

Report

	final.contigs
# contigs (≥ 0 bp)	1253
# contigs (≥ 1000 bp)	1110
Total length (≥ 0 bp)	5565654
Total length (≥ 1000 bp)	5460129
# contigs	1253
Largest contig	31841
Total length	5565654
Reference length	5478683
GC (%)	50.51
Reference GC (%)	50.50
N50	6618
NG50	6713
N75	3855
NG75	3963
L50	265
LG50	259
L75	540
LG75	524
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	29757
# local misassemblies	0
# unaligned contigs	0 + 1 part
Unaligned length	13
Genome fraction (%)	99.277
Duplication ratio	1.023
# N's per 100 kbp	0.00
# mismatches per 100 kbp	29.14
# indels per 100 kbp	0.00
Largest alignment	31841
NA50	6614
NGA50	6713
NA75	3847
NGA75	3961
LA50	266
LGA50	259
LA75	542
LGA75	525

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

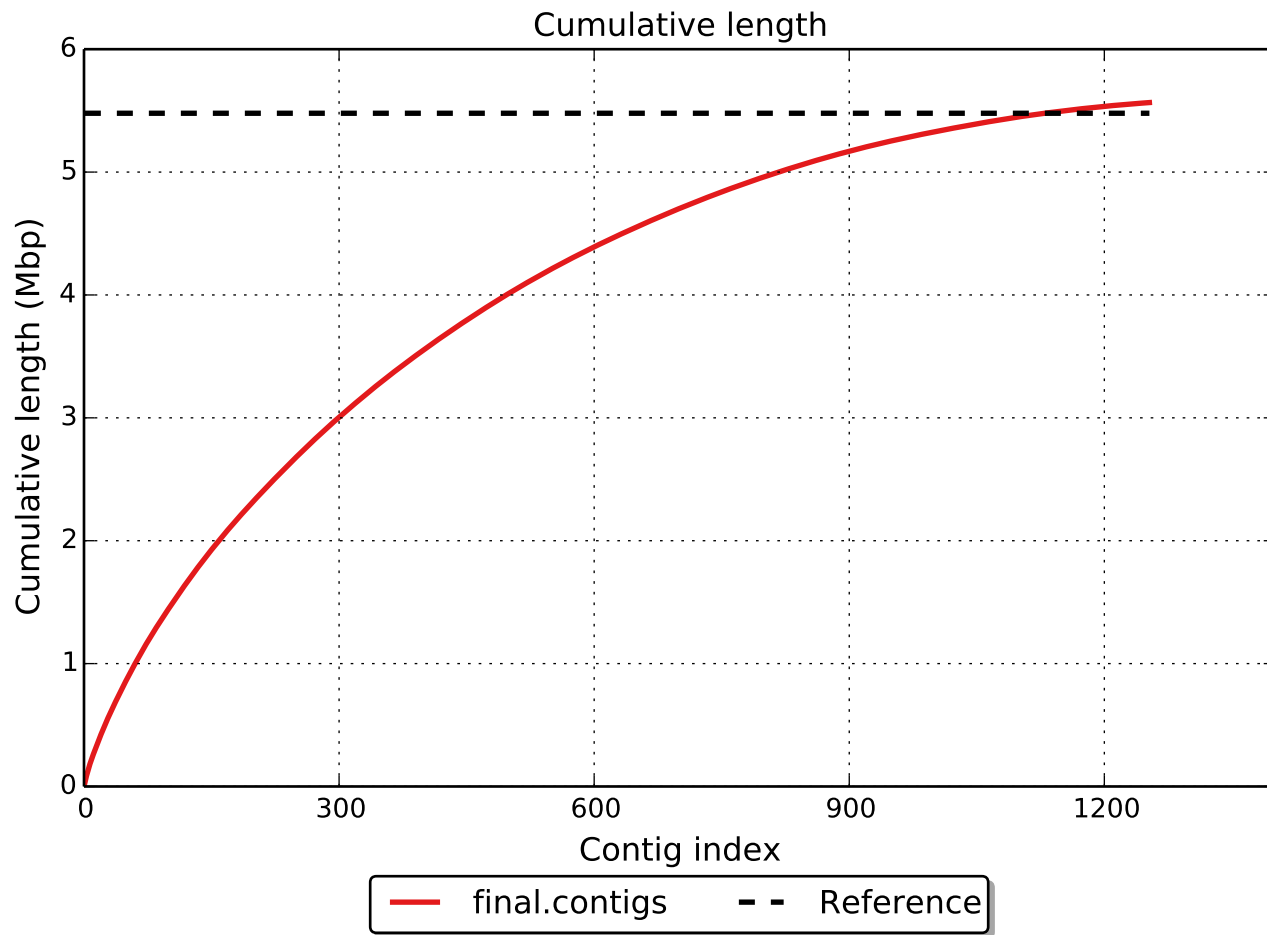
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	1
# misassembled contigs	1
Misassembled contigs length	29757
# local misassemblies	0
# mismatches	1585
# indels	0
# short indels	0
# long indels	0
Indels length	0

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).

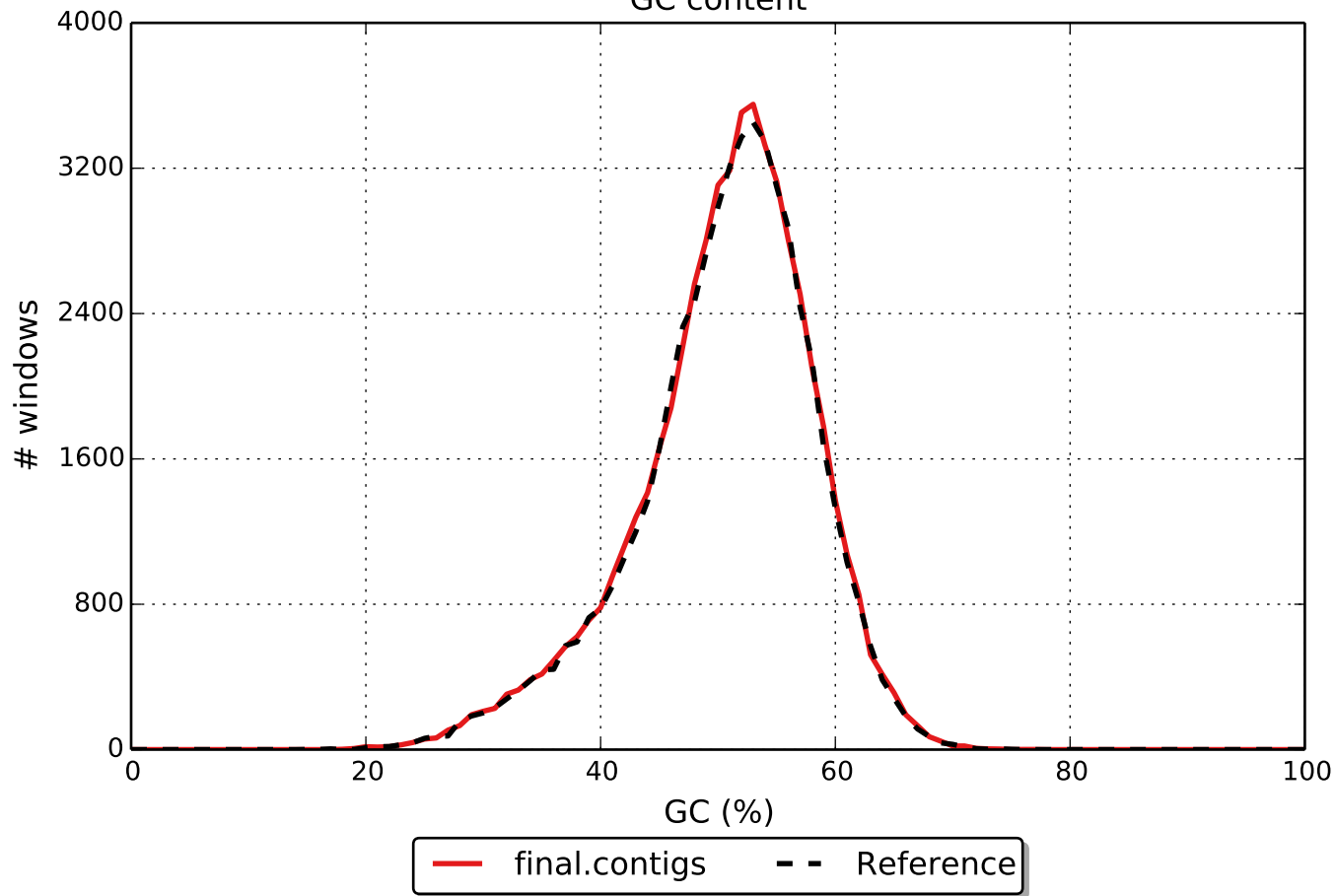
Unaligned report

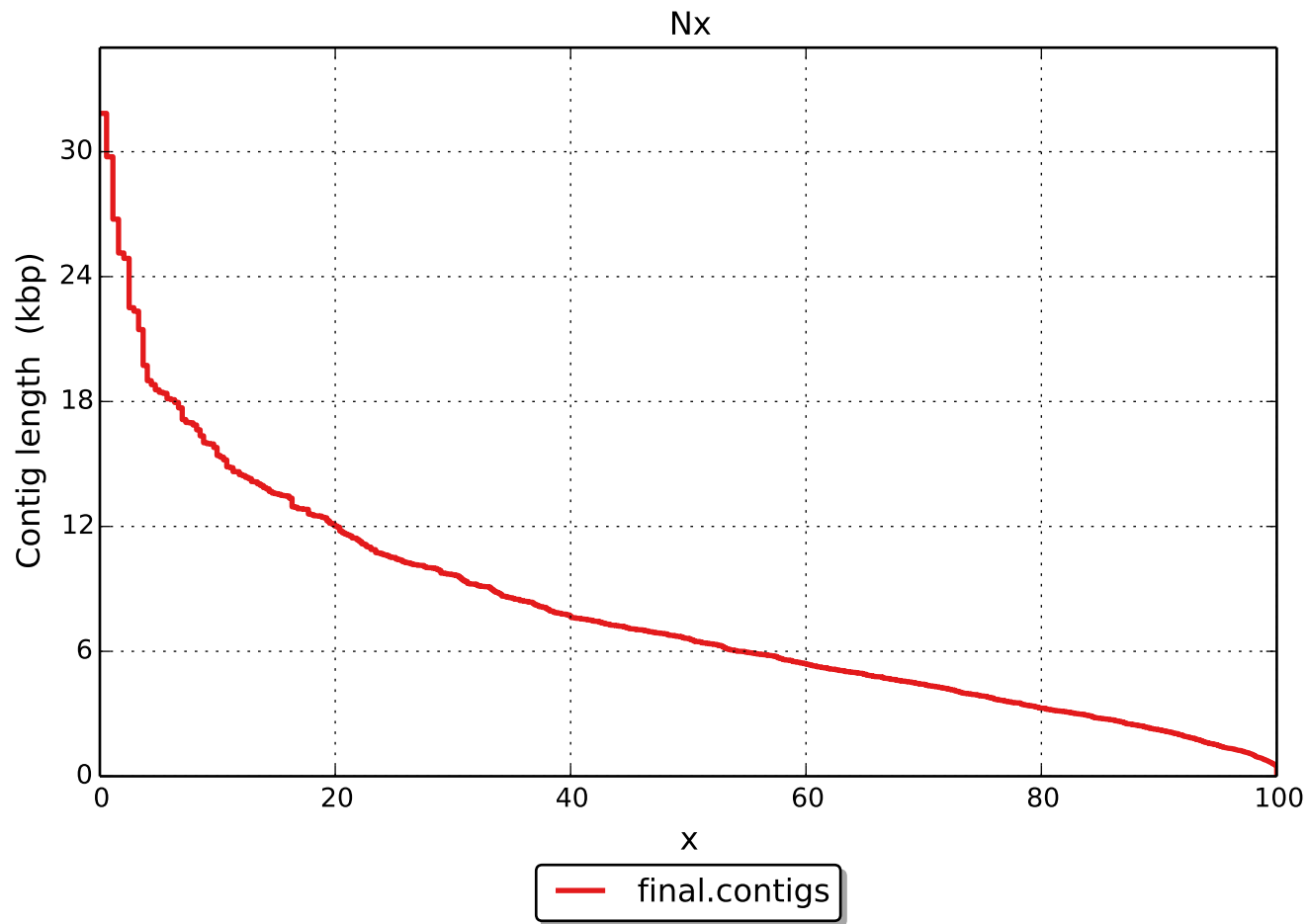
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	13
# N's	0

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).

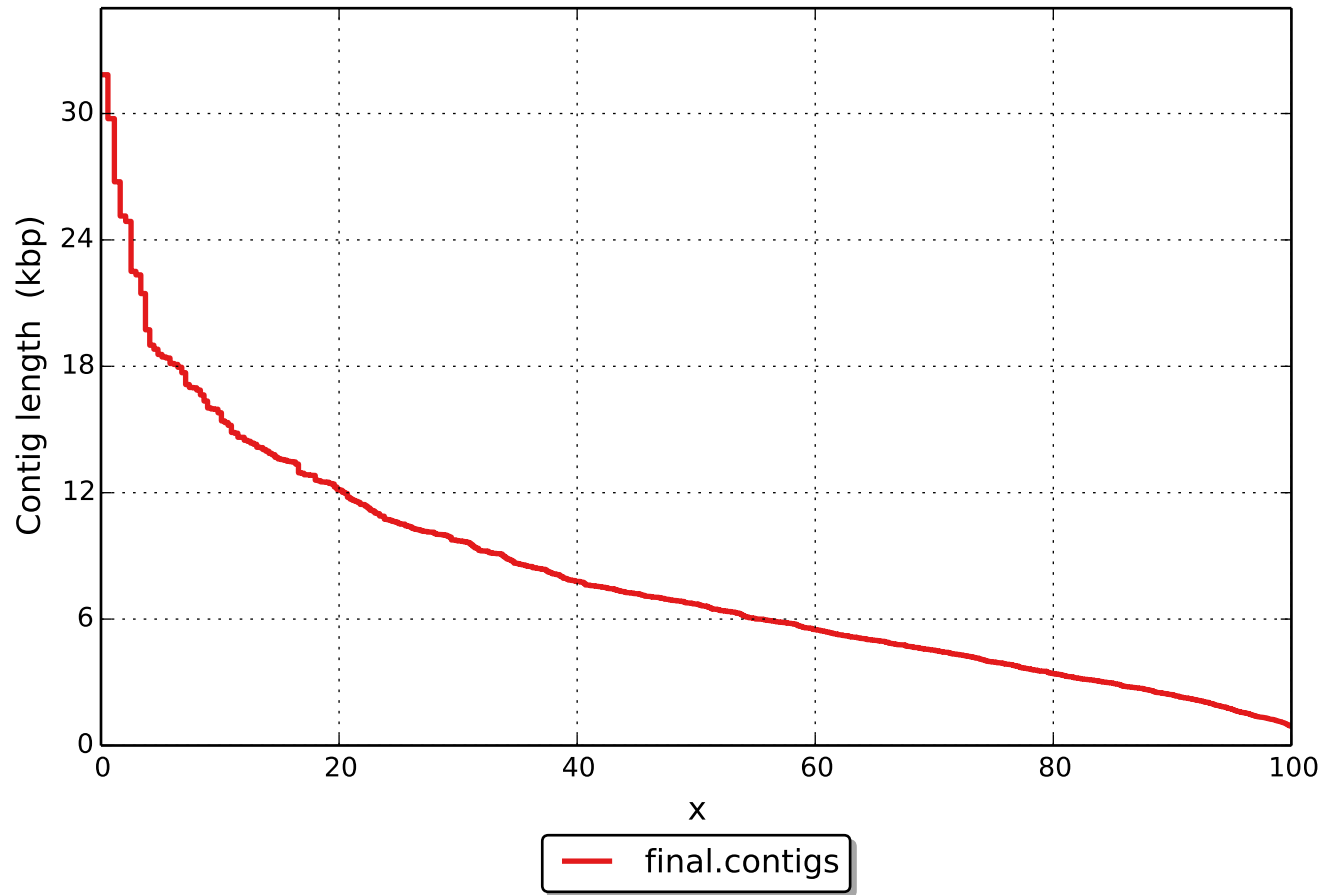


GC content

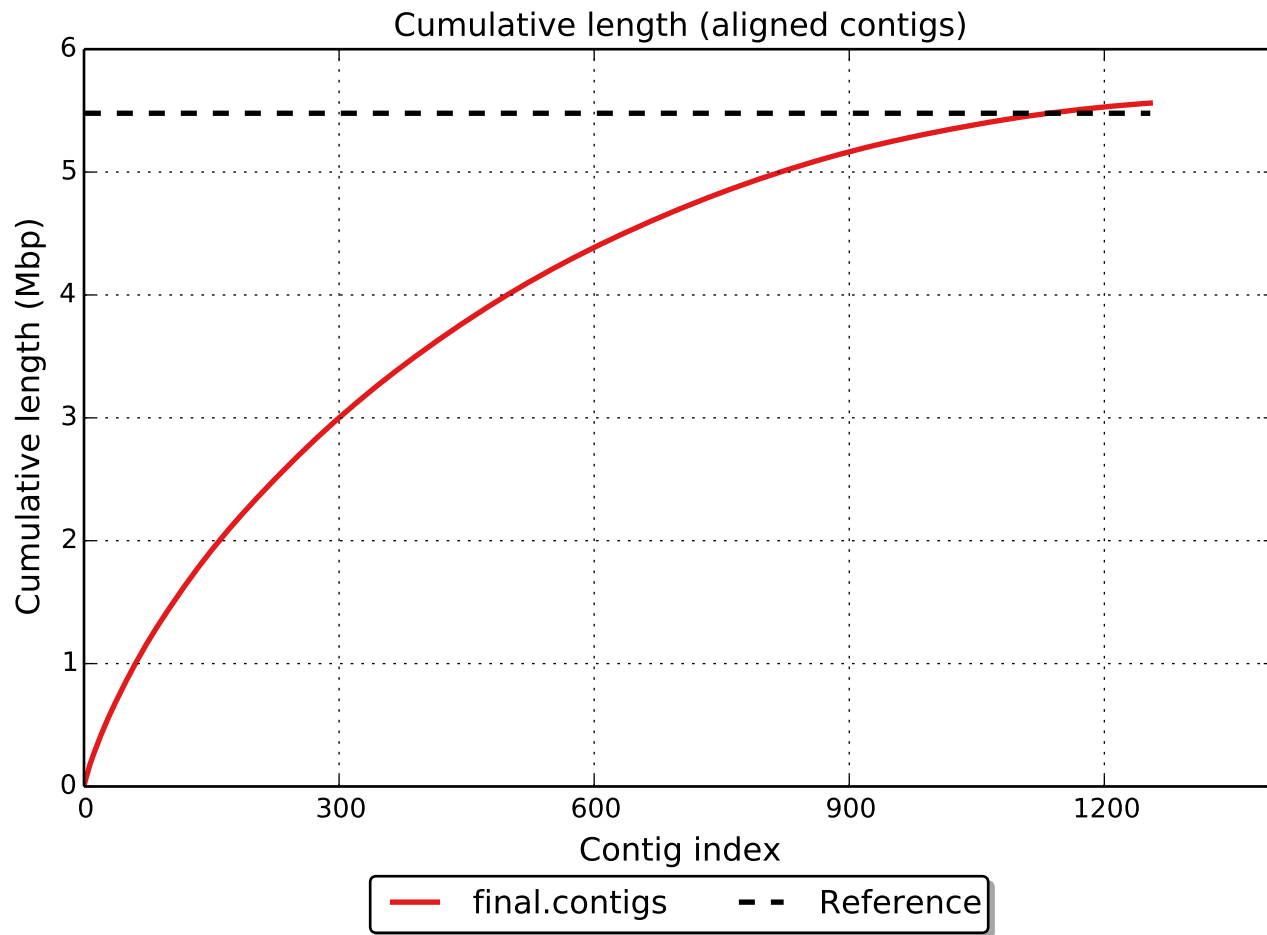




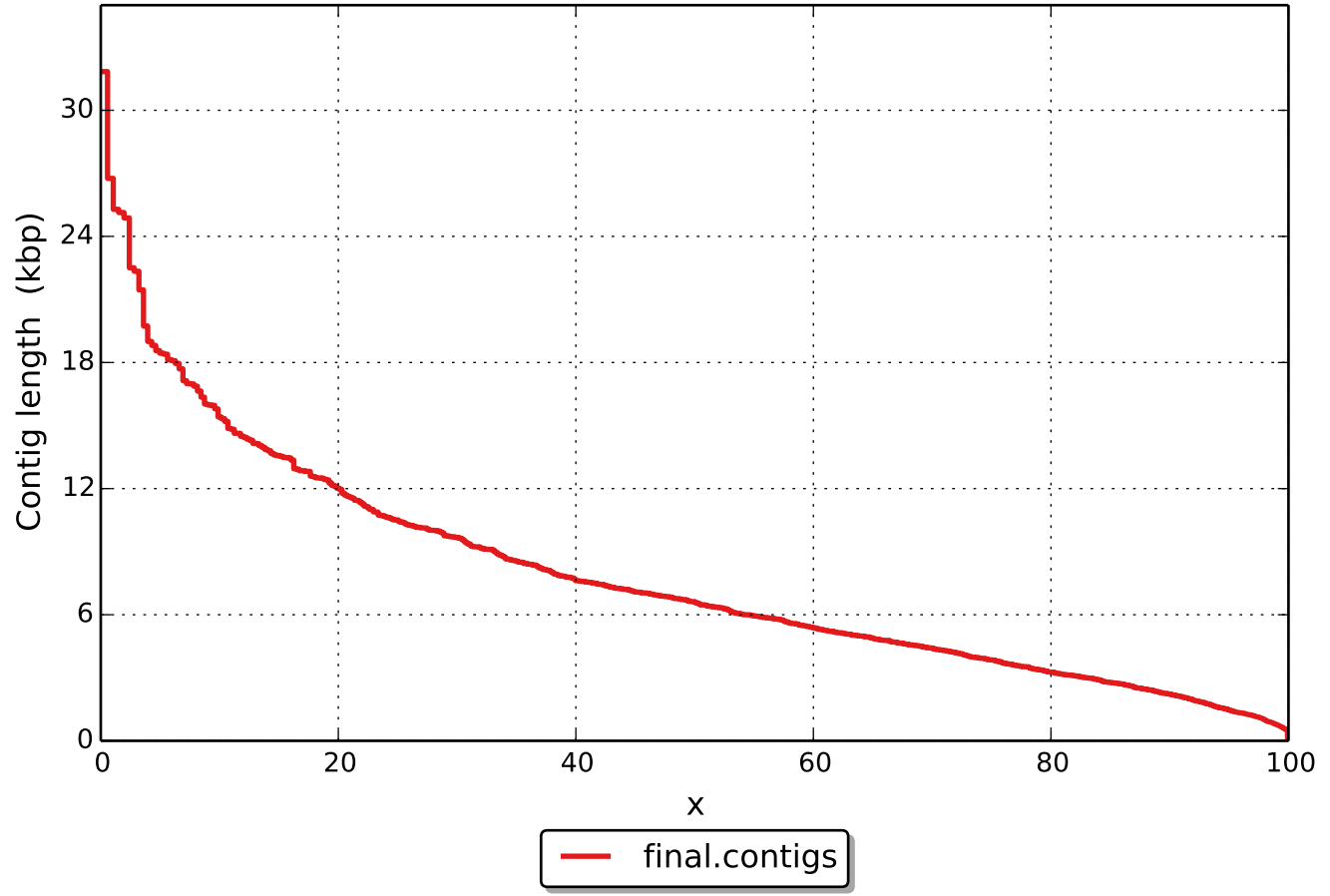
NGx







NAx



NGAx

