

Report

	final.contigs
# contigs (>= 1000 bp)	1444
# contigs (>= 5000 bp)	37
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	3021522
Total length (>= 5000 bp)	222791
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	3158
Largest contig	8536
Total length	4204014
Reference length	4641652
GC (℥)	50.75
Reference GC (℥)	50.79
N50	1741
NG50	1545
N75	920
NG75	759
L50	748
LG50	881
L75	1582
LG75	1977
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (℥)	84.850
Duplication ratio	1.067
# N's per 100 kbp	0.00
# mismatches per 100 kbp	548.62
# indels per 100 kbp	0.23
Largest alignment	8536
NA50	1741
NGA50	1545
NA75	920
NGA75	759
LA50	748
LGA50	881
LA75	1582
LGA75	1977

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

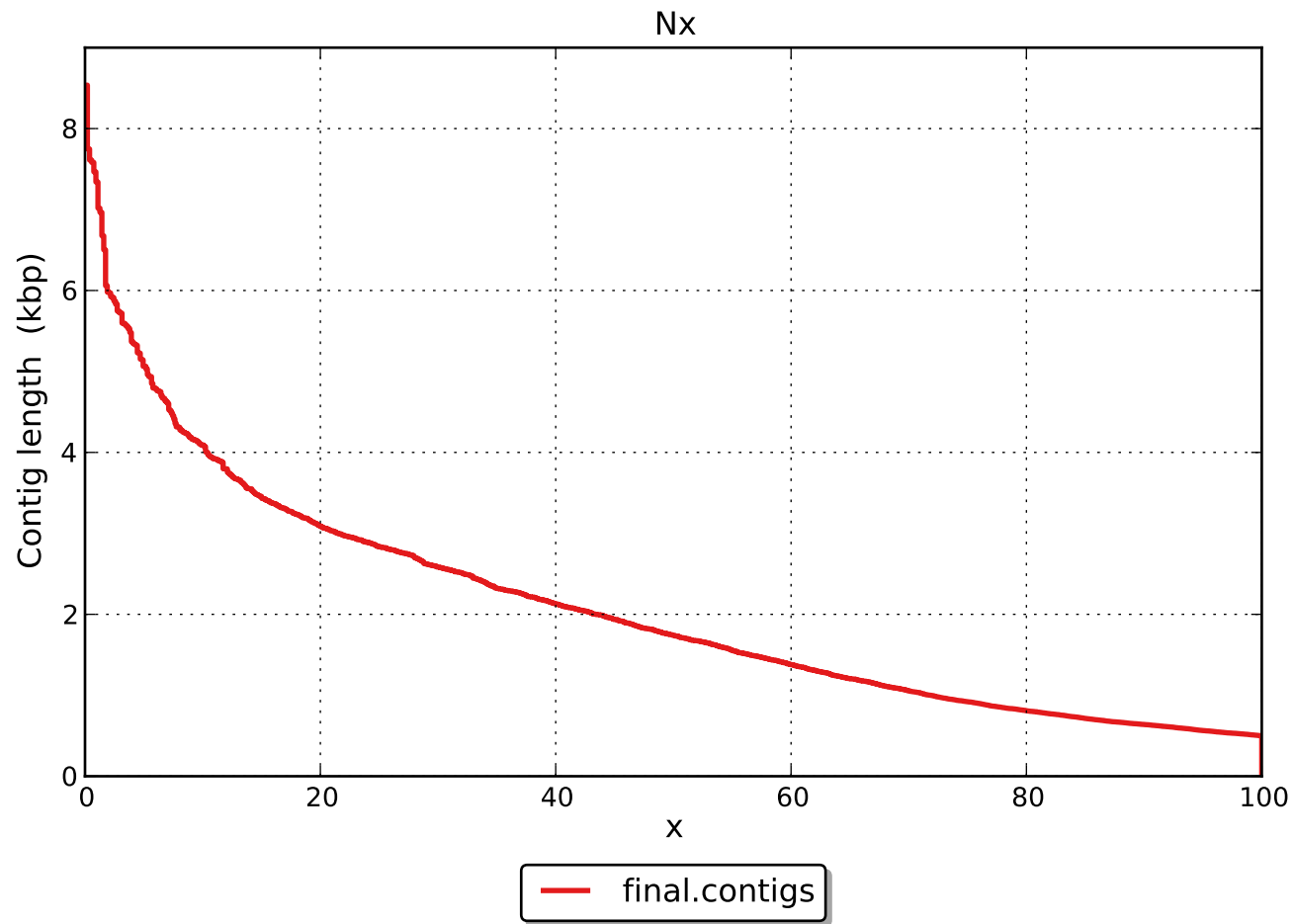
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	21607
# indels	9
# short indels	9
# long indels	0
Indels length	9

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).

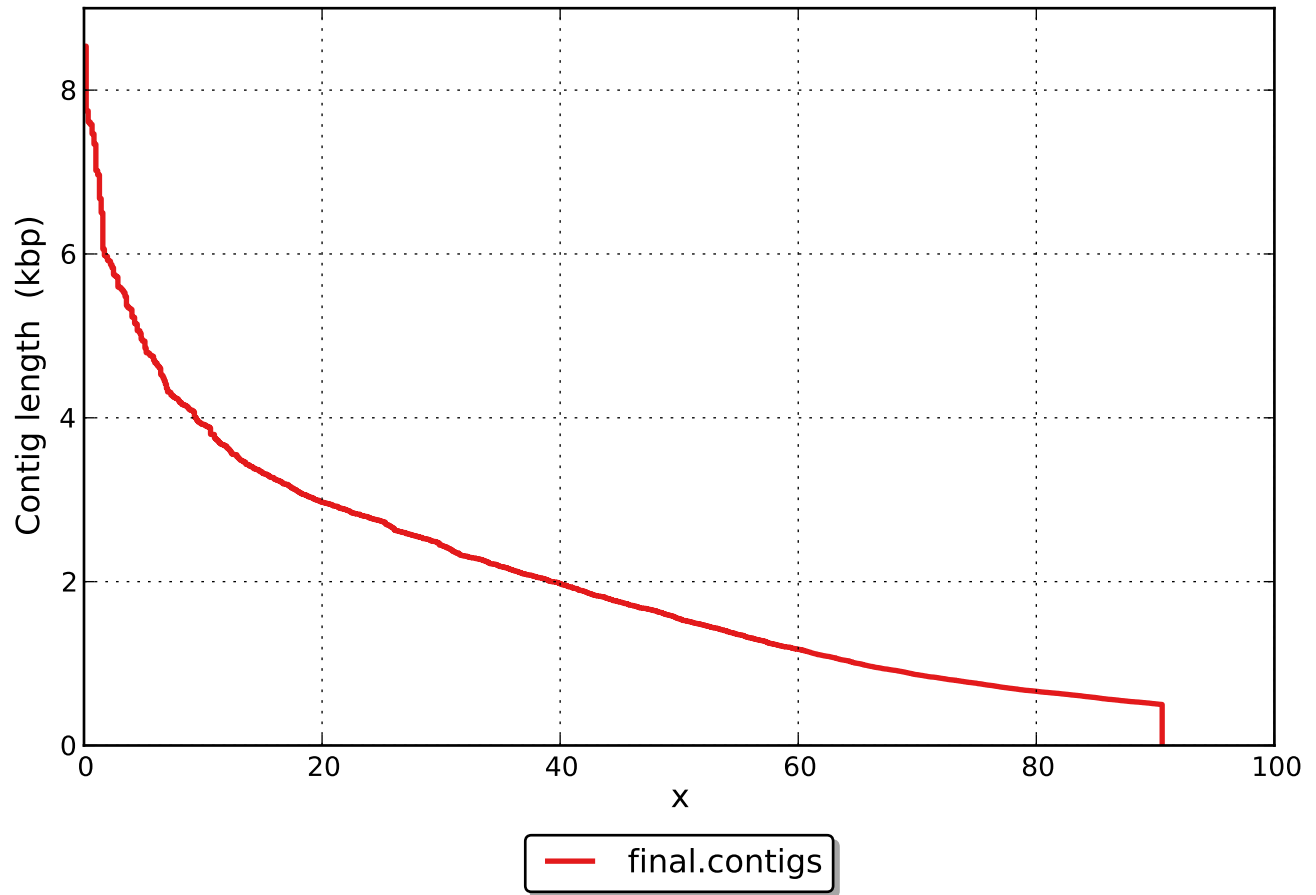
Unaligned report

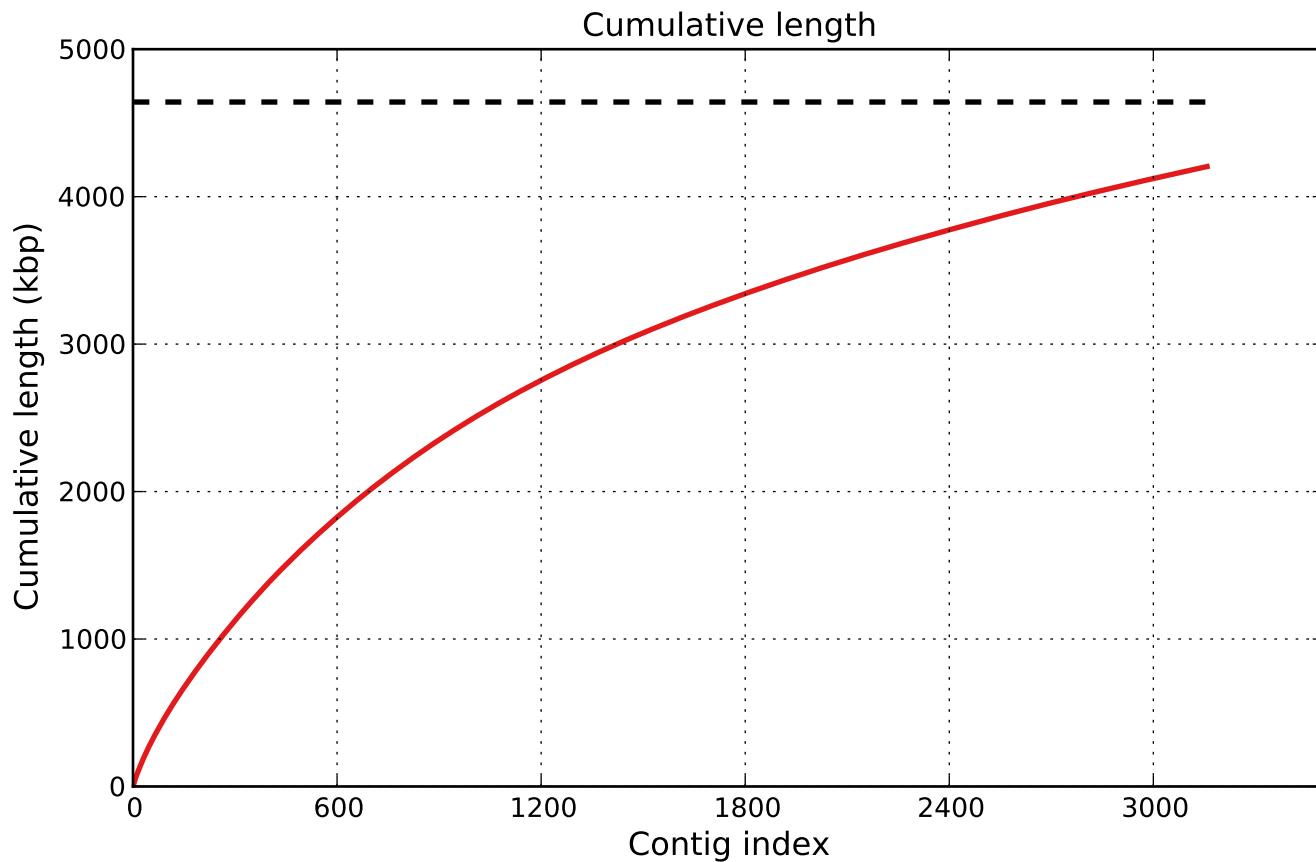
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).



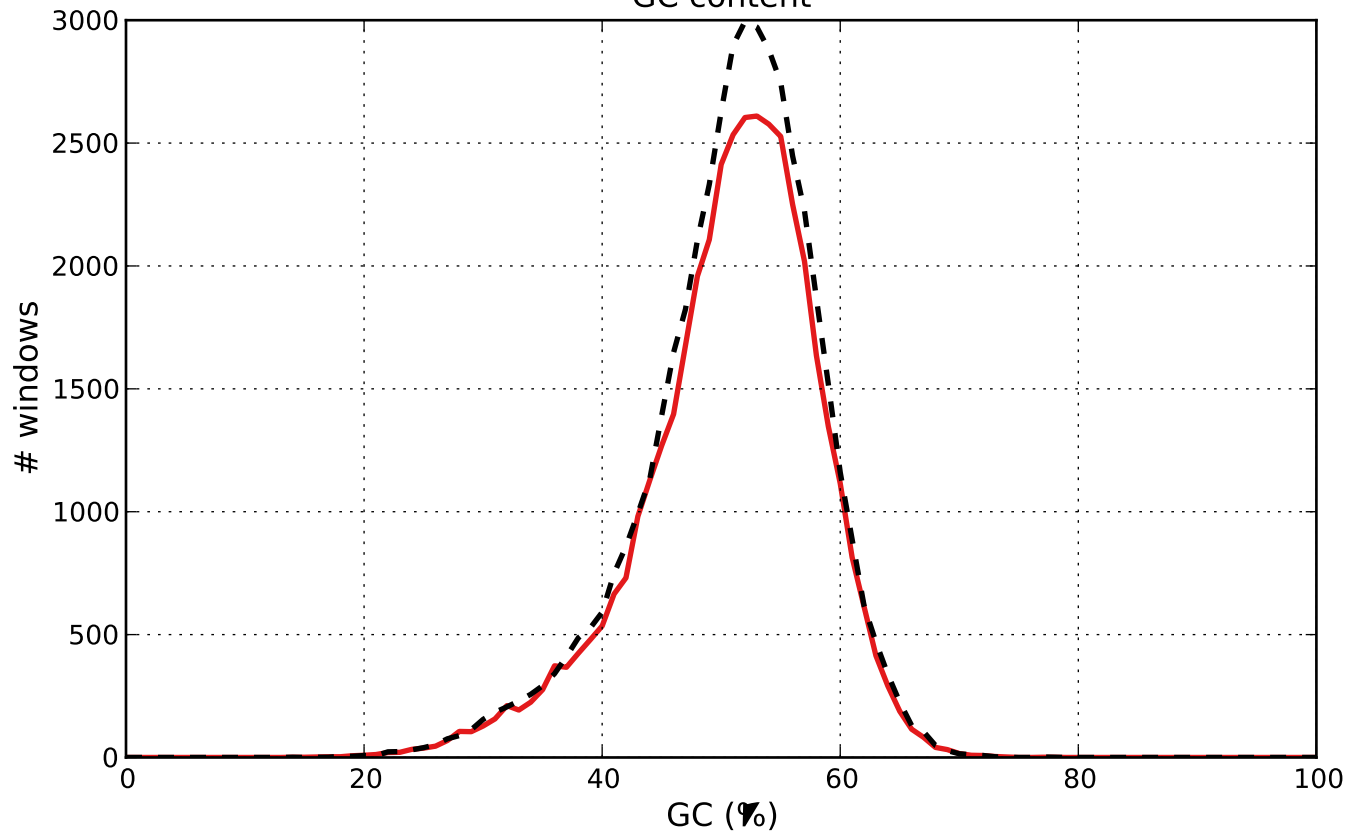
NGx





— final.contigs - - Reference

GC content

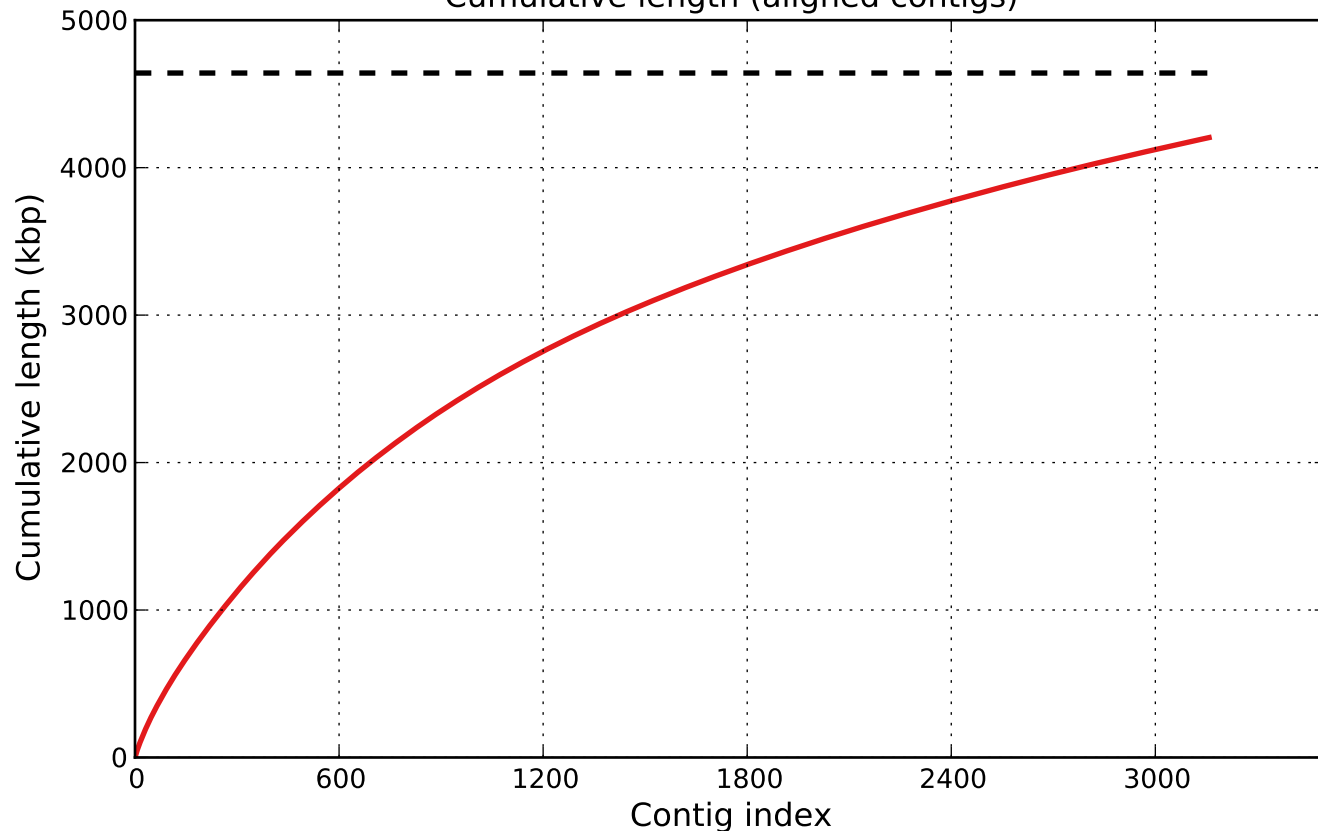


— final.contigs - - Reference

Misassemblies

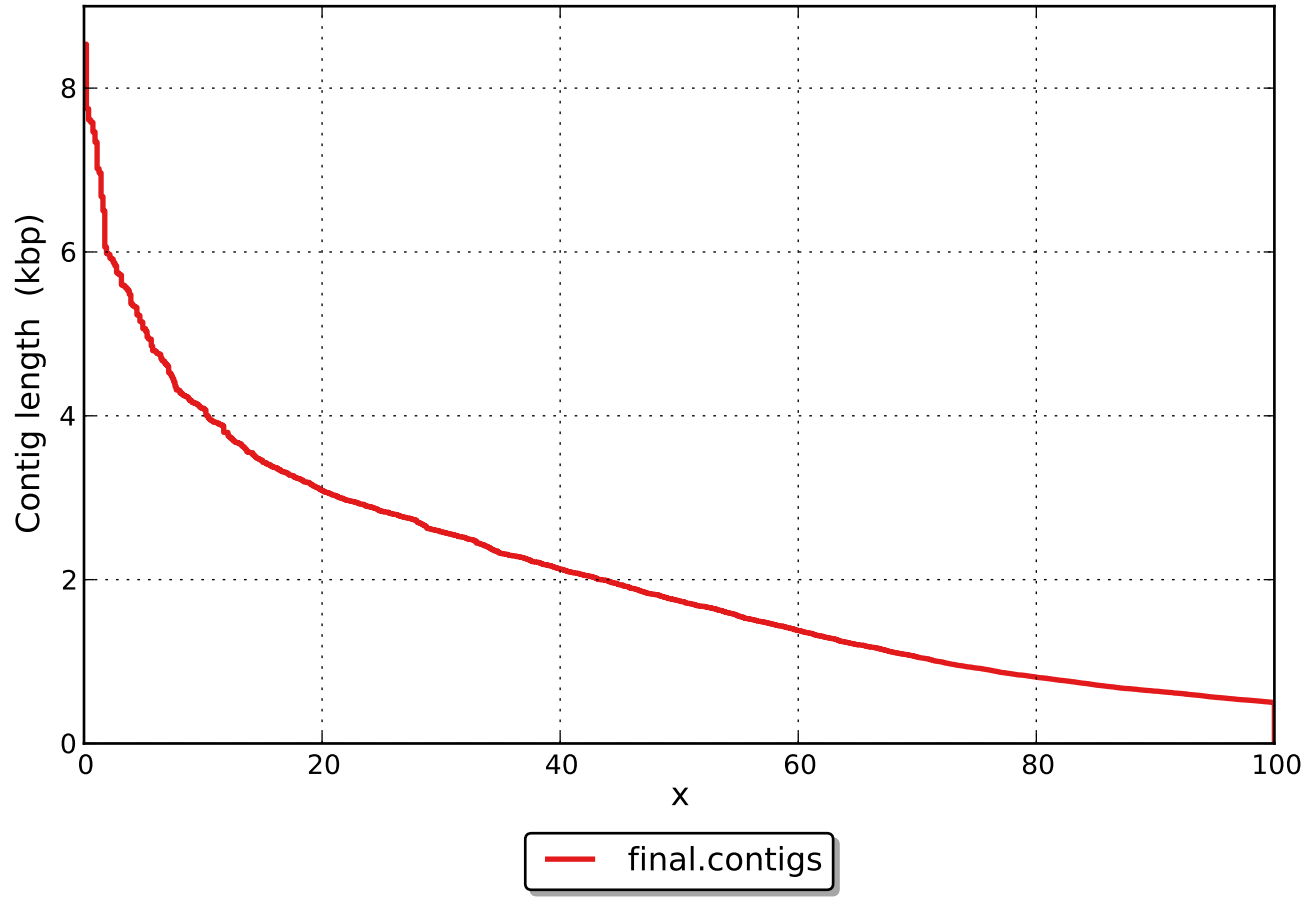


Cumulative length (aligned contigs)

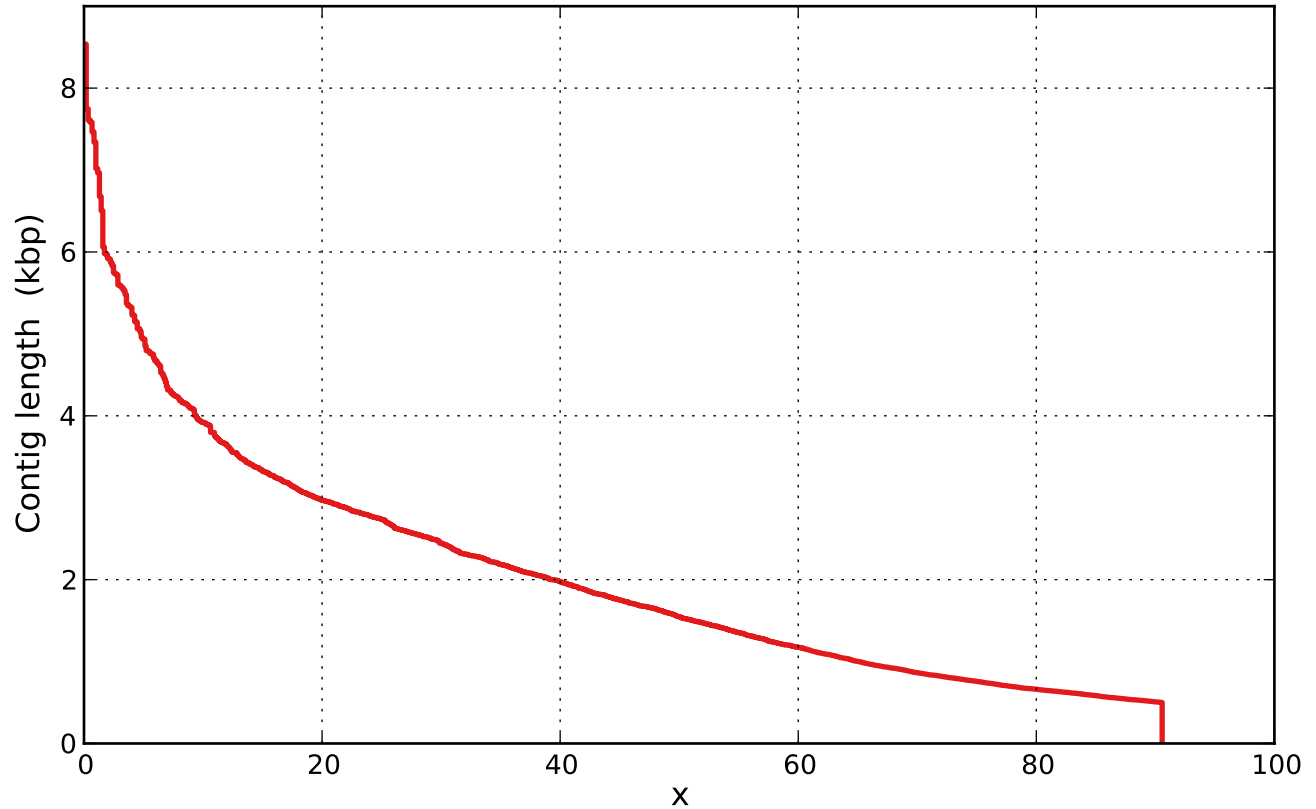


— final.contigs - - Reference

NAx



NGAx



— final.contigs