Report

	final.contigs
# contigs (>= 0 bp)	6861
# contigs (>= 1000 bp)	3821
Total length (>= 0 bp)	11217884
Total length (>= 1000 bp)	9576202
# contigs	5380
Largest contig	12599
Total length	10721602
Reference length	11094646
GC (%)	50.38
Reference GC (%)	50.48
N50	2606
NG50	2534
N75	1575
NG75	1471
L50	1287
LG50	1360
L75	2606
LG75	2790
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	1135
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	93.303
Duplication ratio	1.036
# N's per 100 kbp	0.00
# mismatches per 100 kbp	33.47
# indels per 100 kbp	0.08
Largest alignment	12599
NA50	2606
NGA50	2534
NA75	1575
NGA75	1471
LA50	1287
LGA50	1360
LA75	2606
LGA75	2790

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

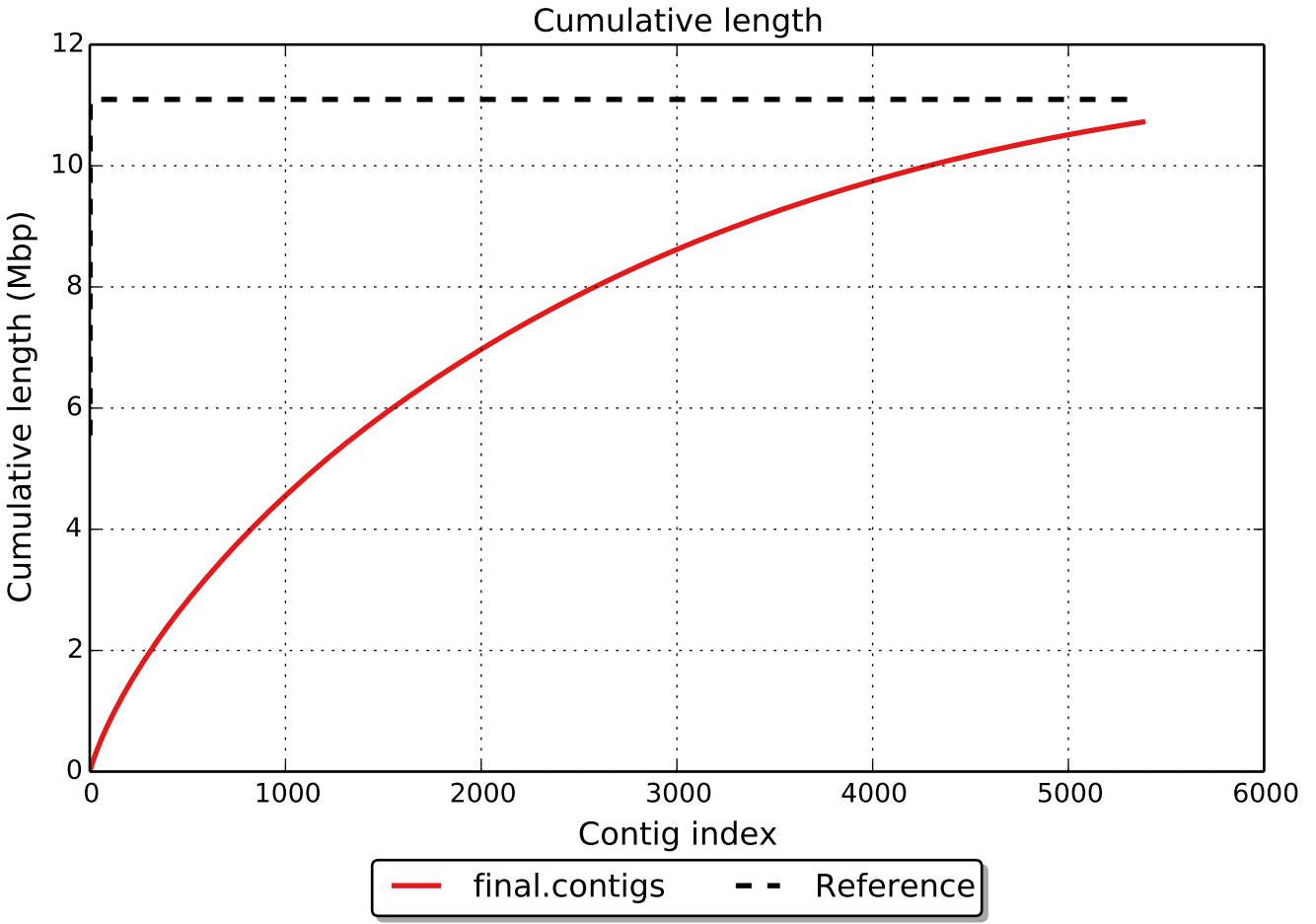
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	1135
# local misassemblies	0
# mismatches	3465
# indels	8
# short indels	6
# long indels	2
Indels length	33

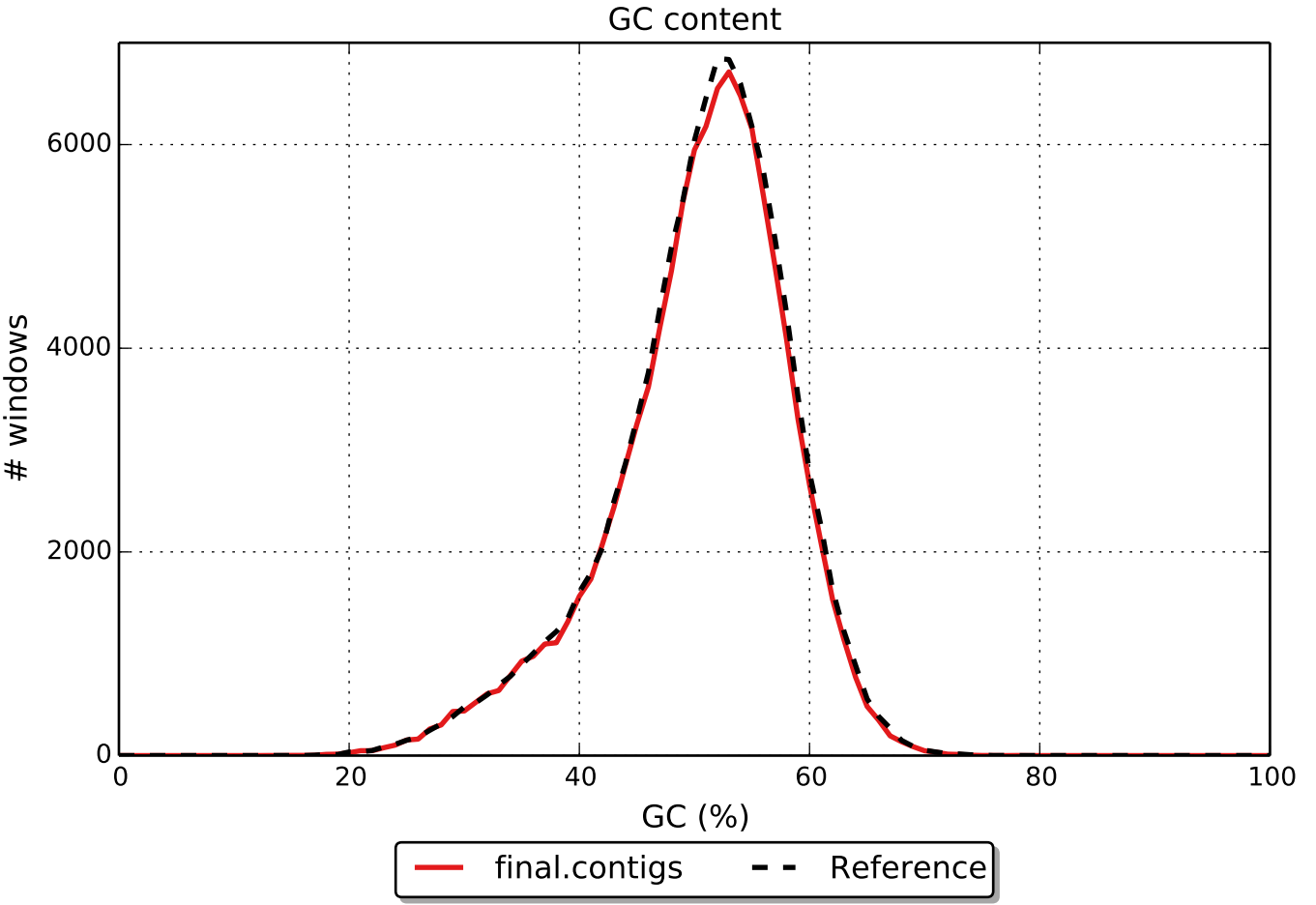
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

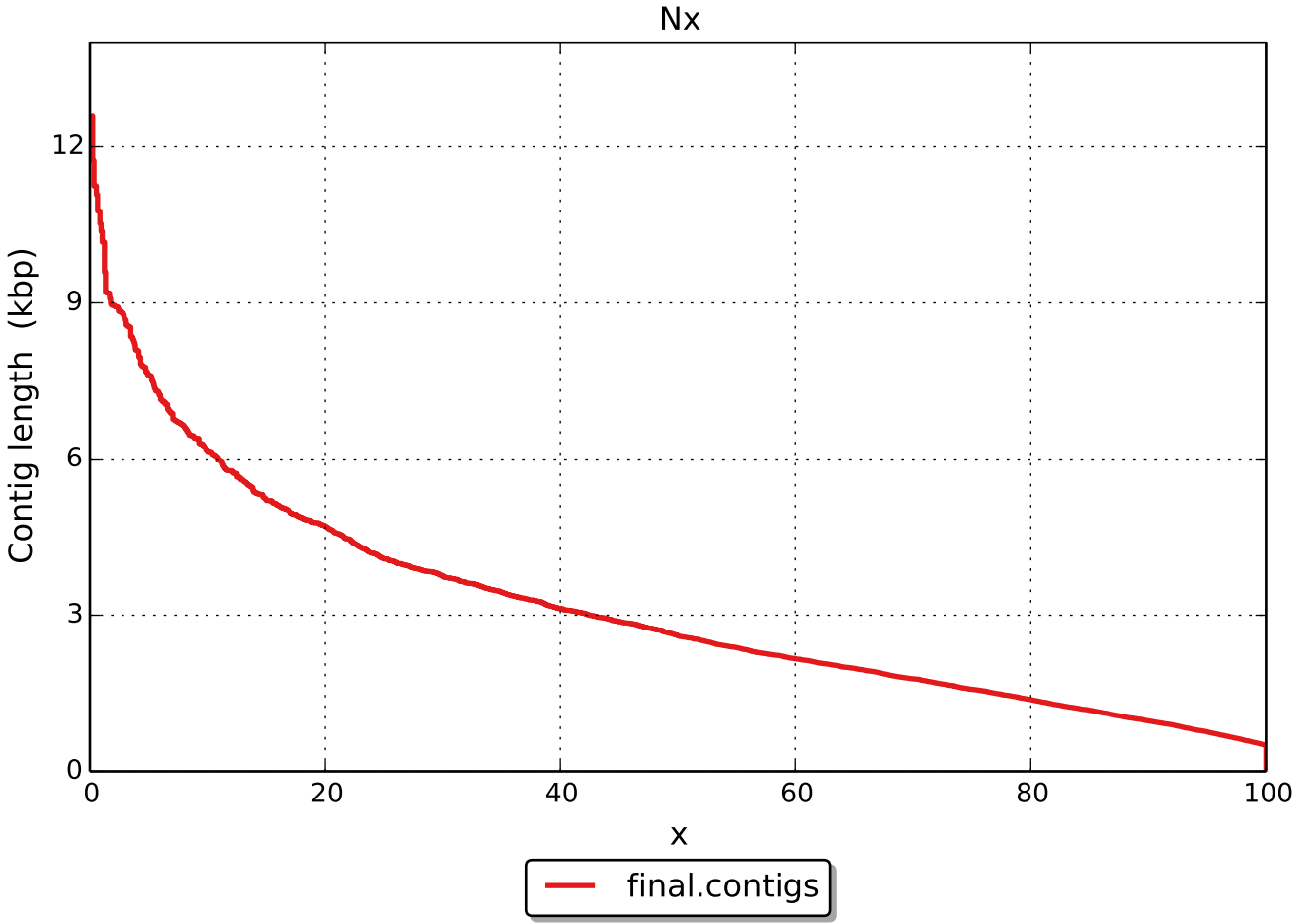
Unaligned report

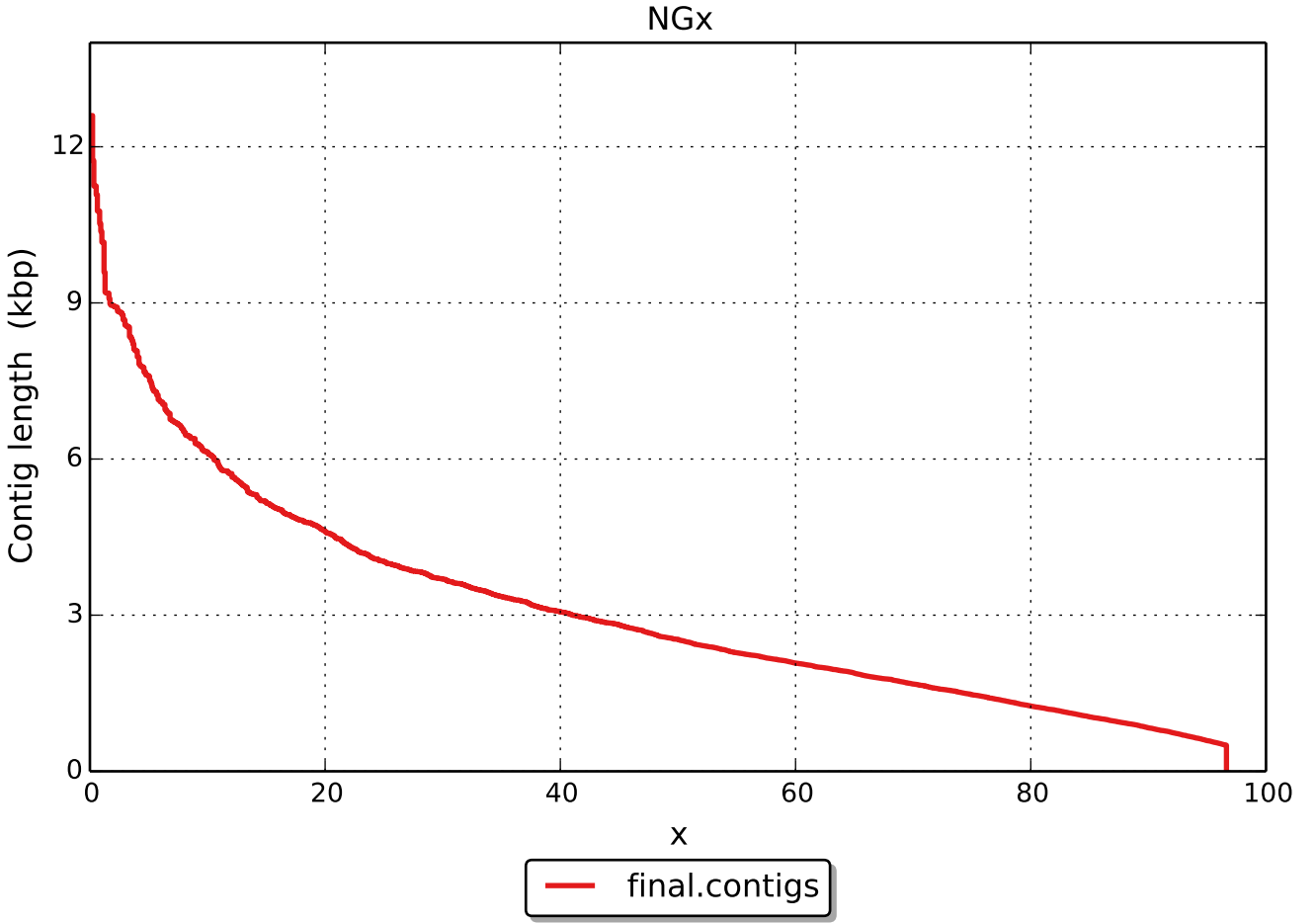
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

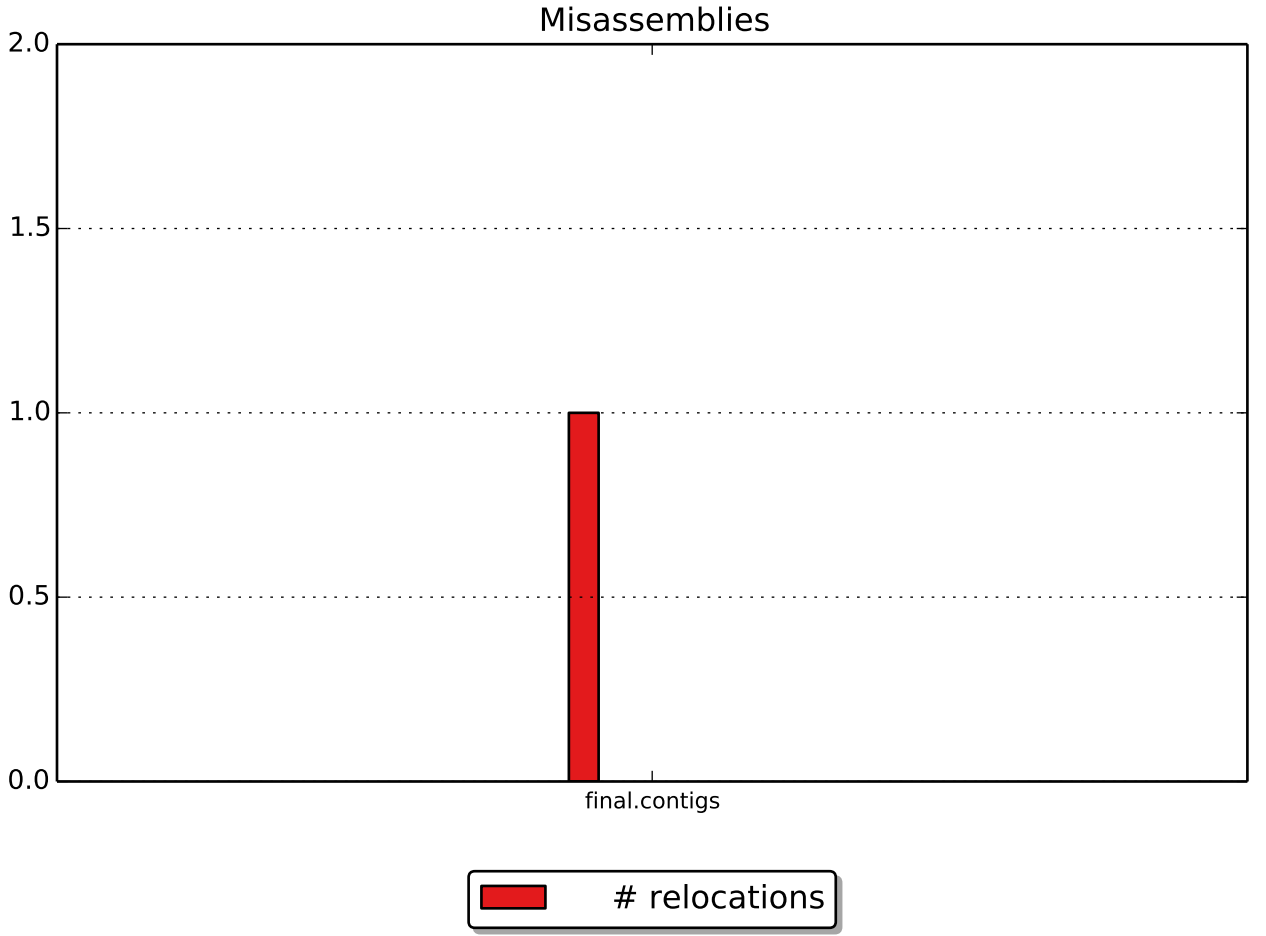
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

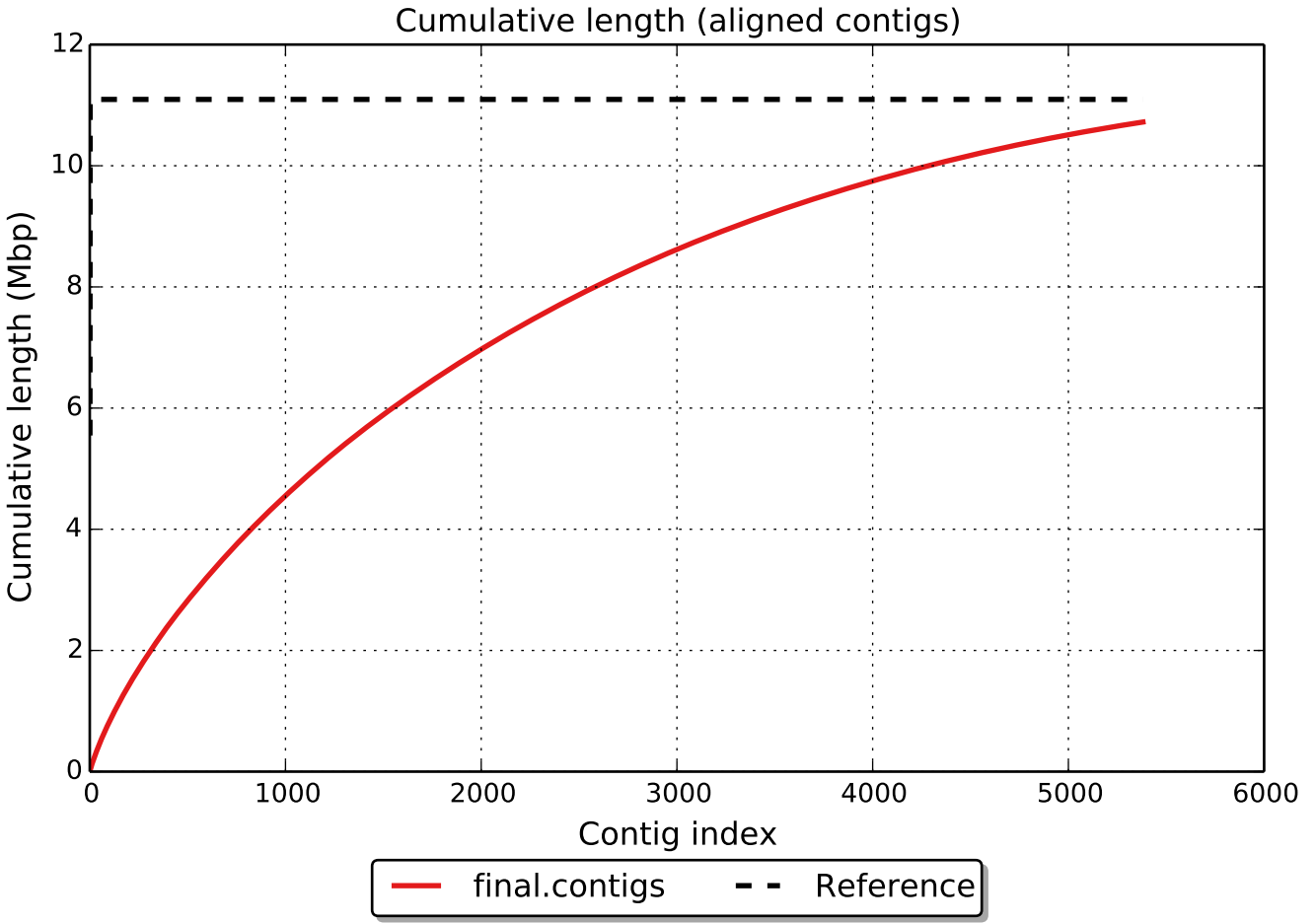

Cumulative length
Cumulative length (Mbp)
Contig index
0
2
4
6
8
10
12
0
1000
2000
3000
4000
5000
6000
final.contigs
Reference

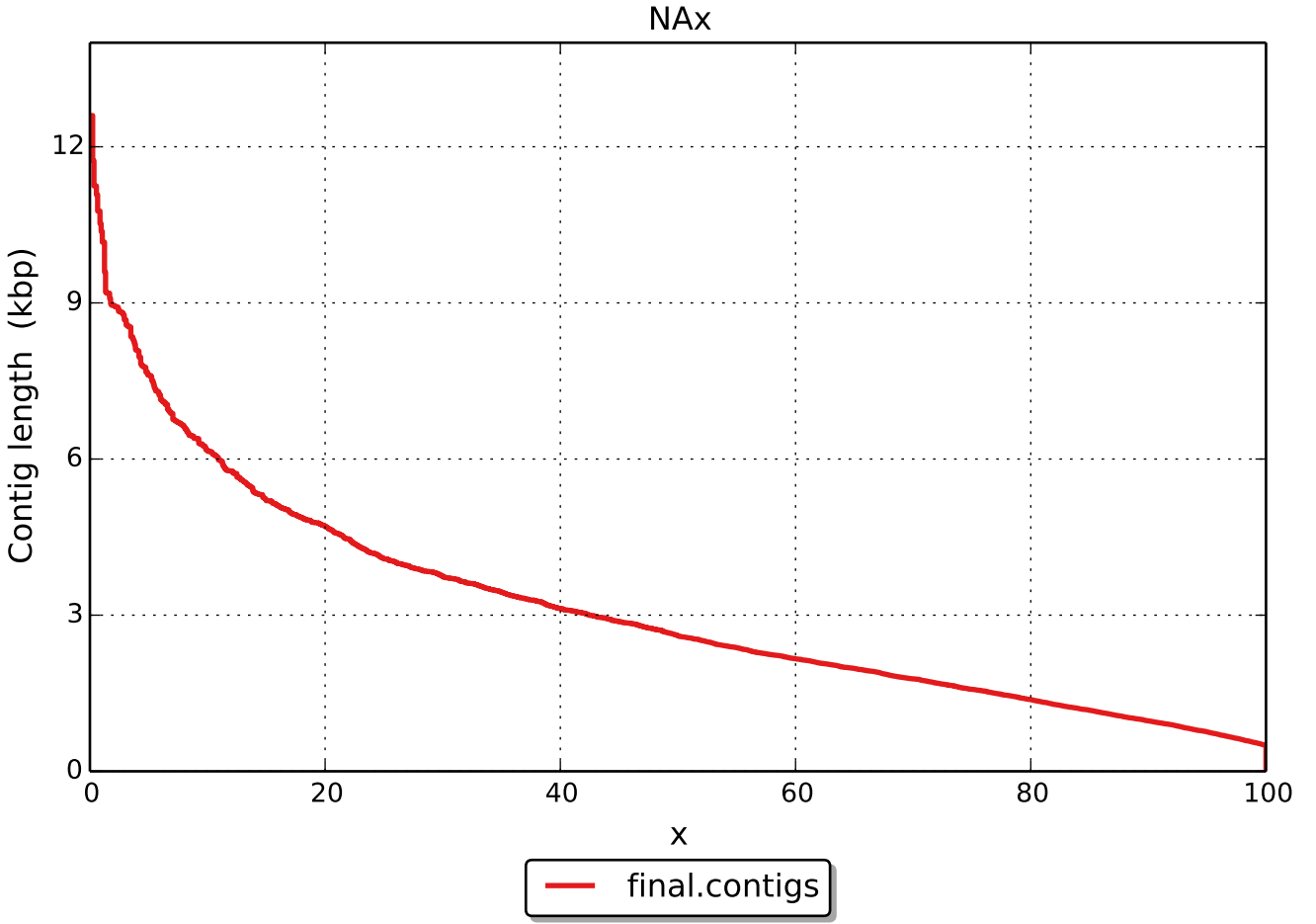

GC content
windows
GC (%)
0
2000
4000
6000
0
20
40
60
80
100
final.contigs
Reference

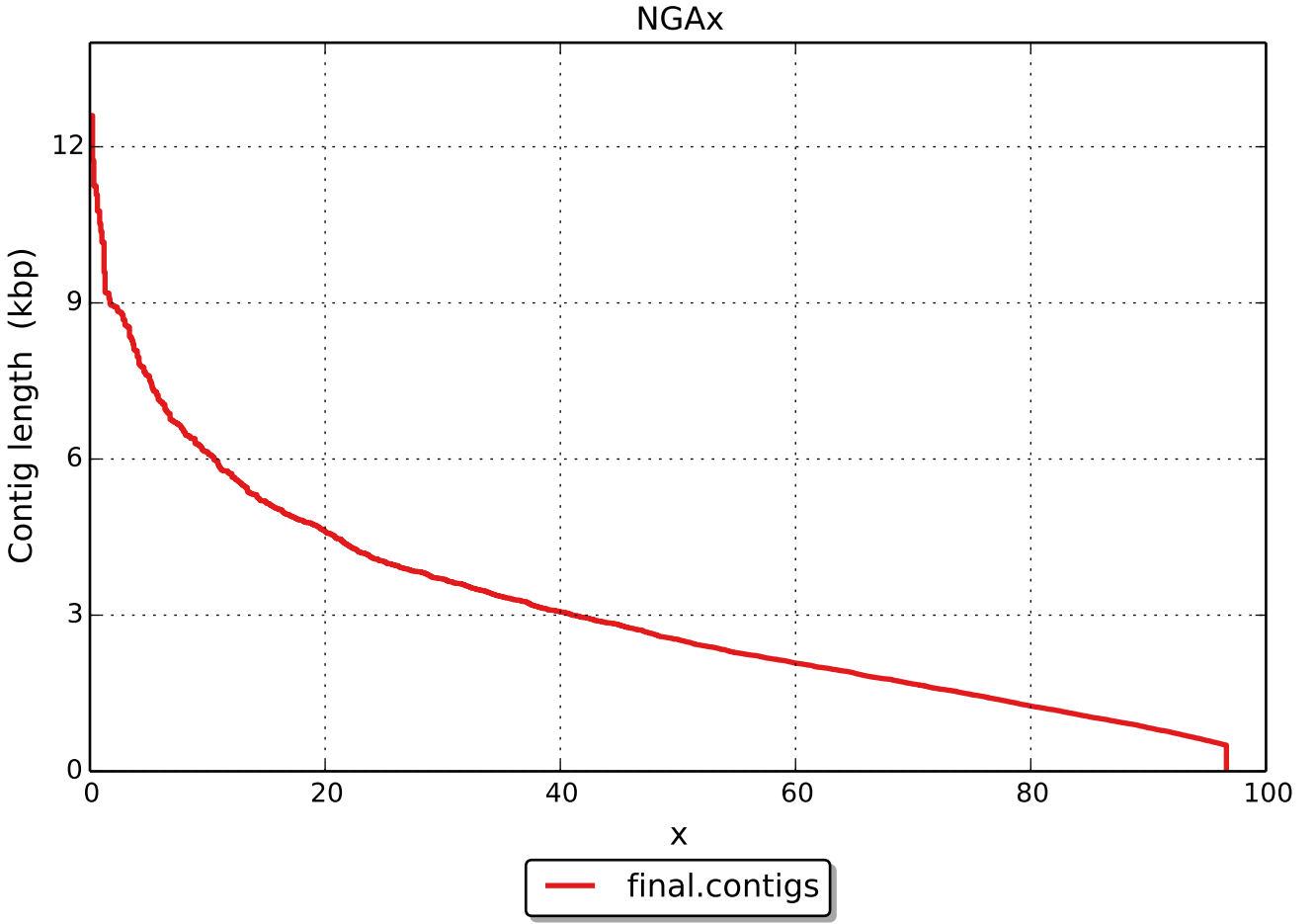

Nx
Contig length (kbp)
12
9
6
3
0
0
20
40
60
80
100
x
final.contigs


NGx
Contig length (kbp)
12
9
6
3
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)
Contig index
0
2
4
6
8
10
12
0
1000
2000
3000
4000
5000
6000
final.contigs
Reference


NAx
Contig length (kbp)
12
9
6
3
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (kbp)
12
9
6
3
0
0
20
40
60
80
100
x
final.contigs