Report

	final.contigs
# contigs (>= 1000 bp)	348
# contigs (>= 5000 bp)	159
# contigs (>= 10000 bp)	65
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	2117338
Total length (>= 5000 bp)	1591421
Total length (>= 10000 bp)	951971
Total length (>= 25000 bp)	25216
Total length (>= 50000 bp)	0
# contigs	469
Largest contig	25216
Total length	2194235
Reference length	4641652
GC (%)	50.63
Reference GC (%)	50.79
N50	8631
N75	4751
L50	81
L75	171
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	5468
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	46.809
Duplication ratio	1.010
# N's per 100 kbp	0.00
# mismatches per 100 kbp	421.92
# indels per 100 kbp	0.00
Largest alignment	25216
NA50	8631
NGA50	-
NA75	4751
LA50	81
LA75	171

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

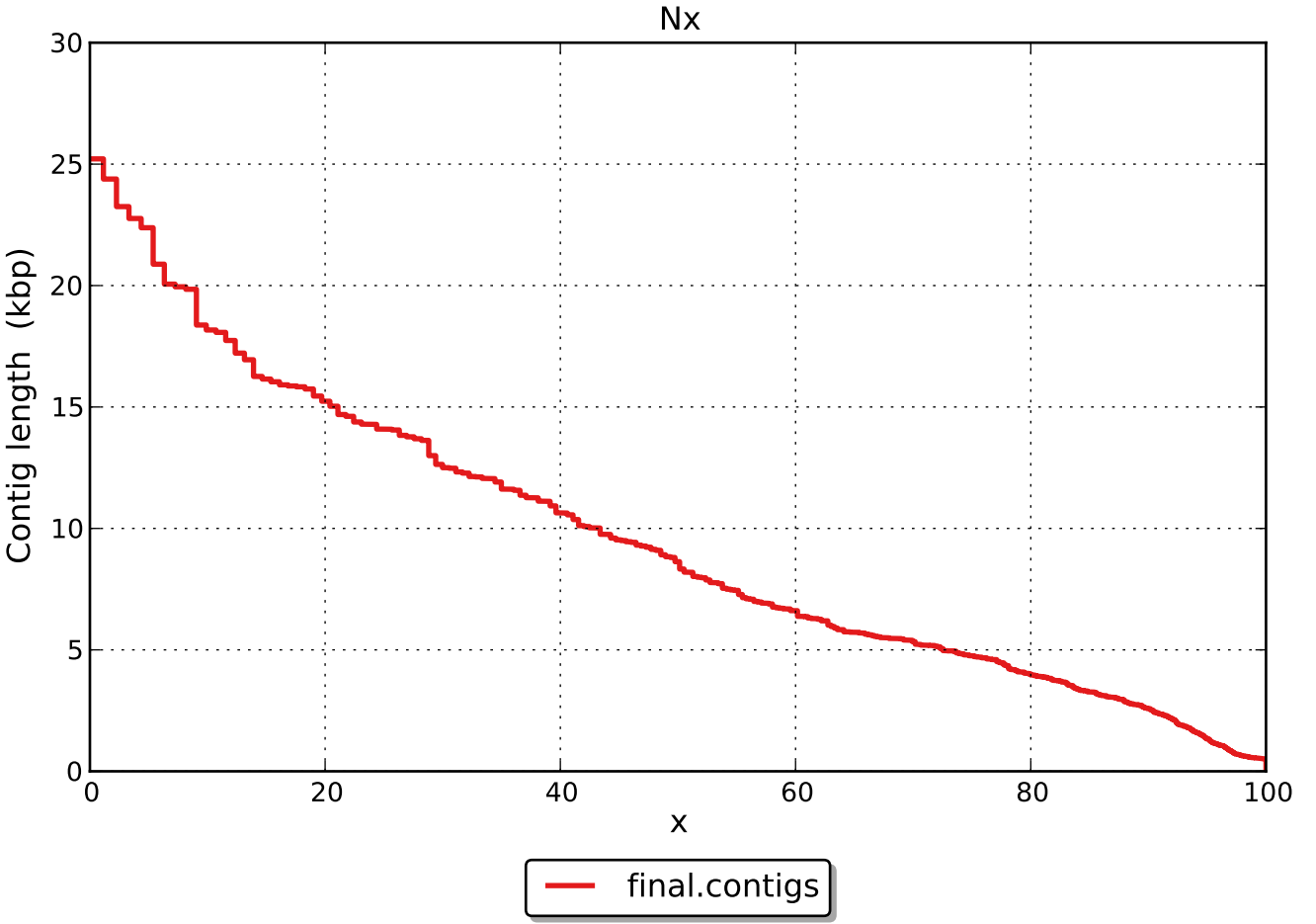
	final.contigs
# misassemblies	1
# relocations	0
# translocations	0
# inversions	1
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	5468
# local misassemblies	0
# mismatches	9167
# indels	0
# short indels	0
# long indels	0
Indels length	0

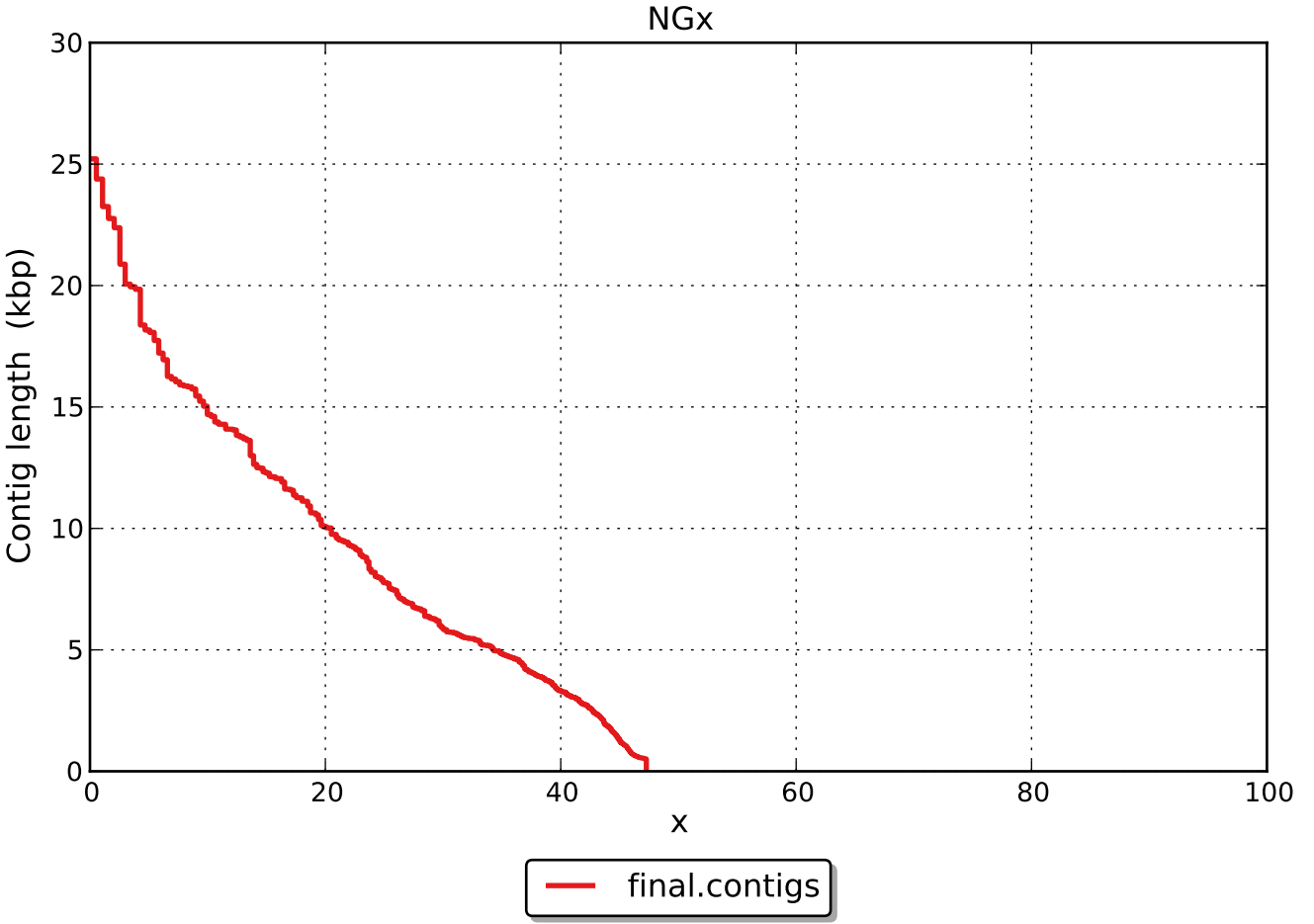
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

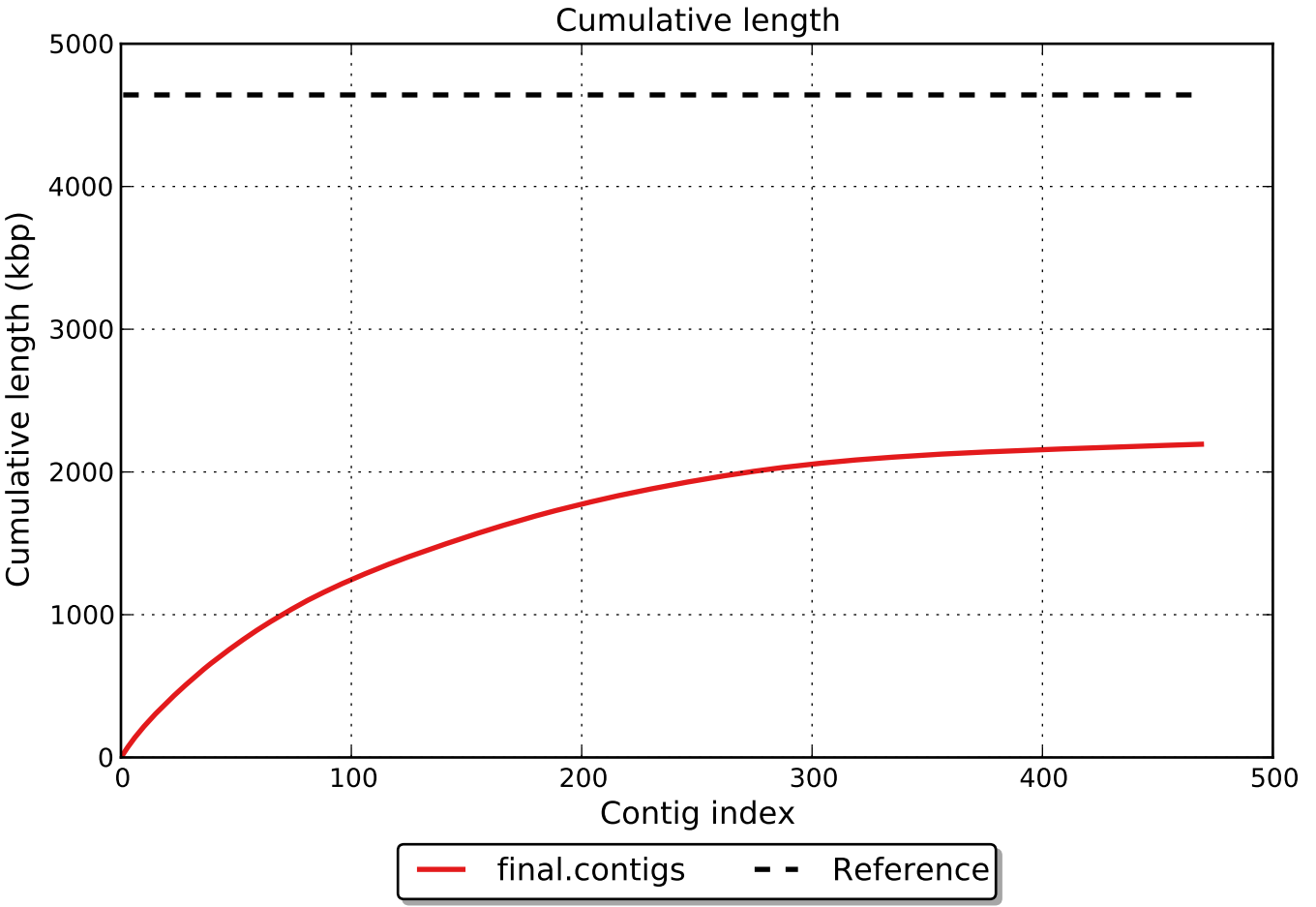
Unaligned report

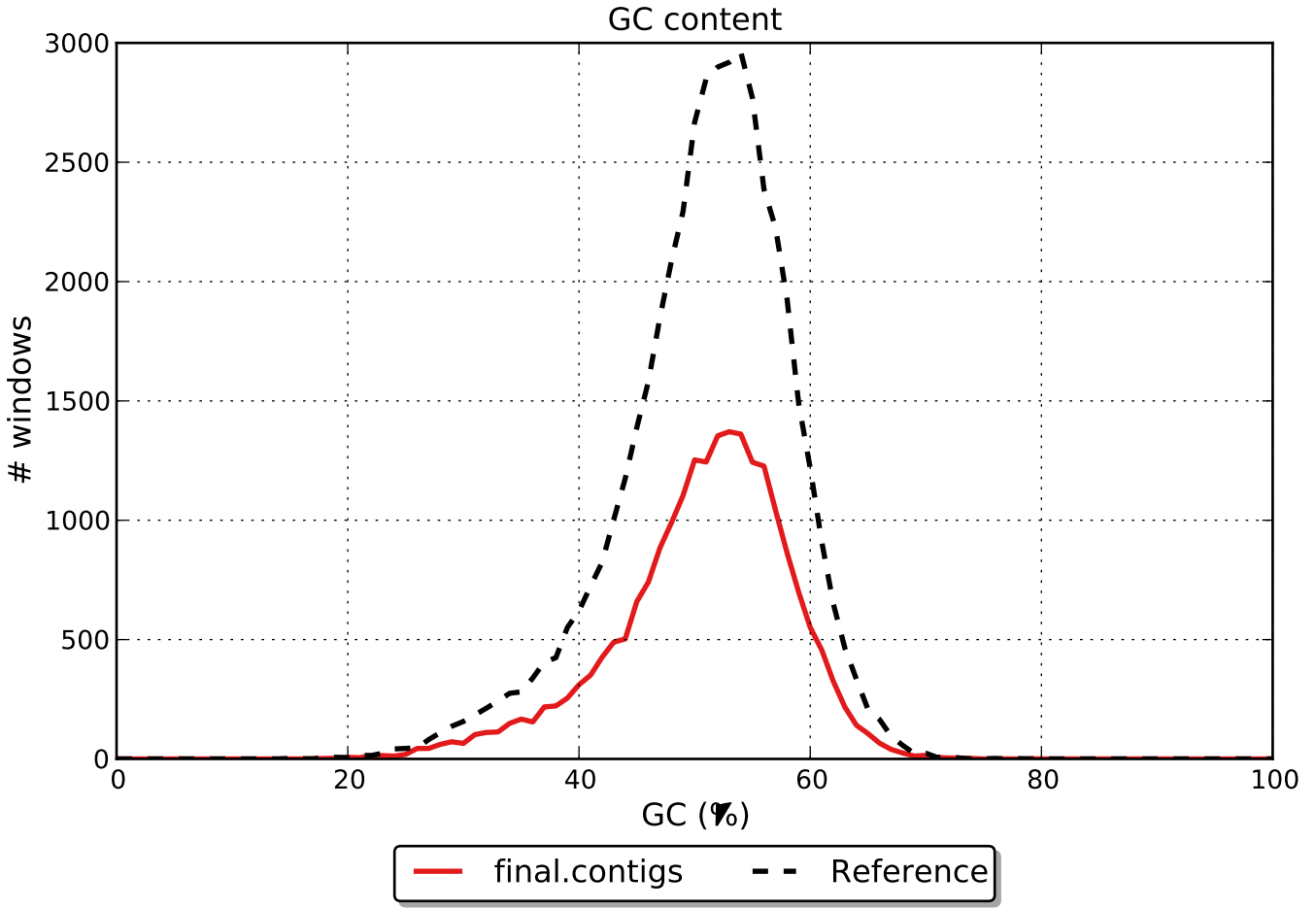
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

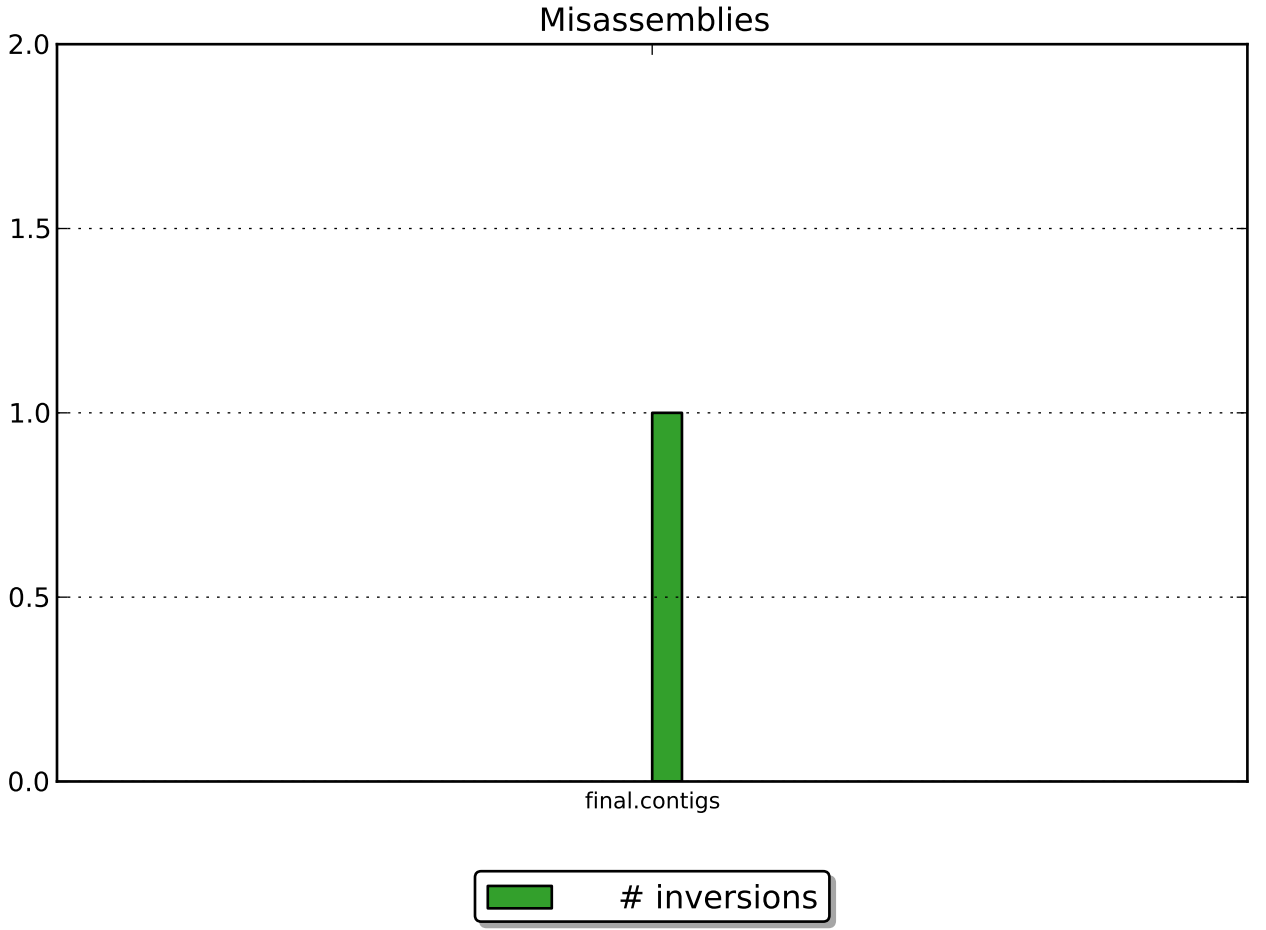
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

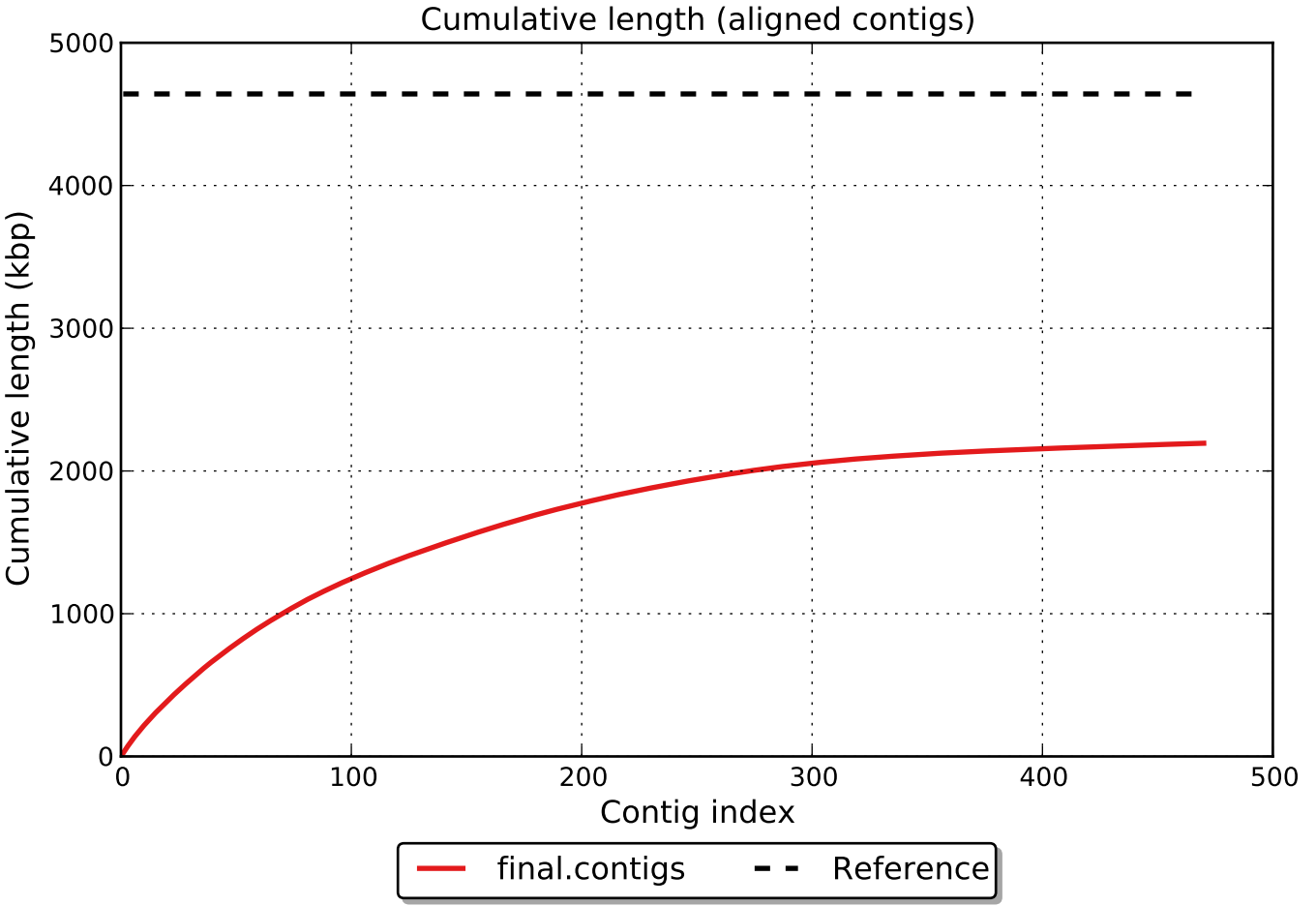

Nx
Contig length (kbp)
30
25
20
15
10
5
0
0
20
40
60
80
100
x
final.contigs

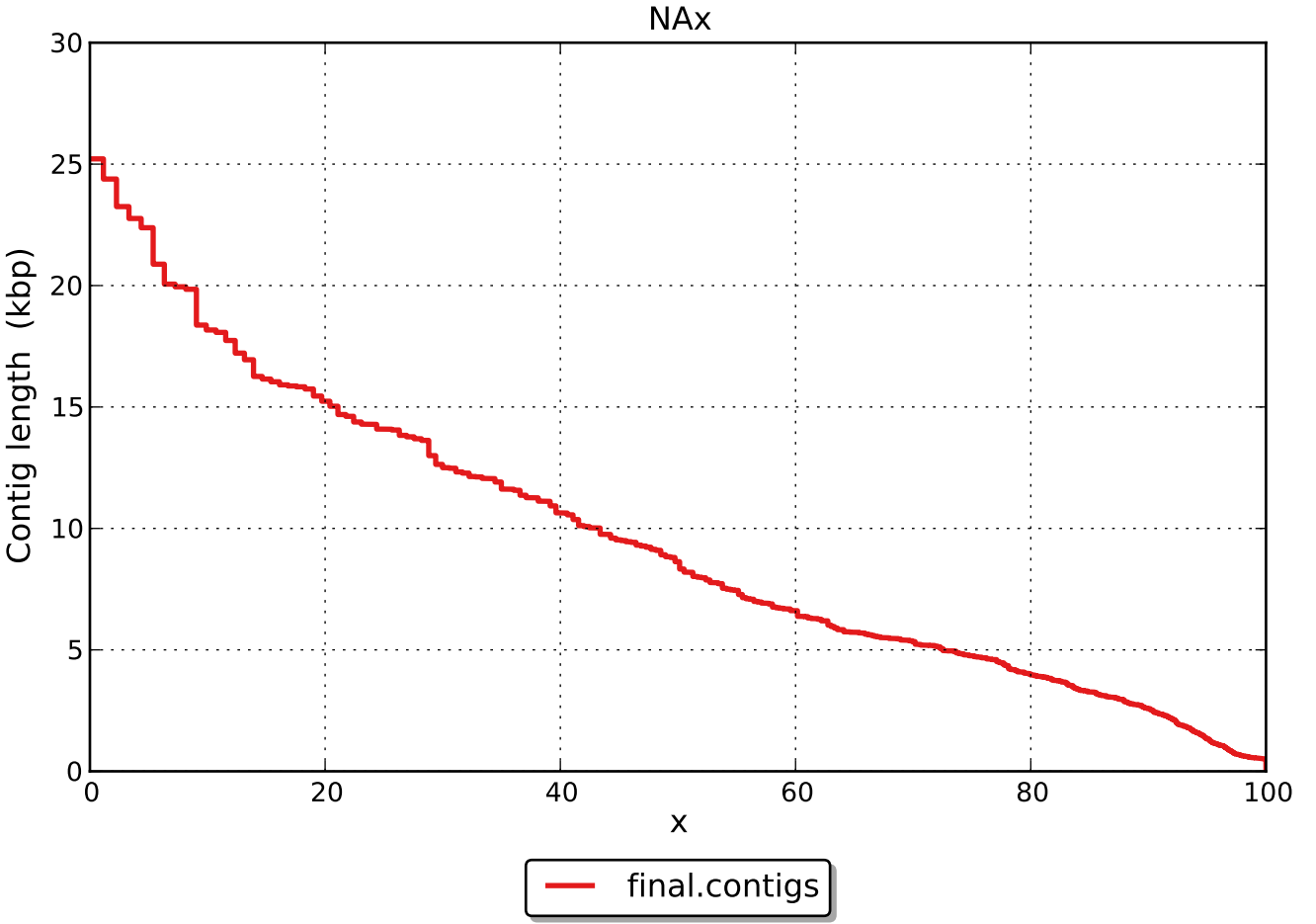

NGx
Contig length (kbp)
30
25
20
15
10
5
0
0
20
40
60
80
100
x
final.contigs

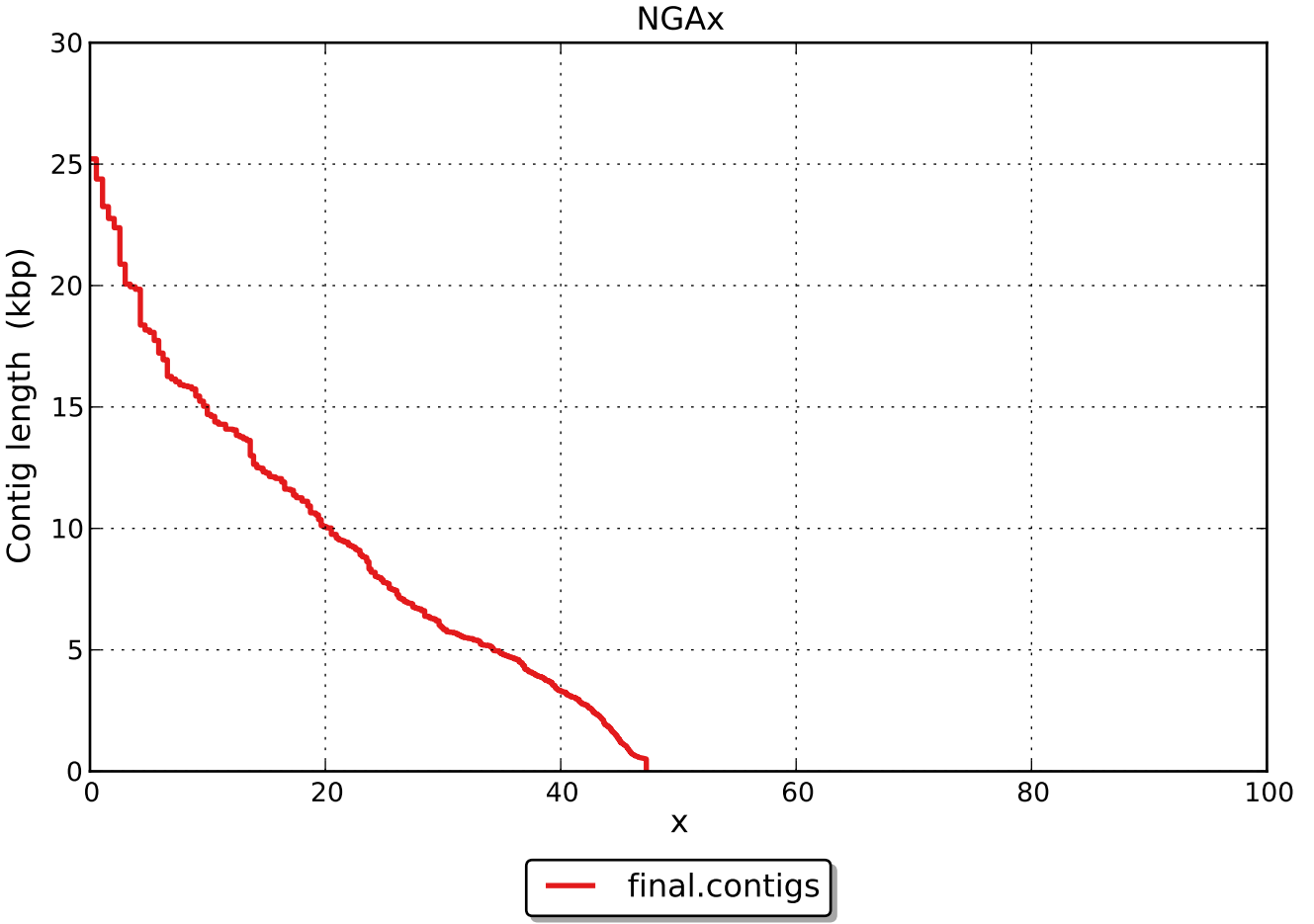

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
100
200
300
400
500
Contig index
final.contigs
Reference


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


Misassemblies
2.0
1.5
1.0
0.5
0.0
final.contigs
inversions


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
100
200
300
400
500
Contig index
final.contigs
Reference


NAx
Contig length (kbp)
30
25
20
15
10
5
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (kbp)
30
25
20
15
10
5
0
0
20
40
60
80
100
x
final.contigs