

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	1112
# contigs ( $\geq 1000$ bp)	921
Total length ( $\geq 0$ bp)	5255716
Total length ( $\geq 1000$ bp)	5119805
# contigs	1112
Largest contig	36412
Total length	5255716
Reference length	5478683
GC (%)	50.28
Reference GC (%)	50.49
N50	8099
NG50	7667
N75	4263
NG75	3865
L50	202
LG50	217
L75	423
LG75	464
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	94.458
Duplication ratio	1.016
# N's per 100 kbp	0.00
# mismatches per 100 kbp	15.36
# indels per 100 kbp	0.12
Largest alignment	36412
NA50	8099
NGA50	7667
NA75	4263
NGA75	3865
LA50	202
LGA50	217
LA75	423
LGA75	464

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

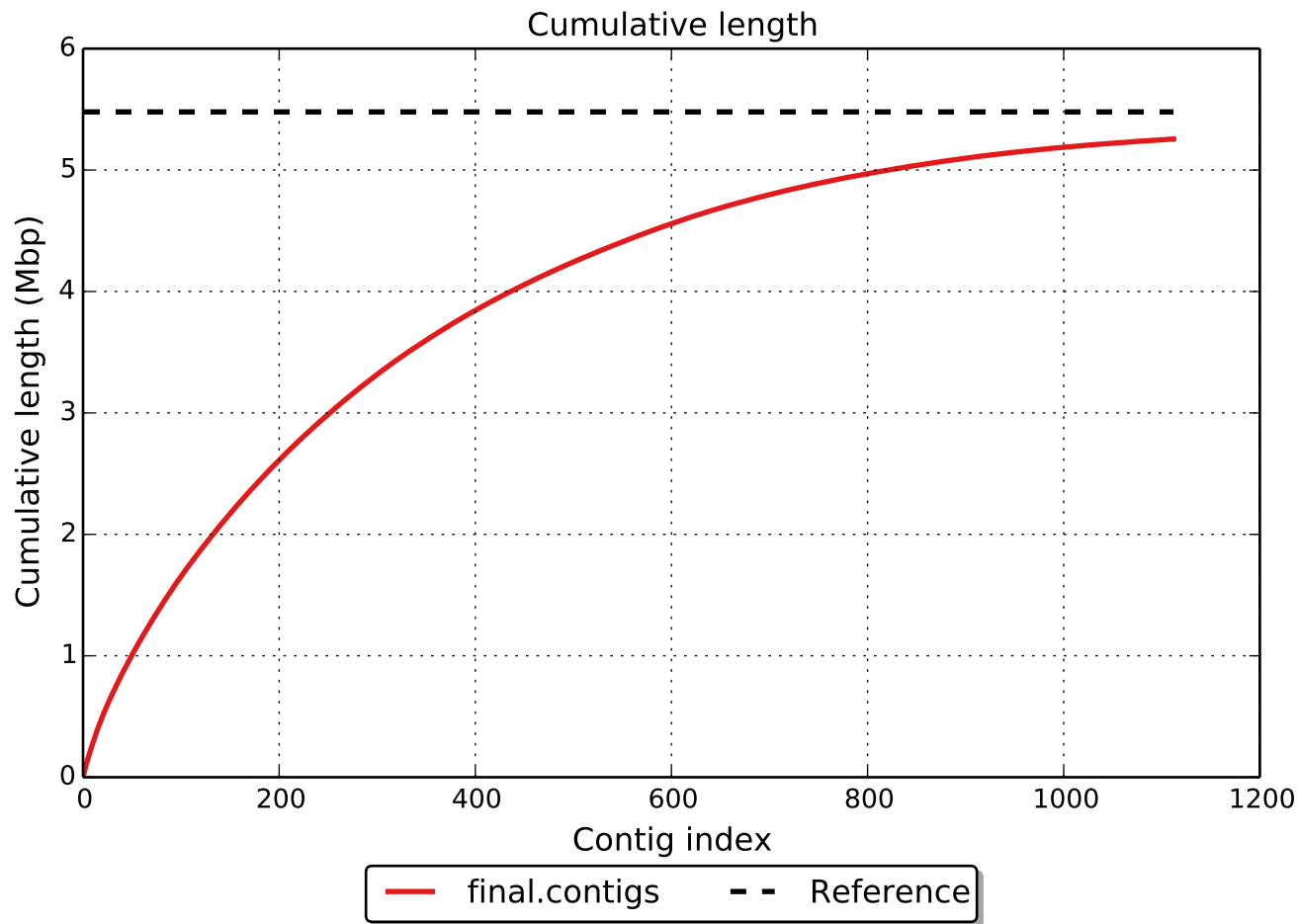
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# mismatches	795
# indels	6
# short indels	4
# long indels	2
Indels length	33

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).

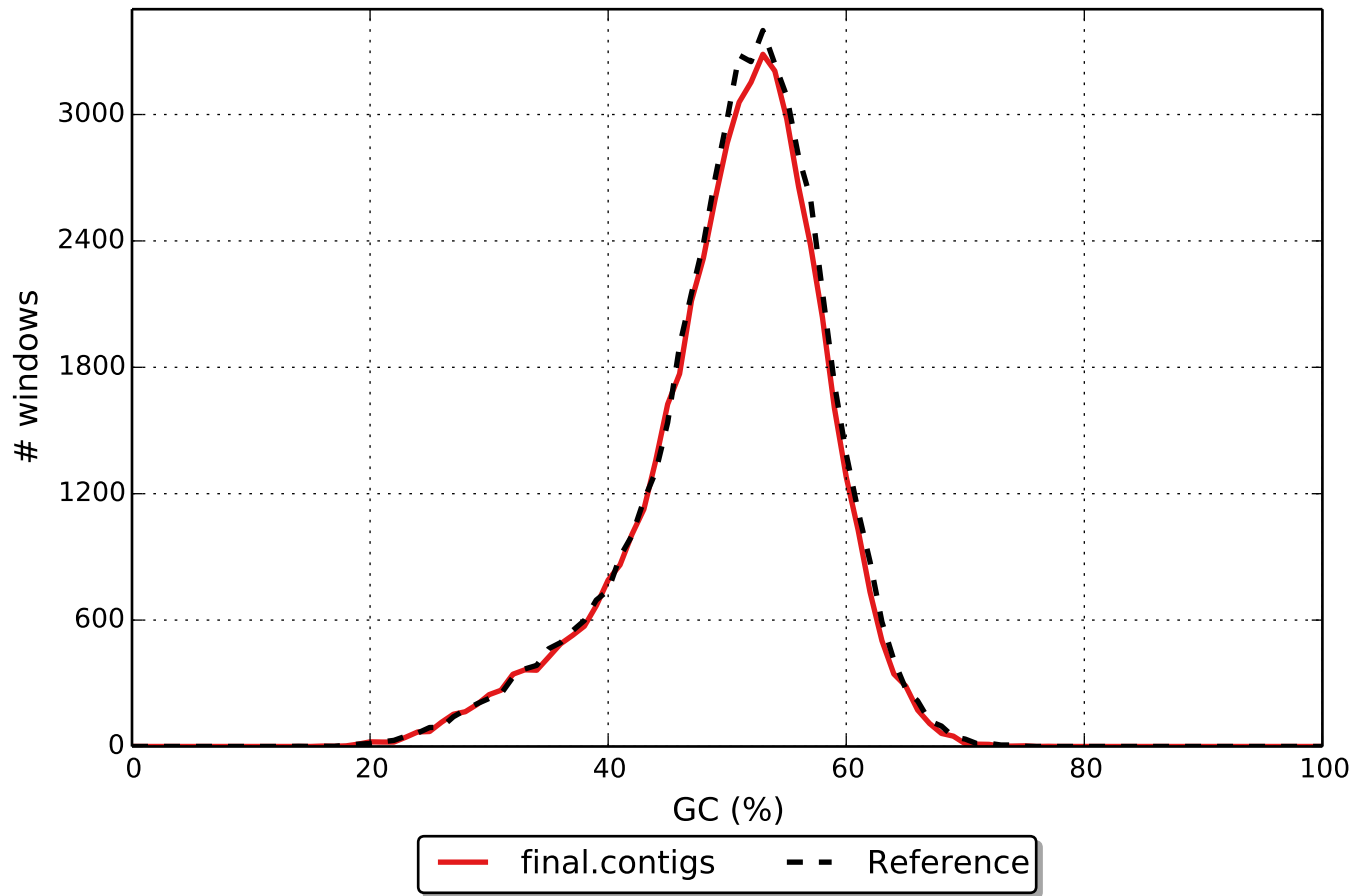
## Unaligned report

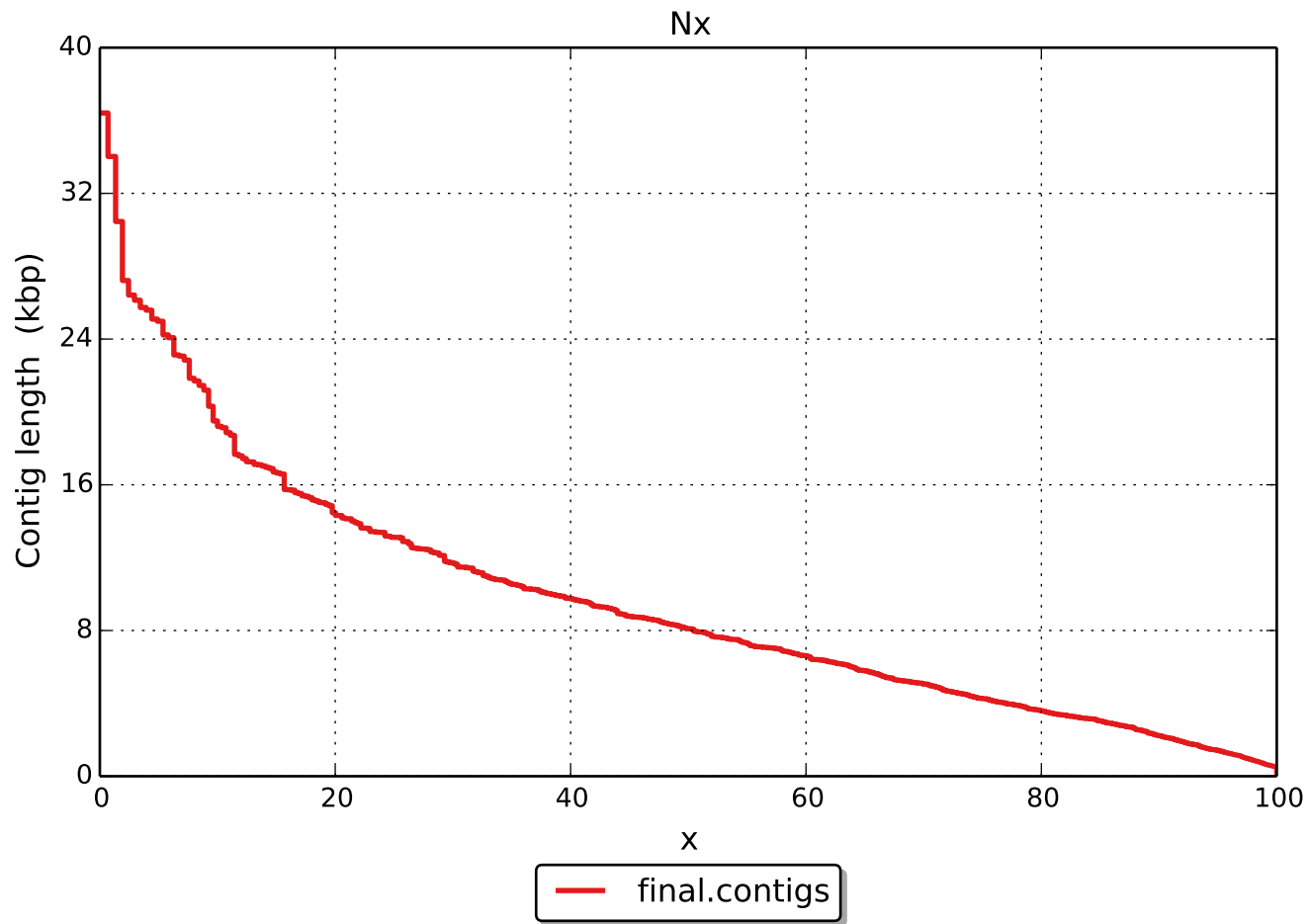
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

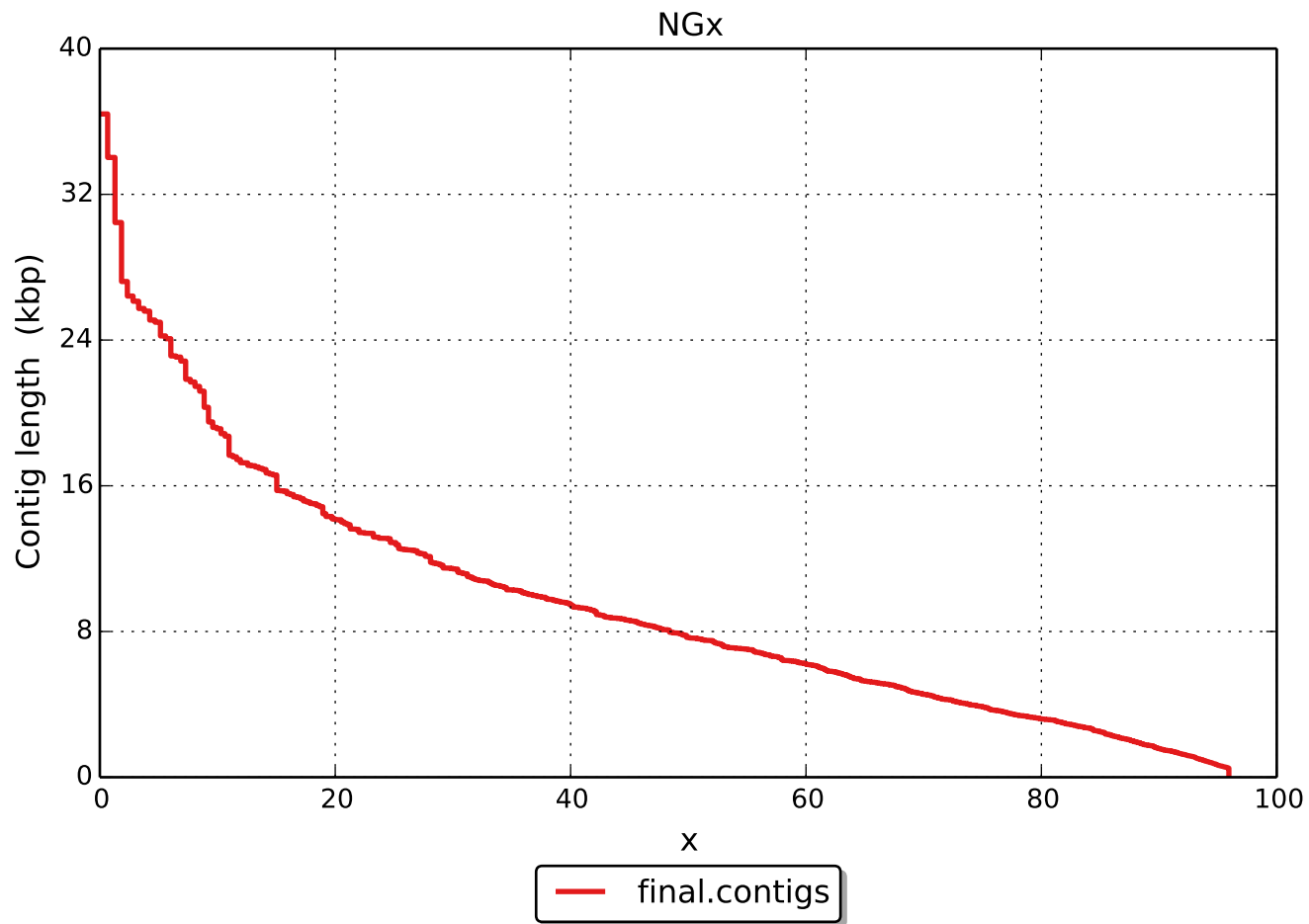
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



GC content



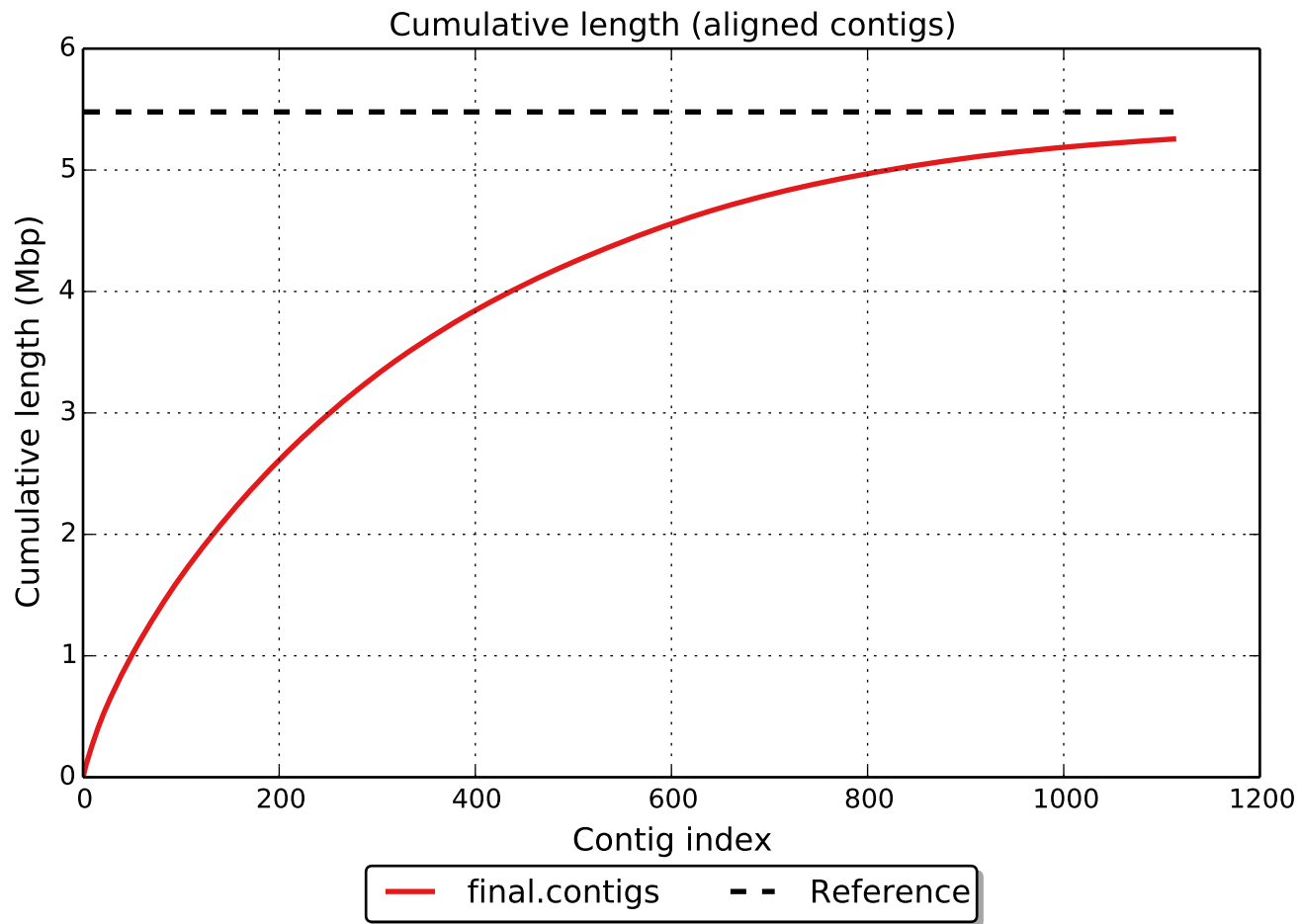


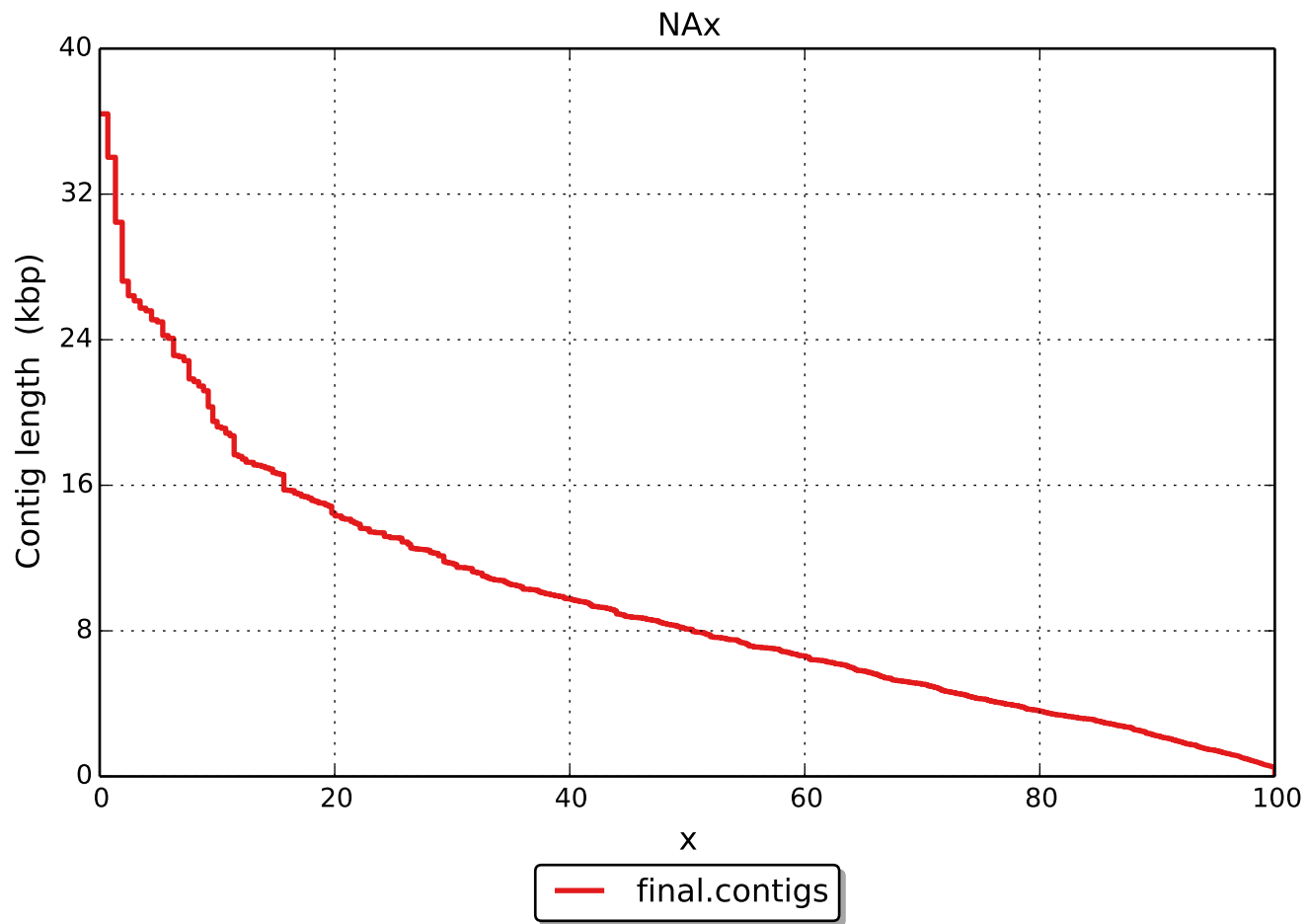


# Misassemblies









# NGAx

