

## Report

	final.contigs
# contigs (>= 1000 bp)	1399
# contigs (>= 5000 bp)	196
# contigs (>= 10000 bp)	17
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4238175
Total length (>= 5000 bp)	1353758
Total length (>= 10000 bp)	190064
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	1914
Largest contig	15182
Total length	4598202
Reference length	4857432
GC (%)	52.15
Reference GC (%)	52.22
N50	3393
NG50	3233
N75	2004
NG75	1790
L50	429
LG50	468
L75	864
LG75	967
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	7463
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	91.456
Duplication ratio	1.035
# N's per 100 kbp	0.00
# mismatches per 100 kbp	515.17
# indels per 100 kbp	0.07
Largest alignment	15182
NA50	3393
NGA50	3233
NA75	2004
NGA75	1790
LA50	429
LGA50	468
LA75	864
LGA75	967

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

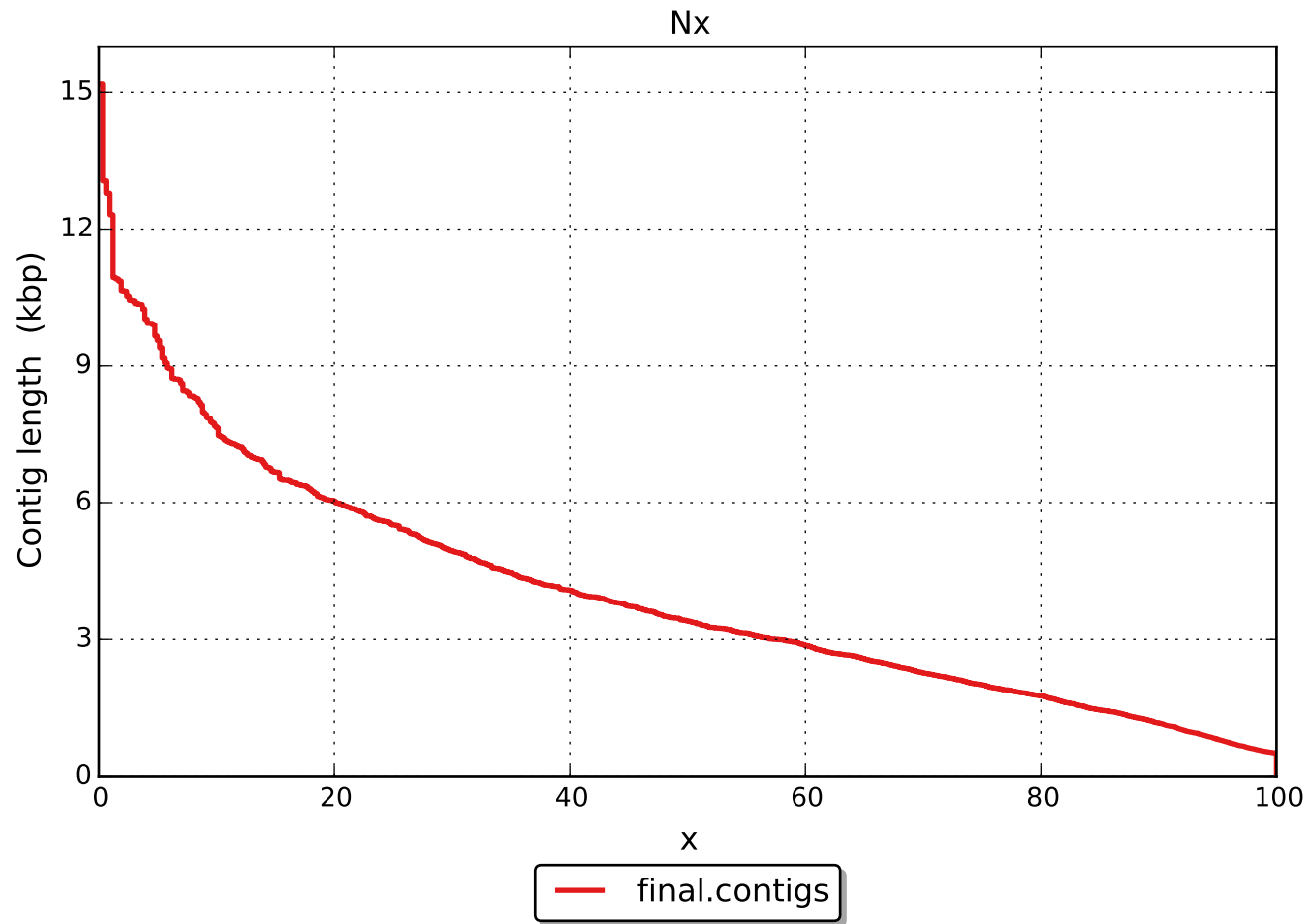
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	7463
# local misassemblies	0
# mismatches	22886
# indels	3
# short indels	3
# long indels	0
Indels length	6

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

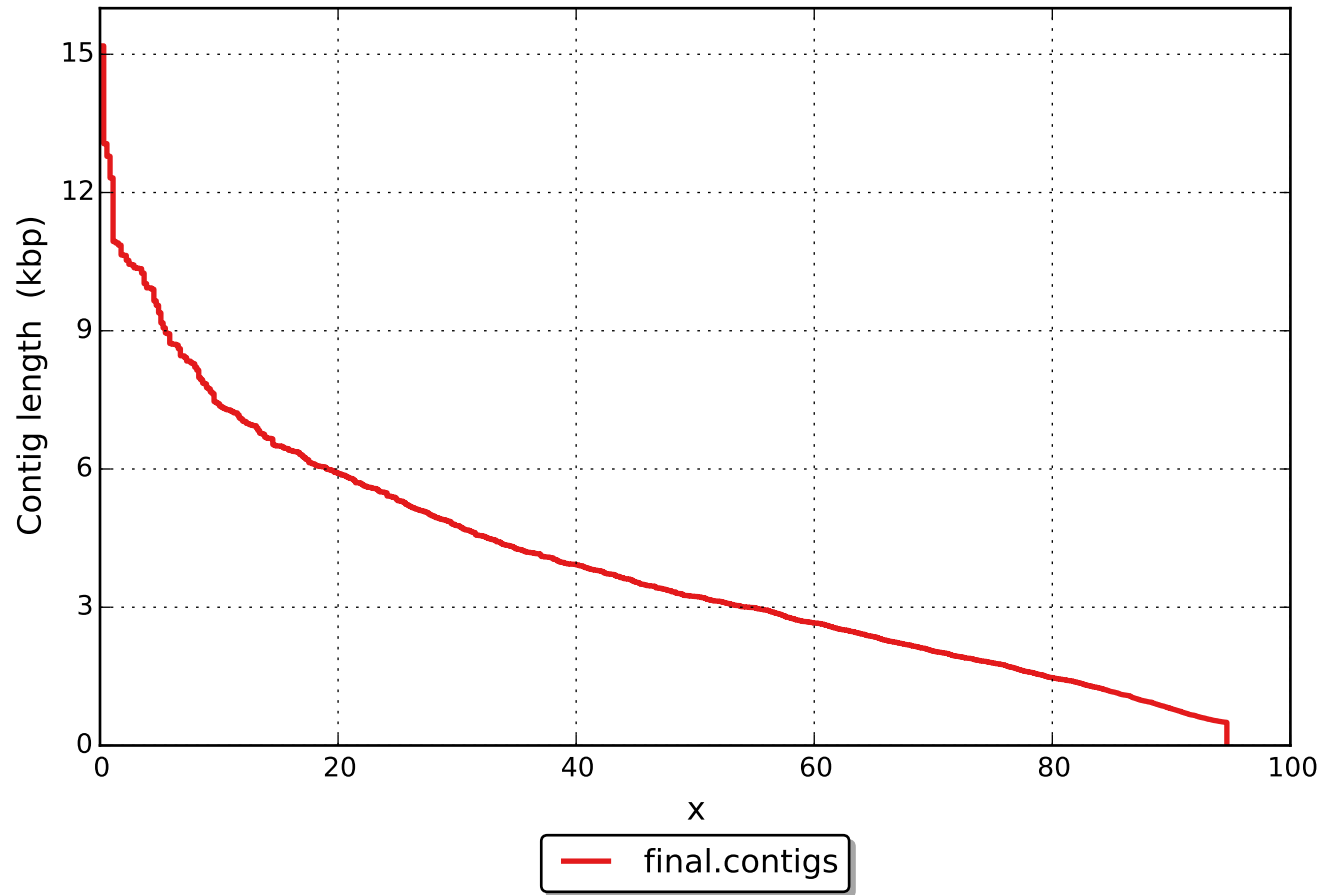
## Unaligned report

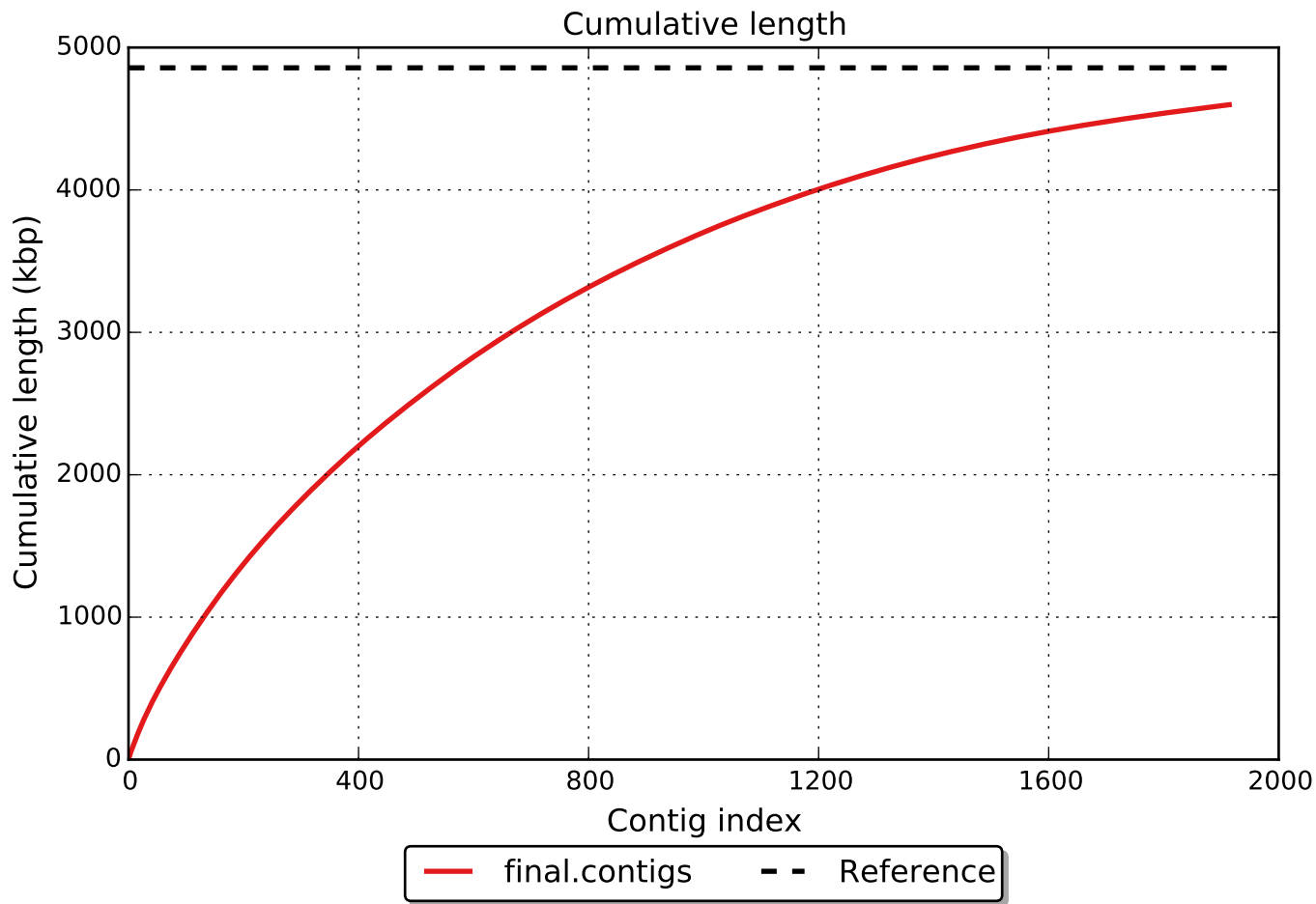
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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

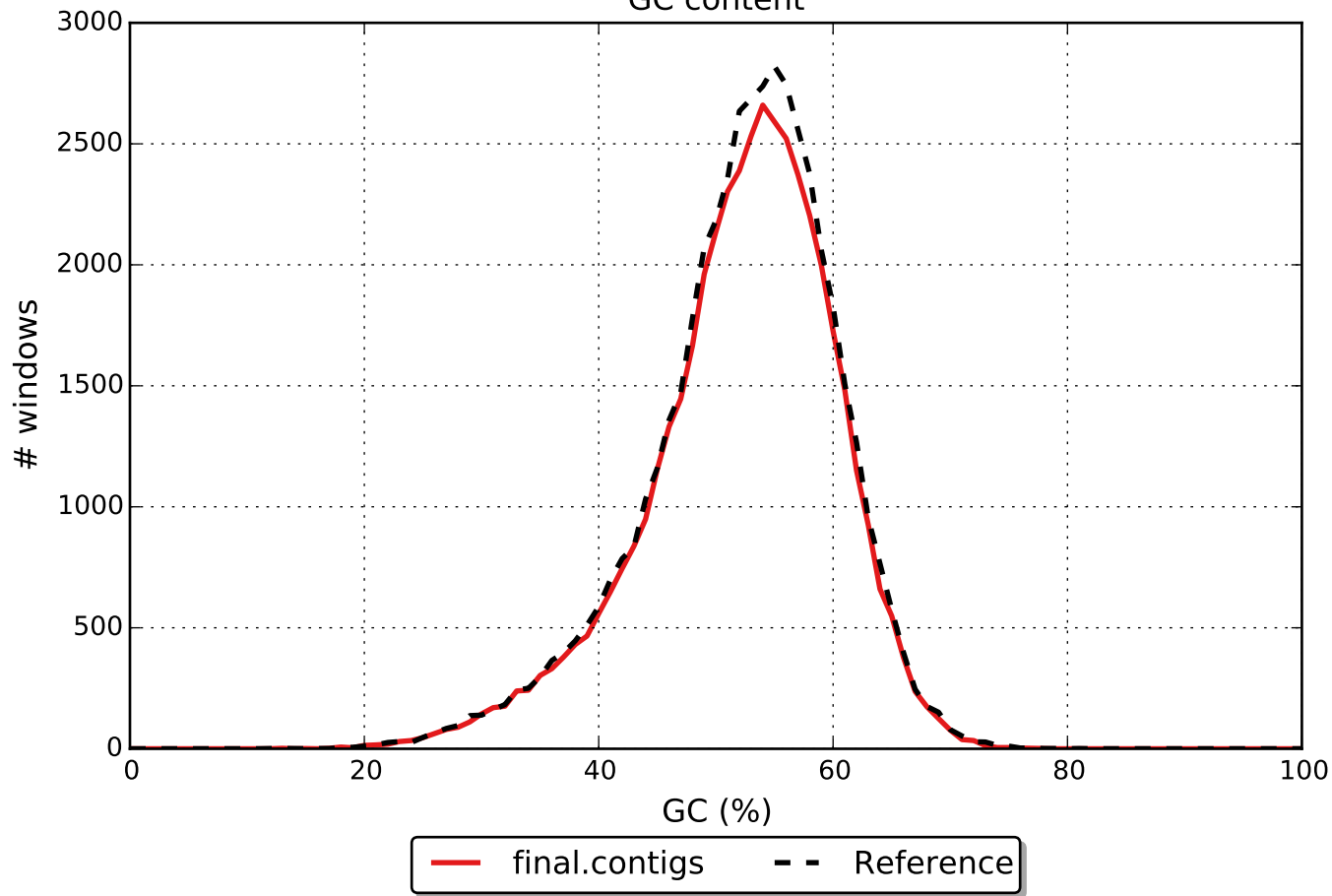


NGx





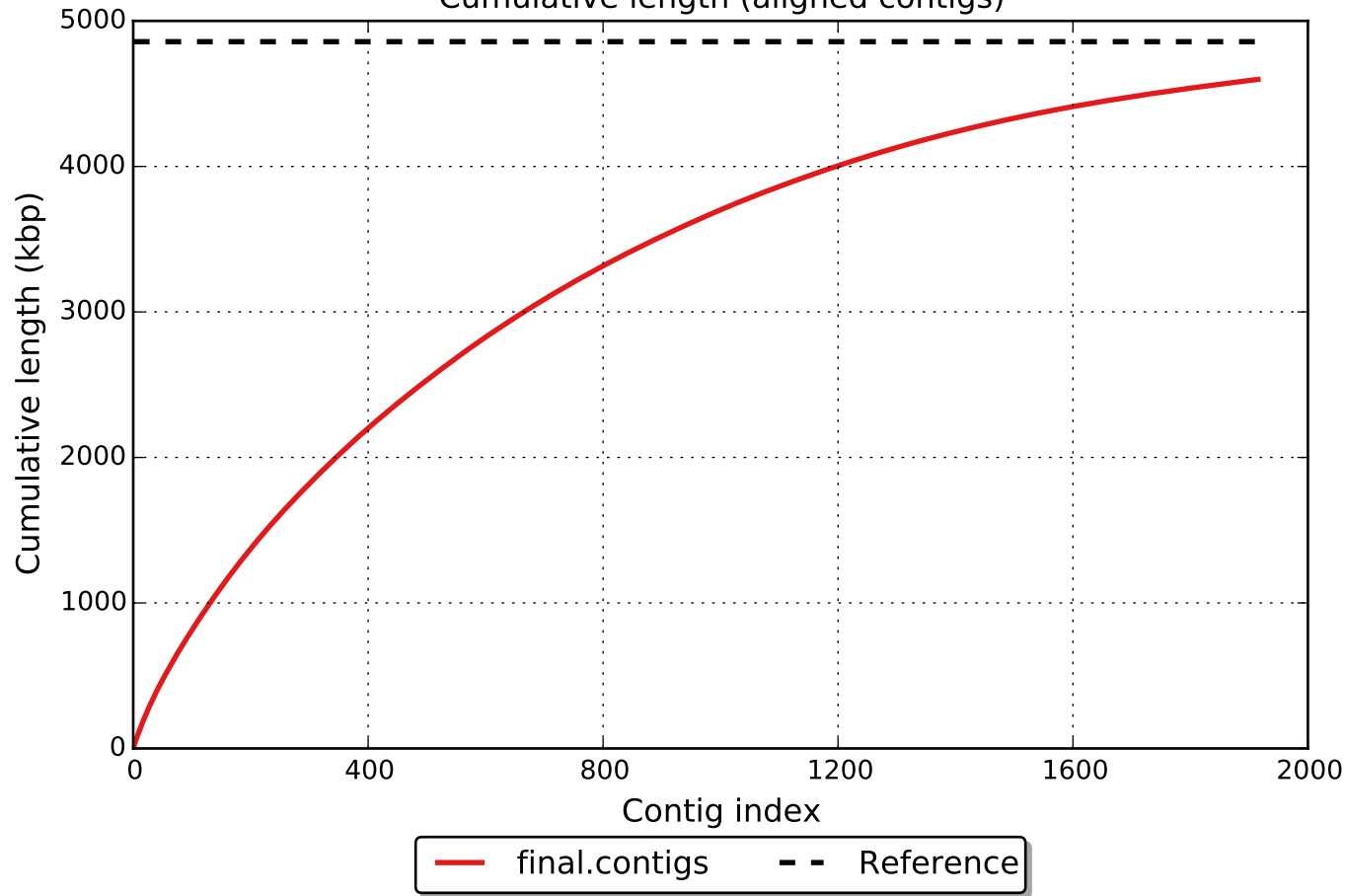
GC content



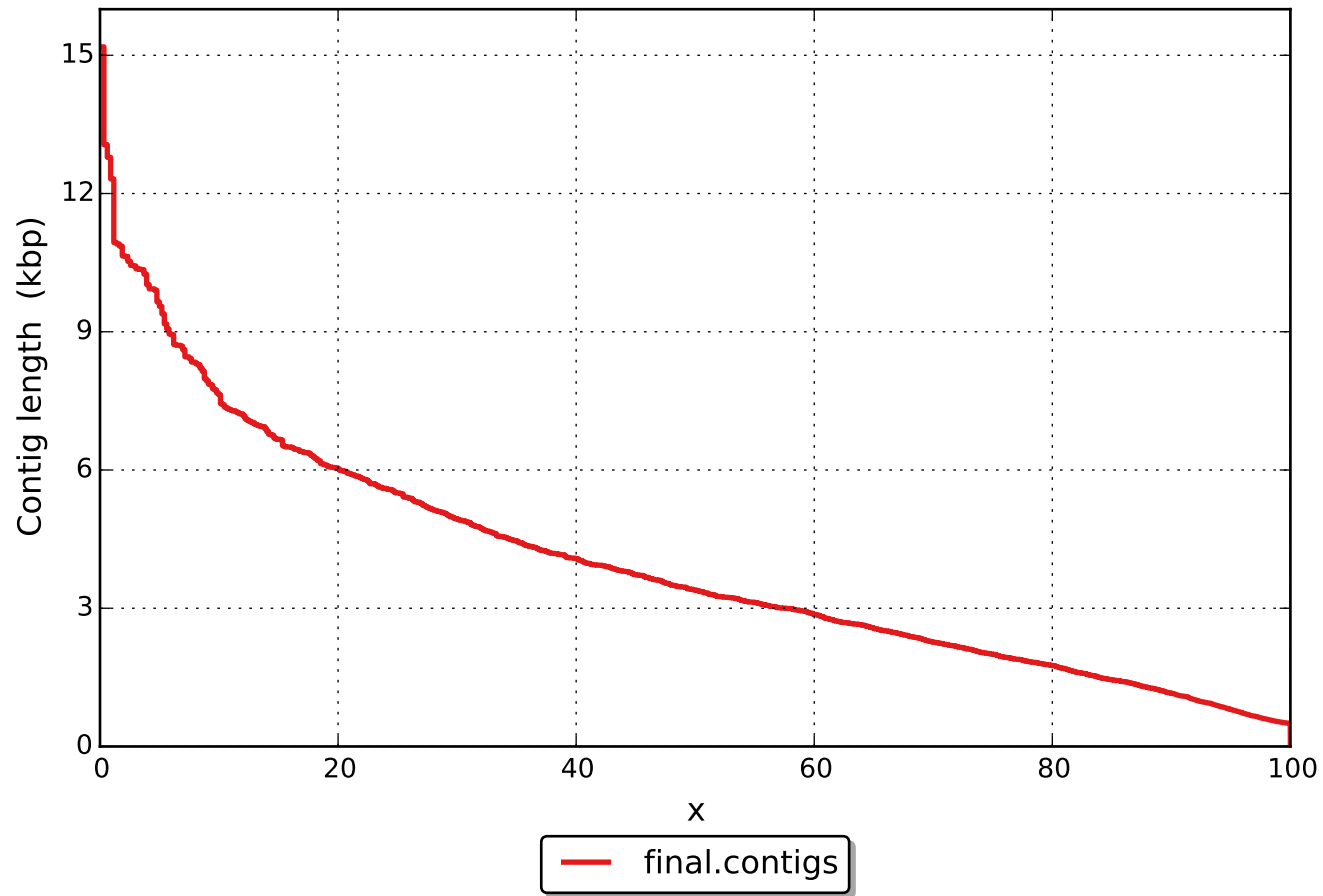




Cumulative length (aligned contigs)



NAx



NGAx

