

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	230
# contigs ( $\geq 1000$ bp)	82
Total length ( $\geq 0$ bp)	663628
Total length ( $\geq 1000$ bp)	607382
# contigs	102
Largest contig	36312
Total length	619642
Reference length	1231960
GC (%)	25.34
Reference GC (%)	25.35
N50	11348
NG50	576
N75	6713
L50	20
LG50	96
L75	37
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.523
Duplication ratio	1.010
# N's per 100 kbp	0.00
# mismatches per 100 kbp	494.66
# indels per 100 kbp	0.00
Largest alignment	36312
NA50	11348
NGA50	573
NA75	6713
LA50	20
LGA50	96
LA75	37

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	6004
# indels	0
# short indels	0
# long indels	0
Indels length	0

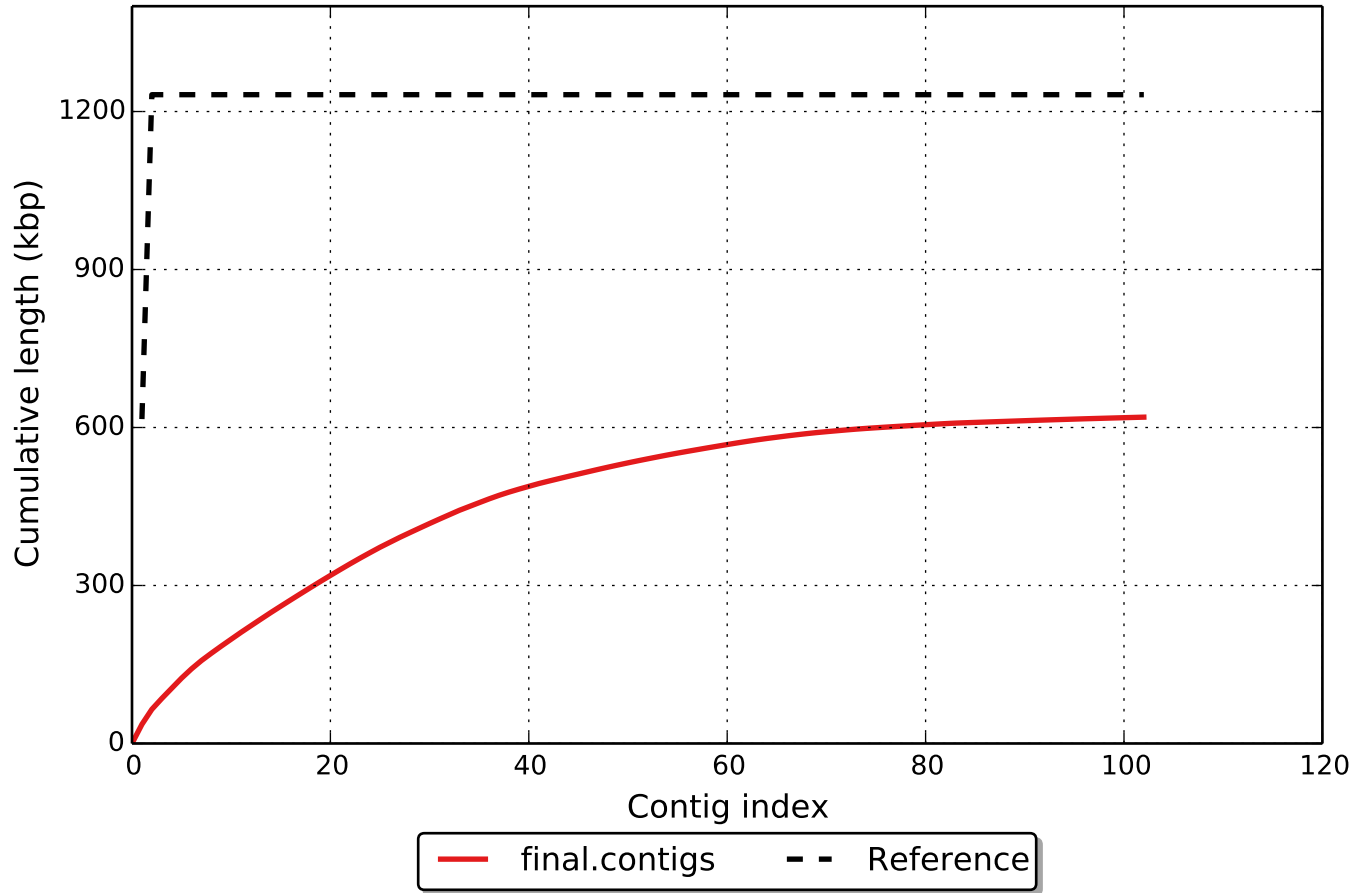
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

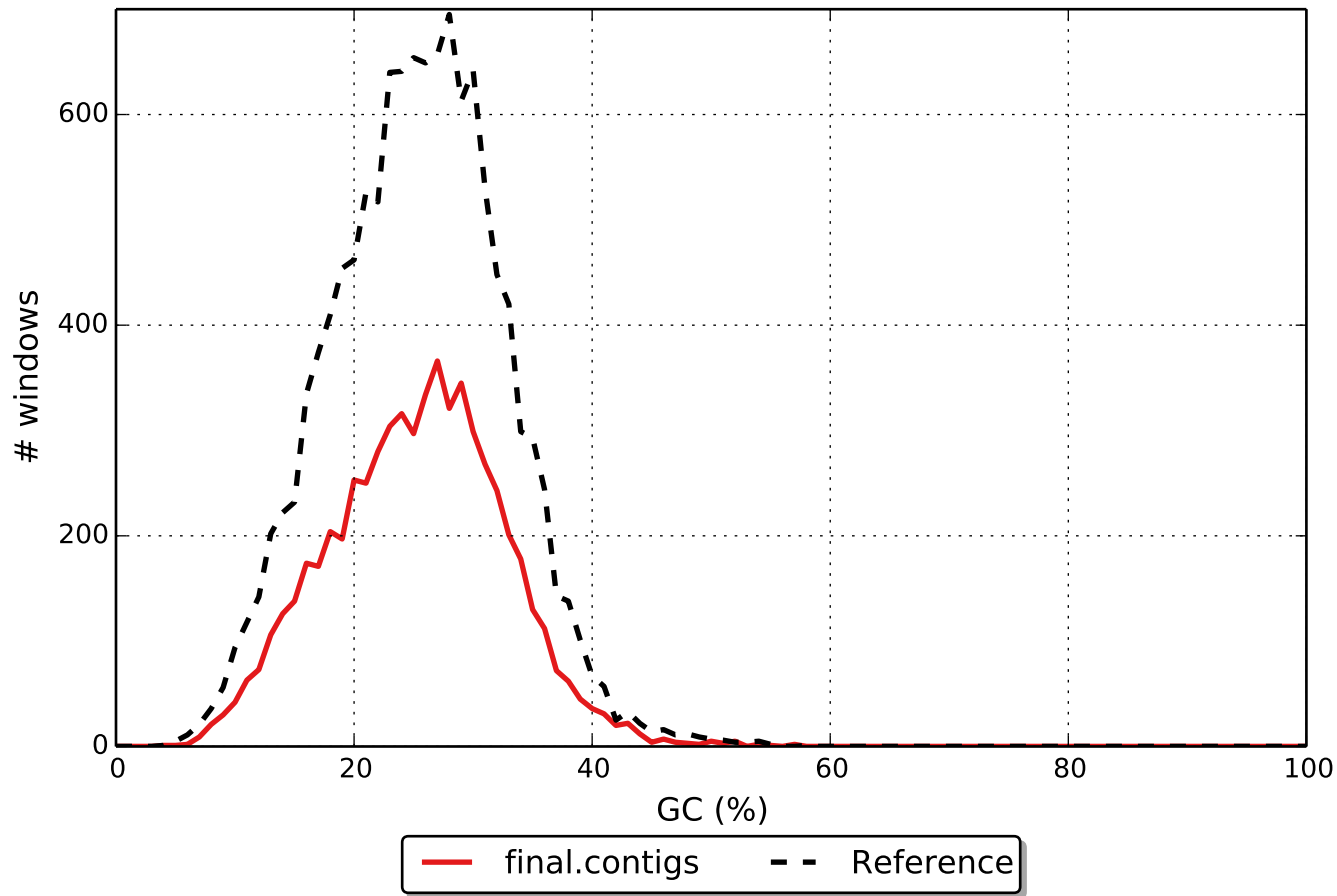
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

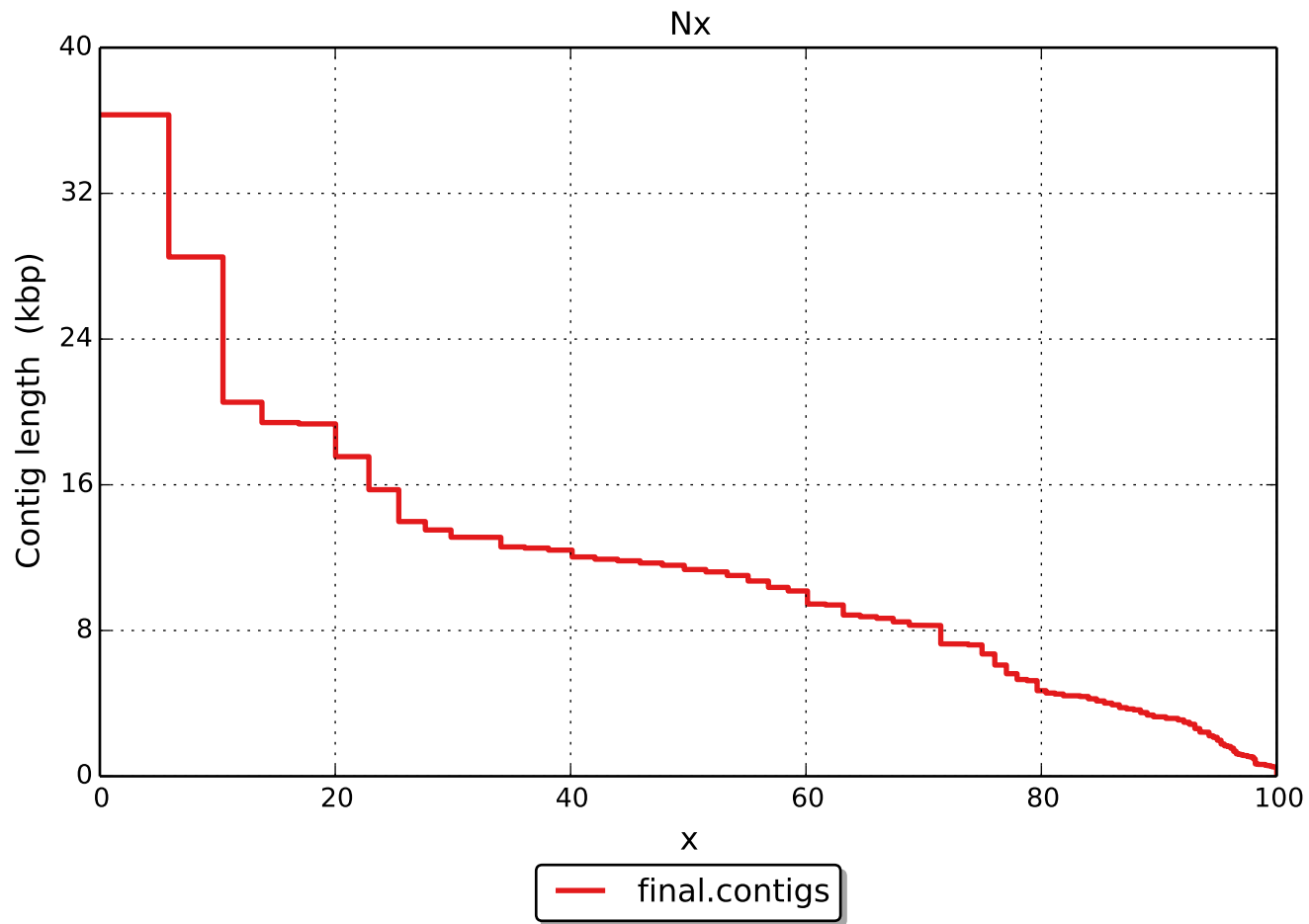
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

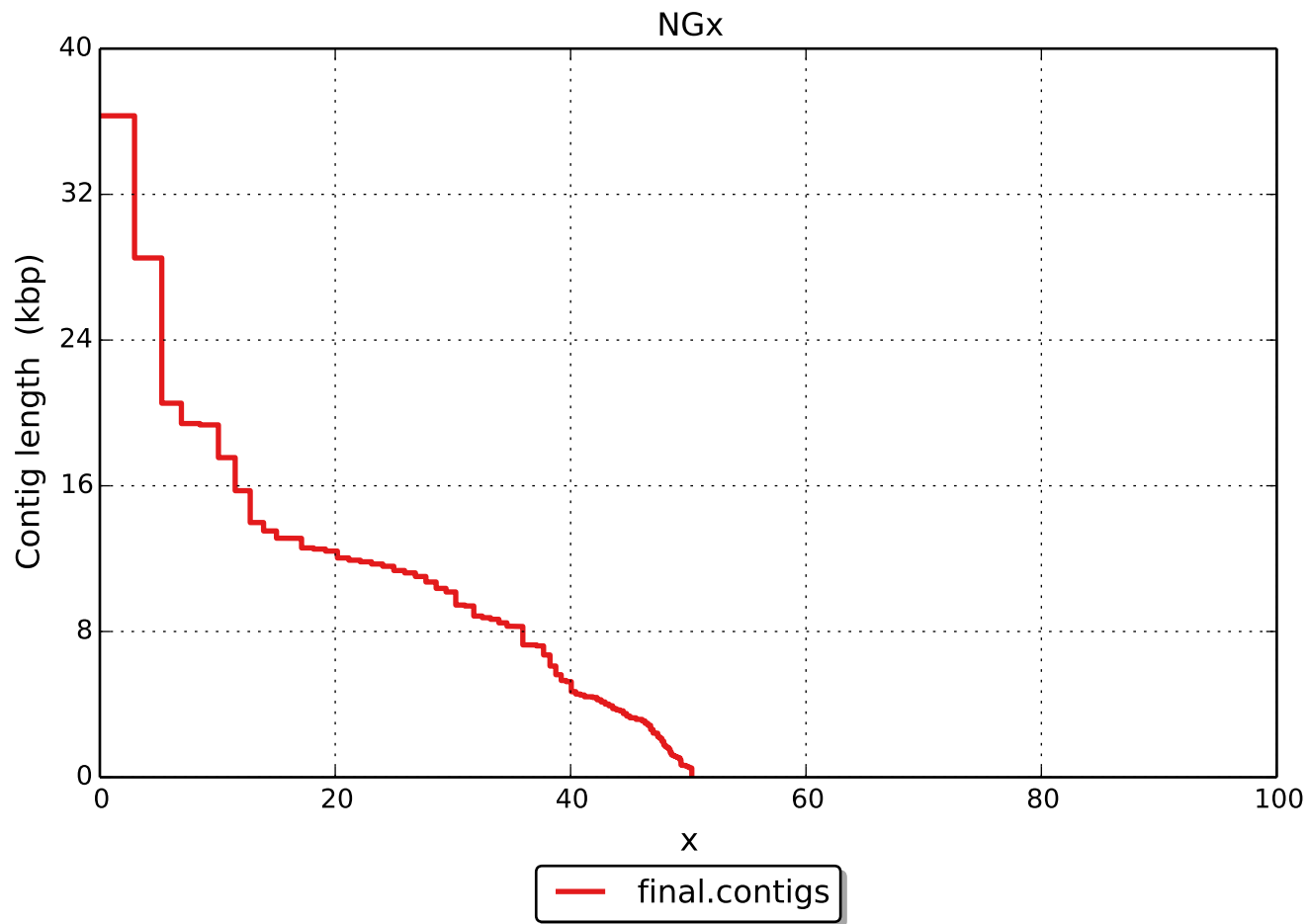
Cumulative length



# GC content





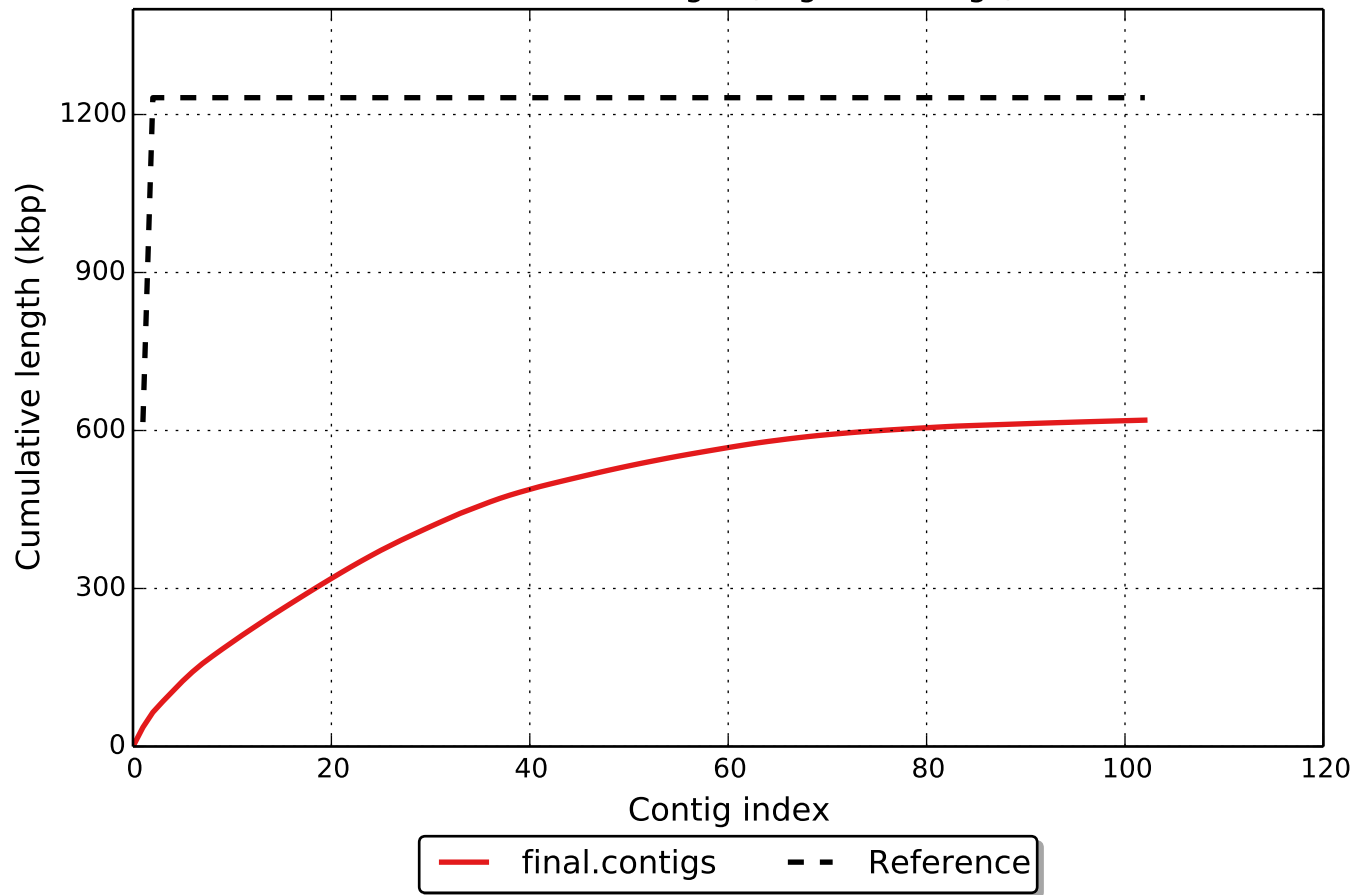


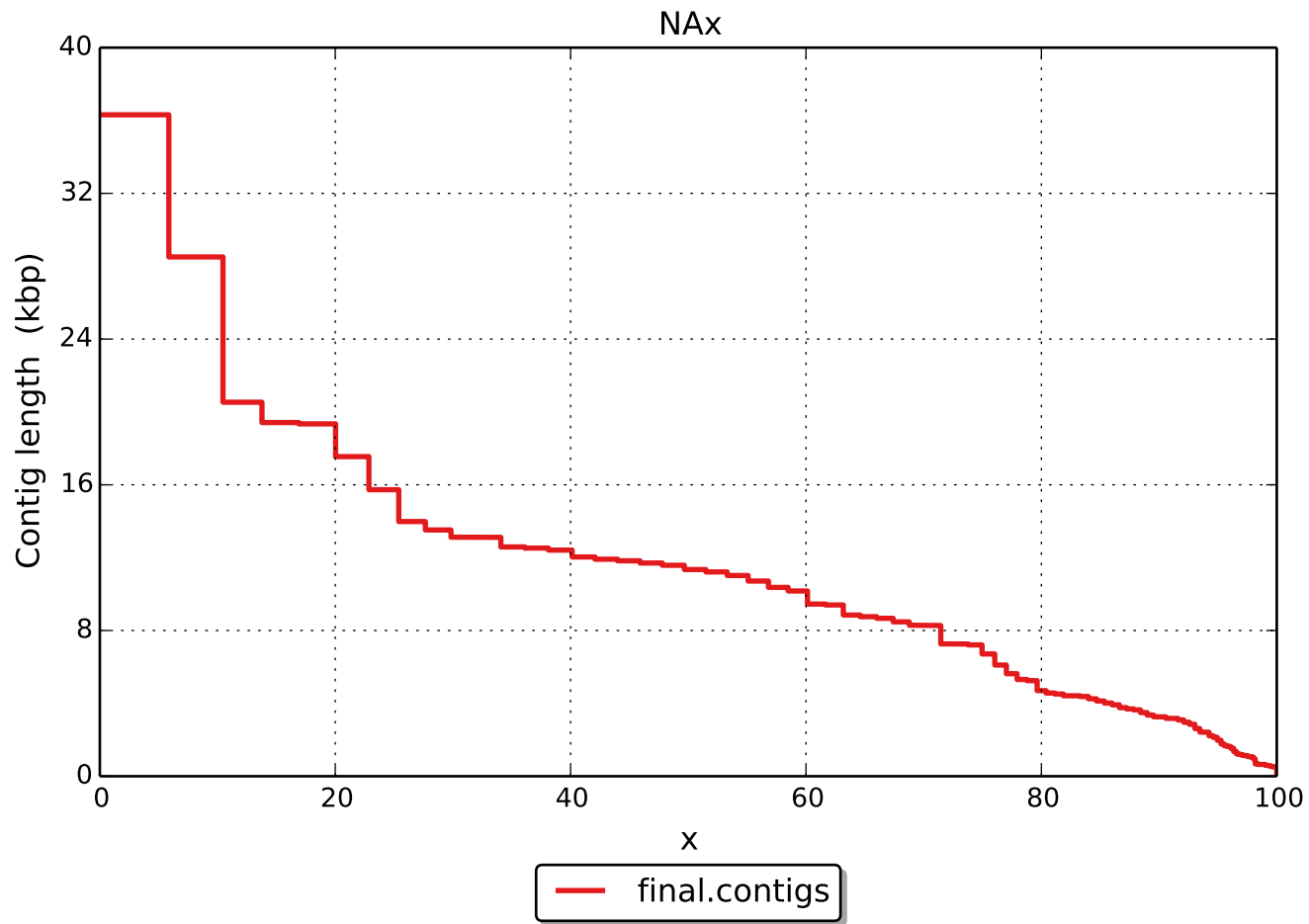
# Misassemblies





Cumulative length (aligned contigs)





NGAx

