Report

	final.contigs
# contigs (>= 1000 bp)	1310
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	1941106
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	4306
Largest contig	3693
Total length	4021855
Reference length	4857432
GC (%)	52.22
Reference GC (%)	52.22
N50	978
NG50	855
N75	700
NG75	568
L50	1381
LG50	1839
L75	2599
LG75	3596
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	1221
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	76.280
Duplication ratio	1.085
# N's per 100 kbp	0.00
# mismatches per 100 kbp	398.89
# indels per 100 kbp	0.11
Largest alignment	3693
NA50	978
NGA50	855
NA75	700
NGA75	567
LA50	1381
LGA50	1839
LA75	2599
LGA75	3597

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

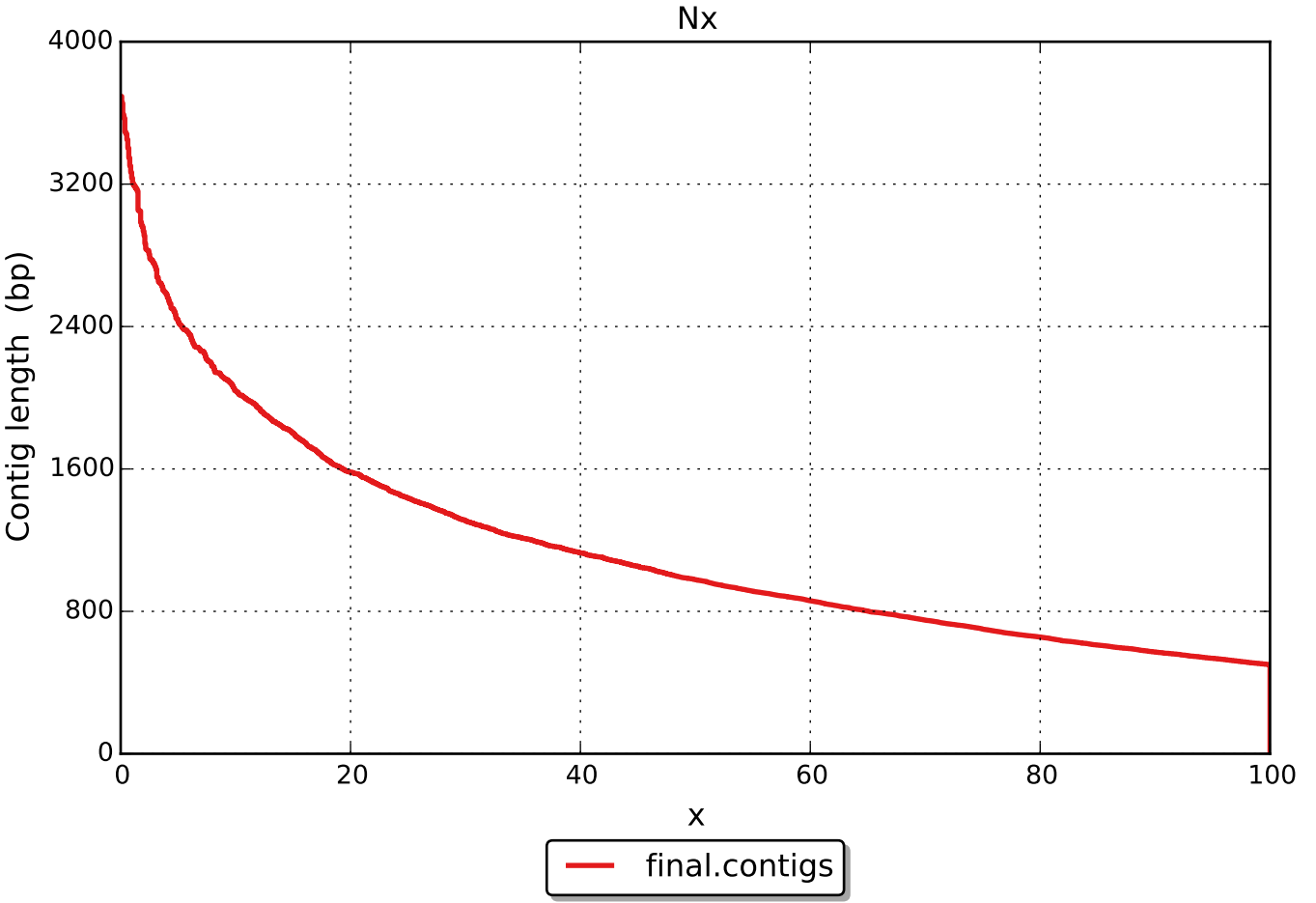
	final.contigs
# misassemblies	1
# relocations	0
# translocations	0
# inversions	1
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	1221
# local misassemblies	0
# mismatches	14780
# indels	4
# short indels	4
# long indels	0
Indels length	4

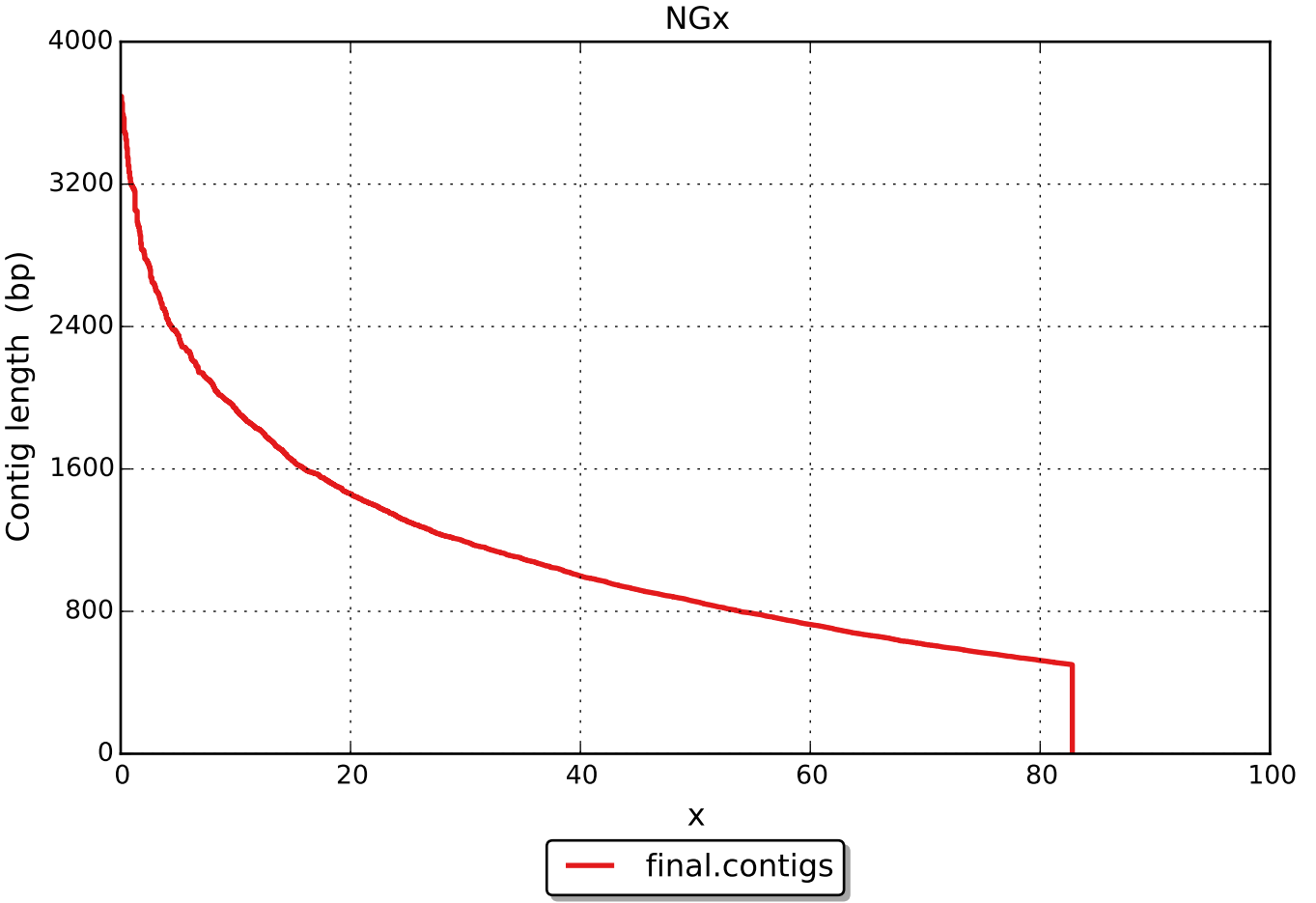
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

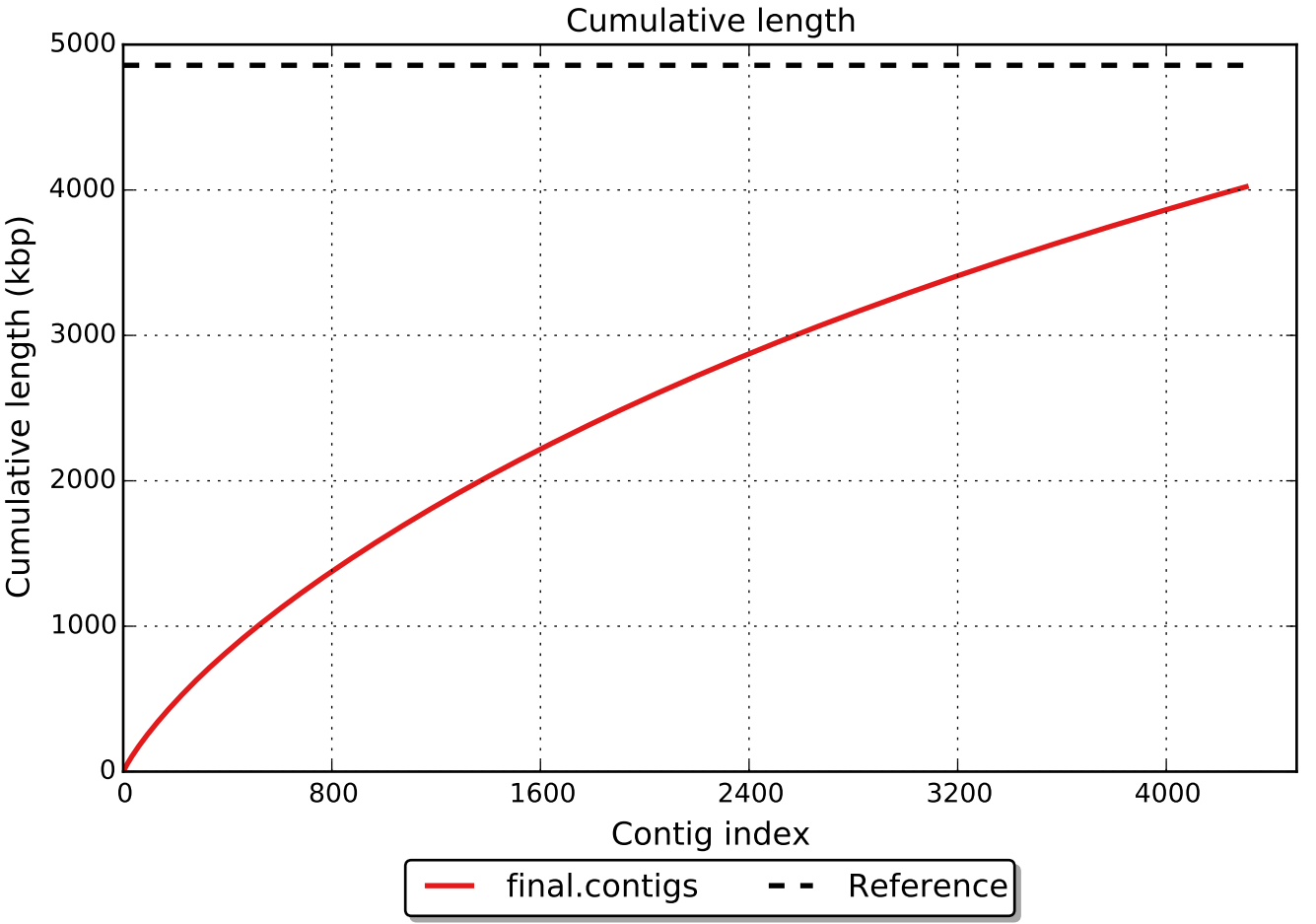
Unaligned report

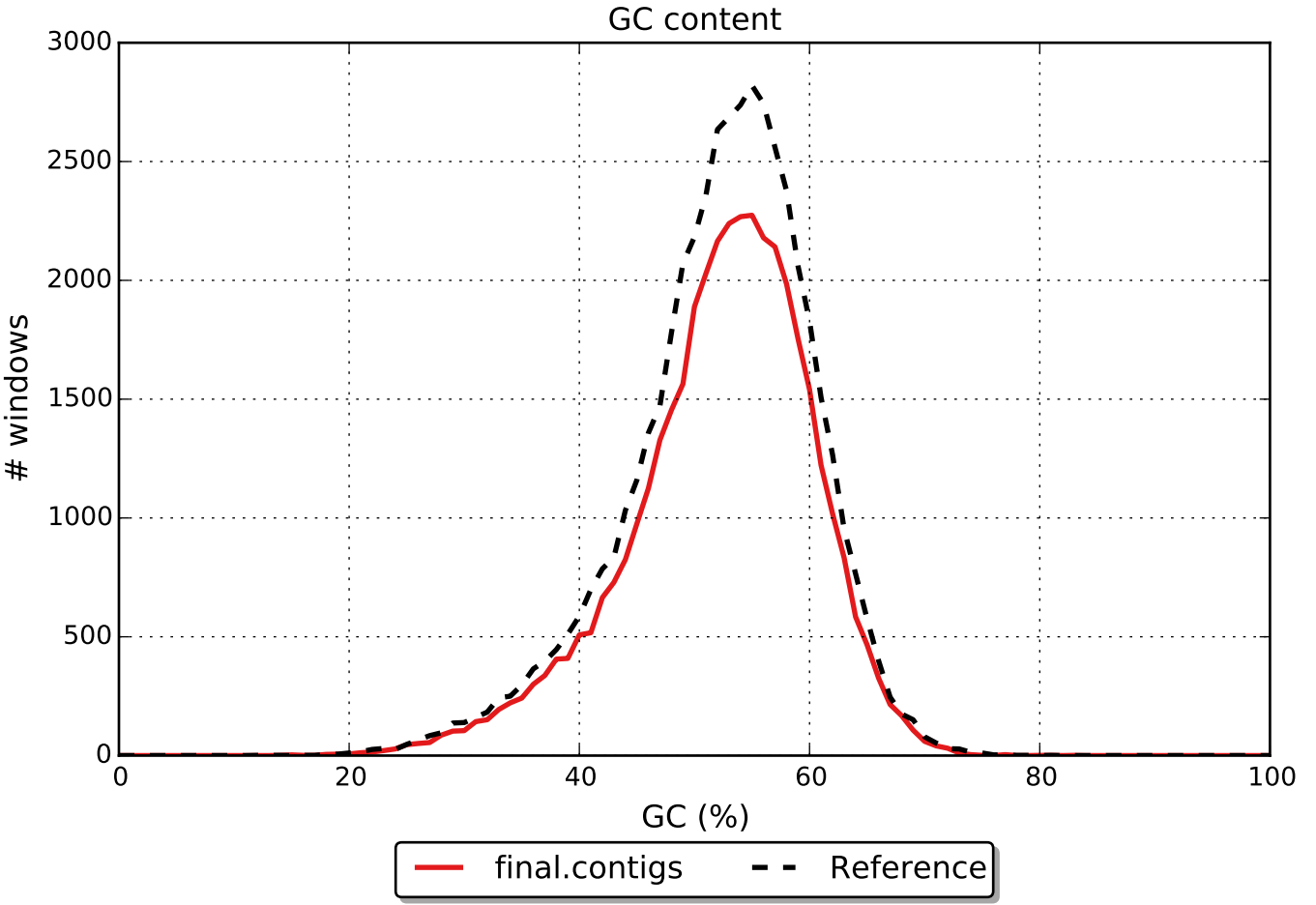
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

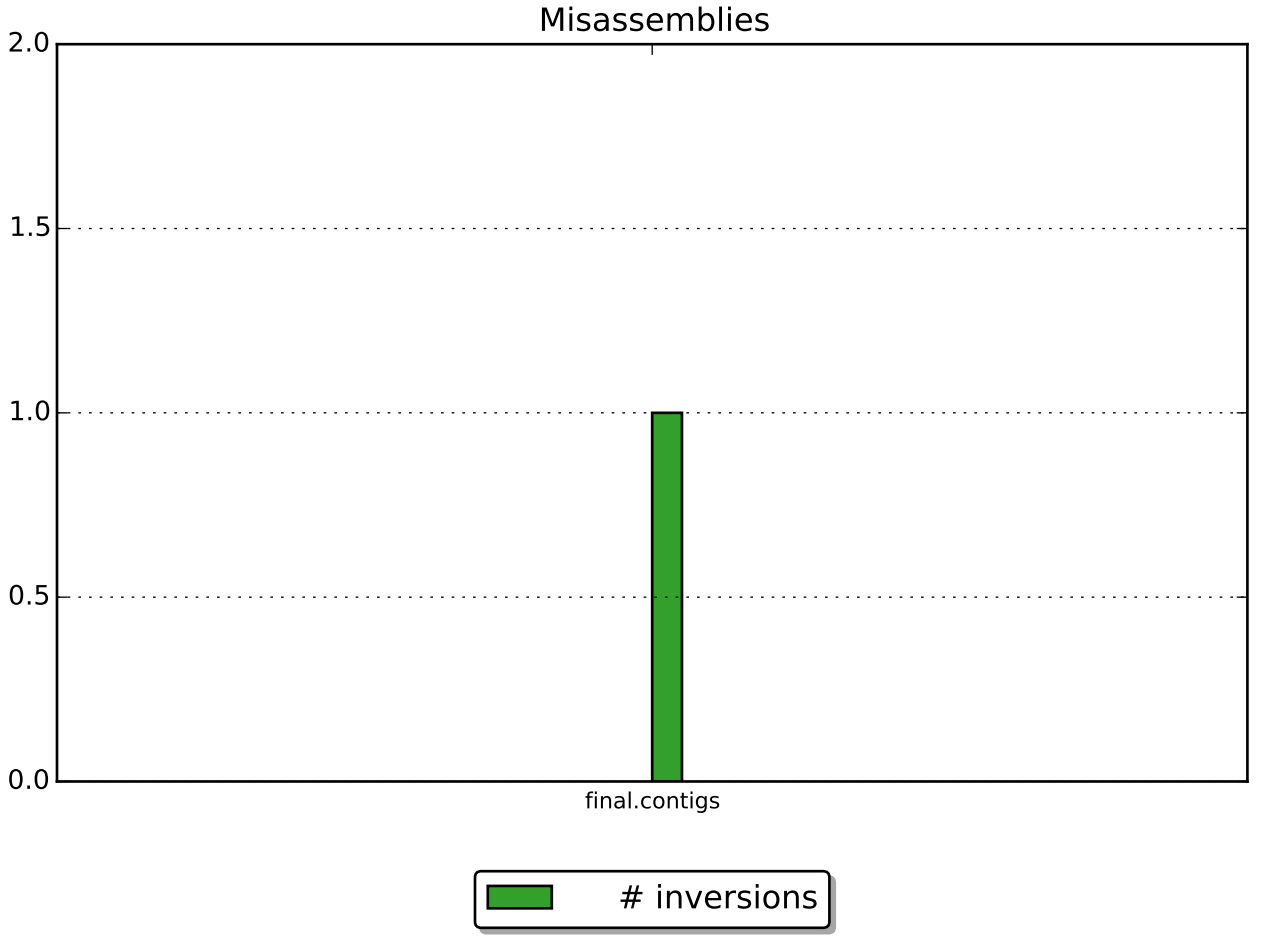
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

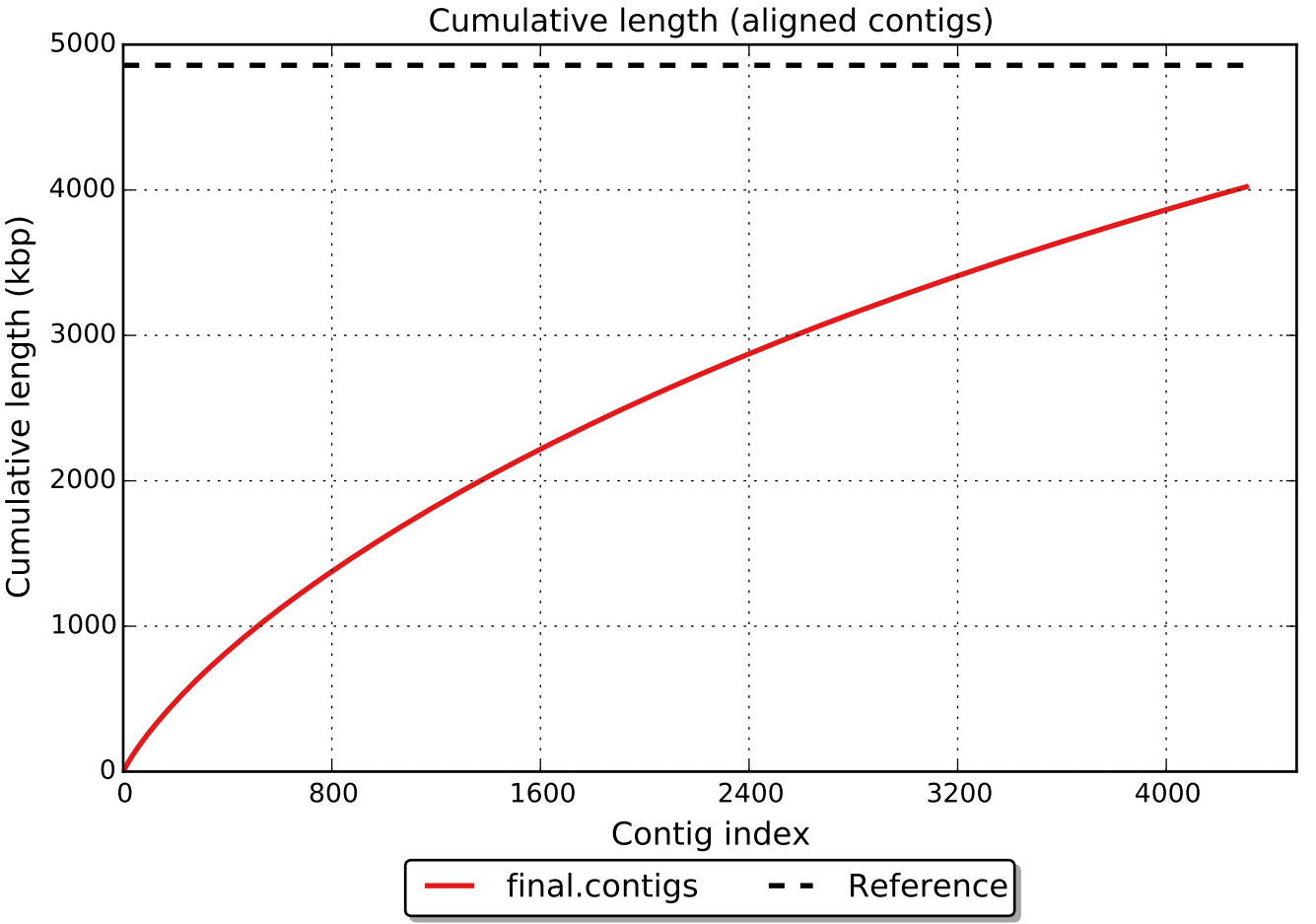

Nx
4000
3200
2400
1600
800
0
Contig length (bp)
0
20
40
60
80
100
x
final.contigs

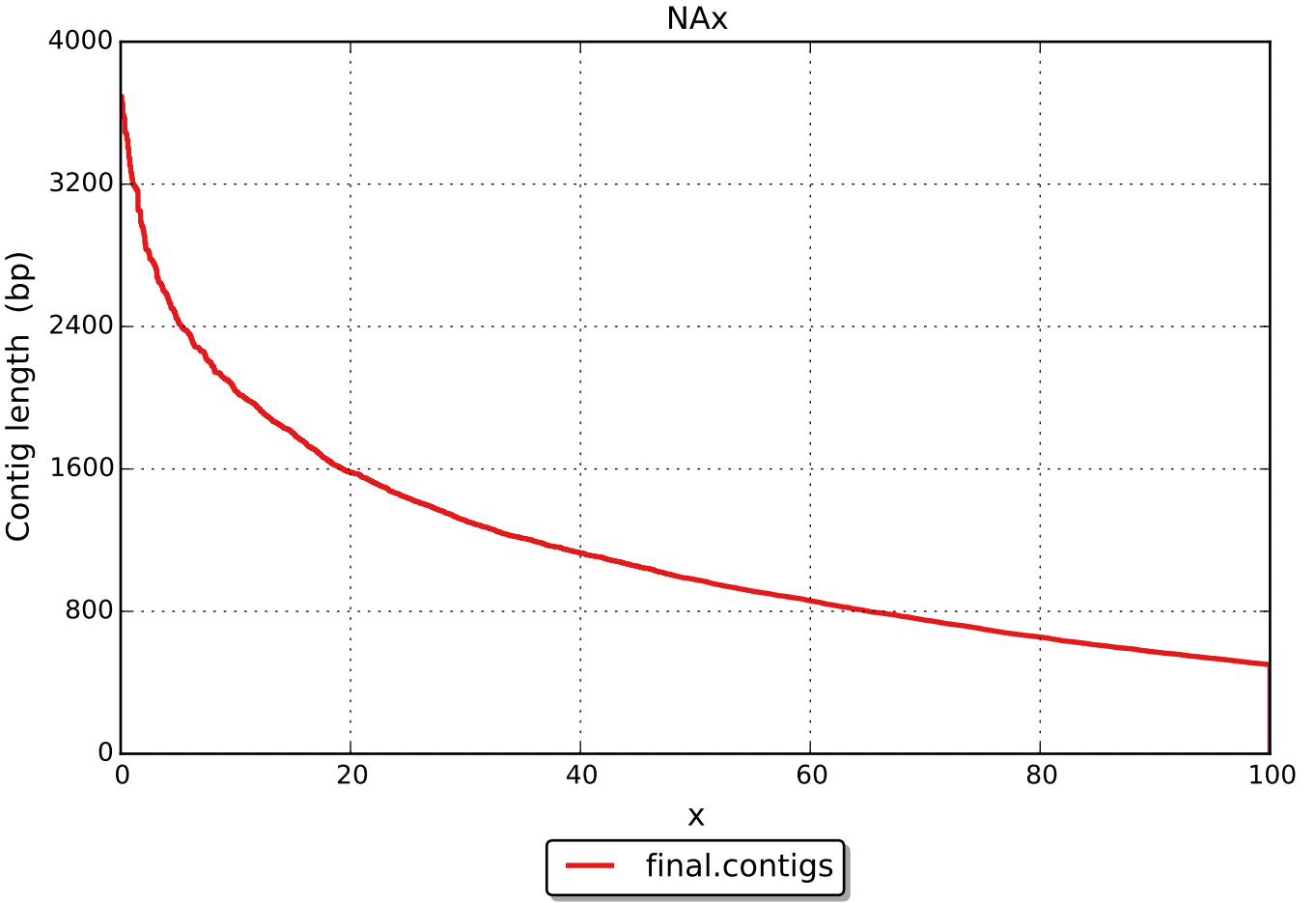

NGx
4000
3200
2400
1600
800
0
Contig length (bp)
0
20
40
60
80
100
x
final.contigs

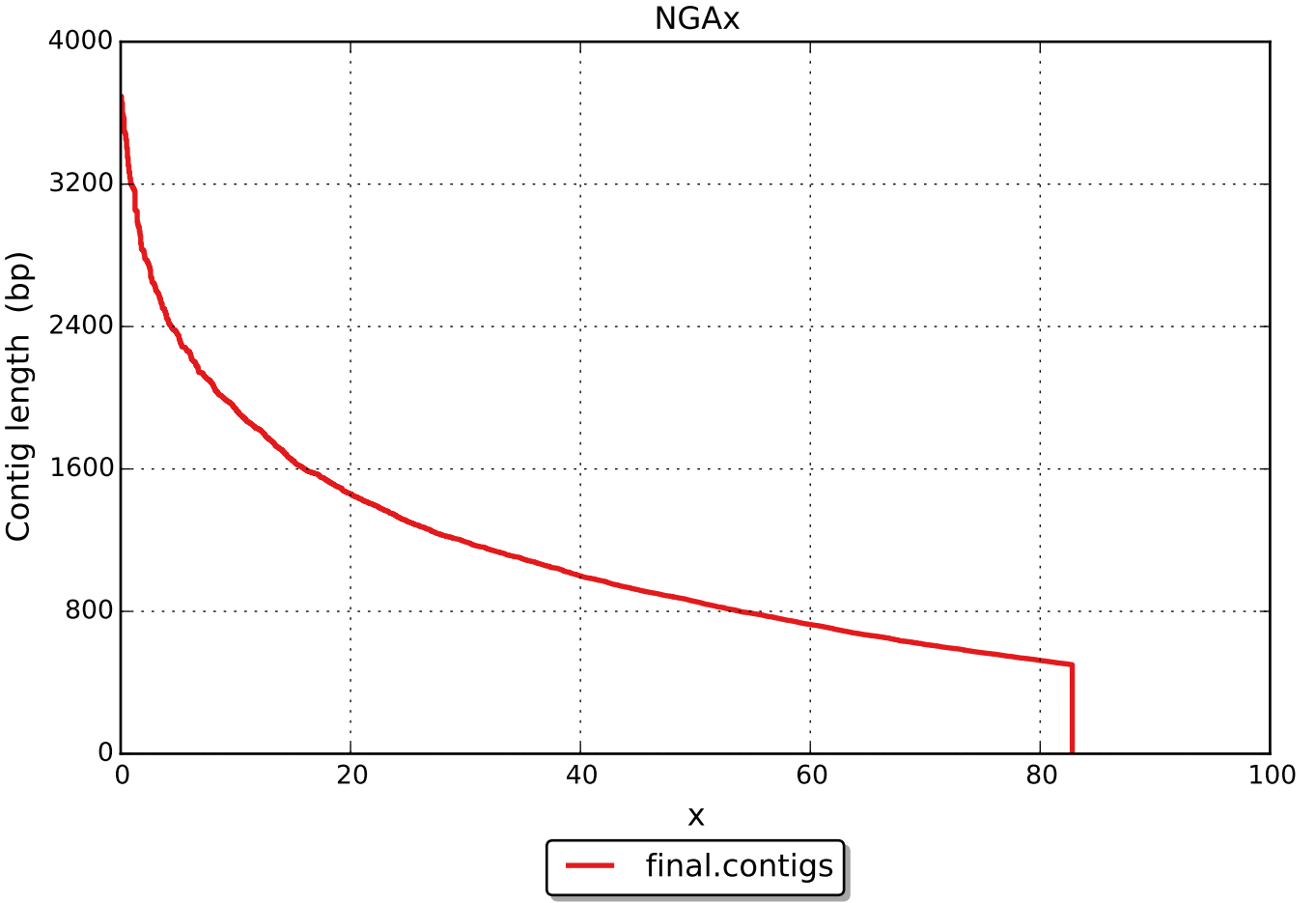

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
800
1600
2400
3200
4000
Contig index
final.contigs
Reference


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


Misassemblies
2.0
1.5
1.0
0.5
0.0
final.contigs
inversions


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