

## Report

	final.contigs
# contigs (>= 1000 bp)	289
# contigs (>= 5000 bp)	227
# contigs (>= 10000 bp)	166
# contigs (>= 25000 bp)	69
# contigs (>= 50000 bp)	12
Total length (>= 1000 bp)	4862475
Total length (>= 5000 bp)	4683840
Total length (>= 10000 bp)	4259289
Total length (>= 25000 bp)	2716212
Total length (>= 50000 bp)	775975
# contigs	304
Largest contig	78170
Total length	4872889
Reference length	4857432
GC (%)	52.22
Reference GC (%)	52.23
N50	26649
NG50	26858
N75	15433
NG75	15433
L50	59
LG50	58
L75	117
LG75	117
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.676
Duplication ratio	1.006
# N's per 100 kbp	0.00
# mismatches per 100 kbp	8.43
# indels per 100 kbp	0.00
Largest alignment	78170
NA50	26649
NGA50	26858
NA75	15433
NGA75	15433
LA50	59
LGA50	58
LA75	117
LGA75	117

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

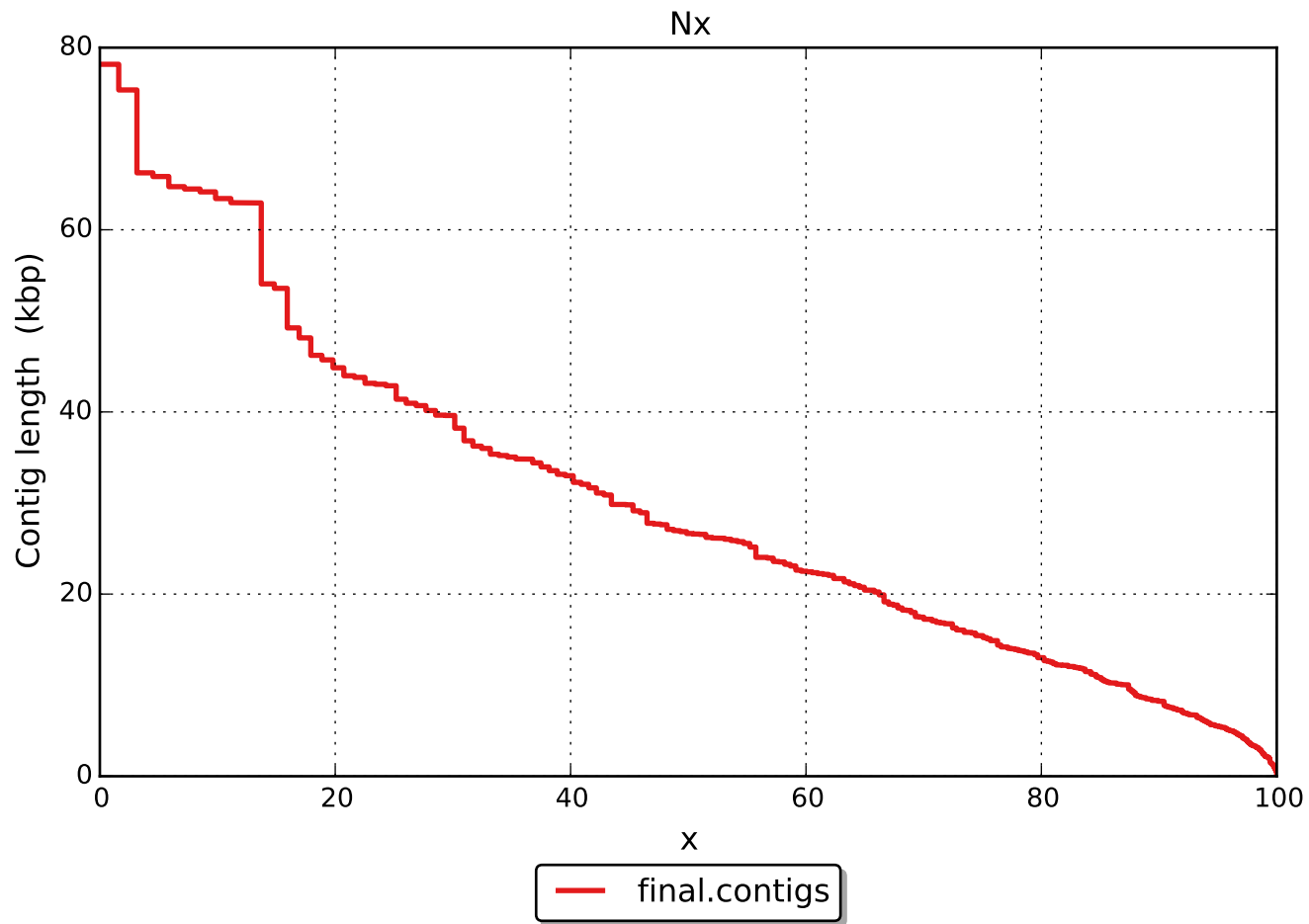
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	408
# indels	0
# short indels	0
# long indels	0
Indels length	0

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).

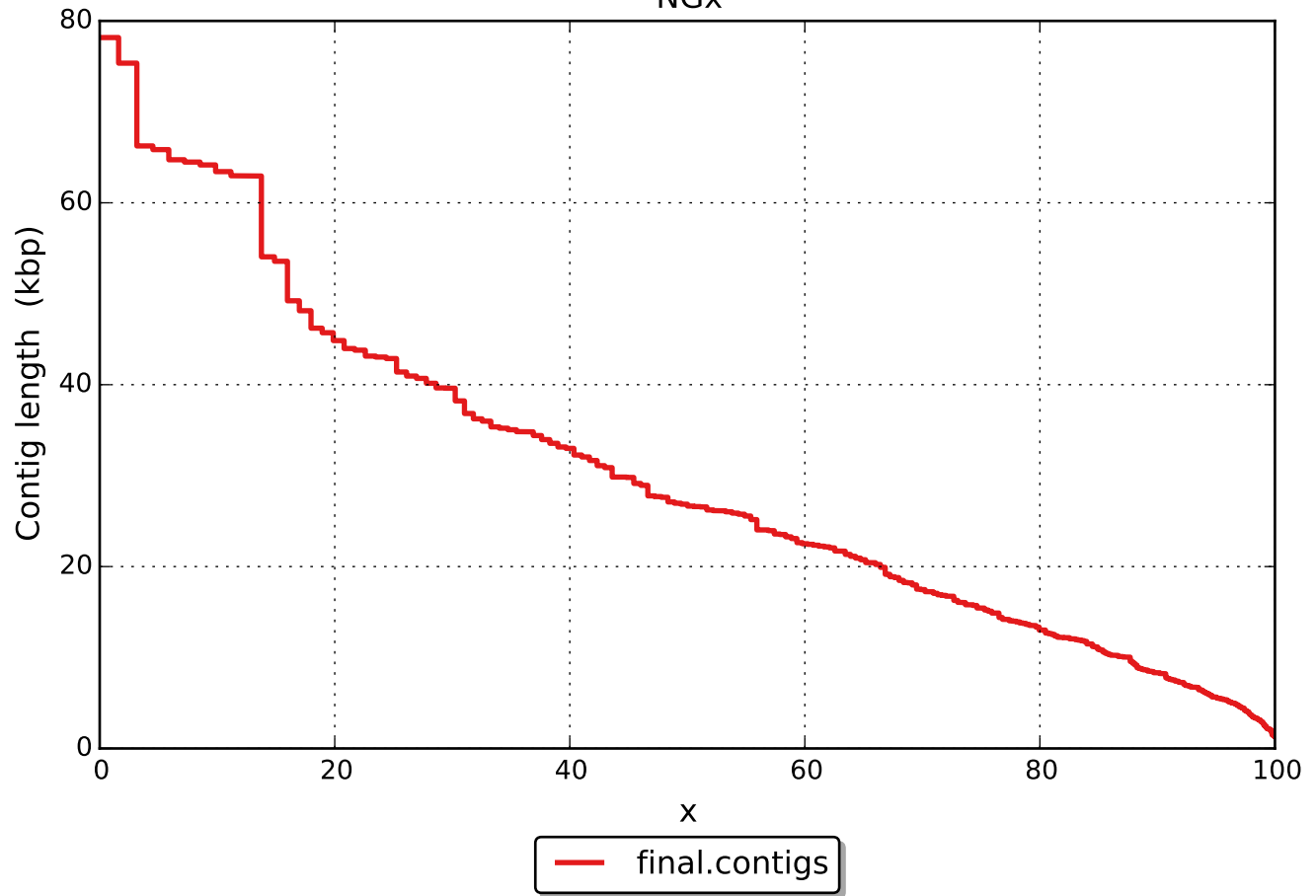
## Unaligned report

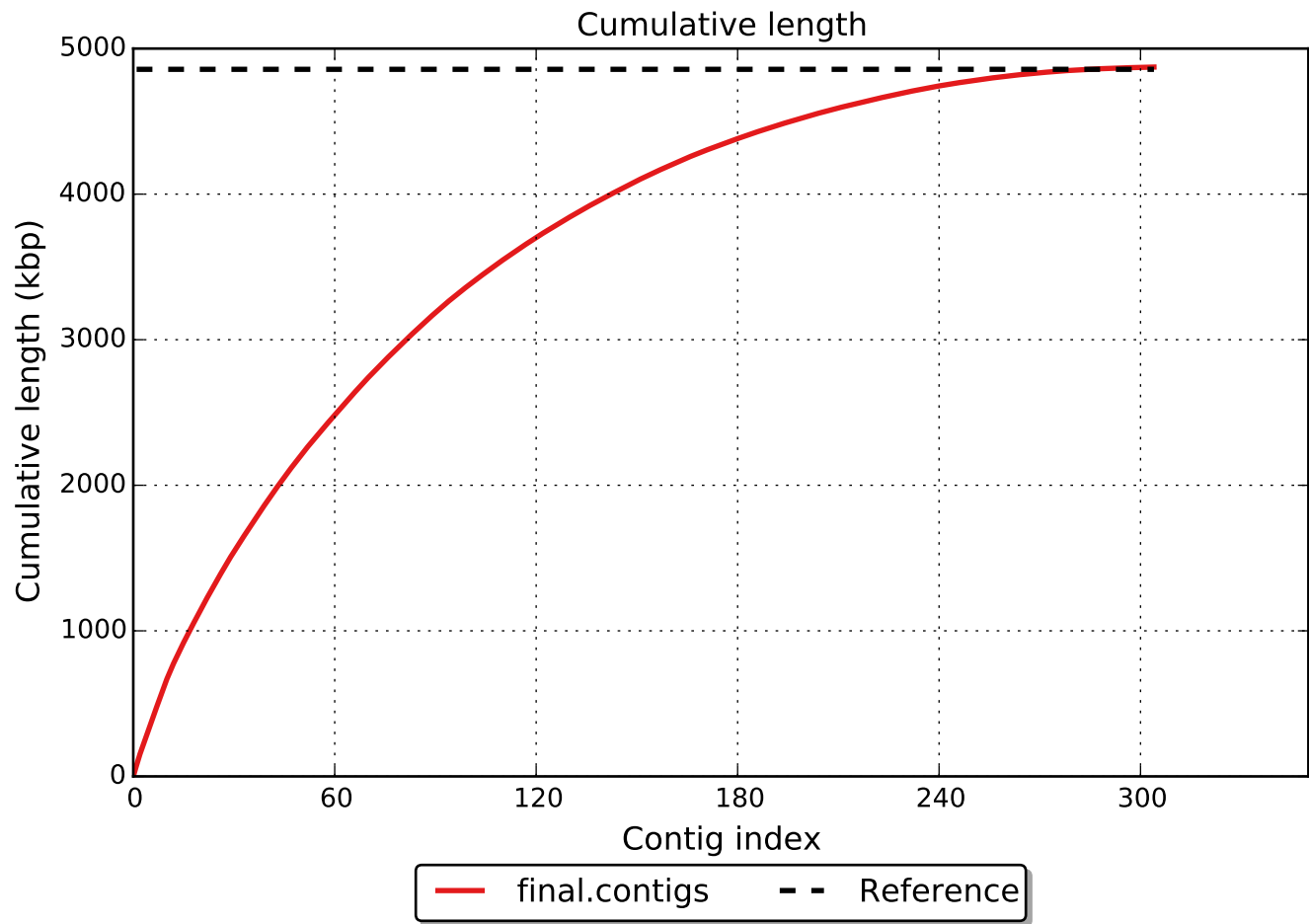
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

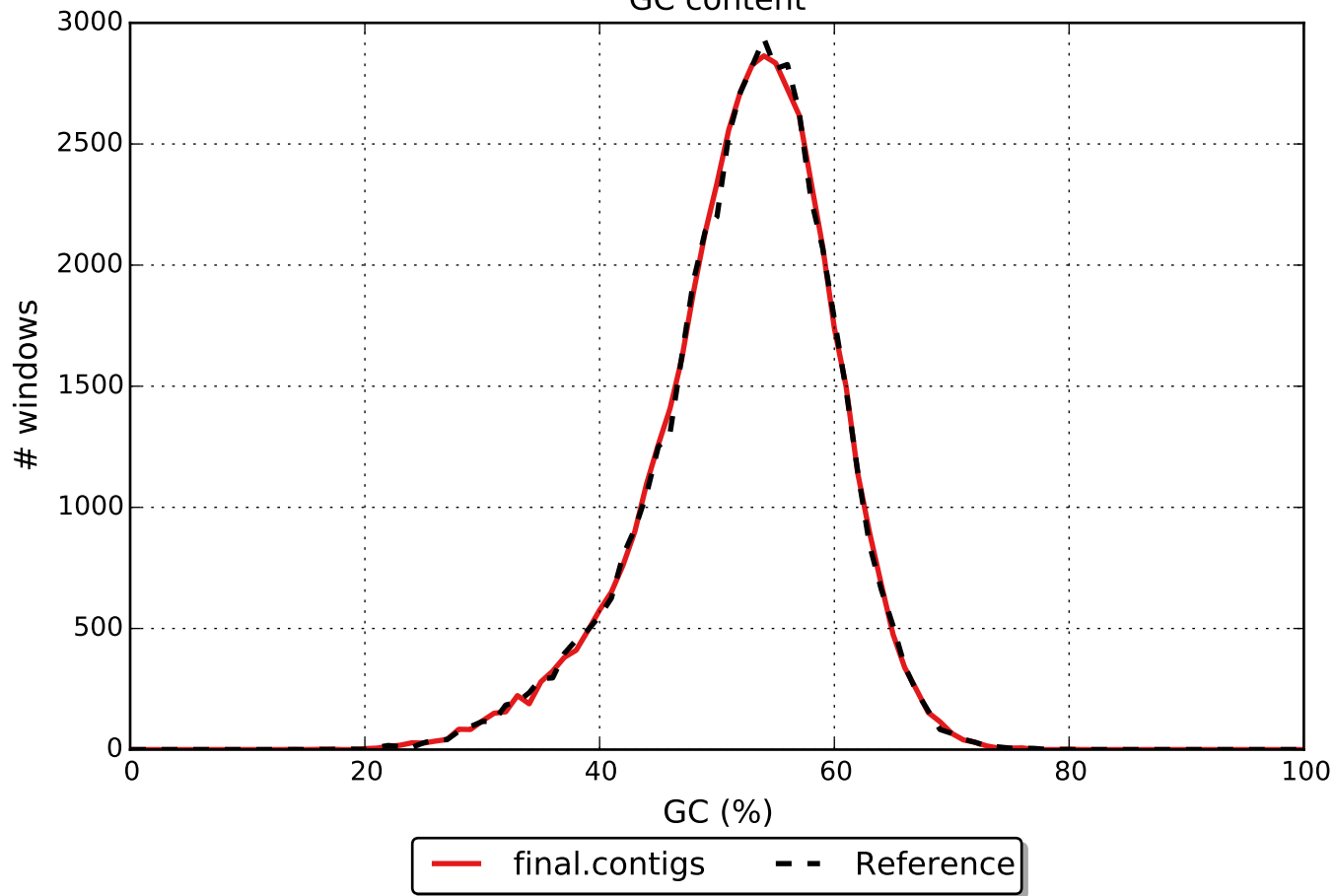


NGx





GC content

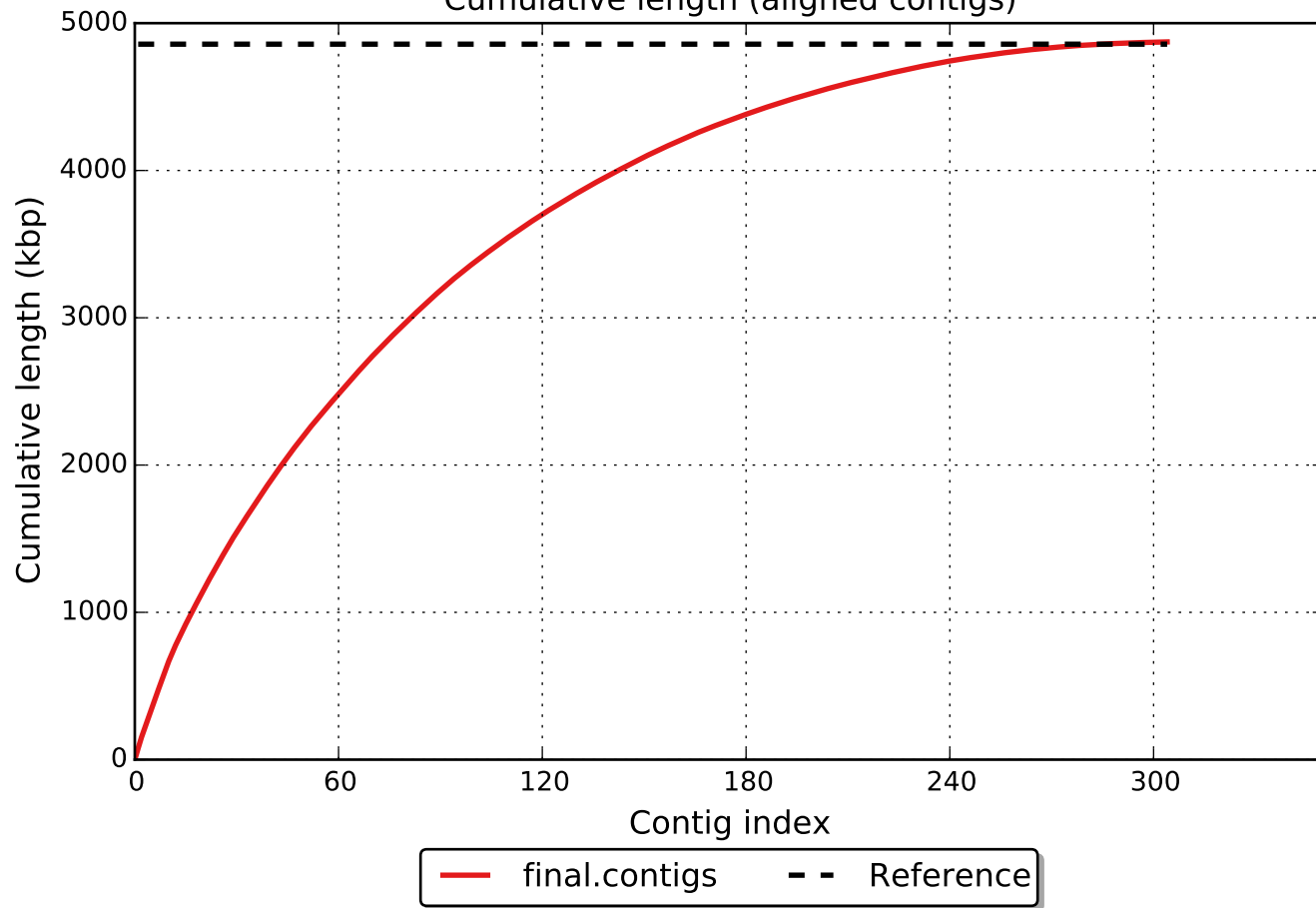


# Misassemblies

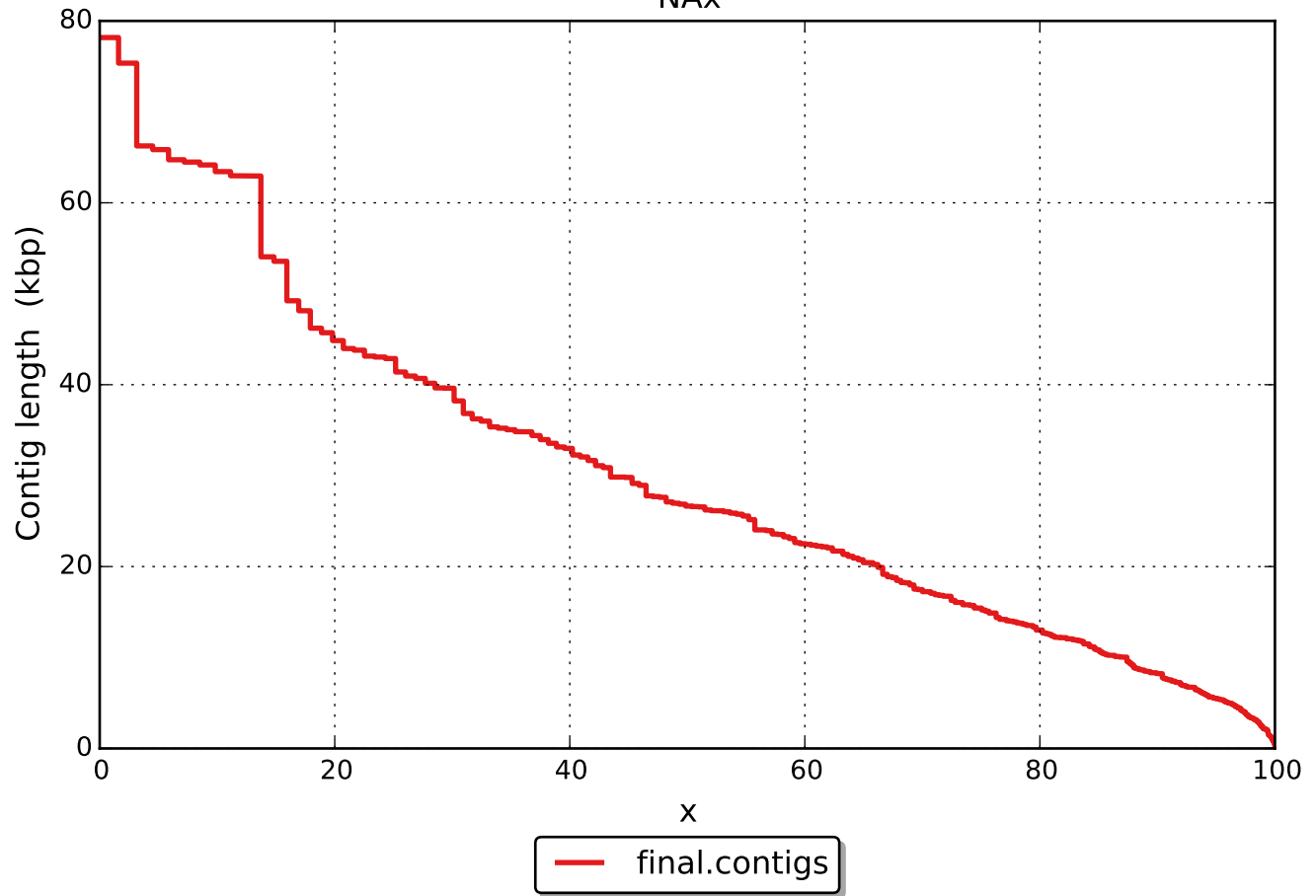




Cumulative length (aligned contigs)



NAx



# NGAx

