

Report

	final.contigs
# contigs (≥ 0 bp)	3176
# contigs (≥ 1000 bp)	1964
Total length (≥ 0 bp)	5071310
Total length (≥ 1000 bp)	4190256
# contigs	3176
Largest contig	9231
Total length	5071310
Reference length	5547323
GC (%)	50.29
Reference GC (%)	50.48
N50	1985
NG50	1828
N75	1222
NG75	1017
L50	802
LG50	927
L75	1614
LG75	1935
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	1177
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	87.878
Duplication ratio	1.040
# N's per 100 kbp	0.00
# mismatches per 100 kbp	43.41
# indels per 100 kbp	0.18
Largest alignment	9231
NA50	1985
NGA50	1828
NA75	1222
NGA75	1016
LA50	802
LGA50	927
LA75	1615
LGA75	1935

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

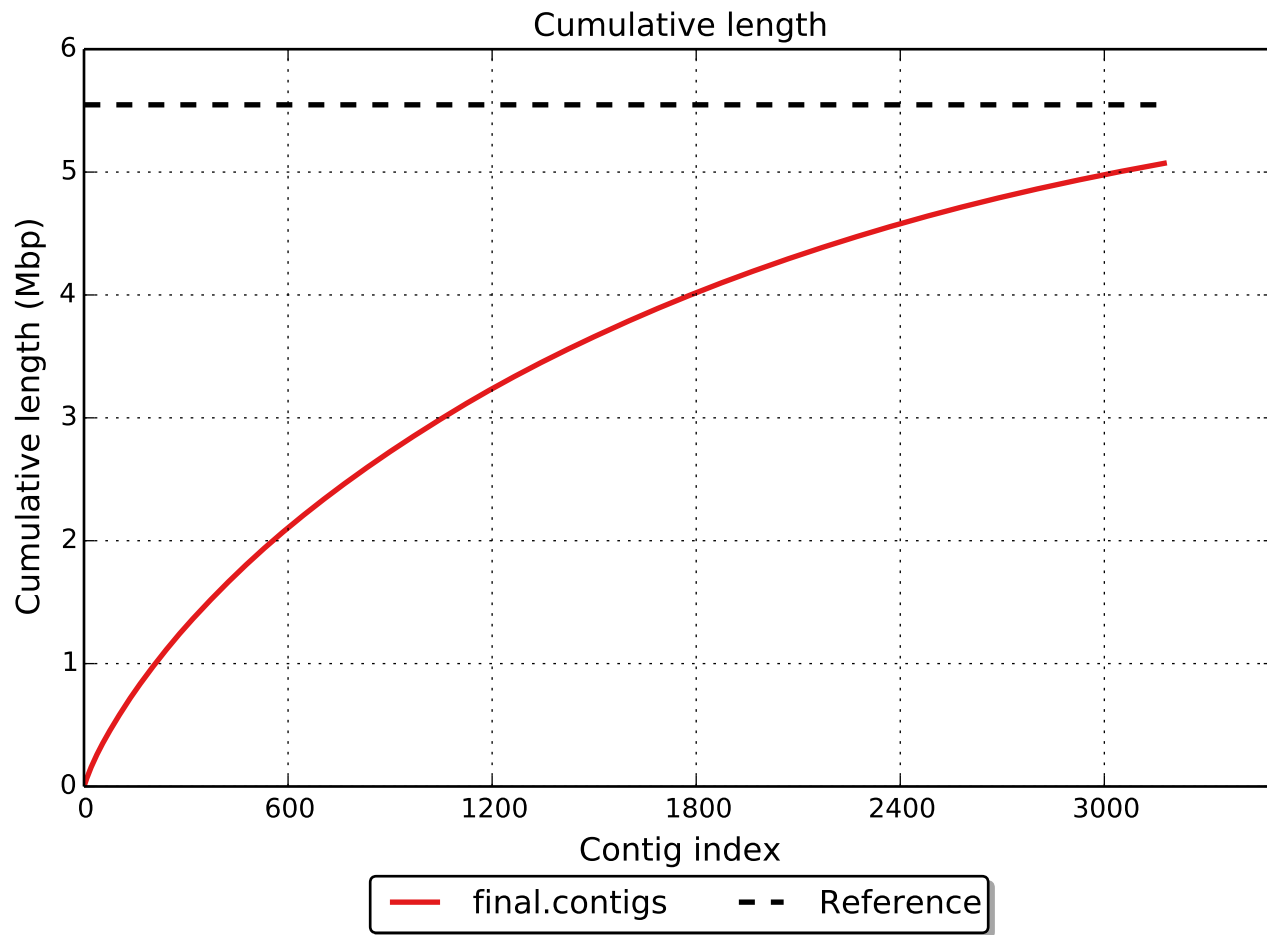
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	1177
# local misassemblies	0
# mismatches	2116
# indels	9
# short indels	7
# long indels	2
Indels length	20

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).

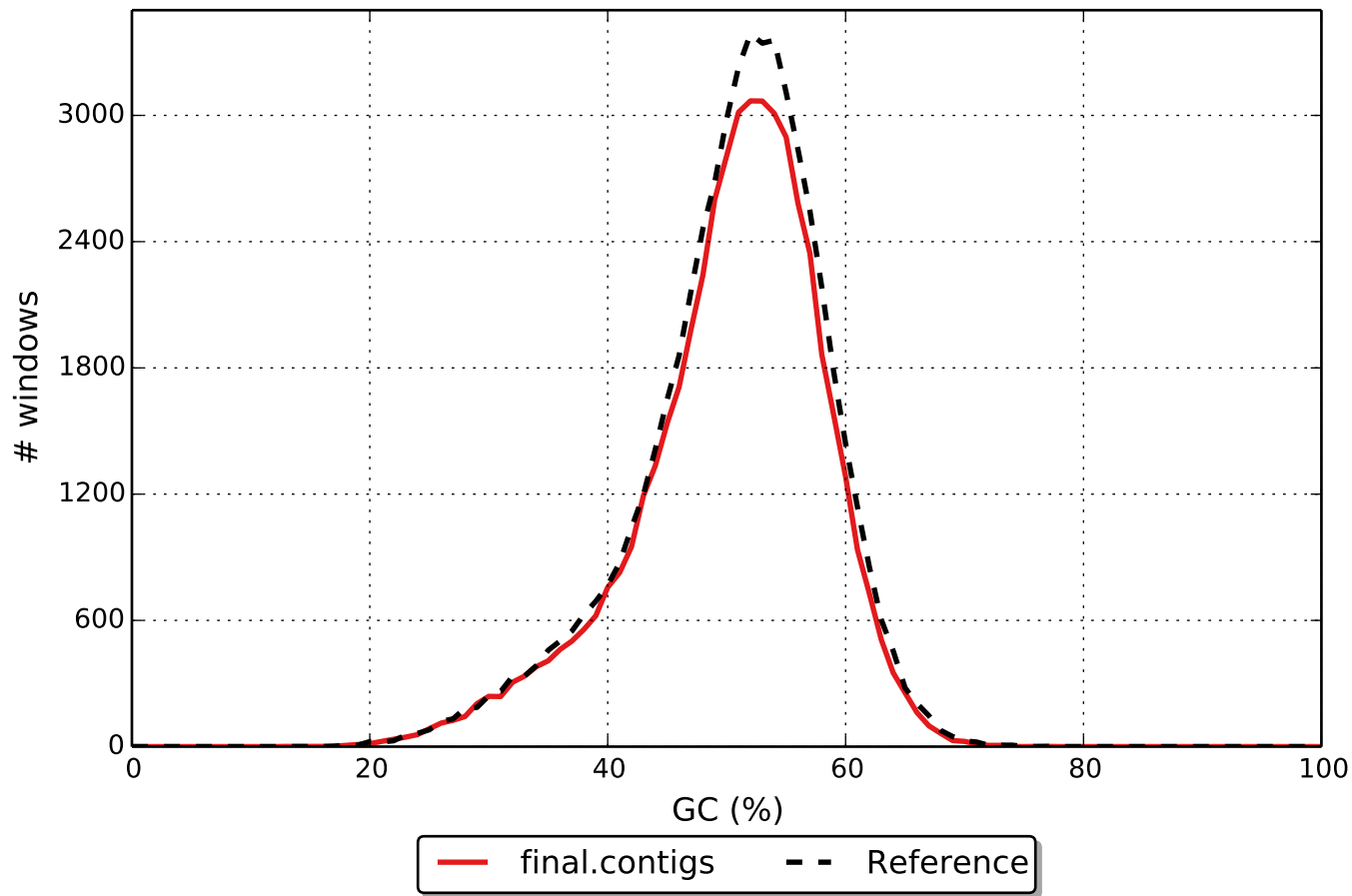
Unaligned report

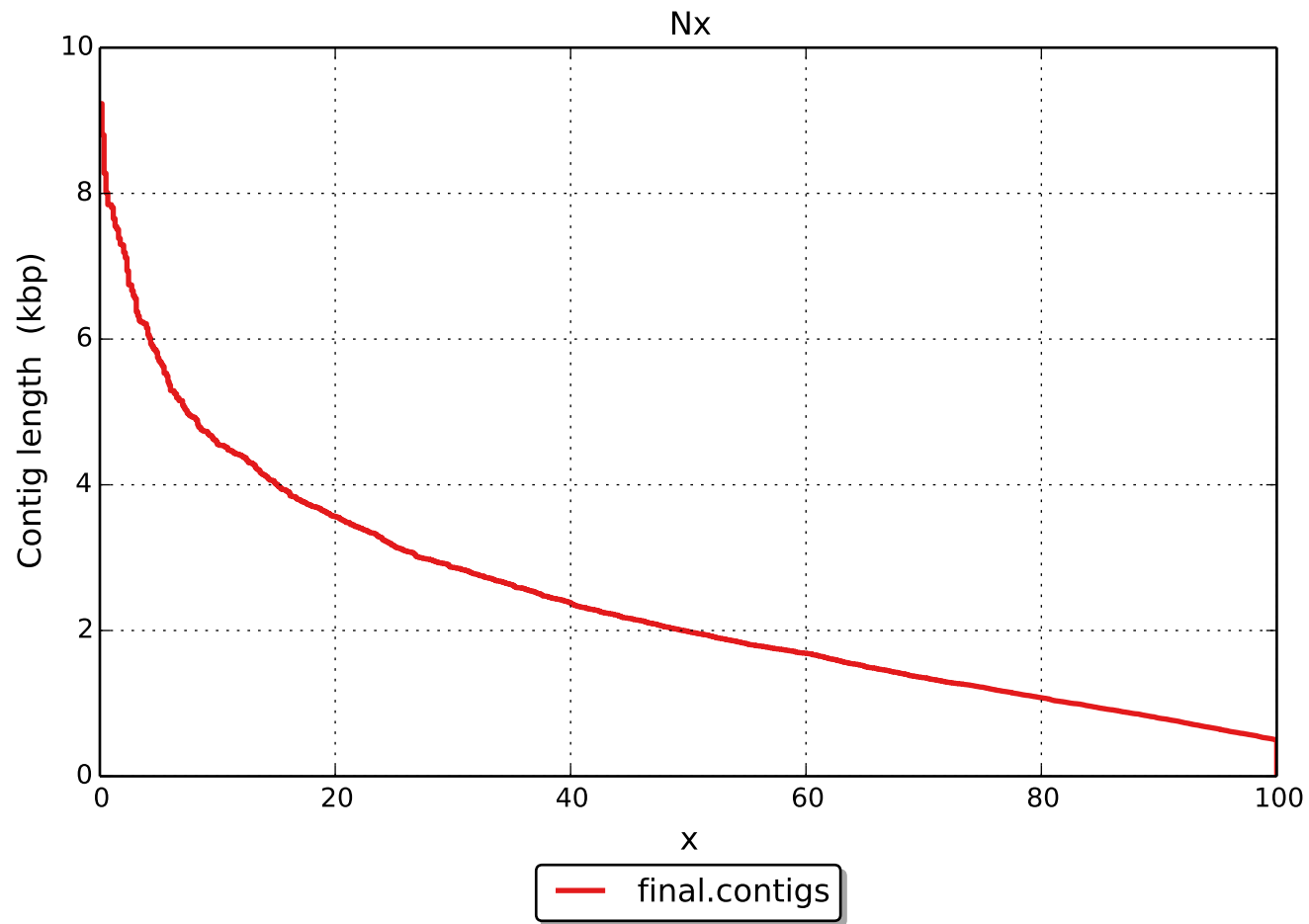
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

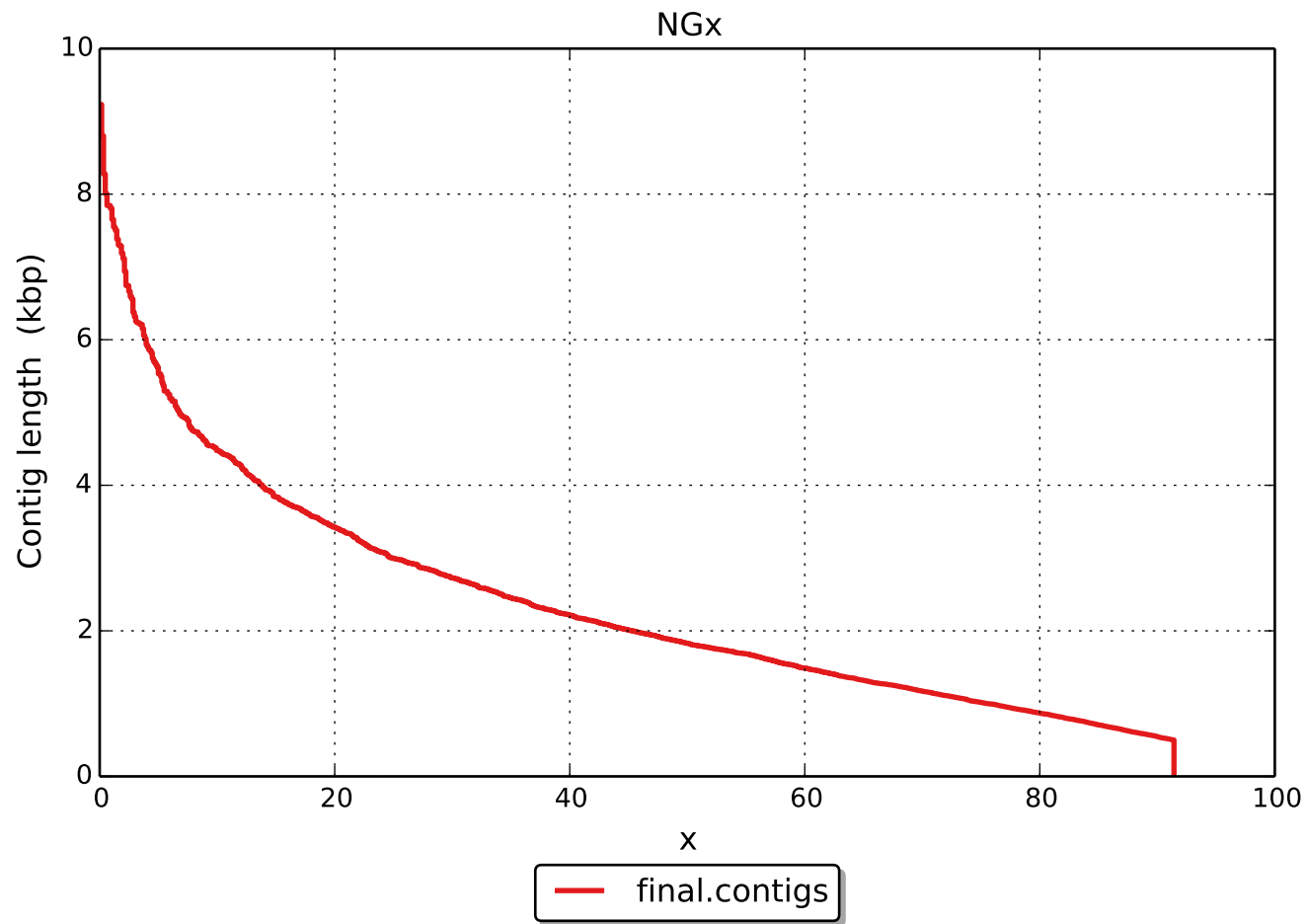
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



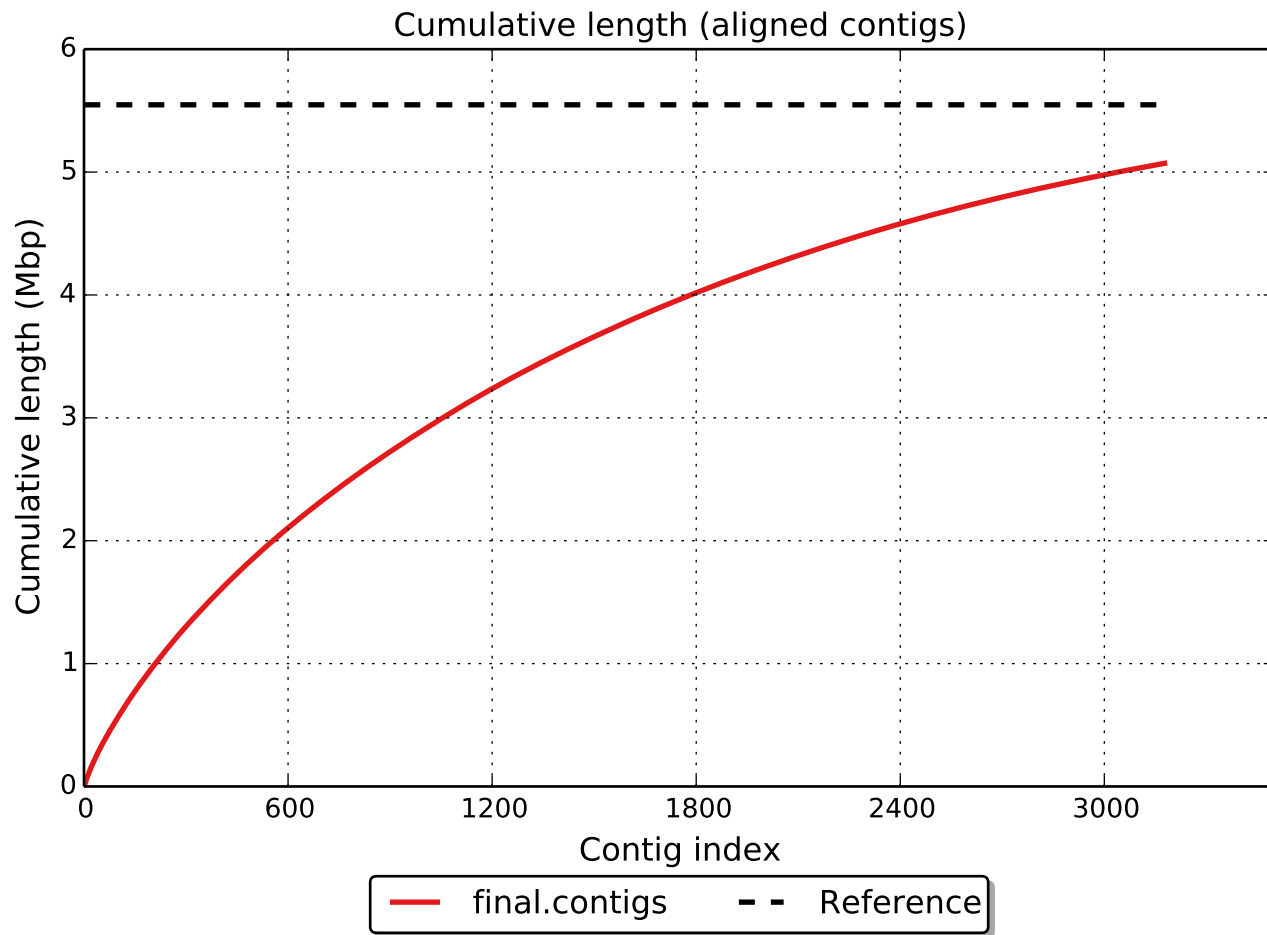
GC content

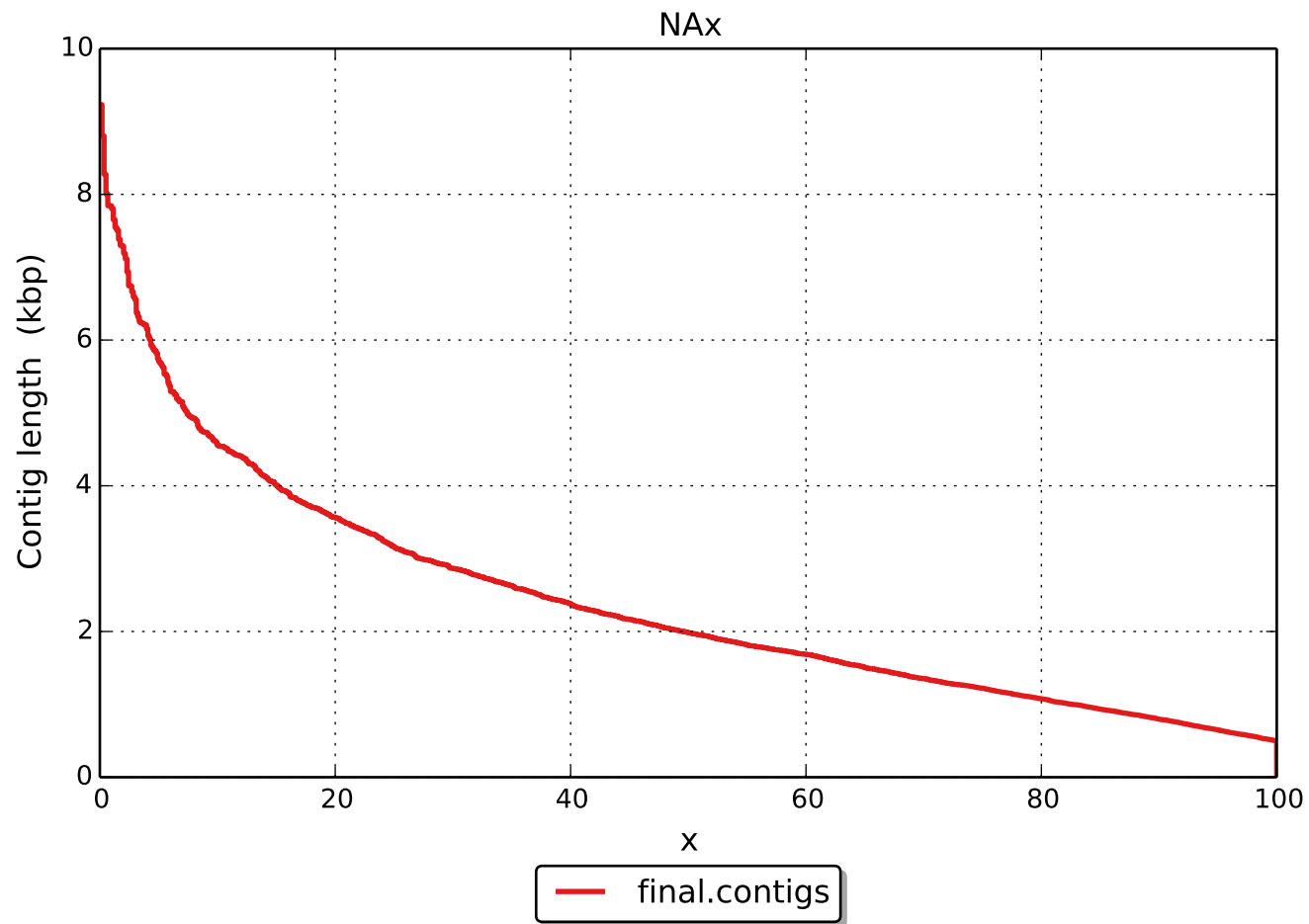












NGAx

