Report

	final.contigs
# contigs (>= 0 bp)	2676
# contigs (>= 1000 bp)	964
Total length (>= 0 bp)	3056744
Total length (>= 1000 bp)	1889807
# contigs	2676
Largest contig	9465
Total length	3056744
Reference length	5478683
GC (%)	50.37
Reference GC (%)	50.49
N50	1321
NG50	597
N75	759
L50	648
LG50	2096
L75	1432
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 1 part
Unaligned length	24
Genome fraction (%)	53.744
Duplication ratio	1.038
# N's per 100 kbp	0.00
# mismatches per 100 kbp	331.37
# indels per 100 kbp	0.07
Largest alignment	9465
NA50	1321
NGA50	597
NA75	759
LA50	648
LGA50	2096
LA75	1432

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

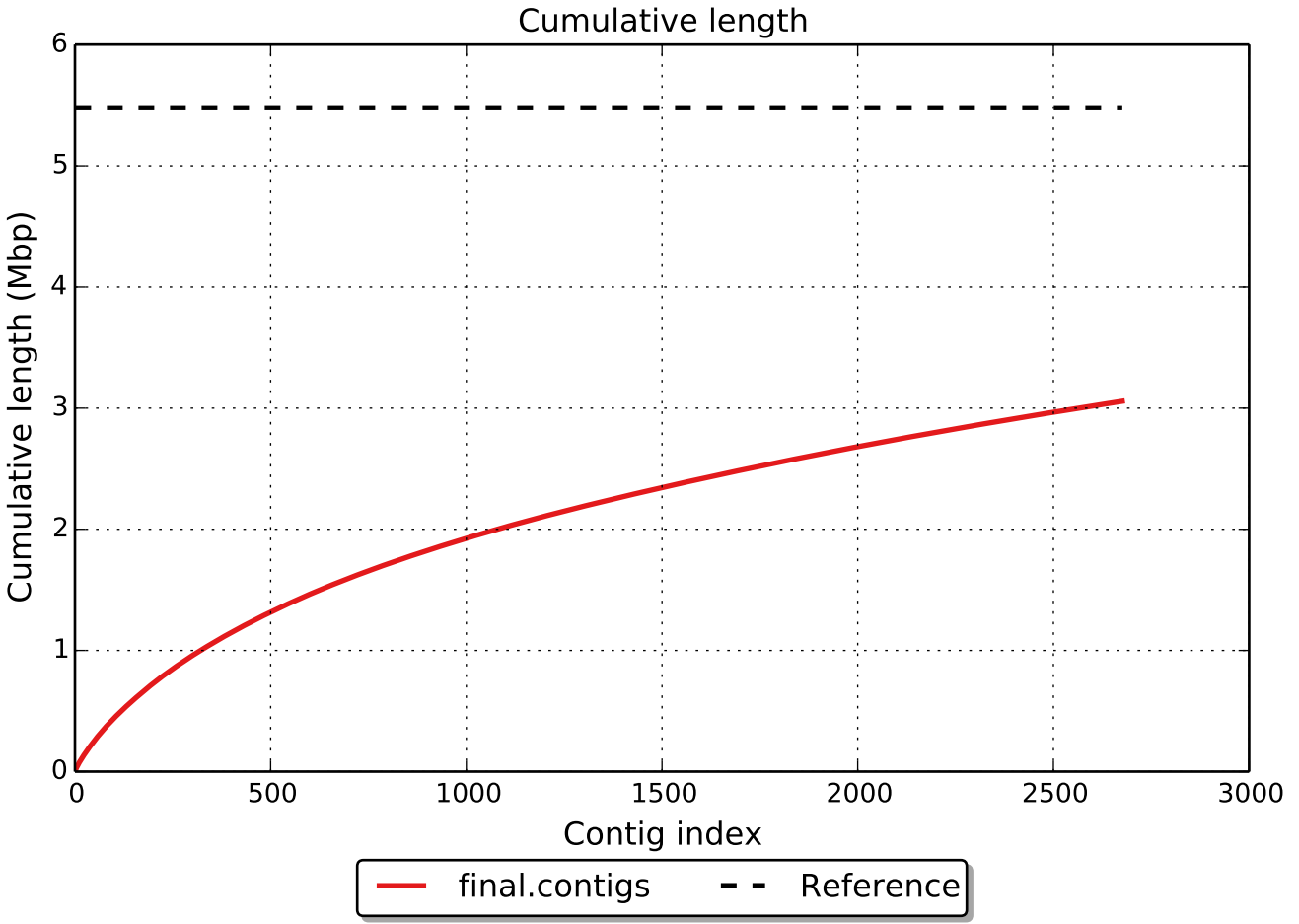
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	9757
# indels	2
# short indels	0
# long indels	2
Indels length	24

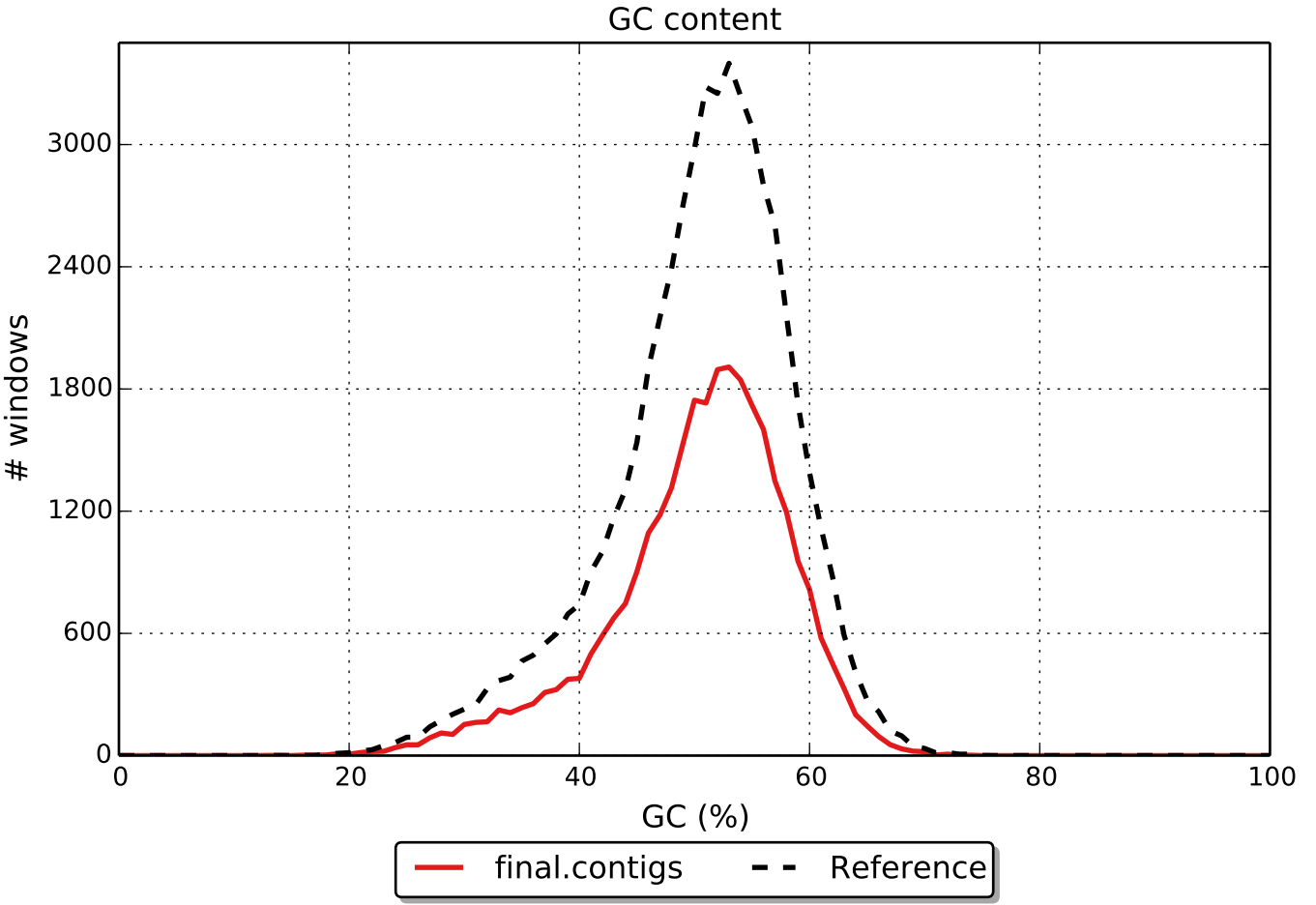
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

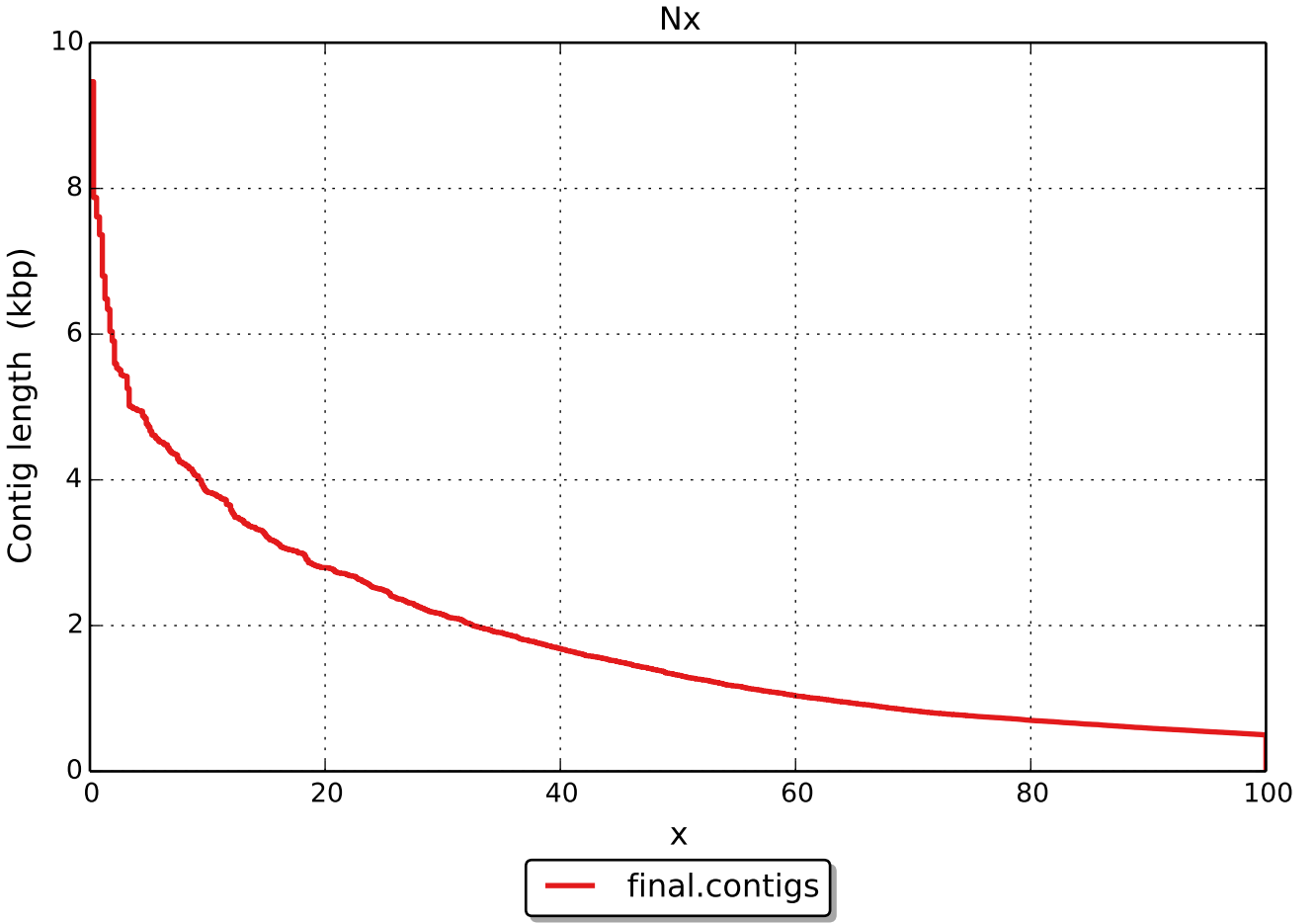
Unaligned report

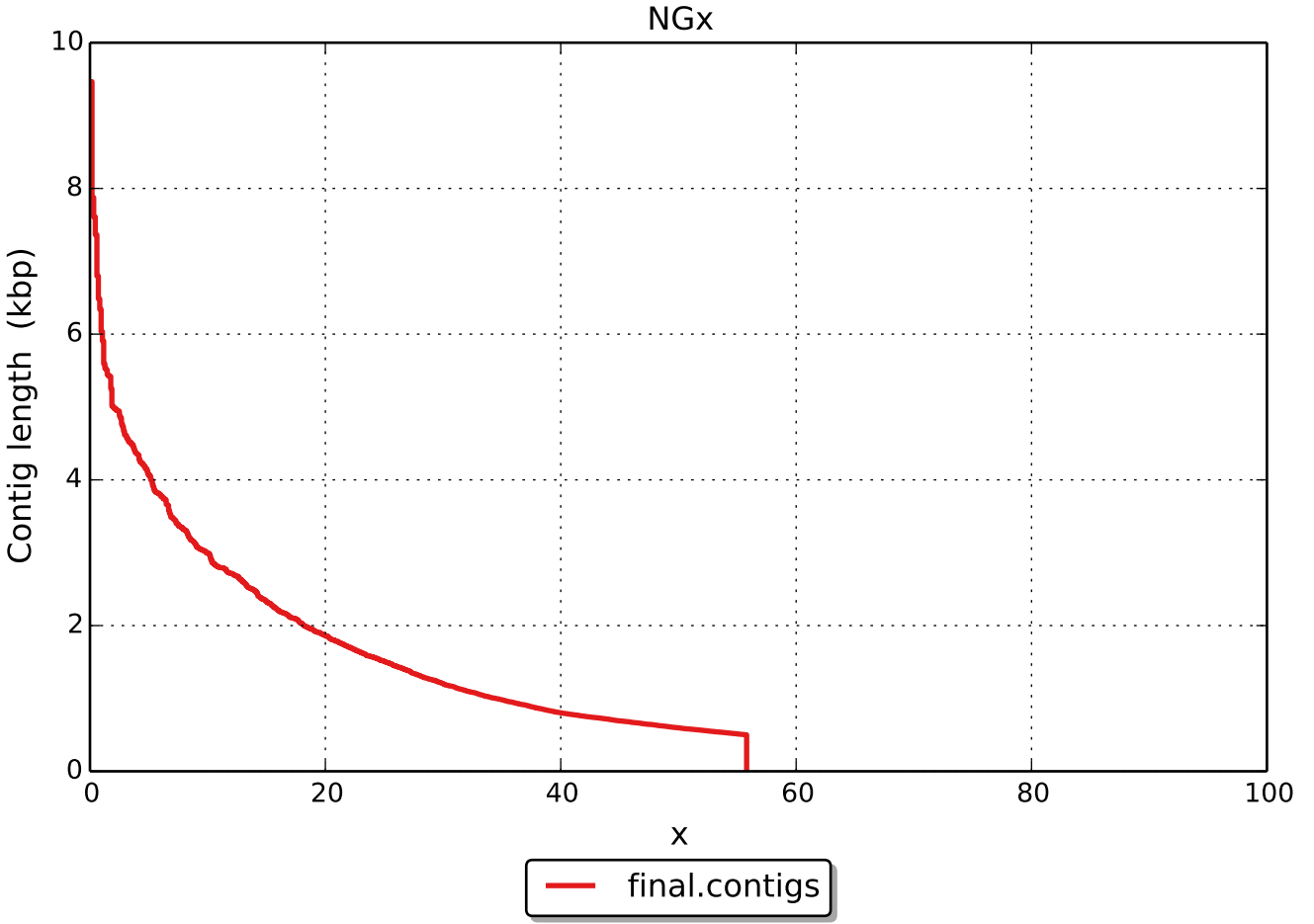
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	24
# N's	0

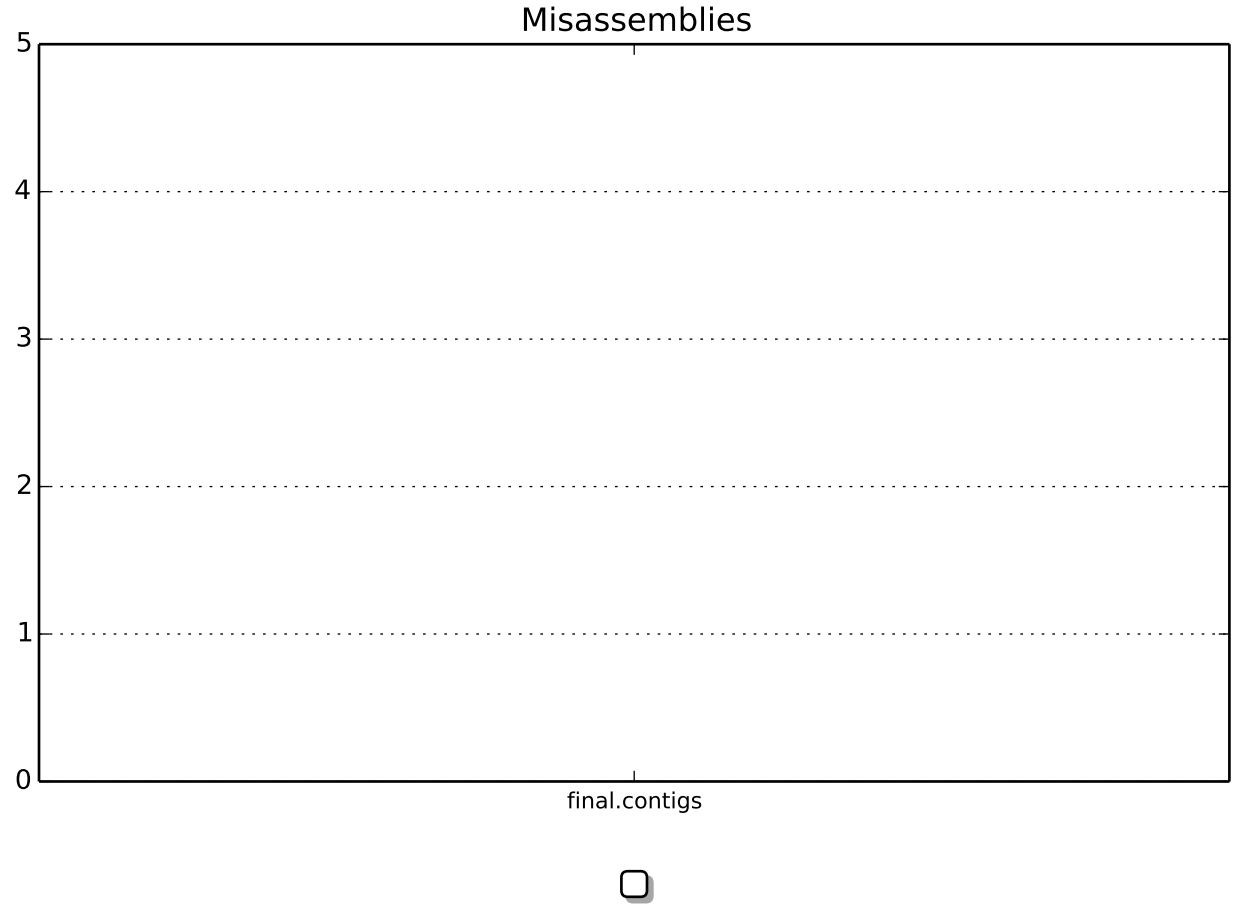
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

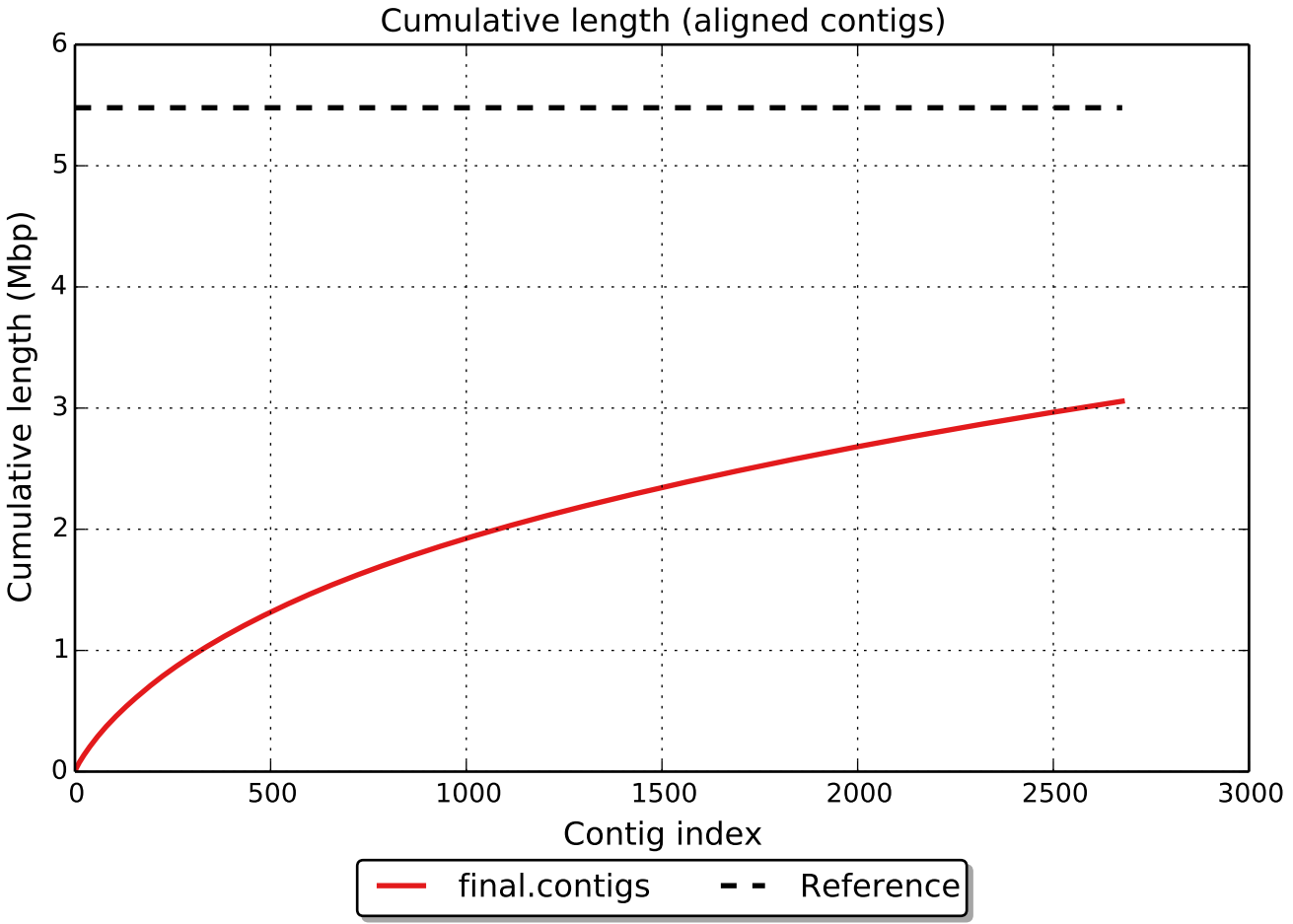

Cumulative length
Cumulative length (Mbp)
0
1
2
3
4
5
6
0
500
1000
1500
2000
2500
3000
Contig index
final.contigs
Reference

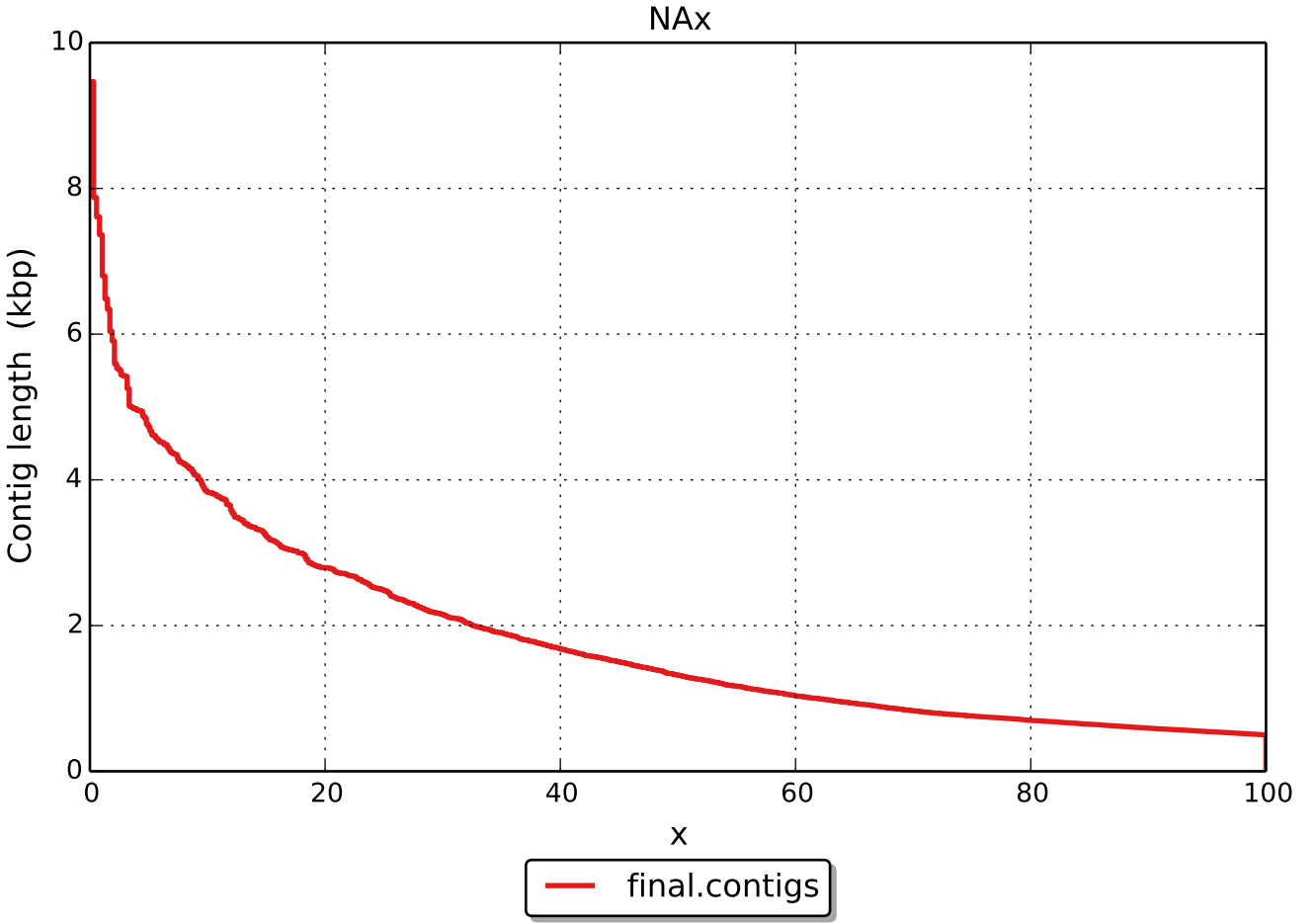

GC content
windows
3000
2400
1800
1200
600
0
0
20
40
60
80
100
GC (%)
final.contigs
Reference

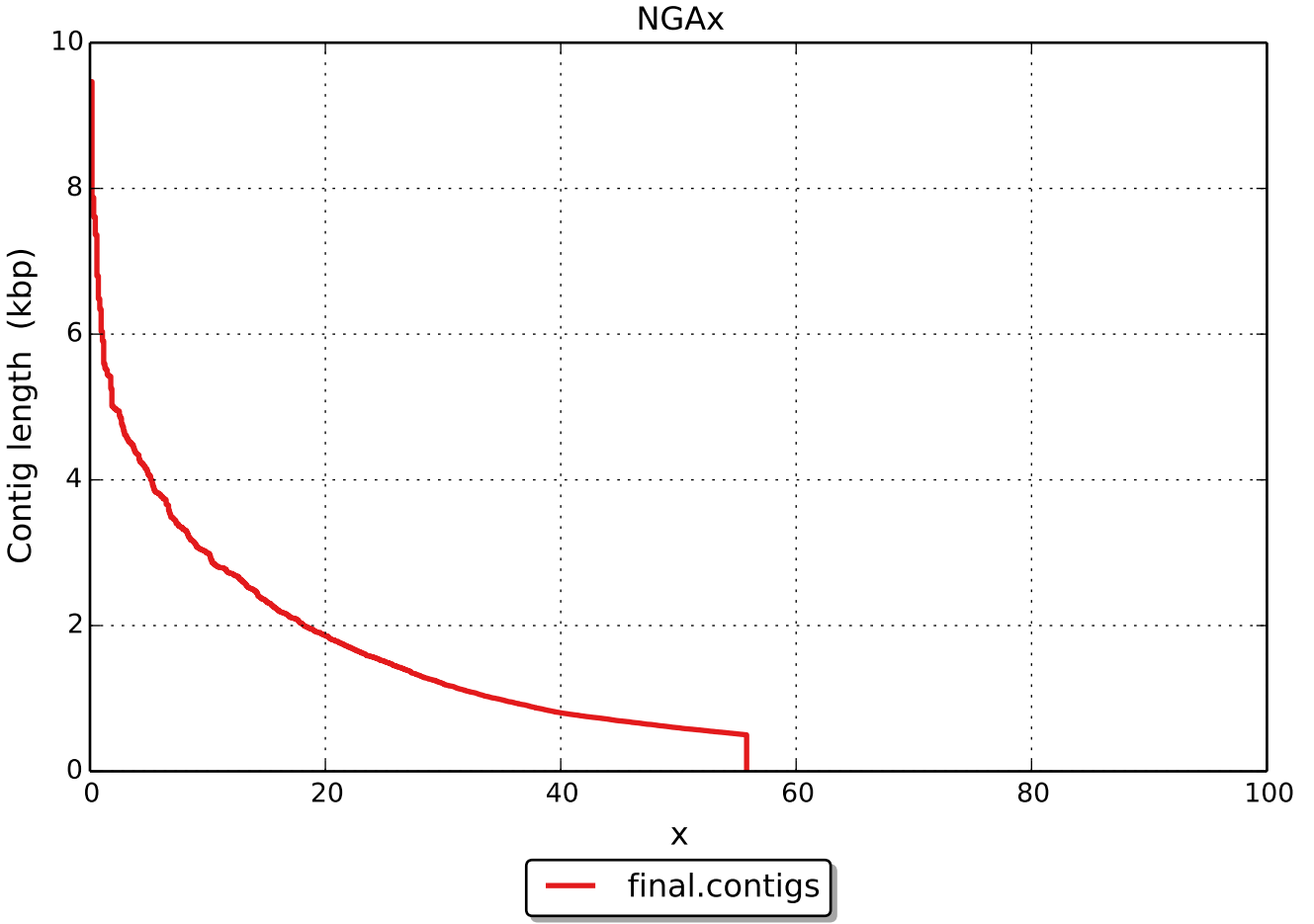

Nx
Contig length (kbp)
10
8
6
4
2
0
0
20
40
60
80
100
x
final.contigs


NGx
Contig length (kbp)
10
8
6
4
2
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
3000
Contig index
final.contigs
Reference


NAx
Contig length (kbp)
10
8
6
4
2
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (kbp)
10
8
6
4
2
0
0
20
40
60
80
100
x
final.contigs