Report

	site_D1_DNA.final.contigs
# contigs (>= 1000 bp)	6
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	11025
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	21
Largest contig	2571
Total length	21303
Reference length	2366980
GC (%)	58.31
Reference GC (%)	60.24
N50	1137
N75	666
L50	6
L75	13
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# structural variations	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 7 part
Unaligned length	7473
Genome fraction (%)	0.381
Duplication ratio	1.533
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2272.98
# indels per 100 kbp	177.40
Largest alignment	2489
Total aligned length	10194
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

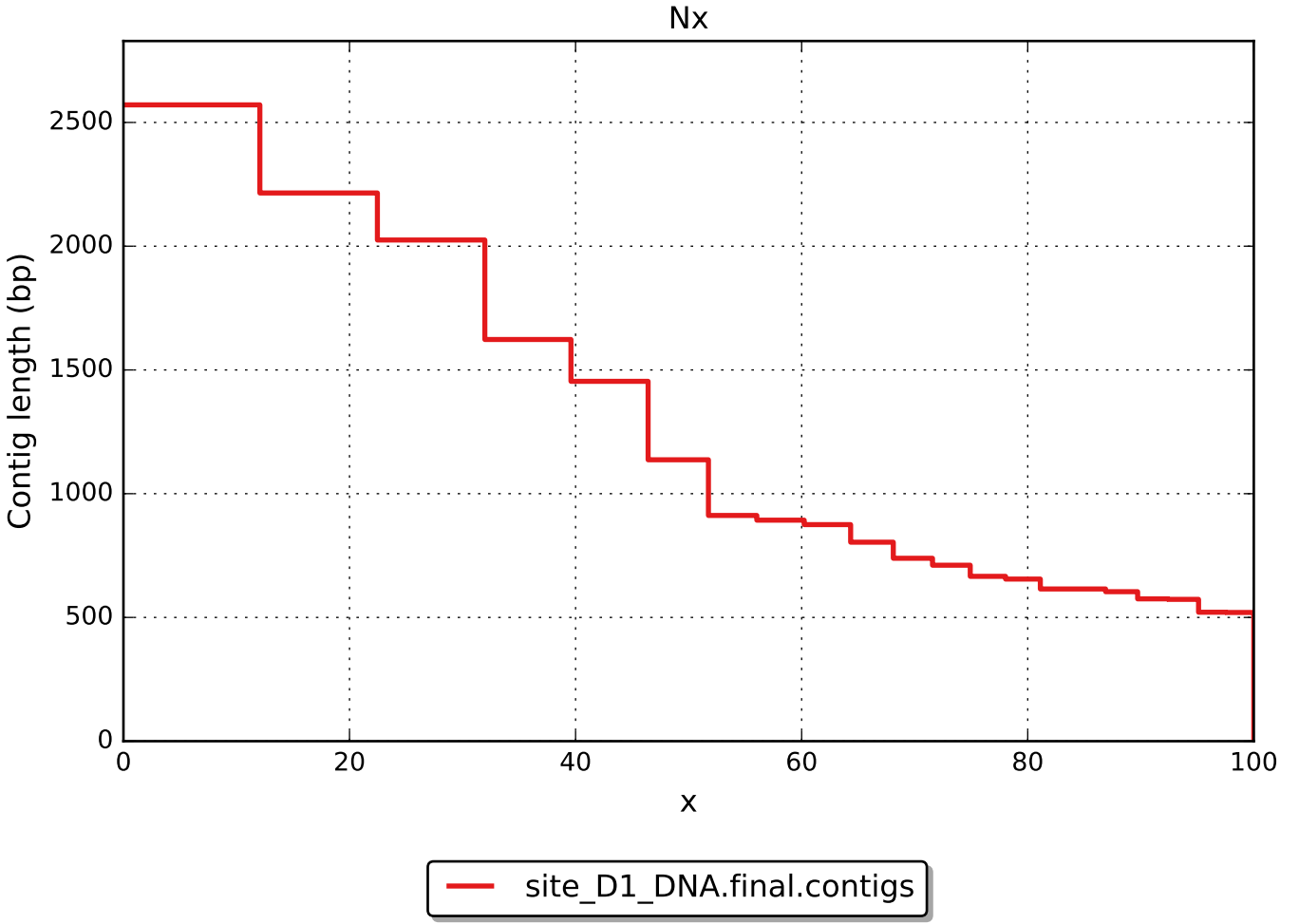
	site_D1_DNA.final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	1
# possible misassemblies	1
# local misassemblies	0
# structural variations	0
# unaligned mis. contigs	0
# mismatches	205
# indels	16
# indels (<= 5 bp)	16
# indels (> 5 bp)	0
Indels length	18

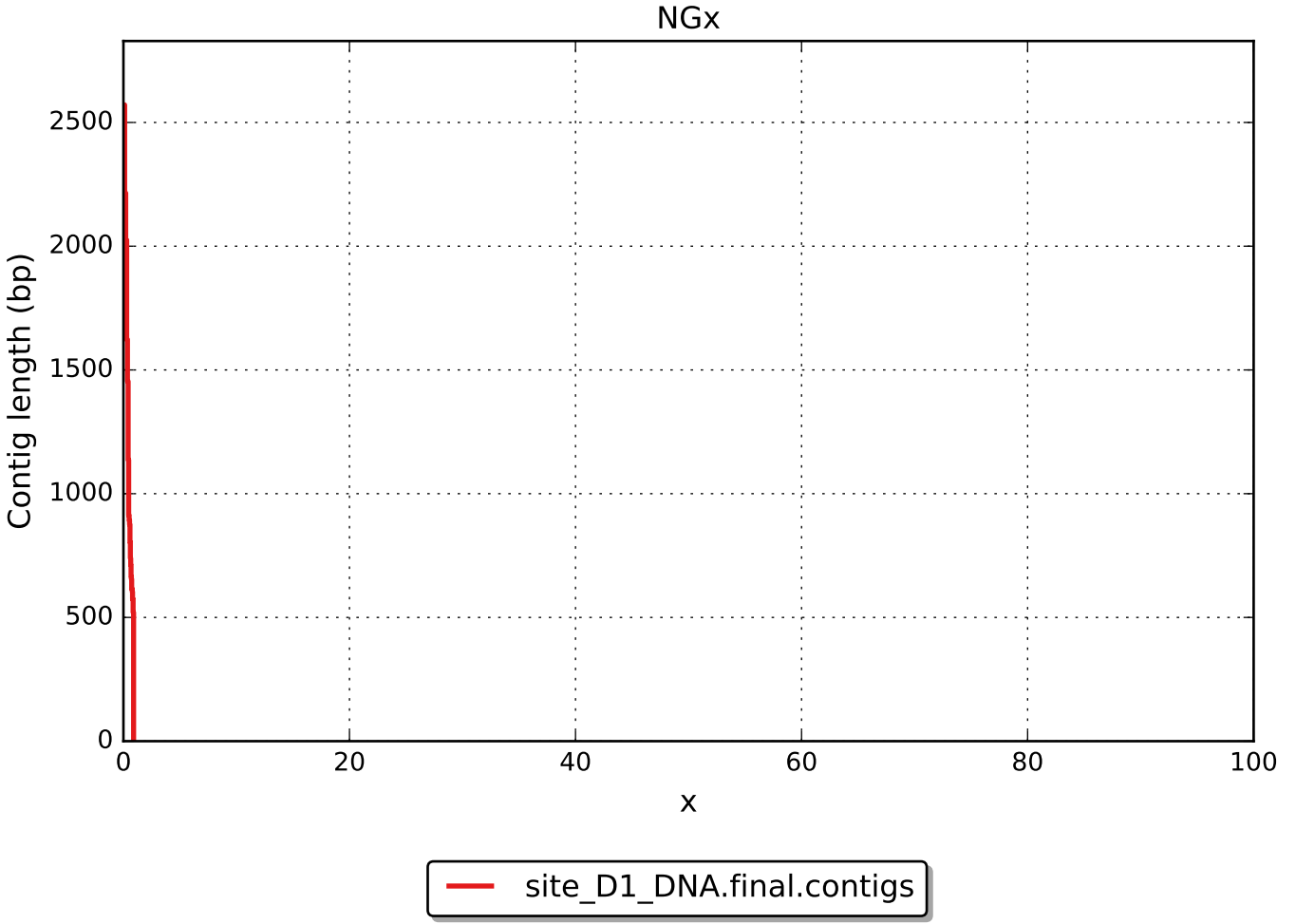
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

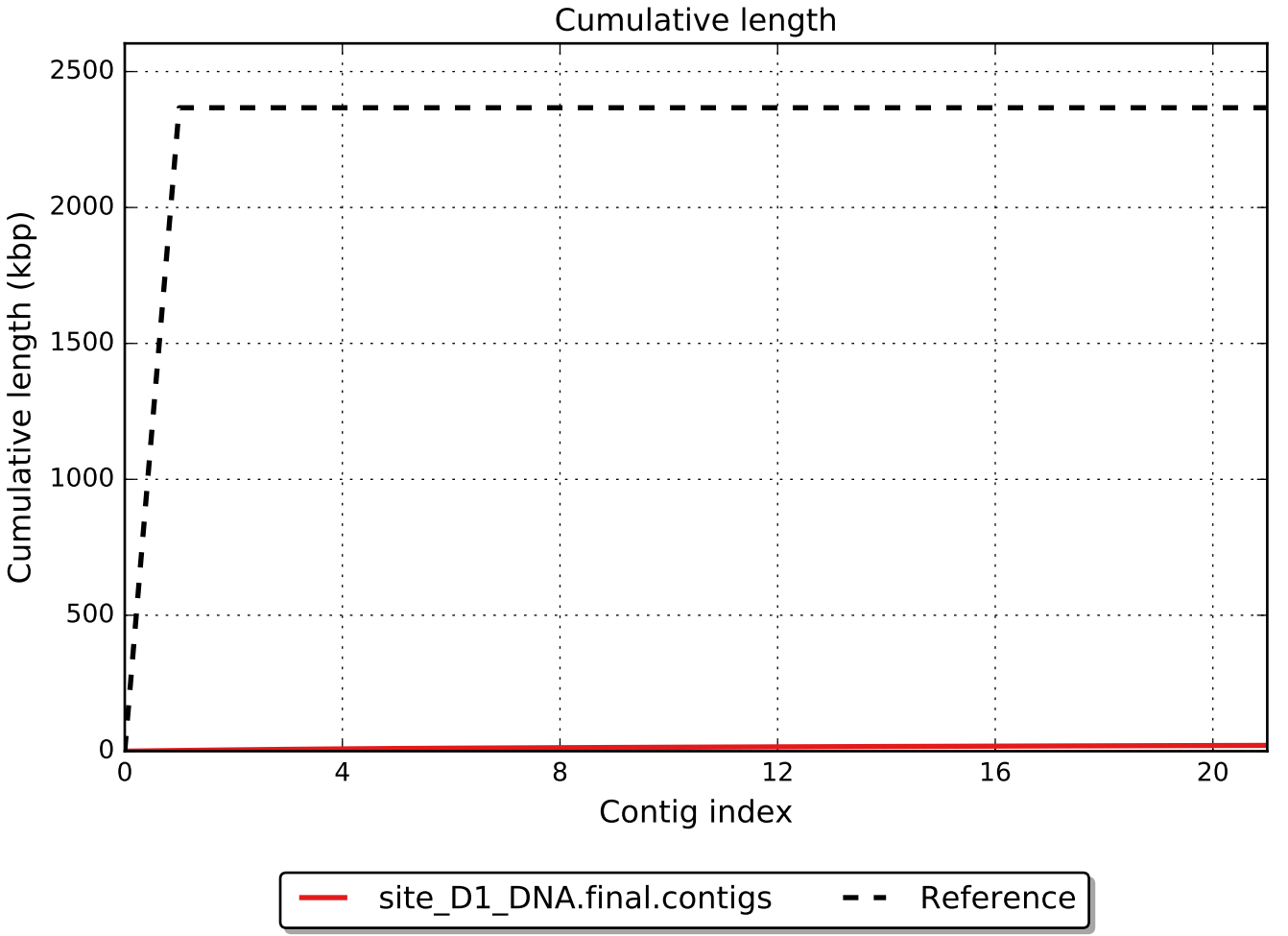
Unaligned report

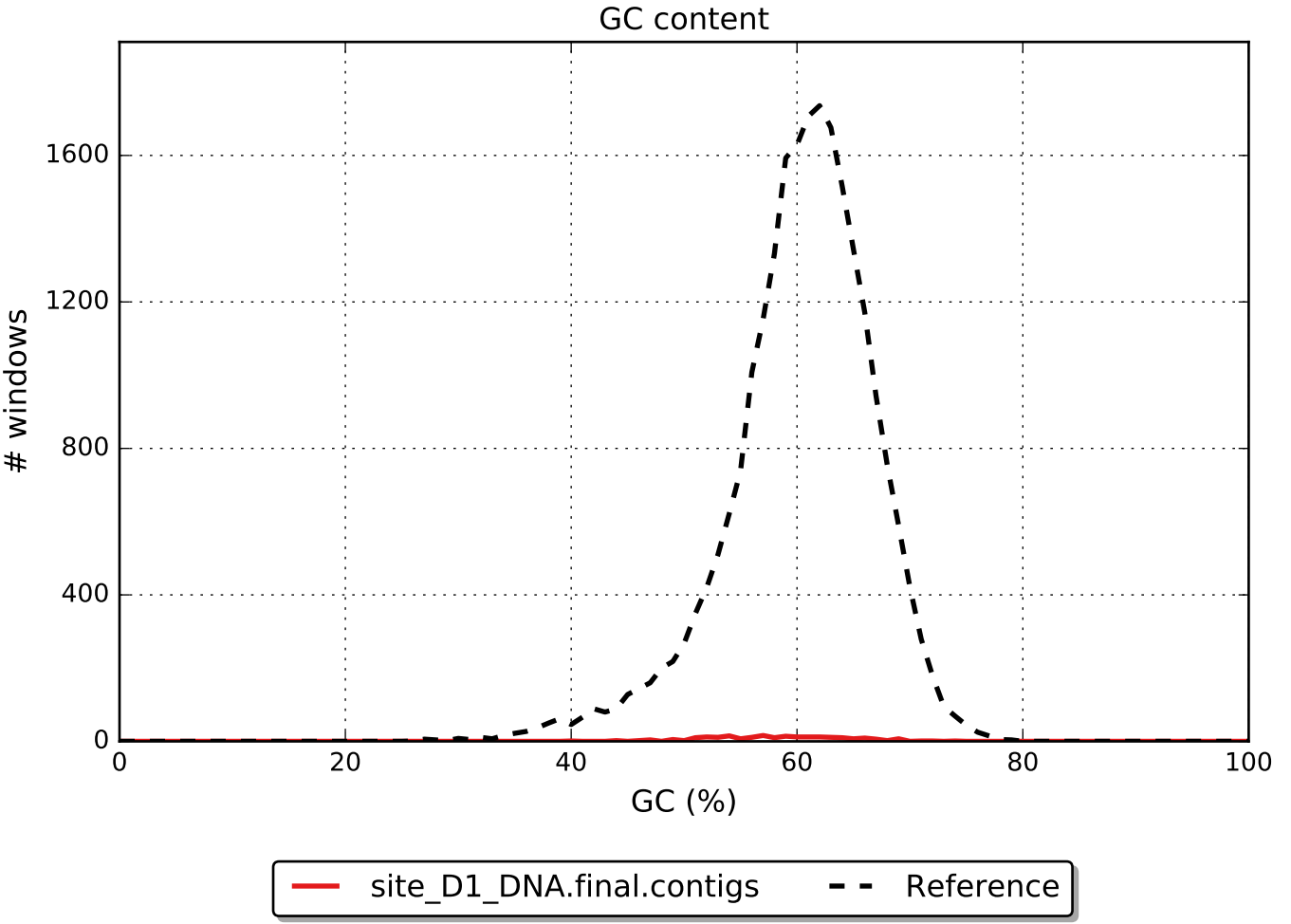
	site_D1_DNA.final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	7
Partially unaligned length	7473
# N's	0

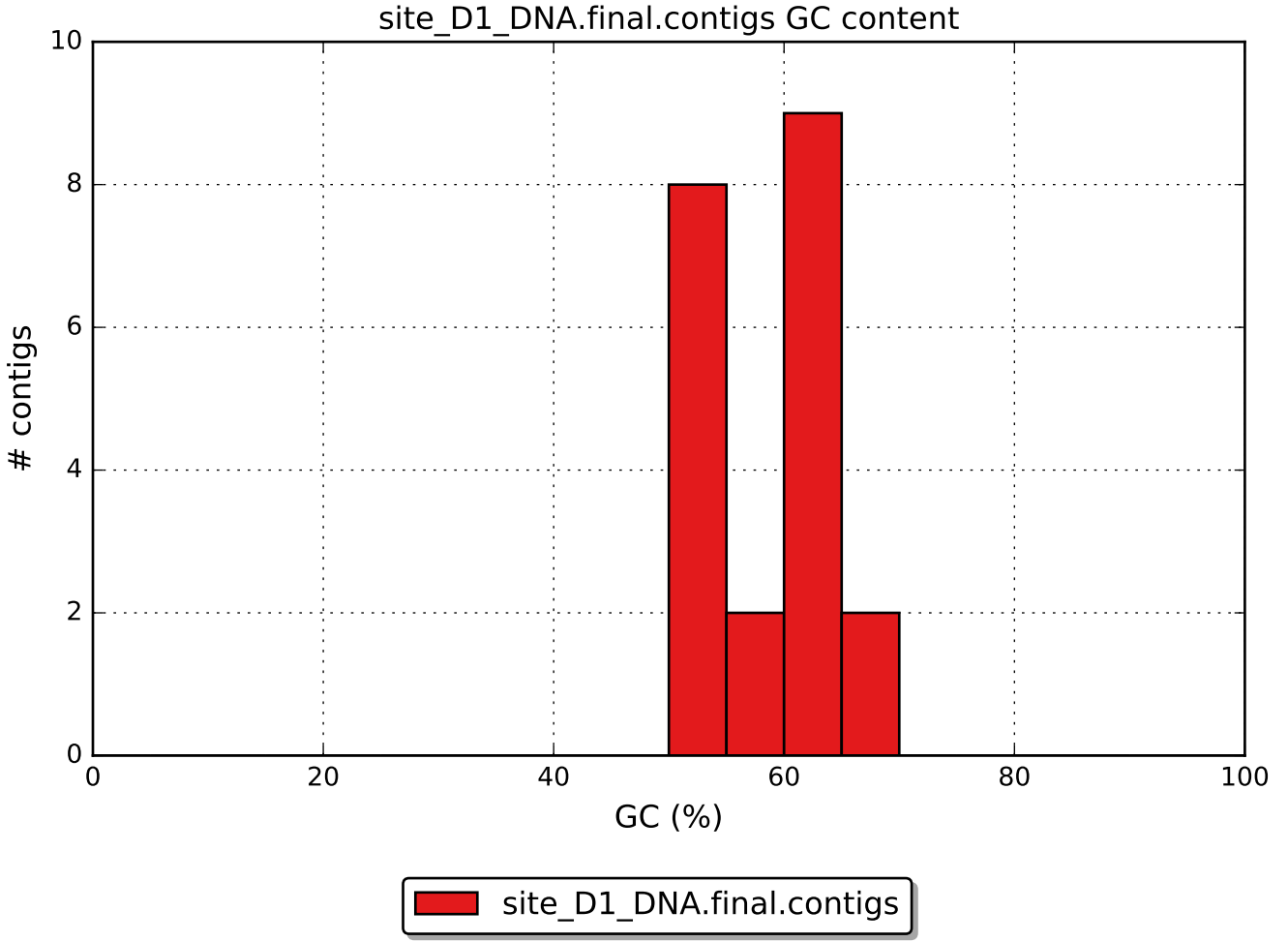
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

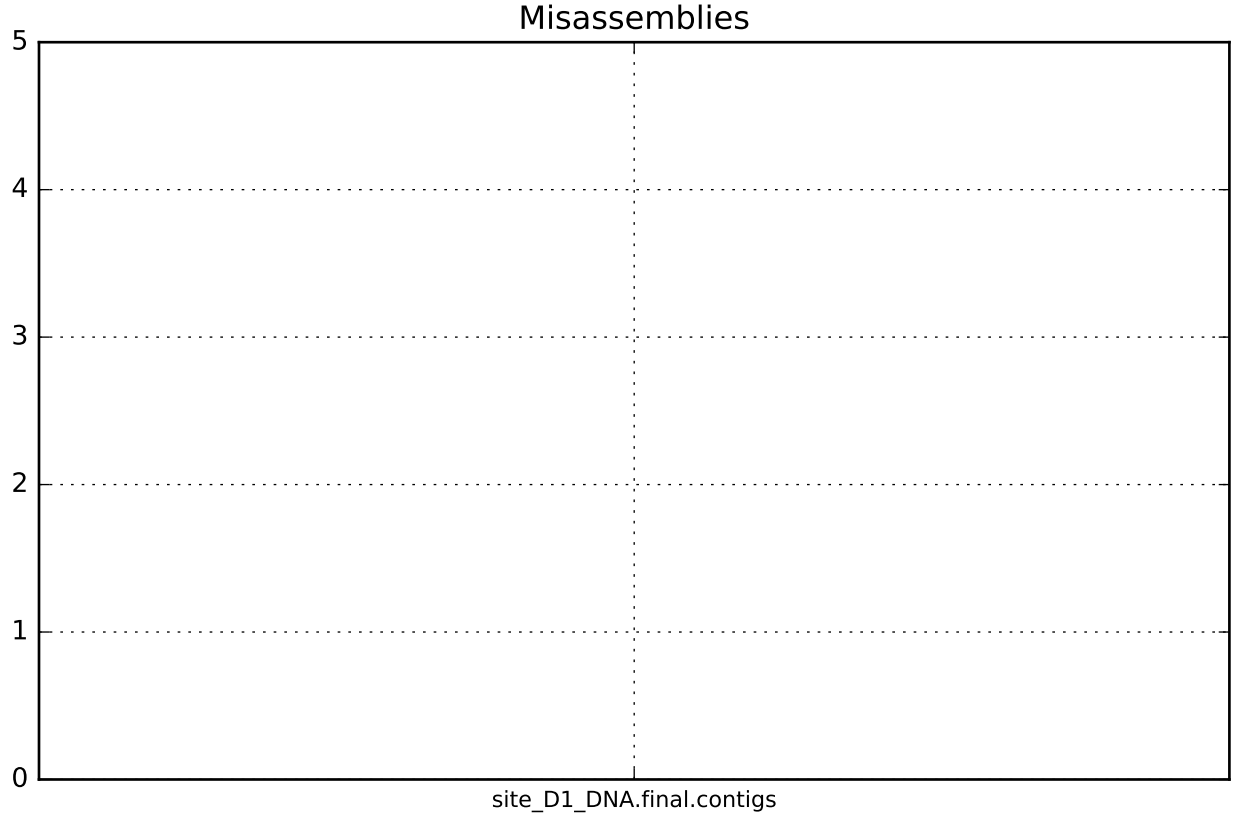

Nx
Contig length (bp)
2500
2000
1500
1000
500
0
0
20
40
60
80
100
x
site_D1_DNA.final.contigs

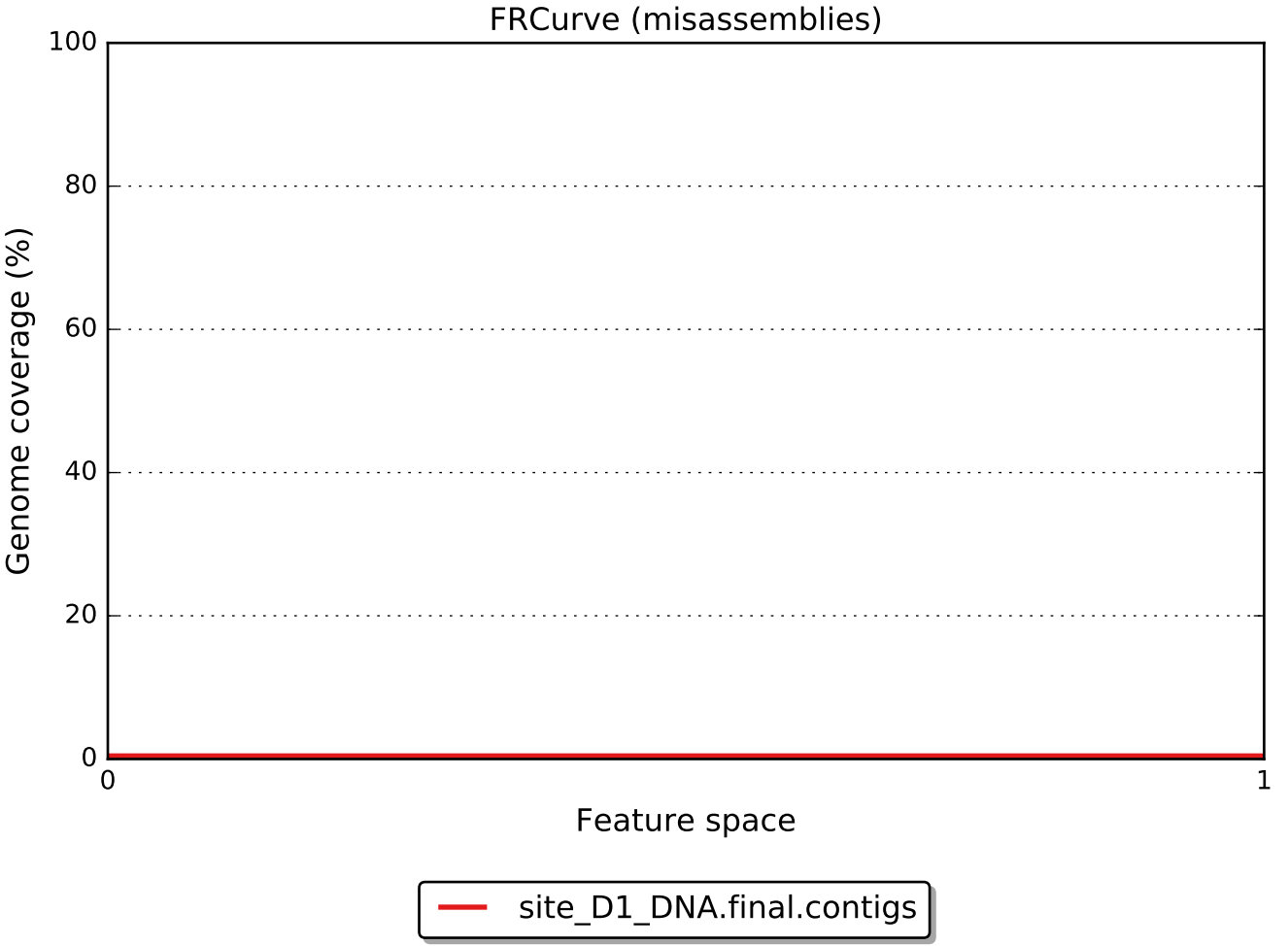

NGx
Contig length (bp)
2500
2000
1500
1000
500
0
0
20
40
60
80
100
x
site_D1_DNA.final.contigs

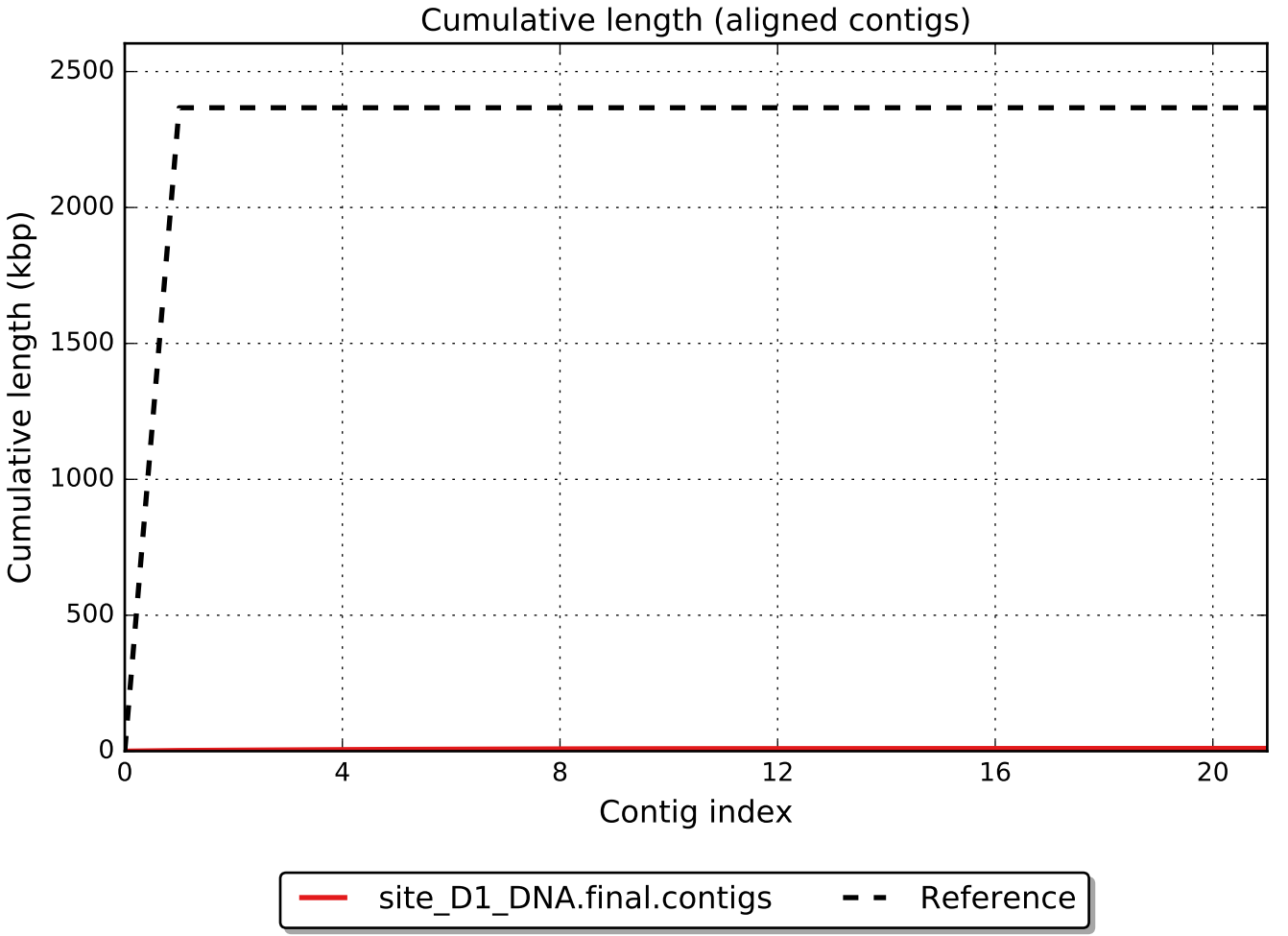

Cumulative length
Cumulative length (kbp)
2500
2000
1500
1000
500
0
0
4
8
12
16
20
Contig index
site_D1_DNA.final.contigs
Reference

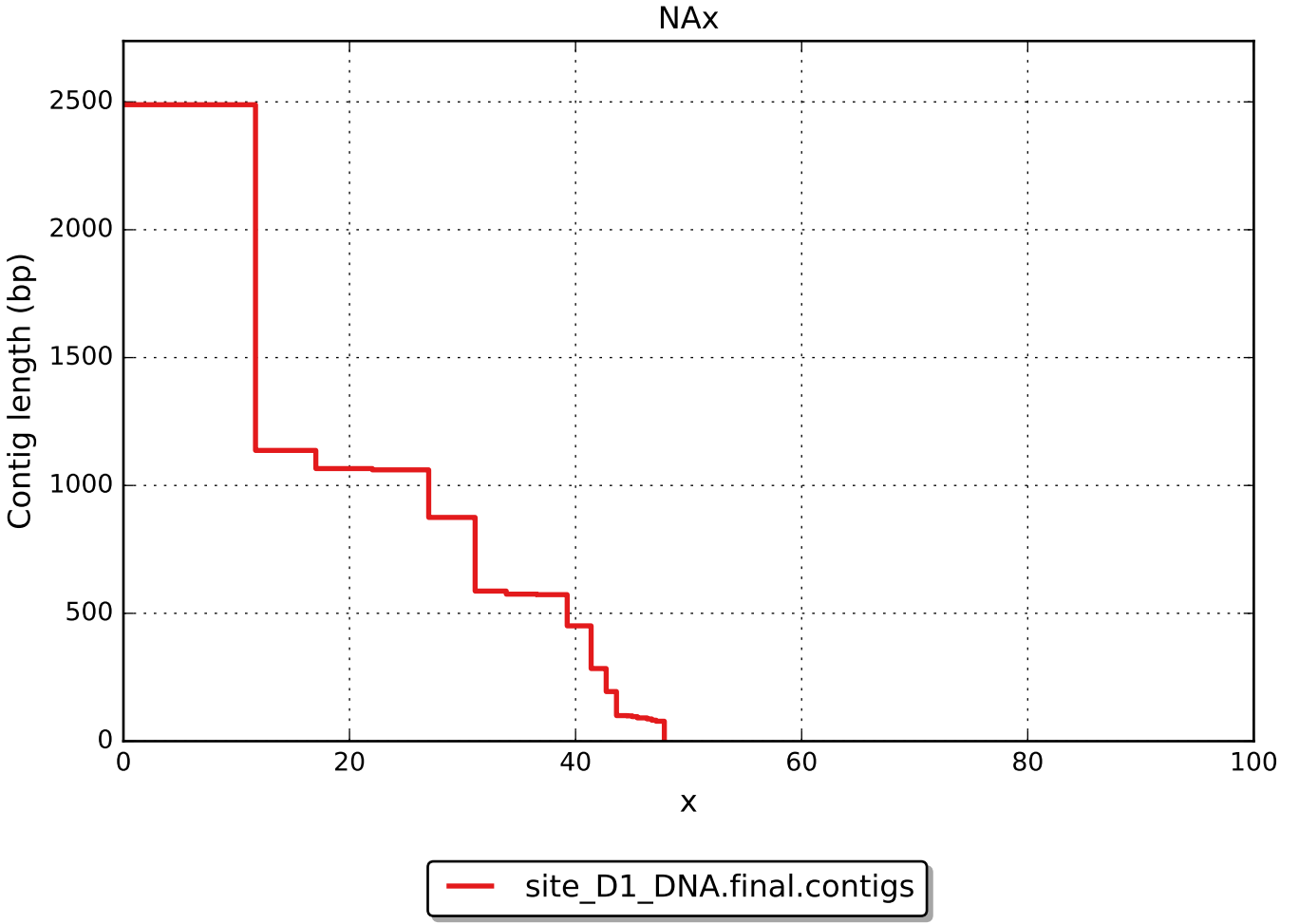

GC content
windows
GC (%)
0
400
800
1200
1600
0
20
40
60
80
100
site_D1_DNA.final.contigs
Reference

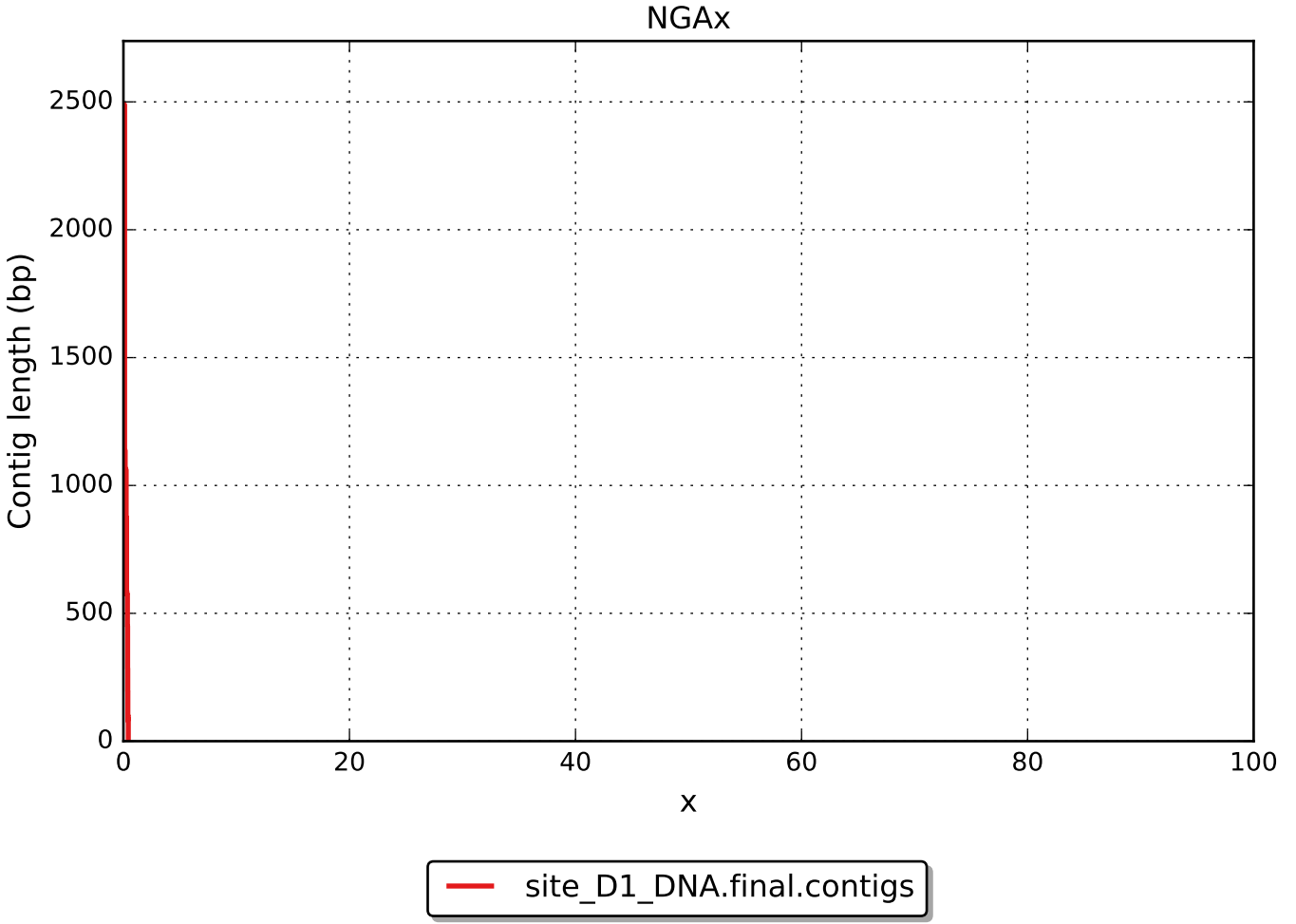

site_D1_DNA.final.contigs GC content
contigs
GC (%)
0
2
4
6
8
10
0
20
40
60
80
100
site_D1_DNA.final.contigs


Misassemblies
5
4
3
2
1
0
site_D1_DNA.final.contigs


FRCurve (misassemblies)
100
80
60
40
20
0
Genome coverage (%)
0
1
Feature space
site_D1_DNA.final.contigs


Cumulative length (aligned contigs)
Cumulative length (kbp)
2500
2000
1500
1000
500
0
0
4
8
12
16
20
Contig index
site_D1_DNA.final.contigs
Reference


NAx
Contig length (bp)
2500
2000
1500
1000
500
0
0
20
40
60
80
100
x
site_D1_DNA.final.contigs


NGAx
Contig length (bp)
2500
2000
1500
1000
500
0
0
20
40
60
80
100
x
site_D1_DNA.final.contigs