

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	214
# contigs ( $\geq 1000$ bp)	189
Total length ( $\geq 0$ bp)	1265788
Total length ( $\geq 1000$ bp)	1249476
# contigs	214
Largest contig	23250
Total length	1265788
Reference length	641799
GC (%)	26.31
Reference GC (%)	26.30
N50	9177
NG50	12294
N75	5658
NG75	10021
L50	49
LG50	19
L75	94
LG75	34
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.503
Duplication ratio	2.002
# N's per 100 kbp	0.00
# mismatches per 100 kbp	522.31
# indels per 100 kbp	0.63
Largest alignment	23250
NA50	763
NGA50	9177
NGA75	5658
LA50	98
LGA50	25
LGA75	48

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	3302
# indels	4
# short indels	3
# long indels	1
Indels length	84

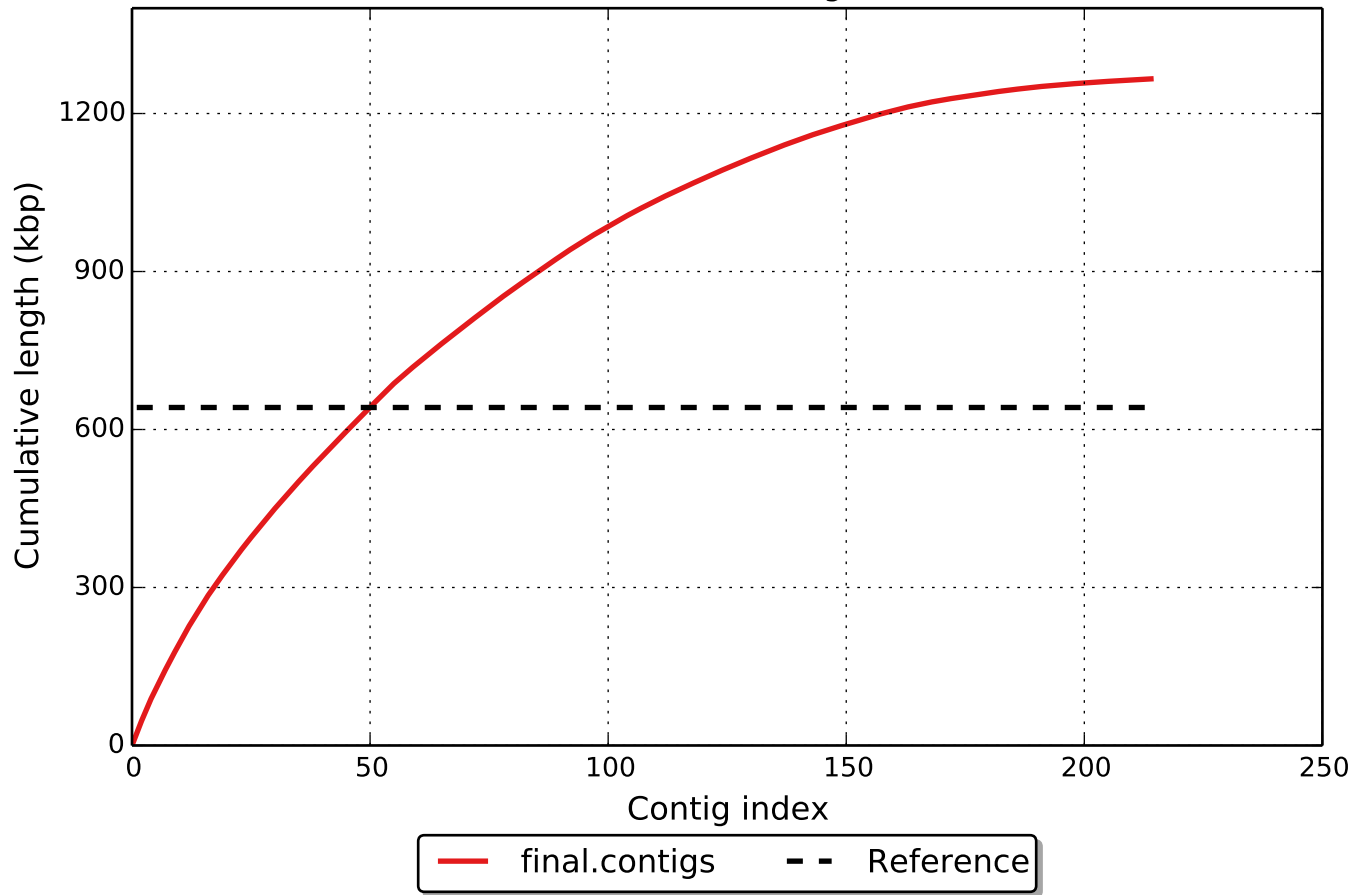
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

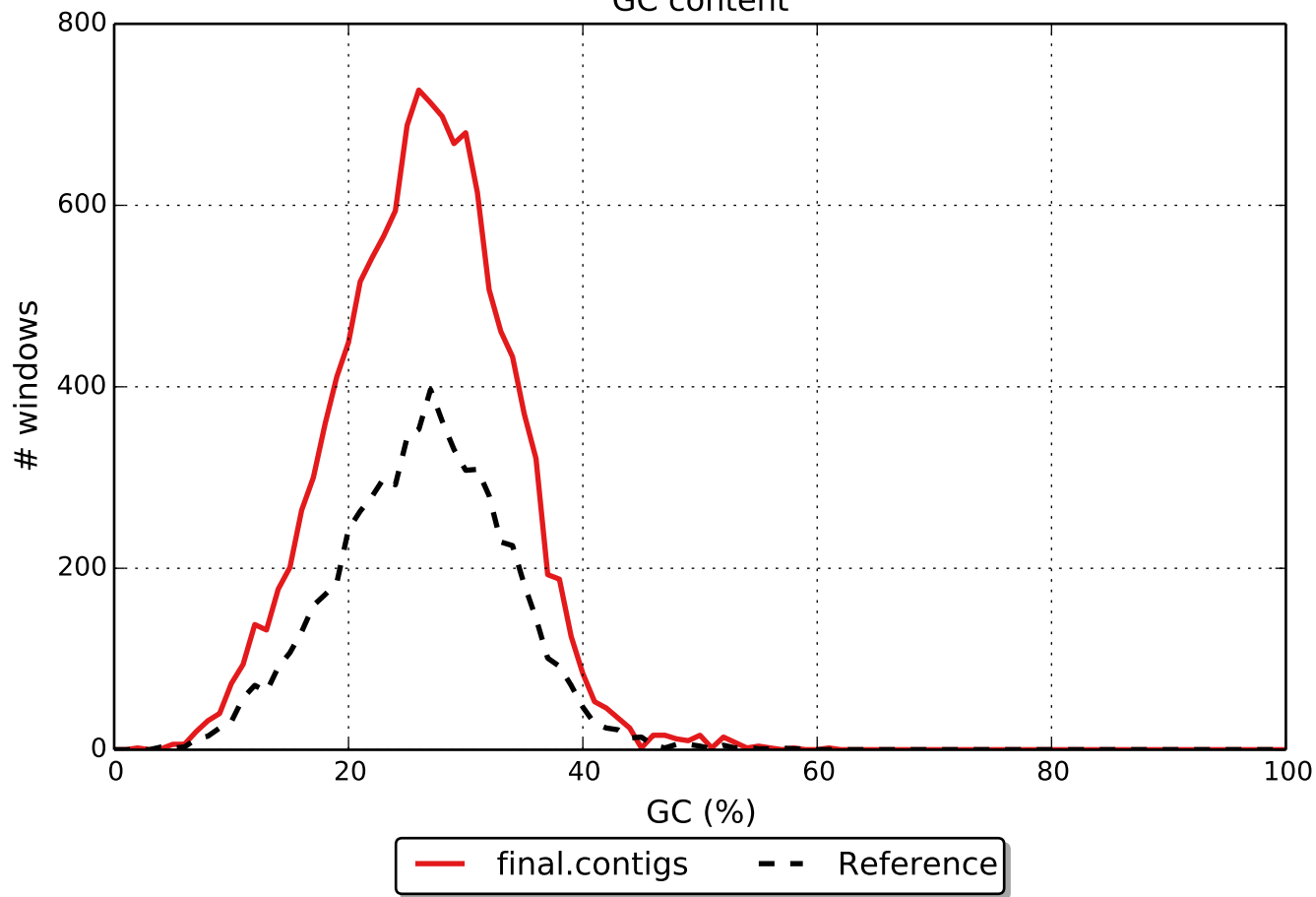
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

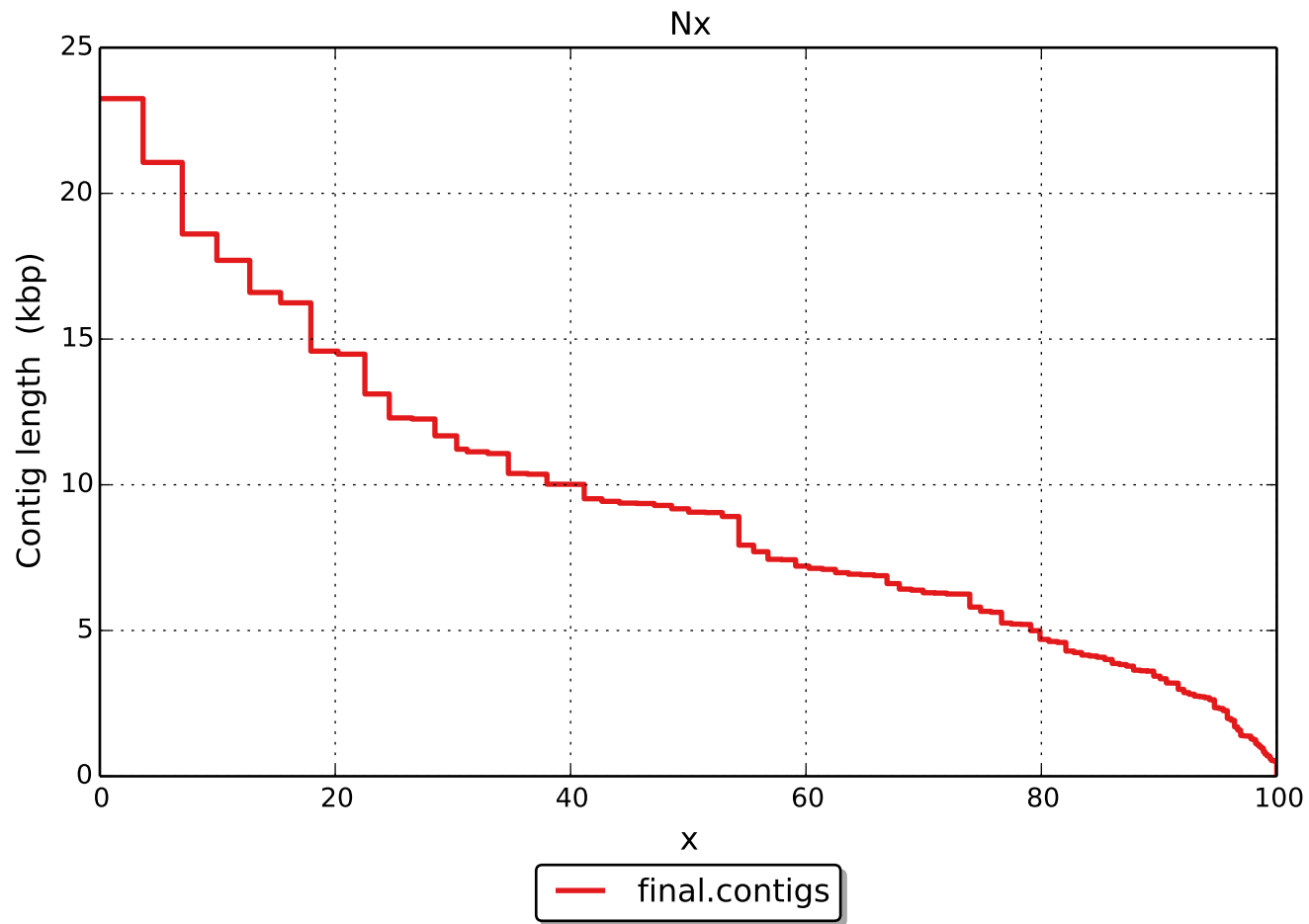
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

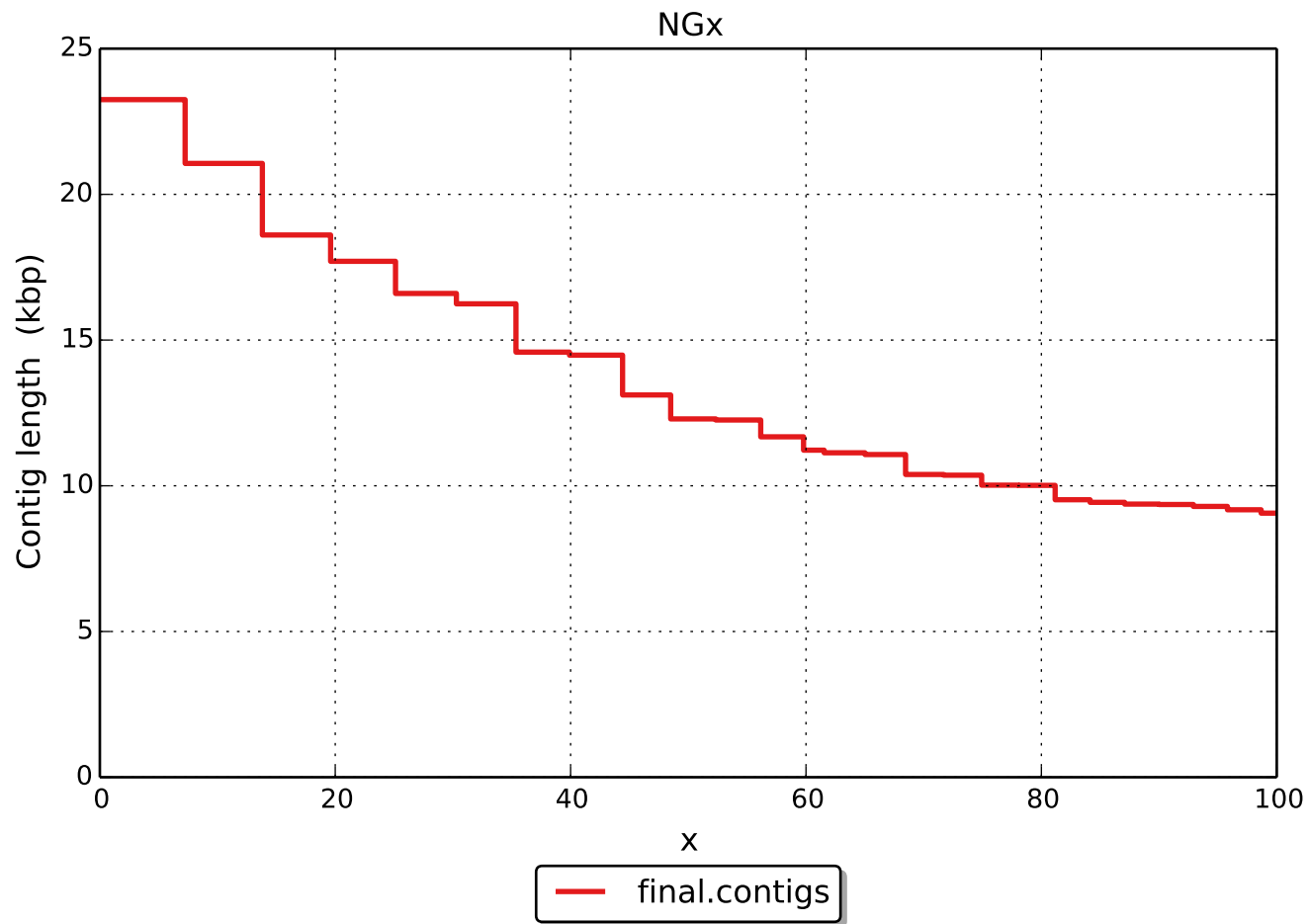
Cumulative length



# GC content





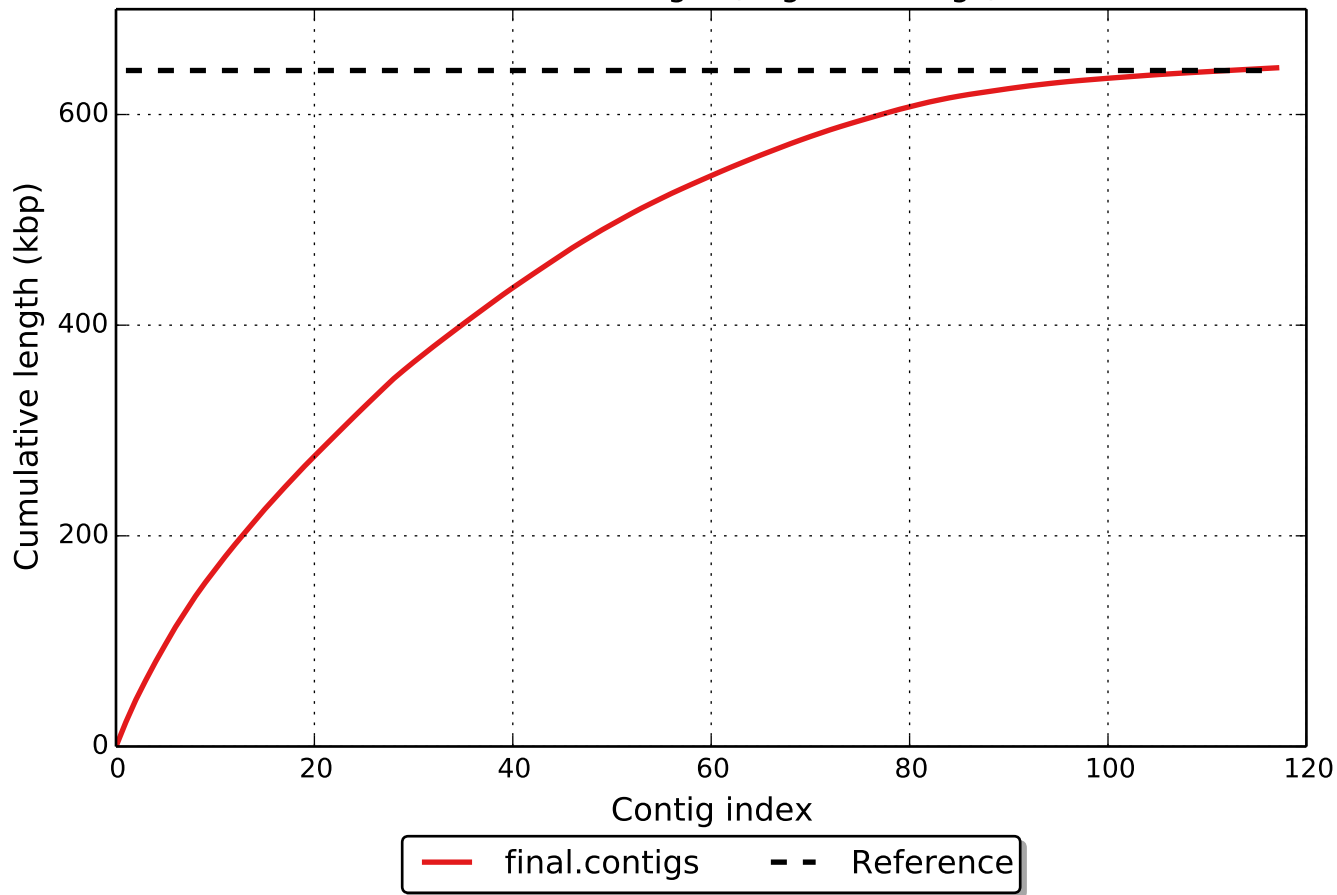


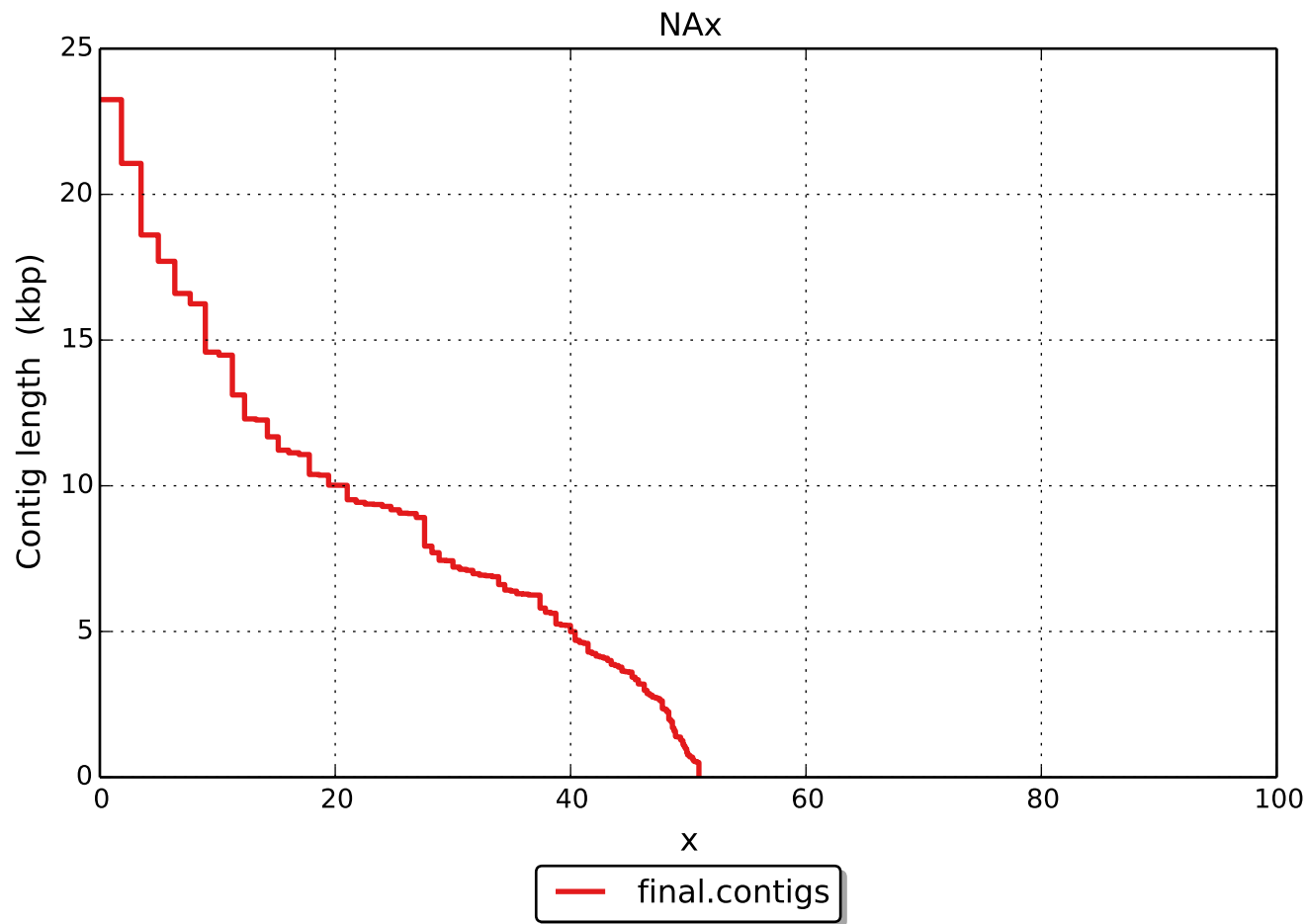
# Misassemblies





Cumulative length (aligned contigs)





# NGAx

