

Report

	final.contigs
# contigs (>= 1000 bp)	1572
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	2422631
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	4116
Largest contig	4666
Total length	4225954
Reference length	4857432
GC (℥)	52.14
Reference GC (℥)	52.22
N50	1106
NG50	998
N75	771
NG75	646
L50	1279
LG50	1579
L75	2423
LG75	3096
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (℥)	83.196
Duplication ratio	1.046
# N's per 100 kbp	0.00
# mismatches per 100 kbp	40.73
# indels per 100 kbp	0.05
Largest alignment	4666
NA50	1106
NGA50	998
NA75	771
NGA75	646
LA50	1279
LGA50	1579
LA75	2423
LGA75	3096

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	1646
# indels	2
# short indels	2
# long indels	0
Indels length	2

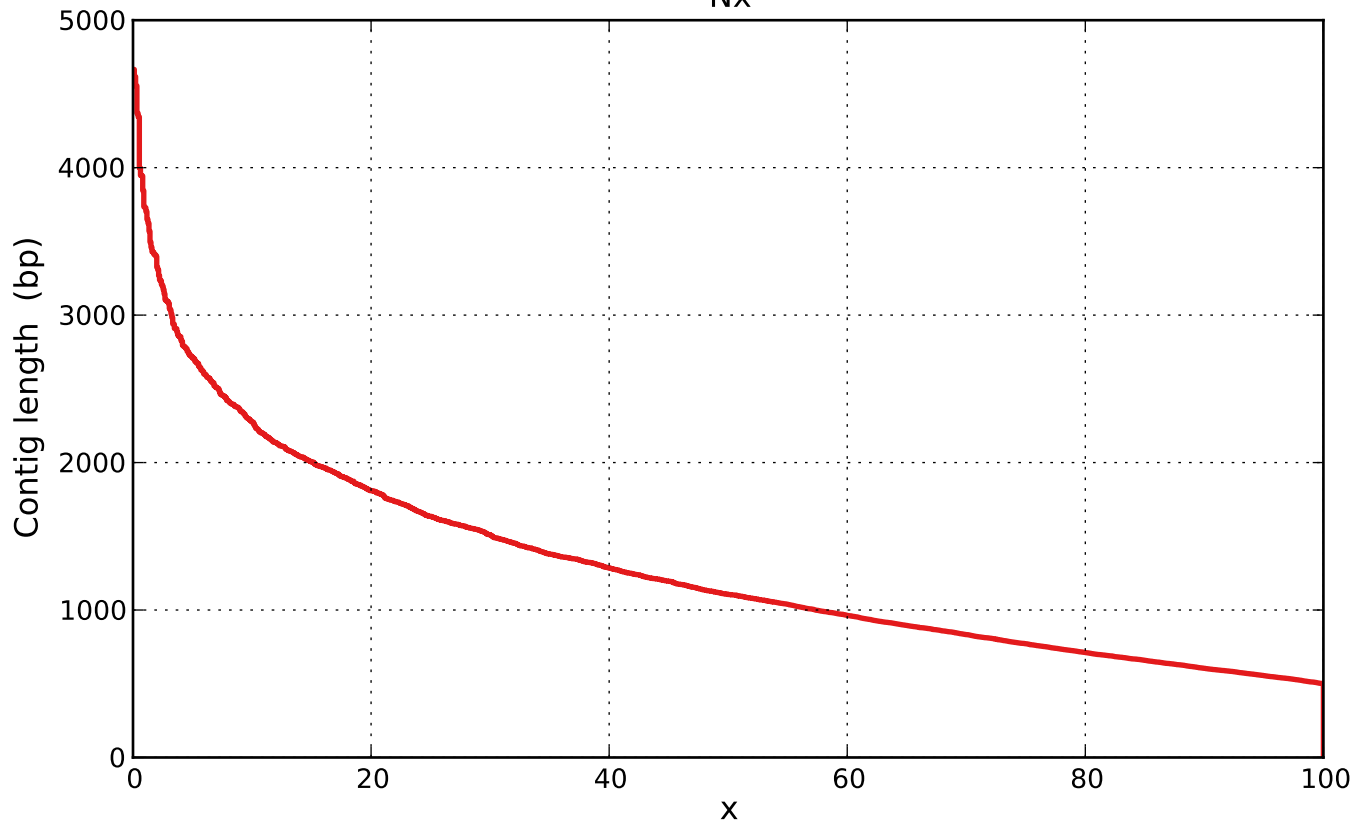
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## 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

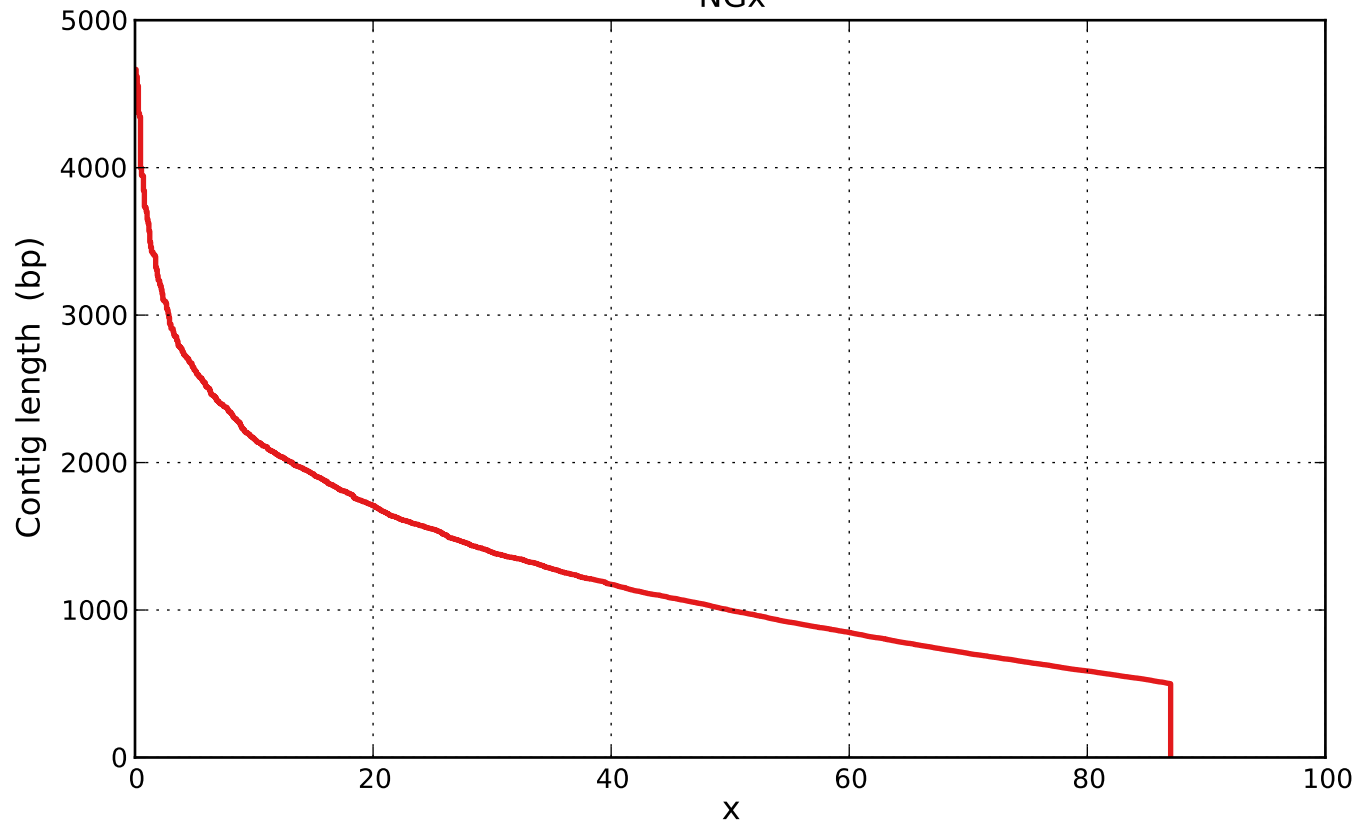
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

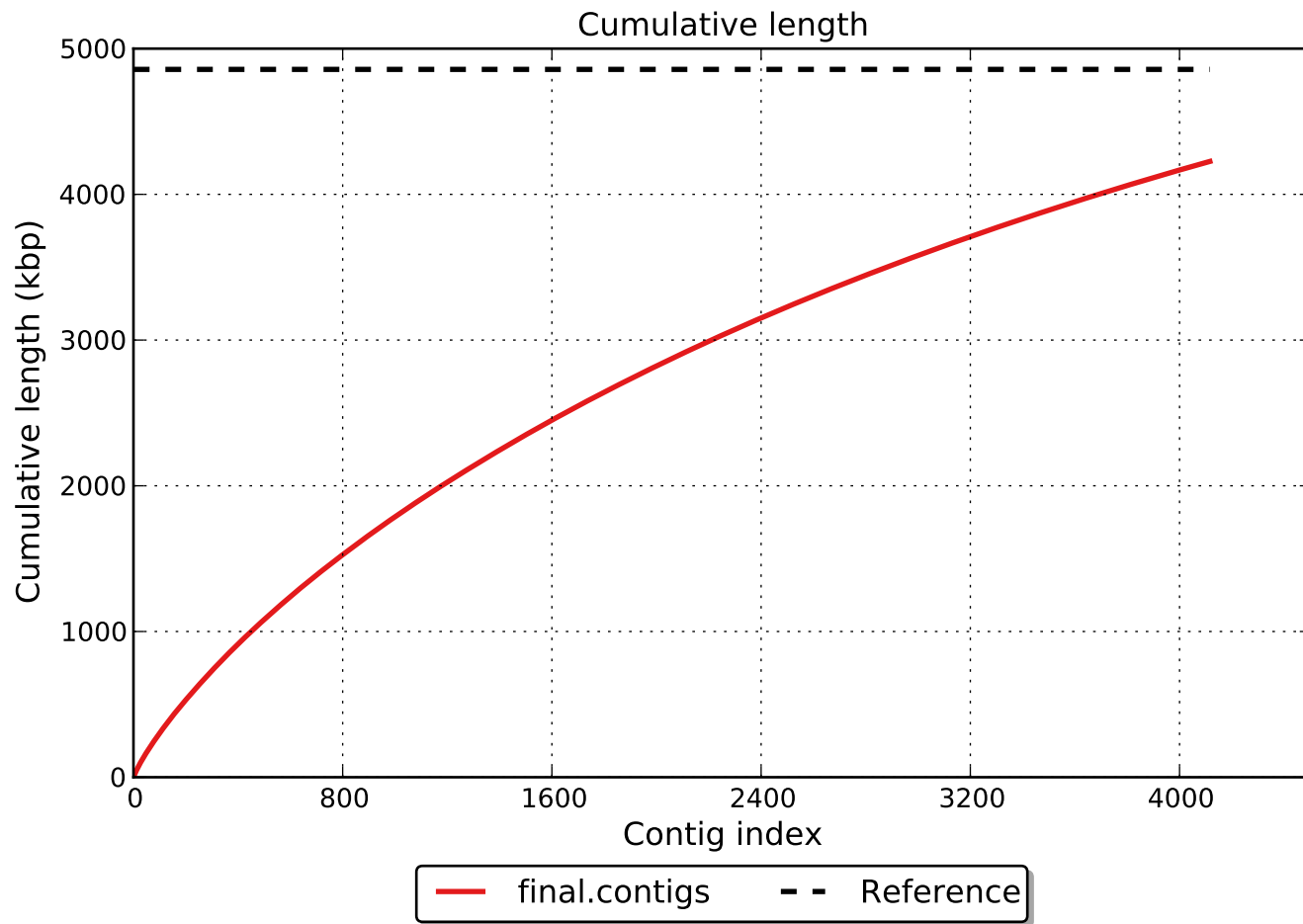


— final.contigs

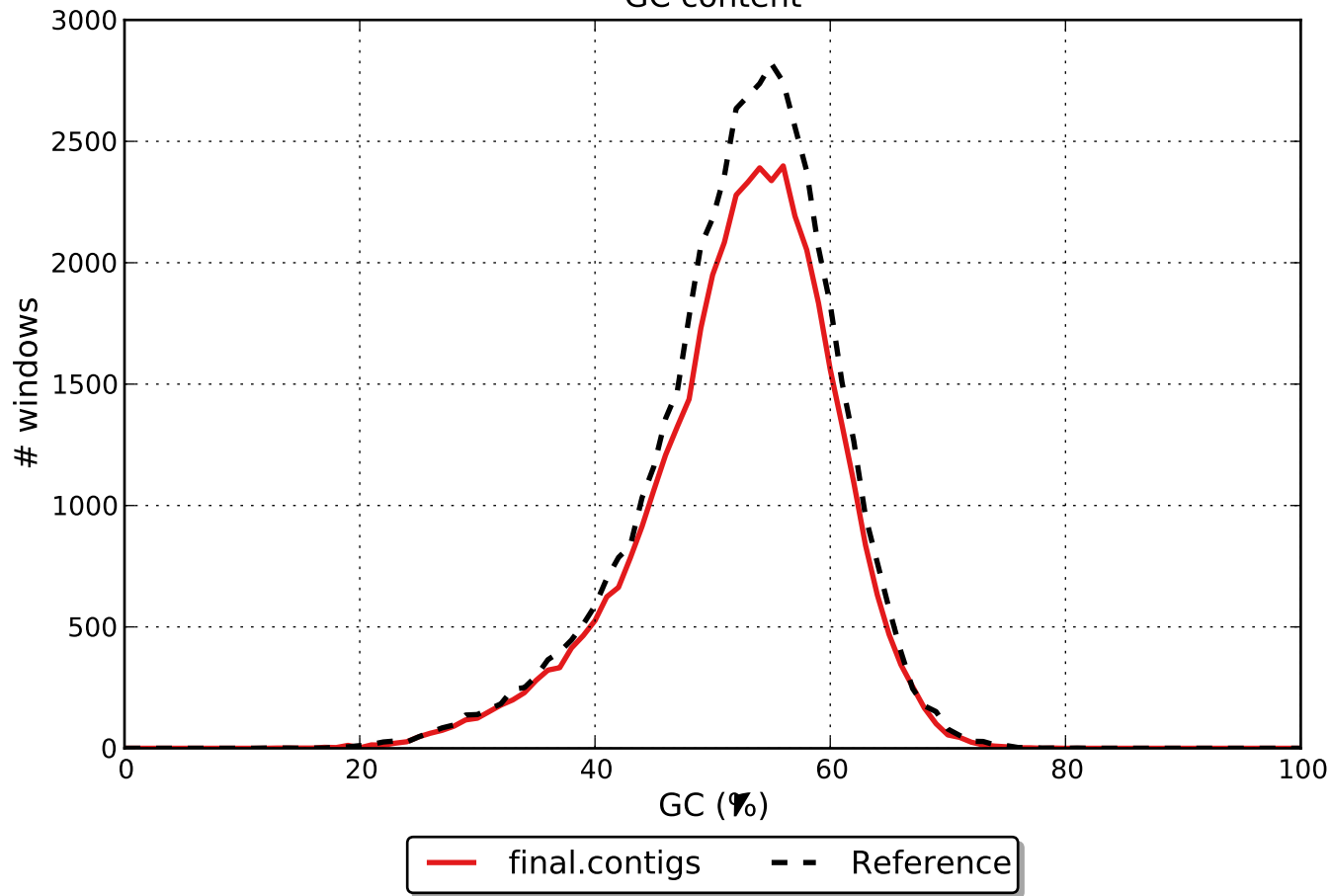
NGx



— final.contigs



GC content

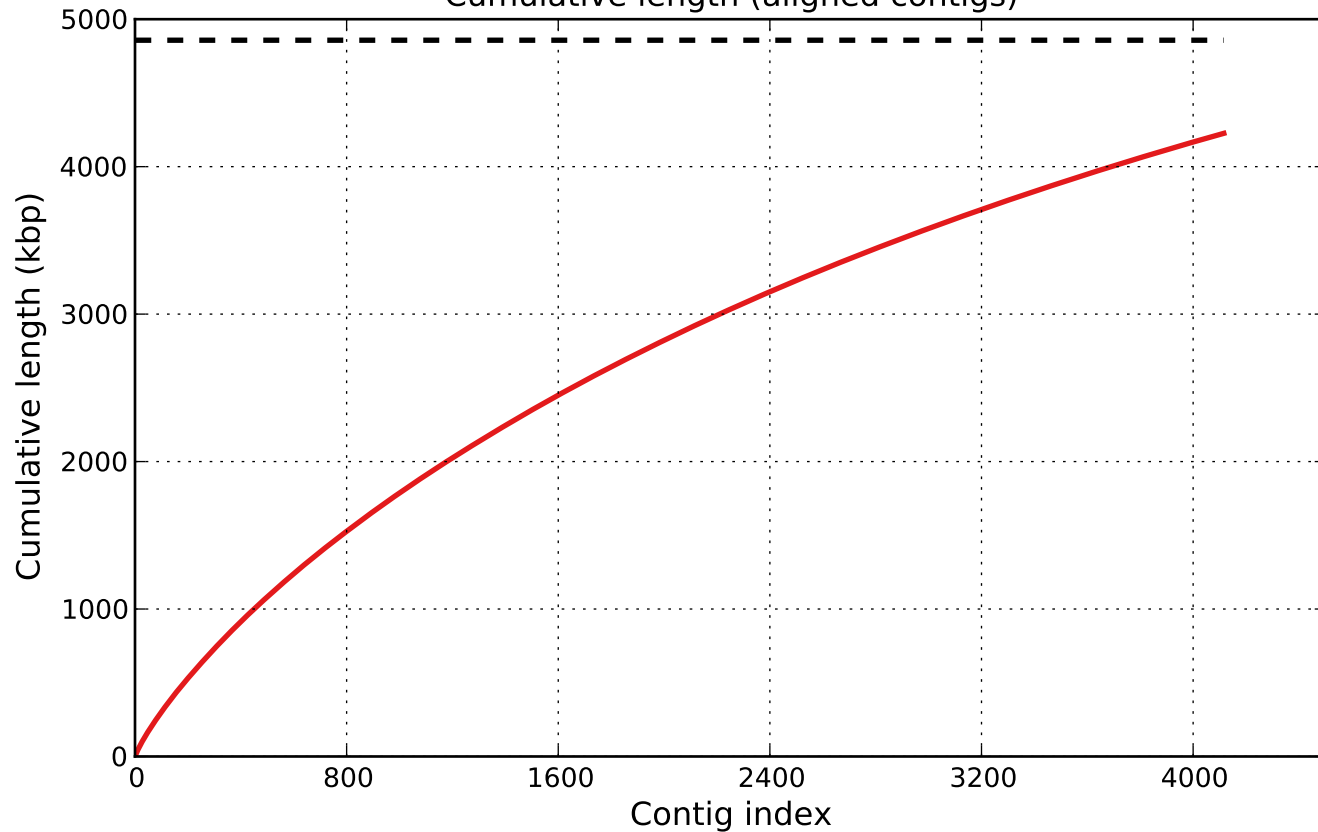


# Misassemblies



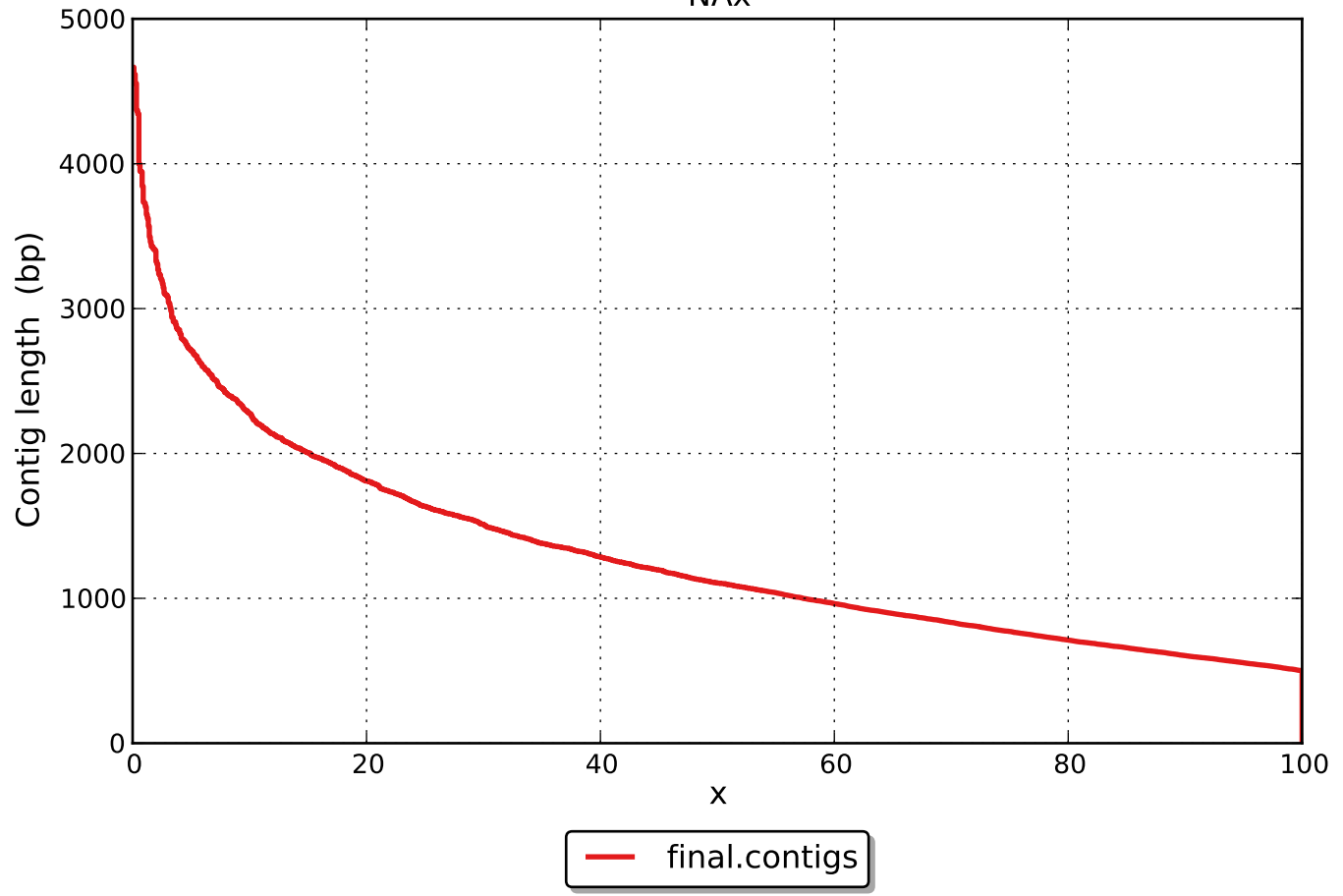


Cumulative length (aligned contigs)



— final.contigs    - - Reference

NAx



NGAx

