Report

	final.contigs
# contigs (>= 0 bp)	1231
# contigs (>= 1000 bp)	1081
Total length (>= 0 bp)	5624502
Total length (>= 1000 bp)	5511564
# contigs	1231
Largest contig	30455
Total length	5624502
Reference length	5547323
GC (%)	50.49
Reference GC (%)	50.49
N50	6926
NG50	7028
N75	3914
NG75	4037
L50	257
LG50	251
L75	526
LG75	511
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	17136
# local misassemblies	0
# unaligned contigs	0 + 2 part
Unaligned length	6052
Genome fraction (%)	99.347
Duplication ratio	1.019
# N's per 100 kbp	0.00
# mismatches per 100 kbp	8.47
# indels per 100 kbp	0.02
Largest alignment	30455
NA50	6926
NGA50	7018
NA75	3897
NGA75	4031
LA50	257
LGA50	252
LA75	527
LGA75	513

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

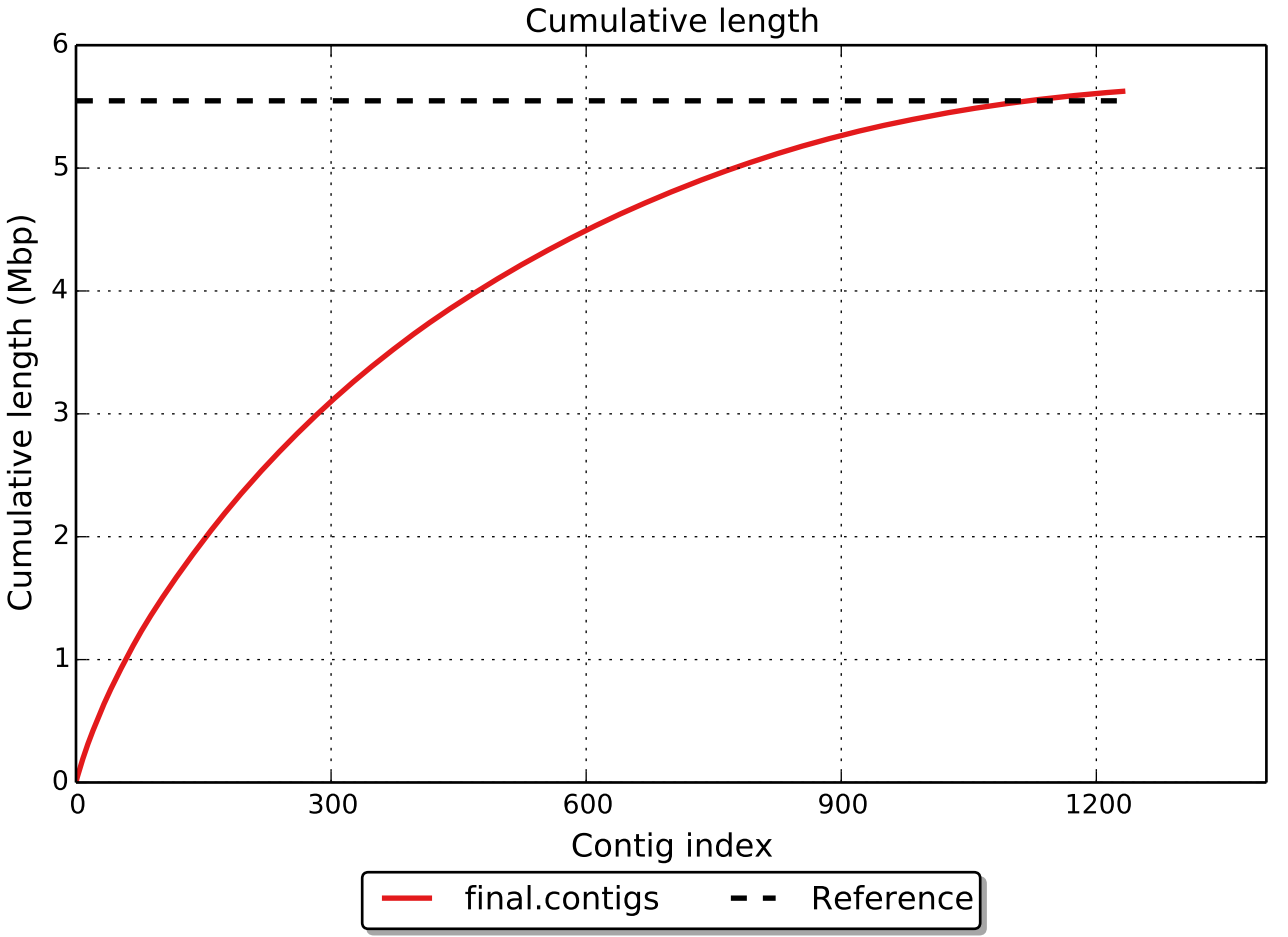
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	2
# misassembled contigs	1
Misassembled contigs length	17136
# local misassemblies	0
# mismatches	467
# indels	1
# short indels	1
# long indels	0
Indels length	1

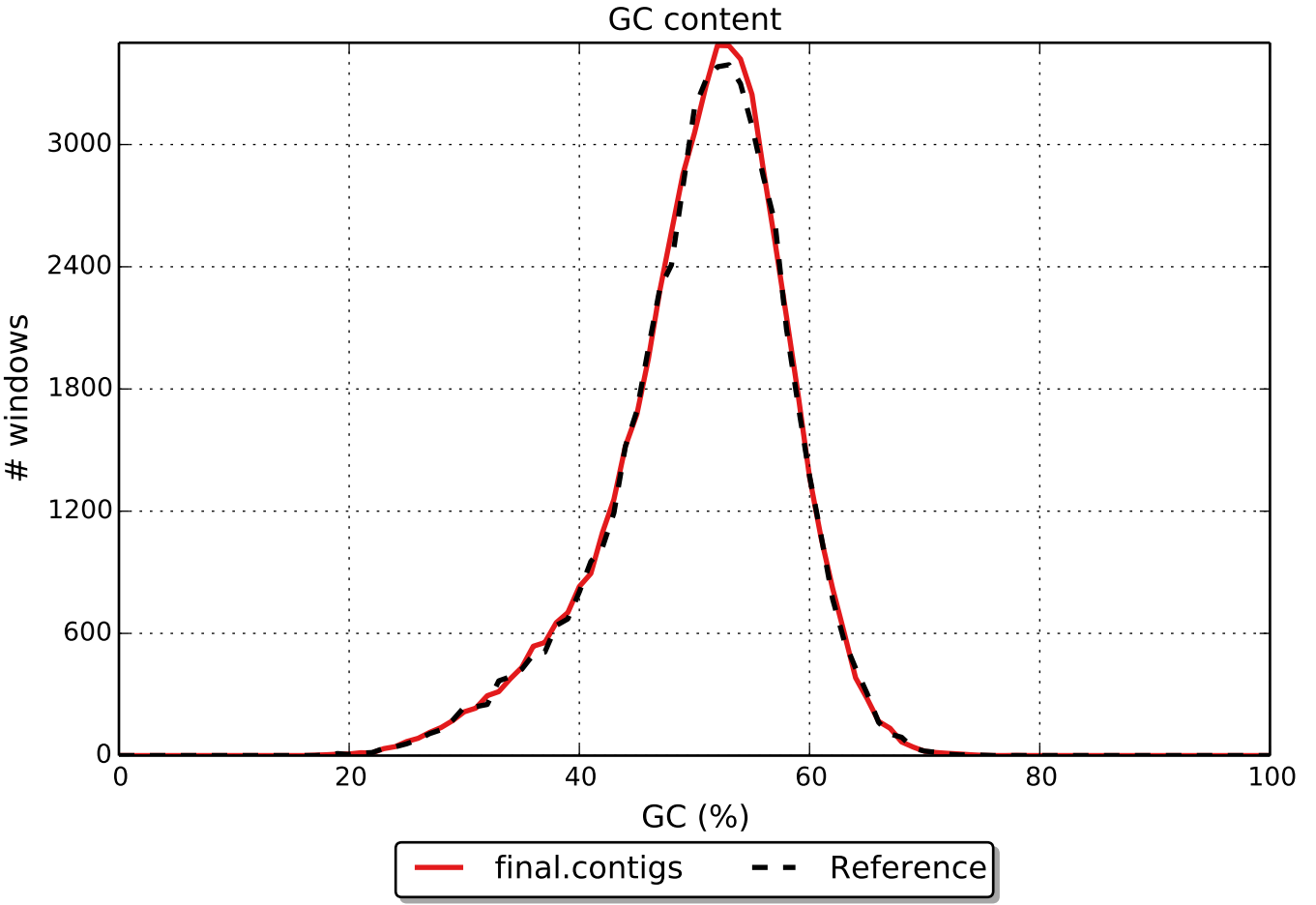
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

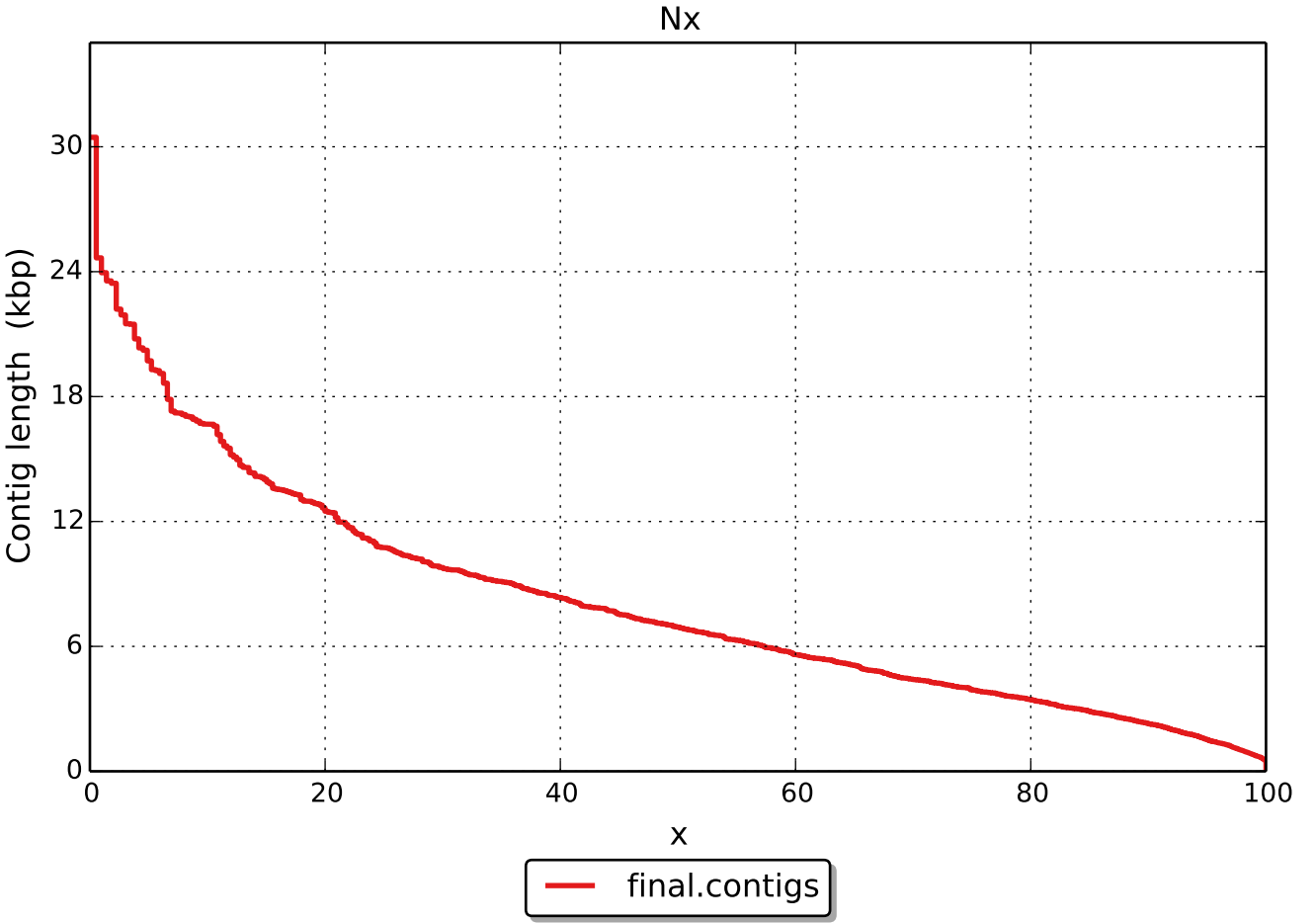
Unaligned report

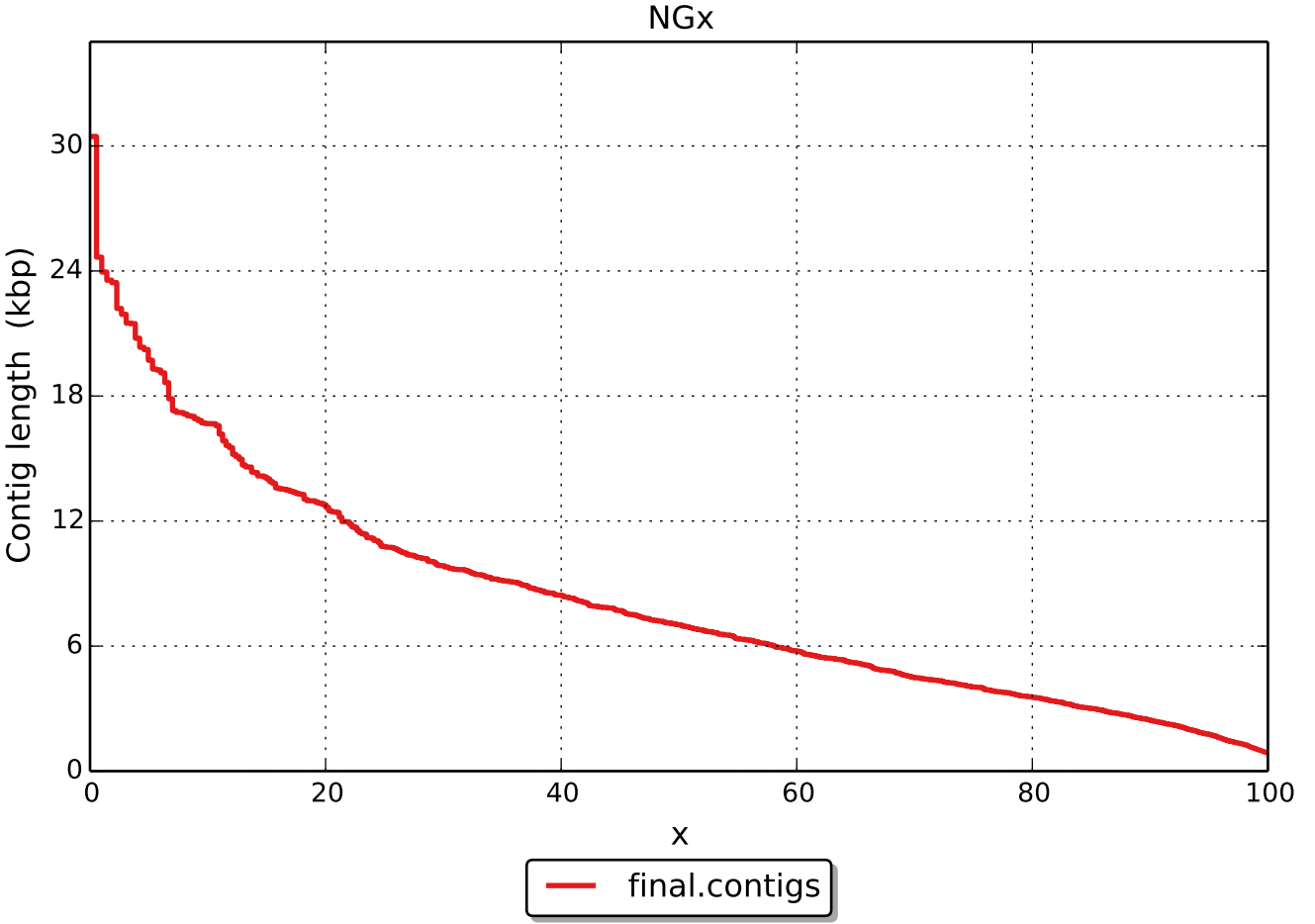
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
# with misassembly	1
# both parts are significant	2
Partially unaligned length	6052
# N's	0

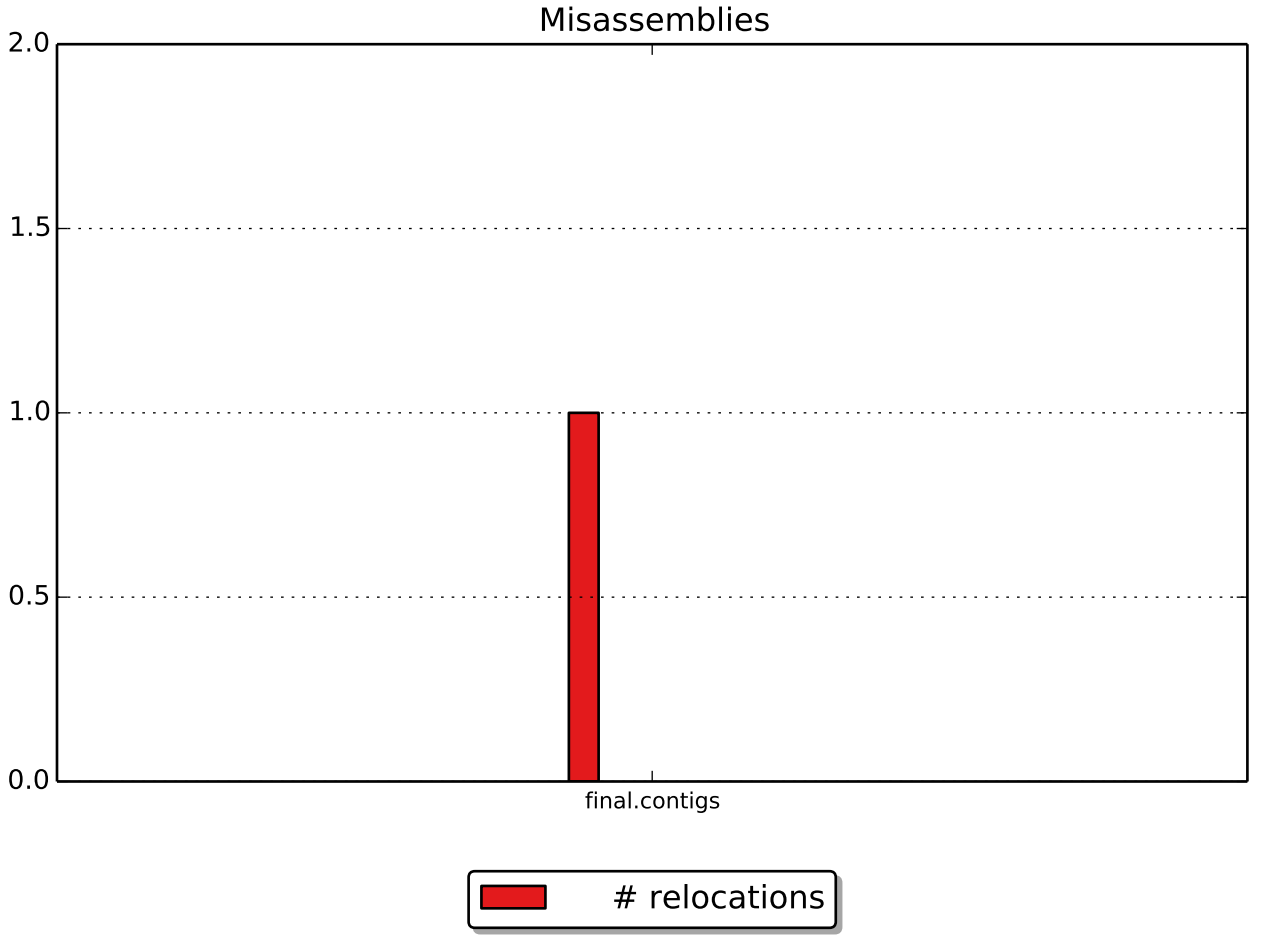
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

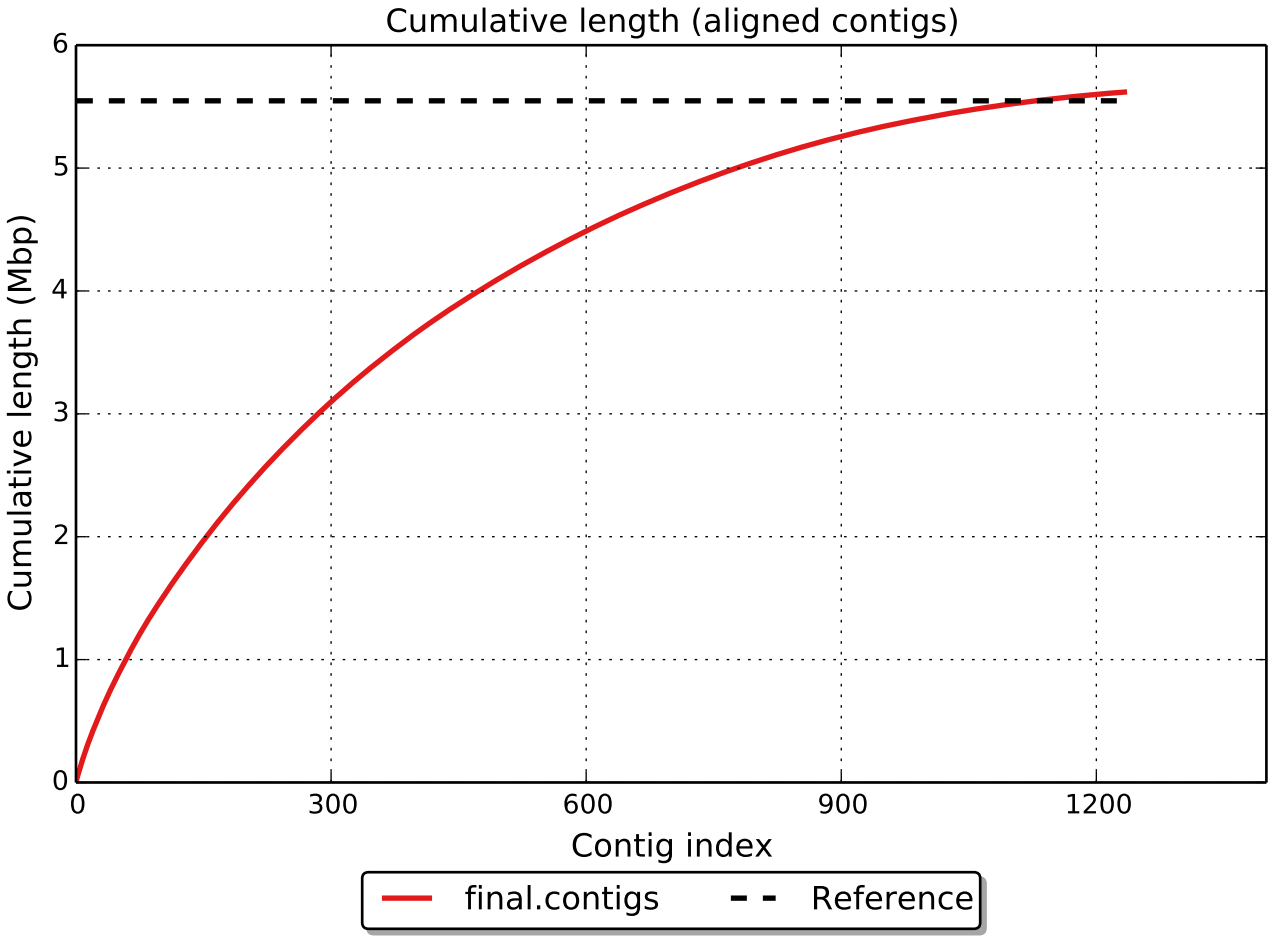

Cumulative length
Cumulative length (Mbp)
0
1
2
3
4
5
6
0
300
600
900
1200
Contig index
final.contigs
Reference

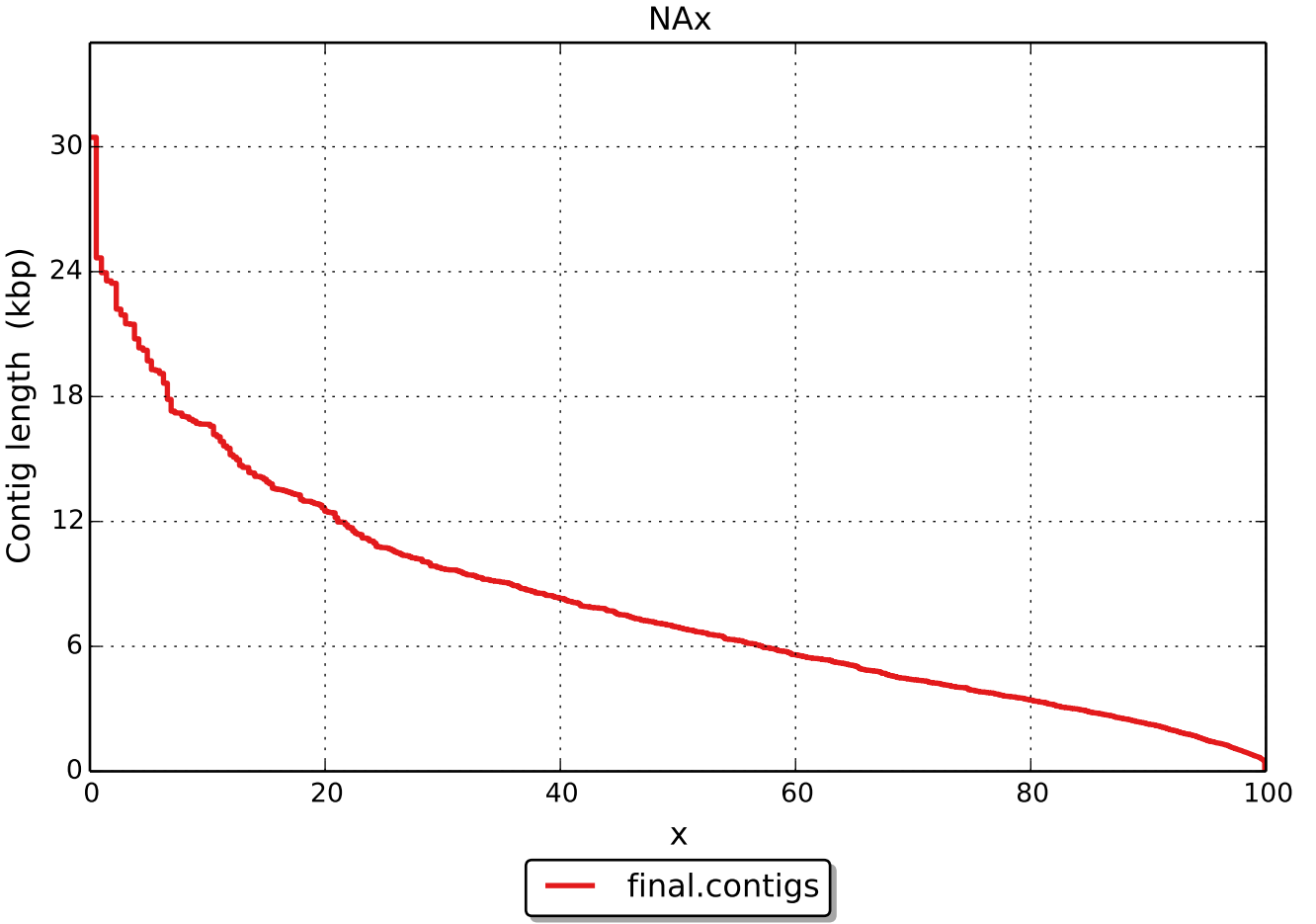

GC content
windows
3000
2400
1800
1200
600
0
0
20
40
60
80
100
GC (%)
final.contigs
Reference

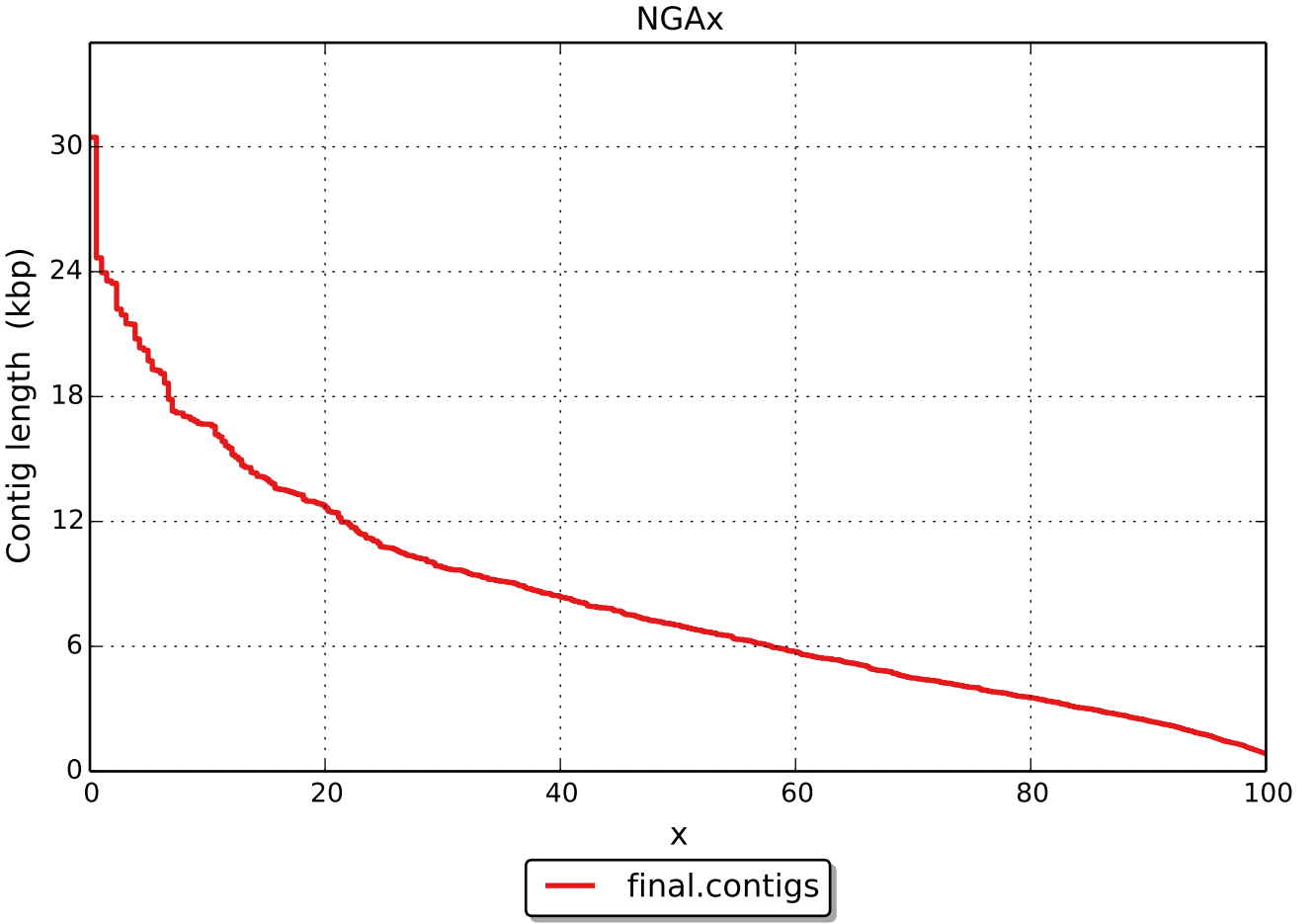

Nx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
final.contigs


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
300
600
900
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