

# Report

	final.contigs
# contigs ( $\geq 1000$ bp)	8
# contigs ( $\geq 5000$ bp)	2
# contigs ( $\geq 10000$ bp)	0
# contigs ( $\geq 25000$ bp)	0
# contigs ( $\geq 50000$ bp)	0
Total length ( $\geq 1000$ bp)	30316
Total length ( $\geq 5000$ bp)	15061
Total length ( $\geq 10000$ bp)	0
Total length ( $\geq 25000$ bp)	0
Total length ( $\geq 50000$ 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
# structural variations	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  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Misassemblies report

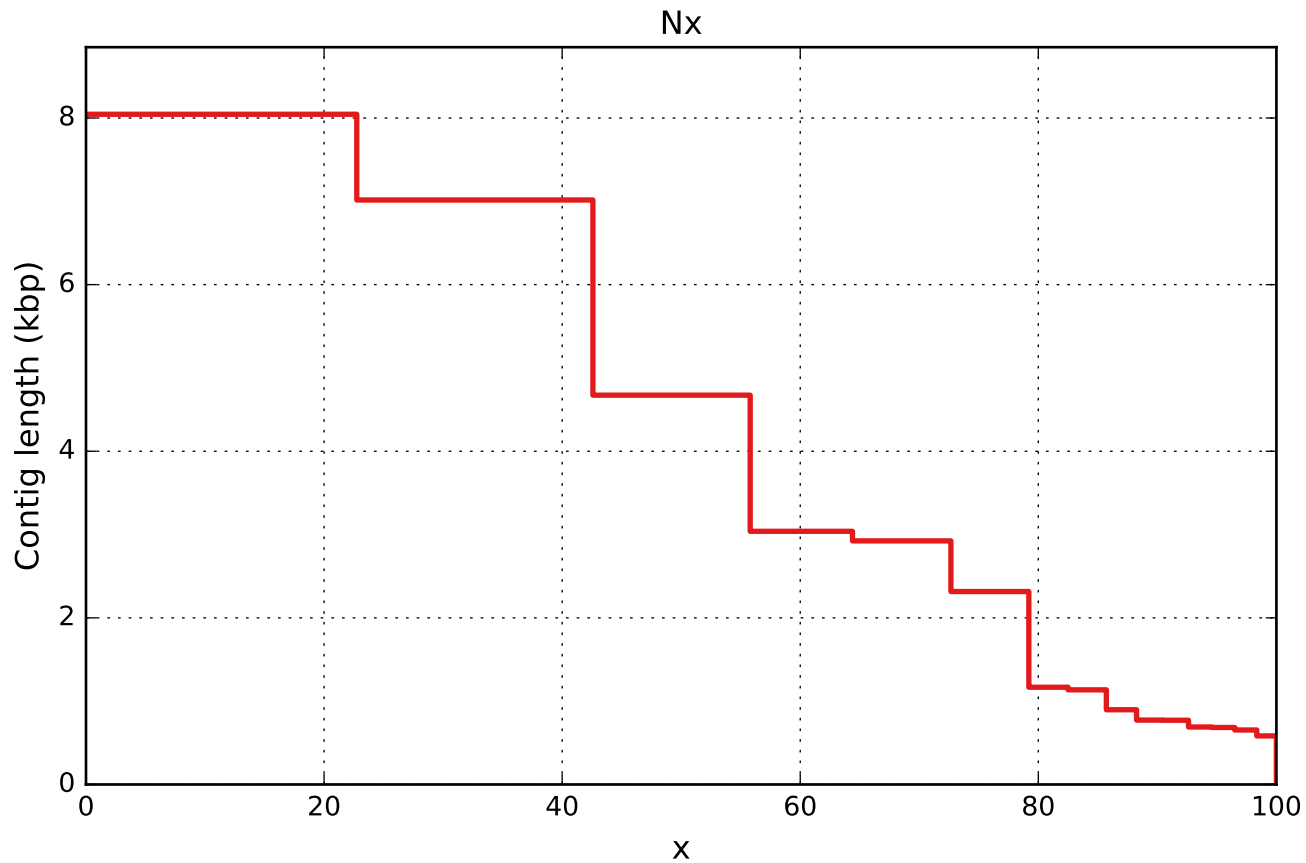
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# structural variations	0
# unaligned mis. contigs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

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## Unaligned report

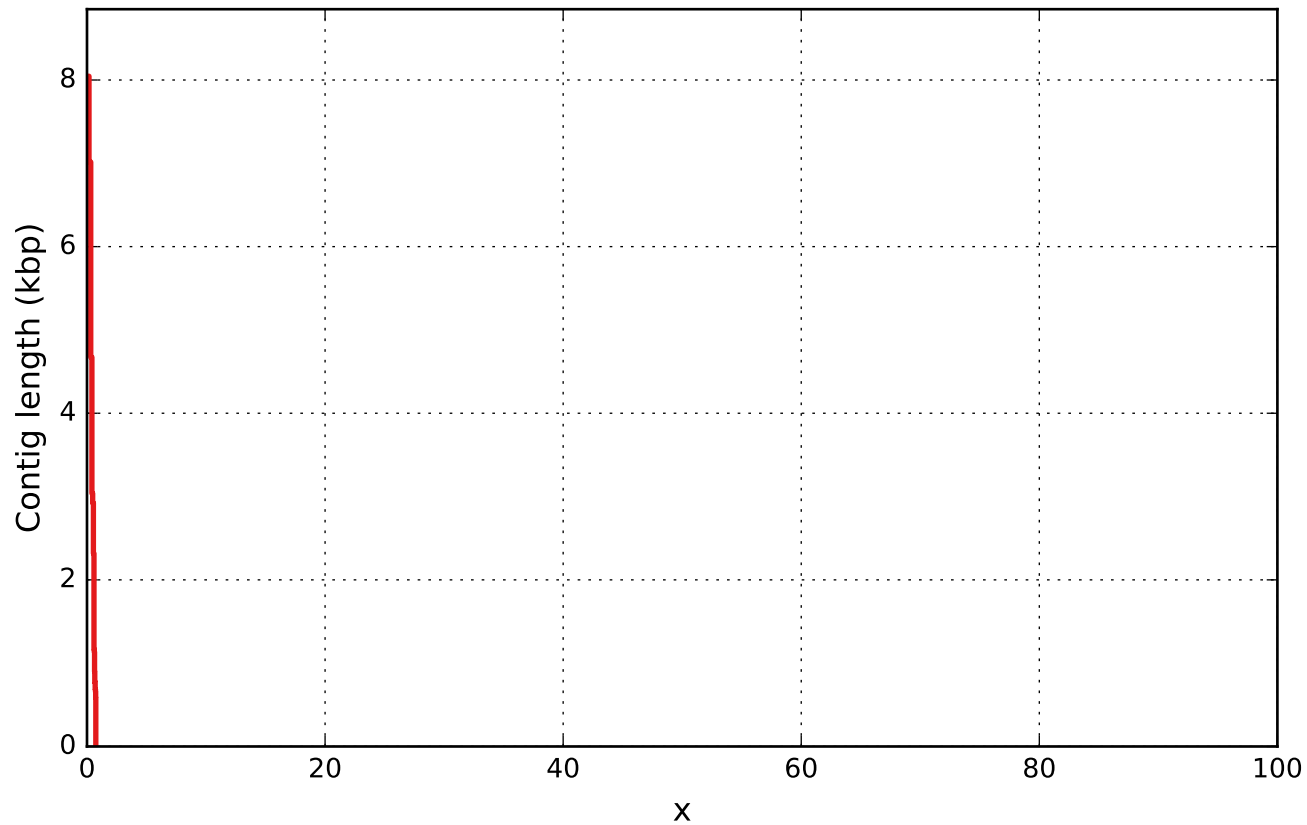
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	8
Partially unaligned length	29534
# N's	0

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).

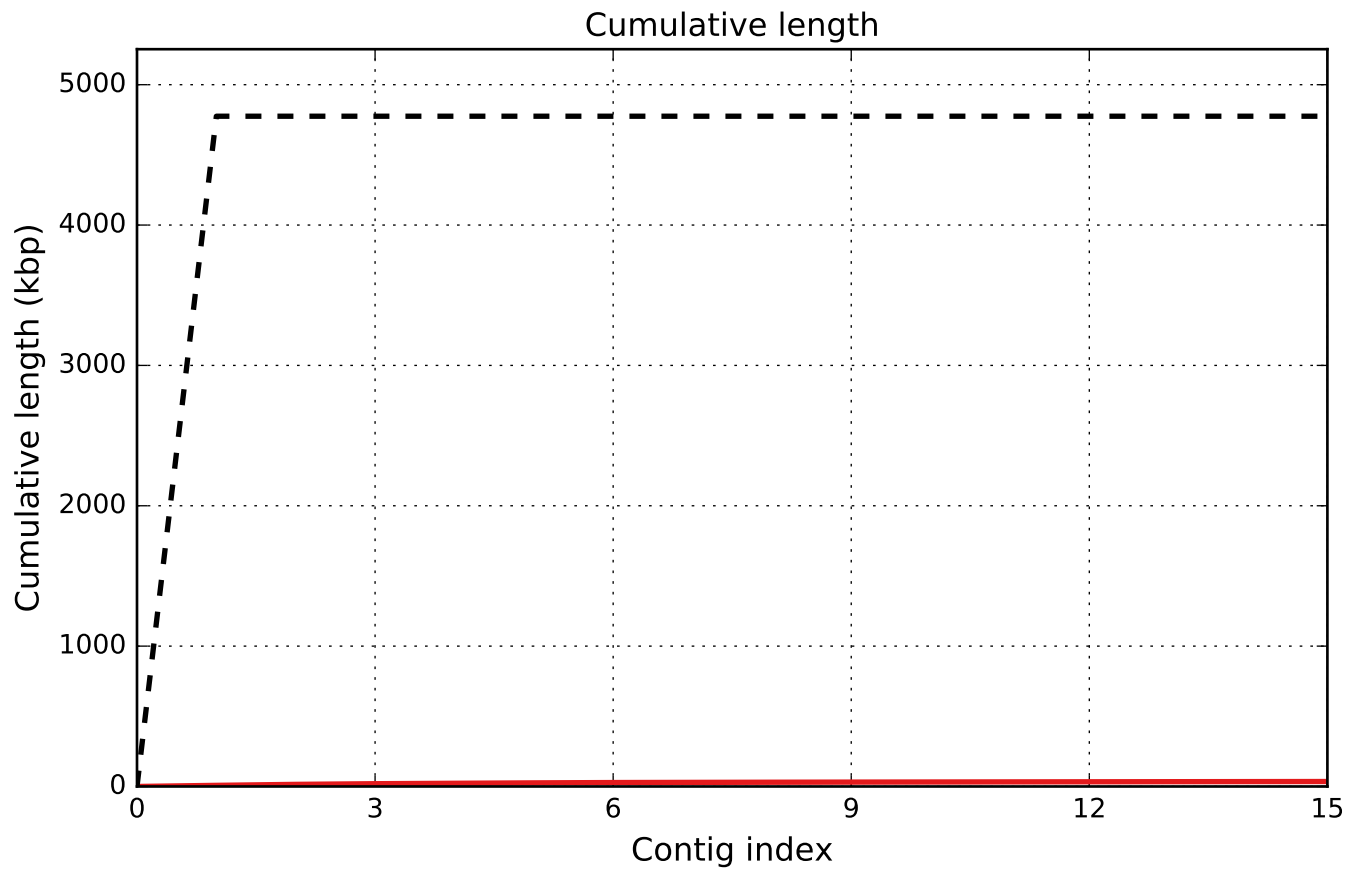


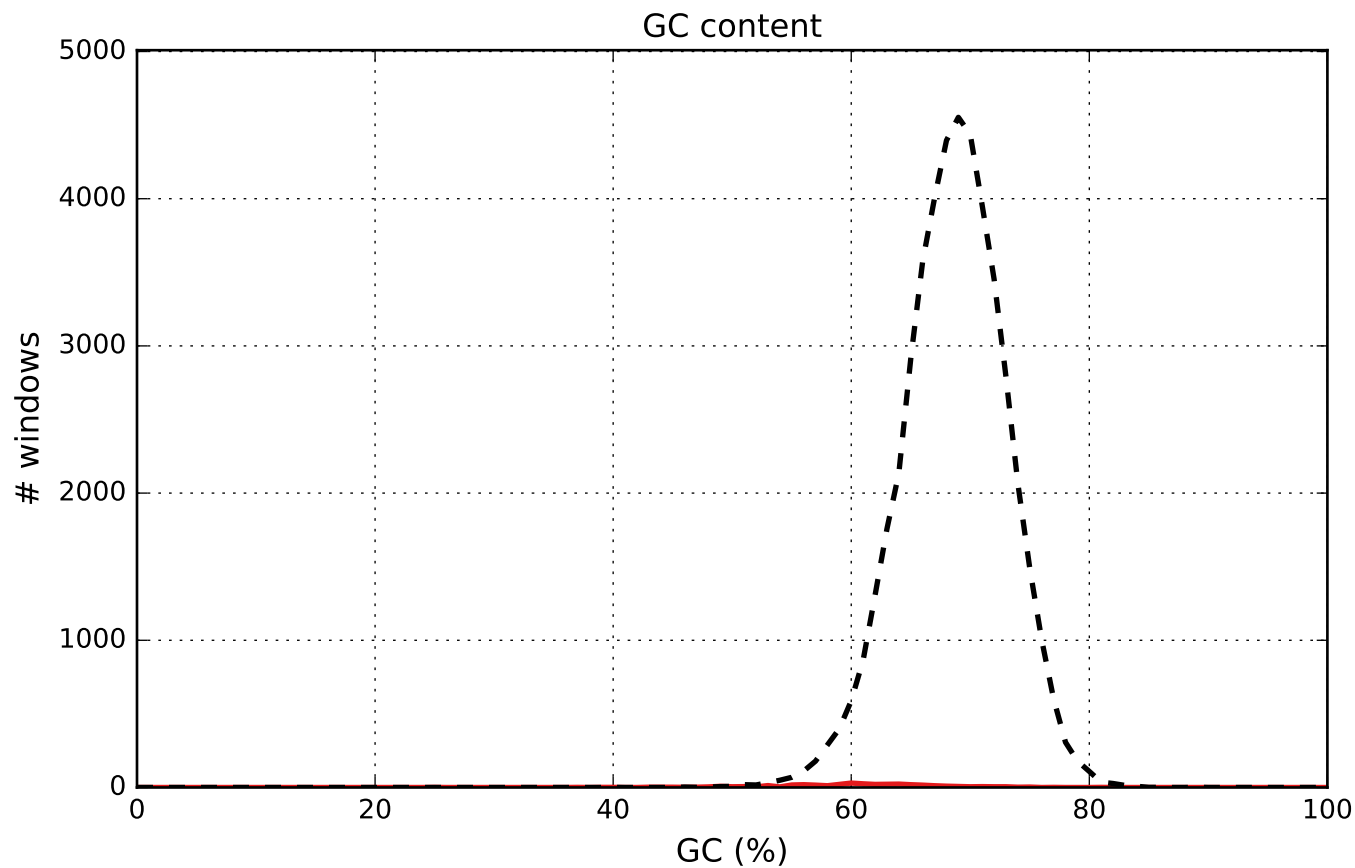
— final.contigs

NGx

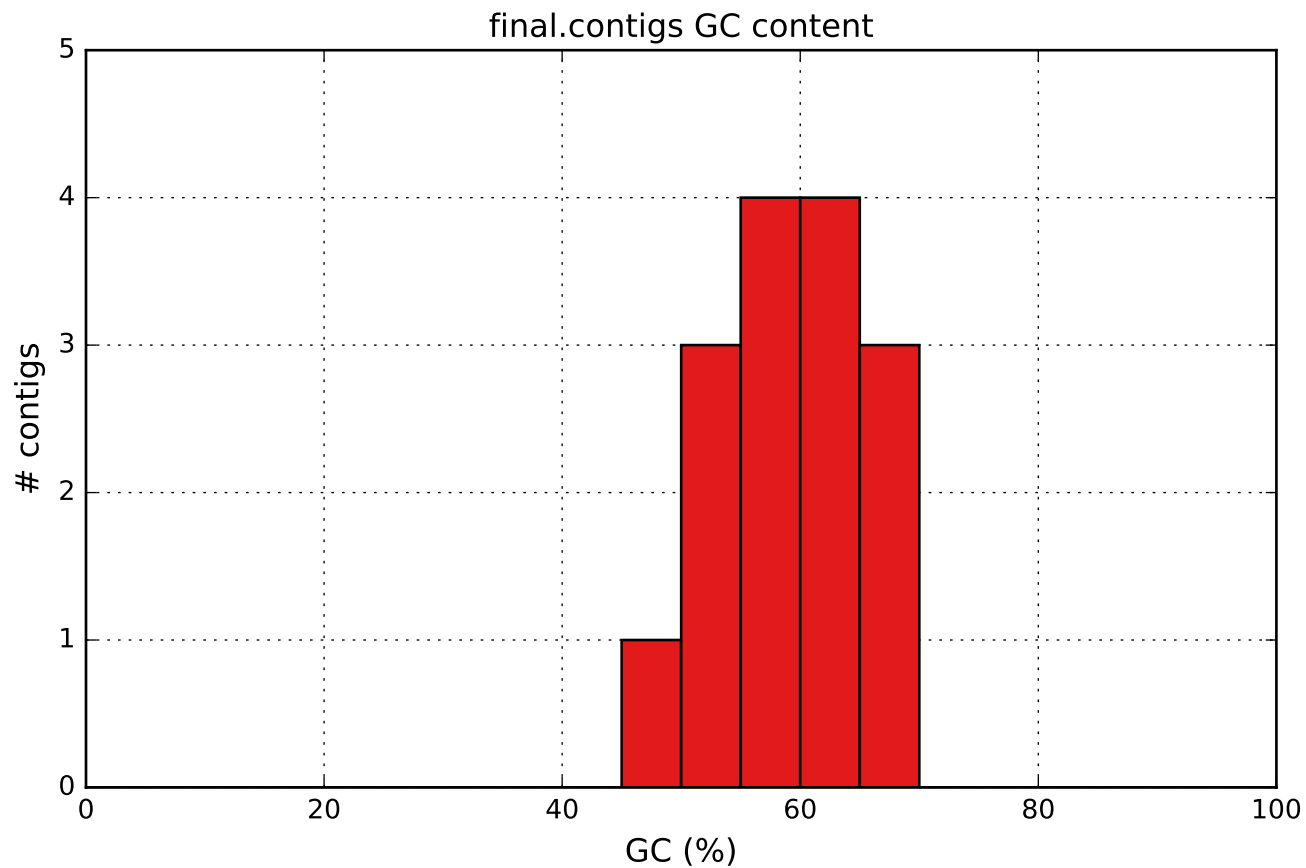


— final.contigs





— final.contigs    - - Reference

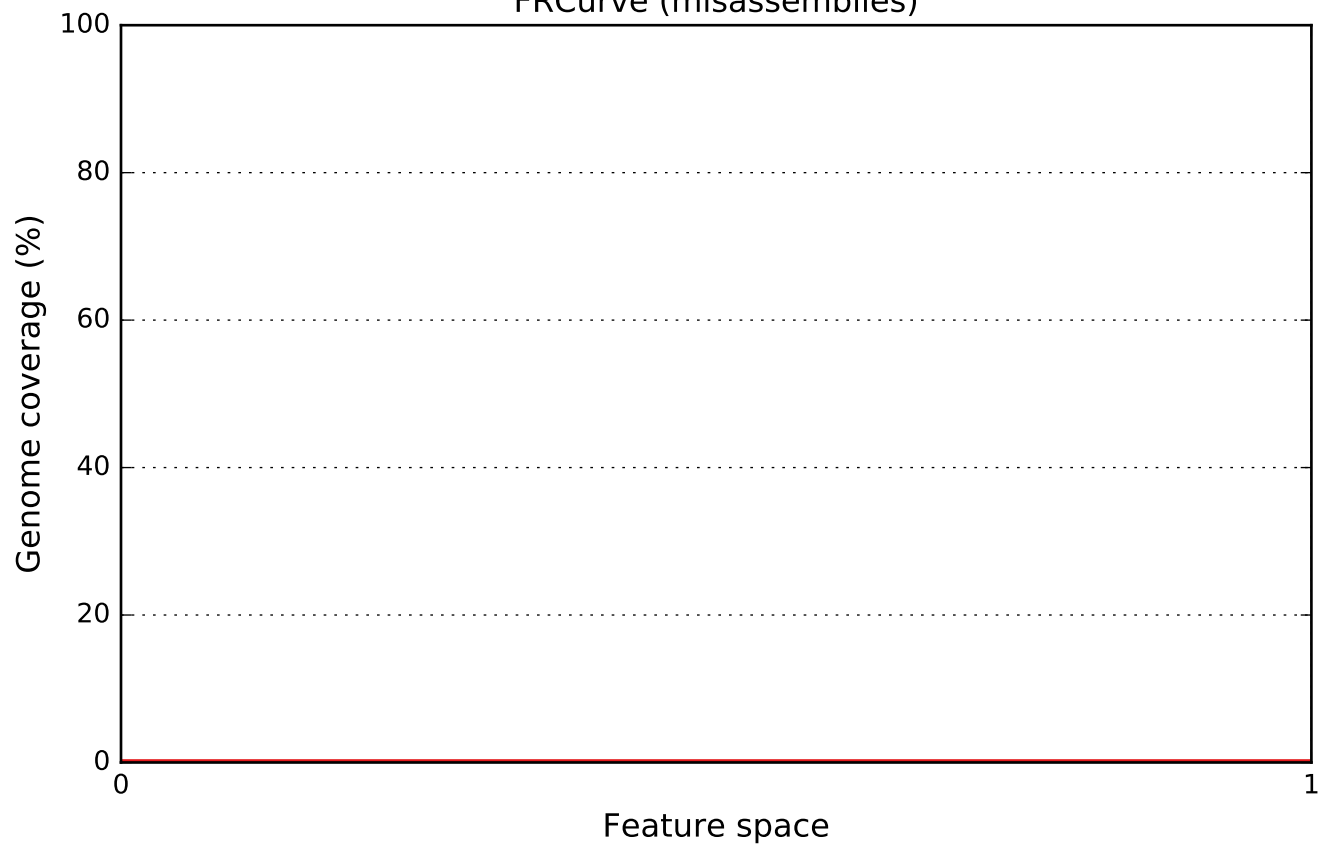


final.contigs



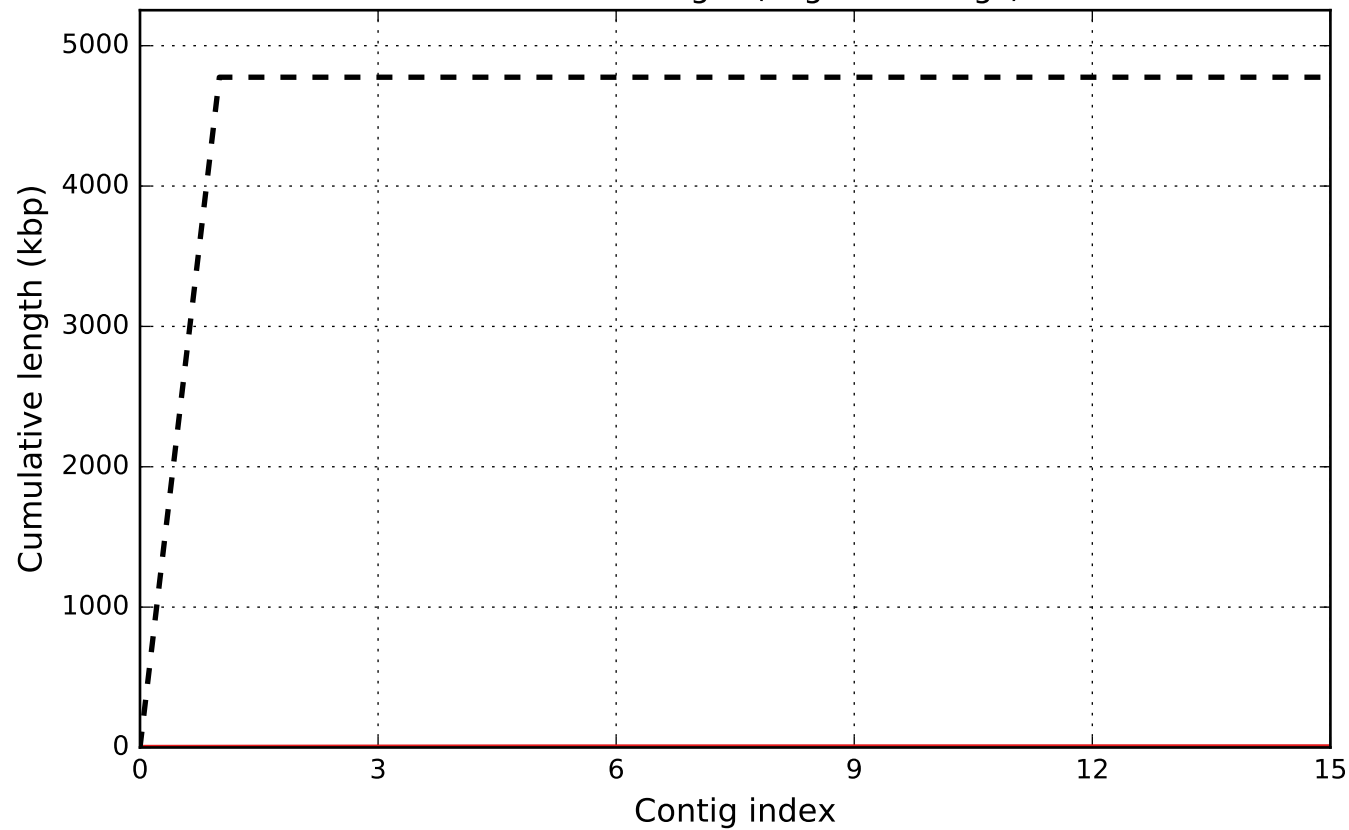


FRCurve (misassemblies)

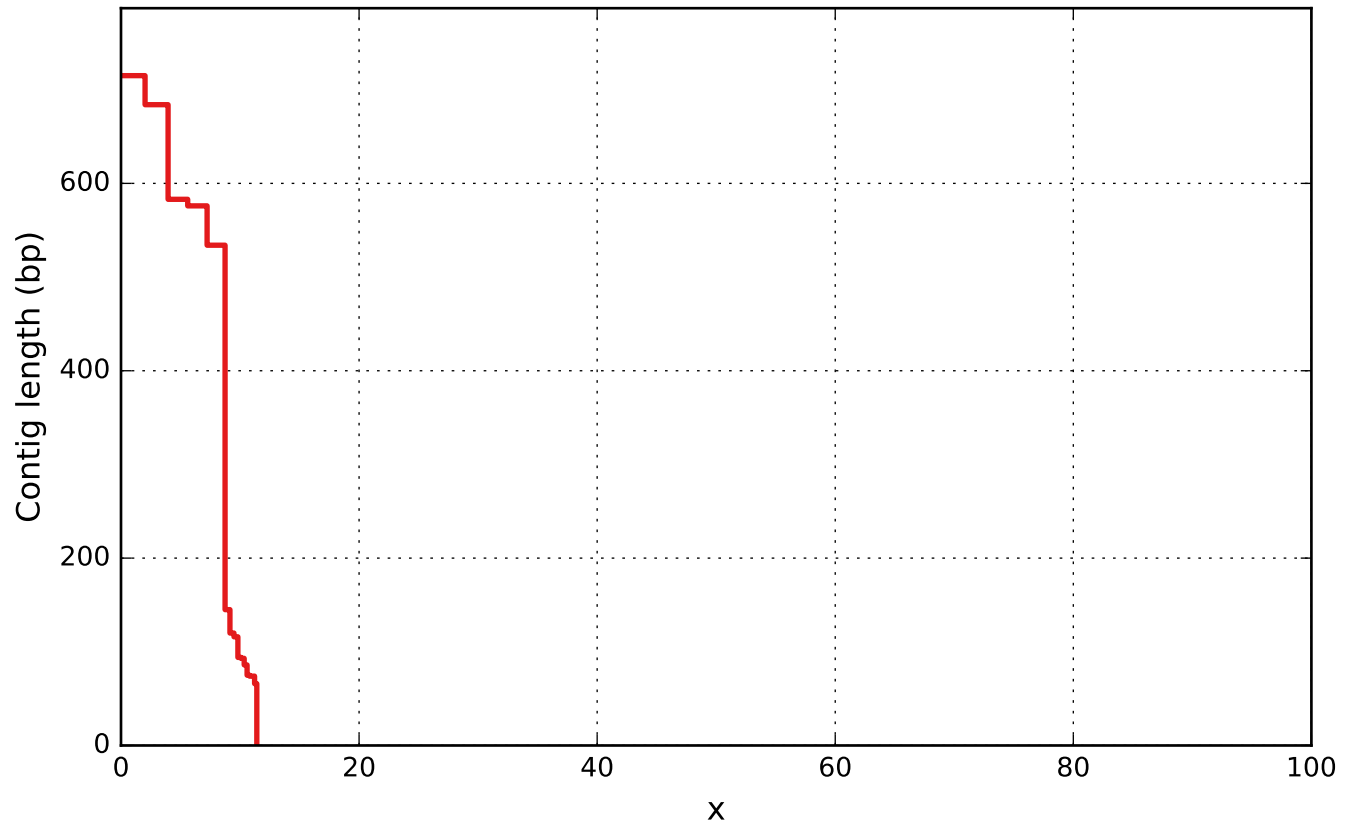


— final.contigs

Cumulative length (aligned contigs)

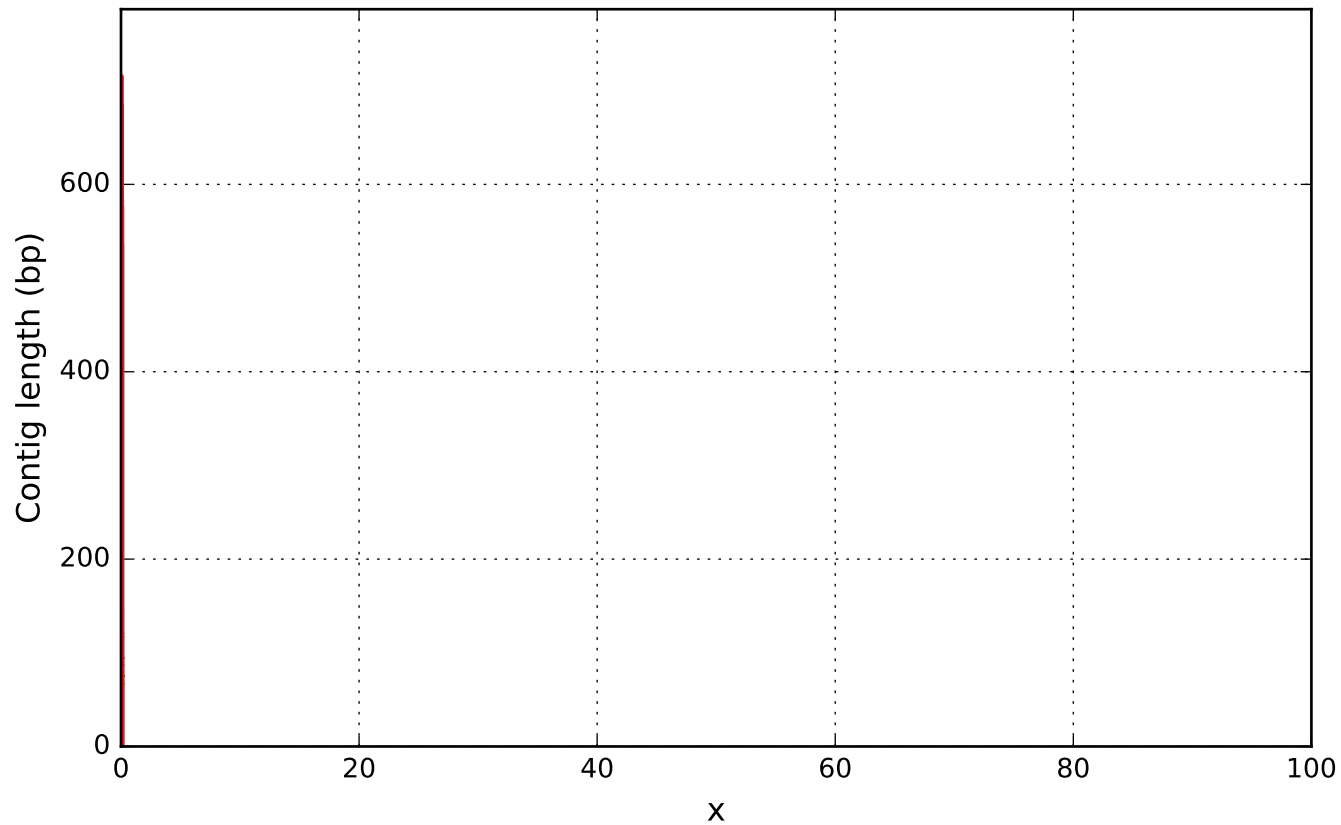


NAx



— final.contigs

NGAx



— final.contigs