

Report

	final.contigs
# contigs (>= 1000 bp)	515
# contigs (>= 5000 bp)	333
# contigs (>= 10000 bp)	168
# contigs (>= 25000 bp)	36
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4881264
Total length (>= 5000 bp)	4373551
Total length (>= 10000 bp)	3210348
Total length (>= 25000 bp)	1219561
Total length (>= 50000 bp)	0
# contigs	536
Largest contig	48657
Total length	4897023
Reference length	4857432
GC (℥)	52.23
Reference GC (℥)	52.23
N50	14063
NG50	14172
N75	7859
NG75	7963
L50	104
LG50	102
L75	221
LG75	218
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (℥)	99.928
Duplication ratio	1.009
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.02
# indels per 100 kbp	0.00
Largest alignment	48657
NA50	14063
NGA50	14172
NA75	7859
NGA75	7963
LA50	104
LGA50	102
LA75	221
LGA75	218

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

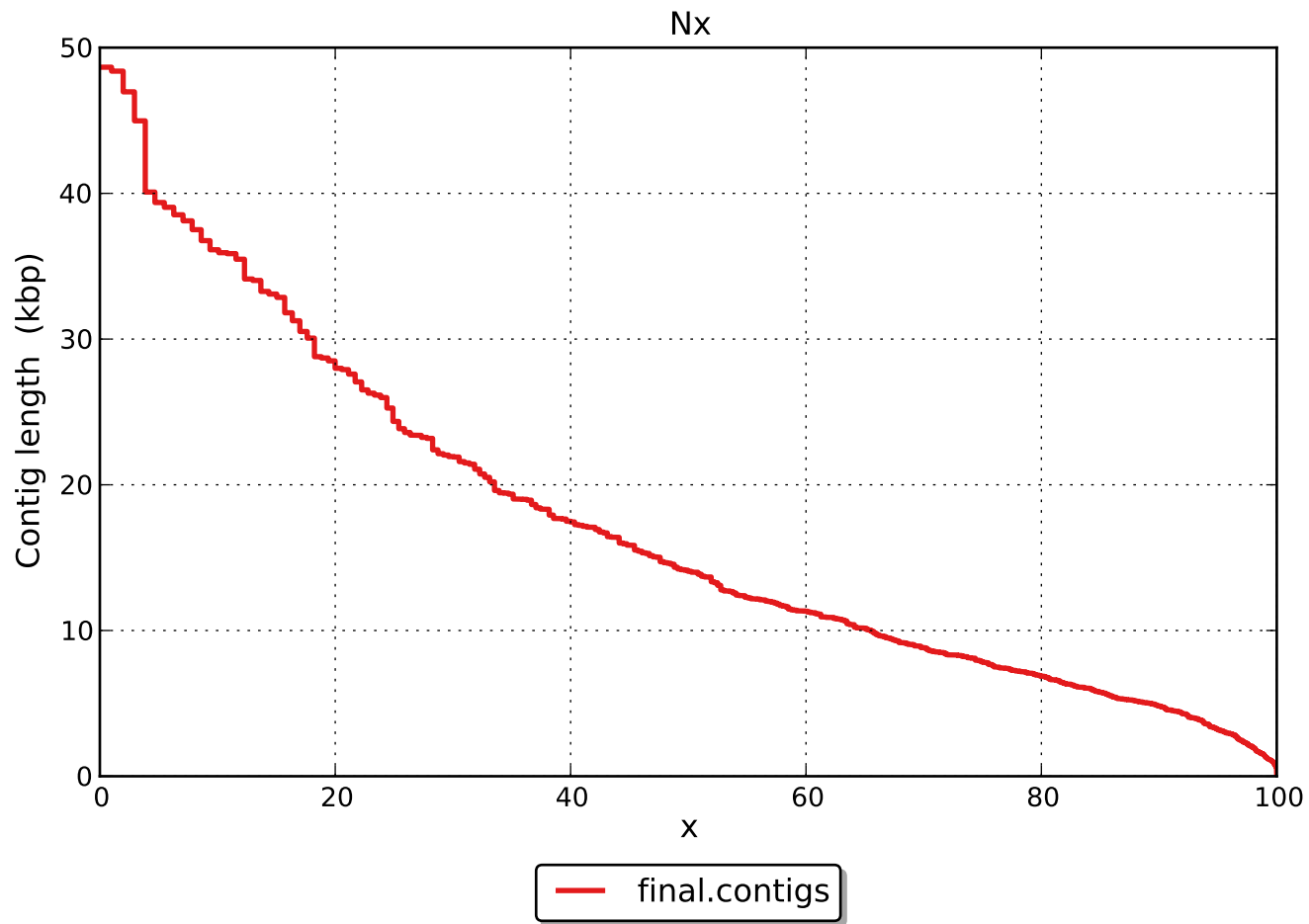
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	1
# indels	0
# short indels	0
# long indels	0
Indels length	0

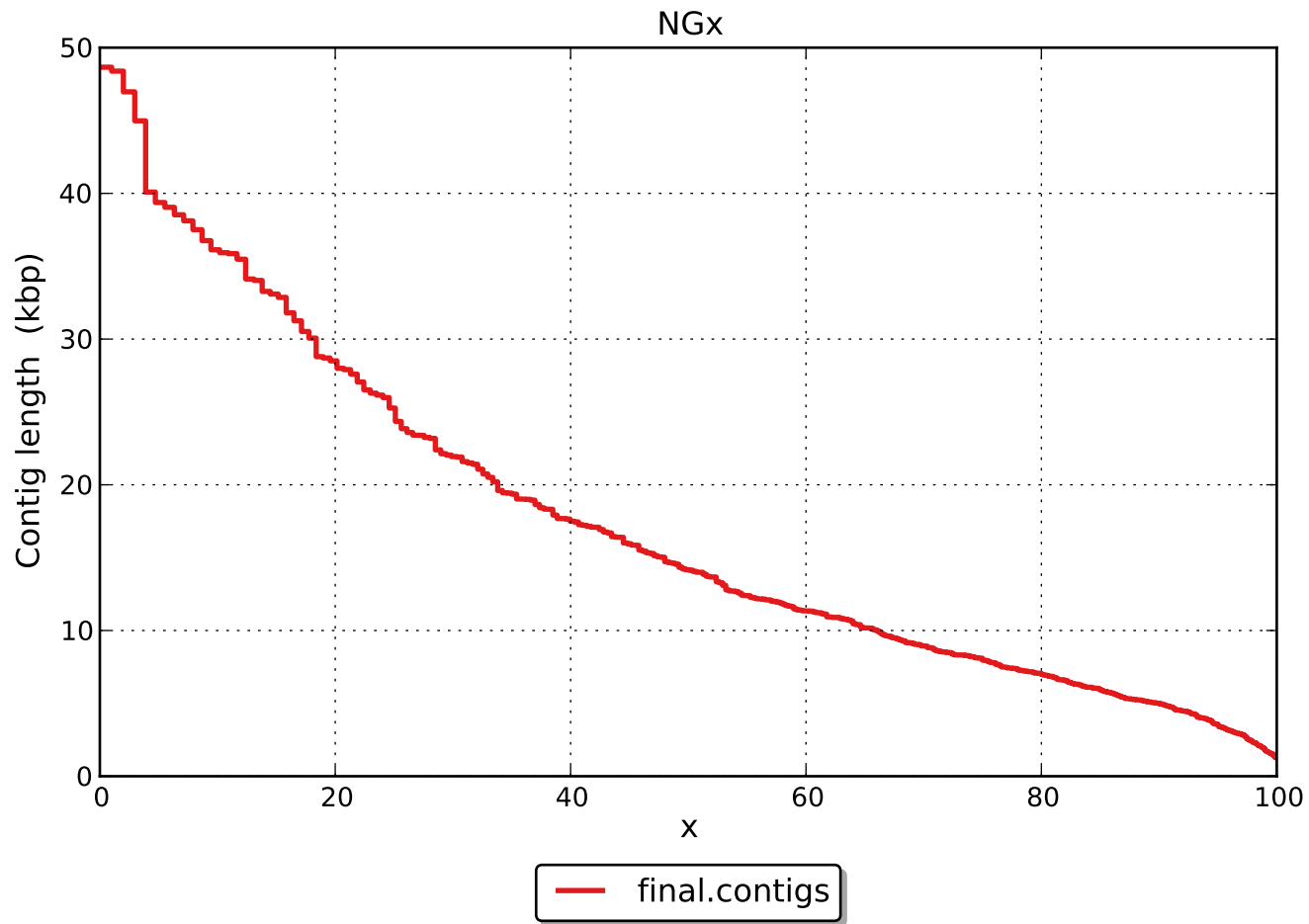
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

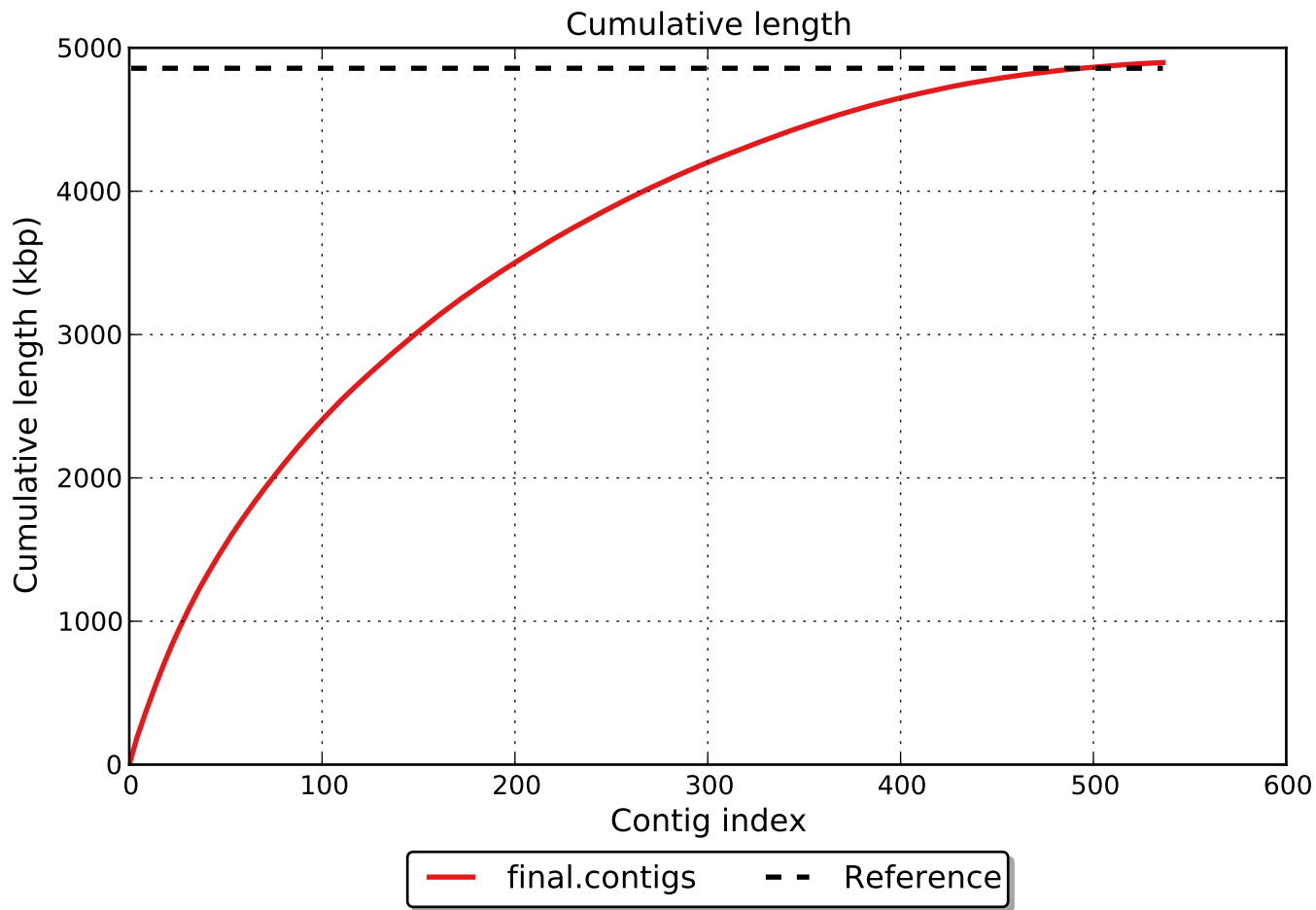
## Unaligned report

	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

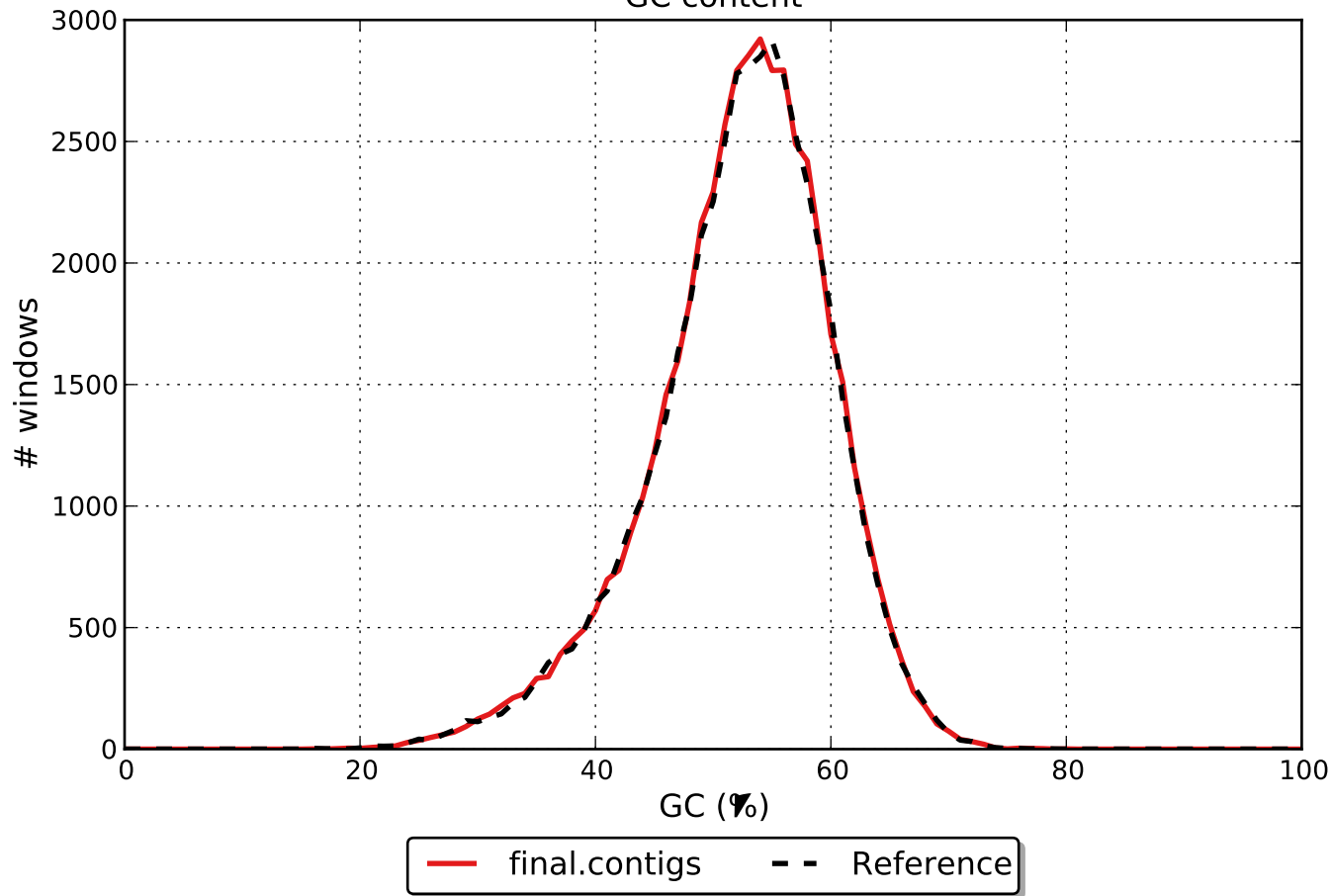
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).







GC content

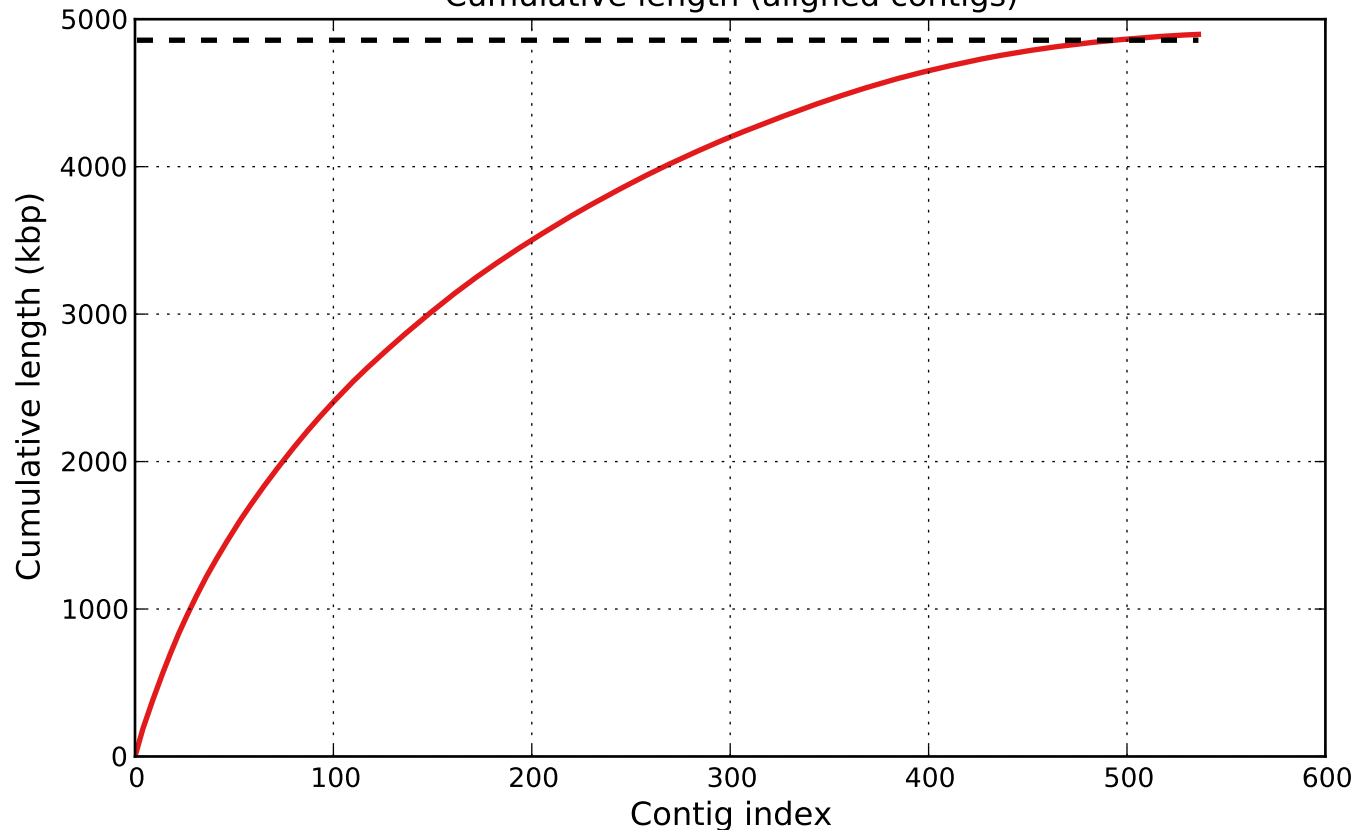


# Misassemblies

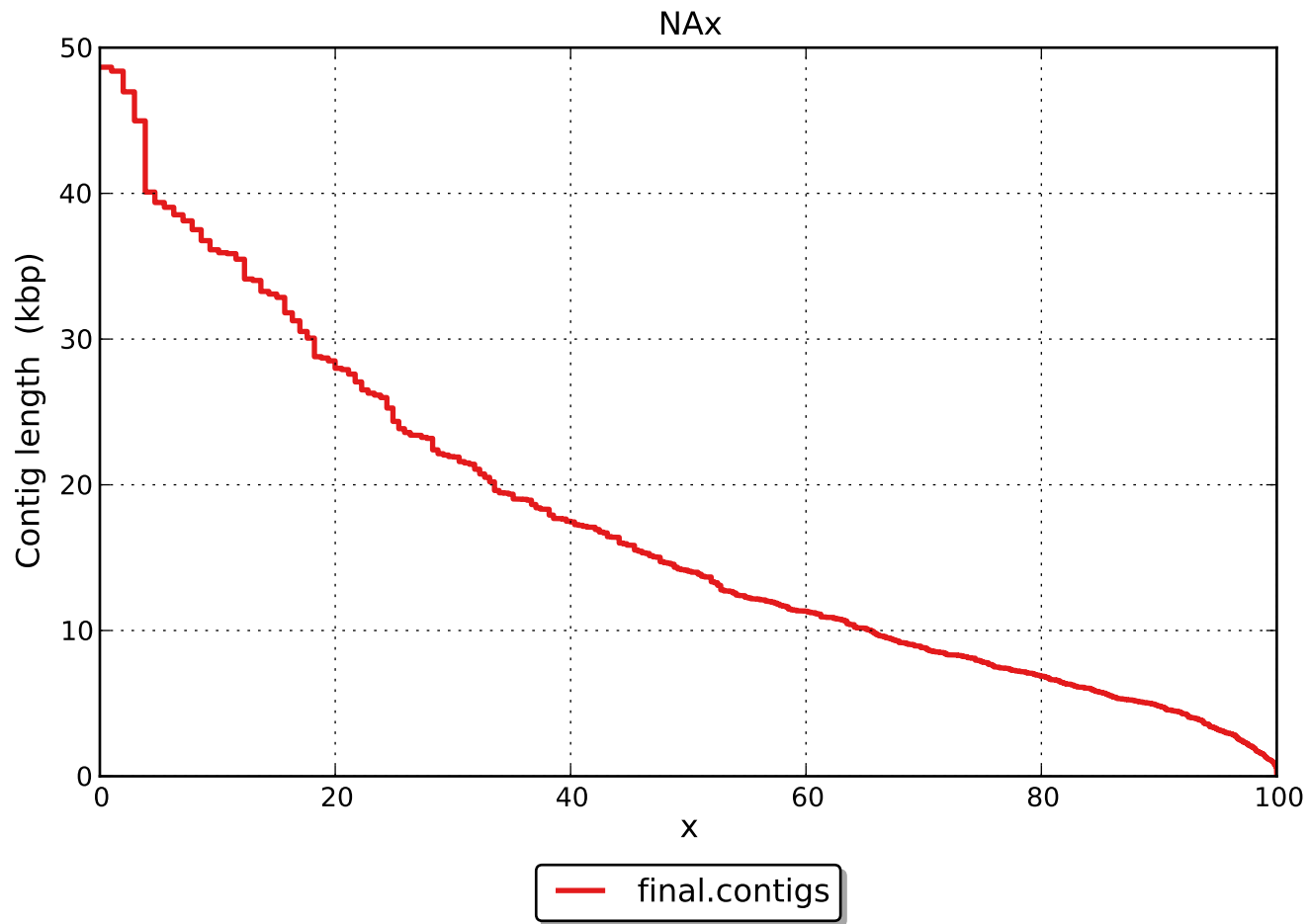




Cumulative length (aligned contigs)



— final.contigs      - - Reference



# NGAx

