

## Report

	final.contigs
# contigs (>= 1000 bp)	482
# contigs (>= 5000 bp)	289
# contigs (>= 10000 bp)	162
# contigs (>= 25000 bp)	33
# contigs (>= 50000 bp)	1
Total length (>= 1000 bp)	4565498
Total length (>= 5000 bp)	4024594
Total length (>= 10000 bp)	3083016
Total length (>= 25000 bp)	1074371
Total length (>= 50000 bp)	50343
# contigs	536
Largest contig	50343
Total length	4603775
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	14242
NG50	14116
N75	8251
NG75	8079
L50	98
LG50	100
L75	203
LG75	207
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# unaligned contigs	0 + 1 part
Unaligned length	27
Genome fraction (%)	98.116
Duplication ratio	1.011
# N's per 100 kbp	0.00
# mismatches per 100 kbp	15.90
# indels per 100 kbp	0.13
Largest alignment	50343
NA50	14242
NGA50	14116
NA75	8251
NGA75	8079
LA50	98
LGA50	100
LA75	203
LGA75	207

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

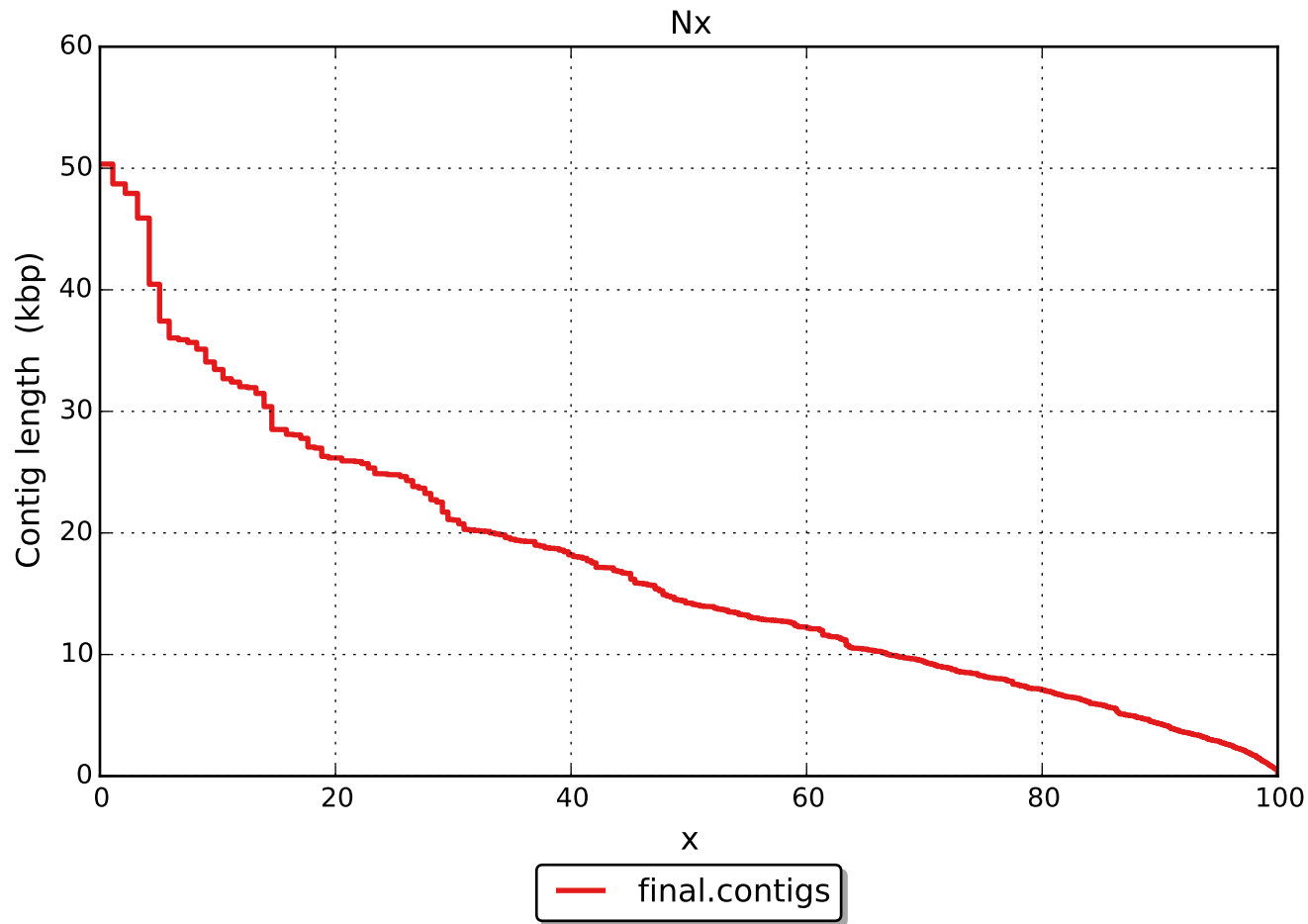
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# mismatches	724
# indels	6
# short indels	6
# long indels	0
Indels length	6

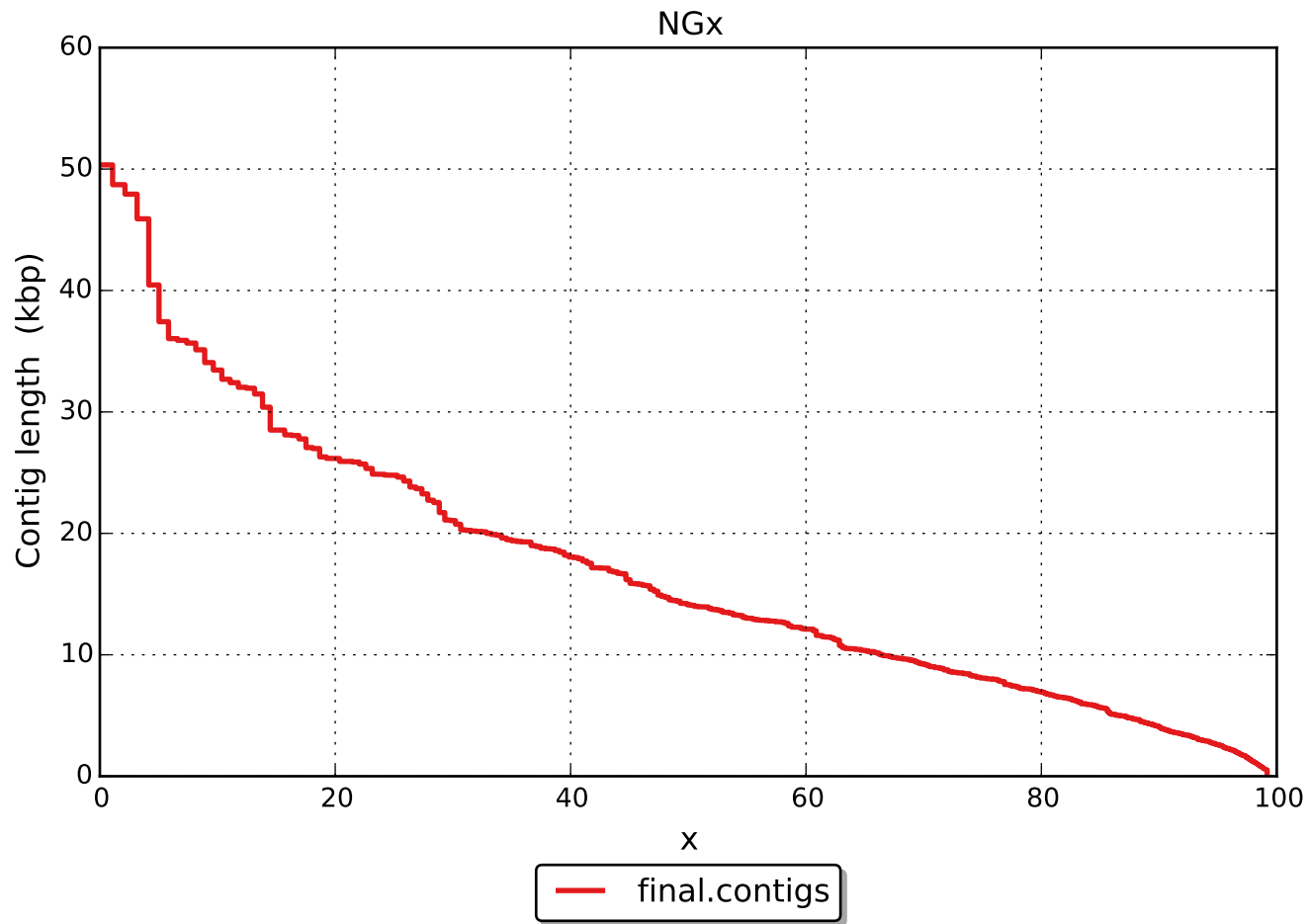
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

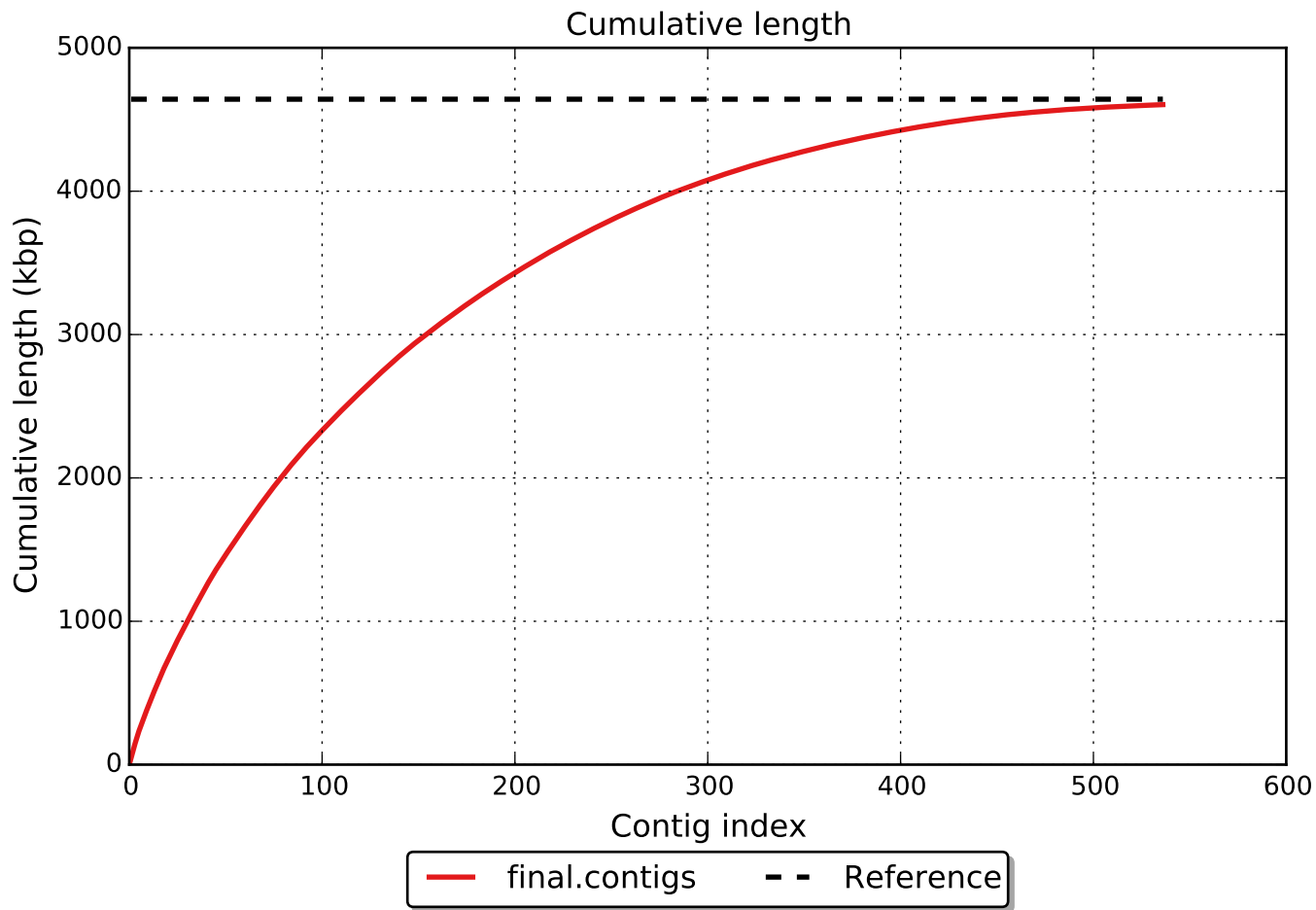
## Unaligned report

	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	27
# N's	0

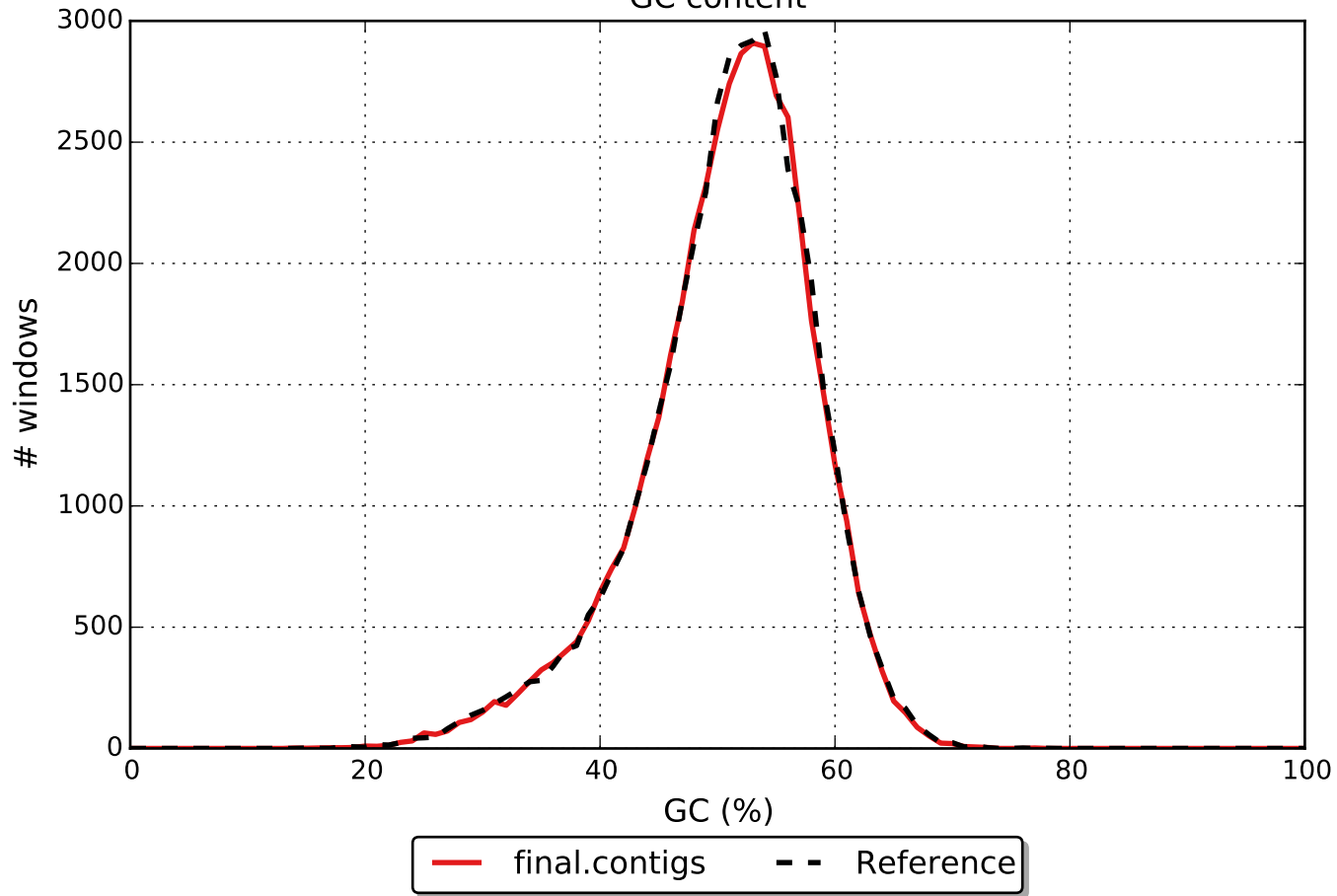
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).







GC content

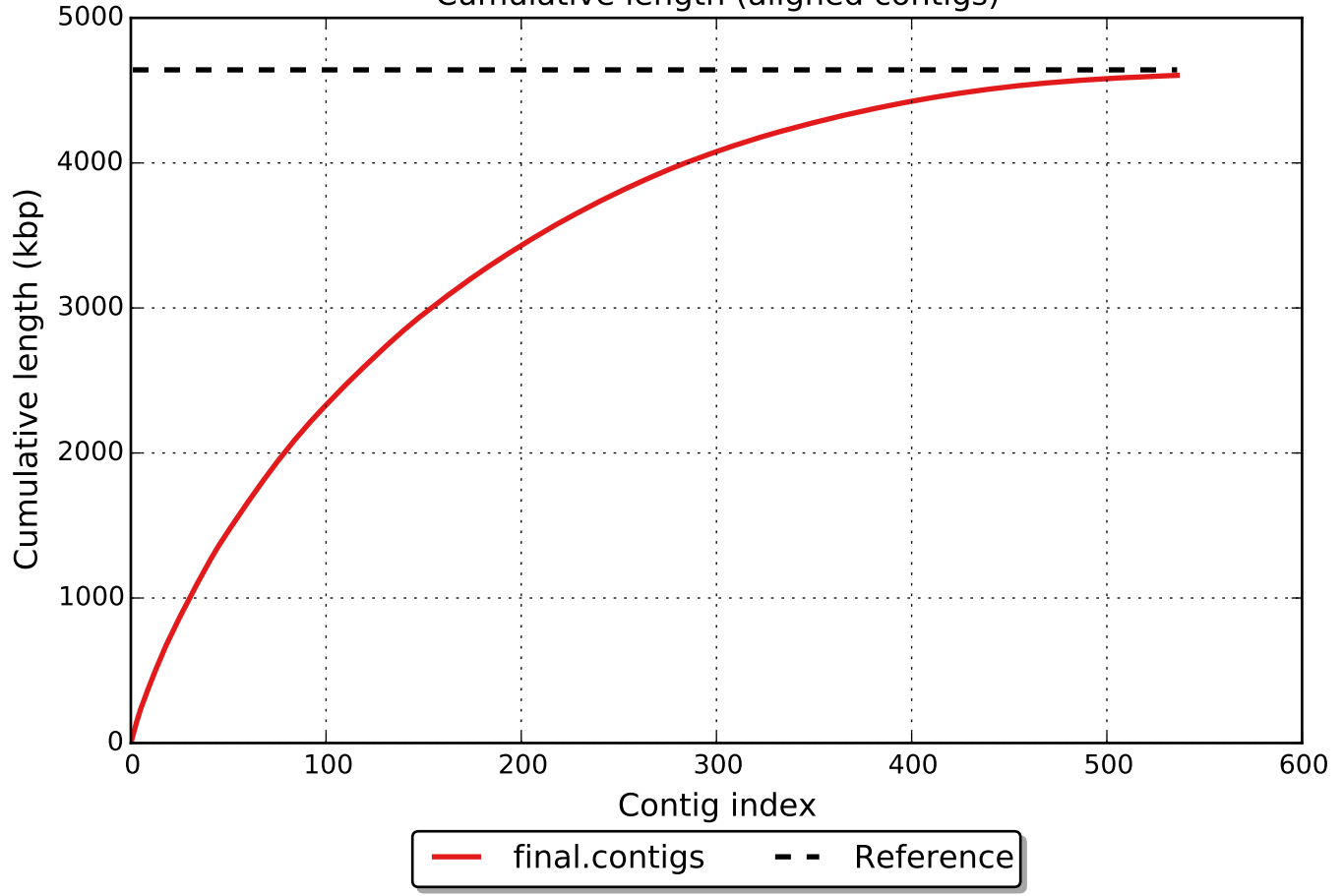


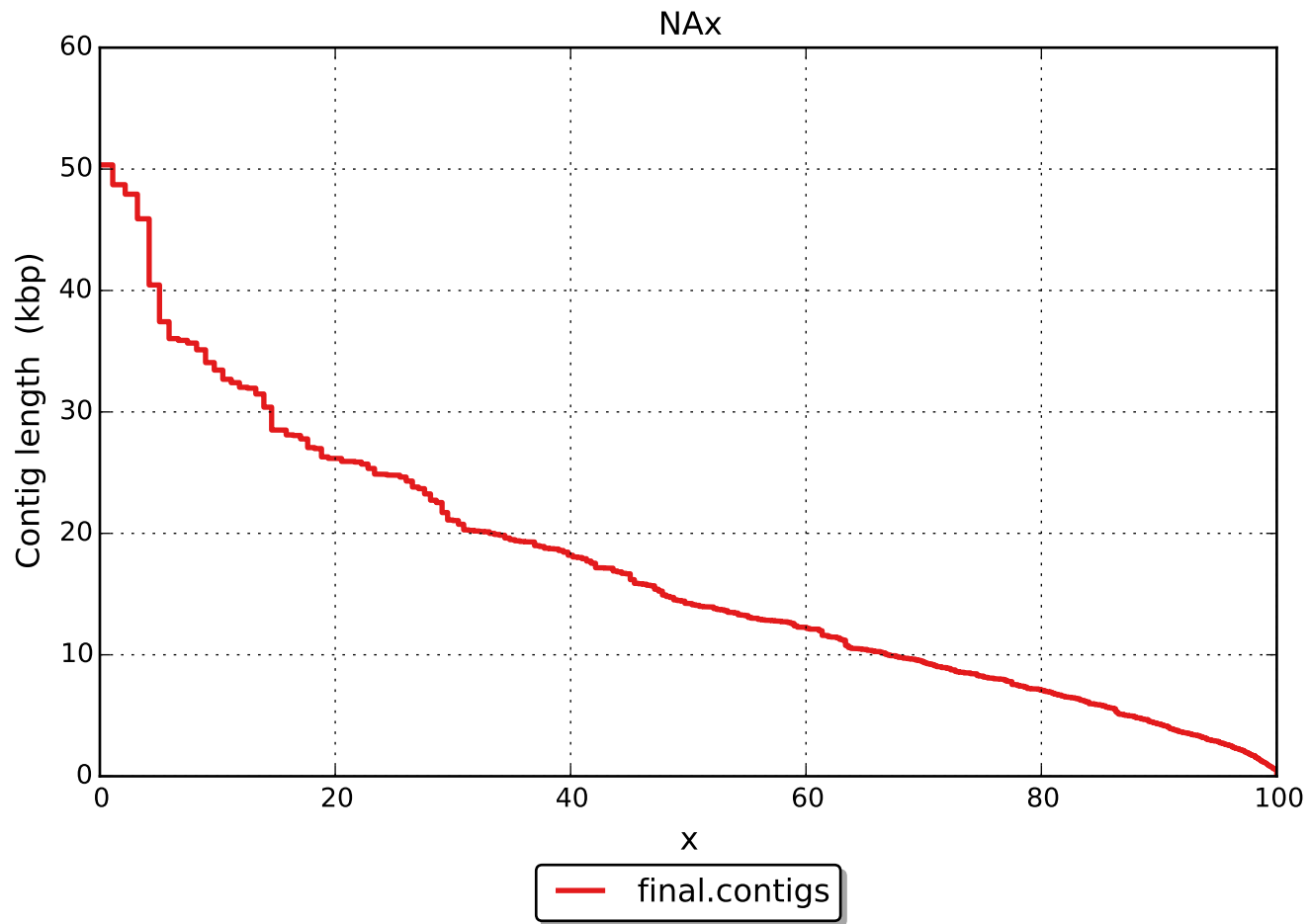
# Misassemblies





Cumulative length (aligned contigs)





NGAx

