Report

	final.contigs
# contigs (>= 0 bp)	818
# contigs (>= 1000 bp)	706
Total length (>= 0 bp)	3729908
Total length (>= 1000 bp)	3642377
# contigs	818
Largest contig	29446
Total length	3729908
Reference length	1892775
GC (%)	32.25
Reference GC (%)	32.25
N50	7320
NG50	11383
N75	4004
NG75	8989
L50	162
LG50	60
L75	332
LG75	107
# misassemblies	5
# misassembled contigs	5
Misassembled contigs length	7629
# local misassemblies	0
# unaligned contigs	217 + 100 part
Unaligned length	1608559
Genome fraction (%)	99.675
Duplication ratio	1.124
# N's per 100 kbp	0.00
# mismatches per 100 kbp	180.69
# indels per 100 kbp	0.42
Largest alignment	29446
NA50	1901
NGA50	7619
NGA75	4506
LA50	307
LGA50	83
LGA75	160

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

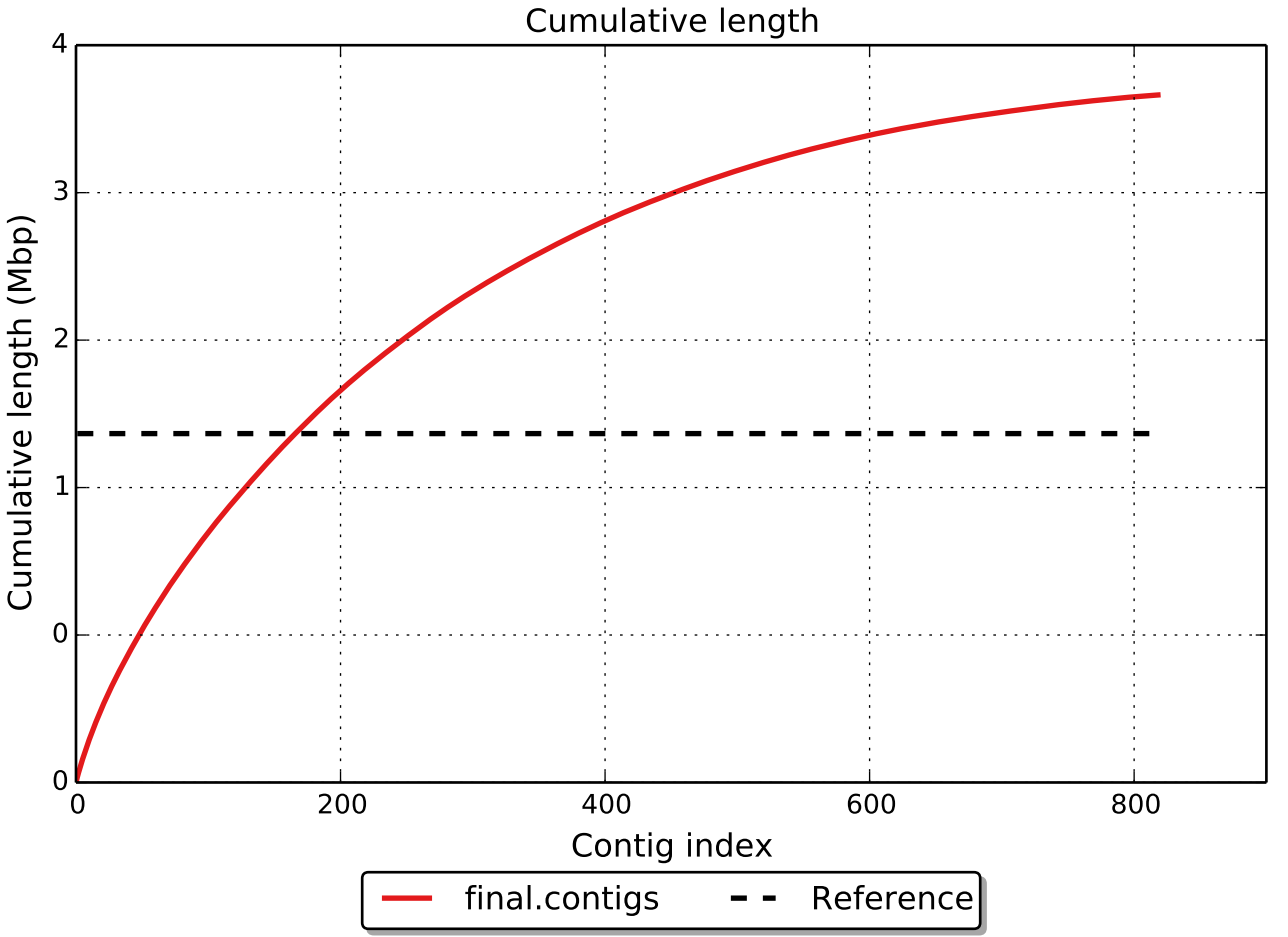
	final.contigs
# misassemblies	5
# relocations	5
# translocations	0
# inversions	0
# possibly misassembled contigs	24
# misassembled contigs	5
Misassembled contigs length	7629
# local misassemblies	0
# mismatches	3409
# indels	8
# short indels	8
# long indels	0
Indels length	8

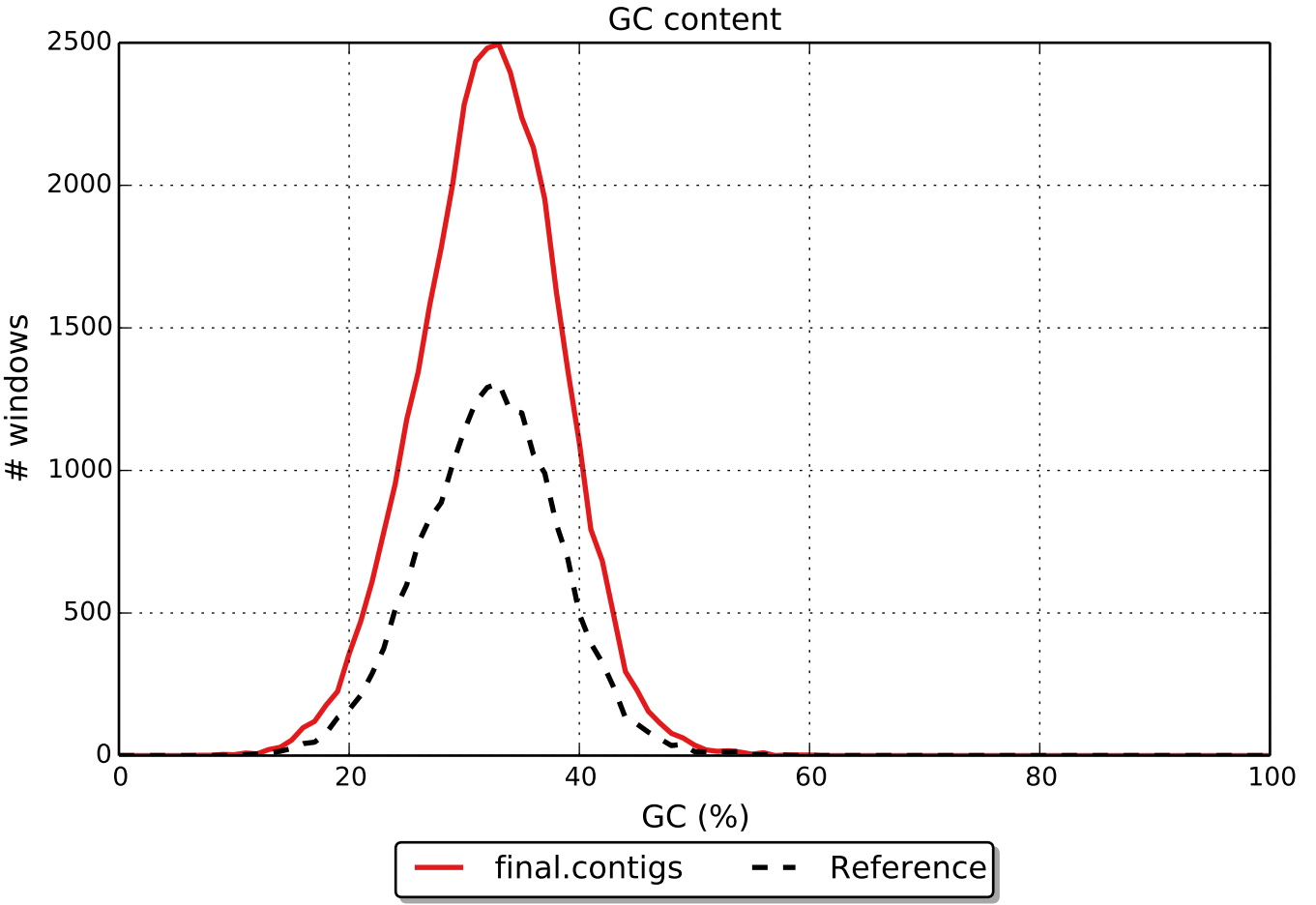
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

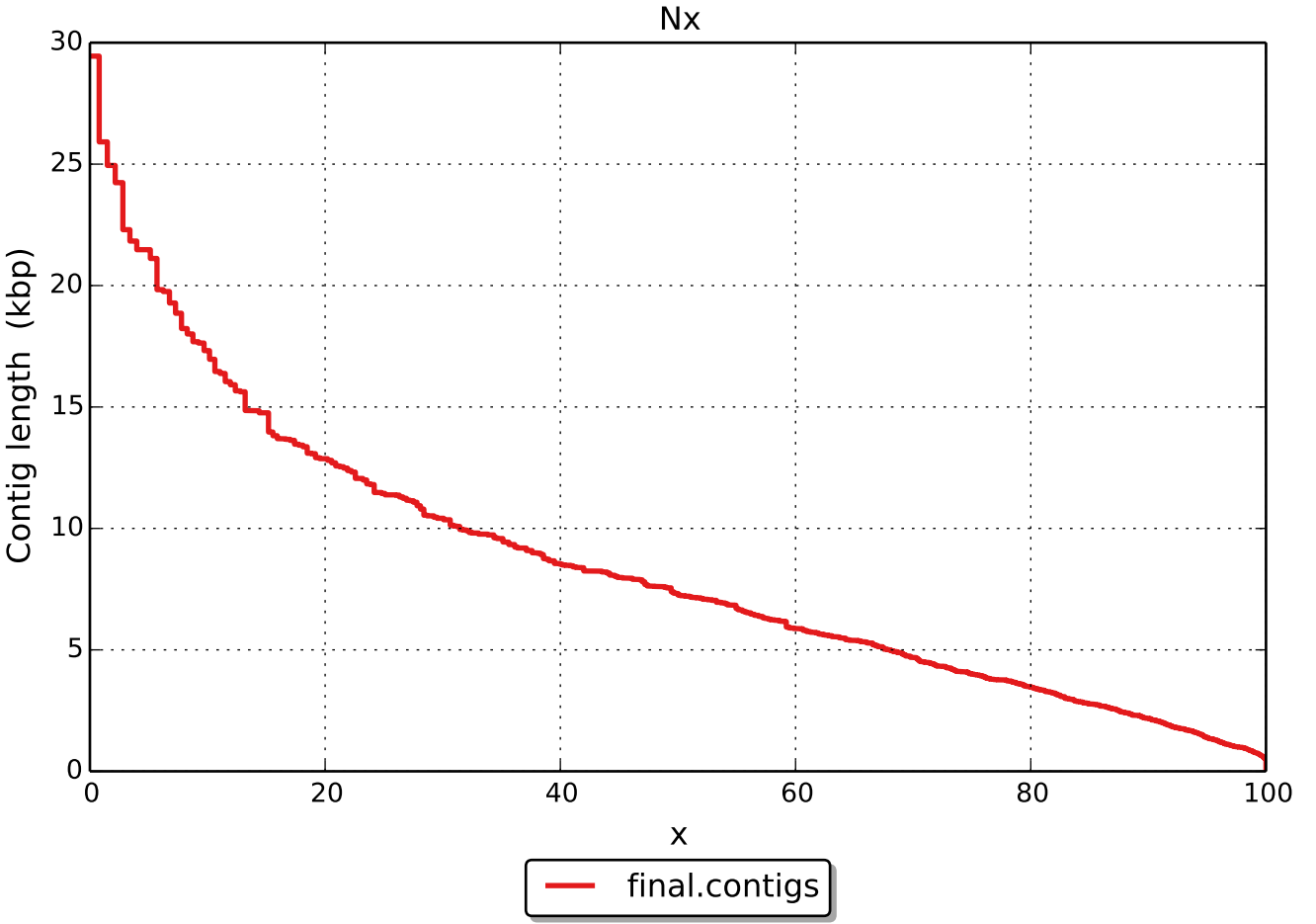
Unaligned report

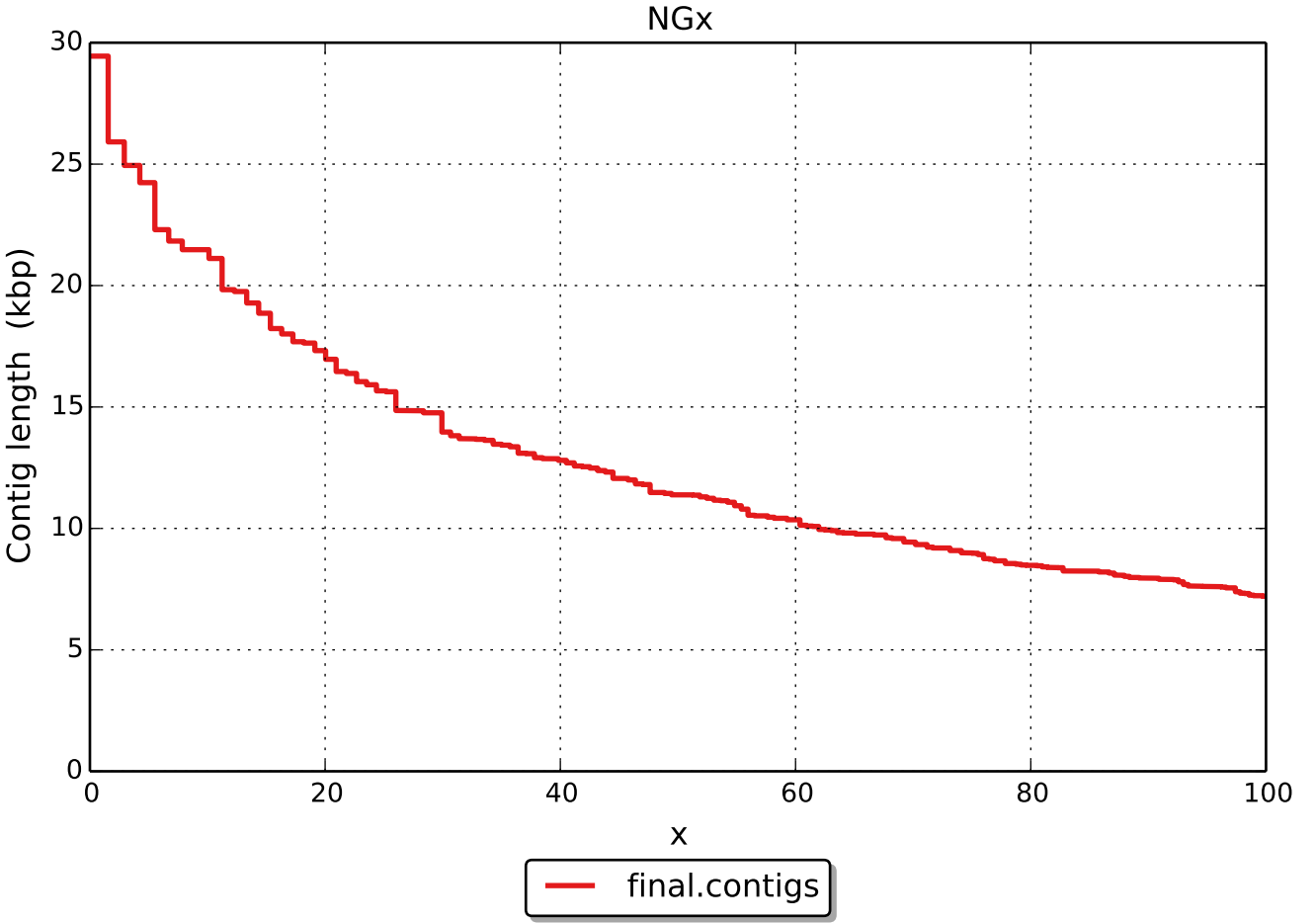
	final.contigs
# fully unaligned contigs	217
Fully unaligned length	1144803
# partially unaligned contigs	100
# with misassembly	6
# both parts are significant	24
Partially unaligned length	463756
# N's	0

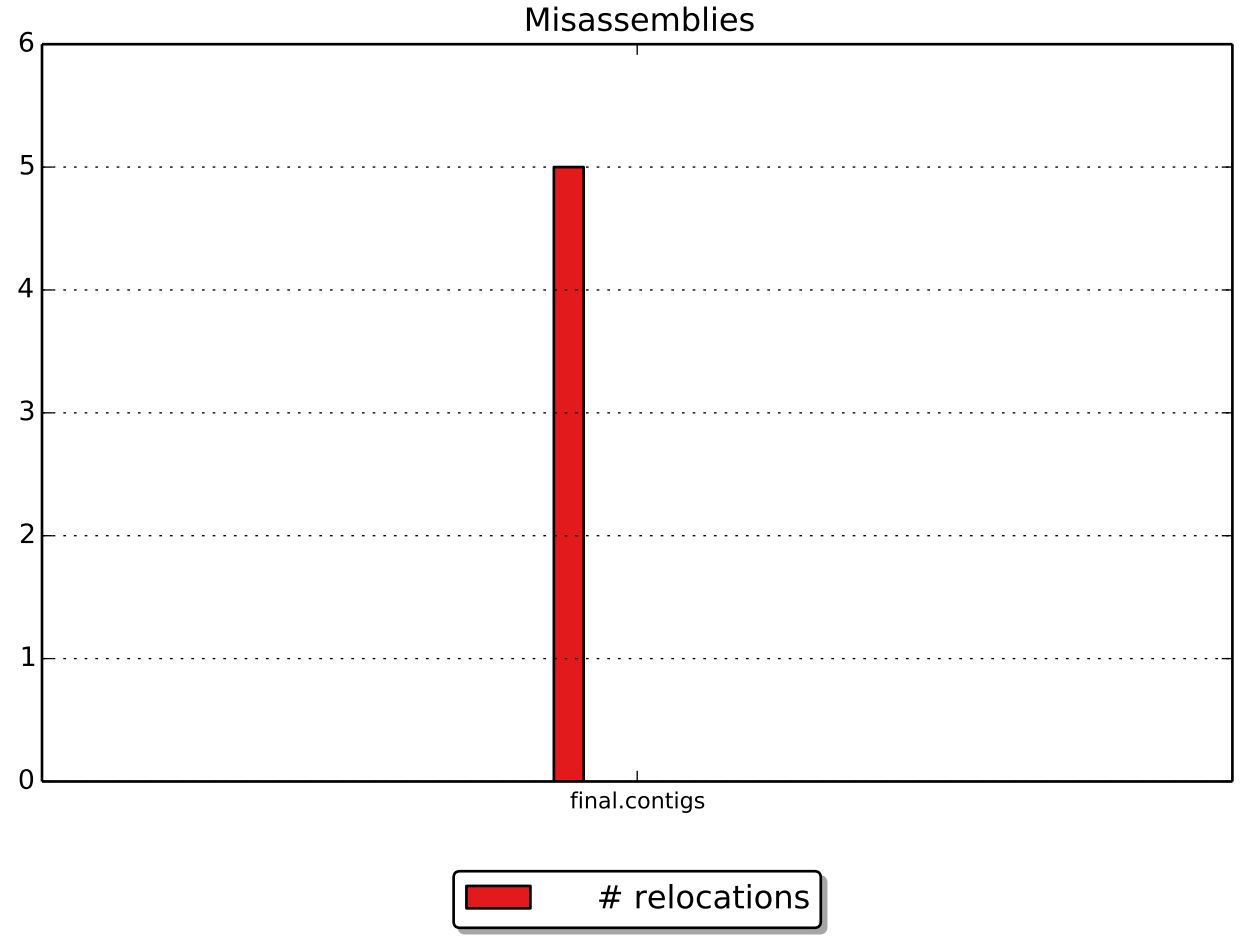
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

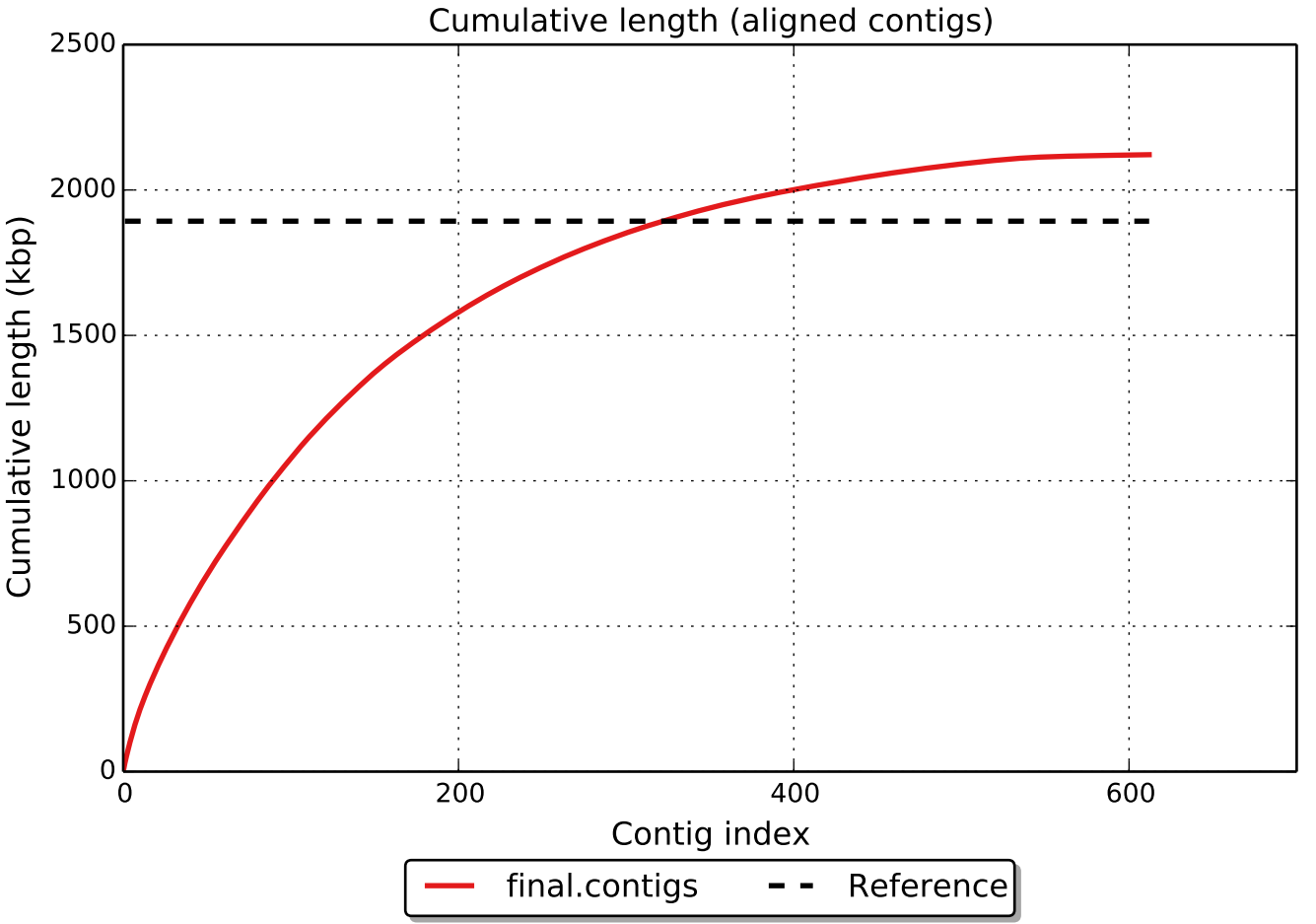

Cumulative length
Cumulative length (Mbp)
4
3
2
1
0
0
200
400
600
800
Contig index
final.contigs
Reference

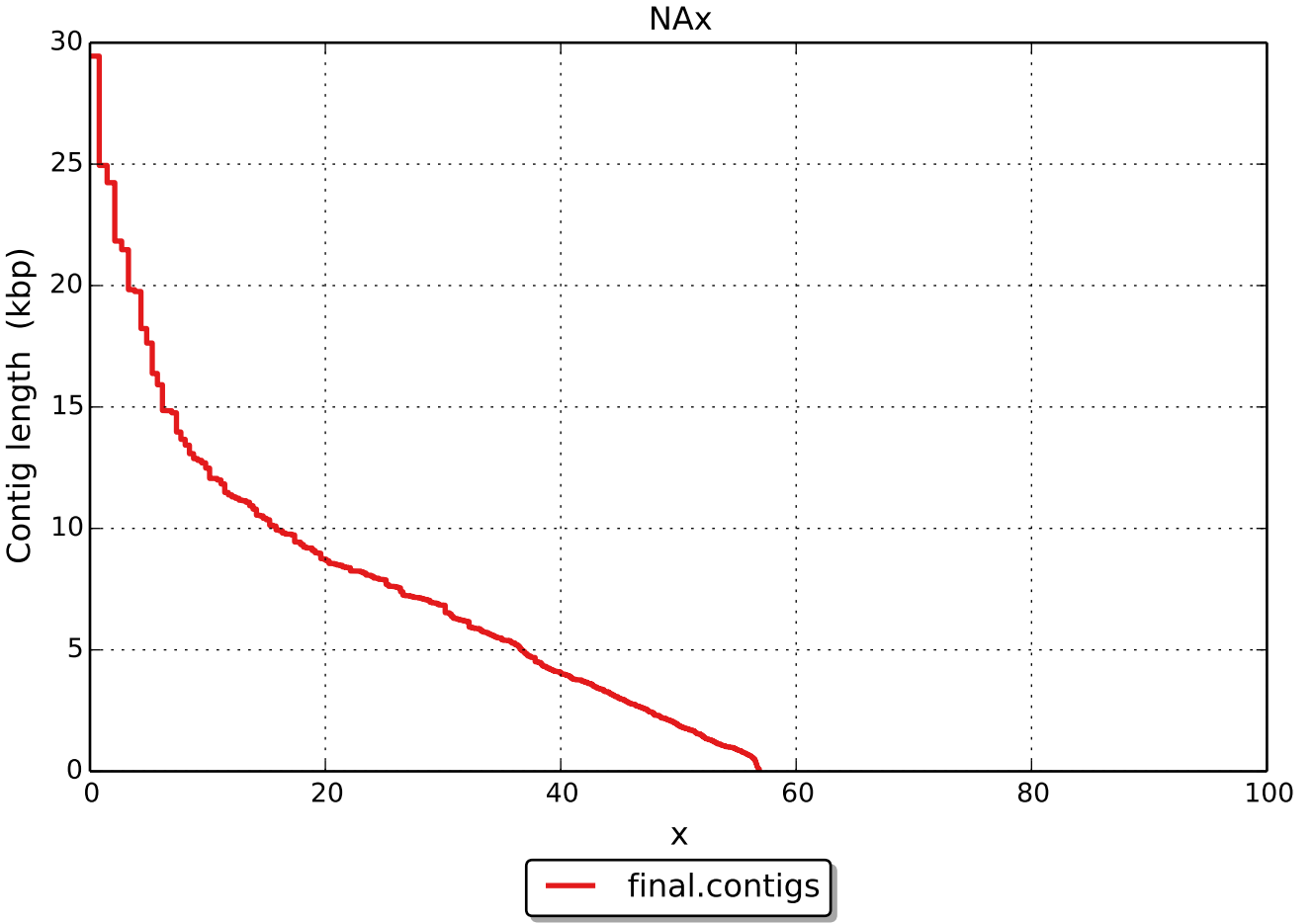

GC content
2500
2000
1500
1000
500
0
windows
0
20
40
60
80
100
GC (%)
final.contigs
Reference

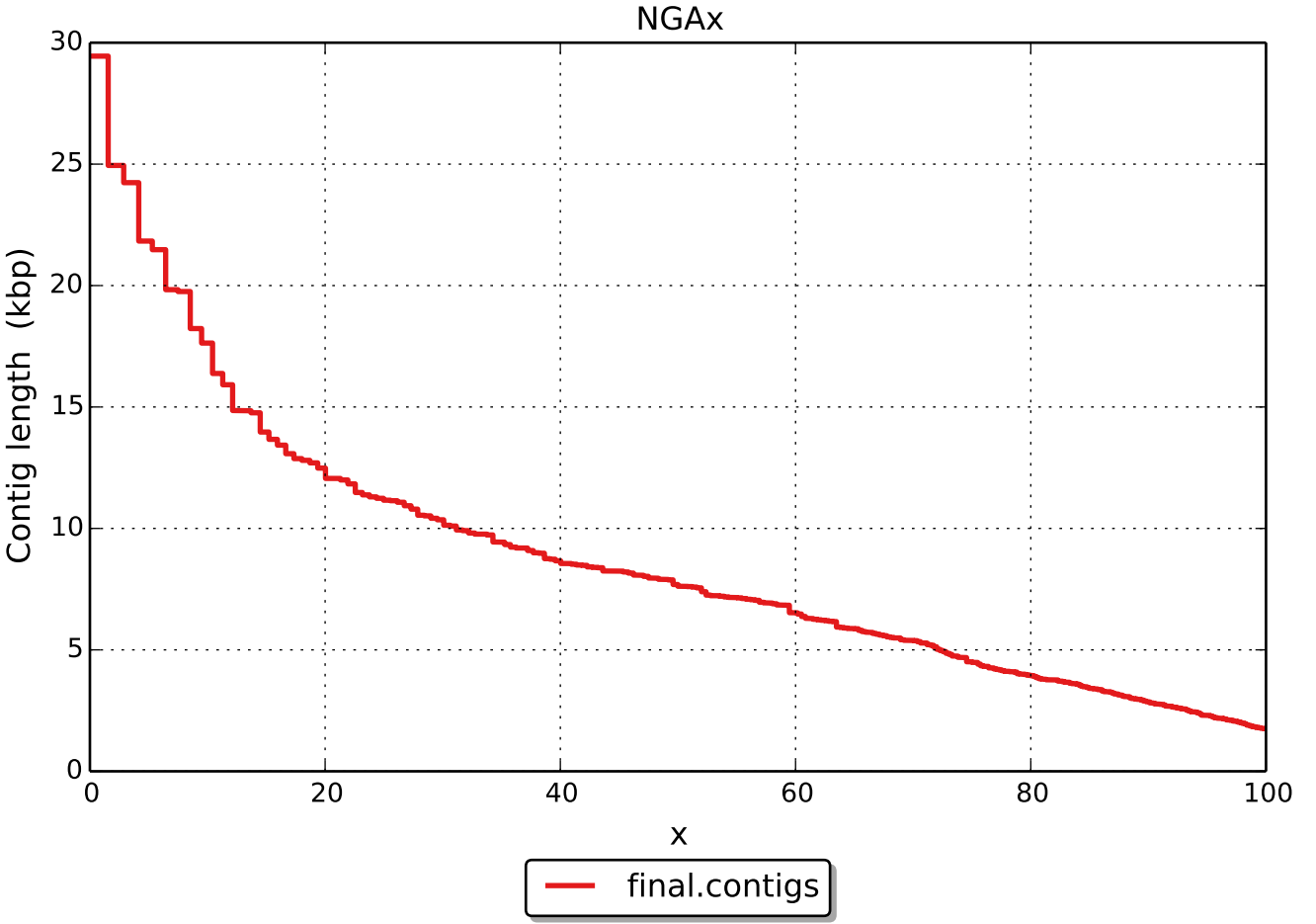

Nx
Contig length (kbp)
30
25
20
15
10
5
0
0
20
40
60
80
100
x
final.contigs


NGx
Contig length (kbp)
30
25
20
15
10
5
0
0
20
40
60
80
100
x
final.contigs


Misassemblies
6
5
4
3
2
1
0
final.contigs
relocations


Cumulative length (aligned contigs)
Cumulative length (kbp)
2500
2000
1500
1000
500
0
0
200
400
600
Contig index
final.contigs
Reference


NAx
Contig length (kbp)
30
25
20
15
10
5
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (kbp)
30
25
20
15
10
5
0
0
20
40
60
80
100
x
final.contigs