

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	2828
# contigs ( $\geq 1000$ bp)	954
Total length ( $\geq 0$ bp)	3152553
Total length ( $\geq 1000$ bp)	1870968
# contigs	2828
Largest contig	7400
Total length	3152553
Reference length	5478683
GC (%)	50.30
Reference GC (%)	50.49
N50	1272
NG50	618
N75	746
L50	692
LG50	2087
L75	1533
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 2 part
Unaligned length	336
Genome fraction (%)	55.364
Duplication ratio	1.039
# N's per 100 kbp	0.00
# mismatches per 100 kbp	314.65
# indels per 100 kbp	0.00
Largest alignment	7400
NA50	1272
NGA50	618
NA75	746
LA50	692
LGA50	2087
LA75	1533

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

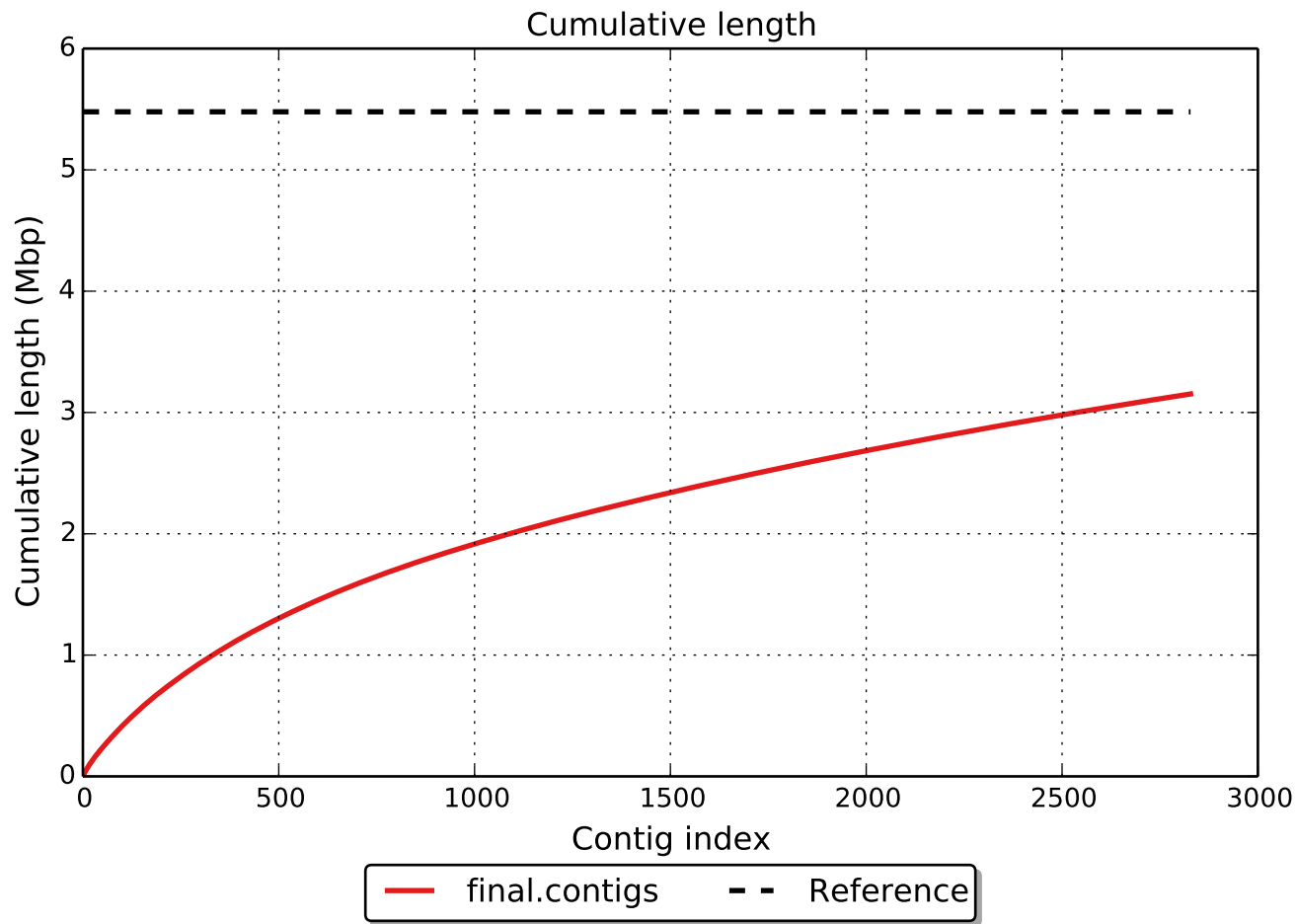
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	9544
# indels	0
# short indels	0
# long indels	0
Indels length	0

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).

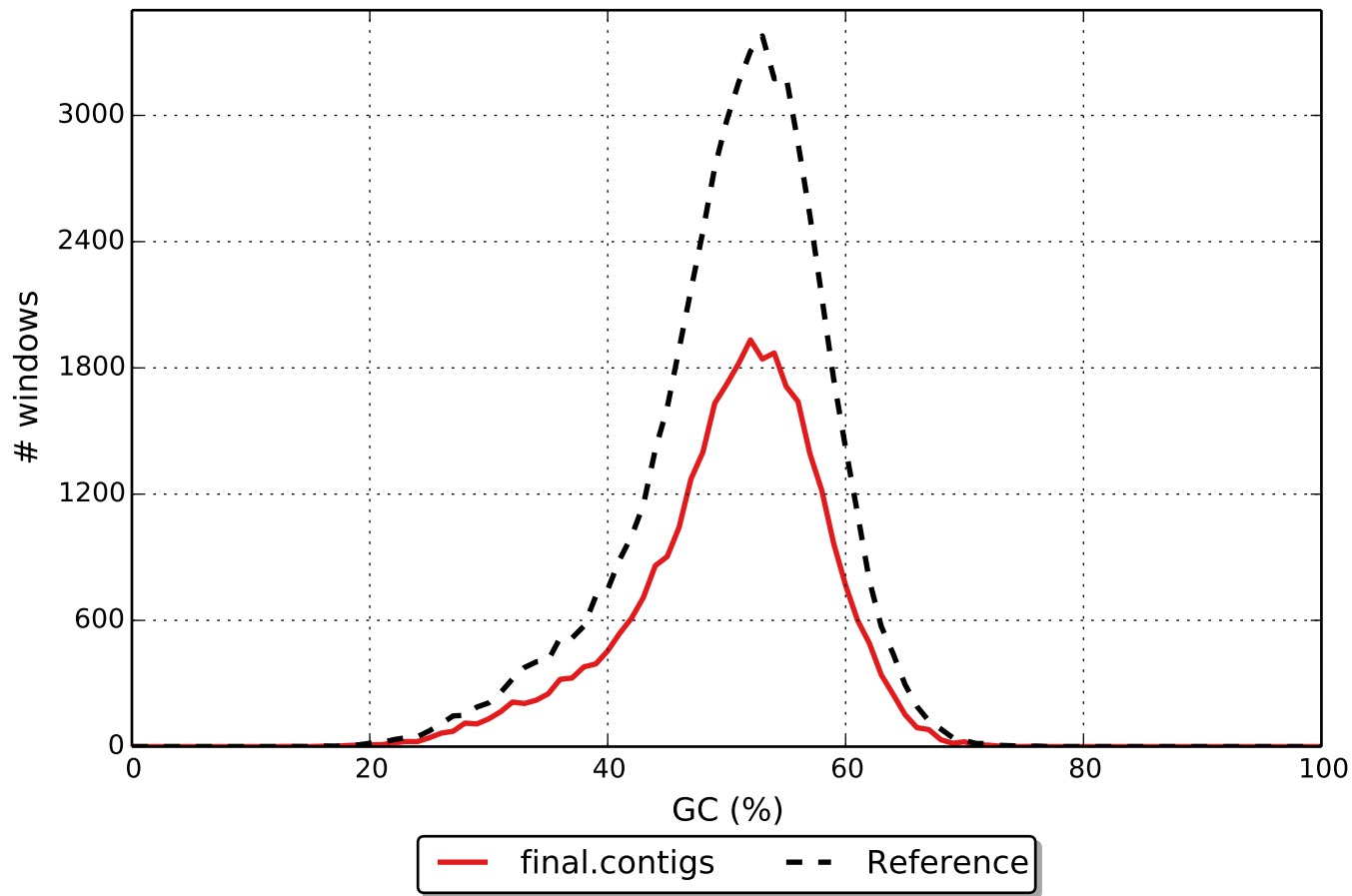
## Unaligned report

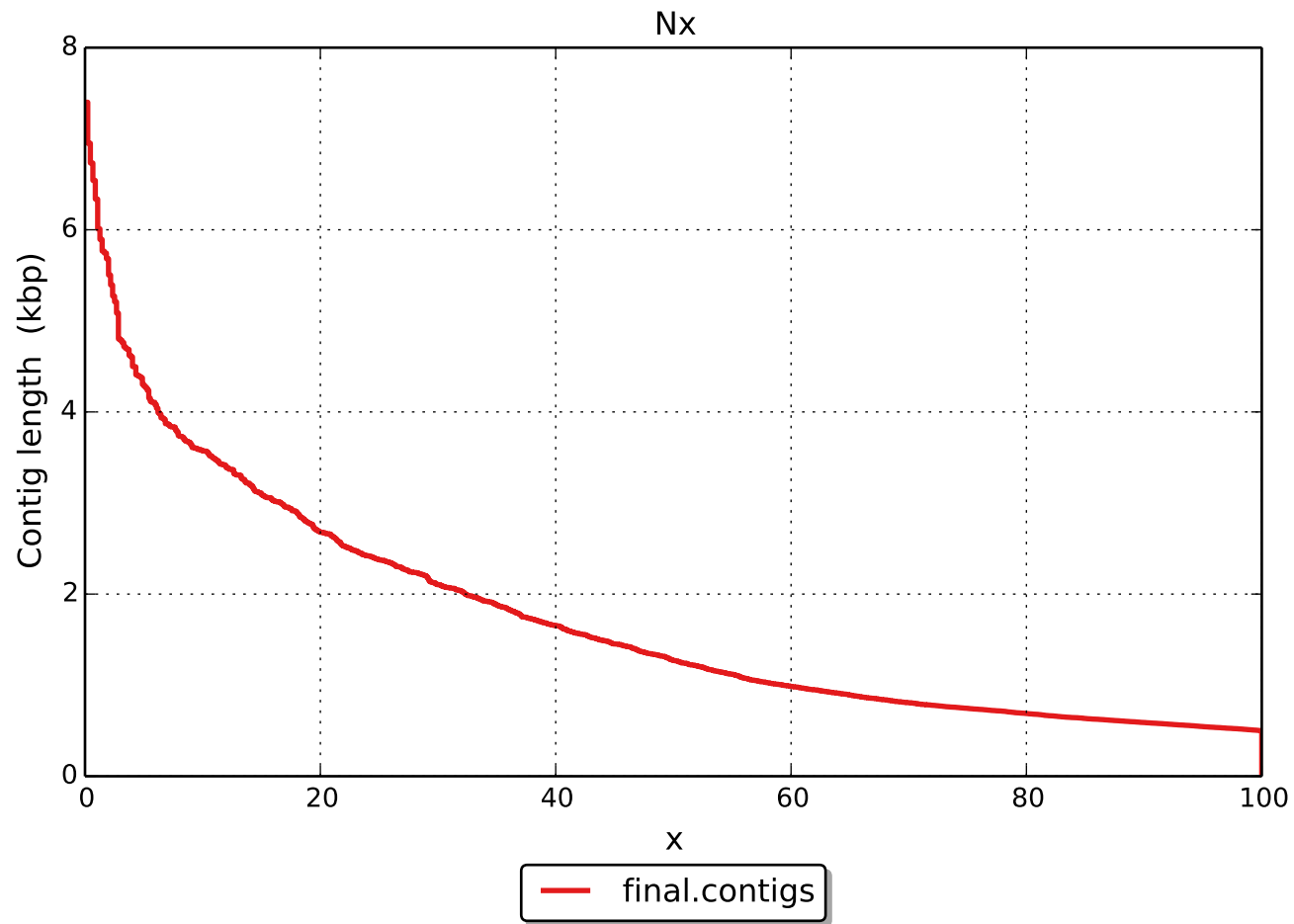
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	0
Partially unaligned length	336
# N's	0

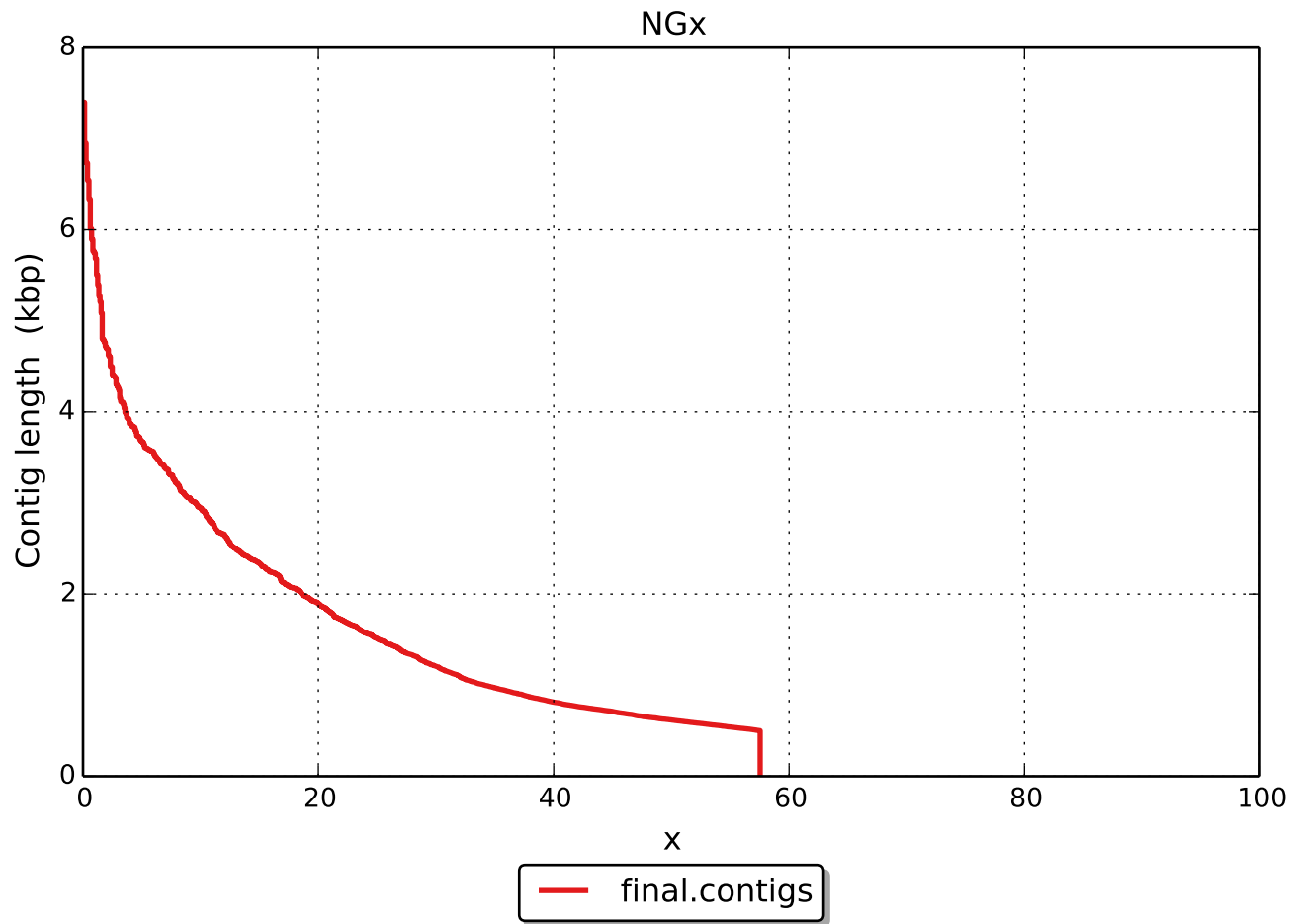
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



GC content



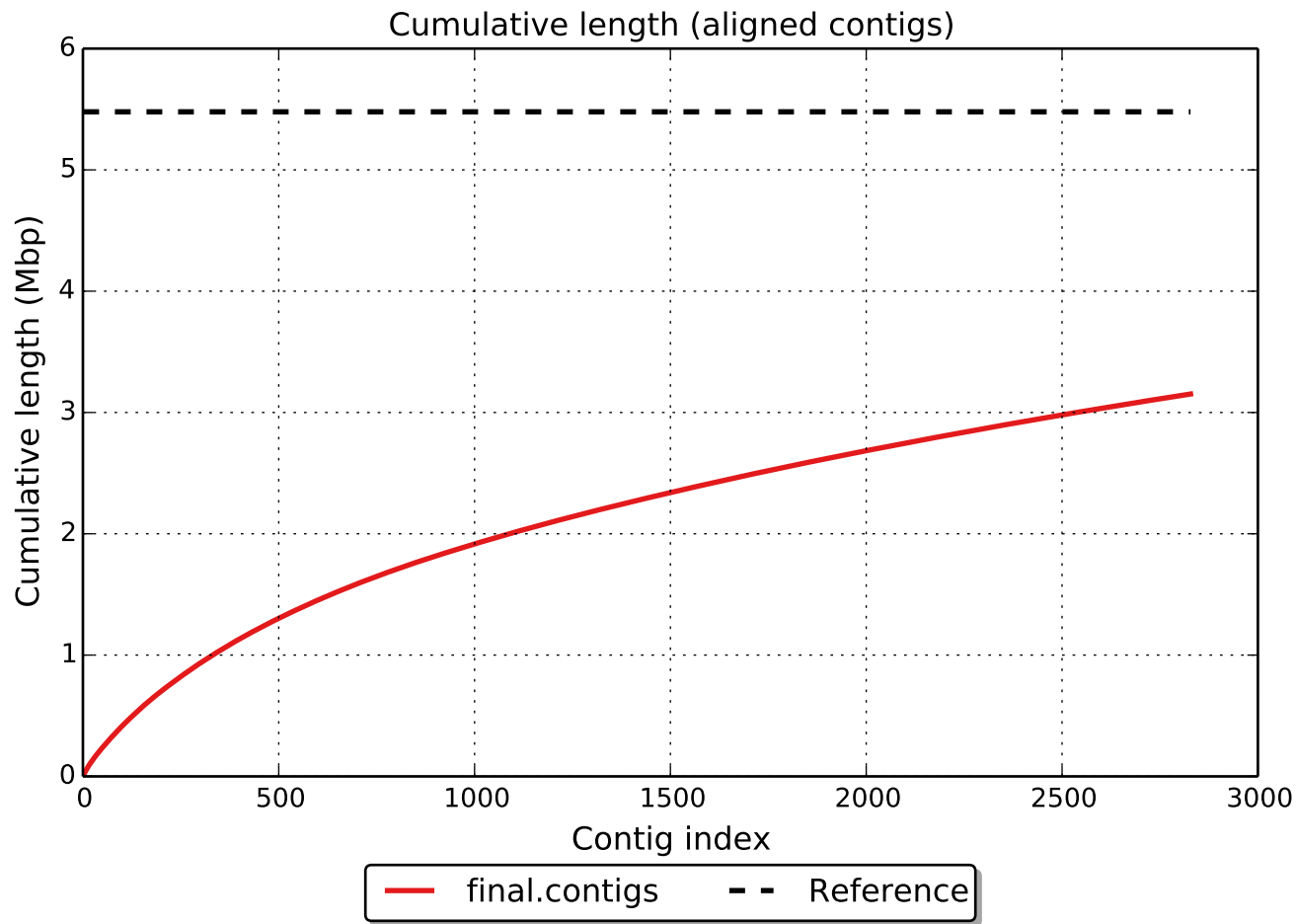


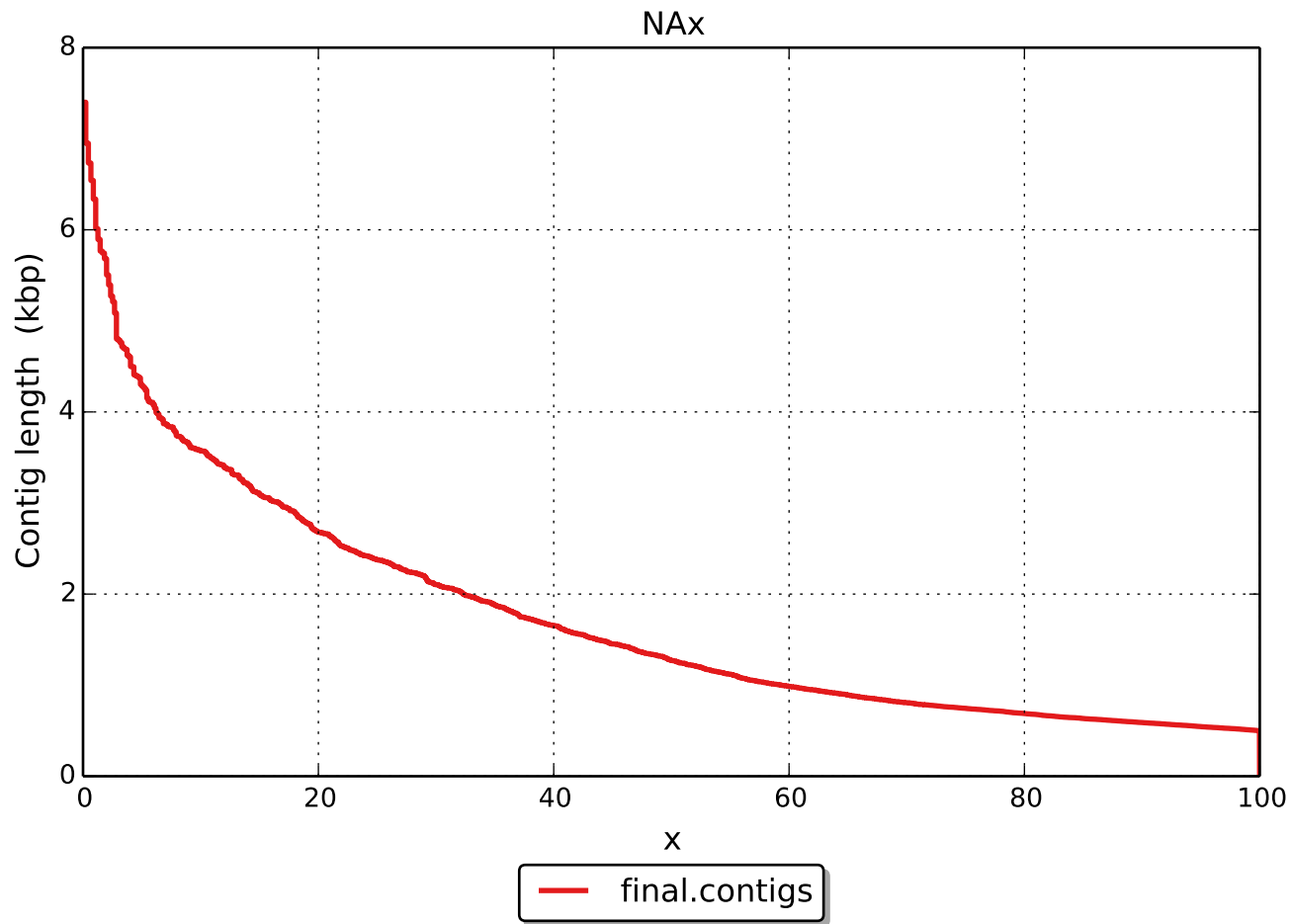


# Misassemblies









NGAx

