

Report

	final.contigs
# contigs (>= 1000 bp)	1533
# contigs (>= 5000 bp)	18
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	2896074
Total length (>= 5000 bp)	108627
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	2833
Largest contig	7697
Total length	3817960
Reference length	4641652
GC (℥)	50.77
Reference GC (℥)	50.79
N50	1618
NG50	1355
N75	1021
NG75	674
L50	763
LG50	1041
L75	1501
LG75	2245
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 2 part
Unaligned length	250
Genome fraction (℥)	80.902
Duplication ratio	1.017
# N's per 100 kbp	0.00
# mismatches per 100 kbp	11.37
# indels per 100 kbp	0.00
Largest alignment	7697
NA50	1618
NGA50	1355
NA75	1021
NGA75	674
LA50	763
LGA50	1041
LA75	1501
LGA75	2245

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

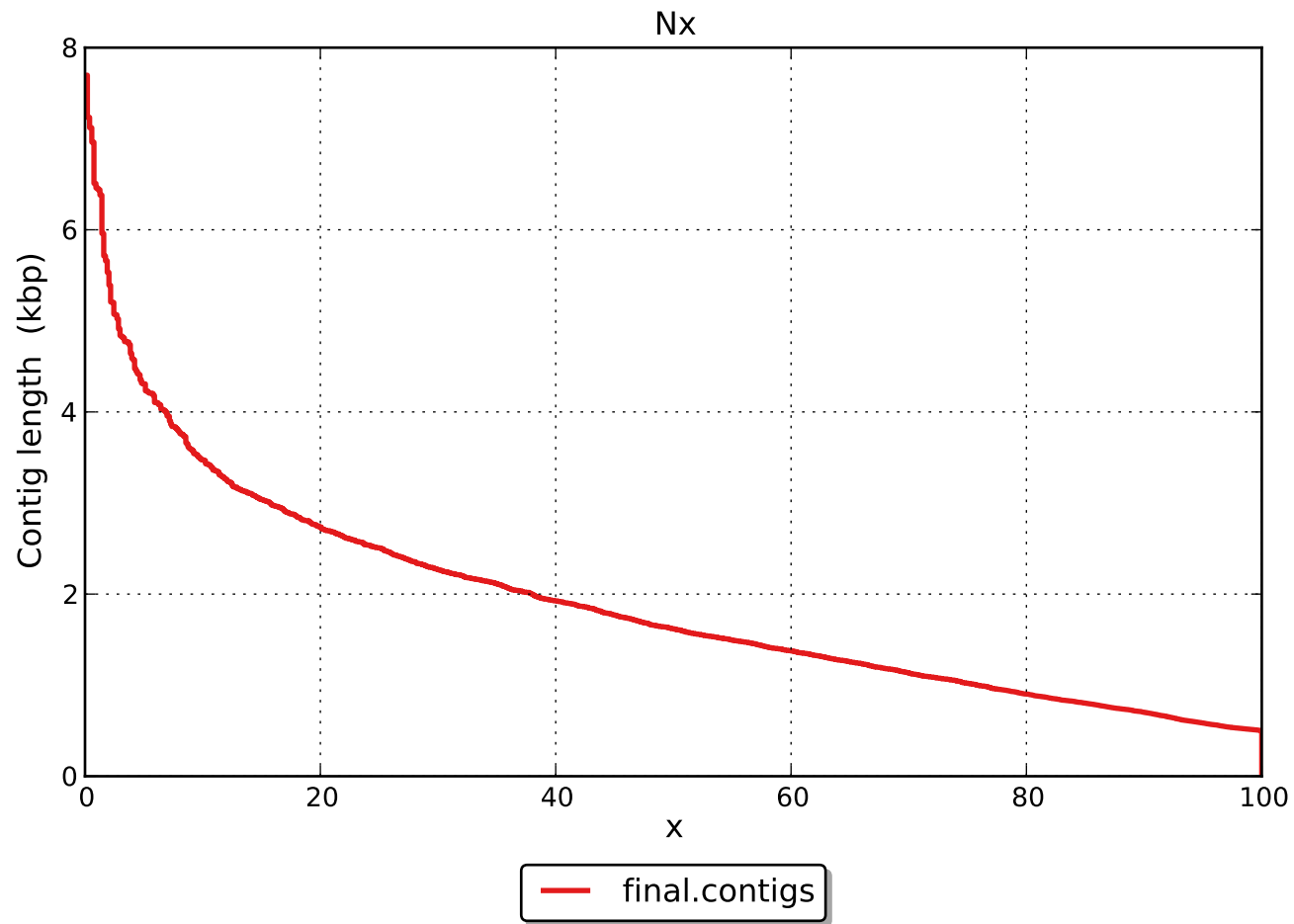
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	427
# indels	0
# short indels	0
# long indels	0
Indels length	0

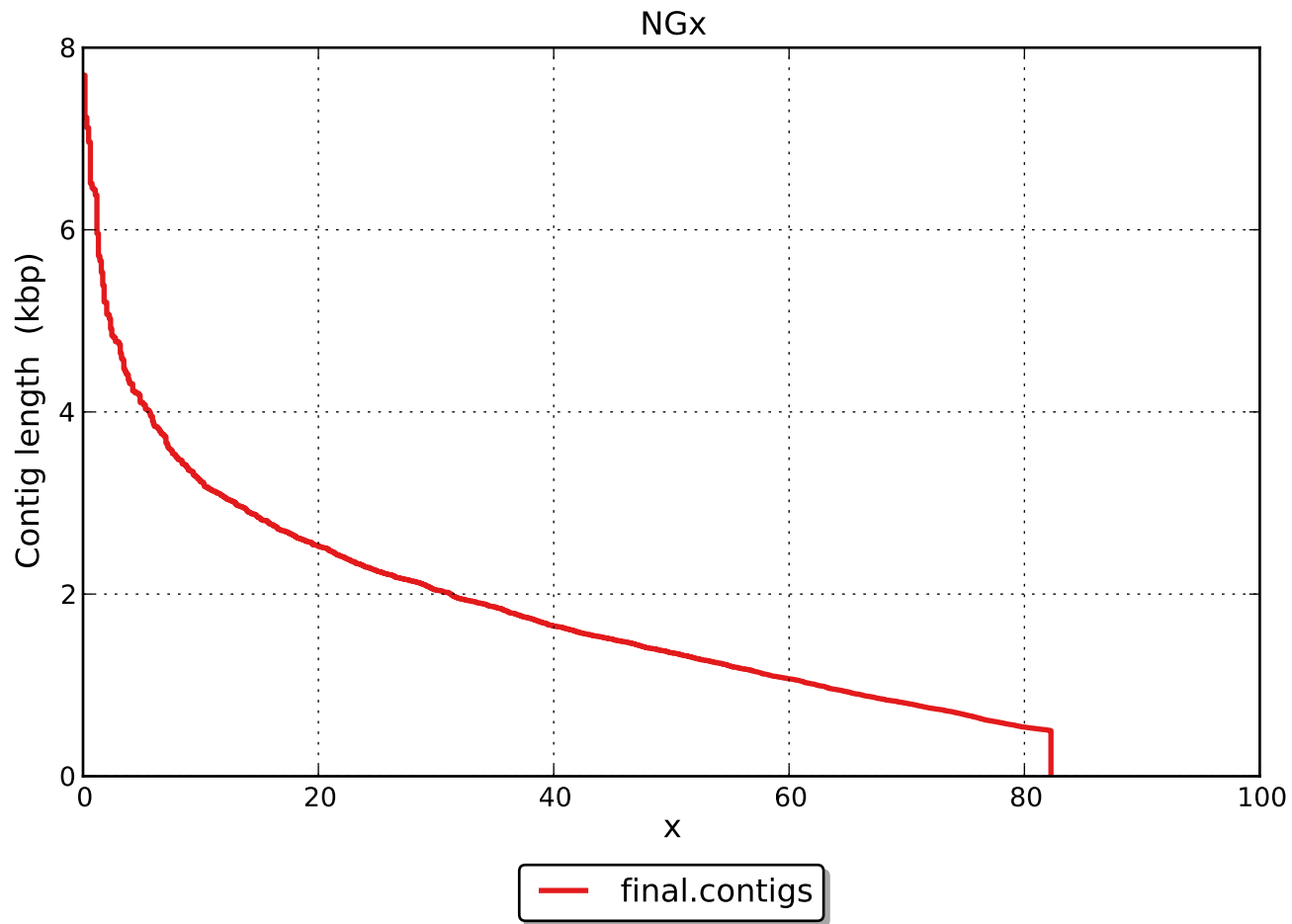
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

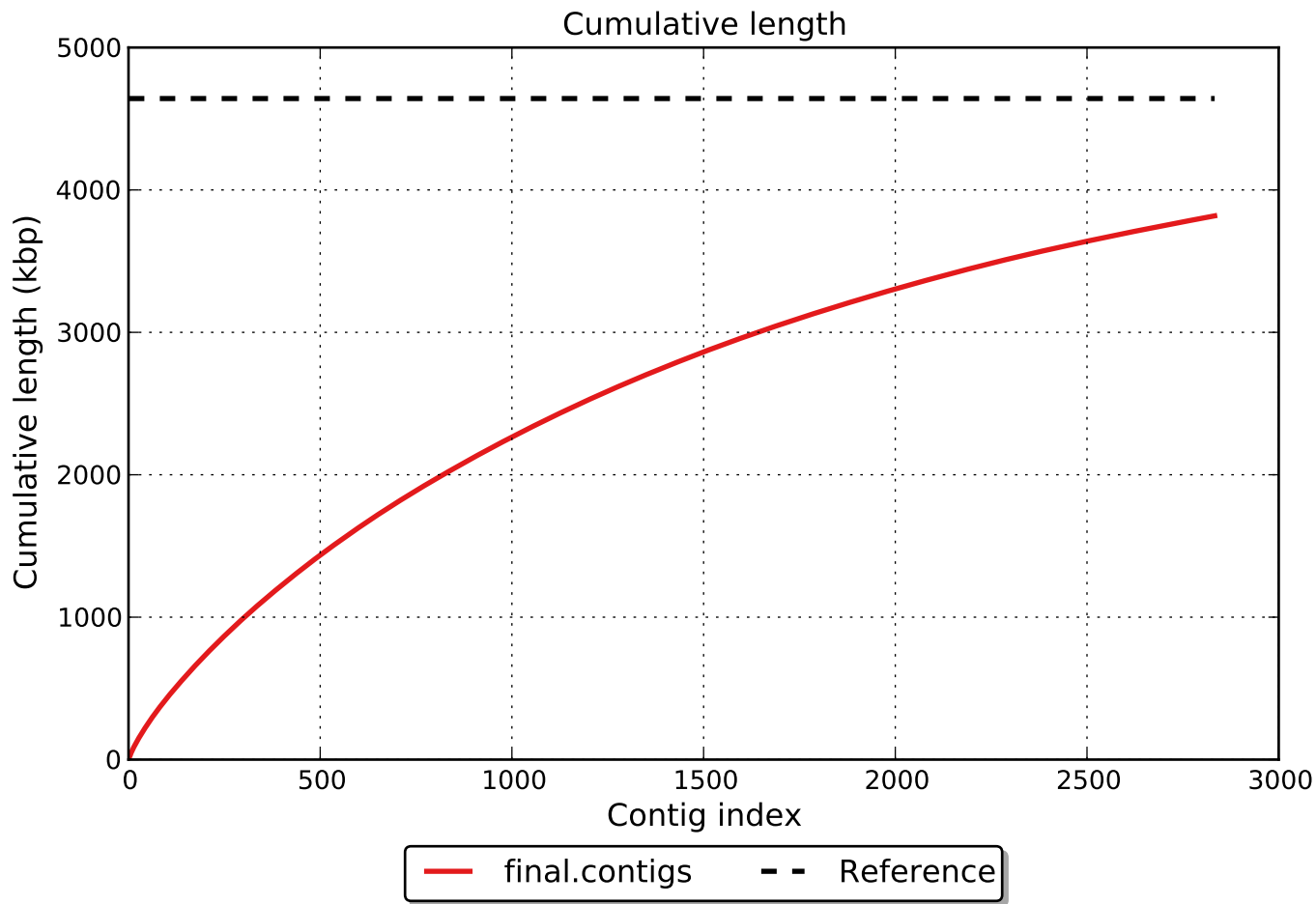
## Unaligned report

	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	0
Partially unaligned length	250
# N's	0

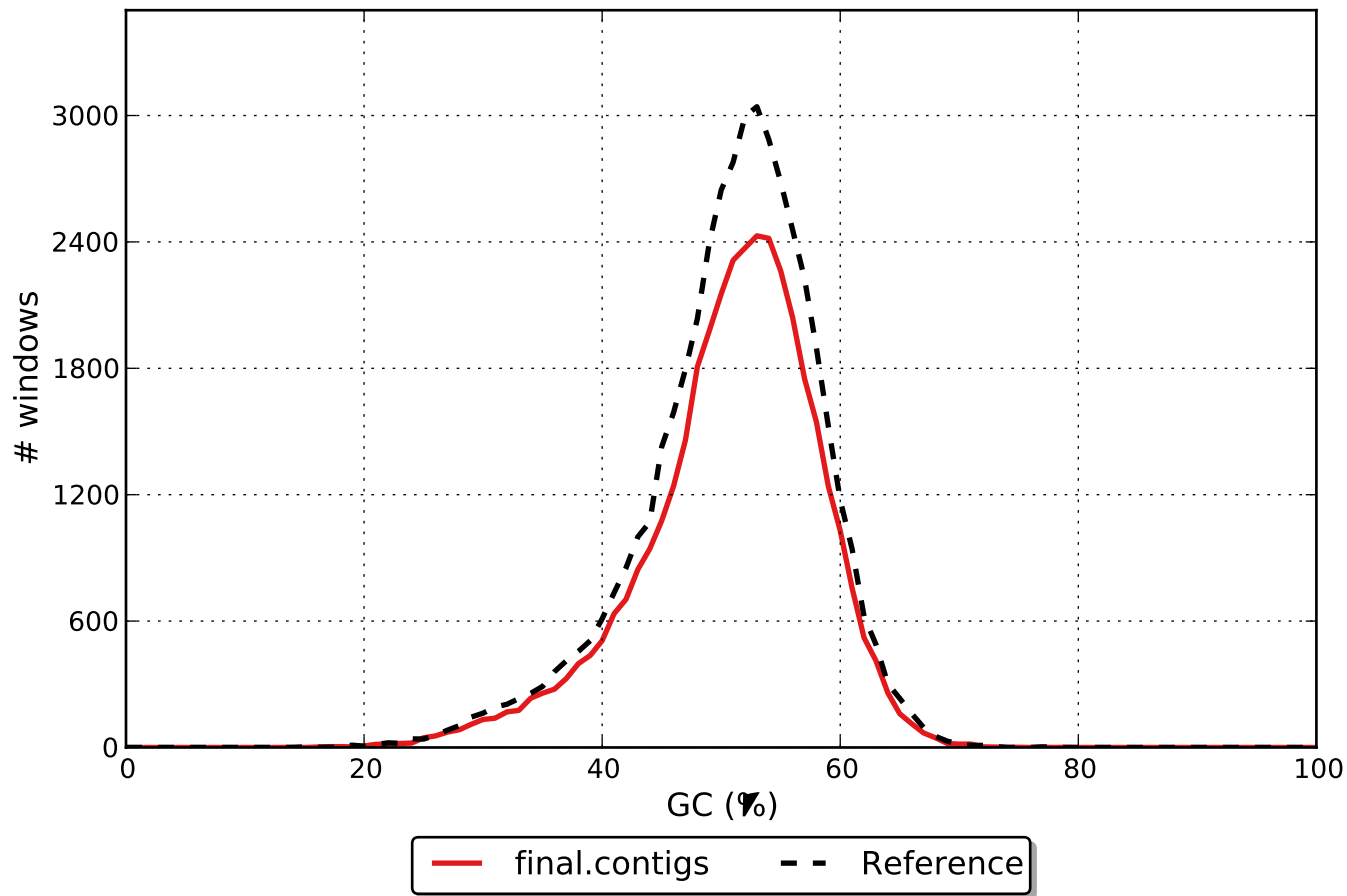
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).







GC content

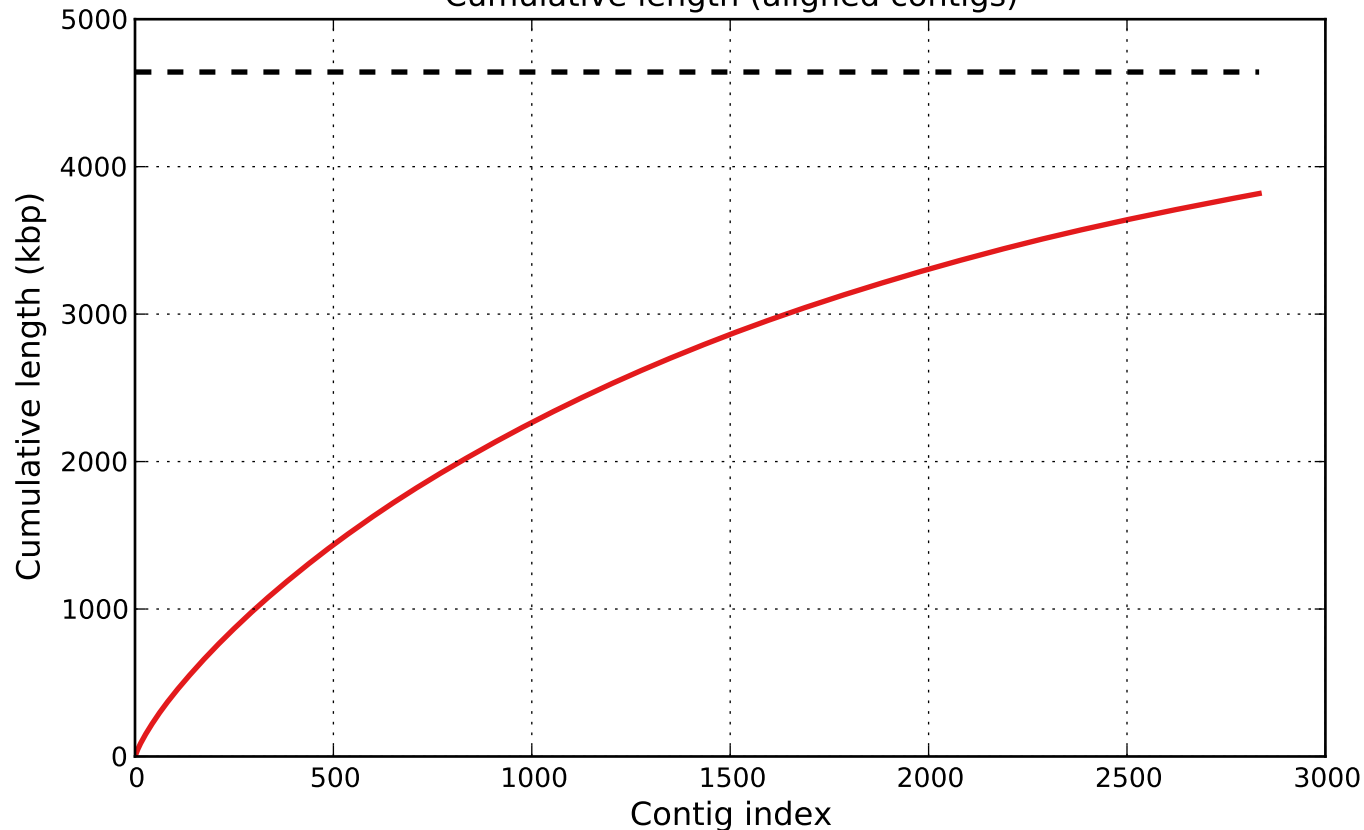


# Misassemblies

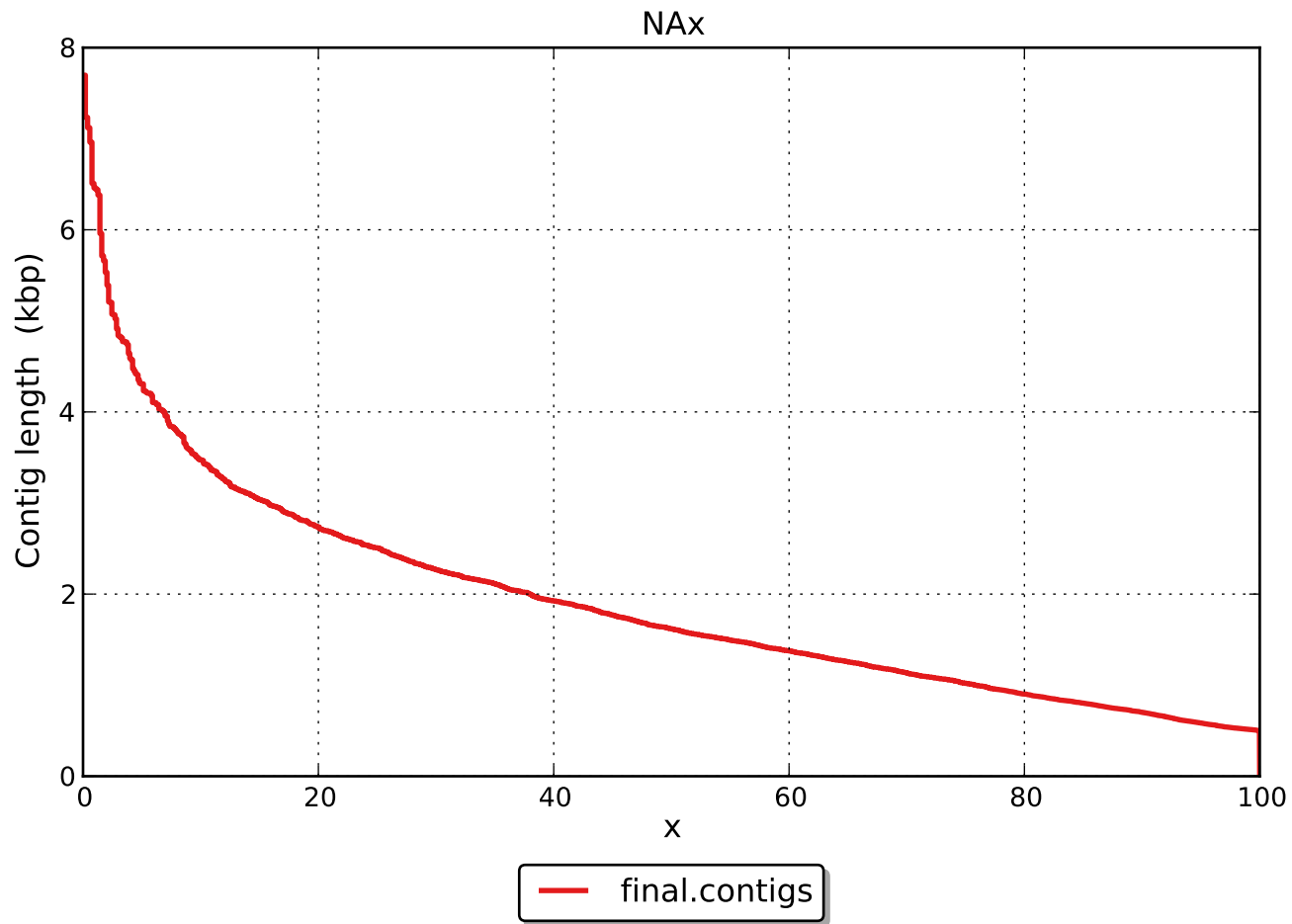




Cumulative length (aligned contigs)



— final.contigs    - - Reference



NGAx

