Report

	final.contigs
# contigs (>= 0 bp)	1974
# contigs (>= 1000 bp)	1196
Total length (>= 0 bp)	3821503
Total length (>= 1000 bp)	3380572
# contigs	1643
Largest contig	18614
Total length	3707914
Reference length	3785550
GC (%)	32.24
Reference GC (%)	32.26
N50	3240
NG50	3161
N75	1709
NG75	1640
L50	352
LG50	364
L75	746
LG75	781
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	94.944
Duplication ratio	1.032
# N's per 100 kbp	0.00
# mismatches per 100 kbp	27.80
# indels per 100 kbp	0.28
Largest alignment	18614
NA50	3240
NGA50	3161
NA75	1709
NGA75	1640
LA50	352
LGA50	364
LA75	746
LGA75	781

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).
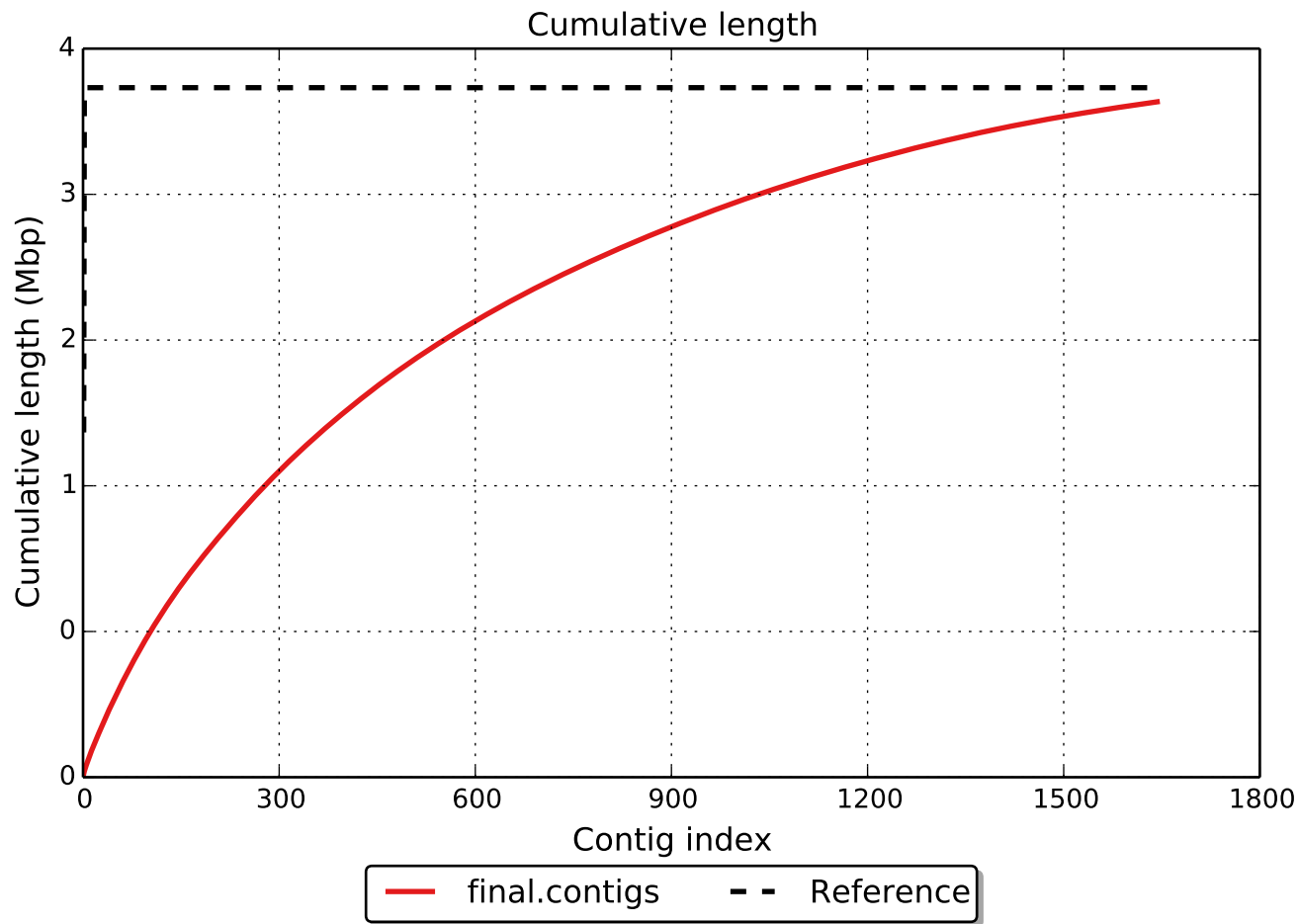
Misassemblies report

	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	999
# indels	10
# short indels	4
# long indels	6
Indels length	72

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).
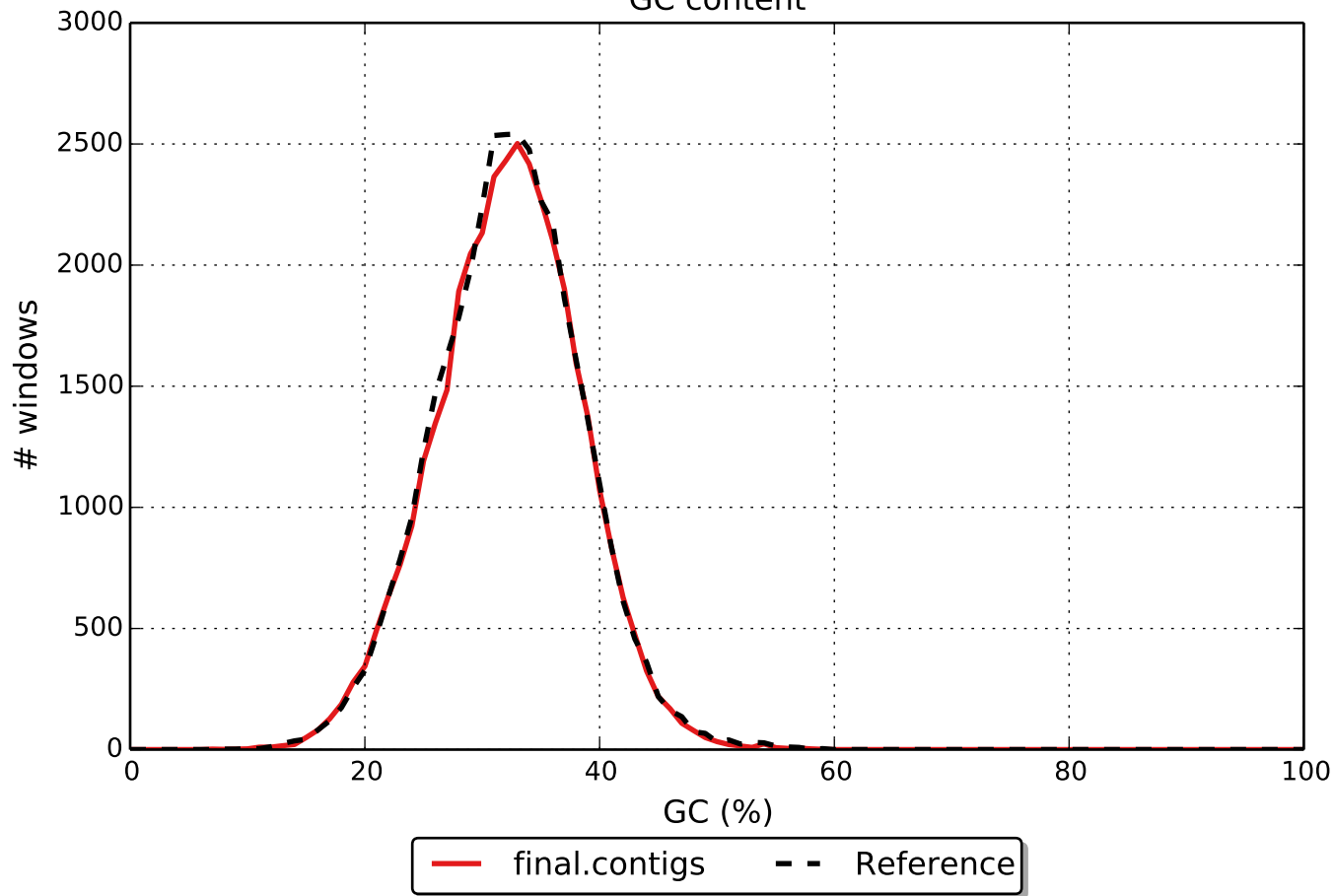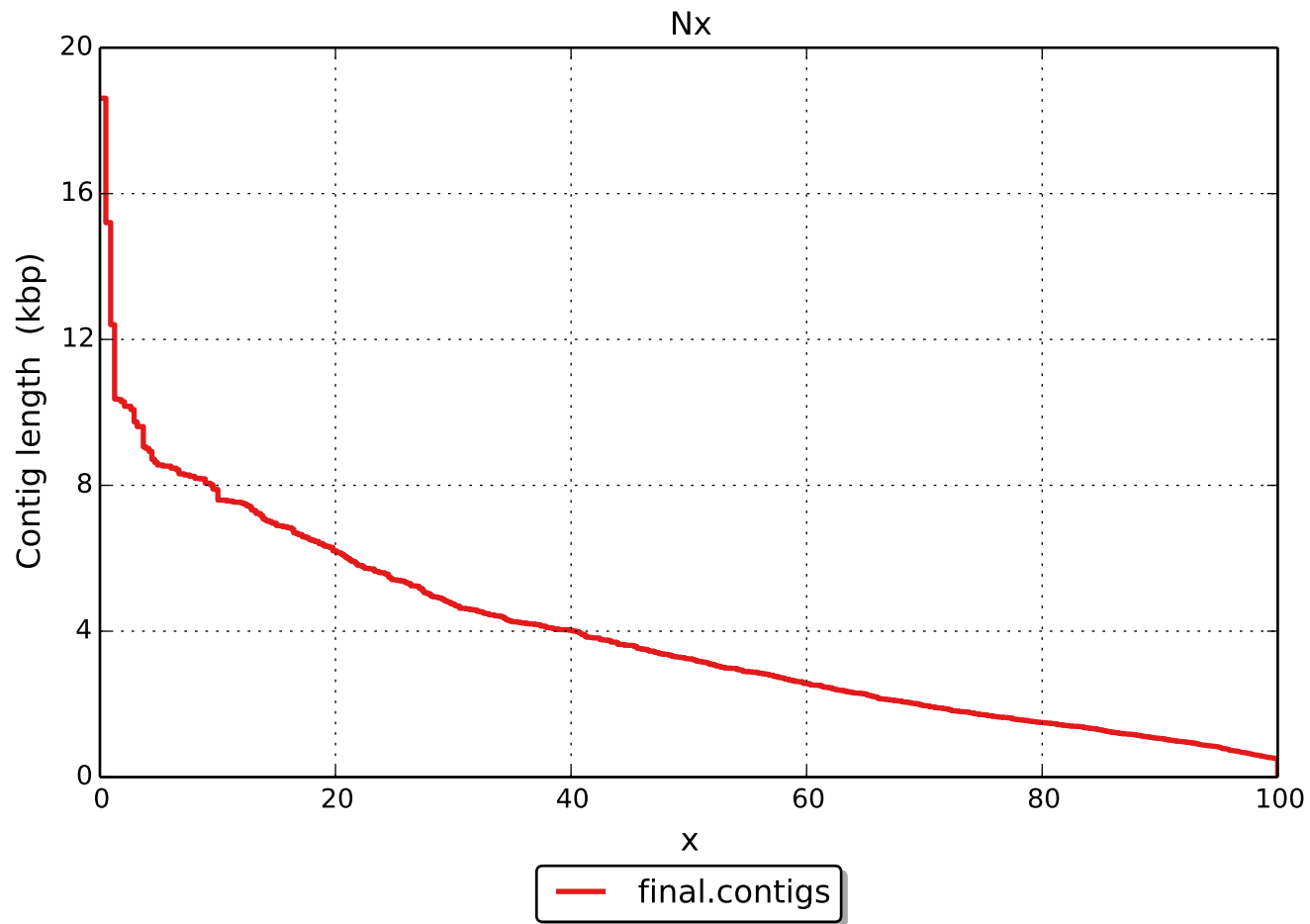
Unaligned report

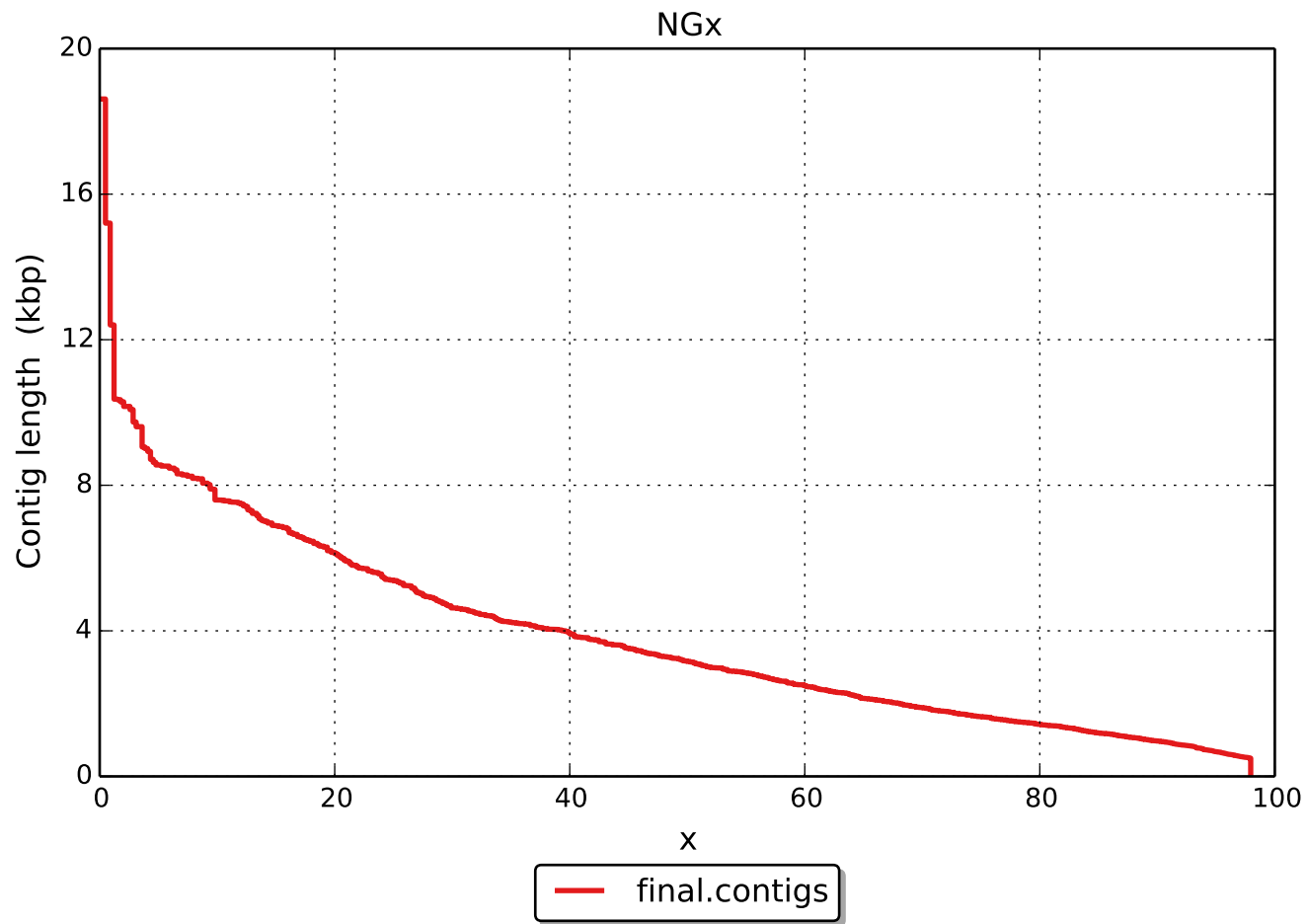|	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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

NGx

Misassemblies

final.contigs

Cumulative length (aligned contigs)

NAx

Contig length (kbp)

x

final.contigs