

Report

	final.contigs
# contigs (≥ 0 bp)	7003
# contigs (≥ 1000 bp)	1400
Total length (≥ 0 bp)	6817146
Total length (≥ 1000 bp)	4405709
# contigs	3021
Largest contig	18257
Total length	5492492
Reference length	11094646
GC (%)	50.31
Reference GC (%)	50.48
N50	3100
N75	1336
L50	494
L75	1152
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 1 part
Unaligned length	11
Genome fraction (%)	48.450
Duplication ratio	1.022
# N's per 100 kbp	0.00
# mismatches per 100 kbp	428.51
# indels per 100 kbp	0.28
Largest alignment	18257
NA50	3100
NA75	1336
LA50	494
LA75	1152

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

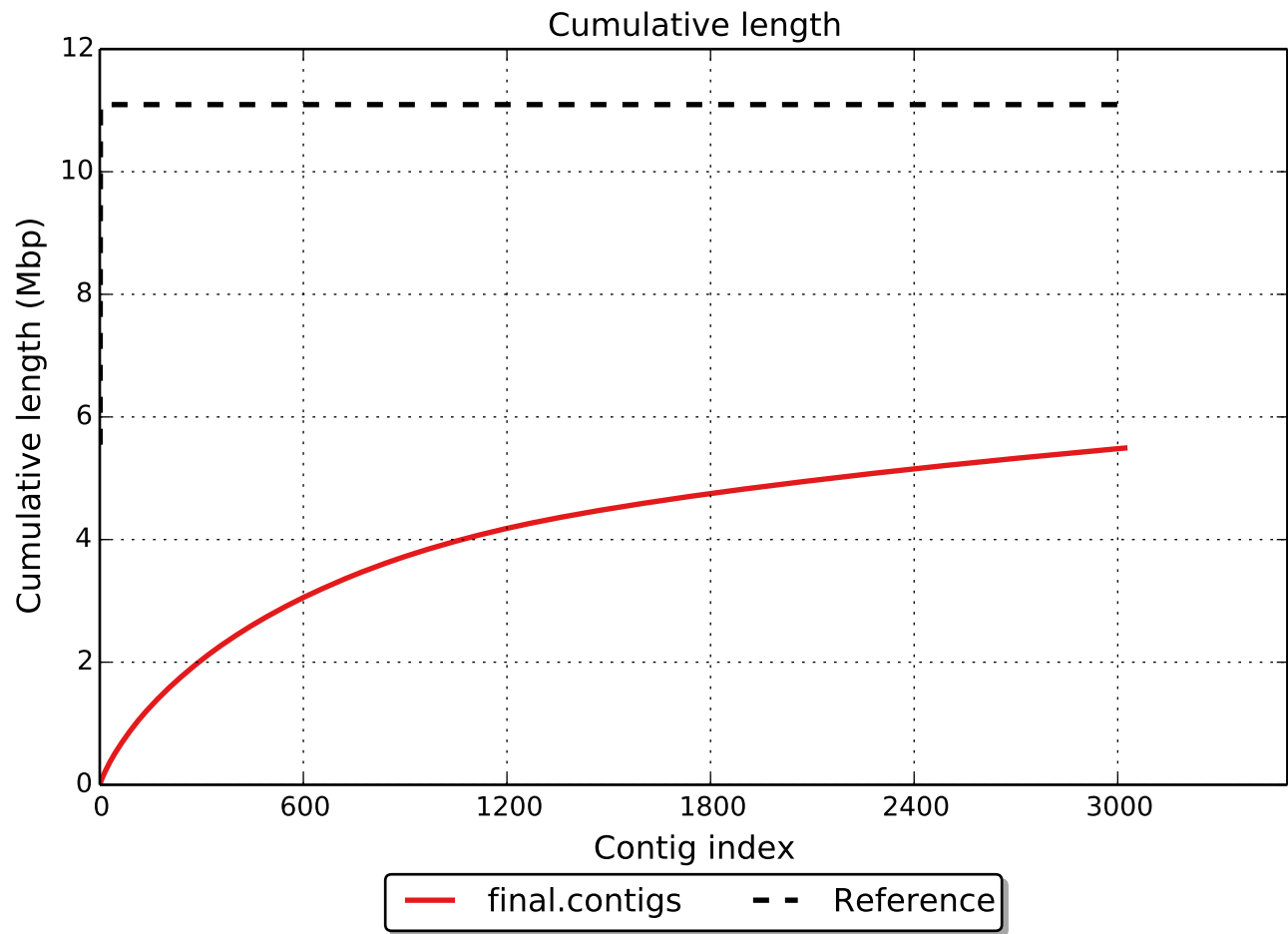
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# mismatches	23034
# indels	15
# short indels	14
# long indels	1
Indels length	21

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).

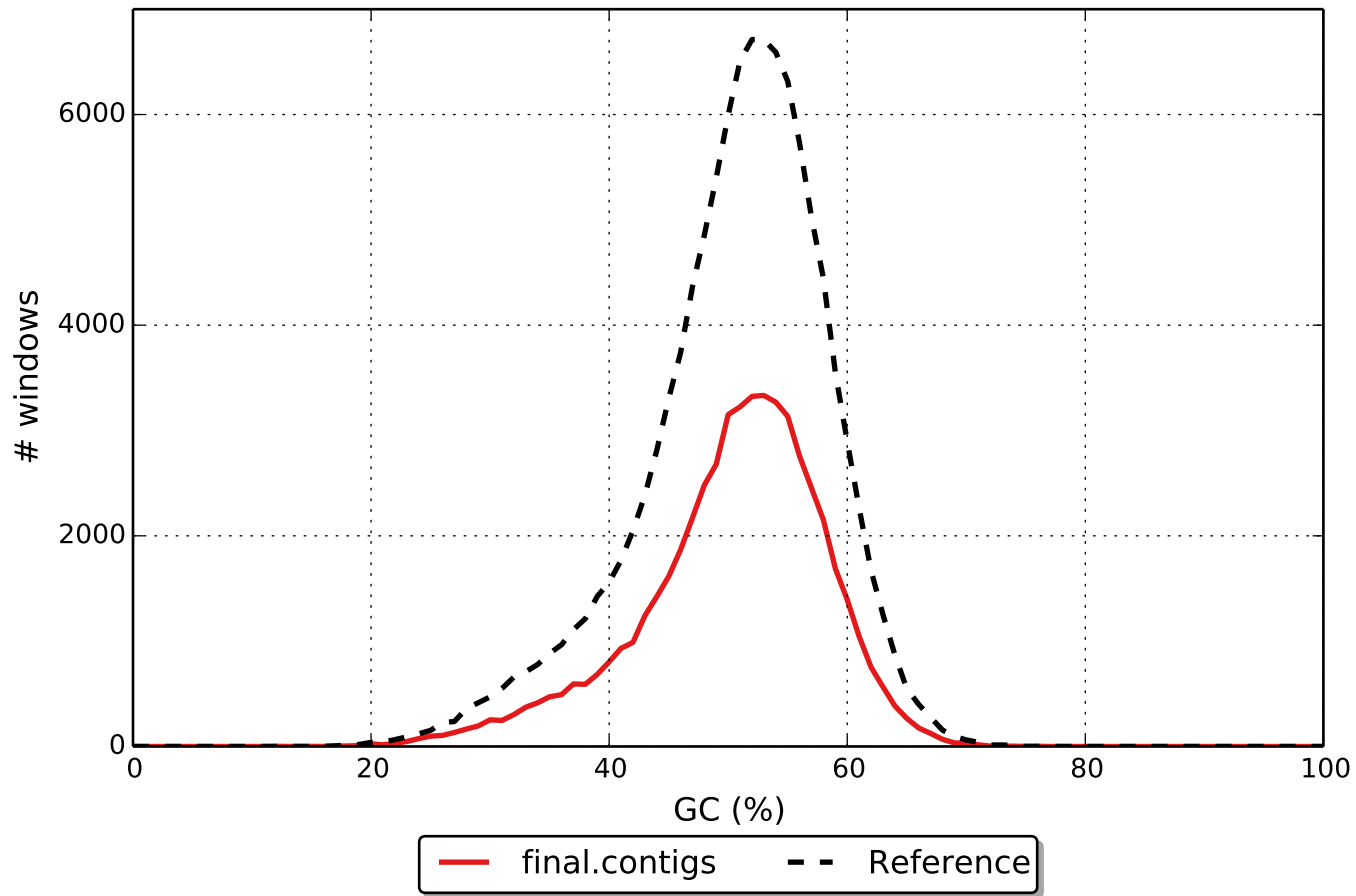
Unaligned report

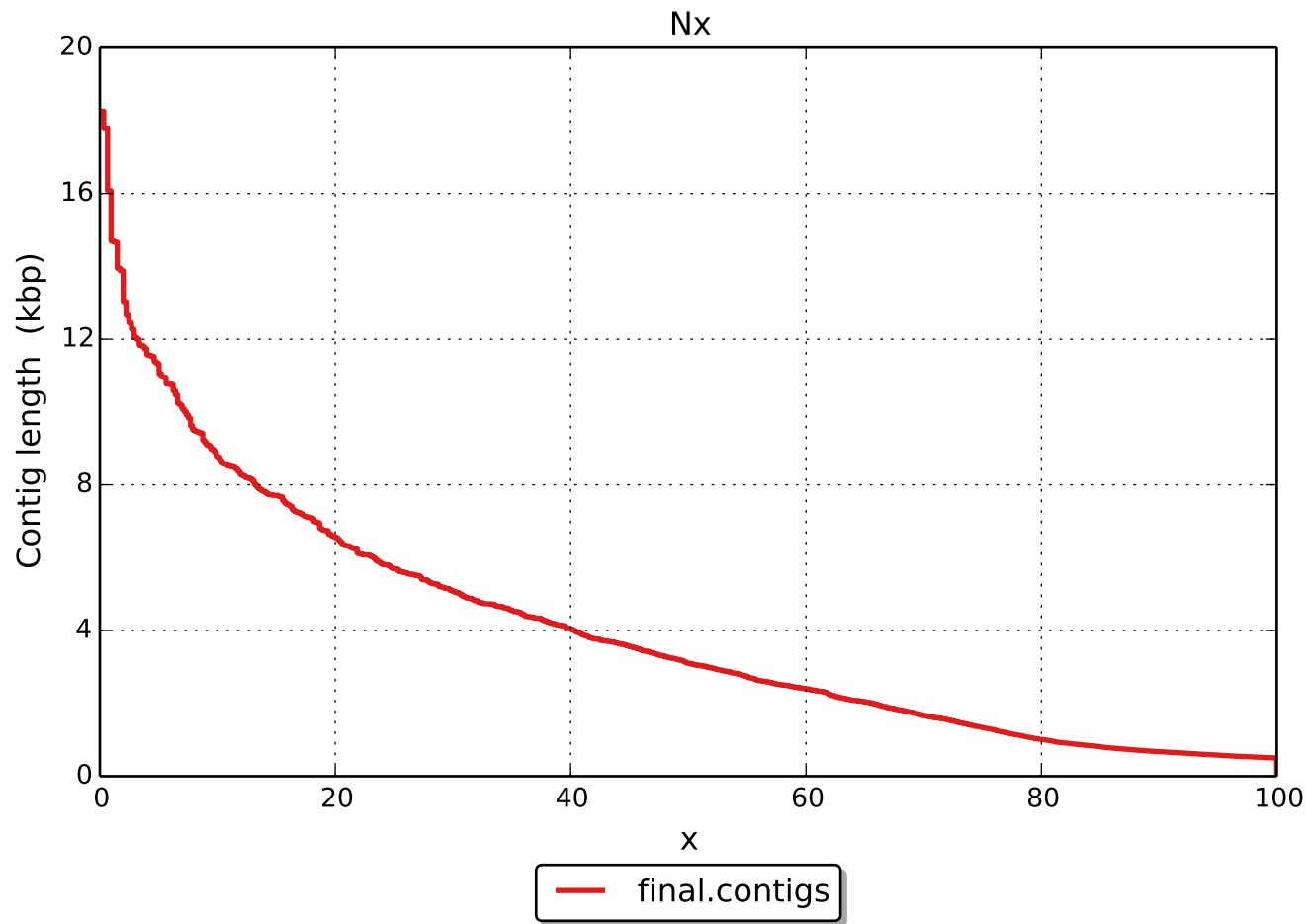
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	11
# N's	0

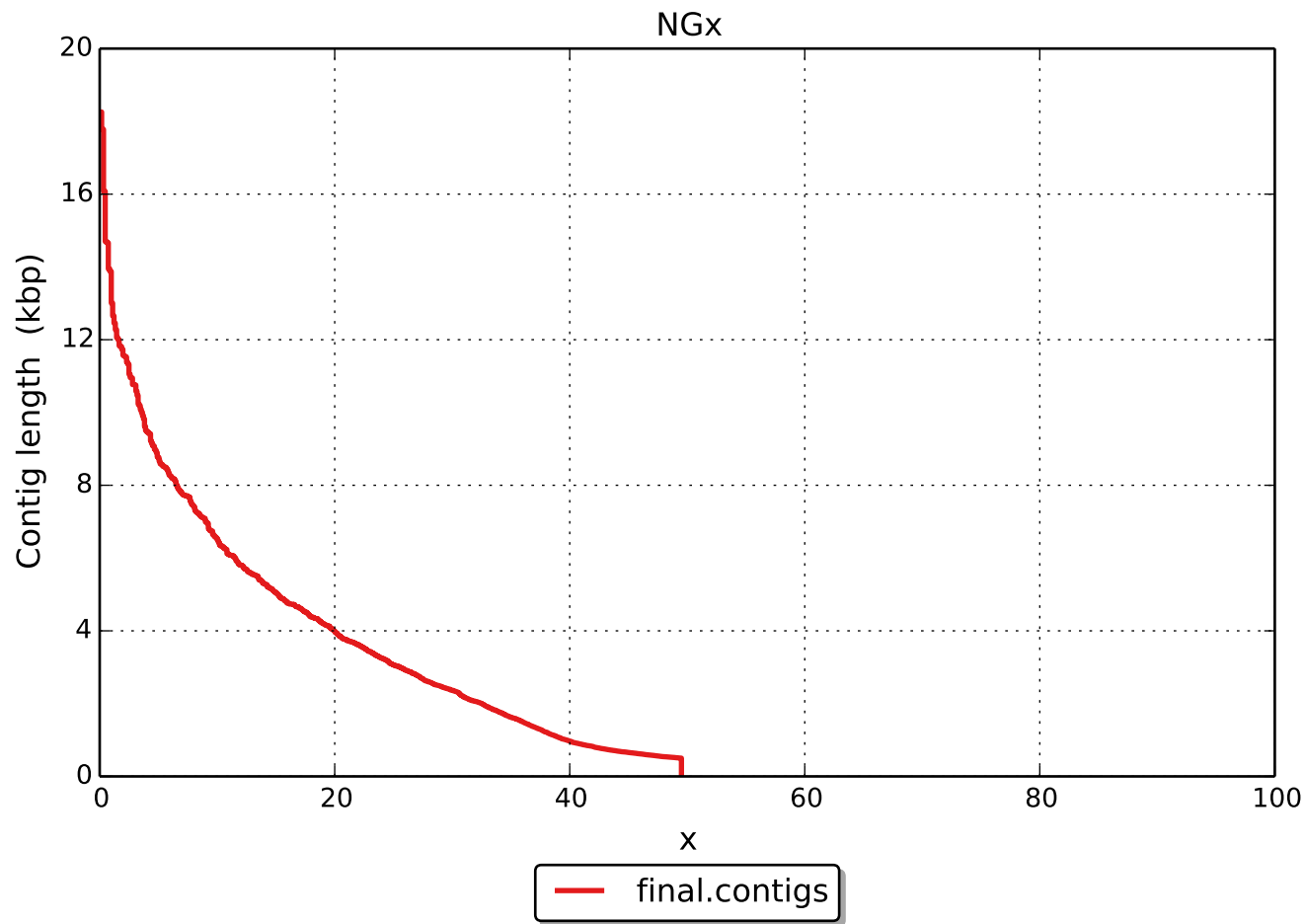
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



GC content







Misassemblies



