

Report

	final.contigs
# contigs (>= 1000 bp)	1414
# contigs (>= 5000 bp)	250
# contigs (>= 10000 bp)	28
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4591976
Total length (>= 5000 bp)	1783102
Total length (>= 10000 bp)	329090
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	1764
Largest contig	17106
Total length	4849540
Reference length	4857432
GC (℥)	52.20
Reference GC (℥)	52.22
N50	3838
NG50	3828
N75	2238
NG75	2237
L50	398
LG50	399
L75	804
LG75	807
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	9233
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (℥)	97.396
Duplication ratio	1.025
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1.80
# indels per 100 kbp	0.00
Largest alignment	17106
NA50	3838
NGA50	3828
NA75	2238
NGA75	2237
LA50	398
LGA50	399
LA75	804
LGA75	807

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

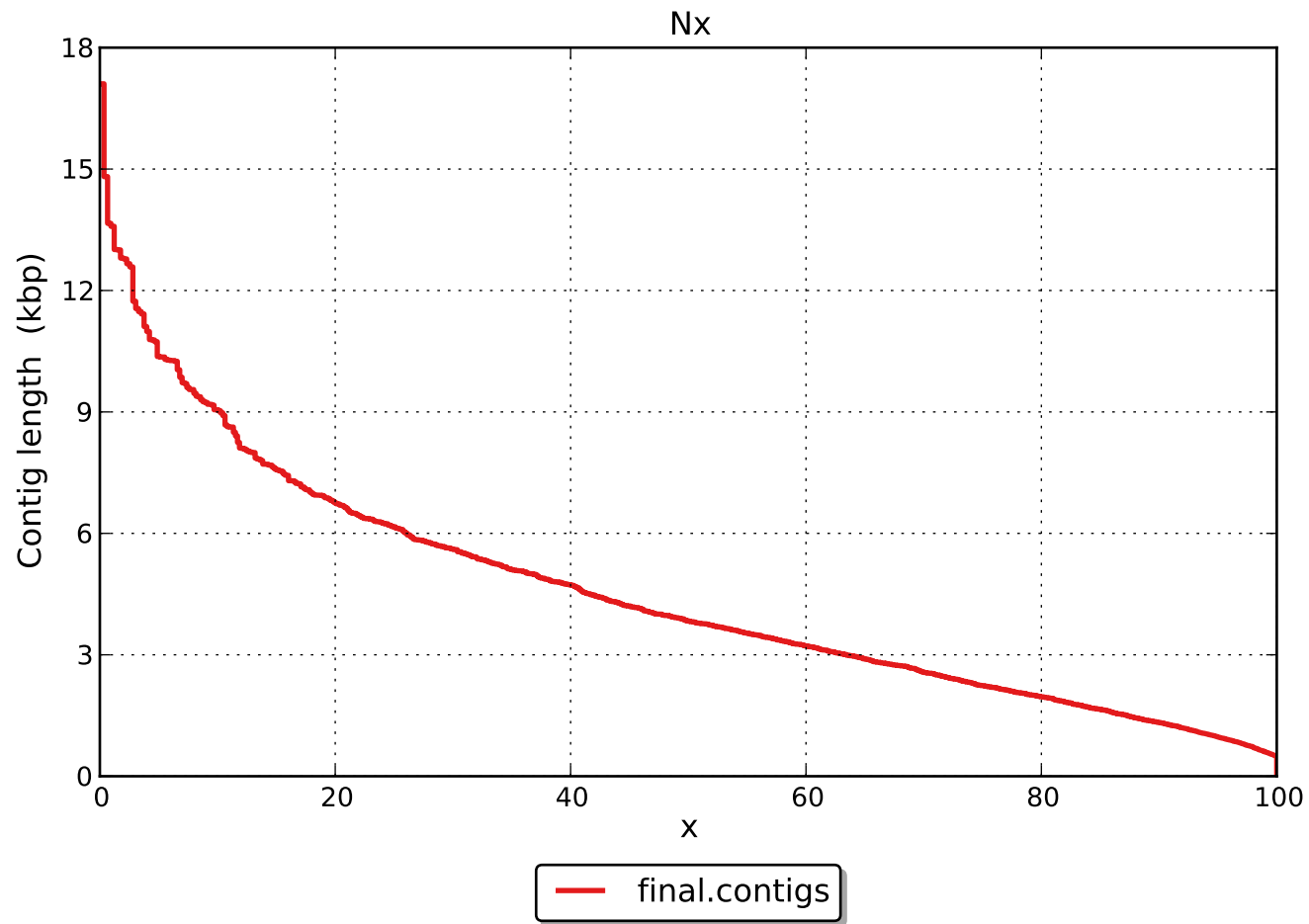
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	9233
# local misassemblies	0
# mismatches	85
# indels	0
# short indels	0
# long indels	0
Indels length	0

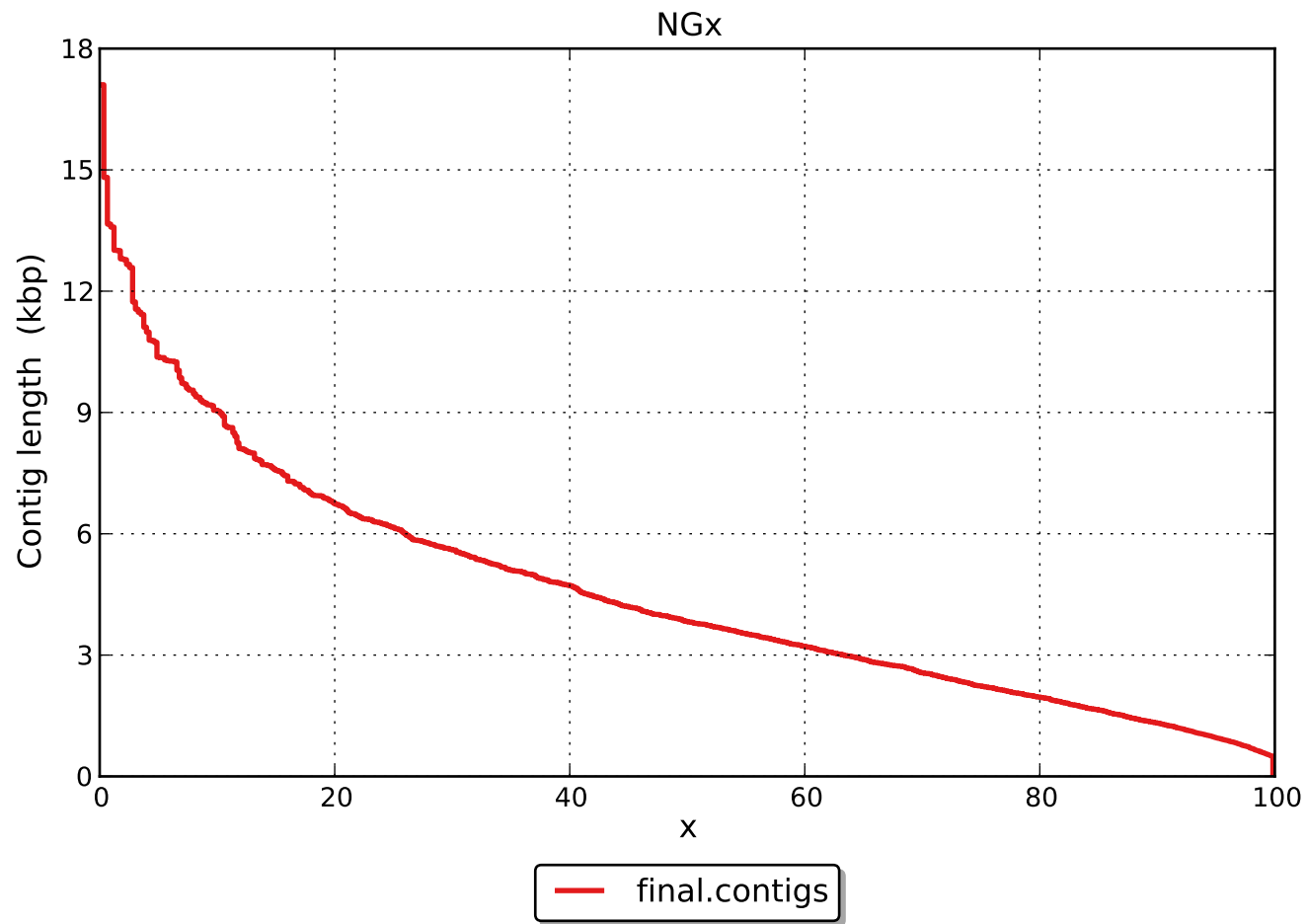
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

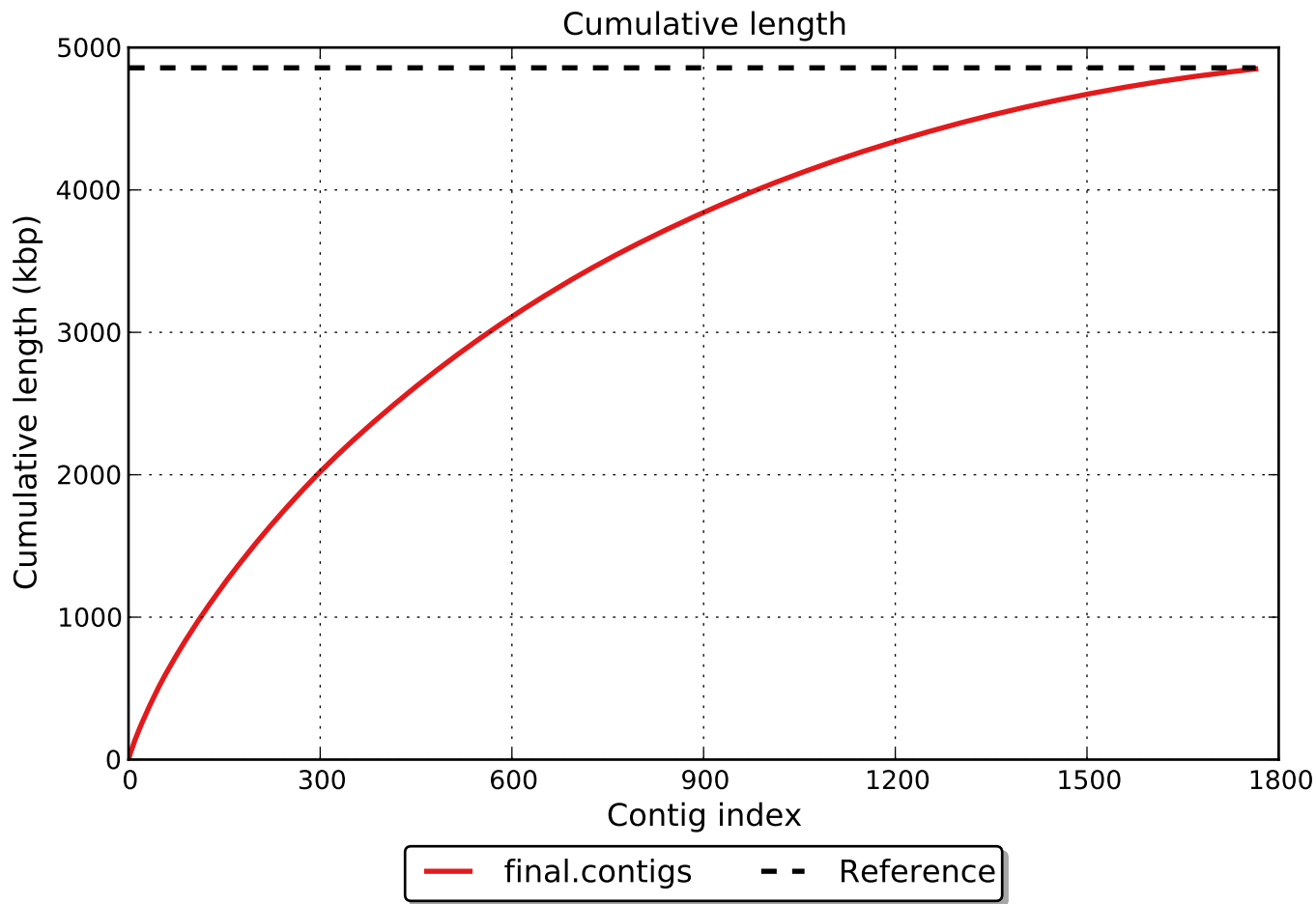
## Unaligned report

	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

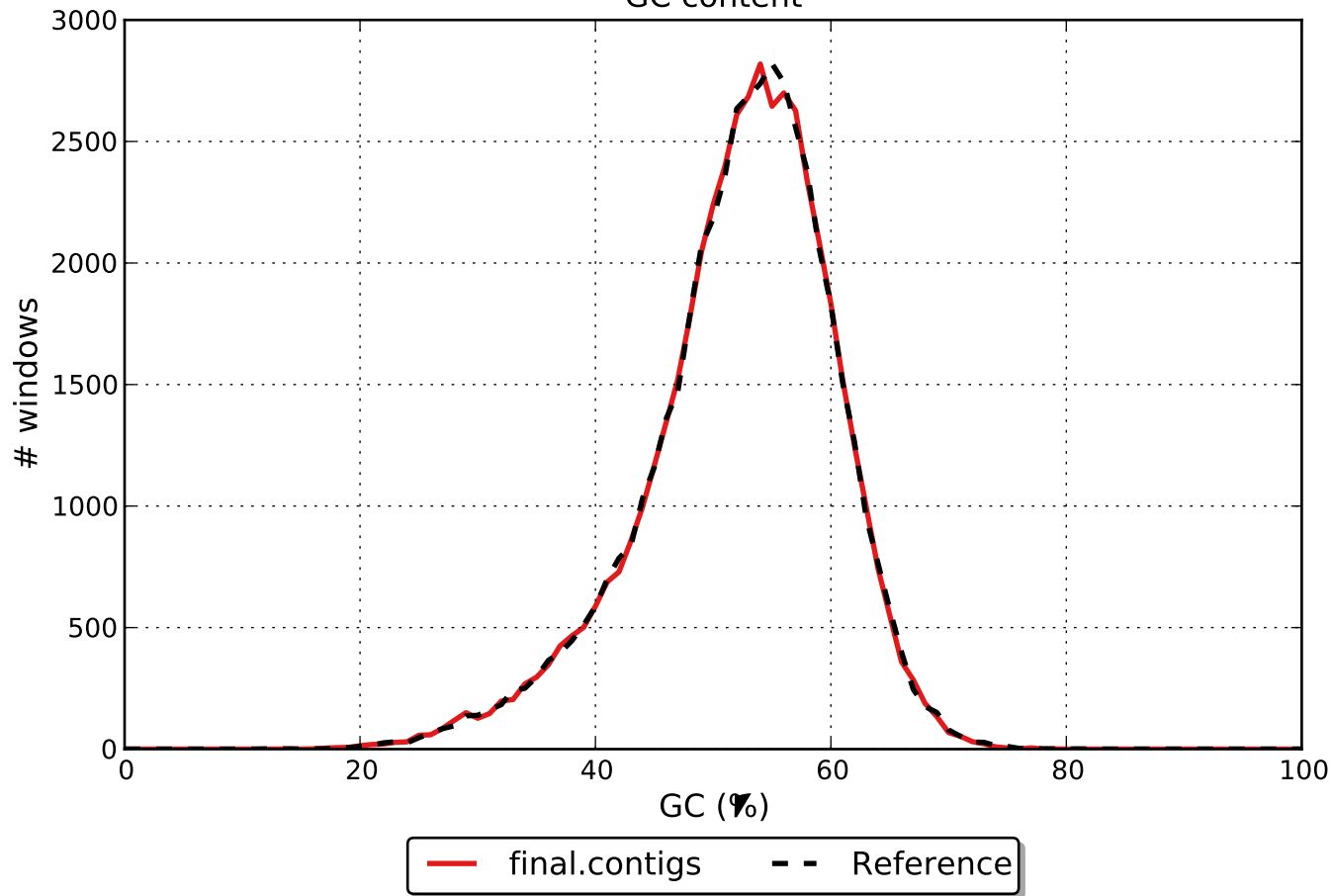
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).







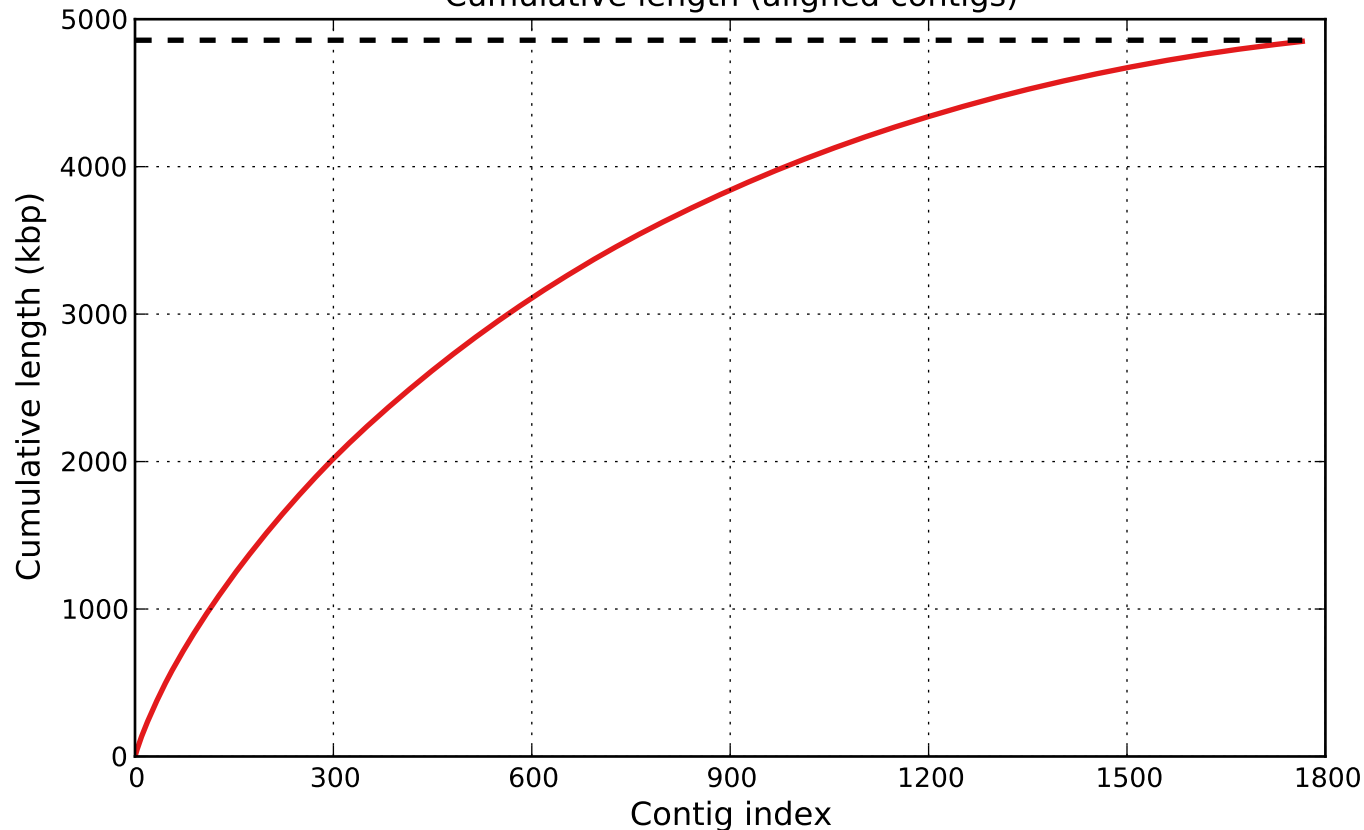
GC content



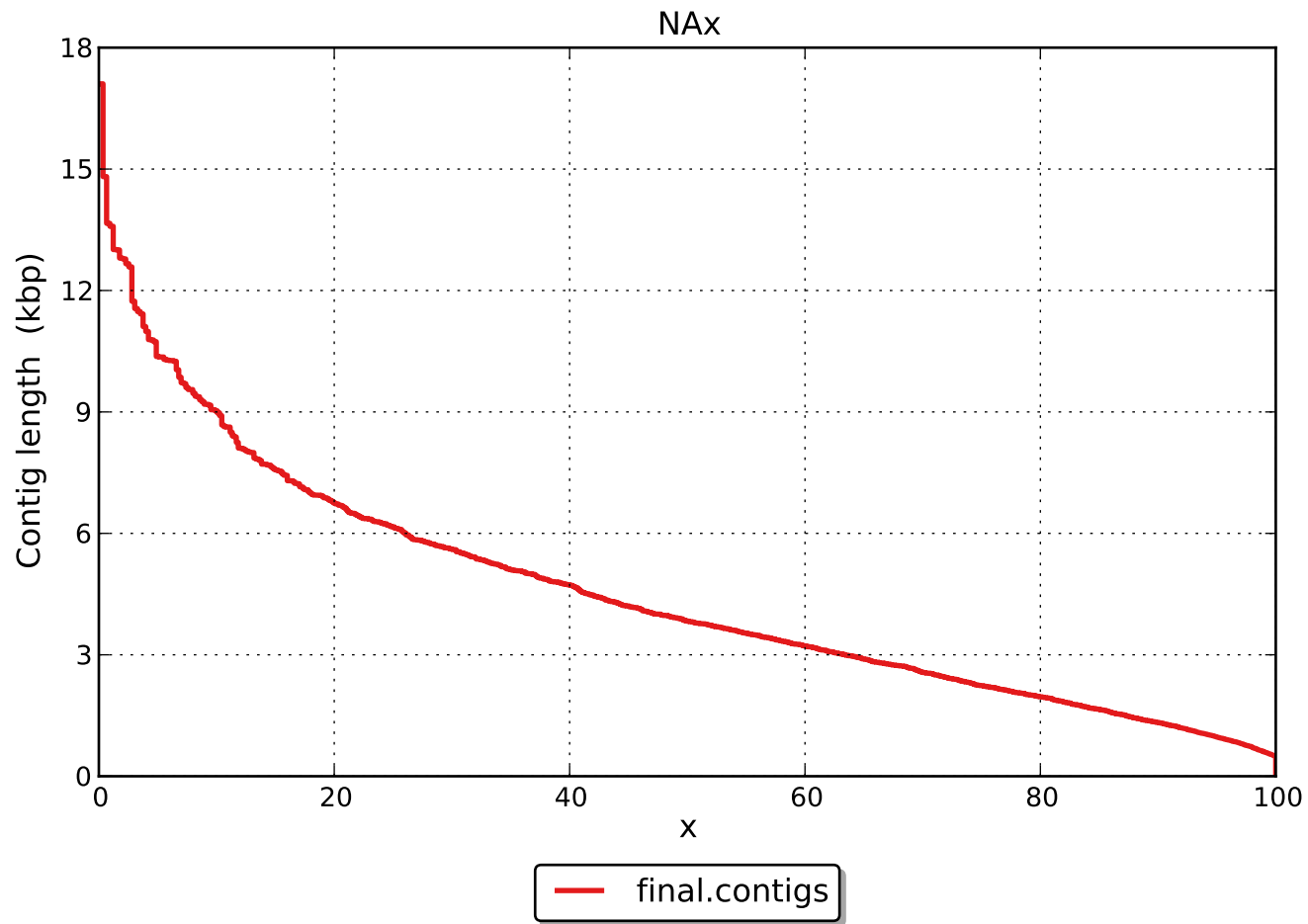




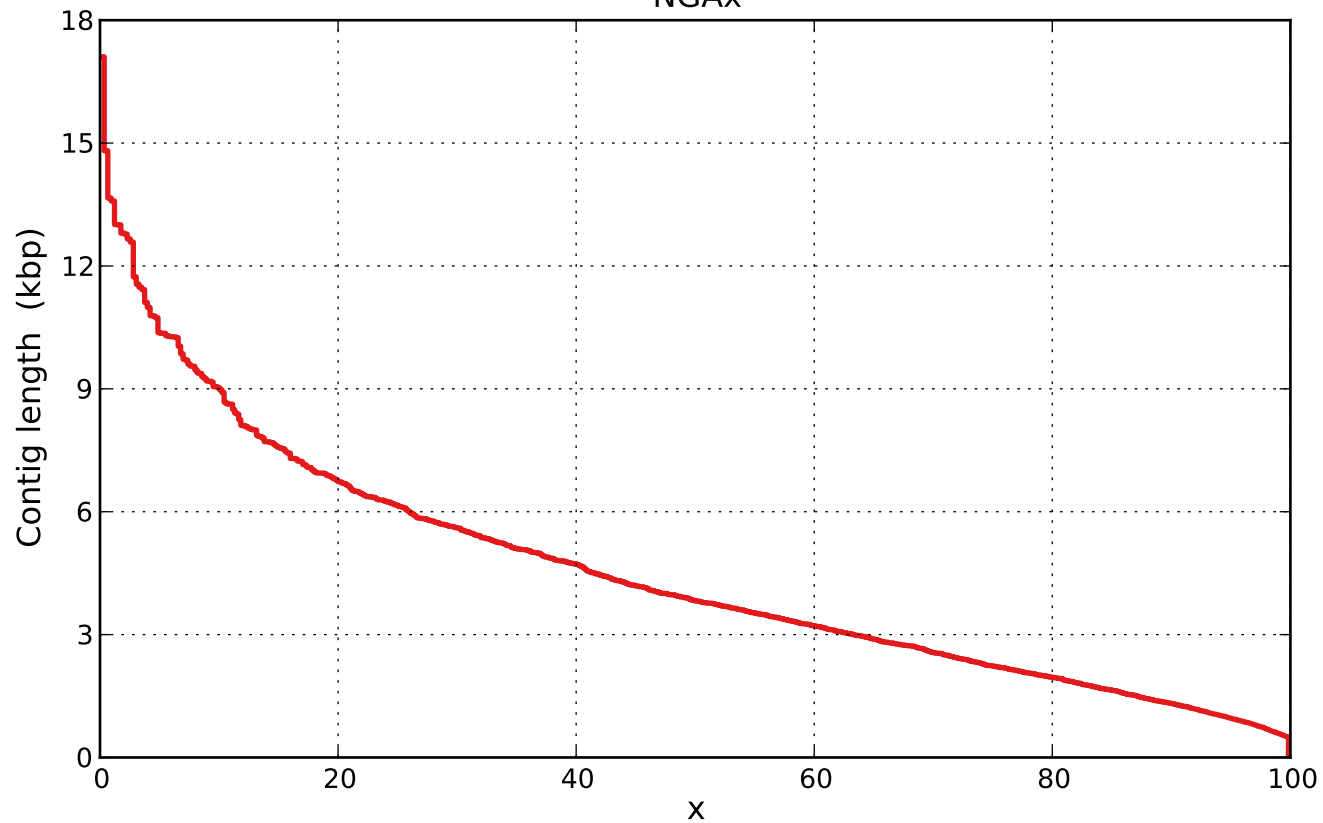
Cumulative length (aligned contigs)



— final.contigs    - - Reference



NGAx



— final.contigs