

## Report

	final.contigs
# contigs (>= 1000 bp)	1699
# contigs (>= 5000 bp)	119
# contigs (>= 10000 bp)	4
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4193692
Total length (>= 5000 bp)	748508
Total length (>= 10000 bp)	41982
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	2387
Largest contig	10907
Total length	4703057
Reference length	4641652
GC (%)	50.79
Reference GC (%)	50.79
N50	2568
NG50	2595
N75	1546
NG75	1596
L50	590
LG50	578
L75	1170
LG75	1141
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	643
# local misassemblies	0
# unaligned contigs	0 + 2 part
Unaligned length	297
Genome fraction (%)	97.375
Duplication ratio	1.040
# N's per 100 kbp	0.00
# mismatches per 100 kbp	50.02
# indels per 100 kbp	0.02
Largest alignment	10907
NA50	2568
NGA50	2595
NA75	1546
NGA75	1596
LA50	590
LGA50	578
LA75	1170
LGA75	1141

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

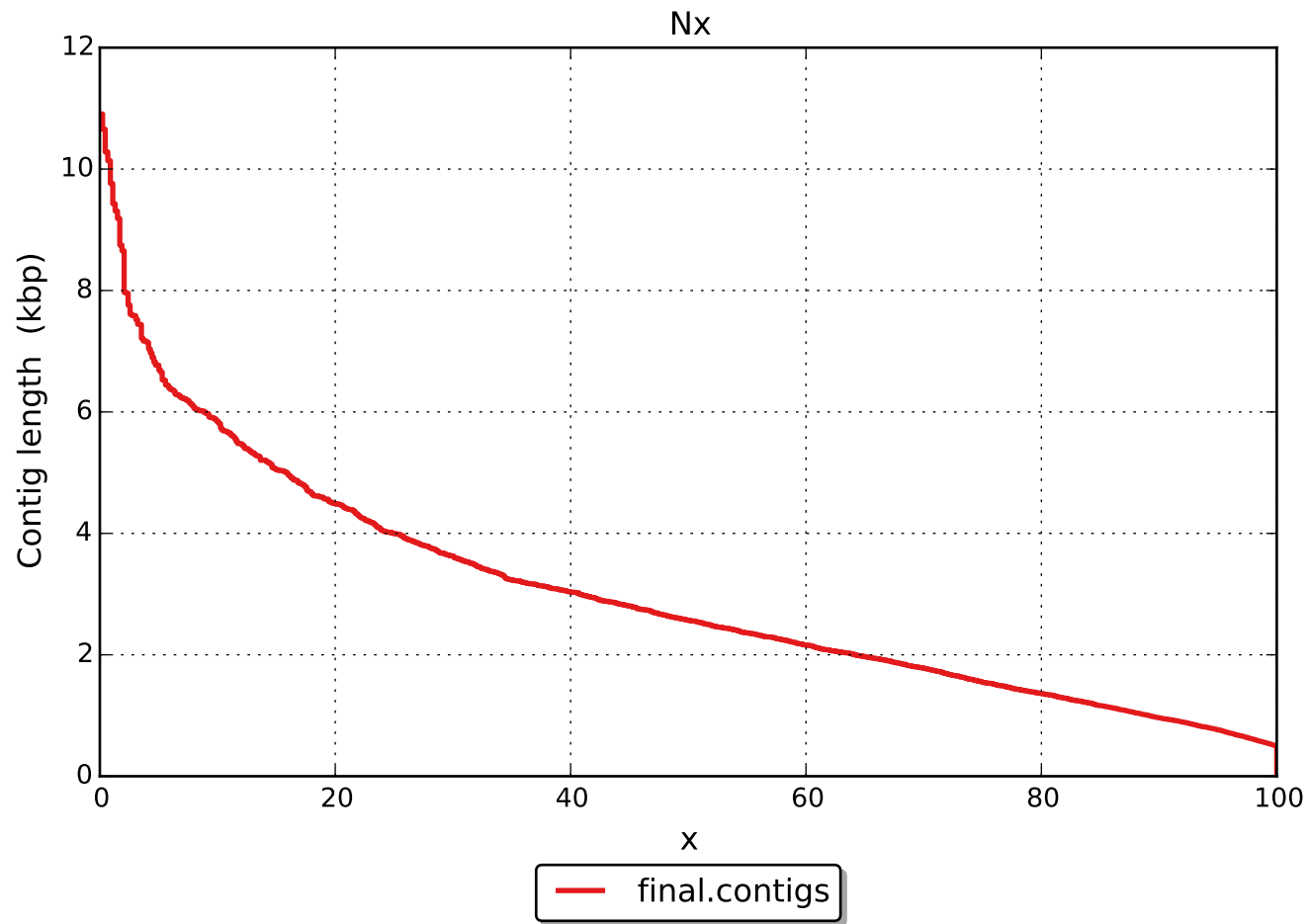
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	643
# local misassemblies	0
# mismatches	2261
# indels	1
# short indels	1
# long indels	0
Indels length	1

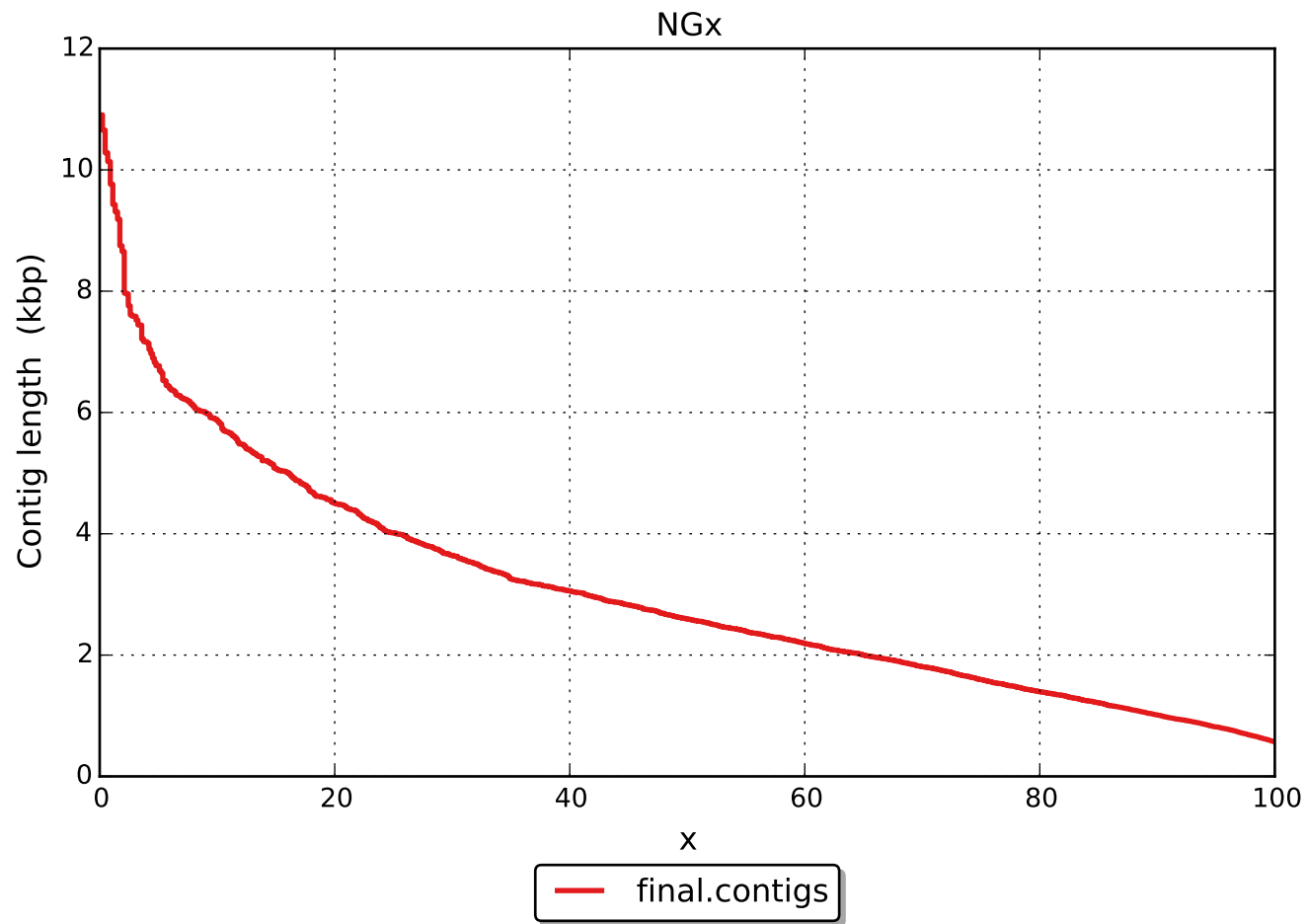
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

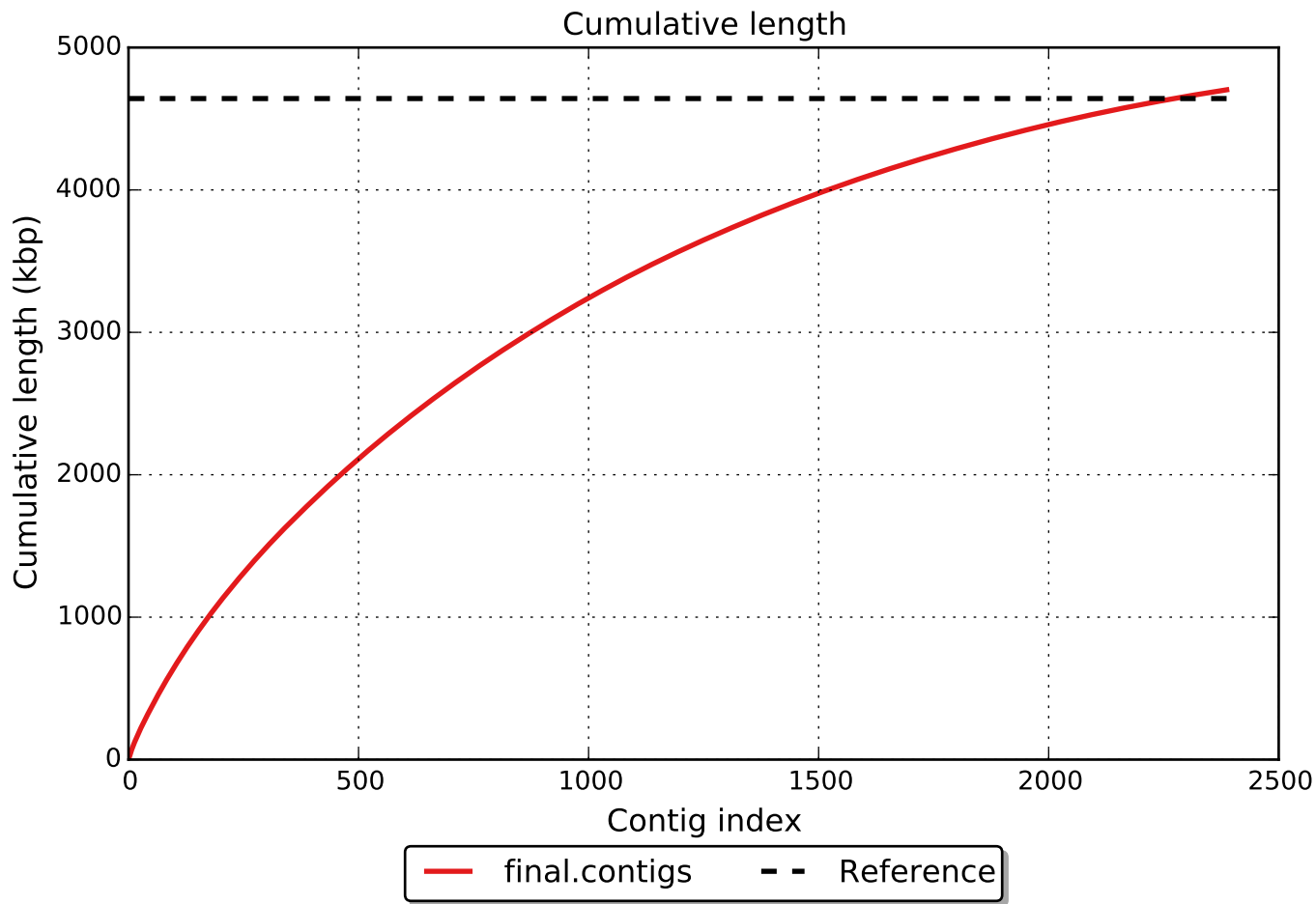
## Unaligned report

	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	0
Partially unaligned length	297
# N's	0

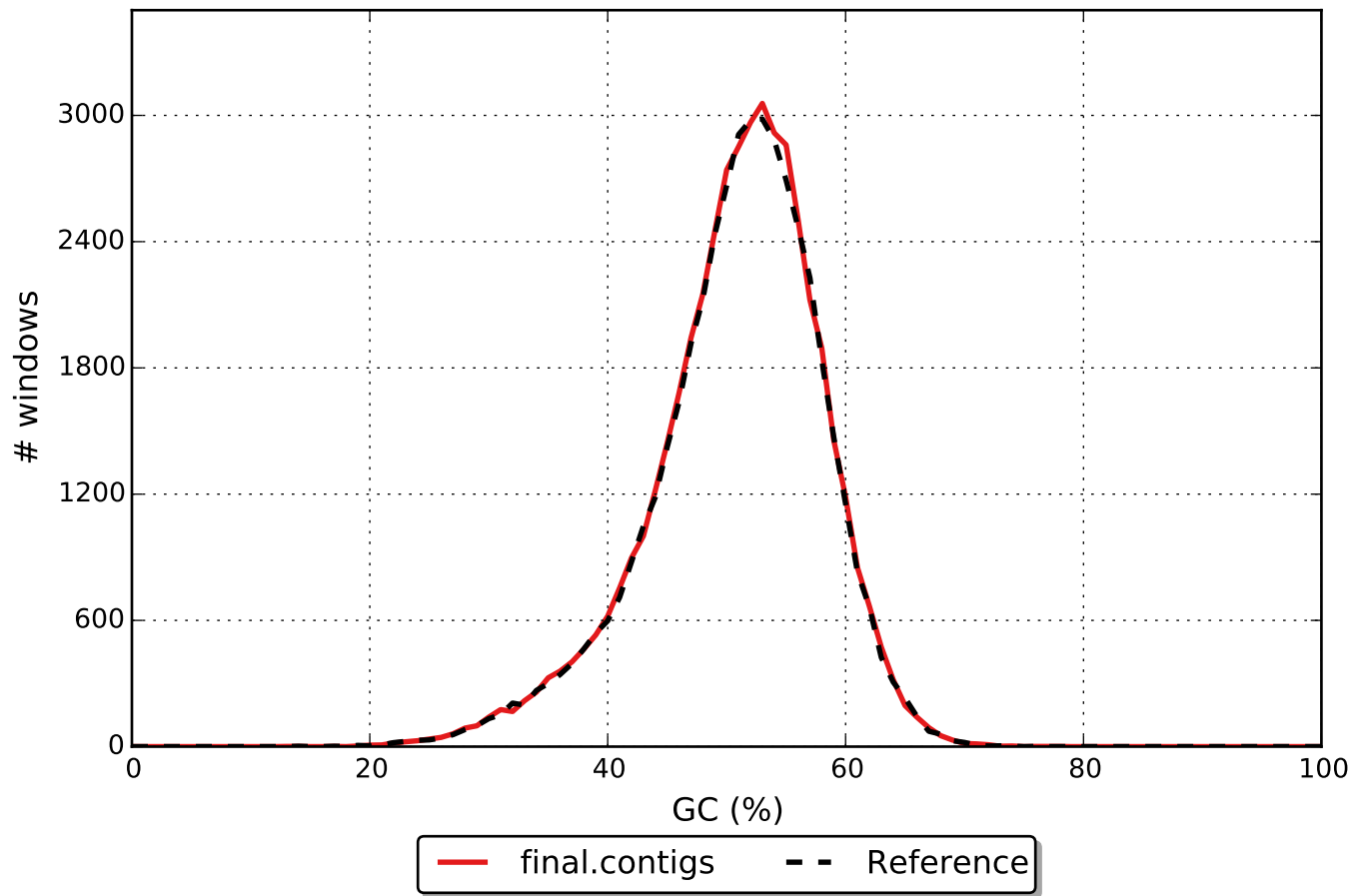
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).







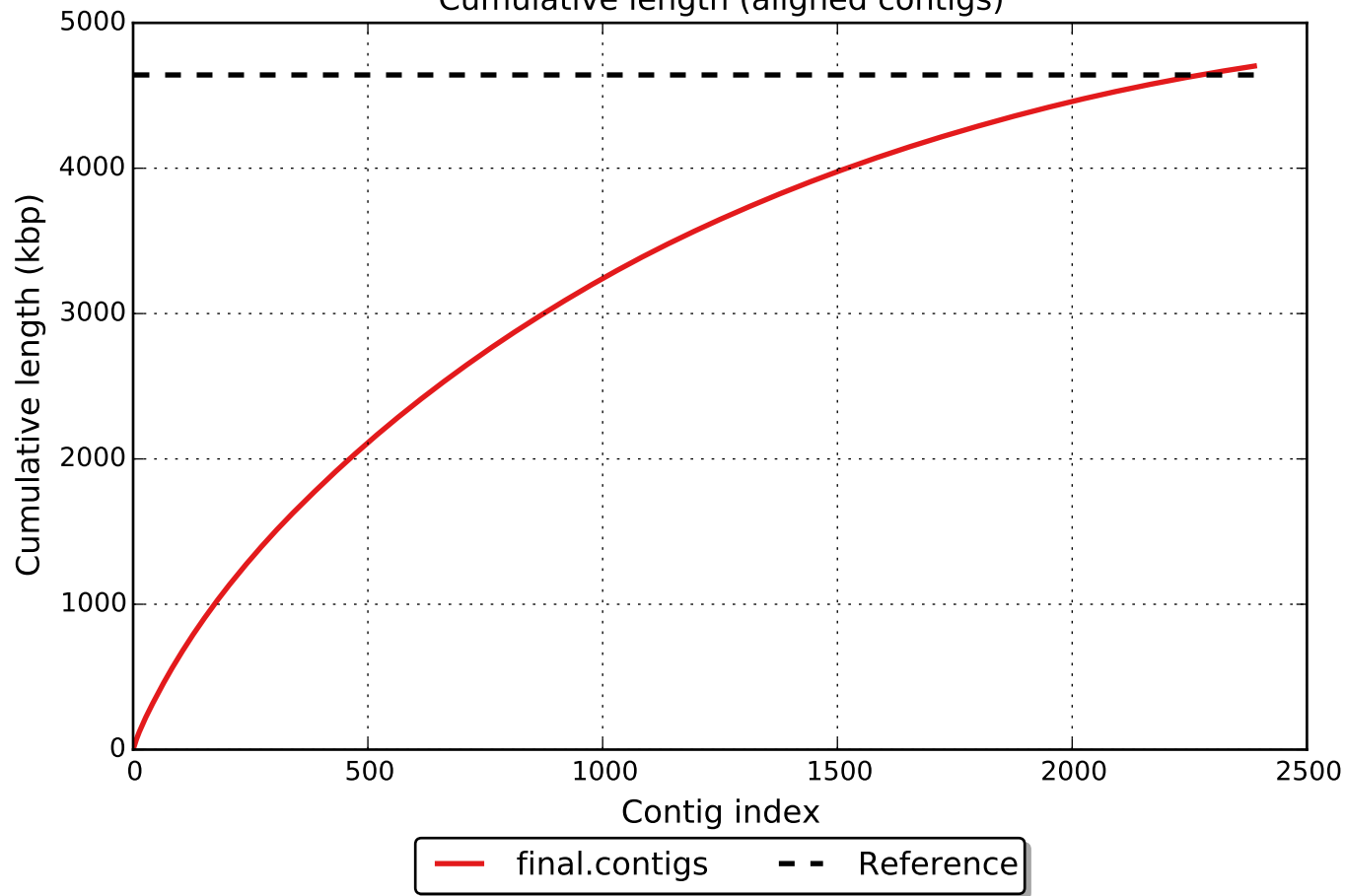
GC content

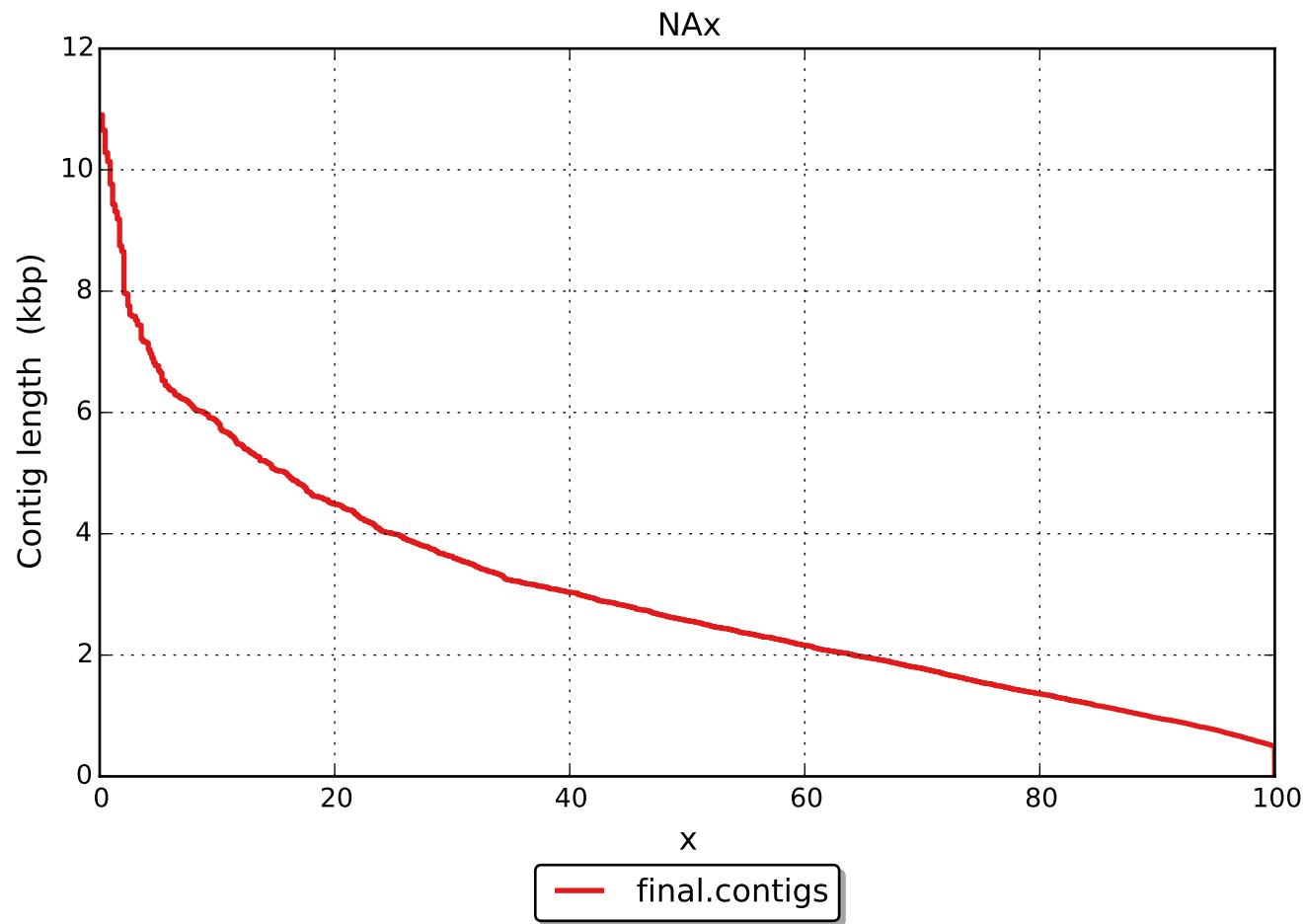






Cumulative length (aligned contigs)





NGAx

