Report

	final.contigs
# contigs (>= 1000 bp)	1321
# contigs (>= 5000 bp)	244
# contigs (>= 10000 bp)	32
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4466539
Total length (>= 5000 bp)	1829105
Total length (>= 10000 bp)	420040
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	1643
Largest contig	18981
Total length	4704300
Reference length	4641652
GC (%)	50.79
Reference GC (%)	50.78
N50	4096
NG50	4175
N75	2348
NG75	2413
L50	360
LG50	352
L75	742
LG75	722
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.930
Duplication ratio	1.024
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1.09
# indels per 100 kbp	0.04
Largest alignment	18981
NA50	4096
NGA50	4175
NA75	2348
NGA75	2413
LA50	360
LGA50	352
LA75	742
LGA75	722

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

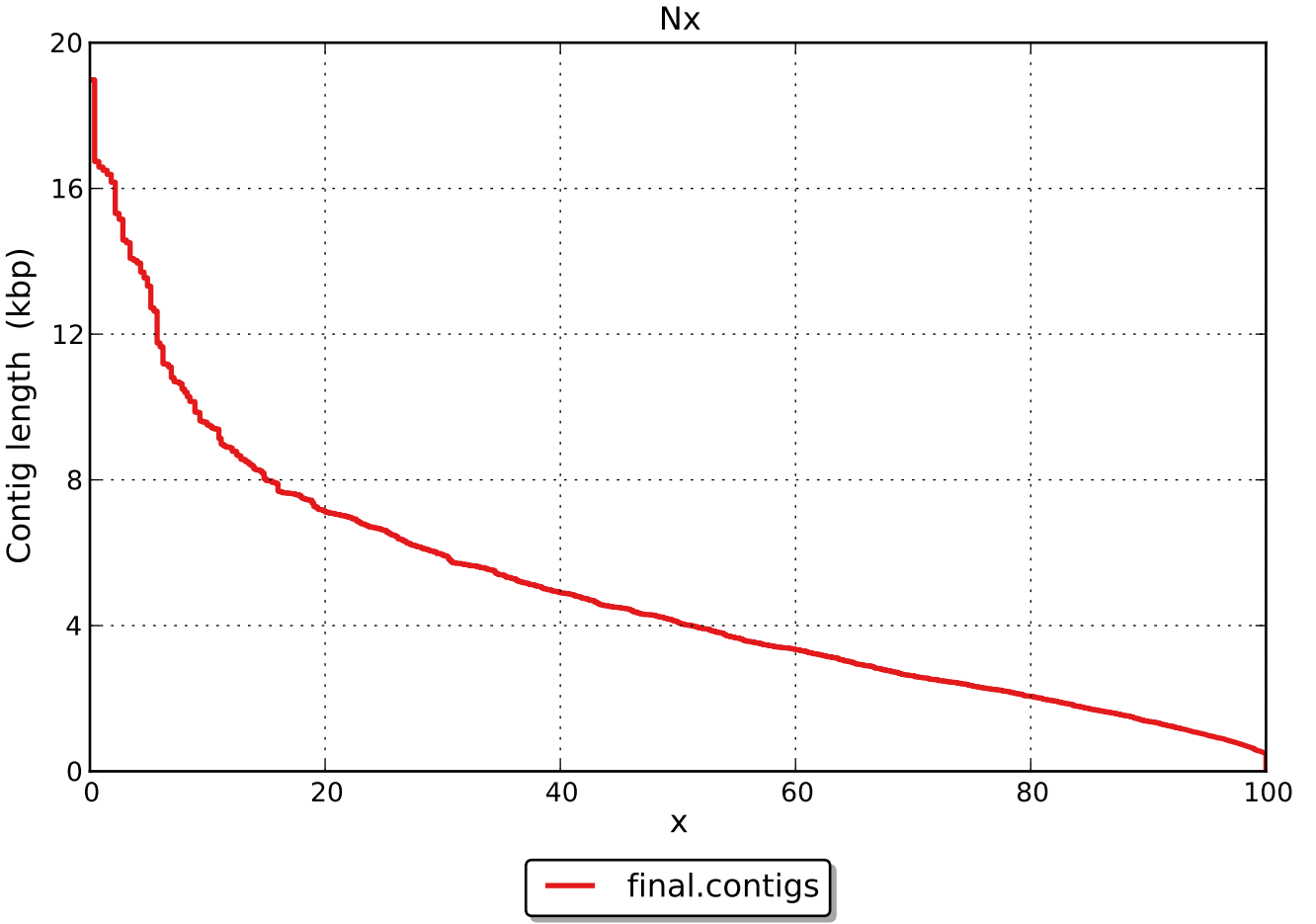
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	50
# indels	2
# short indels	2
# long indels	0
Indels length	2

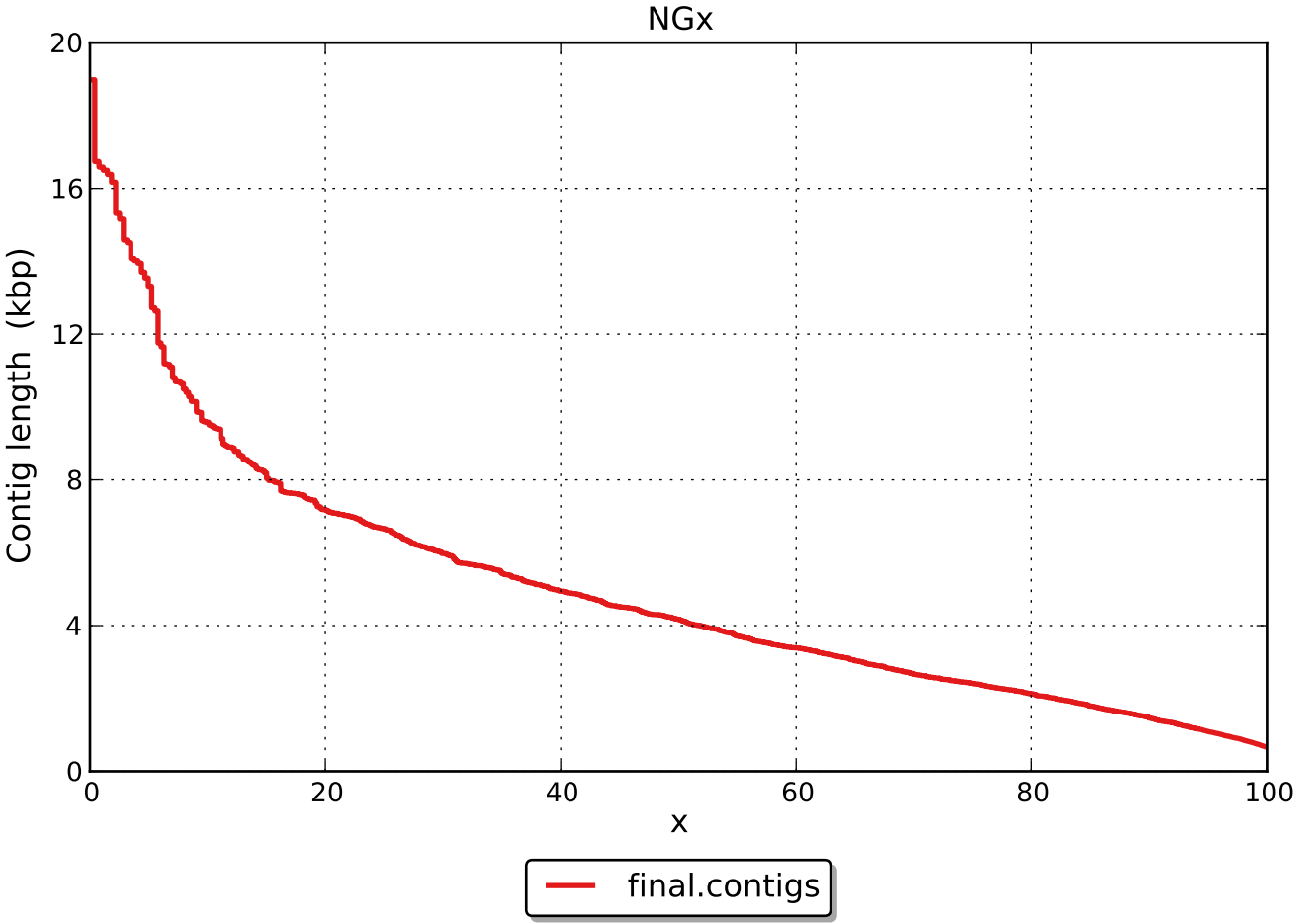
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

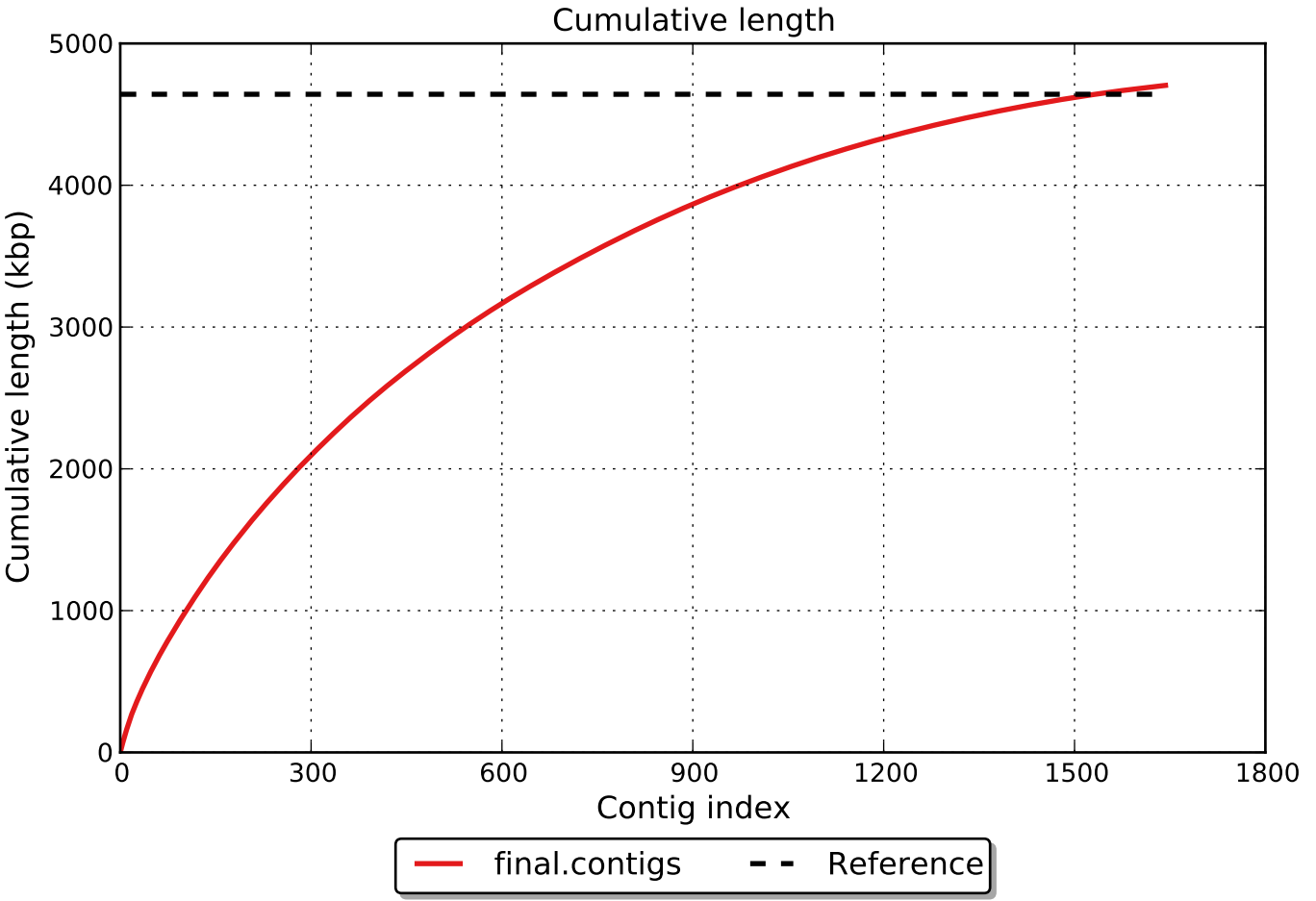
Unaligned report

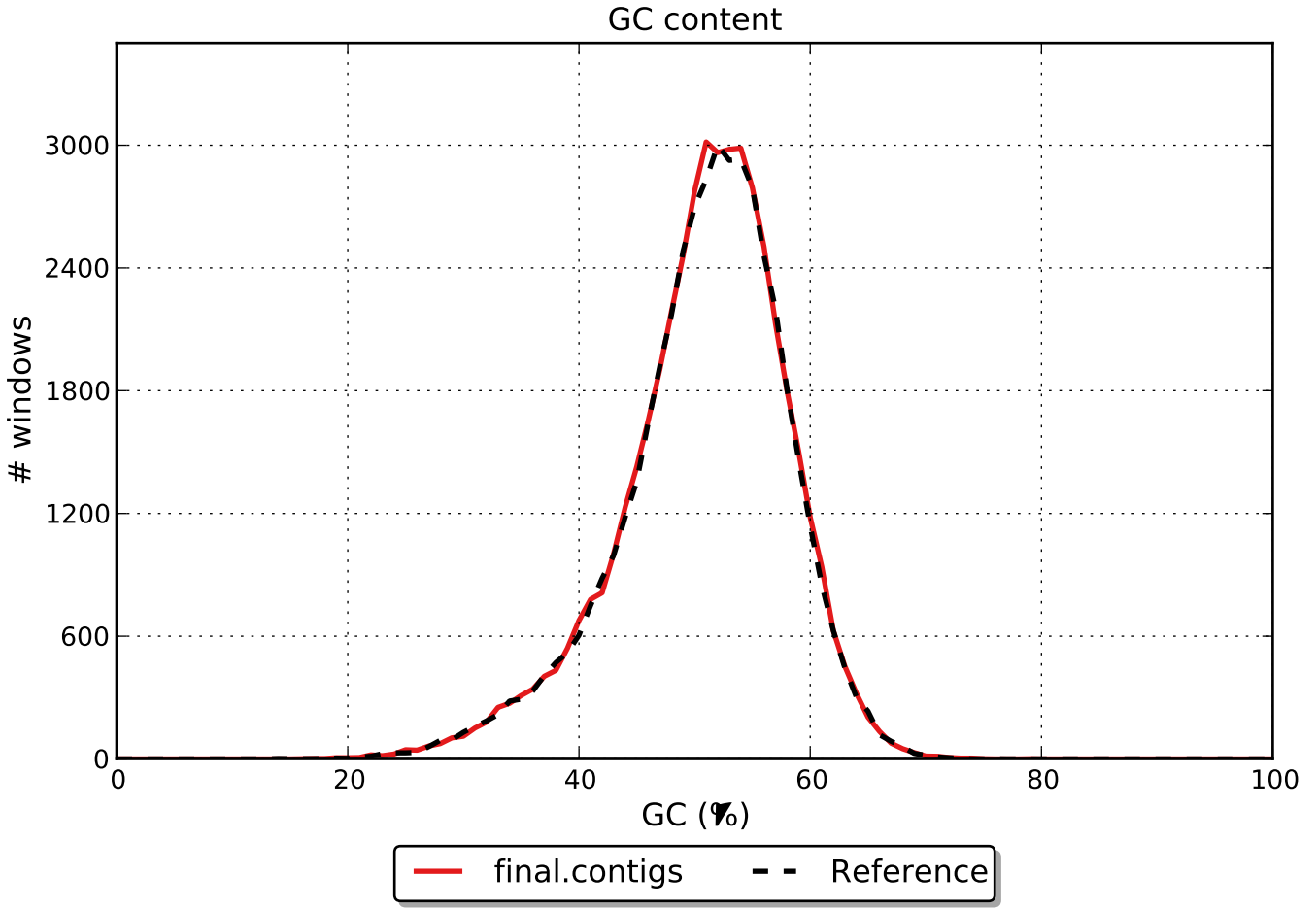
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

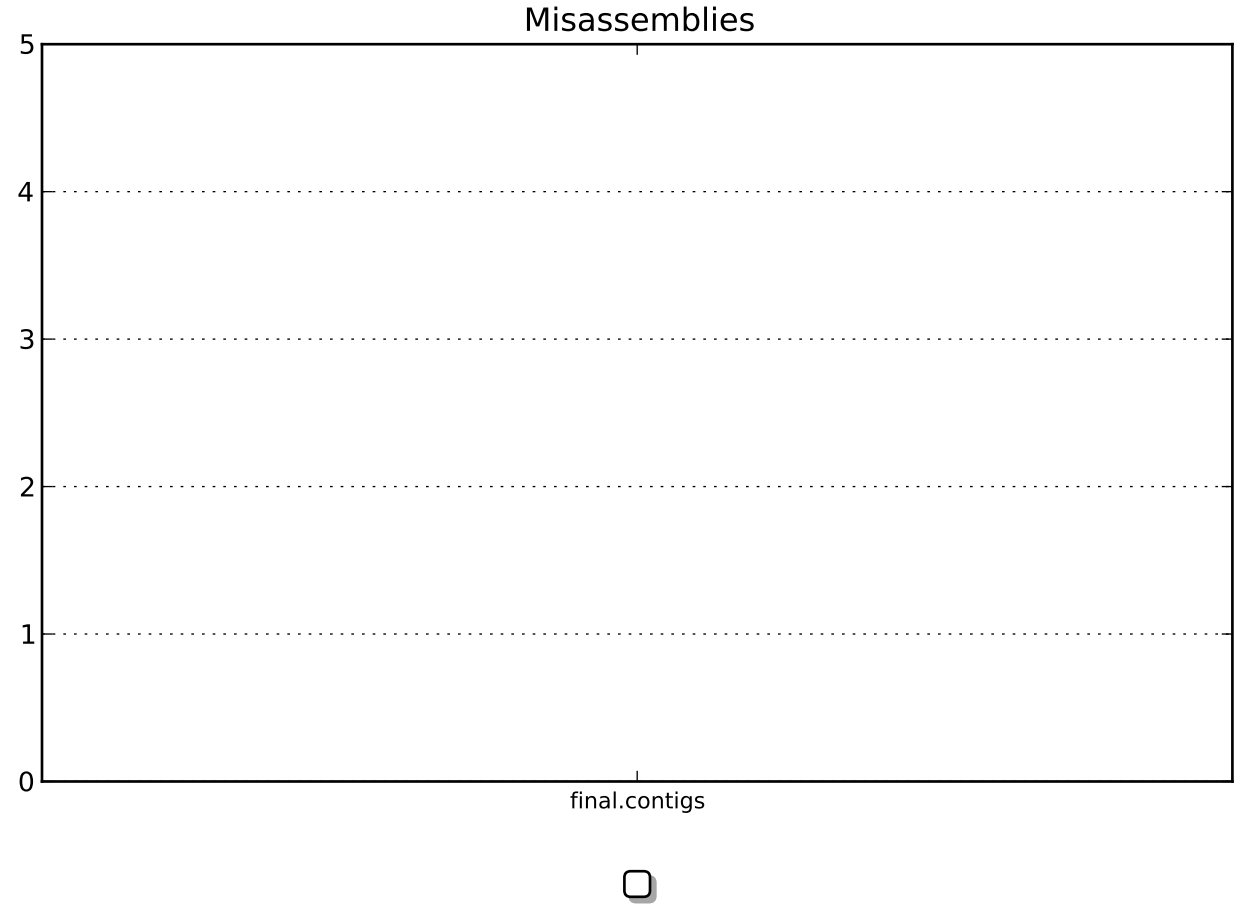
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

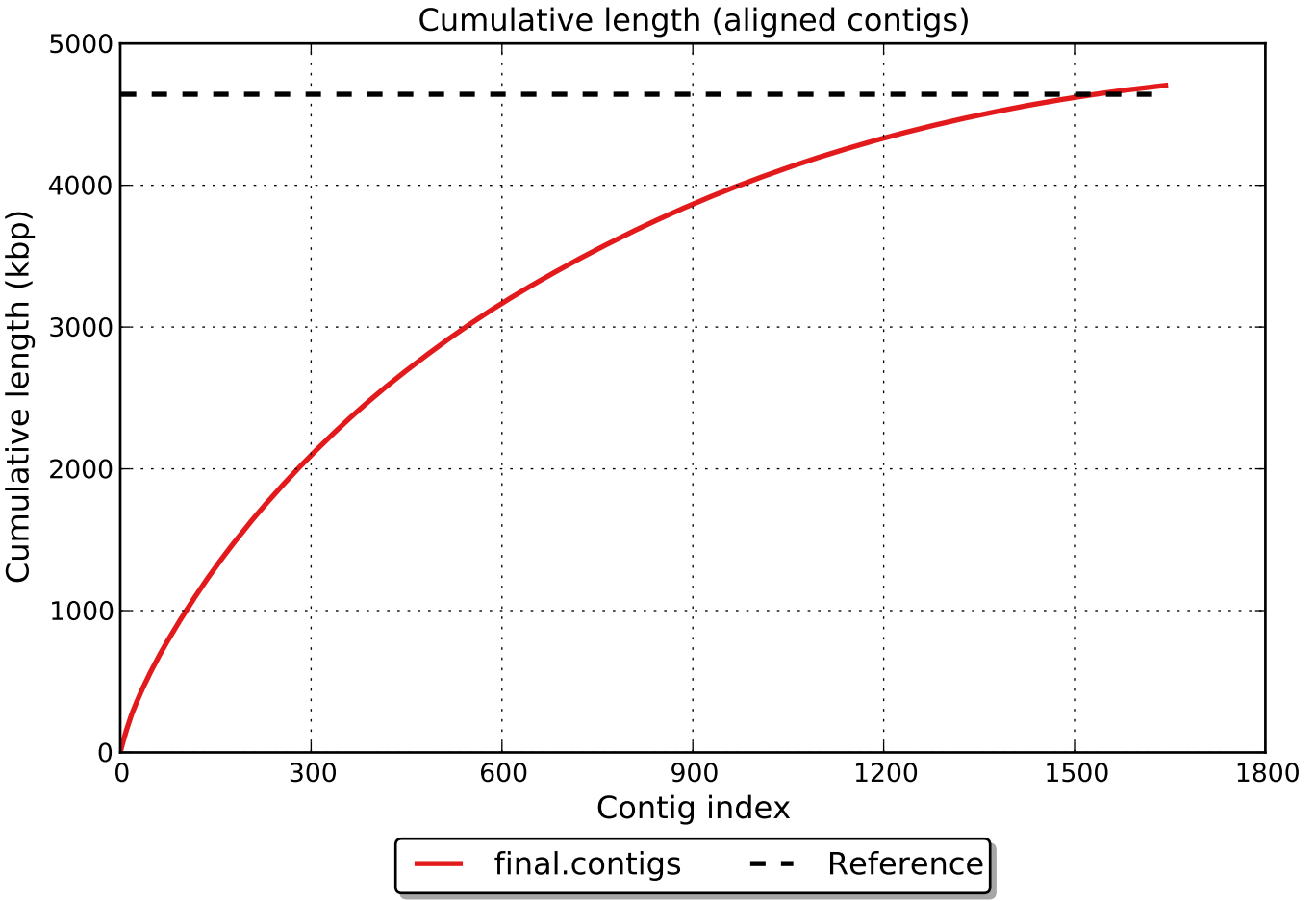

Nx
Contig length (kbp)
20
16
12
8
4
0
0
20
40
60
80
100
x
final.contigs

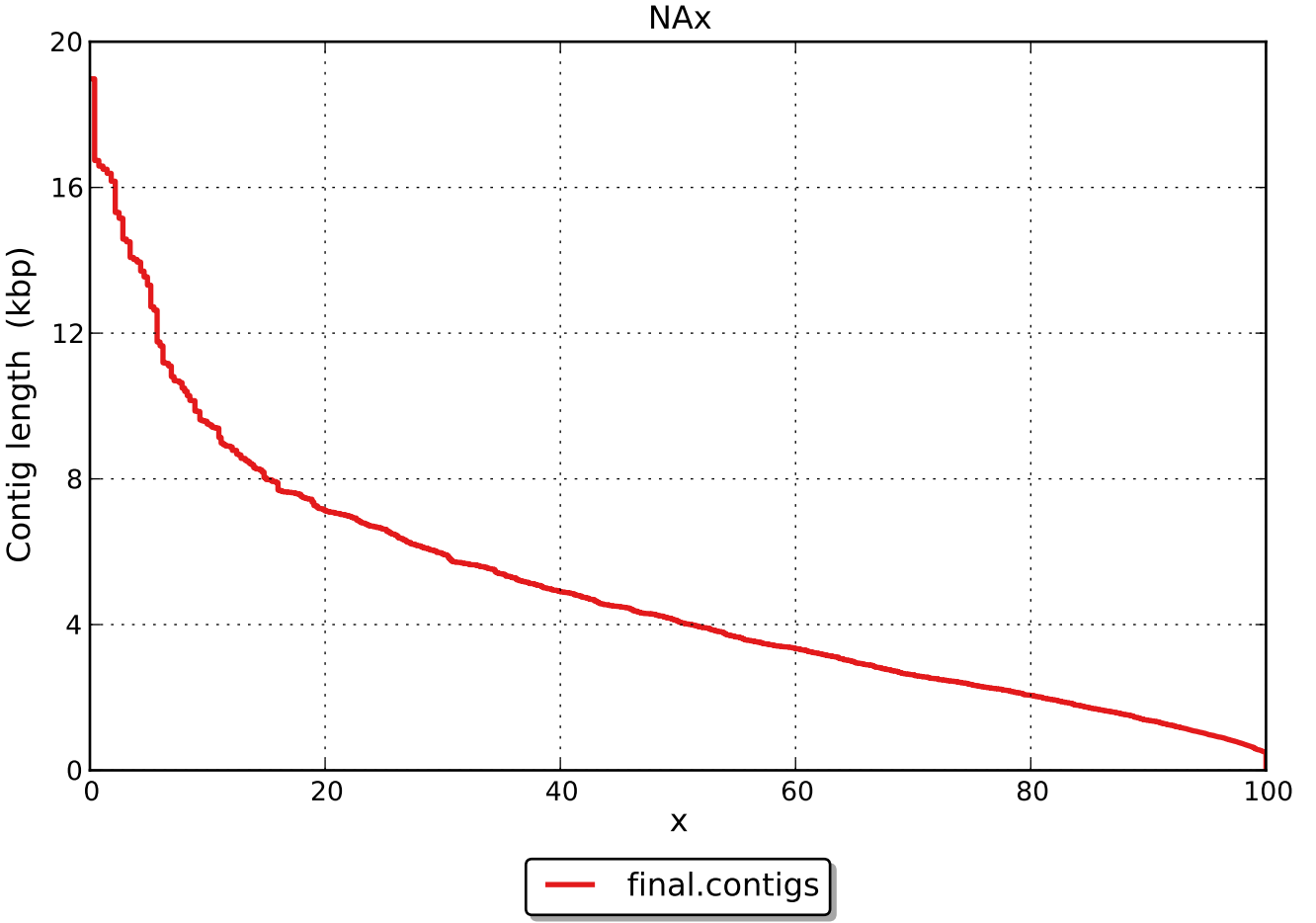

NGx
Contig length (kbp)
20
16
12
8
4
0
0
20
40
60
80
100
x
final.contigs

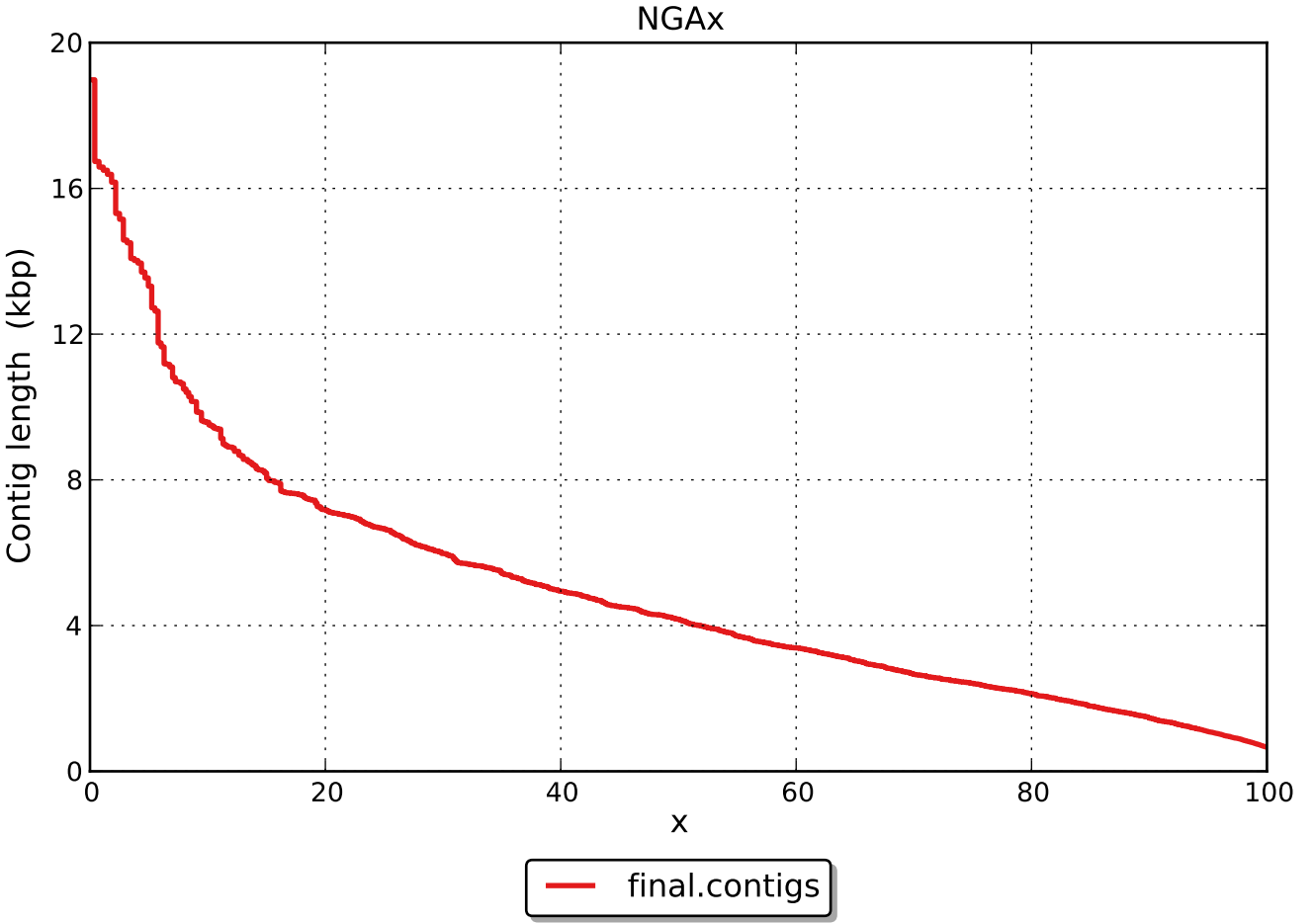

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
300
600
900
1200
1500
1800
Contig index
final.contigs
Reference


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
300
600
900
1200
1500
1800
Contig index
final.contigs
Reference


NAx
Contig length (kbp)
20
16
12
8
4
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (kbp)
20
16
12
8
4
0
0
20
40
60
80
100
x
final.contigs