

## Report

	final.contigs
# contigs (>= 1000 bp)	1723
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	2851451
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	3866
Largest contig	4997
Total length	4386910
Reference length	4641652
GC (%)	50.80
Reference GC (%)	50.78
N50	1288
NG50	1227
N75	853
NG75	786
L50	1146
LG50	1247
L75	2200
LG75	2434
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 4 part
Unaligned length	263
Genome fraction (%)	88.931
Duplication ratio	1.063
# N's per 100 kbp	0.00
# mismatches per 100 kbp	119.94
# indels per 100 kbp	0.12
Largest alignment	4997
NA50	1288
NGA50	1227
NA75	853
NGA75	786
LA50	1146
LGA50	1247
LA75	2200
LGA75	2434

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	1
# mismatches	4951
# indels	5
# short indels	5
# long indels	0
Indels length	5

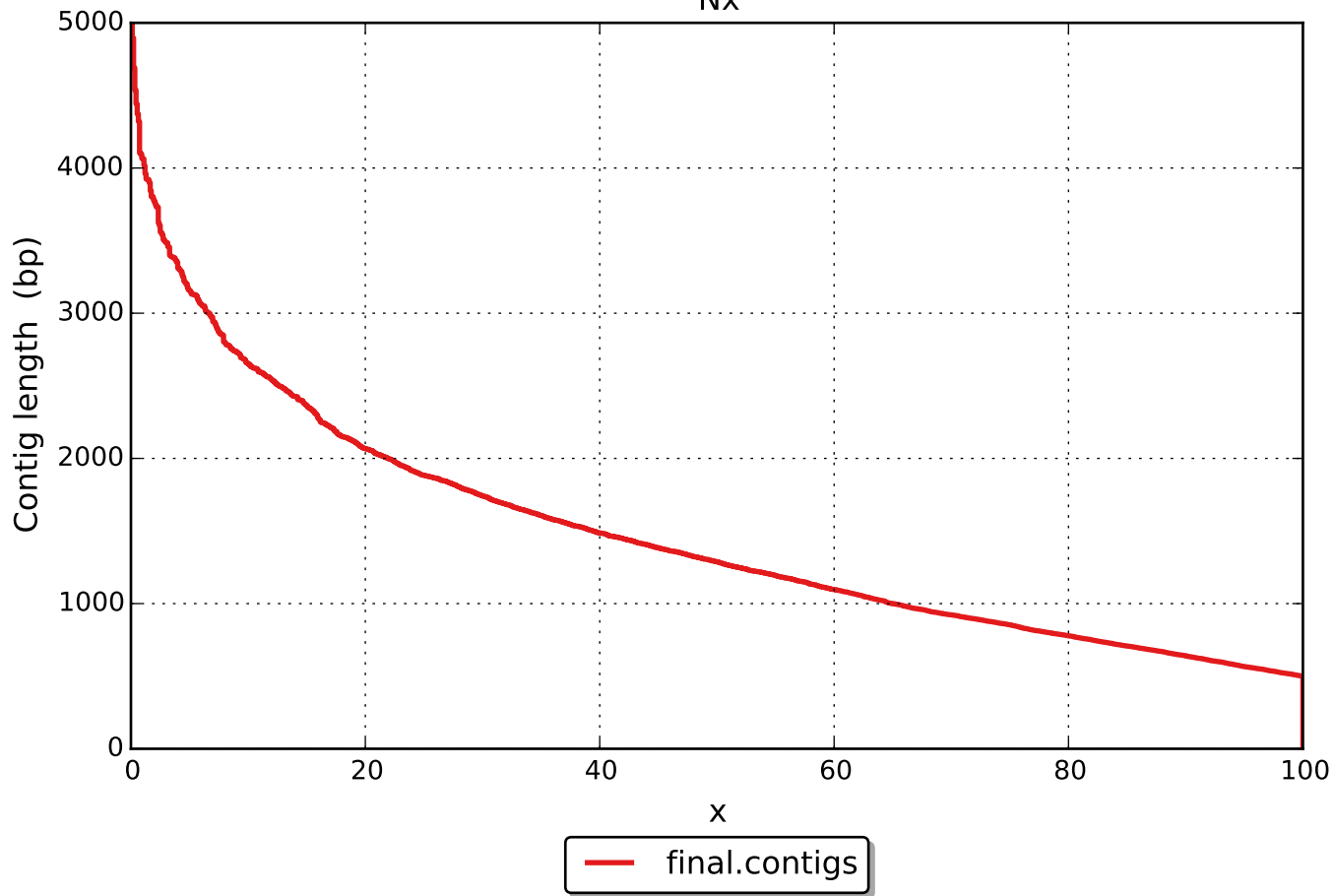
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

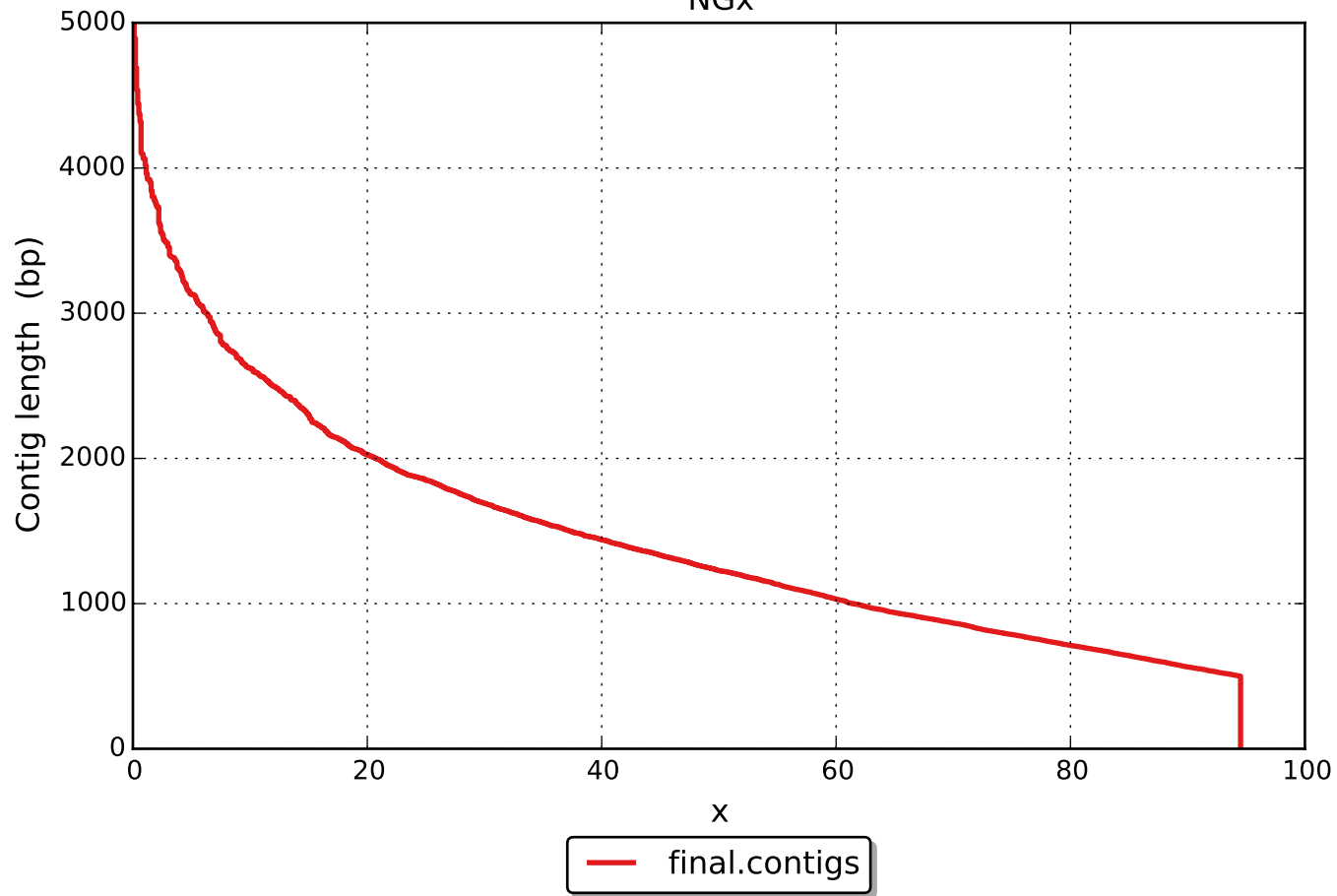
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	4
# with misassembly	0
# both parts are significant	0
Partially unaligned length	263
# N's	0

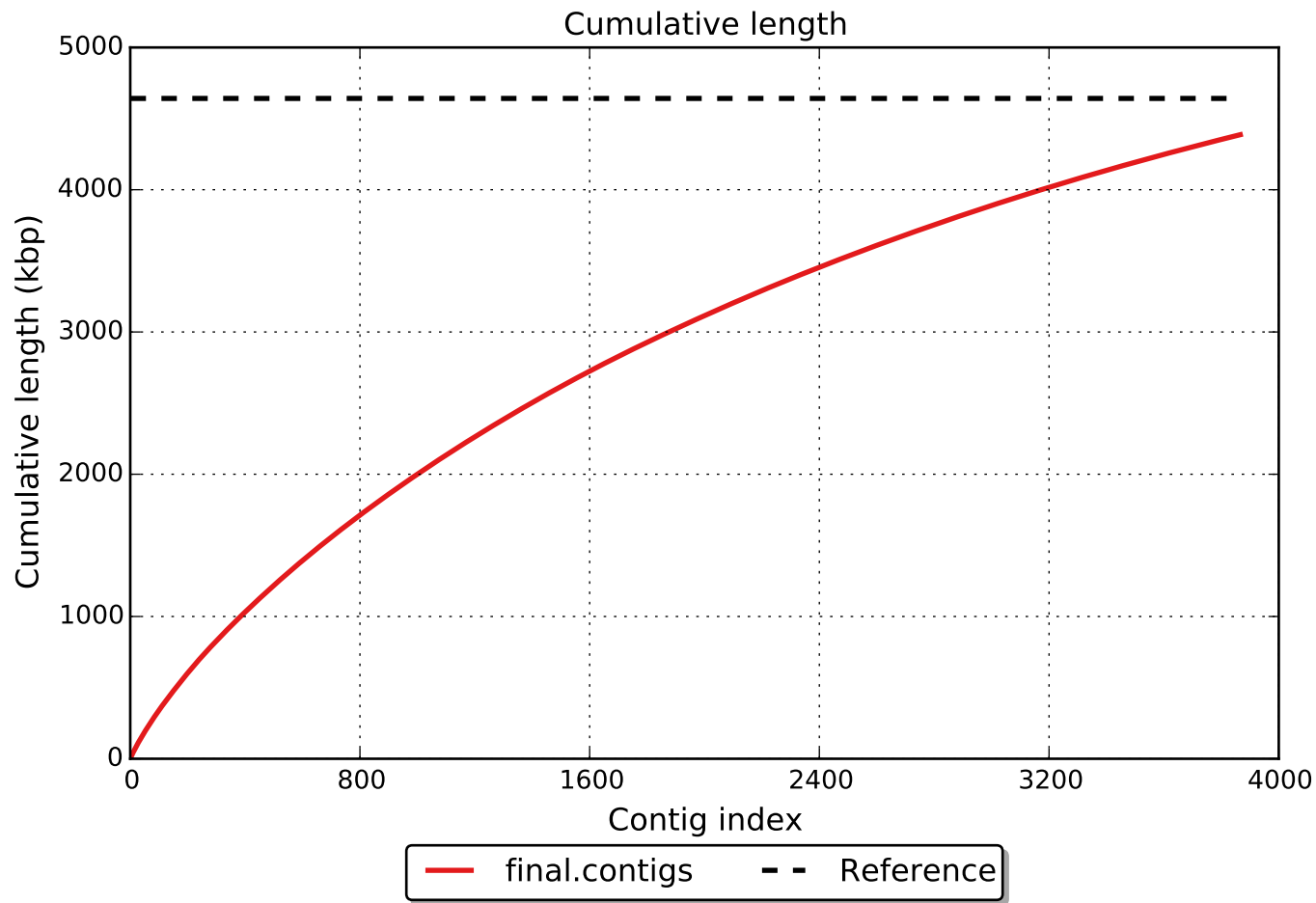
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

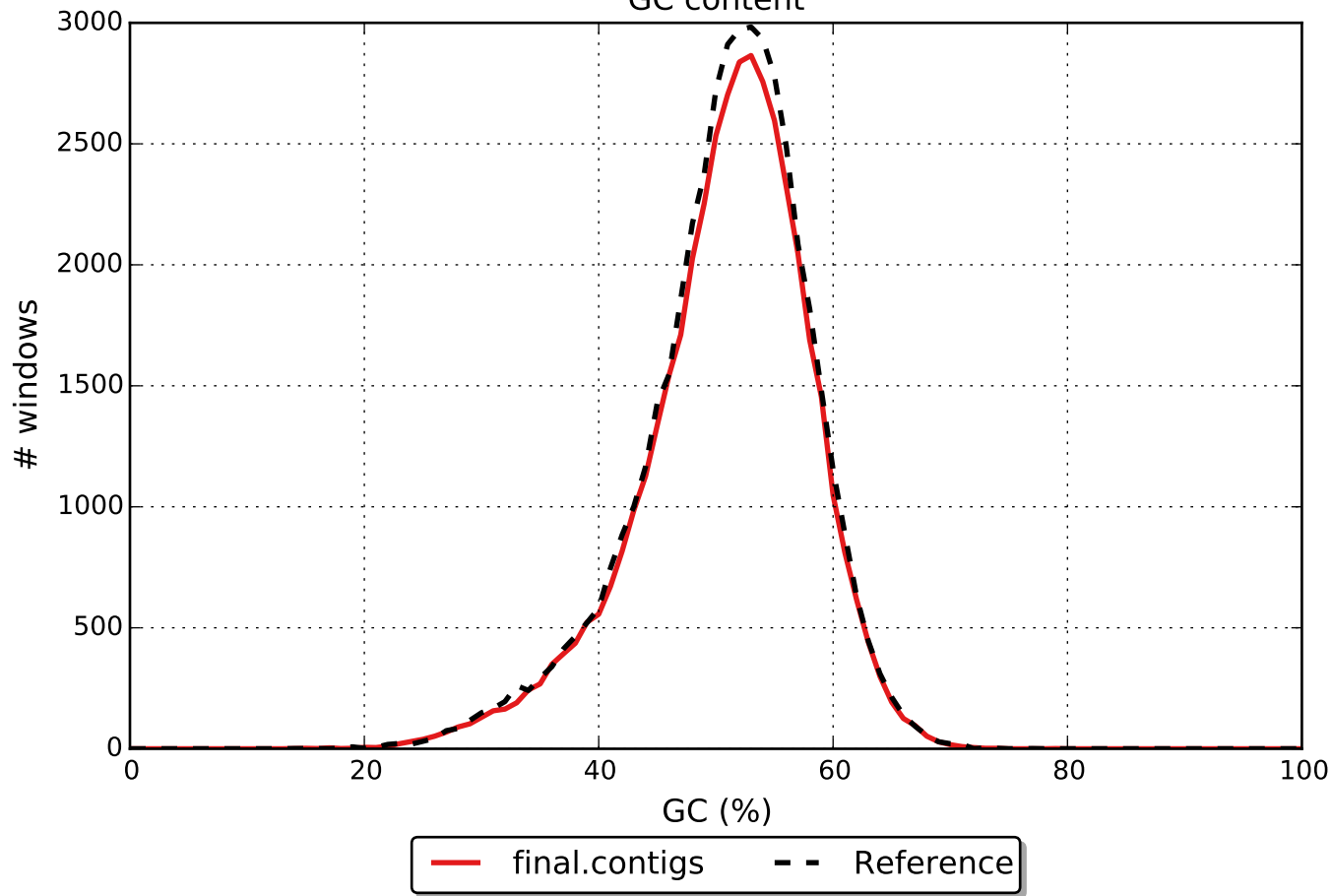


NGx





GC content

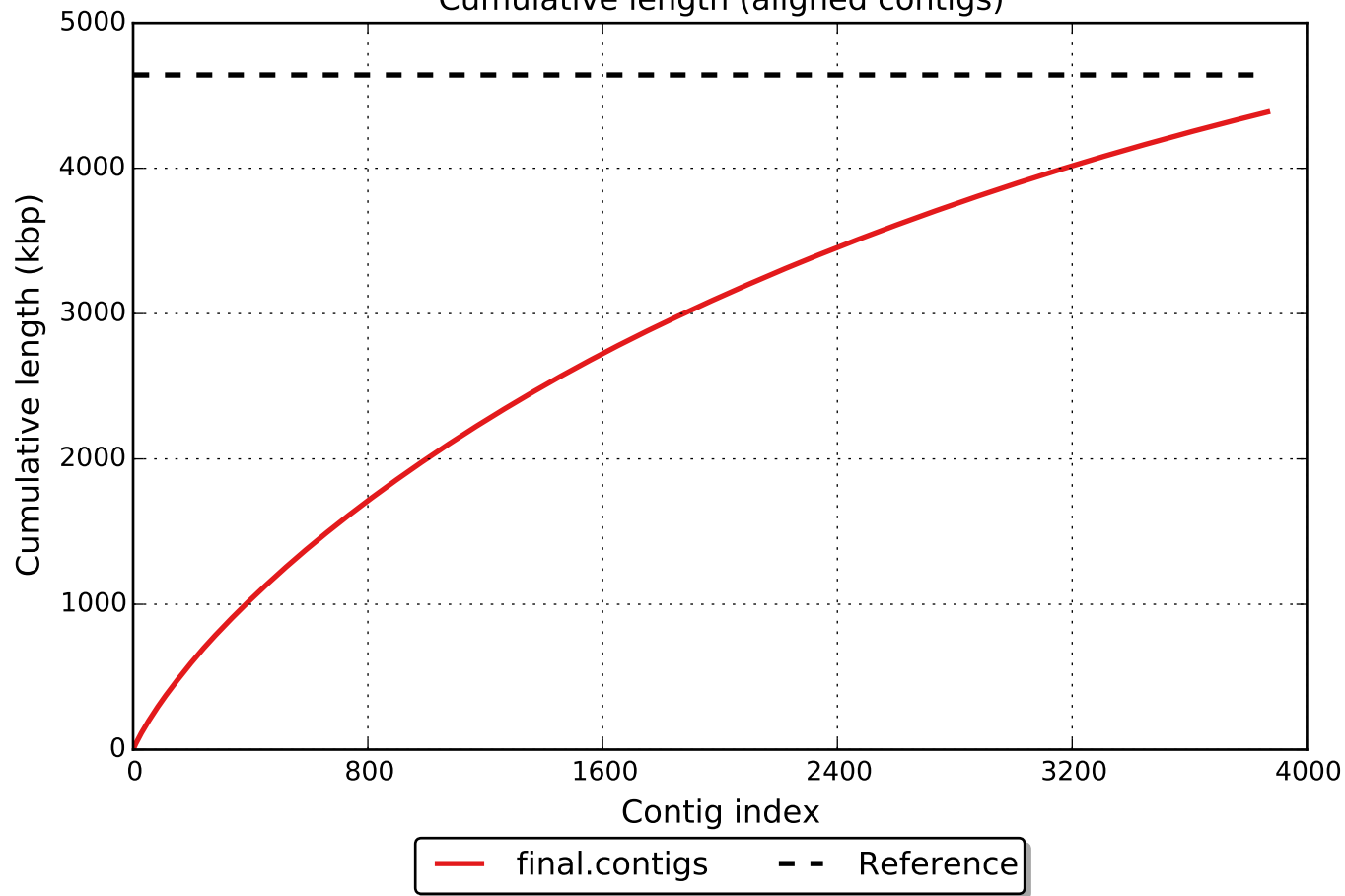


# Misassemblies

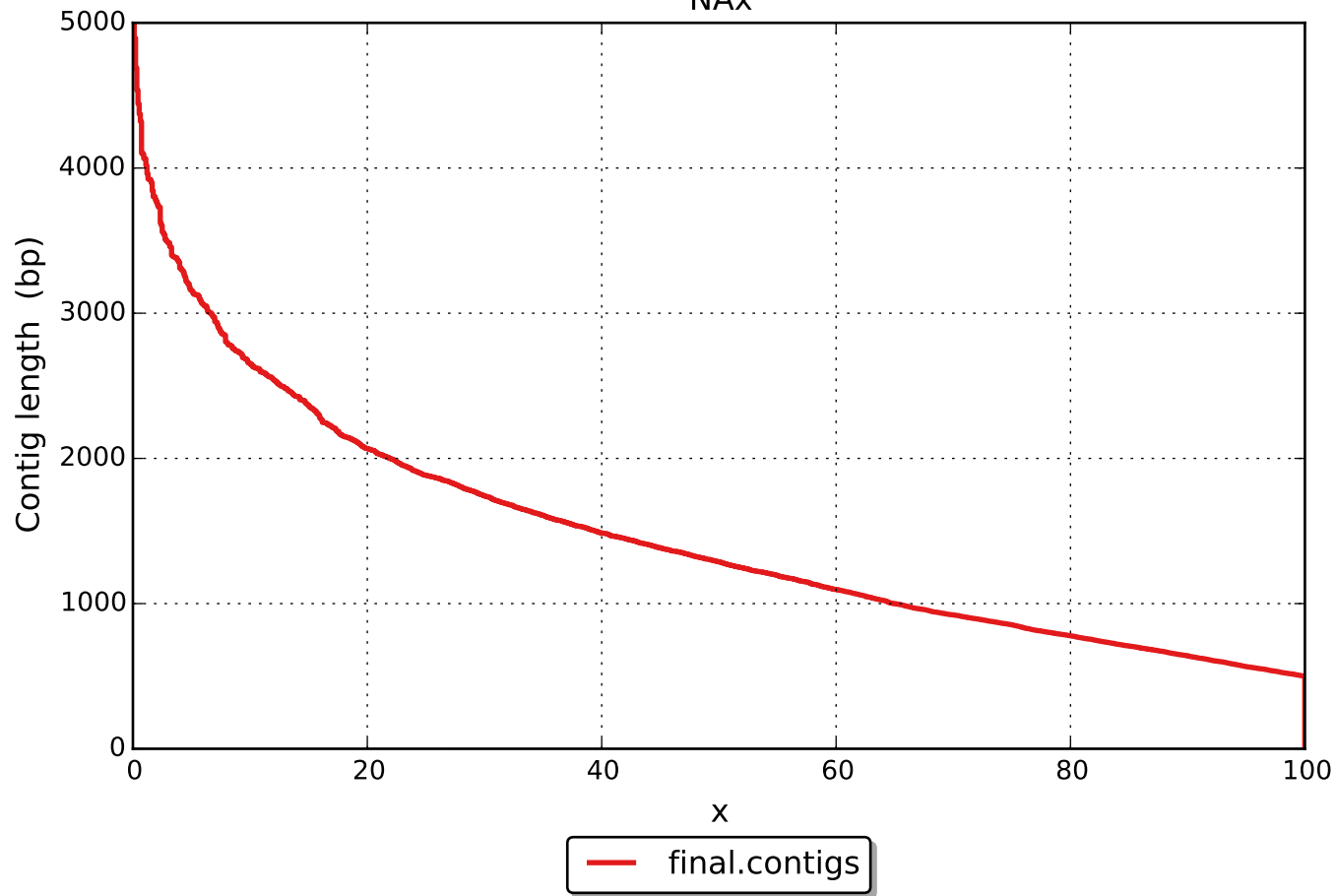




Cumulative length (aligned contigs)



NAx



NGAx

