

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	1184
# contigs ( $\geq 1000$ bp)	388
Total length ( $\geq 0$ bp)	1136553
Total length ( $\geq 1000$ bp)	571254
# contigs	1184
Largest contig	4169
Total length	1136553
Reference length	641799
GC (%)	26.29
Reference GC (%)	26.30
N50	1001
NG50	1359
N75	735
NG75	1108
L50	386
LG50	171
L75	719
LG75	304
# misassemblies	12
# misassembled contigs	12
Misassembled contigs length	14988
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	90.975
Duplication ratio	1.947
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1171.13
# indels per 100 kbp	1.37
Largest alignment	4169
NA50	841
NGA50	1147
NA75	579
NGA75	924
LA50	454
LGA50	201
LA75	859
LGA75	356

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).

## Misassemblies report

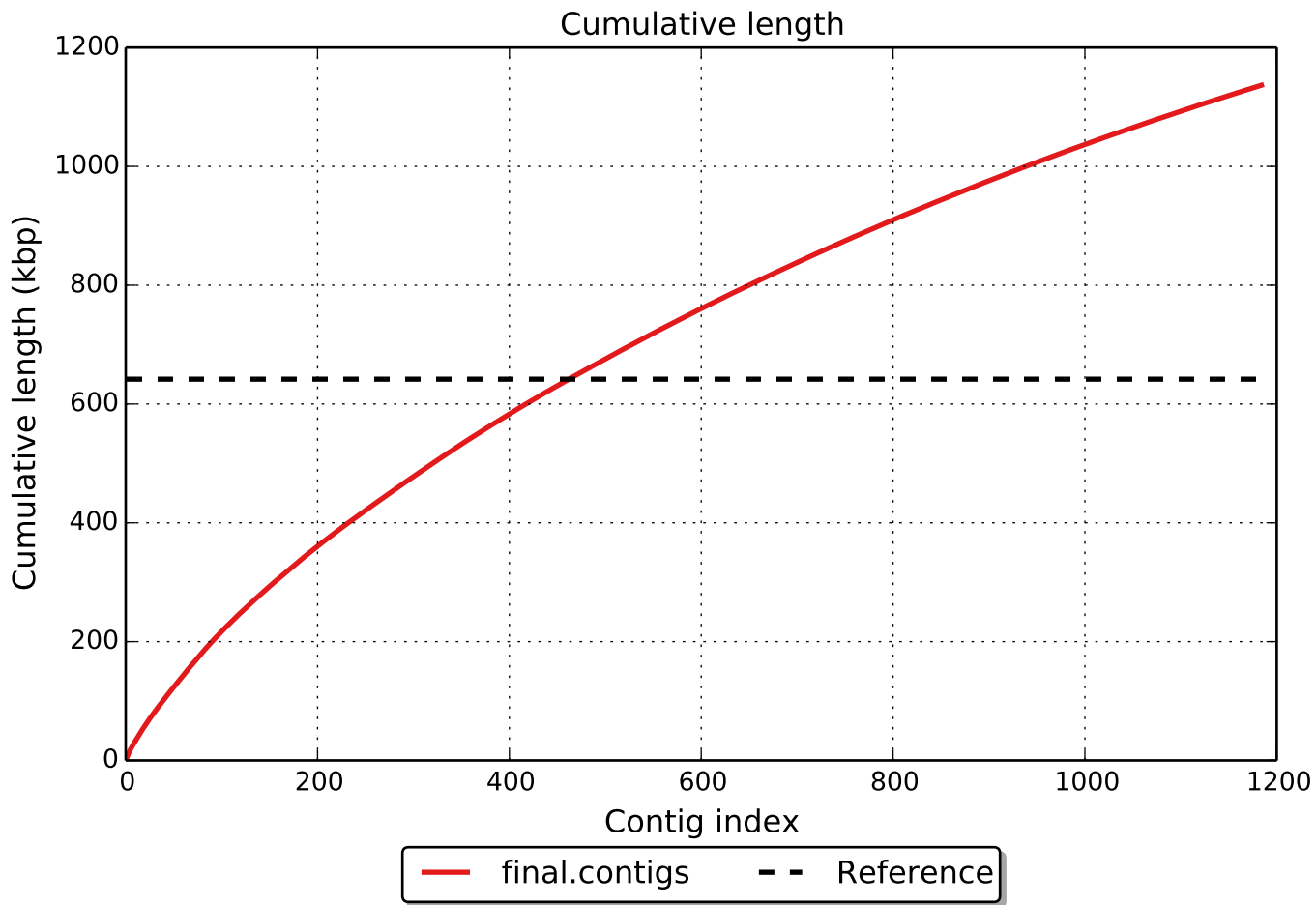
	final.contigs
# misassemblies	12
# relocations	12
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	12
Misassembled contigs length	14988
# local misassemblies	0
# mismatches	6838
# indels	8
# short indels	8
# long indels	0
Indels length	8

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).

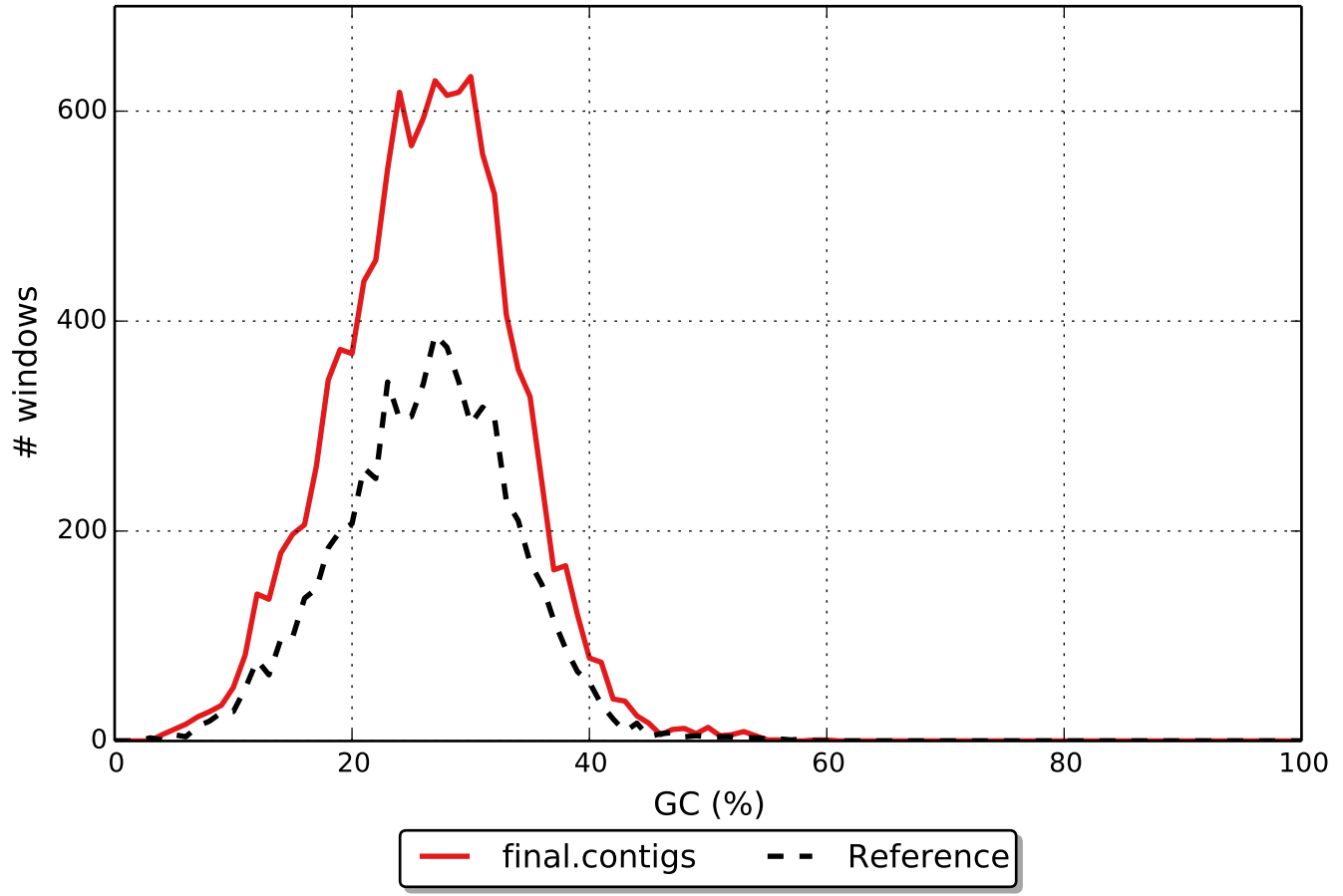
## Unaligned report

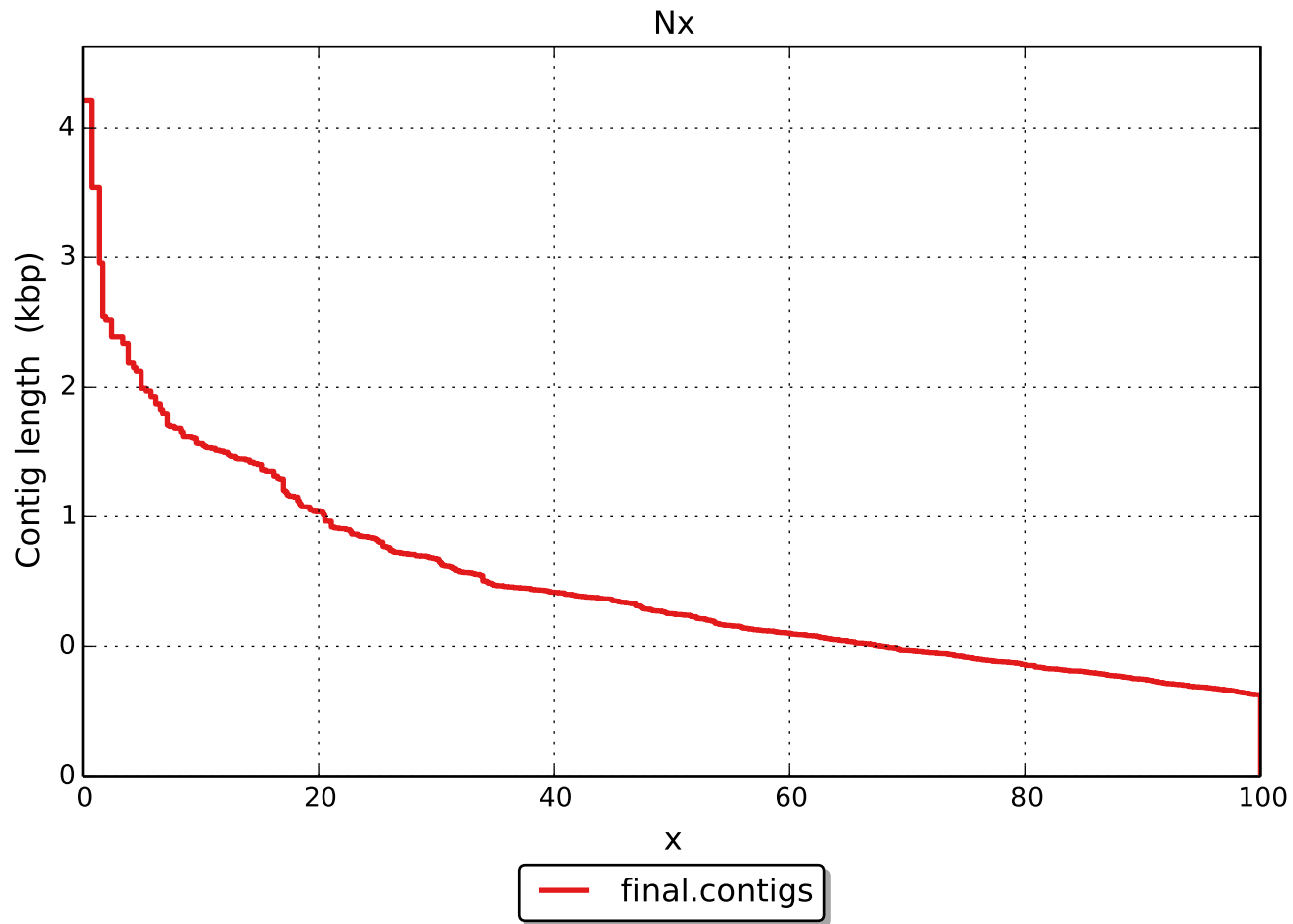
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

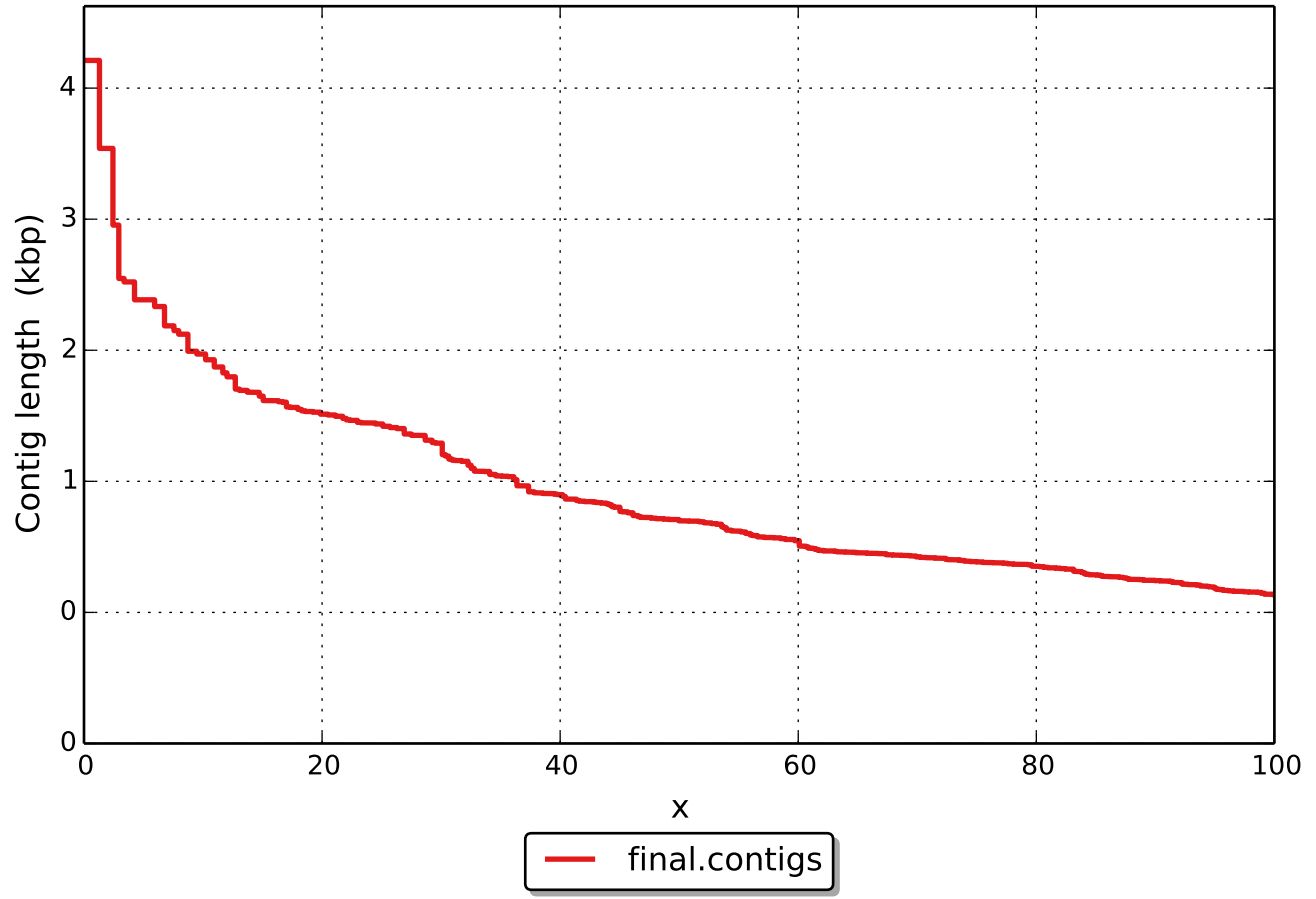


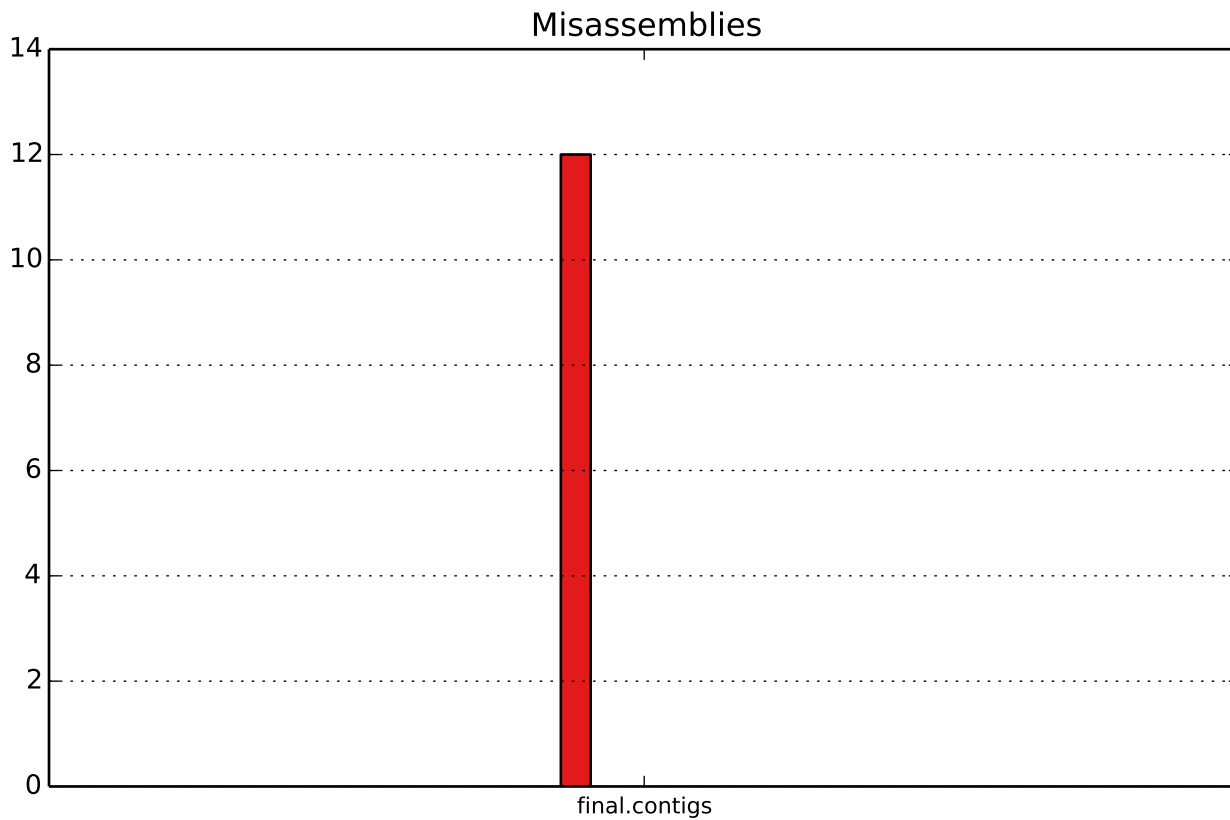
# GC content





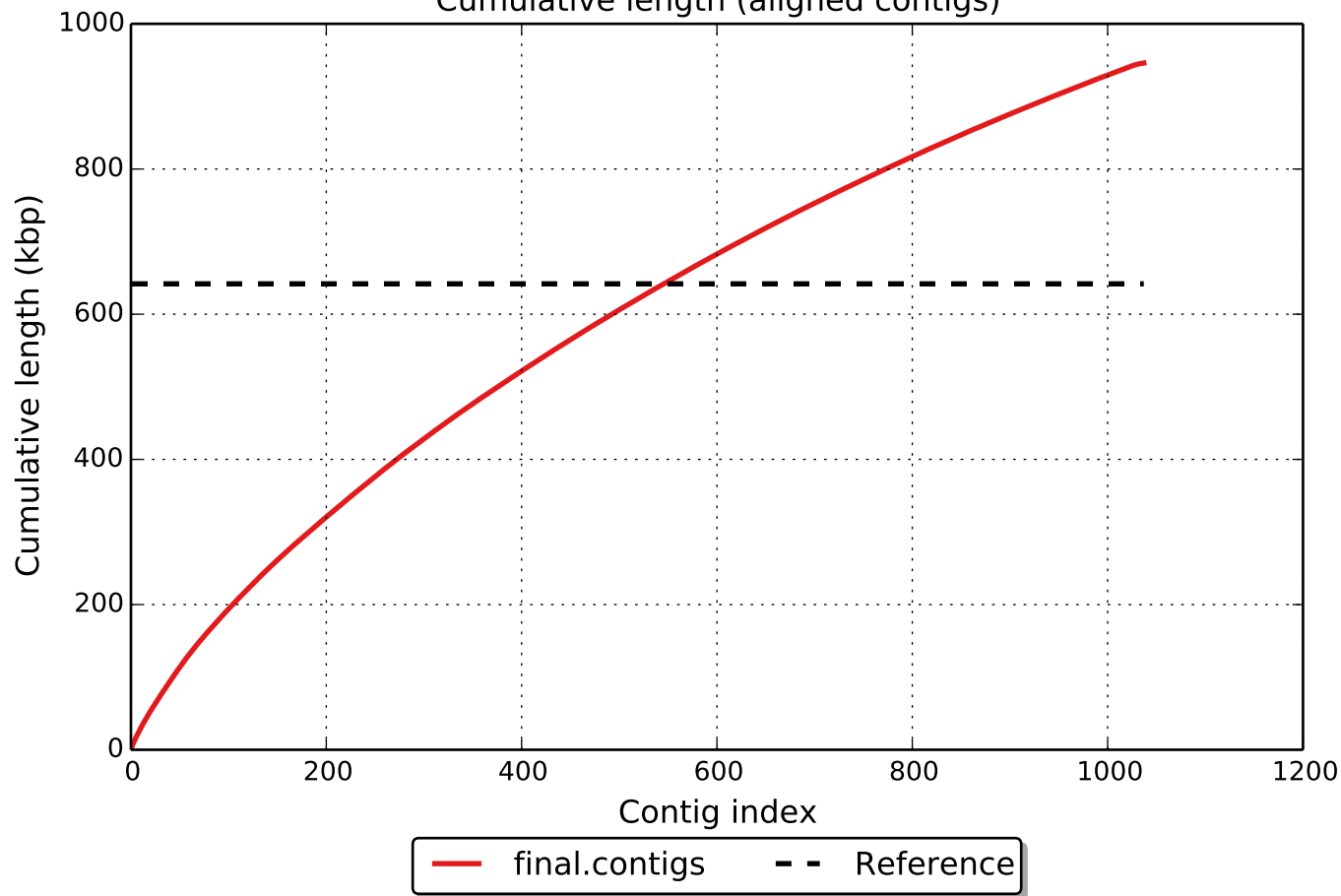
NGx



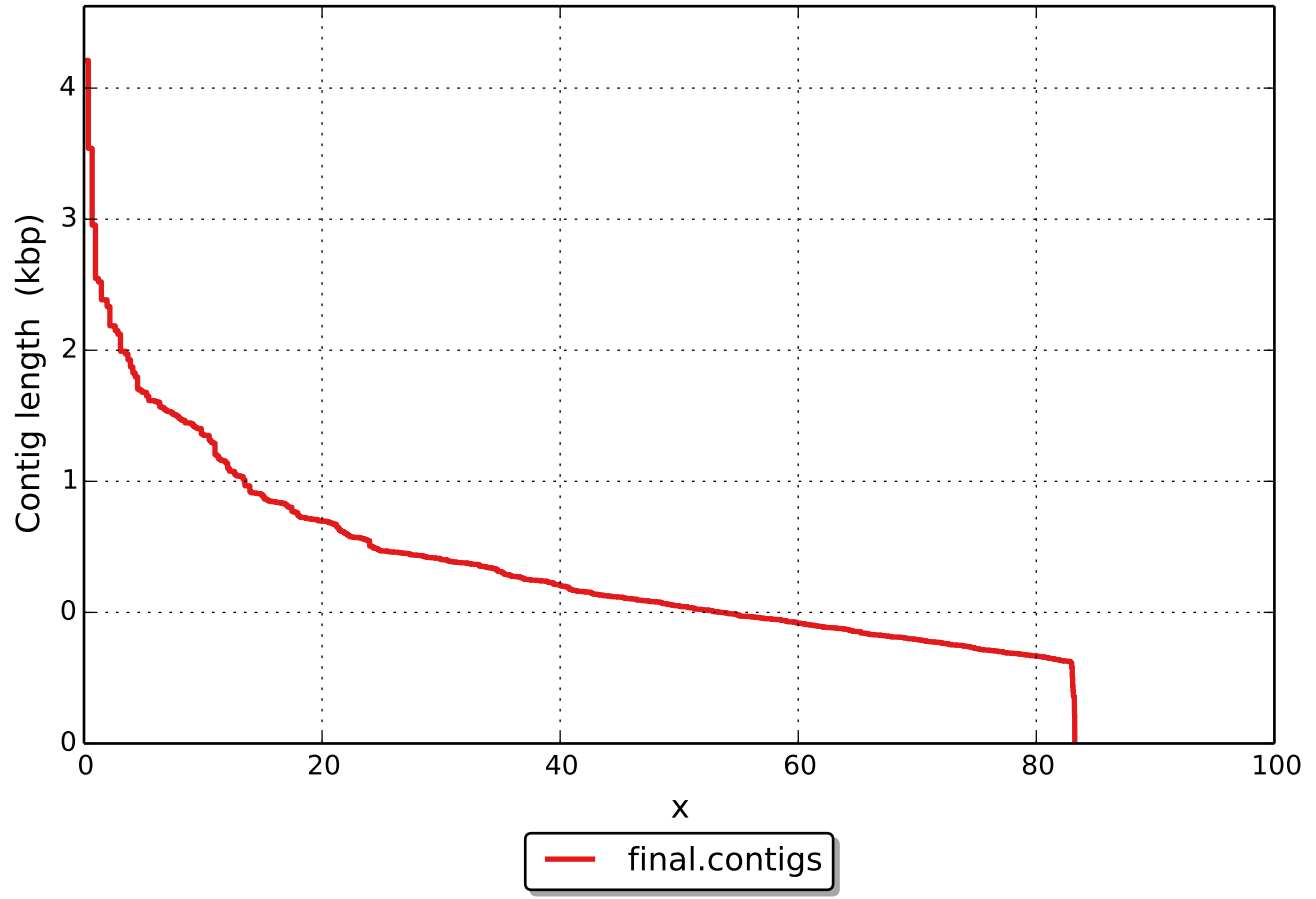




Cumulative length (aligned contigs)



NAx



# NGAx

