

## Report

	final.contigs
# contigs (>= 1000 bp)	754
# contigs (>= 5000 bp)	354
# contigs (>= 10000 bp)	142
# contigs (>= 25000 bp)	13
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4791543
Total length (>= 5000 bp)	3742938
Total length (>= 10000 bp)	2262326
Total length (>= 25000 bp)	398506
Total length (>= 50000 bp)	0
# contigs	842
Largest contig	46253
Total length	4857031
Reference length	4857432
GC (%)	52.21
Reference GC (%)	52.22
N50	9172
NG50	9172
N75	5203
NG75	5203
L50	160
LG50	160
L75	335
LG75	335
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.399
Duplication ratio	1.016
# N's per 100 kbp	0.00
# mismatches per 100 kbp	21.26
# indels per 100 kbp	0.00
Largest alignment	46253
NA50	9172
NGA50	9172
NA75	5203
NGA75	5203
LA50	160
LGA50	160
LA75	335
LGA75	335

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

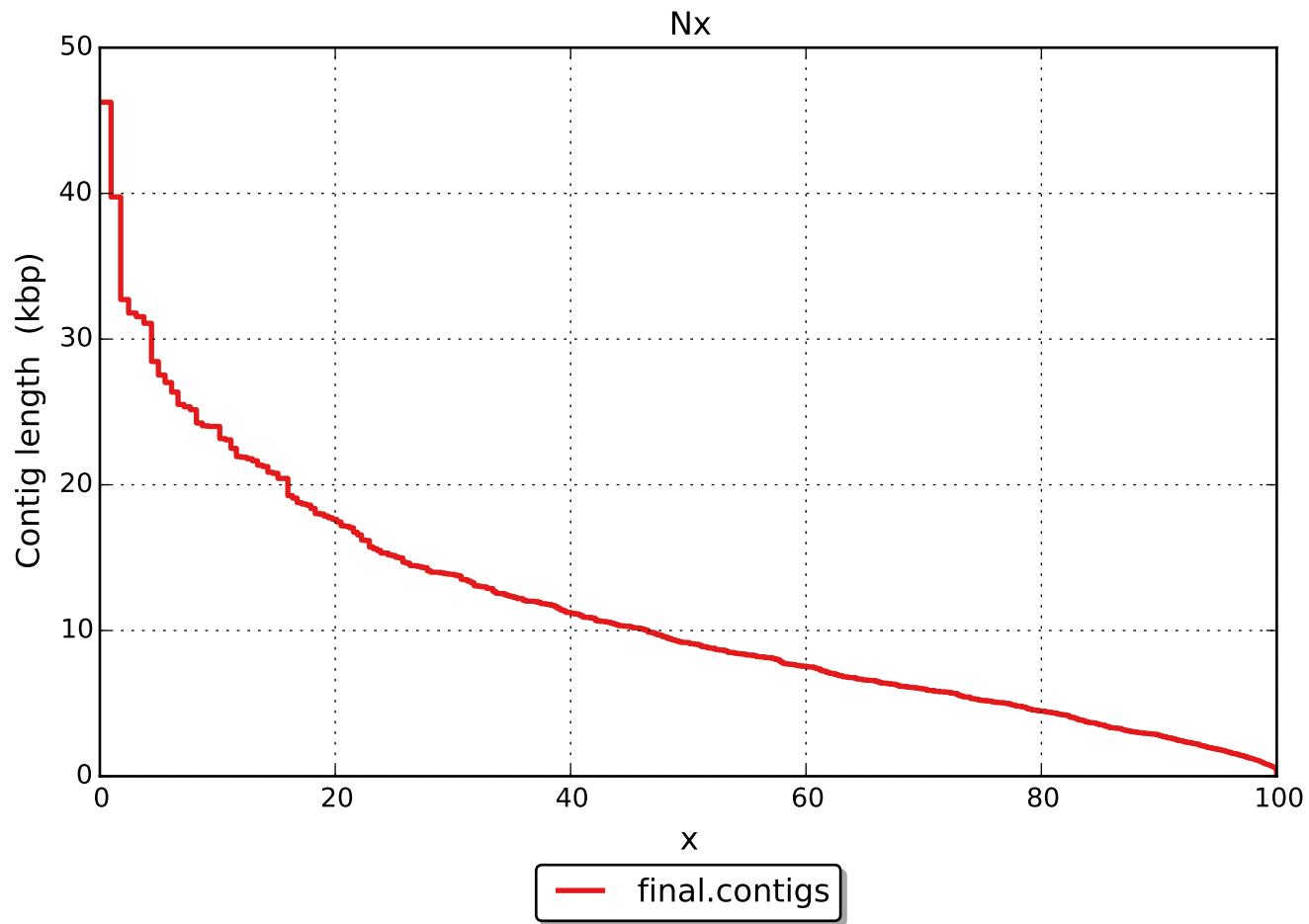
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	1016
# indels	0
# short indels	0
# long indels	0
Indels length	0

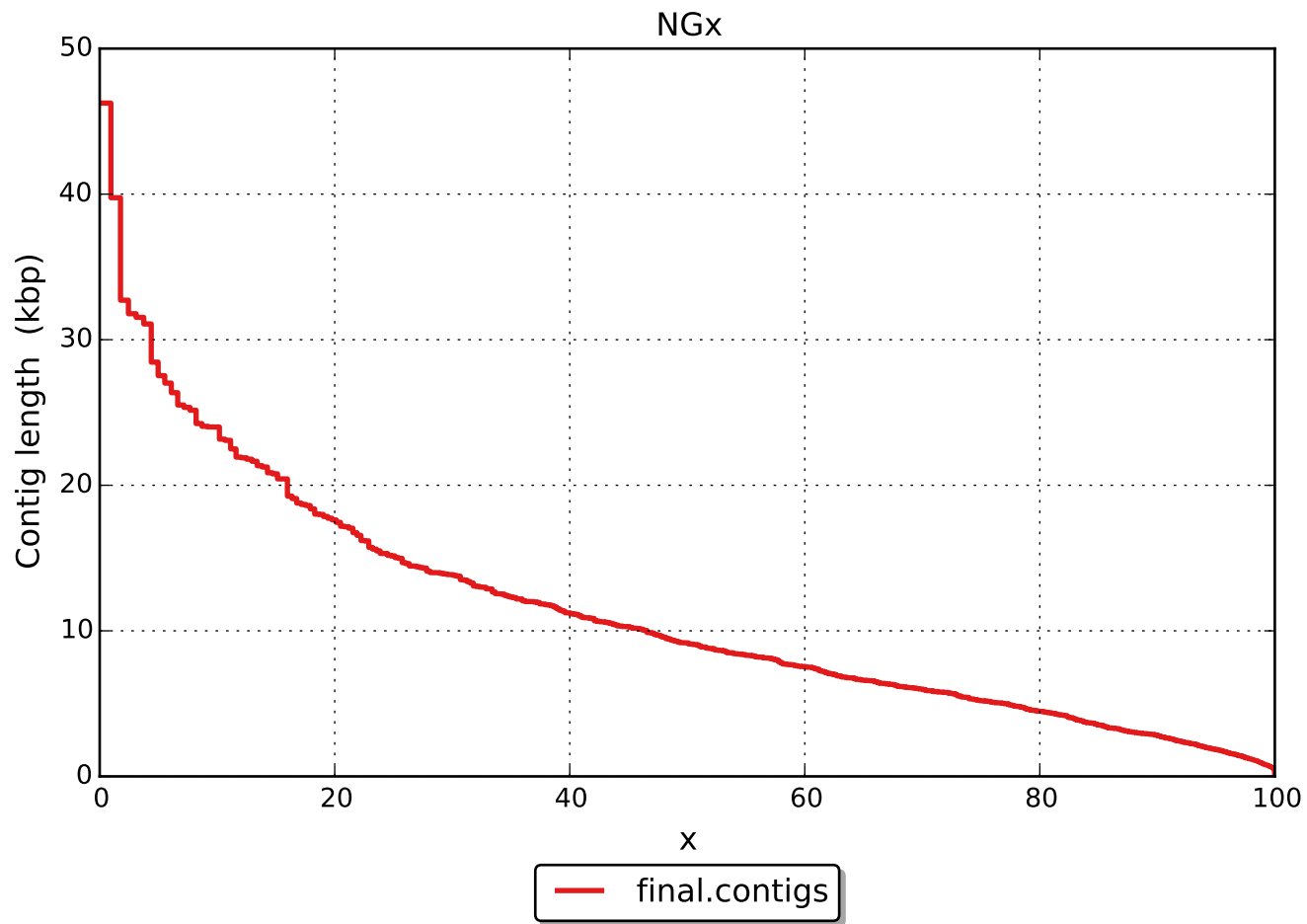
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

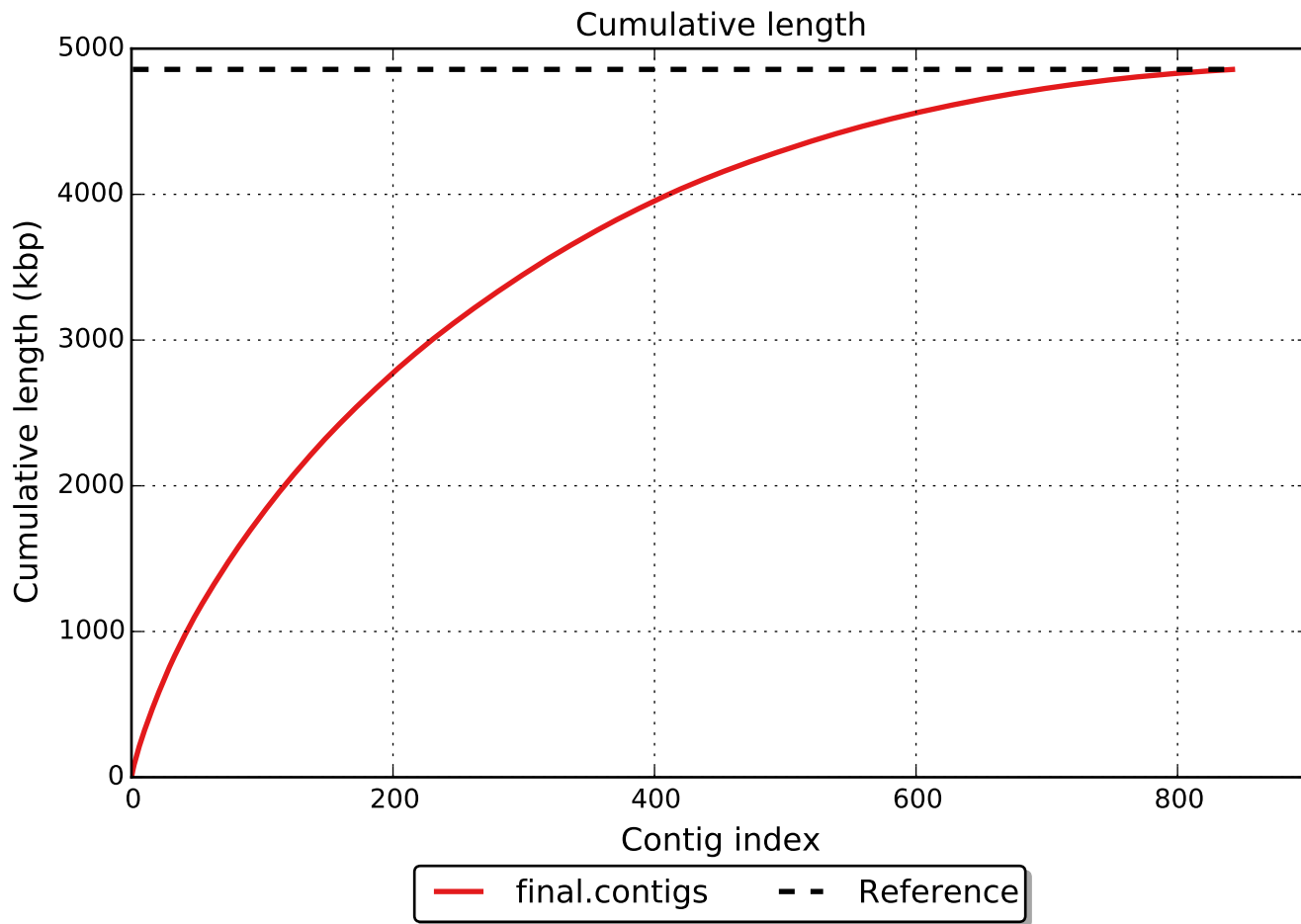
## Unaligned report

	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

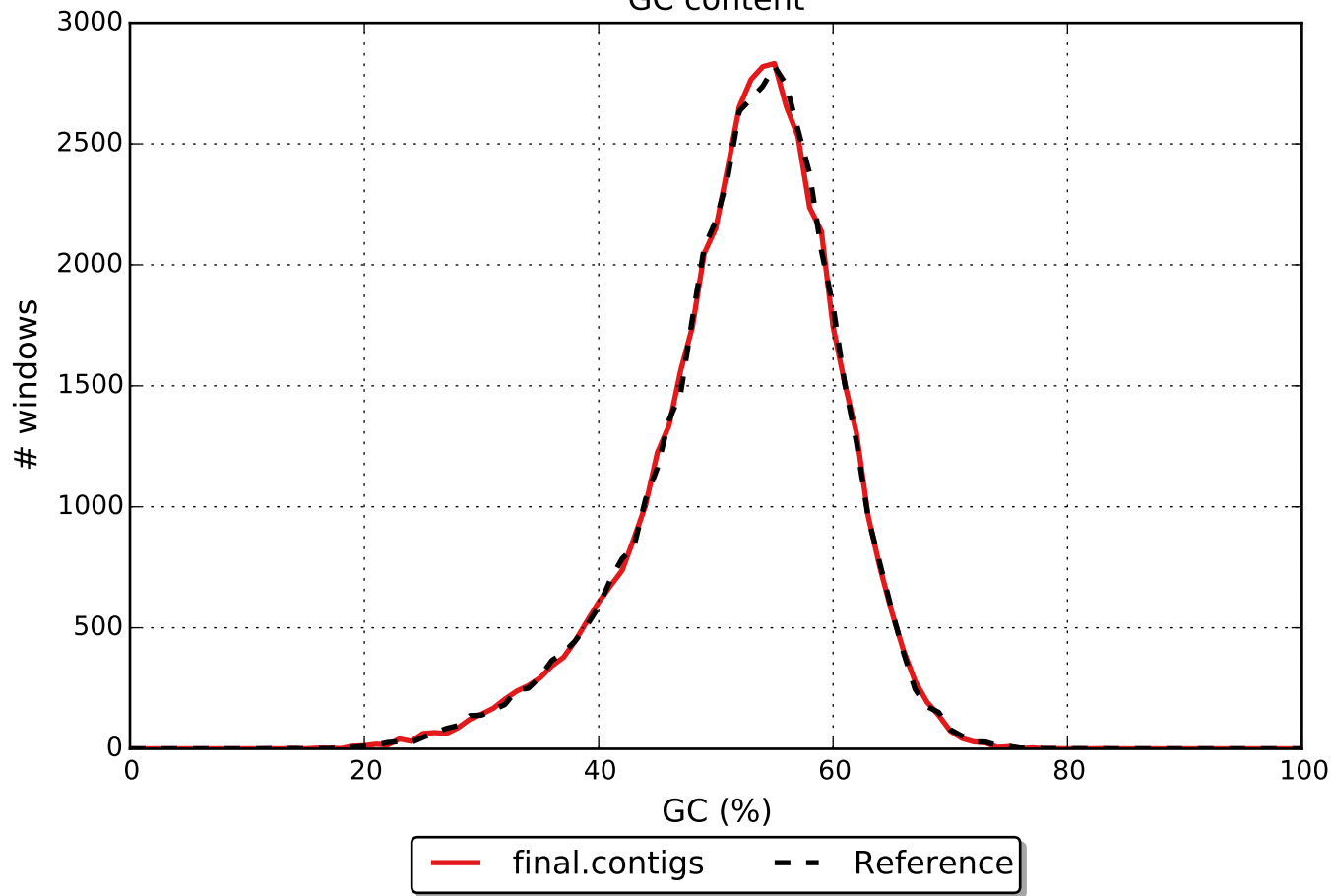
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).







GC content

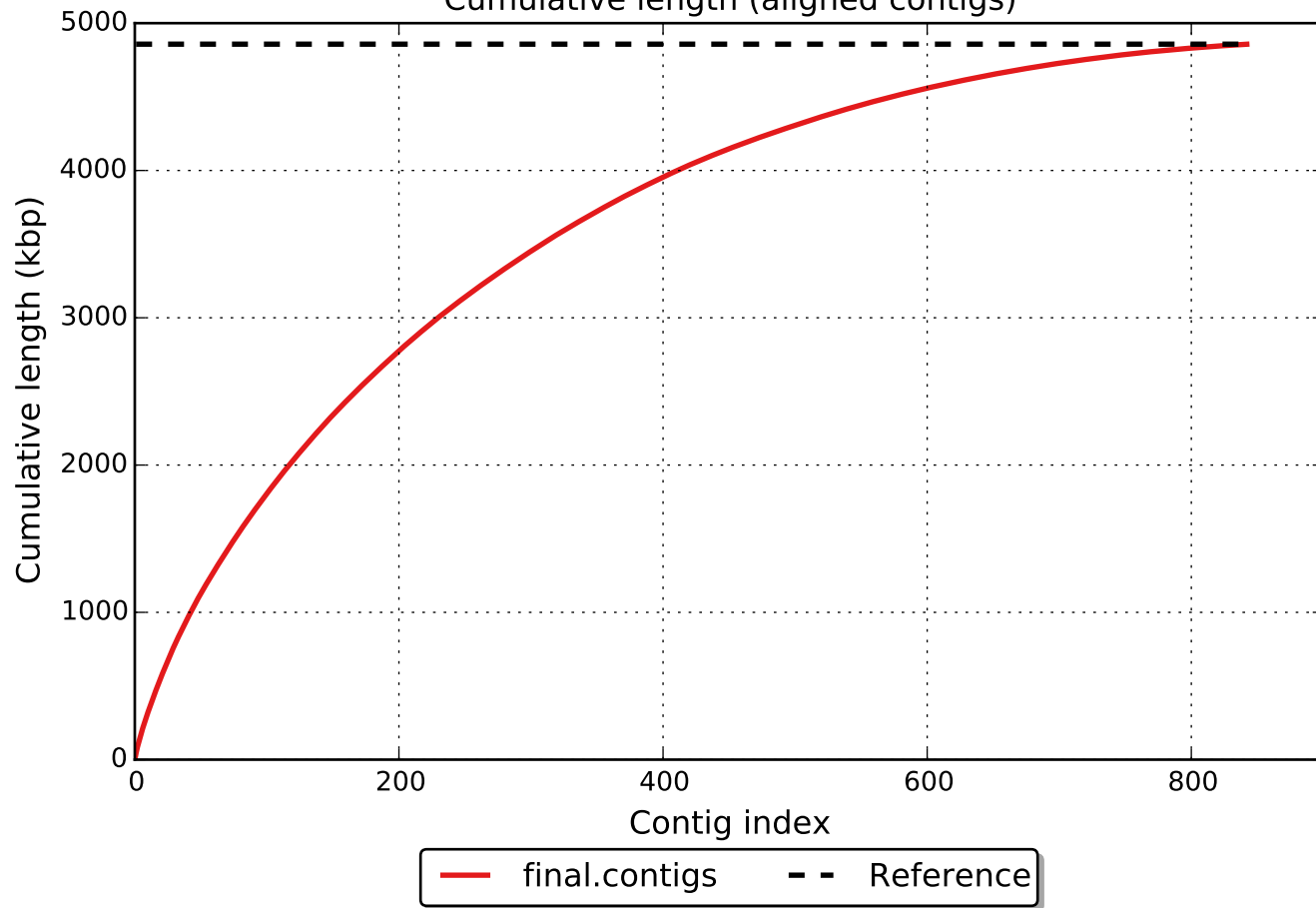


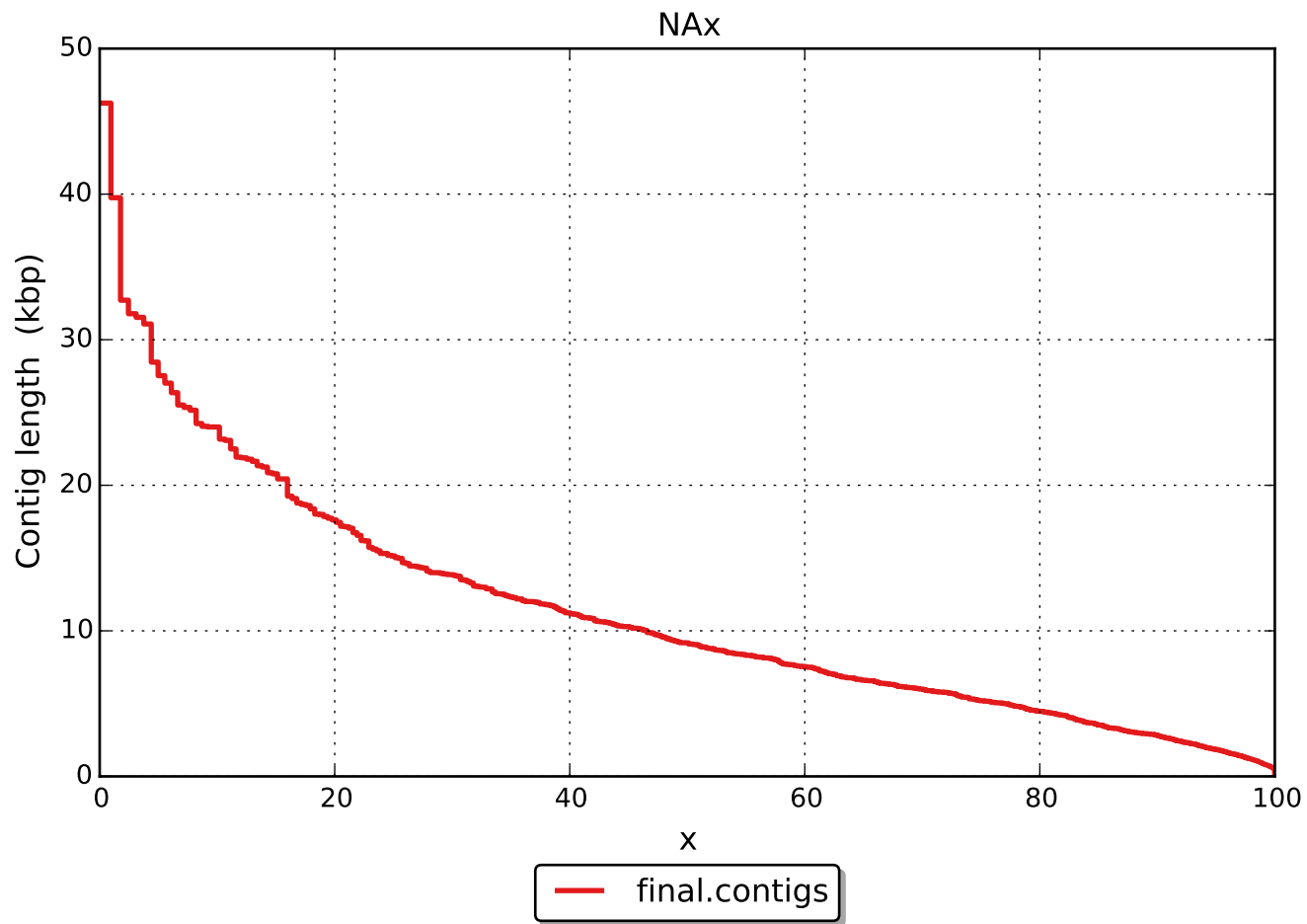
# Misassemblies





Cumulative length (aligned contigs)





# NGAx

