

## Report

	final.contigs
# contigs ( $\geq 1000$ bp)	17
# contigs ( $\geq 5000$ bp)	5
# contigs ( $\geq 10000$ bp)	2
# contigs ( $\geq 25000$ bp)	0
# contigs ( $\geq 50000$ bp)	0
Total length ( $\geq 1000$ bp)	71423
Total length ( $\geq 5000$ bp)	43946
Total length ( $\geq 10000$ bp)	25014
Total length ( $\geq 25000$ bp)	0
Total length ( $\geq 50000$ bp)	0
# contigs	31
Largest contig	13783
Total length	81705
Reference length	4010516
GC (%)	52.93
Reference GC (%)	60.05
N50	5324
N75	2097
L50	5
L75	11
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned mis. contigs	3
# unaligned contigs	0 + 21 part
Unaligned length	72885
Genome fraction (%)	0.047
Duplication ratio	4.672
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1588.98
# indels per 100 kbp	105.93
Largest alignment	363
Total aligned length	3138
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

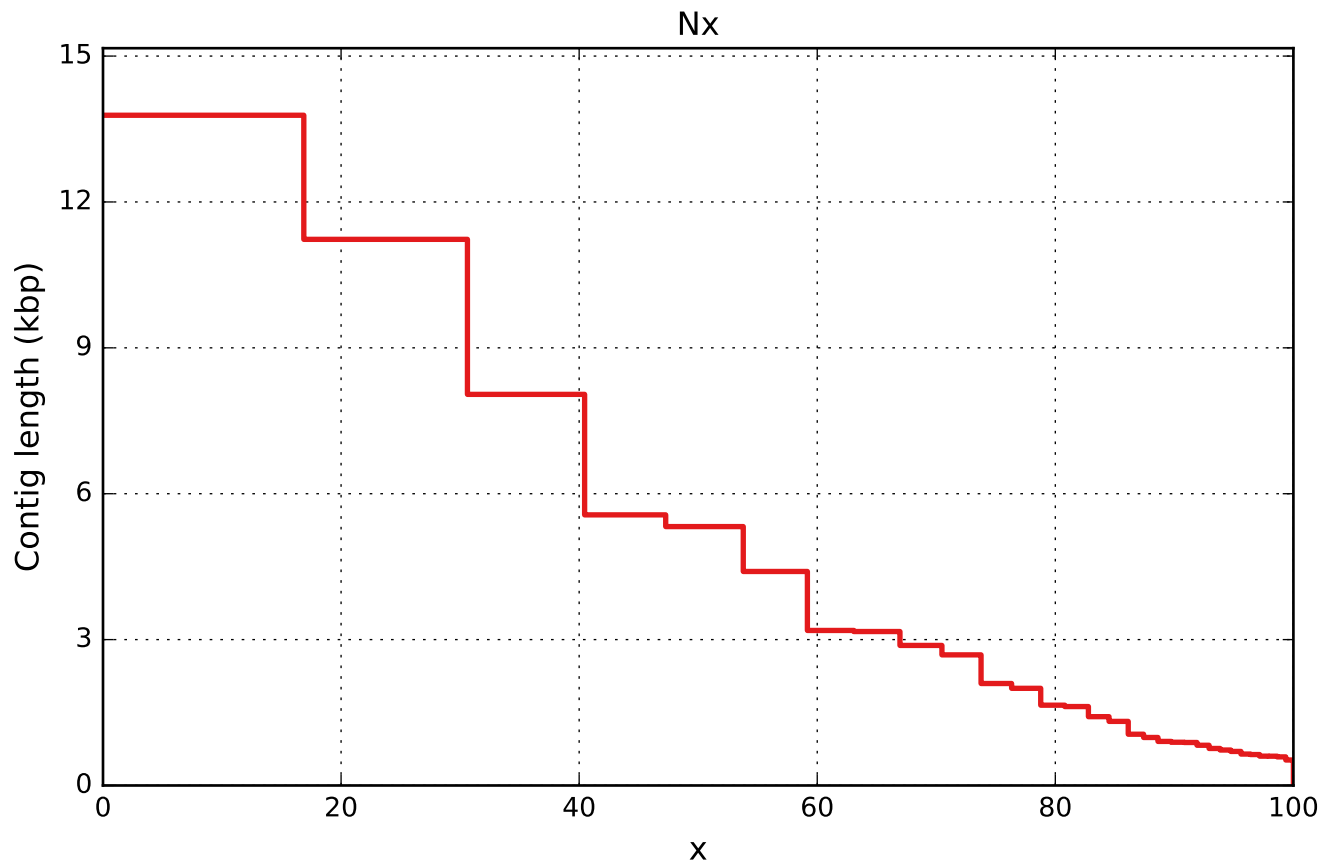
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	1
# unaligned mis. contigs	3
# mismatches	30
# indels	2
# indels ( $\leq 5$ bp)	2
# indels ( $> 5$ bp)	0
Indels length	2

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

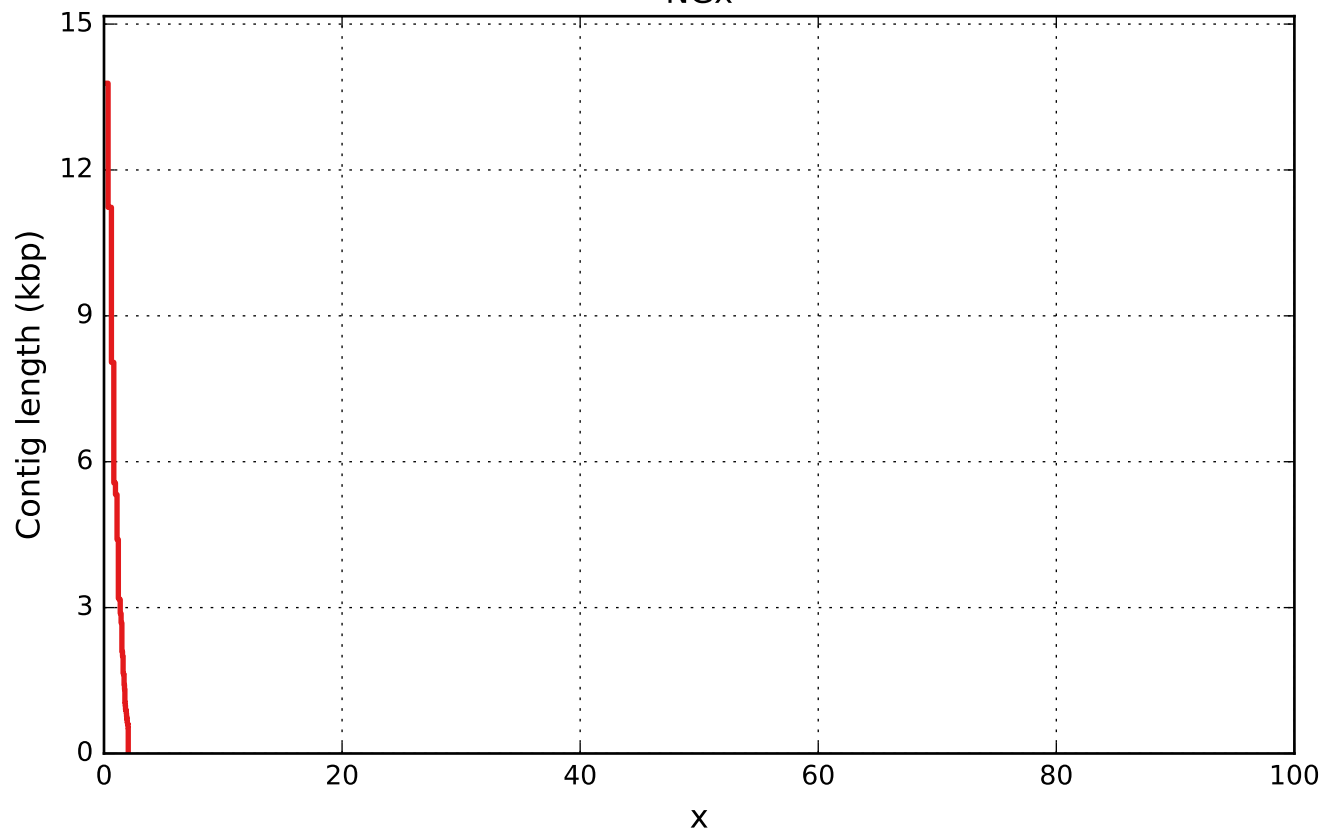
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	21
Partially unaligned length	72885
# N's	0

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).

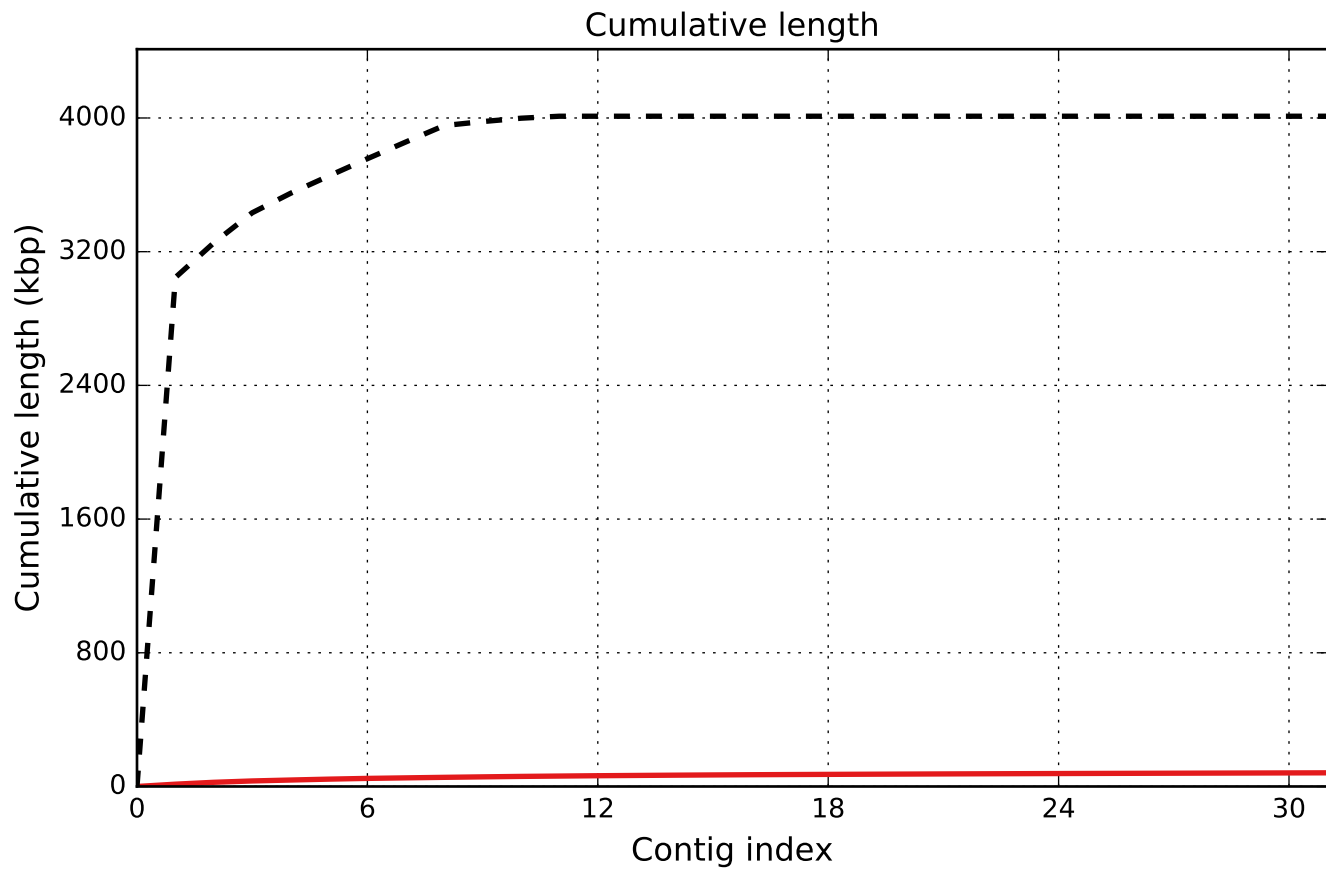


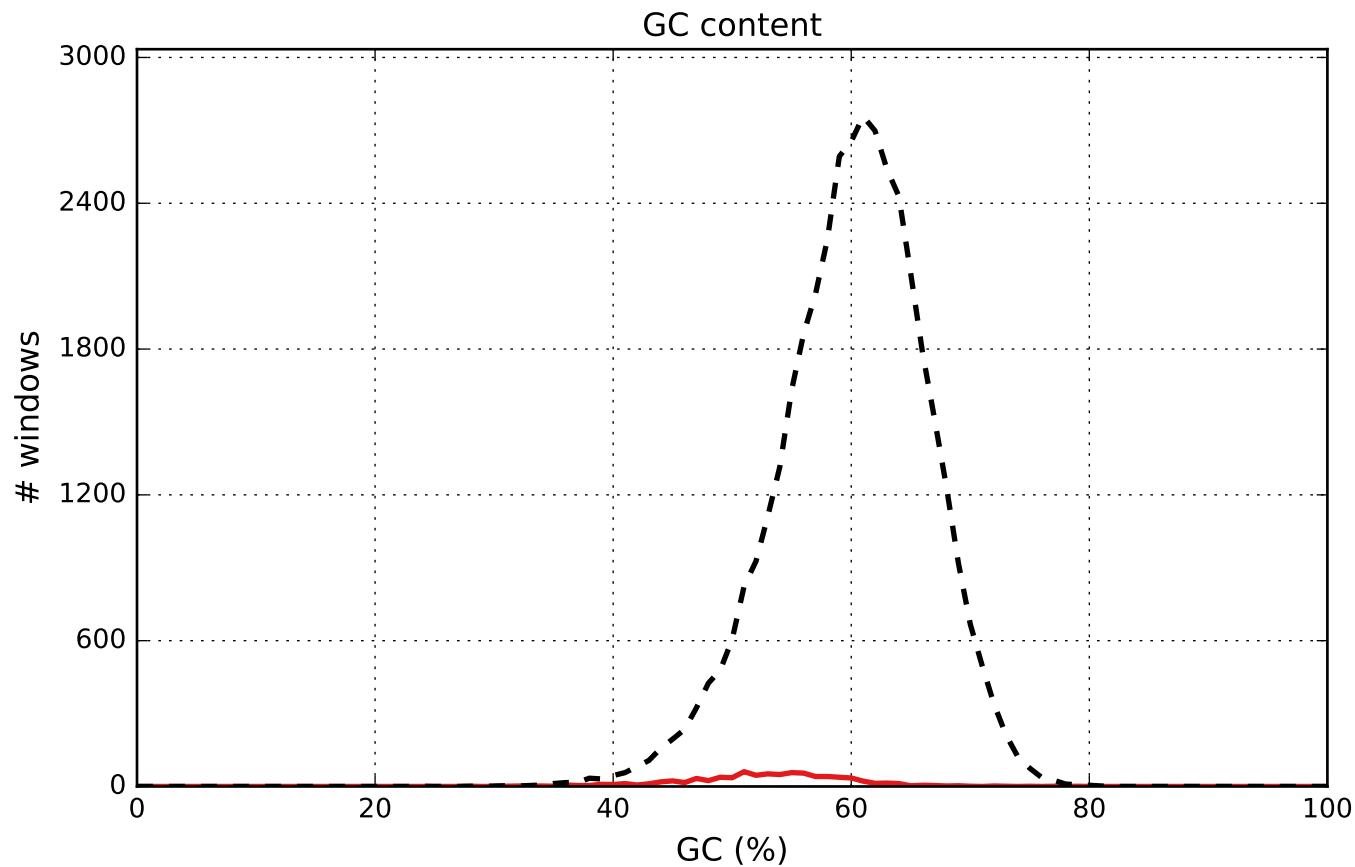
— final.contigs

NGx

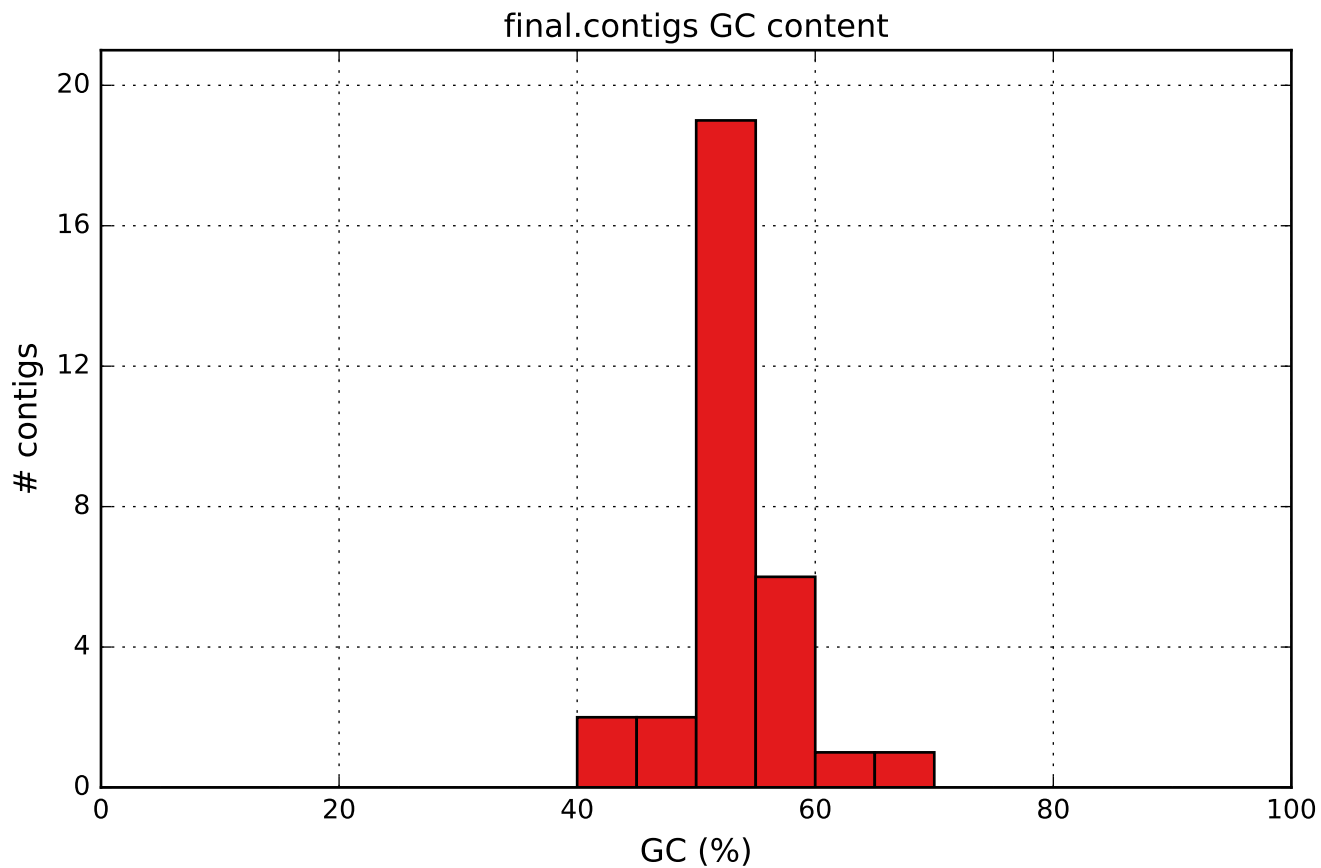


— final.contigs



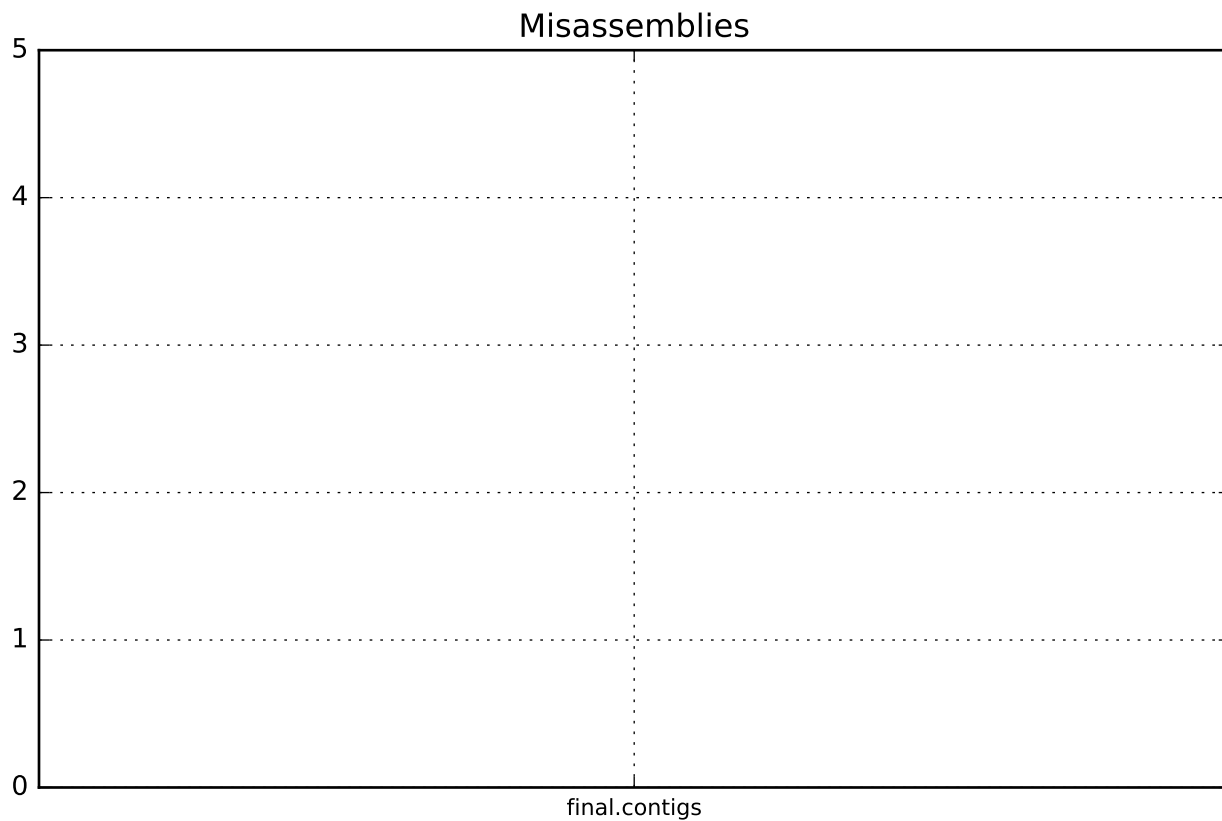


— final.contigs    - - Reference

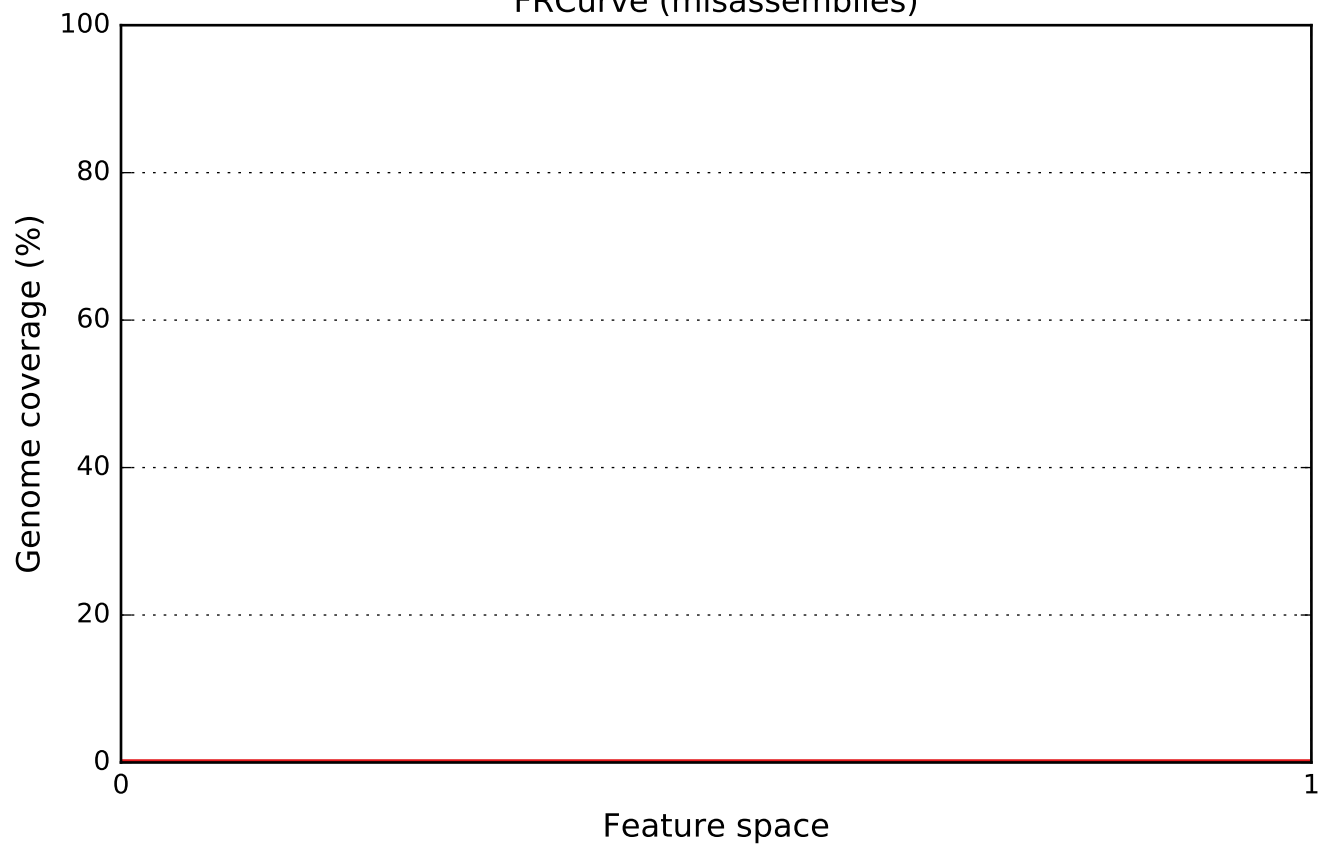


final.contigs



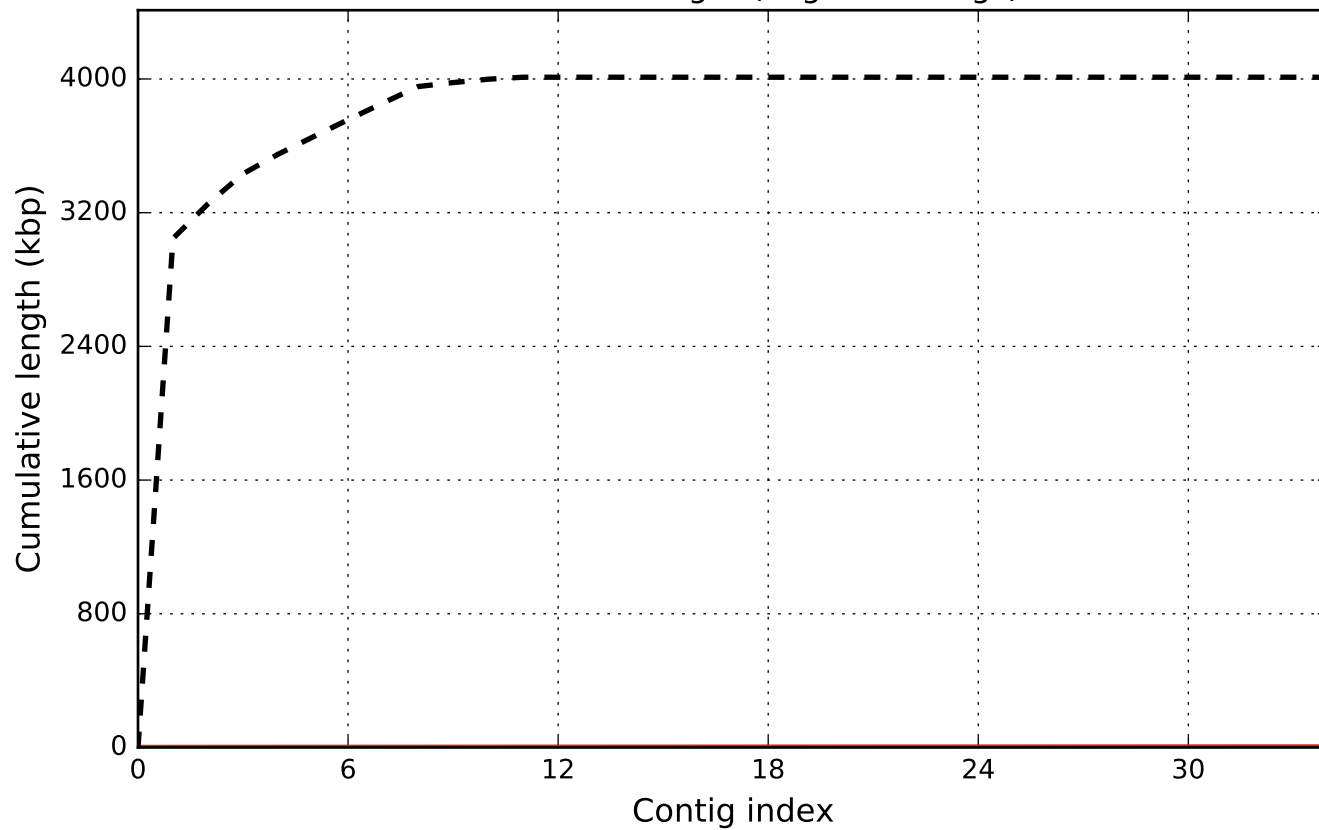


FRCurve (misassemblies)



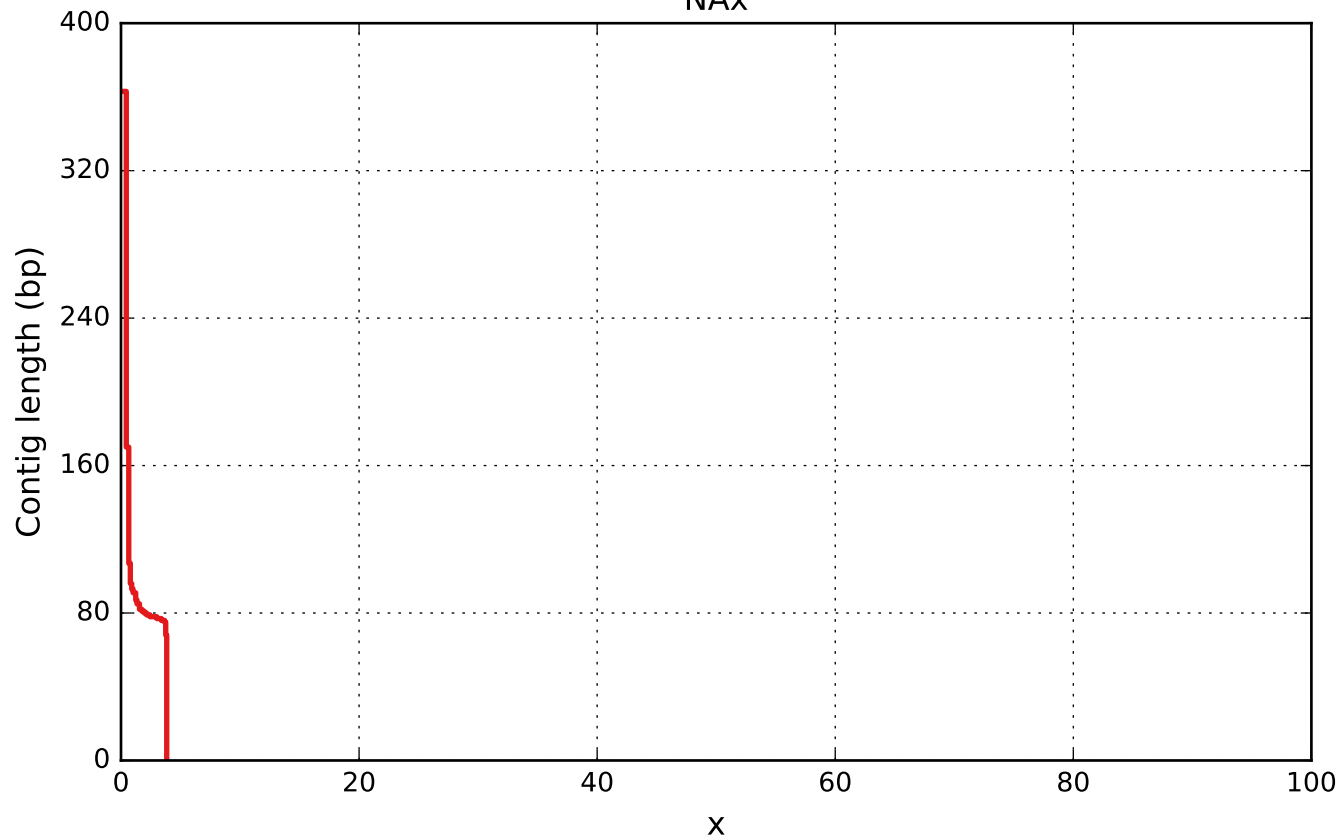
— final.contigs

Cumulative length (aligned contigs)



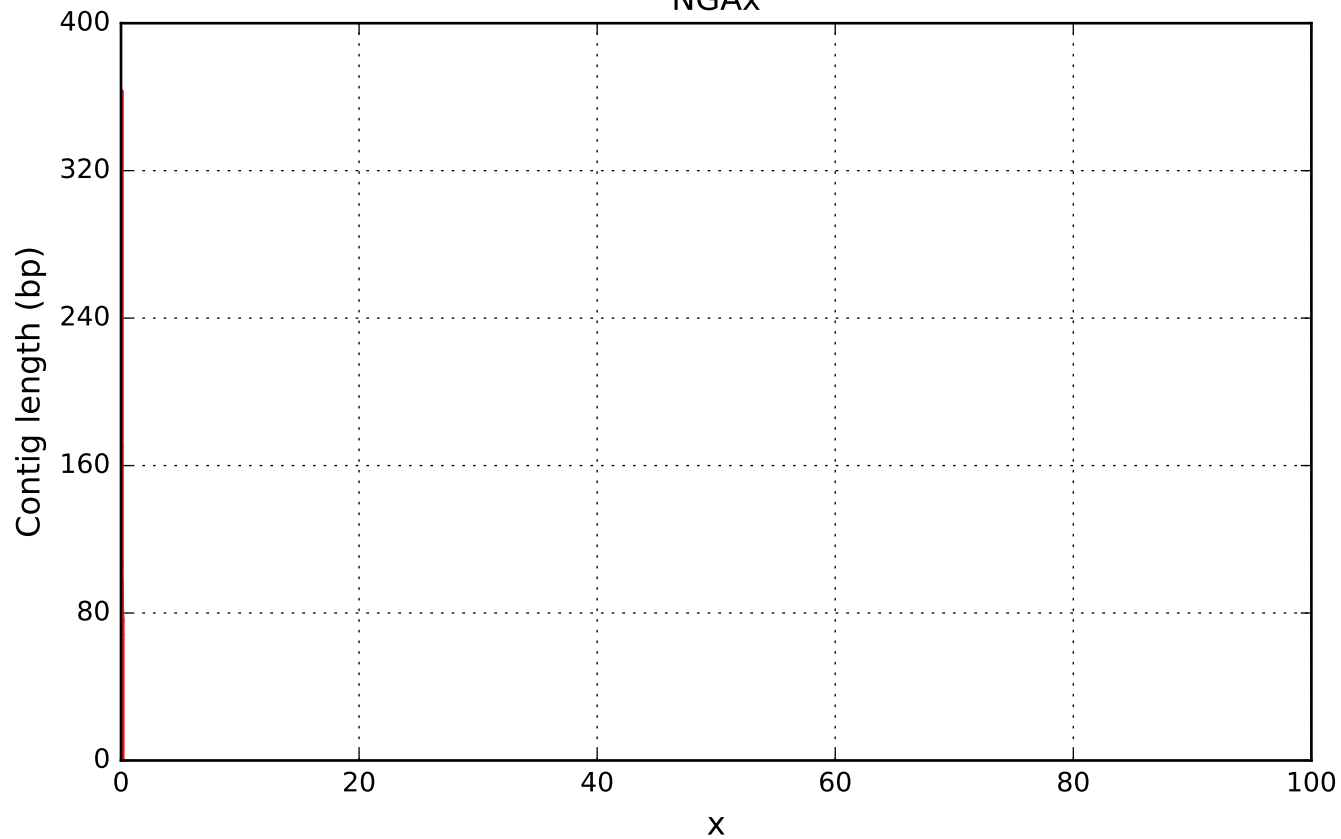
— final.contigs    - - Reference

NAx



— final.contigs

NGAx



— final.contigs