

Report

	final.contigs
# contigs (>= 1000 bp)	895
# contigs (>= 5000 bp)	348
# contigs (>= 10000 bp)	87
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4507316
Total length (>= 5000 bp)	3034468
Total length (>= 10000 bp)	1237627
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	1033
Largest contig	24083
Total length	4609479
Reference length	4641652
GC (℥)	50.74
Reference GC (℥)	50.79
N50	6553
NG50	6480
N75	4002
NG75	3952
L50	221
LG50	223
L75	443
LG75	449
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (℥)	97.768
Duplication ratio	1.016
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.35
# indels per 100 kbp	0.00
Largest alignment	24083
NA50	6553
NGA50	6480
NA75	4002
NGA75	3952
LA50	221
LGA50	223
LA75	443
LGA75	449

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

## Misassemblies report

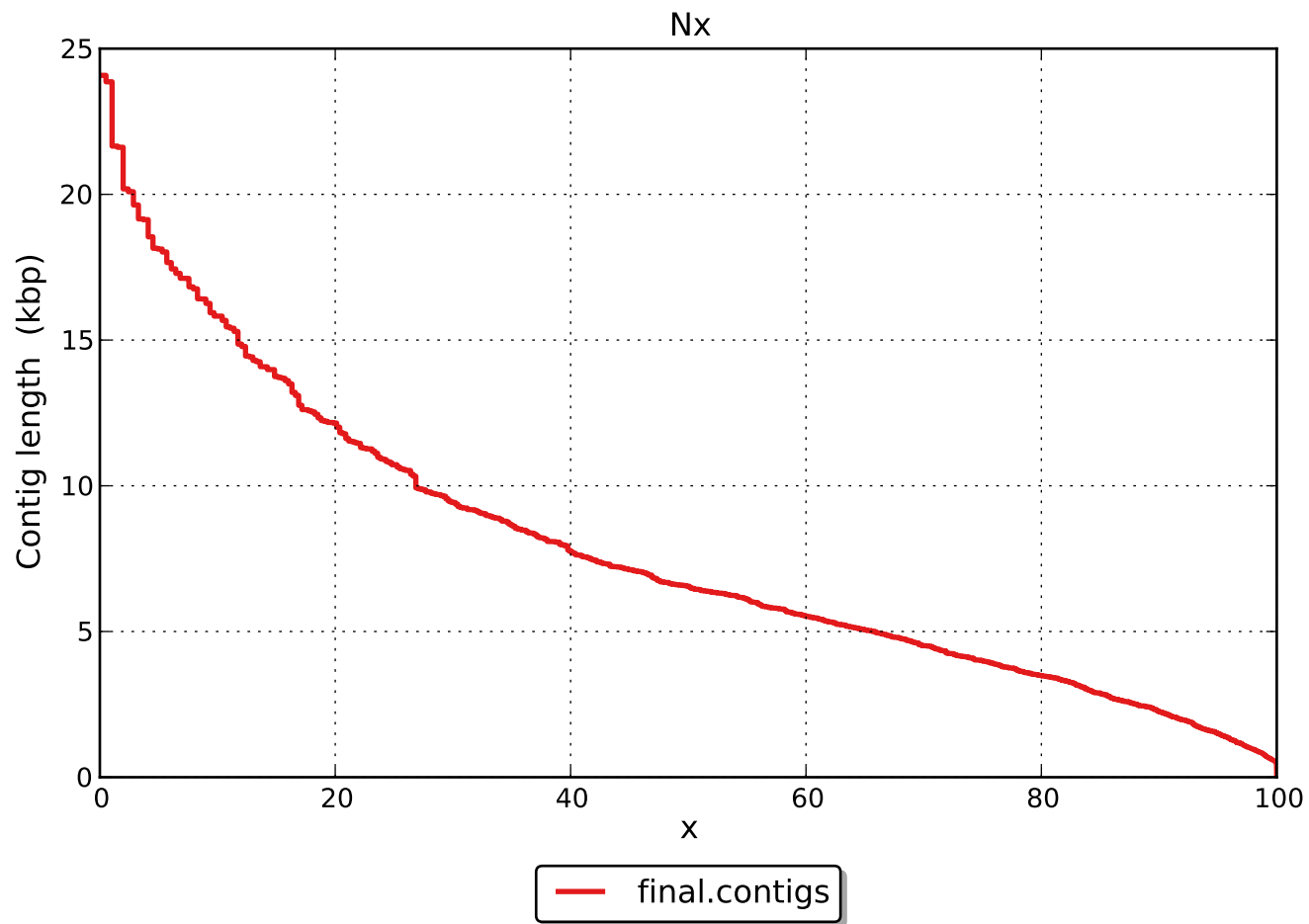
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	16
# indels	0
# short indels	0
# long indels	0
Indels length	0

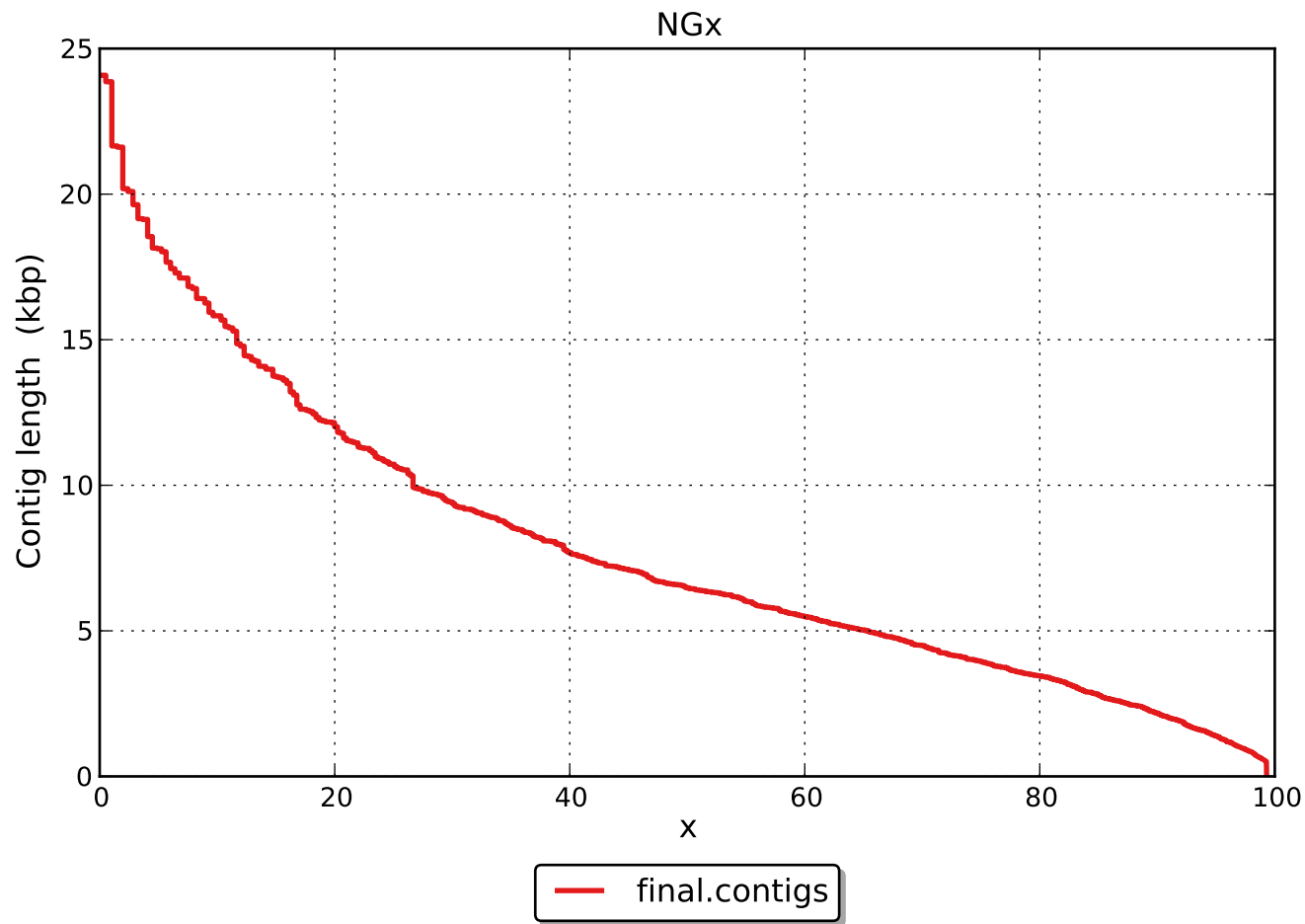
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

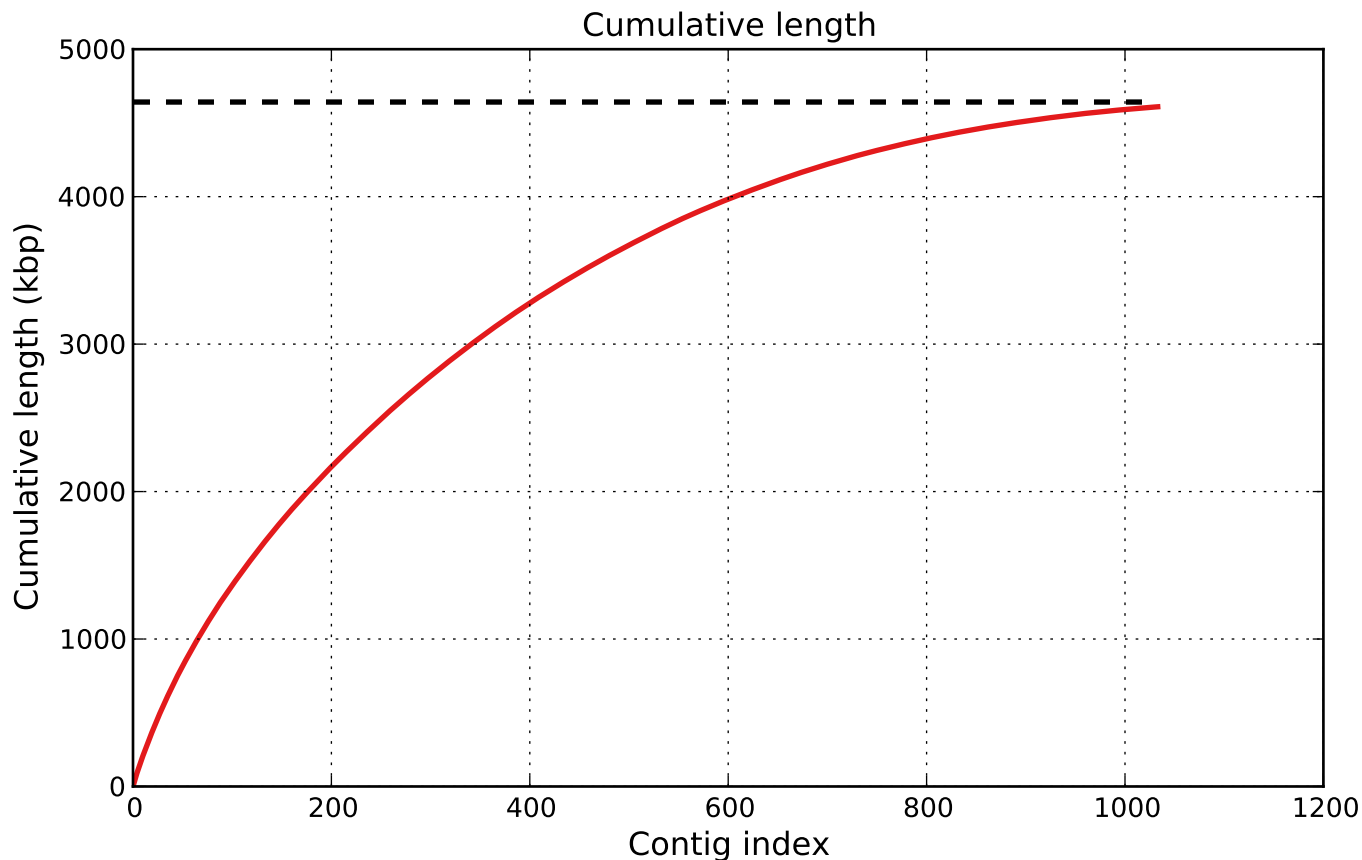
## Unaligned report

	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

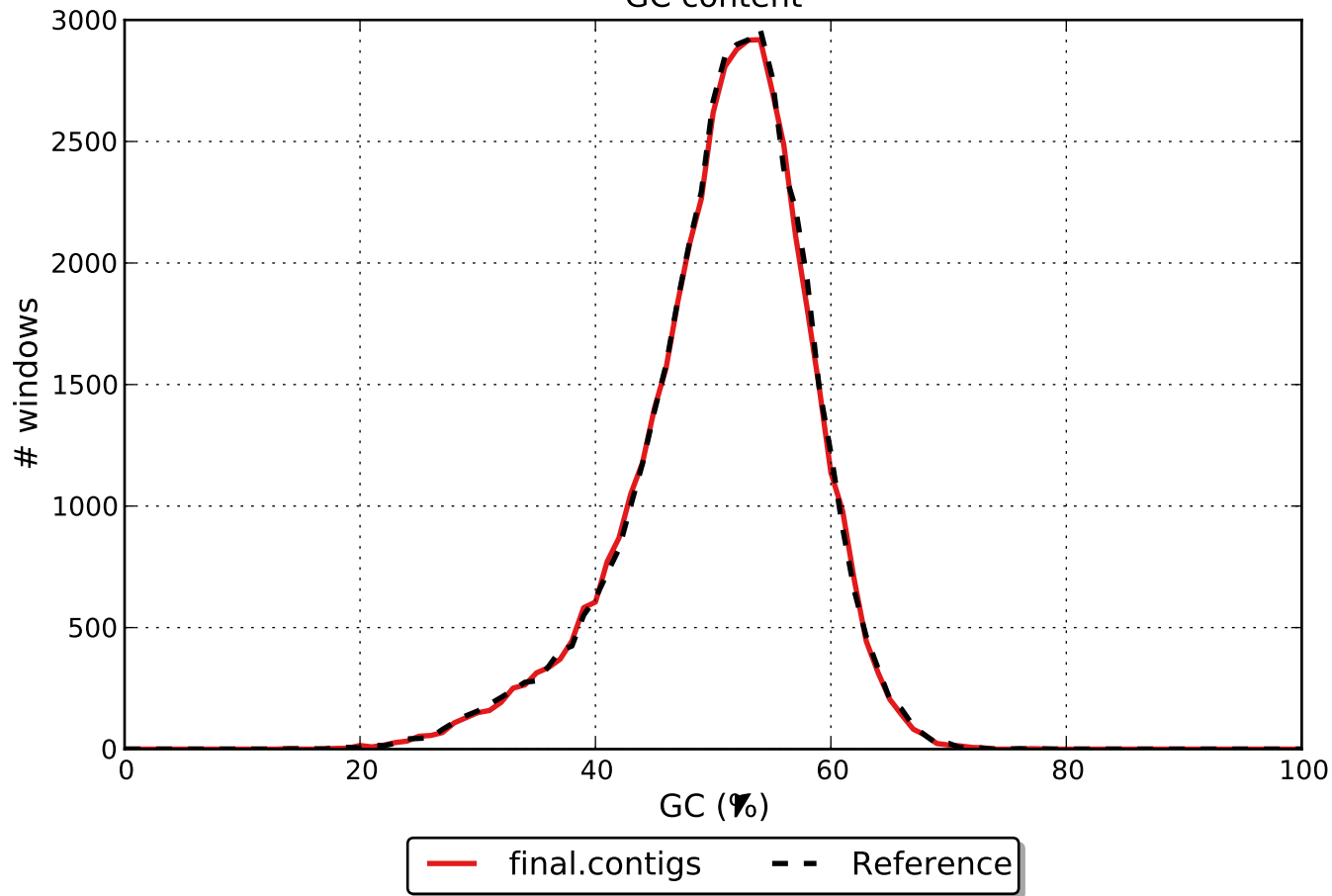
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).







GC content

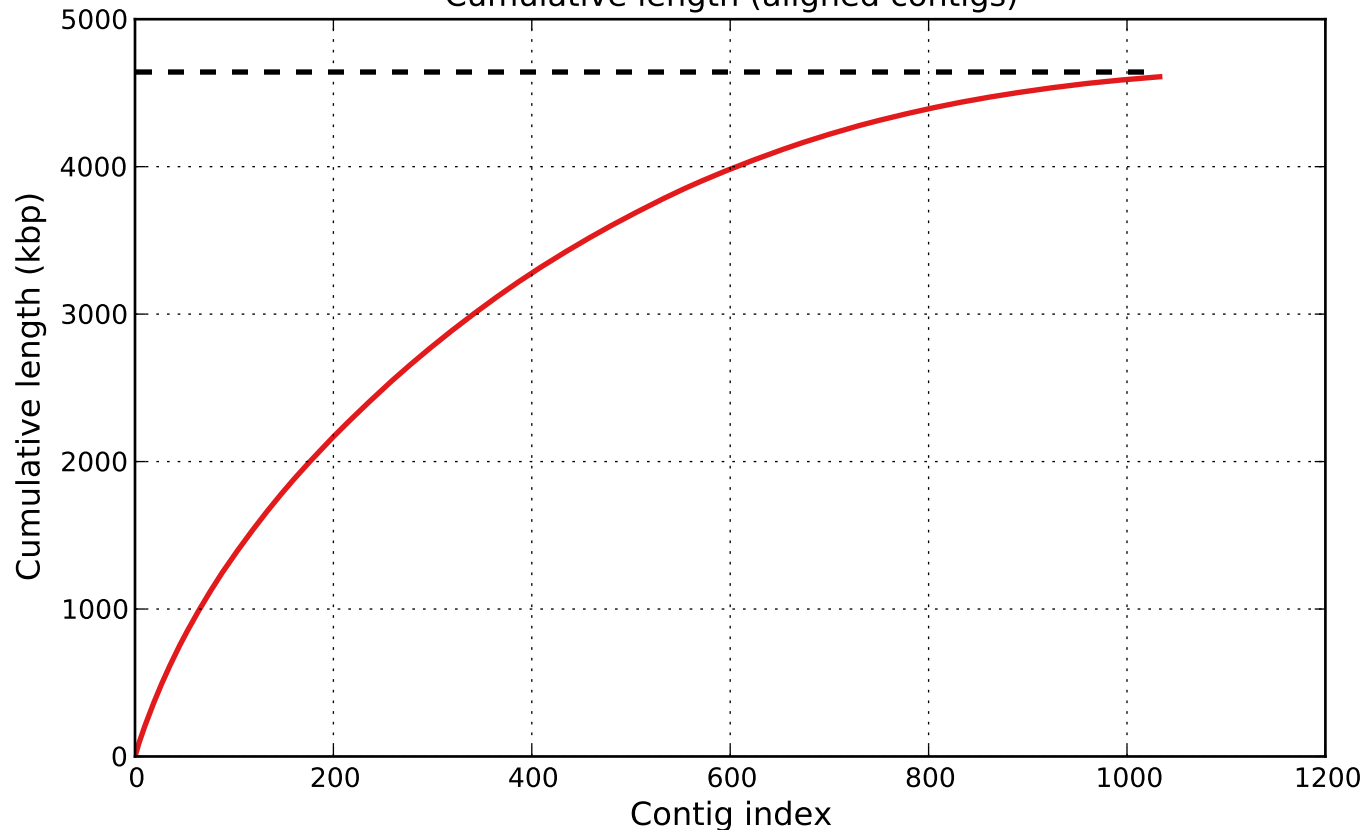


# Misassemblies

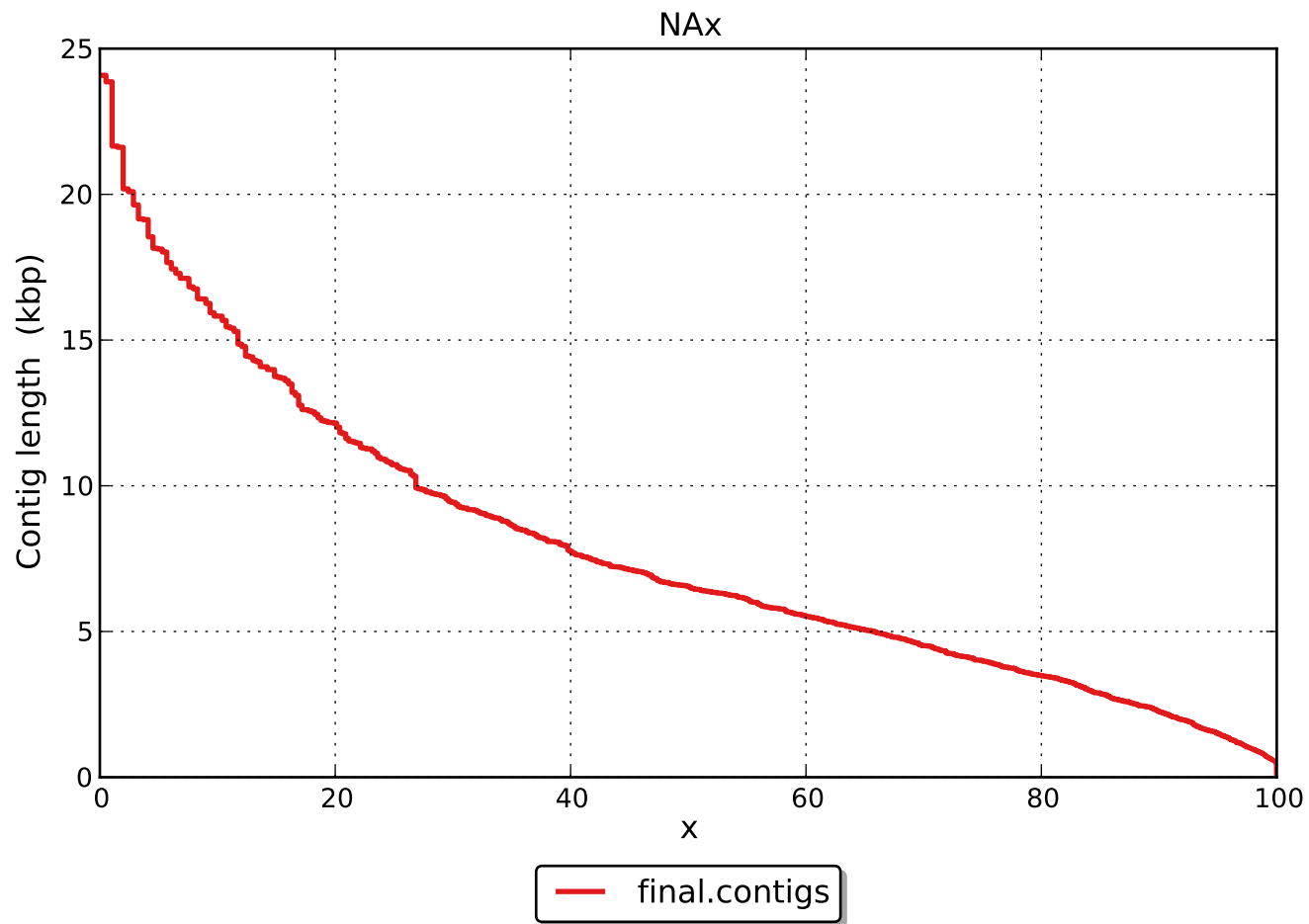




Cumulative length (aligned contigs)



— final.contigs    - - Reference



# NGAx

