Report

	final.contigs
# contigs (>= 1000 bp)	1646
# contigs (>= 5000 bp)	154
# contigs (>= 10000 bp)	7
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4389337
Total length (>= 5000 bp)	995334
Total length (>= 10000 bp)	78604
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	2261
Largest contig	13587
Total length	4837859
Reference length	4857432
GC (%)	52.19
Reference GC (%)	52.22
N50	2890
NG50	2877
N75	1710
NG75	1689
L50	529
LG50	533
L75	1069
LG75	1078
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	96.675
Duplication ratio	1.030
# N's per 100 kbp	0.00
# mismatches per 100 kbp	4.60
# indels per 100 kbp	0.00
Largest alignment	13587
NA50	2890
NGA50	2877
NA75	1710
NGA75	1689
LA50	529
LGA50	533
LA75	1069
LGA75	1078

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

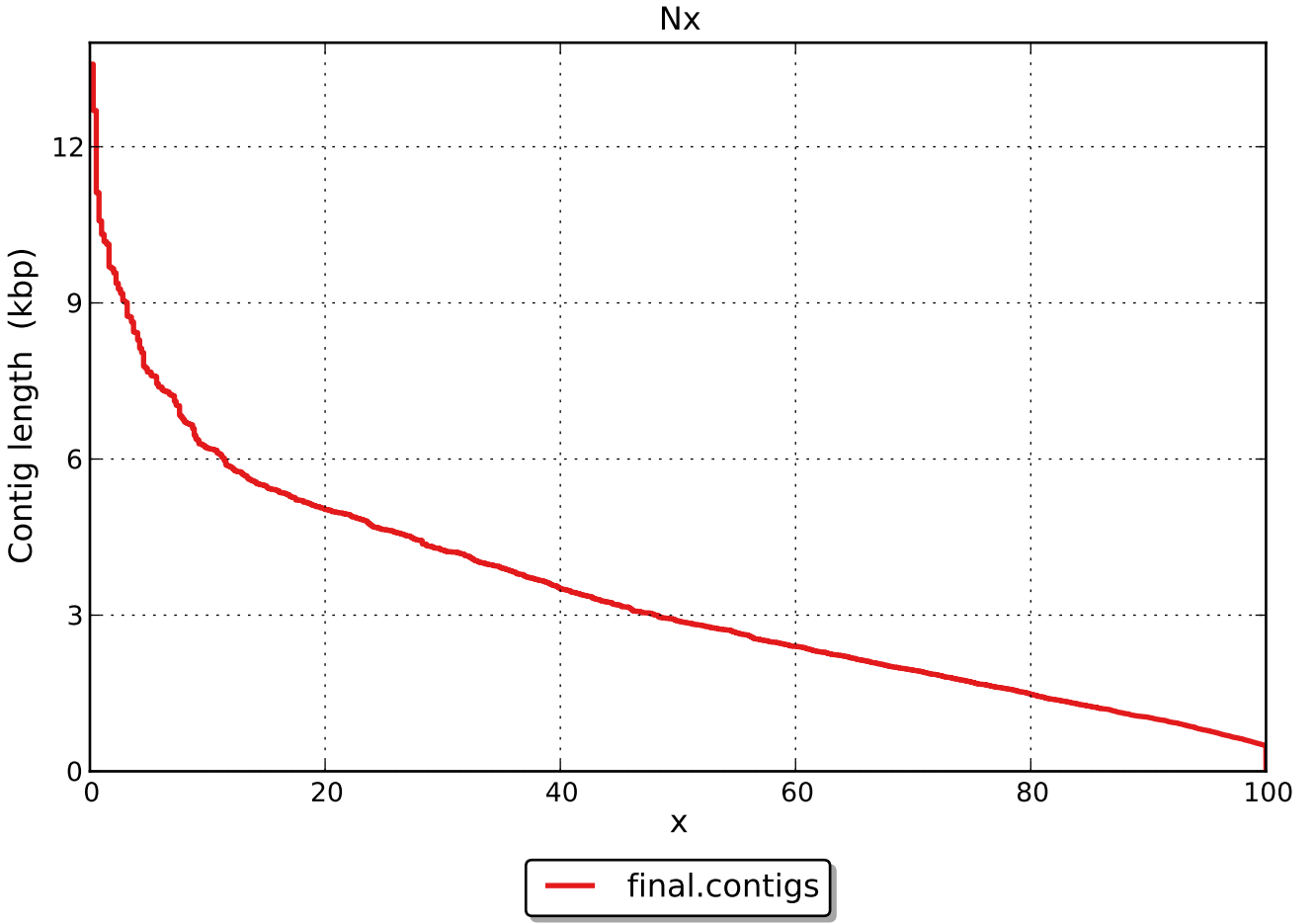
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	216
# indels	0
# short indels	0
# long indels	0
Indels length	0

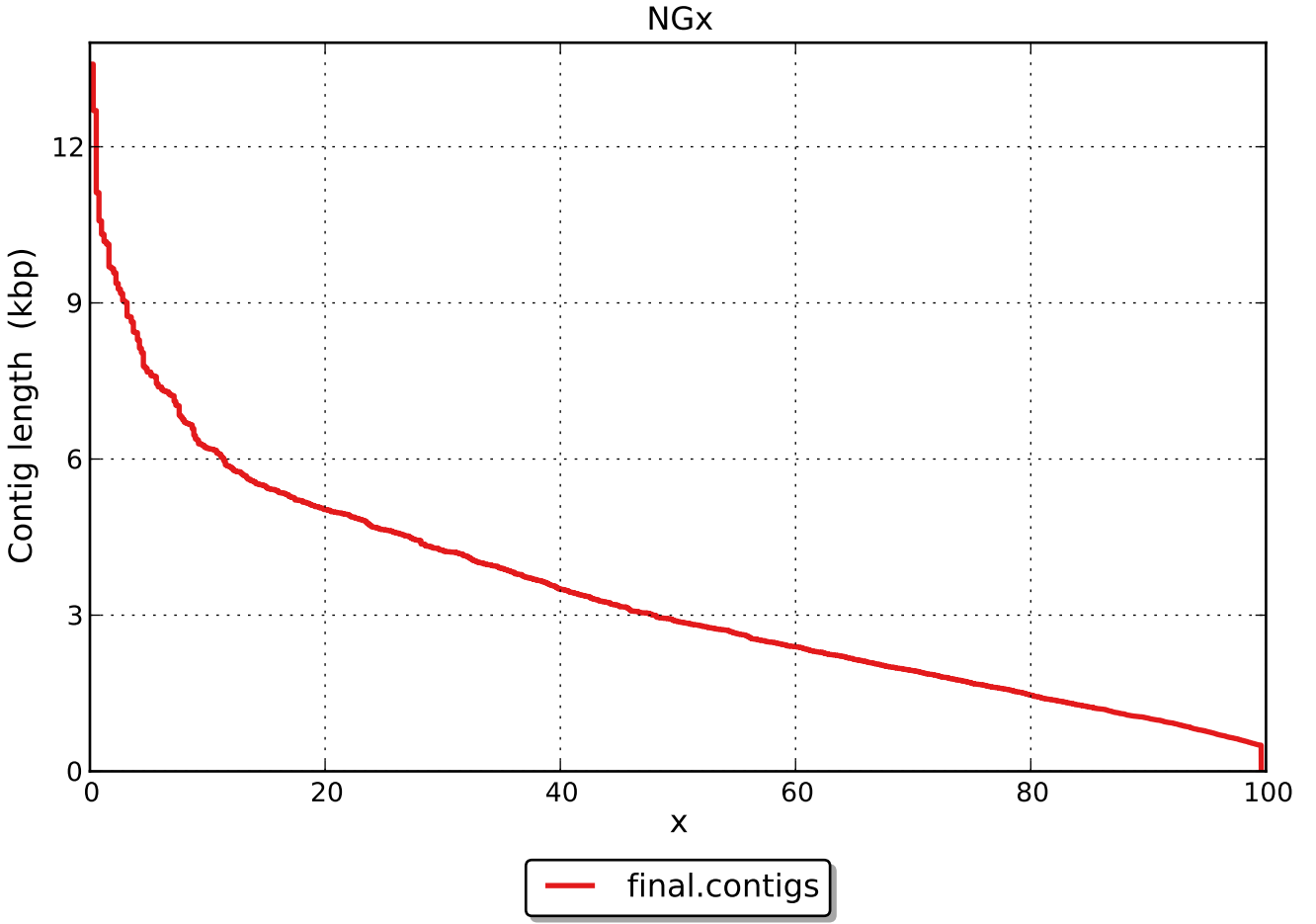
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

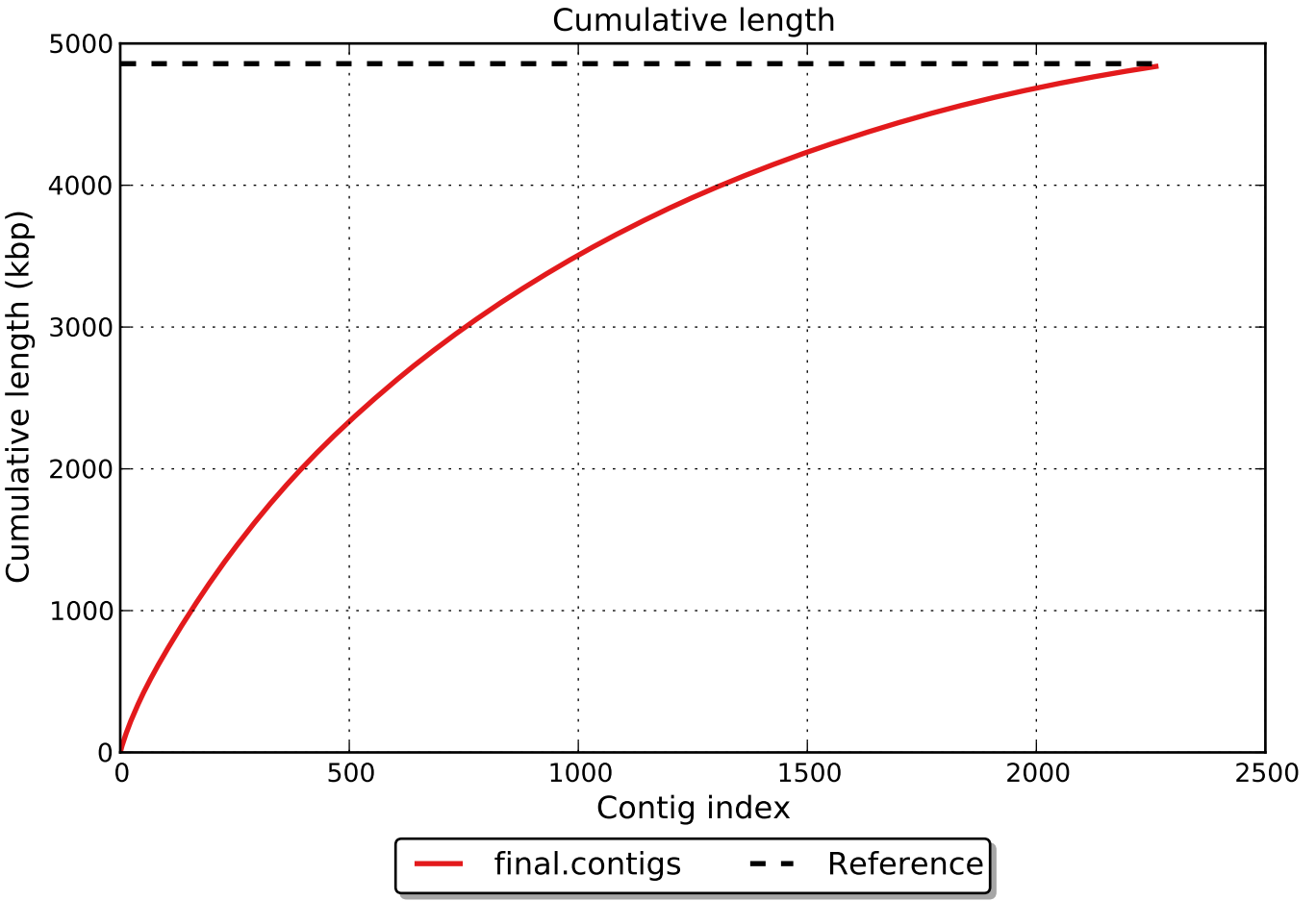
Unaligned report

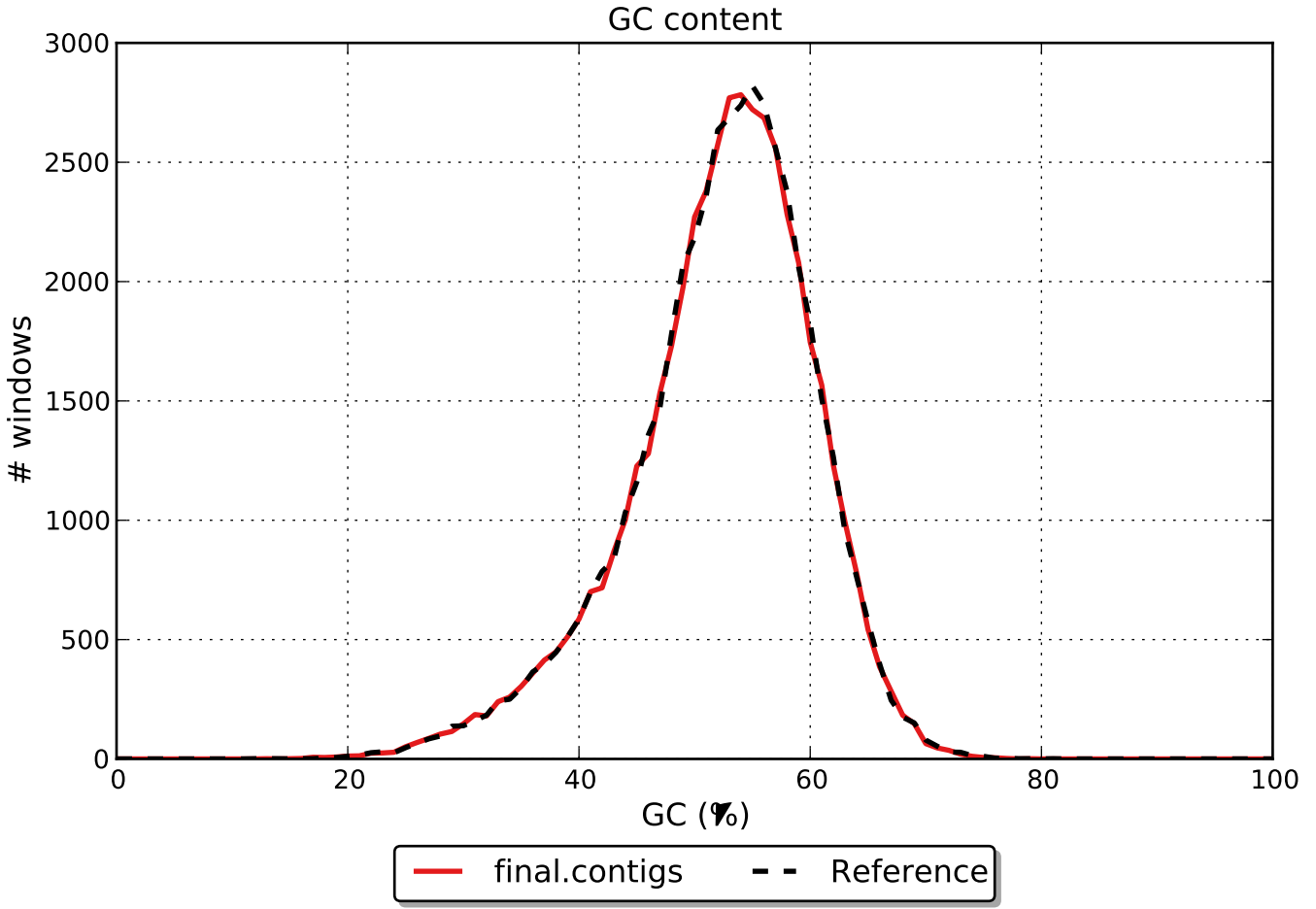
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

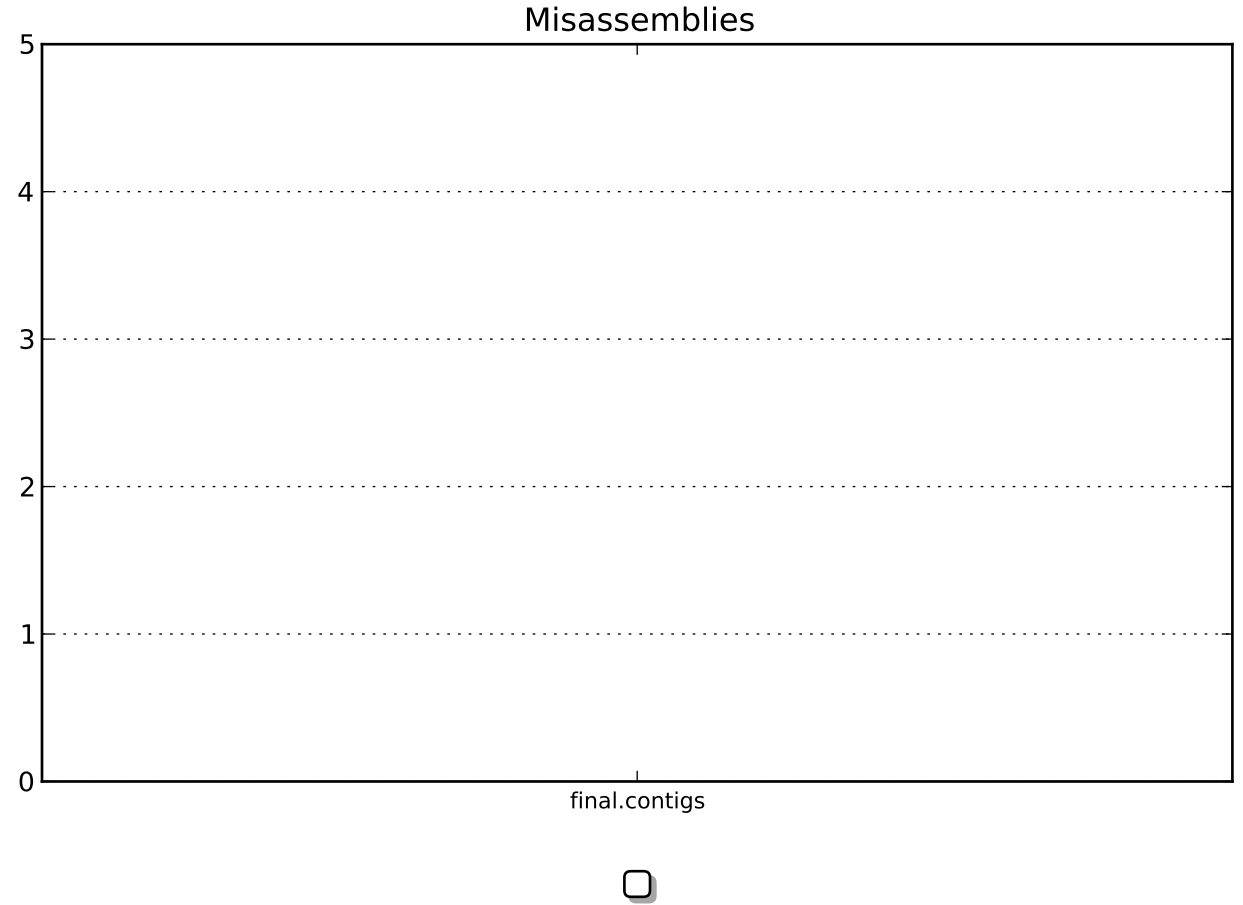
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

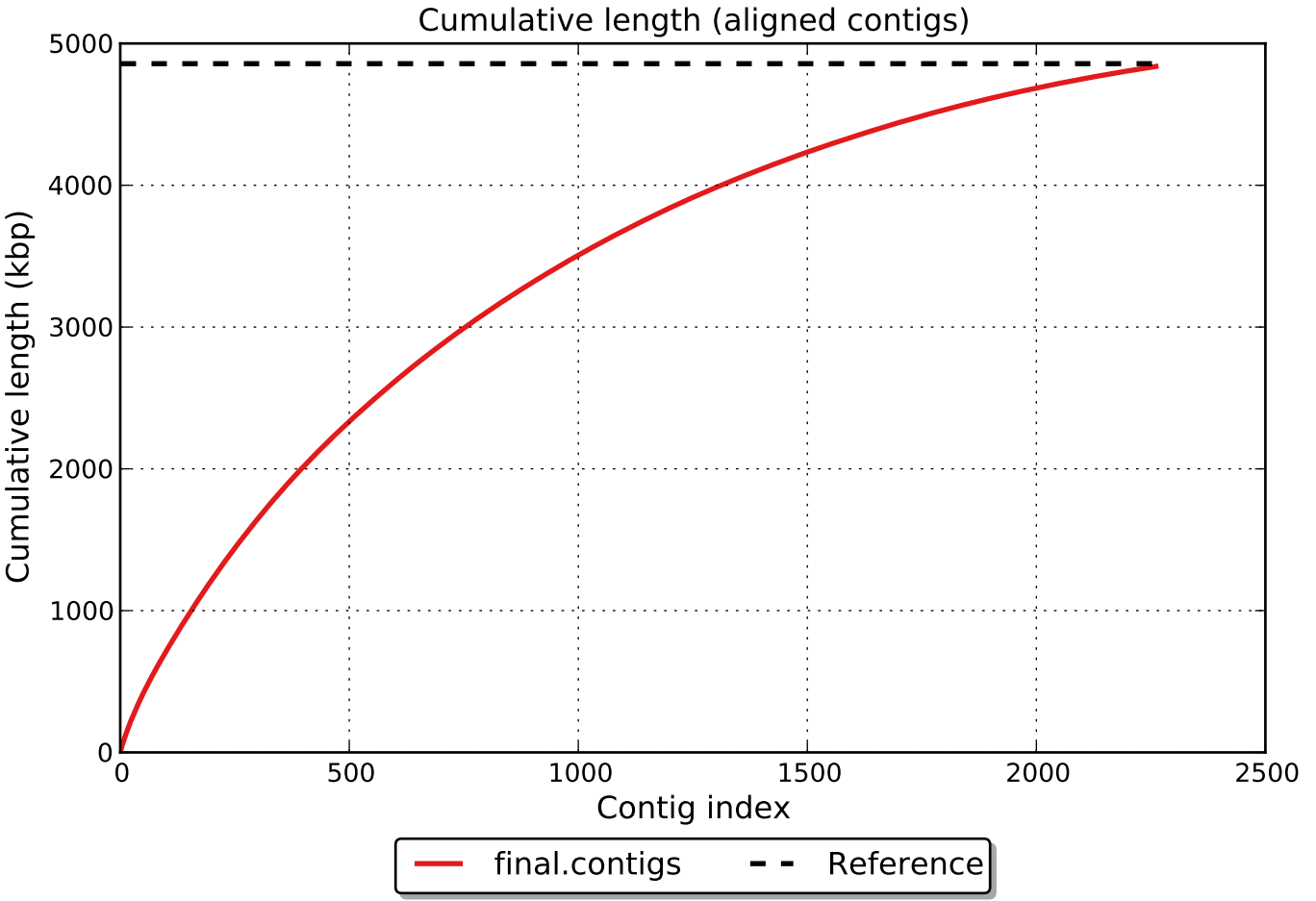

Nx
Contig length (kbp)
0
3
6
9
12
0
20
40
60
80
100
x
final.contigs

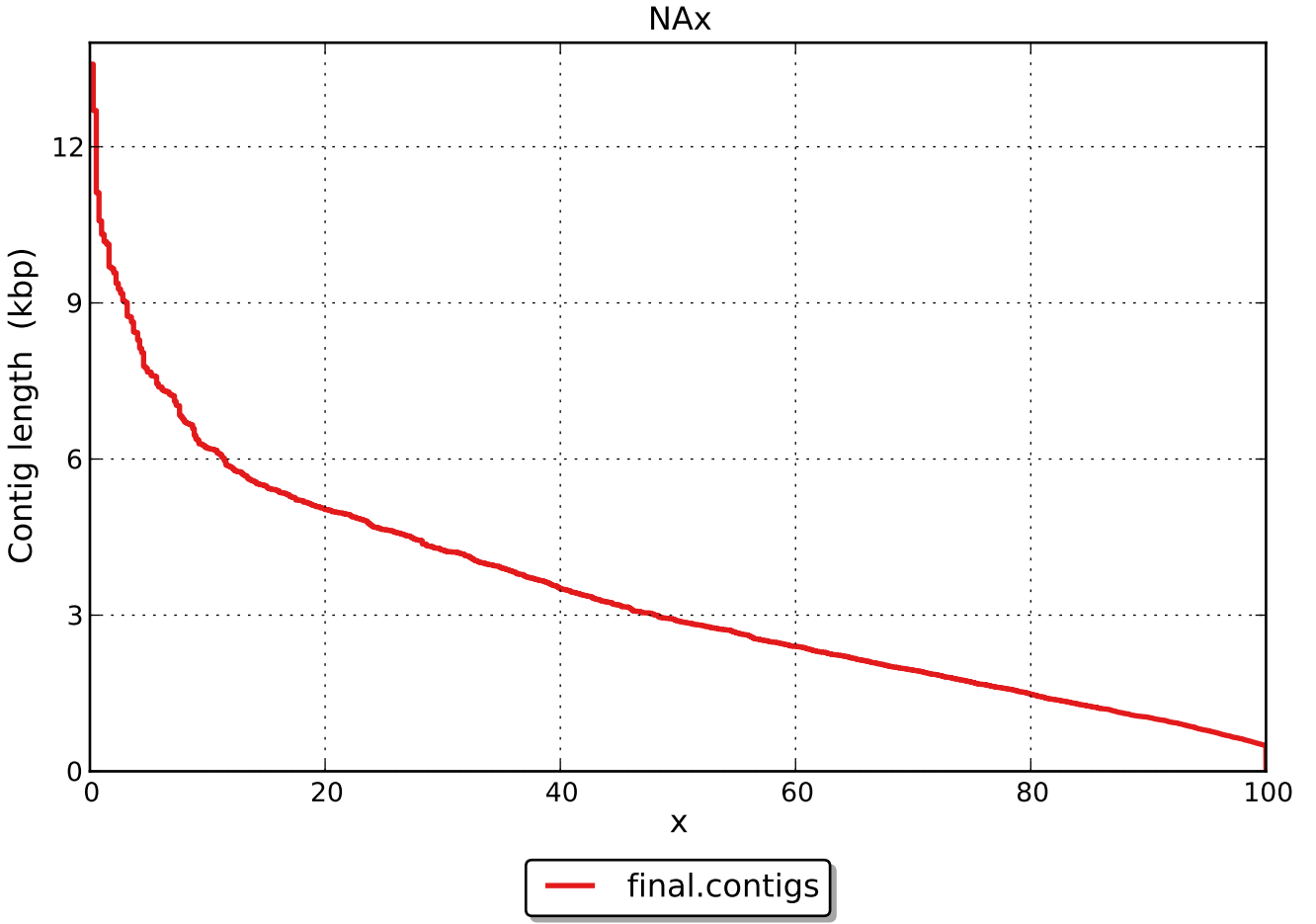

NGx
Contig length (kbp)
0
3
6
9
12
0
20
40
60
80
100
x
final.contigs

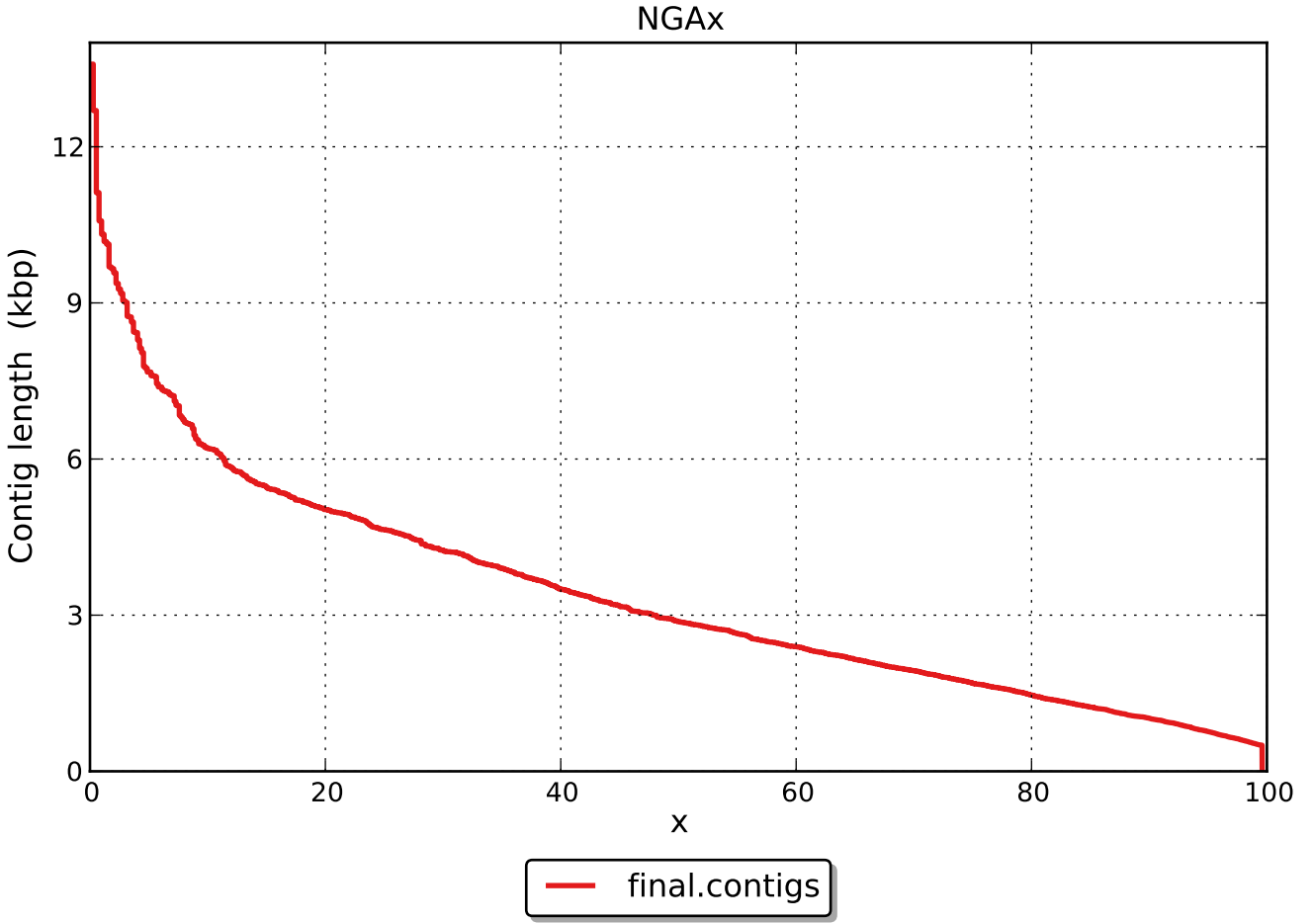

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
500
1000
1500
2000
2500
Contig index
final.contigs
Reference


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
500
1000
1500
2000
2500
Contig index
final.contigs
Reference


NAx
Contig length (kbp)
0
3
6
9
12
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (kbp)
0
3
6
9
12
0
20
40
60
80
100
x
final.contigs