Report

	final.contigs
# contigs (>= 1000 bp)	911
# contigs (>= 5000 bp)	373
# contigs (>= 10000 bp)	104
# contigs (>= 25000 bp)	2
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4757985
Total length (>= 5000 bp)	3355755
Total length (>= 10000 bp)	1497469
Total length (>= 25000 bp)	50984
Total length (>= 50000 bp)	0
# contigs	1041
Largest contig	25535
Total length	4853255
Reference length	4857432
GC (%)	52.21
Reference GC (%)	52.22
N50	7024
NG50	7024
N75	4158
NG75	4158
L50	217
LG50	217
L75	436
LG75	436
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.372
Duplication ratio	1.016
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2.16
# indels per 100 kbp	0.00
Largest alignment	25535
NA50	7024
NGA50	7024
NA75	4158
NGA75	4158
LA50	217
LGA50	217
LA75	436
LGA75	436

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

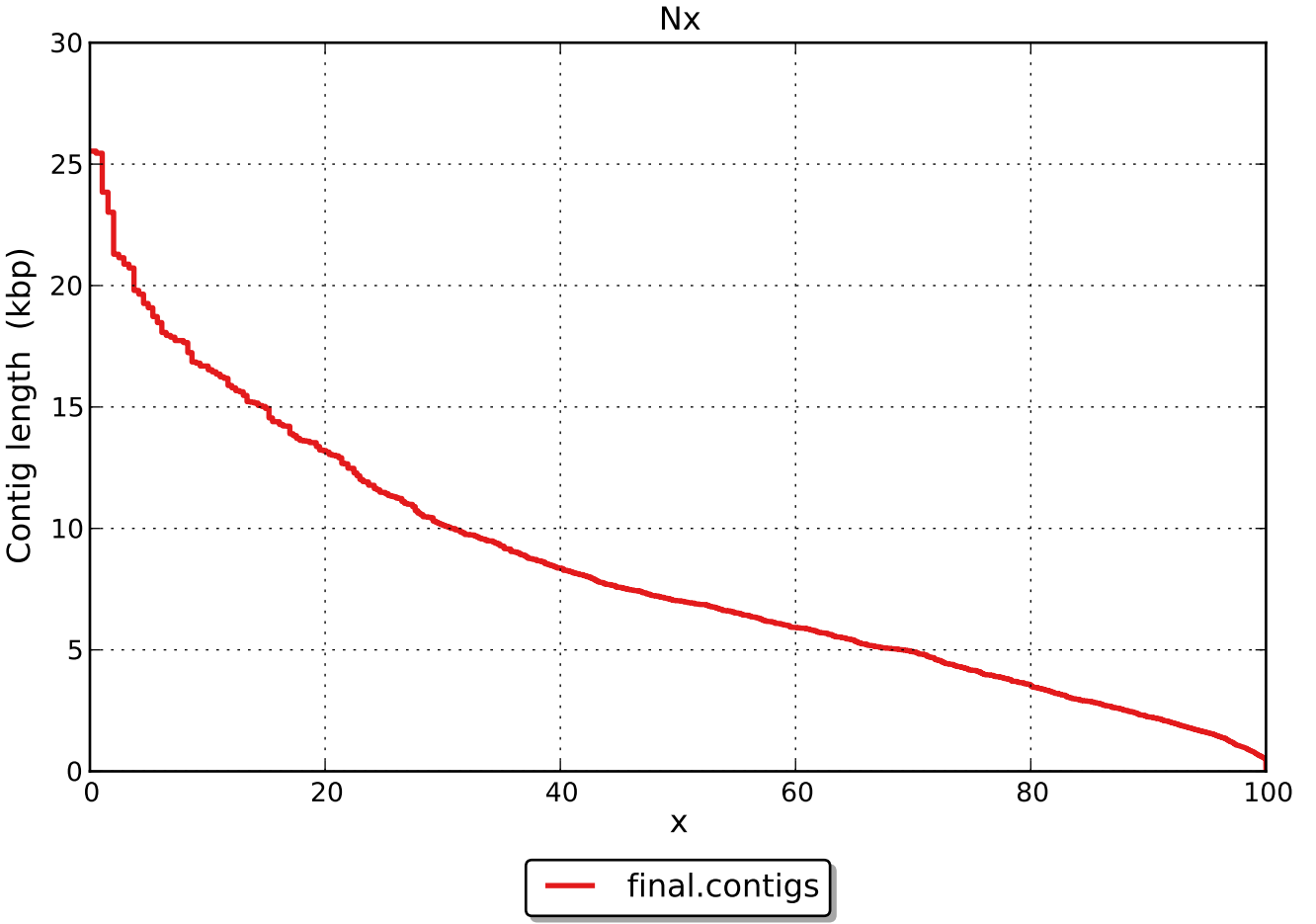
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	103
# indels	0
# short indels	0
# long indels	0
Indels length	0

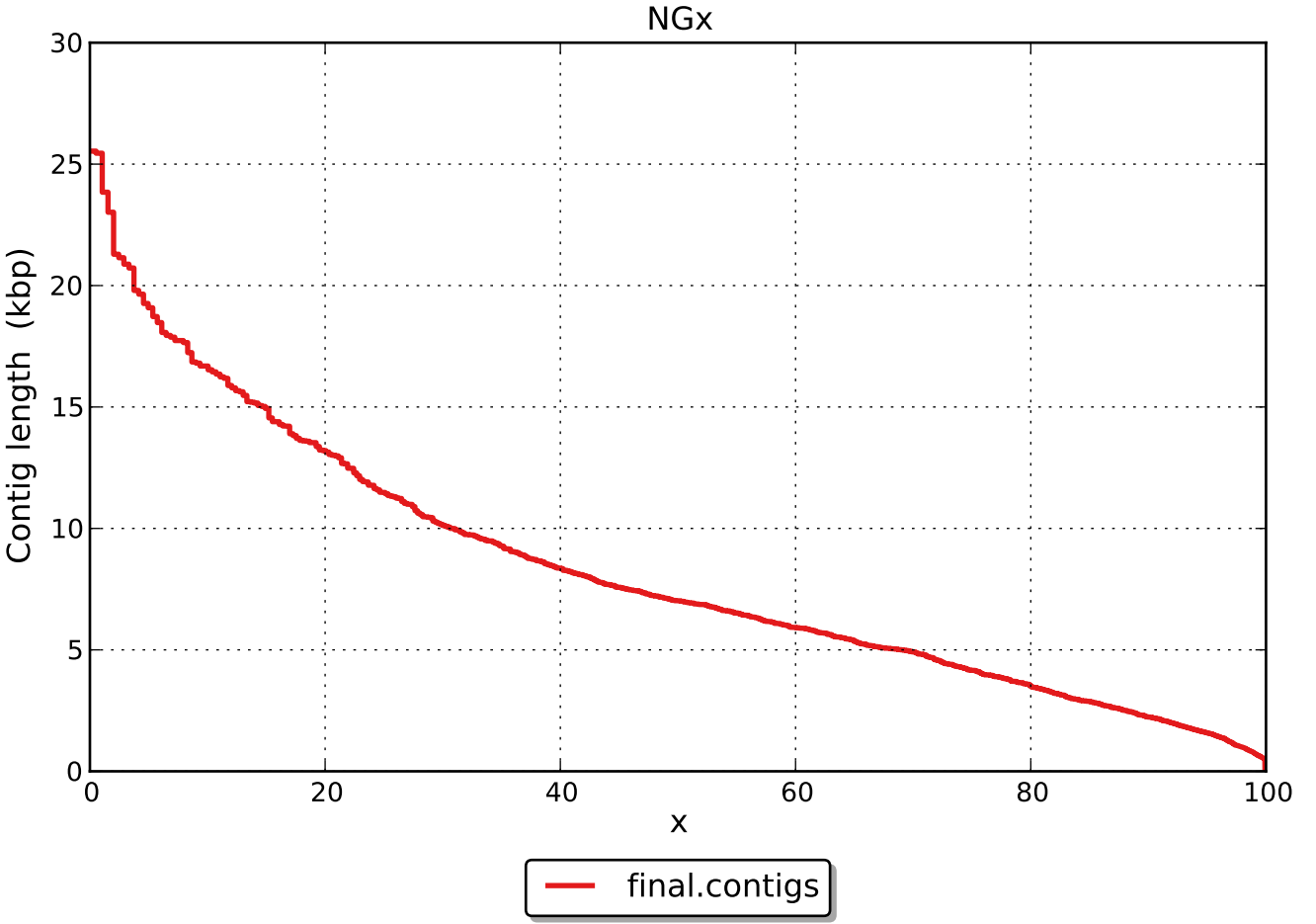
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

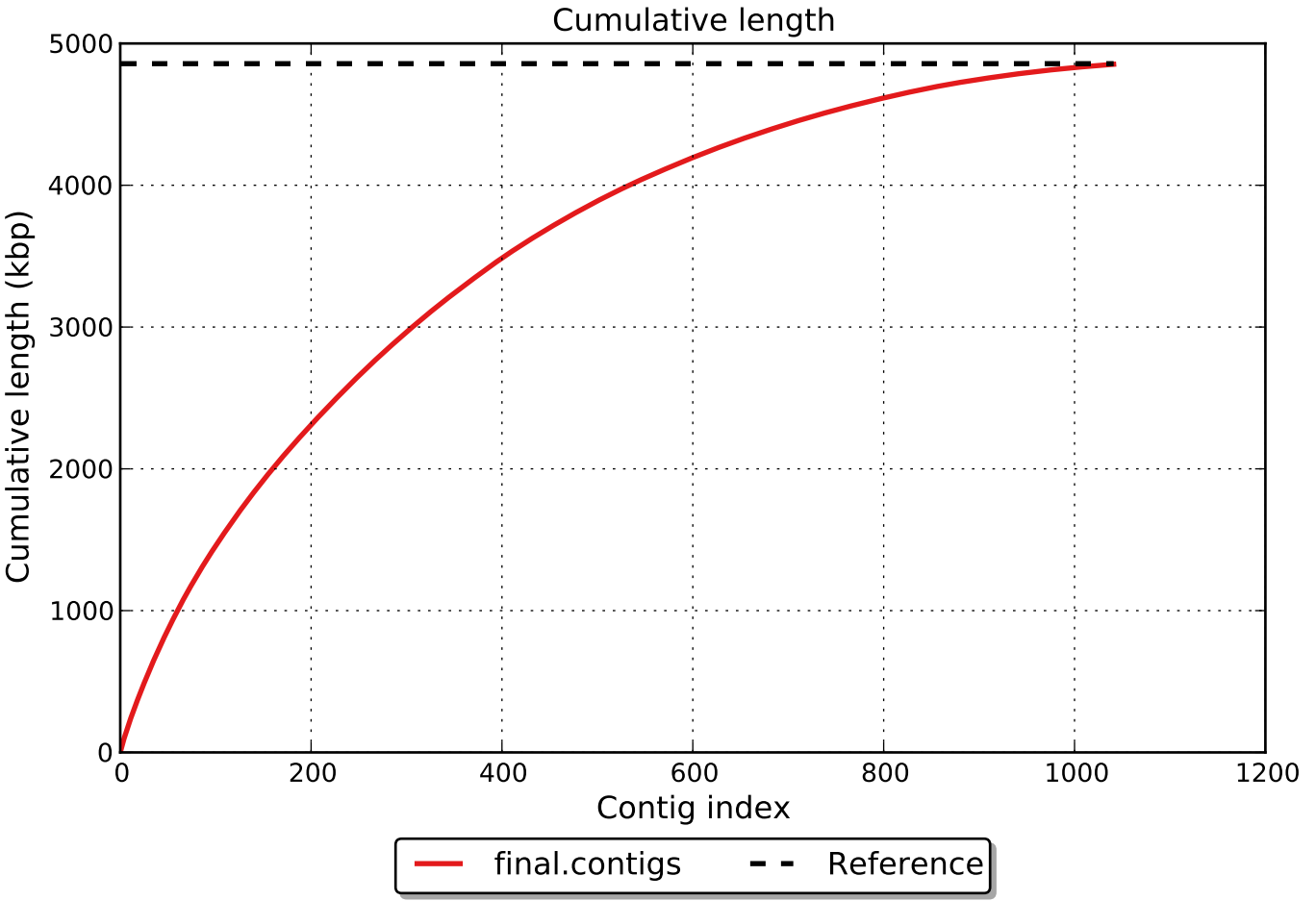
Unaligned report

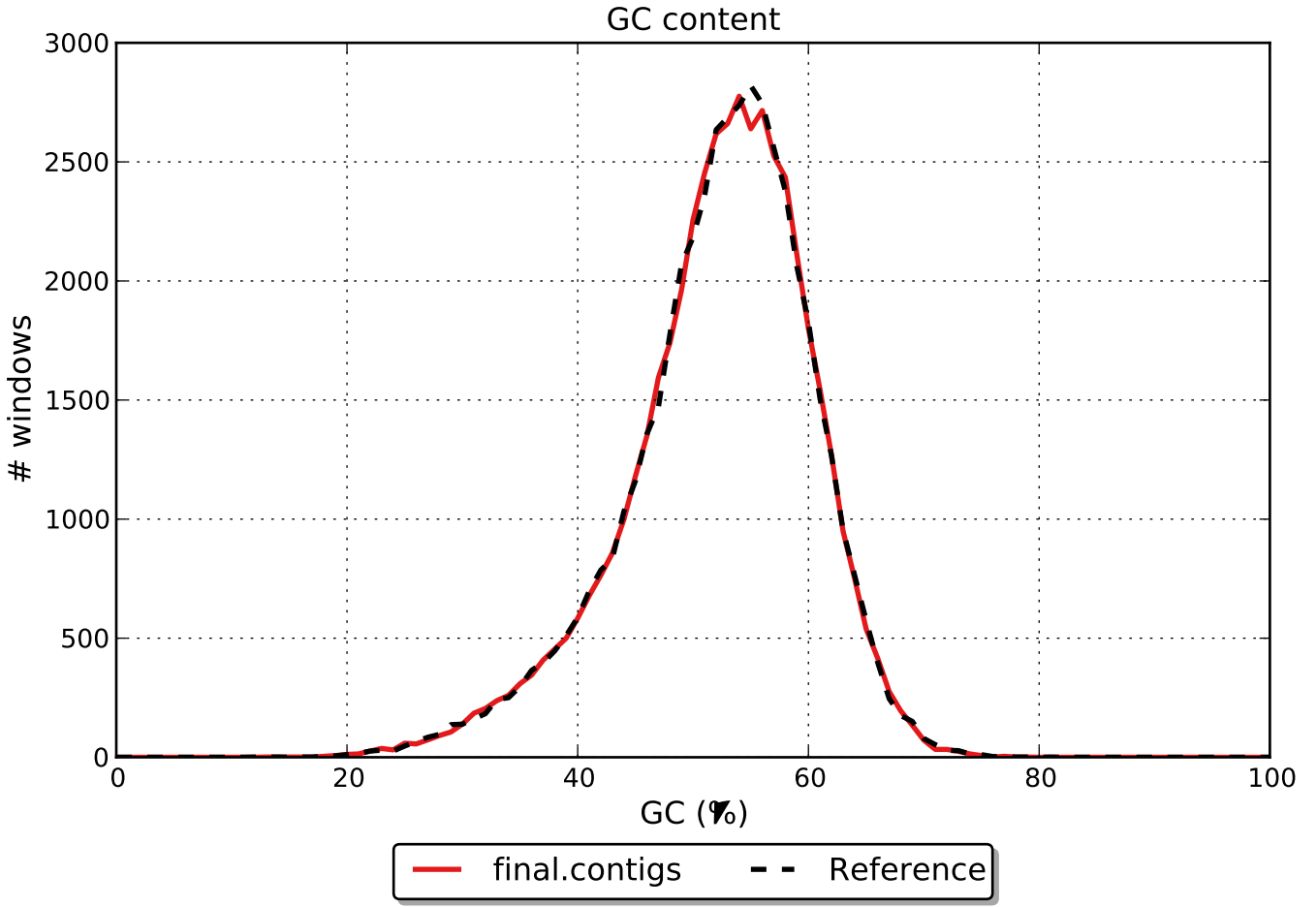
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

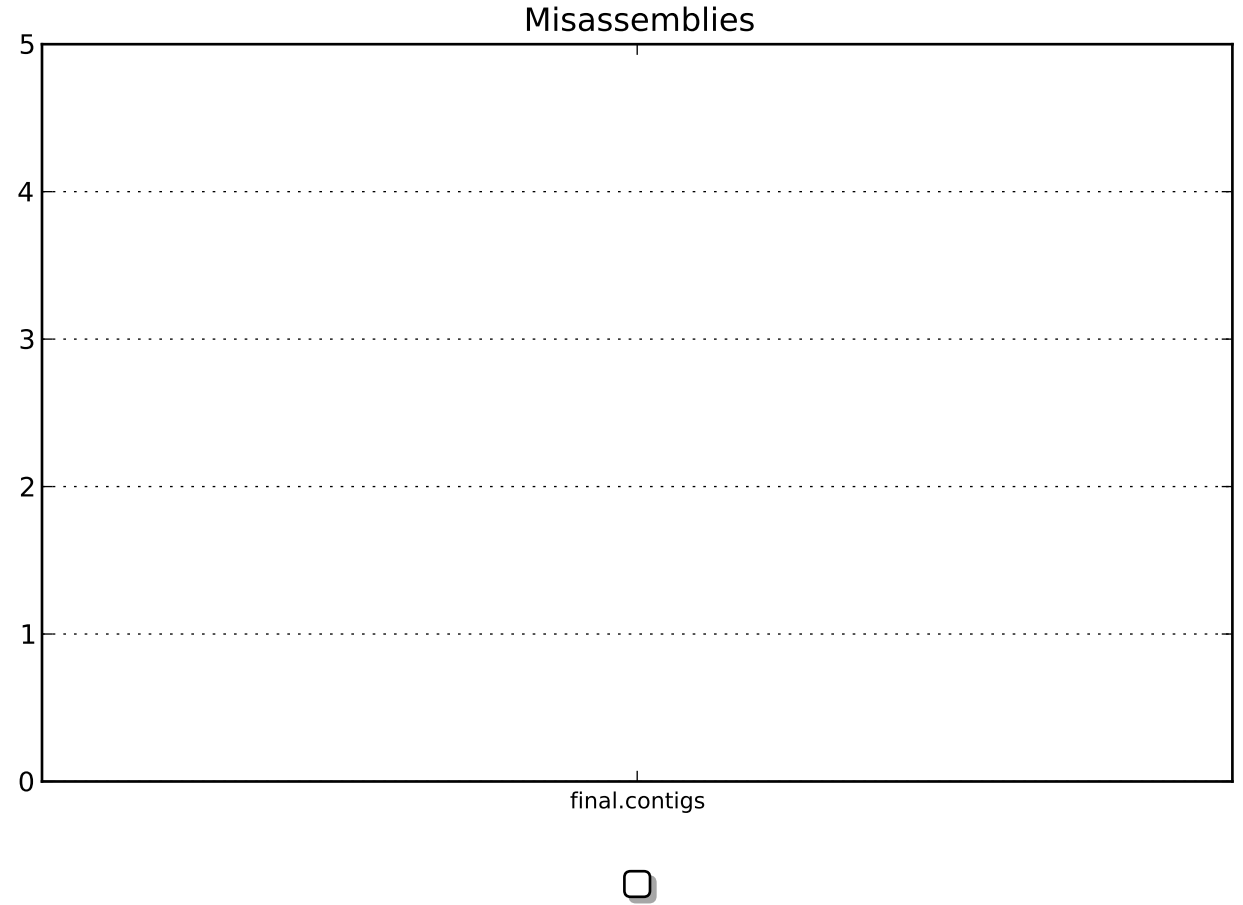
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

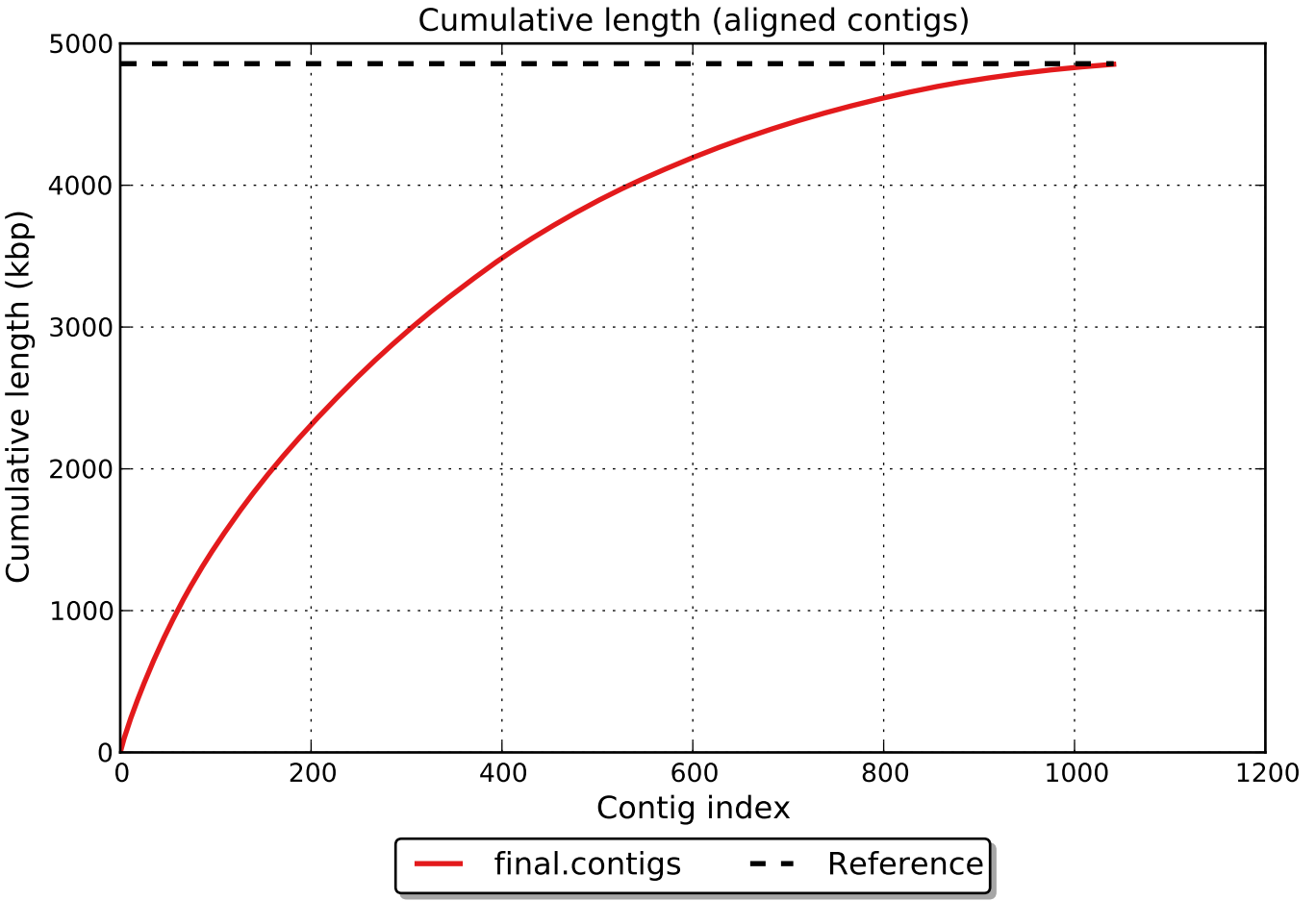

Nx
Contig length (kbp)
30
25
20
15
10
5
0
0
20
40
60
80
100
x
final.contigs

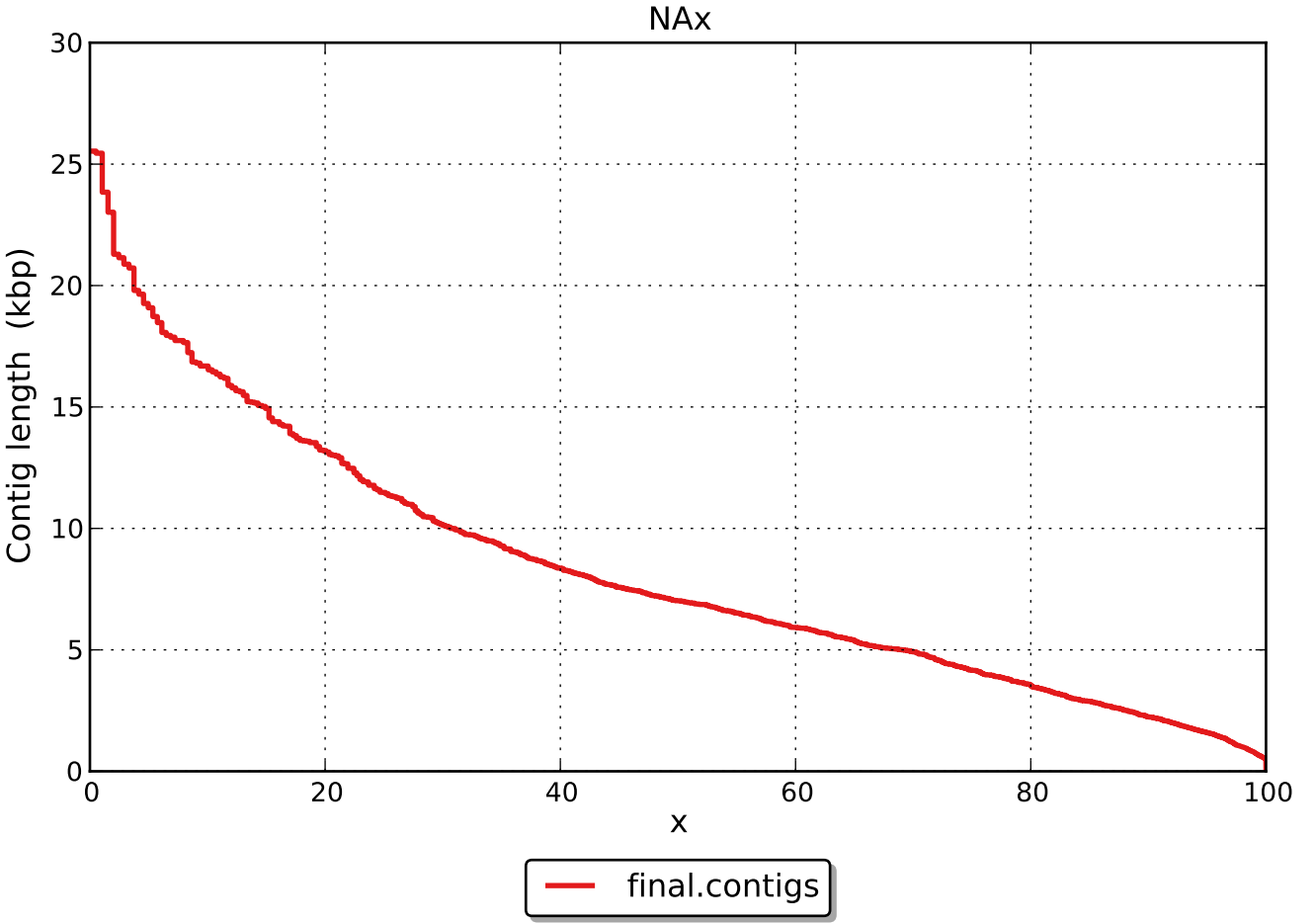

NGx
Contig length (kbp)
30
25
20
15
10
5
0
0
20
40
60
80
100
x
final.contigs

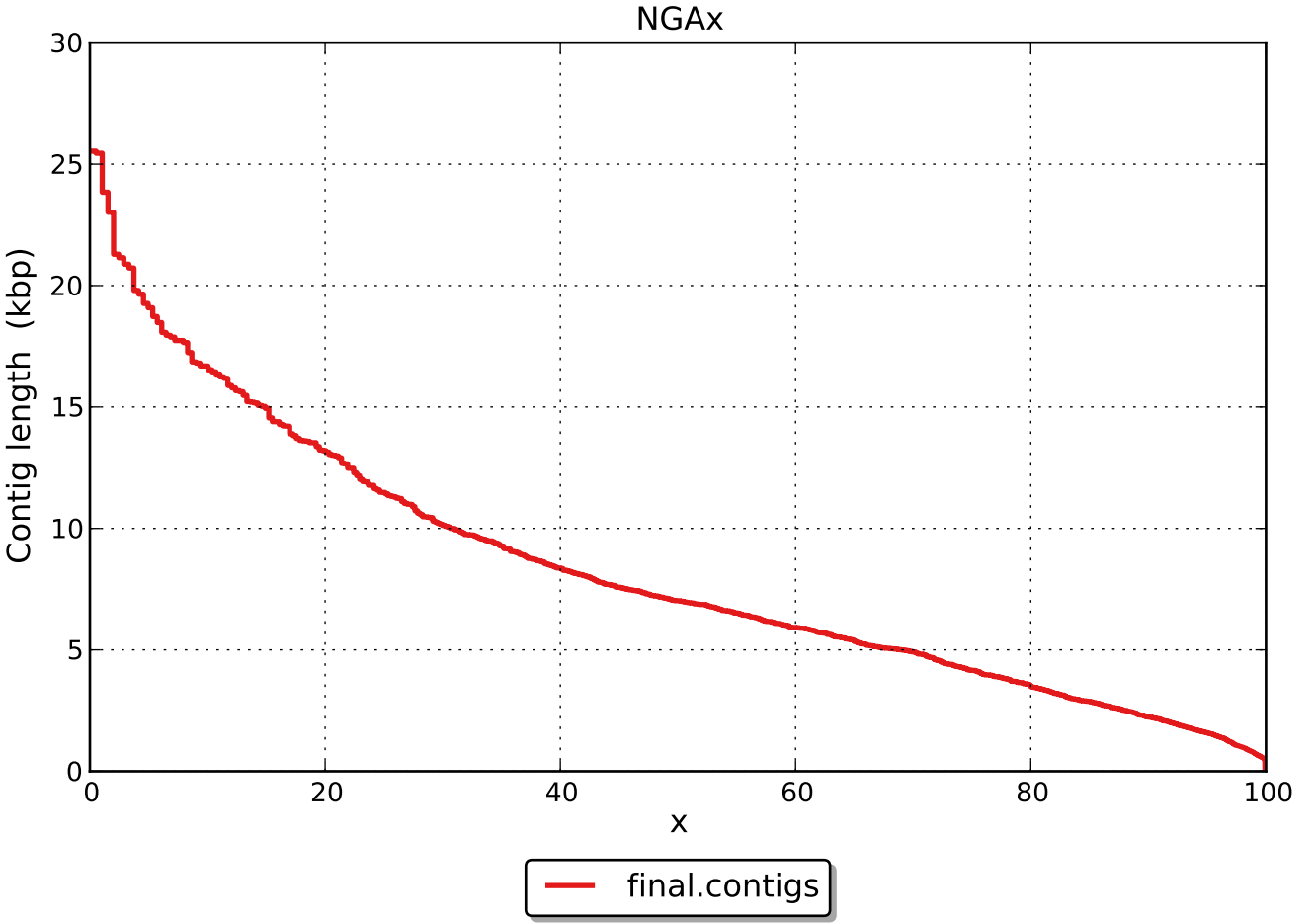

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
200
400
600
800
1000
1200
Contig index
final.contigs
Reference


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
200
400
600
800
1000
1200
Contig index
final.contigs
Reference


NAx
Contig length (kbp)
30
25
20
15
10
5
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (kbp)
30
25
20
15
10
5
0
0
20
40
60
80
100
x
final.contigs