

## Report

	final.contigs
# contigs (>= 1000 bp)	359
# contigs (>= 5000 bp)	255
# contigs (>= 10000 bp)	180
# contigs (>= 25000 bp)	54
# contigs (>= 50000 bp)	9
Total length (>= 1000 bp)	4868721
Total length (>= 5000 bp)	4565312
Total length (>= 10000 bp)	4030964
Total length (>= 25000 bp)	1993270
Total length (>= 50000 bp)	567634
# contigs	375
Largest contig	78175
Total length	4880557
Reference length	4857432
GC (%)	52.23
Reference GC (%)	52.23
N50	20934
NG50	21045
N75	12784
NG75	12795
L50	74
LG50	73
L75	148
LG75	147
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.674
Duplication ratio	1.008
# N's per 100 kbp	0.00
# mismatches per 100 kbp	9.79
# indels per 100 kbp	0.00
Largest alignment	78175
NA50	20934
NGA50	21045
NA75	12784
NGA75	12795
LA50	74
LGA50	73
LA75	148
LGA75	147

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

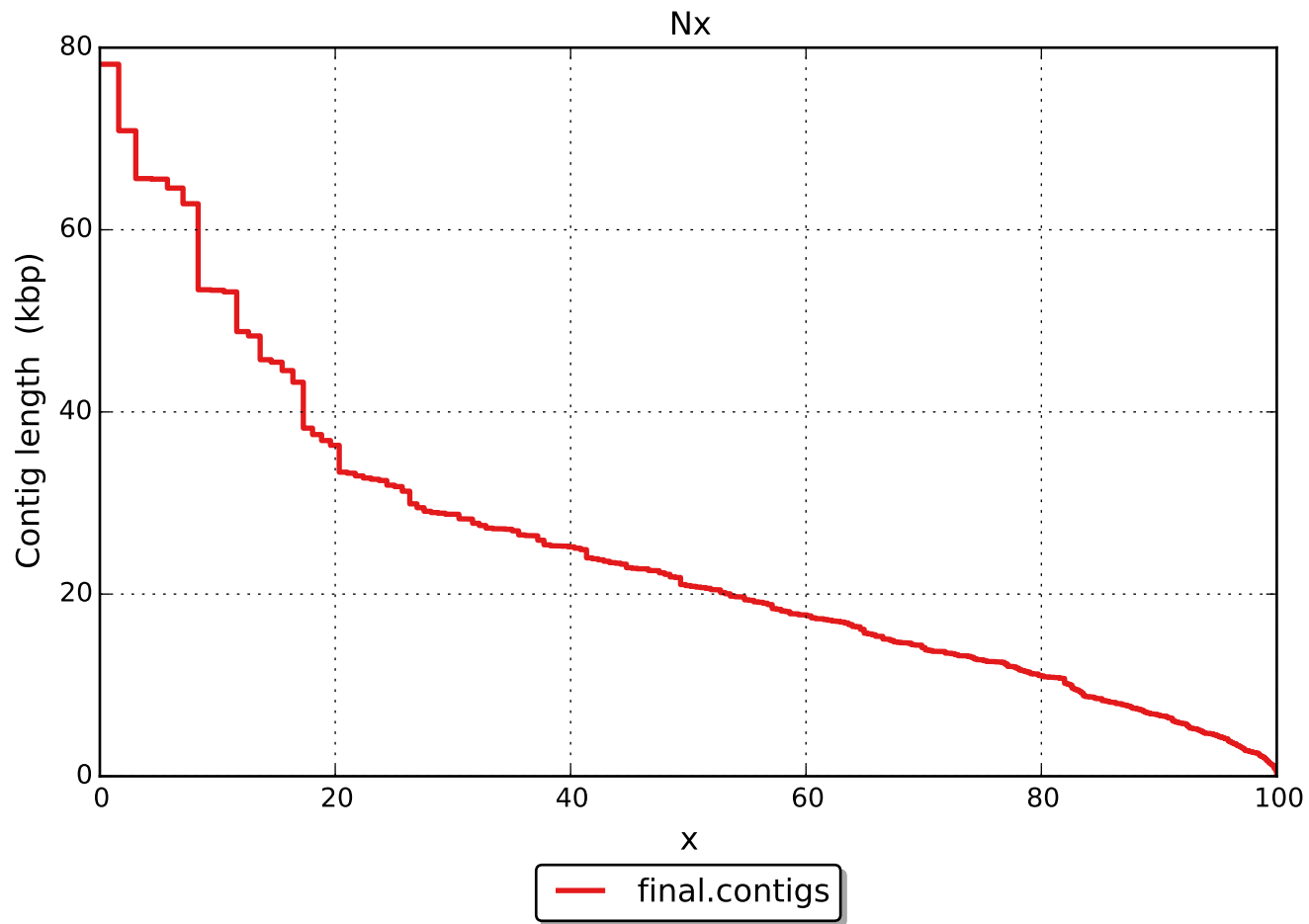
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	474
# indels	0
# short indels	0
# long indels	0
Indels length	0

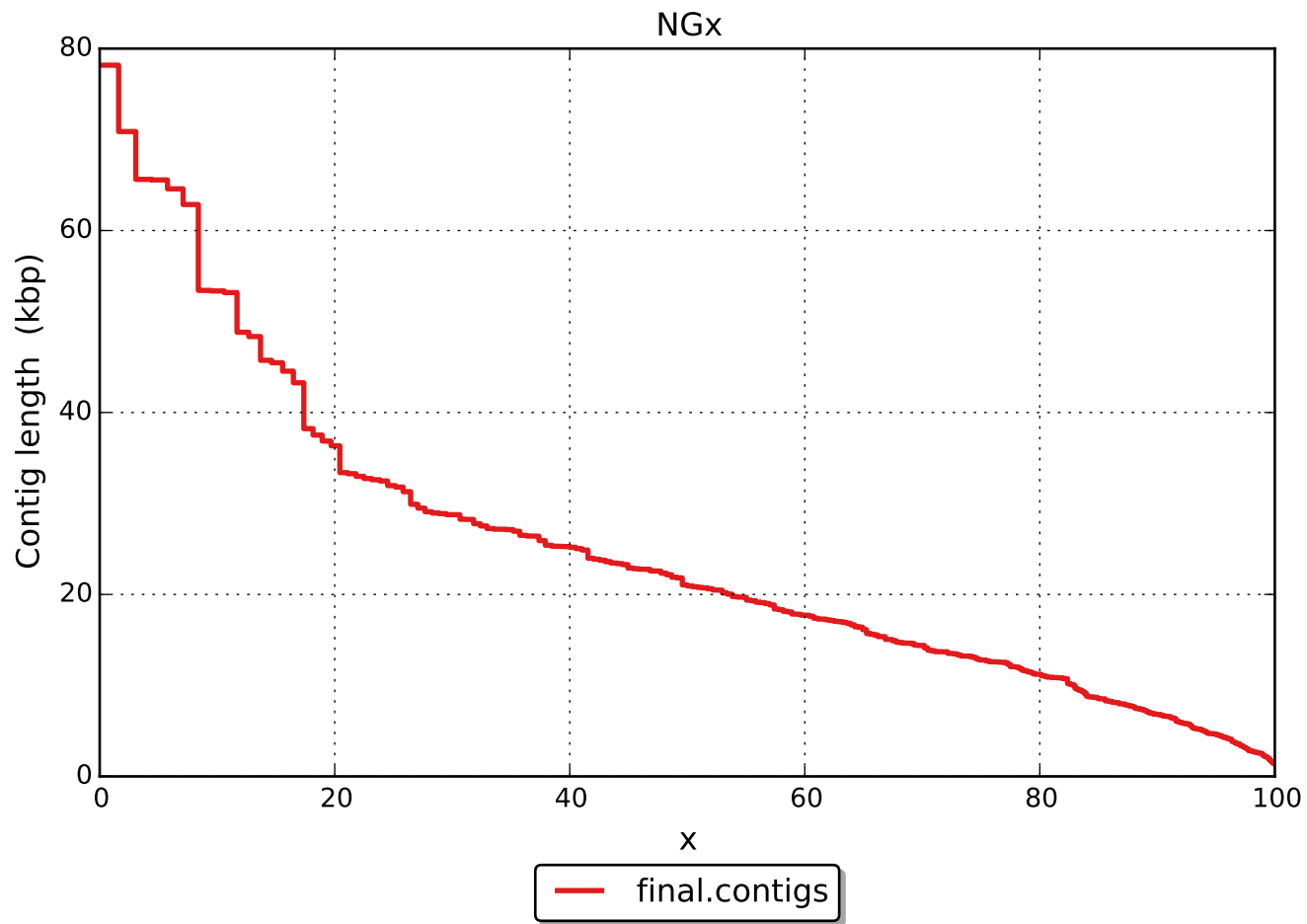
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

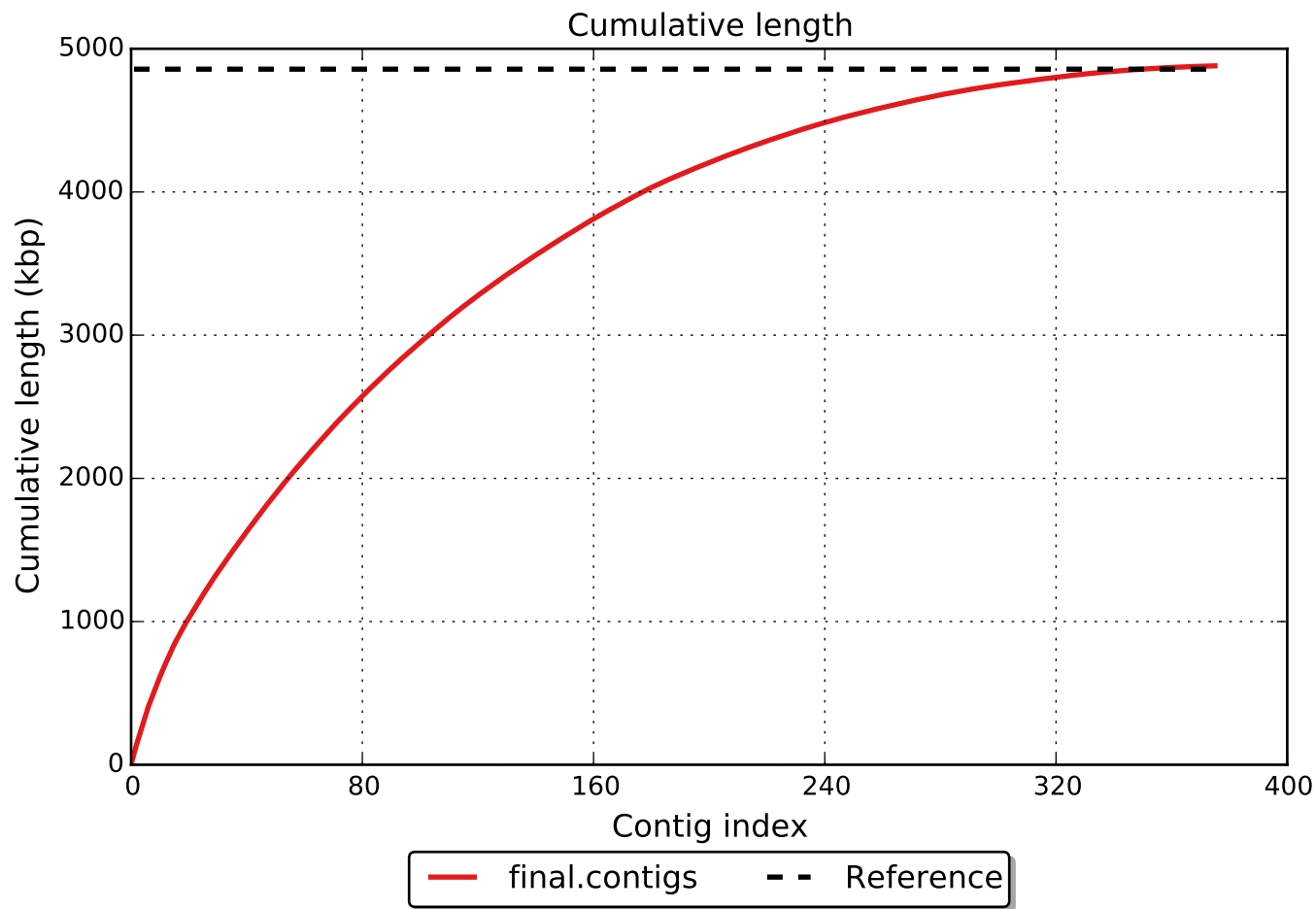
## Unaligned report

	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

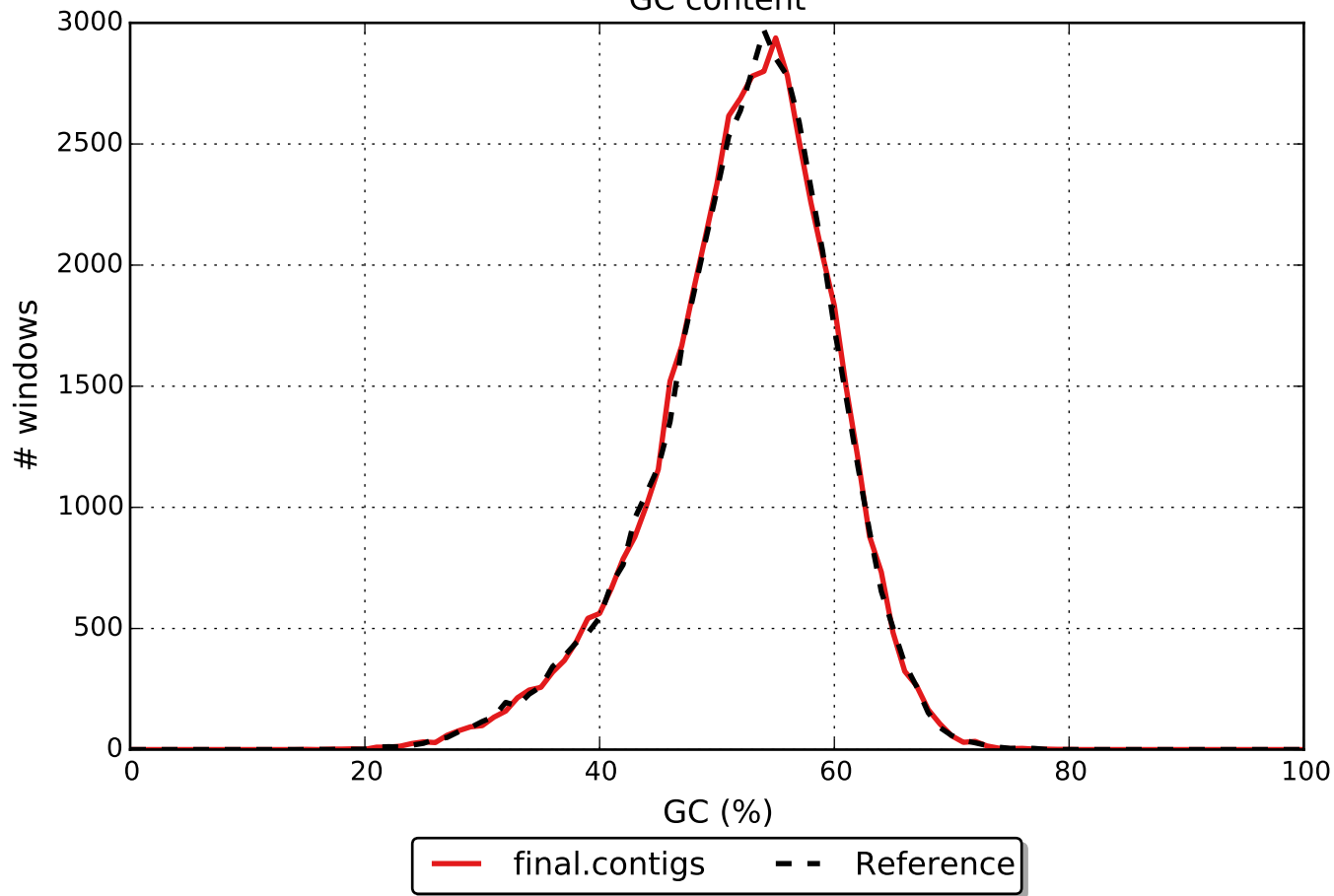
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).







GC content

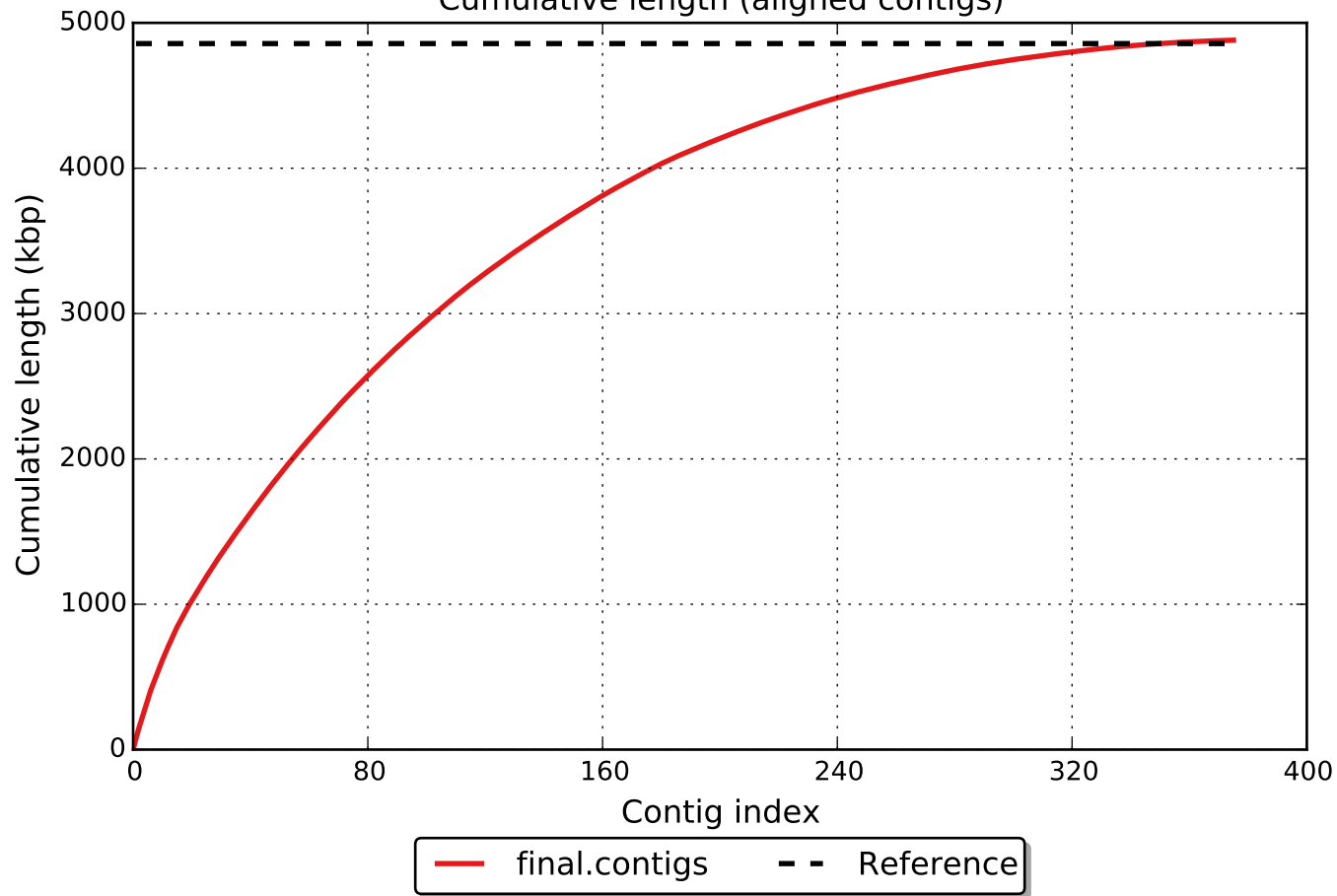


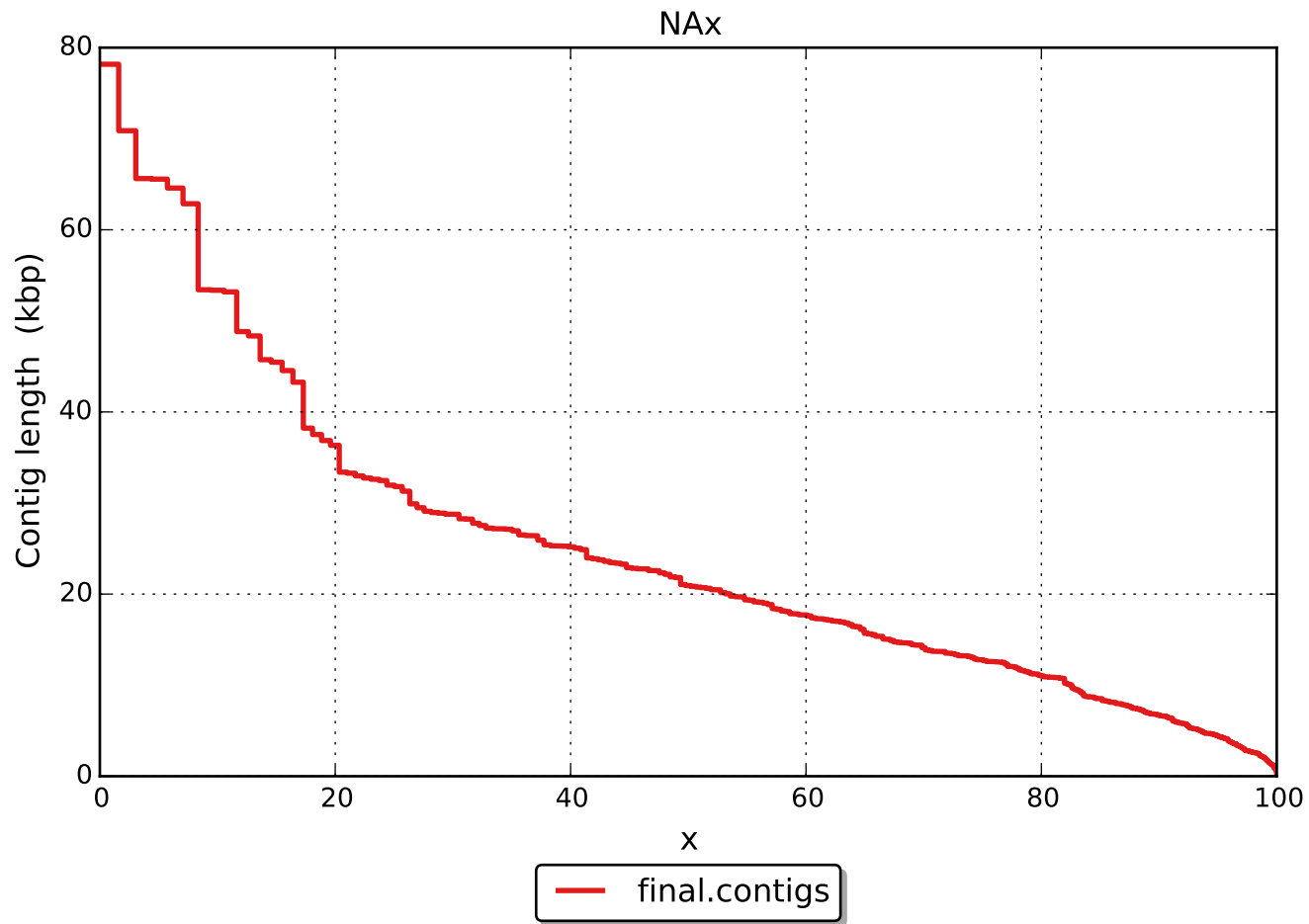
# Misassemblies





Cumulative length (aligned contigs)





NGAx

