

Report

	final.contigs
# contigs (≥ 0 bp)	2662
# contigs (≥ 1000 bp)	1842
Total length (≥ 0 bp)	5134996
Total length (≥ 1000 bp)	4534879
# contigs	2662
Largest contig	12599
Total length	5134996
Reference length	5547323
GC (%)	50.27
Reference GC (%)	50.48
N50	2539
NG50	2343
N75	1519
NG75	1276
L50	636
LG50	721
L75	1290
LG75	1512
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	1135
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	89.514
Duplication ratio	1.034
# N's per 100 kbp	0.00
# mismatches per 100 kbp	32.83
# indels per 100 kbp	0.16
Largest alignment	12599
NA50	2539
NGA50	2343
NA75	1519
NGA75	1276
LA50	636
LGA50	721
LA75	1290
LGA75	1512

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

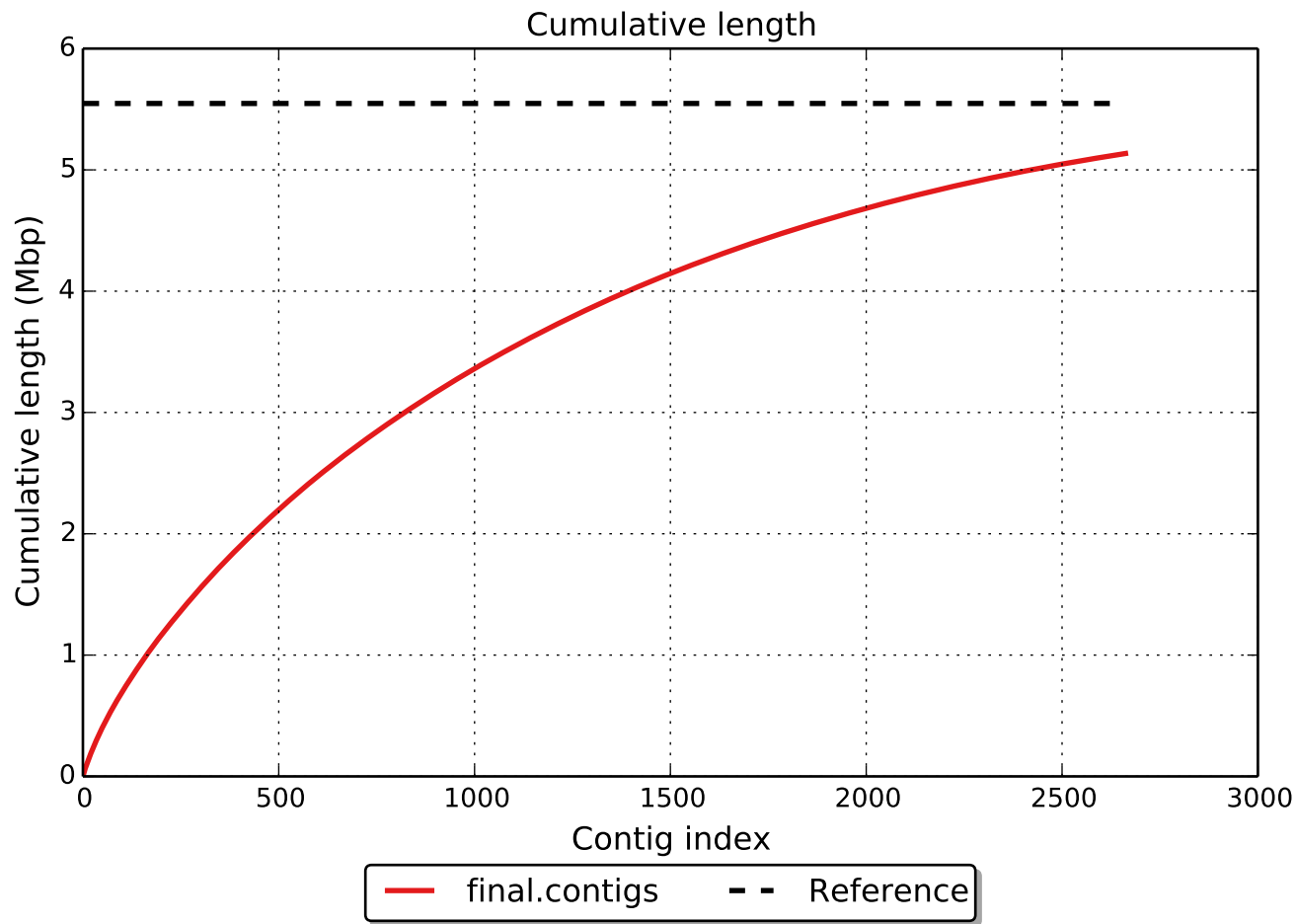
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	1135
# local misassemblies	0
# mismatches	1630
# indels	8
# short indels	6
# long indels	2
Indels length	33

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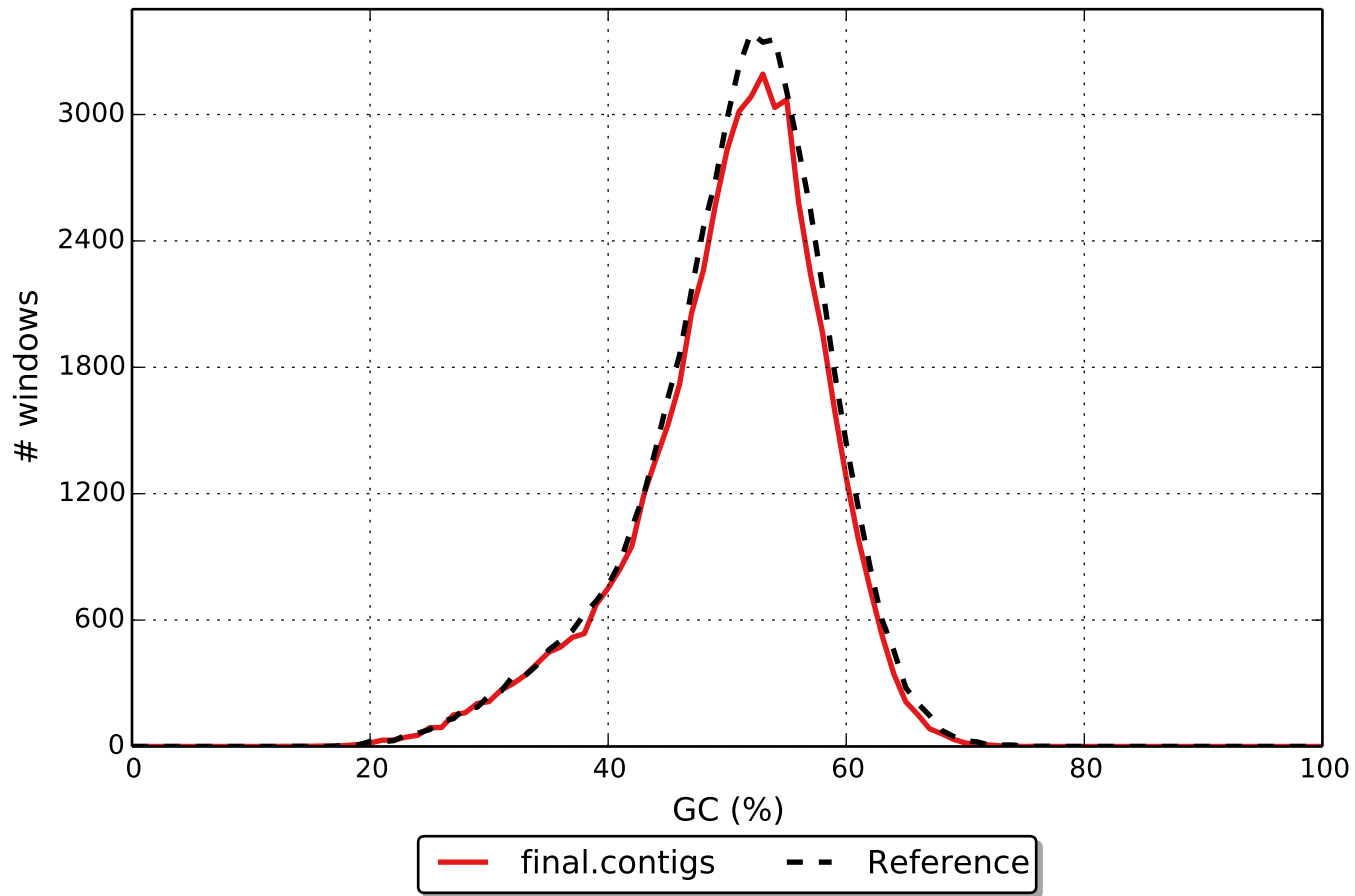
Unaligned report

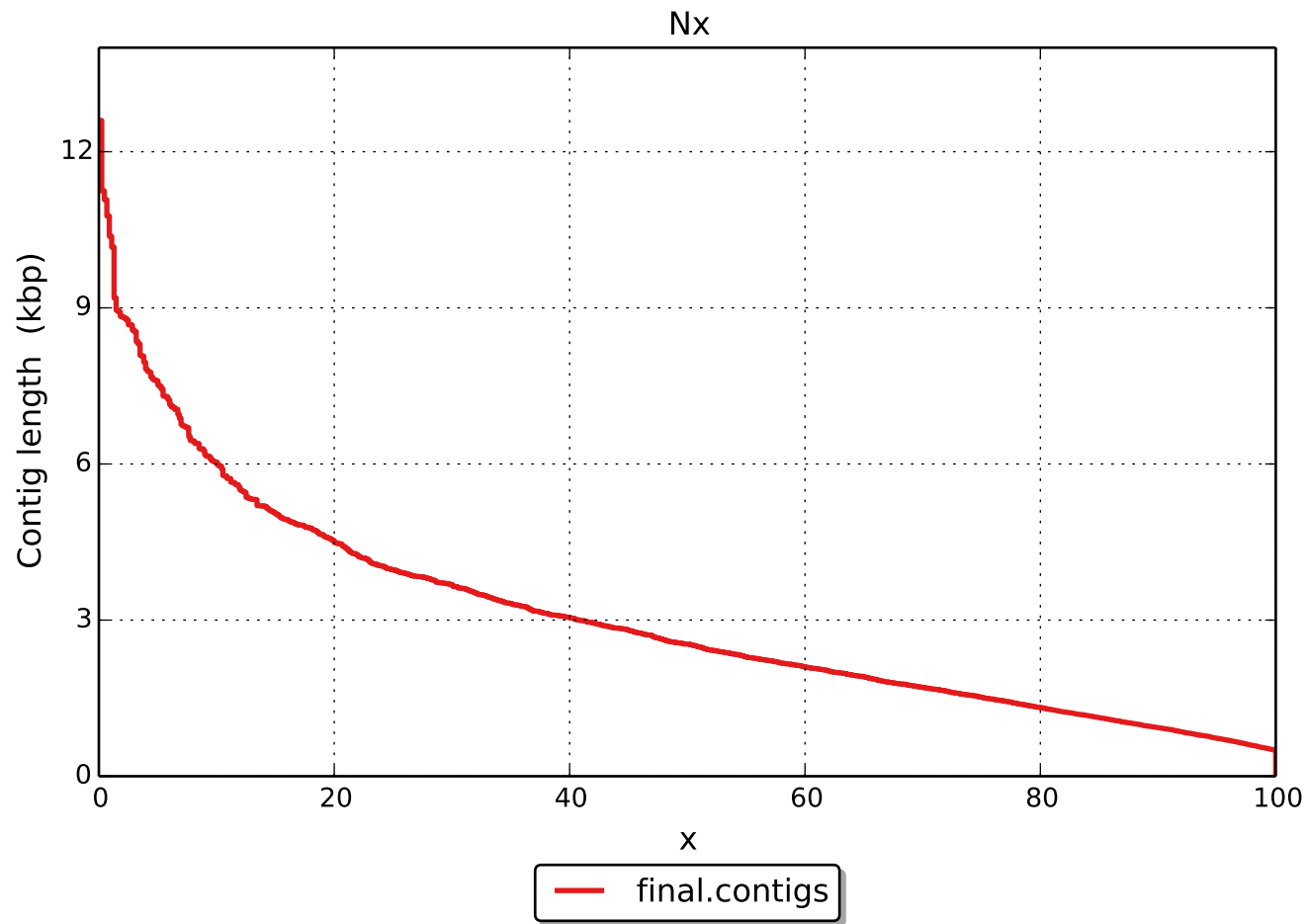
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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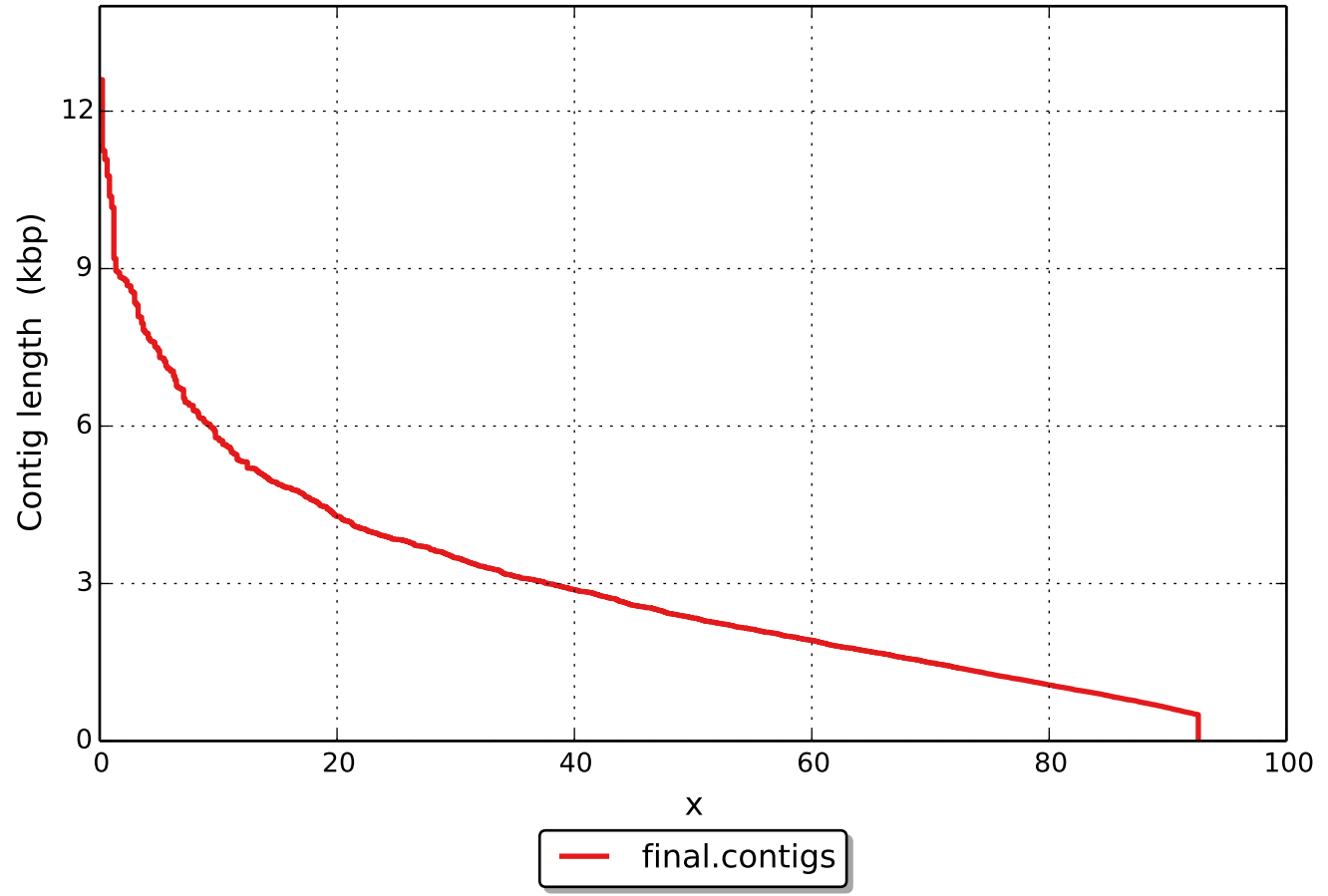


GC content

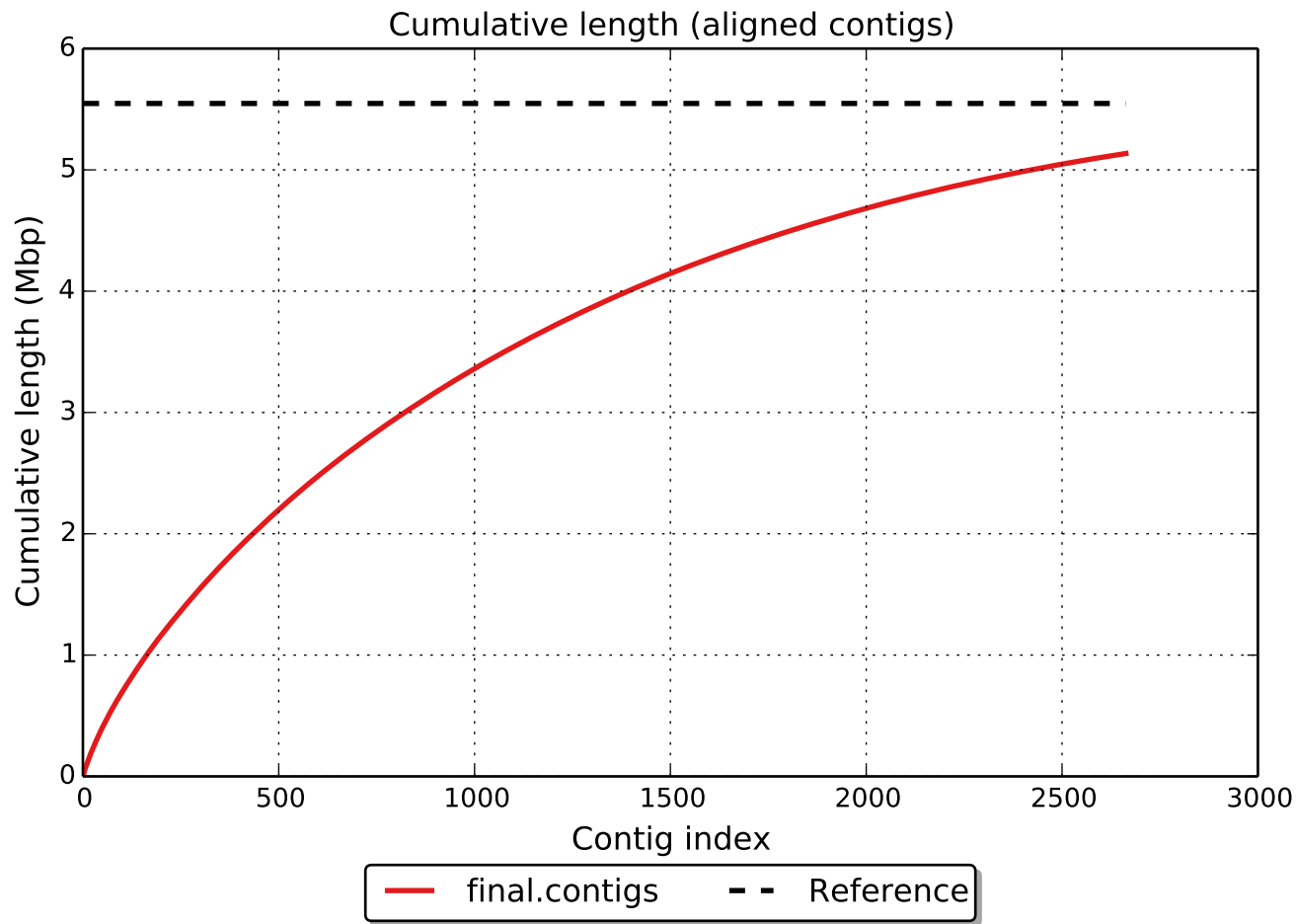


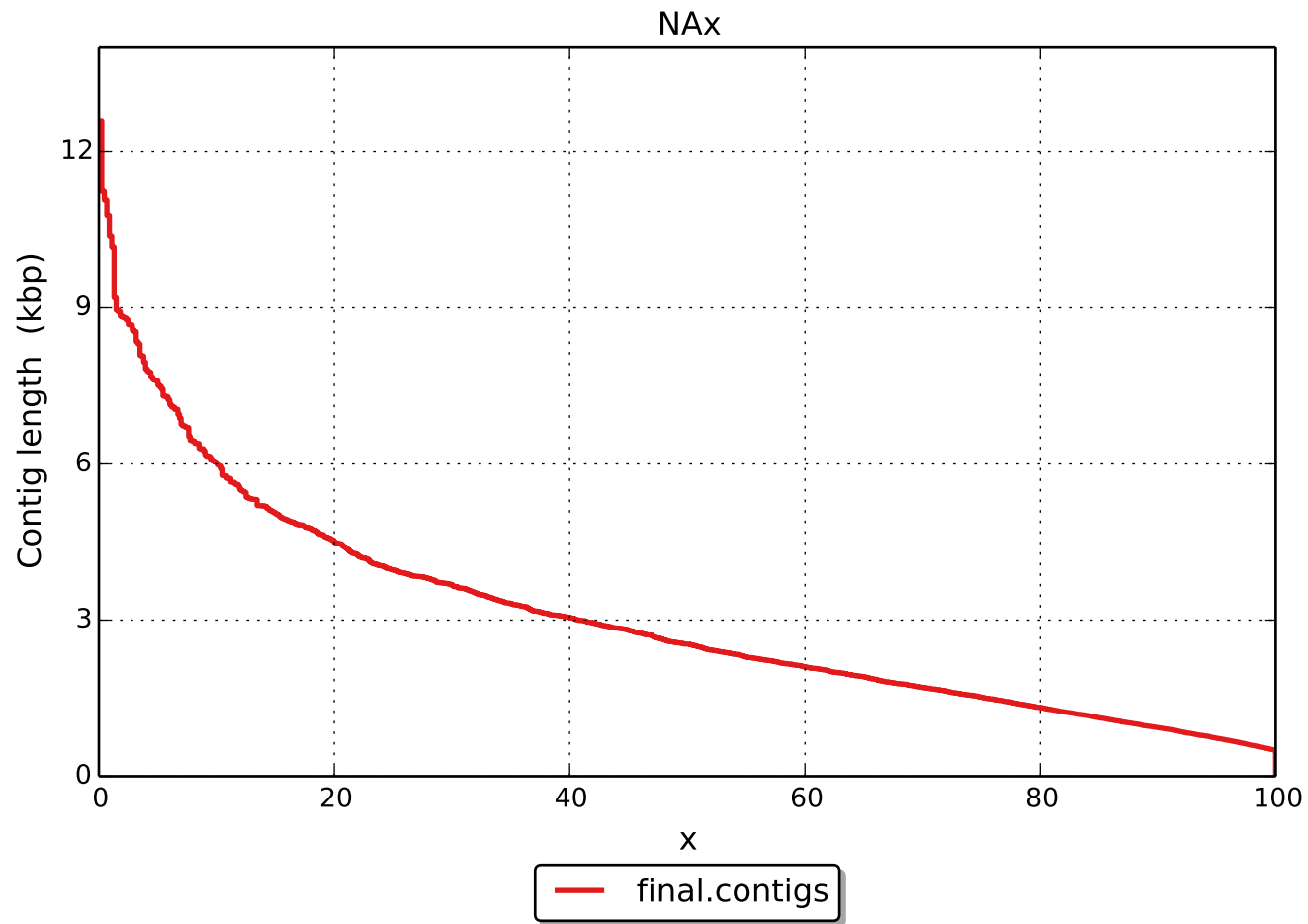


NGx









NGAx

