

Report

	final.contigs
# contigs (≥ 0 bp)	279
# contigs (≥ 1000 bp)	270
Total length (≥ 0 bp)	3709906
Total length (≥ 1000 bp)	3703431
# contigs	279
Largest contig	74321
Total length	3709906
Reference length	1892775
GC (%)	32.27
Reference GC (%)	32.28
N50	21538
NG50	33551
N75	12583
NG75	26655
L50	56
LG50	22
L75	111
LG75	38
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	116 + 54 part
Unaligned length	1799836
Genome fraction (%)	99.972
Duplication ratio	1.009
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.42
# indels per 100 kbp	0.00
Largest alignment	63635
NA50	4008
NGA50	27696
NGA75	18440
LA50	90
LGA50	25
LGA75	46

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

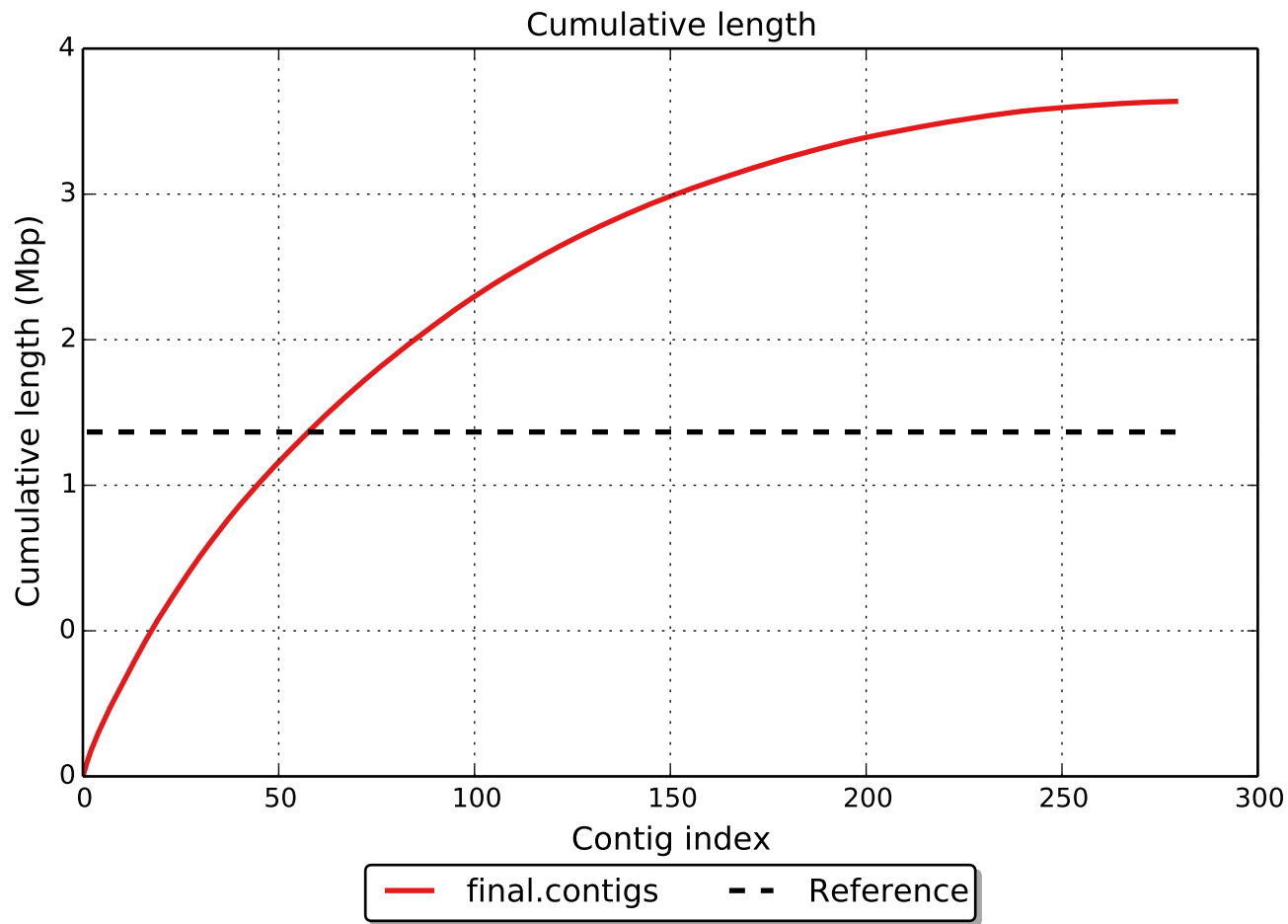
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	8
# indels	0
# short indels	0
# long indels	0
Indels length	0

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).

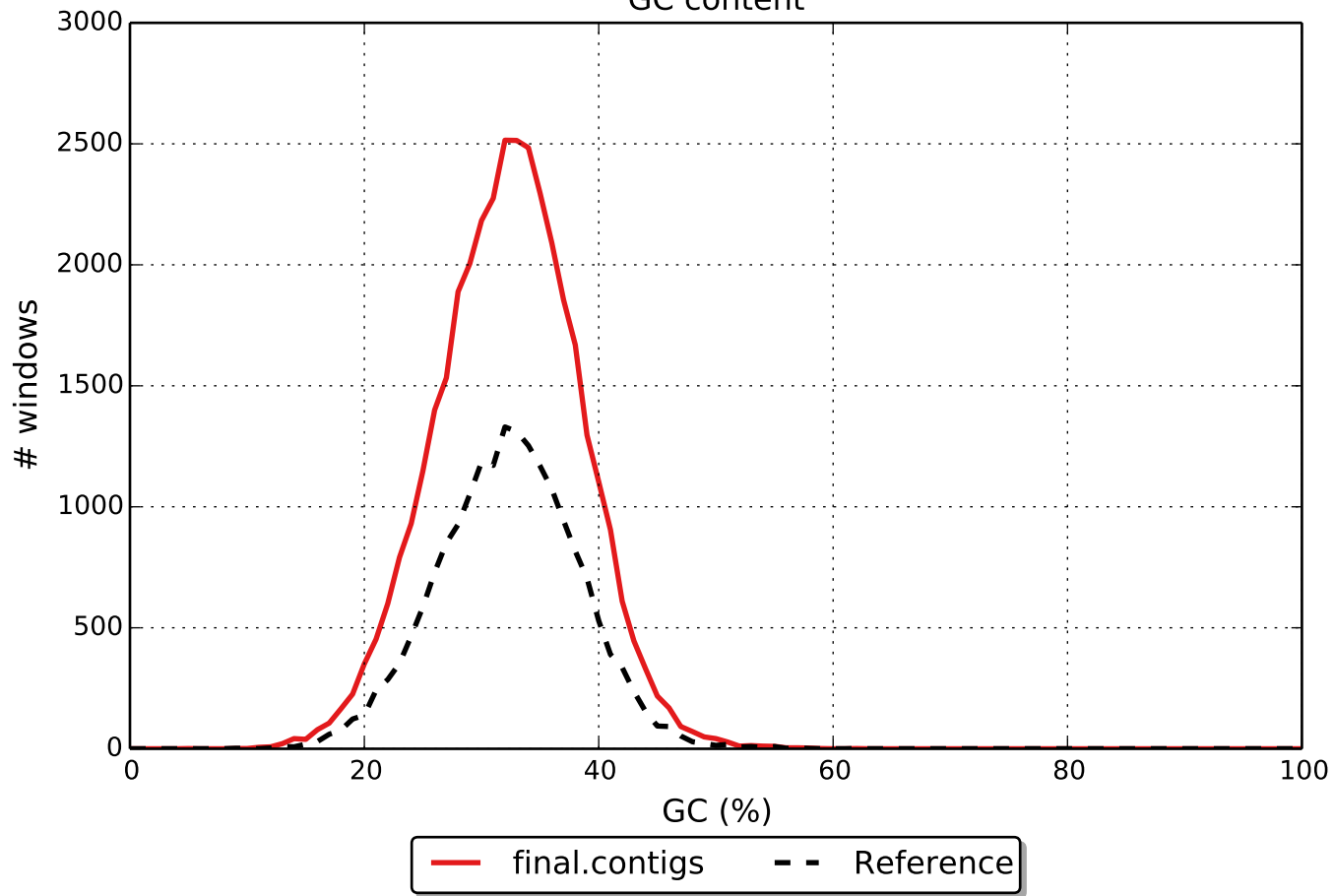
Unaligned report

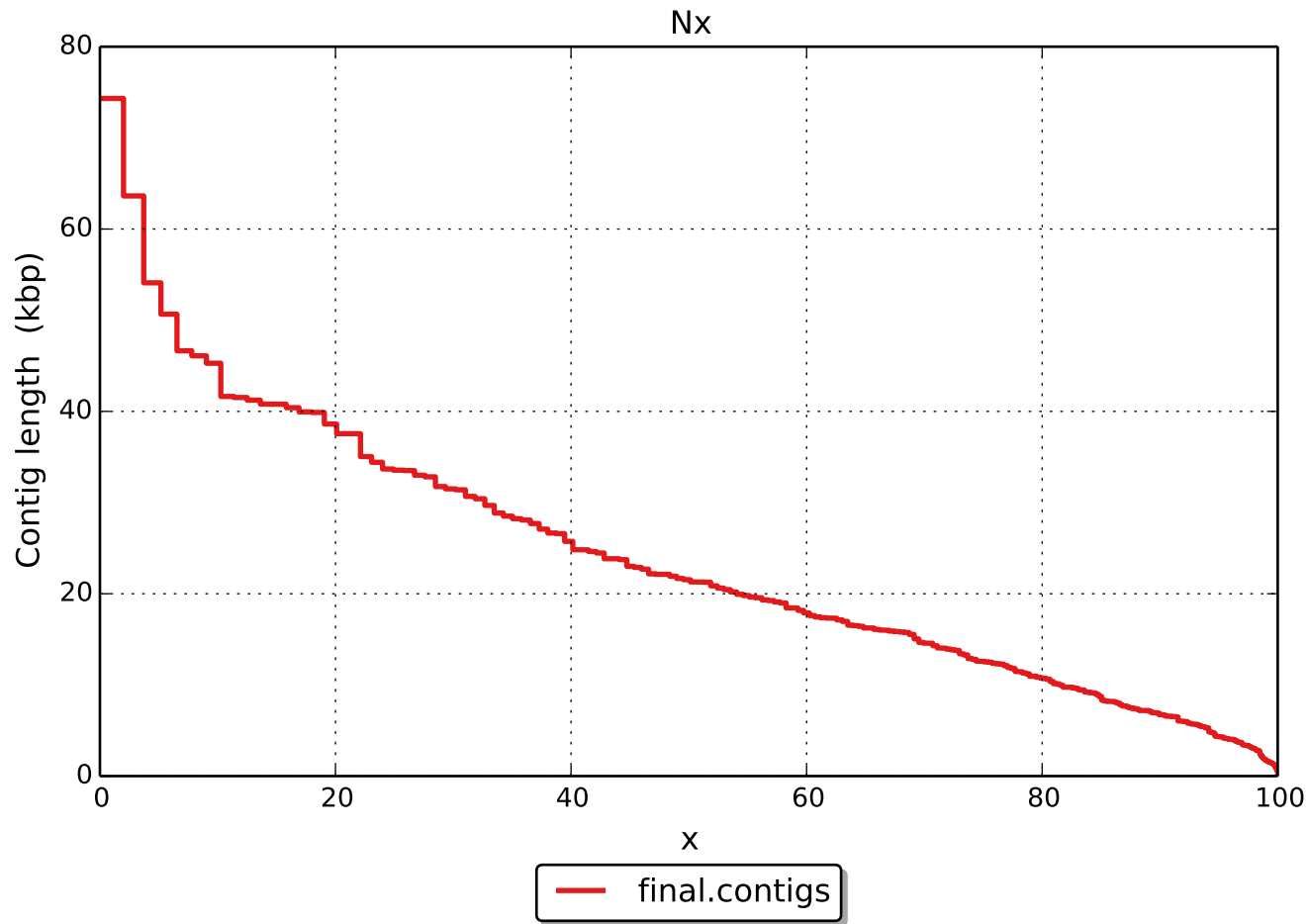
	final.contigs
# fully unaligned contigs	116
Fully unaligned length	1126186
# partially unaligned contigs	54
# with misassembly	7
# both parts are significant	0
Partially unaligned length	673650
# N's	0

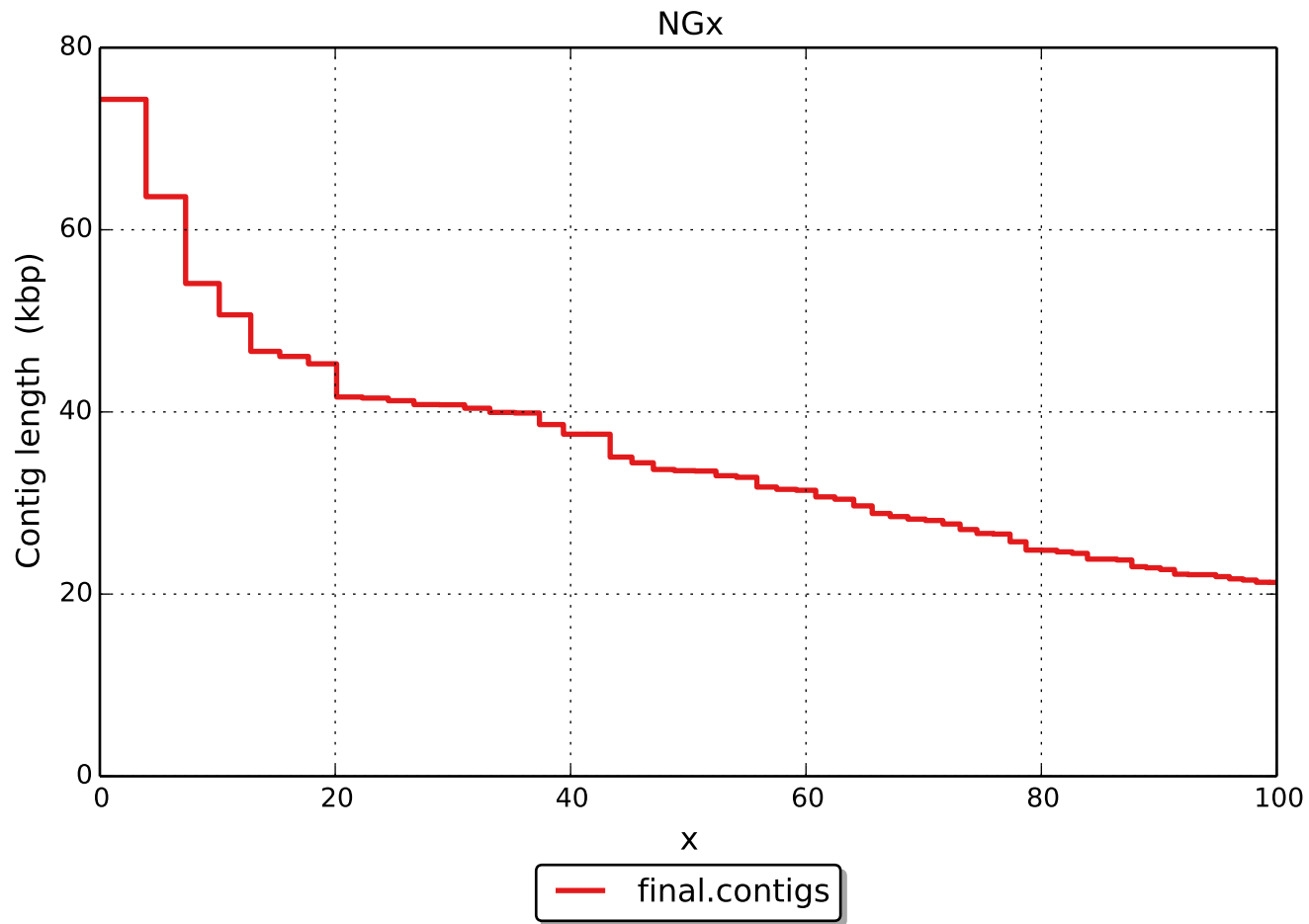
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



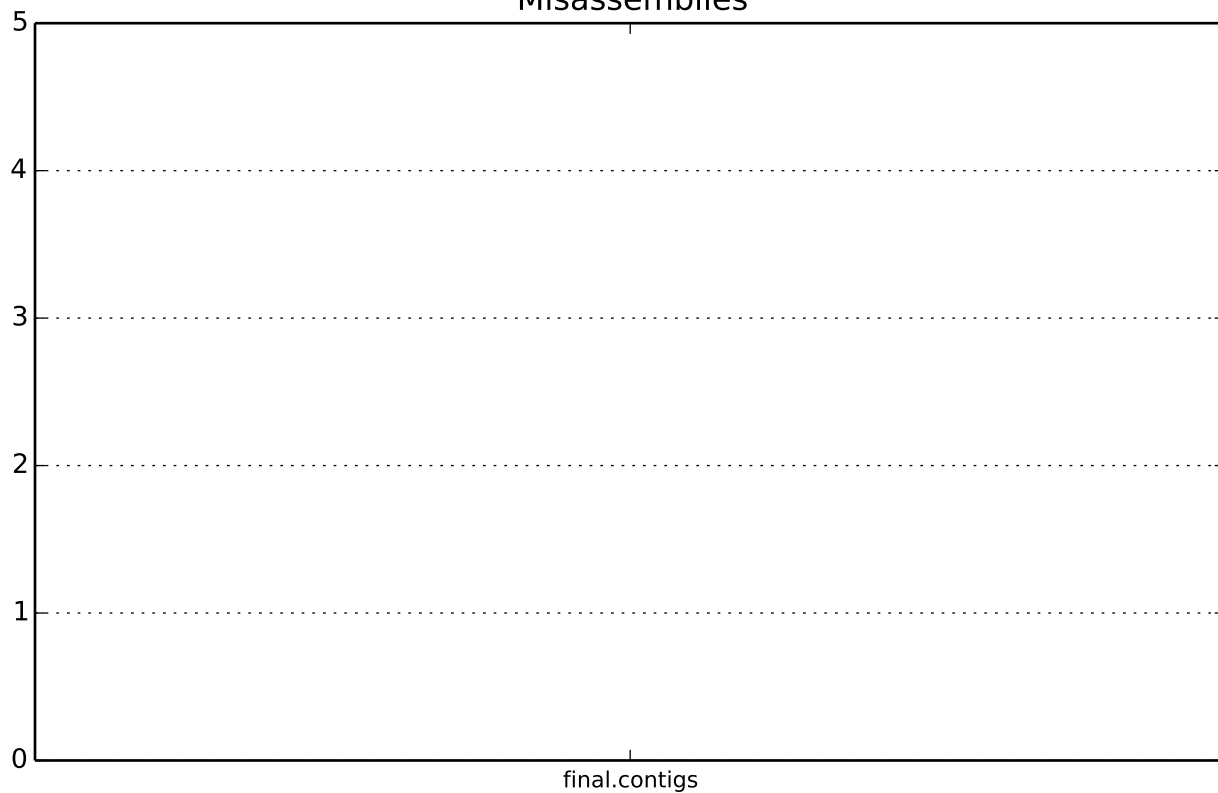
GC content



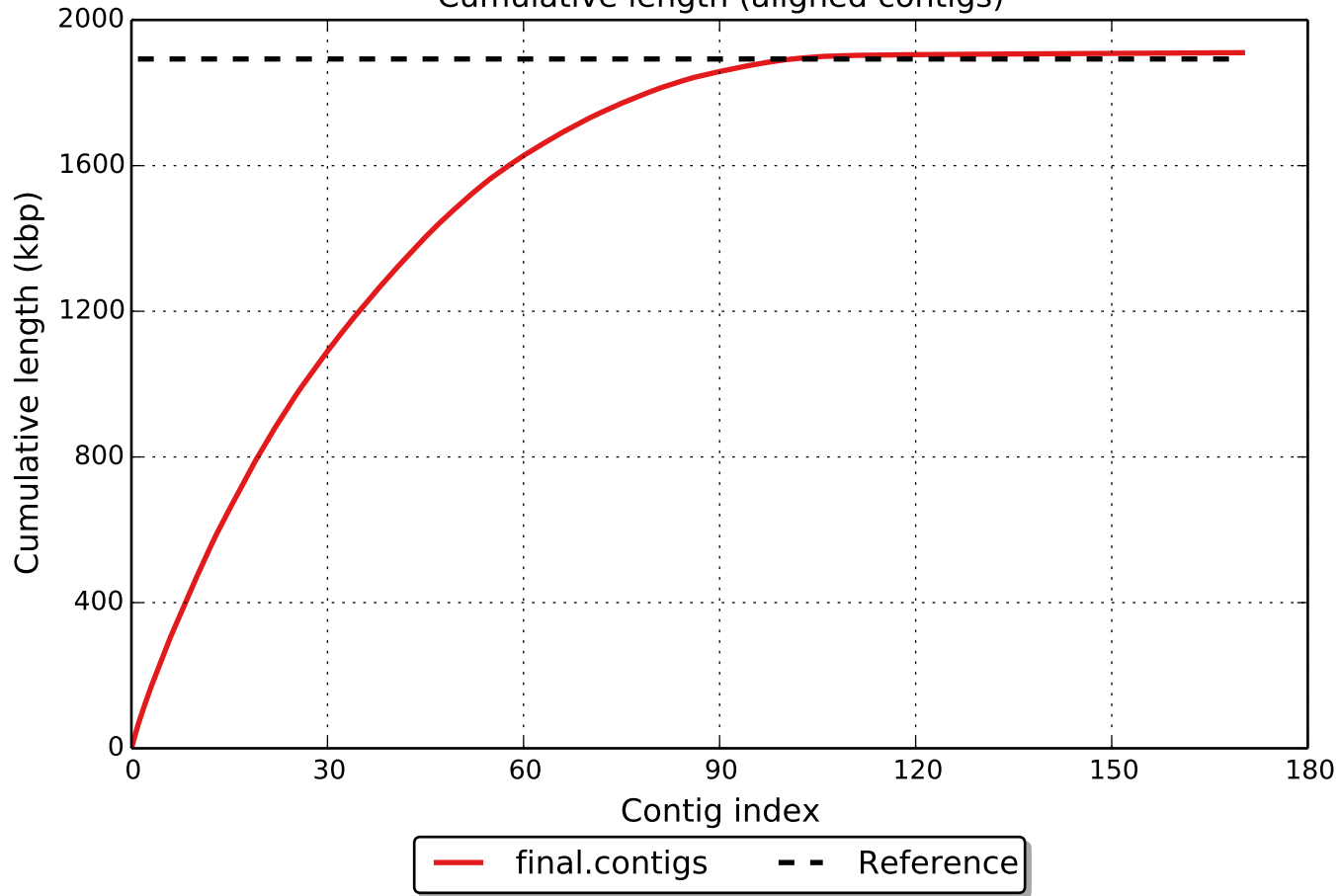




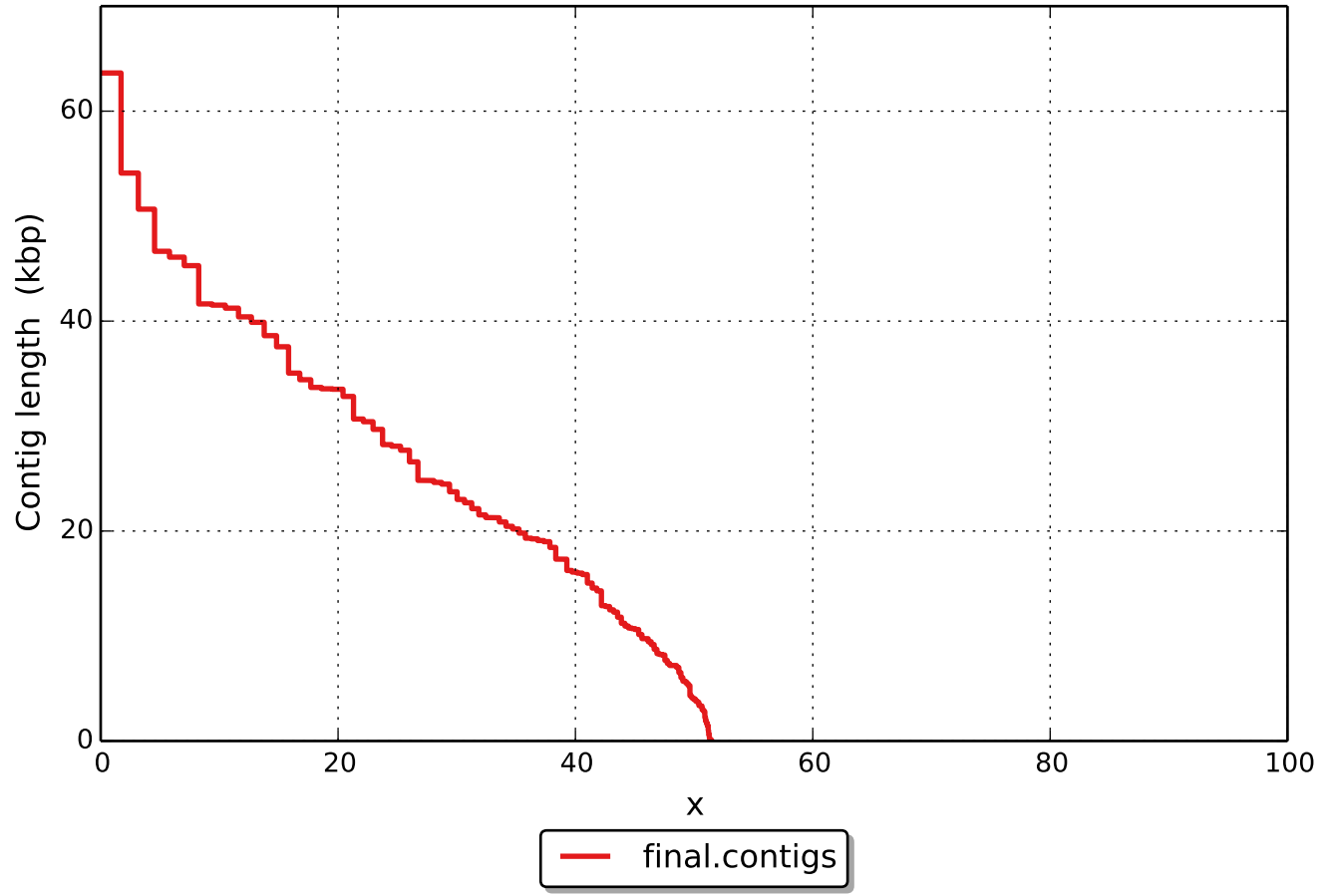
Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

