

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	516
# contigs ( $\geq 1000$ bp)	354
Total length ( $\geq 0$ bp)	1261696
Total length ( $\geq 1000$ bp)	1166163
# contigs	450
Largest contig	17588
Total length	1236944
Reference length	1231960
GC (%)	25.38
Reference GC (%)	25.34
N50	3892
NG50	3892
N75	2341
NG75	2360
L50	99
LG50	99
L75	202
LG75	200
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.029
Duplication ratio	1.032
# N's per 100 kbp	0.00
# mismatches per 100 kbp	42.23
# indels per 100 kbp	0.00
Largest alignment	17588
NA50	3892
NGA50	3892
NA75	2341
NGA75	2360
LA50	99
LGA50	99
LA75	202
LGA75	200

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	510
# indels	0
# short indels	0
# long indels	0
Indels length	0

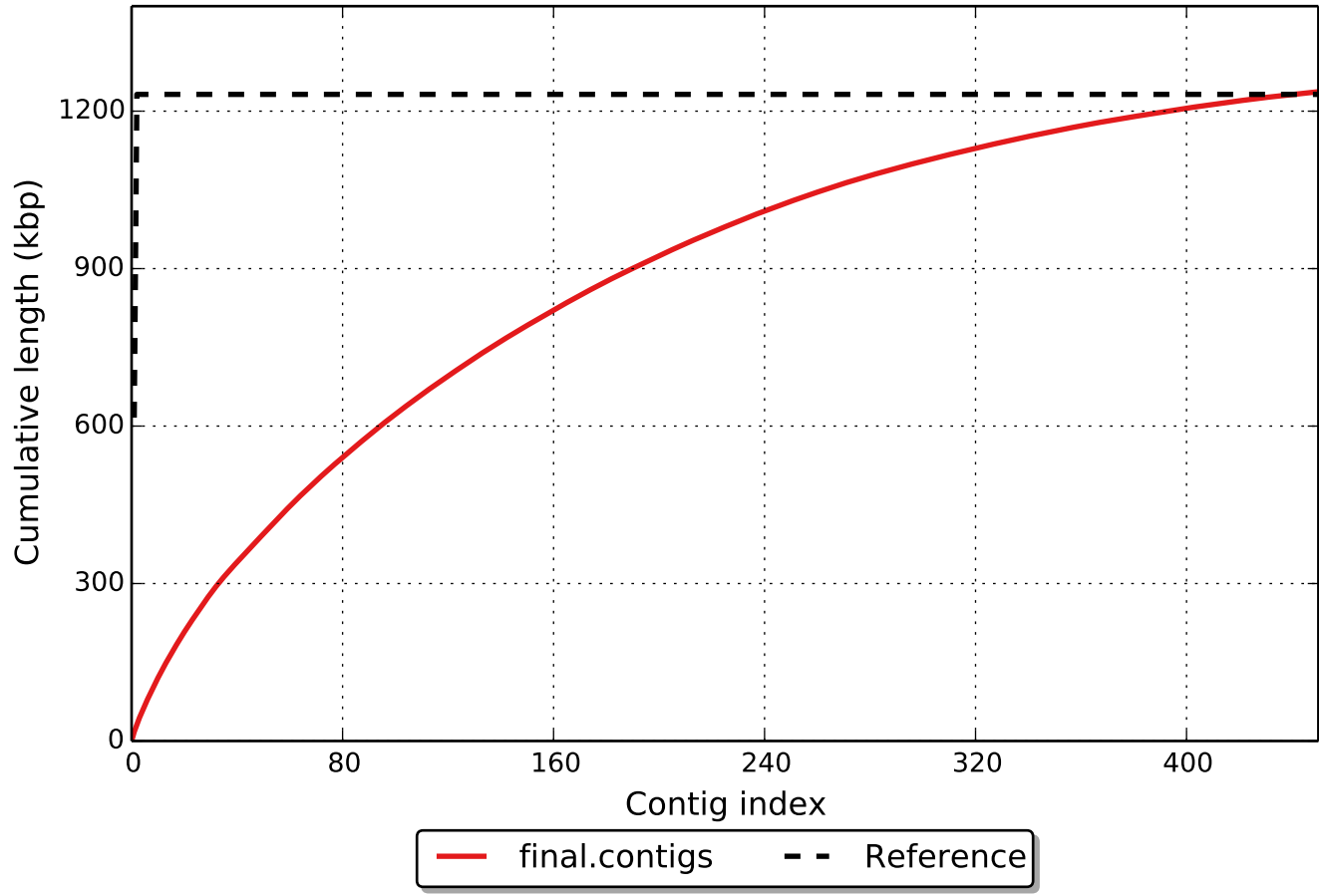
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

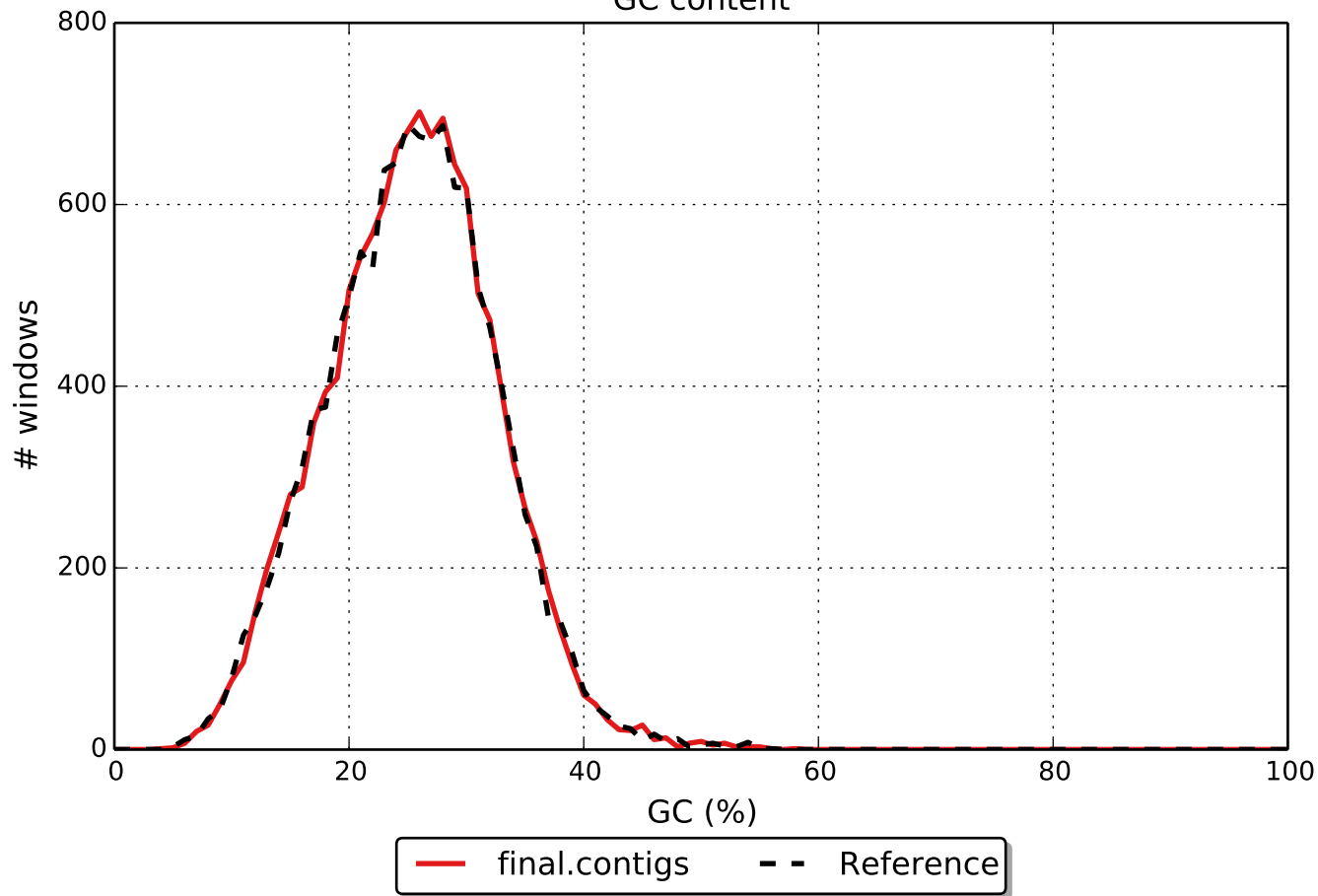
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

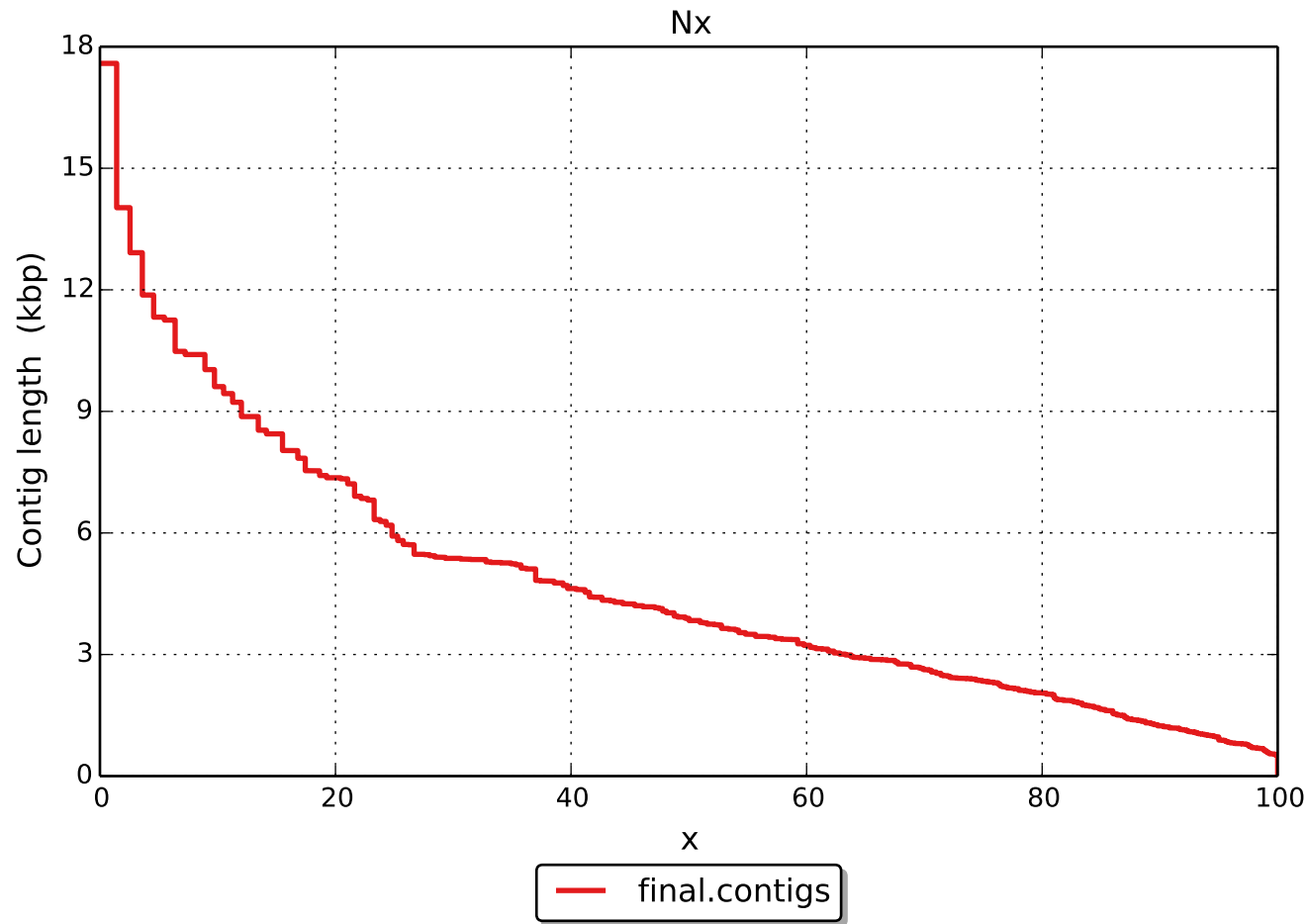
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

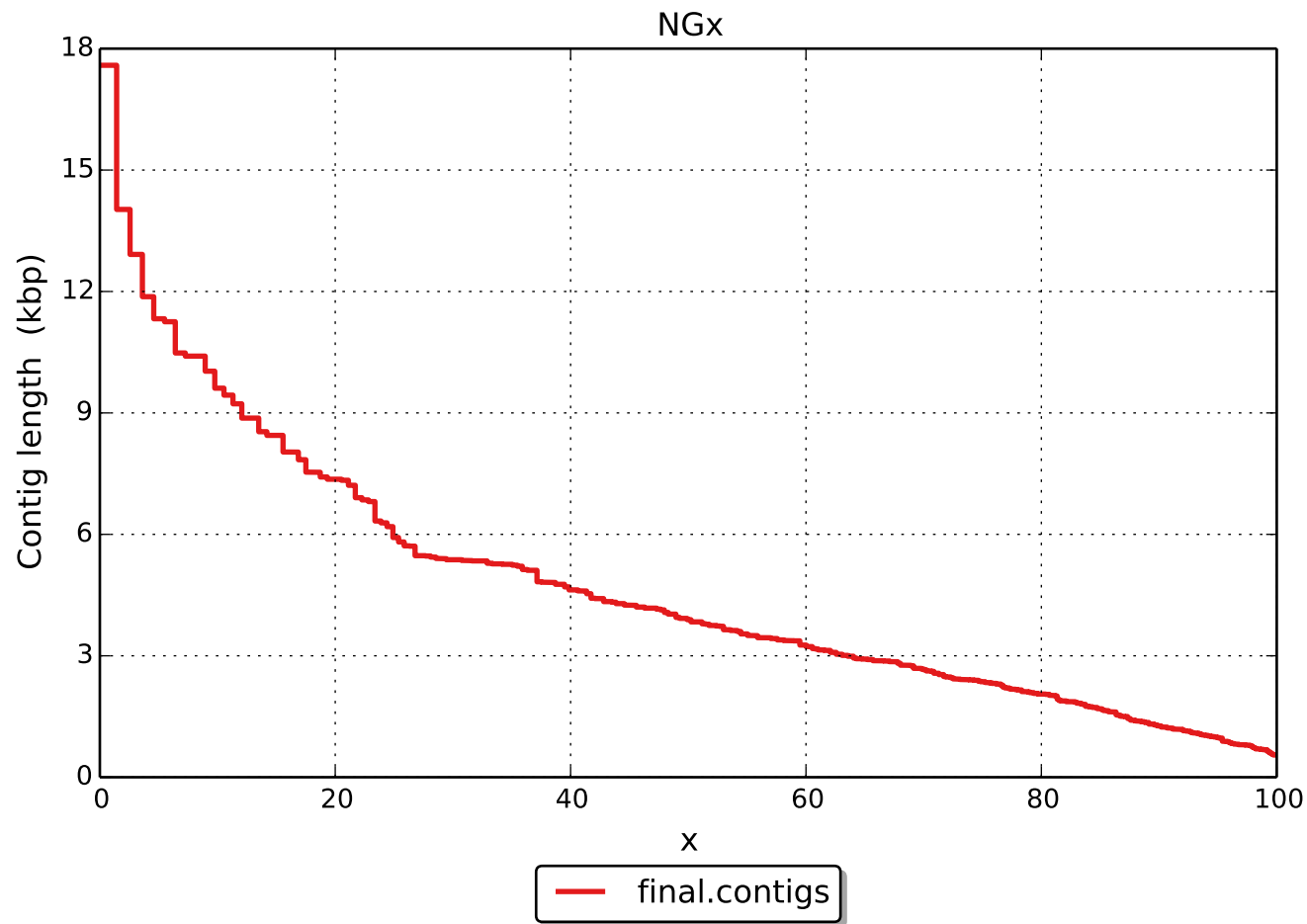
Cumulative length



GC content





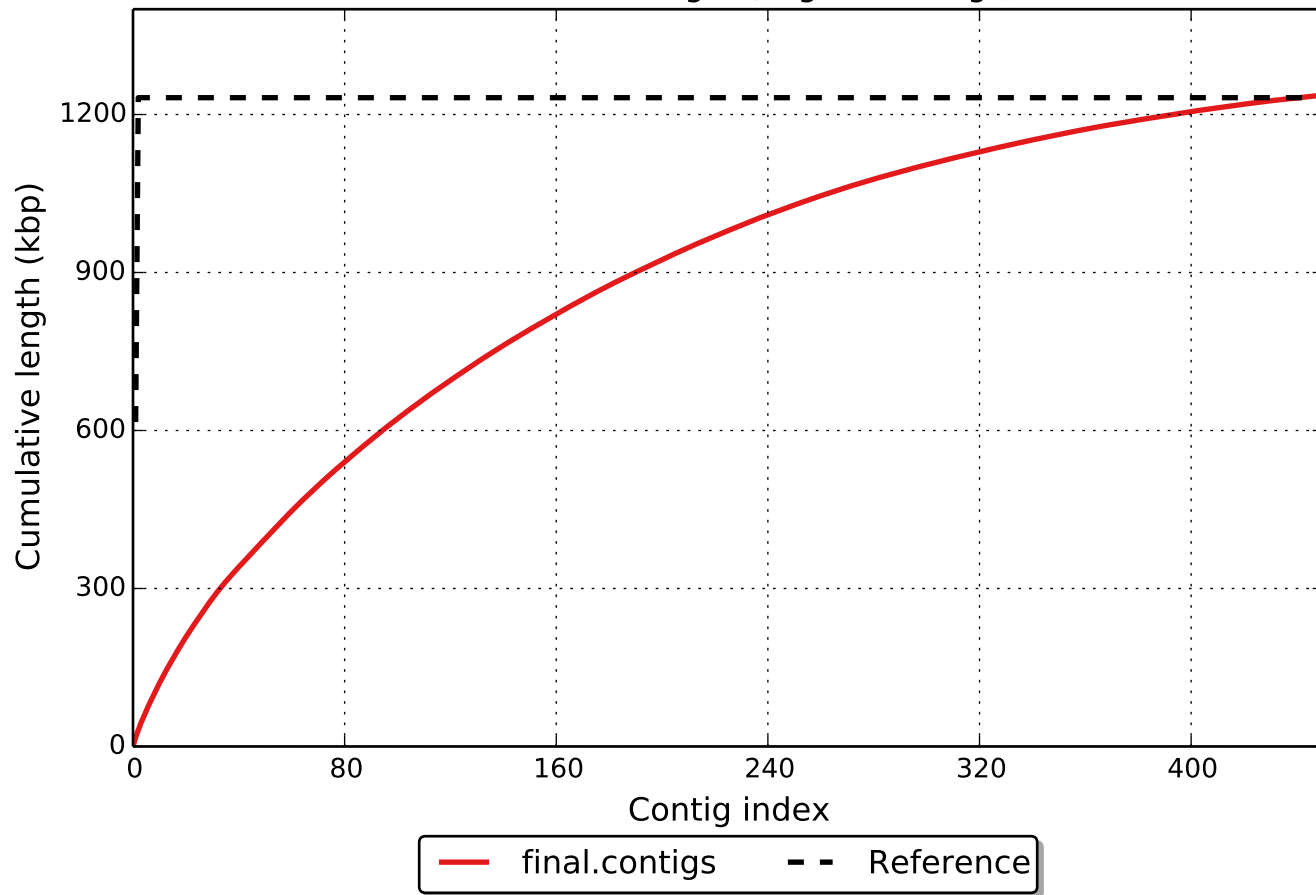


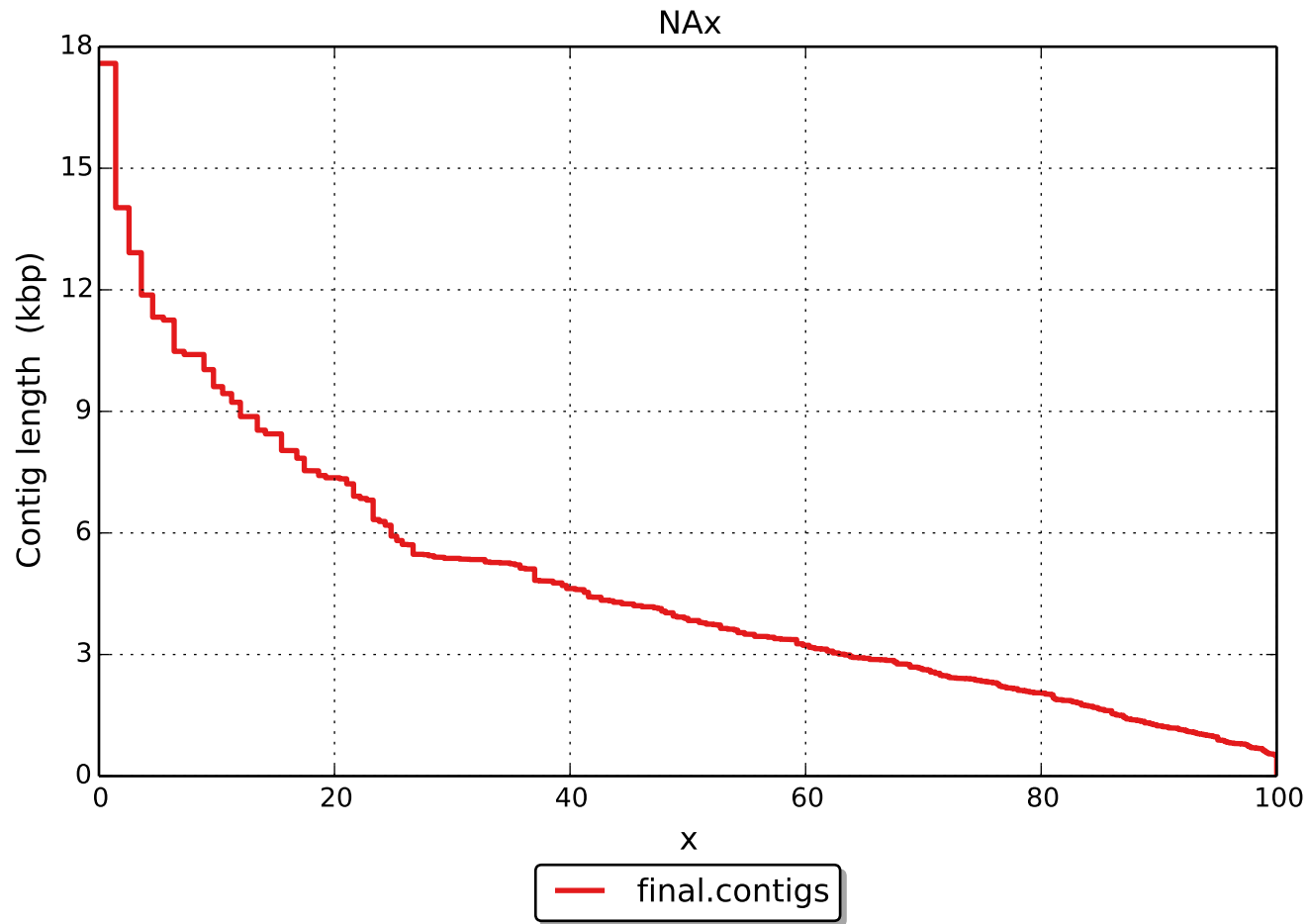
# Misassemblies





Cumulative length (aligned contigs)





# NGAx

