Report

|	final.contigs
# contigs (>= 0 bp)	1067
# contigs (>= 1000 bp)	481
Total length (>= 0 bp)	1228210
Total length (>= 1000 bp)	802880
# contigs	1067
Largest contig	7521
Total length	1228210
Reference length	641799
GC (%)	26.31
Reference GC (%)	26.30
N50	1261
NG50	1916
N75	867
NG75	1503
L50	313
LG50	121
L75	608
LG75	217
# misassemblies	30
# misassembled contigs	30
Misassembled contigs length	48591
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	93.782
Duplication ratio	2.041
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1453.58
# indels per 100 kbp	1.33
Largest alignment	7521
NA50	1214
NGA50	1861
NA75	833
NGA75	1460
LA50	321
LGA50	124
LA75	625
LGA75	222

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	30
# relocations	30
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	30
Misassembled contigs length	48591
# local misassemblies	0
# mismatches	8749
# indels	8
# short indels	8
# long indels	0
Indels length	8

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).
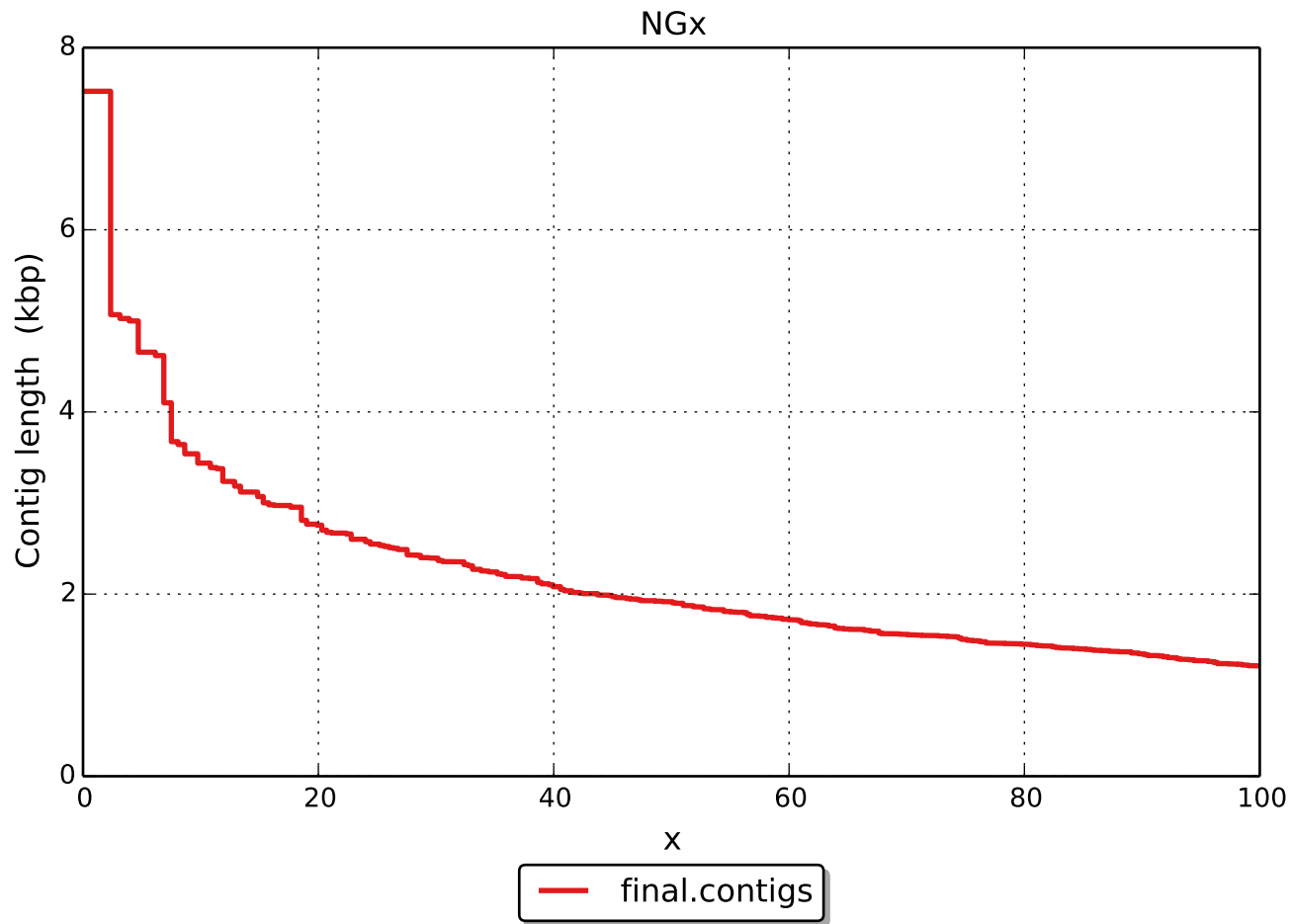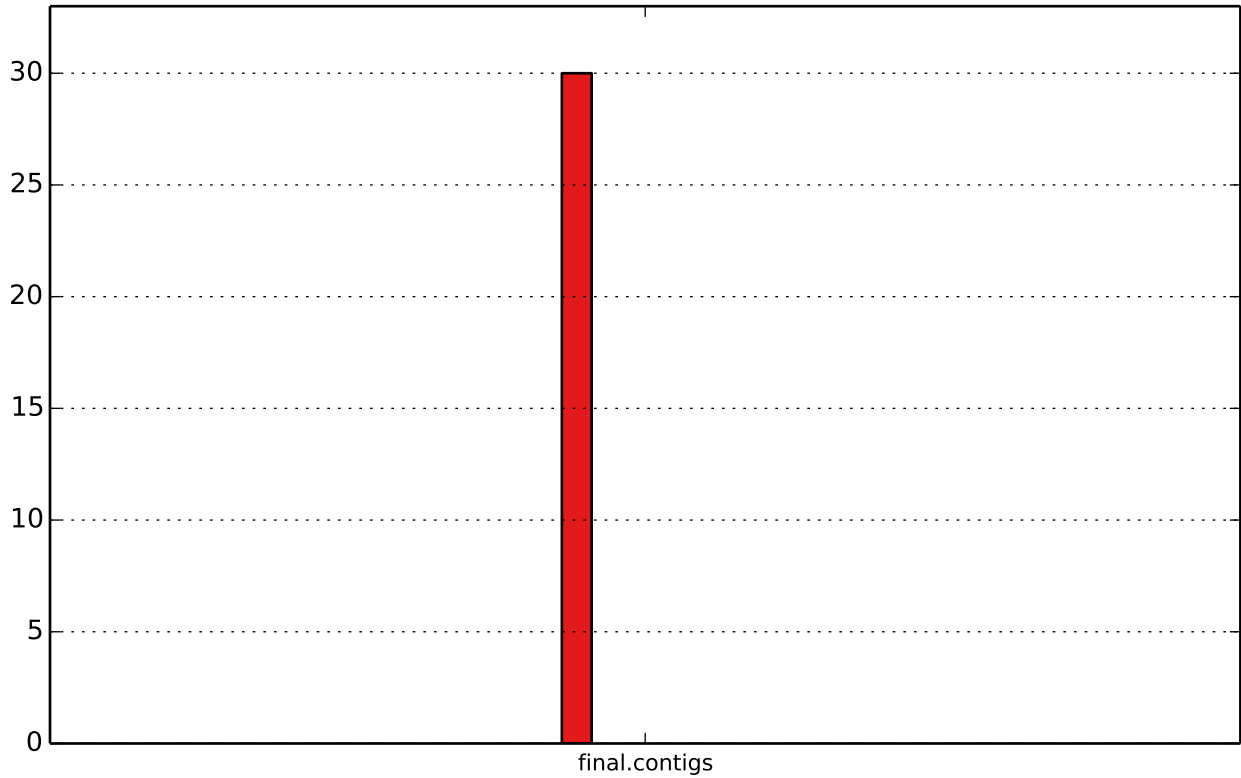
Cumulative length

Misassemblies

final.contigs

relocations
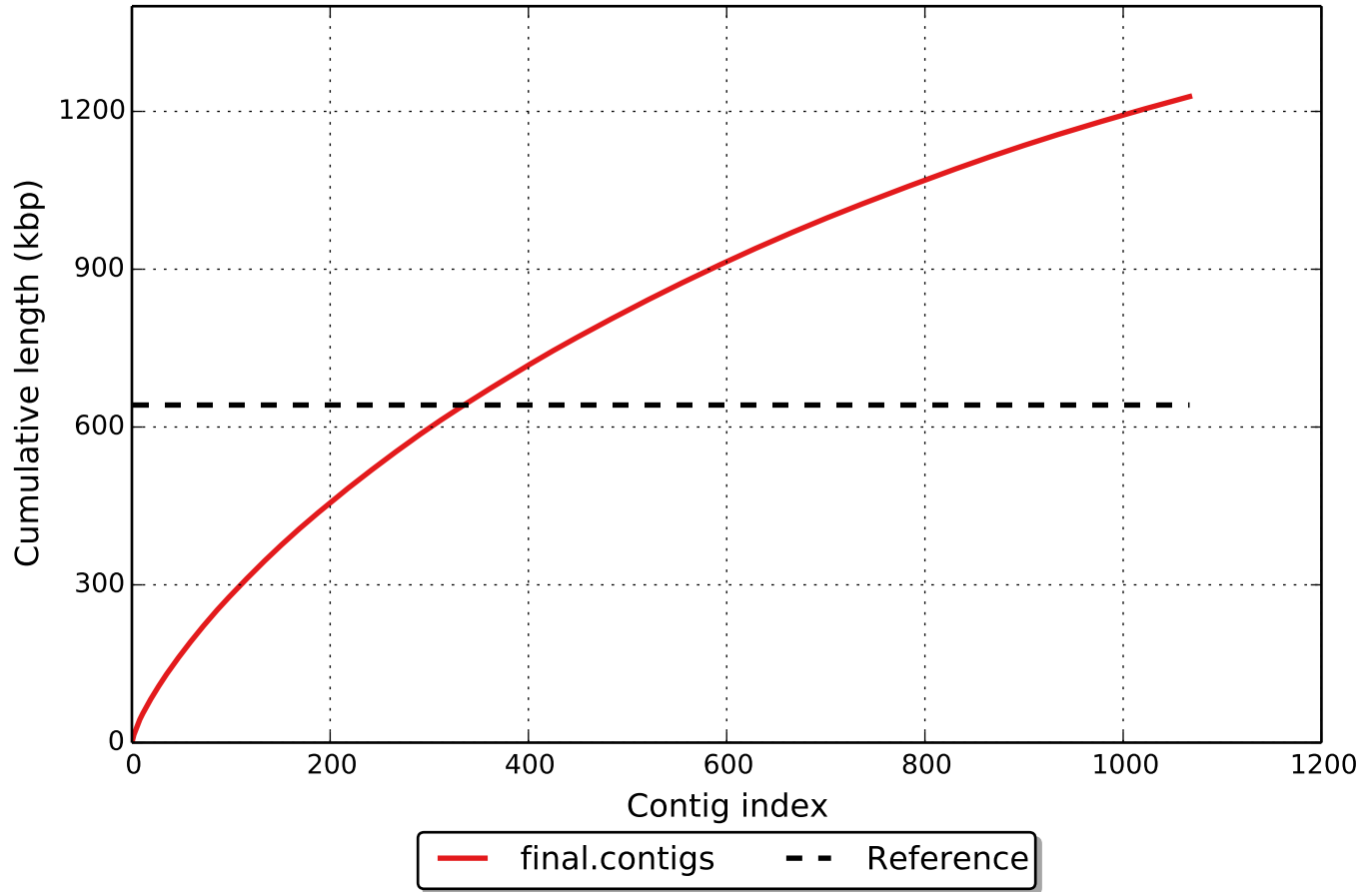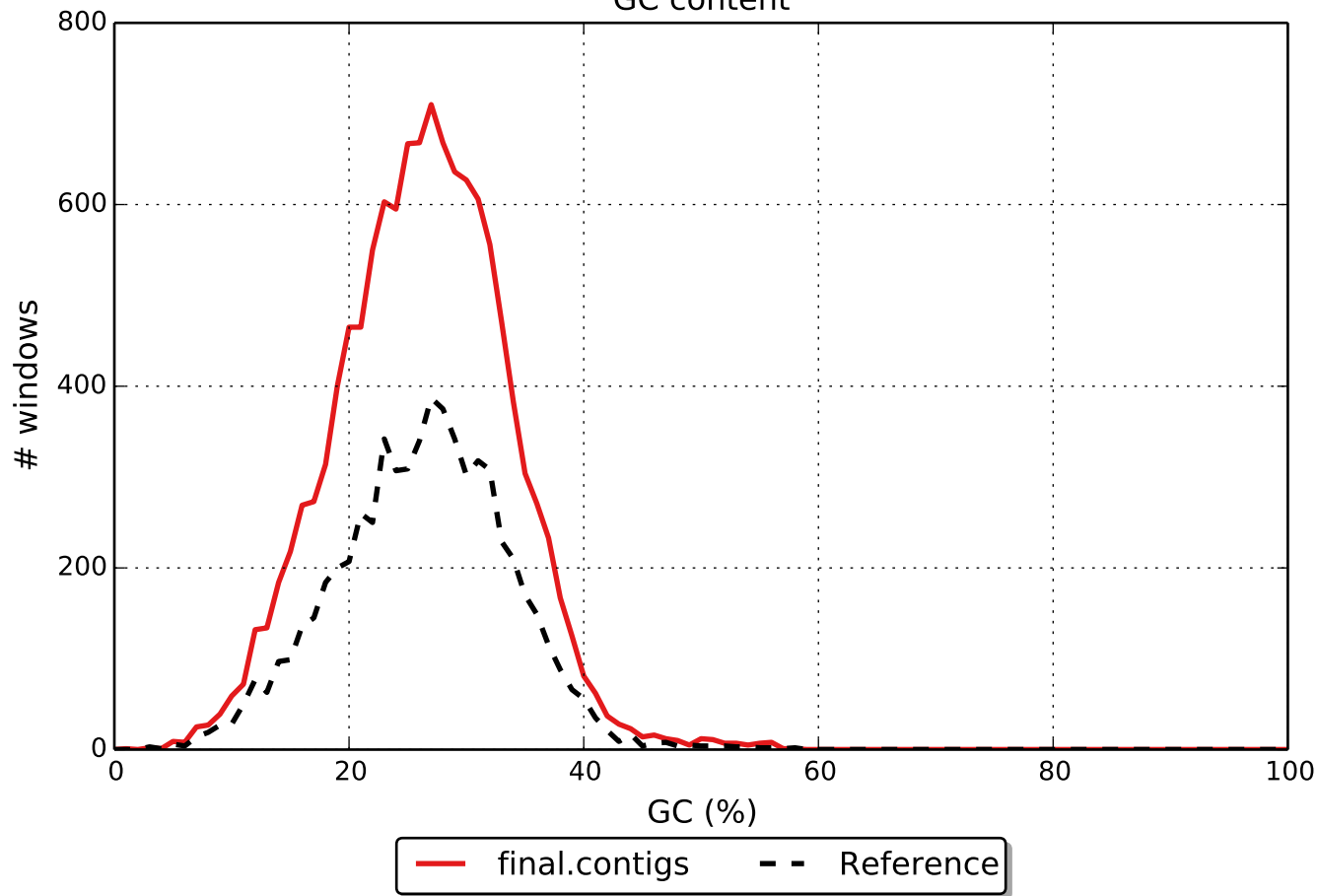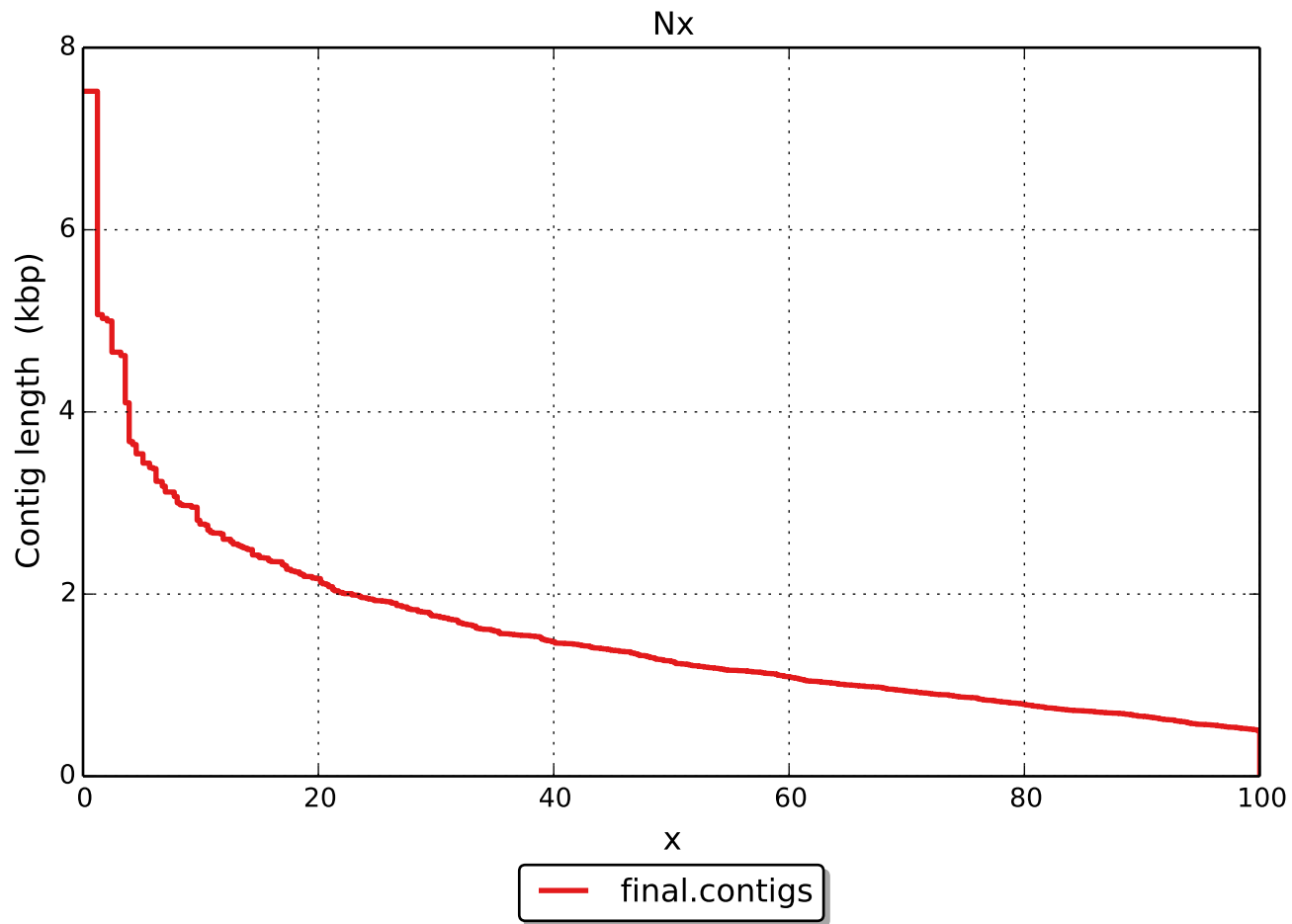
Cumulative length (aligned contigs)