

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	1378
# contigs ( $\geq 1000$ bp)	266
Total length ( $\geq 0$ bp)	1026645
Total length ( $\geq 1000$ bp)	436254
# contigs	826
Largest contig	5316
Total length	826744
Reference length	1283598
GC (%)	26.39
Reference GC (%)	26.30
N50	1045
NG50	698
N75	733
L50	244
LG50	514
L75	484
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	61.439
Duplication ratio	1.048
# N's per 100 kbp	0.00
# mismatches per 100 kbp	254.49
# indels per 100 kbp	0.00
Largest alignment	5316
NA50	1045
NGA50	698
NA75	733
LA50	244
LGA50	514
LA75	484

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	2007
# indels	0
# short indels	0
# long indels	0
Indels length	0

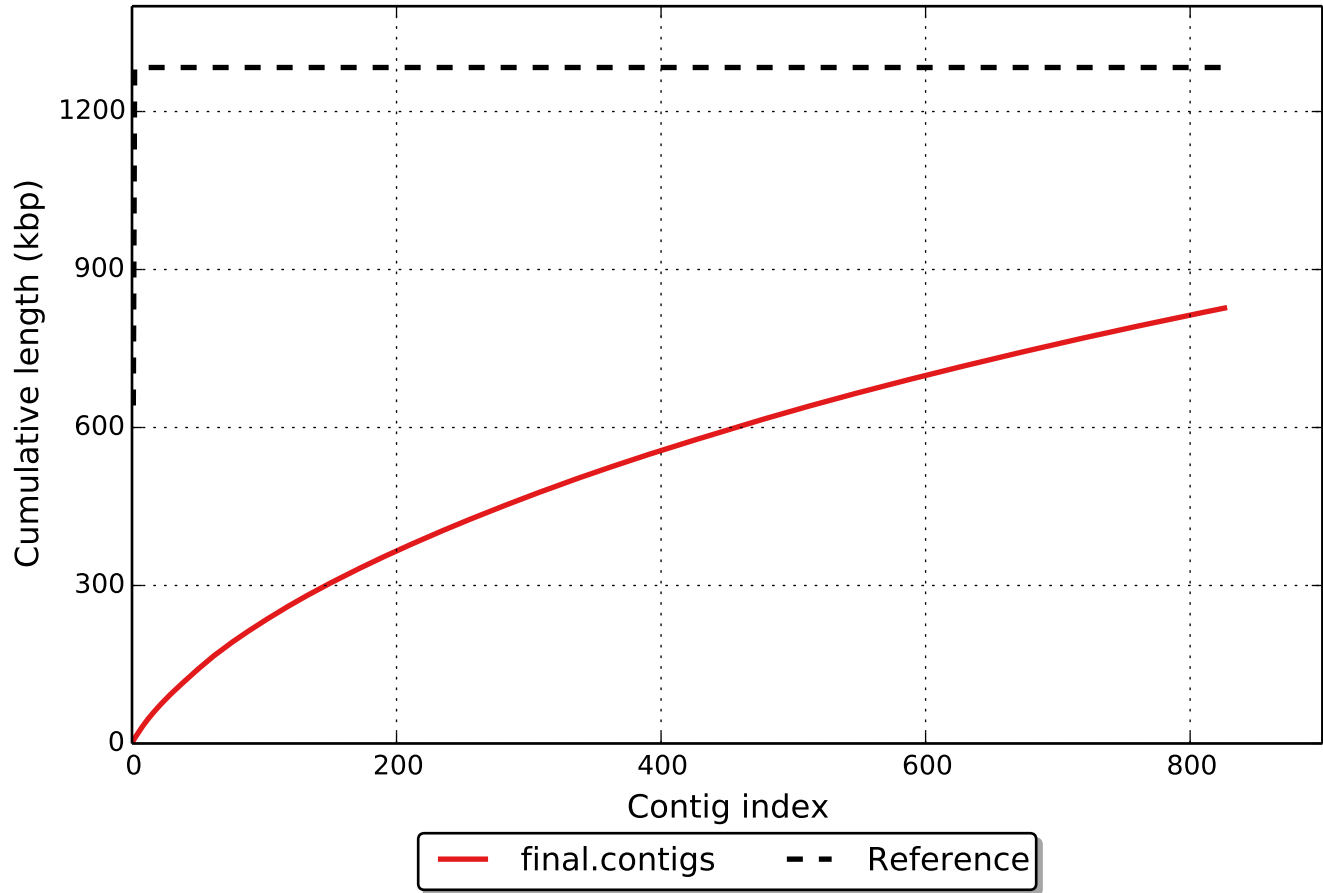
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

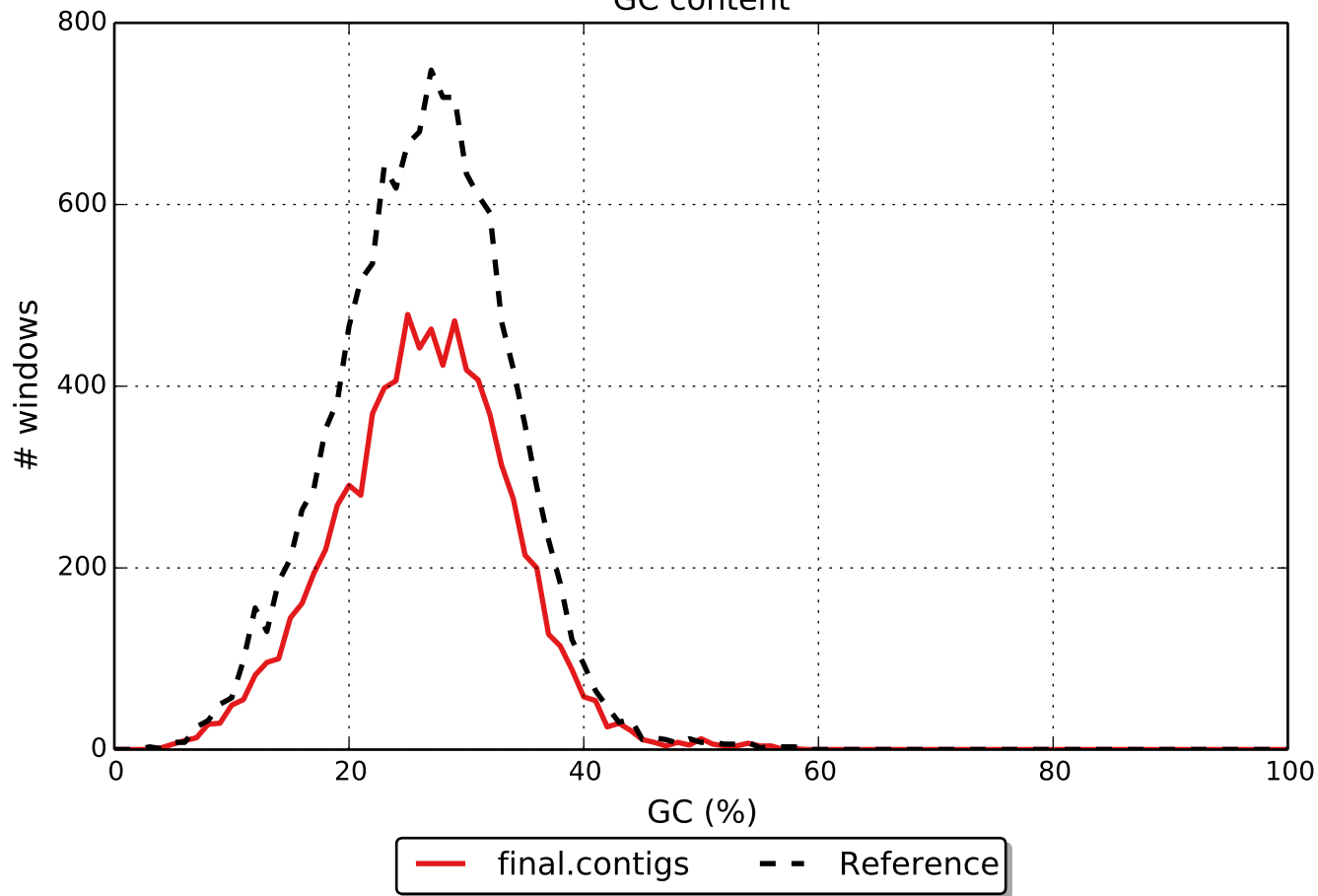
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

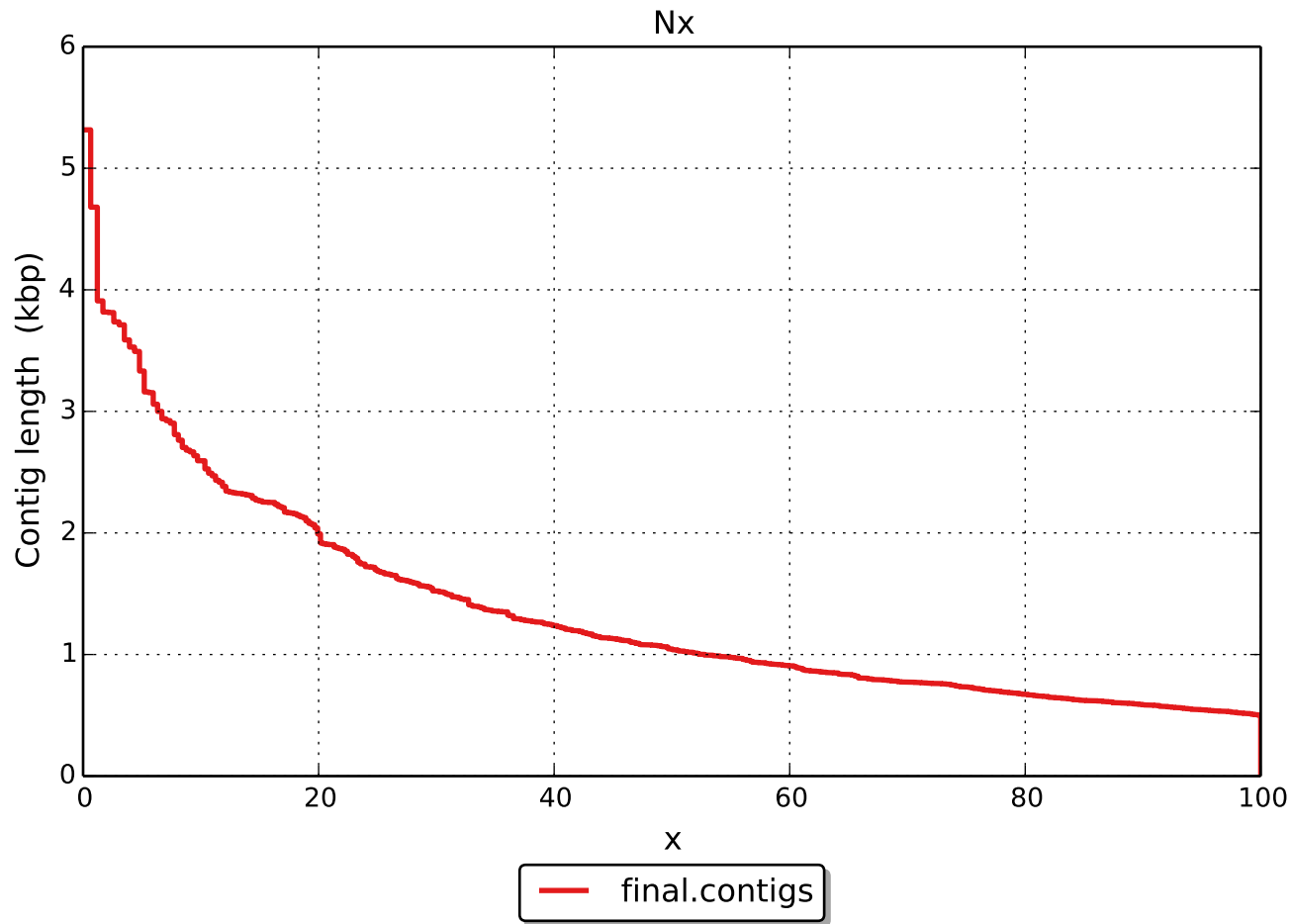
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Cumulative length

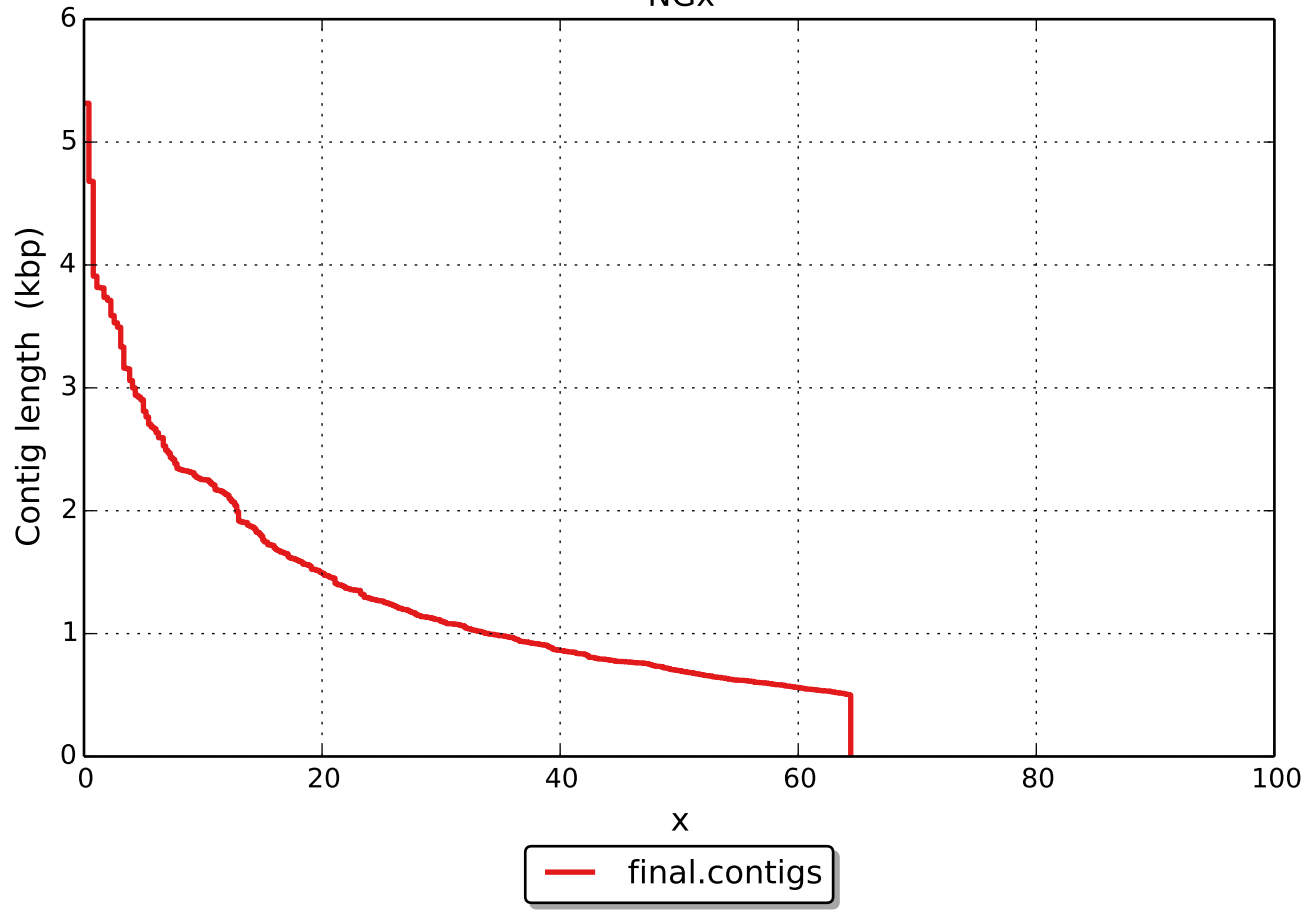


GC content





NGx

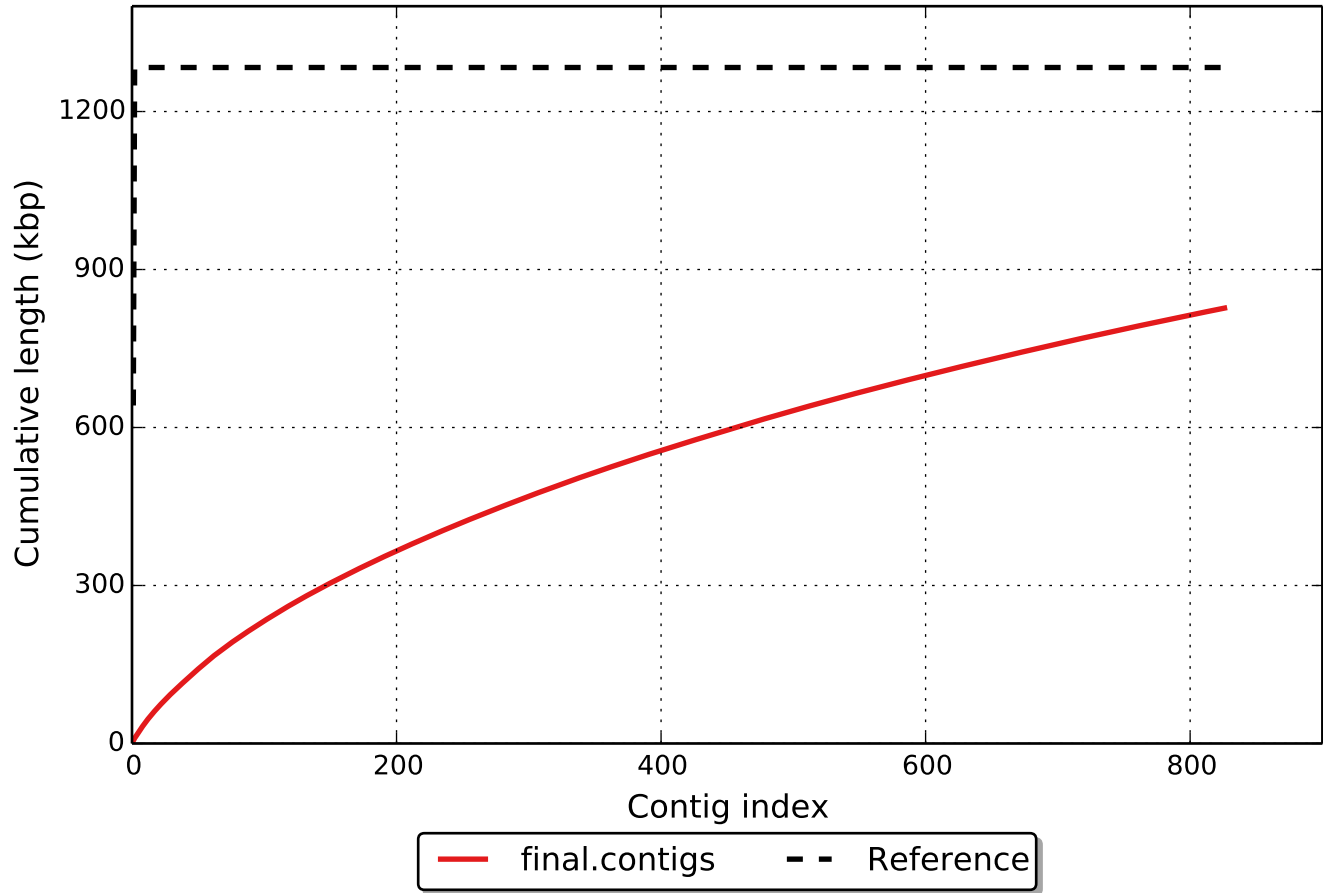


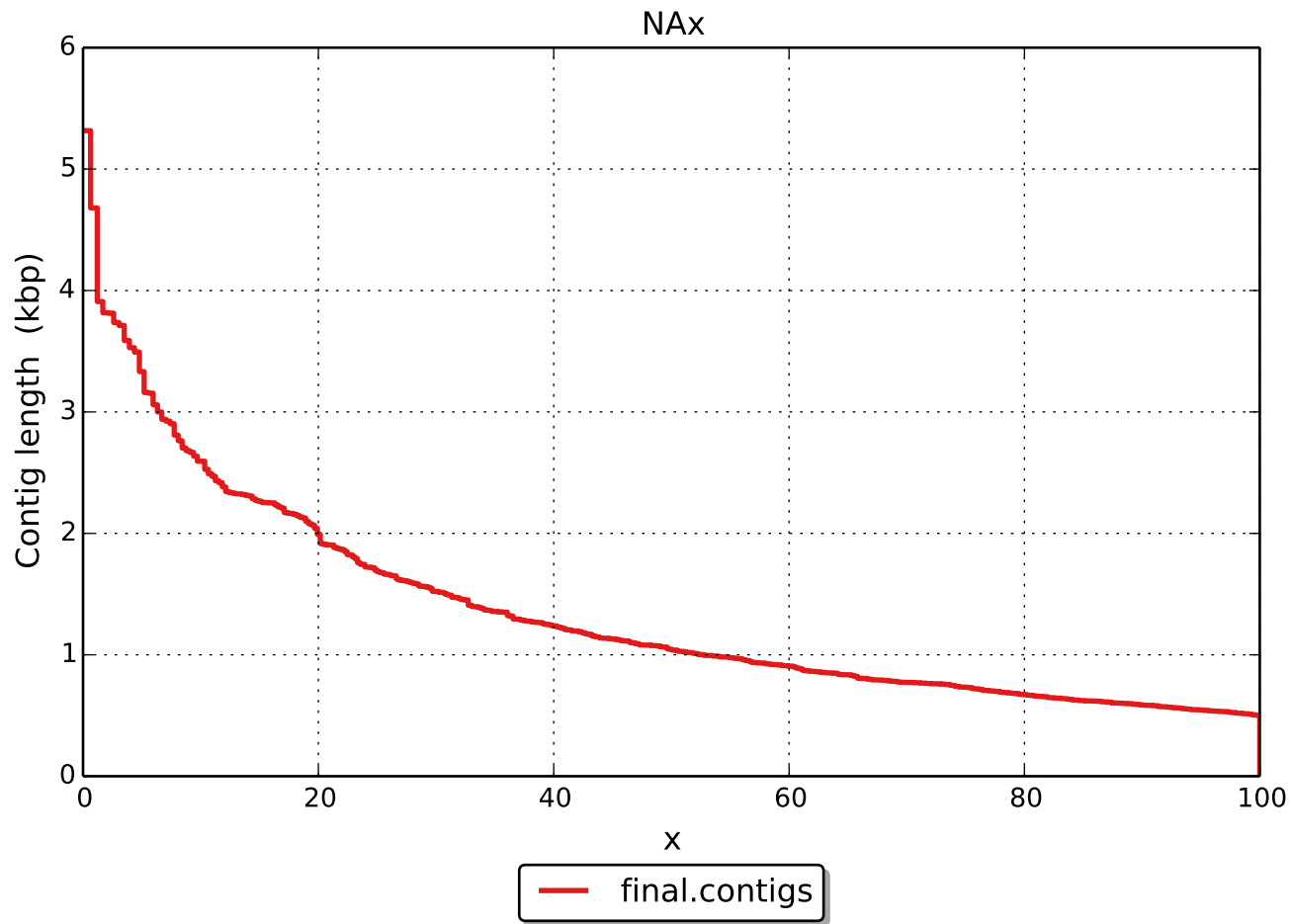
# Misassemblies





Cumulative length (aligned contigs)





NGAx

