

Report

	final.contigs
# contigs (≥ 0 bp)	3195
# contigs (≥ 1000 bp)	1972
Total length (≥ 0 bp)	5095518
Total length (≥ 1000 bp)	4206616
# contigs	3195
Largest contig	9231
Total length	5095518
Reference length	5547323
GC (%)	50.29
Reference GC (%)	50.48
N50	1984
NG50	1835
N75	1219
NG75	1025
L50	806
LG50	924
L75	1624
LG75	1927
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	1177
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	88.157
Duplication ratio	1.042
# N's per 100 kbp	0.00
# mismatches per 100 kbp	50.51
# indels per 100 kbp	0.18
Largest alignment	9231
NA50	1984
NGA50	1835
NA75	1219
NGA75	1025
LA50	806
LGA50	924
LA75	1624
LGA75	1927

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

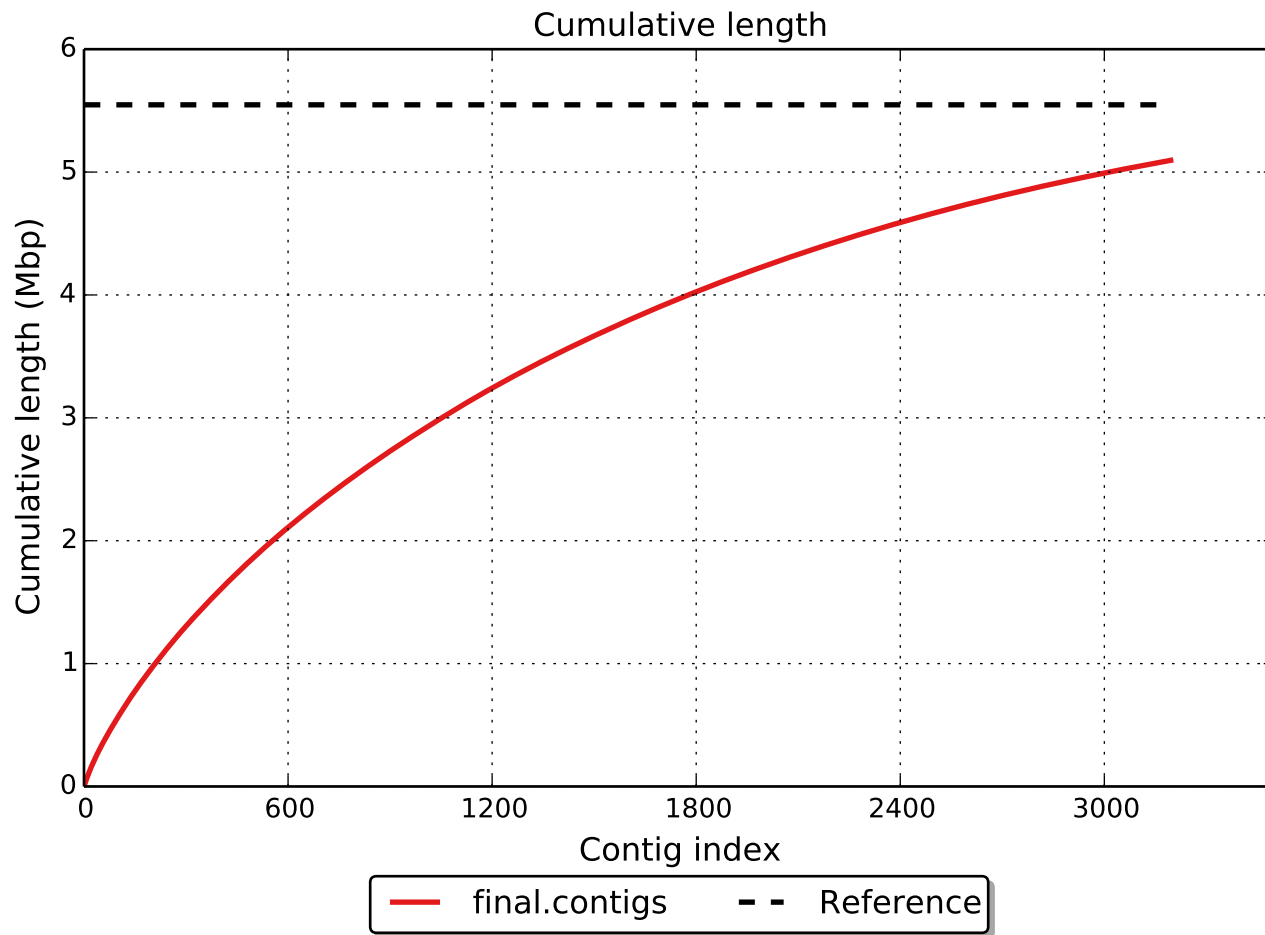
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	1177
# local misassemblies	0
# mismatches	2470
# indels	9
# short indels	7
# long indels	2
Indels length	20

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).

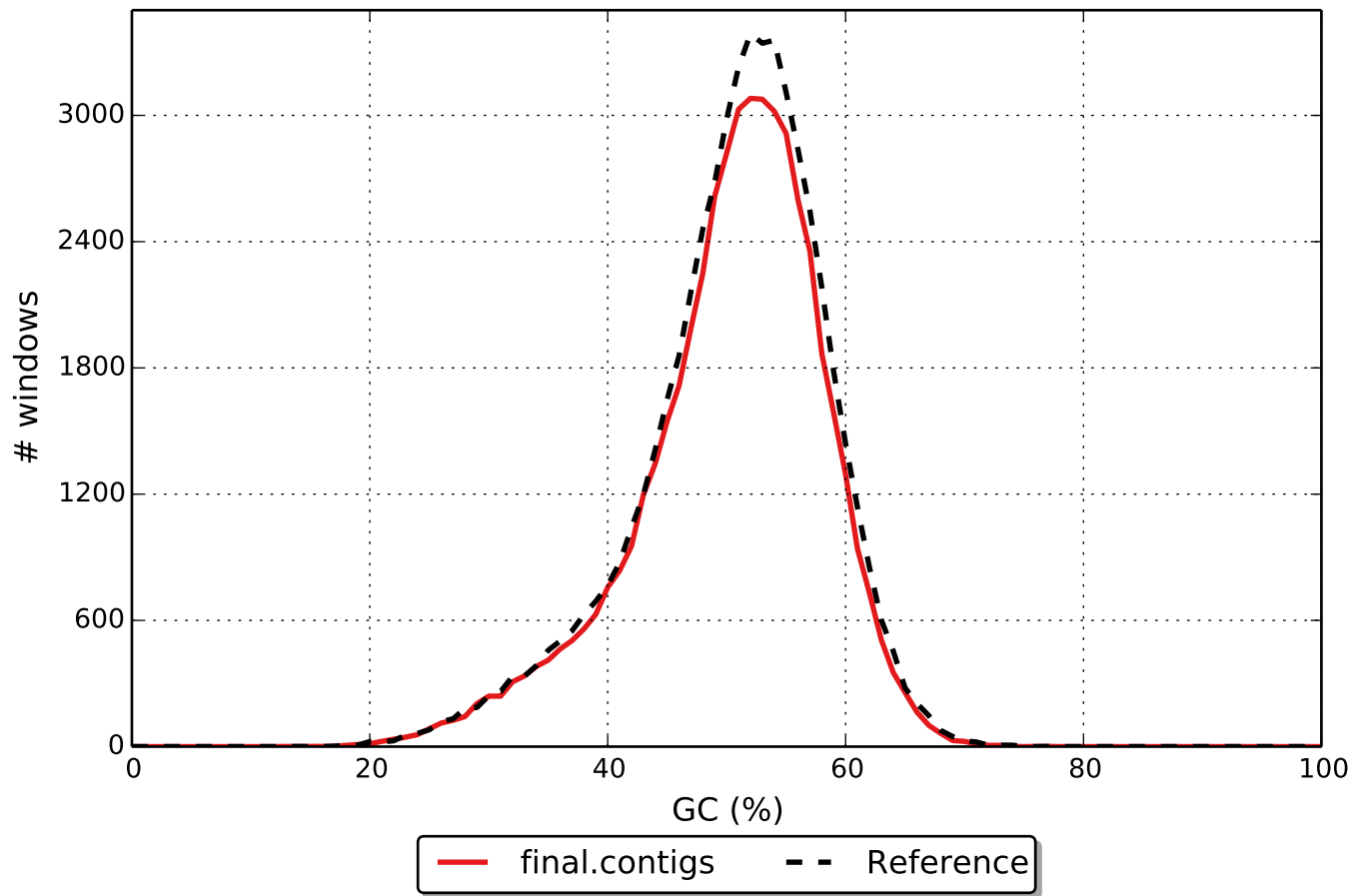
Unaligned report

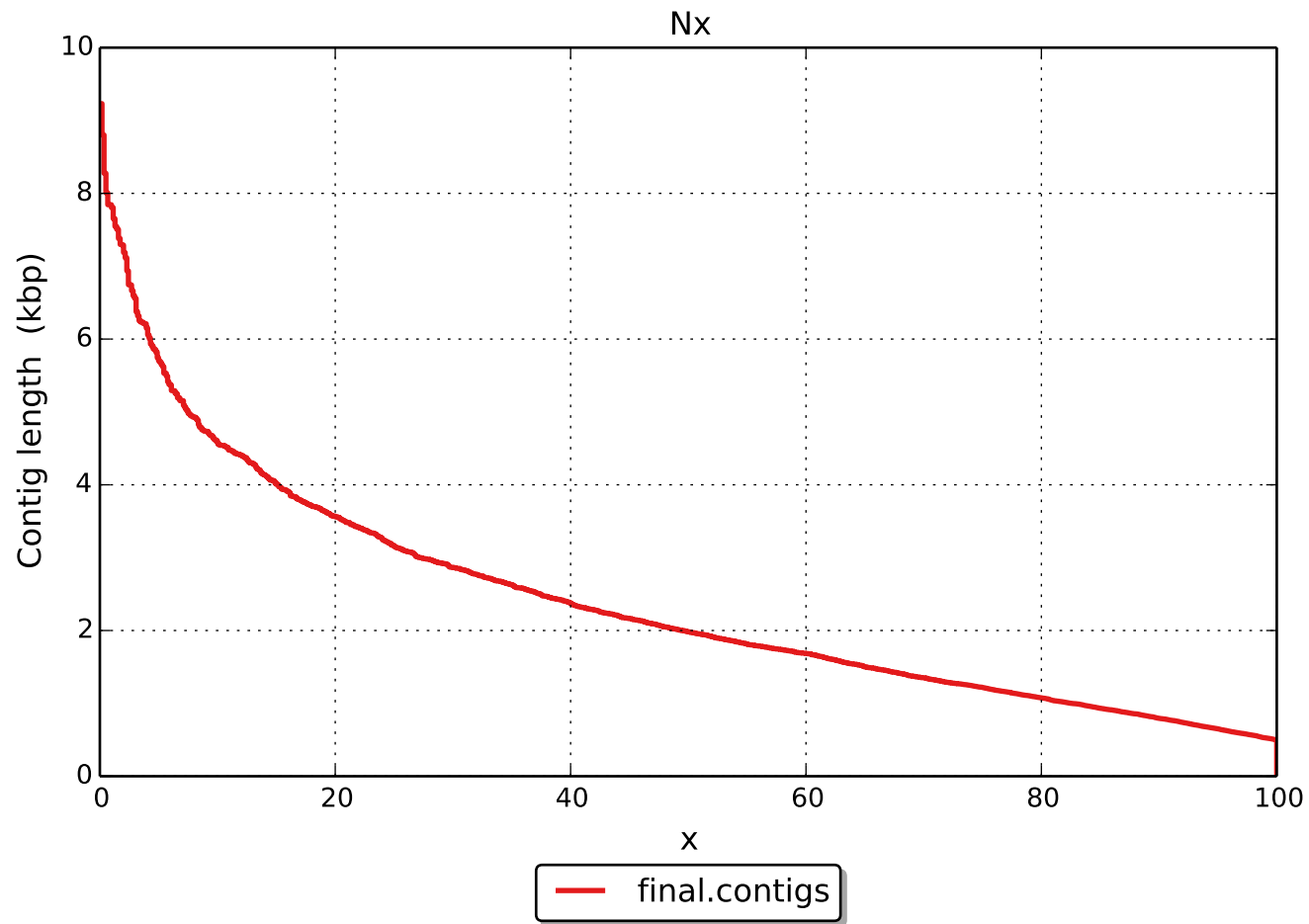
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

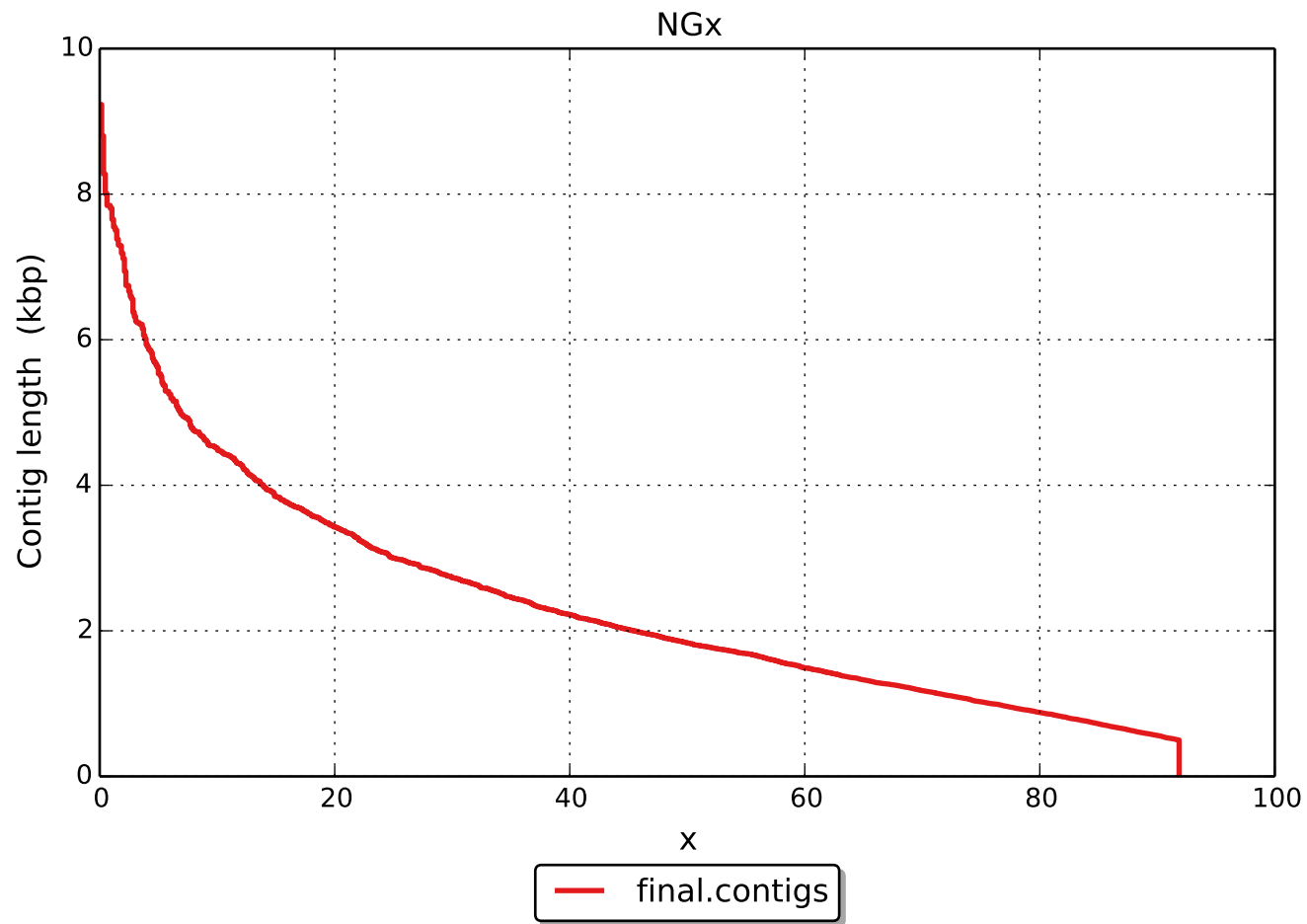
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



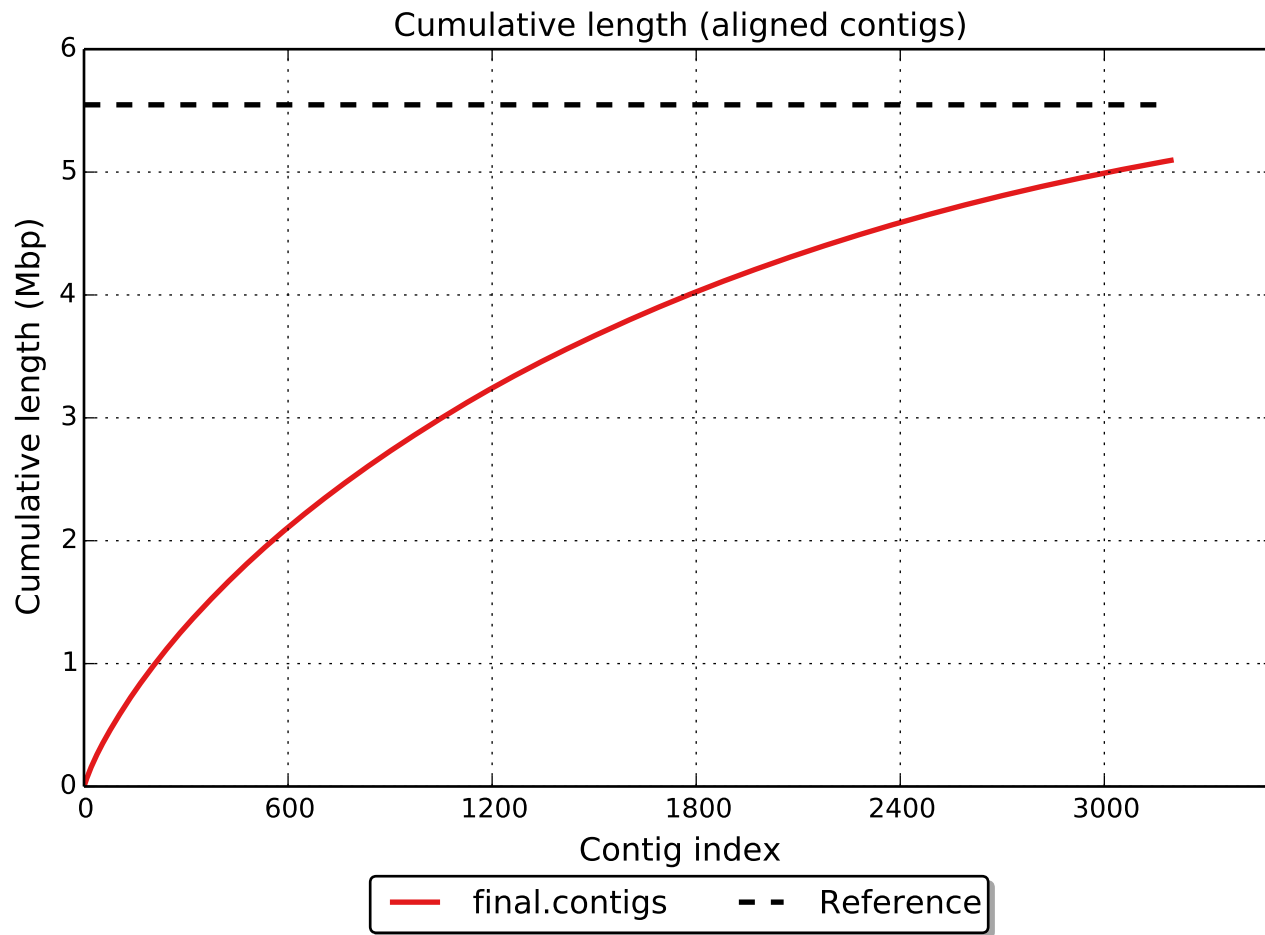
GC content

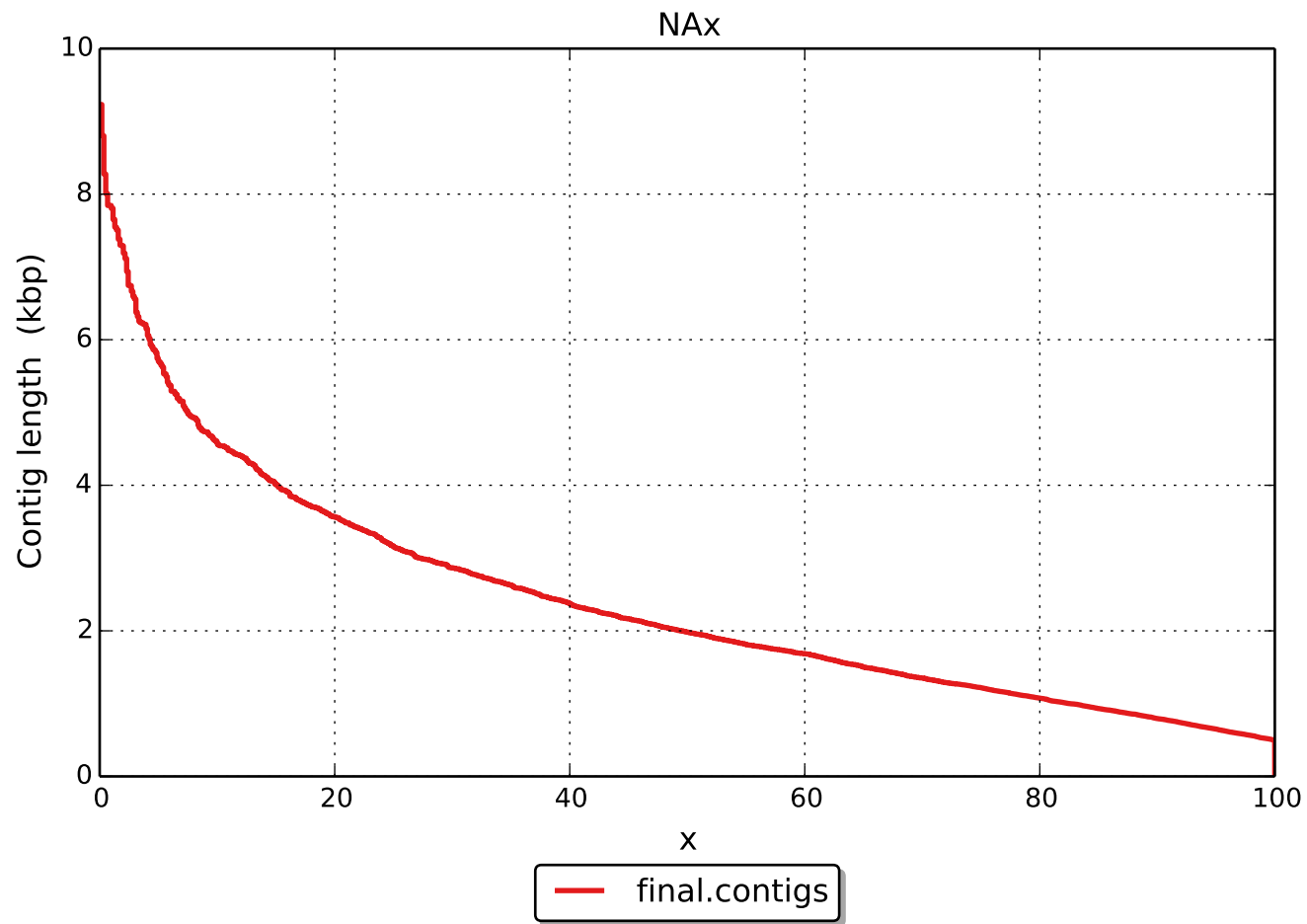












NGAx

