

Report

	final.contigs
# contigs (≥ 0 bp)	10681
# contigs (≥ 1000 bp)	1918
Total length (≥ 0 bp)	8011239
Total length (≥ 1000 bp)	3760775
# contigs	5504
Largest contig	9465
Total length	6209297
Reference length	10957366
GC (%)	50.34
Reference GC (%)	50.49
N50	1300
NG50	608
N75	751
L50	1338
LG50	4181
L75	2964
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 3 part
Unaligned length	360
Genome fraction (%)	82.095
Duplication ratio	1.058
# N's per 100 kbp	0.00
# mismatches per 100 kbp	550.31
# indels per 100 kbp	0.09
Largest alignment	9465
NA50	1300
NGA50	607
NA75	751
LA50	1338
LGA50	4182
LA75	2964

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

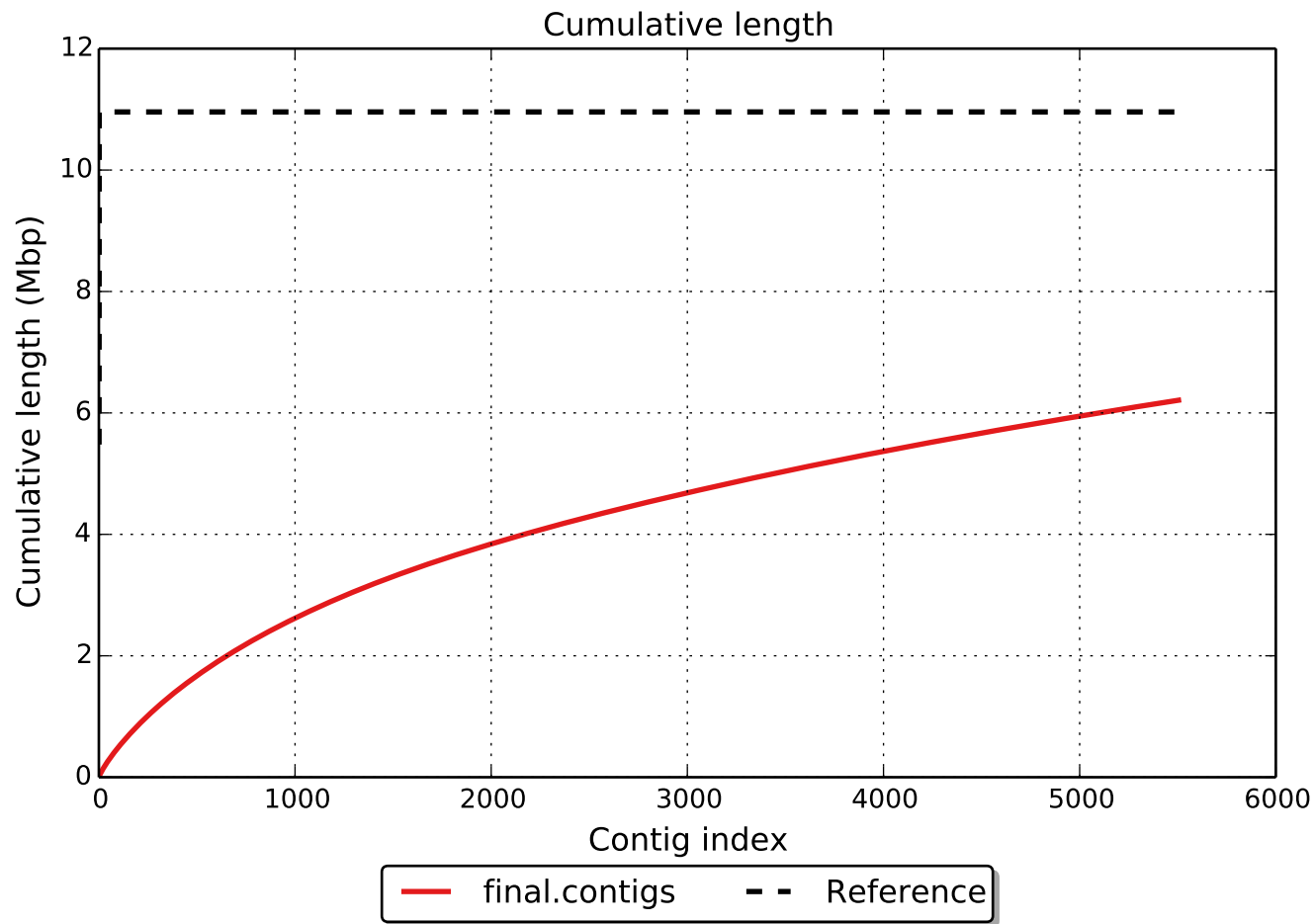
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	49503
# indels	8
# short indels	5
# long indels	3
Indels length	49

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).

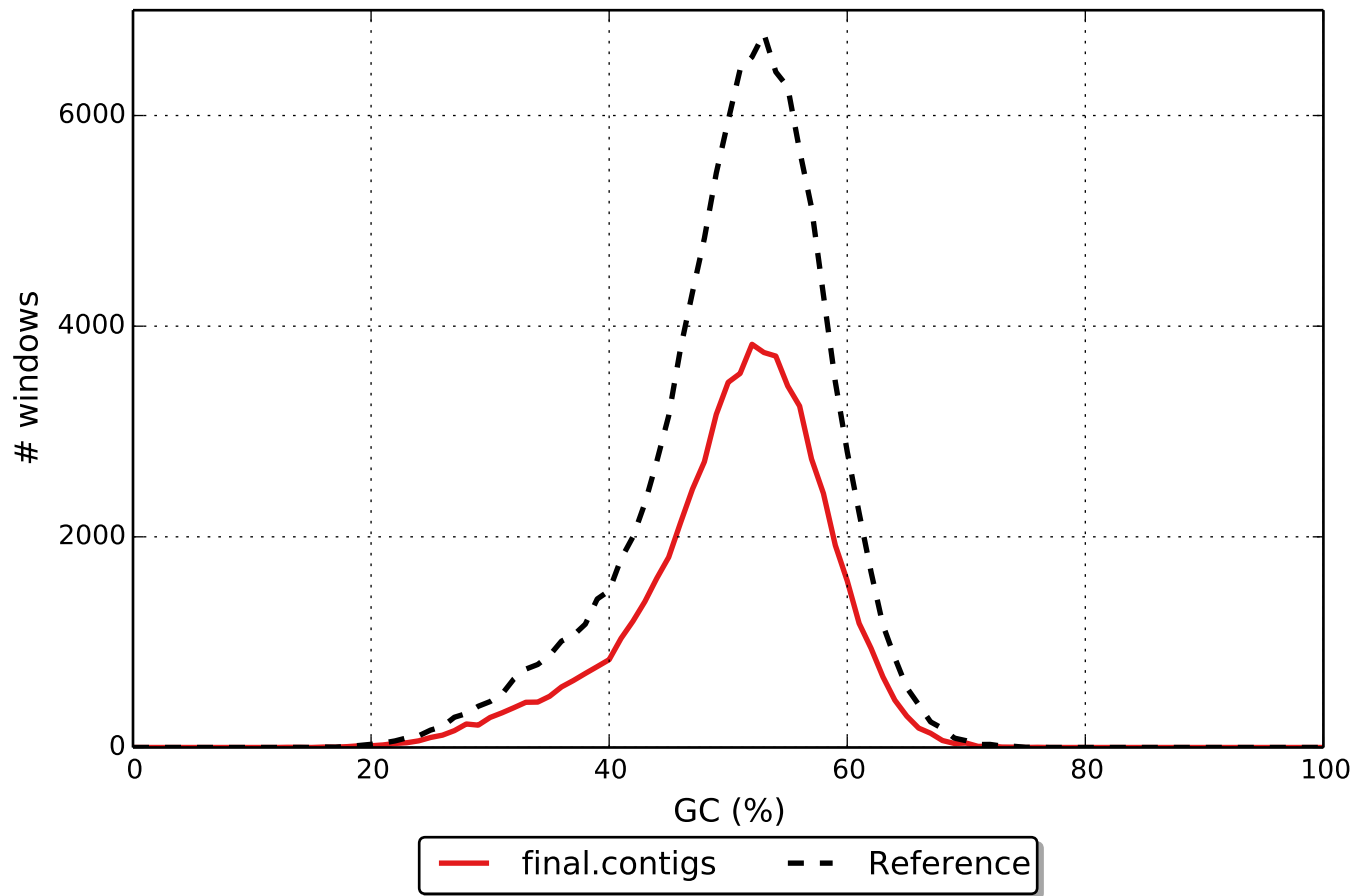
Unaligned report

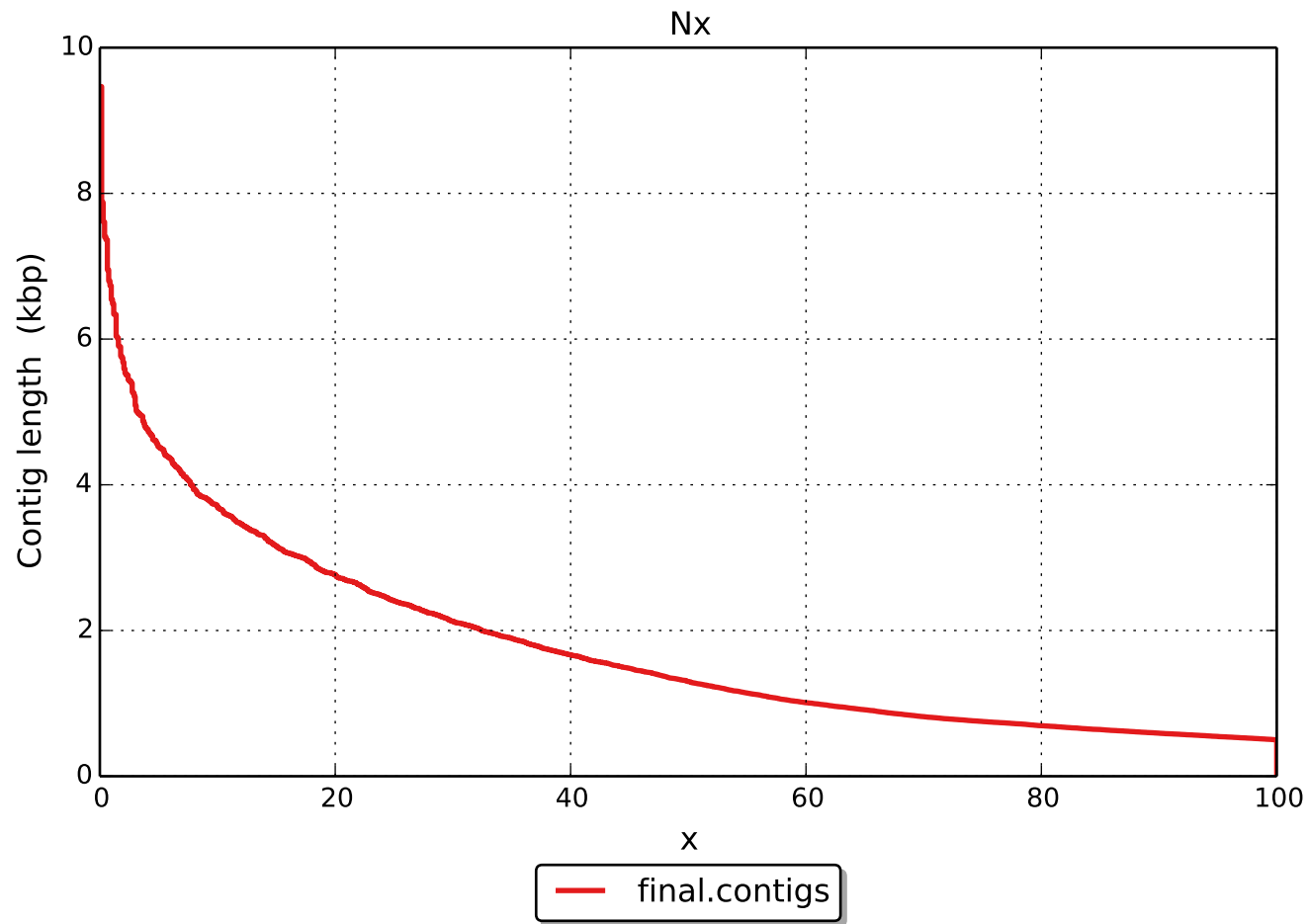
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	3
# with misassembly	0
# both parts are significant	0
Partially unaligned length	360
# N's	0

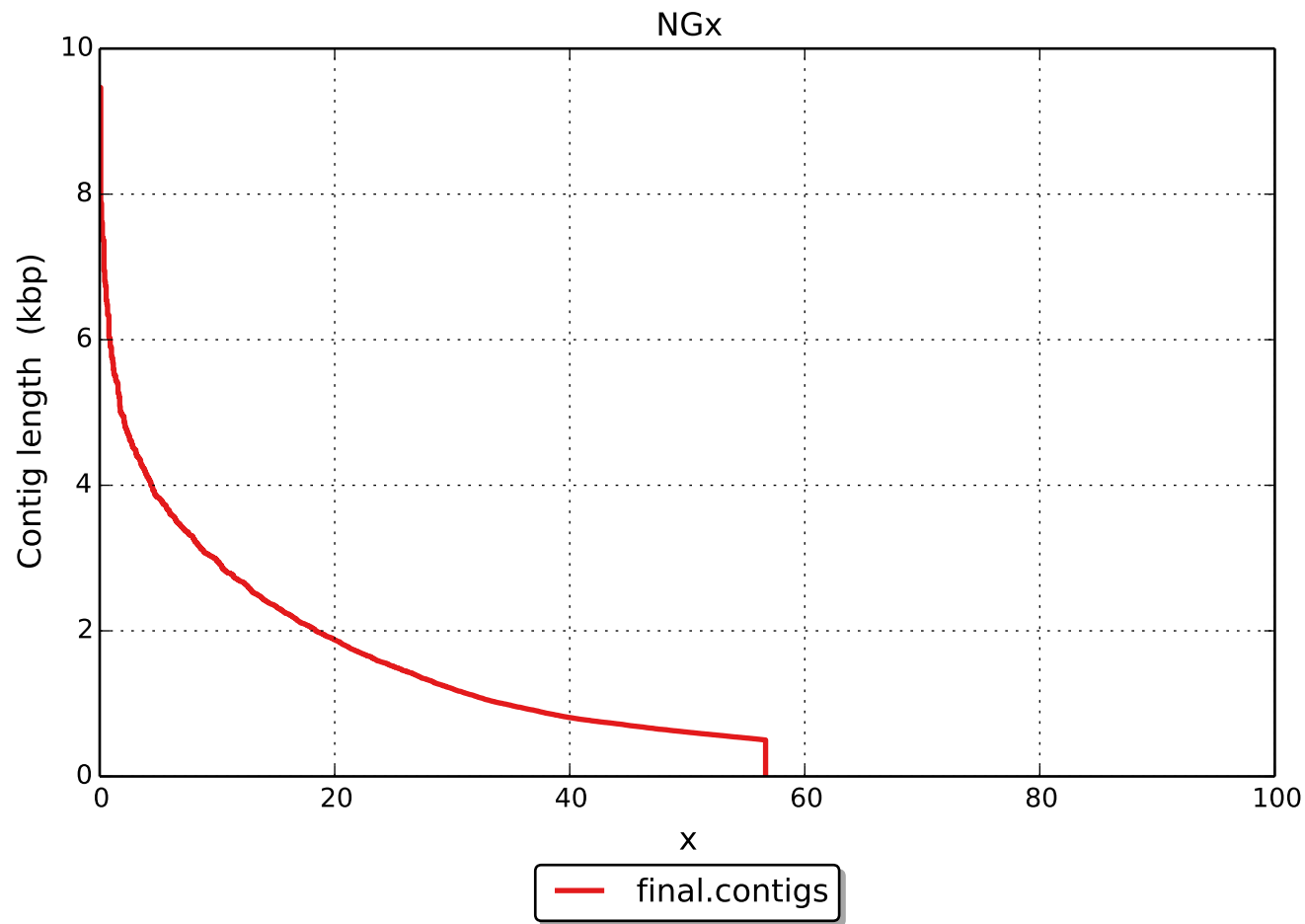
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



GC content







Misassemblies



