

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	2105
# contigs ( $\geq 1000$ bp)	1665
Total length ( $\geq 0$ bp)	5624709
Total length ( $\geq 1000$ bp)	5291927
# contigs	2105
Largest contig	16890
Total length	5624709
Reference length	5547323
GC (%)	50.50
Reference GC (%)	50.49
N50	3676
NG50	3732
N75	2203
NG75	2253
L50	478
LG50	468
L75	969
LG75	943
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 1 part
Unaligned length	180
Genome fraction (%)	97.999
Duplication ratio	1.035
# N's per 100 kbp	0.00
# mismatches per 100 kbp	29.12
# indels per 100 kbp	0.04
Largest alignment	16890
NA50	3676
NGA50	3732
NA75	2203
NGA75	2253
LA50	478
LGA50	468
LA75	969
LGA75	943

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

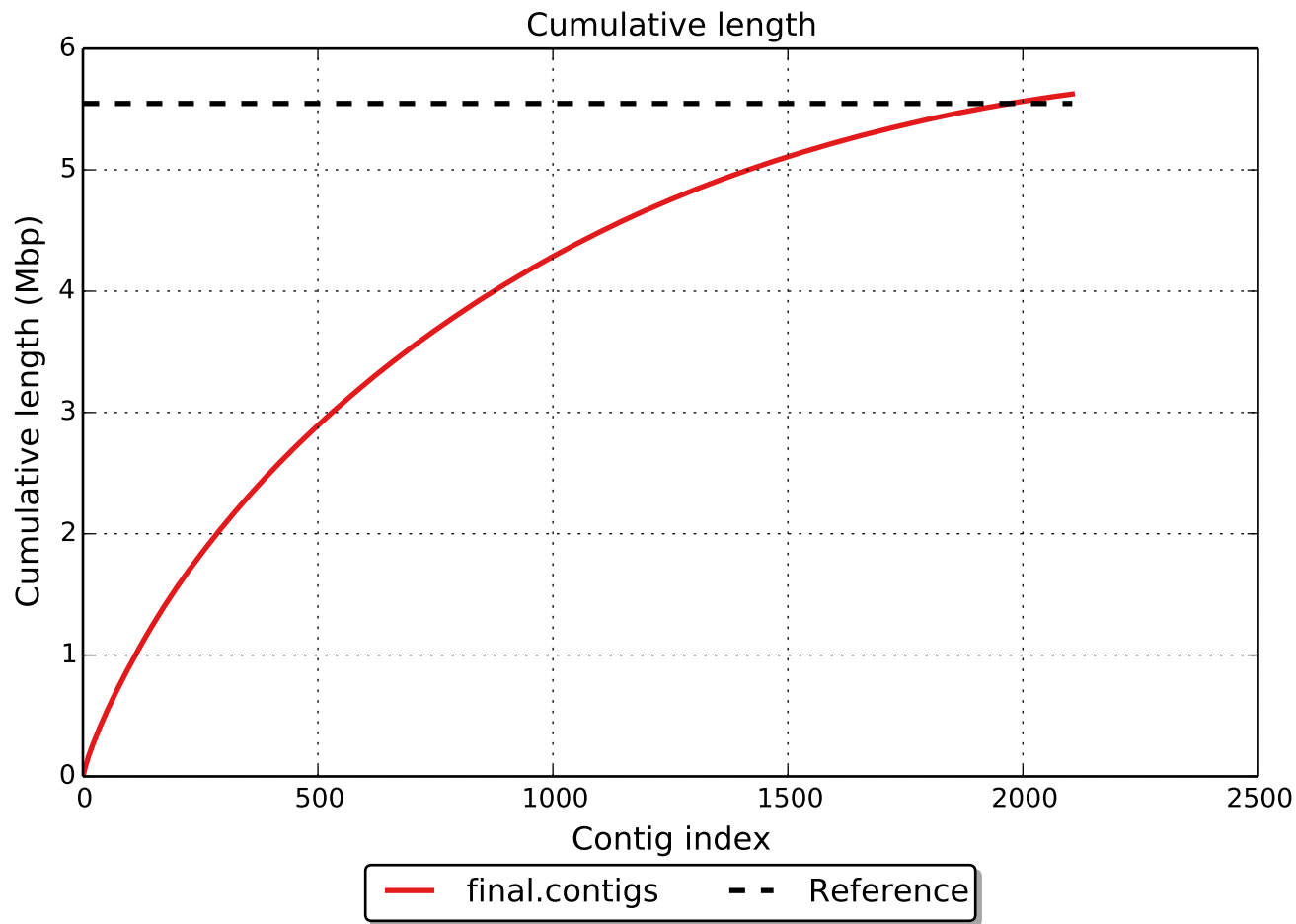
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	1583
# indels	2
# short indels	1
# long indels	1
Indels length	24

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).

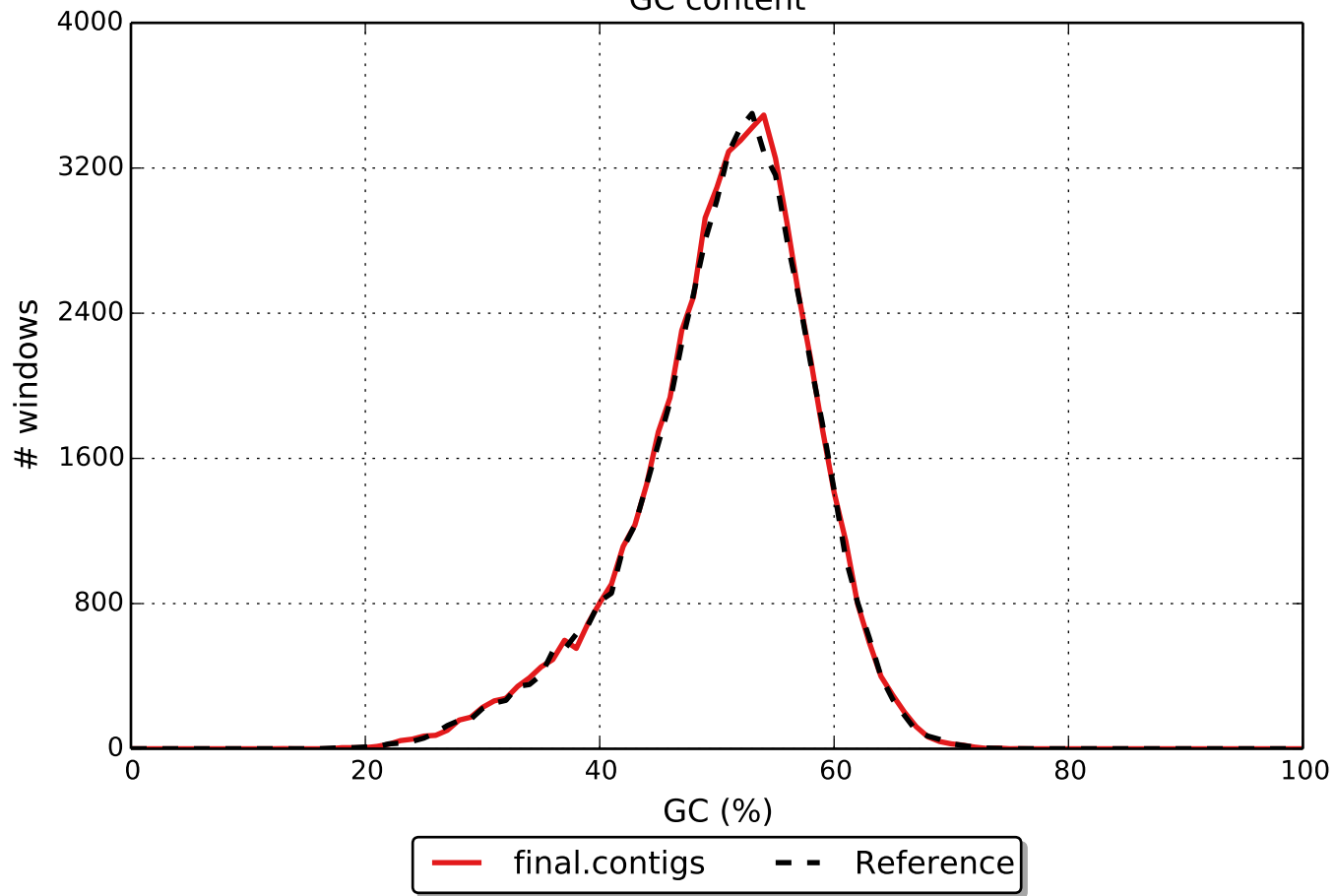
## Unaligned report

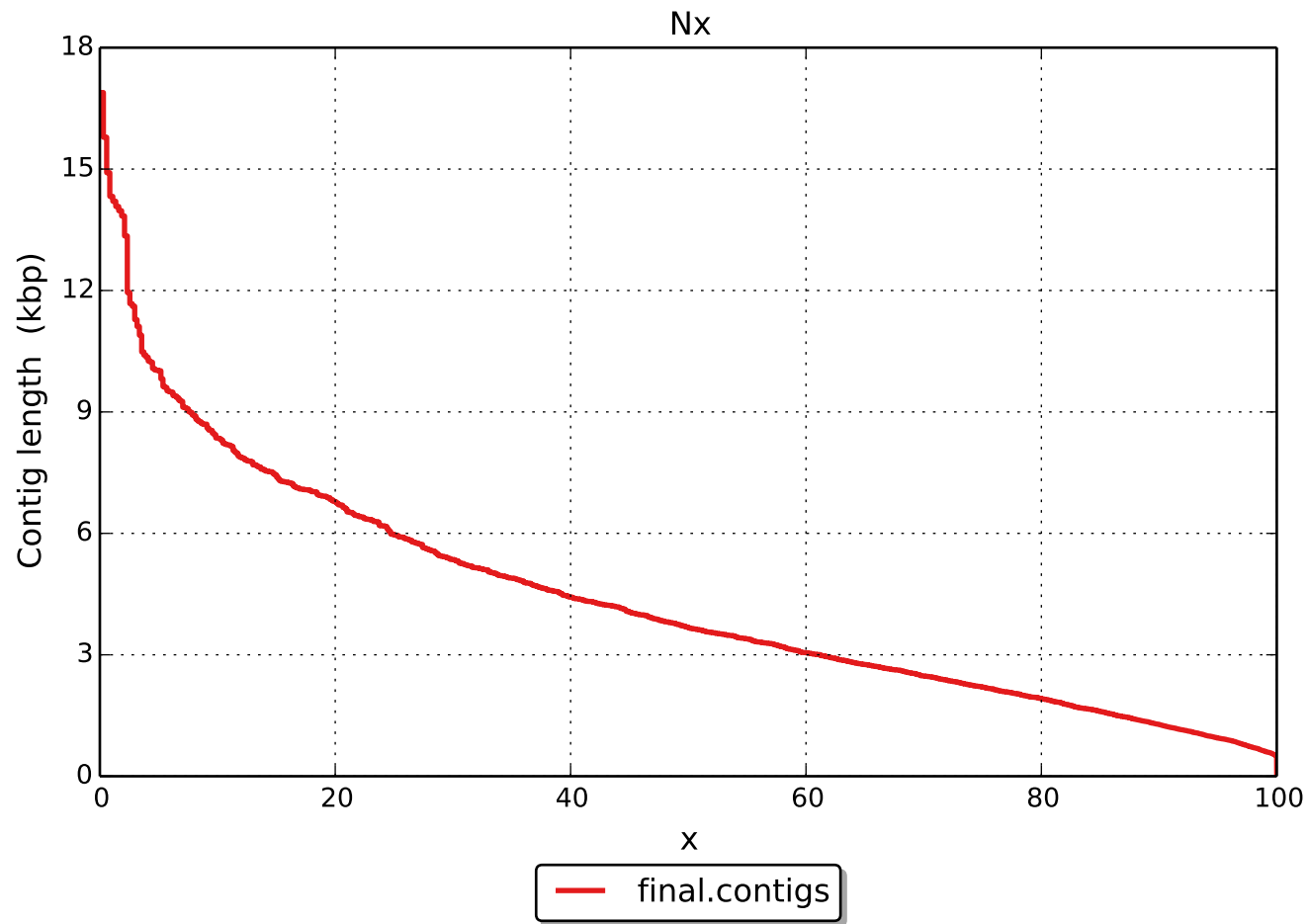
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	180
# N's	0

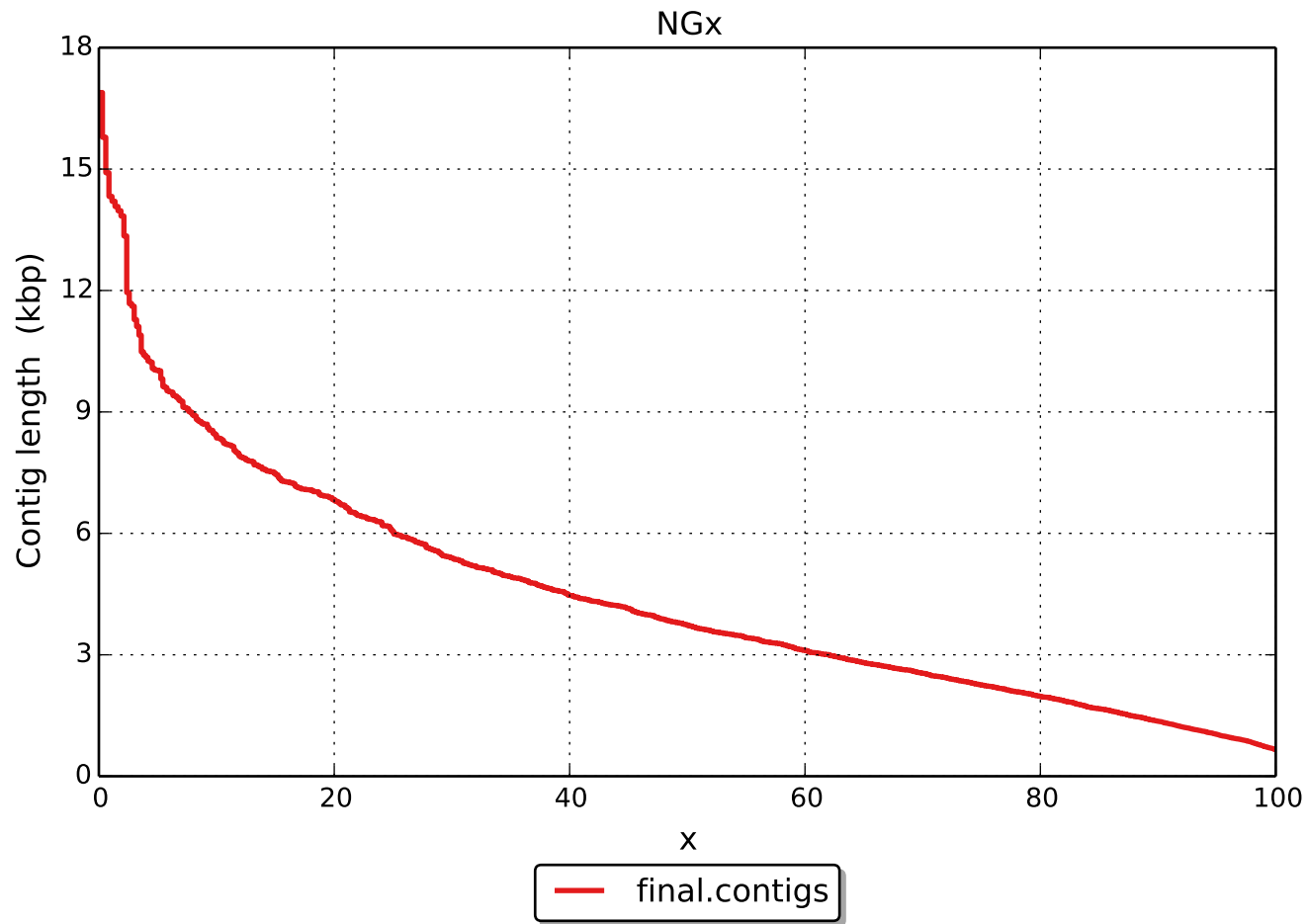
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



# GC content



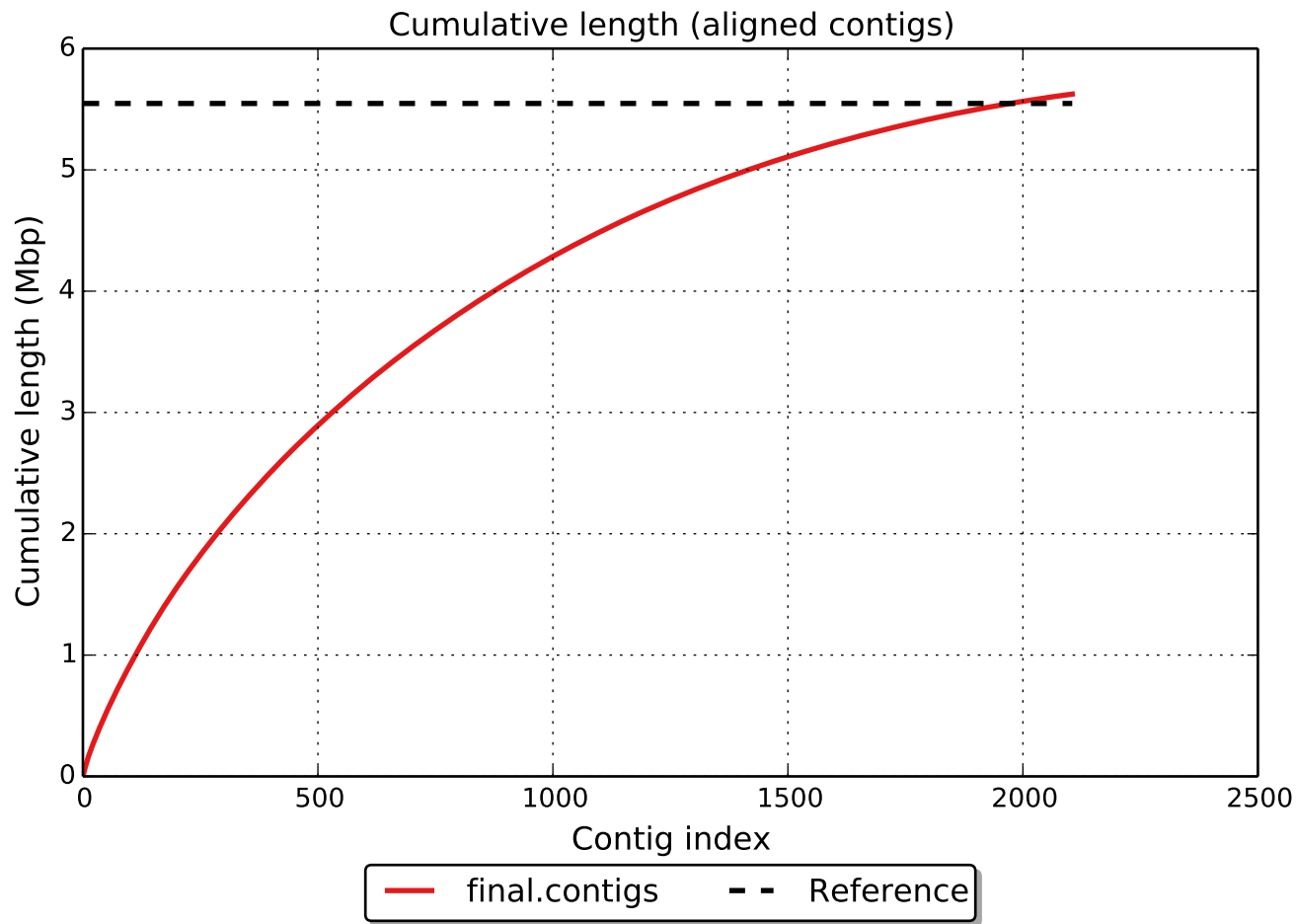


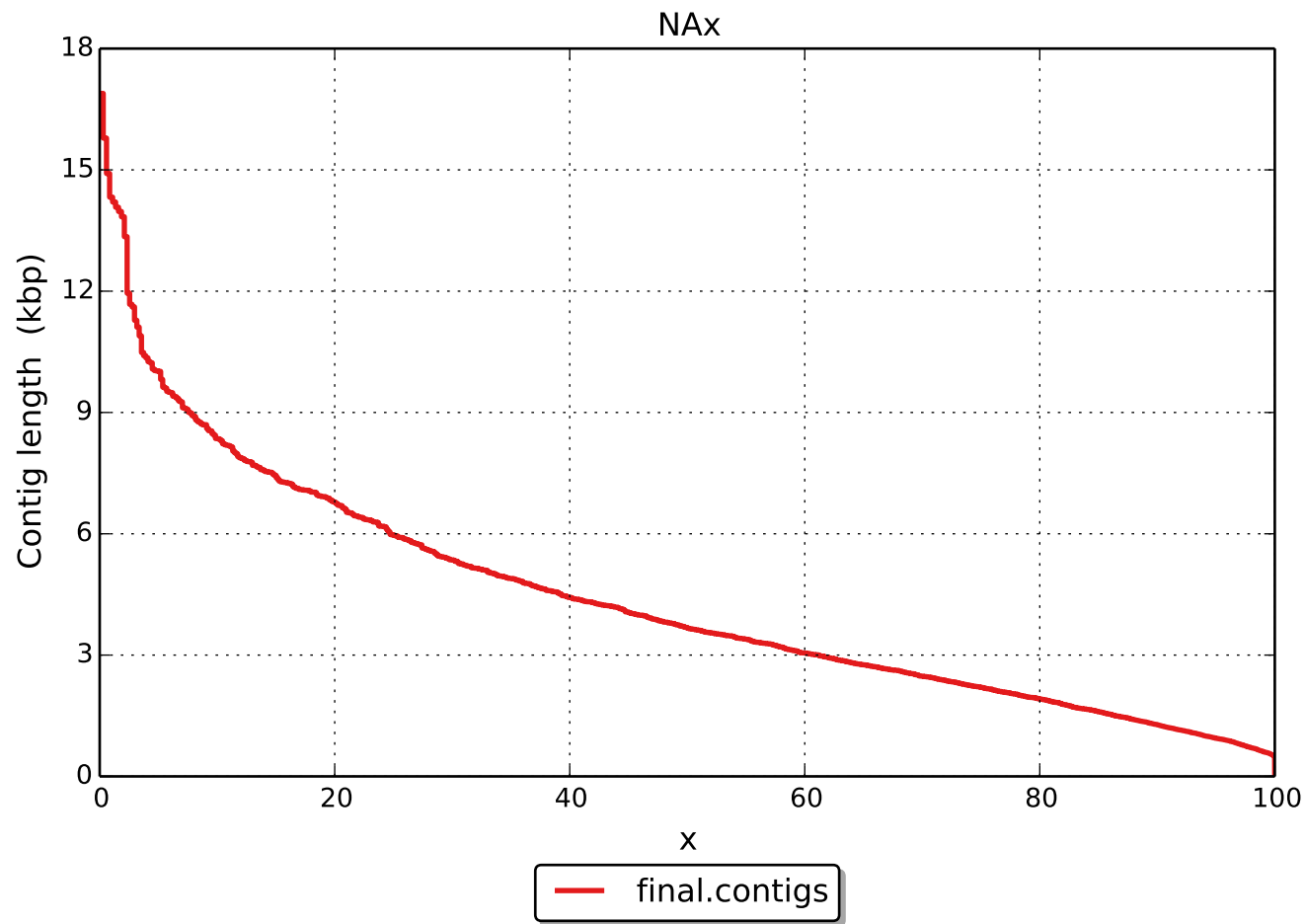


# Misassemblies









# NGAx

