

Report

	final.contigs
# contigs (>= 0 bp)	85
# contigs (>= 1000 bp)	81
Total length (>= 0 bp)	1290586
Total length (>= 1000 bp)	1288922
# contigs	83
Largest contig	60549
Total length	1289930
Reference length	1283598
GC (%)	26.31
Reference GC (%)	26.31
N50	23452
NG50	23452
N75	14400
NG75	14400
L50	17
LG50	17
L75	34
LG75	34
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.978
Duplication ratio	1.005
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.23
# indels per 100 kbp	0.00
Largest alignment	60549
NA50	23452
NGA50	23452
NA75	14400
NGA75	14400
LA50	17
LGA50	17
LA75	34
LGA75	34

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	0
# mismatches	3
# indels	0
# short indels	0
# long indels	0
Indels length	0

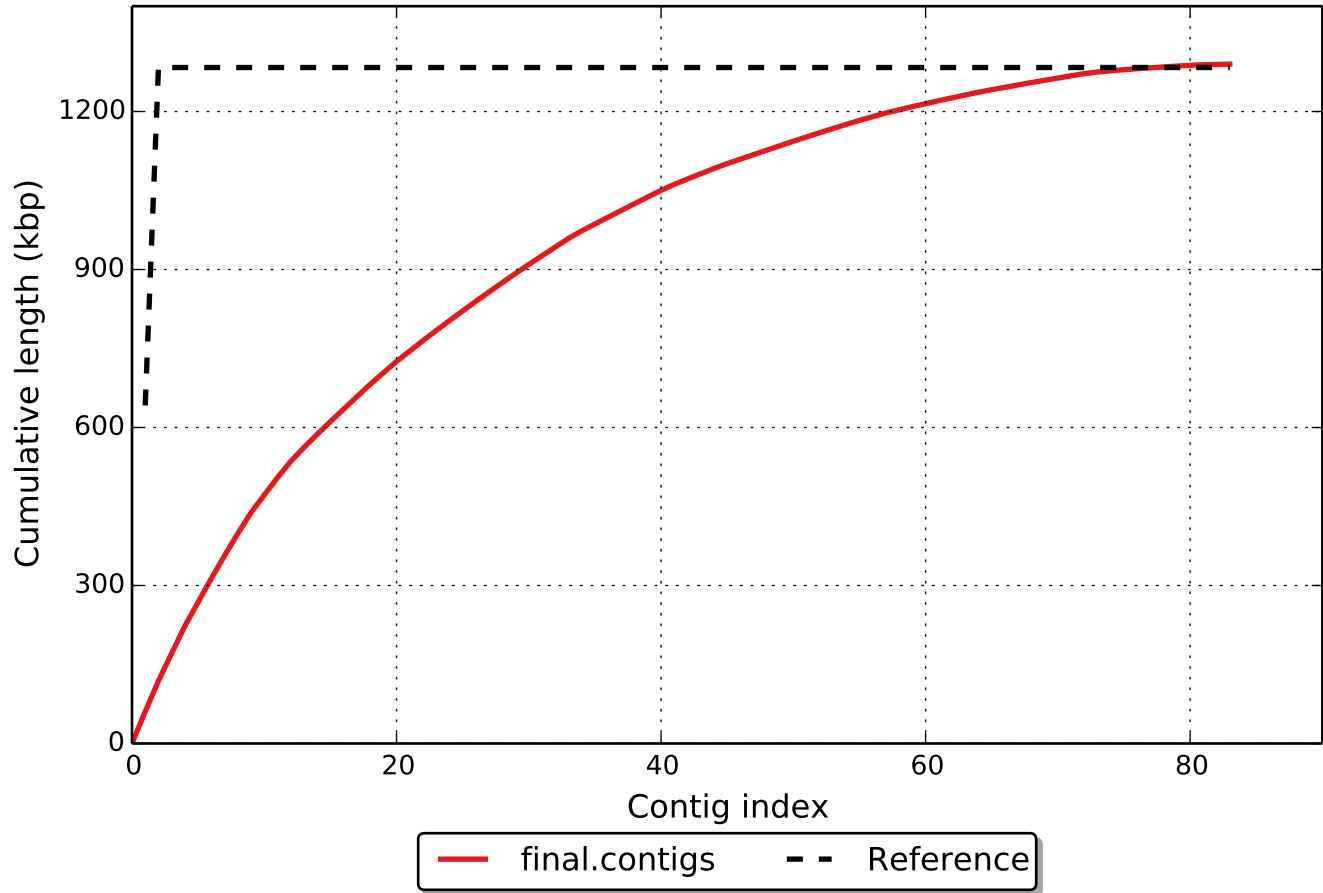
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

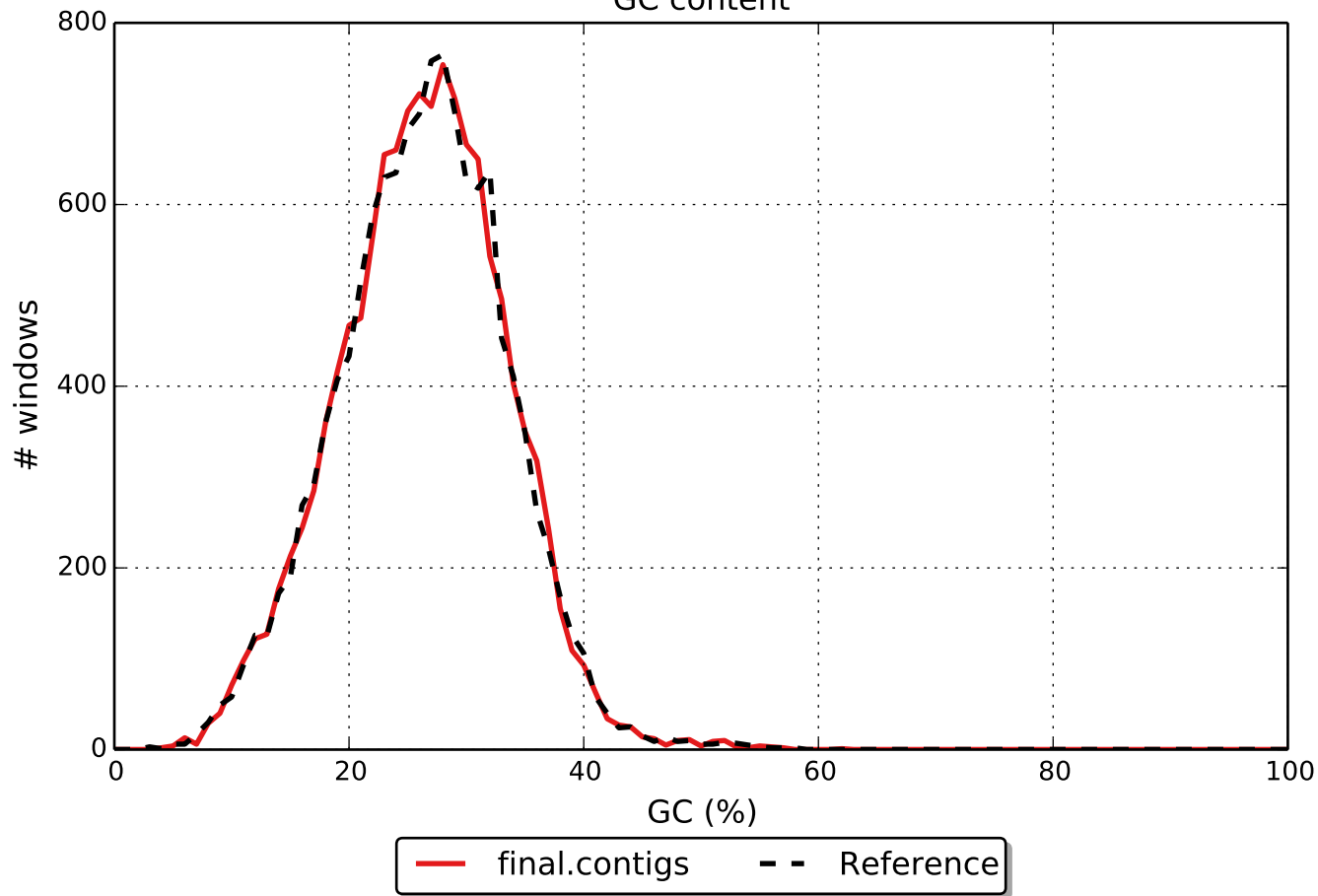
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

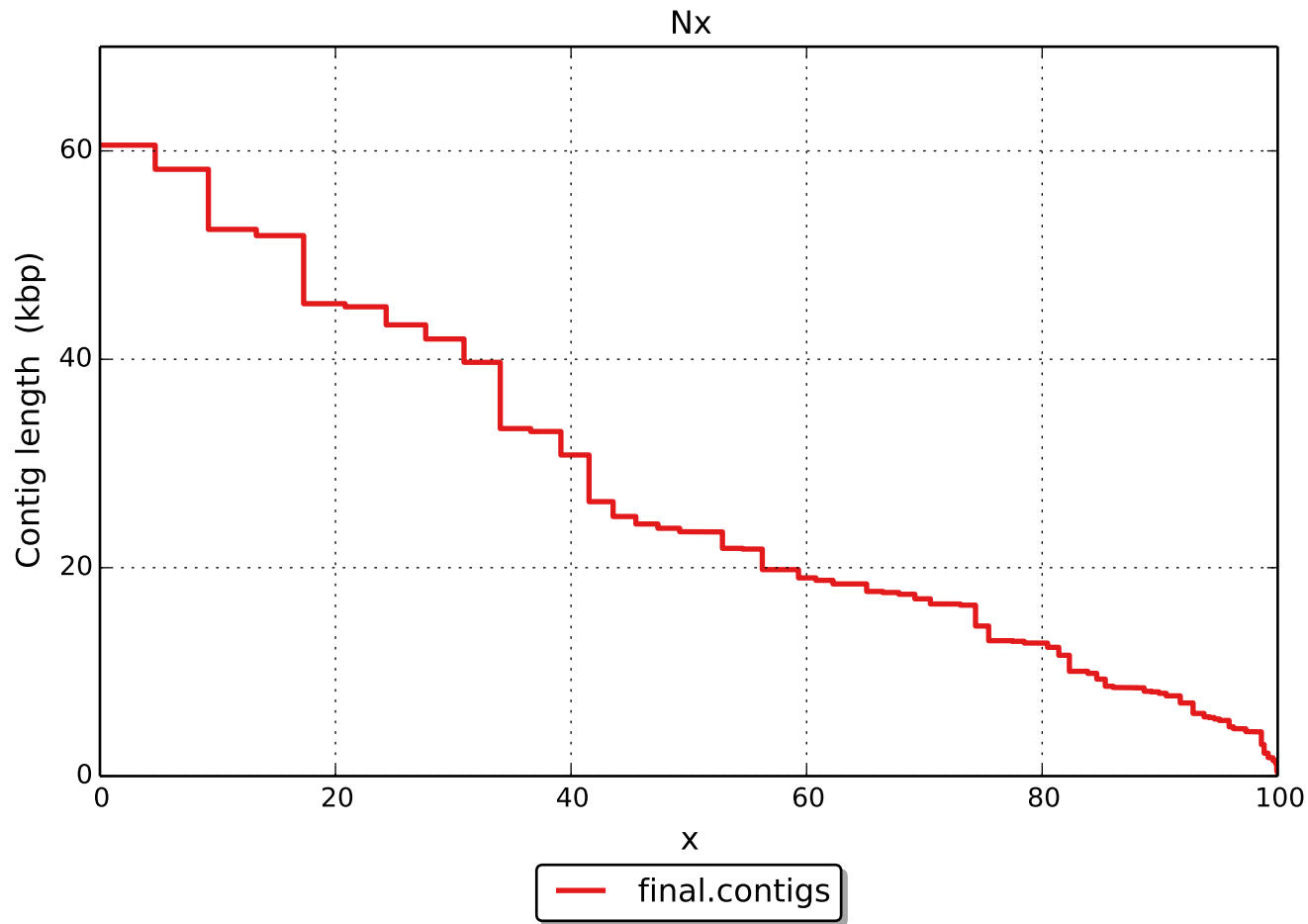
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Cumulative length

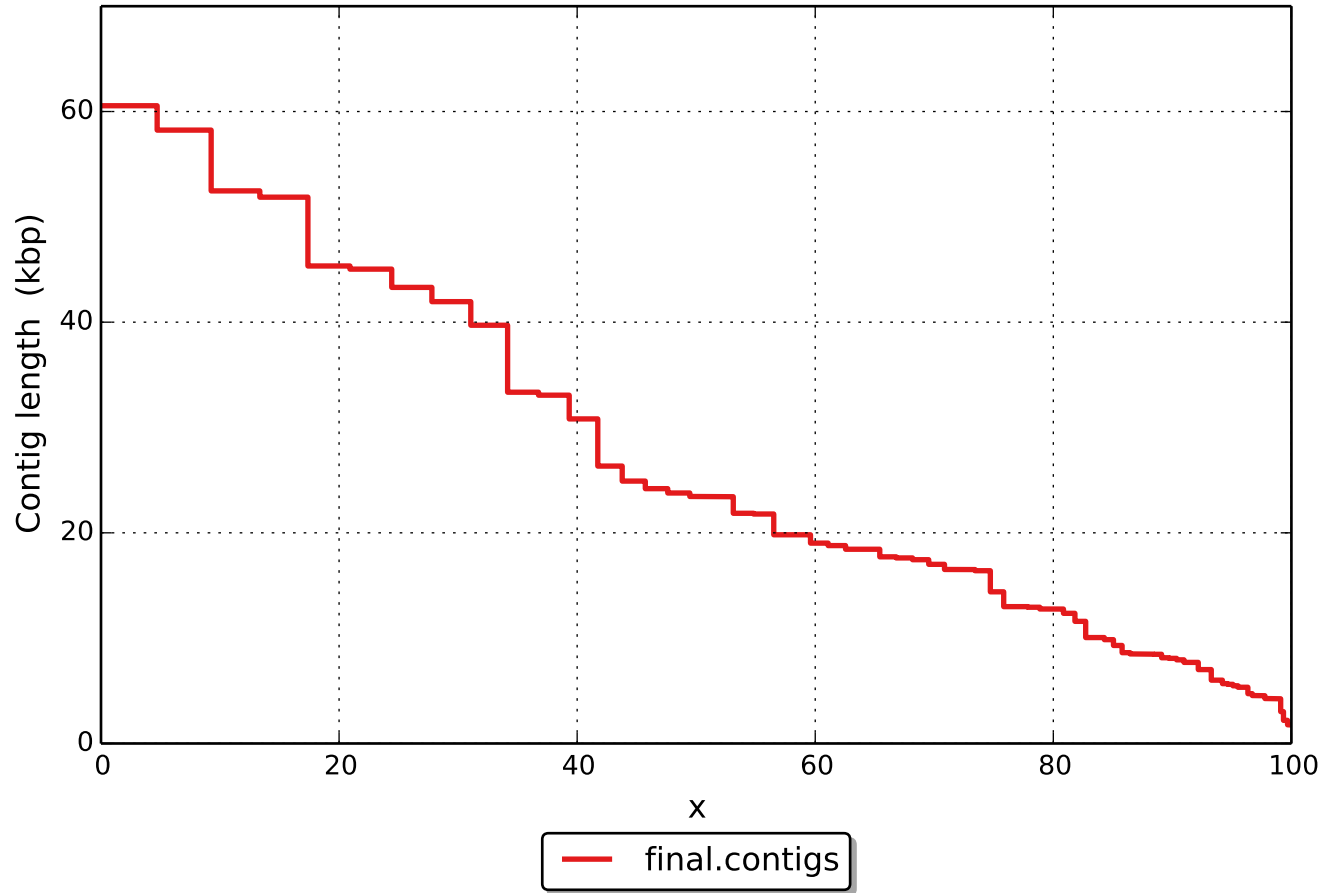


GC content





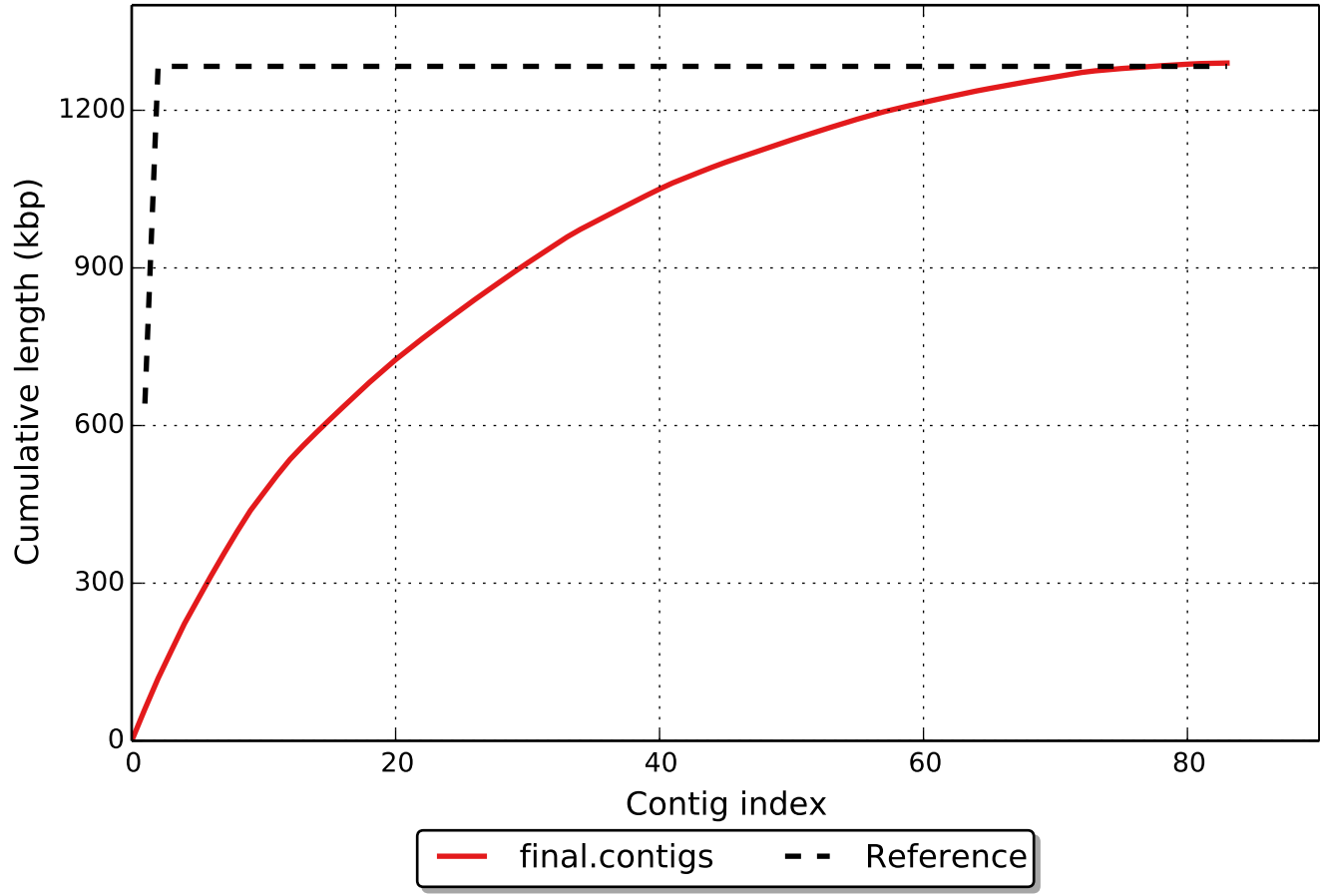
NGx



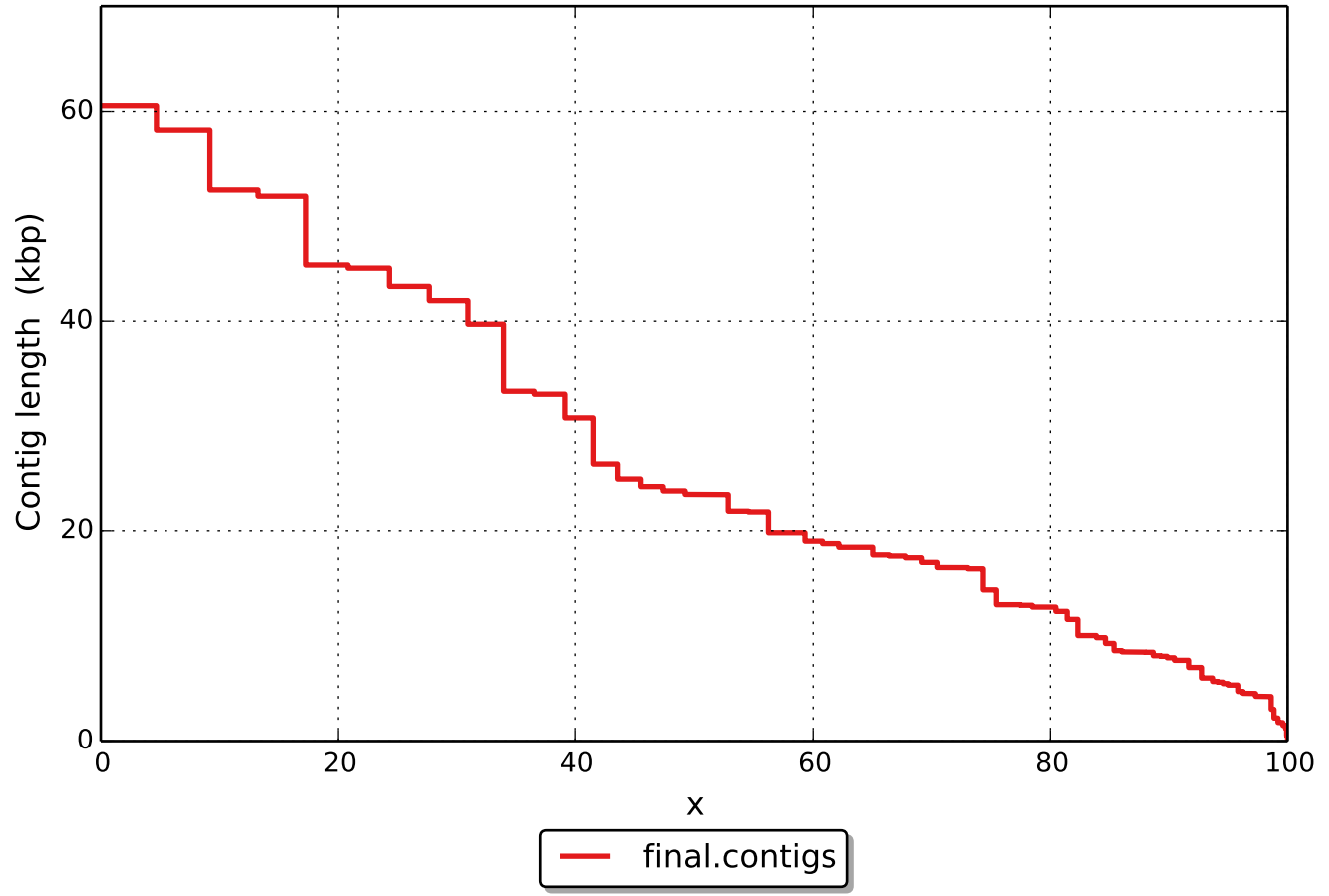
Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

