Report

	final.contigs
# contigs (>= 0 bp)	754
# contigs (>= 1000 bp)	439
Total length (>= 0 bp)	1328406
Total length (>= 1000 bp)	1140822
# contigs	631
Largest contig	11378
Total length	1284116
Reference length	1283598
GC (%)	26.29
Reference GC (%)	26.30
N50	2787
NG50	2797
N75	1631
NG75	1636
L50	149
LG50	148
L75	301
LG75	300
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	918
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	96.969
Duplication ratio	1.033
# N's per 100 kbp	0.00
# mismatches per 100 kbp	16.15
# indels per 100 kbp	0.00
Largest alignment	11378
NA50	2787
NGA50	2797
NA75	1631
NGA75	1636
LA50	149
LGA50	148
LA75	301
LGA75	300

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

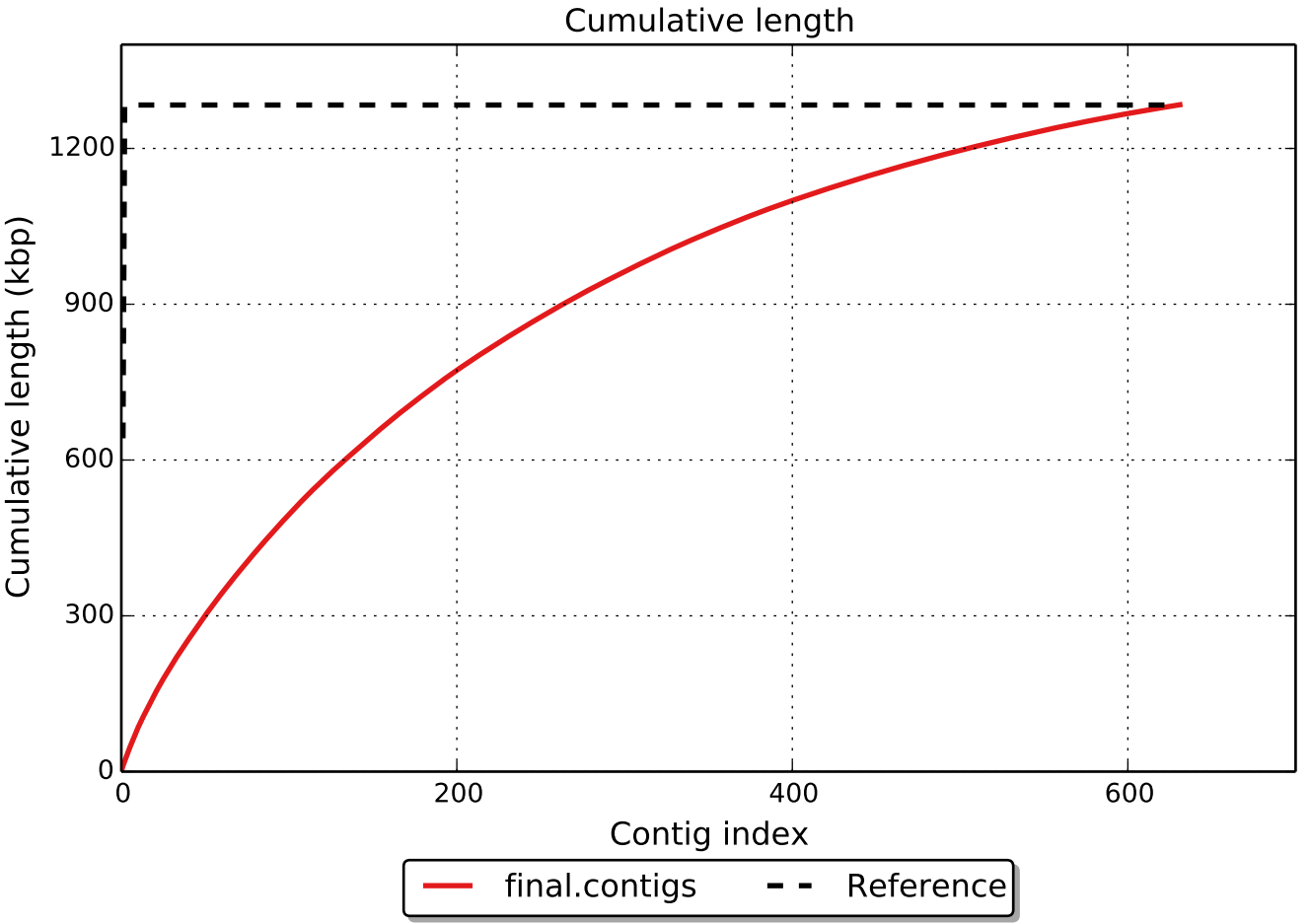
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	918
# local misassemblies	0
# mismatches	201
# indels	0
# short indels	0
# long indels	0
Indels length	0

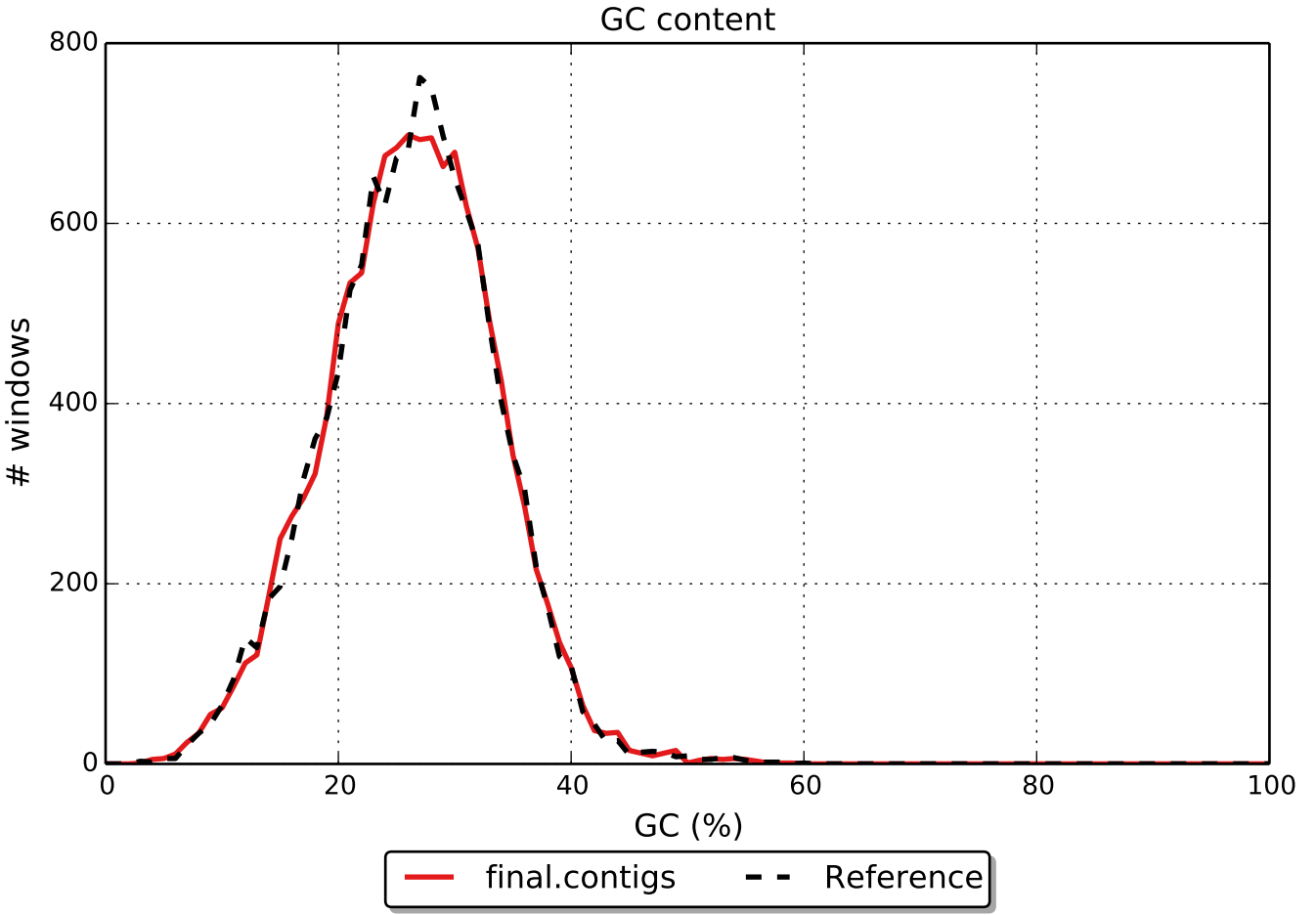
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

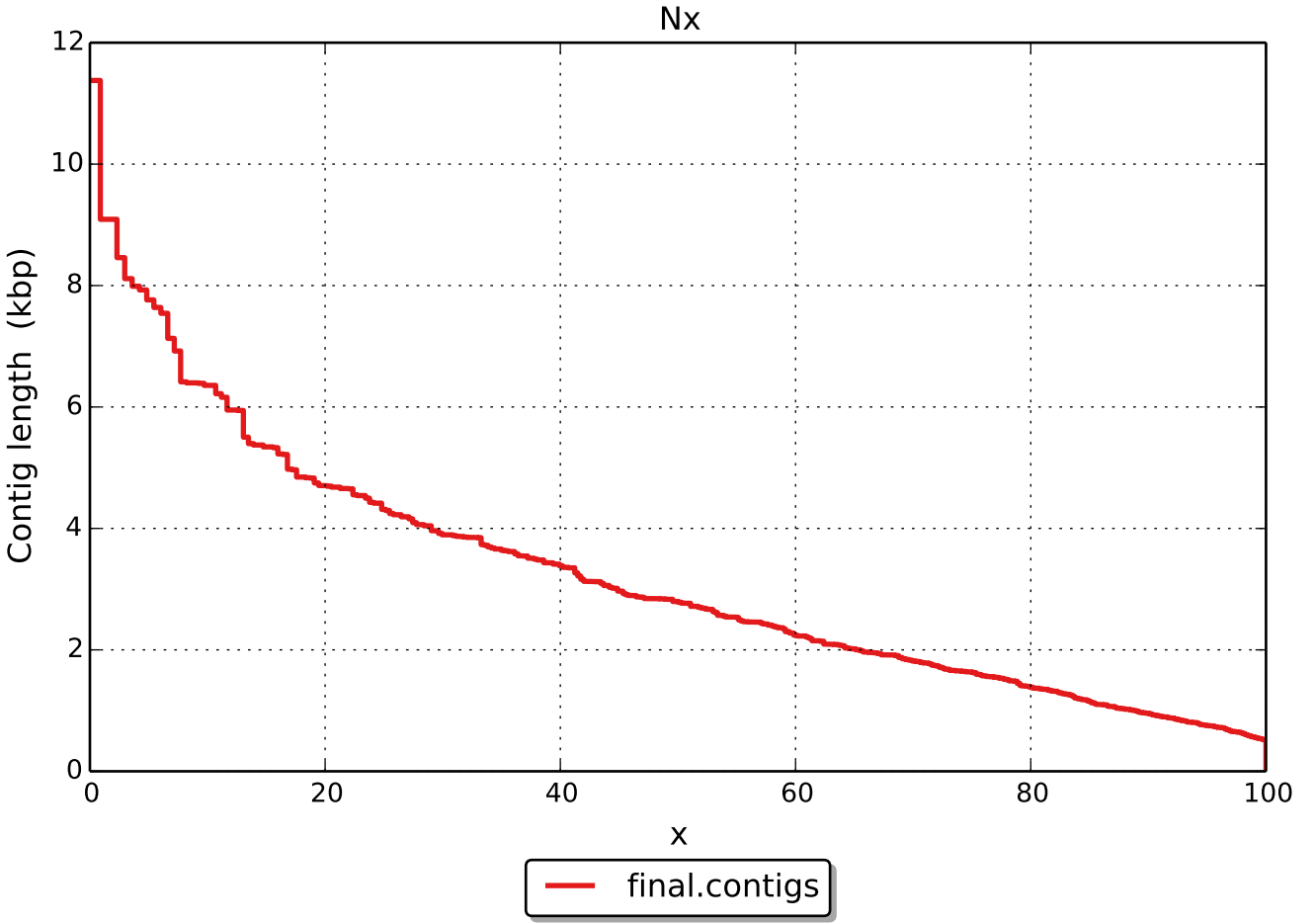
Unaligned report

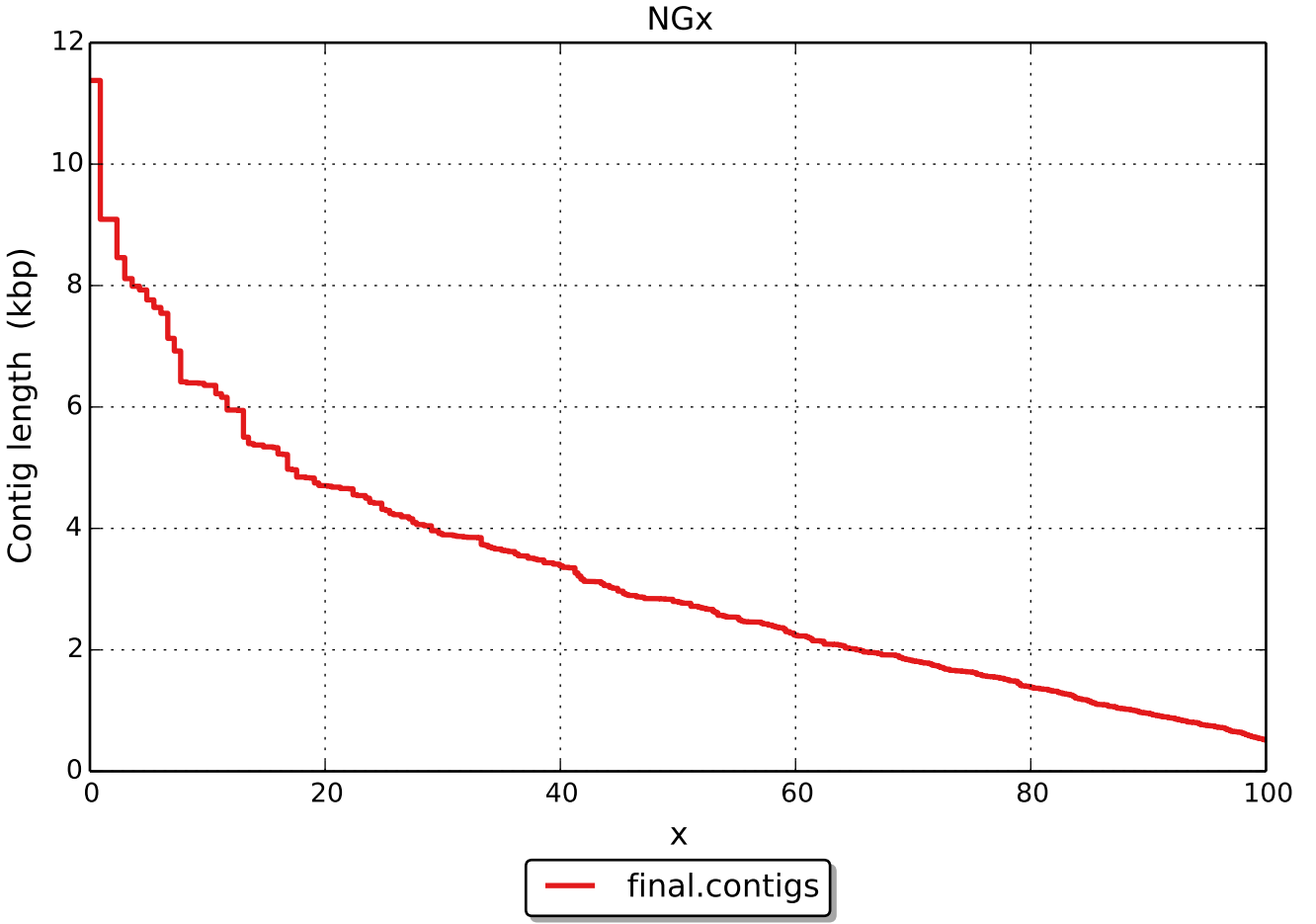
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

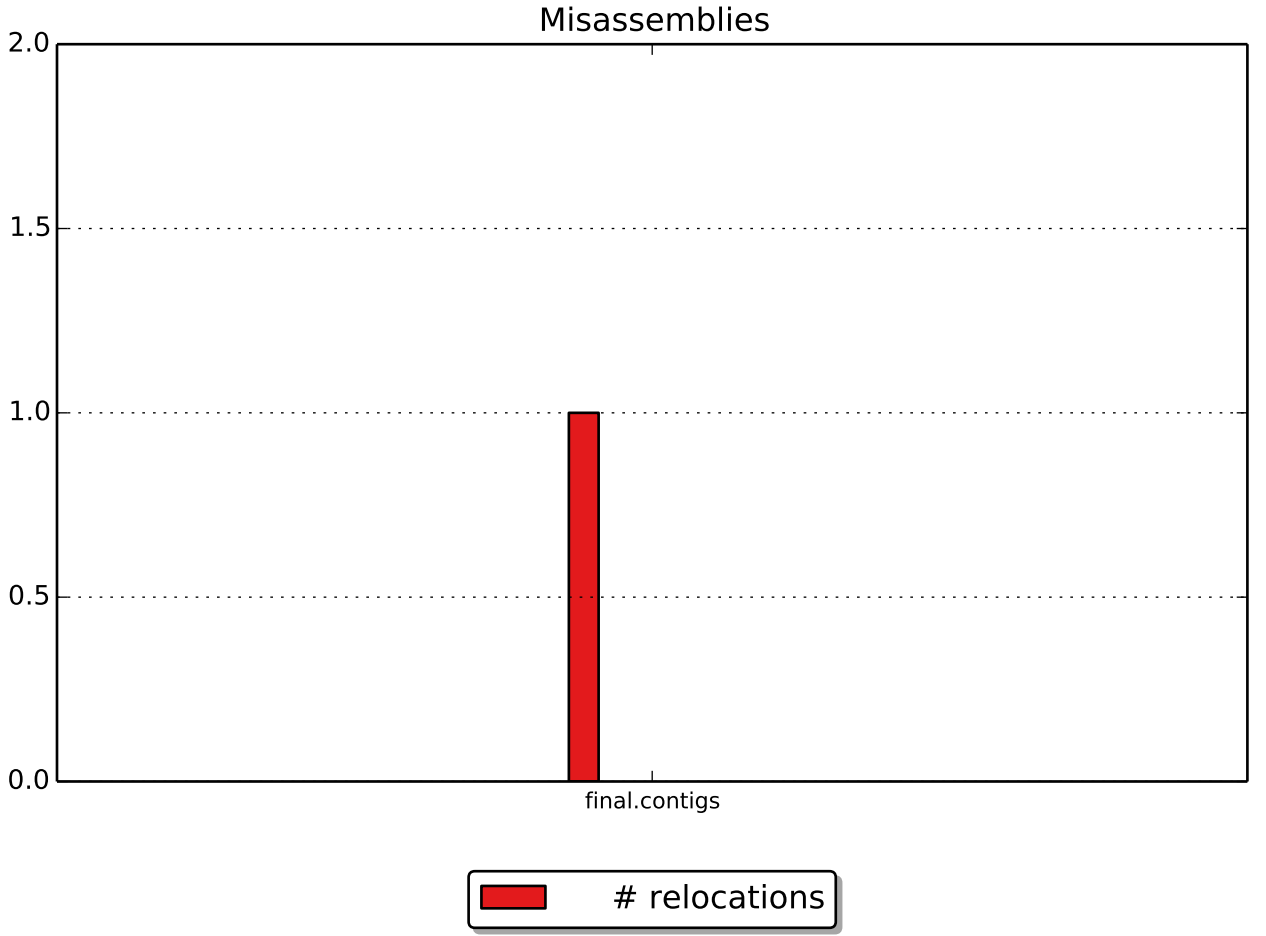
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

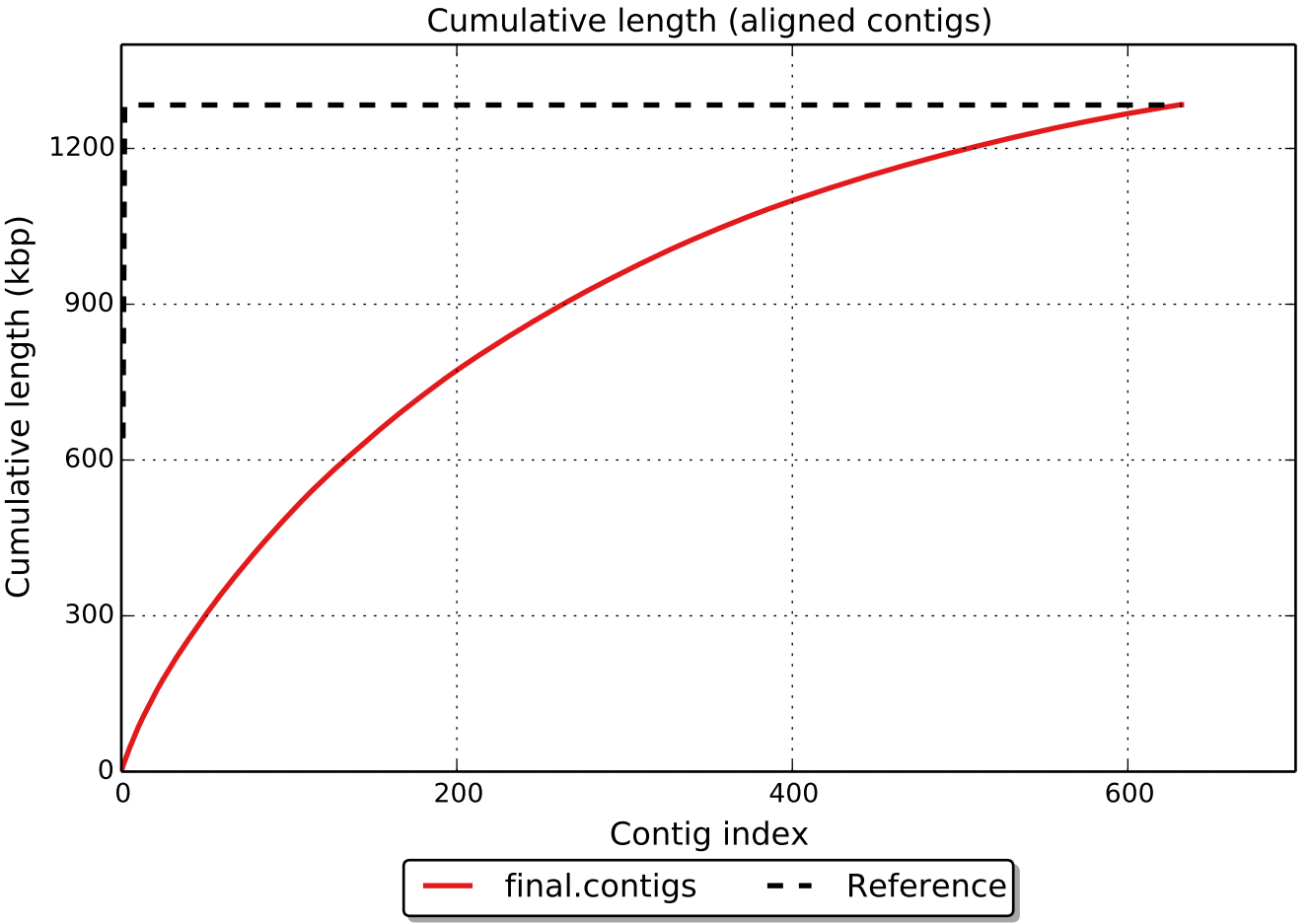

Cumulative length
Cumulative length (kbp)
0
300
600
900
1200
0
200
400
600
Contig index
final.contigs
Reference

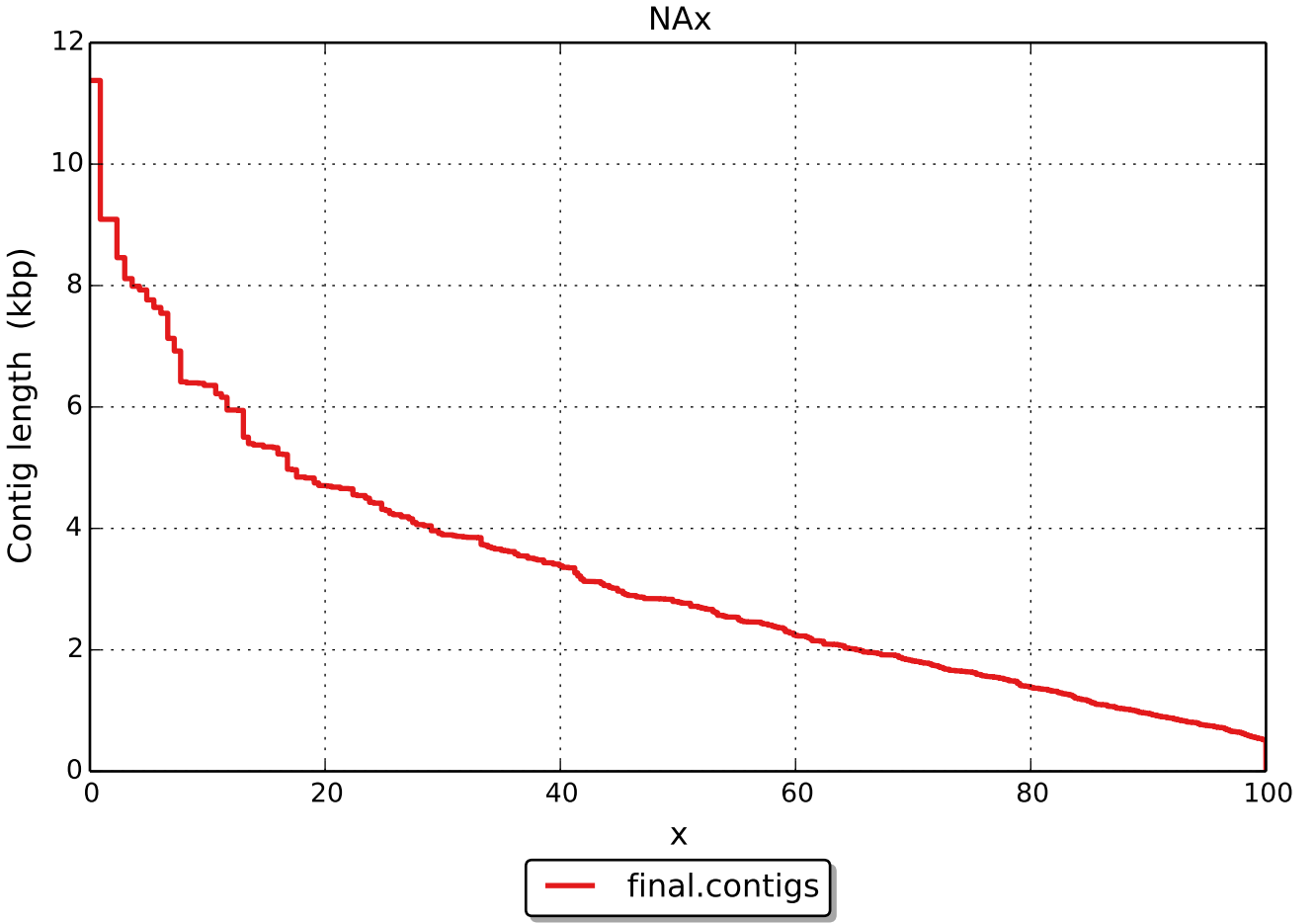

GC content
800
600
400
200
0
windows
0
20
40
60
80
100
GC (%)
final.contigs
Reference

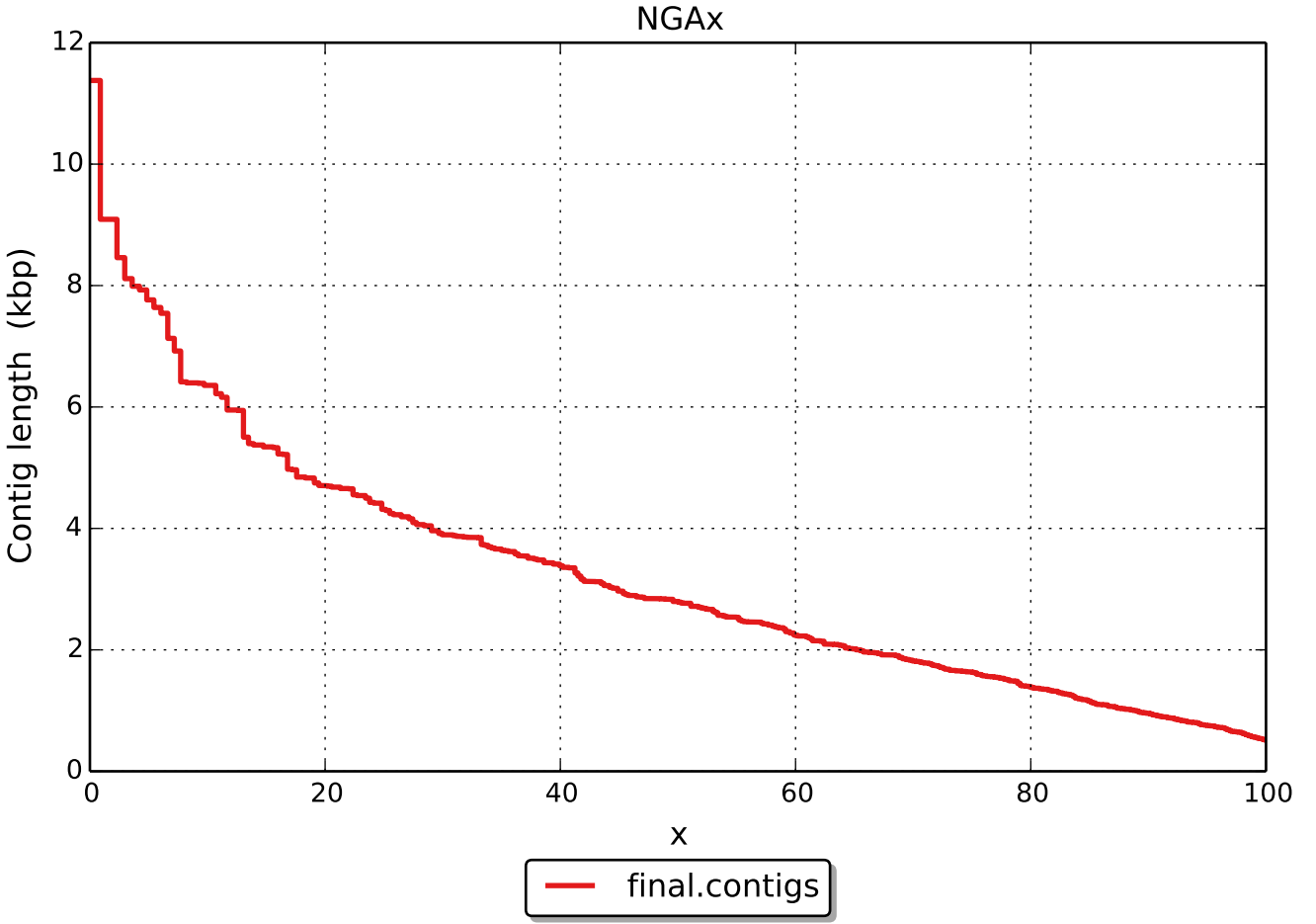

Nx
Contig length (kbp)
0
2
4
6
8
10
12
0
20
40
60
80
100
x
final.contigs


NGx
Contig length (kbp)
0
2
4
6
8
10
12
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 (kbp)
0
300
600
900
1200
0
200
400
600
Contig index
final.contigs
Reference


NAx
Contig length (kbp)
0
2
4
6
8
10
12
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (kbp)
0
2
4
6
8
10
12
0
20
40
60
80
100
x
final.contigs