

# Report

	final.contigs
# contigs ( $\geq 0$ bp)	442
# contigs ( $\geq 1000$ bp)	299
Total length ( $\geq 0$ bp)	1255175
Total length ( $\geq 1000$ bp)	1159107
# contigs	442
Largest contig	25883
Total length	1255175
Reference length	641799
GC (%)	26.27
Reference GC (%)	26.30
N50	4710
NG50	7681
N75	2567
NG75	5790
L50	79
LG50	26
L75	171
LG75	51
# misassemblies	5
# misassembled contigs	5
Misassembled contigs length	10256
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	96.805
Duplication ratio	2.020
# N's per 100 kbp	0.00
# mismatches per 100 kbp	653.48
# indels per 100 kbp	0.32
Largest alignment	25883
NA50	665
NGA50	4614
NGA75	2490
LA50	203
LGA50	41
LGA75	89

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	5
# relocations	5
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	5
Misassembled contigs length	10256
# local misassemblies	0
# mismatches	4060
# indels	2
# short indels	2
# long indels	0
Indels length	2

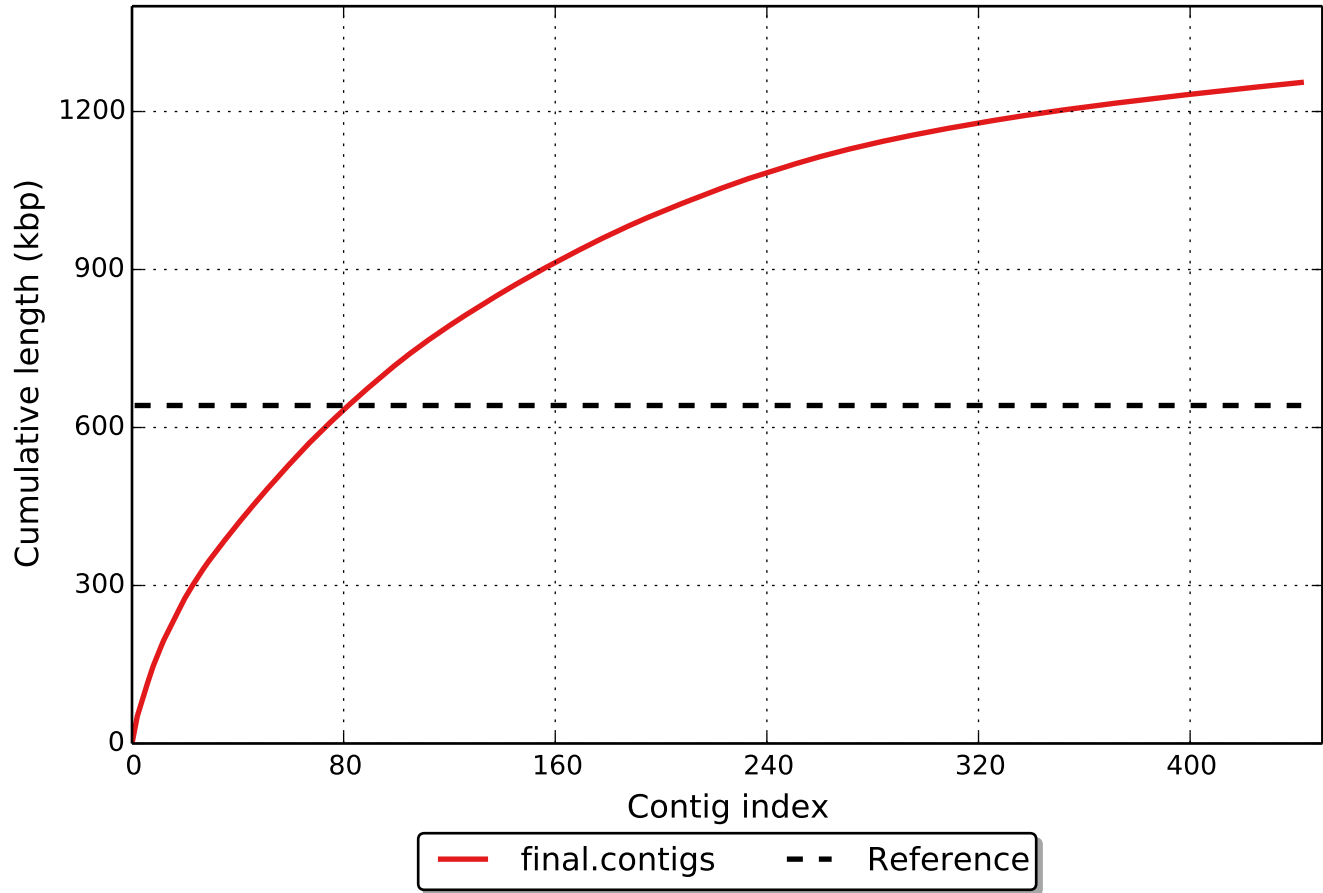
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

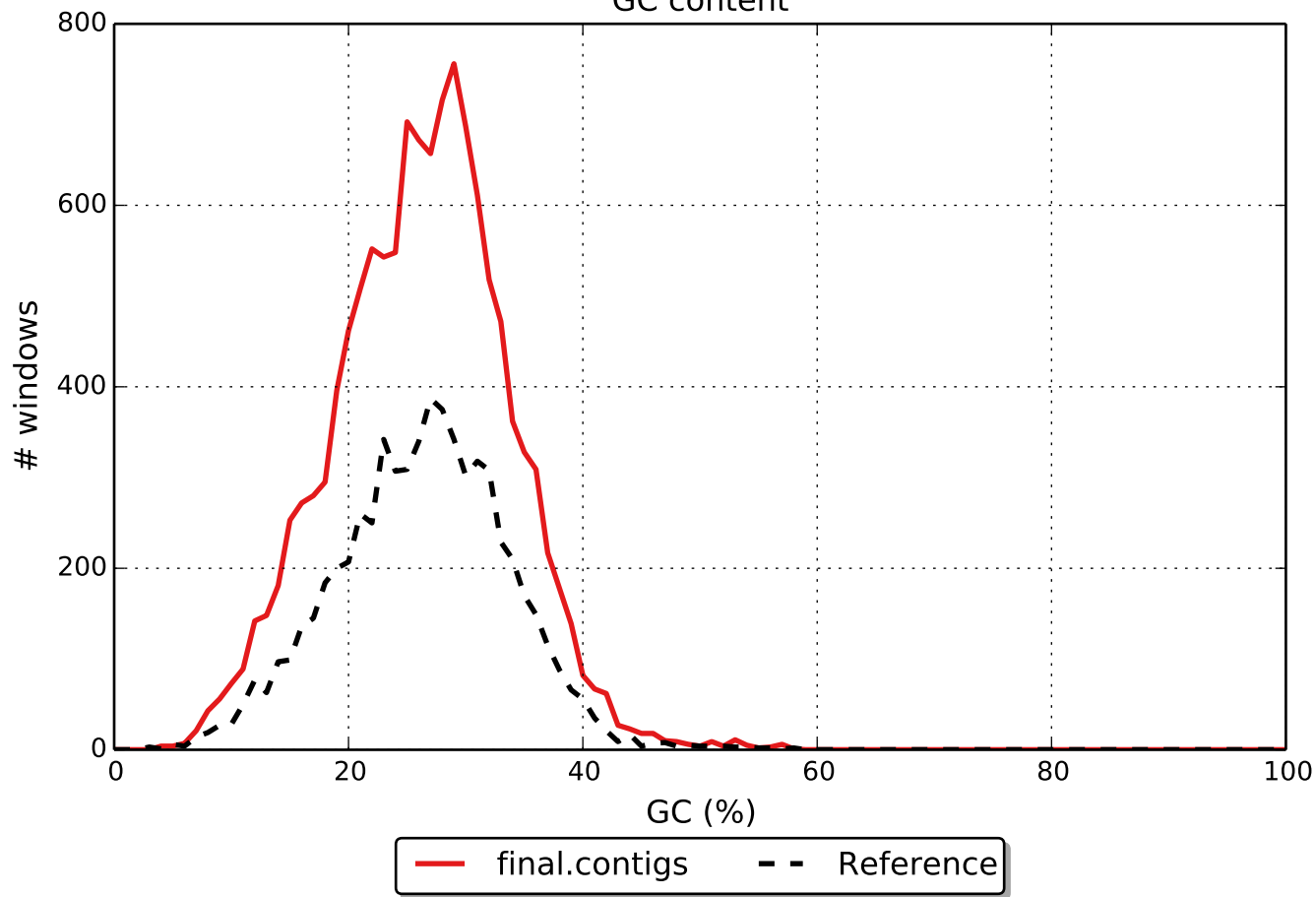
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

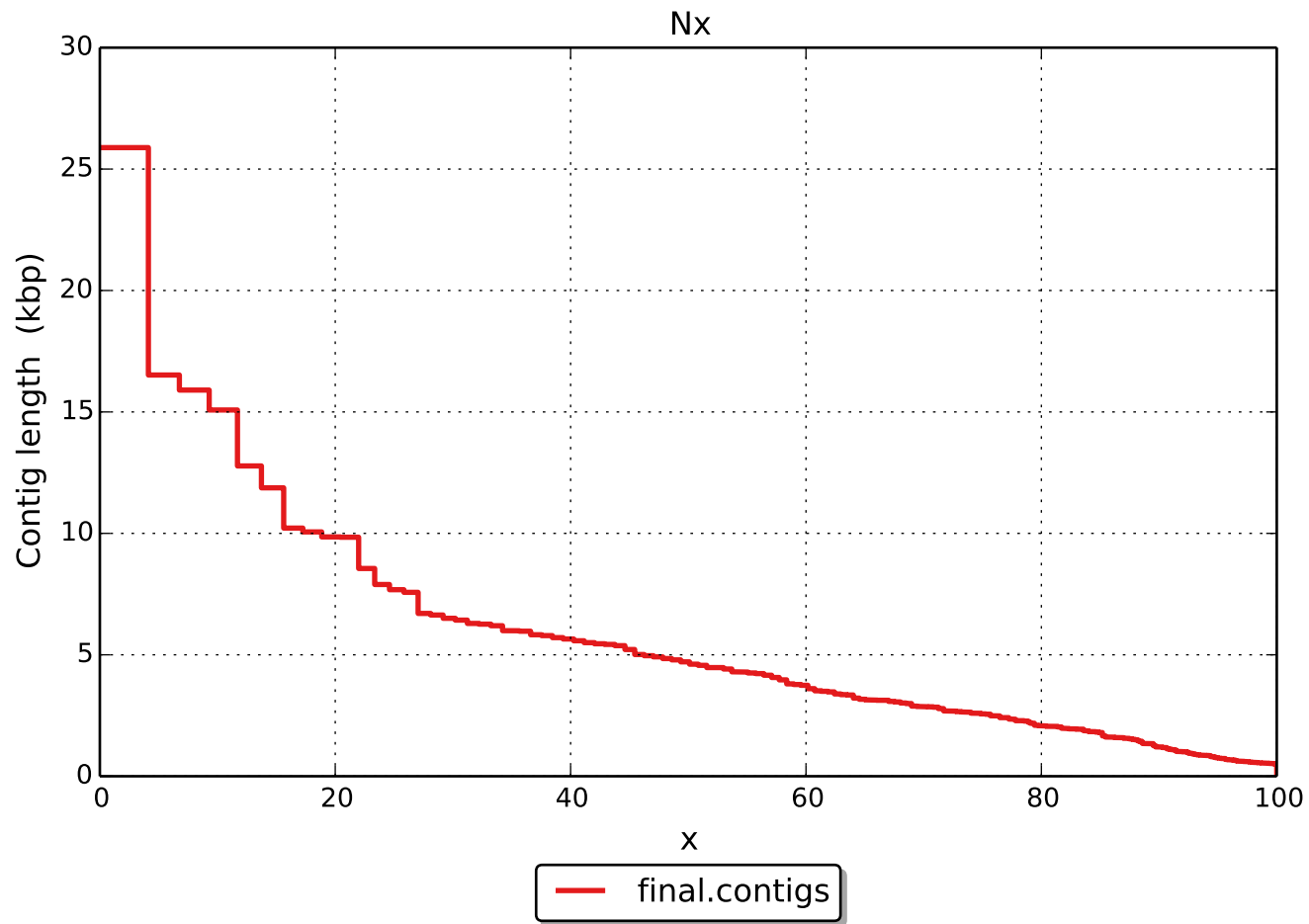
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

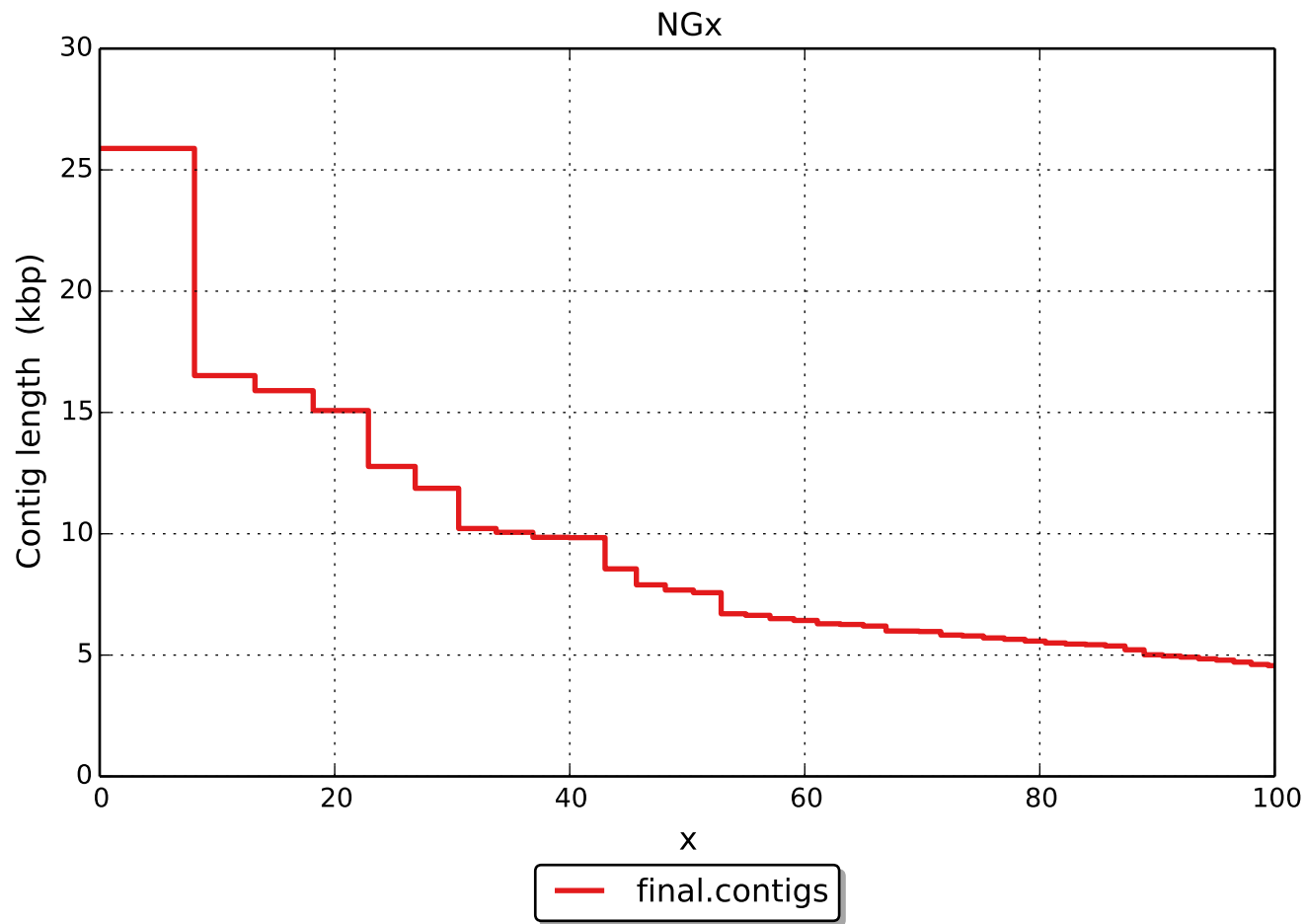
Cumulative length

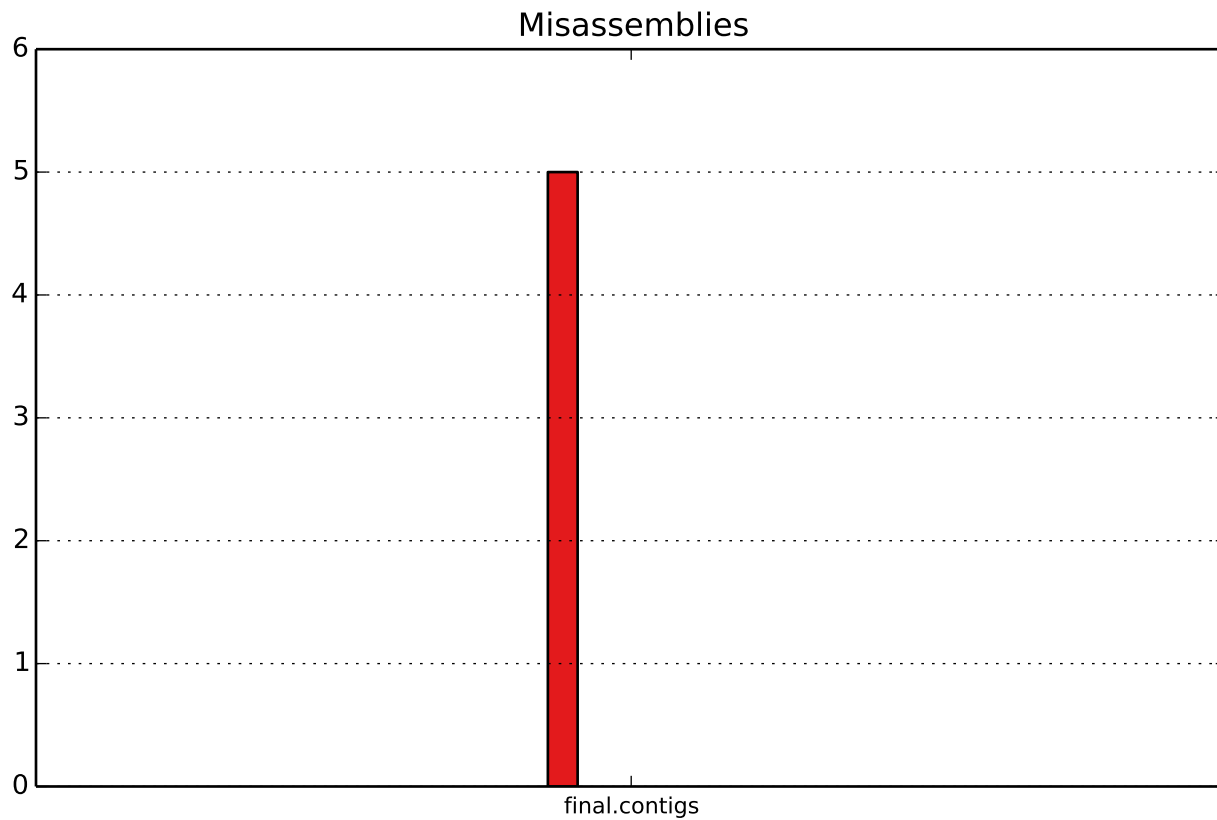


# GC content



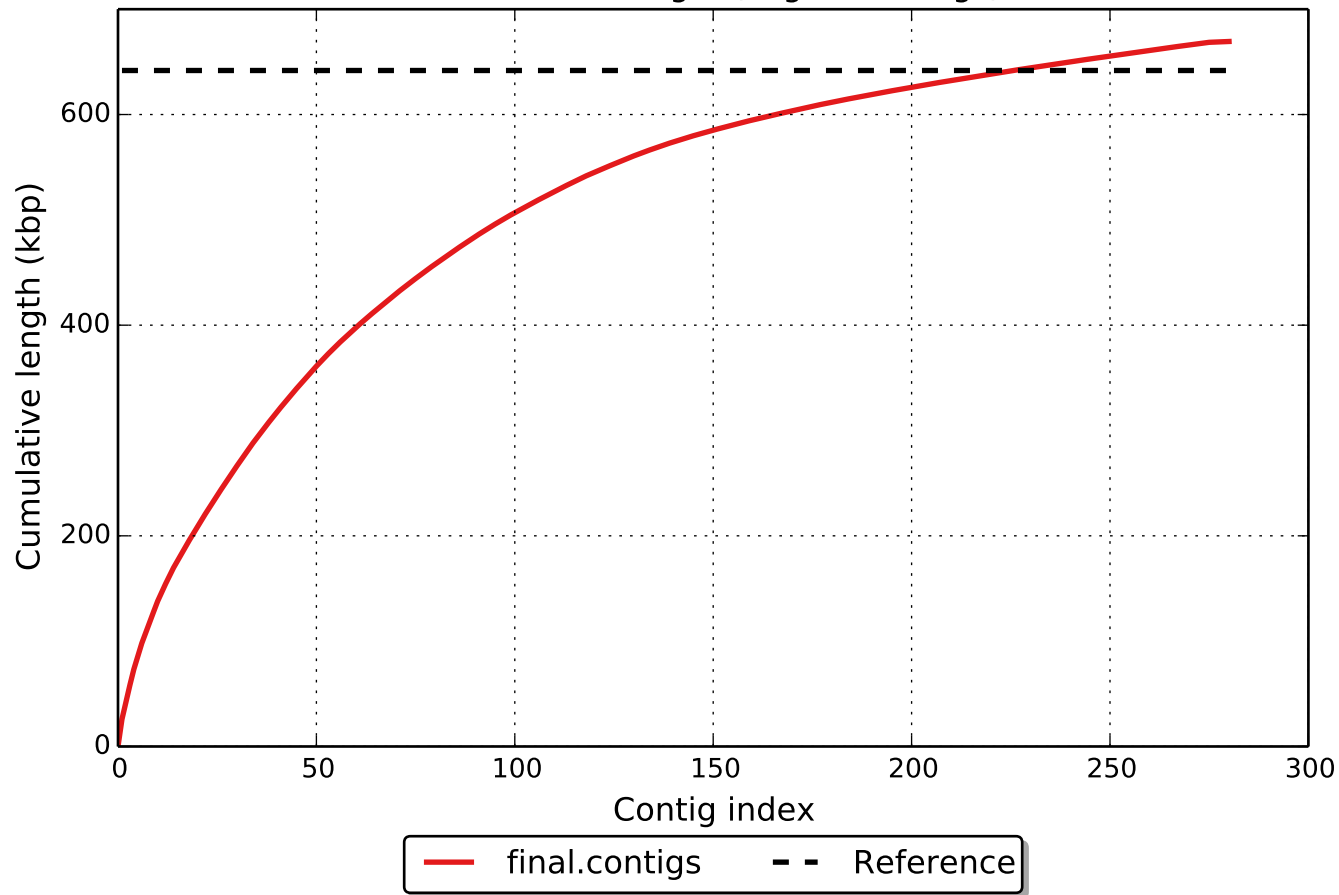


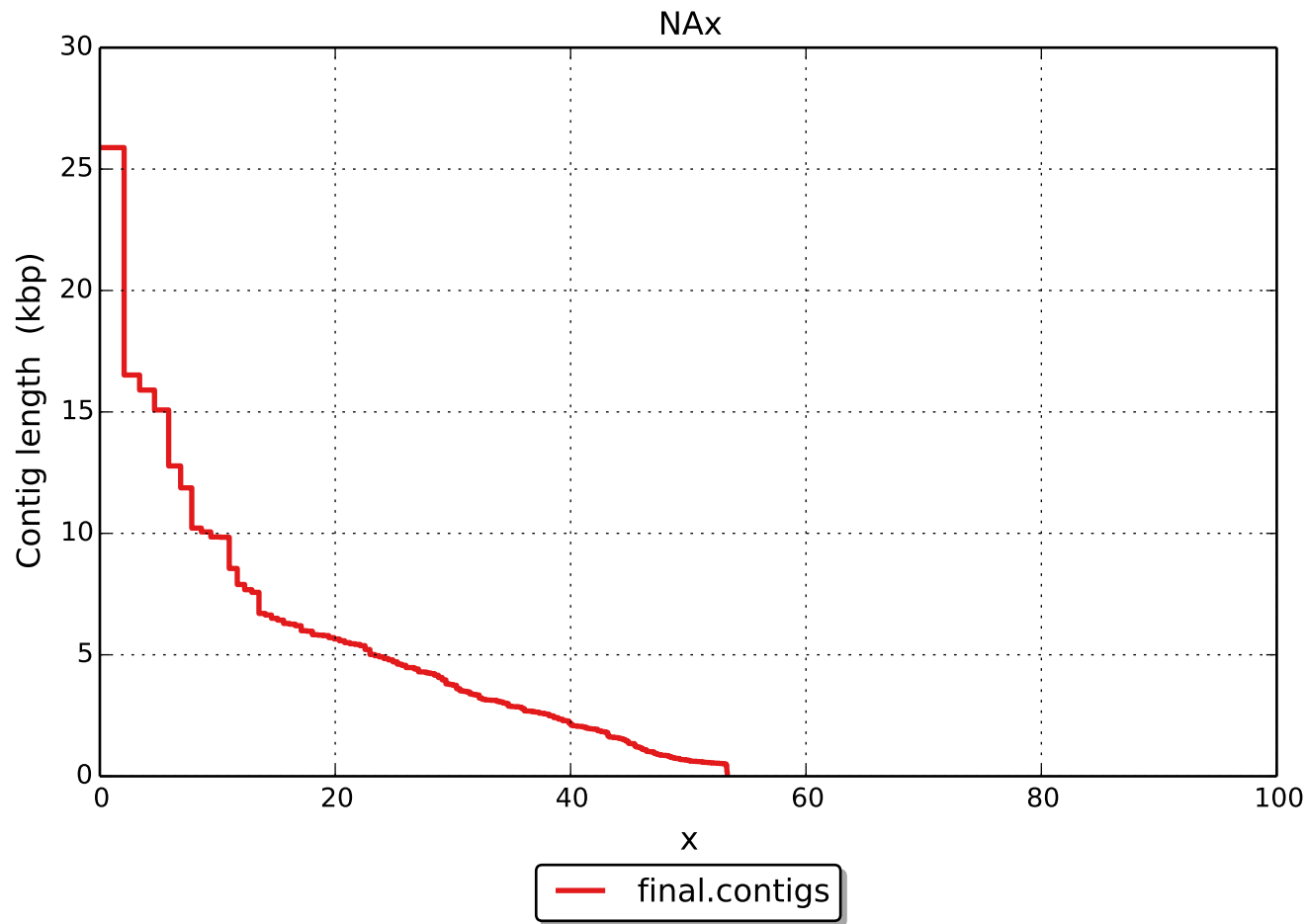






Cumulative length (aligned contigs)





# NGAx

