Report

	final.contigs
# contigs (>= 0 bp)	1396
# contigs (>= 1000 bp)	1129
Total length (>= 0 bp)	5269518
Total length (>= 1000 bp)	5078297
# contigs	1396
Largest contig	29757
Total length	5269518
Reference length	5478683
GC (%)	50.25
Reference GC (%)	50.49
N50	5916
NG50	5609
N75	3268
NG75	2992
L50	262
LG50	280
L75	562
LG75	612
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# unaligned contigs	0 + 1 part
Unaligned length	6073
Genome fraction (%)	94.110
Duplication ratio	1.021
# N's per 100 kbp	0.00
# mismatches per 100 kbp	24.30
# indels per 100 kbp	0.06
Largest alignment	27862
NA50	5911
NGA50	5601
NA75	3266
NGA75	2986
LA50	263
LGA50	281
LA75	564
LGA75	614

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

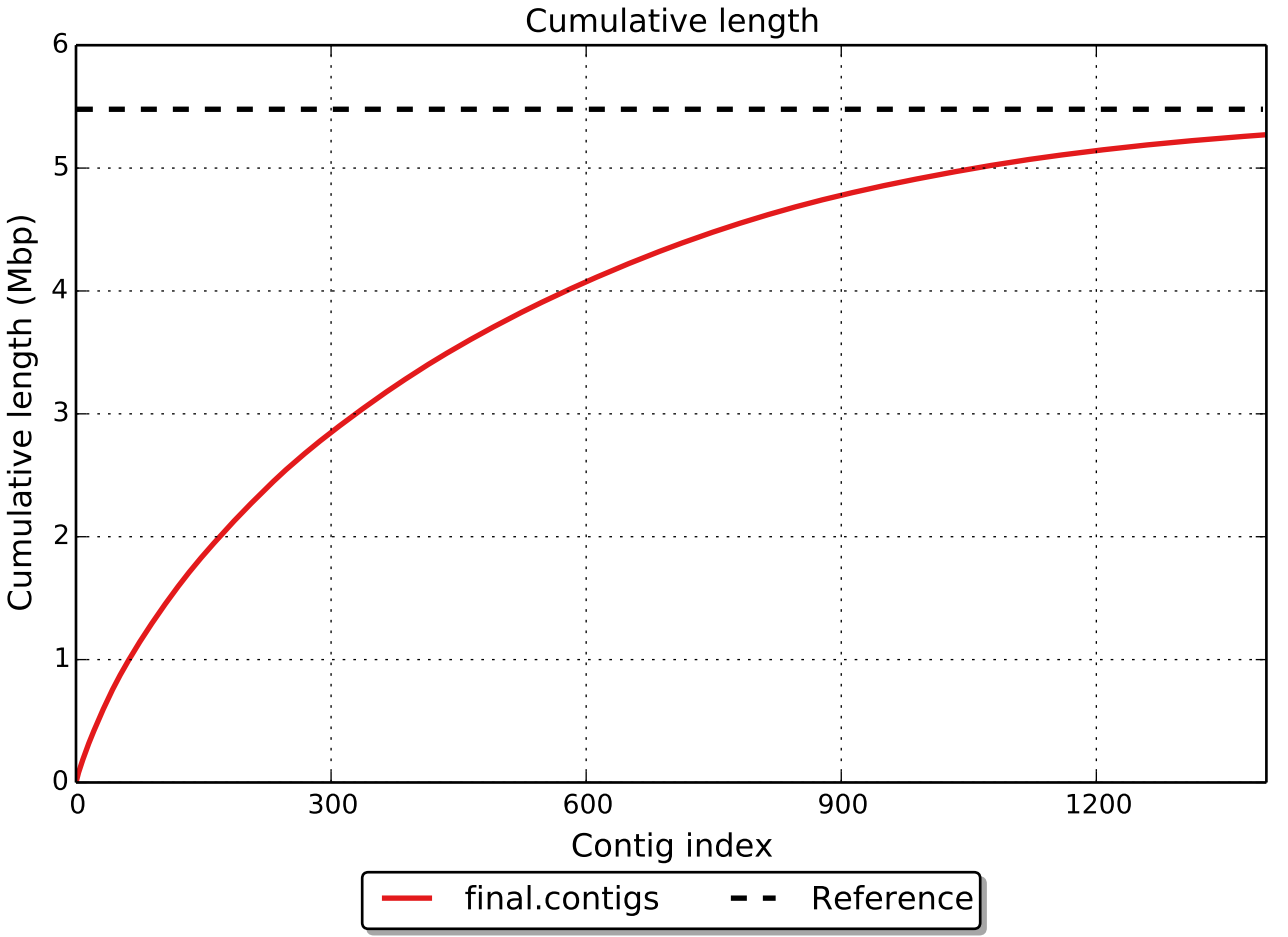
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	1
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# mismatches	1253
# indels	3
# short indels	1
# long indels	2
Indels length	31

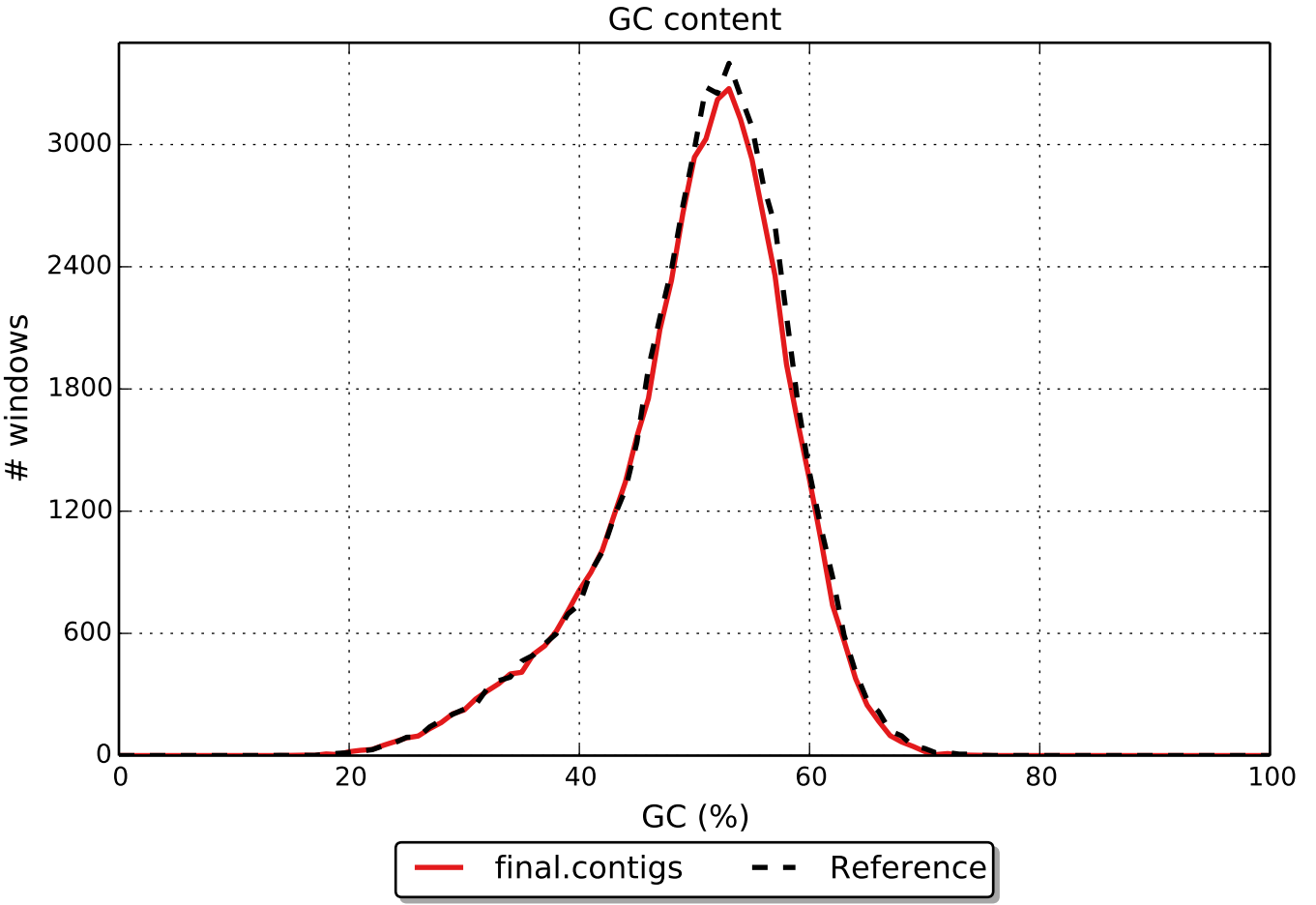
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

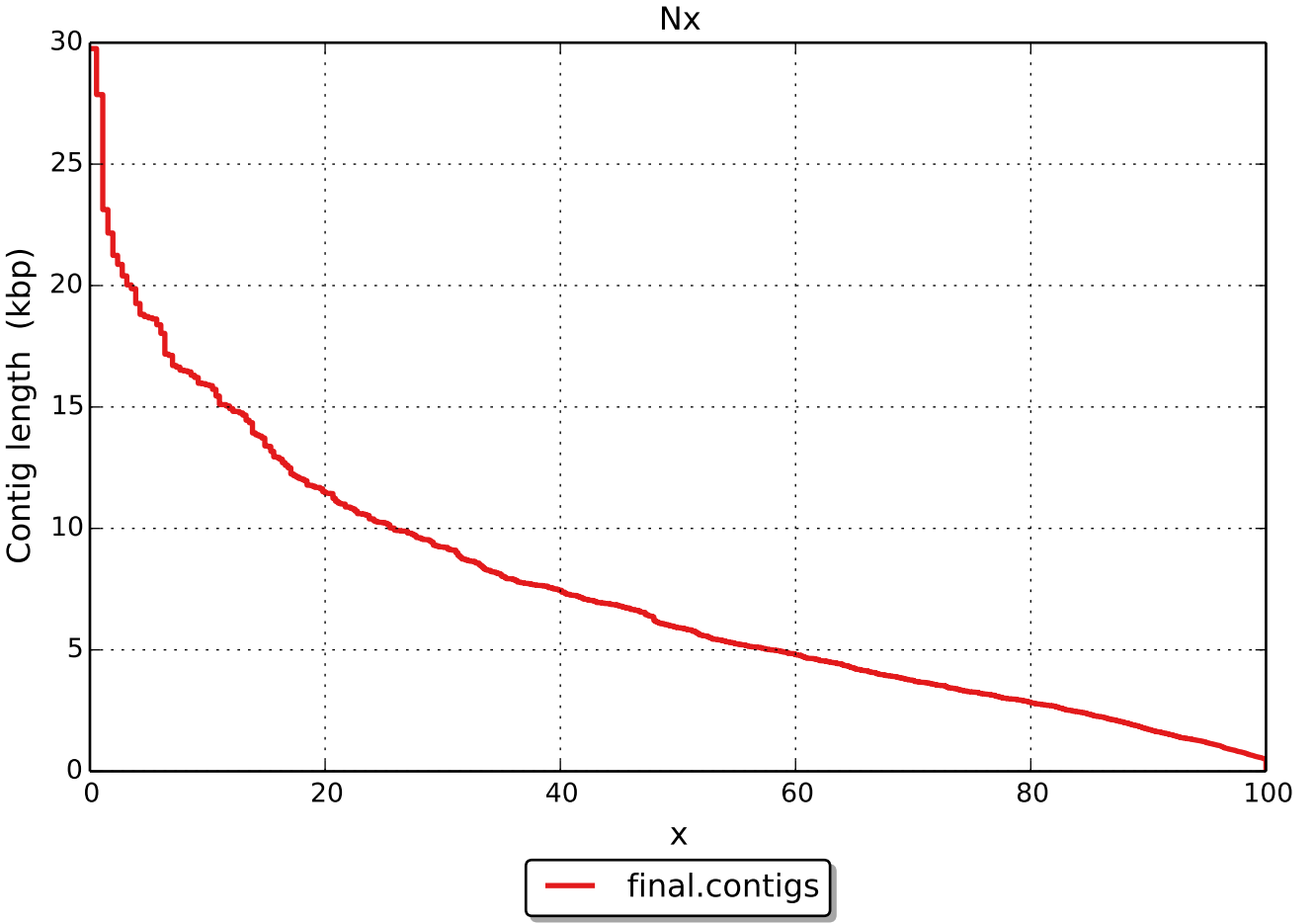
Unaligned report

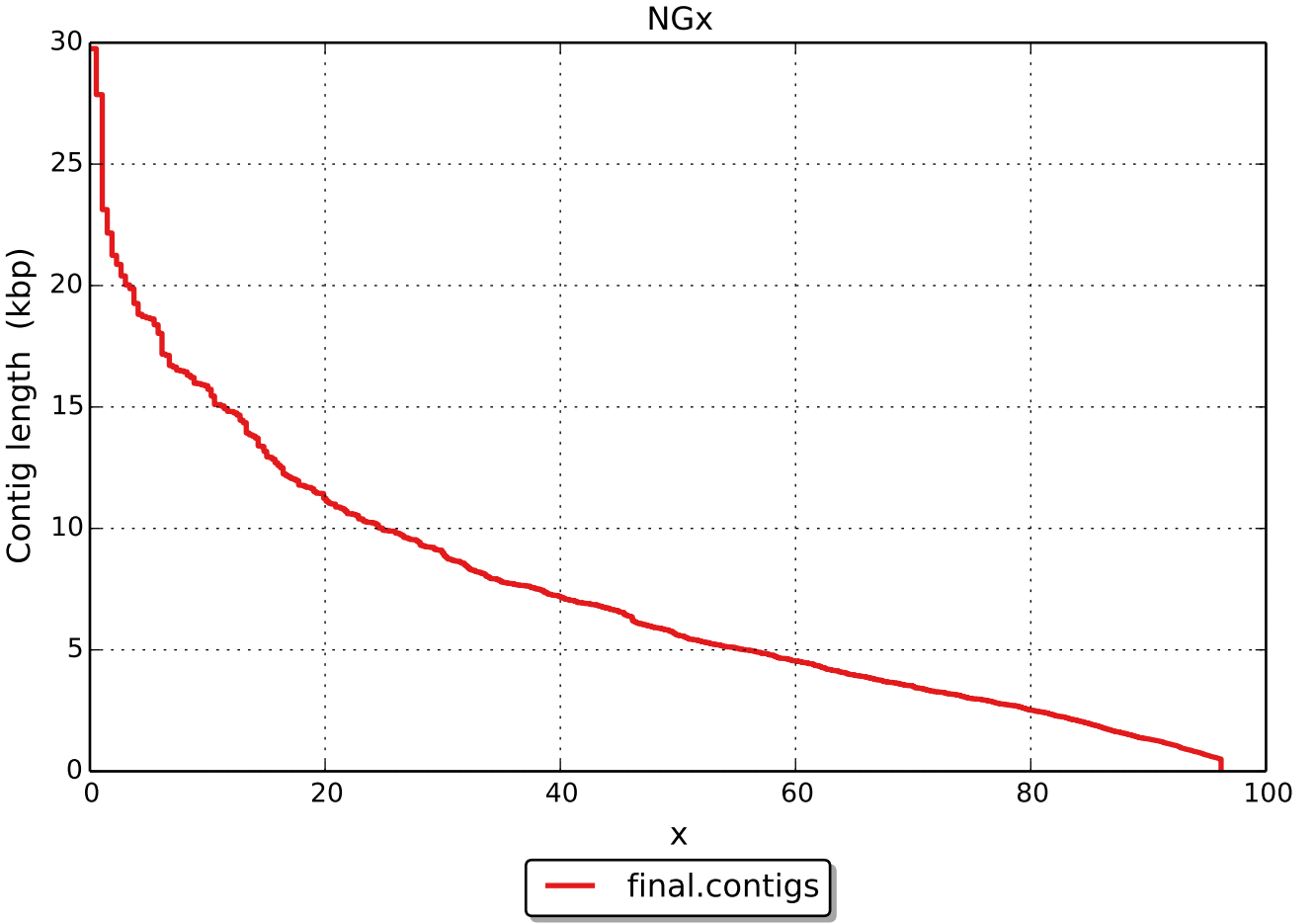
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	1
Partially unaligned length	6073
# N's	0

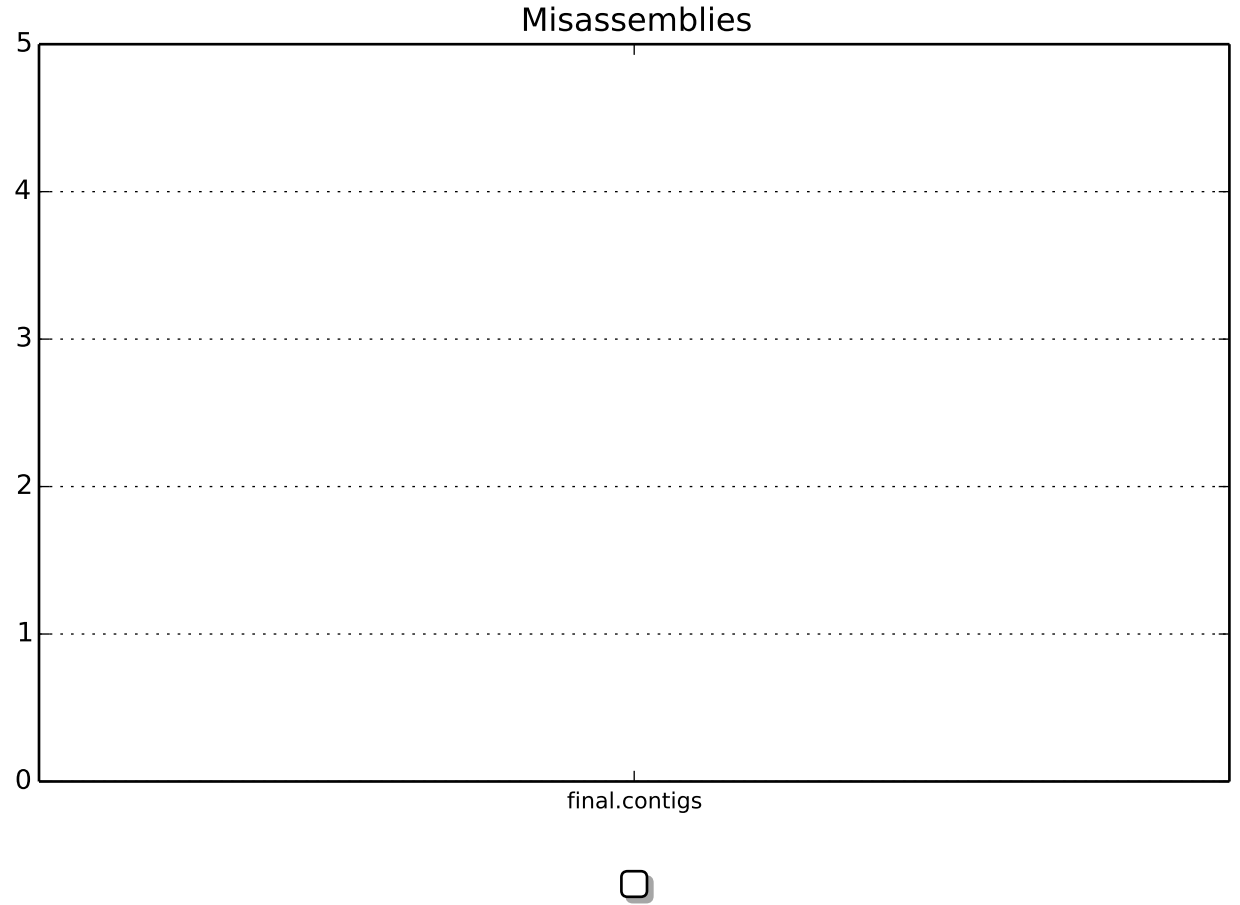
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

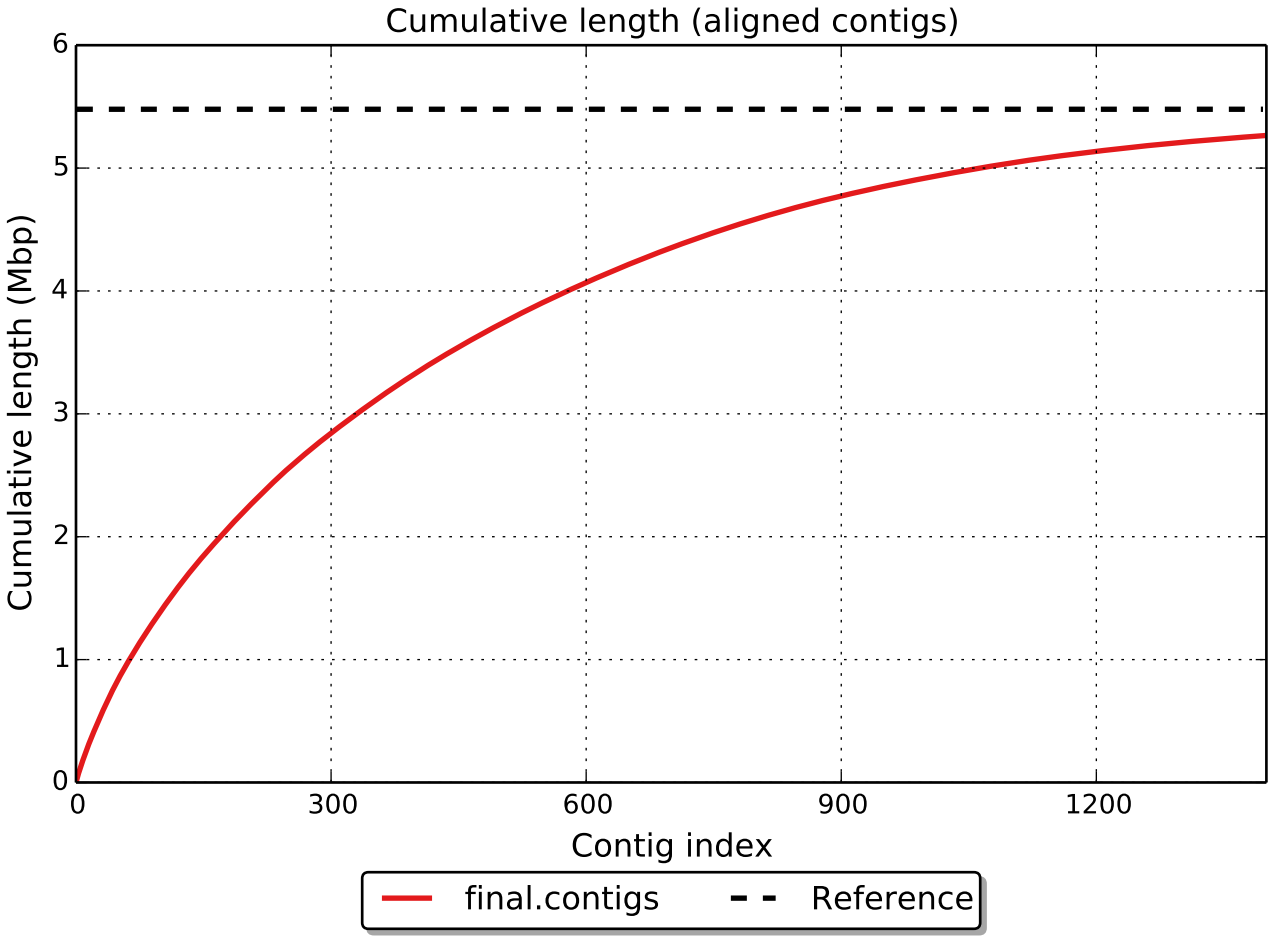

Cumulative length
Cumulative length (Mbp)
0
1
2
3
4
5
6
0
300
600
900
1200
Contig index
final.contigs
Reference

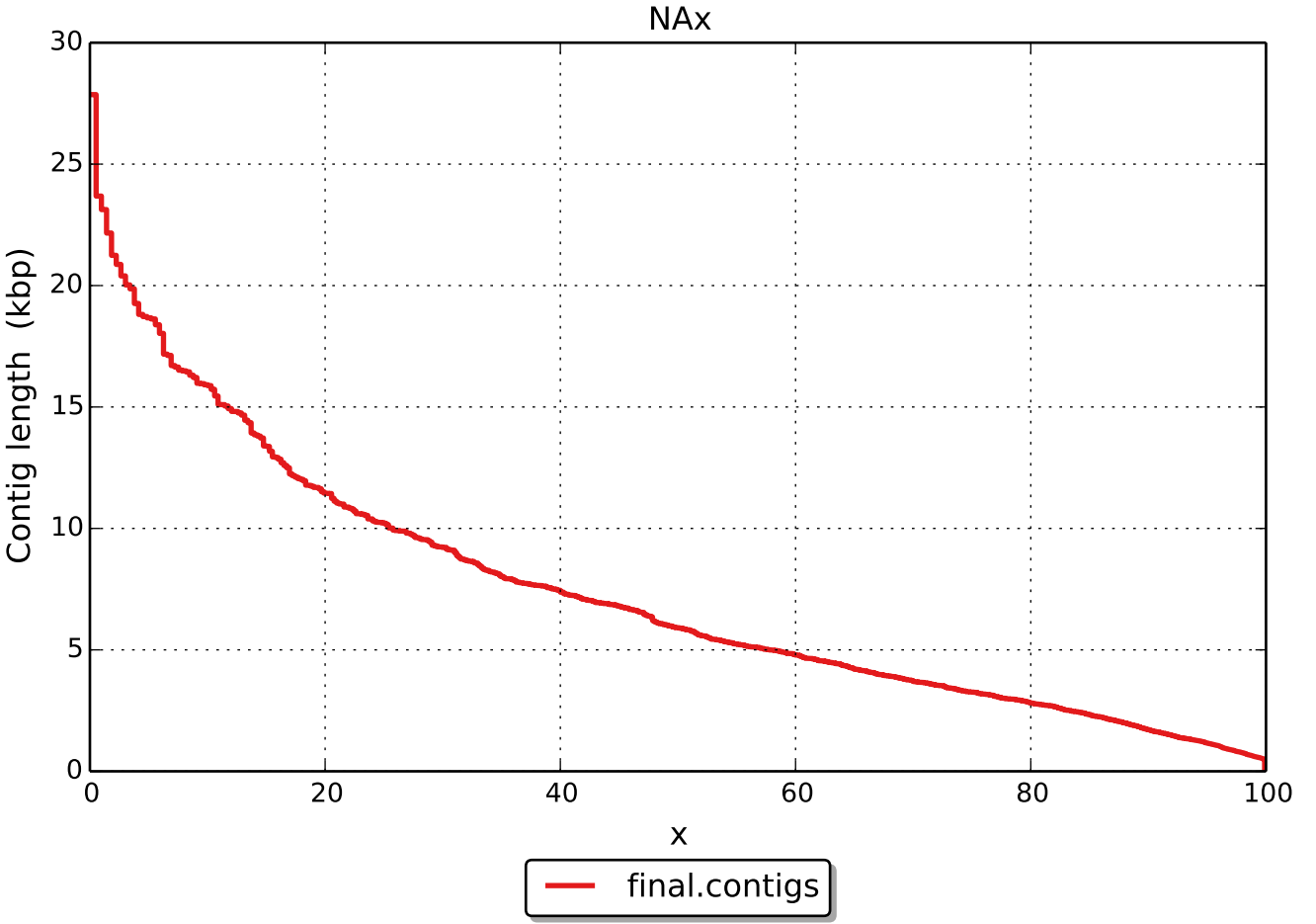

GC content
windows
3000
2400
1800
1200
600
0
0
20
40
60
80
100
GC (%)
final.contigs
Reference

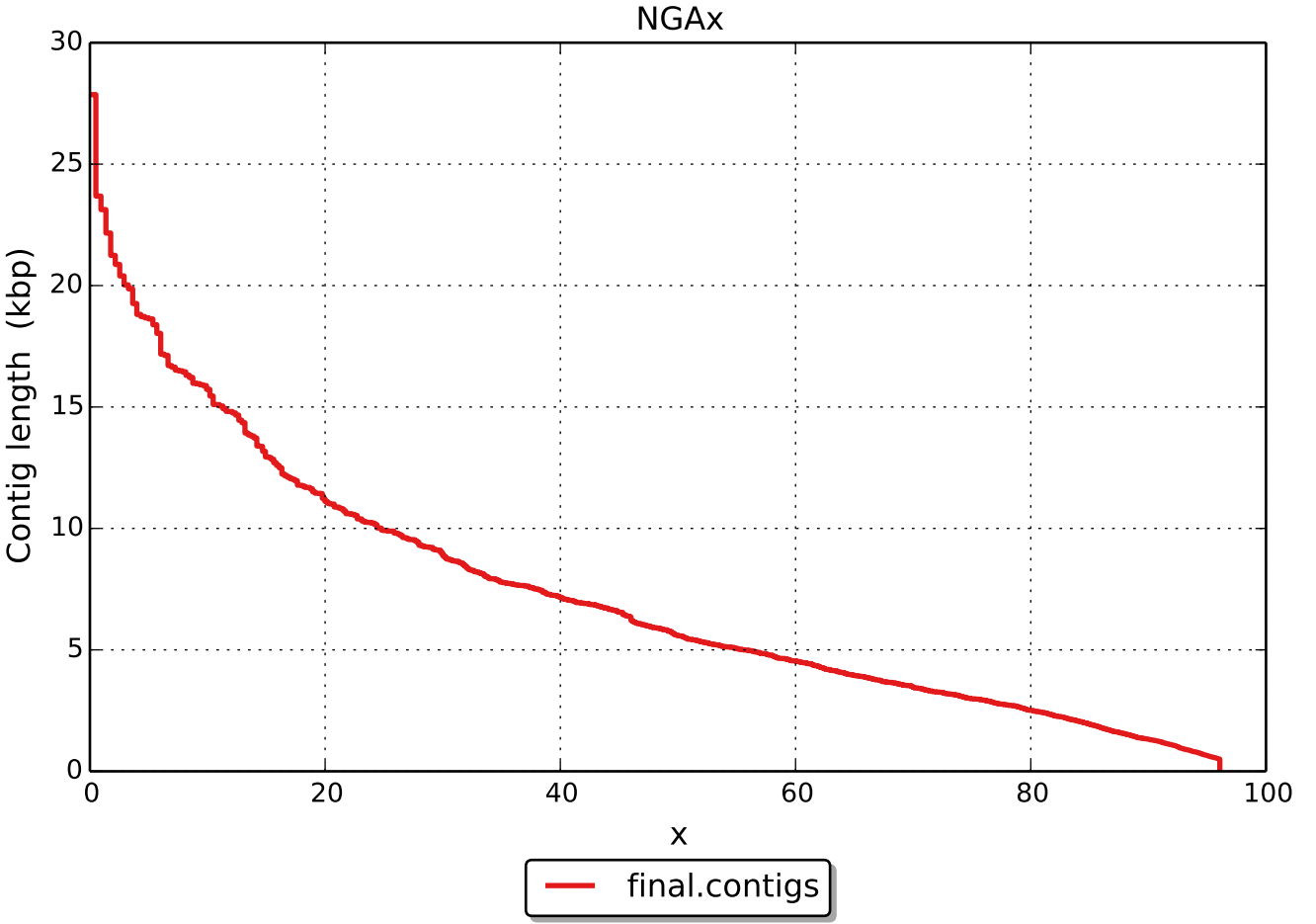

Nx
Contig length (kbp)
30
25
20
15
10
5
0
0
20
40
60
80
100
x
final.contigs


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


Misassemblies
5
4
3
2
1
0
final.contigs


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
1
2
3
4
5
6
0
300
600
900
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