Report

	final.contigs
# contigs (>= 0 bp)	1673
# contigs (>= 1000 bp)	1247
# contigs (>= 5000 bp)	256
# contigs (>= 10000 bp)	36
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	4627932
Total length (>= 1000 bp)	4364470
Total length (>= 5000 bp)	1914809
Total length (>= 10000 bp)	448567
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	1523
Largest contig	18990
Total length	4568606
Reference length	4641652
GC (%)	50.73
Reference GC (%)	50.79
N50	4364
NG50	4285
N75	2430
NG75	2360
L50	336
LG50	344
L75	683
LG75	705
# misassemblies	10
# misassembled contigs	10
Misassembled contigs length	46159
# local misassemblies	8
# unaligned contigs	1 + 5 part
Unaligned length	1694
Genome fraction (%)	96.437
Duplication ratio	1.020
# N's per 100 kbp	0.00
# mismatches per 100 kbp	324.56
# indels per 100 kbp	0.47
Largest alignment	18990
NA50	4316
NGA50	4255
NA75	2422
NGA75	2347
LA50	338
LGA50	347
LA75	687
LGA75	710

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).
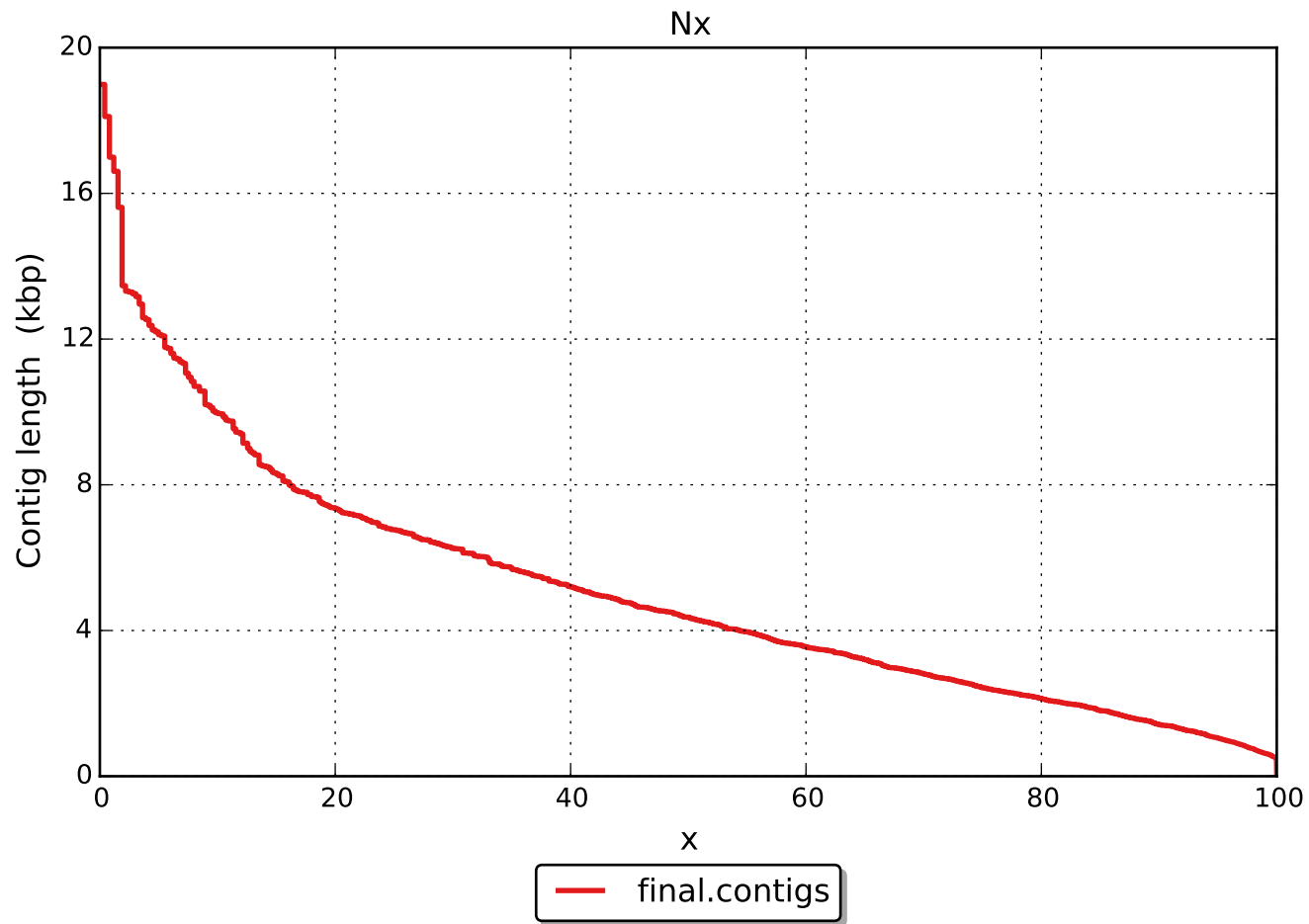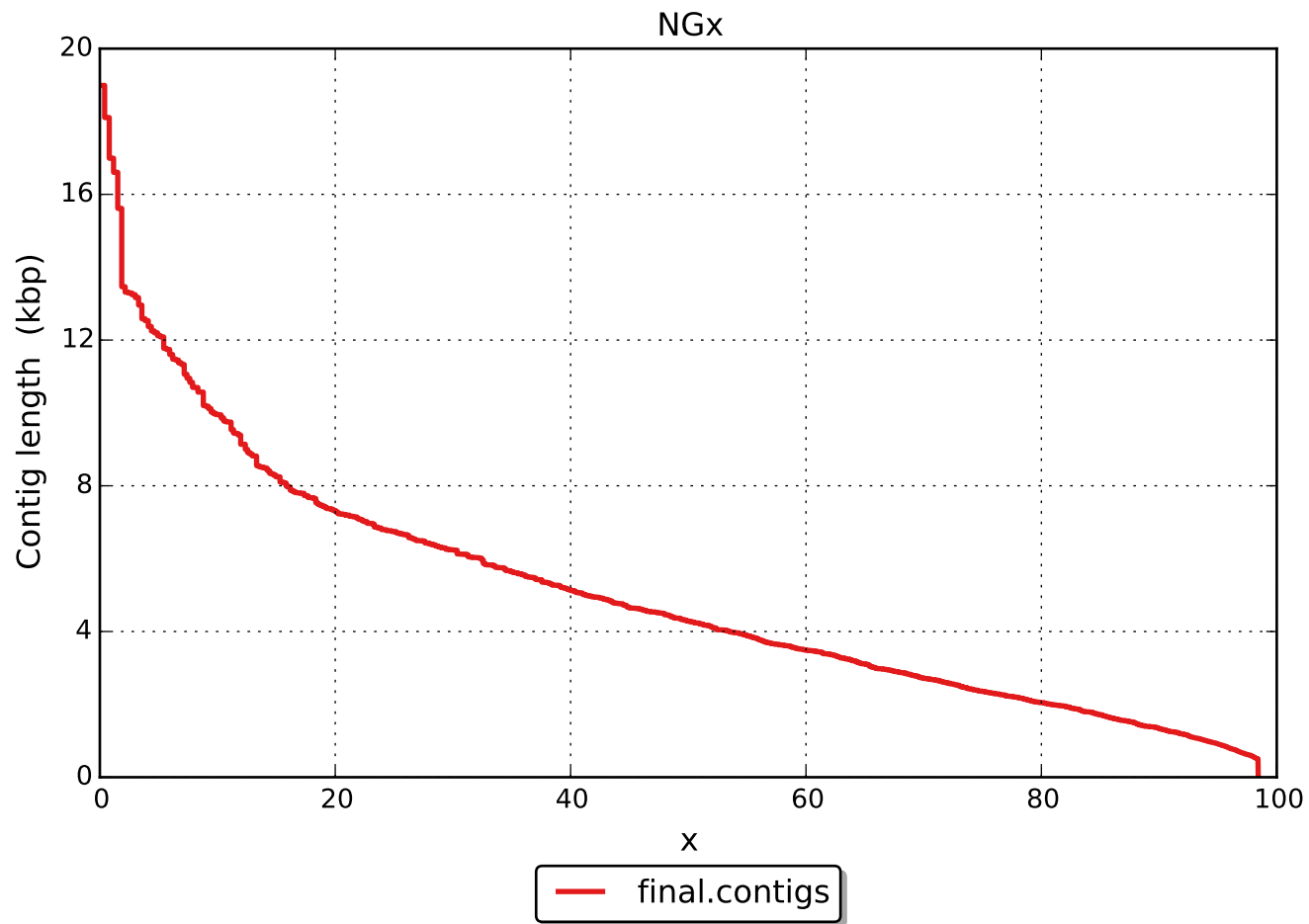
Misassemblies report

	final.contigs
# misassemblies	10
# relocations	10
# translocations	0
# inversions	0
# misassembled contigs	10
Misassembled contigs length	46159
# local misassemblies	8
# mismatches	14528
# indels	21
# short indels	20
# long indels	1
Indels length	107

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	1
Fully unaligned length	1556
# partially unaligned contigs	5
# with misassembly	0
# both parts are significant	0
Partially unaligned length	138
# N's	0

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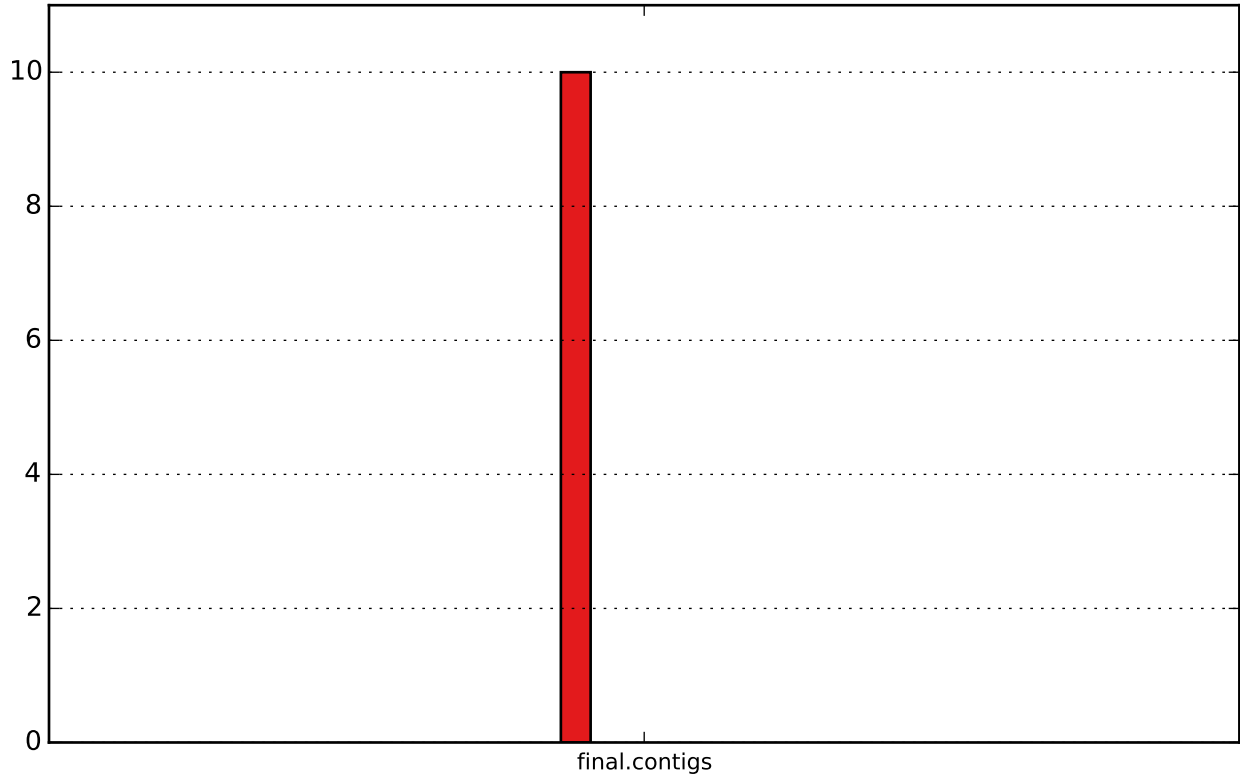(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).
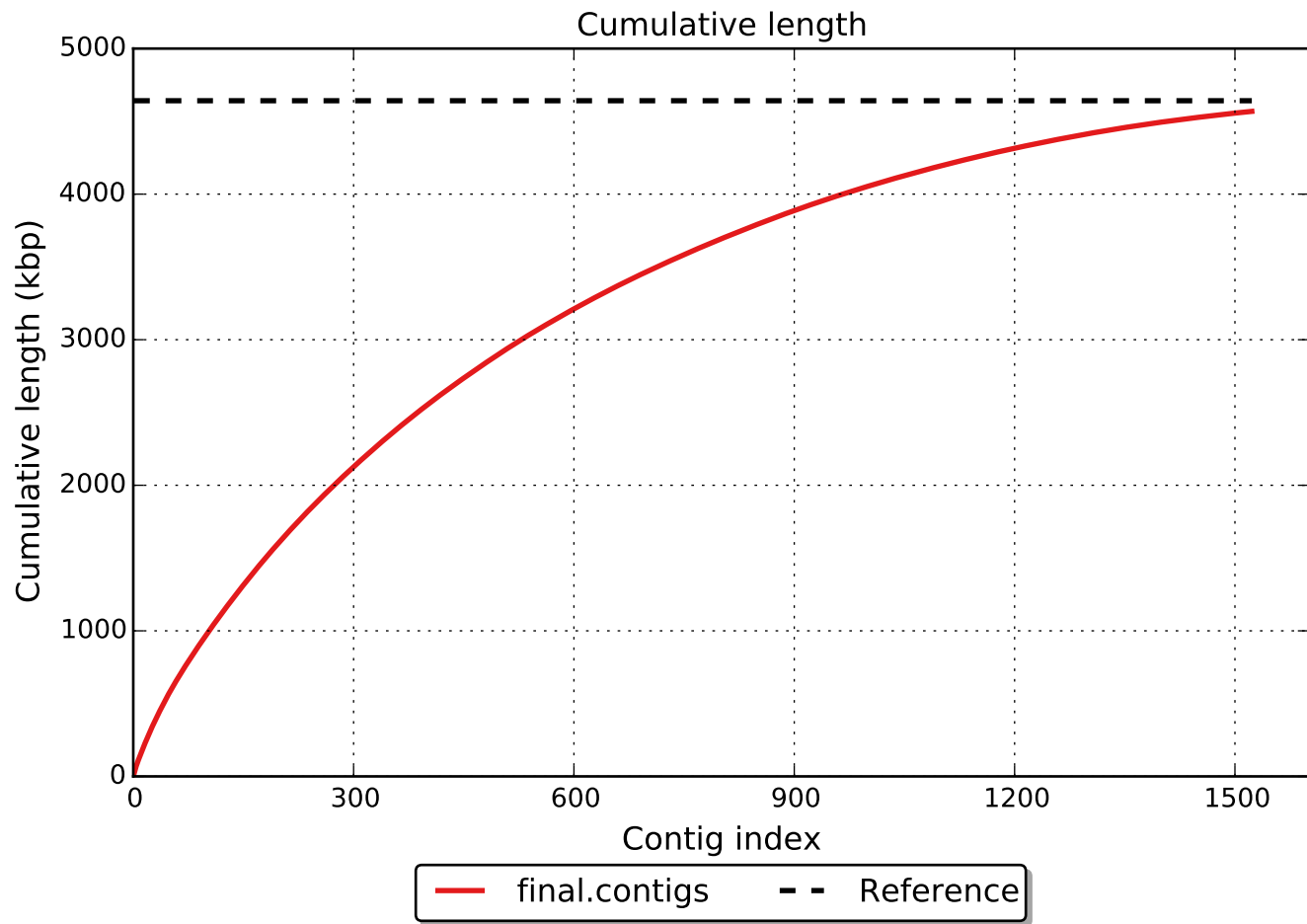
Cumulative length

GC content

Misassemblies

final.contigs

relocations
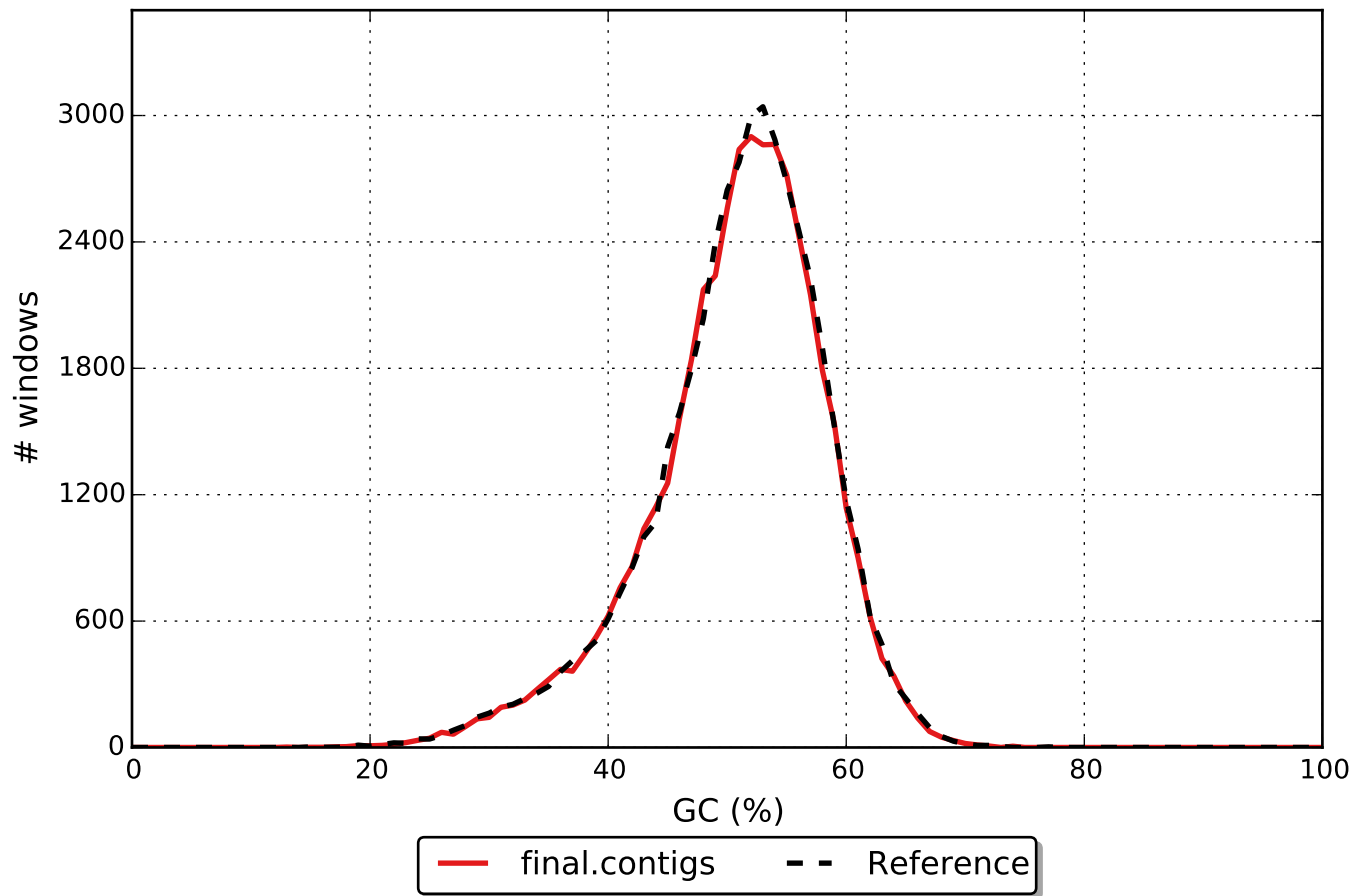
Cumulative length (aligned contigs)

NGAx