

Report

	final.contigs
# contigs (≥ 0 bp)	1545
# contigs (≥ 1000 bp)	760
Total length (≥ 0 bp)	2922380
Total length (≥ 1000 bp)	2392622
# contigs	1545
Largest contig	18257
Total length	2922380
Reference length	5547323
GC (%)	50.09
Reference GC (%)	50.48
N50	3204
NG50	591
N75	1452
L50	260
LG50	1272
L75	595
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	51.540
Duplication ratio	1.022
# N's per 100 kbp	0.00
# mismatches per 100 kbp	436.75
# indels per 100 kbp	0.21
Largest alignment	18257
NA50	3204
NGA50	591
NA75	1452
LA50	260
LGA50	1272
LA75	595

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

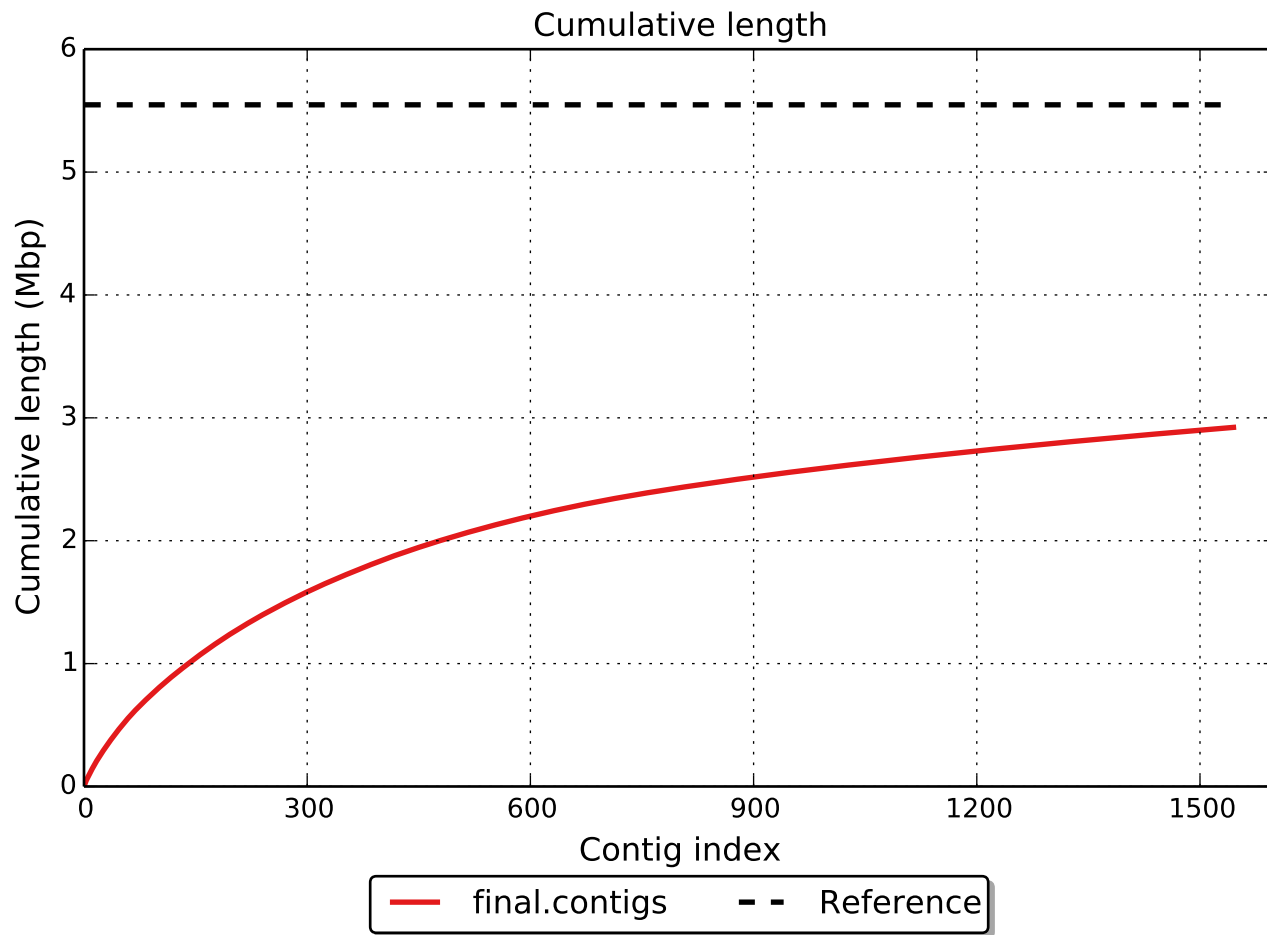
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# mismatches	12487
# indels	6
# short indels	5
# long indels	1
Indels length	12

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).

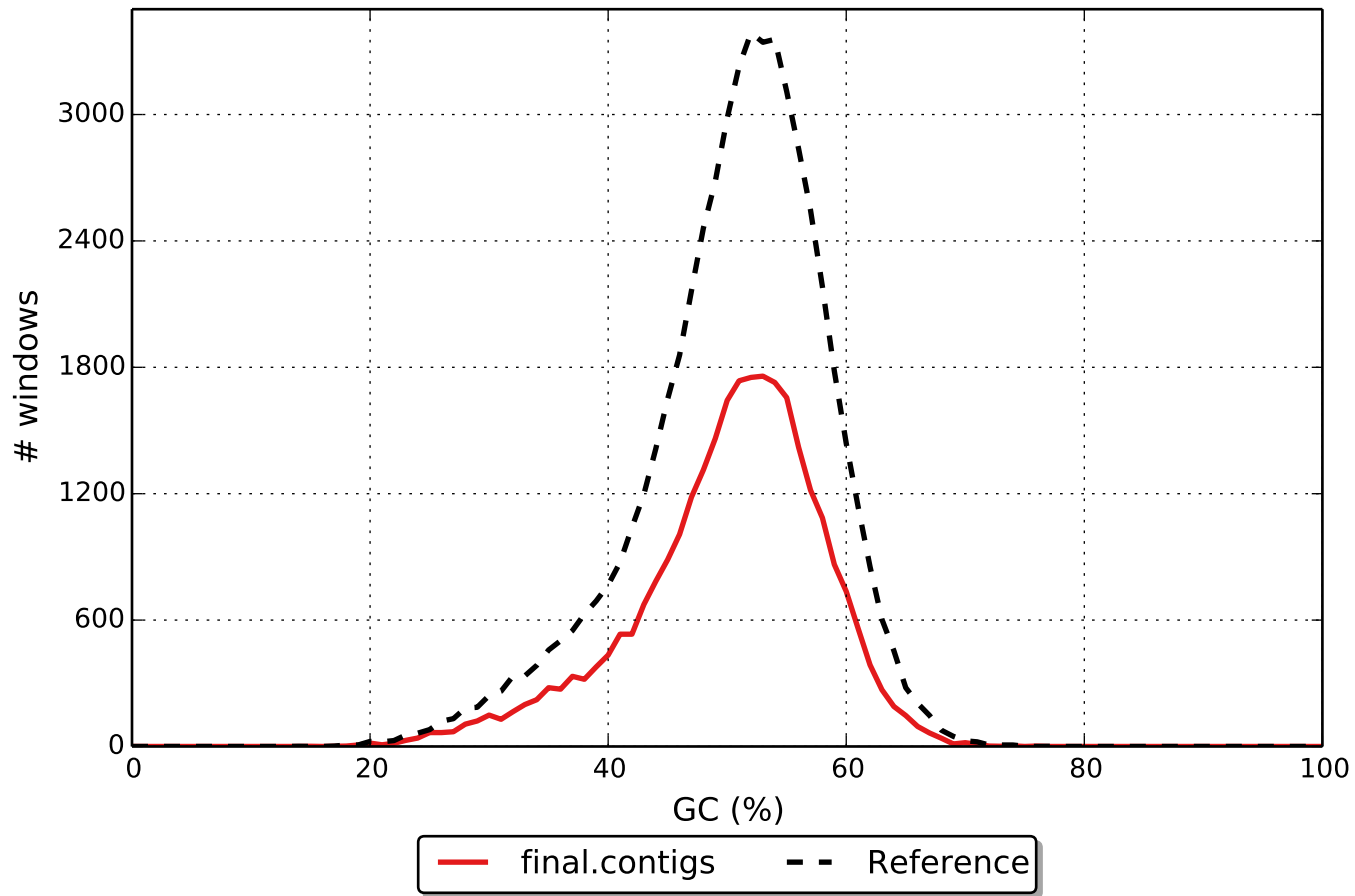
Unaligned report

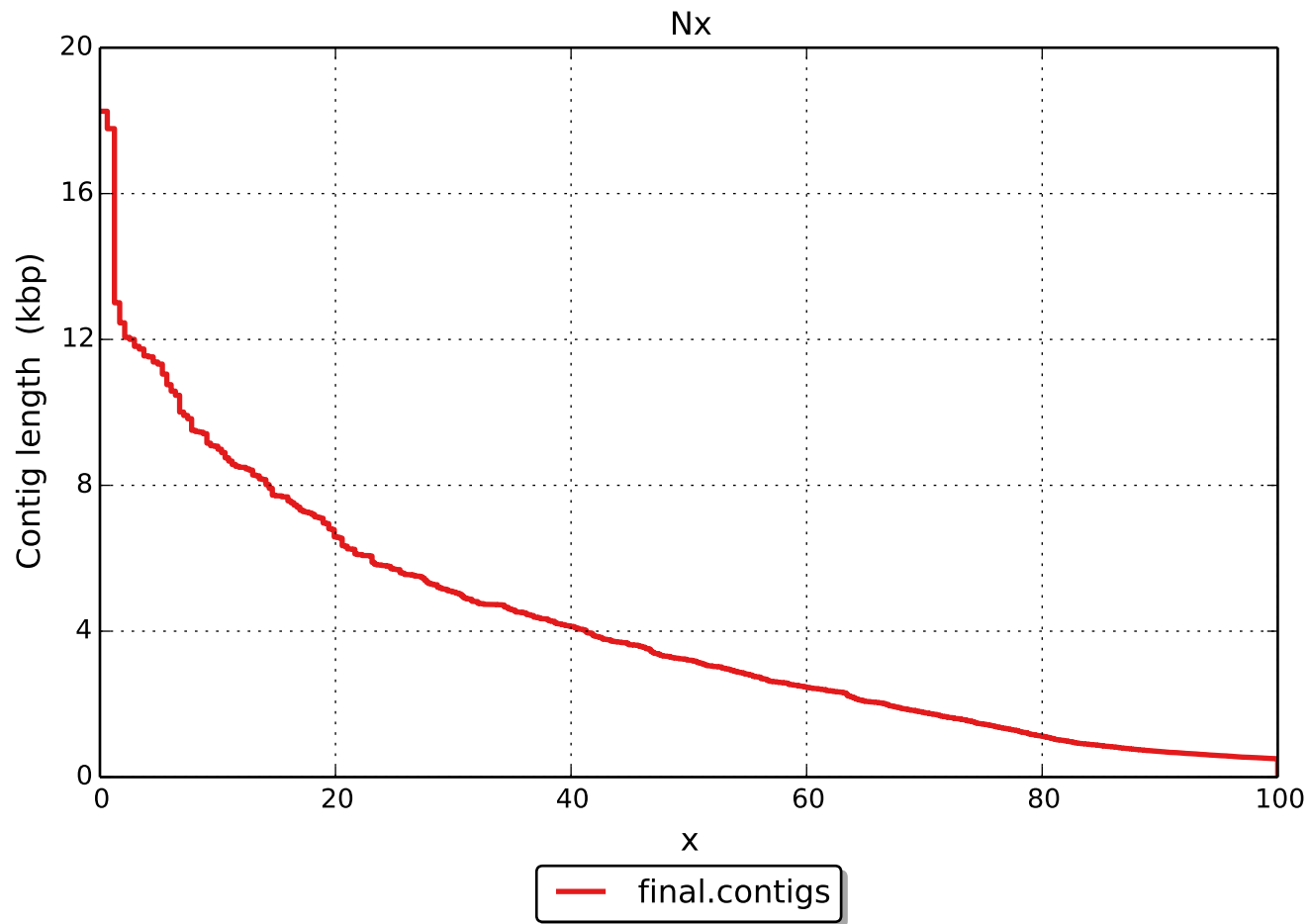
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

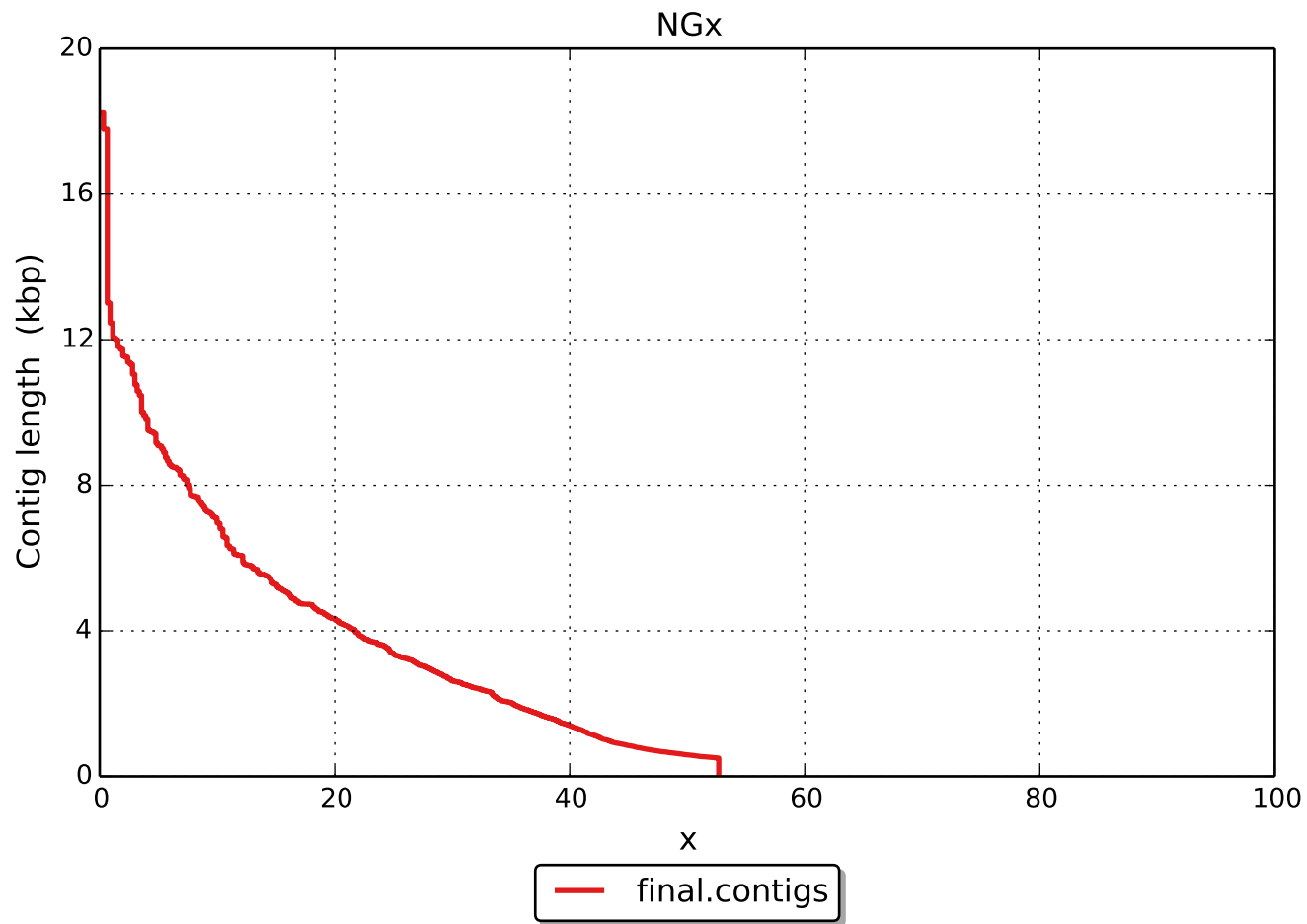
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



GC content







Misassemblies



