

## Report

	final.contigs
# contigs (>= 1000 bp)	1793
# contigs (>= 5000 bp)	20
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	3291335
Total length (>= 5000 bp)	121456
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	3407
Largest contig	8916
Total length	4456752
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	1533
NG50	1482
N75	979
NG75	923
L50	939
LG50	1000
L75	1845
LG75	1991
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	91.151
Duplication ratio	1.053
# N's per 100 kbp	0.00
# mismatches per 100 kbp	84.66
# indels per 100 kbp	0.17
Largest alignment	8916
NA50	1533
NGA50	1482
NA75	979
NGA75	923
LA50	939
LGA50	1000
LA75	1845
LGA75	1991

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

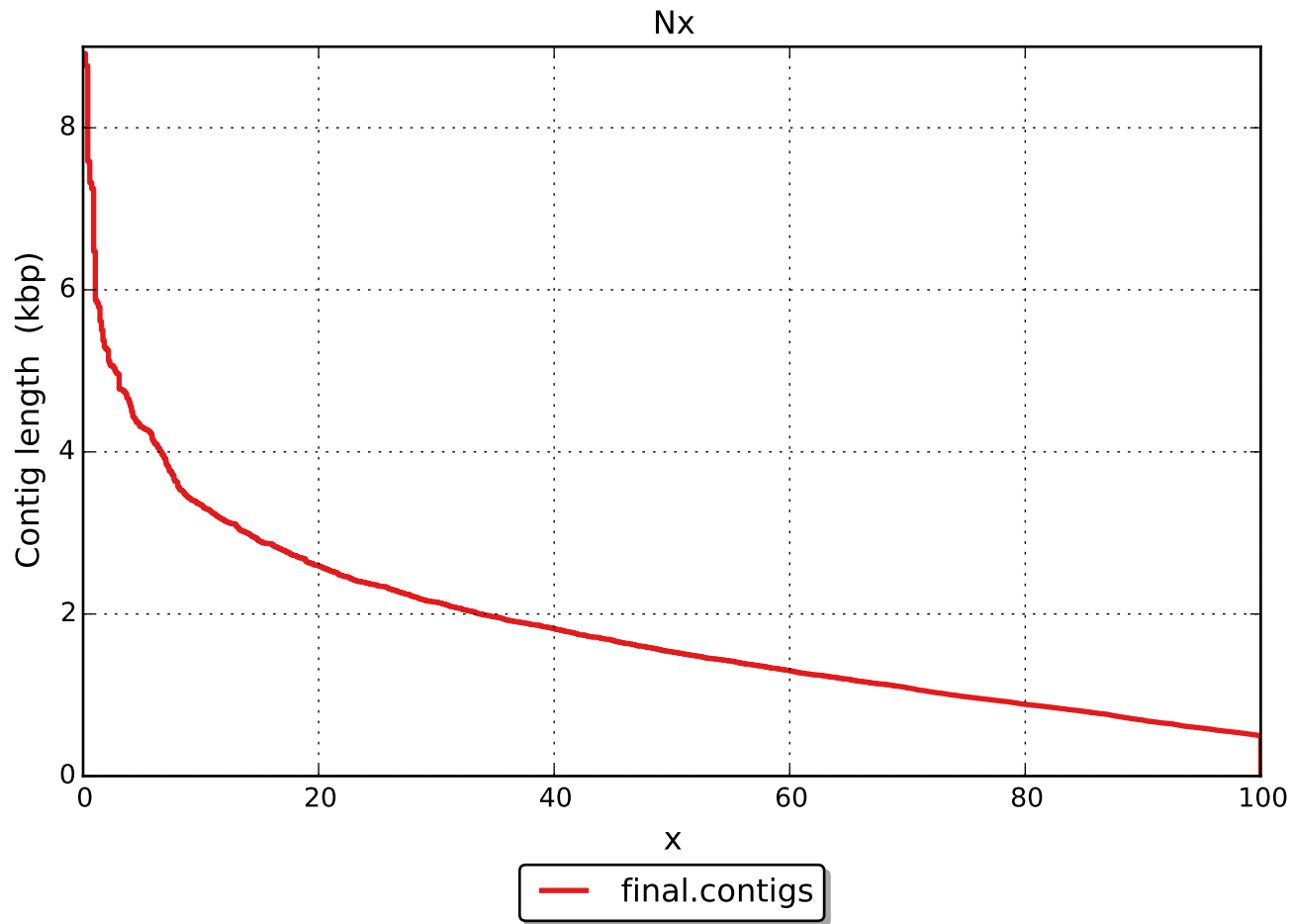
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# mismatches	3582
# indels	7
# short indels	7
# long indels	0
Indels length	7

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).

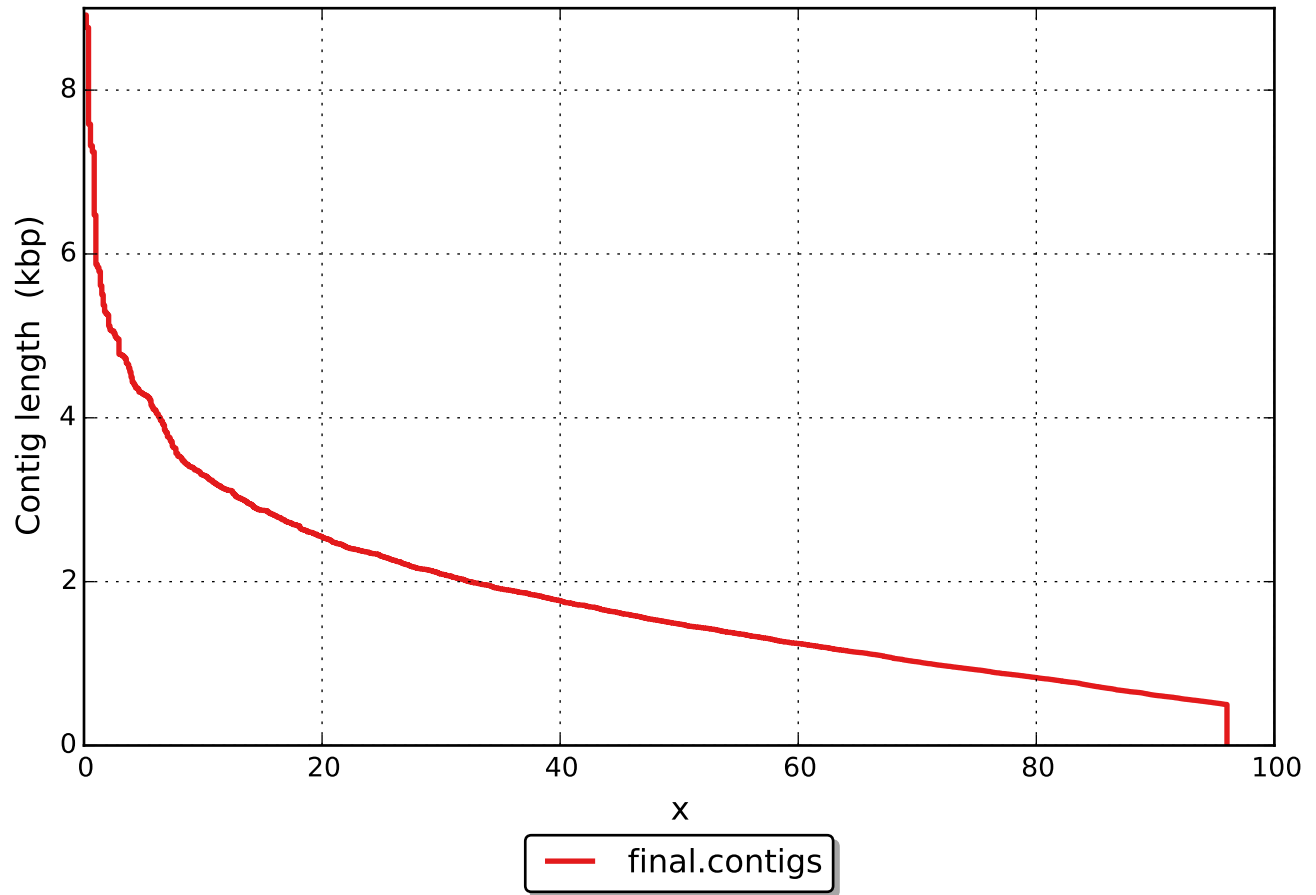
## Unaligned report

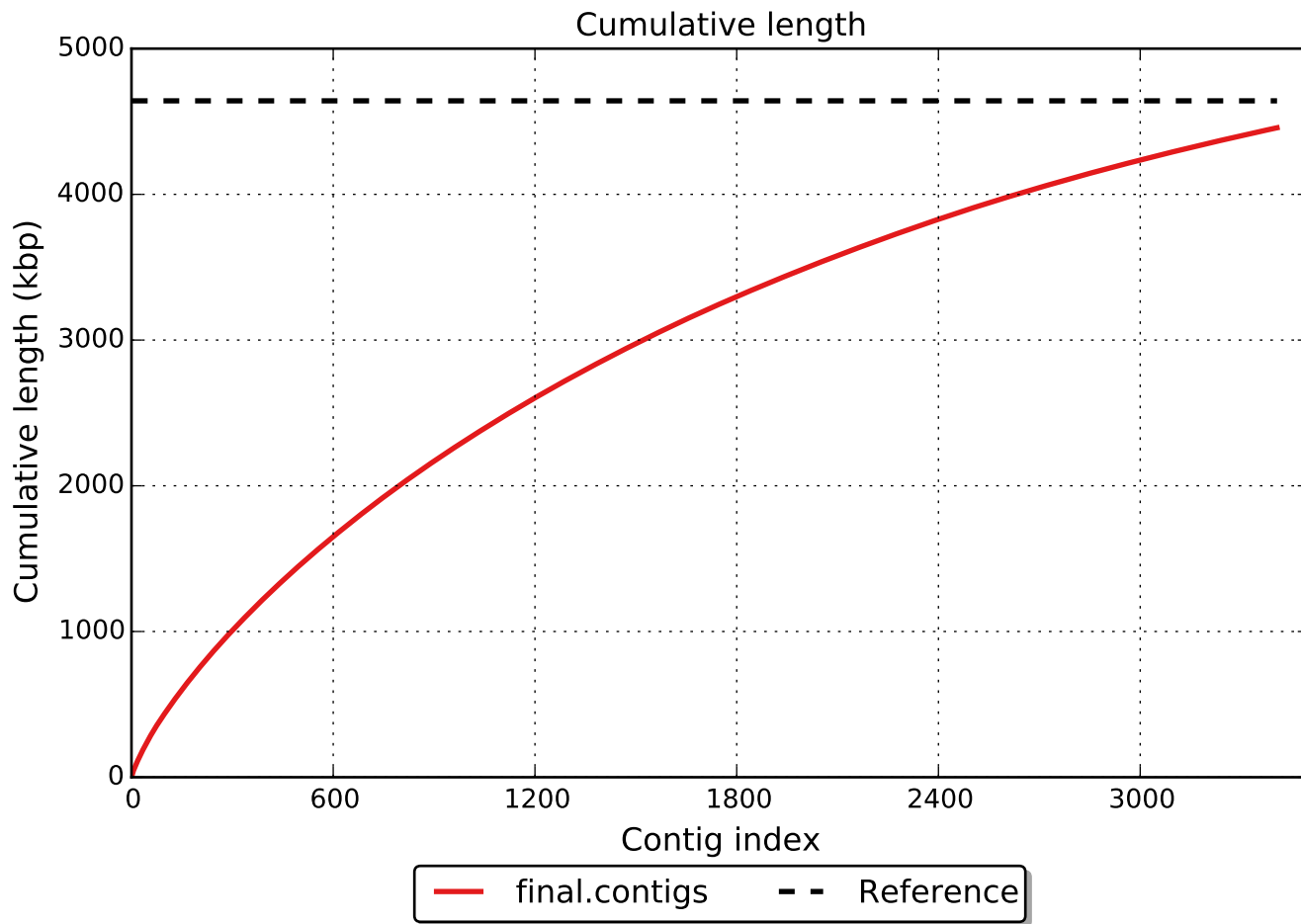
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

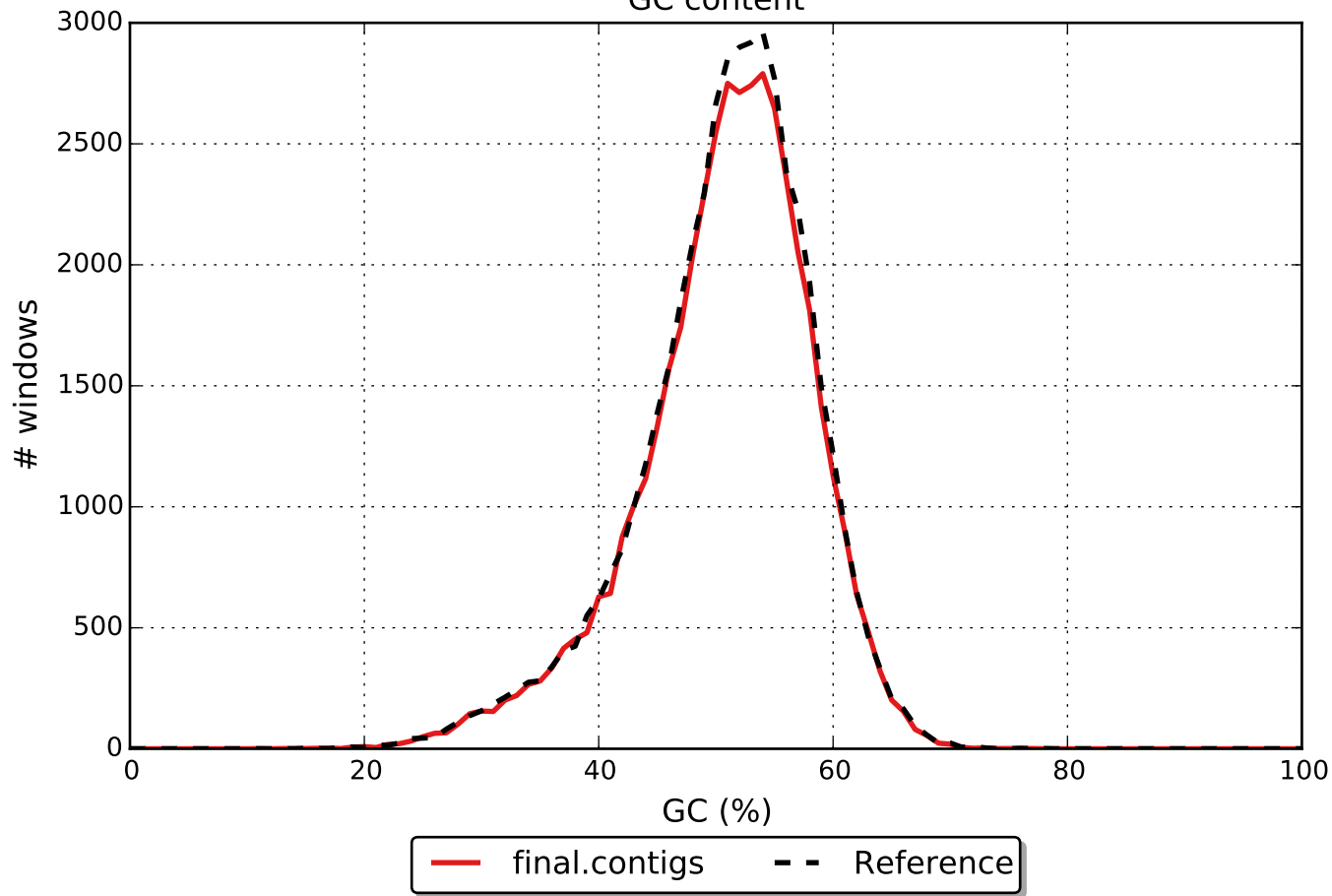


NGx





GC content

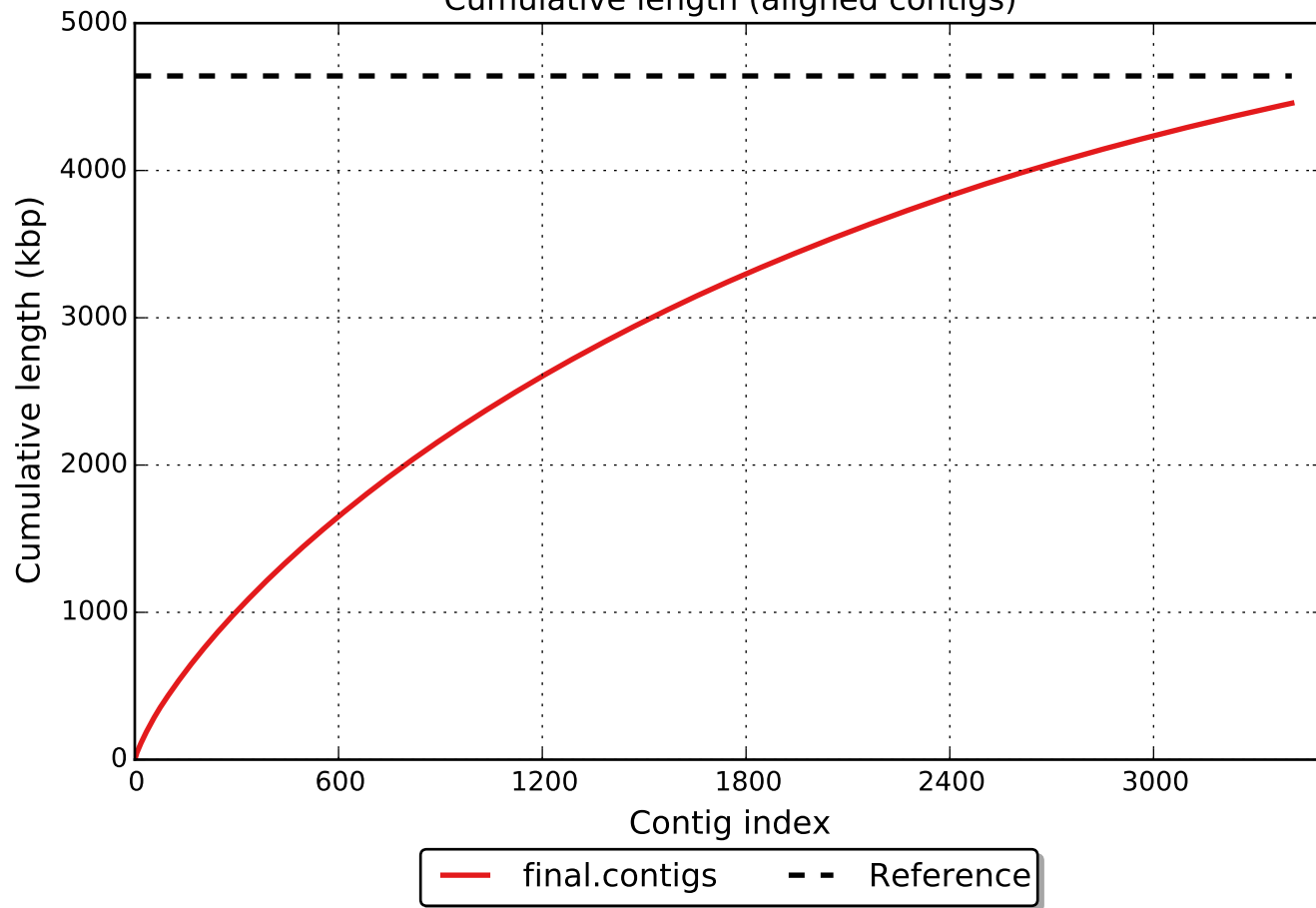


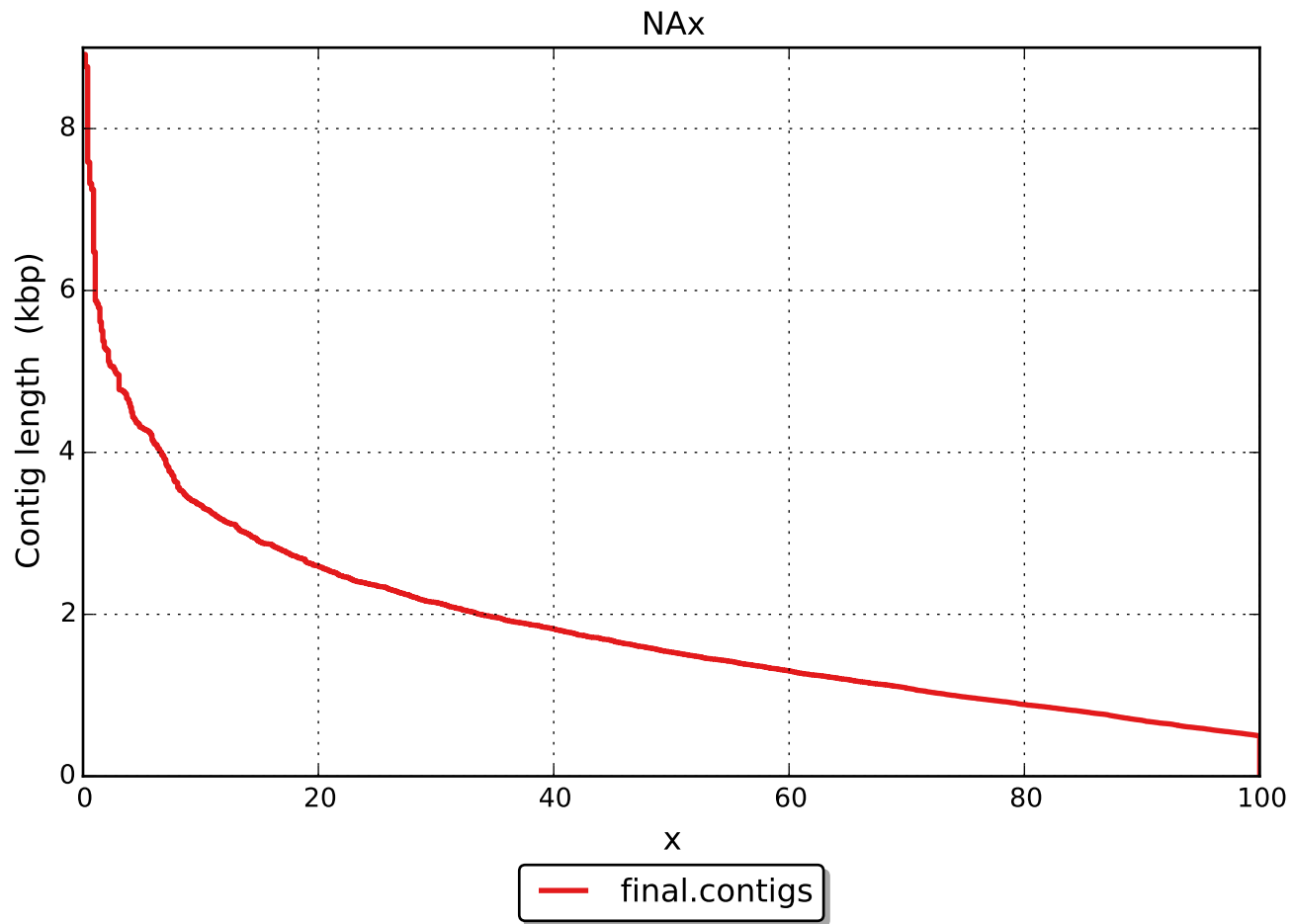
# Misassemblies





Cumulative length (aligned contigs)





NGAx

