

Report

	final.contigs
# contigs (>= 1000 bp)	1722
# contigs (>= 5000 bp)	89
# contigs (>= 10000 bp)	2
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4020298
Total length (>= 5000 bp)	559709
Total length (>= 10000 bp)	24013
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	2586
Largest contig	12951
Total length	4651337
Reference length	4641652
GC (℥)	50.78
Reference GC (℥)	50.79
N50	2301
NG50	2309
N75	1404
NG75	1409
L50	636
LG50	633
L75	1278
LG75	1273
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (℥)	96.880
Duplication ratio	1.034
# N's per 100 kbp	0.00
# mismatches per 100 kbp	5.98
# indels per 100 kbp	0.04
Largest alignment	12951
NA50	2301
NGA50	2309
NA75	1404
NGA75	1409
LA50	636
LGA50	633
LA75	1278
LGA75	1273

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

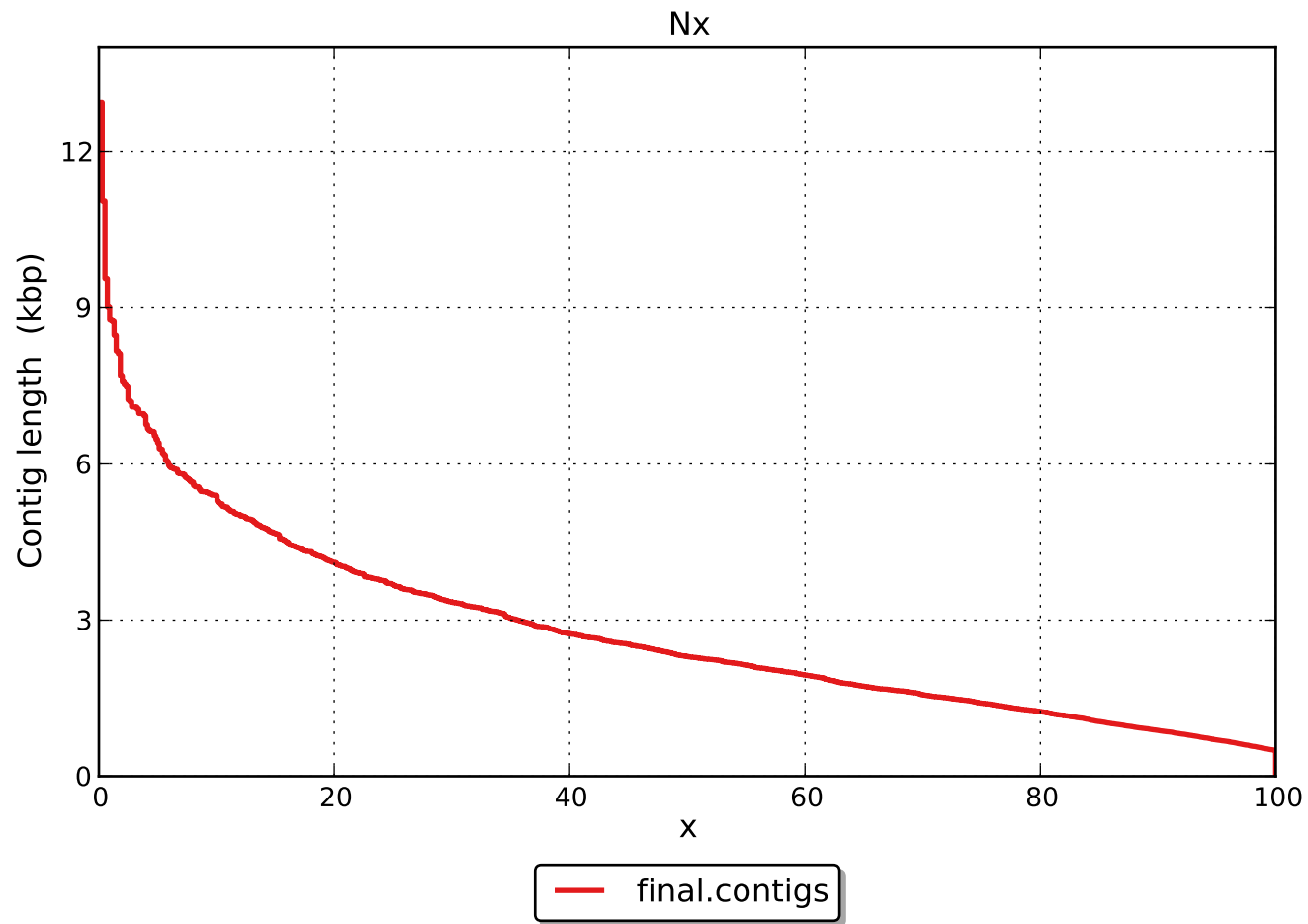
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	269
# indels	2
# short indels	2
# long indels	0
Indels length	2

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).

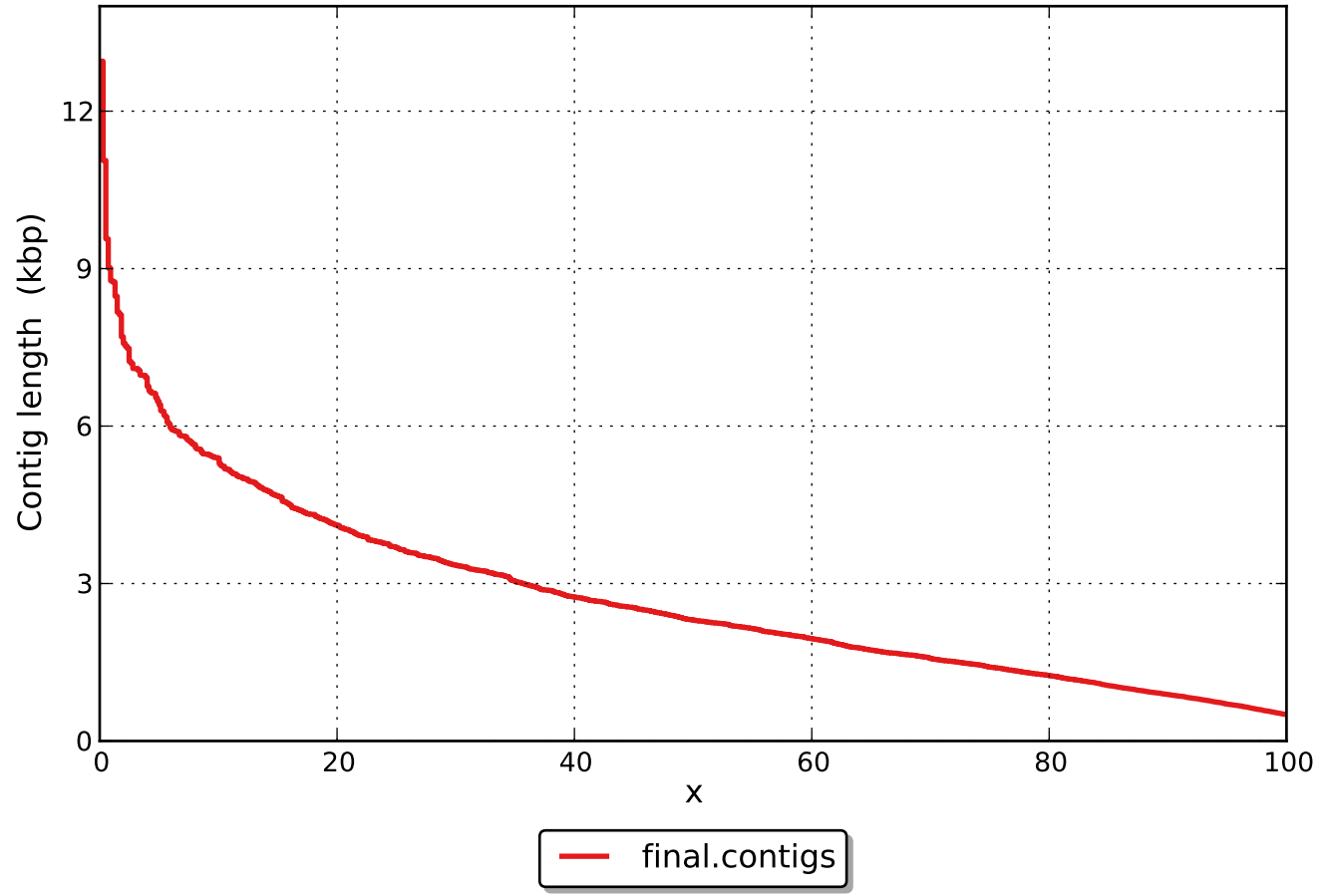
## Unaligned report

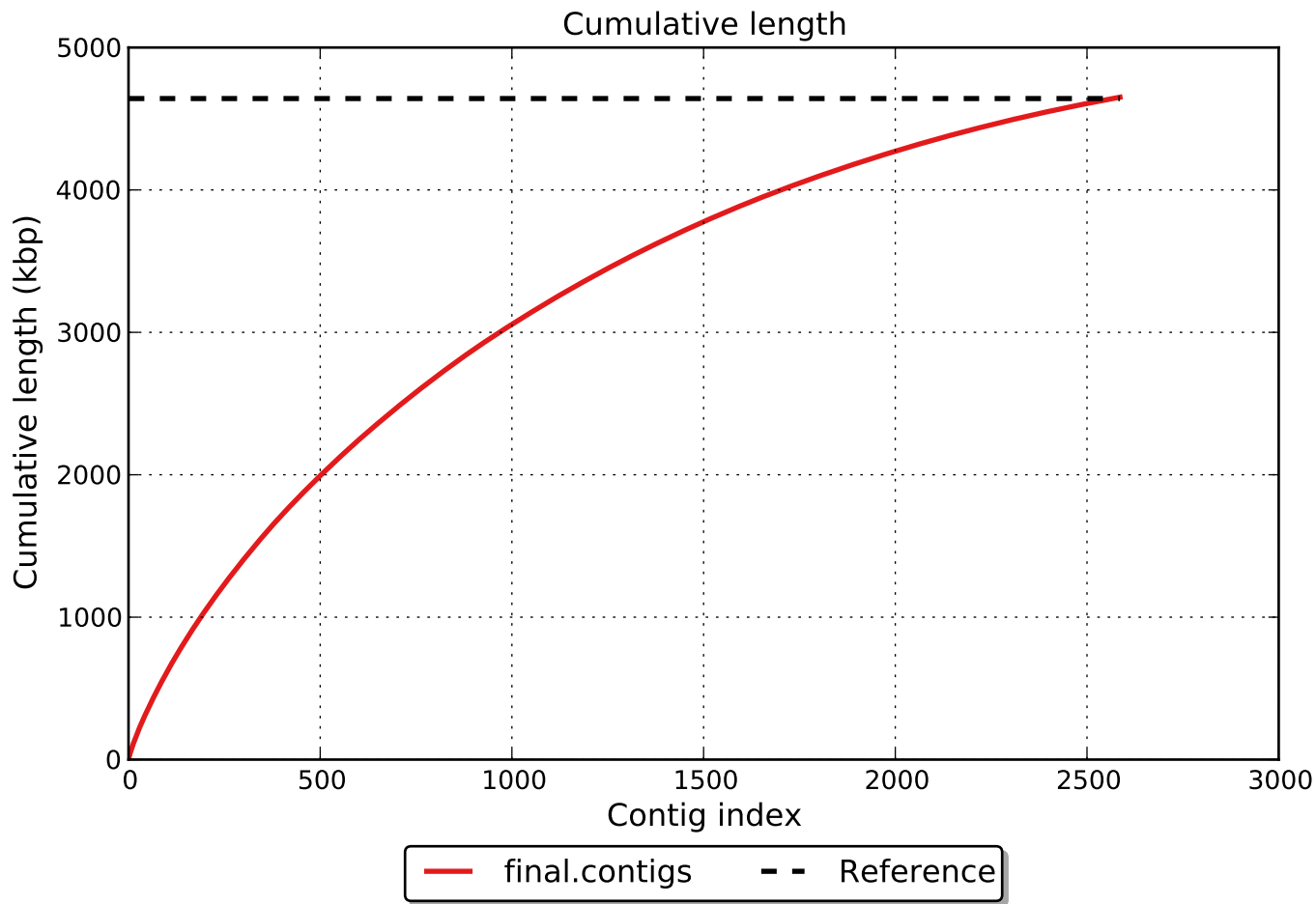
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

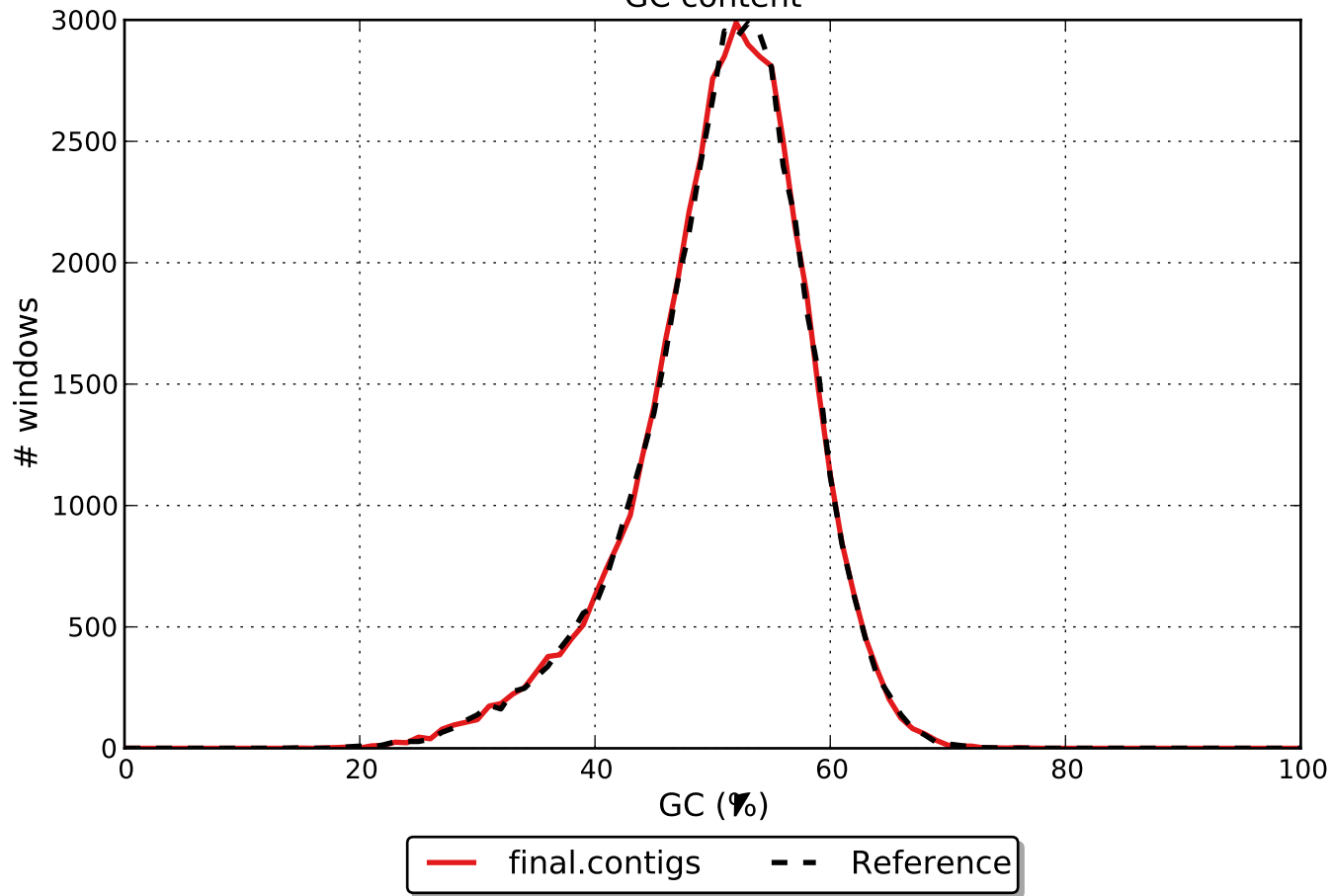


NGx





GC content

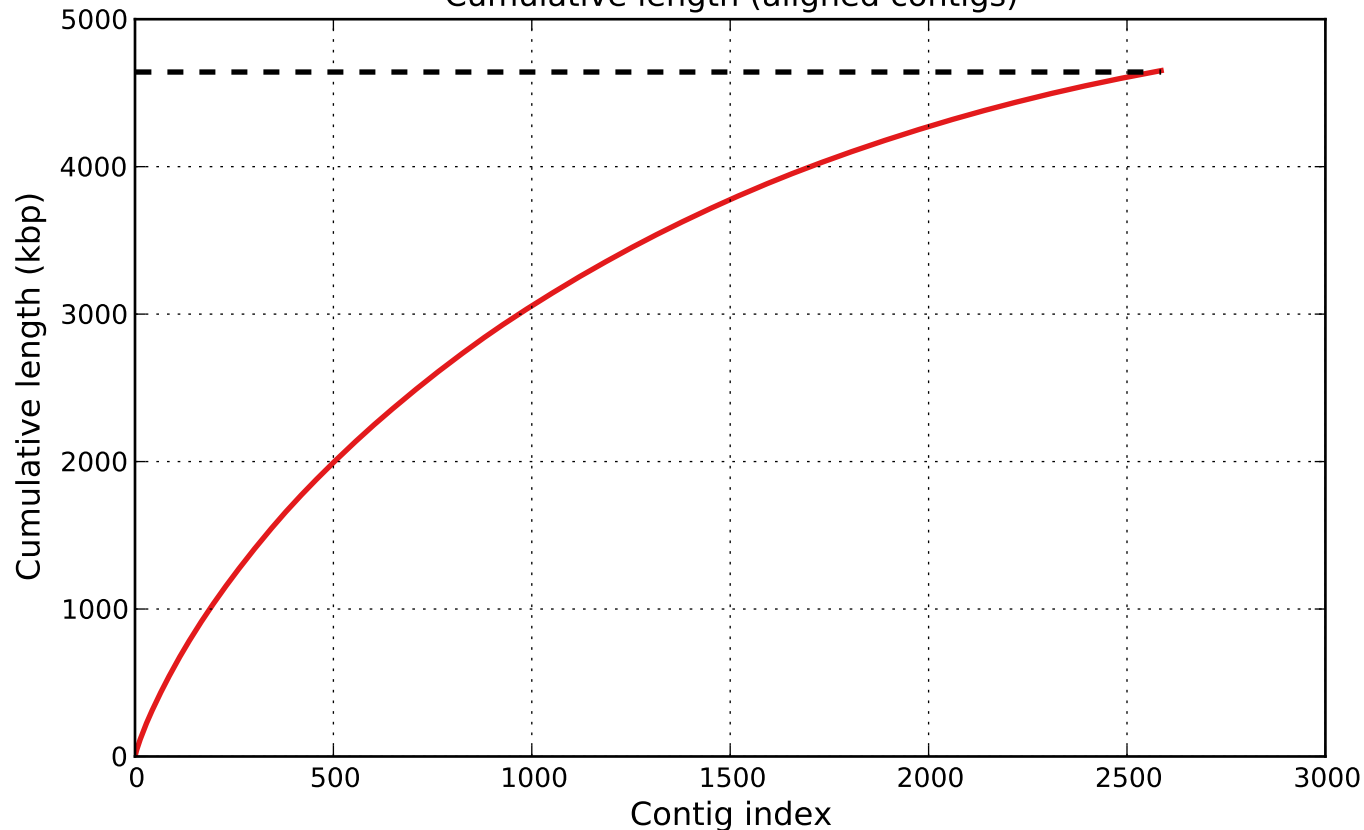


# Misassemblies

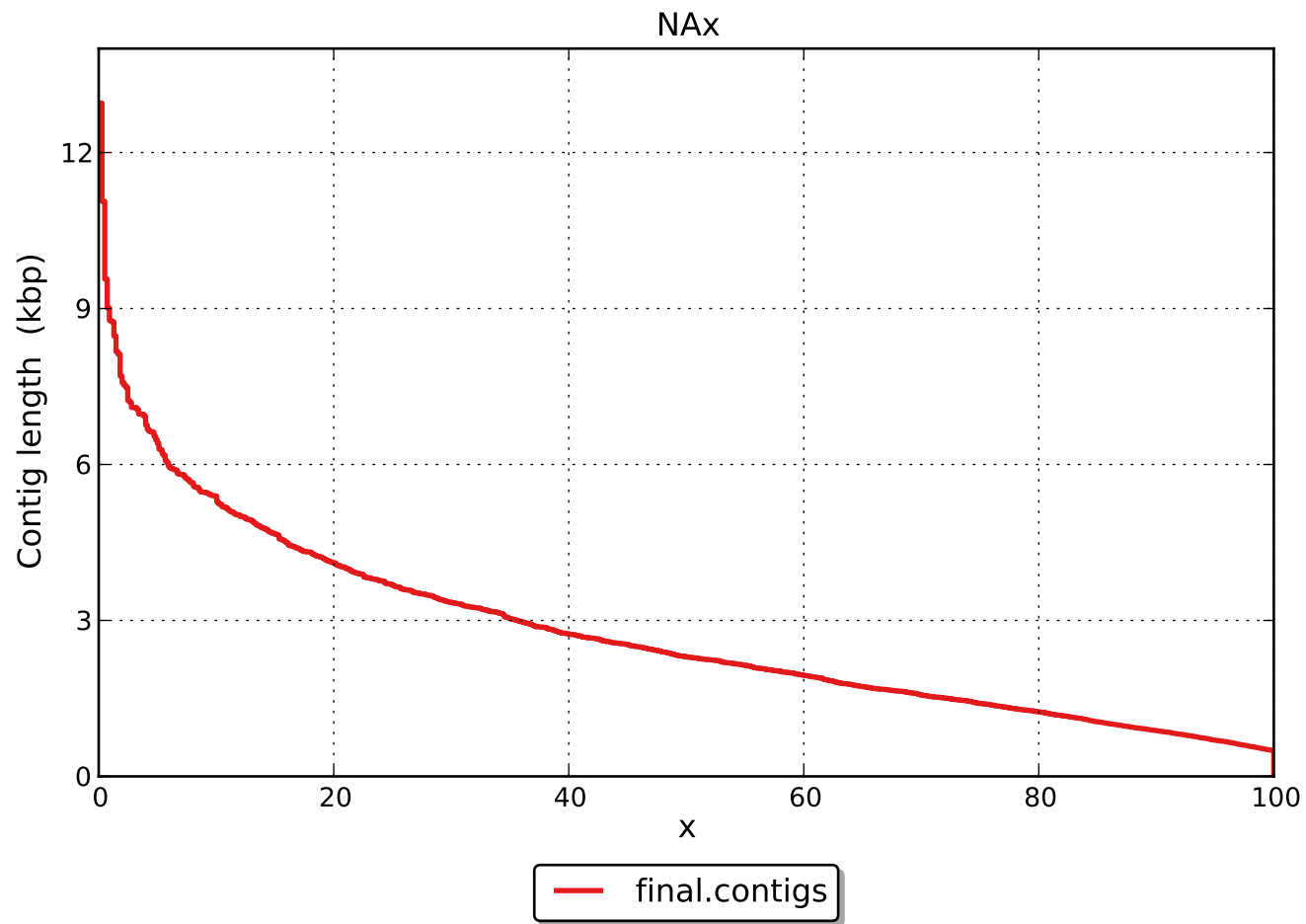




Cumulative length (aligned contigs)



— final.contigs    - - Reference



NGAx

