

# Report

	final.contigs
# contigs (>= 1000 bp)	6
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	8733
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	14
Largest contig	1954
Total length	14569
Reference length	1424092
GC (%)	46.00
Reference GC (%)	38.87
N50	1233
N75	823
L50	5
L75	9
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# structural variations	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 4 part
Unaligned length	5094
Genome fraction (%)	0.534
Duplication ratio	1.247
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2762.79
# indels per 100 kbp	144.72
Largest alignment	1307
Total aligned length	8278
NA50	638
NGA50	-
LA50	9

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

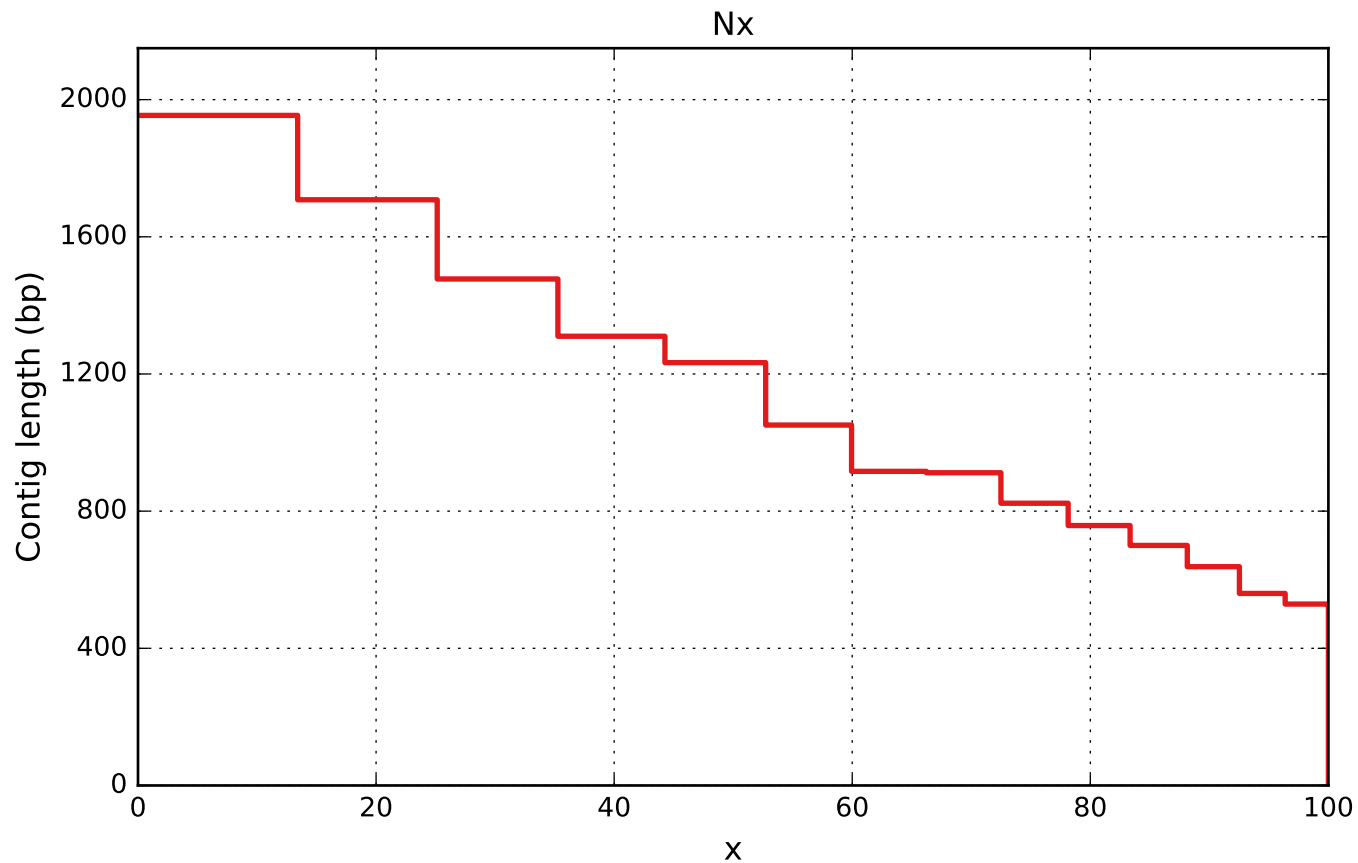
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	1
# possible misassemblies	1
# local misassemblies	0
# structural variations	0
# unaligned mis. contigs	0
# mismatches	210
# indels	11
# indels ( $\leq 5$ bp)	11
# indels ( $> 5$ bp)	0
Indels length	12

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).

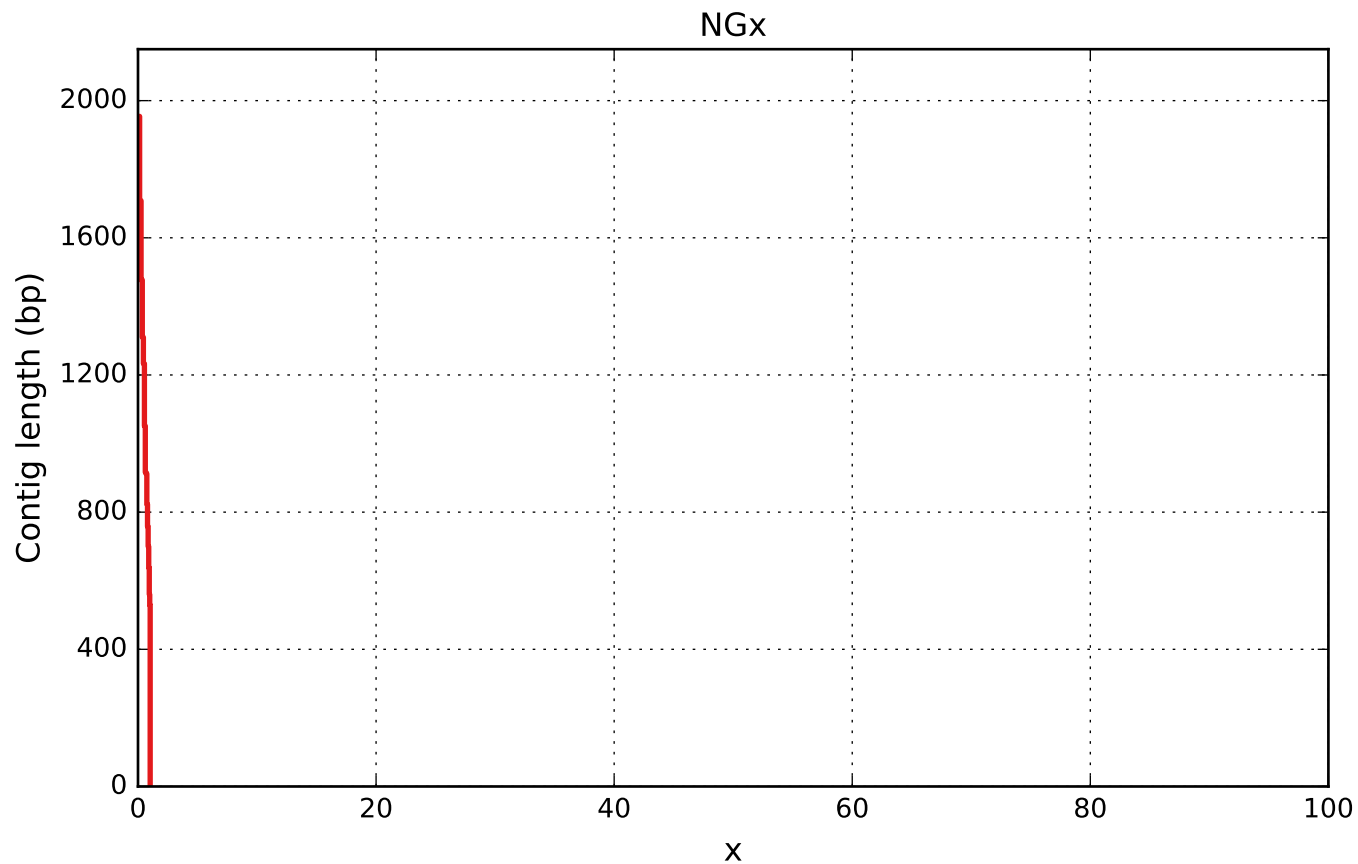
## Unaligned report

	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	4
Partially unaligned length	5094
# N's	0

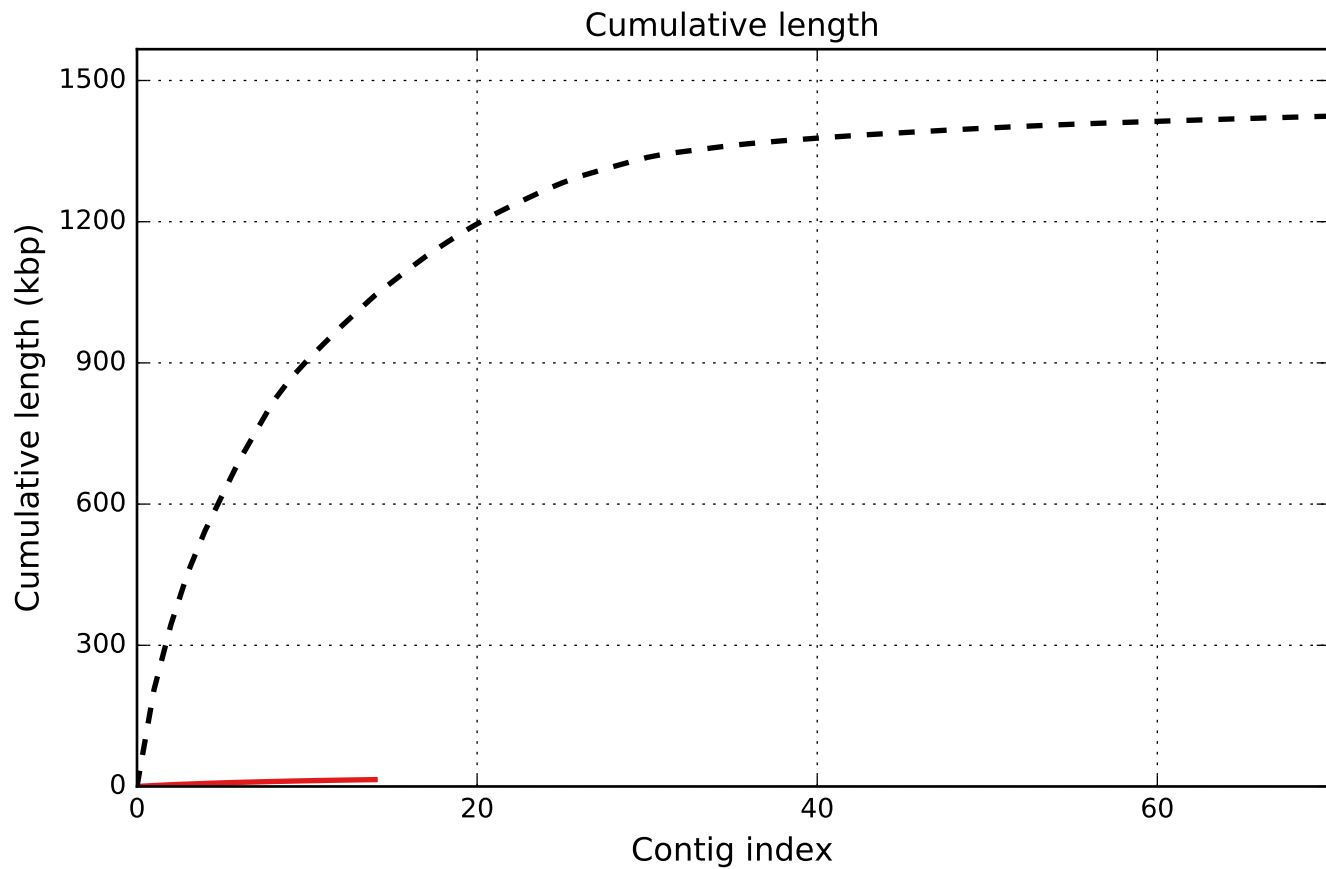
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



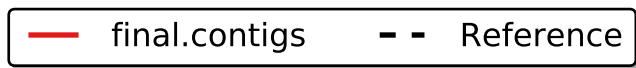
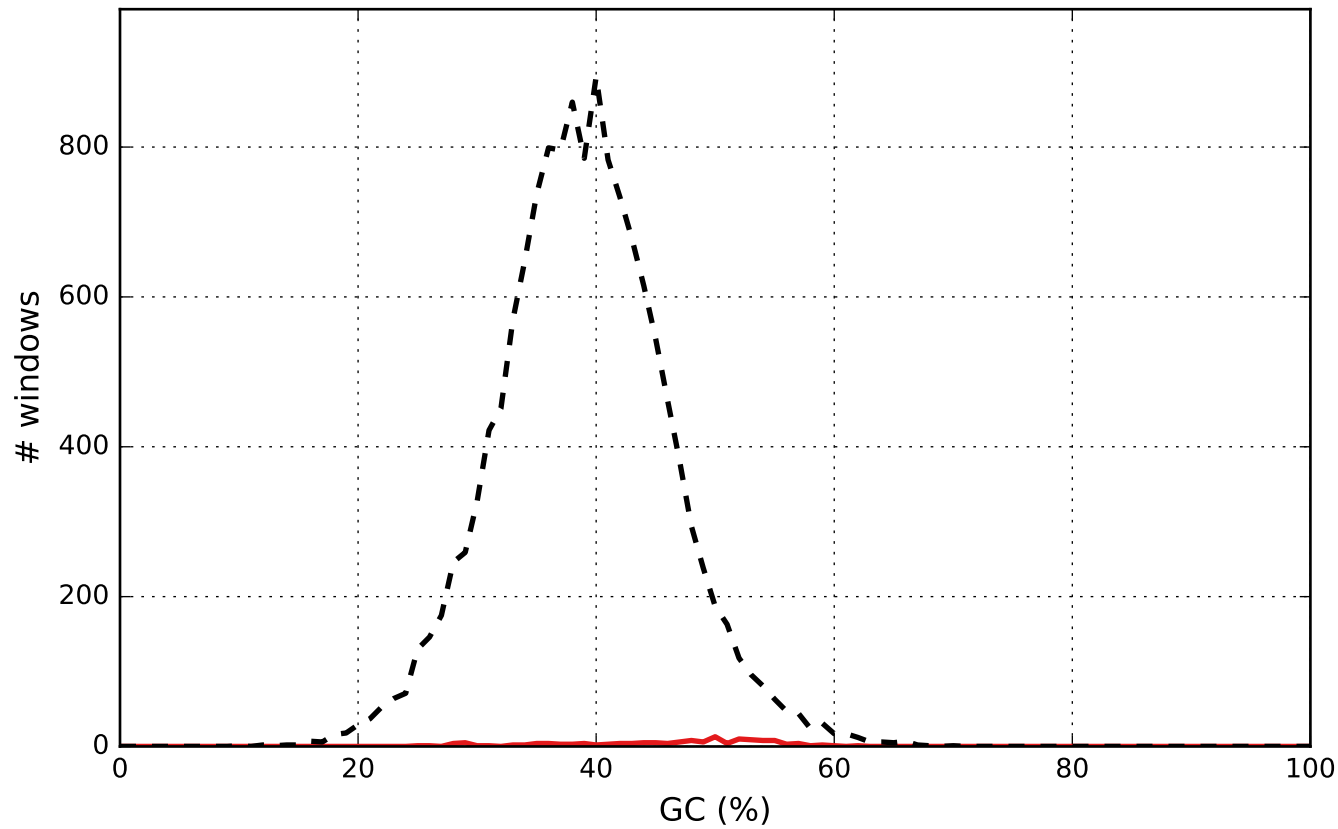
— final.contigs

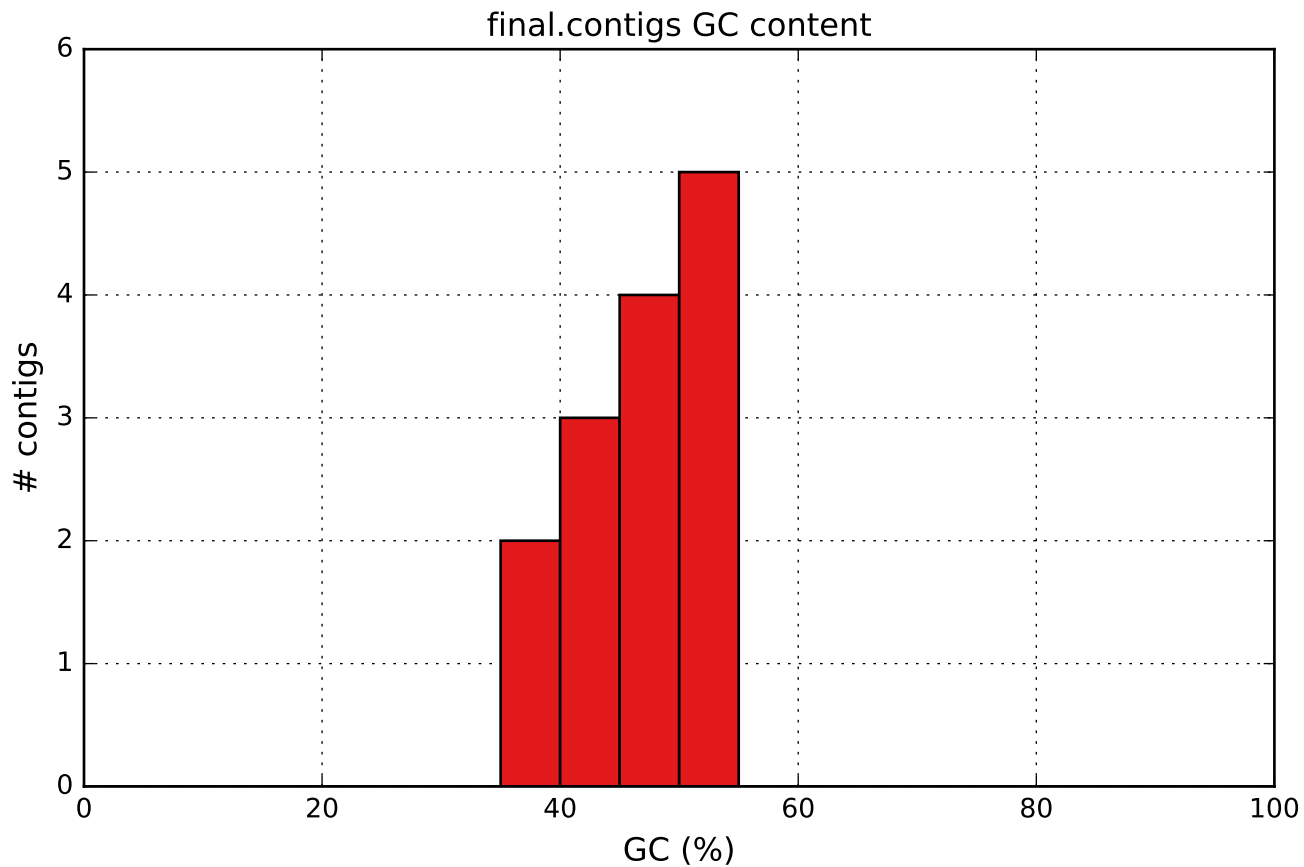


— final.contigs



# GC content



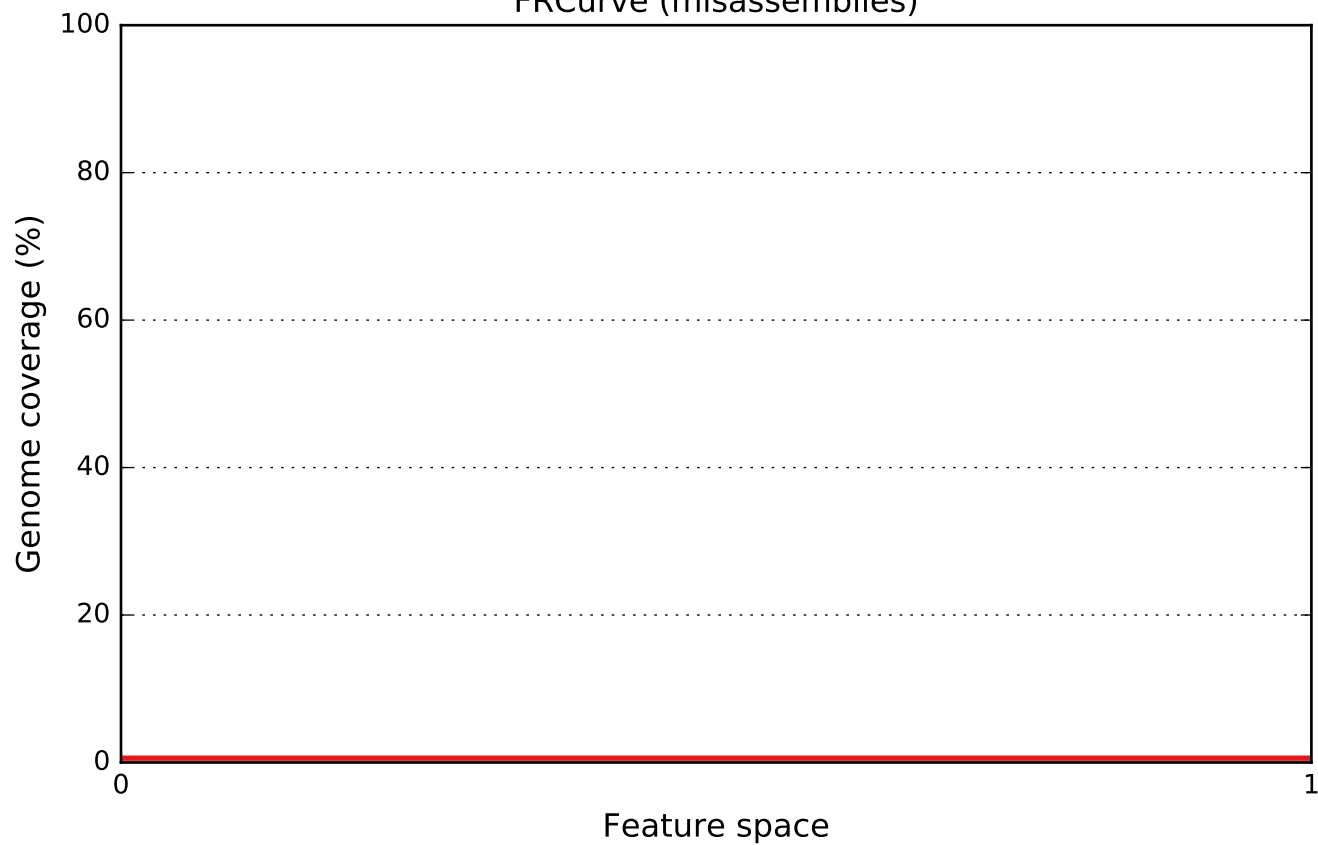


final.contigs



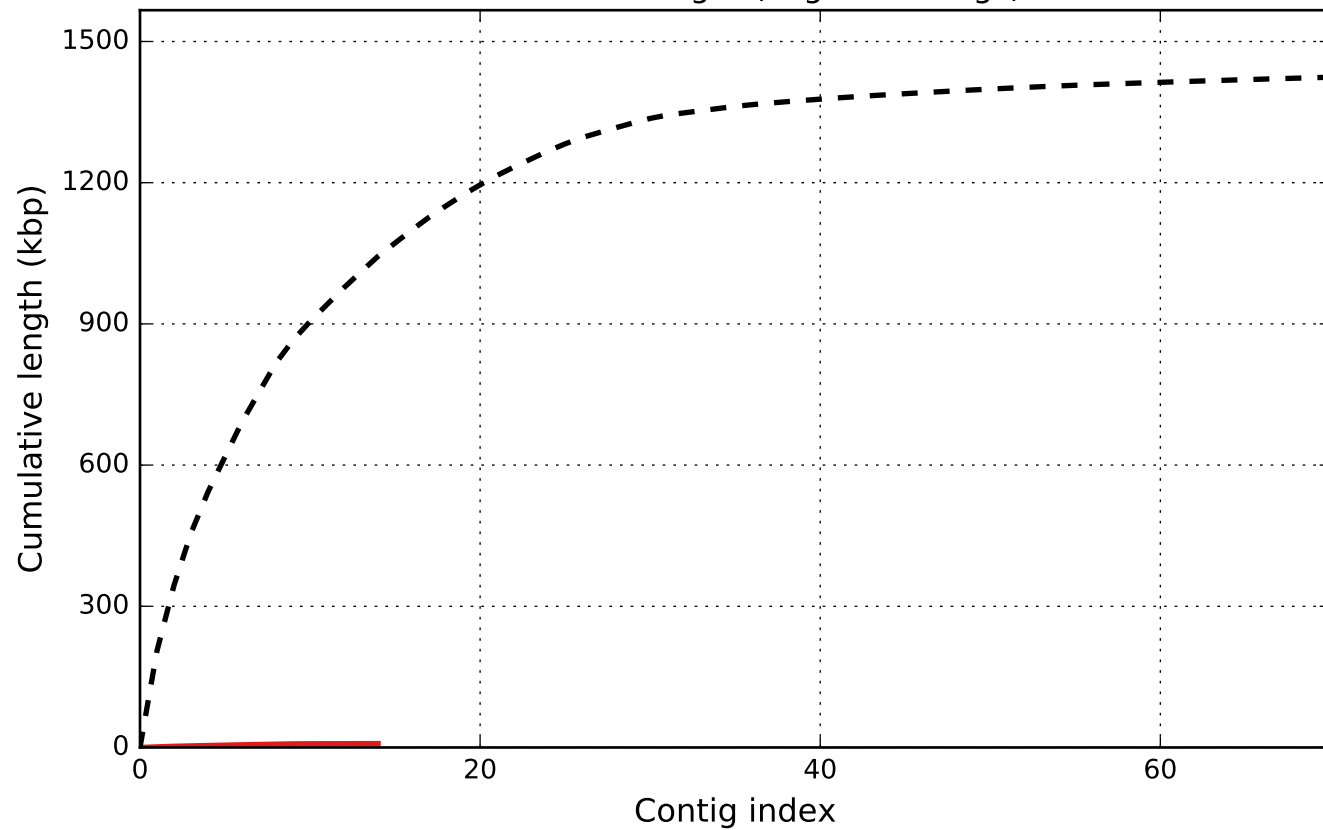


FRCurve (misassemblies)

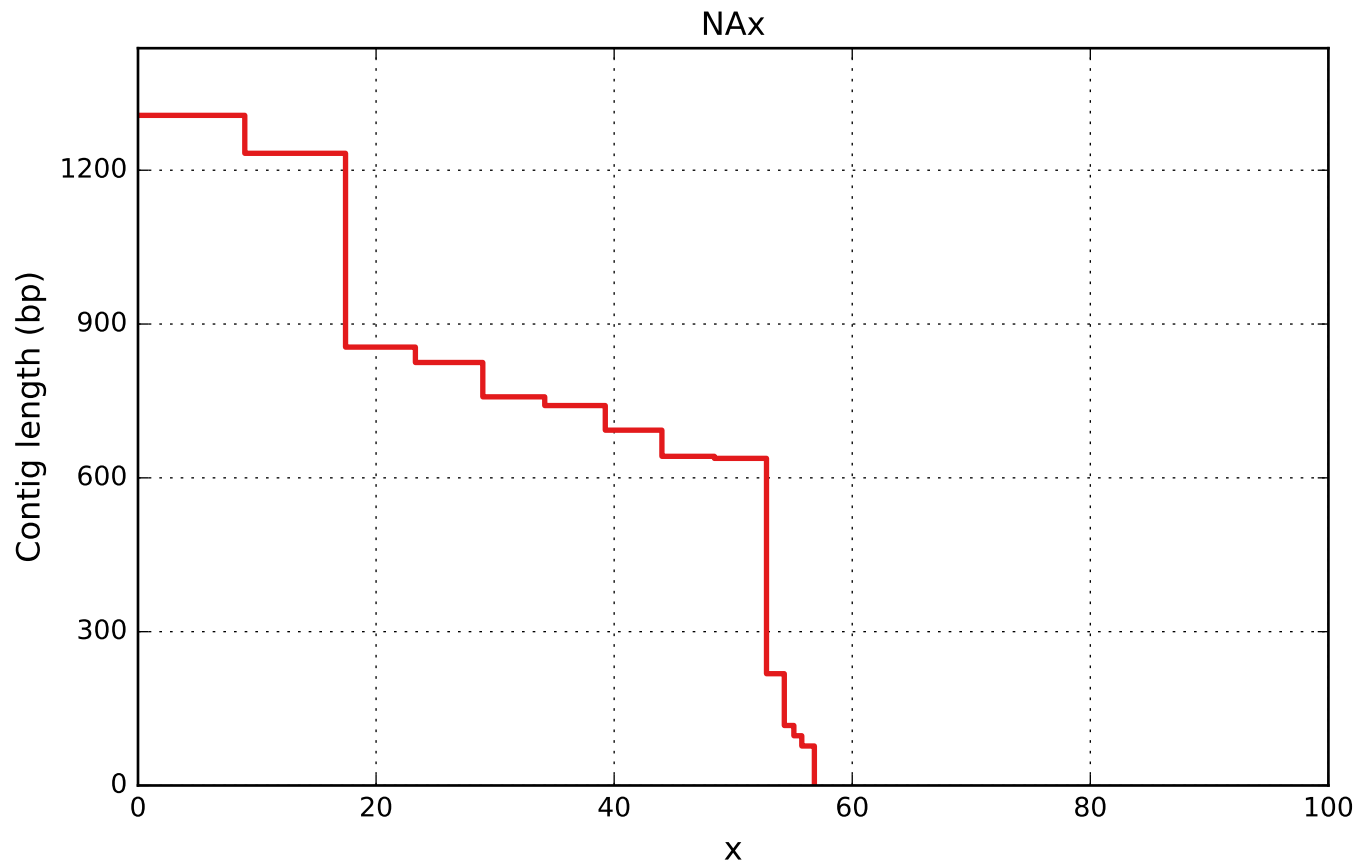


— final.contigs

Cumulative length (aligned contigs)

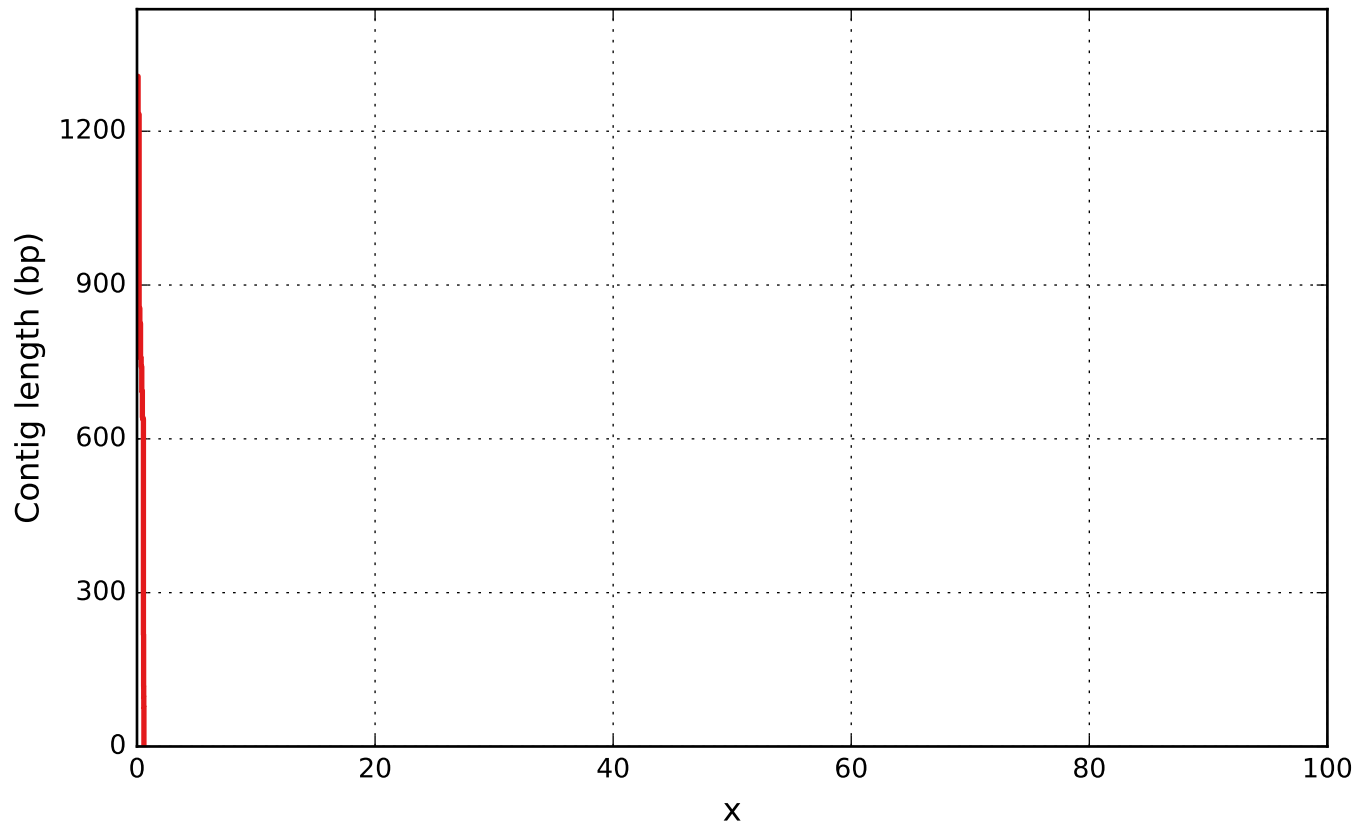


— final.contigs    - - Reference



— final.contigs

NGAx



— final.contigs