

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	866
# contigs ( $\geq 1000$ bp)	472
Total length ( $\geq 0$ bp)	1281421
Total length ( $\geq 1000$ bp)	1046424
# contigs	721
Largest contig	11393
Total length	1230533
Reference length	1231960
GC (%)	25.37
Reference GC (%)	25.34
N50	2195
NG50	2195
N75	1304
NG75	1291
L50	186
LG50	186
L75	364
LG75	365
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	95.981
Duplication ratio	1.041
# N's per 100 kbp	0.00
# mismatches per 100 kbp	36.79
# indels per 100 kbp	0.00
Largest alignment	11393
NA50	2195
NGA50	2195
NA75	1304
NGA75	1291
LA50	186
LGA50	186
LA75	364
LGA75	365

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).

## Misassemblies report

	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# mismatches	435
# indels	0
# short indels	0
# long indels	0
Indels length	0

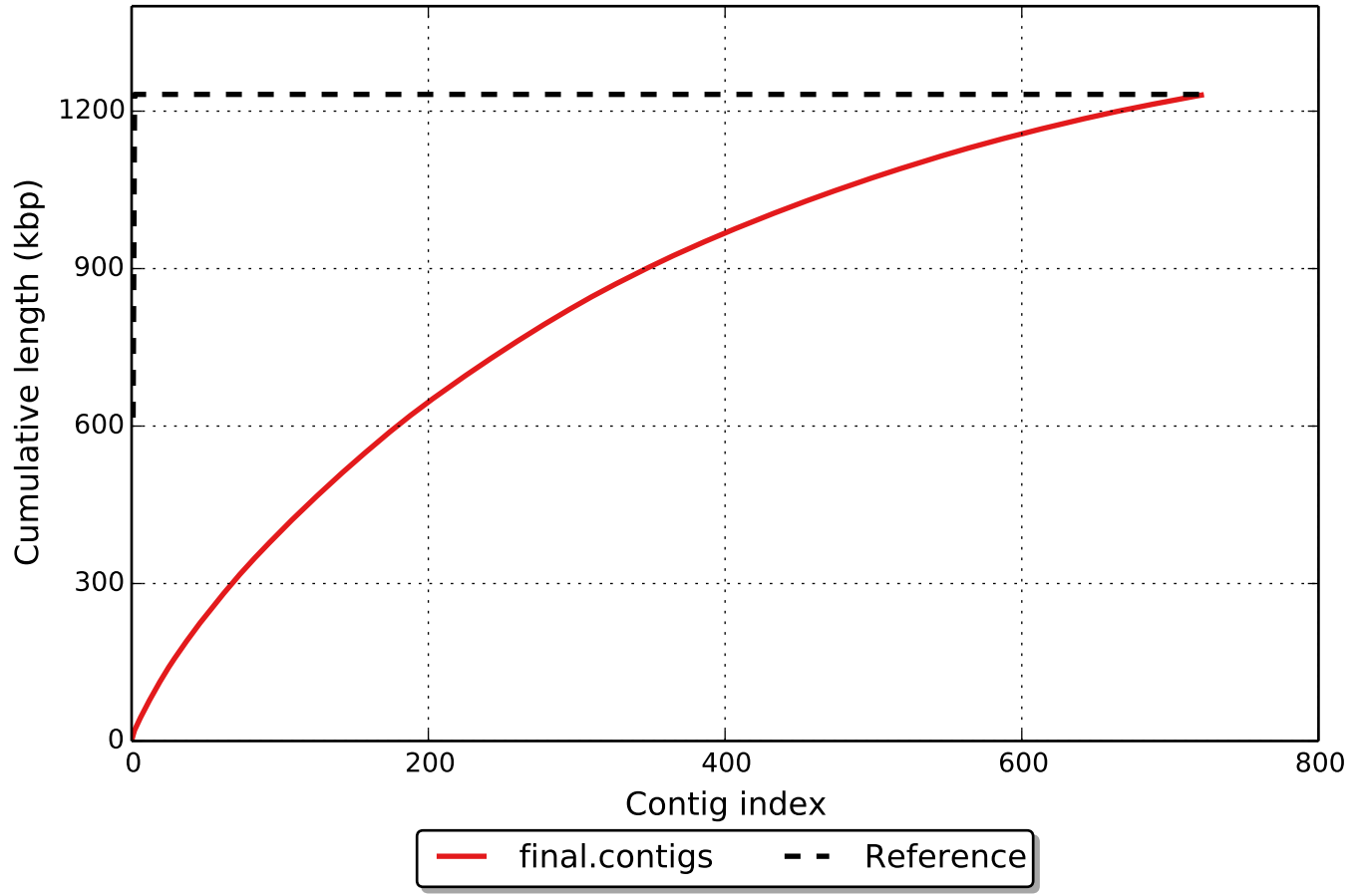
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

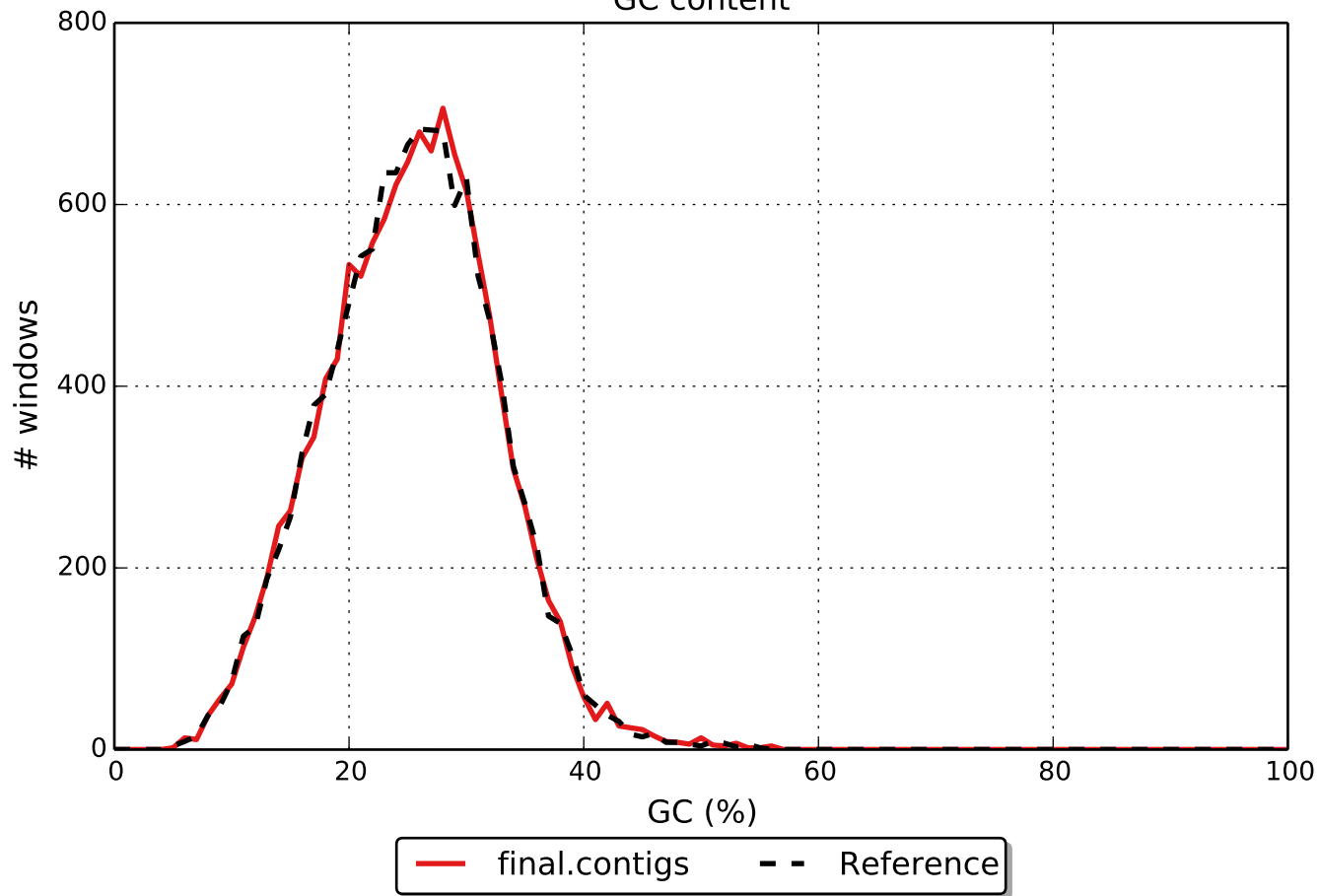
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

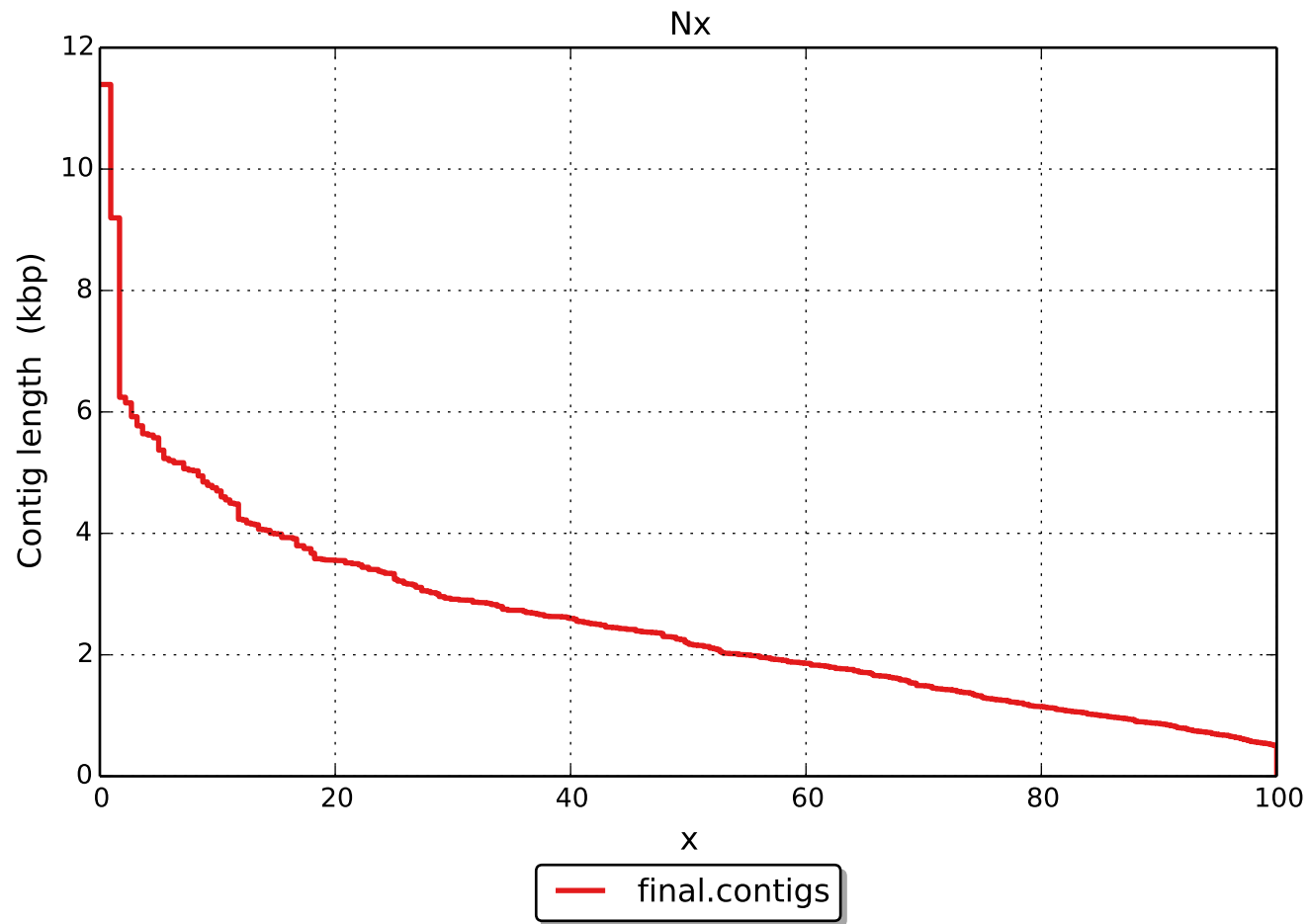
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

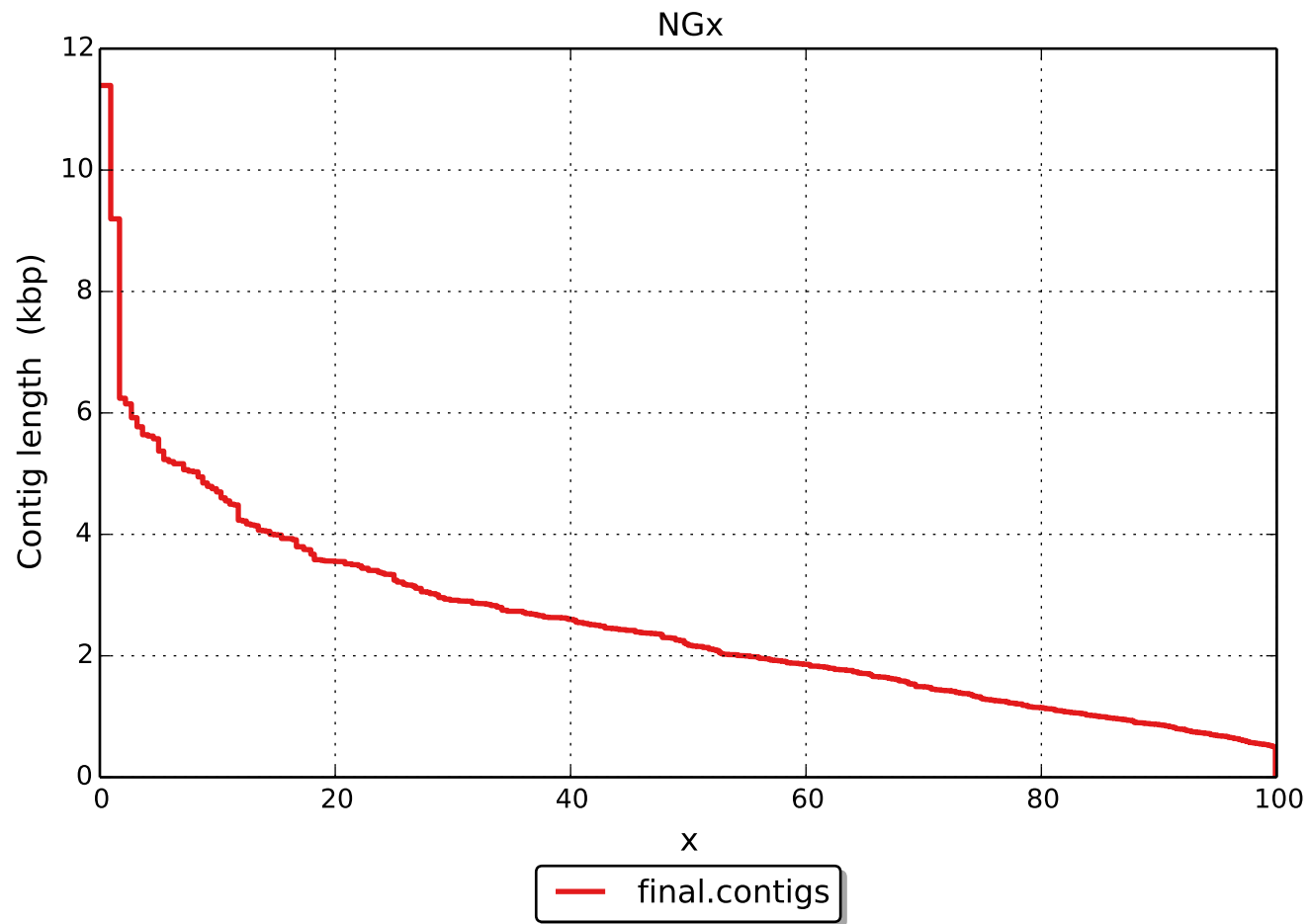
Cumulative length



GC content







# Misassemblies





Cumulative length (aligned contigs)

