

Report

	final.contigs
# contigs (>= 1000 bp)	1504
# contigs (>= 5000 bp)	32
# contigs (>= 10000 bp)	2
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	3170474
Total length (>= 5000 bp)	204792
Total length (>= 10000 bp)	20163
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	3299
Largest contig	10101
Total length	4406532
Reference length	4857432
GC (℥)	52.20
Reference GC (℥)	52.22
N50	1734
NG50	1561
N75	924
NG75	759
L50	771
LG50	908
L75	1644
LG75	2049
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (℥)	85.209
Duplication ratio	1.065
# N's per 100 kbp	0.00
# mismatches per 100 kbp	555.19
# indels per 100 kbp	0.05
Largest alignment	10101
NA50	1734
NGA50	1561
NA75	924
NGA75	759
LA50	771
LGA50	908
LA75	1644
LGA75	2049

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

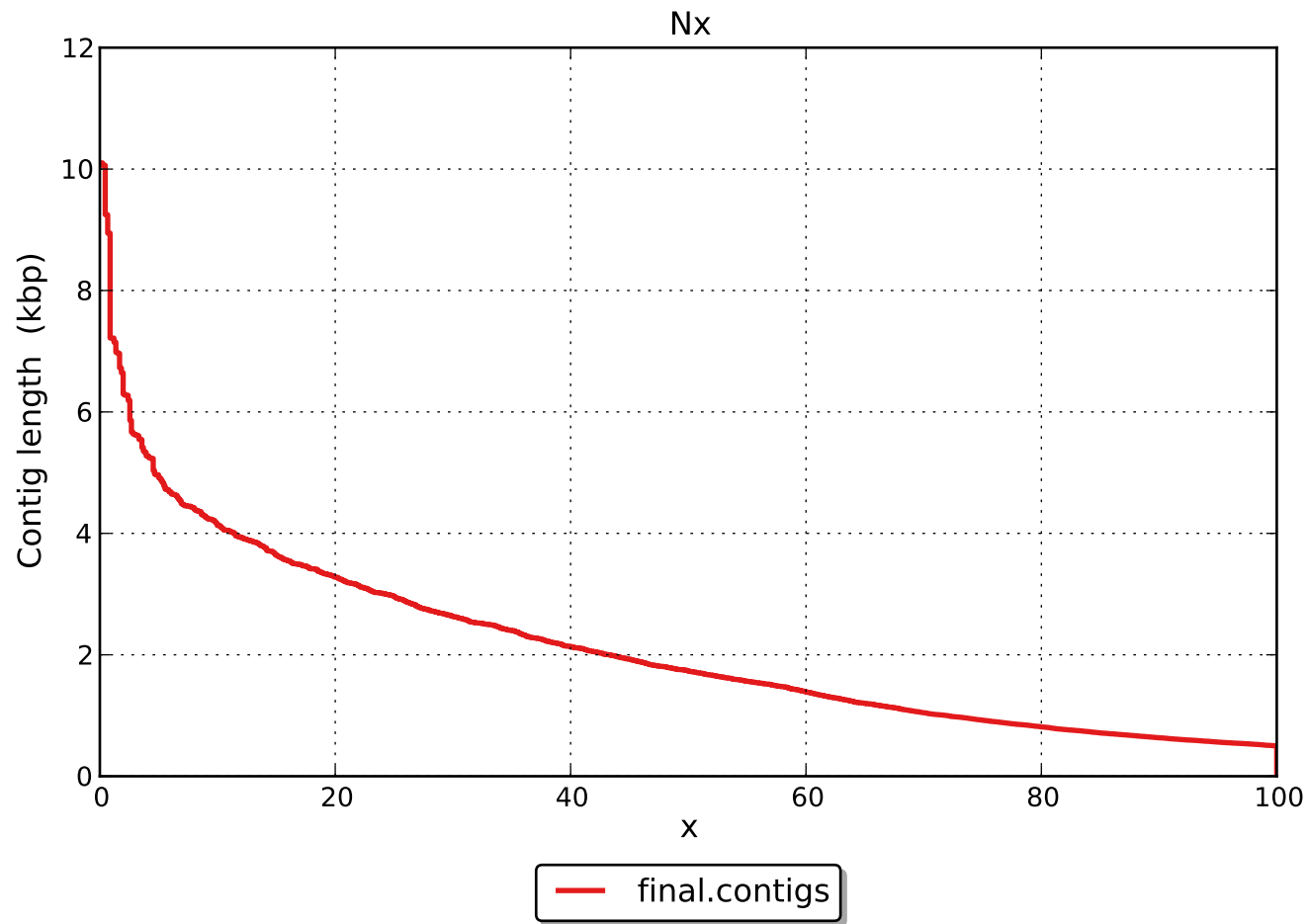
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	22979
# indels	2
# short indels	2
# long indels	0
Indels length	2

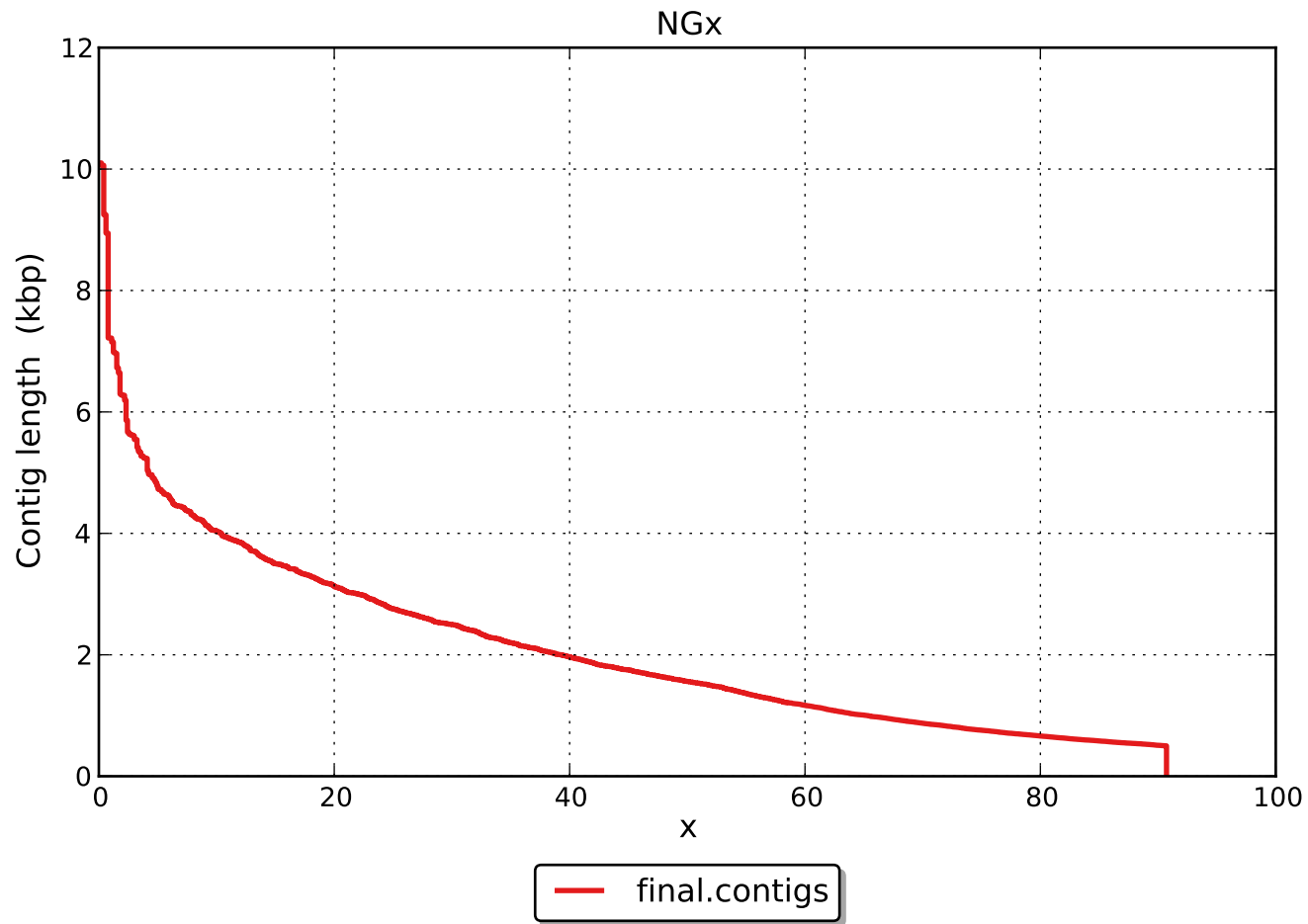
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

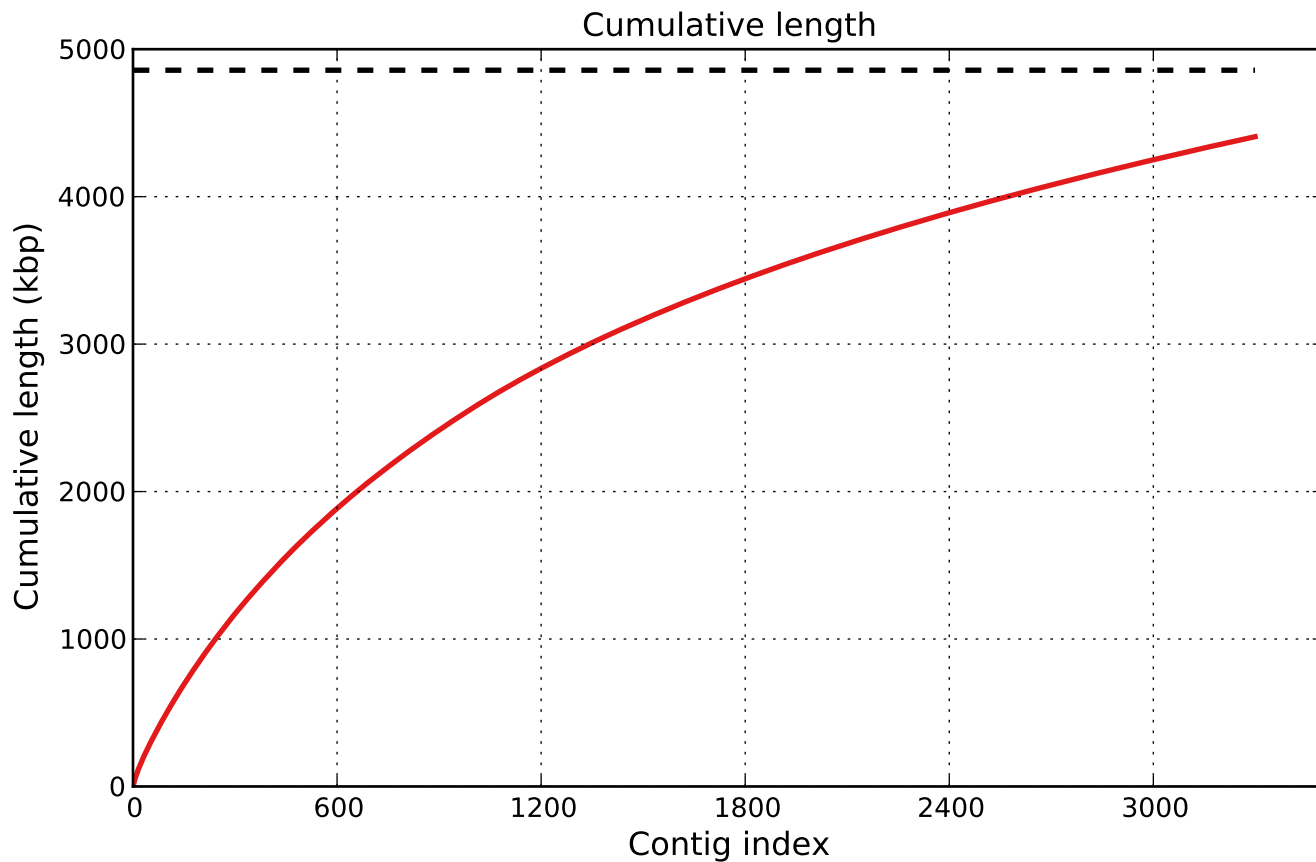
## Unaligned report

	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

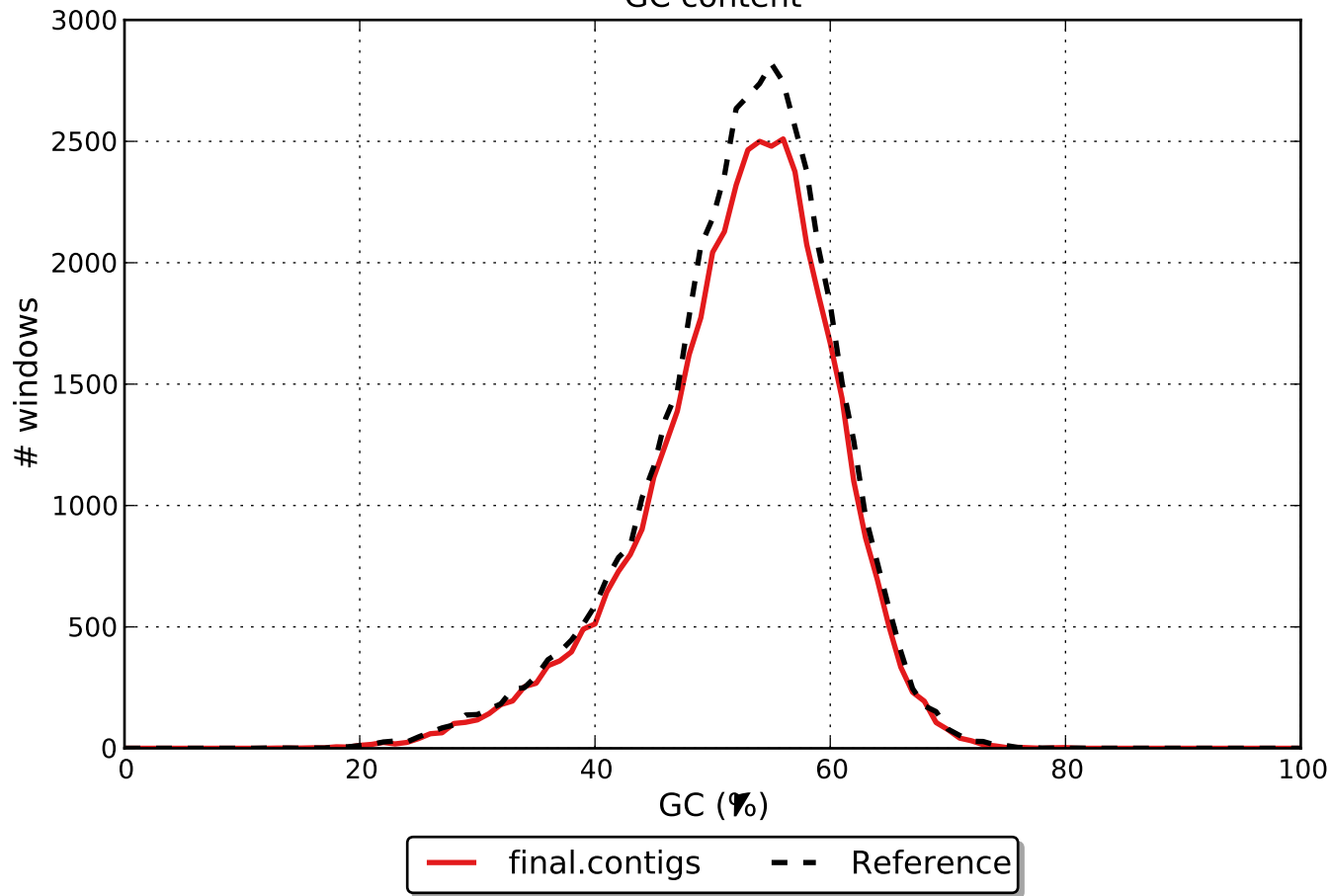
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).







GC content

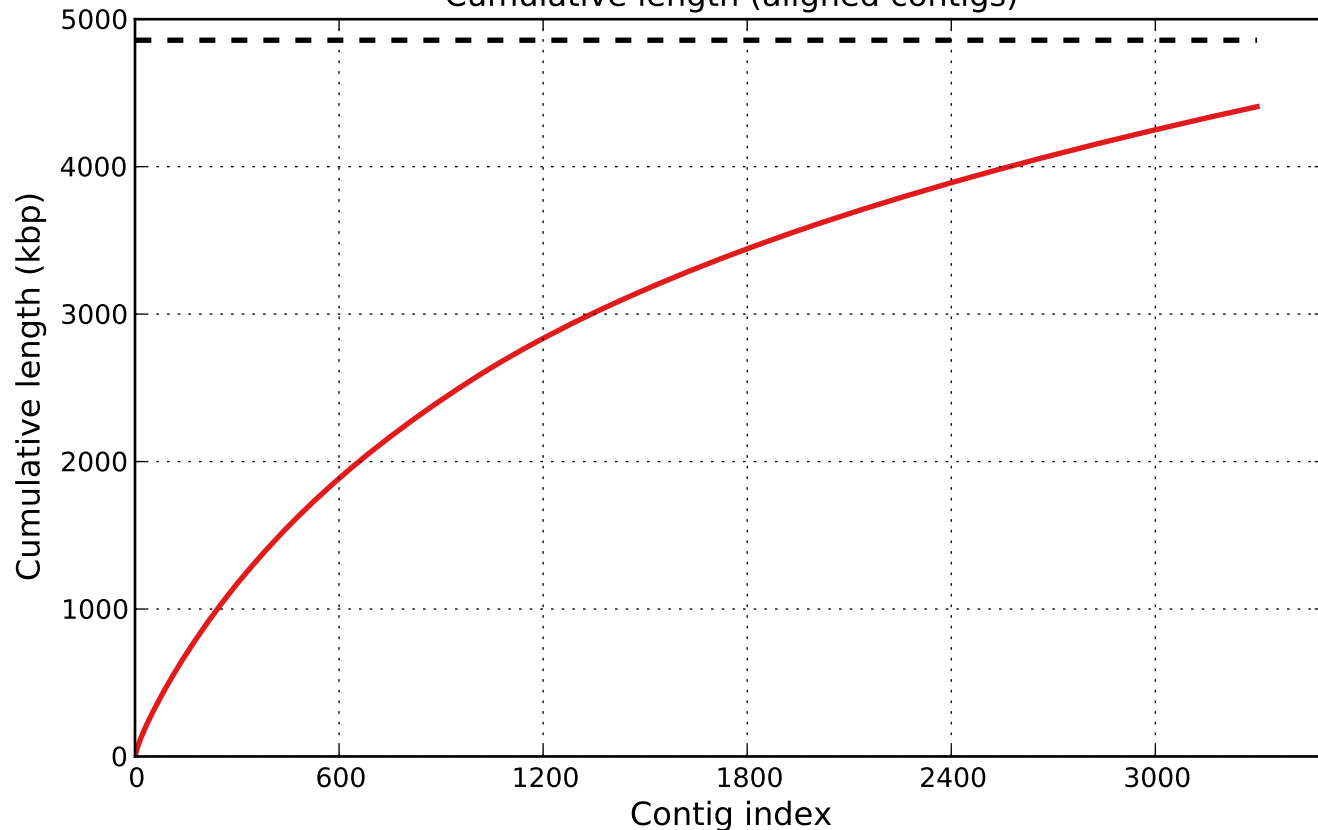


# Misassemblies

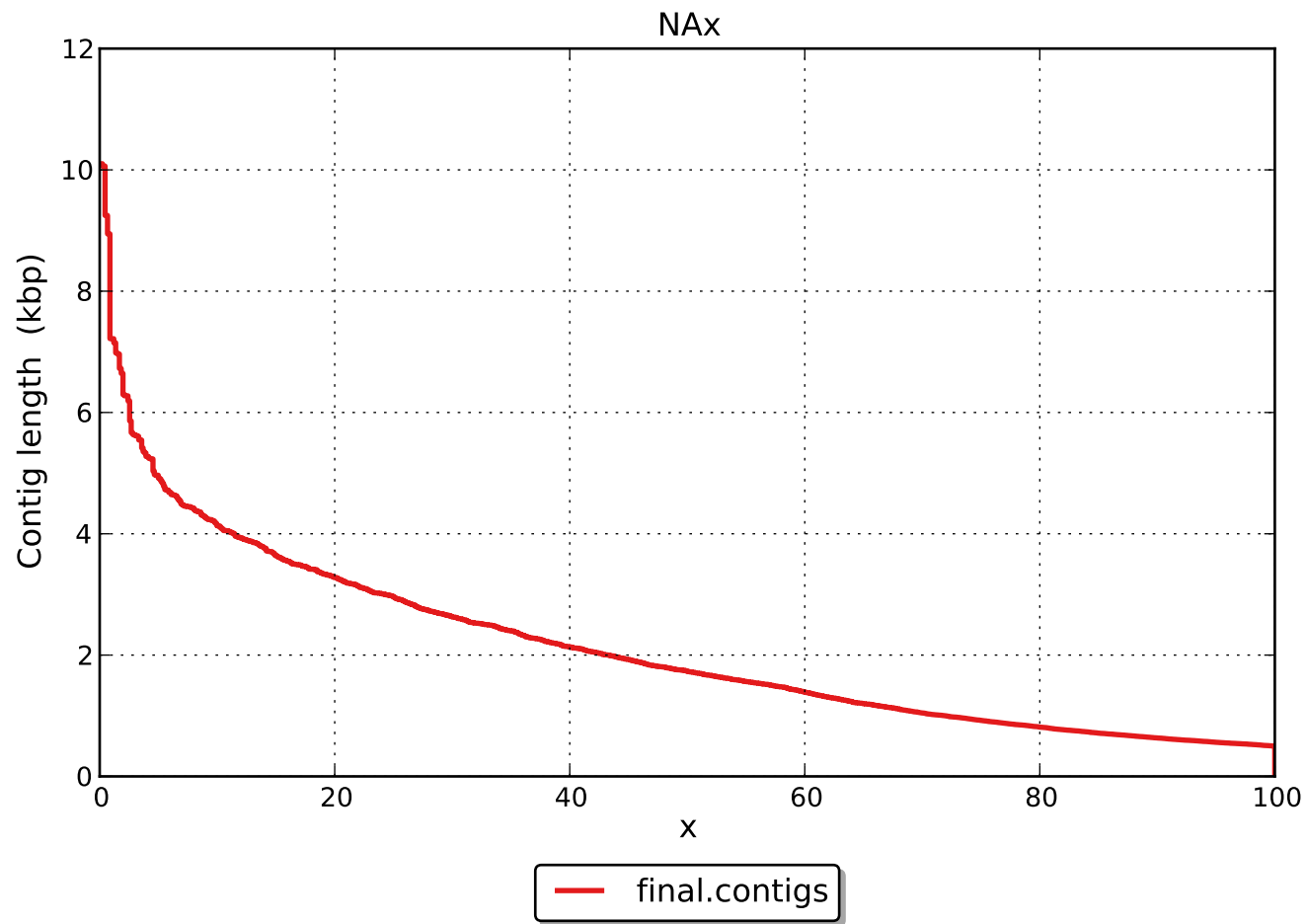




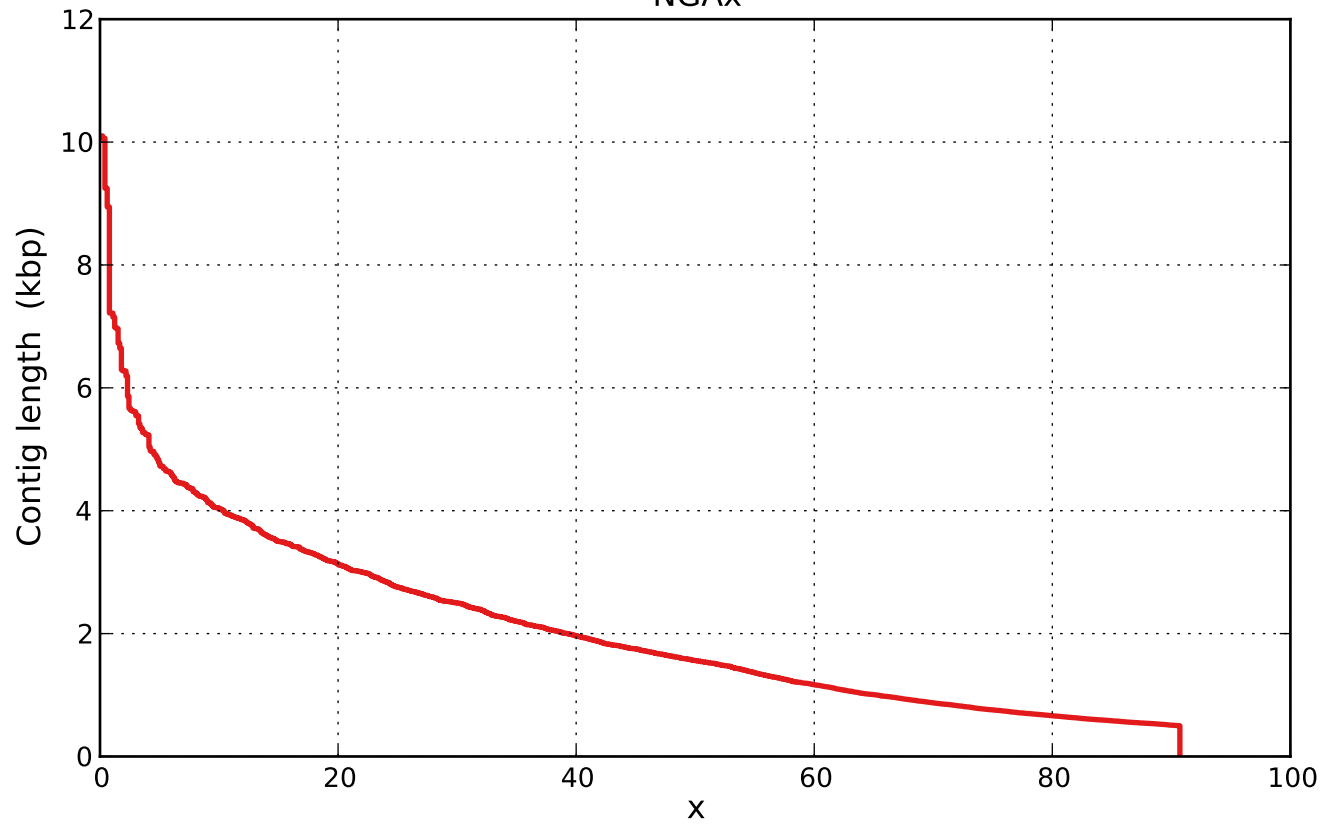
Cumulative length (aligned contigs)



— final.contigs      - - Reference



NGAx



— final.contigs