Report

	final.contigs
# contigs (>= 0 bp)	348
# contigs (>= 1000 bp)	270
Total length (>= 0 bp)	3729883
Total length (>= 1000 bp)	3703431
# contigs	279
Largest contig	74321
Total length	3709906
Reference length	3785550
GC (%)	32.27
Reference GC (%)	32.27
N50	21538
NG50	21285
N75	12583
NG75	12276
L50	56
LG50	58
L75	111
LG75	116
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.548
Duplication ratio	1.005
# N's per 100 kbp	0.00
# mismatches per 100 kbp	6.97
# indels per 100 kbp	0.00
Largest alignment	74321
NA50	21538
NGA50	21285
NA75	12583
NGA75	12276
LA50	56
LGA50	58
LA75	111
LGA75	116

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

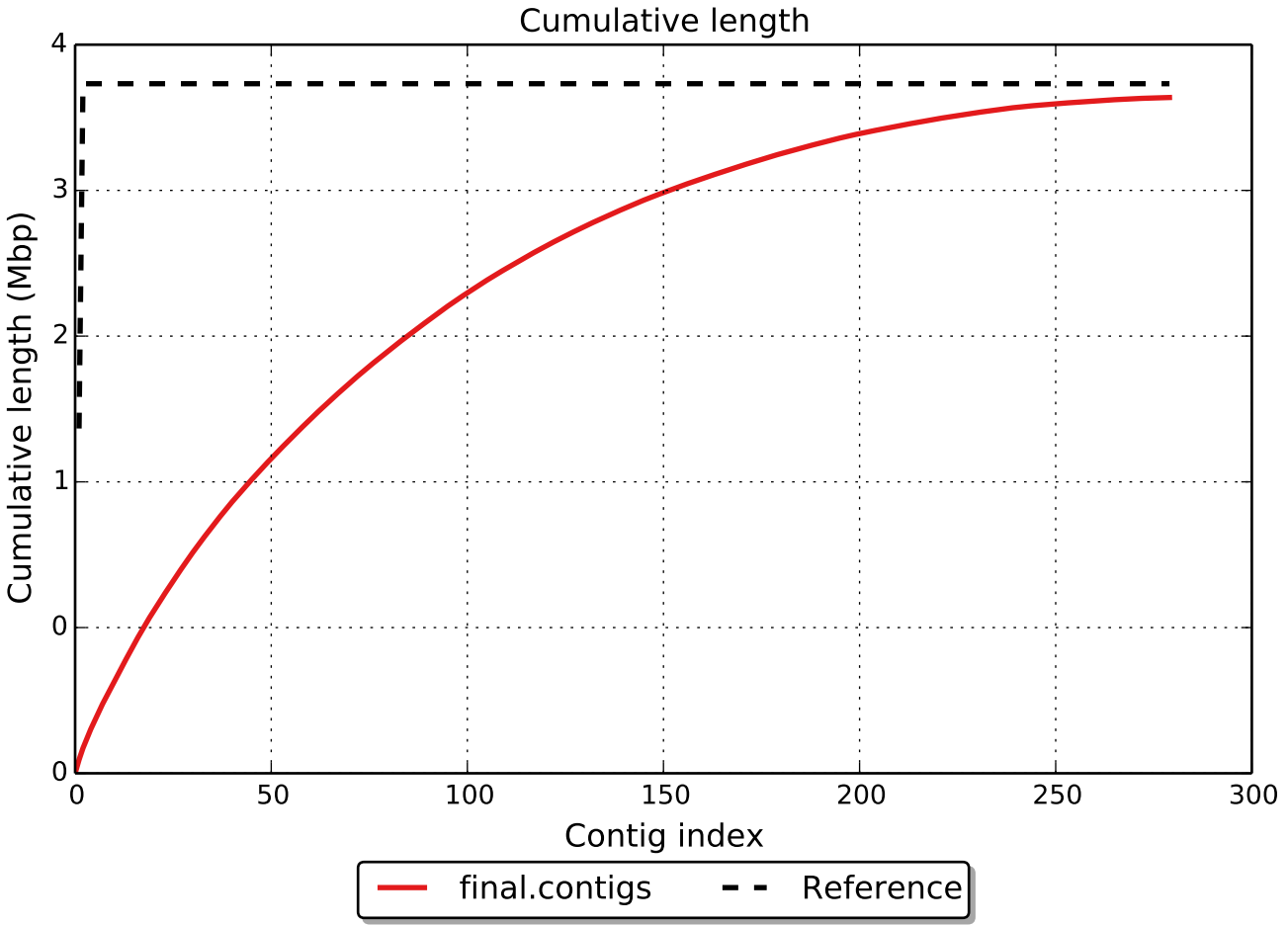
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	260
# indels	0
# short indels	0
# long indels	0
Indels length	0

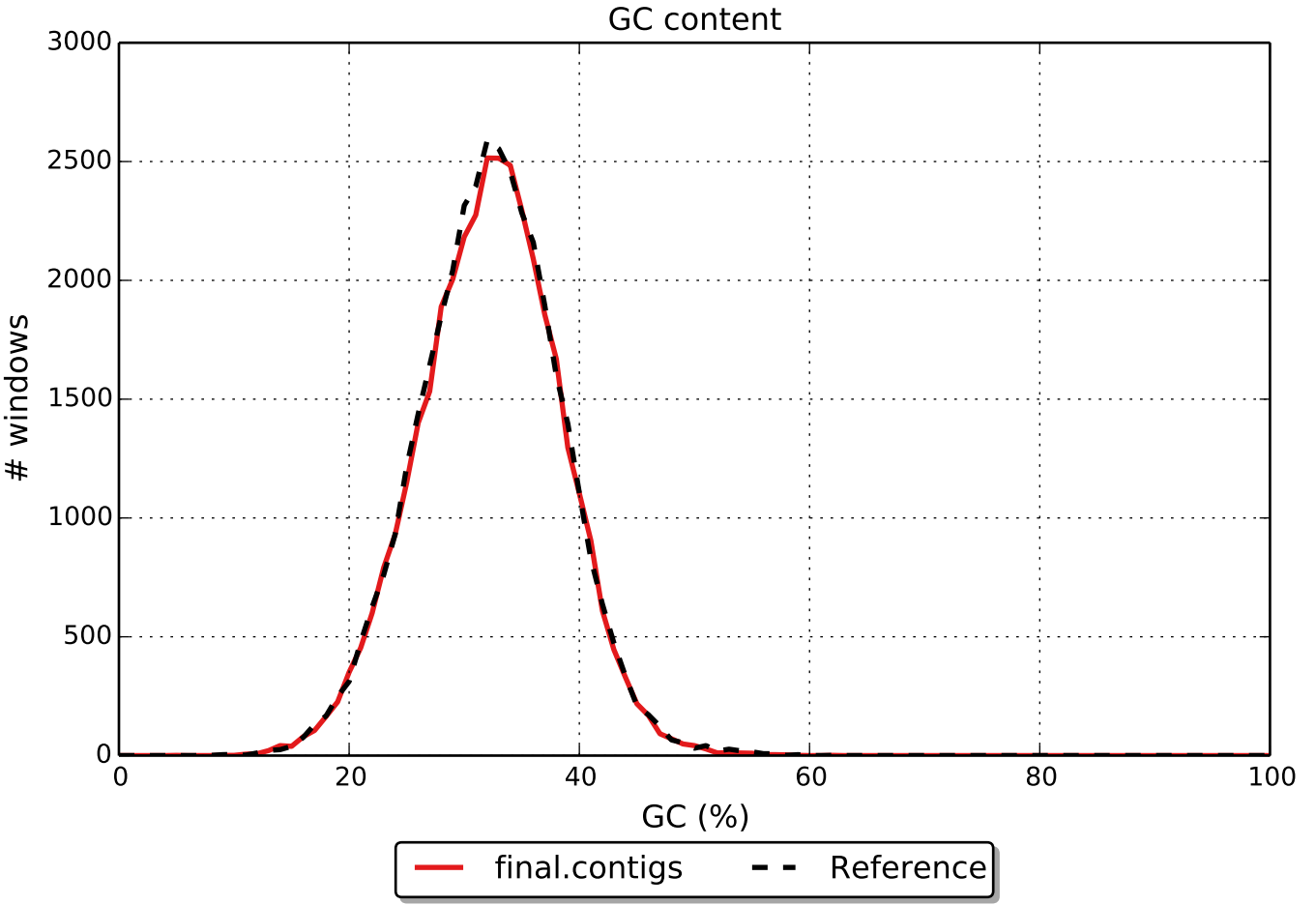
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

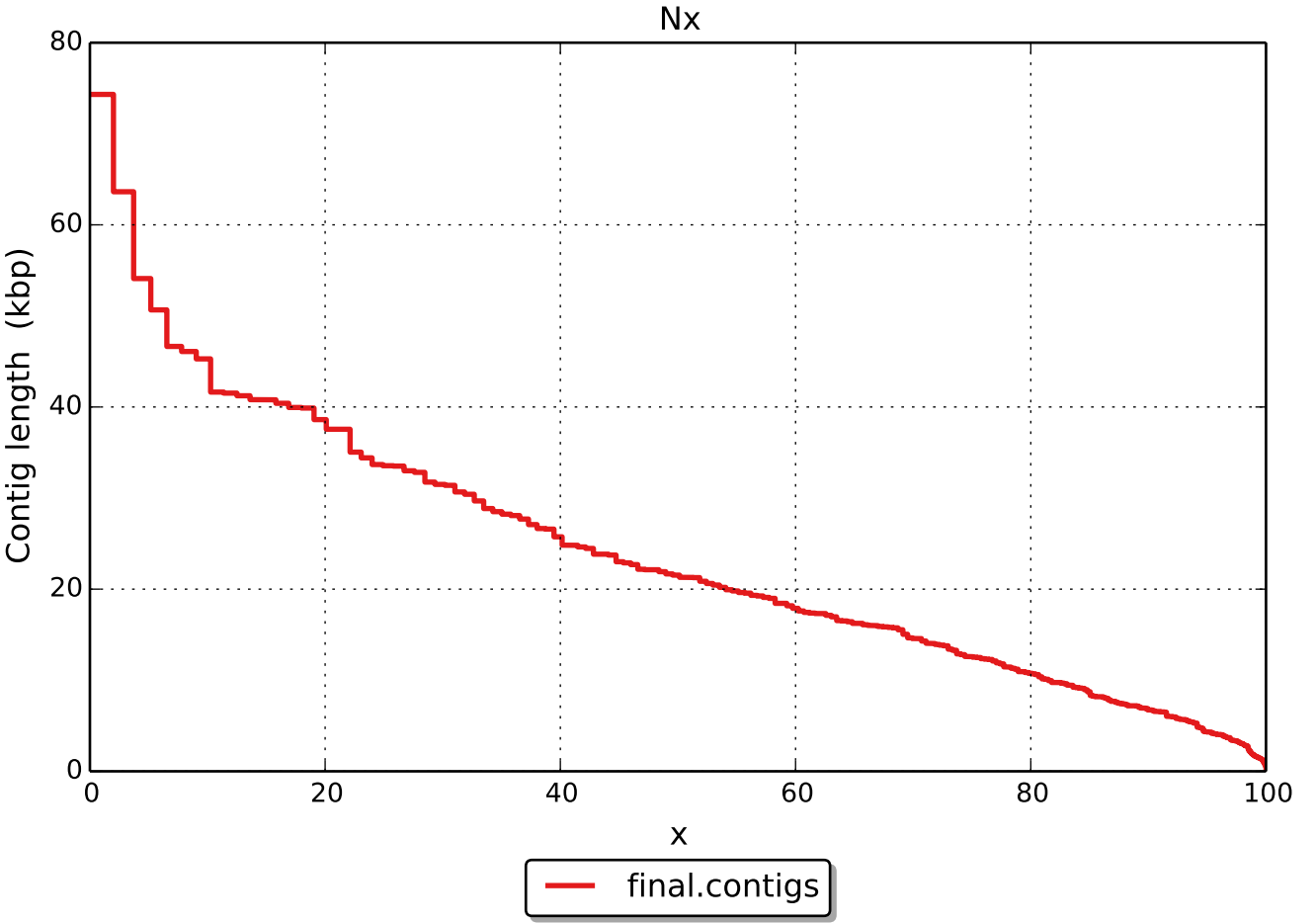
Unaligned report

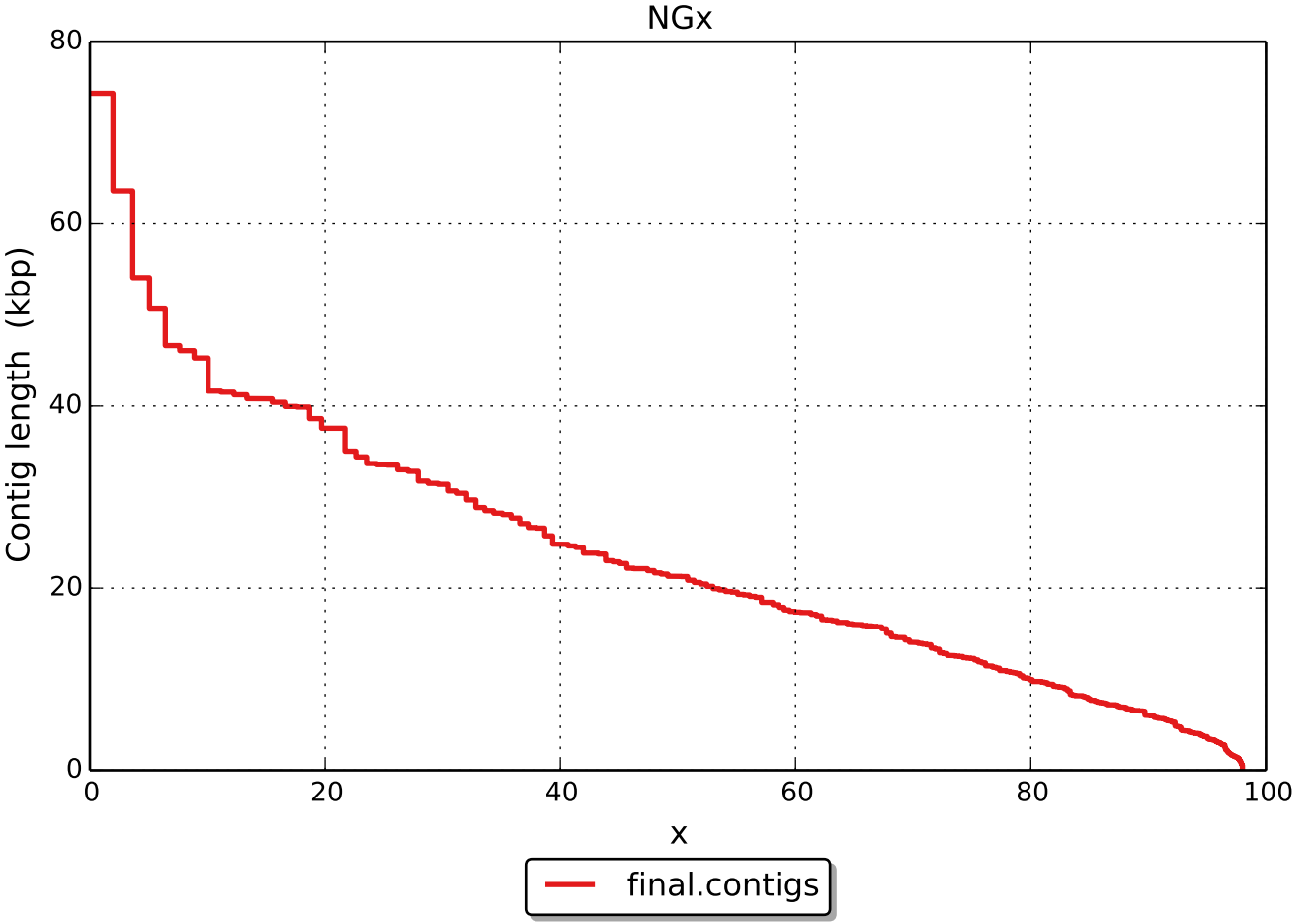
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

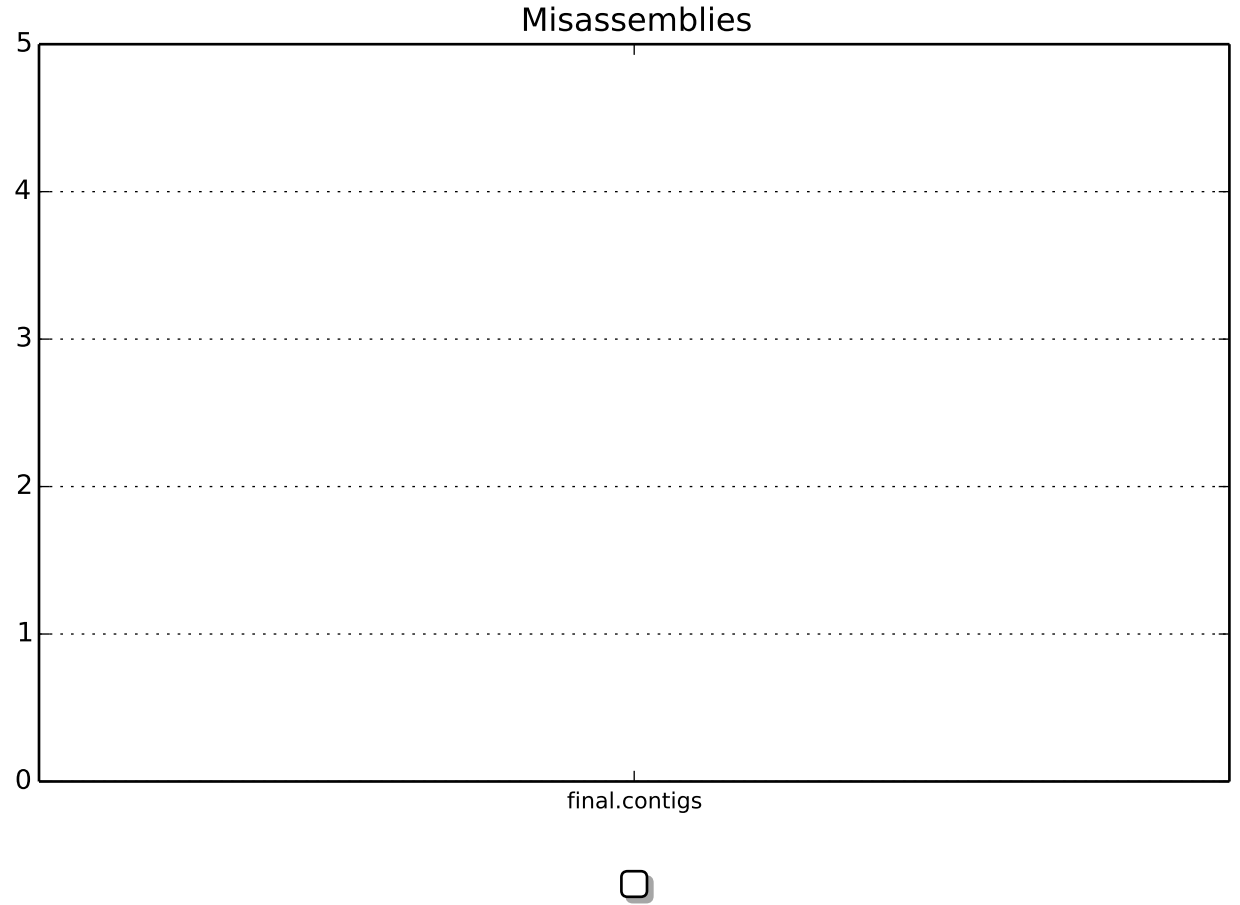
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

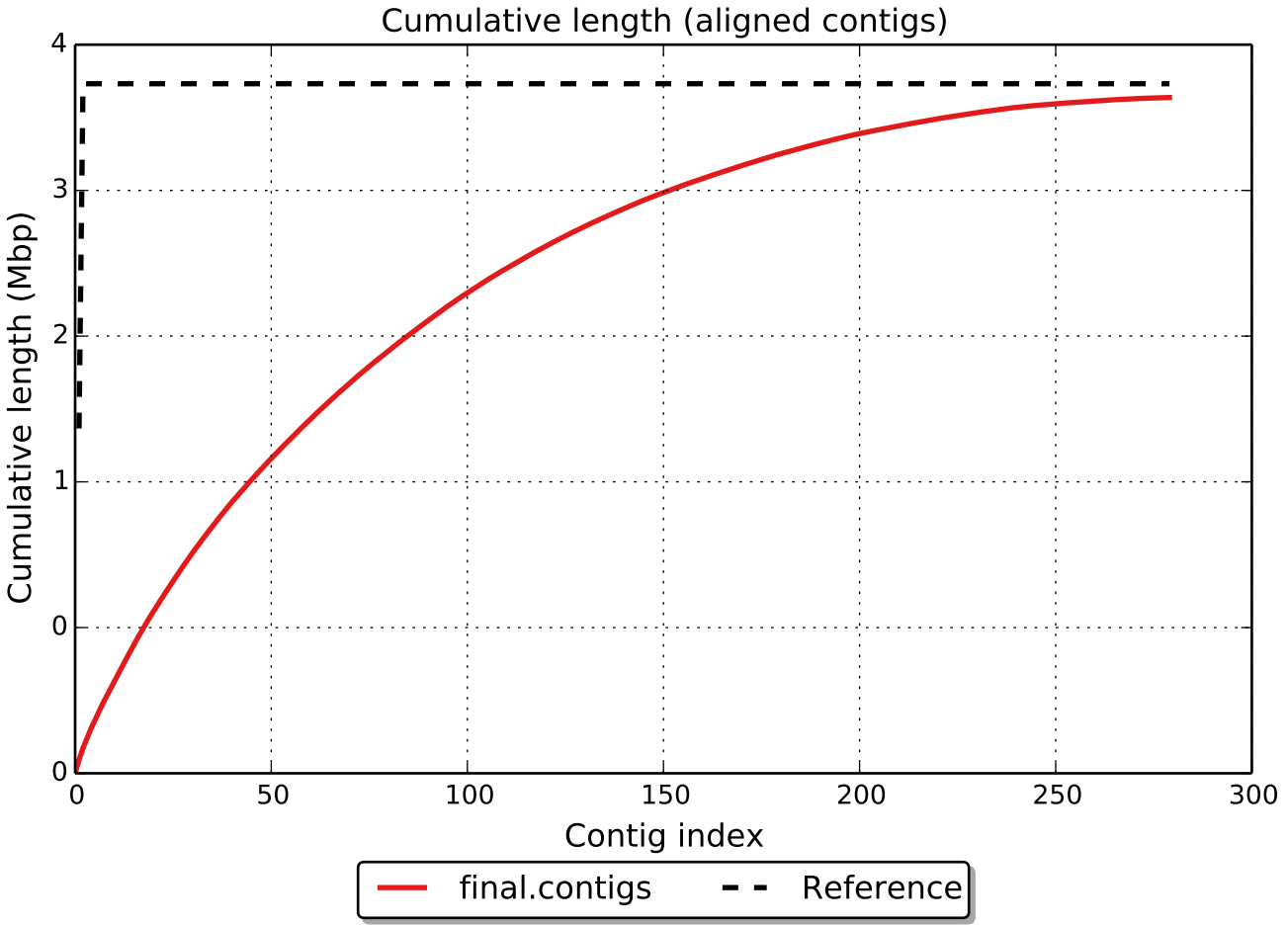

Cumulative length
Cumulative length (Mbp)
Contig index
0
1
2
3
4
0
50
100
150
200
250
300
final.contigs
Reference

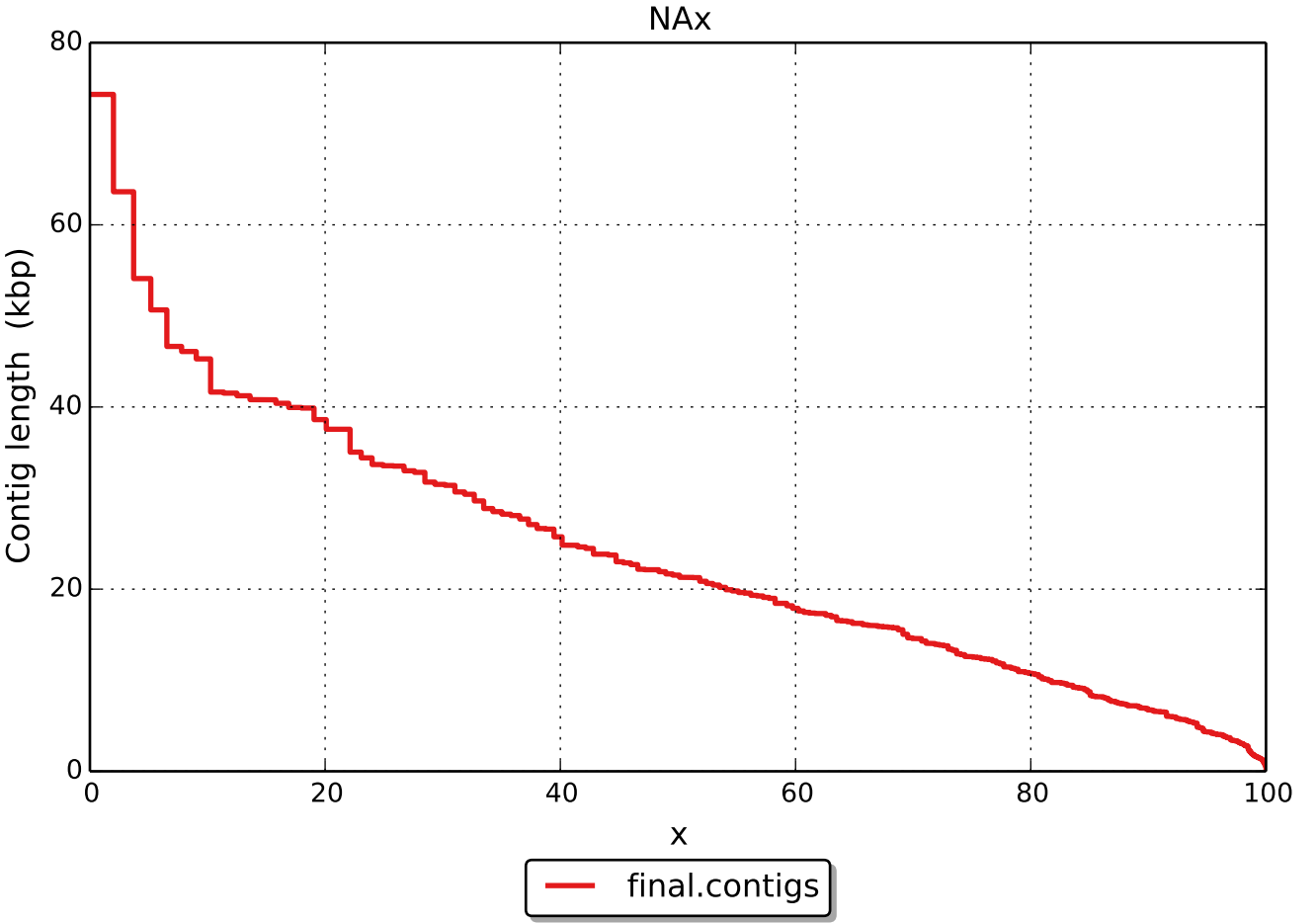

GC content
3000
2500
2000
1500
1000
500
0
windows
0
20
40
60
80
100
GC (%)
final.contigs
Reference

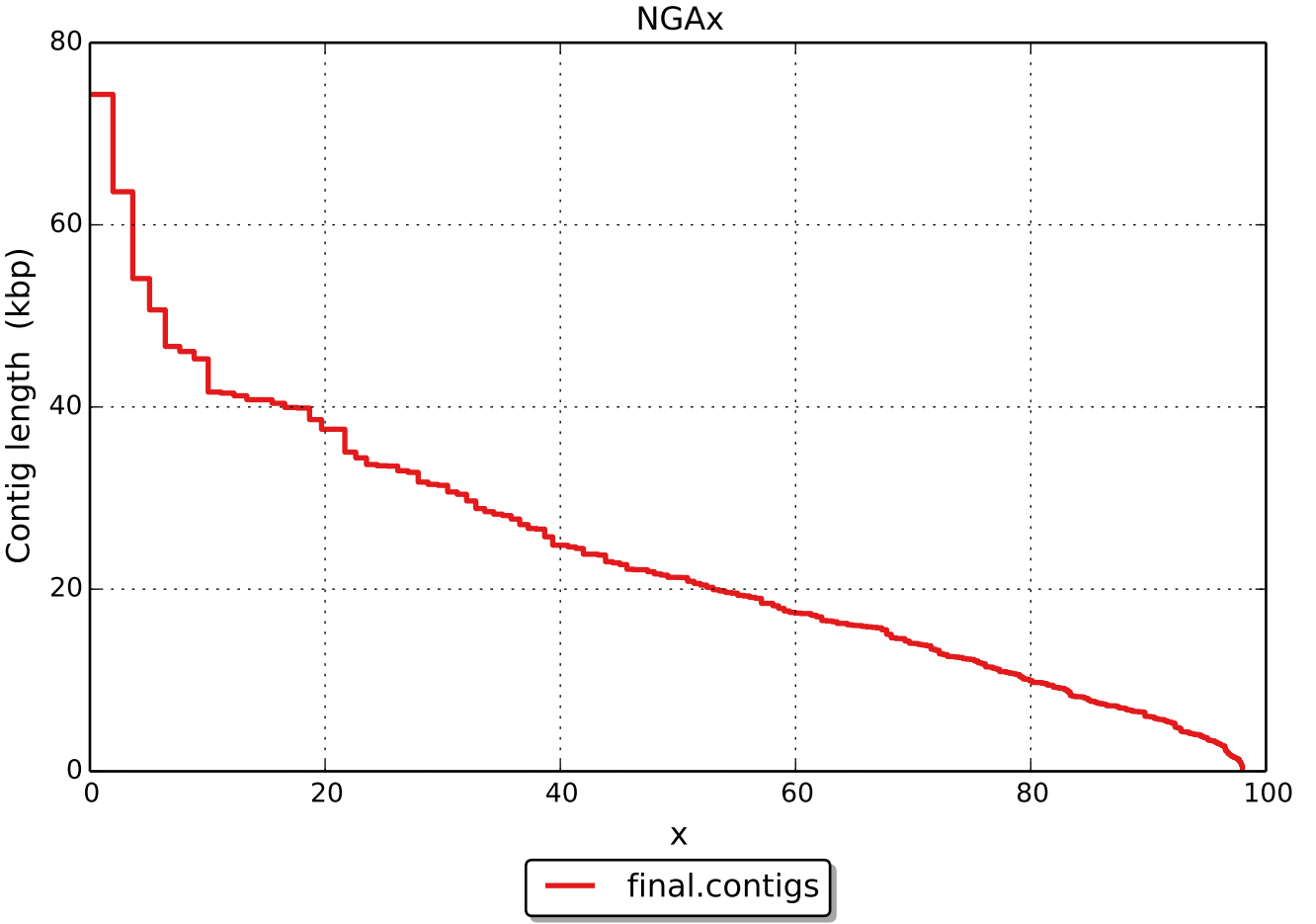

Nx
Contig length (kbp)
80
60
40
20
0
0
20
40
60
80
100
x
final.contigs


NGx
Contig length (kbp)
80
60
40
20
0
0
20
40
60
80
100
x
final.contigs


Misassemblies
5
4
3
2
1
0
final.contigs


Cumulative length (aligned contigs)
Cumulative length (Mbp)
Contig index
0
1
2
3
4
0
50
100
150
200
250
300
final.contigs
Reference


NAx
Contig length (kbp)
80
60
40
20
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (kbp)
80
60
40
20
0
0
20
40
60
80
100
x
final.contigs