Report

	final.contigs
# contigs (>= 1000 bp)	1269
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	1820356
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	4150
Largest contig	3756
Total length	3856134
Reference length	4857432
GC (%)	52.20
Reference GC (%)	52.22
N50	962
NG50	824
N75	714
NG75	547
L50	1379
LG50	1943
L75	2547
LG75	3744
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	75.711
Duplication ratio	1.049
# N's per 100 kbp	0.00
# mismatches per 100 kbp	88.81
# indels per 100 kbp	0.00
Largest alignment	3756
NA50	962
NGA50	824
NA75	714
NGA75	547
LA50	1380
LGA50	1943
LA75	2547
LGA75	3744

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

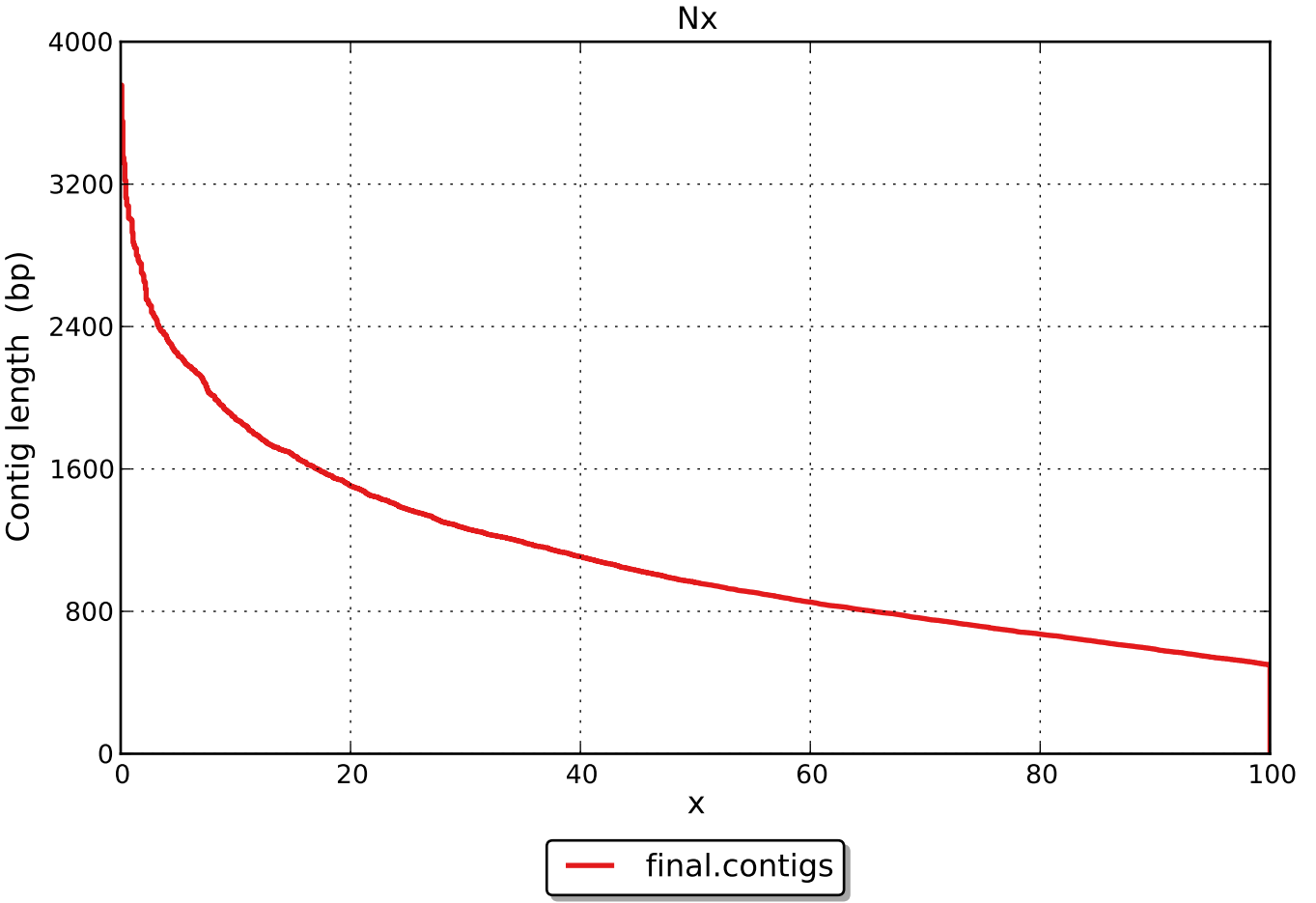
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	3266
# indels	0
# short indels	0
# long indels	0
Indels length	0

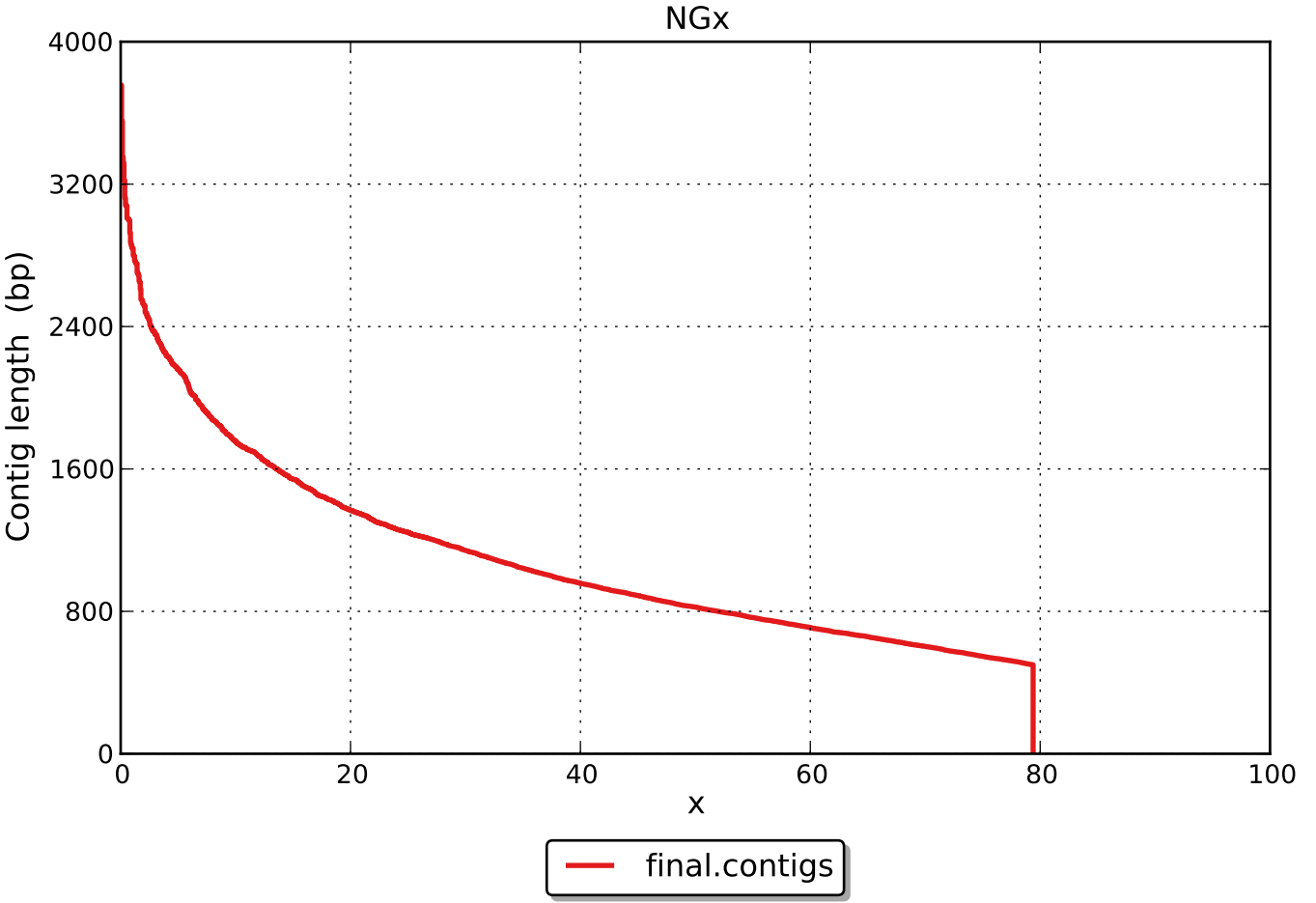
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

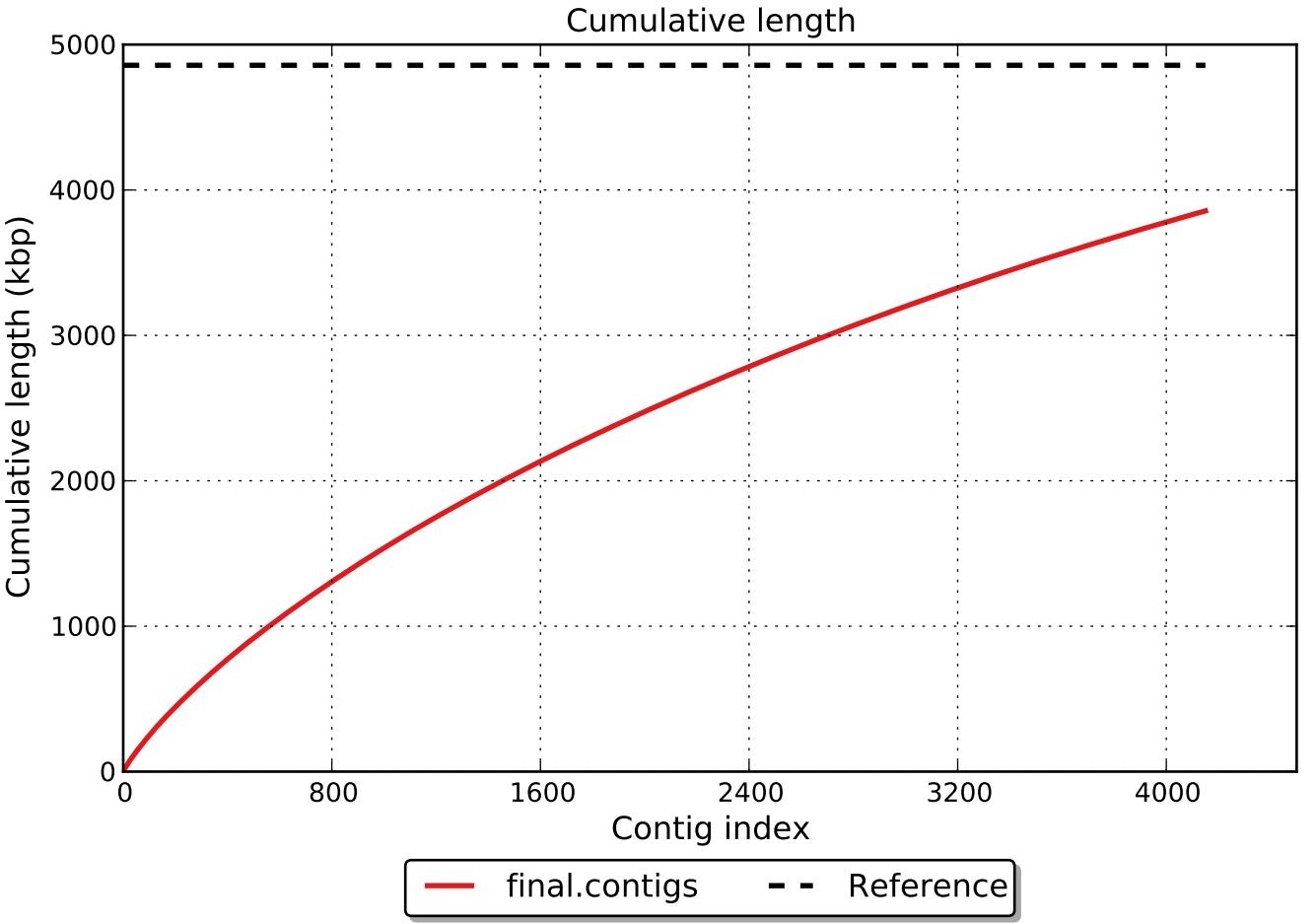
Unaligned report

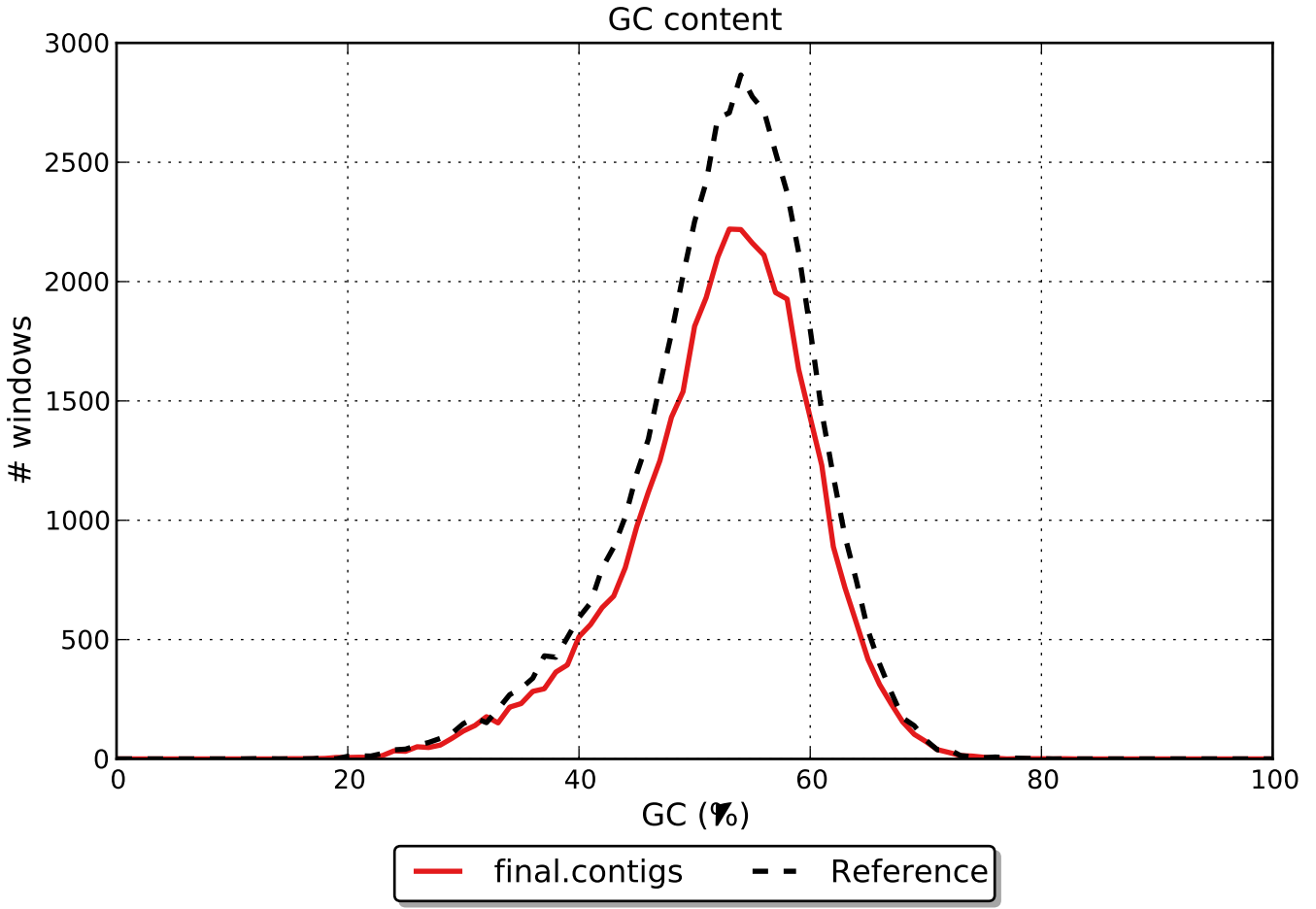
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

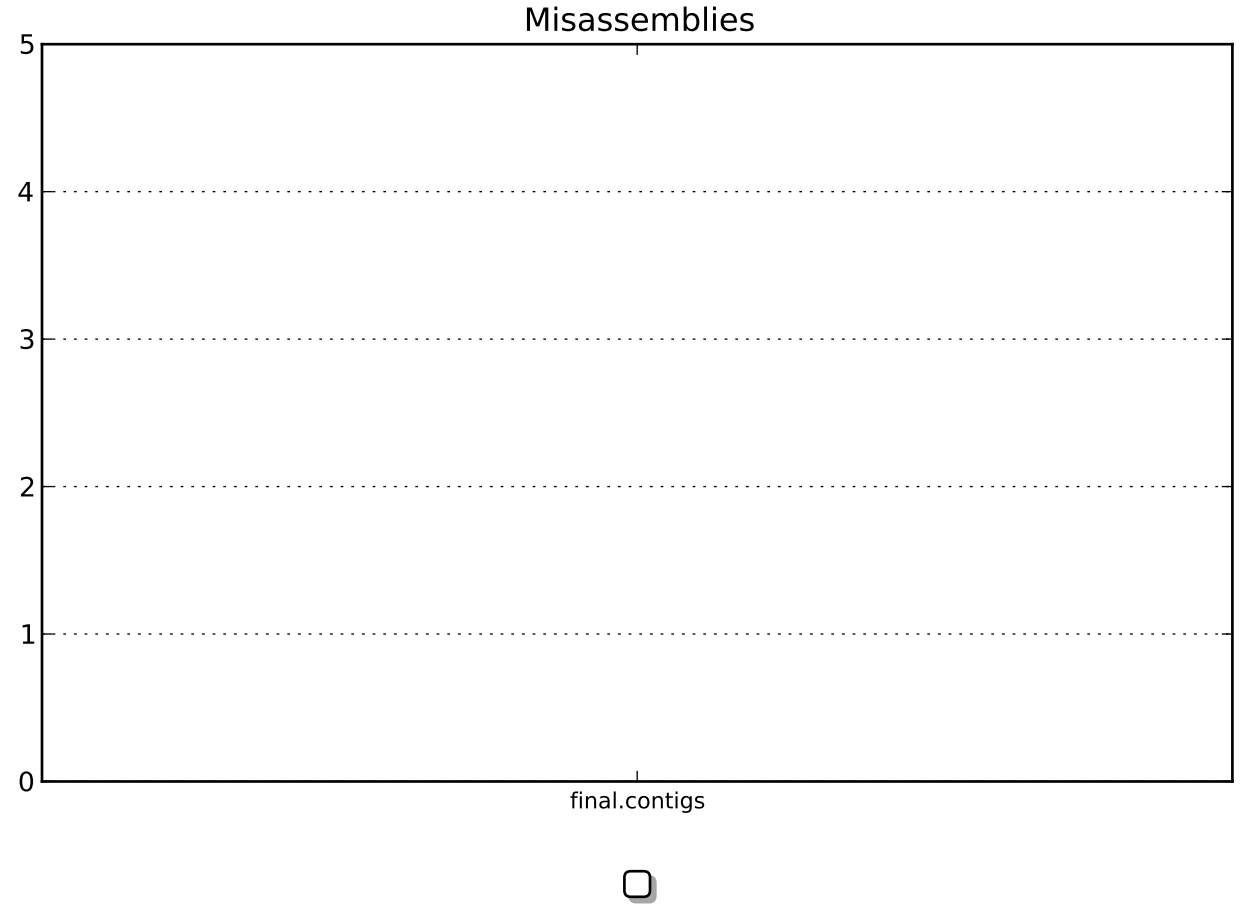
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

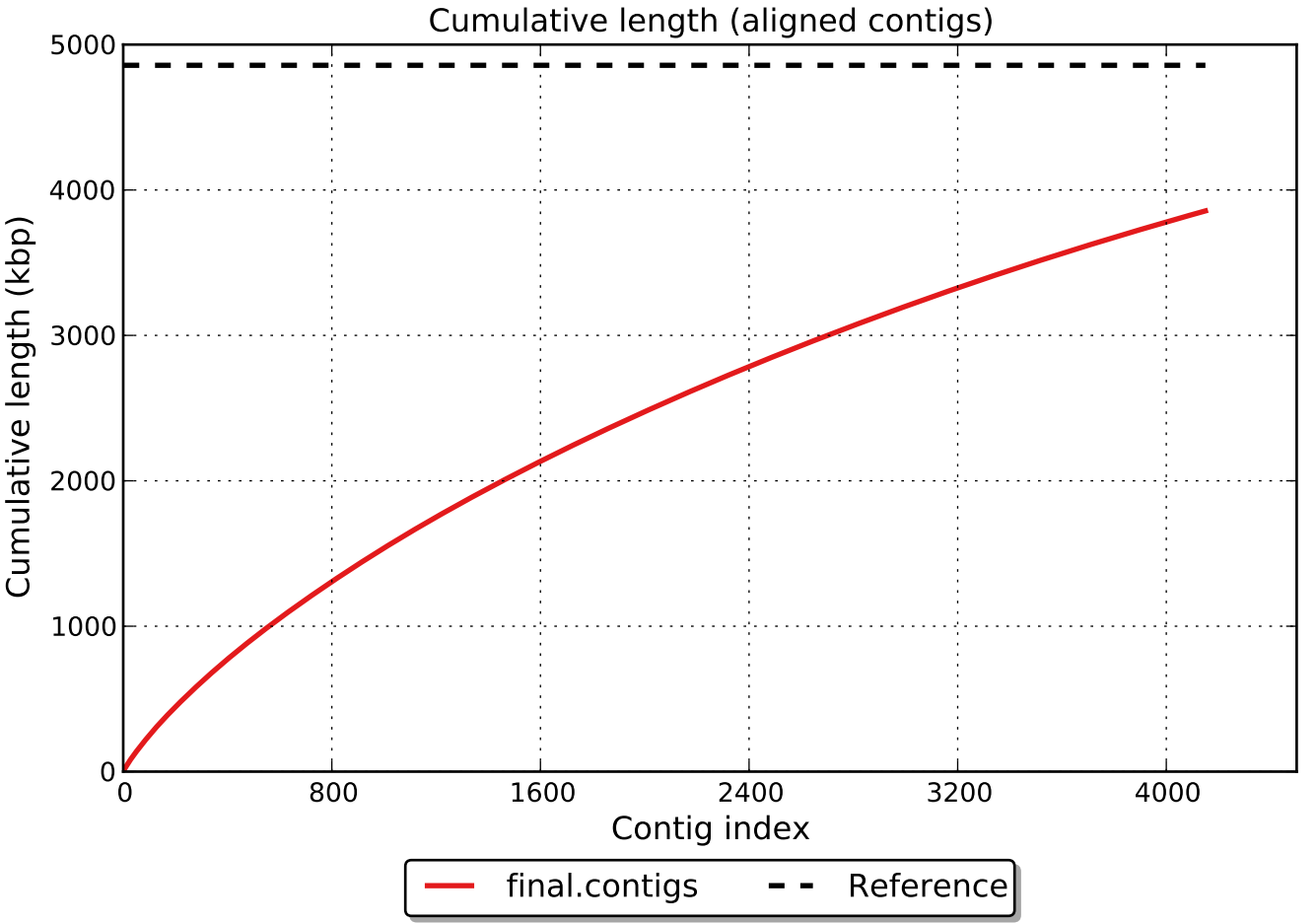

Nx
4000
3200
2400
1600
800
0
Contig length (bp)
0
20
40
60
80
100
x
final.contigs

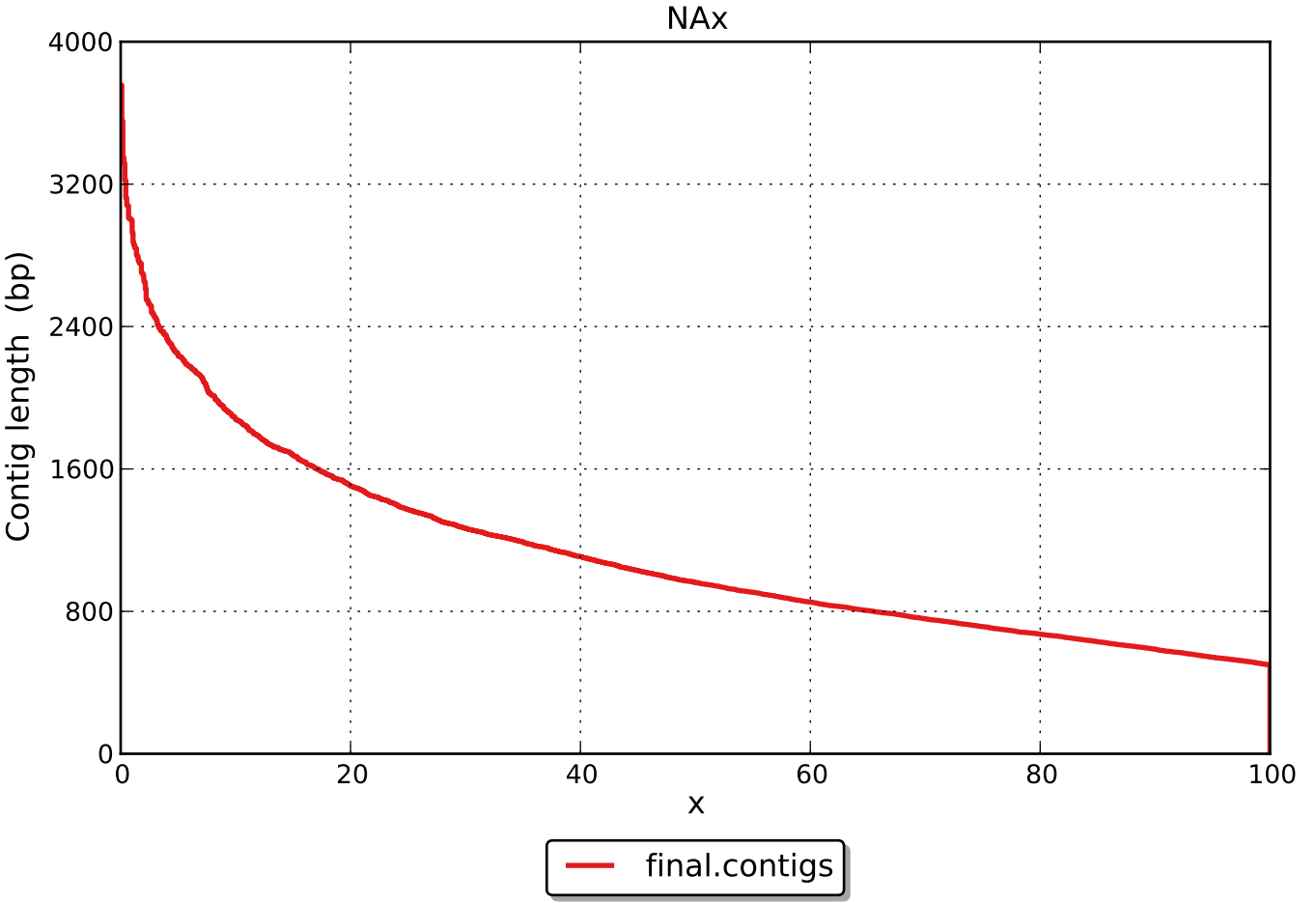

NGx
4000
3200
2400
1600
800
0
Contig length (bp)
0
20
40
60
80
100
x
final.contigs

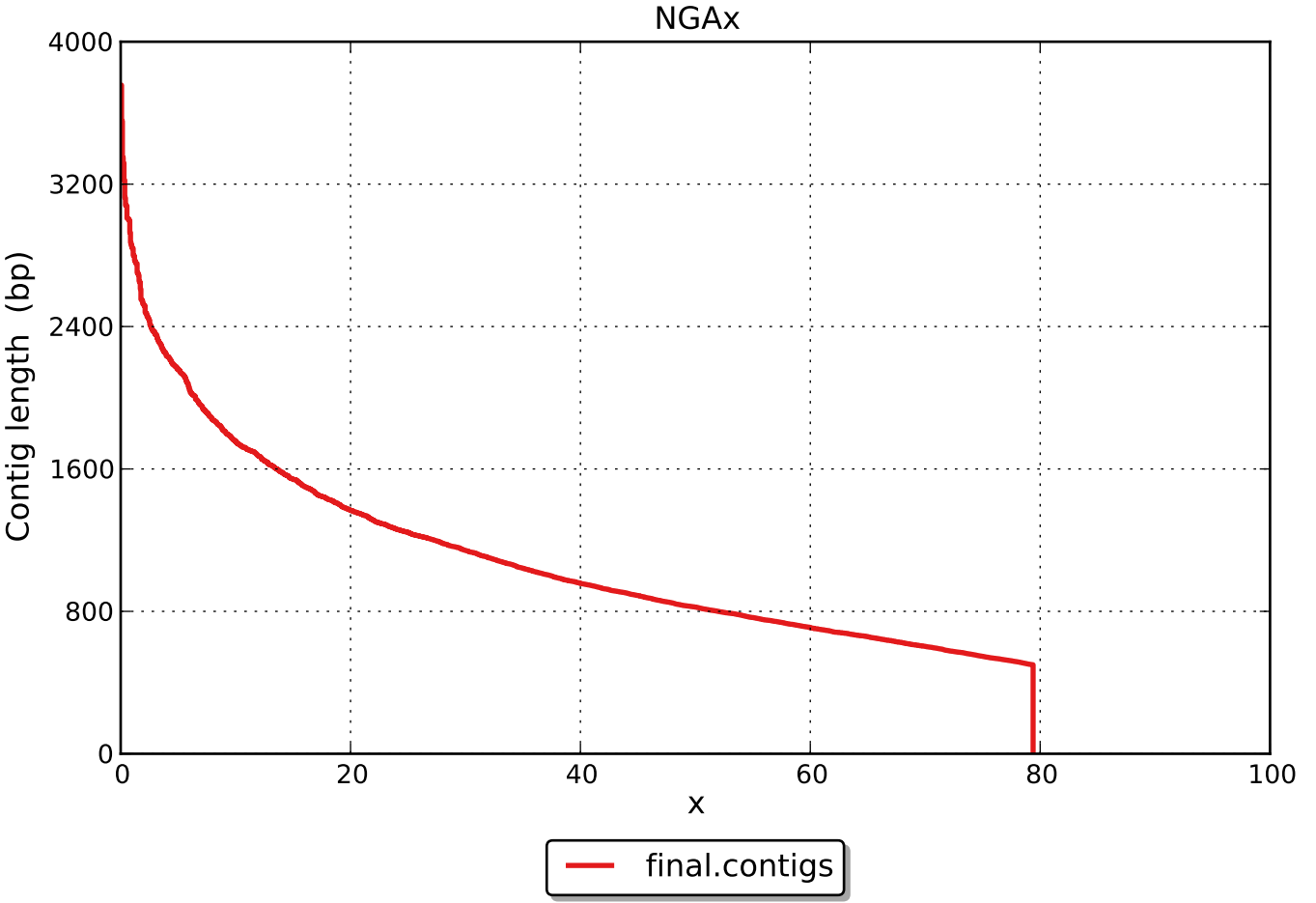

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
800
1600
2400
3200
4000
Contig index
final.contigs
Reference


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
800
1600
2400
3200
4000
Contig index
final.contigs
Reference


NAx
4000
3200
2400
1600
800
0
Contig length (bp)
0
20
40
60
80
100
x
final.contigs


NGAx
4000
3200
2400
1600
800
0
Contig length (bp)
0
20
40
60
80
100
x
final.contigs