Report

	final.contigs
# contigs (>= 0 bp)	1626
# contigs (>= 1000 bp)	1349
Total length (>= 0 bp)	5624049
Total length (>= 1000 bp)	5414515
# contigs	1626
Largest contig	23946
Total length	5624049
Reference length	5547323
GC (%)	50.46
Reference GC (%)	50.49
N50	5182
NG50	5202
N75	2955
NG75	3058
L50	346
LG50	339
L75	702
LG75	683
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 1 part
Unaligned length	1459
Genome fraction (%)	98.861
Duplication ratio	1.025
# N's per 100 kbp	0.00
# mismatches per 100 kbp	28.26
# indels per 100 kbp	0.00
Largest alignment	23946
NA50	5182
NGA50	5202
NA75	2955
NGA75	3058
LA50	346
LGA50	339
LA75	702
LGA75	683

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).
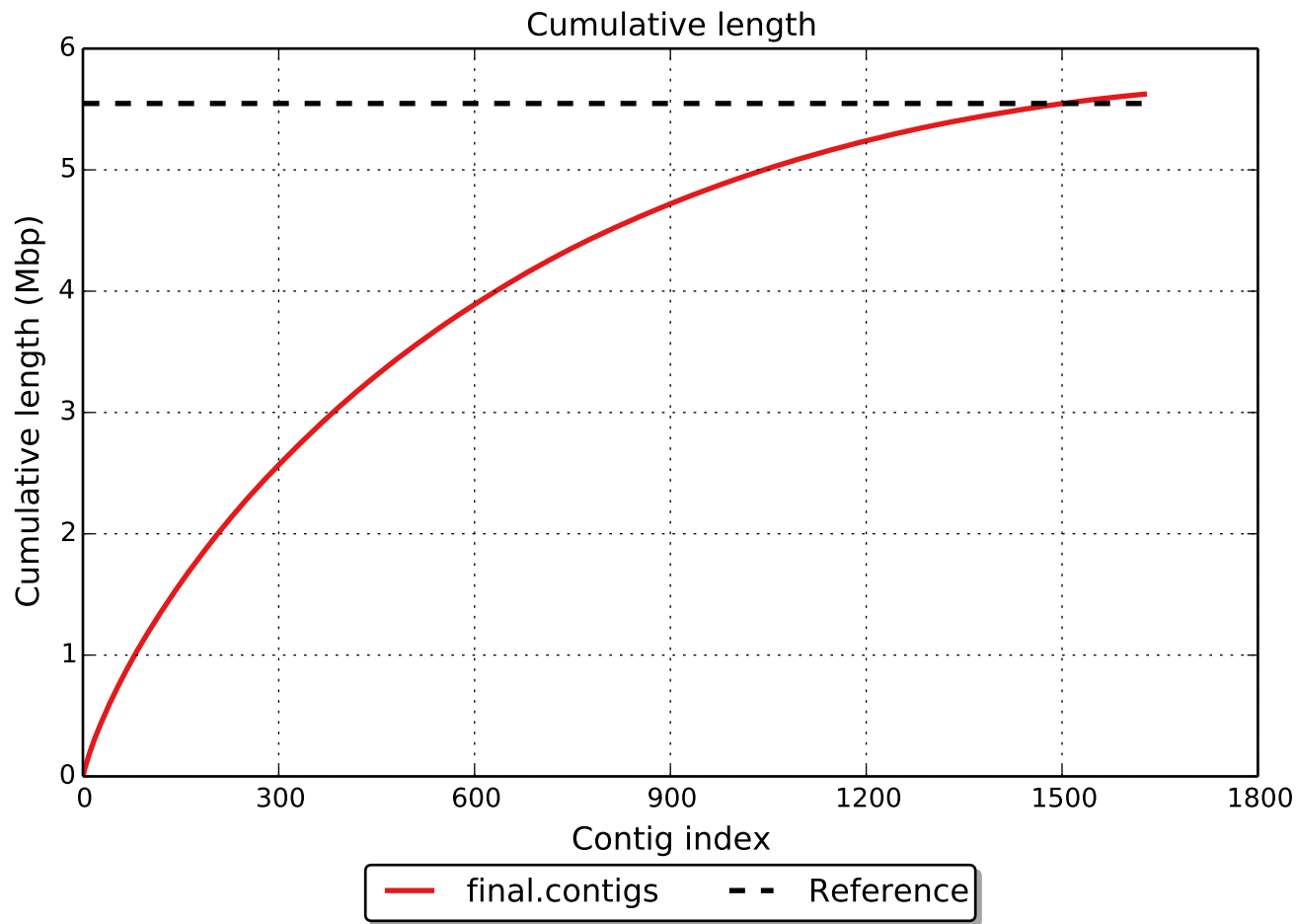
Misassemblies report

	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	1
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	1550
# 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
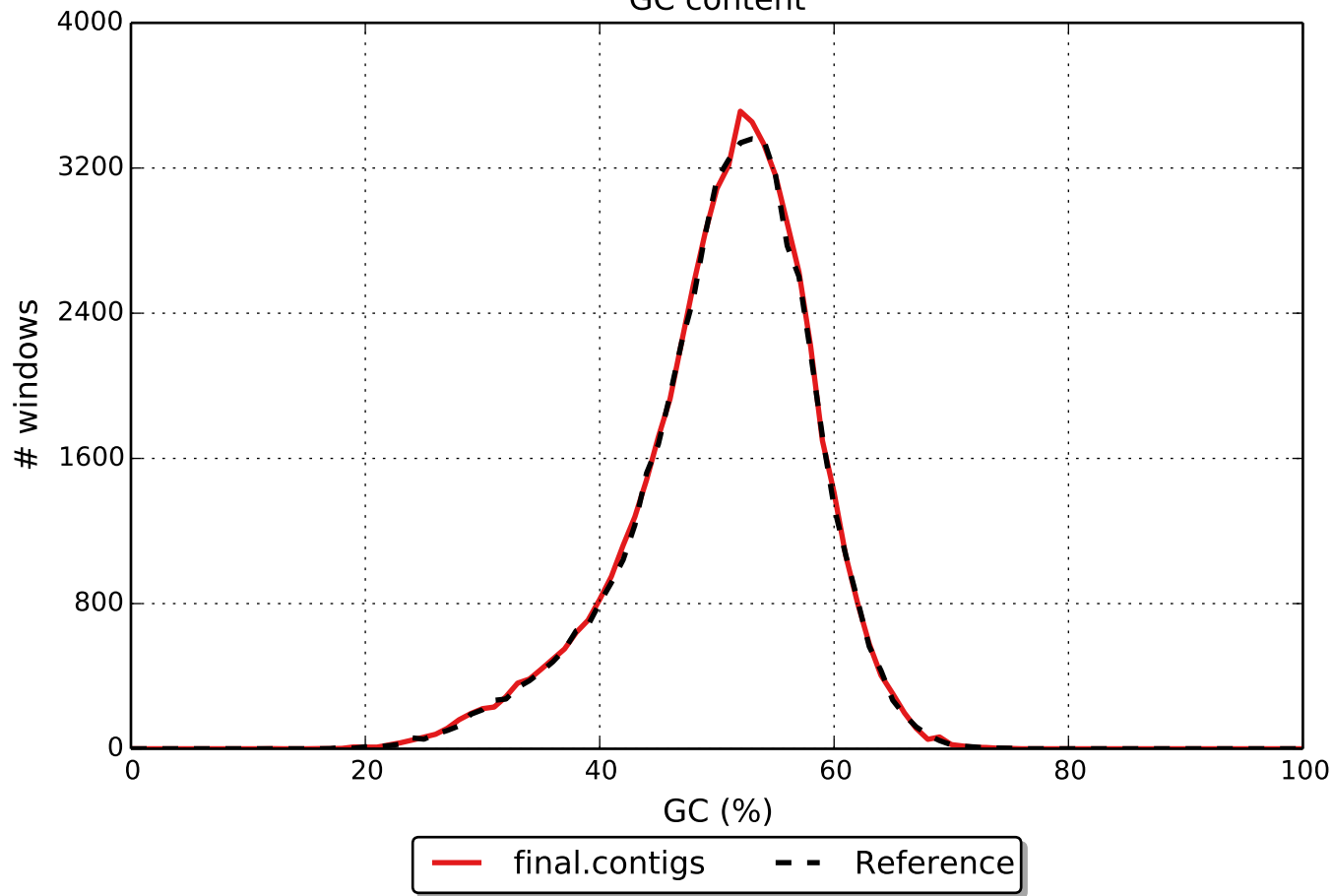
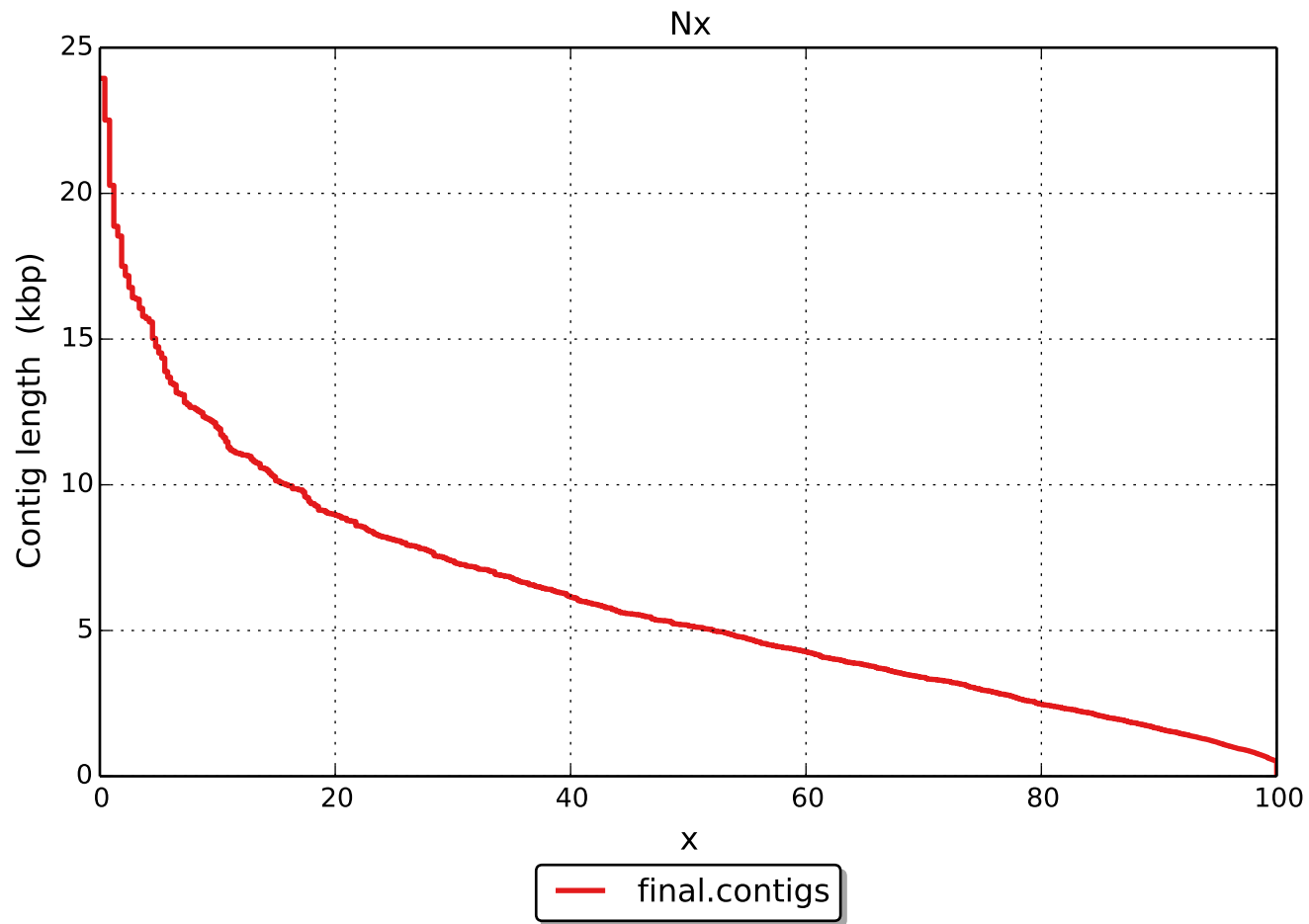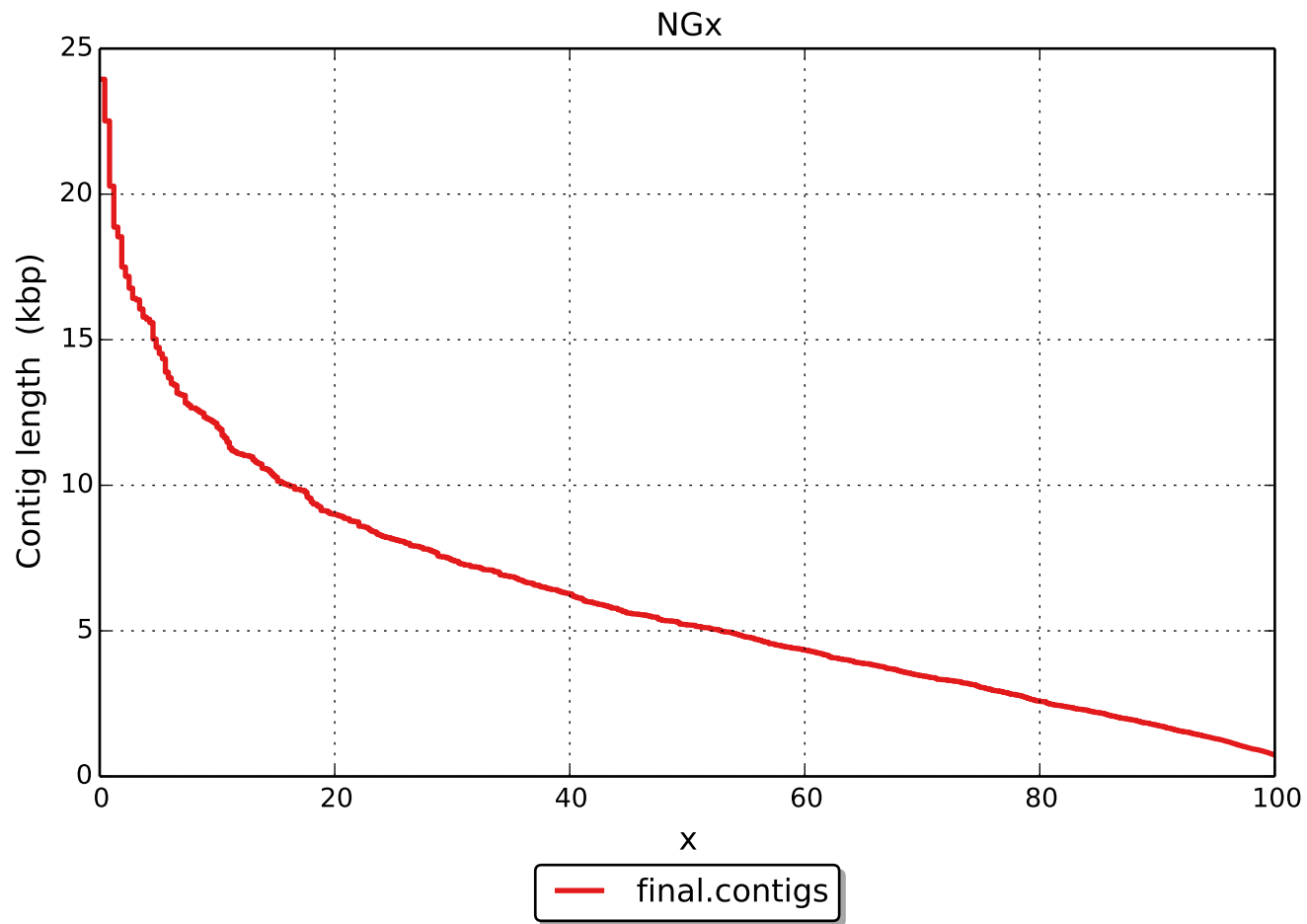|	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	1
Partially unaligned length	1459
# N's	0

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

Nx

Contig length (kbp)

x

final.contigs

NGx

Misassemblies

final.contigs

Cumulative length (aligned contigs)