

Report

	final.contigs
# contigs (>= 1000 bp)	217
# contigs (>= 5000 bp)	172
# contigs (>= 10000 bp)	143
# contigs (>= 25000 bp)	66
# contigs (>= 50000 bp)	20
Total length (>= 1000 bp)	4549760
Total length (>= 5000 bp)	4445537
Total length (>= 10000 bp)	4223740
Total length (>= 25000 bp)	2959535
Total length (>= 50000 bp)	1358550
# contigs	235
Largest contig	105740
Total length	4562347
Reference length	4641652
GC (℥)	50.74
Reference GC (℥)	50.79
N50	33685
NG50	33314
N75	19315
NG75	18542
L50	43
LG50	45
L75	88
LG75	91
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	7
# unaligned contigs	0 + 1 part
Unaligned length	53
Genome fraction (℥)	98.209
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	57.65
# indels per 100 kbp	9.59
Largest alignment	105740
NA50	33685
NGA50	33314
NA75	19315
NGA75	18542
LA50	43
LGA50	45
LA75	88
LGA75	91

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

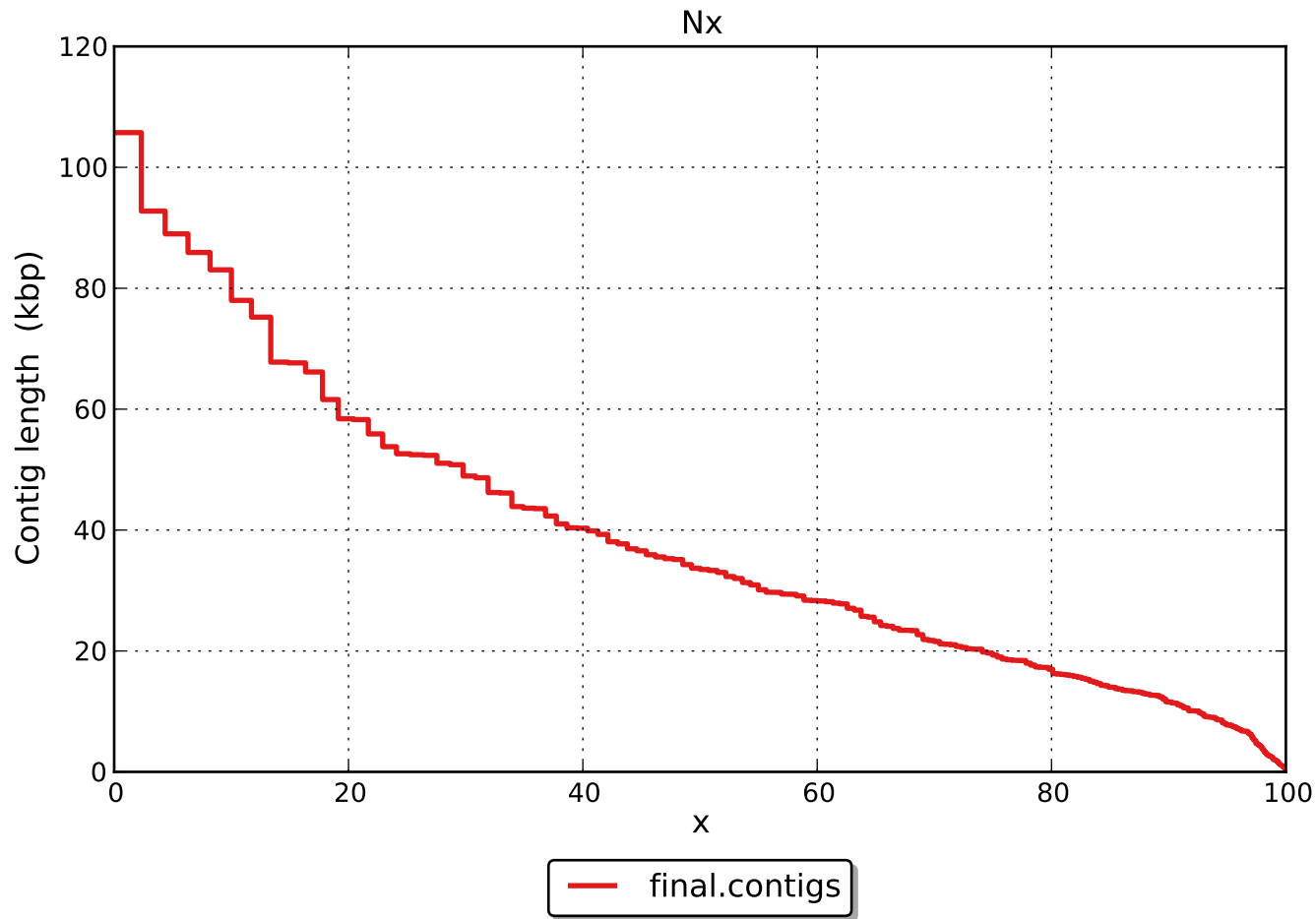
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	7
# mismatches	2628
# indels	437
# short indels	431
# long indels	6
Indels length	757

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).

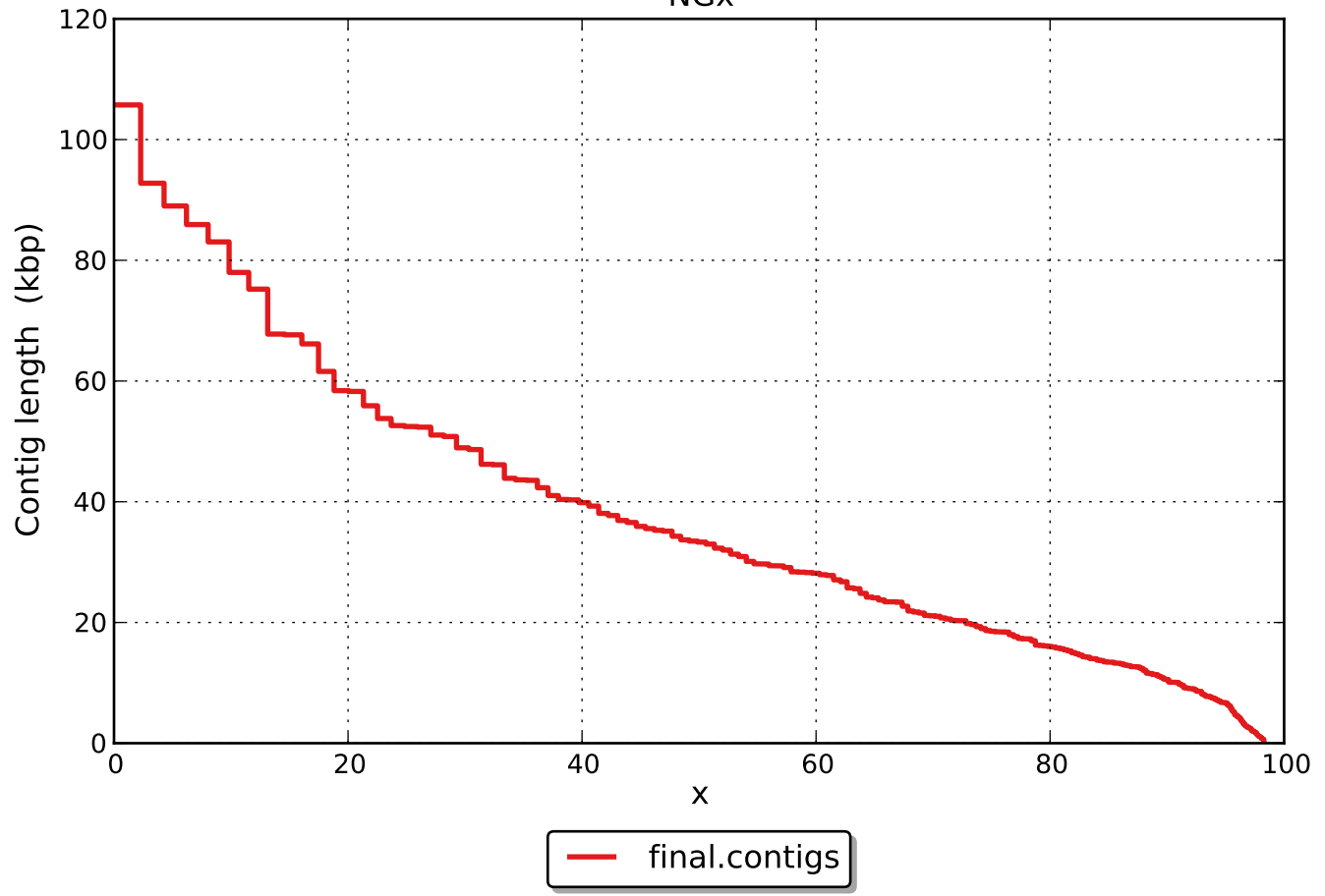
## Unaligned report

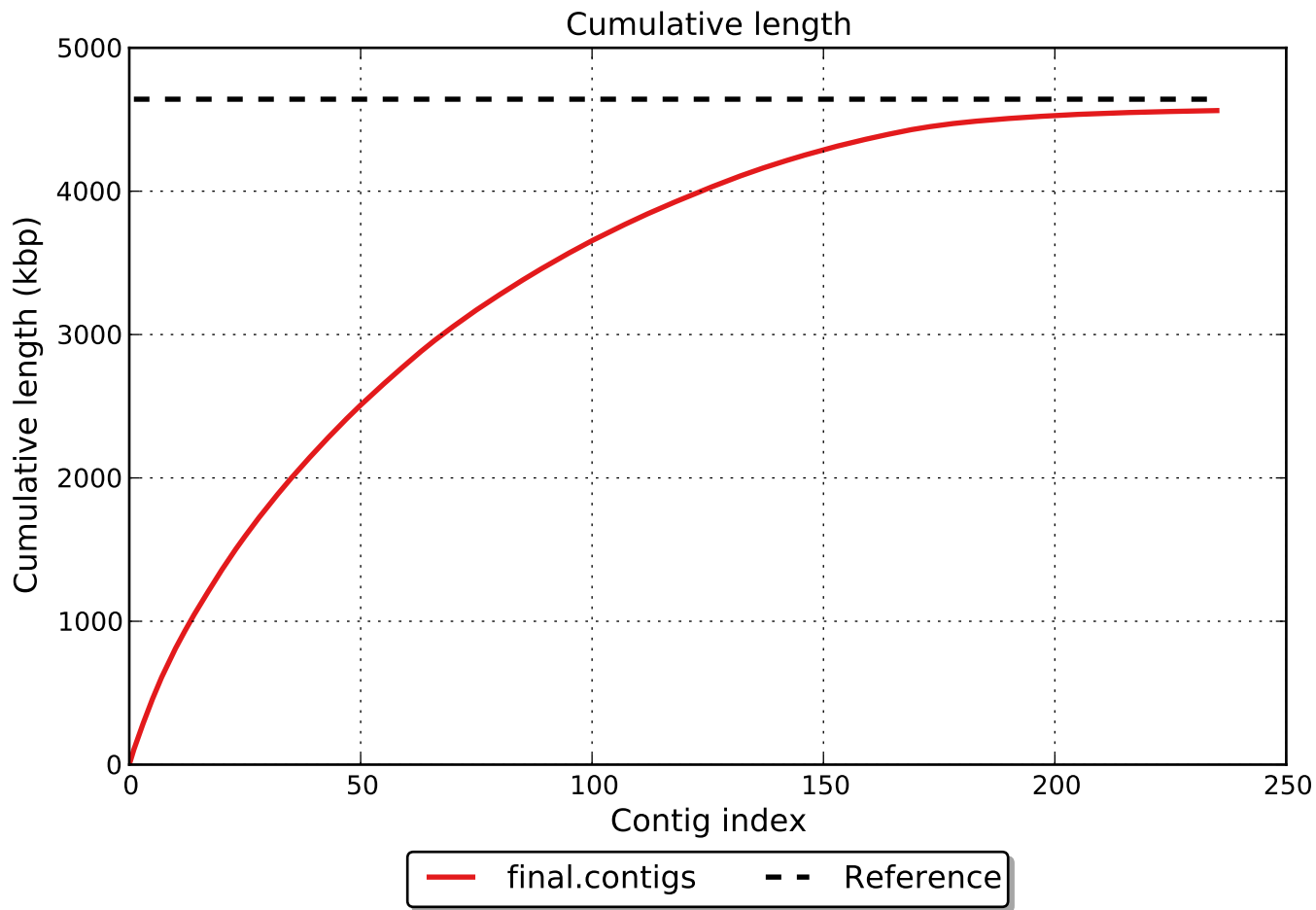
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	53
# N's	0

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).

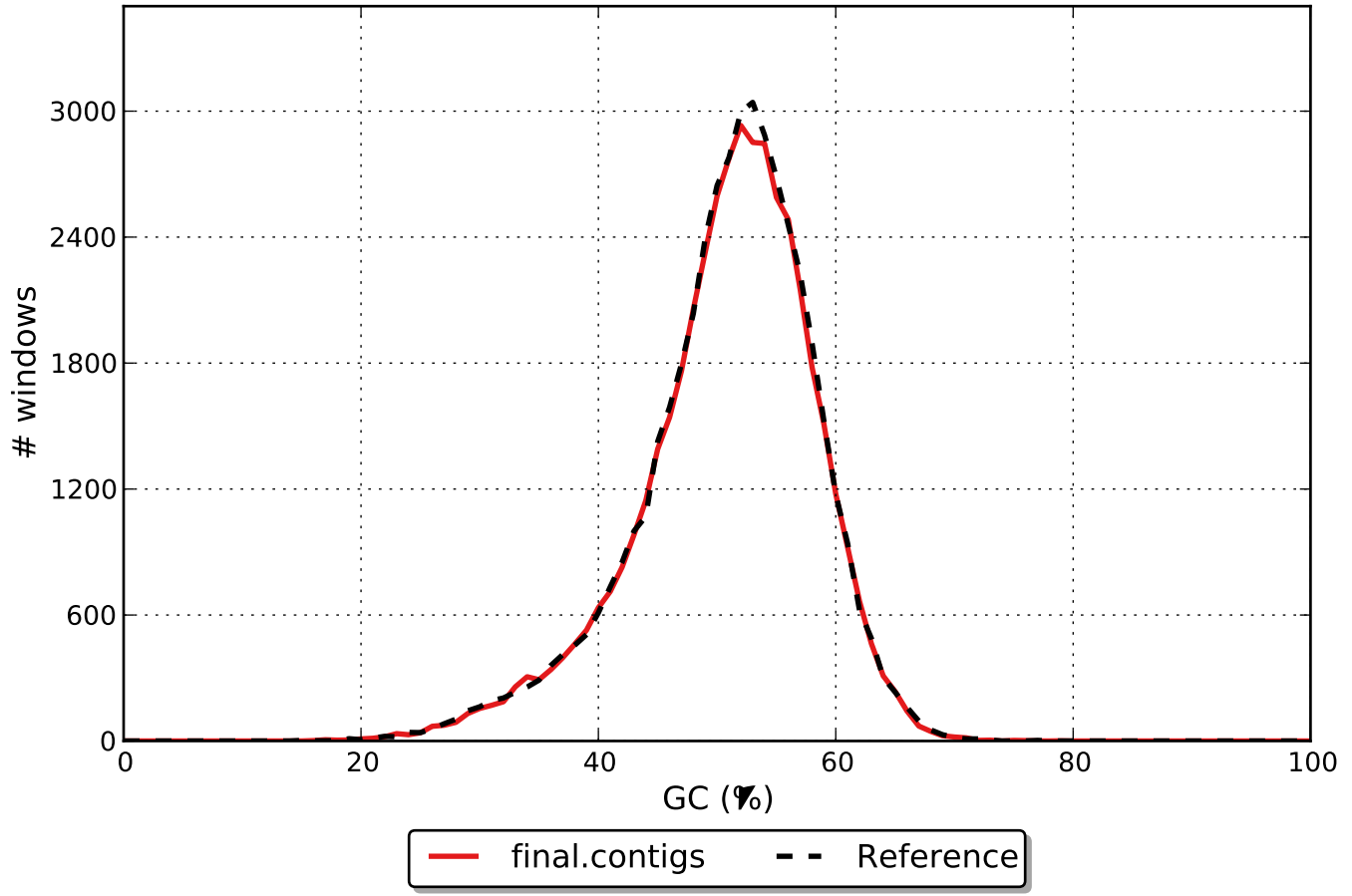


NGx





GC content

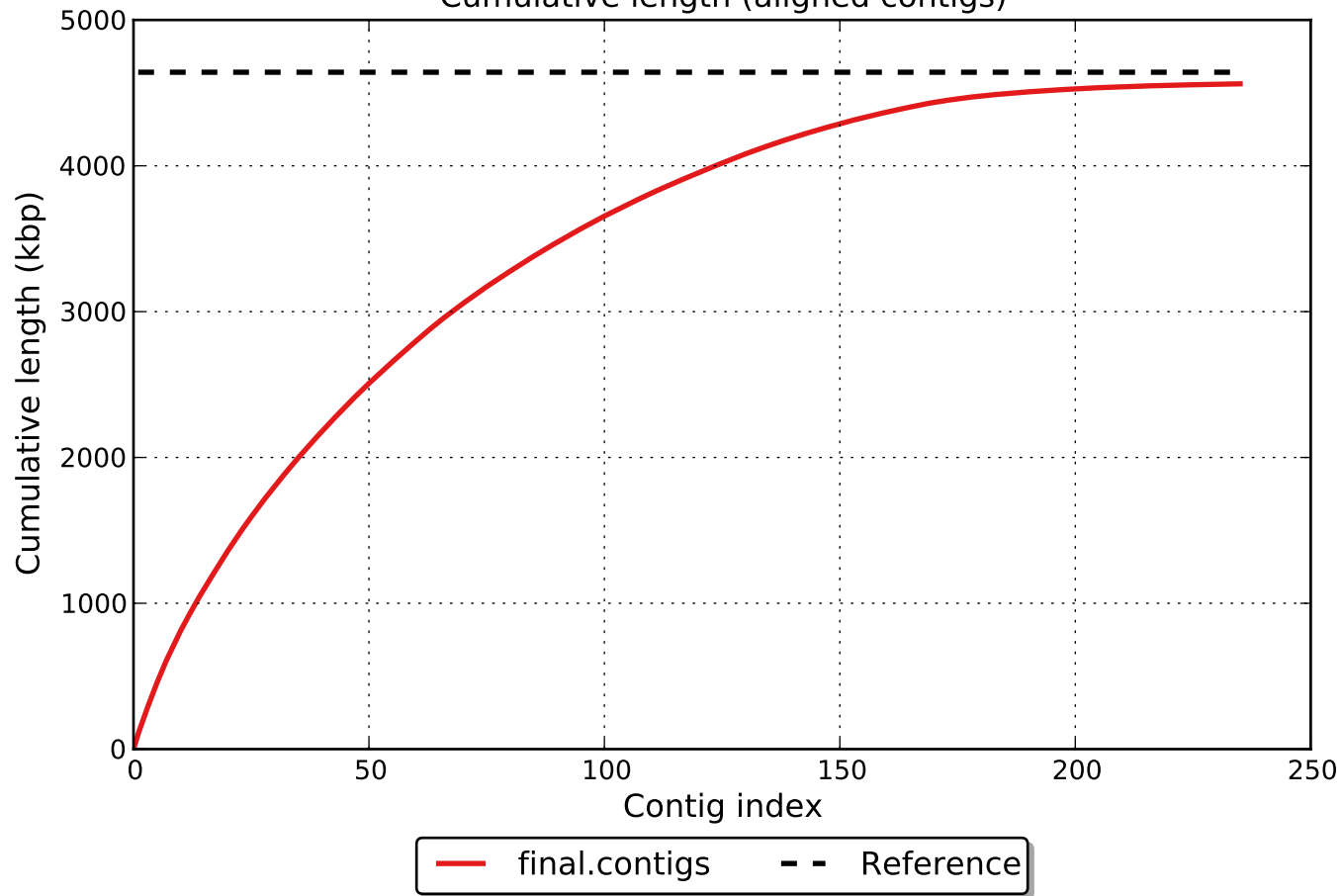


# Misassemblies

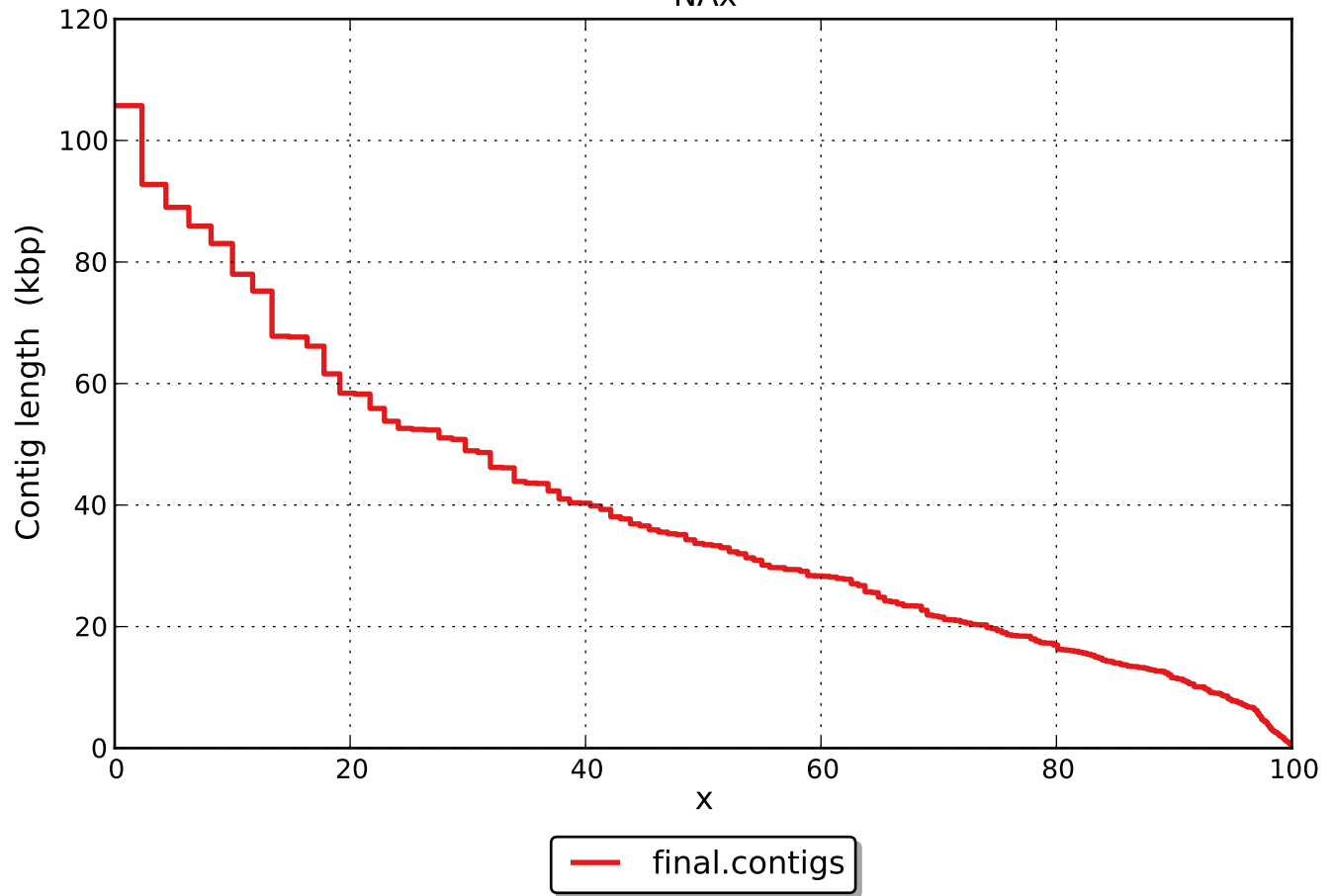




Cumulative length (aligned contigs)



NAx



# NGAx

