Report

	final.contigs
# contigs (>= 1000 bp)	711
# contigs (>= 5000 bp)	343
# contigs (>= 10000 bp)	126
# contigs (>= 25000 bp)	10
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4532792
Total length (>= 5000 bp)	3521706
Total length (>= 10000 bp)	1959553
Total length (>= 25000 bp)	295277
Total length (>= 50000 bp)	0
# contigs	805
Largest contig	45348
Total length	4602596
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	9051
NG50	8818
N75	5232
NG75	5109
L50	162
LG50	165
L75	330
LG75	336
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	15101
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	97.931
Duplication ratio	1.013
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.64
# indels per 100 kbp	0.00
Largest alignment	45348
NA50	8912
NGA50	8818
NA75	5232
NGA75	5109
LA50	163
LGA50	165
LA75	330
LGA75	336

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

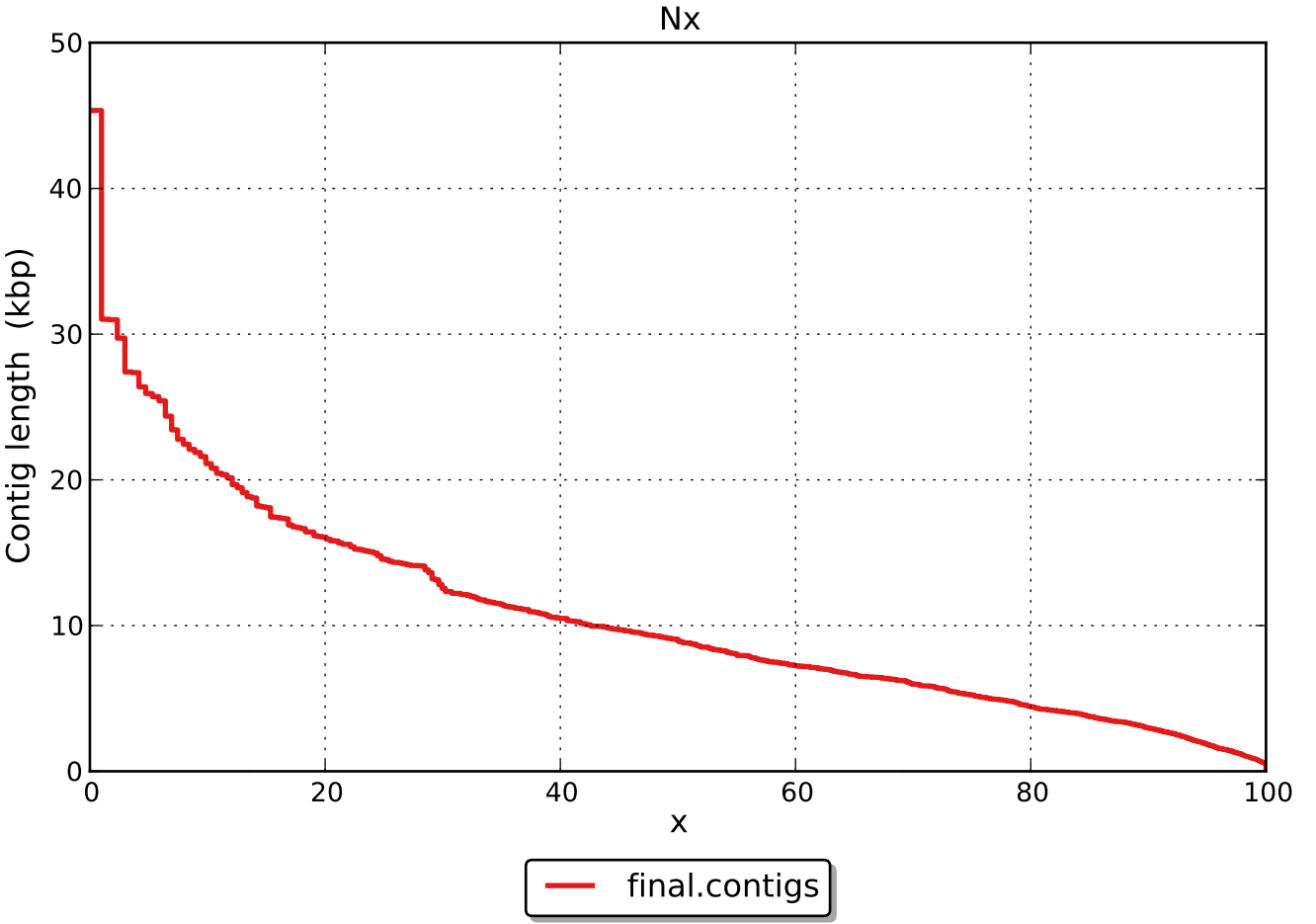
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	15101
# local misassemblies	0
# mismatches	29
# indels	0
# short indels	0
# long indels	0
Indels length	0

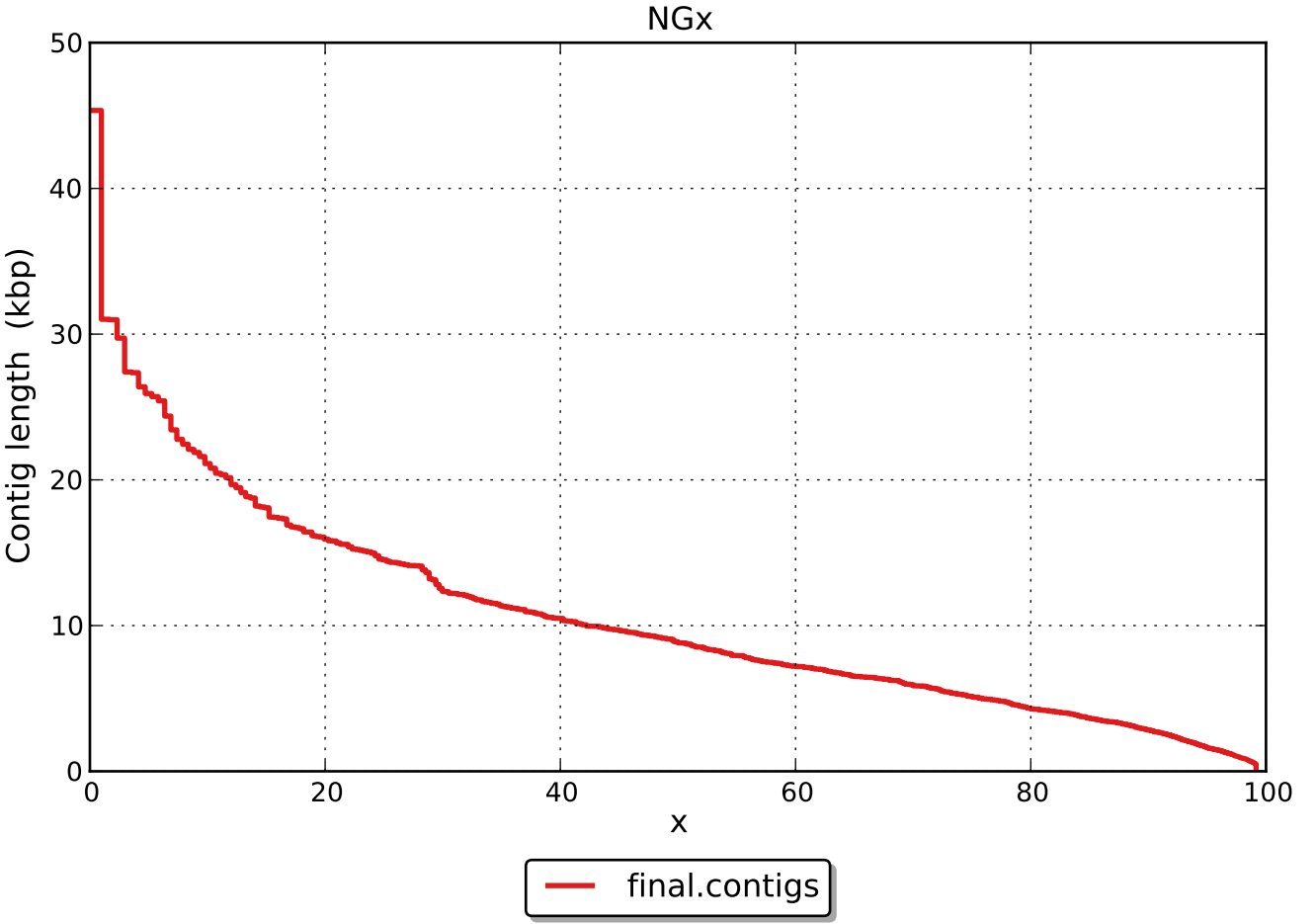
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

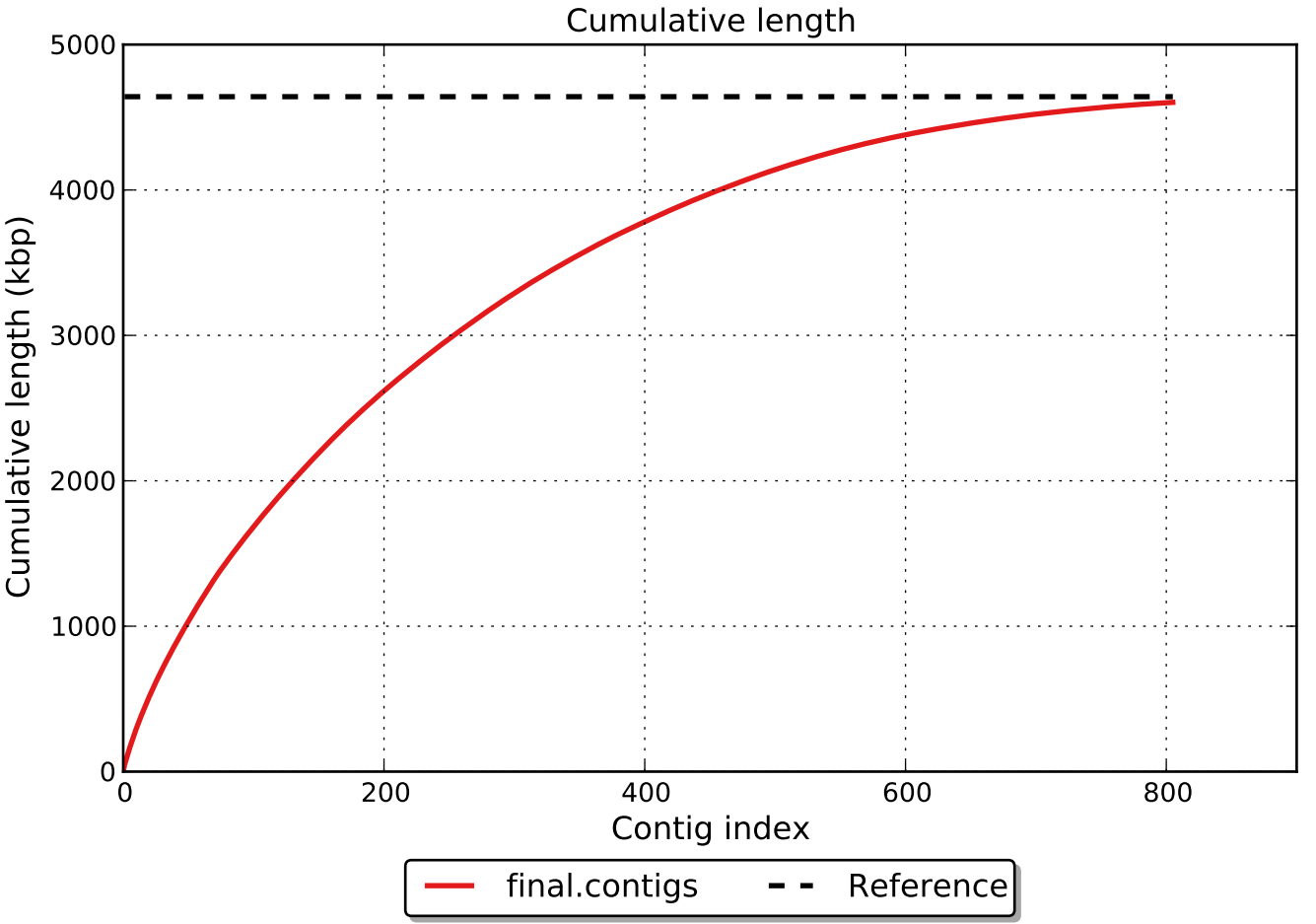
Unaligned report

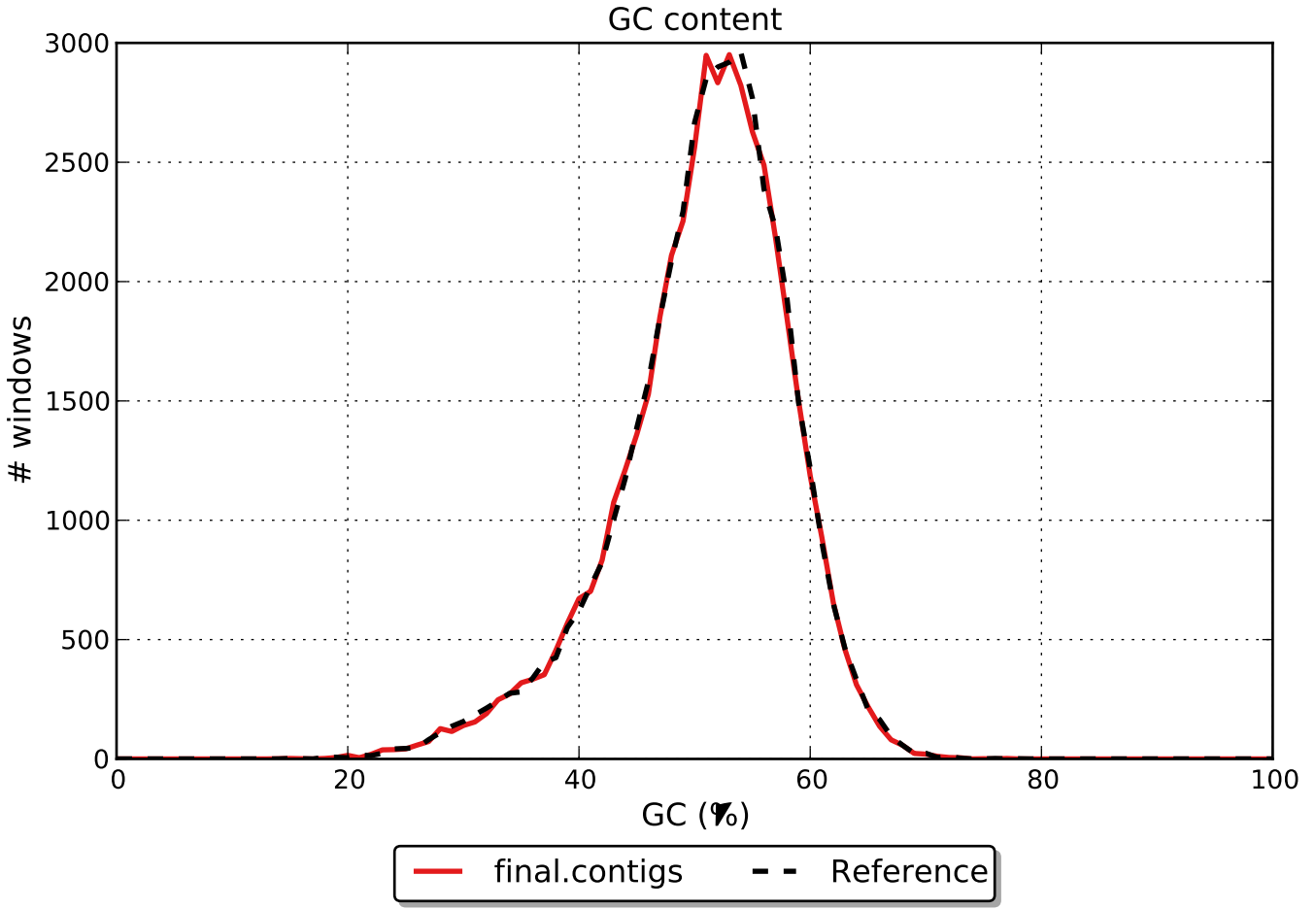
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

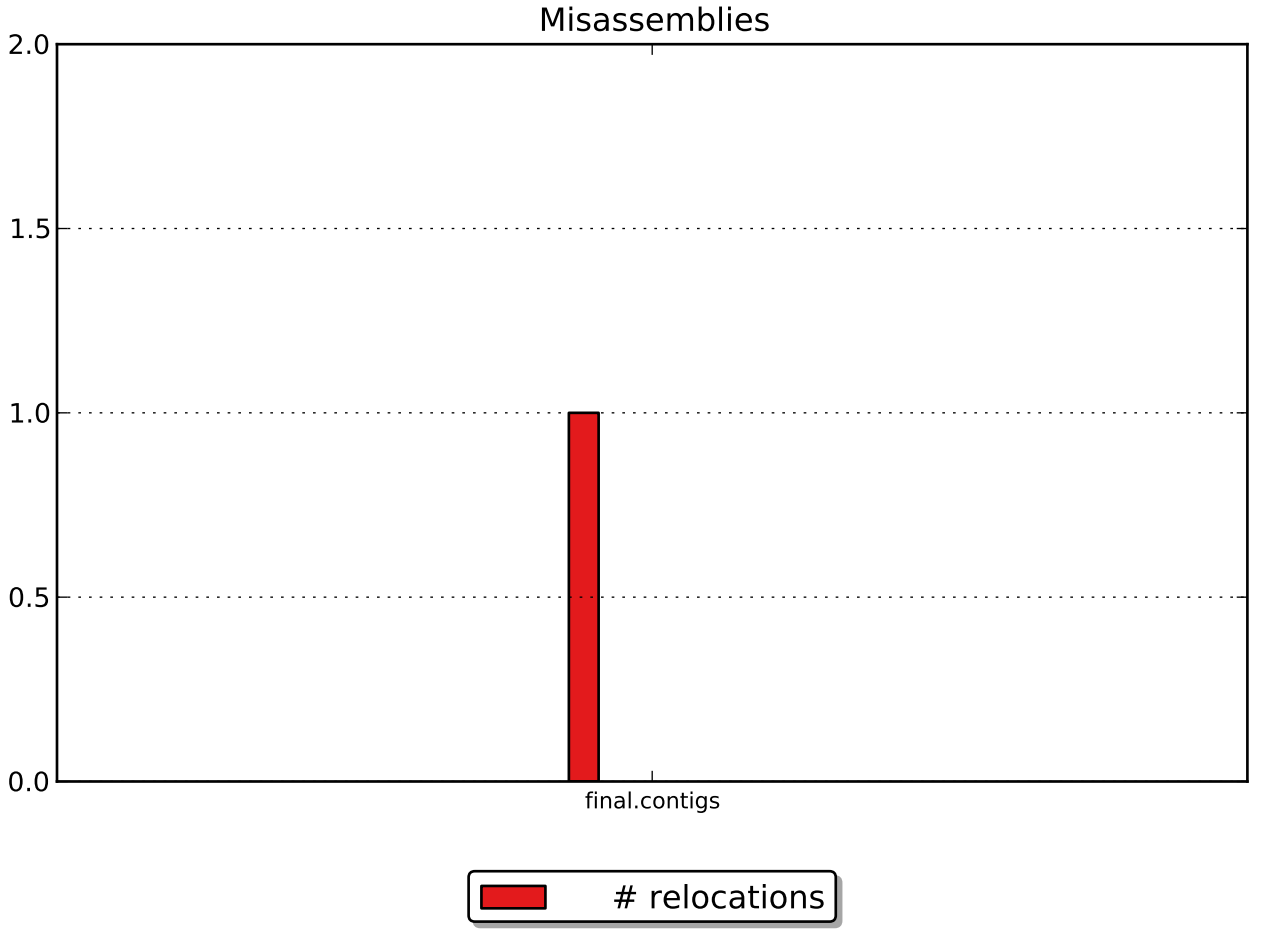
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

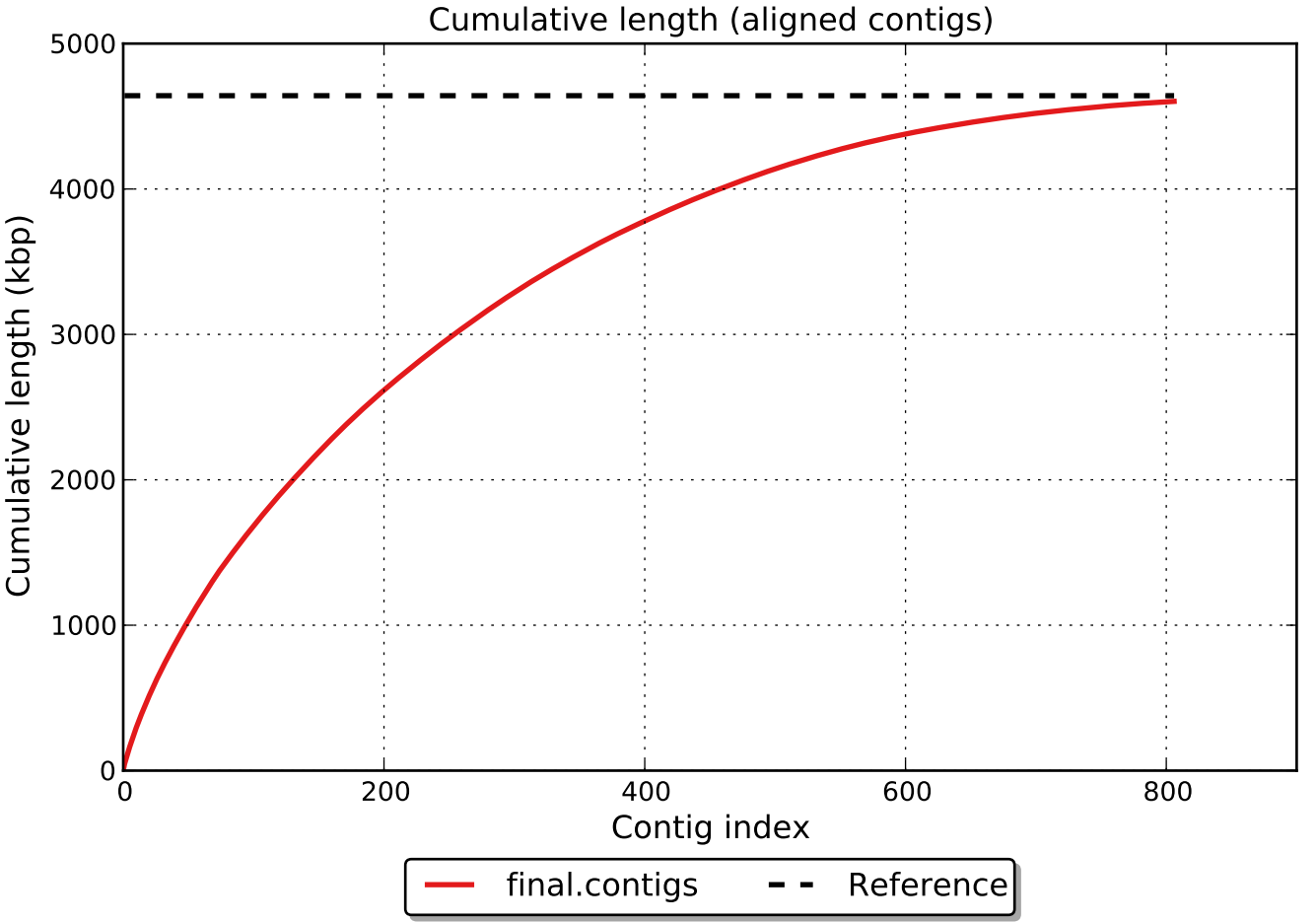

Nx
Contig length (kbp)
50
40
30
20
10
0
0
20
40
60
80
100
x
final.contigs

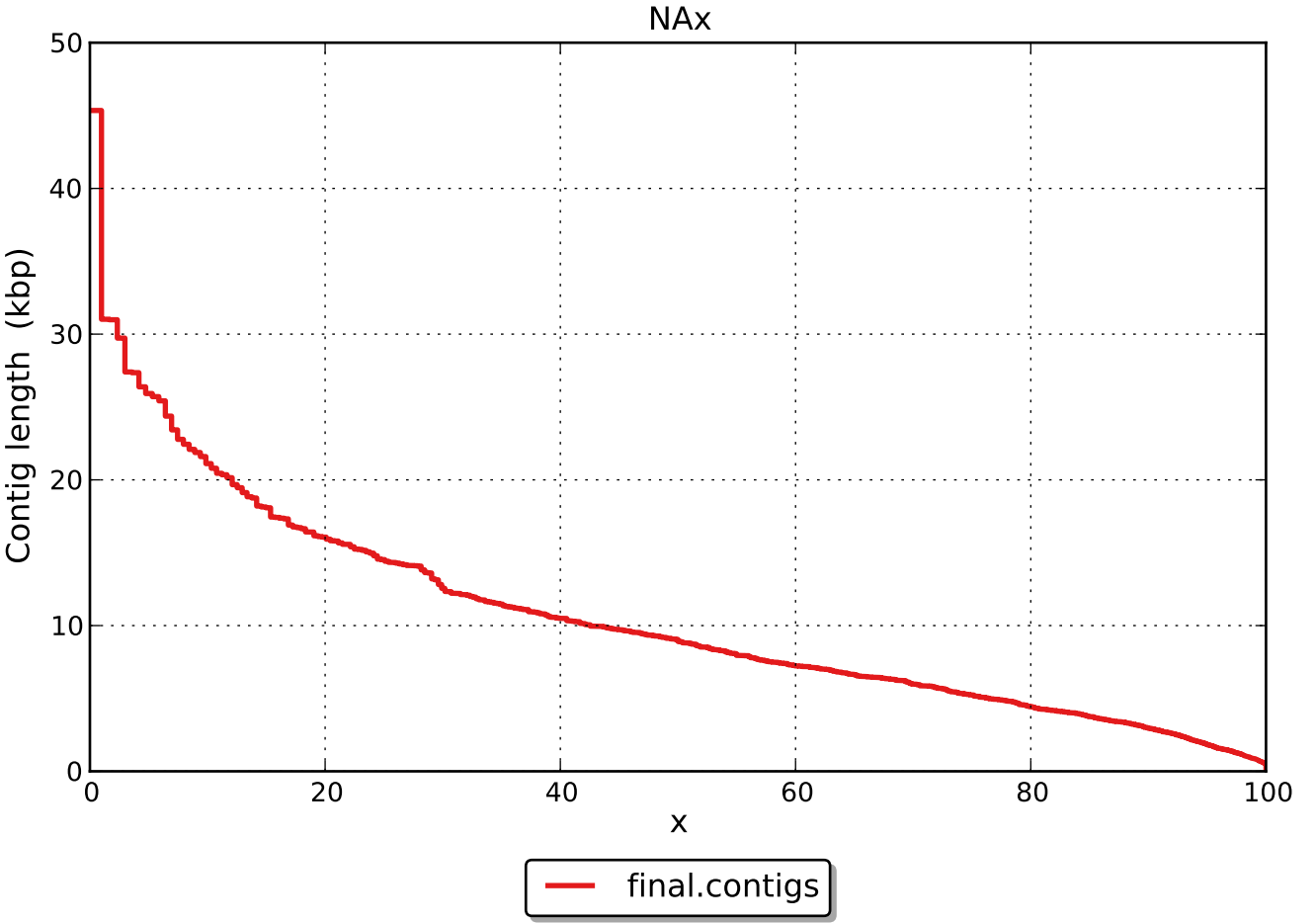

NGx
Contig length (kbp)
50
40
30
20
10
0
0
20
40
60
80
100
x
final.contigs

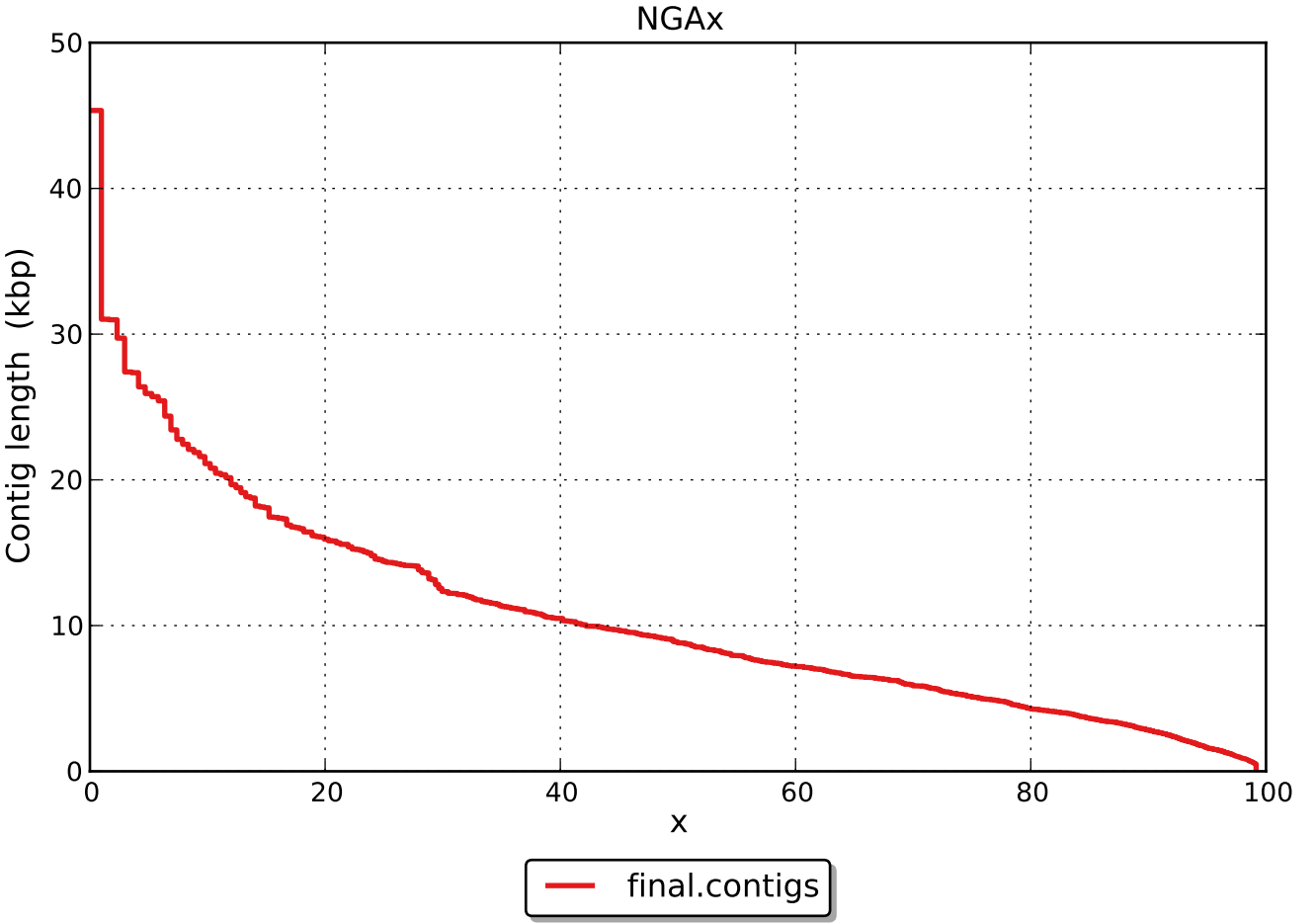

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
200
400
600
800
Contig index
final.contigs
Reference


GC content
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
relocations


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)
50
40
30
20
10
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (kbp)
50
40
30
20
10
0
0
20
40
60
80
100
x
final.contigs