

Report

	final.contigs
# contigs (>= 1000 bp)	671
# contigs (>= 5000 bp)	324
# contigs (>= 10000 bp)	137
# contigs (>= 25000 bp)	7
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4378994
Total length (>= 5000 bp)	3391793
Total length (>= 10000 bp)	2084597
Total length (>= 25000 bp)	198815
Total length (>= 50000 bp)	0
# contigs	813
Largest contig	35550
Total length	4472076
Reference length	4641652
GC (℥)	50.74
Reference GC (℥)	50.78
N50	9424
NG50	8865
N75	5167
NG75	4759
L50	153
LG50	162
L75	317
LG75	343
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	5468
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (℥)	94.936
Duplication ratio	1.015
# N's per 100 kbp	0.00
# mismatches per 100 kbp	519.63
# indels per 100 kbp	0.05
Largest alignment	35550
NA50	9424
NGA50	8865
NA75	5167
NGA75	4759
LA50	153
LGA50	162
LA75	317
LGA75	343

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

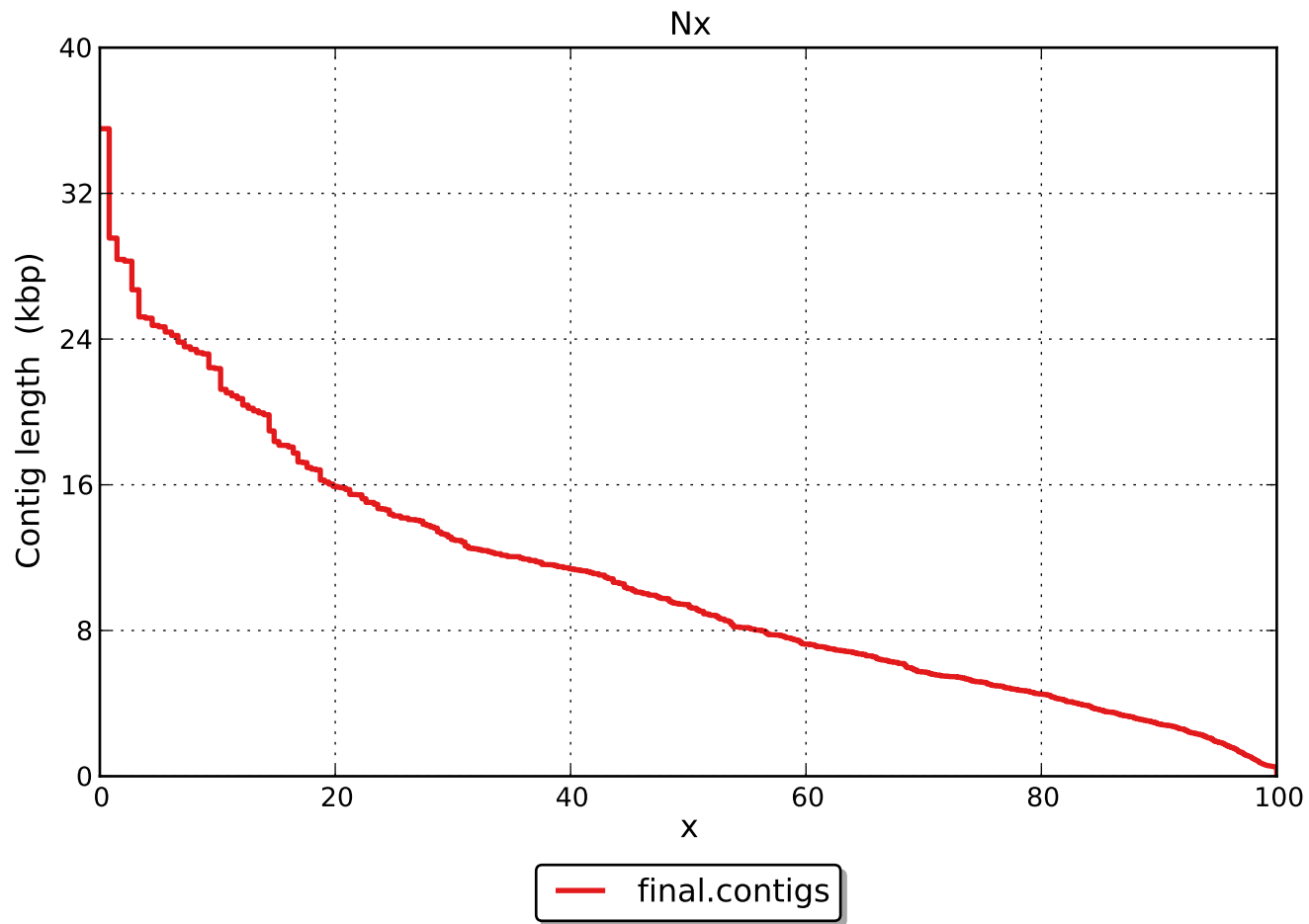
	final.contigs
# misassemblies	1
# relocations	0
# translocations	0
# inversions	1
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	5468
# local misassemblies	0
# mismatches	22898
# indels	2
# short indels	2
# long indels	0
Indels length	2

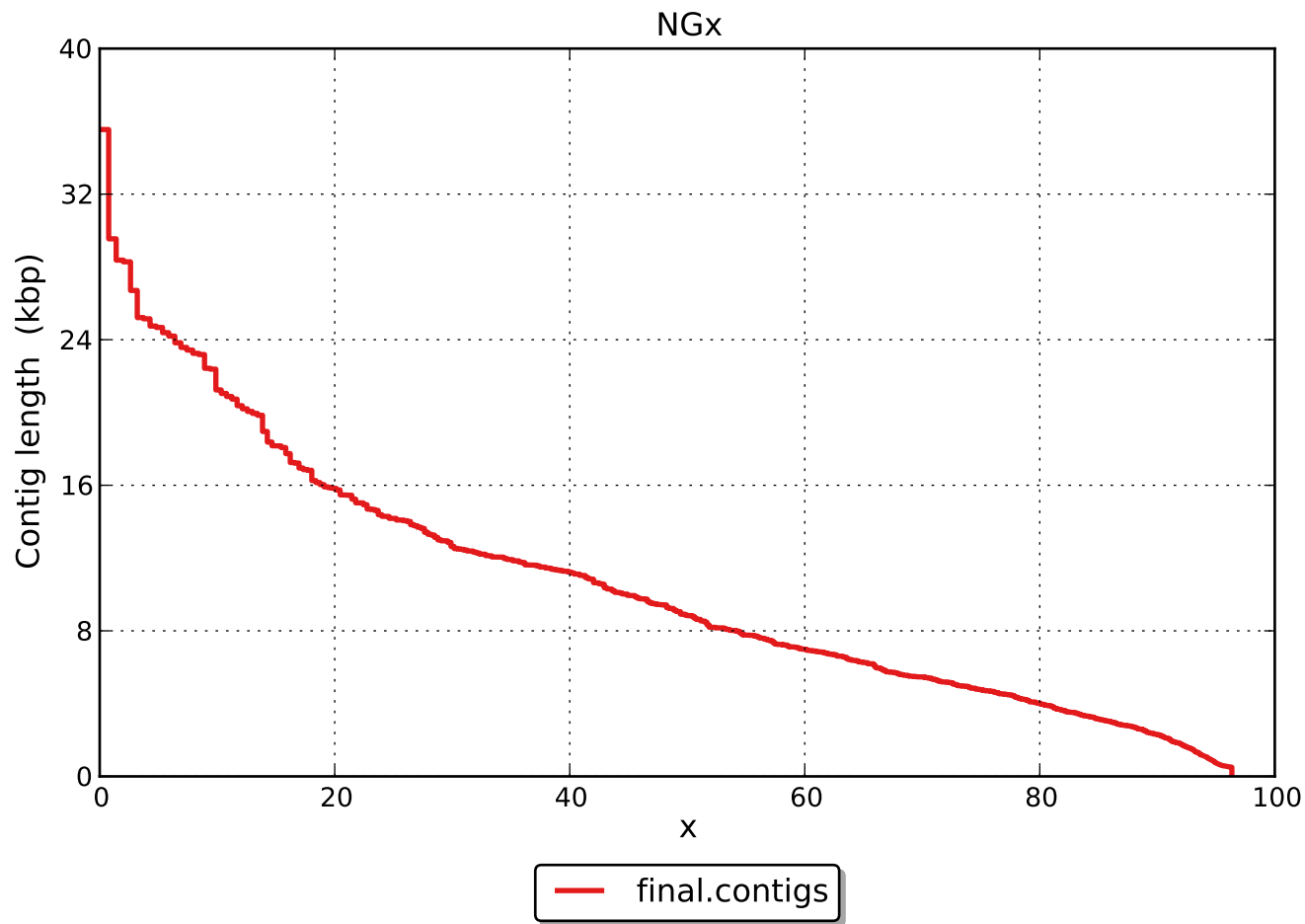
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

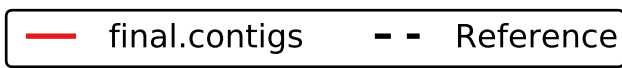
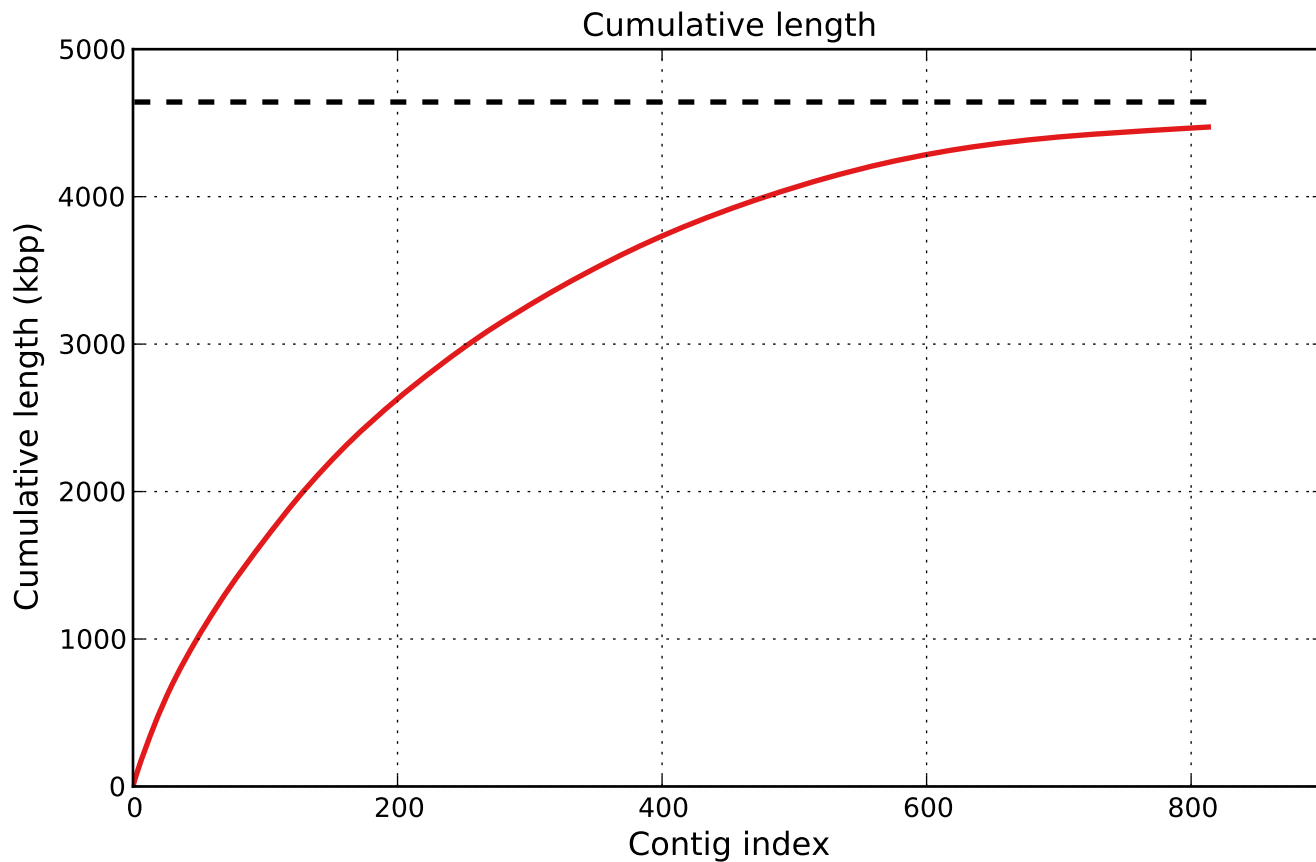
## Unaligned report

	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

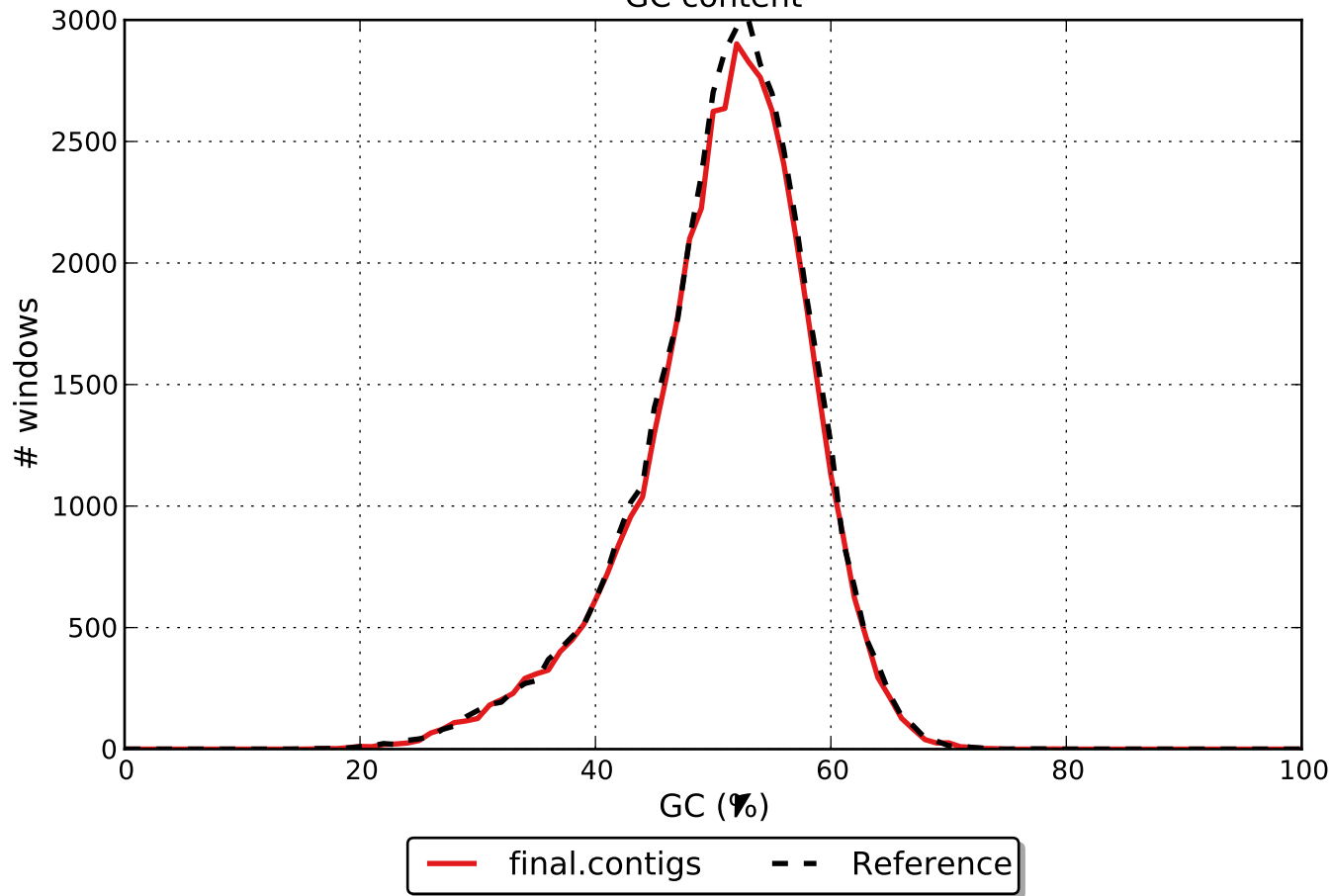
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

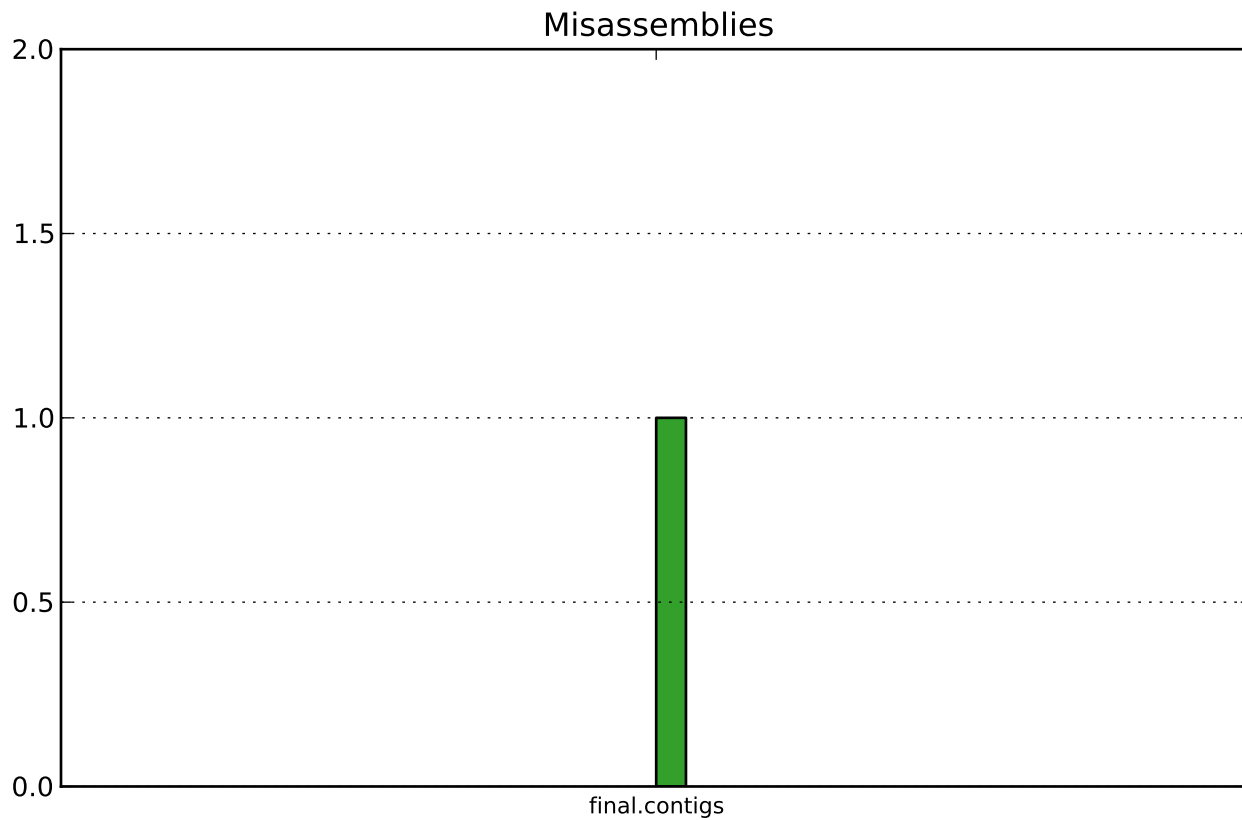






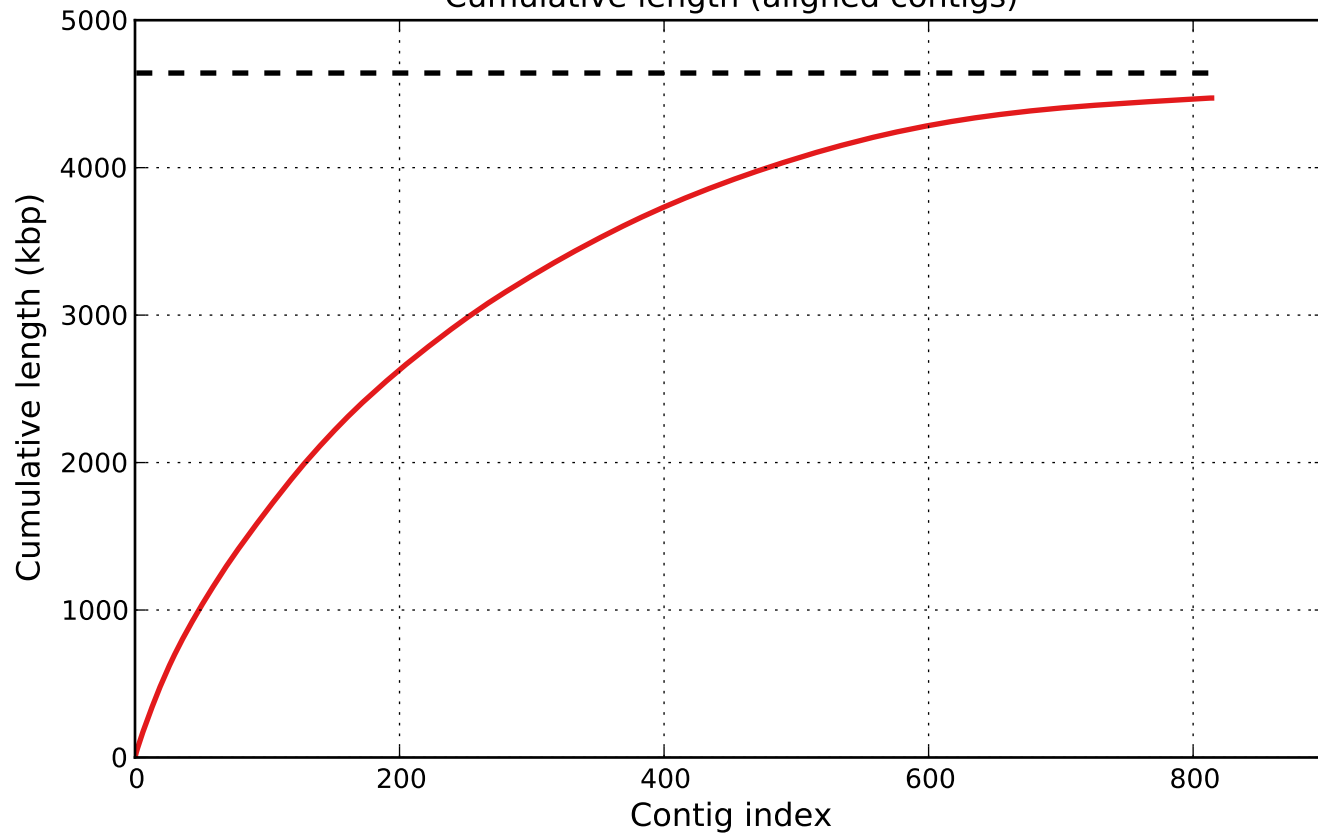
GC content



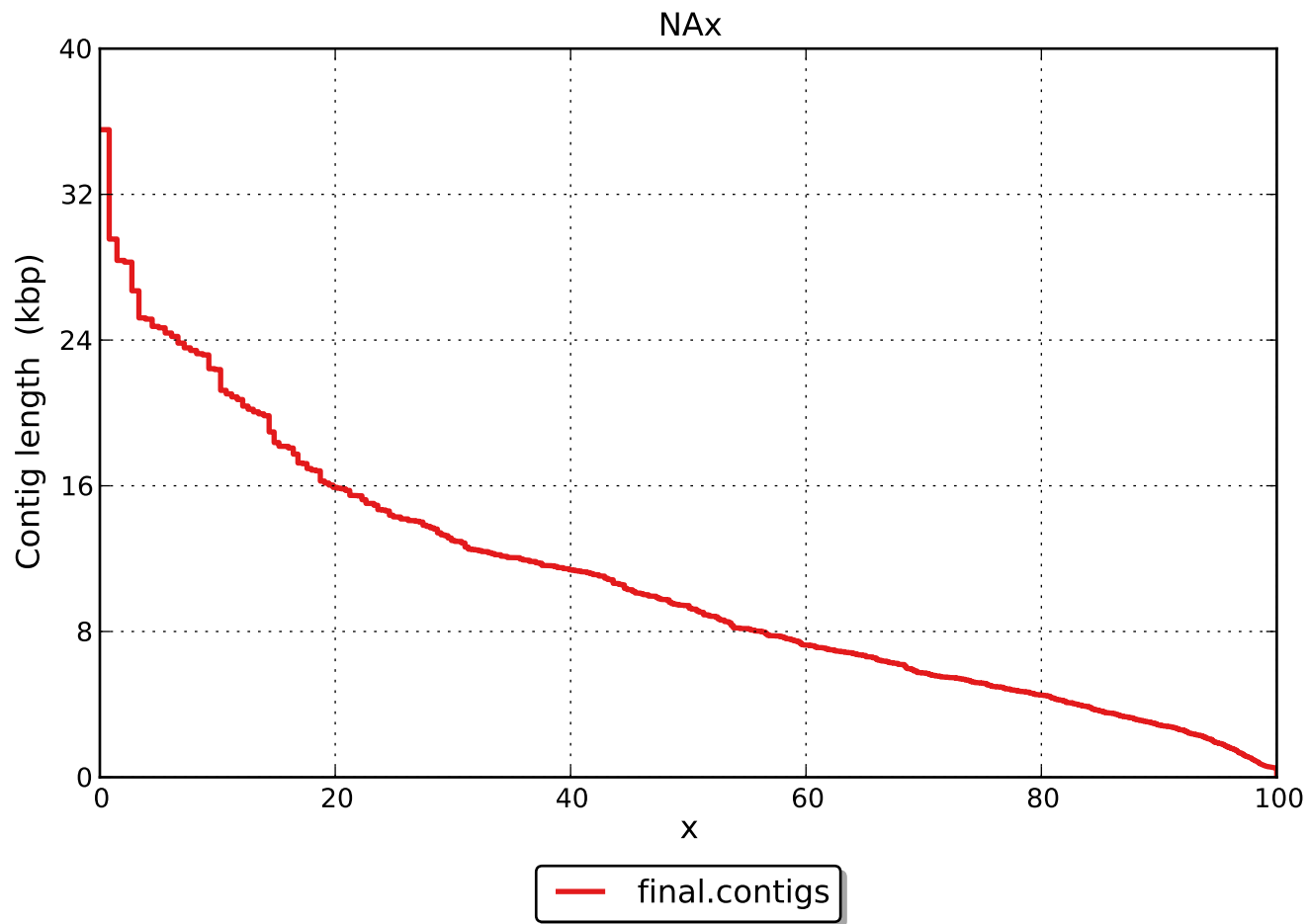




Cumulative length (aligned contigs)



— final.contigs      - - Reference



# NGAx

