Report

	final.contigs
# contigs (>= 1000 bp)	1498
# contigs (>= 5000 bp)	2
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	2255071
Total length (>= 5000 bp)	11412
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	4192
Largest contig	5936
Total length	4162906
Reference length	4641652
GC (%)	50.82
Reference GC (%)	50.78
N50	1056
NG50	982
N75	757
NG75	660
L50	1330
LG50	1565
L75	2500
LG75	3010
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	1094
# local misassemblies	2
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	83.958
Duplication ratio	1.068
# N's per 100 kbp	0.00
# mismatches per 100 kbp	177.21
# indels per 100 kbp	0.10
Largest alignment	5936
NA50	1056
NGA50	982
NA75	757
NGA75	660
LA50	1330
LGA50	1565
LA75	2500
LGA75	3010

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	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	1094
# local misassemblies	2
# mismatches	6906
# indels	4
# short indels	4
# long indels	0
Indels length	4

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
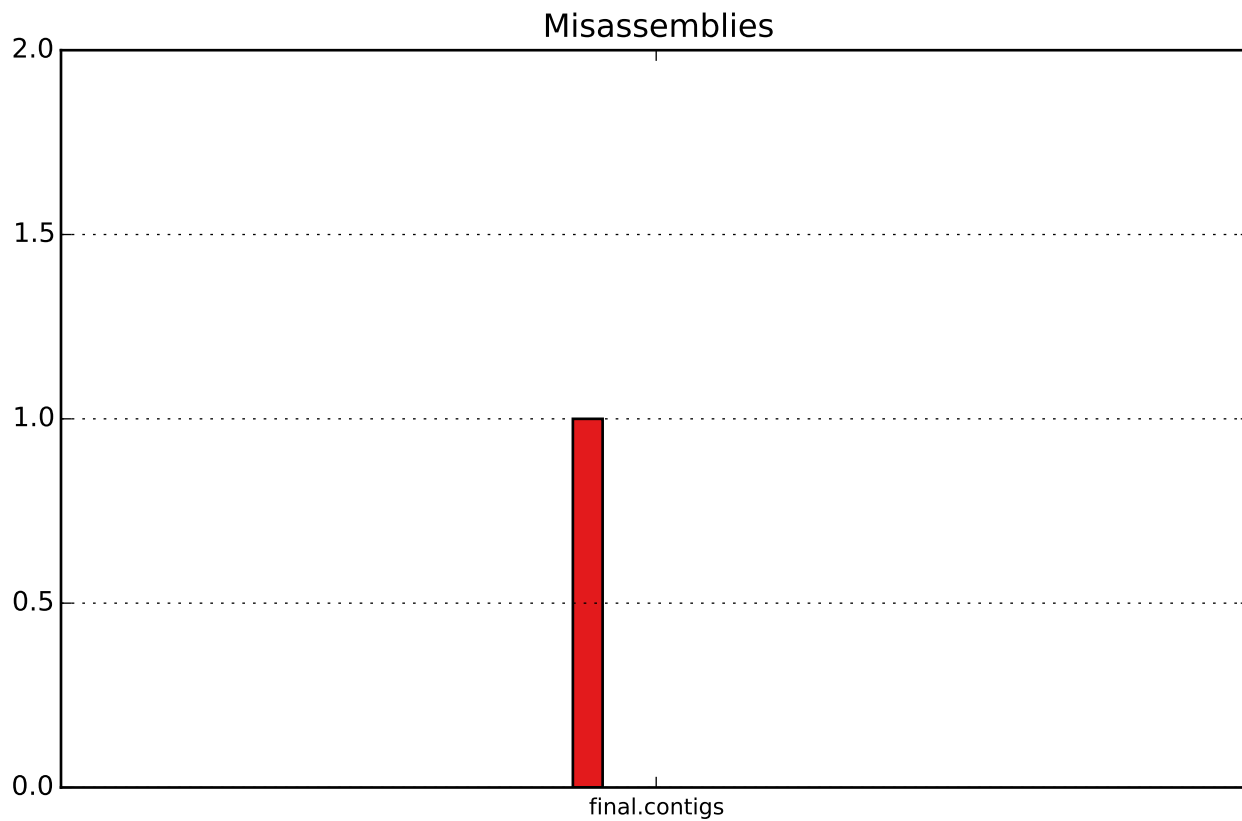(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

NGx

final.contigs

Cumulative length

GC content

Misassemblies

final.contigs

relocations
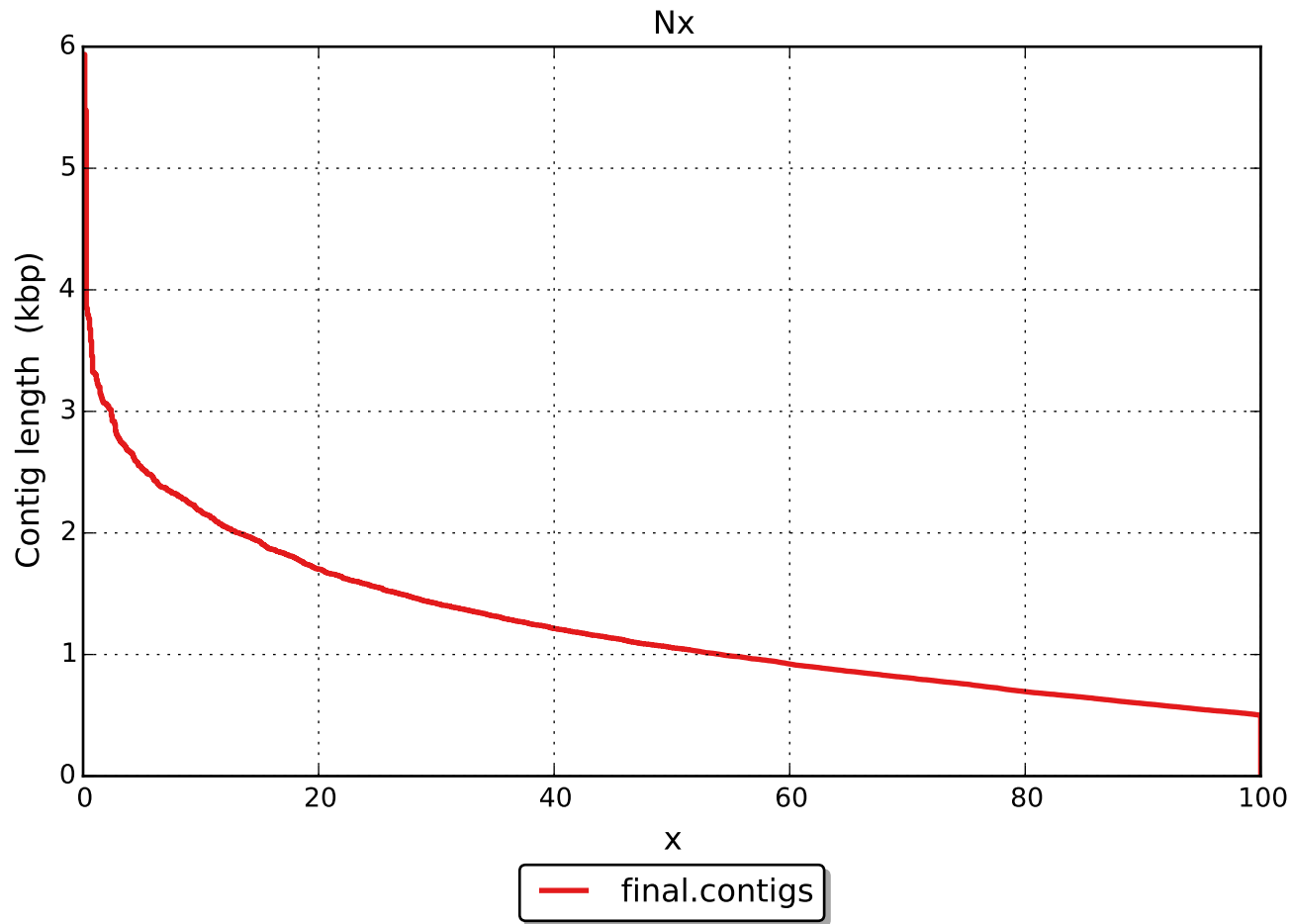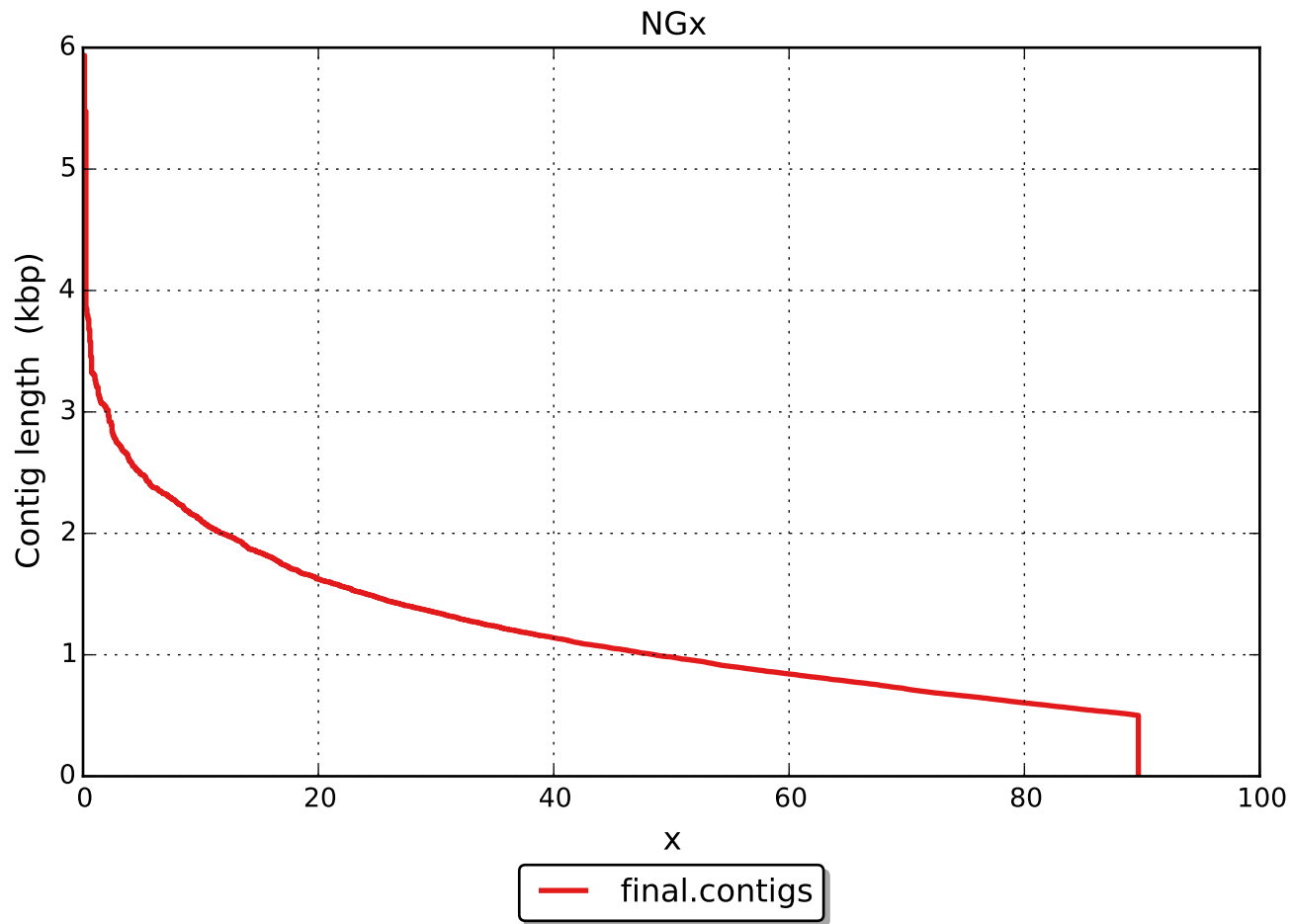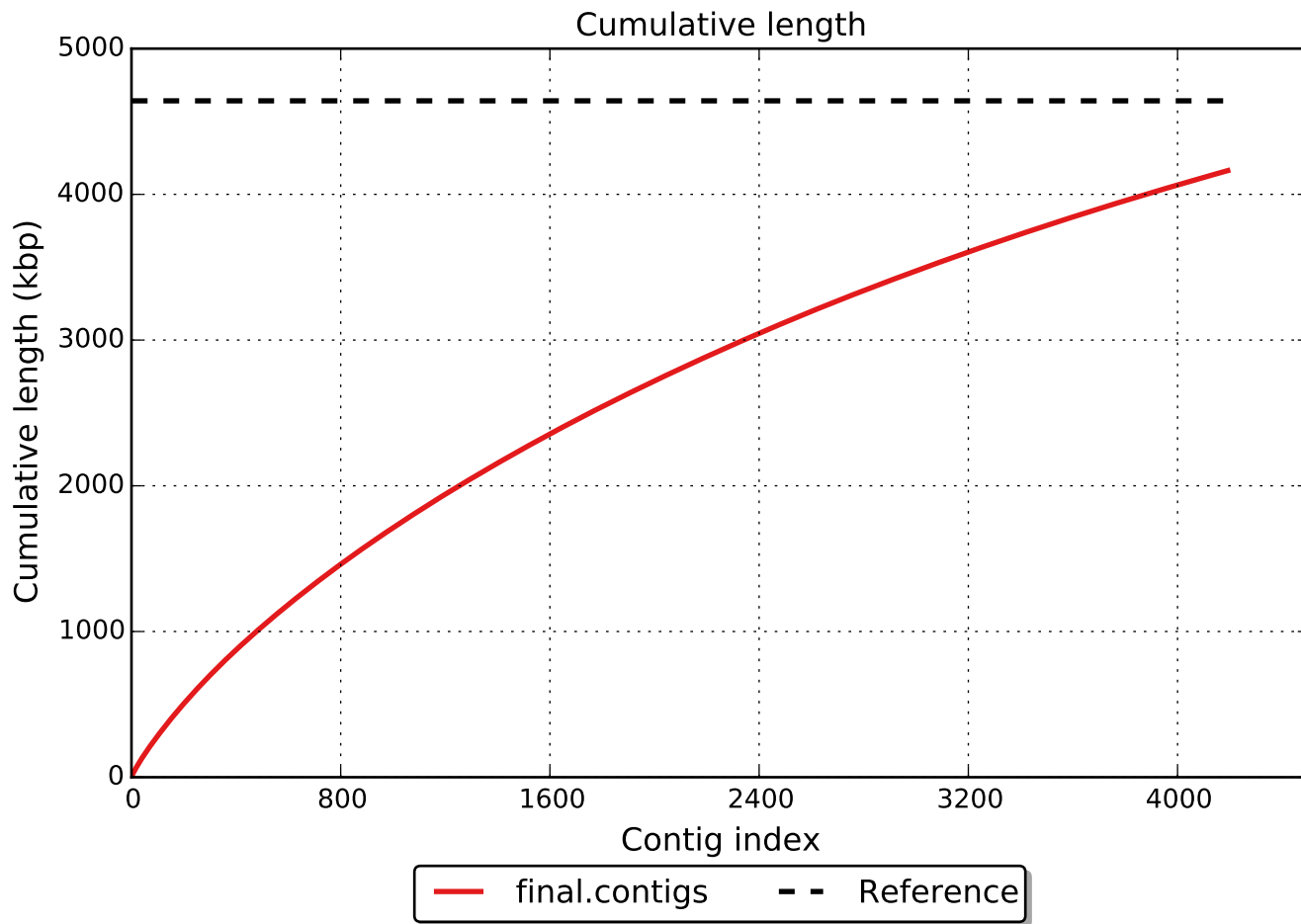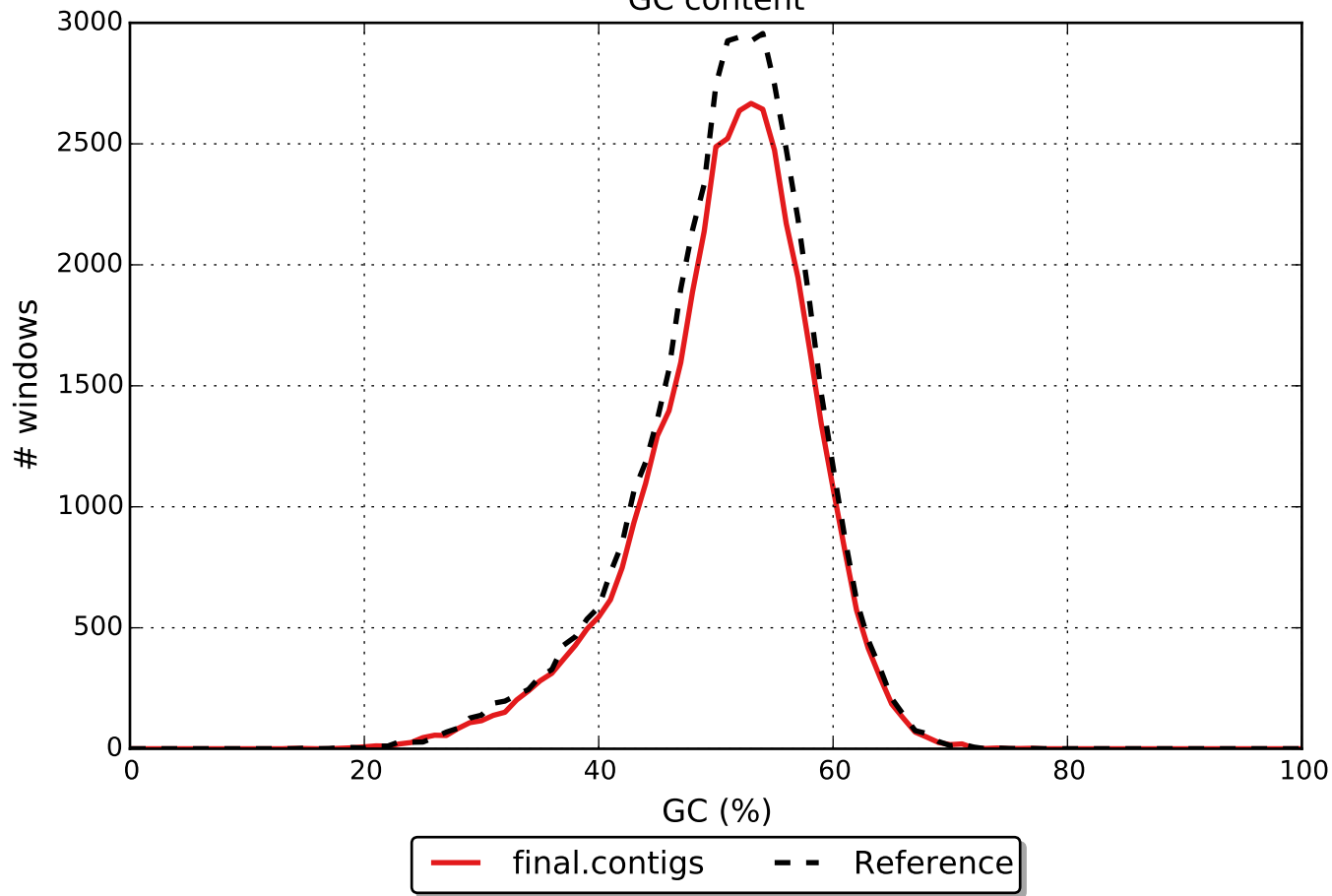
Cumulative length (aligned contigs)