

Report

	final.contigs
# contigs (≥ 0 bp)	1147
# contigs (≥ 1000 bp)	425
Total length (≥ 0 bp)	1183787
Total length (≥ 1000 bp)	670223
# contigs	1147
Largest contig	4490
Total length	1183787
Reference length	641799
GC (%)	26.32
Reference GC (%)	26.30
N50	1117
NG50	1639
N75	776
NG75	1266
L50	351
LG50	145
L75	675
LG75	258
# misassemblies	21
# misassembled contigs	21
Misassembled contigs length	29556
# local misassemblies	0
# unaligned contigs	0 + 2 part
Unaligned length	299
Genome fraction (%)	91.543
Duplication ratio	2.014
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1406.25
# indels per 100 kbp	1.02
Largest alignment	4490
NA50	1060
NGA50	1579
NA75	720
NGA75	1225
LA50	365
LGA50	150
LA75	706
LGA75	268

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

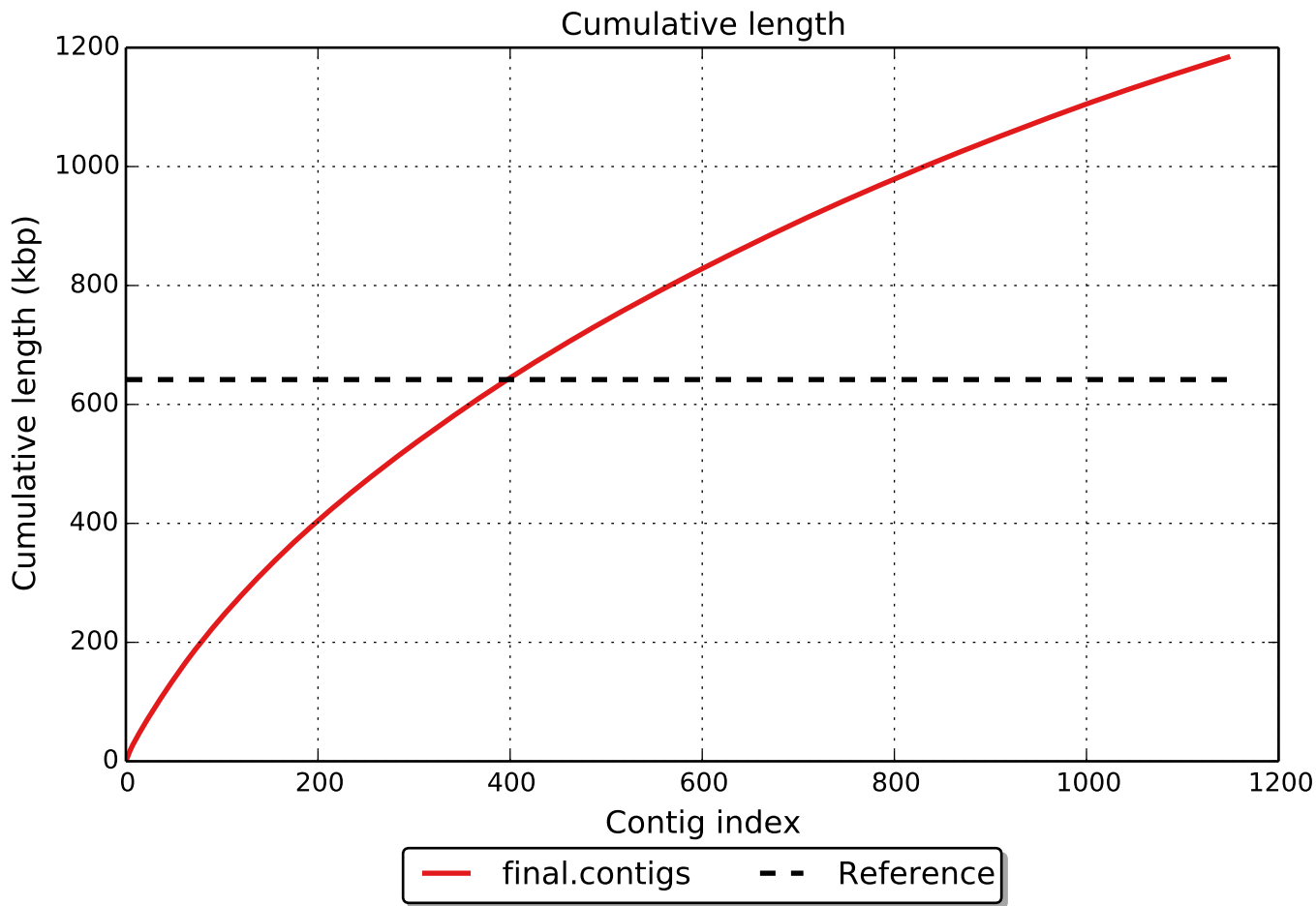
	final.contigs
# misassemblies	21
# relocations	20
# translocations	0
# inversions	1
# possibly misassembled contigs	0
# misassembled contigs	21
Misassembled contigs length	29556
# local misassemblies	0
# mismatches	8262
# indels	6
# short indels	6
# long indels	0
Indels length	6

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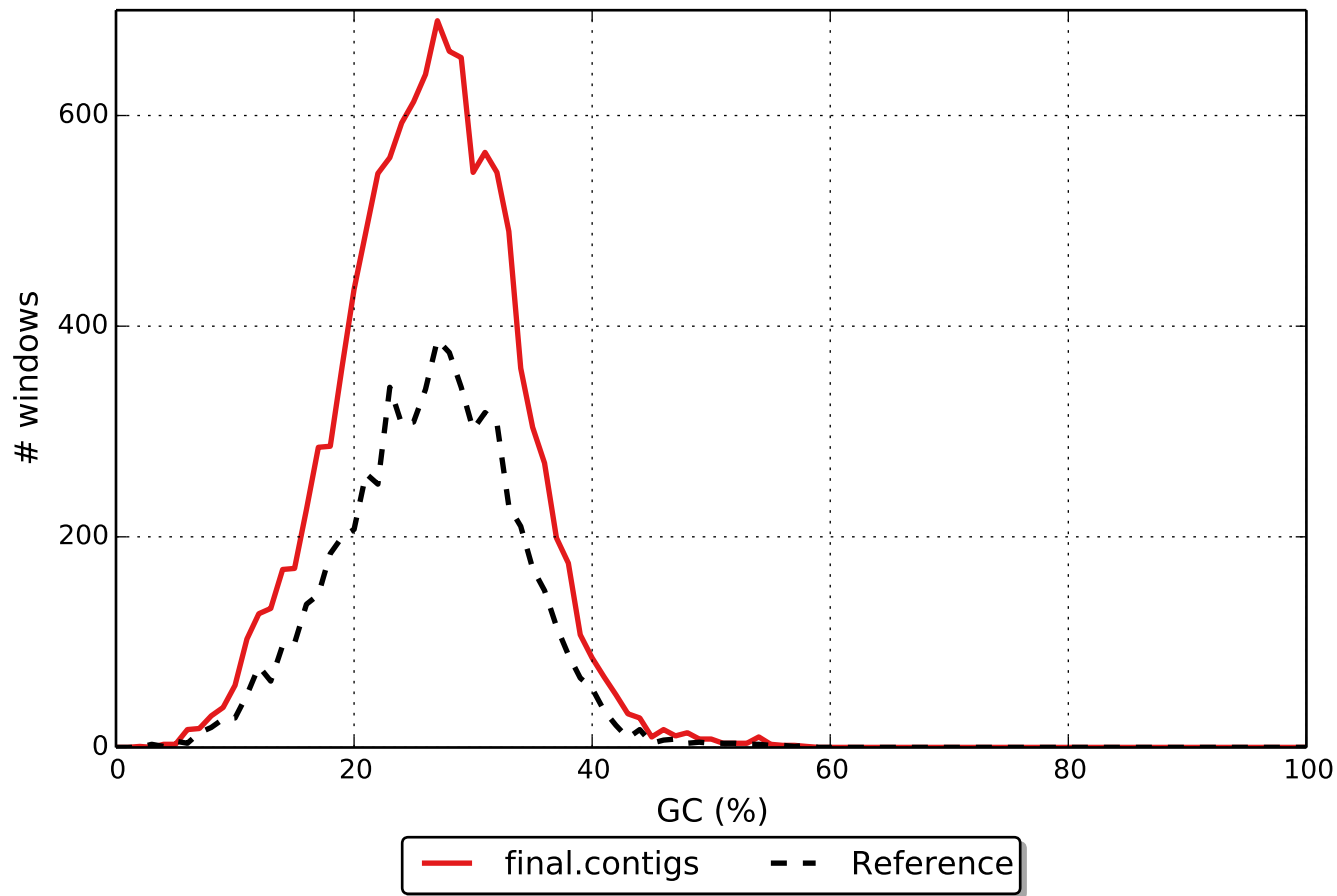
Unaligned report

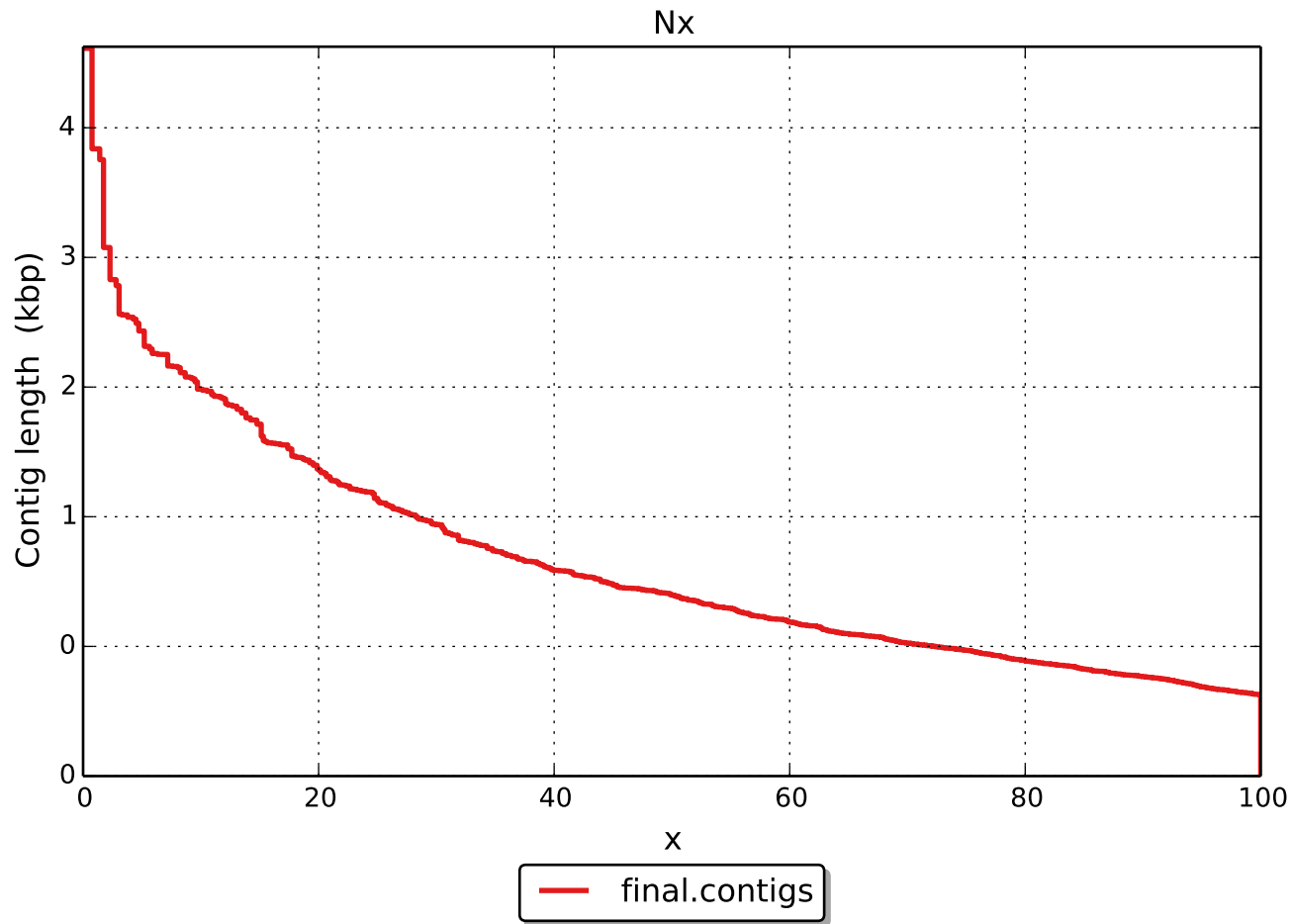
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	0
Partially unaligned length	299
# N's	0

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).

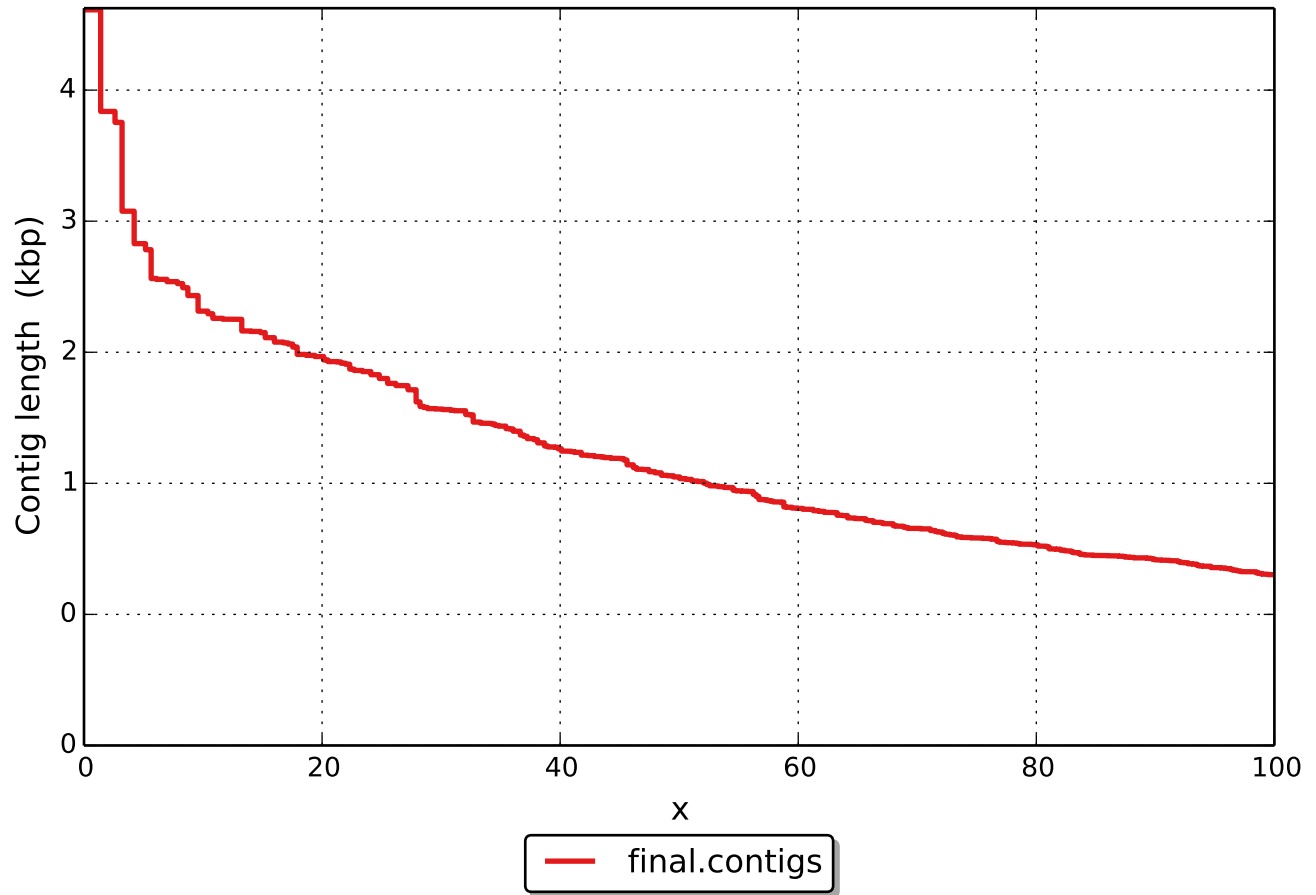


GC content

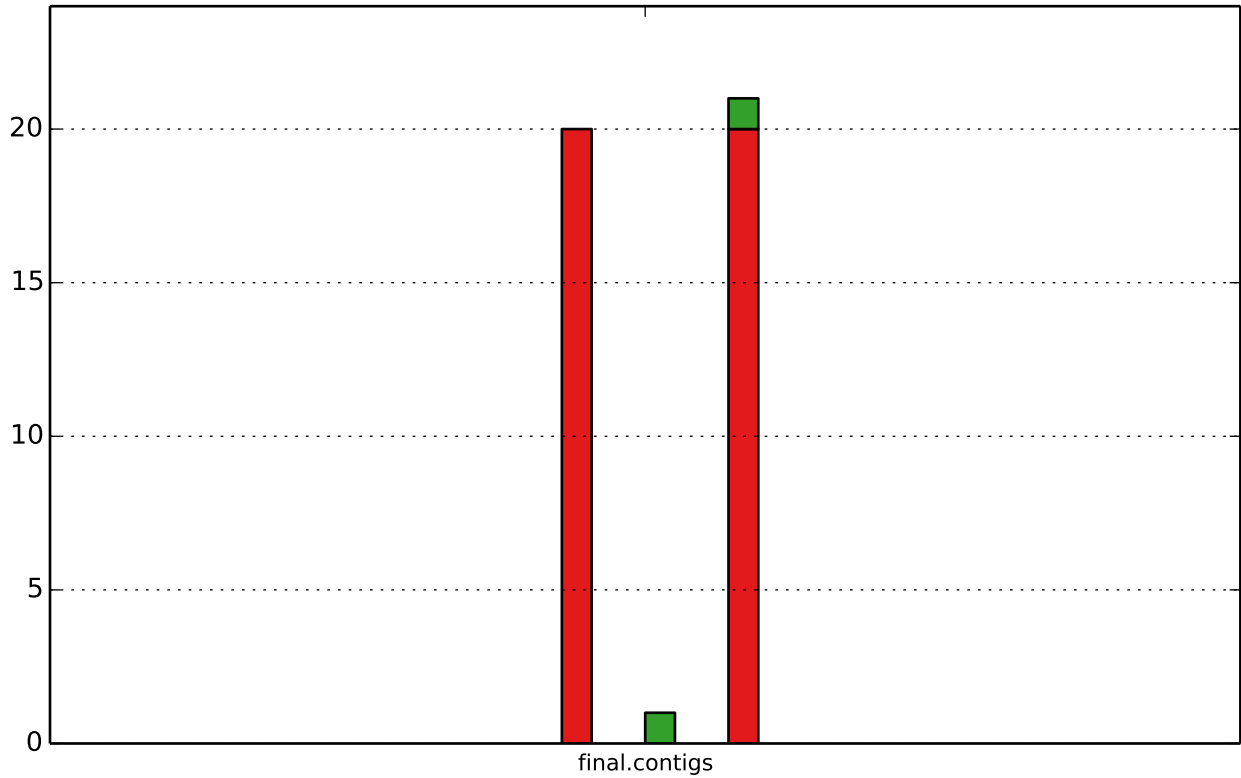




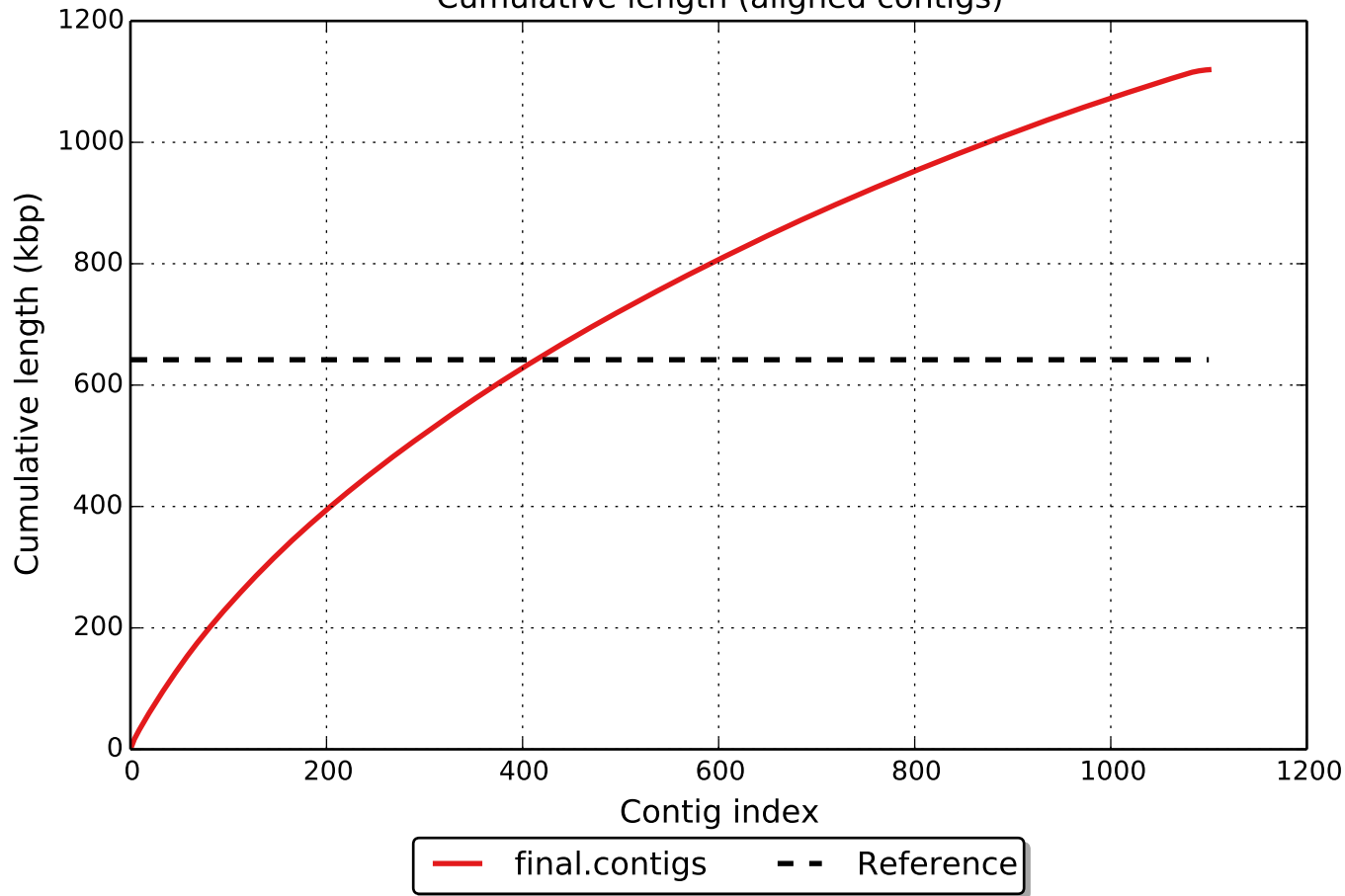
NGx



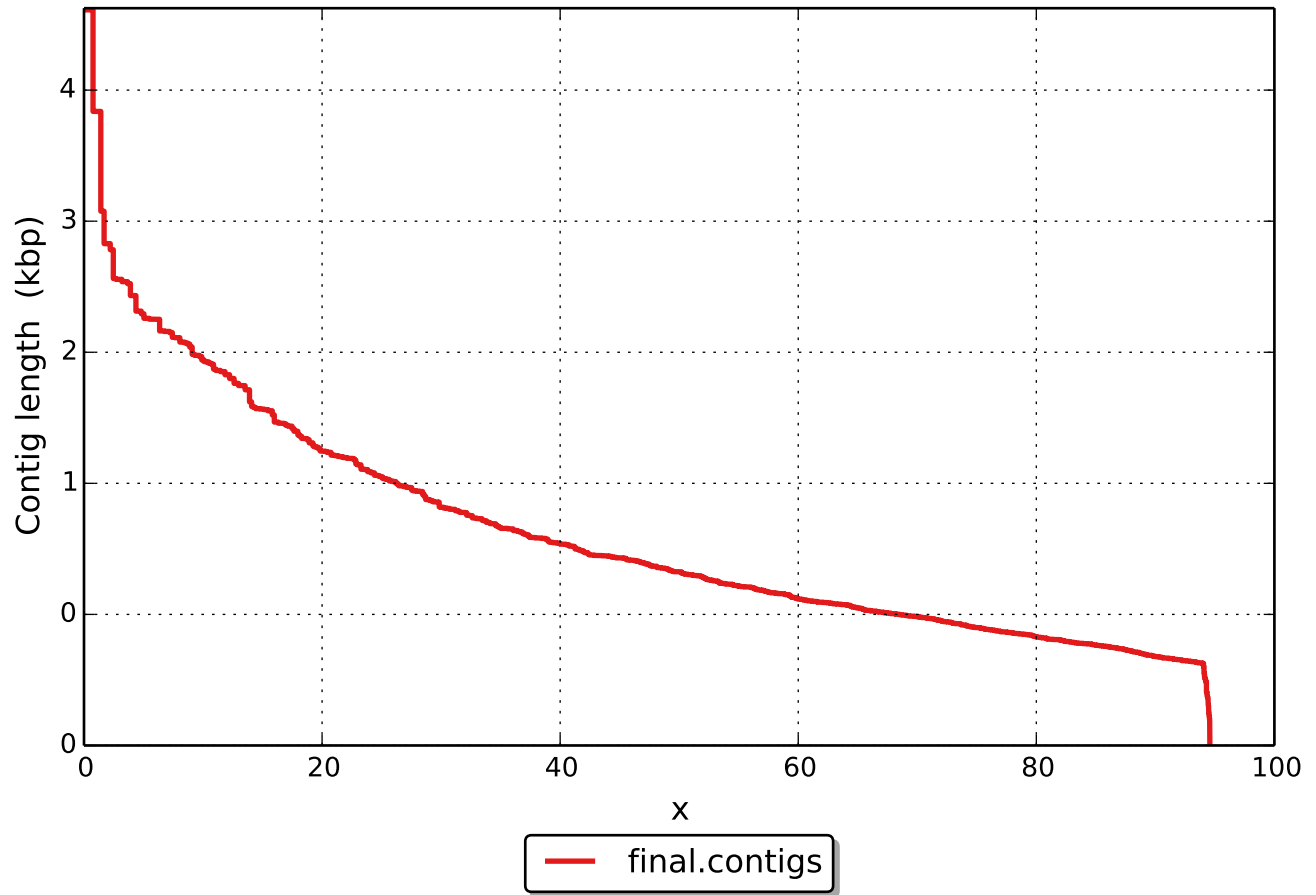
Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

