

Report

	final.contigs
# contigs (≥ 0 bp)	4228
# contigs (≥ 1000 bp)	1798
Total length (≥ 0 bp)	4695699
Total length (≥ 1000 bp)	2946430
# contigs	4228
Largest contig	6941
Total length	4695699
Reference length	5478683
GC (%)	50.30
Reference GC (%)	50.49
N50	1236
NG50	1073
N75	834
NG75	670
L50	1259
LG50	1599
L75	2429
LG75	3216
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	81.998
Duplication ratio	1.045
# N's per 100 kbp	0.00
# mismatches per 100 kbp	55.87
# indels per 100 kbp	0.13
Largest alignment	6941
NA50	1236
NGA50	1073
NA75	834
NGA75	670
LA50	1259
LGA50	1599
LA75	2429
LGA75	3217

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

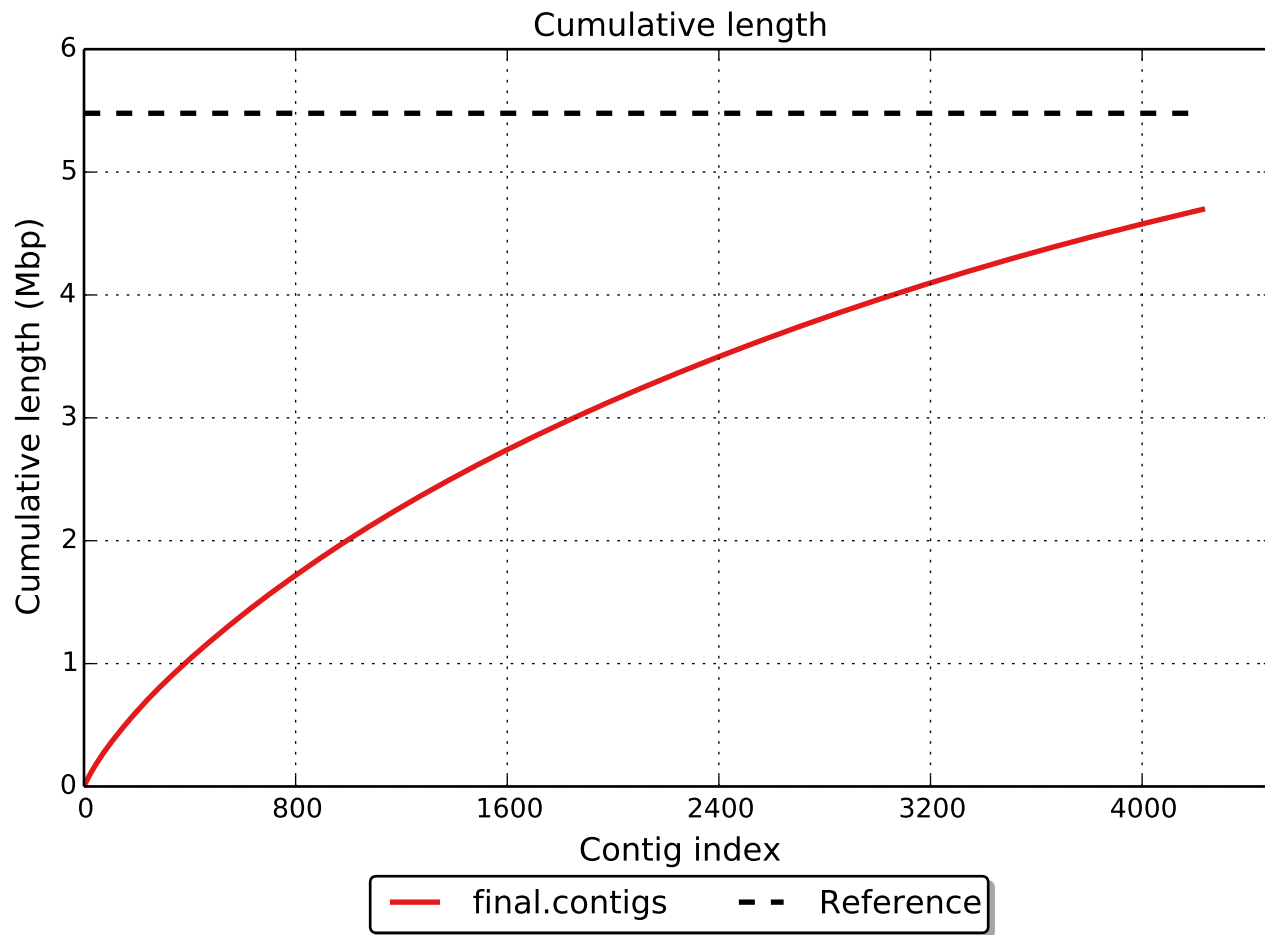
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	2510
# indels	6
# short indels	4
# long indels	2
Indels length	46

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).

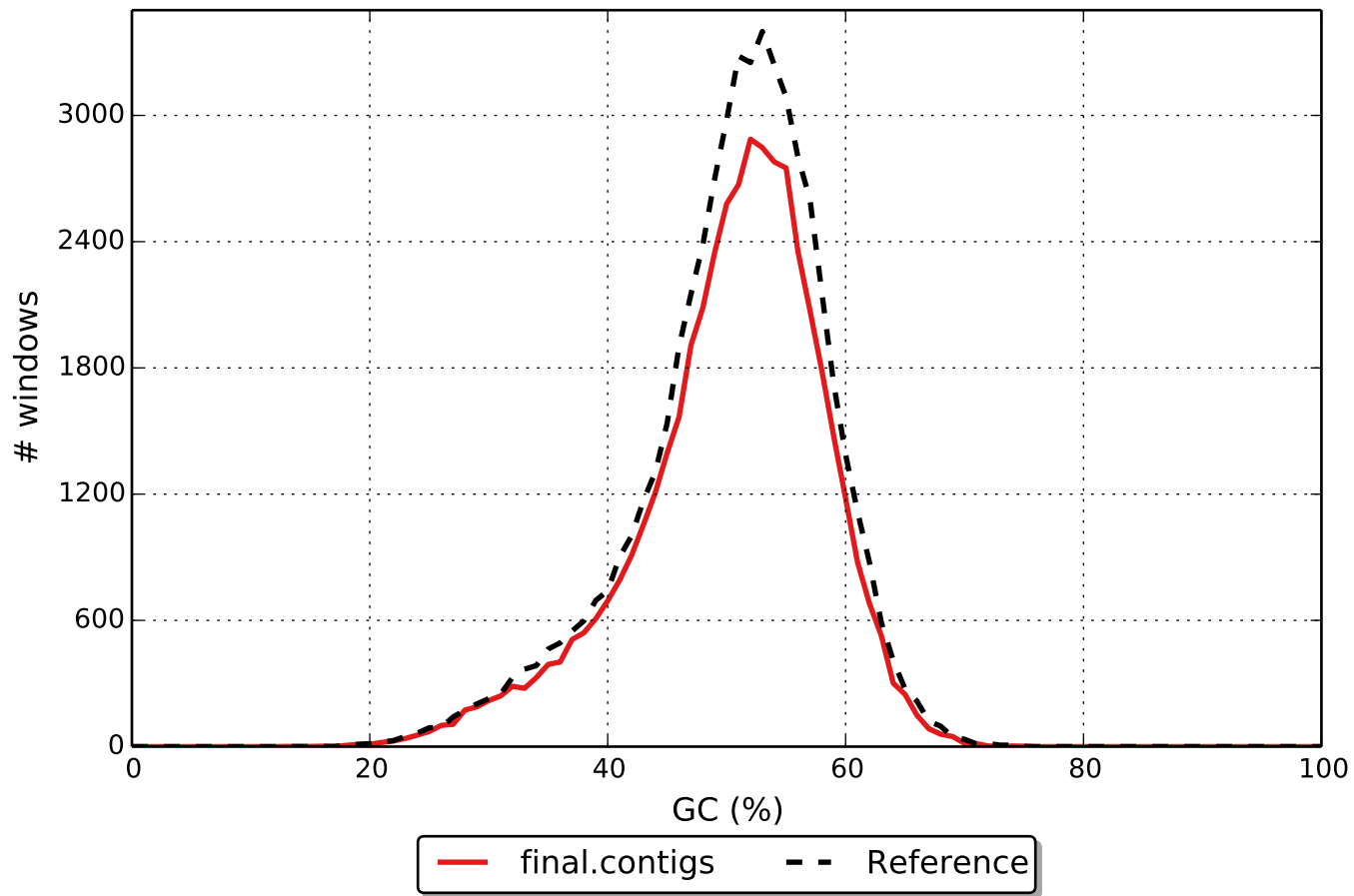
Unaligned report

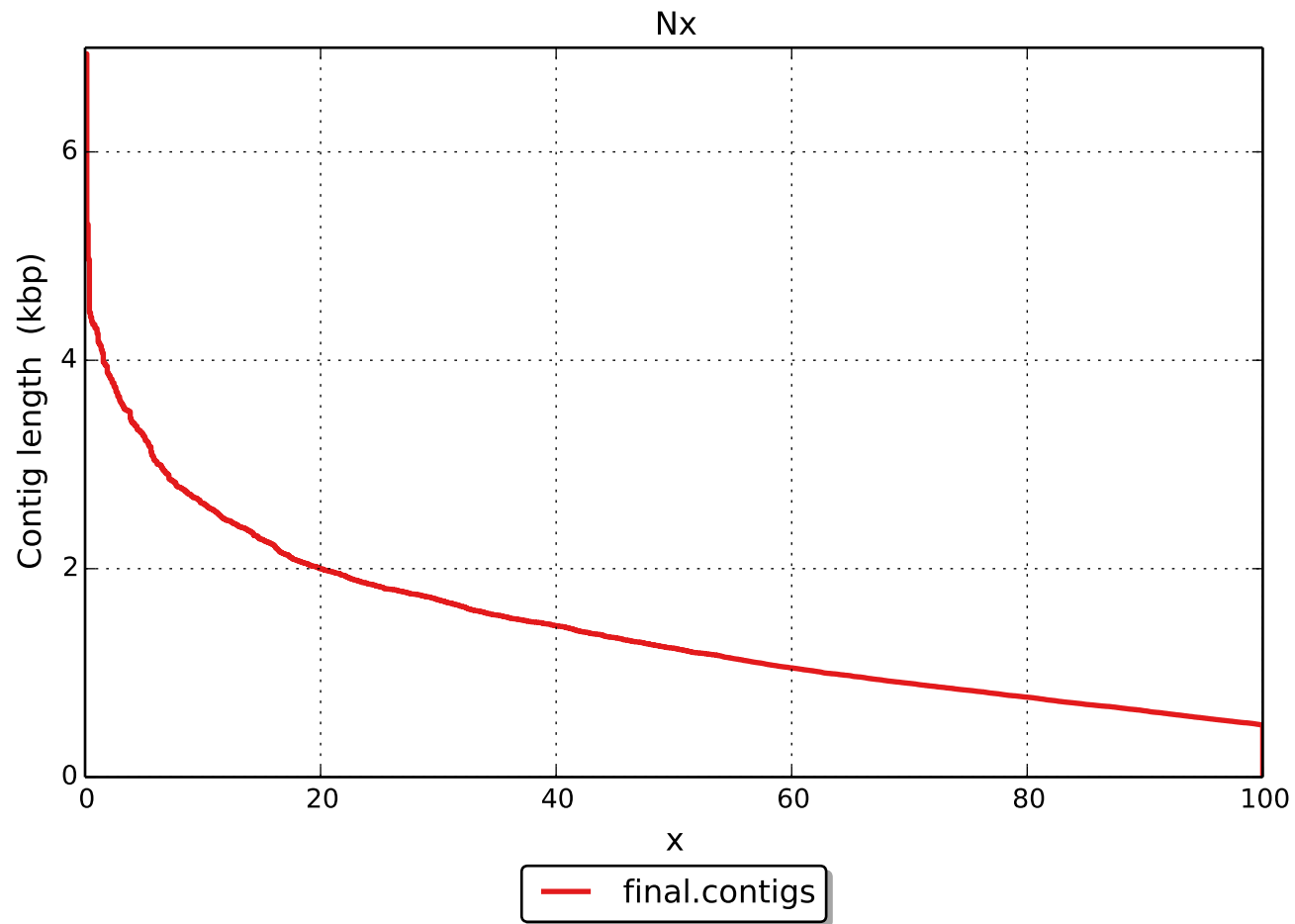
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

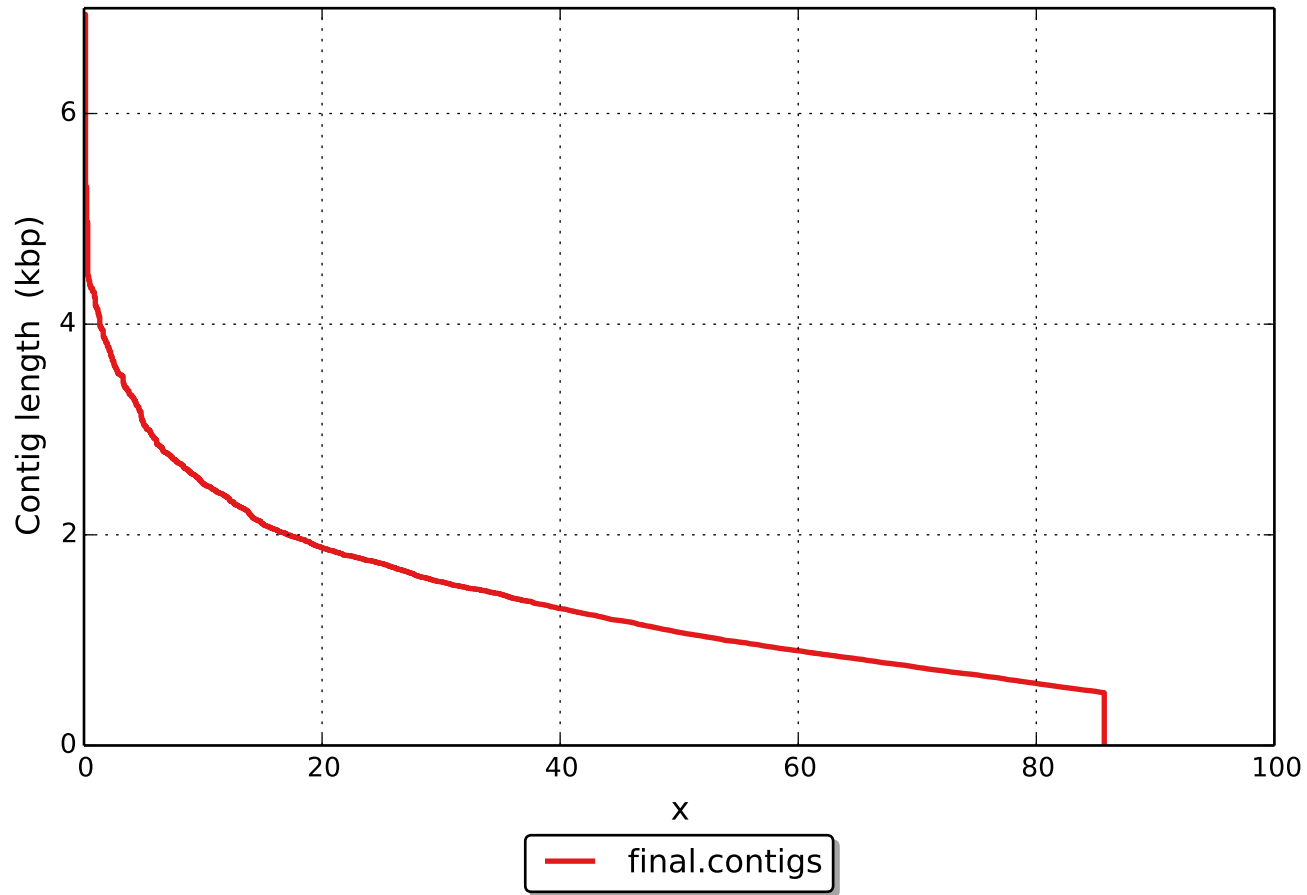


GC content



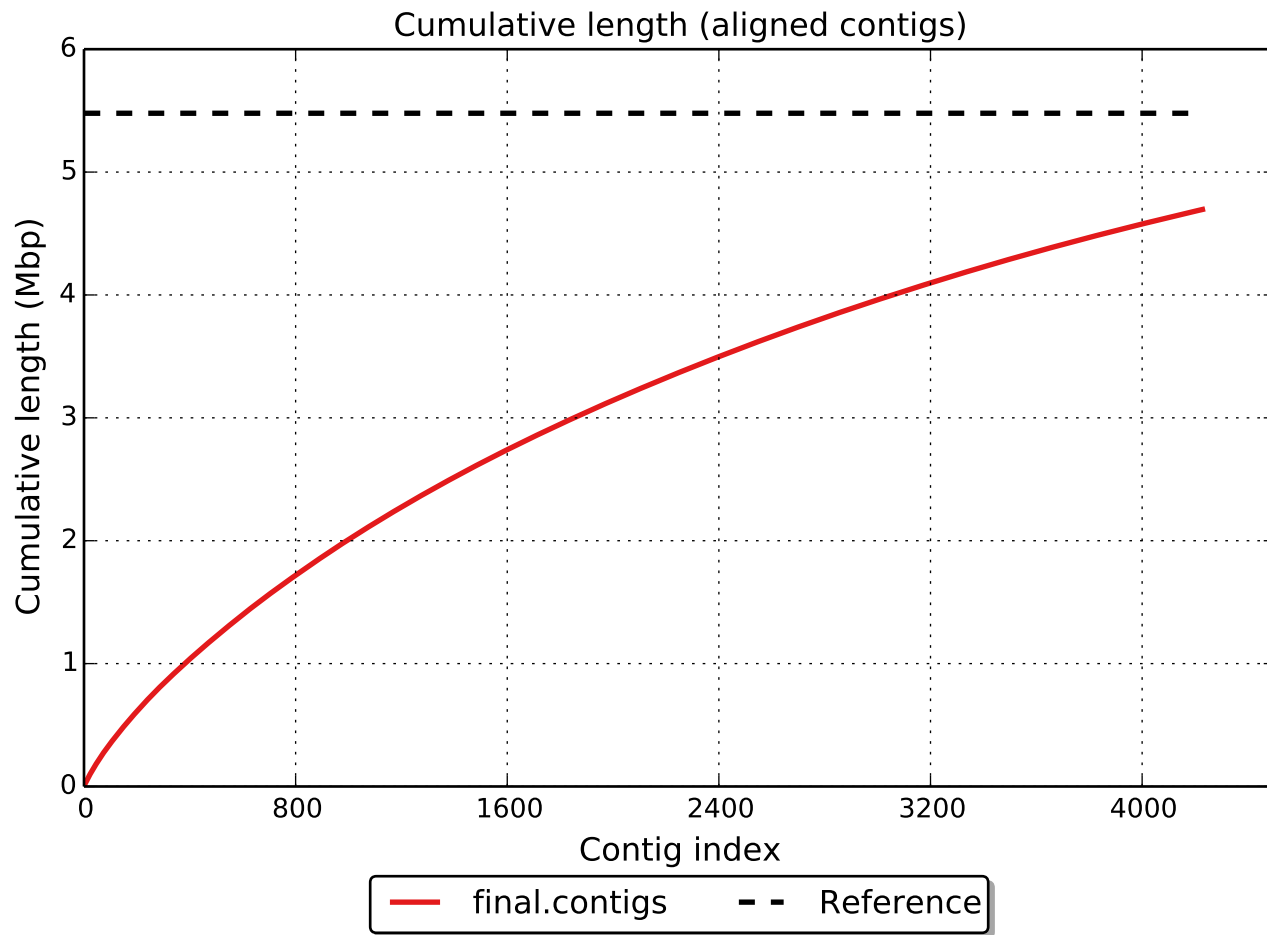


NGx

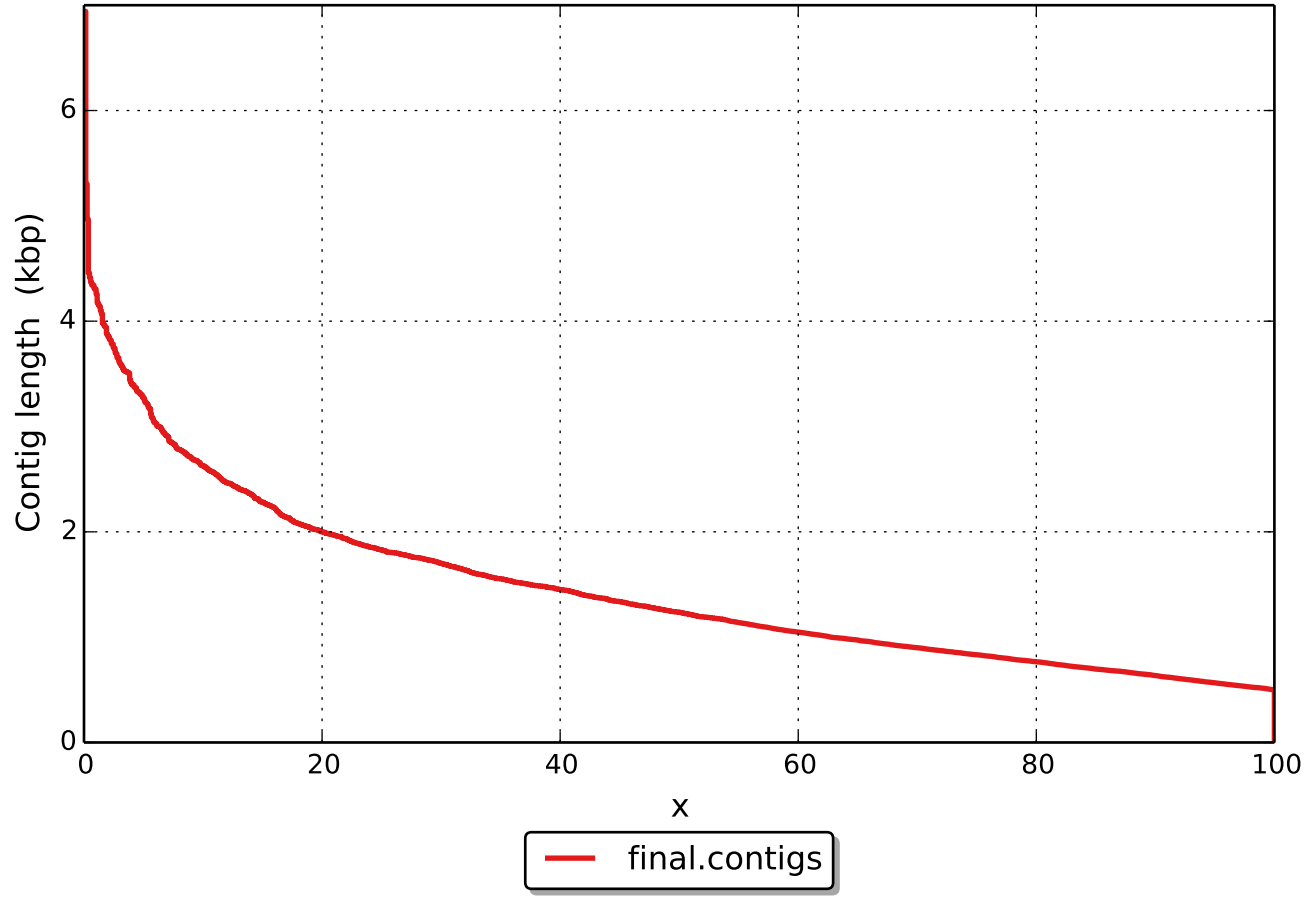


Misassemblies





NAx



NGAx

