Report

	final.contigs
# contigs (>= 0 bp)	699
# contigs (>= 1000 bp)	570
Total length (>= 0 bp)	5267968
Total length (>= 1000 bp)	5178832
# contigs	699
Largest contig	54248
Total length	5267968
Reference length	5547323
GC (%)	50.31
Reference GC (%)	50.48
N50	13457
NG50	12941
N75	7955
NG75	7057
L50	116
LG50	126
L75	239
LG75	267
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# unaligned contigs	0 + 4 part
Unaligned length	42862
Genome fraction (%)	93.227
Duplication ratio	1.010
# N's per 100 kbp	0.00
# mismatches per 100 kbp	11.70
# indels per 100 kbp	0.10
Largest alignment	54248
NA50	13378
NGA50	12824
NA75	7619
NGA75	6772
LA50	118
LGA50	129
LA75	244
LGA75	273

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

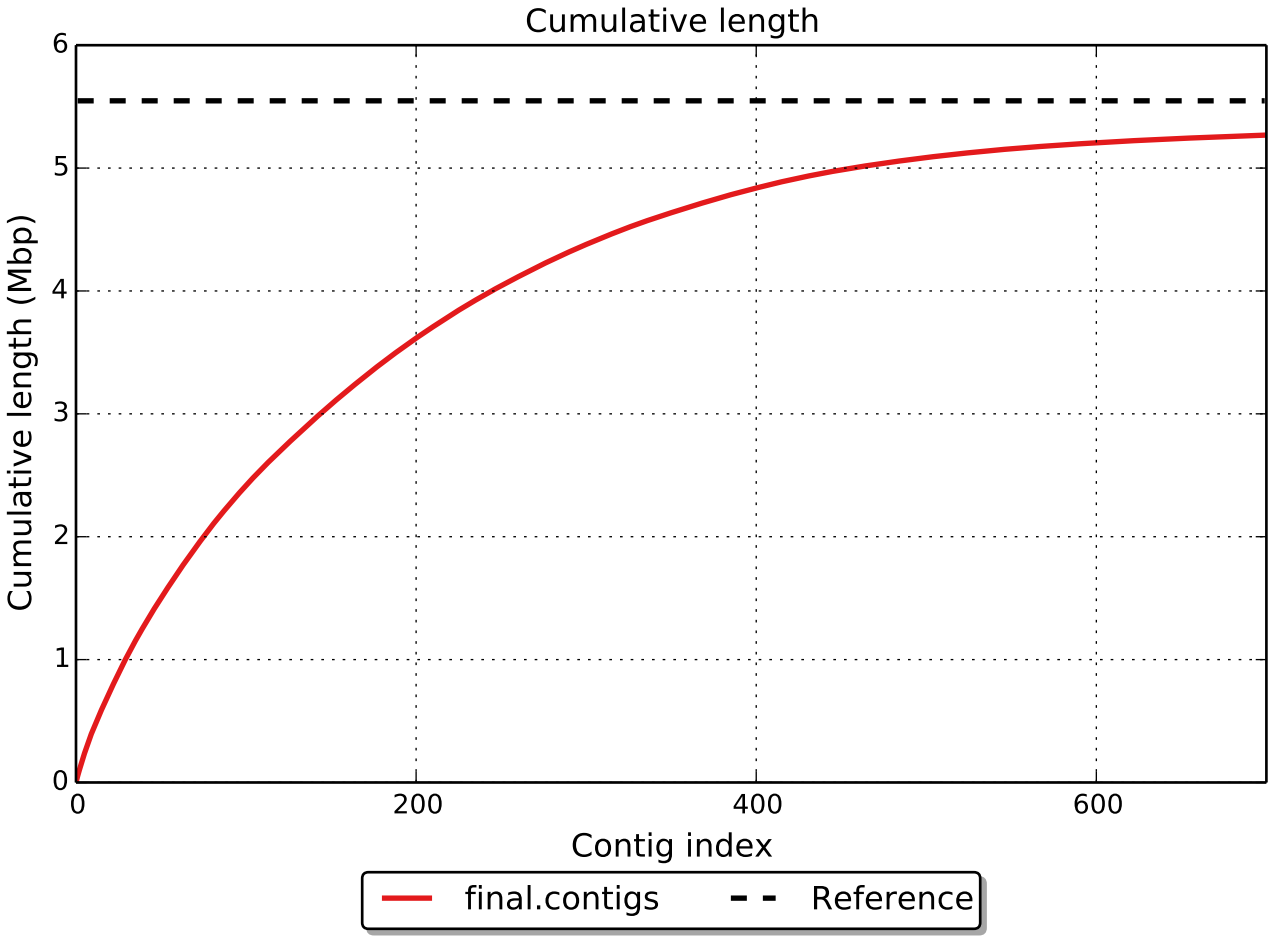
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	4
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# mismatches	605
# indels	5
# short indels	4
# long indels	1
Indels length	10

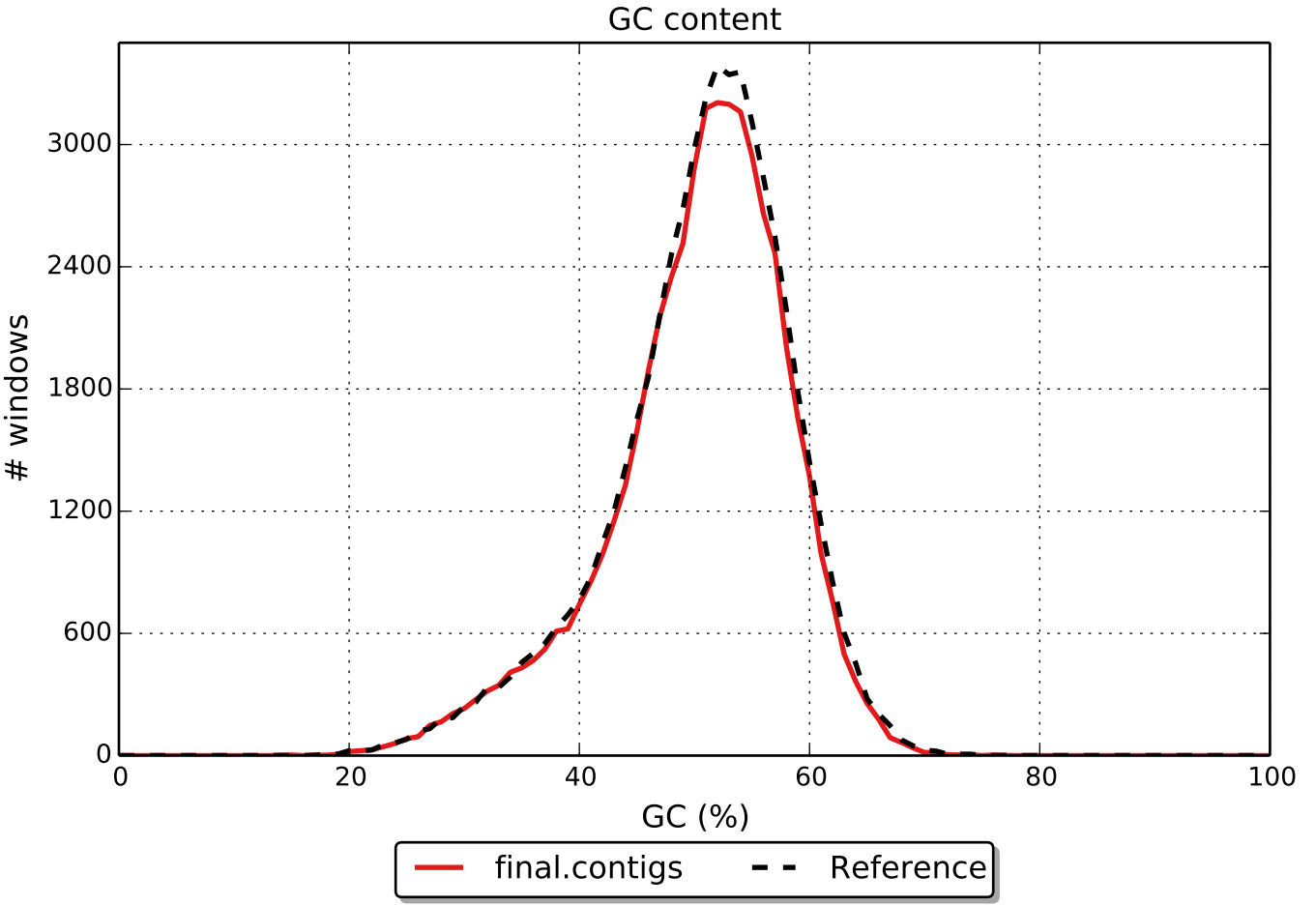
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

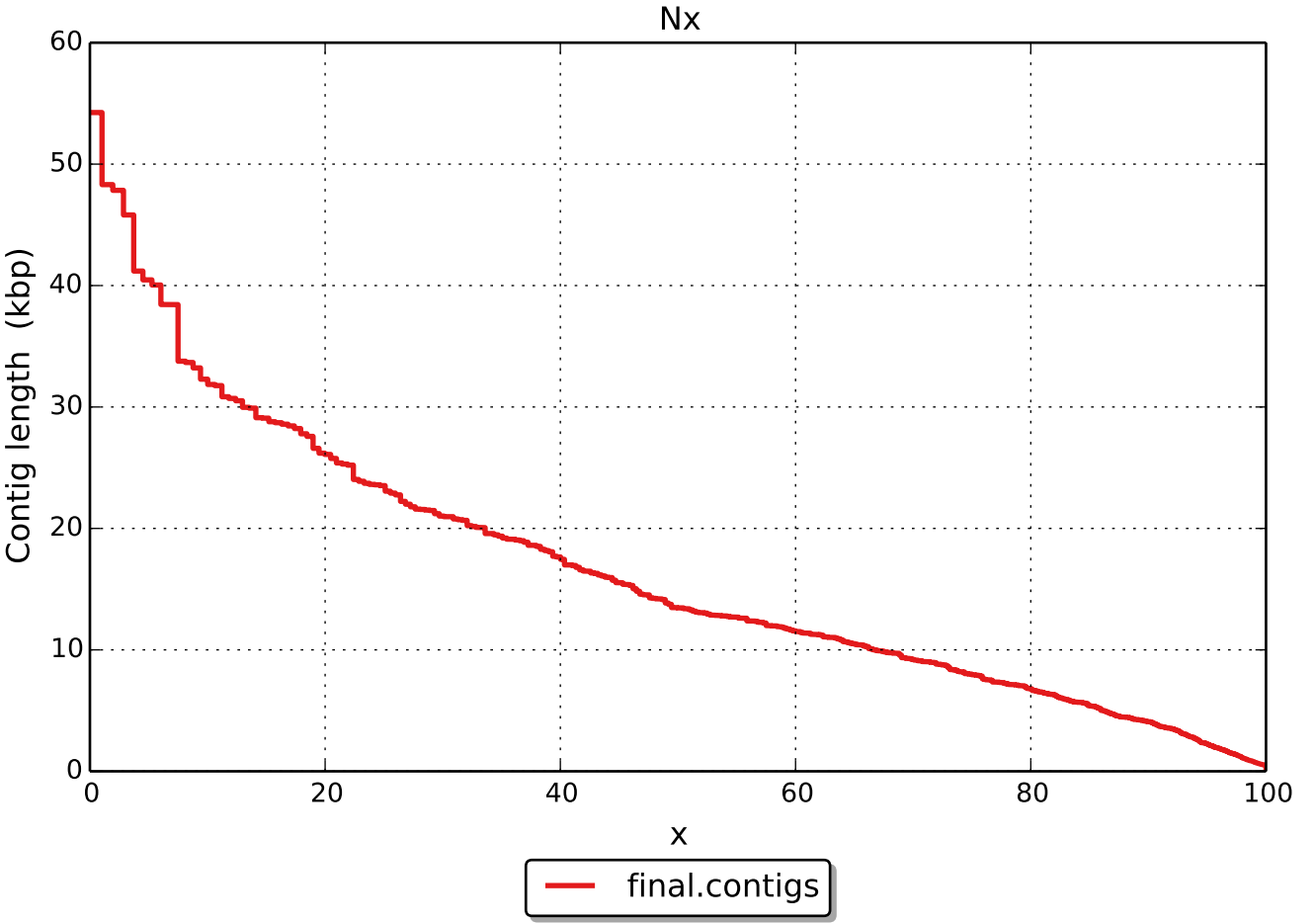
Unaligned report

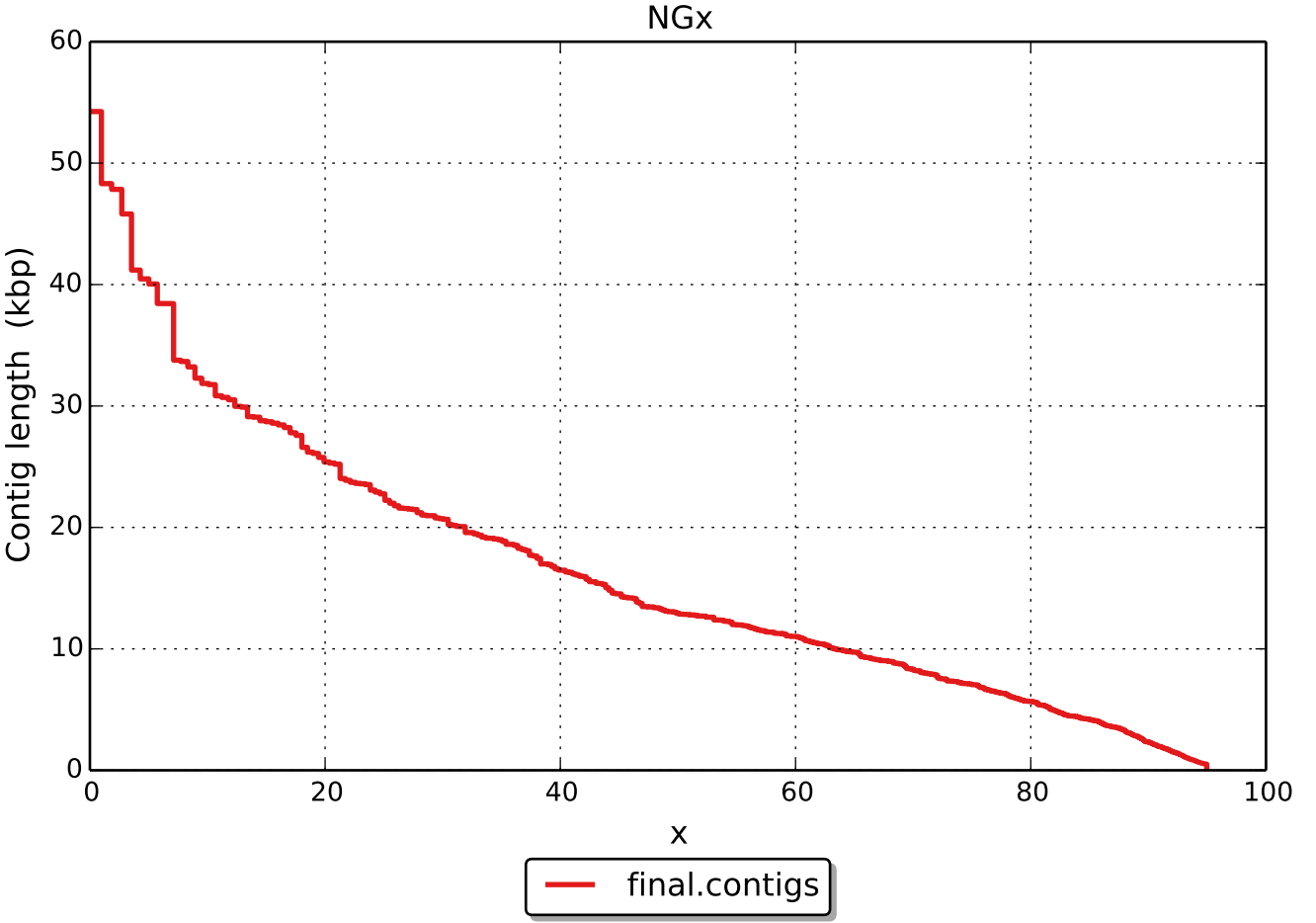
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	4
# with misassembly	0
# both parts are significant	4
Partially unaligned length	42862
# N's	0

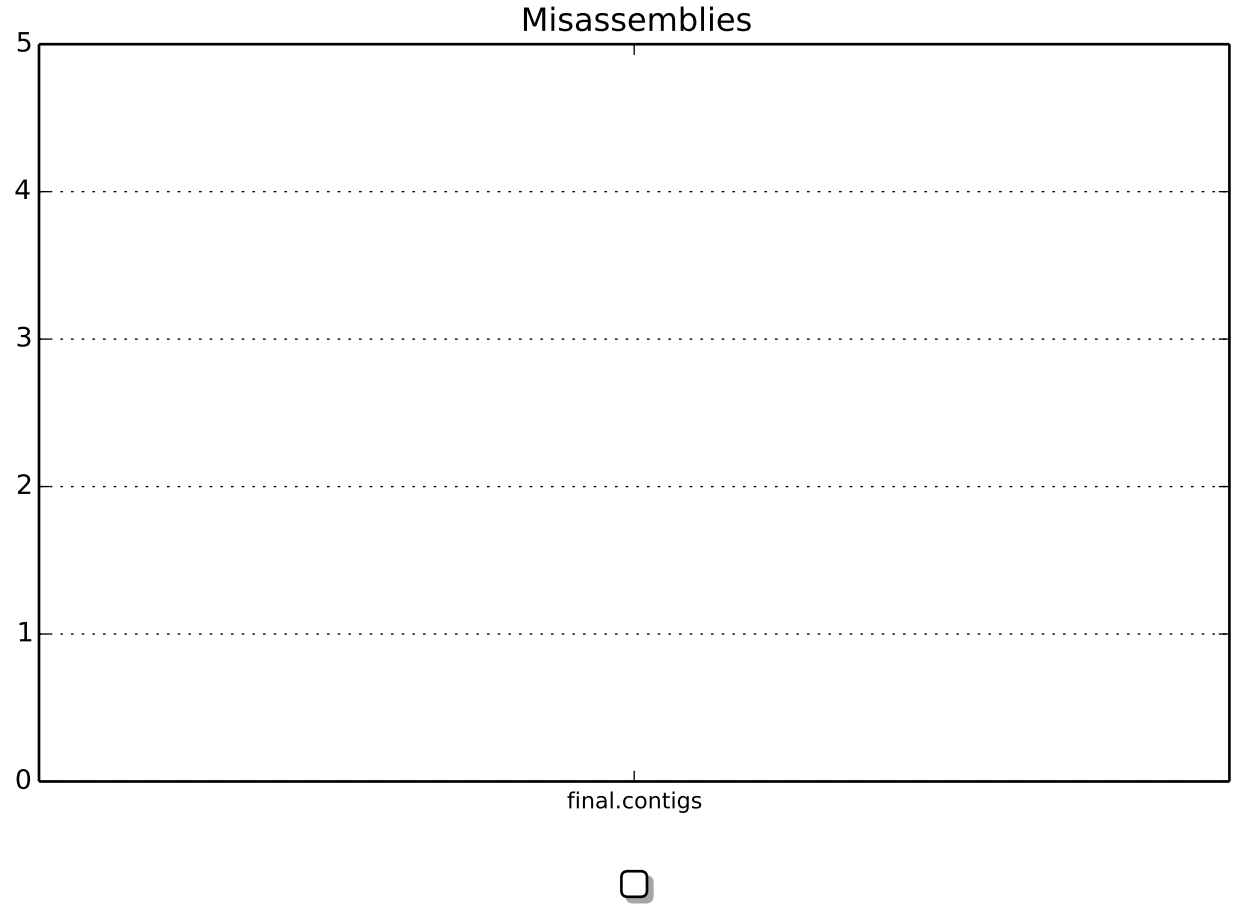
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

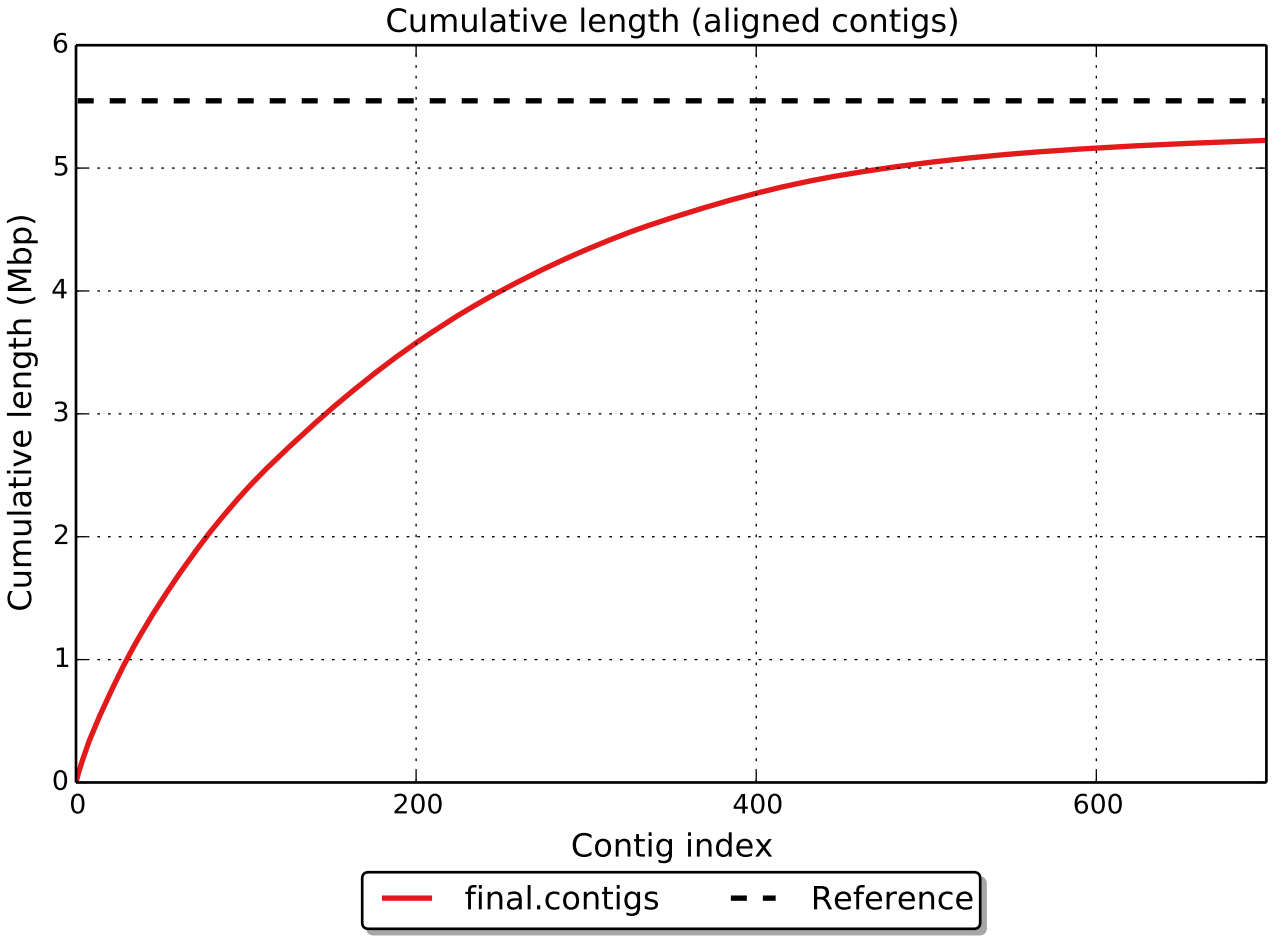

Cumulative length
Cumulative length (Mbp)
0
1
2
3
4
5
6
0
200
400
600
Contig index
final.contigs
Reference

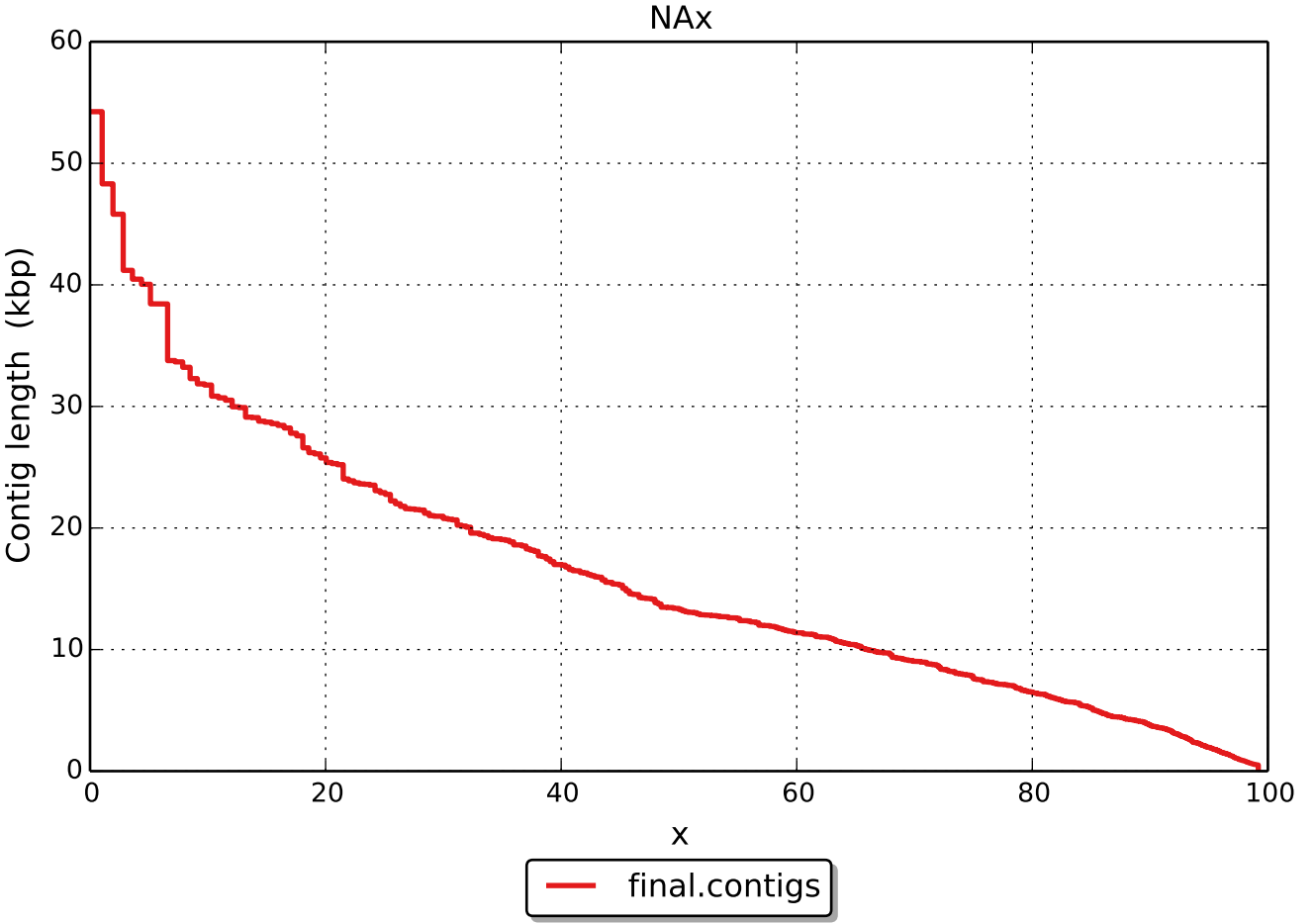

GC content
windows
3000
2400
1800
1200
600
0
0
20
40
60
80
100
GC (%)
final.contigs
Reference

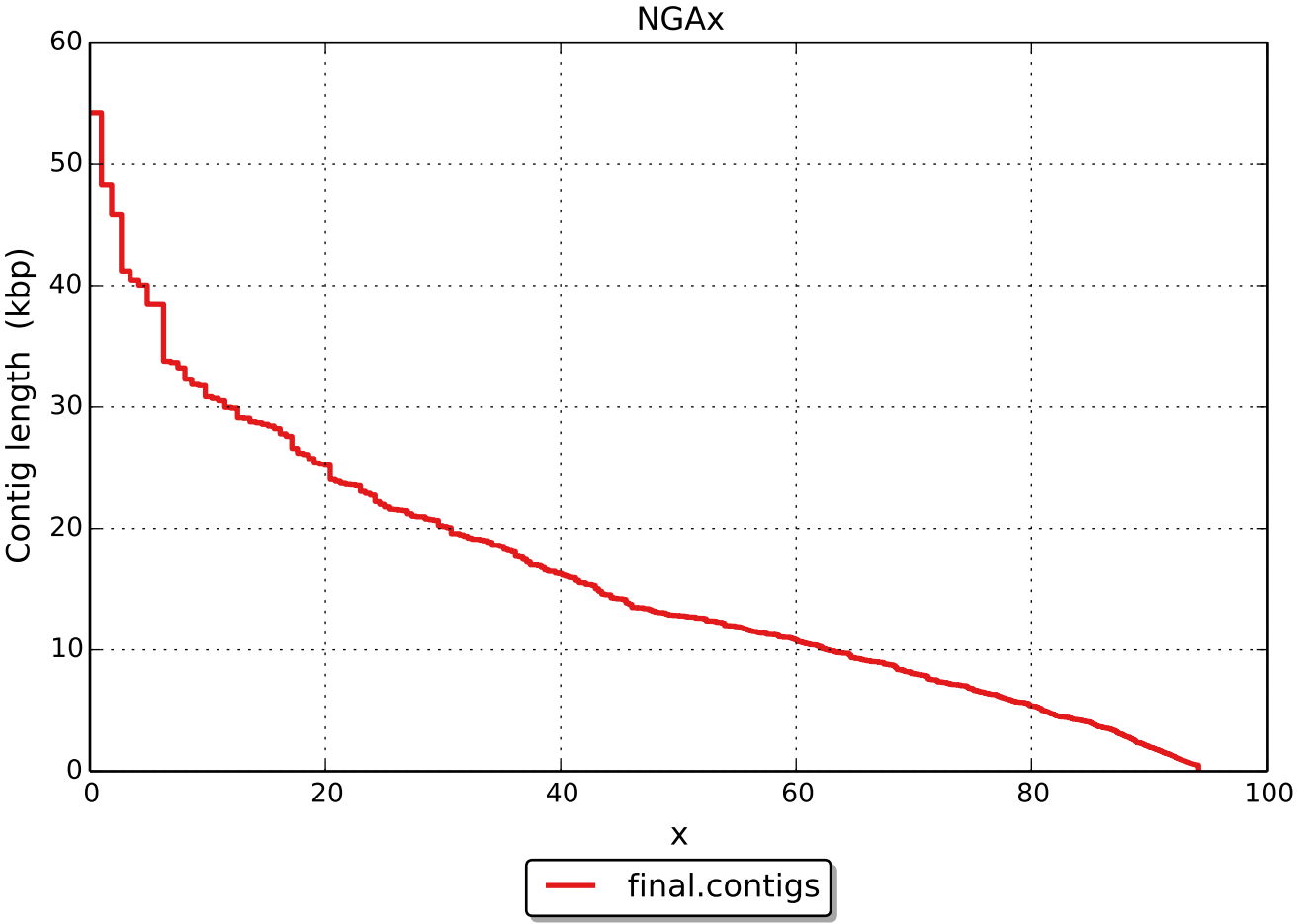

Nx
Contig length (kbp)
60
50
40
30
20
10
0
0
20
40
60
80
100
x
final.contigs


NGx
Contig length (kbp)
0
10
20
30
40
50
60
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
200
400
600
Contig index
final.contigs
Reference


NAx
Contig length (kbp)
60
50
40
30
20
10
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (kbp)
60
50
40
30
20
10
0
0
20
40
60
80
100
x
final.contigs