

Report

	final.contigs
# contigs (≥ 0 bp)	2293
# contigs (≥ 1000 bp)	1347
Total length (≥ 0 bp)	4977193
Total length (≥ 1000 bp)	4329001
# contigs	2293
Largest contig	18257
Total length	4977193
Reference length	5547323
GC (%)	50.29
Reference GC (%)	50.48
N50	3539
NG50	3055
N75	1795
NG75	1221
L50	416
LG50	503
L75	908
LG75	1194
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	87.073
Duplication ratio	1.030
# N's per 100 kbp	0.00
# mismatches per 100 kbp	596.70
# indels per 100 kbp	0.14
Largest alignment	18257
NA50	3539
NGA50	3055
NA75	1795
NGA75	1221
LA50	416
LGA50	503
LA75	908
LGA75	1194

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

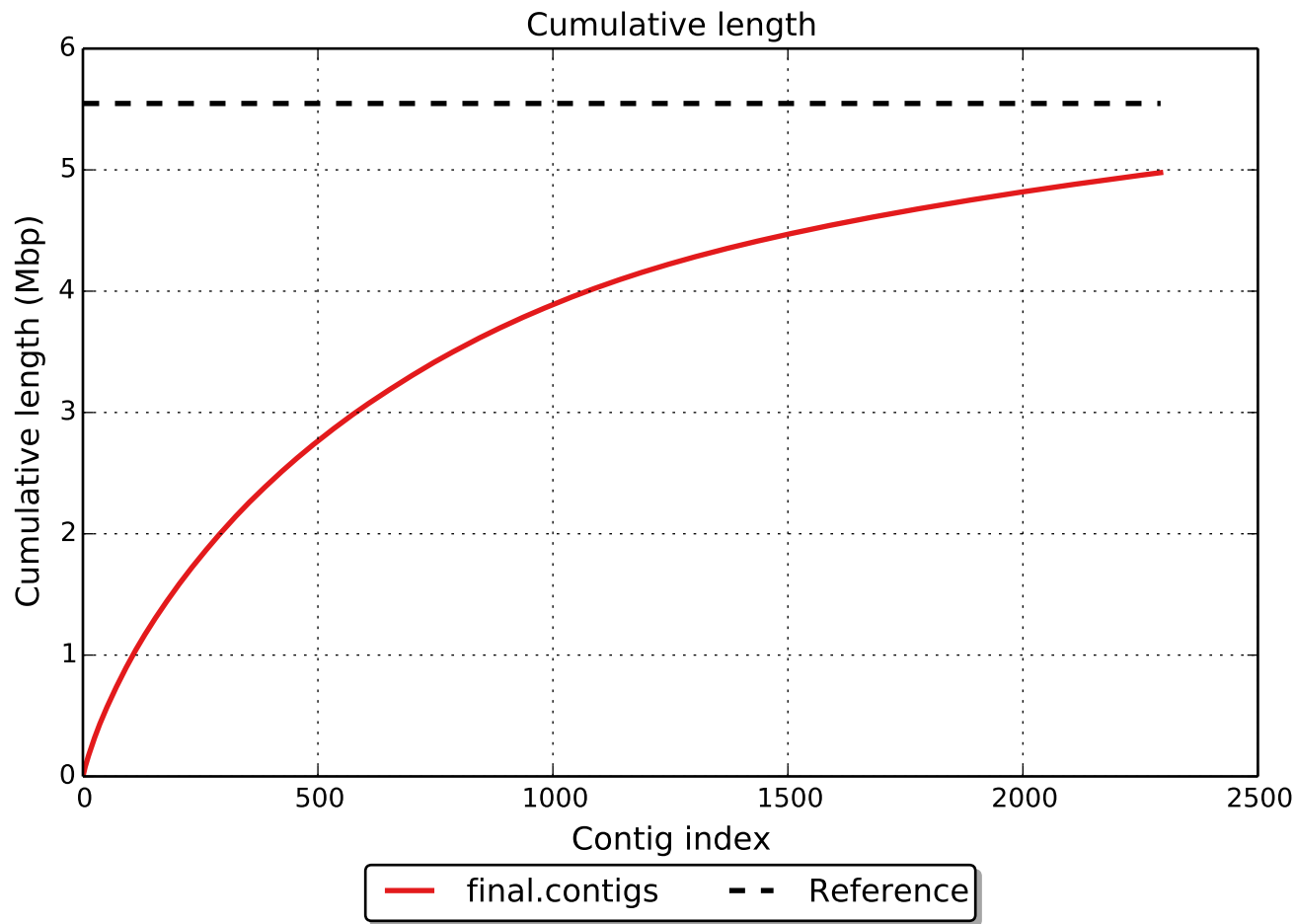
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# mismatches	28822
# indels	7
# short indels	6
# long indels	1
Indels length	13

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).

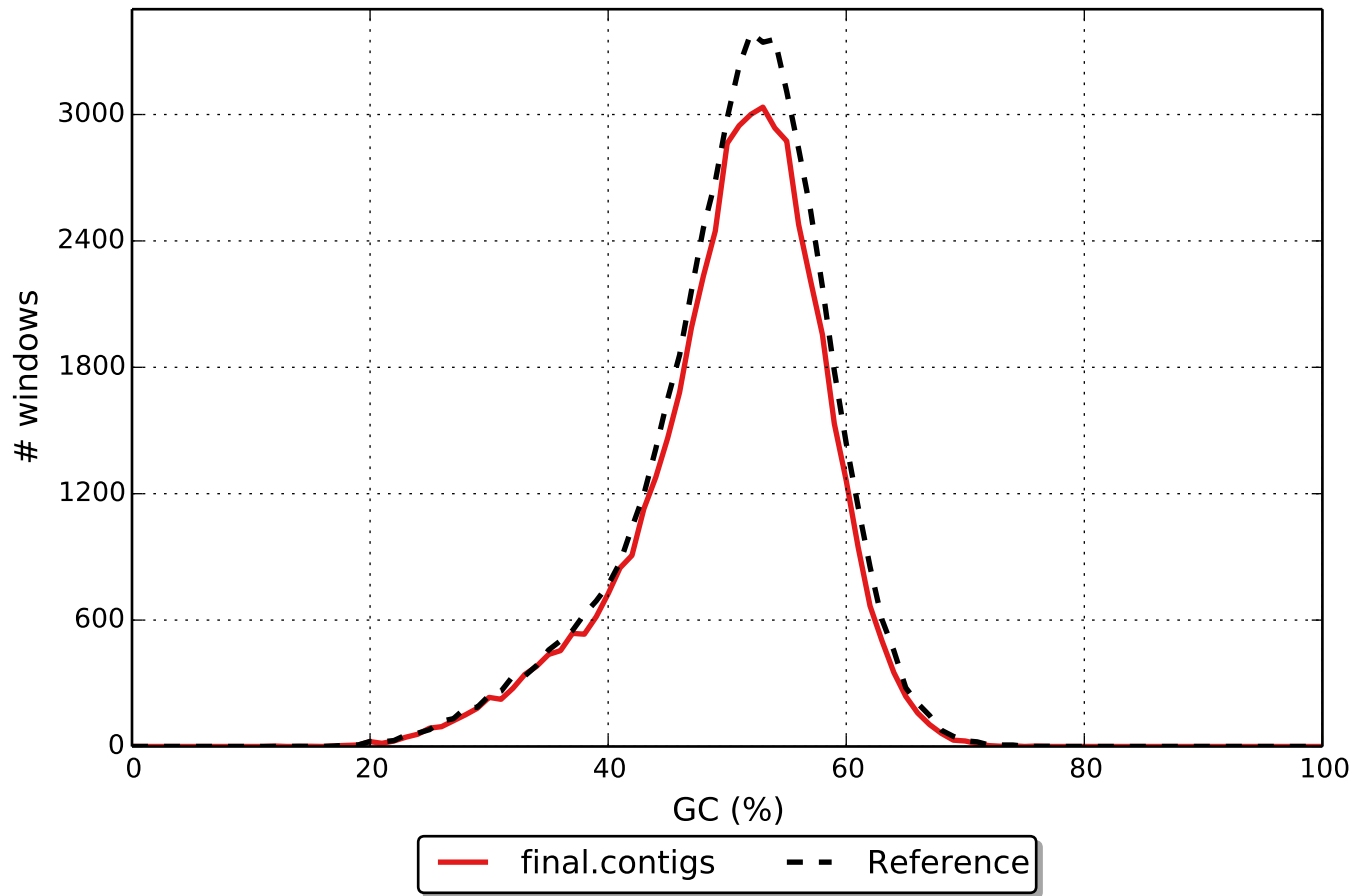
Unaligned report

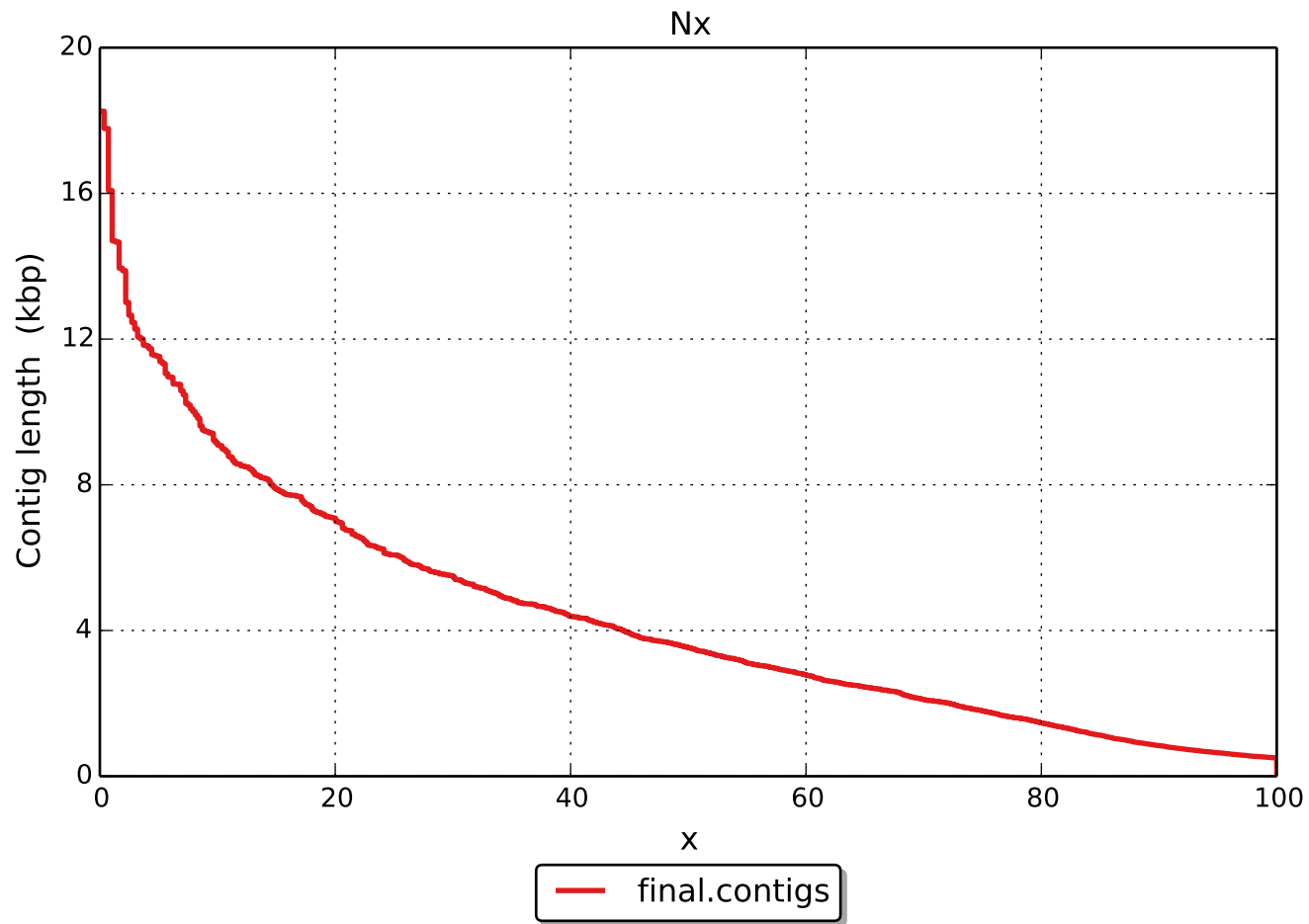
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

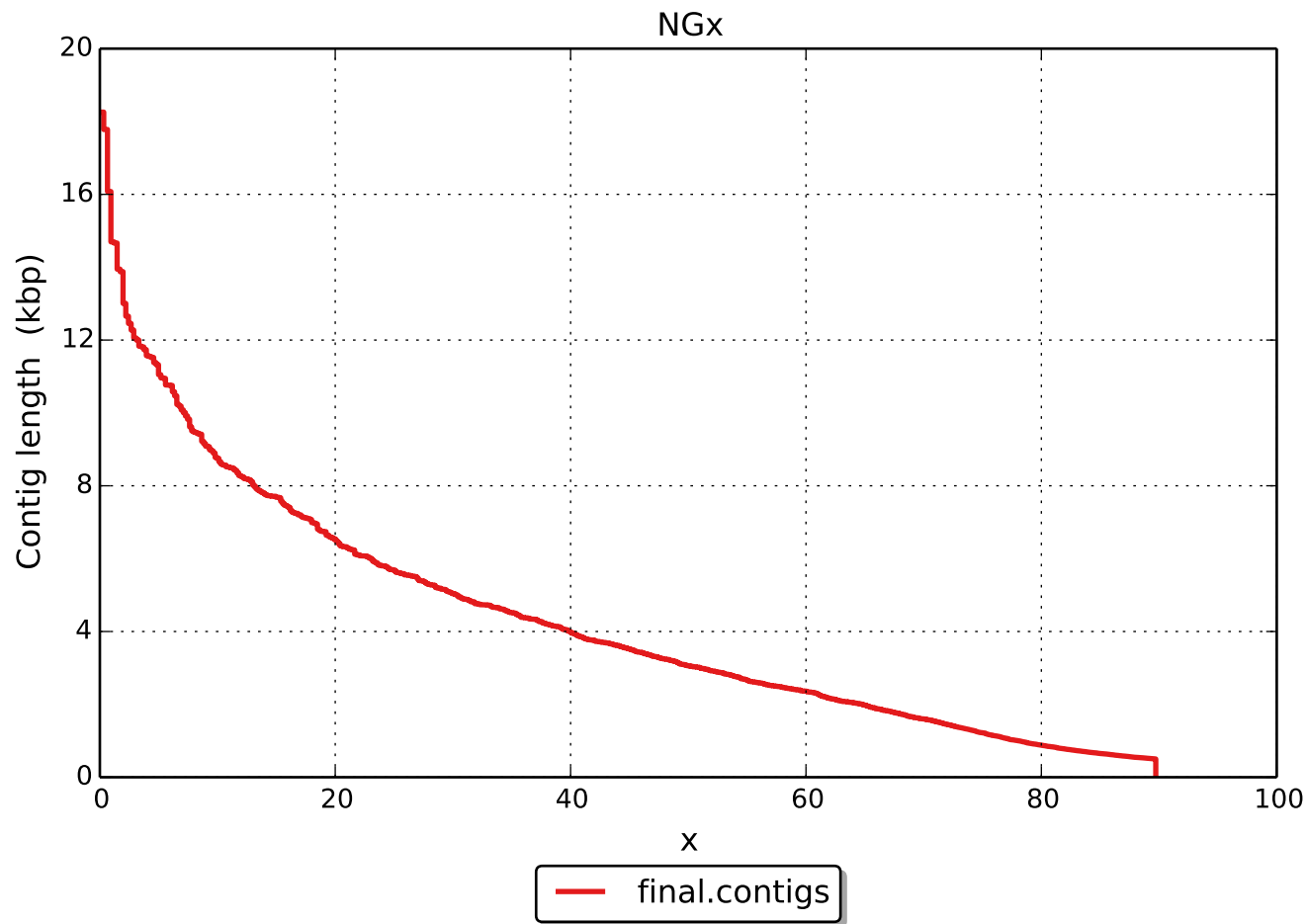
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



GC content







Misassemblies



