

Report

	final.contigs
# contigs (>= 1000 bp)	930
# contigs (>= 5000 bp)	8
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	1584081
Total length (>= 5000 bp)	46837
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	2882
Largest contig	6821
Total length	2917017
Reference length	4857432
GC (%)	52.10
Reference GC (%)	52.22
N50	1083
NG50	634
N75	709
L50	810
LG50	2014
L75	1655
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 1 part
Unaligned length	57
Genome fraction (%)	57.279
Duplication ratio	1.048
# N's per 100 kbp	0.00
# mismatches per 100 kbp	345.87
# indels per 100 kbp	0.07
Largest alignment	6821
NA50	1083
NGA50	634
NA75	709
LA50	810
LGA50	2014
LA75	1655

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

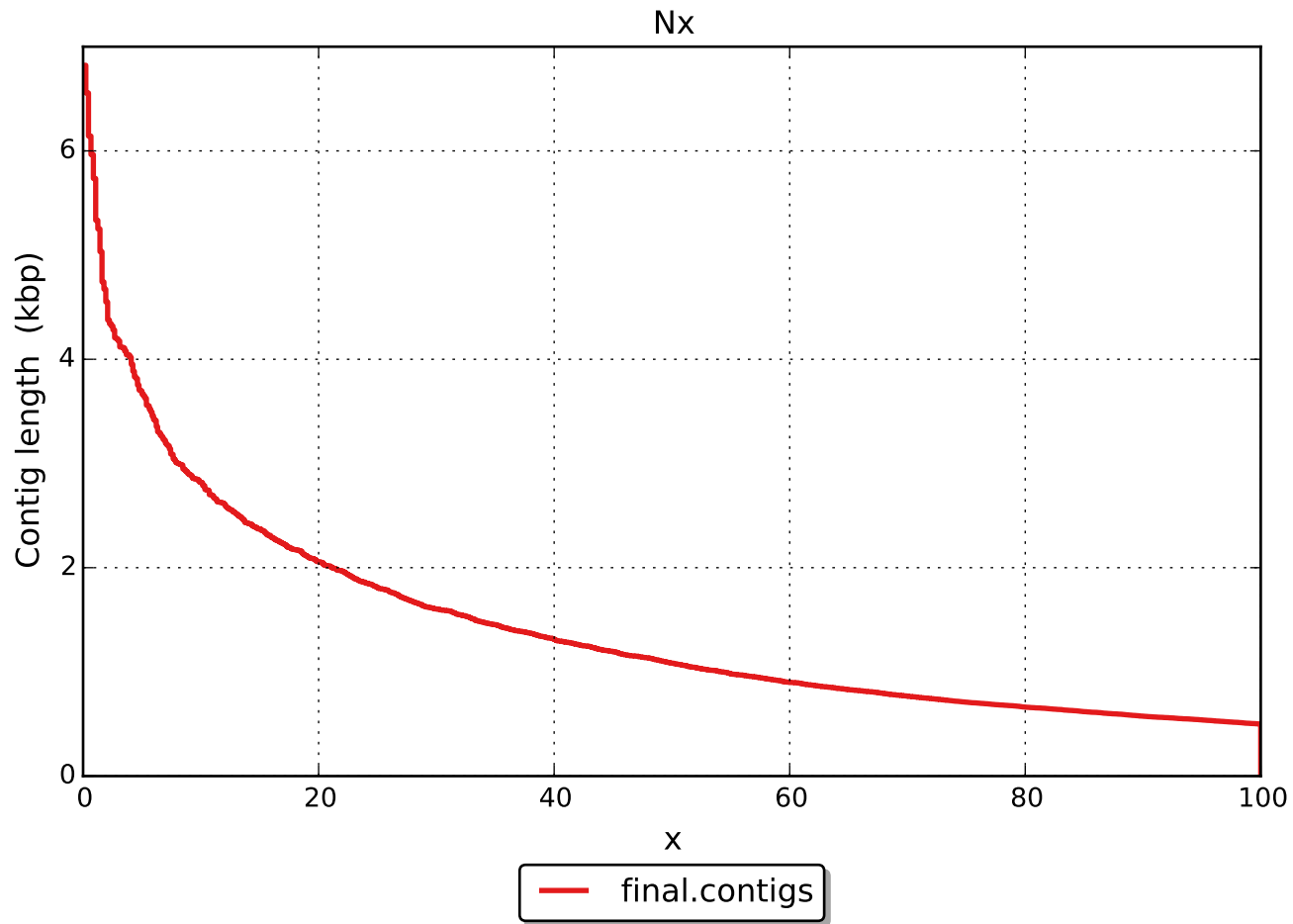
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# mismatches	9623
# indels	2
# short indels	2
# long indels	0
Indels length	2

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).

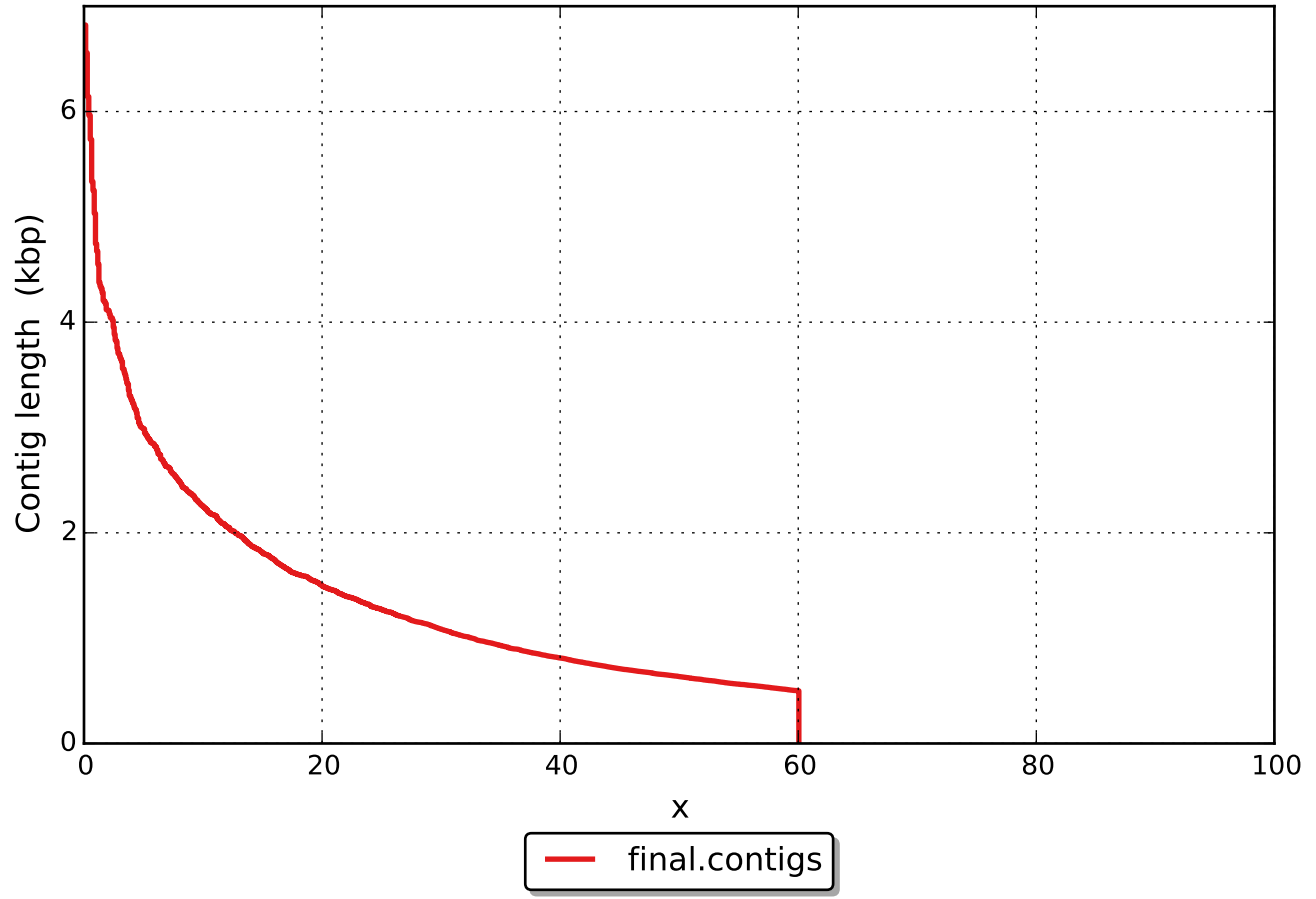
Unaligned report

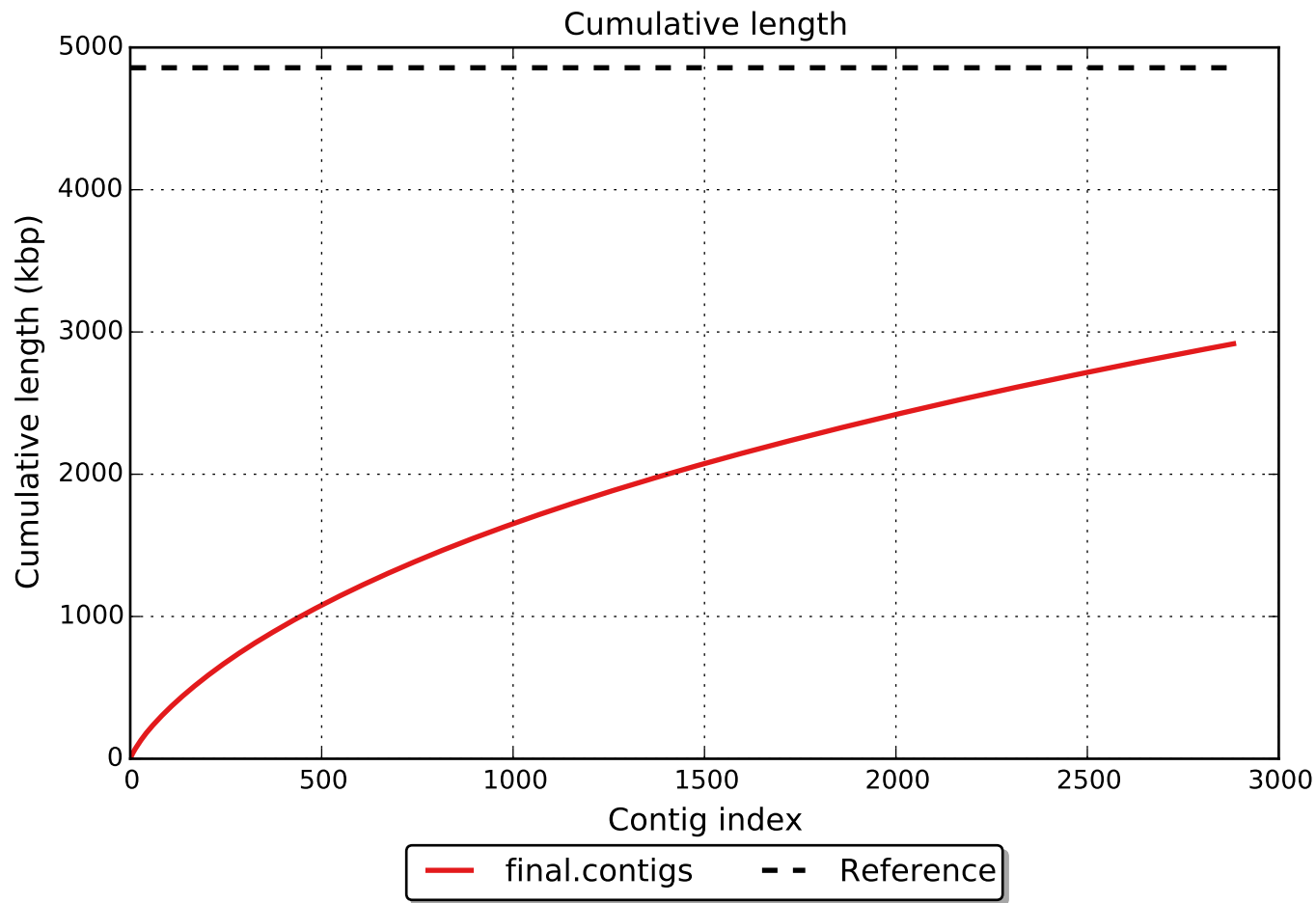
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	57
# N's	0

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).

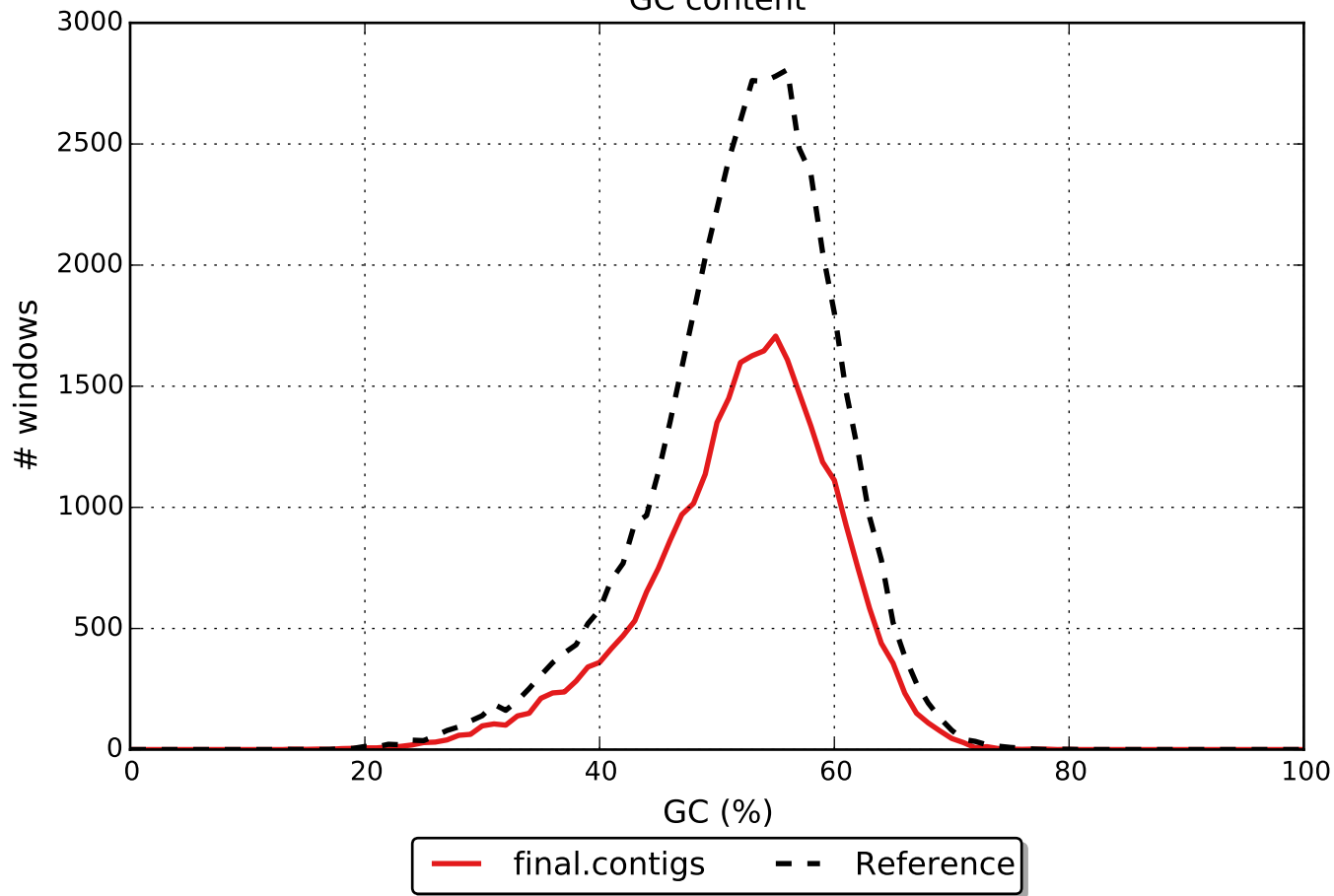


NGx





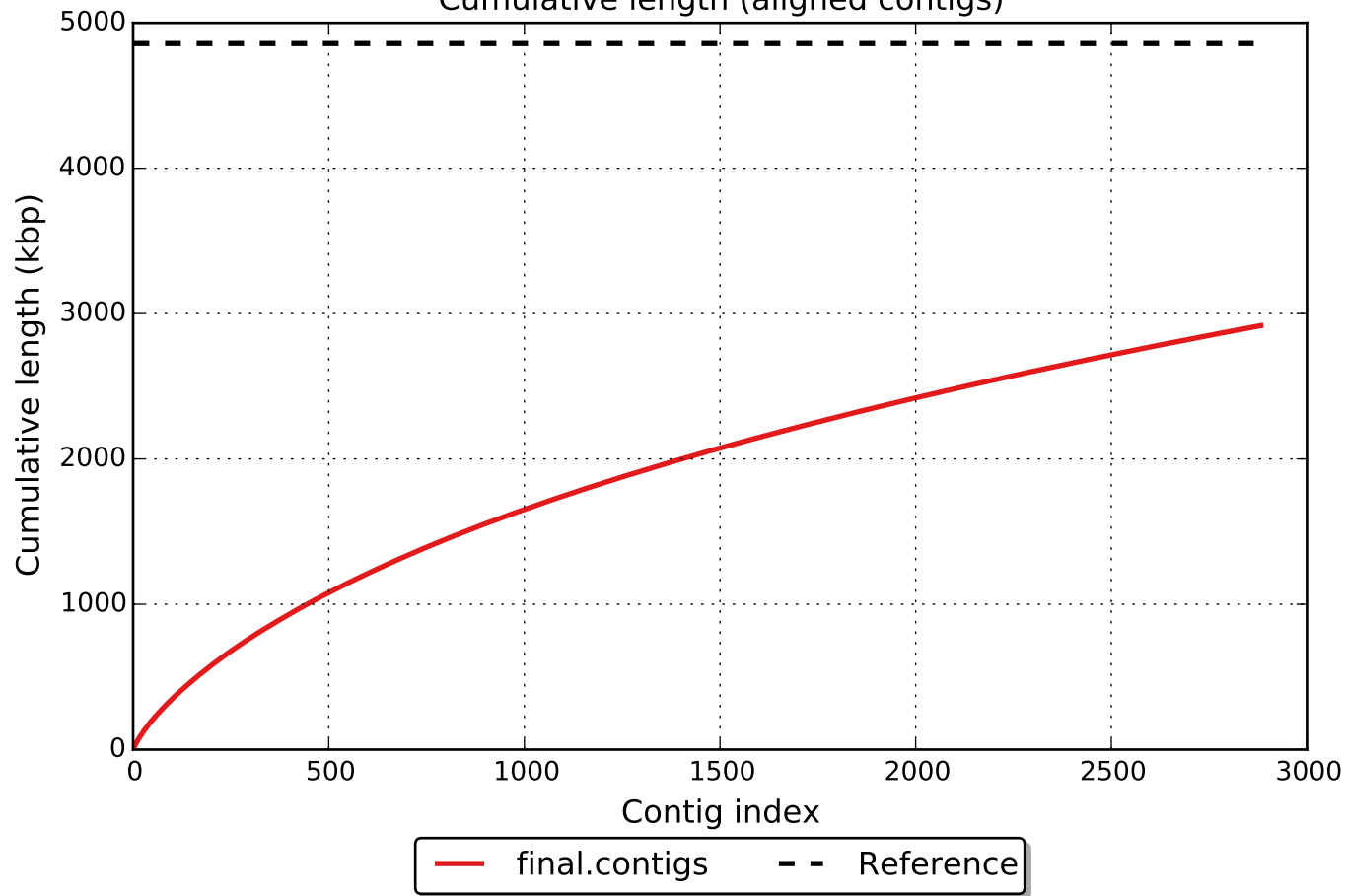
GC content



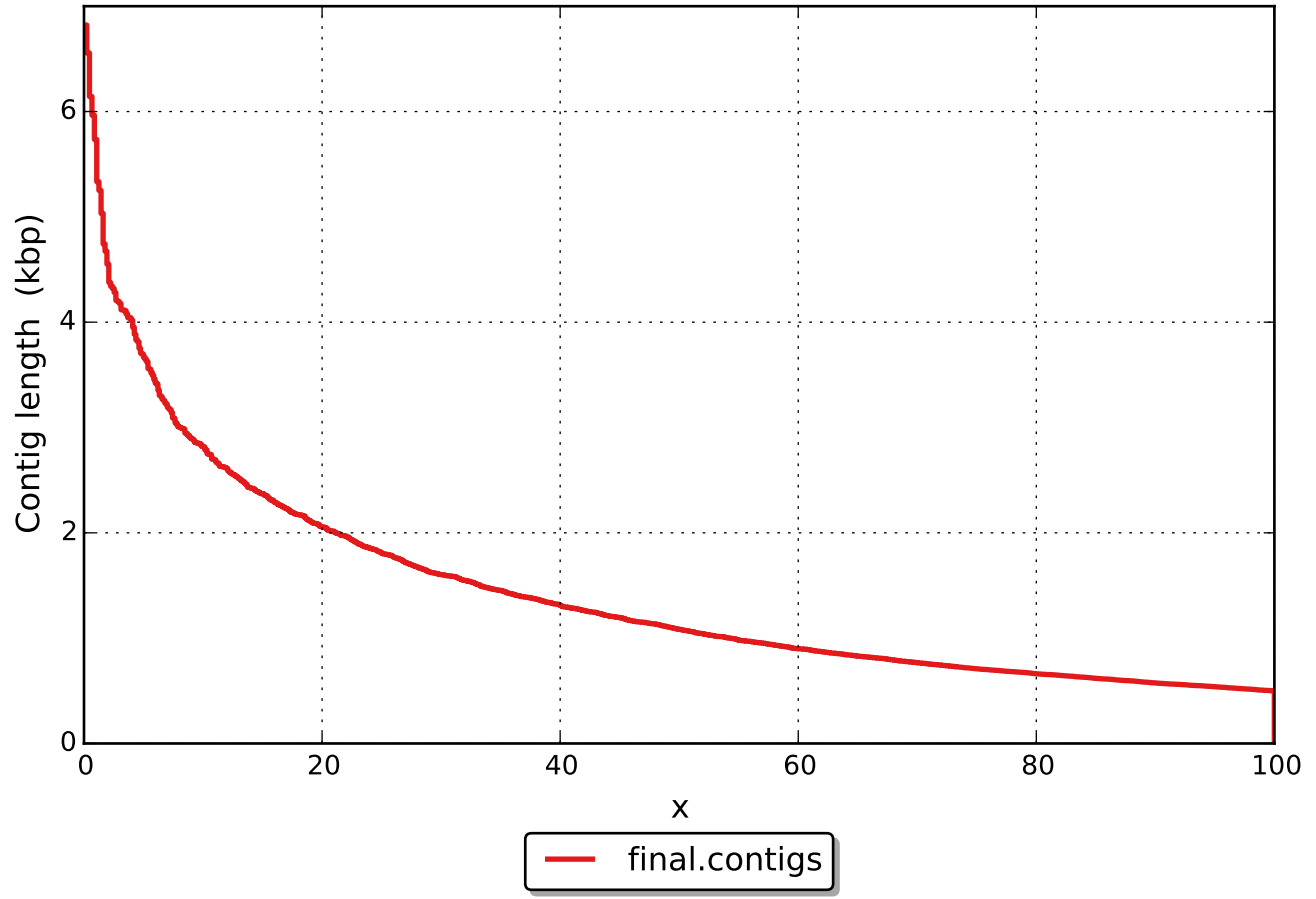
Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

