

Report

	final.contigs
# contigs (≥ 0 bp)	3109
# contigs (≥ 1000 bp)	48
# contigs (≥ 5000 bp)	1
# contigs (≥ 10000 bp)	0
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 0 bp)	1489995
Total length (≥ 1000 bp)	63684
Total length (≥ 5000 bp)	5132
Total length (≥ 10000 bp)	0
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	1011
Largest contig	5132
Total length	677196
Reference length	4641652
GC (%)	50.73
Reference GC (%)	50.79
N50	648
N75	563
L50	409
L75	691
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	1694
# local misassemblies	0
# unaligned contigs	731 + 5 part
Unaligned length	490871
Genome fraction (%)	4.012
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	663.27
# indels per 100 kbp	0.54
Largest alignment	5132
NGA50	-

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

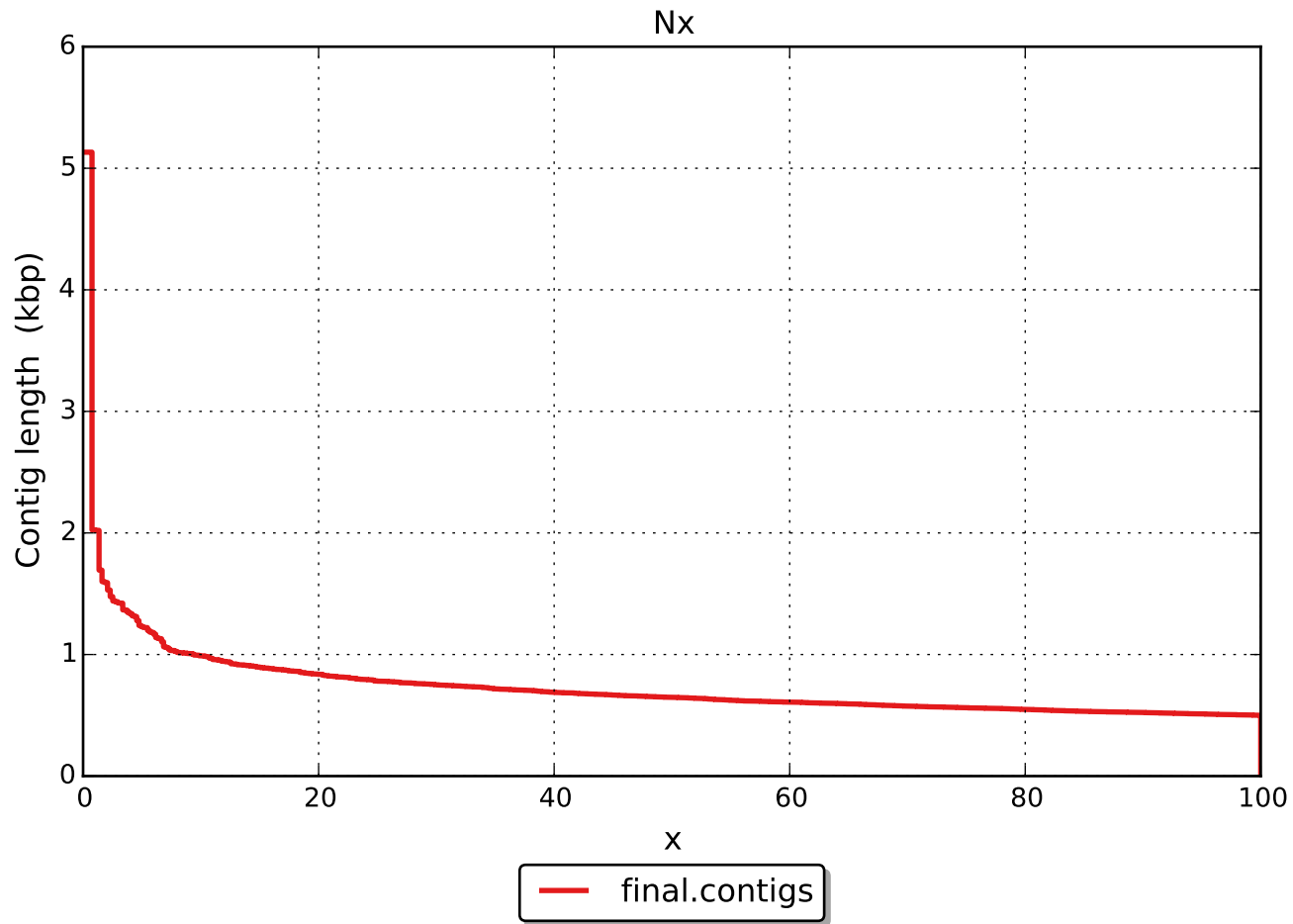
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# misassembled contigs	1
Misassembled contigs length	1694
# local misassemblies	0
# mismatches	1235
# indels	1
# short indels	1
# long indels	0
Indels length	1

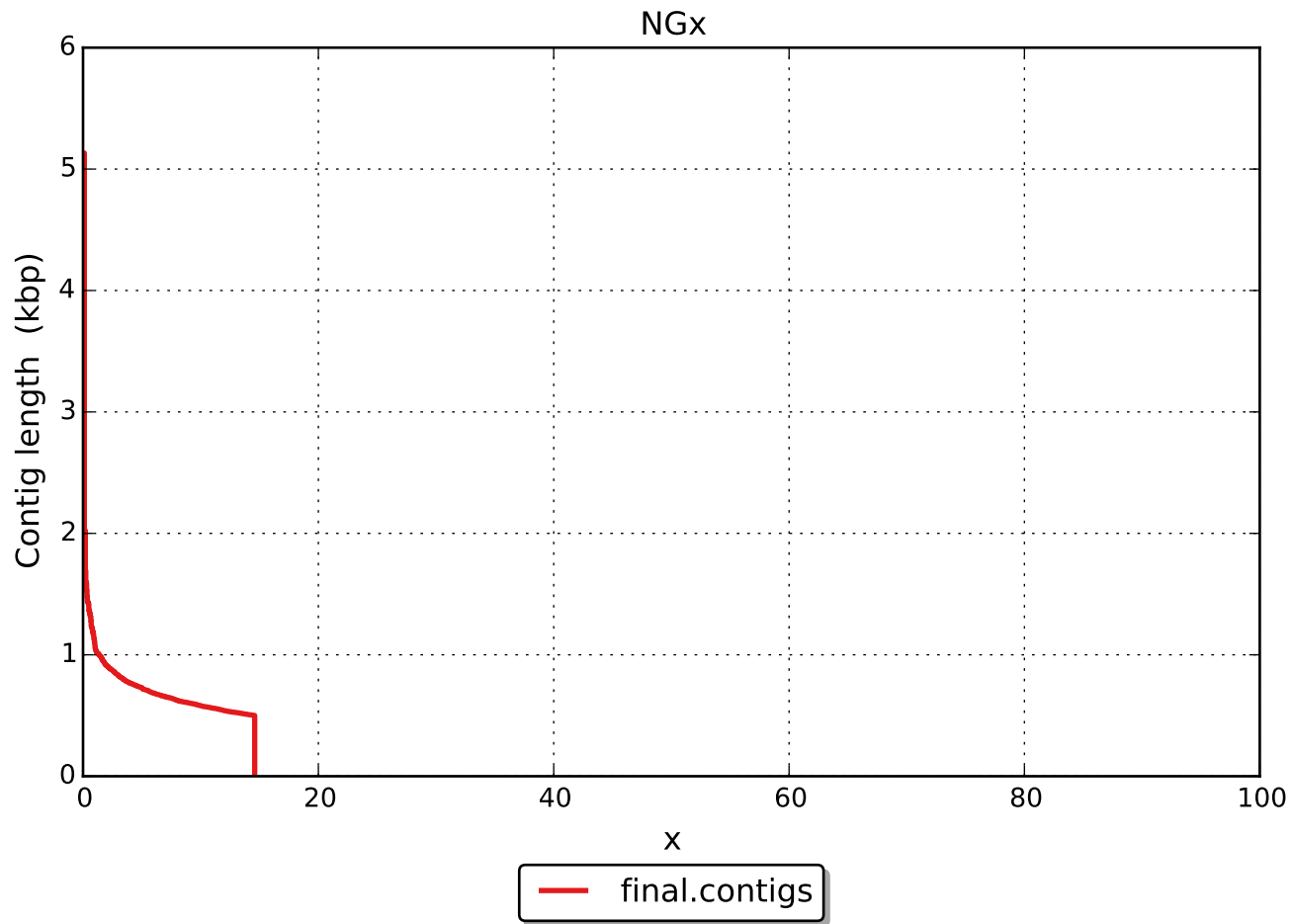
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

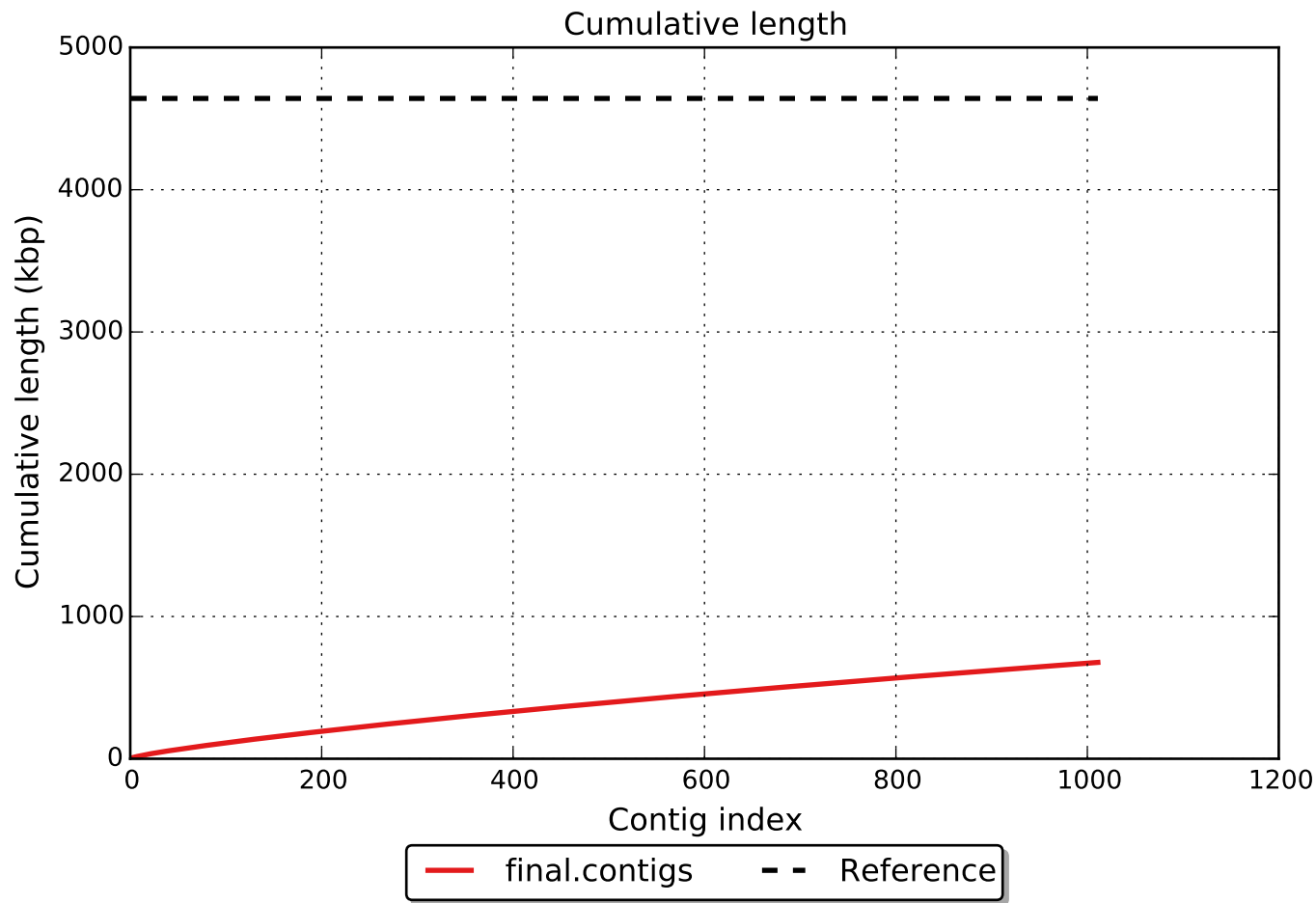
Unaligned report

	final.contigs
# fully unaligned contigs	731
Fully unaligned length	488301
# partially unaligned contigs	5
# with misassembly	0
# both parts are significant	1
Partially unaligned length	2570
# N's	0

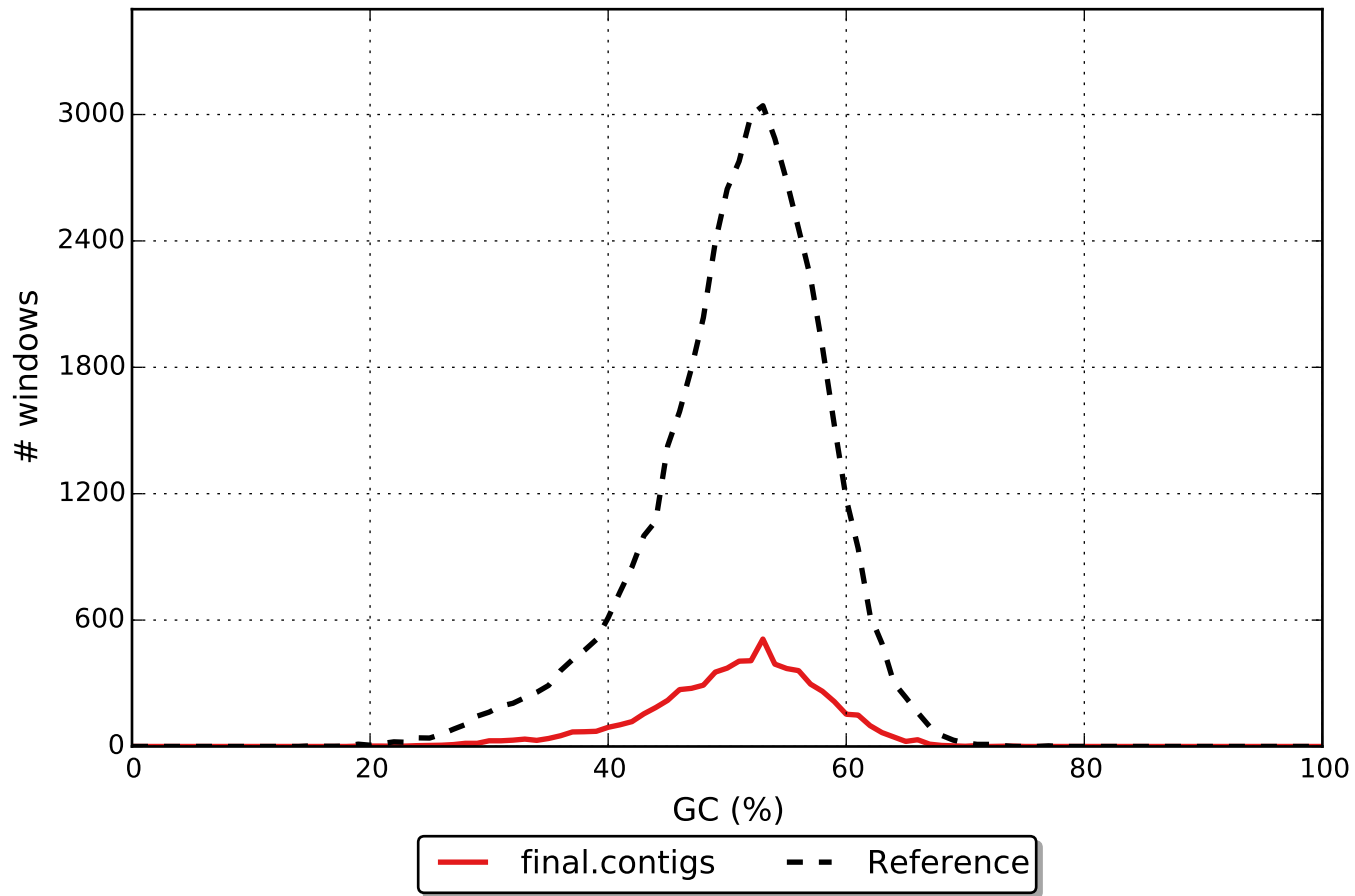
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).







GC content





Cumulative length (aligned contigs)

