

Report

	final.contigs
# contigs (≥ 0 bp)	1251
# contigs (≥ 1000 bp)	1109
Total length (≥ 0 bp)	5555729
Total length (≥ 1000 bp)	5451026
# contigs	1251
Largest contig	31841
Total length	5555729
Reference length	5478683
GC (%)	50.51
Reference GC (%)	50.50
N50	6614
NG50	6710
N75	3852
NG75	3946
L50	265
LG50	259
L75	540
LG75	525
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	29757
# local misassemblies	0
# unaligned contigs	0 + 1 part
Unaligned length	13
Genome fraction (%)	99.187
Duplication ratio	1.022
# N's per 100 kbp	0.00
# mismatches per 100 kbp	23.78
# indels per 100 kbp	0.00
Largest alignment	31841
NA50	6572
NGA50	6676
NA75	3847
NGA75	3944
LA50	266
LGA50	260
LA75	541
LGA75	526

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

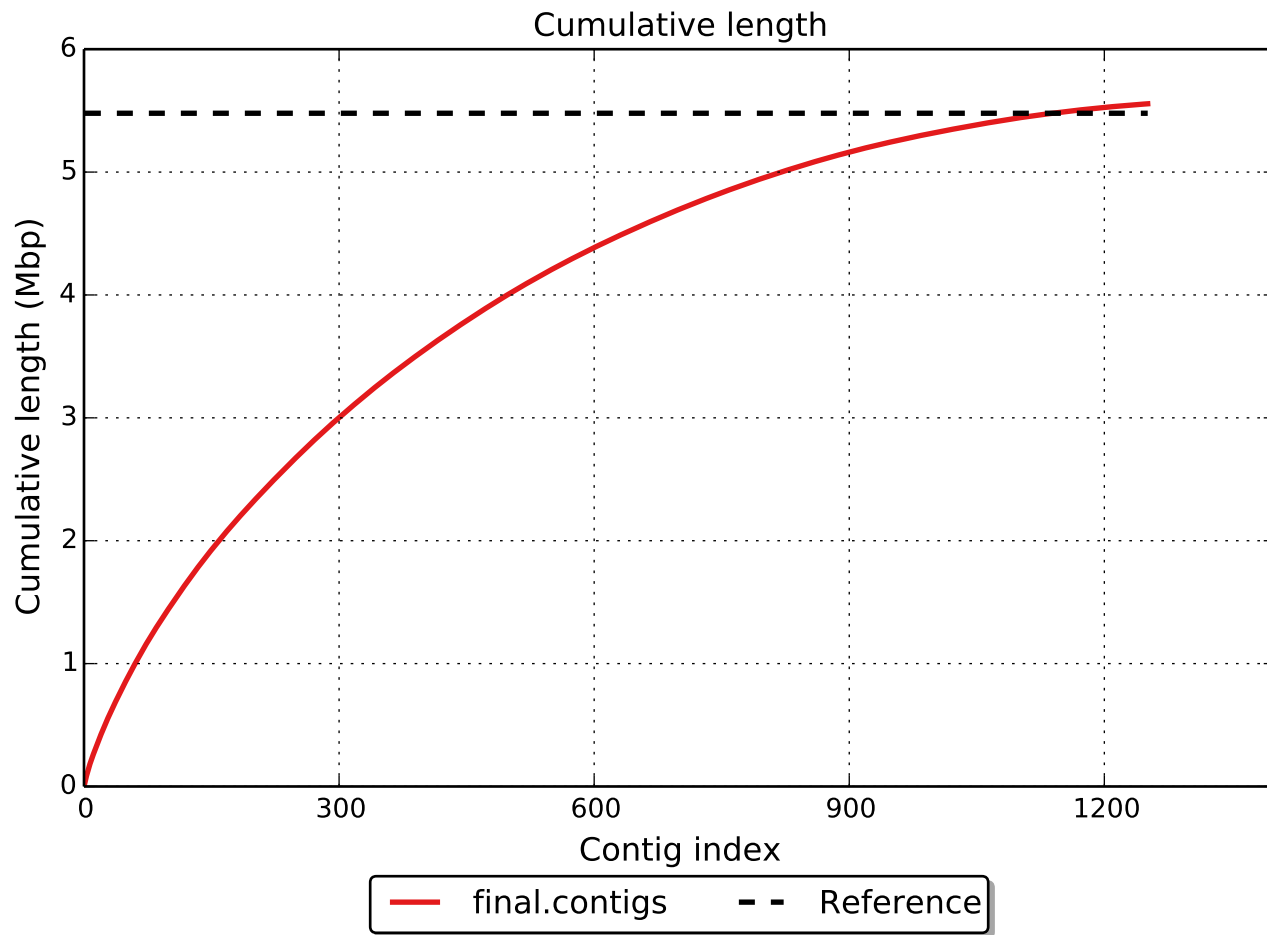
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	1
# misassembled contigs	1
Misassembled contigs length	29757
# local misassemblies	0
# mismatches	1292
# indels	0
# short indels	0
# long indels	0
Indels length	0

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).

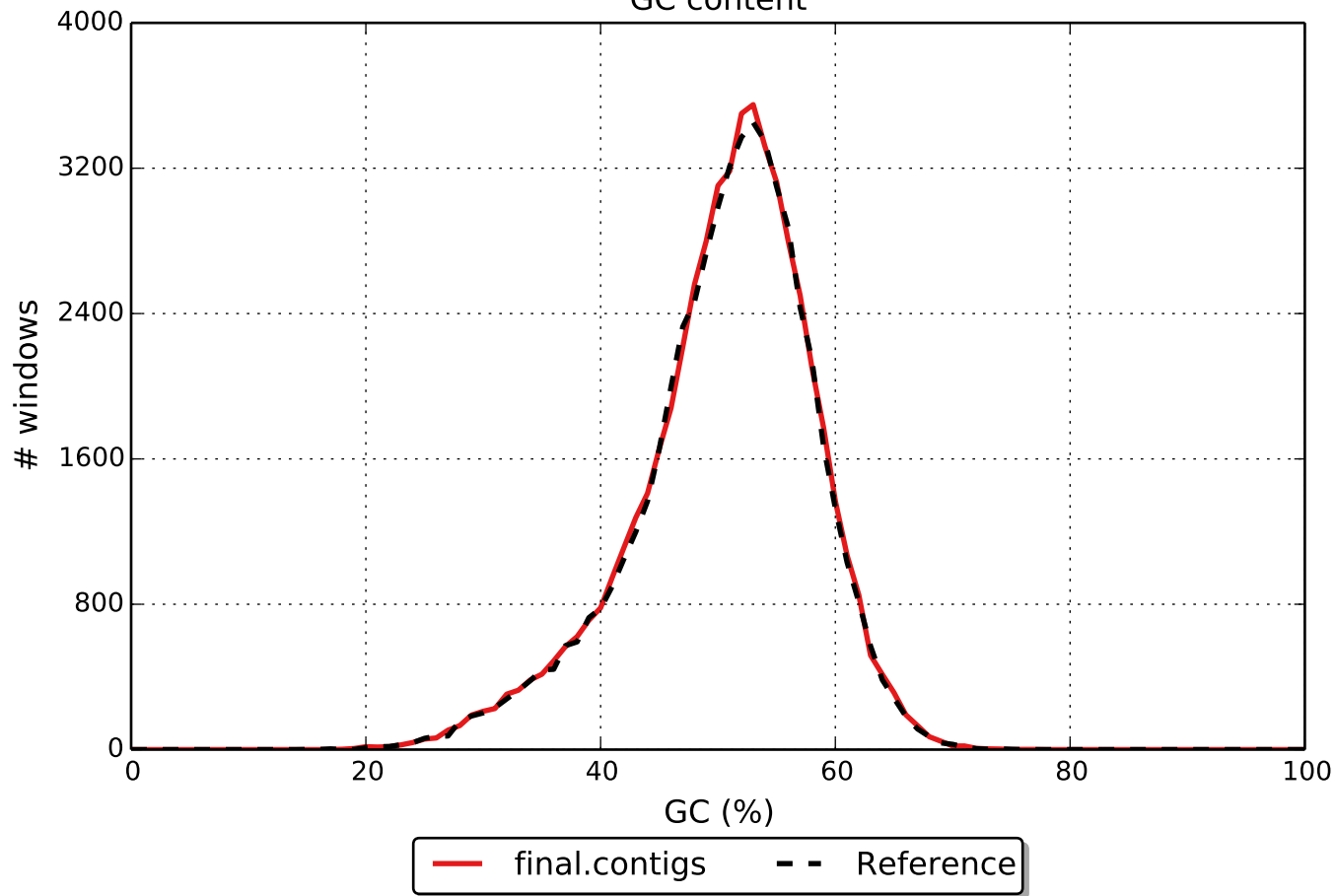
Unaligned report

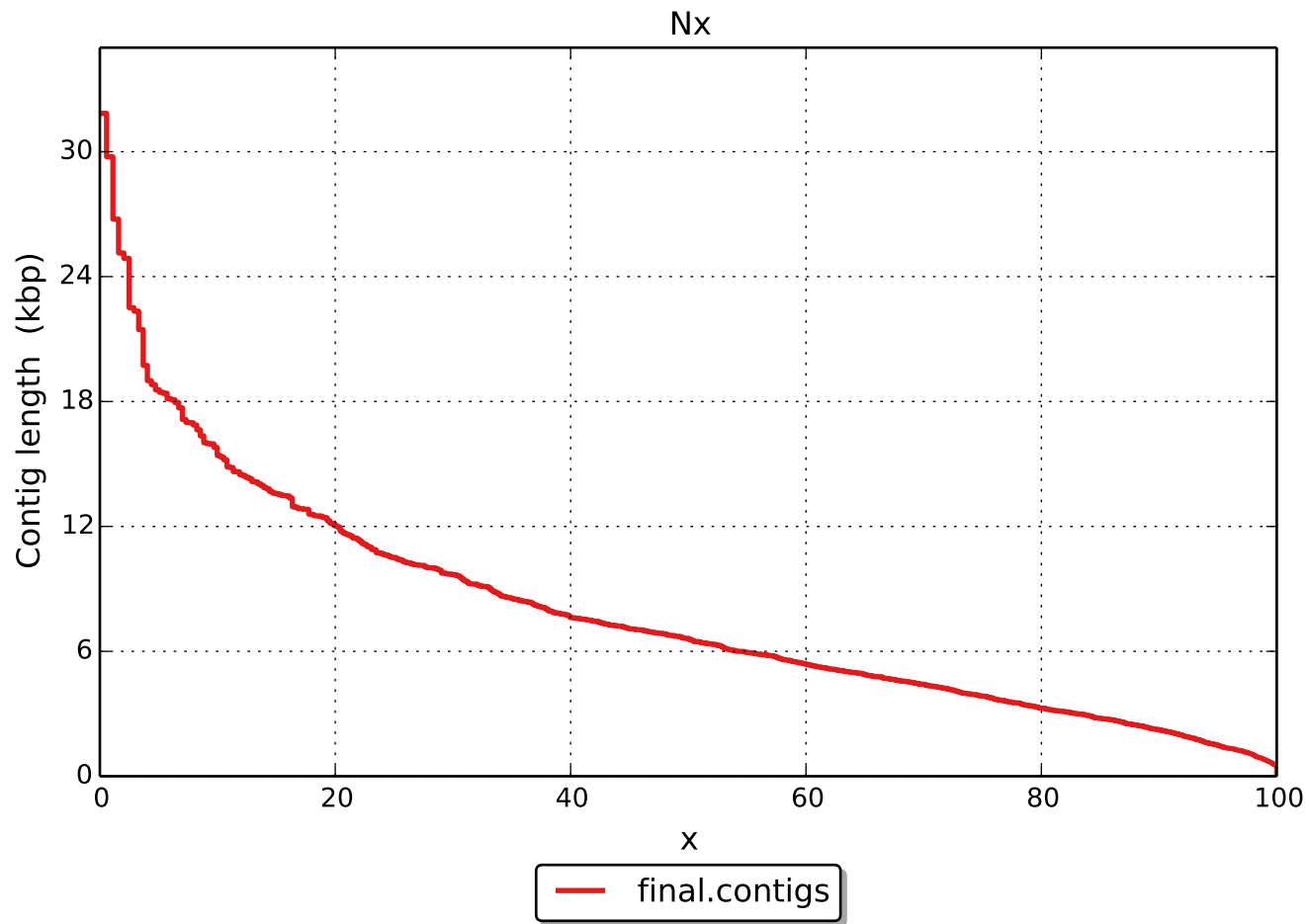
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	13
# N's	0

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).

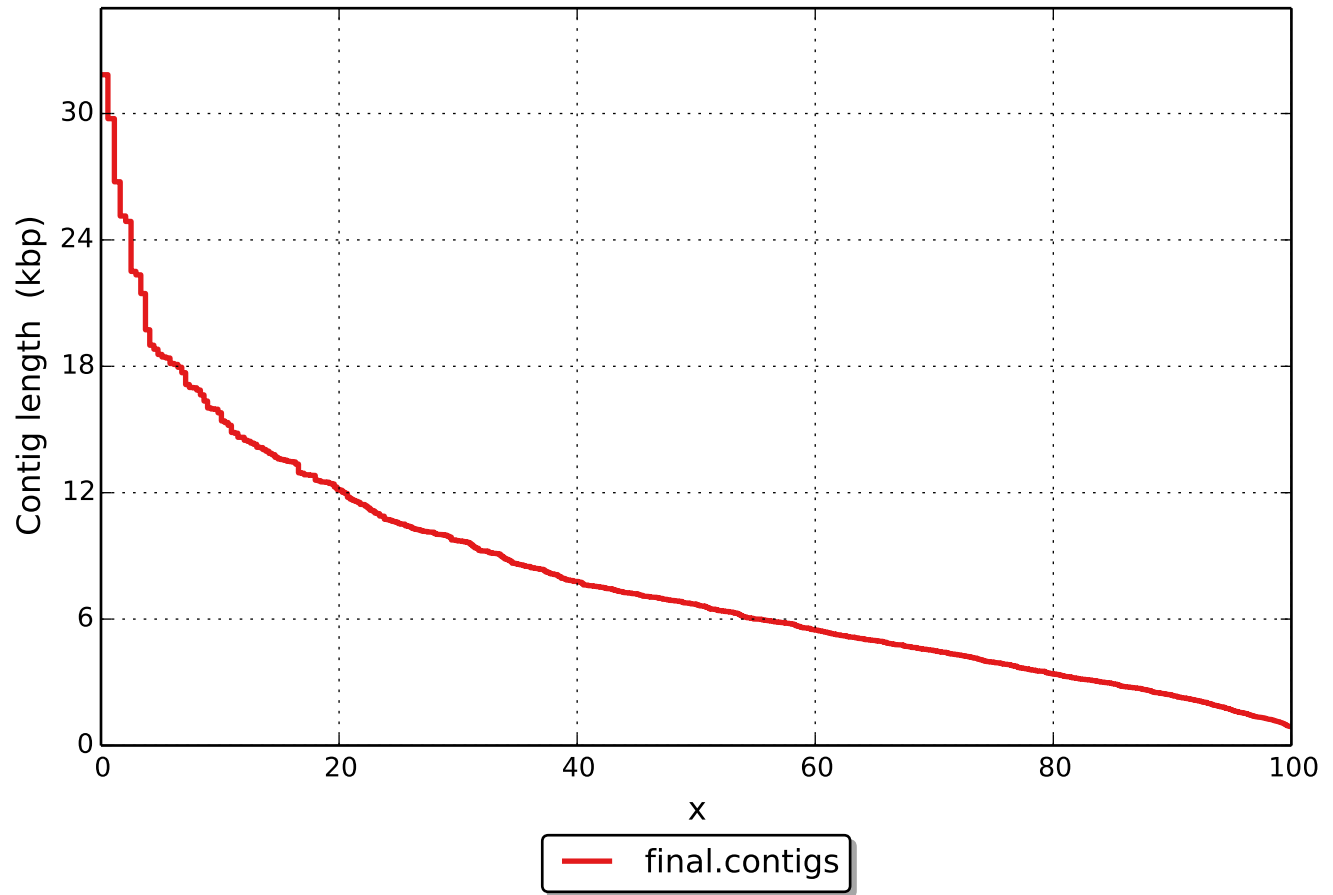


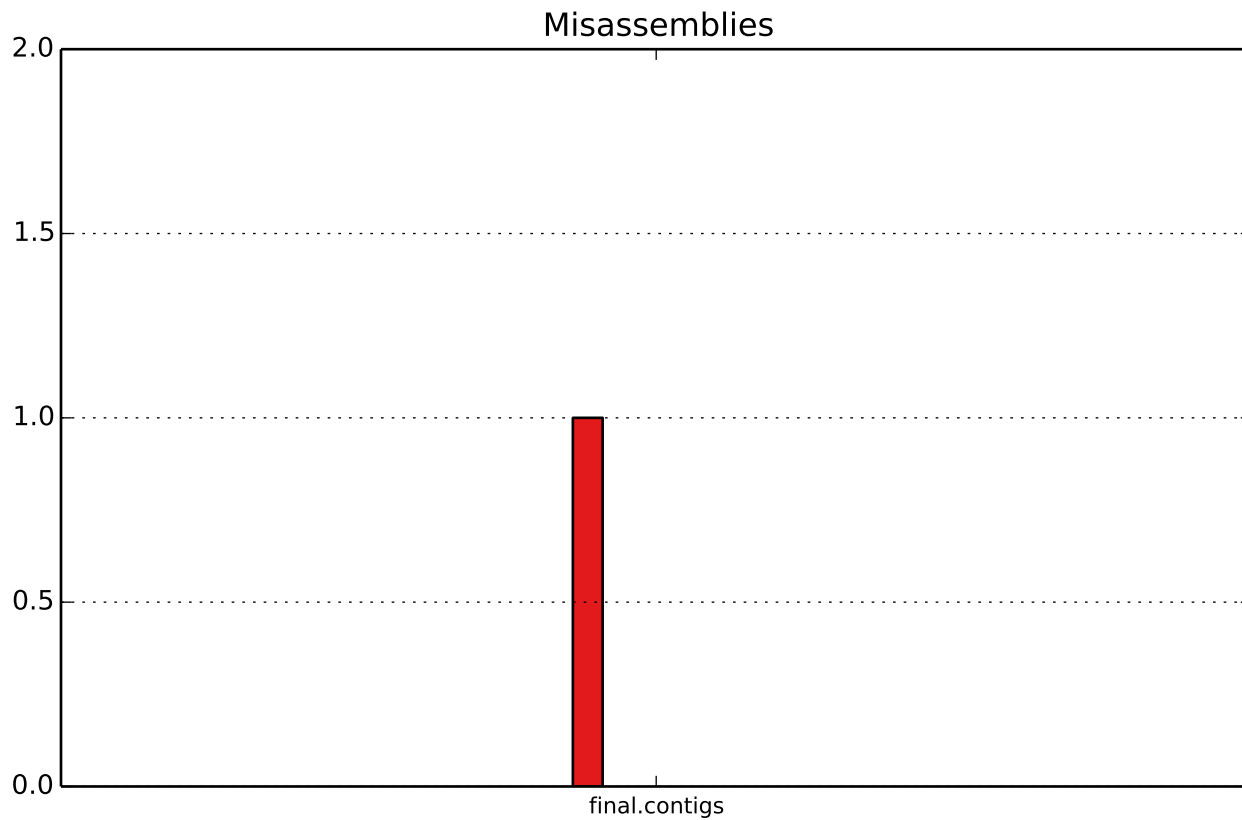
GC content

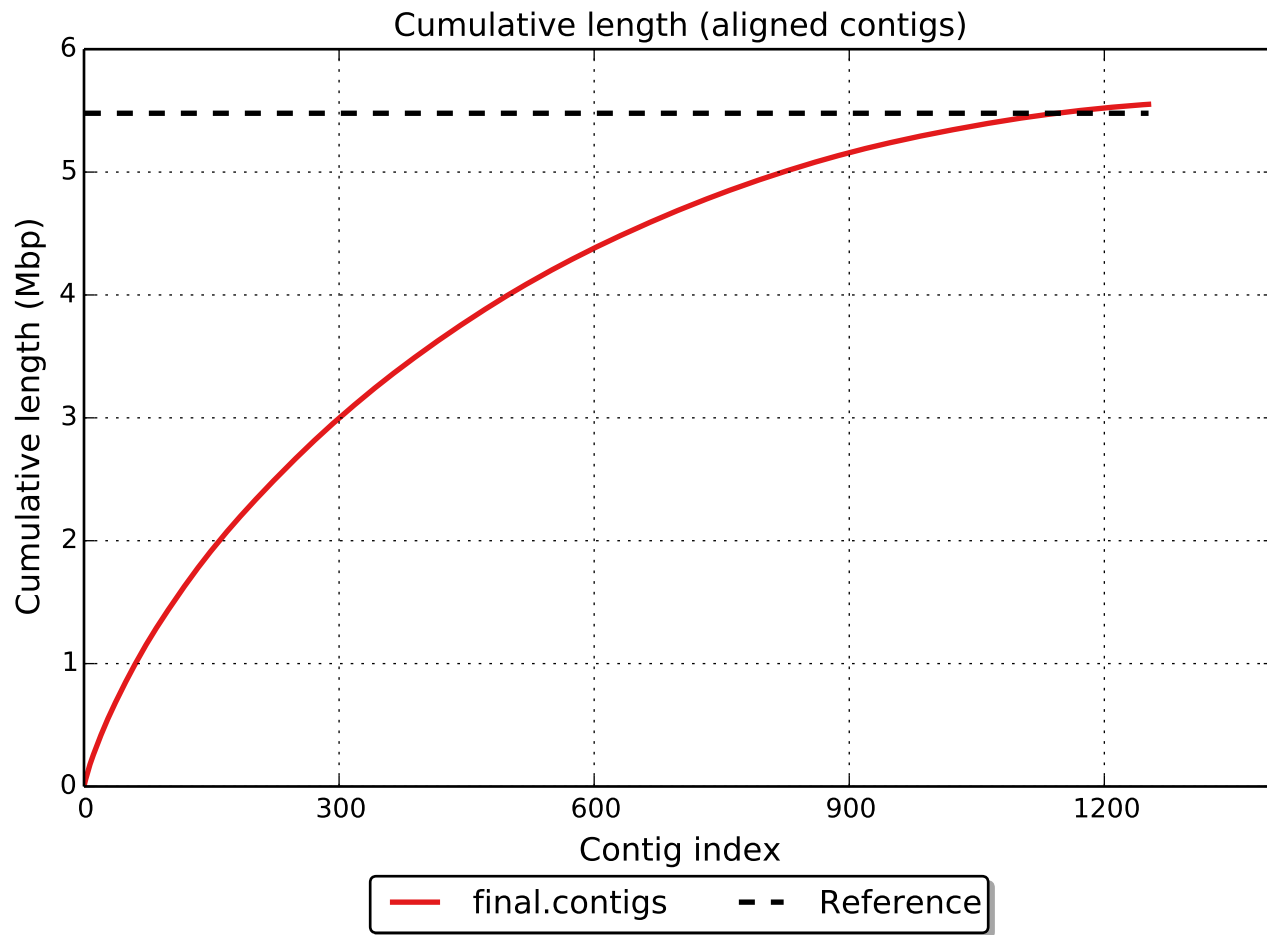




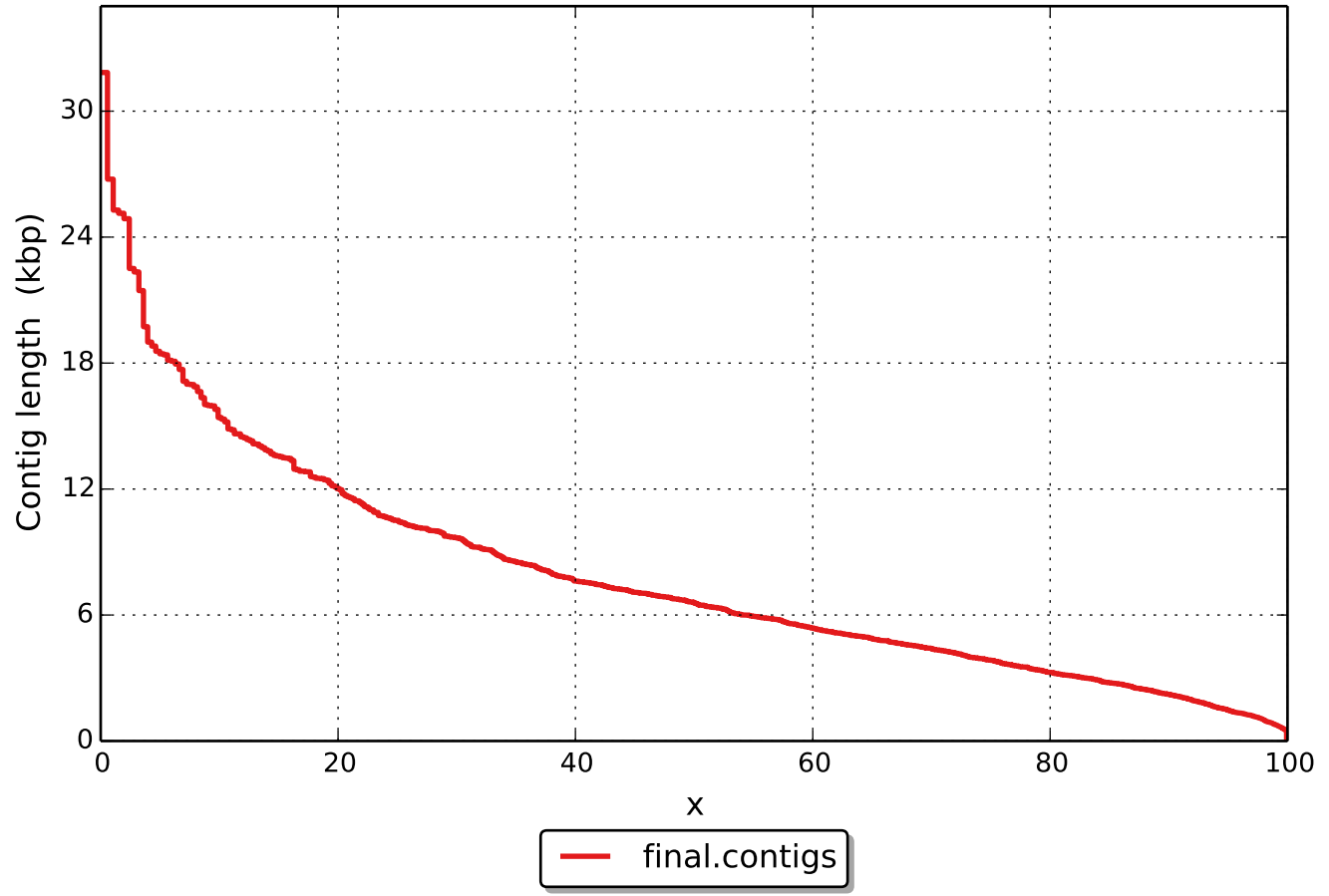
NGx







NAx



NGAx

