

## Report

	final.contigs
# contigs (>= 0 bp)	99
# contigs (>= 1000 bp)	97
Total length (>= 0 bp)	1291392
Total length (>= 1000 bp)	1290438
# contigs	97
Largest contig	45036
Total length	1290438
Reference length	1283598
GC (%)	26.29
Reference GC (%)	26.31
N50	19749
NG50	19749
N75	12569
NG75	12768
L50	23
LG50	23
L75	44
LG75	43
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.950
Duplication ratio	1.006
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.00
Largest alignment	45036
NA50	19749
NGA50	19749
NA75	12569
NGA75	12768
LA50	23
LGA50	23
LA75	44
LGA75	43

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

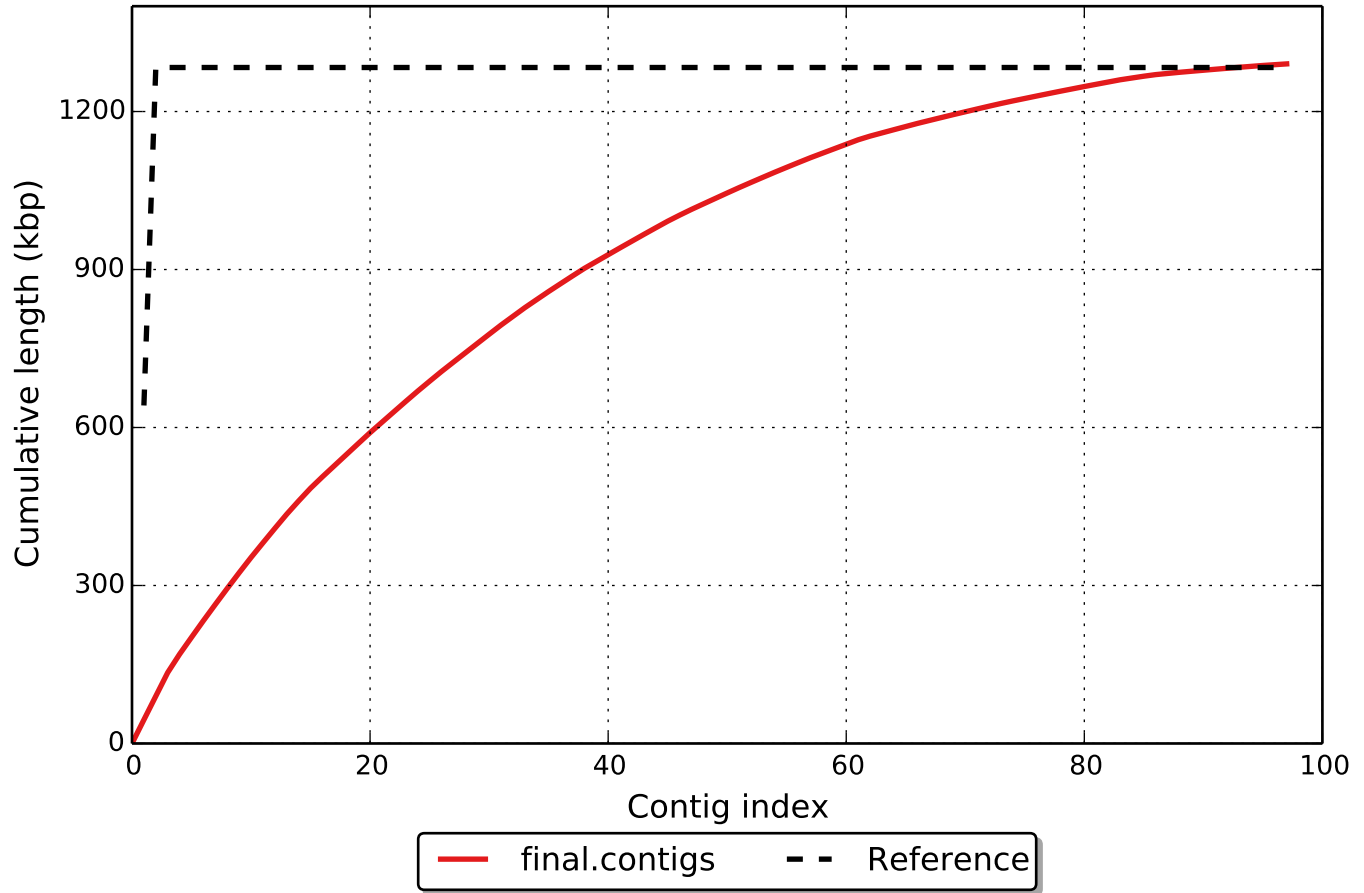
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

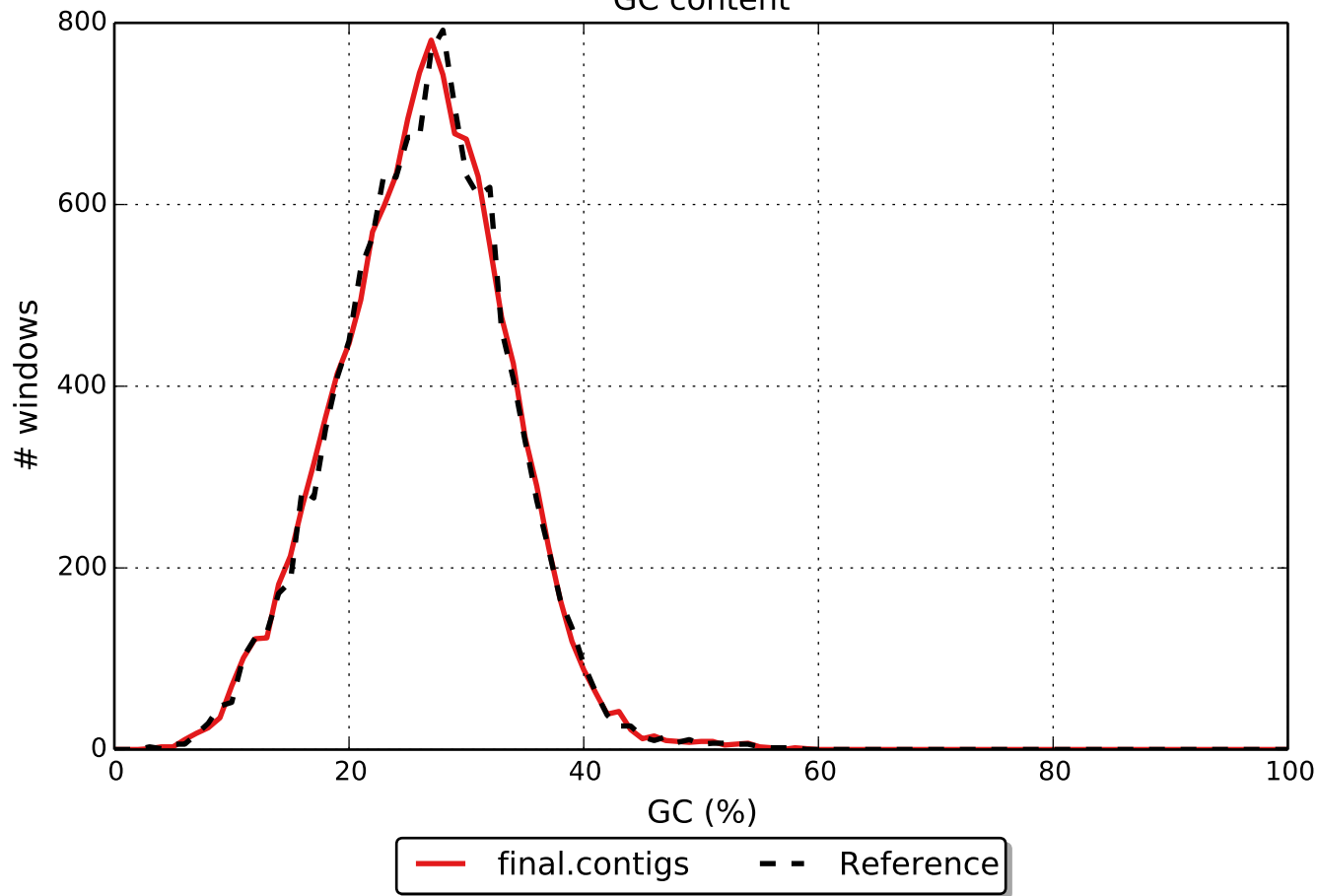
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

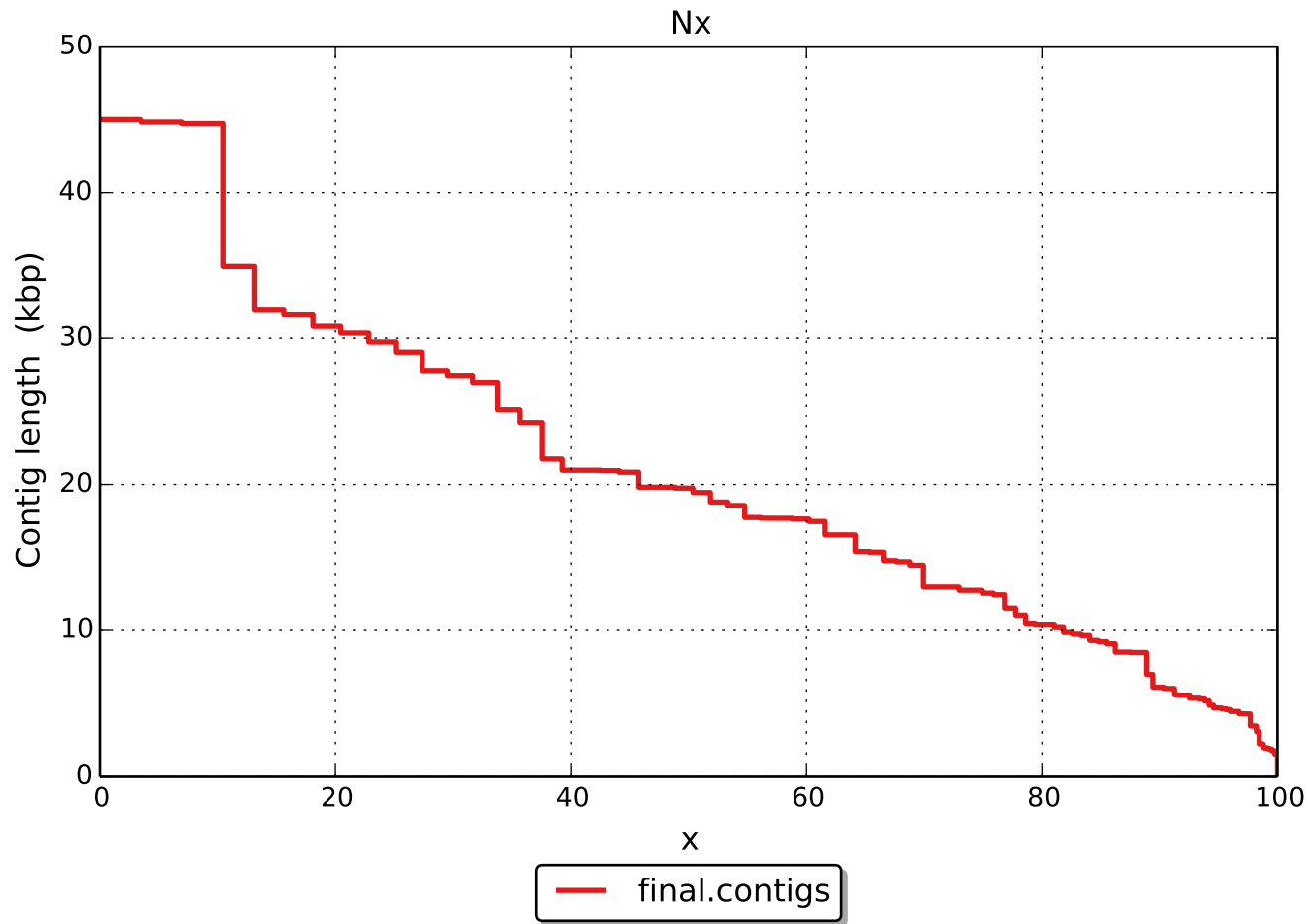
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

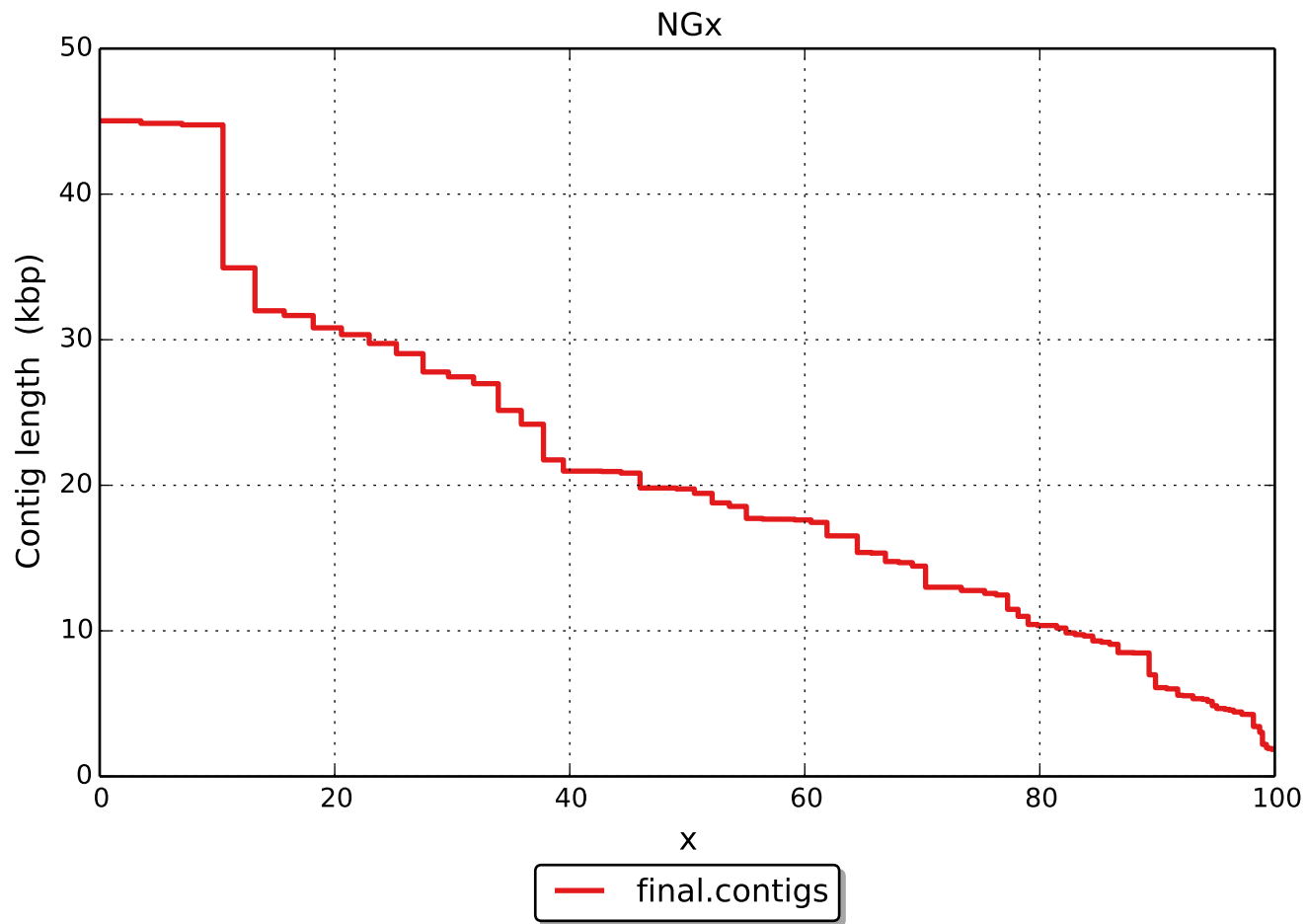
Cumulative length



GC content





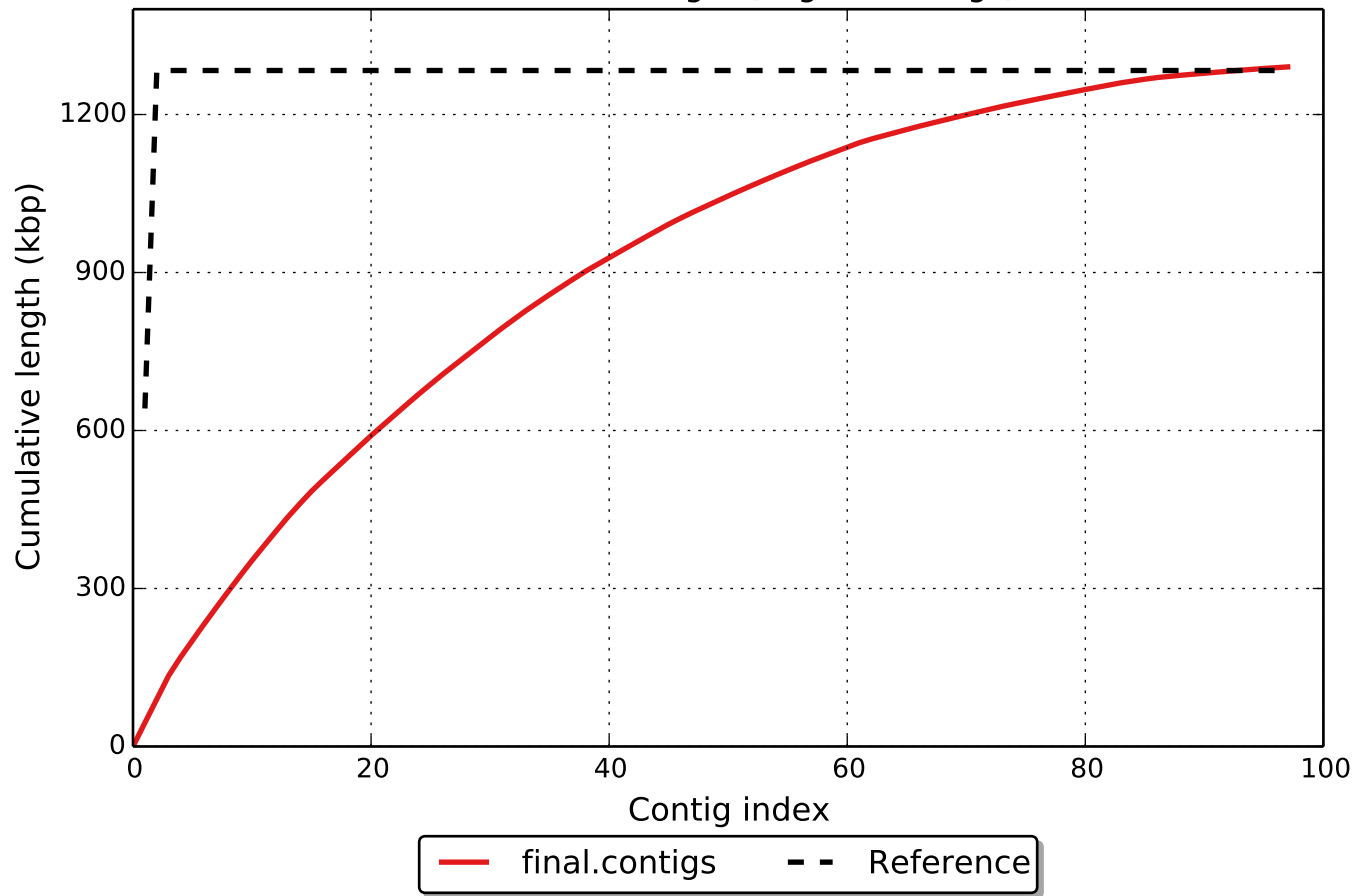


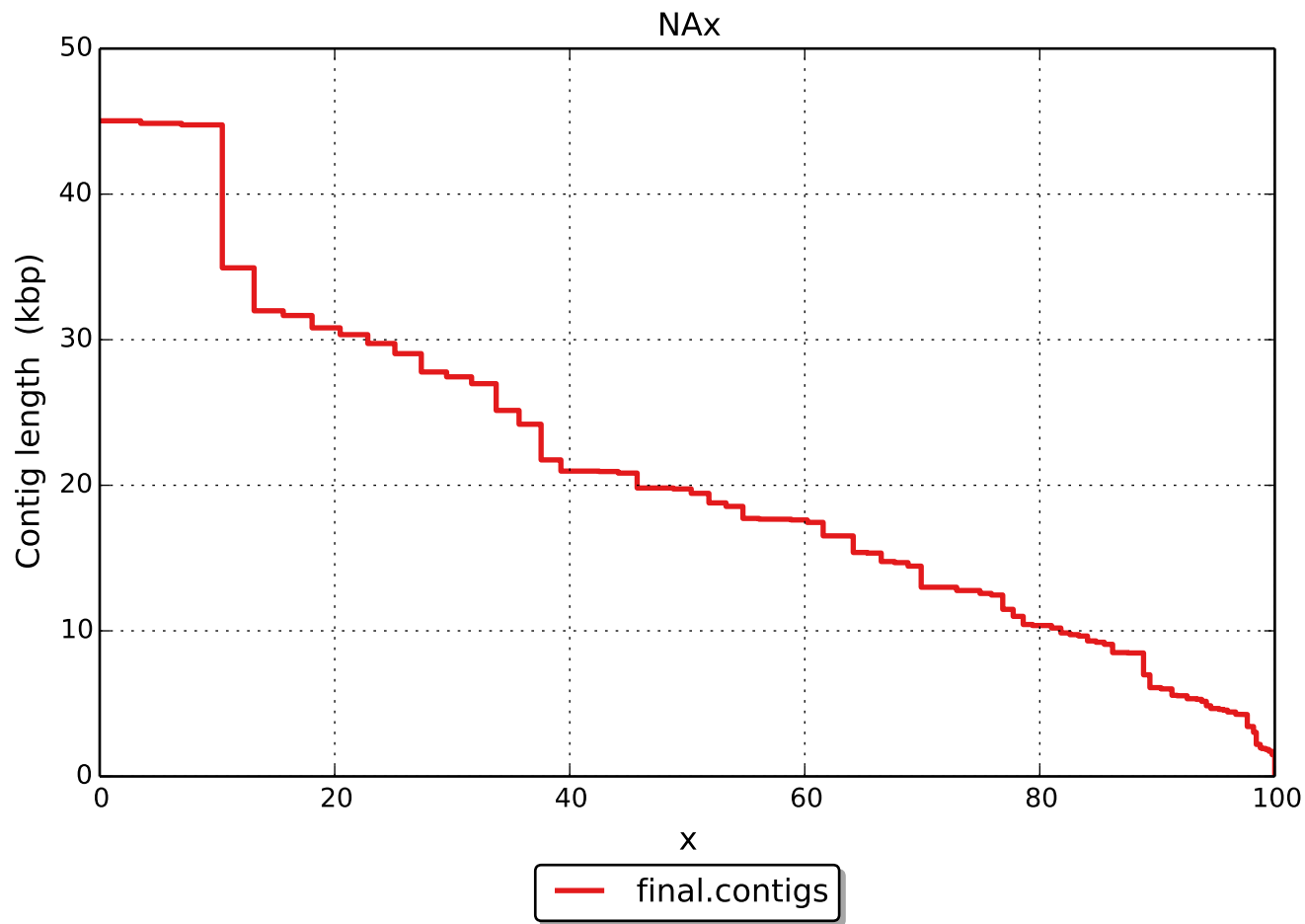
# Misassemblies





Cumulative length (aligned contigs)





# NGAx

