

Report

	final.contigs
# contigs (≥ 0 bp)	2839
# contigs (≥ 1000 bp)	883
Total length (≥ 0 bp)	3013046
Total length (≥ 1000 bp)	1685965
# contigs	2839
Largest contig	8603
Total length	3013046
Reference length	5547323
GC (%)	50.35
Reference GC (%)	50.49
N50	1132
NG50	560
N75	718
L50	714
LG50	2387
L75	1572
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 1 part
Unaligned length	25
Genome fraction (%)	52.260
Duplication ratio	1.039
# N's per 100 kbp	0.00
# mismatches per 100 kbp	304.59
# indels per 100 kbp	0.07
Largest alignment	8603
NA50	1132
NGA50	560
NA75	718
LA50	714
LGA50	2387
LA75	1572

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

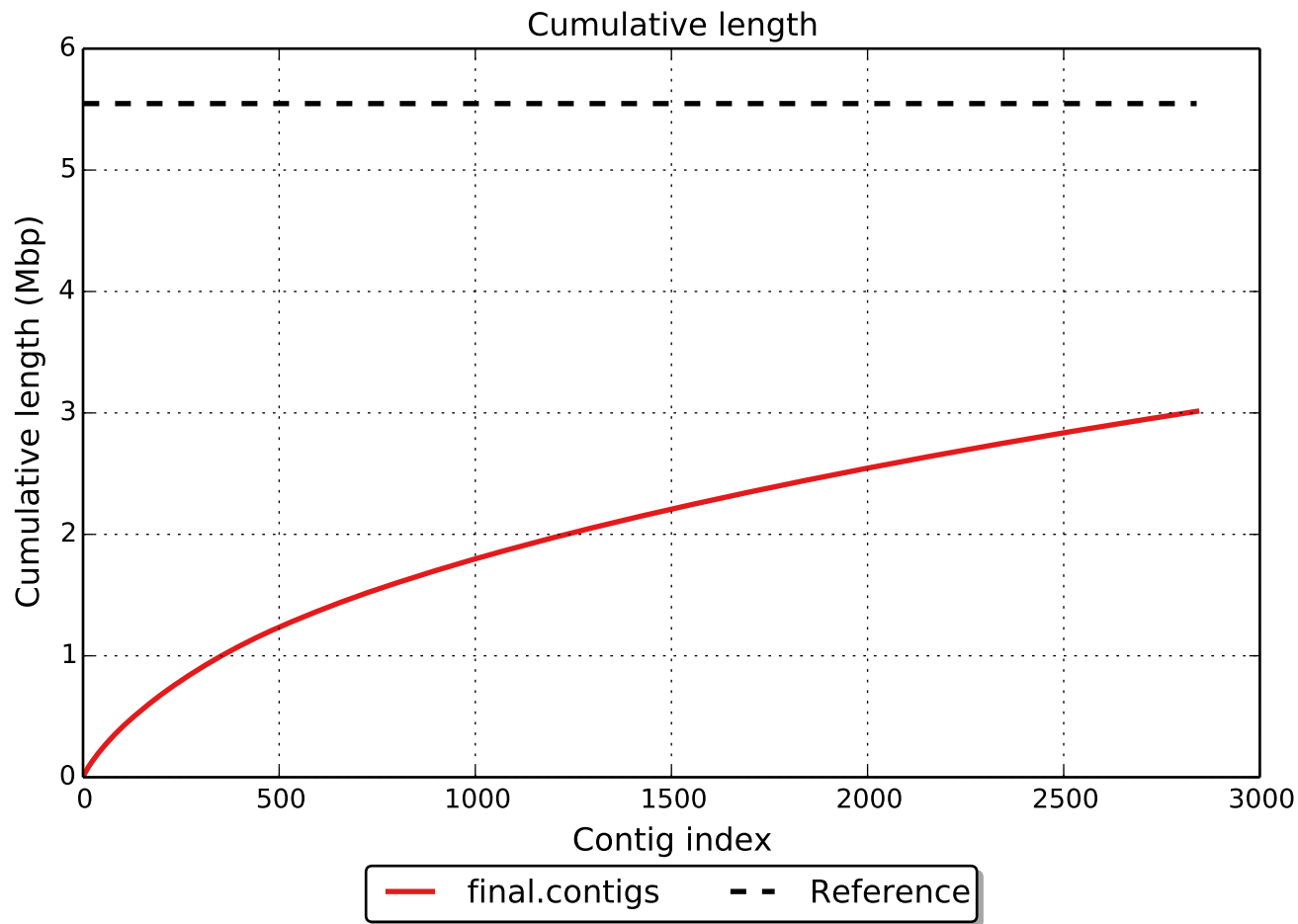
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	8830
# indels	2
# short indels	2
# long indels	0
Indels length	5

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).

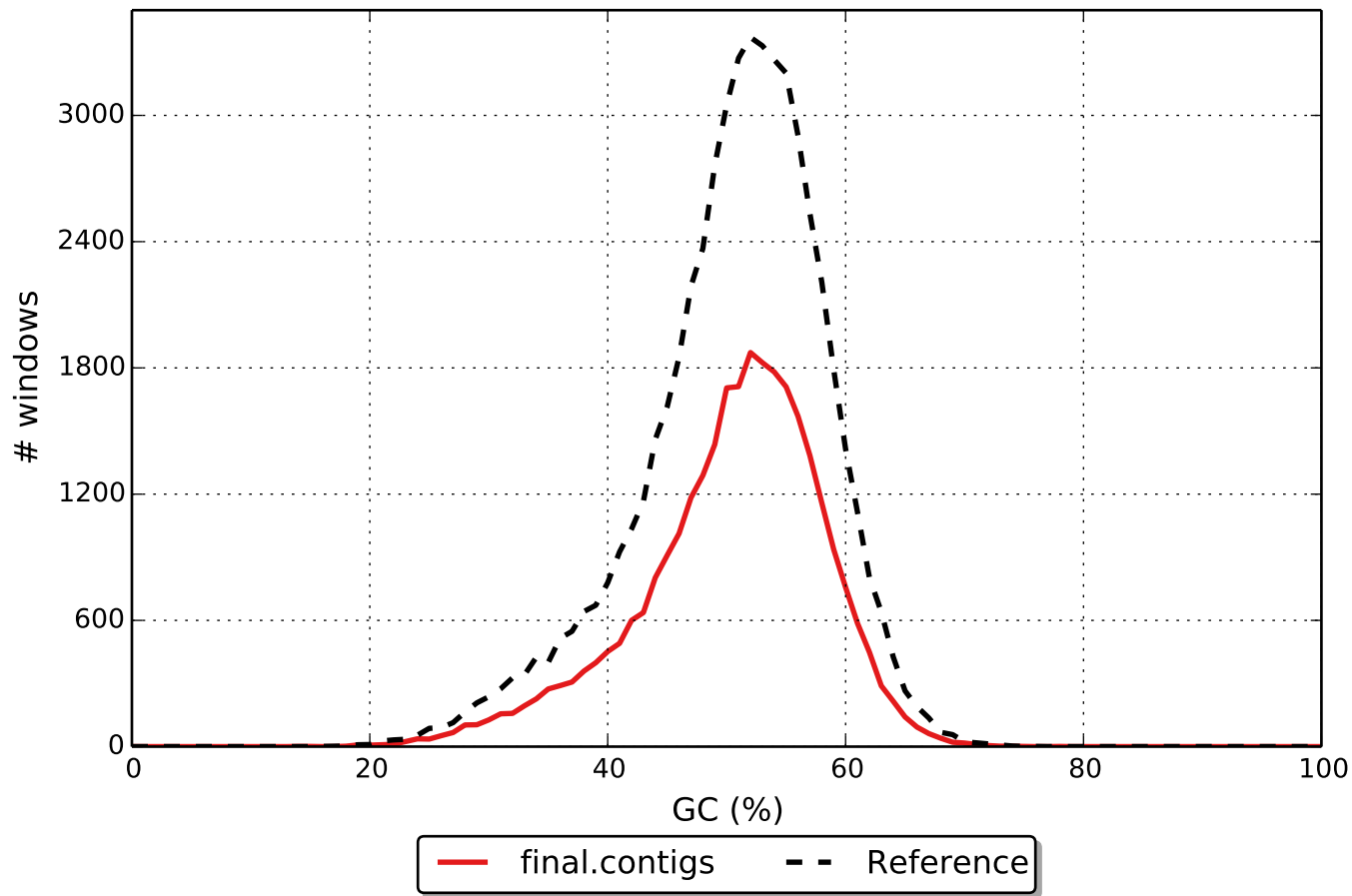
Unaligned report

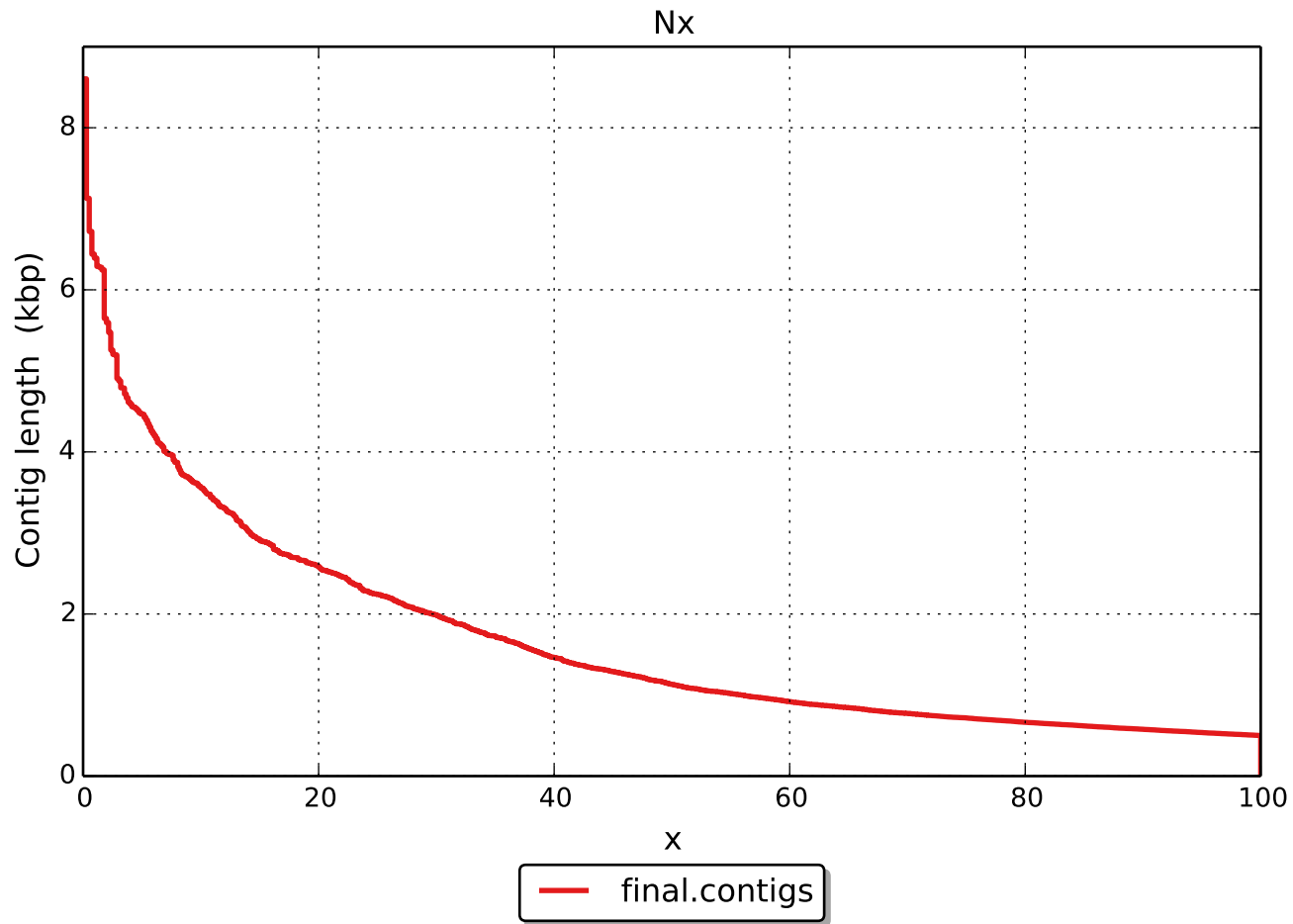
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	25
# N's	0

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).

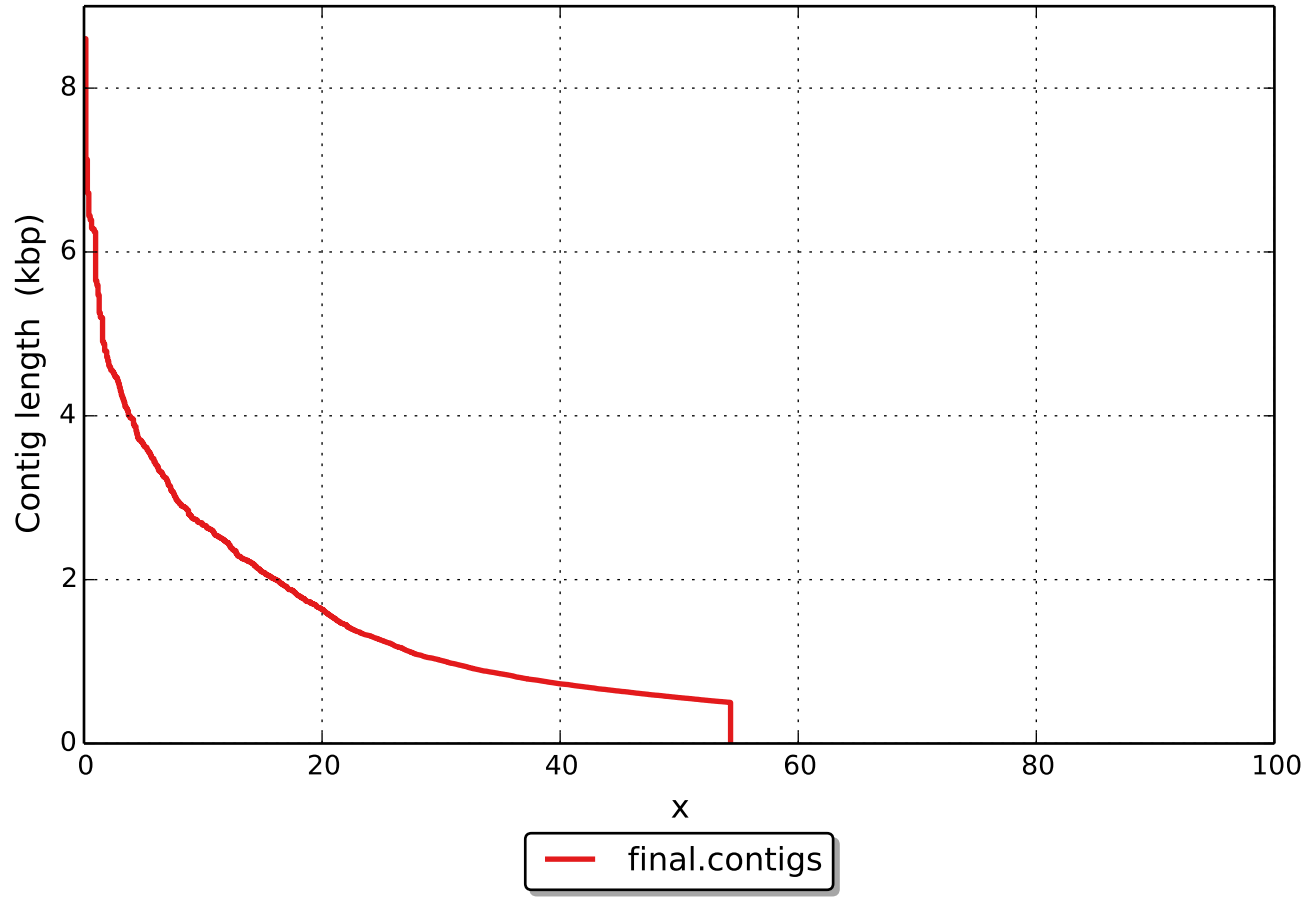


GC content



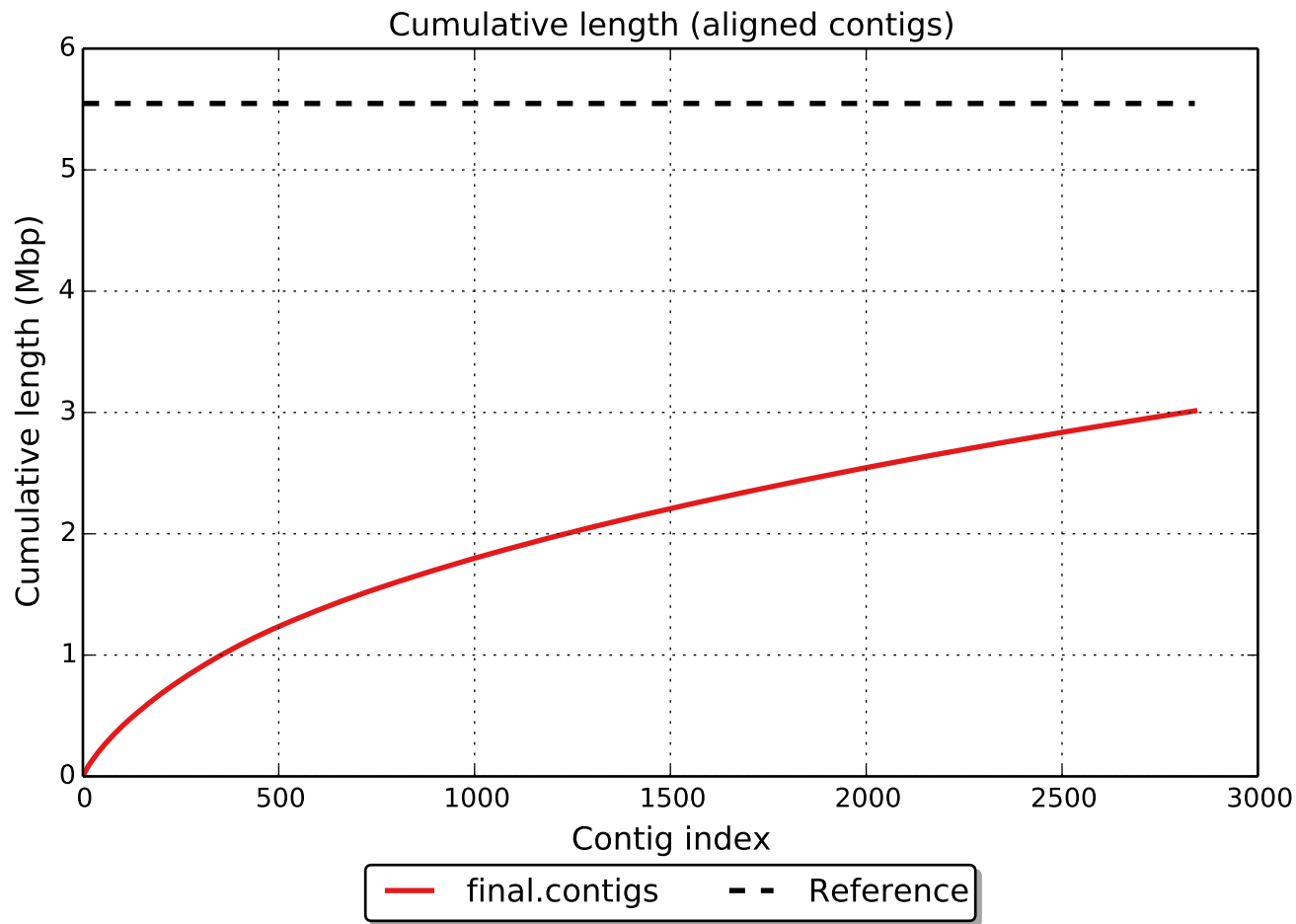


NGx

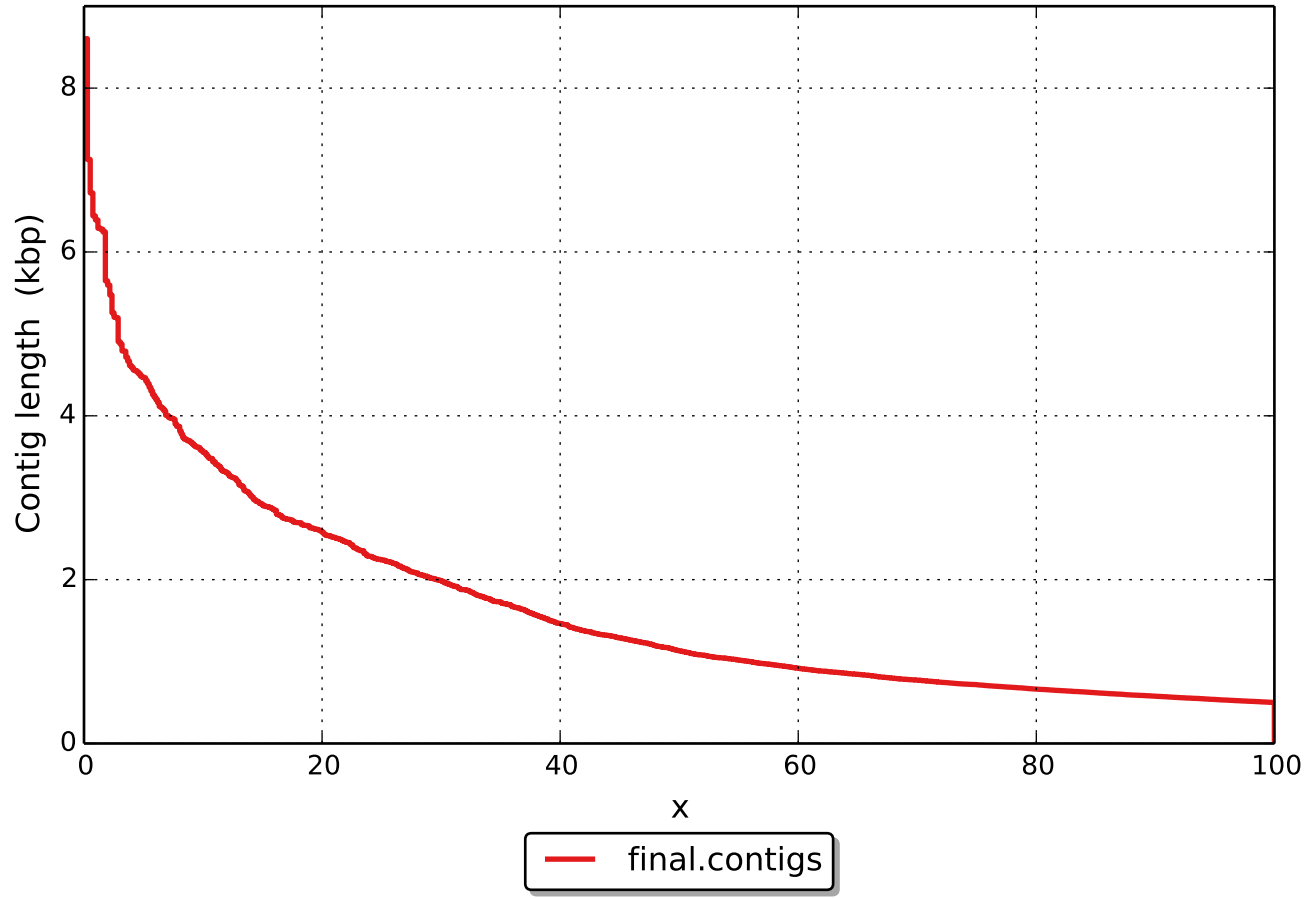


Misassemblies





NAx



NGAx

