Report

	final.contigs
# contigs (>= 1000 bp)	675
# contigs (>= 5000 bp)	354
# contigs (>= 10000 bp)	136
# contigs (>= 25000 bp)	17
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4635389
Total length (>= 5000 bp)	3748891
Total length (>= 10000 bp)	2196745
Total length (>= 25000 bp)	496844
Total length (>= 50000 bp)	0
# contigs	750
Largest contig	39629
Total length	4690367
Reference length	4641652
GC (%)	50.79
Reference GC (%)	50.79
N50	9534
NG50	9640
N75	5624
NG75	5696
L50	152
LG50	149
L75	311
LG75	304
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.801
Duplication ratio	1.013
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.04
# indels per 100 kbp	0.00
Largest alignment	39629
NA50	9534
NGA50	9640
NA75	5624
NGA75	5696
LA50	152
LGA50	149
LA75	311
LGA75	304

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

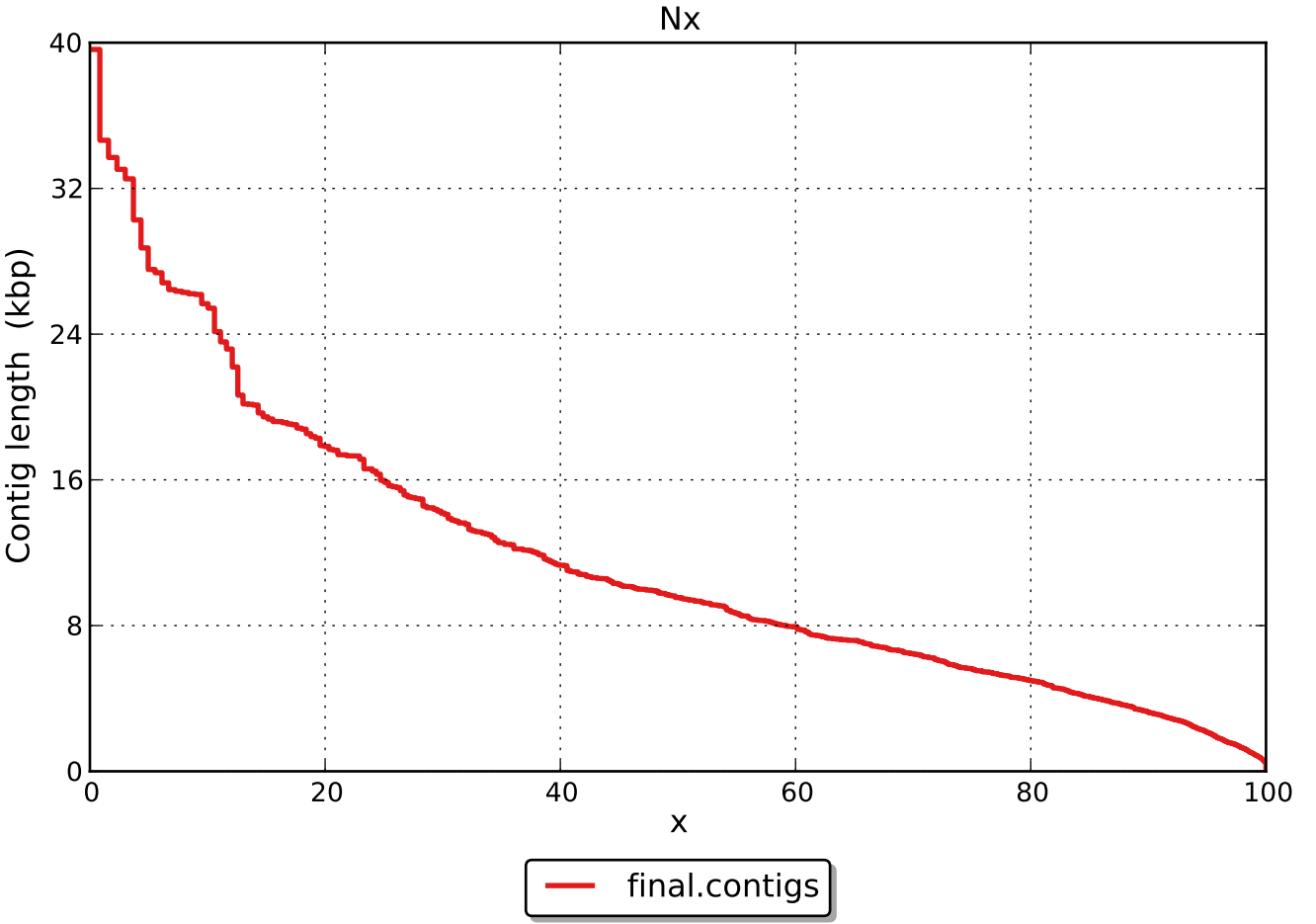
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	2
# indels	0
# short indels	0
# long indels	0
Indels length	0

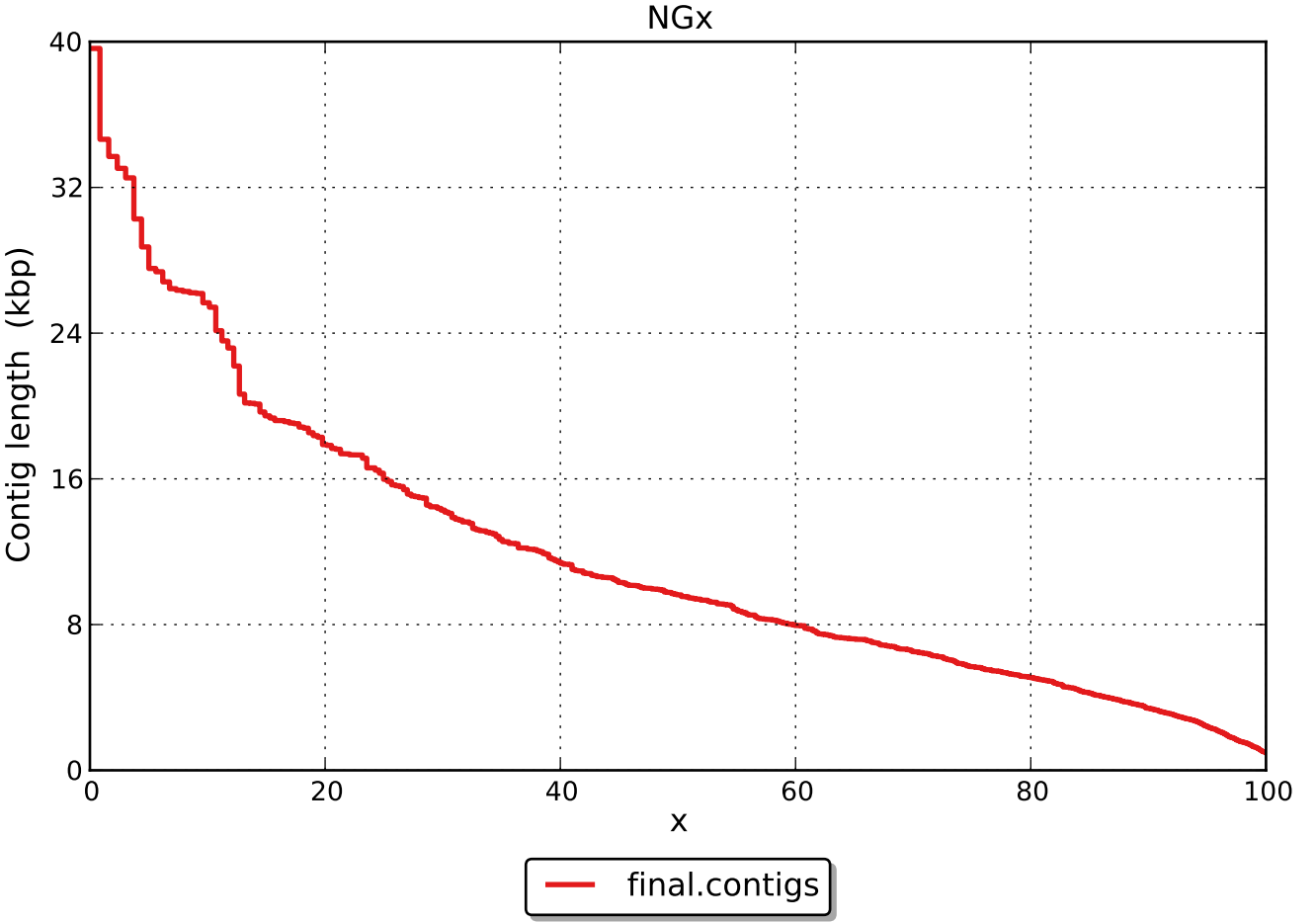
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

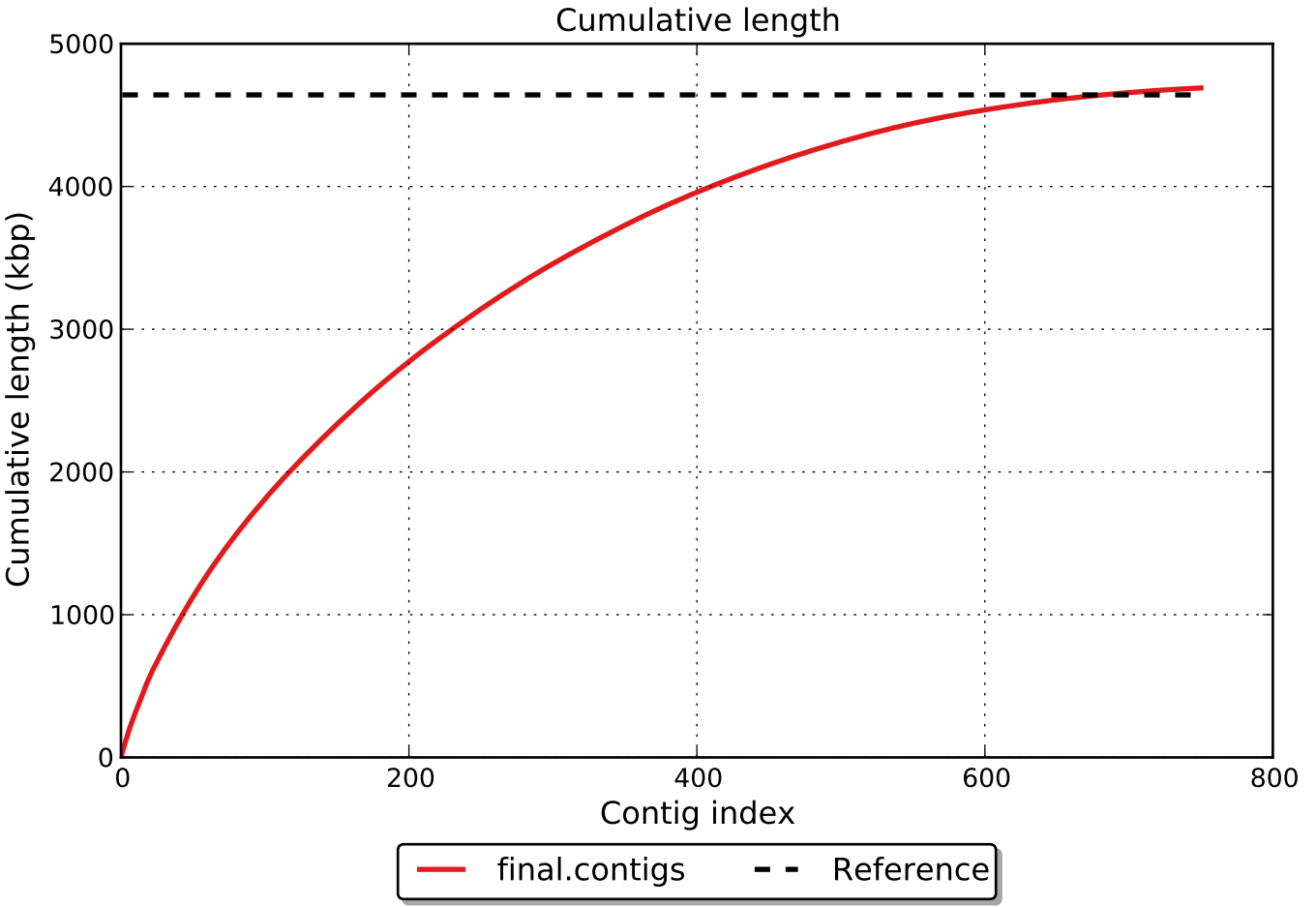
Unaligned report

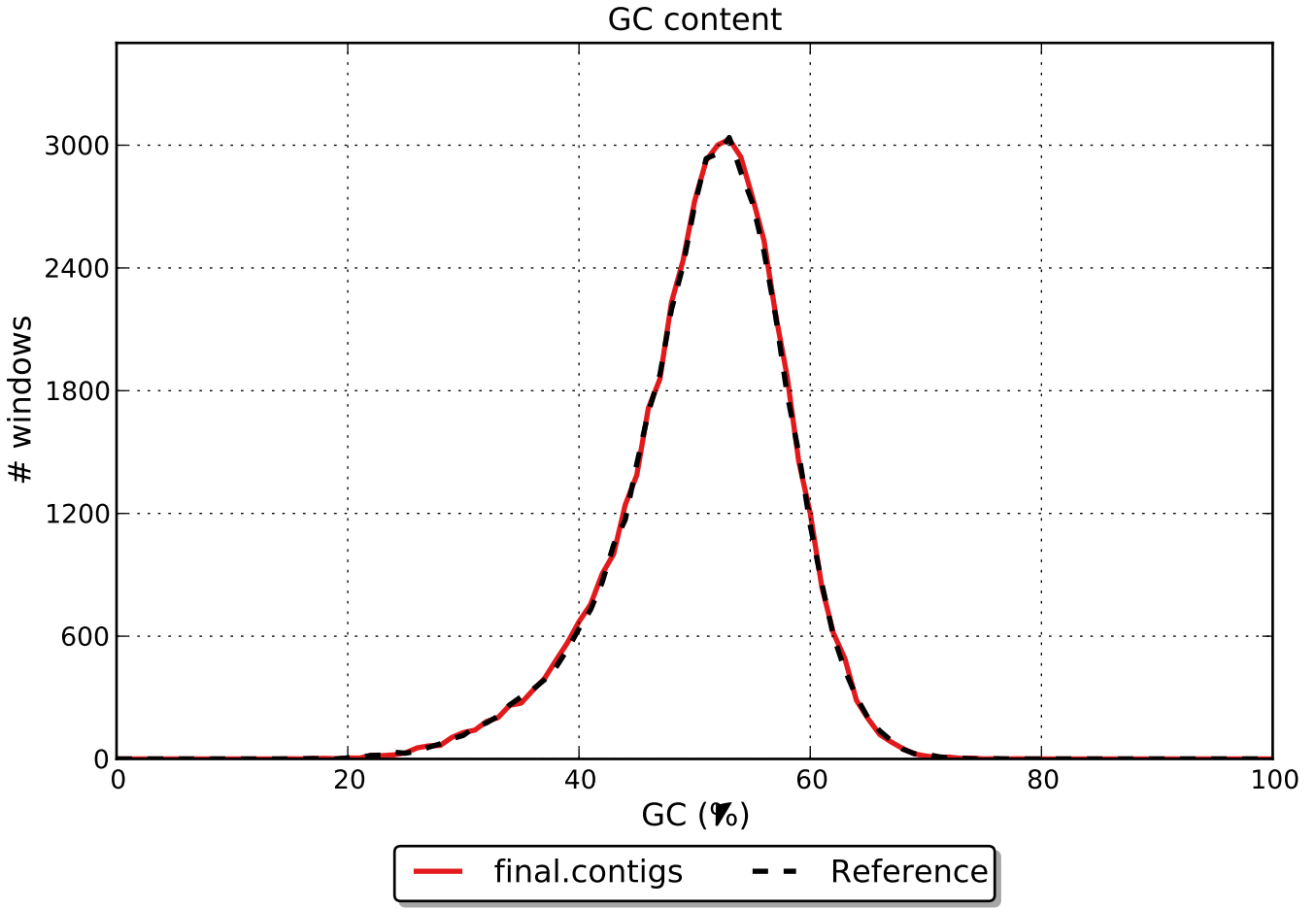
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

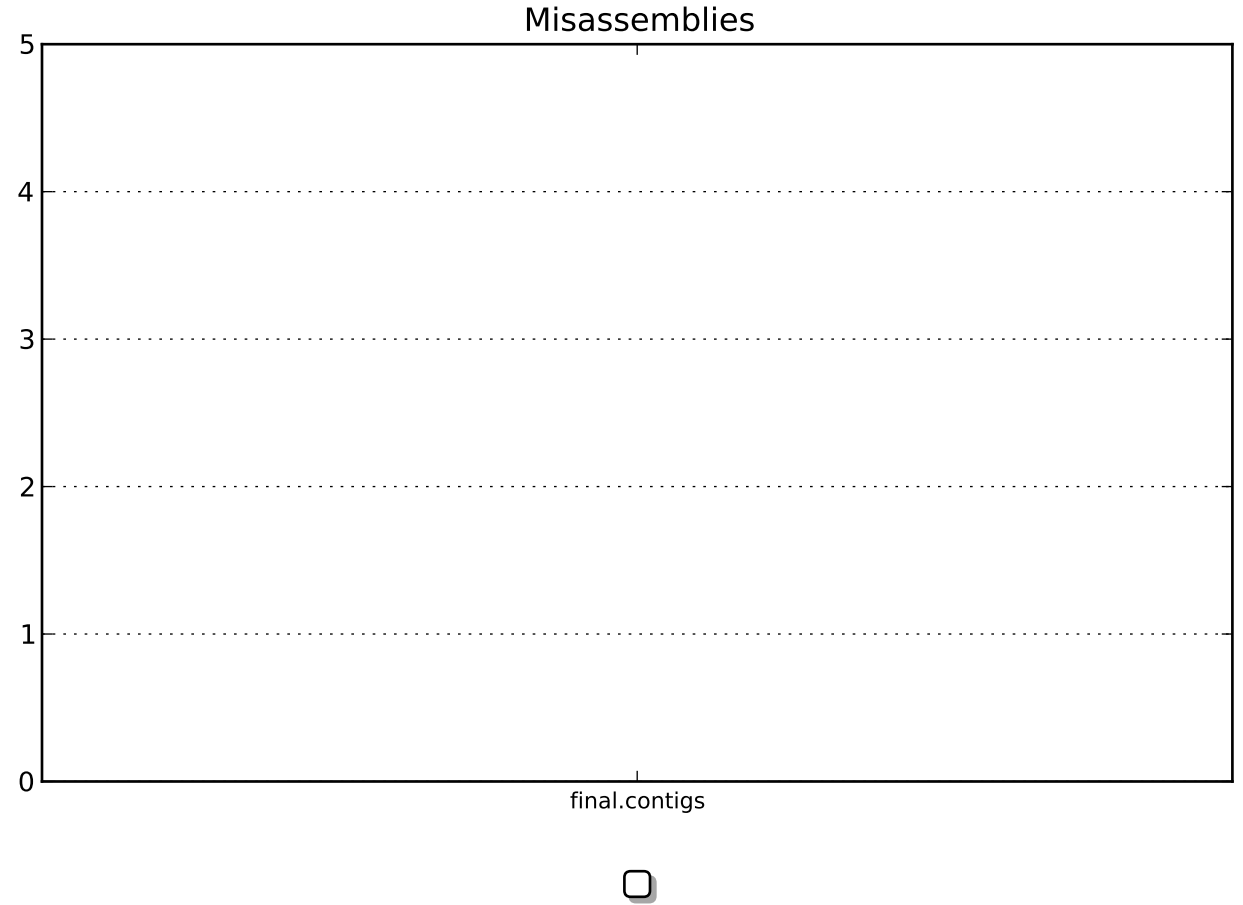
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

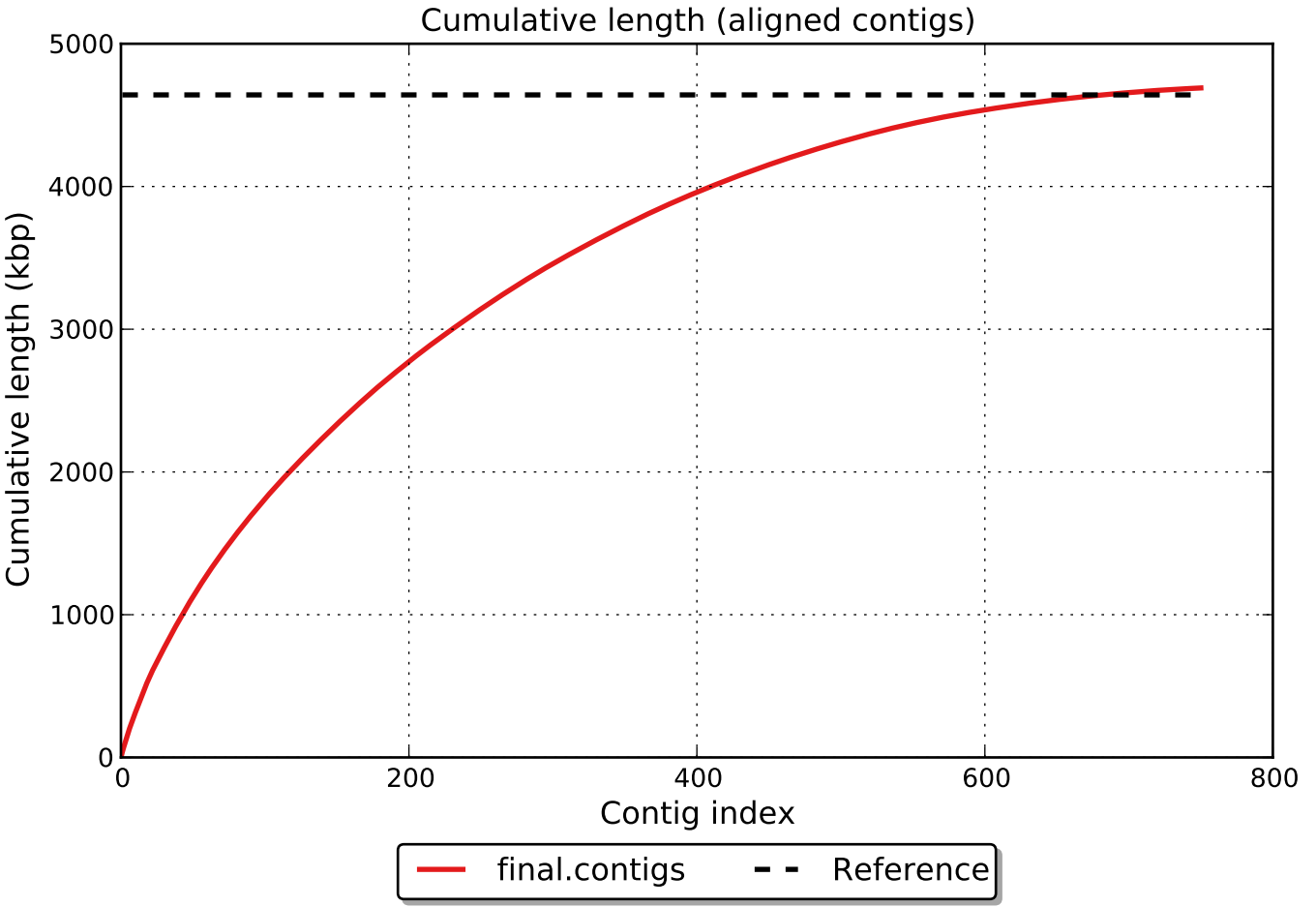

Nx
Contig length (kbp)
40
32
24
16
8
0
0
20
40
60
80
100
x
final.contigs

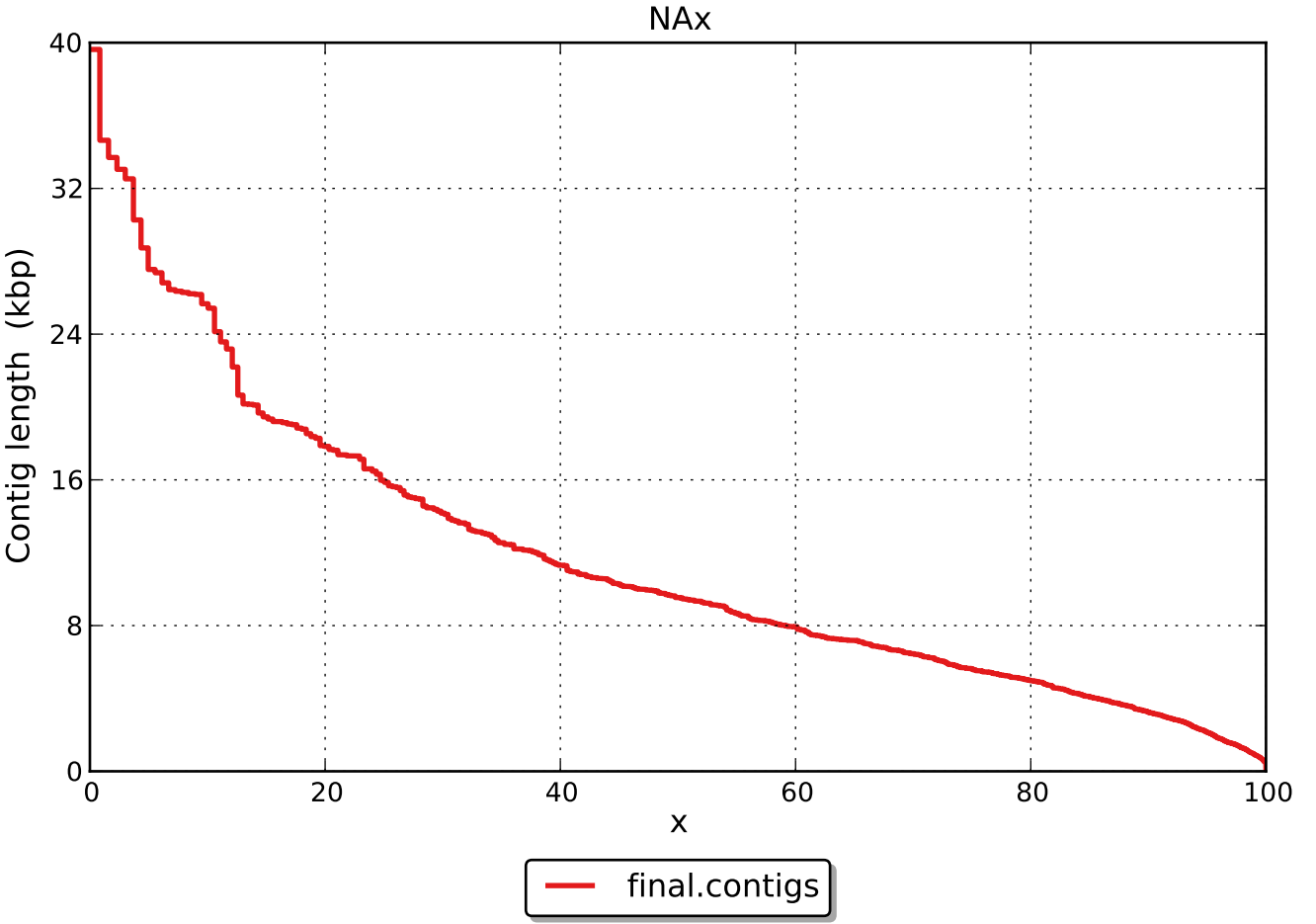

NGx
Contig length (kbp)
40
32
24
16
8
0
0
20
40
60
80
100
x
final.contigs

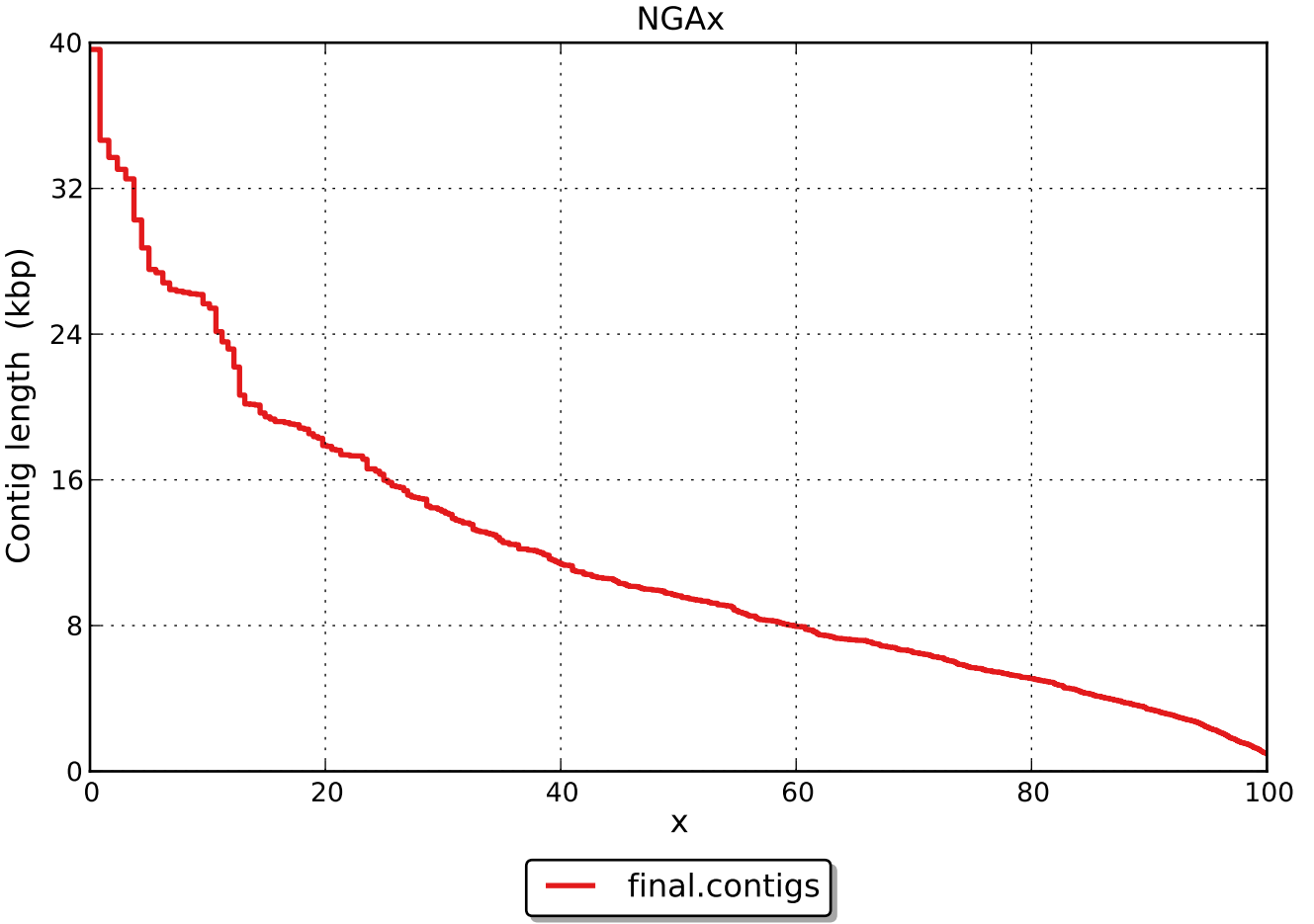

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
200
400
600
800
Contig index
final.contigs
Reference


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
200
400
600
800
Contig index
final.contigs
Reference


NAx
Contig length (kbp)
40
32
24
16
8
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (kbp)
40
32
24
16
8
0
0
20
40
60
80
100
x
final.contigs