

## Report

	final.contigs
# contigs (>= 0 bp)	3709
# contigs (>= 1000 bp)	104
# contigs (>= 5000 bp)	77
# contigs (>= 10000 bp)	70
# contigs (>= 25000 bp)	53
# contigs (>= 50000 bp)	32
Total length (>= 0 bp)	5926161
Total length (>= 1000 bp)	4571365
Total length (>= 5000 bp)	4510045
Total length (>= 10000 bp)	4456018
Total length (>= 25000 bp)	4171467
Total length (>= 50000 bp)	3422302
# contigs	341
Largest contig	268374
Total length	4707896
Reference length	4641652
GC (%)	50.73
Reference GC (%)	50.79
N50	88899
NG50	95621
N75	44899
NG75	46813
L50	17
LG50	16
L75	35
LG75	34
# misassemblies	4
# misassembled contigs	4
Misassembled contigs length	71117
# local misassemblies	5
# unaligned contigs	15 + 6 part
Unaligned length	9138
Genome fraction (%)	98.636
Duplication ratio	1.026
# N's per 100 kbp	0.00
# mismatches per 100 kbp	17.76
# indels per 100 kbp	0.13
Largest alignment	268374
NA50	88899
NGA50	95621
NA75	44896
NGA75	46186
LA50	17
LGA50	16
LA75	35
LGA75	34

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	4
# relocations	4
# translocations	0
# inversions	0
# misassembled contigs	4
Misassembled contigs length	71117
# local misassemblies	5
# mismatches	813
# indels	6
# short indels	6
# long indels	0
Indels length	6

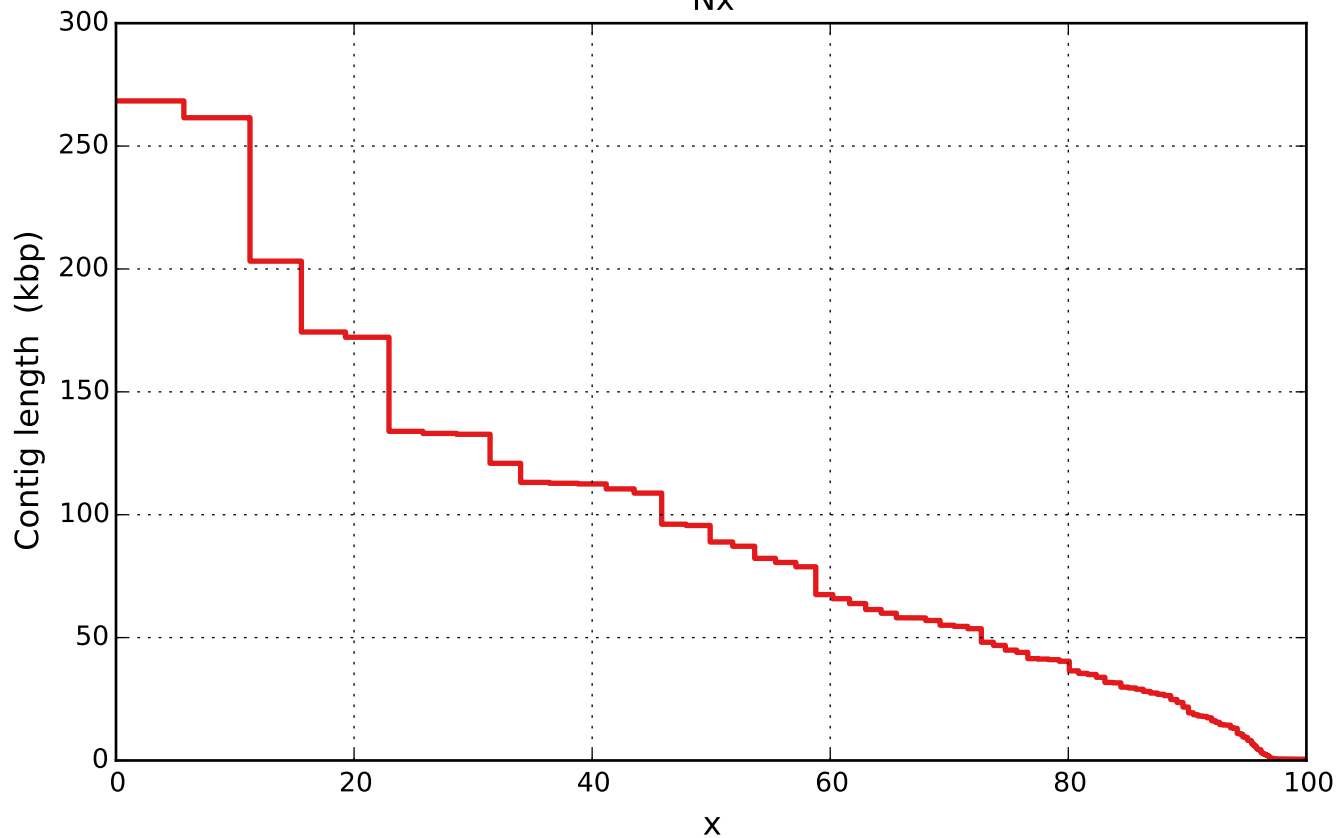
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	final.contigs
# fully unaligned contigs	15
Fully unaligned length	8134
# partially unaligned contigs	6
# with misassembly	0
# both parts are significant	0
Partially unaligned length	1004
# N's	0

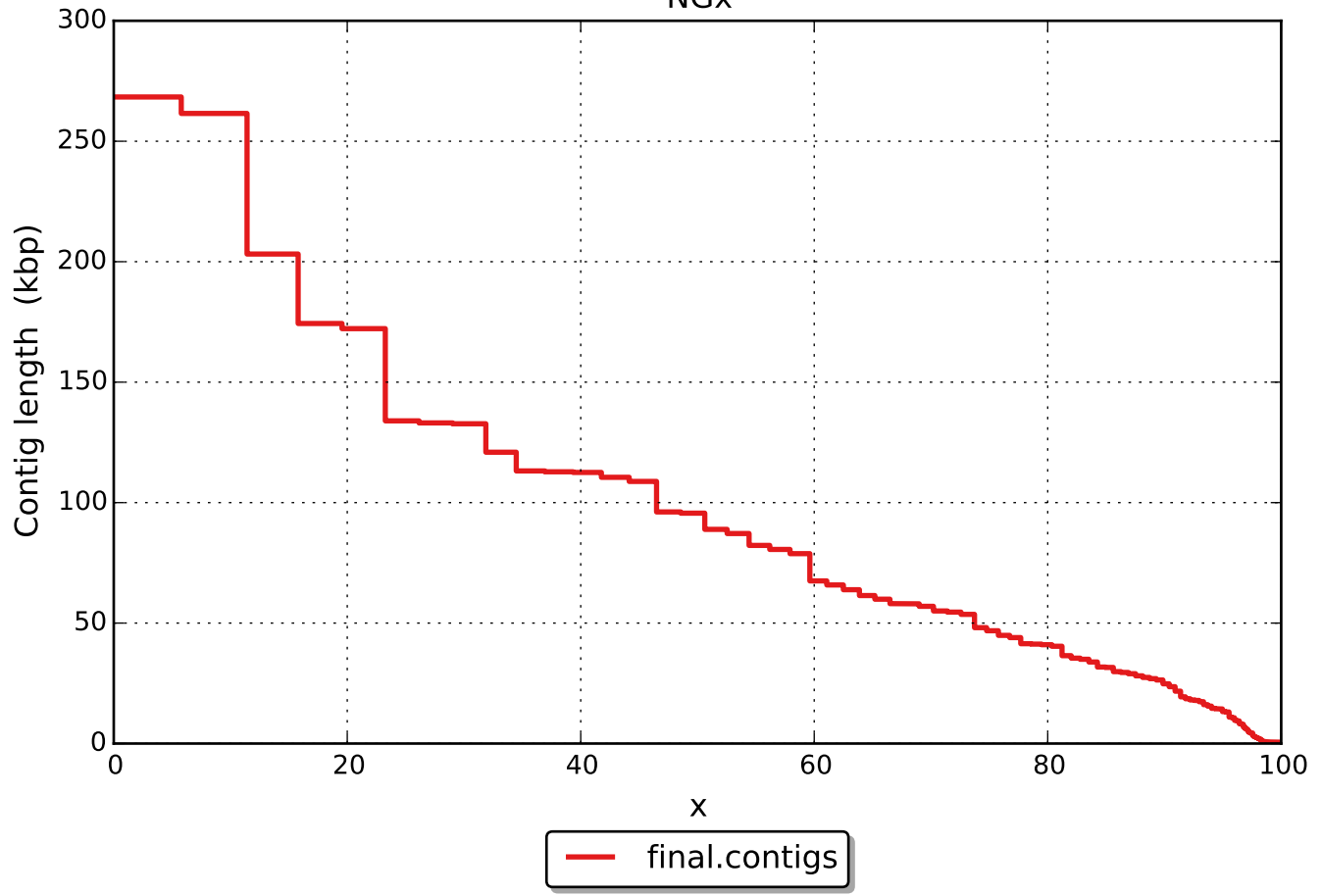
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

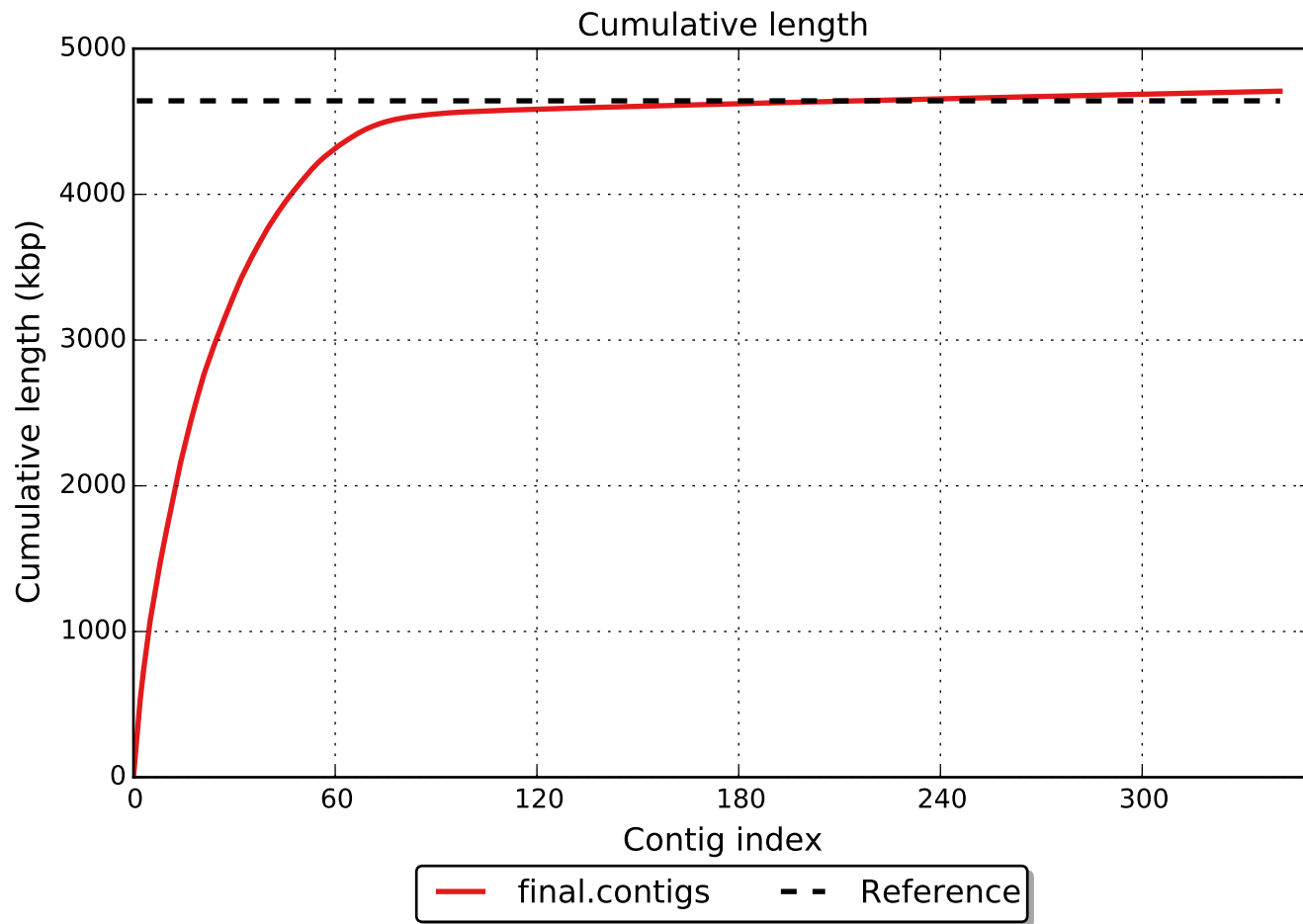
Nx



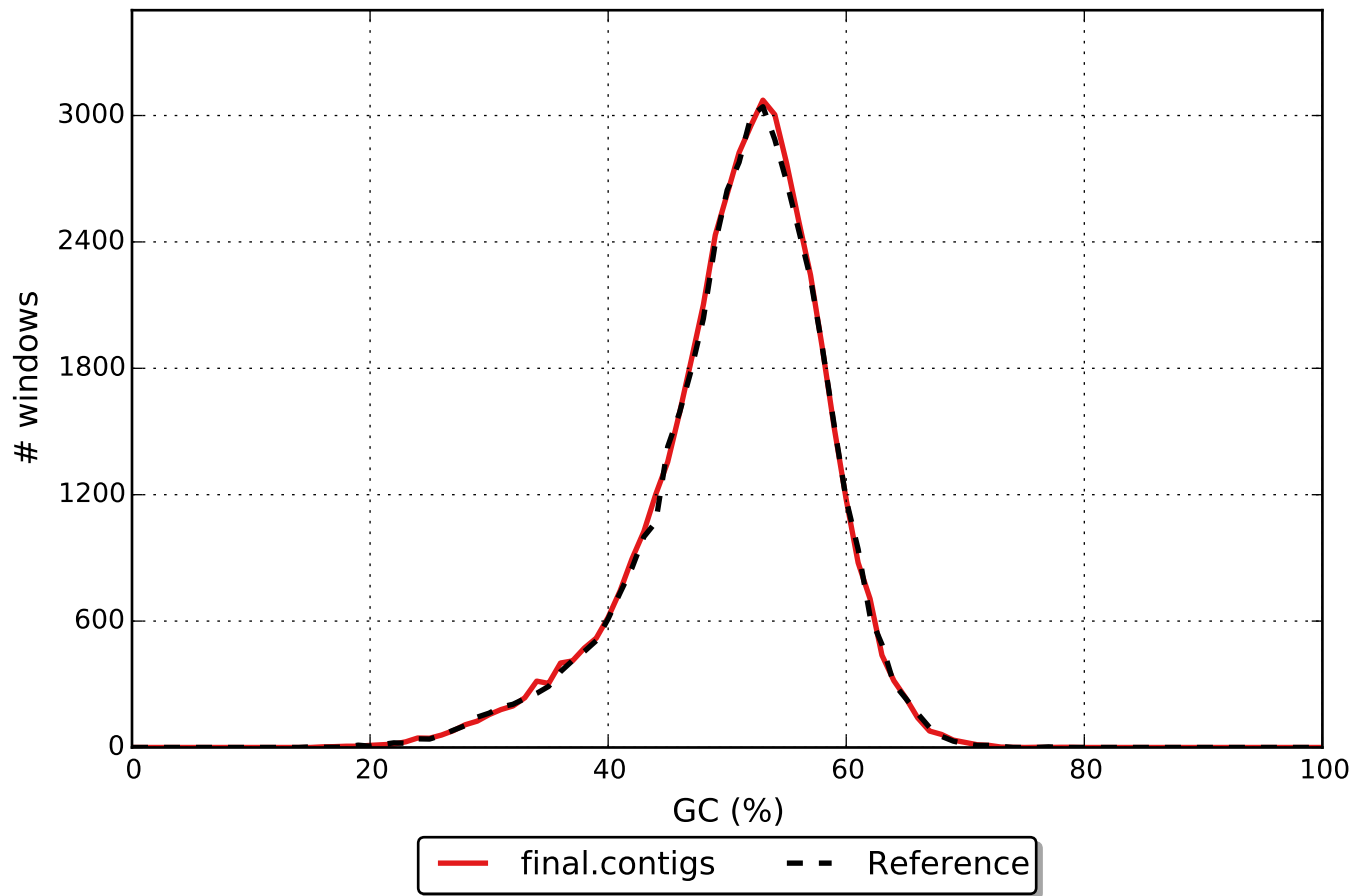
— final.contigs

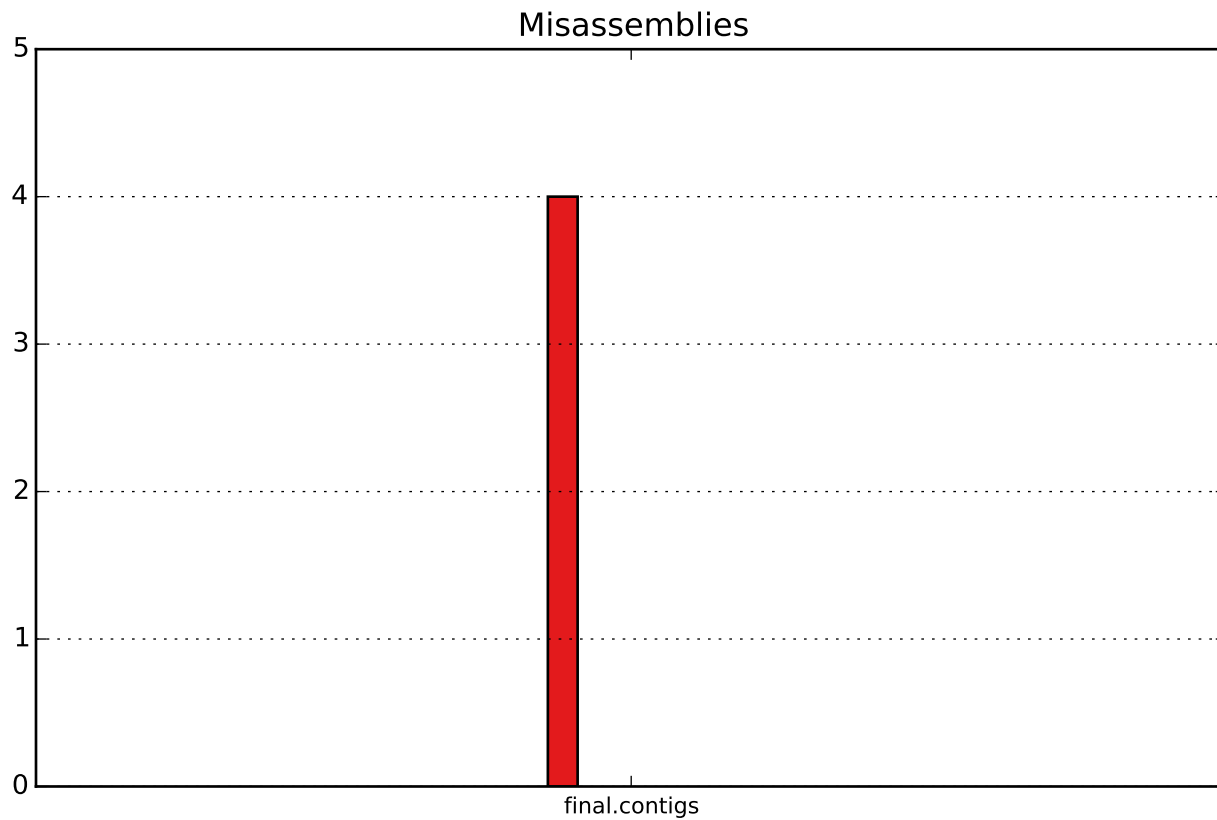
NGx





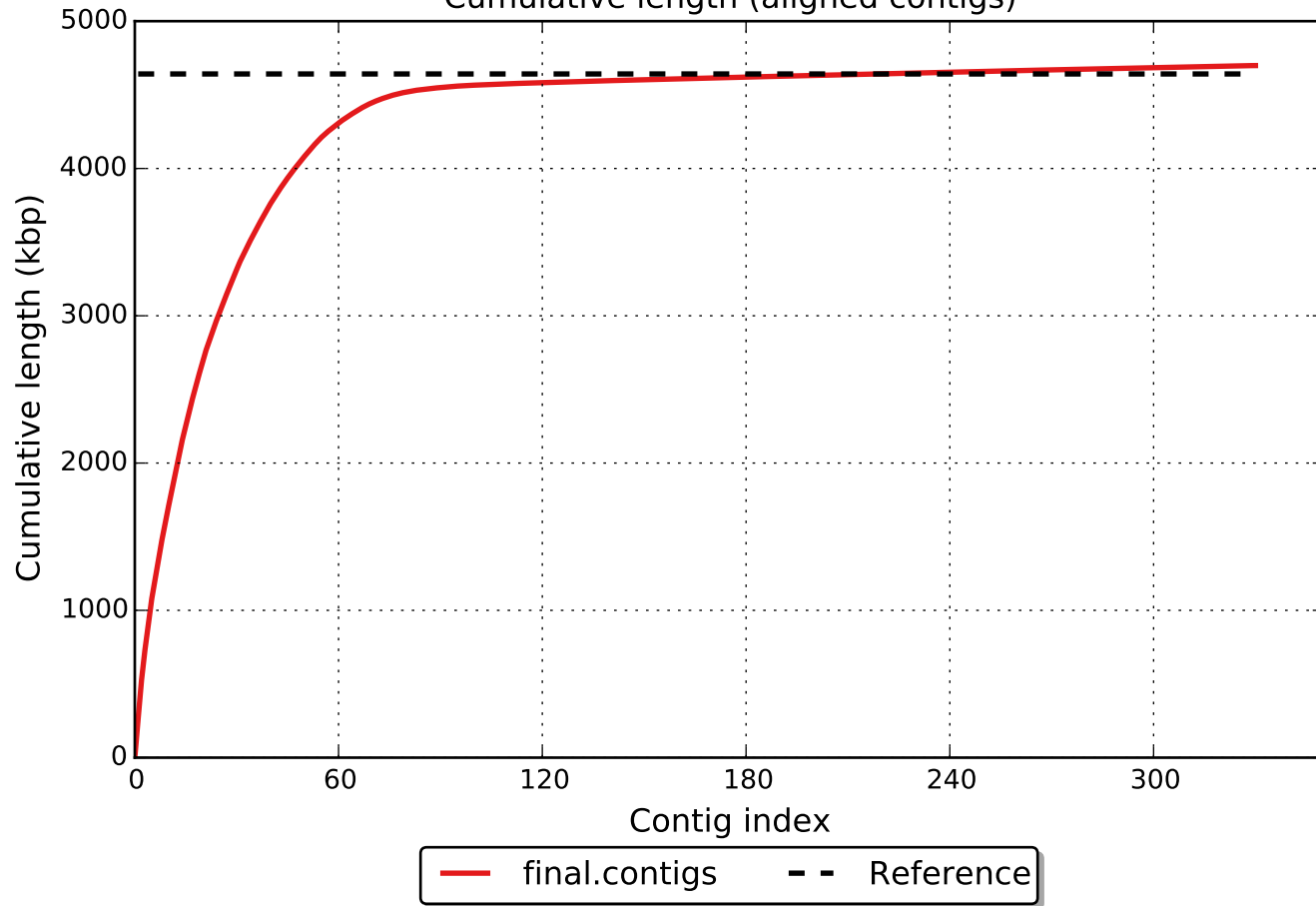
GC content



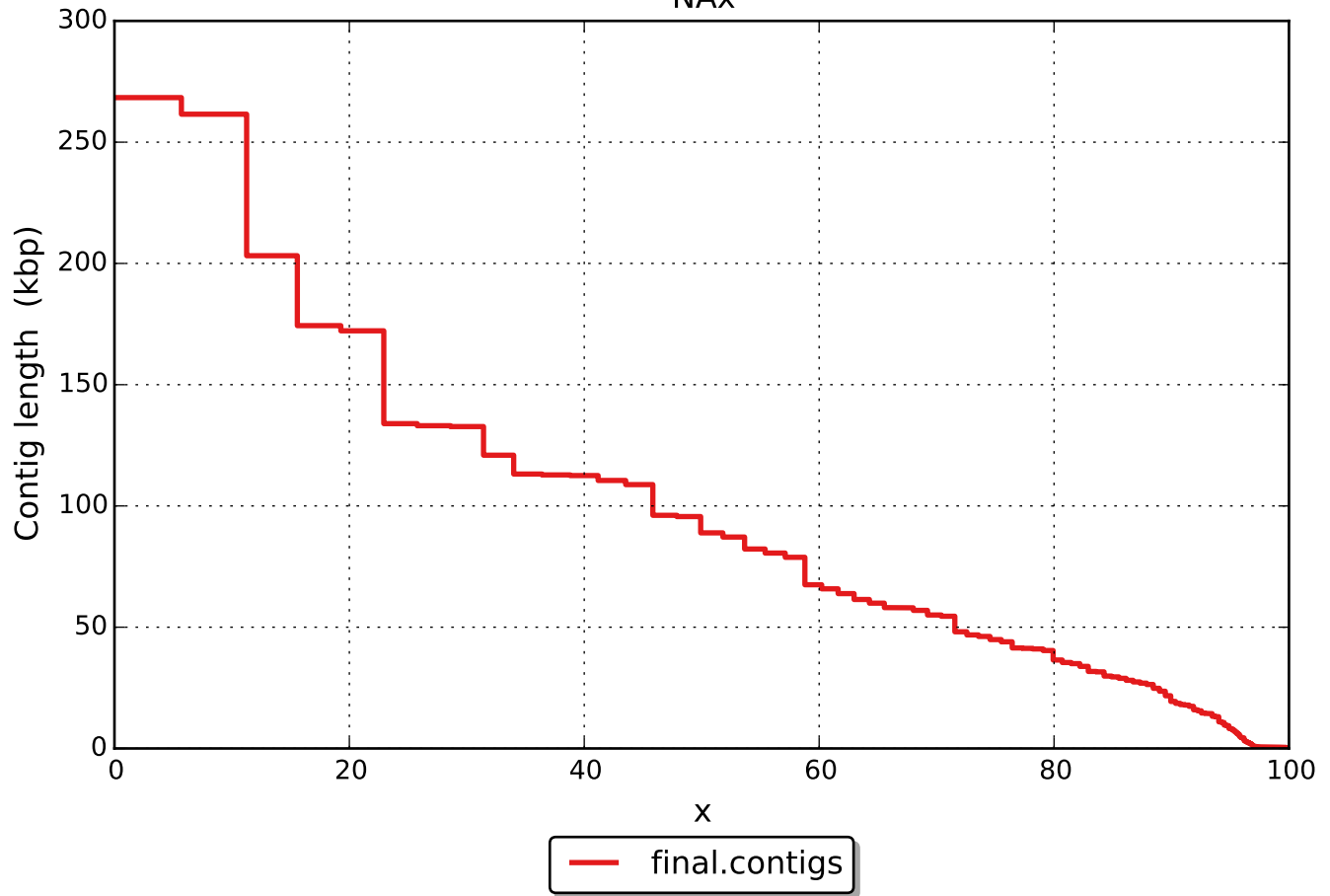




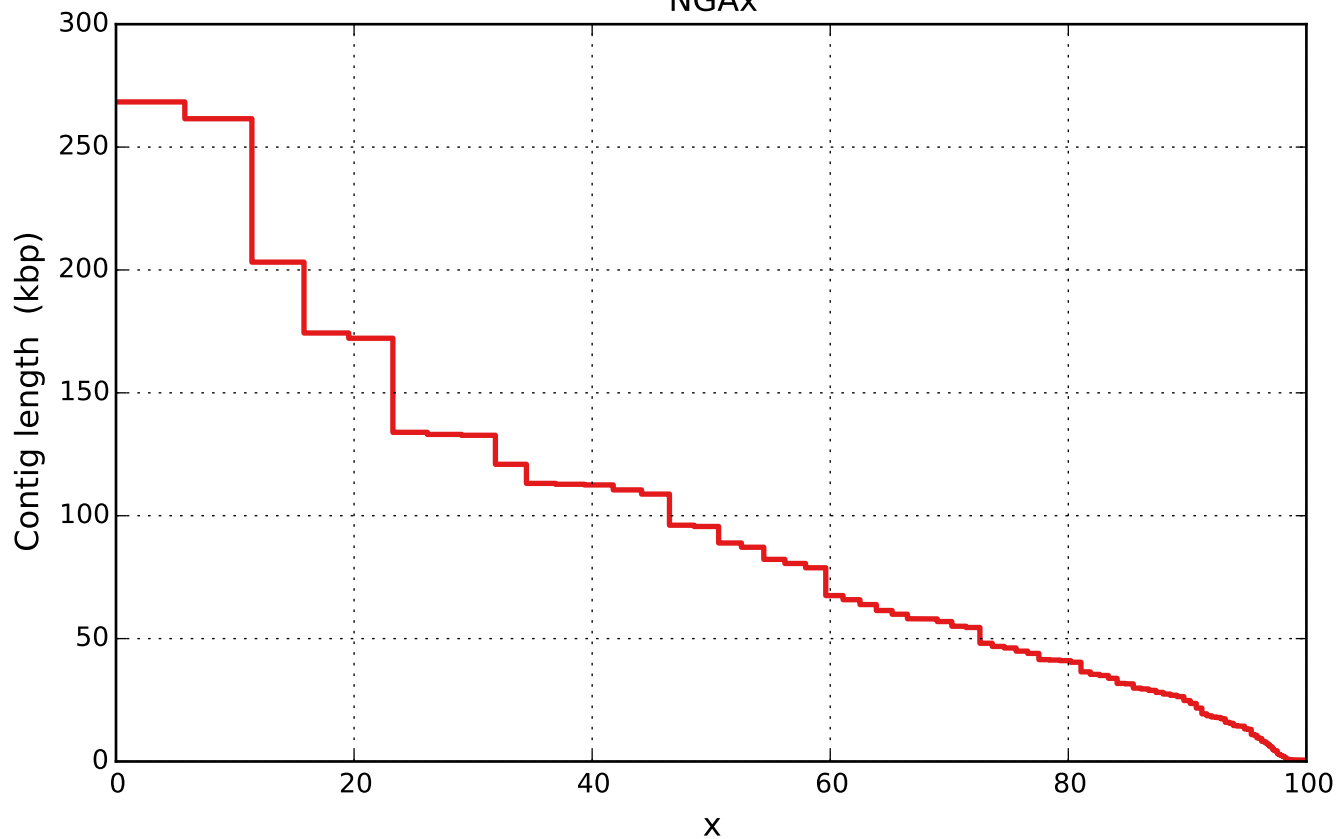
Cumulative length (aligned contigs)



NAx



NGAx



— final.contigs