Report

	site_D3_DNA.final.contigs
# contigs (>= 1000 bp)	4
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	5986
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	6
Largest contig	2387
Total length	7651
Reference length	4282232
GC (%)	58.79
Reference GC (%)	66.99
N50	1190
N75	1054
L50	3
L75	4
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 3 part
Unaligned length	4662
Genome fraction (%)	0.045
Duplication ratio	1.567
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2515.72
# indels per 100 kbp	471.70
Largest alignment	977
Total aligned length	1894
NGA50	-

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

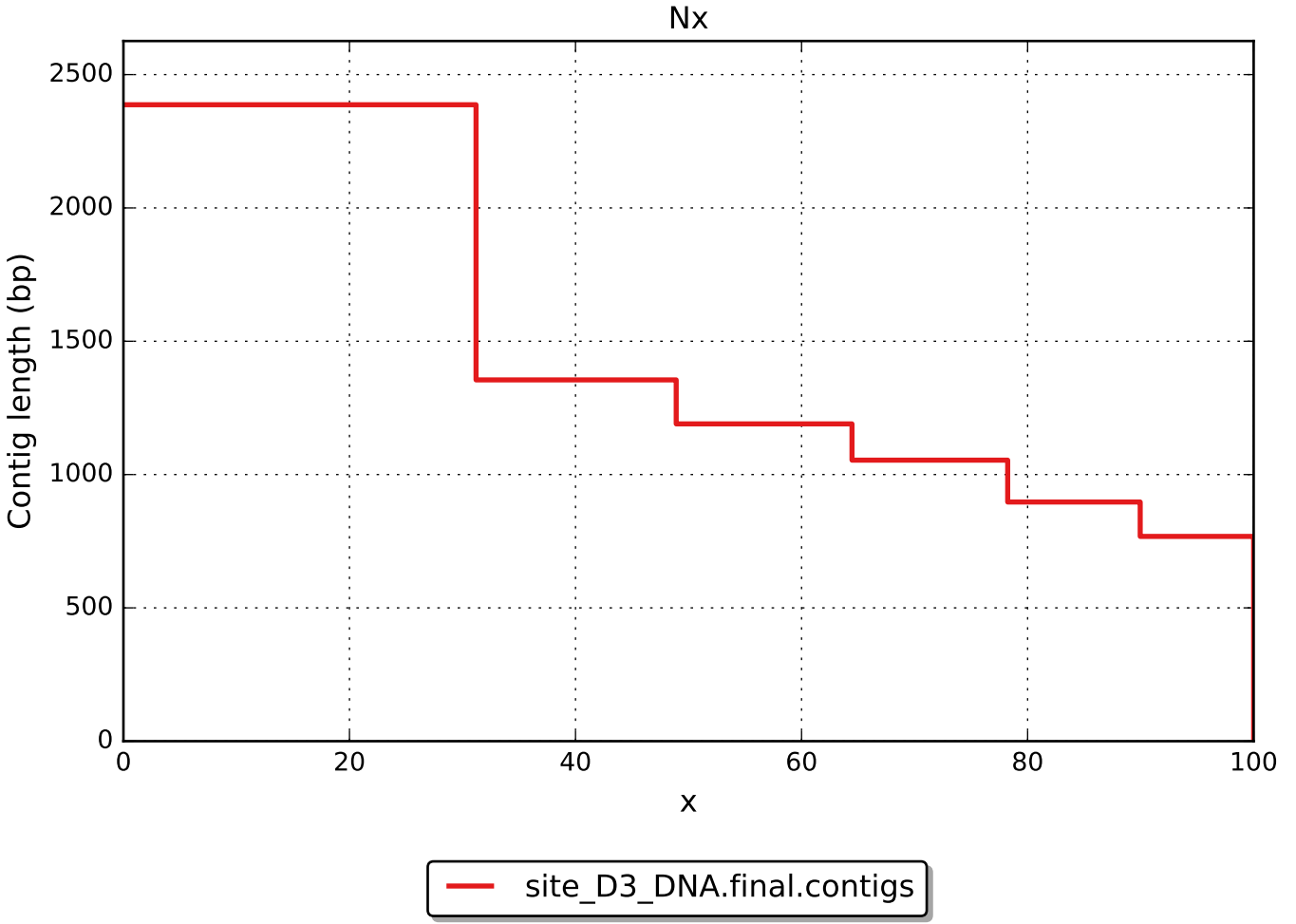
	site_D3_DNA.final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	48
# indels	9
# indels (<= 5 bp)	9
# indels (> 5 bp)	0
Indels length	14

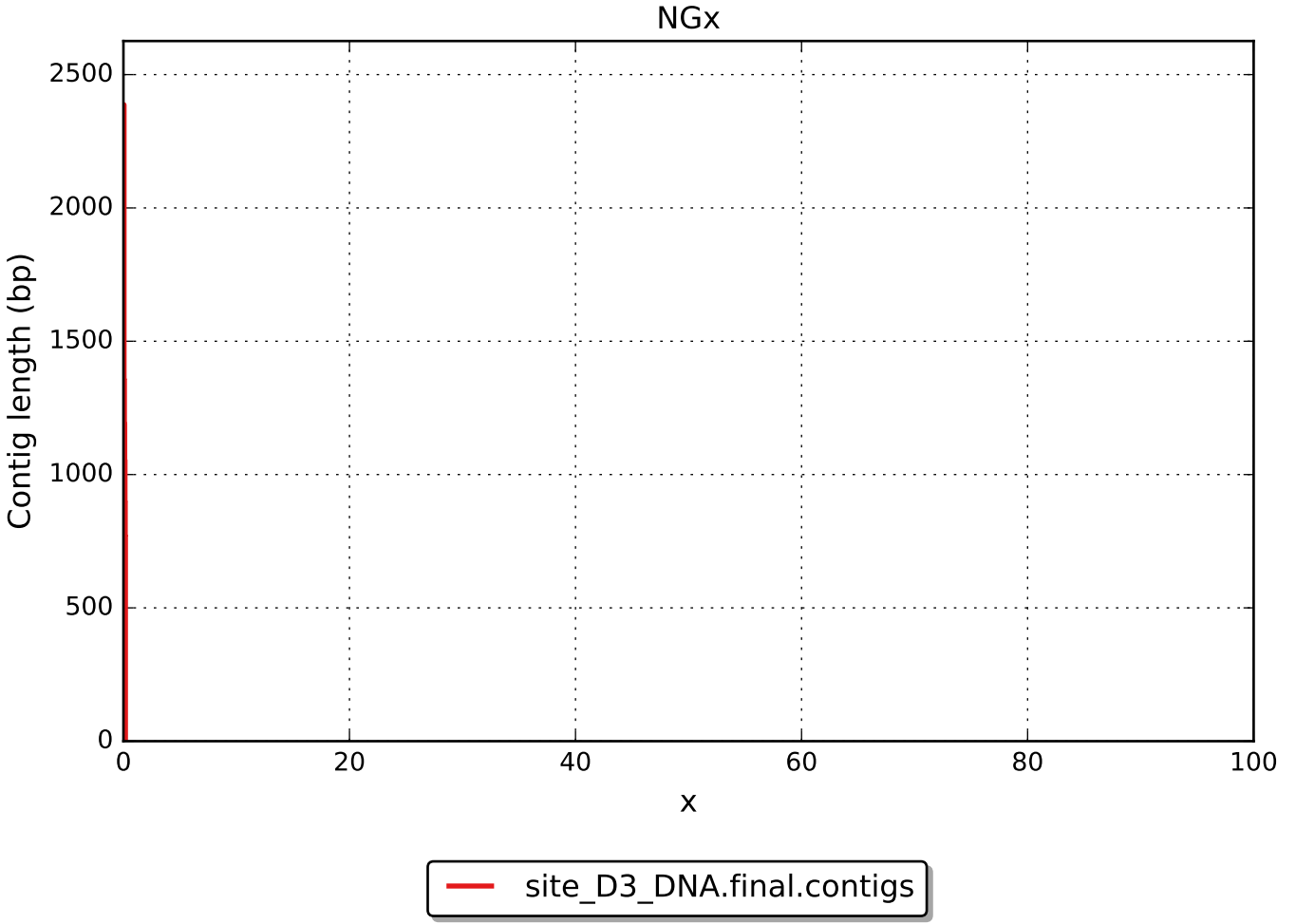
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

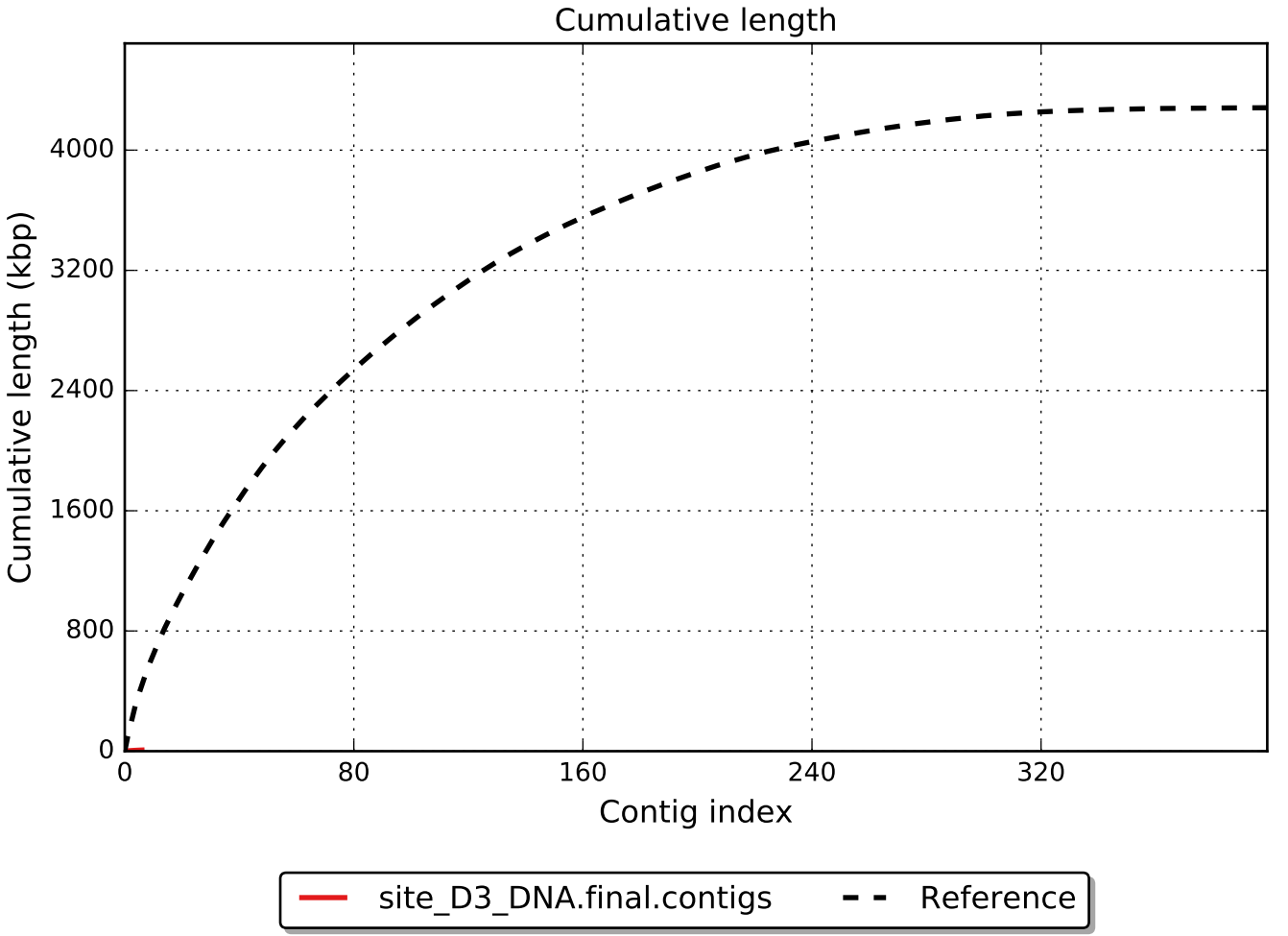
Unaligned report

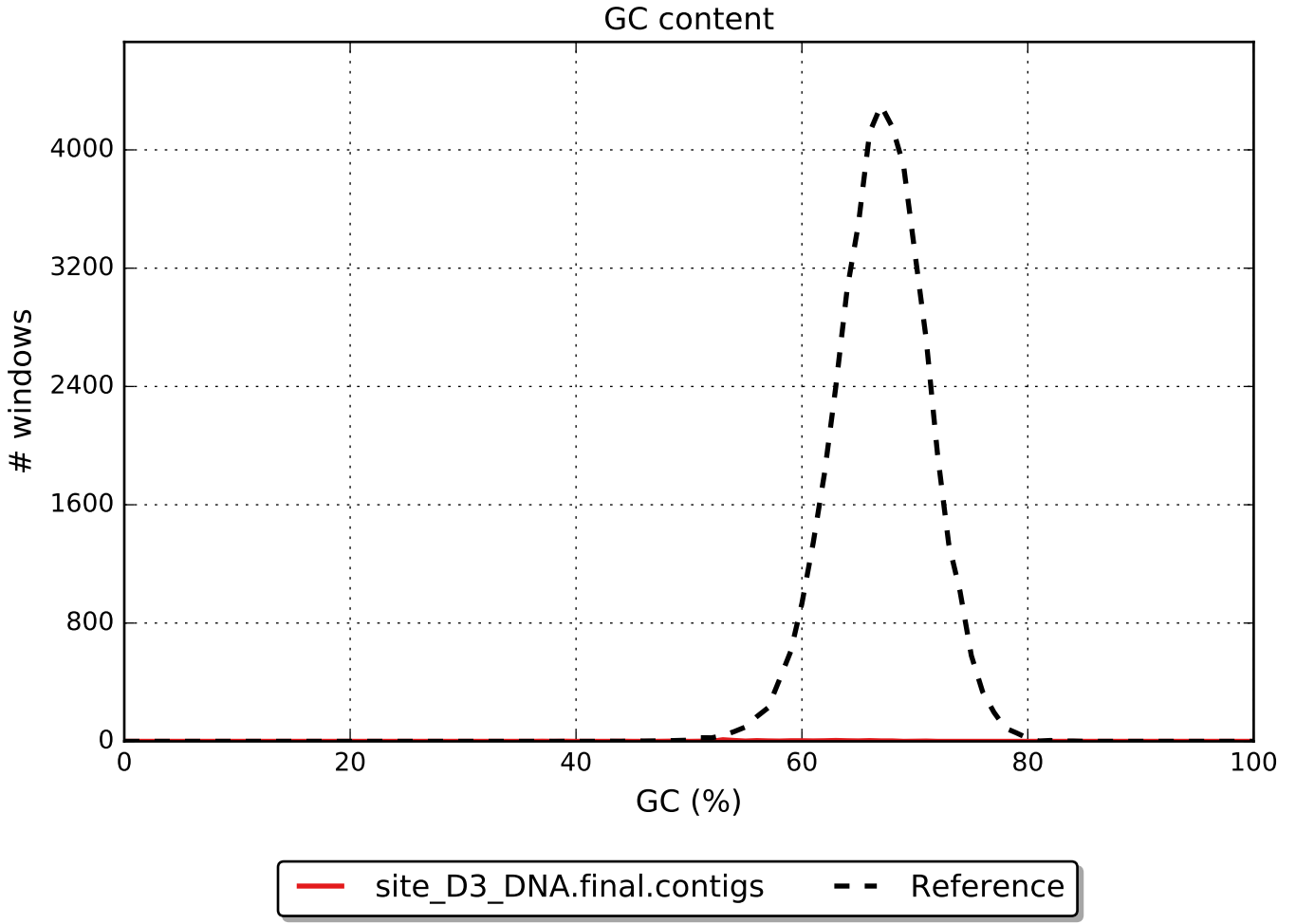
	site_D3_DNA.final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	3
Partially unaligned length	4662
# N's	0

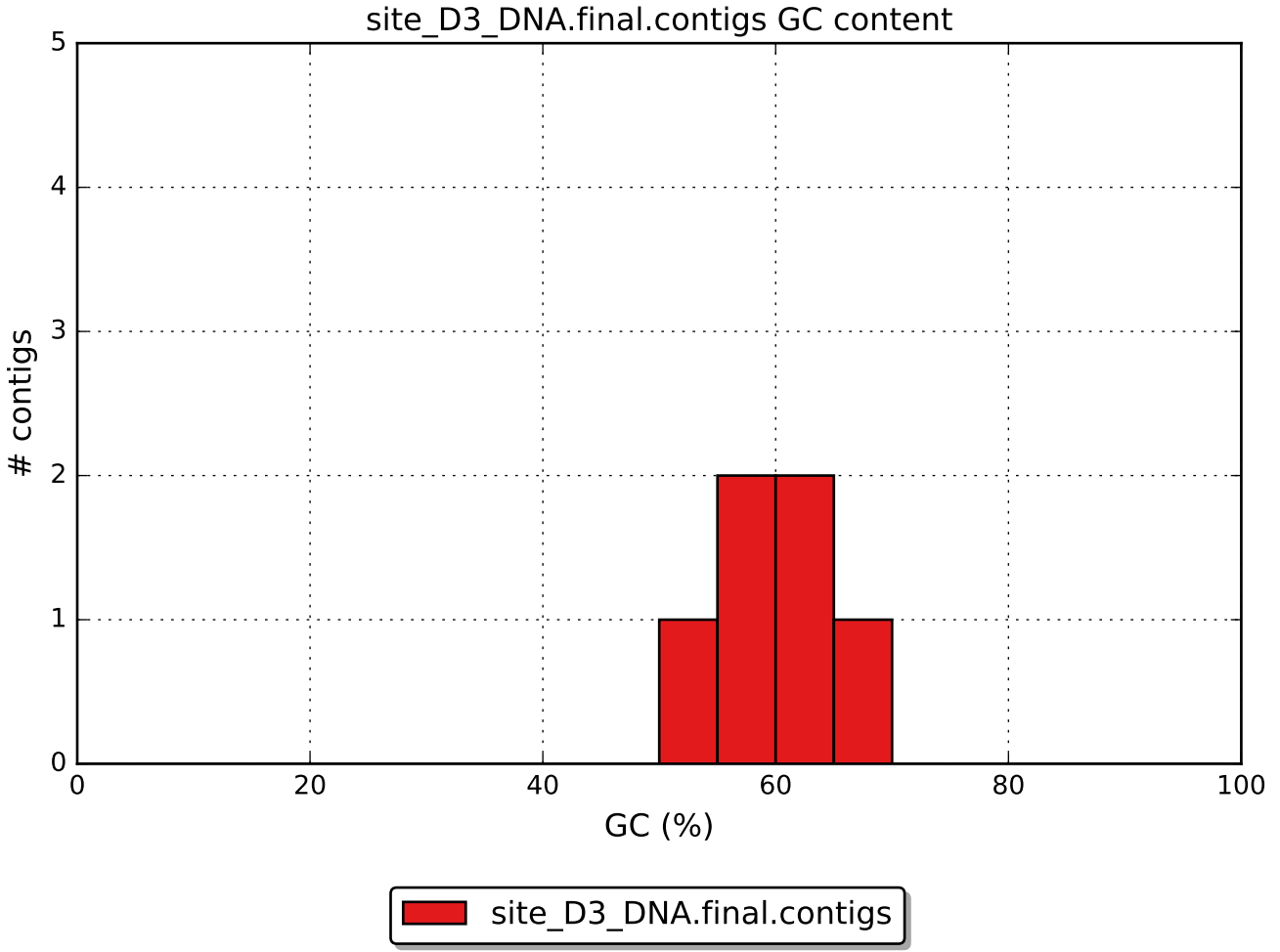
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

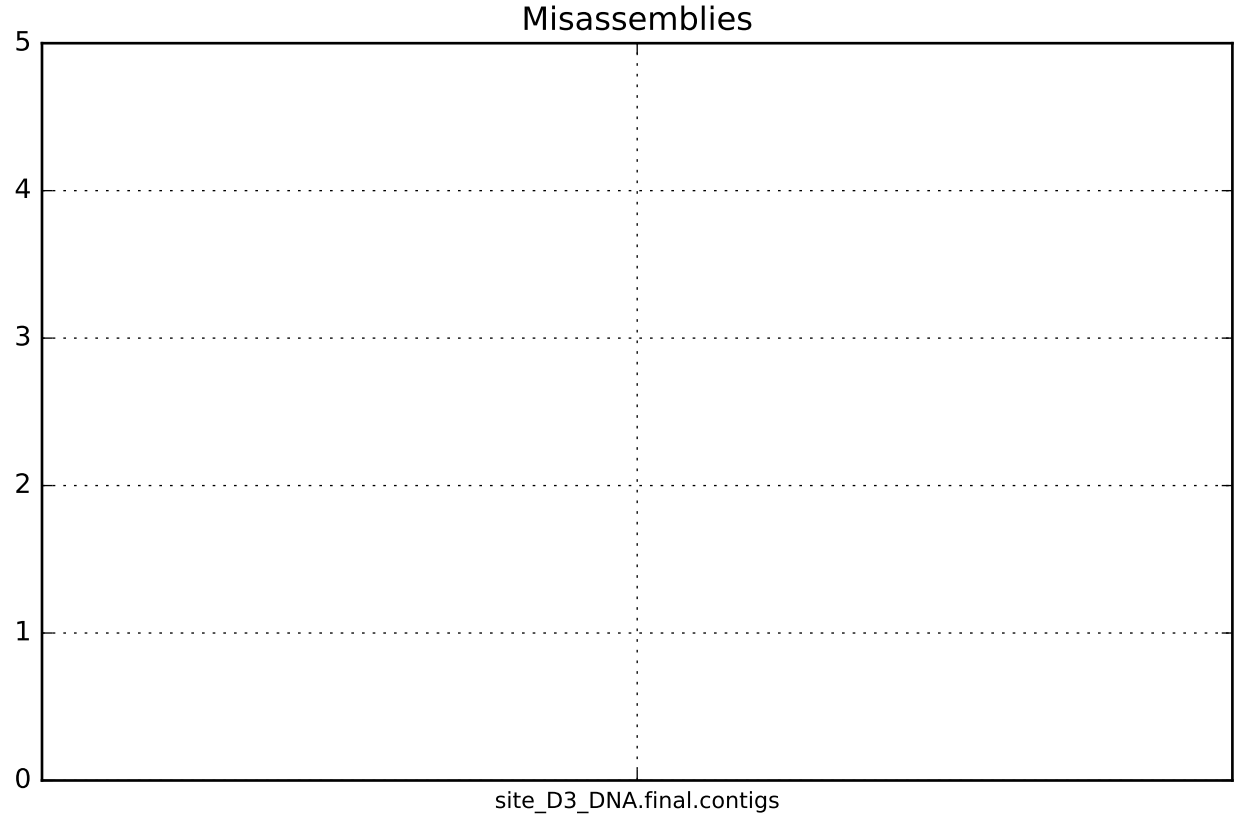

Nx
Contig length (bp)
2500
2000
1500
1000
500
0
0
20
40
60
80
100
x
site_D3_DNA.final.contigs

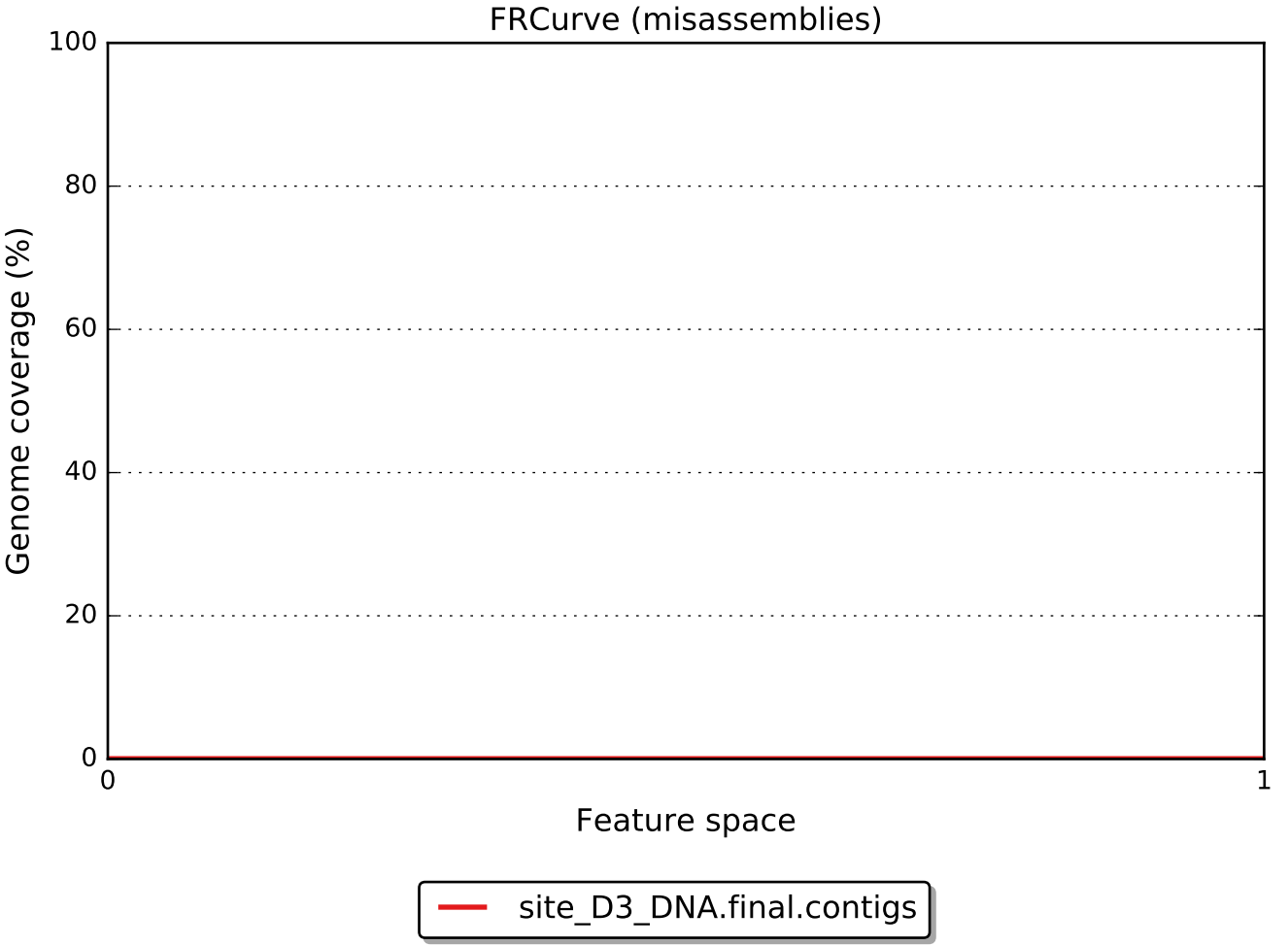

NGx
Contig length (bp)
2500
2000
1500
1000
500
0
0
20
40
60
80
100
x
site_D3_DNA.final.contigs

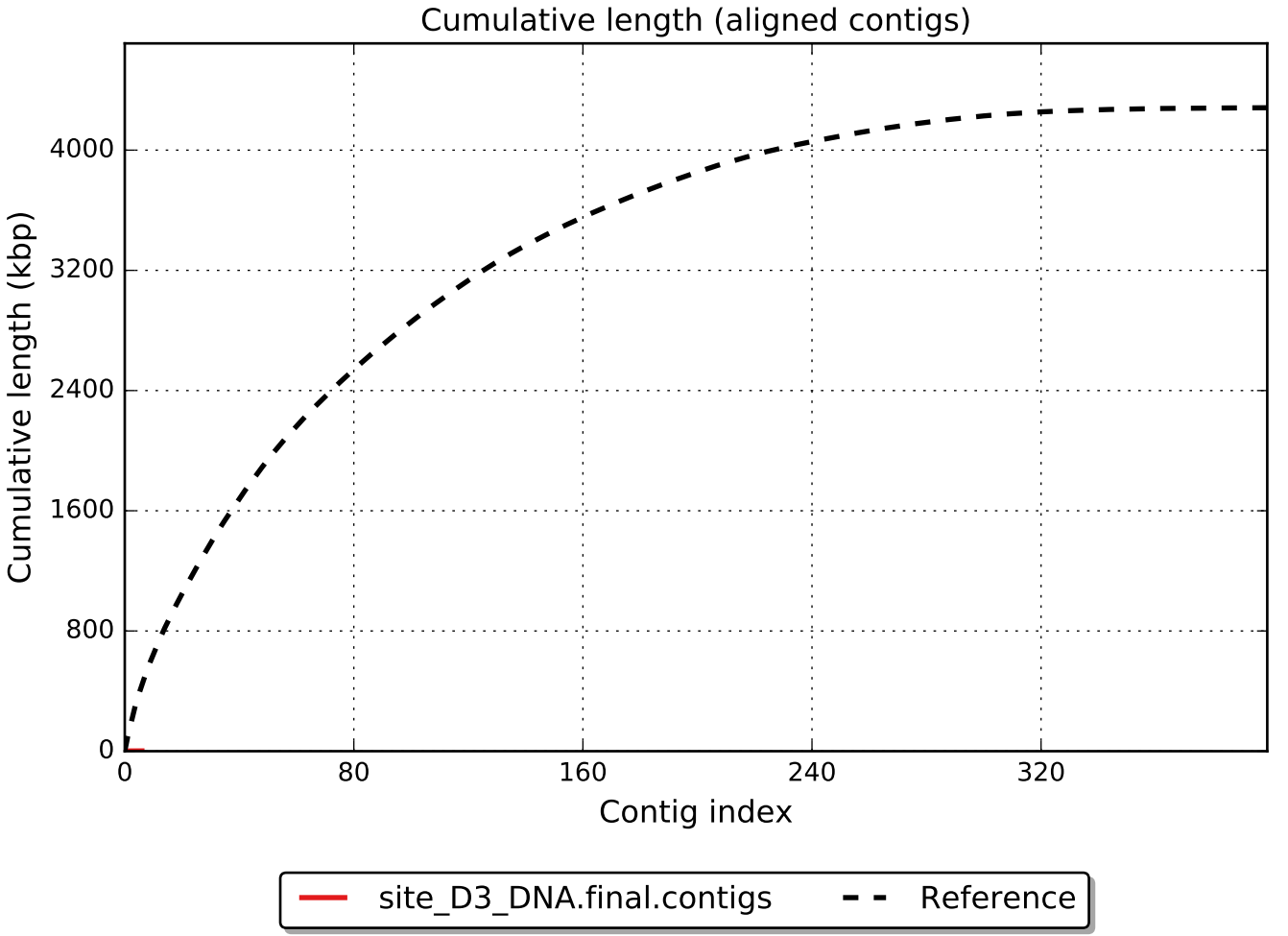

Cumulative length
Cumulative length (kbp)
4000
3200
2400
1600
800
0
0
80
160
240
320
Contig index
site_D3_DNA.final.contigs
Reference

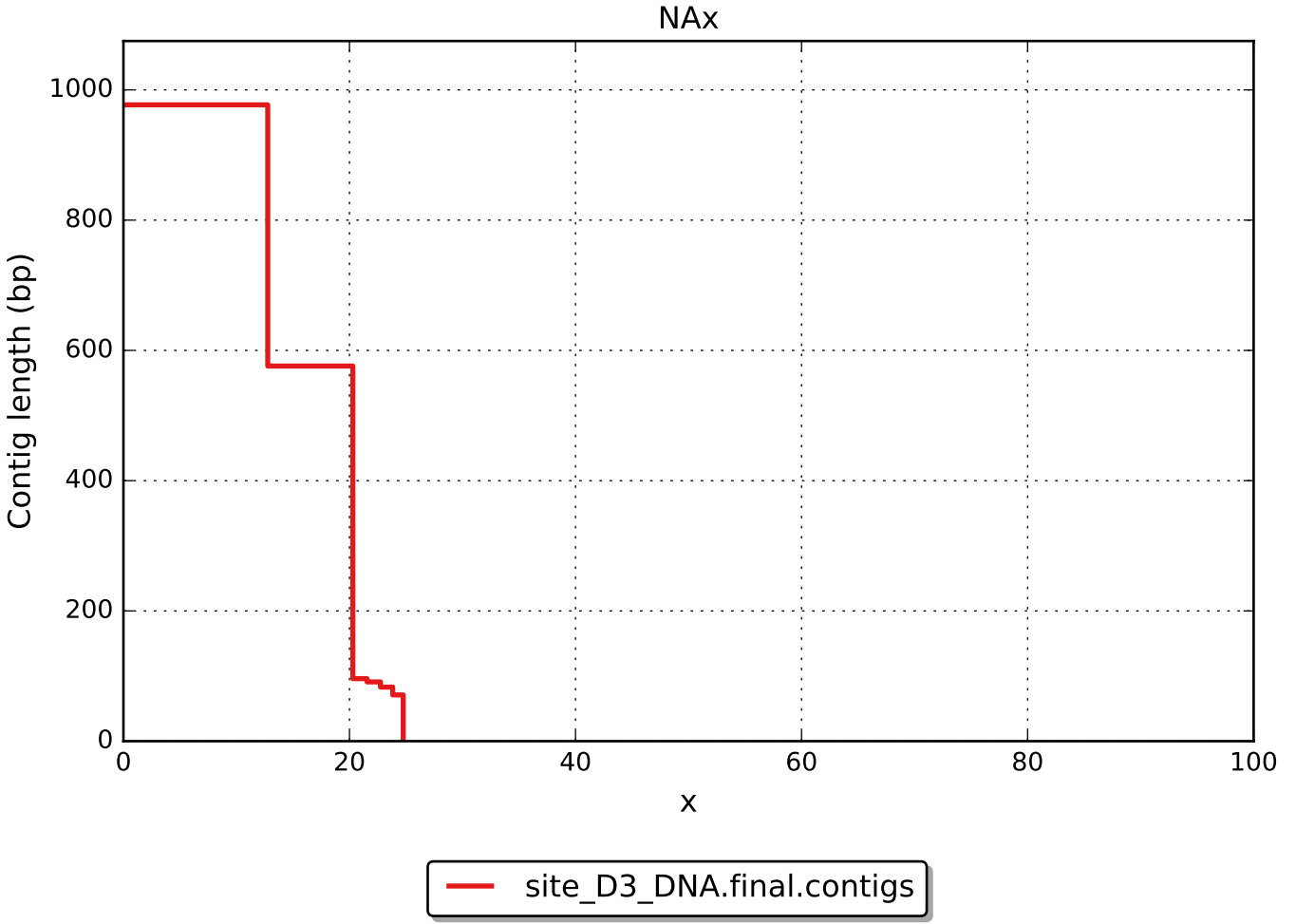

GC content
windows
GC (%)
0
800
1600
2400
3200
4000
0
20
40
60
80
100
site_D3_DNA.final.contigs
Reference

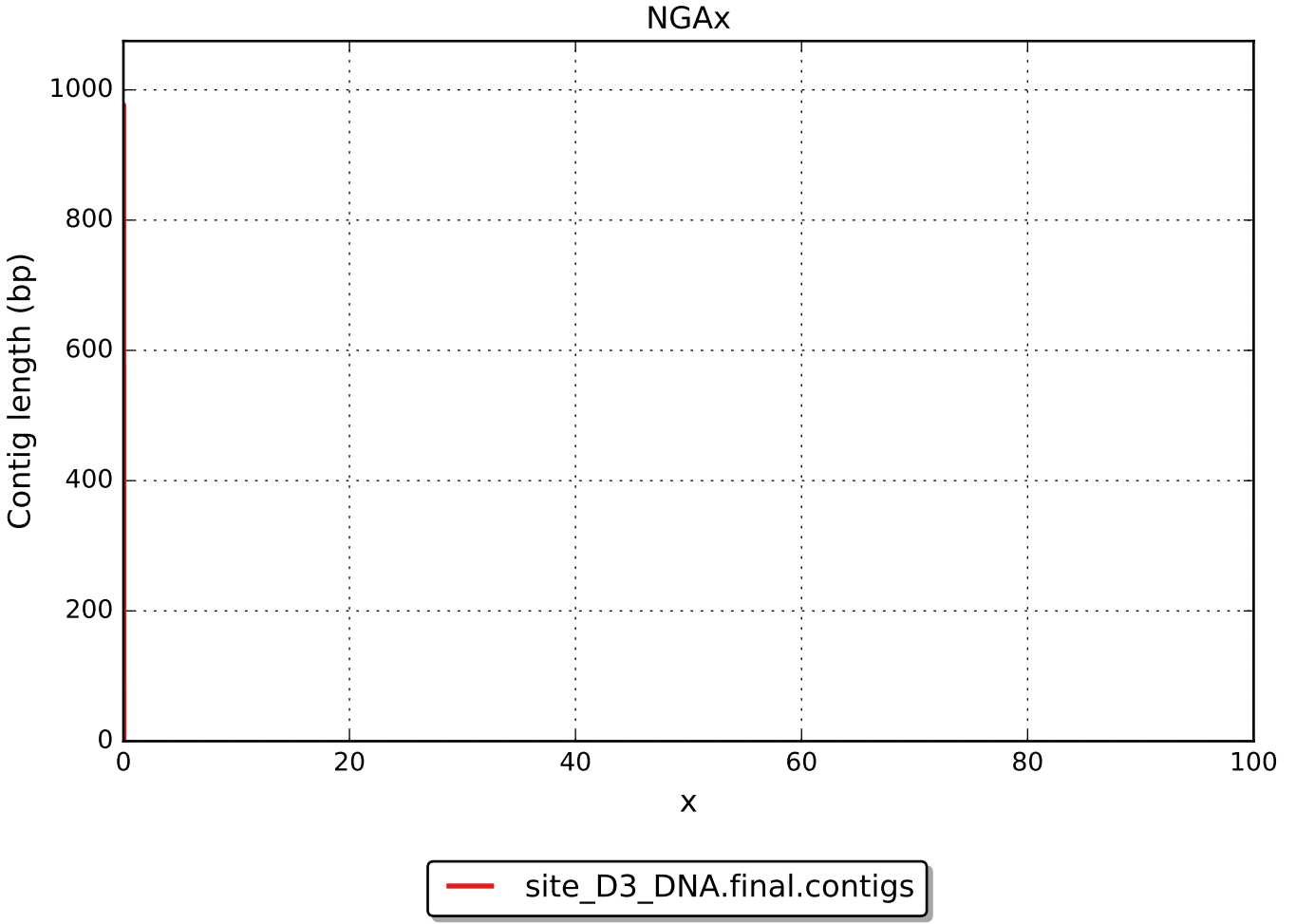

site_D3_DNA.final.contigs GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
site_D3_DNA.final.contigs


Misassemblies
5
4
3
2
1
0
site_D3_DNA.final.contigs


FRCurve (misassemblies)
100
80
60
40
20
0
Genome coverage (%)
0
1
Feature space
site_D3_DNA.final.contigs


Cumulative length (aligned contigs)
Cumulative length (kbp)
4000
3200
2400
1600
800
0
0
80
160
240
320
Contig index
site_D3_DNA.final.contigs
Reference


NAx
Contig length (bp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
site_D3_DNA.final.contigs


NGAx
Contig length (bp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
site_D3_DNA.final.contigs