

## Report

	final.contigs
# contigs (>= 0 bp)	2139
# contigs (>= 1000 bp)	1620
Total length (>= 0 bp)	5223475
Total length (>= 1000 bp)	4845548
# contigs	2139
Largest contig	15765
Total length	5223475
Reference length	5478683
GC (%)	50.29
Reference GC (%)	50.49
N50	3457
NG50	3293
N75	1963
NG75	1757
L50	470
LG50	508
L75	970
LG75	1073
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	4159
# local misassemblies	0
# unaligned contigs	0 + 1 part
Unaligned length	2369
Genome fraction (%)	92.548
Duplication ratio	1.030
# N's per 100 kbp	0.00
# mismatches per 100 kbp	22.38
# indels per 100 kbp	0.10
Largest alignment	15765
NA50	3457
NGA50	3280
NA75	1959
NGA75	1757
LA50	471
LGA50	509
LA75	971
LGA75	1074

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

## Misassemblies report

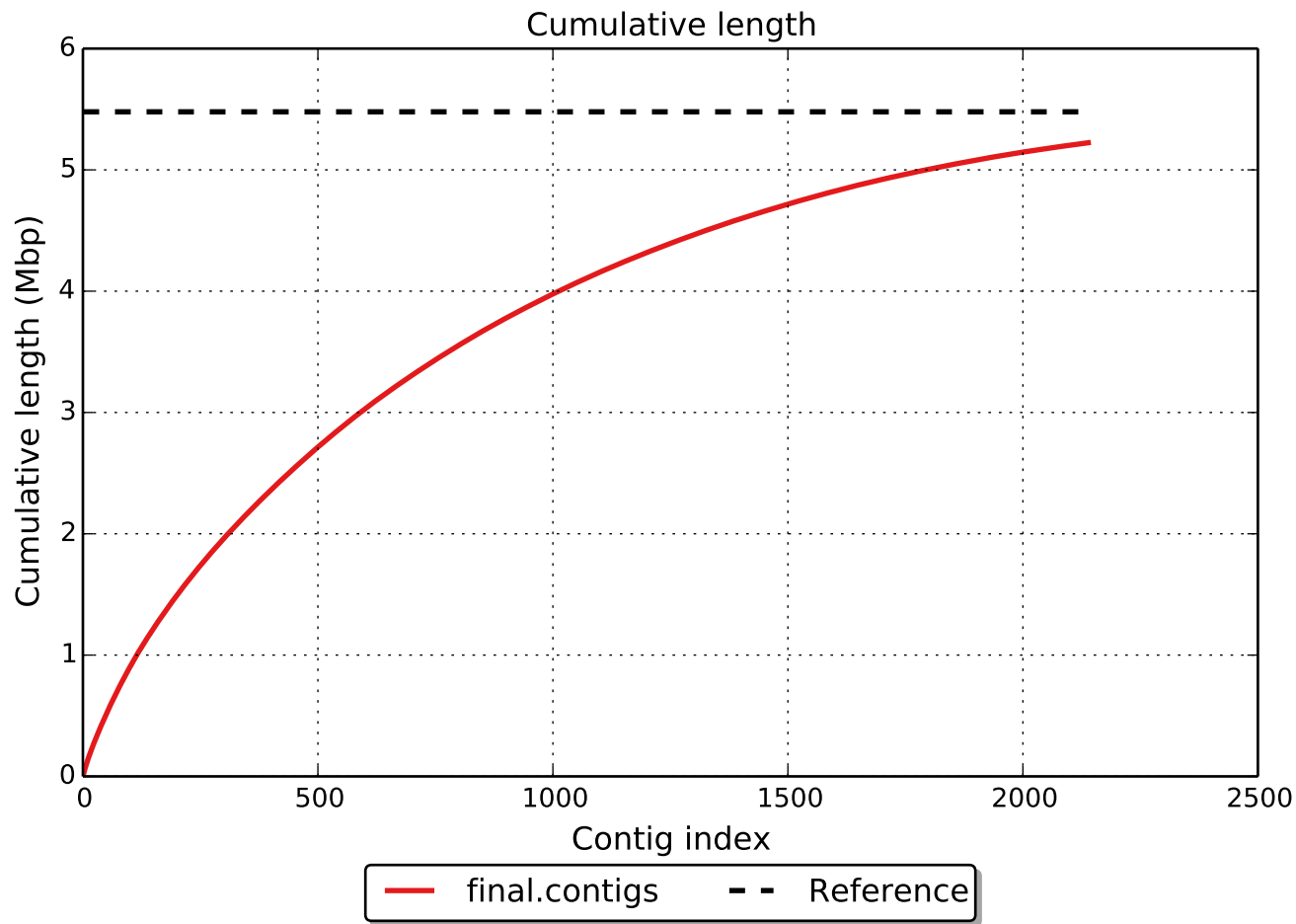
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	1
# misassembled contigs	1
Misassembled contigs length	4159
# local misassemblies	0
# mismatches	1135
# indels	5
# short indels	3
# long indels	2
Indels length	28

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).

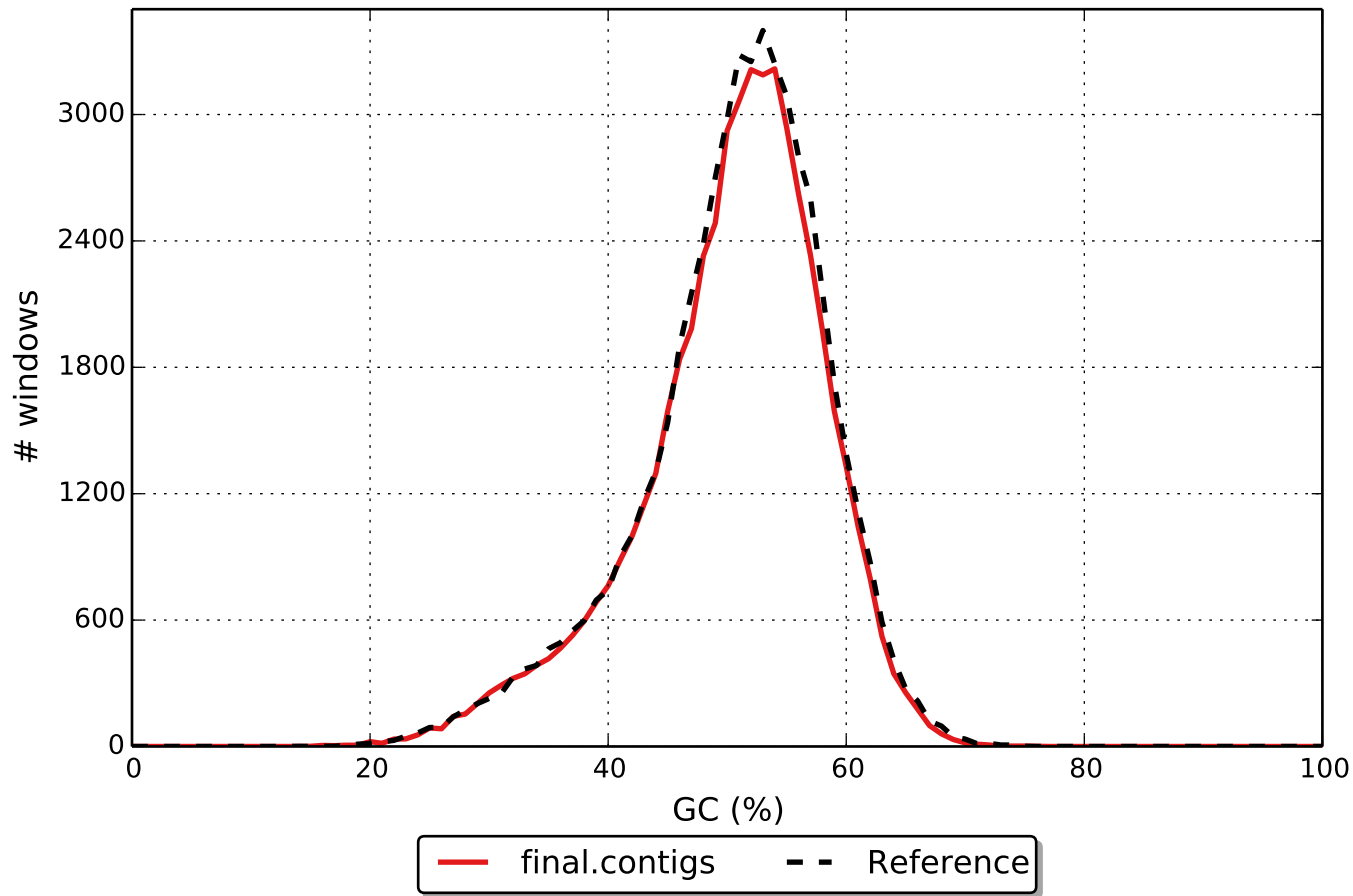
## Unaligned report

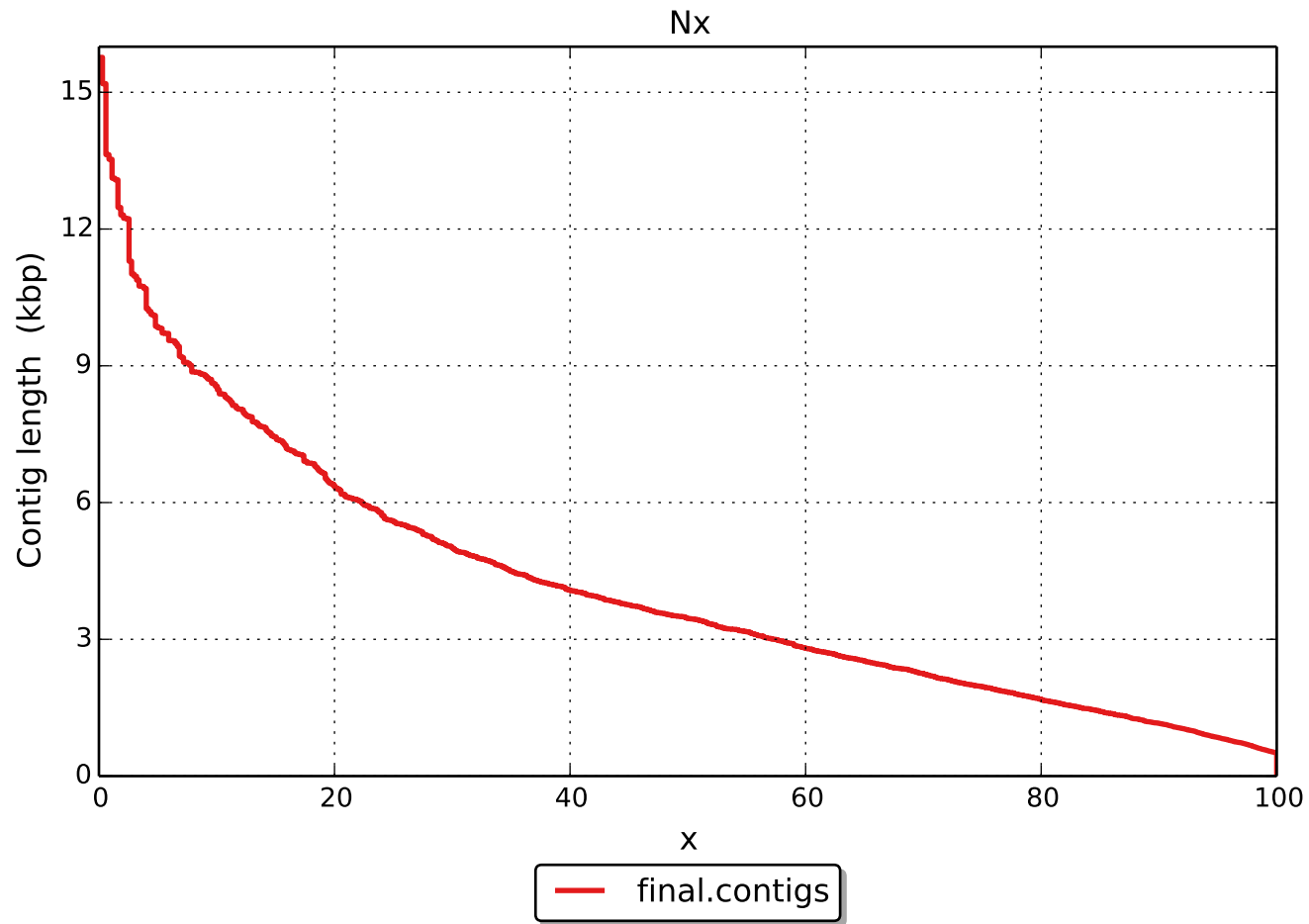
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	1
Partially unaligned length	2369
# N's	0

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).

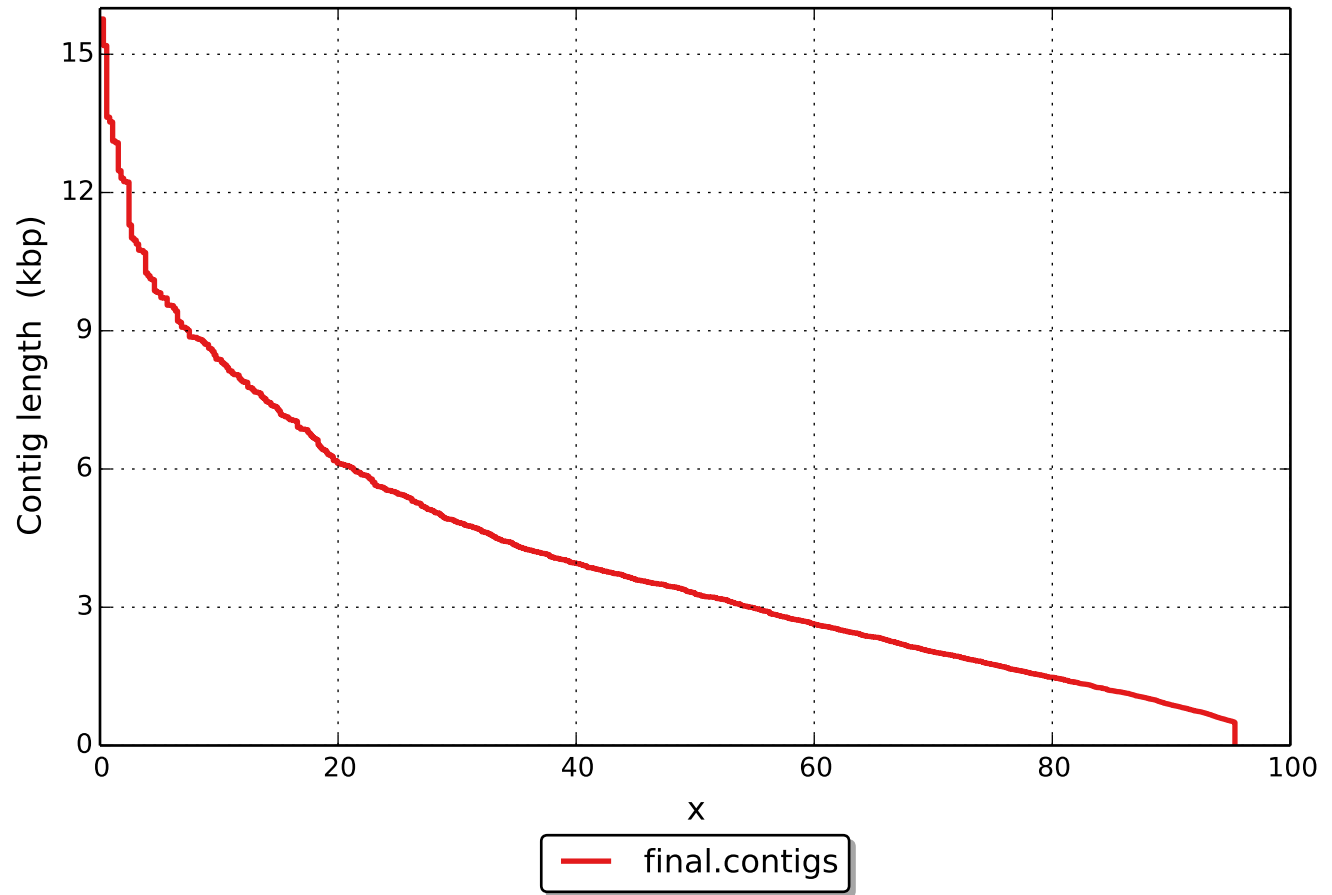


GC content





NGx

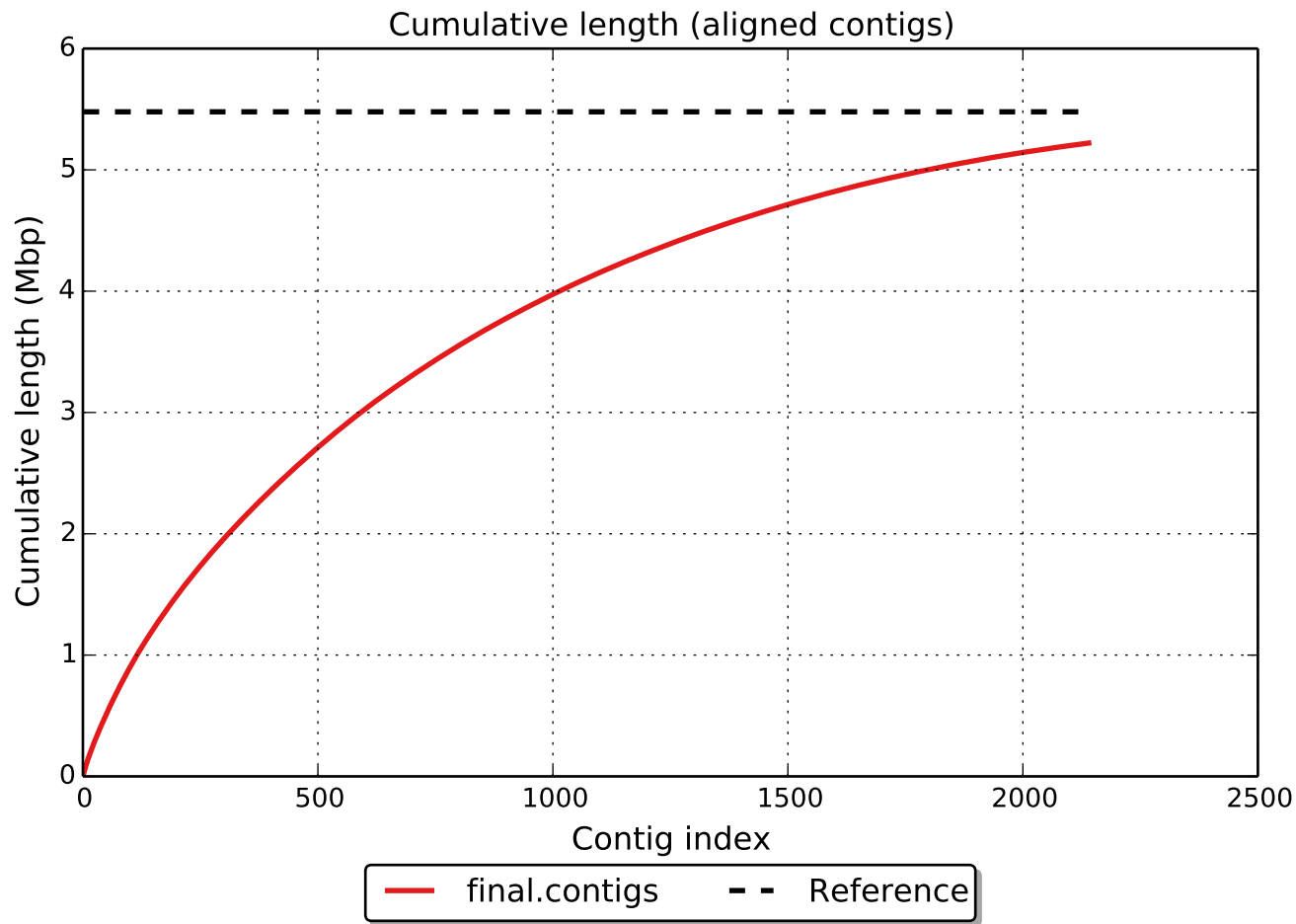


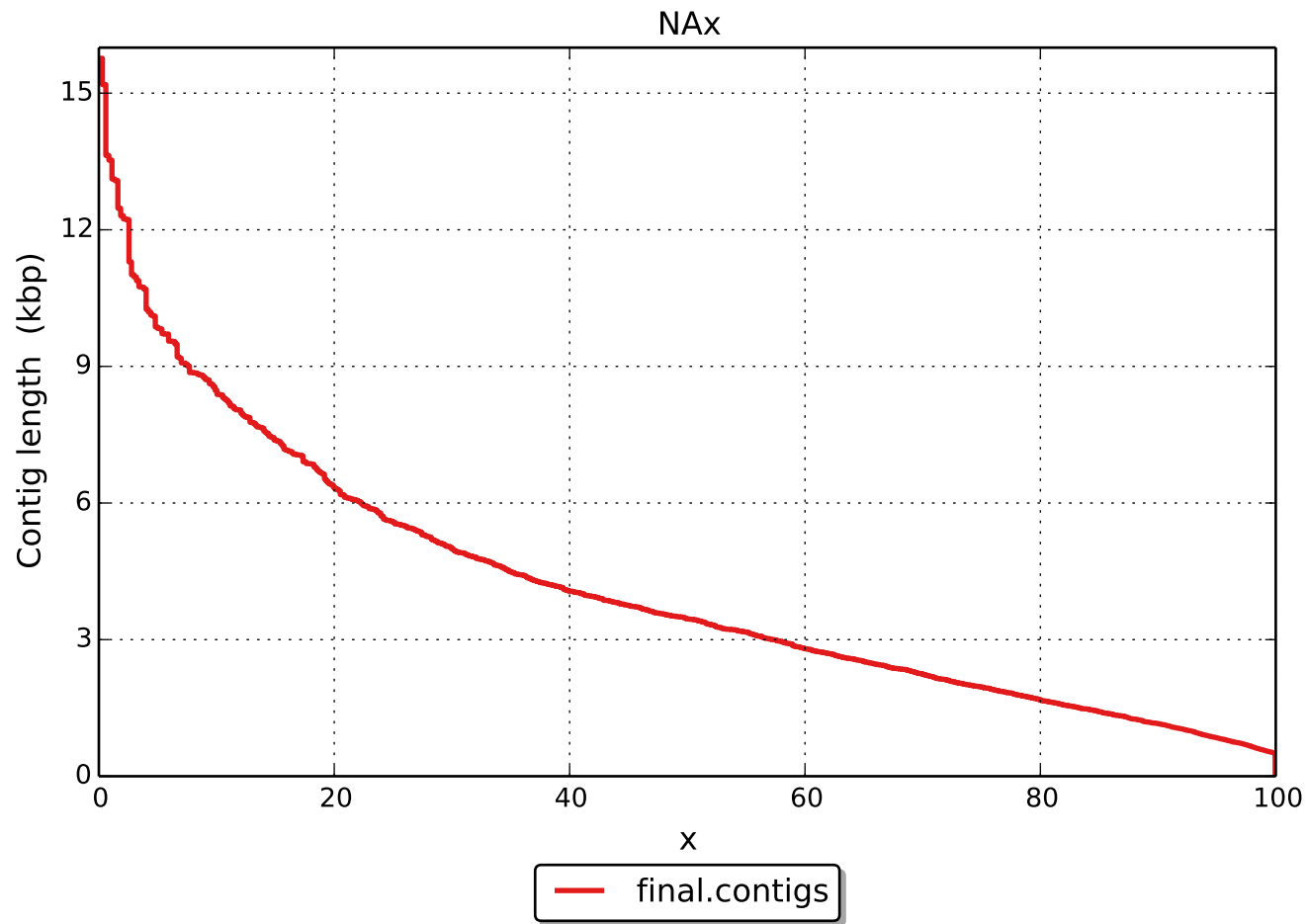
# Misassemblies



 # relocations







# NGAx

