Report

	final.contigs
# contigs (>= 0 bp)	2206
# contigs (>= 1000 bp)	1383
Total length (>= 0 bp)	4958288
Total length (>= 1000 bp)	4403979
# contigs	2206
Largest contig	18963
Total length	4958288
Reference length	5478683
GC (%)	50.26
Reference GC (%)	50.49
N50	3641
NG50	3208
N75	1873
NG75	1363
L50	417
LG50	493
L75	889
LG75	1131
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	87.878
Duplication ratio	1.030
# N's per 100 kbp	0.00
# mismatches per 100 kbp	600.83
# indels per 100 kbp	0.08
Largest alignment	18963
NA50	3641
NGA50	3208
NA75	1873
NGA75	1363
LA50	417
LGA50	493
LA75	889
LGA75	1131

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

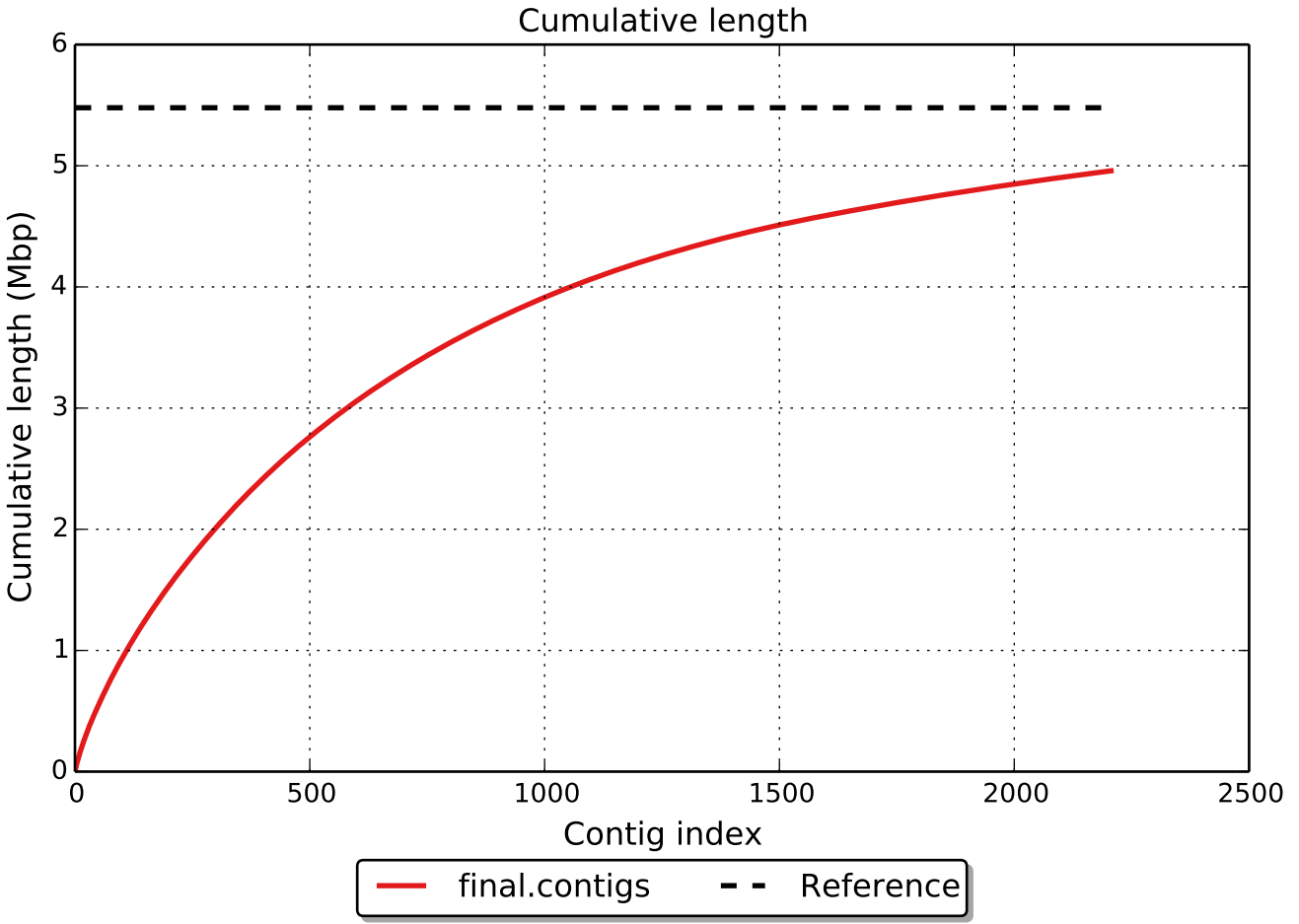
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	28927
# indels	4
# short indels	2
# long indels	2
Indels length	26

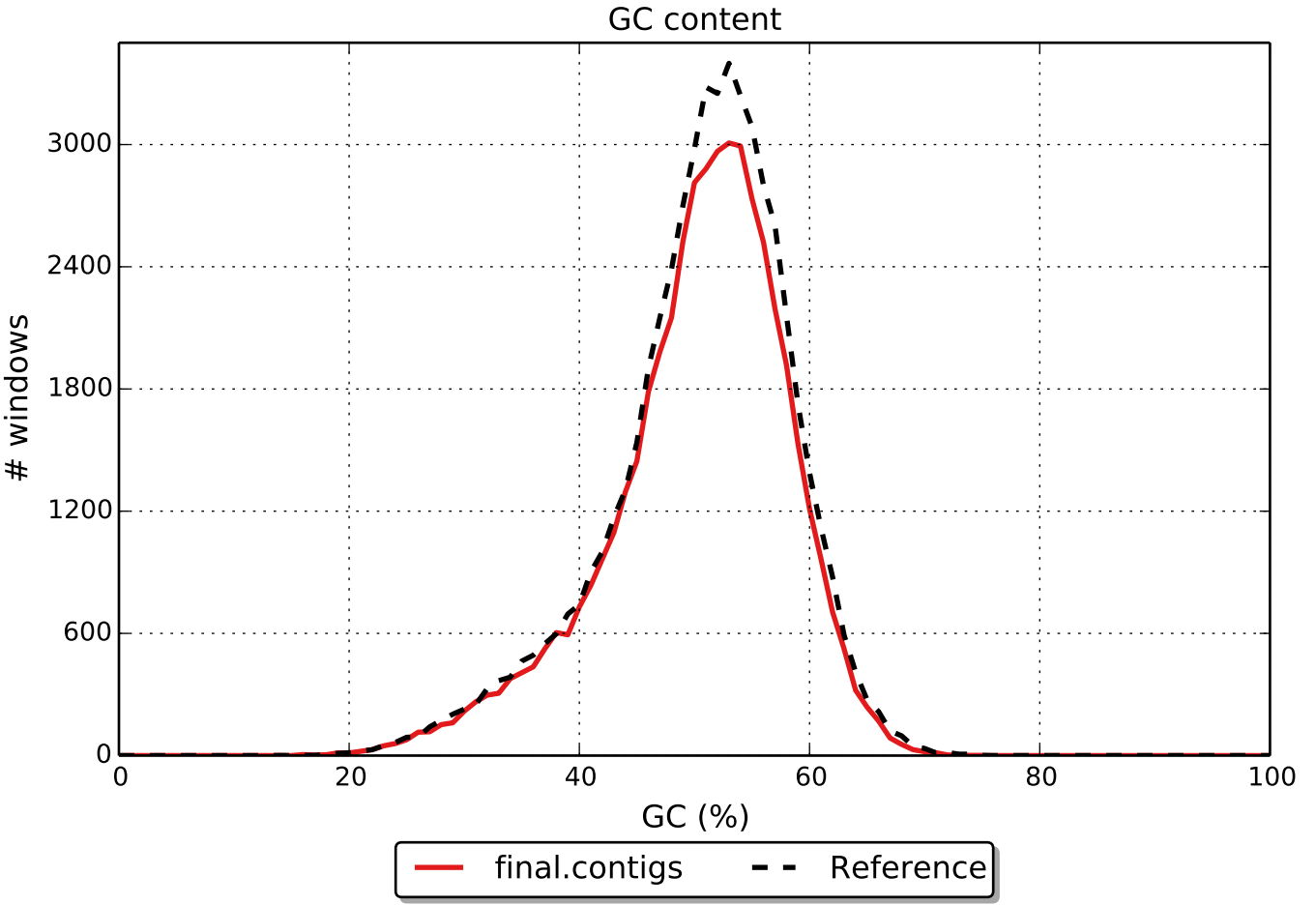
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

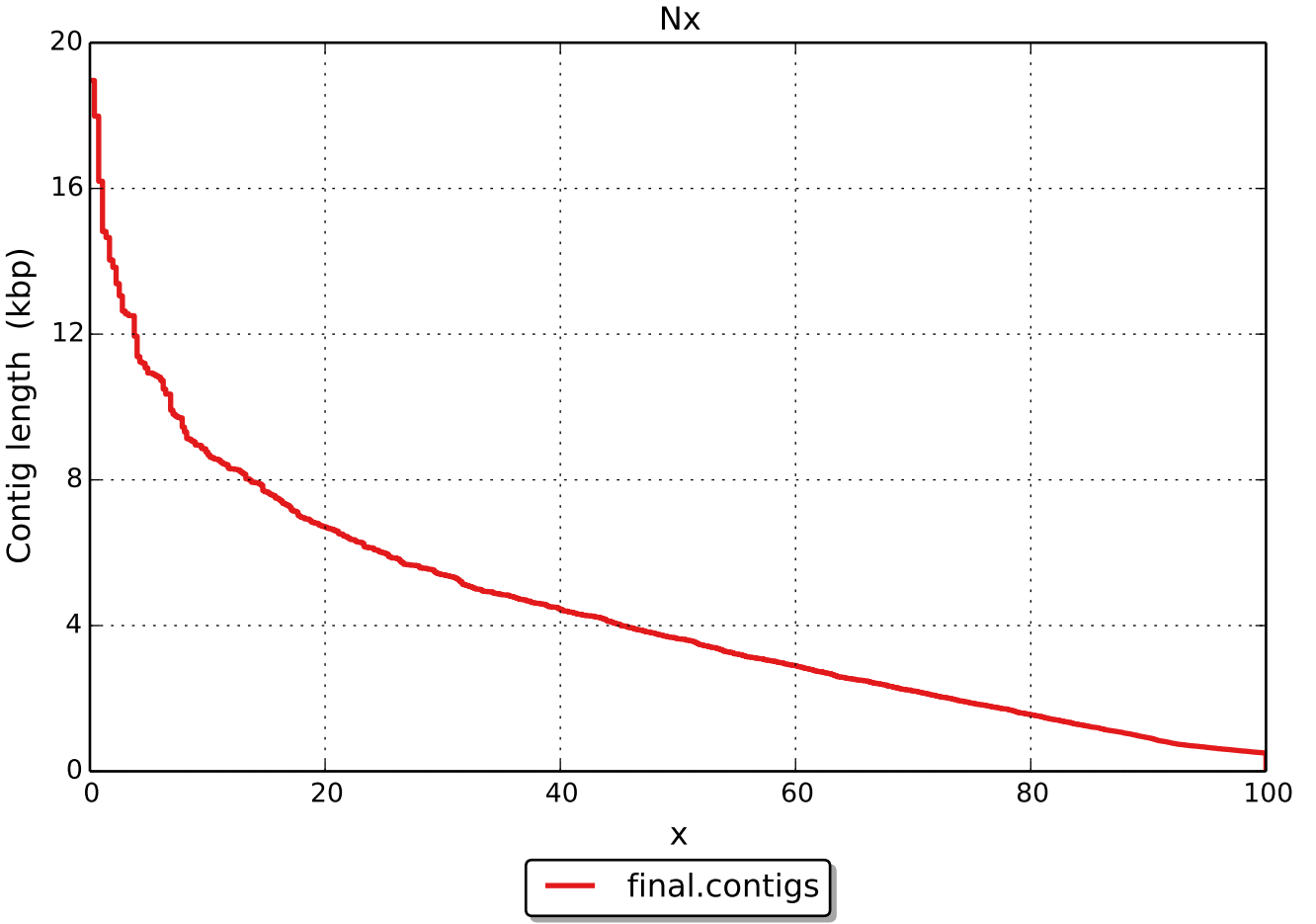
Unaligned report

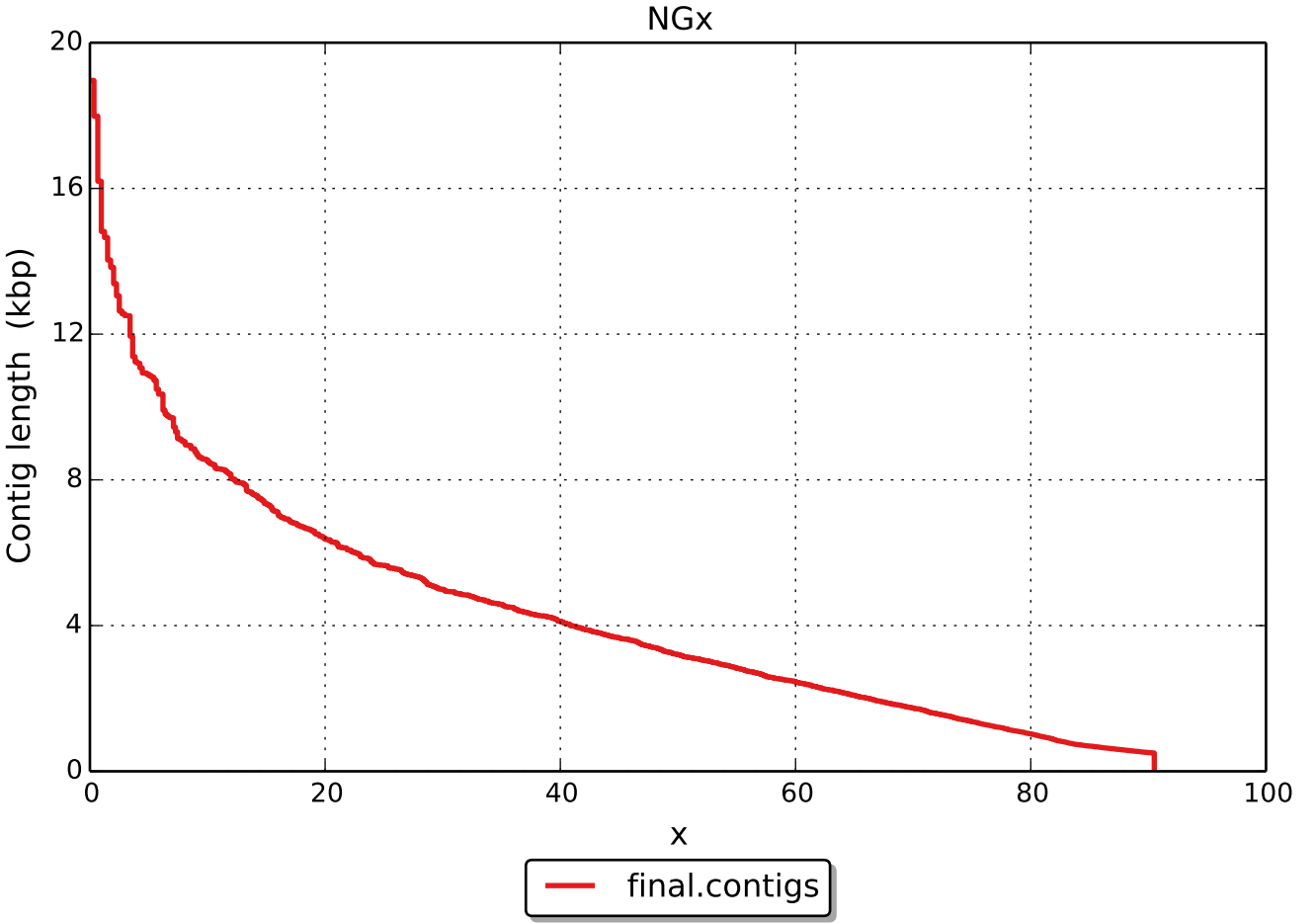
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

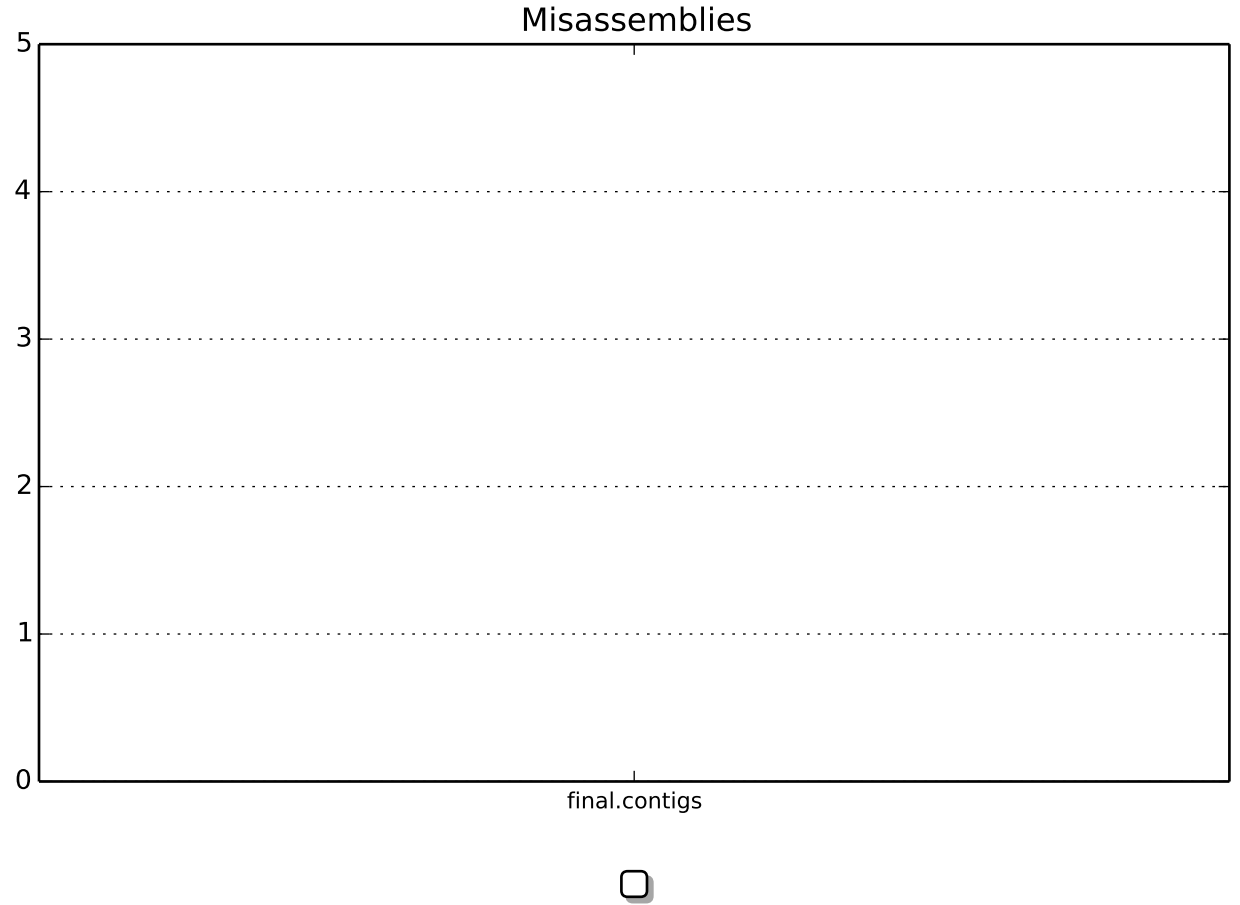
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

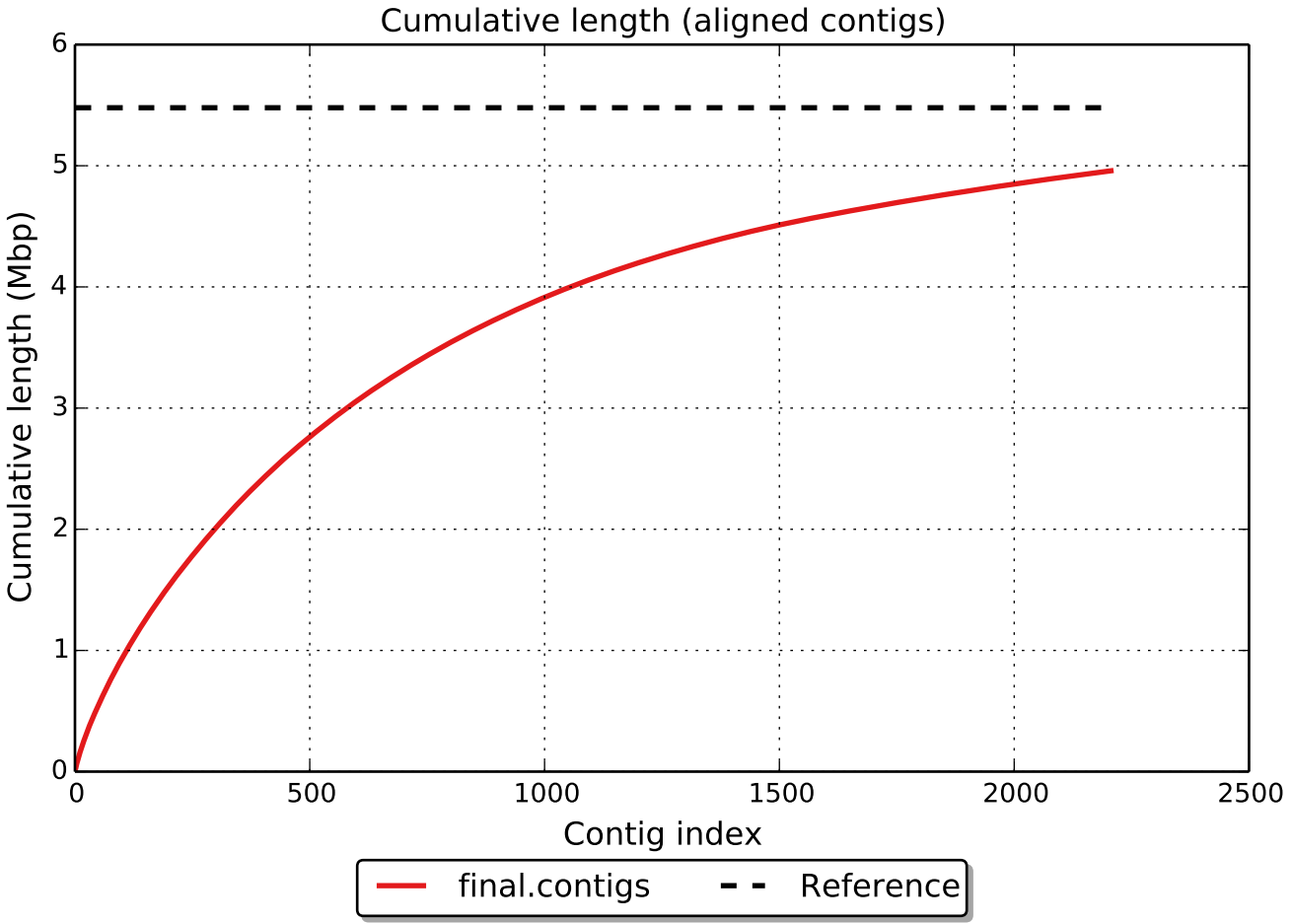

Cumulative length
Cumulative length (Mbp)
0
1
2
3
4
5
6
0
500
1000
1500
2000
2500
Contig index
final.contigs
Reference

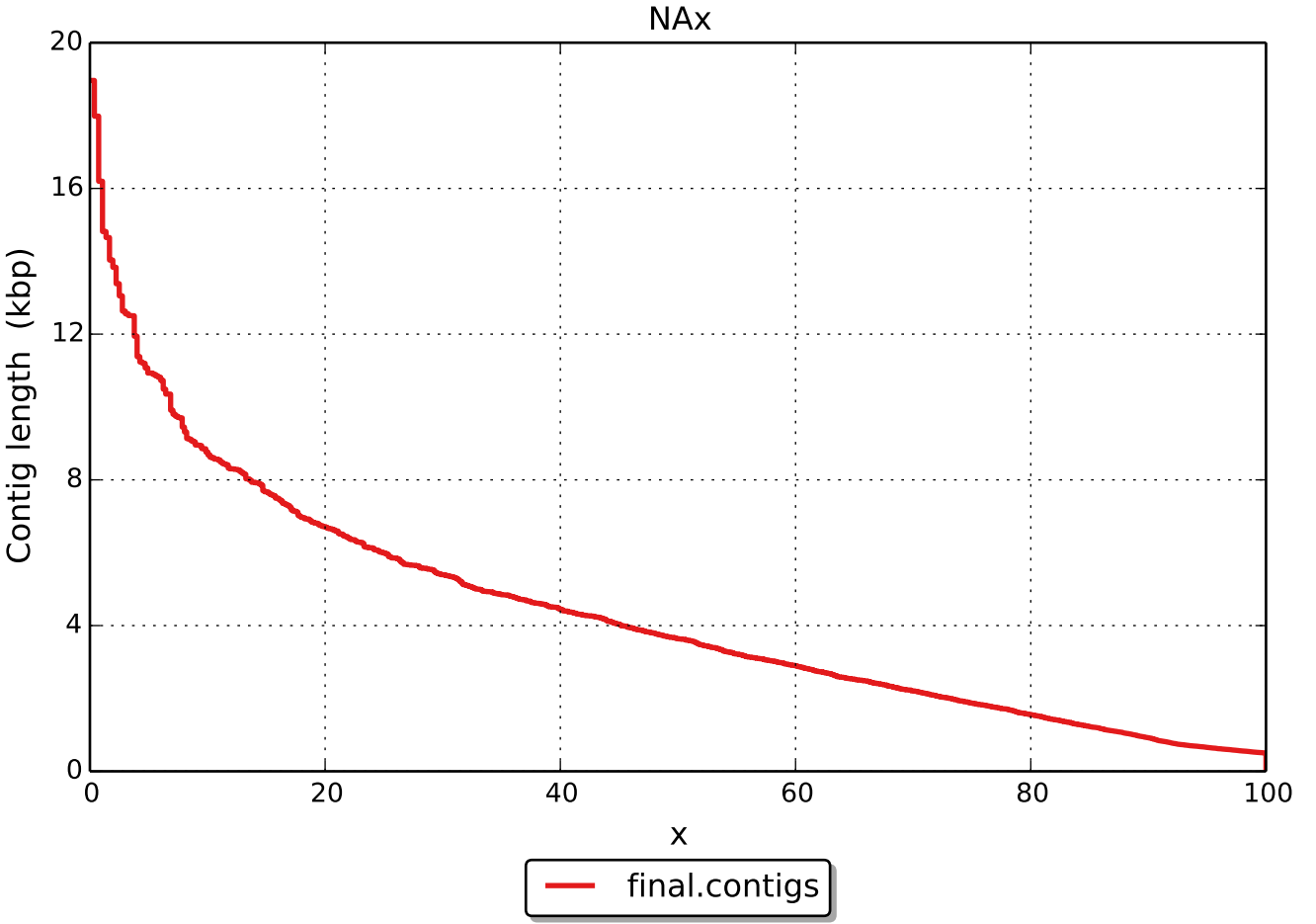

GC content
windows
3000
2400
1800
1200
600
0
0
20
40
60
80
100
GC (%)
final.contigs
Reference

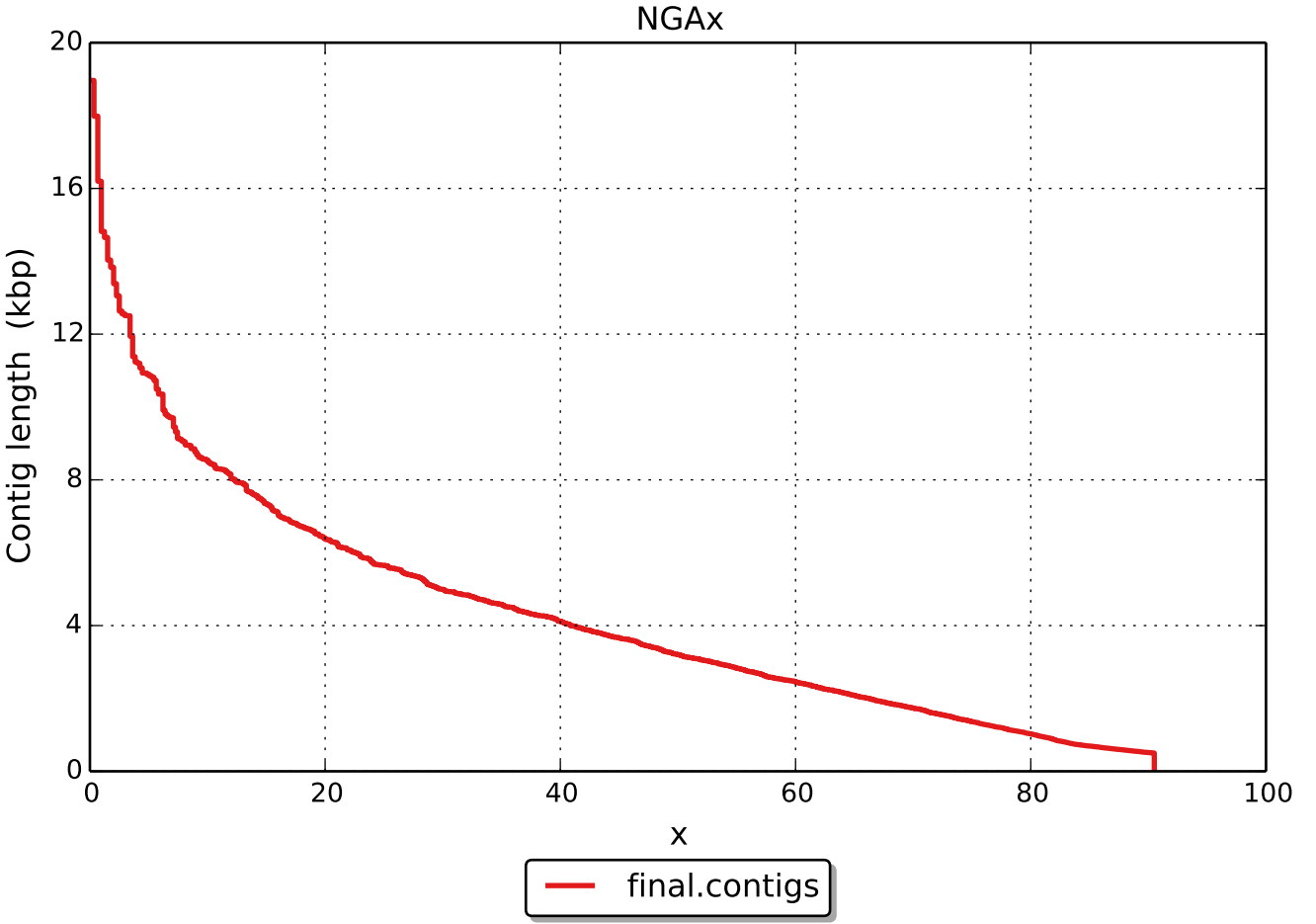

Nx
Contig length (kbp)
20
16
12
8
4
0
0
20
40
60
80
100
x
final.contigs


NGx
Contig length (kbp)
20
16
12
8
4
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
500
1000
1500
2000
2500
Contig index
final.contigs
Reference


NAx
Contig length (kbp)
20
16
12
8
4
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (kbp)
20
16
12
8
4
0
0
20
40
60
80
100
x
final.contigs