

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	11043
# contigs ( $\geq 1000$ bp)	1822
Total length ( $\geq 0$ bp)	8080274
Total length ( $\geq 1000$ bp)	3618008
# contigs	5605
Largest contig	10039
Total length	6195528
Reference length	11094646
GC (%)	50.33
Reference GC (%)	50.48
N50	1217
NG50	588
N75	736
L50	1347
LG50	4408
L75	3035
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 1 part
Unaligned length	25
Genome fraction (%)	81.559
Duplication ratio	1.057
# N's per 100 kbp	0.00
# mismatches per 100 kbp	557.73
# indels per 100 kbp	0.15
Largest alignment	10039
NA50	1217
NGA50	588
NA75	736
LA50	1347
LGA50	4408
LA75	3035

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

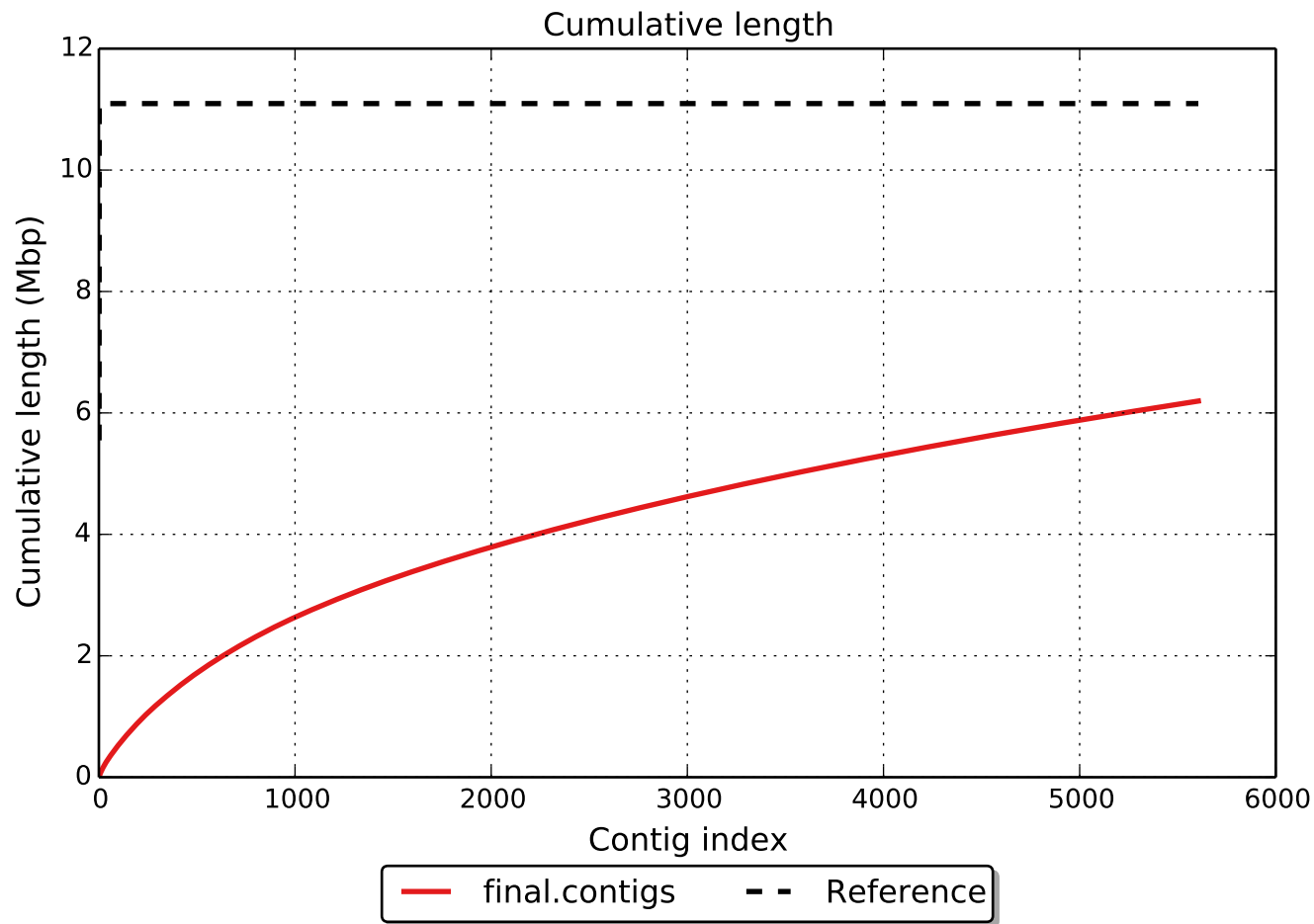
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	50467
# indels	14
# short indels	13
# long indels	1
Indels length	22

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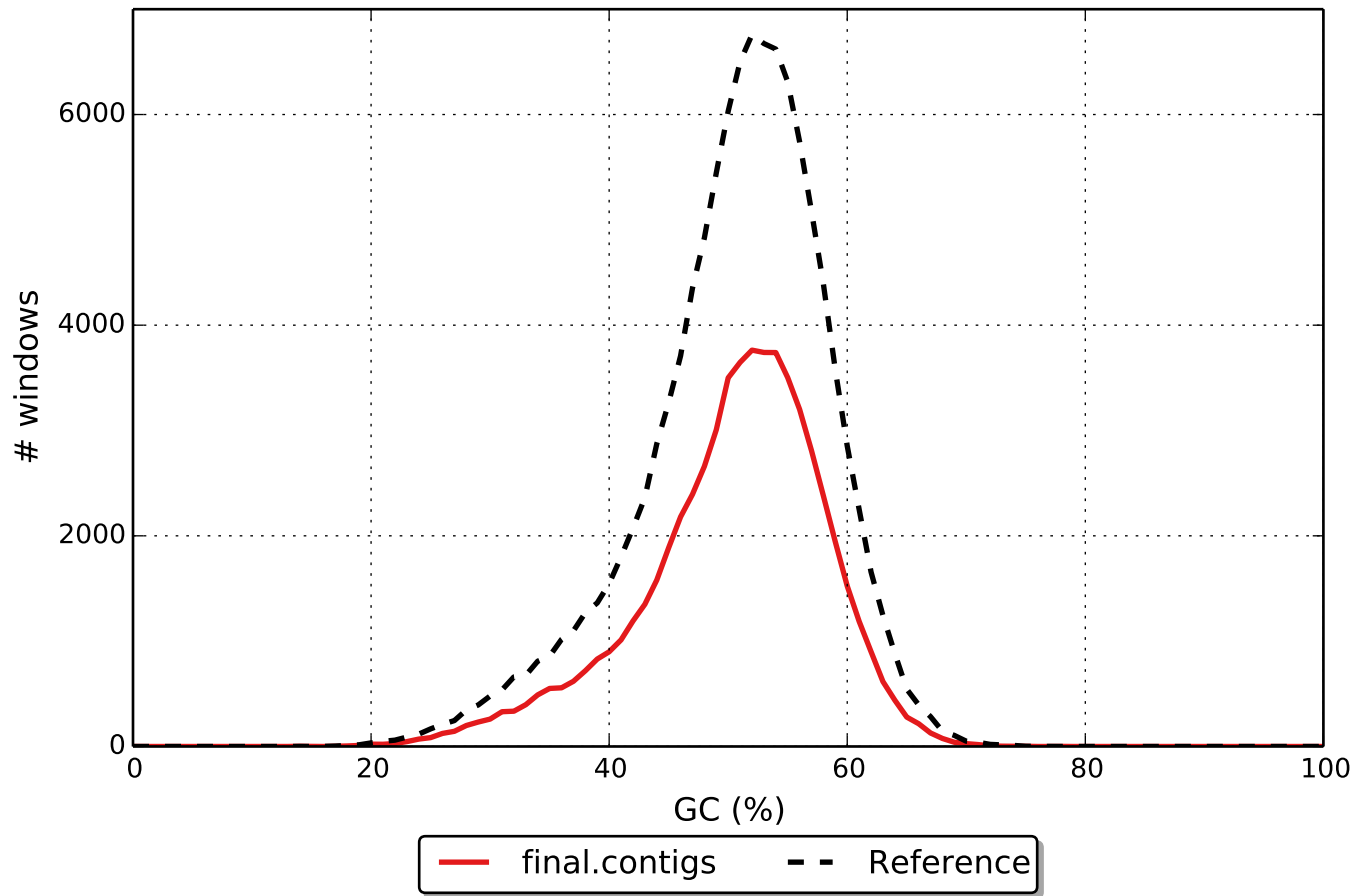
## Unaligned report

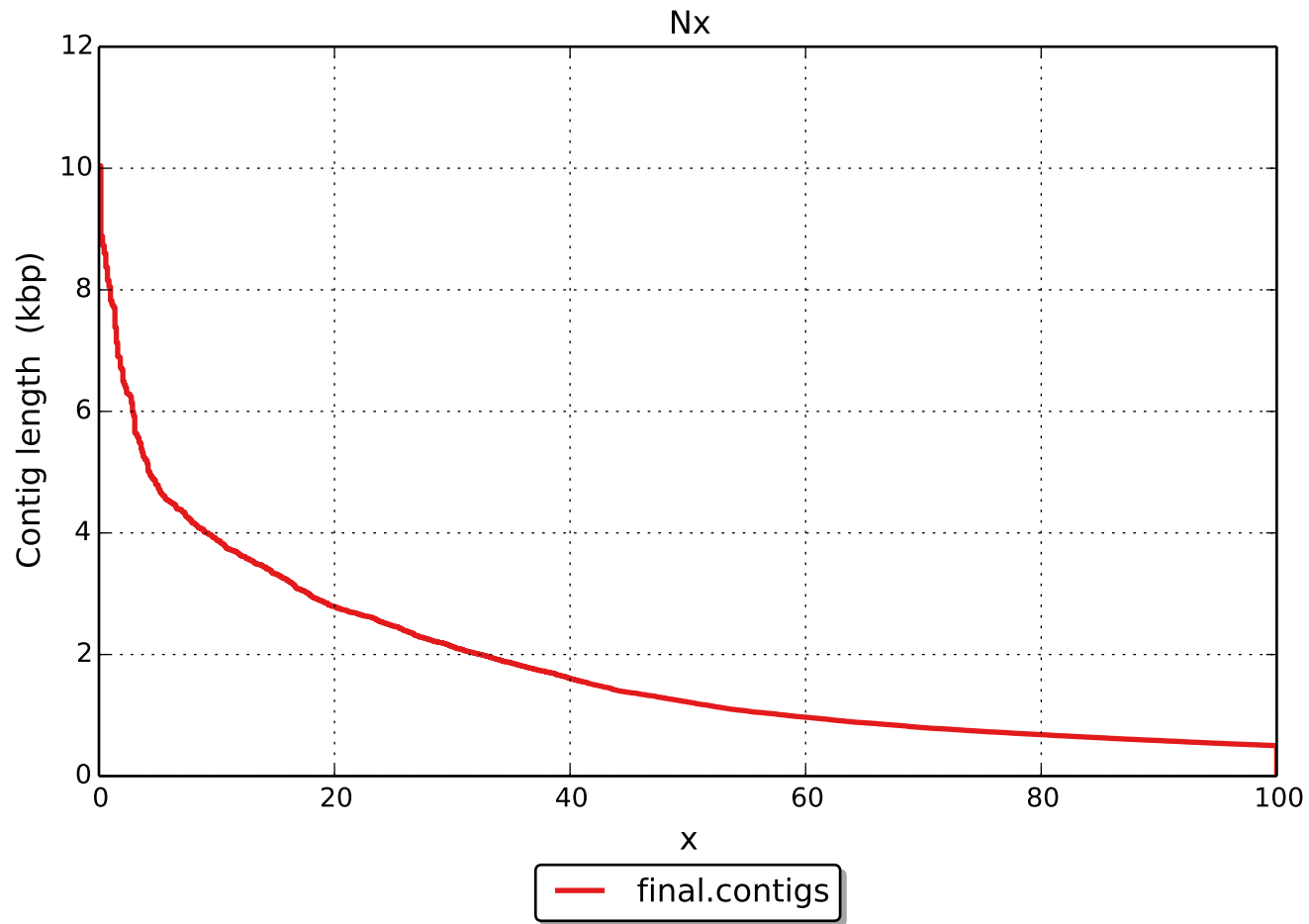
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	25
# N's	0

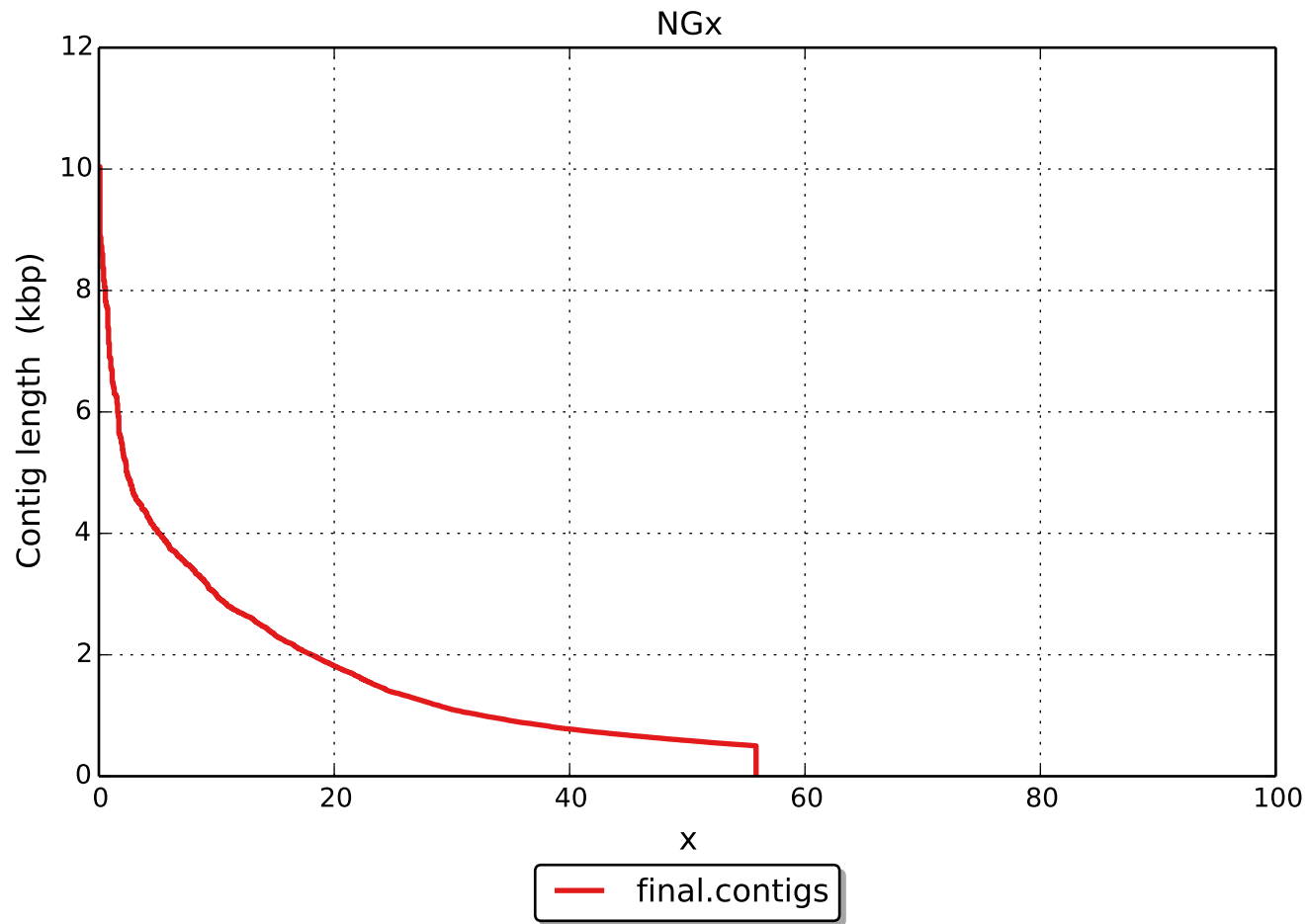
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



GC content



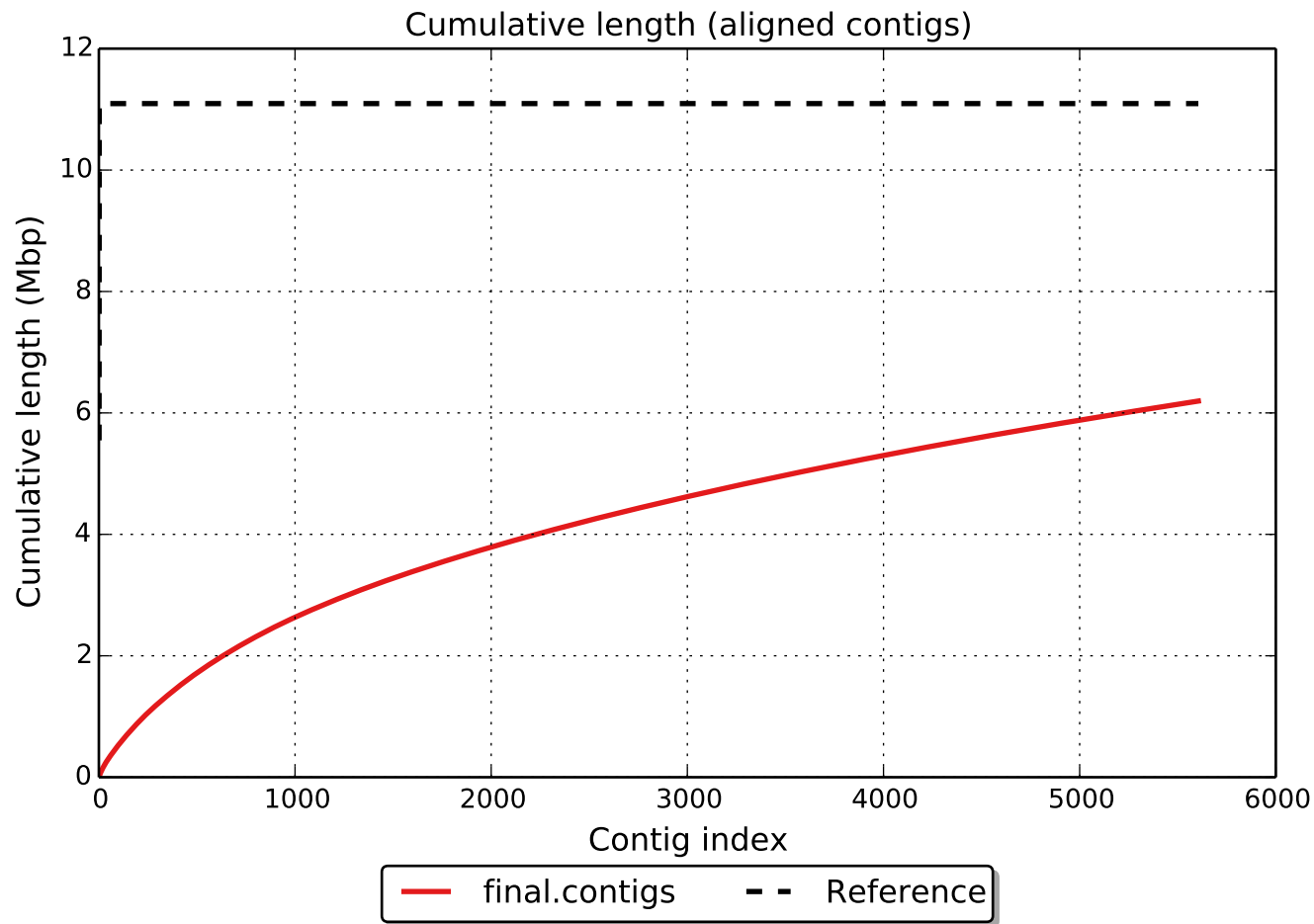


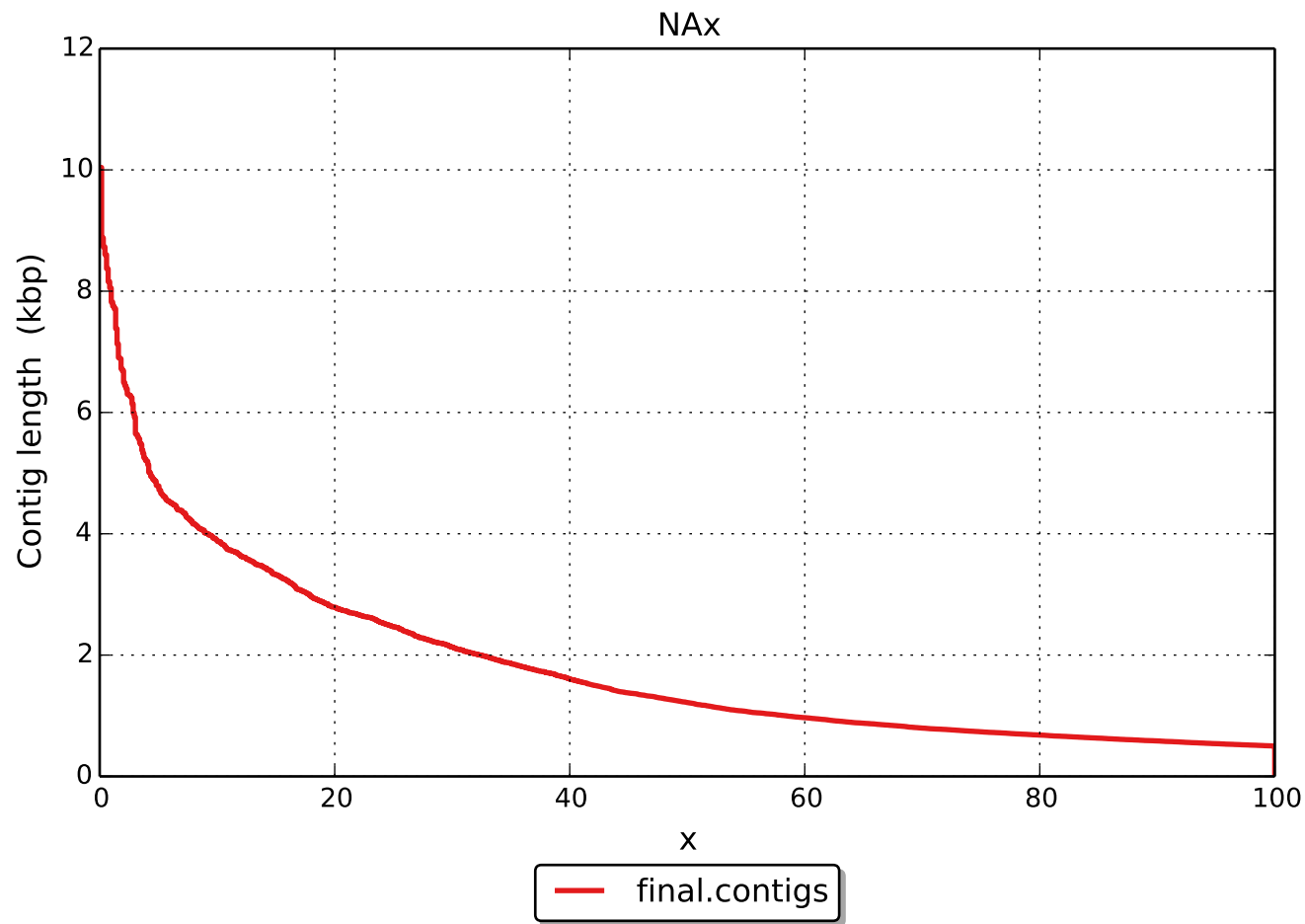


# Misassemblies









NGAx

