

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	165
# contigs ( $\geq 1000$ bp)	145
Total length ( $\geq 0$ bp)	1244674
Total length ( $\geq 1000$ bp)	1234563
# contigs	153
Largest contig	38663
Total length	1240083
Reference length	1231960
GC (%)	25.35
Reference GC (%)	25.35
N50	12232
NG50	12232
N75	8270
NG75	8270
L50	34
LG50	34
L75	65
LG75	65
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.731
Duplication ratio	1.009
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.73
# indels per 100 kbp	0.00
Largest alignment	38663
NA50	12232
NGA50	12232
NA75	8270
NGA75	8270
LA50	34
LGA50	34
LA75	65
LGA75	65

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
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	9
# indels	0
# short indels	0
# long indels	0
Indels length	0

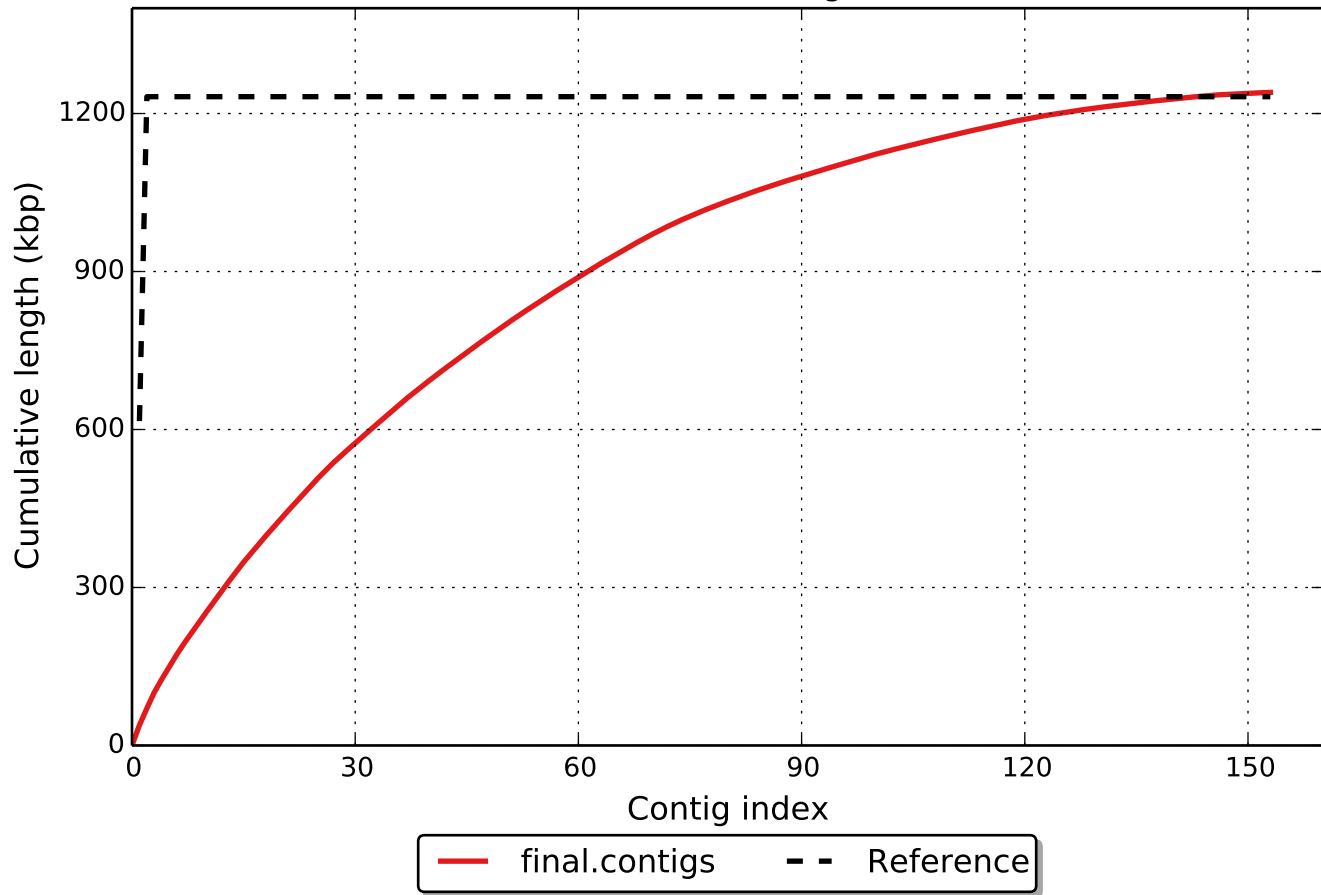
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

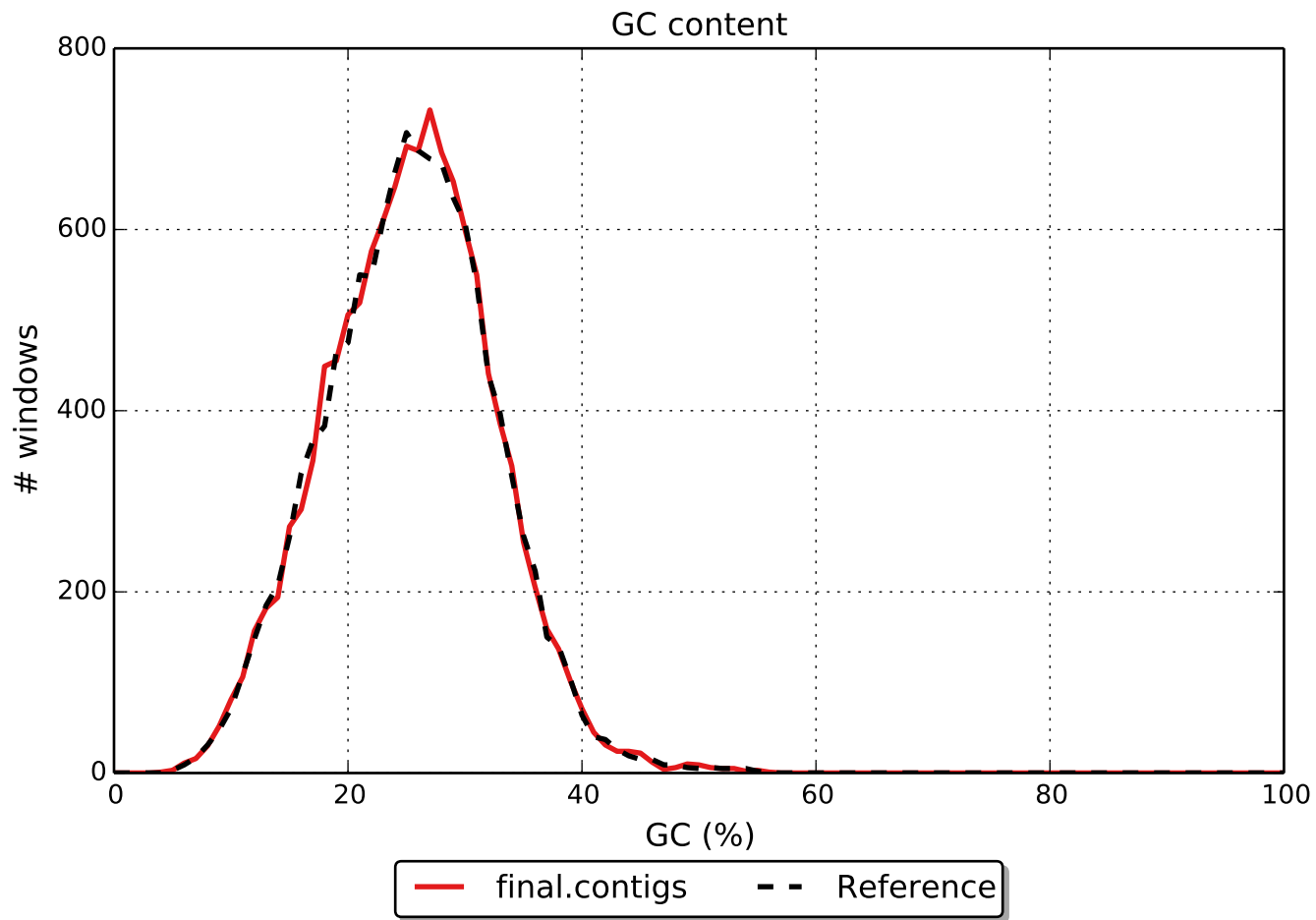
## Unaligned report

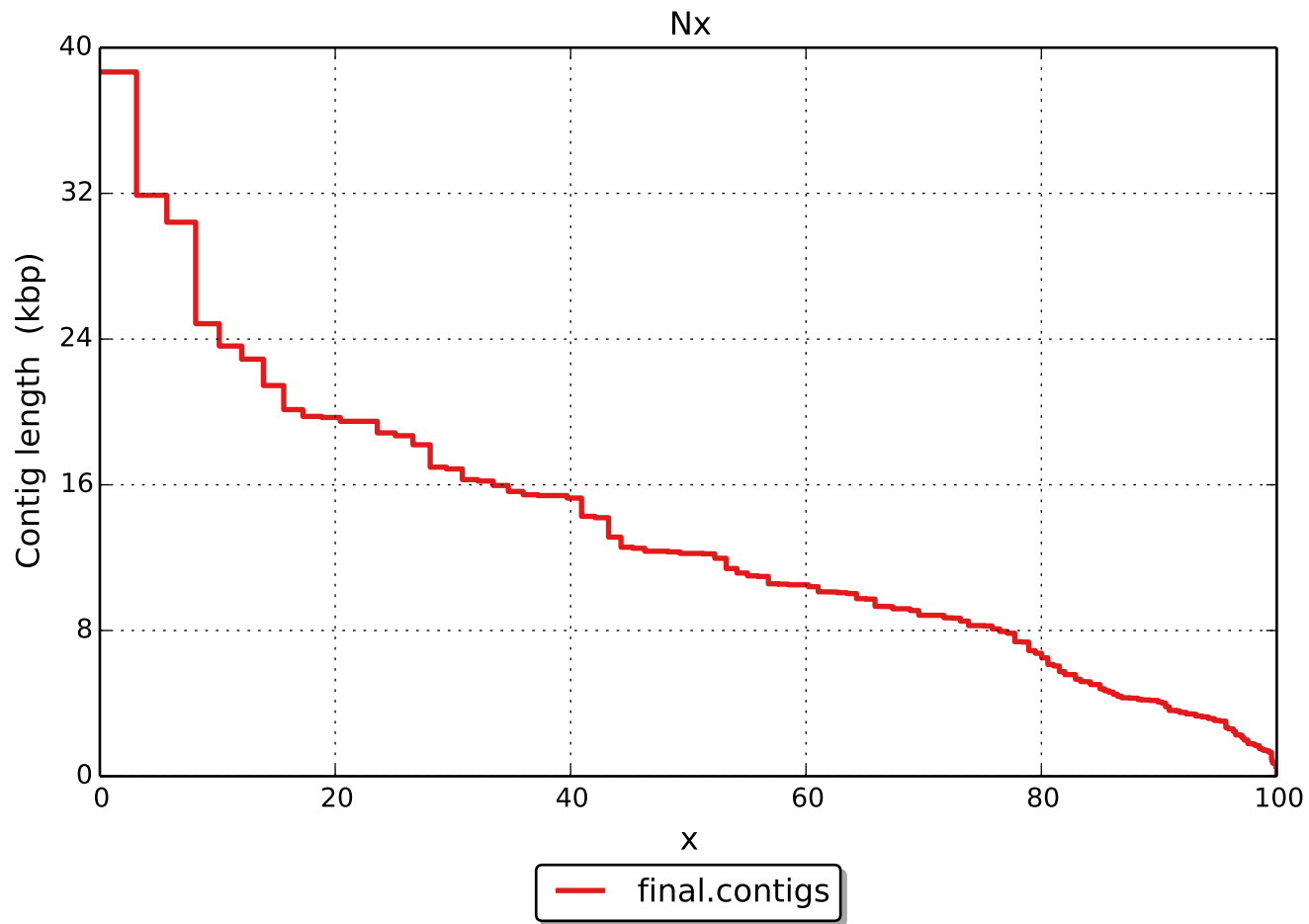
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

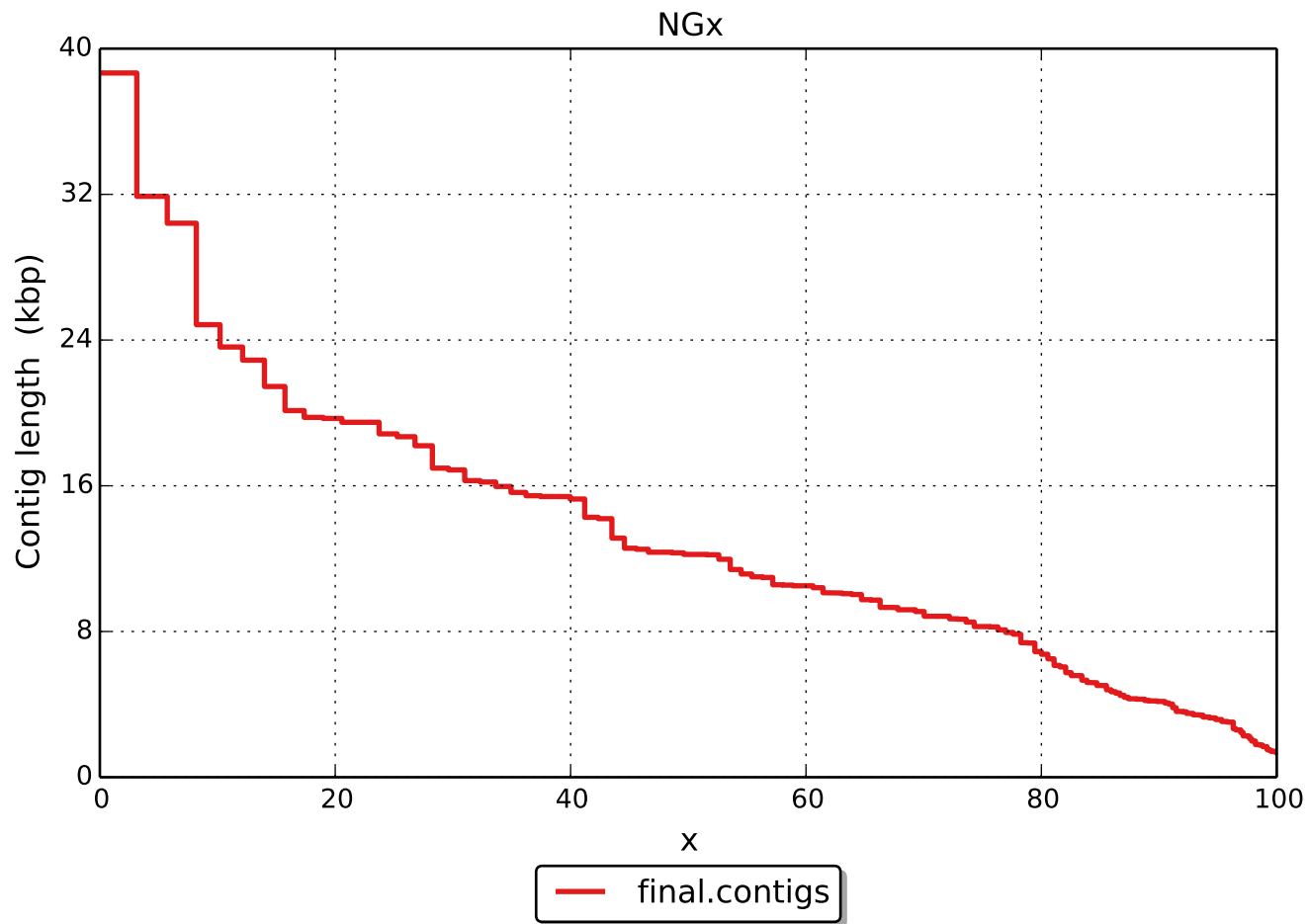
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Cumulative length







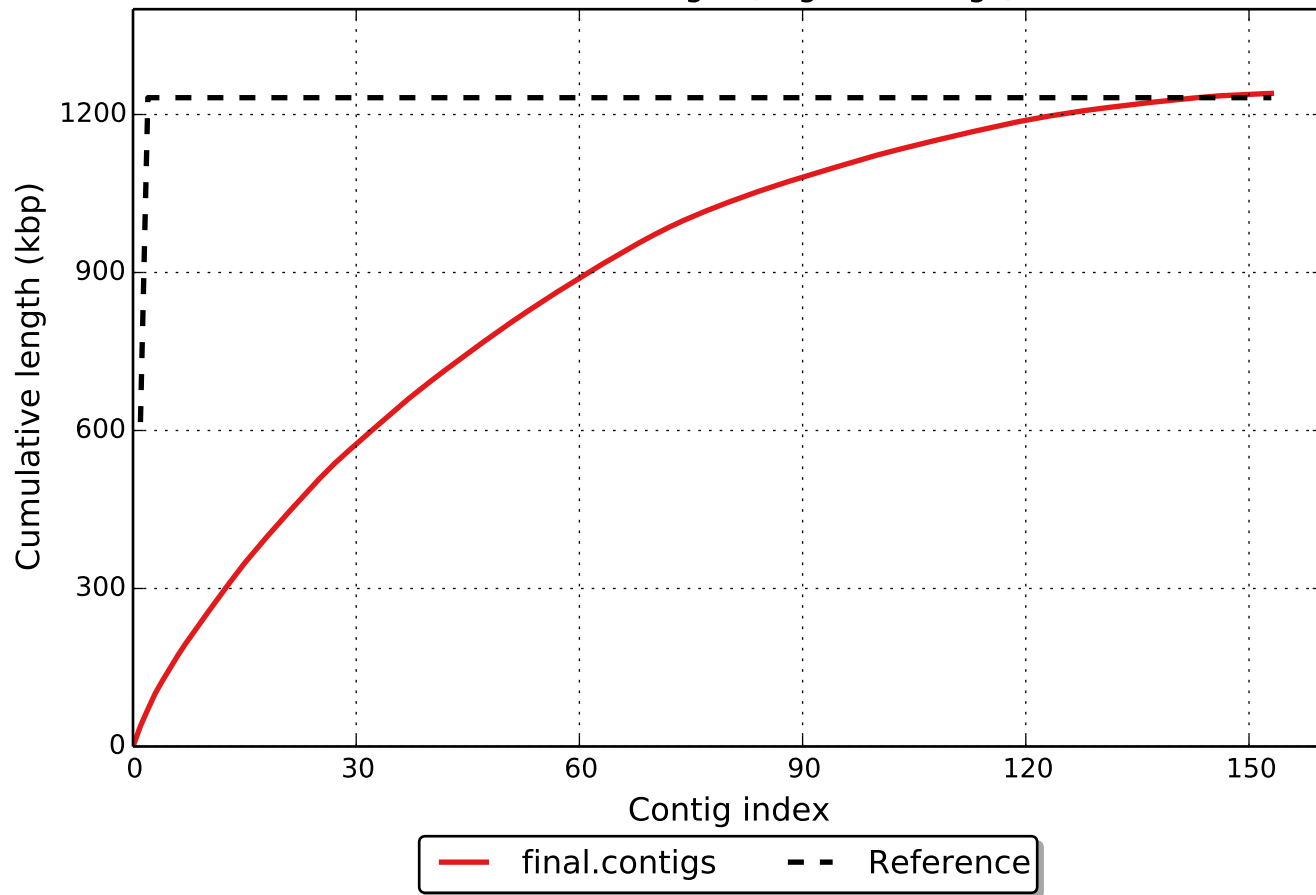


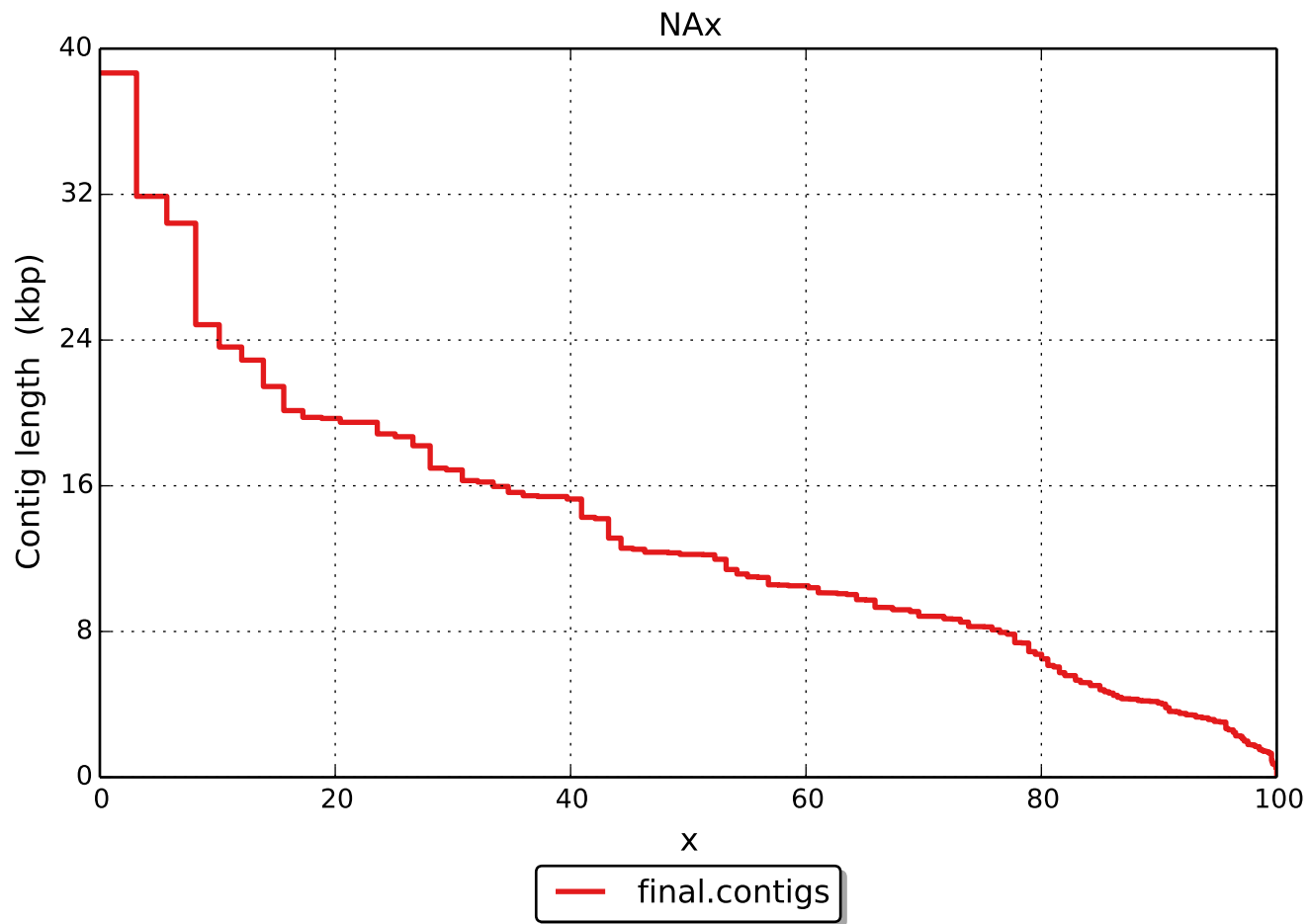
# Misassemblies





Cumulative length (aligned contigs)





# NGAx

