

Report

	final.contigs
# contigs (≥ 0 bp)	1132
# contigs (≥ 1000 bp)	411
Total length (≥ 0 bp)	1125341
Total length (≥ 1000 bp)	613540
# contigs	1132
Largest contig	4336
Total length	1125341
Reference length	615980
GC (%)	25.40
Reference GC (%)	25.34
N50	1043
NG50	1465
N75	749
NG75	1187
L50	362
LG50	153
L75	675
LG75	271
# misassemblies	17
# misassembled contigs	16
Misassembled contigs length	21539
# local misassemblies	0
# unaligned contigs	2 + 1 part
Unaligned length	1386
Genome fraction (%)	90.495
Duplication ratio	2.016
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1408.60
# indels per 100 kbp	0.72
Largest alignment	4336
NA50	1013
NGA50	1409
NA75	719
NGA75	1156
LA50	370
LGA50	157
LA75	695
LGA75	277

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	17
# relocations	17
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	16
Misassembled contigs length	21539
# local misassemblies	0
# mismatches	7852
# indels	4
# short indels	4
# long indels	0
Indels length	4

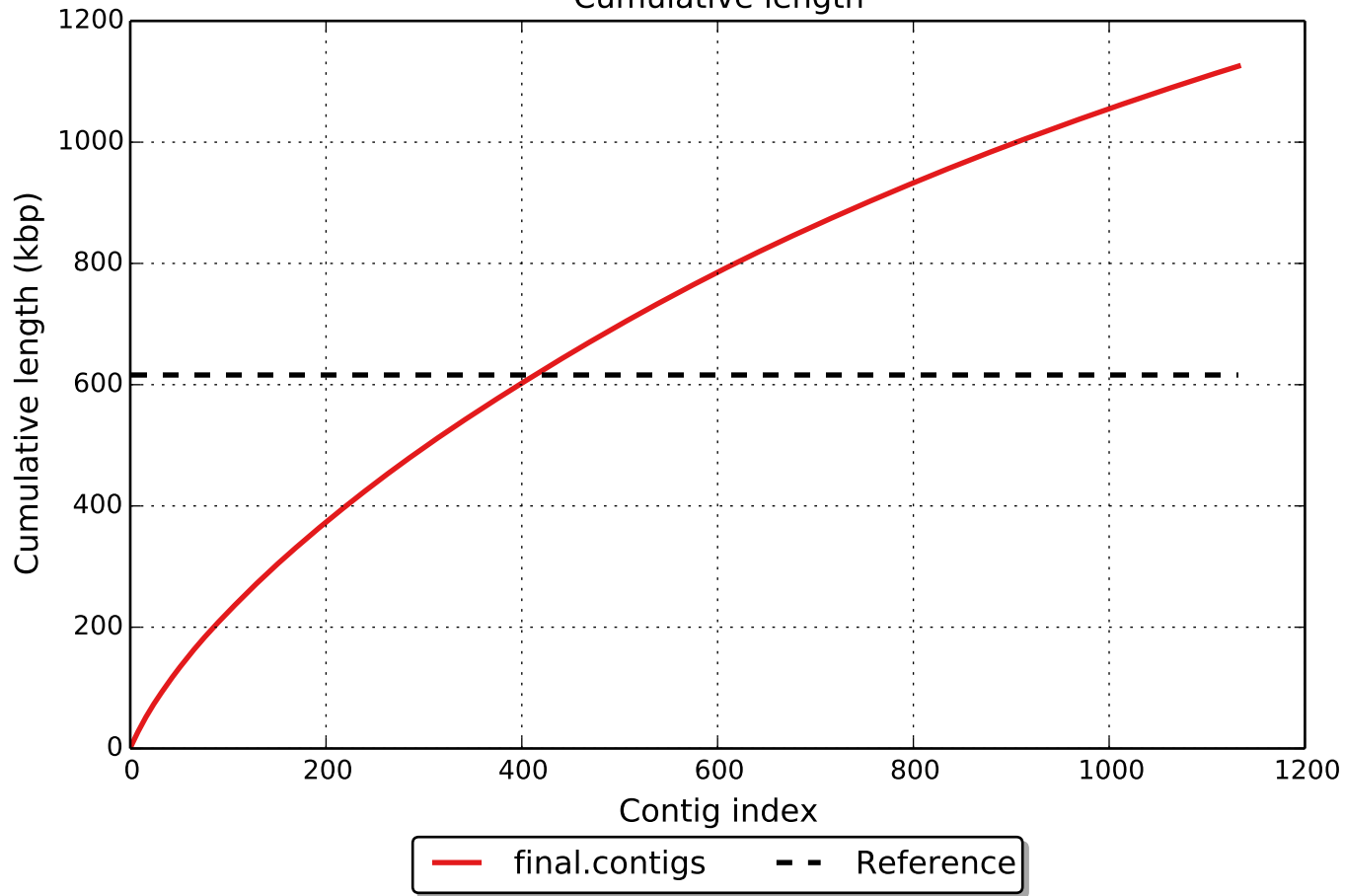
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

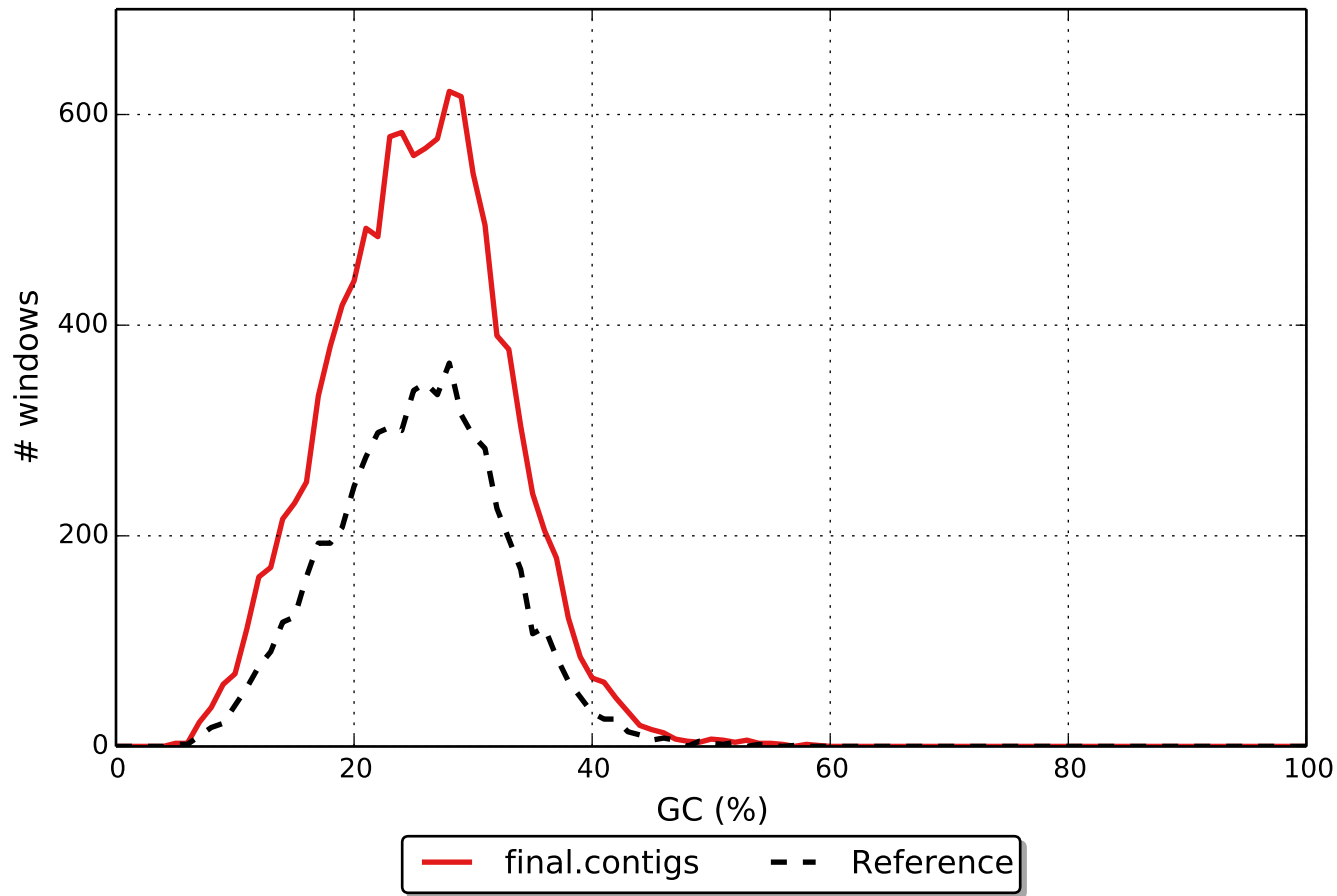
	final.contigs
# fully unaligned contigs	2
Fully unaligned length	1205
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	181
# N's	0

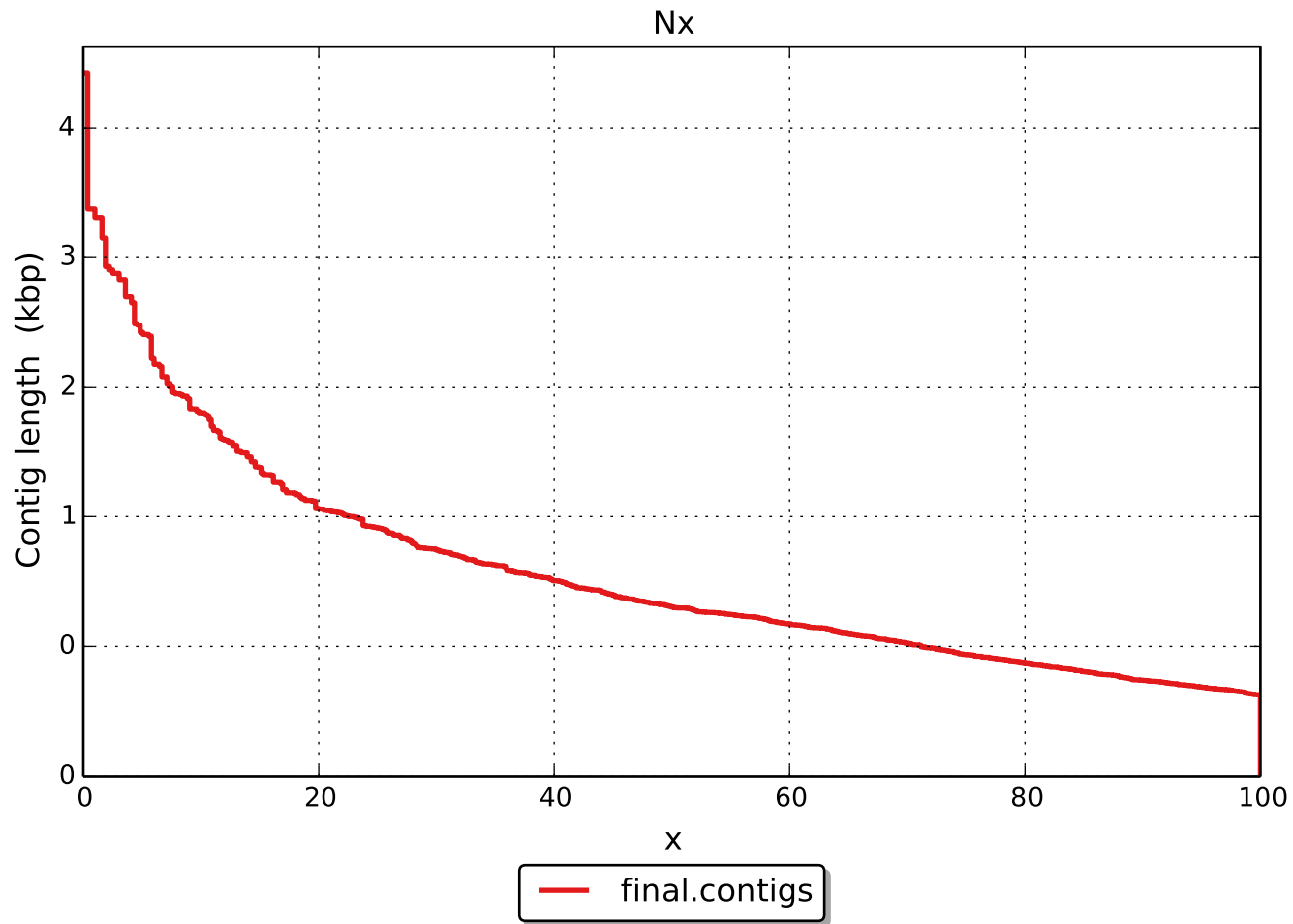
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Cumulative length

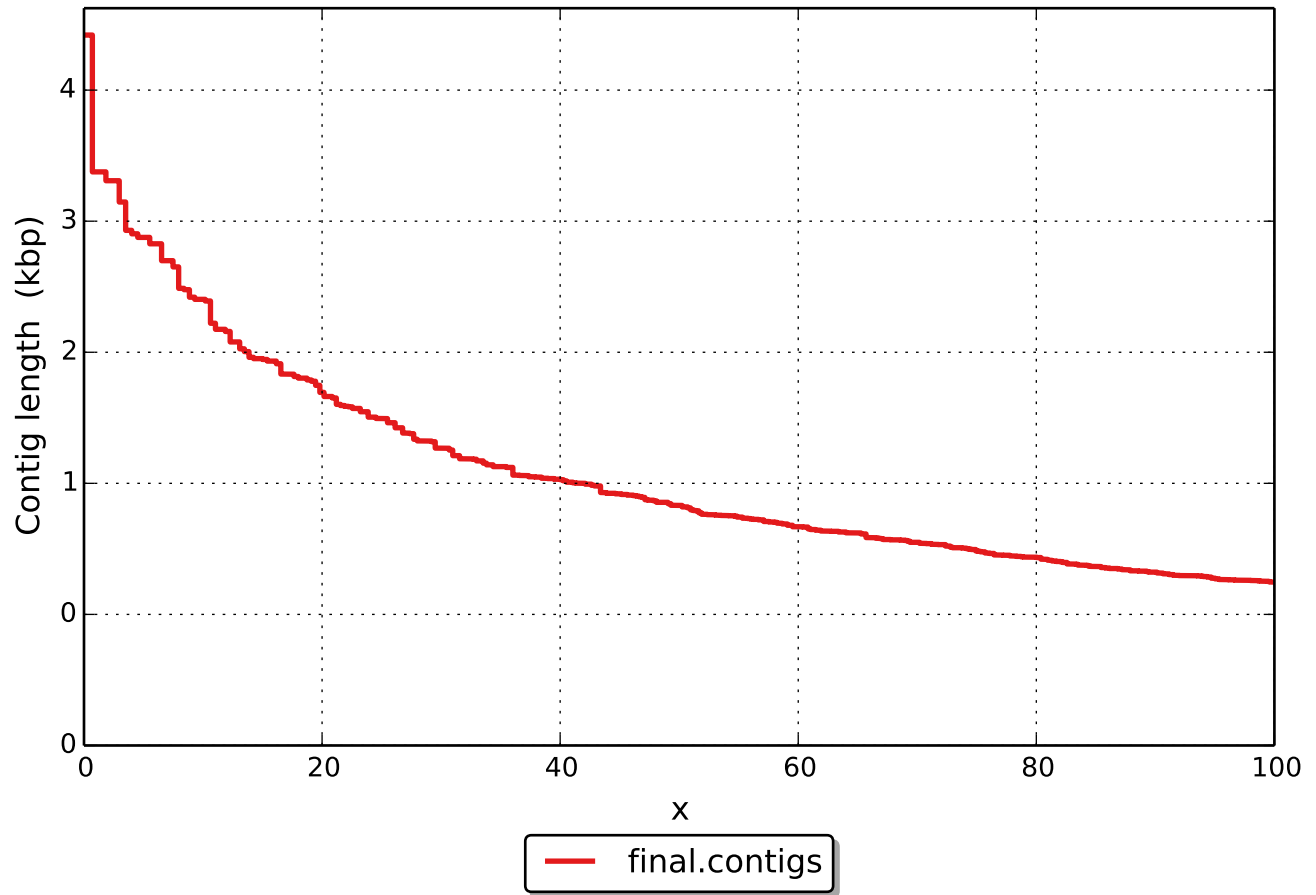


GC content

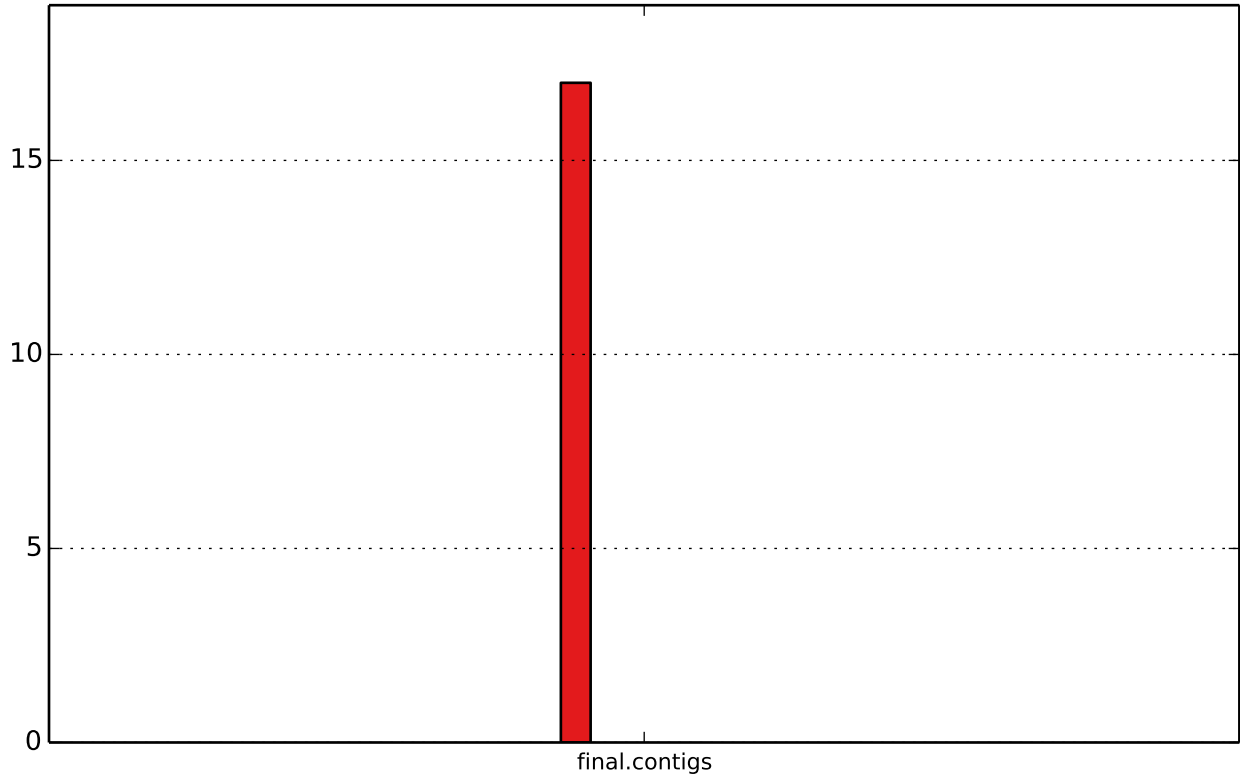




NGx

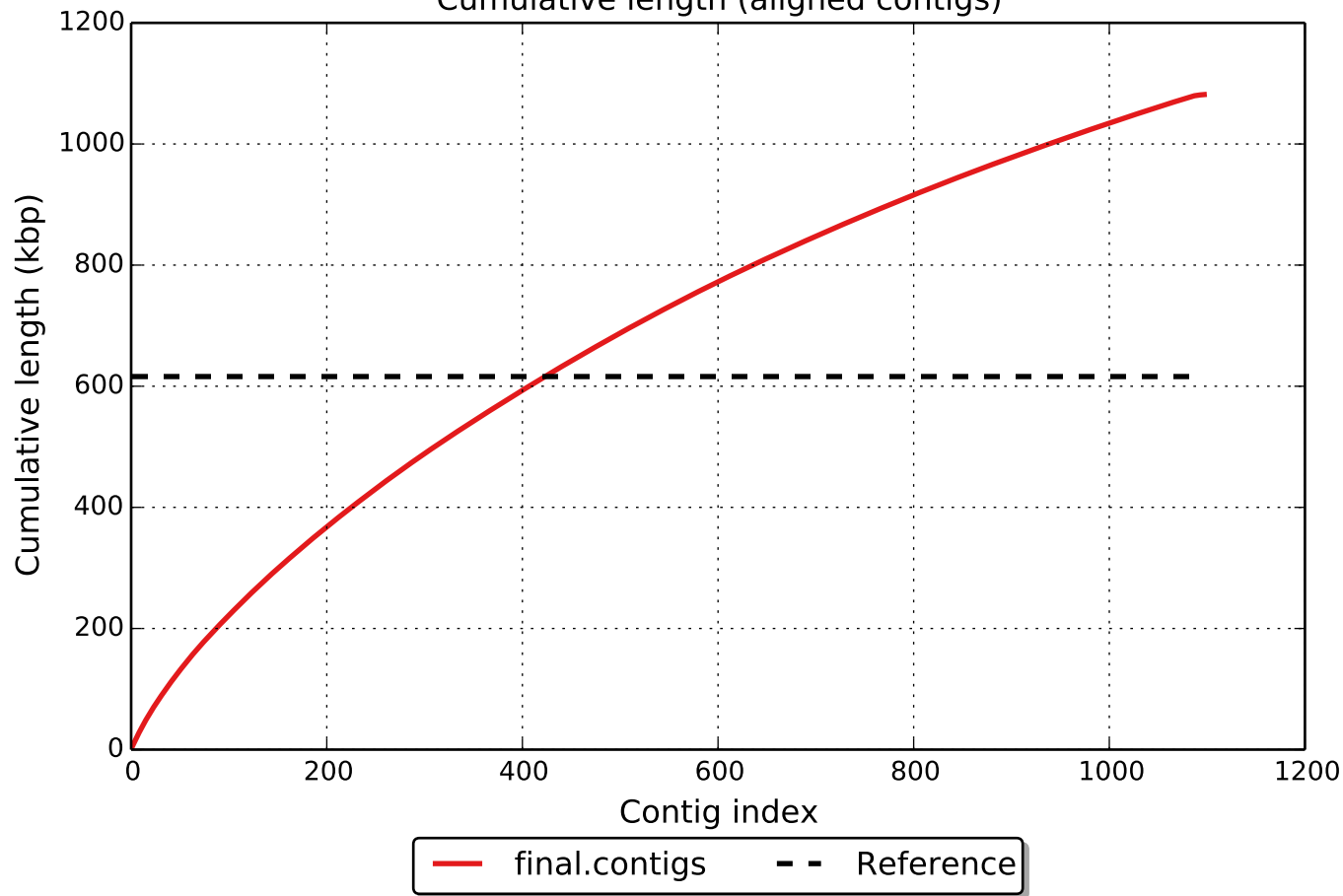


Misassemblies

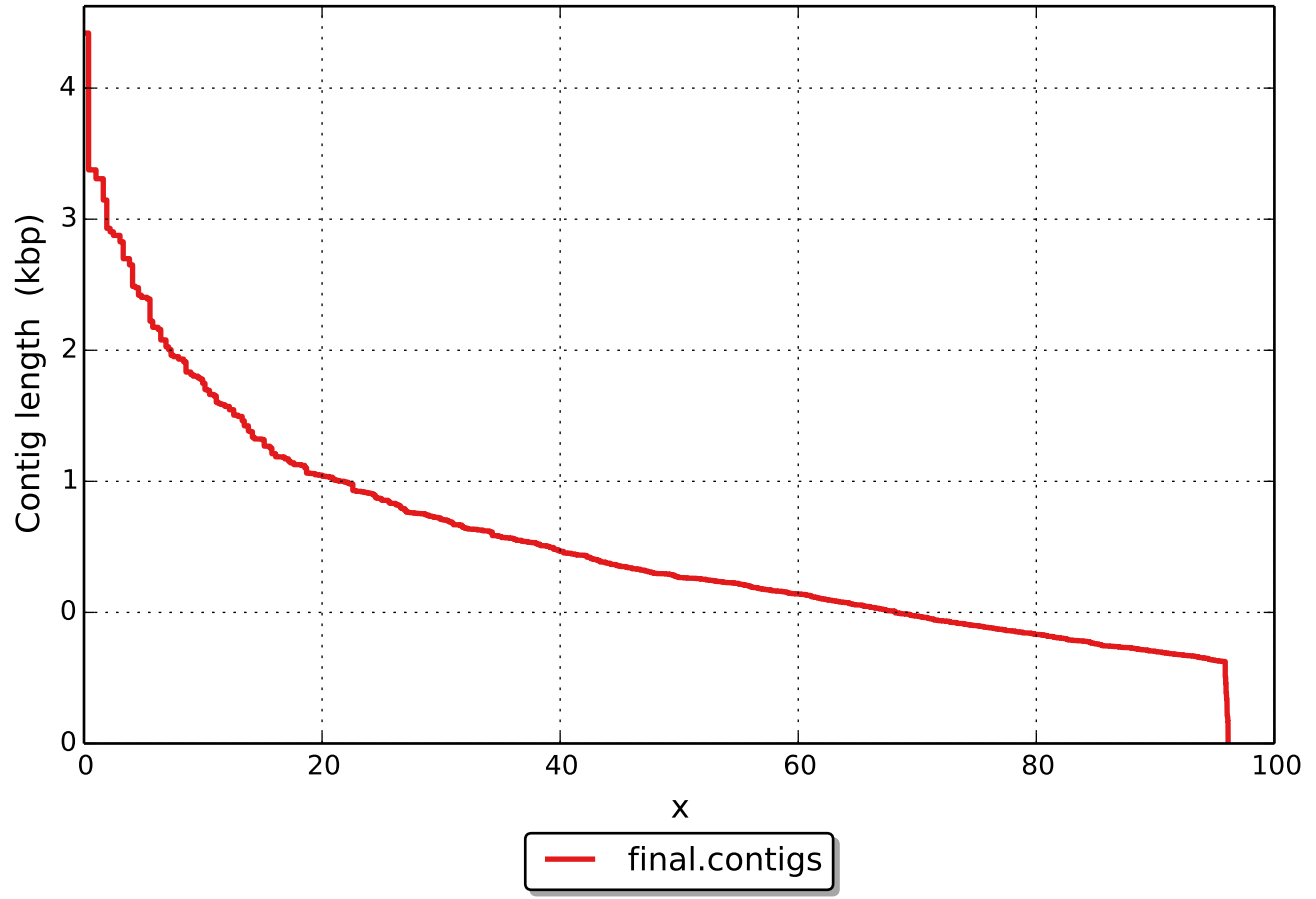


 # relocations

Cumulative length (aligned contigs)



NAx



NGAx

