Report

	final.contigs
# contigs (>= 0 bp)	1642
# contigs (>= 1000 bp)	1414
Total length (>= 0 bp)	5574789
Total length (>= 1000 bp)	5407881
# contigs	1642
Largest contig	24393
Total length	5574789
Reference length	5478683
GC (%)	50.50
Reference GC (%)	50.50
N50	4742
NG50	4836
N75	2900
NG75	2991
L50	362
LG50	352
L75	738
LG75	713
# misassemblies	4
# misassembled contigs	4
Misassembled contigs length	37200
# local misassemblies	0
# unaligned contigs	0 + 2 part
Unaligned length	13598
Genome fraction (%)	98.795
Duplication ratio	1.027
# N's per 100 kbp	0.00
# mismatches per 100 kbp	28.56
# indels per 100 kbp	0.00
Largest alignment	24393
NA50	4701
NGA50	4821
NA75	2856
NGA75	2968
LA50	364
LGA50	354
LA75	743
LGA75	718

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

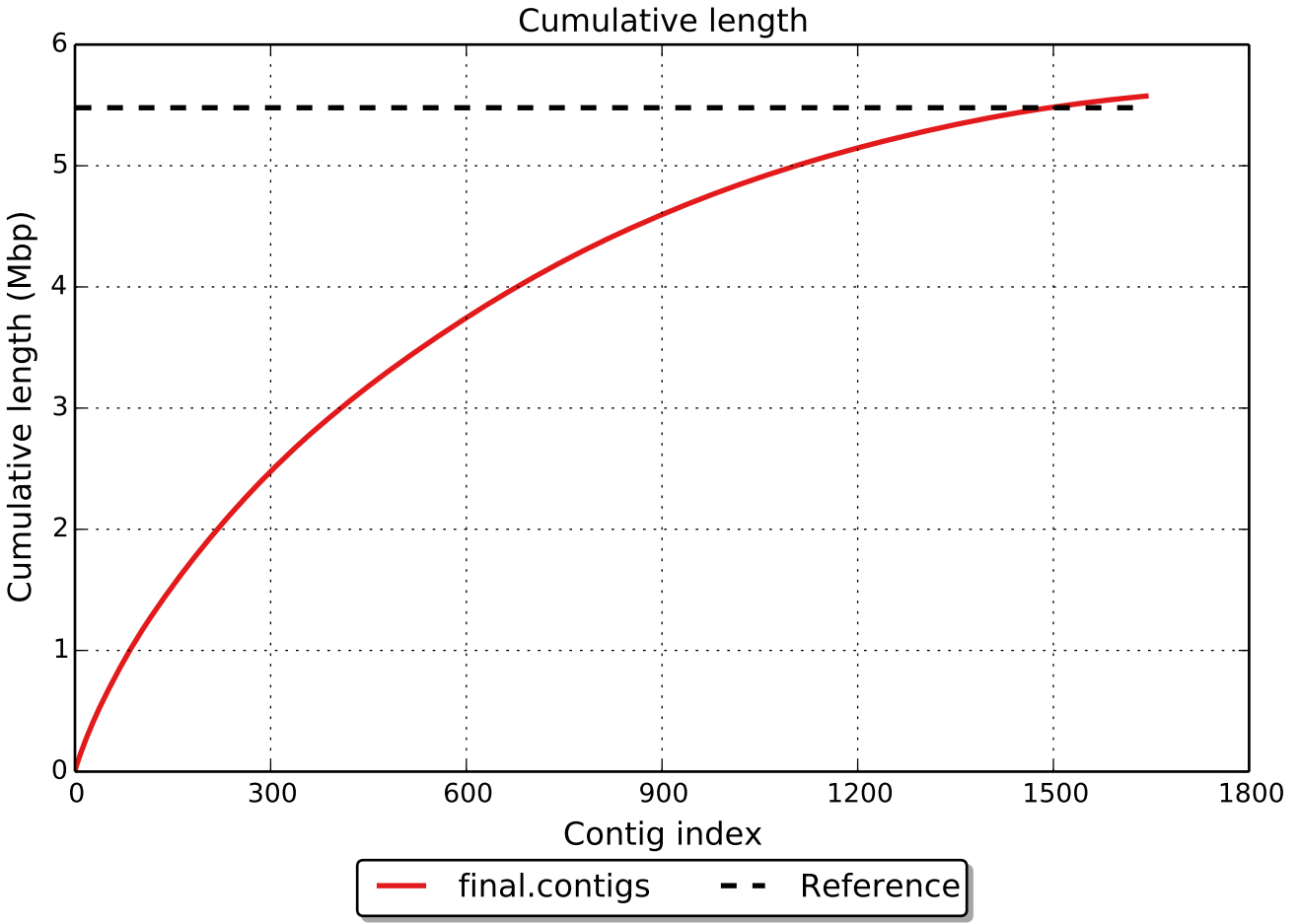
	final.contigs
# misassemblies	4
# relocations	4
# translocations	0
# inversions	0
# possibly misassembled contigs	3
# misassembled contigs	4
Misassembled contigs length	37200
# local misassemblies	0
# mismatches	1546
# indels	0
# short indels	0
# long indels	0
Indels length	0

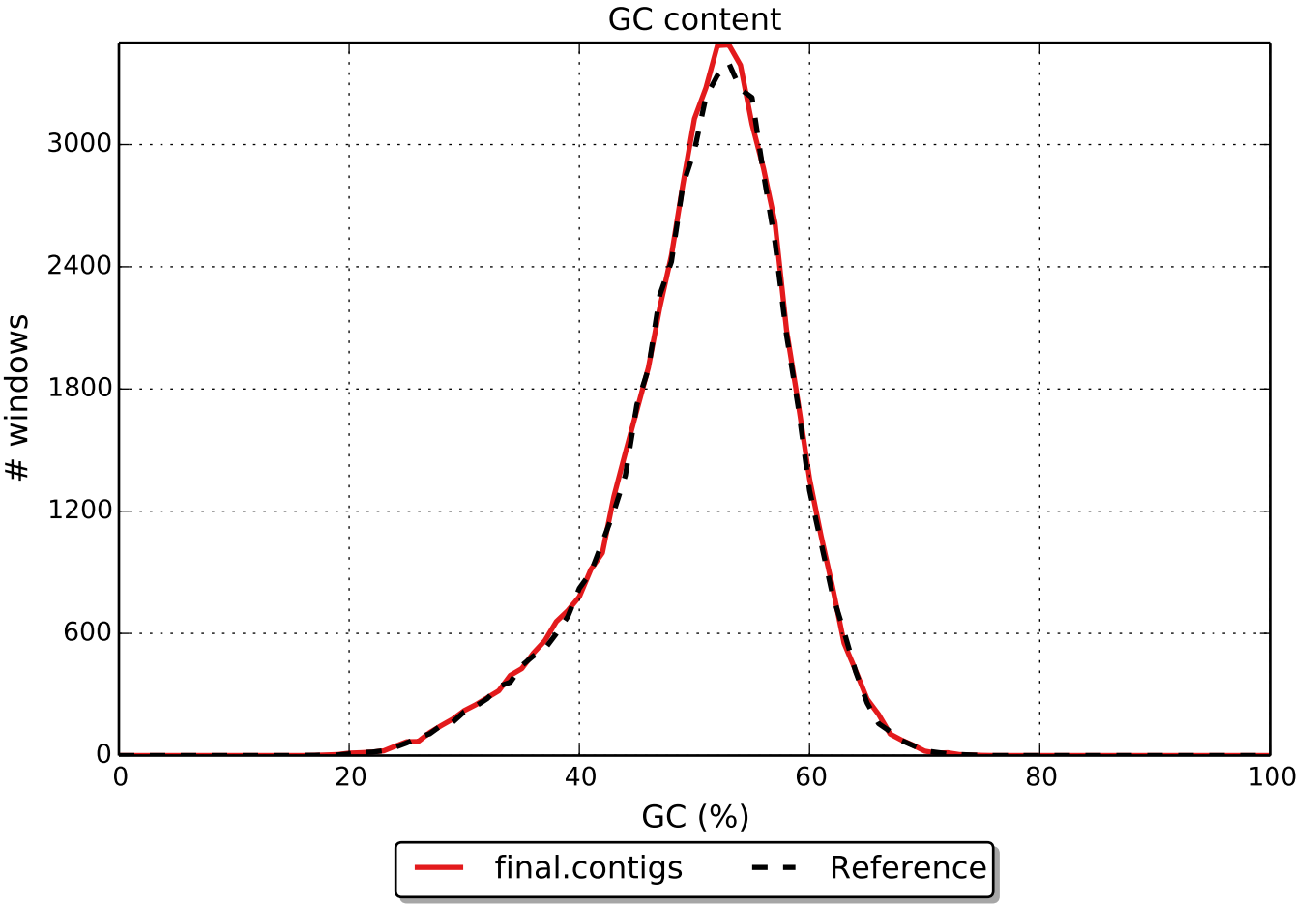
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

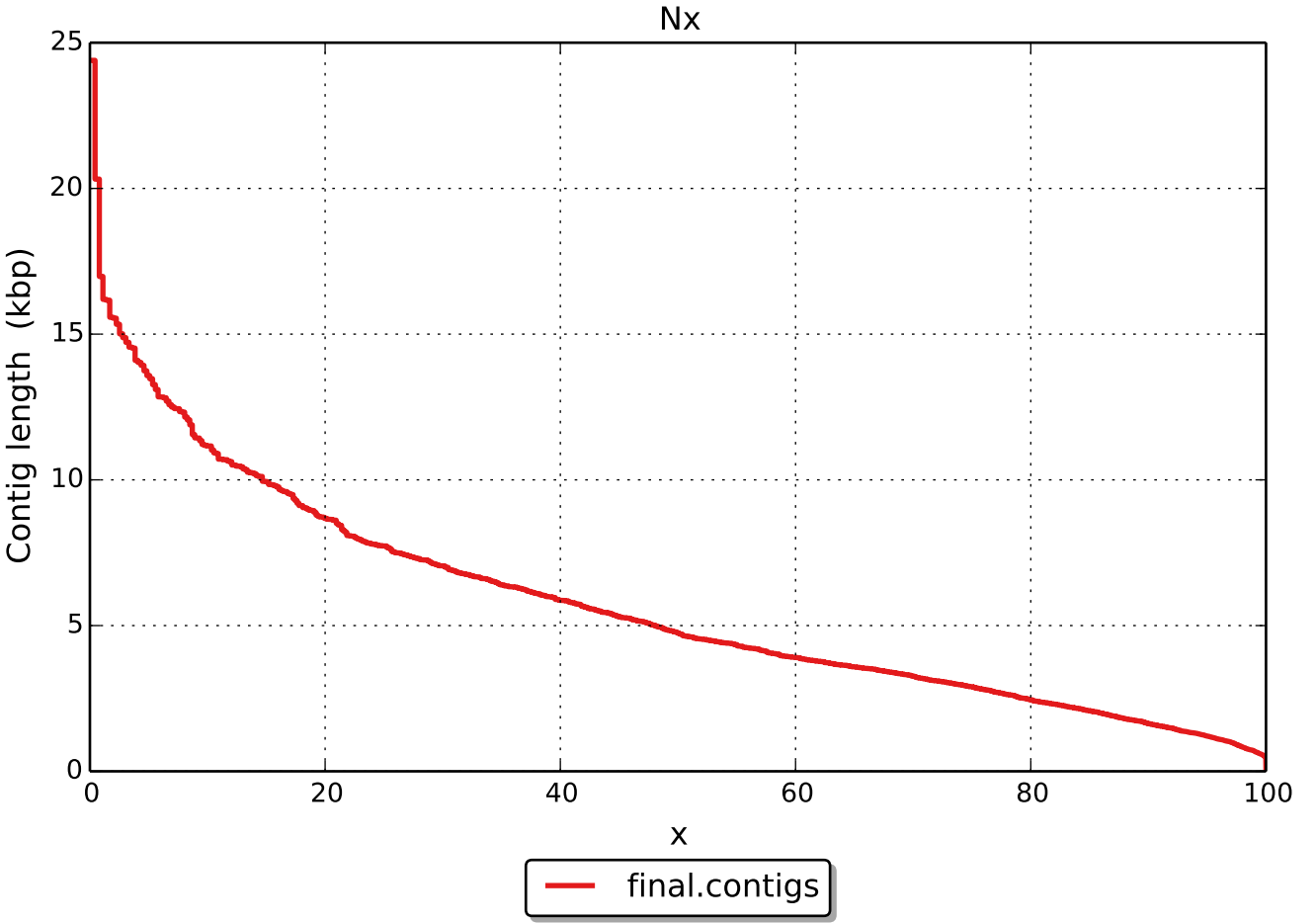
Unaligned report

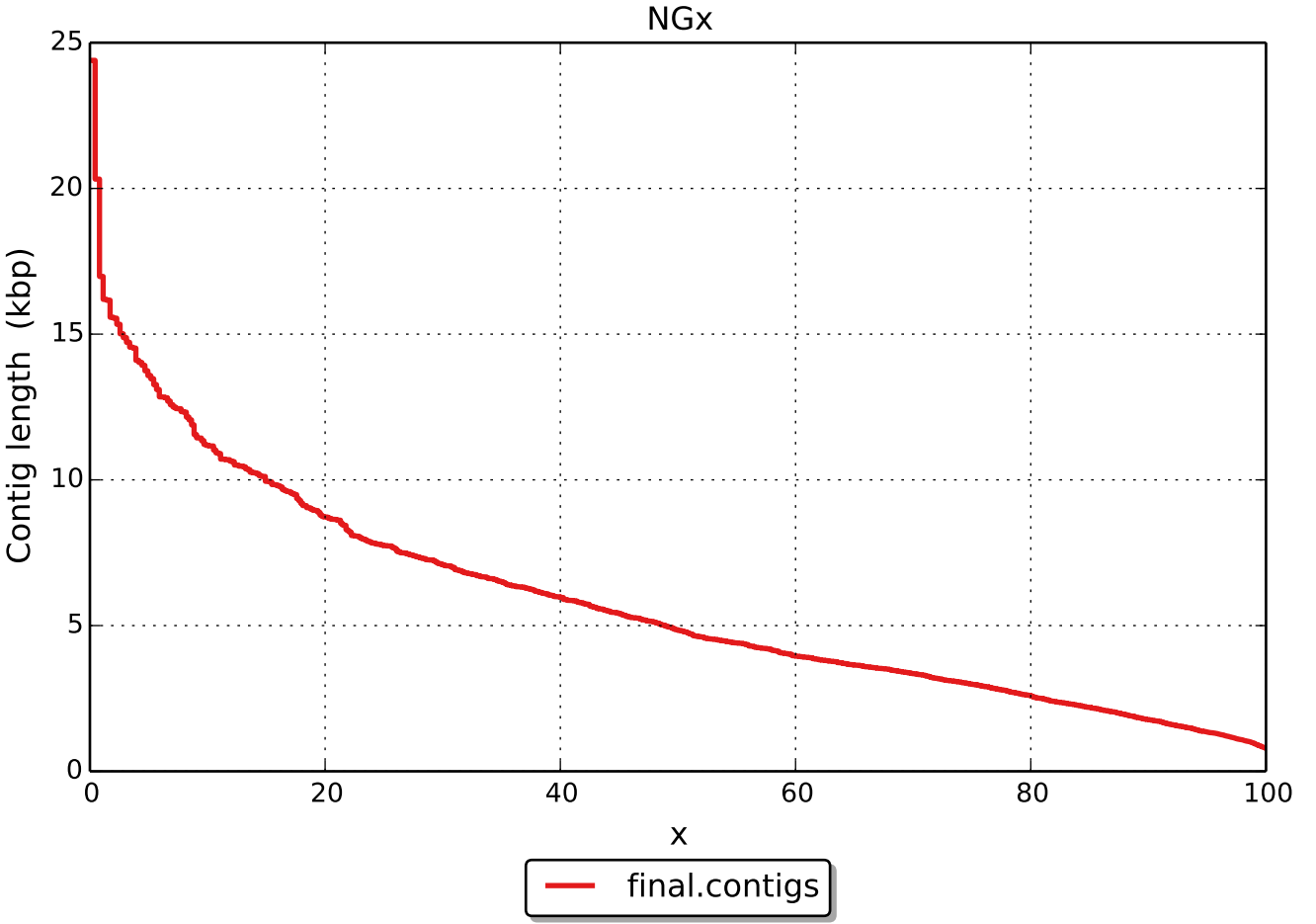
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	2
Partially unaligned length	13598
# N's	0

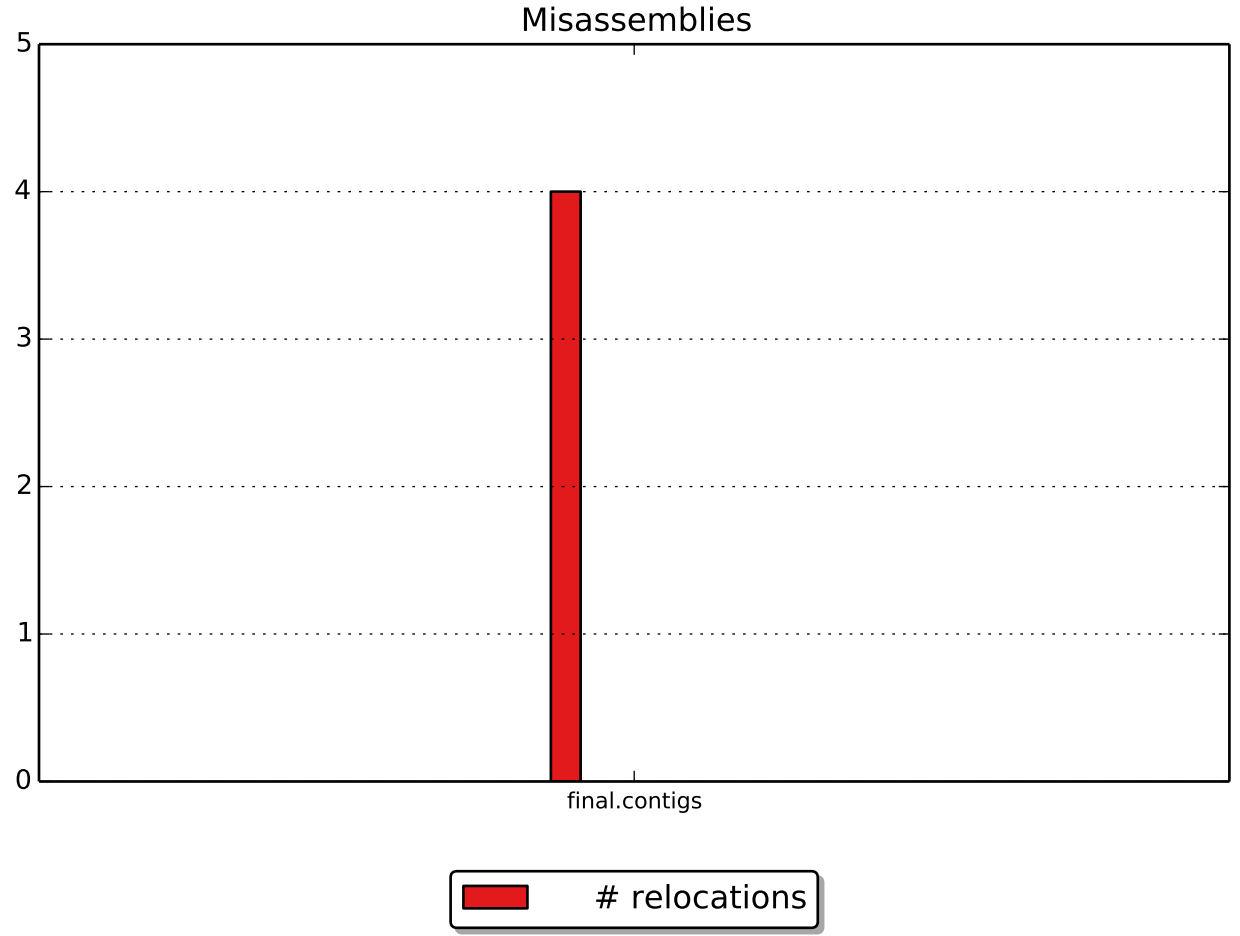
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

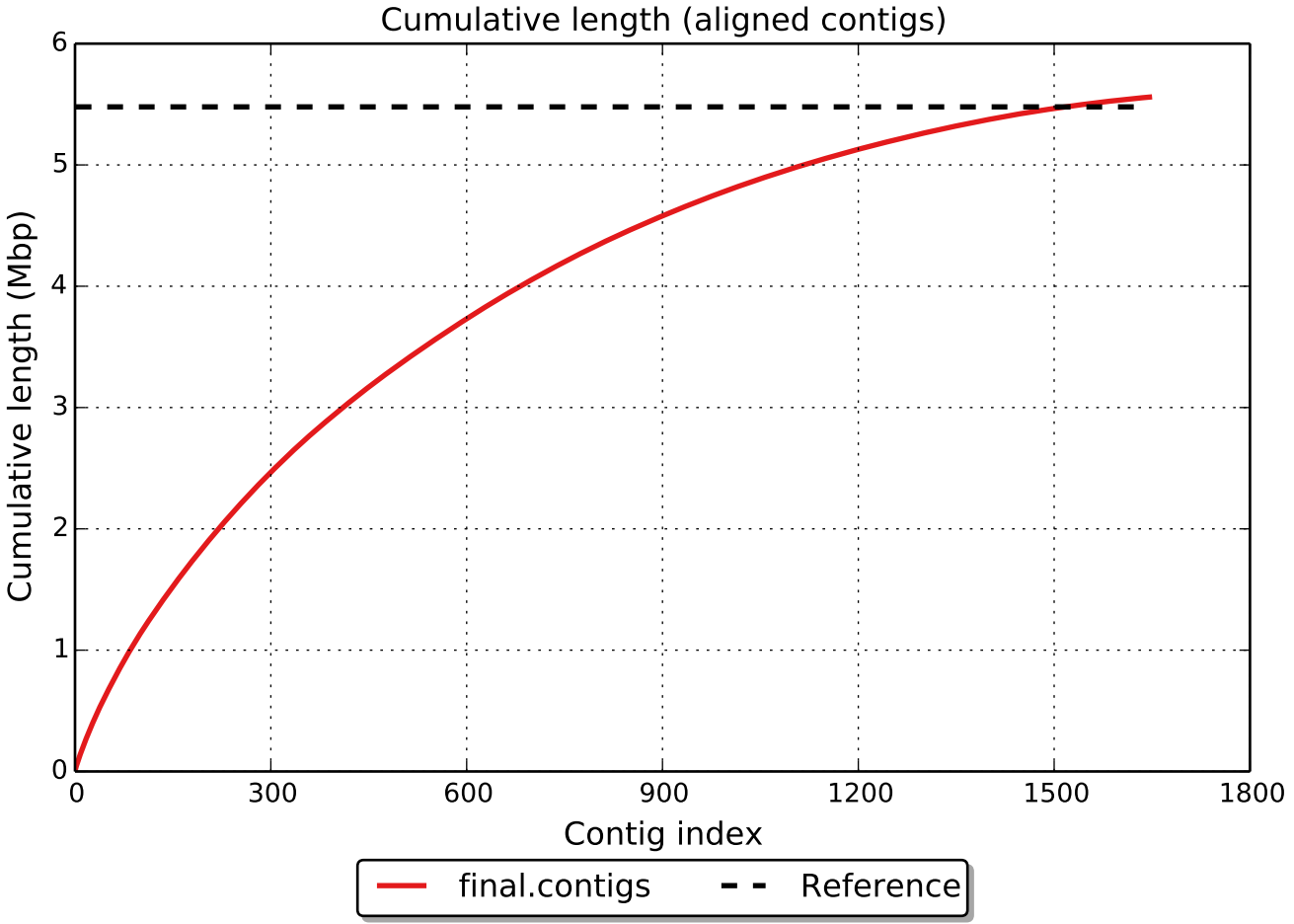

Cumulative length
Cumulative length (Mbp)
0
1
2
3
4
5
6
0
300
600
900
1200
1500
1800
Contig index
final.contigs
Reference

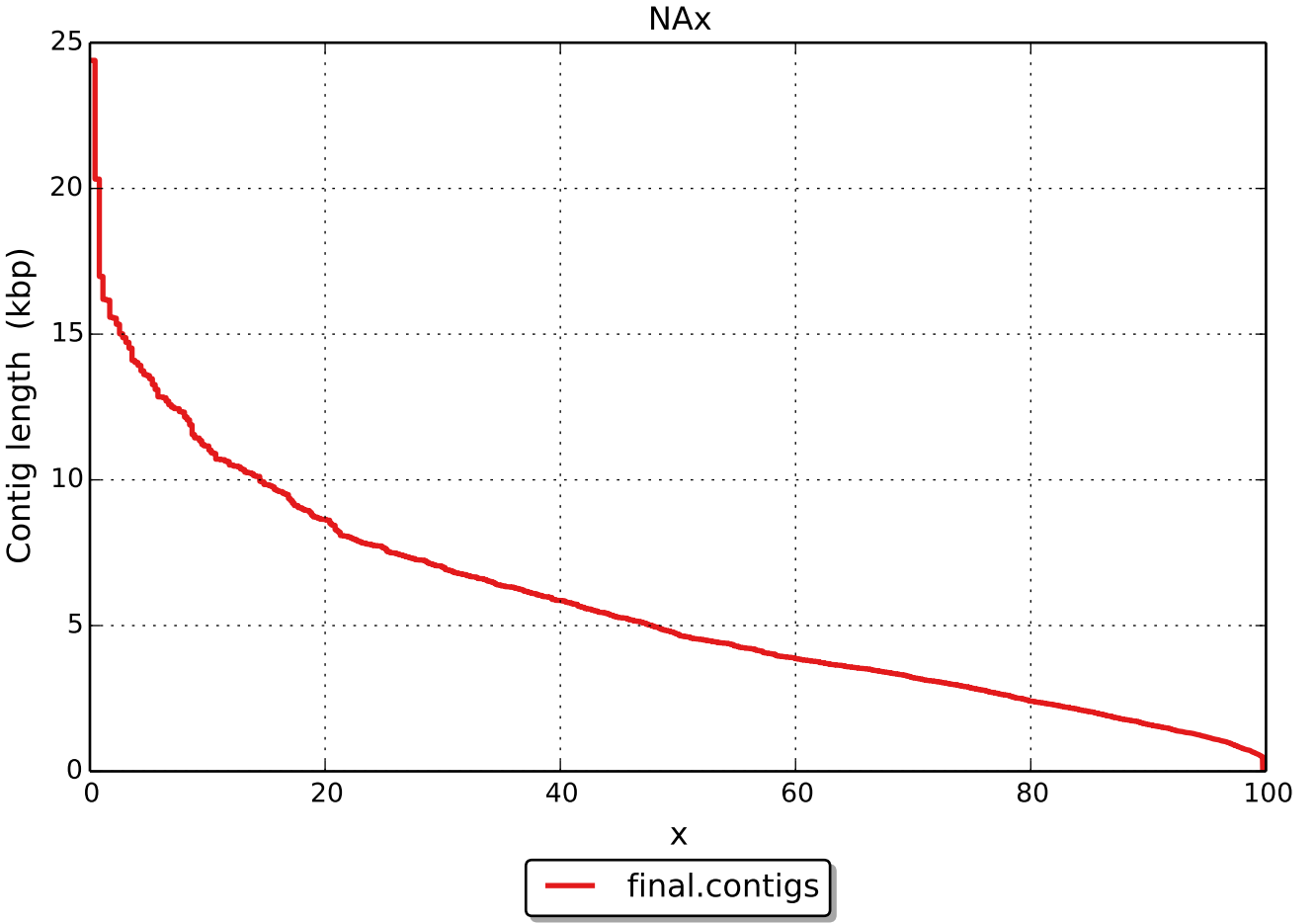

GC content
windows
3000
2400
1800
1200
600
0
0
20
40
60
80
100
GC (%)
final.contigs
Reference

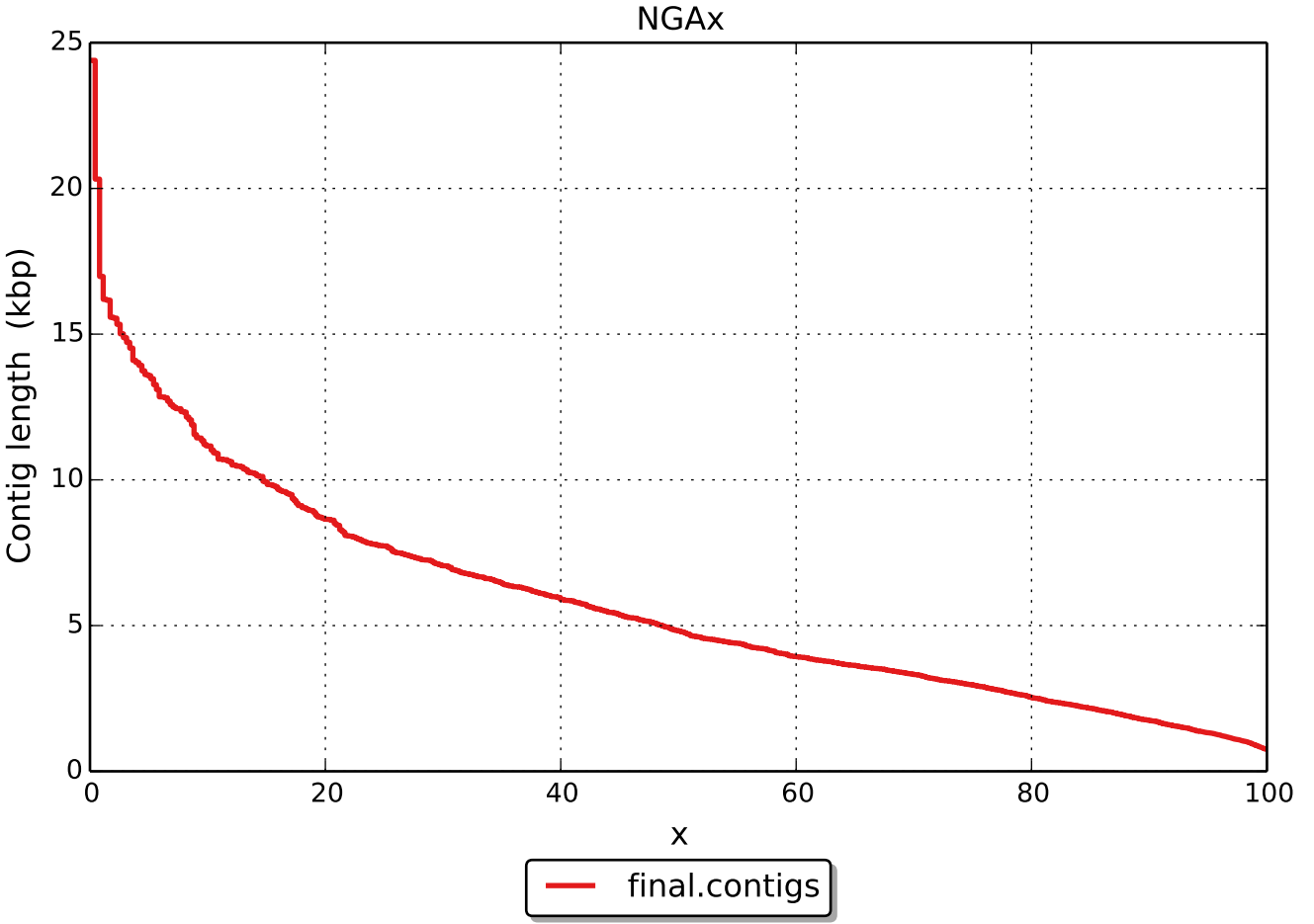

Nx
Contig length (kbp)
25
20
15
10
5
0
0
20
40
60
80
100
x
final.contigs


NGx
Contig length (kbp)
25
20
15
10
5
0
0
20
40
60
80
100
x
final.contigs


Misassemblies
5
4
3
2
1
0
final.contigs
relocations


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
1
2
3
4
5
6
0
300
600
900
1200
1500
1800
Contig index
final.contigs
Reference


NAx
Contig length (kbp)
25
20
15
10
5
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (kbp)
25
20
15
10
5
0
0
20
40
60
80
100
x
final.contigs