

Report

	final.contigs
# contigs (>= 0 bp)	2675
# contigs (>= 1000 bp)	1941
Total length (>= 0 bp)	5518100
Total length (>= 1000 bp)	4976786
# contigs	2675
Largest contig	12275
Total length	5518100
Reference length	5478683
GC (%)	50.49
Reference GC (%)	50.49
N50	2716
NG50	2732
N75	1643
NG75	1659
L50	641
LG50	633
L75	1289
LG75	1271
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	7696
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	97.309
Duplication ratio	1.035
# N's per 100 kbp	0.00
# mismatches per 100 kbp	26.13
# indels per 100 kbp	0.02
Largest alignment	12275
NA50	2716
NGA50	2723
NA75	1643
NGA75	1659
LA50	641
LGA50	634
LA75	1290
LGA75	1272

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

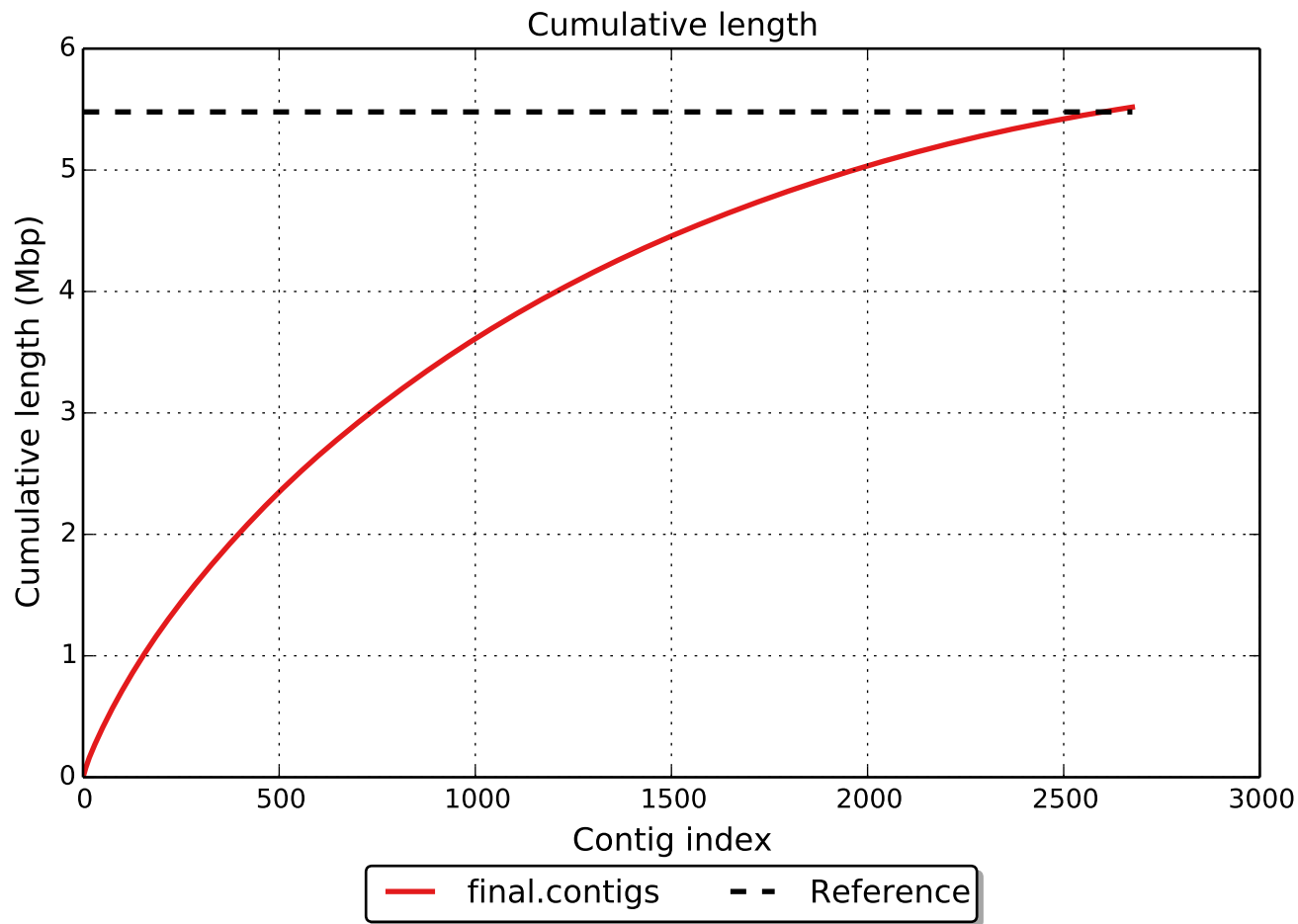
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	7696
# local misassemblies	0
# mismatches	1393
# indels	1
# short indels	0
# long indels	1
Indels length	9

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).

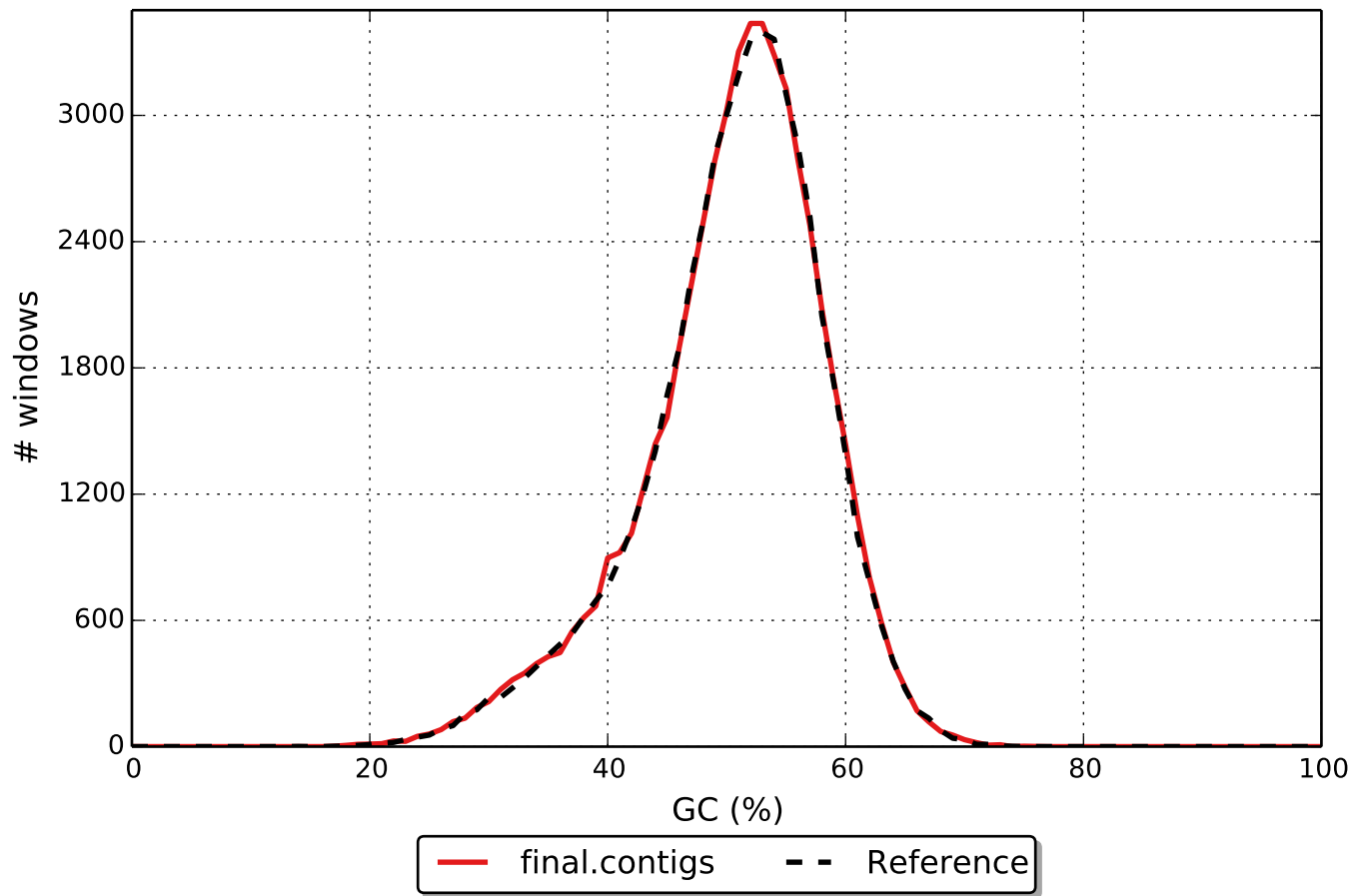
Unaligned report

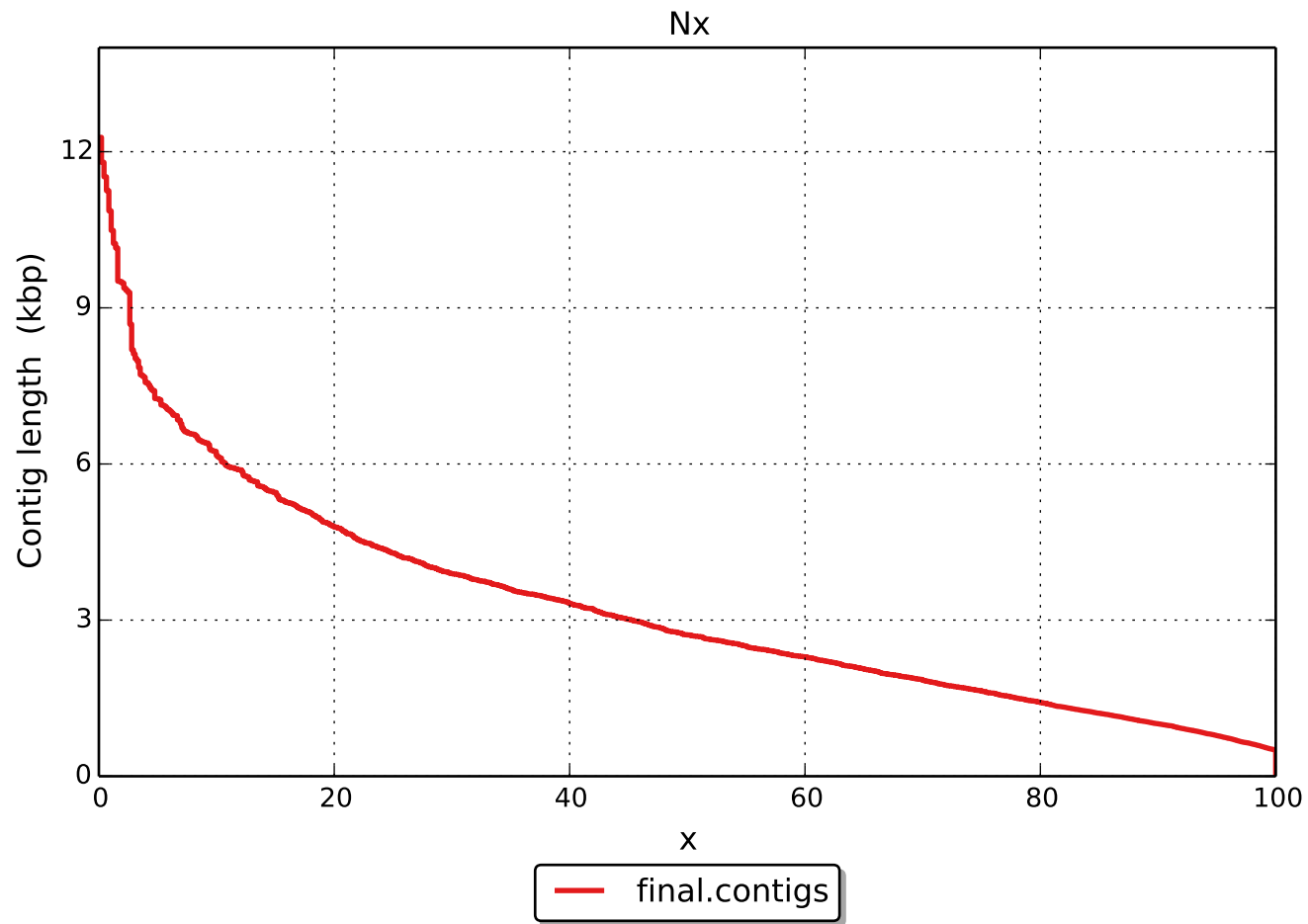
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

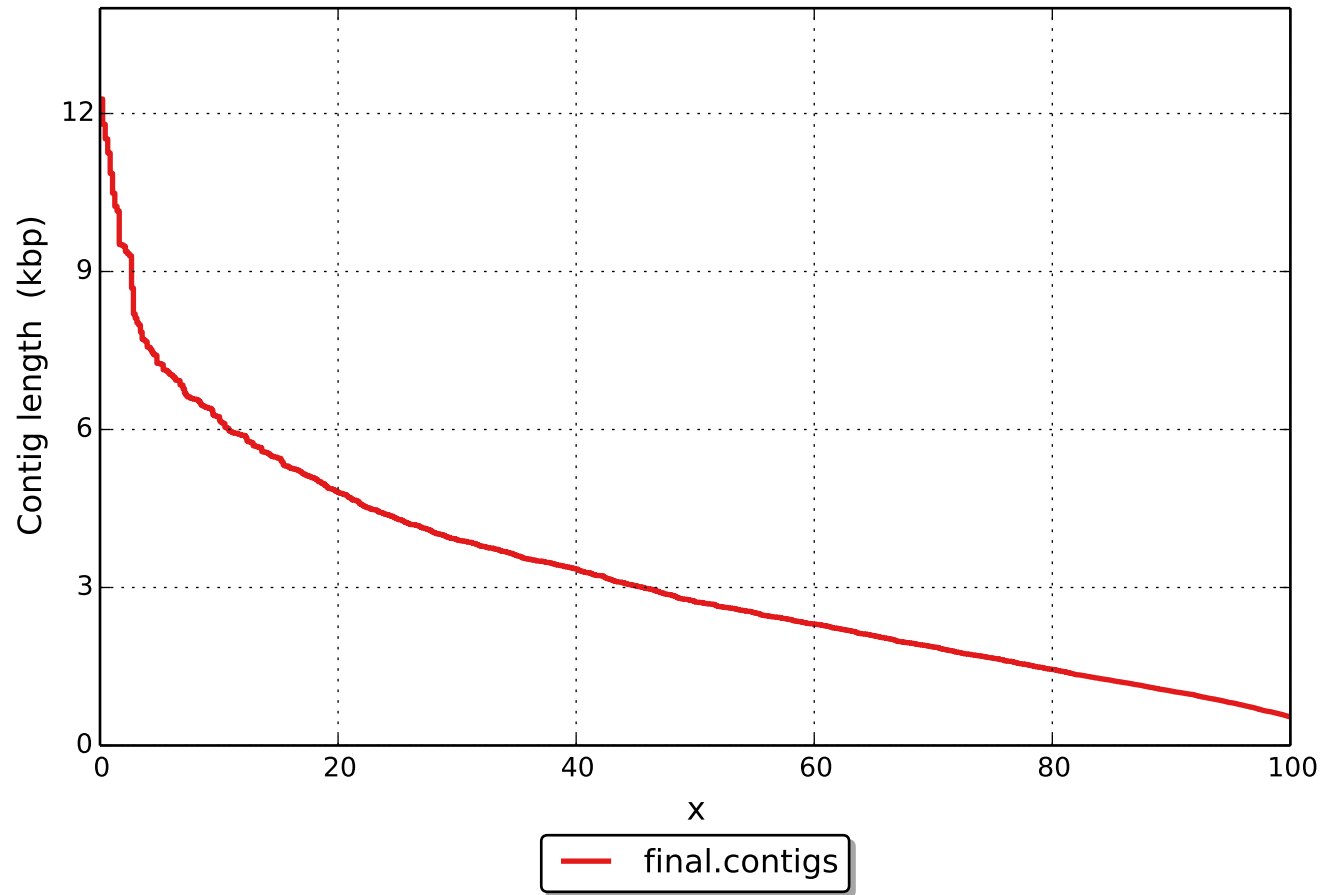


GC content

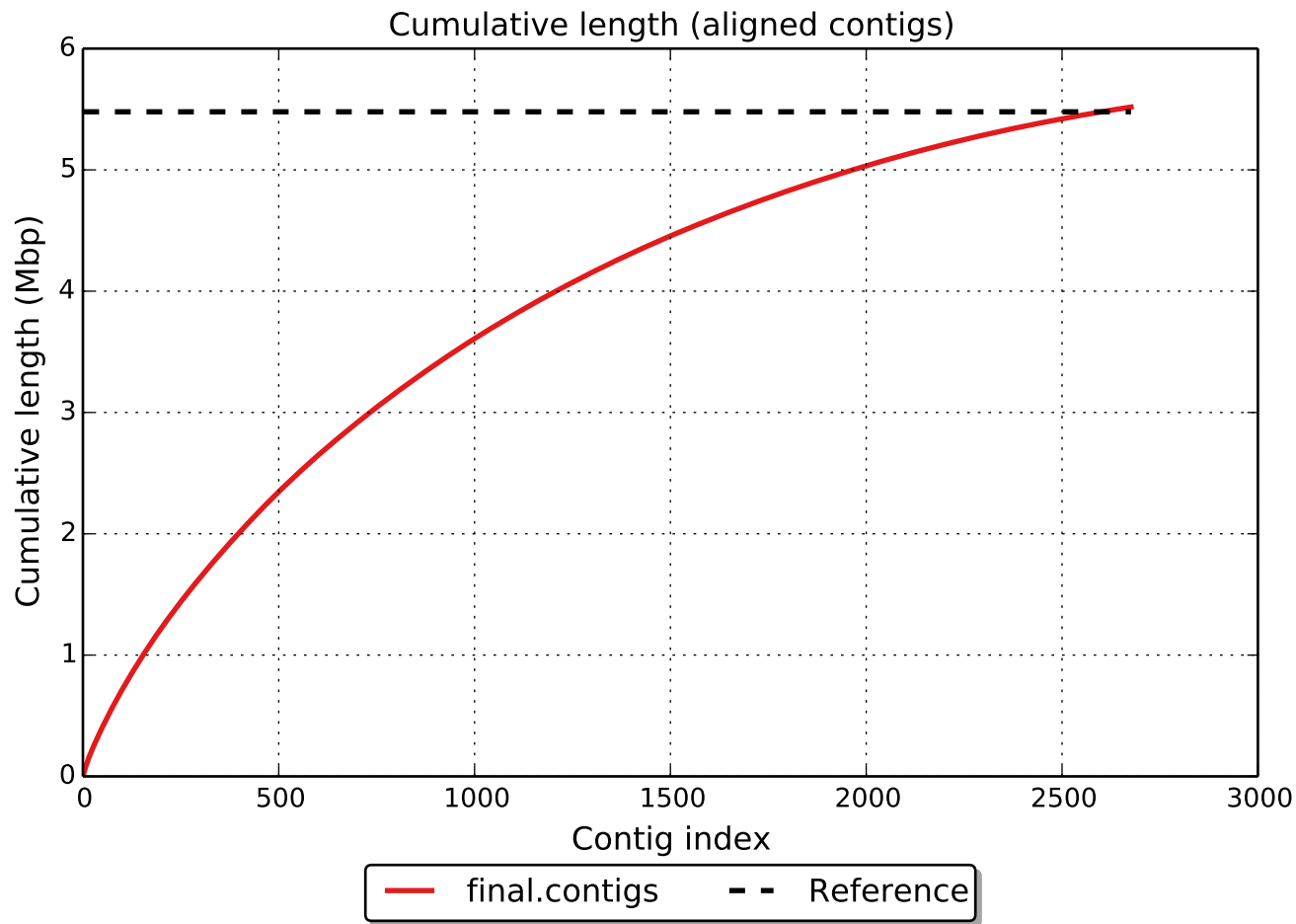


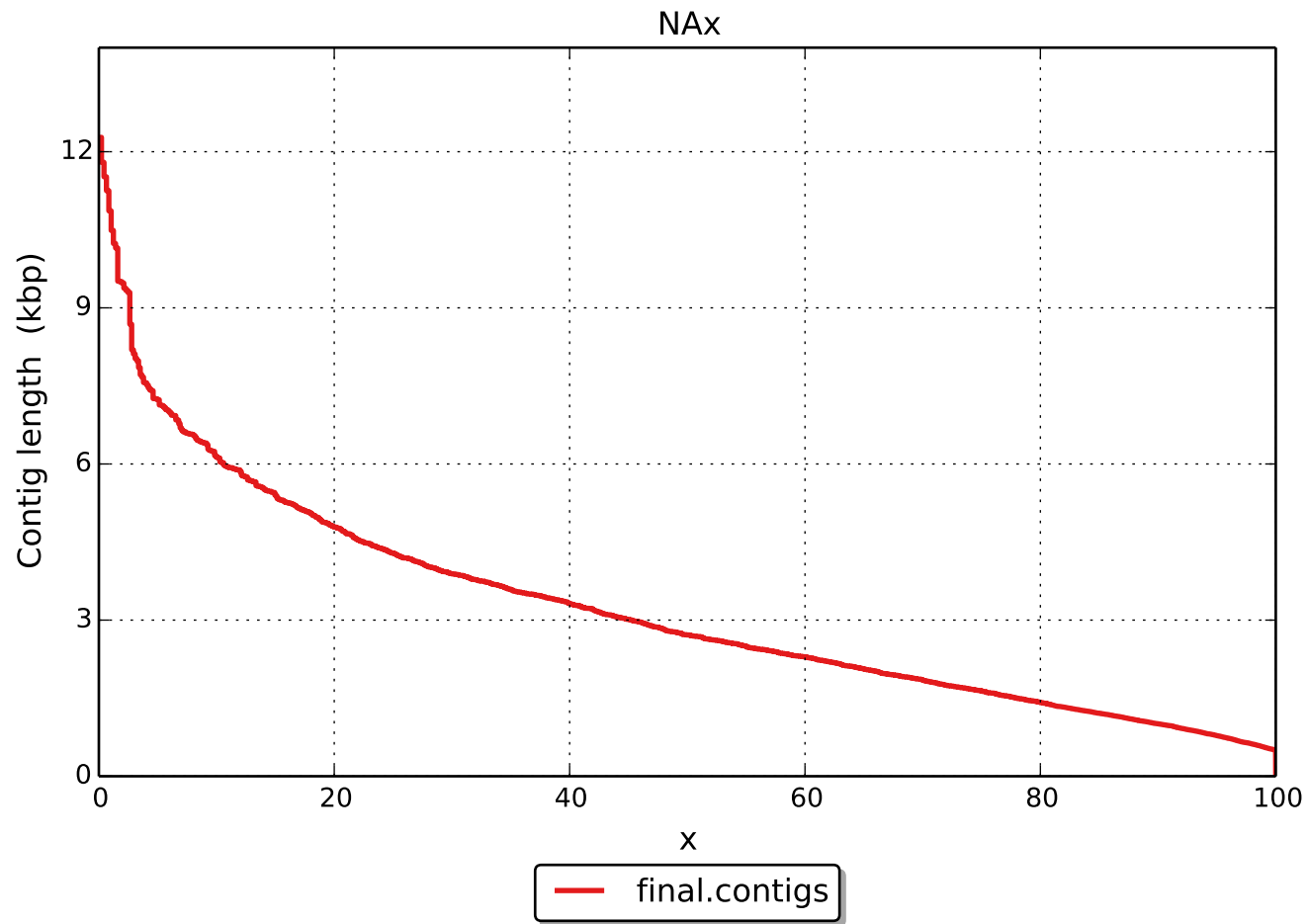


NGx









NGAx

