

## Report

	final.contigs
# contigs (>= 0 bp)	3264
# contigs (>= 1000 bp)	2001
Total length (>= 0 bp)	5161357
Total length (>= 1000 bp)	4245796
# contigs	3264
Largest contig	10098
Total length	5161357
Reference length	5478683
GC (%)	50.27
Reference GC (%)	50.49
N50	1978
NG50	1879
N75	1217
NG75	1076
L50	835
LG50	917
L75	1662
LG75	1870
# misassemblies	2
# misassembled contigs	2
Misassembled contigs length	3732
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	90.269
Duplication ratio	1.044
# N's per 100 kbp	0.00
# mismatches per 100 kbp	46.26
# indels per 100 kbp	0.20
Largest alignment	10098
NA50	1978
NGA50	1879
NA75	1216
NGA75	1076
LA50	835
LGA50	917
LA75	1662
LGA75	1870

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

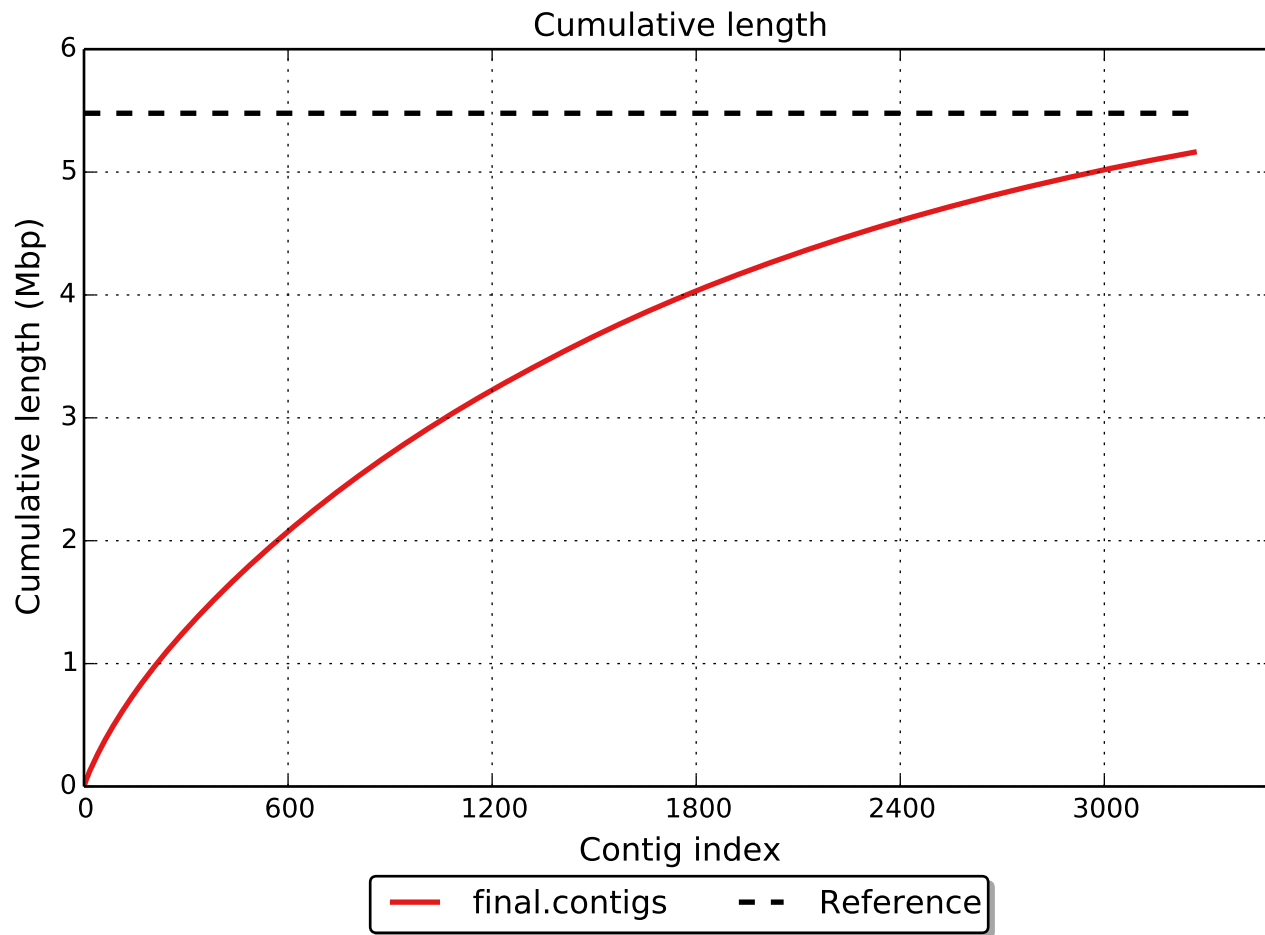
	final.contigs
# misassemblies	2
# relocations	2
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	2
Misassembled contigs length	3732
# local misassemblies	1
# mismatches	2288
# indels	10
# short indels	10
# long indels	0
Indels length	14

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).

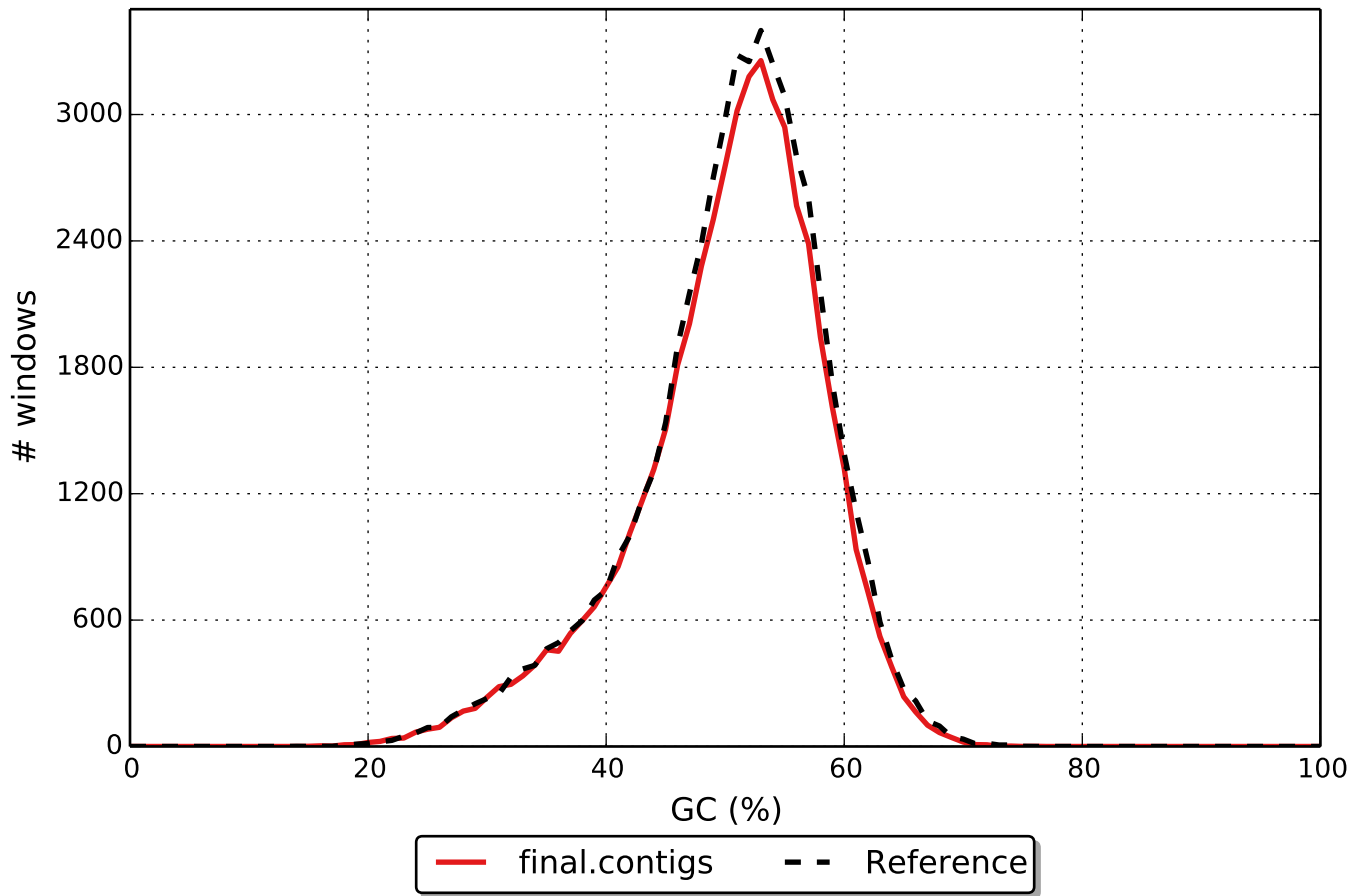
## Unaligned report

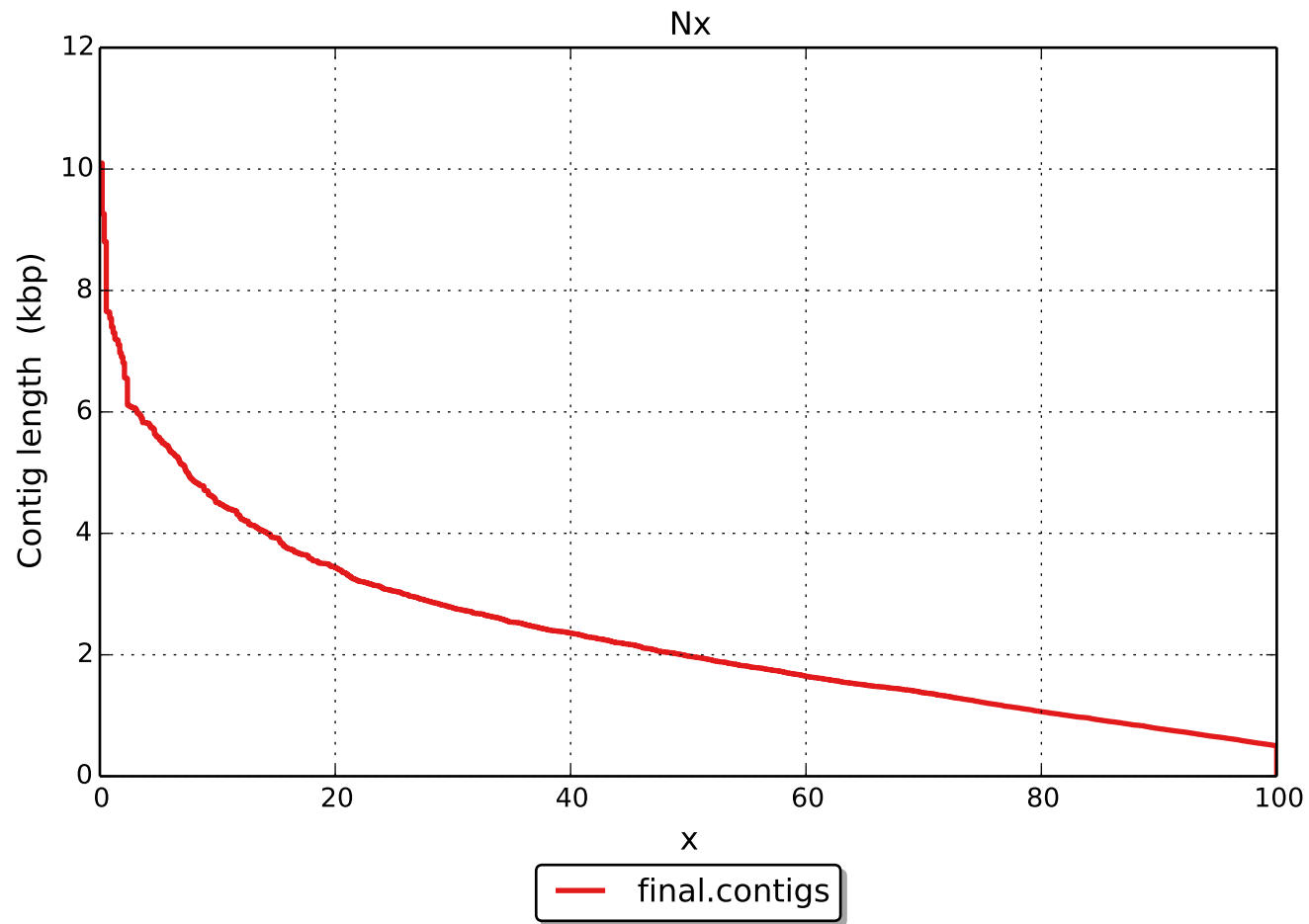
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

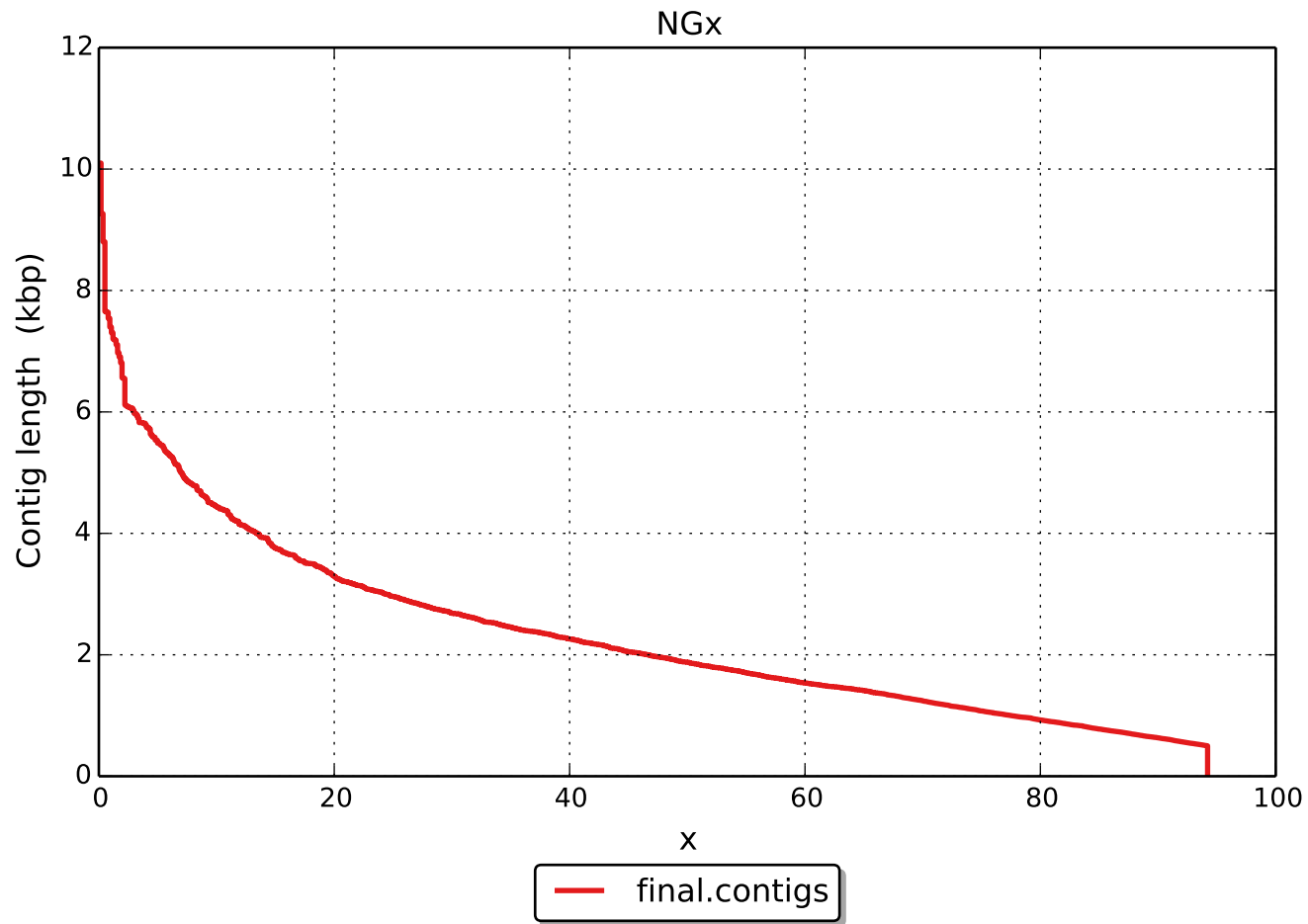
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



GC content

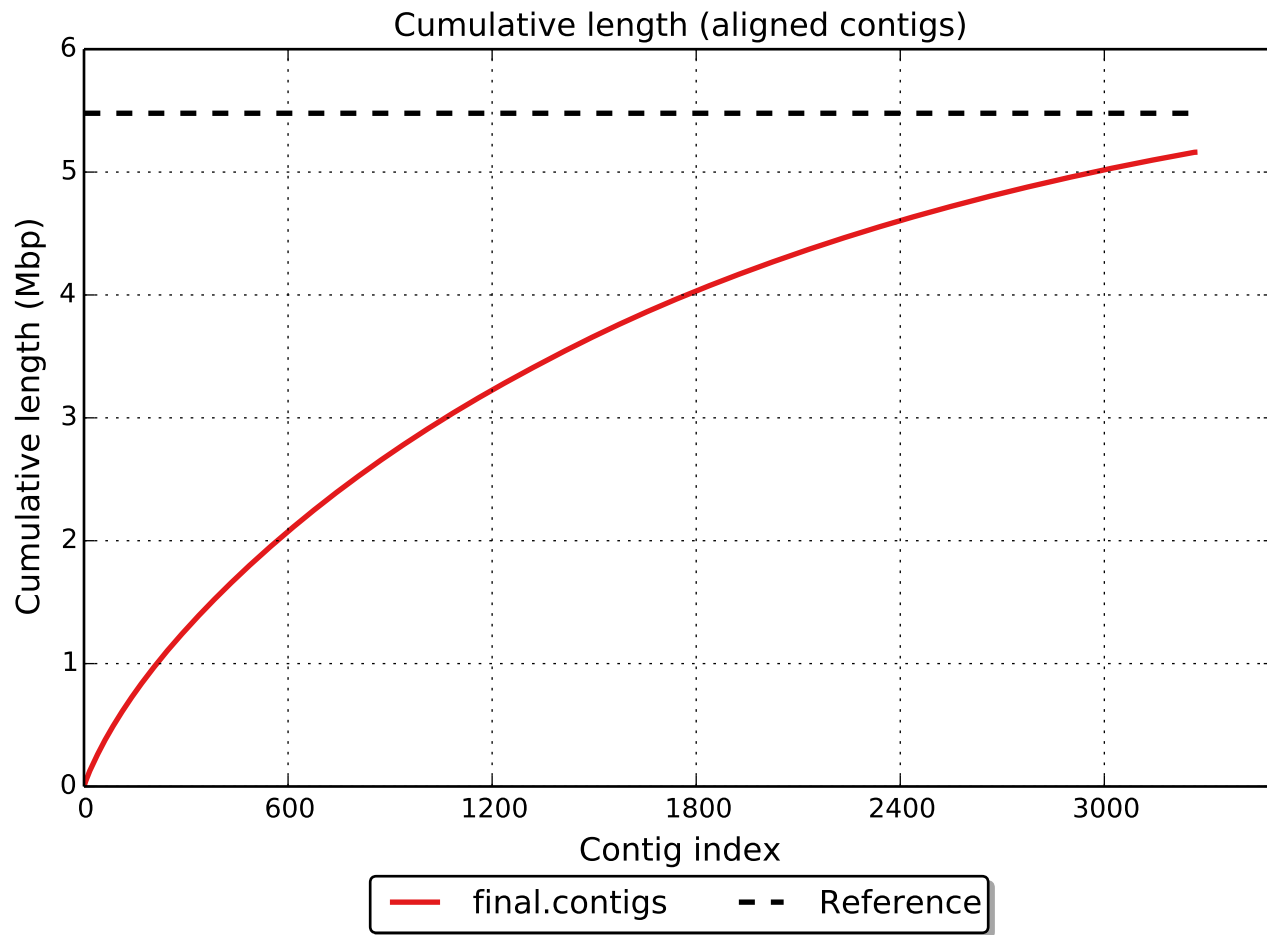


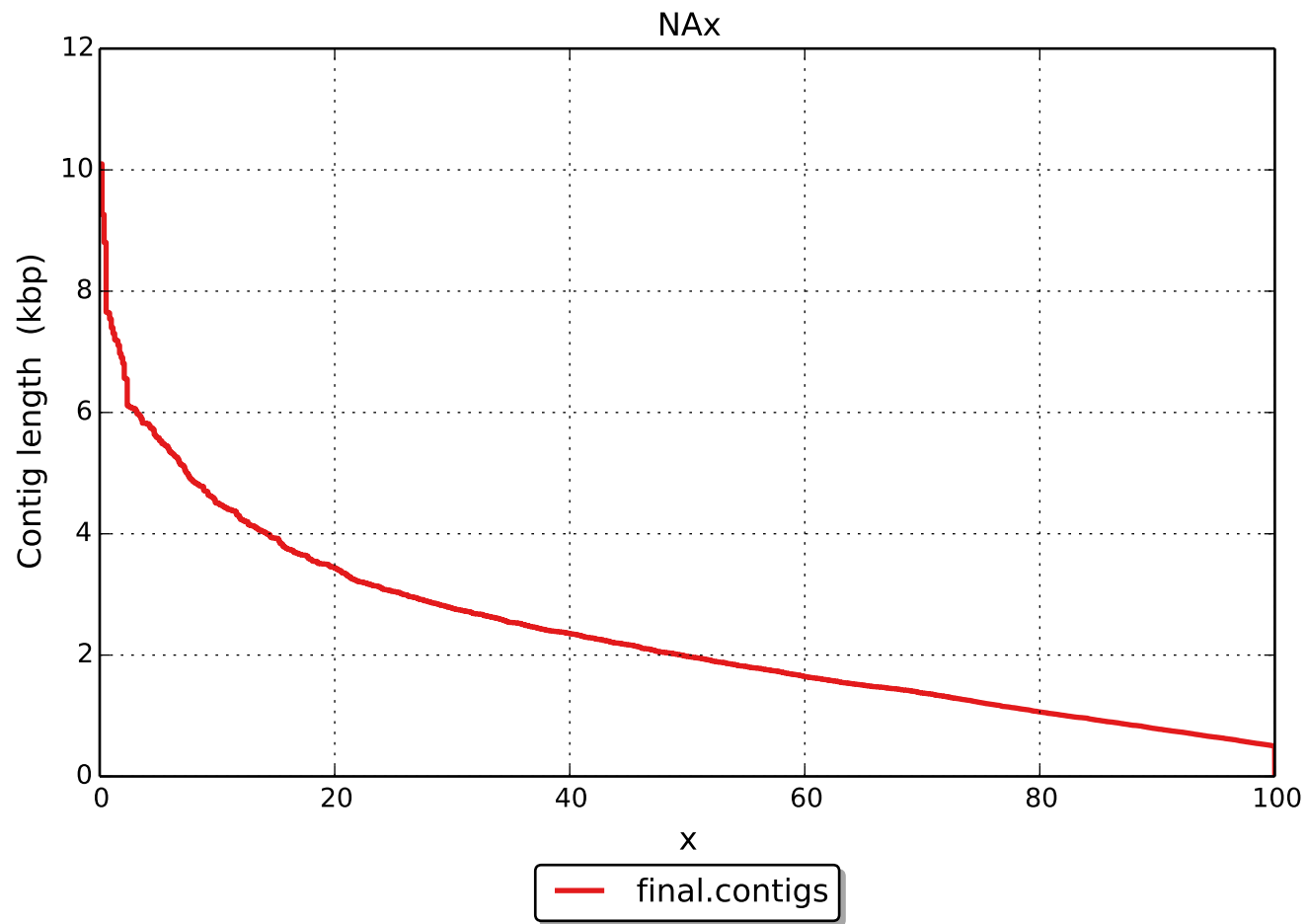












NGAx

