

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	1044
# contigs ( $\geq 1000$ bp)	415
Total length ( $\geq 0$ bp)	1155507
Total length ( $\geq 1000$ bp)	713639
# contigs	1044
Largest contig	5316
Total length	1155507
Reference length	641799
GC (%)	26.32
Reference GC (%)	26.30
N50	1219
NG50	1910
N75	789
NG75	1397
L50	292
LG50	120
L75	587
LG75	218
# misassemblies	8
# misassembled contigs	8
Misassembled contigs length	7612
# local misassemblies	0
# unaligned contigs	0 + 1 part
Unaligned length	452
Genome fraction (%)	91.561
Duplication ratio	1.966
# N's per 100 kbp	0.00
# mismatches per 100 kbp	943.95
# indels per 100 kbp	0.68
Largest alignment	5316
NA50	772
NGA50	1266
NGA75	920
LA50	429
LGA50	163
LGA75	314

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).

## Misassemblies report

	final.contigs
# misassemblies	8
# relocations	8
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	8
Misassembled contigs length	7612
# local misassemblies	0
# mismatches	5547
# indels	4
# short indels	4
# long indels	0
Indels length	4

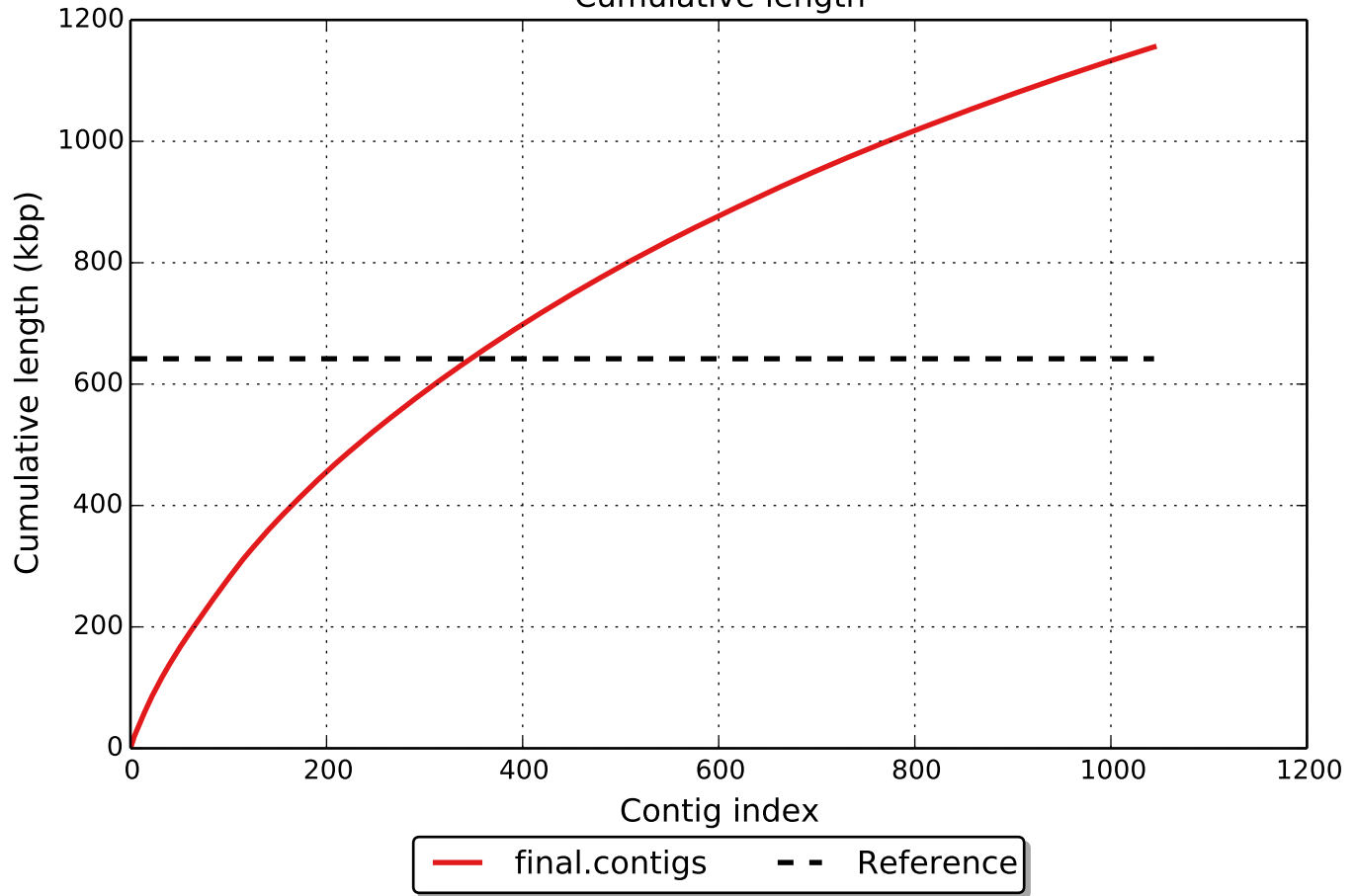
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

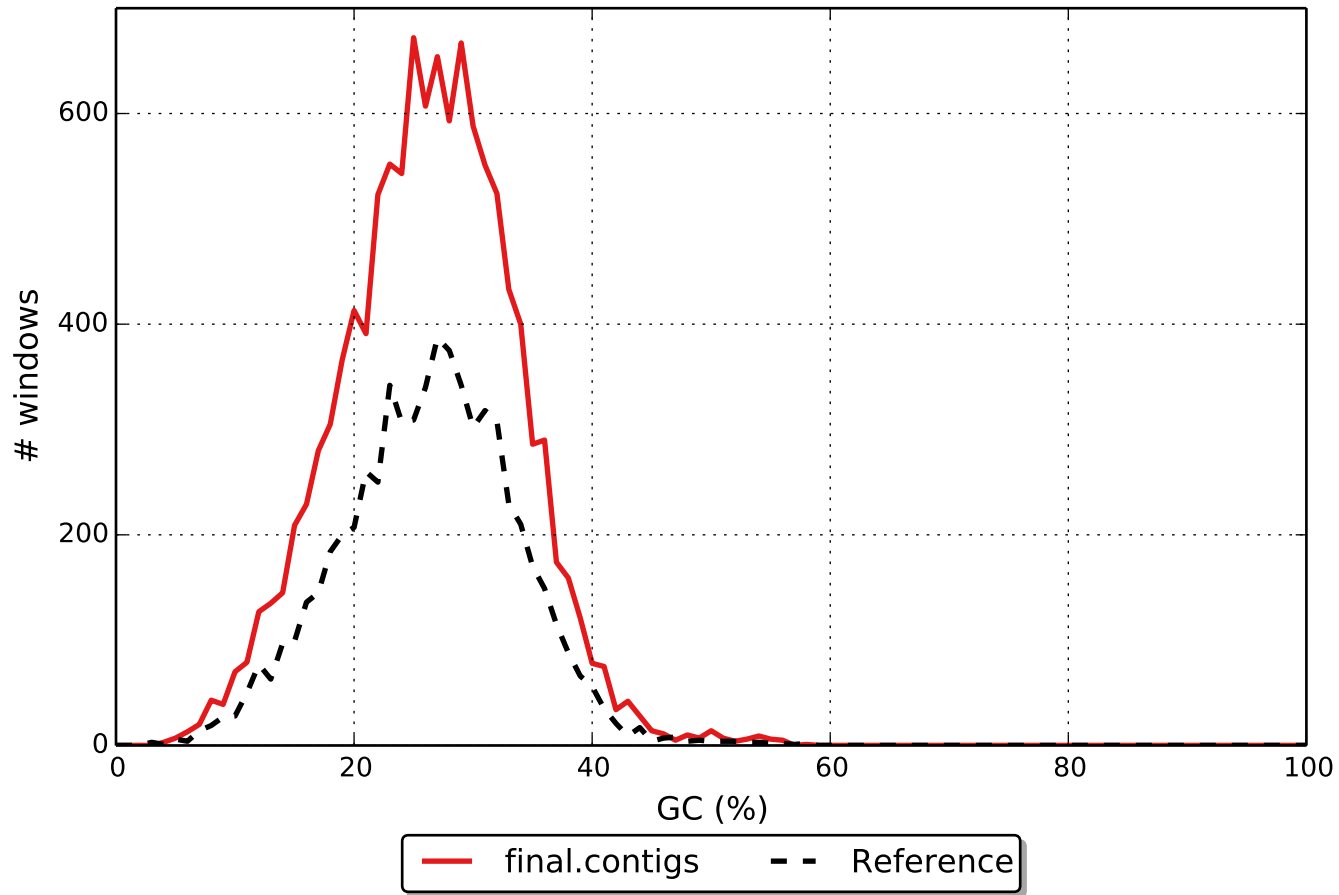
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	452
# N's	0

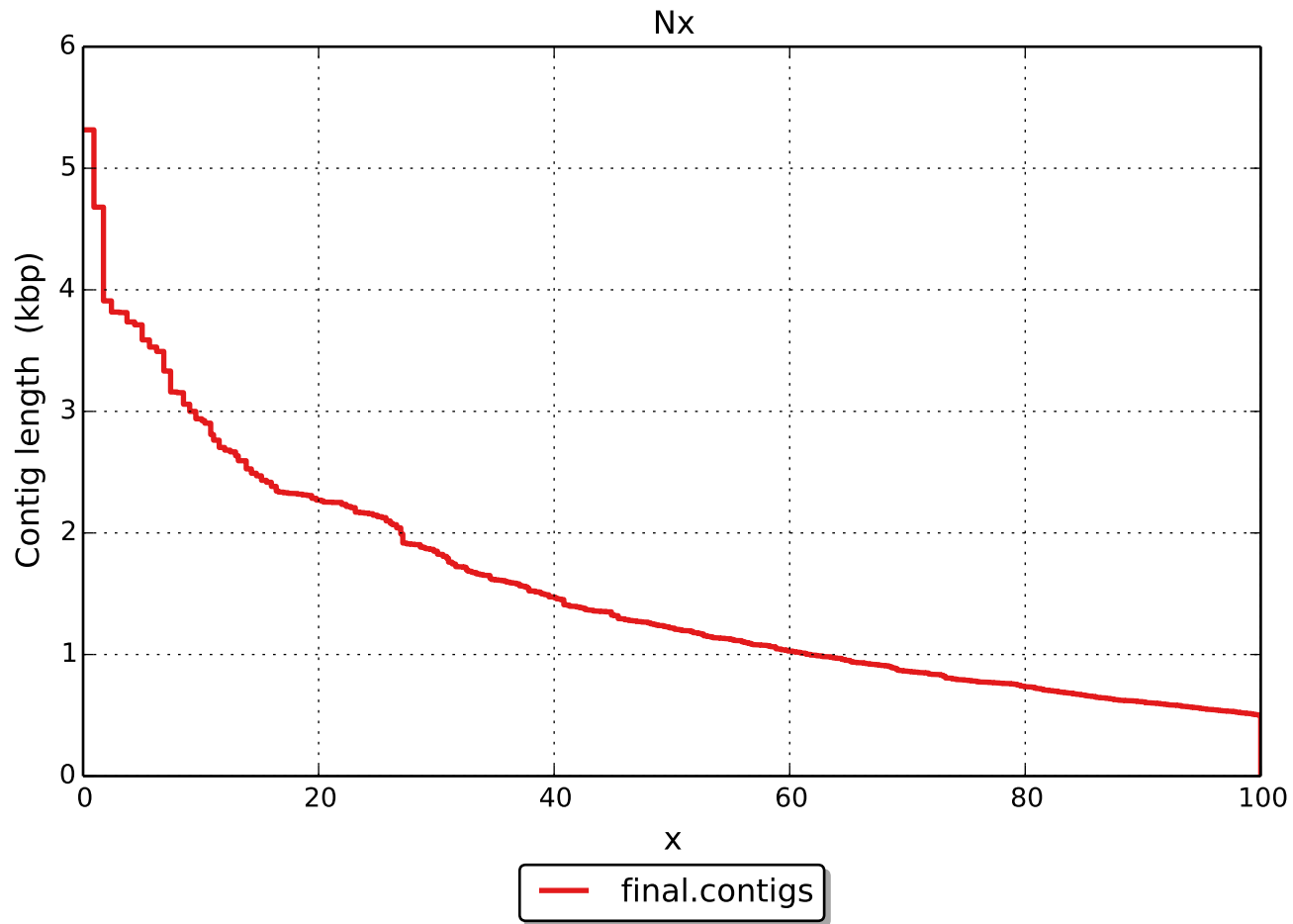
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Cumulative length

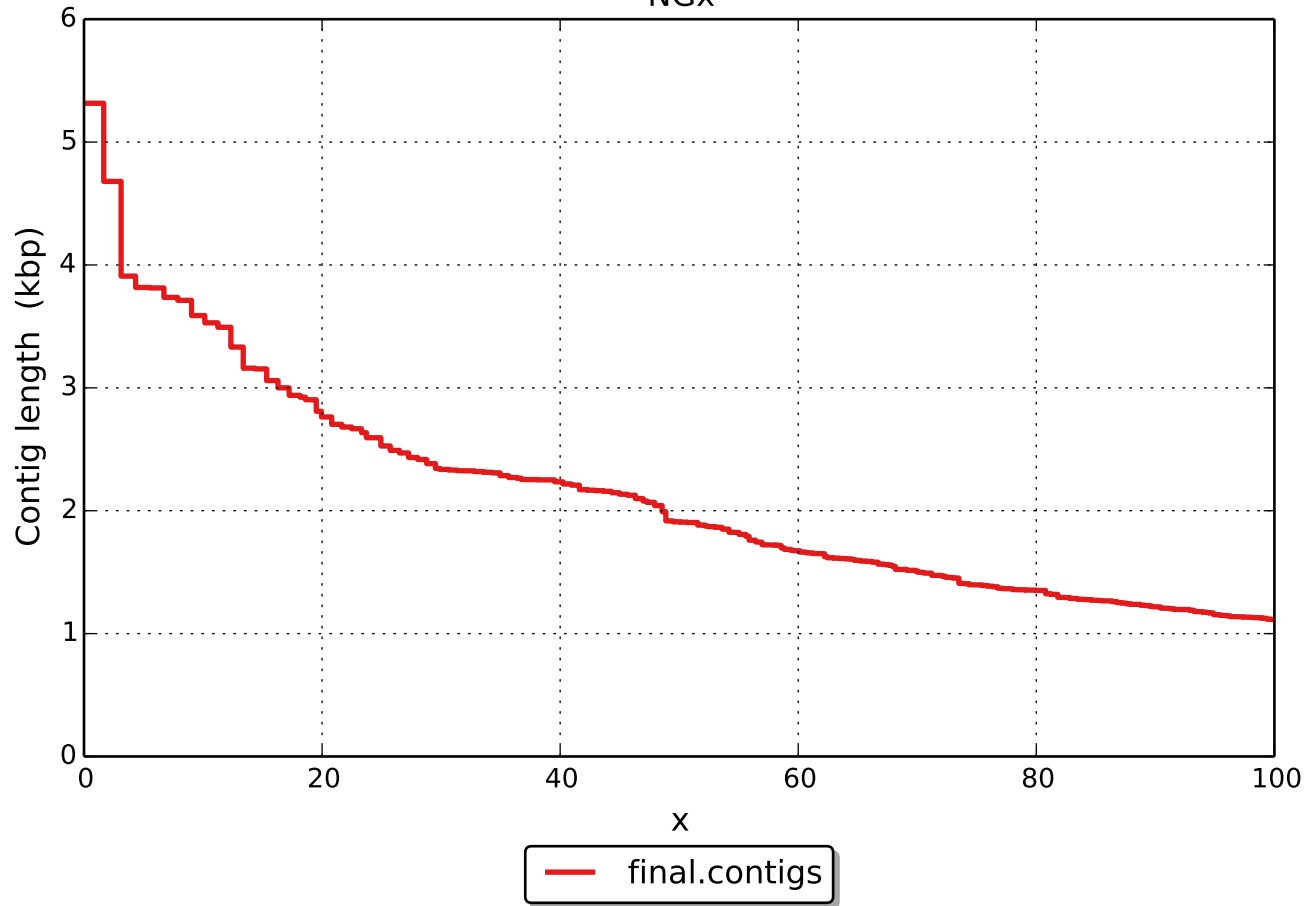


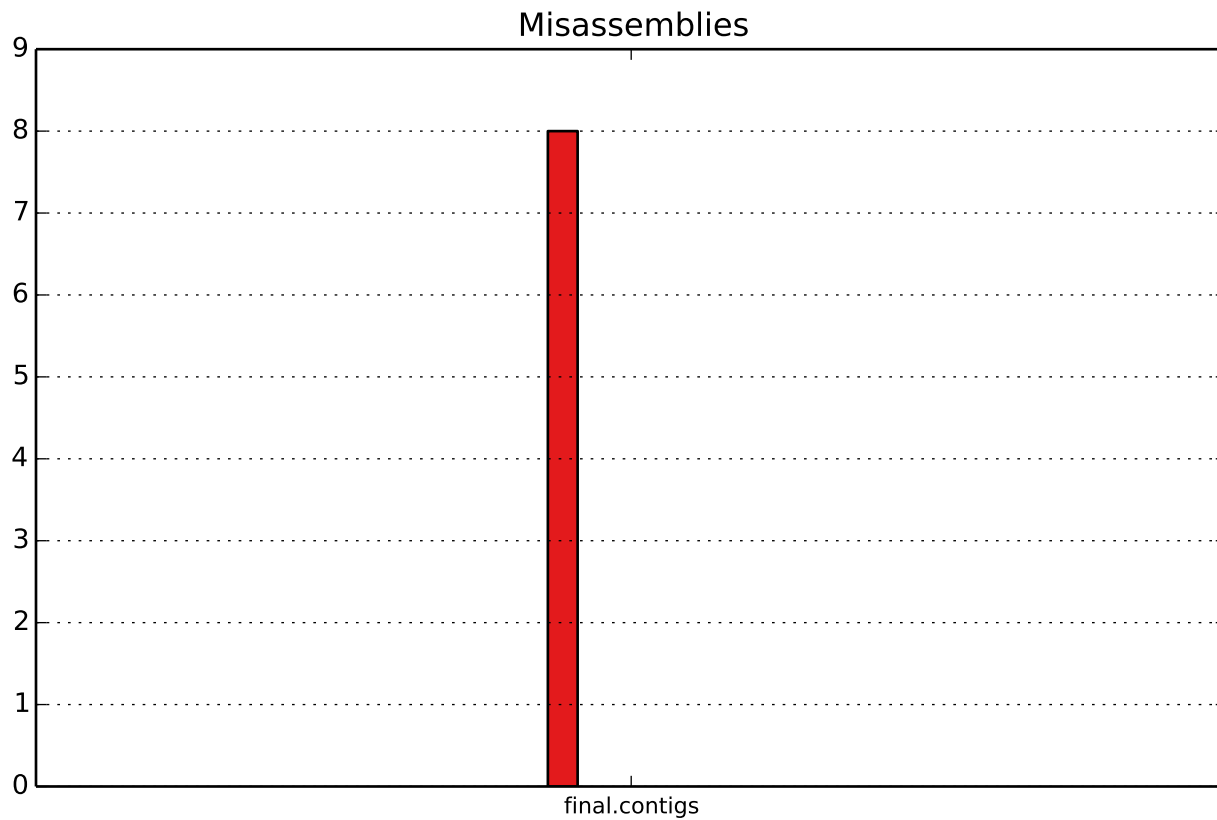
# GC content



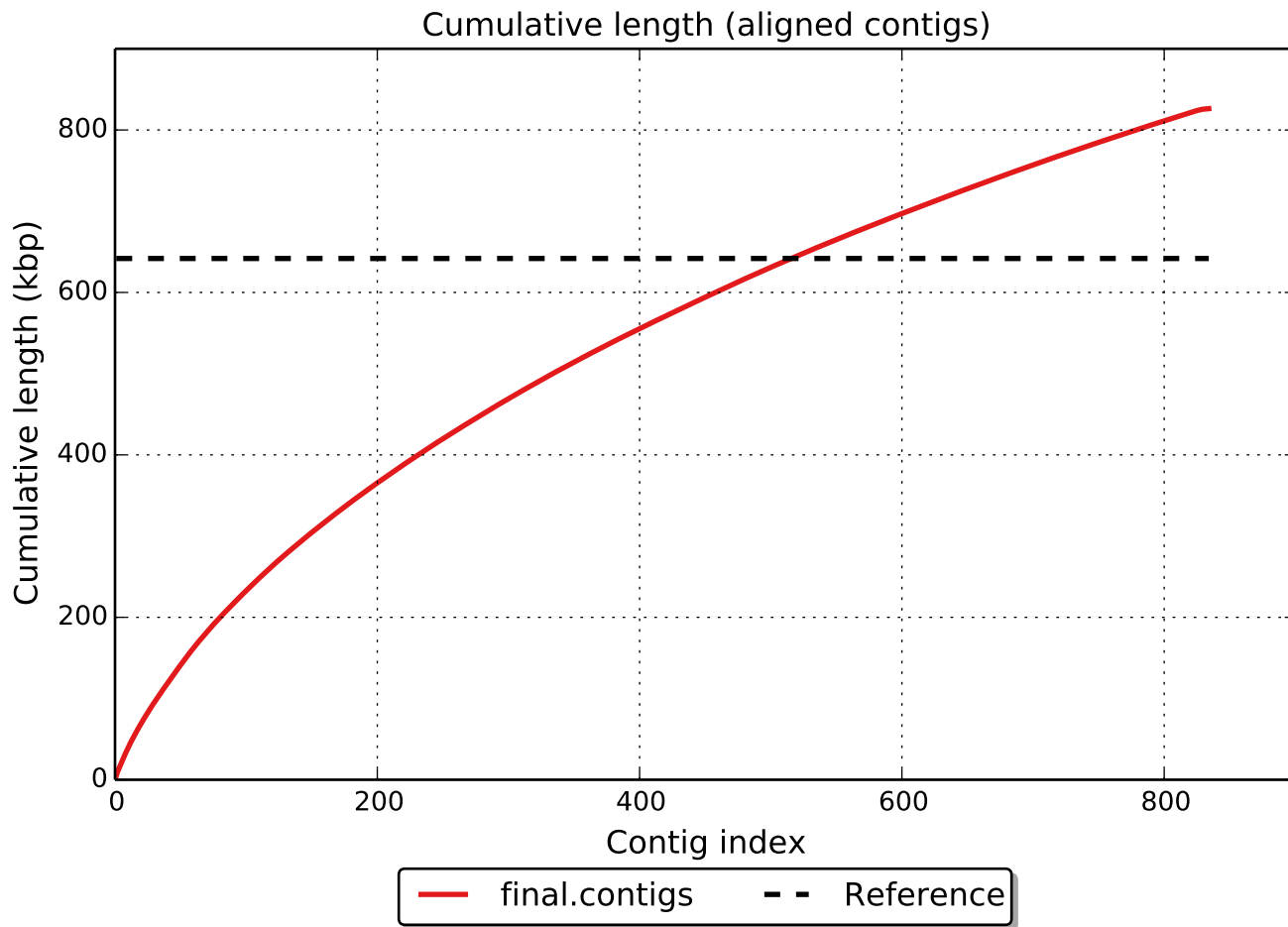


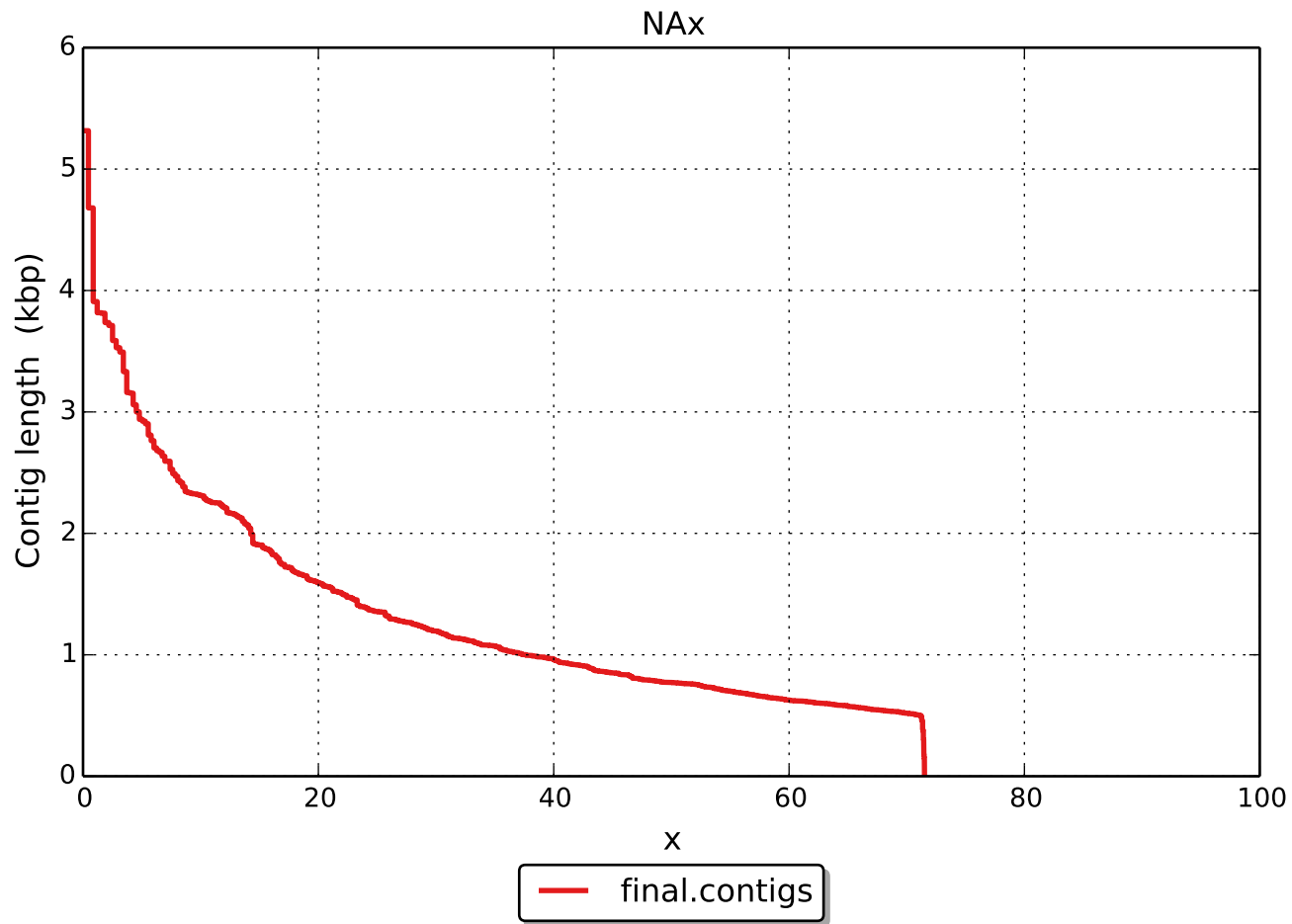
NGx











NGAx

