

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	6680
# contigs ( $\geq 1000$ bp)	1466
Total length ( $\geq 0$ bp)	6750421
Total length ( $\geq 1000$ bp)	4538844
# contigs	2864
Largest contig	18963
Total length	5460626
Reference length	10957366
GC (%)	50.28
Reference GC (%)	50.49
N50	3267
N75	1475
L50	487
L75	1100
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	48.824
Duplication ratio	1.021
# N's per 100 kbp	0.00
# mismatches per 100 kbp	429.26
# indels per 100 kbp	0.06
Largest alignment	18963
NA50	3267
NA75	1475
LA50	487
LA75	1100

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

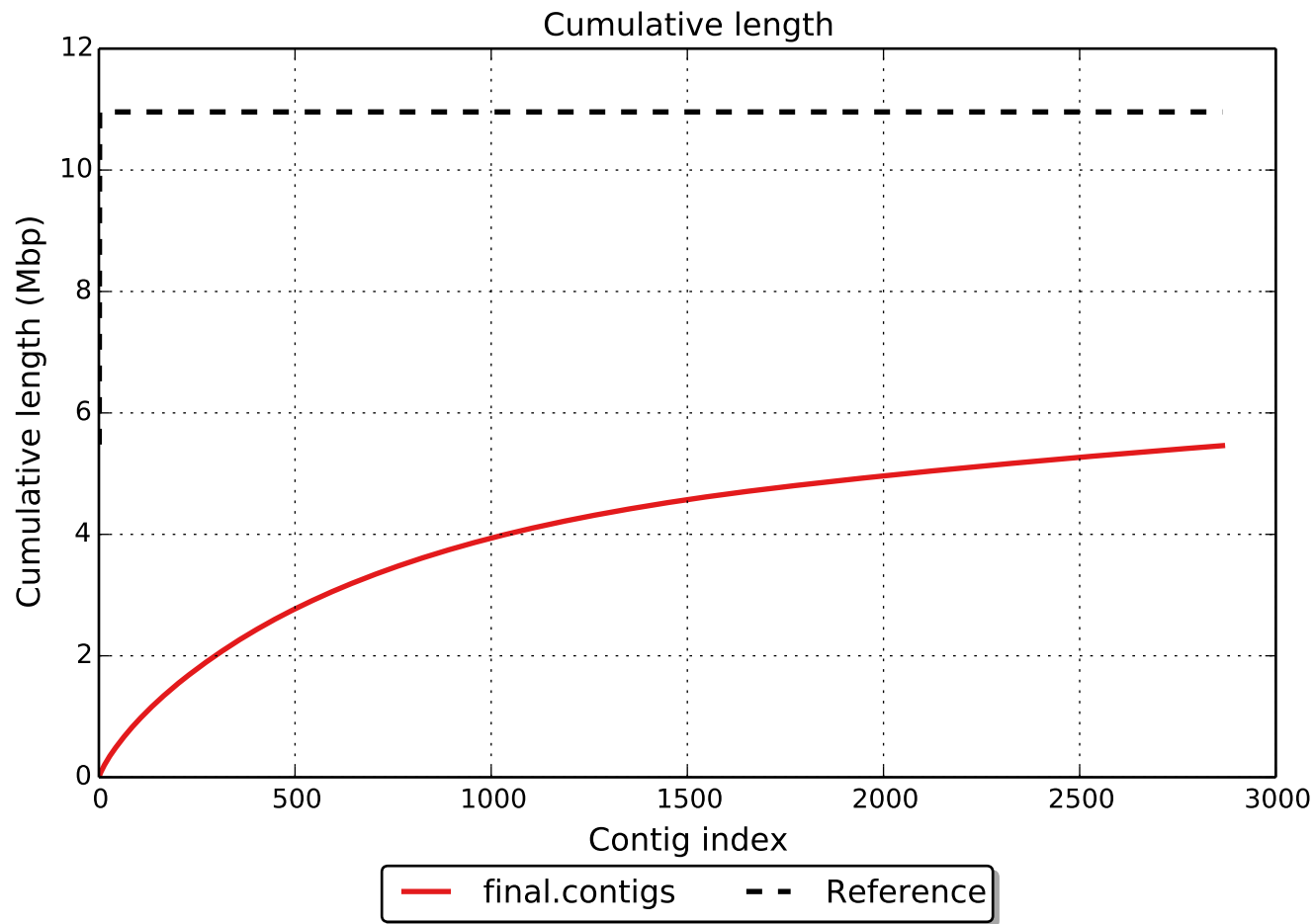
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# mismatches	22965
# indels	3
# short indels	0
# long indels	3
Indels length	42

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).

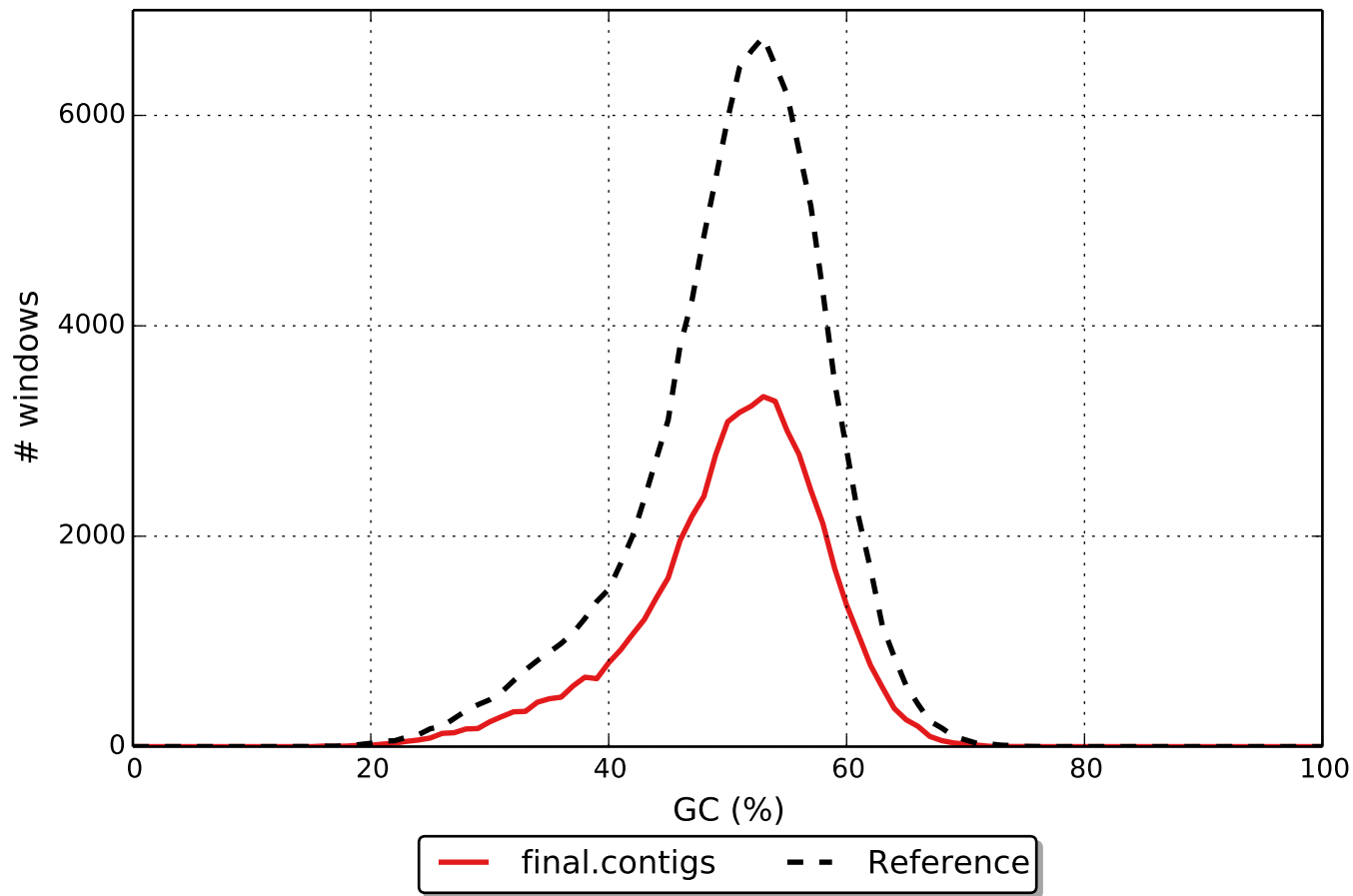
## Unaligned report

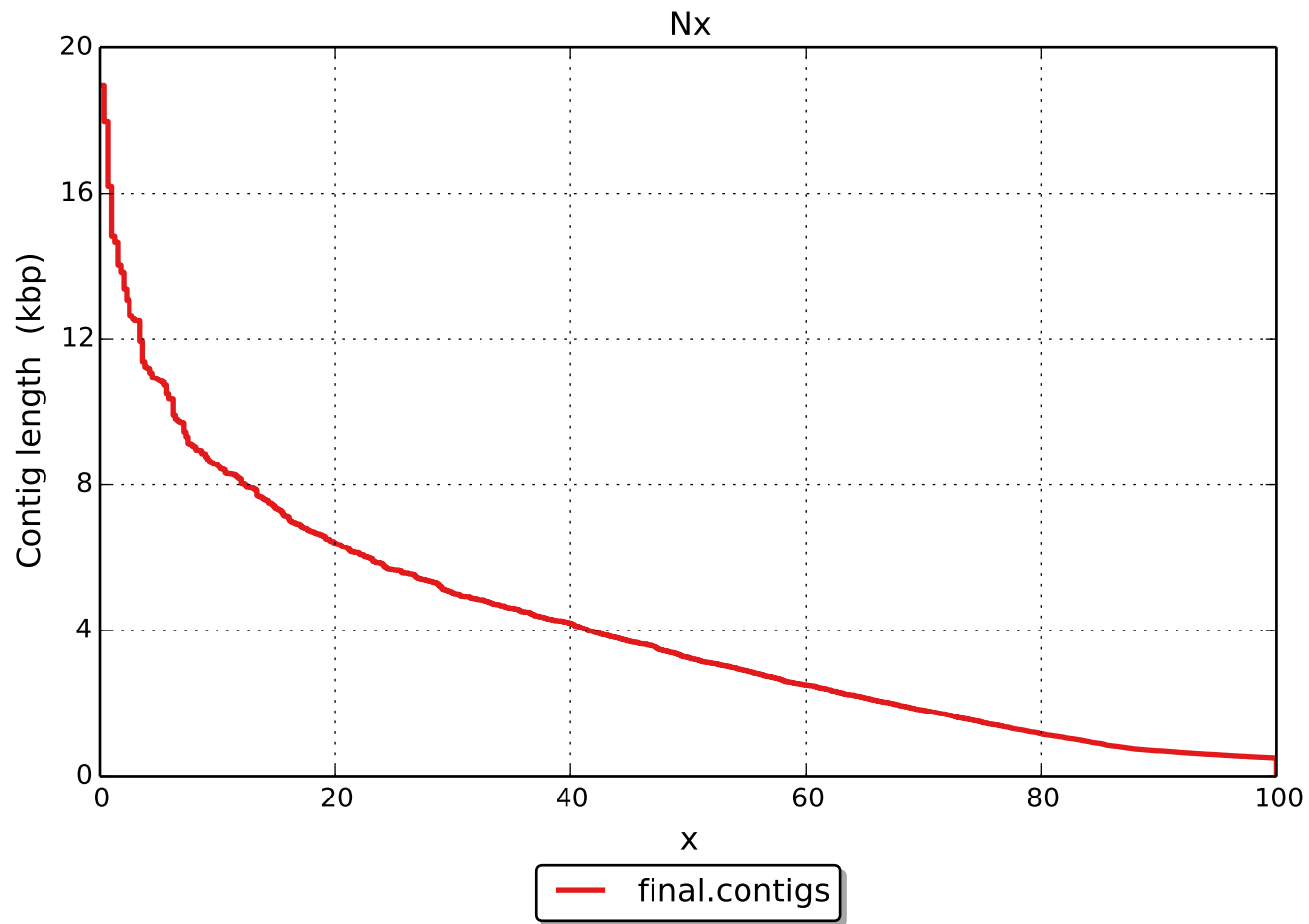
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

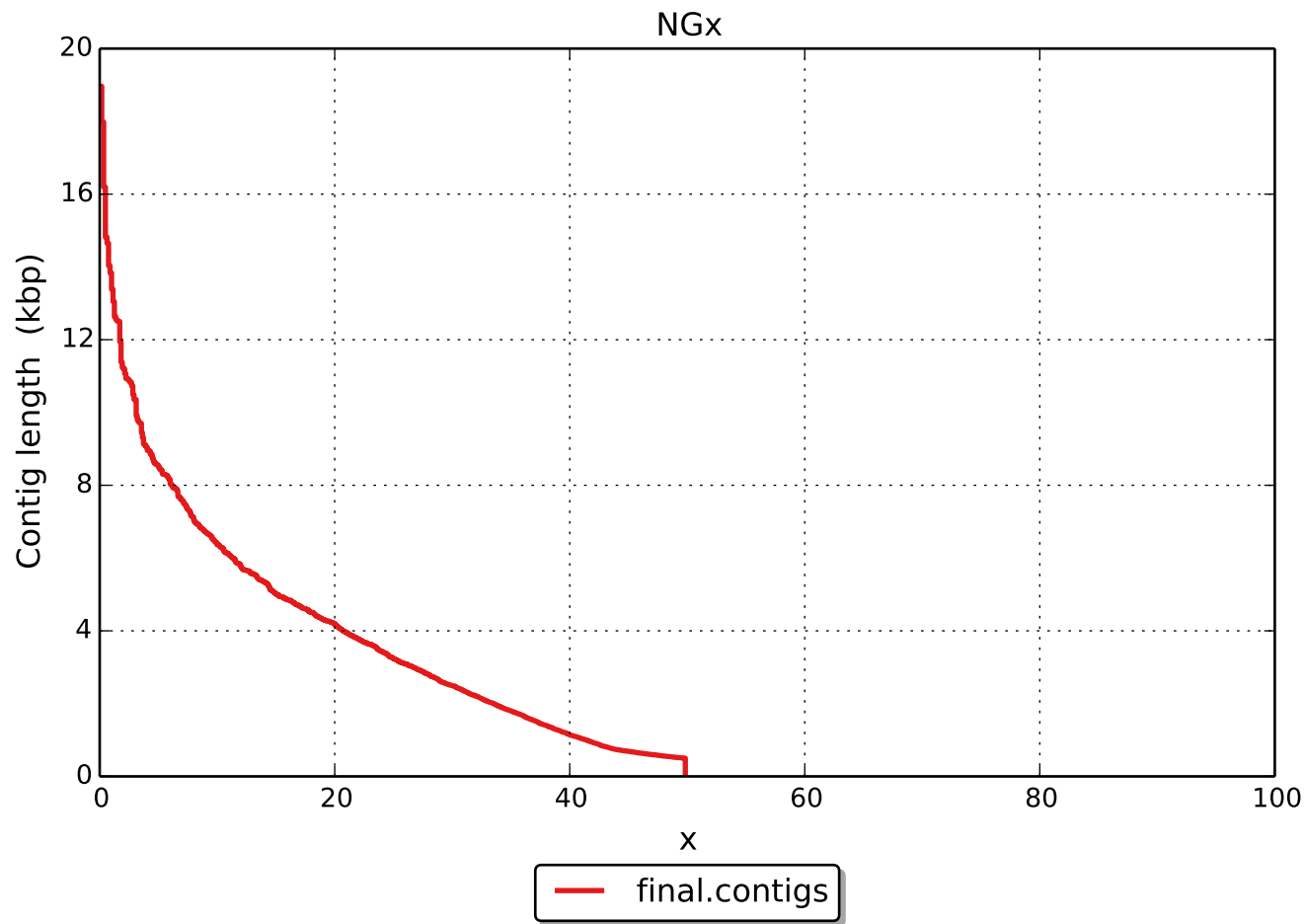
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



GC content







# Misassemblies





