Report

	final.contigs
# contigs (>= 0 bp)	275
# contigs (>= 1000 bp)	155
Total length (>= 0 bp)	669346
Total length (>= 1000 bp)	590588
# contigs	275
Largest contig	25883
Total length	669346
Reference length	641799
GC (%)	26.32
Reference GC (%)	26.30
N50	4473
NG50	4614
N75	2222
NG75	2490
L50	44
LG50	41
L75	98
LG75	89
# misassemblies	5
# misassembled contigs	5
Misassembled contigs length	10256
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	96.805
Duplication ratio	1.077
# N's per 100 kbp	0.00
# mismatches per 100 kbp	645.27
# indels per 100 kbp	0.32
Largest alignment	25883
NA50	4473
NGA50	4614
NA75	2181
NGA75	2490
LA50	44
LGA50	41
LA75	98
LGA75	89

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

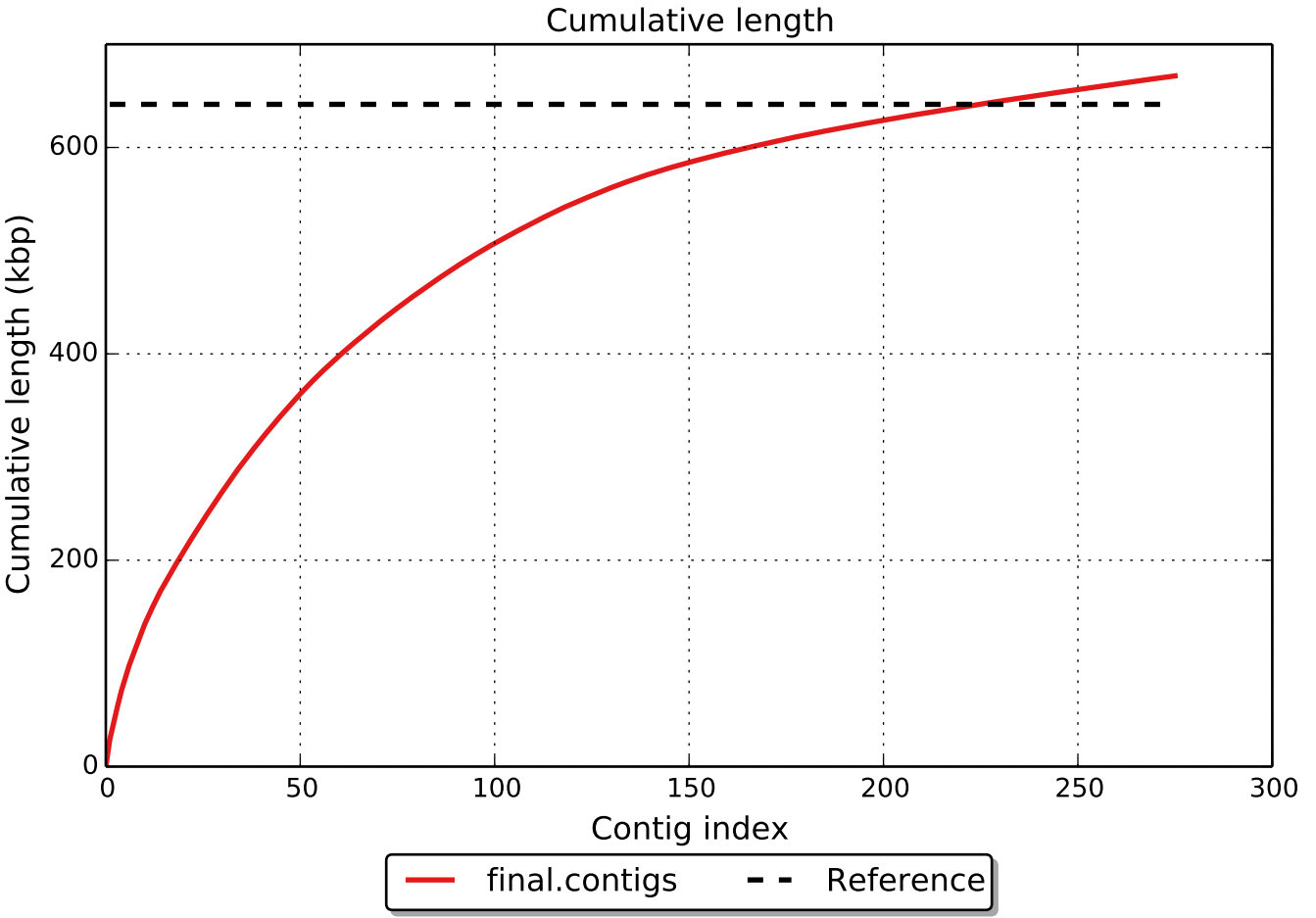
	final.contigs
# misassemblies	5
# relocations	5
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	5
Misassembled contigs length	10256
# local misassemblies	0
# mismatches	4009
# indels	2
# short indels	2
# long indels	0
Indels length	2

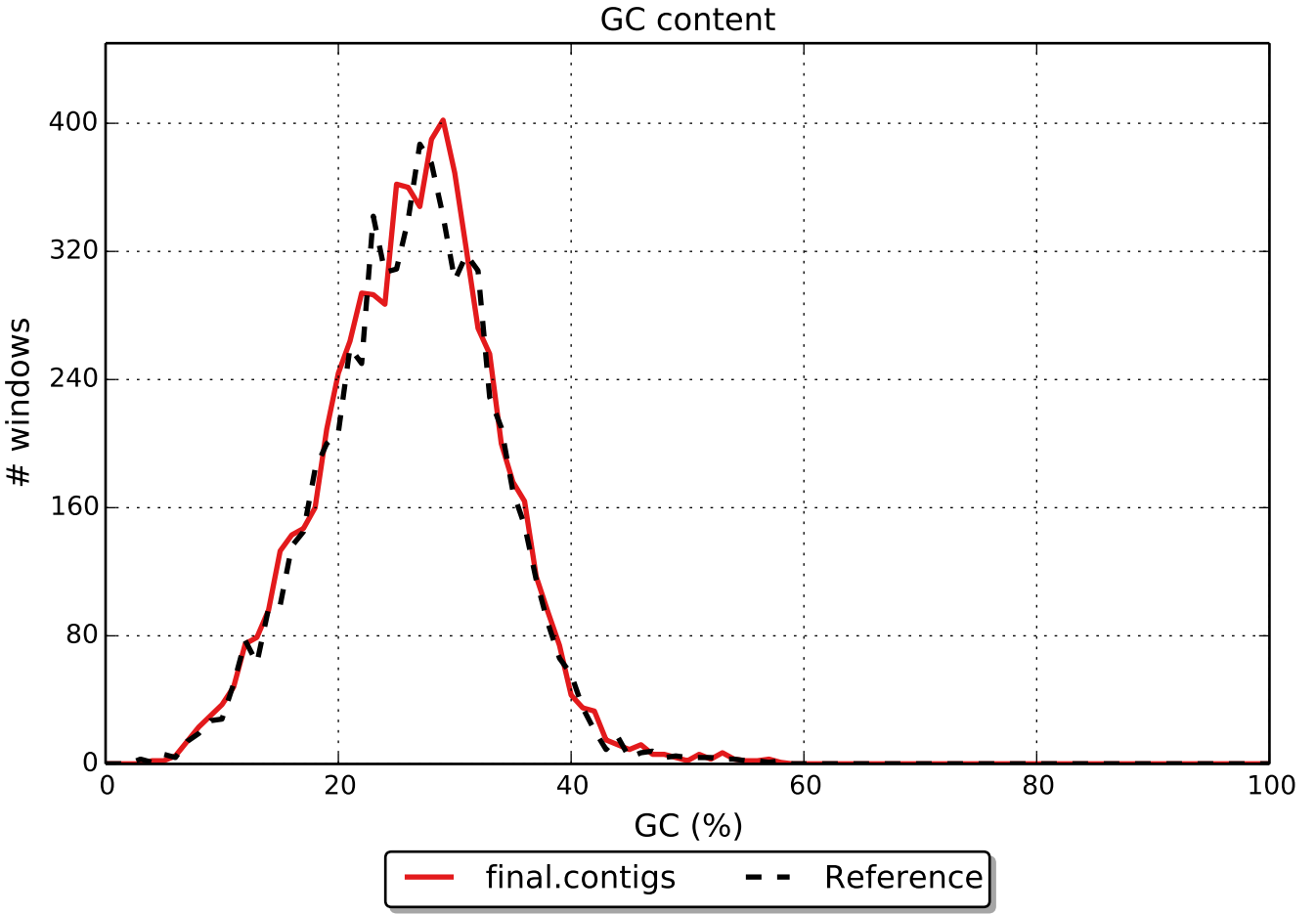
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

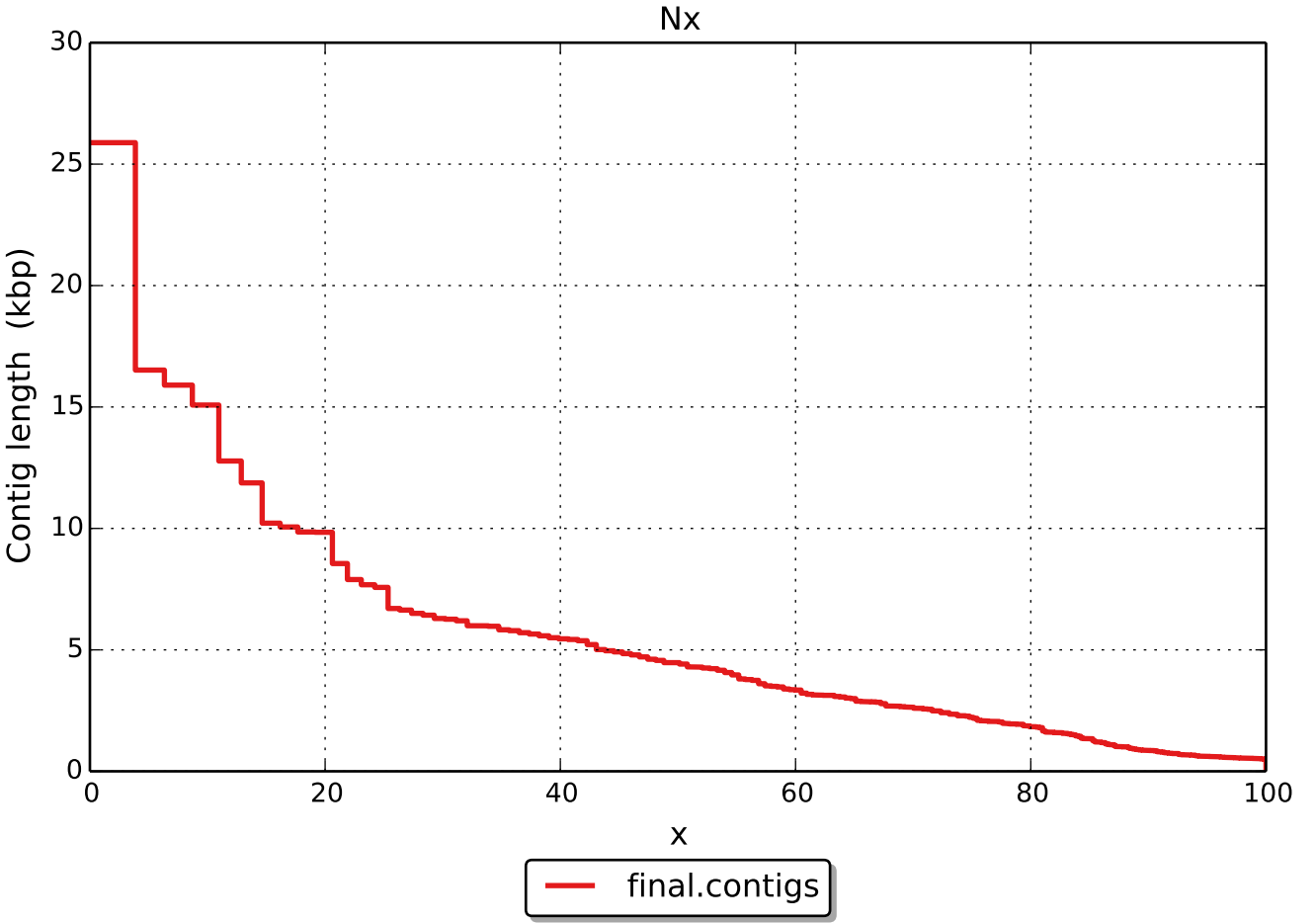
Unaligned report

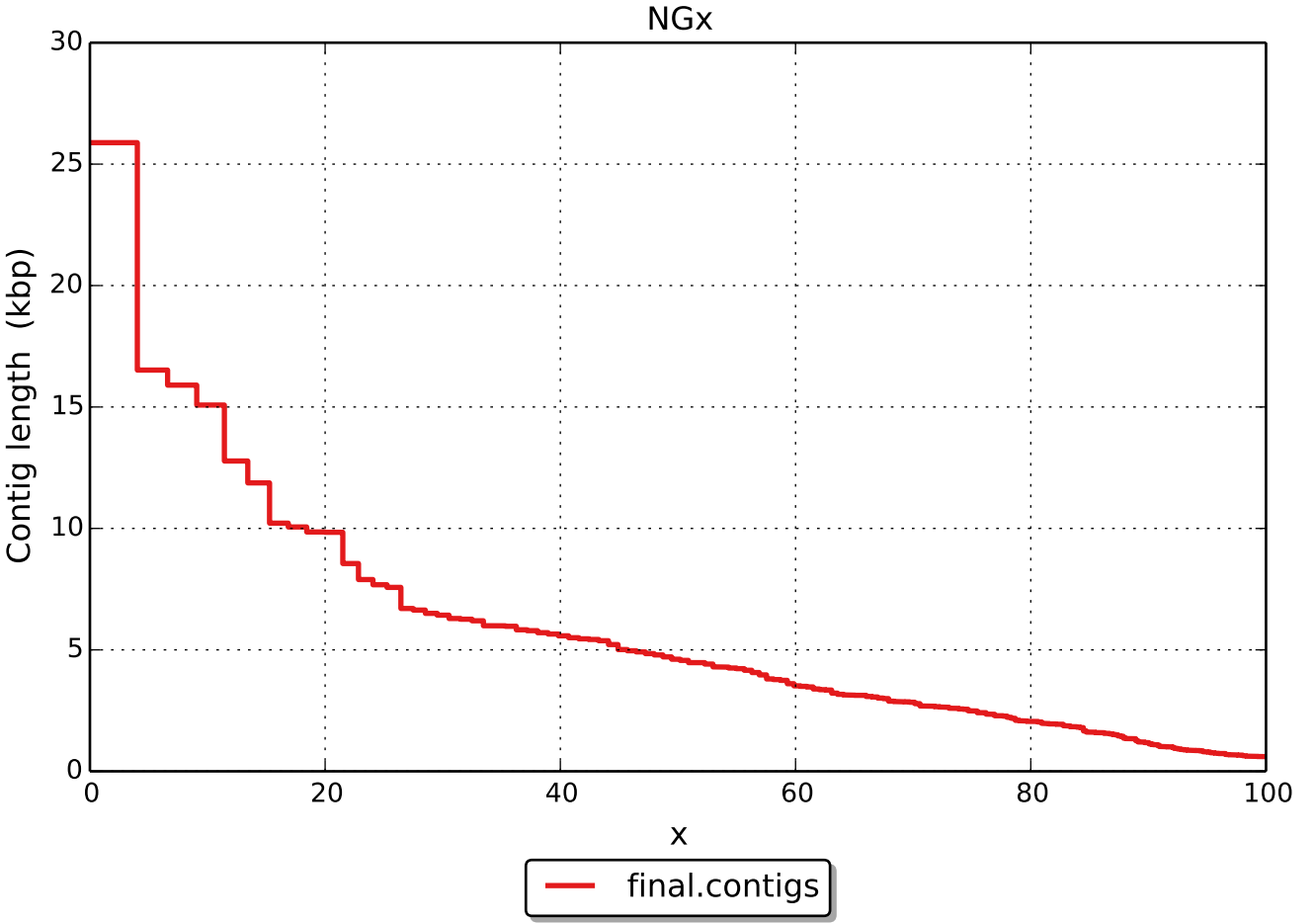
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

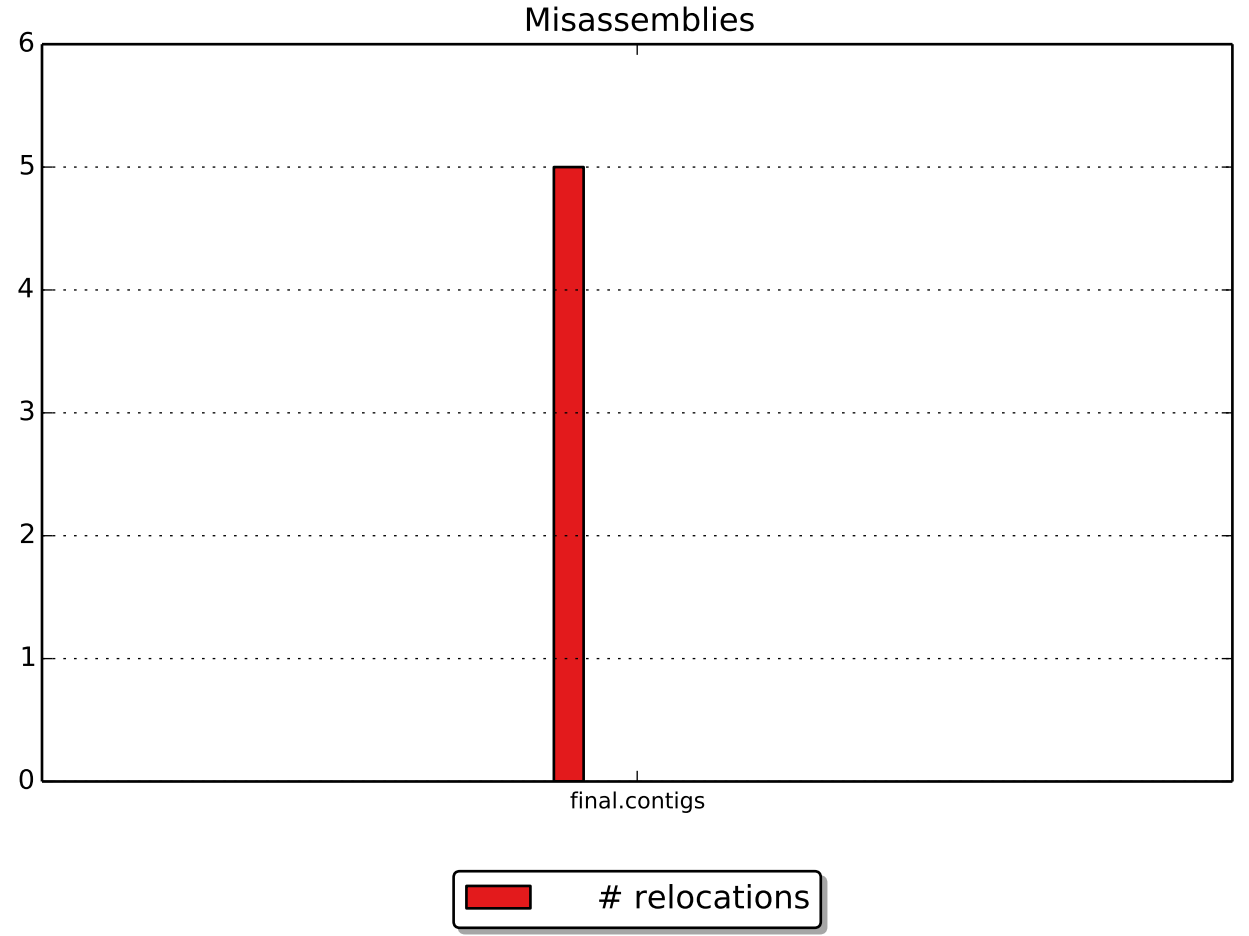
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

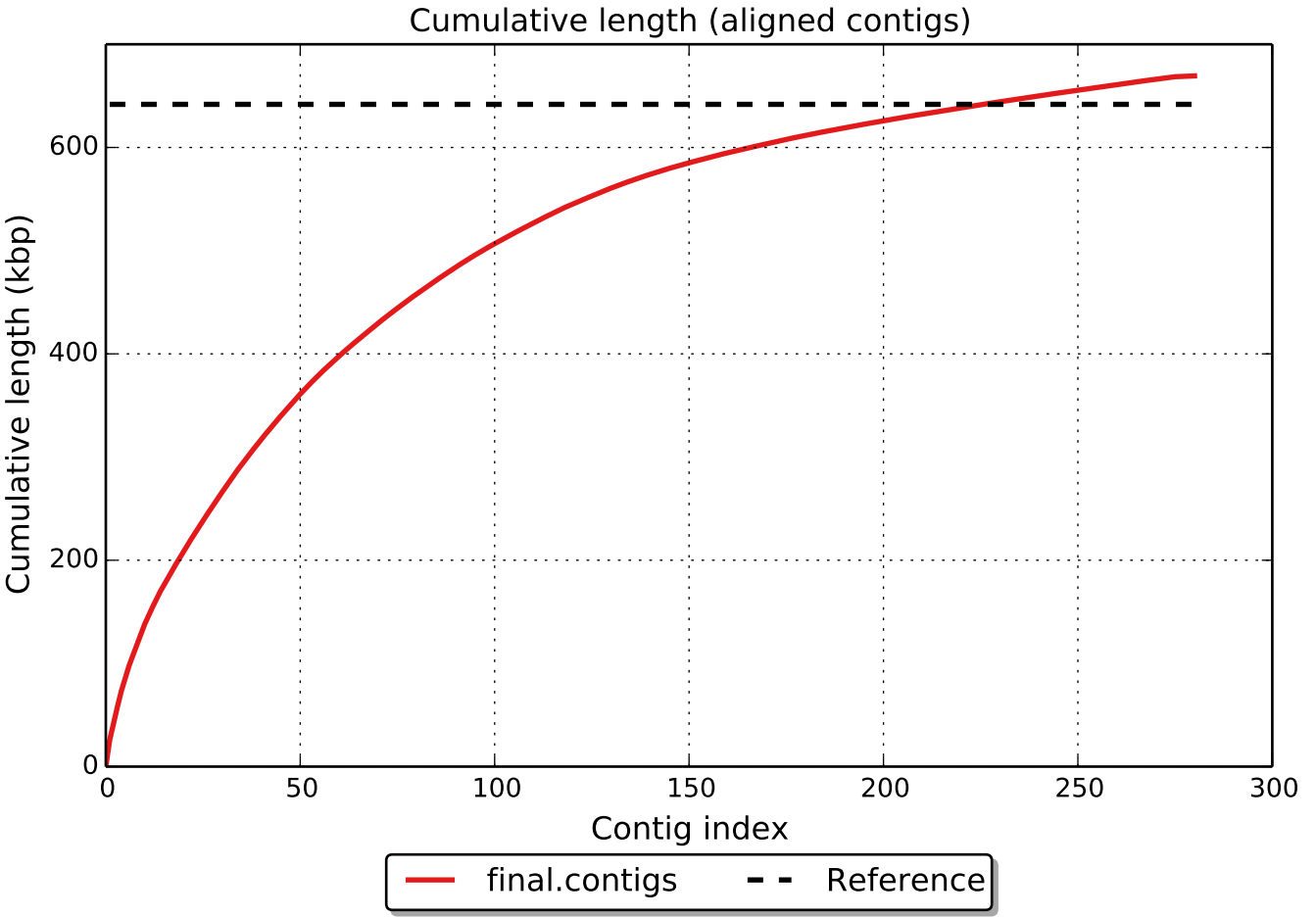

Cumulative length
Cumulative length (kbp)
0
200
400
600
0
50
100
150
200
250
300
Contig index
final.contigs
Reference

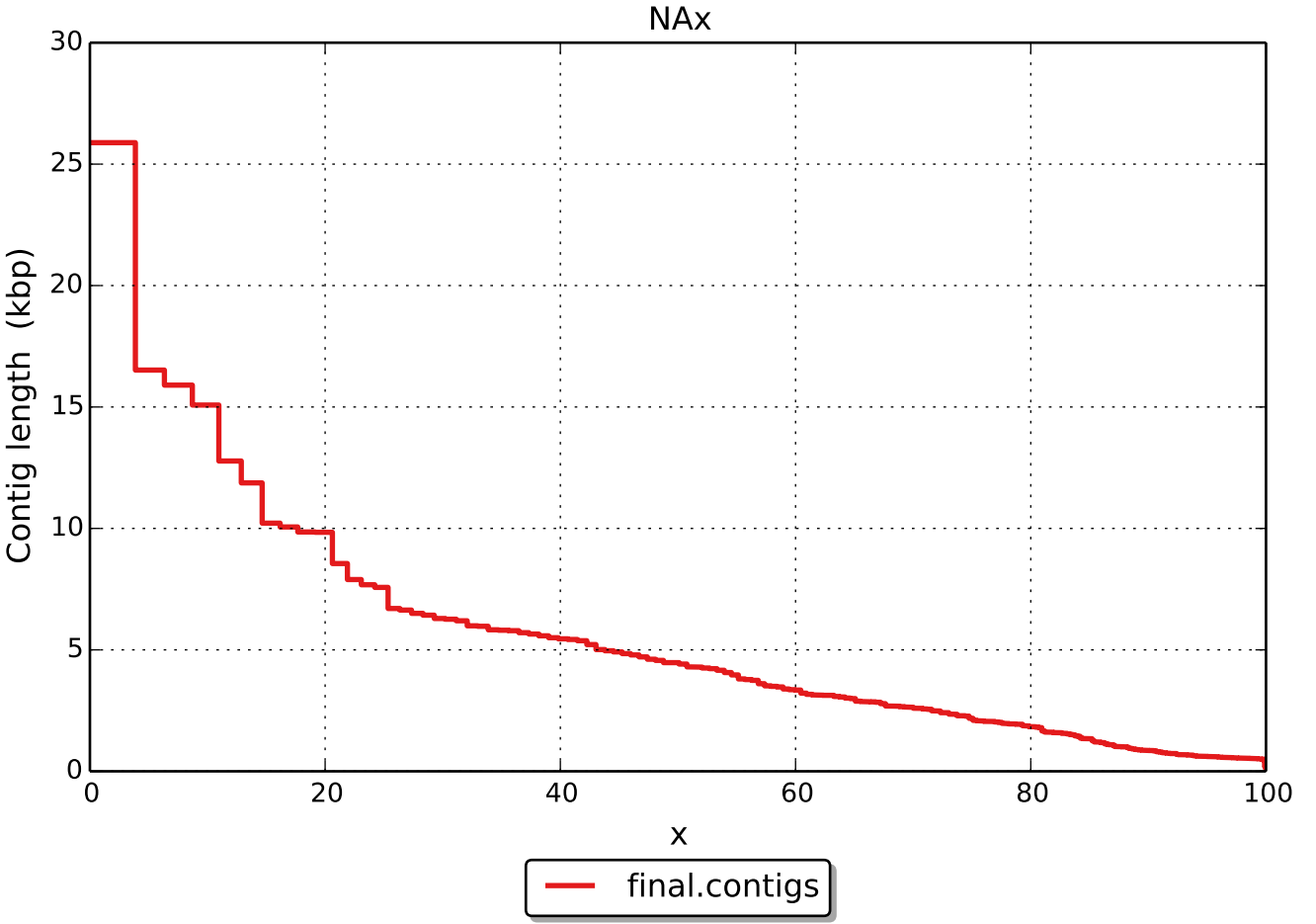

GC content
windows
GC (%)
0
80
160
240
320
400
0
20
40
60
80
100
final.contigs
Reference

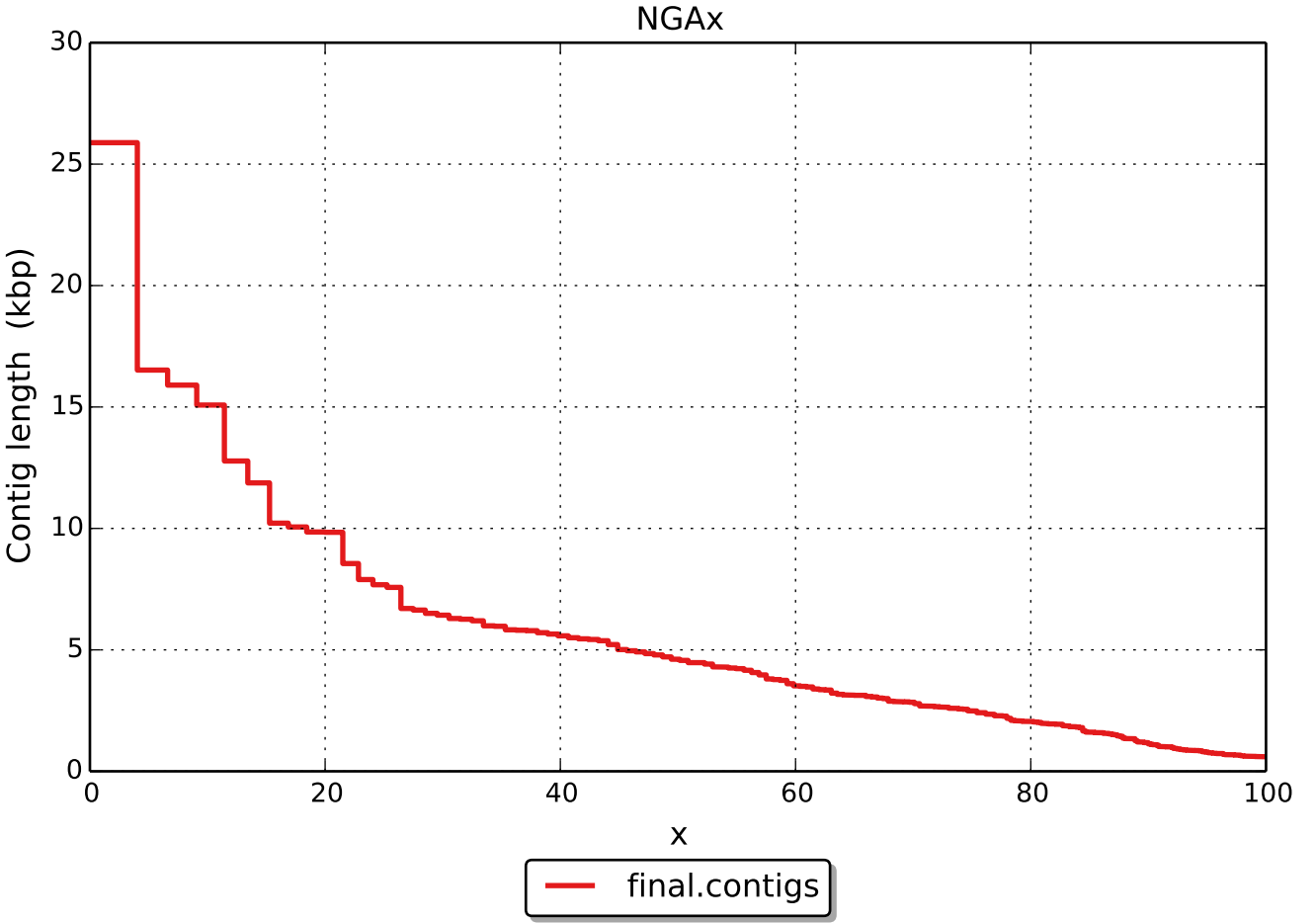

Nx
Contig length (kbp)
30
25
20
15
10
5
0
0
20
40
60
80
100
x
final.contigs


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)
0
200
400
600
0
50
100
150
200
250
300
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