

Report

	final.contigs
# contigs (>= 1000 bp)	1620
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	2491835
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	4279
Largest contig	4666
Total length	4375877
Reference length	4857432
GC (℥)	52.17
Reference GC (℥)	52.22
N50	1102
NG50	1024
N75	767
NG75	676
L50	1332
LG50	1558
L75	2523
LG75	3025
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (℥)	85.567
Duplication ratio	1.053
# N's per 100 kbp	0.00
# mismatches per 100 kbp	75.79
# indels per 100 kbp	0.05
Largest alignment	4666
NA50	1102
NGA50	1024
NA75	767
NGA75	676
LA50	1332
LGA50	1558
LA75	2523
LGA75	3025

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	3150
# indels	2
# short indels	2
# long indels	0
Indels length	2

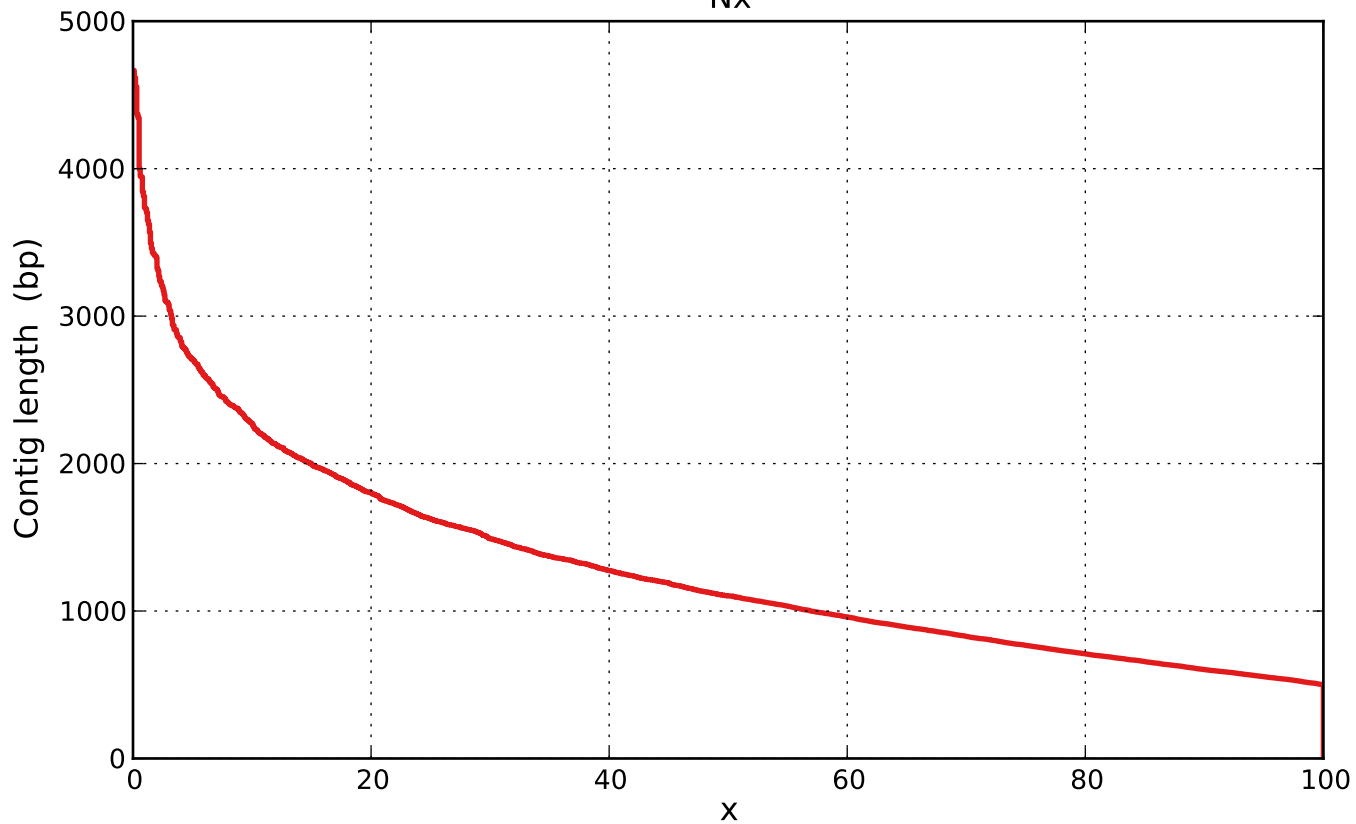
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## 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

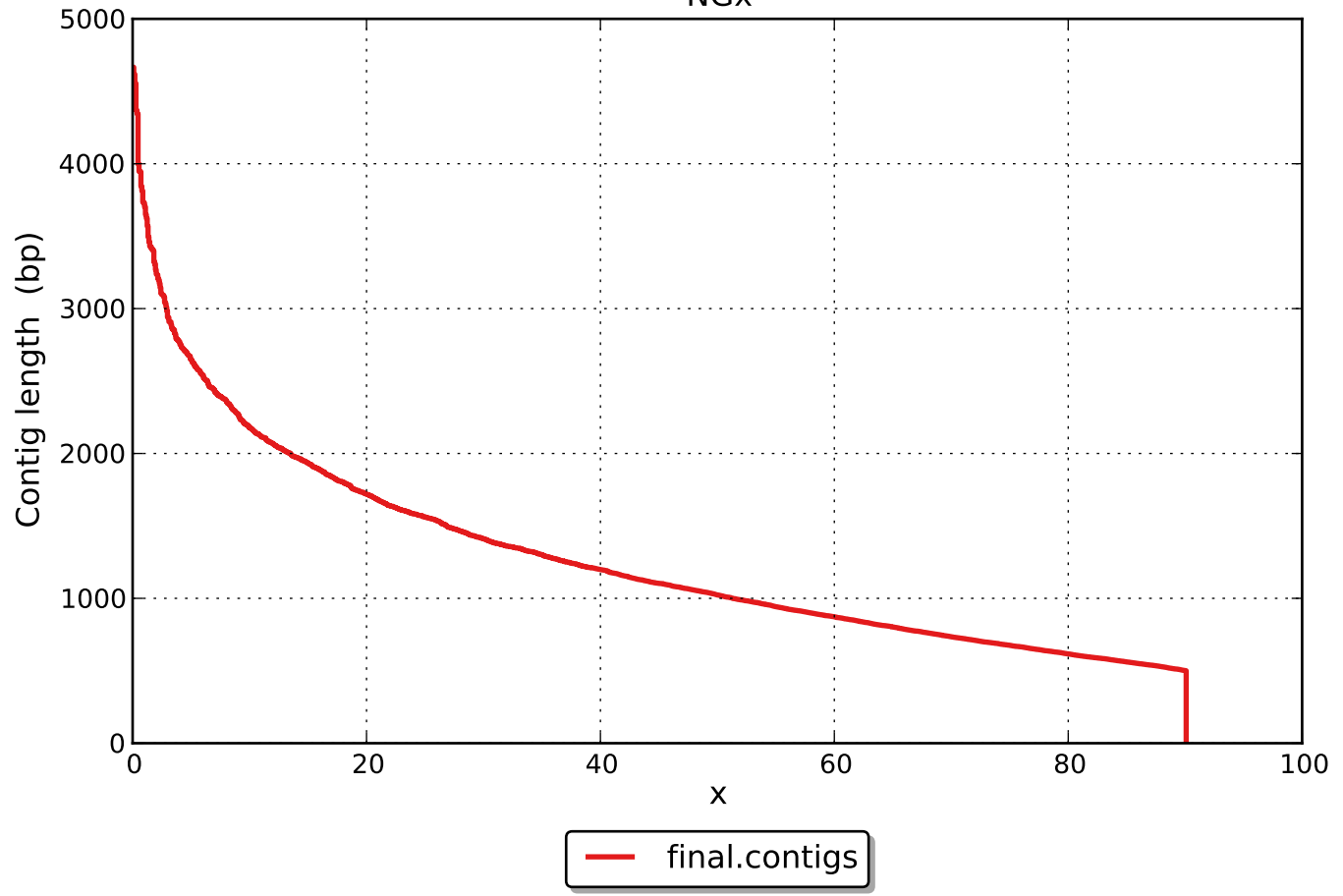
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

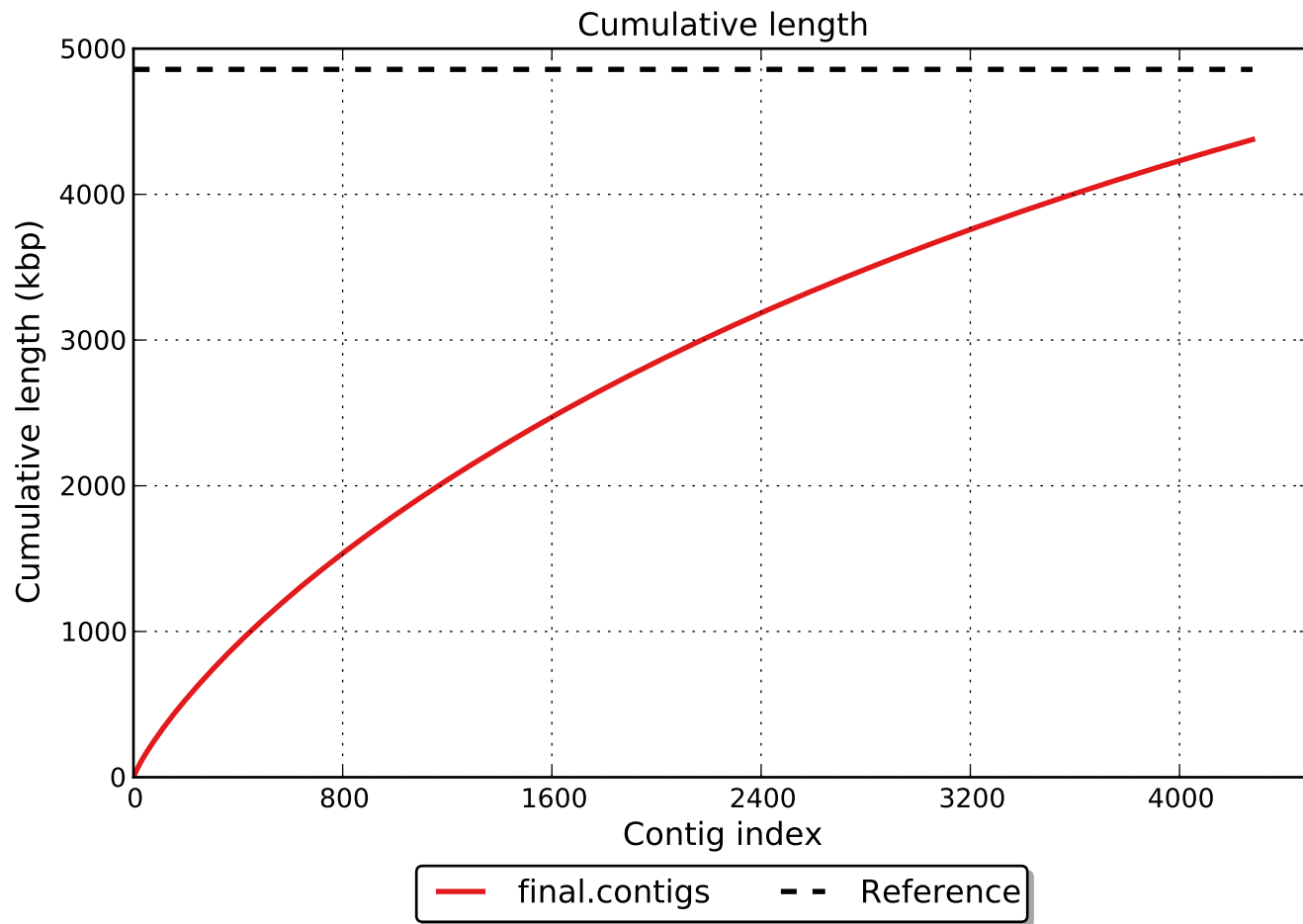
Nx



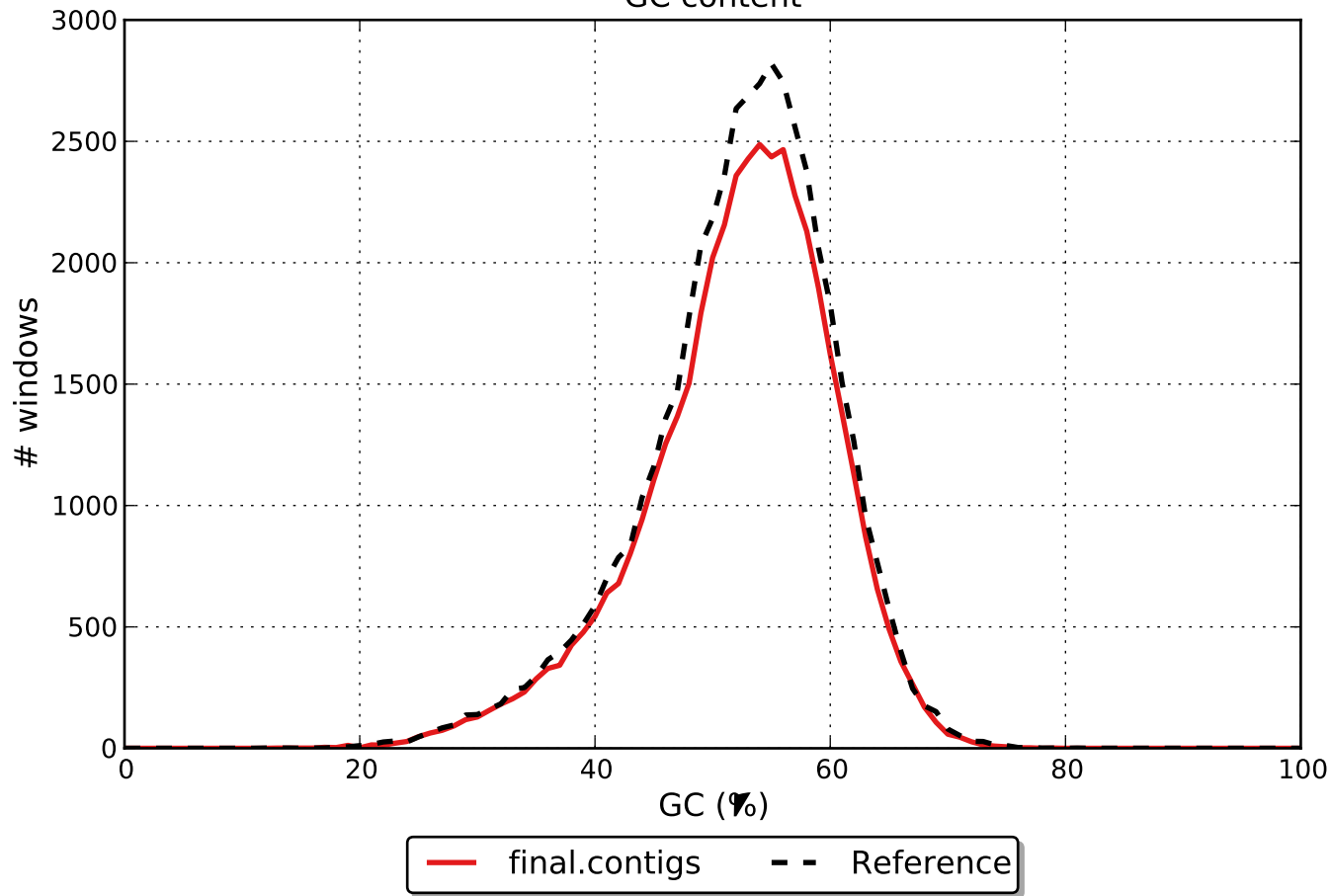
— final.contigs

NGx





GC content

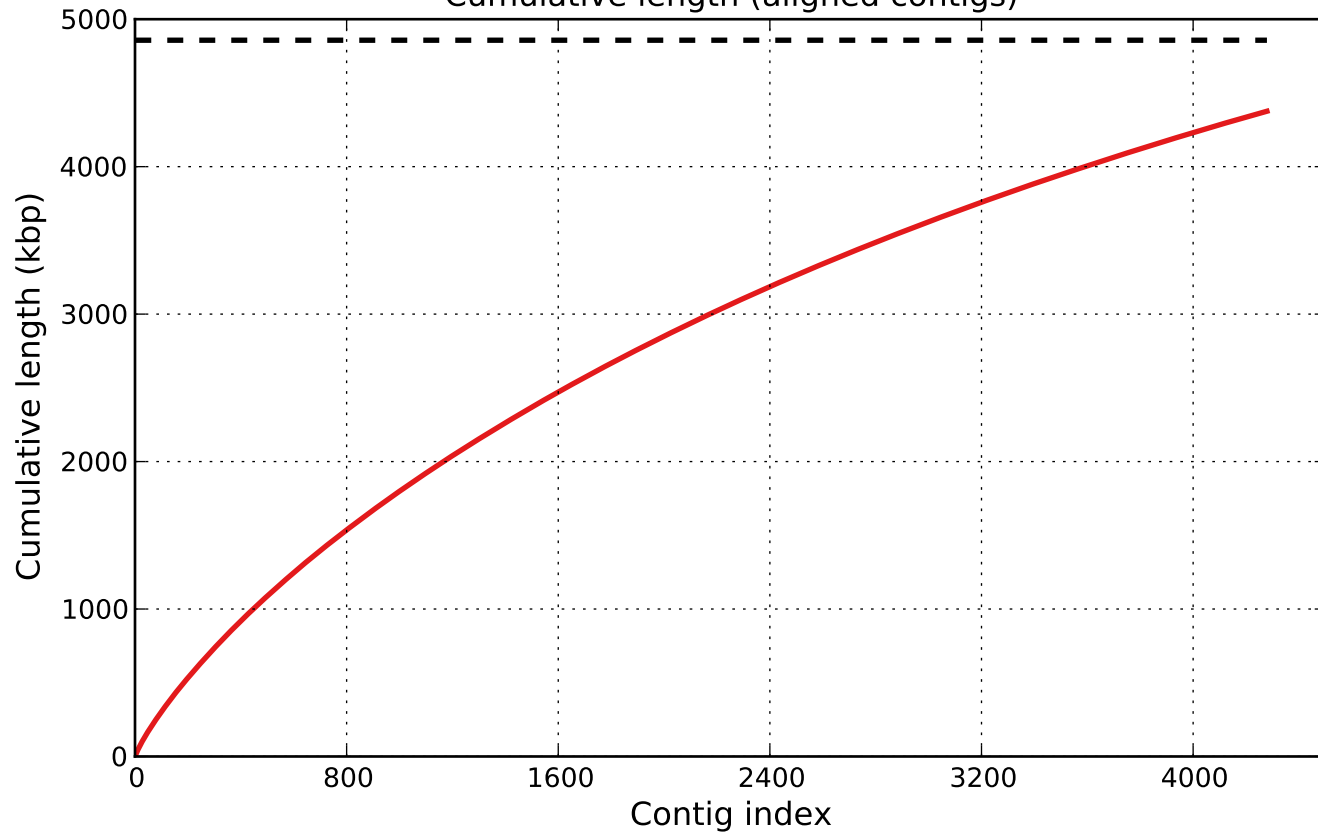


# Misassemblies



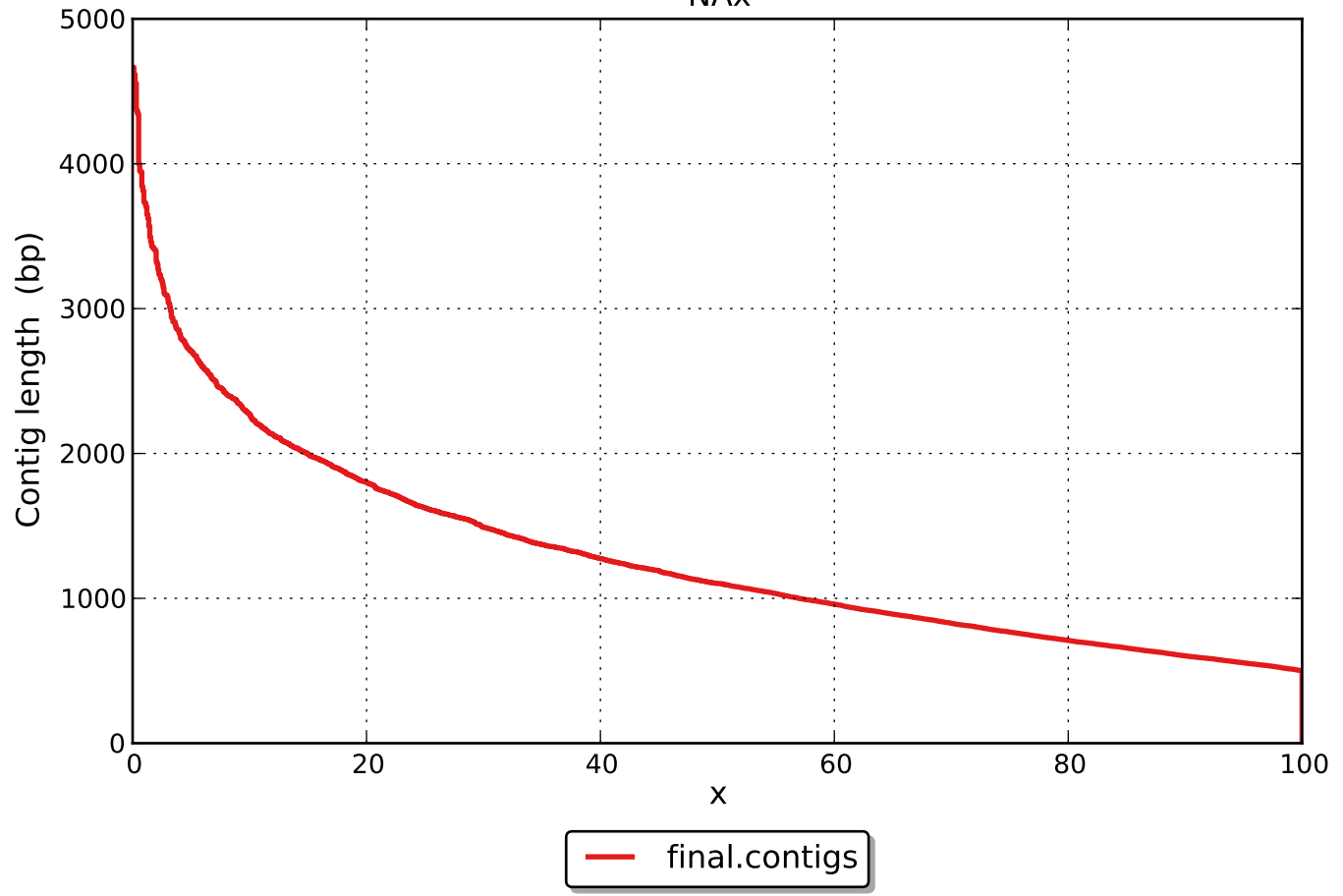


Cumulative length (aligned contigs)

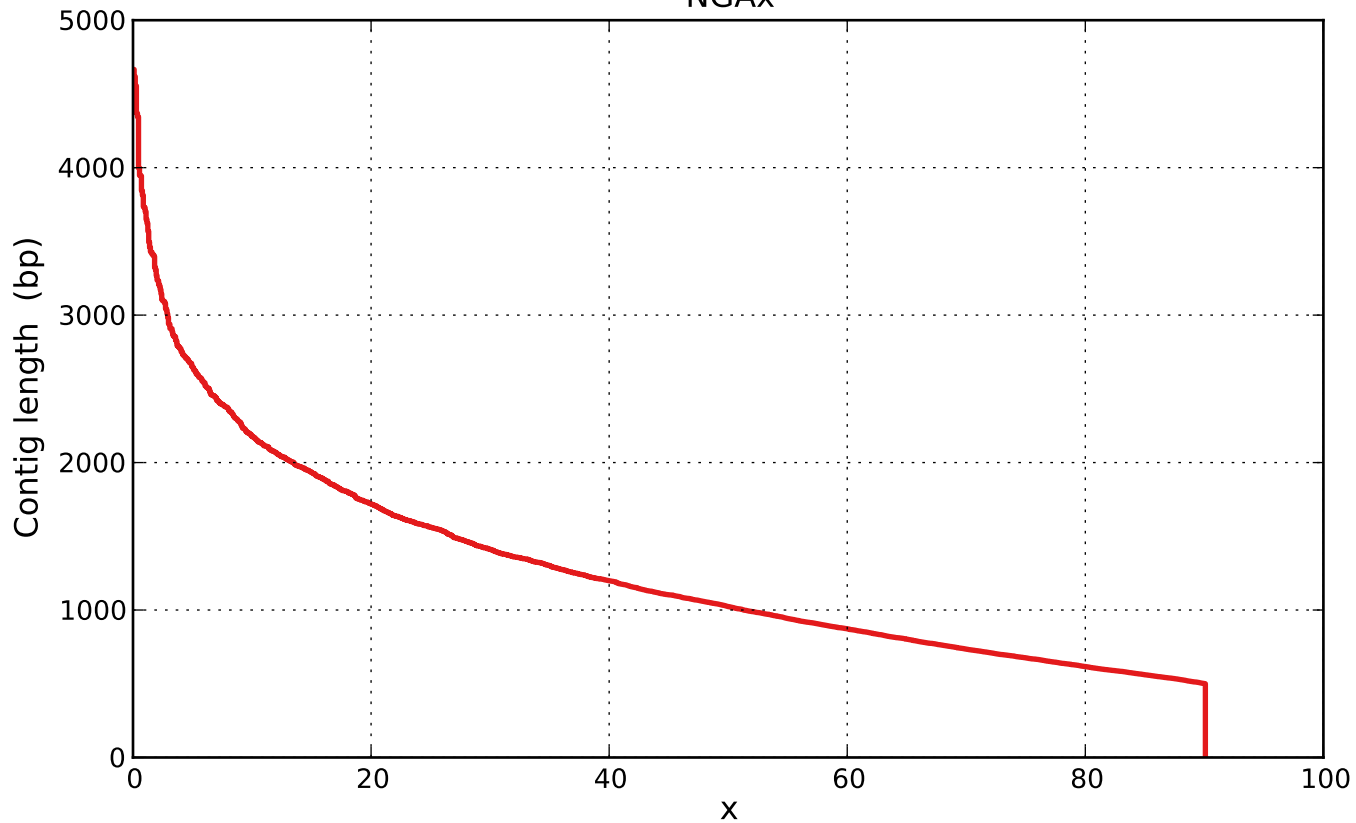


— final.contigs    - - Reference

NAx



NGAx



— final.contigs