

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	108
# contigs ( $\geq 1000$ bp)	108
Total length ( $\geq 0$ bp)	1315019
Total length ( $\geq 1000$ bp)	1315019
# contigs	108
Largest contig	53647
Total length	1315019
Reference length	641799
GC (%)	26.27
Reference GC (%)	26.30
N50	19444
NG50	29739
N75	11480
NG75	24186
L50	23
LG50	9
L75	46
LG75	15
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	49 + 5 part
Unaligned length	622807
Genome fraction (%)	99.874
Duplication ratio	1.080
# N's per 100 kbp	0.00
# mismatches per 100 kbp	206.56
# indels per 100 kbp	0.94
Largest alignment	53647
NA50	2224
NGA50	18788
NGA75	12418
LA50	51
LGA50	11
LGA75	21

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	2
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	1324
# indels	6
# short indels	6
# long indels	0
Indels length	6

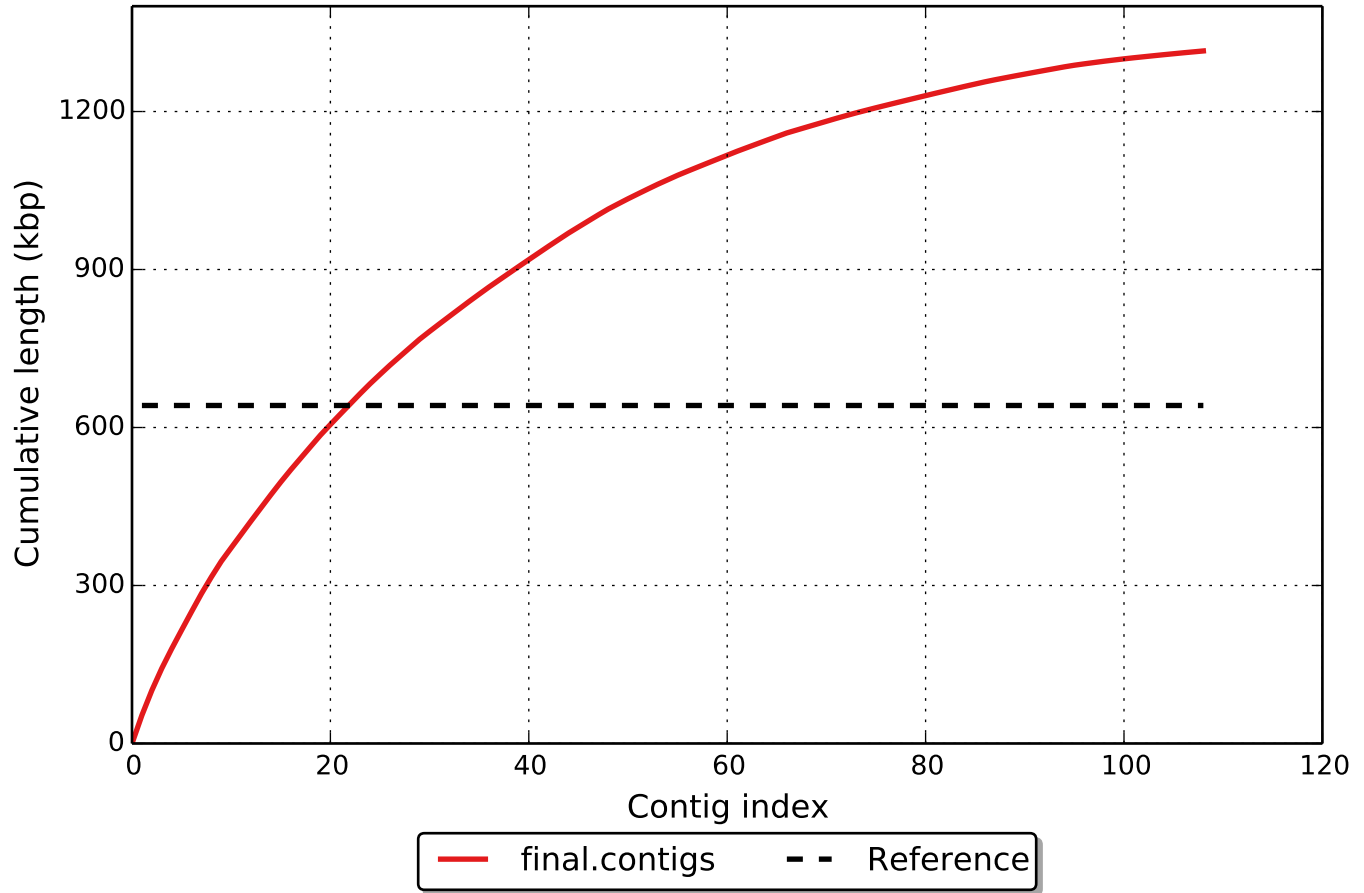
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

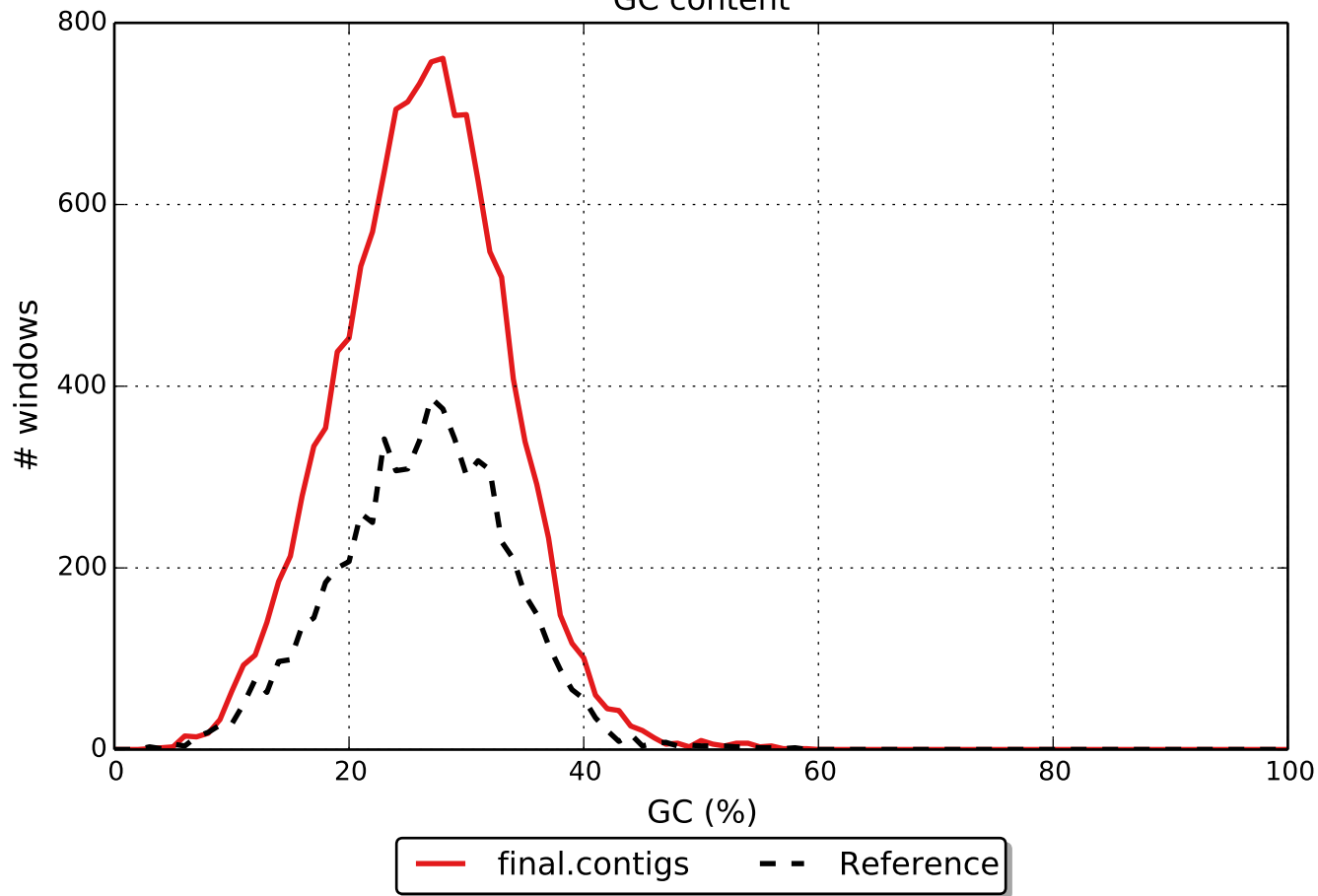
	final.contigs
# fully unaligned contigs	49
Fully unaligned length	582502
# partially unaligned contigs	5
# with misassembly	0
# both parts are significant	2
Partially unaligned length	40305
# N's	0

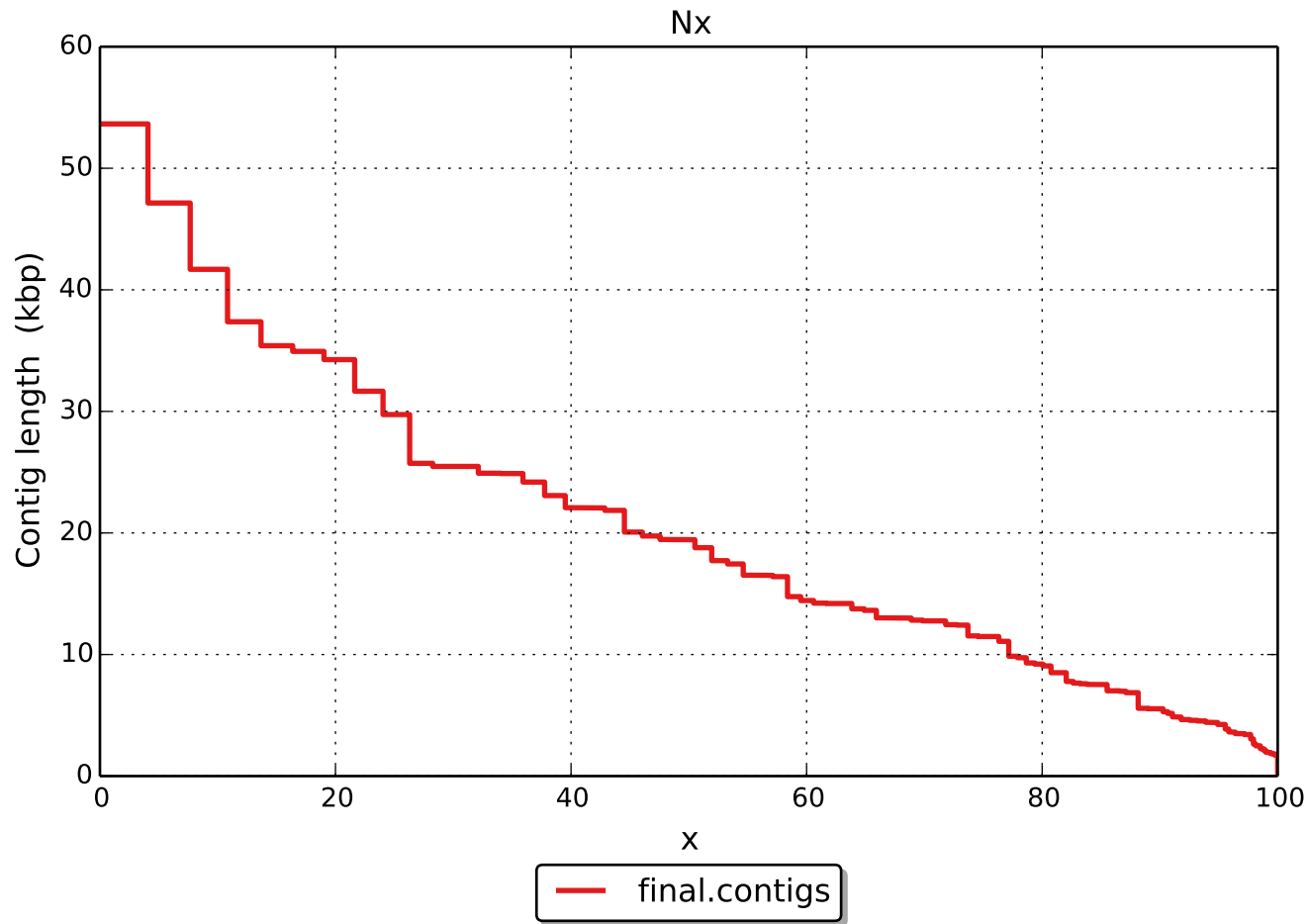
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

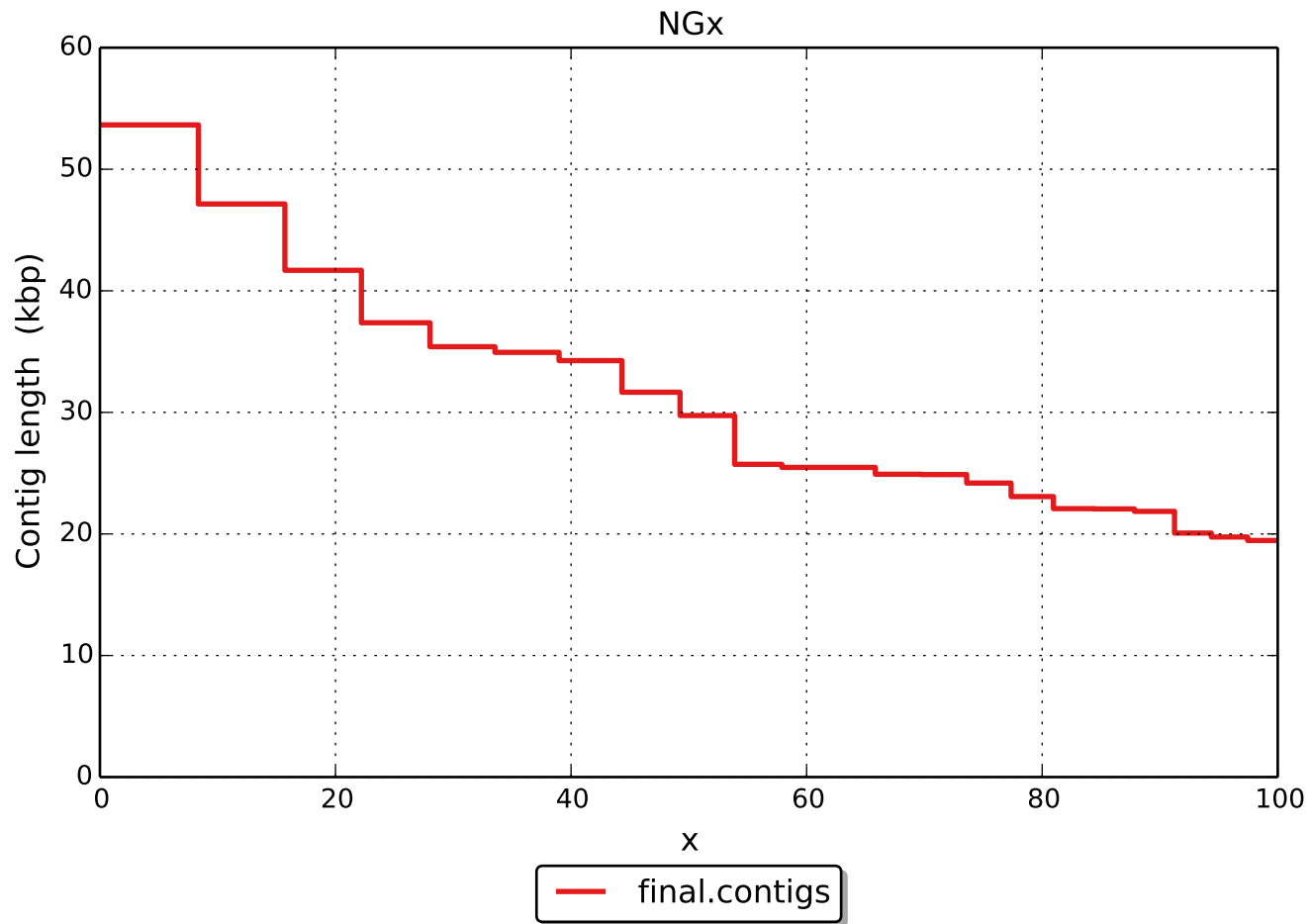
Cumulative length



GC content





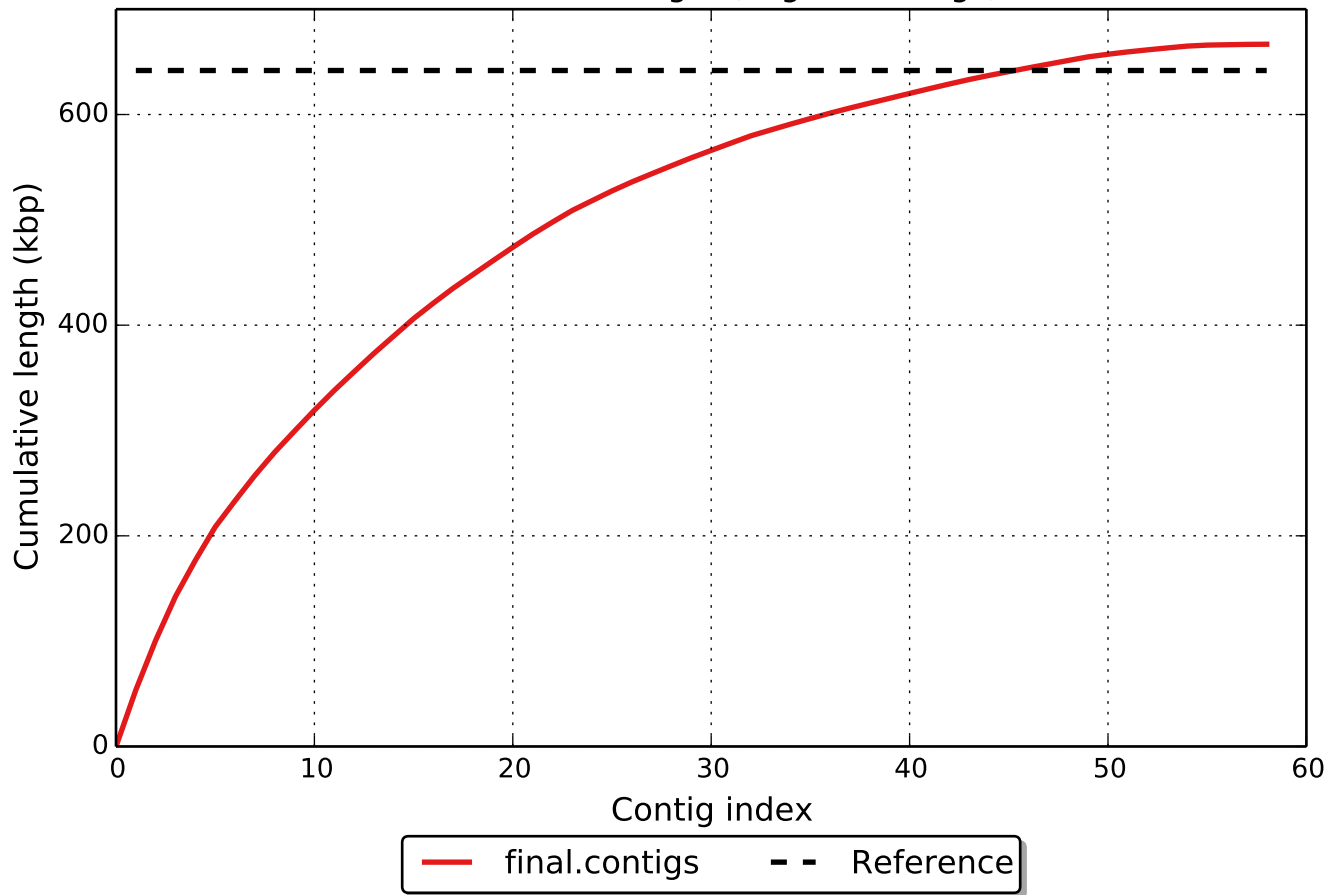


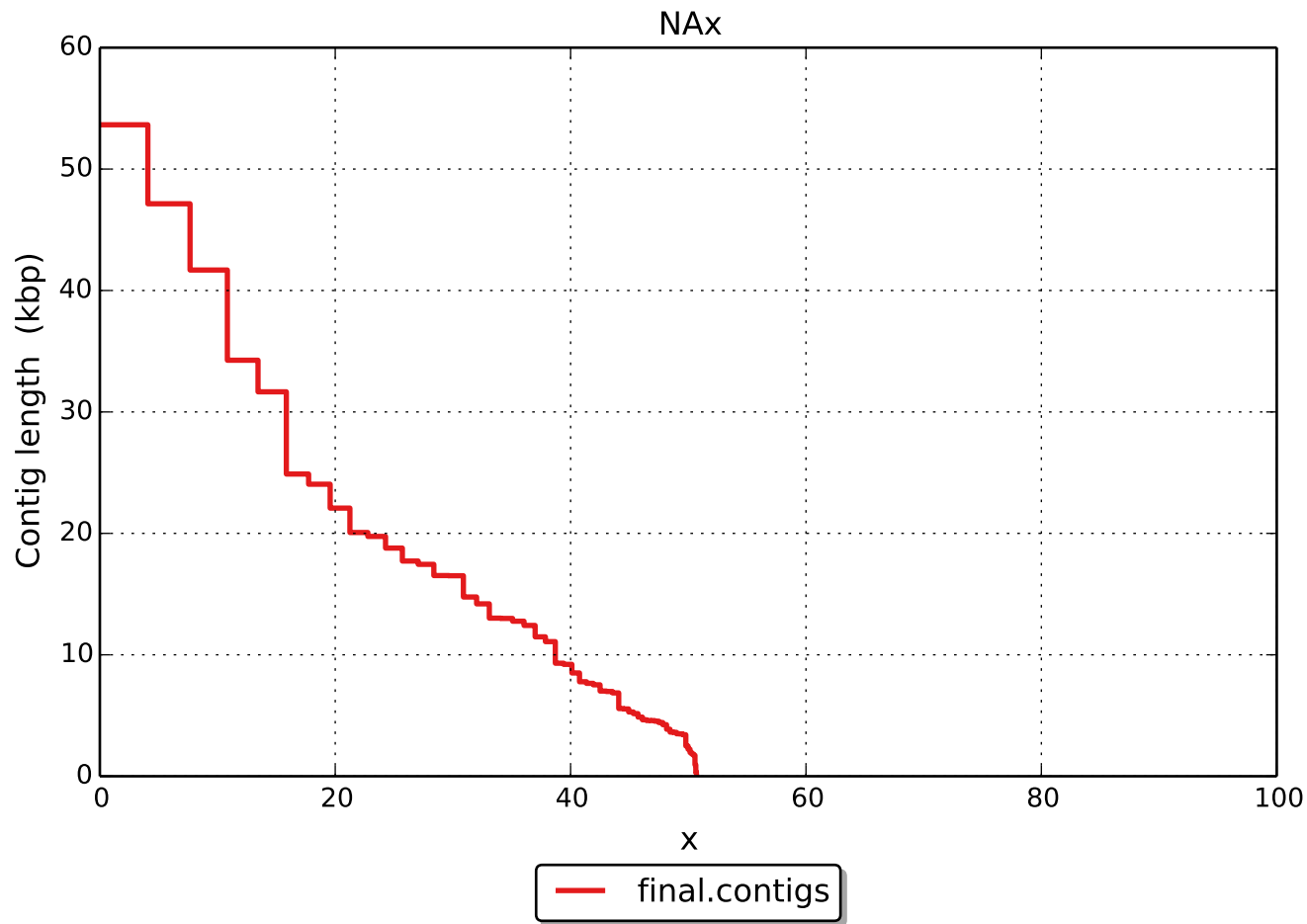
# Misassemblies



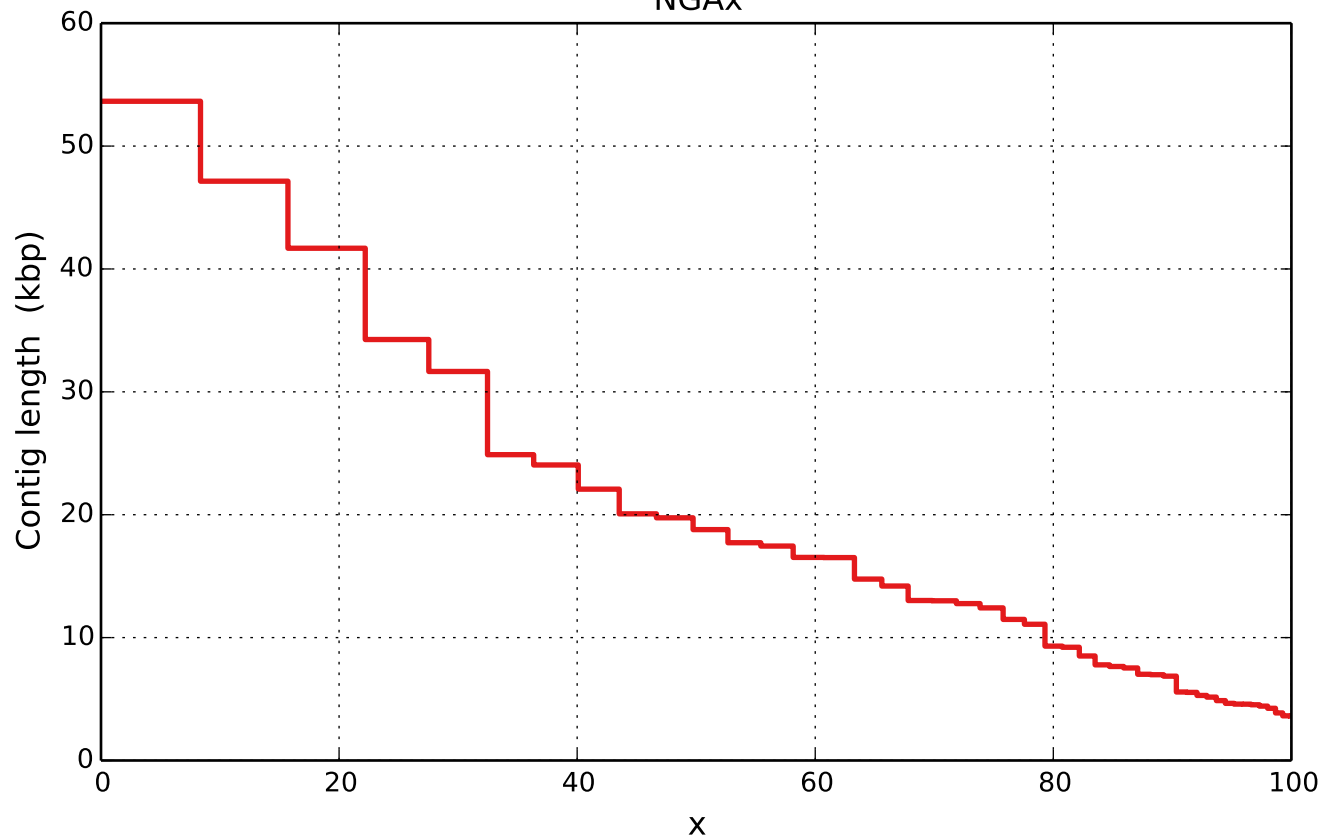


Cumulative length (aligned contigs)





NGAx



— final.contigs