Report

|	final.contigs
# contigs (>= 0 bp)	768
# contigs (>= 1000 bp)	486
Total length (>= 0 bp)	1268602
Total length (>= 1000 bp)	1066196
# contigs	768
Largest contig	9818
Total length	1268602
Reference length	641799
GC (%)	26.30
Reference GC (%)	26.30
N50	2059
NG50	3296
N75	1294
NG75	2506
L50	187
LG50	64
L75	386
LG75	120
# misassemblies	38
# misassembled contigs	38
Misassembled contigs length	89858
# local misassemblies	0
# unaligned contigs	1 + 3 part
Unaligned length	1828
Genome fraction (%)	96.277
Duplication ratio	2.050
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1934.44
# indels per 100 kbp	1.78
Largest alignment	9818
NA50	1984
NGA50	3194
NA75	1226
NGA75	2431
LA50	196
LGA50	66
LA75	405
LGA75	126

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	38
# relocations	38
# translocations	0
# inversions	0
# possibly misassembled contigs	2
# misassembled contigs	38
Misassembled contigs length	89858
# local misassemblies	0
# mismatches	11953
# indels	11
# short indels	10
# long indels	1
Indels length	24

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	894
# partially unaligned contigs	3
# with misassembly	0
# both parts are significant	1
Partially unaligned length	934
# 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).
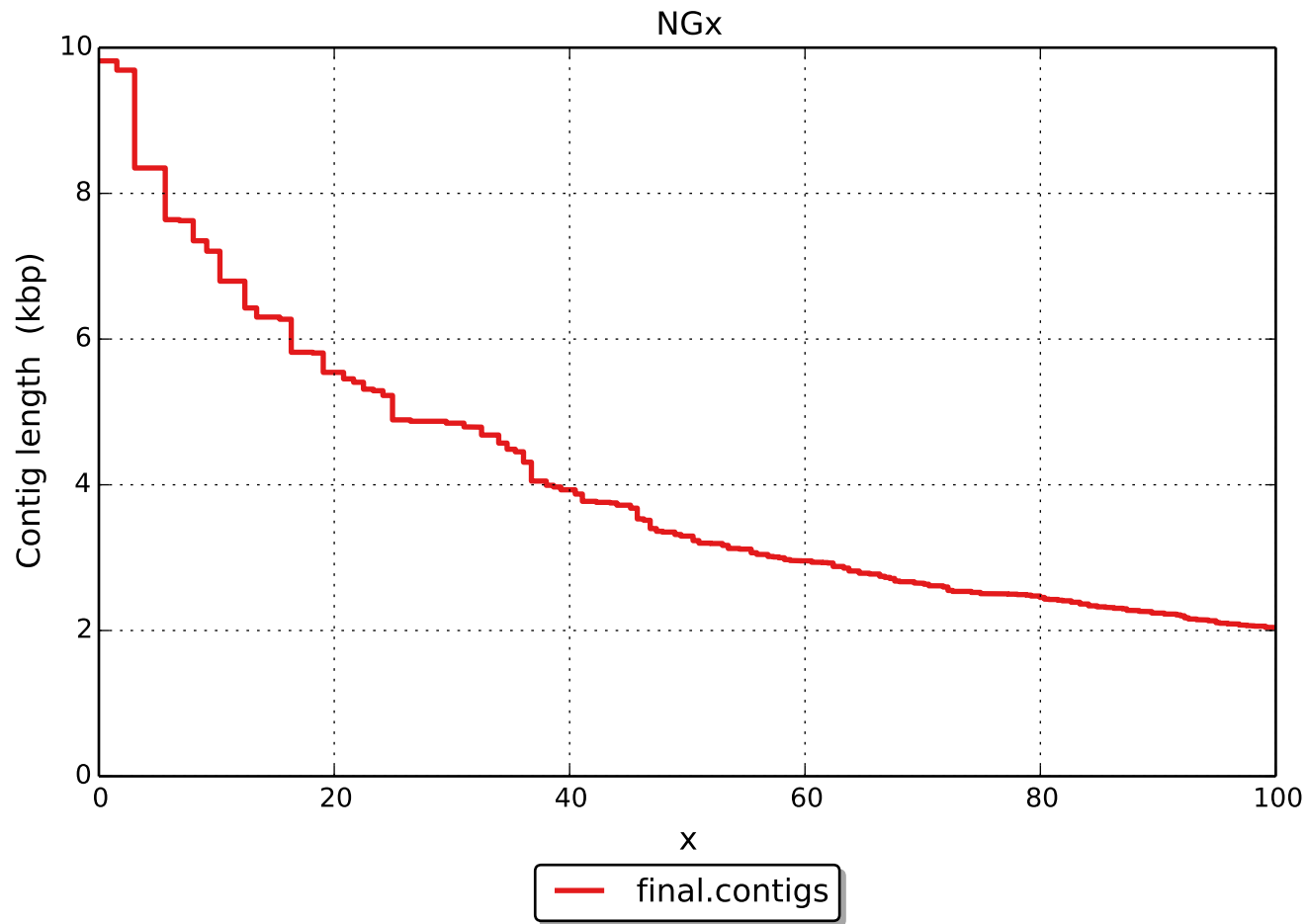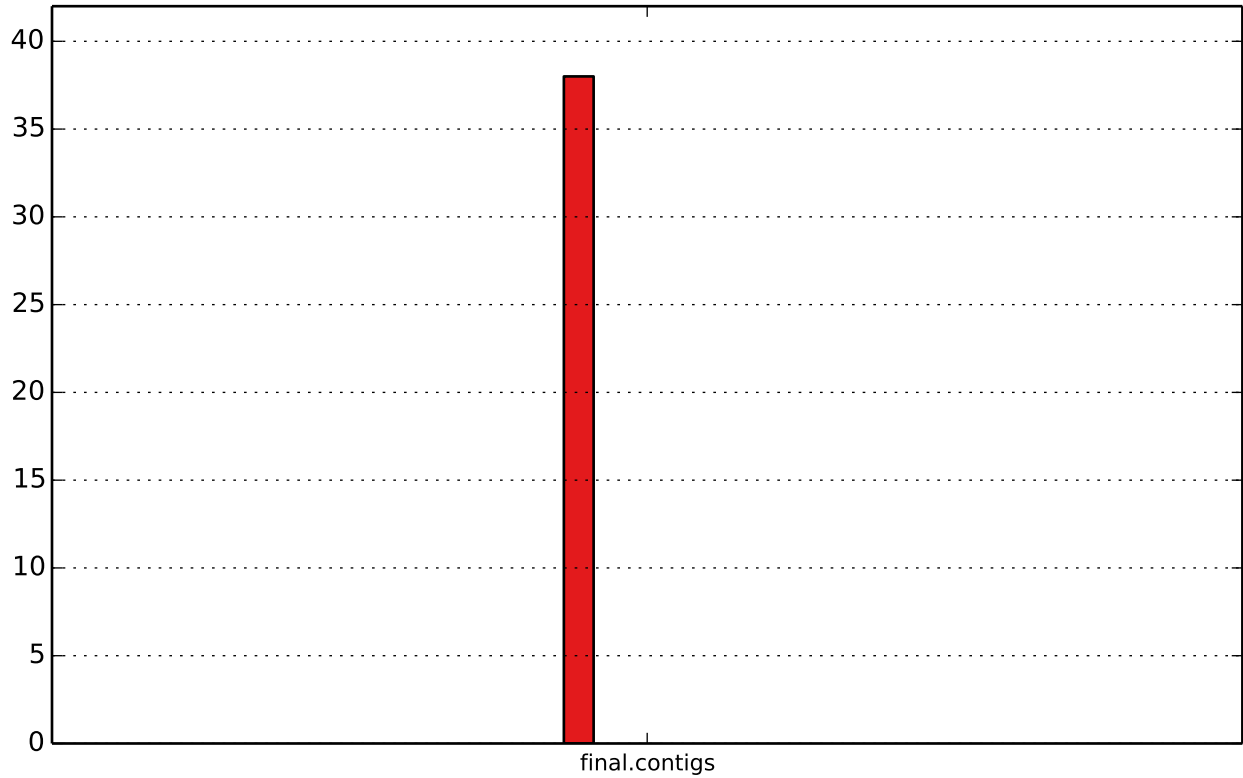
Cumulative length

GC content

Nx

Misassemblies

final.contigs

relocations
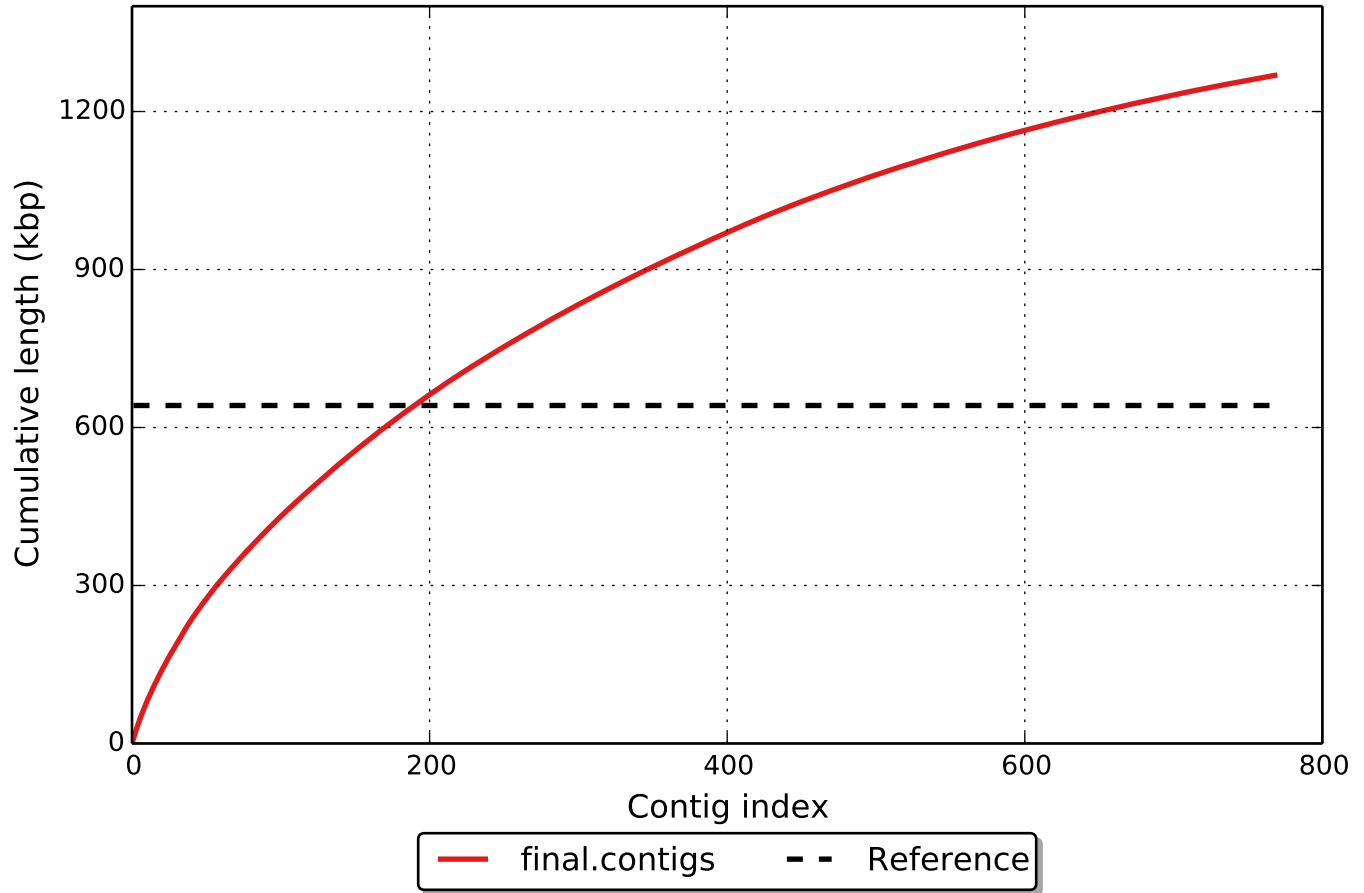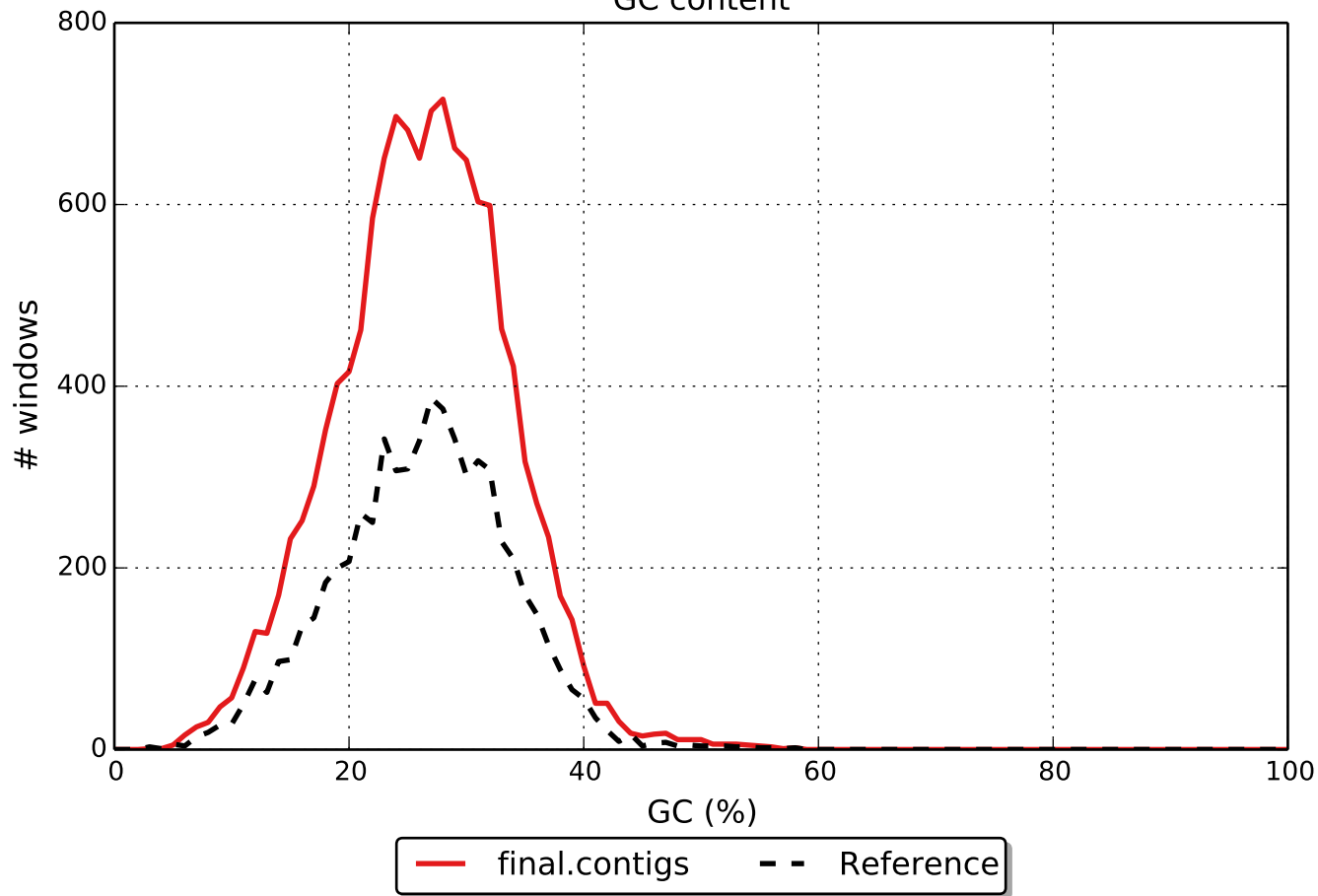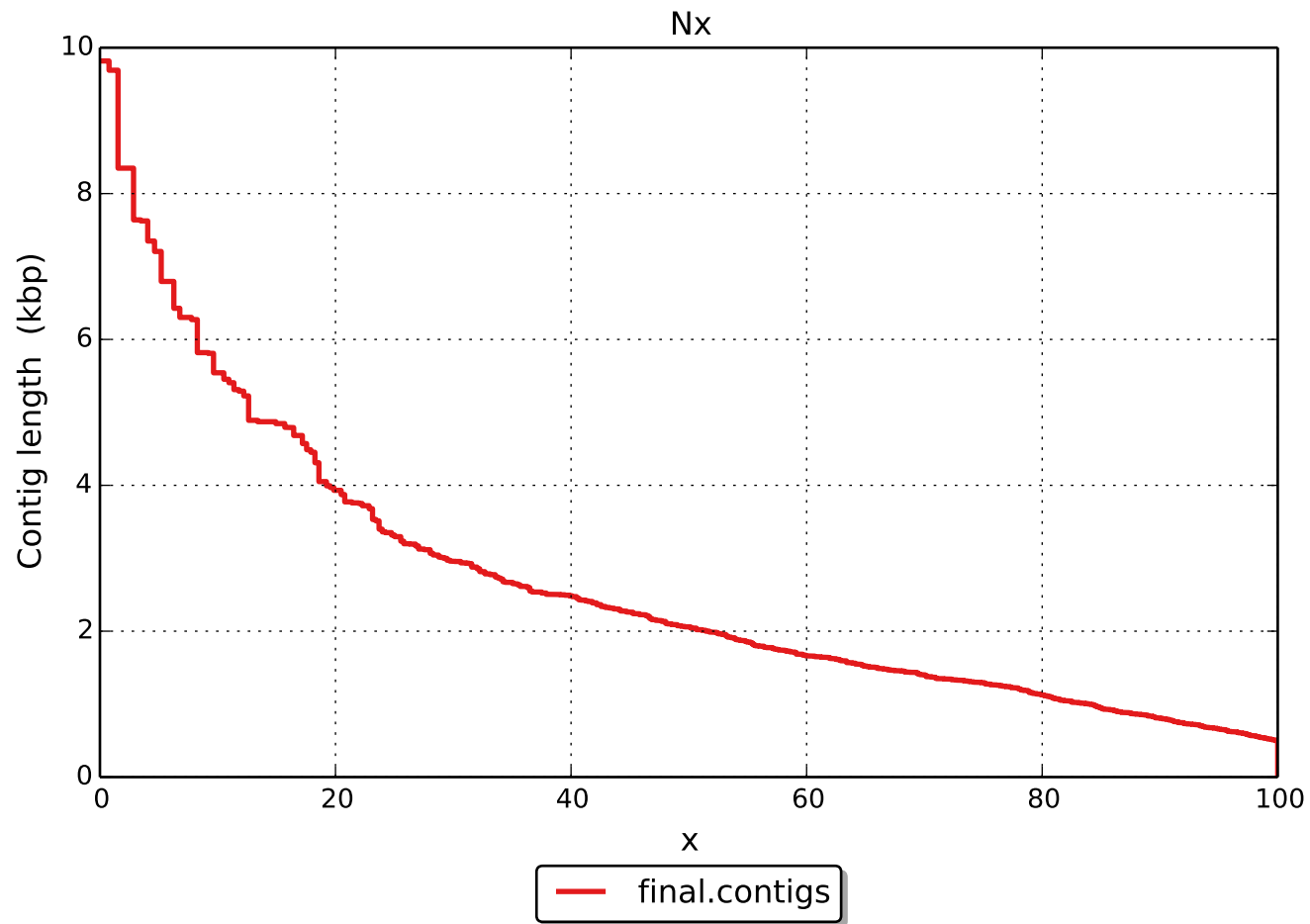
Cumulative length (aligned contigs)