

## Report

	final.contigs
# contigs (>= 1000 bp)	1377
# contigs (>= 5000 bp)	259
# contigs (>= 10000 bp)	29
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4653558
Total length (>= 5000 bp)	1921608
Total length (>= 10000 bp)	355340
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	1717
Largest contig	15687
Total length	4899243
Reference length	4857432
GC (%)	52.22
Reference GC (%)	52.22
N50	3992
NG50	4008
N75	2394
NG75	2426
L50	378
LG50	372
L75	773
LG75	760
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	97.790
Duplication ratio	1.031
# N's per 100 kbp	0.00
# mismatches per 100 kbp	39.14
# indels per 100 kbp	0.02
Largest alignment	15687
NA50	3992
NGA50	4008
NA75	2393
NGA75	2426
LA50	378
LGA50	372
LA75	773
LGA75	760

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

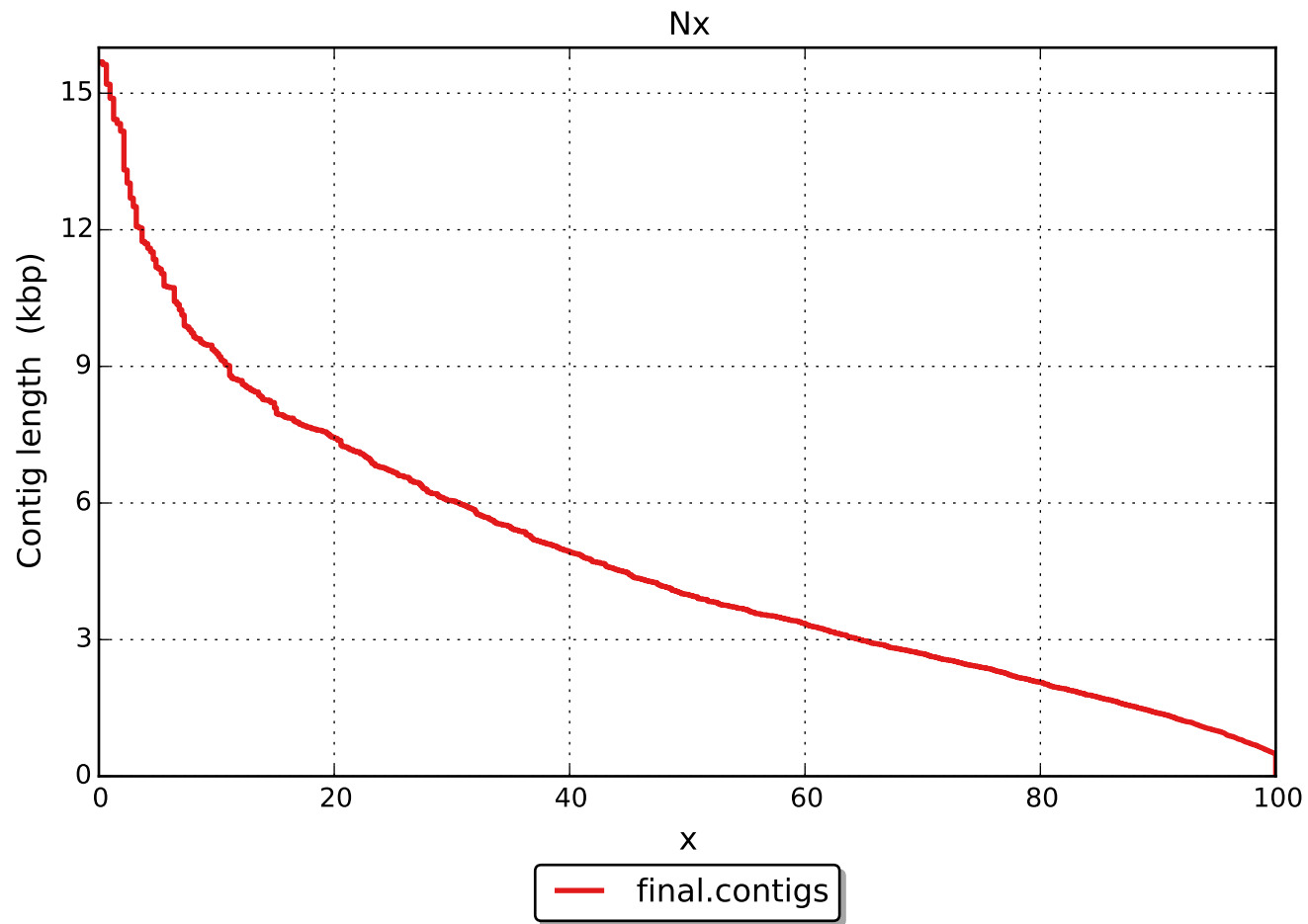
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# mismatches	1859
# indels	1
# short indels	1
# long indels	0
Indels length	1

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).

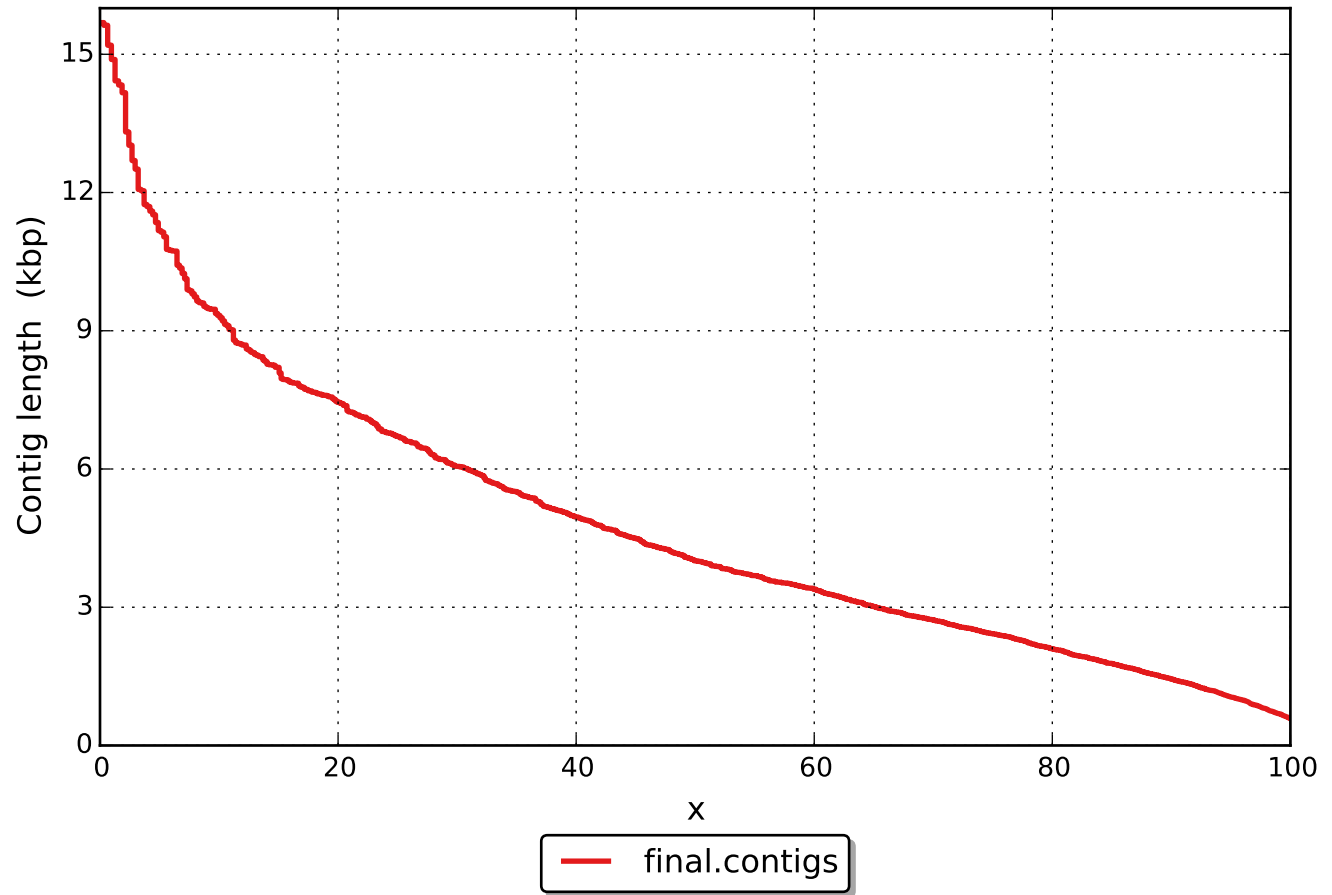
## Unaligned report

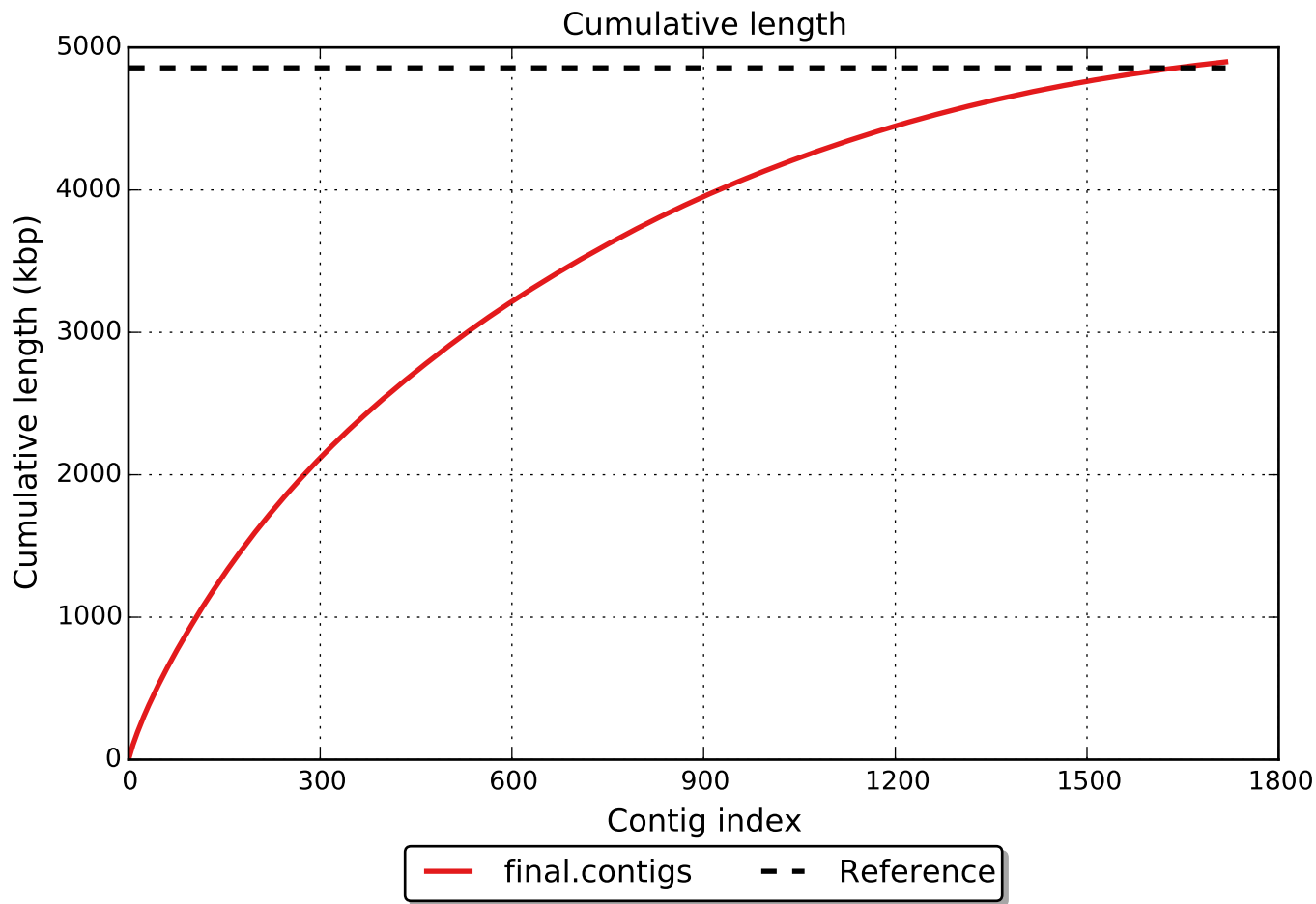
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

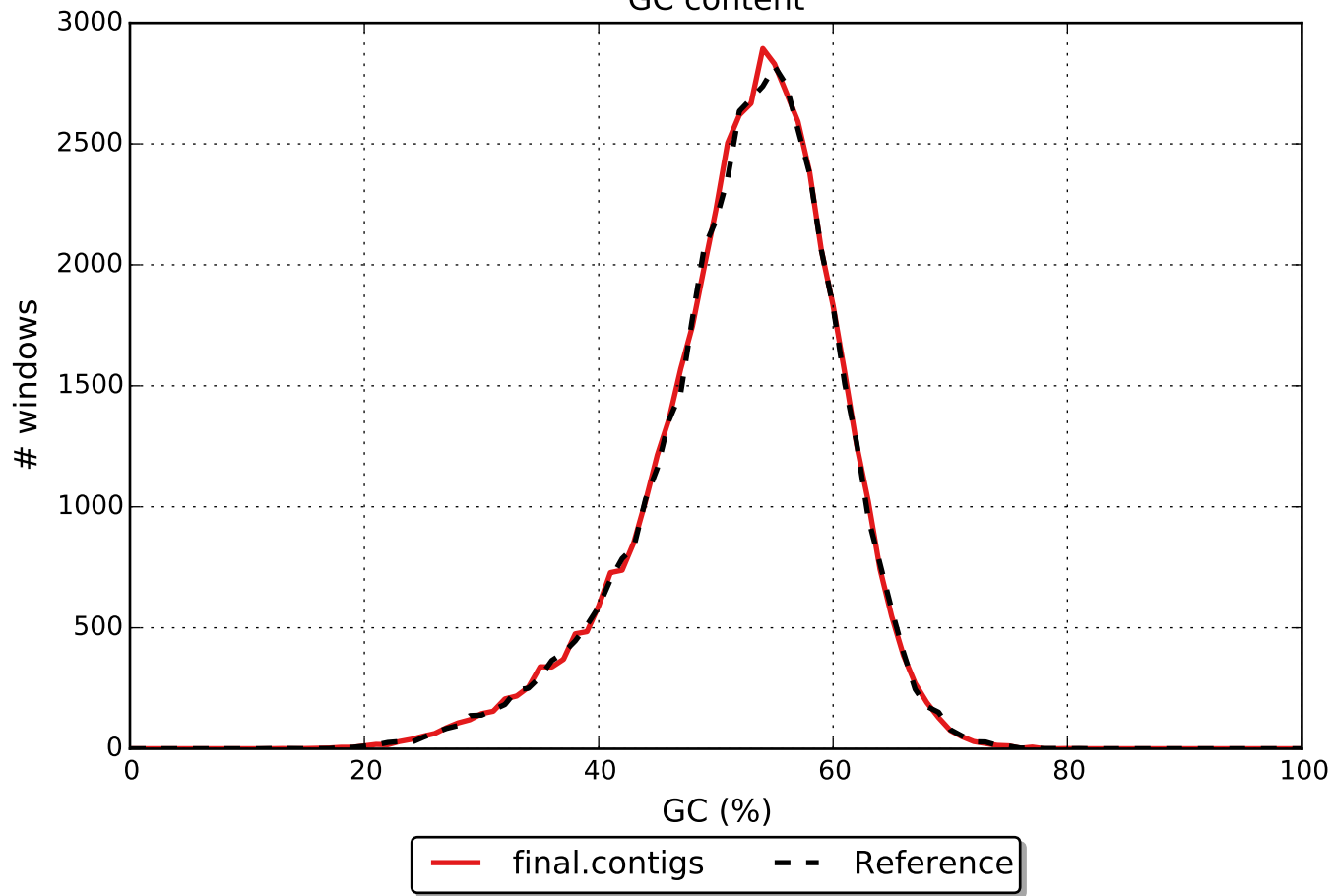


NGx





# GC content

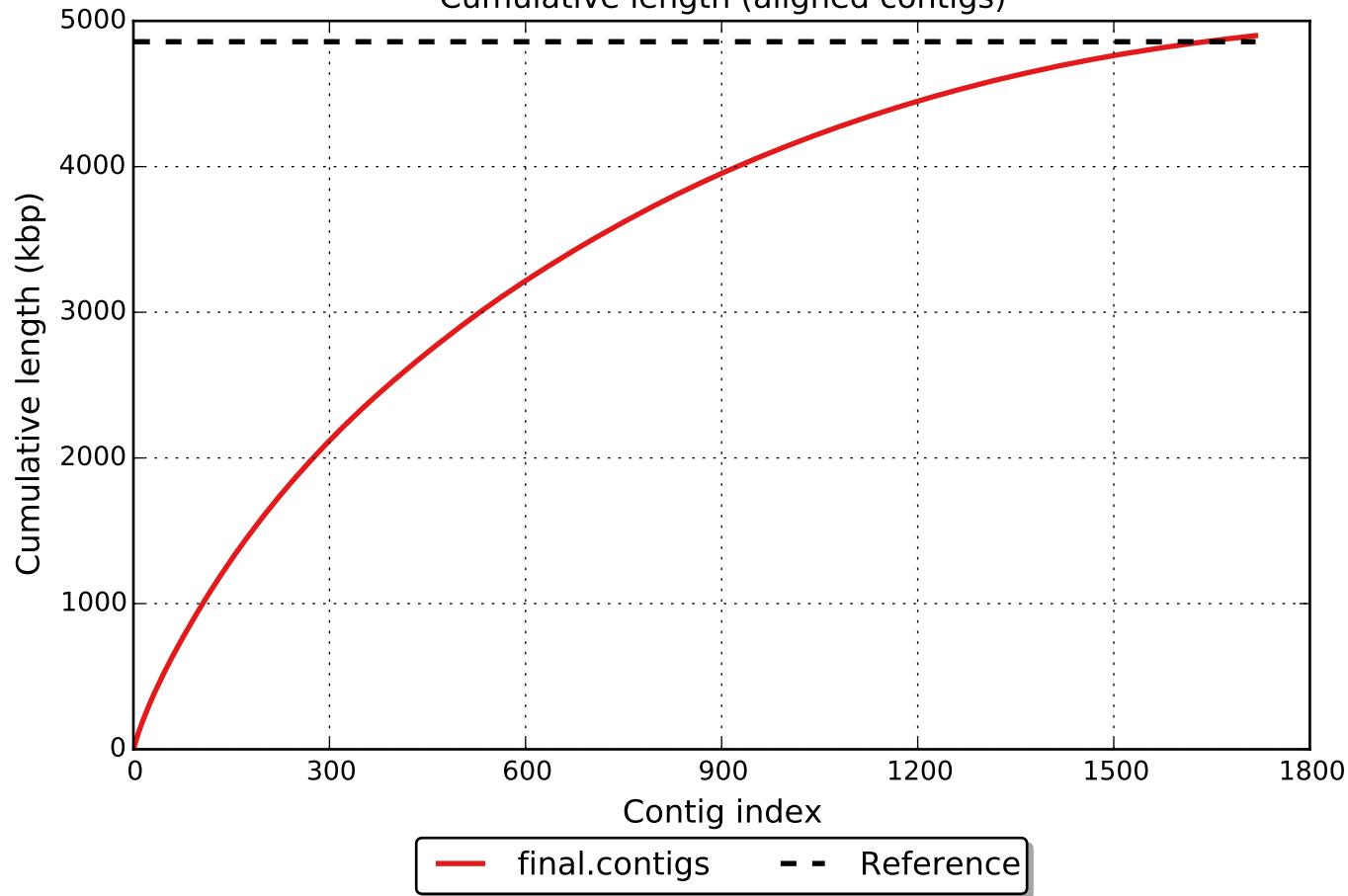


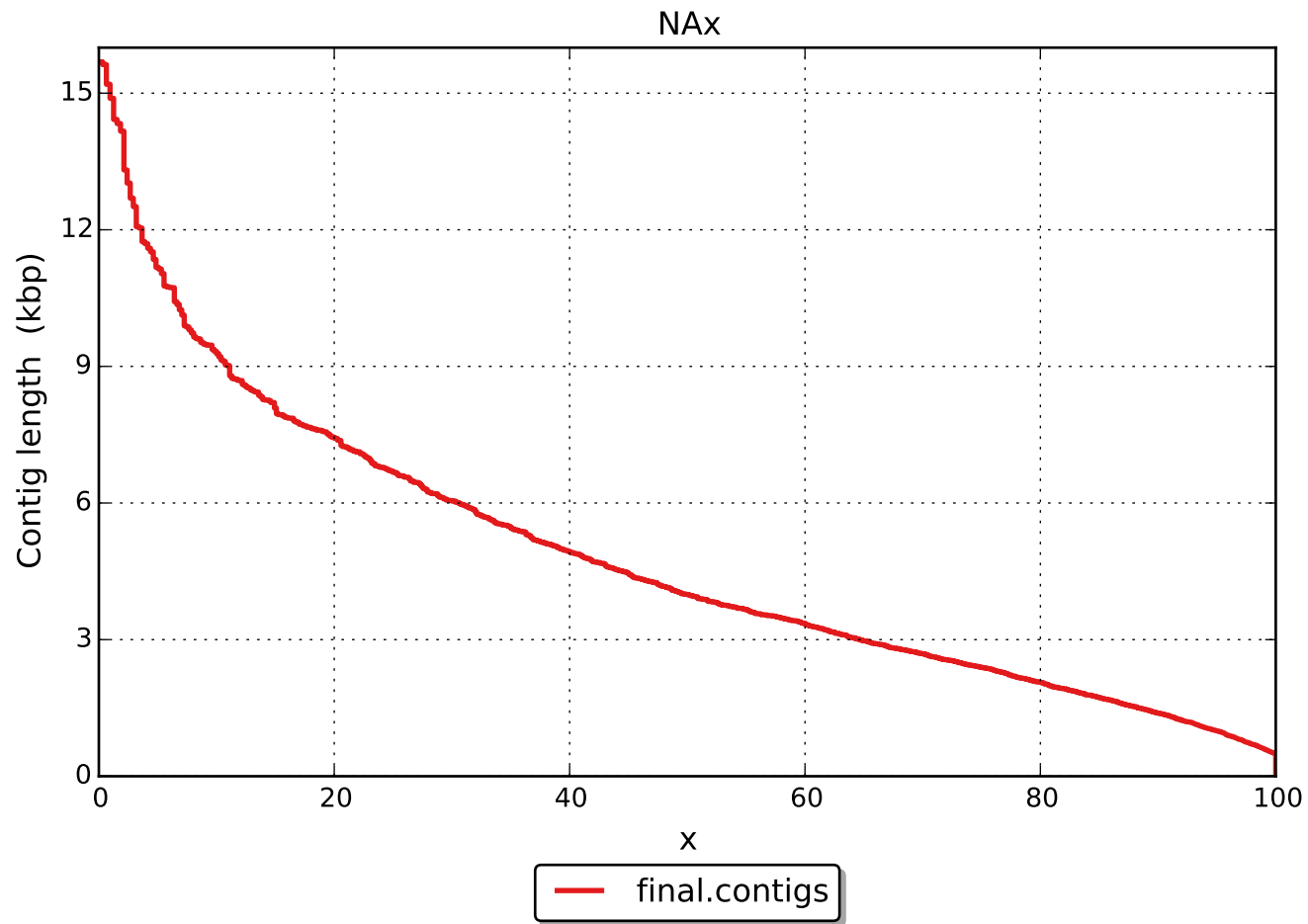
# Misassemblies





Cumulative length (aligned contigs)





NGAx

