Report

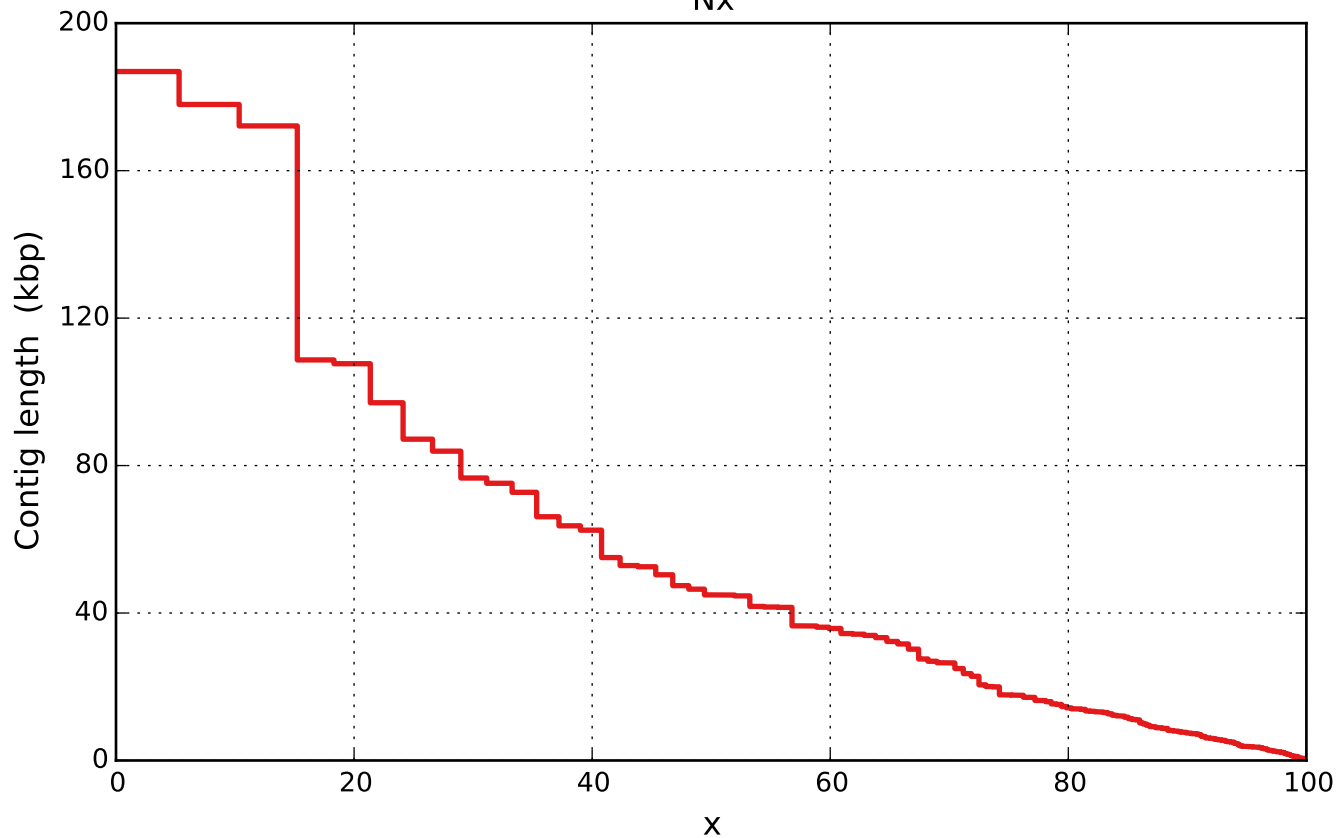|	contigs
# contigs (>= 1000 bp)	191
# contigs (>= 5000 bp)	115
# contigs (>= 10000 bp)	77
# contigs (>= 25000 bp)	41
# contigs (>= 50000 bp)	18
Total length (>= 1000 bp)	3500435
Total length (>= 5000 bp)	3310428
Total length (>= 10000 bp)	3042124
Total length (>= 25000 bp)	2484656
Total length (>= 50000 bp)	1648997
# contigs	231
Largest contig	186891
Total length	3525828
Reference length	4641652
GC (%)	50.86
Reference GC (%)	50.79
N50	44923
NG50	31609
N75	17761
NG75	1329
L50	21
LG50	36
L75	49
LG75	175
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	66116
# local misassemblies	3
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	74.323
Duplication ratio	1.022
# N's per 100 kbp	0.00
# mismatches per 100 kbp	995.83
# indels per 100 kbp	0.81
Largest alignment	186891
NA50	44923
NGA50	31609
NA75	17731
NGA75	1329
LA50	21
LGA50	36
LA75	50
LGA75	176

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

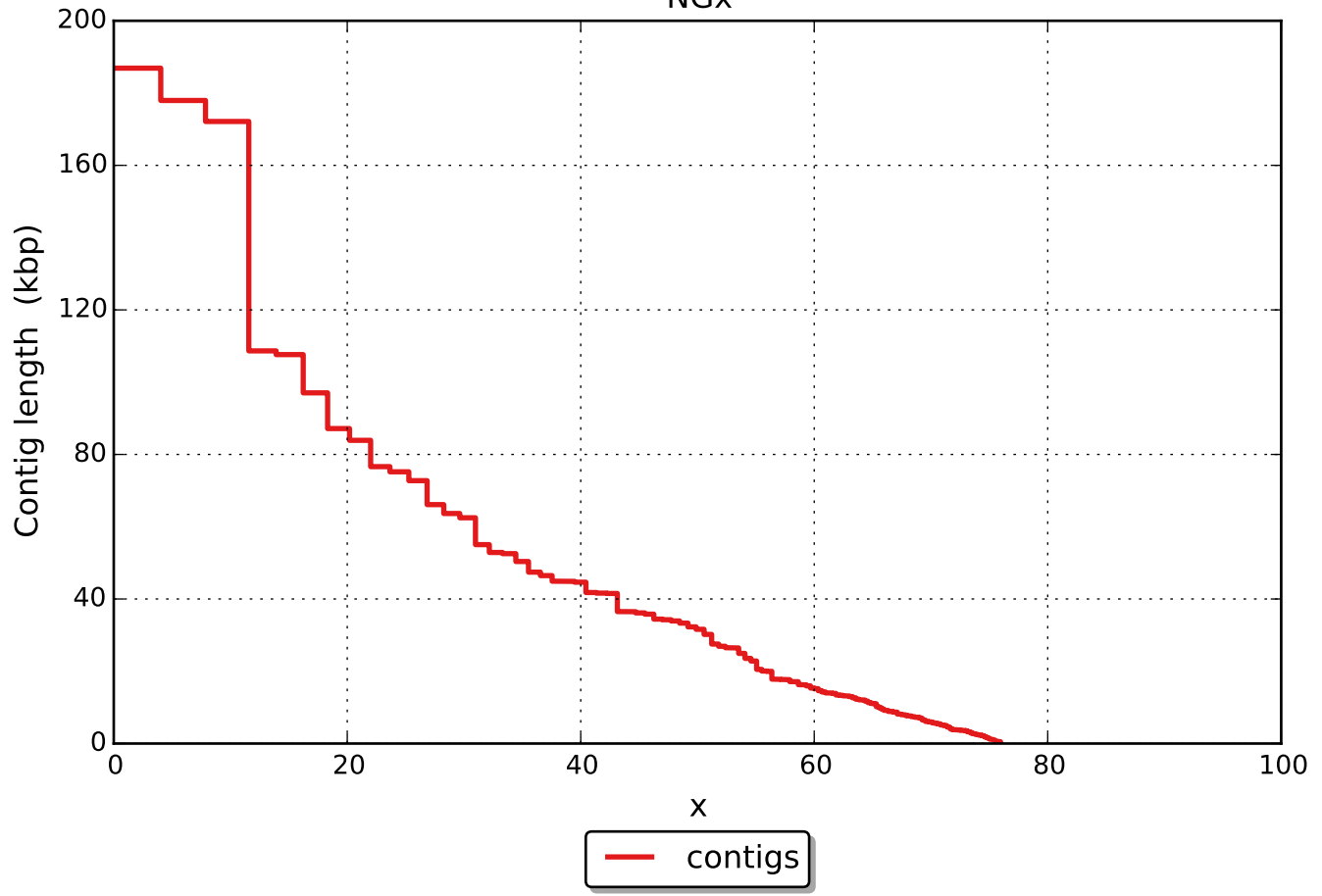|	contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	66116
# local misassemblies	3
# mismatches	34354
# indels	28
# short indels	28
# long indels	0
Indels length	34

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

	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).
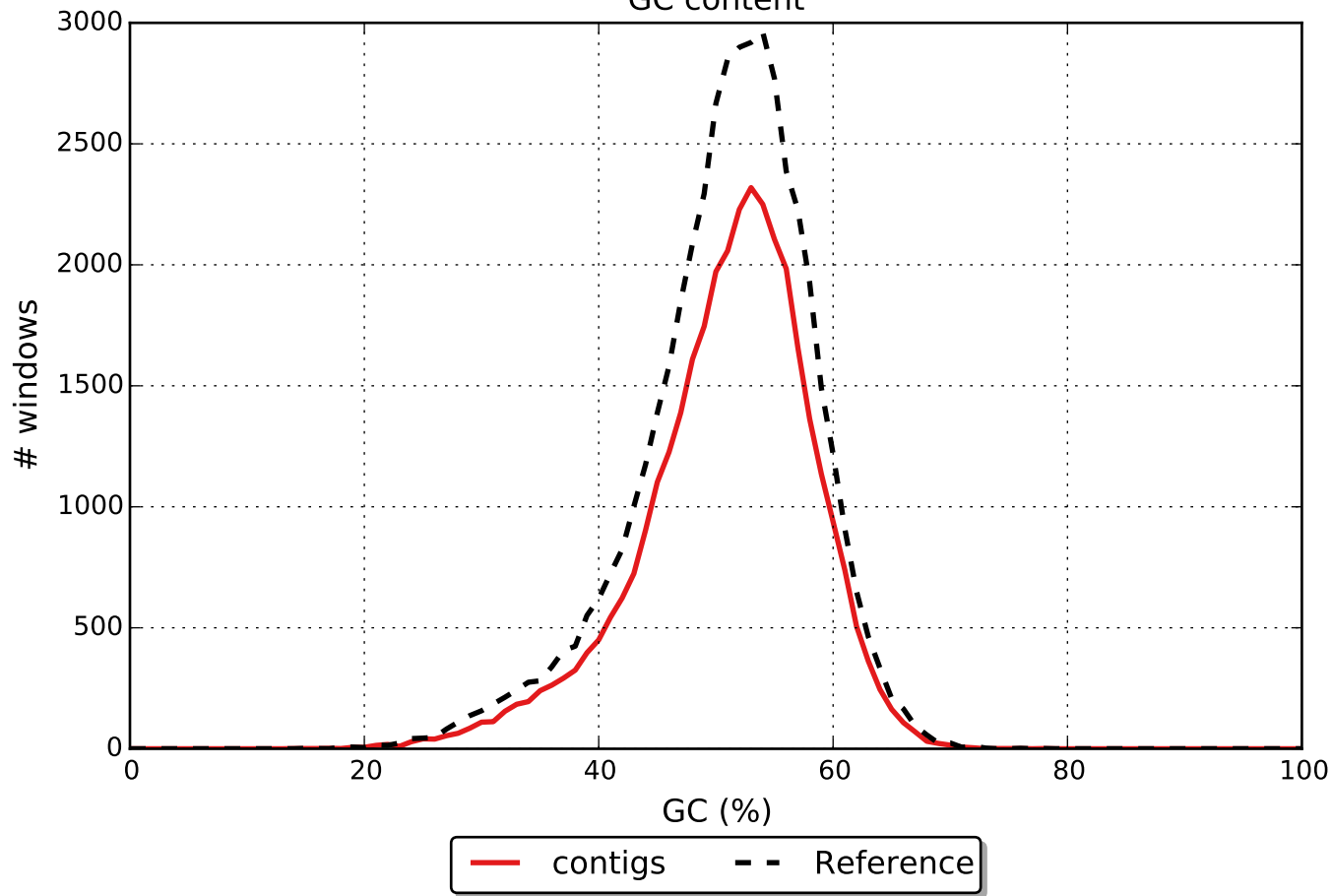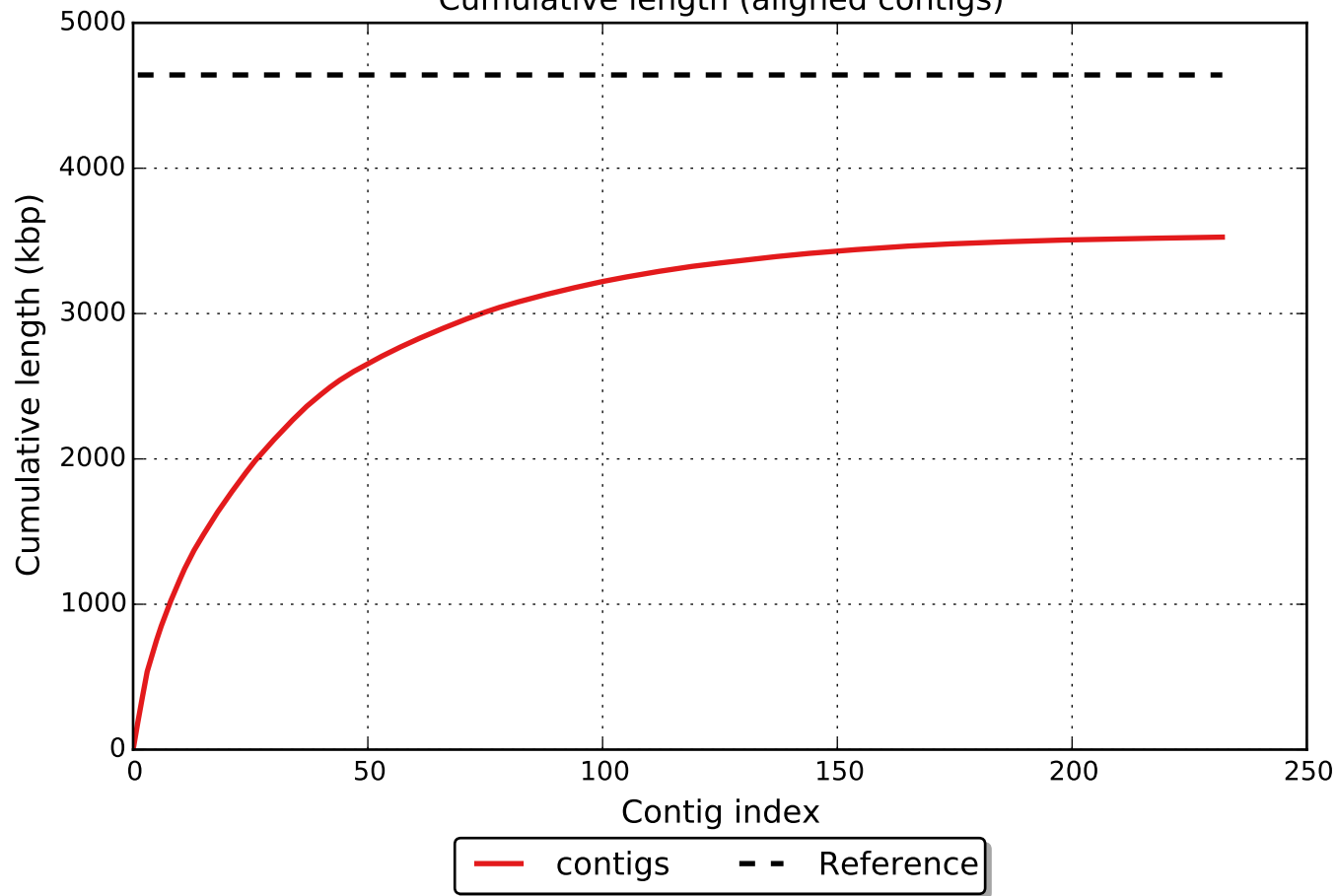
NGx

Cumulative length

GC content

windows

GC (%)

contigs — — Reference
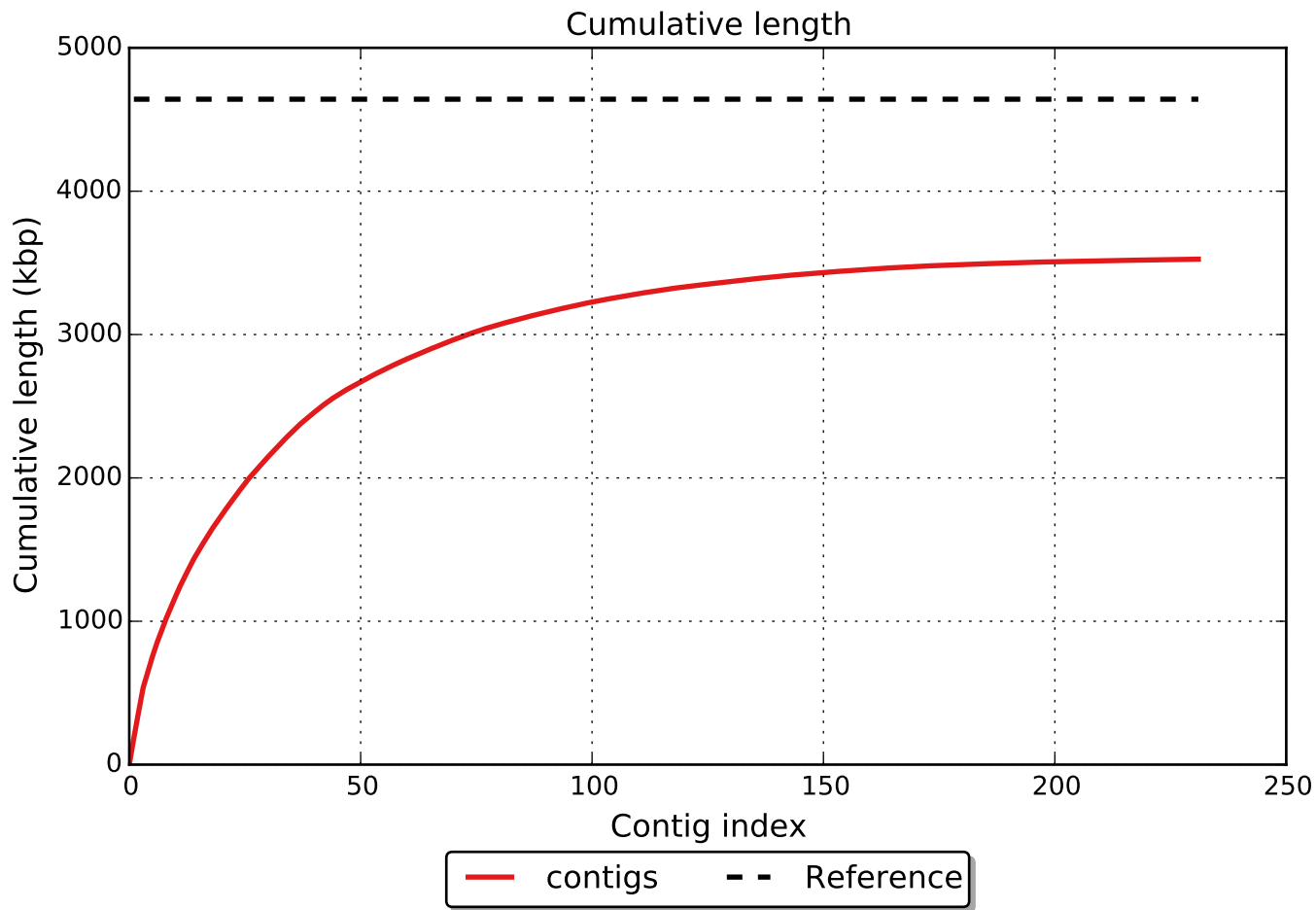
Cumulative length (aligned contigs)