

Report

	final.contigs
# contigs (≥ 0 bp)	3336
# contigs (≥ 1000 bp)	2126
Total length (≥ 0 bp)	5446885
Total length (≥ 1000 bp)	4557235
# contigs	3336
Largest contig	10098
Total length	5446885
Reference length	5478683
GC (%)	50.48
Reference GC (%)	50.49
N50	2022
NG50	2015
N75	1264
NG75	1251
L50	862
LG50	869
L75	1706
LG75	1725
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 2 part
Unaligned length	1351
Genome fraction (%)	95.210
Duplication ratio	1.044
# N's per 100 kbp	0.00
# mismatches per 100 kbp	39.59
# indels per 100 kbp	0.00
Largest alignment	10098
NA50	2022
NGA50	2015
NA75	1264
NGA75	1248
LA50	862
LGA50	870
LA75	1707
LGA75	1726

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

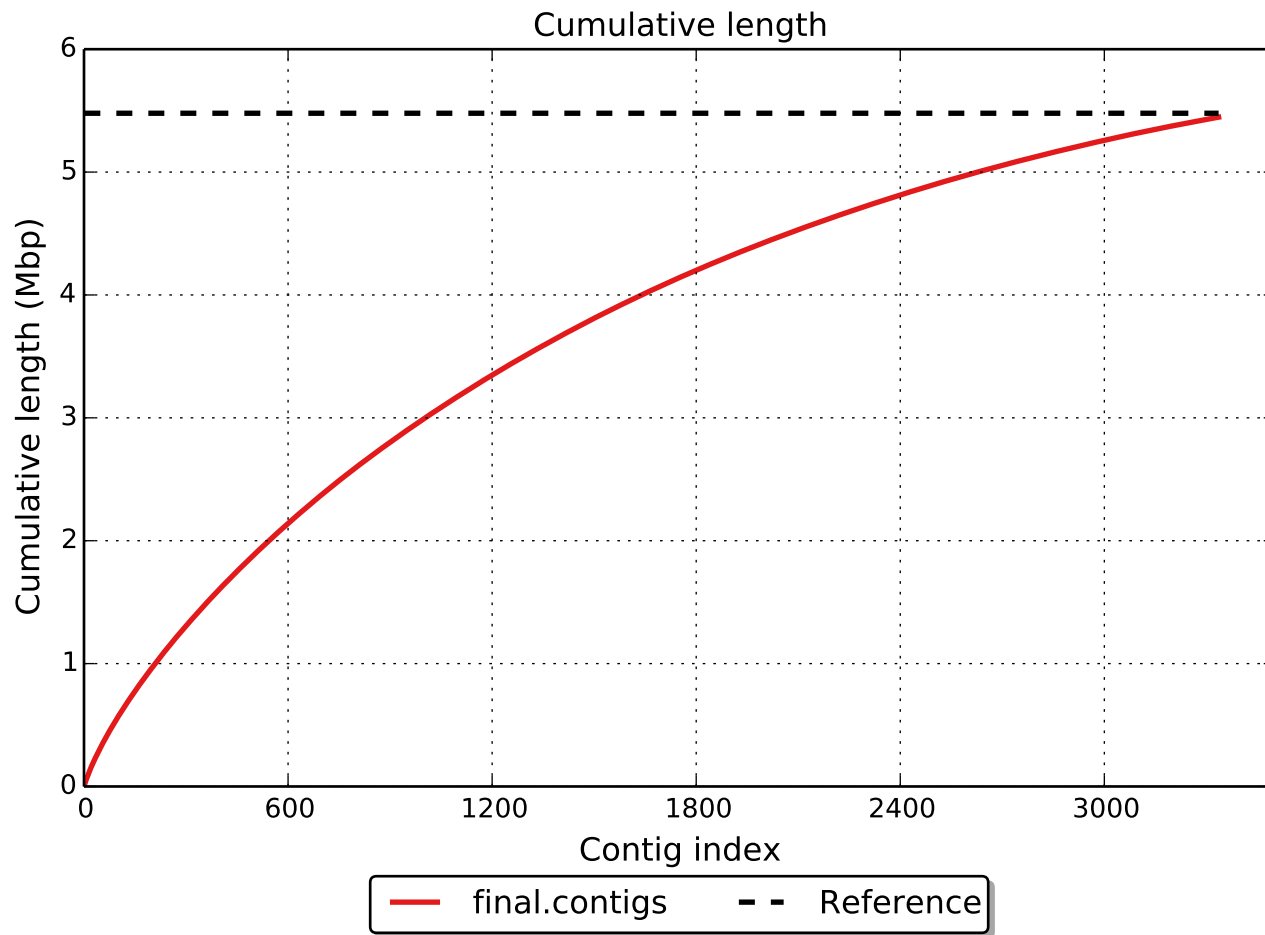
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	1
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# mismatches	2065
# indels	0
# short indels	0
# long indels	0
Indels length	0

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).

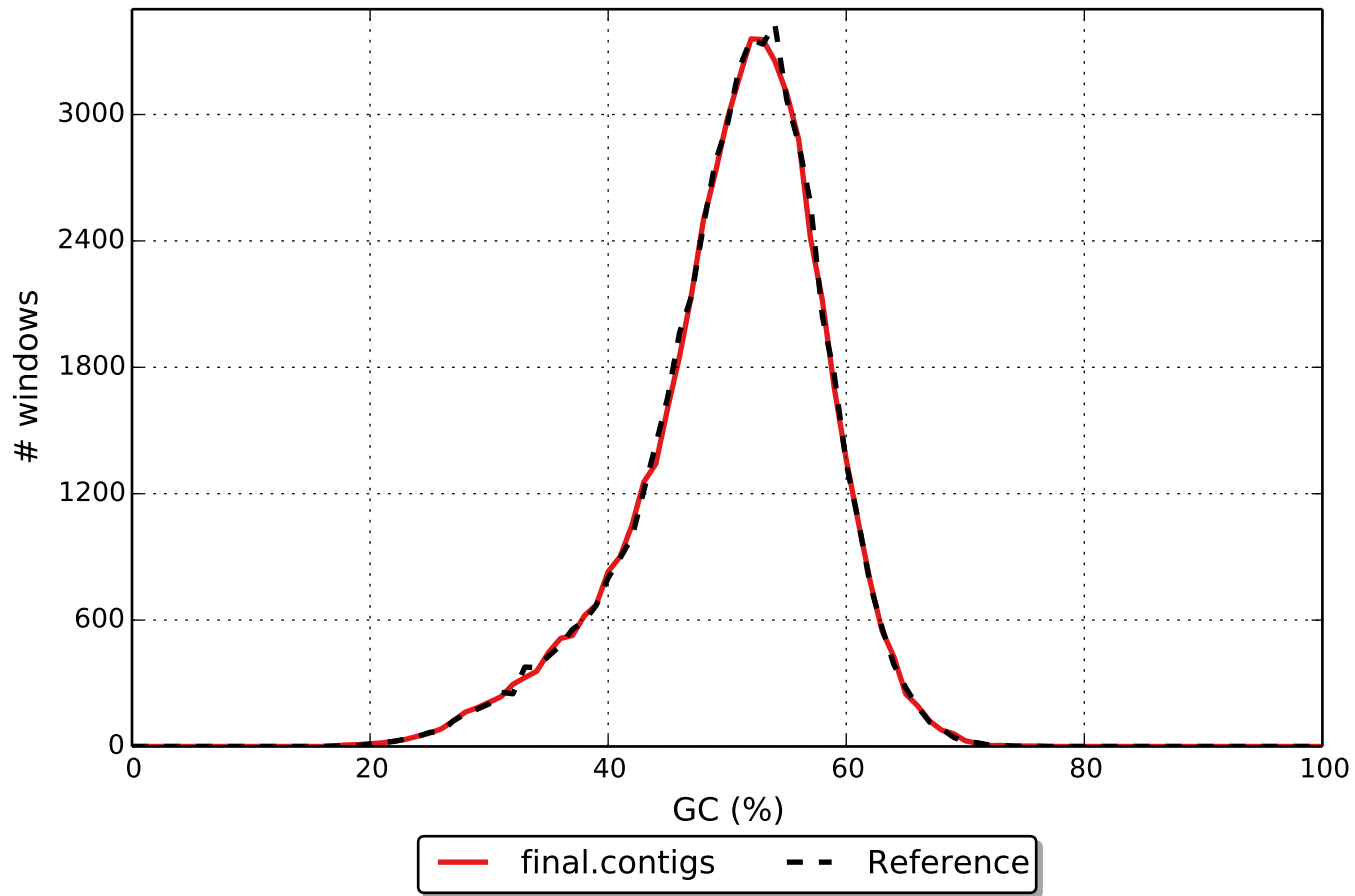
Unaligned report

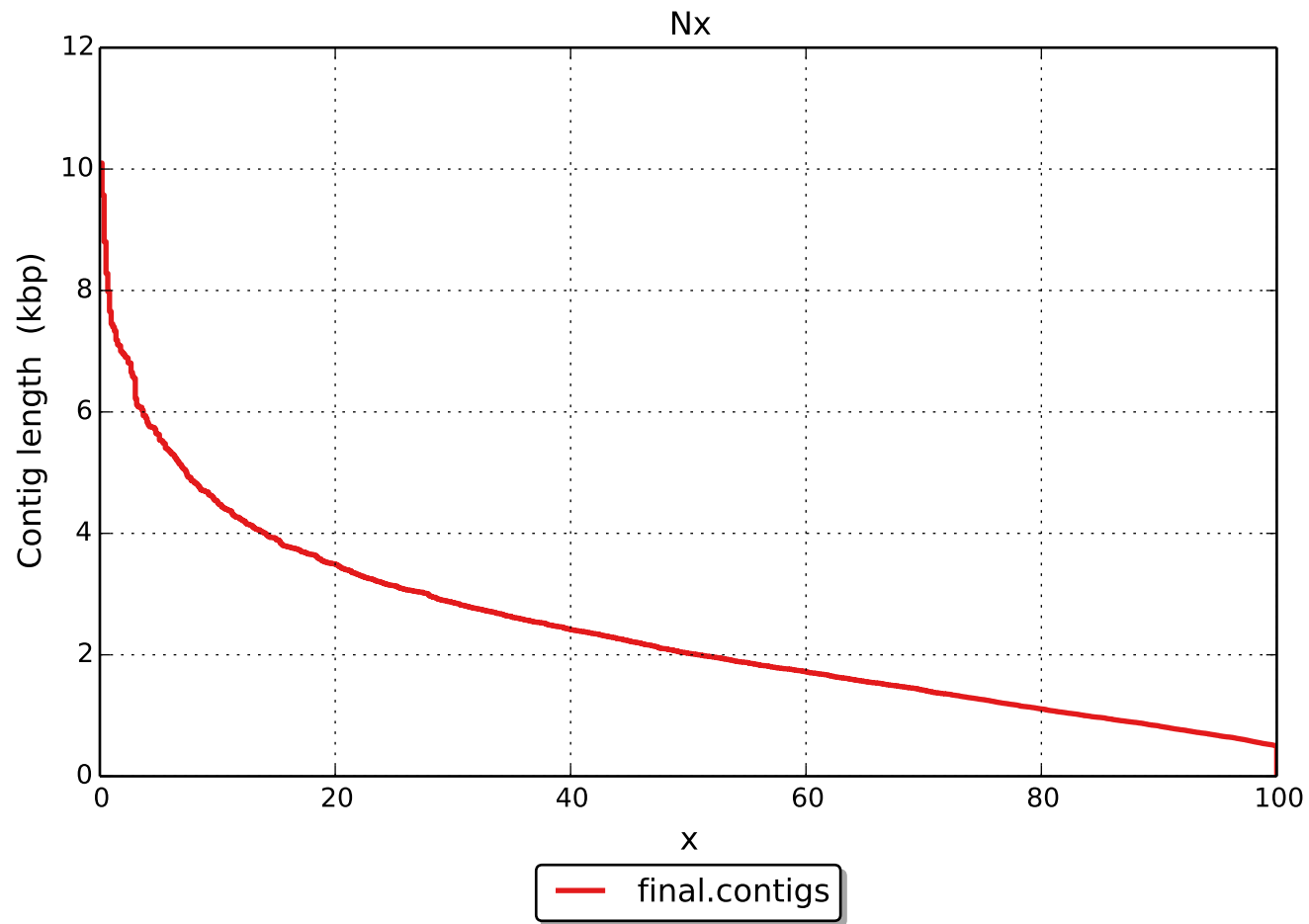
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	1
Partially unaligned length	1351
# N's	0

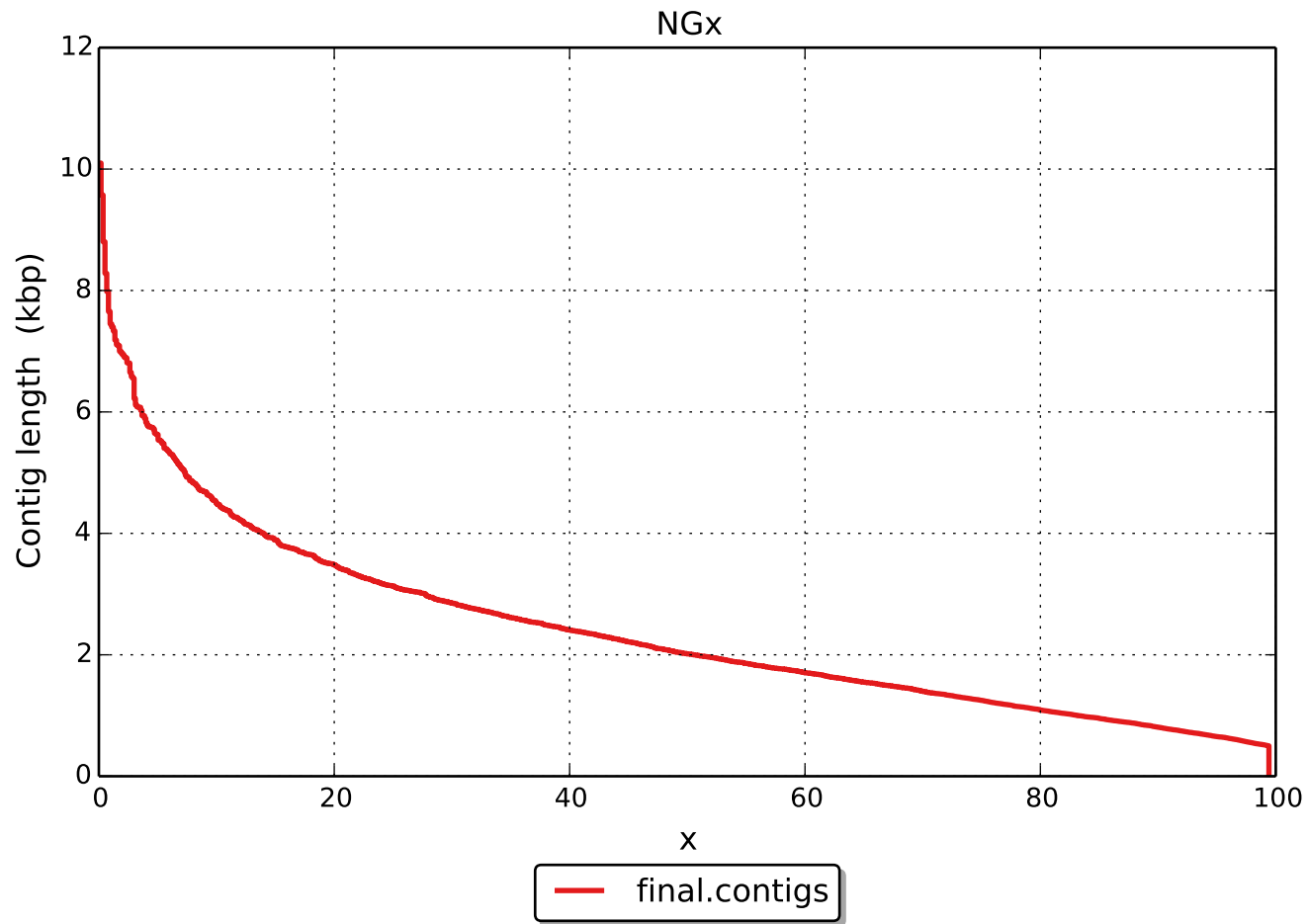
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



GC content







Misassemblies



