

Report

	final.contigs
# contigs (>= 1000 bp)	1591
# contigs (>= 5000 bp)	61
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	3582094
Total length (>= 5000 bp)	386438
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	2795
Largest contig	9194
Total length	4411427
Reference length	4857432
GC (%)	52.20
Reference GC (%)	52.22
N50	2109
NG50	1895
N75	1205
NG75	952
L50	655
LG50	766
L75	1343
LG75	1654
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	85.651
Duplication ratio	1.060
# N's per 100 kbp	0.00
# mismatches per 100 kbp	580.13
# indels per 100 kbp	0.22
Largest alignment	9194
NA50	2109
NGA50	1895
NA75	1205
NGA75	952
LA50	655
LGA50	766
LA75	1343
LGA75	1654

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

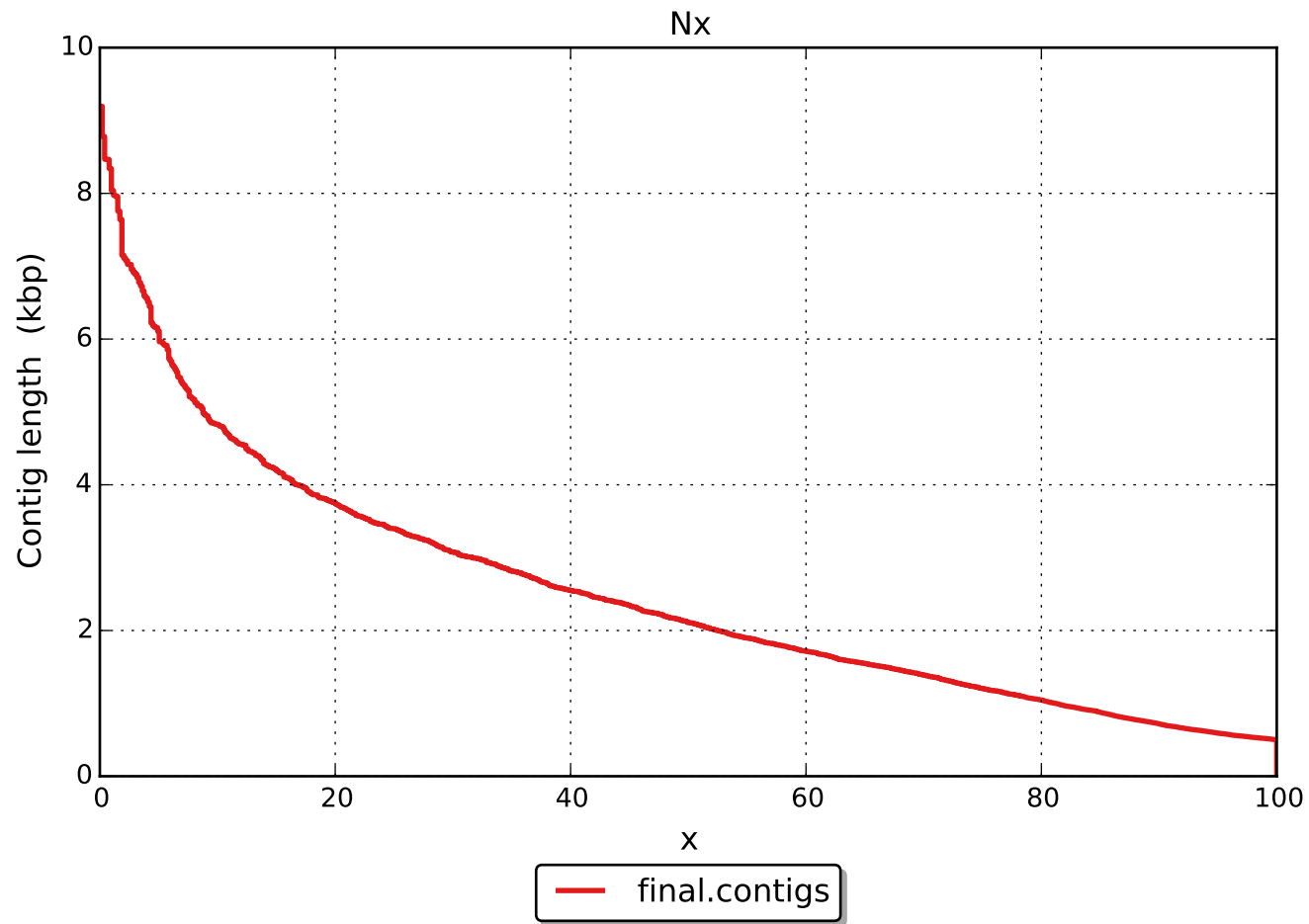
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# mismatches	24136
# indels	9
# short indels	9
# long indels	0
Indels length	12

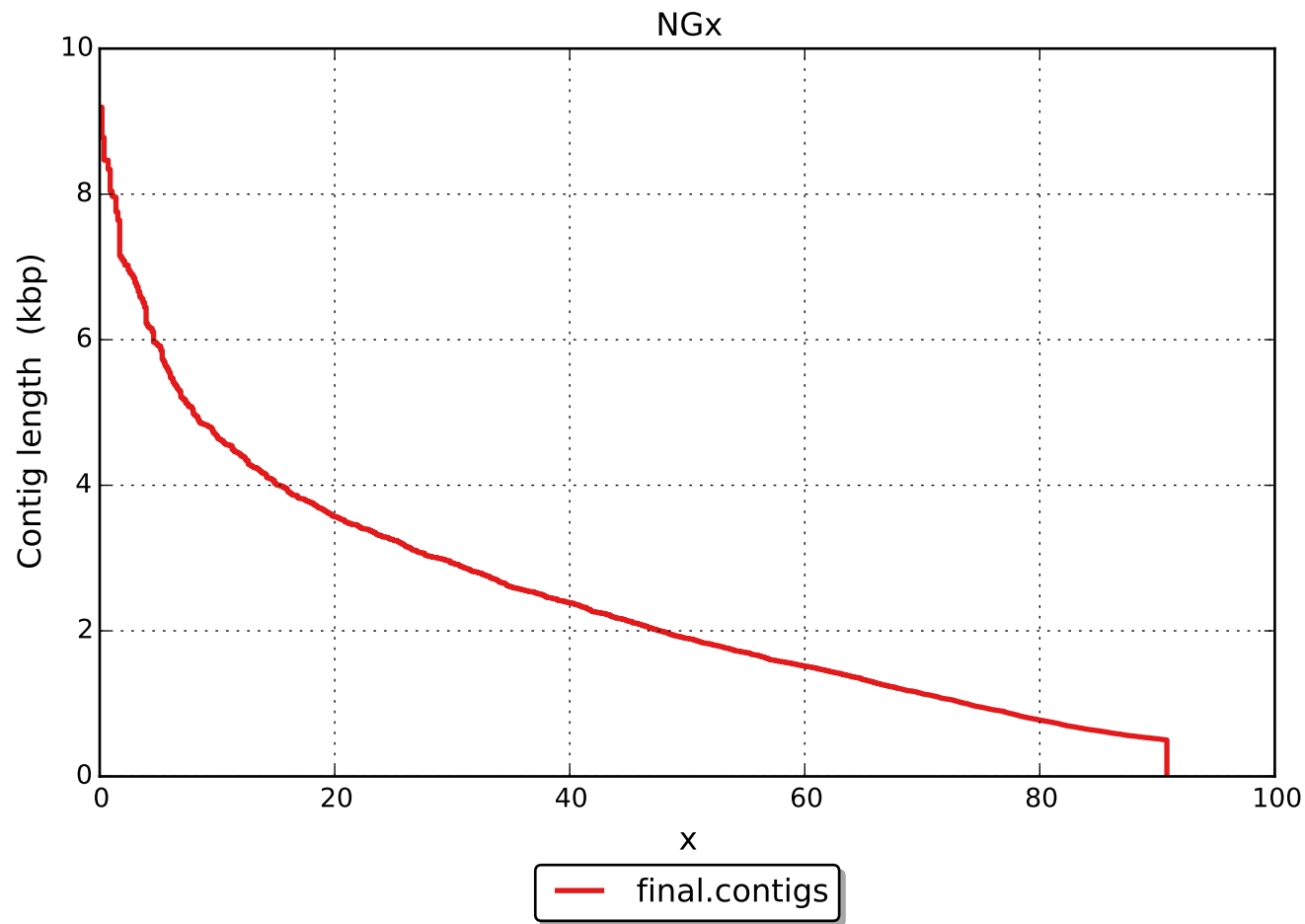
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

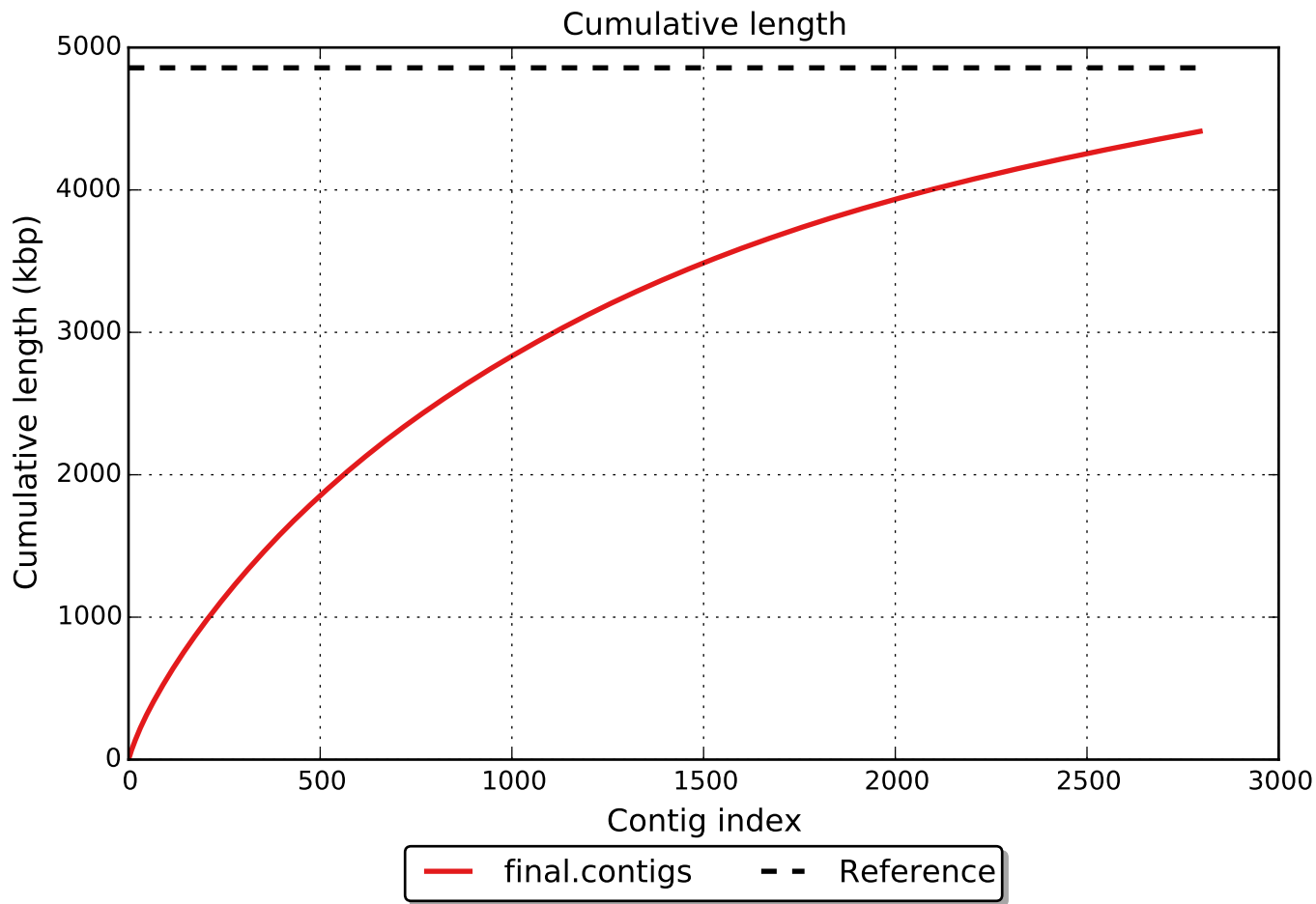
Unaligned report

	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

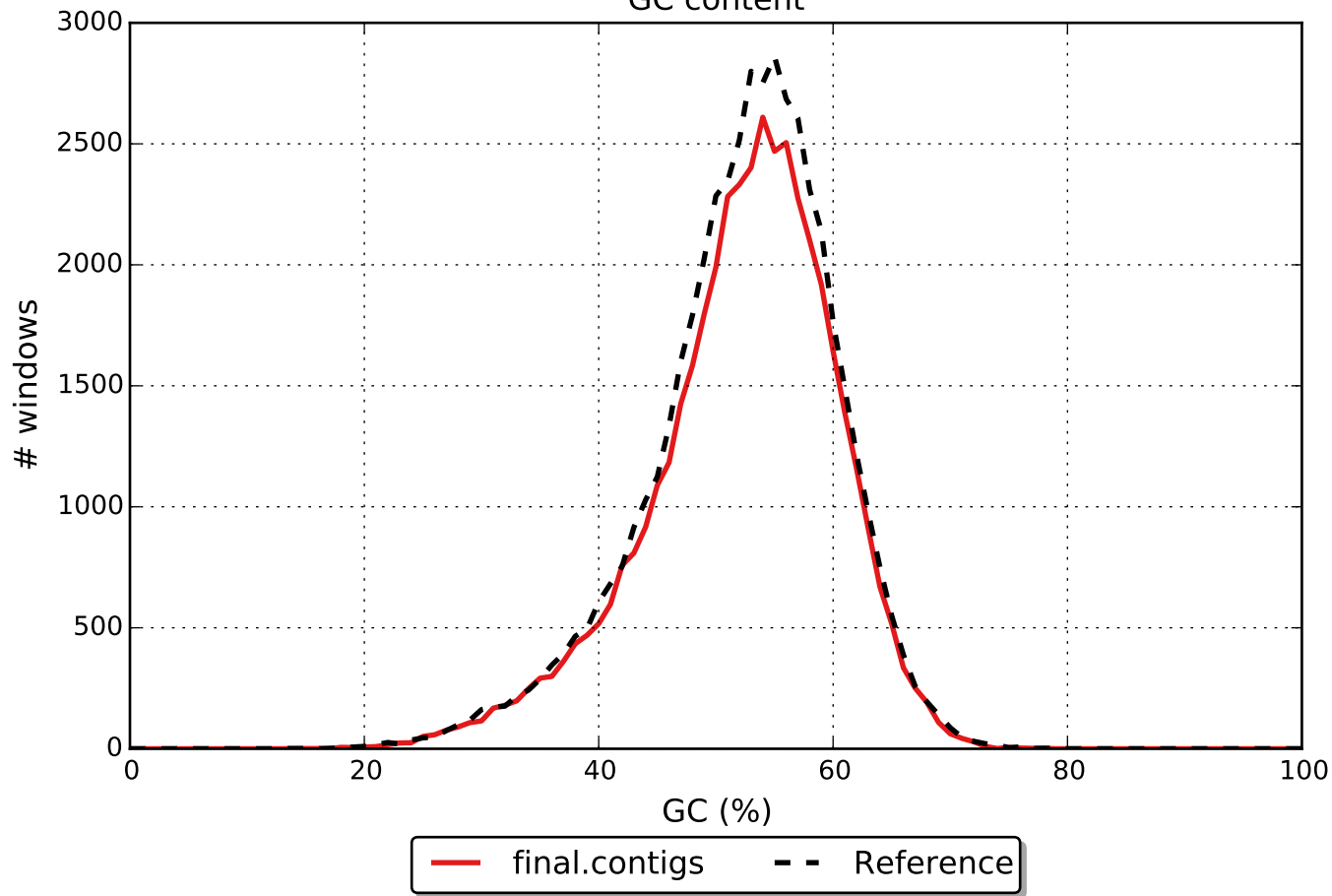
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).







GC content



Misassemblies



Cumulative length (aligned contigs)

