

## Report

	final.contigs
# contigs ( $\geq 1000$ bp)	5
# contigs ( $\geq 5000$ bp)	2
# contigs ( $\geq 10000$ bp)	1
# contigs ( $\geq 25000$ bp)	1
# contigs ( $\geq 50000$ bp)	0
Total length ( $\geq 1000$ bp)	52633
Total length ( $\geq 5000$ bp)	46083
Total length ( $\geq 10000$ bp)	40848
Total length ( $\geq 25000$ bp)	40848
Total length ( $\geq 50000$ bp)	0
# contigs	7
Largest contig	40848
Total length	53938
Reference length	4235068
GC (%)	48.31
Reference GC (%)	68.44
N50	40848
N75	40848
L50	1
L75	1
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 5 part
Unaligned length	51878
Genome fraction (%)	0.016
Duplication ratio	3.116
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1059.00
# indels per 100 kbp	605.14
Largest alignment	277
Total aligned length	914
NGA50	-

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).

## Misassemblies report

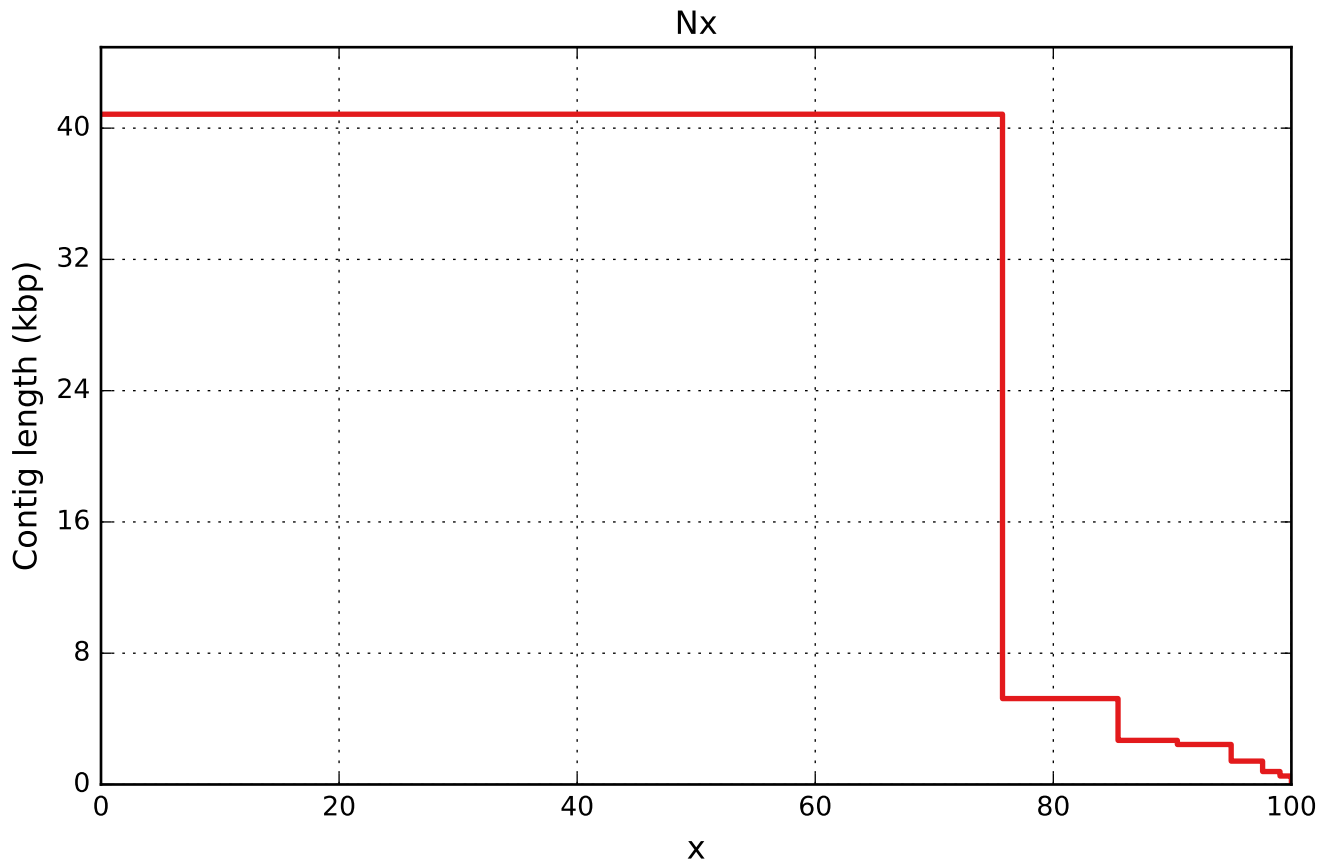
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	7
# indels	4
# indels (<= 5 bp)	4
# indels (> 5 bp)	0
Indels length	6

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

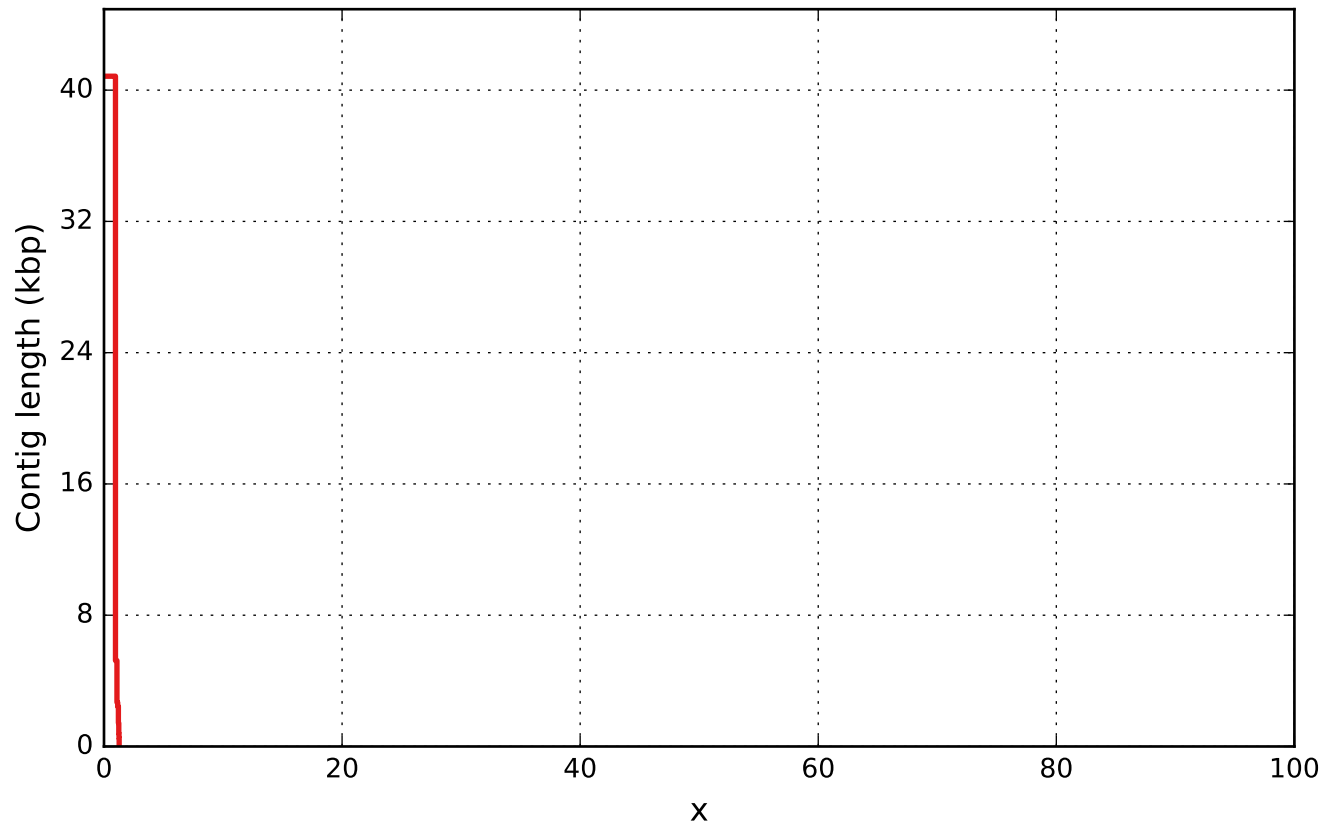
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	5
Partially unaligned length	51878
# N's	0

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).

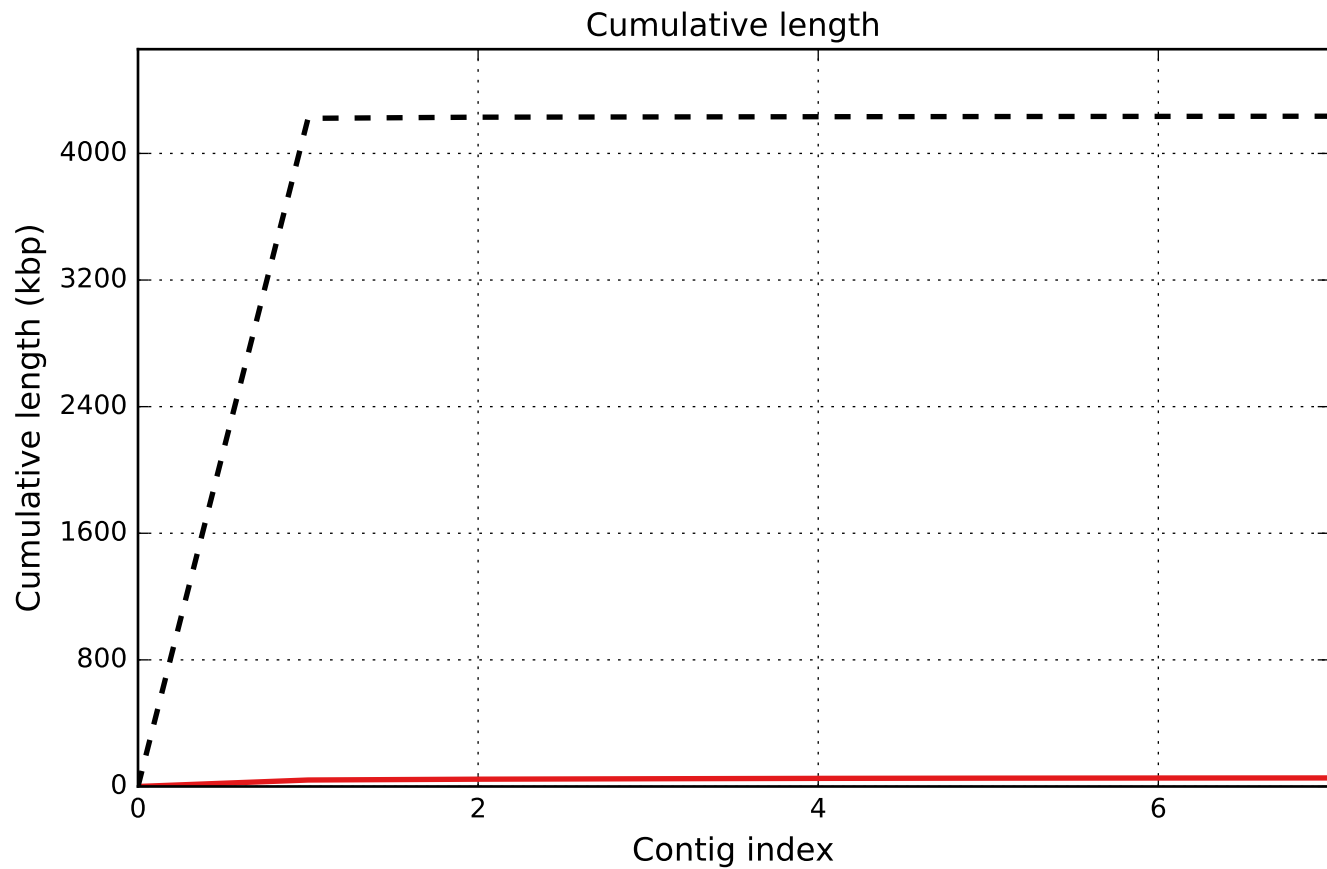


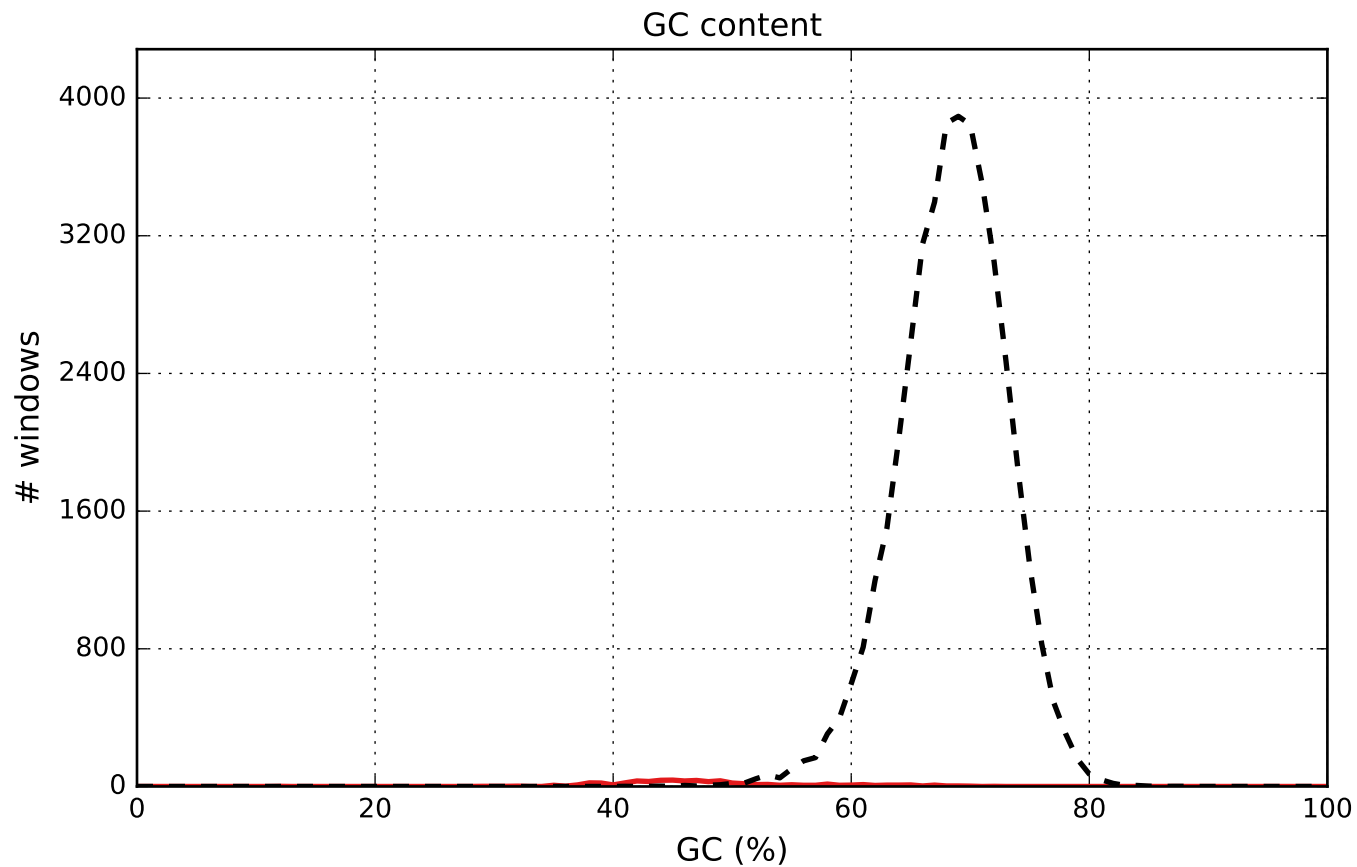
— final.contigs

NGx

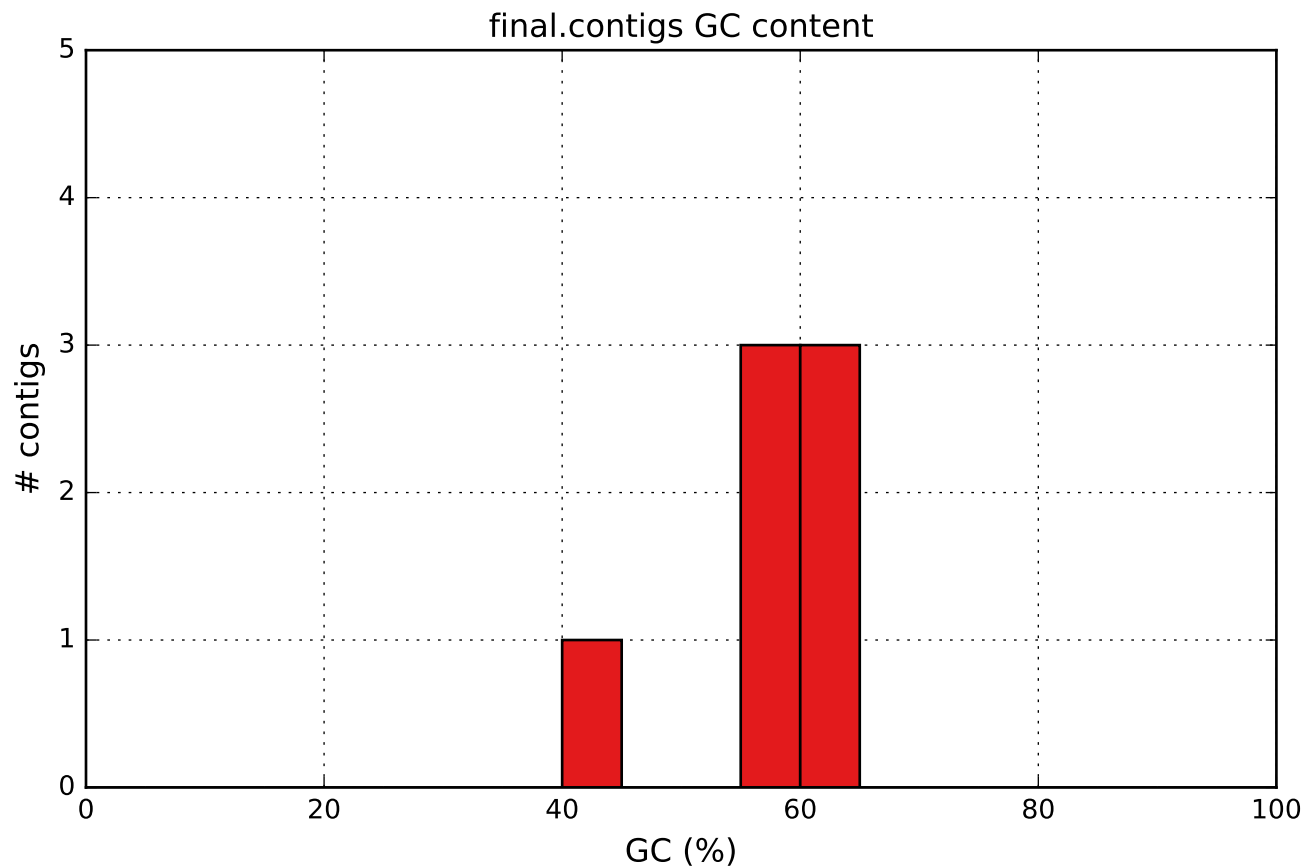


— final.contigs





— final.contigs    - - Reference

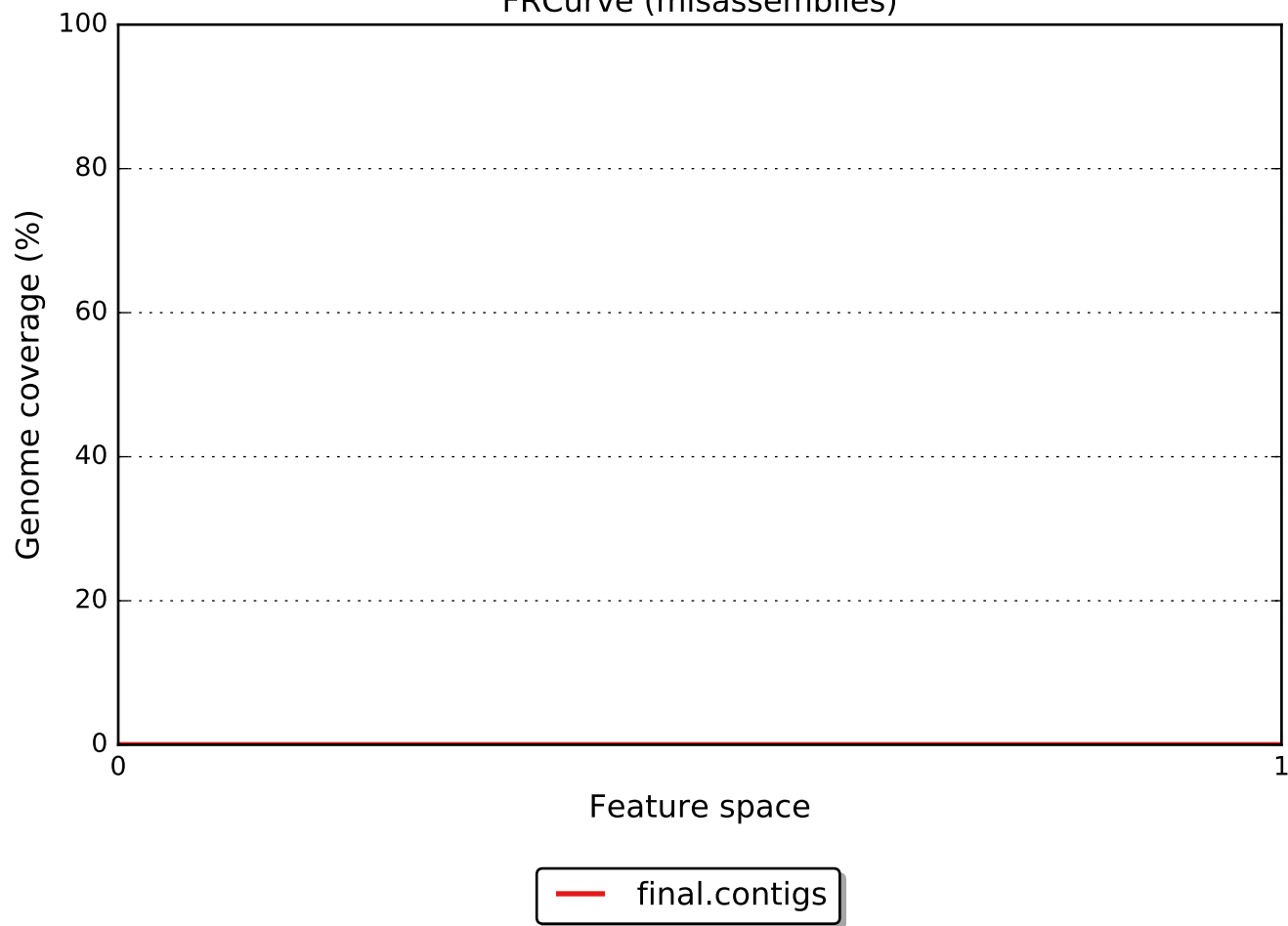


final.contigs

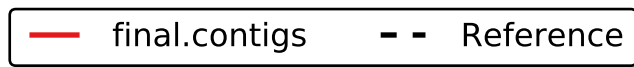
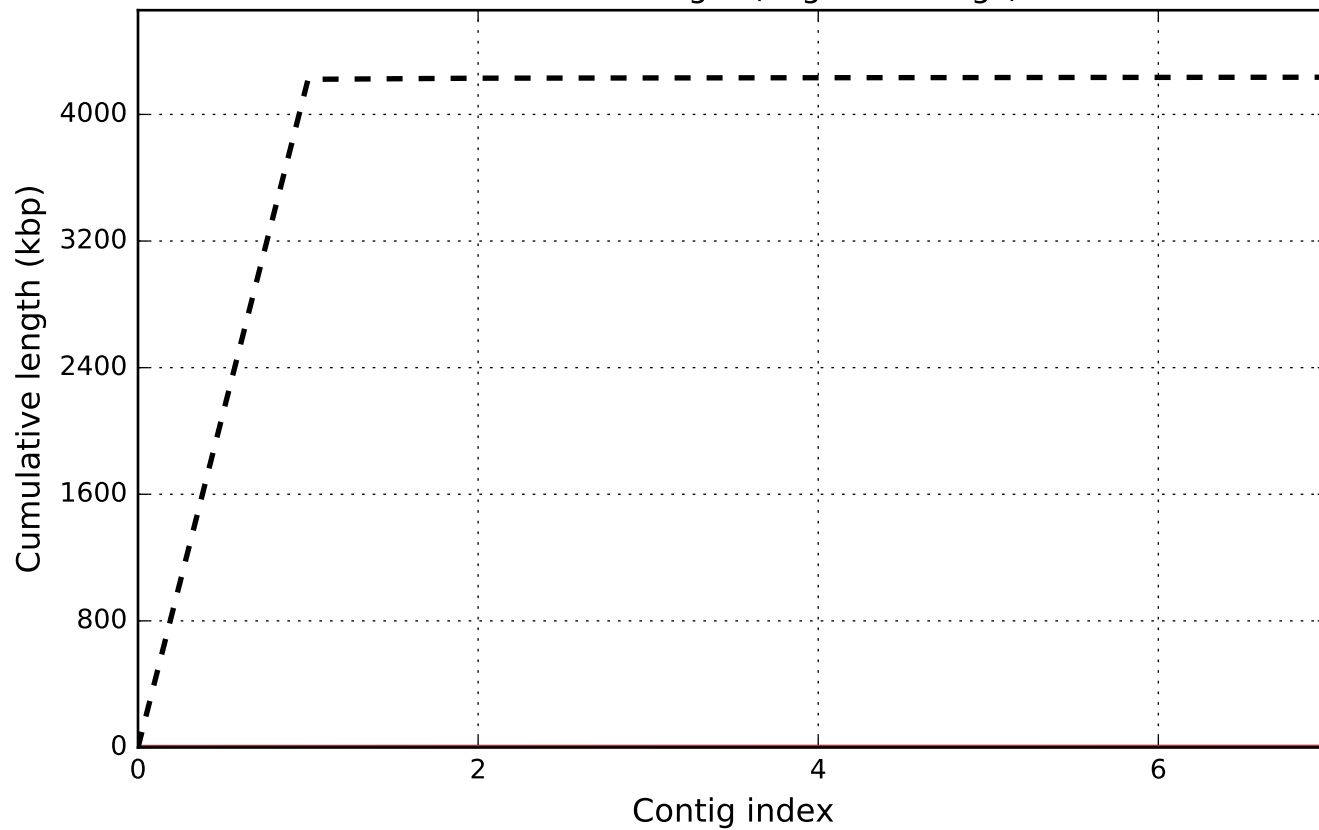




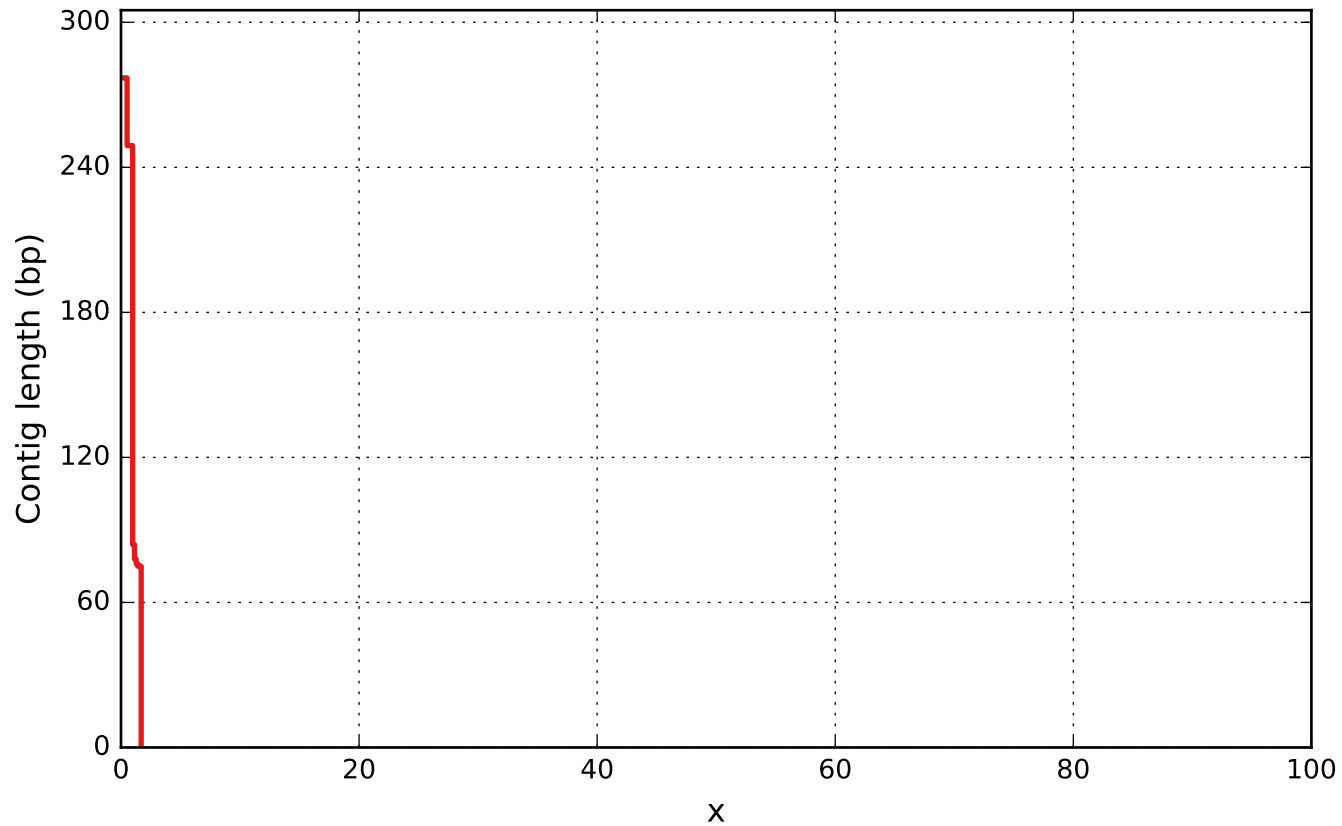
FRCurve (misassemblies)



Cumulative length (aligned contigs)

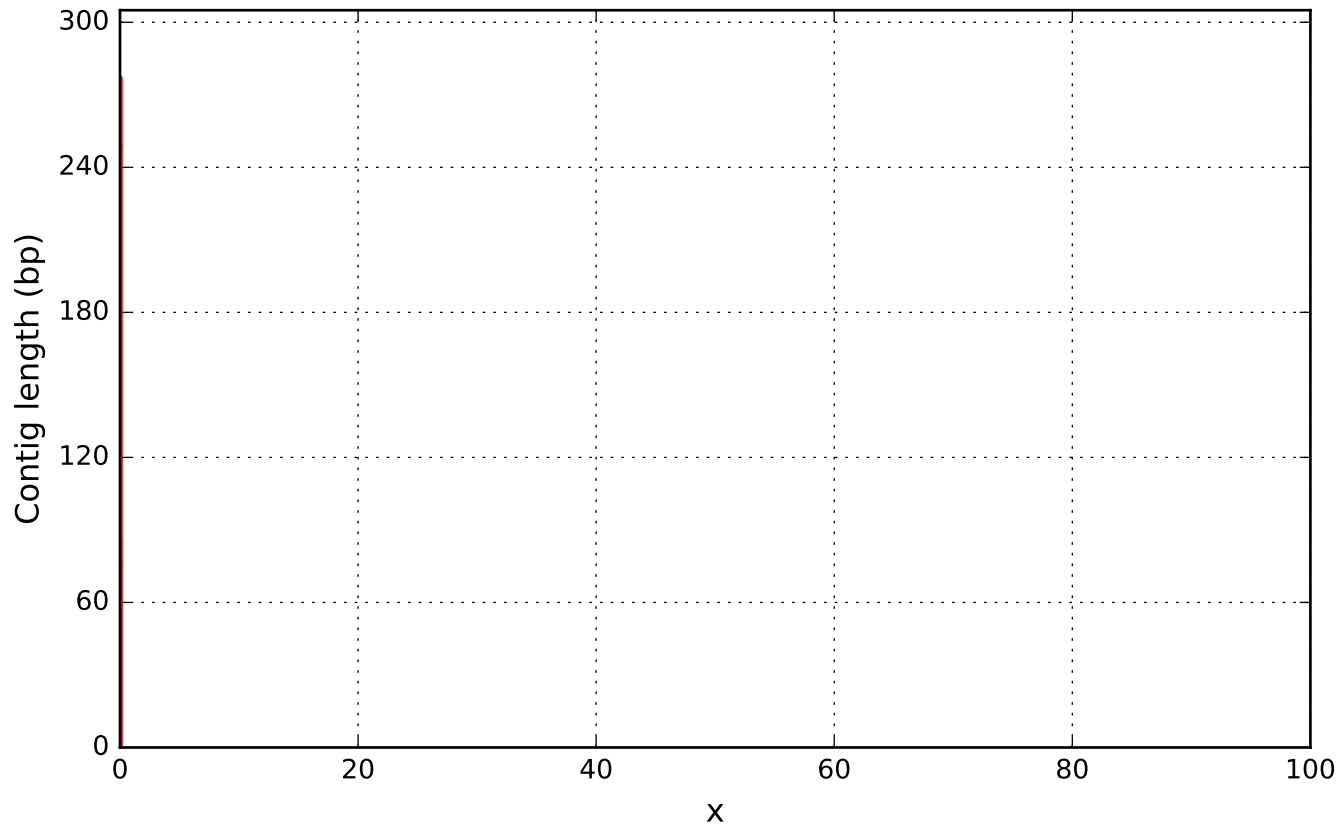


NAx



— final.contigs

NGAx



— final.contigs