Report

	final.contigs
# contigs (>= 0 bp)	1719
# contigs (>= 1000 bp)	1327
Total length (>= 0 bp)	5224062
Total length (>= 1000 bp)	4940152
# contigs	1719
Largest contig	23734
Total length	5224062
Reference length	5547323
GC (%)	50.30
Reference GC (%)	50.48
N50	4722
NG50	4441
N75	2565
NG75	2236
L50	345
LG50	380
L75	715
LG75	817
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	2818
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	91.881
Duplication ratio	1.025
# N's per 100 kbp	0.00
# mismatches per 100 kbp	32.06
# indels per 100 kbp	0.18
Largest alignment	23734
NA50	4722
NGA50	4441
NA75	2564
NGA75	2234
LA50	345
LGA50	380
LA75	715
LGA75	817

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

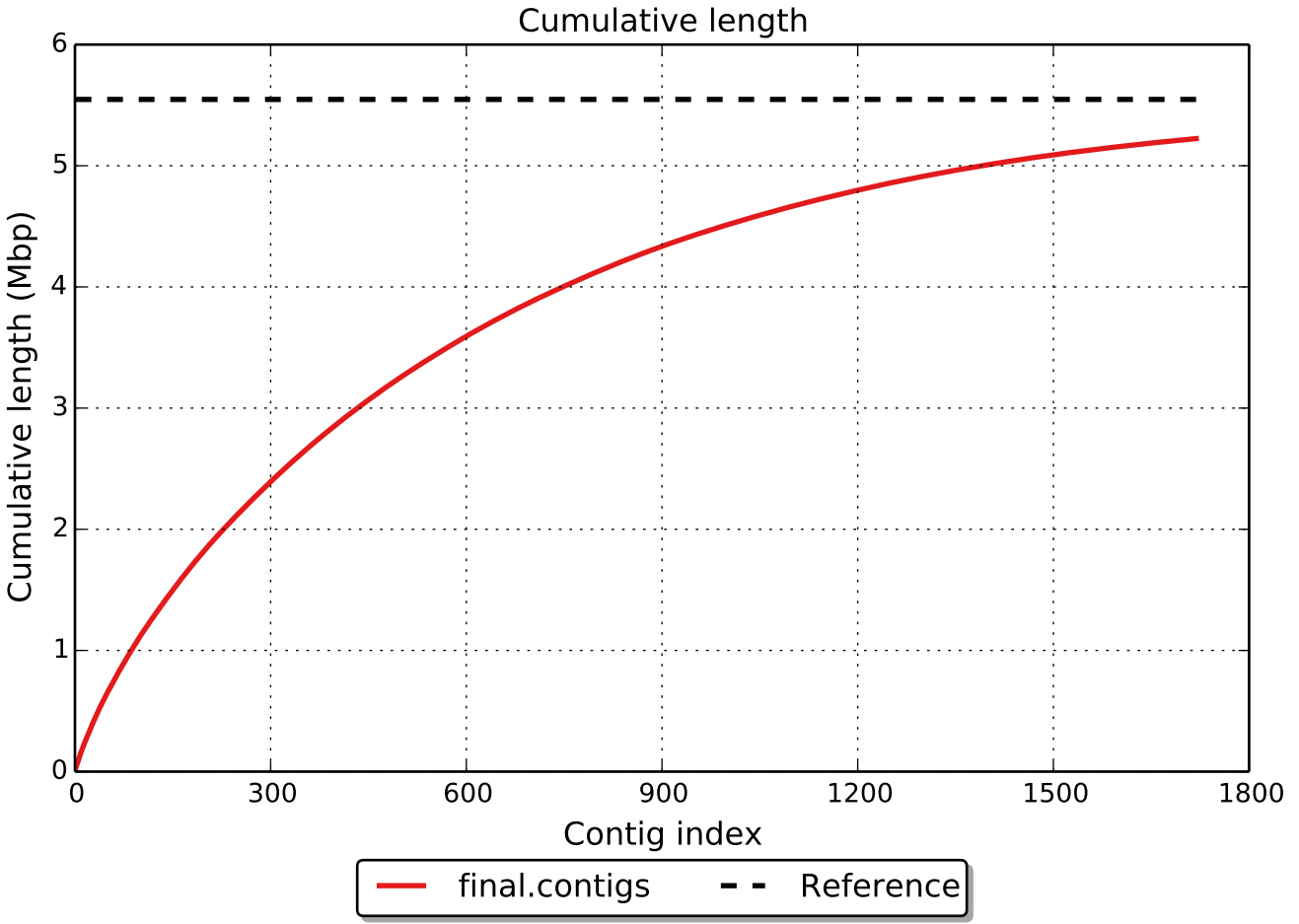
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	2818
# local misassemblies	0
# mismatches	1634
# indels	9
# short indels	8
# long indels	1
Indels length	14

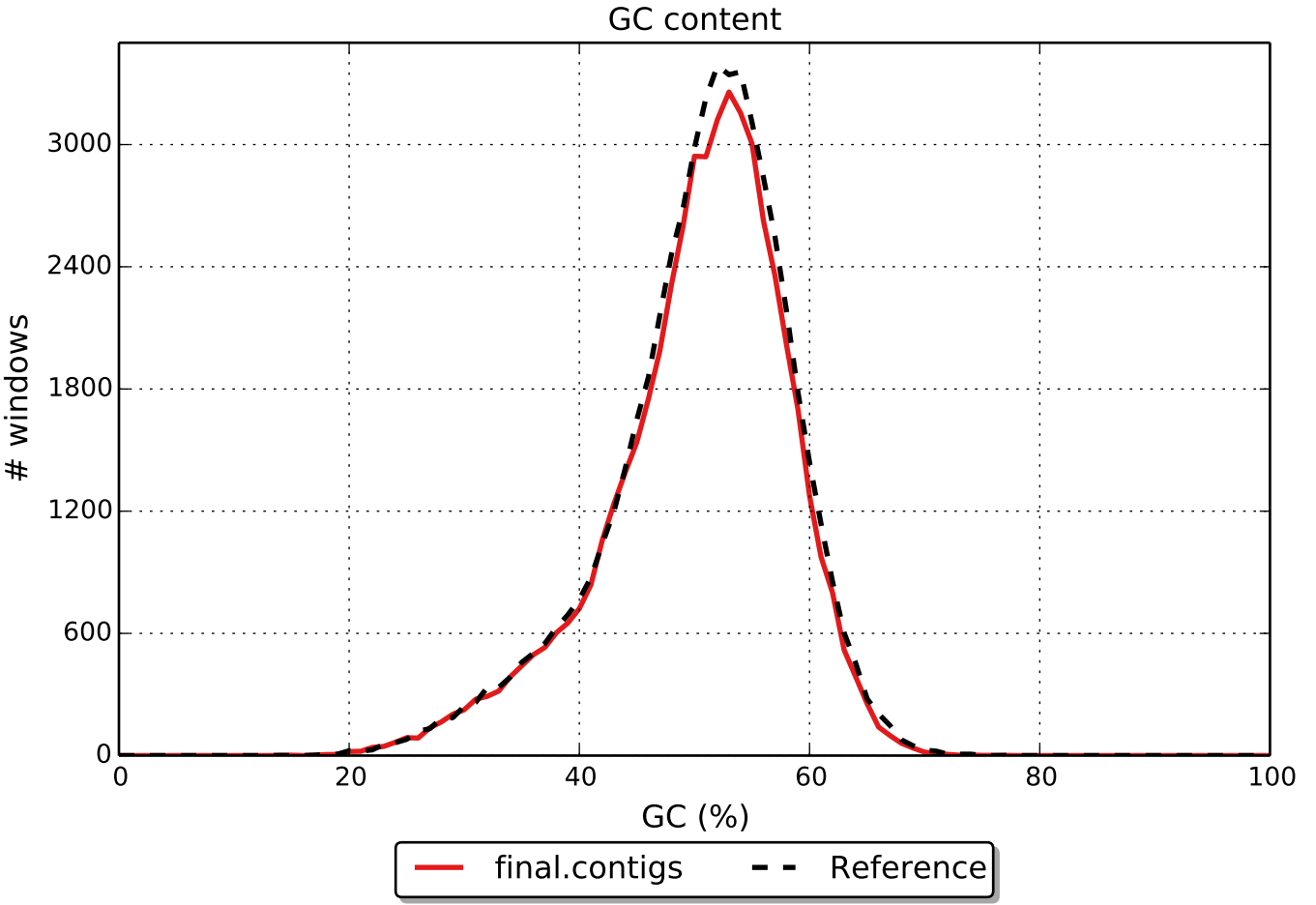
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

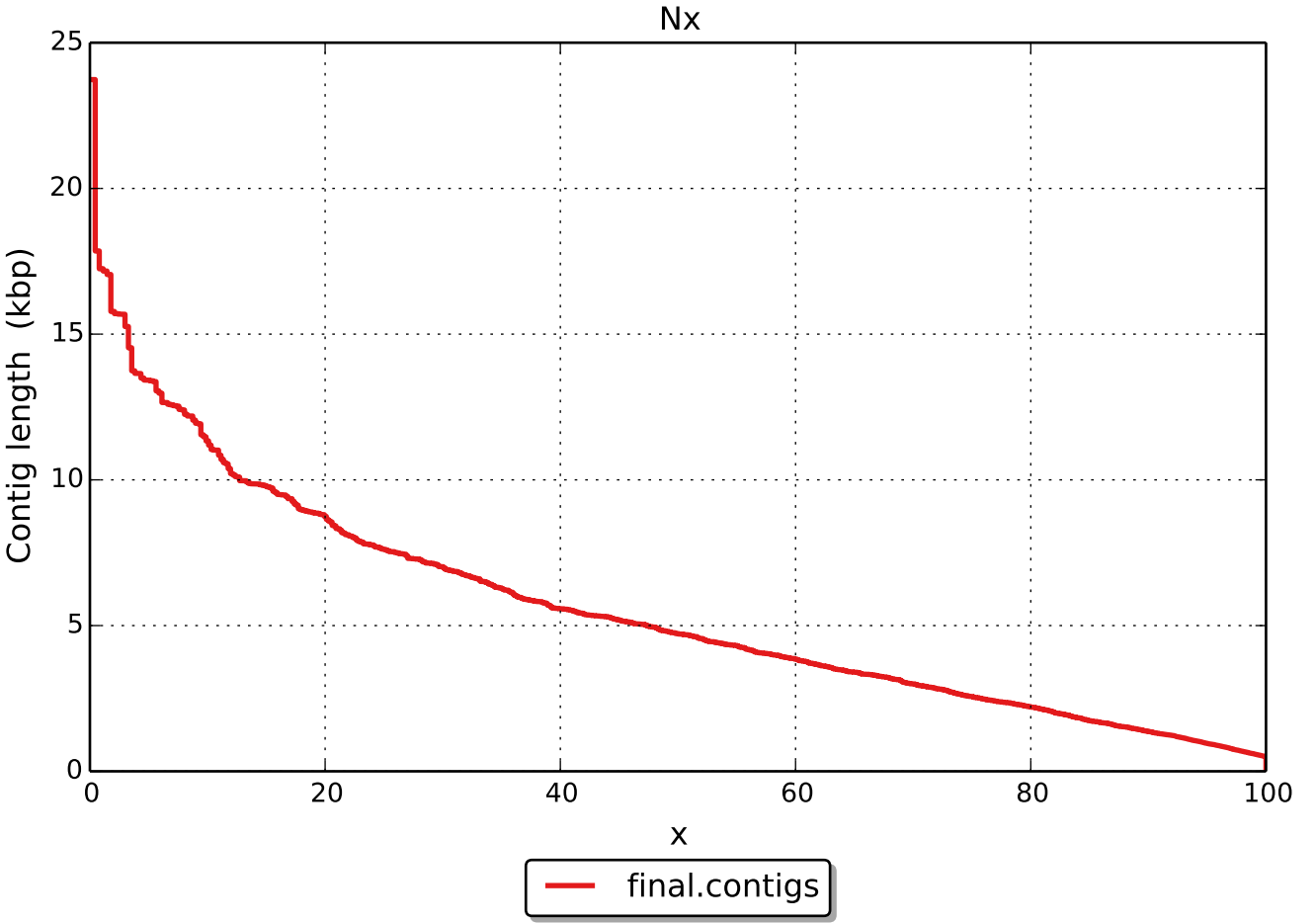
Unaligned report

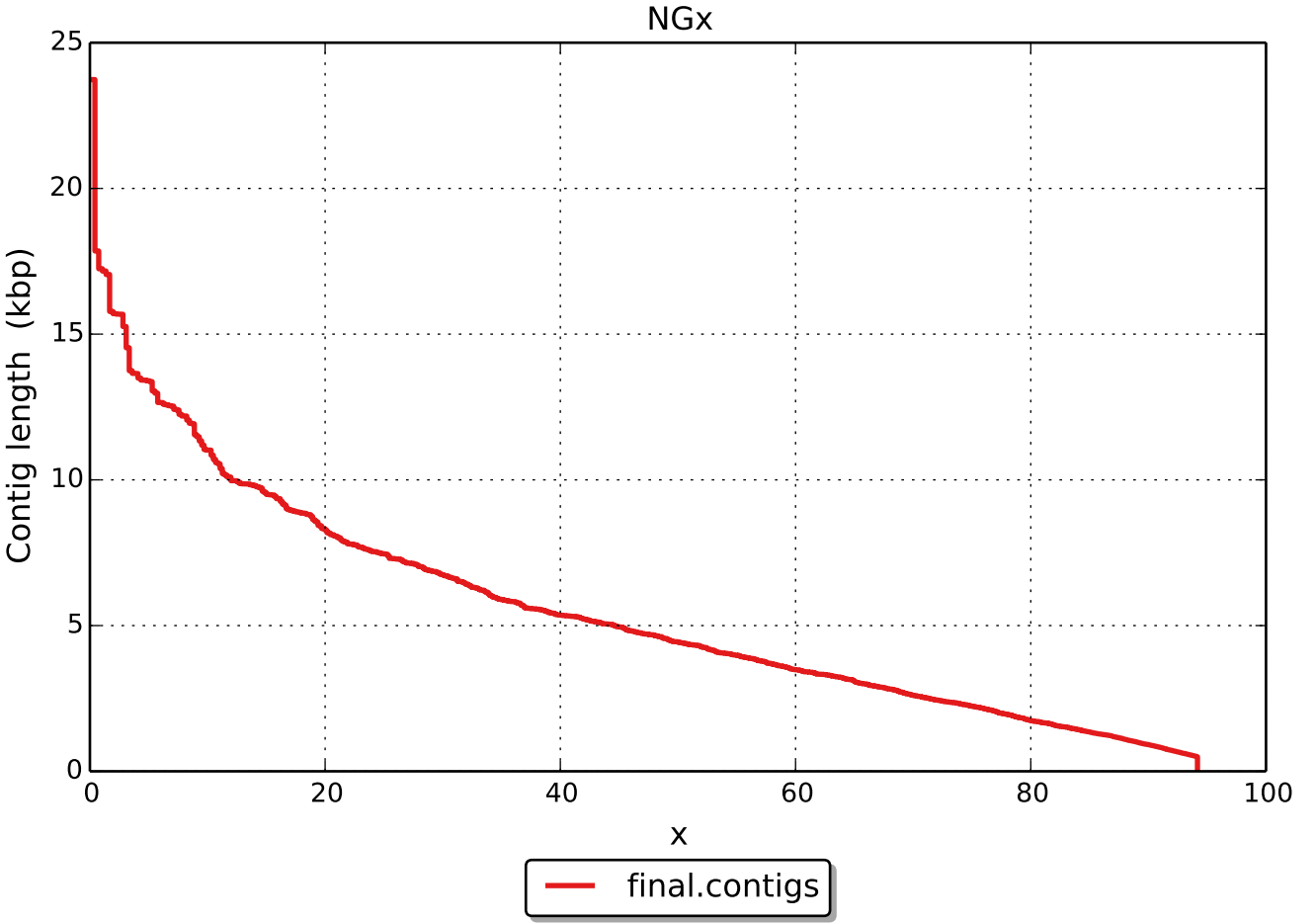
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

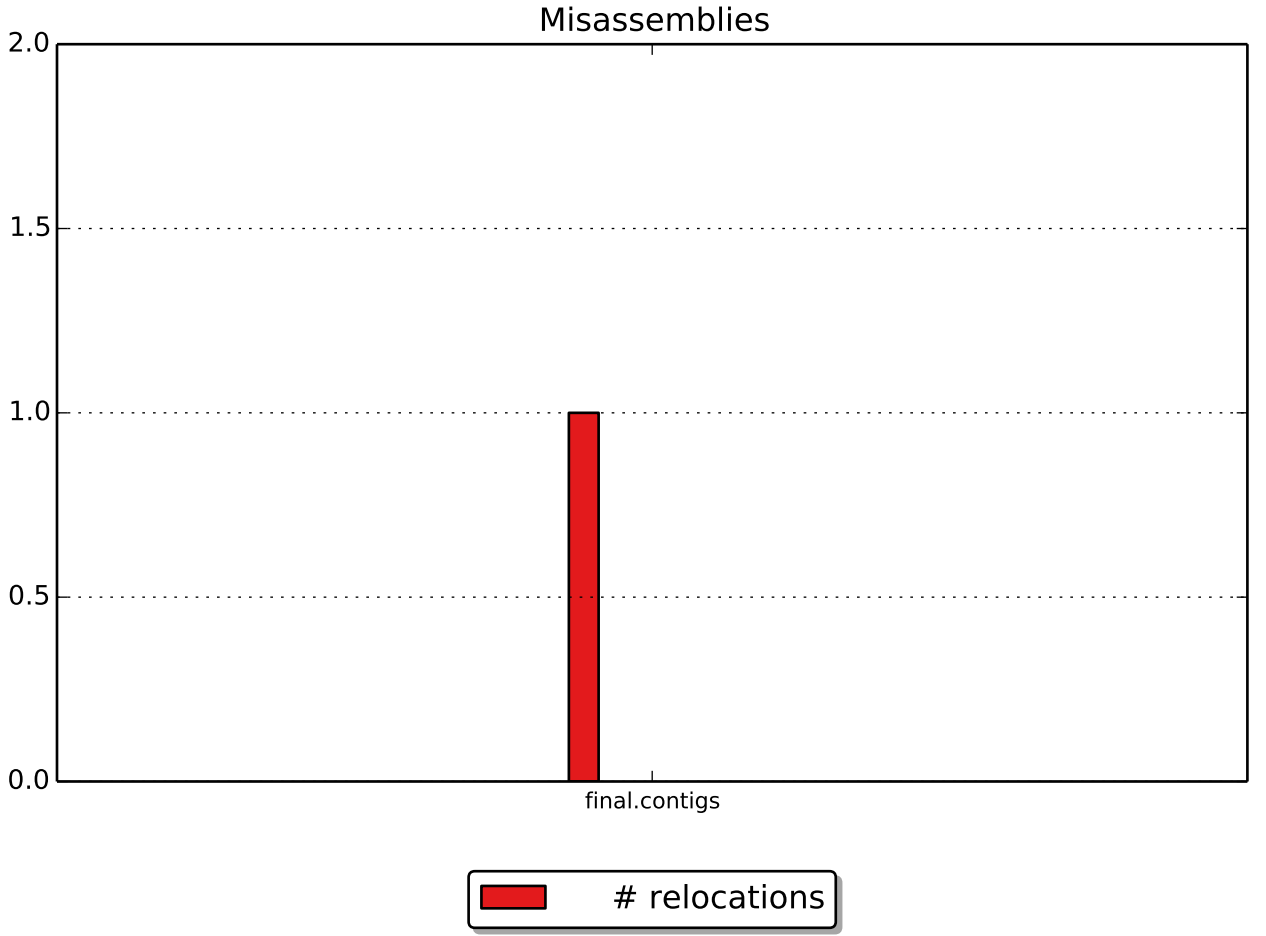
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

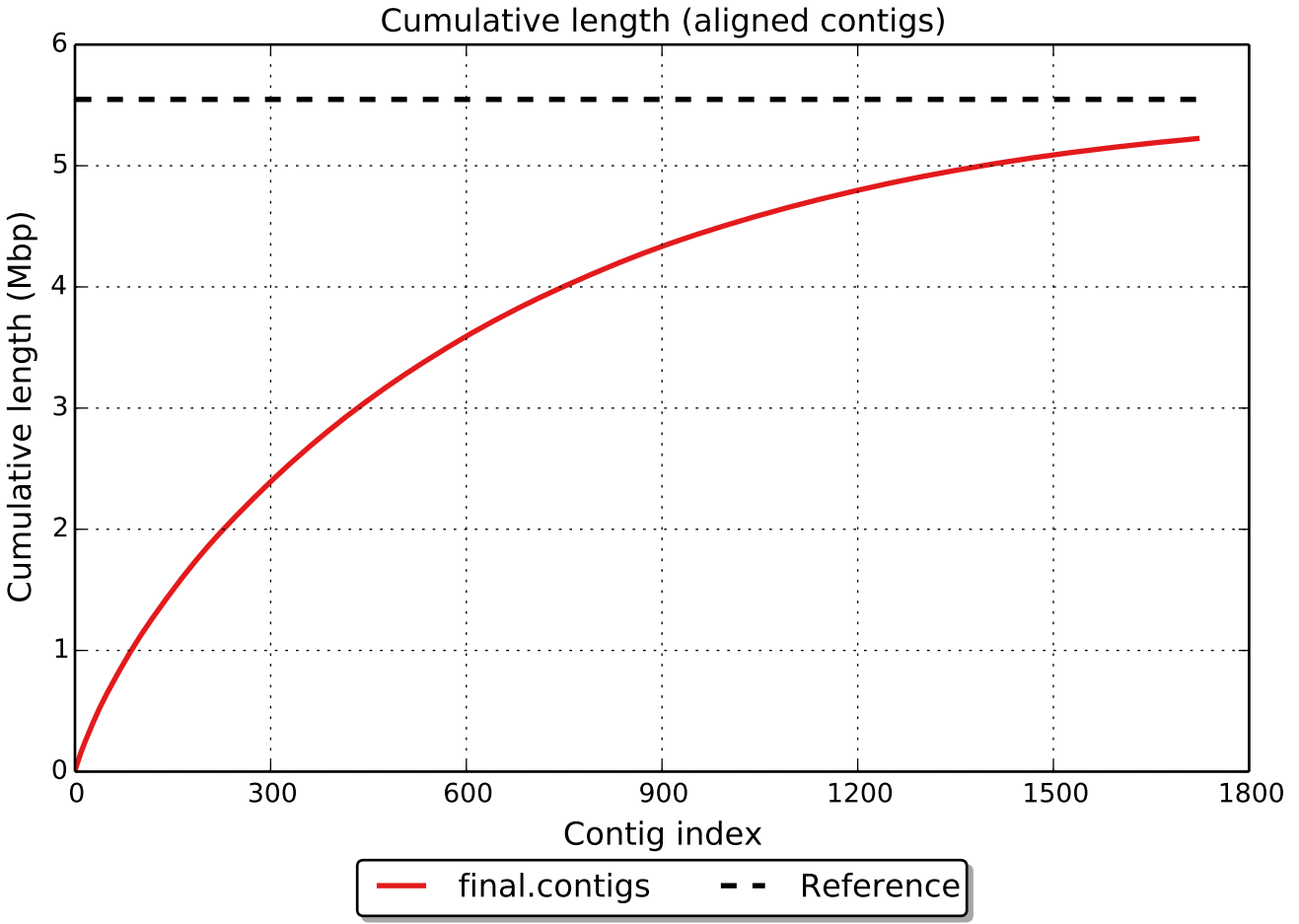

Cumulative length
Cumulative length (Mbp)
0
1
2
3
4
5
6
0
300
600
900
1200
1500
1800
Contig index
final.contigs
Reference

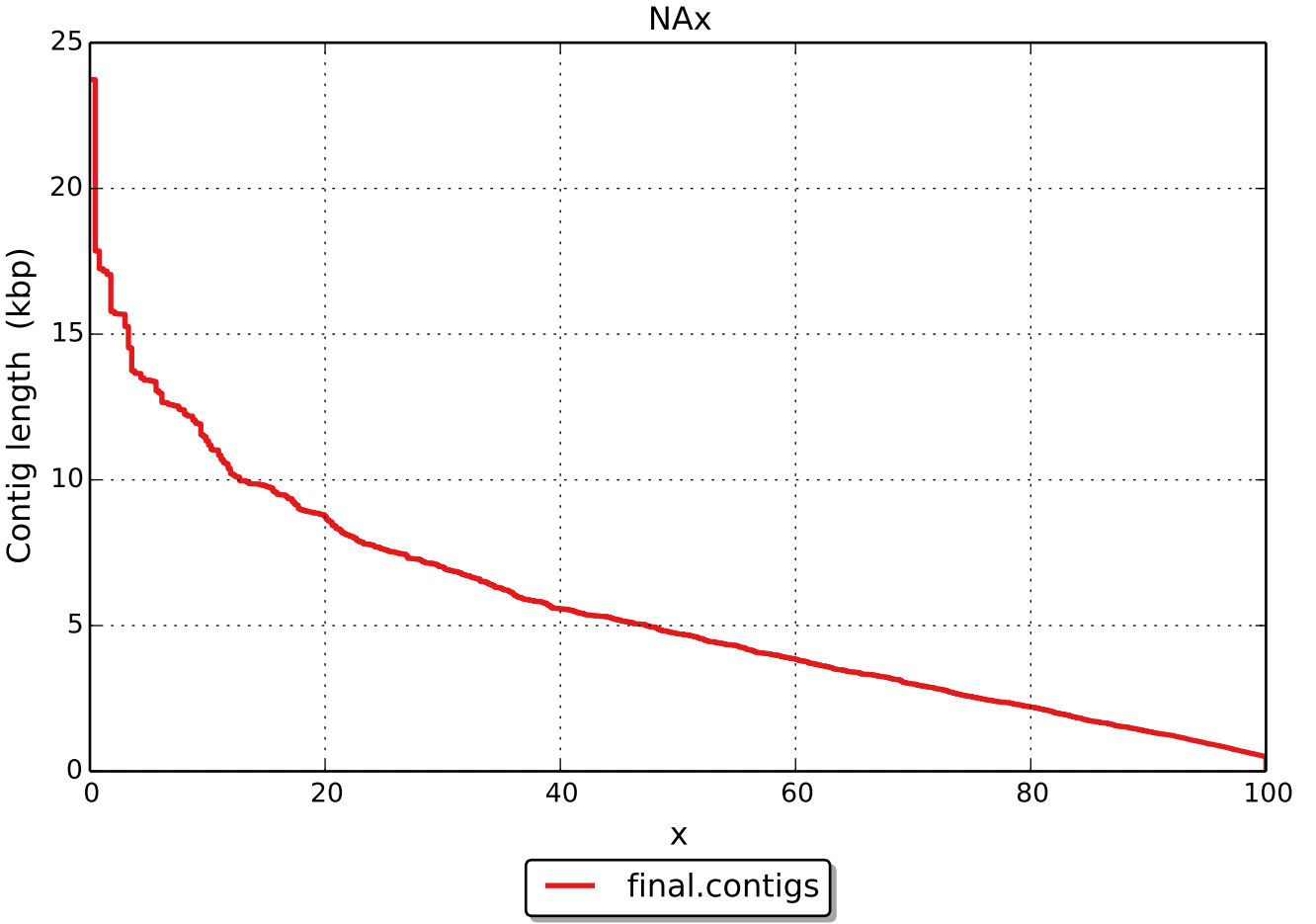

GC content
windows
3000
2400
1800
1200
600
0
0
20
40
60
80
100
GC (%)
final.contigs
Reference

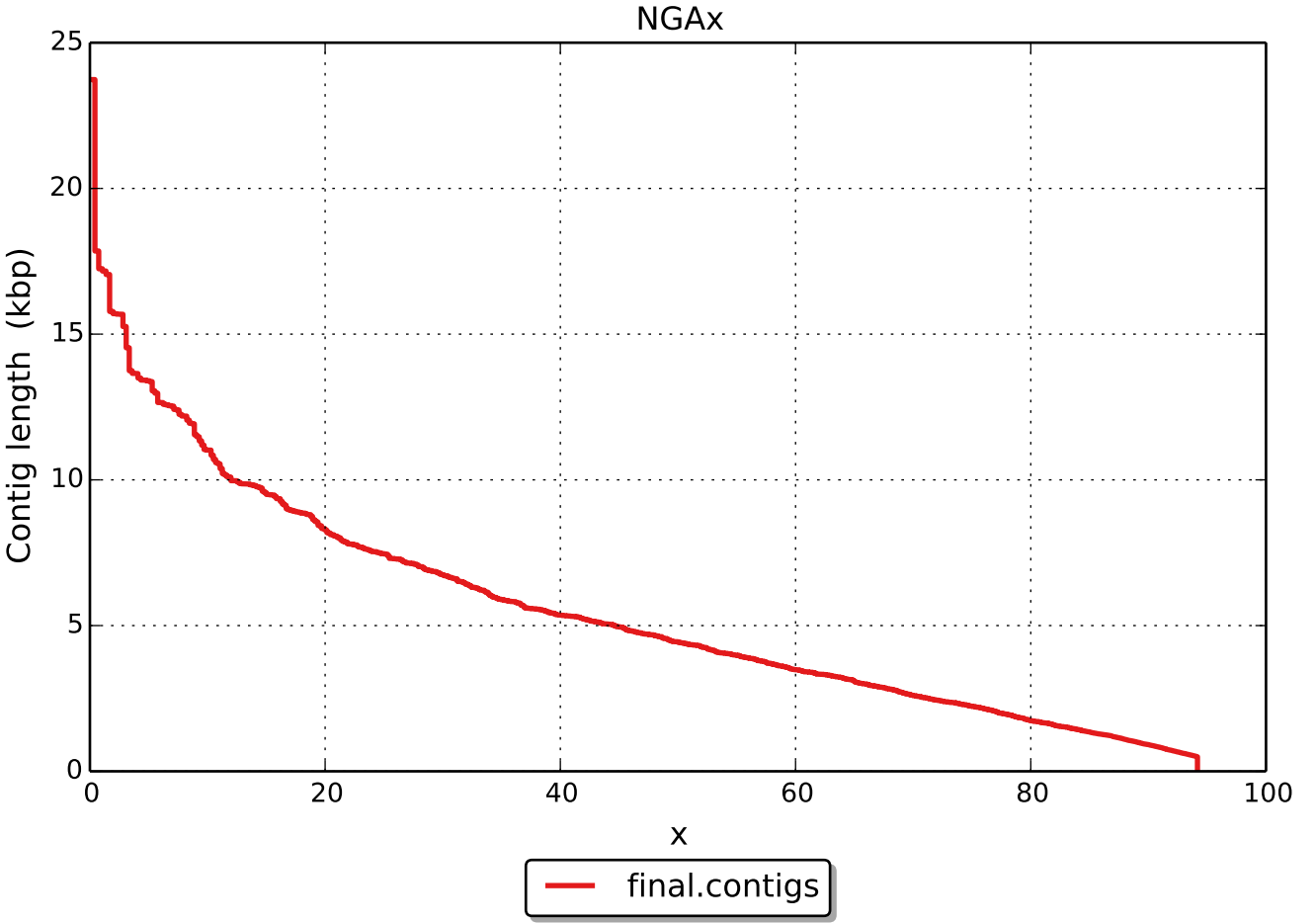

Nx
Contig length (kbp)
25
20
15
10
5
0
0
20
40
60
80
100
x
final.contigs


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


Misassemblies
2.0
1.5
1.0
0.5
0.0
final.contigs
relocations


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
1
2
3
4
5
6
0
300
600
900
1200
1500
1800
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