Report

	final.contigs
# contigs (>= 0 bp)	589
# contigs (>= 1000 bp)	469
Total length (>= 0 bp)	5221055
Total length (>= 1000 bp)	5140933
# contigs	589
Largest contig	72554
Total length	5221055
Reference length	5547323
GC (%)	50.29
Reference GC (%)	50.48
N50	18218
NG50	17383
N75	9367
NG75	8046
L50	92
LG50	101
L75	190
LG75	218
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# unaligned contigs	0 + 1 part
Unaligned length	7919
Genome fraction (%)	93.348
Duplication ratio	1.007
# N's per 100 kbp	0.00
# mismatches per 100 kbp	10.56
# indels per 100 kbp	0.15
Largest alignment	72554
NA50	18218
NGA50	17361
NA75	9264
NGA75	8041
LA50	92
LGA50	102
LA75	191
LGA75	219

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

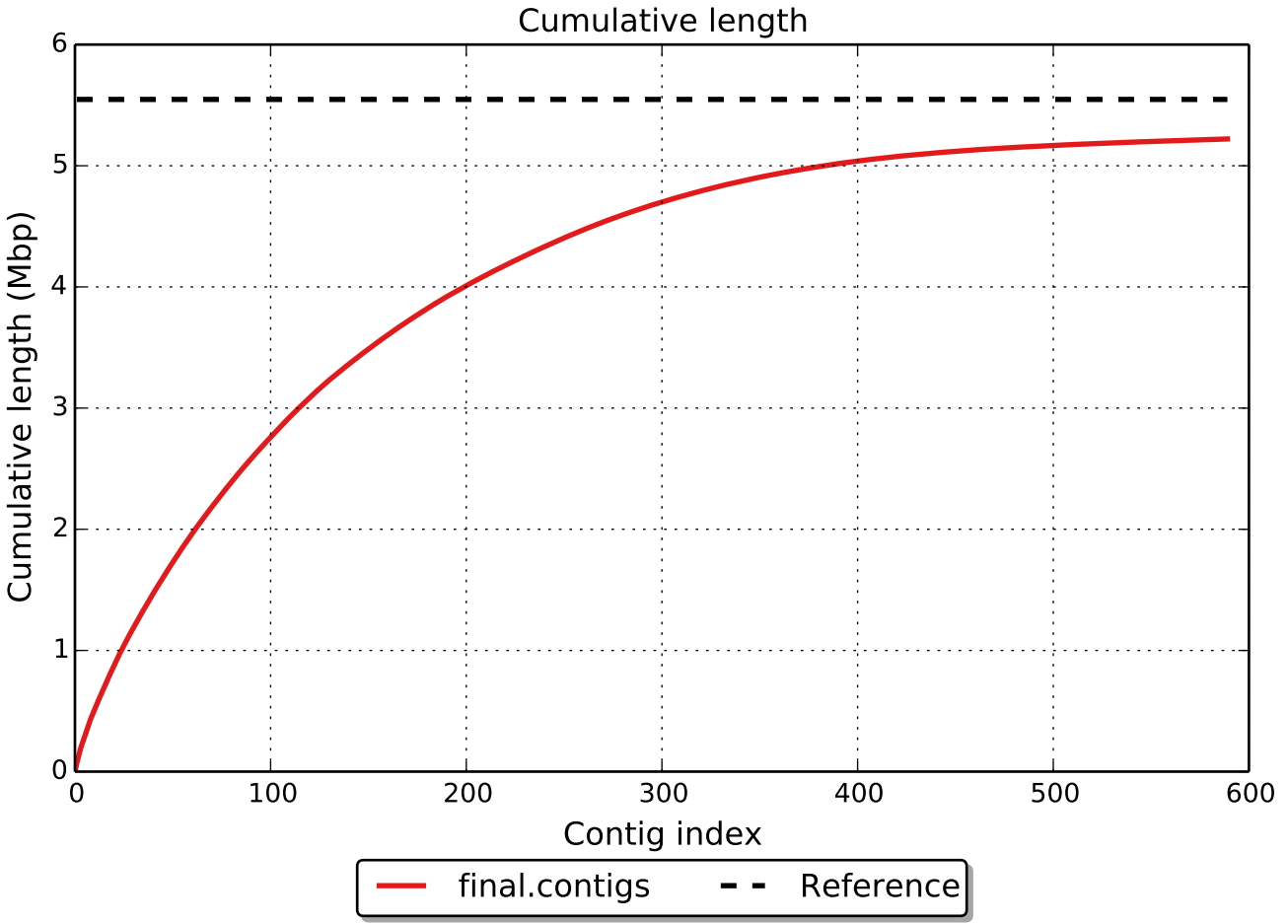
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	1
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# mismatches	547
# indels	8
# short indels	6
# long indels	2
Indels length	74

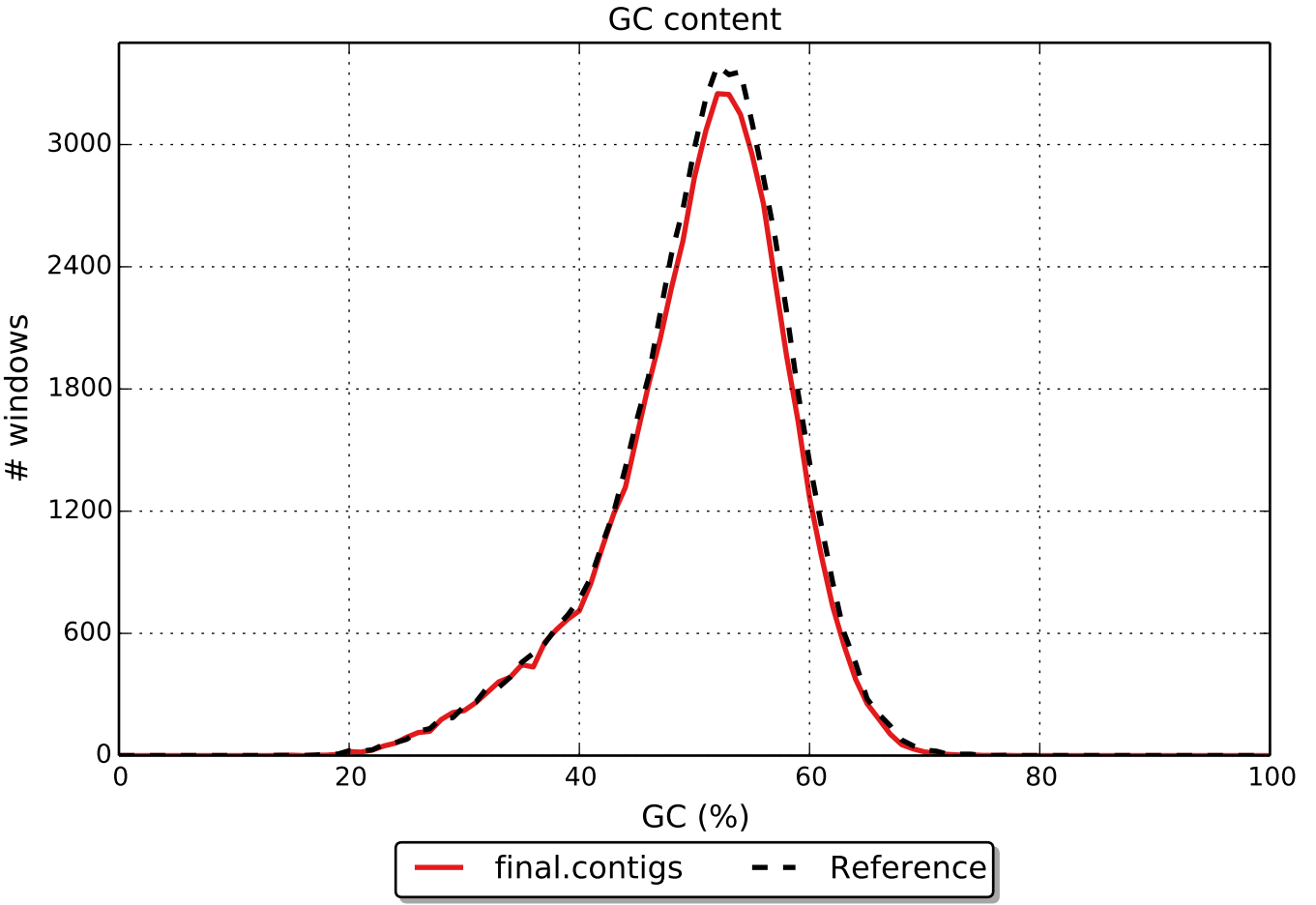
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

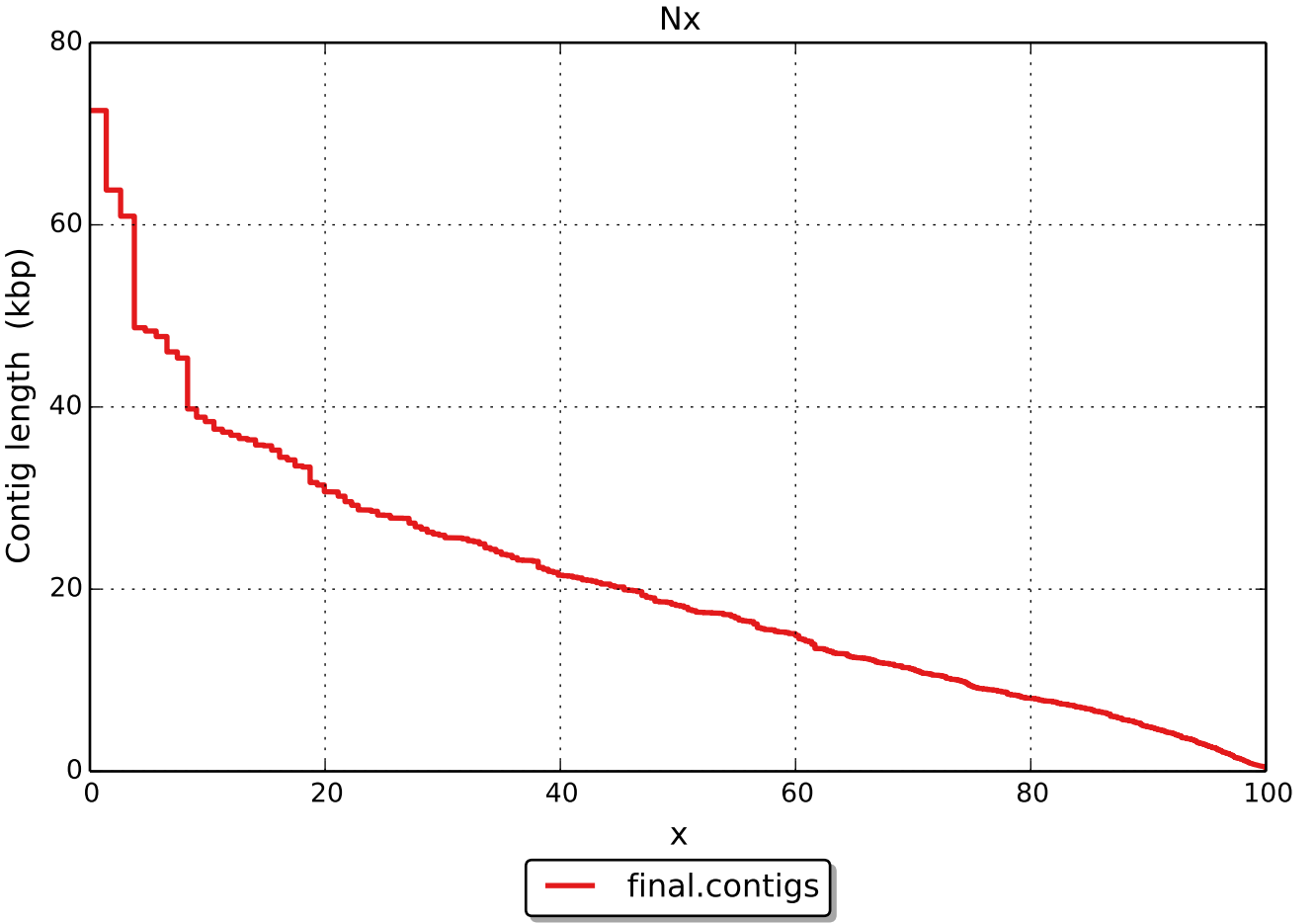
Unaligned report

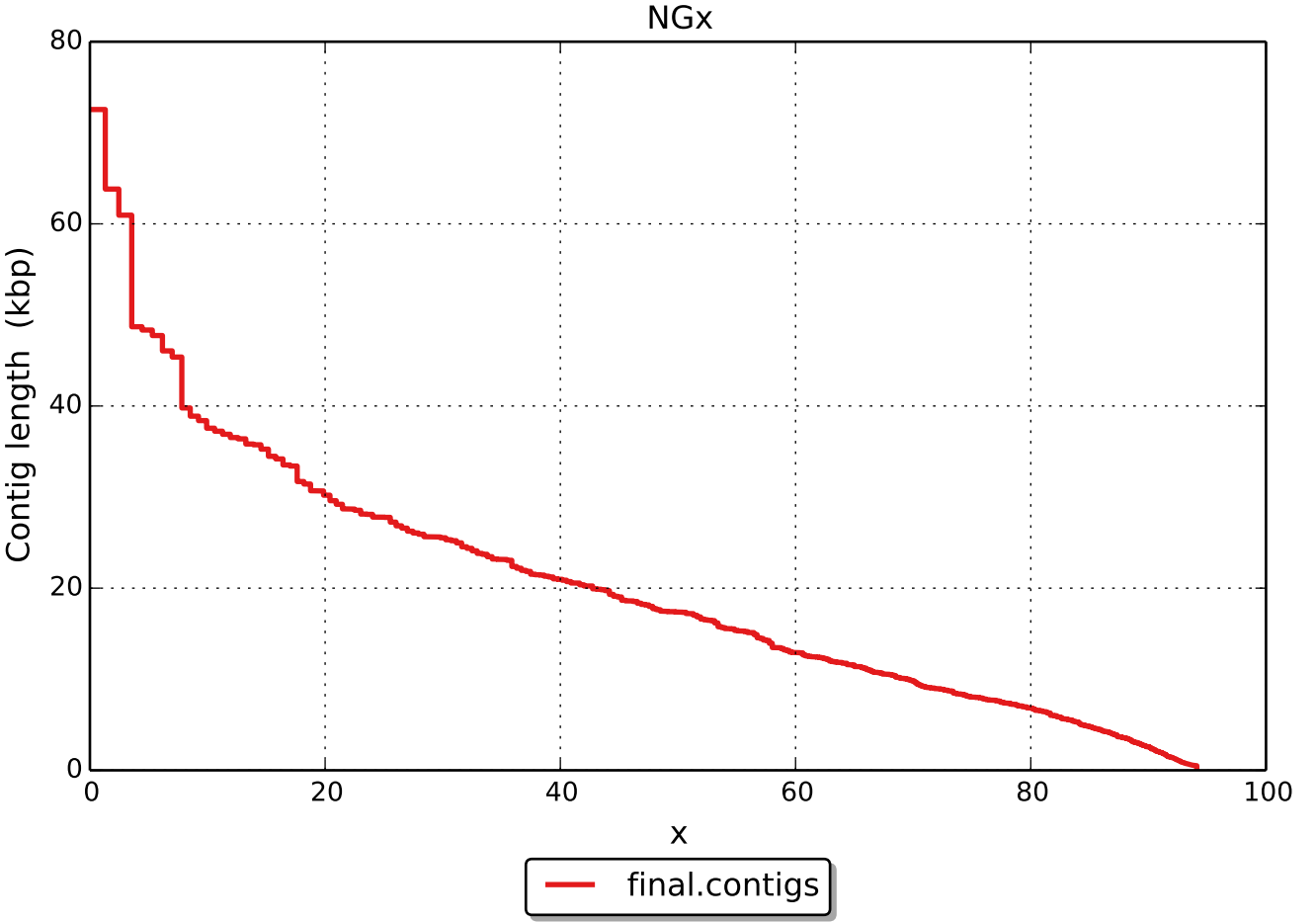
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	1
Partially unaligned length	7919
# N's	0

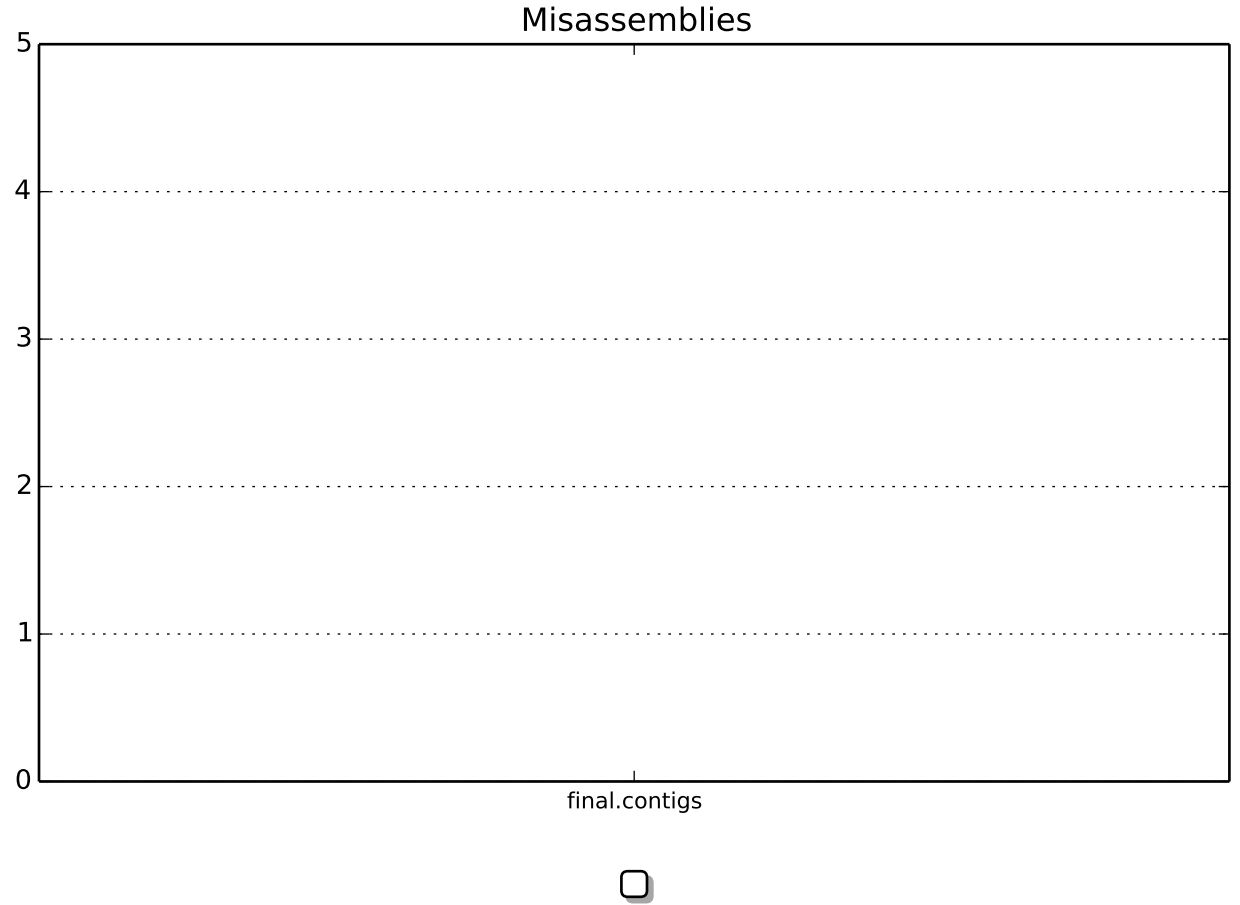
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

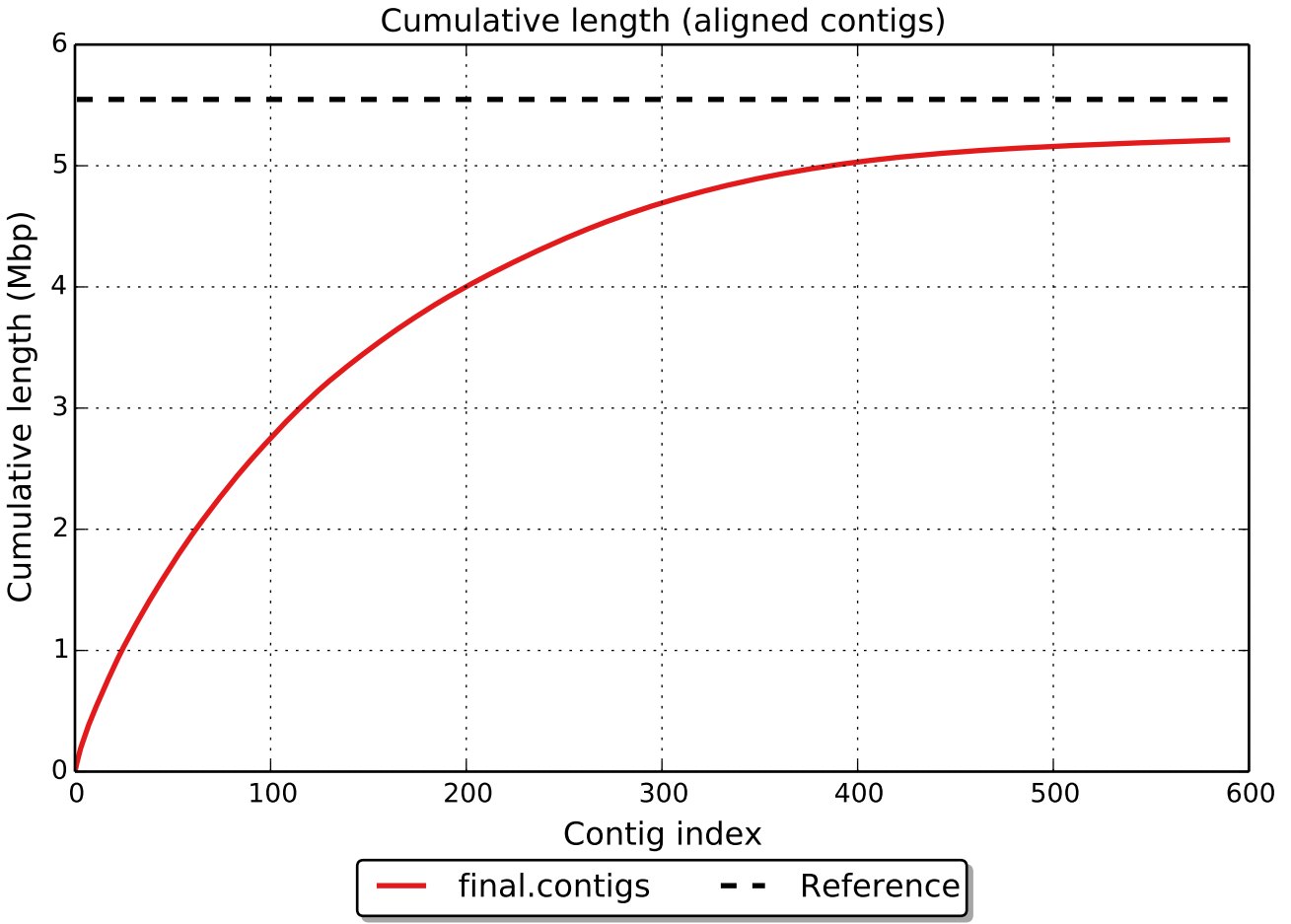

Cumulative length
Cumulative length (Mbp)
0
1
2
3
4
5
6
0
100
200
300
400
500
600
Contig index
final.contigs
Reference

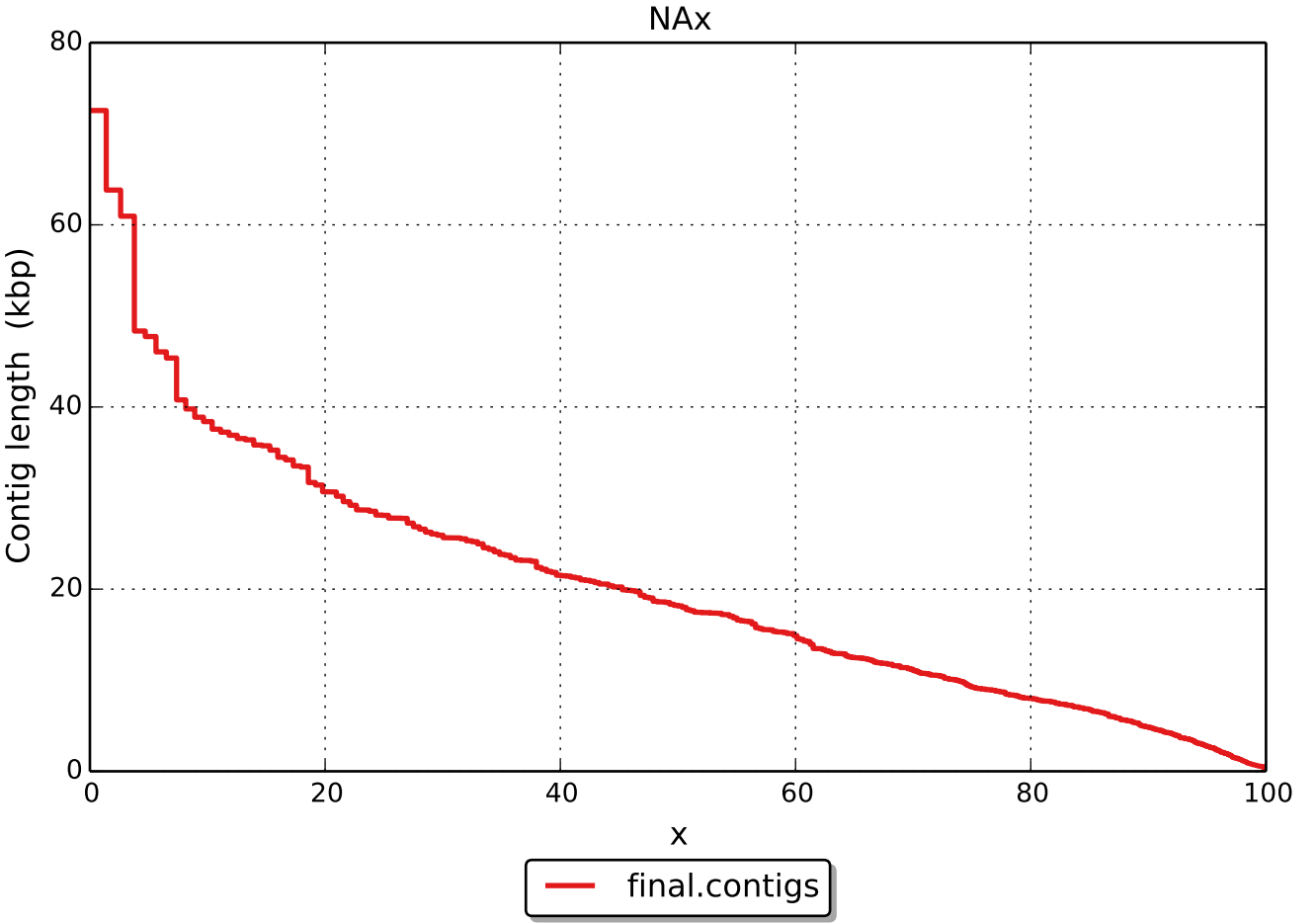

GC content
windows
3000
2400
1800
1200
600
0
0
20
40
60
80
100
GC (%)
final.contigs
Reference

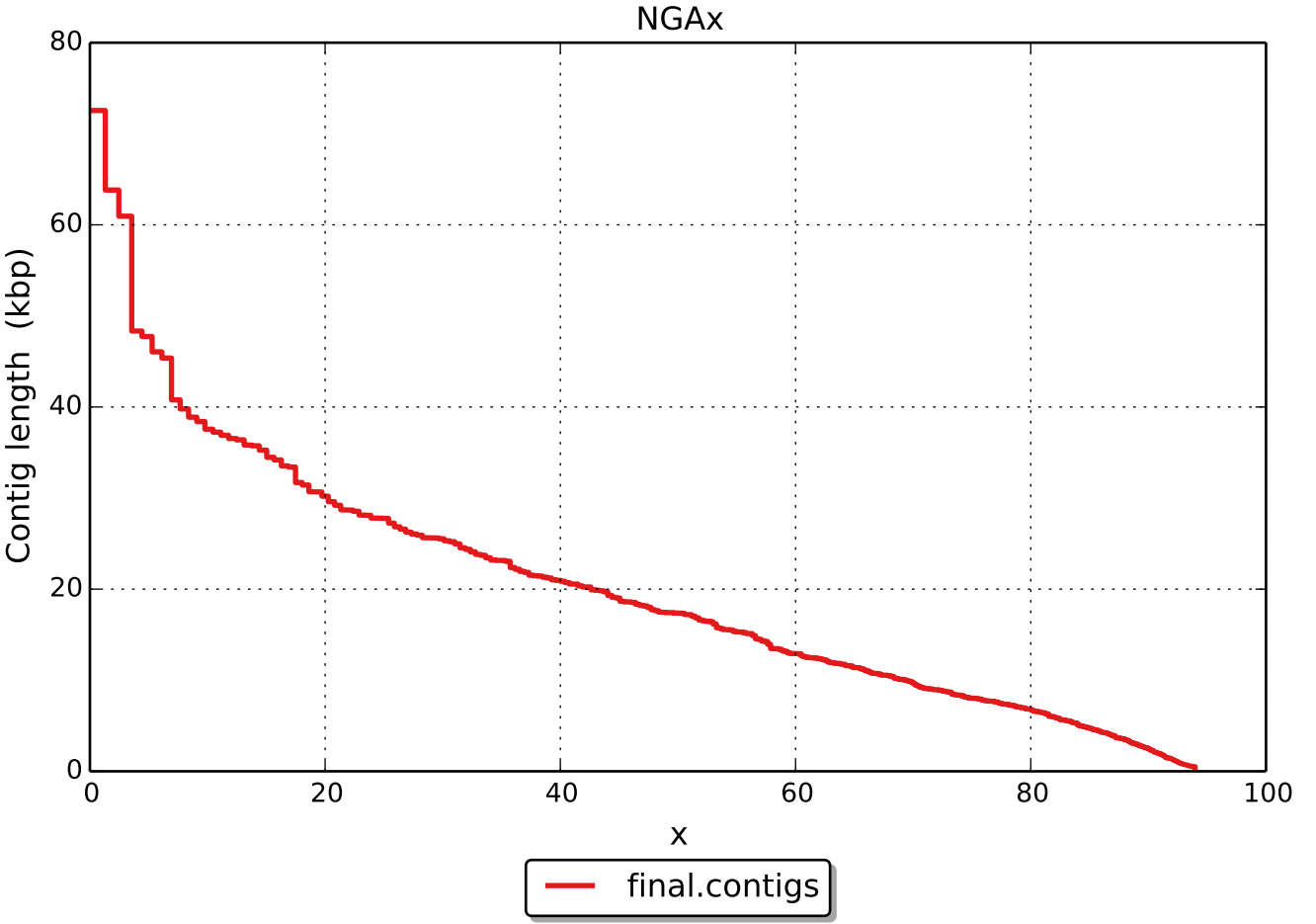

Nx
Contig length (kbp)
80
60
40
20
0
0
20
40
60
80
100
x
final.contigs


NGx
Contig length (kbp)
80
60
40
20
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)
Contig index
0
1
2
3
4
5
6
0
100
200
300
400
500
600
final.contigs
Reference


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


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