

Report

	final.contigs
# contigs (>= 1000 bp)	99
# contigs (>= 5000 bp)	74
# contigs (>= 10000 bp)	68
# contigs (>= 25000 bp)	50
# contigs (>= 50000 bp)	34
Total length (>= 1000 bp)	4554027
Total length (>= 5000 bp)	4498418
Total length (>= 10000 bp)	4454662
Total length (>= 25000 bp)	4168582
Total length (>= 50000 bp)	3606295
# contigs	113
Largest contig	246979
Total length	4563917
Reference length	4641652
GC (℥)	50.75
Reference GC (℥)	50.79
N50	95645
NG50	95535
N75	56778
NG75	54951
L50	15
LG50	16
L75	31
LG75	32
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	9
# unaligned contigs	0 + 1 part
Unaligned length	53
Genome fraction (℥)	98.269
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	58.89
# indels per 100 kbp	9.56
Largest alignment	246979
NA50	95645
NGA50	95535
NA75	56778
NGA75	54951
LA50	15
LGA50	16
LA75	31
LGA75	32

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	9
# mismatches	2686
# indels	436
# short indels	430
# long indels	6
Indels length	786

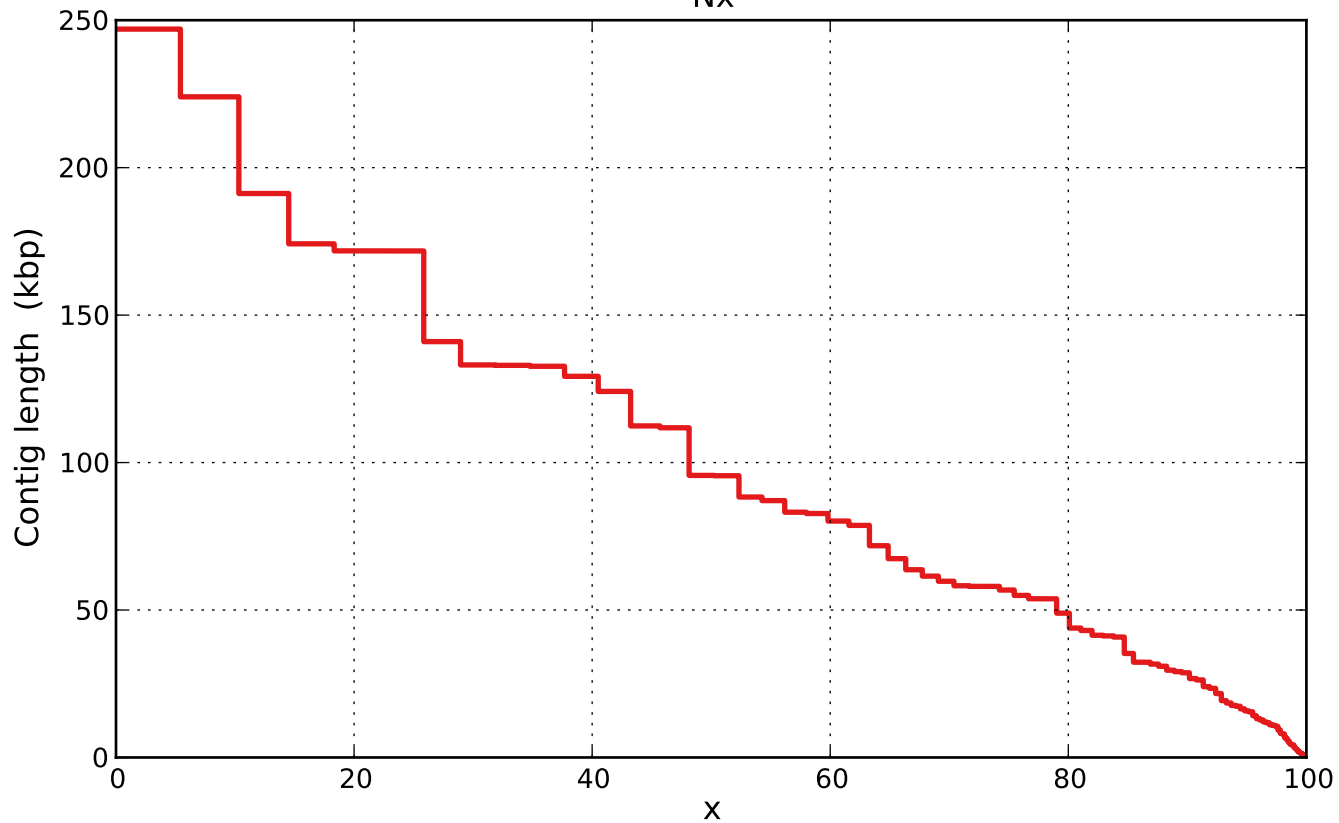
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	53
# N's	0

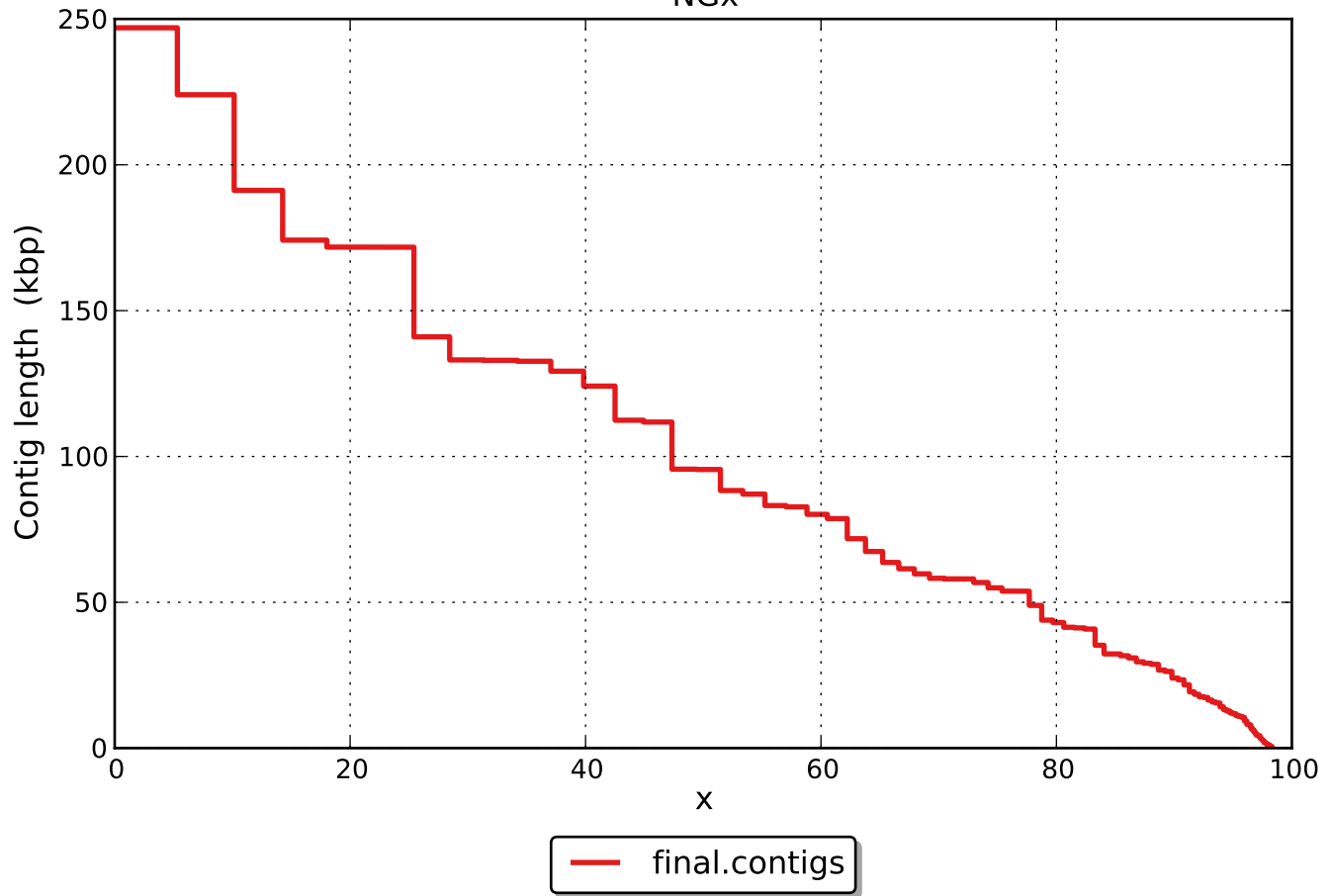
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

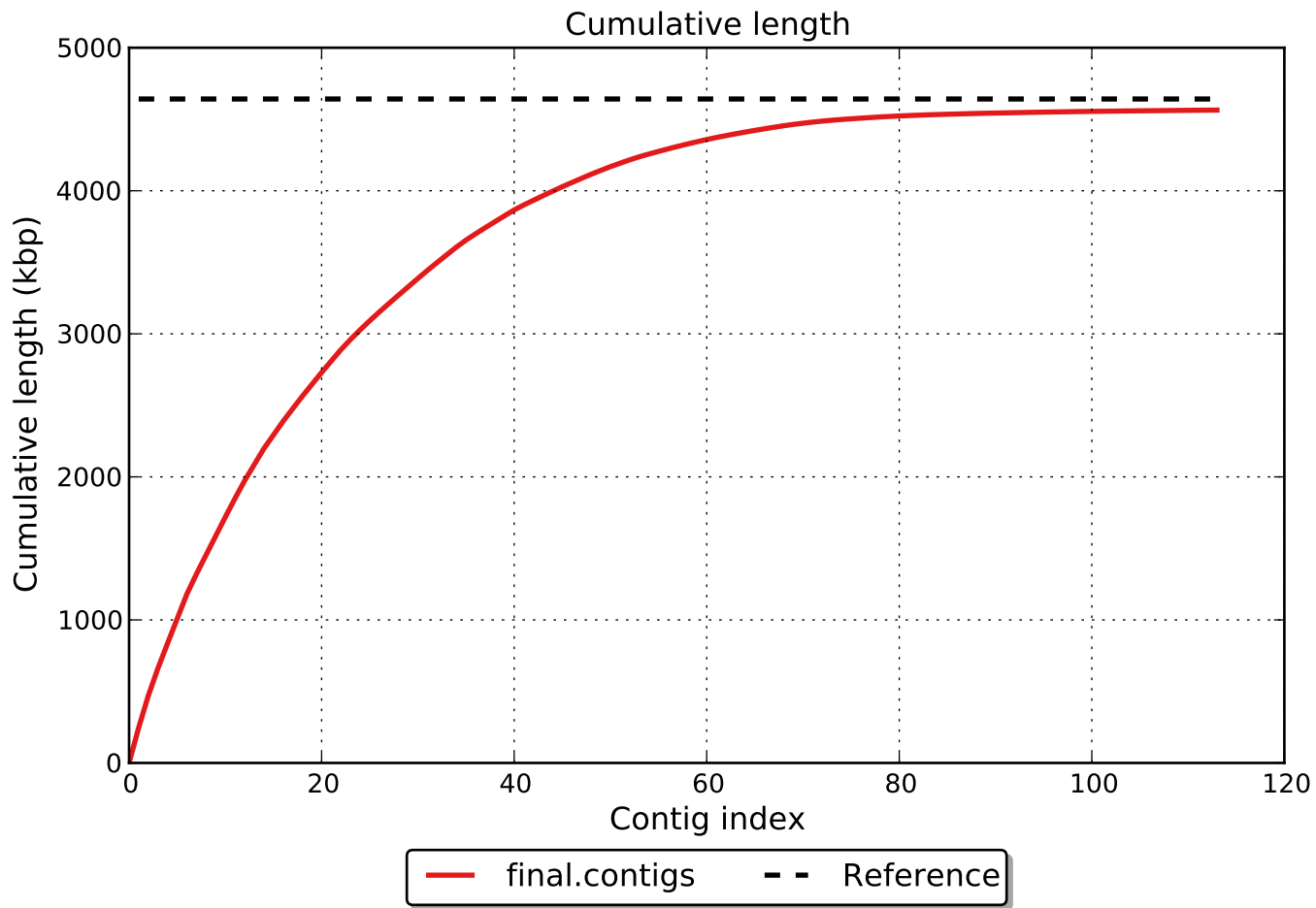
Nx



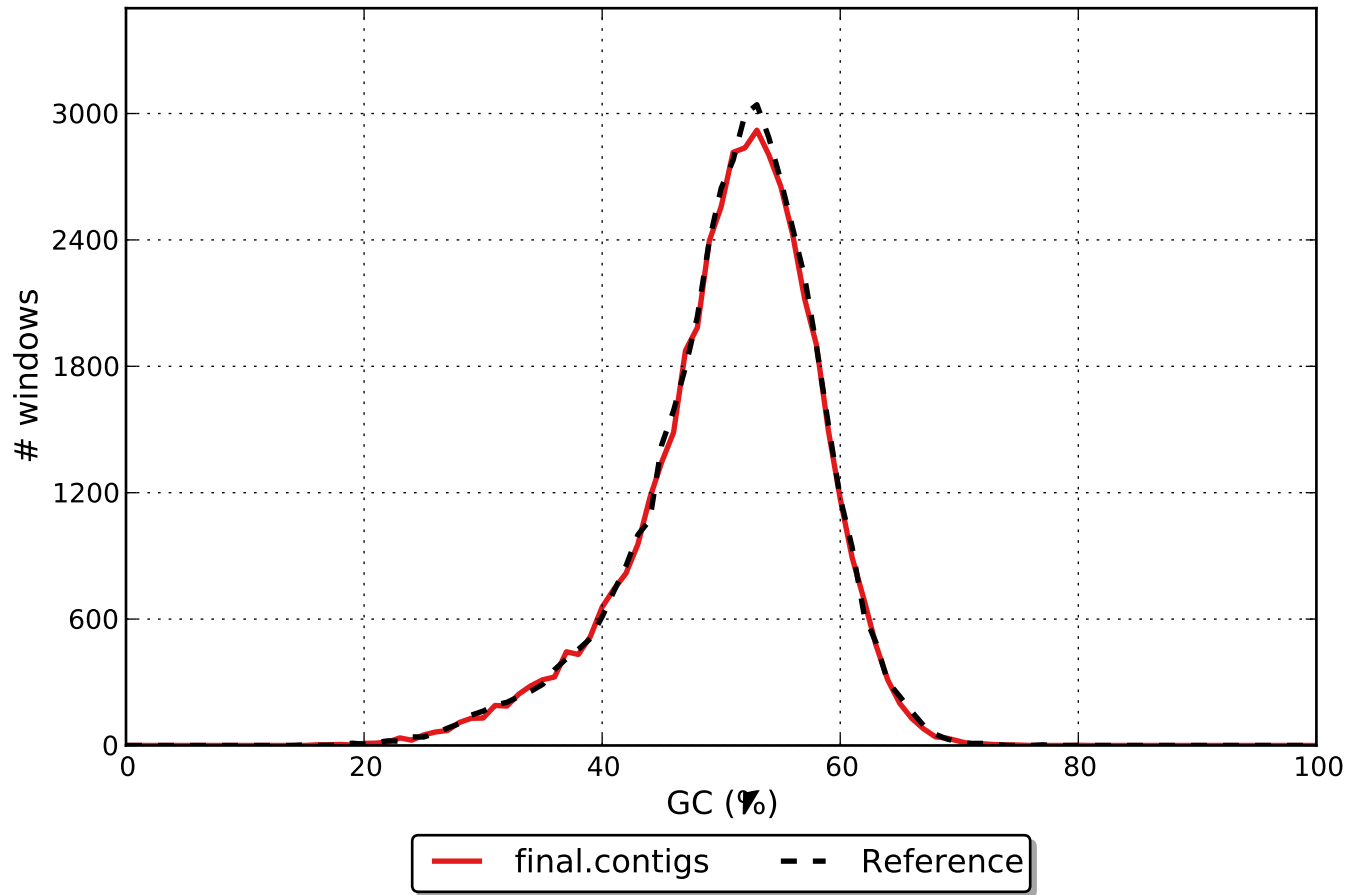
— final.contigs

NGx





GC content

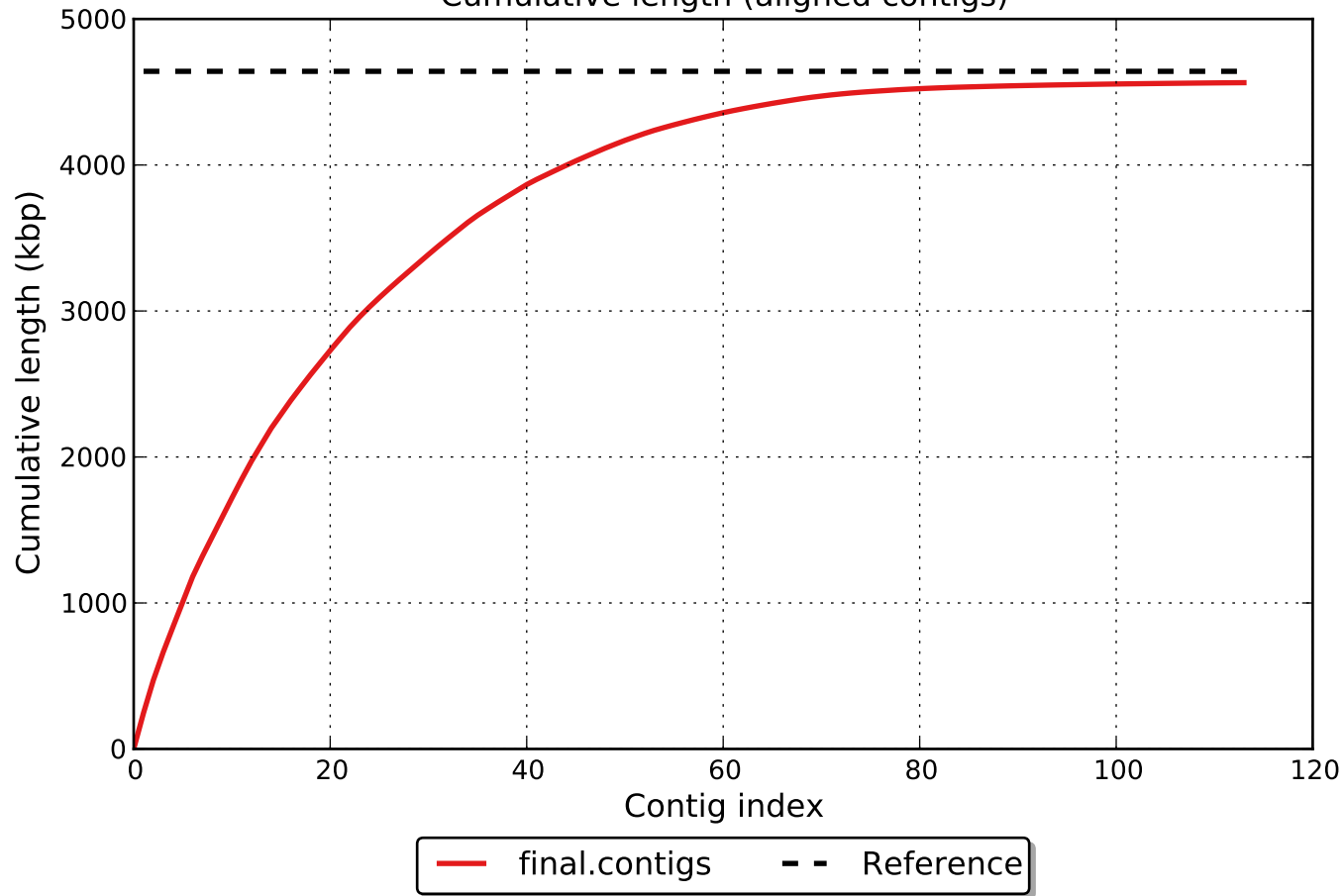


# Misassemblies

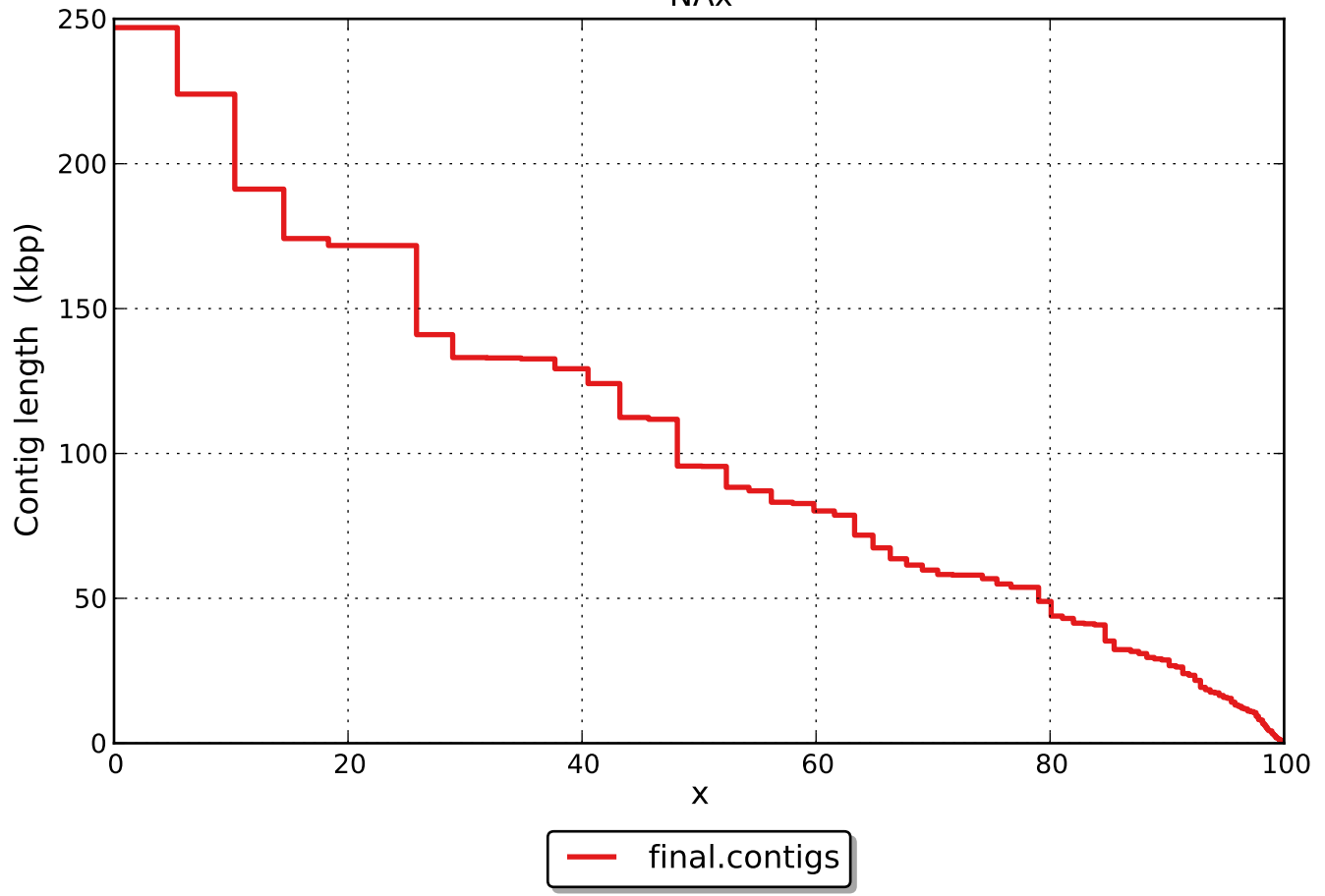




Cumulative length (aligned contigs)



NAx



NGAx

