

## Report

	final.contigs
# contigs (>= 1000 bp)	1902
# contigs (>= 5000 bp)	41
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	3943603
Total length (>= 5000 bp)	240581
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	3021
Largest contig	9054
Total length	4769120
Reference length	4857432
GC (%)	52.21
Reference GC (%)	52.22
N50	1956
NG50	1930
N75	1208
NG75	1172
L50	799
LG50	821
L75	1569
LG75	1624
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	93.968
Duplication ratio	1.045
# N's per 100 kbp	0.00
# mismatches per 100 kbp	63.49
# indels per 100 kbp	0.00
Largest alignment	9054
NA50	1956
NGA50	1930
NA75	1208
NGA75	1172
LA50	799
LGA50	821
LA75	1569
LGA75	1624

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

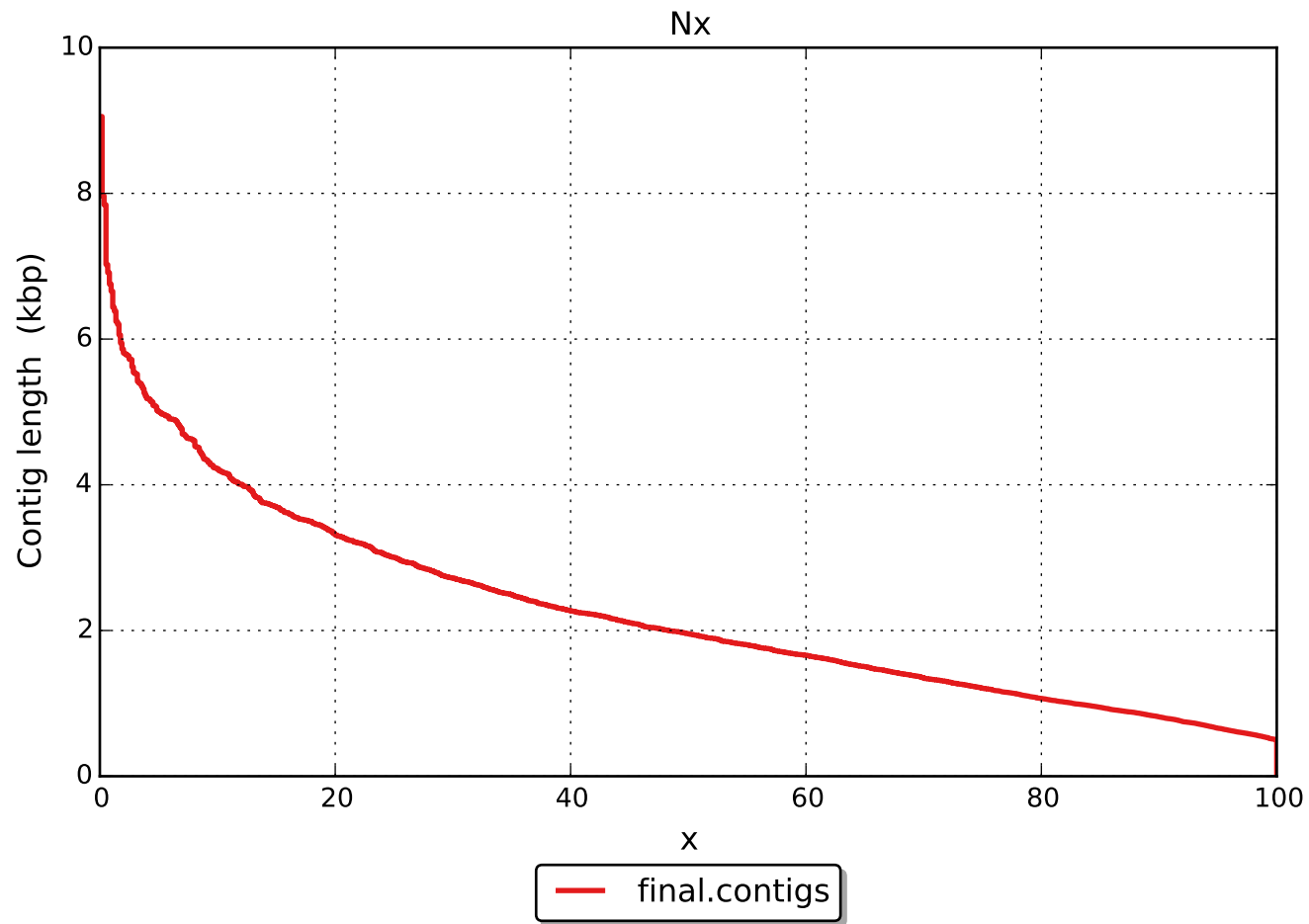
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	2898
# indels	0
# short indels	0
# long indels	0
Indels length	0

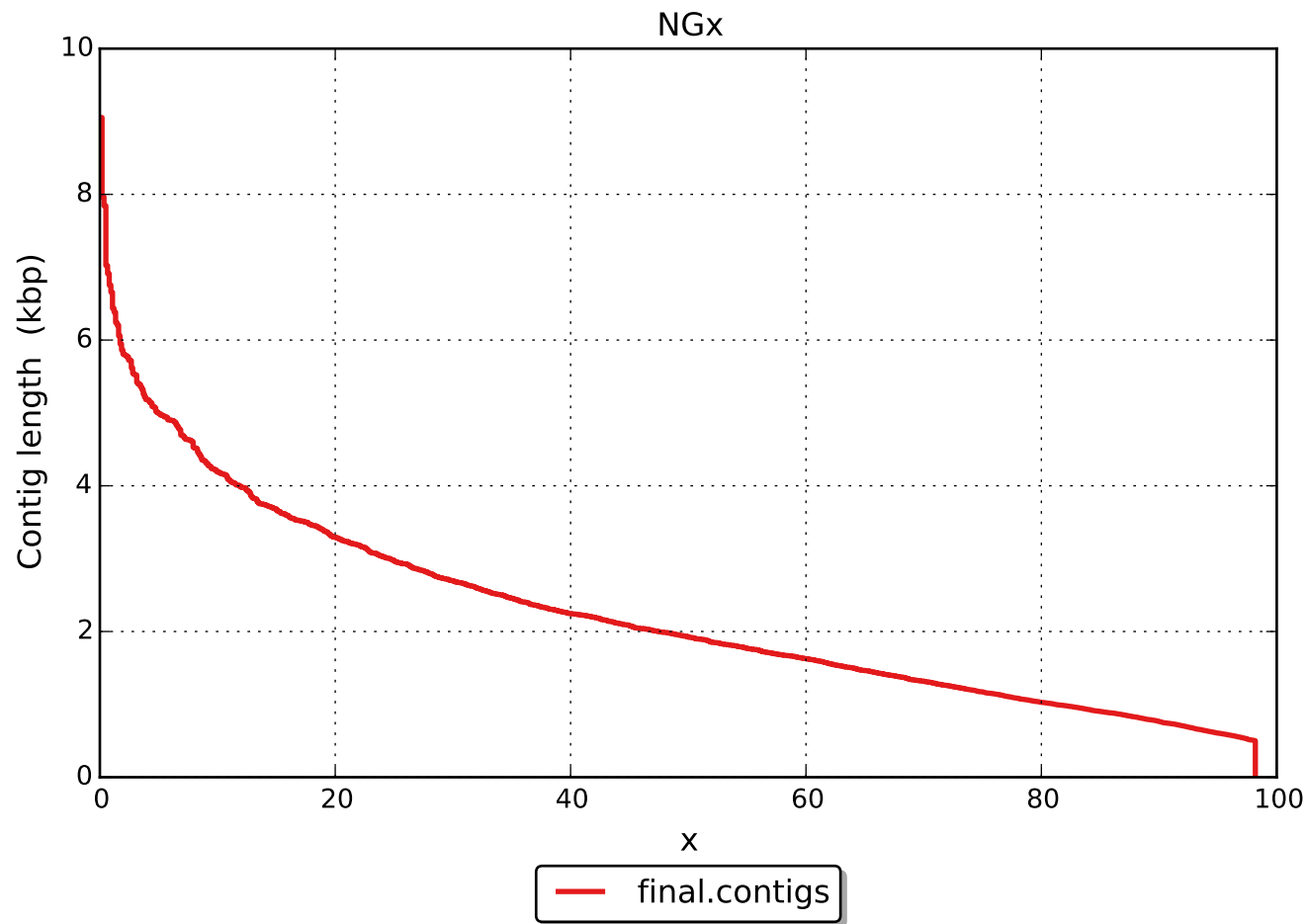
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

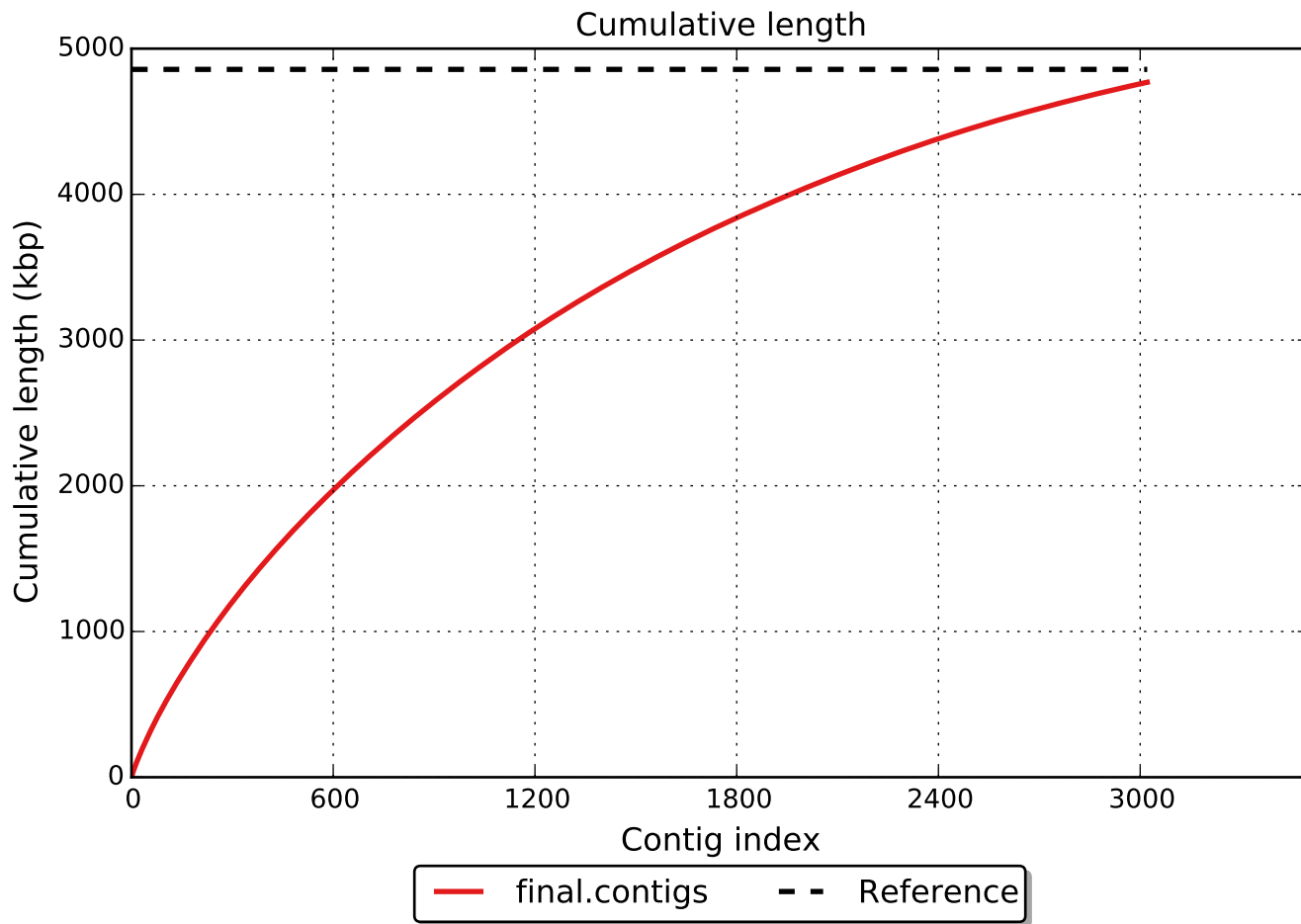
## Unaligned report

	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

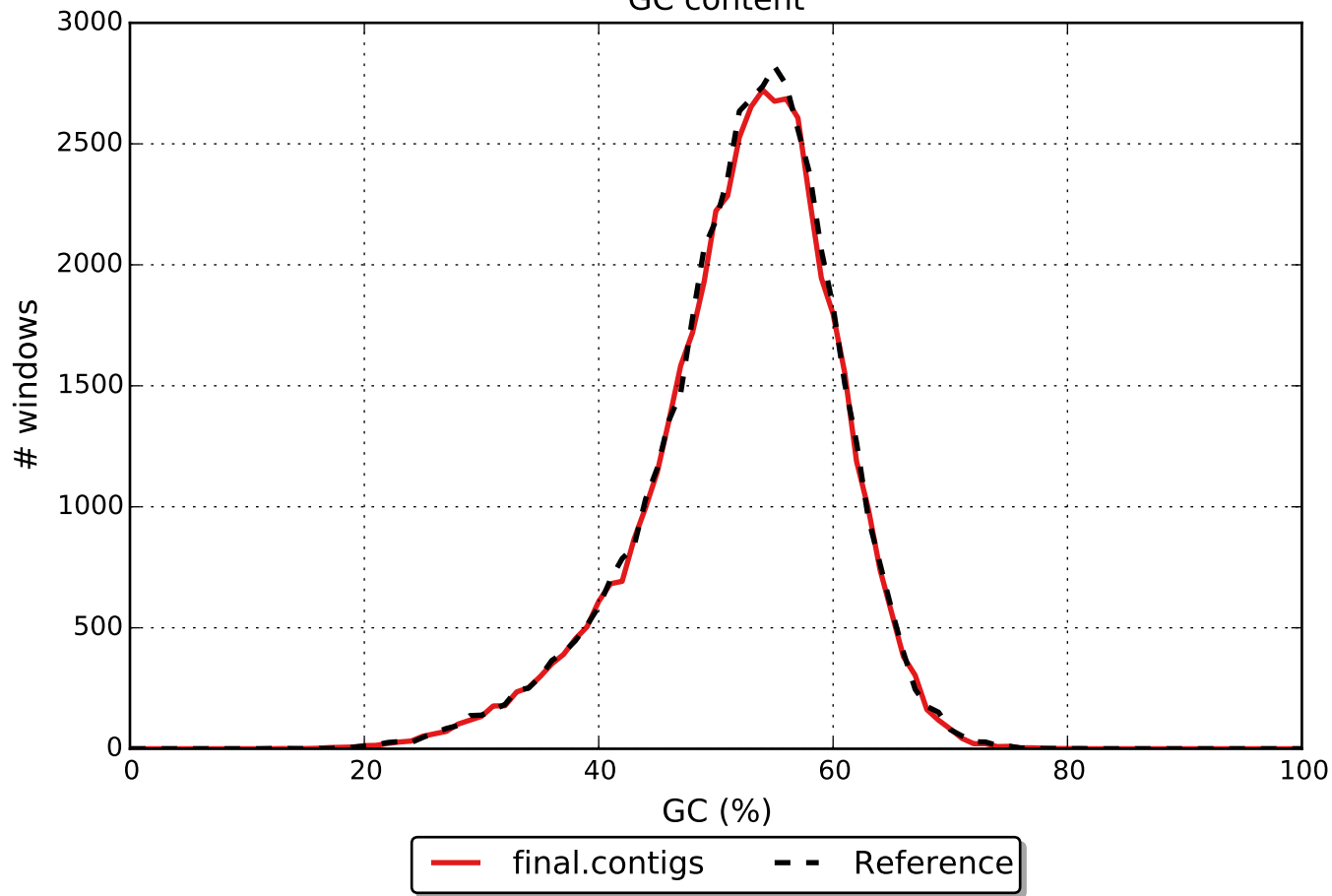
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).







GC content

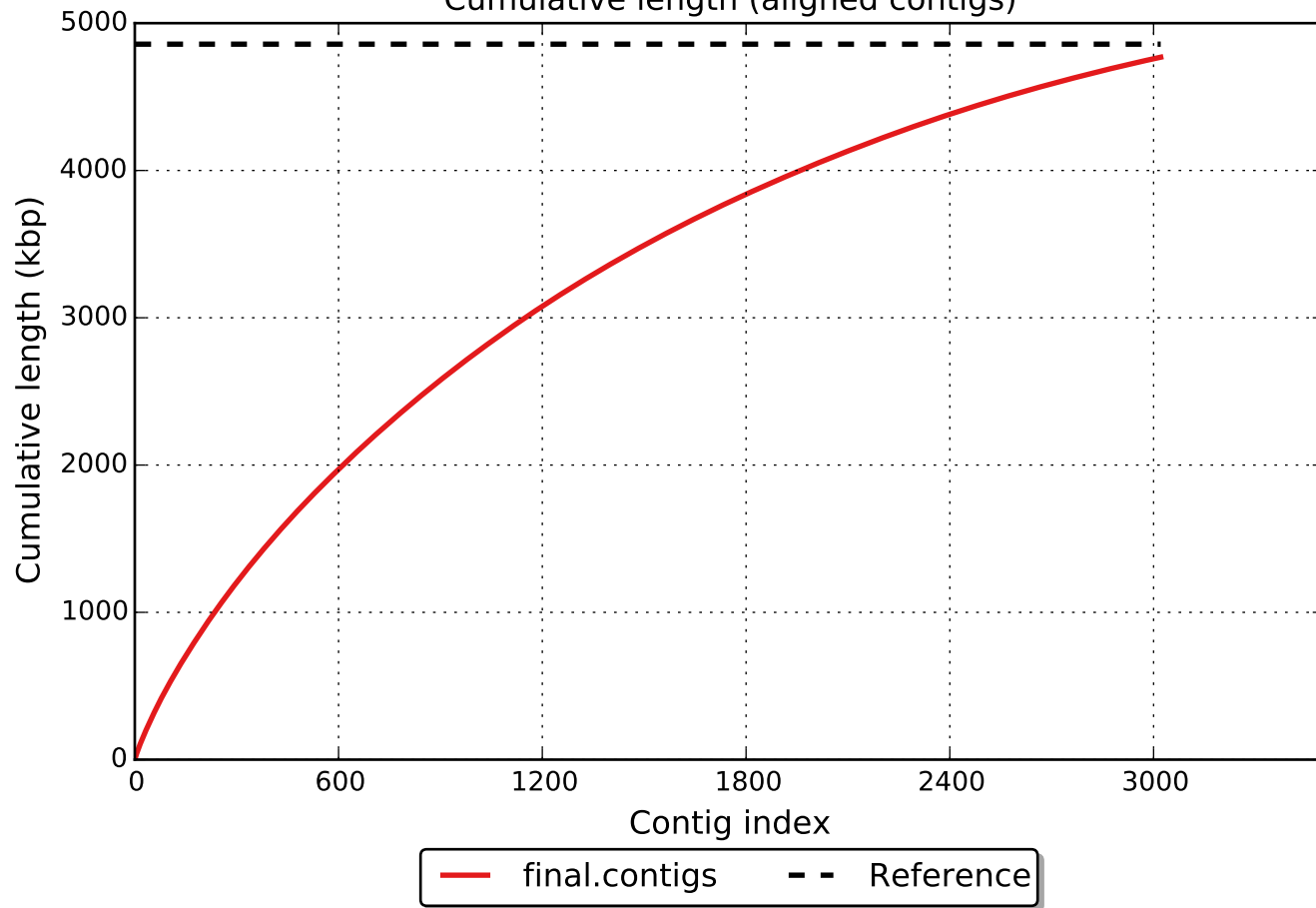


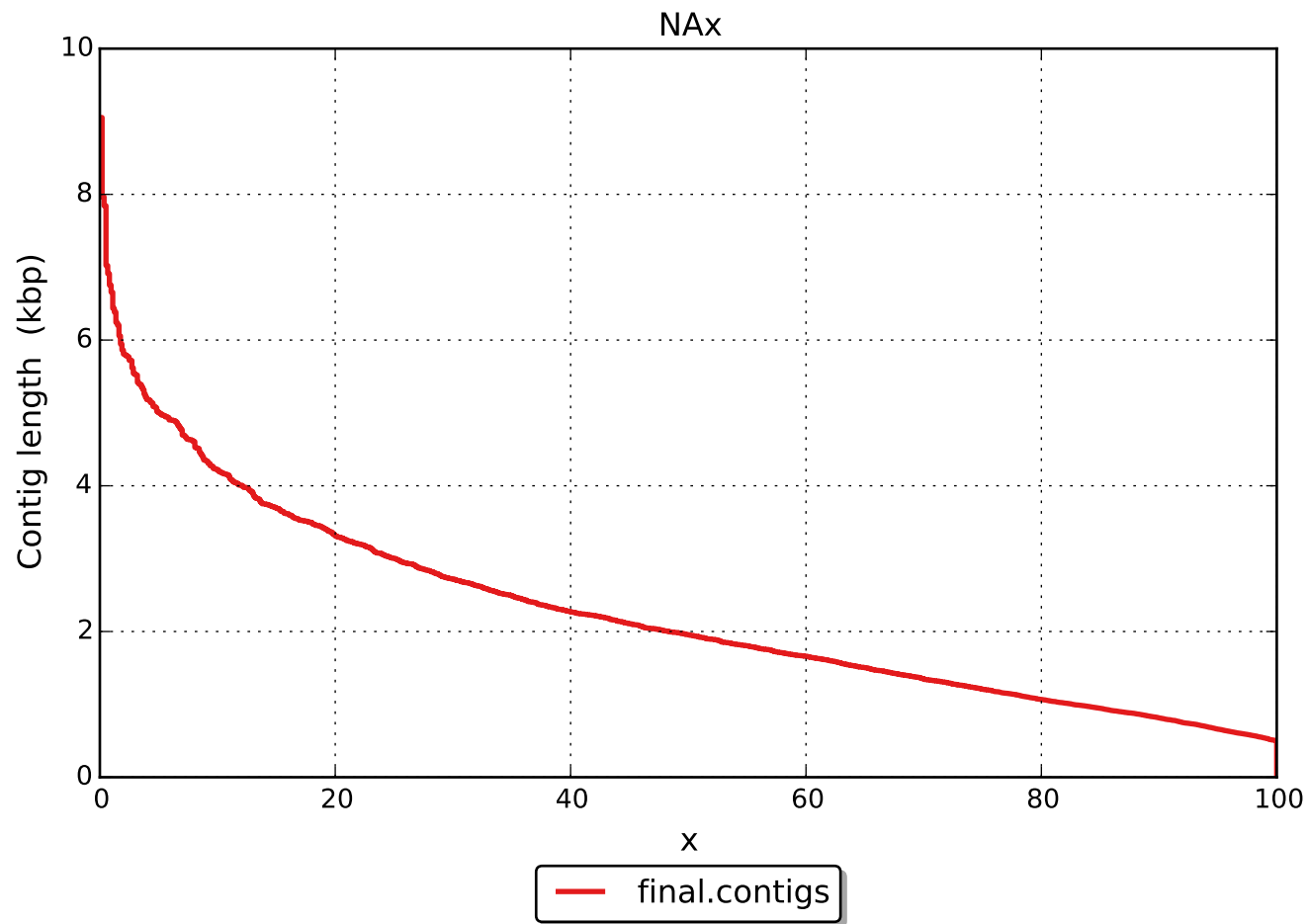
# Misassemblies





Cumulative length (aligned contigs)





NGAx

