Report

	final.contigs
# contigs (>= 0 bp)	2282
# contigs (>= 1000 bp)	1382
Total length (>= 0 bp)	5003124
Total length (>= 1000 bp)	4400255
# contigs	2282
Largest contig	18963
Total length	5003124
Reference length	5478683
GC (%)	50.27
Reference GC (%)	50.49
N50	3627
NG50	3200
N75	1829
NG75	1363
L50	424
LG50	494
L75	909
LG75	1134
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	88.532
Duplication ratio	1.031
# N's per 100 kbp	0.00
# mismatches per 100 kbp	623.27
# indels per 100 kbp	0.08
Largest alignment	18963
NA50	3627
NGA50	3200
NA75	1829
NGA75	1363
LA50	424
LGA50	494
LA75	909
LGA75	1134

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

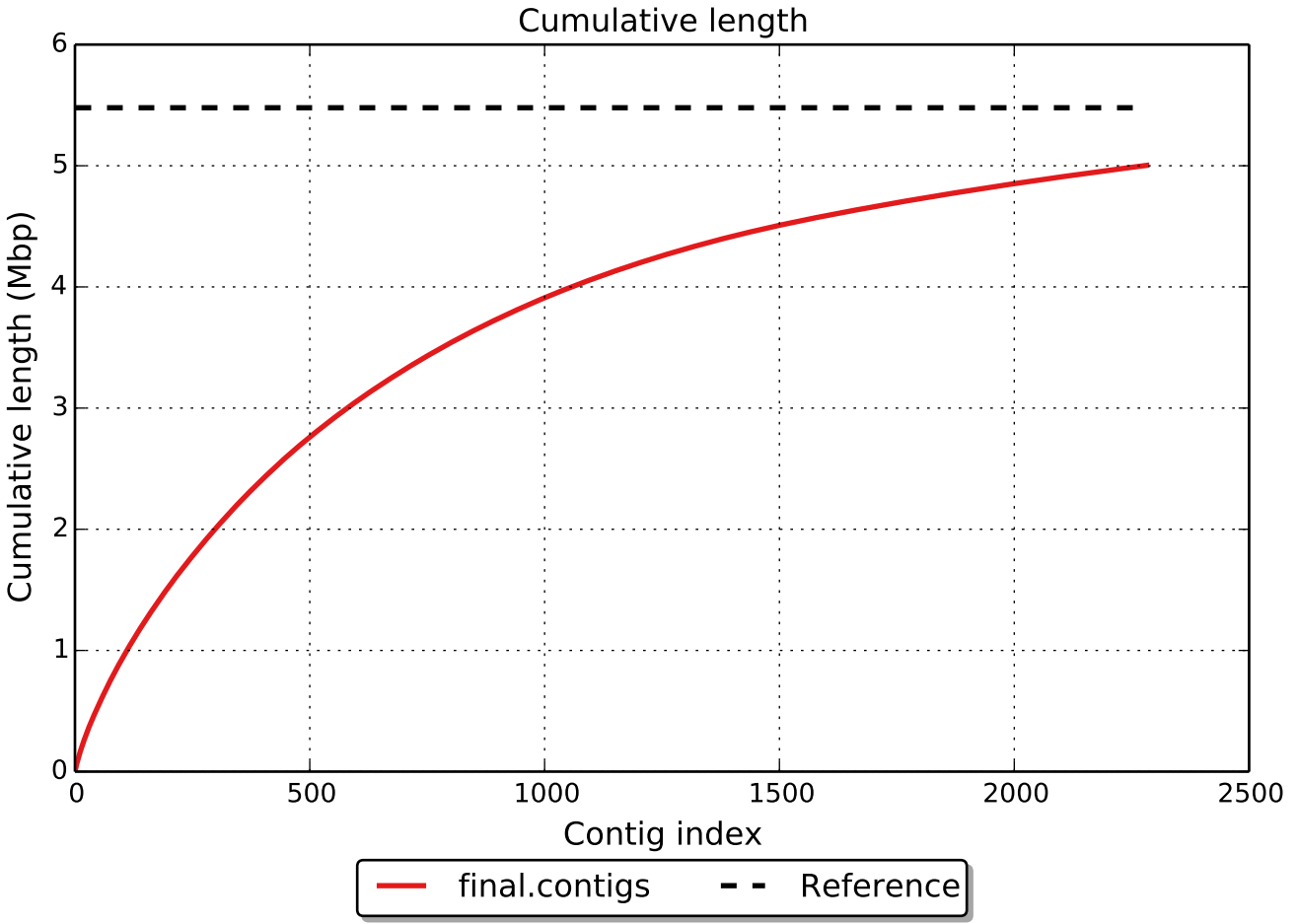
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# mismatches	30231
# indels	4
# short indels	2
# long indels	2
Indels length	26

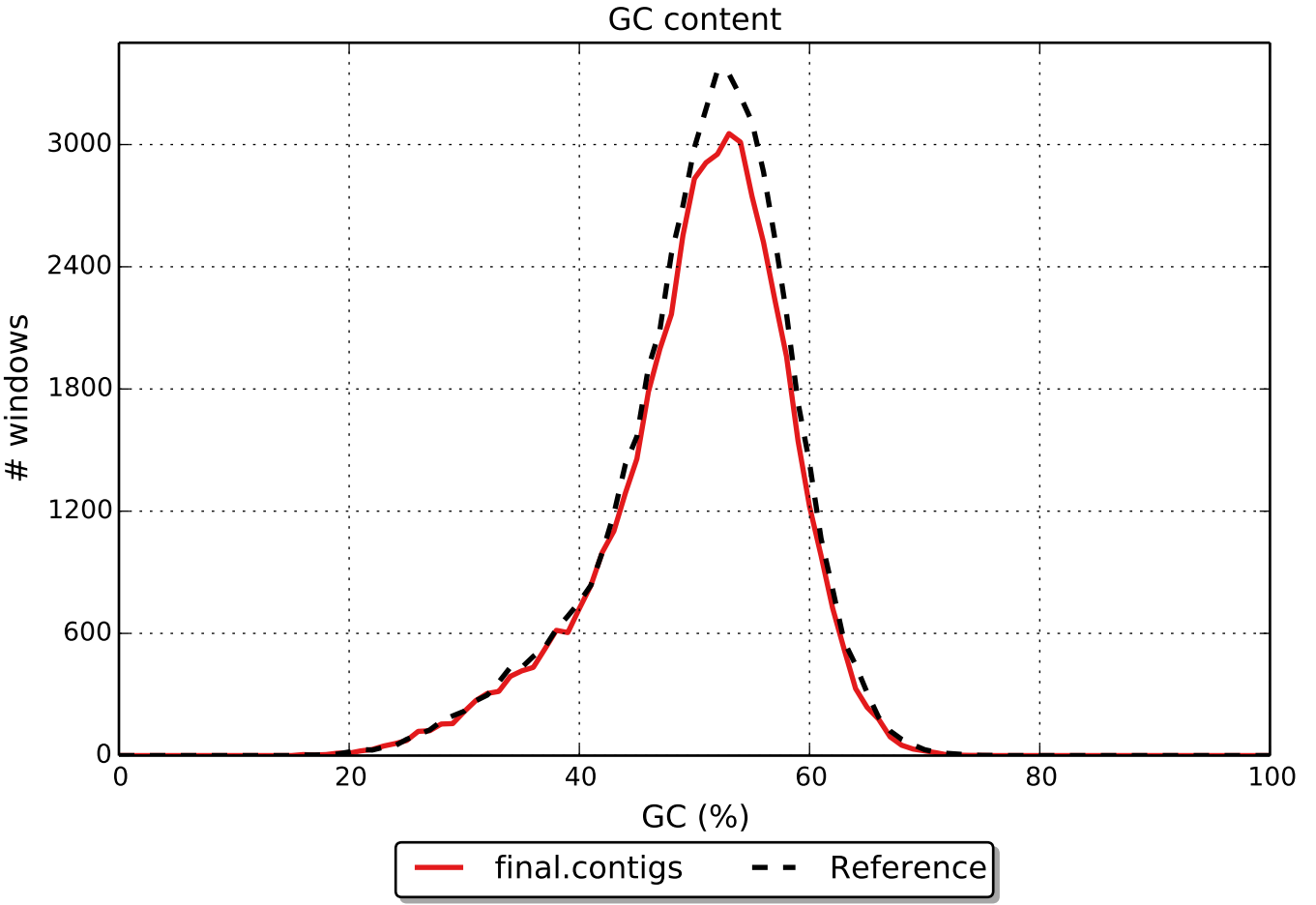
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

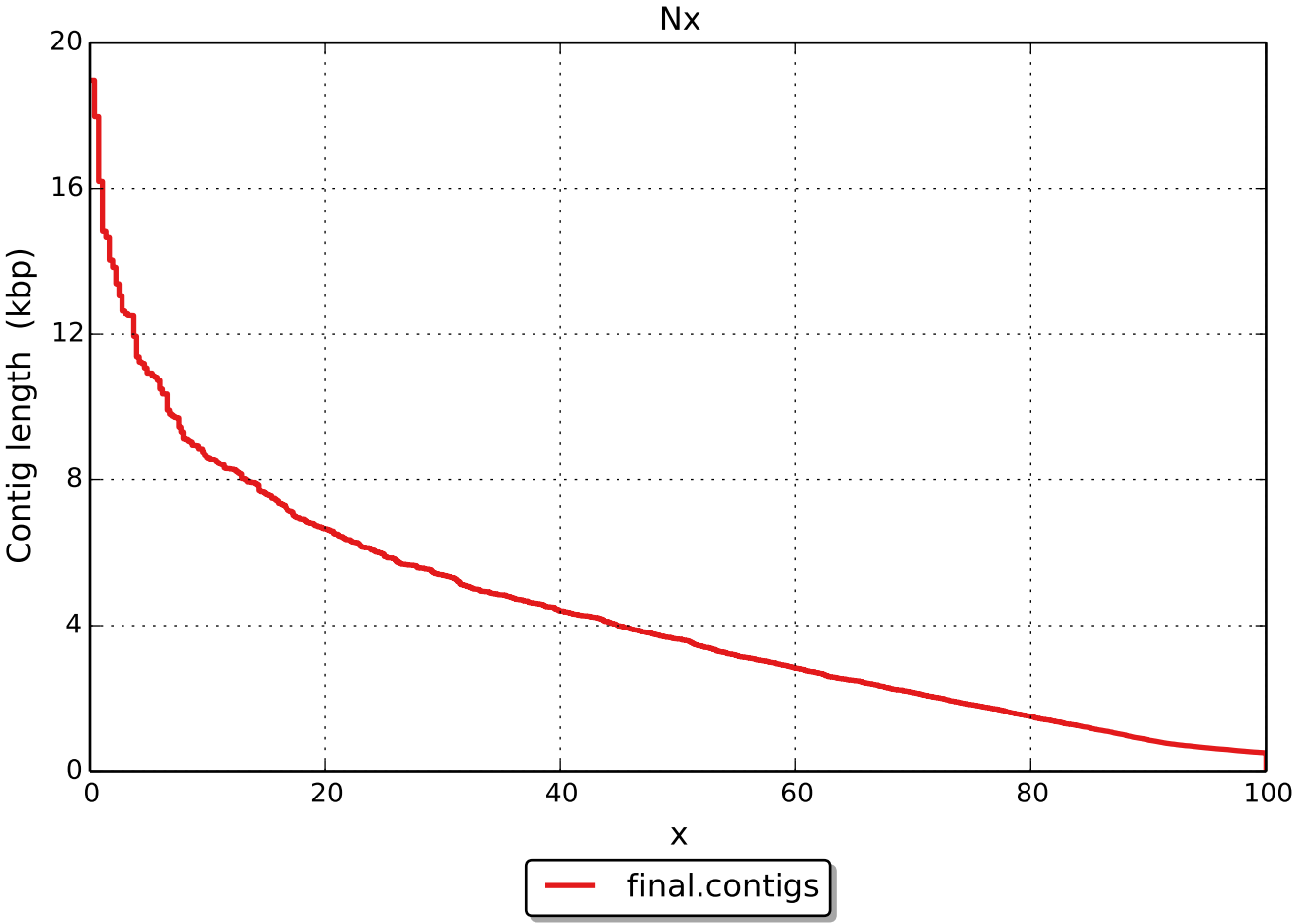
Unaligned report

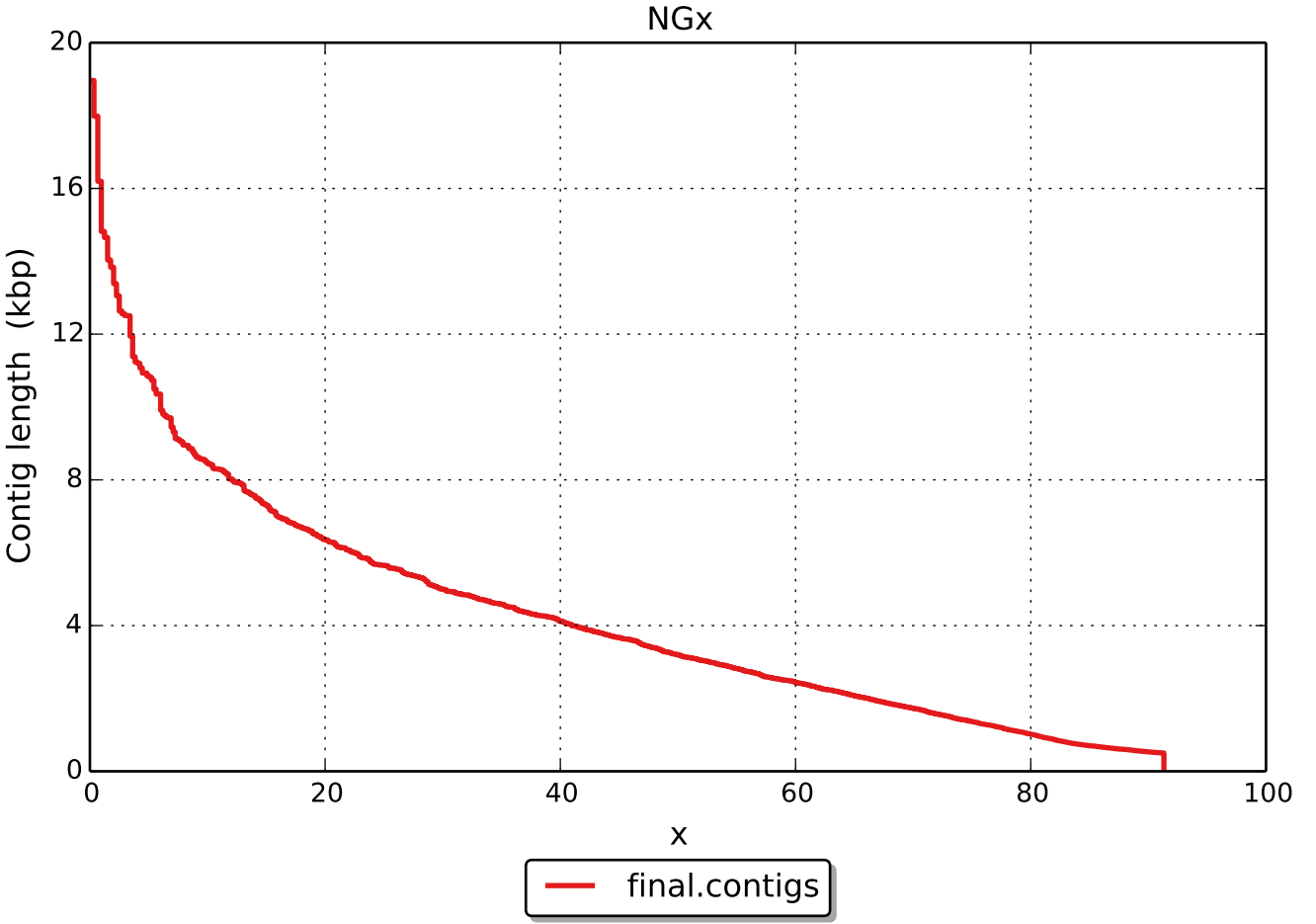
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

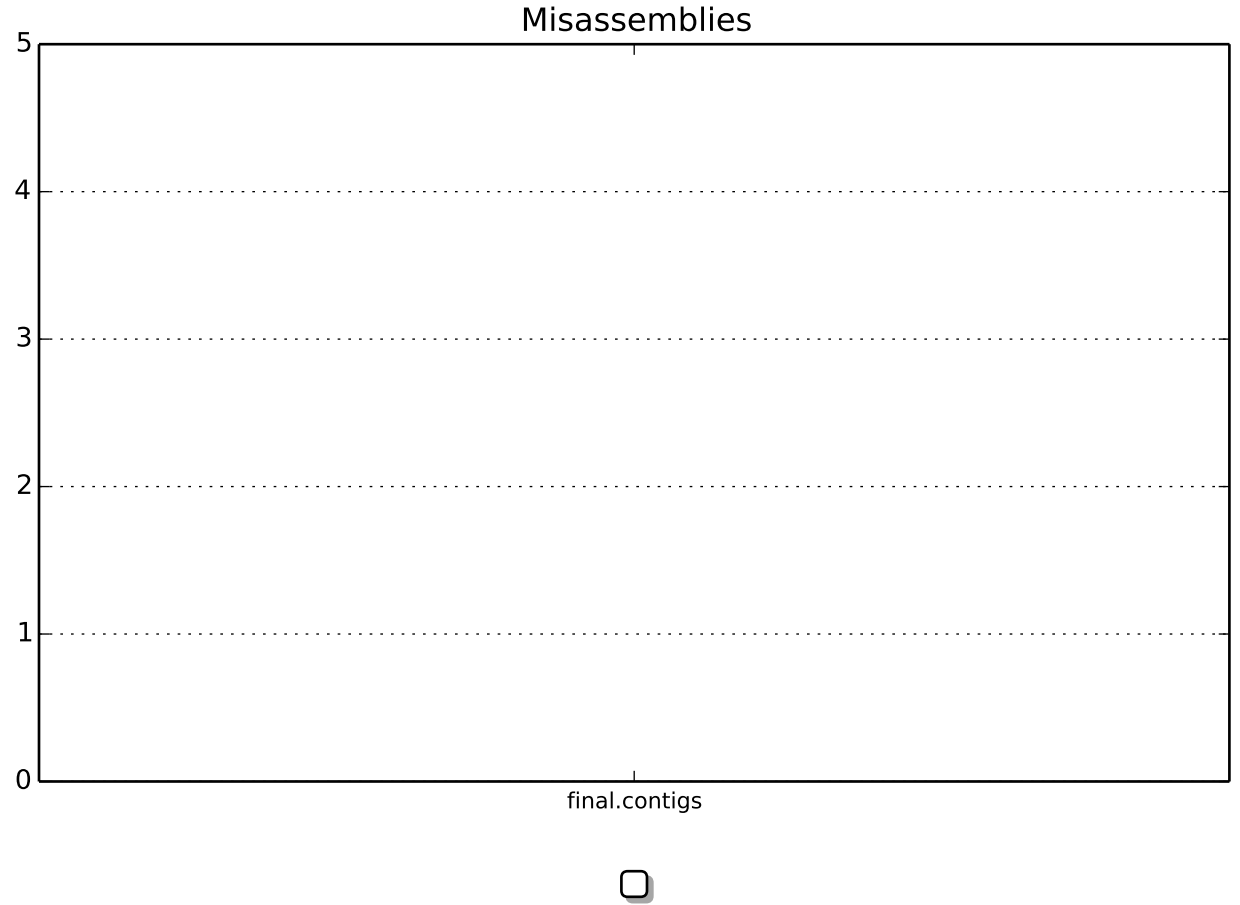
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

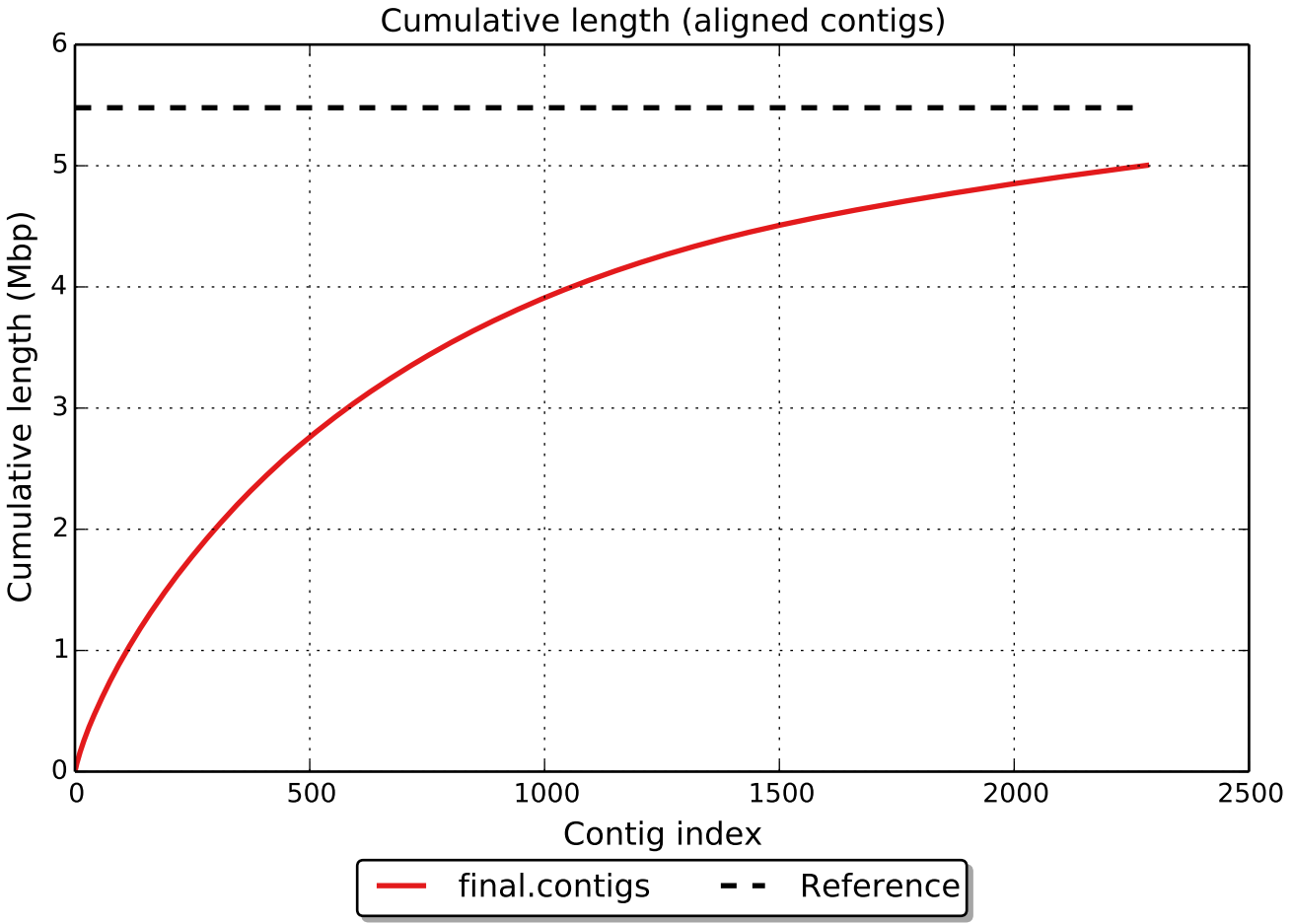

Cumulative length
Cumulative length (Mbp)
0
1
2
3
4
5
6
0
500
1000
1500
2000
2500
Contig index
final.contigs
Reference

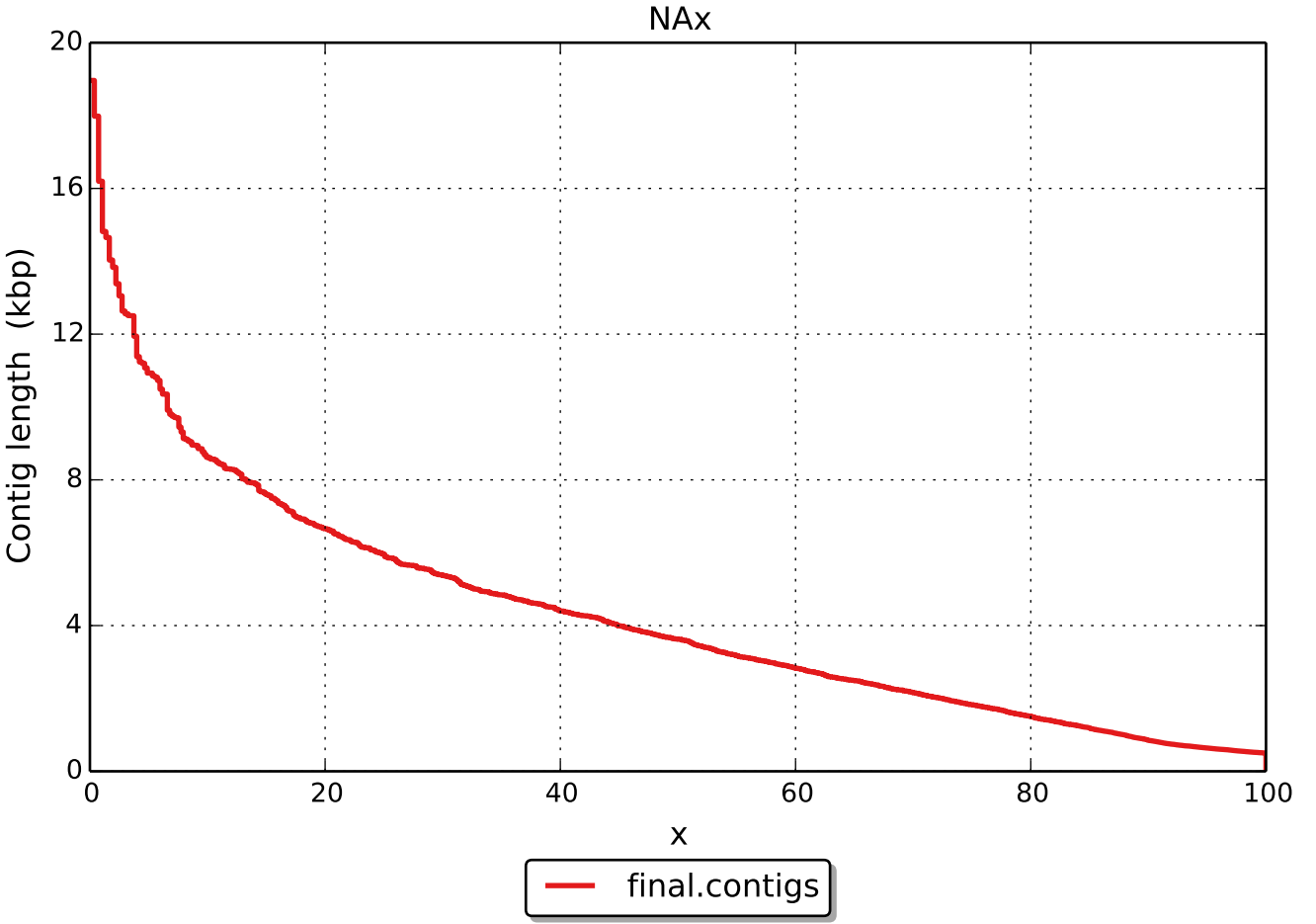

GC content
windows
3000
2400
1800
1200
600
0
0
20
40
60
80
100
GC (%)
final.contigs
Reference

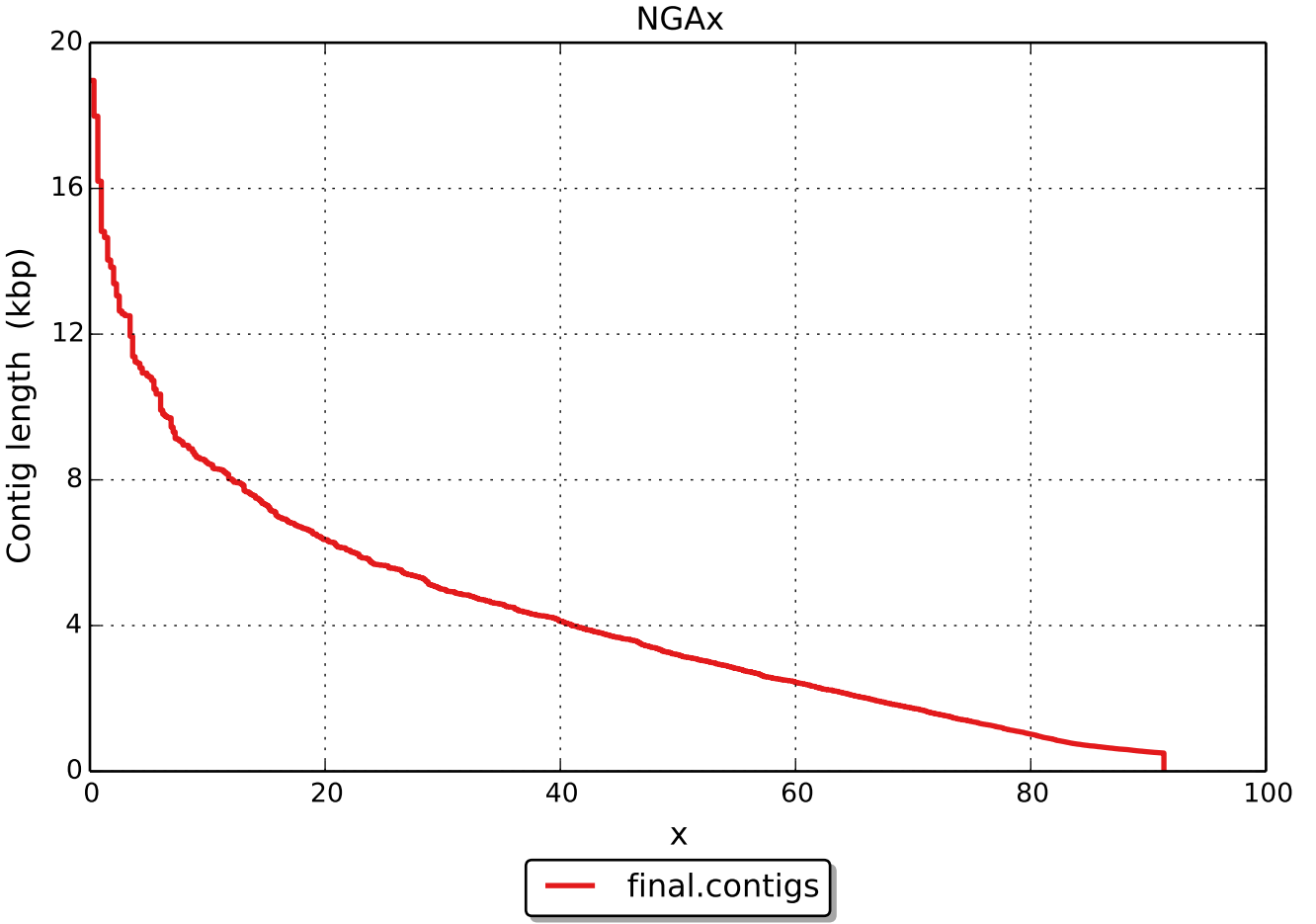

Nx
Contig length (kbp)
20
16
12
8
4
0
0
20
40
60
80
100
x
final.contigs


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