Report

	final.contigs
# contigs (>= 1000 bp)	1725
# contigs (>= 5000 bp)	2
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	2821651
Total length (>= 5000 bp)	11285
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	3960
Largest contig	5697
Total length	4418030
Reference length	4857432
GC (%)	52.20
Reference GC (%)	52.22
N50	1235
NG50	1146
N75	836
NG75	732
L50	1173
LG50	1358
L75	2263
LG75	2683
# misassemblies	2
# misassembled contigs	2
Misassembled contigs length	4628
# local misassemblies	1
# unaligned contigs	0 + 1 part
Unaligned length	16
Genome fraction (%)	86.364
Duplication ratio	1.053
# N's per 100 kbp	0.00
# mismatches per 100 kbp	104.53
# indels per 100 kbp	0.05
Largest alignment	5697
NA50	1235
NGA50	1146
NA75	836
NGA75	732
LA50	1174
LGA50	1360
LA75	2264
LGA75	2684

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).
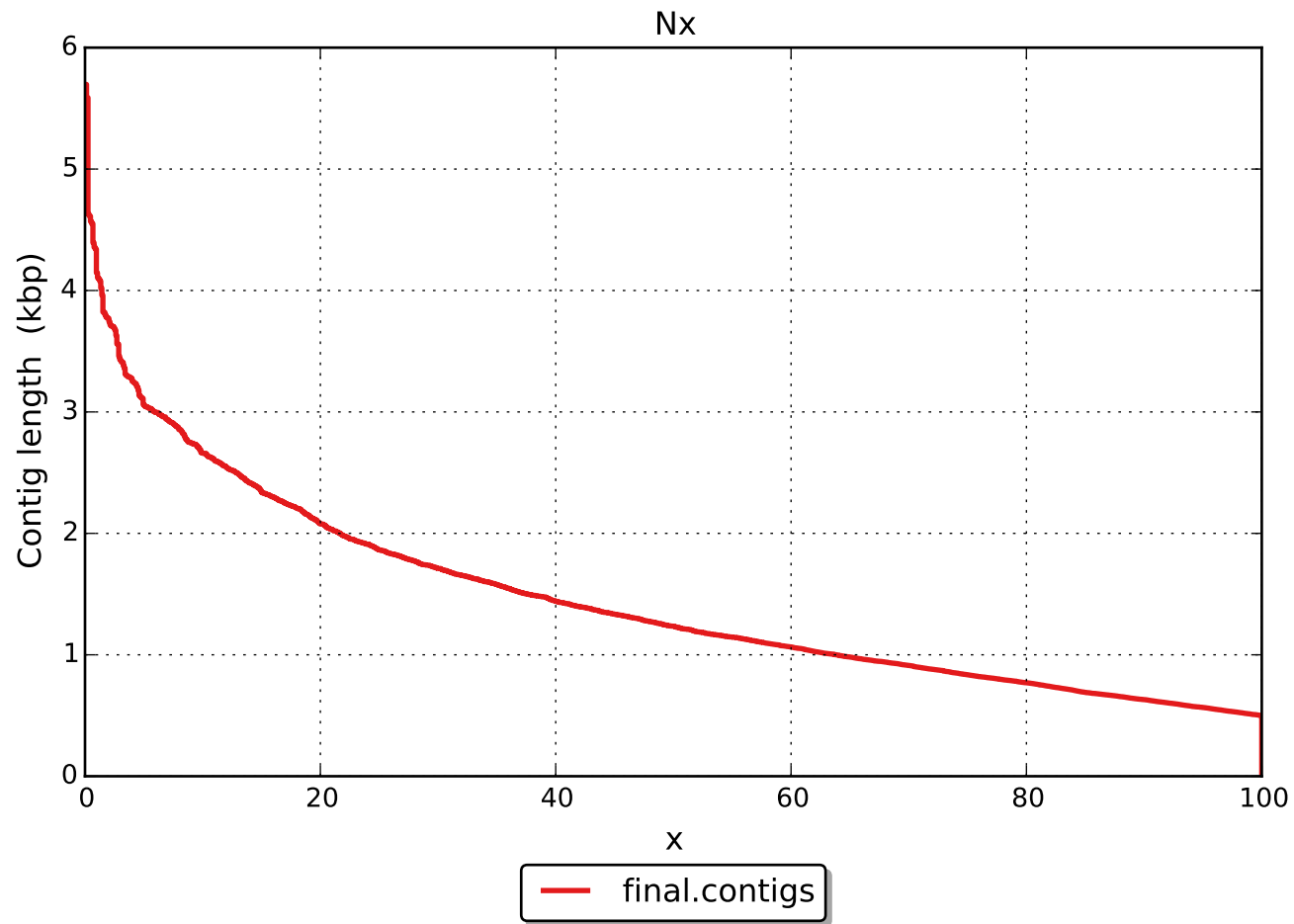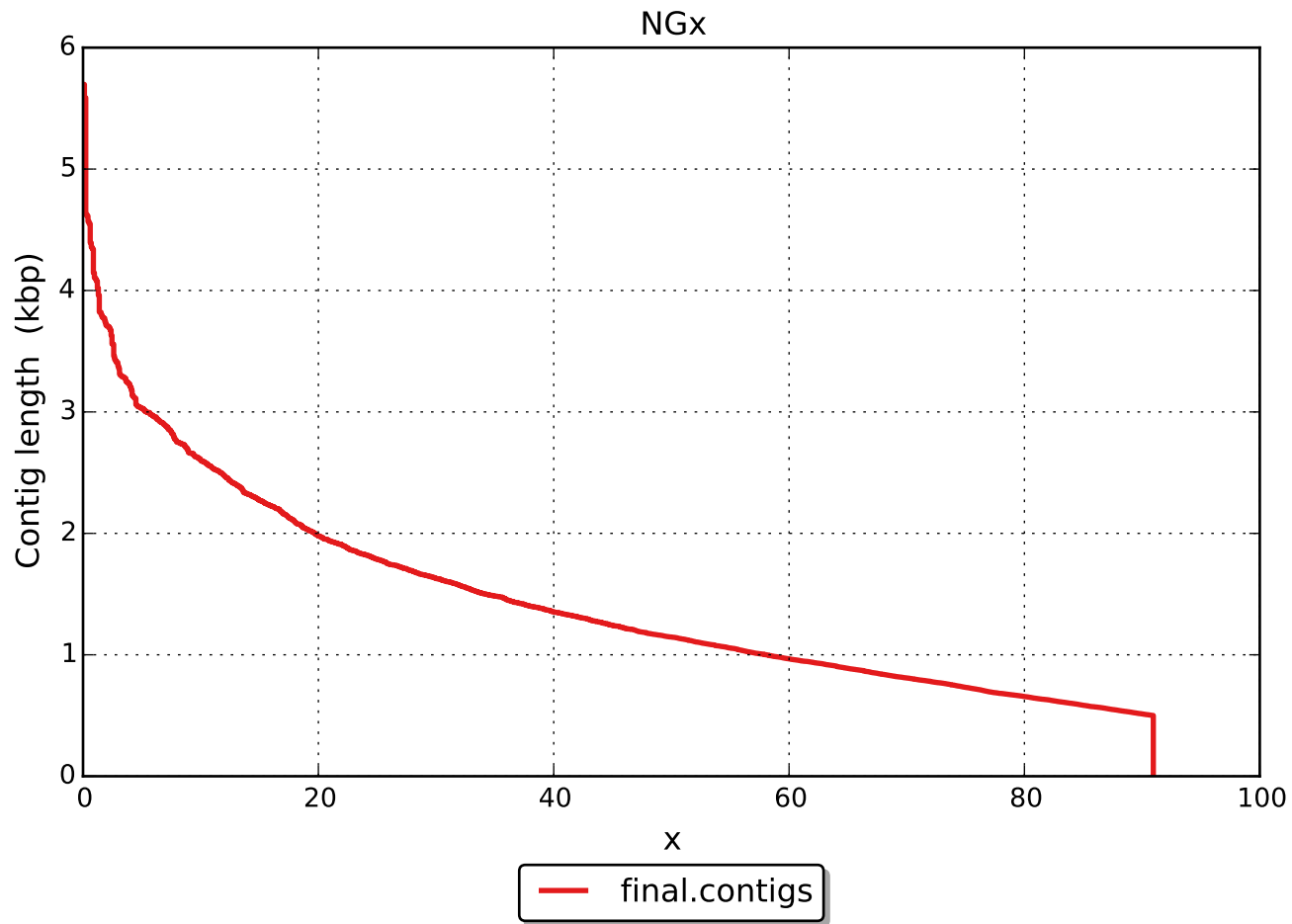
Misassemblies report

	final.contigs
# misassemblies	2
# relocations	2
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	2
Misassembled contigs length	4628
# local misassemblies	1
# mismatches	4385
# indels	2
# short indels	2
# long indels	0
Indels length	2

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).
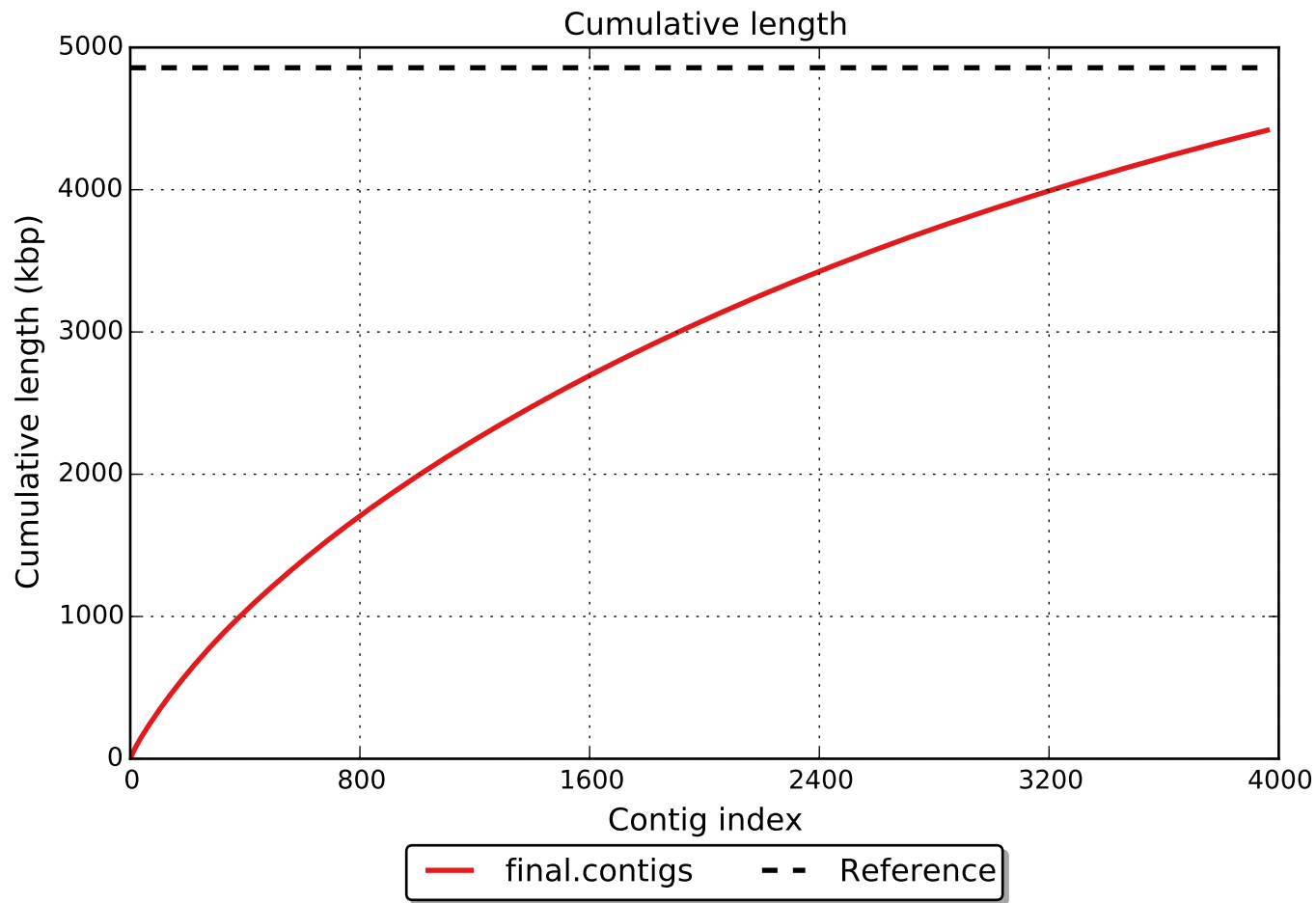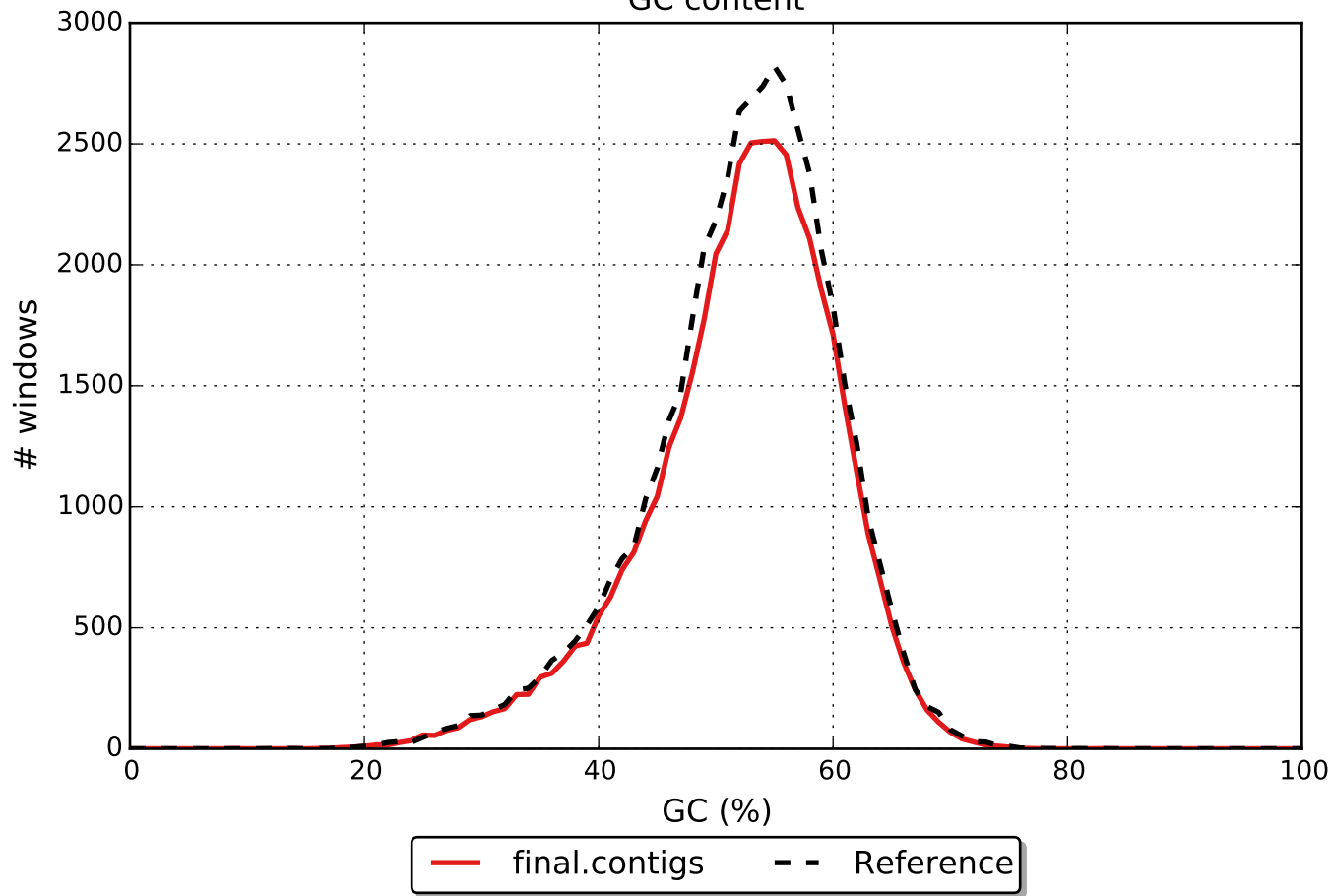
Unaligned report

	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	16
# N's	0

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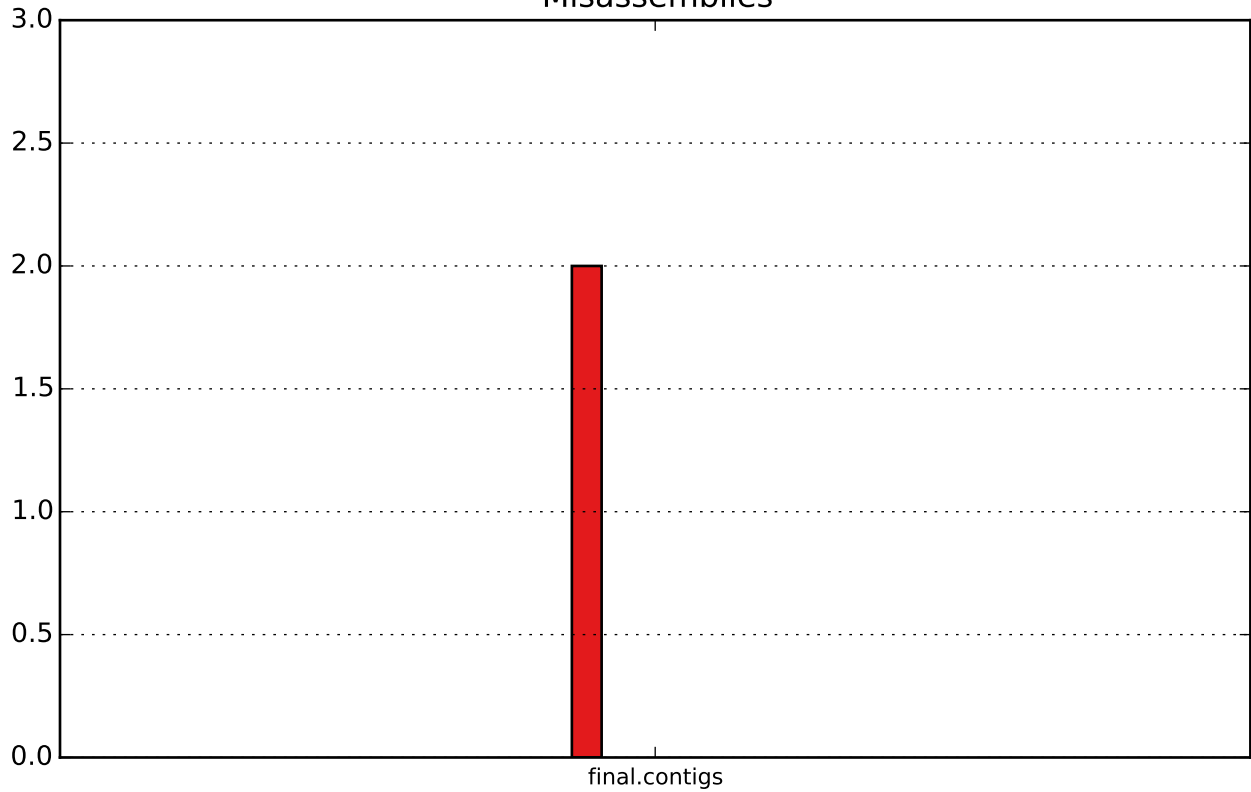(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Nx

Cumulative length

GC content

Cumulative length (aligned contigs)