Report

	final.contigs
# contigs (>= 1000 bp)	1769
# contigs (>= 5000 bp)	100
# contigs (>= 10000 bp)	2
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4259984
Total length (>= 5000 bp)	624614
Total length (>= 10000 bp)	20616
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	2558
Largest contig	10576
Total length	4836990
Reference length	4857432
GC (%)	52.19
Reference GC (%)	52.22
N50	2506
NG50	2499
N75	1476
NG75	1460
L50	627
LG50	631
L75	1250
LG75	1261
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	95.837
Duplication ratio	1.039
# N's per 100 kbp	0.00
# mismatches per 100 kbp	46.29
# indels per 100 kbp	0.00
Largest alignment	10576
NA50	2506
NGA50	2499
NA75	1476
NGA75	1460
LA50	627
LGA50	631
LA75	1250
LGA75	1261

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

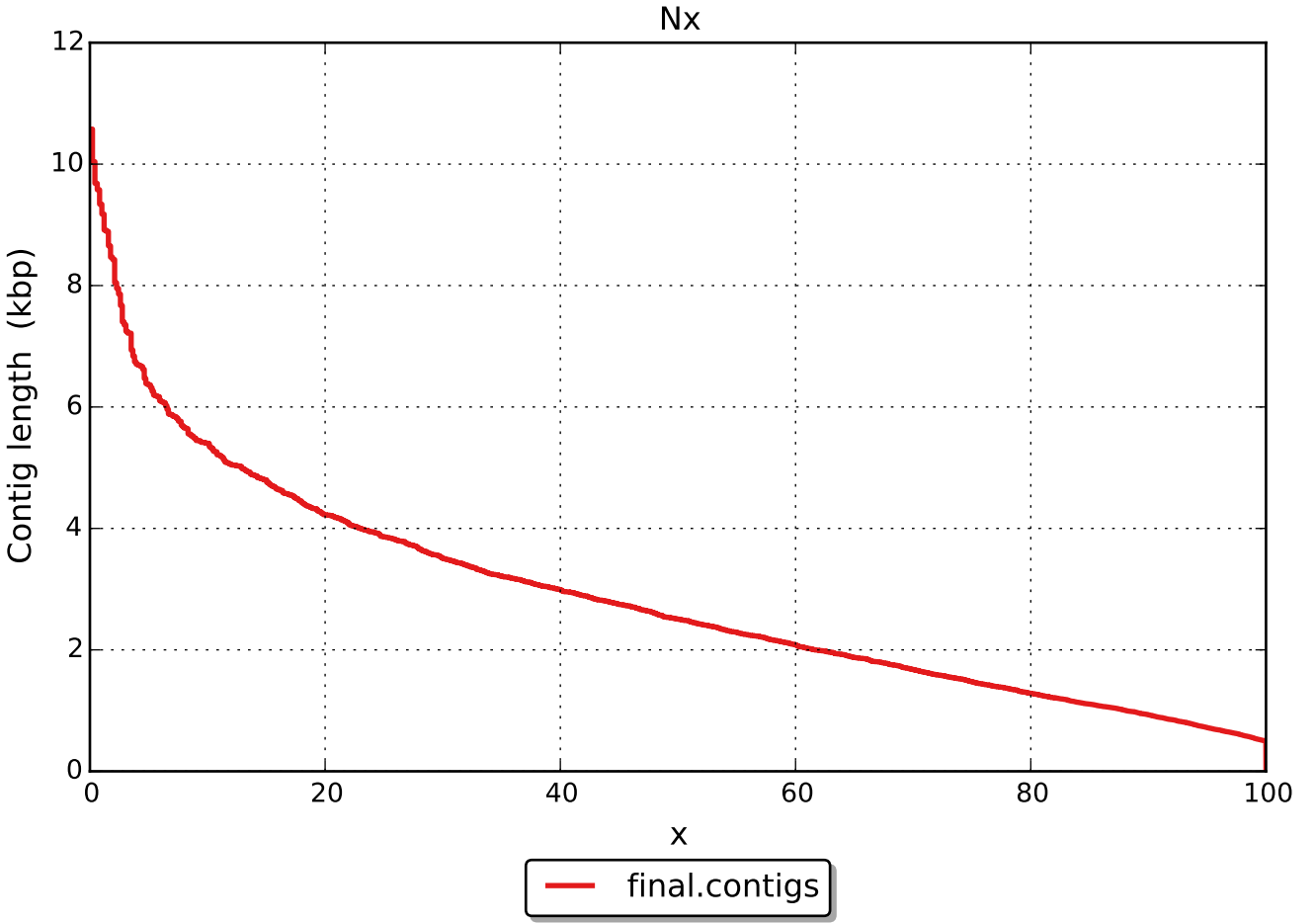
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	2155
# indels	0
# short indels	0
# long indels	0
Indels length	0

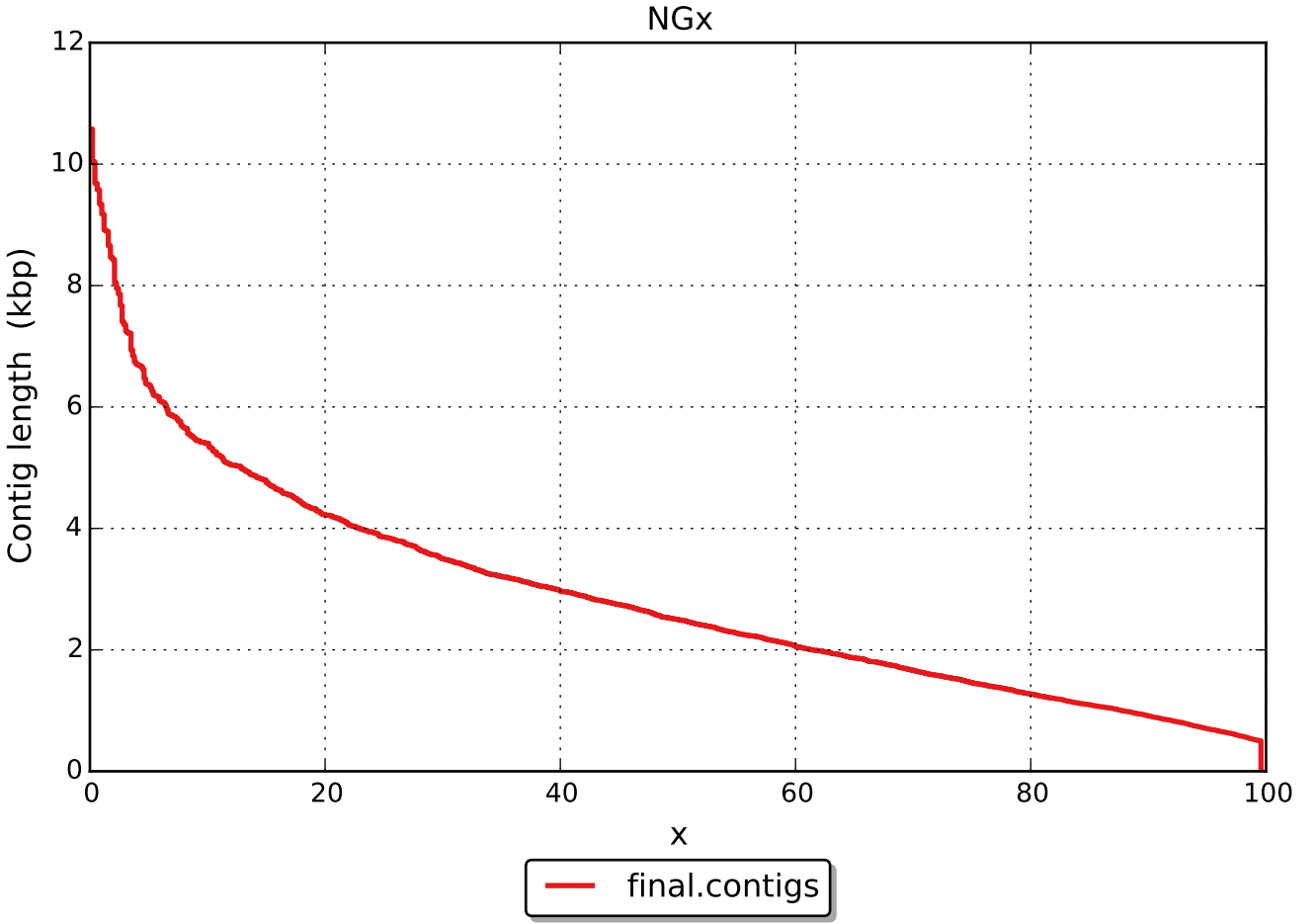
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

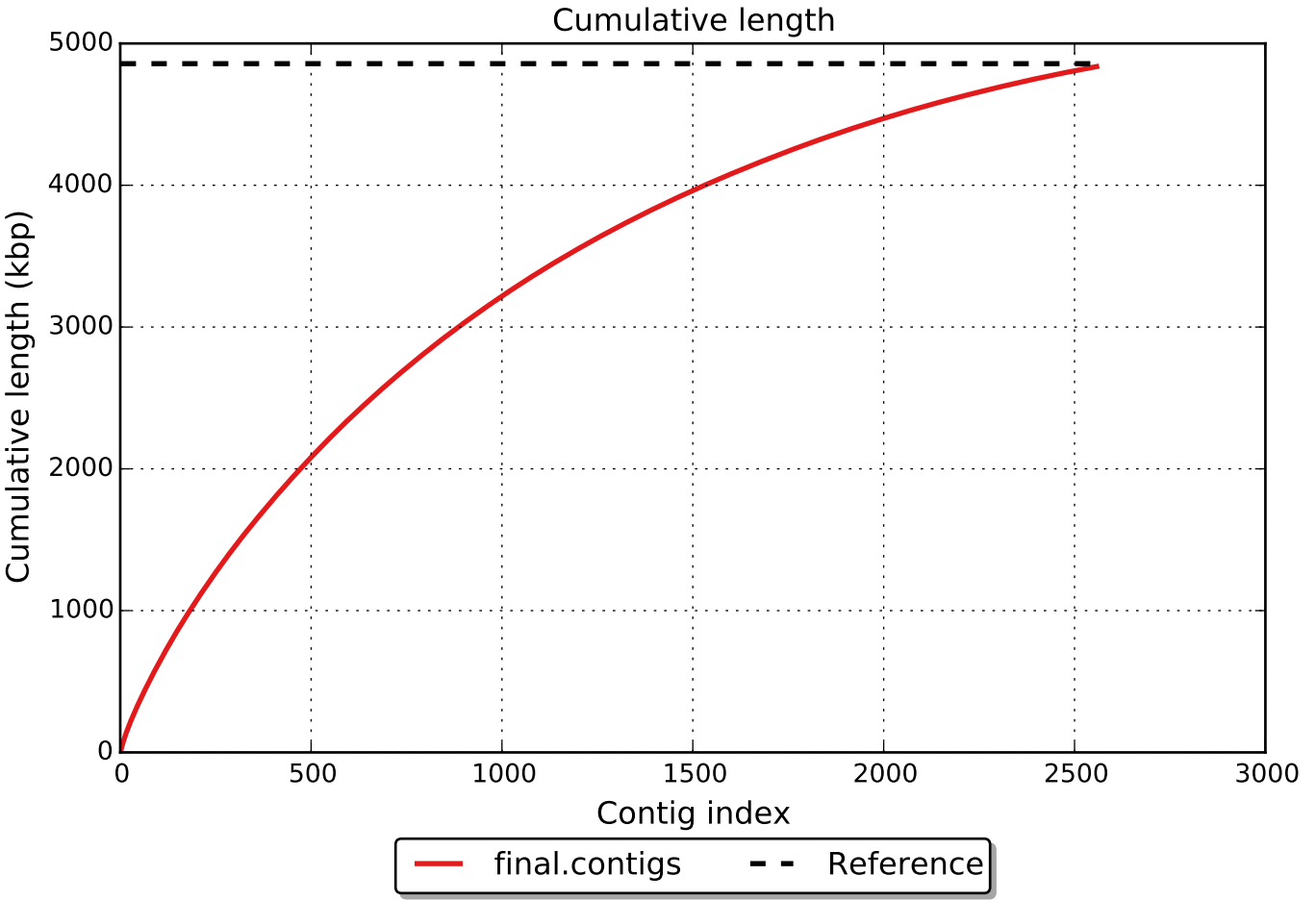
Unaligned report

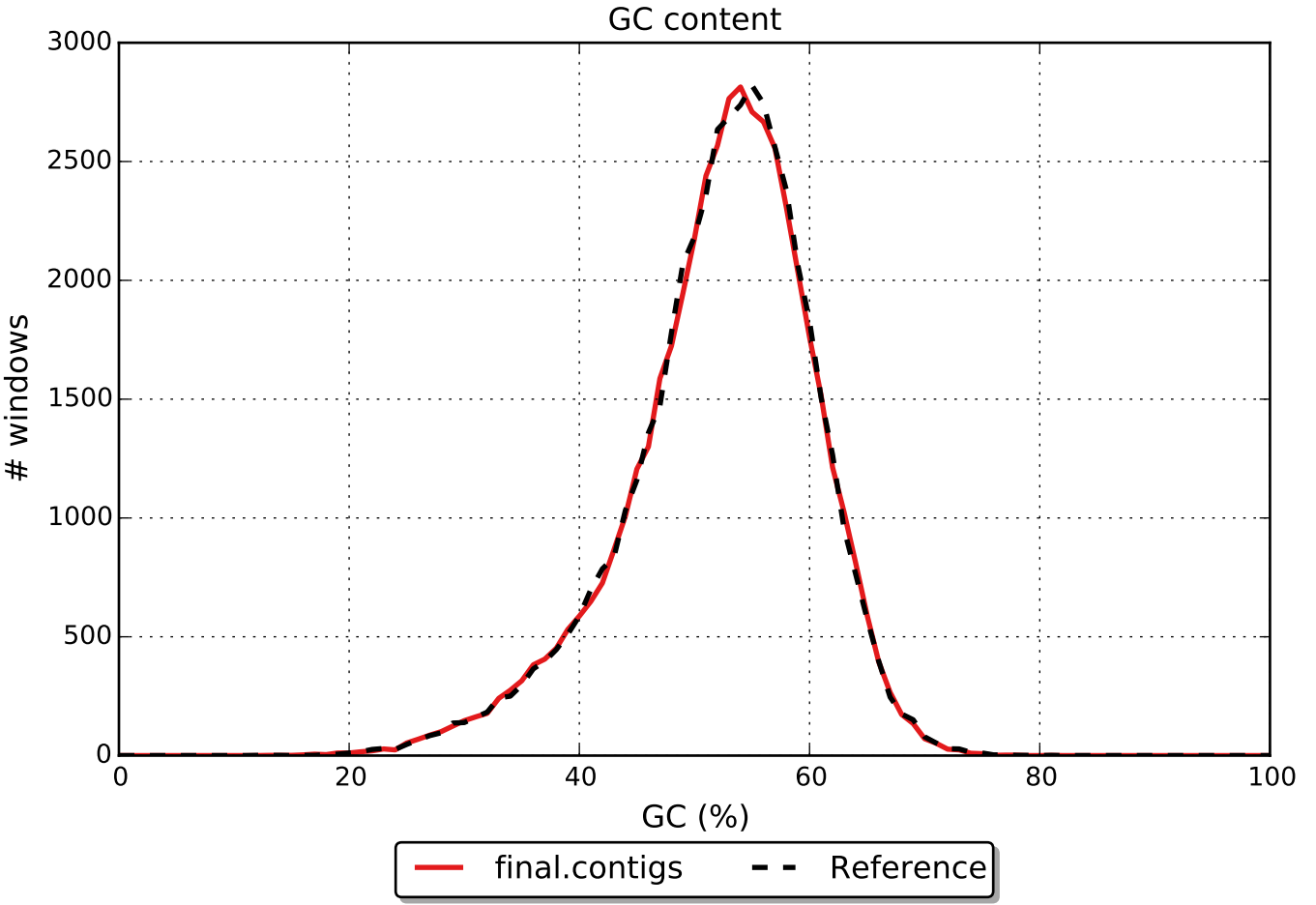
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

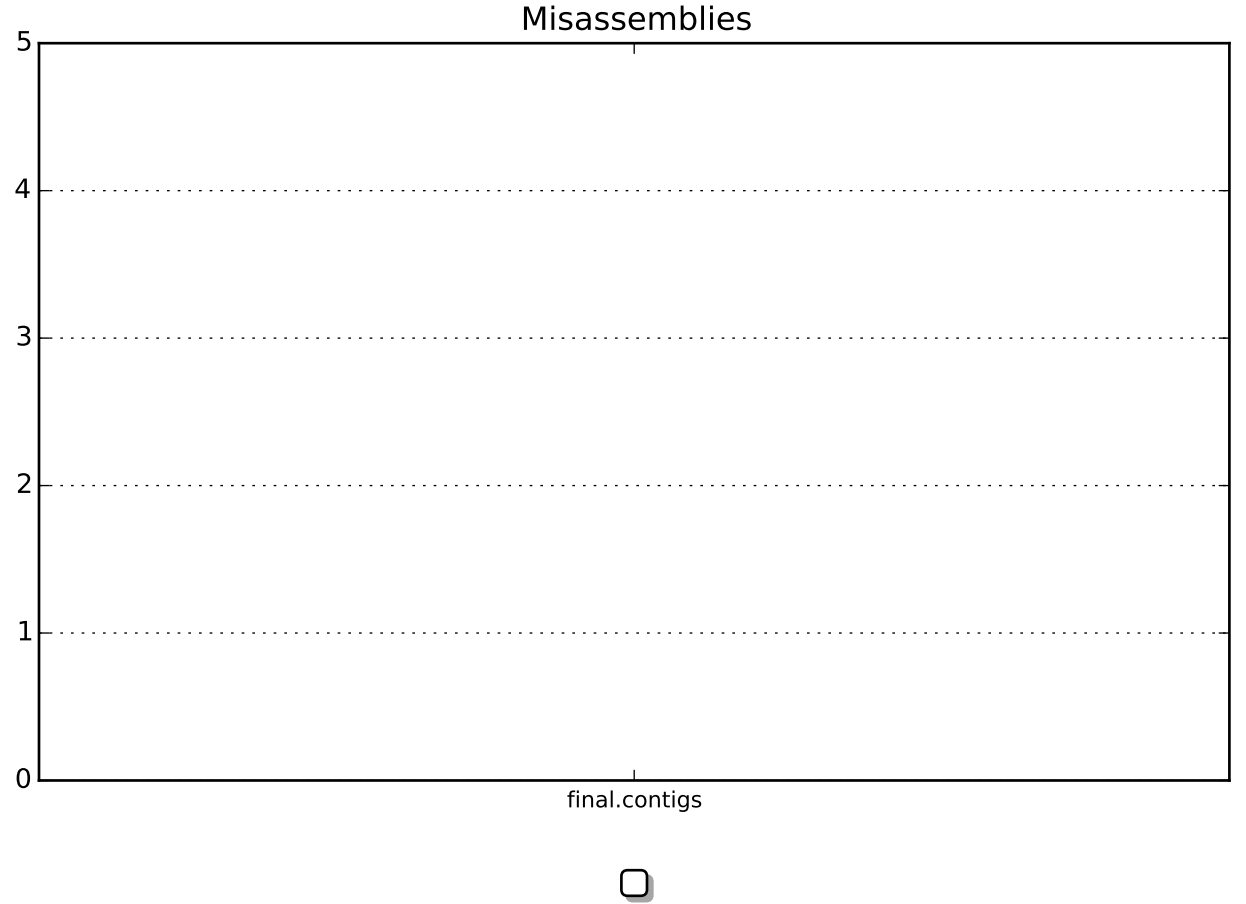
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

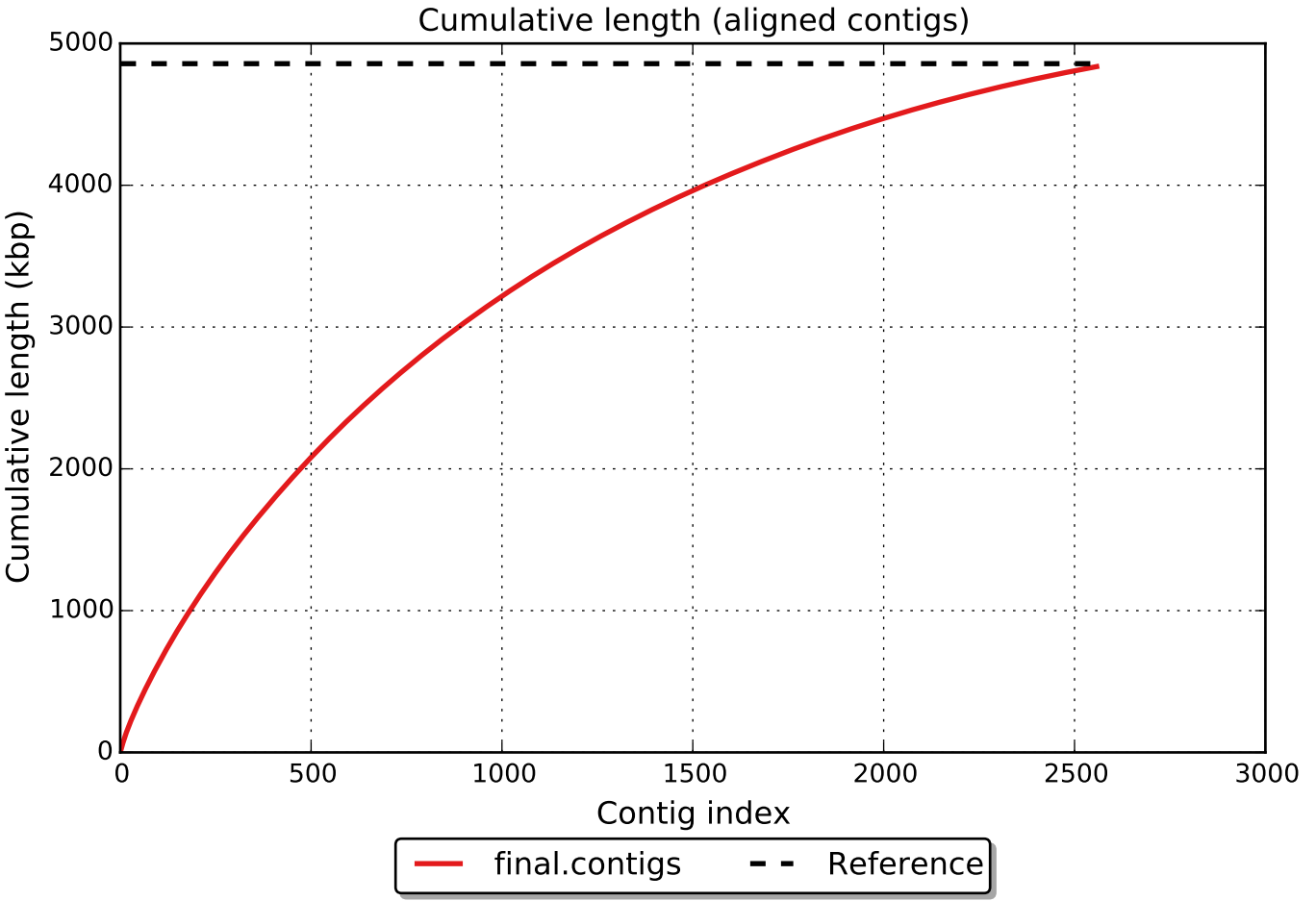

Nx
Contig length (kbp)
x
0
2
4
6
8
10
12
0
20
40
60
80
100
final.contigs

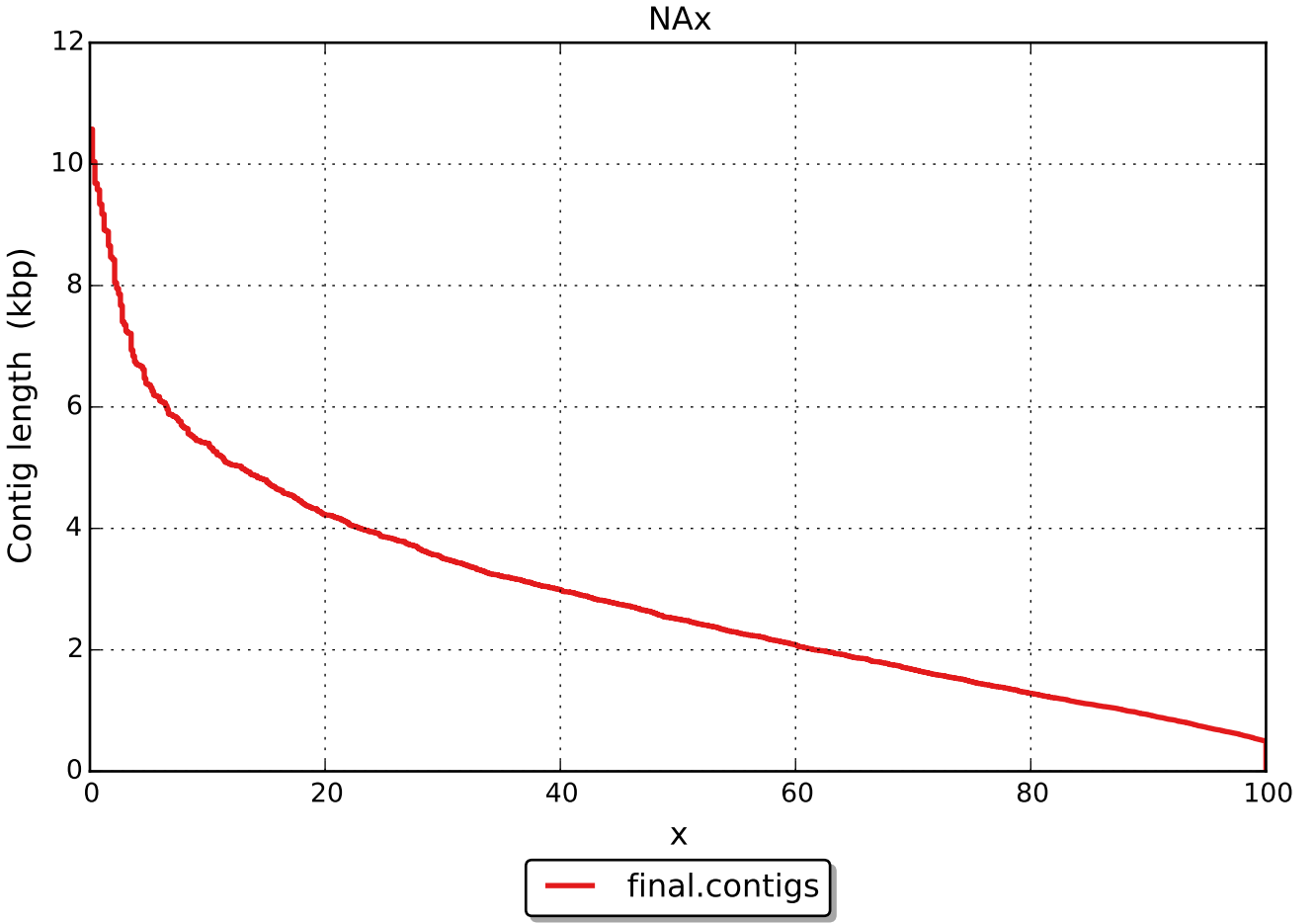

NGx
Contig length (kbp)
0
2
4
6
8
10
12
0
20
40
60
80
100
x
final.contigs

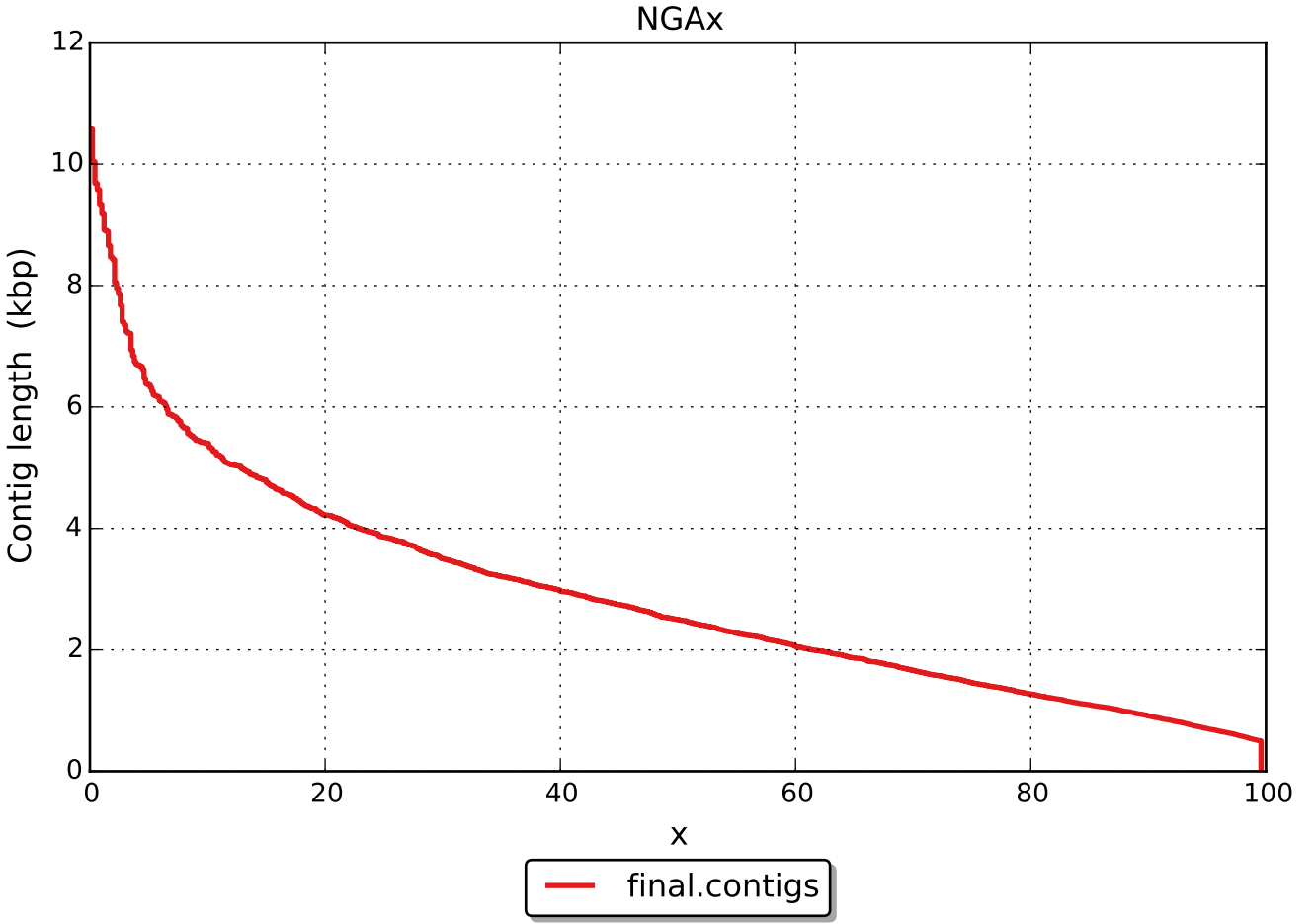

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
500
1000
1500
2000
2500
3000
Contig index
final.contigs
Reference


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
3000
Contig index
final.contigs
Reference


NAx
Contig length (kbp)
0
2
4
6
8
10
12
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (kbp)
0
2
4
6
8
10
12
0
20
40
60
80
100
x
final.contigs