

## Report

	final.contigs
# contigs (>= 1000 bp)	868
# contigs (>= 5000 bp)	14
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	1722248
Total length (>= 5000 bp)	89632
Total length (>= 10000 bp)	10101
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	2481
Largest contig	10101
Total length	2821838
Reference length	4857432
GC (℥)	52.24
Reference GC (℥)	52.22
N50	1329
NG50	629
N75	756
L50	594
LG50	1779
L75	1326
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (℥)	55.791
Duplication ratio	1.041
# N's per 100 kbp	0.00
# mismatches per 100 kbp	305.87
# indels per 100 kbp	0.00
Largest alignment	10101
NA50	1329
NGA50	629
NA75	756
LA50	594
LGA50	1779
LA75	1326

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

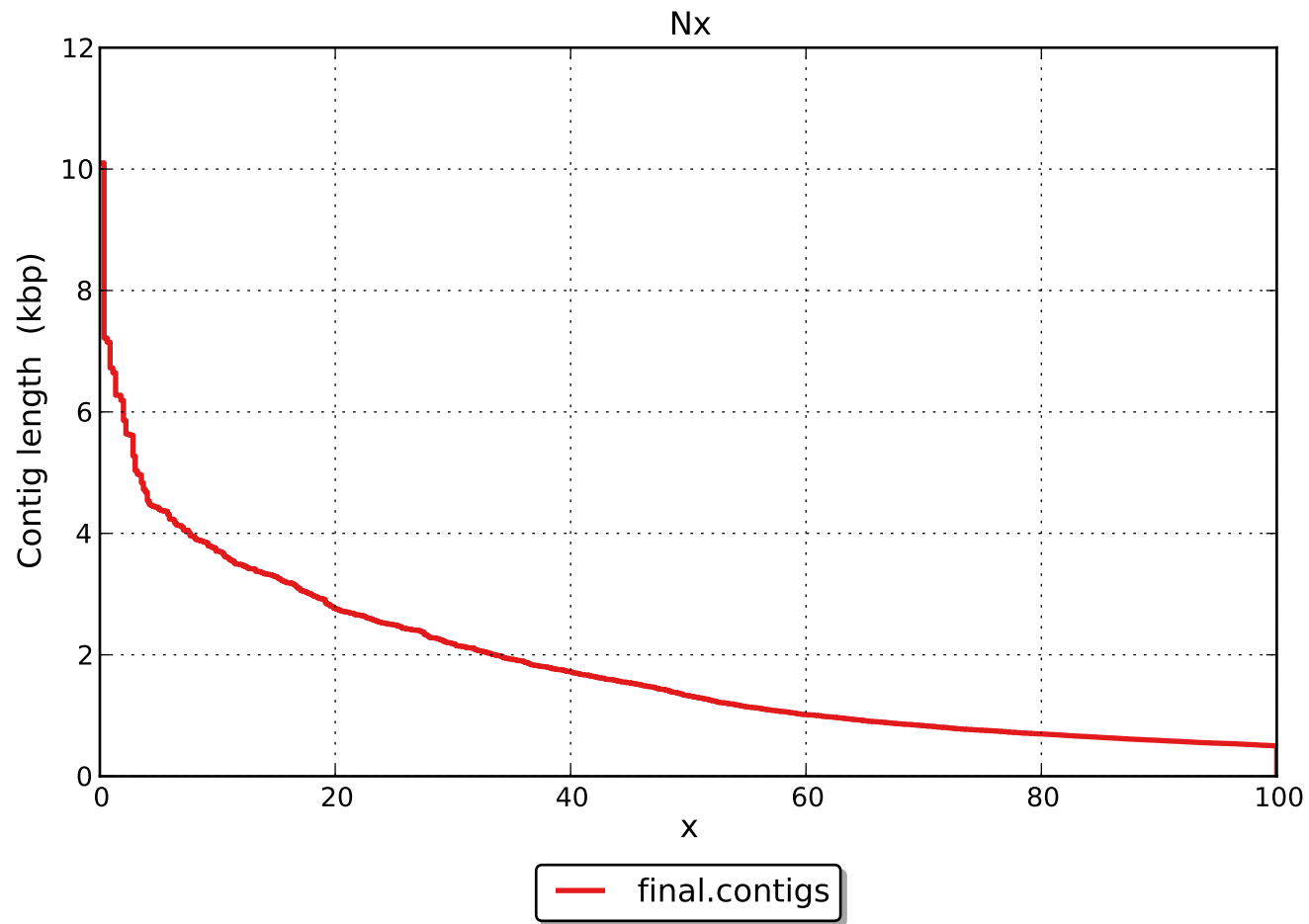
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	8289
# indels	0
# short indels	0
# long indels	0
Indels length	0

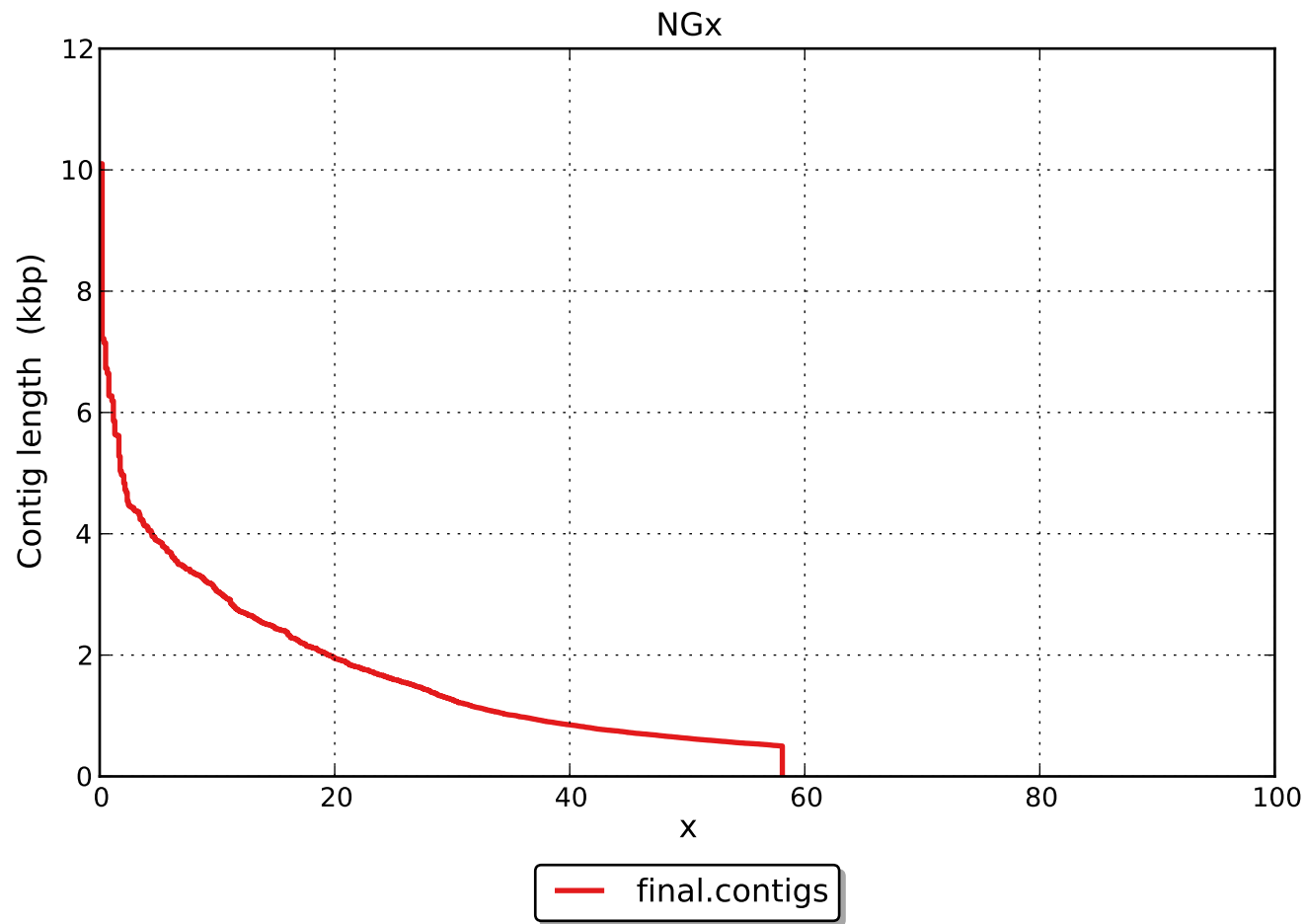
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

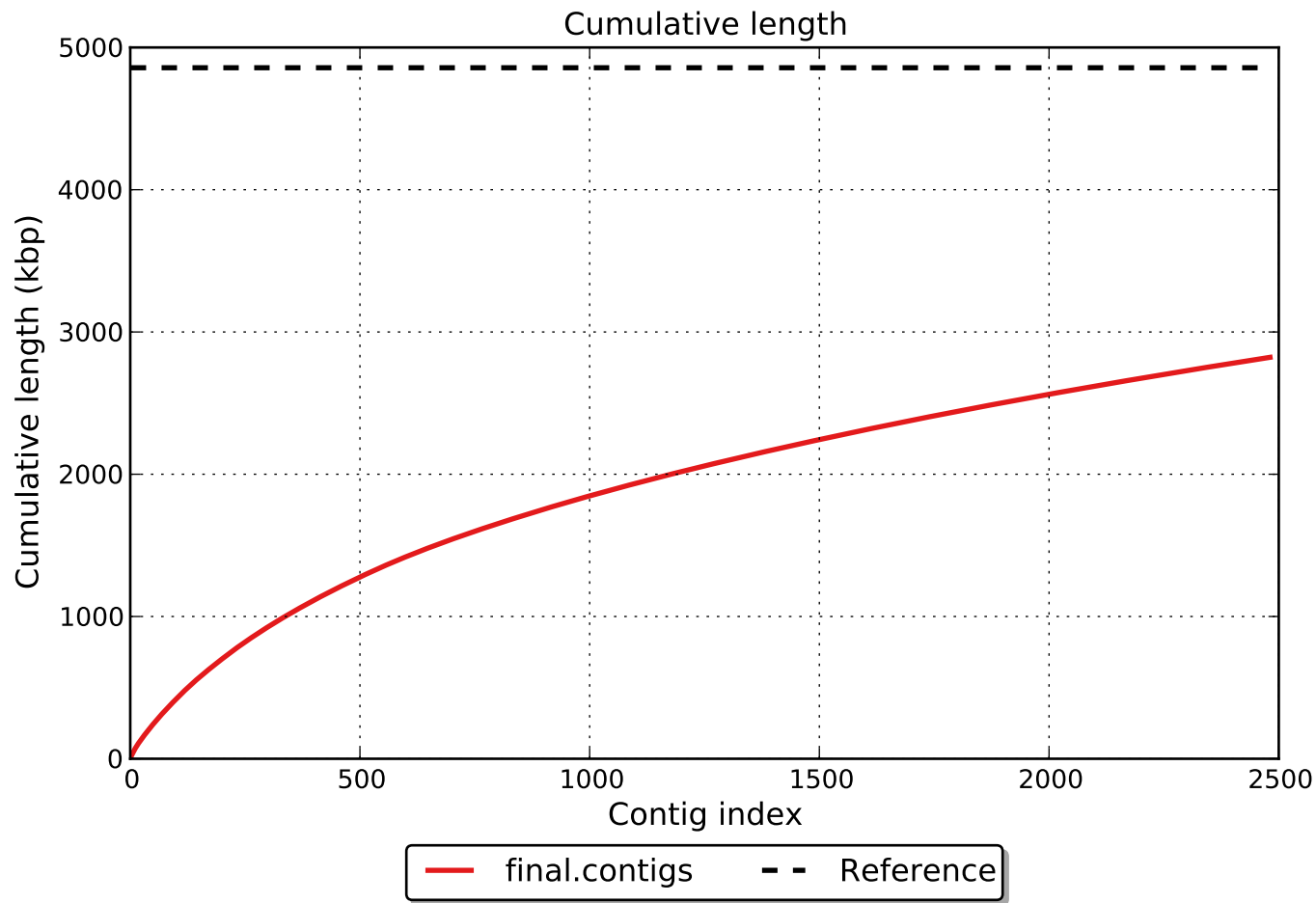
## Unaligned report

	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

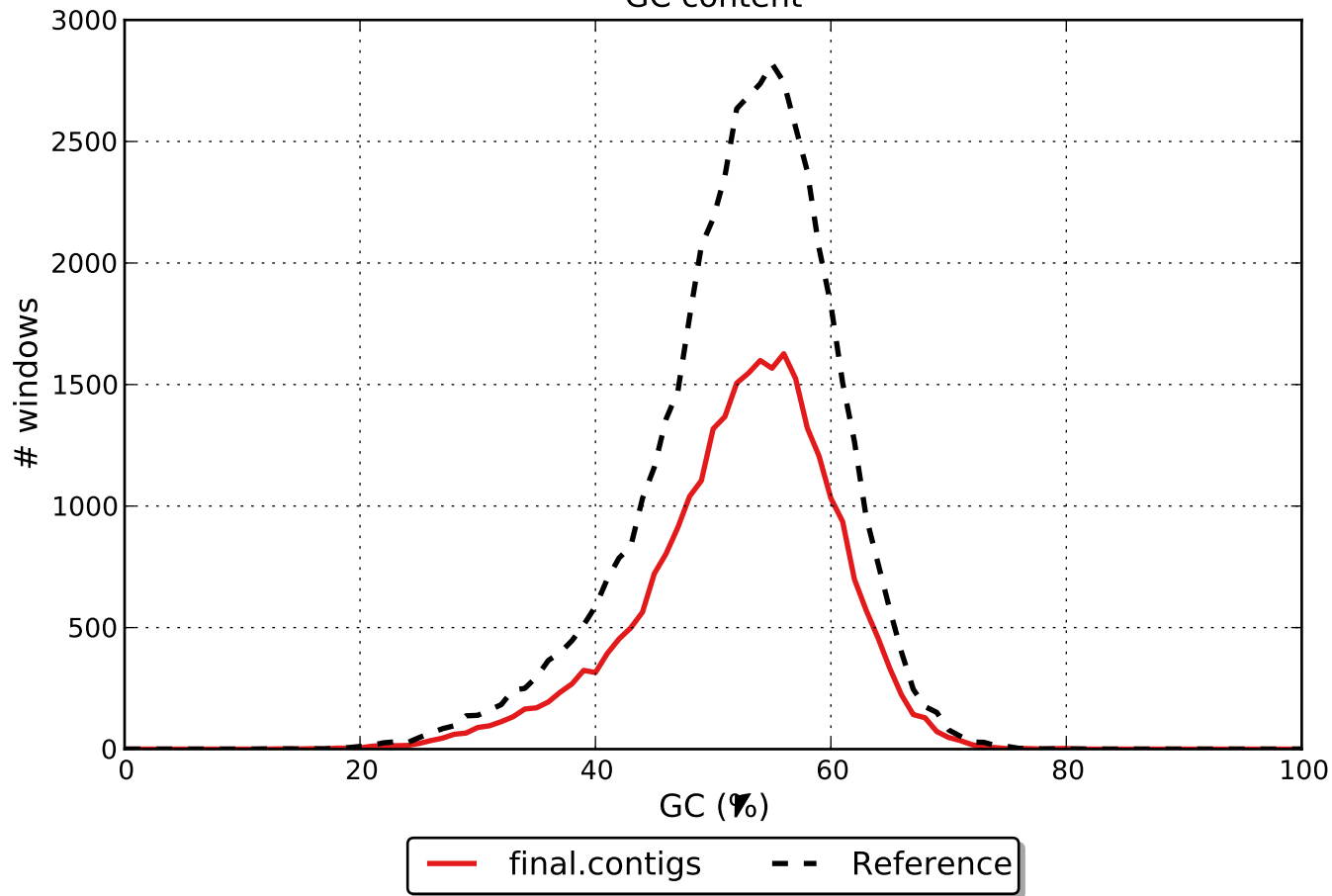
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



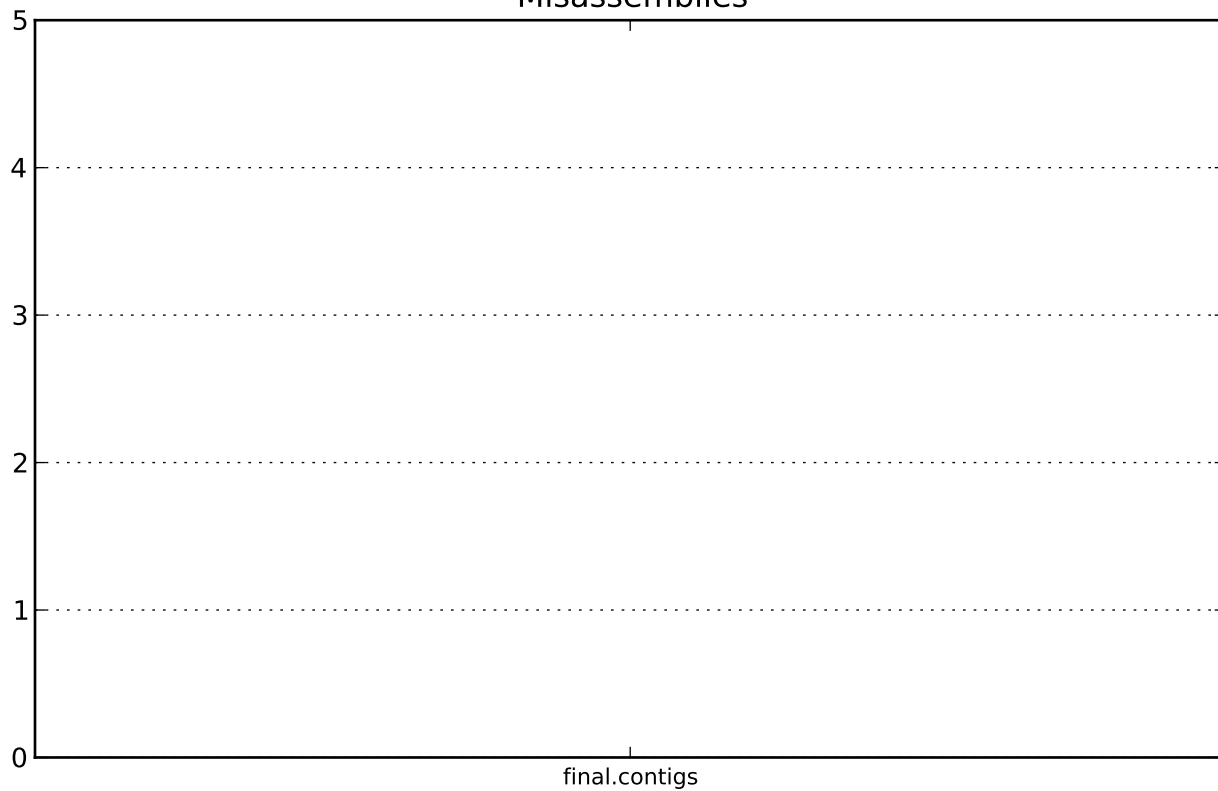




GC content

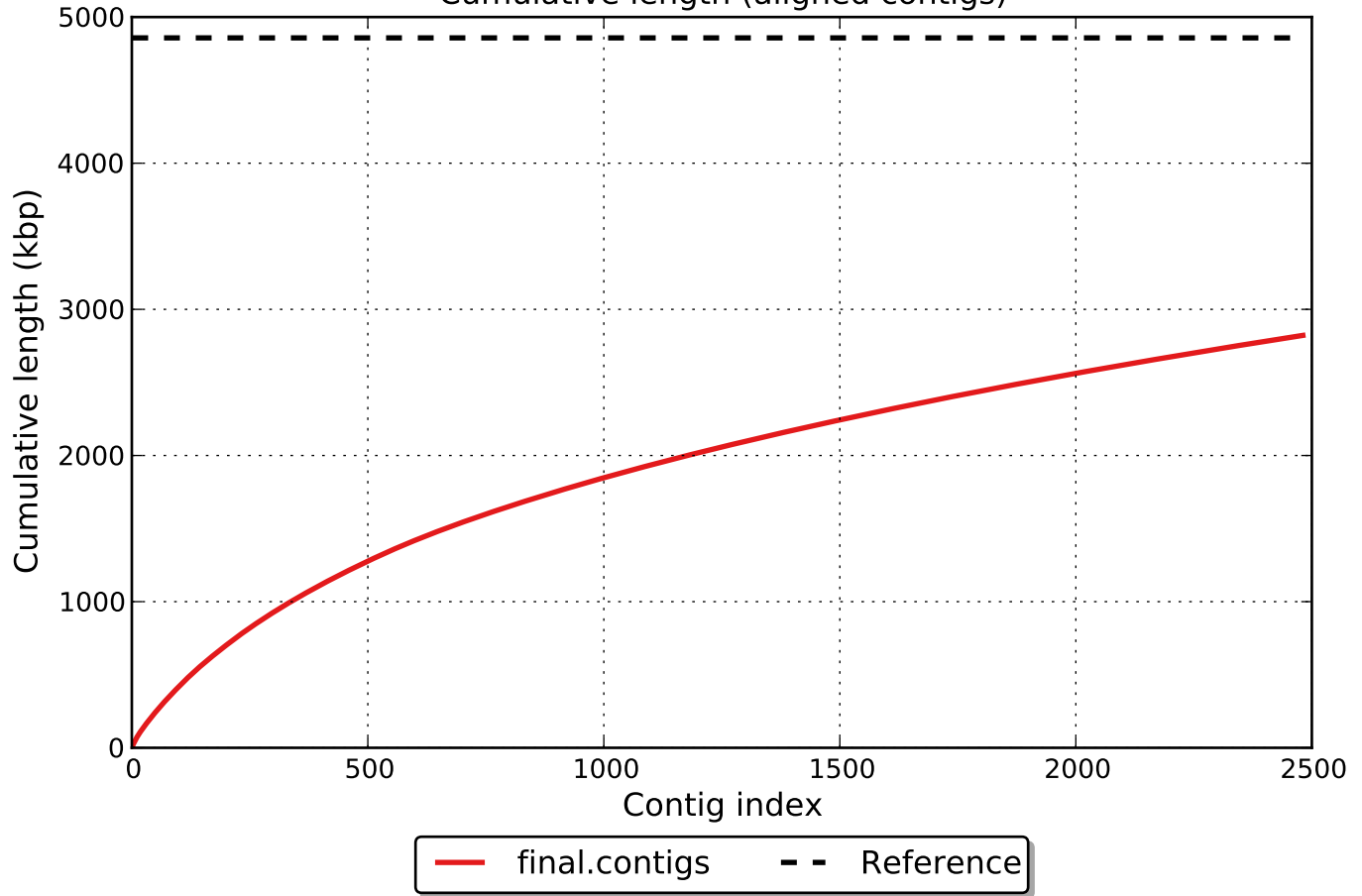


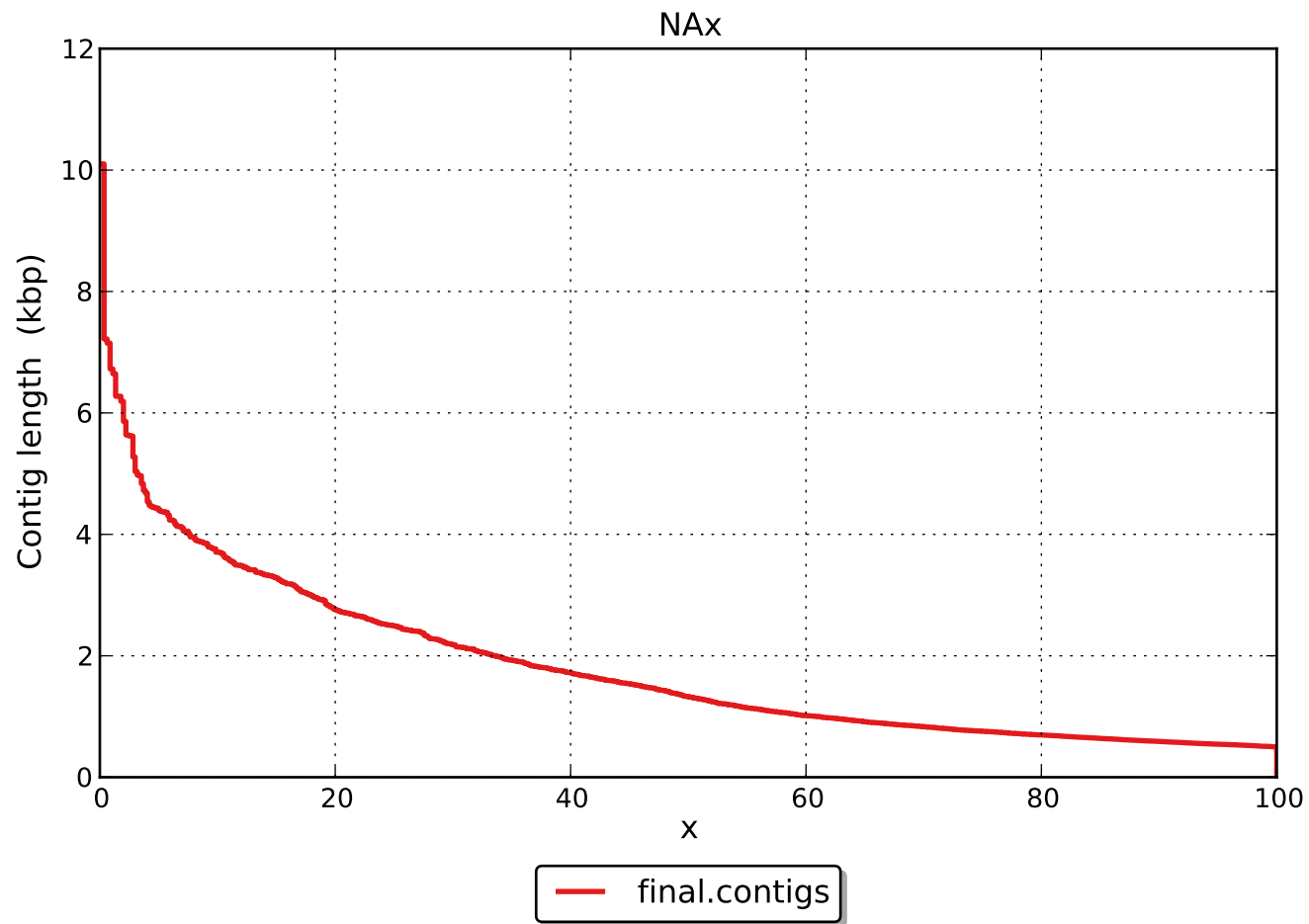
# Misassemblies





Cumulative length (aligned contigs)





NGAx

