Report

	final.contigs
# contigs (>= 0 bp)	985
# contigs (>= 1000 bp)	225
Total length (>= 0 bp)	889754
Total length (>= 1000 bp)	510290
# contigs	563
Largest contig	9129
Total length	736895
Reference length	1283598
GC (%)	26.33
Reference GC (%)	26.30
N50	1740
NG50	633
N75	844
L50	118
LG50	395
L75	272
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	90.160
Duplication ratio	1.049
# N's per 100 kbp	0.00
# mismatches per 100 kbp	601.14
# indels per 100 kbp	0.00
Largest alignment	9129
NA50	1740
NGA50	633
NA75	844
LA50	118
LGA50	395
LA75	272

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

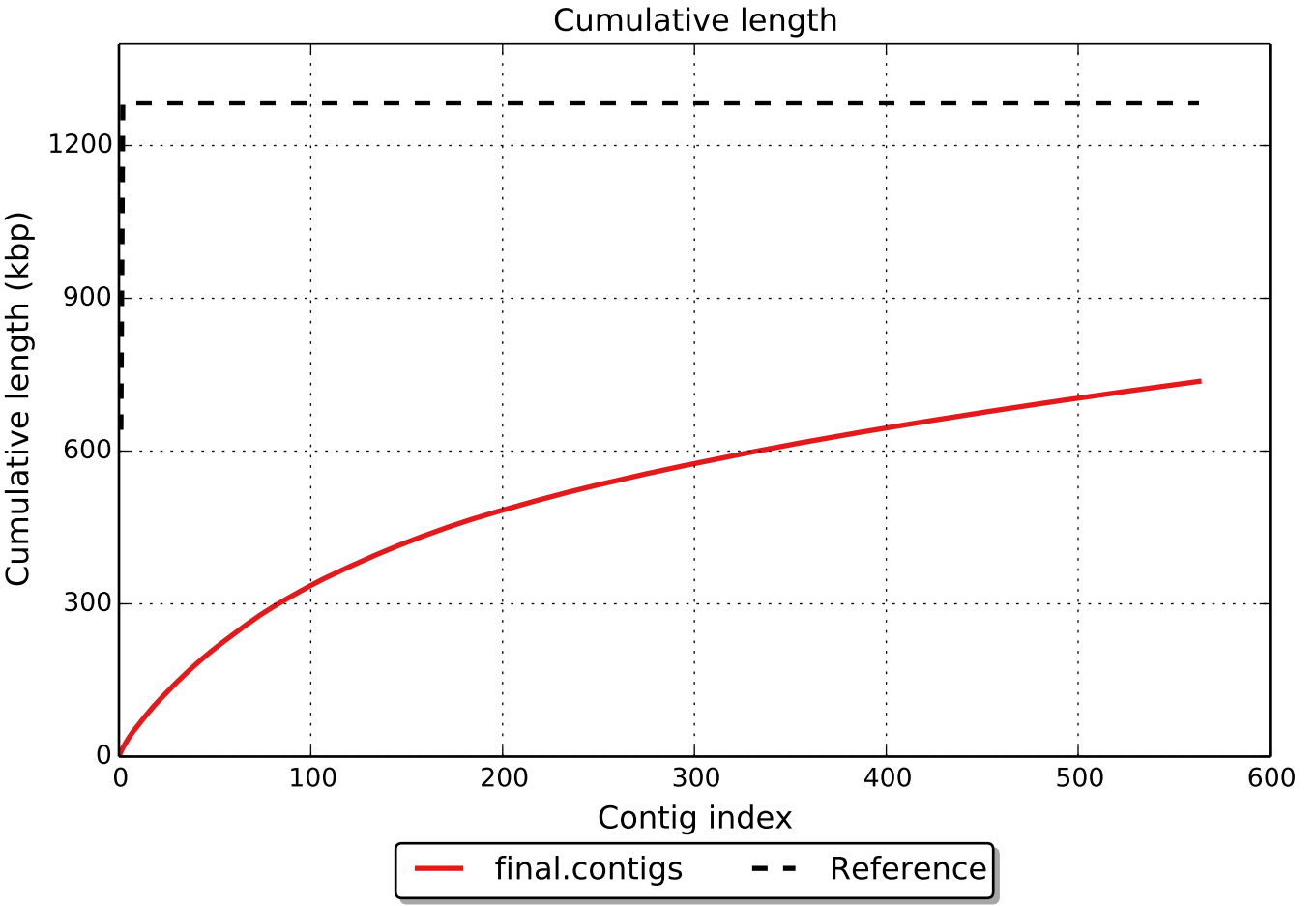
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	6957
# indels	0
# short indels	0
# long indels	0
Indels length	0

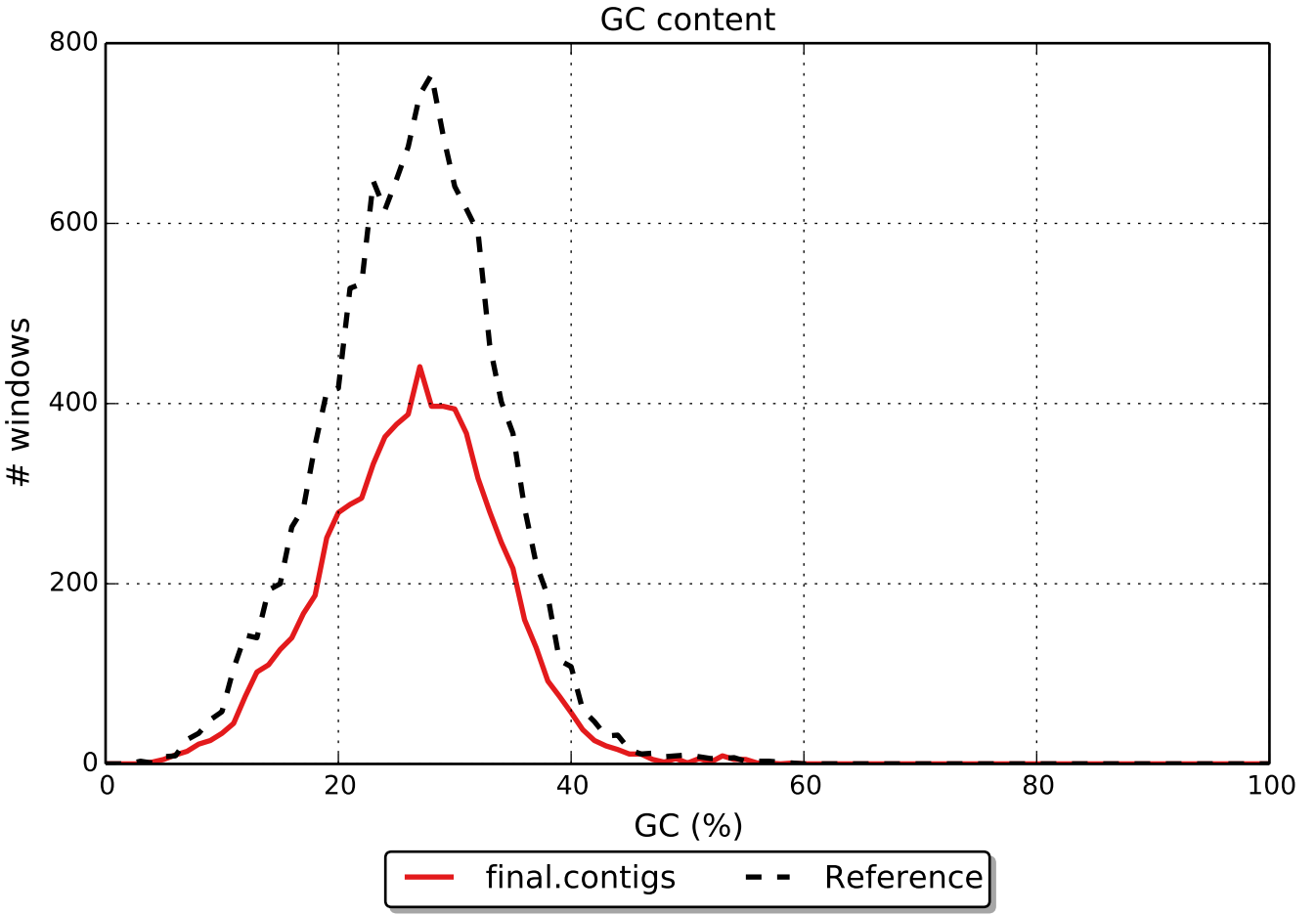
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

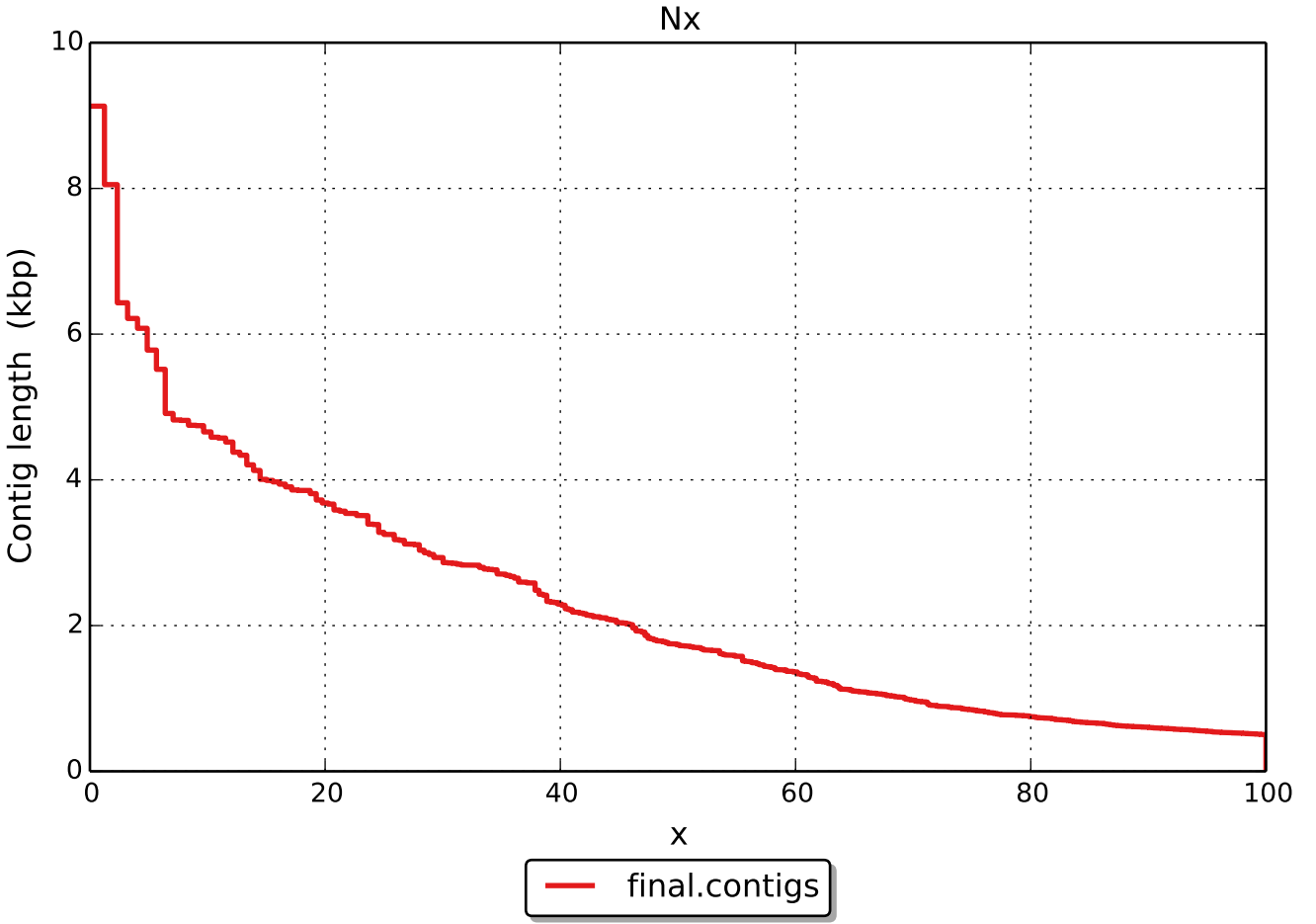
Unaligned report

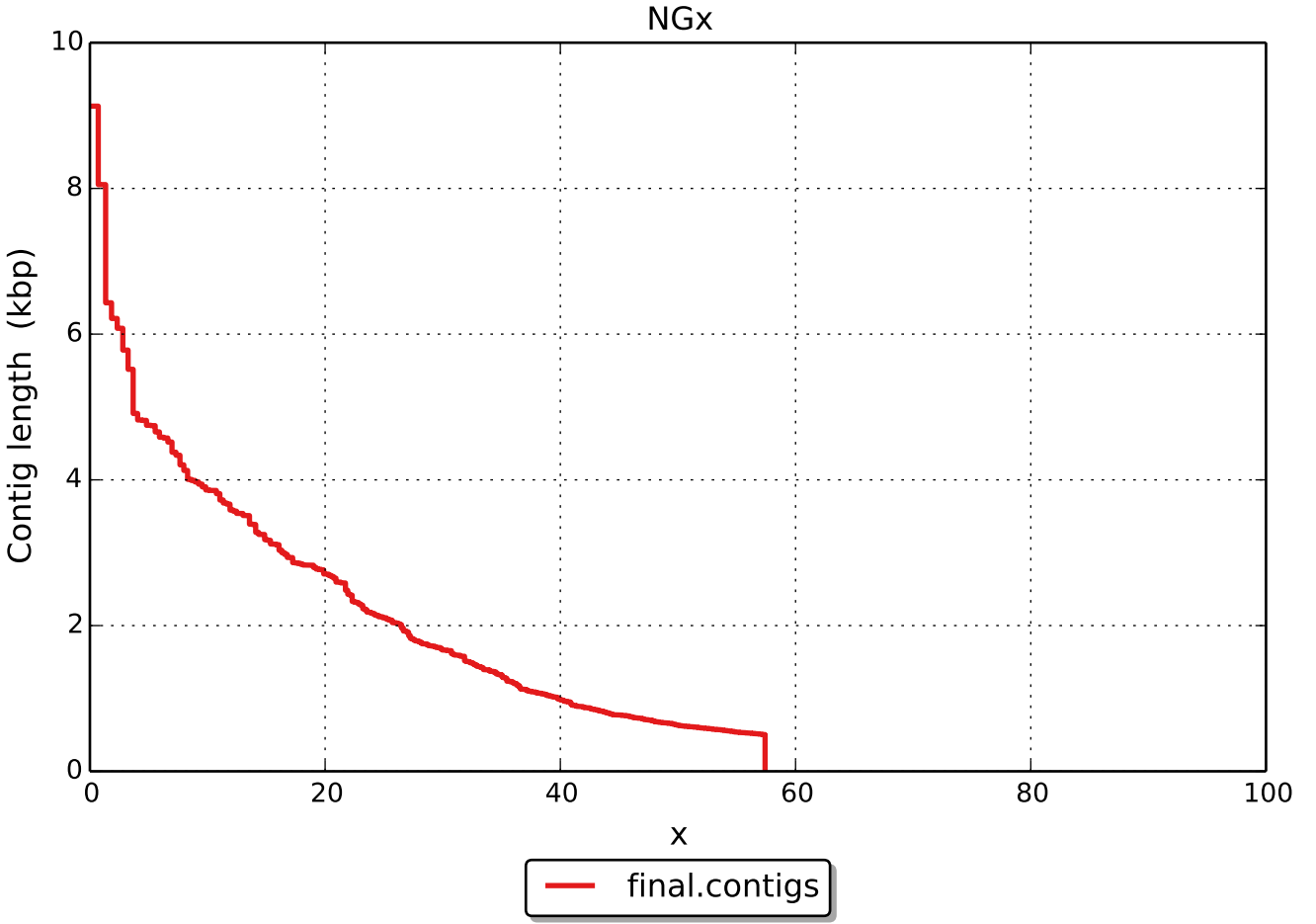
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

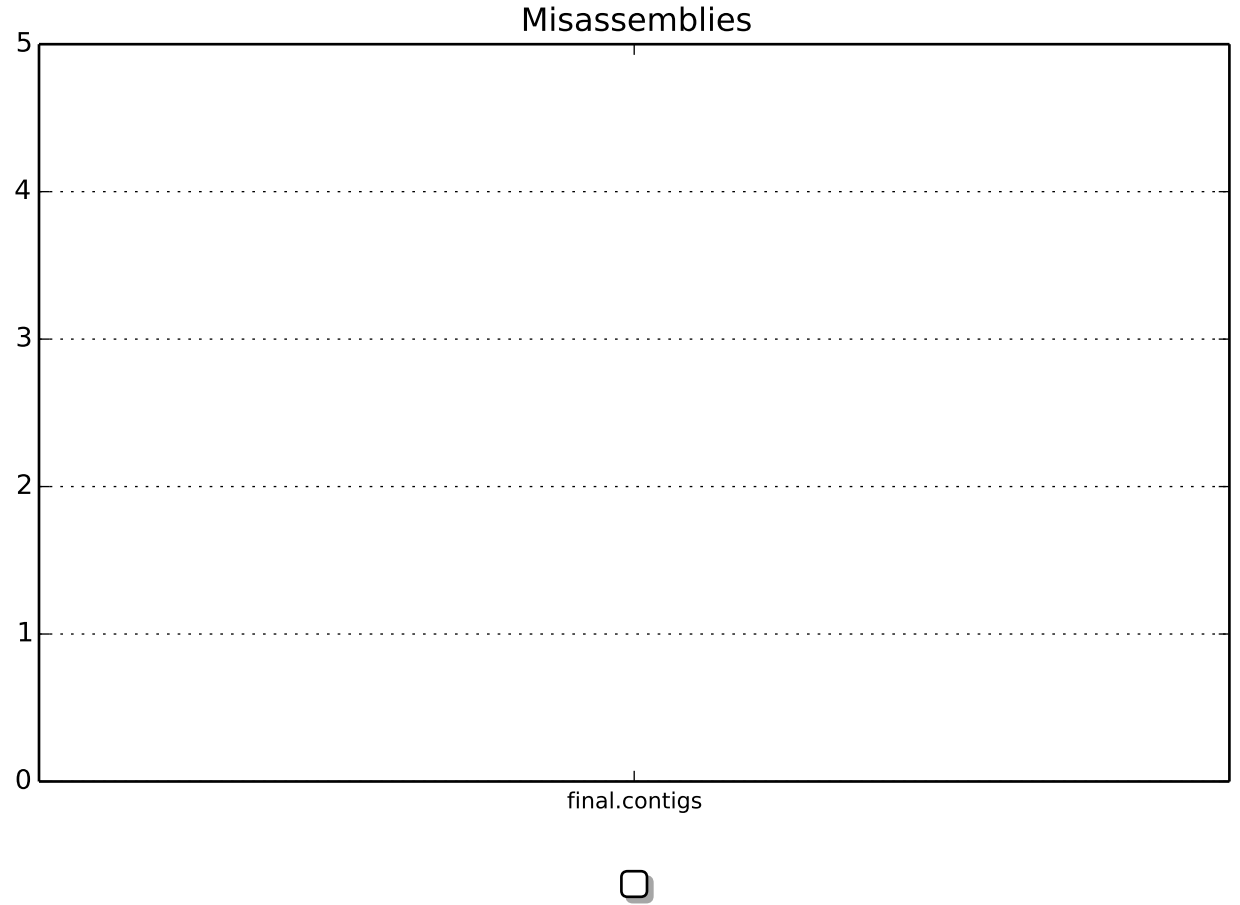
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

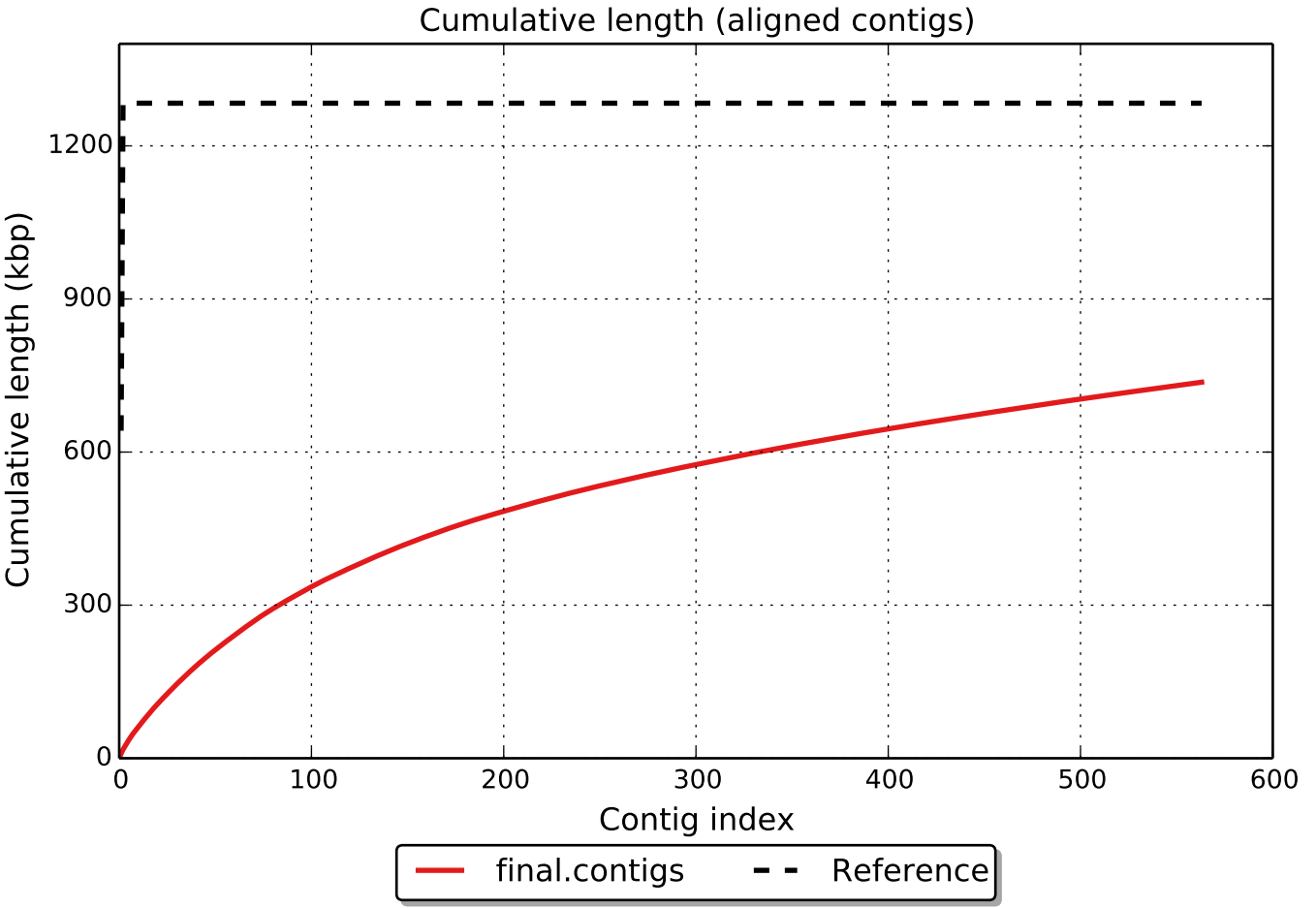

Cumulative length
Cumulative length (kbp)
1200
900
600
300
0
0
100
200
300
400
500
600
Contig index
final.contigs
Reference

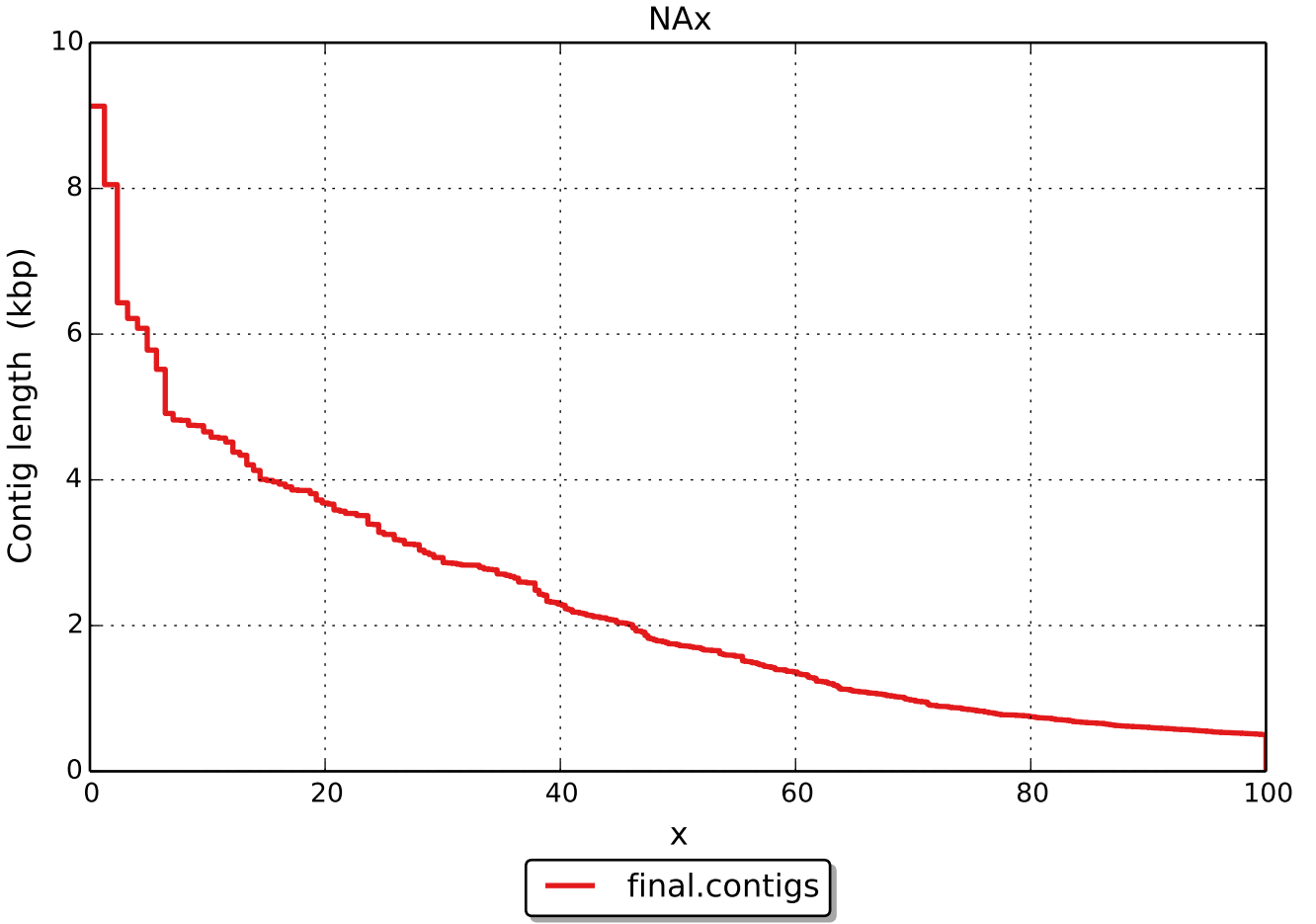

GC content
800
600
400
200
0
windows
0
20
40
60
80
100
GC (%)
final.contigs
Reference

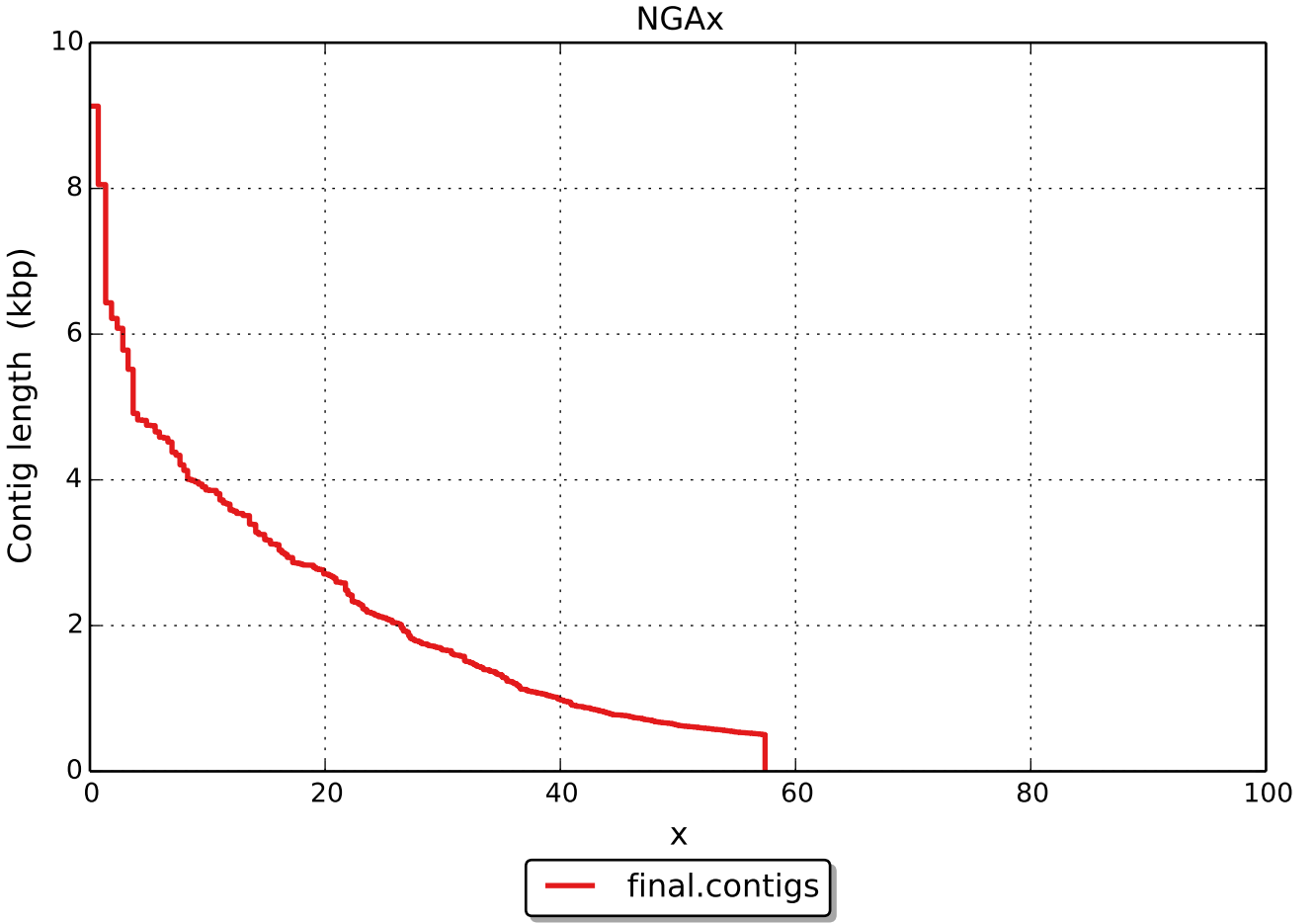

Nx
Contig length (kbp)
10
8
6
4
2
0
0
20
40
60
80
100
x
final.contigs


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


Misassemblies
5
4
3
2
1
0
final.contigs


Cumulative length (aligned contigs)
Cumulative length (kbp)
1200
900
600
300
0
0
100
200
300
400
500
600
Contig index
final.contigs
Reference


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


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