Report

	final.contigs
# contigs (>= 1000 bp)	92
# contigs (>= 5000 bp)	72
# contigs (>= 10000 bp)	67
# contigs (>= 25000 bp)	53
# contigs (>= 50000 bp)	34
Total length (>= 1000 bp)	4549180
Total length (>= 5000 bp)	4508520
Total length (>= 10000 bp)	4469795
Total length (>= 25000 bp)	4253771
Total length (>= 50000 bp)	3595787
# contigs	104
Largest contig	209435
Total length	4557558
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	95681
NG50	95542
N75	56609
NG75	54942
L50	15
LG50	16
L75	31
LG75	32
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	9
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.146
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	57.93
# indels per 100 kbp	9.44
Largest alignment	209435
NA50	95681
NGA50	95542
NA75	56609
NGA75	54942
LA50	15
LGA50	16
LA75	31
LGA75	32

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

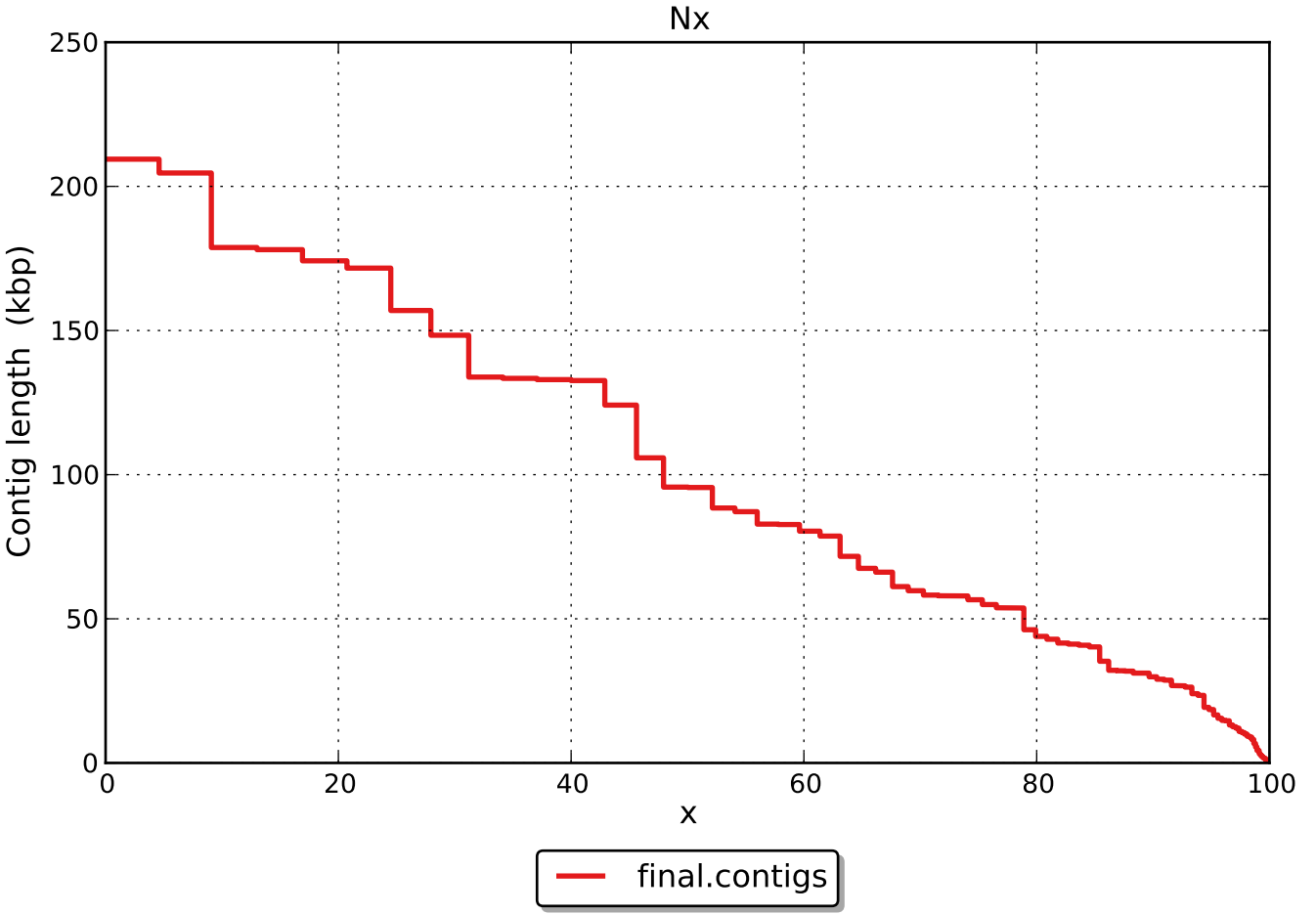
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	9
# mismatches	2639
# indels	430
# short indels	430
# long indels	0
Indels length	596

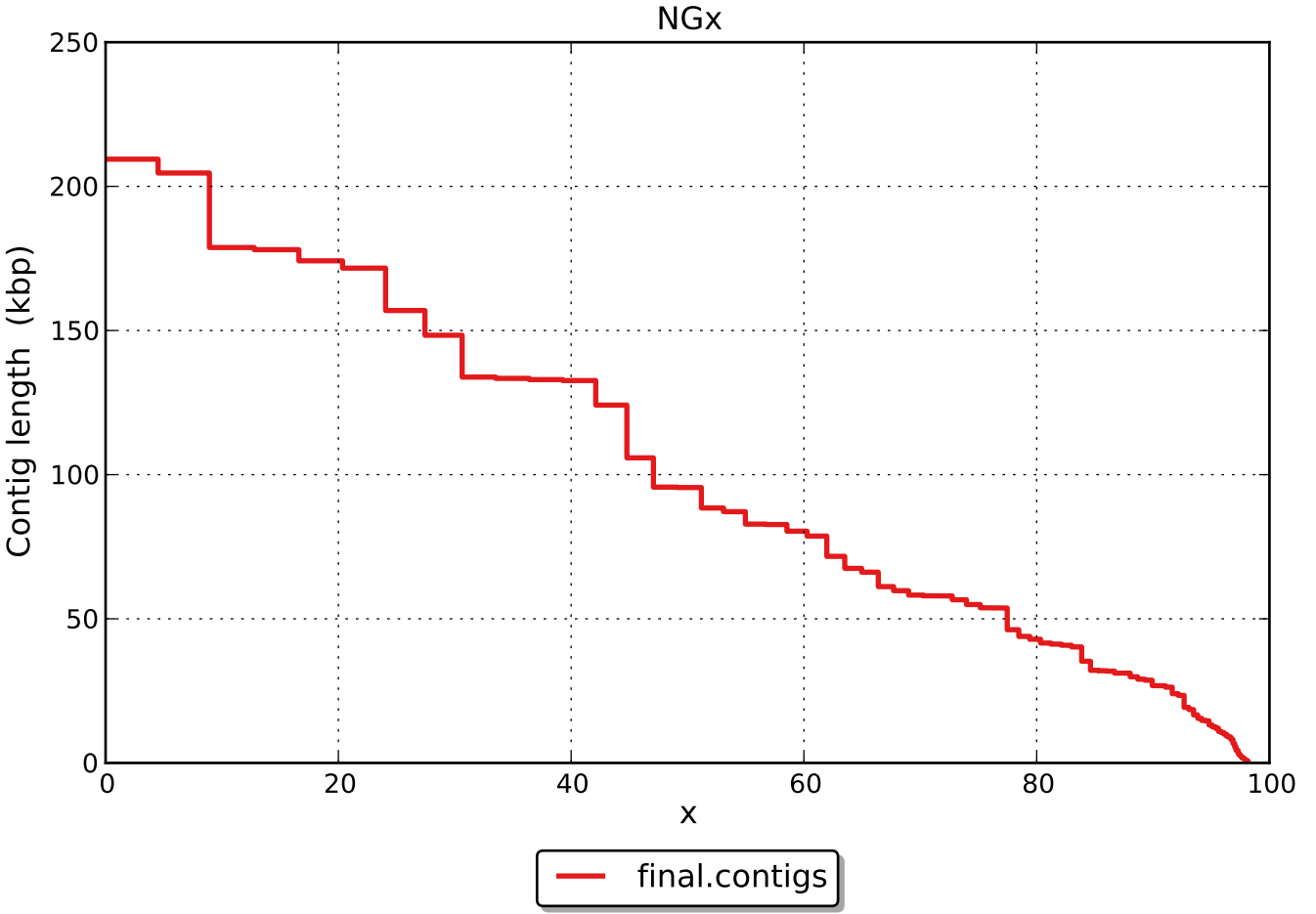
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

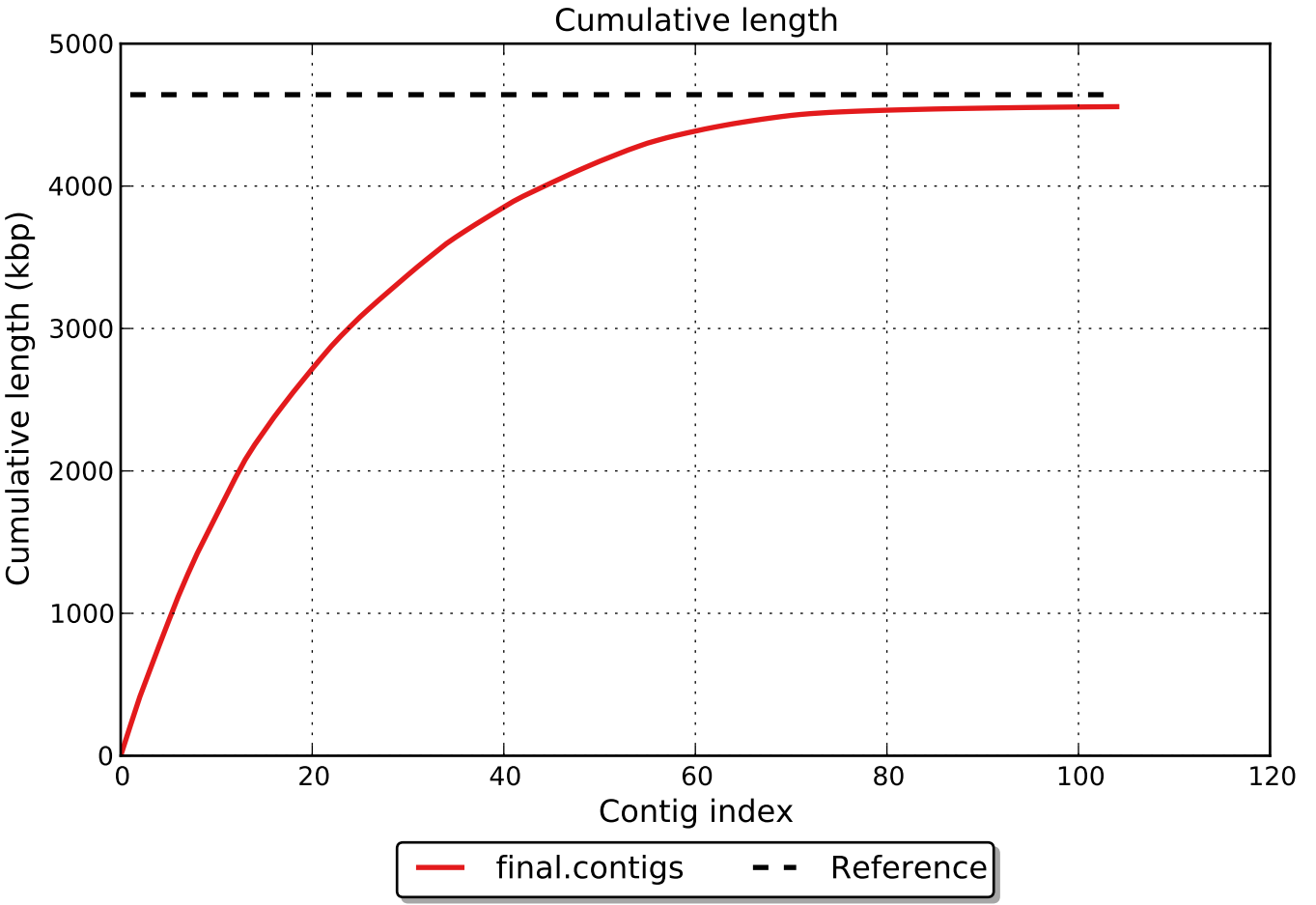
Unaligned report

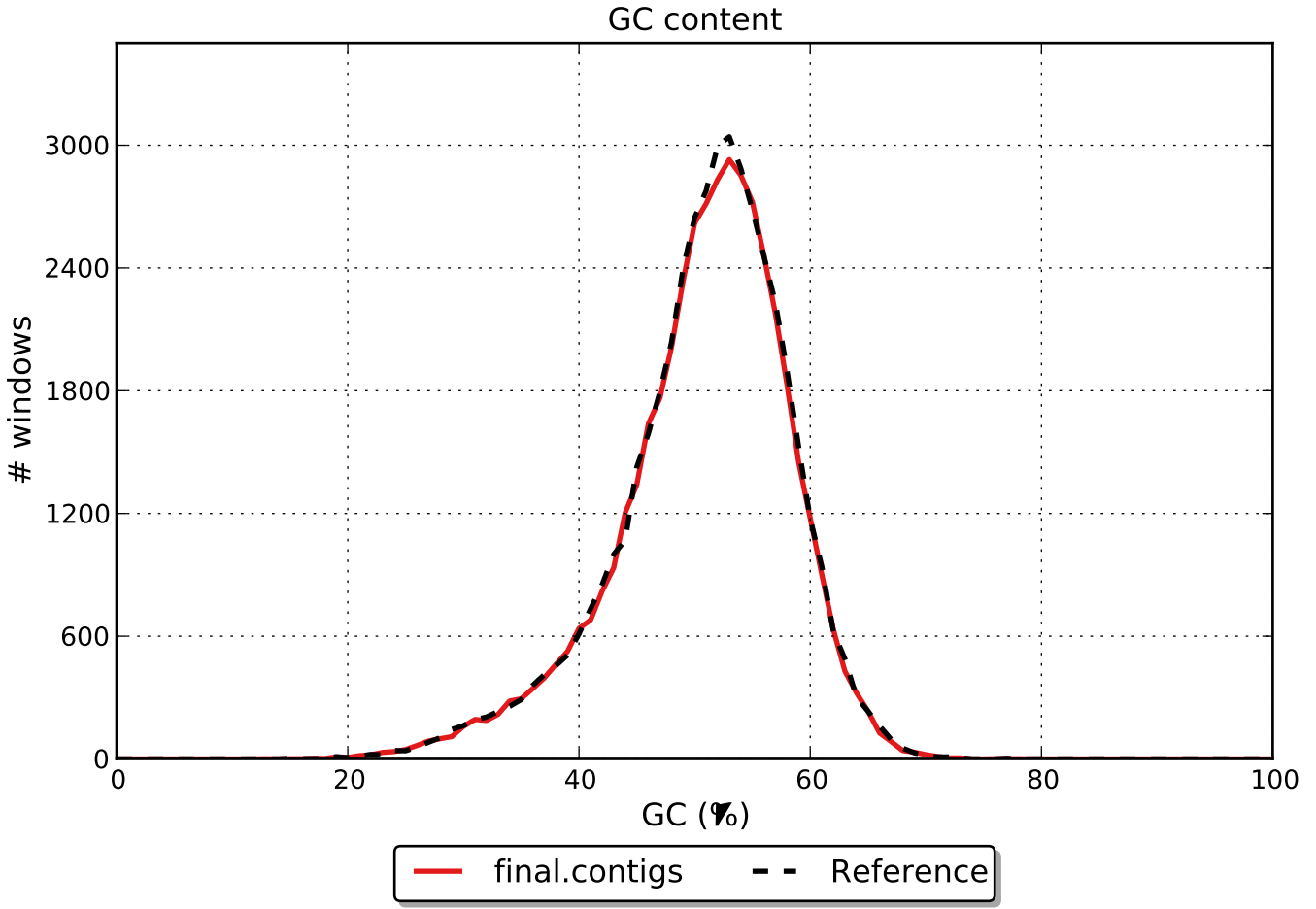
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

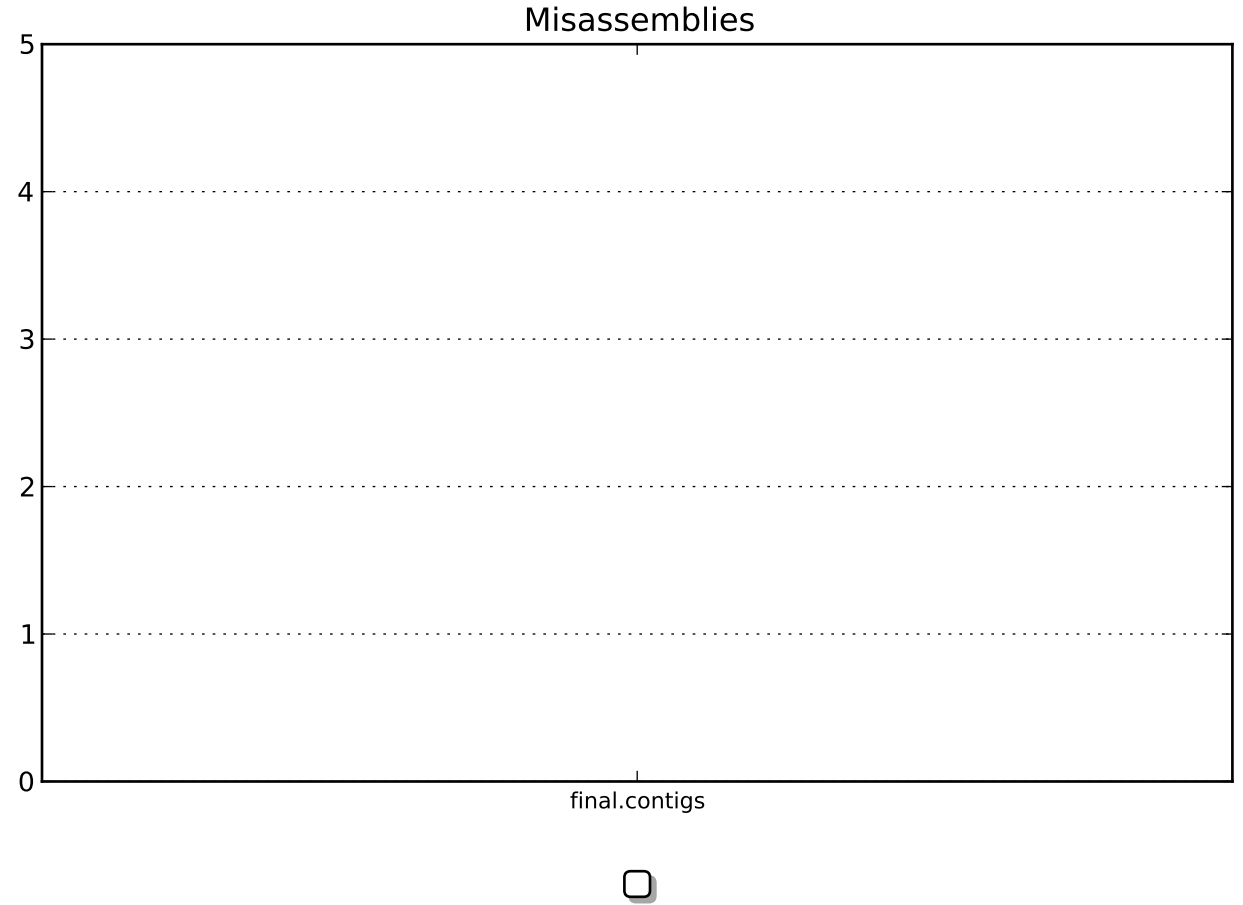
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

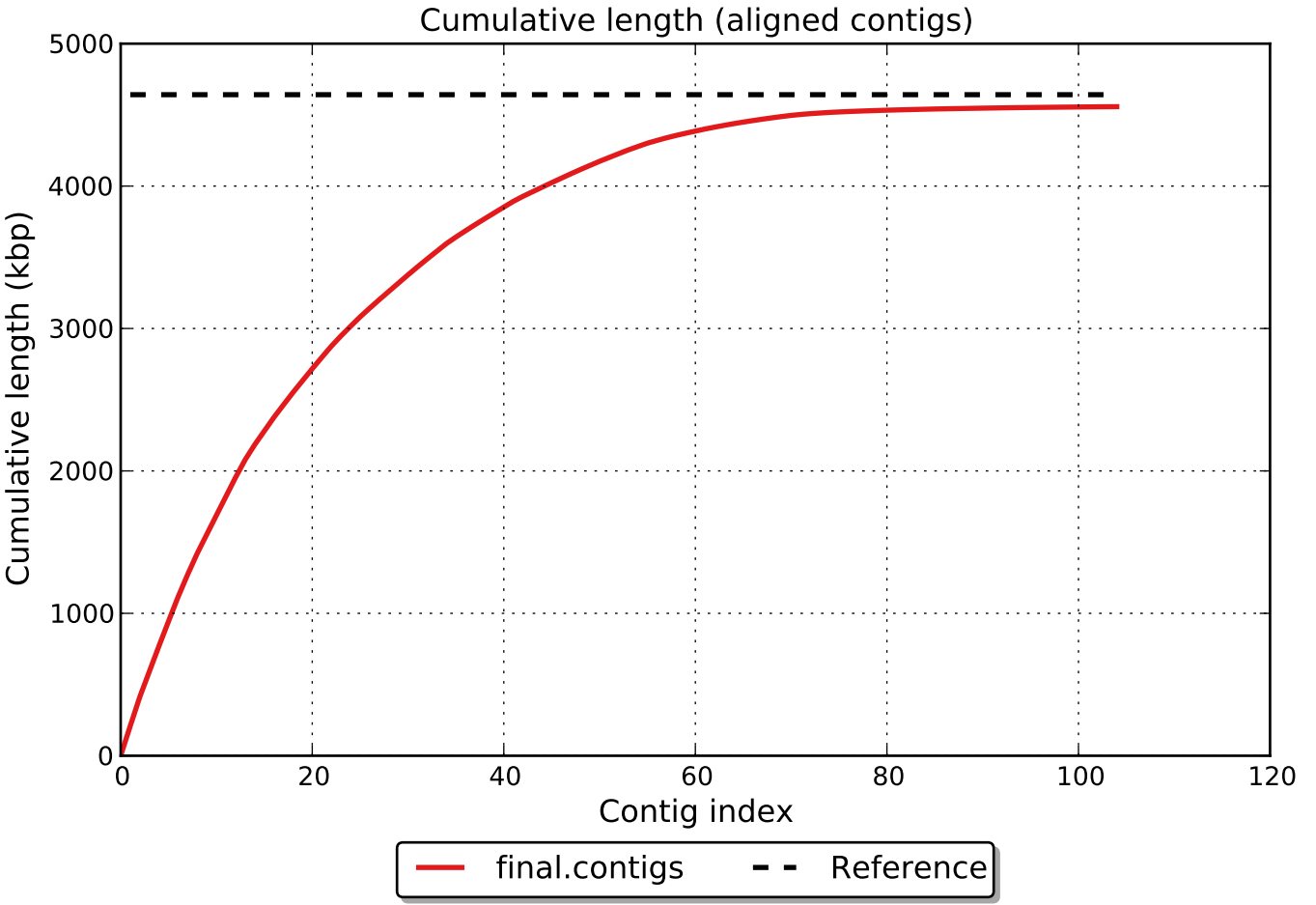

Nx
Contig length (kbp)
250
200
150
100
50
0
0
20
40
60
80
100
x
final.contigs

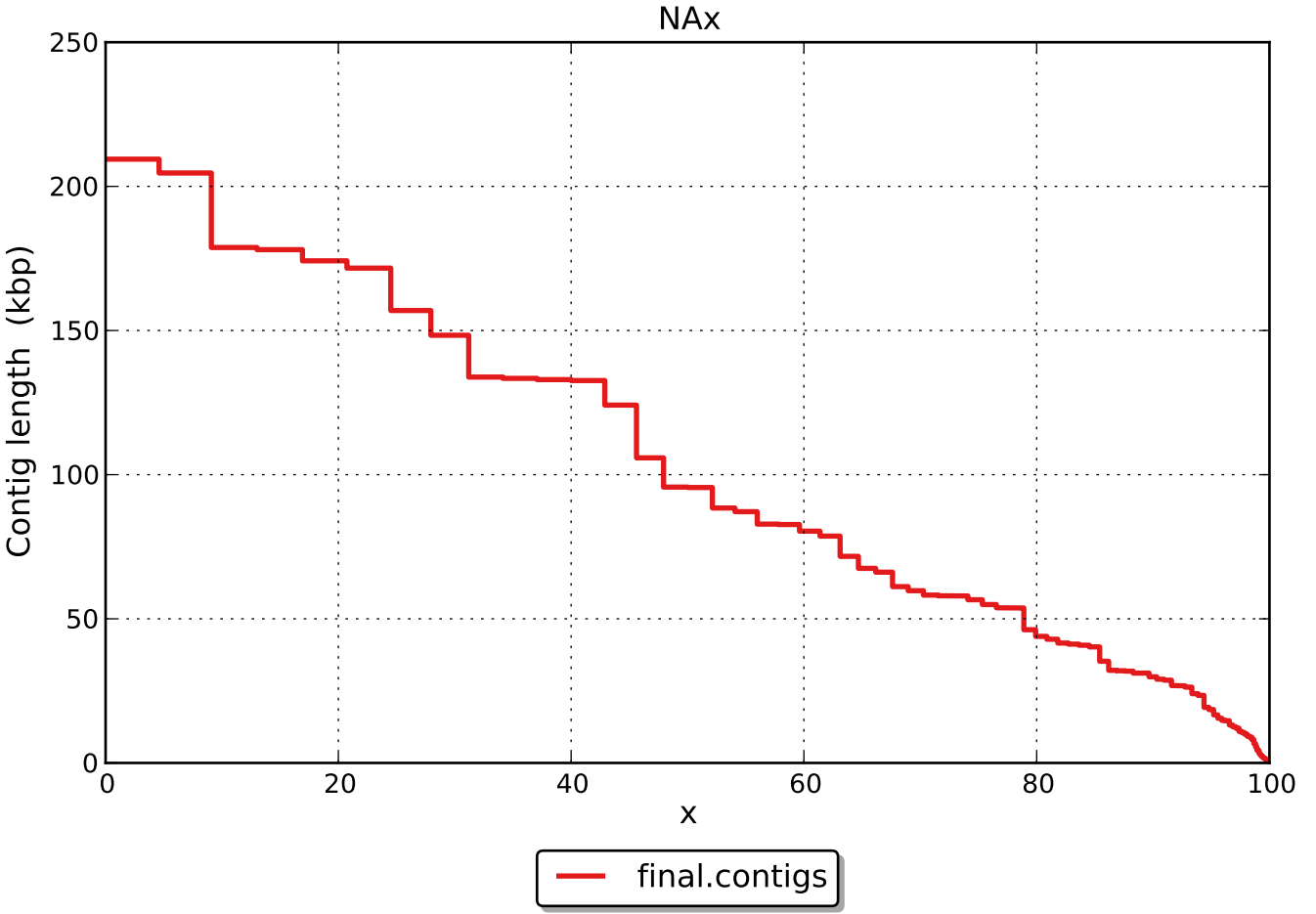

NGx
Contig length (kbp)
250
200
150
100
50
0
0
20
40
60
80
100
x
final.contigs

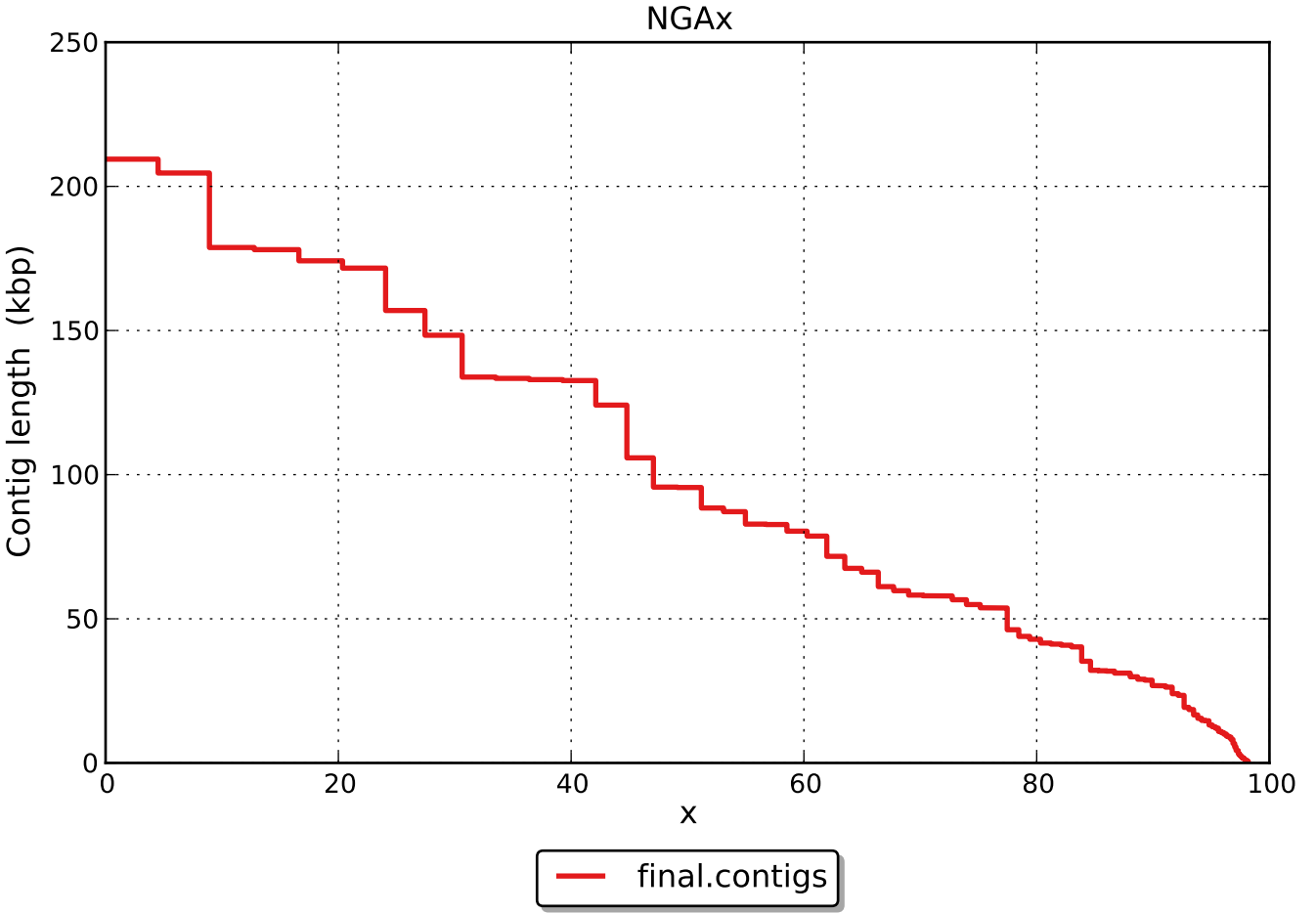

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
100
120
Contig index
final.contigs
Reference


GC content
windows
GC (%)
0
600
1200
1800
2400
3000
0
20
40
60
80
100
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
20
40
60
80
100
120
Contig index
final.contigs
Reference


NAx
Contig length (kbp)
250
200
150
100
50
0
0
20
40
60
80
100
x
final.contigs


NGAx
250
200
150
100
50
0
Contig length (kbp)
0
20
40
60
80
100
x
final.contigs