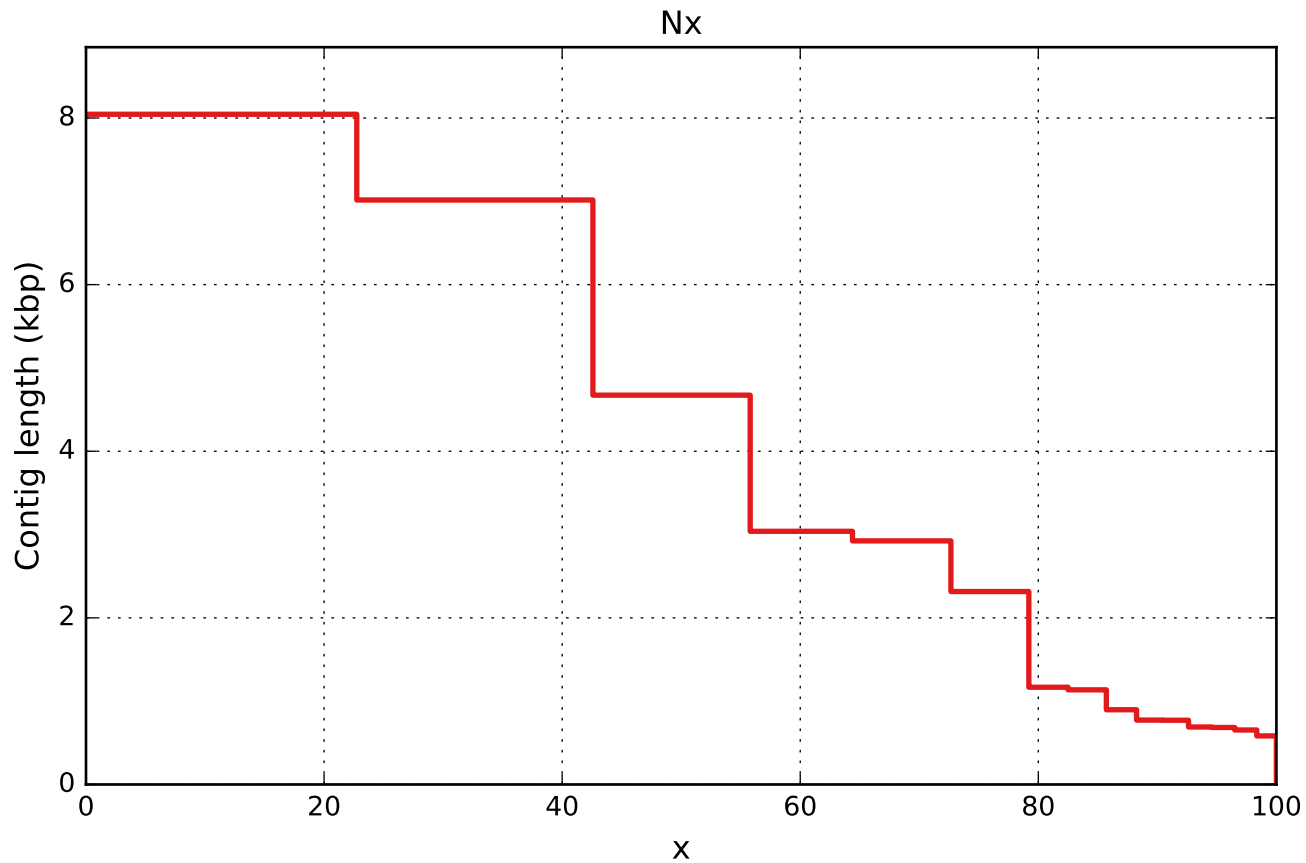
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	100
# indels	14
# indels (<= 5 bp)	14
# indels (> 5 bp)	0
Indels length	22

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

## Unaligned report

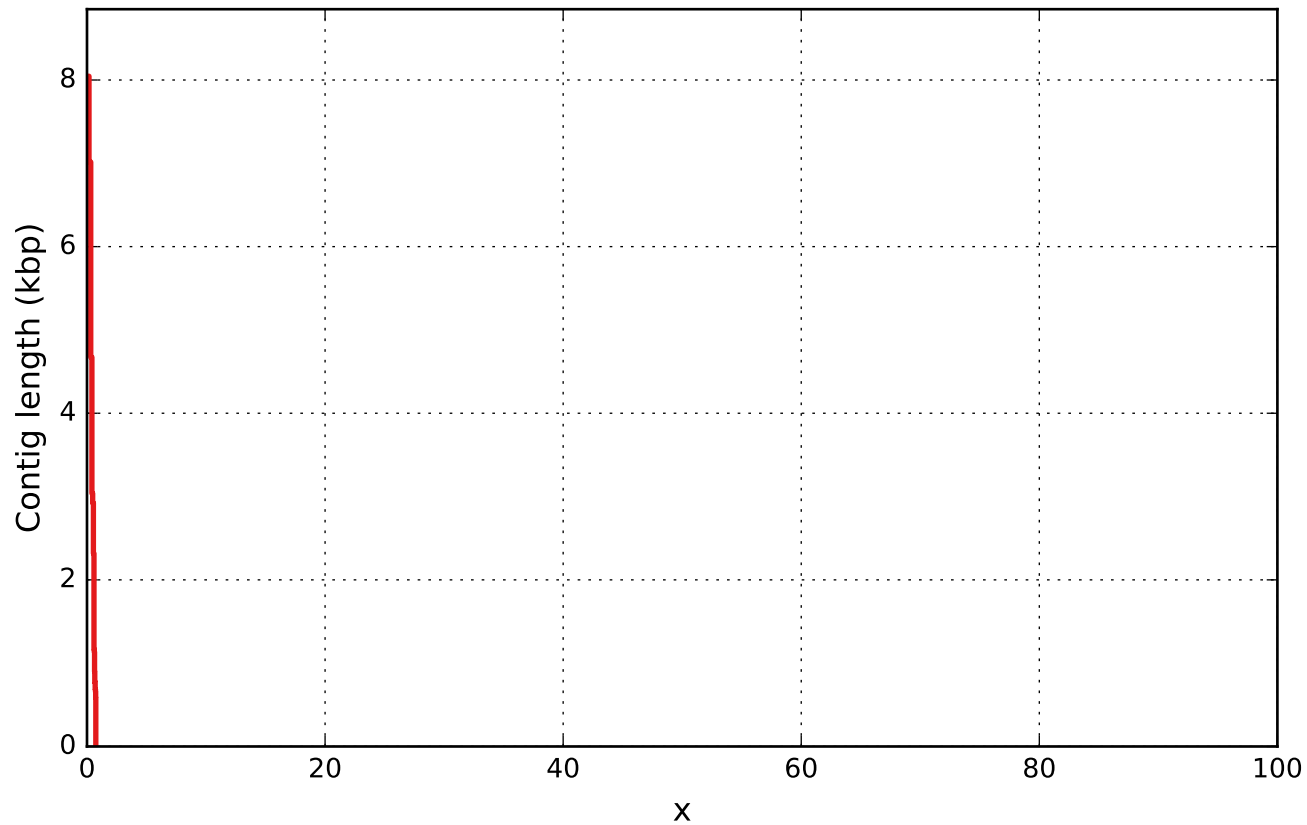
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	8
Partially unaligned length	29534
# N's	0

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

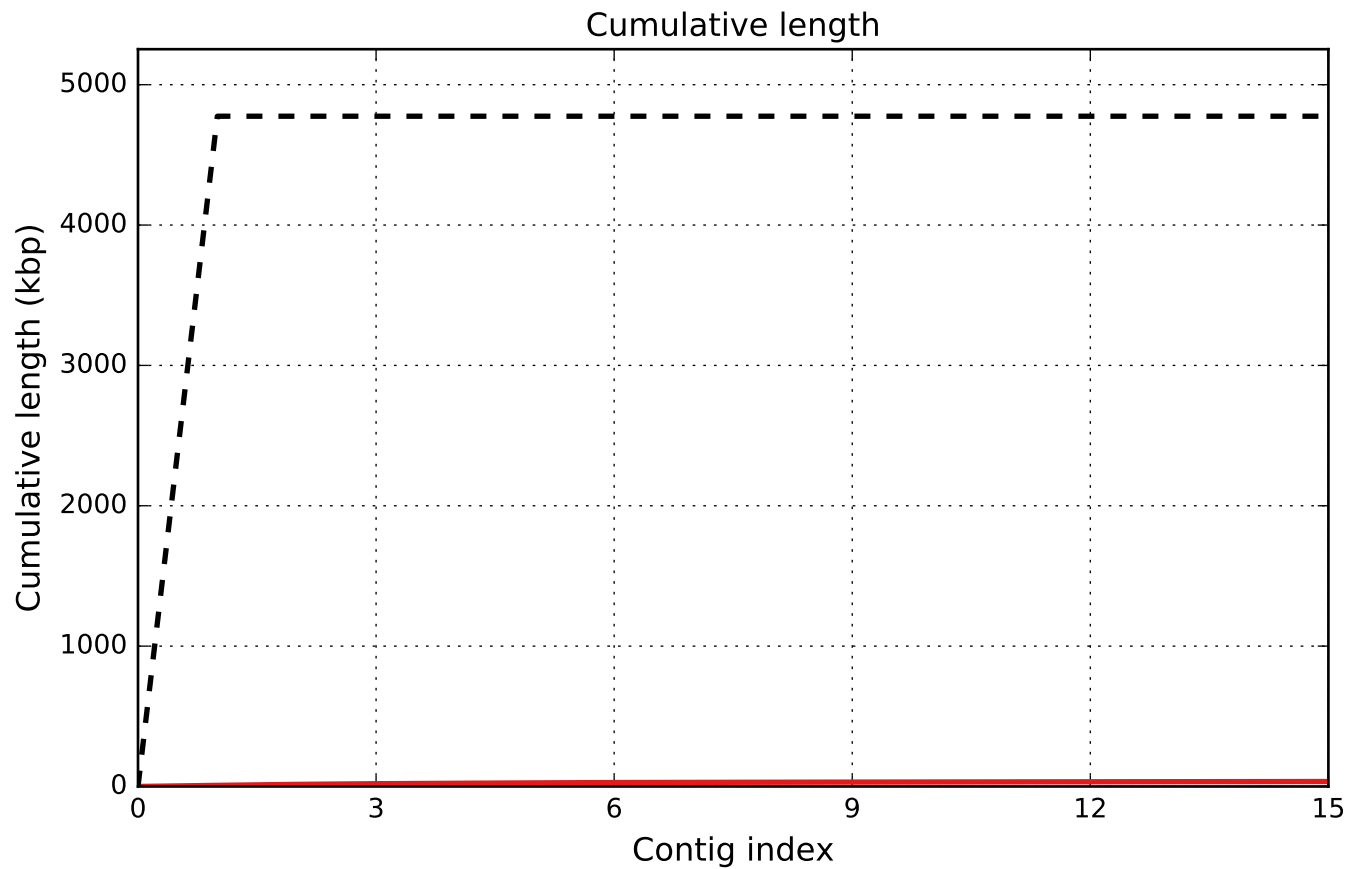


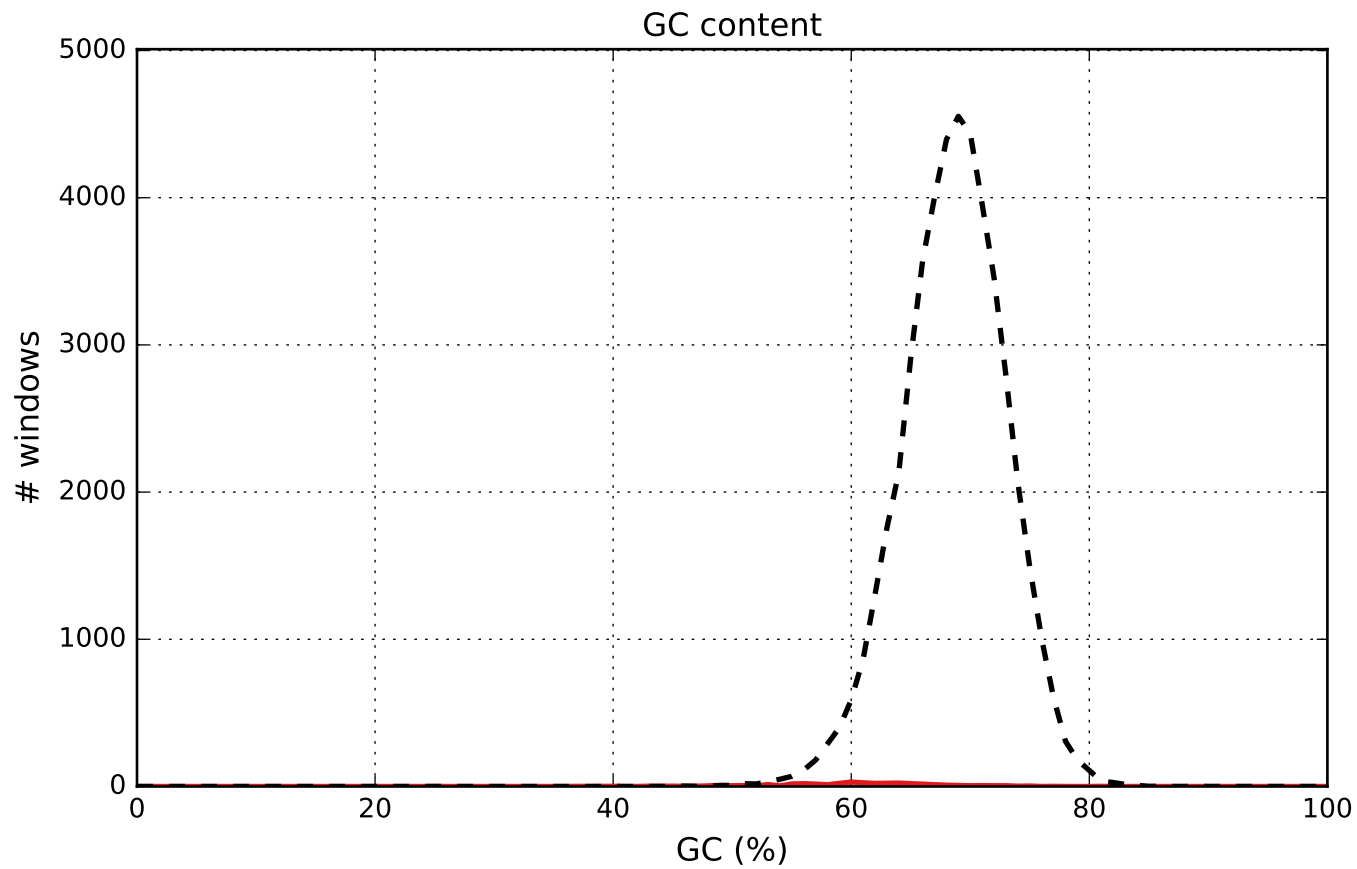
— final.contigs

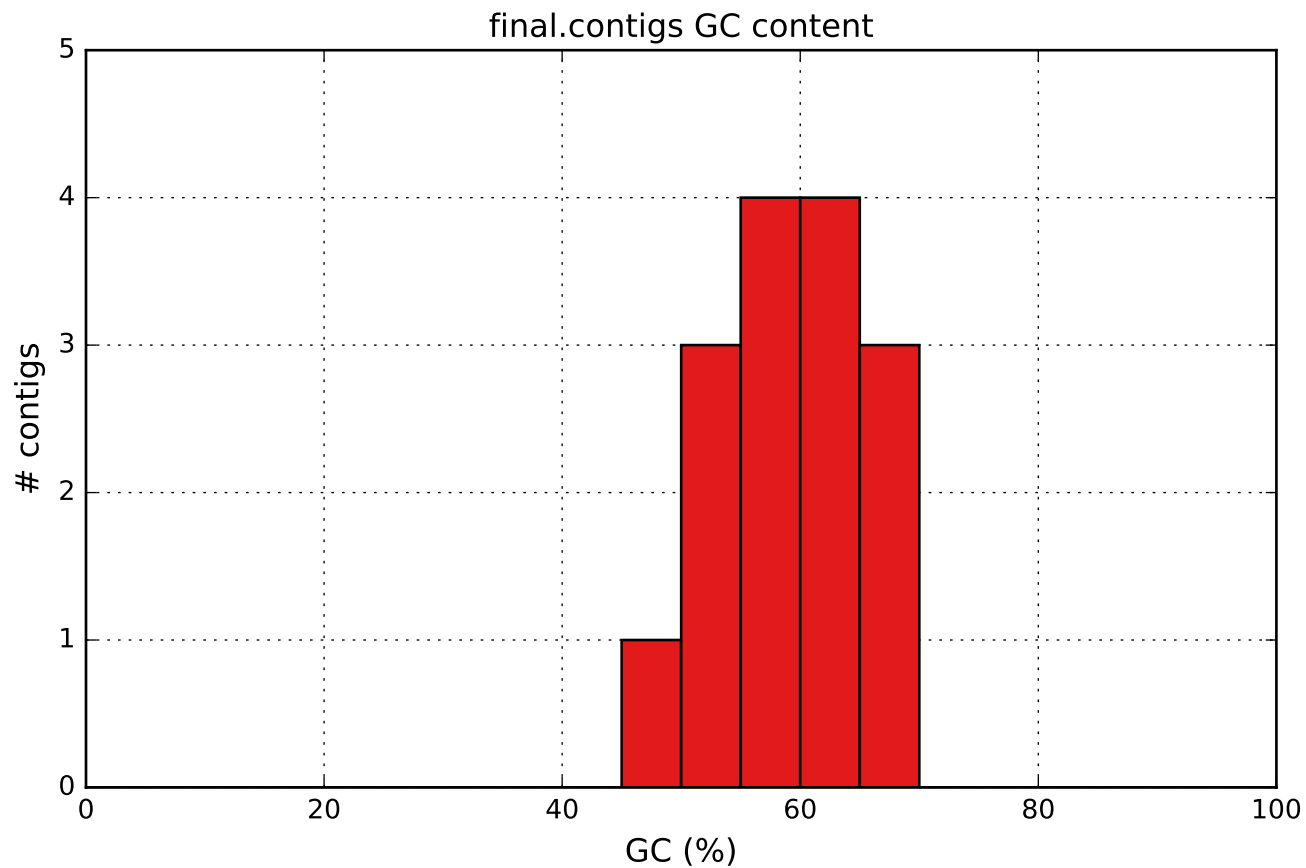
NGx



— final.contigs





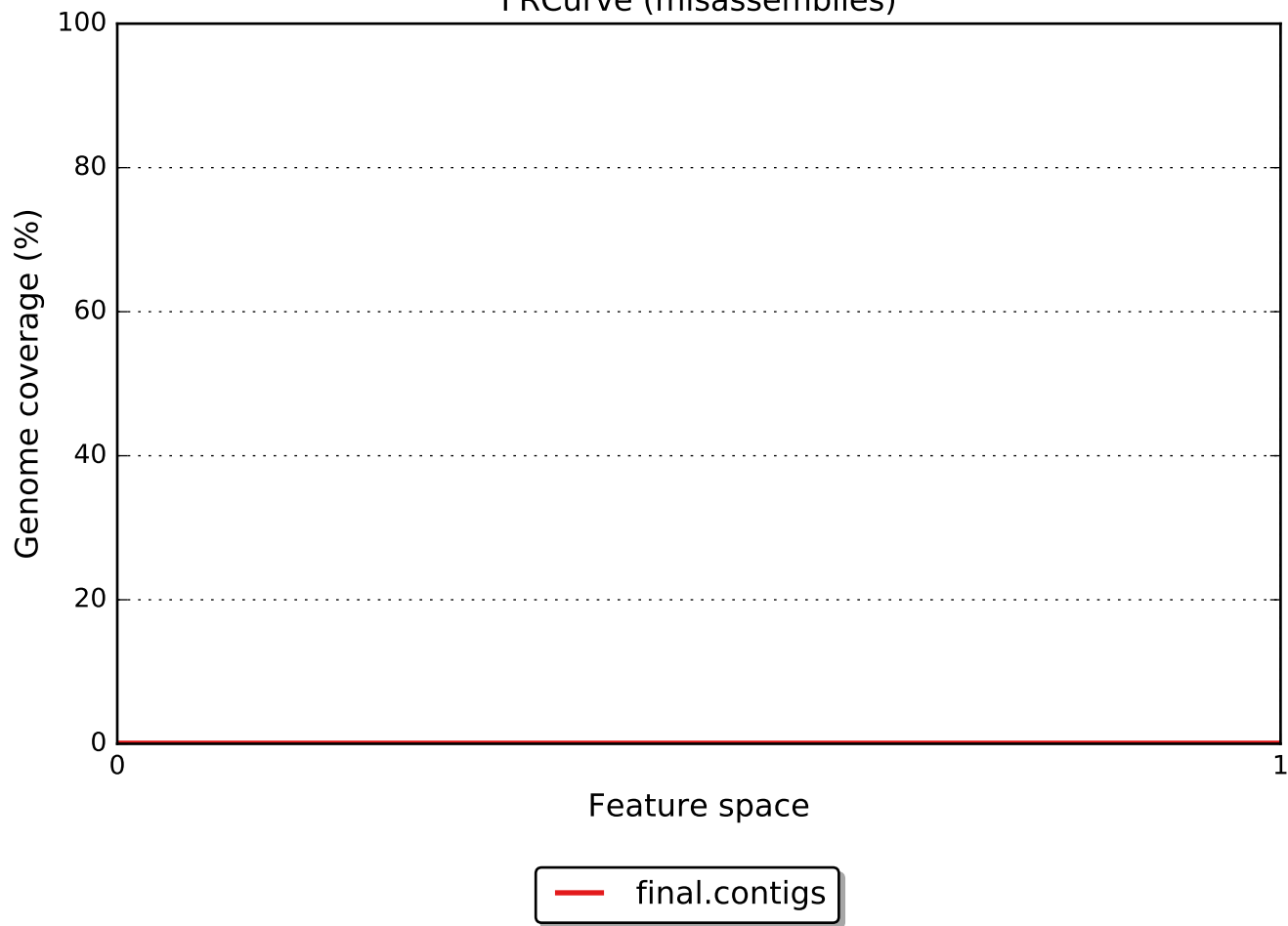


final.contigs

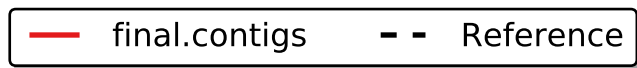
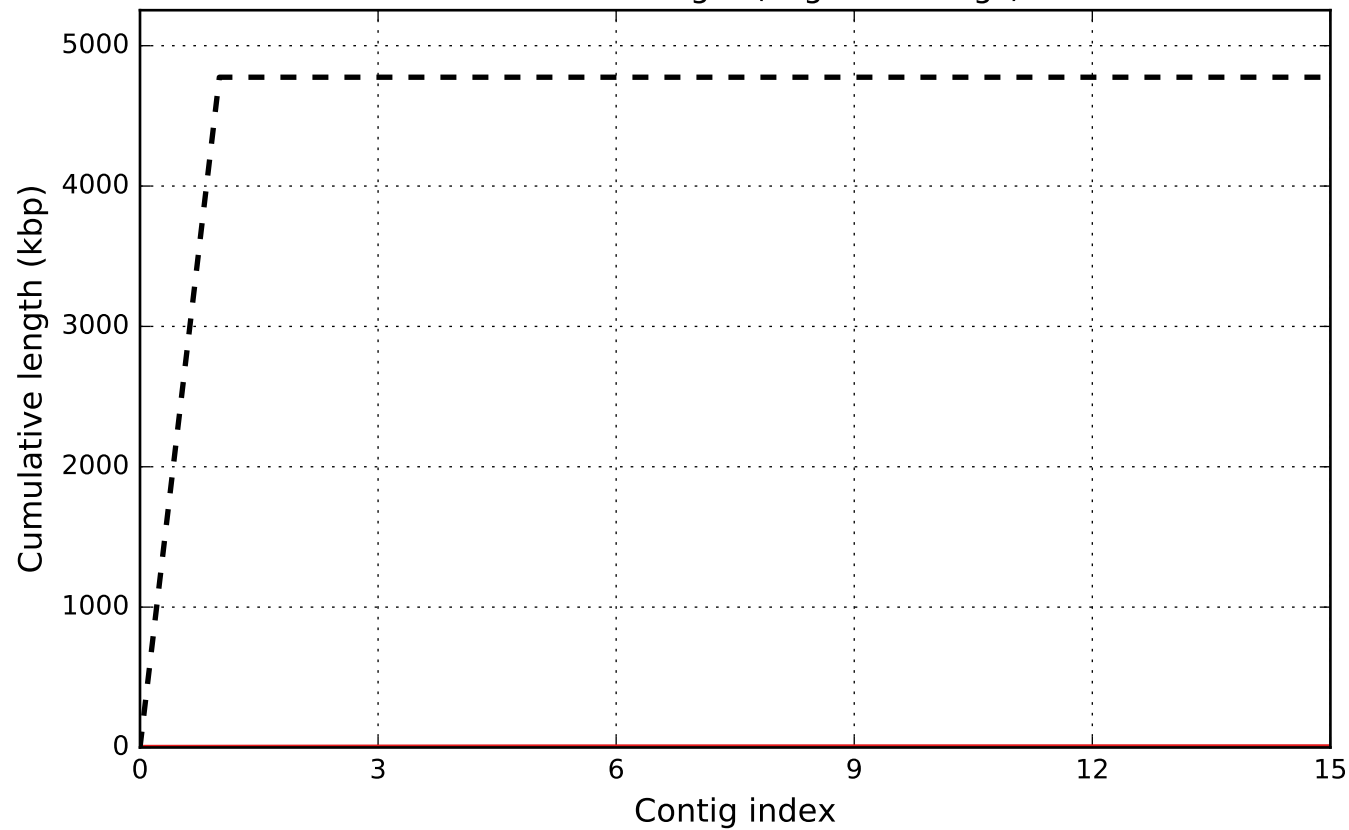




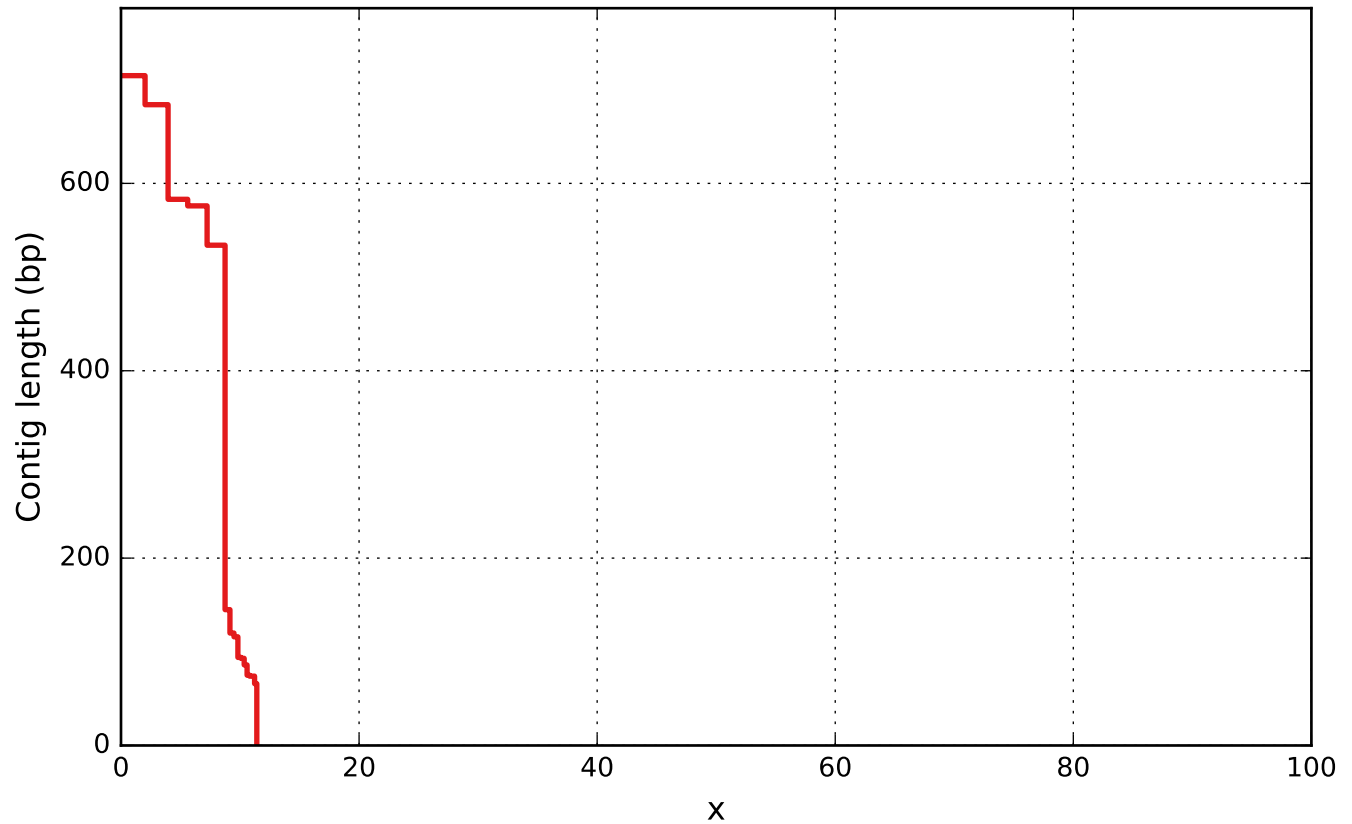
FRCurve (misassemblies)



Cumulative length (aligned contigs)

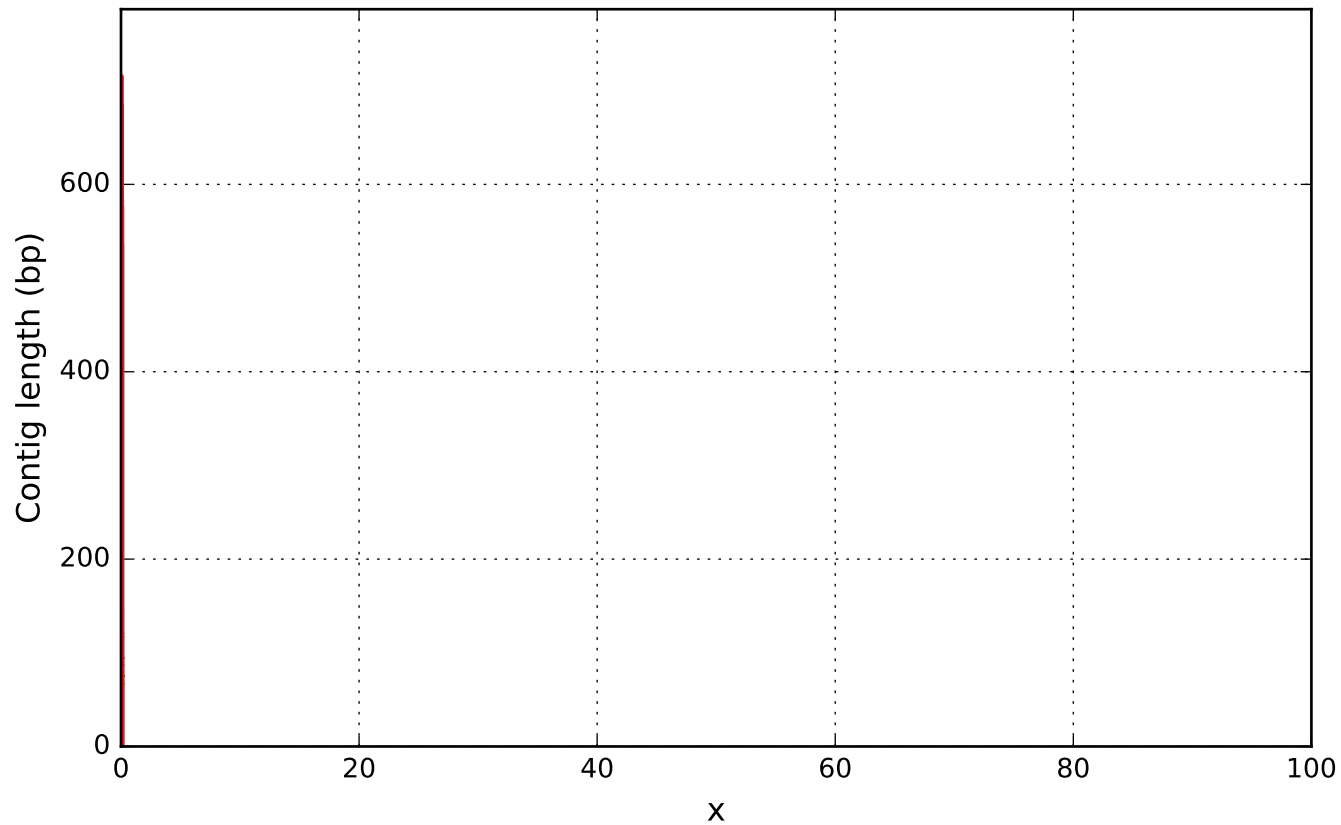


NAx



— final.contigs

NGAx



— final.contigs