Report

	final.contigs
# contigs (>= 0 bp)	2766
# contigs (>= 1000 bp)	939
Total length (>= 0 bp)	3182482
Total length (>= 1000 bp)	1932043
# contigs	2766
Largest contig	10039
Total length	3182482
Reference length	5547323
GC (%)	50.31
Reference GC (%)	50.48
N50	1313
NG50	620
N75	758
L50	638
LG50	2030
L75	1466
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	55.201
Duplication ratio	1.039
# N's per 100 kbp	0.00
# mismatches per 100 kbp	343.48
# indels per 100 kbp	0.07
Largest alignment	10039
NA50	1313
NGA50	620
NA75	758
LA50	638
LGA50	2030
LA75	1466

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

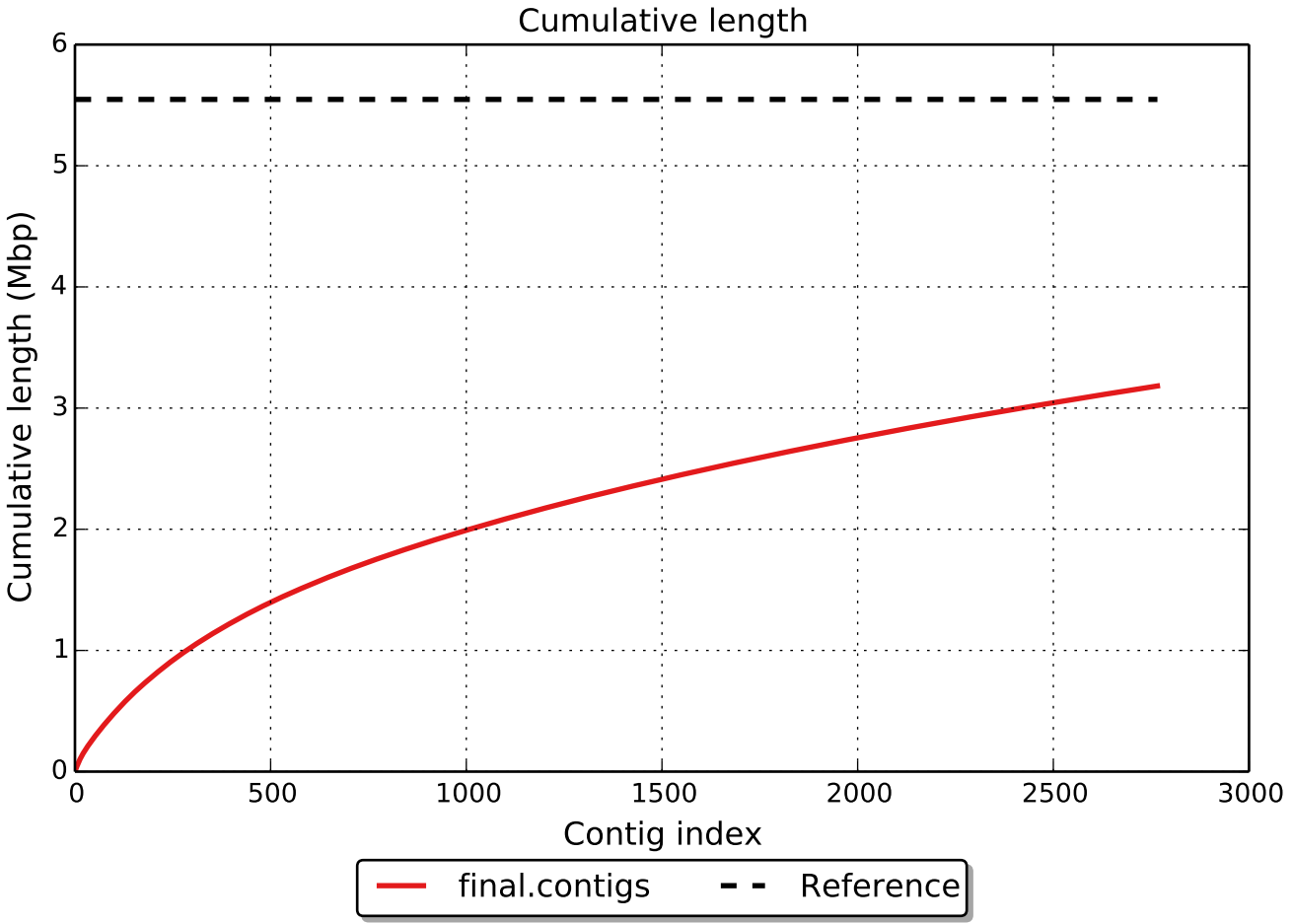
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	10518
# indels	2
# short indels	2
# long indels	0
Indels length	3

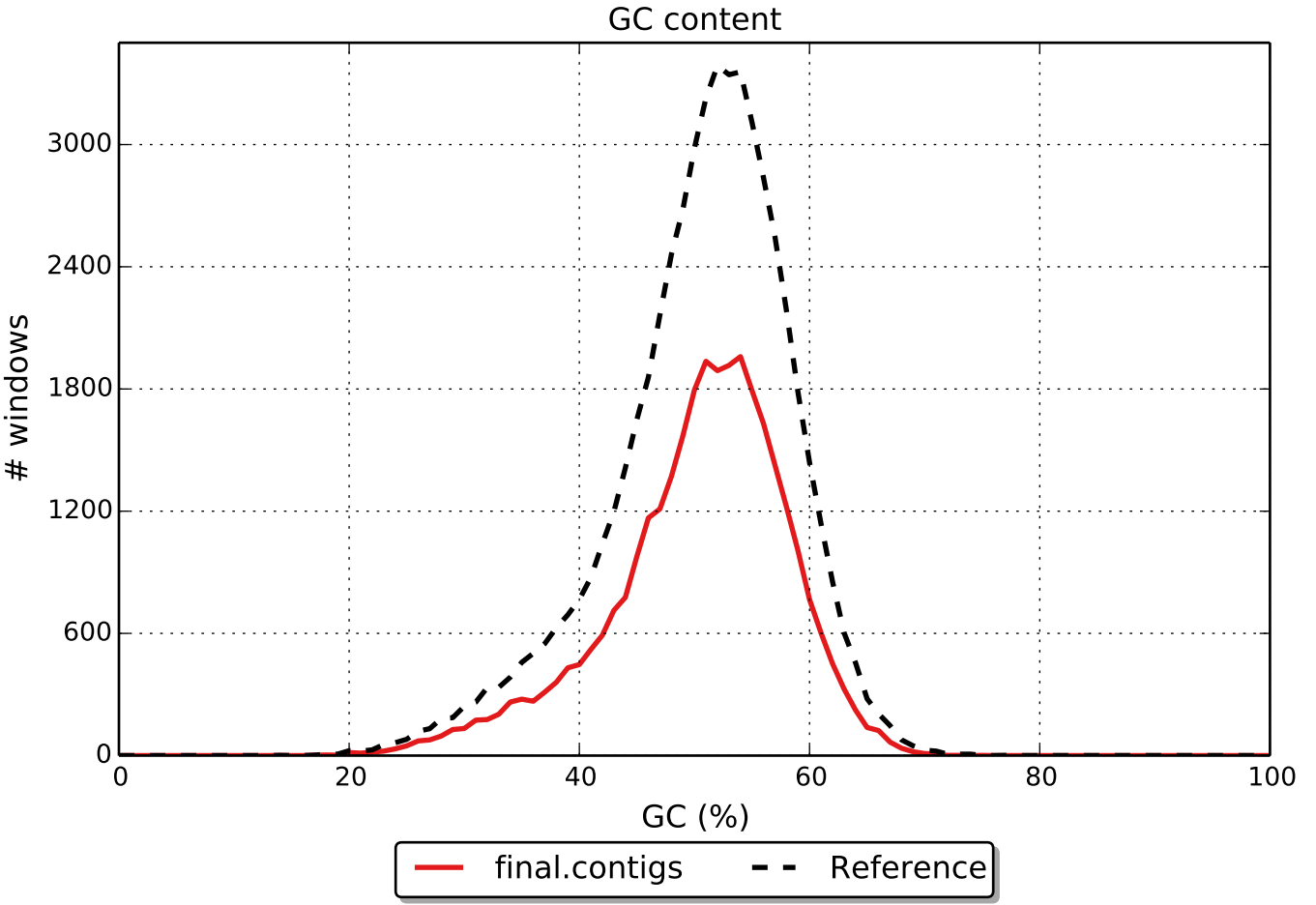
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

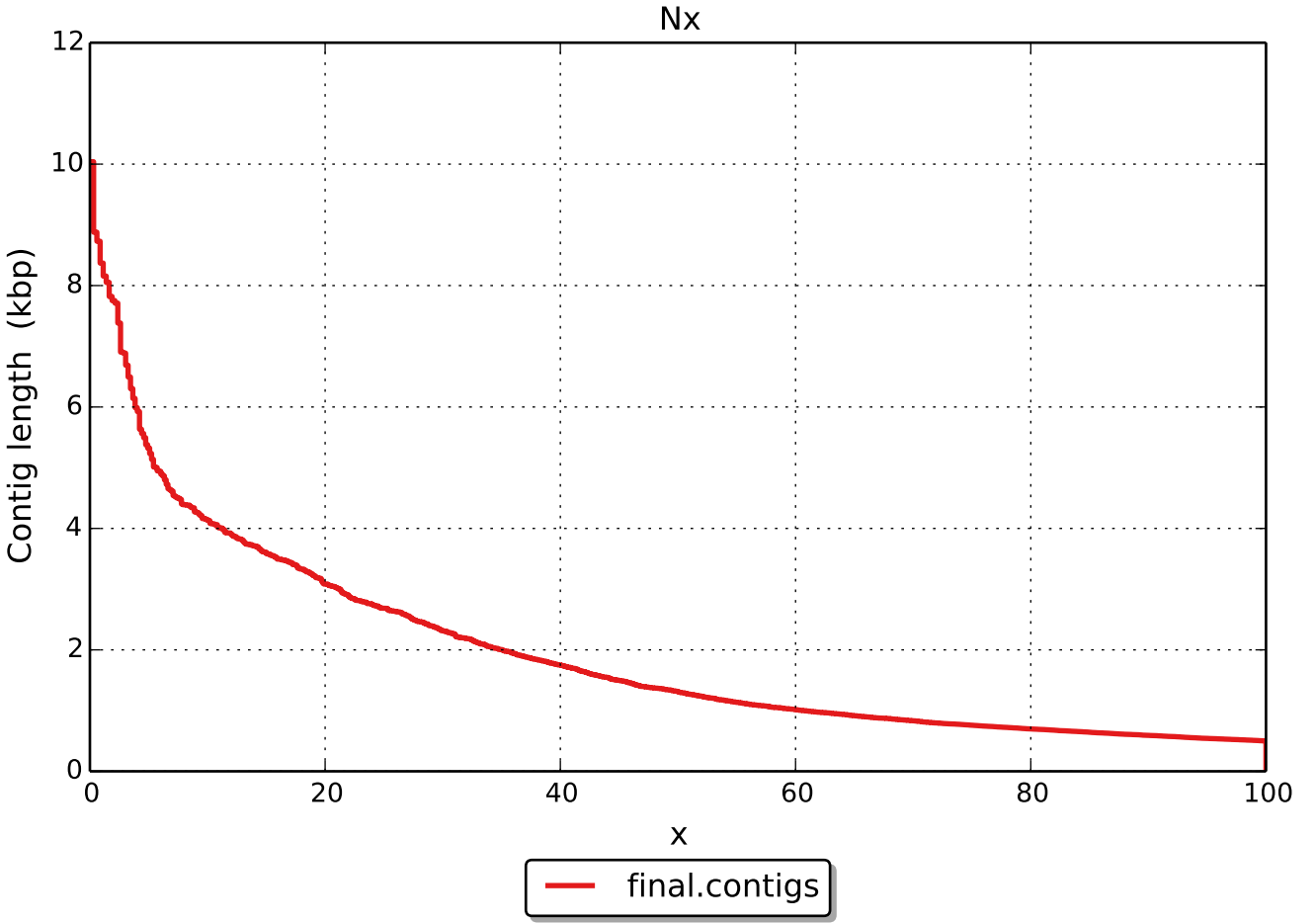
Unaligned report

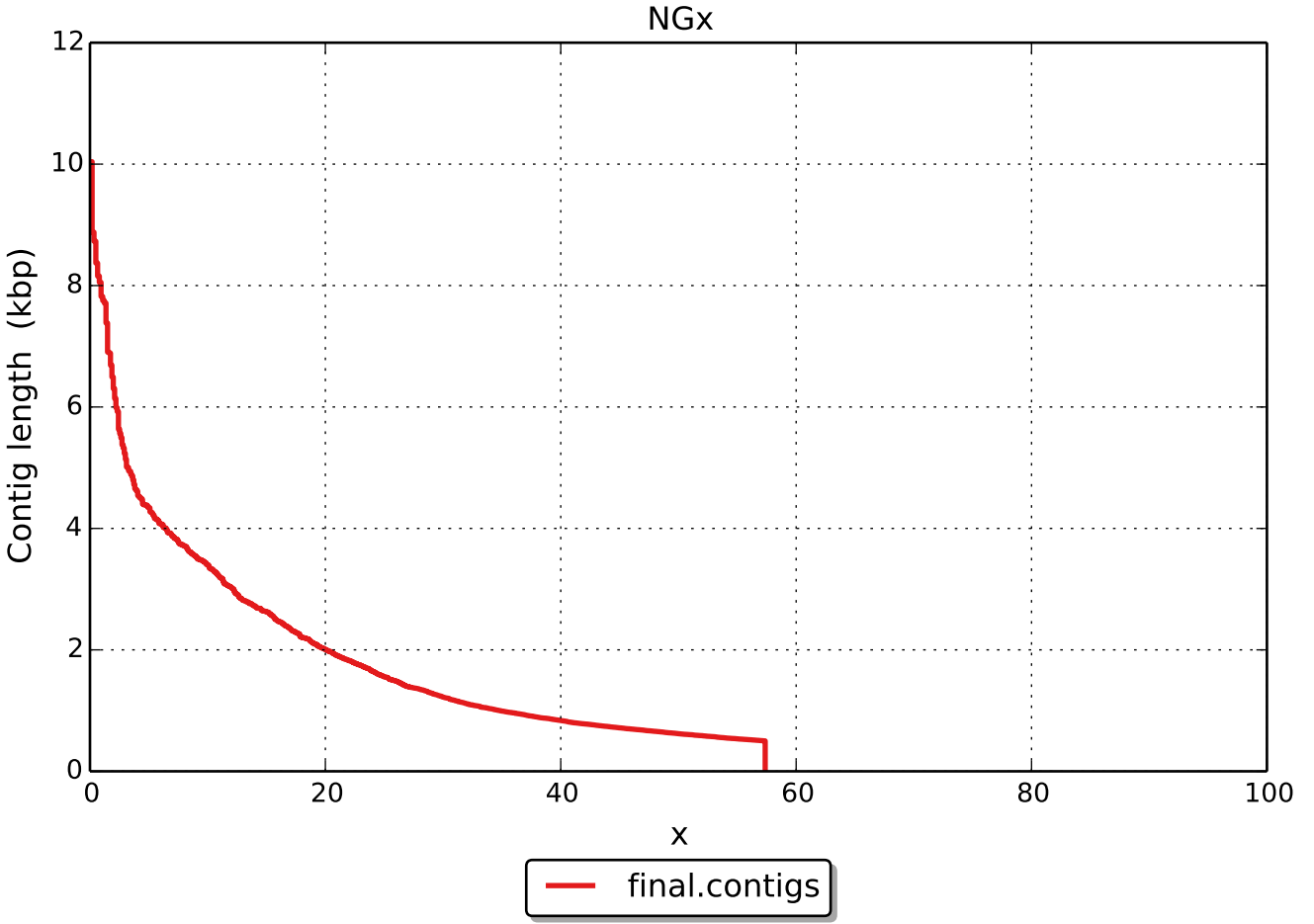
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

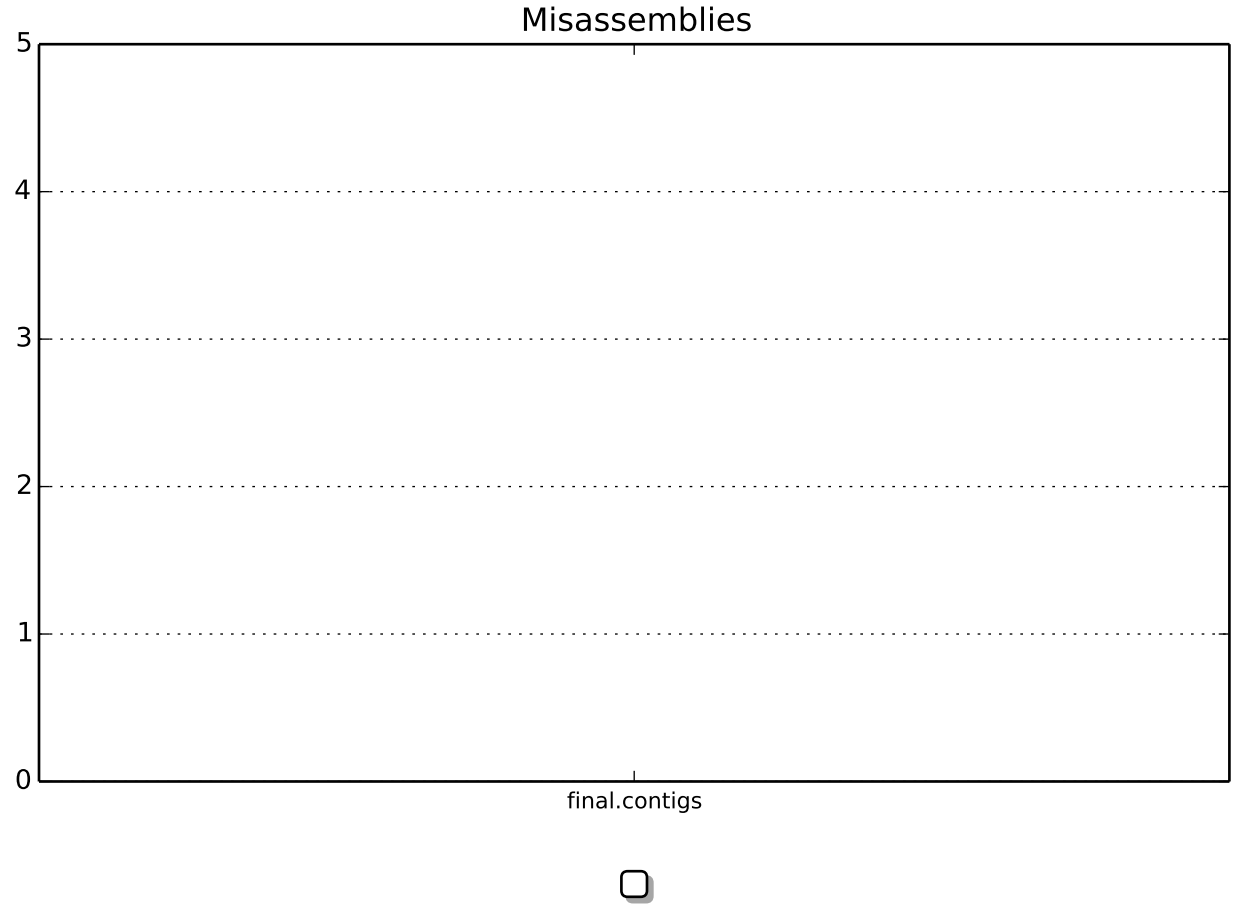
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

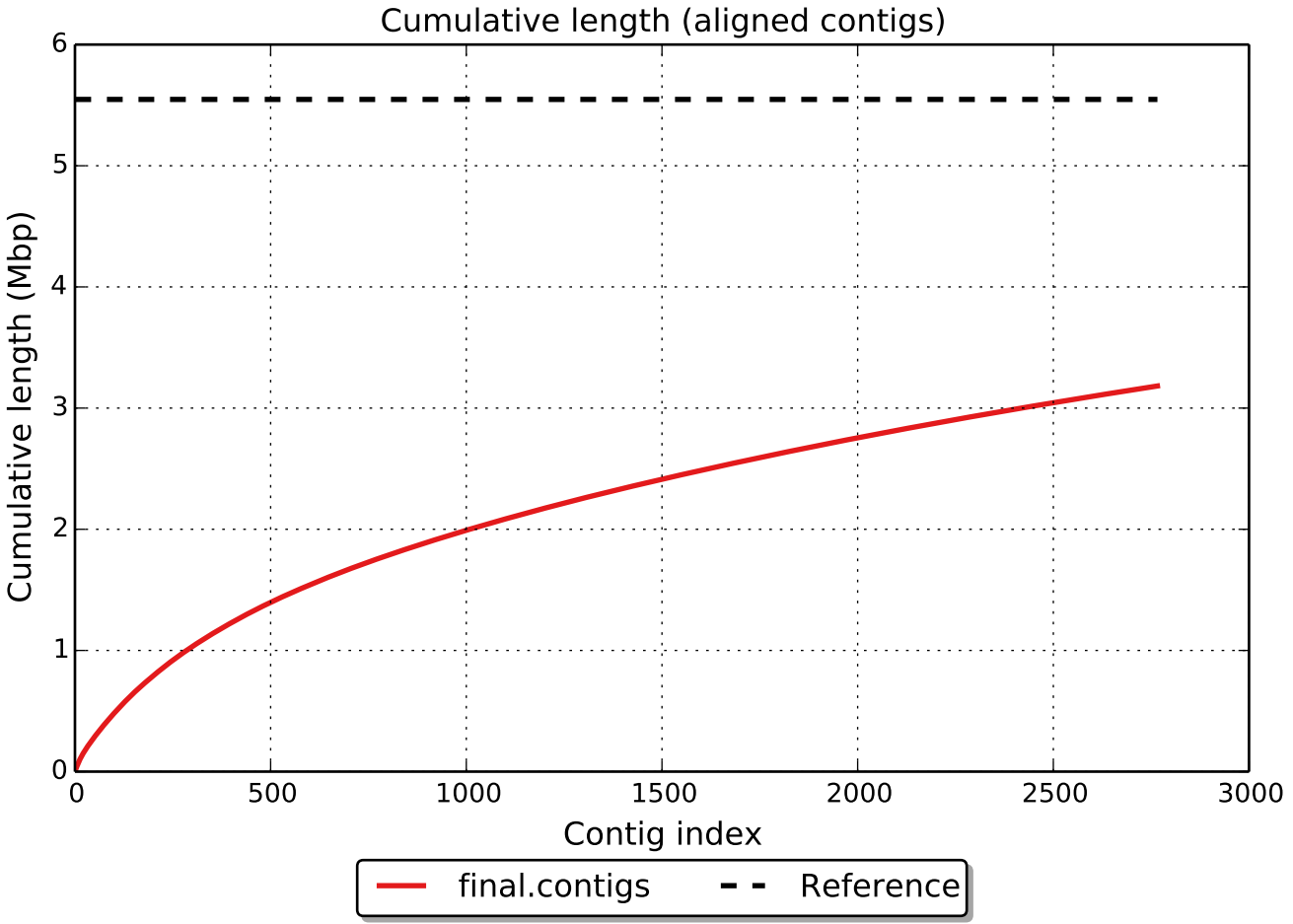

Cumulative length
Cumulative length (Mbp)
0
1
2
3
4
5
6
0
500
1000
1500
2000
2500
3000
Contig index
final.contigs
Reference

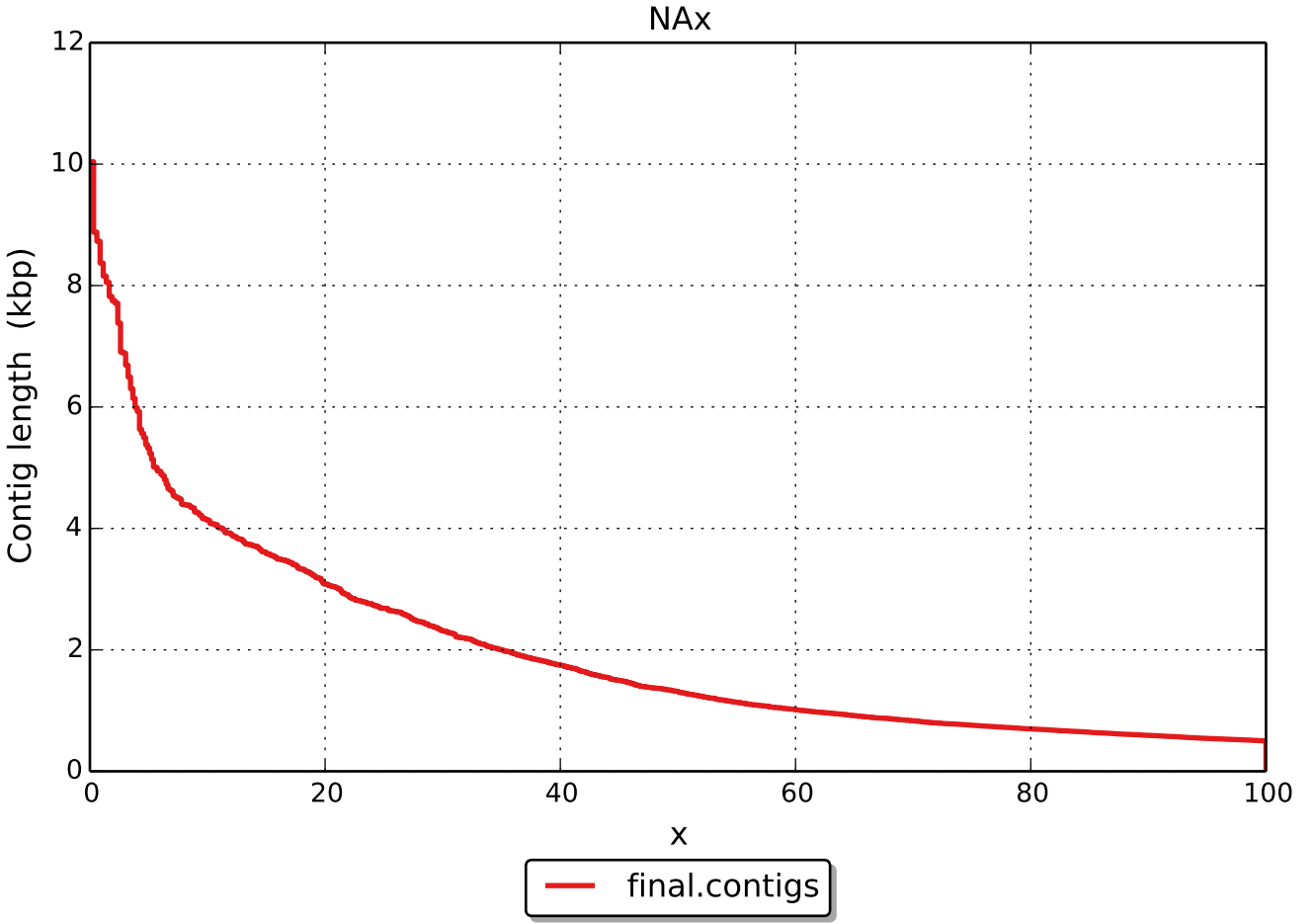

GC content
windows
3000
2400
1800
1200
600
0
0
20
40
60
80
100
GC (%)
final.contigs
Reference

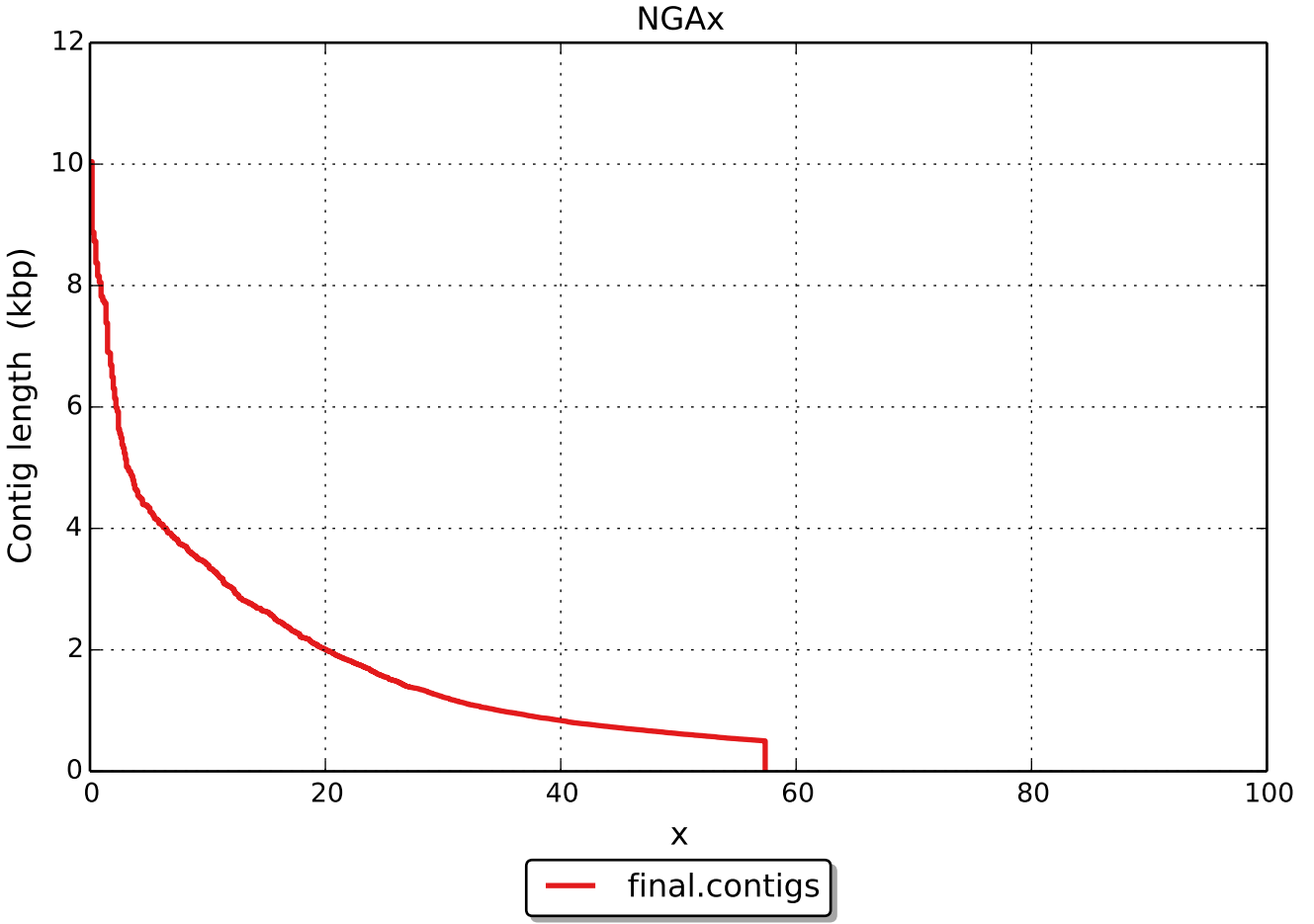

Nx
Contig length (kbp)
x
0
2
4
6
8
10
12
0
20
40
60
80
100
final.contigs


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


Misassemblies
5
4
3
2
1
0
final.contigs


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
1
2
3
4
5
6
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)
x
0
2
4
6
8
10
12
0
20
40
60
80
100
final.contigs