Report

	final.contigs
# contigs (>= 1000 bp)	737
# contigs (>= 5000 bp)	345
# contigs (>= 10000 bp)	129
# contigs (>= 25000 bp)	10
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4619967
Total length (>= 5000 bp)	3551586
Total length (>= 10000 bp)	2022594
Total length (>= 25000 bp)	306431
Total length (>= 50000 bp)	0
# contigs	898
Largest contig	46220
Total length	4729063
Reference length	4857432
GC (%)	52.17
Reference GC (%)	52.22
N50	8481
NG50	8222
N75	5000
NG75	4693
L50	167
LG50	175
L75	345
LG75	364
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	95.770
Duplication ratio	1.017
# N's per 100 kbp	0.00
# mismatches per 100 kbp	526.68
# indels per 100 kbp	0.04
Largest alignment	46220
NA50	8481
NGA50	8222
NA75	5000
NGA75	4693
LA50	167
LGA50	175
LA75	345
LGA75	364

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

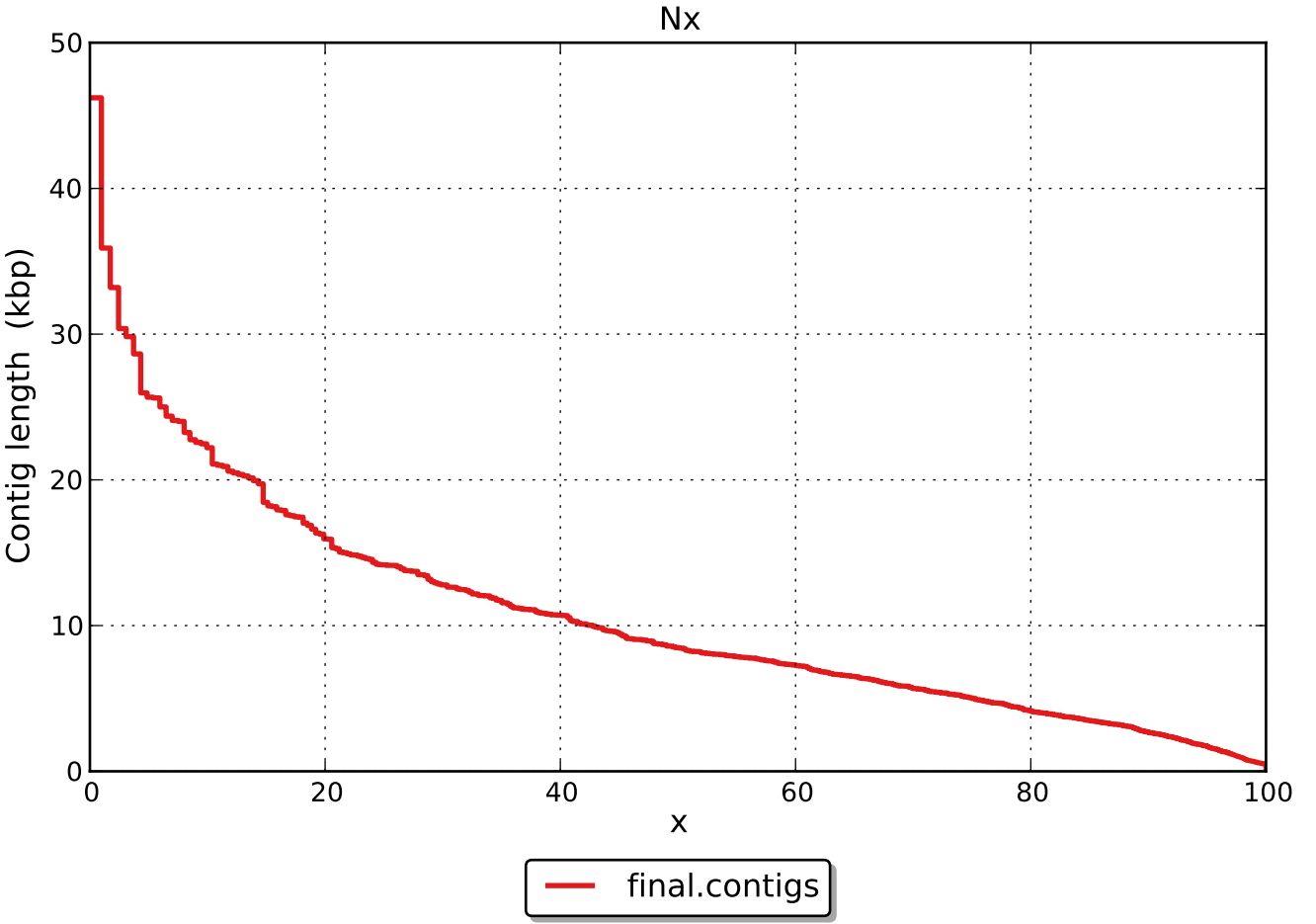
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	24501
# indels	2
# short indels	2
# long indels	0
Indels length	2

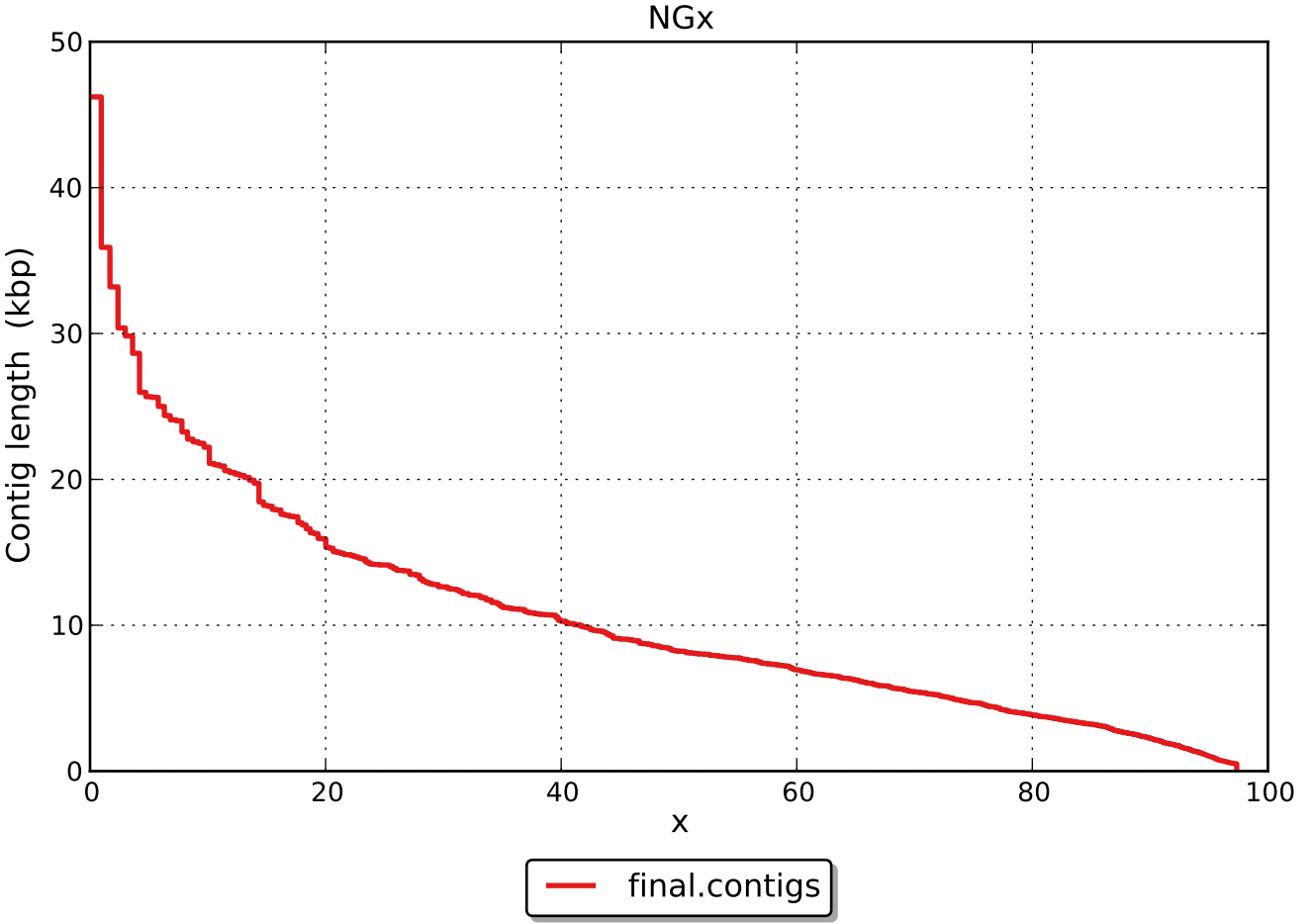
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

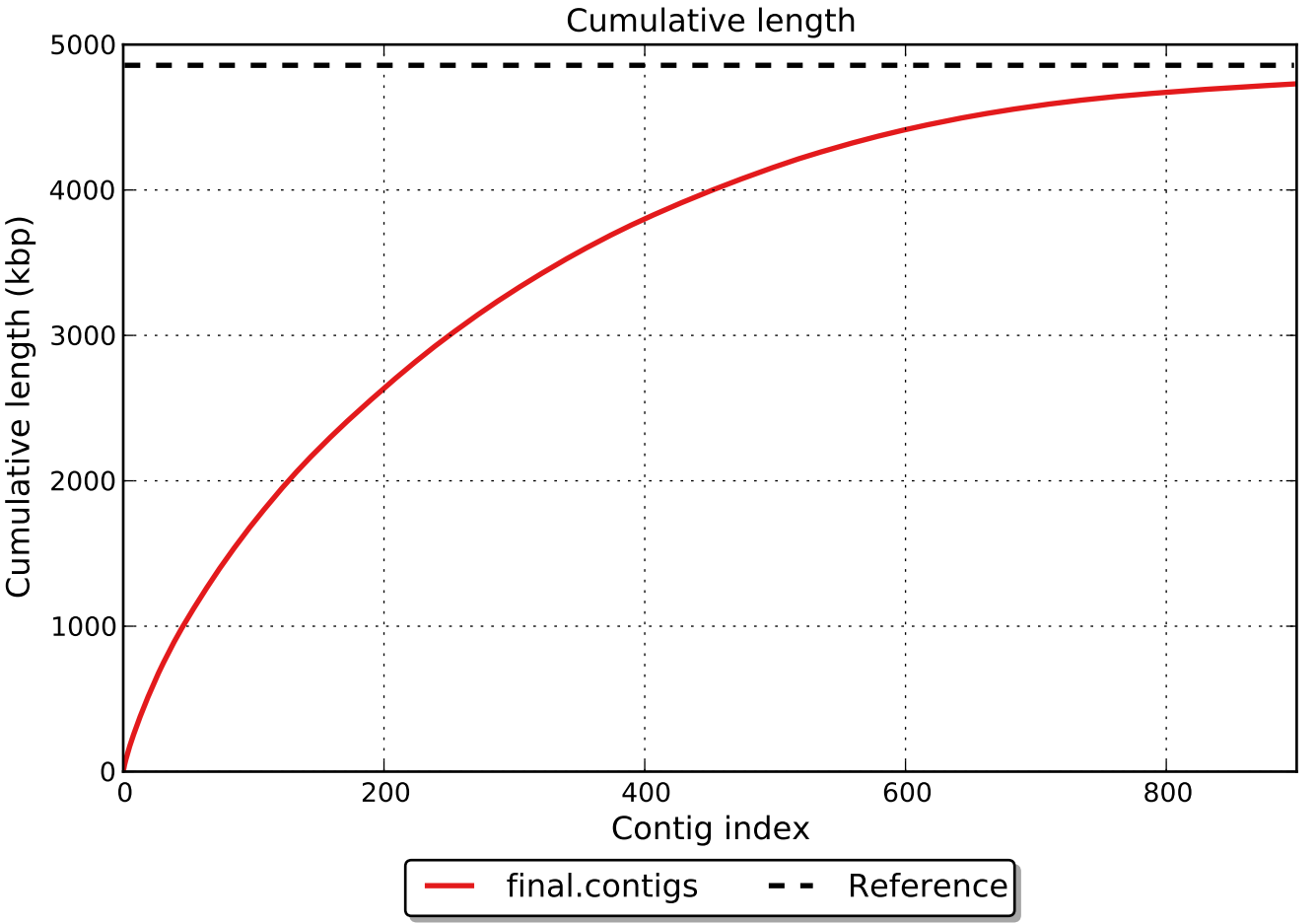
Unaligned report

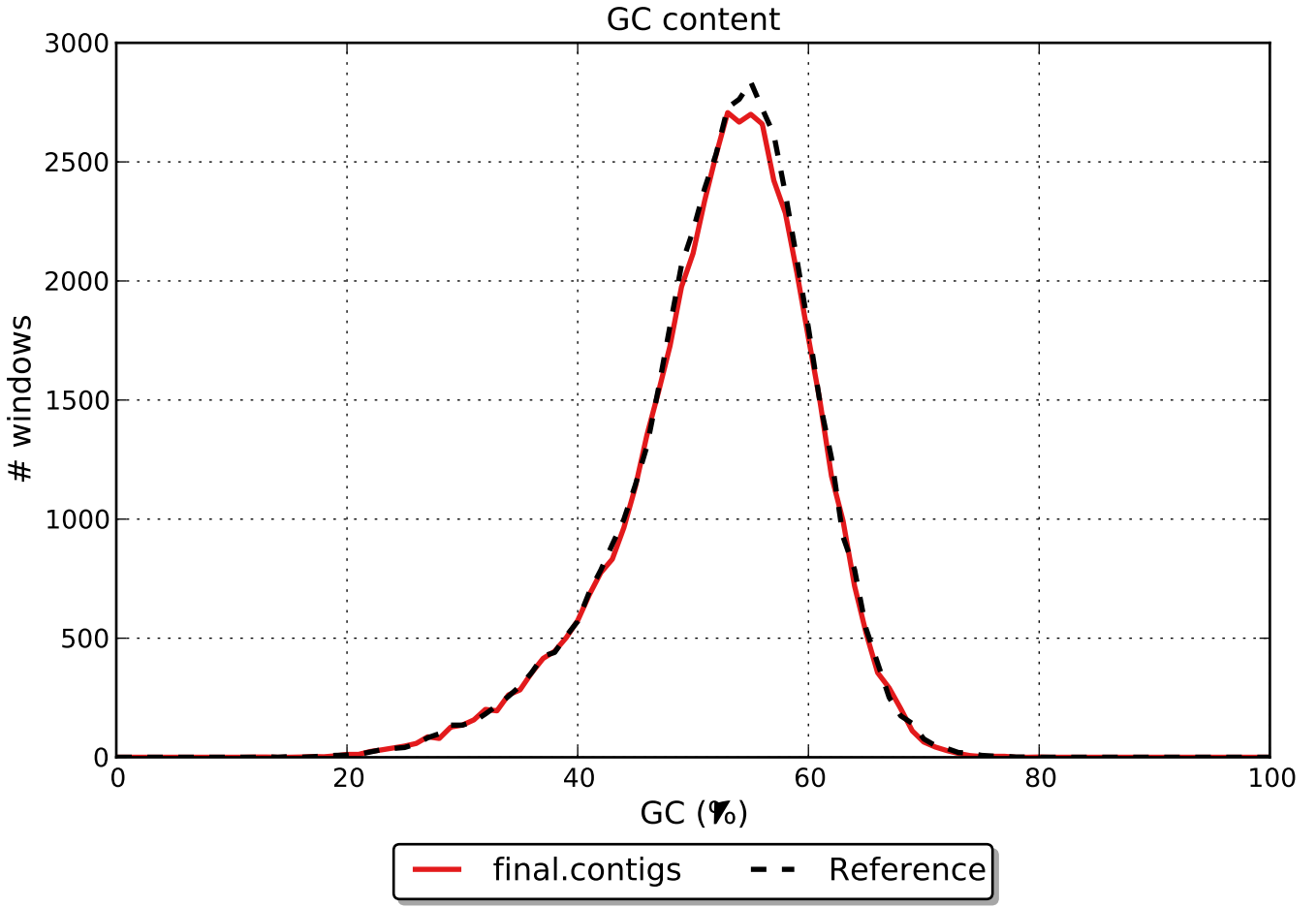
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

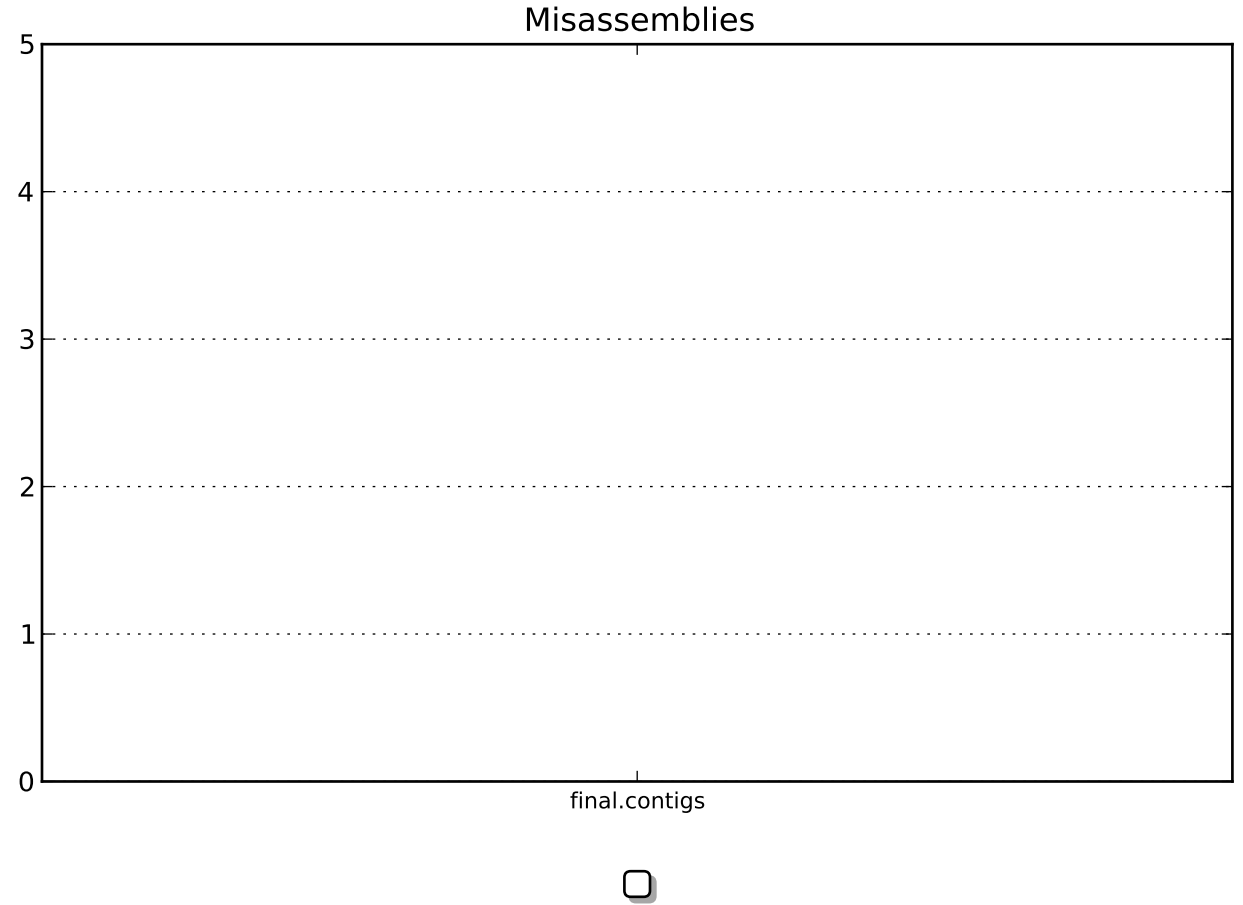
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

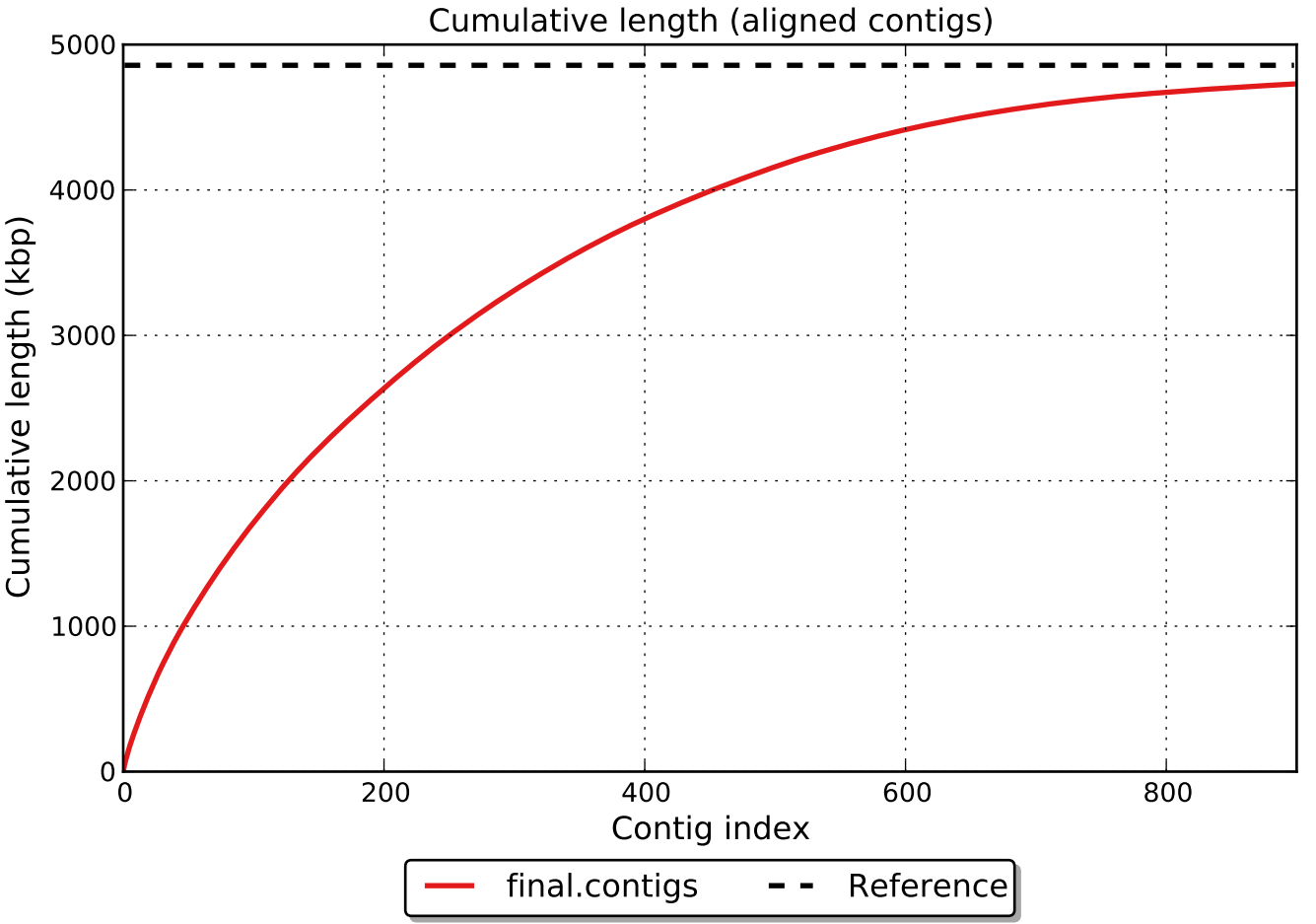

Nx
Contig length (kbp)
50
40
30
20
10
0
0
20
40
60
80
100
x
final.contigs

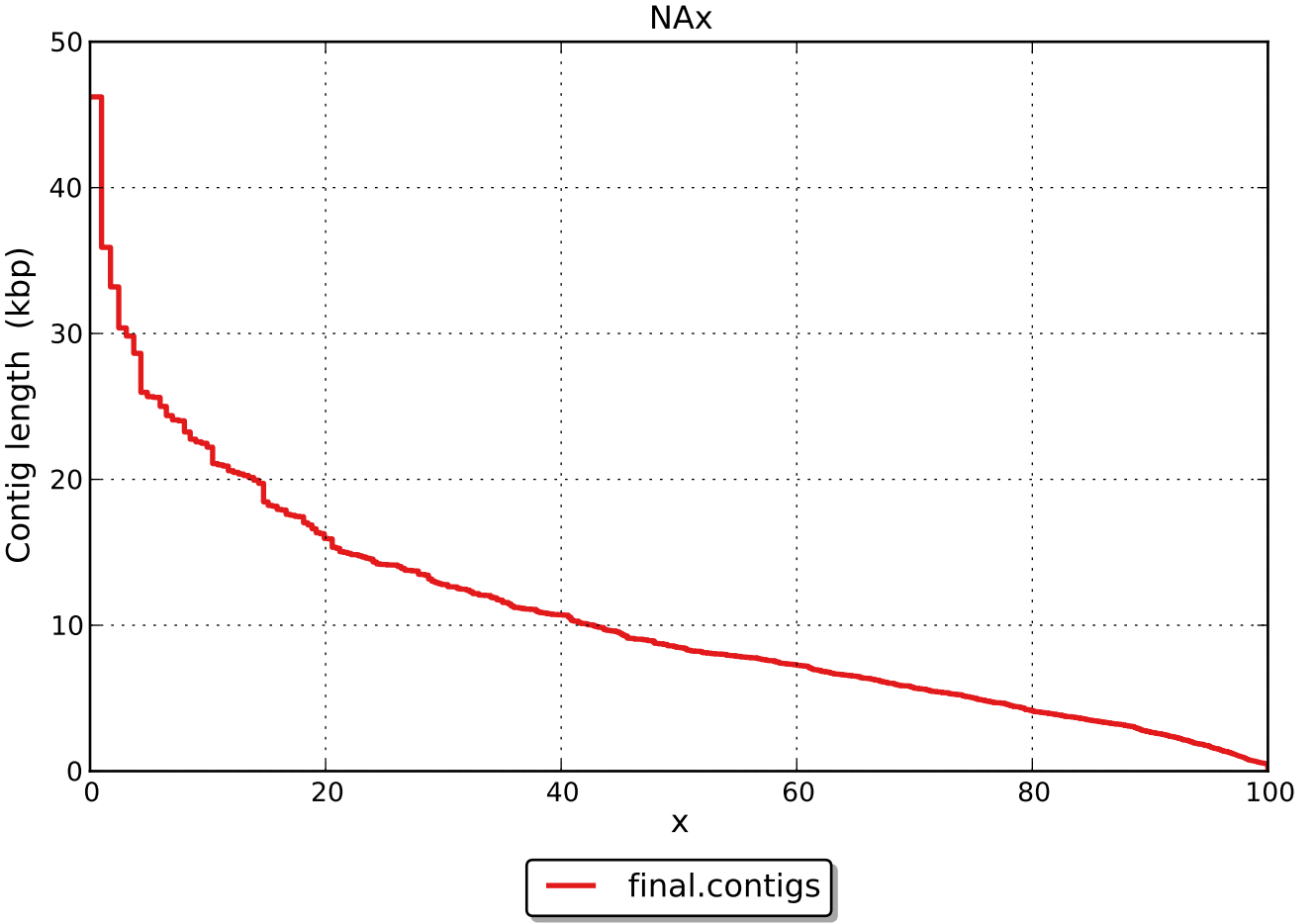

NGx
Contig length (kbp)
50
40
30
20
10
0
0
20
40
60
80
100
x
final.contigs

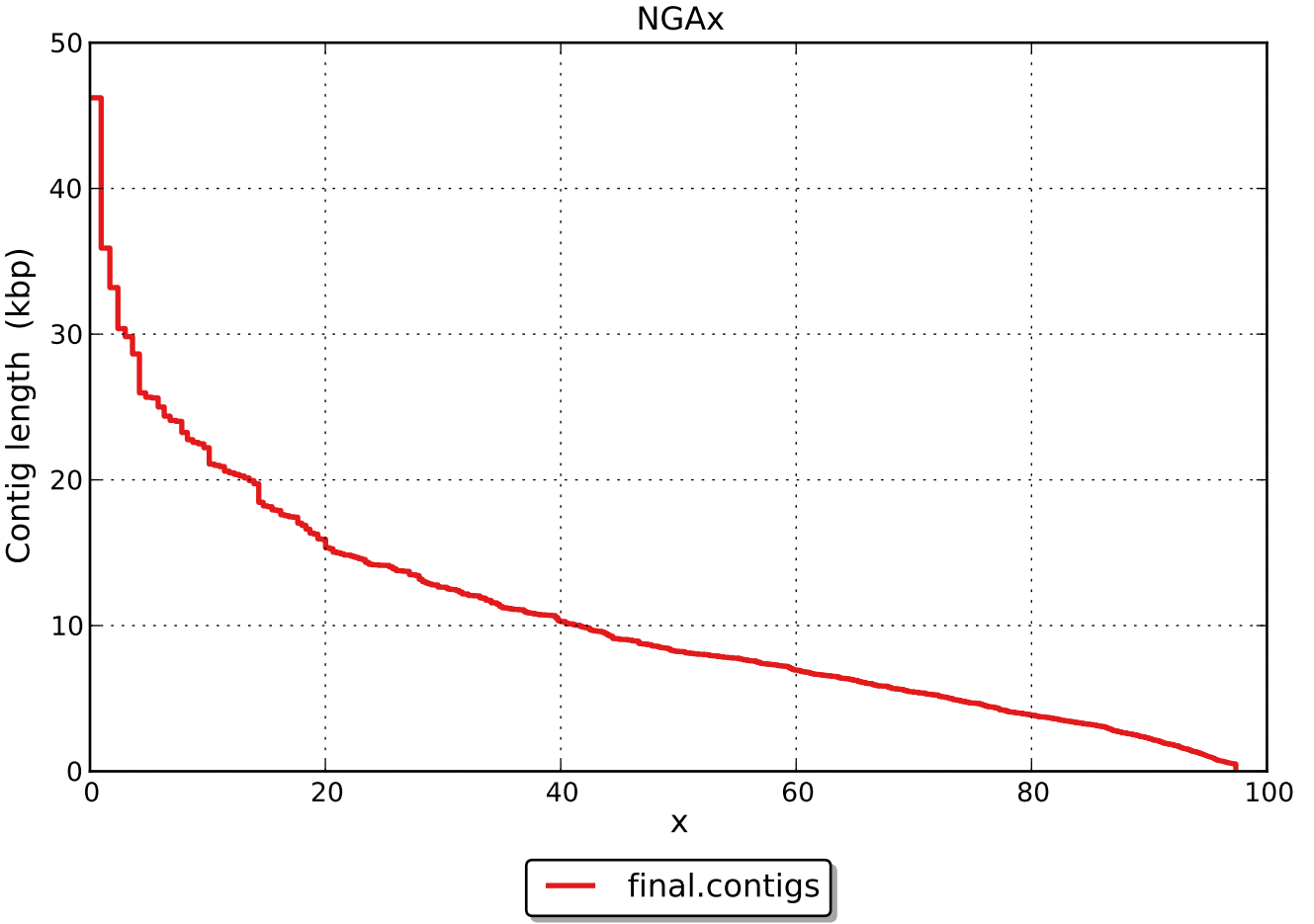

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
200
400
600
800
Contig index
final.contigs
Reference


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


Misassemblies
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)
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