

Report

	final.contigs
# contigs (>= 1000 bp)	151
# contigs (>= 5000 bp)	133
# contigs (>= 10000 bp)	111
# contigs (>= 25000 bp)	67
# contigs (>= 50000 bp)	28
Total length (>= 1000 bp)	4650220
Total length (>= 5000 bp)	4591524
Total length (>= 10000 bp)	4418440
Total length (>= 25000 bp)	3618843
Total length (>= 50000 bp)	2254123
# contigs	157
Largest contig	177974
Total length	4654357
Reference length	4641652
GC (℥)	50.79
Reference GC (℥)	50.79
N50	48434
NG50	48434
N75	27972
NG75	28189
L50	30
LG50	30
L75	63
LG75	62
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (℥)	99.989
Duplication ratio	1.003
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.00
Largest alignment	177974
NA50	48434
NGA50	48434
NA75	27972
NGA75	28189
LA50	30
LGA50	30
LA75	63
LGA75	62

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

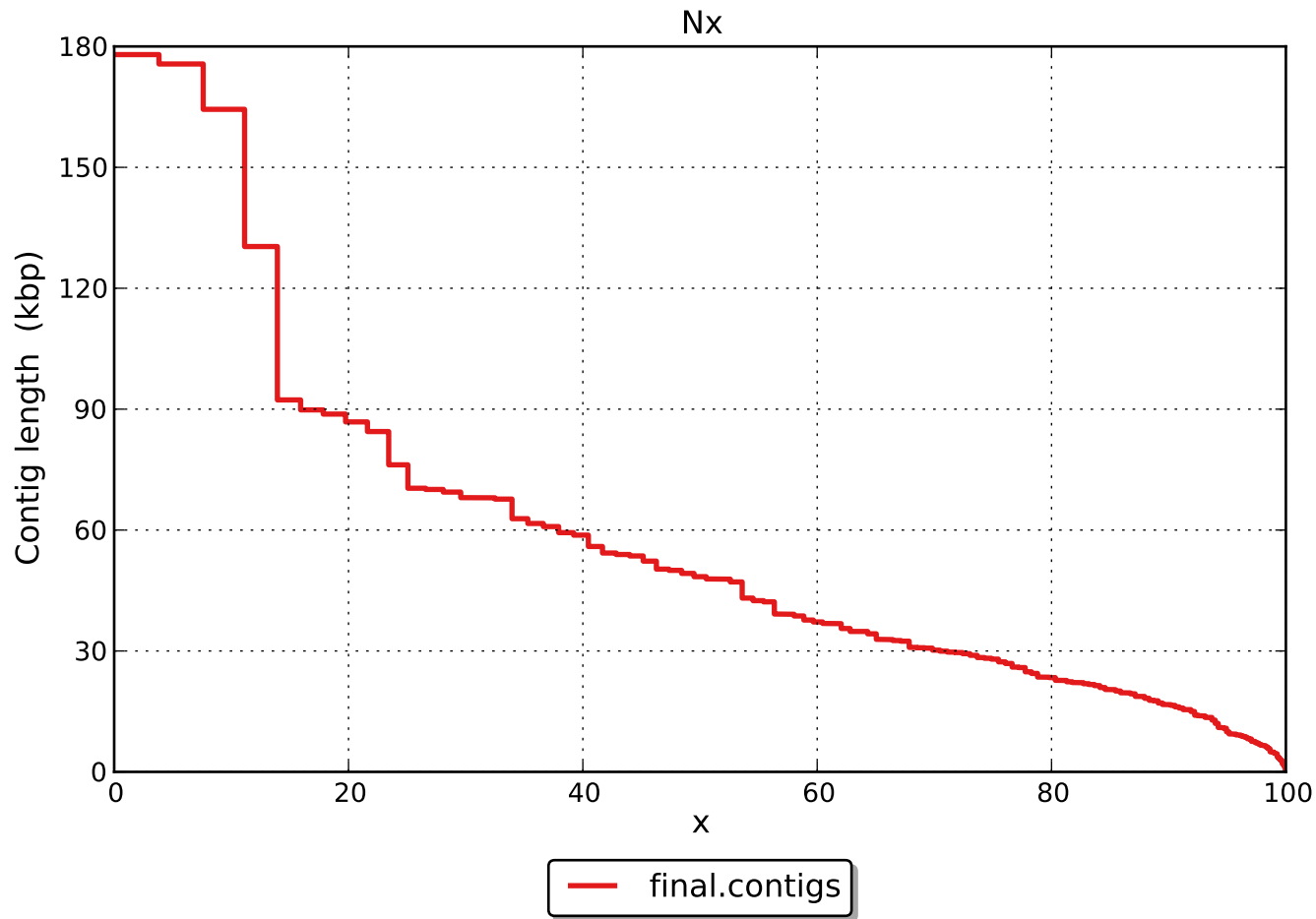
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	0
# indels	0
# short indels	0
# long indels	0
Indels length	0

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).

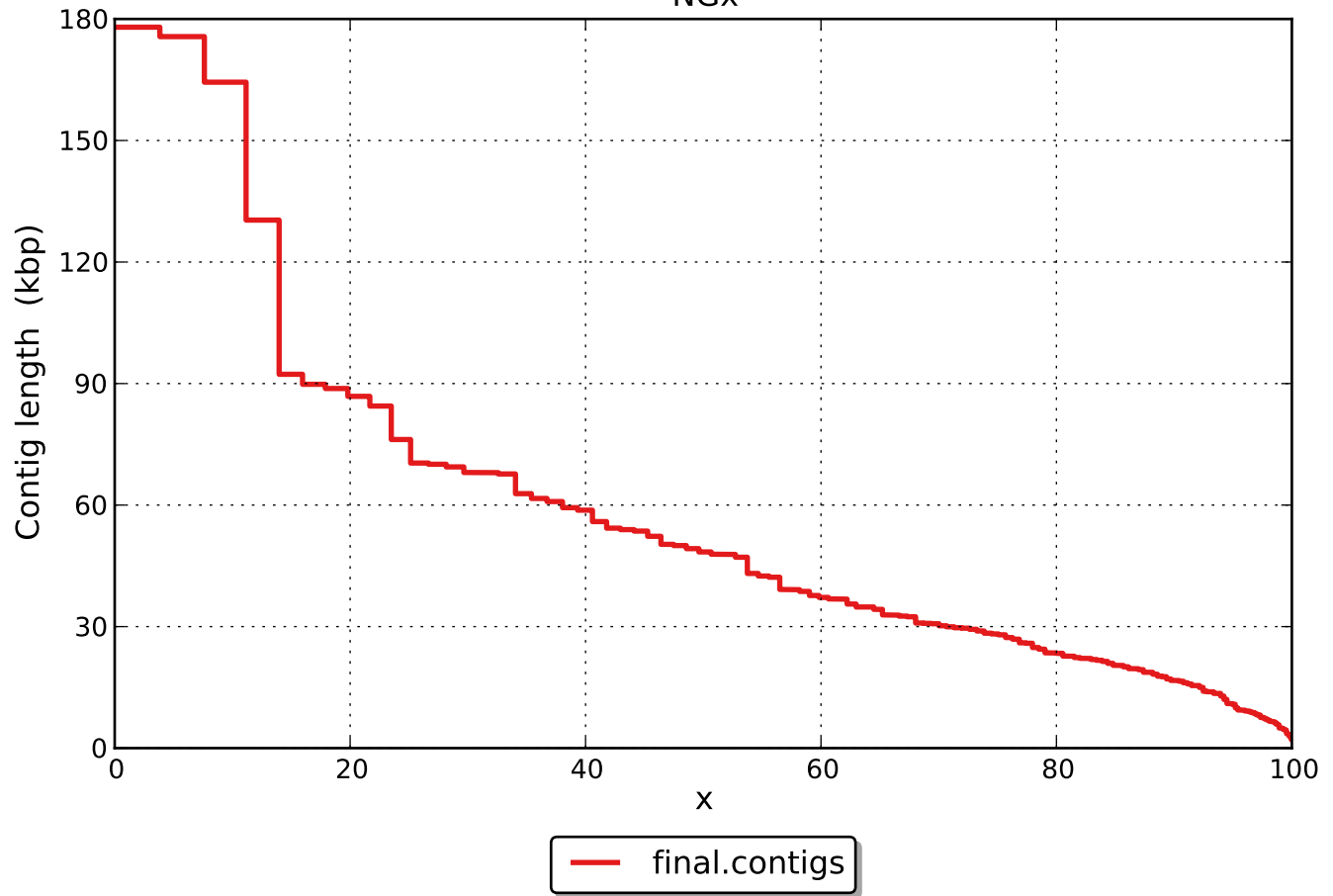
## Unaligned report

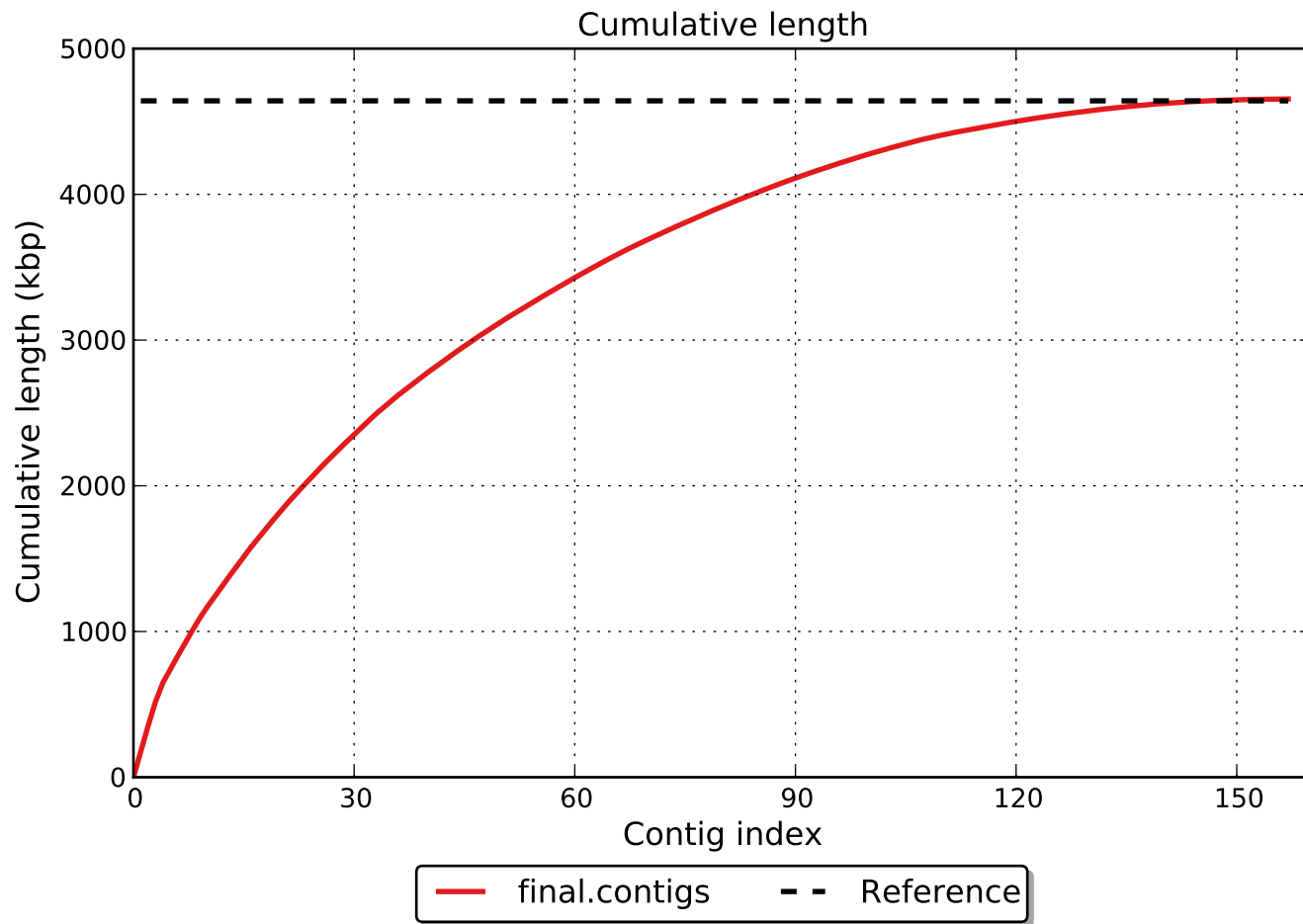
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

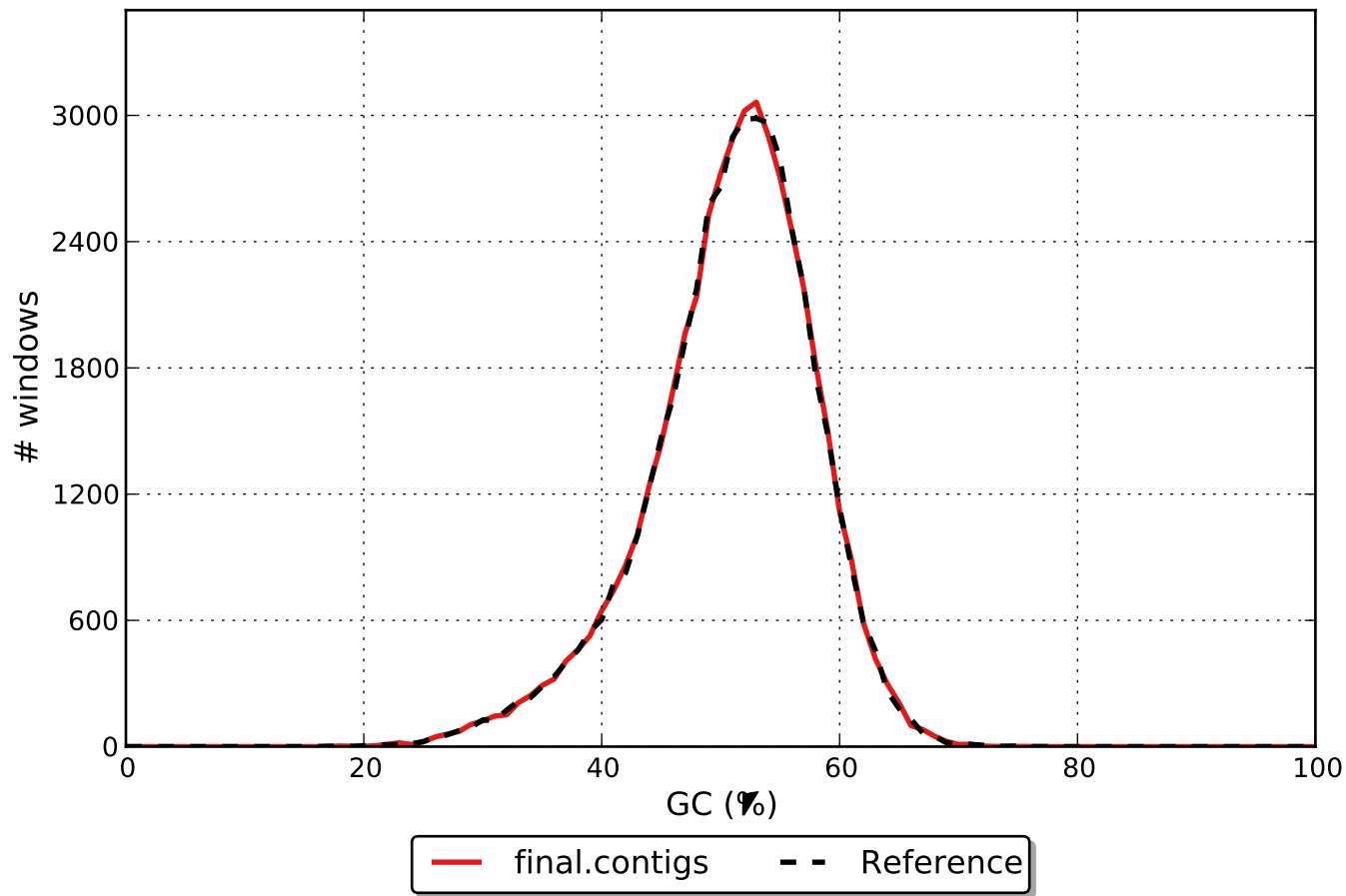


NGx





# GC content

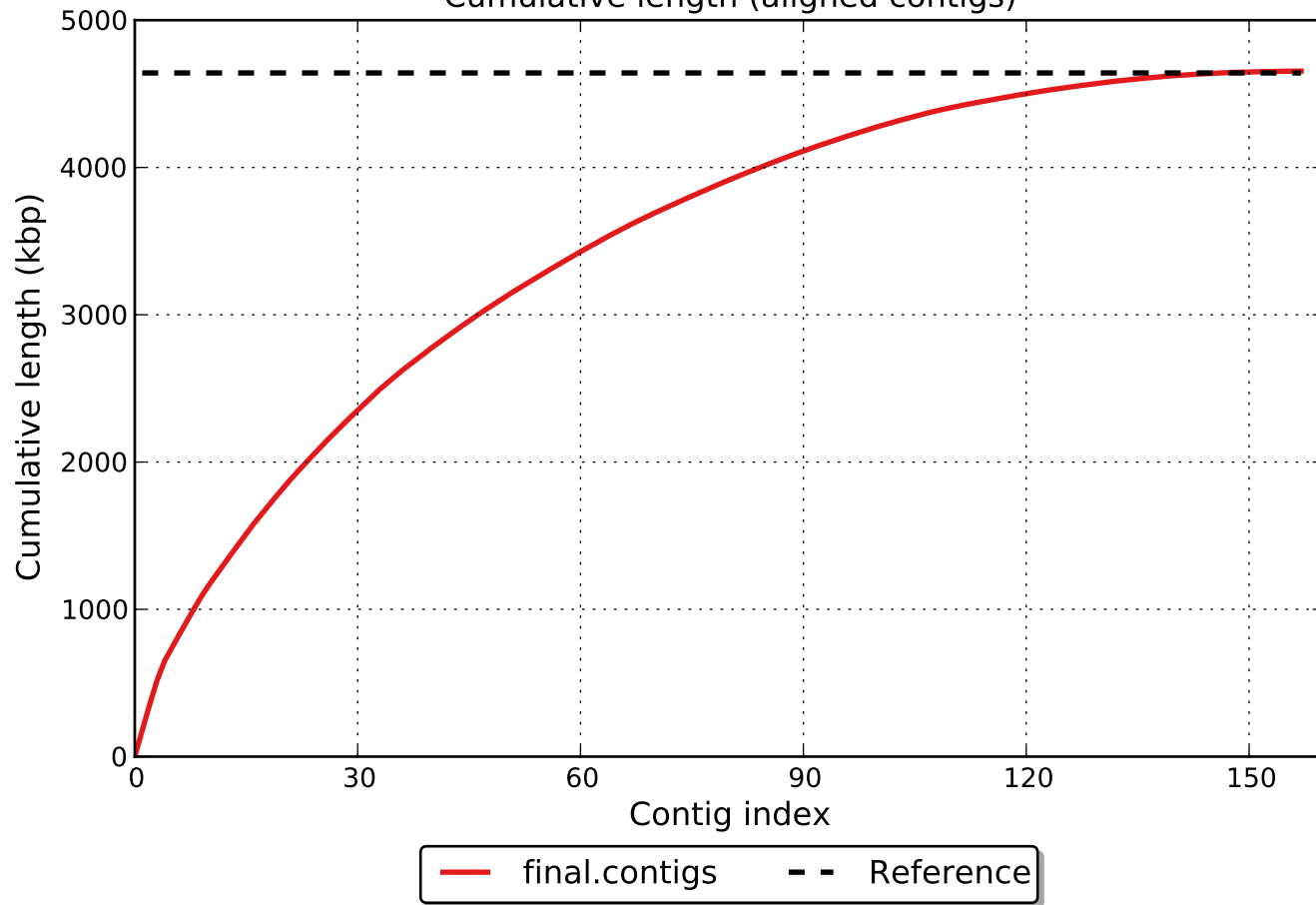


# Misassemblies

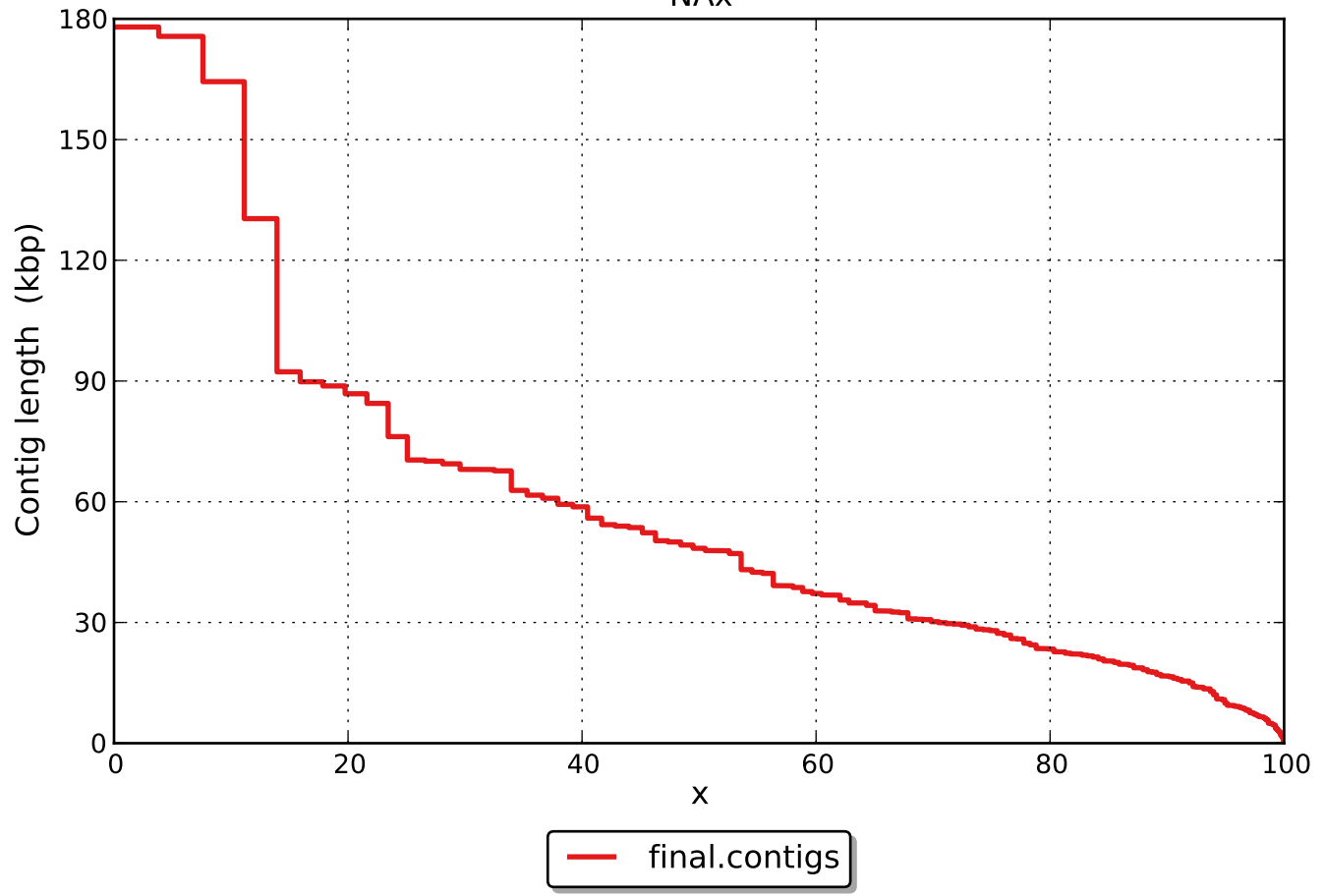




Cumulative length (aligned contigs)



NAx



# NGAx

