

Report

	final.contigs
# contigs (>= 1000 bp)	1461
# contigs (>= 5000 bp)	3
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	2275633
Total length (>= 5000 bp)	16039
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	4236
Largest contig	5668
Total length	4216337
Reference length	4857432
GC (℥)	52.19
Reference GC (℥)	52.22
N50	1059
NG50	950
N75	738
NG75	619
L50	1299
LG50	1619
L75	2501
LG75	3213
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (℥)	80.631
Duplication ratio	1.077
# N's per 100 kbp	0.00
# mismatches per 100 kbp	370.71
# indels per 100 kbp	0.20
Largest alignment	5668
NA50	1059
NGA50	950
NA75	738
NGA75	619
LA50	1299
LGA50	1619
LA75	2501
LGA75	3213

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

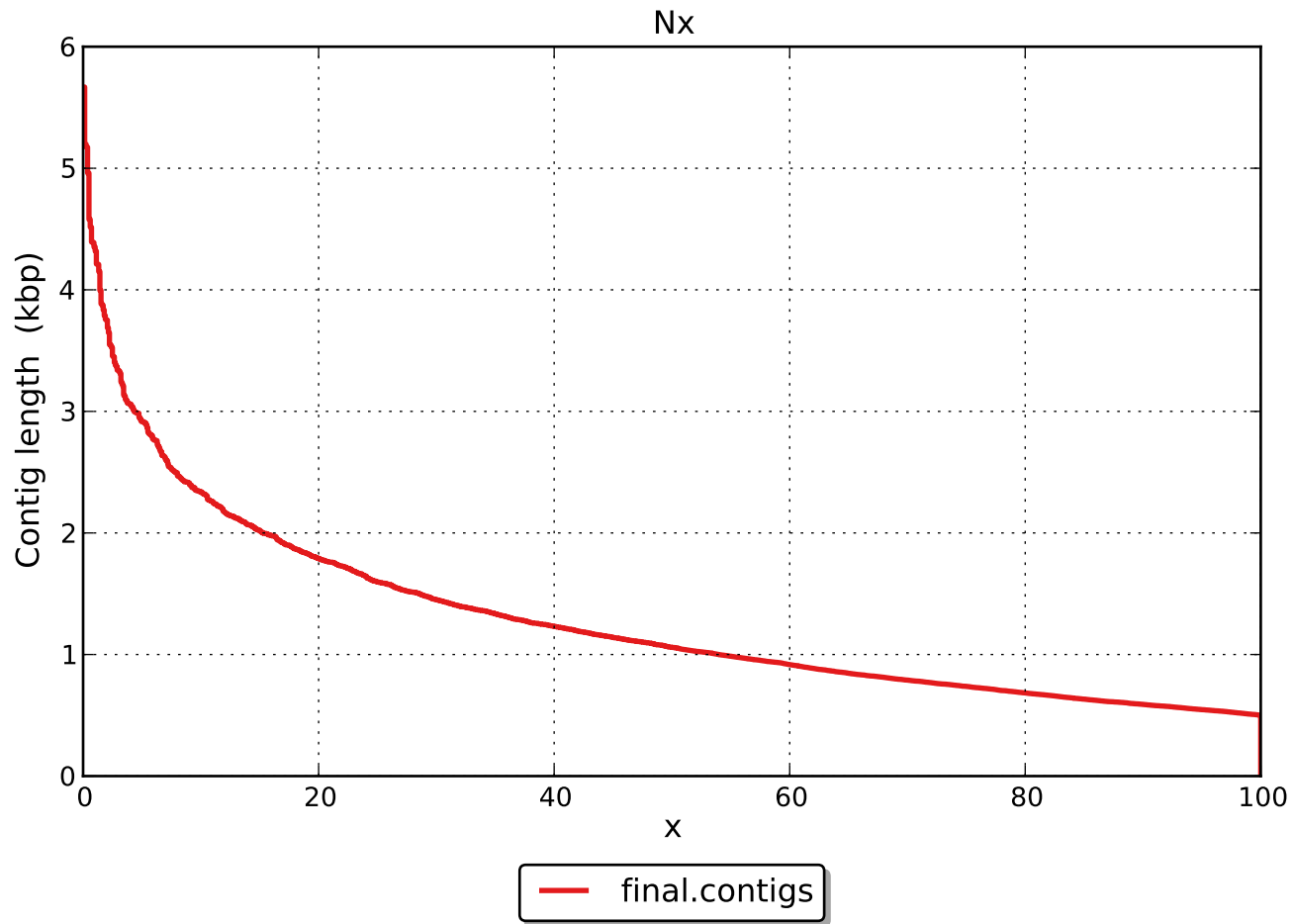
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	14519
# indels	8
# short indels	8
# long indels	0
Indels length	8

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).

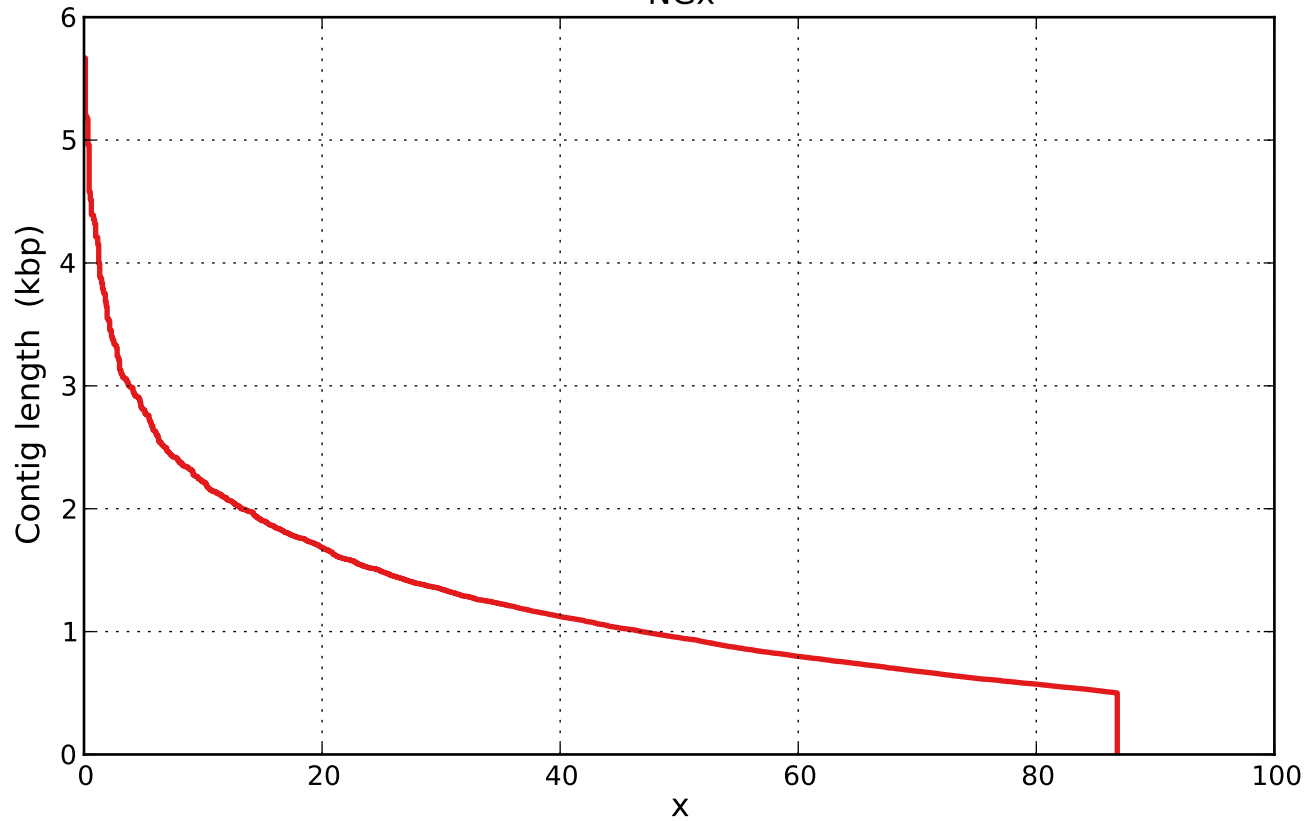
## Unaligned report

	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

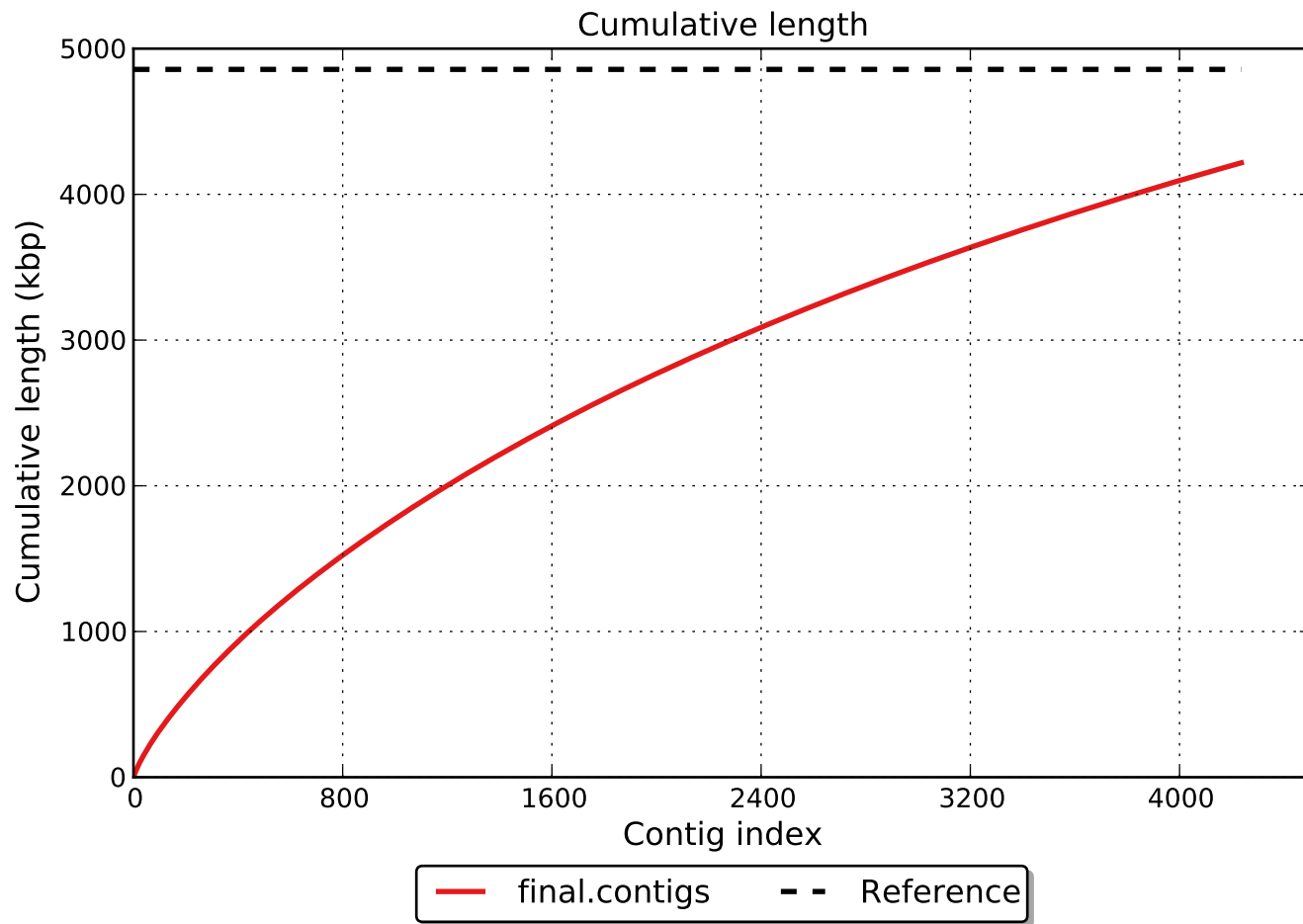
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



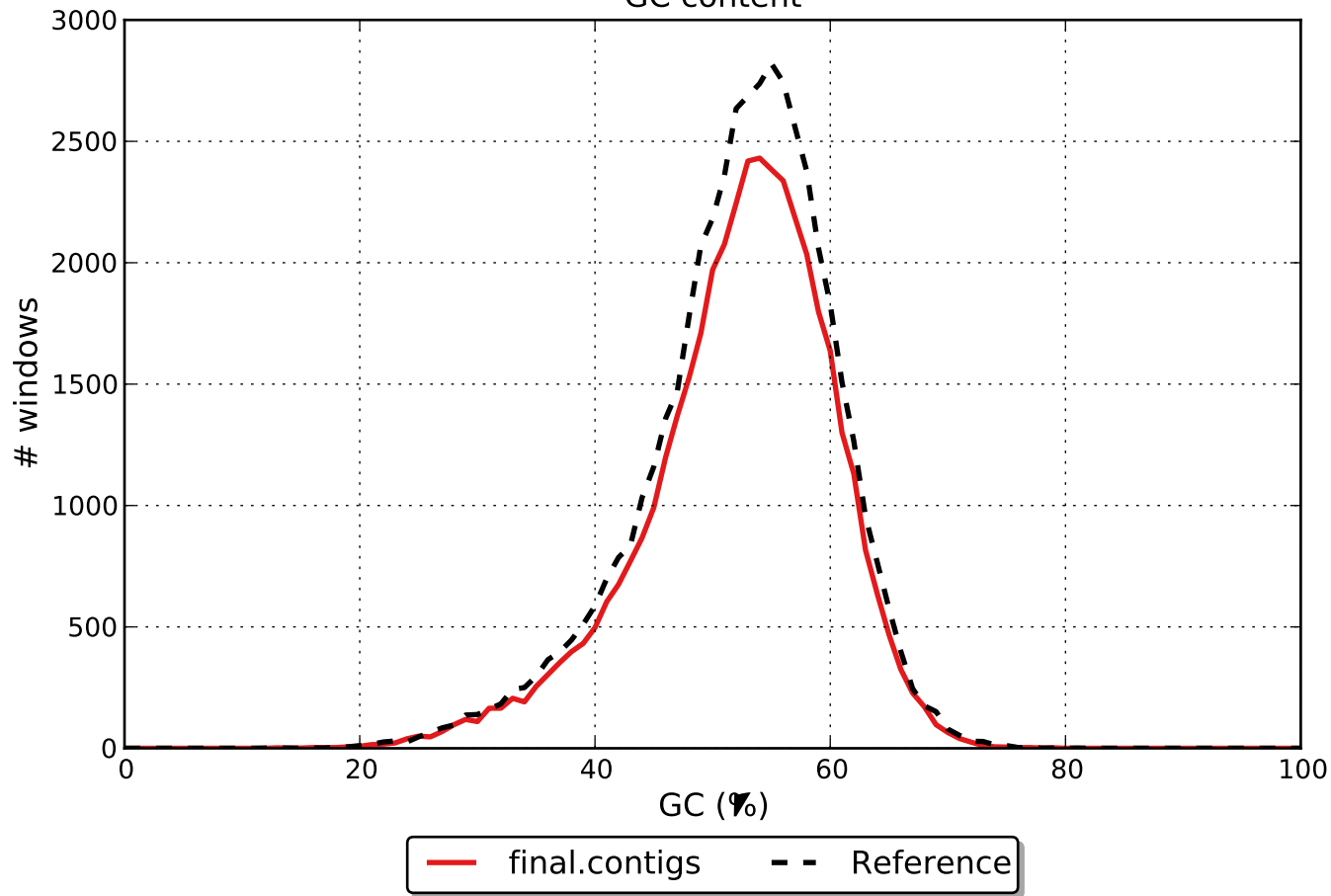
NGx



— final.contigs



GC content

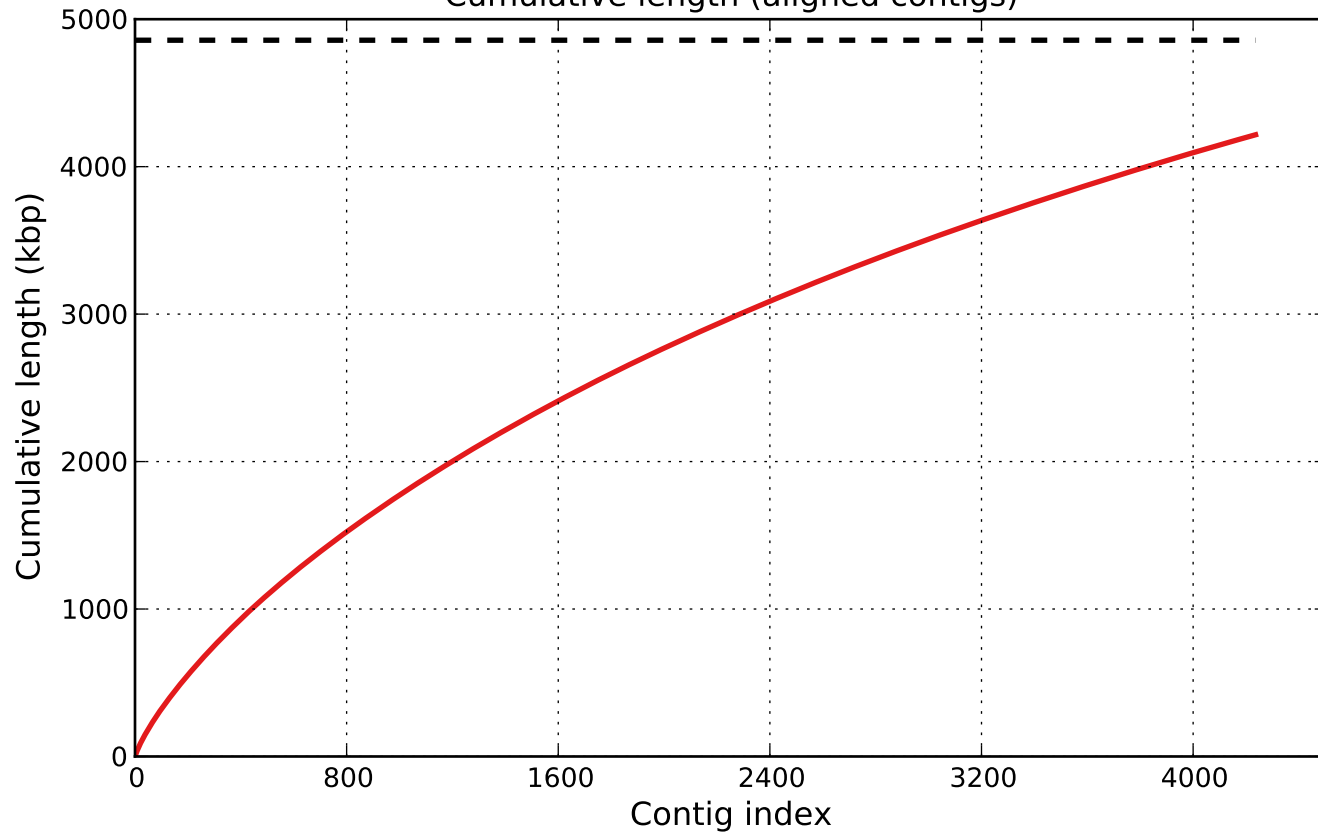


# Misassemblies

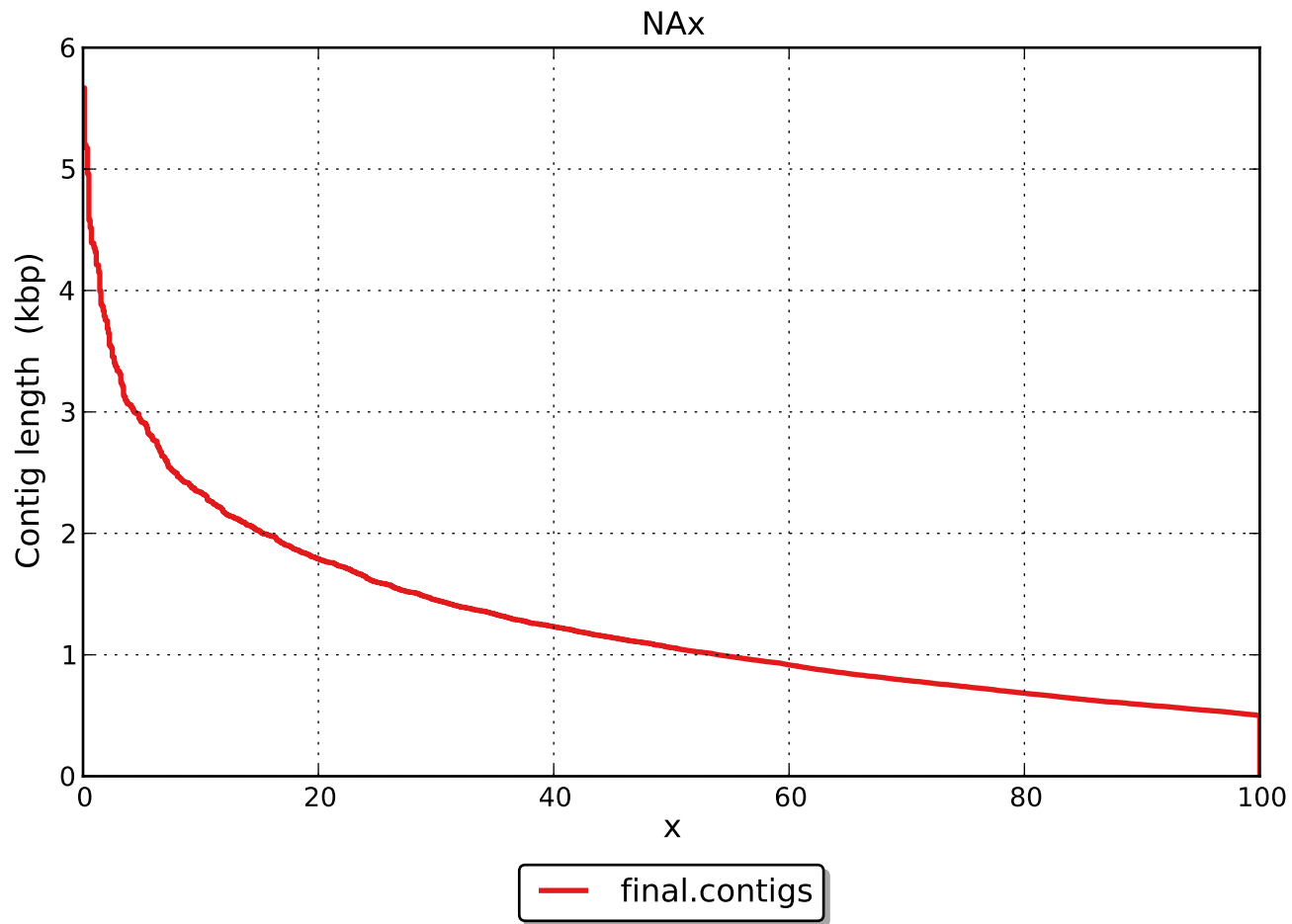




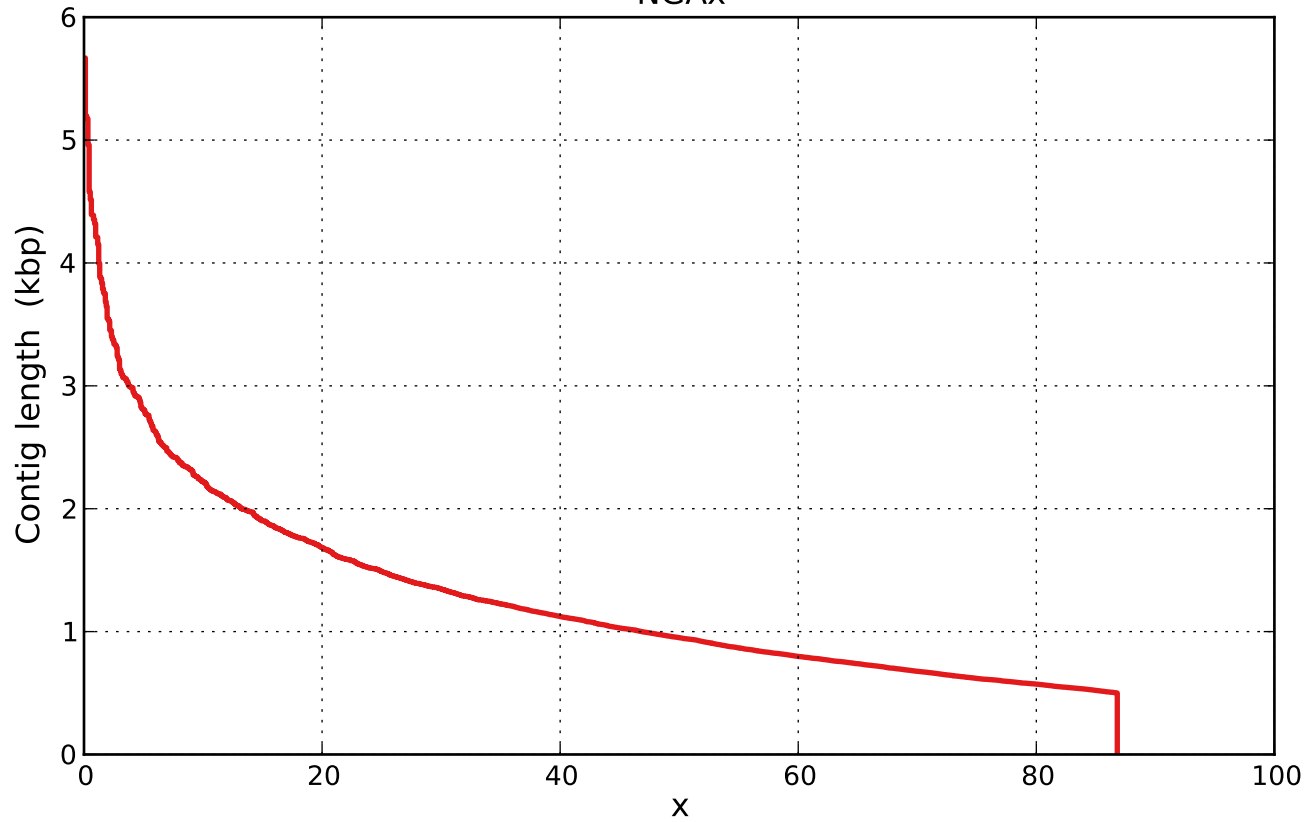
Cumulative length (aligned contigs)



— final.contigs    - - Reference



NGAx



— final.contigs