Report

	final.contigs
# contigs (>= 1000 bp)	1336
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	1922468
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	4485
Largest contig	4645
Total length	4136702
Reference length	4857432
GC (%)	52.22
Reference GC (%)	52.22
N50	959
NG50	863
N75	707
NG75	594
L50	1486
LG50	1882
L75	2745
LG75	3577
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	78.850
Duplication ratio	1.080
# N's per 100 kbp	0.00
# mismatches per 100 kbp	289.58
# indels per 100 kbp	0.10
Largest alignment	4645
NA50	959
NGA50	863
NA75	707
NGA75	594
LA50	1486
LGA50	1882
LA75	2745
LGA75	3578

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

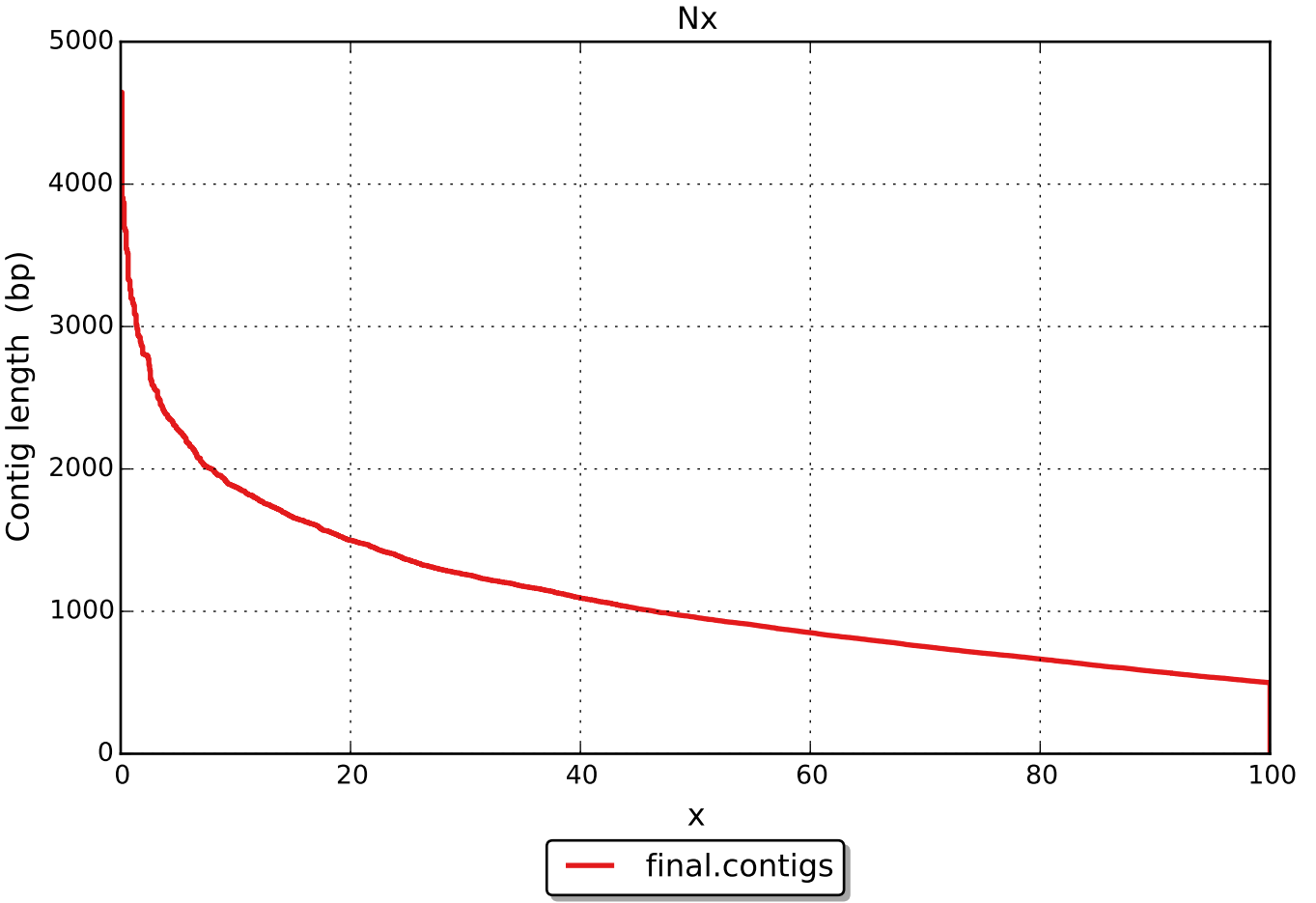
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# mismatches	11091
# indels	4
# short indels	4
# long indels	0
Indels length	4

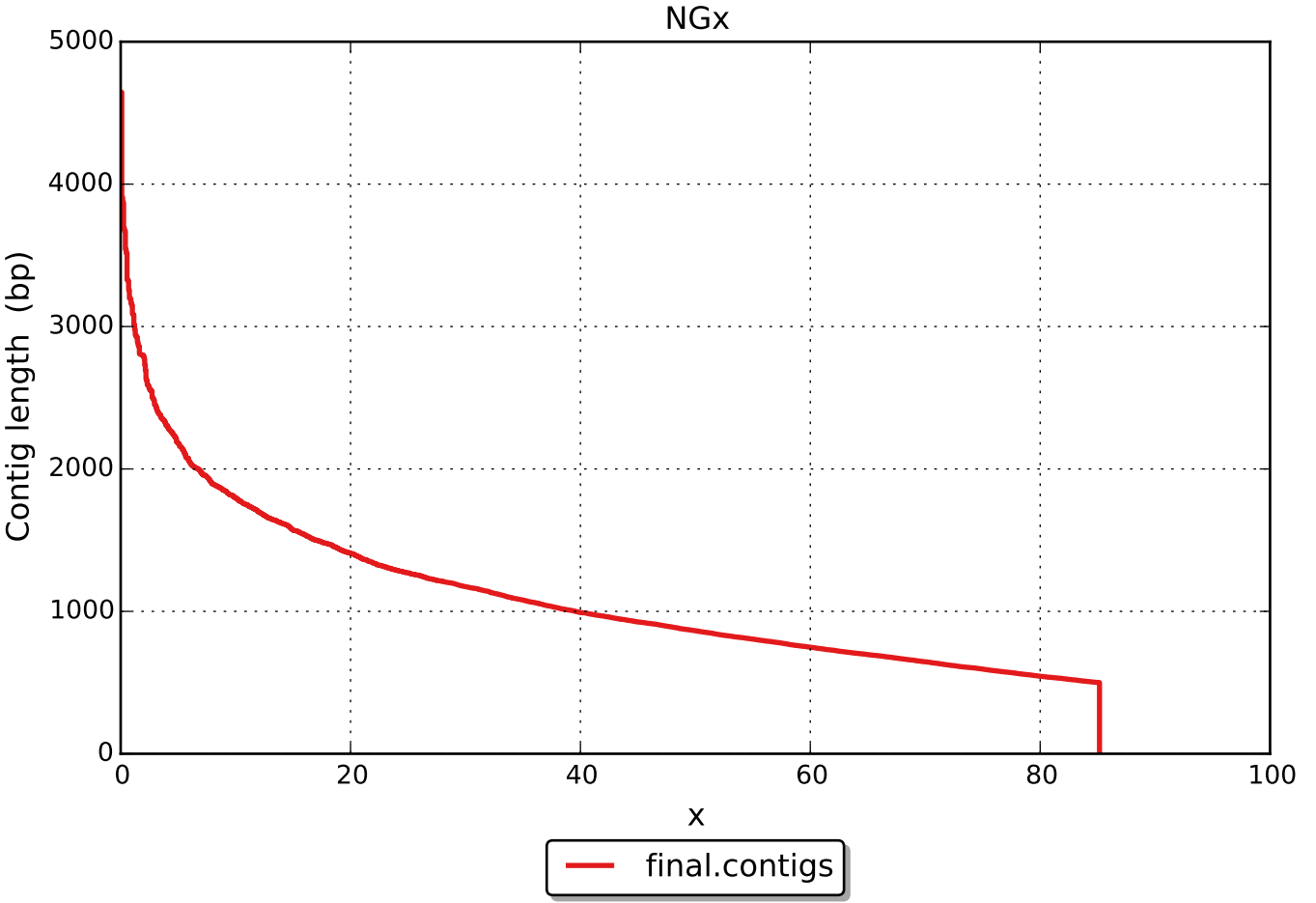
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

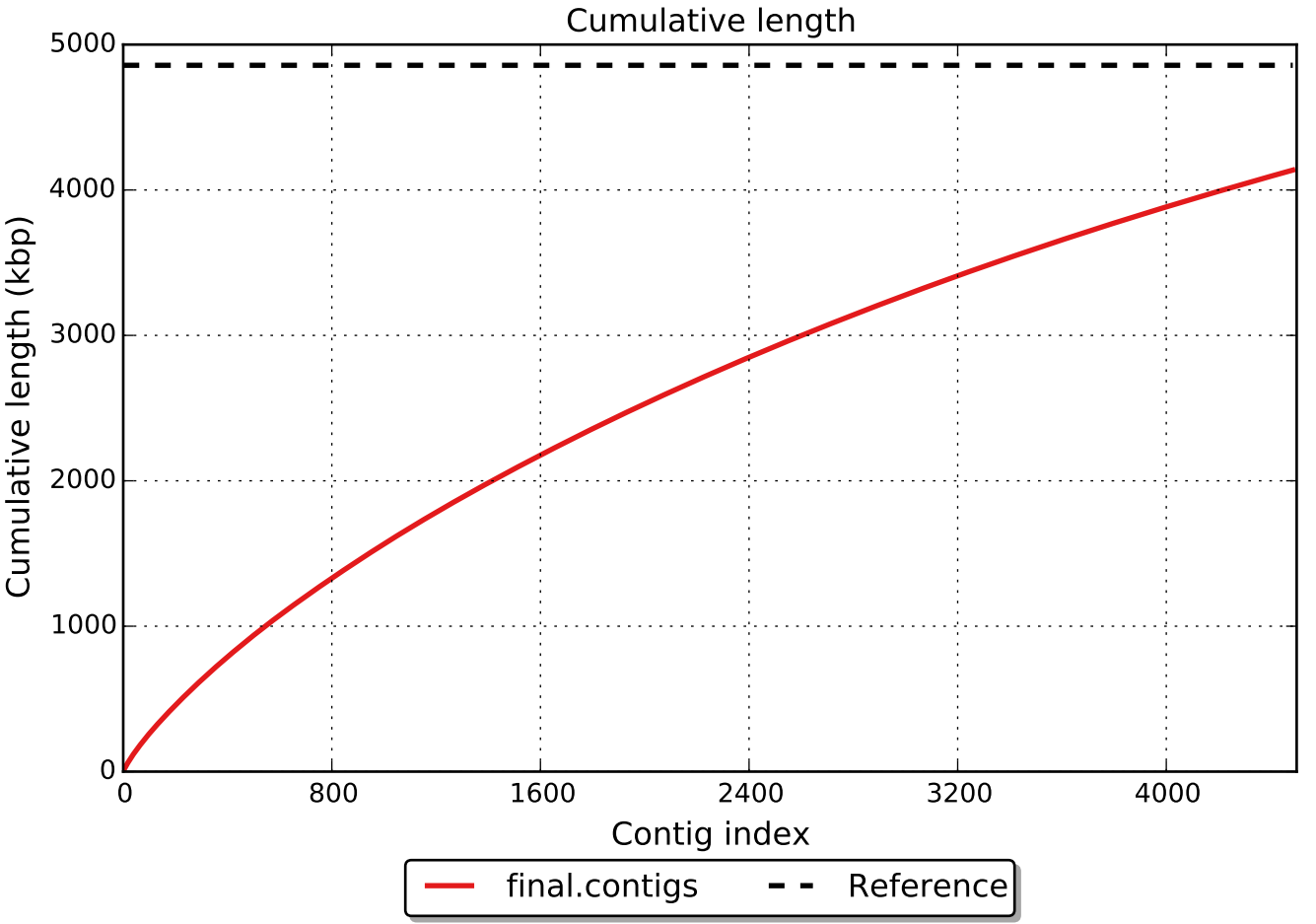
Unaligned report

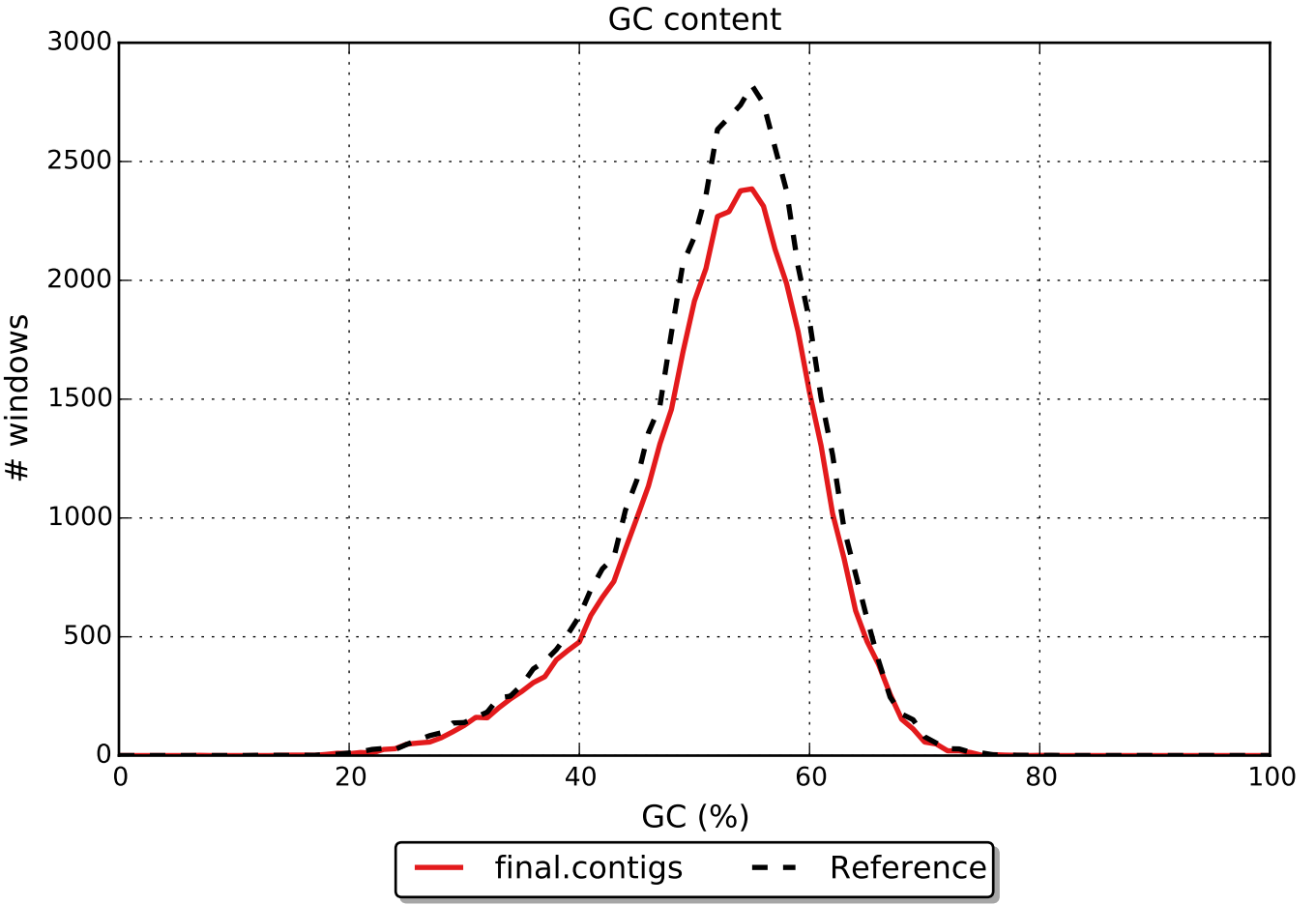
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

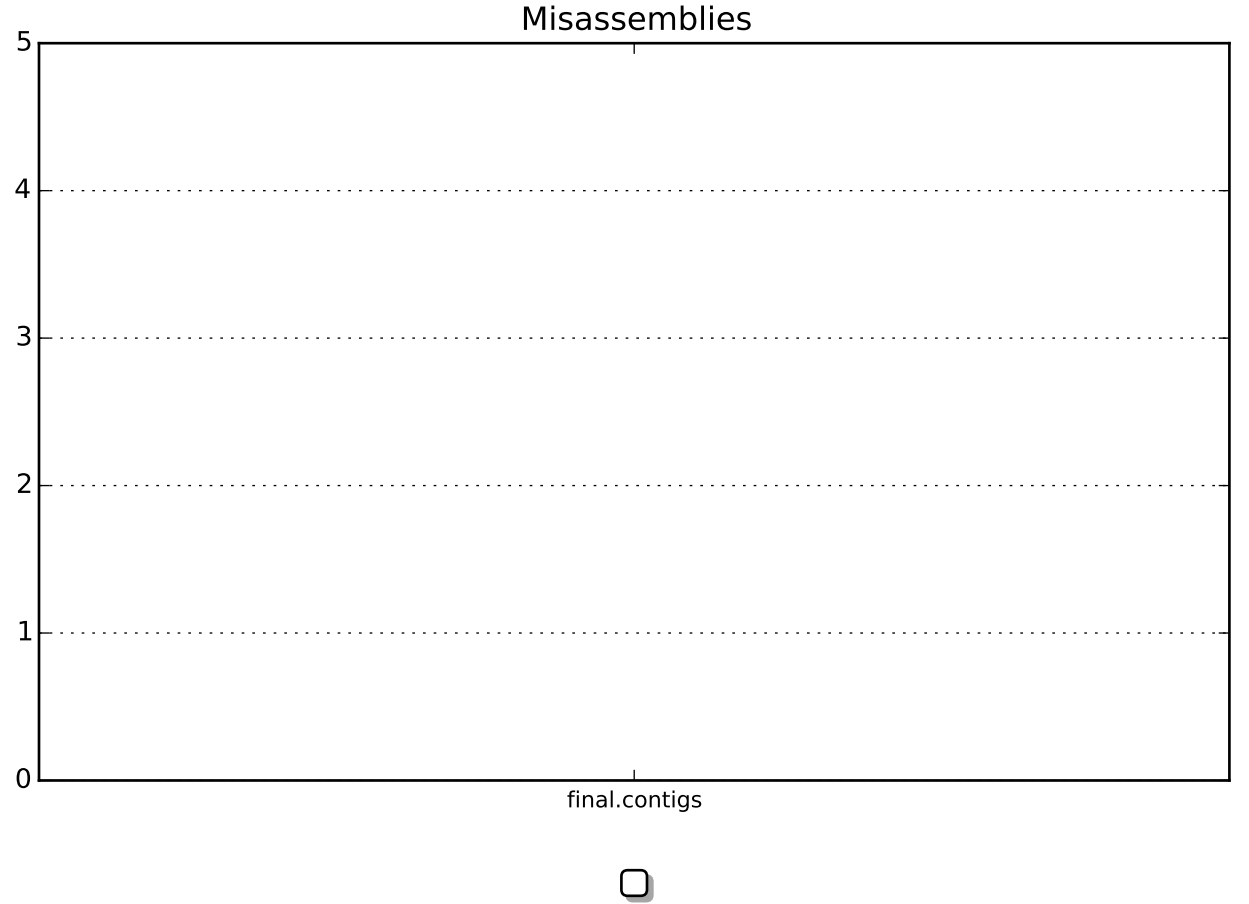
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

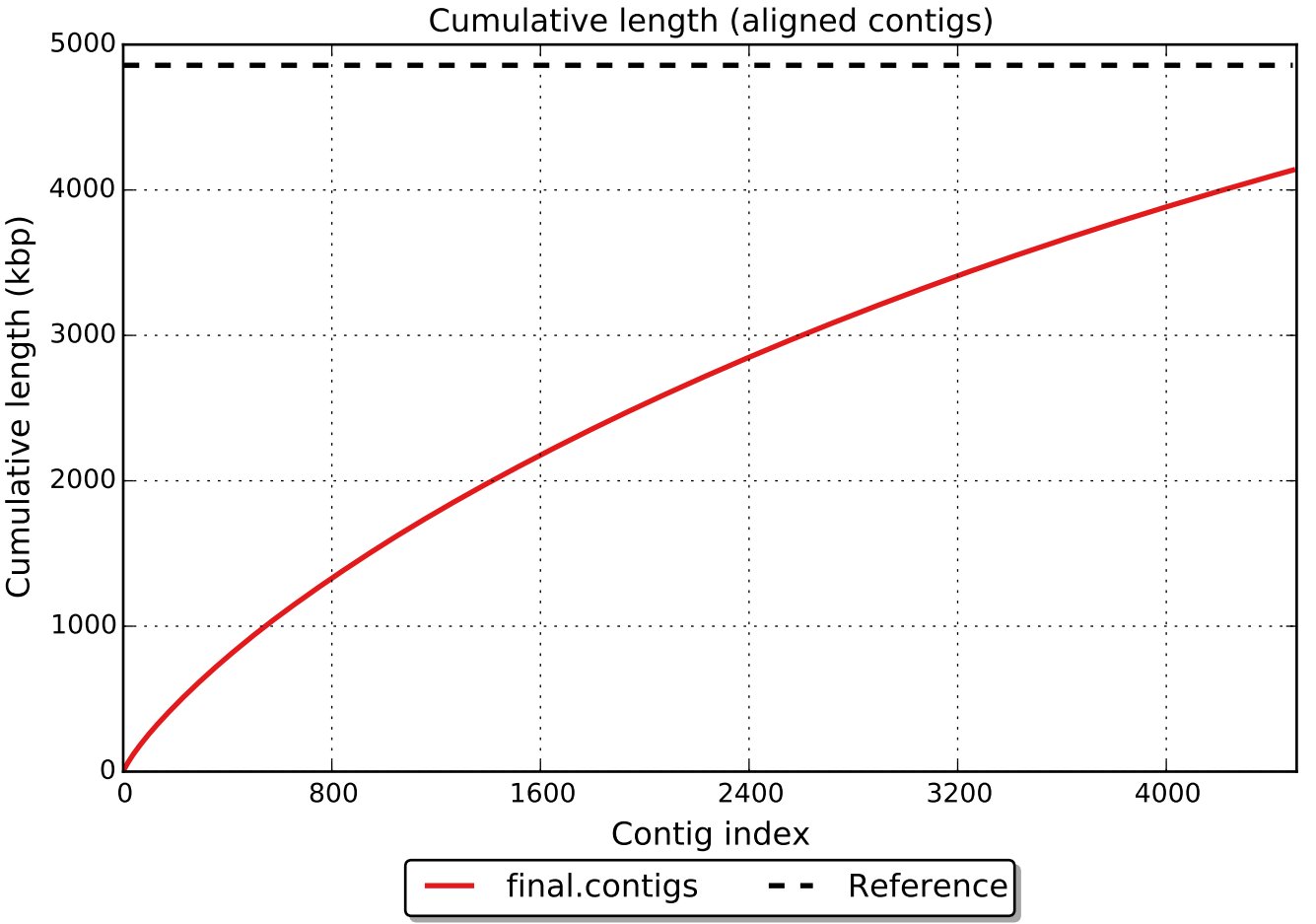

Nx
5000
4000
3000
2000
1000
0
Contig length (bp)
0
20
40
60
80
100
x
final.contigs

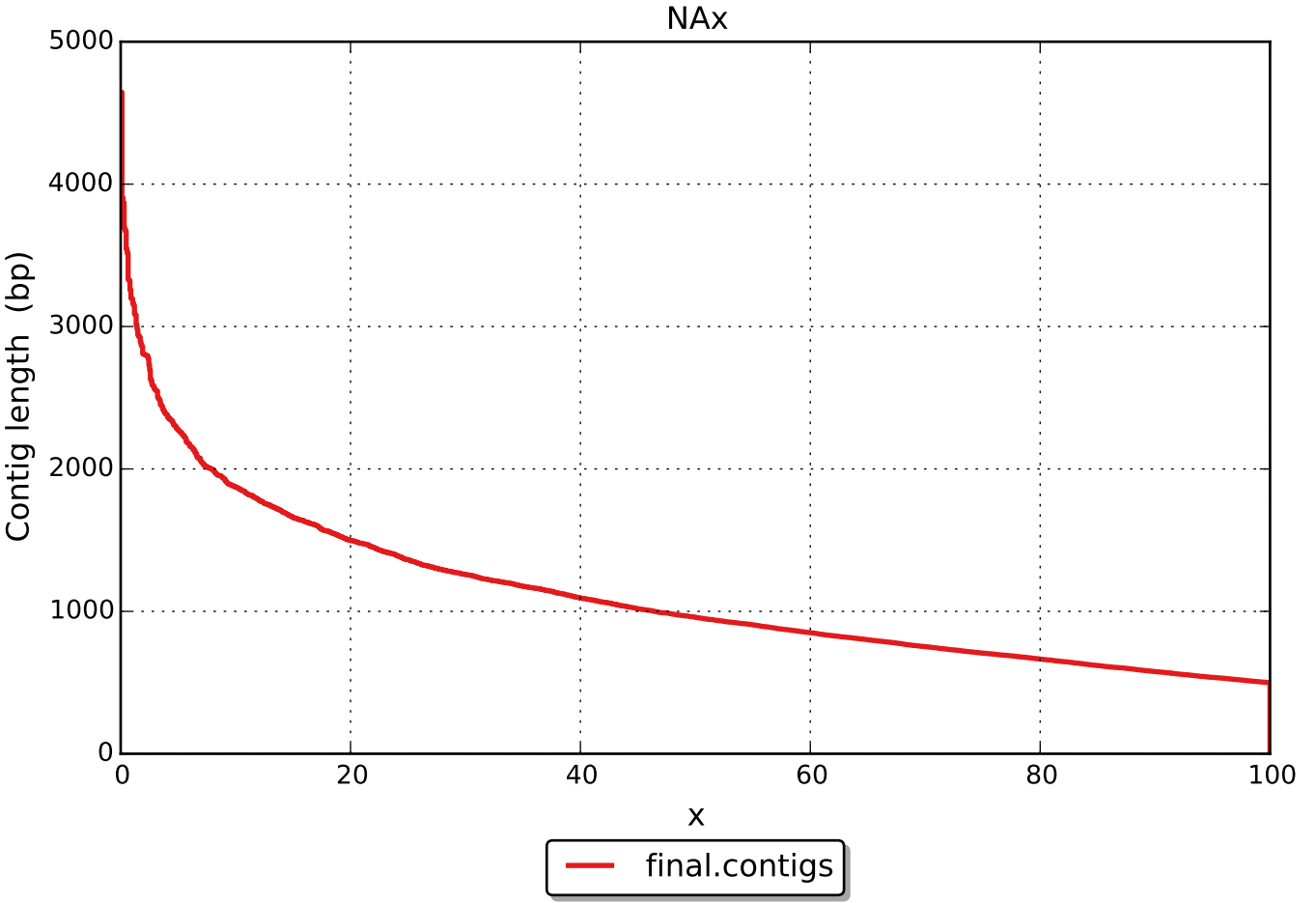

NGx
5000
4000
3000
2000
1000
0
Contig length (bp)
0
20
40
60
80
100
x
final.contigs

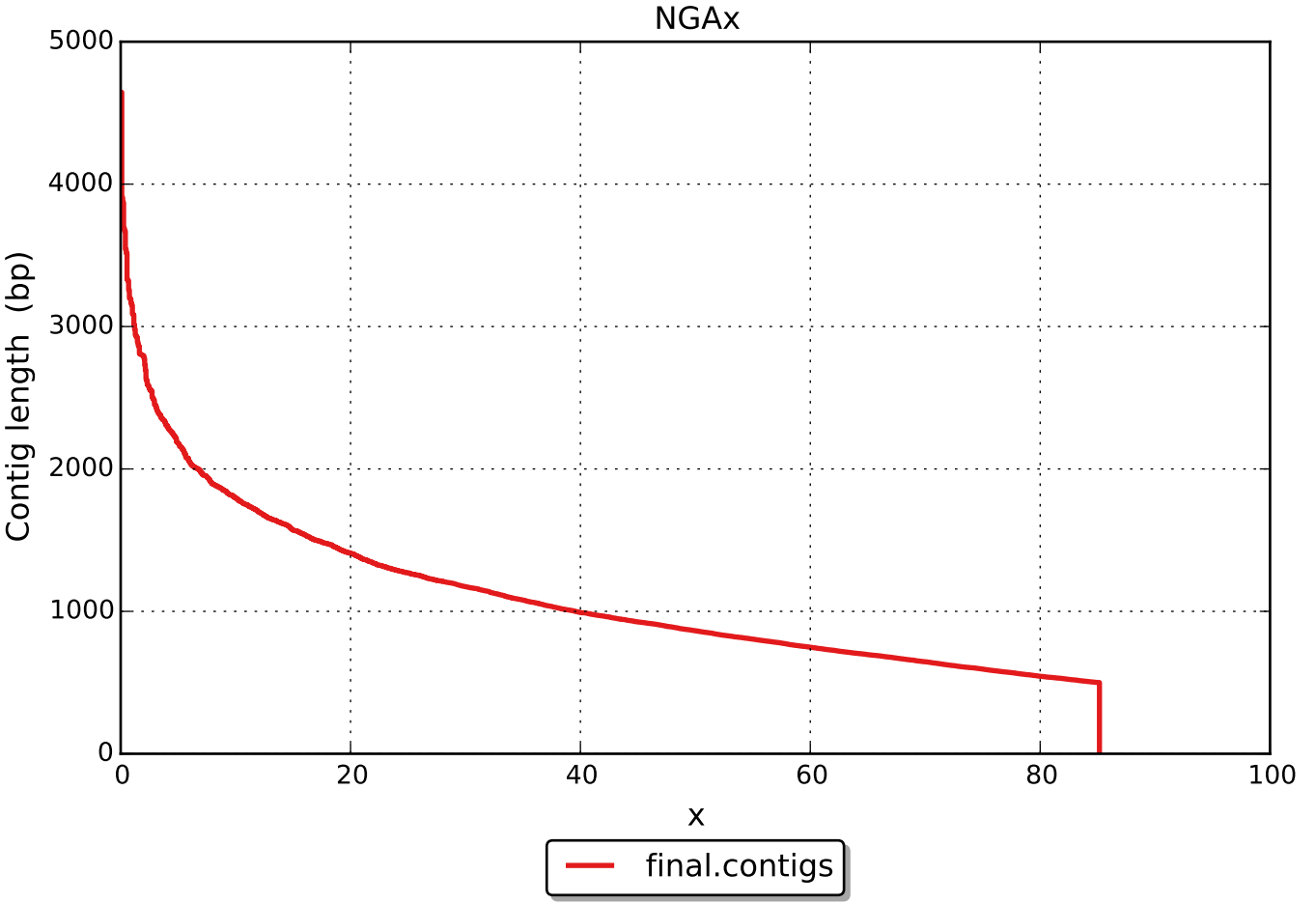

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
800
1600
2400
3200
4000
Contig index
final.contigs
Reference


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
5000
4000
3000
2000
1000
0
Contig length (bp)
0
20
40
60
80
100
x
final.contigs


NGAx
5000
4000
3000
2000
1000
0
Contig length (bp)
0
20
40
60
80
100
x
final.contigs