Report

	final.contigs
# contigs (>= 1000 bp)	394
# contigs (>= 5000 bp)	270
# contigs (>= 10000 bp)	171
# contigs (>= 25000 bp)	44
# contigs (>= 50000 bp)	3
Total length (>= 1000 bp)	4655708
Total length (>= 5000 bp)	4301266
Total length (>= 10000 bp)	3551731
Total length (>= 25000 bp)	1467479
Total length (>= 50000 bp)	169638
# contigs	415
Largest contig	62774
Total length	4671997
Reference length	4641652
GC (%)	50.78
Reference GC (%)	50.78
N50	19101
NG50	19115
N75	10184
NG75	10301
L50	84
LG50	83
L75	167
LG75	165
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.933
Duplication ratio	1.007
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.02
# indels per 100 kbp	0.00
Largest alignment	62774
NA50	19101
NGA50	19115
NA75	10184
NGA75	10301
LA50	84
LGA50	83
LA75	167
LGA75	165

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

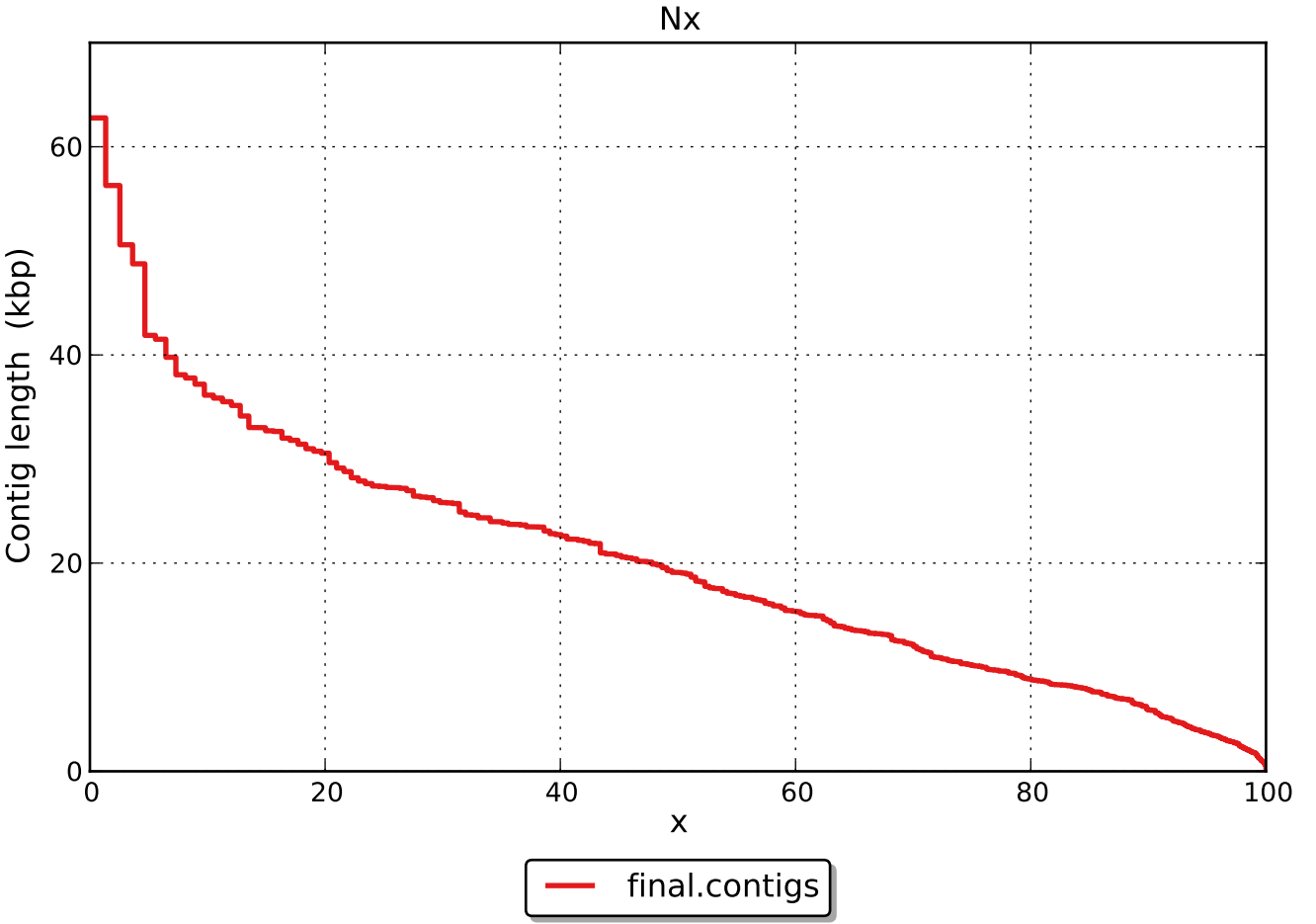
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	1
# indels	0
# short indels	0
# long indels	0
Indels length	0

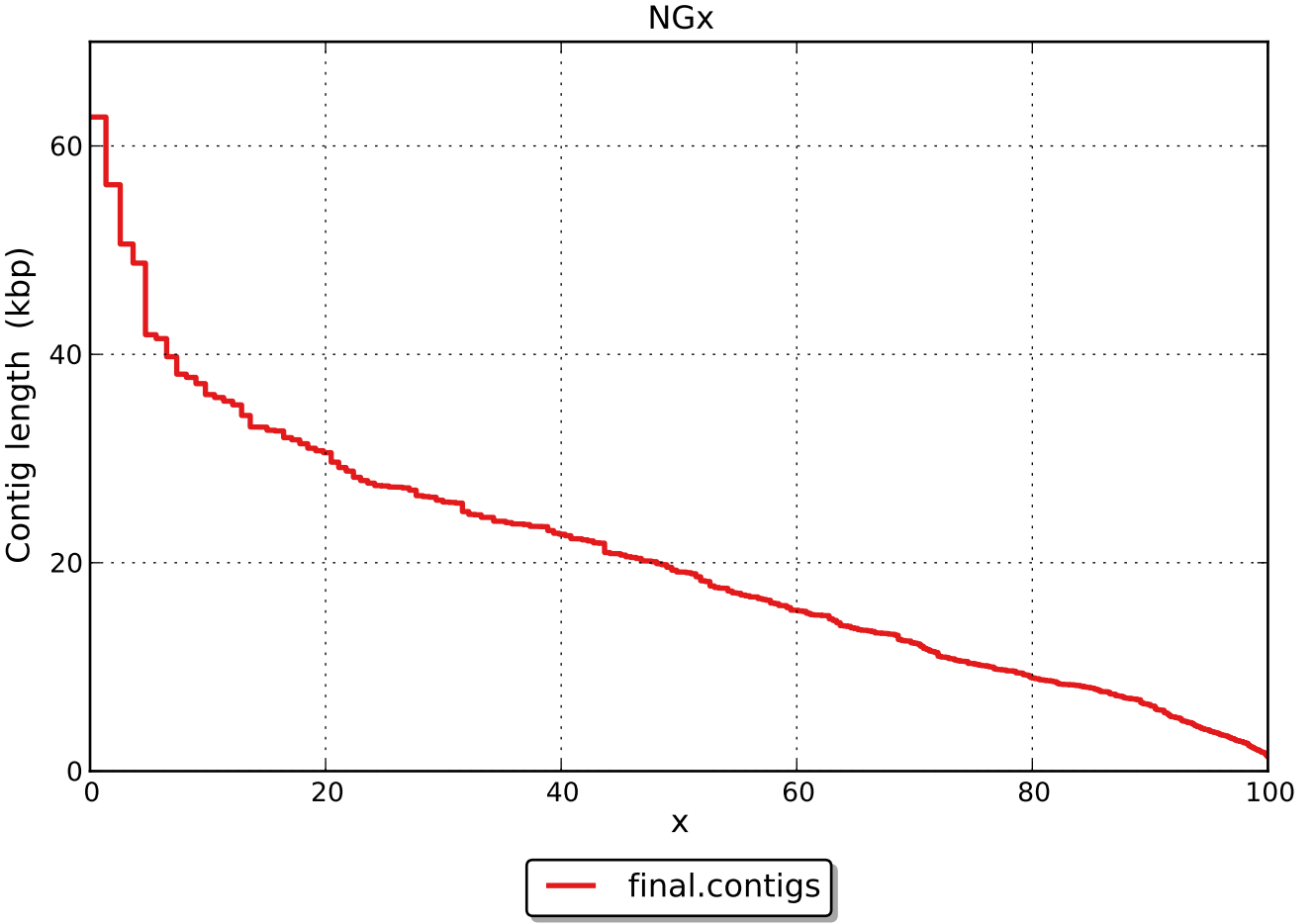
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

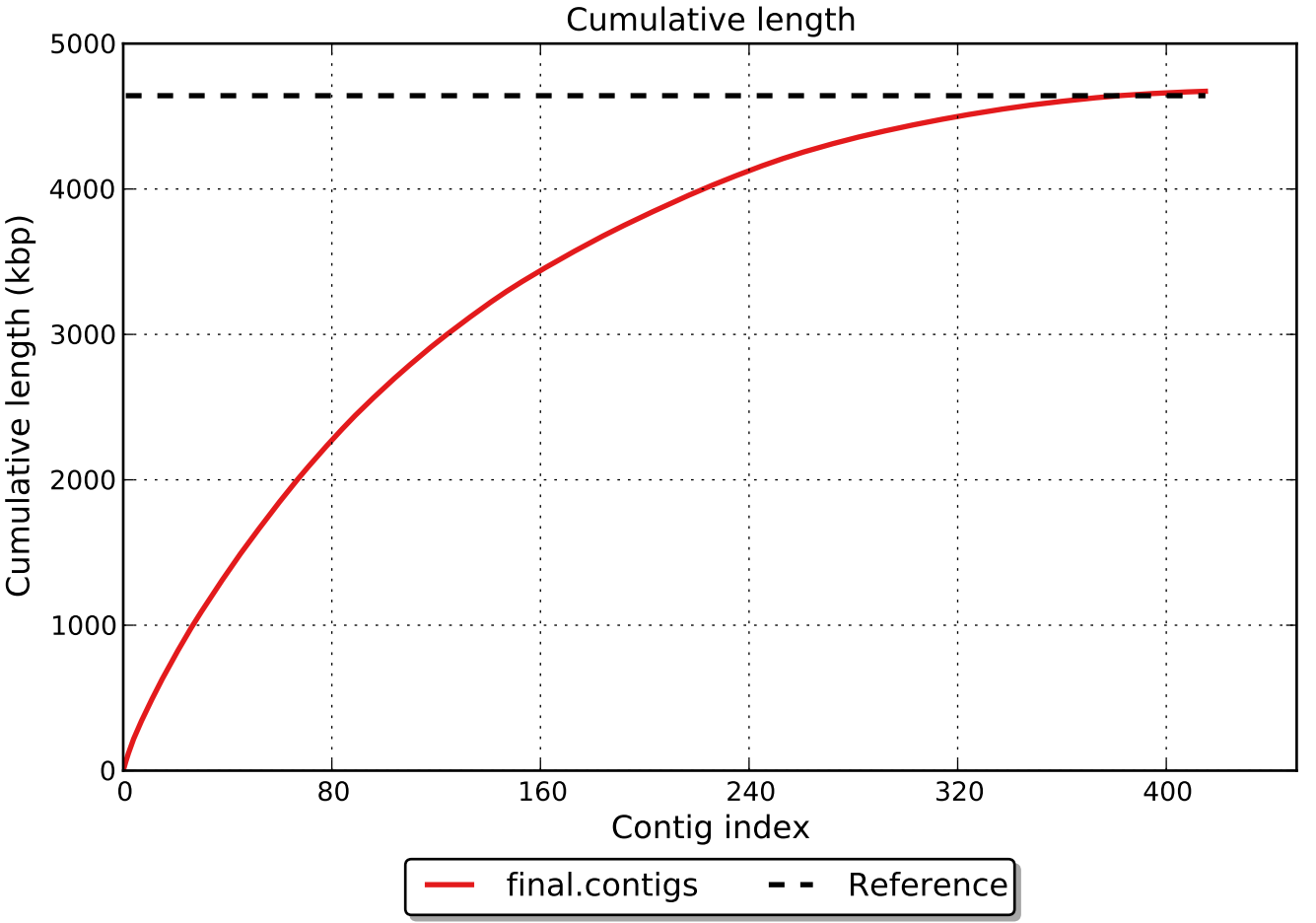
Unaligned report

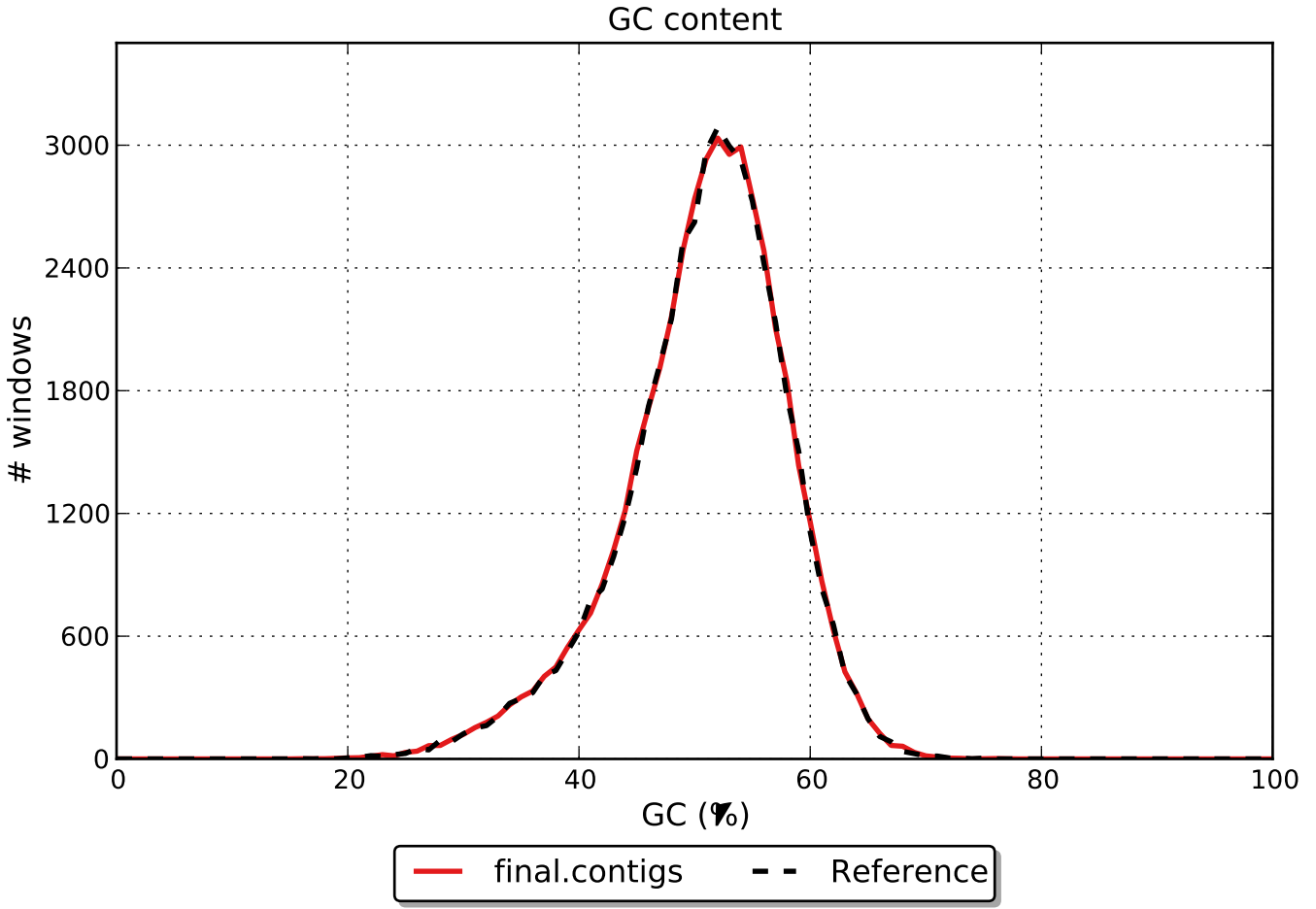
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

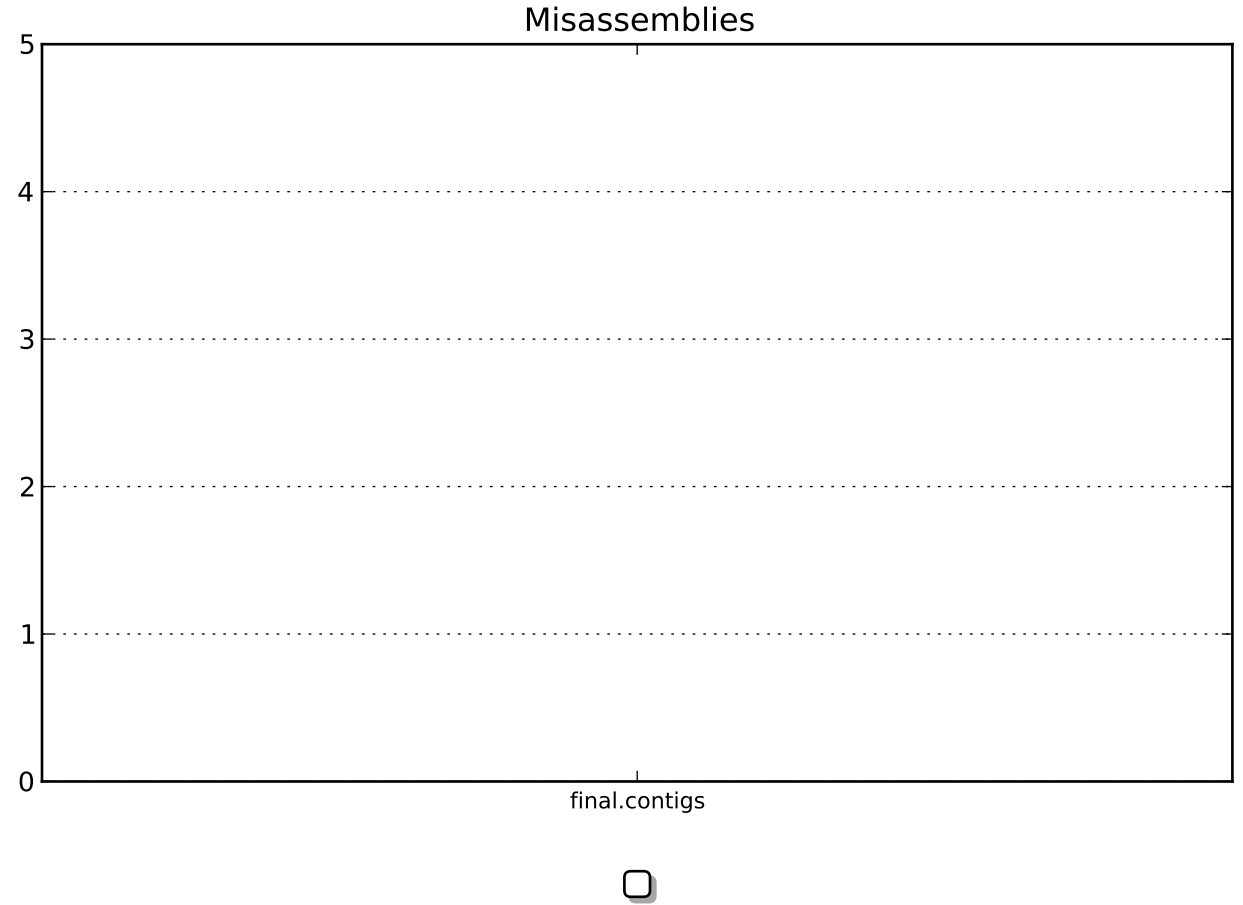
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

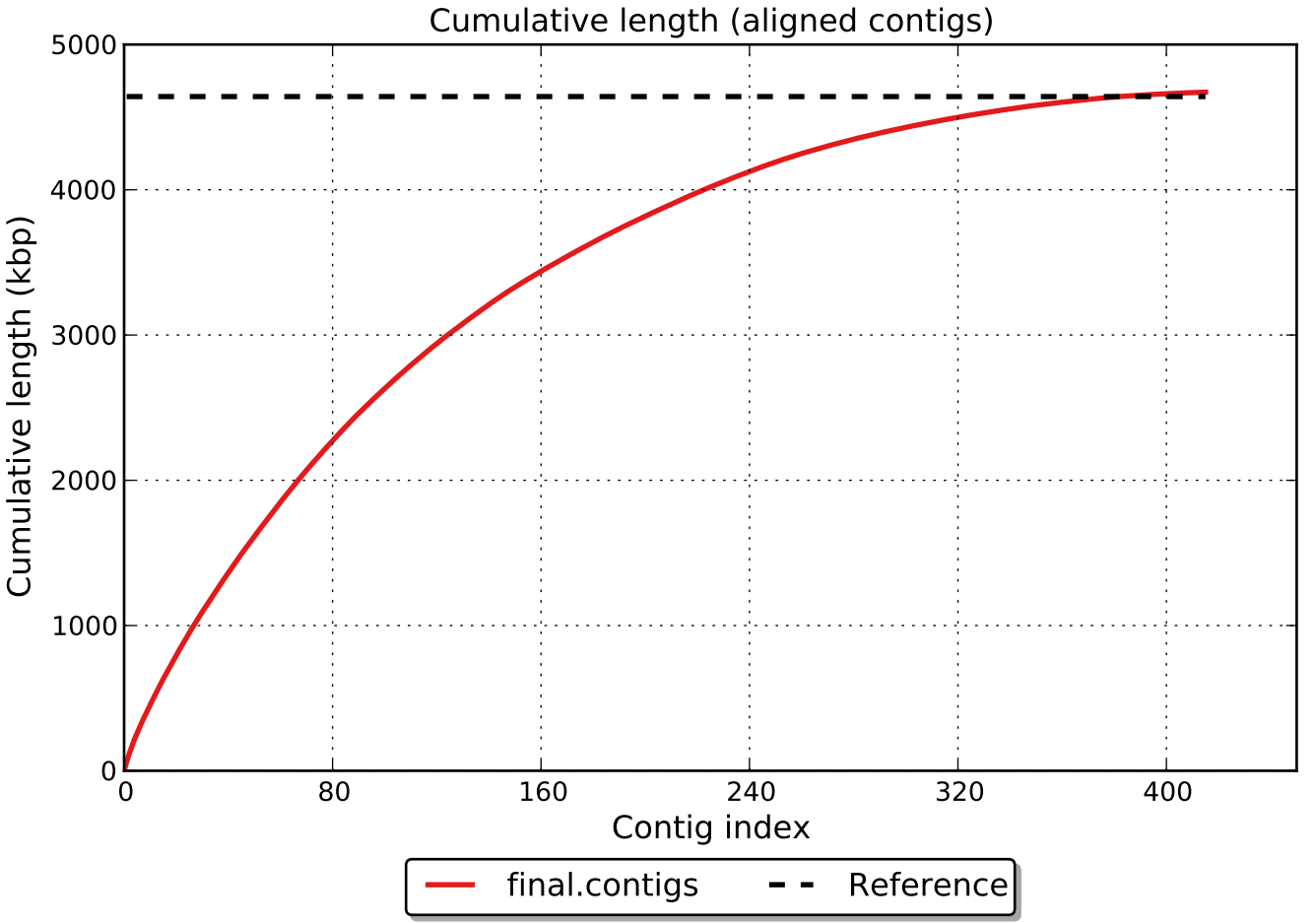

Nx
Contig length (kbp)
0
20
40
60
0
20
40
60
80
100
x
final.contigs

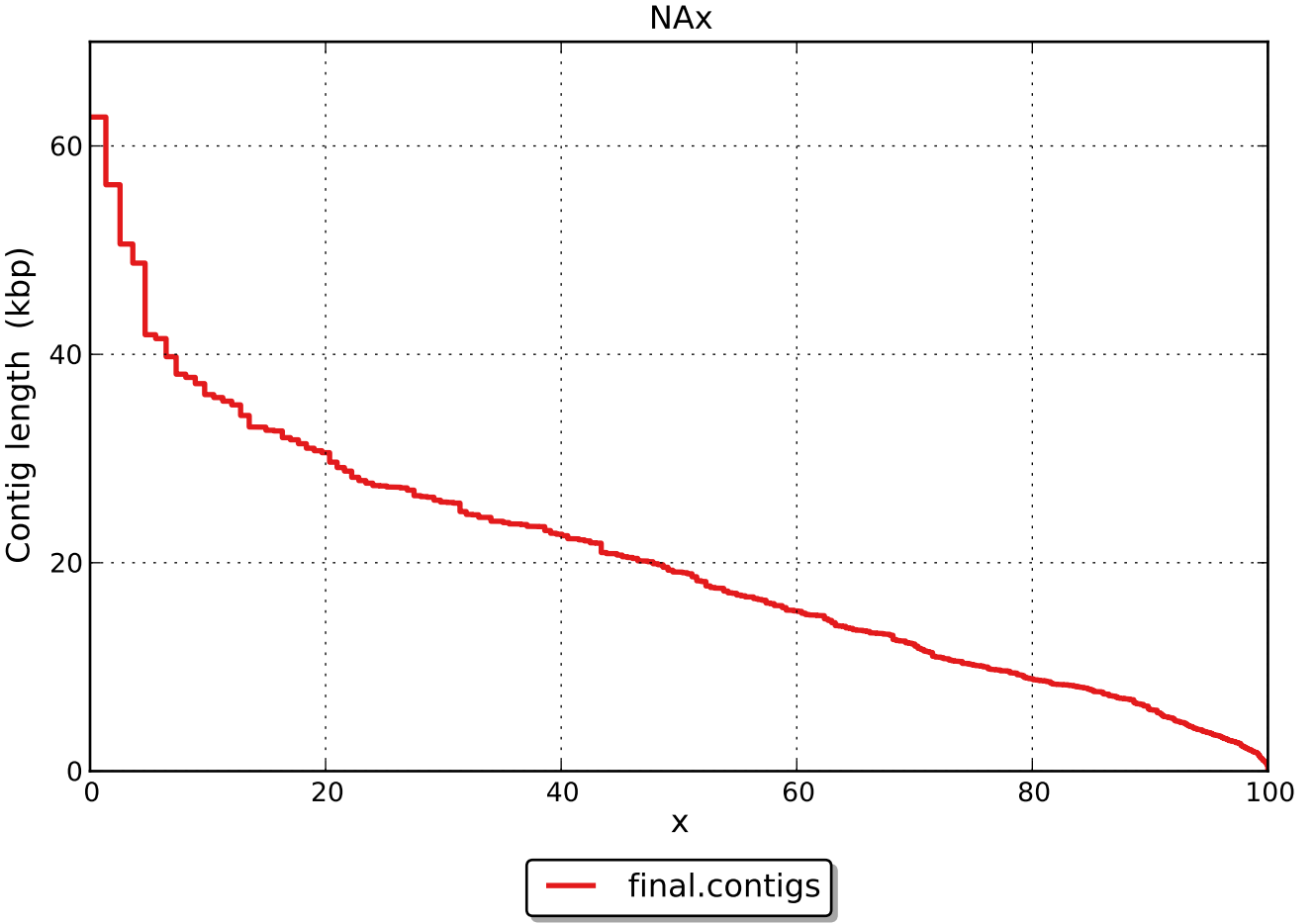

NGx
Contig length (kbp)
0
20
40
60
0
20
40
60
80
100
x
final.contigs

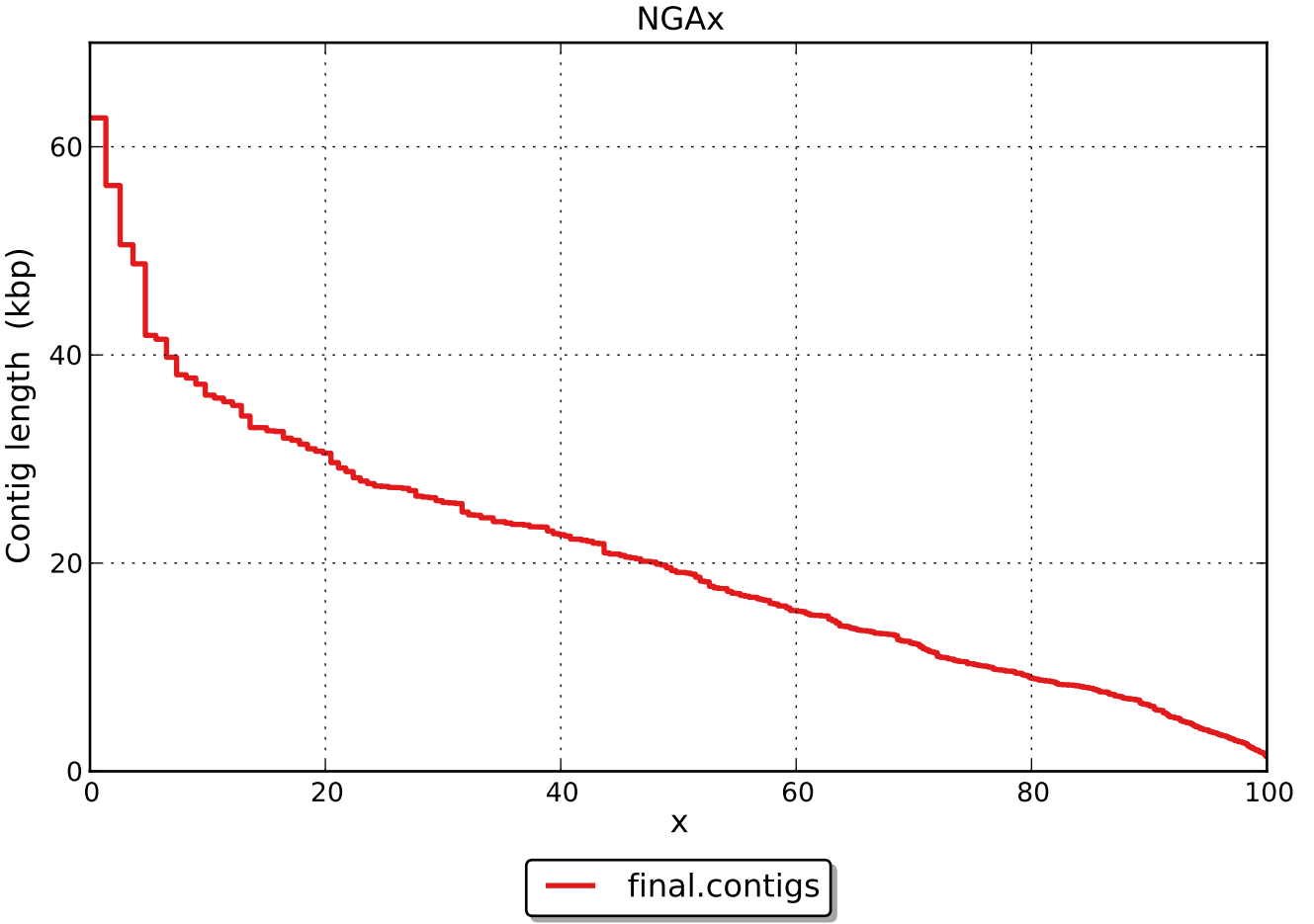

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
80
160
240
320
400
Contig index
final.contigs
Reference


GC content
windows
3000
2400
1800
1200
600
0
0
20
40
60
80
100
GC (%)
final.contigs
Reference


Misassemblies
5
4
3
2
1
0
final.contigs


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
80
160
240
320
400
Contig index
final.contigs
Reference


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


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