

## Report

	final.contigs
# contigs (>= 1000 bp)	618
# contigs (>= 5000 bp)	340
# contigs (>= 10000 bp)	158
# contigs (>= 25000 bp)	19
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4809470
Total length (>= 5000 bp)	4041918
Total length (>= 10000 bp)	2721086
Total length (>= 25000 bp)	626560
Total length (>= 50000 bp)	0
# contigs	671
Largest contig	46180
Total length	4846952
Reference length	4857432
GC (%)	52.20
Reference GC (%)	52.22
N50	11524
NG50	11524
N75	6727
NG75	6592
L50	131
LG50	131
L75	270
LG75	272
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.556
Duplication ratio	1.012
# N's per 100 kbp	0.00
# mismatches per 100 kbp	15.94
# indels per 100 kbp	0.15
Largest alignment	46180
NA50	11524
NGA50	11524
NA75	6727
NGA75	6592
LA50	131
LGA50	131
LA75	270
LGA75	272

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

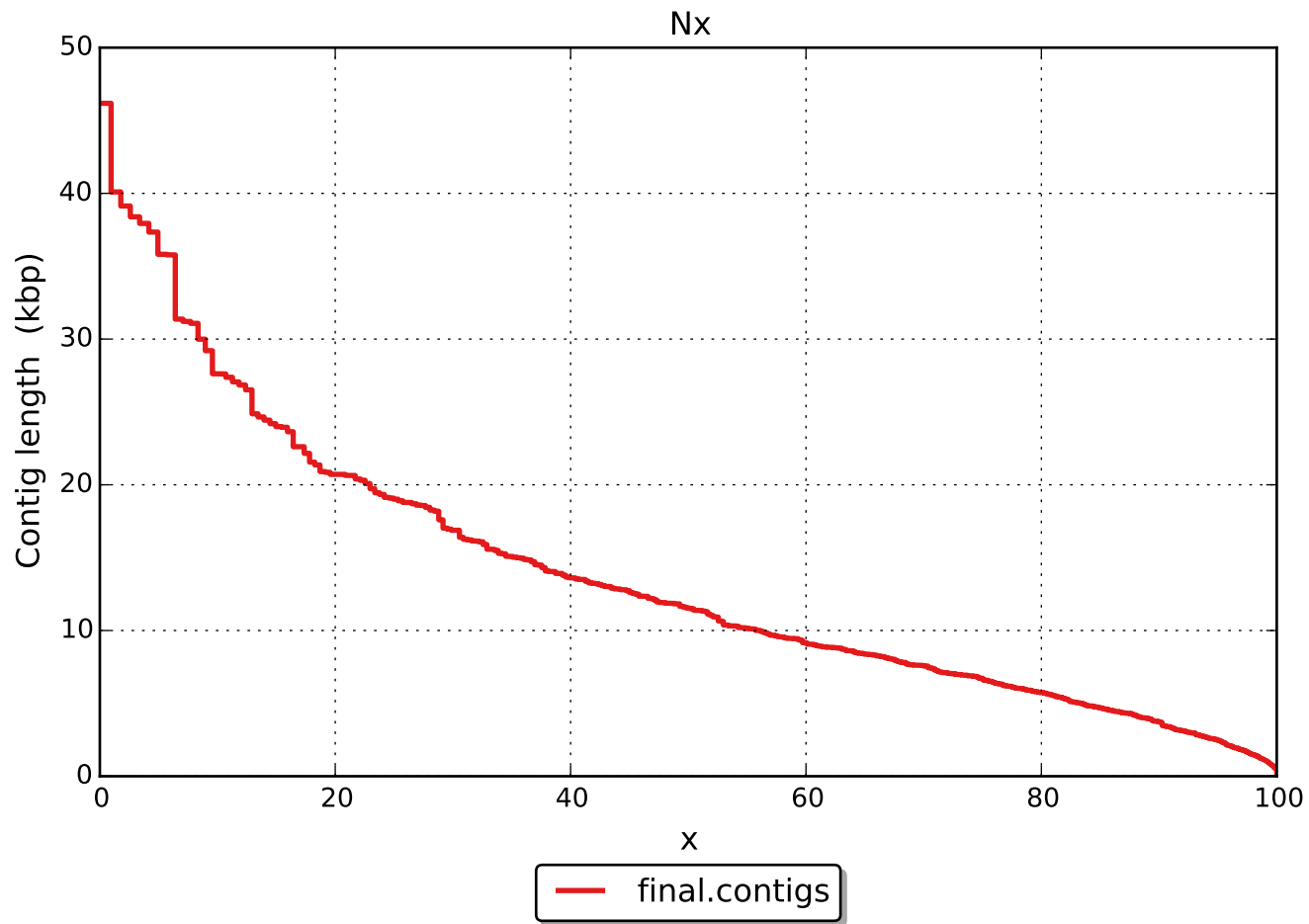
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	763
# indels	7
# short indels	6
# long indels	1
Indels length	69

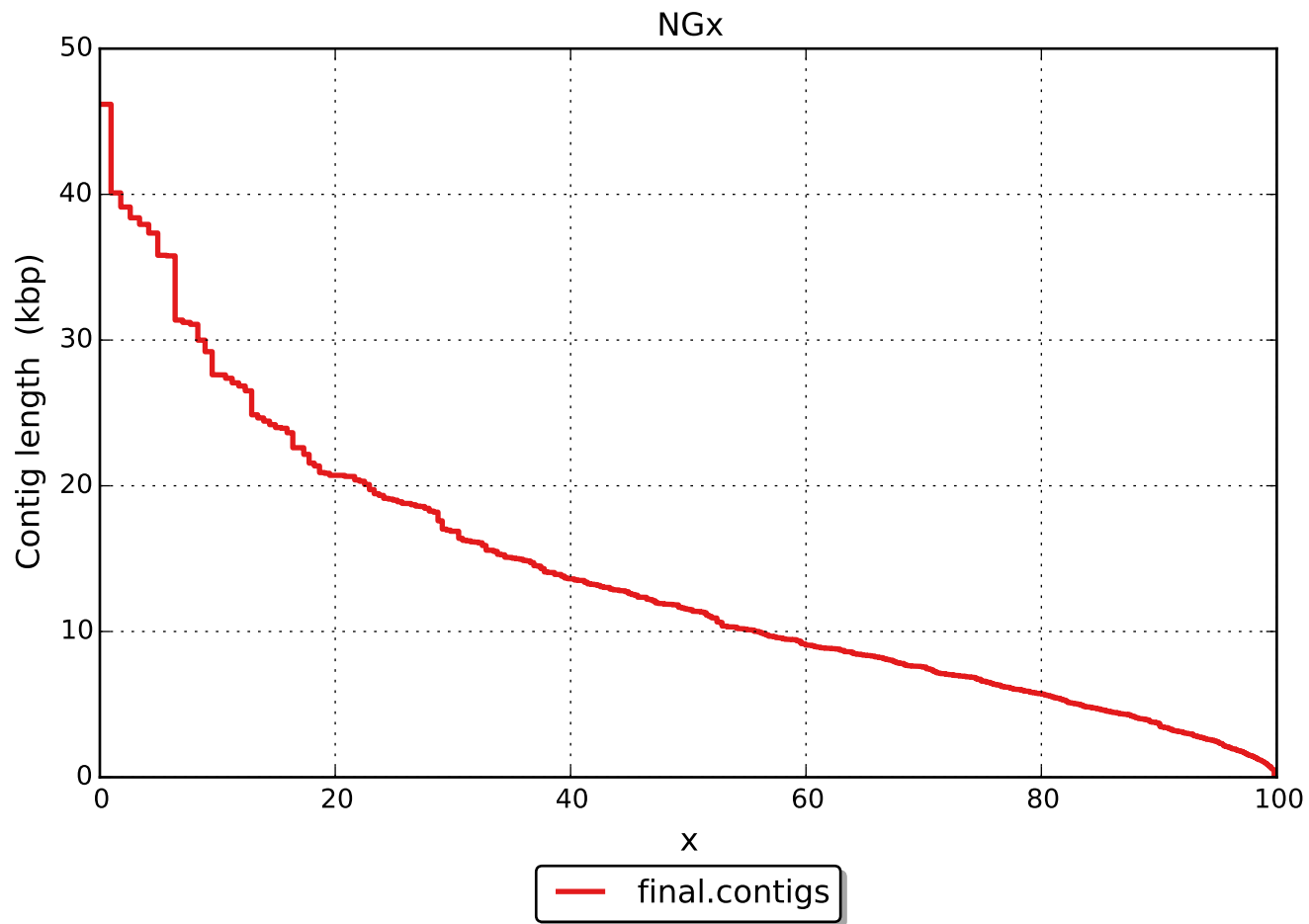
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

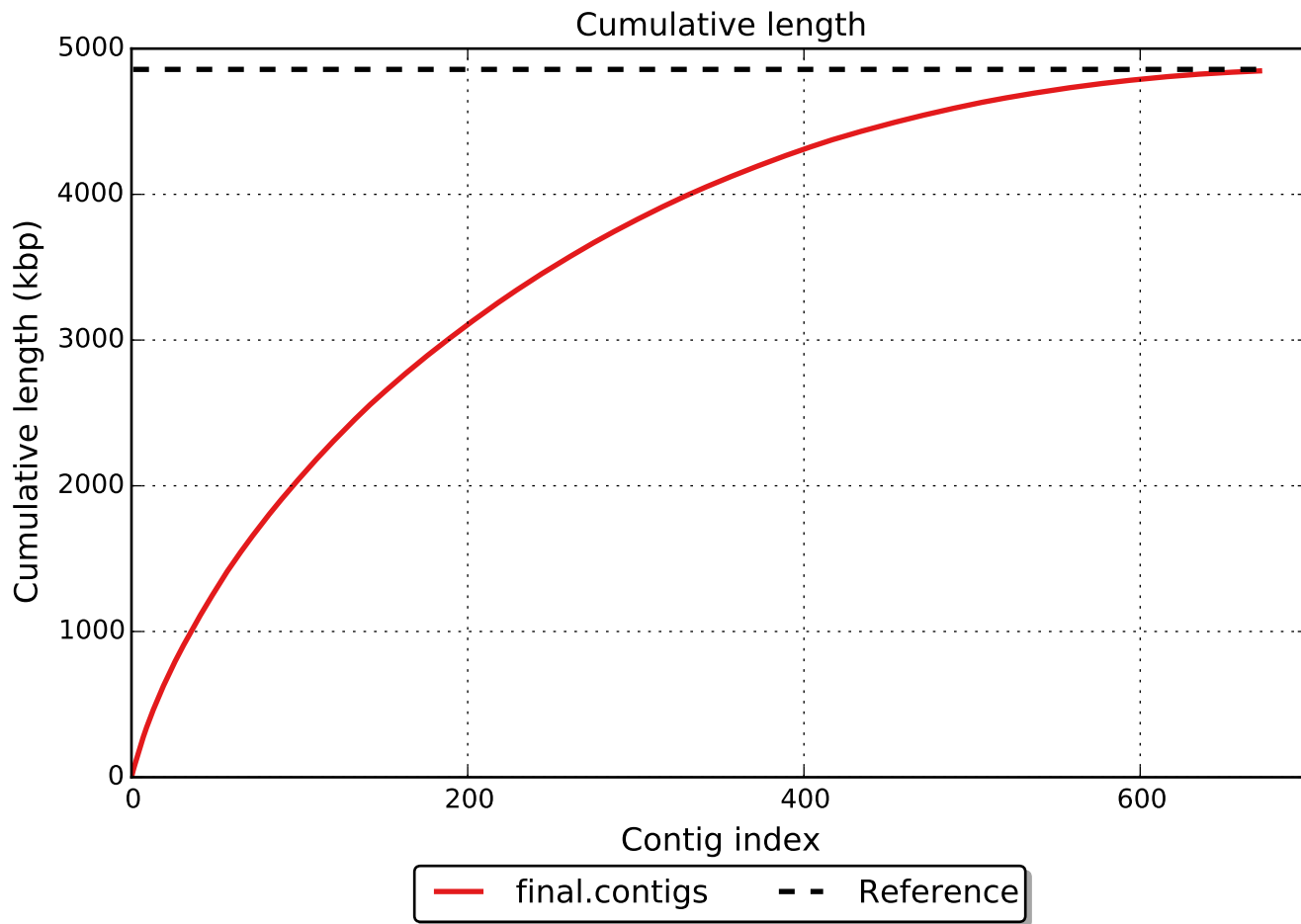
## Unaligned report

	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

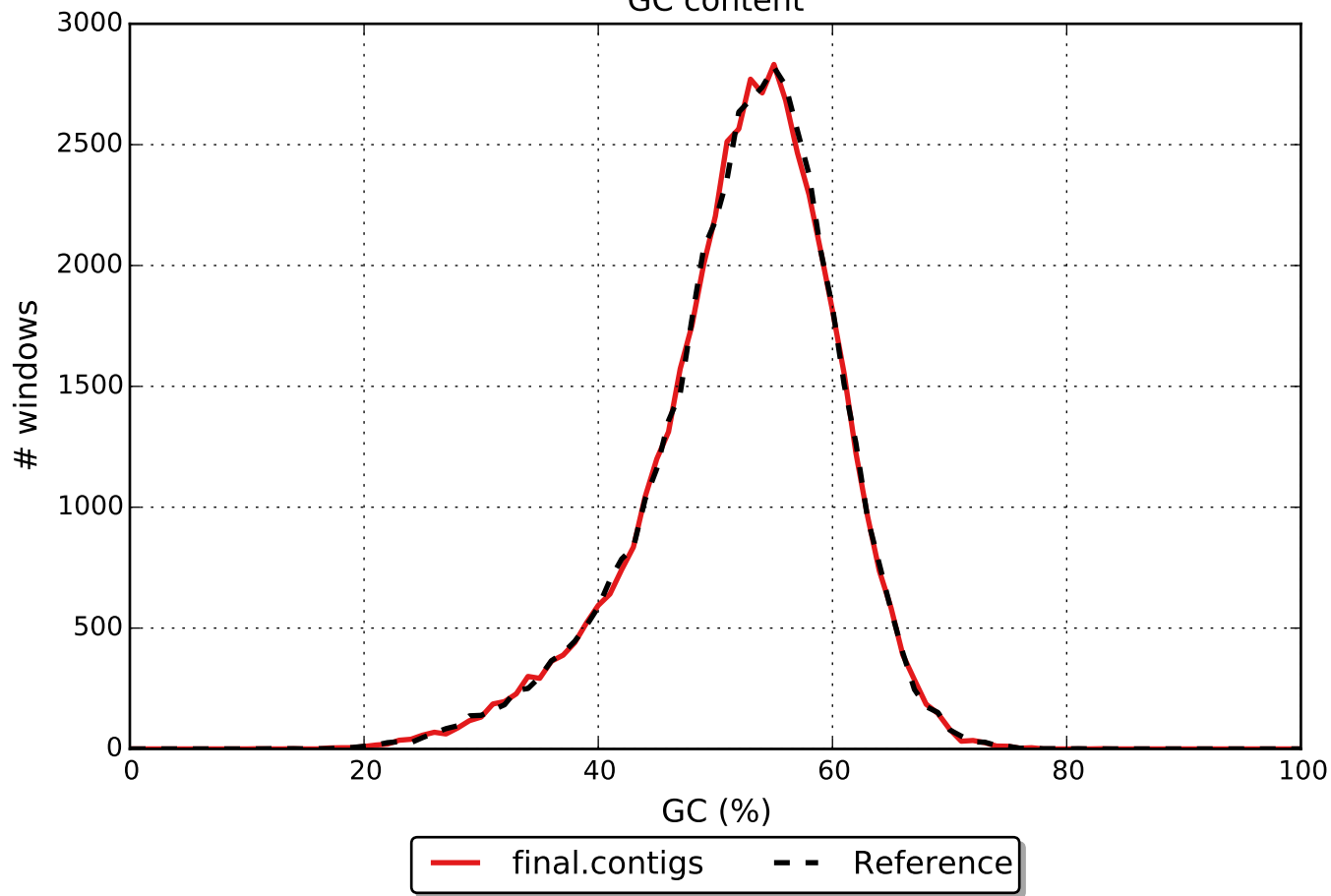
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).







GC content

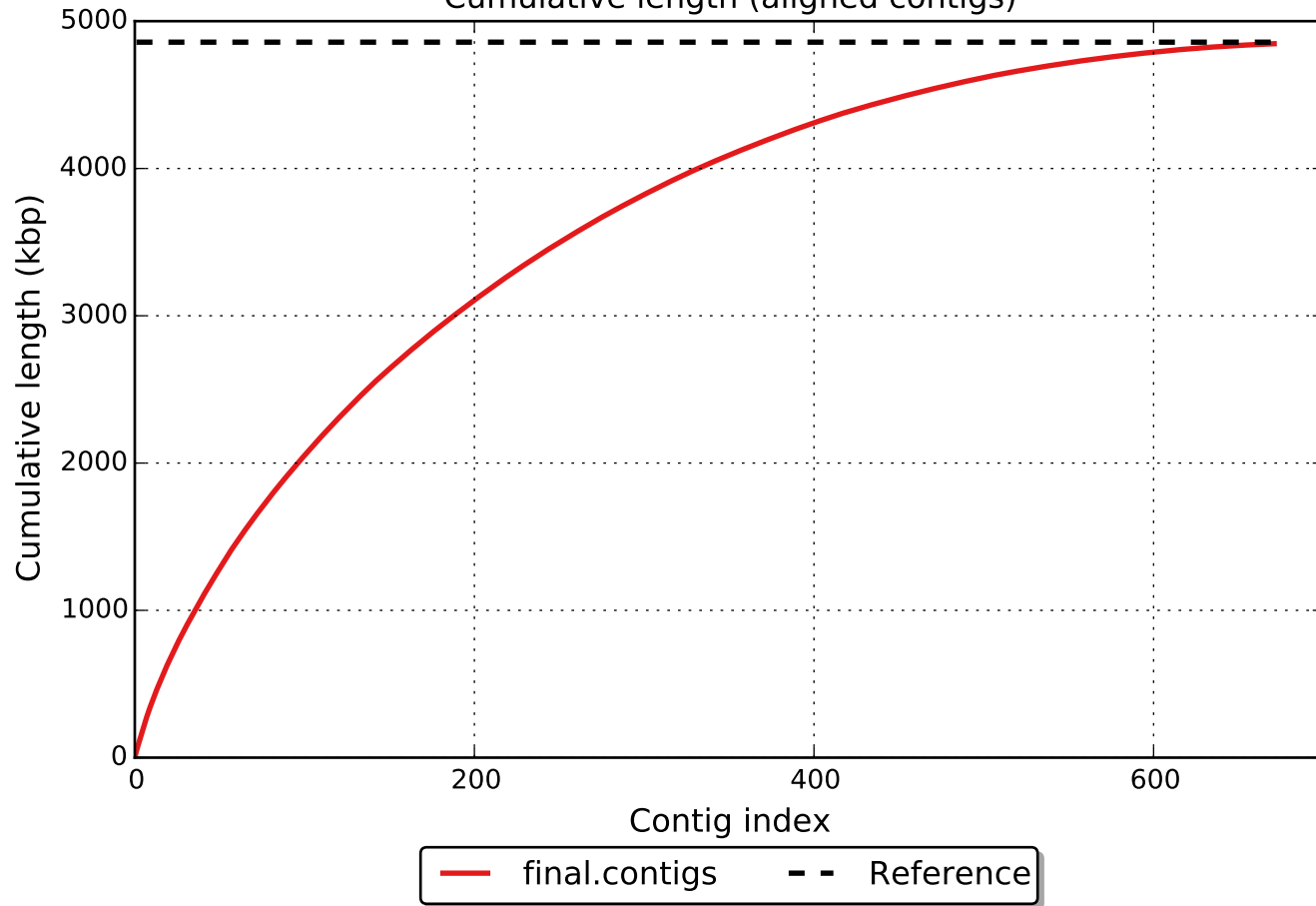


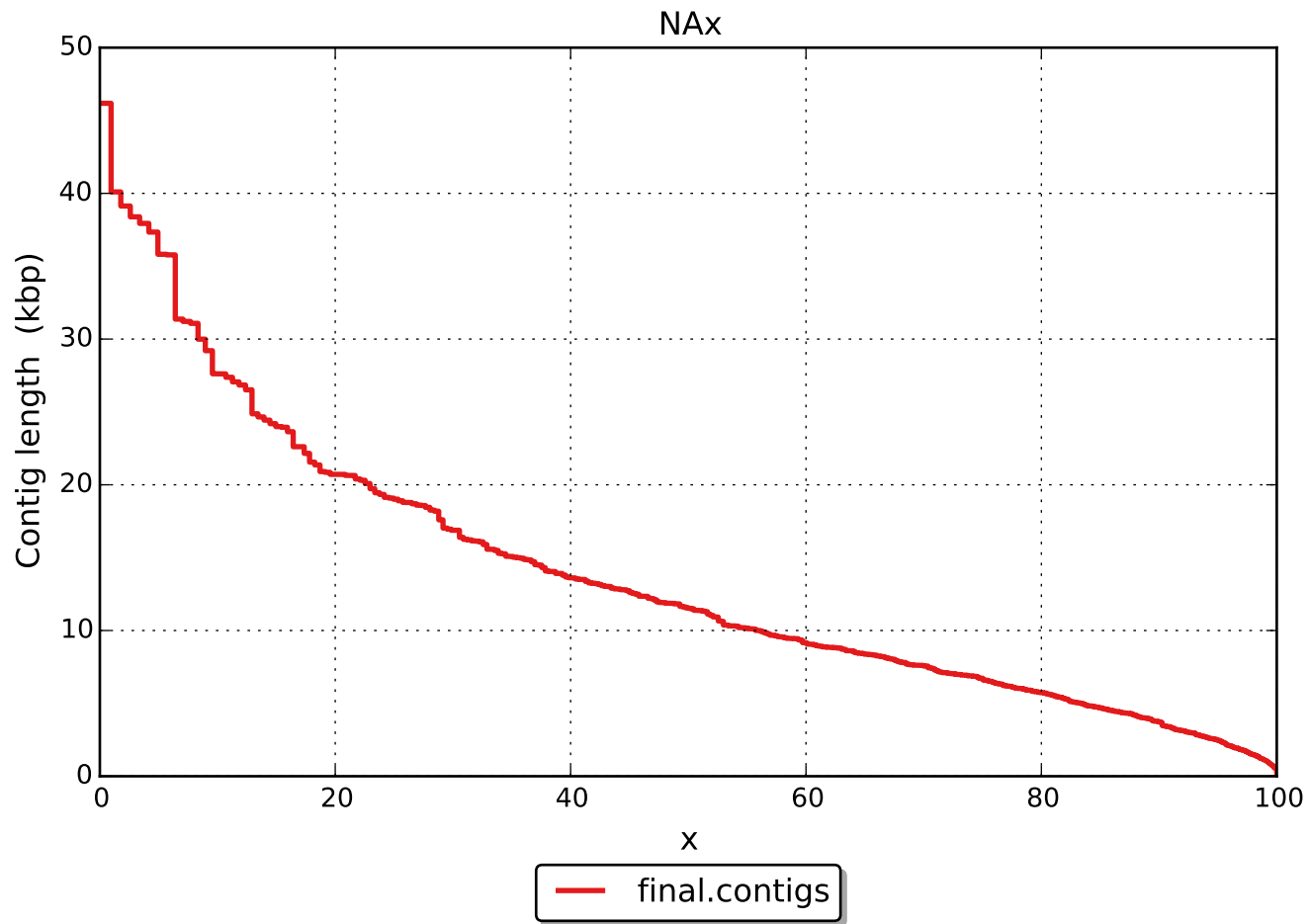
# Misassemblies





Cumulative length (aligned contigs)





# NGAx

