Report

	final.contigs
# contigs (>= 0 bp)	687
# contigs (>= 1000 bp)	644
Total length (>= 0 bp)	5662450
Total length (>= 1000 bp)	5630141
# contigs	687
Largest contig	47562
Total length	5662450
Reference length	5547323
GC (%)	50.50
Reference GC (%)	50.49
N50	12744
NG50	13137
N75	7647
NG75	7860
L50	134
LG50	130
L75	277
LG75	266
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	19930
# local misassemblies	0
# unaligned contigs	0 + 3 part
Unaligned length	28335
Genome fraction (%)	99.531
Duplication ratio	1.020
# N's per 100 kbp	0.00
# mismatches per 100 kbp	21.44
# indels per 100 kbp	0.00
Largest alignment	47562
NA50	12643
NGA50	12744
NA75	7482
NGA75	7842
LA50	137
LGA50	132
LA75	282
LGA75	270

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

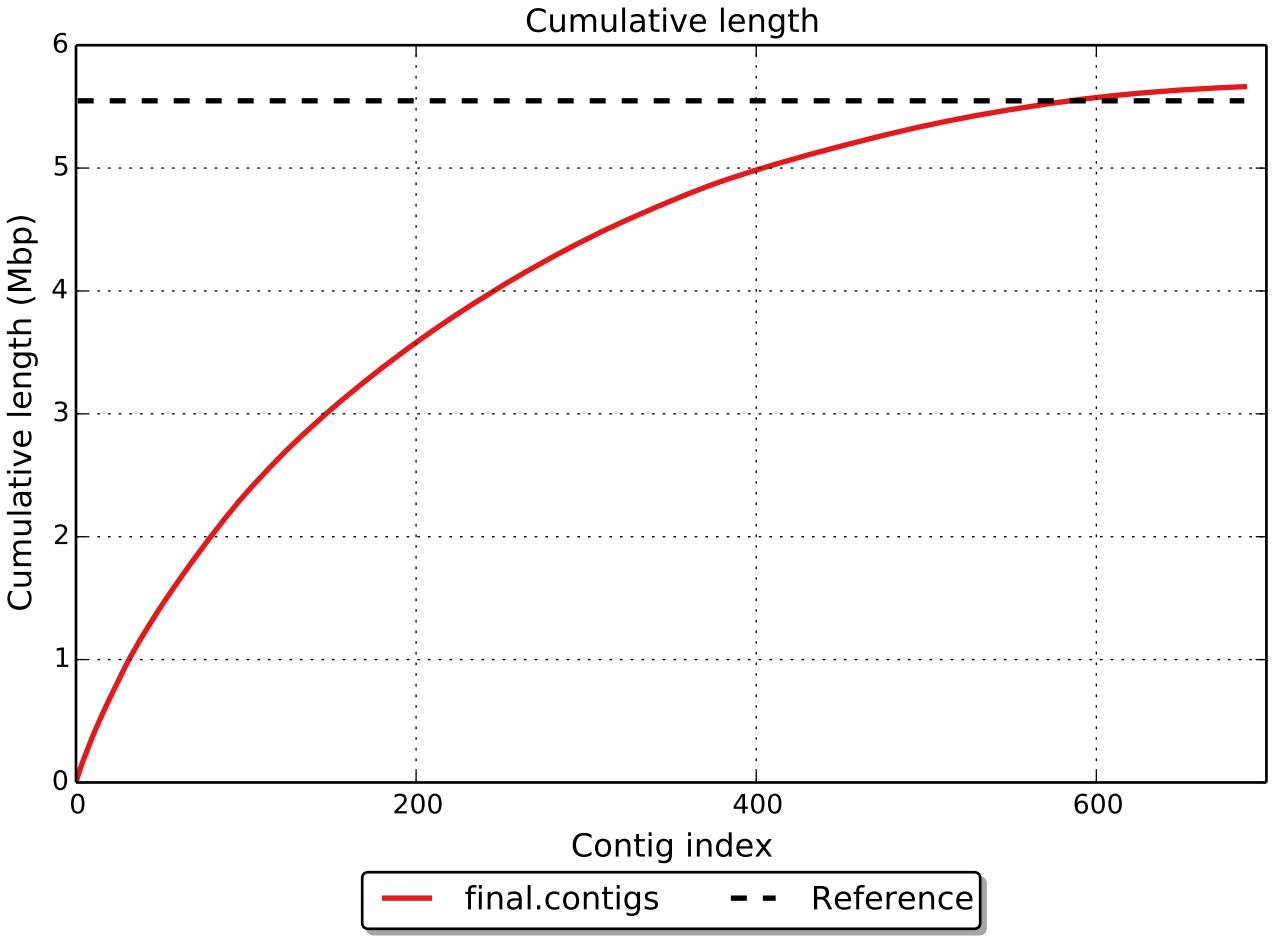
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	4
# misassembled contigs	1
Misassembled contigs length	19930
# local misassemblies	0
# mismatches	1184
# indels	0
# short indels	0
# long indels	0
Indels length	0

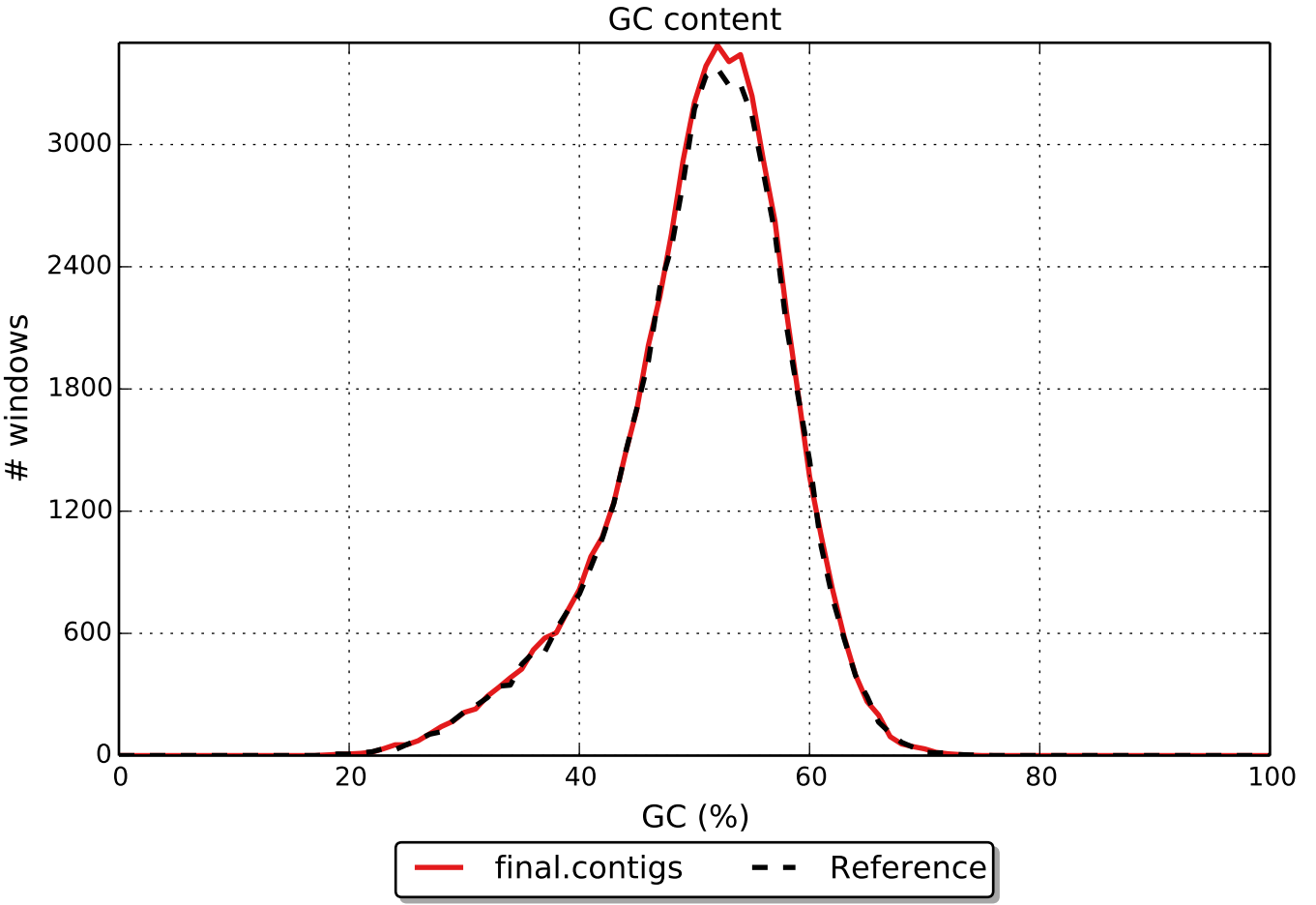
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

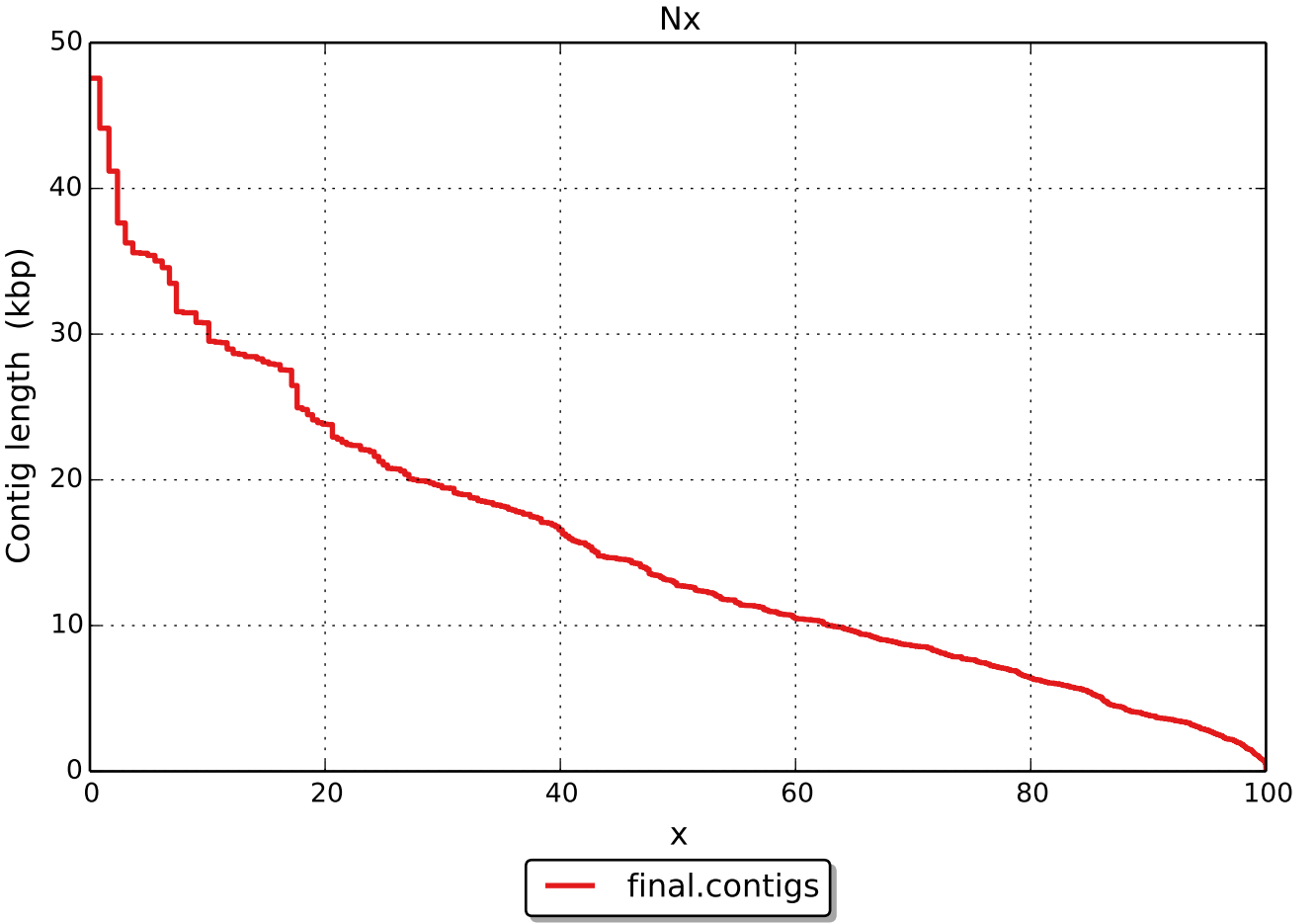
Unaligned report

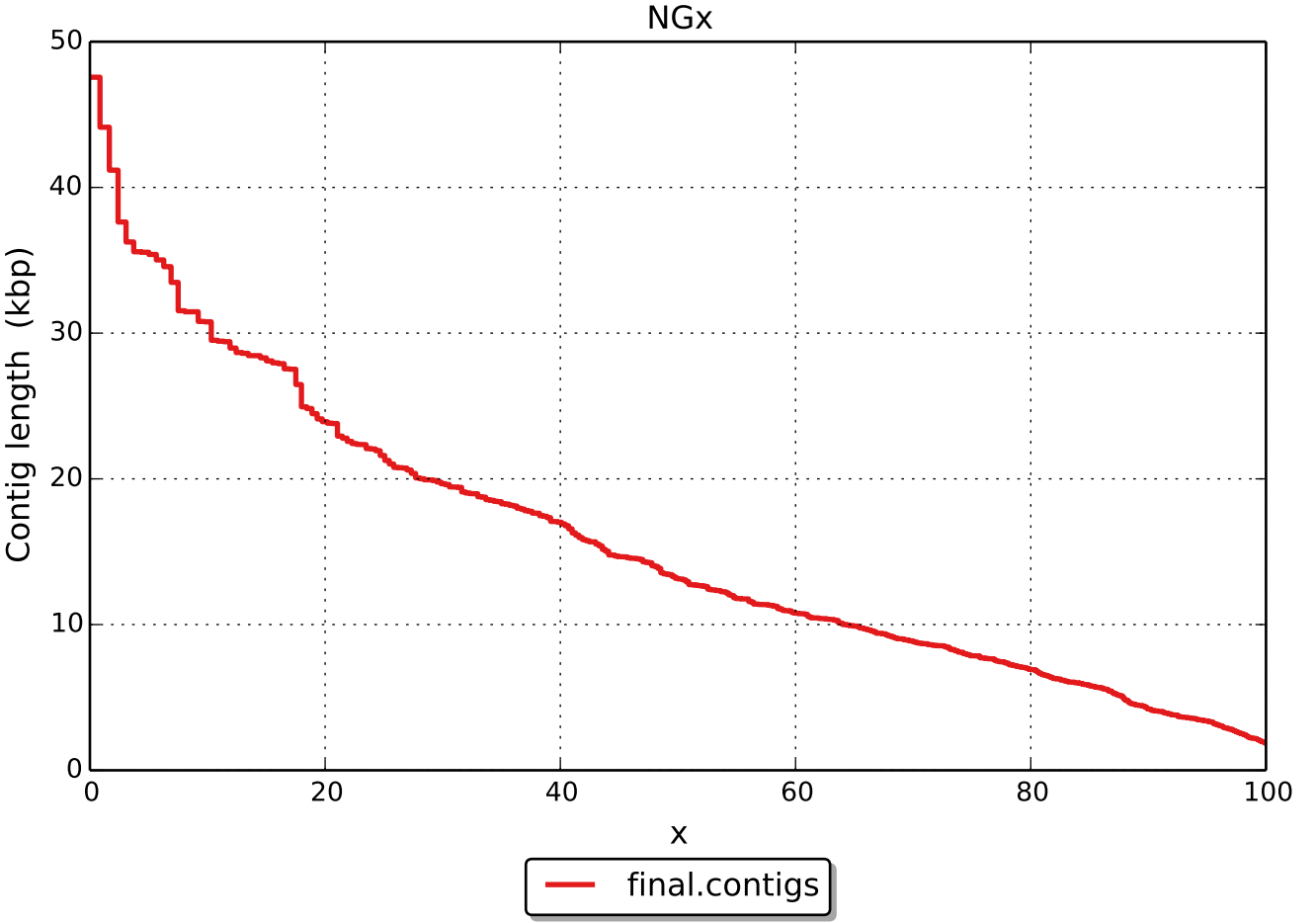
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	3
# with misassembly	0
# both parts are significant	3
Partially unaligned length	28335
# N's	0

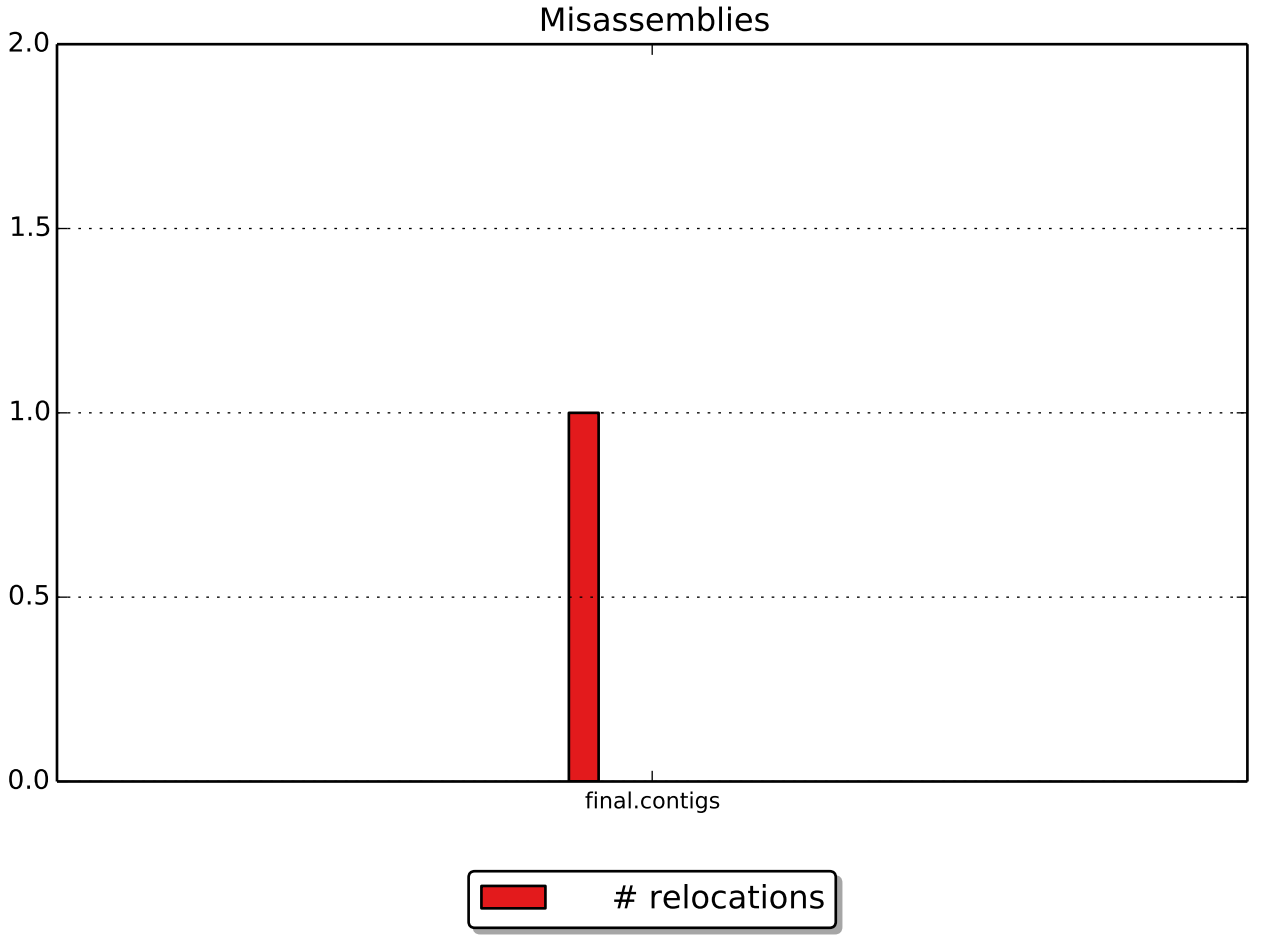
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

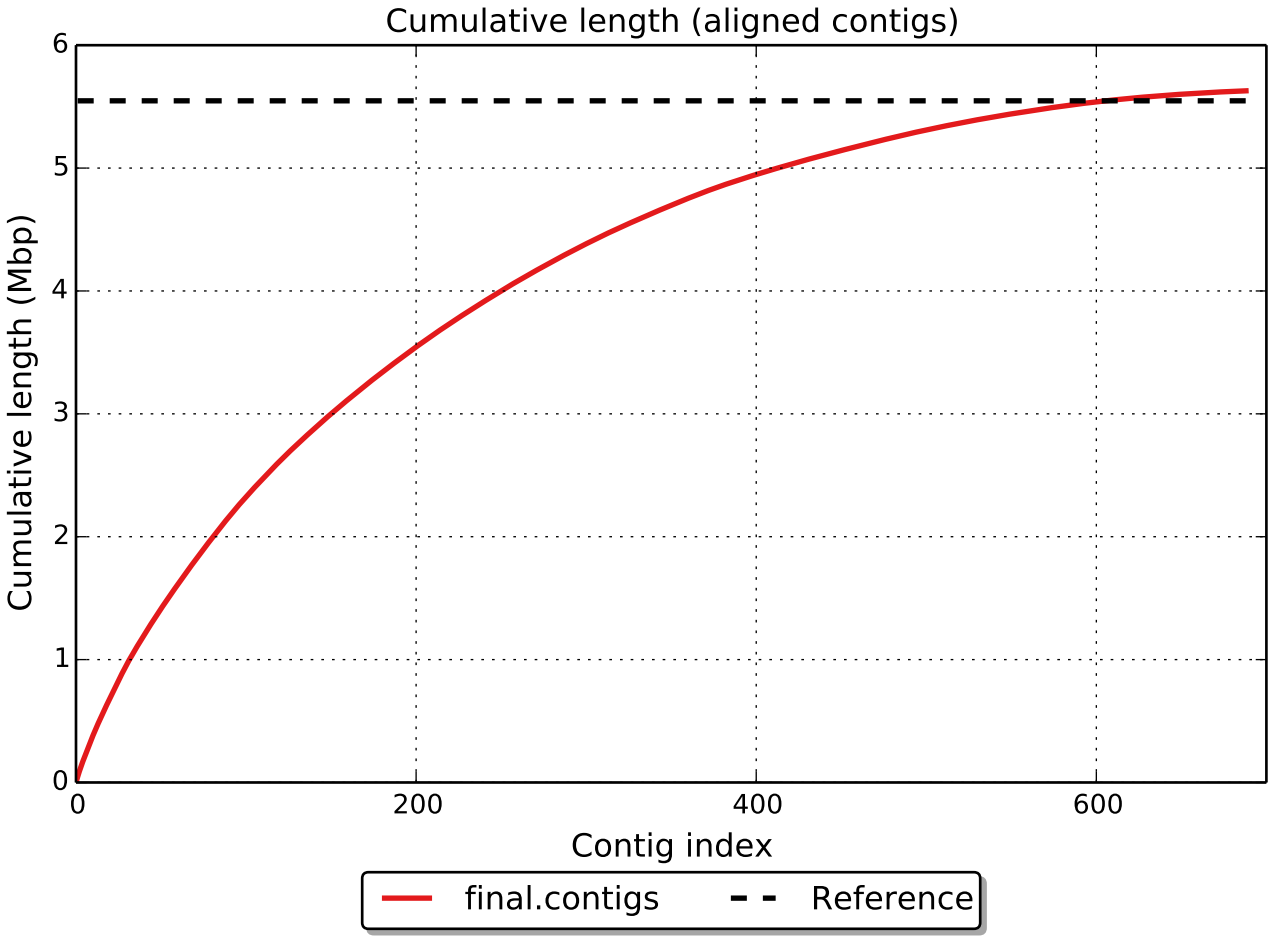

Cumulative length
Cumulative length (Mbp)
0
1
2
3
4
5
6
0
200
400
600
Contig index
final.contigs
Reference

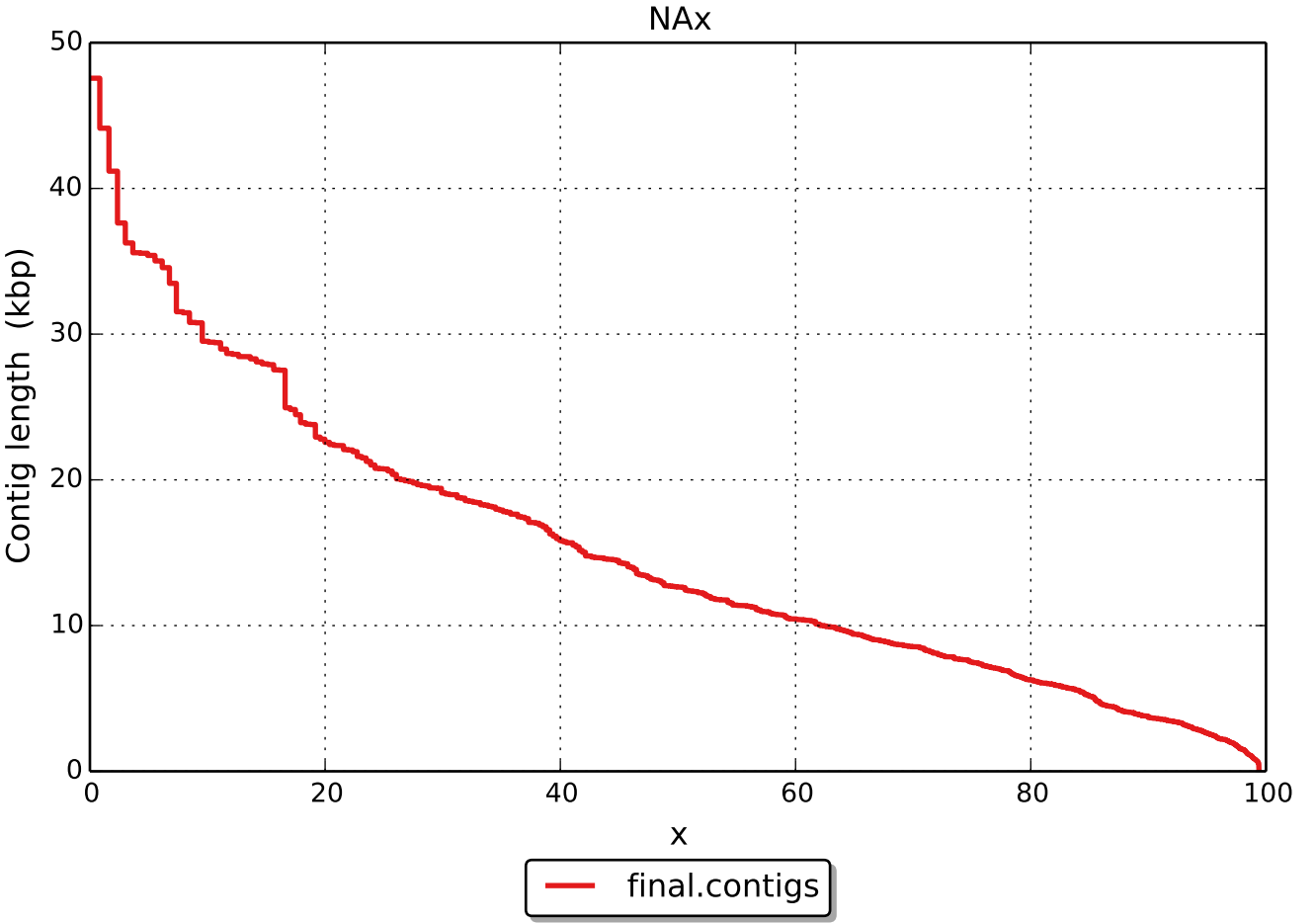

GC content
windows
3000
2400
1800
1200
600
0
0
20
40
60
80
100
GC (%)
final.contigs
Reference

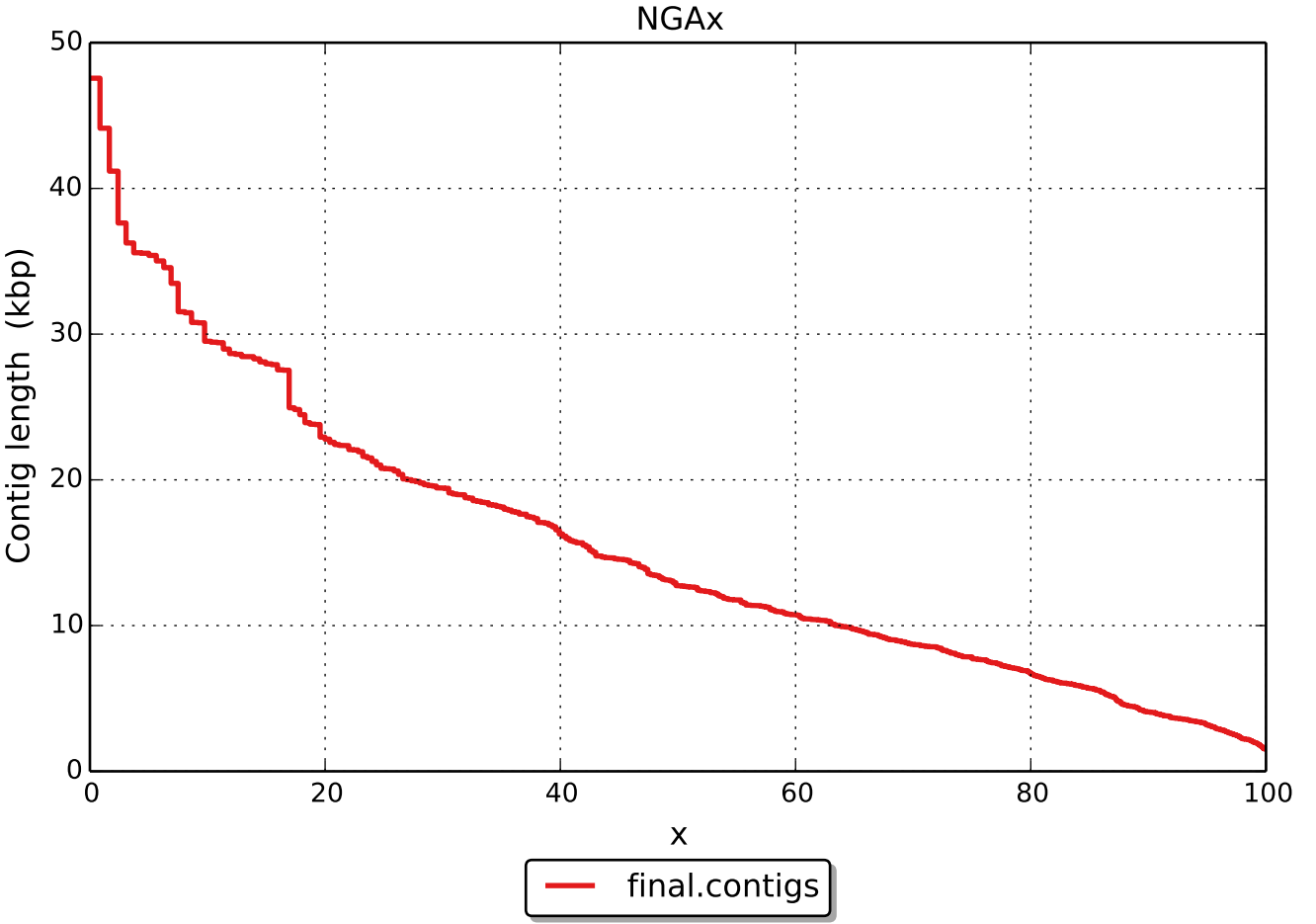

Nx
Contig length (kbp)
50
40
30
20
10
0
0
20
40
60
80
100
x
final.contigs


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


Misassemblies
2.0
1.5
1.0
0.5
0.0
final.contigs
relocations


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


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