

## Report

	final.contigs
# contigs (>= 0 bp)	4212
# contigs (>= 1000 bp)	1853
Total length (>= 0 bp)	4690387
Total length (>= 1000 bp)	3000633
# contigs	4212
Largest contig	5549
Total length	4690387
Reference length	5547323
GC (%)	50.29
Reference GC (%)	50.48
N50	1228
NG50	1077
N75	837
NG75	650
L50	1261
LG50	1635
L75	2419
LG75	3291
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	80.733
Duplication ratio	1.047
# N's per 100 kbp	0.00
# mismatches per 100 kbp	55.46
# indels per 100 kbp	0.07
Largest alignment	5549
NA50	1228
NGA50	1077
NA75	837
NGA75	650
LA50	1261
LGA50	1635
LA75	2419
LGA75	3291

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

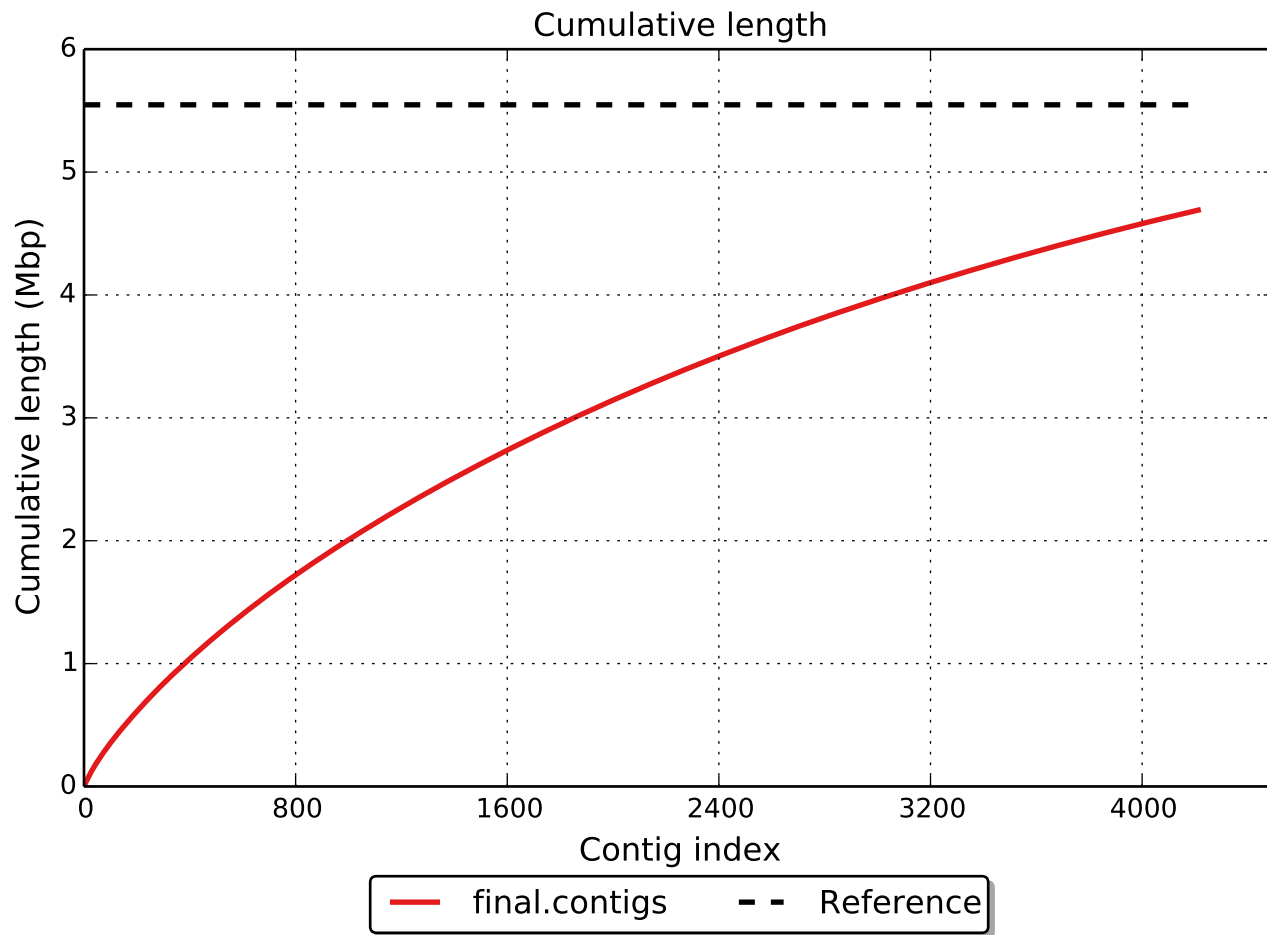
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	2484
# indels	3
# short indels	2
# long indels	1
Indels length	8

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).

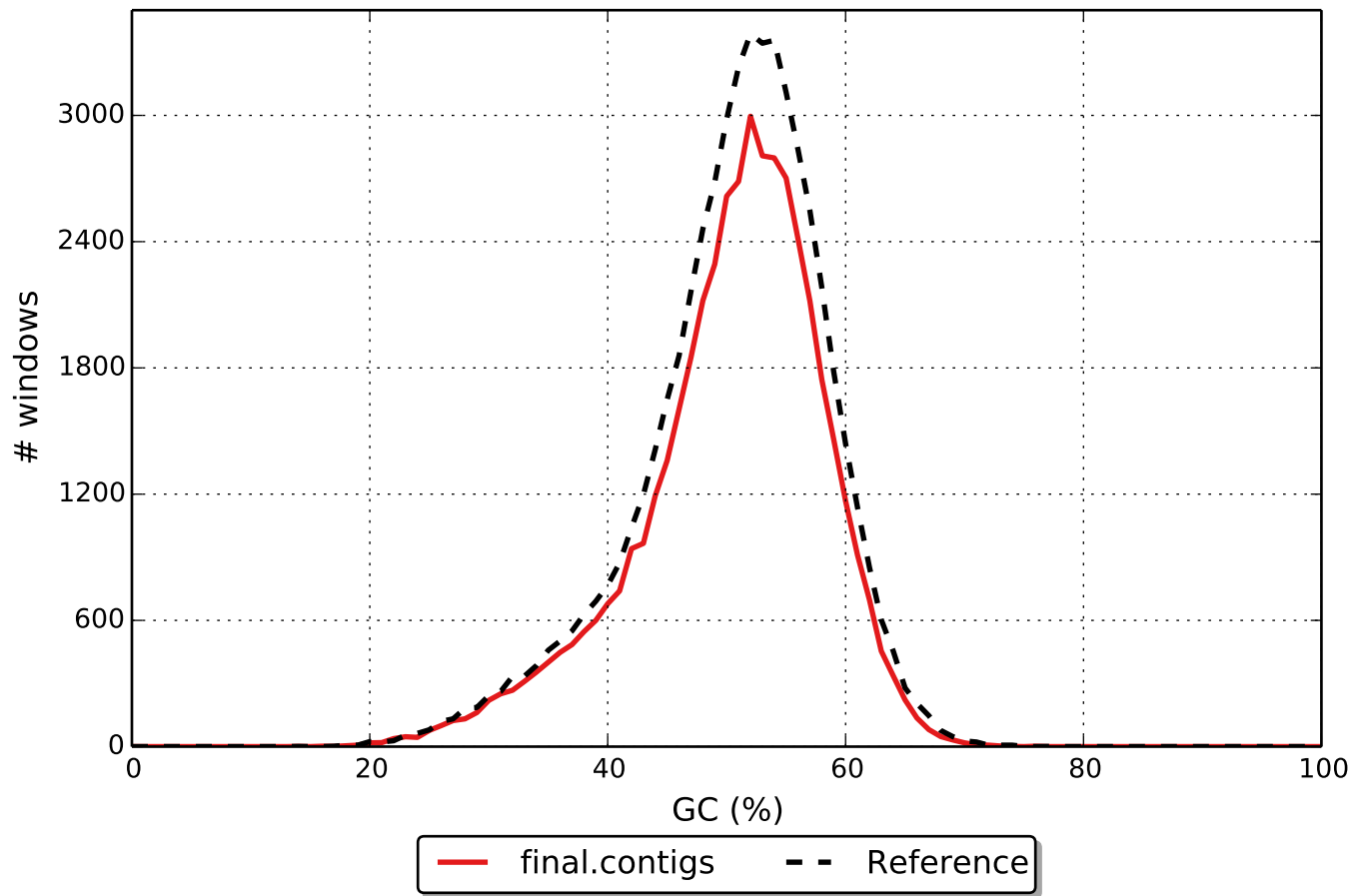
## Unaligned report

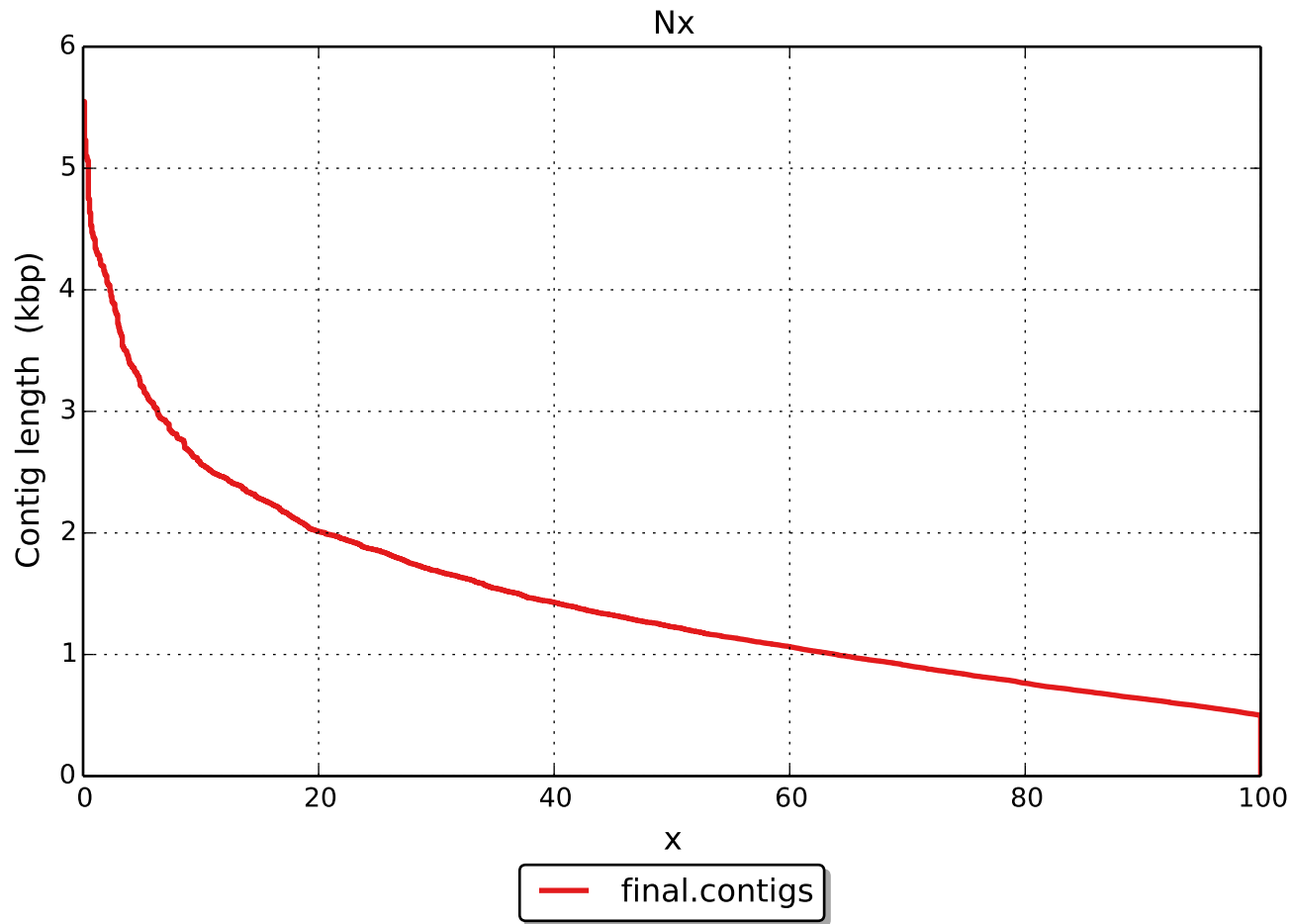
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

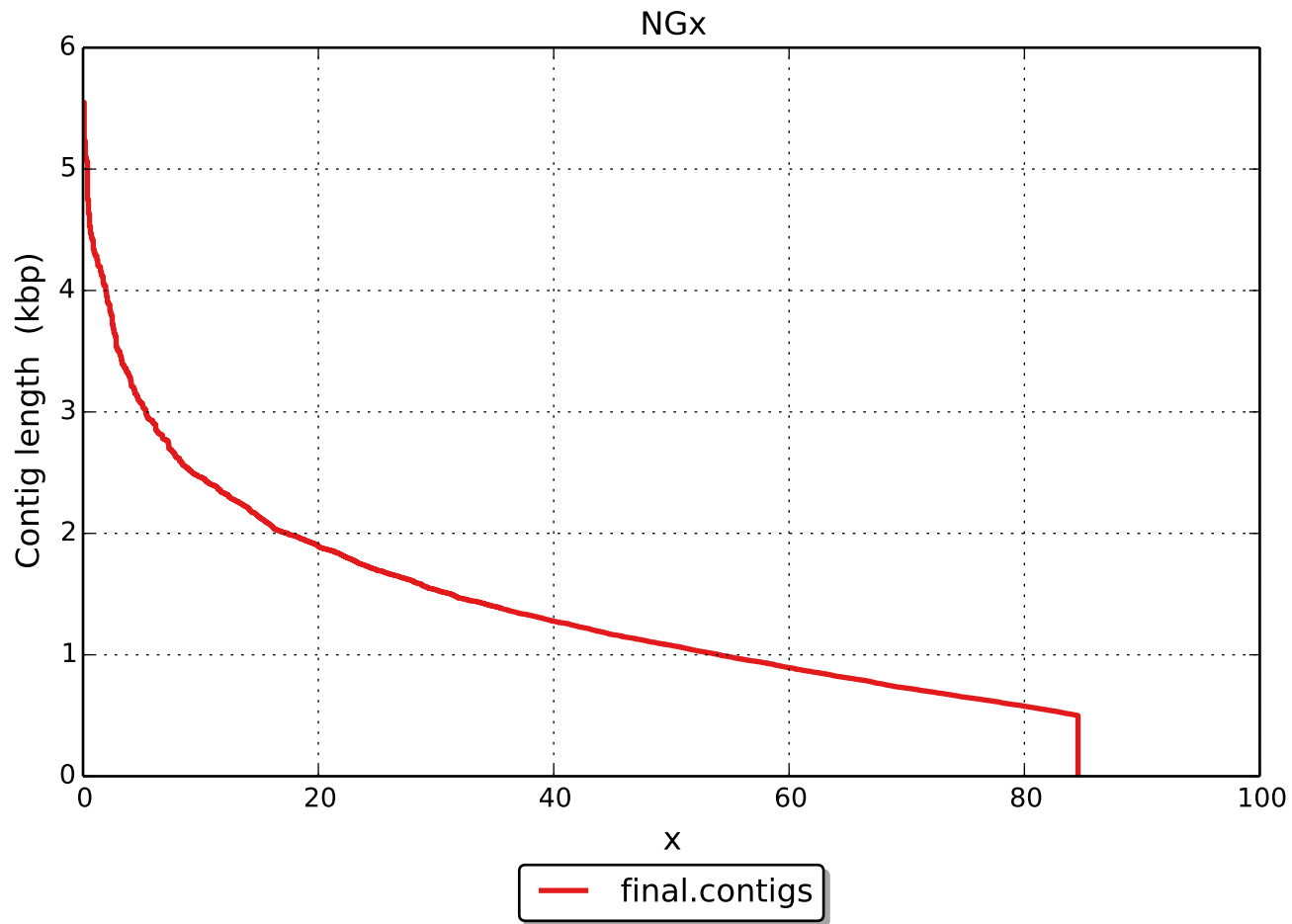
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



GC content



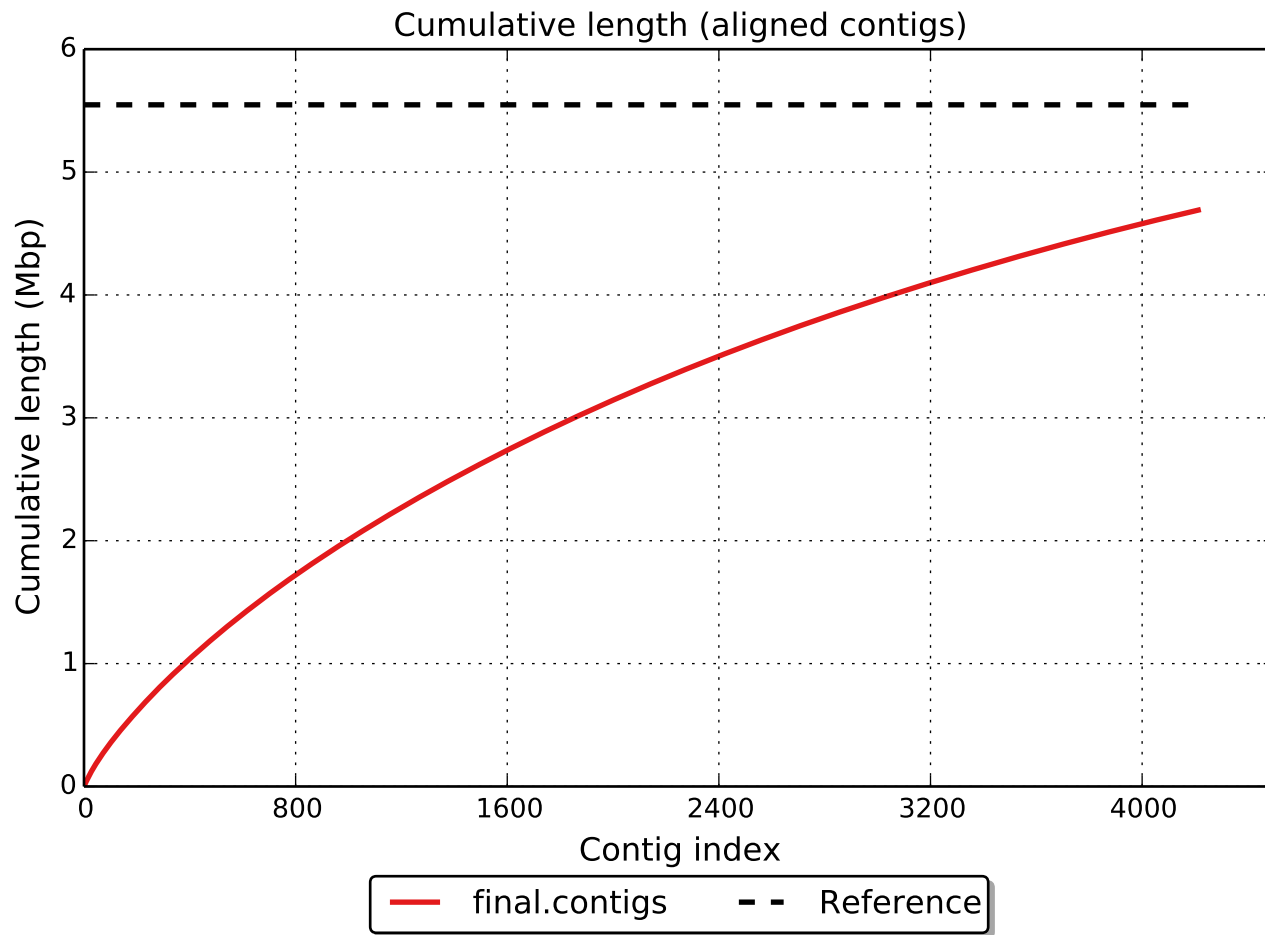


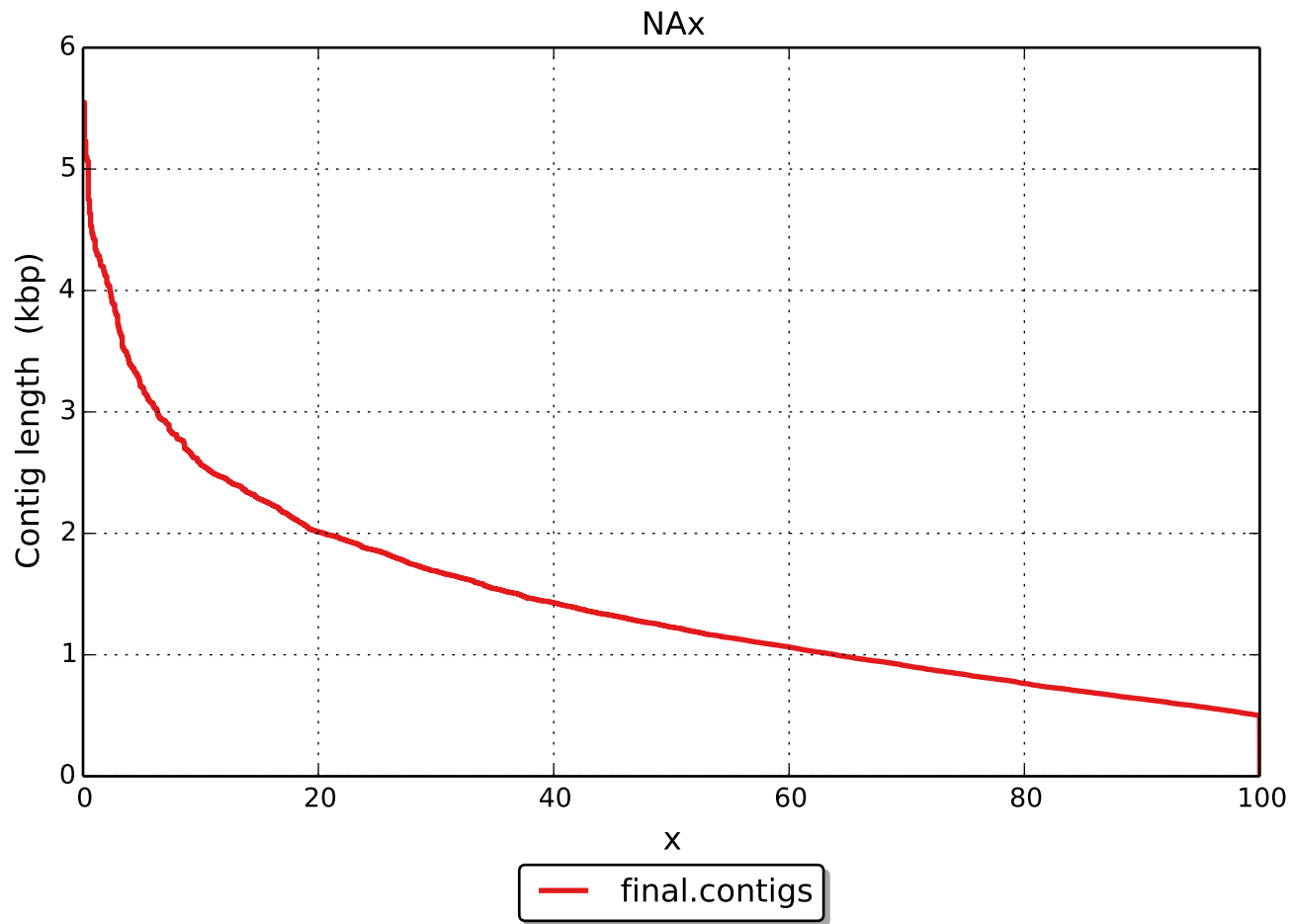


# Misassemblies









NGAx

