

## Report

	final.contigs
# contigs (>= 0 bp)	346
# contigs (>= 1000 bp)	262
Total length (>= 0 bp)	1308412
Total length (>= 1000 bp)	1256062
# contigs	318
Largest contig	23356
Total length	1298209
Reference length	1283598
GC (%)	26.30
Reference GC (%)	26.30
N50	6054
NG50	6098
N75	3538
NG75	3592
L50	65
LG50	64
L75	136
LG75	133
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.203
Duplication ratio	1.020
# N's per 100 kbp	0.00
# mismatches per 100 kbp	15.55
# indels per 100 kbp	0.16
Largest alignment	23356
NA50	6054
NGA50	6098
NA75	3538
NGA75	3592
LA50	65
LGA50	64
LA75	136
LGA75	133

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	198
# indels	2
# short indels	2
# long indels	0
Indels length	2

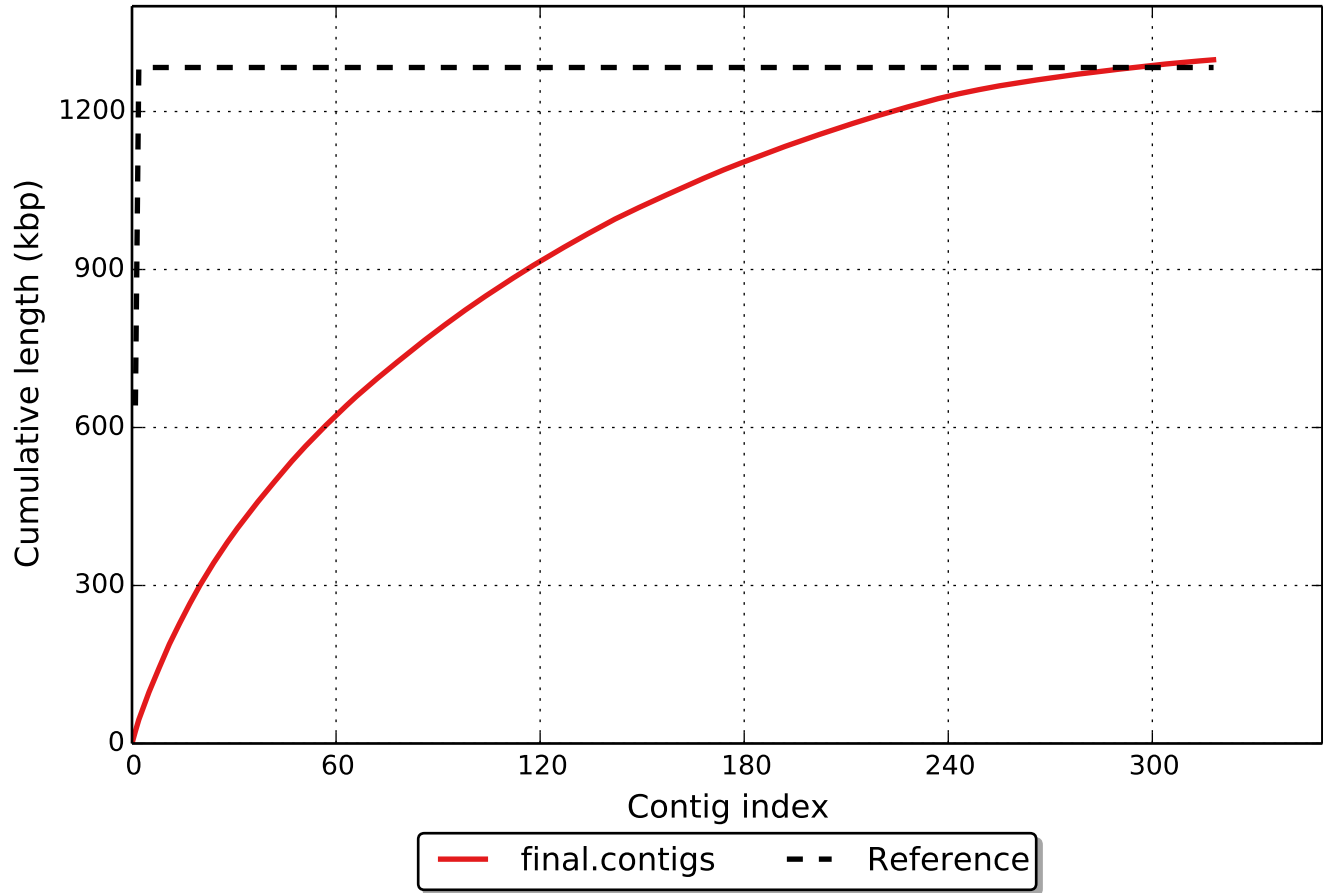
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

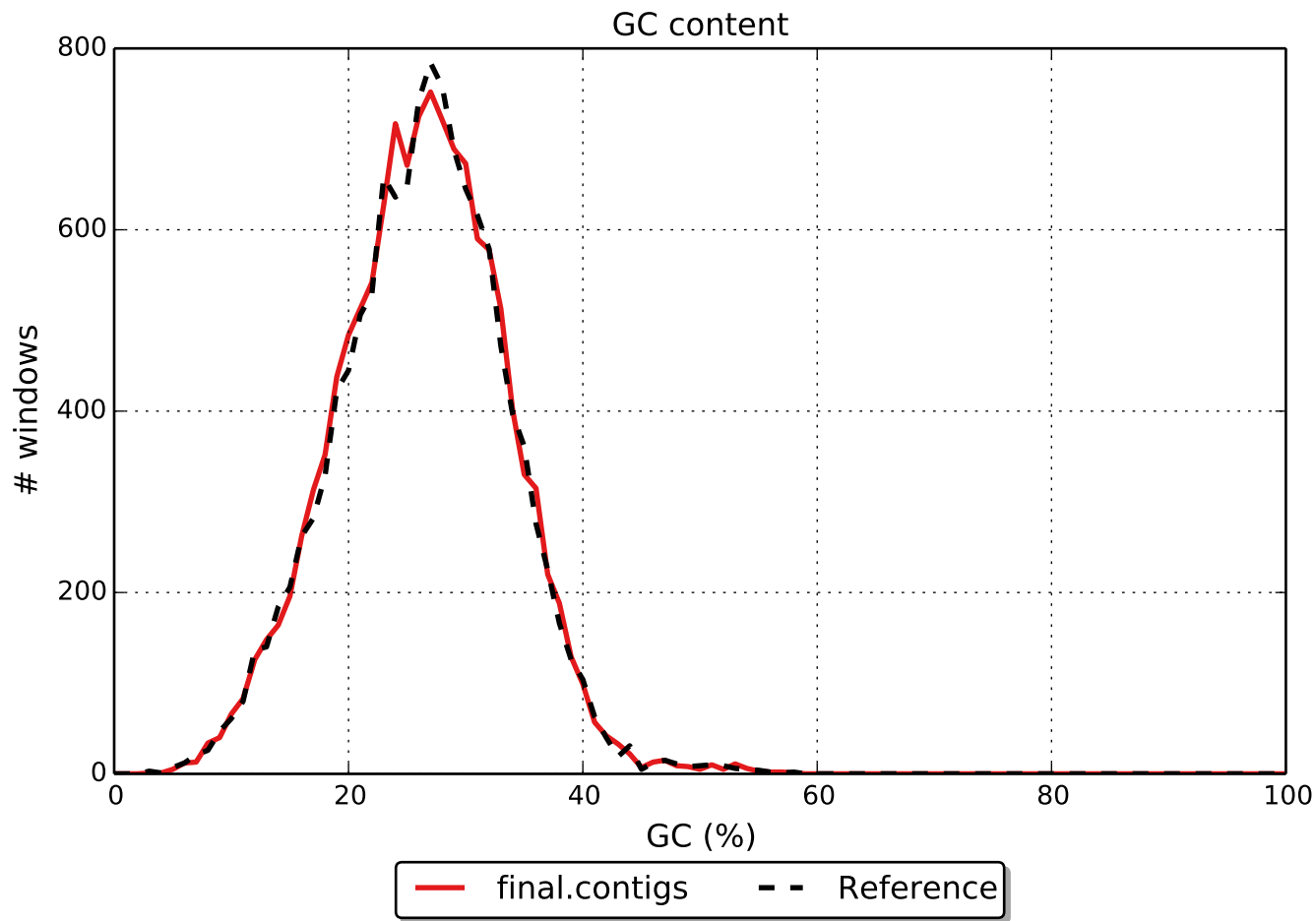
## Unaligned report

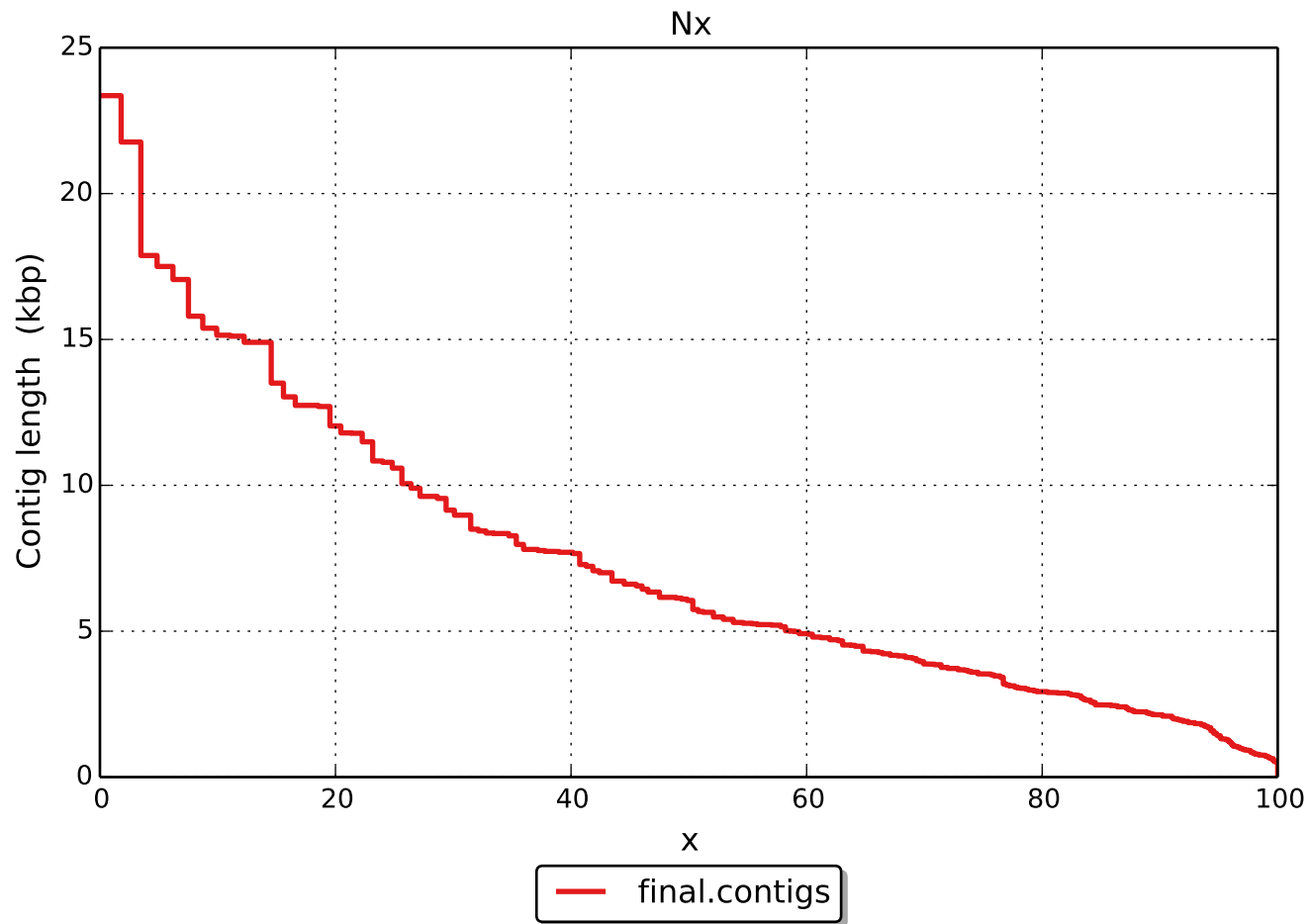
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

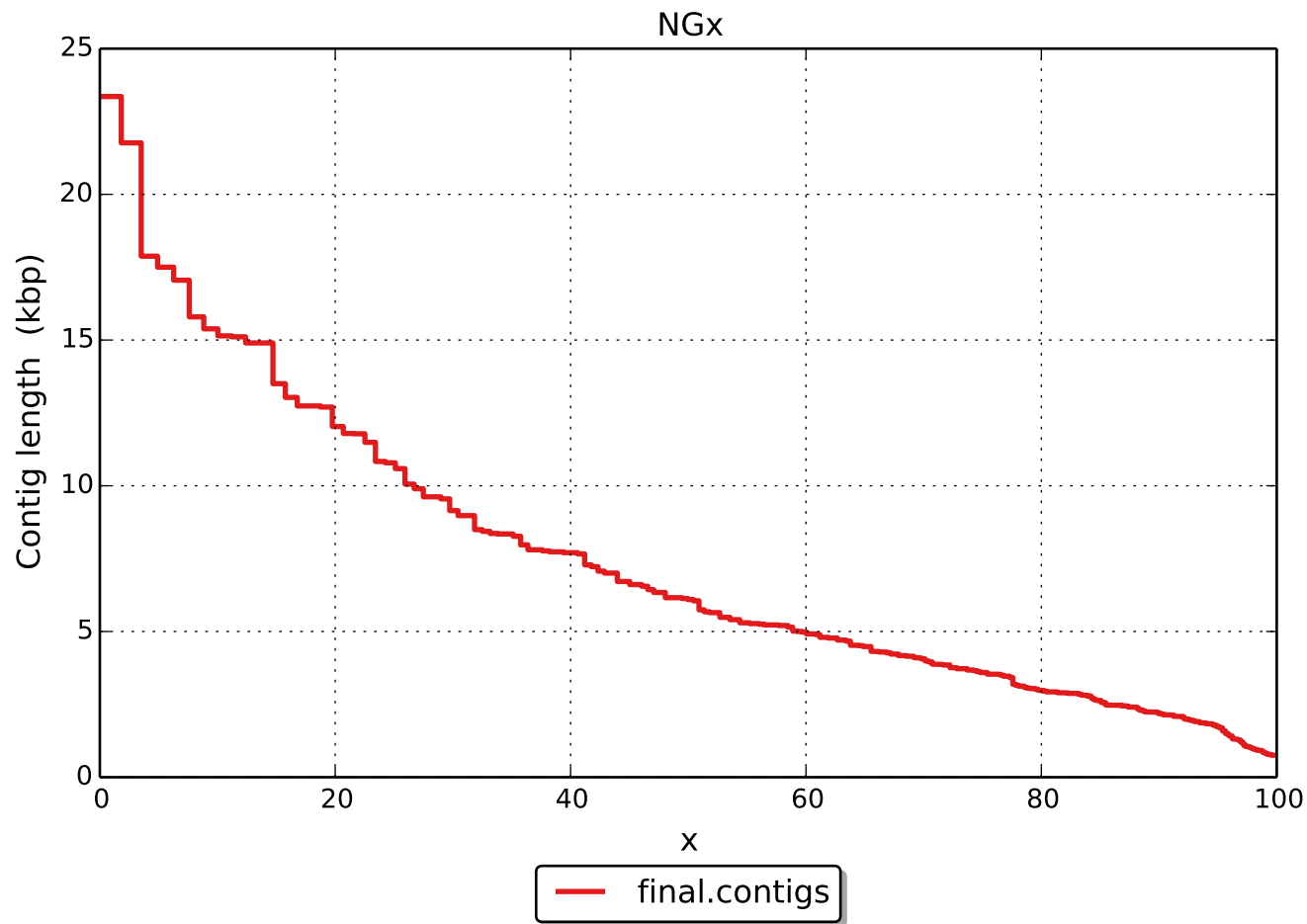
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Cumulative length







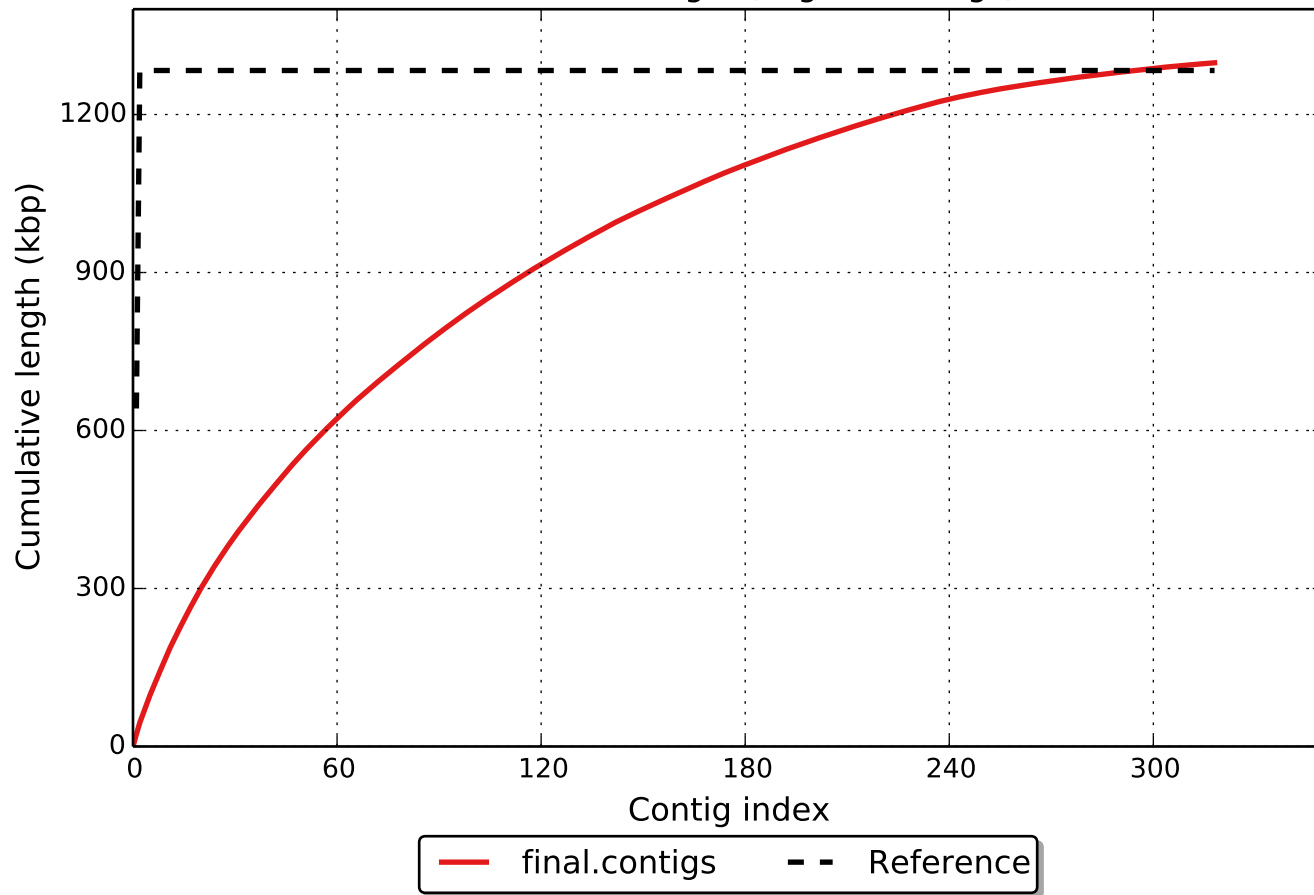


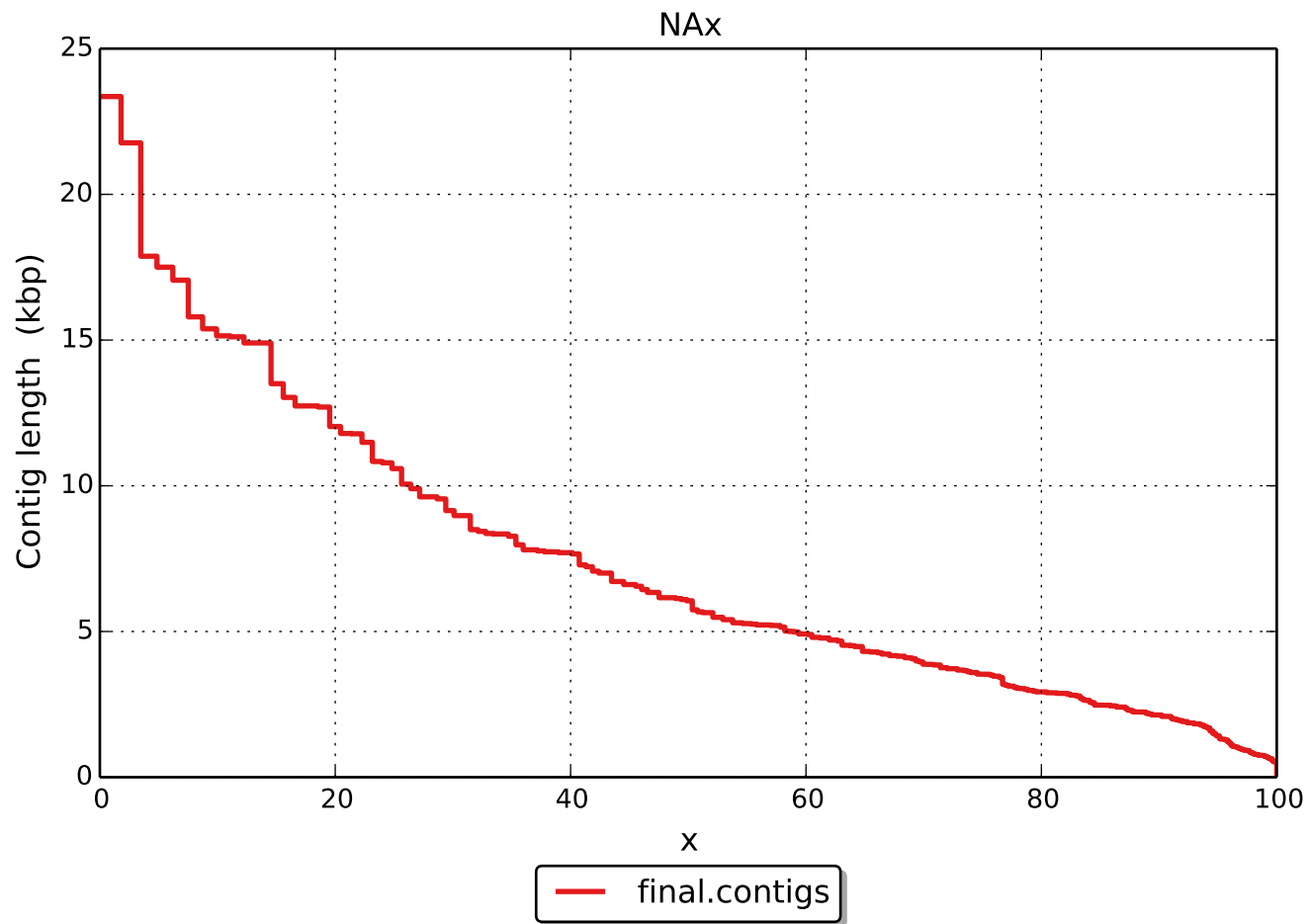
# Misassemblies





Cumulative length (aligned contigs)





# NGAx

