

Report

	final.contigs
# contigs (>= 1000 bp)	1140
# contigs (>= 5000 bp)	335
# contigs (>= 10000 bp)	62
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4788038
Total length (>= 5000 bp)	2679466
Total length (>= 10000 bp)	813583
Total length (>= 25000 bp)	33760
Total length (>= 50000 bp)	0
# contigs	1339
Largest contig	33760
Total length	4932156
Reference length	4857432
GC (℥)	52.24
Reference GC (℥)	52.23
N50	5381
NG50	5455
N75	3194
NG75	3276
L50	294
LG50	287
L75	591
LG75	573
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (℥)	99.493
Duplication ratio	1.021
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.46
# indels per 100 kbp	0.00
Largest alignment	33760
NA50	5381
NGA50	5455
NA75	3194
NGA75	3276
LA50	294
LGA50	287
LA75	591
LGA75	573

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

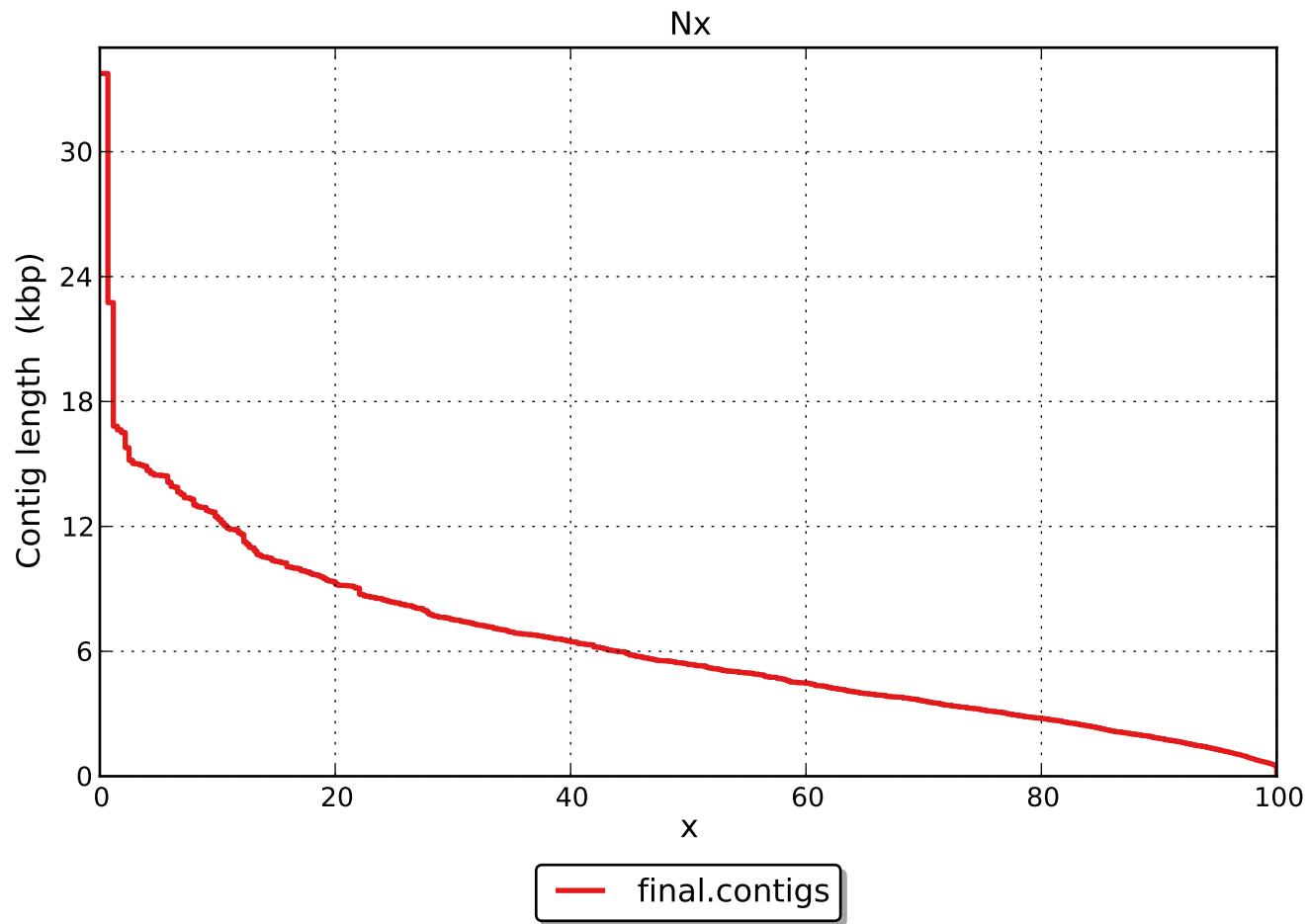
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	22
# indels	0
# short indels	0
# long indels	0
Indels length	0

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).

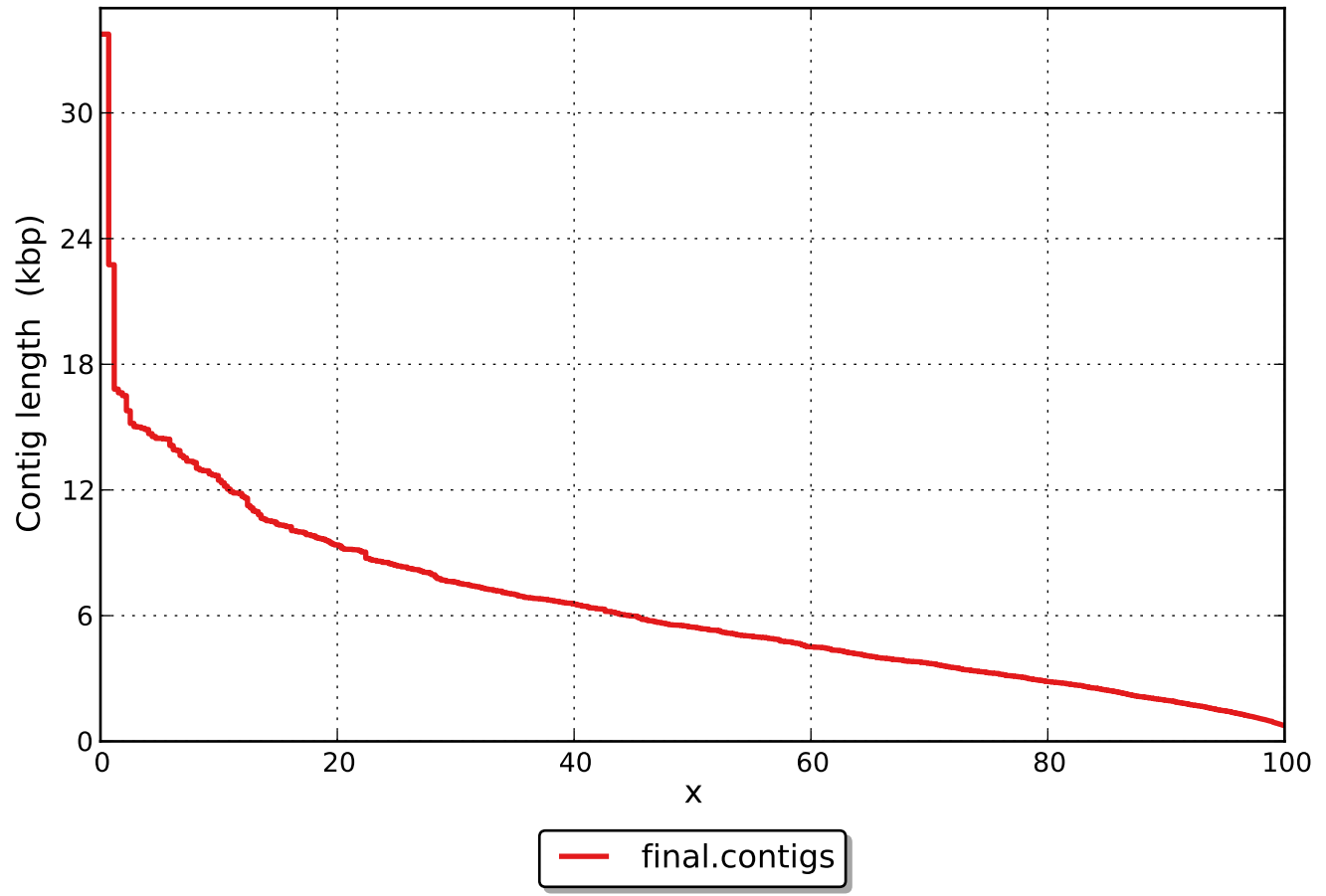
## Unaligned report

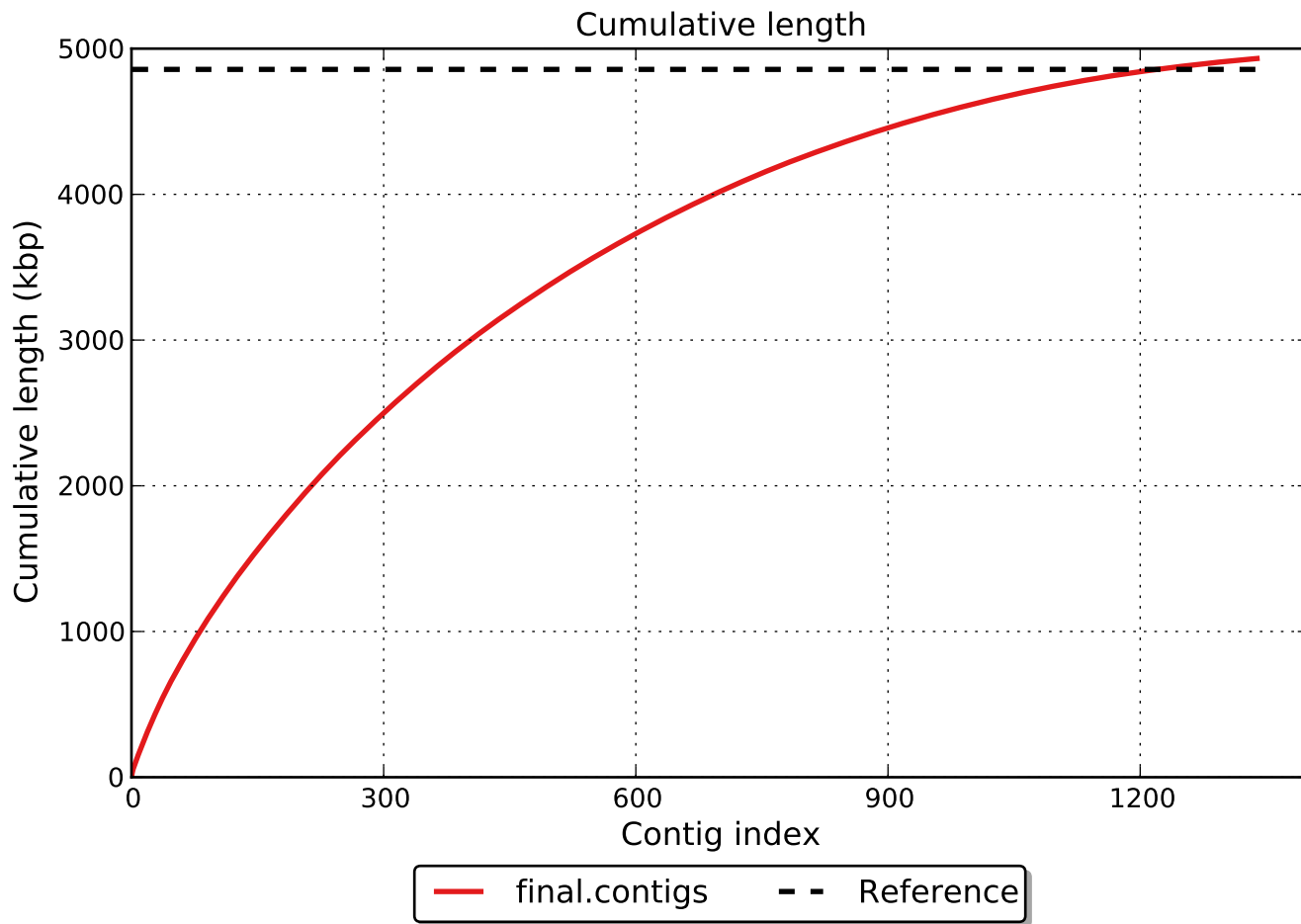
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

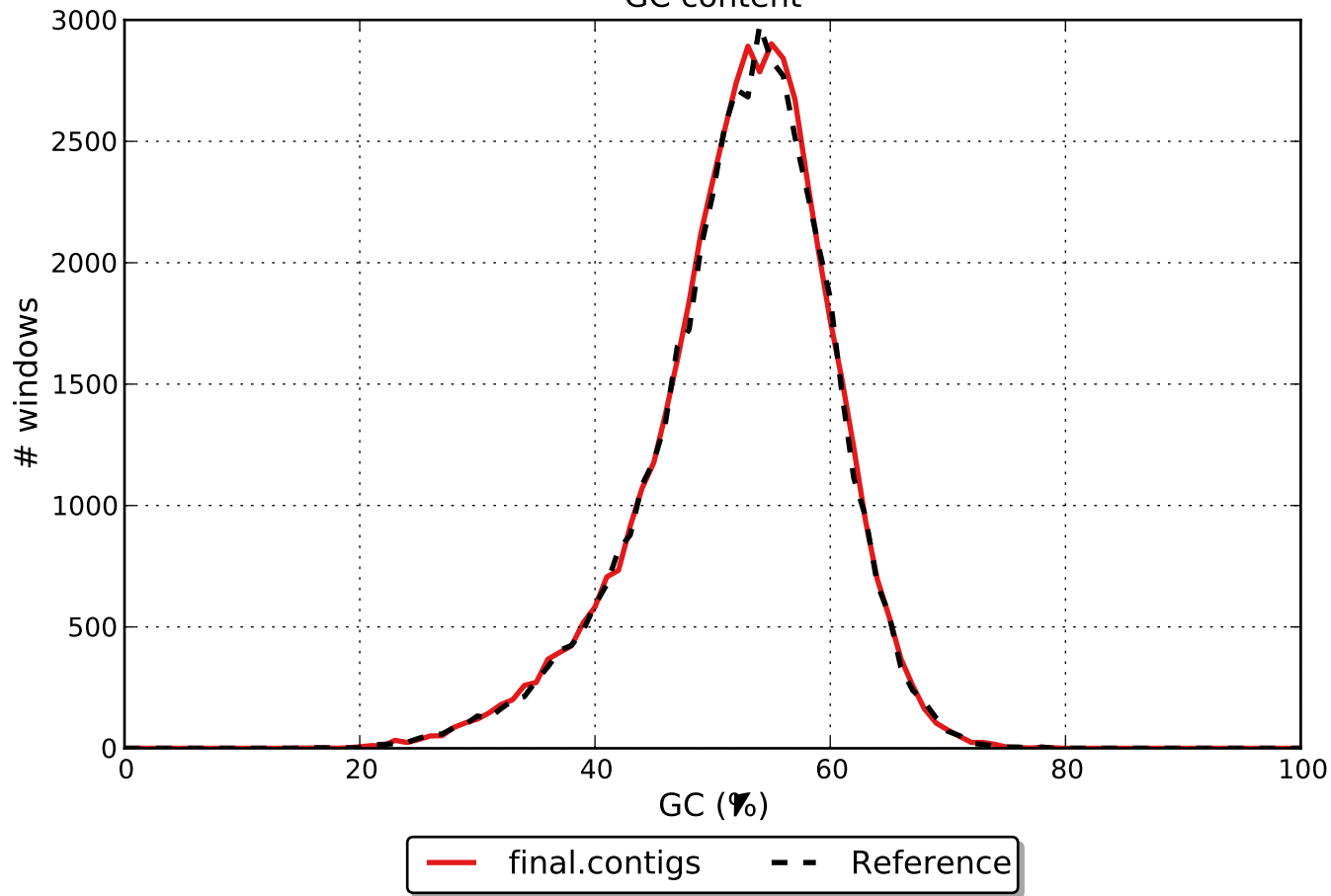


NGx





GC content

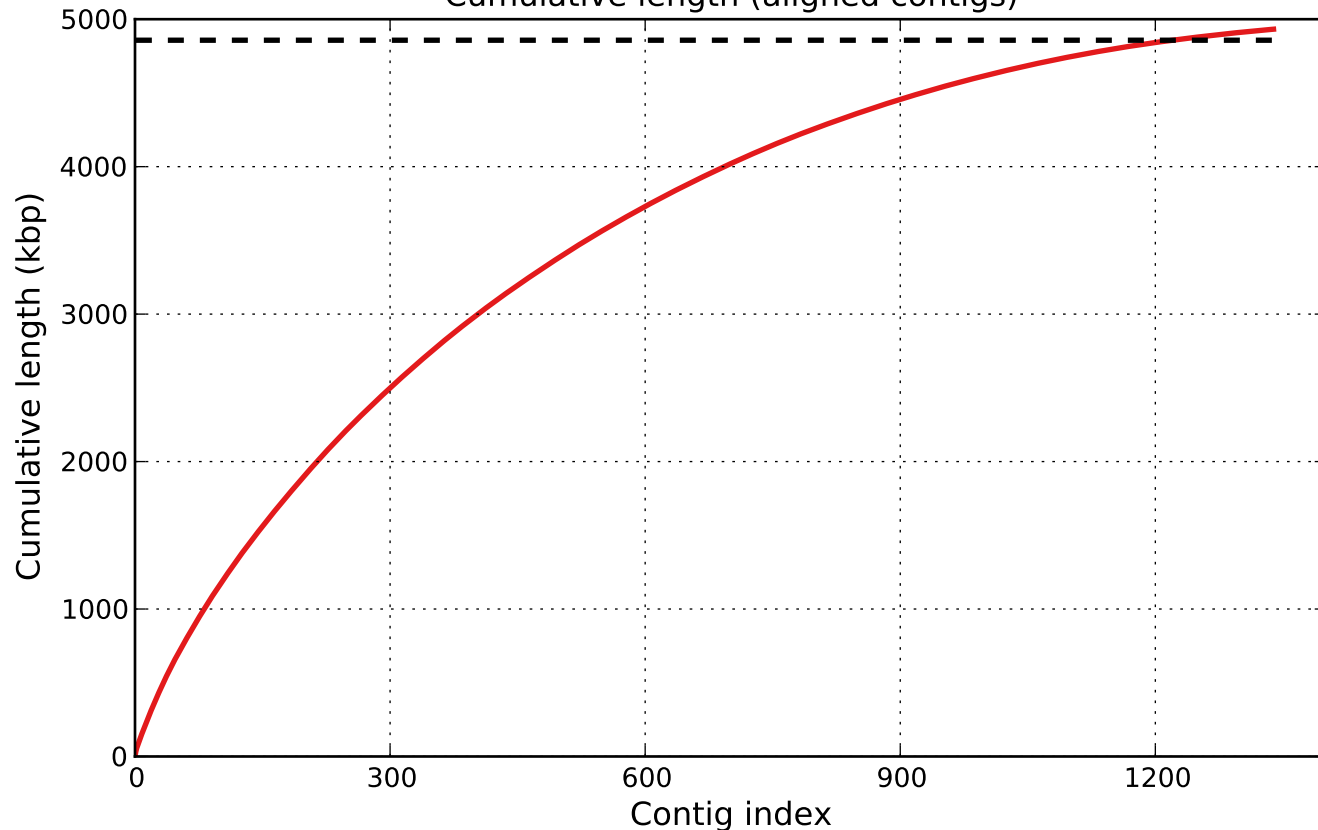


# Misassemblies



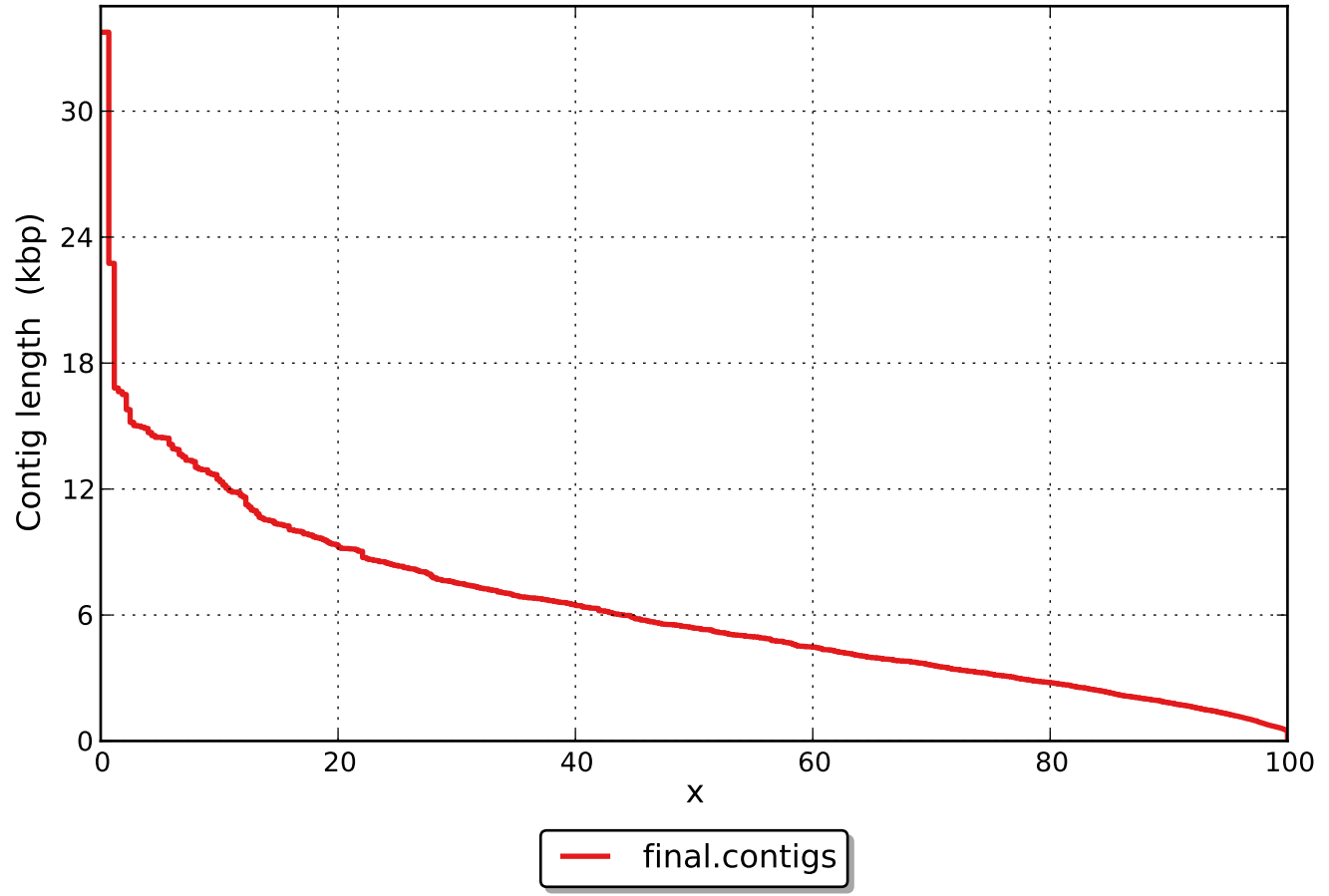


Cumulative length (aligned contigs)



— final.contigs    - - Reference

NAx



# NGAx

