

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	3769
# contigs ( $\geq 1000$ bp)	1609
Total length ( $\geq 0$ bp)	4801484
Total length ( $\geq 1000$ bp)	3311028
# contigs	3769
Largest contig	9465
Total length	4801484
Reference length	5478683
GC (%)	50.34
Reference GC (%)	50.49
N50	1610
NG50	1374
N75	861
NG75	684
L50	893
LG50	1120
L75	1922
LG75	2588
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 2 part
Unaligned length	336
Genome fraction (%)	82.873
Duplication ratio	1.057
# N's per 100 kbp	0.00
# mismatches per 100 kbp	541.67
# indels per 100 kbp	0.09
Largest alignment	9465
NA50	1610
NGA50	1374
NA75	861
NGA75	684
LA50	893
LGA50	1120
LA75	1922
LGA75	2588

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

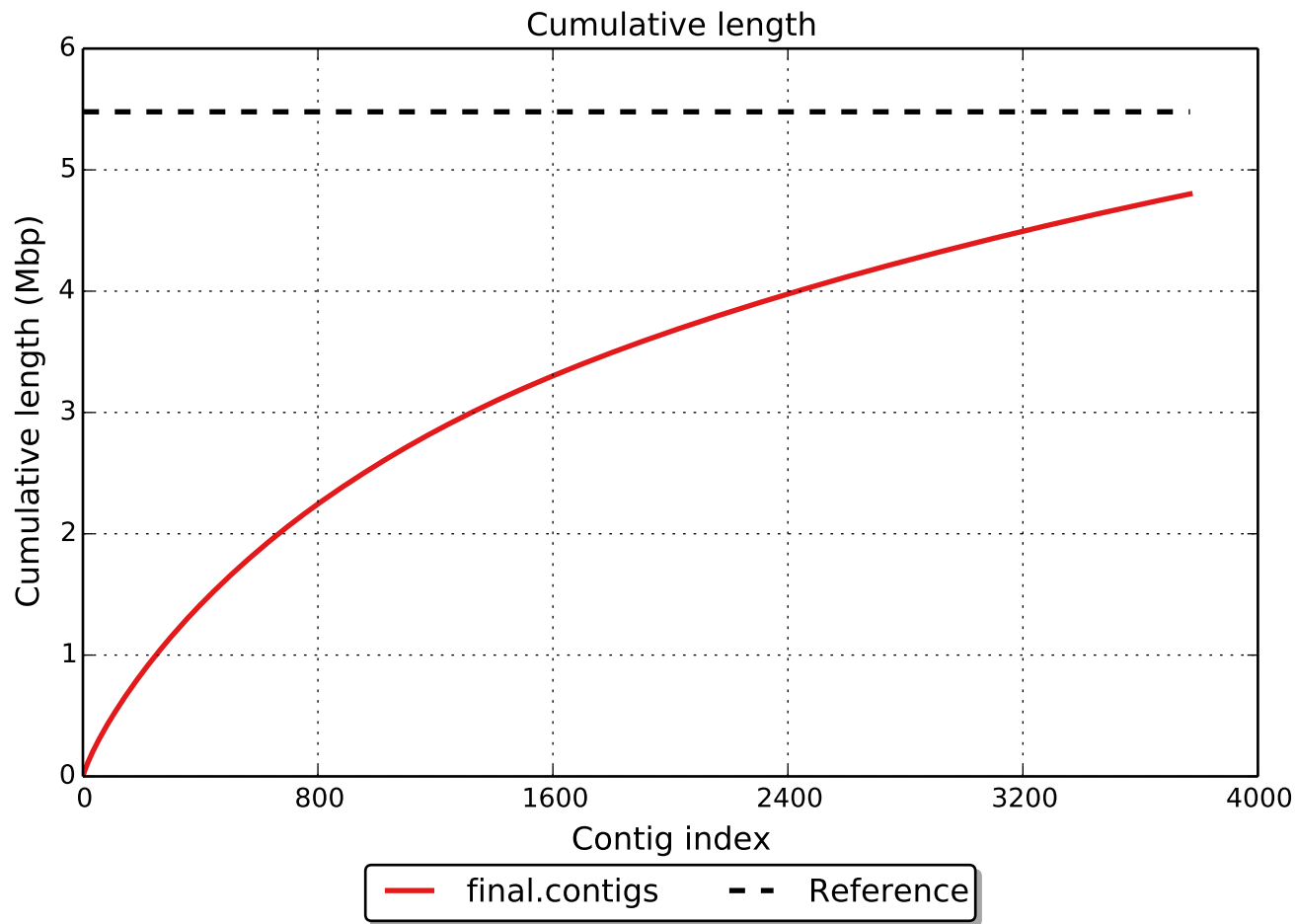
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	24594
# indels	4
# short indels	3
# long indels	1
Indels length	23

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).

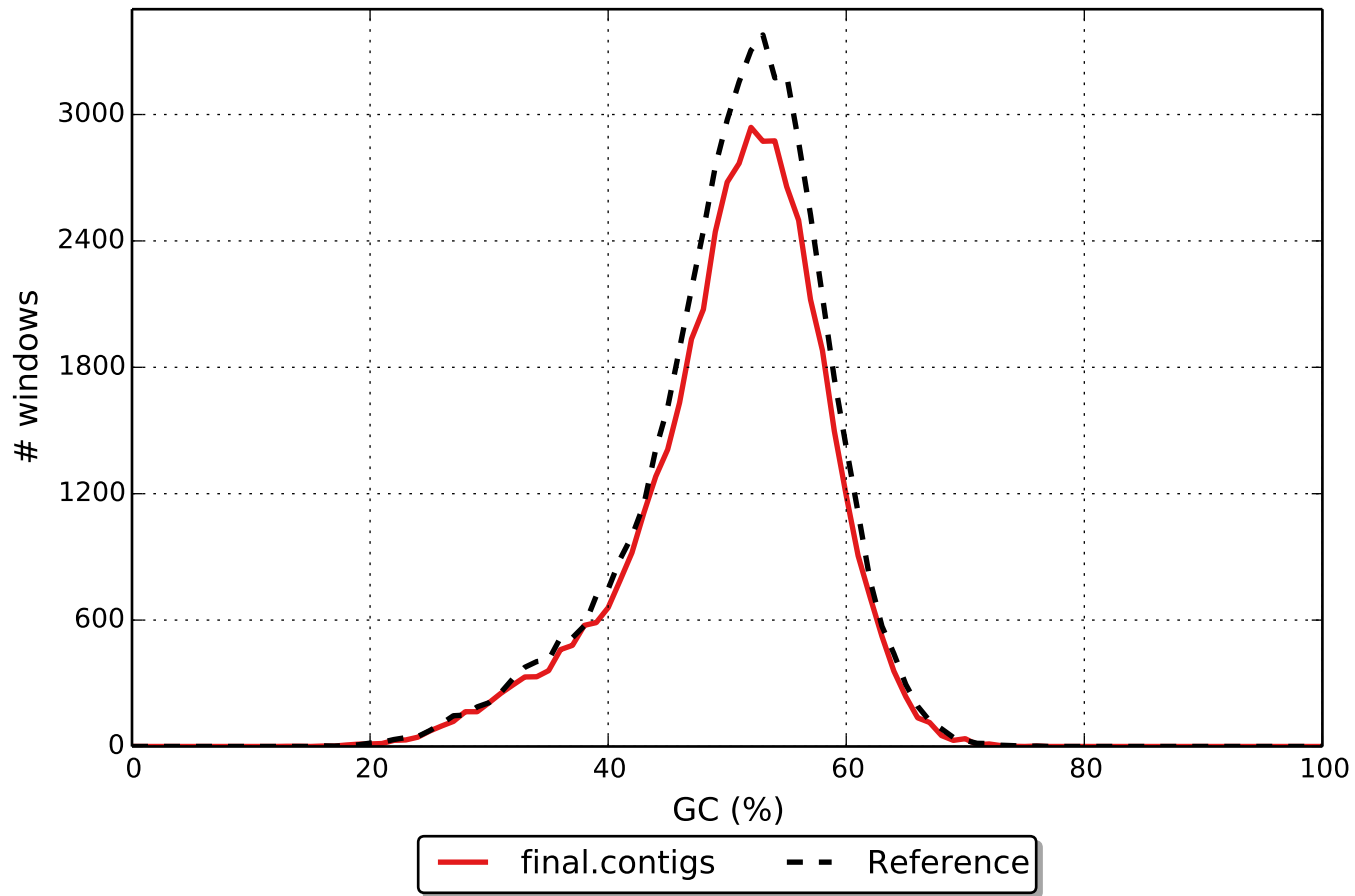
## Unaligned report

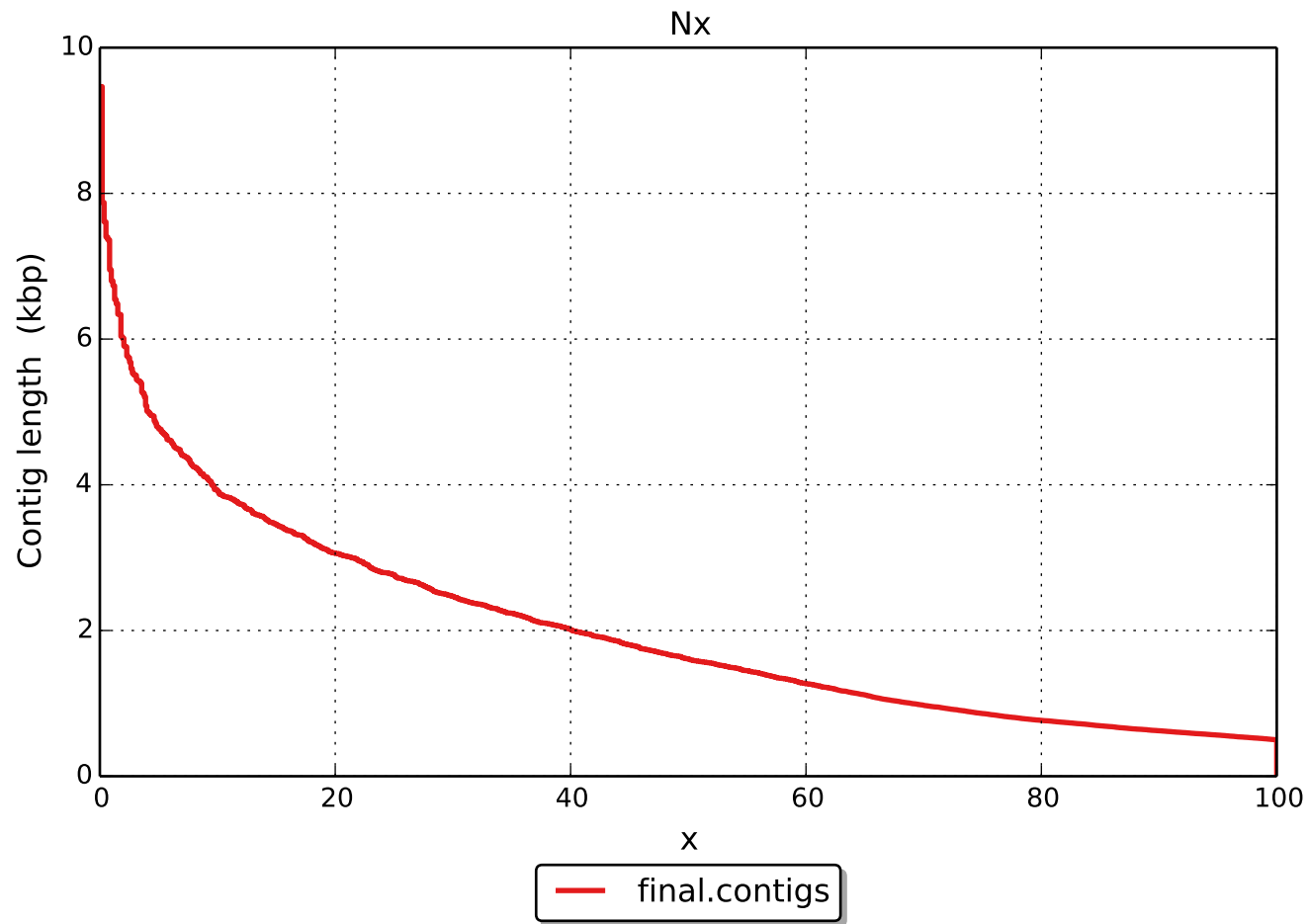
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	0
Partially unaligned length	336
# N's	0

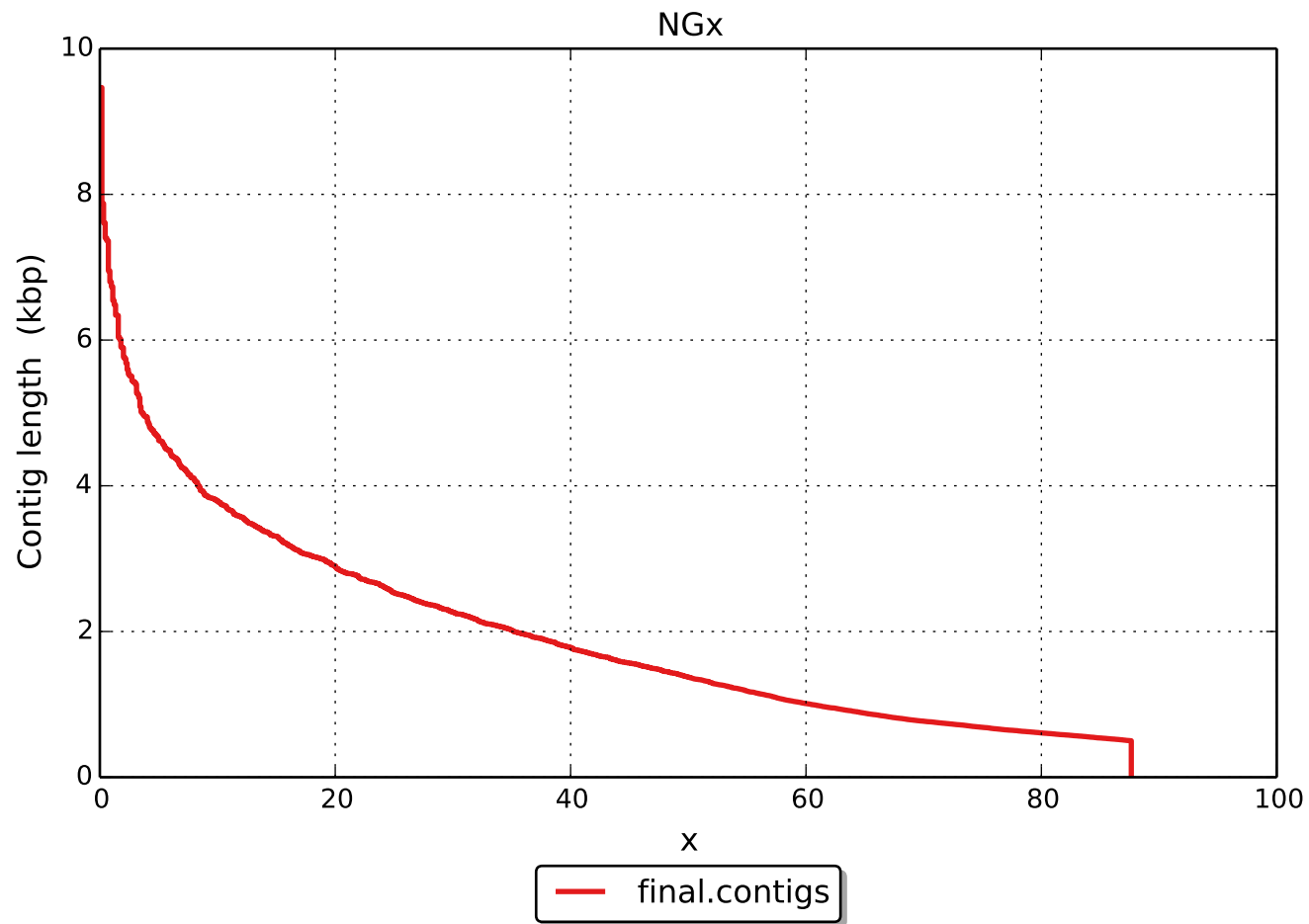
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



GC content



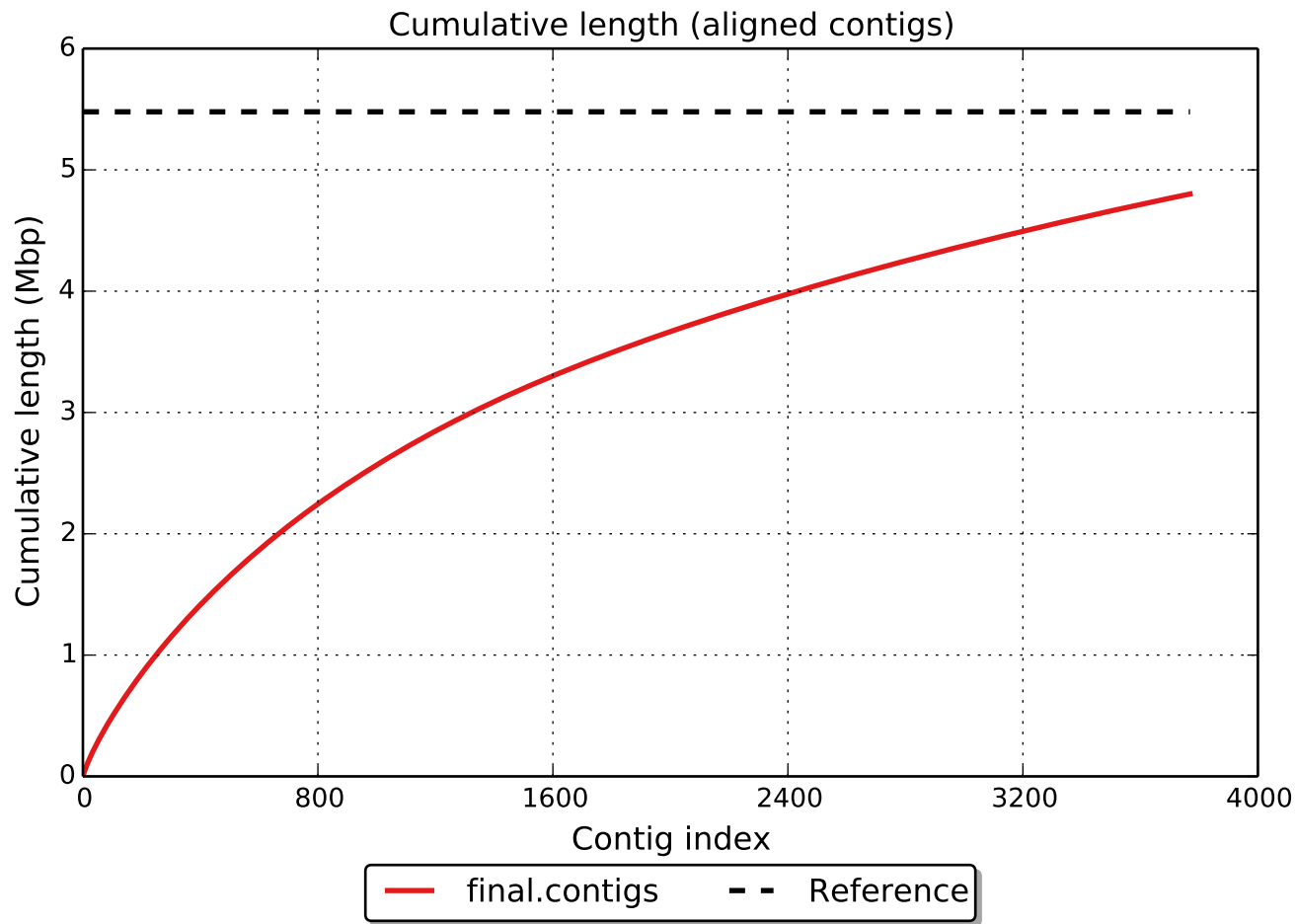


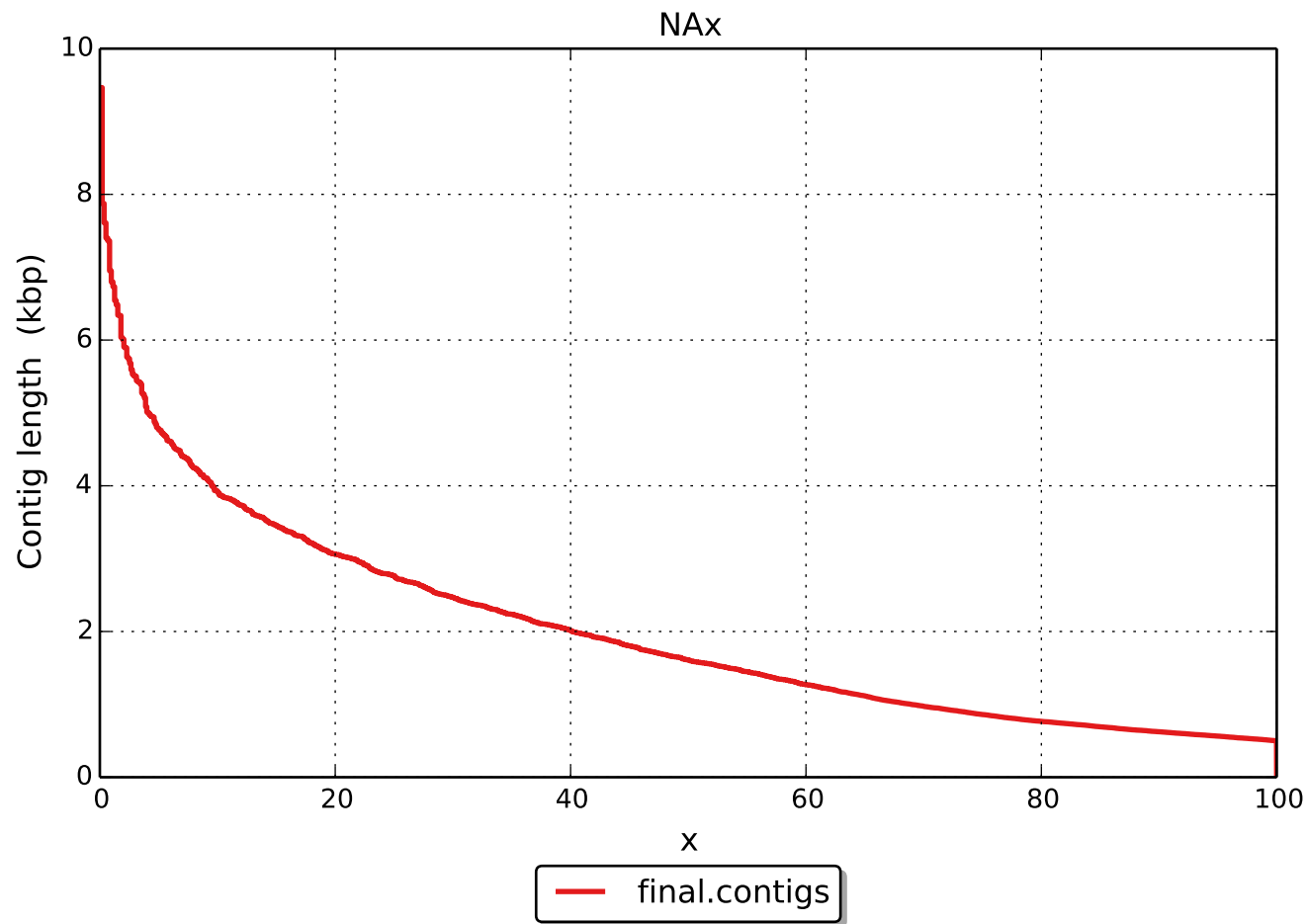


# Misassemblies









NGAx

