

## Report

	final.contigs
# contigs (>= 0 bp)	1919
# contigs (>= 1000 bp)	694
# contigs (>= 5000 bp)	325
# contigs (>= 10000 bp)	132
# contigs (>= 25000 bp)	8
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	4850290
Total length (>= 1000 bp)	4448339
Total length (>= 5000 bp)	3410710
Total length (>= 10000 bp)	2038742
Total length (>= 25000 bp)	241570
Total length (>= 50000 bp)	0
# contigs	780
Largest contig	42357
Total length	4512970
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	8866
NG50	8768
N75	5057
NG75	4753
L50	156
LG50	163
L75	320
LG75	340
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	4 + 0 part
Unaligned length	2223
Genome fraction (%)	96.815
Duplication ratio	1.004
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.60
# indels per 100 kbp	0.00
Largest alignment	42357
NA50	8866
NGA50	8768
NA75	5057
NGA75	4753
LA50	156
LGA50	163
LA75	320
LGA75	340

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

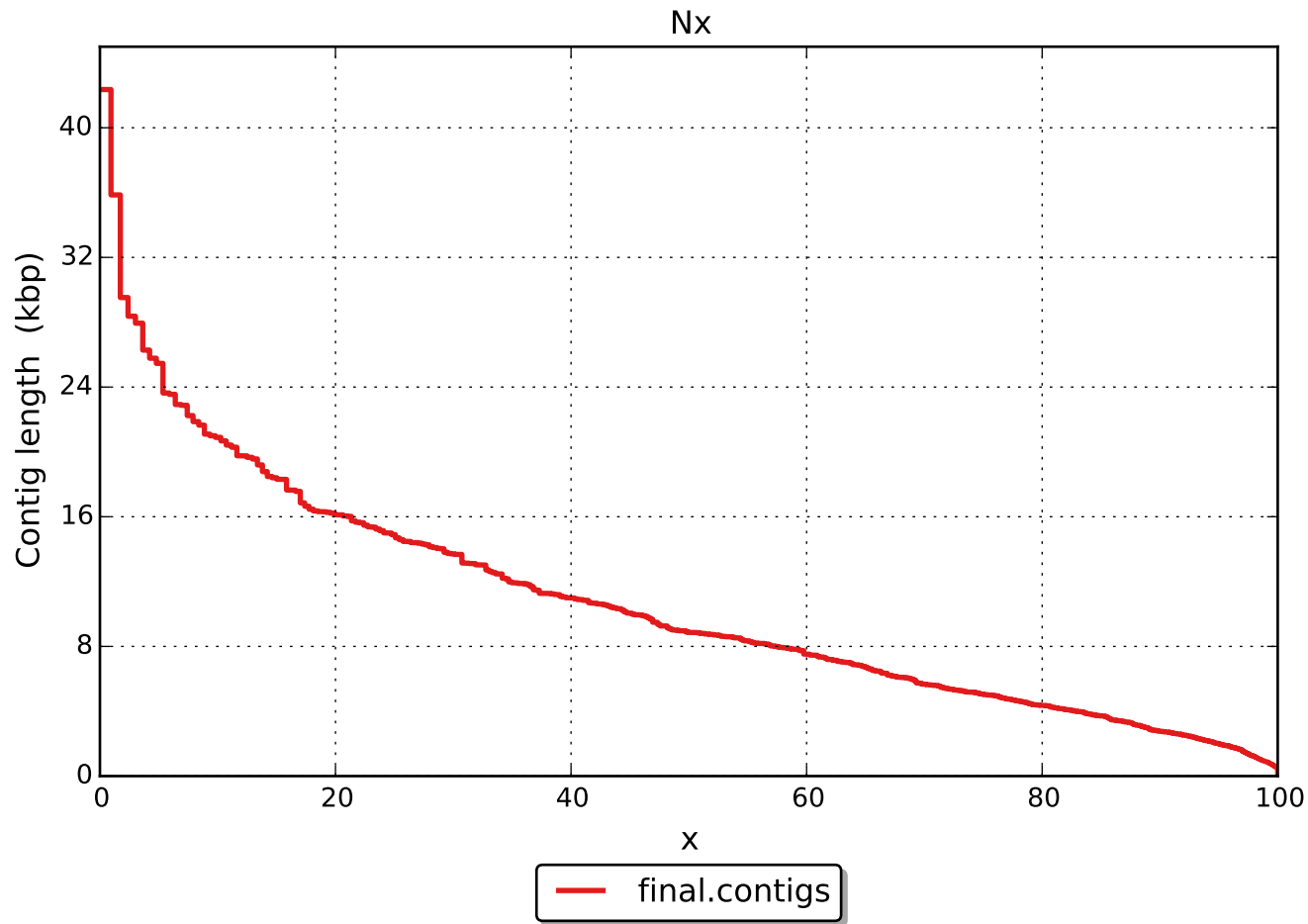
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	27
# indels	0
# short indels	0
# long indels	0
Indels length	0

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).

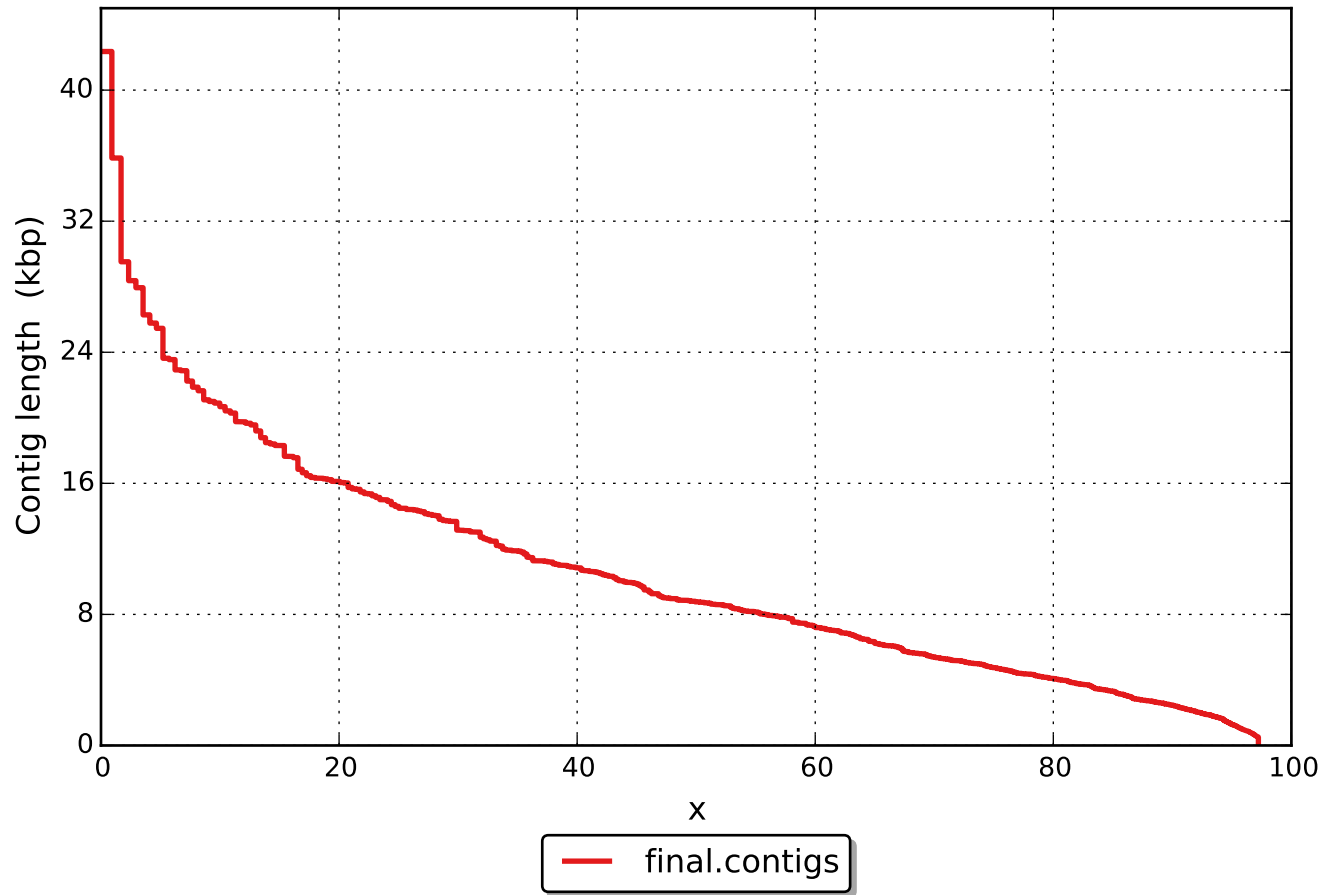
## Unaligned report

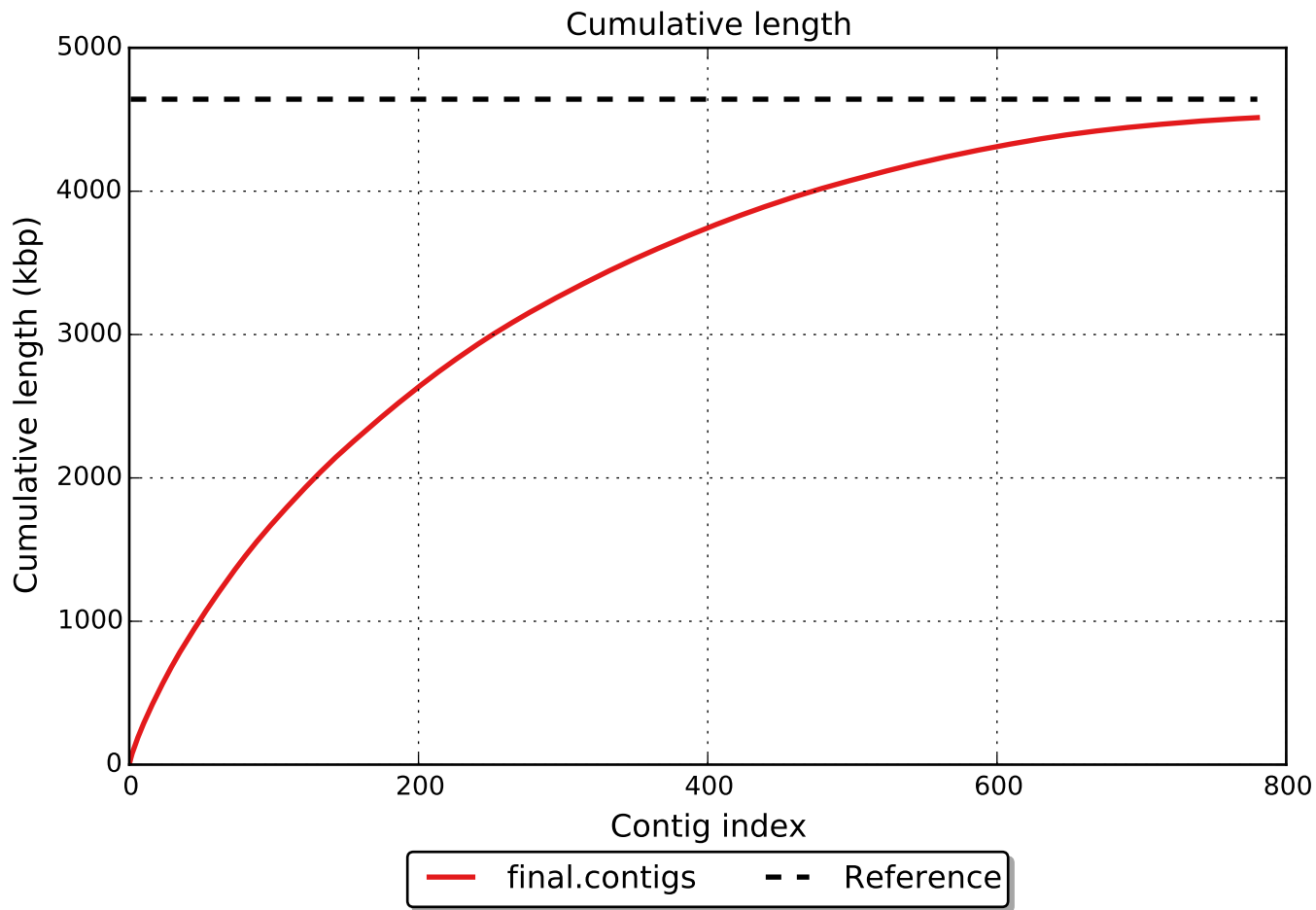
	final.contigs
# fully unaligned contigs	4
Fully unaligned length	2223
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

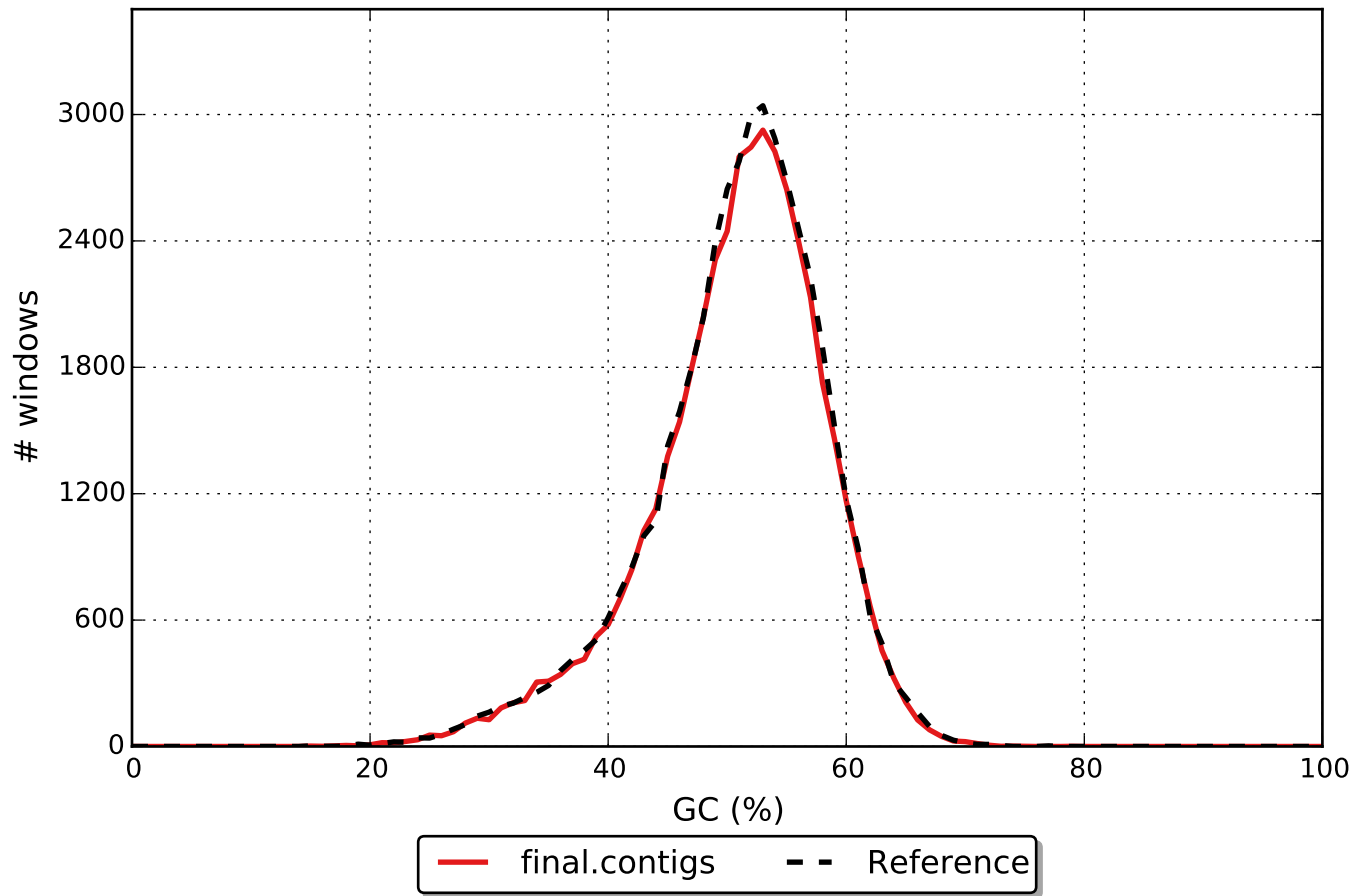


NGx





GC content

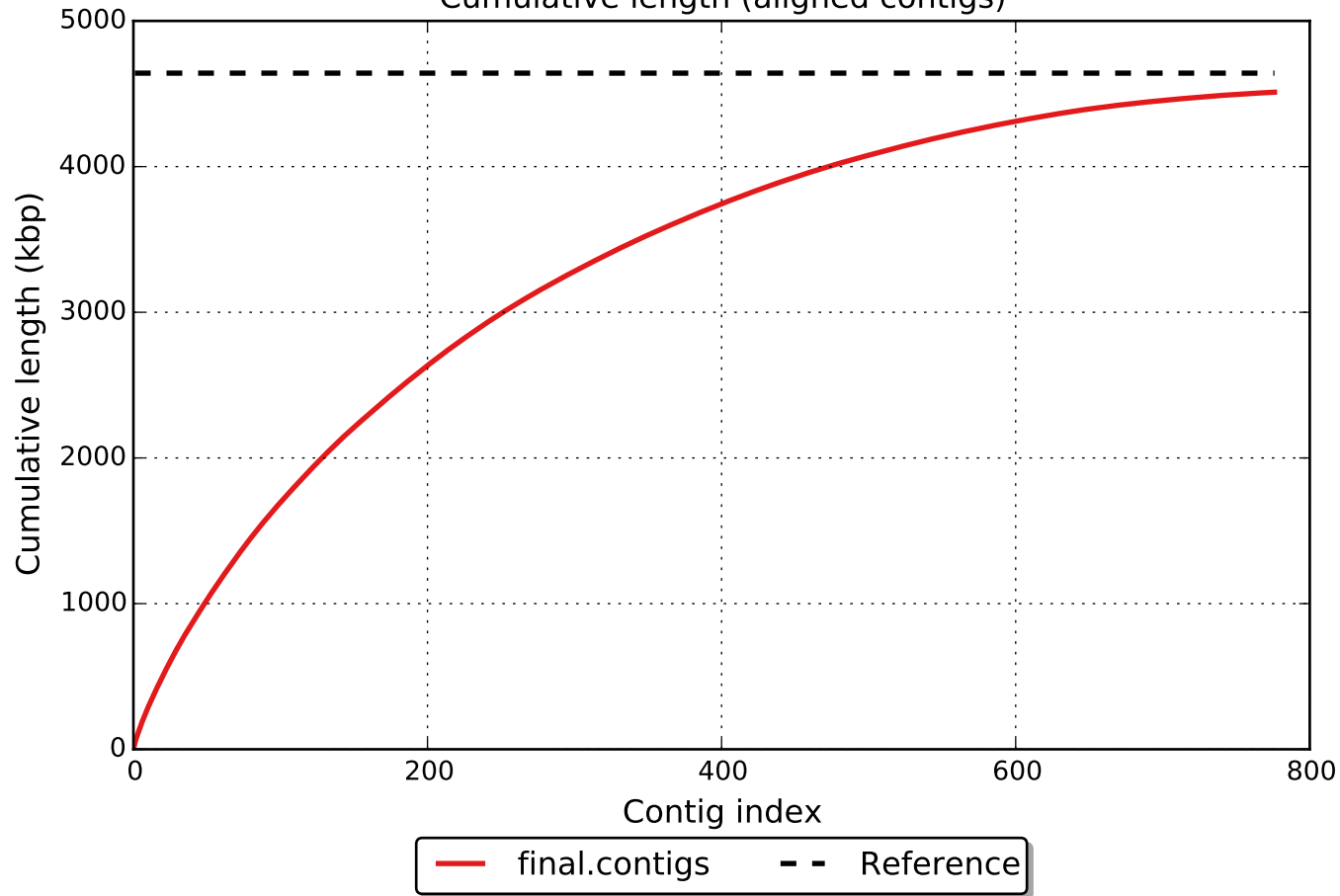


# Misassemblies

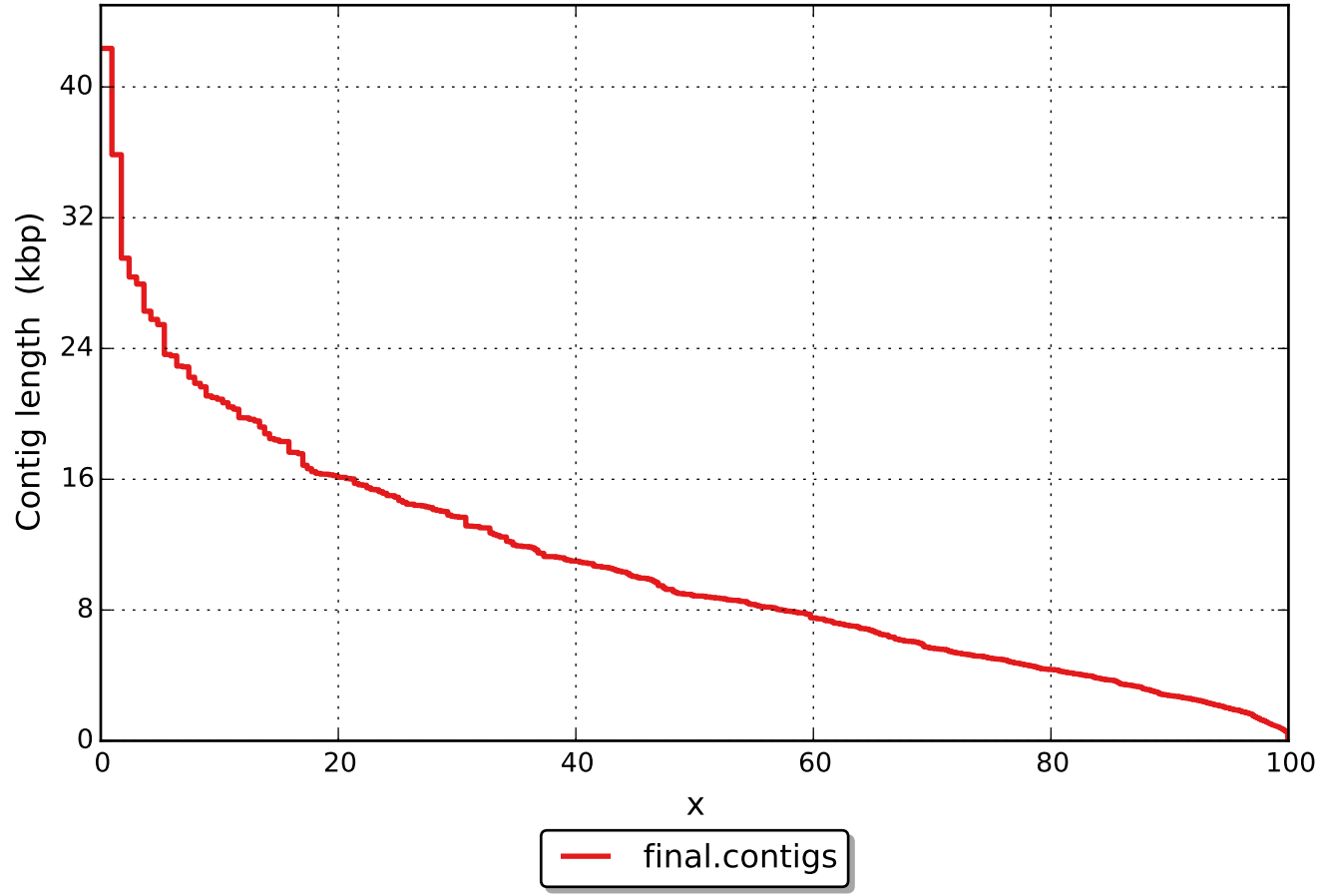




Cumulative length (aligned contigs)



NAx



# NGAx

