

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	1367
# contigs ( $\geq 1000$ bp)	475
Total length ( $\geq 0$ bp)	1320525
Total length ( $\geq 1000$ bp)	793833
# contigs	1031
Largest contig	7521
Total length	1197829
Reference length	1283598
GC (%)	26.32
Reference GC (%)	26.30
N50	1270
NG50	1199
N75	876
NG75	796
L50	302
LG50	337
L75	587
LG75	664
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	90.916
Duplication ratio	1.052
# N's per 100 kbp	0.00
# mismatches per 100 kbp	68.04
# indels per 100 kbp	0.17
Largest alignment	7521
NA50	1270
NGA50	1199
NA75	876
NGA75	796
LA50	302
LGA50	337
LA75	587
LGA75	664

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).

## Misassemblies report

	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	794
# indels	2
# short indels	2
# long indels	0
Indels length	2

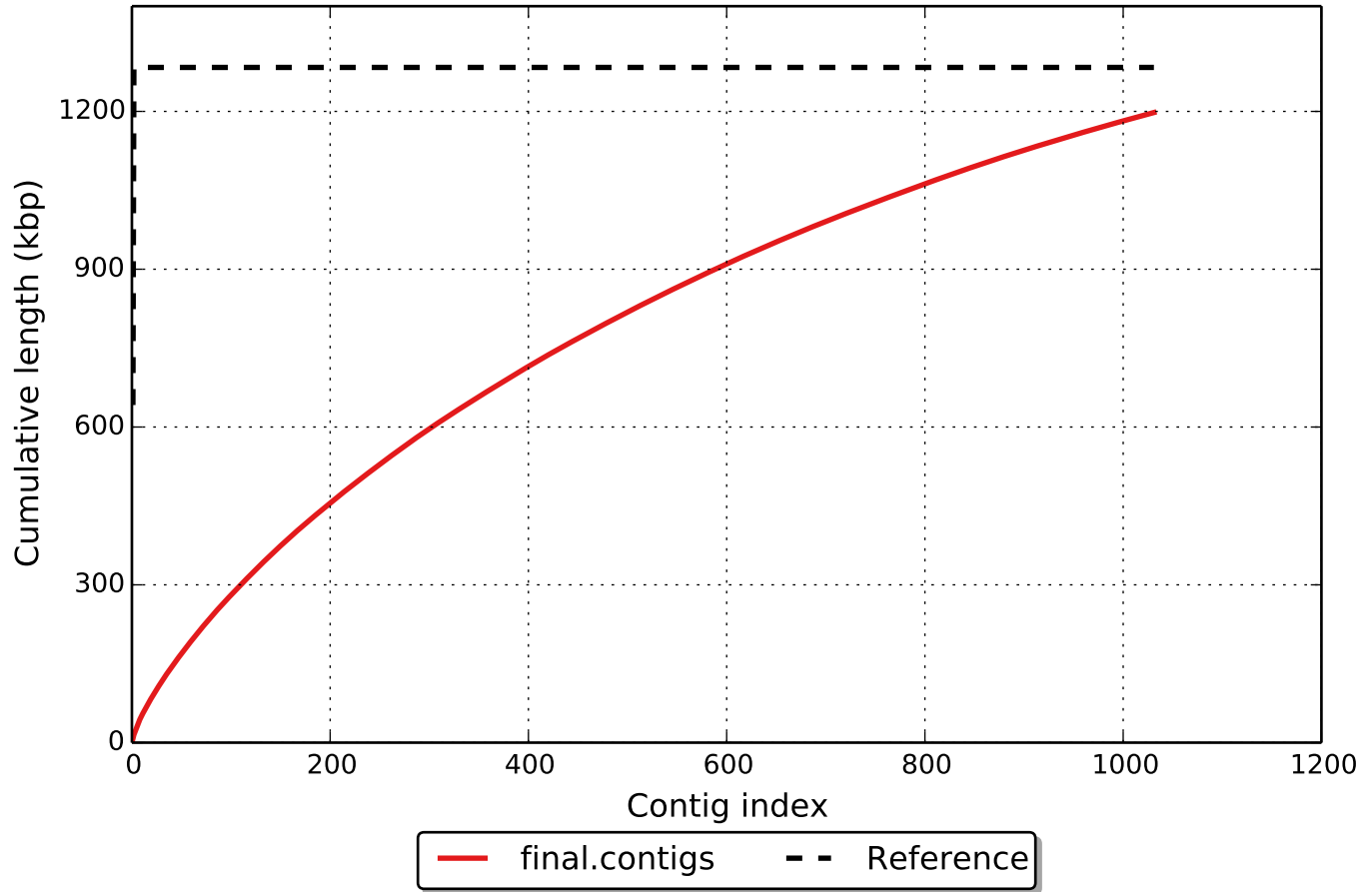
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

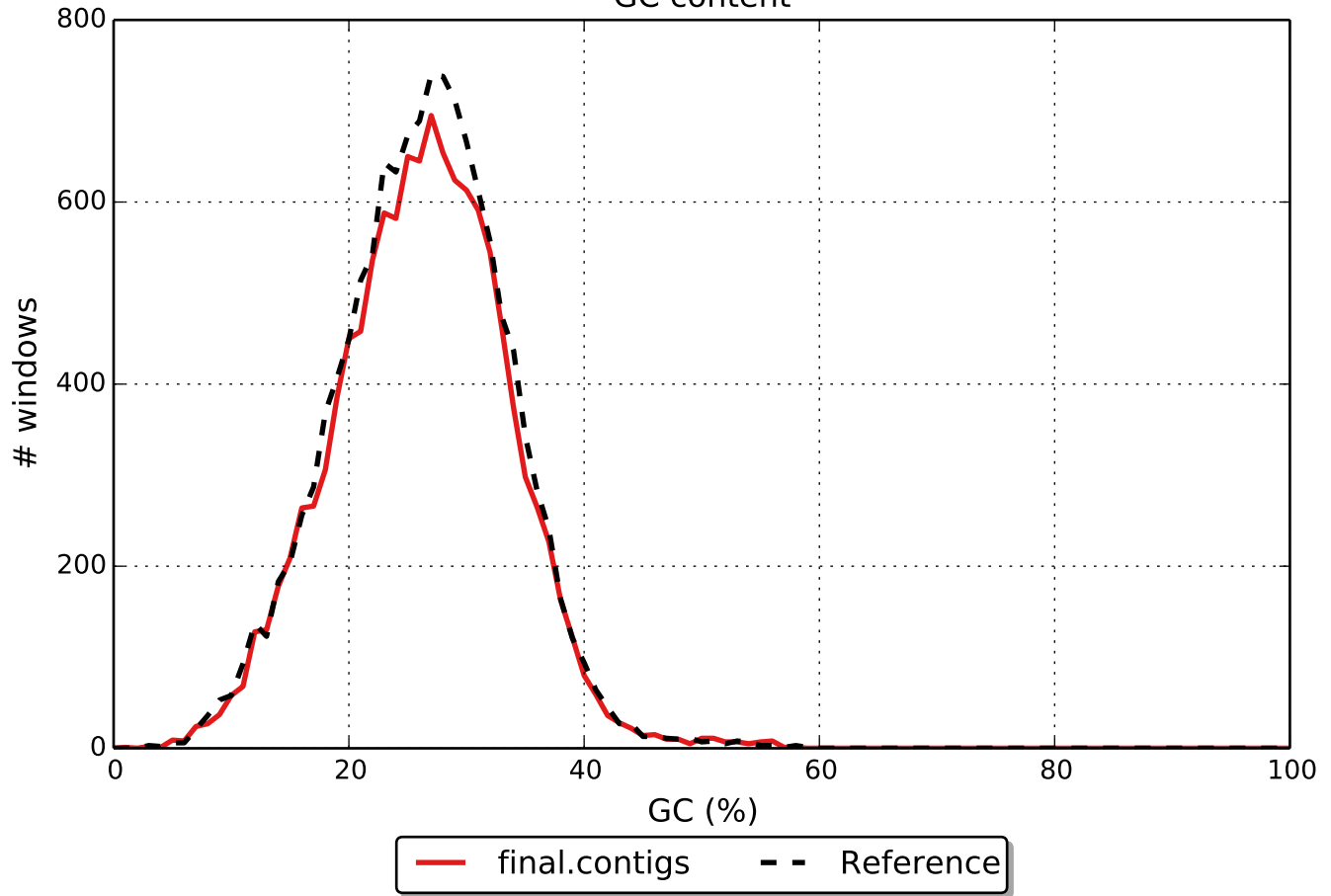
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

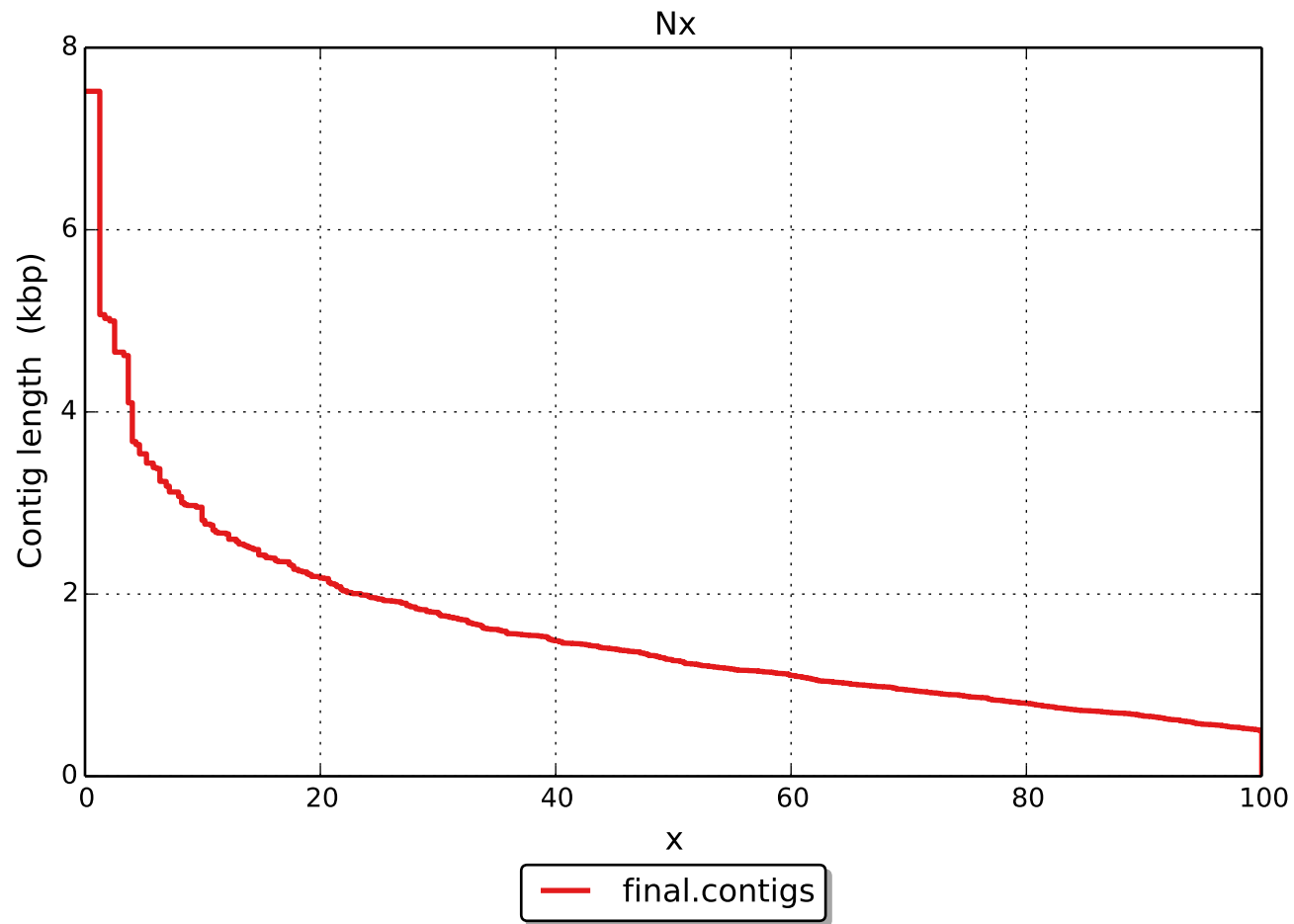
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

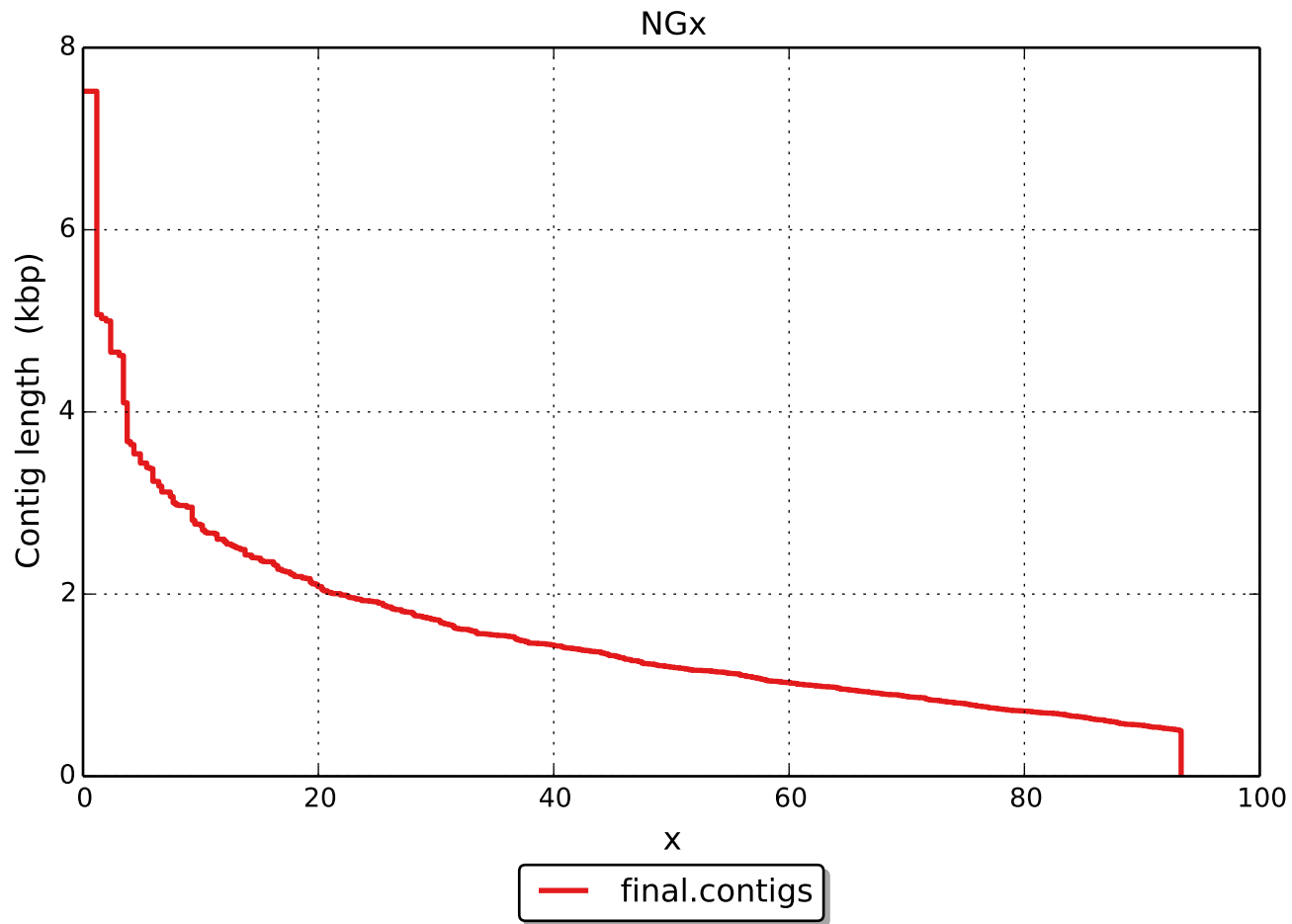
Cumulative length



GC content





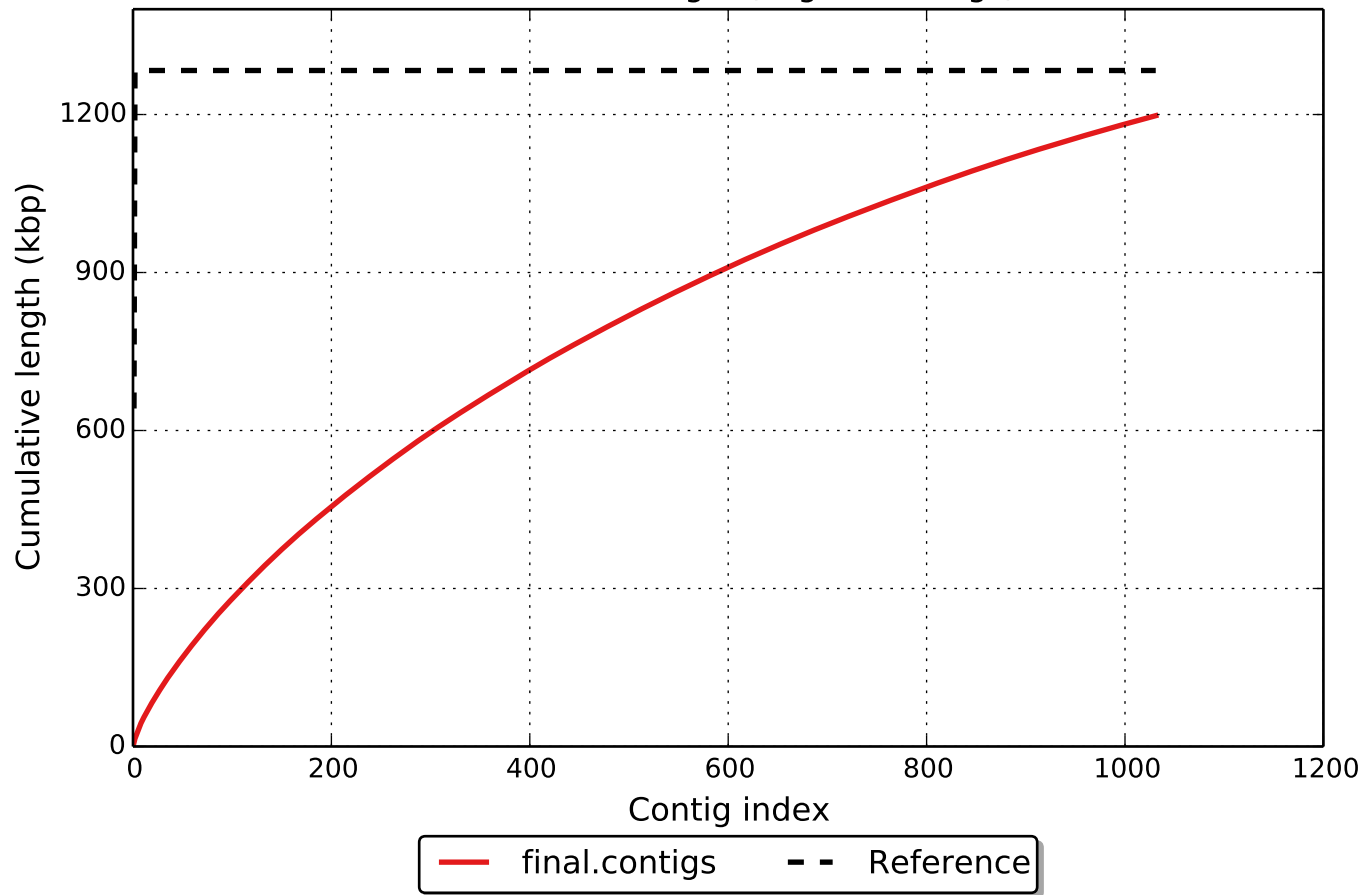


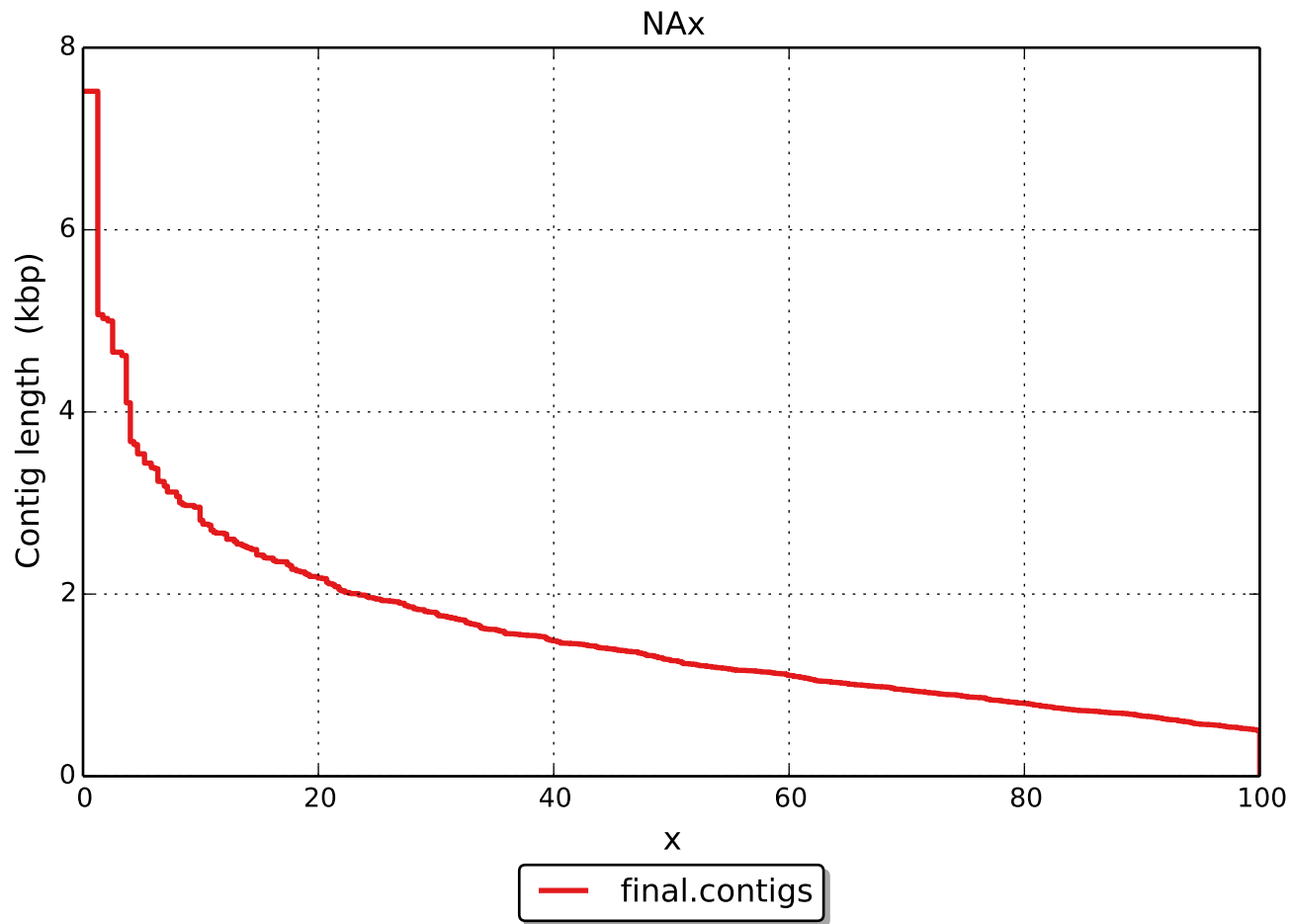
# Misassemblies





Cumulative length (aligned contigs)





NGAx

