

Report

	final.contigs
# contigs (>= 1000 bp)	1945
# contigs (>= 5000 bp)	45
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4043224
Total length (>= 5000 bp)	266818
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	3054
Largest contig	8333
Total length	4859519
Reference length	4857432
GC (%)	52.23
Reference GC (%)	52.23
N50	1960
NG50	1960
N75	1222
NG75	1222
L50	805
LG50	804
L75	1585
LG75	1584
# misassemblies	2
# misassembled contigs	2
Misassembled contigs length	1545
# local misassemblies	0
# unaligned contigs	0 + 3 part
Unaligned length	377
Genome fraction (%)	95.624
Duplication ratio	1.046
# N's per 100 kbp	0.00
# mismatches per 100 kbp	57.10
# indels per 100 kbp	0.04
Largest alignment	8333
NA50	1960
NGA50	1960
NA75	1222
NGA75	1222
LA50	805
LGA50	804
LA75	1585
LGA75	1584

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

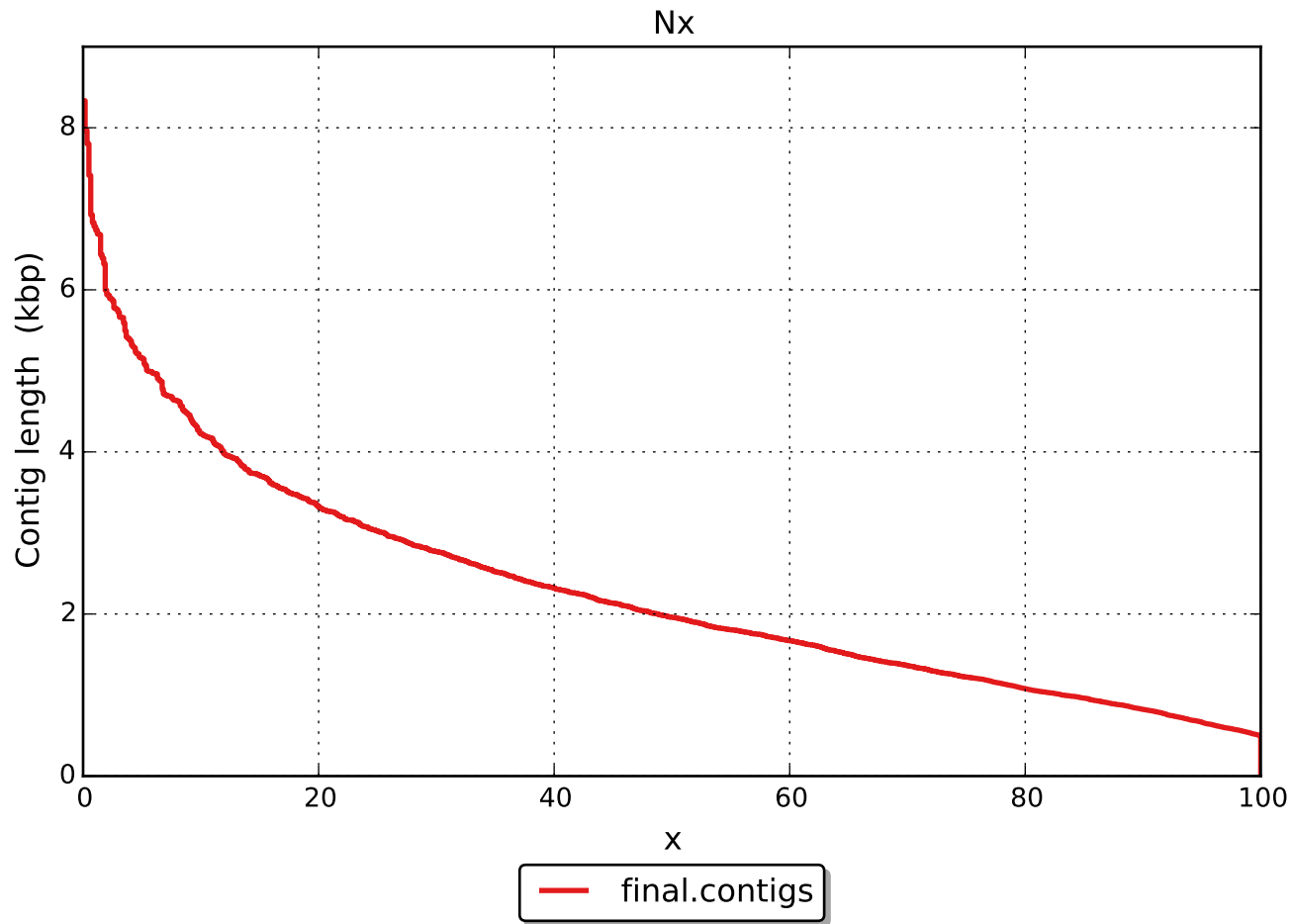
	final.contigs
# misassemblies	2
# relocations	0
# translocations	0
# inversions	2
# possibly misassembled contigs	0
# misassembled contigs	2
Misassembled contigs length	1545
# local misassemblies	0
# mismatches	2652
# indels	2
# short indels	2
# long indels	0
Indels length	2

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).

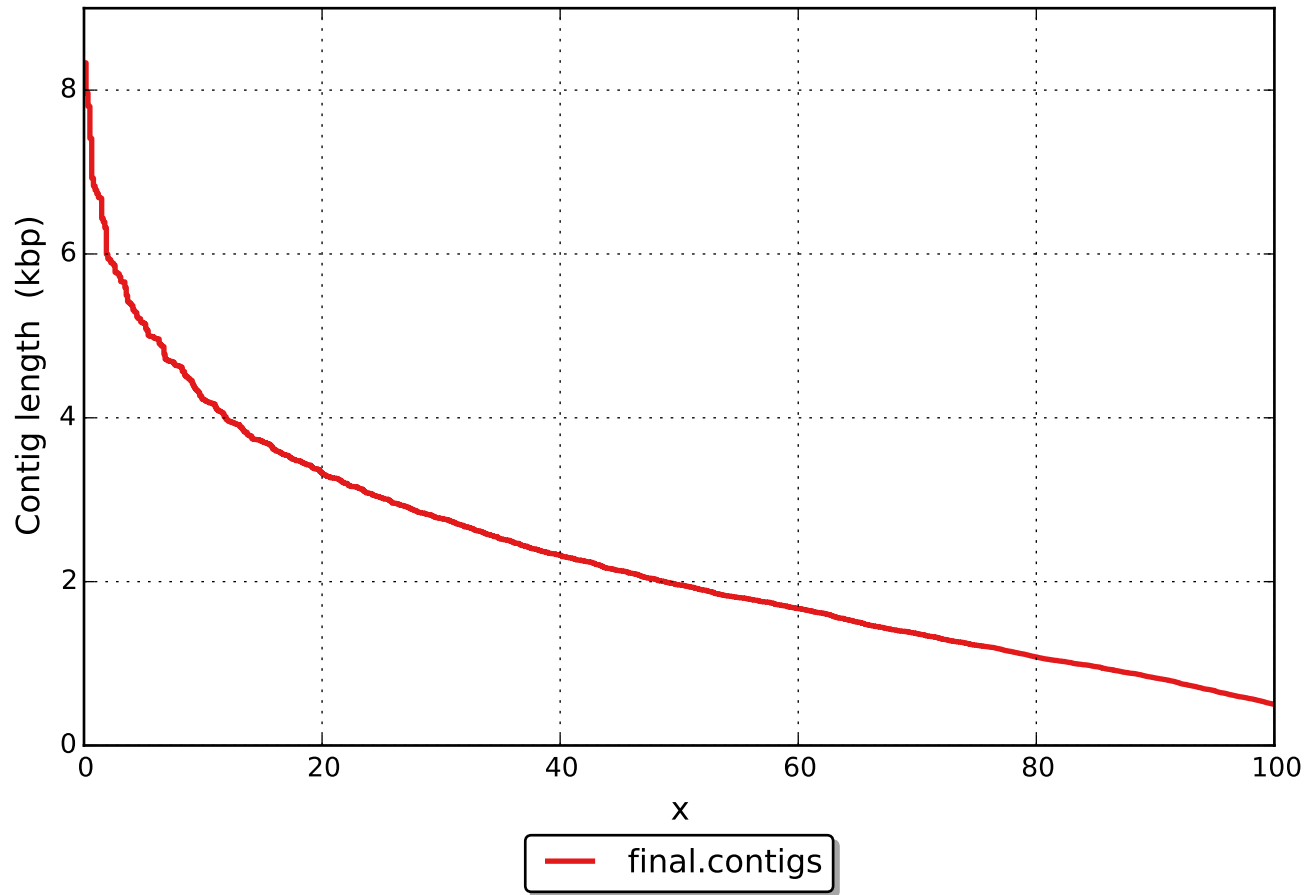
Unaligned report

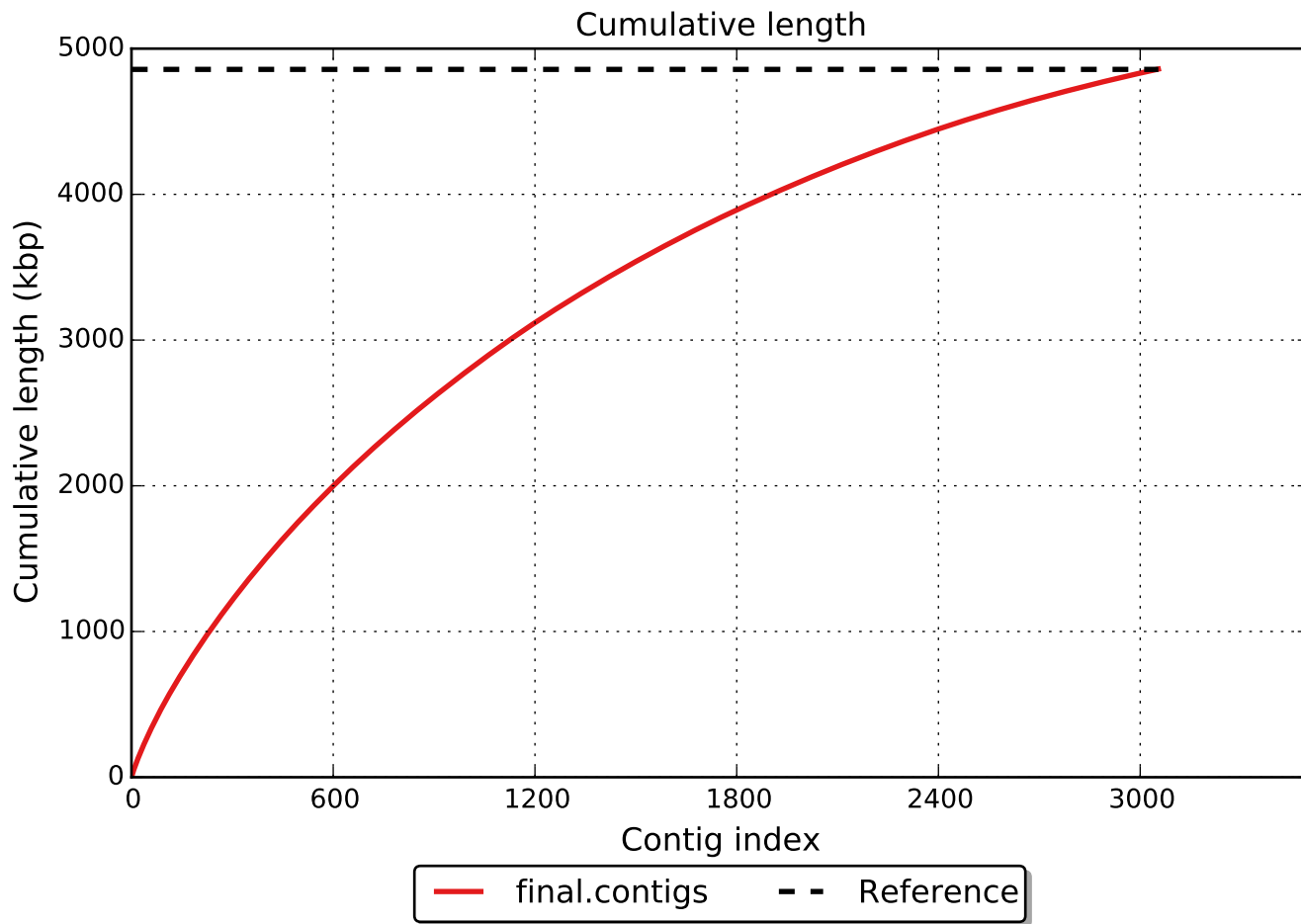
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	3
# with misassembly	0
# both parts are significant	0
Partially unaligned length	377
# N's	0

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).

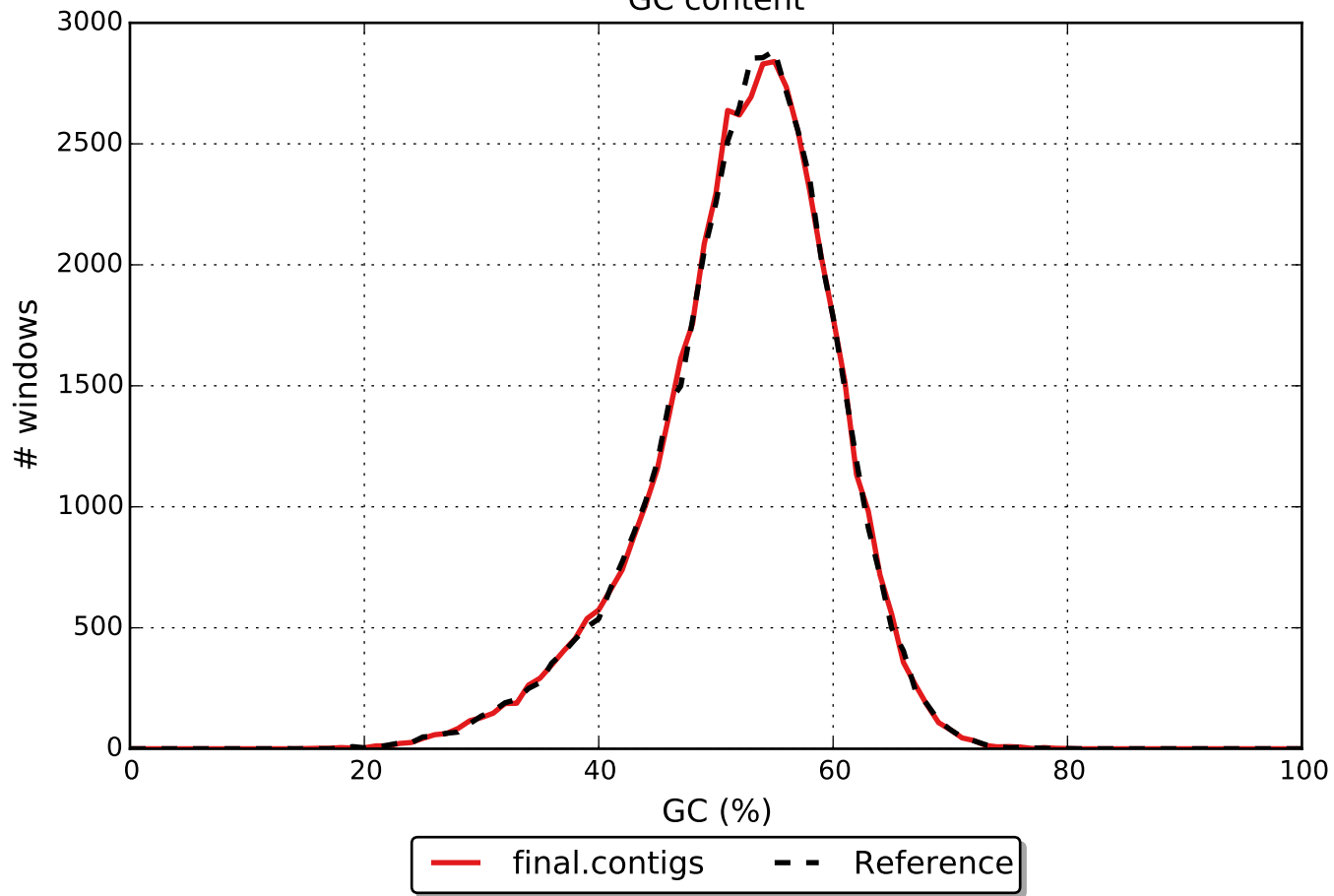


NGx

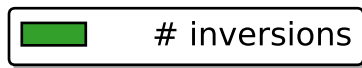
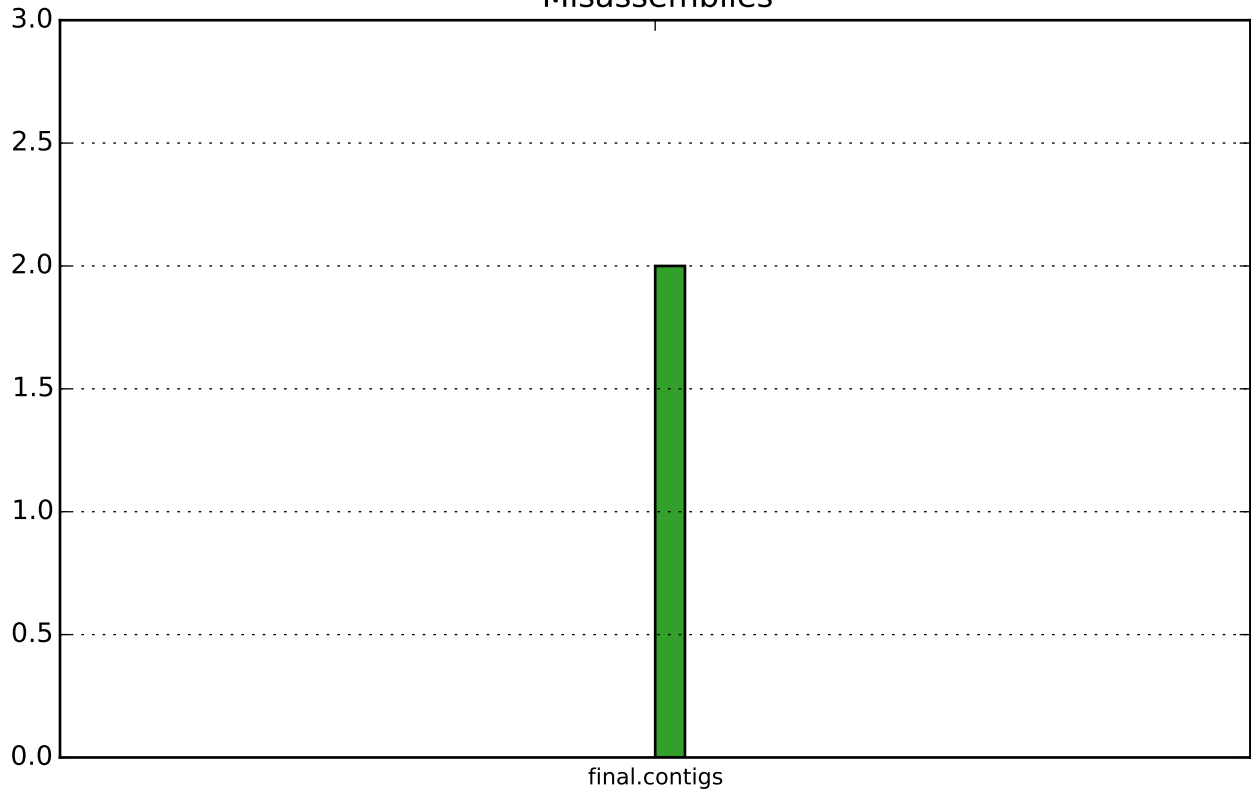




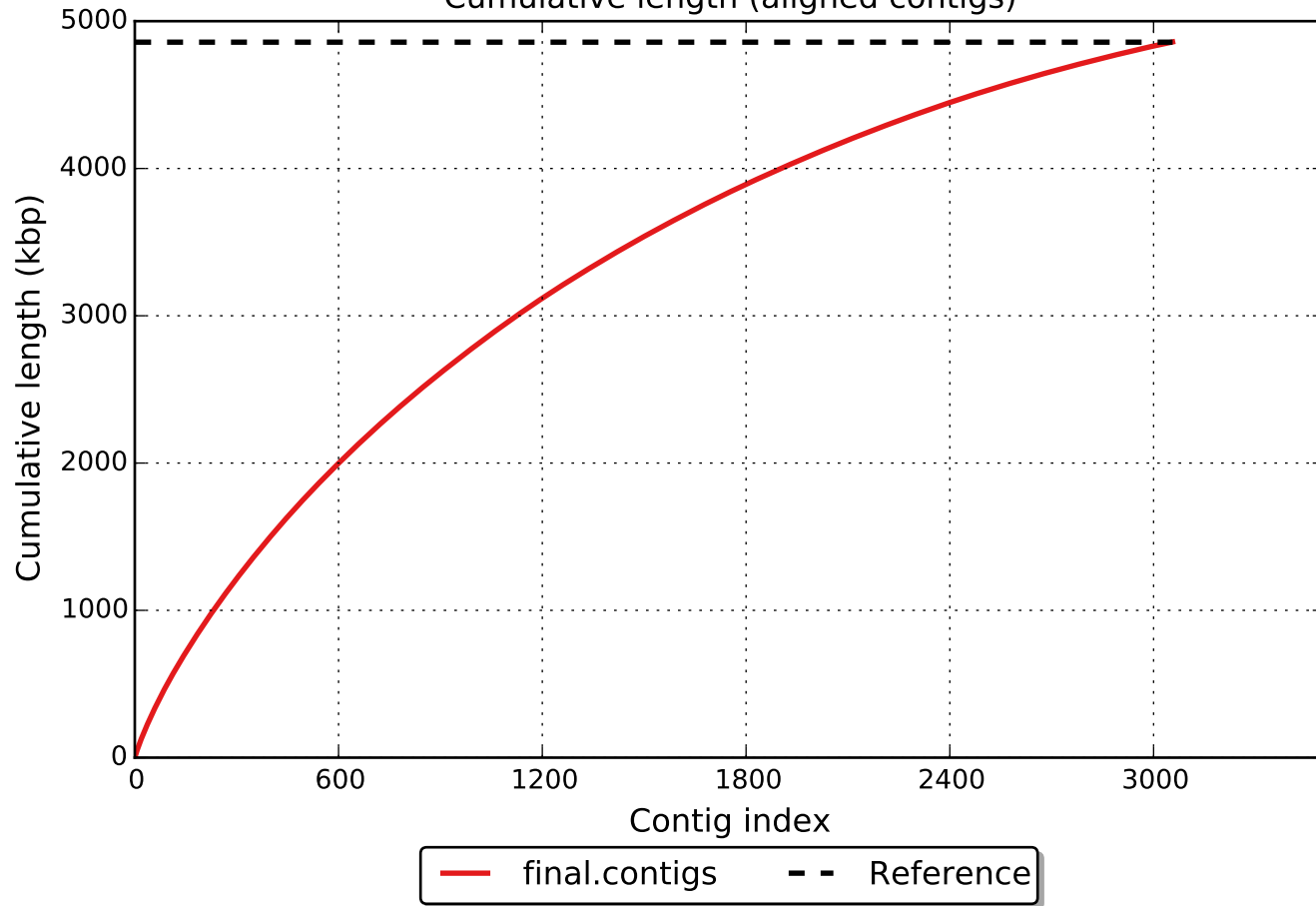
GC content



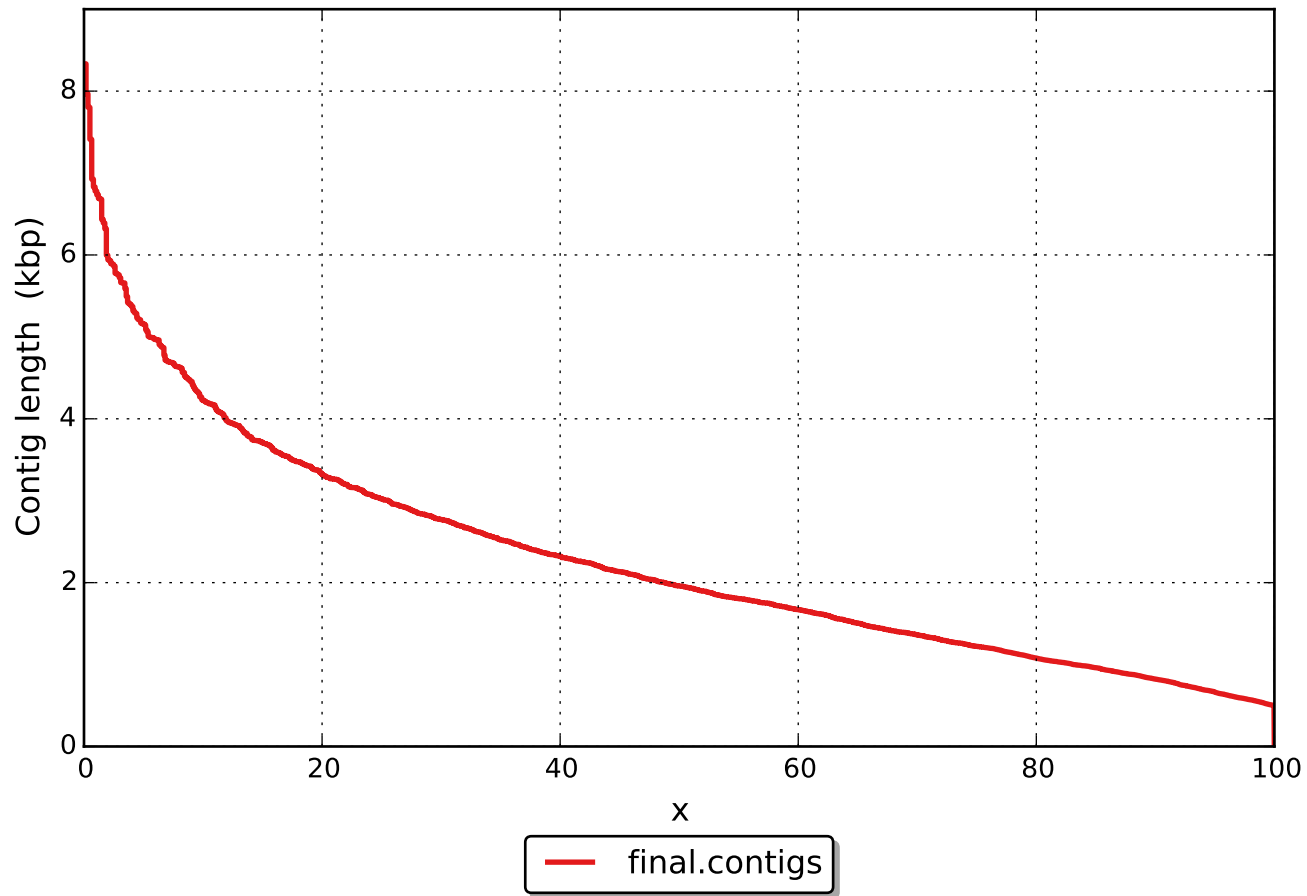
Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

