Report

	final.contigs
# contigs (>= 1000 bp)	1128
# contigs (>= 5000 bp)	284
# contigs (>= 10000 bp)	63
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4459463
Total length (>= 5000 bp)	2261777
Total length (>= 10000 bp)	790814
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	1350
Largest contig	24295
Total length	4625308
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	4891
NG50	4888
N75	2992
NG75	2948
L50	295
LG50	296
L75	595
LG75	600
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	97.488
Duplication ratio	1.022
# N's per 100 kbp	0.00
# mismatches per 100 kbp	9.24
# indels per 100 kbp	0.00
Largest alignment	24295
NA50	4891
NGA50	4888
NA75	2992
NGA75	2948
LA50	295
LGA50	296
LA75	595
LGA75	600

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

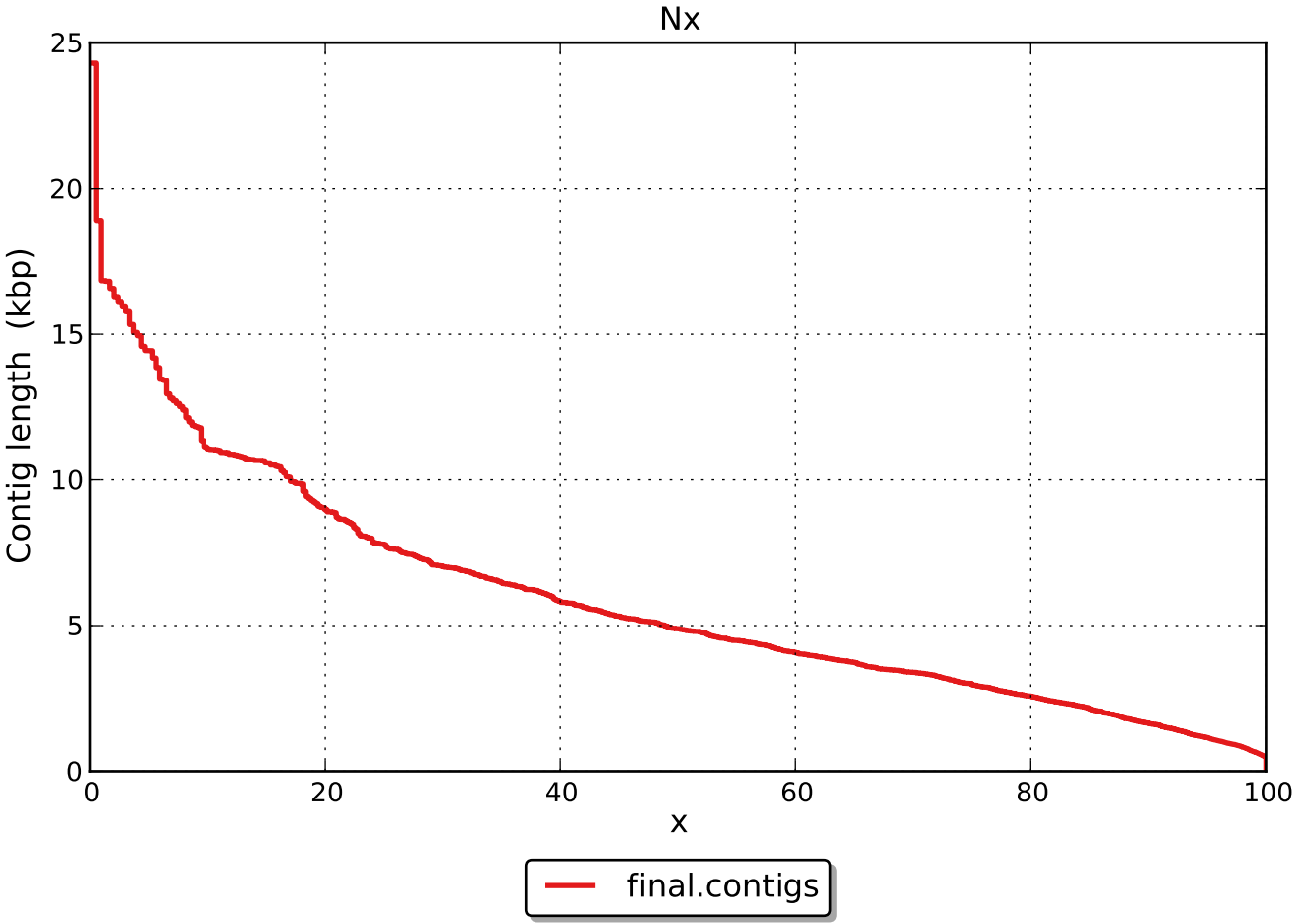
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	418
# indels	0
# short indels	0
# long indels	0
Indels length	0

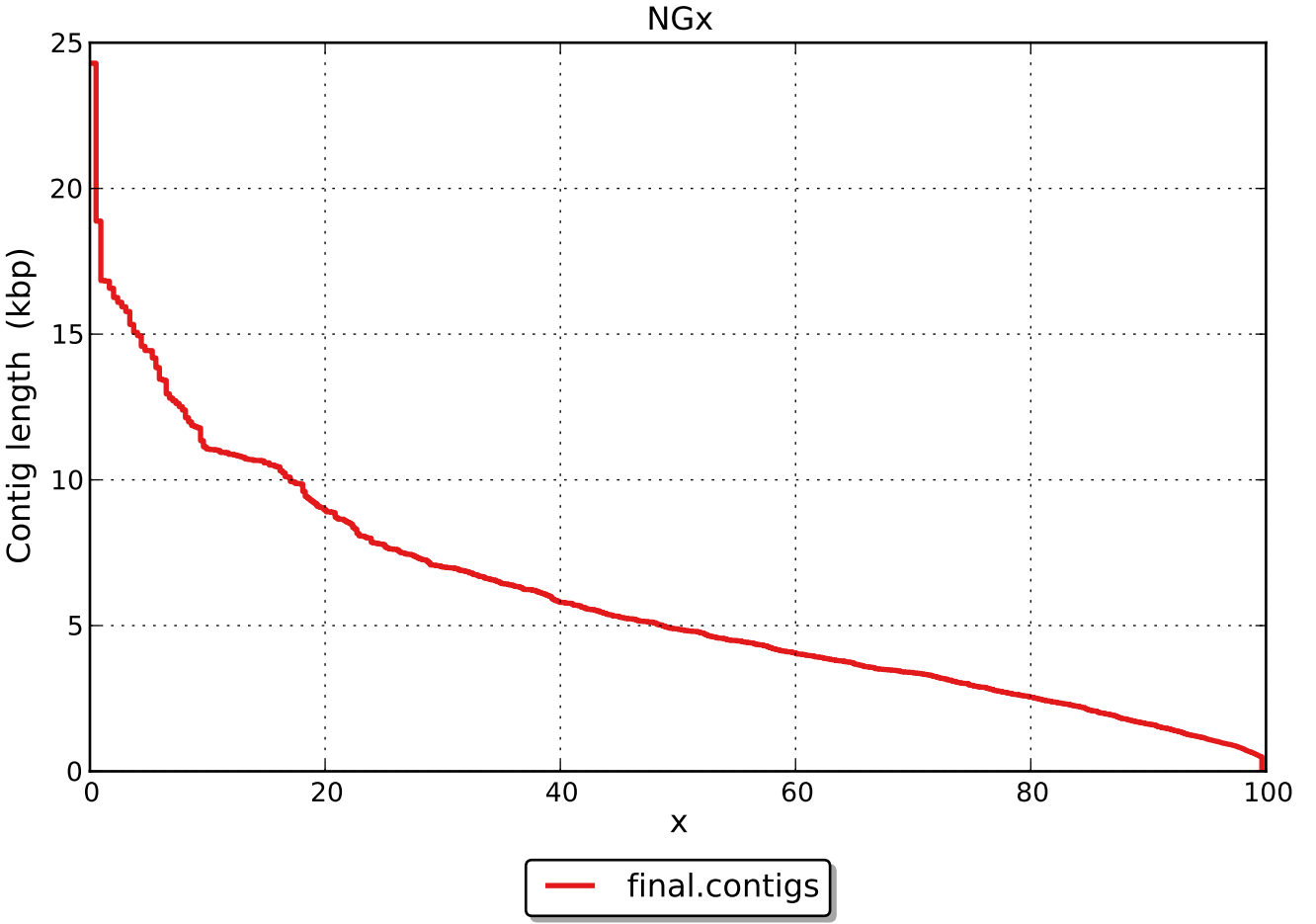
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

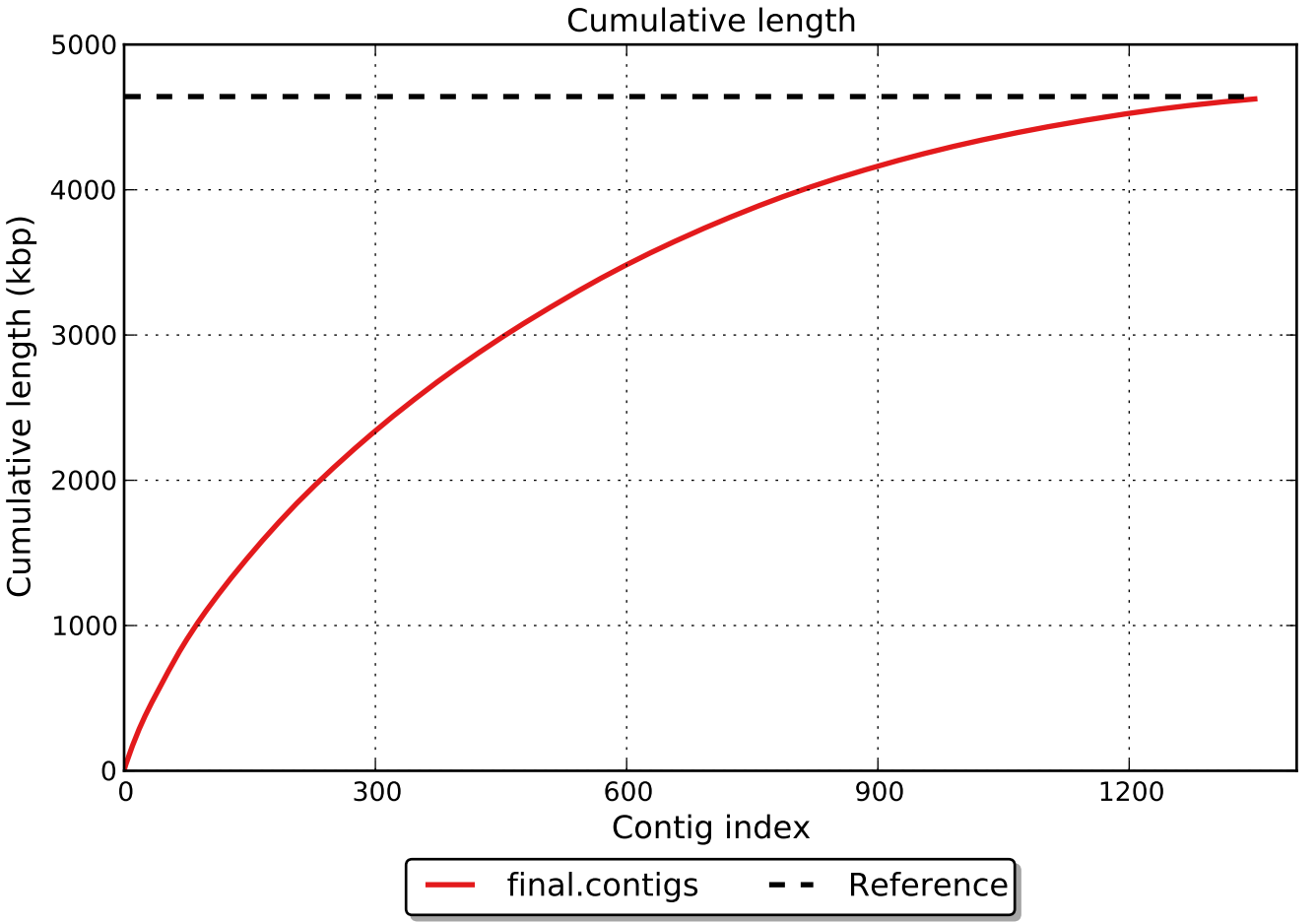
Unaligned report

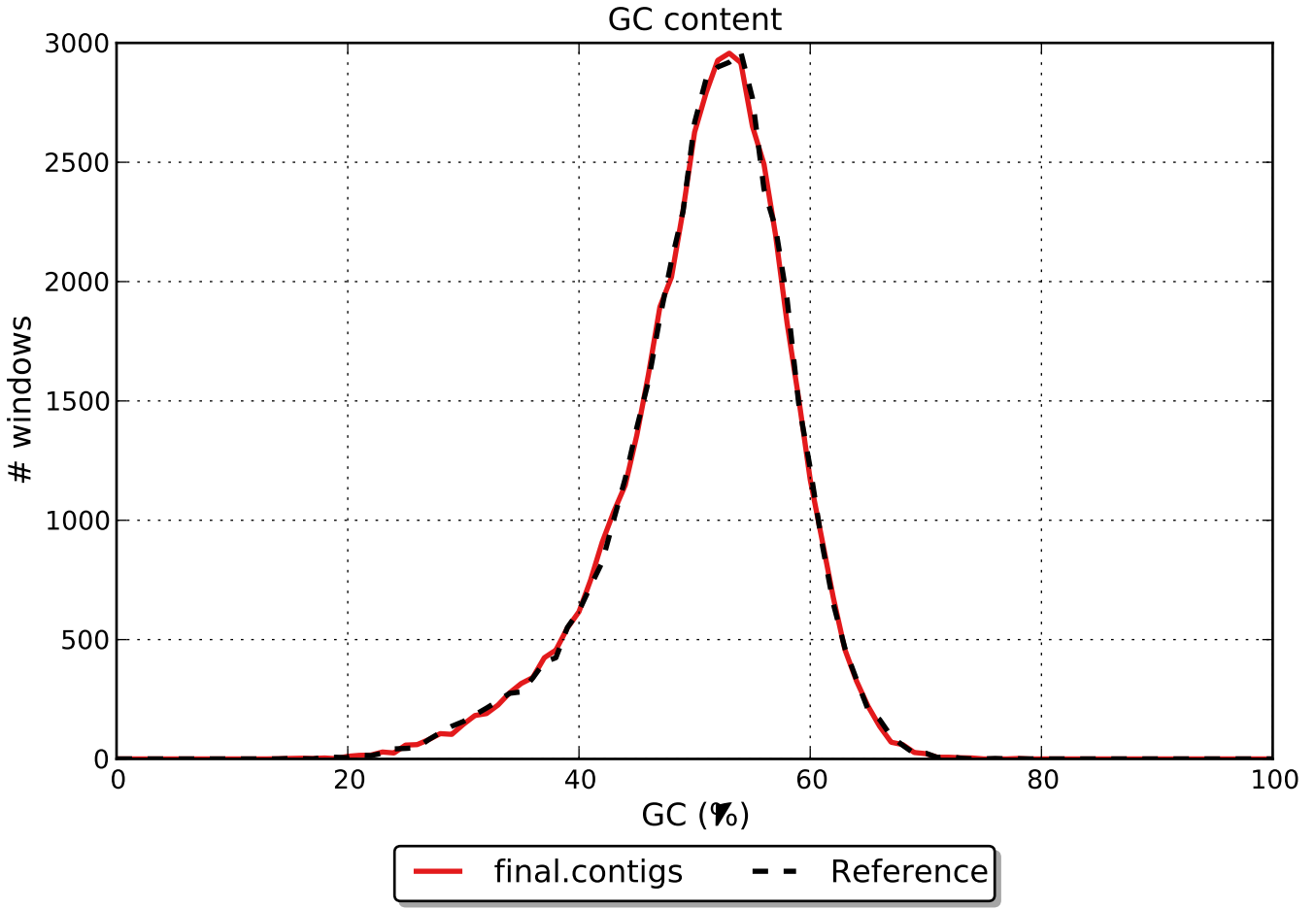
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

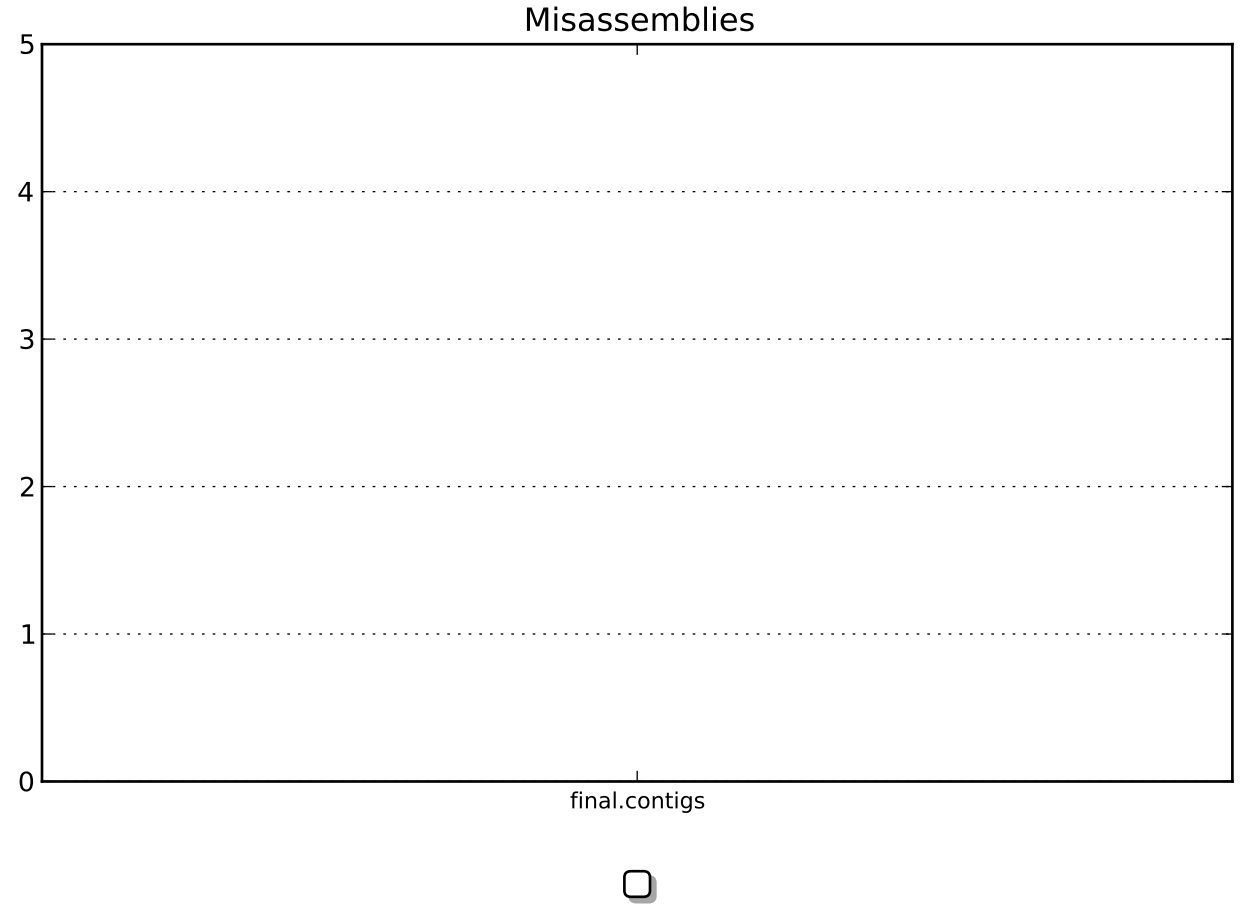
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

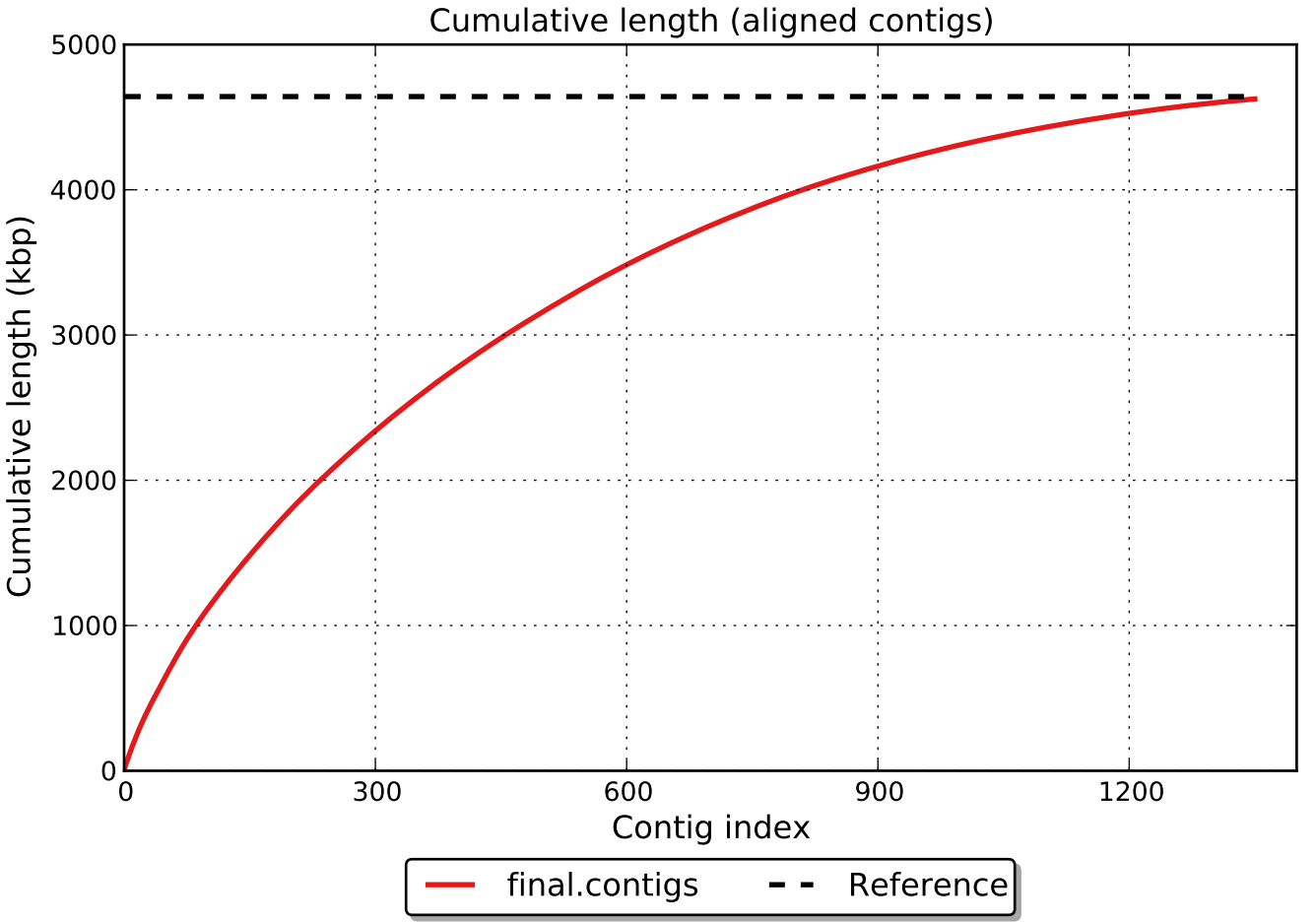

Nx
Contig length (kbp)
25
20
15
10
5
0
0
20
40
60
80
100
x
final.contigs

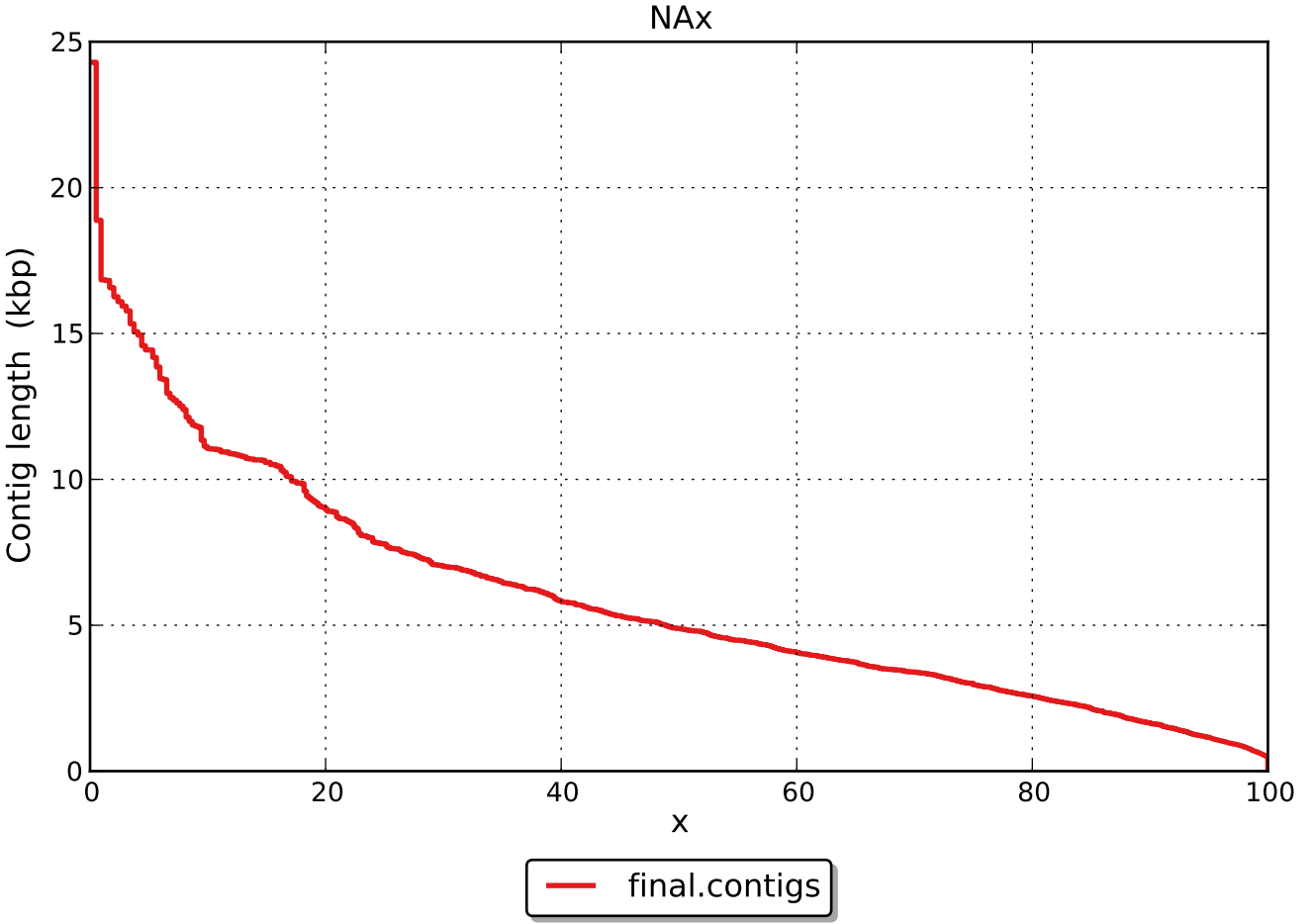

NGx
Contig length (kbp)
25
20
15
10
5
0
0
20
40
60
80
100
x
final.contigs

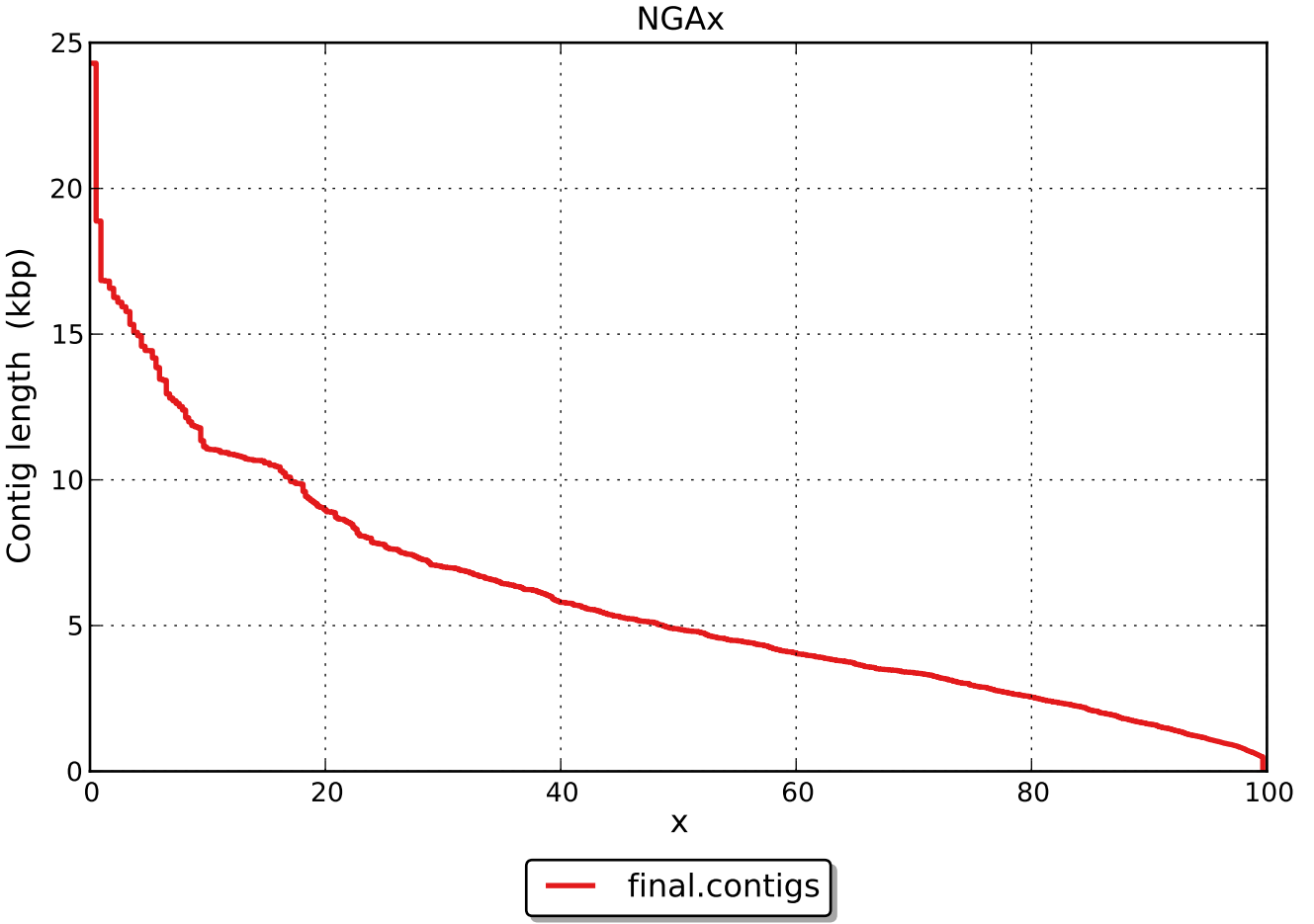

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
300
600
900
1200
Contig index
final.contigs
Reference


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


Misassemblies
5
4
3
2
1
0
final.contigs


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
300
600
900
1200
Contig index
final.contigs
Reference


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


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