Report

|	final.contigs
# contigs (>= 0 bp)	666
# contigs (>= 1000 bp)	423
Total length (>= 0 bp)	1270220
Total length (>= 1000 bp)	1134938
# contigs	558
Largest contig	11592
Total length	1232902
Reference length	1231960
GC (%)	25.33
Reference GC (%)	25.33
N50	2927
NG50	2927
N75	1757
NG75	1757
L50	137
LG50	137
L75	268
LG75	268
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	97.121
Duplication ratio	1.030
# N's per 100 kbp	0.00
# mismatches per 100 kbp	27.16
# indels per 100 kbp	0.00
Largest alignment	11592
NA50	2924
NGA50	2924
NA75	1757
NGA75	1757
LA50	137
LGA50	137
LA75	268
LGA75	268

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	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	325
# indels	0
# short indels	0
# long indels	0
Indels length	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).

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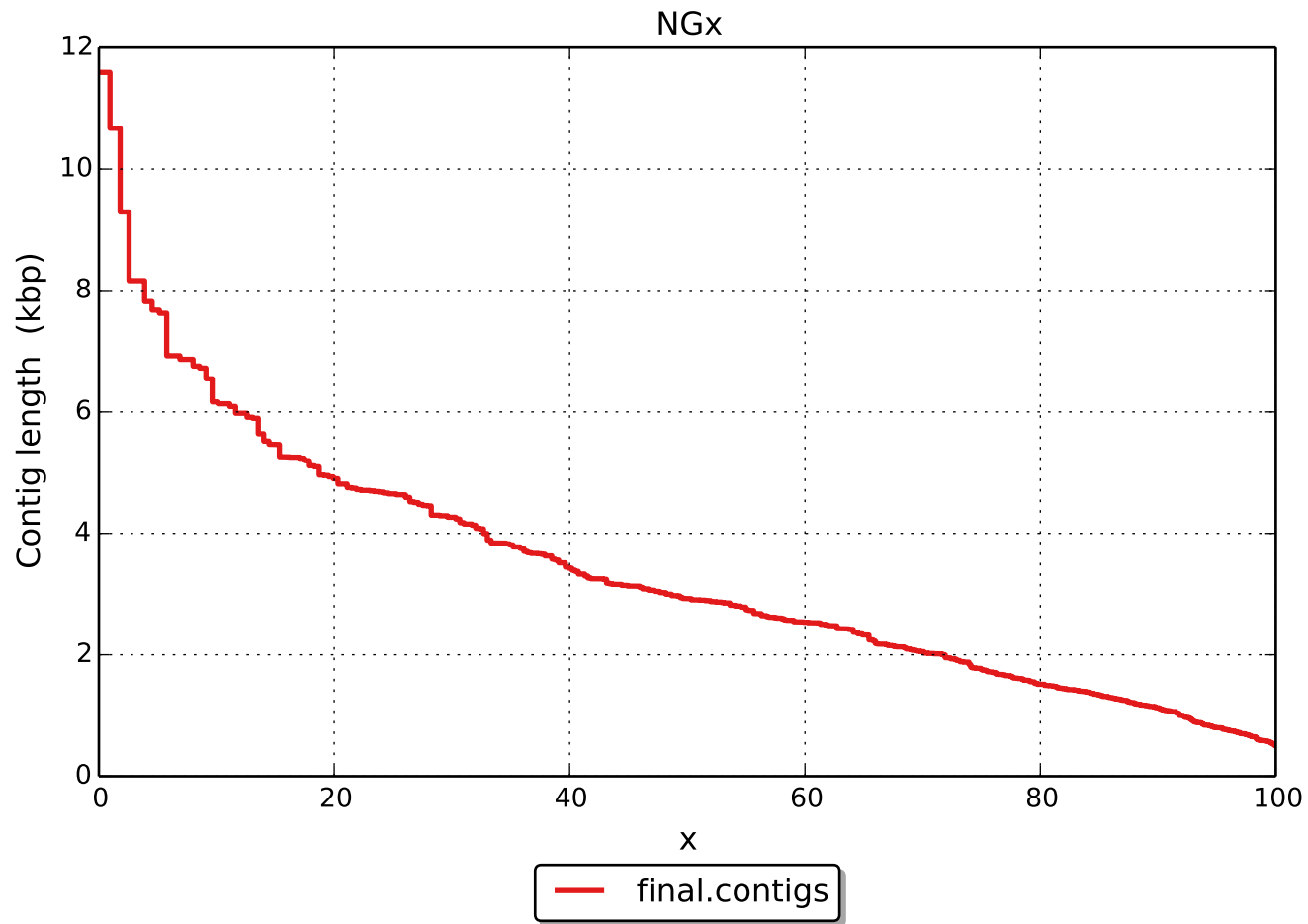(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Cumulative length
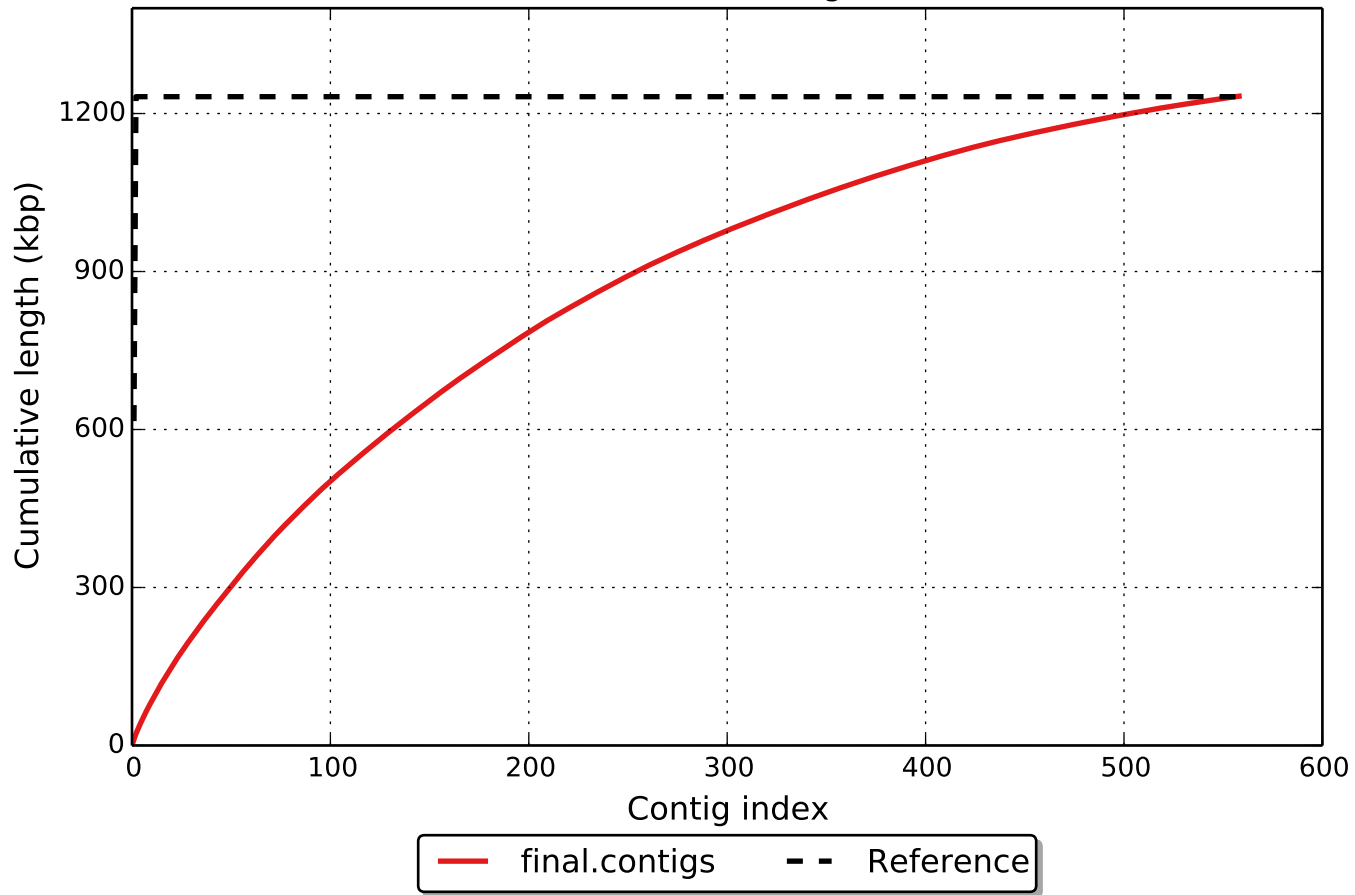
GC content

Misassemblies

final.contigs
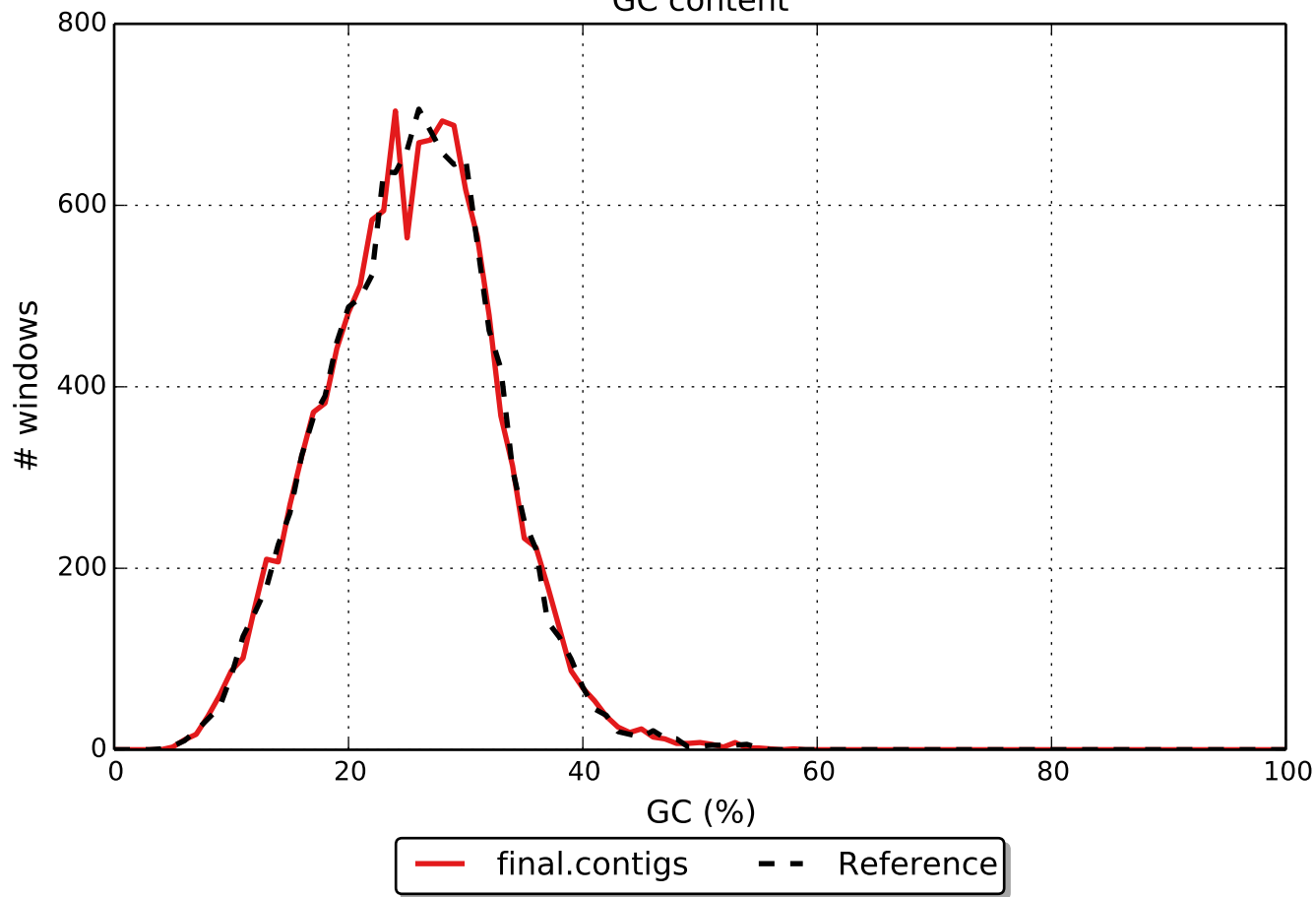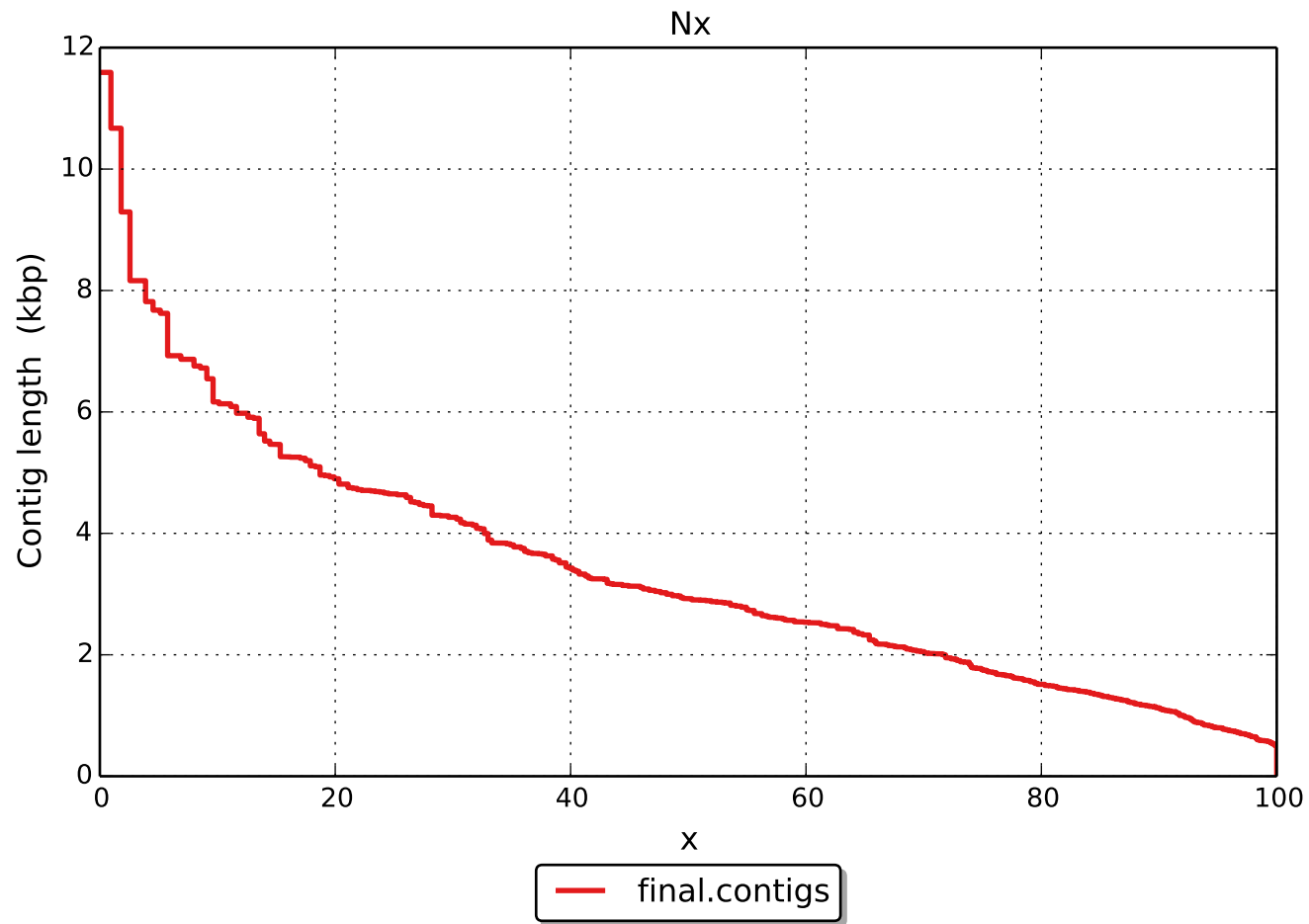
Cumulative length (aligned contigs)

NGAx