

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	643
# contigs ( $\geq 1000$ bp)	430
Total length ( $\geq 0$ bp)	2584523
Total length ( $\geq 1000$ bp)	2445134
# contigs	643
Largest contig	39846
Total length	2584523
Reference length	5547323
GC (%)	50.13
Reference GC (%)	50.48
N50	8416
N75	4208
L50	95
L75	201
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	46.269
Duplication ratio	1.007
# N's per 100 kbp	0.00
# mismatches per 100 kbp	424.67
# indels per 100 kbp	0.00
Largest alignment	39846
NA50	8416
NA75	4208
LA50	95
LA75	201

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

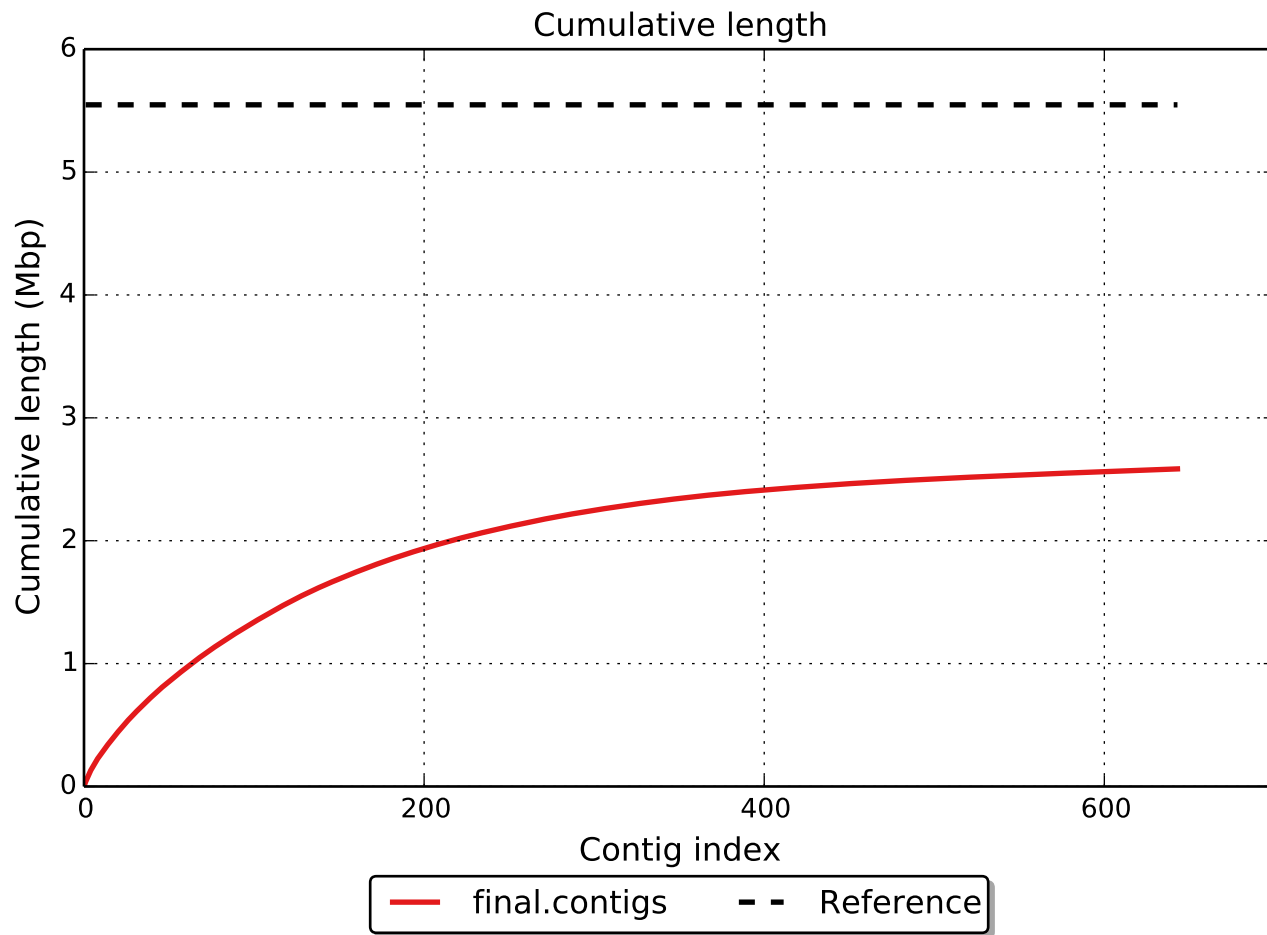
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	10900
# indels	0
# short indels	0
# long indels	0
Indels length	0

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).

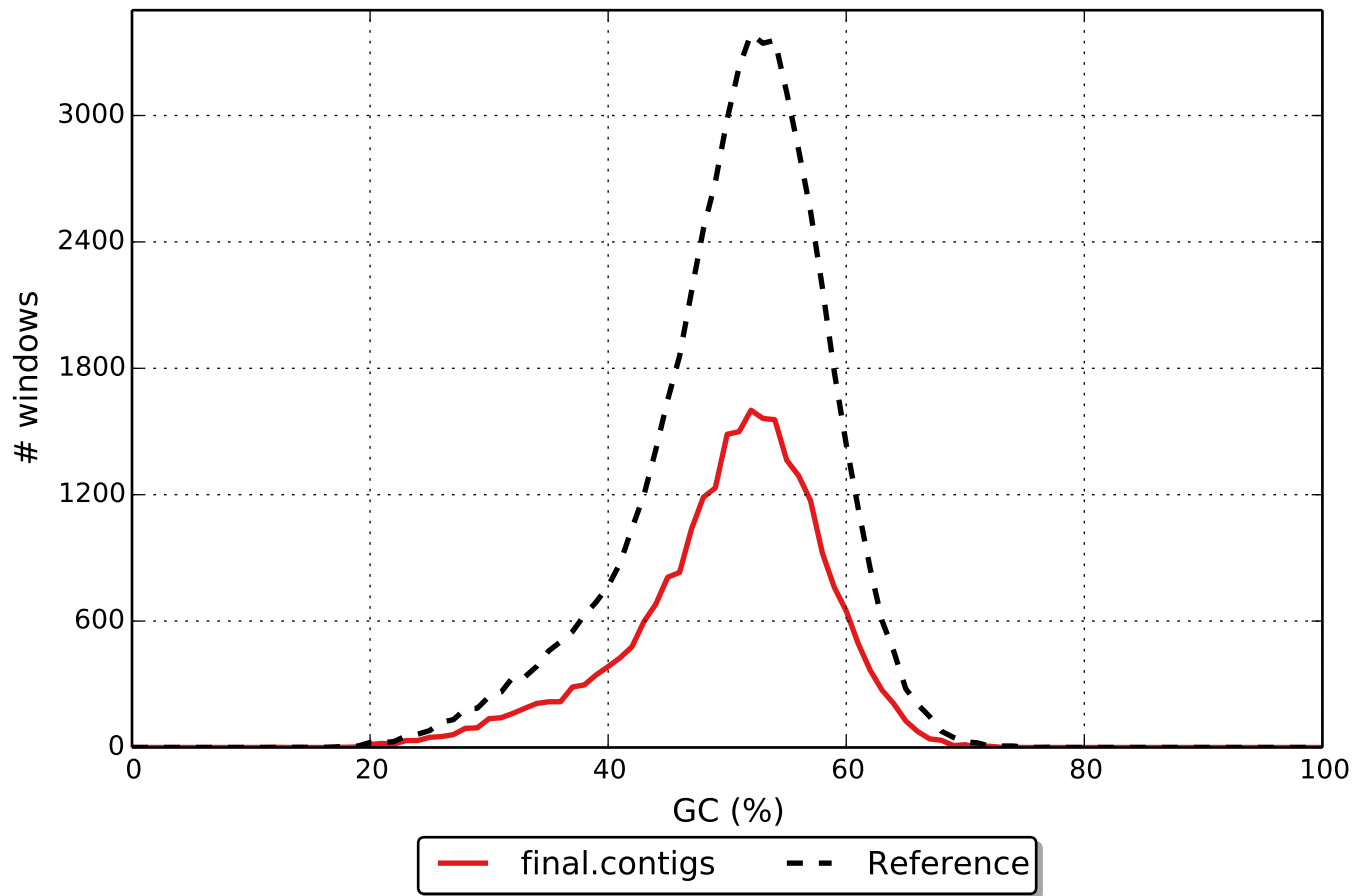
## Unaligned report

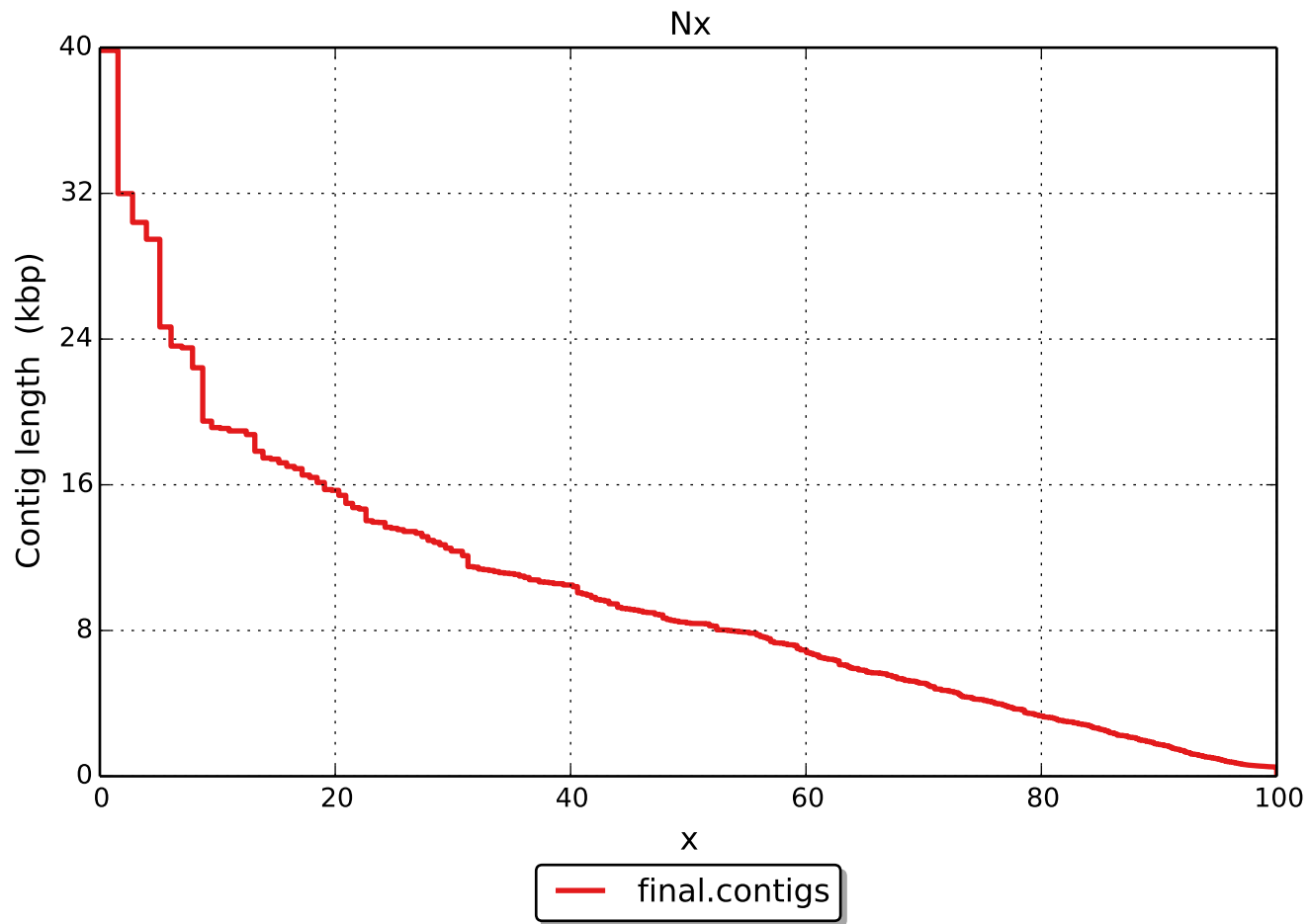
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

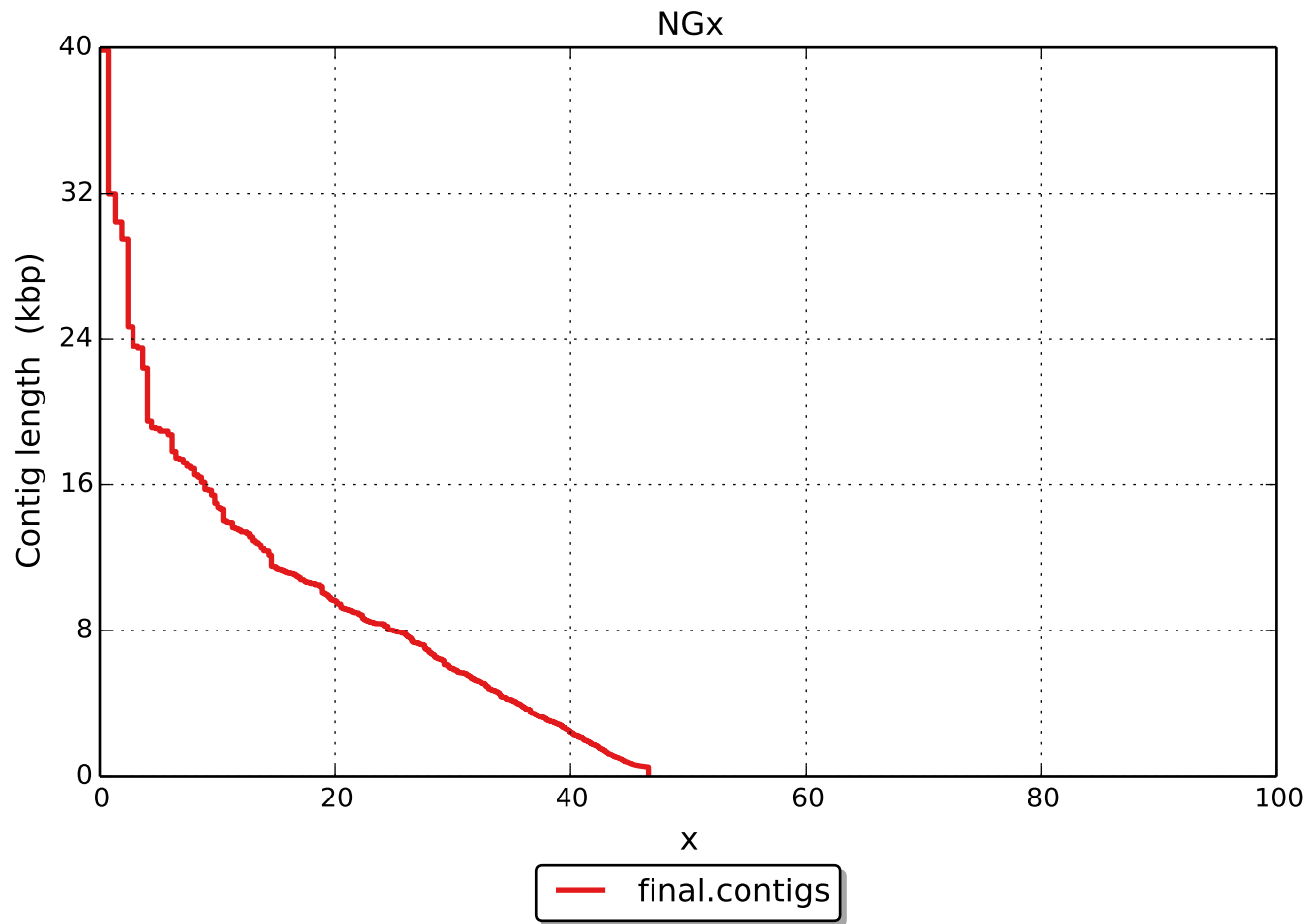
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



GC content



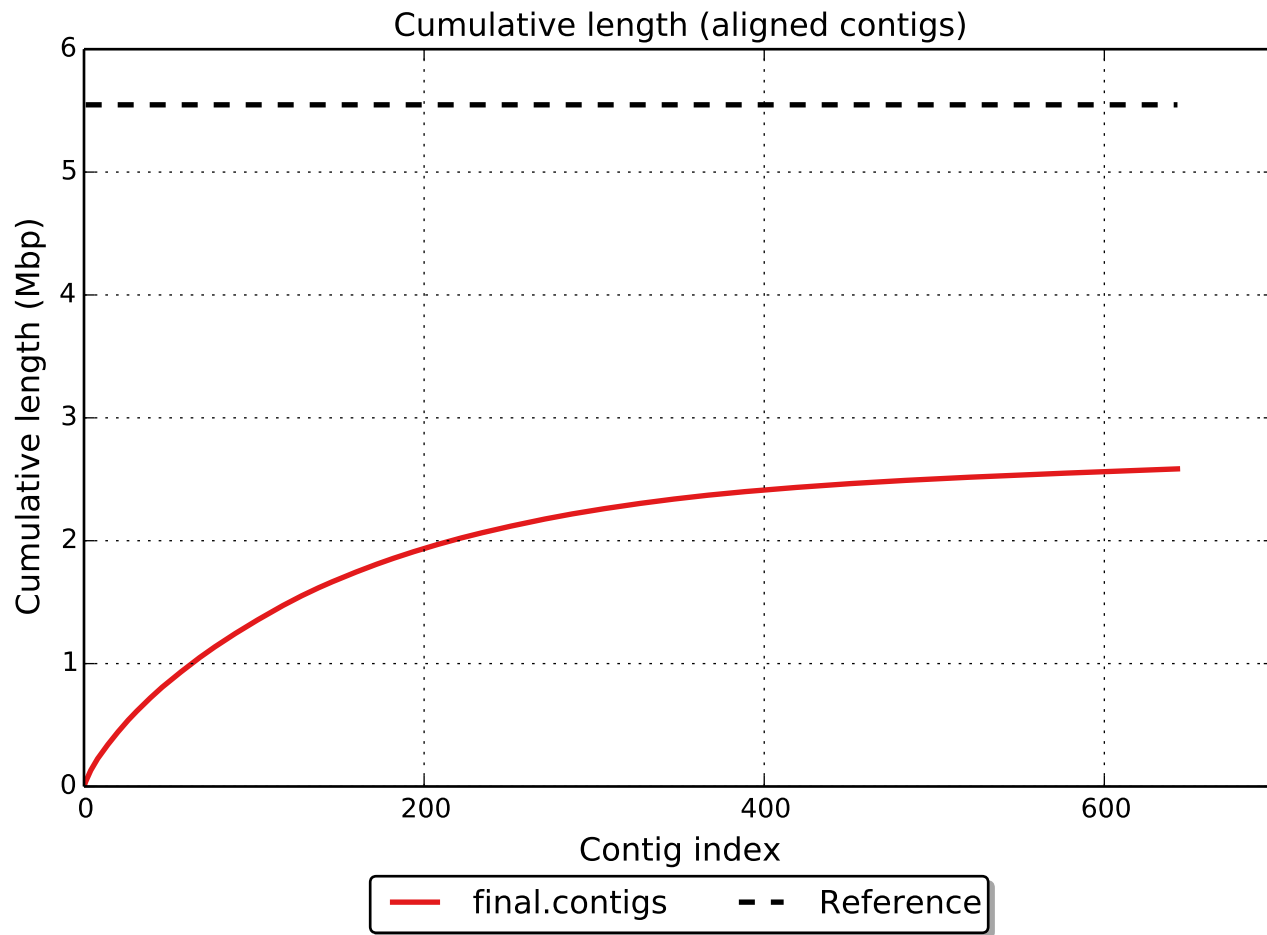


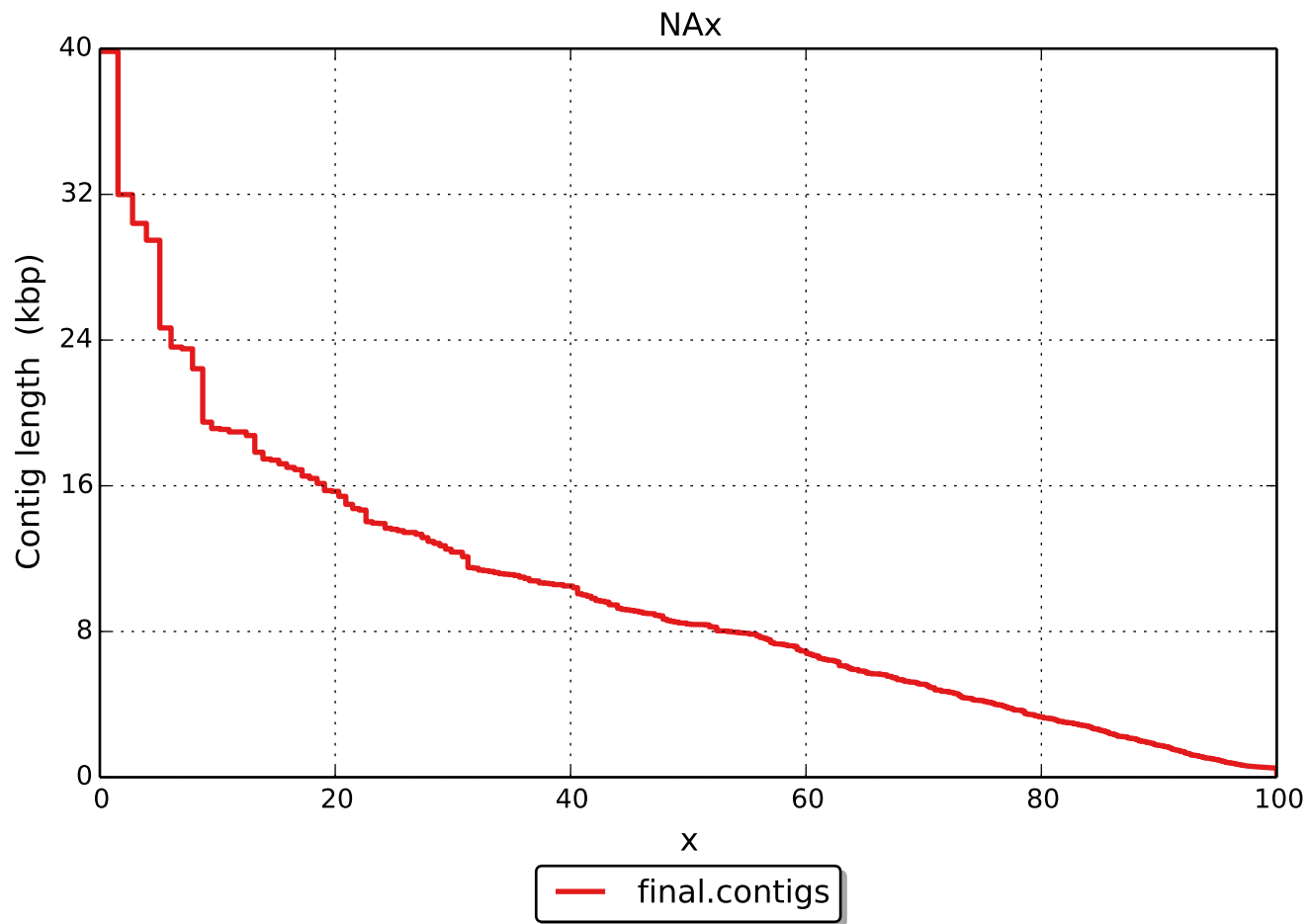


# Misassemblies









NGAx

