

## Report

	final.contigs
# contigs (>= 1000 bp)	8
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	15908
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	10
Largest contig	3891
Total length	17172
Reference length	1669890
GC (%)	30.15
Reference GC (%)	32.21
N50	2409
N75	1431
L50	3
L75	6
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 8 part
Unaligned length	15282
Genome fraction (%)	0.024
Duplication ratio	4.655
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1231.53
# indels per 100 kbp	246.31
Largest alignment	87
Total aligned length	782
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

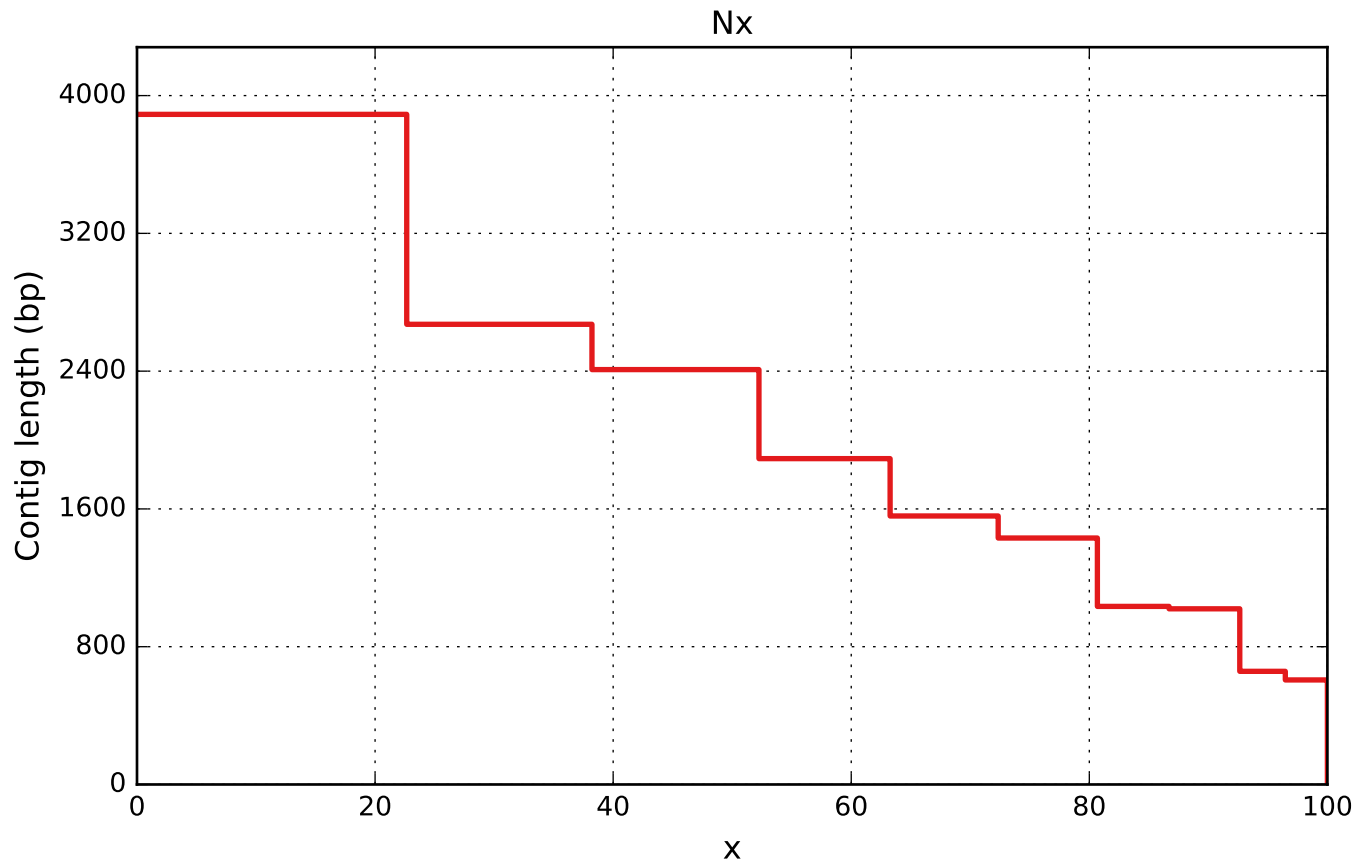
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	5
# indels	1
# indels (<= 5 bp)	1
# indels (> 5 bp)	0
Indels length	1

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).

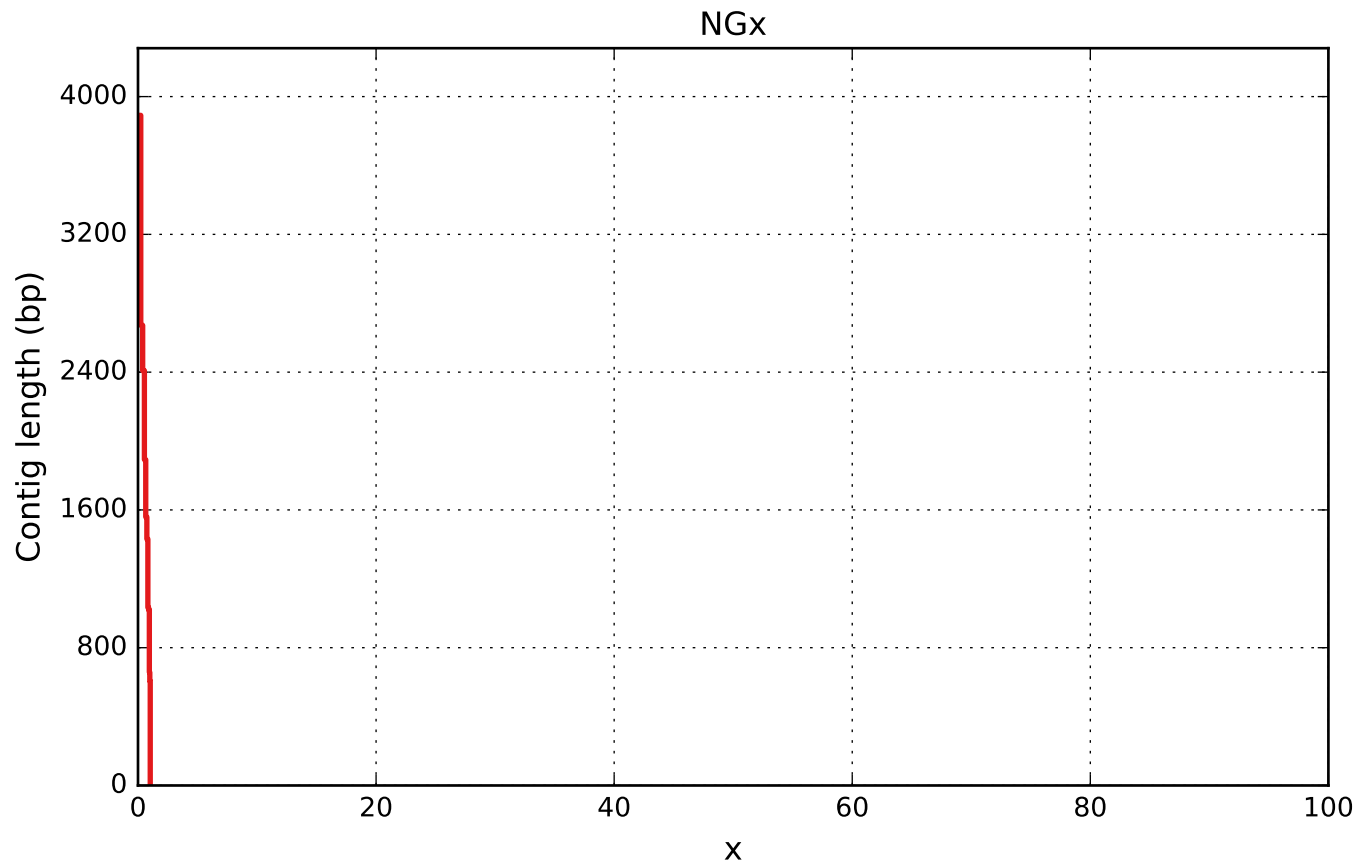
## Unaligned report

	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	8
Partially unaligned length	15282
# N's	0

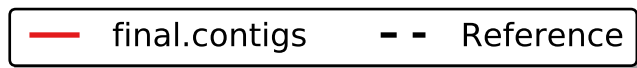
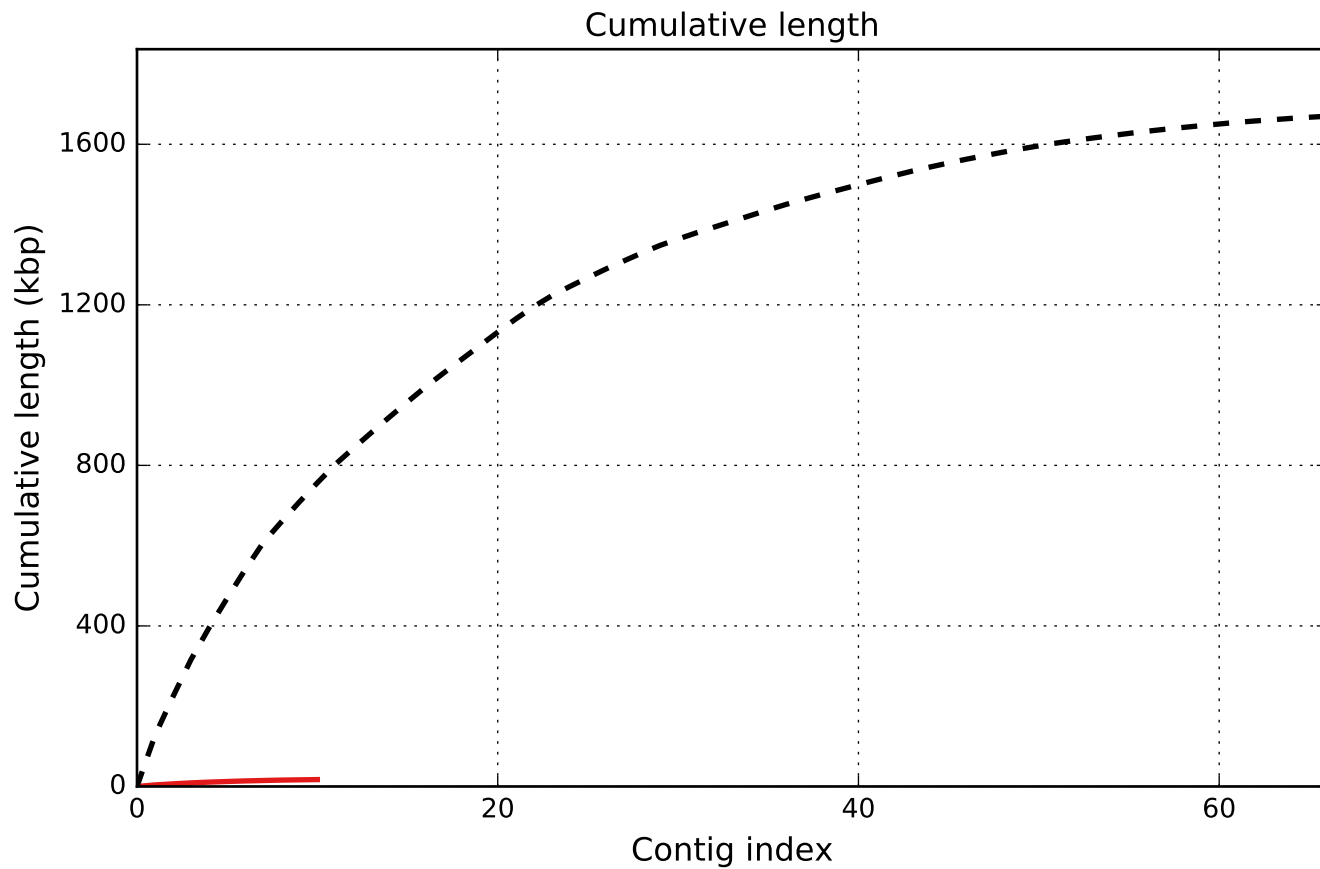
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

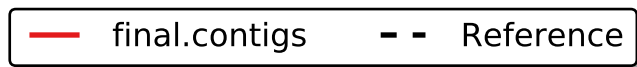
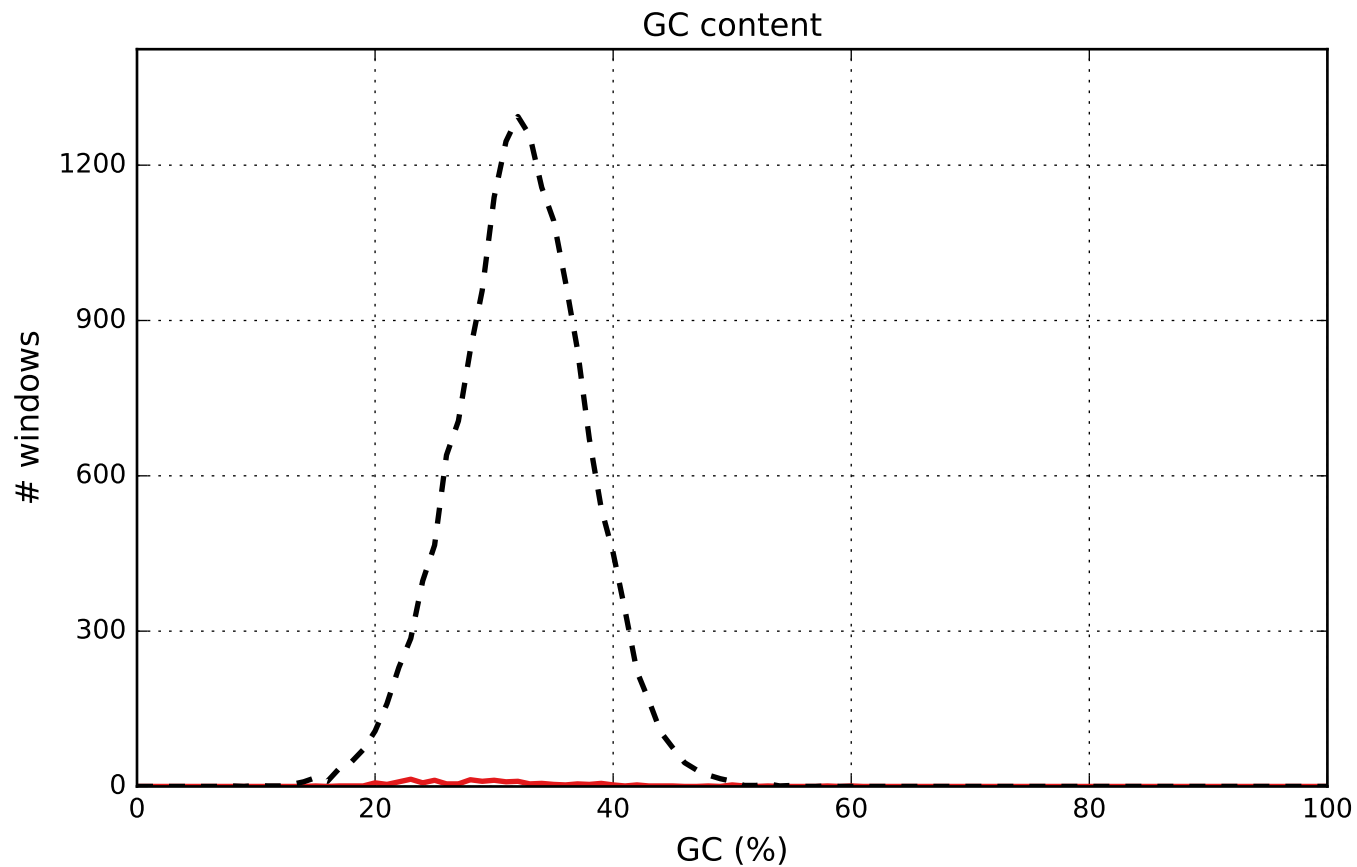


— final.contigs

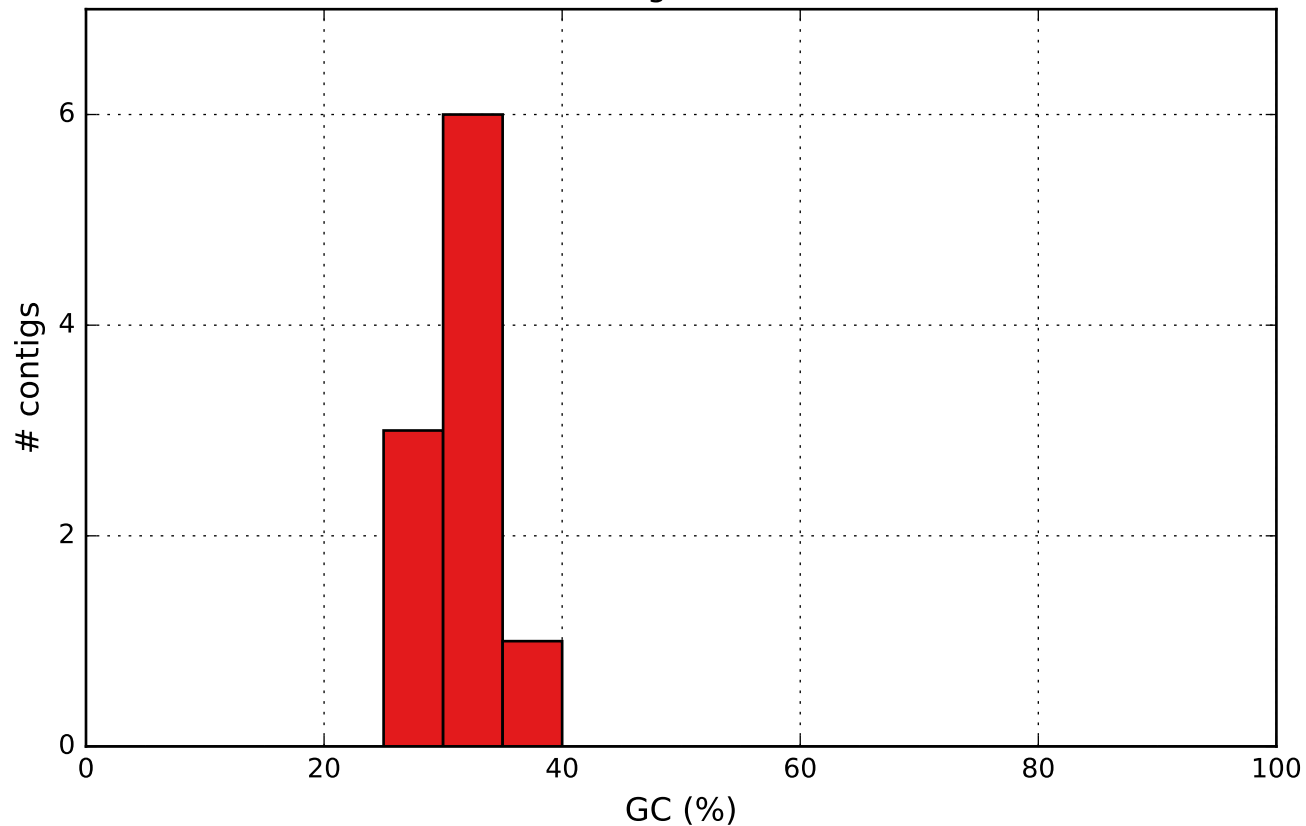


— final.contigs





final.contigs GC content

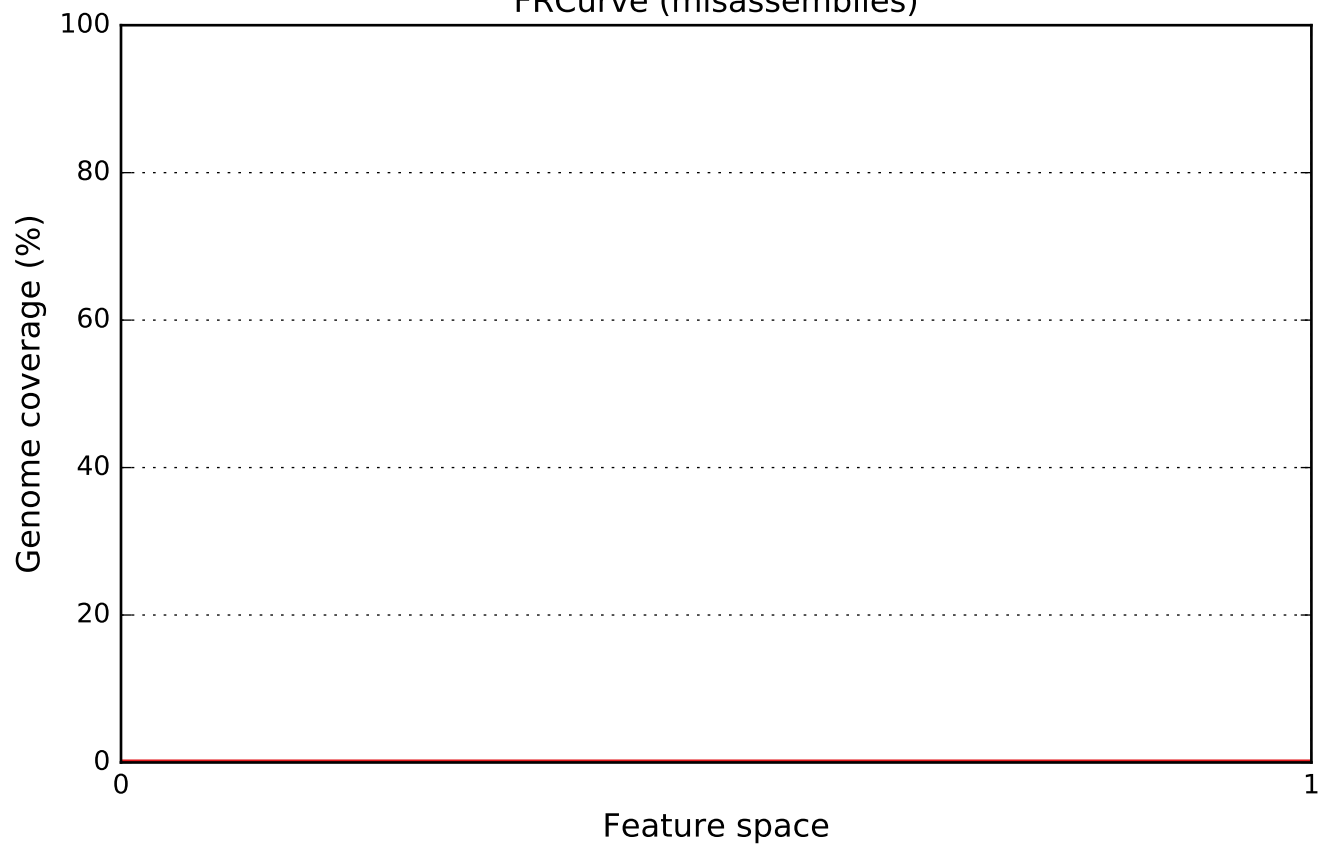


final.contigs



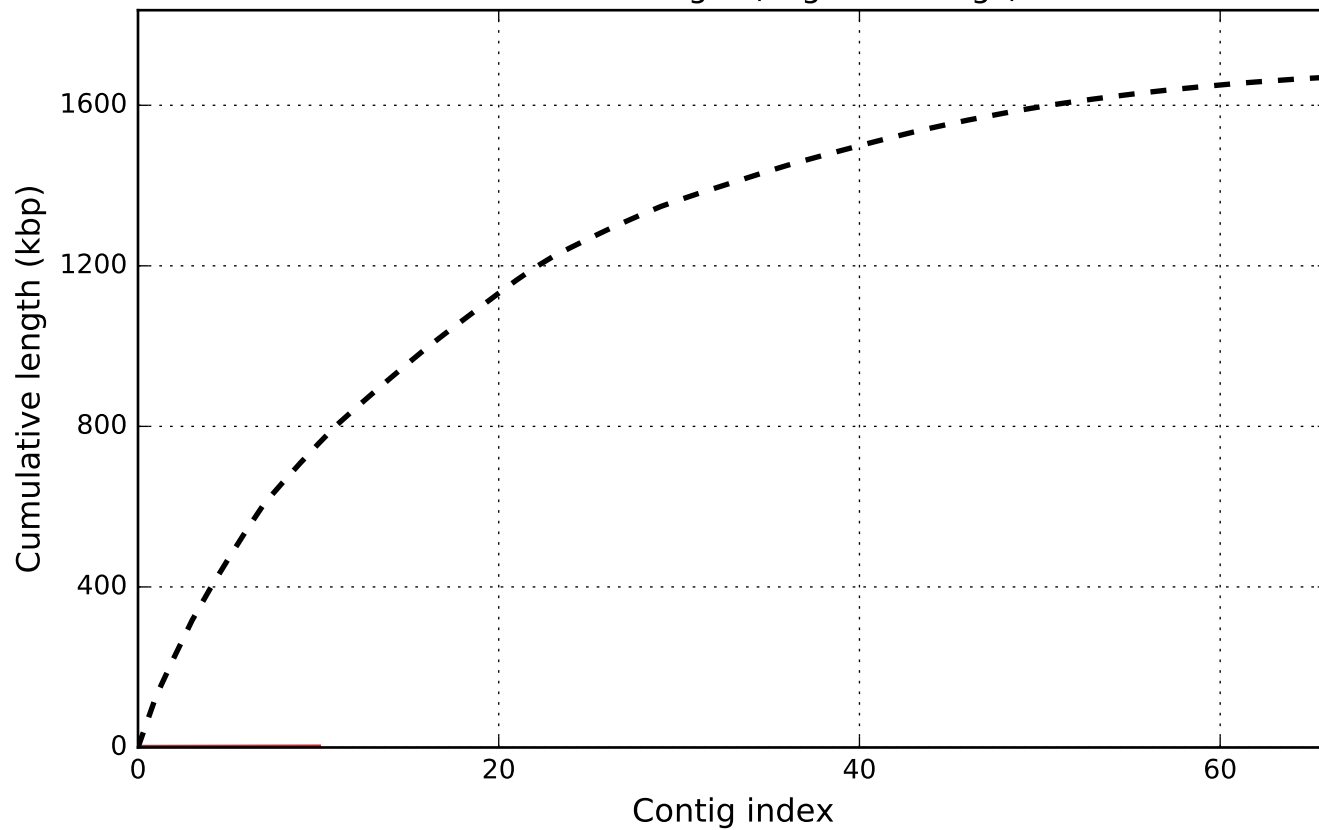


FRCurve (misassemblies)



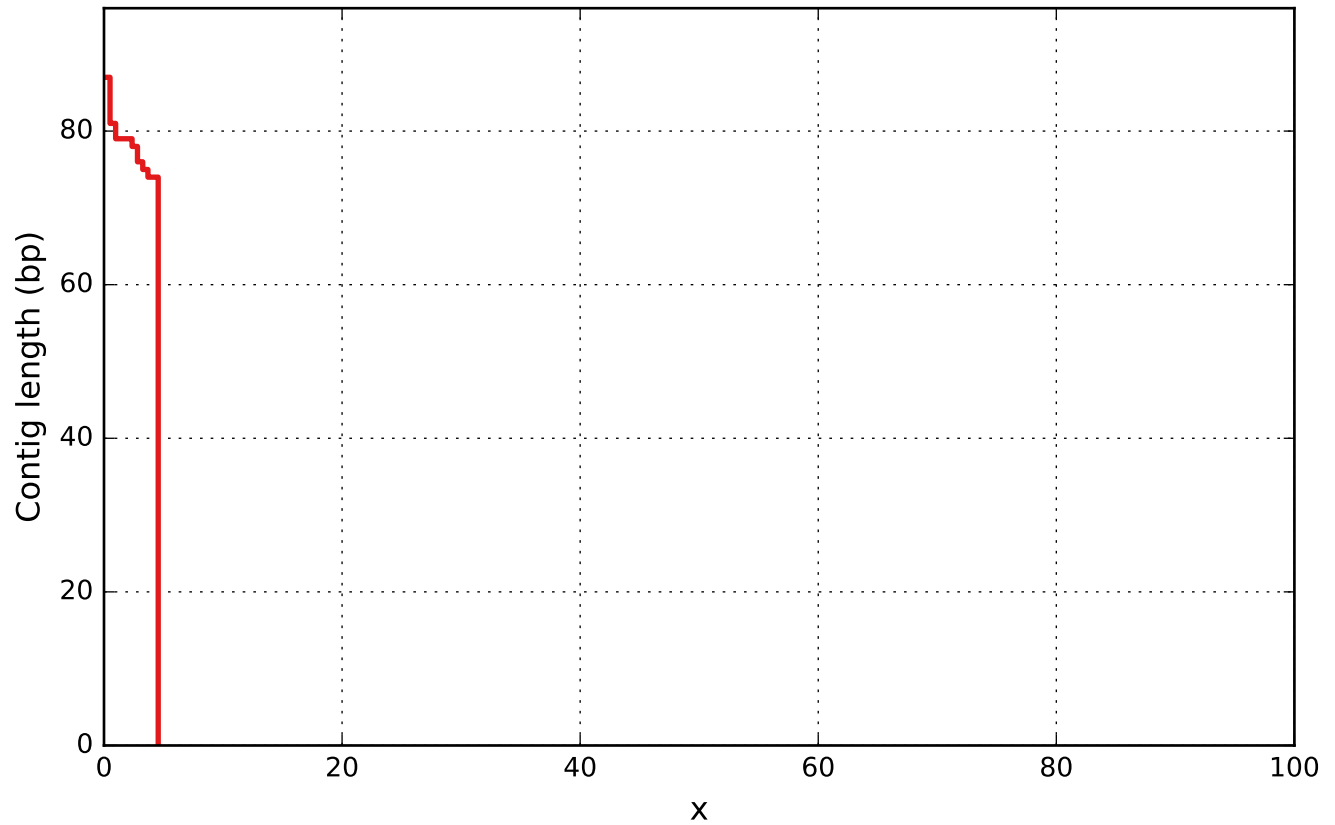
— final.contigs

Cumulative length (aligned contigs)



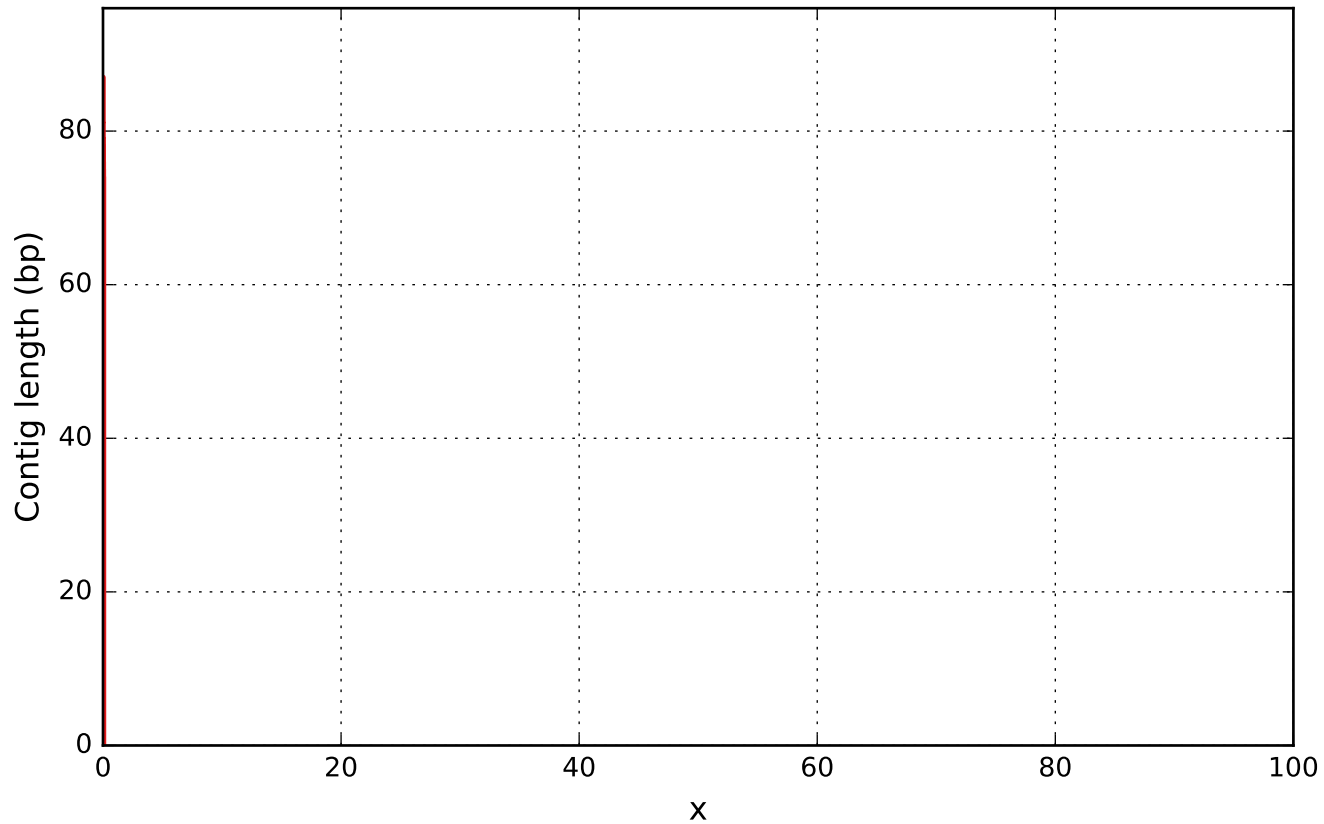
— final.contigs    - - Reference

NAx



— final.contigs

NGAx



— final.contigs