

## Report

	final.contigs
# contigs ( $\geq$ 1000 bp)	649
# contigs ( $\geq$ 5000 bp)	103
# contigs ( $\geq$ 10000 bp)	10
# contigs ( $\geq$ 25000 bp)	0
# contigs ( $\geq$ 50000 bp)	0
Total length ( $\geq$ 1000 bp)	2052196
Total length ( $\geq$ 5000 bp)	737510
Total length ( $\geq$ 10000 bp)	131590
Total length ( $\geq$ 25000 bp)	0
Total length ( $\geq$ 50000 bp)	0
# contigs	974
Largest contig	18460
Total length	2274007
Reference length	4641652
GC (%)	50.91
Reference GC (%)	50.79
N50	3444
N75	1954
L50	202
L75	419
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	48.134
Duplication ratio	1.018
# N's per 100 kbp	0.00
# mismatches per 100 kbp	380.04
# indels per 100 kbp	0.04
Largest alignment	18460
NA50	3444
NGA50	-
NA75	1954
LA50	202
LA75	419

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

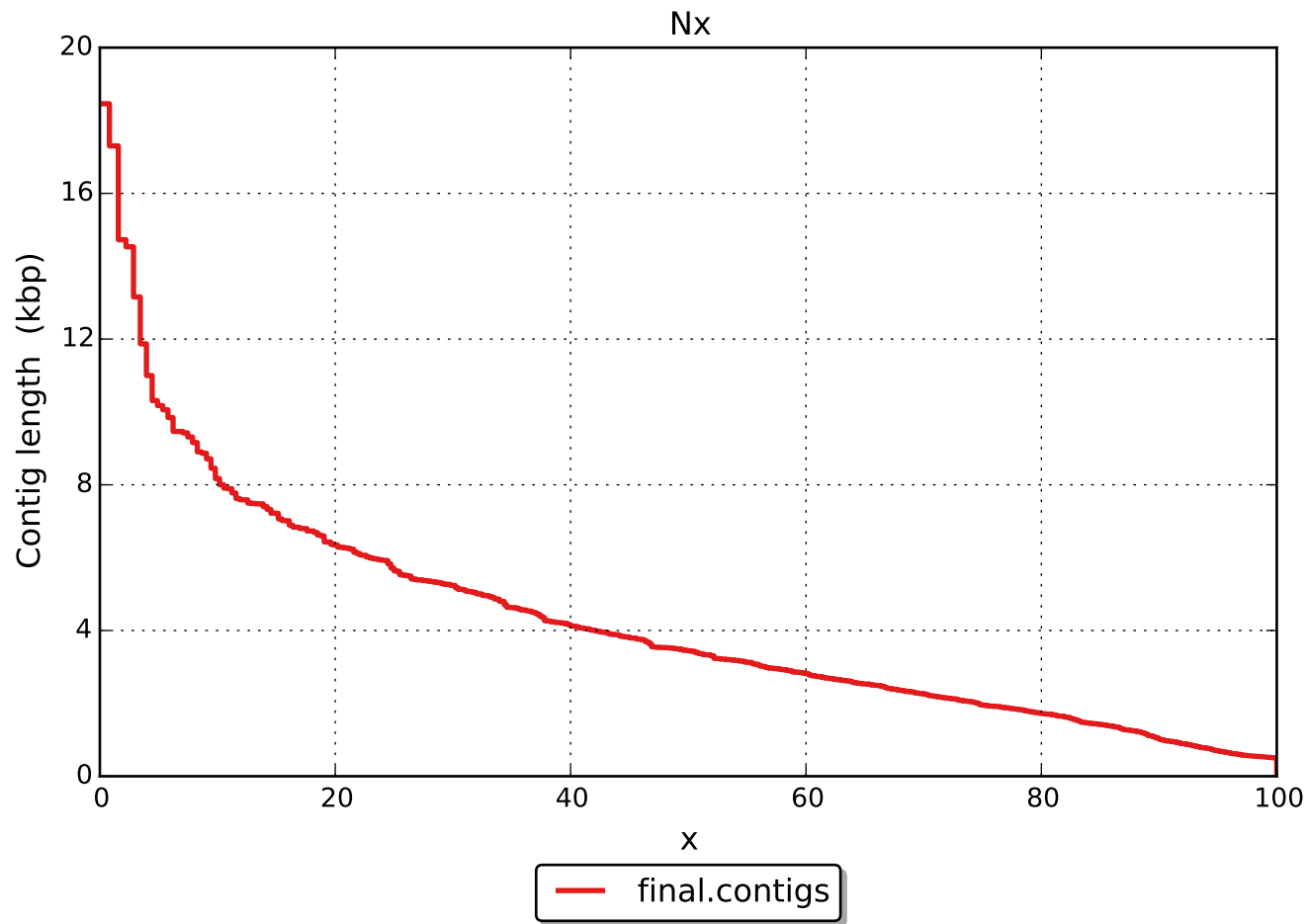
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# mismatches	8491
# indels	1
# short indels	1
# long indels	0
Indels length	1

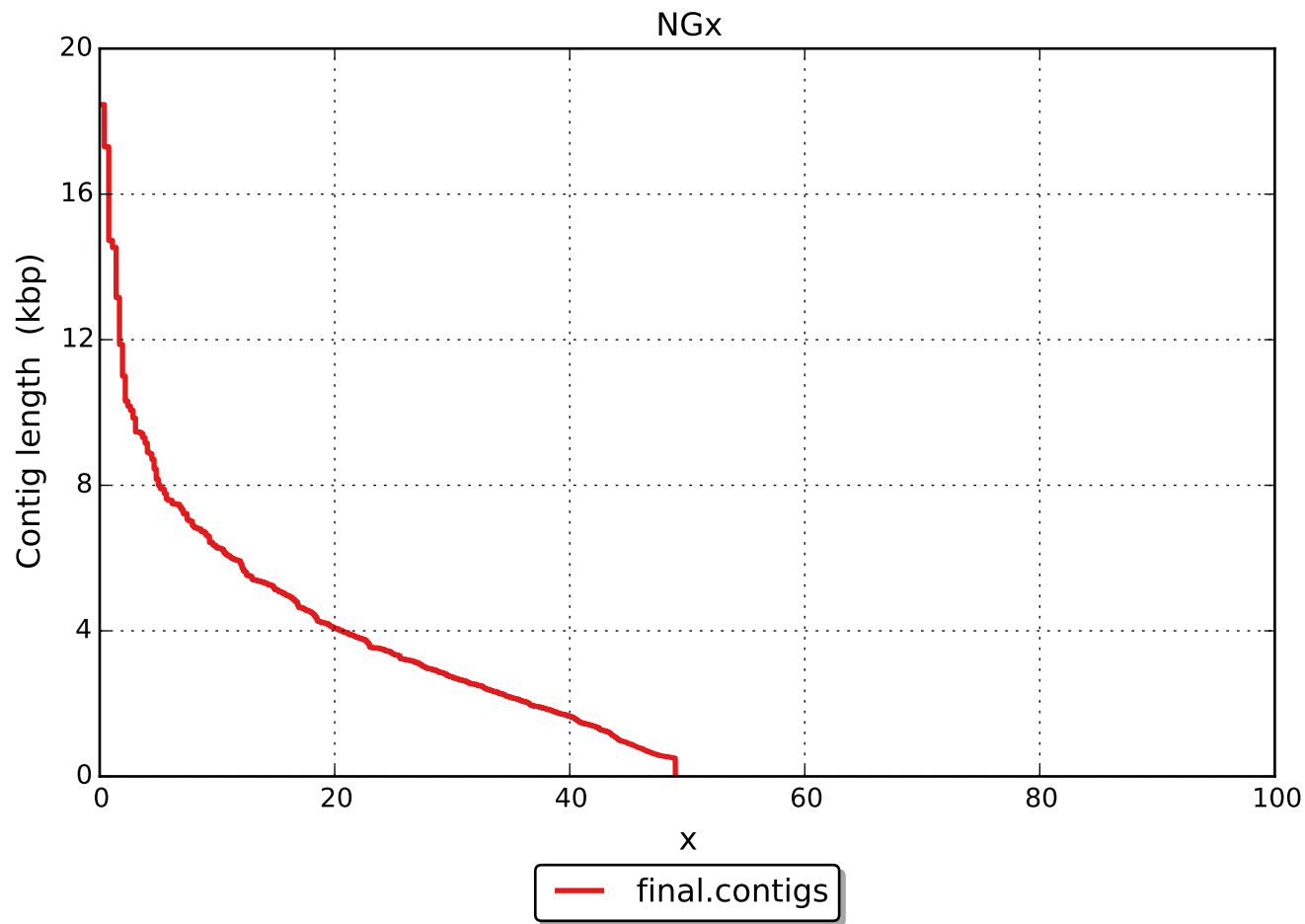
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

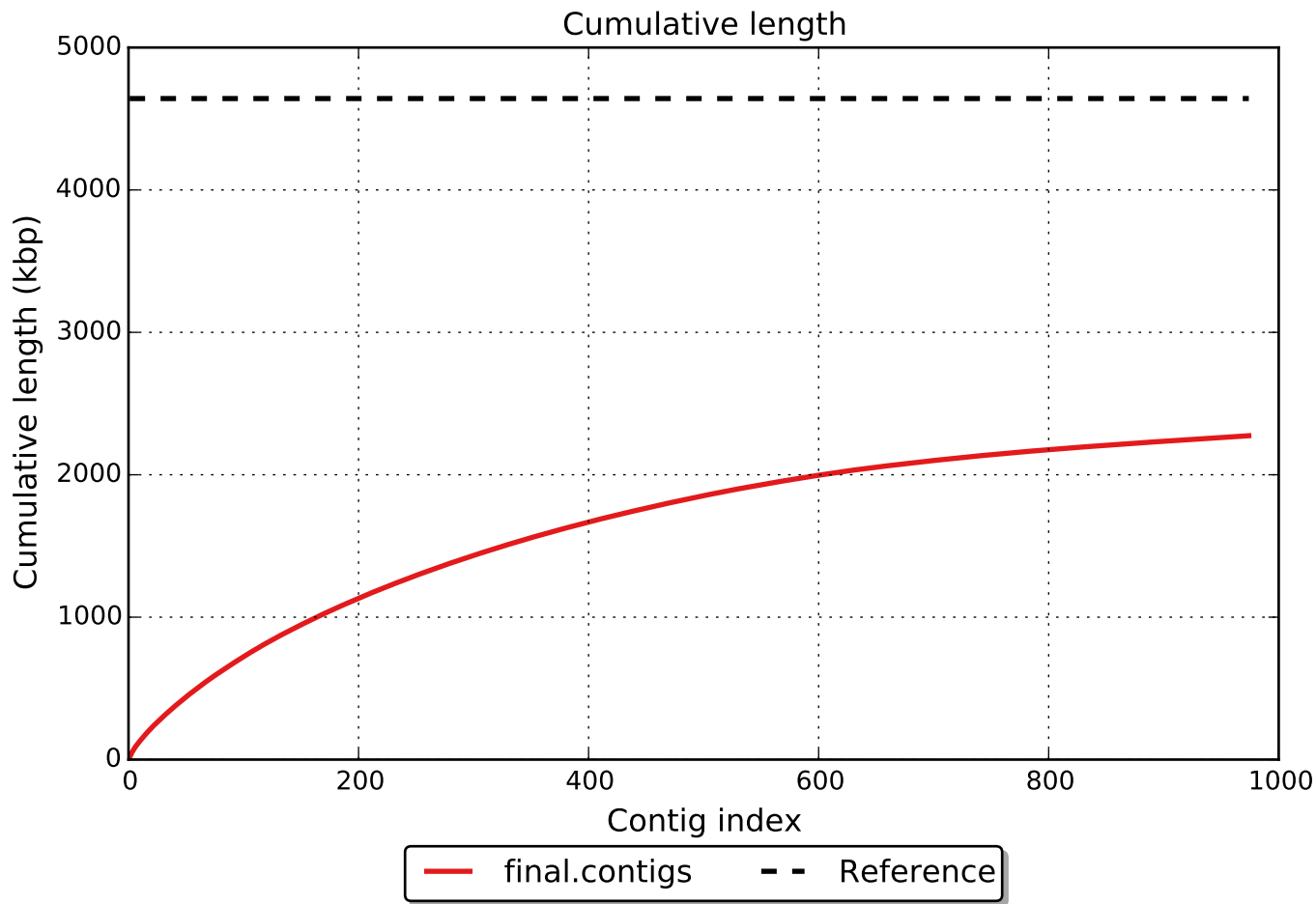
## Unaligned report

	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

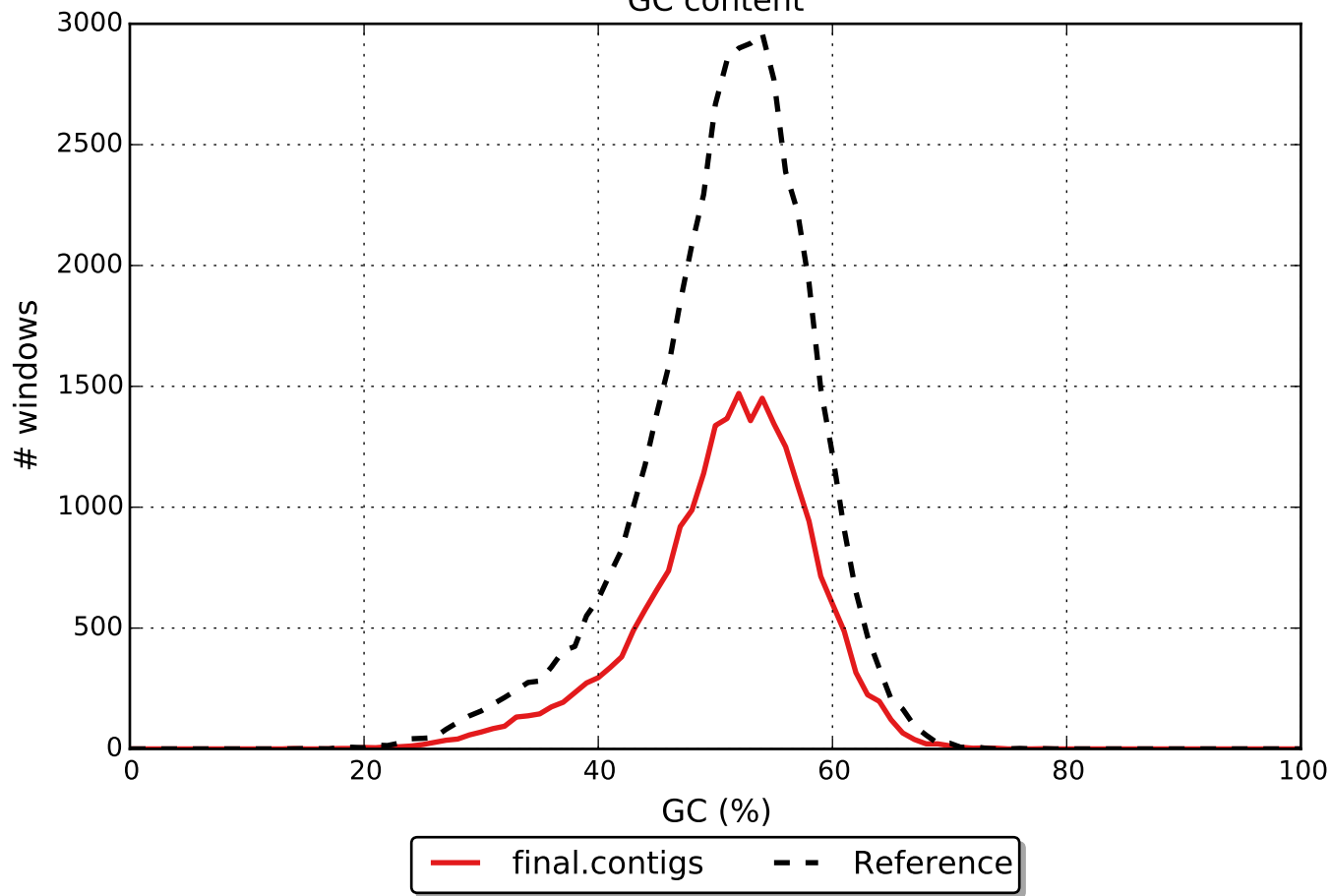
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).







# GC content

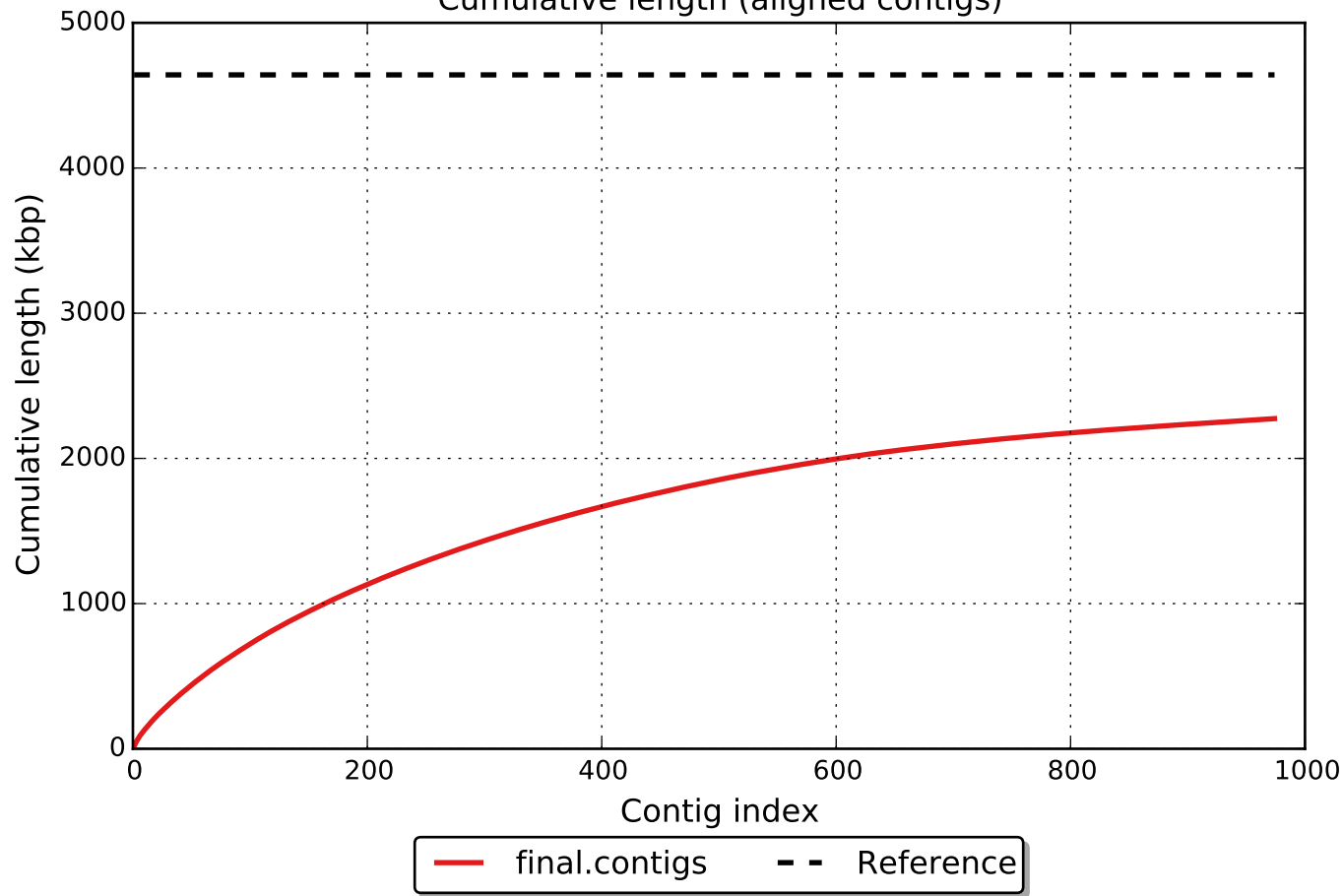


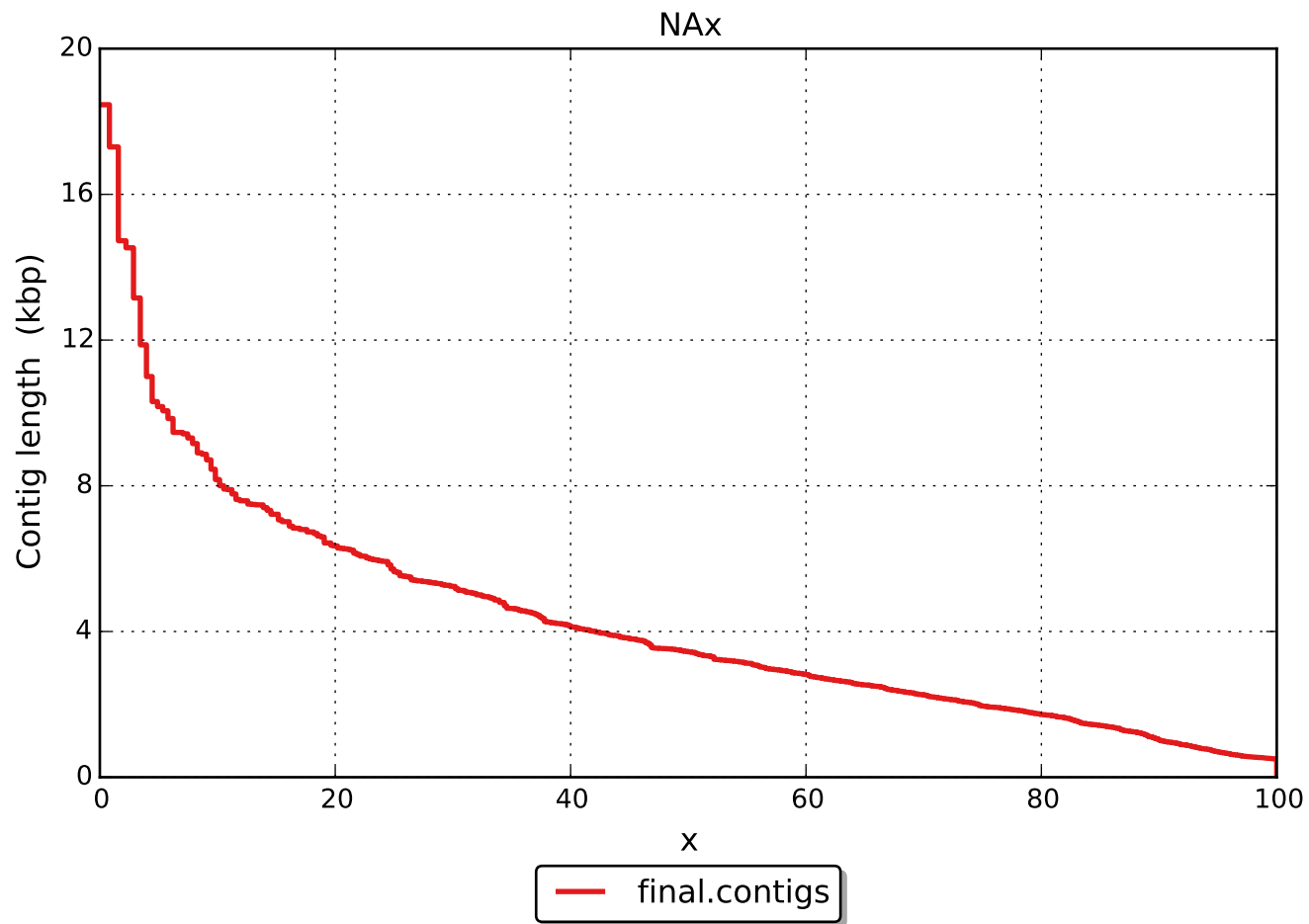
# Misassemblies





Cumulative length (aligned contigs)





NGAx

