Report

	final.contigs
# contigs (>= 0 bp)	398
# contigs (>= 1000 bp)	282
Total length (>= 0 bp)	1210327
Total length (>= 1000 bp)	1131590
# contigs	398
Largest contig	15816
Total length	1210327
Reference length	615980
GC (%)	25.34
Reference GC (%)	25.34
N50	4867
NG50	8316
N75	2738
NG75	6006
L50	76
LG50	27
L75	159
LG75	49
# misassemblies	5
# misassembled contigs	5
Misassembled contigs length	4545
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	97.456
Duplication ratio	2.016
# N's per 100 kbp	0.00
# mismatches per 100 kbp	658.16
# indels per 100 kbp	0.00
Largest alignment	15816
NA50	693
NGA50	4800
NGA75	2523
LA50	185
LGA50	39
LGA75	83

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

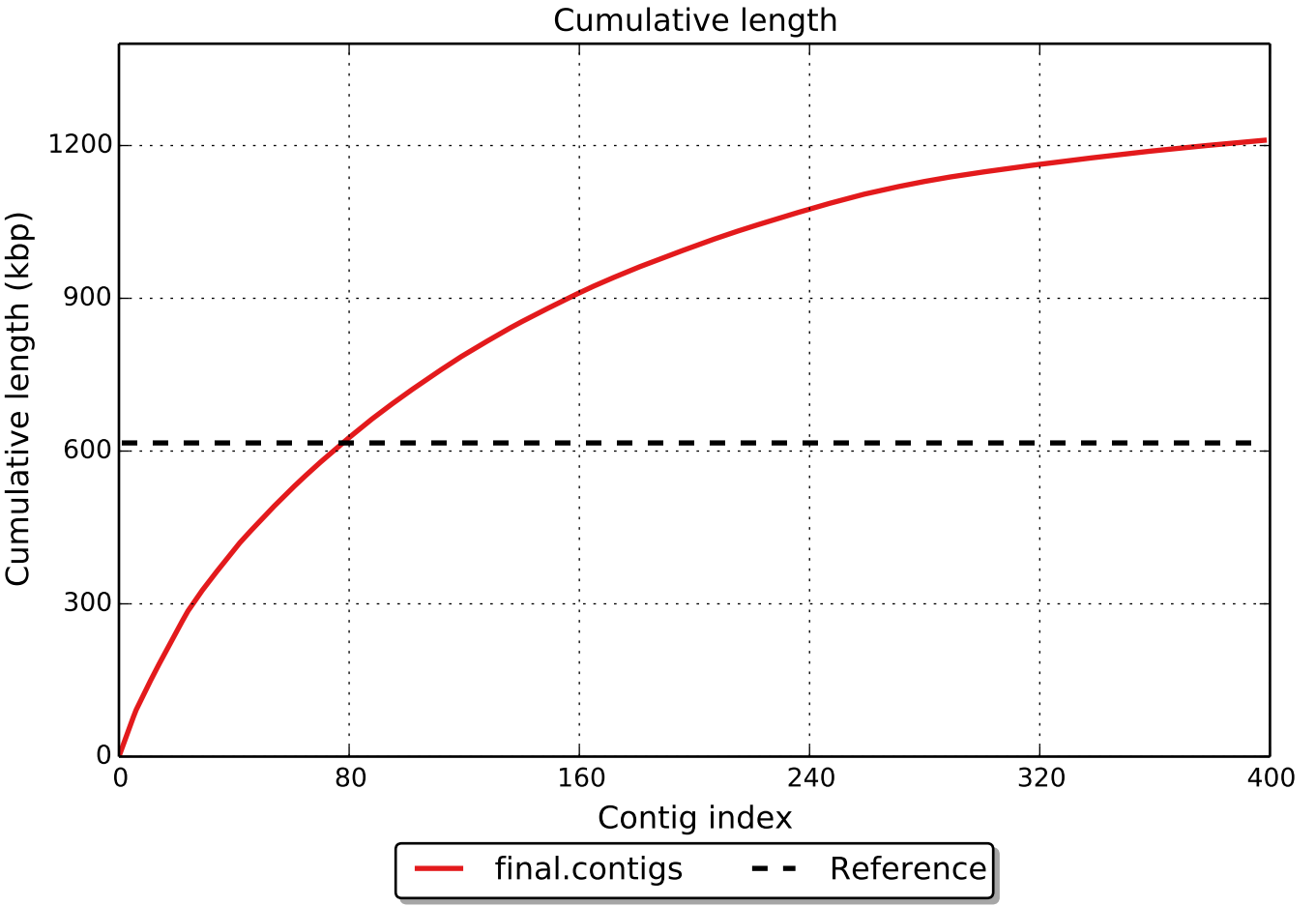
	final.contigs
# misassemblies	5
# relocations	5
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	5
Misassembled contigs length	4545
# local misassemblies	0
# mismatches	3951
# indels	0
# short indels	0
# long indels	0
Indels length	0

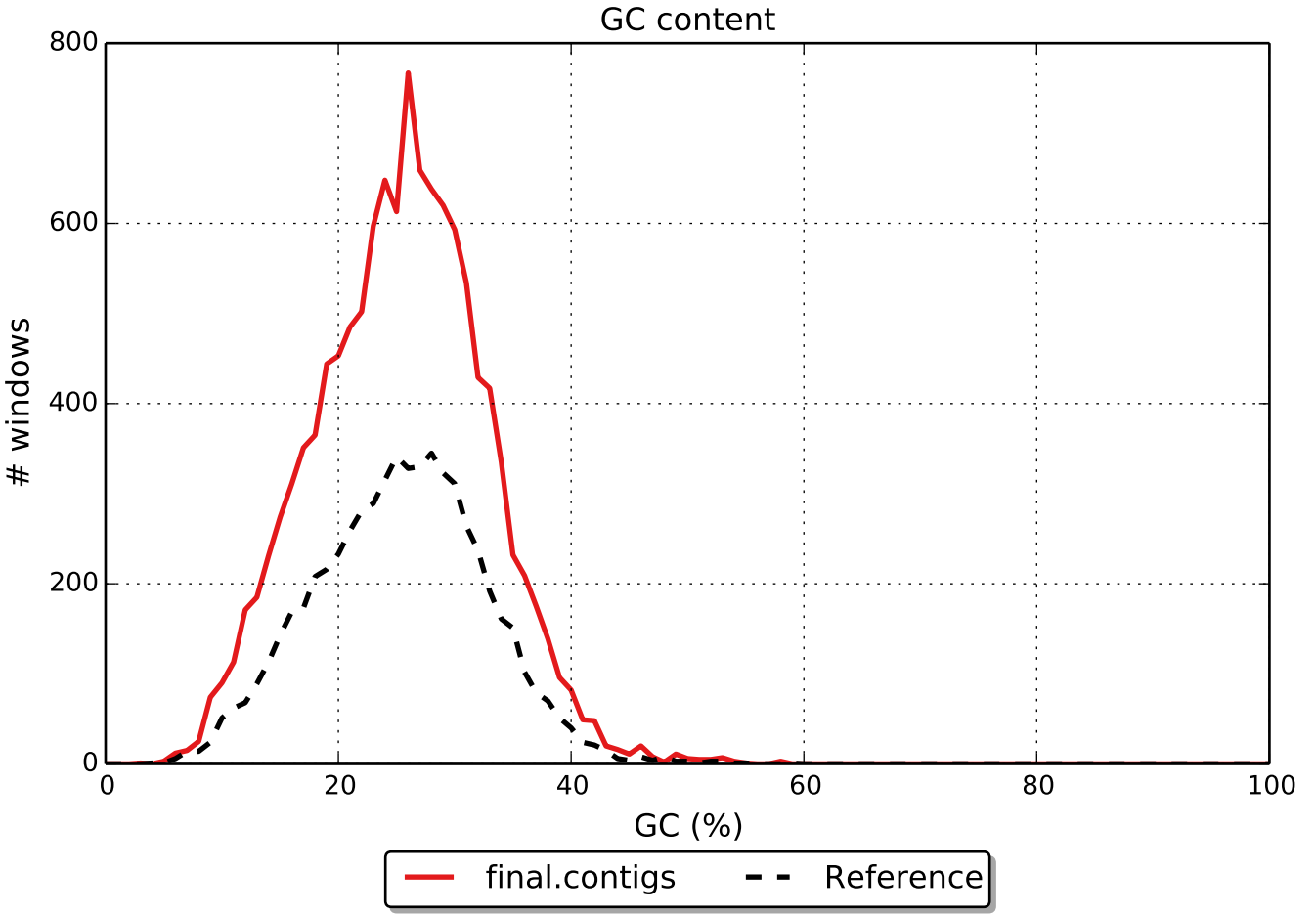
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

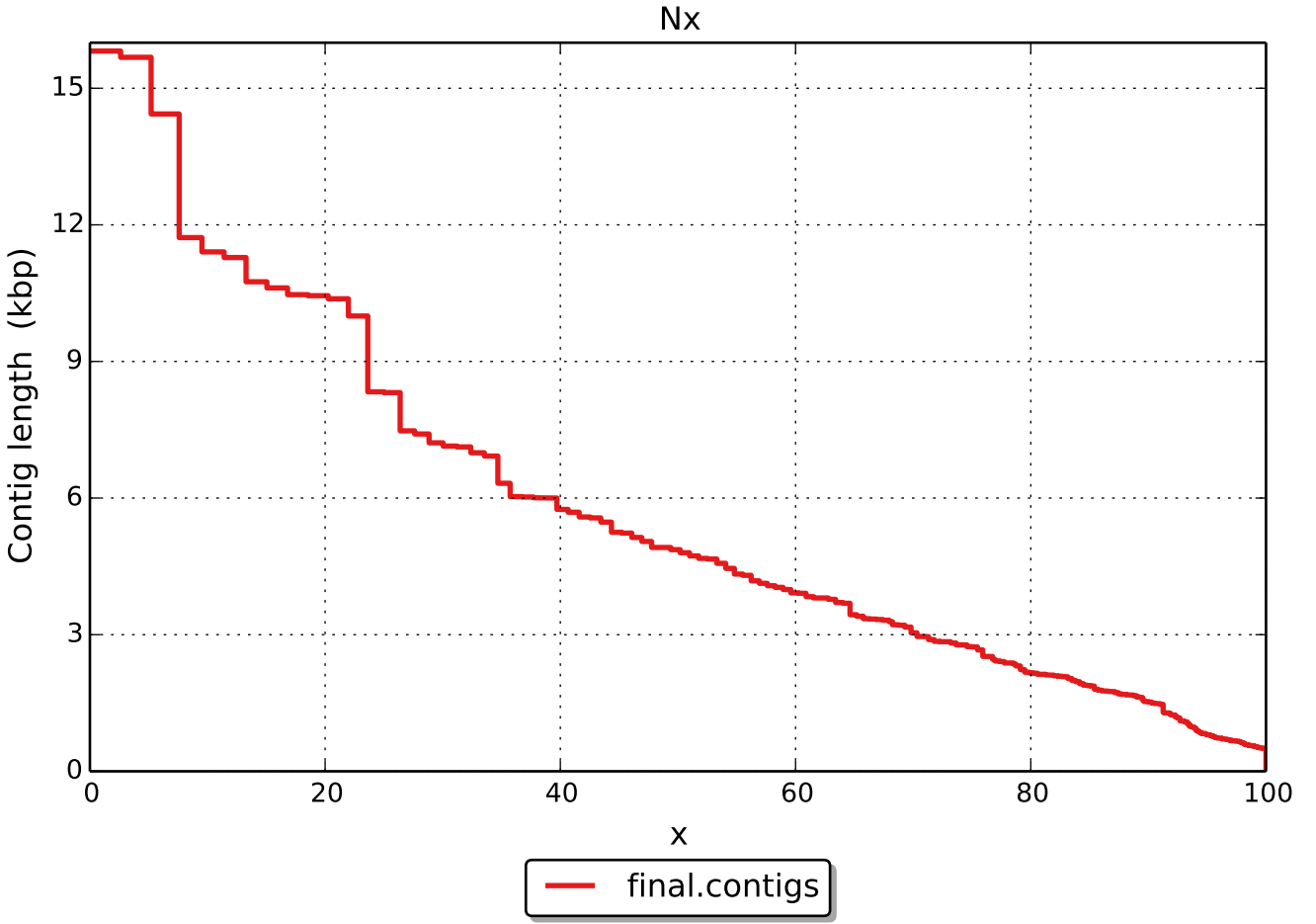
Unaligned report

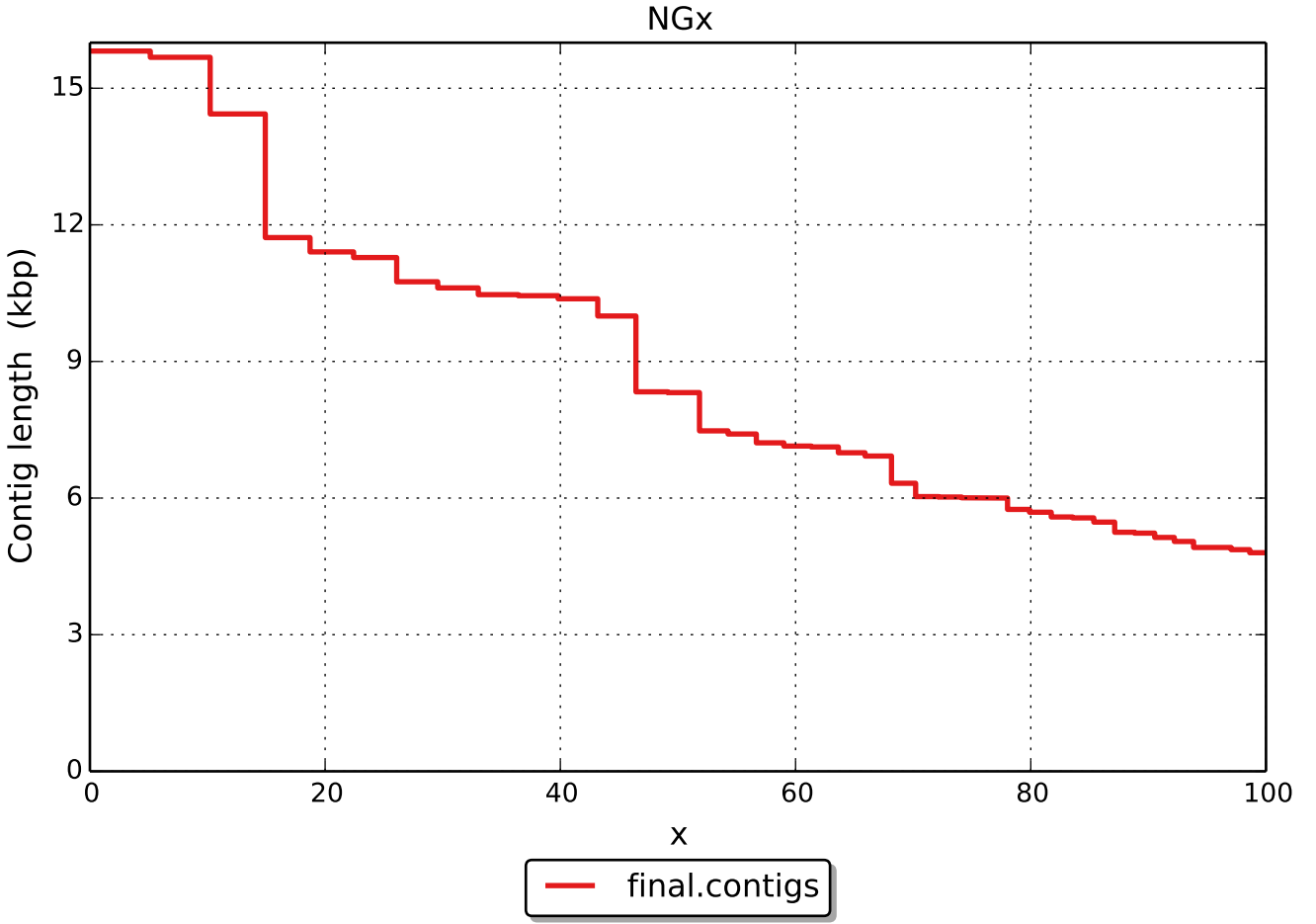
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

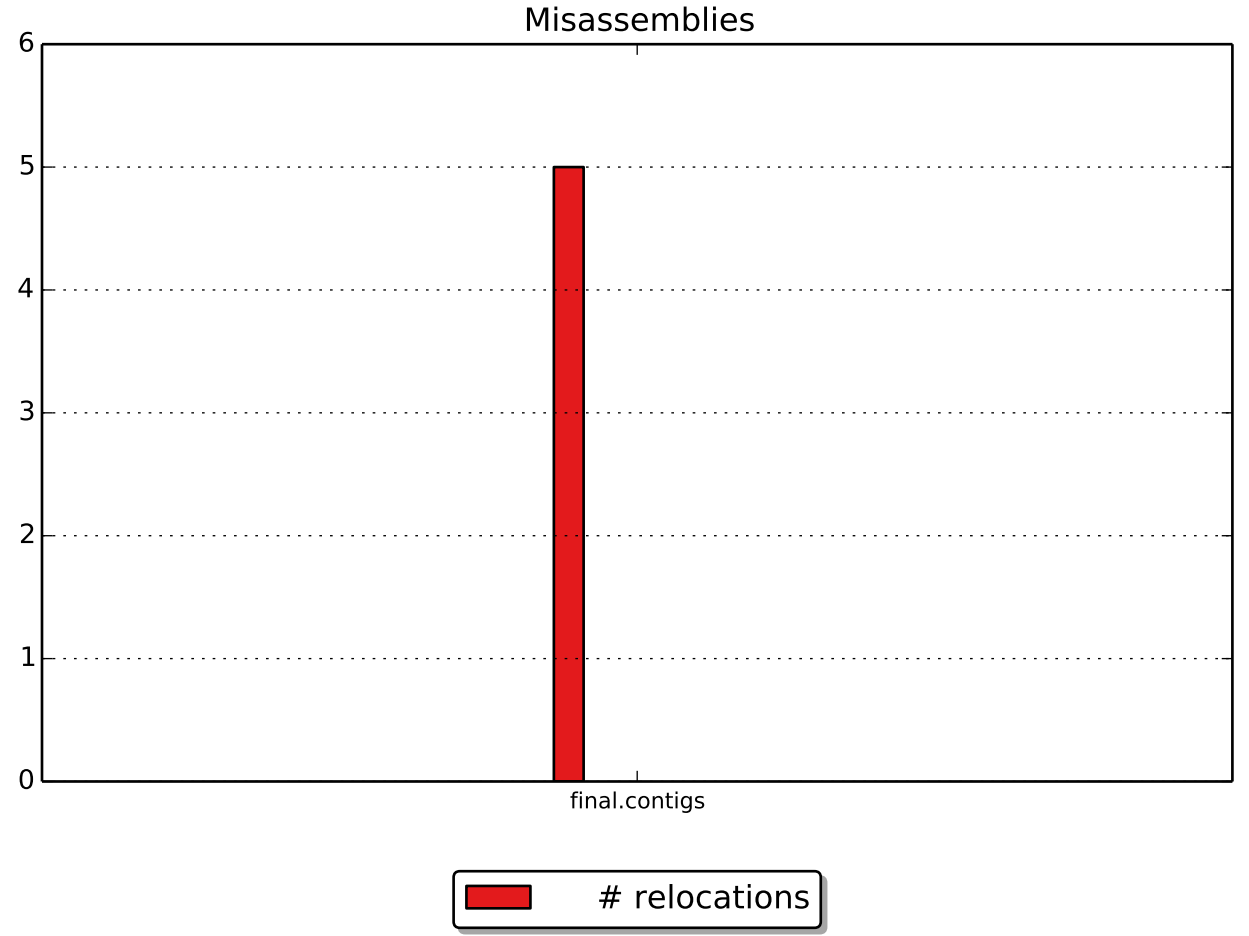
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

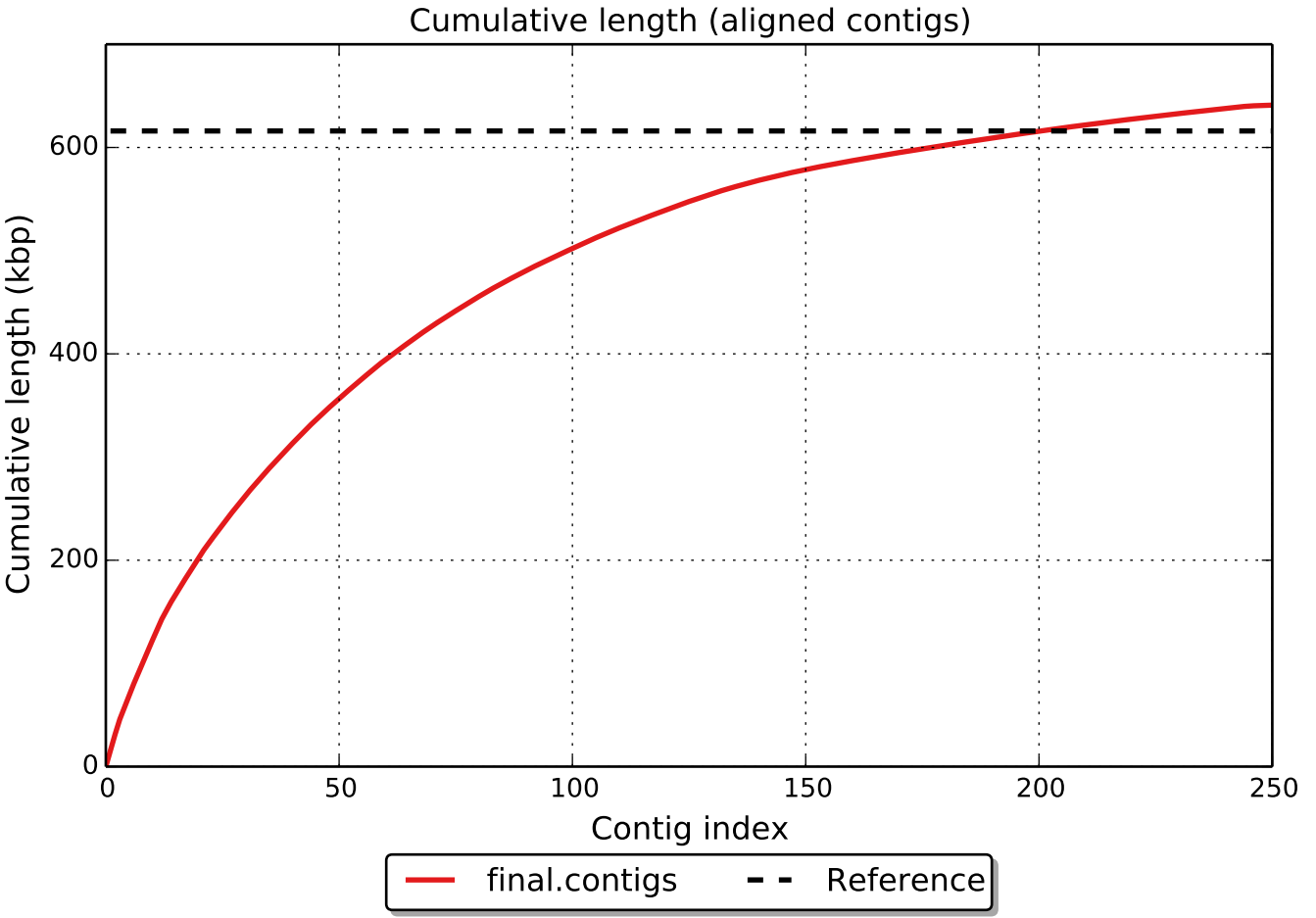

Cumulative length
Cumulative length (kbp)
1200
900
600
300
0
0
80
160
240
320
400
Contig index
final.contigs
Reference

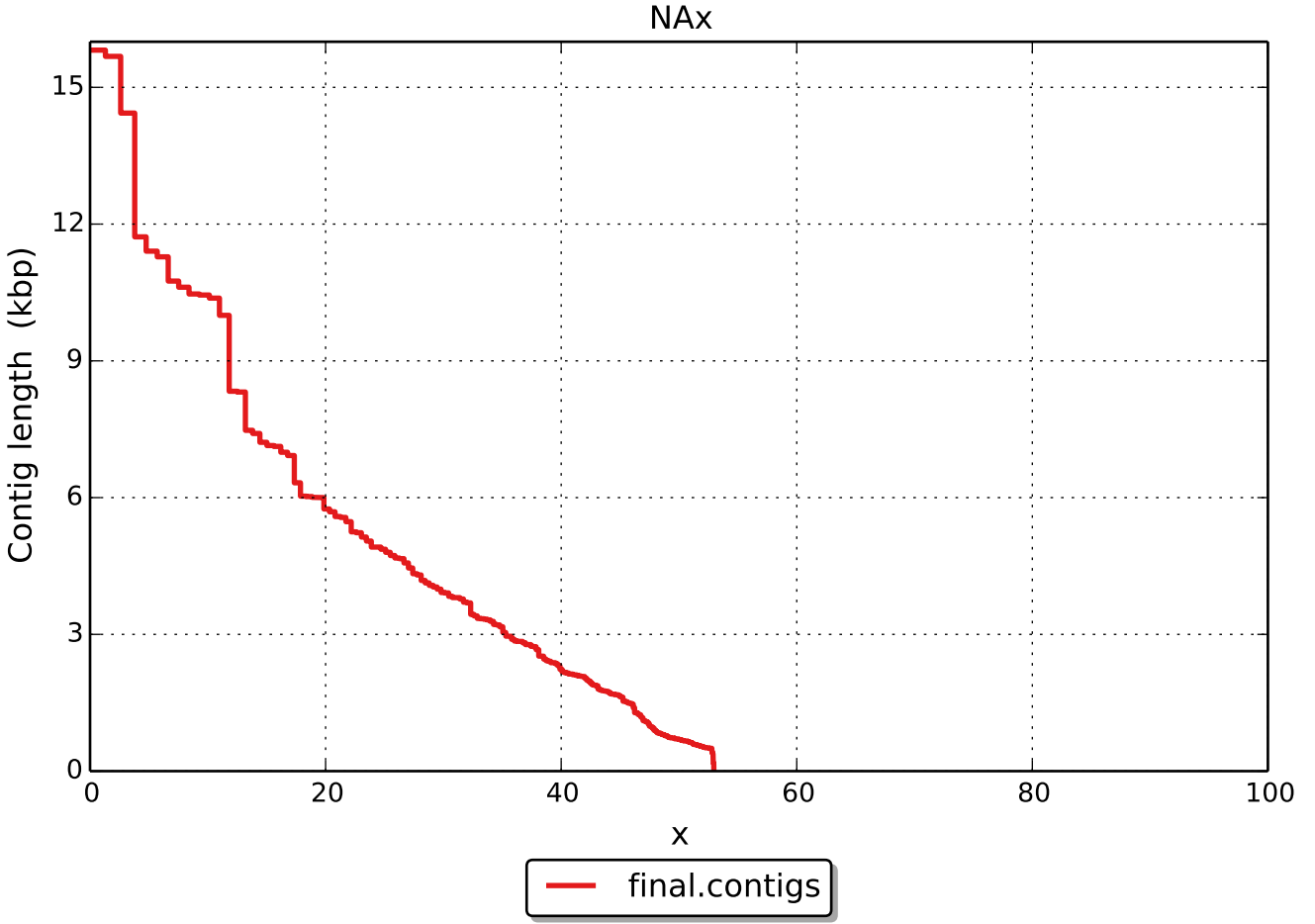

GC content
800
600
400
200
0
windows
0
20
40
60
80
100
GC (%)
final.contigs
Reference

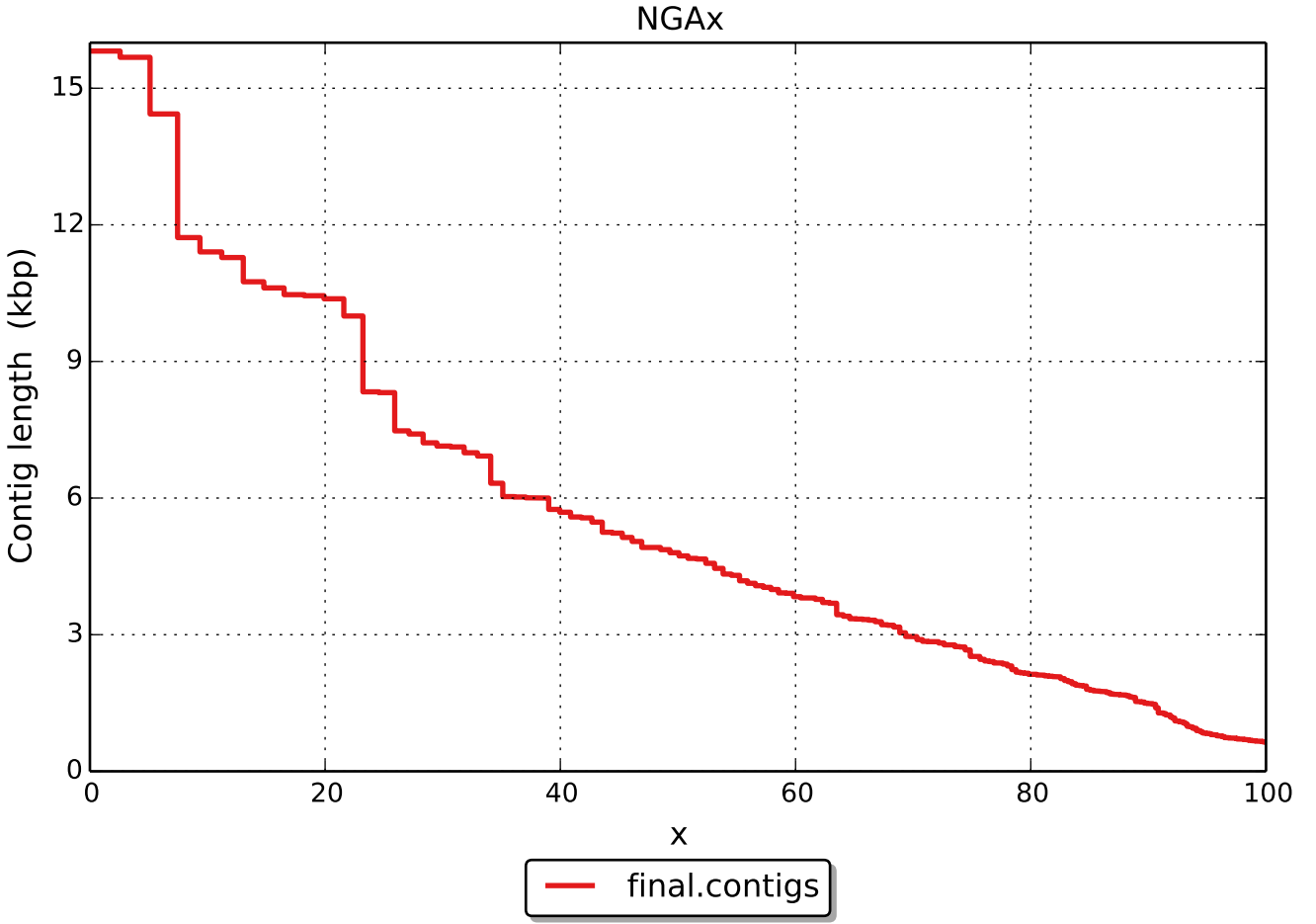

Nx
Contig length (kbp)
15
12
9
6
3
0
0
20
40
60
80
100
x
final.contigs


NGx
Contig length (kbp)
15
12
9
6
3
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)
0
200
400
600
0
50
100
150
200
250
Contig index
final.contigs
Reference


NAx
Contig length (kbp)
15
12
9
6
3
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (kbp)
15
12
9
6
3
0
0
20
40
60
80
100
x
final.contigs