

## Report

	final.contigs
# contigs ( $\geq 1000$ bp)	364
# contigs ( $\geq 5000$ bp)	164
# contigs ( $\geq 10000$ bp)	66
# contigs ( $\geq 25000$ bp)	6
# contigs ( $\geq 50000$ bp)	0
Total length ( $\geq 1000$ bp)	2289646
Total length ( $\geq 5000$ bp)	1744137
Total length ( $\geq 10000$ bp)	1056581
Total length ( $\geq 25000$ bp)	179209
Total length ( $\geq 50000$ bp)	0
# contigs	491
Largest contig	35905
Total length	2371991
Reference length	4857432
GC (%)	52.01
Reference GC (%)	52.22
N50	8937
N75	4693
L50	80
L75	172
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	48.382
Duplication ratio	1.009
# N's per 100 kbp	0.00
# mismatches per 100 kbp	426.02
# indels per 100 kbp	0.00
Largest alignment	35905
NA50	8937
NGA50	-
NA75	4693
LA50	80
LA75	172

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

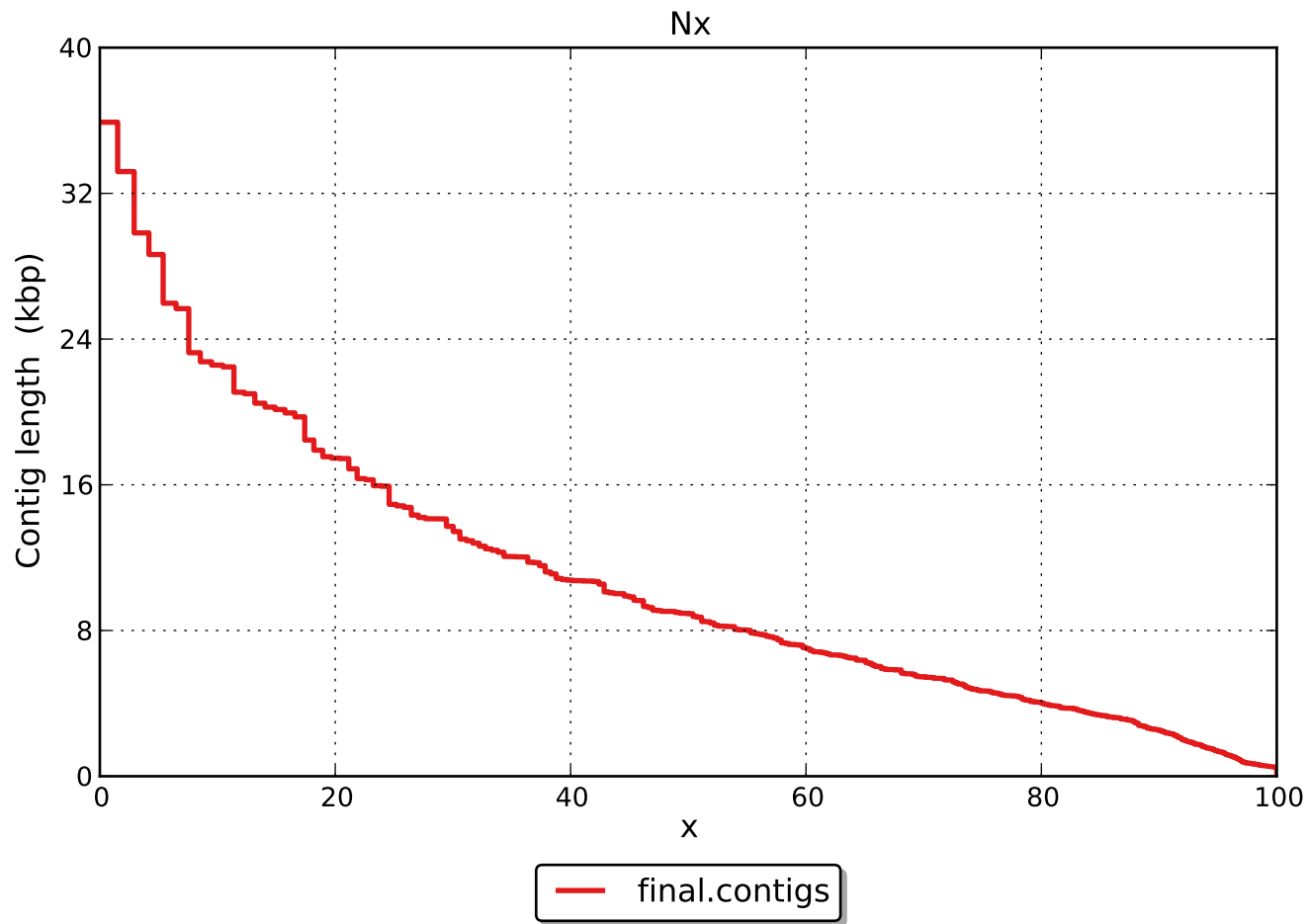
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	10012
# indels	0
# short indels	0
# long indels	0
Indels length	0

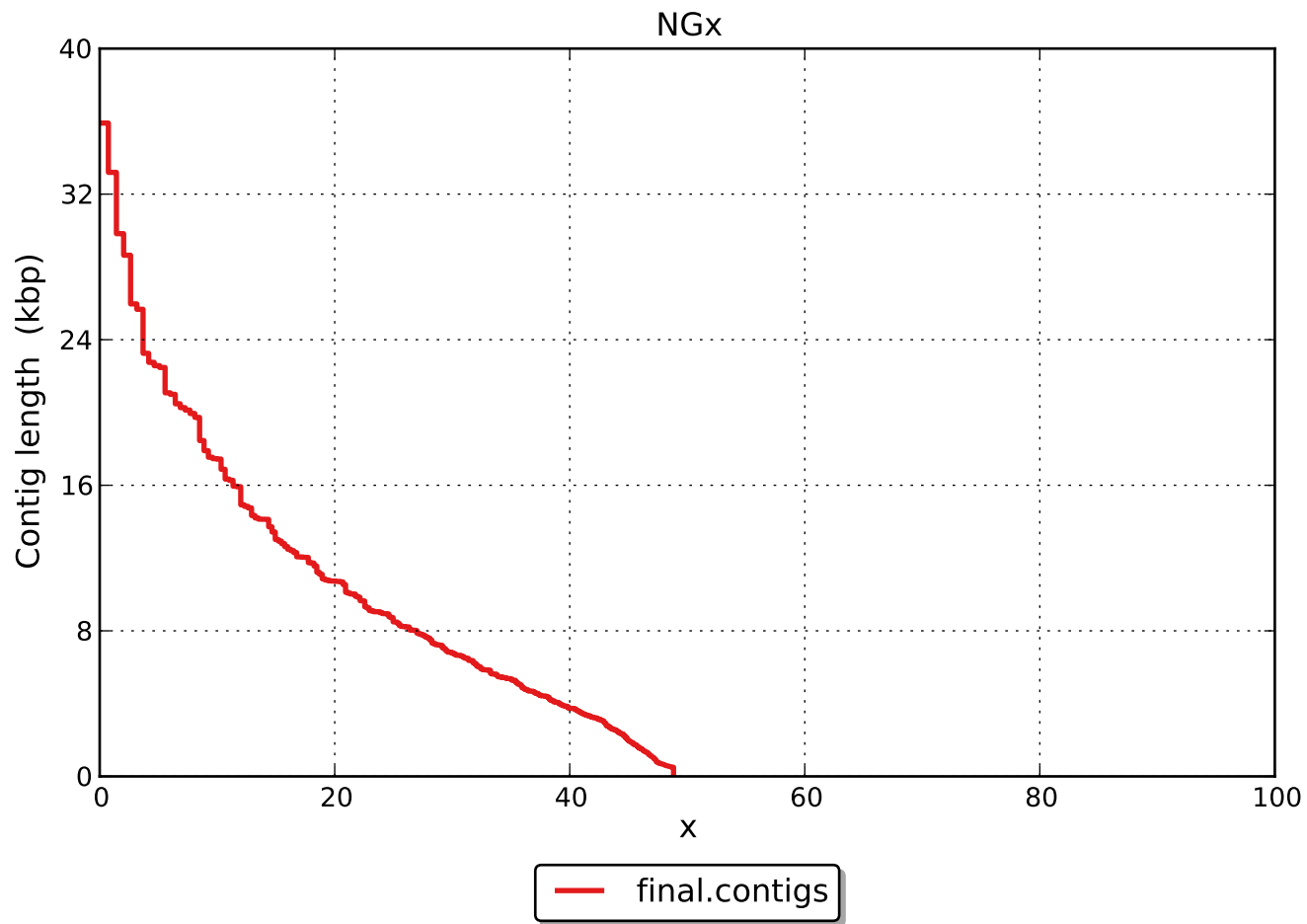
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

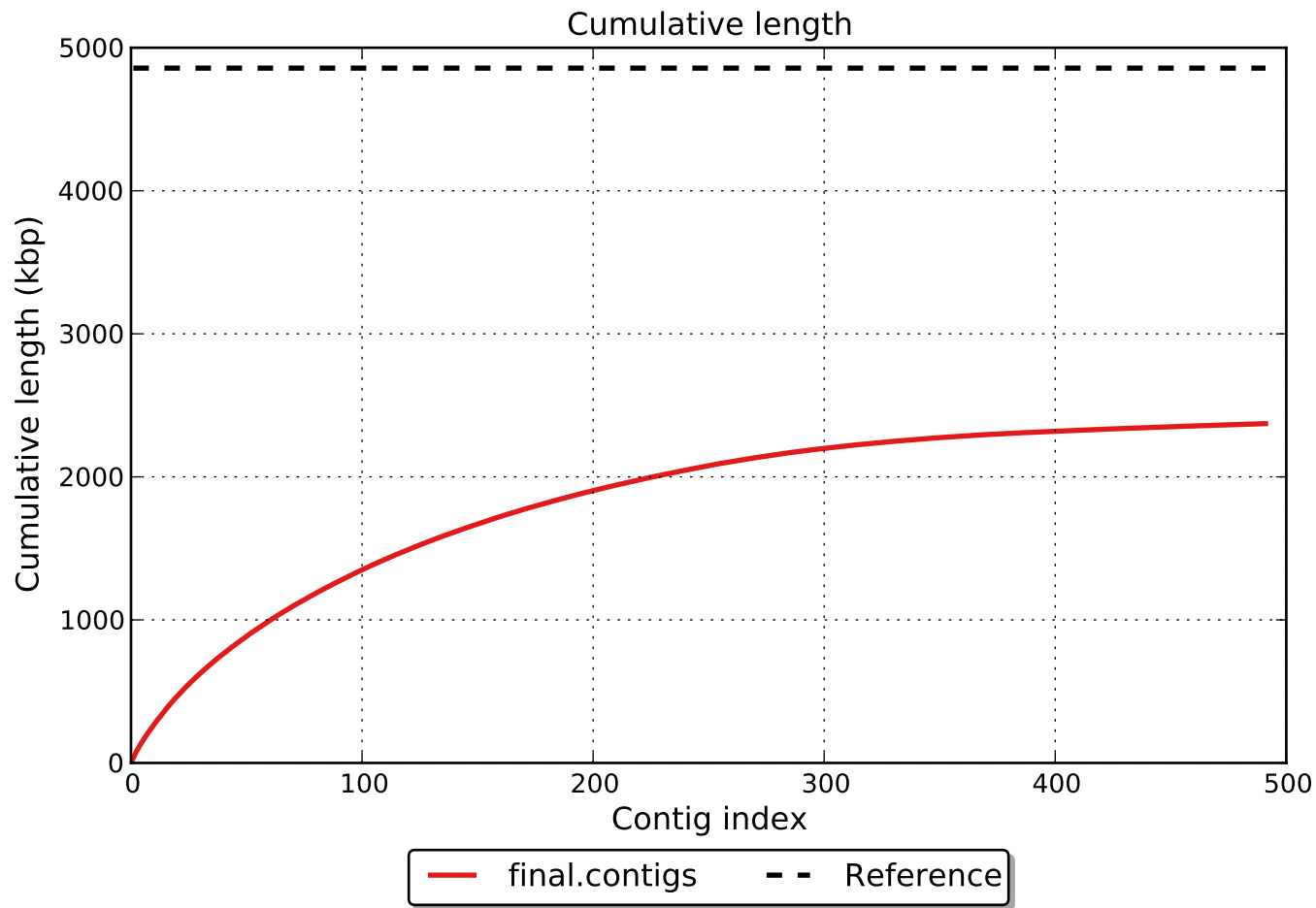
## Unaligned report

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

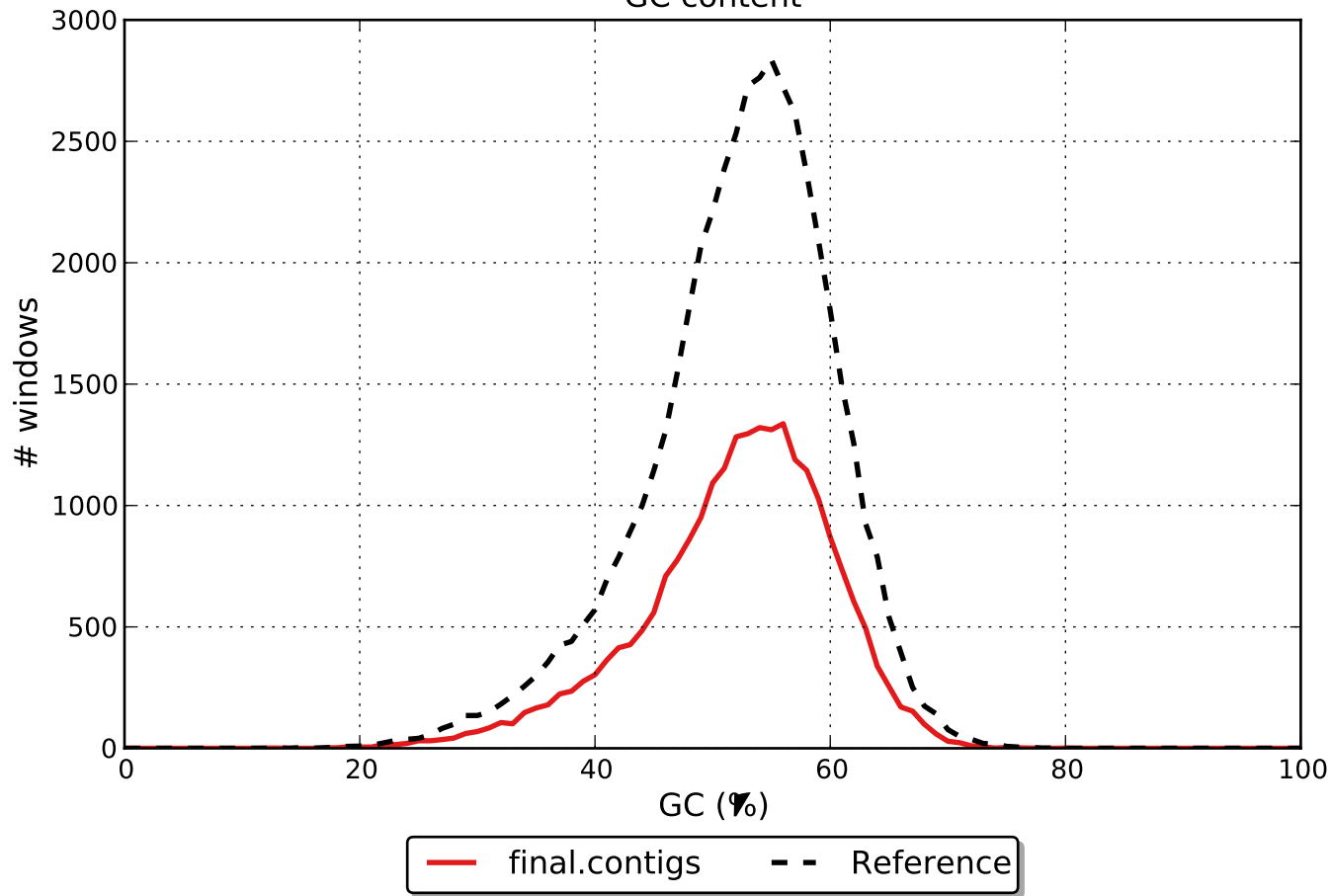
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).







GC content

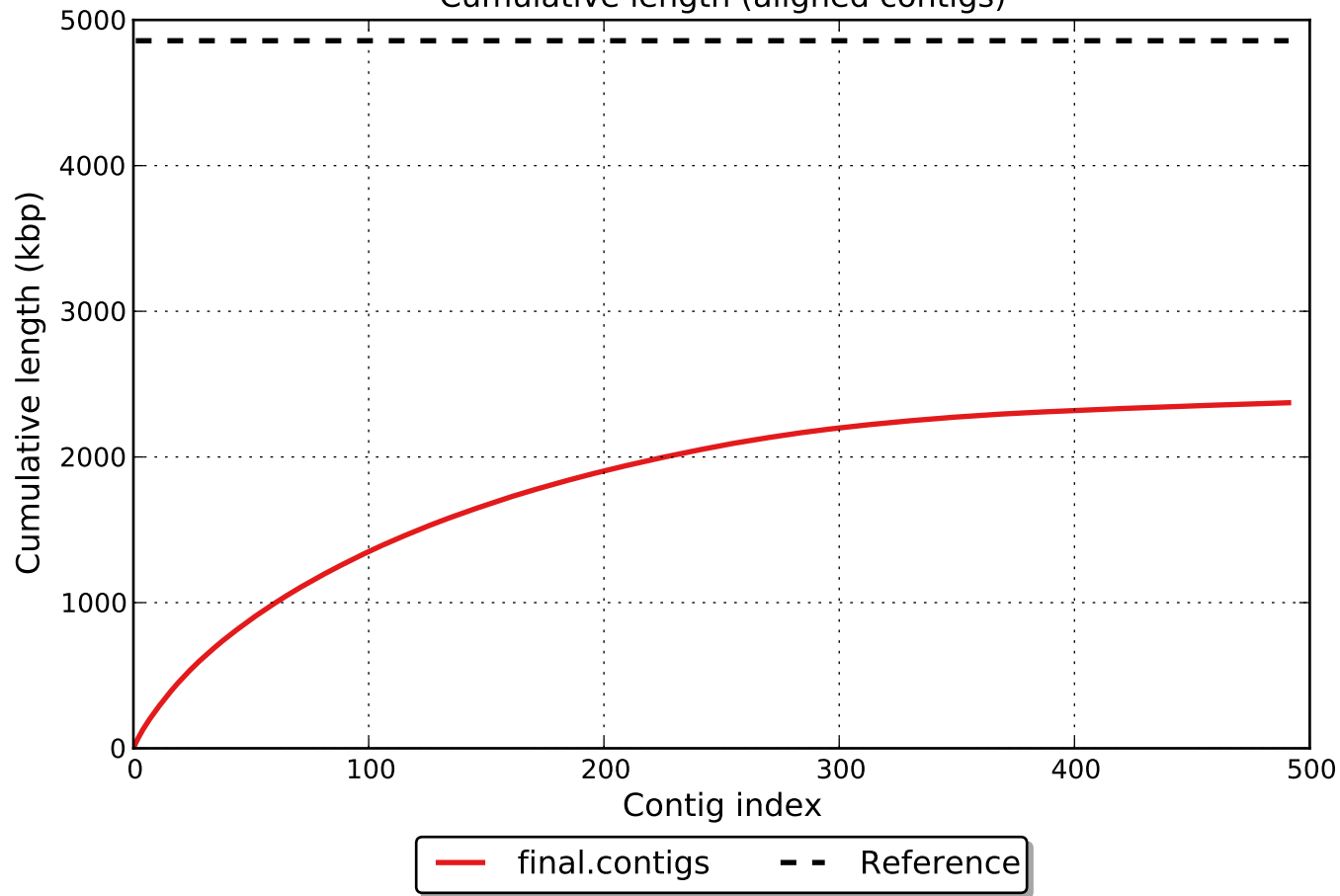


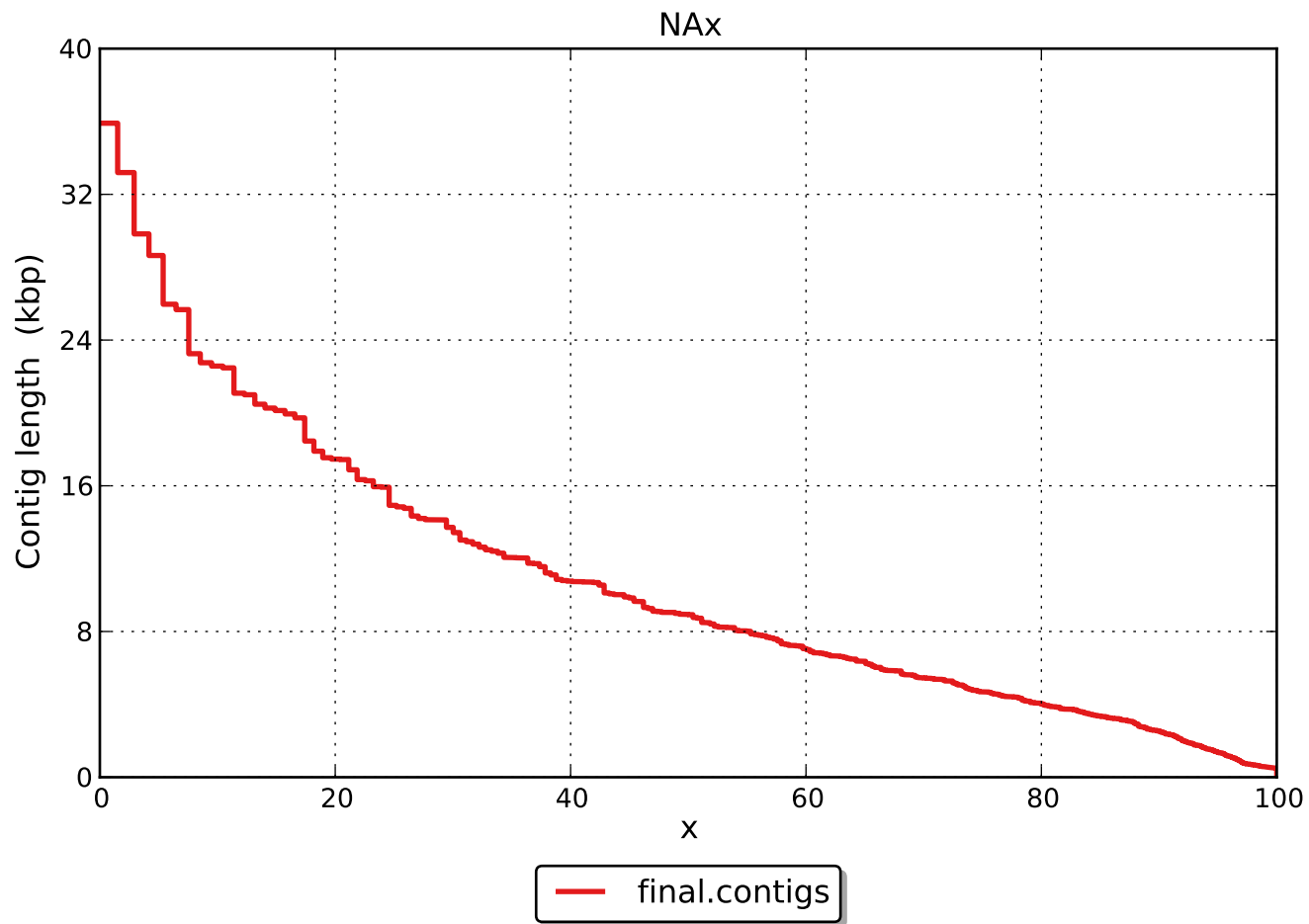
# Misassemblies



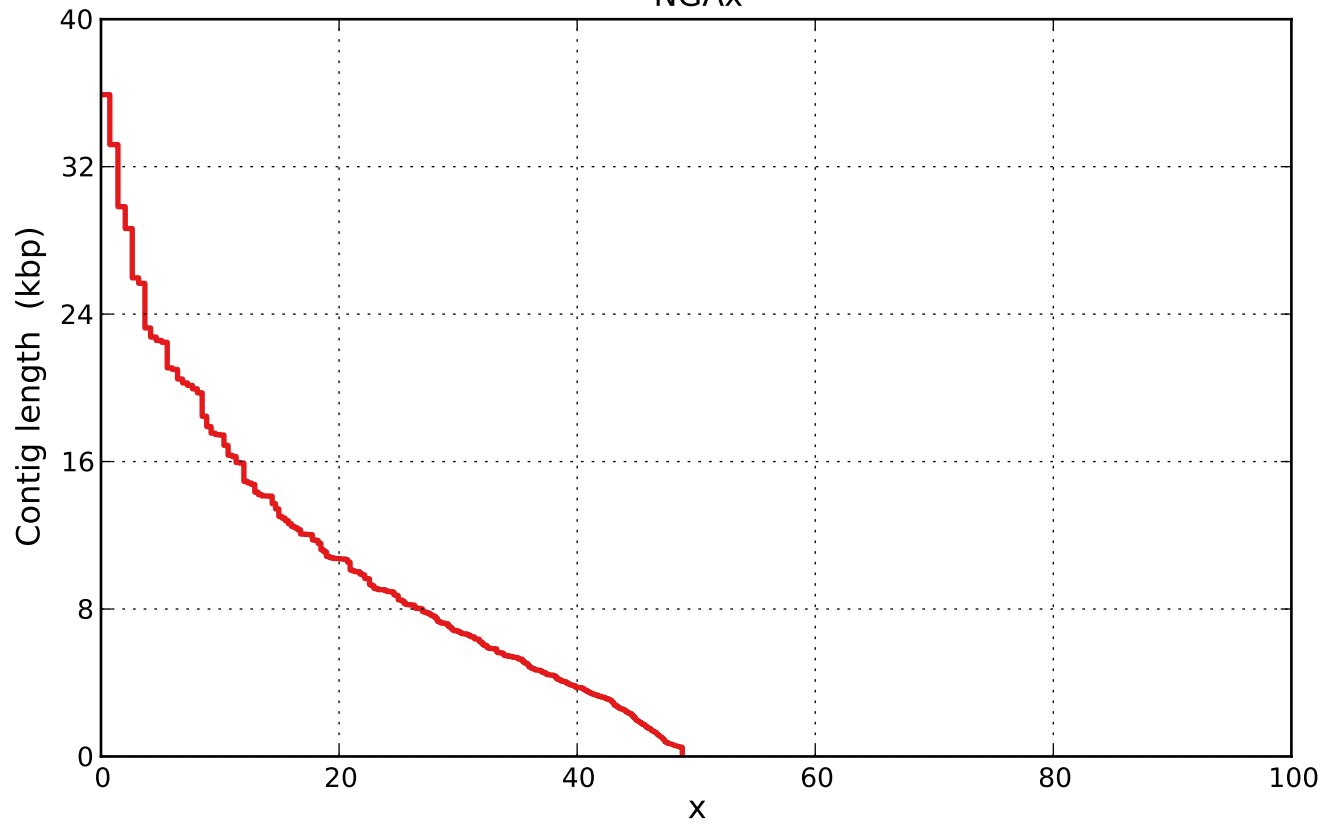


Cumulative length (aligned contigs)





NGAx



— final.contigs