

Report

	final.contigs
# contigs (≥ 0 bp)	4885
# contigs (≥ 1000 bp)	1513
Total length (≥ 0 bp)	4507996
Total length (≥ 1000 bp)	2122821
# contigs	4885
Largest contig	4132
Total length	4507996
Reference length	5478683
GC (%)	50.25
Reference GC (%)	50.49
N50	965
NG50	853
N75	716
NG75	573
L50	1647
LG50	2183
L75	3006
LG75	4141
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	77.053
Duplication ratio	1.068
# N's per 100 kbp	0.00
# mismatches per 100 kbp	246.19
# indels per 100 kbp	0.24
Largest alignment	4132
NA50	965
NGA50	853
NA75	716
NGA75	573
LA50	1647
LGA50	2183
LA75	3006
LGA75	4141

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

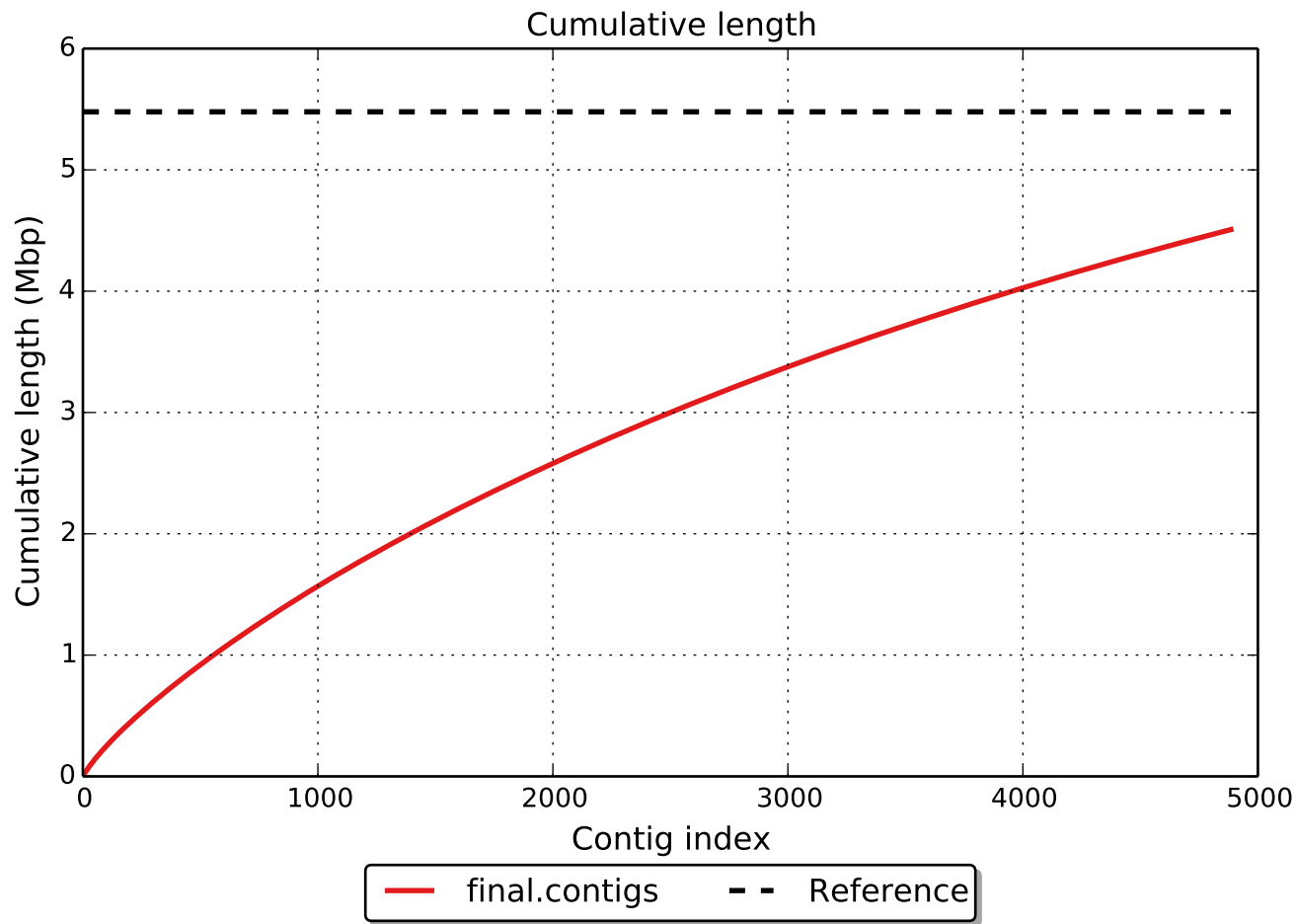
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# mismatches	10393
# indels	10
# short indels	6
# long indels	4
Indels length	62

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).

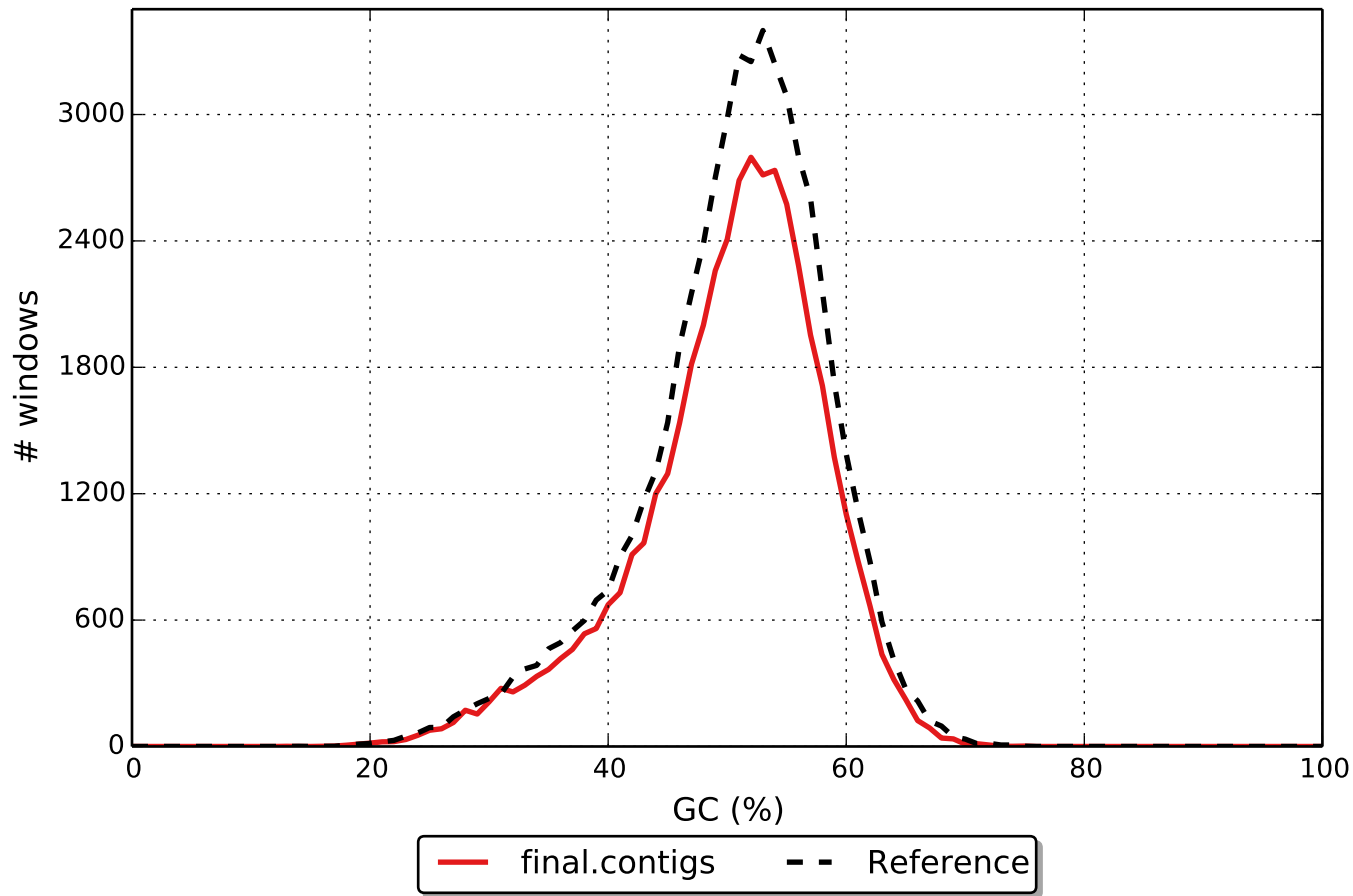
Unaligned report

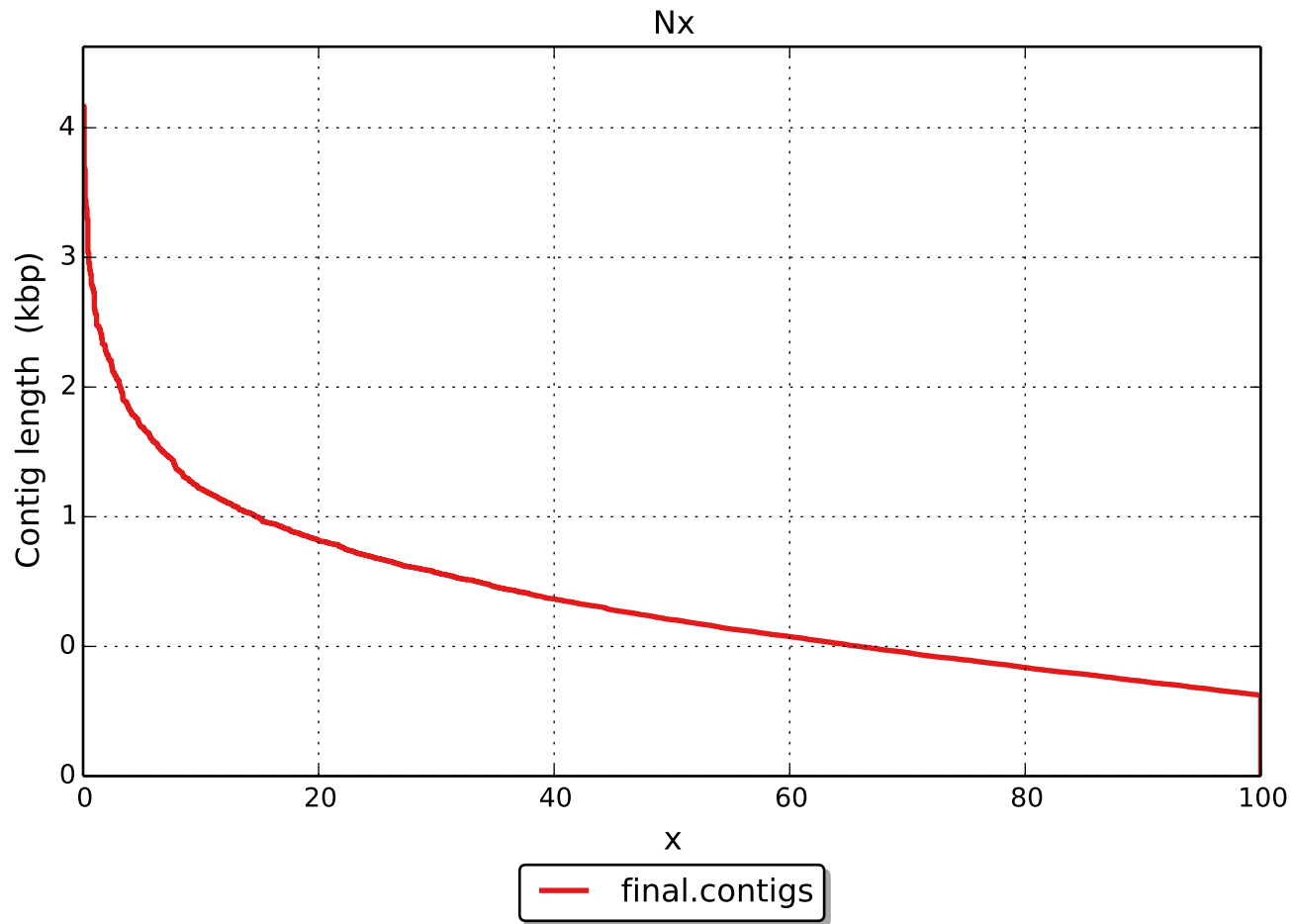
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

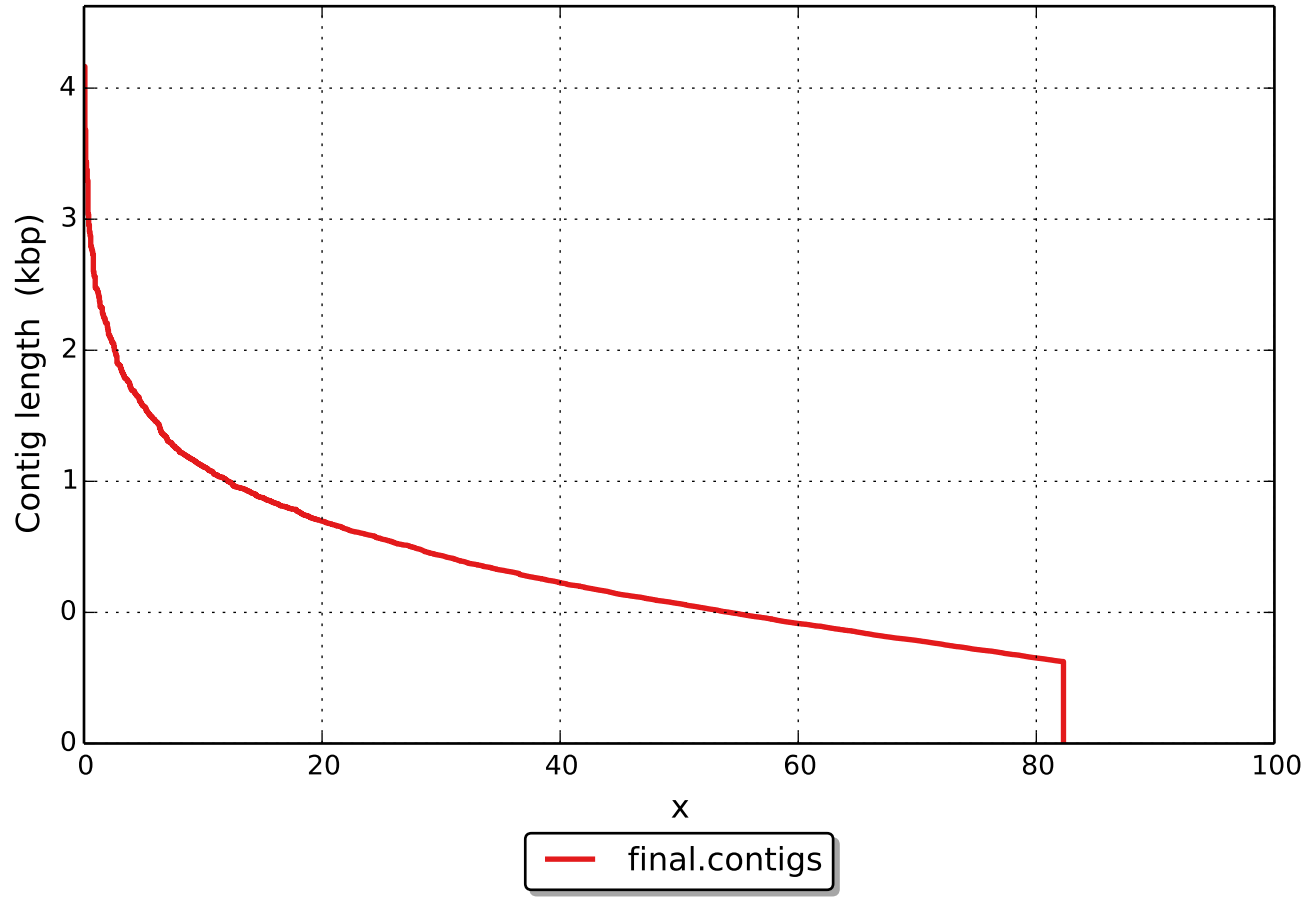


GC content



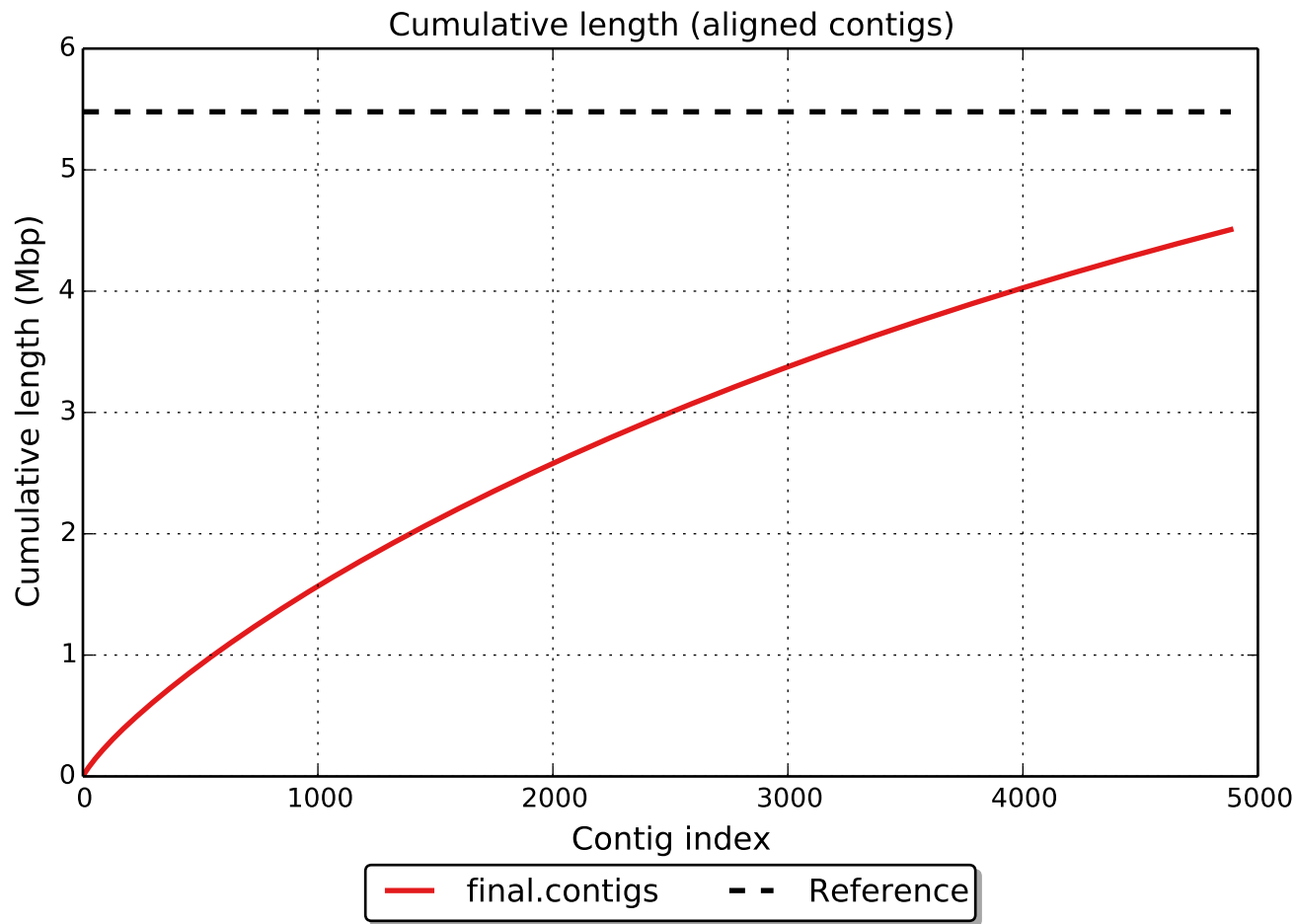


NGx

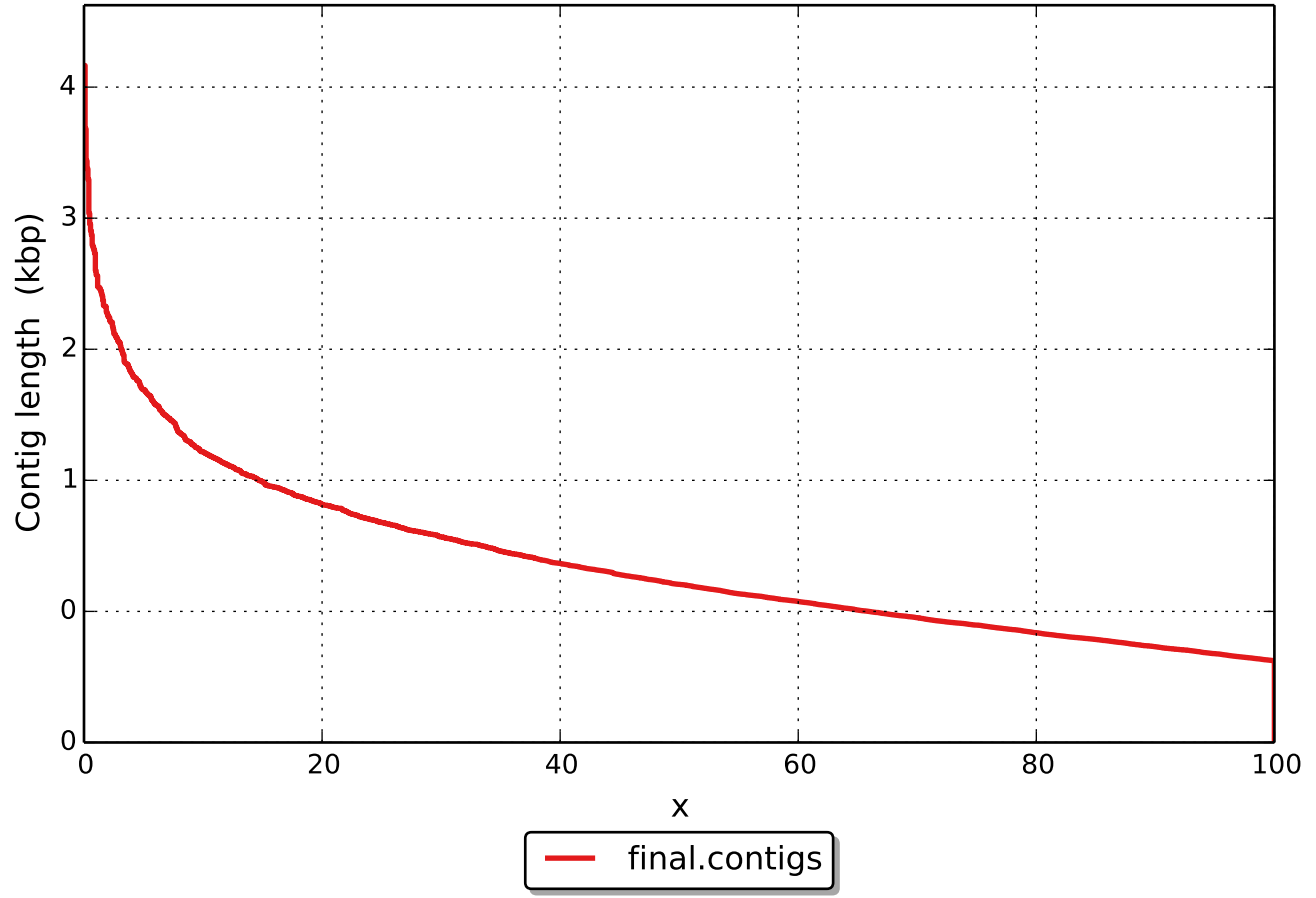


Misassemblies





NAx



NGAx

