Report

	final.contigs
# contigs (>= 0 bp)	1113
# contigs (>= 1000 bp)	921
Total length (>= 0 bp)	5235177
Total length (>= 1000 bp)	5097308
# contigs	1113
Largest contig	33527
Total length	5235177
Reference length	5547323
GC (%)	50.29
Reference GC (%)	50.48
N50	7835
NG50	7246
N75	4231
NG75	3654
L50	202
LG50	223
L75	426
LG75	485
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	2233
# local misassemblies	3
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	92.833
Duplication ratio	1.017
# N's per 100 kbp	0.00
# mismatches per 100 kbp	44.27
# indels per 100 kbp	0.33
Largest alignment	33527
NA50	7835
NGA50	7246
NA75	4231
NGA75	3654
LA50	202
LGA50	223
LA75	426
LGA75	485

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

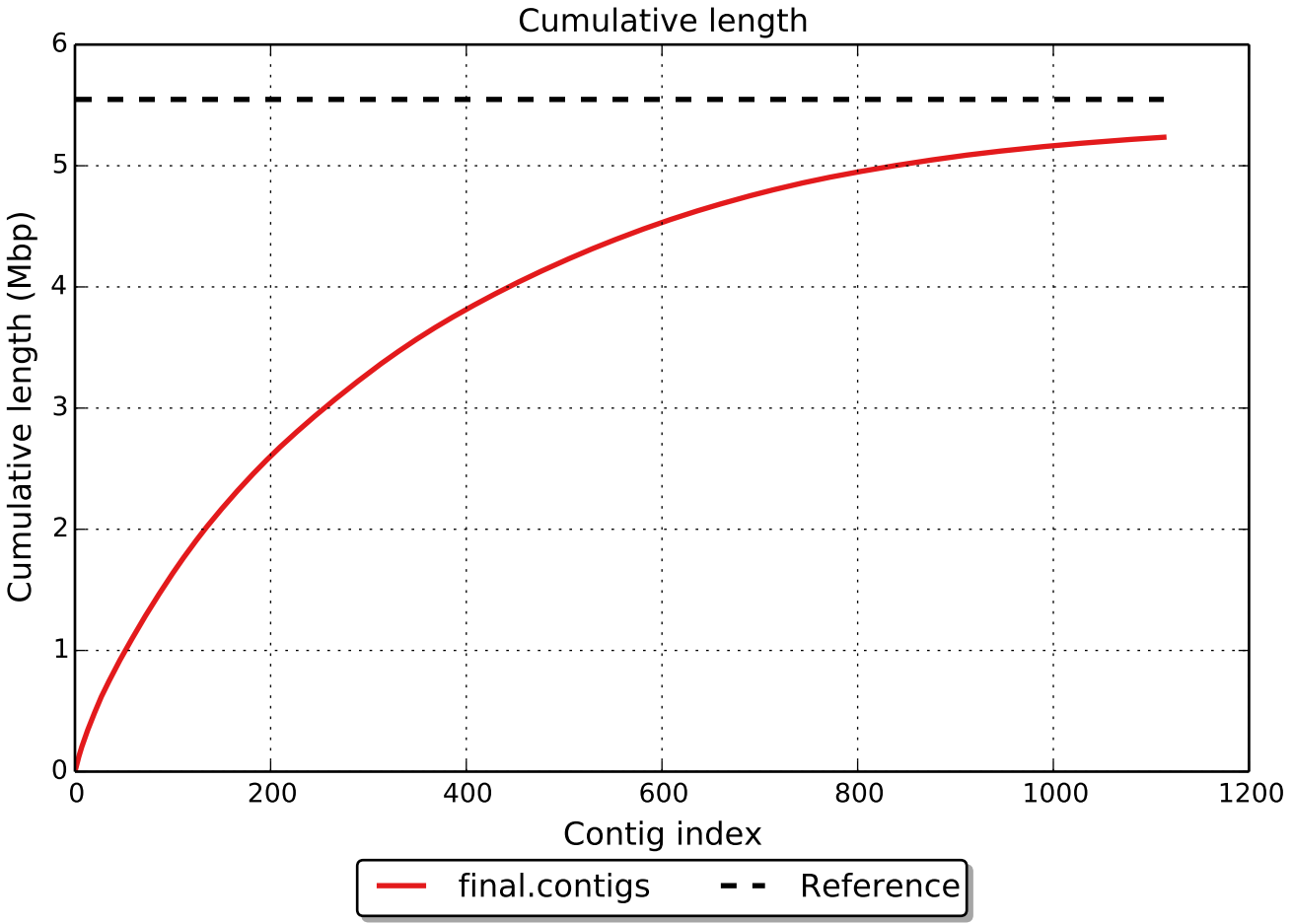
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	2233
# local misassemblies	3
# mismatches	2280
# indels	17
# short indels	16
# long indels	1
Indels length	22

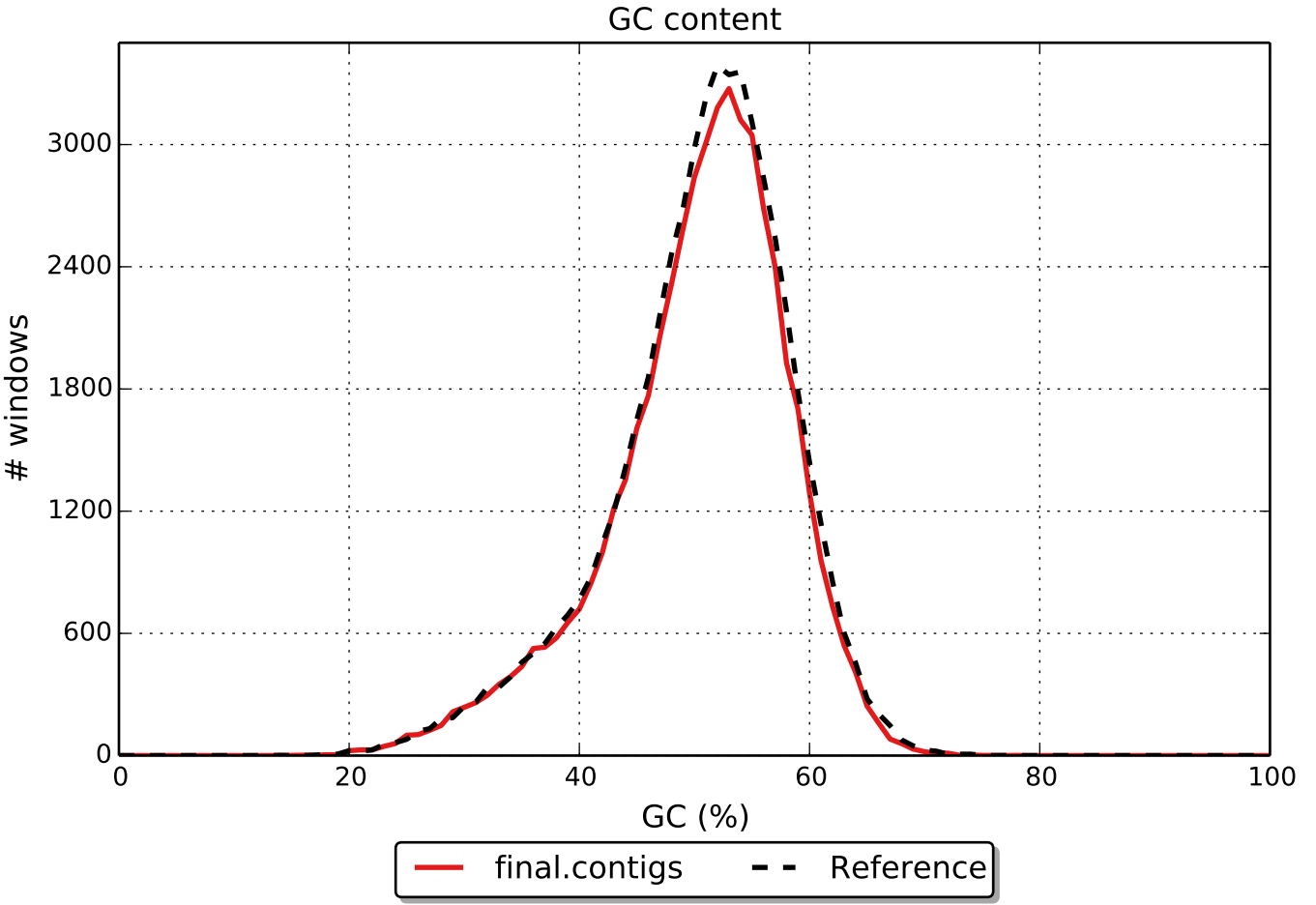
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

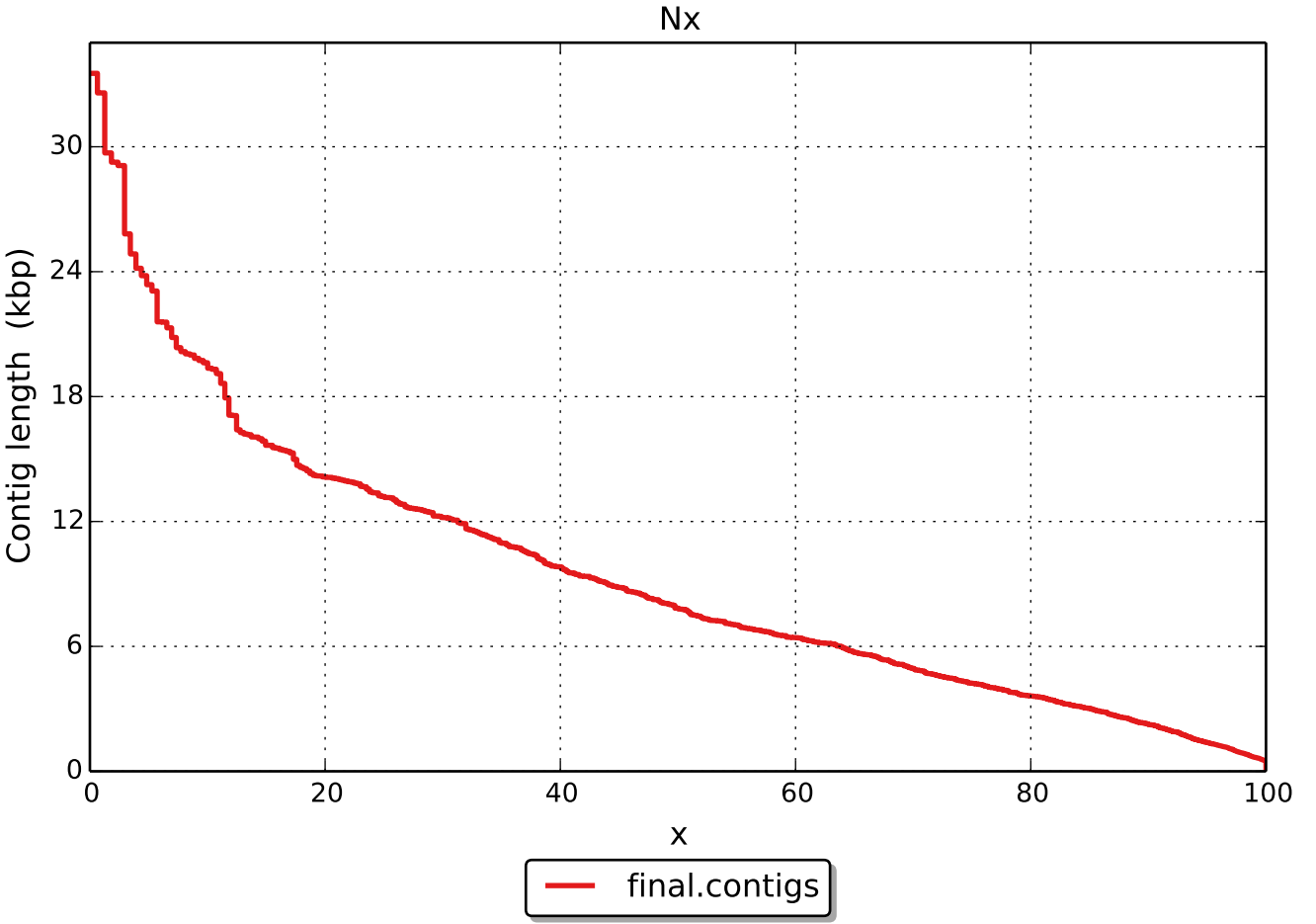
Unaligned report

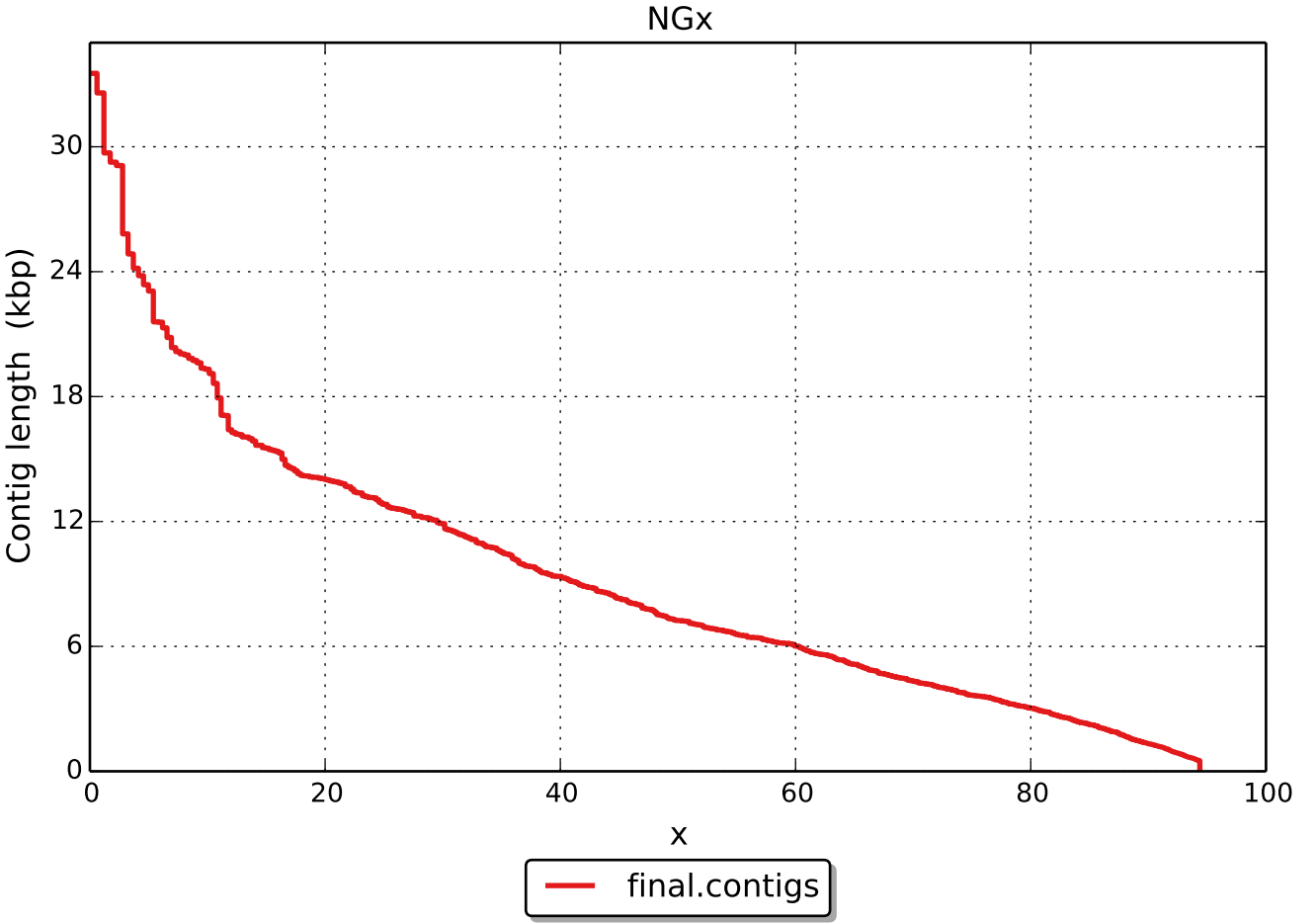
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

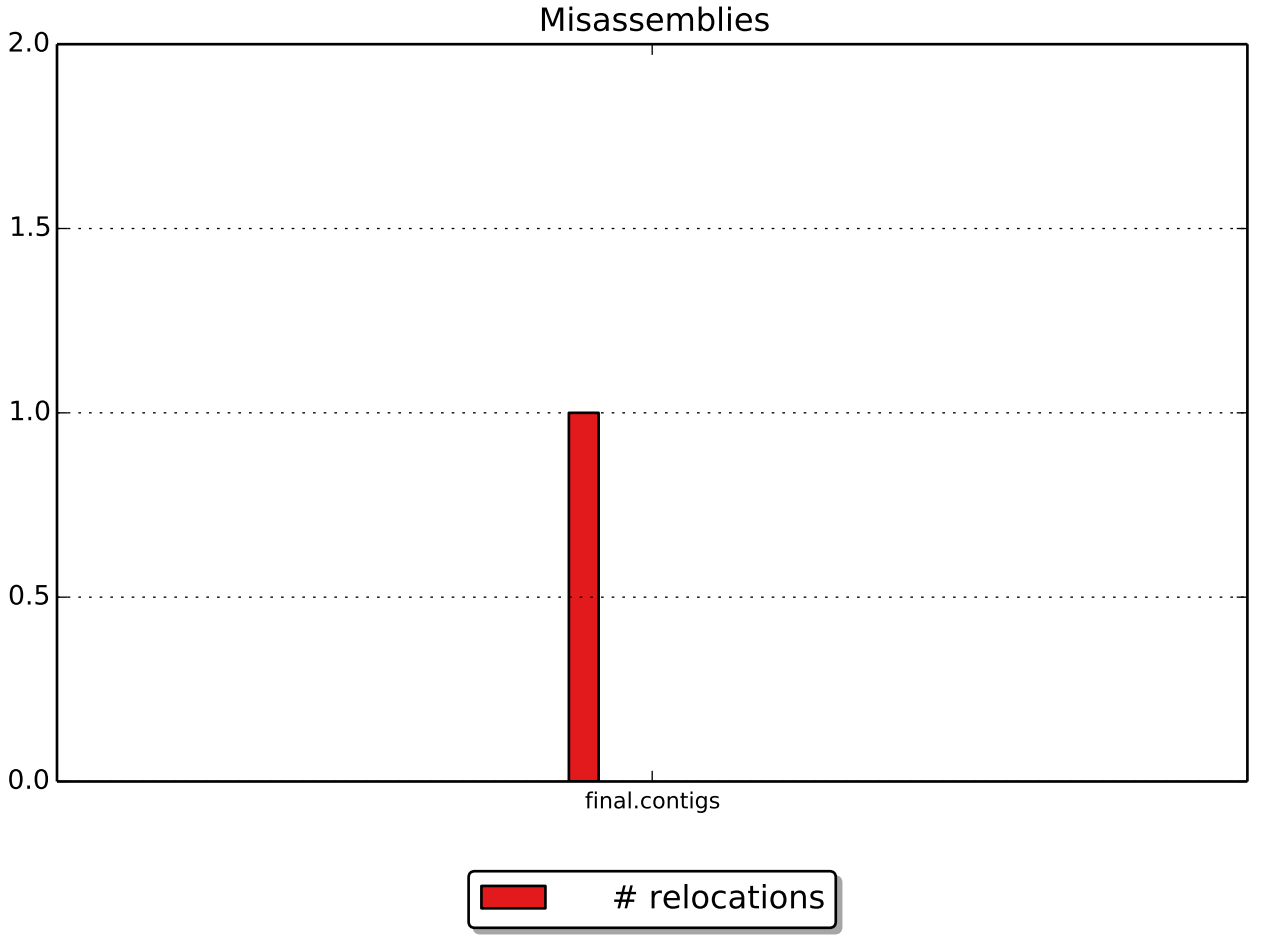
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

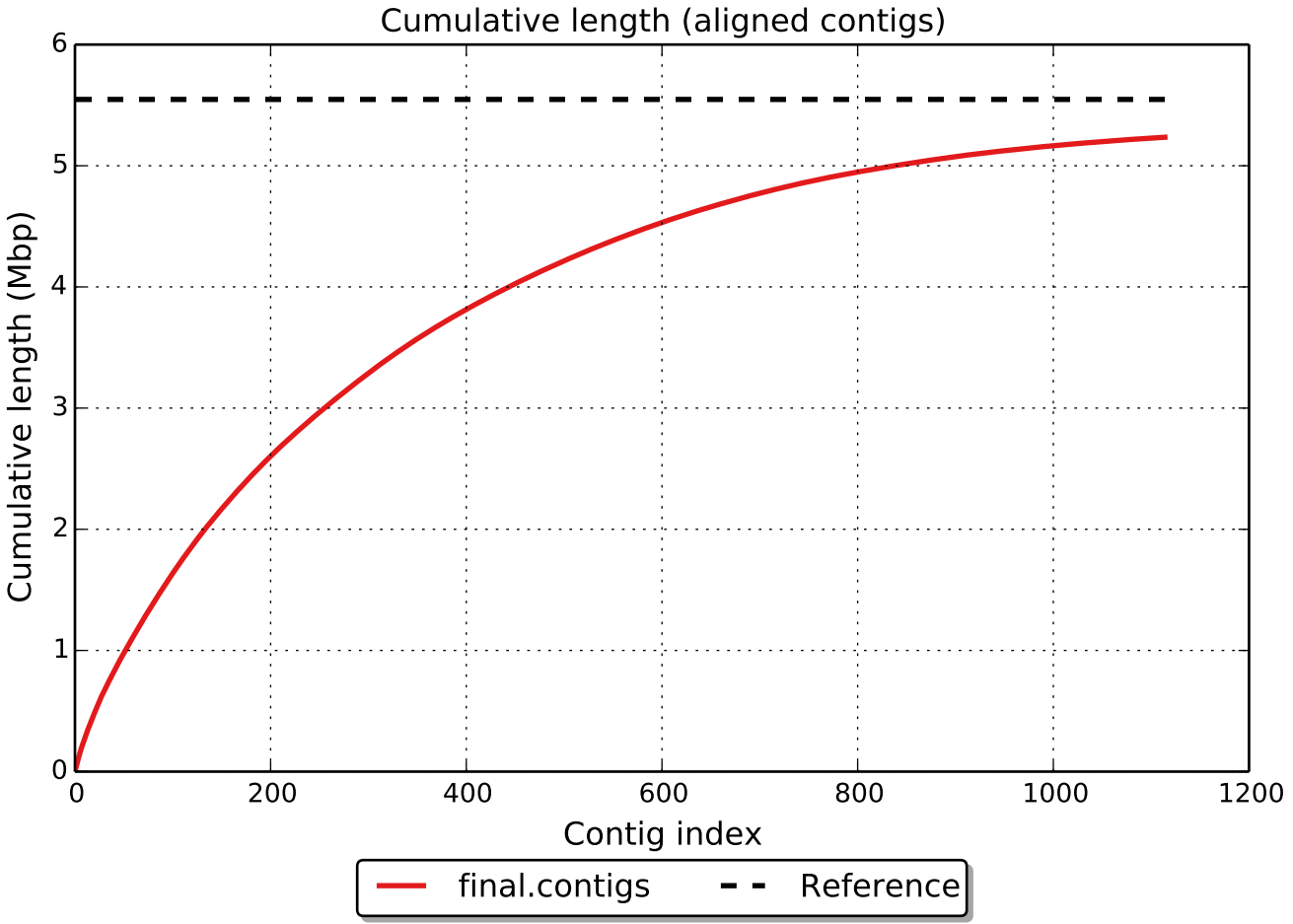

Cumulative length
Cumulative length (Mbp)
0
1
2
3
4
5
6
0
200
400
600
800
1000
1200
Contig index
final.contigs
Reference

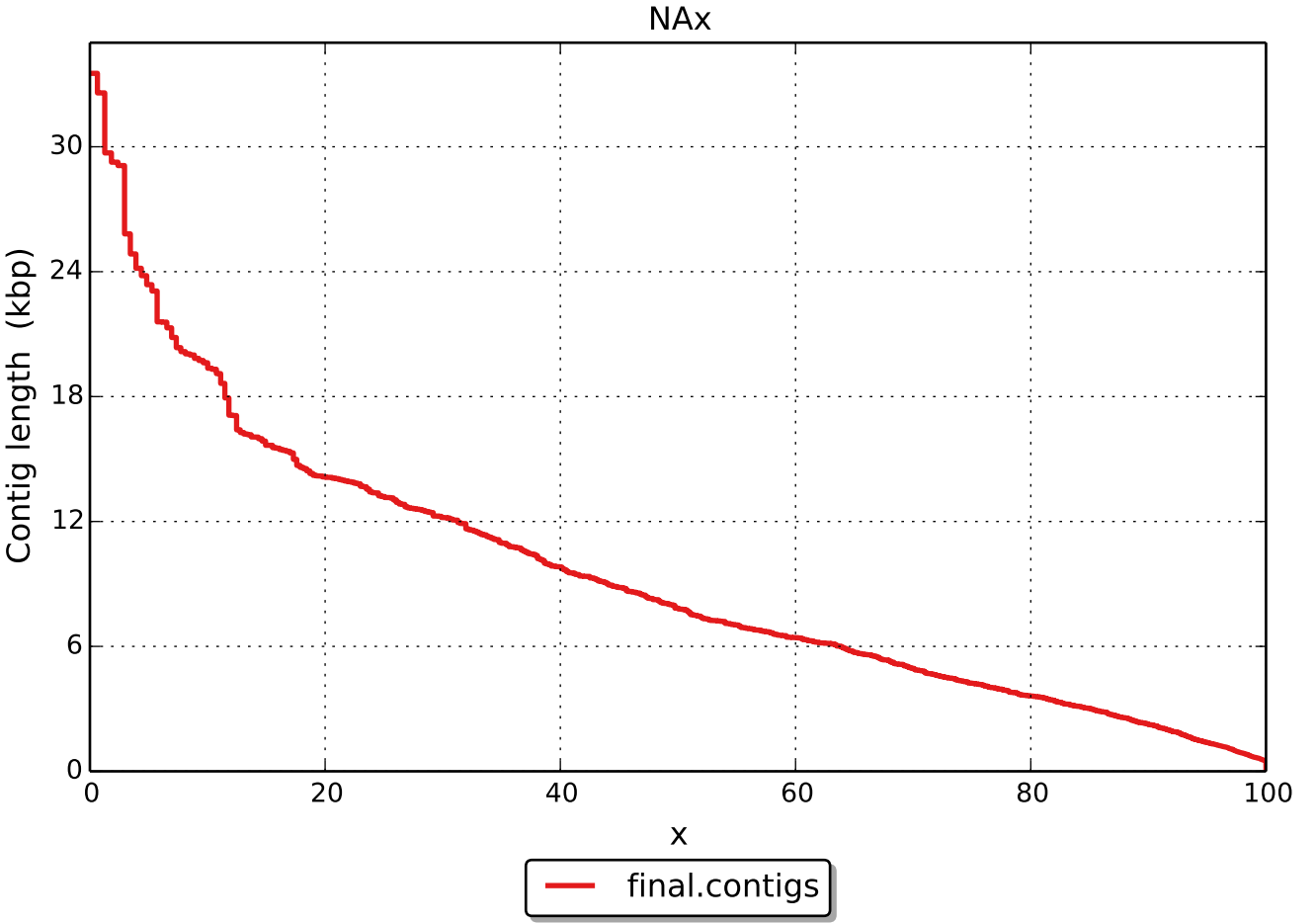

GC content
windows
3000
2400
1800
1200
600
0
0
20
40
60
80
100
GC (%)
final.contigs
Reference

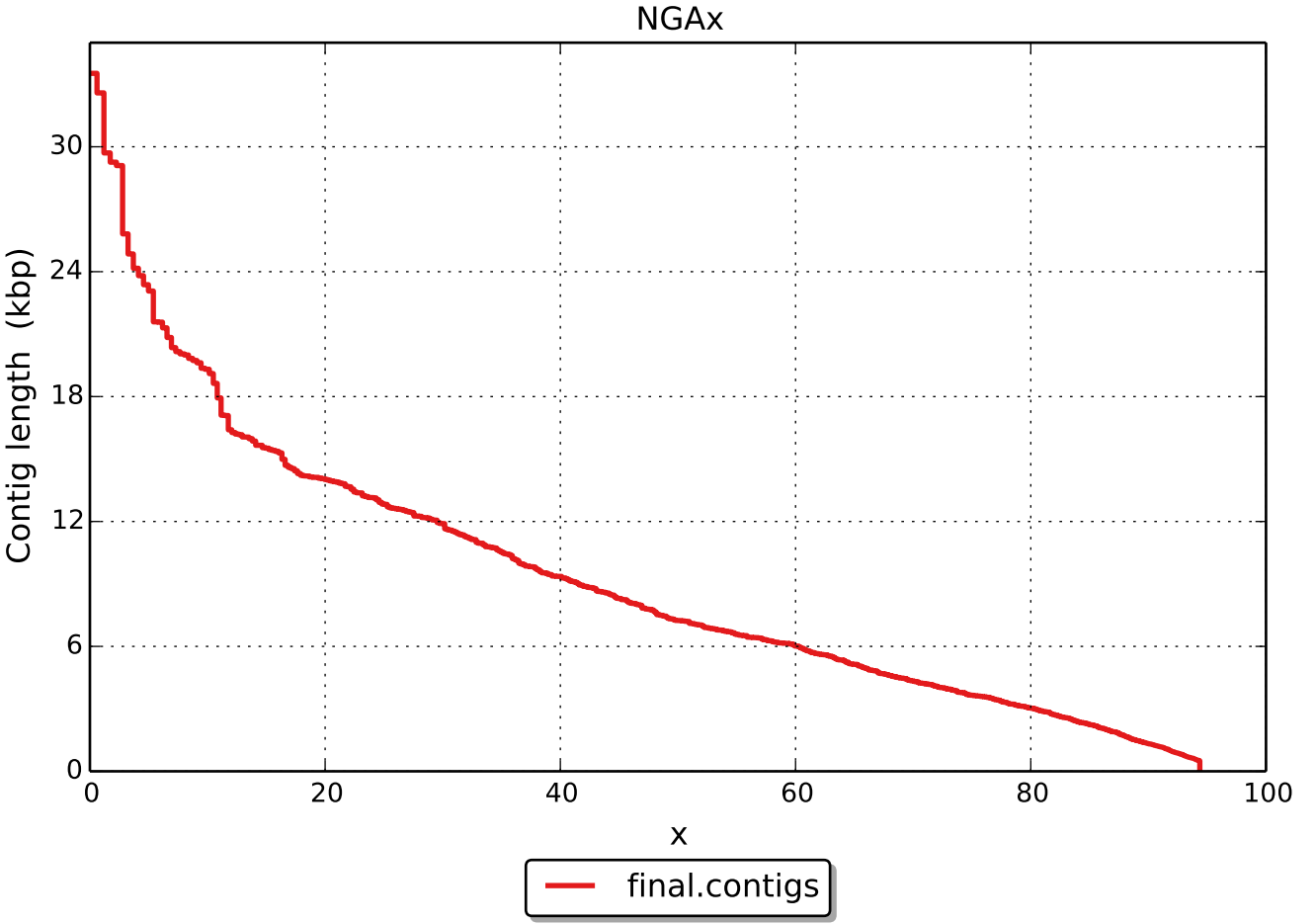

Nx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
final.contigs


NGx
Contig length (kbp)
30
24
18
12
6
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
800
1000
1200
Contig index
final.contigs
Reference


NAx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
final.contigs