Report

	final.contigs
# contigs (>= 0 bp)	933
# contigs (>= 1000 bp)	854
Total length (>= 0 bp)	5523724
Total length (>= 1000 bp)	5466430
# contigs	933
Largest contig	38712
Total length	5523724
Reference length	5478683
GC (%)	50.50
Reference GC (%)	50.50
N50	8814
NG50	8904
N75	5262
NG75	5313
L50	199
LG50	196
L75	399
LG75	393
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.508
Duplication ratio	1.013
# N's per 100 kbp	0.00
# mismatches per 100 kbp	4.88
# indels per 100 kbp	0.00
Largest alignment	38712
NA50	8814
NGA50	8904
NA75	5262
NGA75	5313
LA50	199
LGA50	196
LA75	399
LGA75	393

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).
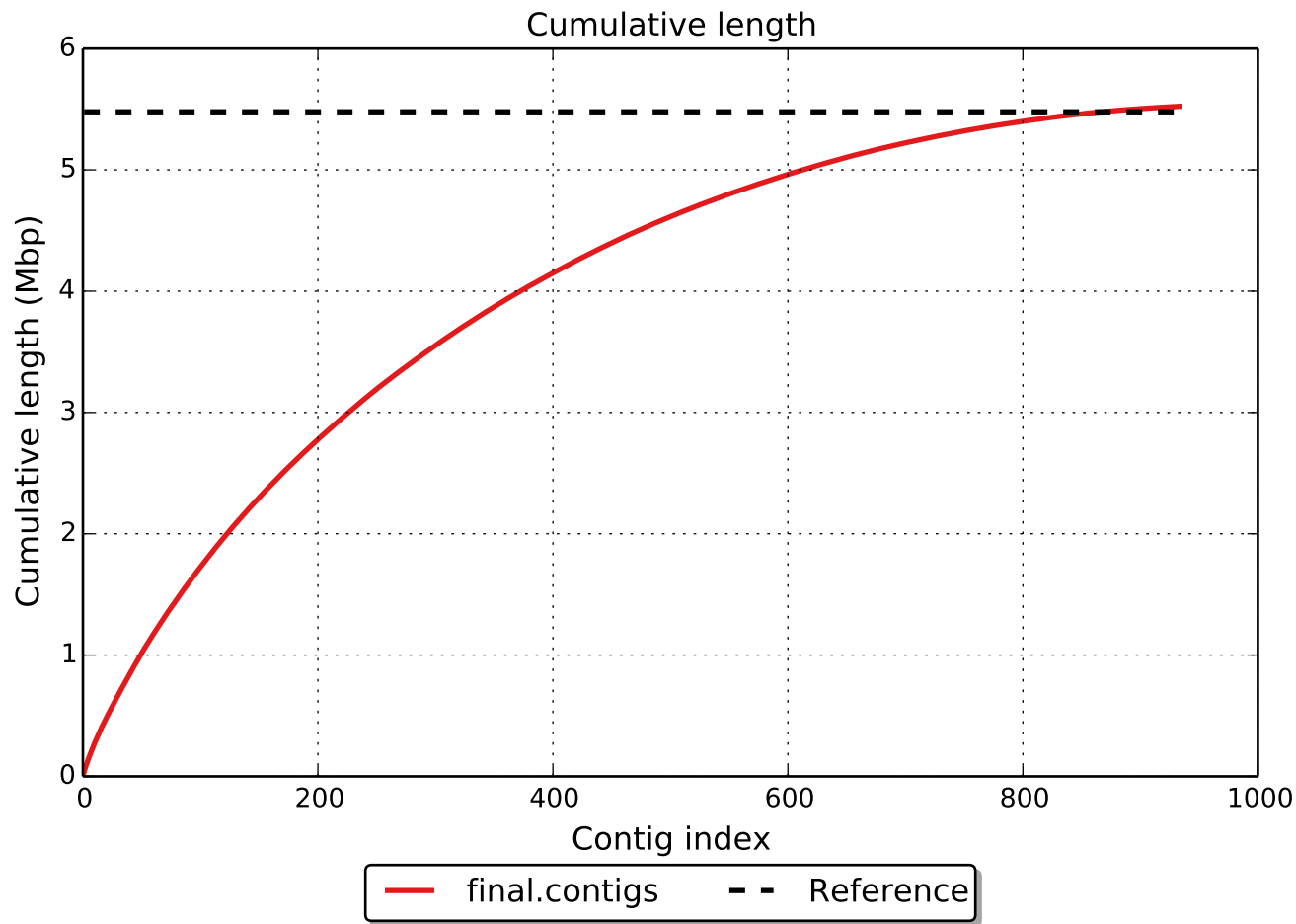
Misassemblies report

	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	266
# 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).
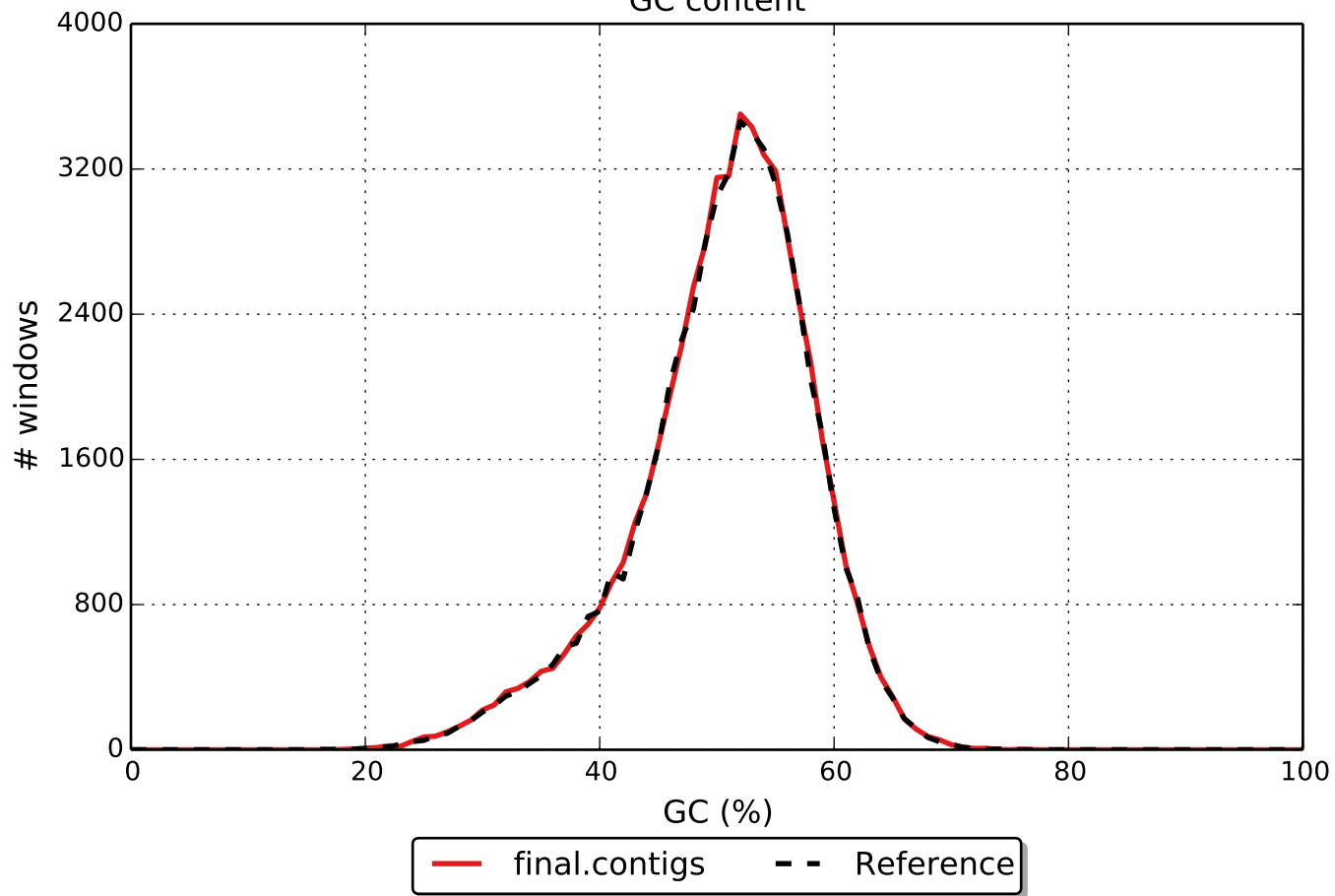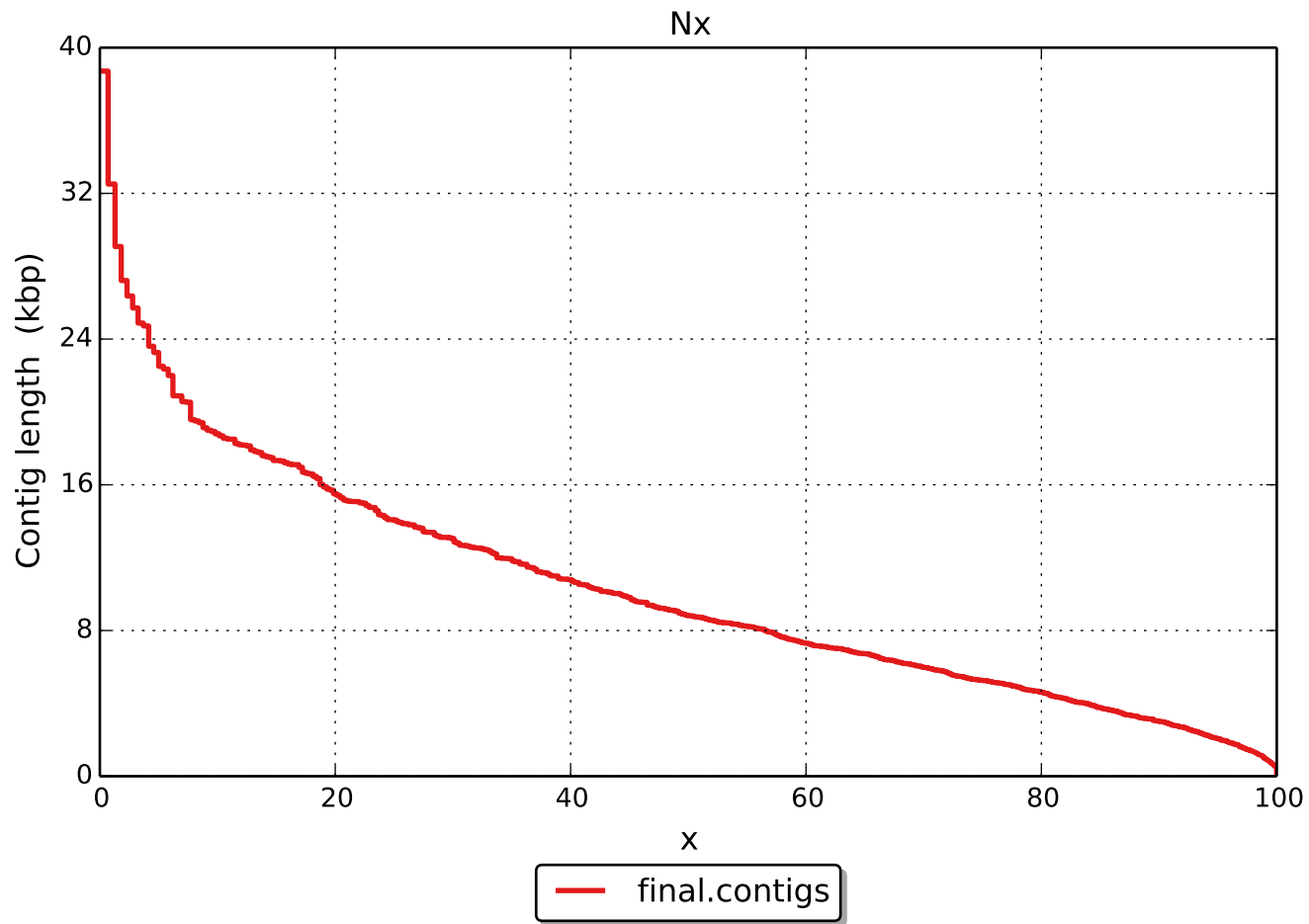
Unaligned report

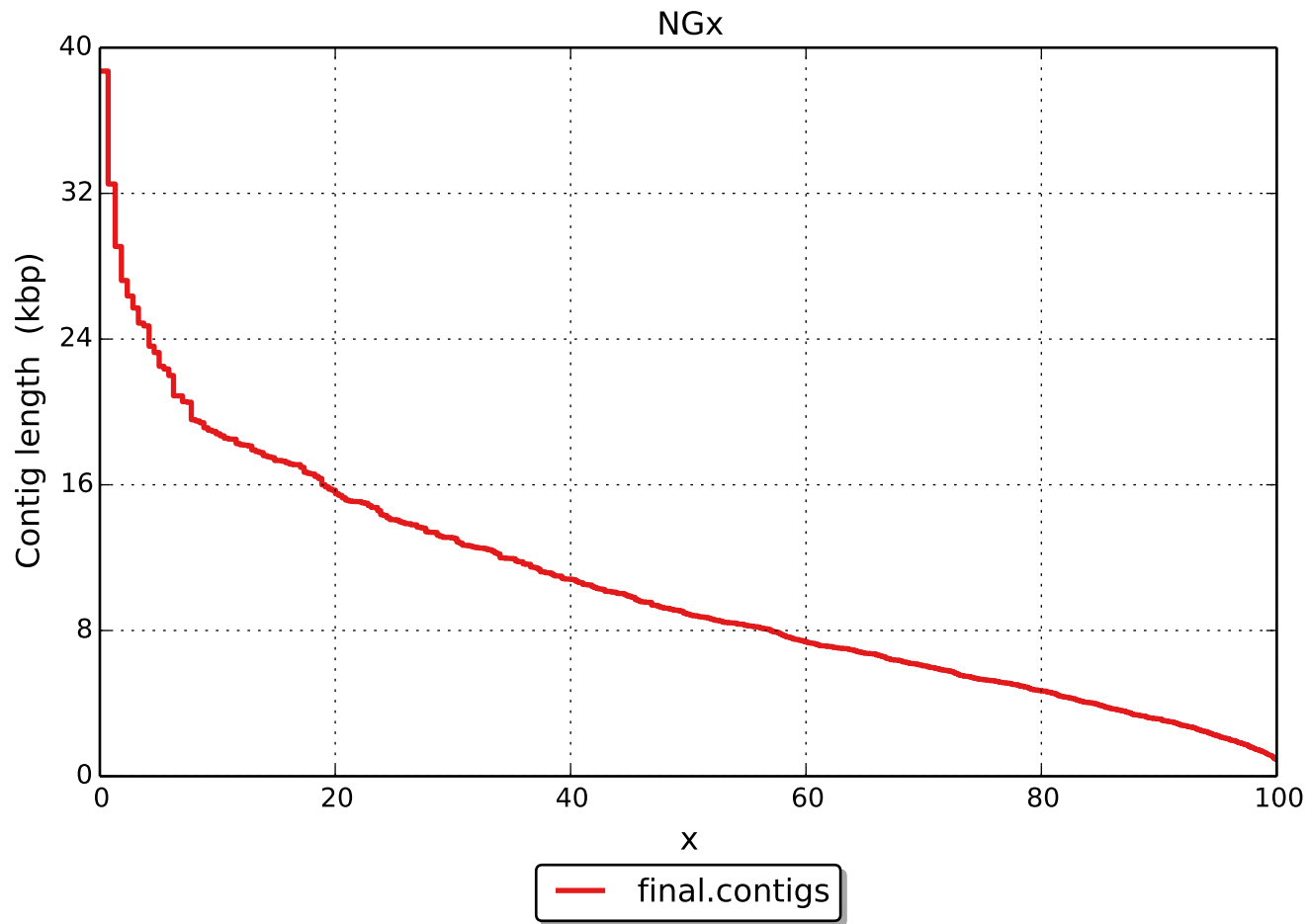|	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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

NGx

Contig length (kbp) vs x

final.contigs

Misassemblies

final.contigs

Cumulative length (aligned contigs)