Report

	final.contigs
# contigs (>= 1000 bp)	1785
# contigs (>= 5000 bp)	51
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	3754806
Total length (>= 5000 bp)	313285
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	2878
Largest contig	9722
Total length	4551826
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	1970
NG50	1937
N75	1214
NG75	1173
L50	744
LG50	767
L75	1477
LG75	1534
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	93.743
Duplication ratio	1.046
# N's per 100 kbp	0.00
# mismatches per 100 kbp	62.19
# indels per 100 kbp	0.00
Largest alignment	9722
NA50	1970
NGA50	1937
NA75	1214
NGA75	1173
LA50	744
LGA50	767
LA75	1477
LGA75	1534

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).
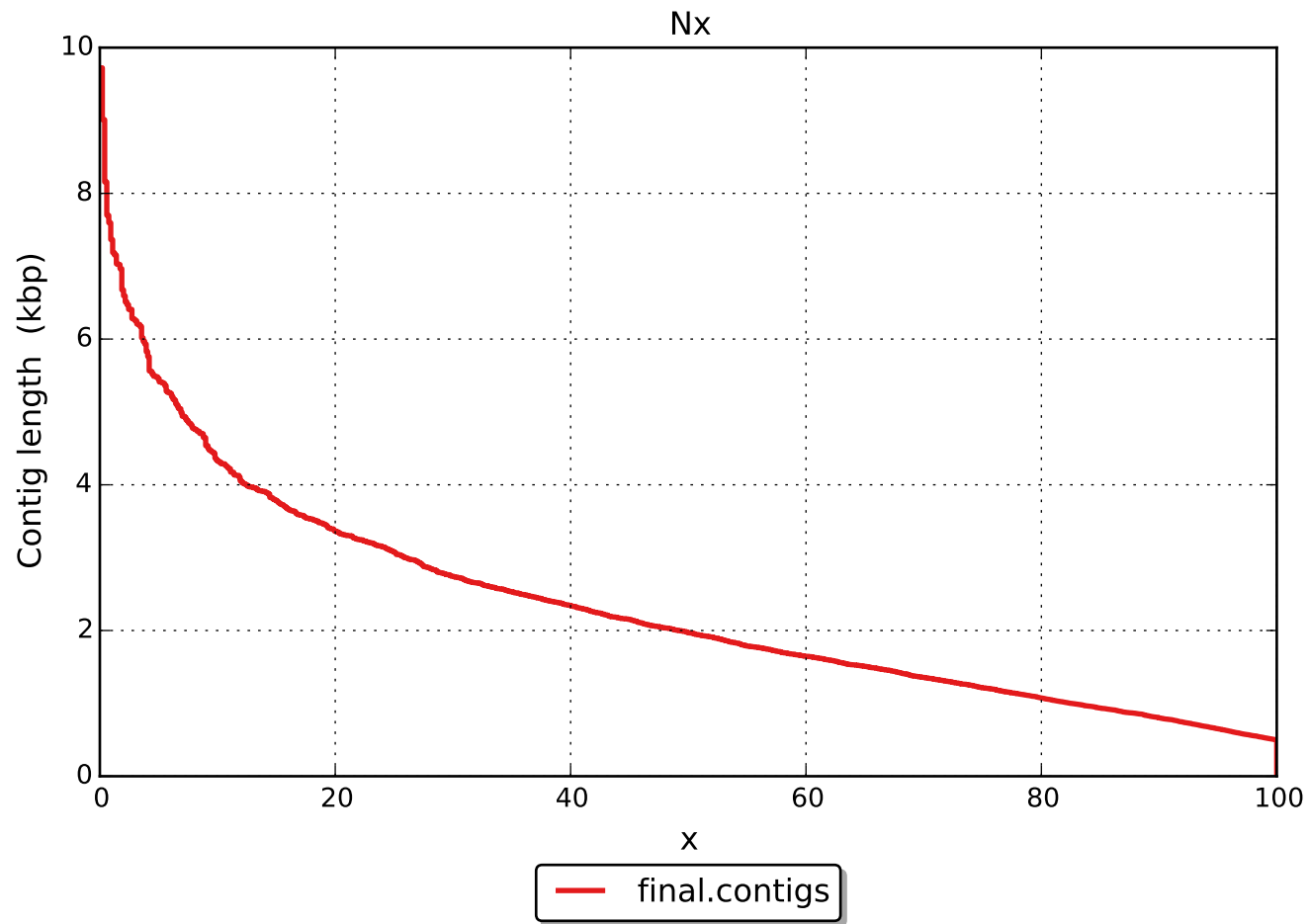
Misassemblies report

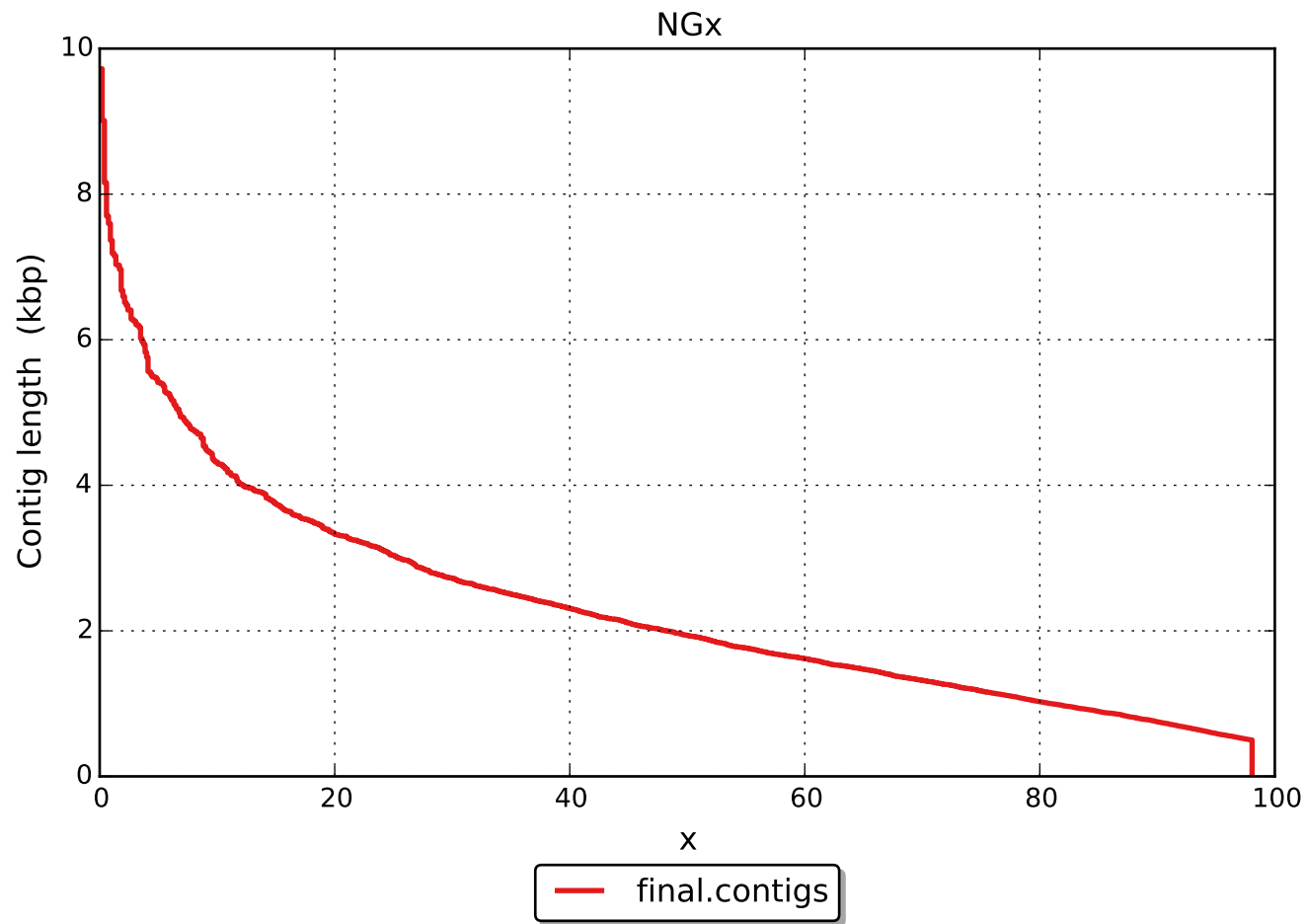|	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# mismatches	2706
# indels	0
# short indels	0
# long indels	0
Indels length	0

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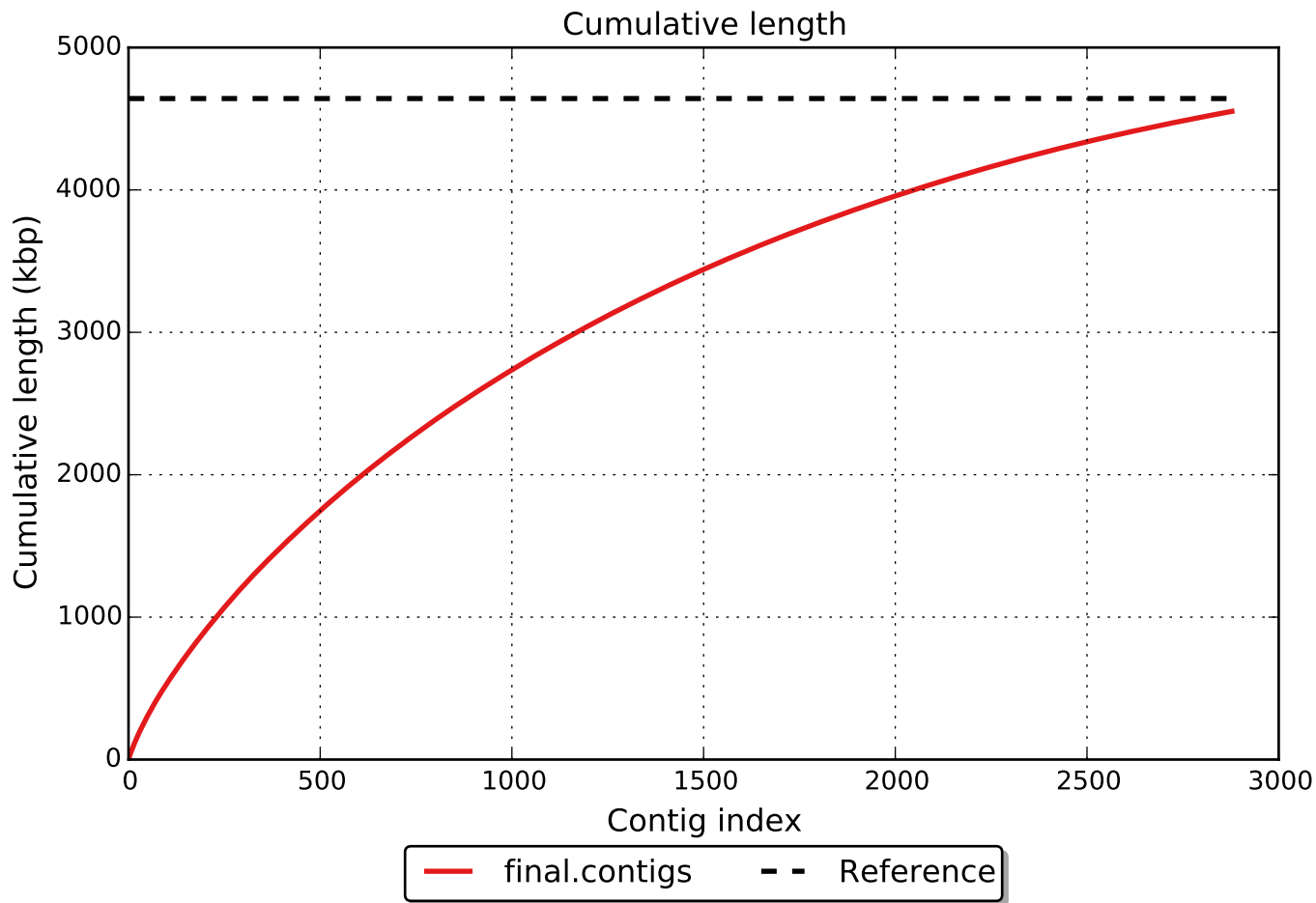
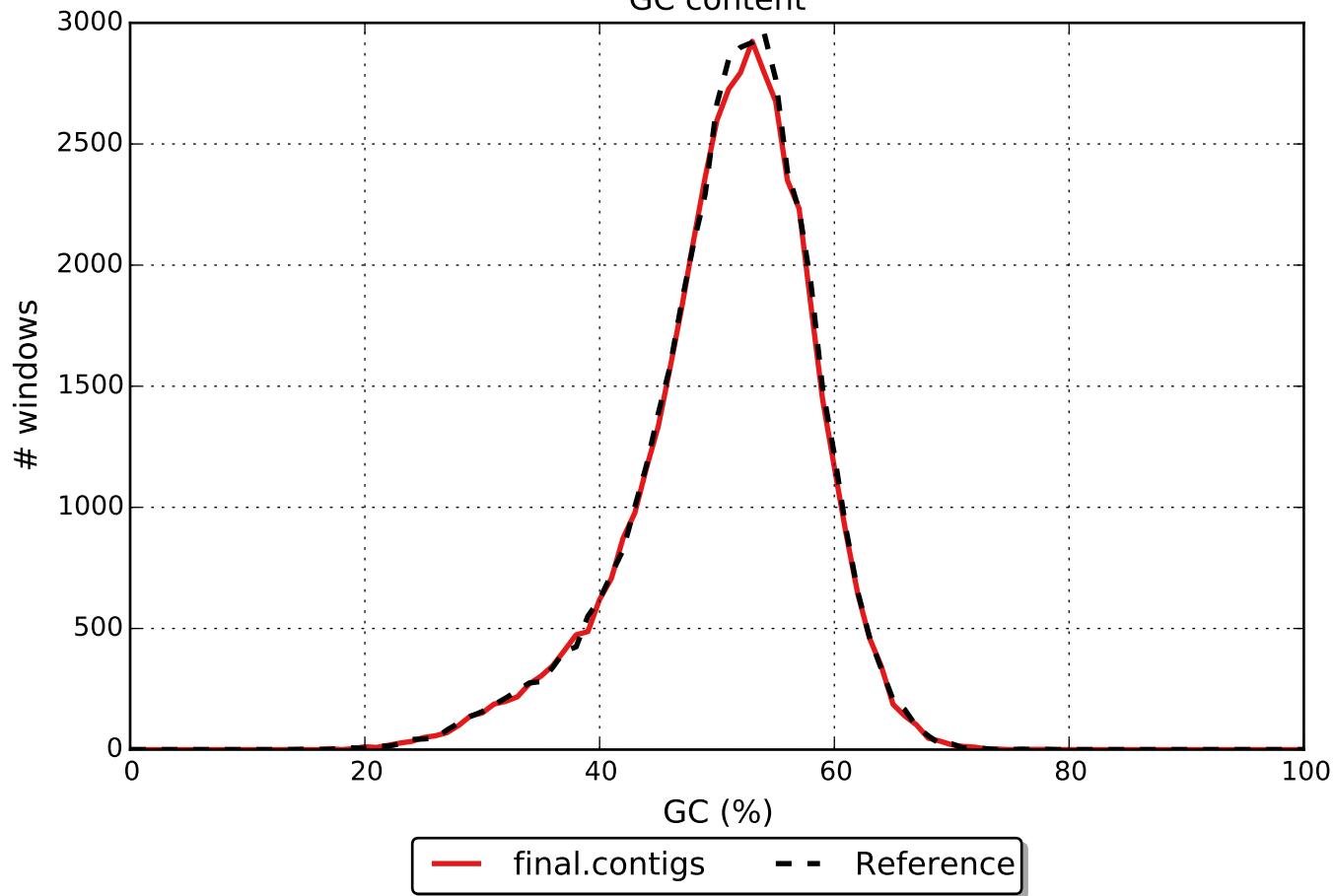|	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

Nx

Contig length (kbp) vs x

final.contigs

Cumulative length

Cumulative length (kbp) vs Contig index

Legend: final.contigs — Reference

Misassemblies

final.contigs

Cumulative length (aligned contigs)

NGAx