

Report

	final.contigs
# contigs (≥ 0 bp)	2732
# contigs (≥ 1000 bp)	1988
Total length (≥ 0 bp)	5614506
Total length (≥ 1000 bp)	5065513
# contigs	2732
Largest contig	12599
Total length	5614506
Reference length	5547323
GC (%)	50.49
Reference GC (%)	50.49
N50	2711
NG50	2738
N75	1635
NG75	1673
L50	657
LG50	644
L75	1325
LG75	1295
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	97.323
Duplication ratio	1.040
# N's per 100 kbp	0.00
# mismatches per 100 kbp	39.25
# indels per 100 kbp	0.00
Largest alignment	12599
NA50	2711
NGA50	2738
NA75	1635
NGA75	1673
LA50	657
LGA50	644
LA75	1325
LGA75	1295

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

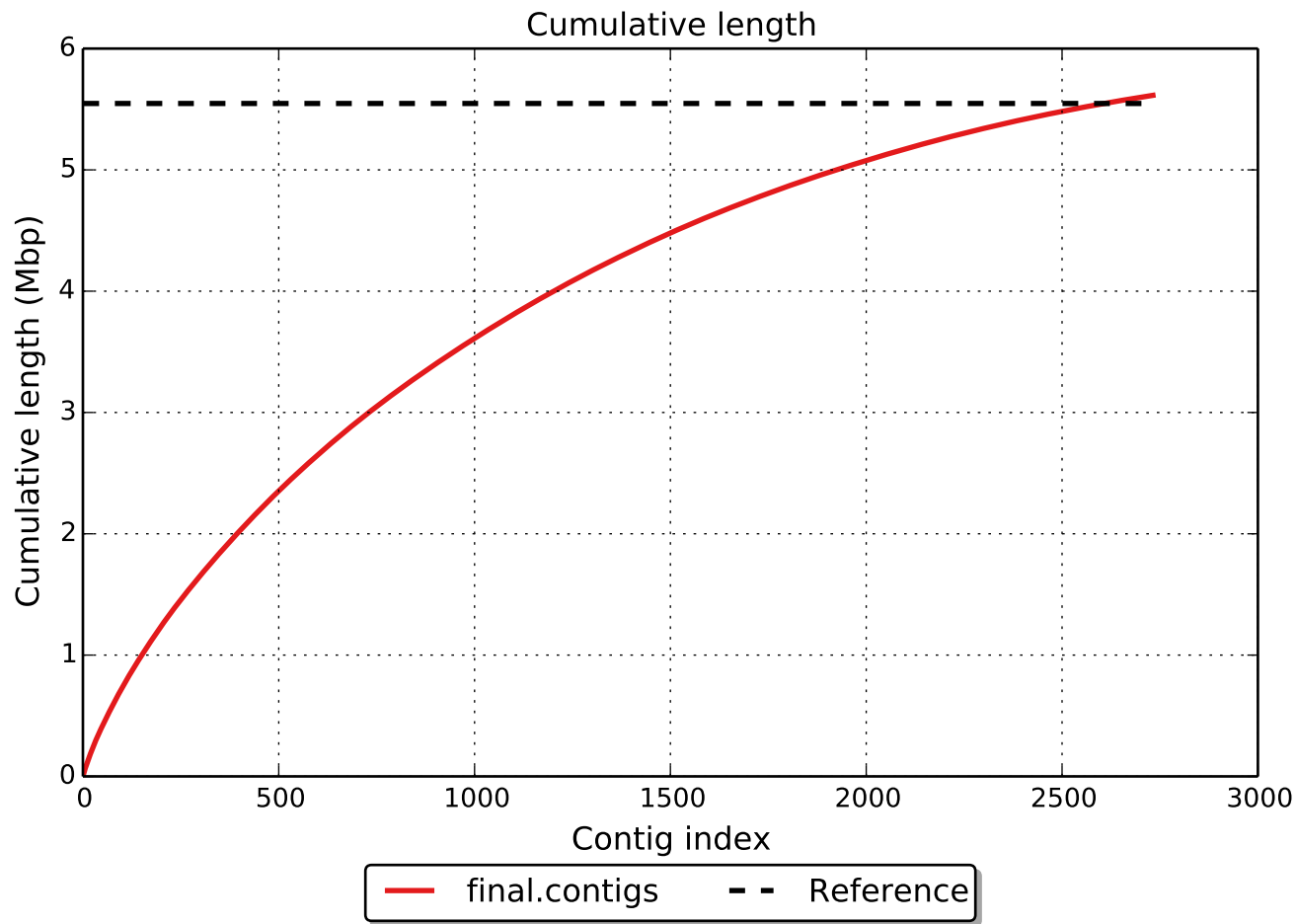
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	2119
# indels	0
# short indels	0
# long indels	0
Indels length	0

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).

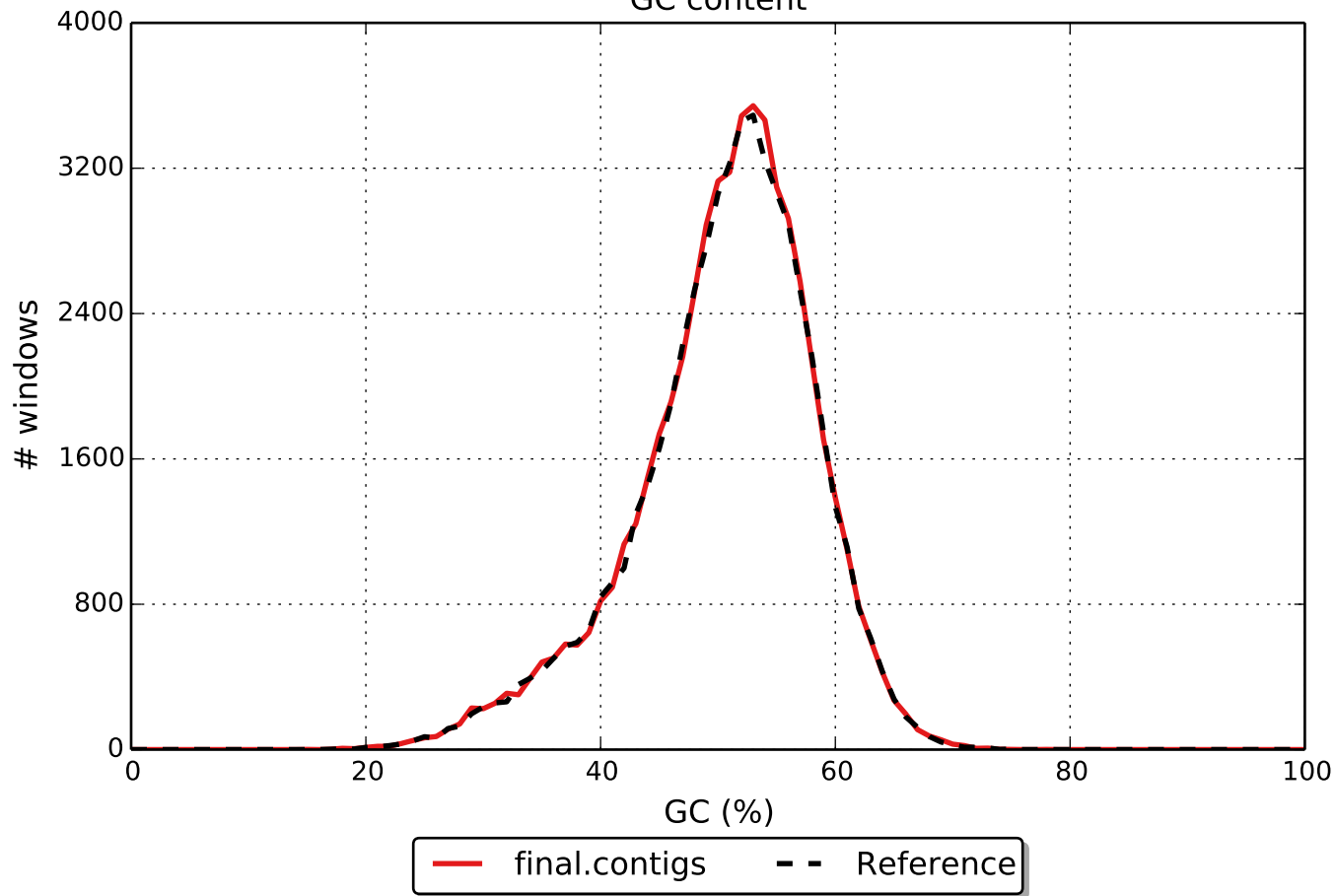
Unaligned report

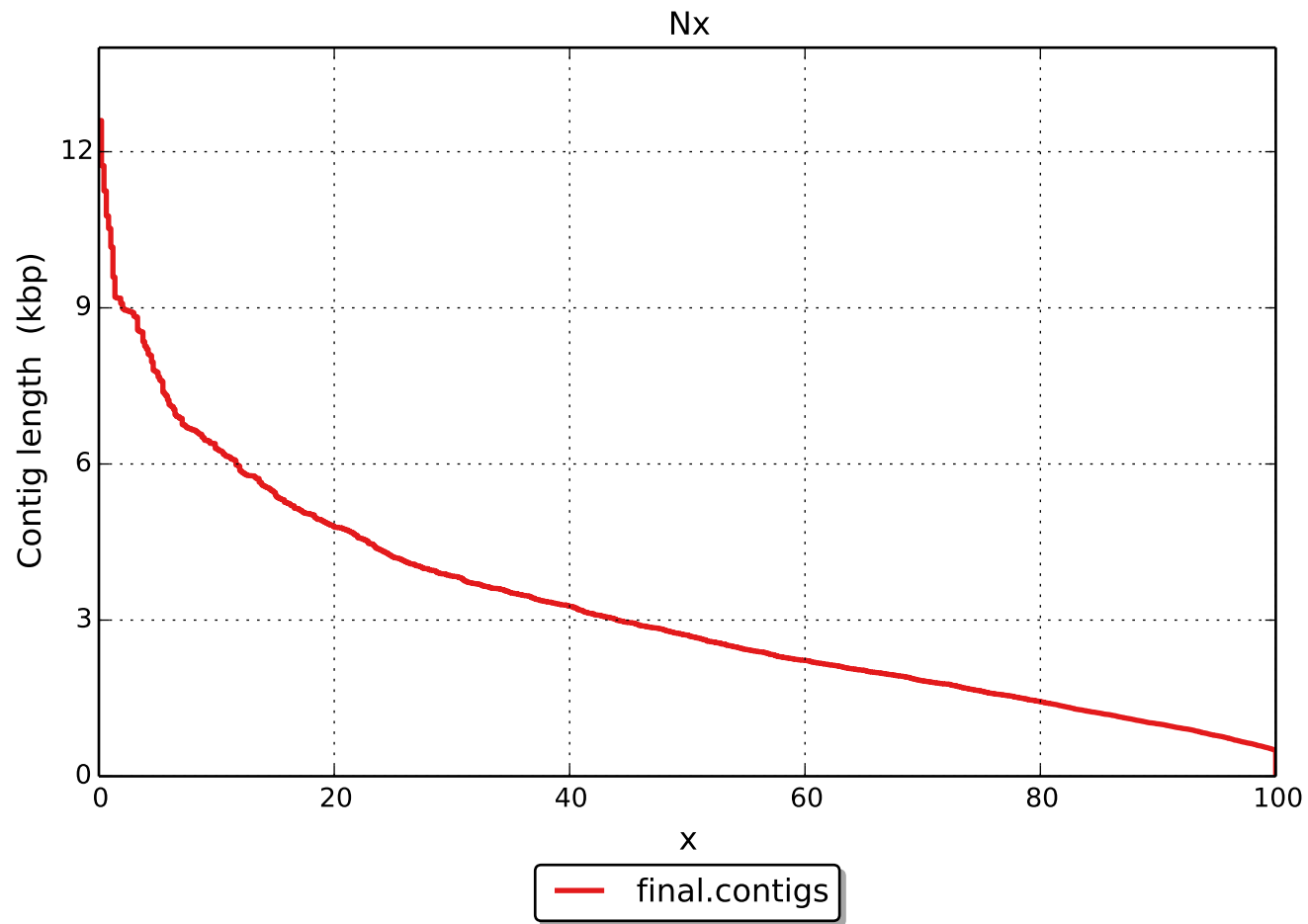
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

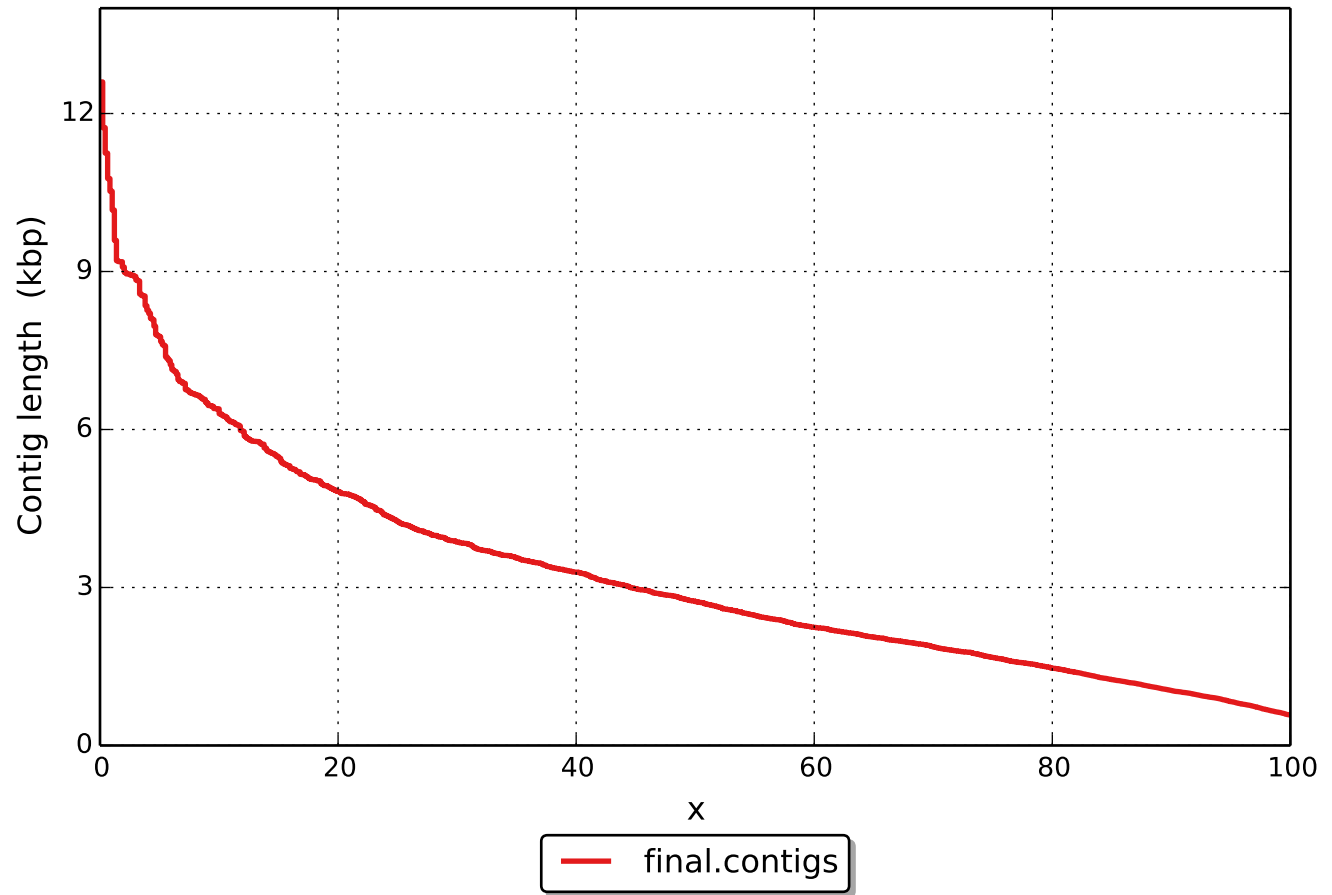


GC content



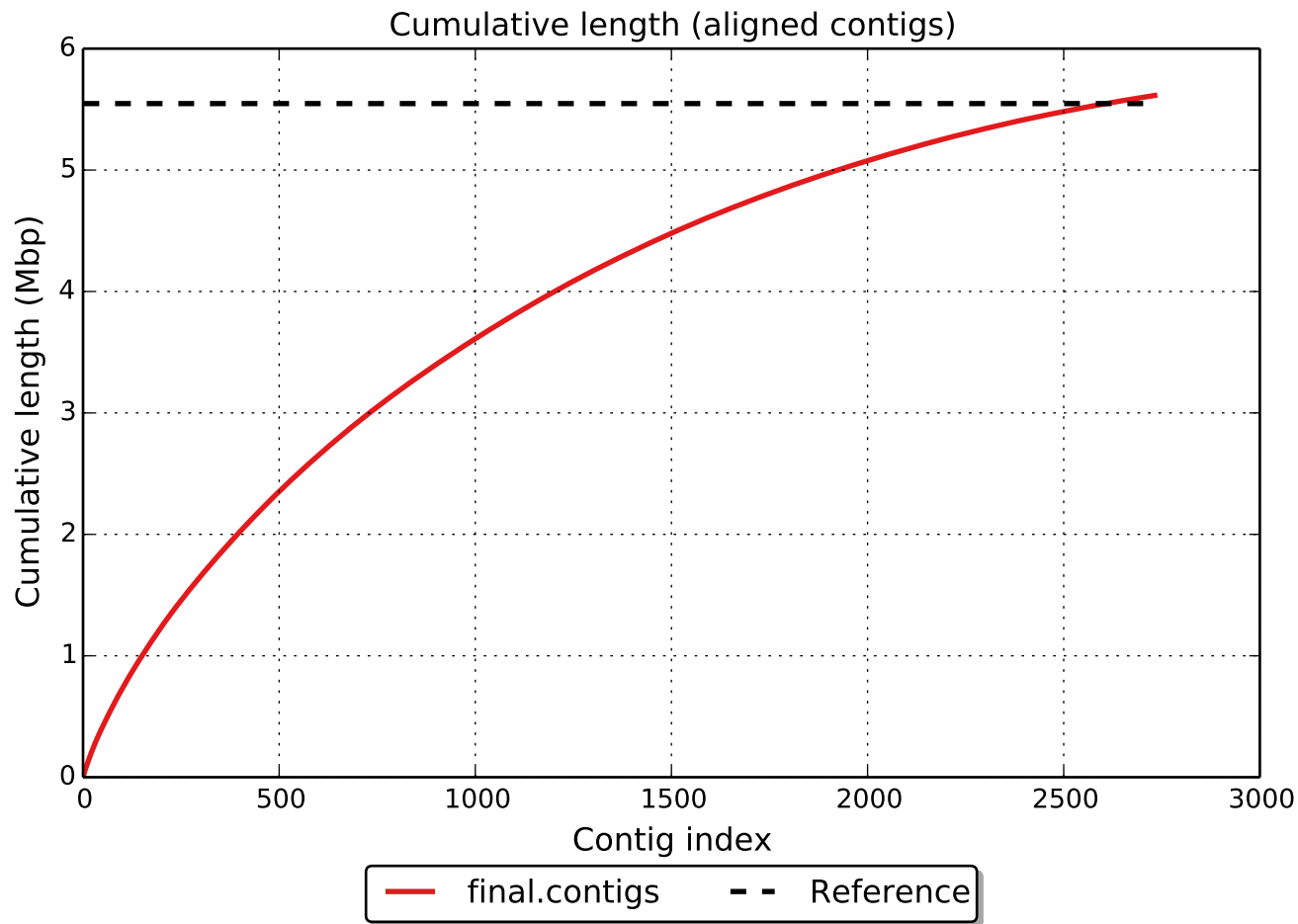


NGx

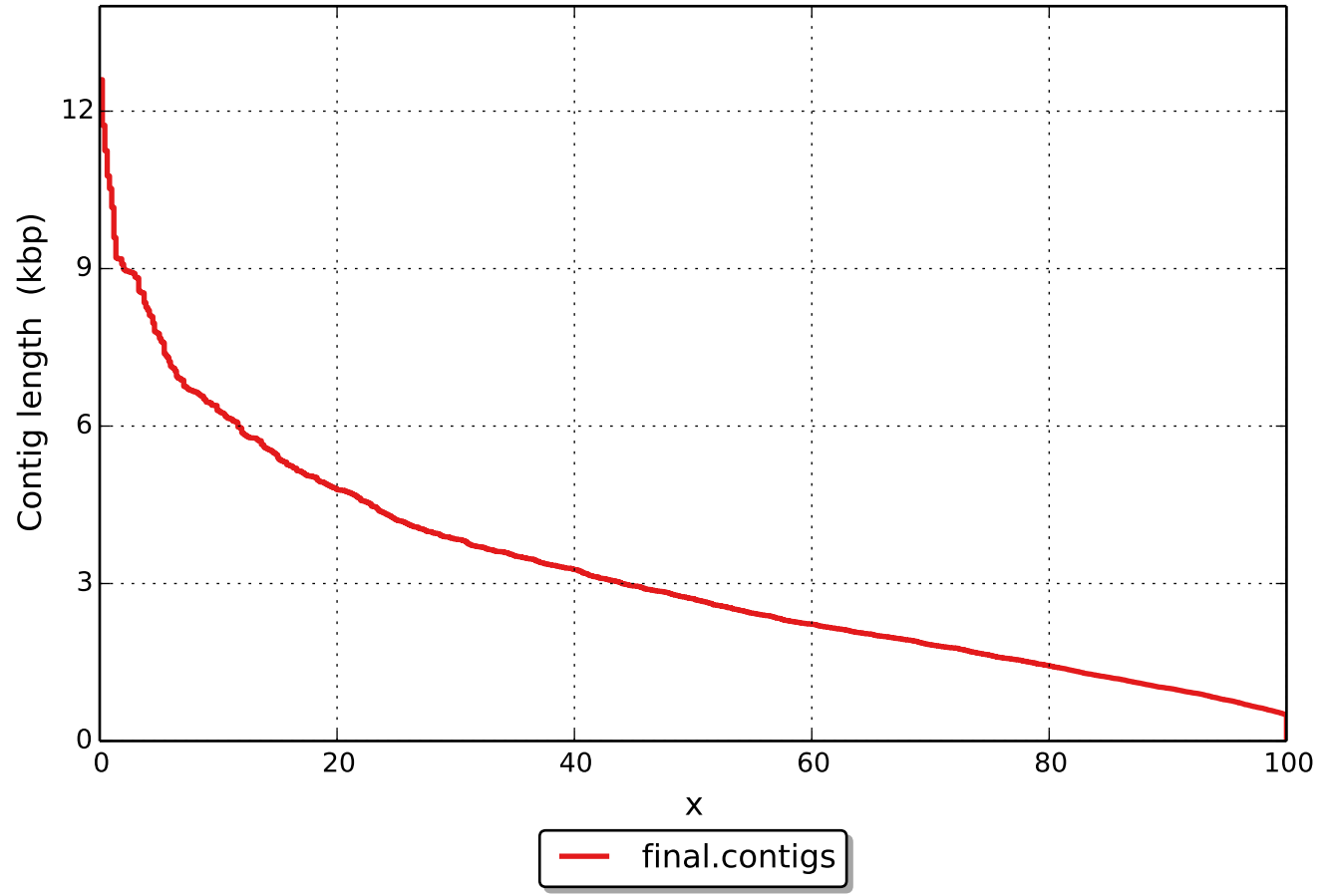


Misassemblies





NAx



NGAx

