

# Report

	final.contigs
# contigs ( $\geq 1000$ bp)	8
# contigs ( $\geq 5000$ bp)	3
# contigs ( $\geq 10000$ bp)	1
# contigs ( $\geq 25000$ bp)	0
# contigs ( $\geq 50000$ bp)	0
Total length ( $\geq 1000$ bp)	38847
Total length ( $\geq 5000$ bp)	29924
Total length ( $\geq 10000$ bp)	12904
Total length ( $\geq 25000$ bp)	0
Total length ( $\geq 50000$ bp)	0
# contigs	19
Largest contig	12904
Total length	46733
Reference length	3261541
GC (%)	54.46
Reference GC (%)	56.74
N50	8486
N75	1582
L50	3
L75	6
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# structural variations	0
# unaligned mis. contigs	1
# unaligned contigs	0 + 15 part
Unaligned length	42305
Genome fraction (%)	0.102
Duplication ratio	1.331
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2736.02
# indels per 100 kbp	150.33
Largest alignment	721
Total aligned length	3737
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

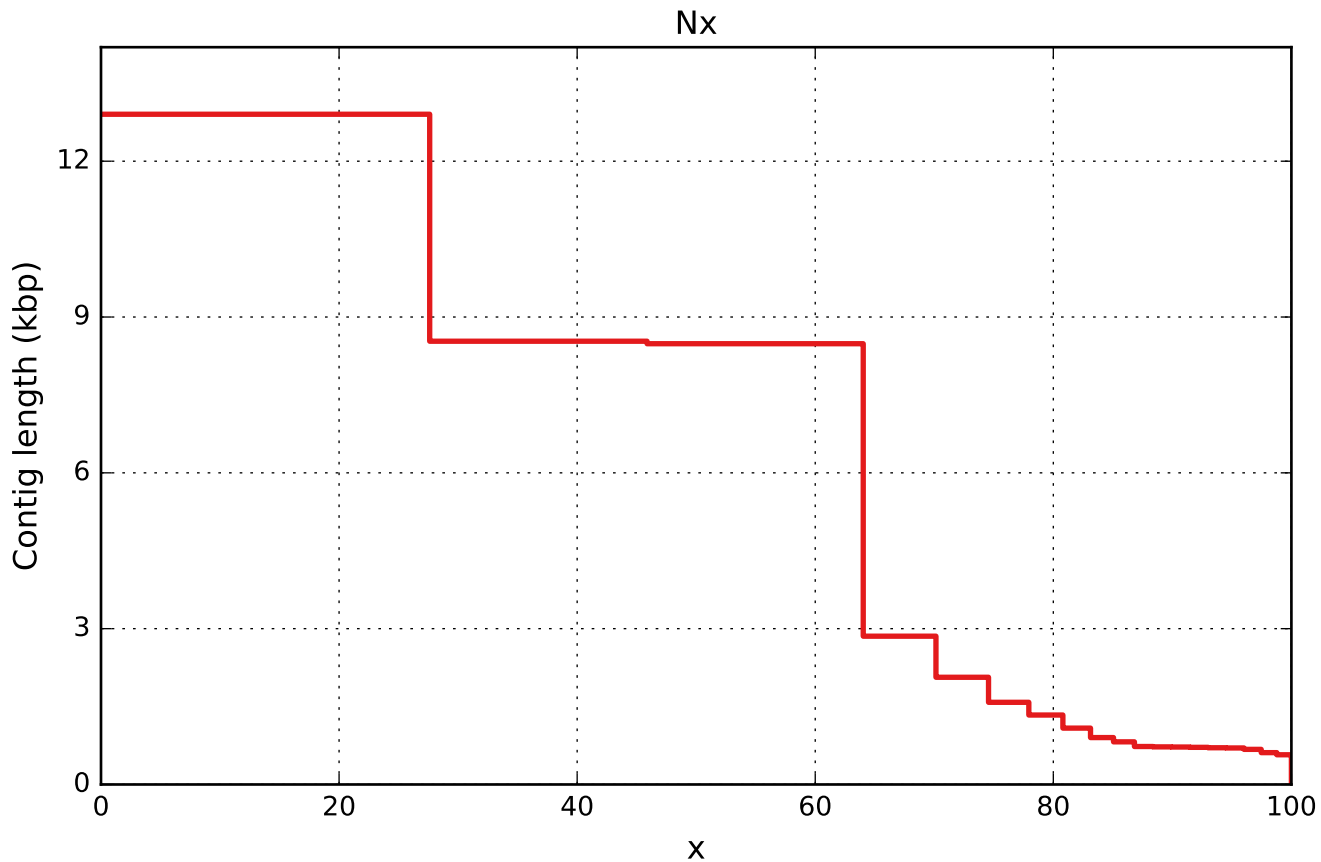
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# structural variations	0
# unaligned mis. contigs	1
# mismatches	91
# indels	5
# indels ( $\leq 5$ bp)	5
# indels ( $> 5$ bp)	0
Indels length	5

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## Unaligned report

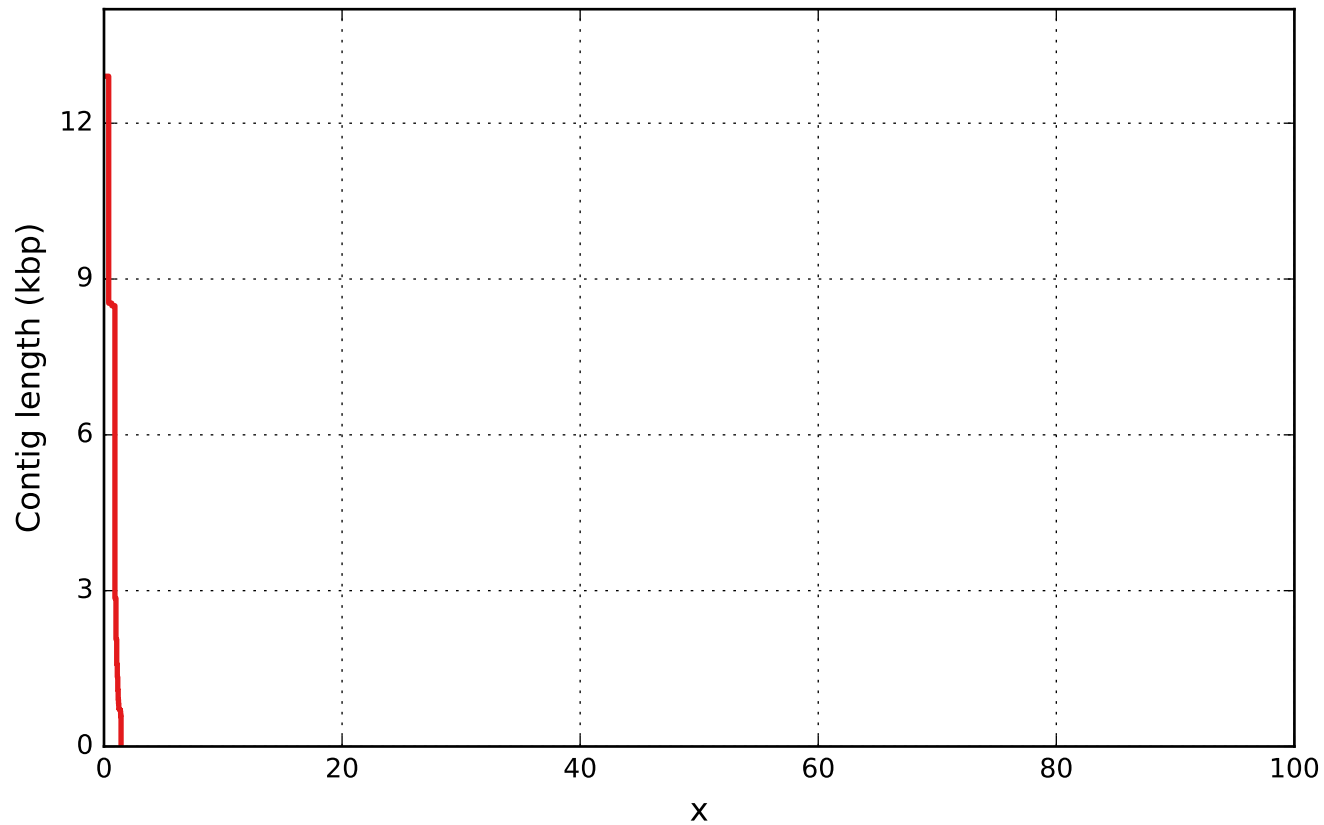
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	15
Partially unaligned length	42305
# N's	0

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).

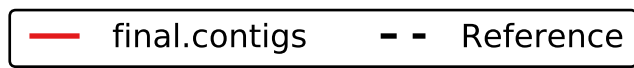
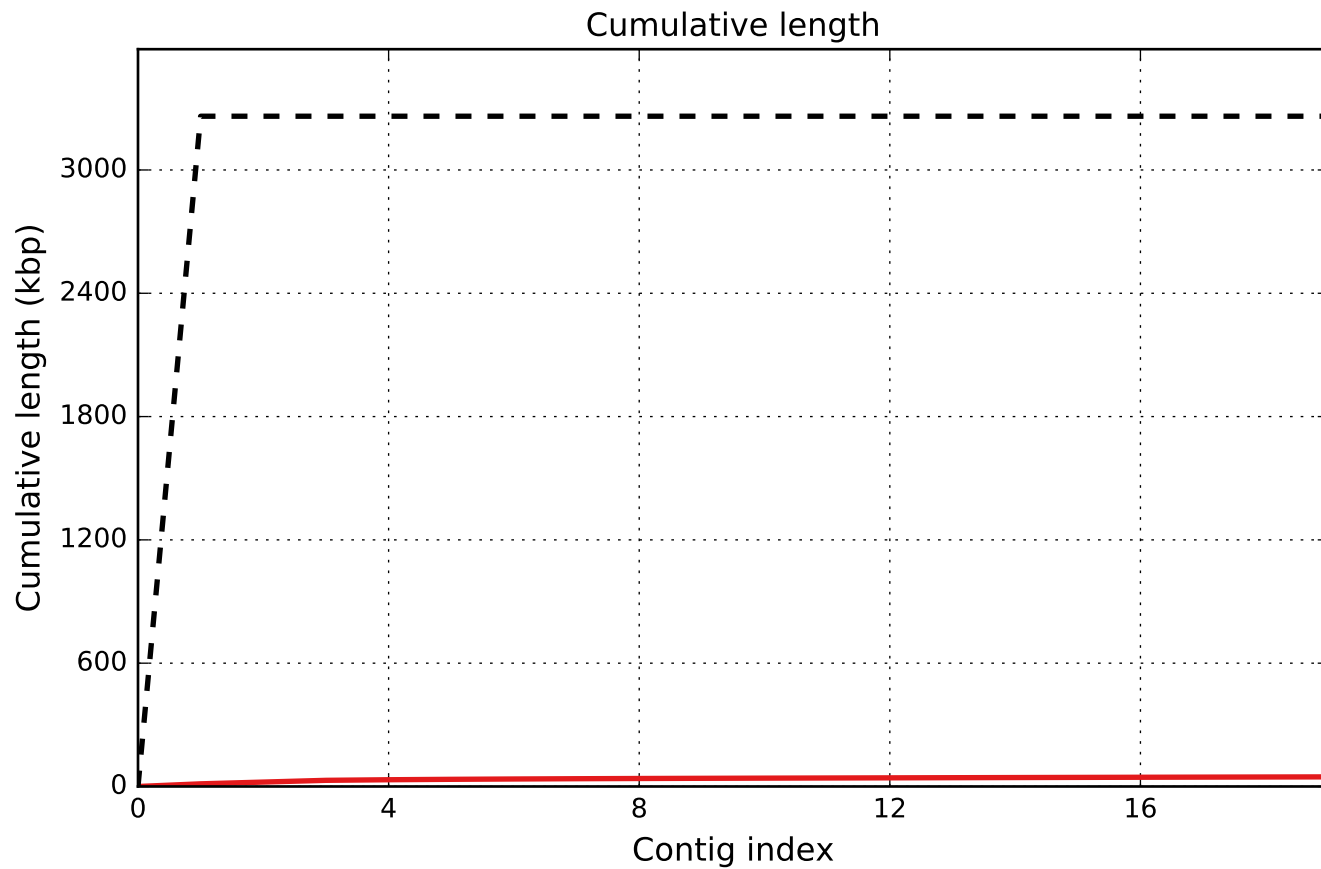


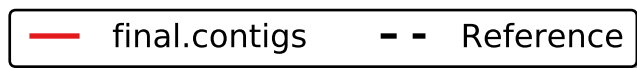
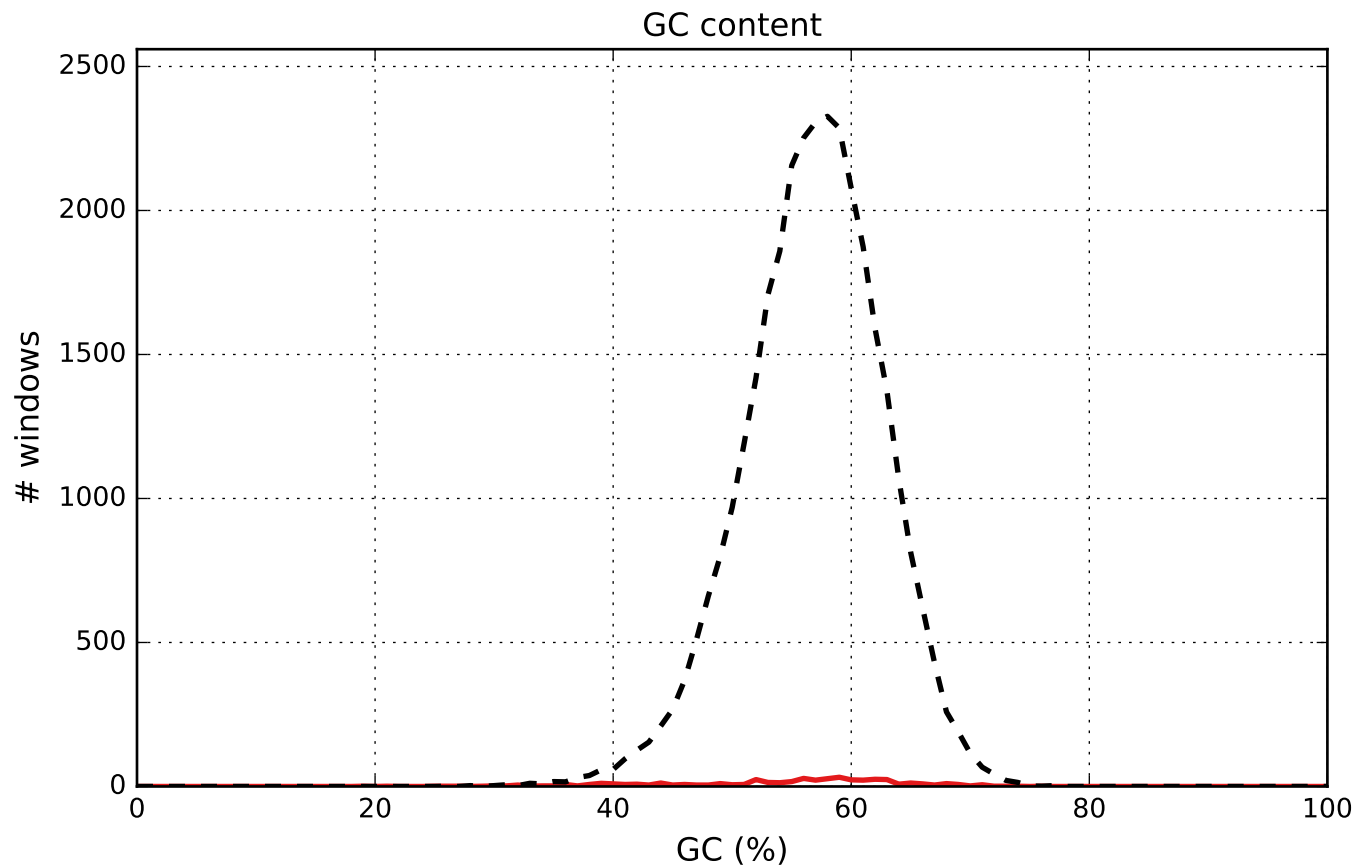
— final.contigs

NGx

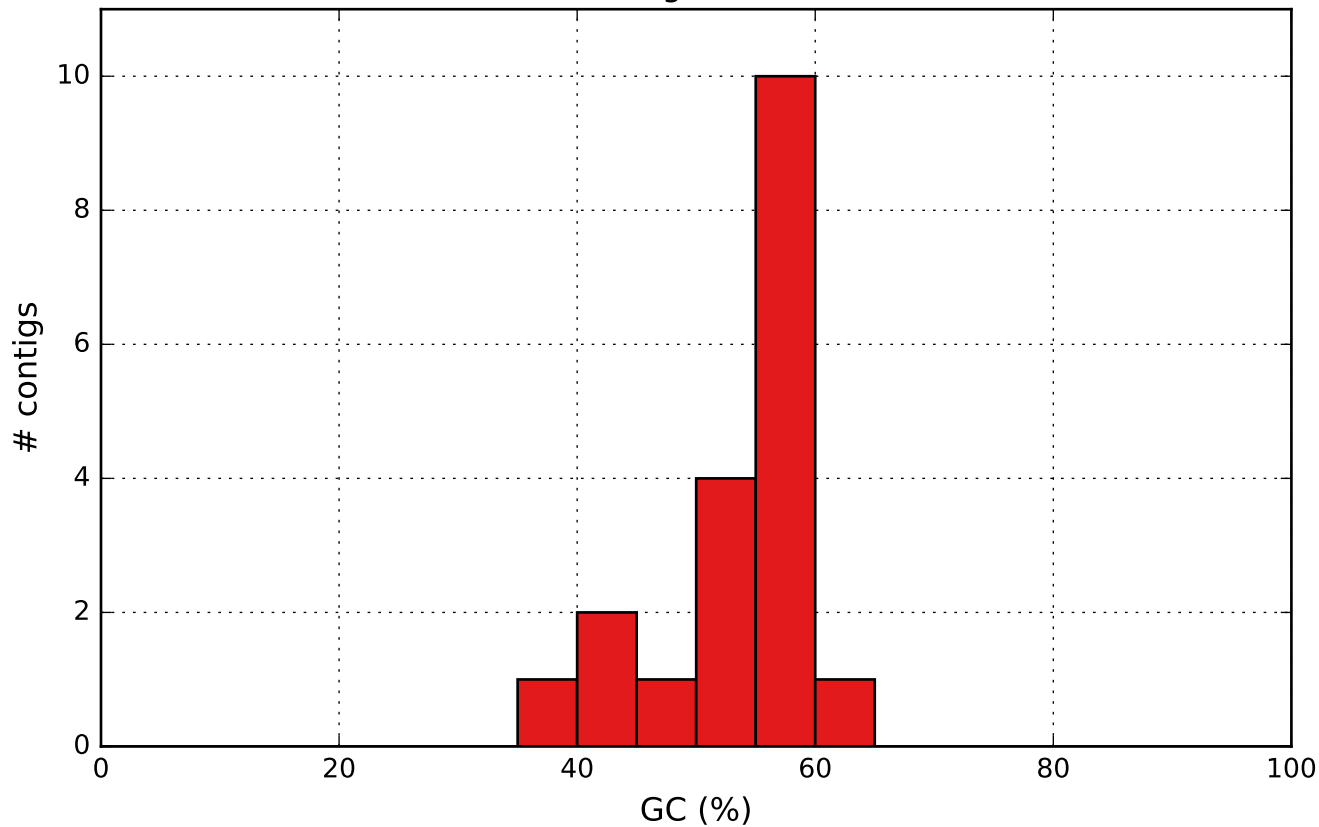


— final.contigs





final.contigs GC content

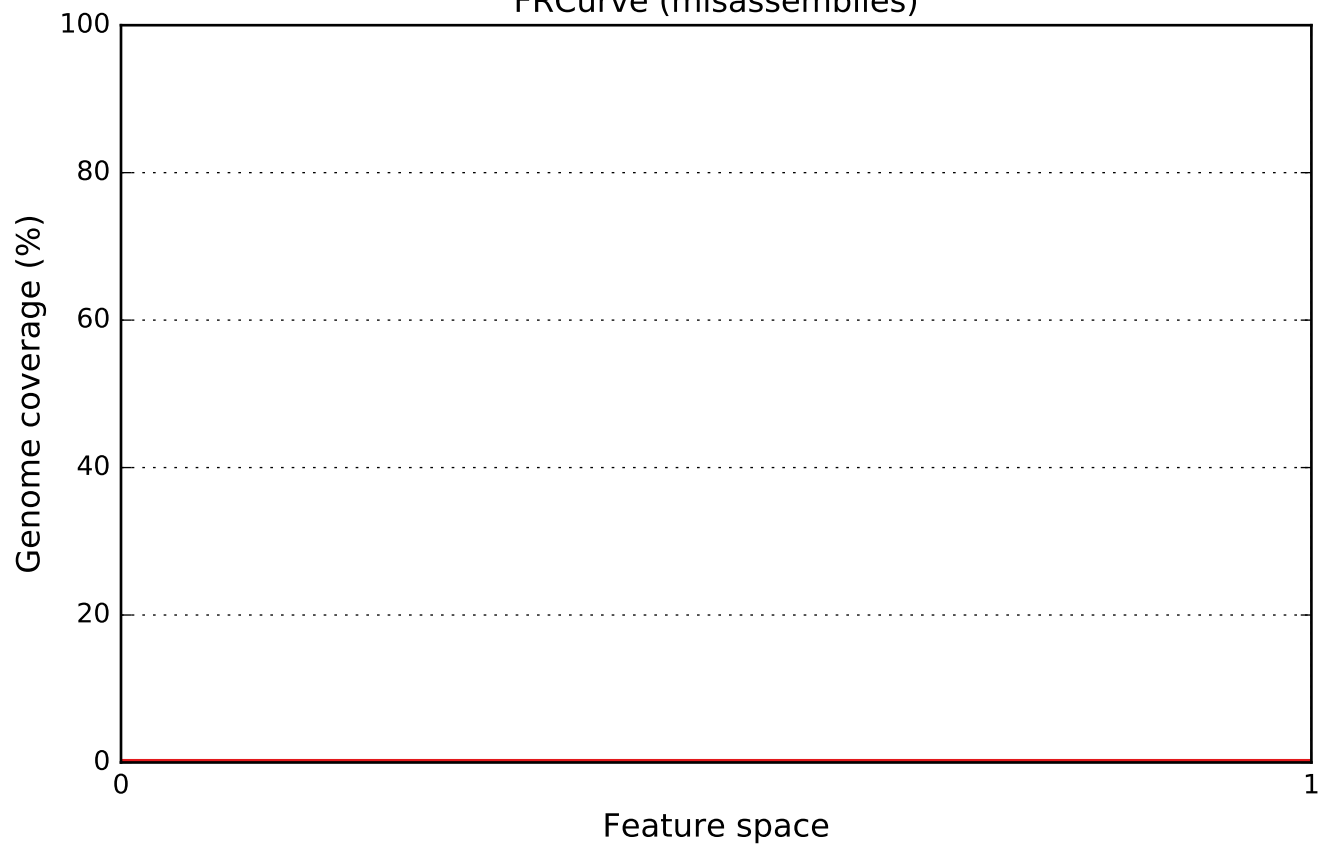


final.contigs



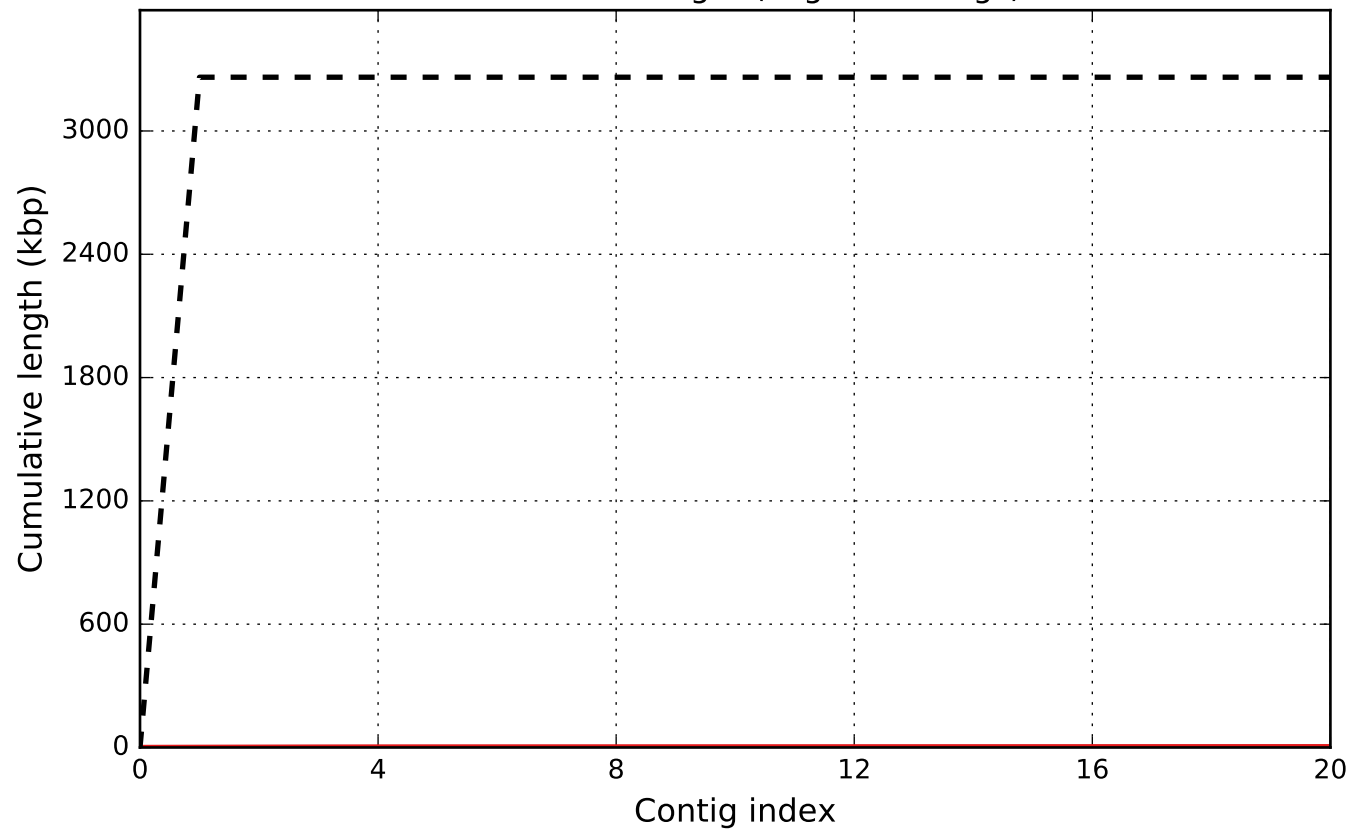


FRCurve (misassemblies)



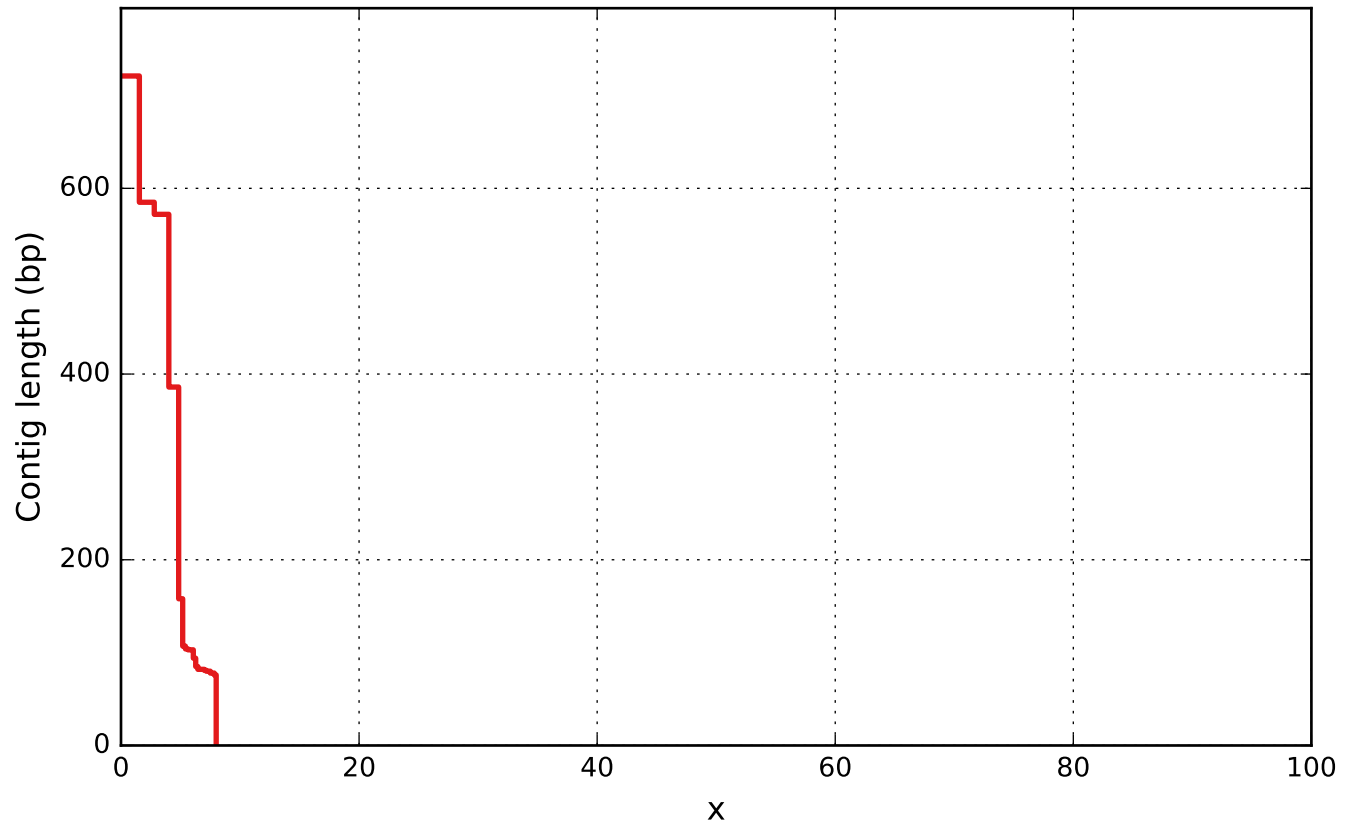
— final.contigs

Cumulative length (aligned contigs)



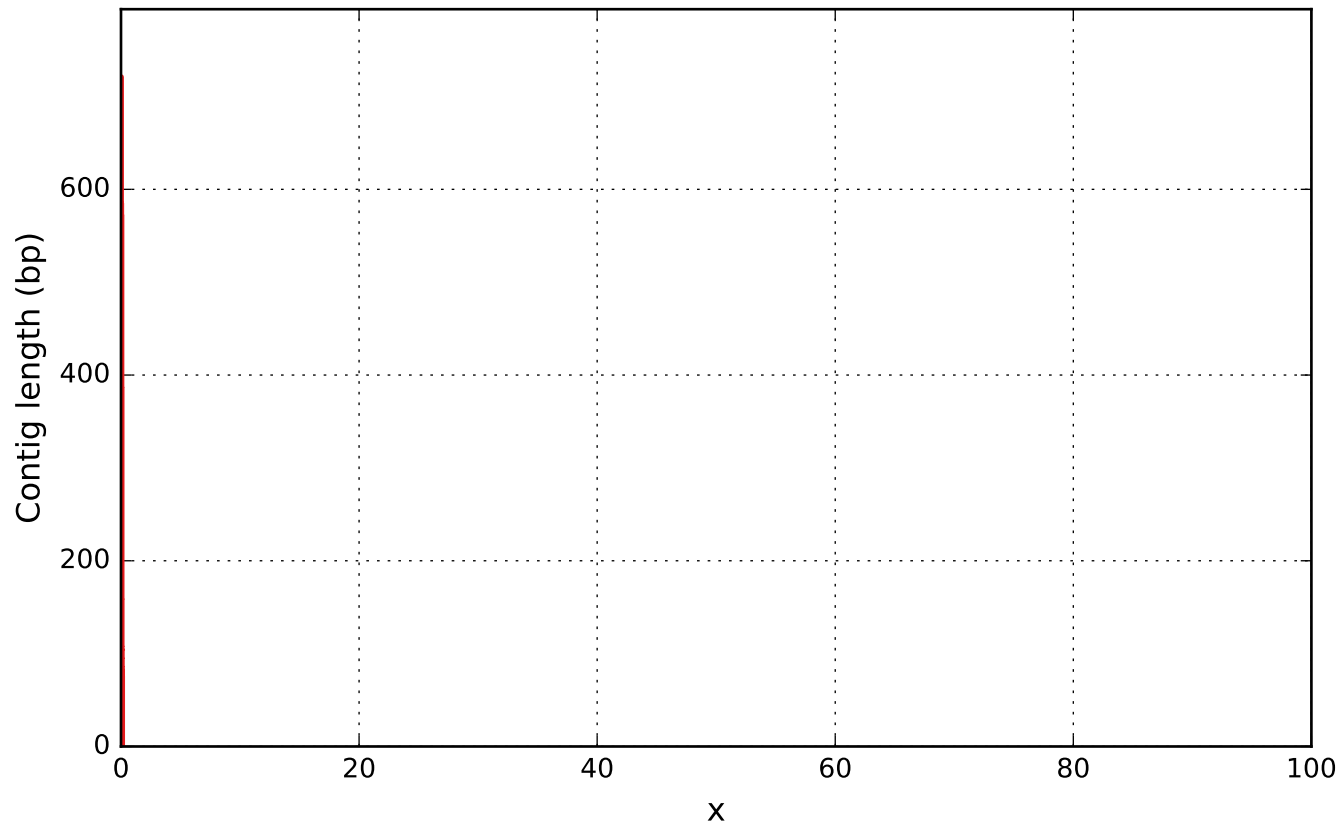
— final.contigs    - - Reference

NAx



— final.contigs

NGAx



— final.contigs