Report

	final.contigs
# contigs (>= 0 bp)	1476
# contigs (>= 1000 bp)	640
Total length (>= 0 bp)	2570112
Total length (>= 1000 bp)	2013087
# contigs	1476
Largest contig	16077
Total length	2570112
Reference length	5547323
GC (%)	50.57
Reference GC (%)	50.48
N50	3012
N75	1197
L50	235
L75	562
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 1 part
Unaligned length	11
Genome fraction (%)	45.360
Duplication ratio	1.021
# N's per 100 kbp	0.00
# mismatches per 100 kbp	418.84
# indels per 100 kbp	0.36
Largest alignment	16077
NA50	3012
NA75	1197
LA50	235
LA75	562

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

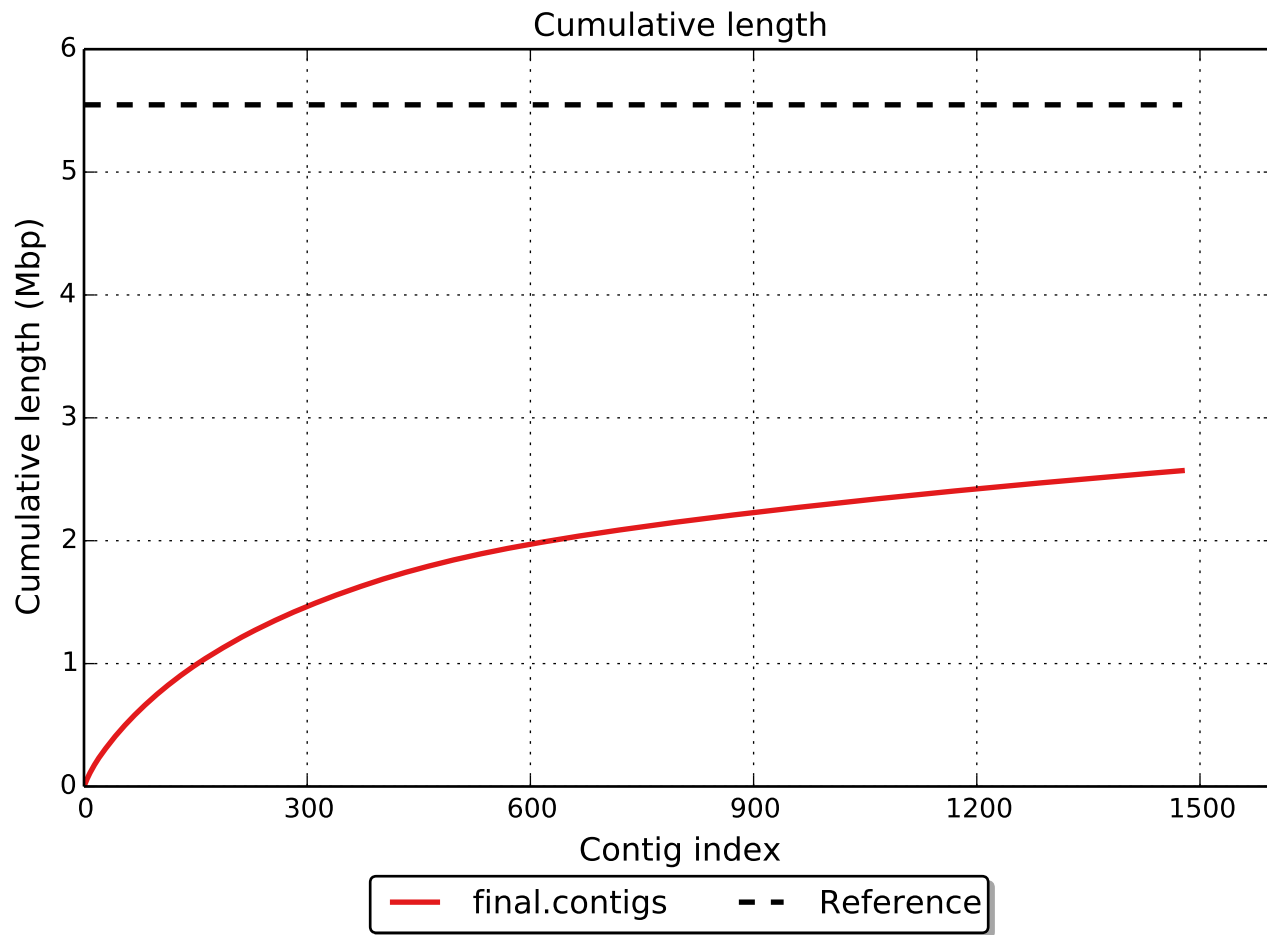|	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	10539
# indels	9
# short indels	9
# long indels	0
Indels length	9

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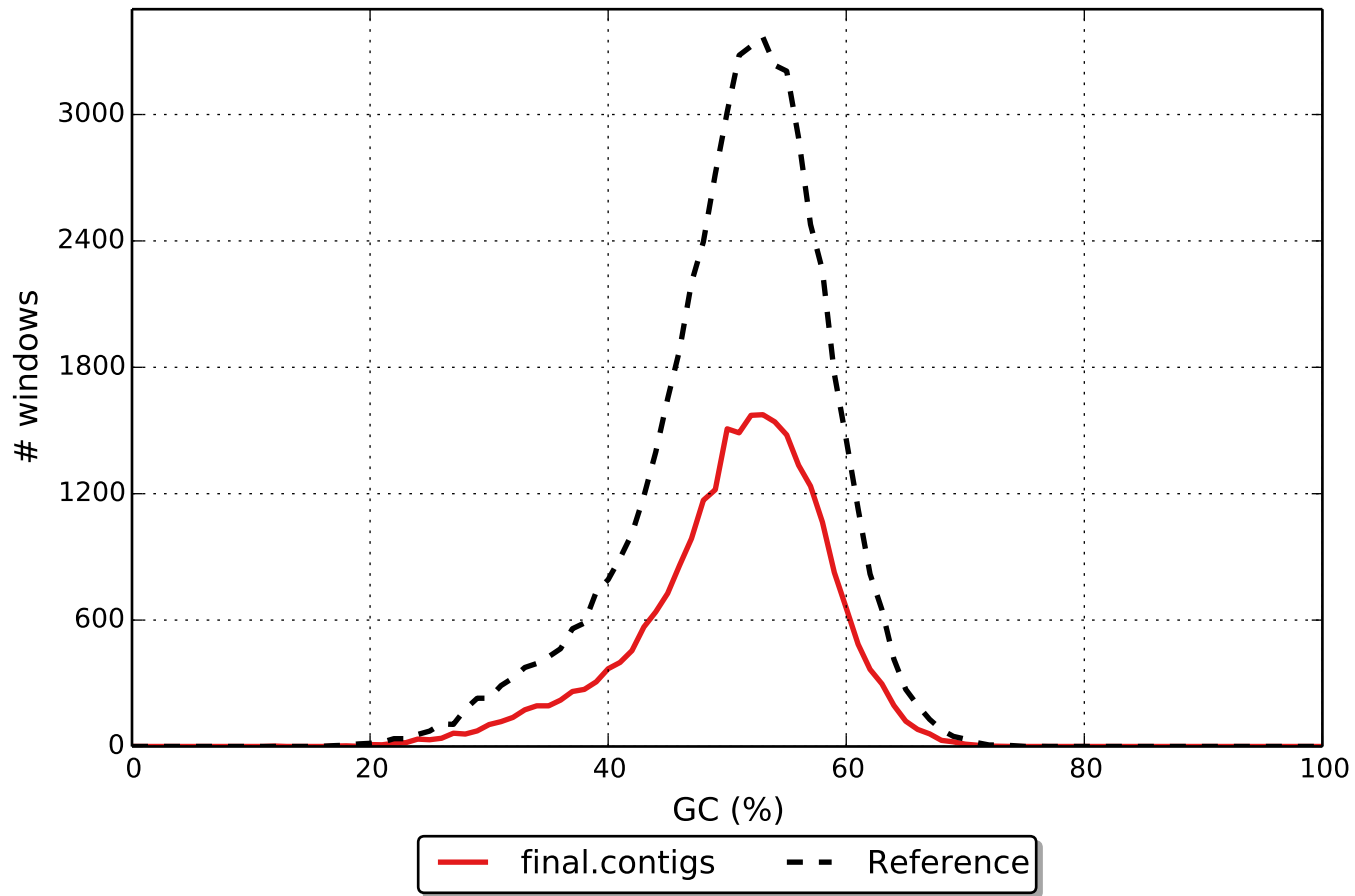
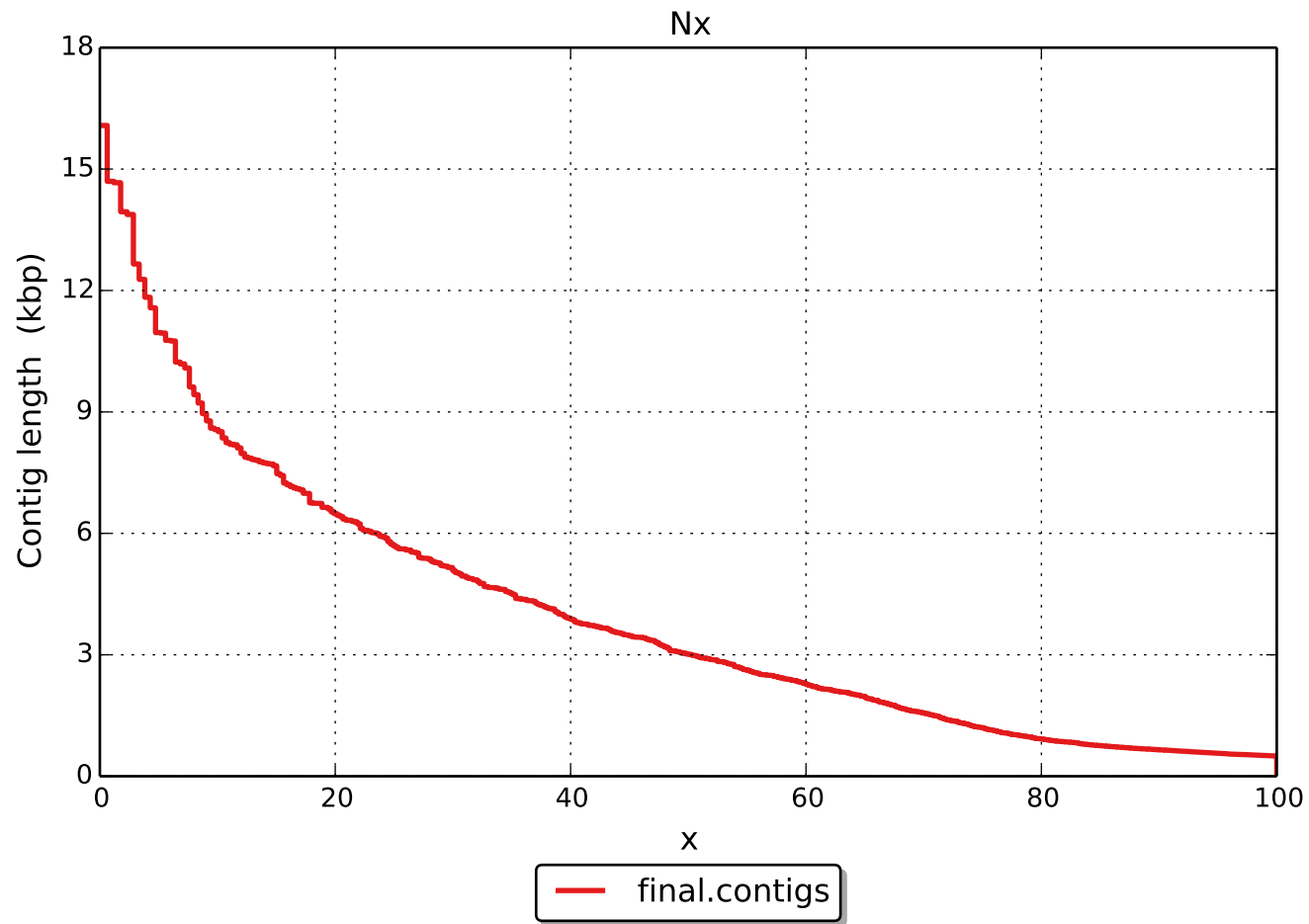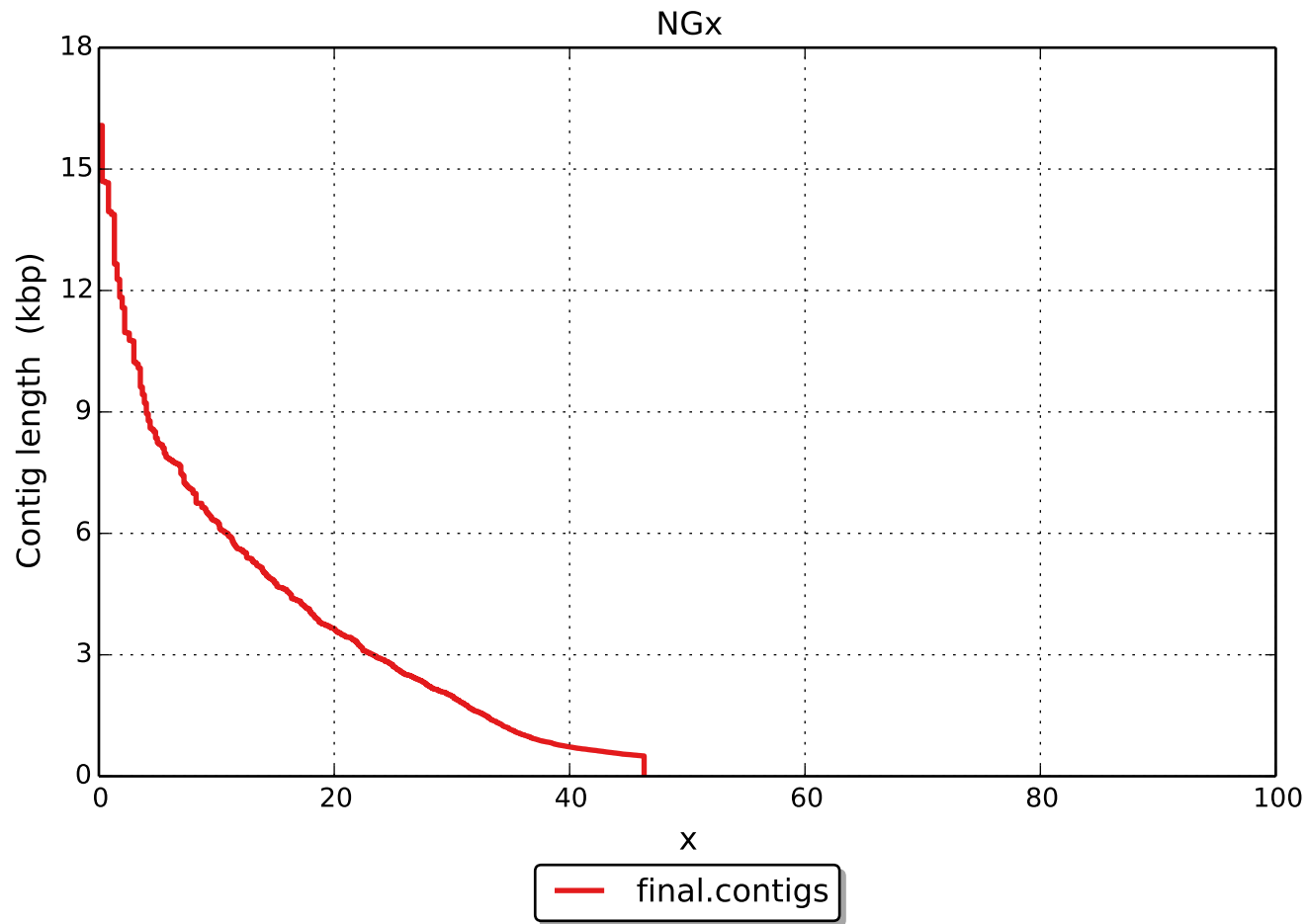|	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	11
# N's	0

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).

Cumulative length

GC content

Misassemblies

final.contigs

Cumulative length (aligned contigs)