

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	376
# contigs ( $\geq 1000$ bp)	277
Total length ( $\geq 0$ bp)	3732082
Total length ( $\geq 1000$ bp)	3692267
# contigs	300
Largest contig	75385
Total length	3709797
Reference length	3785550
GC (%)	32.26
Reference GC (%)	32.26
N50	19328
NG50	18744
N75	12313
NG75	11908
L50	60
LG50	62
L75	120
LG75	125
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	97.513
Duplication ratio	1.005
# N's per 100 kbp	0.00
# mismatches per 100 kbp	15.60
# indels per 100 kbp	0.11
Largest alignment	75385
NA50	19328
NGA50	18744
NA75	12313
NGA75	11908
LA50	60
LGA50	62
LA75	120
LGA75	125

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

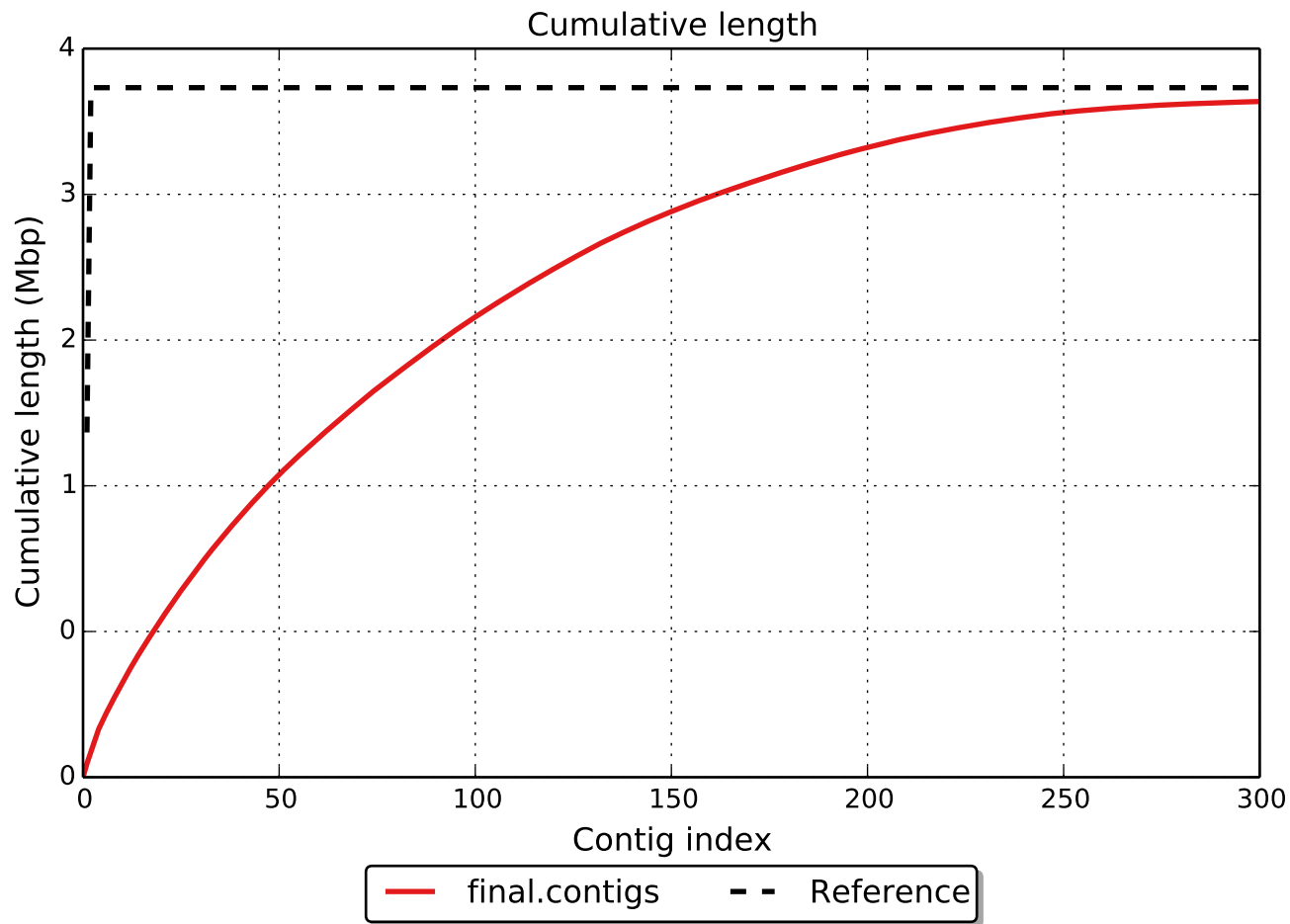
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	576
# indels	4
# short indels	4
# long indels	0
Indels length	4

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).

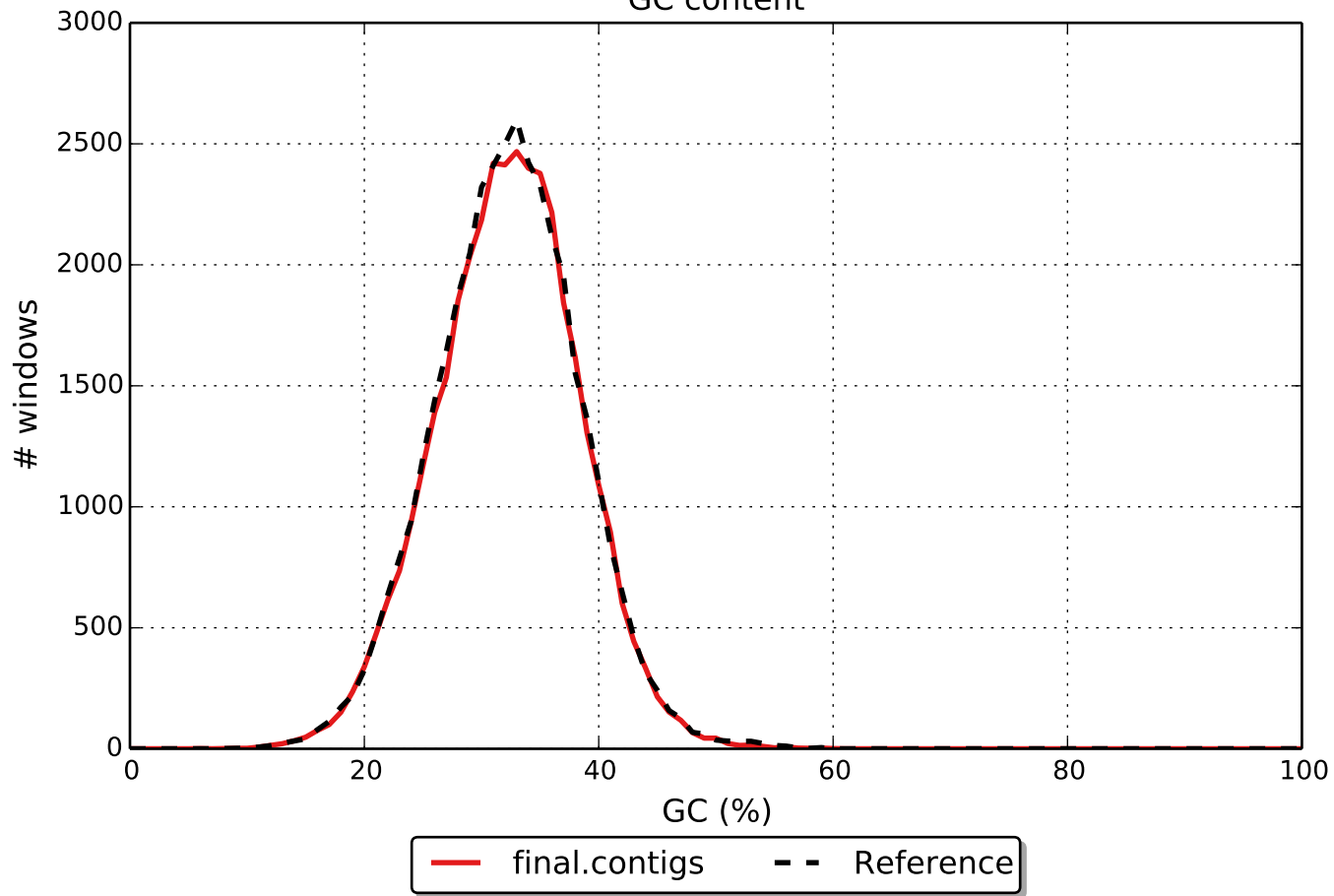
## Unaligned report

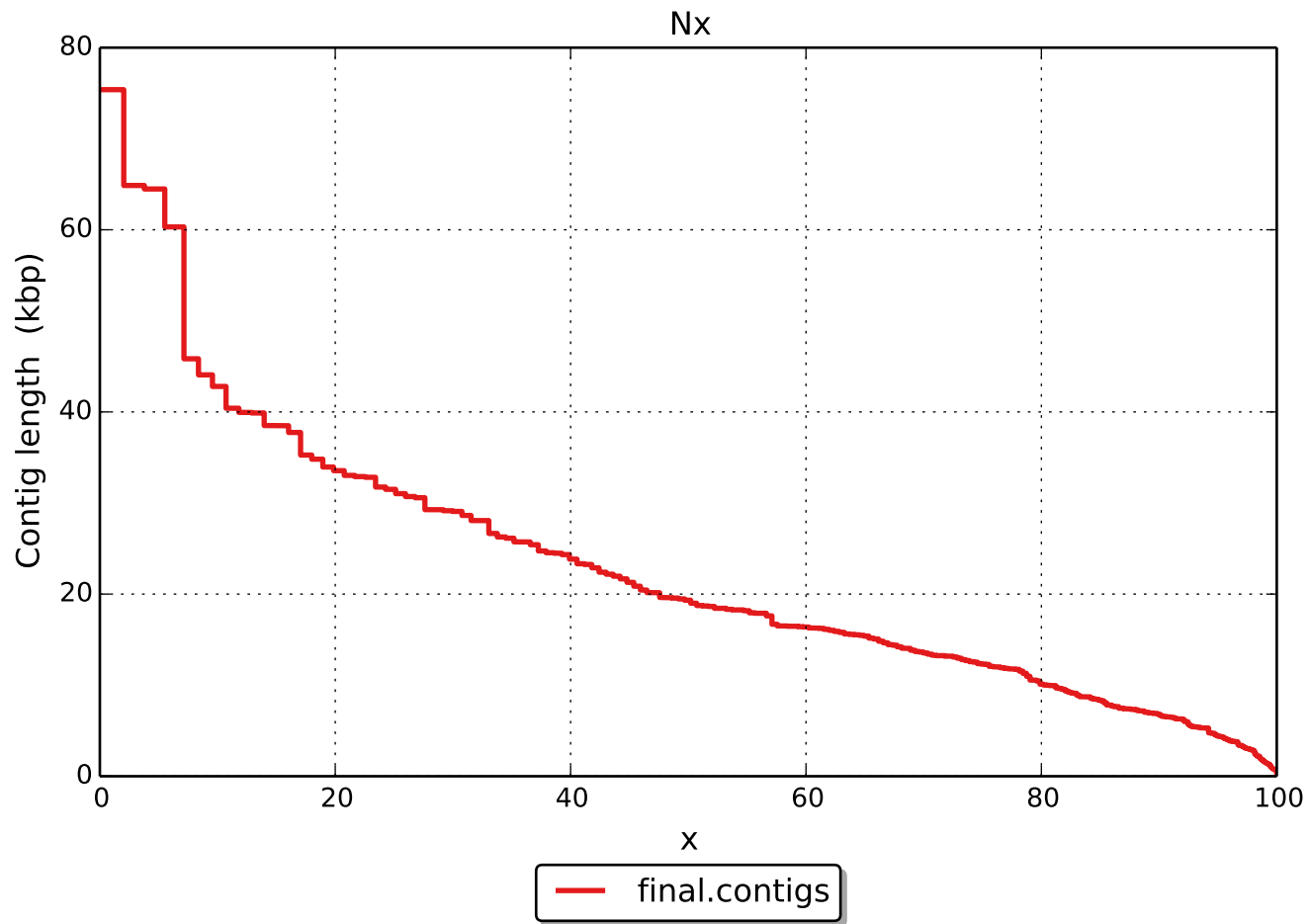
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

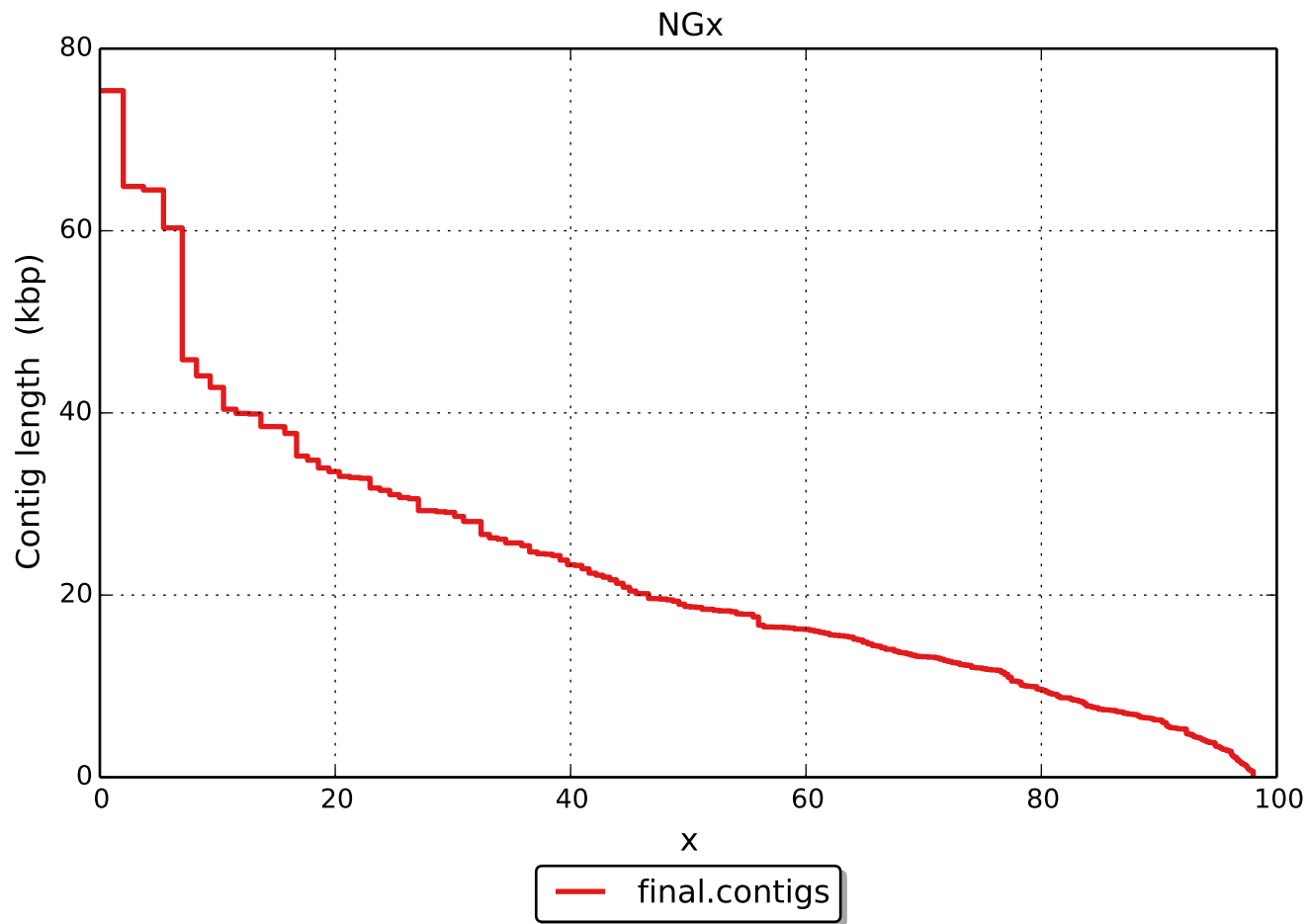
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



GC content



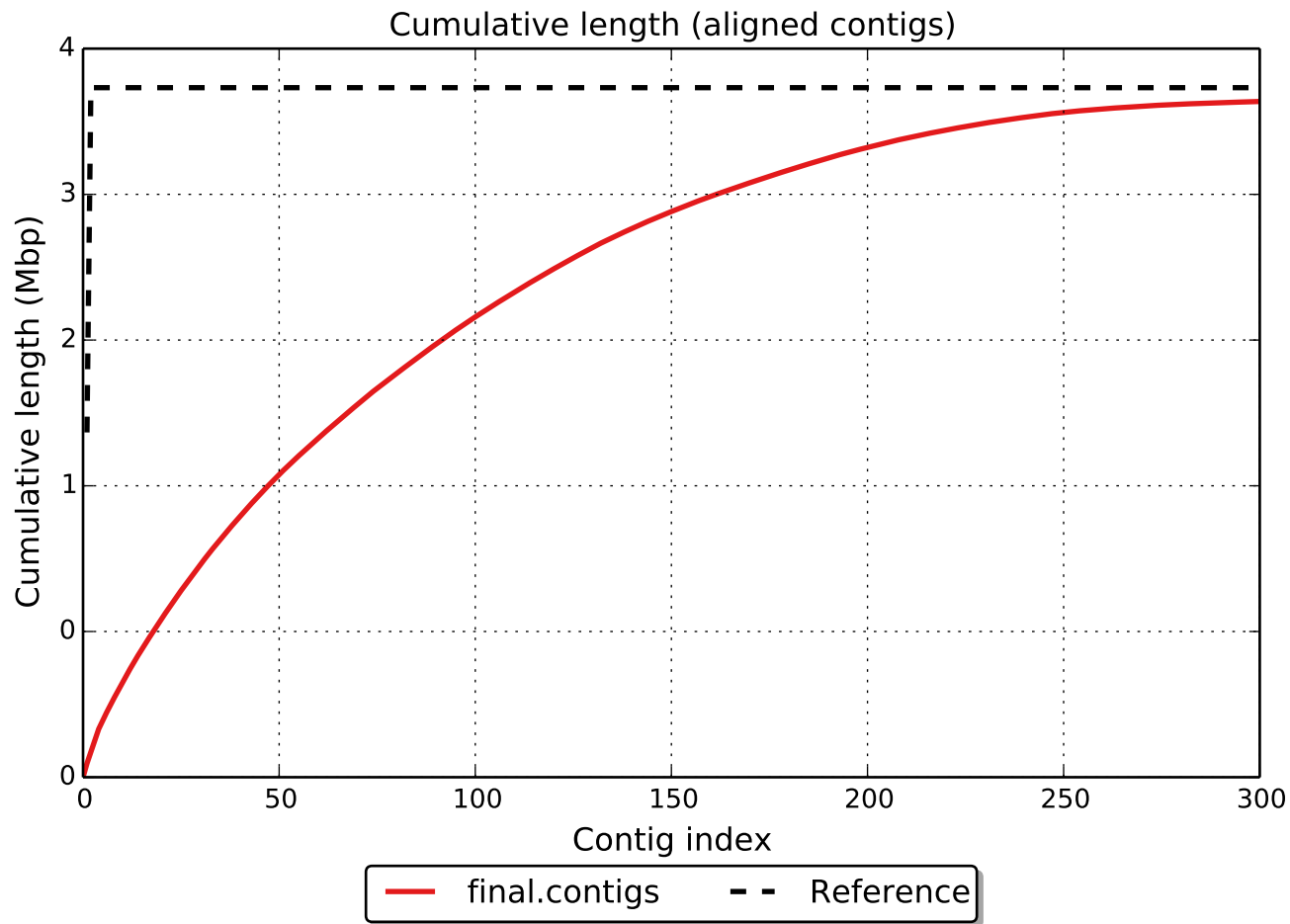


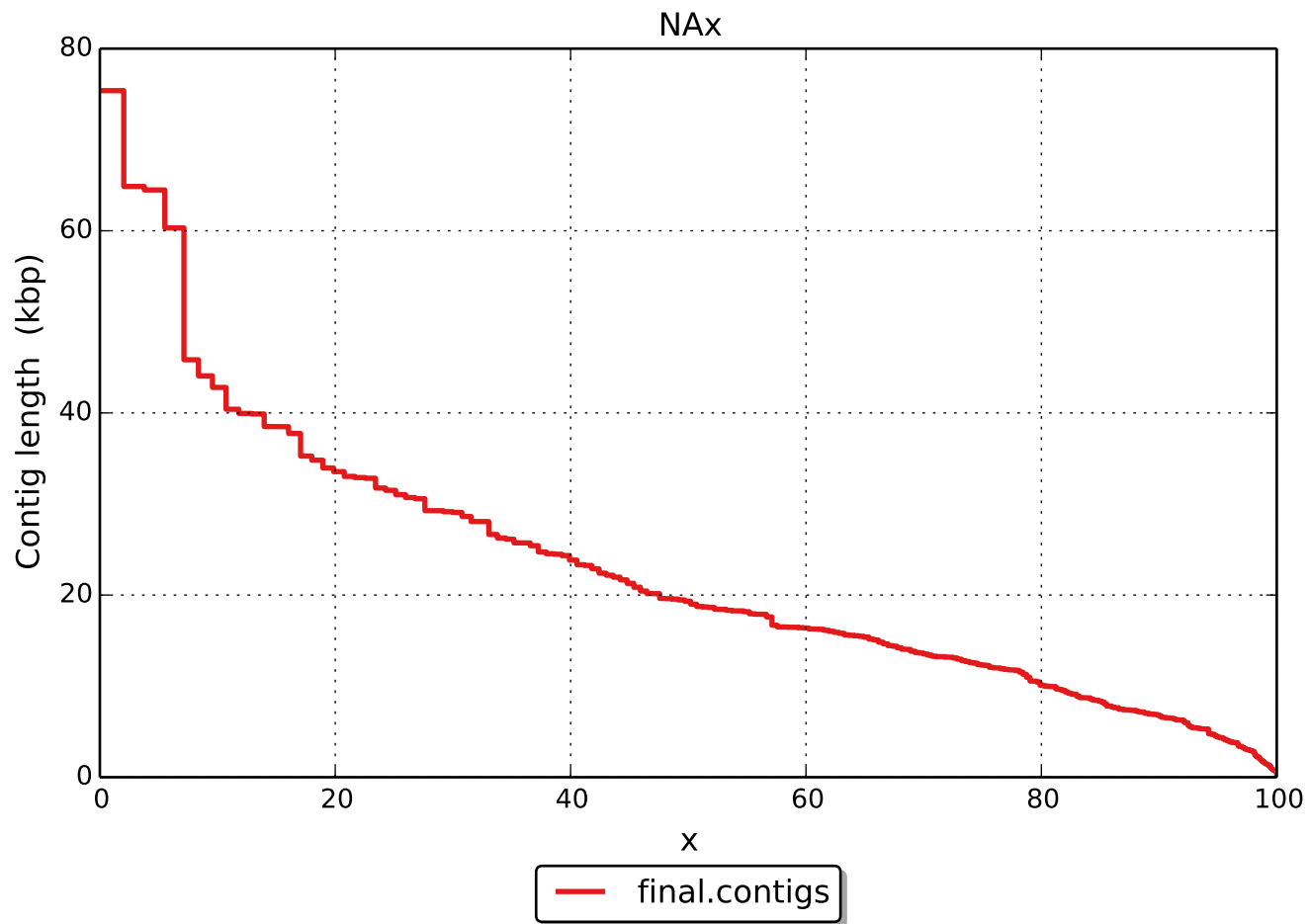


# Misassemblies









# NGAx

