

Report

	final.contigs
# contigs (>= 0 bp)	522
# contigs (>= 1000 bp)	495
Total length (>= 0 bp)	5522502
Total length (>= 1000 bp)	5503535
# contigs	522
Largest contig	67238
Total length	5522502
Reference length	5478683
GC (%)	50.51
Reference GC (%)	50.50
N50	17940
NG50	18317
N75	9618
NG75	9821
L50	95
LG50	94
L75	200
LG75	197
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.911
Duplication ratio	1.009
# N's per 100 kbp	0.00
# mismatches per 100 kbp	8.26
# indels per 100 kbp	0.00
Largest alignment	67238
NA50	17940
NGA50	18317
NA75	9618
NGA75	9821
LA50	95
LGA50	94
LA75	200
LGA75	197

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

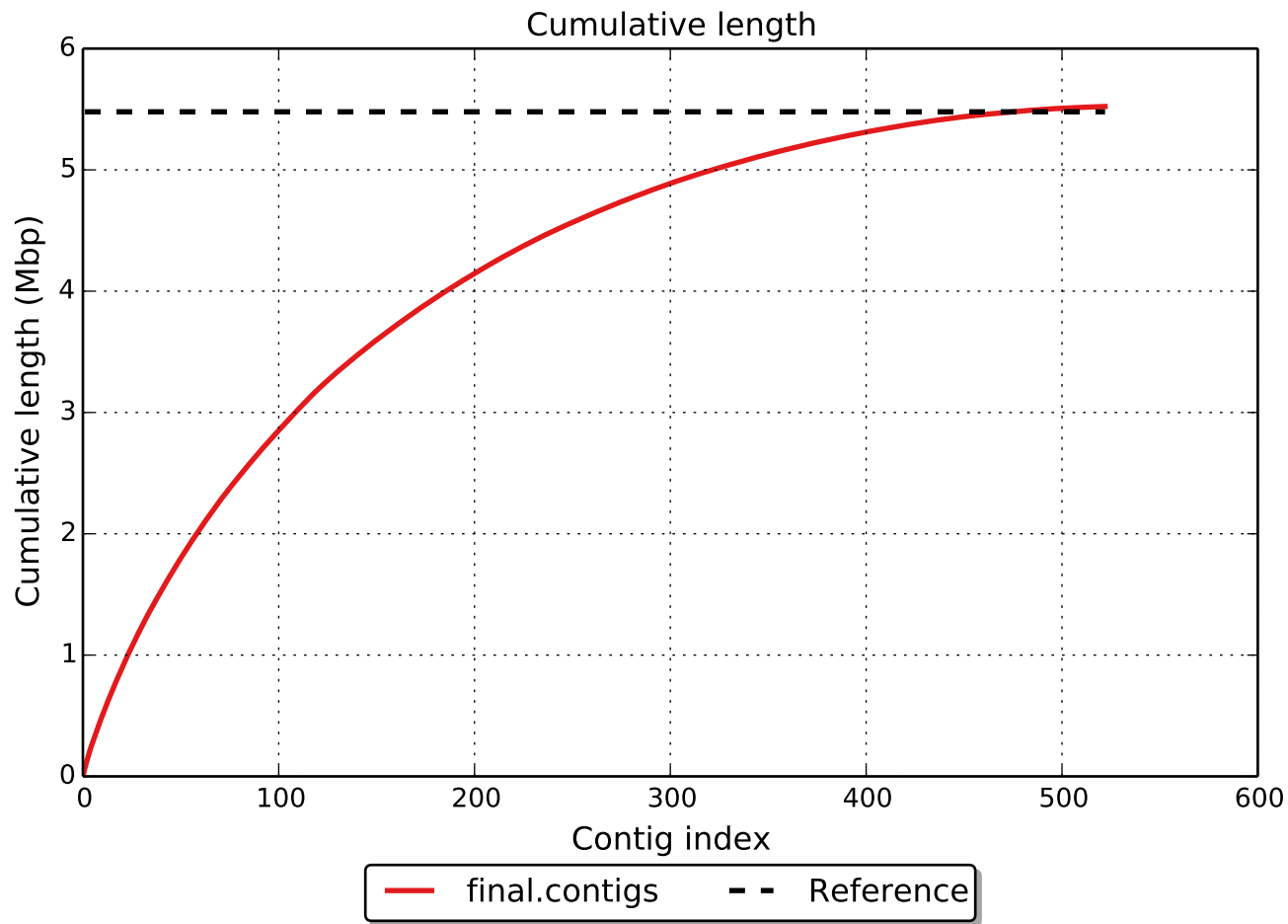
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	452
# indels	0
# short indels	0
# long indels	0
Indels length	0

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).

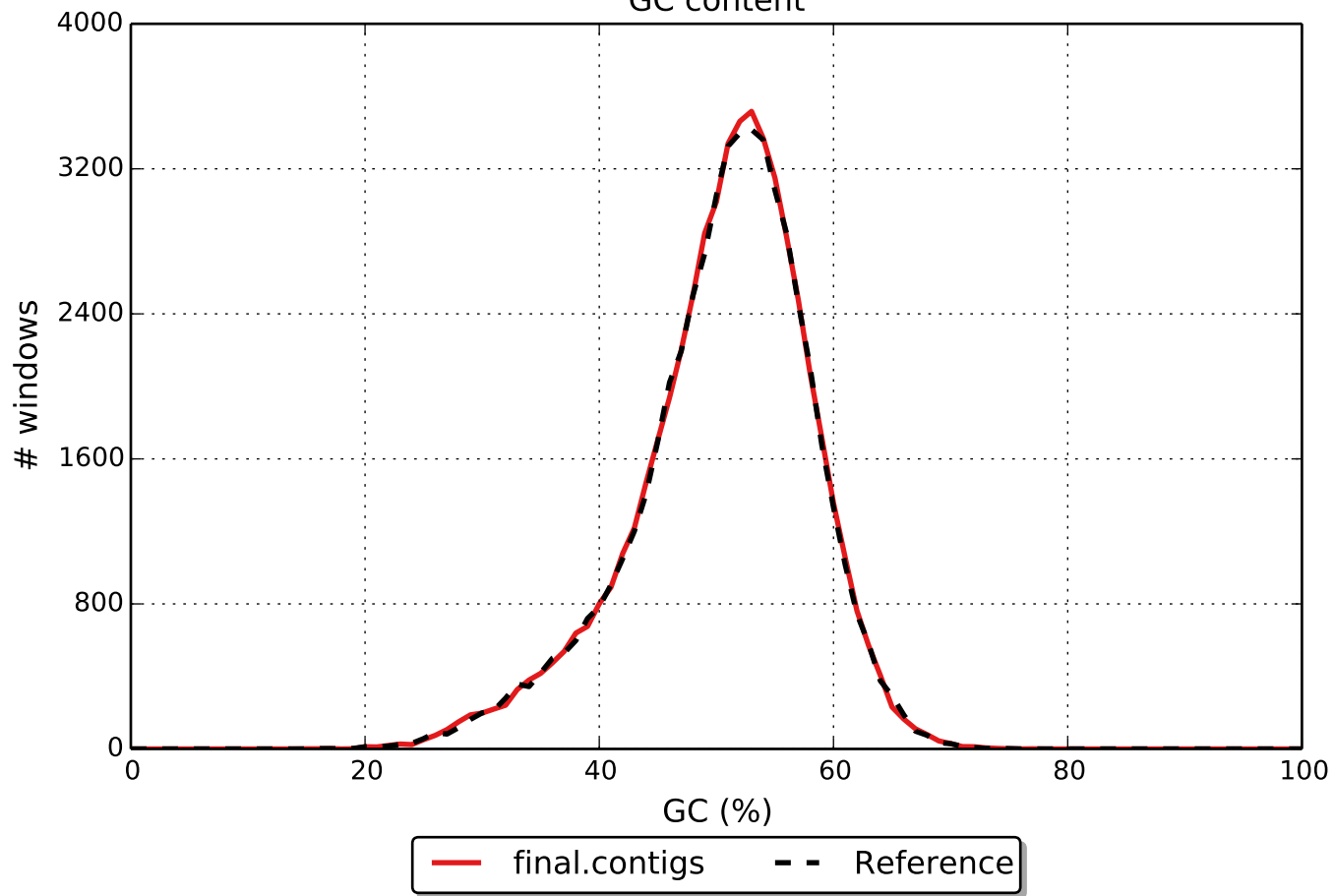
Unaligned report

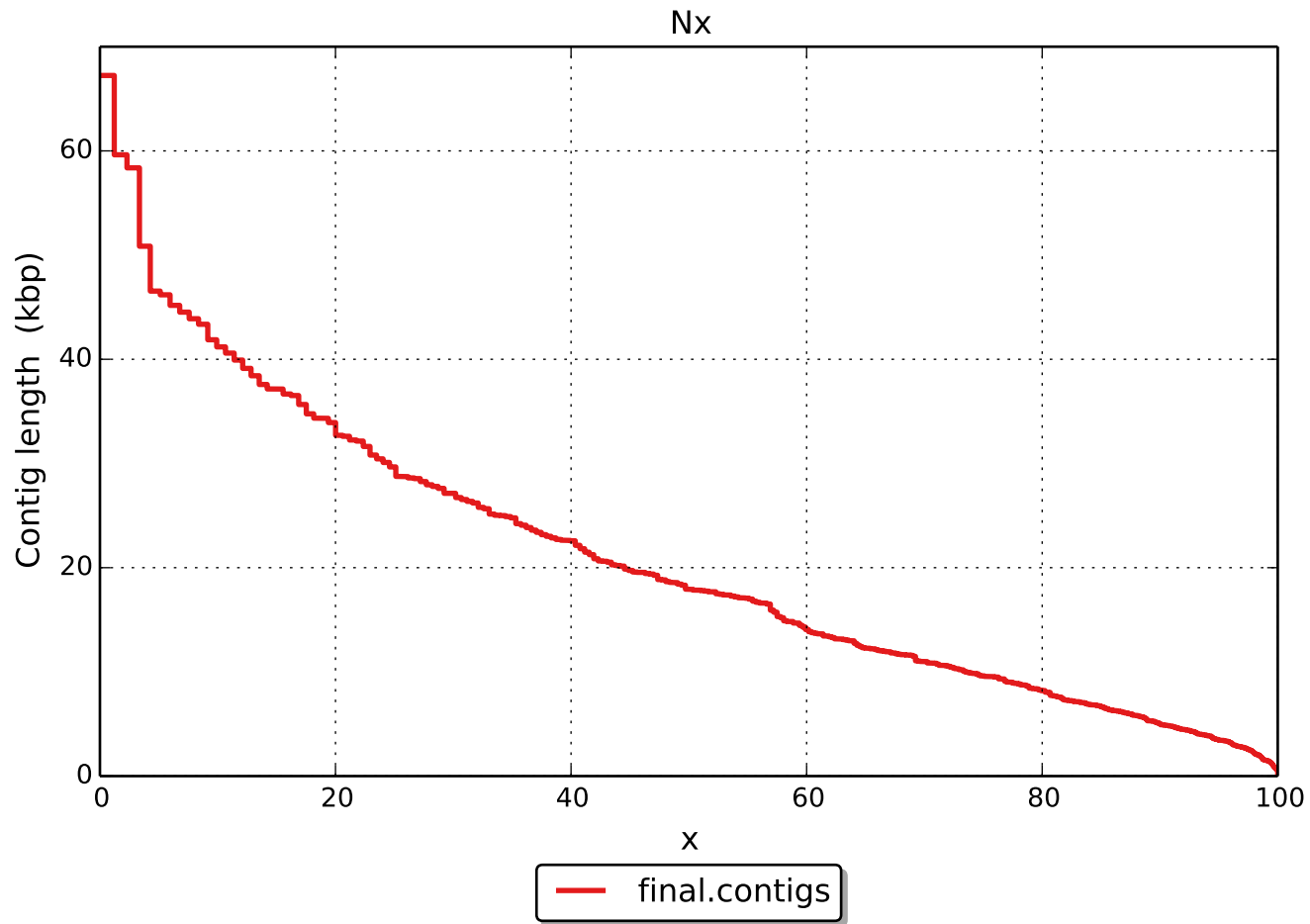
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

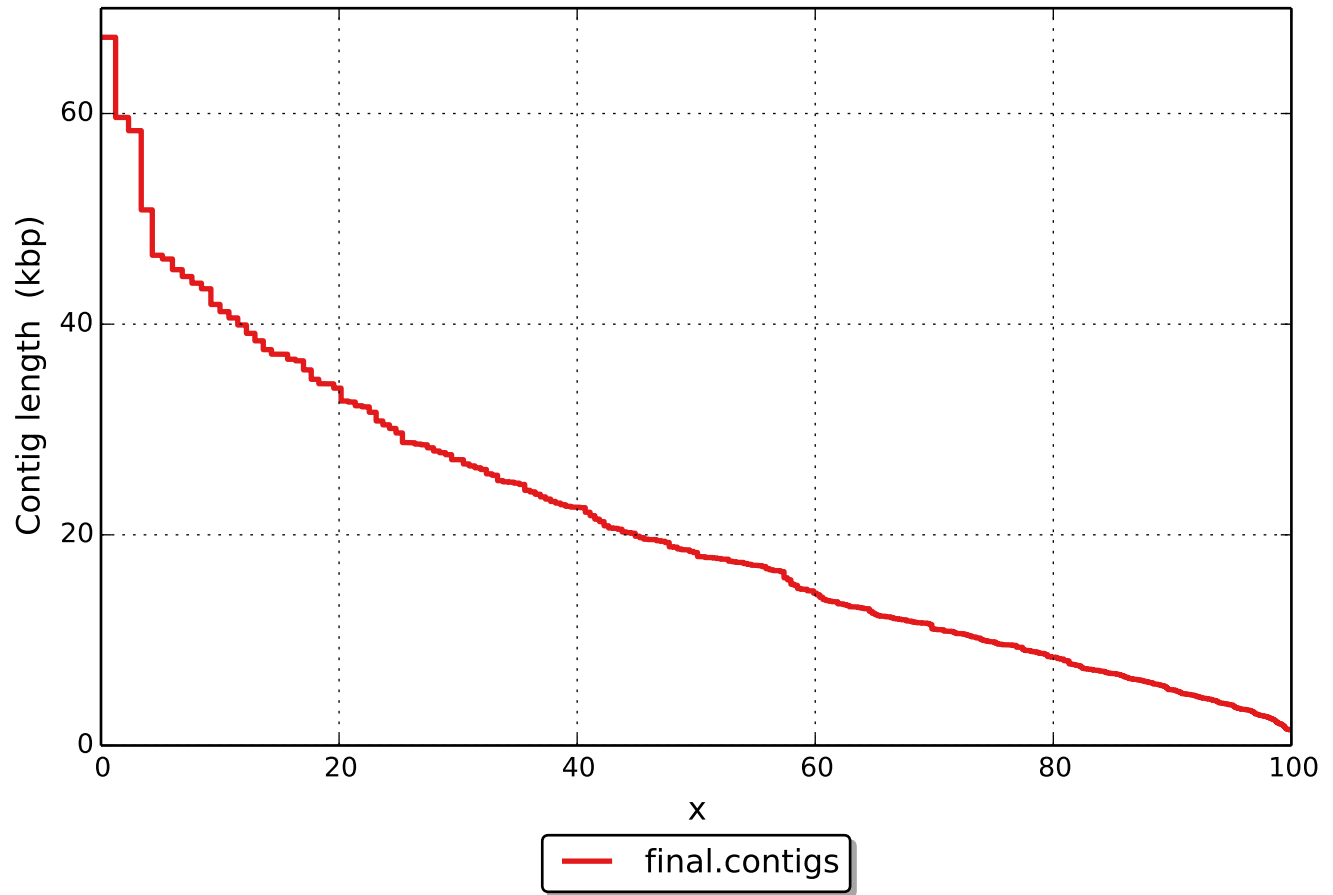


GC content



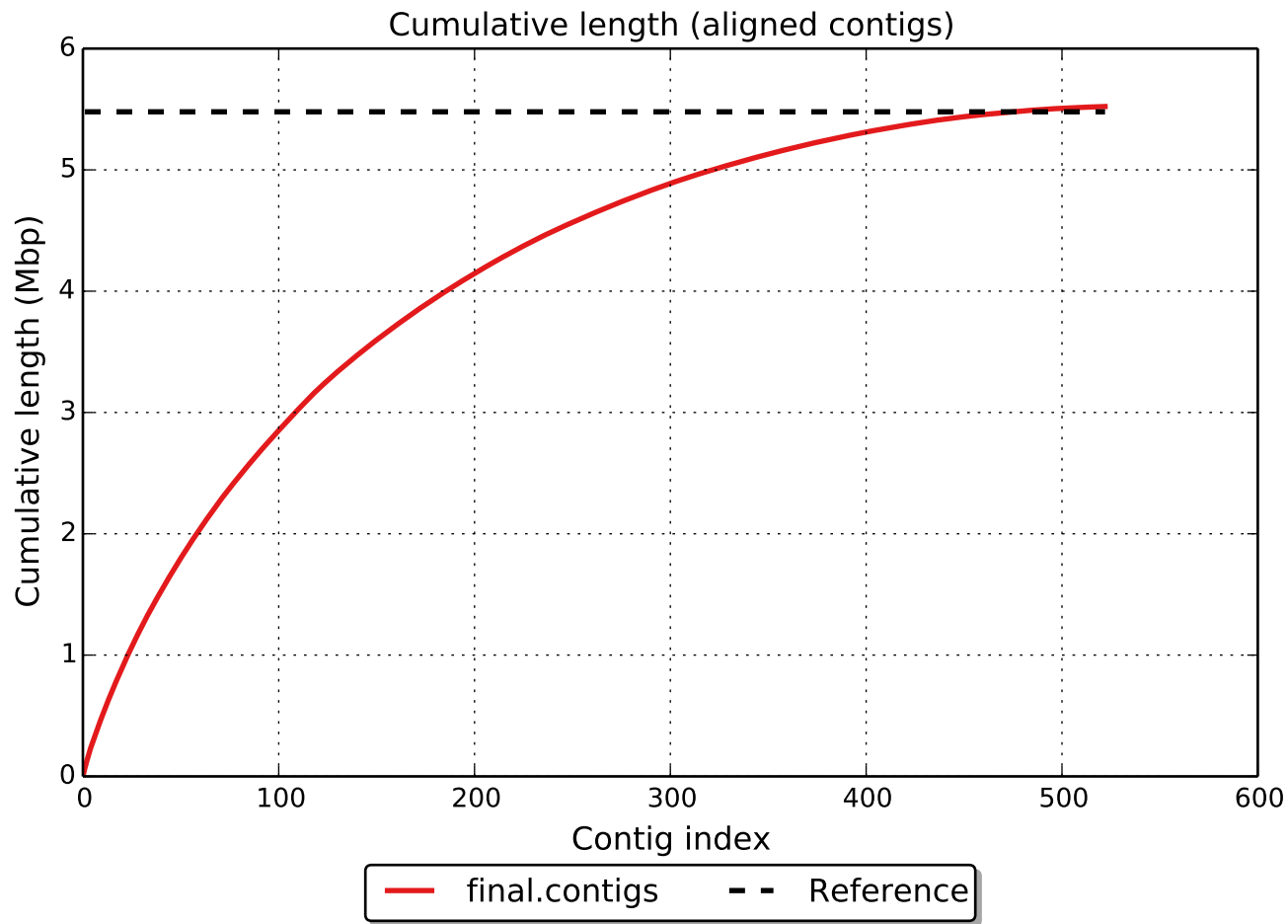


NGx

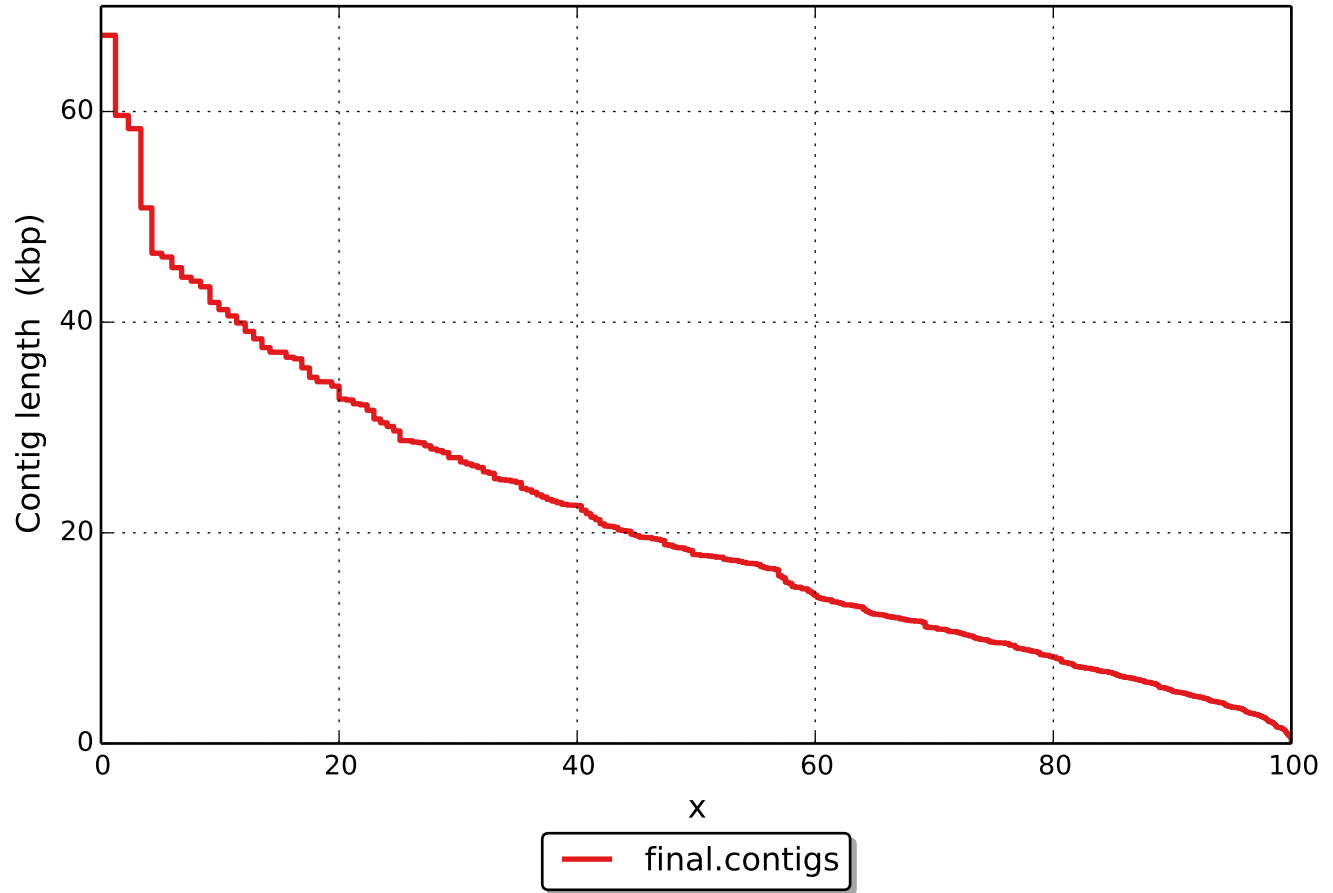


Misassemblies





NAx



NGAx

