

Report

	final.contigs
# contigs (>= 1000 bp)	1232
# contigs (>= 5000 bp)	209
# contigs (>= 10000 bp)	20
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	3941829
Total length (>= 5000 bp)	1493007
Total length (>= 10000 bp)	238163
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	1940
Largest contig	21375
Total length	4418700
Reference length	4641652
GC (℥)	50.75
Reference GC (℥)	50.78
N50	3554
NG50	3393
N75	1965
NG75	1702
L50	380
LG50	412
L75	796
LG75	887
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (℥)	91.352
Duplication ratio	1.042
# N's per 100 kbp	0.00
# mismatches per 100 kbp	597.27
# indels per 100 kbp	0.02
Largest alignment	21375
NA50	3554
NGA50	3393
NA75	1965
NGA75	1702
LA50	380
LGA50	412
LA75	796
LGA75	887

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

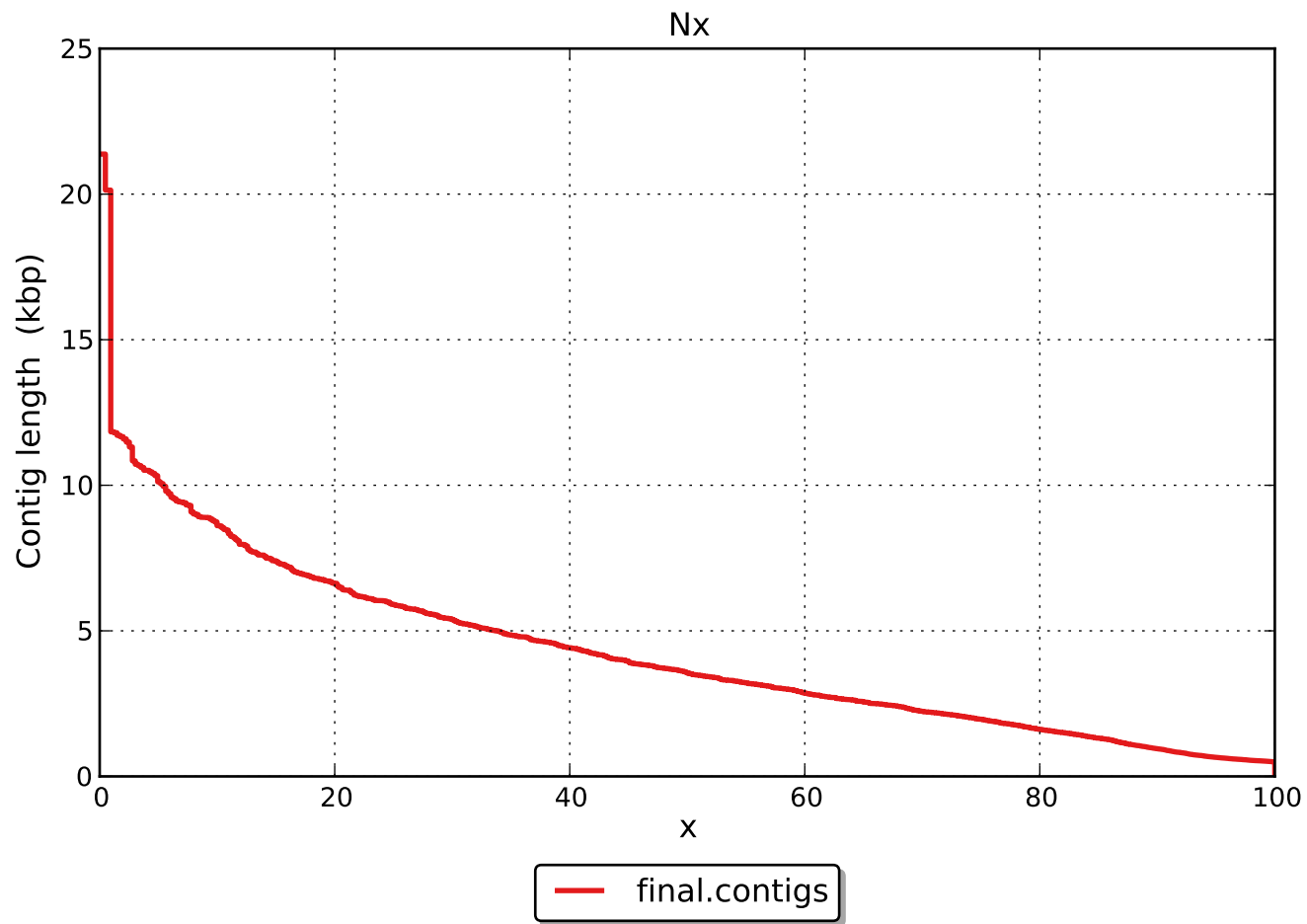
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	25326
# indels	1
# short indels	1
# long indels	0
Indels length	1

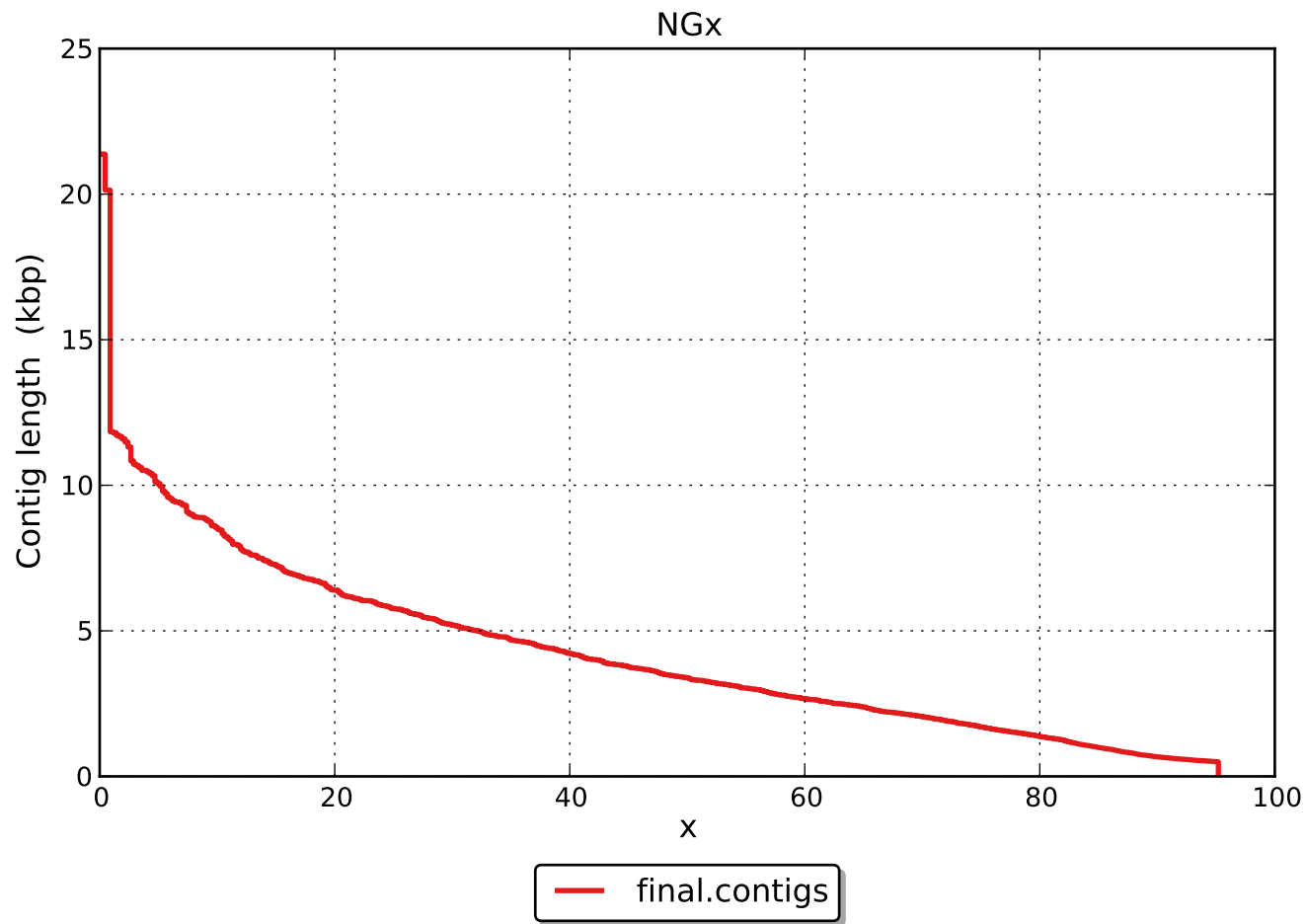
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

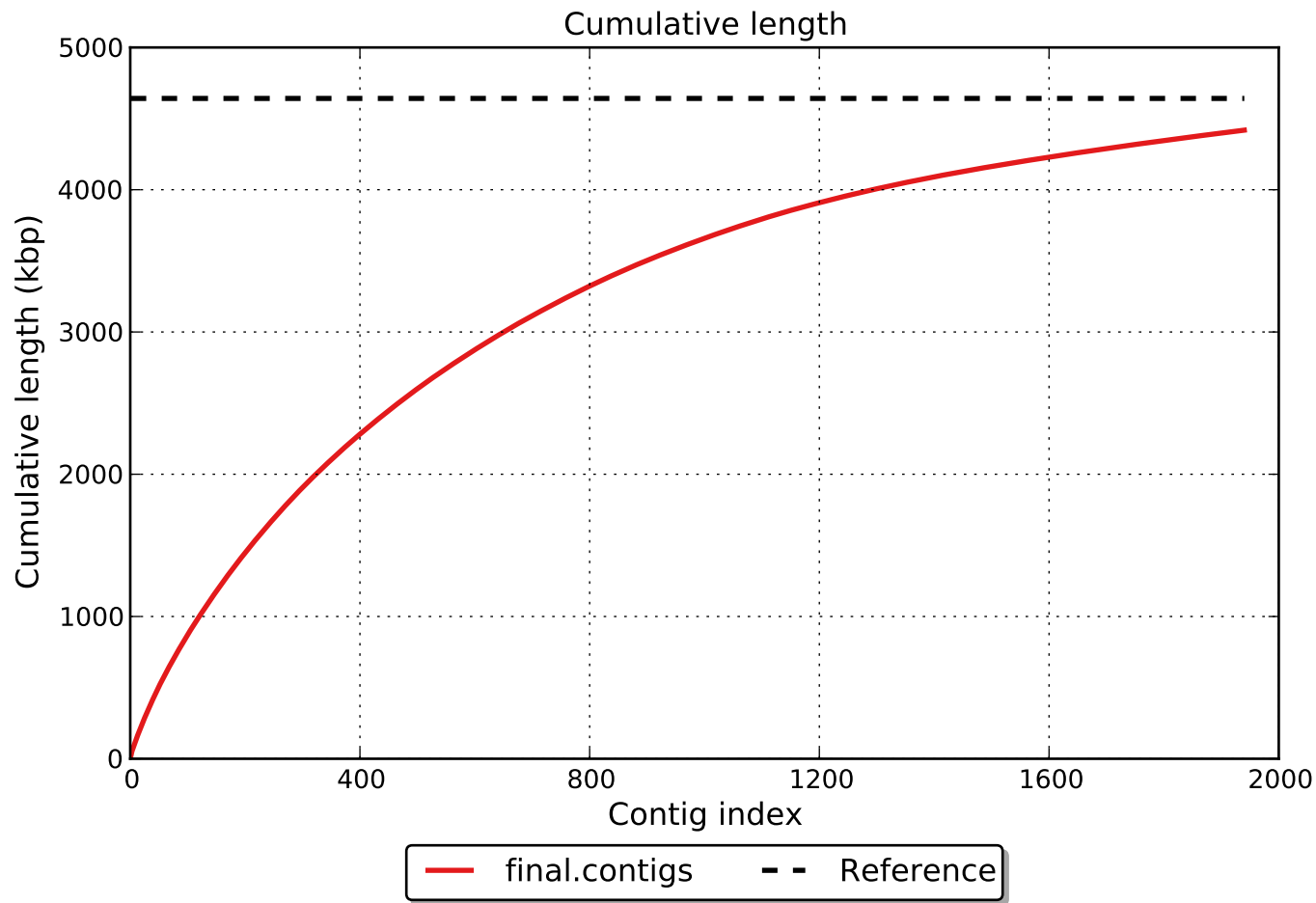
## Unaligned report

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

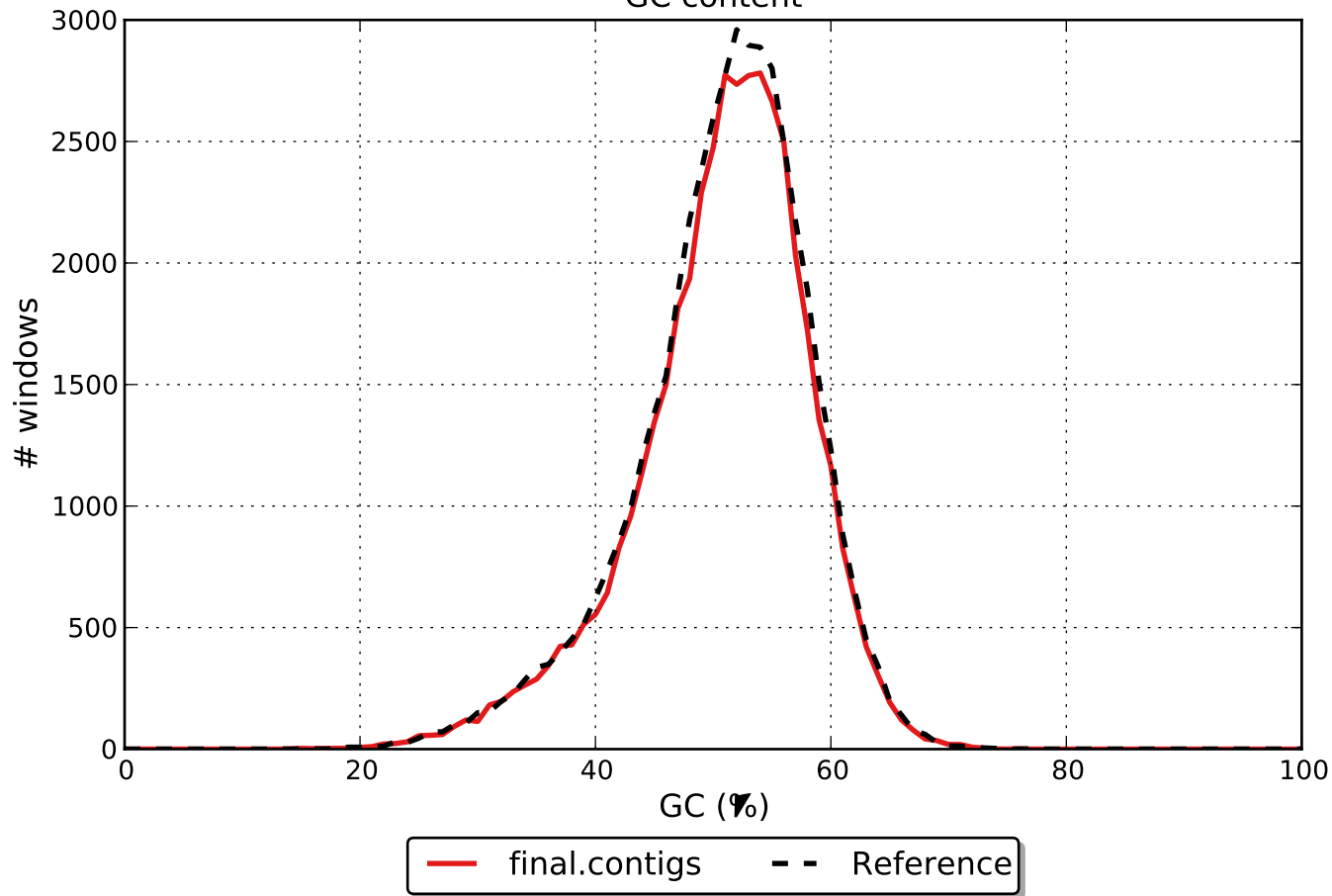
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).







GC content

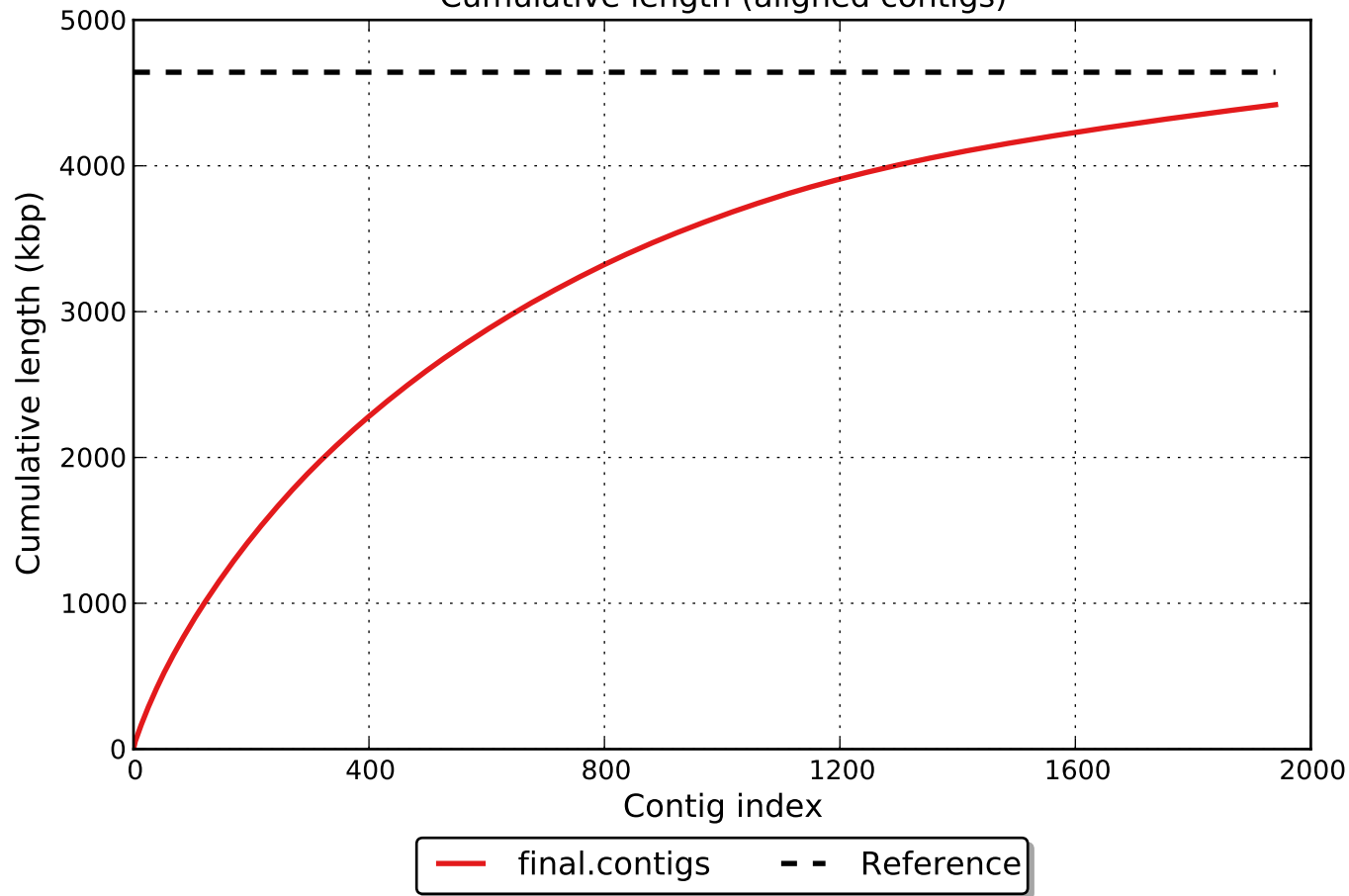


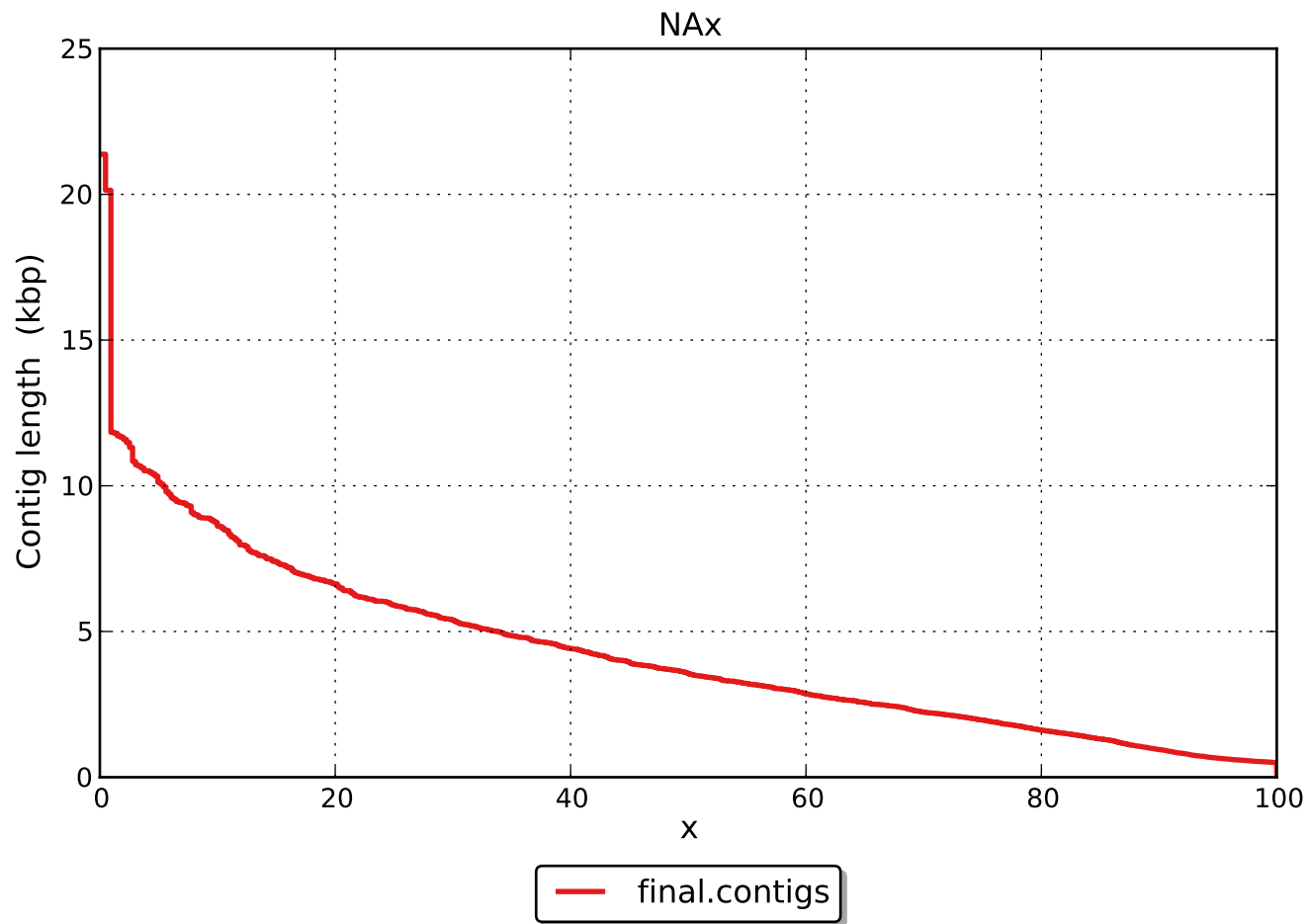
# Misassemblies





Cumulative length (aligned contigs)





NGAx

