

# Report

	final.contigs
# contigs (>= 1000 bp)	2
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	3027
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	5
Largest contig	1842
Total length	4711
Reference length	4638566
GC (%)	38.10
Reference GC (%)	41.62
N50	1185
N75	605
L50	2
L75	3
# 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	2745
Genome fraction (%)	0.009
Duplication ratio	4.540
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2540.42
# indels per 100 kbp	0.00
Largest alignment	207
Total aligned length	509
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

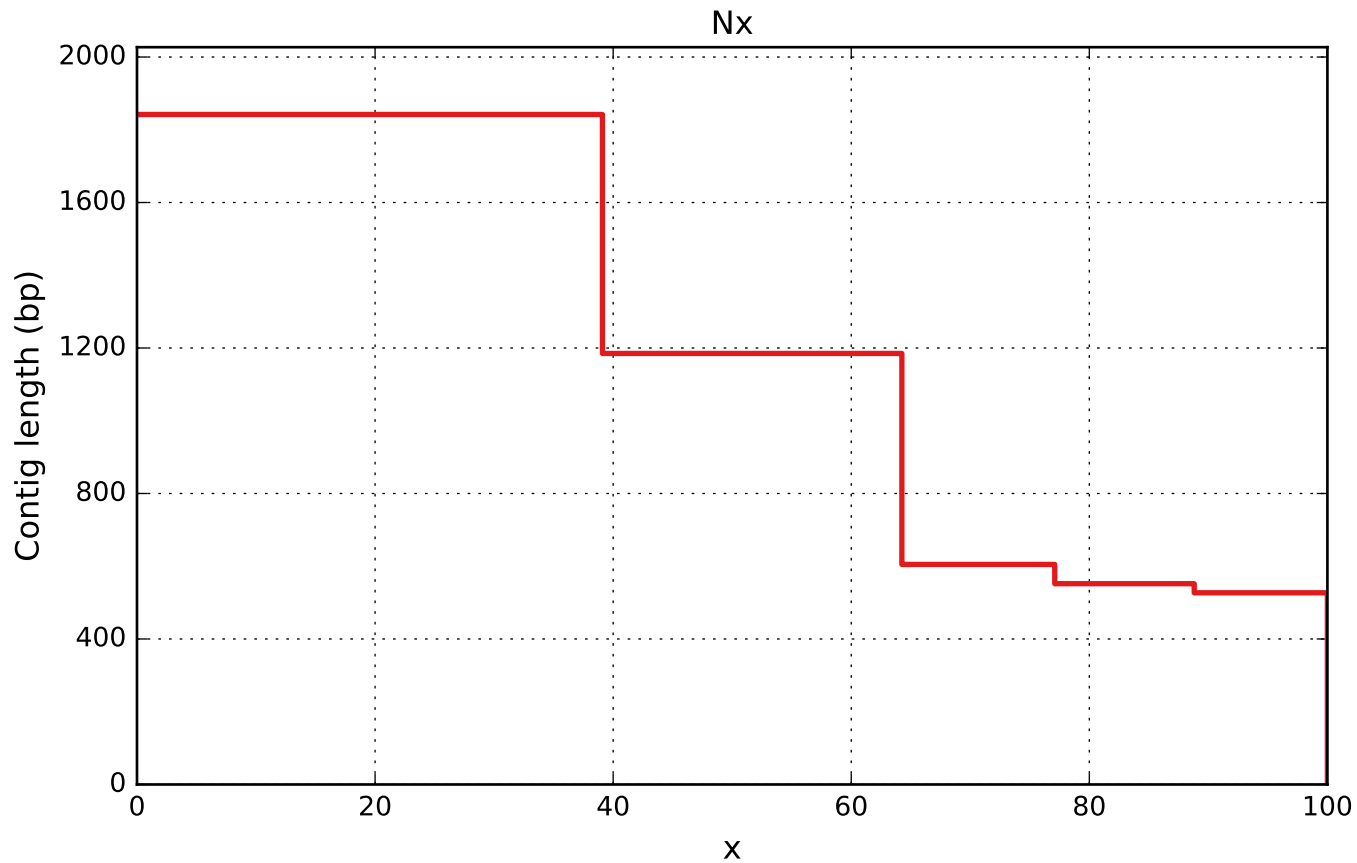
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# structural variations	0
# unaligned mis. contigs	0
# mismatches	11
# indels	0
# indels ( $\leq 5$ bp)	0
# indels ( $> 5$ bp)	0
Indels length	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).

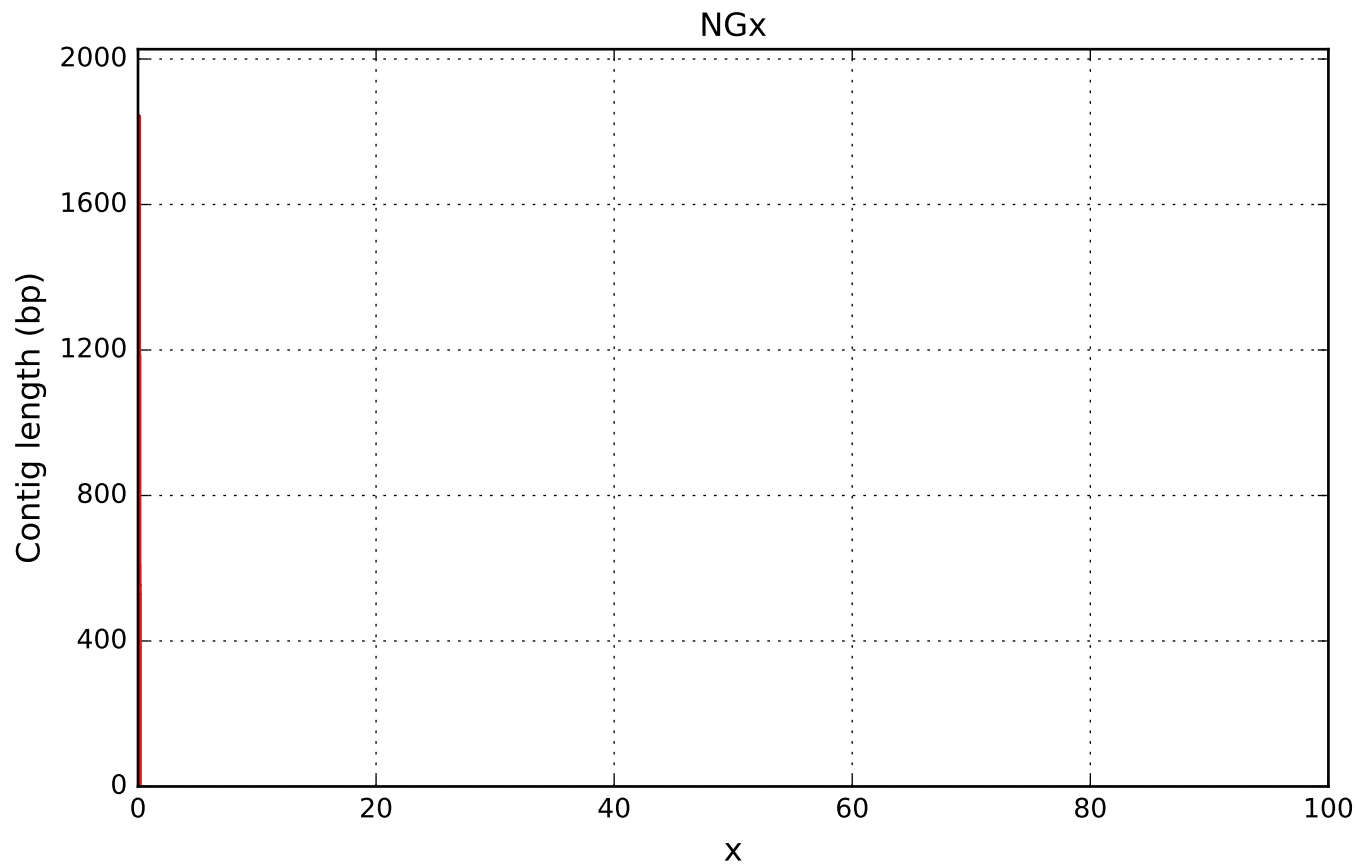
## Unaligned report

	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
Partially unaligned length	2745
# N's	0

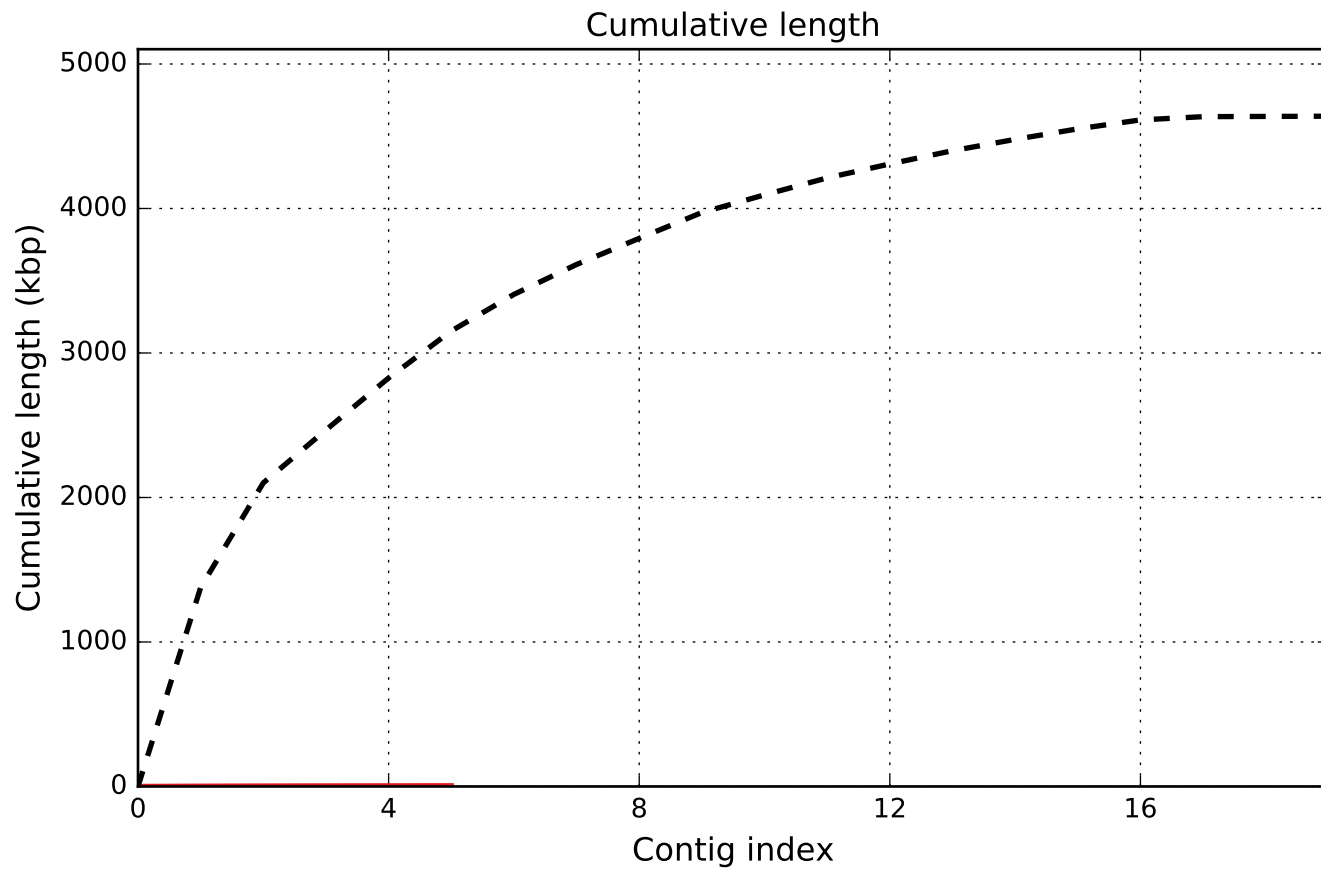
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

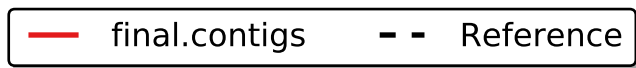
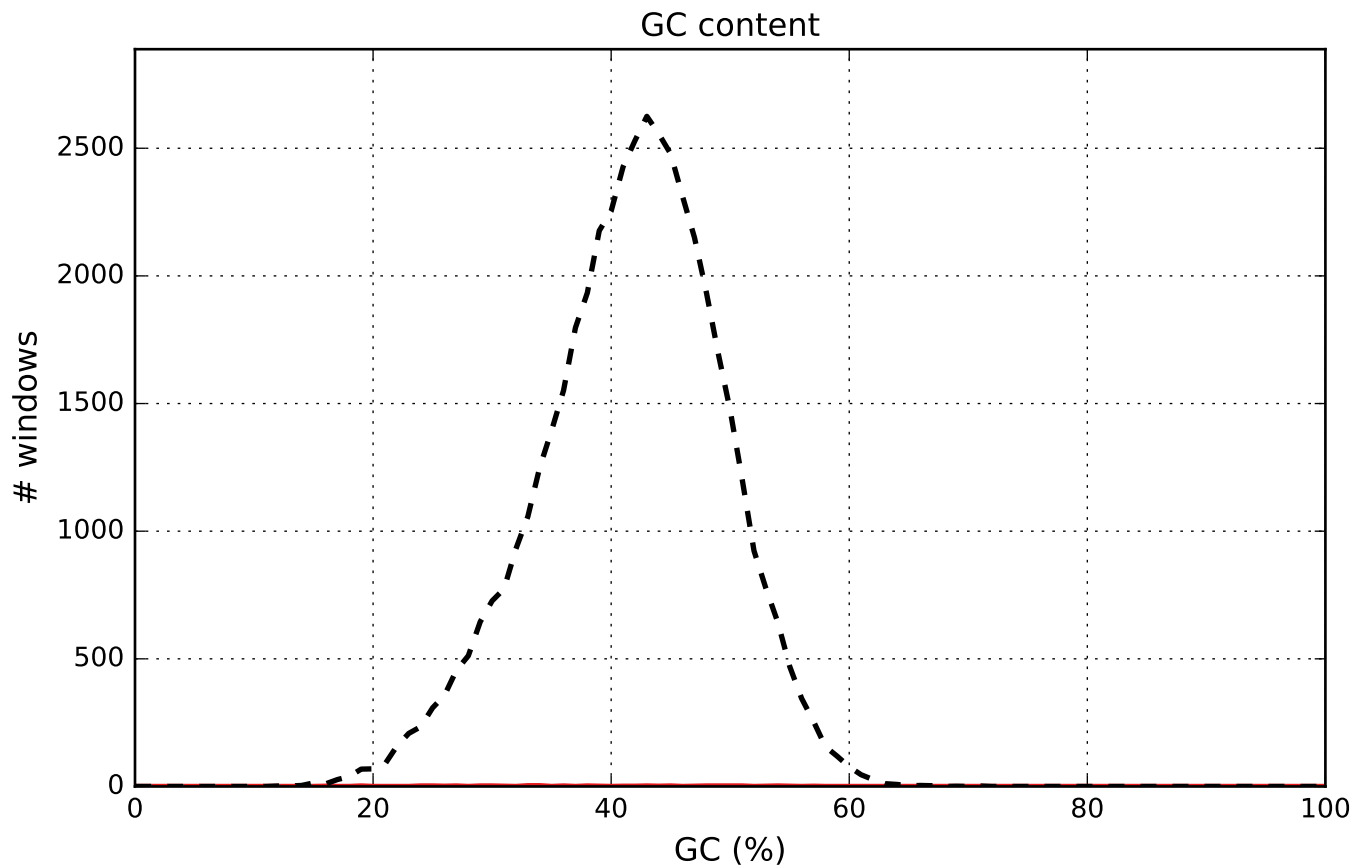


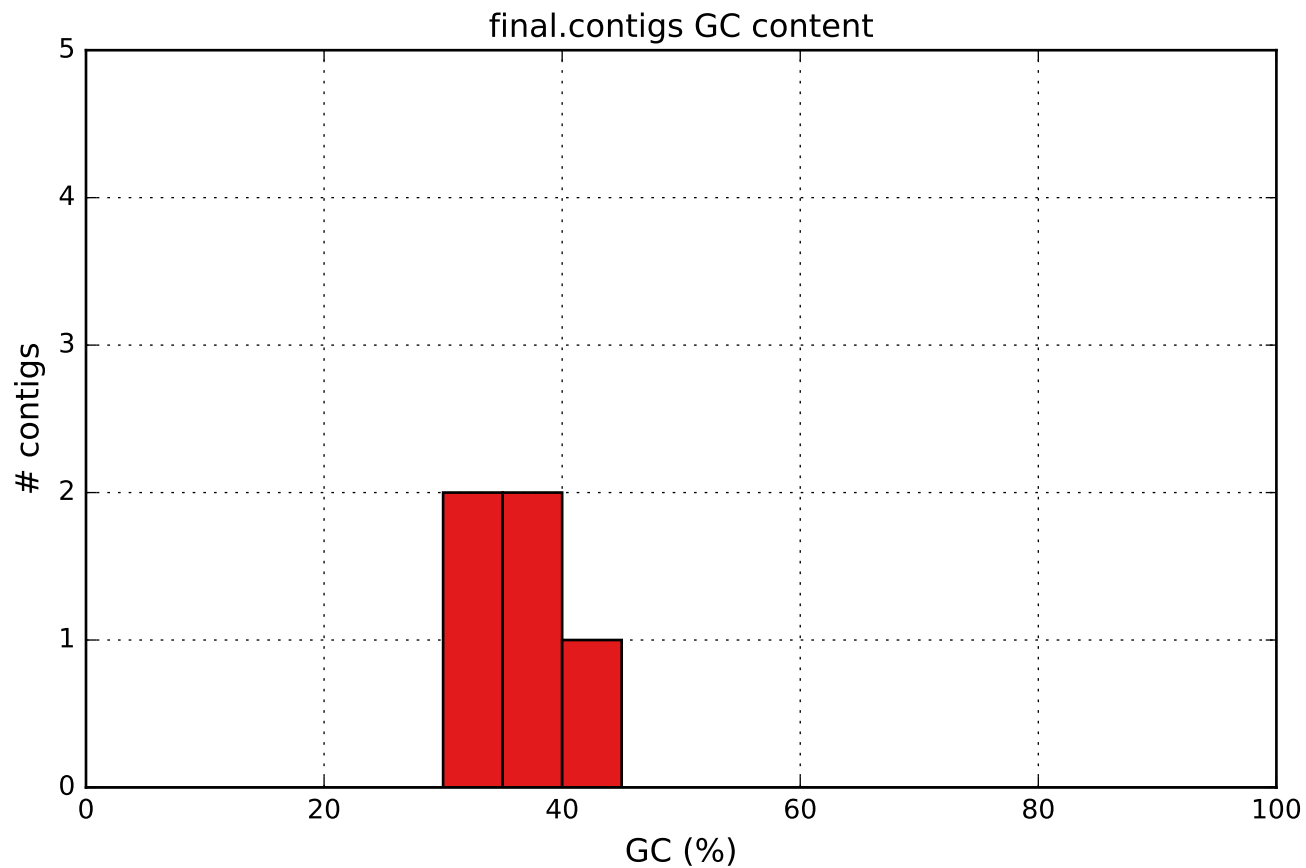
— final.contigs



— final.contigs





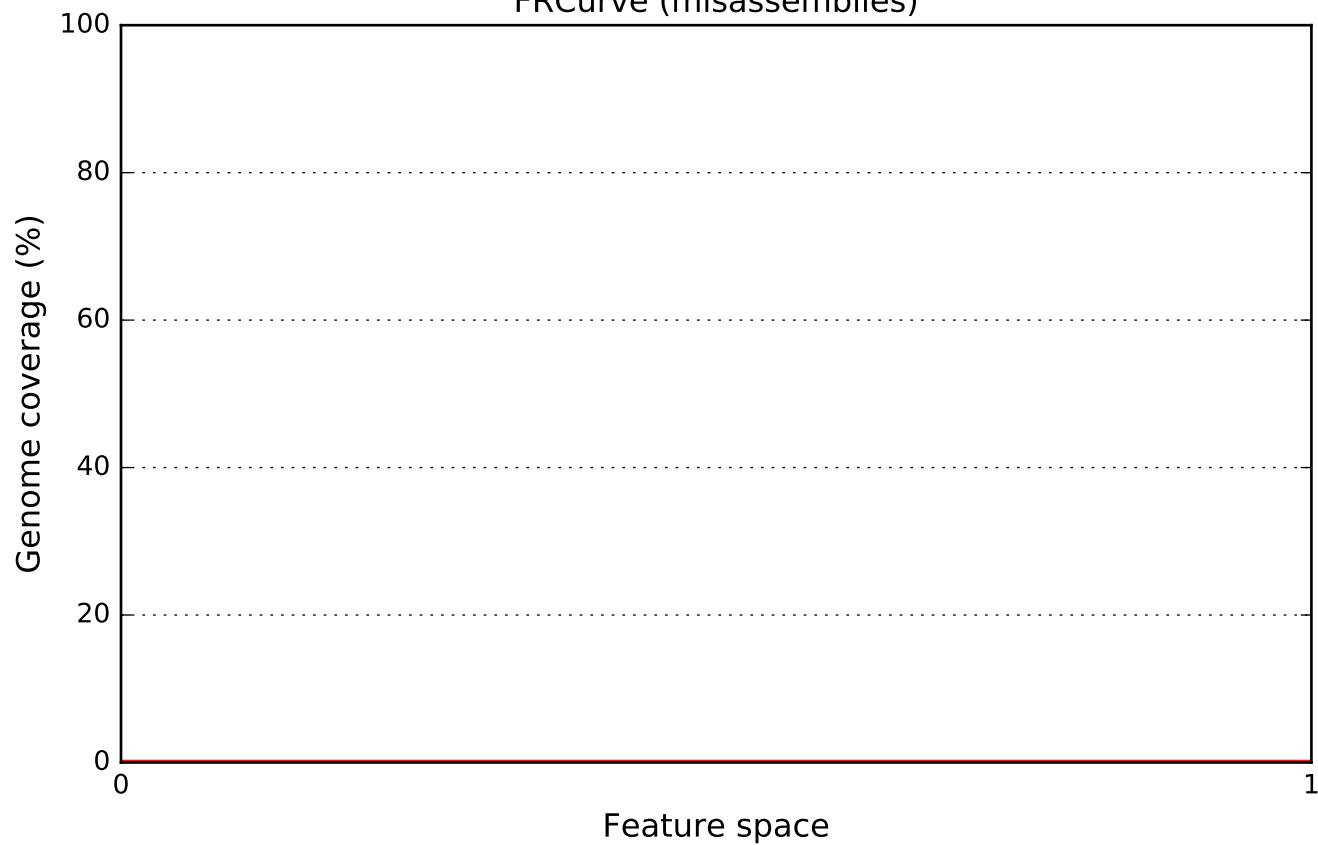


 final.contigs



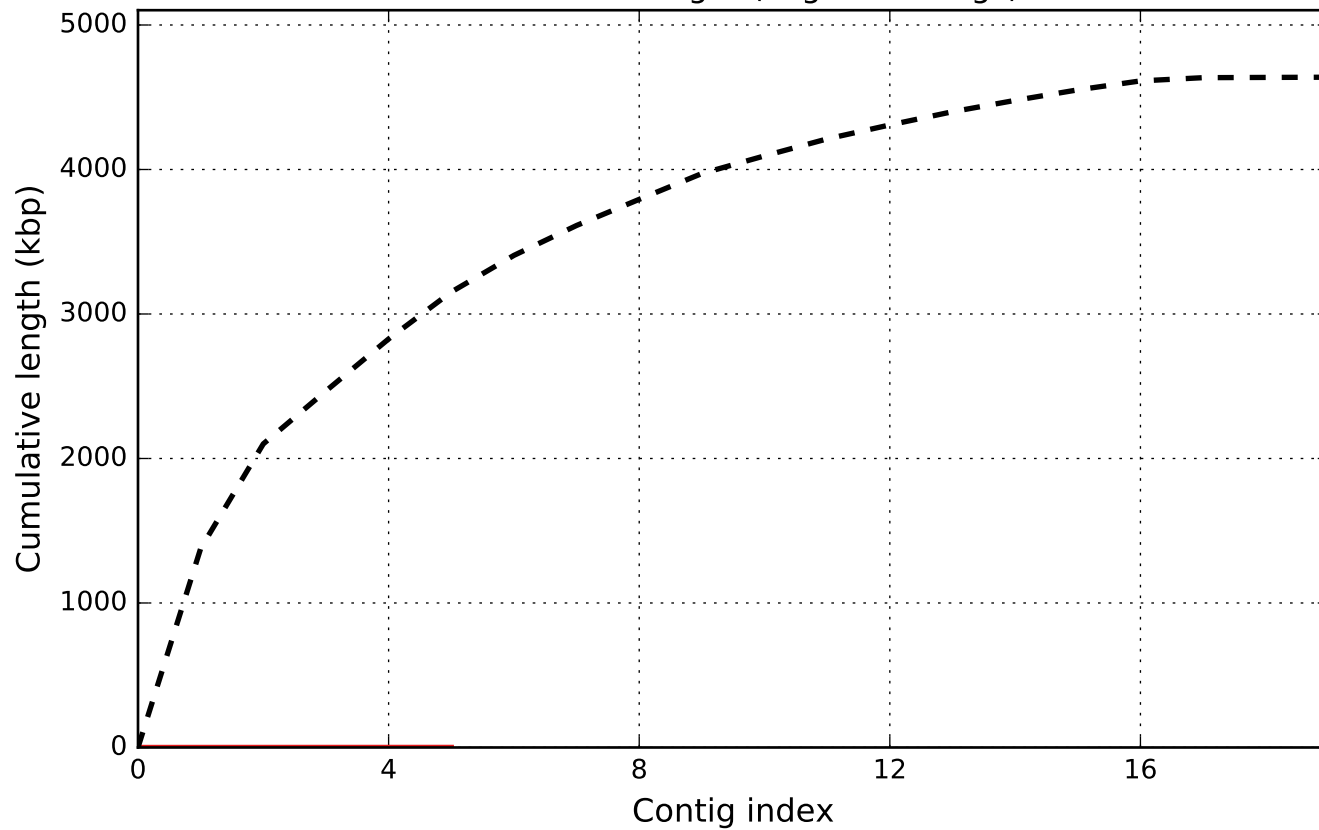


FRCurve (misassemblies)



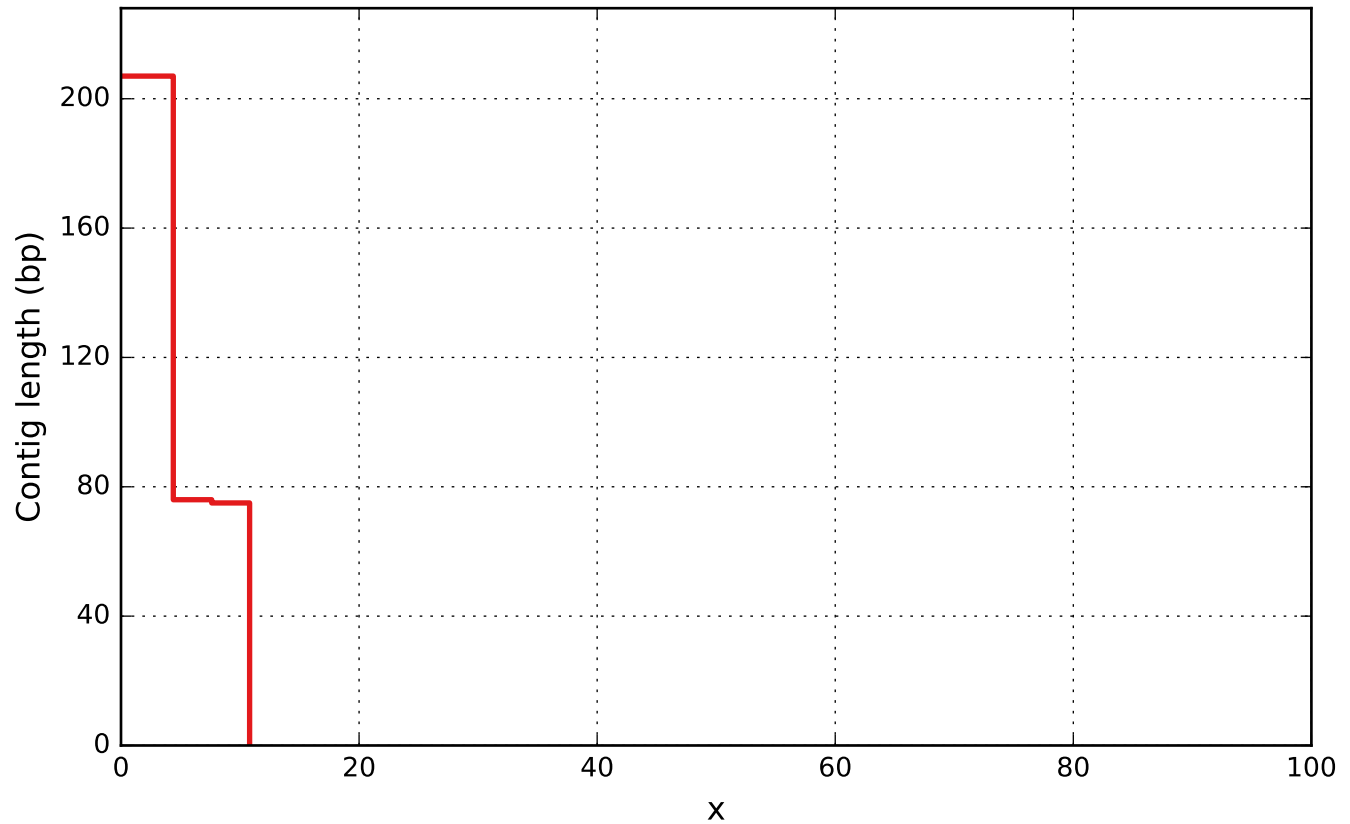
— final.contigs

Cumulative length (aligned contigs)



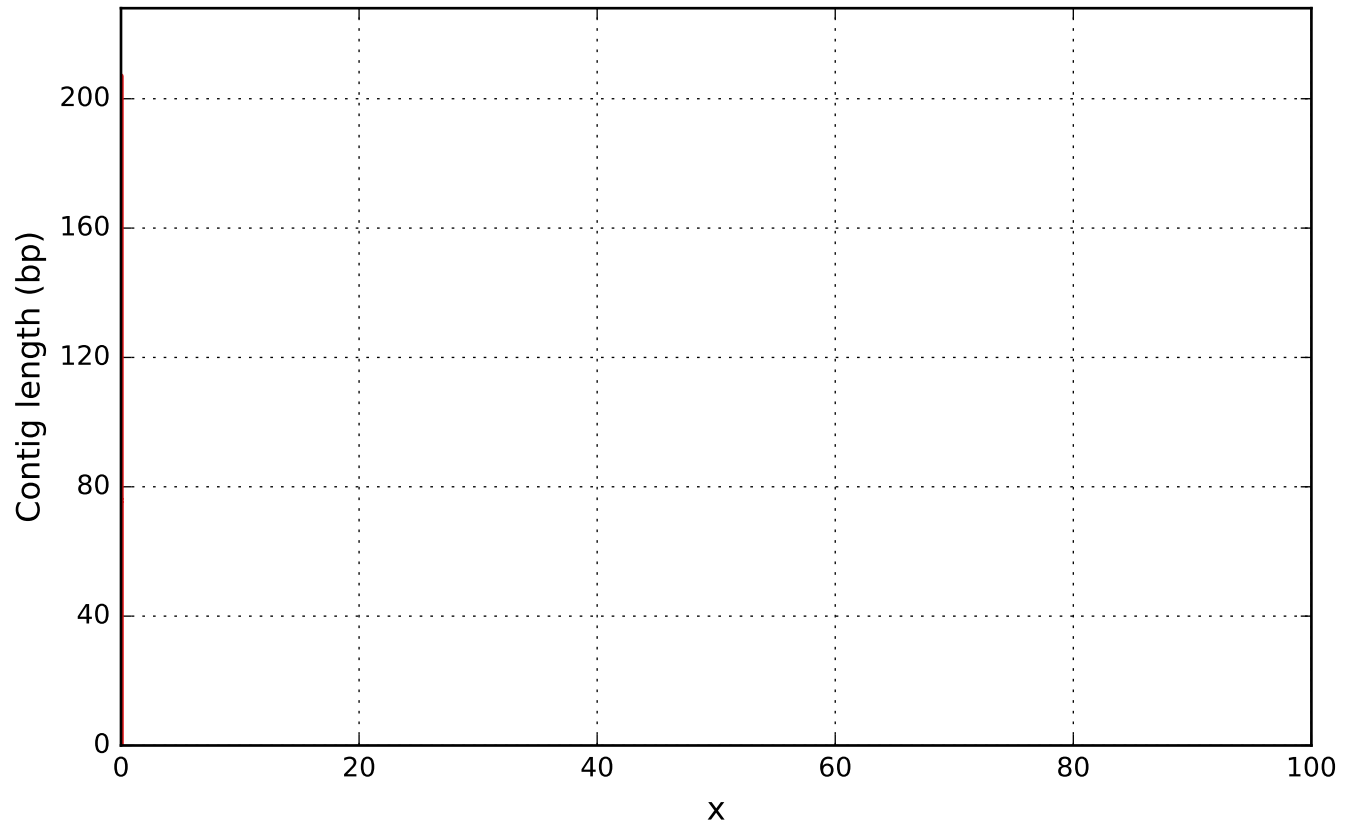
— final.contigs    - - Reference

NAx



— final.contigs

NGAx



— final.contigs