

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	69
# contigs ( $\geq 1000$ bp)	67
Total length ( $\geq 0$ bp)	1236567
Total length ( $\geq 1000$ bp)	1235477
# contigs	69
Largest contig	70492
Total length	1236567
Reference length	615980
GC (%)	25.34
Reference GC (%)	25.33
N50	28564
NG50	43757
N75	17290
NG75	39955
L50	14
LG50	6
L75	29
LG75	9
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	34 + 0 part
Unaligned length	617774
Genome fraction (%)	99.928
Duplication ratio	1.005
# N's per 100 kbp	0.00
# mismatches per 100 kbp	3.74
# indels per 100 kbp	0.00
Largest alignment	53282
NA50	545
NGA50	29046
NGA75	17462
LA50	35
LGA50	8
LGA75	15

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
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	23
# indels	0
# short indels	0
# long indels	0
Indels length	0

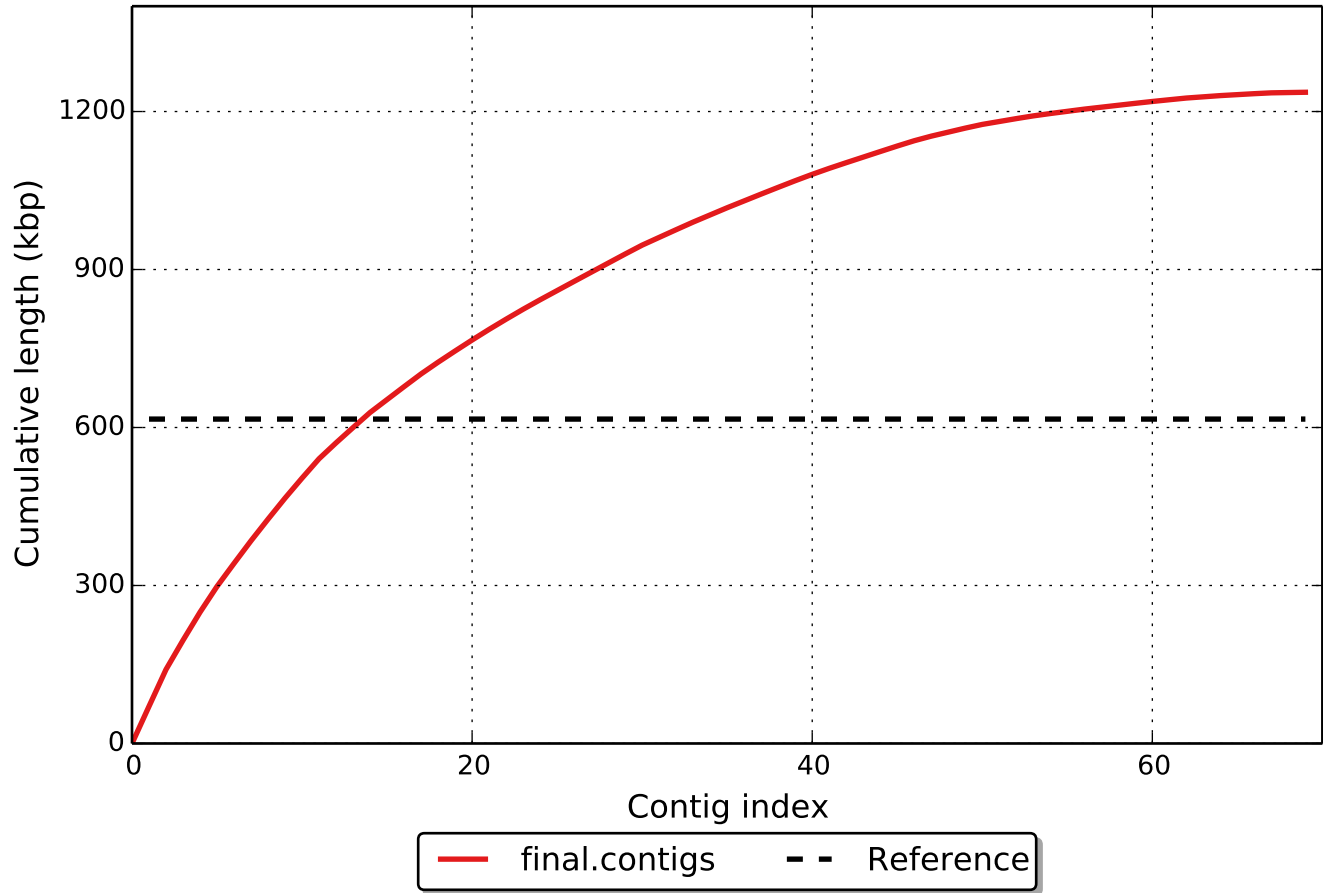
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

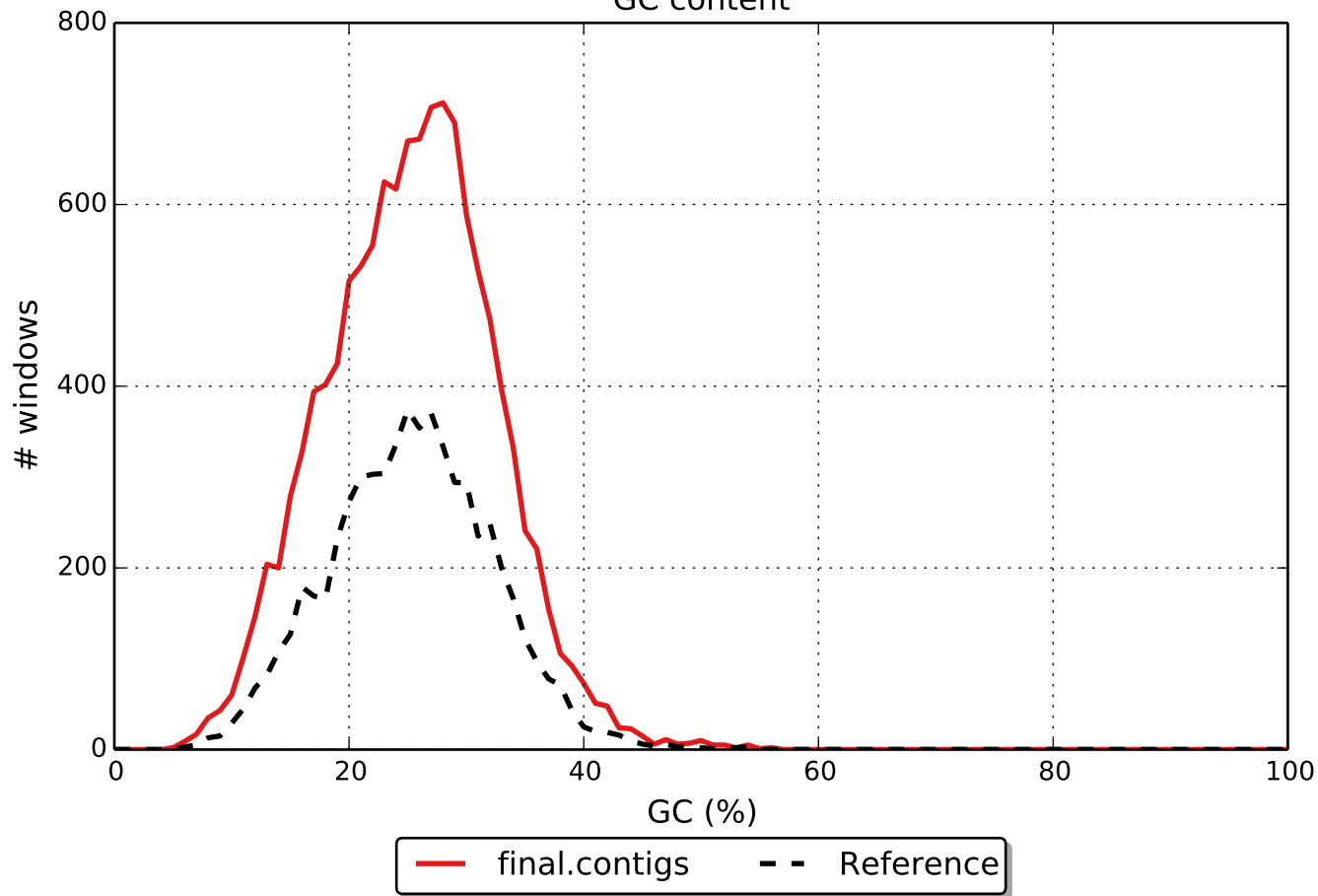
	final.contigs
# fully unaligned contigs	34
Fully unaligned length	617774
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

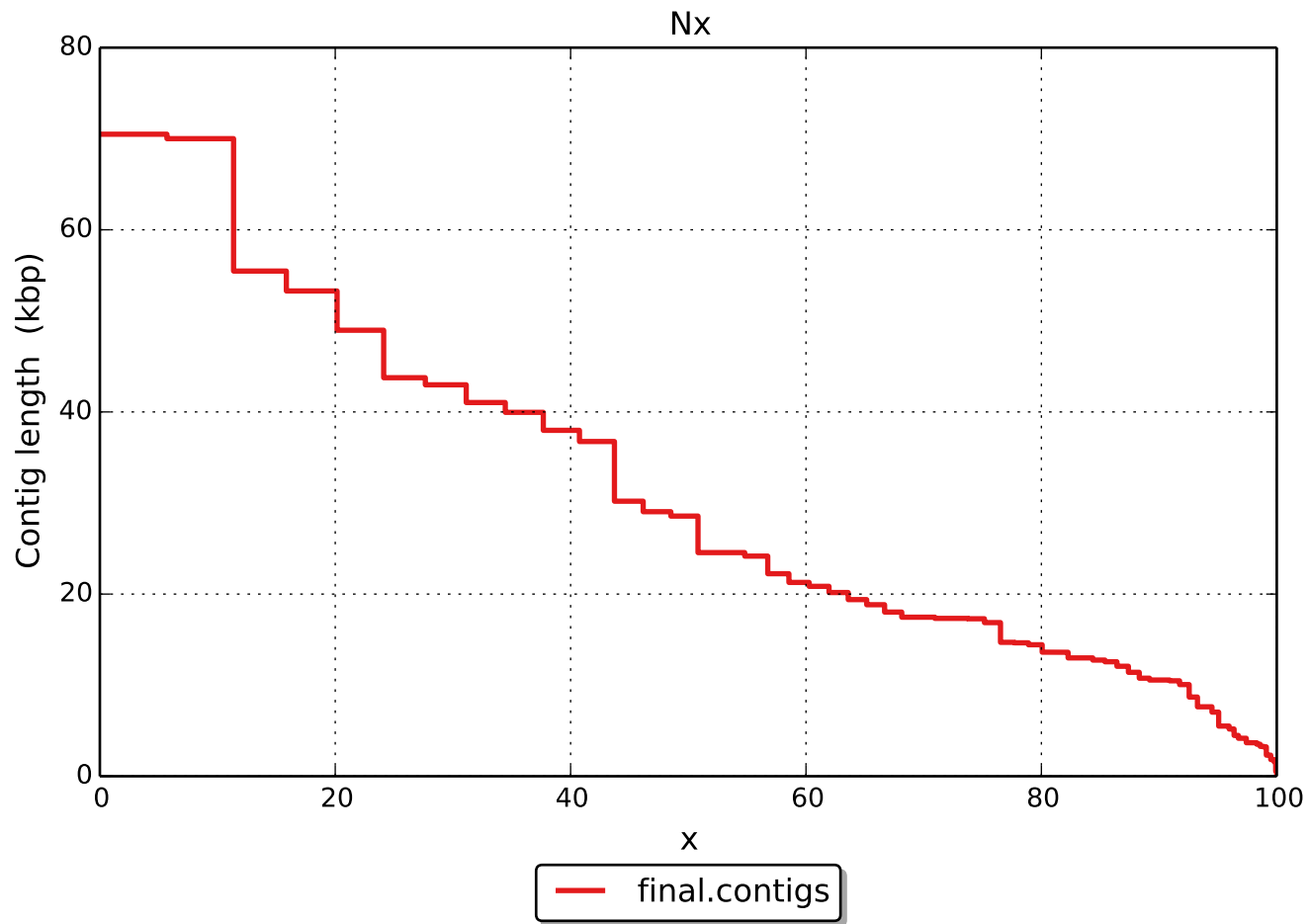
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

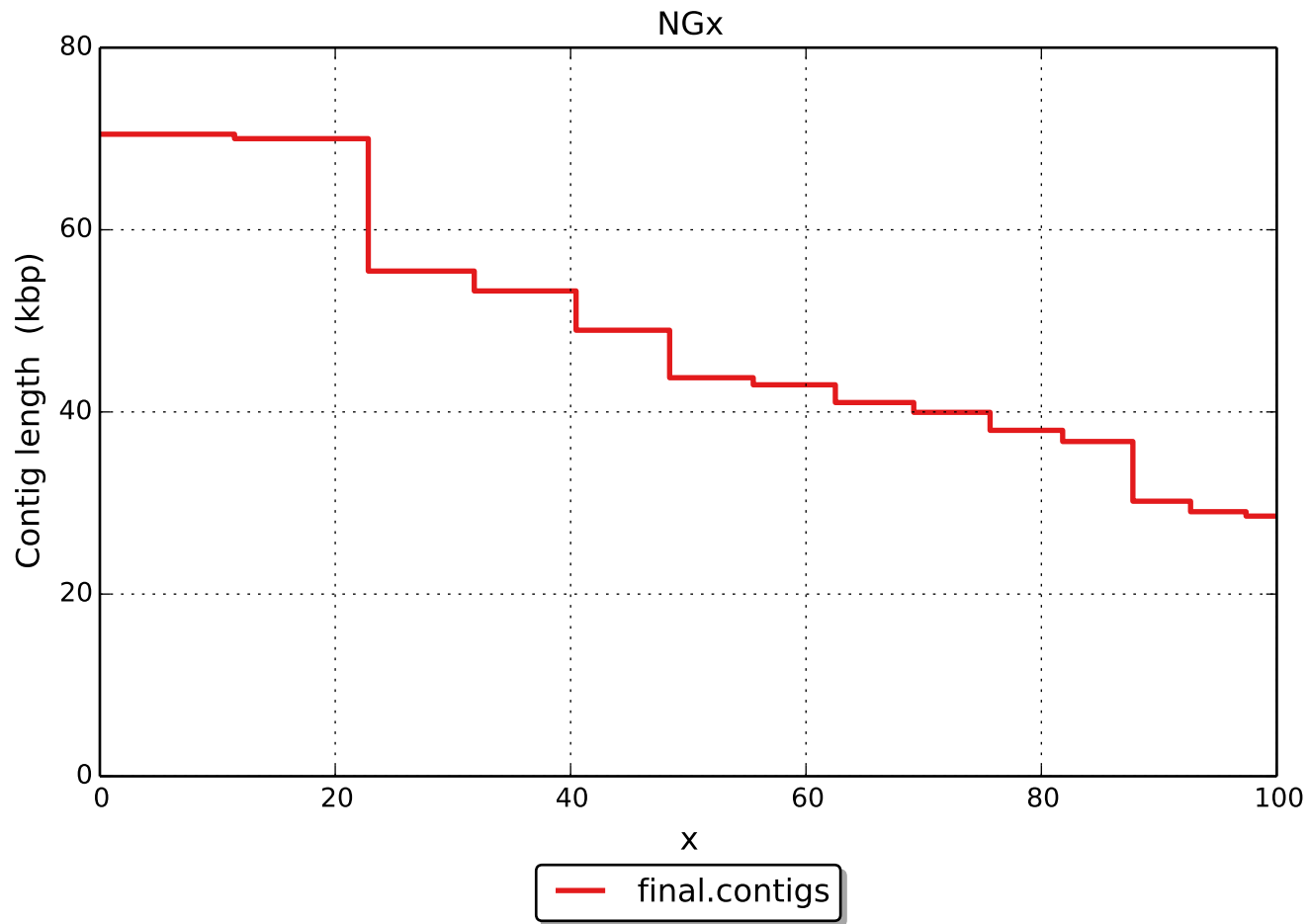
Cumulative length



GC content





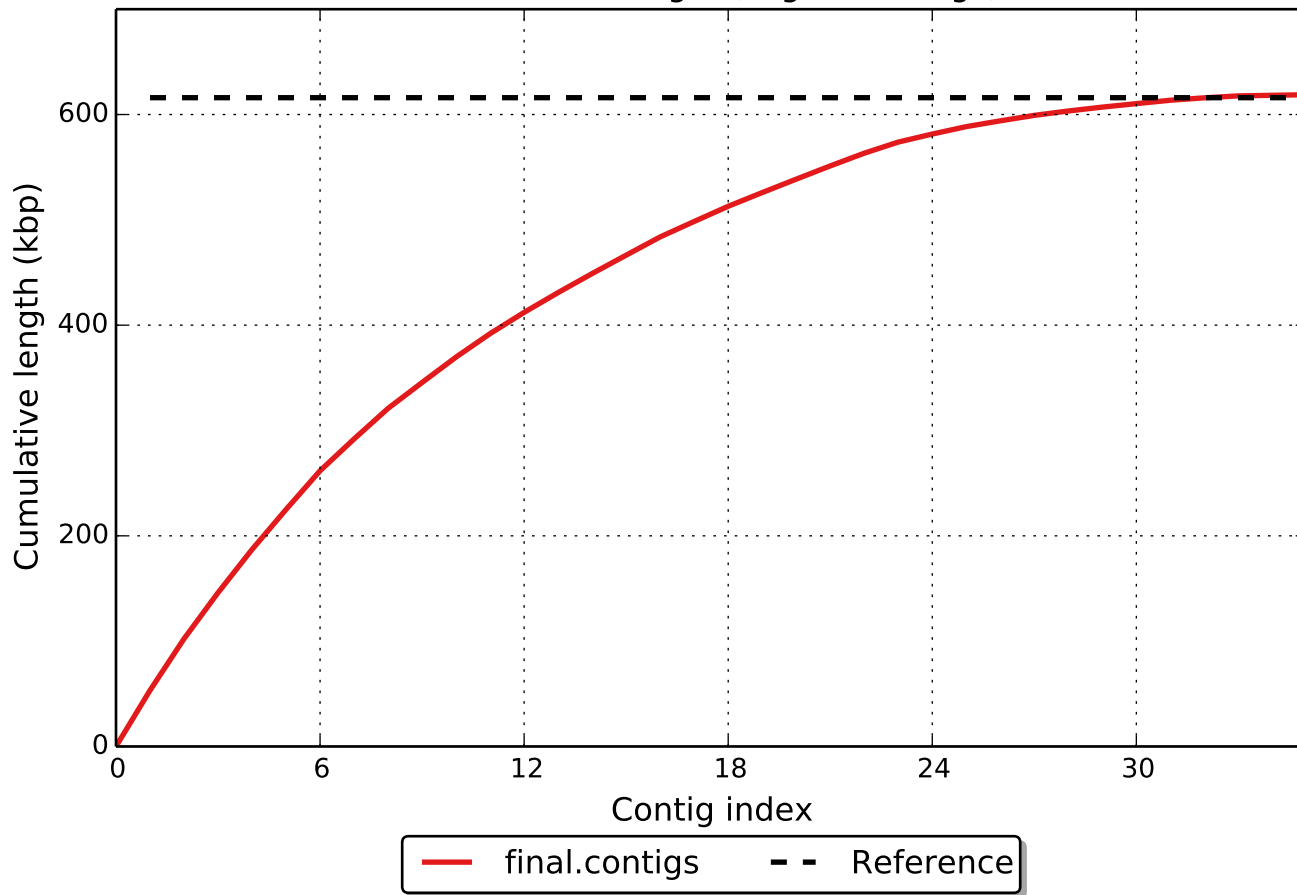


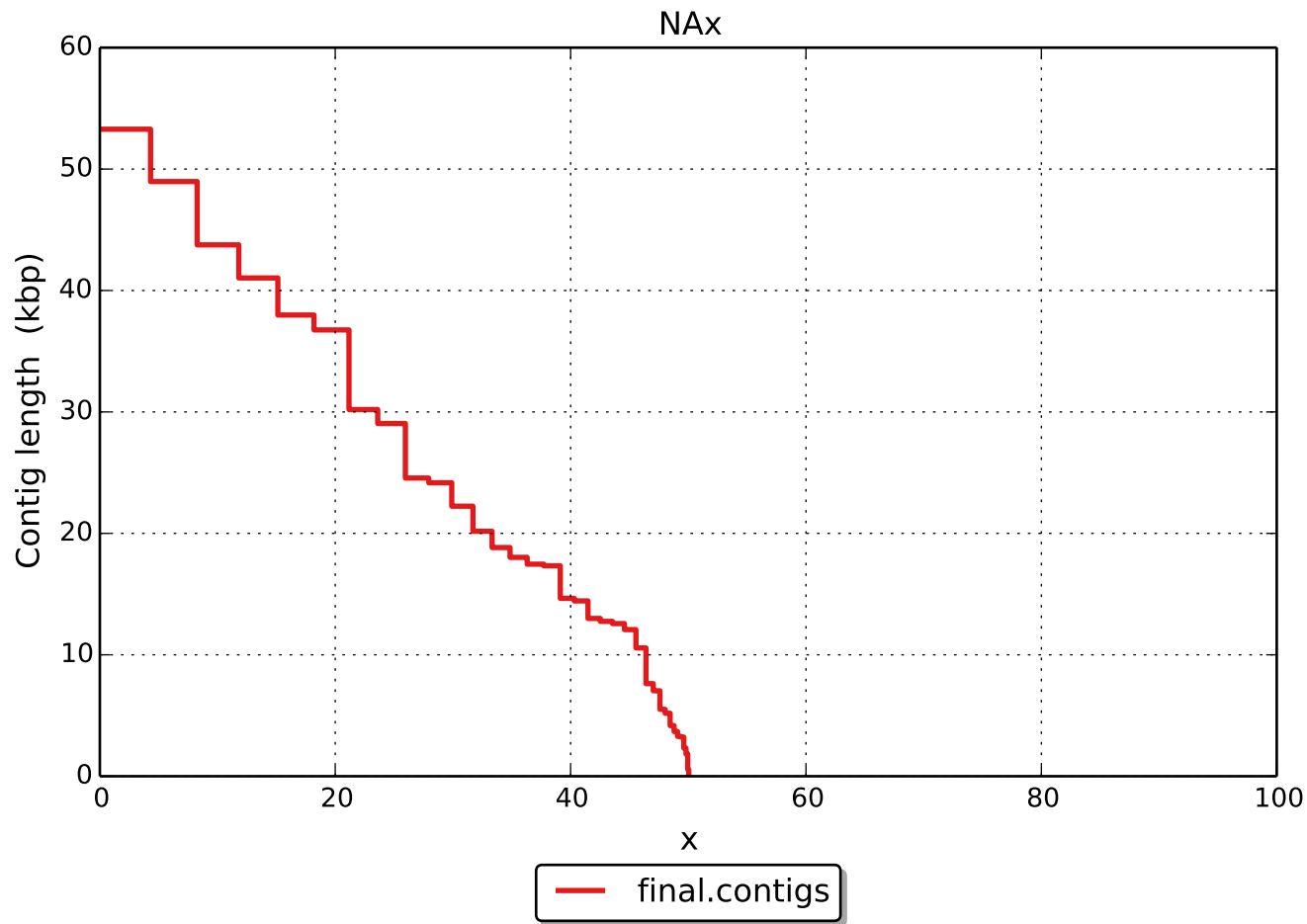
# Misassemblies





Cumulative length (aligned contigs)





NGAx

