

Report

	final.contigs
# contigs (≥ 0 bp)	3537
# contigs (≥ 1000 bp)	837
Total length (≥ 0 bp)	5926674
Total length (≥ 1000 bp)	4935545
# contigs	1246
Largest contig	42944
Total length	5203656
Reference length	10957366
GC (%)	50.28
Reference GC (%)	50.49
N50	8213
N75	4256
L50	181
L75	389
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 2 part
Unaligned length	228
Genome fraction (%)	47.168
Duplication ratio	1.007
# N's per 100 kbp	0.00
# mismatches per 100 kbp	429.27
# indels per 100 kbp	0.14
Largest alignment	42944
NA50	8213
NA75	4256
LA50	181
LA75	389

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

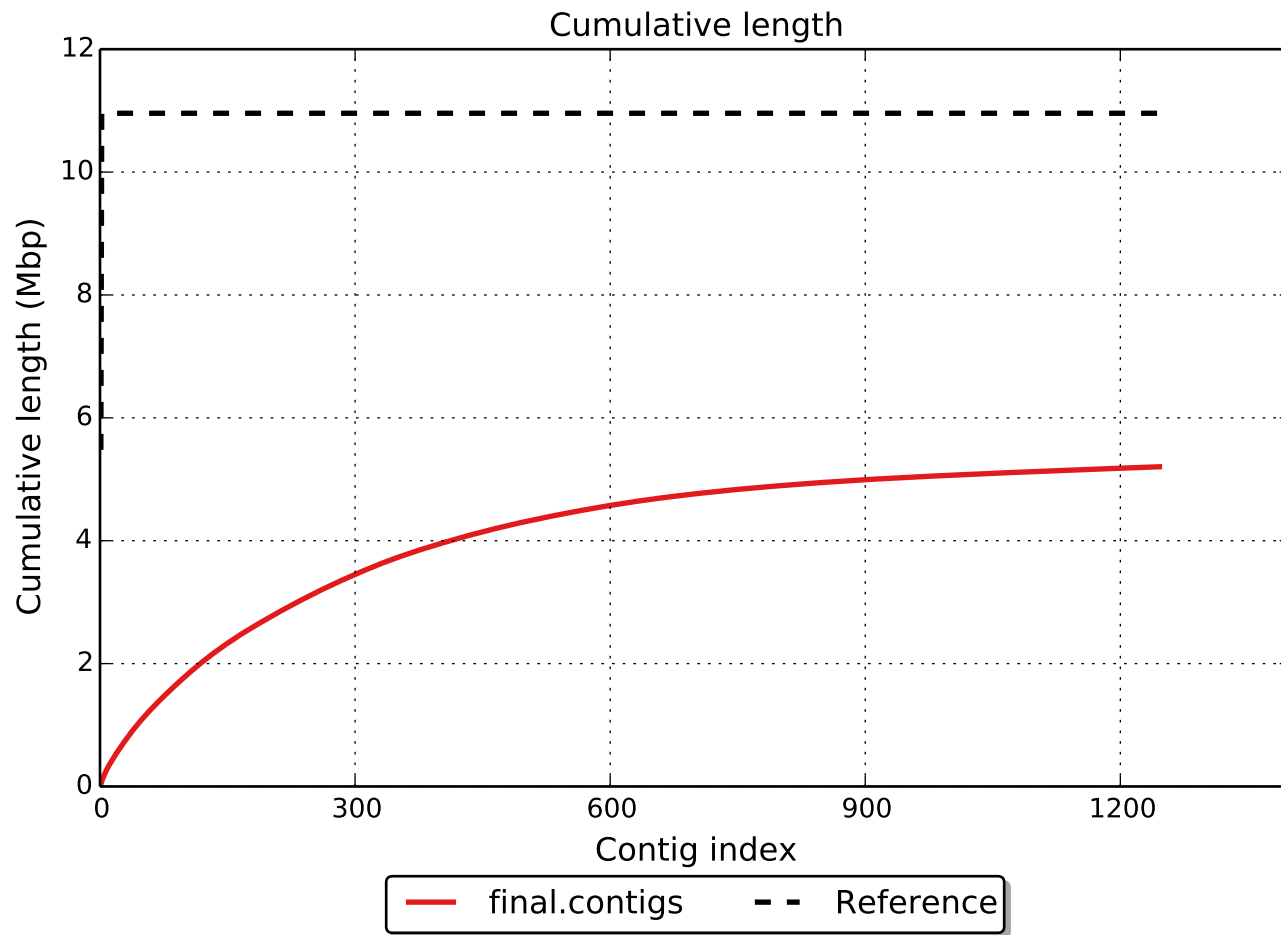
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# mismatches	22186
# indels	7
# short indels	5
# long indels	2
Indels length	29

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).

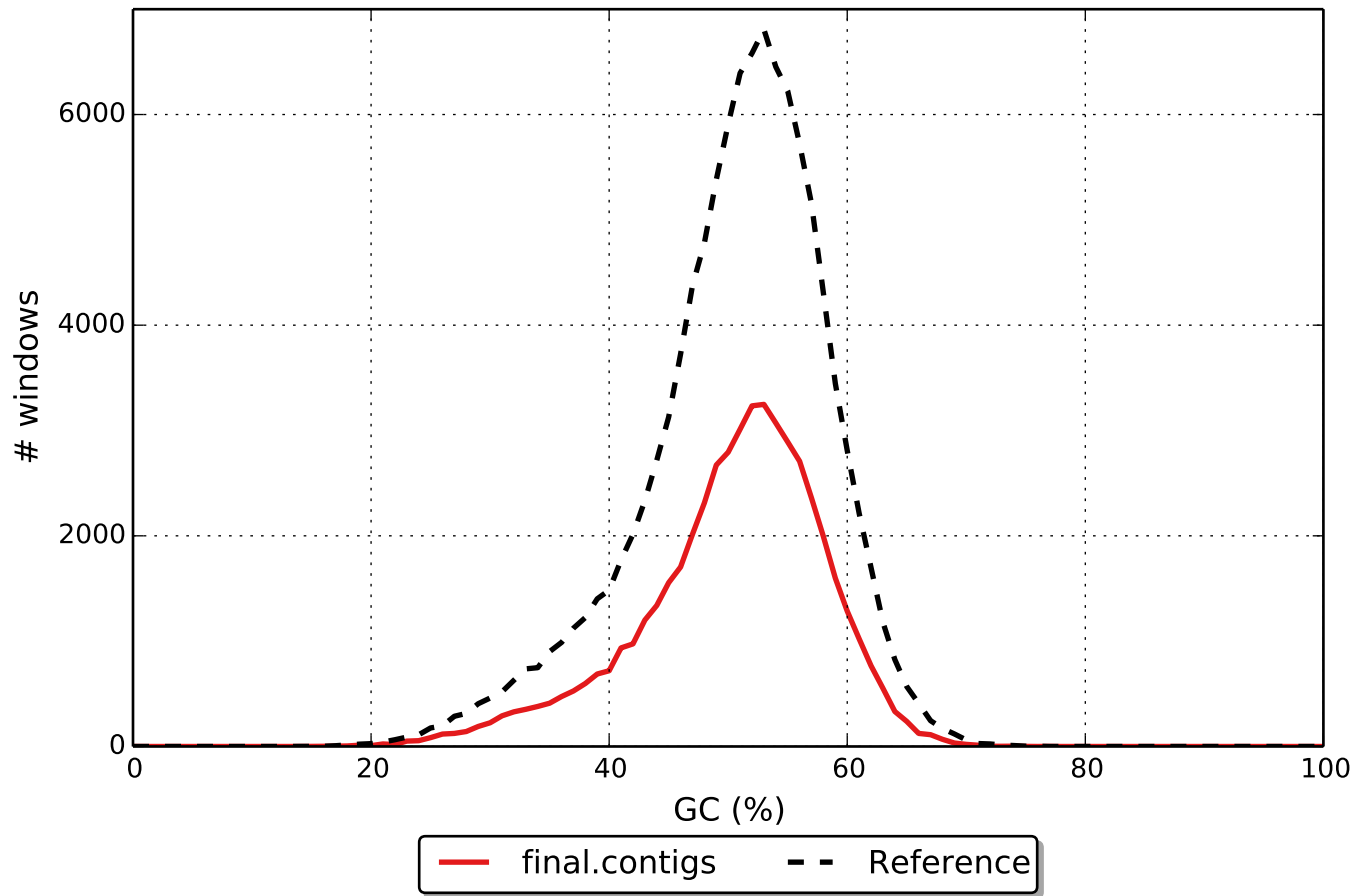
Unaligned report

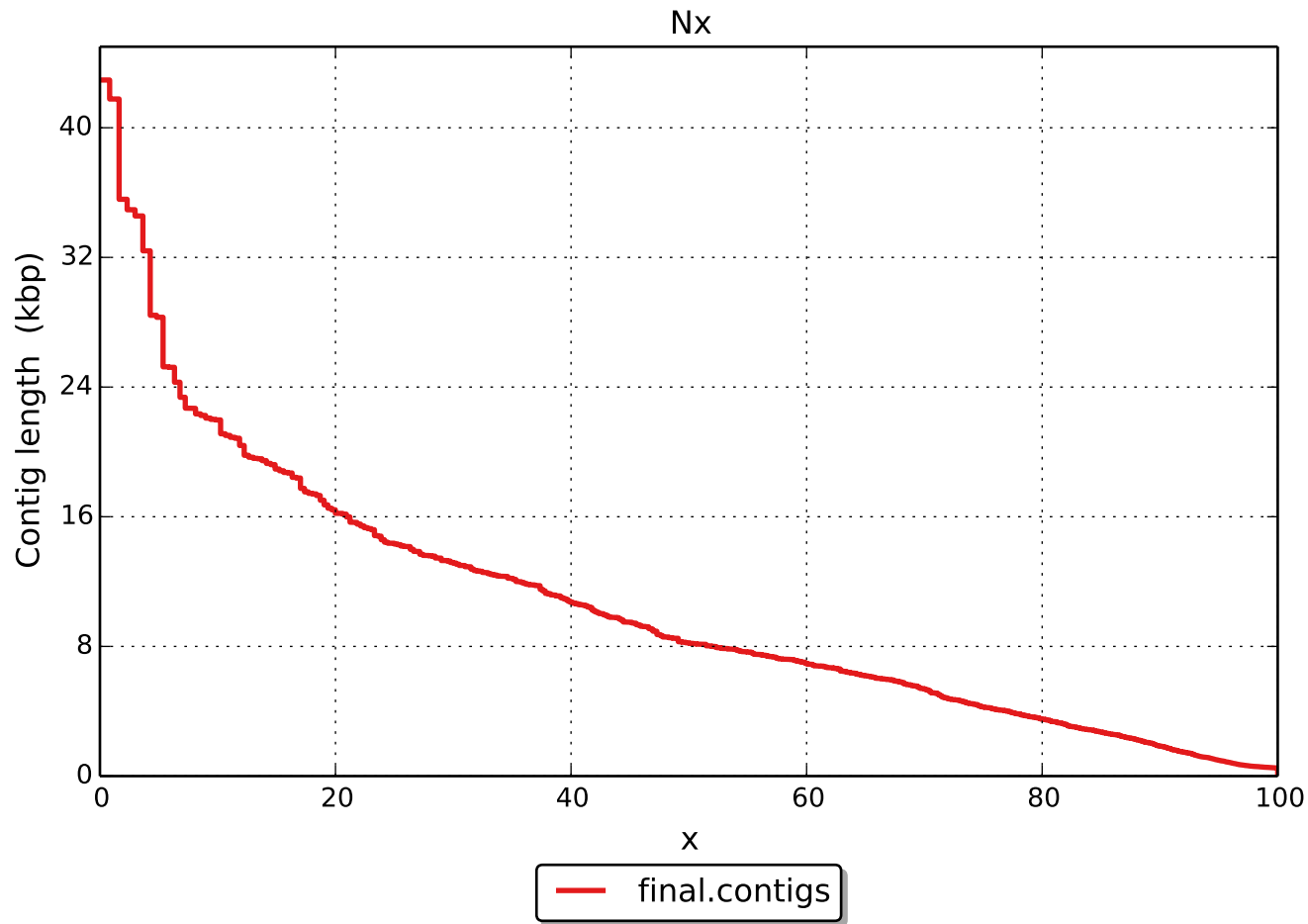
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	0
Partially unaligned length	228
# N's	0

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).

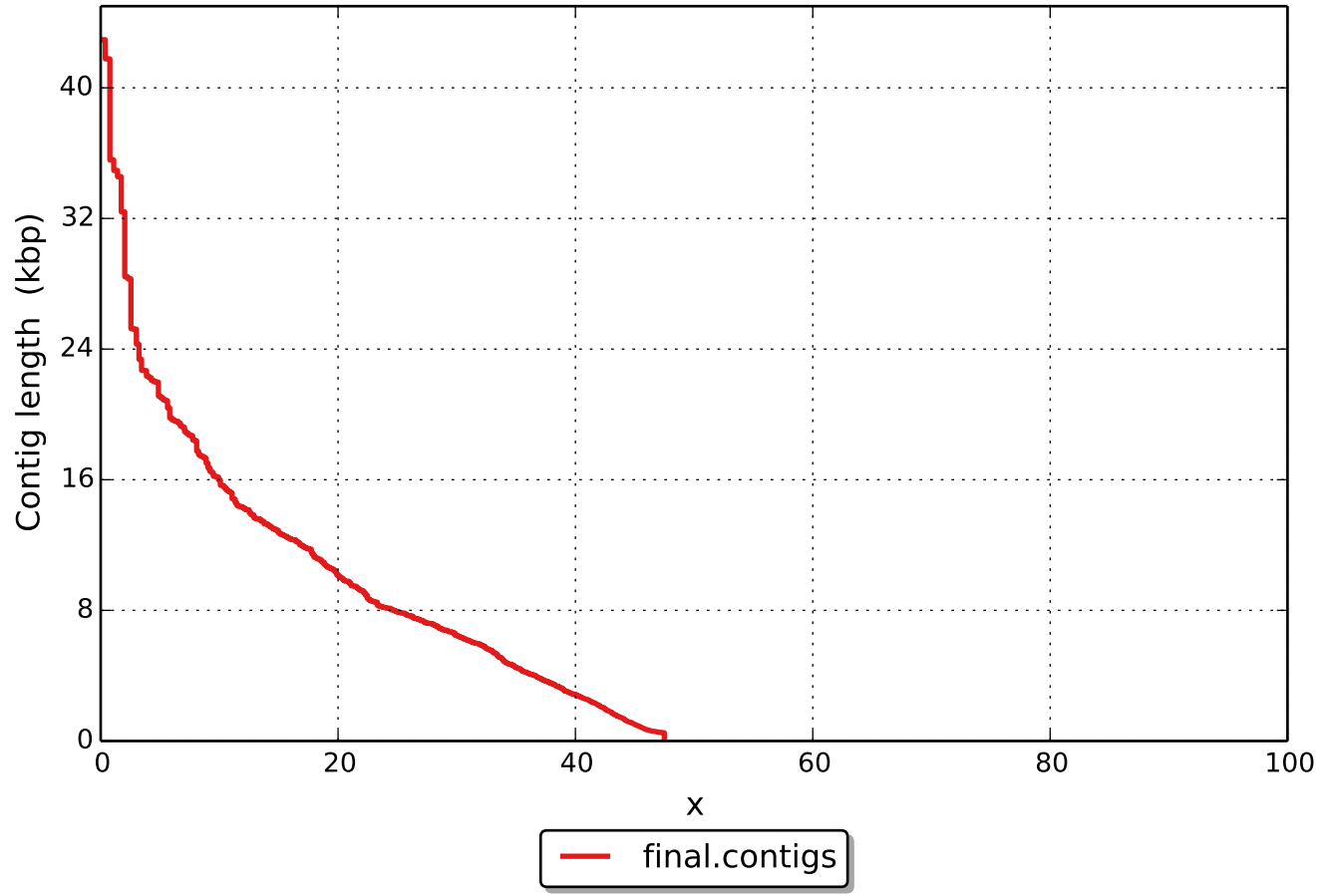


GC content



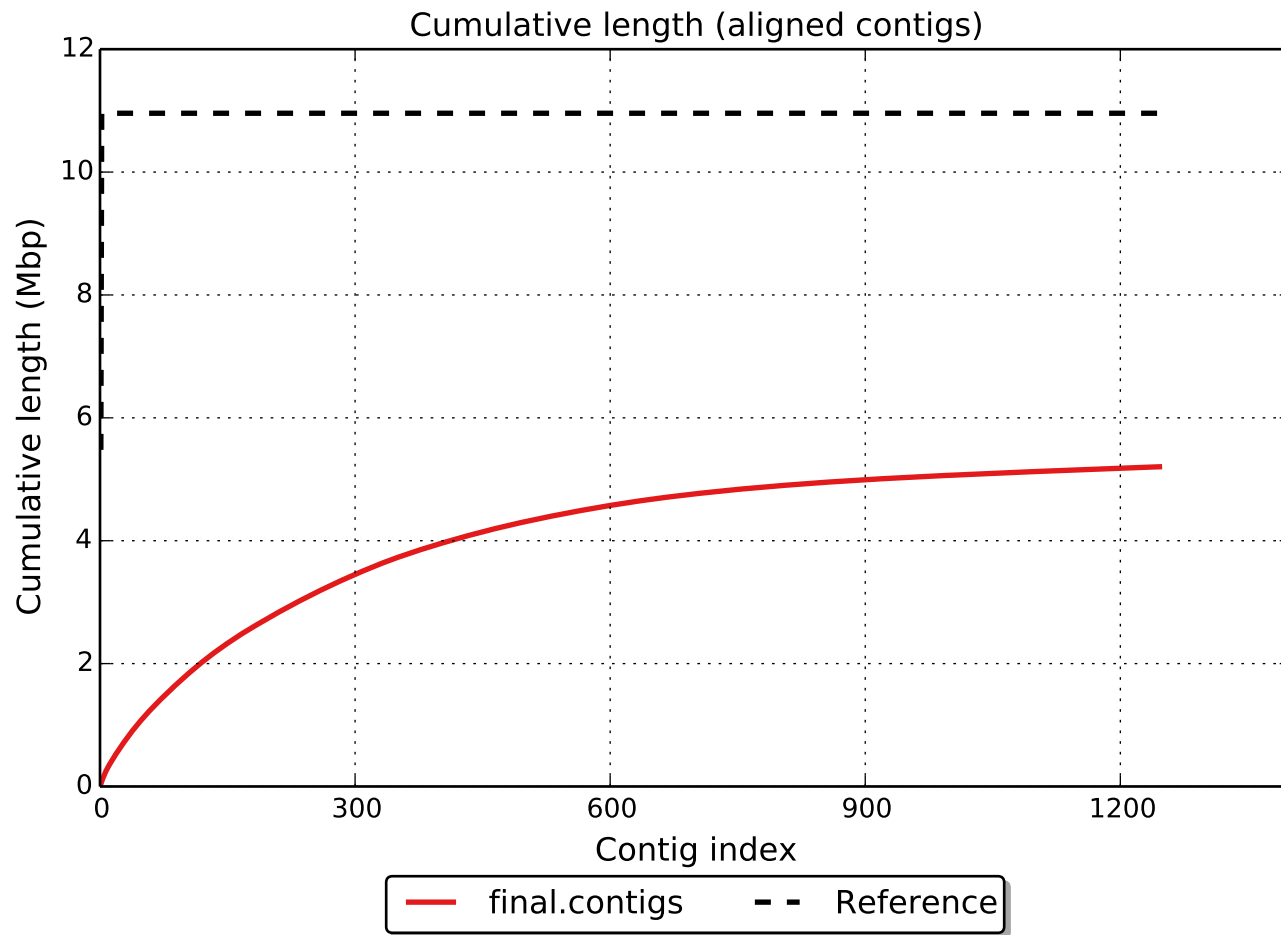


NGx

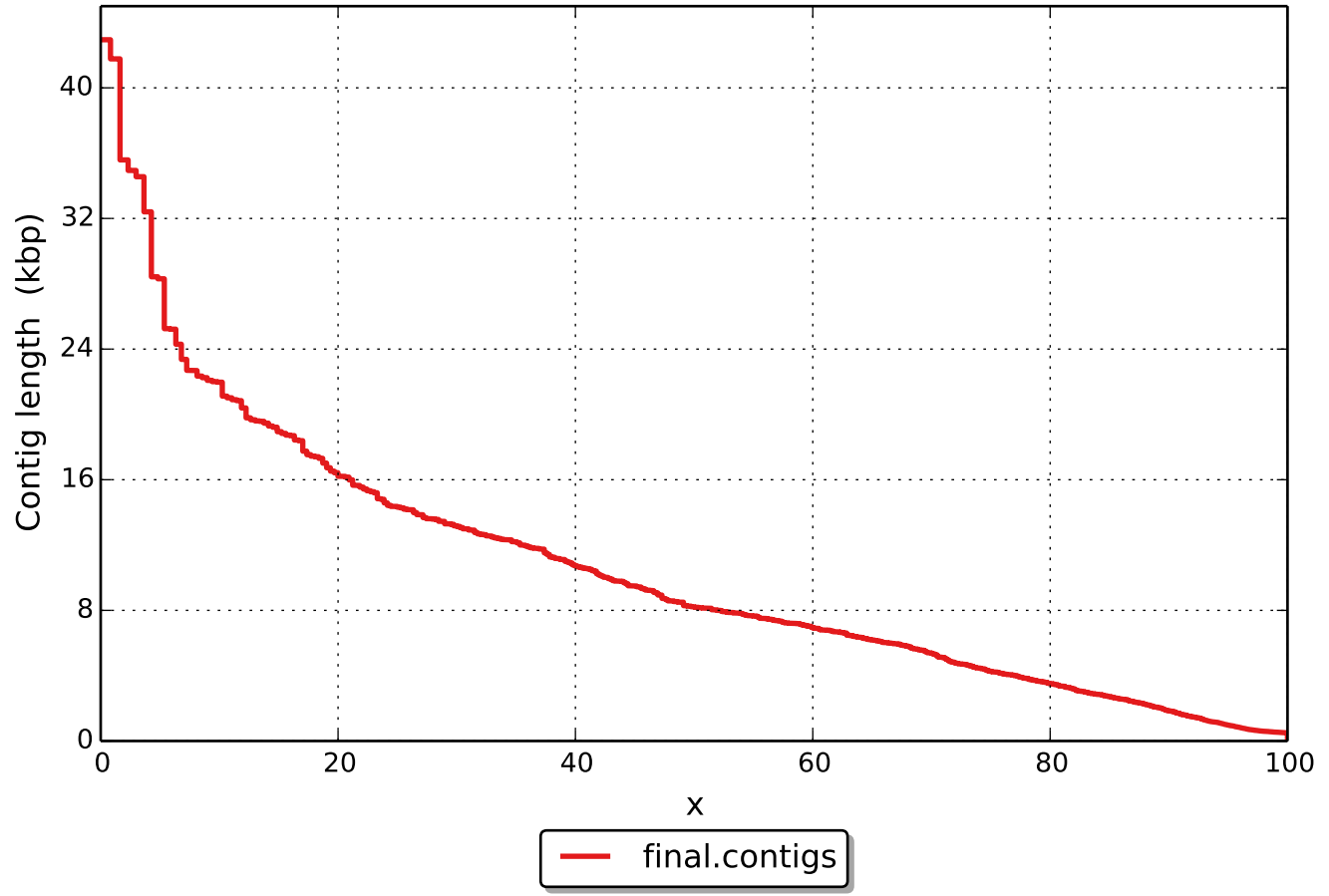


Misassemblies





NAx



NGAx

