Report

	final.contigs
# contigs (>= 1000 bp)	1118
# contigs (>= 5000 bp)	299
# contigs (>= 10000 bp)	64
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4554959
Total length (>= 5000 bp)	2423018
Total length (>= 10000 bp)	832279
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	1315
Largest contig	21070
Total length	4701129
Reference length	4641652
GC (%)	50.79
Reference GC (%)	50.78
N50	5148
NG50	5193
N75	3064
NG75	3171
L50	285
LG50	279
L75	578
LG75	564
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.238
Duplication ratio	1.021
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.20
# indels per 100 kbp	0.00
Largest alignment	21070
NA50	5148
NGA50	5193
NA75	3064
NGA75	3171
LA50	285
LGA50	279
LA75	578
LGA75	564

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

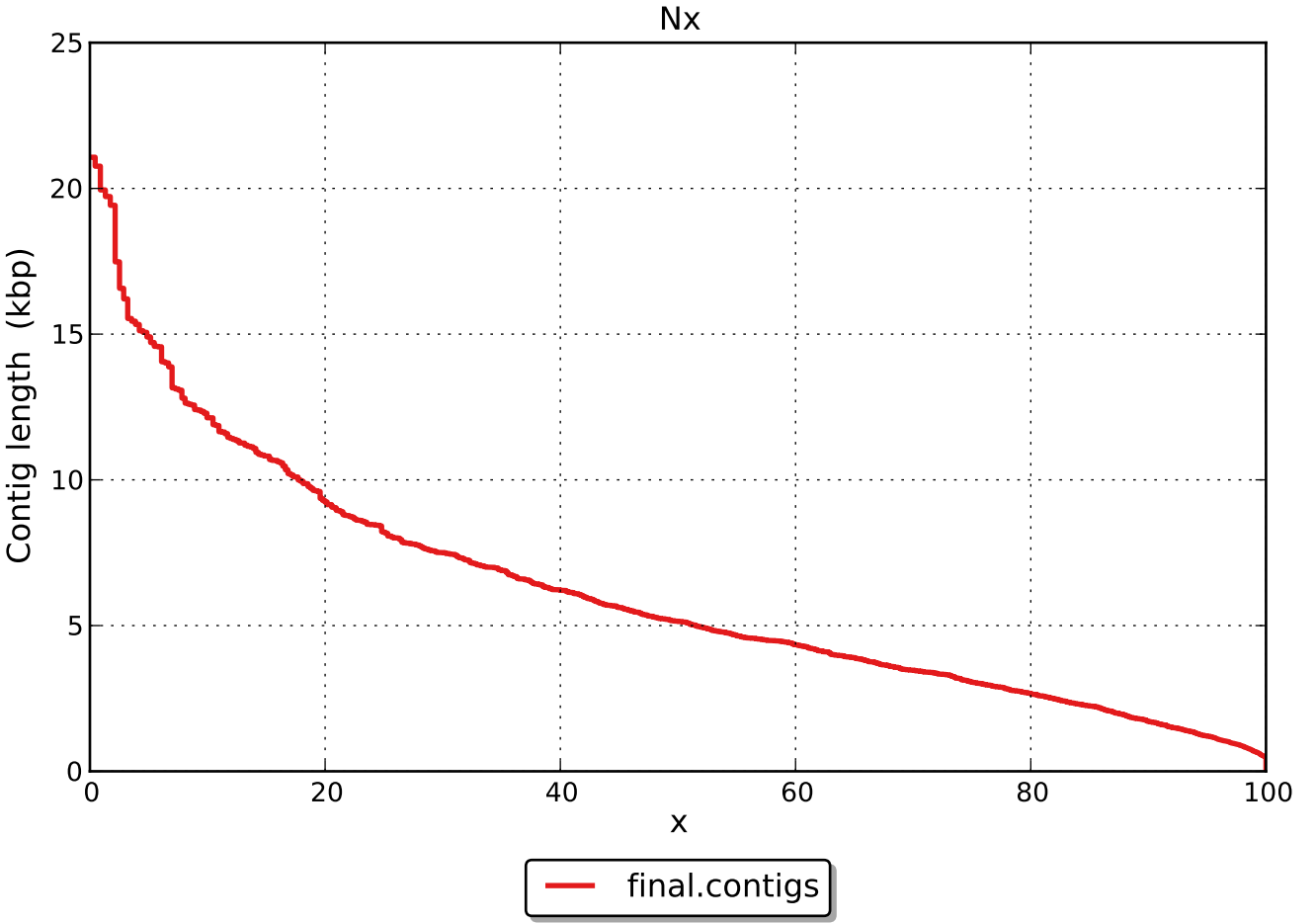
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	9
# indels	0
# short indels	0
# long indels	0
Indels length	0

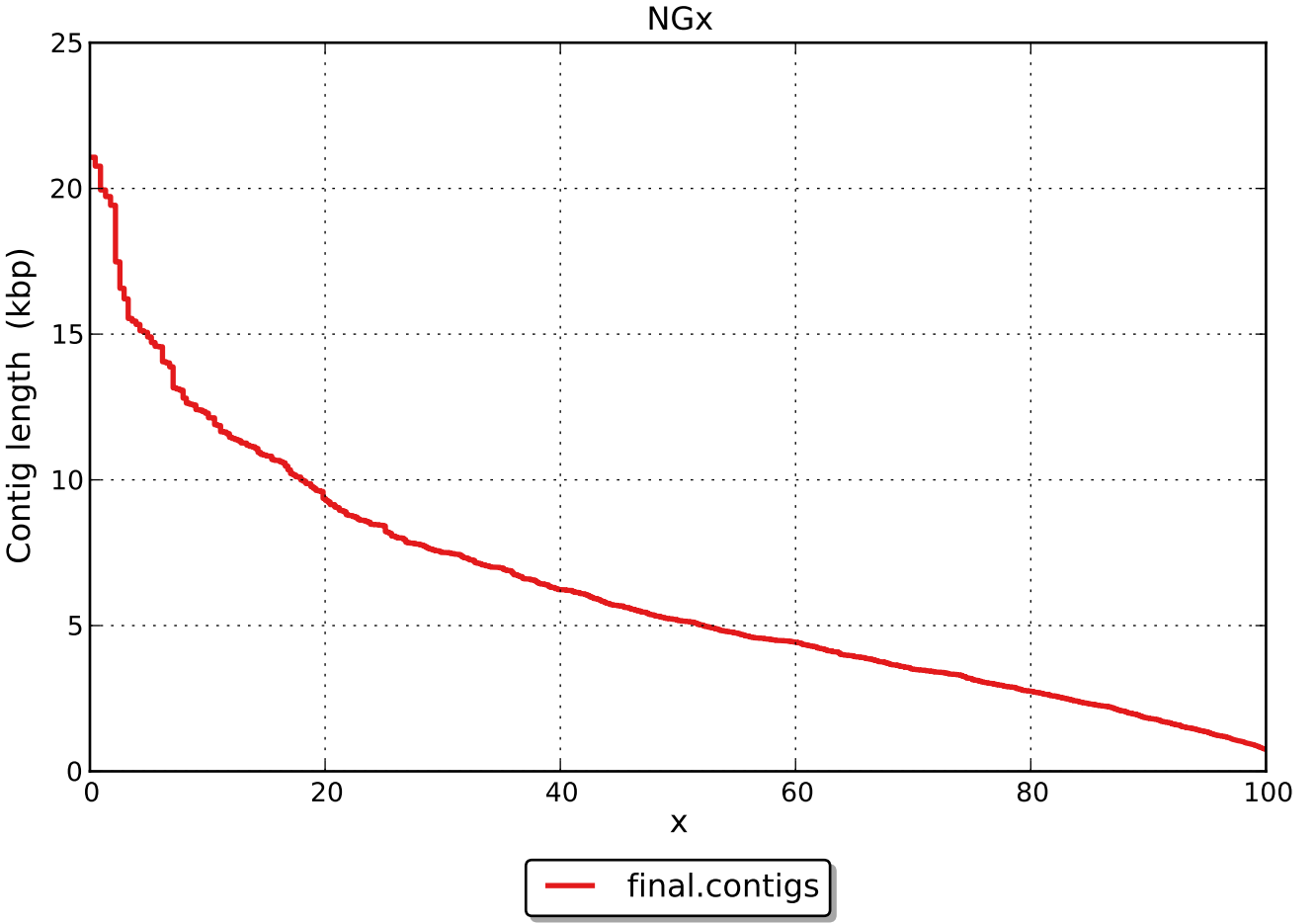
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

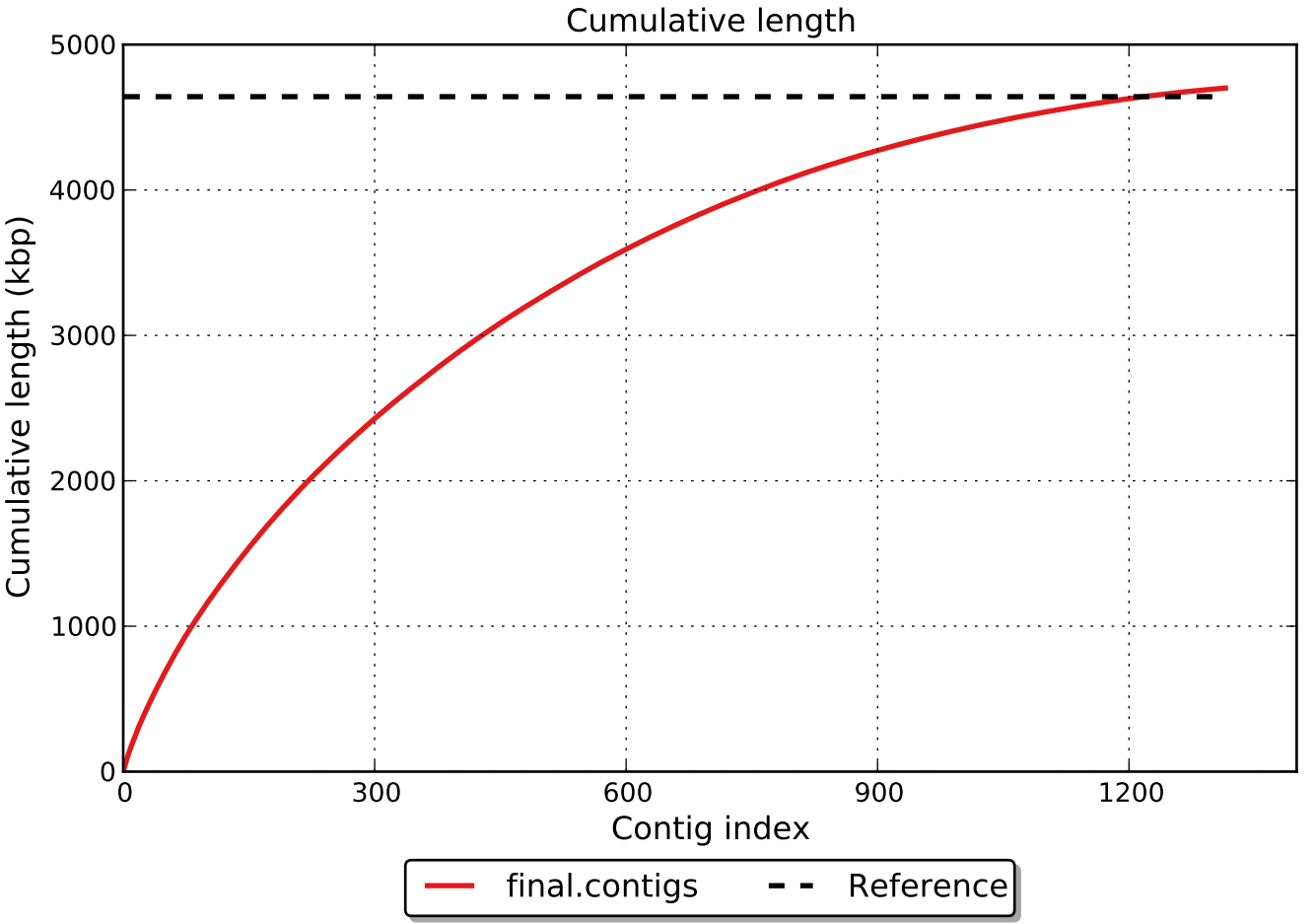
Unaligned report

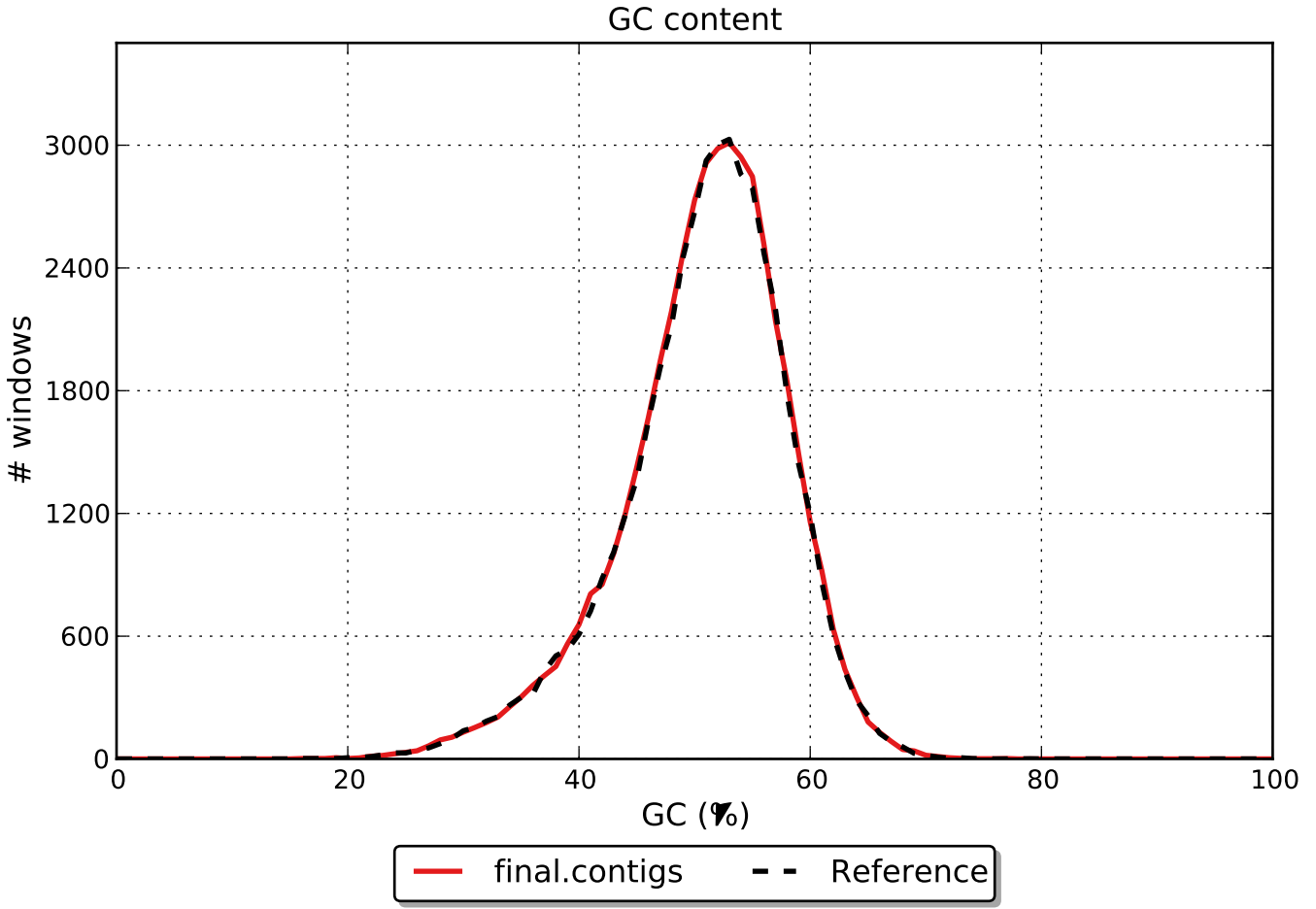
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

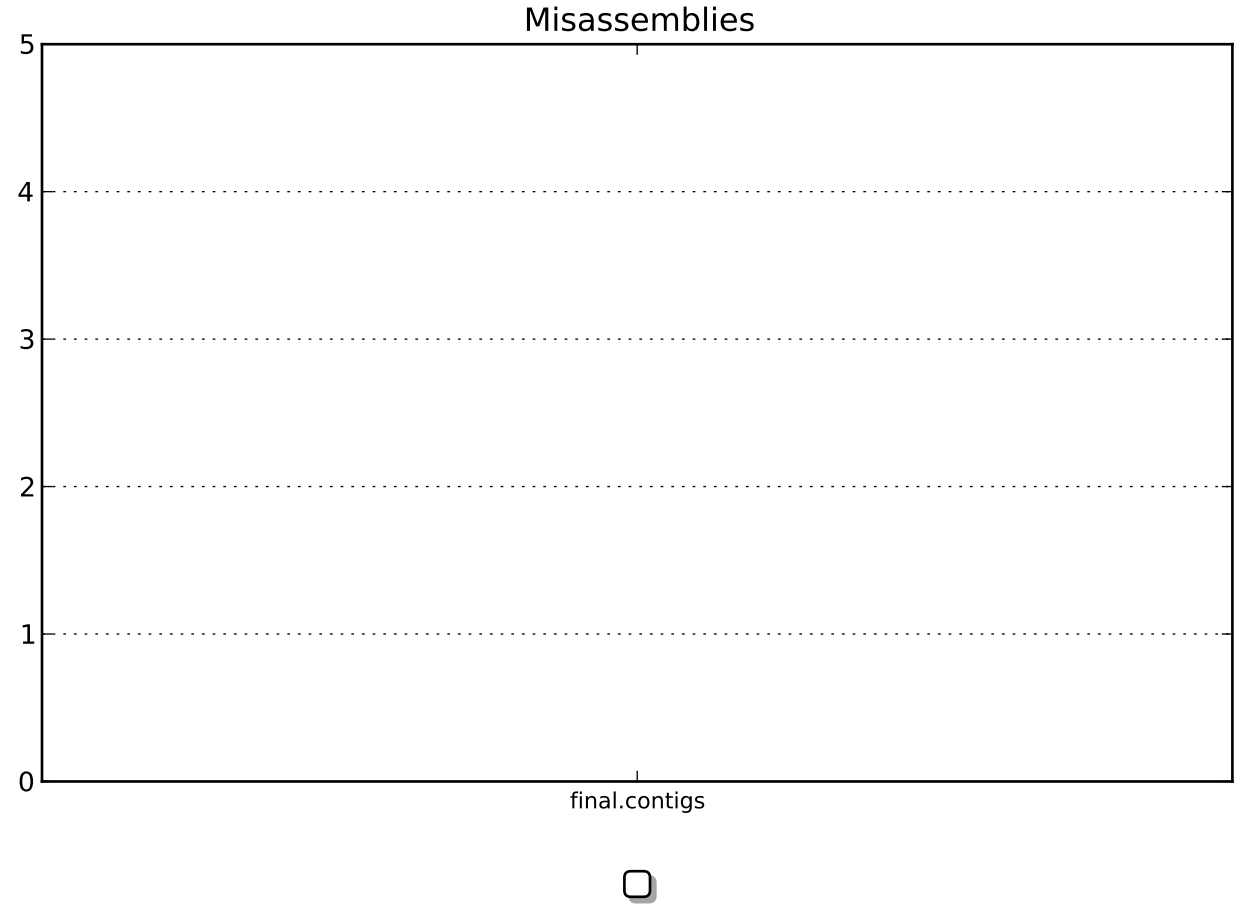
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

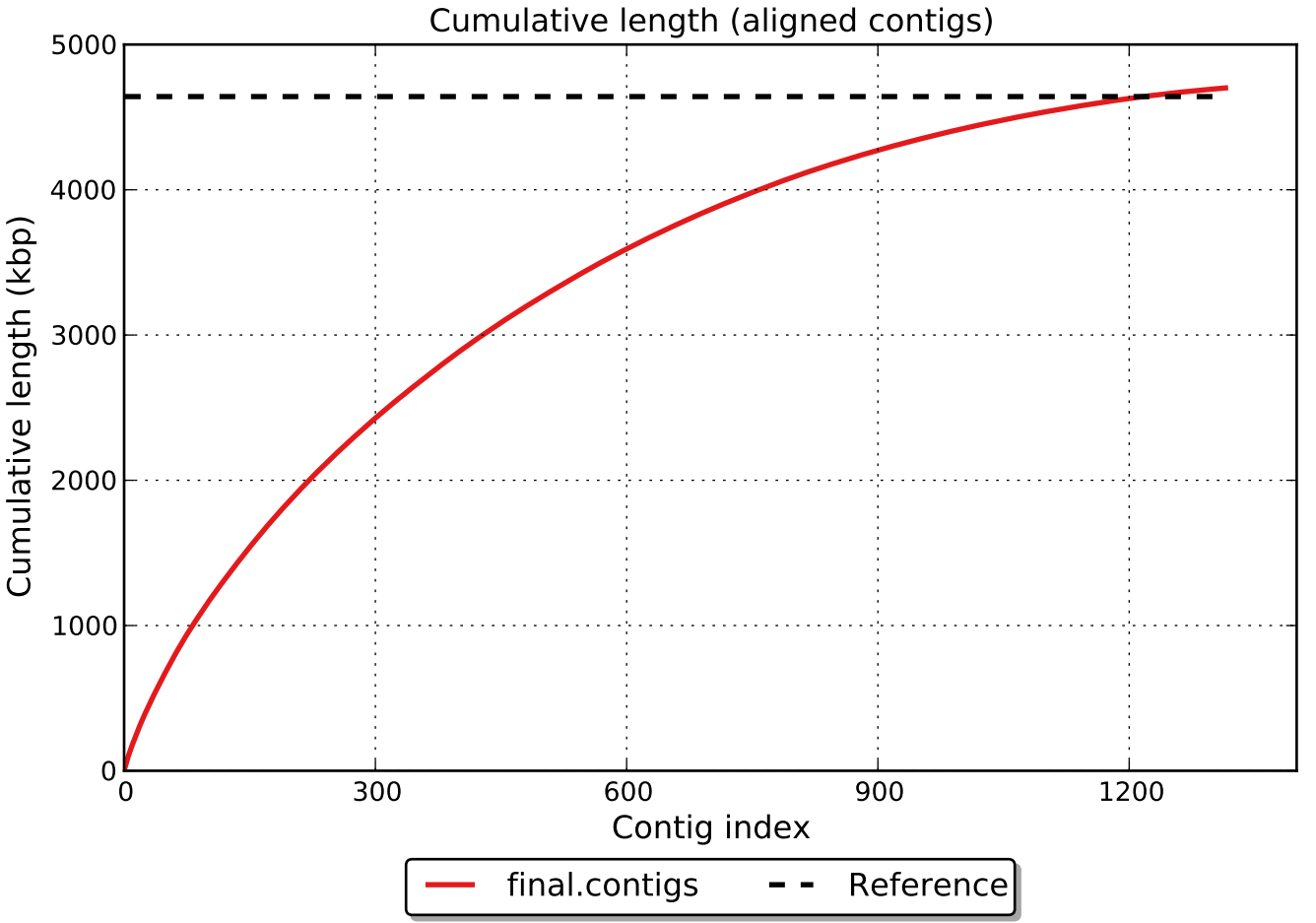

Nx
Contig length (kbp)
25
20
15
10
5
0
0
20
40
60
80
100
x
final.contigs

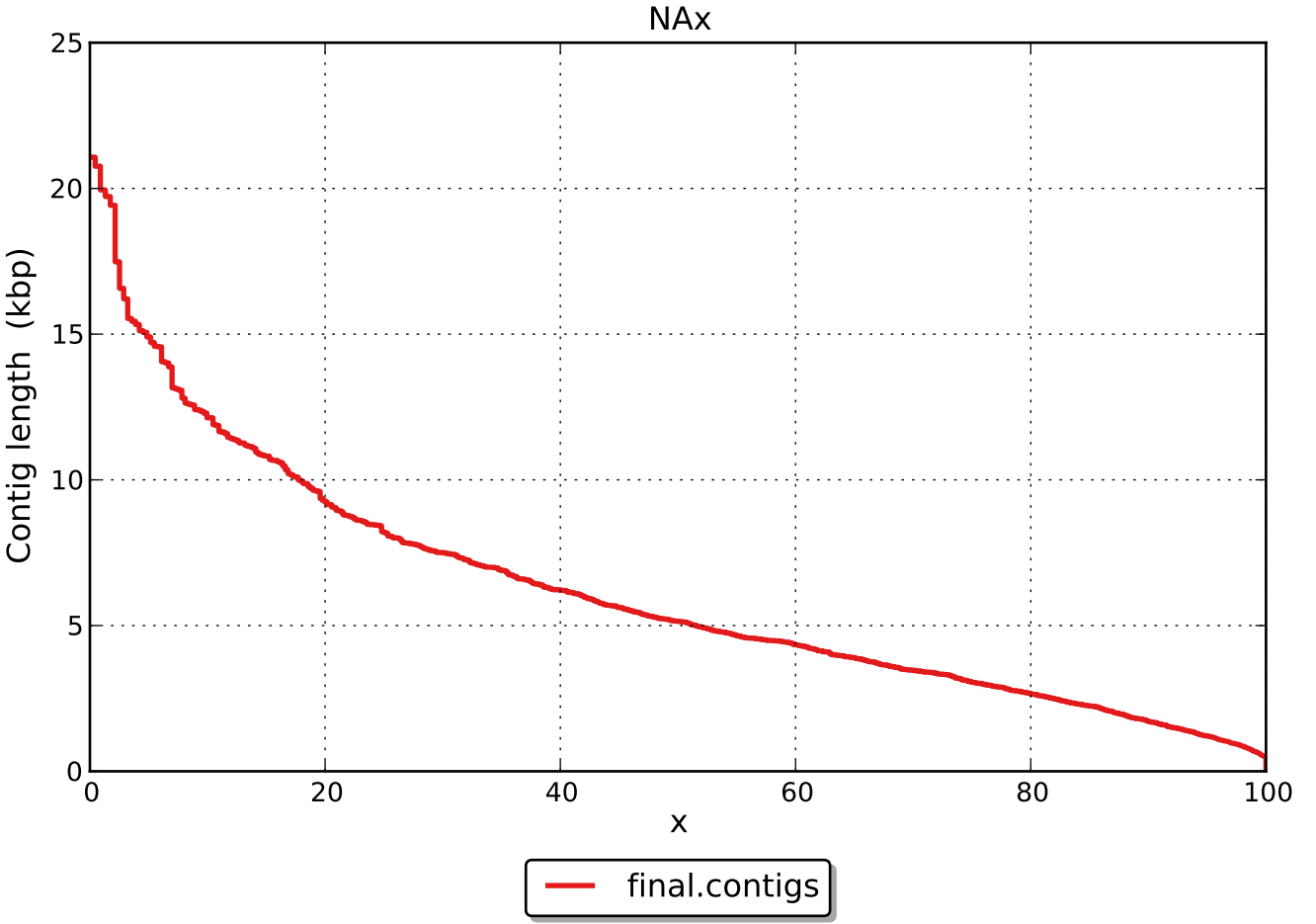

NGx
Contig length (kbp)
25
20
15
10
5
0
0
20
40
60
80
100
x
final.contigs

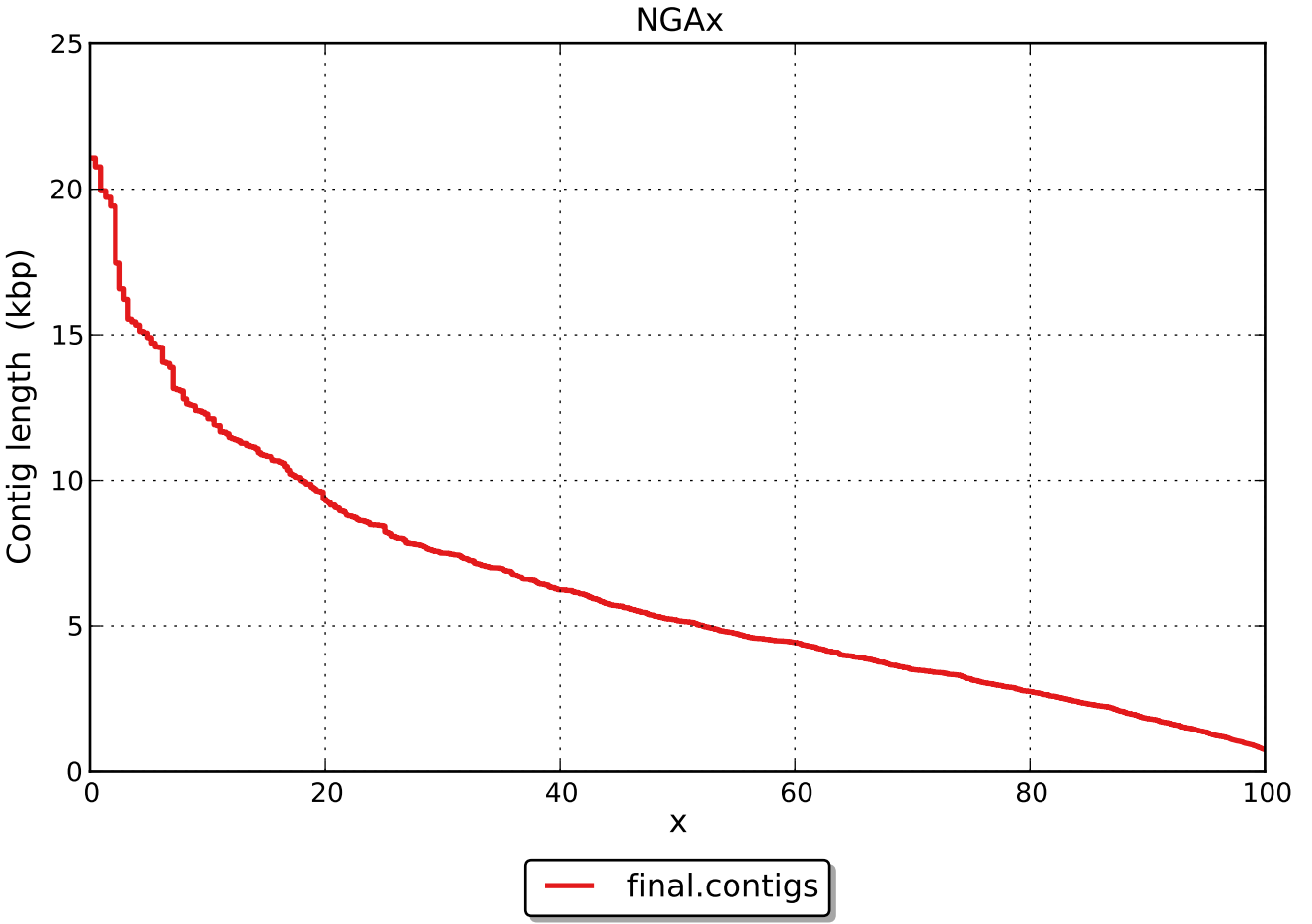

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
300
600
900
1200
Contig index
final.contigs
Reference


GC content
windows
GC (%)
0
600
1200
1800
2400
3000
0
20
40
60
80
100
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
300
600
900
1200
Contig index
final.contigs
Reference


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


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