Report

	final.contigs
# contigs (>= 0 bp)	656
# contigs (>= 1000 bp)	619
Total length (>= 0 bp)	5519343
Total length (>= 1000 bp)	5493330
# contigs	656
Largest contig	58672
Total length	5519343
Reference length	5478683
GC (%)	50.51
Reference GC (%)	50.50
N50	13489
NG50	13503
N75	7178
NG75	7265
L50	131
LG50	130
L75	269
LG75	264
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 2 part
Unaligned length	5177
Genome fraction (%)	99.490
Duplication ratio	1.012
# N's per 100 kbp	0.00
# mismatches per 100 kbp	12.62
# indels per 100 kbp	0.04
Largest alignment	58672
NA50	13420
NGA50	13489
NA75	7178
NGA75	7257
LA50	132
LGA50	130
LA75	269
LGA75	265

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

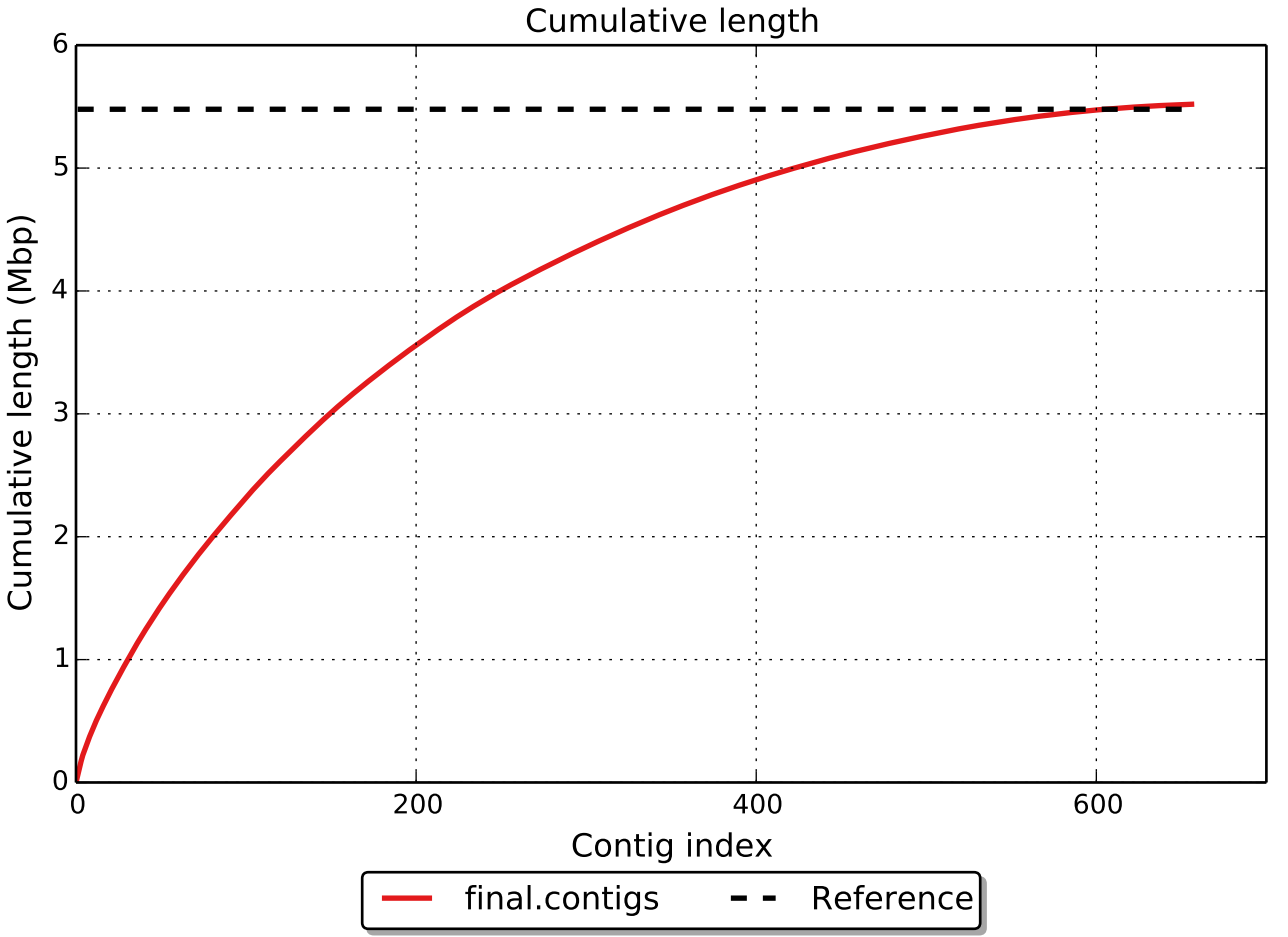
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	2
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	688
# indels	2
# short indels	2
# long indels	0
Indels length	2

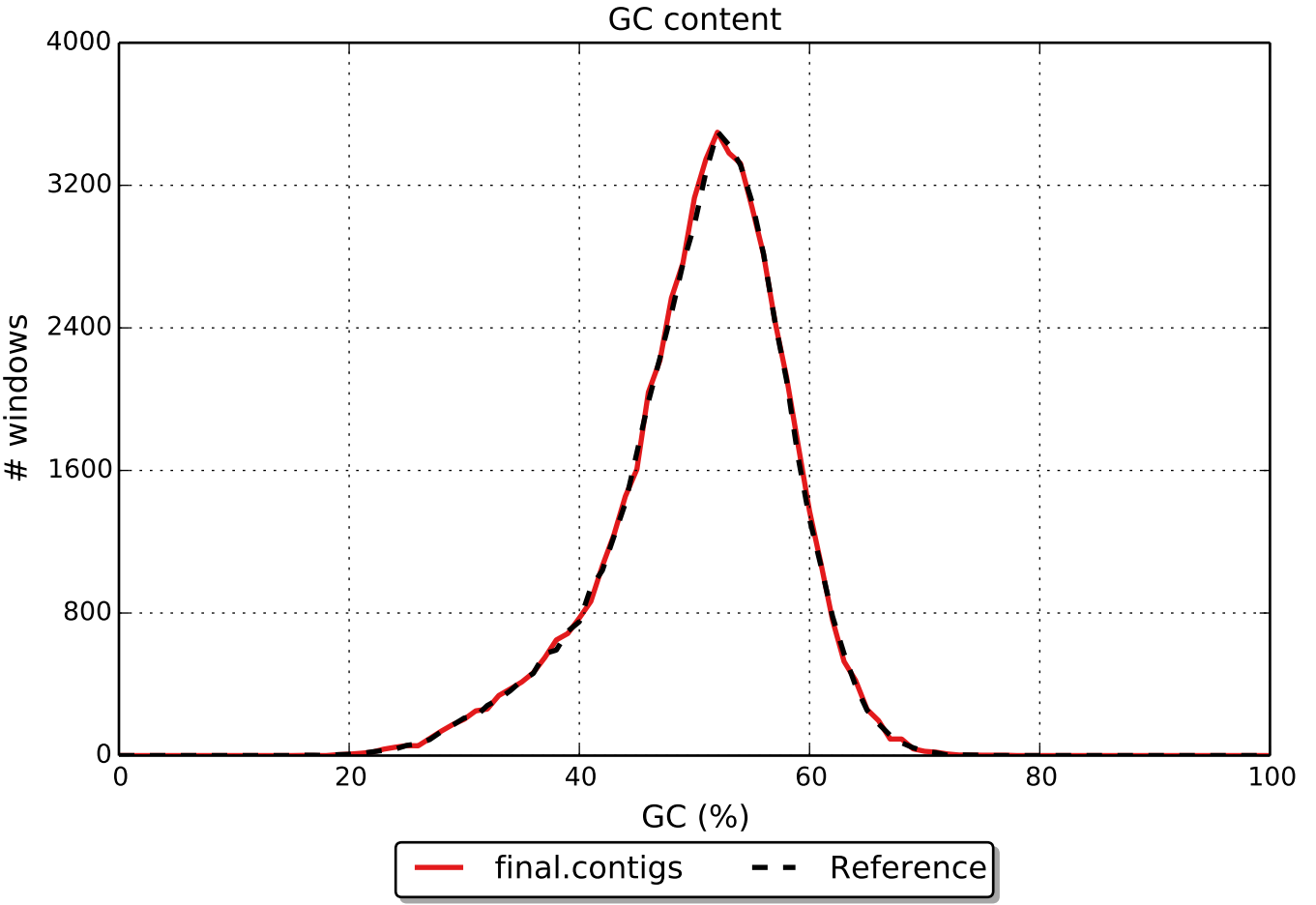
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

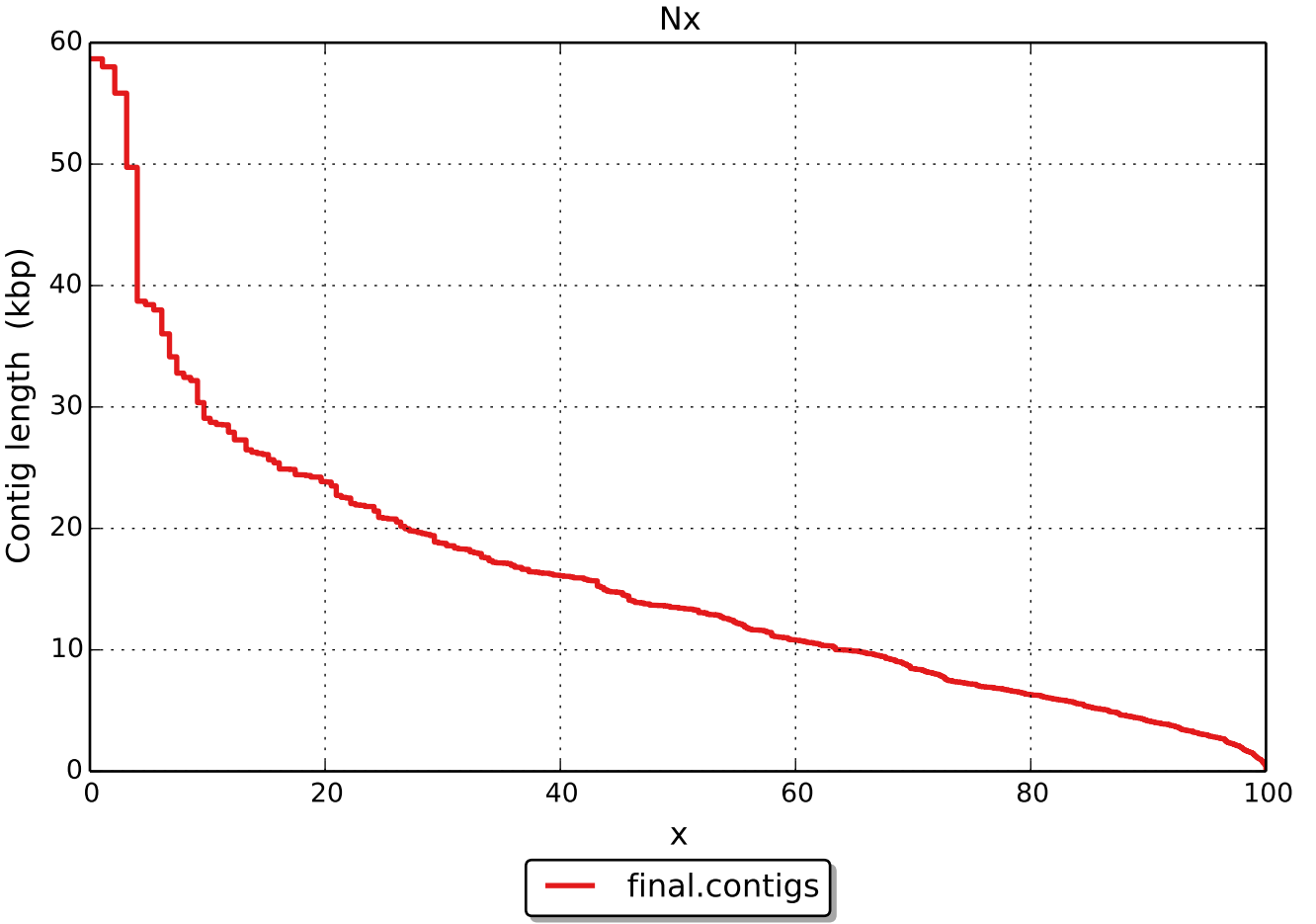
Unaligned report

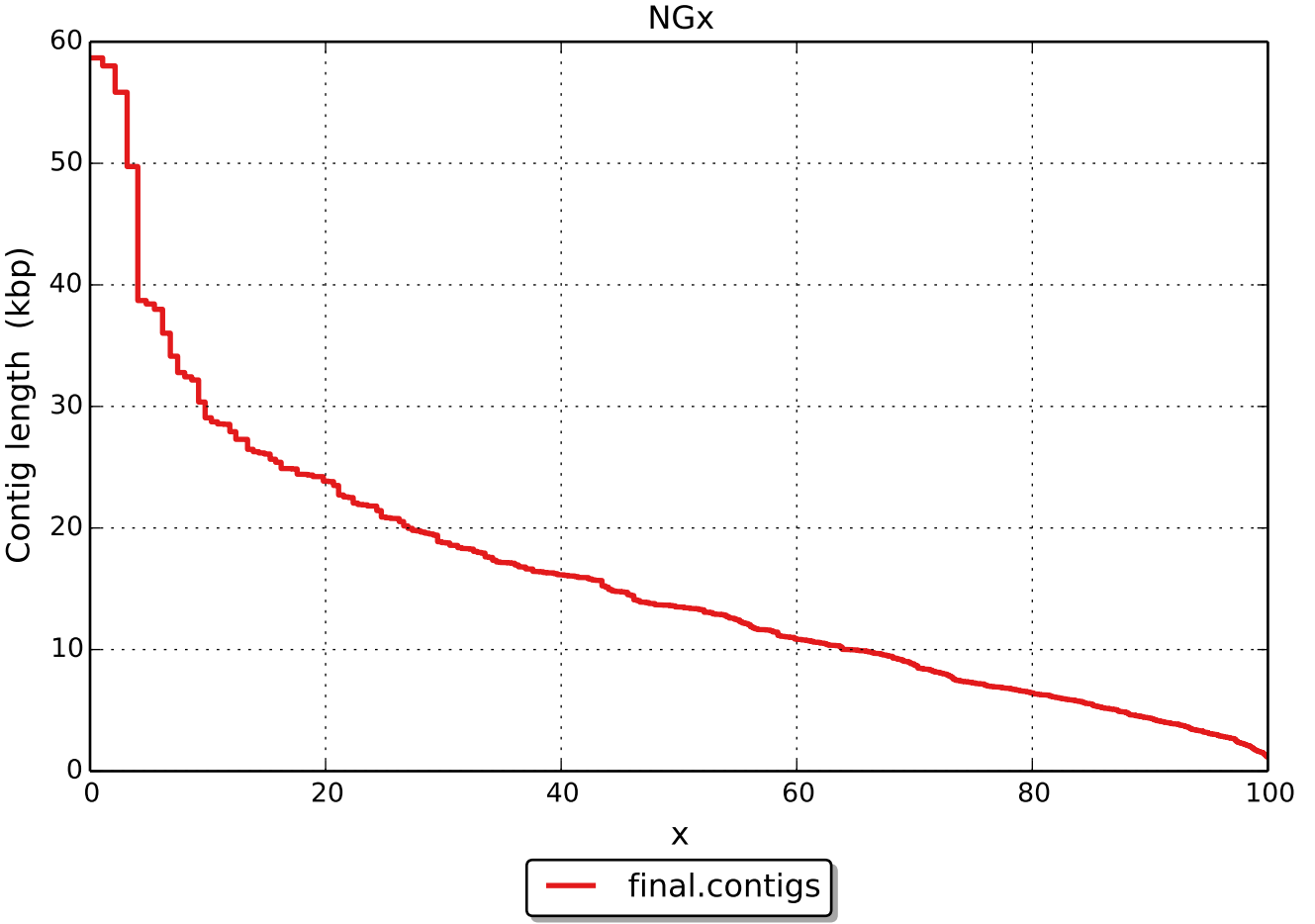
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	2
Partially unaligned length	5177
# N's	0

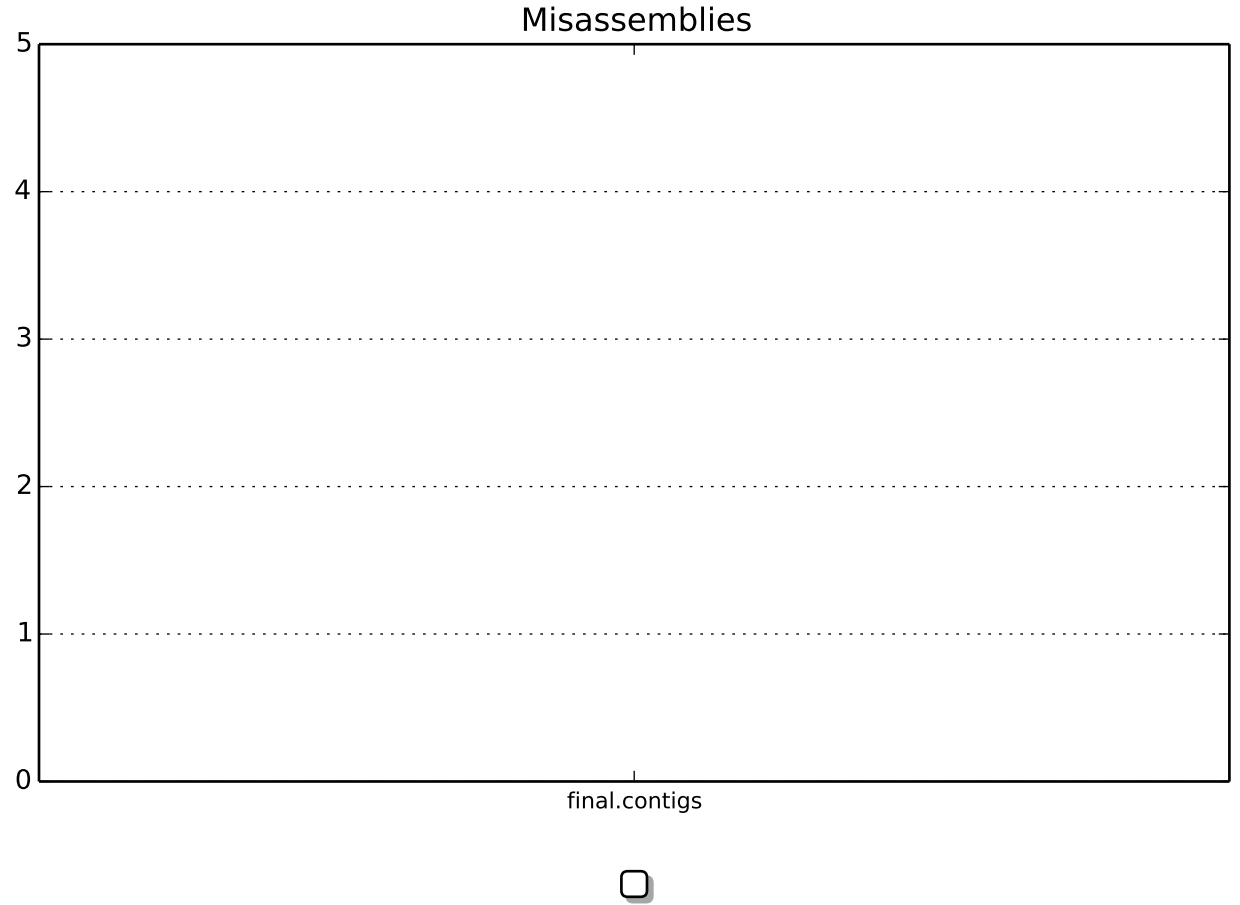
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

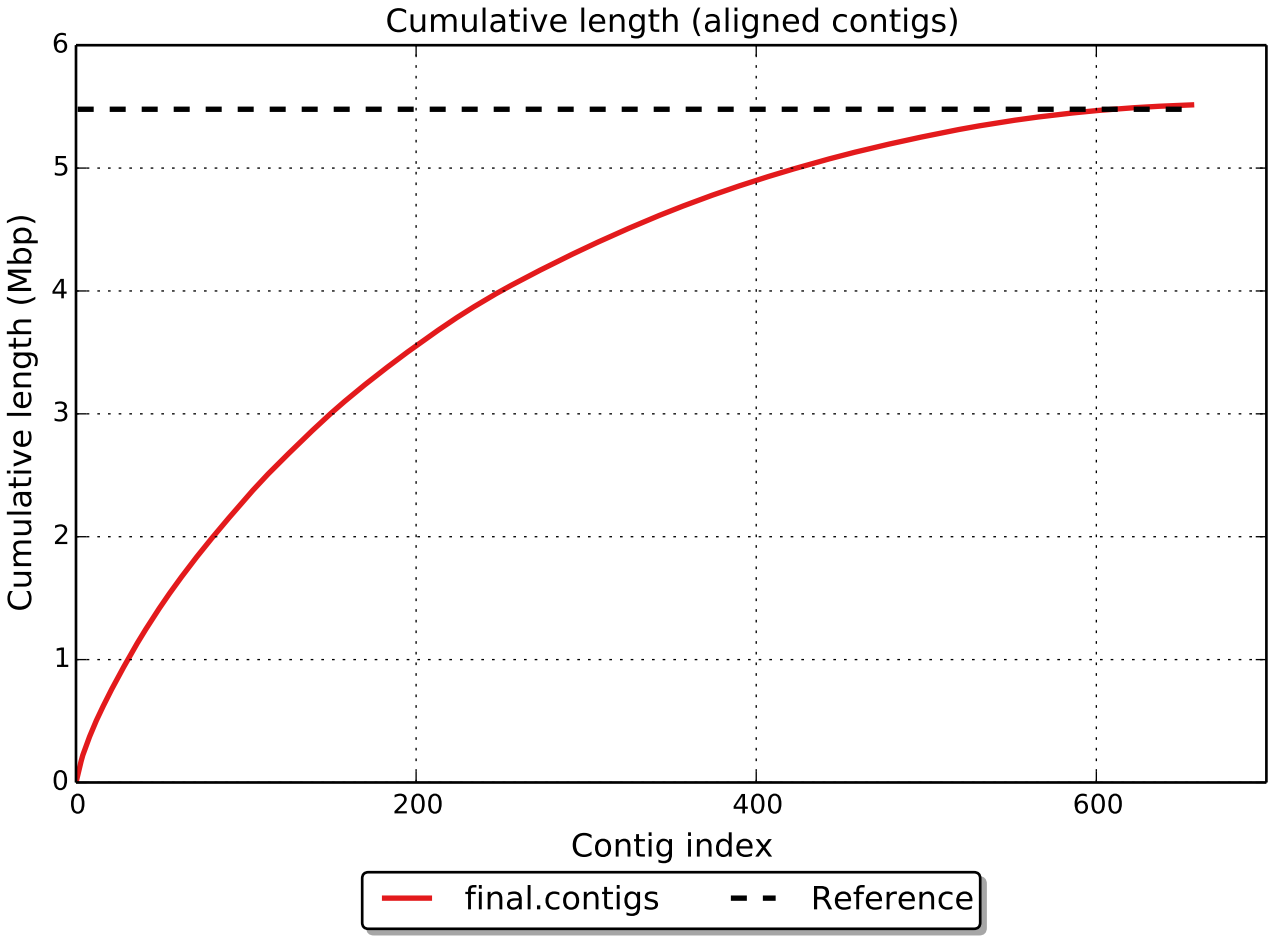

Cumulative length
Cumulative length (Mbp)
0
1
2
3
4
5
6
0
200
400
600
Contig index
final.contigs
Reference

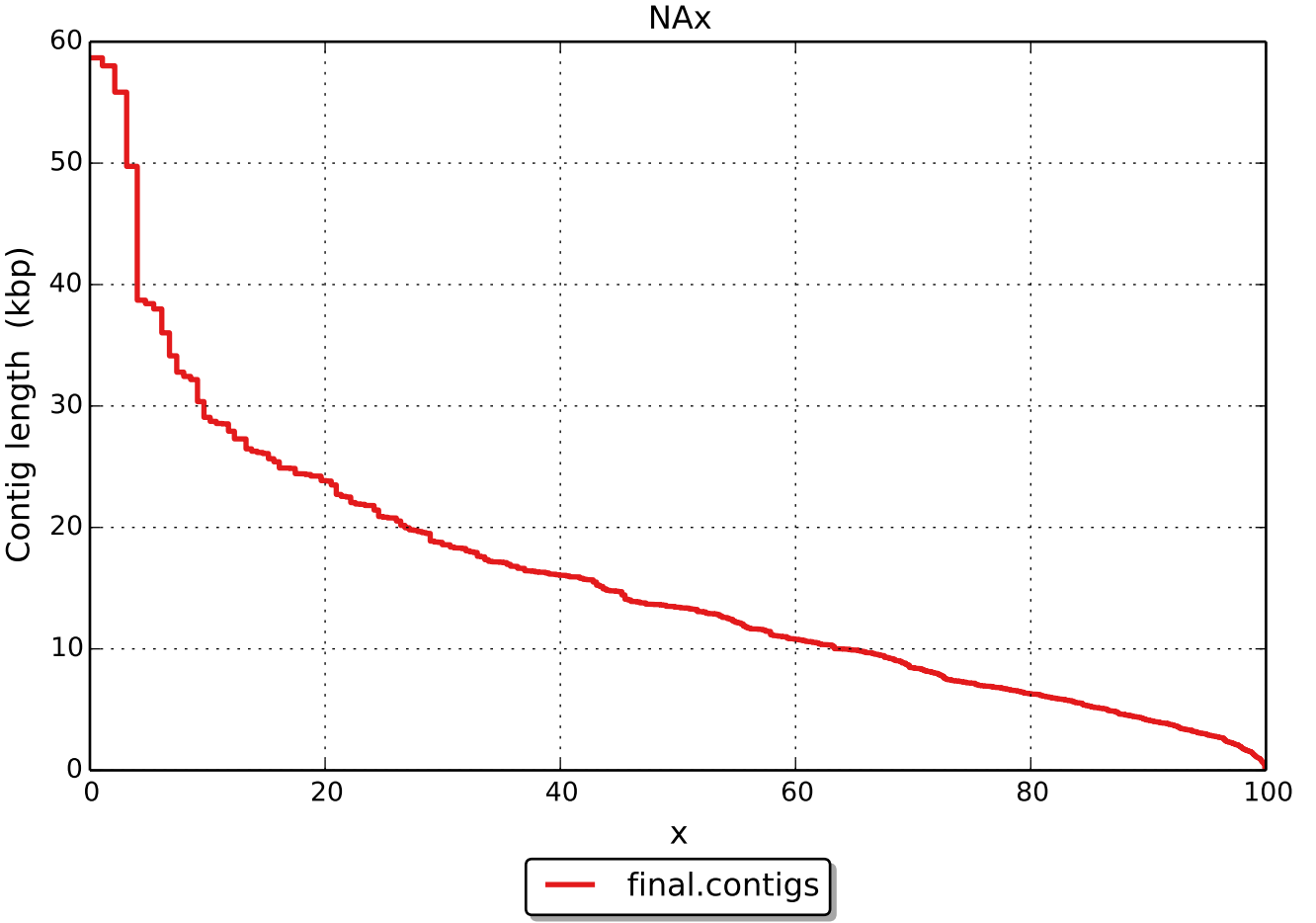

GC content
4000
3200
2400
1600
800
0
windows
0
20
40
60
80
100
GC (%)
final.contigs
Reference

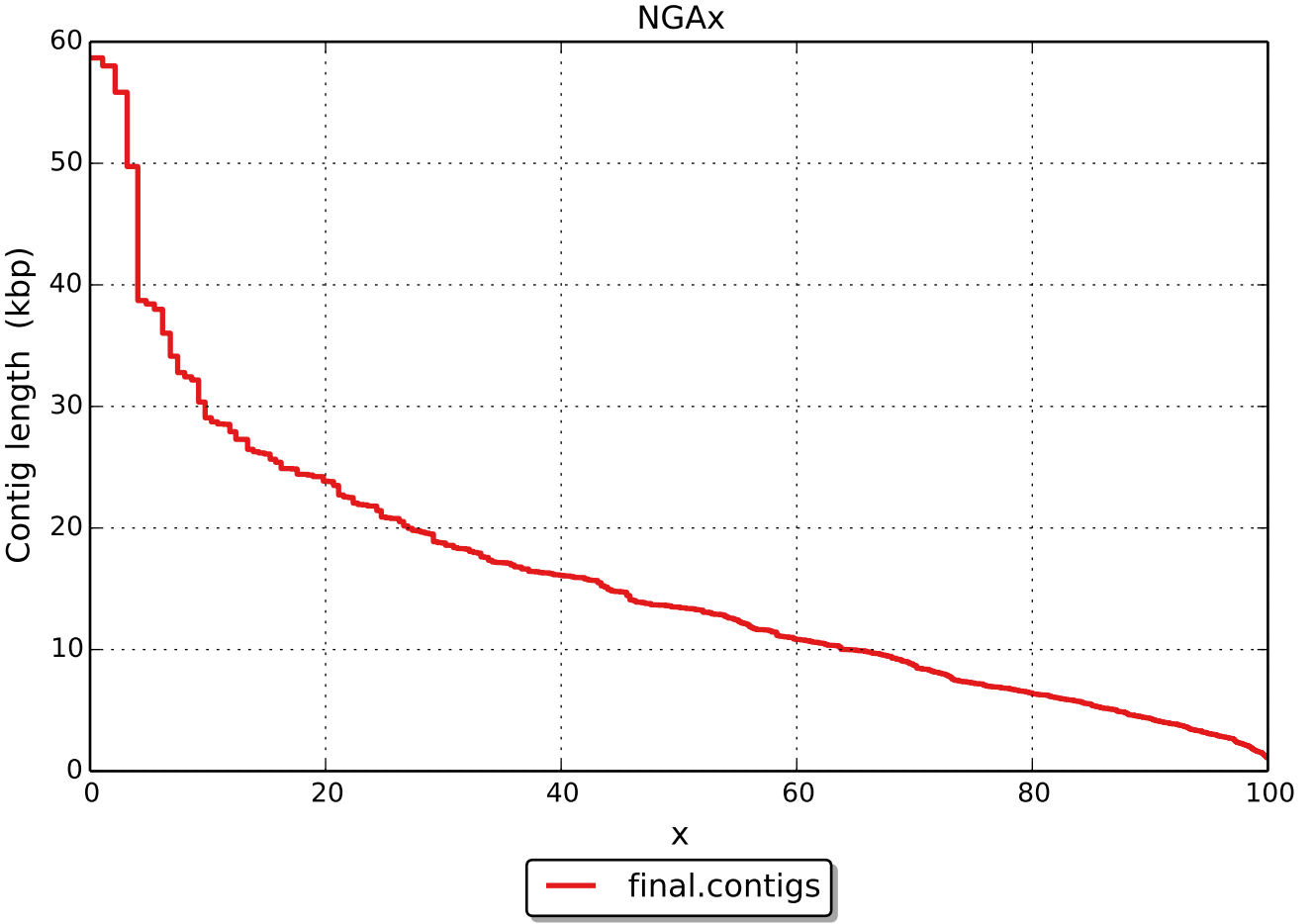

Nx
Contig length (kbp)
60
50
40
30
20
10
0
0
20
40
60
80
100
x
final.contigs


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)
0
10
20
30
40
50
60
0
20
40
60
80
100
x
final.contigs


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