Report

	final.contigs
# contigs (>= 0 bp)	13758
# contigs (>= 1000 bp)	2178
Total length (>= 0 bp)	9265457
Total length (>= 1000 bp)	3273005
# contigs	7747
Largest contig	7611
Total length	7134998
Reference length	10957366
GC (%)	50.38
Reference GC (%)	50.49
N50	940
NG50	675
N75	688
L50	2482
LG50	4904
L75	4717
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	62.233
Duplication ratio	1.046
# N's per 100 kbp	0.00
# mismatches per 100 kbp	203.28
# indels per 100 kbp	0.09
Largest alignment	7611
NA50	940
NGA50	675
NA75	688
LA50	2482
LGA50	4904
LA75	4717

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).
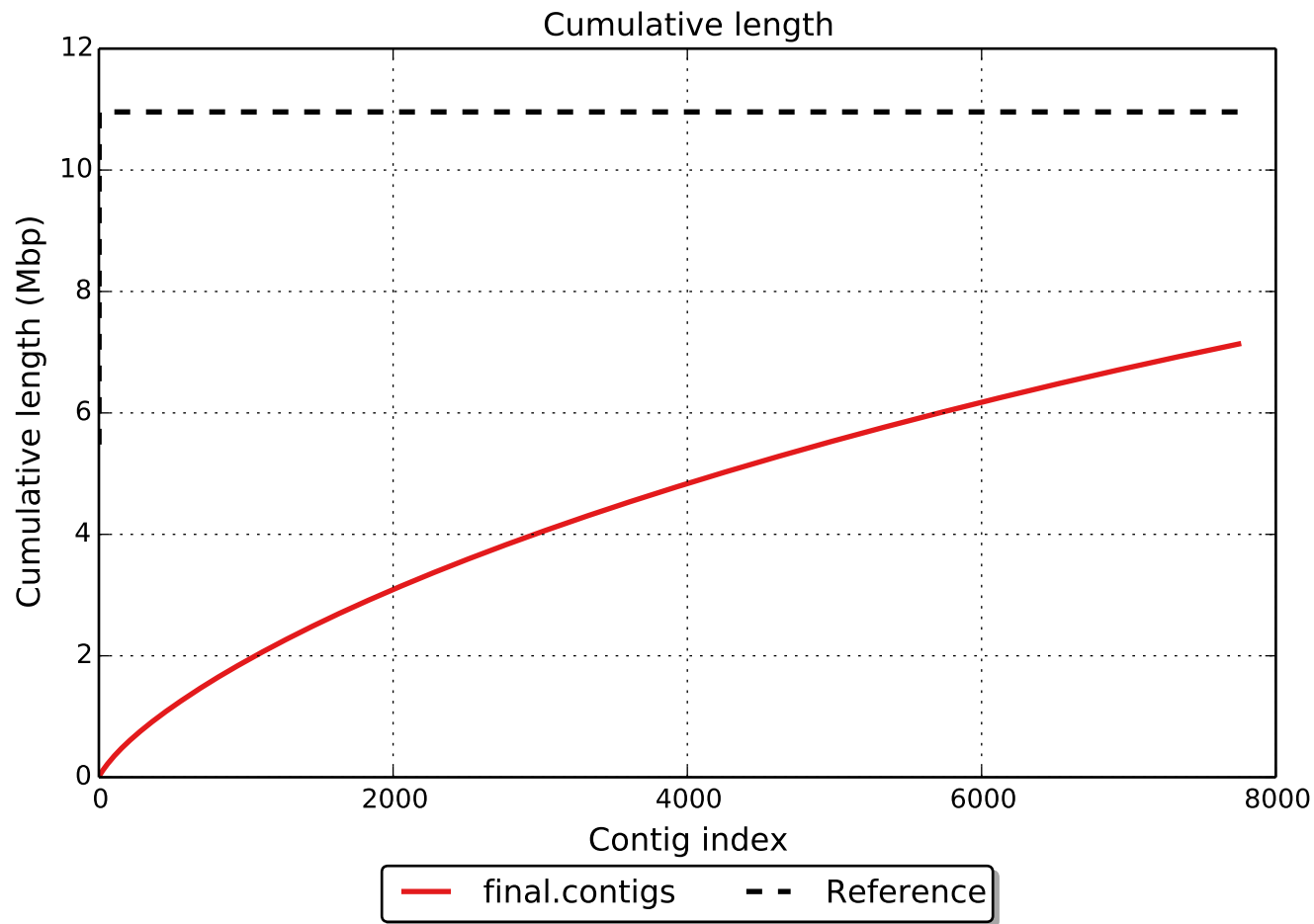
Misassemblies report

	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	13862
# indels	6
# short indels	4
# long indels	2
Indels length	16

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).
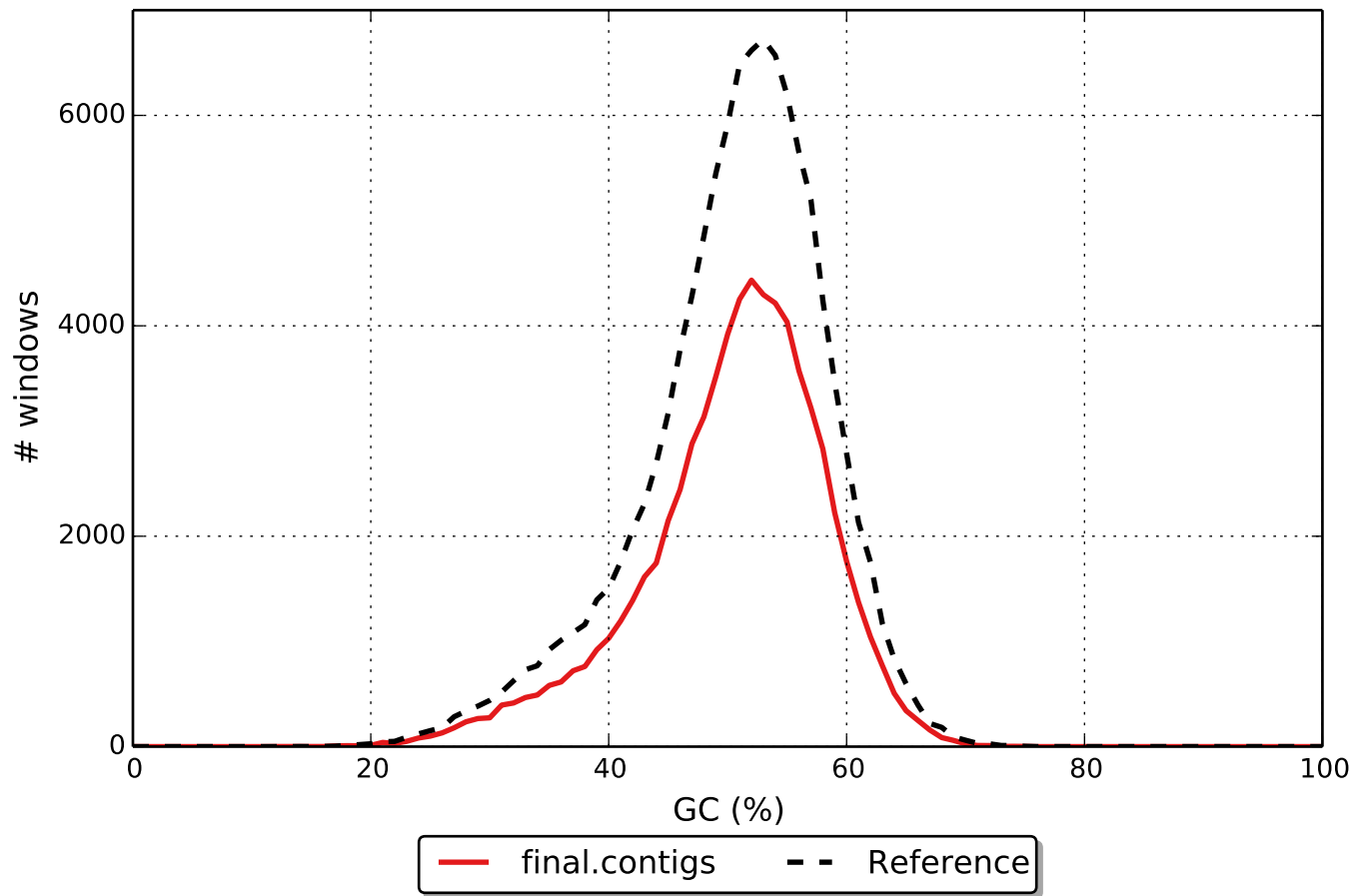
Unaligned report

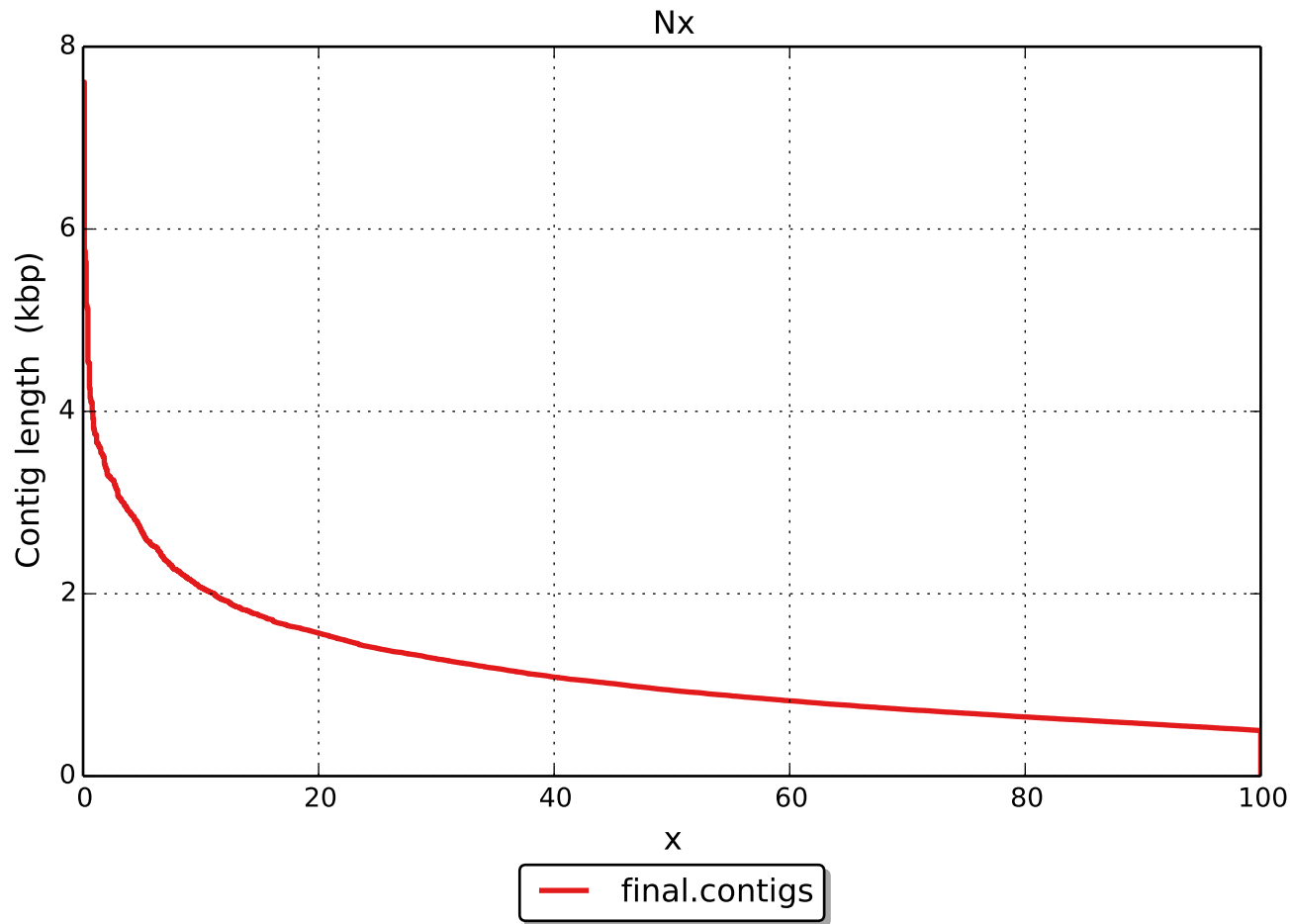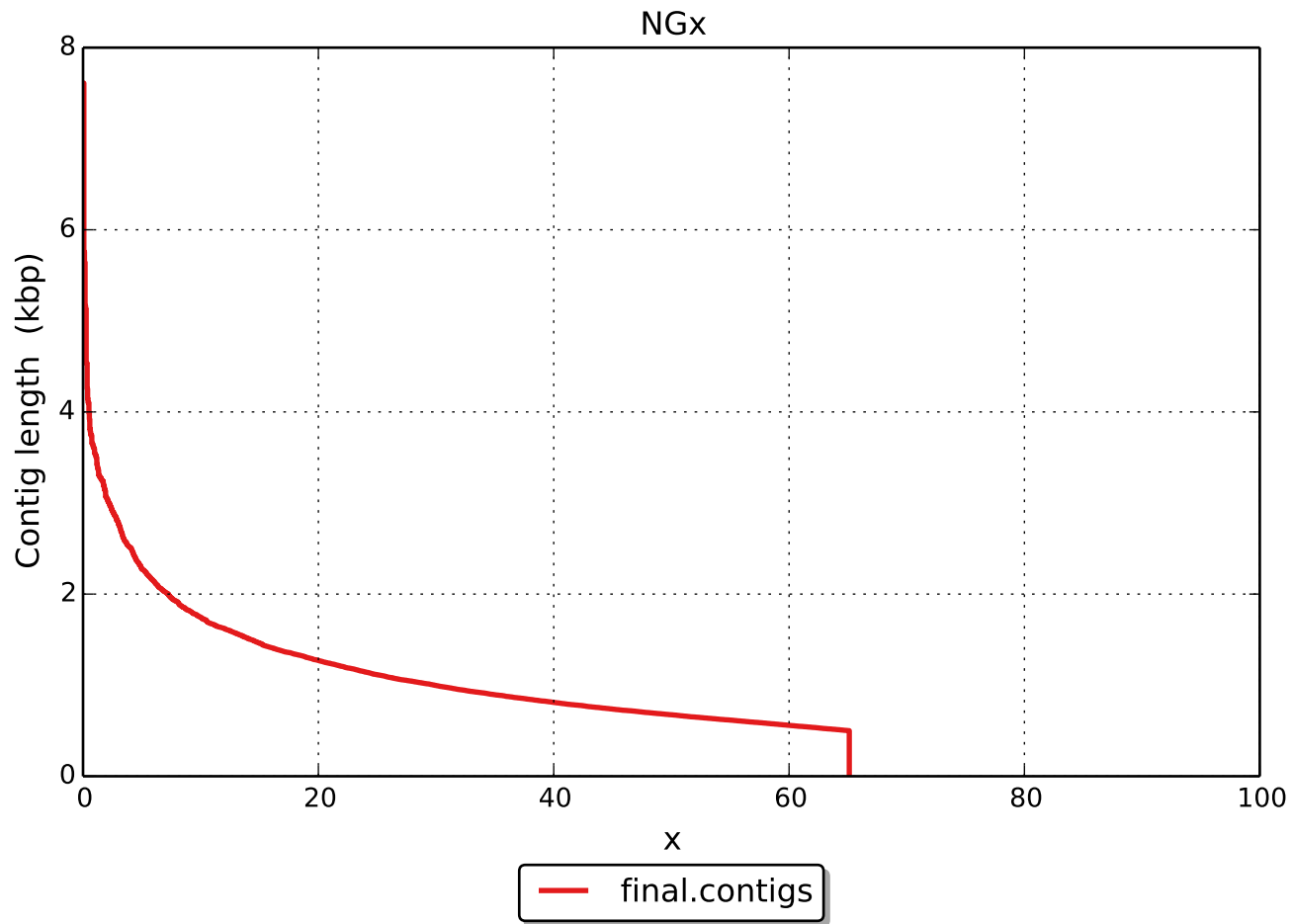|	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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

final.contigs

Cumulative length (aligned contigs)