

Report

	final.contigs
# contigs (≥ 0 bp)	230
# contigs (≥ 1000 bp)	82
Total length (≥ 0 bp)	663628
Total length (≥ 1000 bp)	607382
# contigs	102
Largest contig	36312
Total length	619642
Reference length	1231960
GC (%)	25.34
Reference GC (%)	25.35
N50	11348
NG50	576
N75	6713
L50	20
LG50	96
L75	37
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	50.056
Duplication ratio	1.005
# N's per 100 kbp	0.00
# mismatches per 100 kbp	421.94
# indels per 100 kbp	0.00
Largest alignment	36312
NA50	11348
NGA50	573
NA75	6713
LA50	20
LGA50	96
LA75	37

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	0
# mismatches	2602
# indels	0
# short indels	0
# long indels	0
Indels length	0

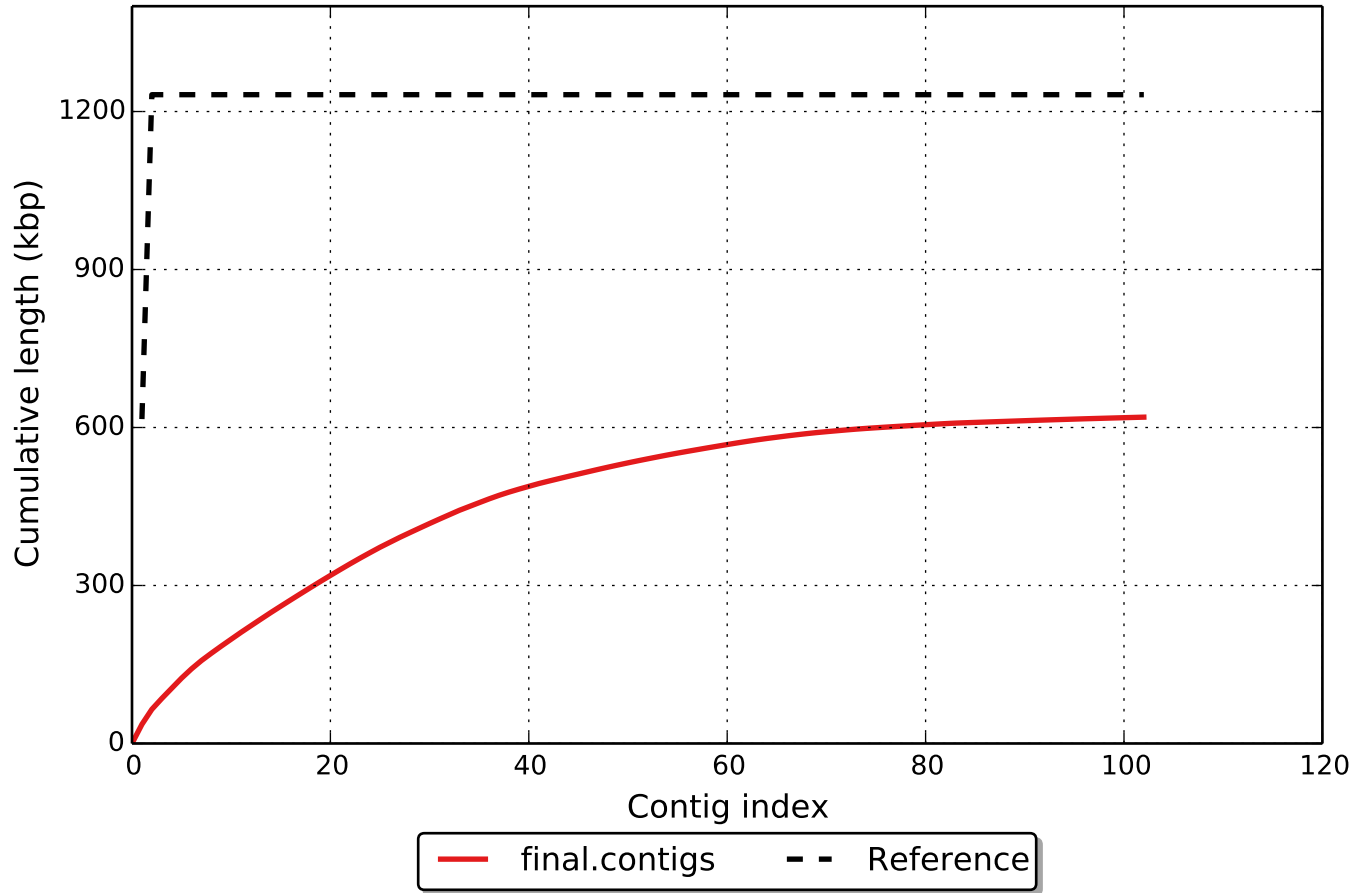
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

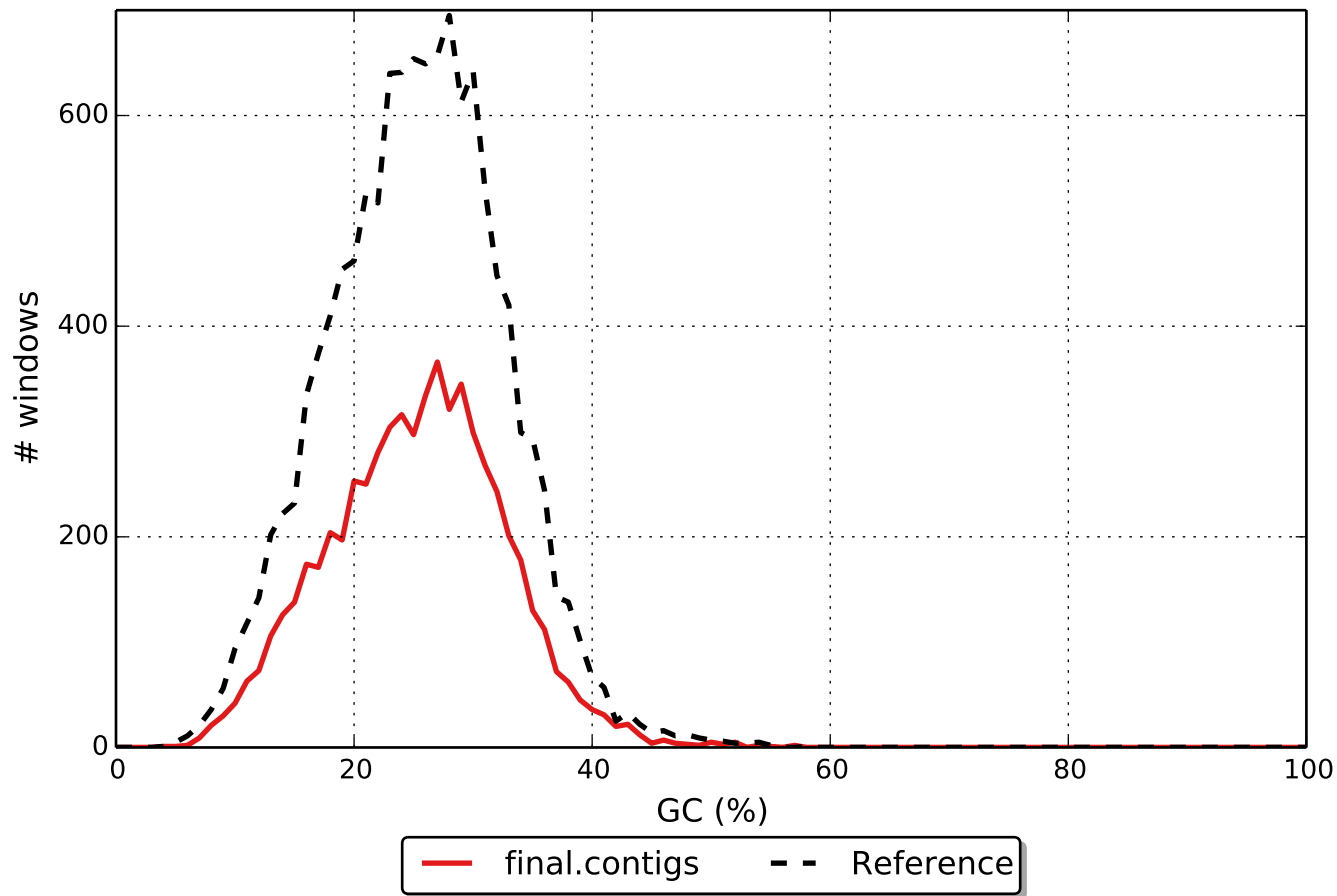
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

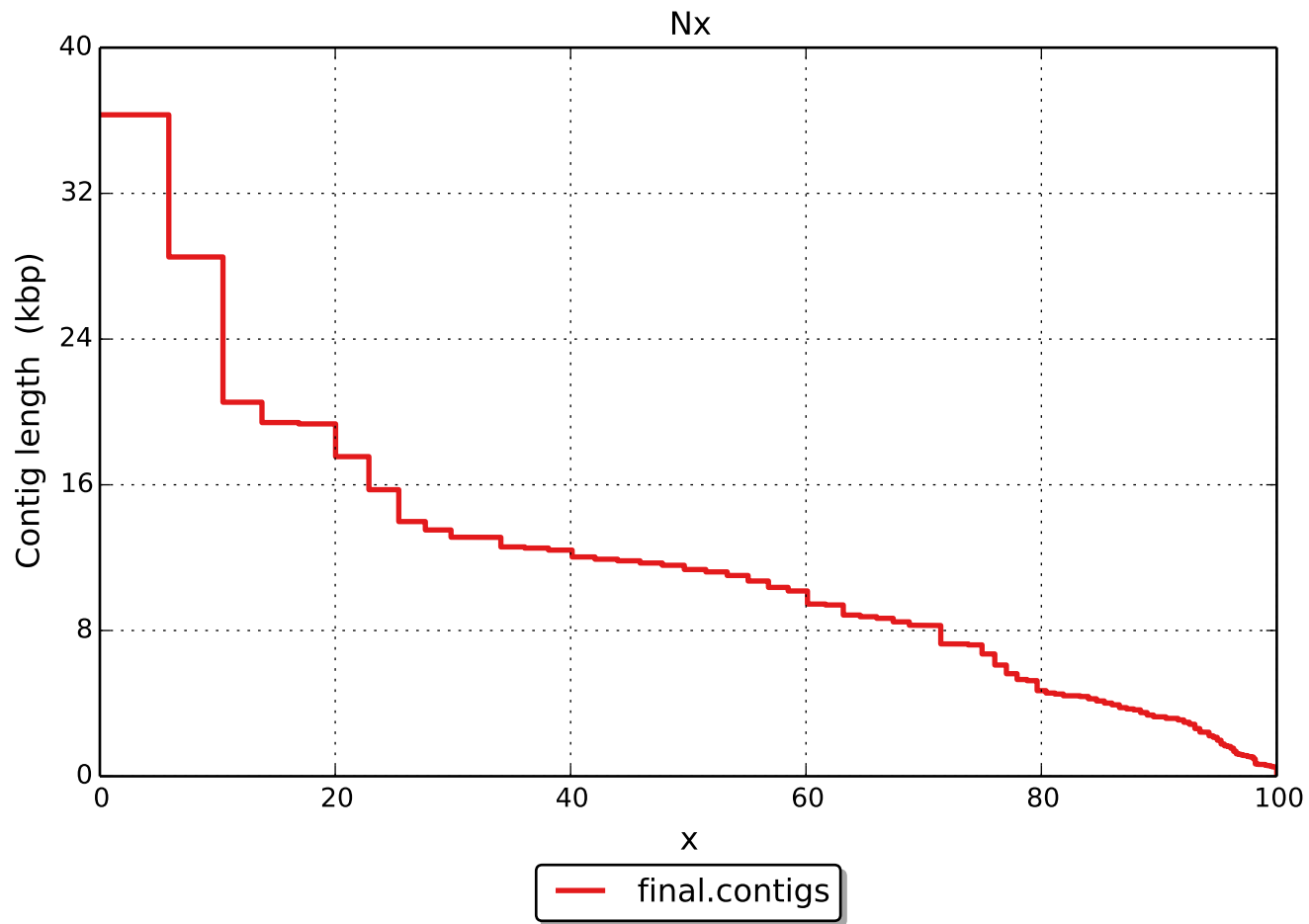
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

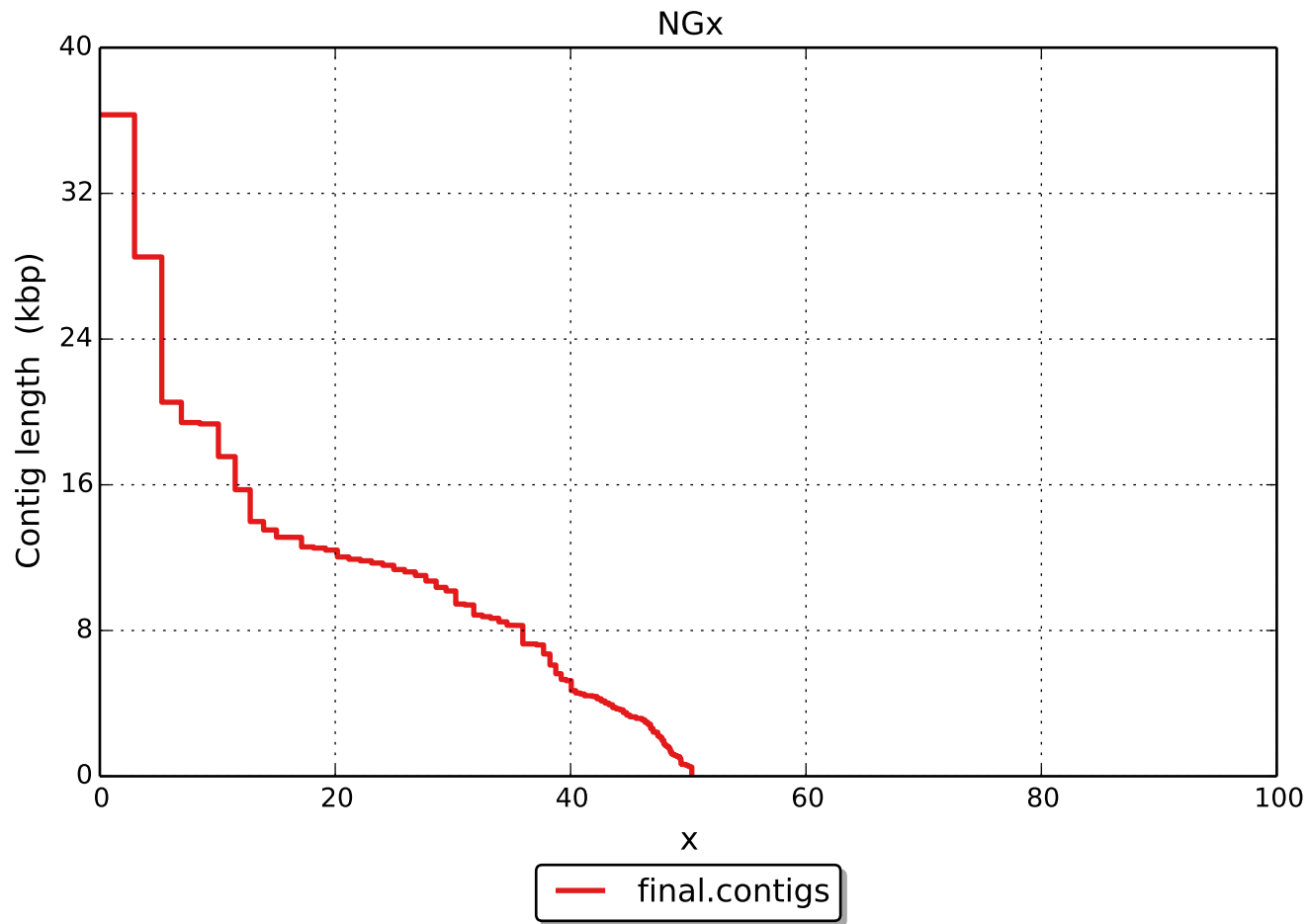
Cumulative length



GC content







Misassemblies



Cumulative length (aligned contigs)

