Report

	site_D1_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)	5313
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	12
Largest contig	1809
Total length	10868
Reference length	3098747
GC (%)	50.45
Reference GC (%)	49.73
N50	791
N75	712
L50	5
L75	8
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# structural variations	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 5 part
Unaligned length	4458
Genome fraction (%)	0.092
Duplication ratio	2.260
# N's per 100 kbp	0.00
# mismatches per 100 kbp	3102.96
# indels per 100 kbp	282.09
Largest alignment	1467
Total aligned length	3334
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

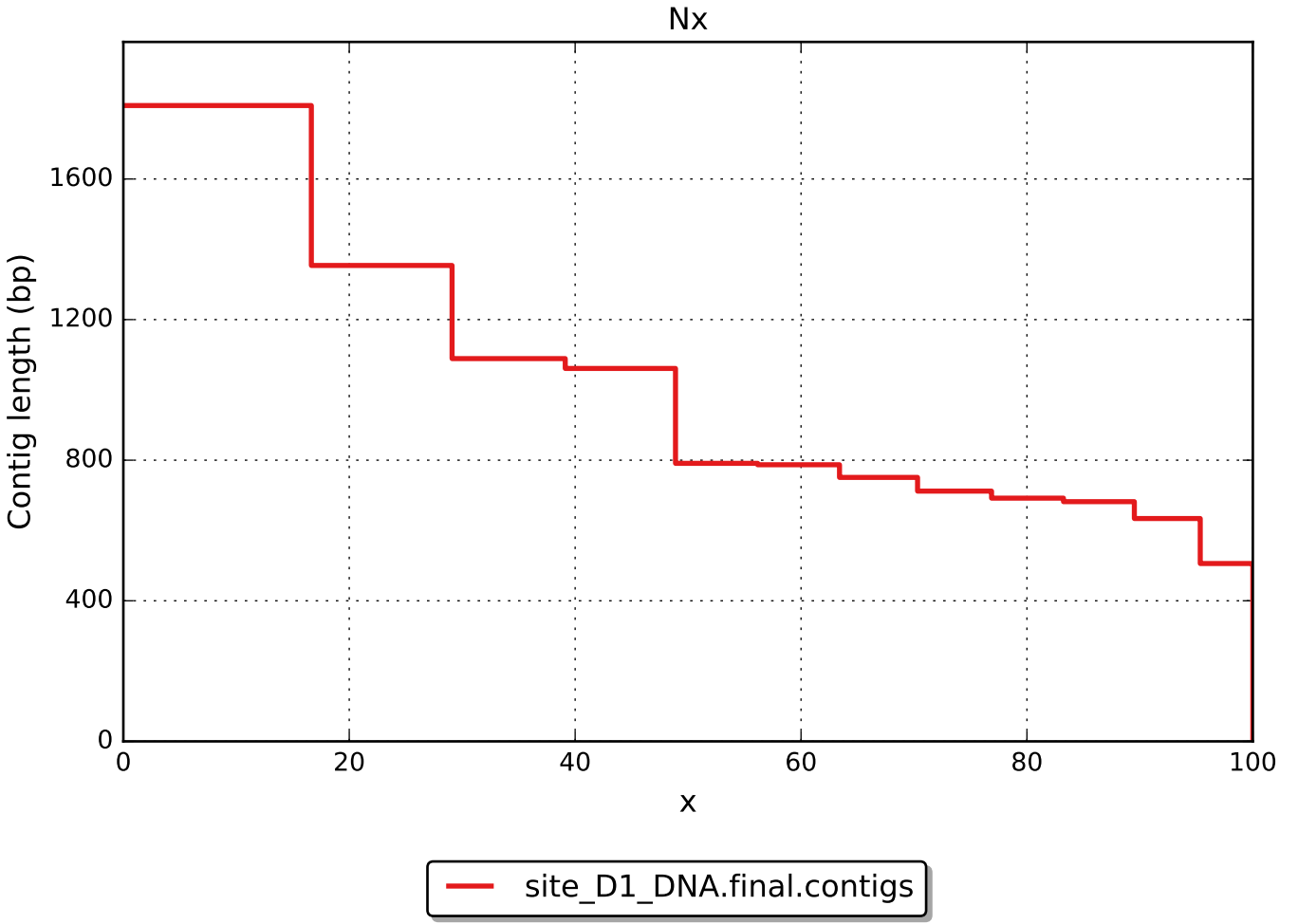
	site_D1_DNA.final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# structural variations	0
# unaligned mis. contigs	0
# mismatches	88
# indels	8
# indels (<= 5 bp)	8
# indels (> 5 bp)	0
Indels length	8

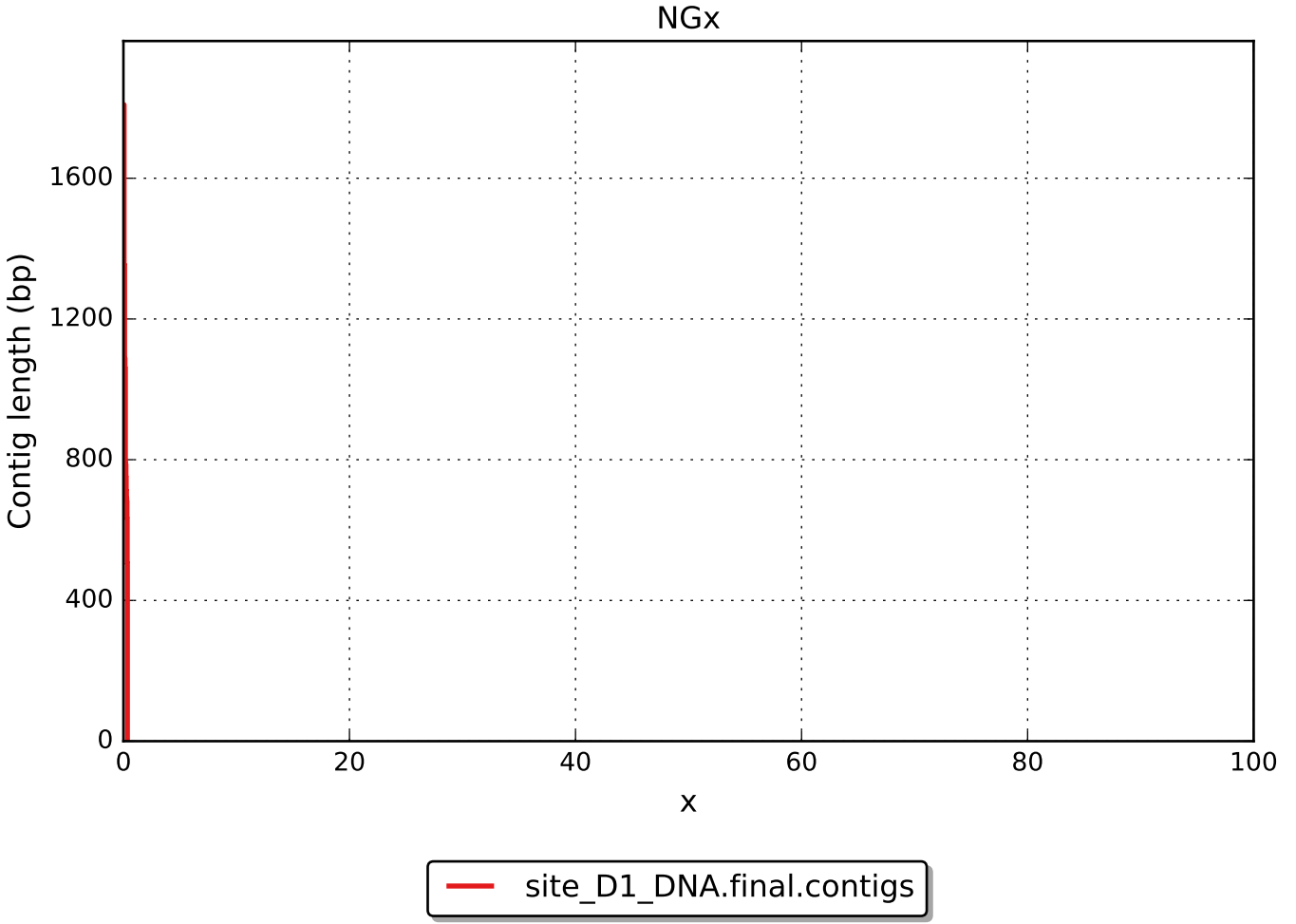
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

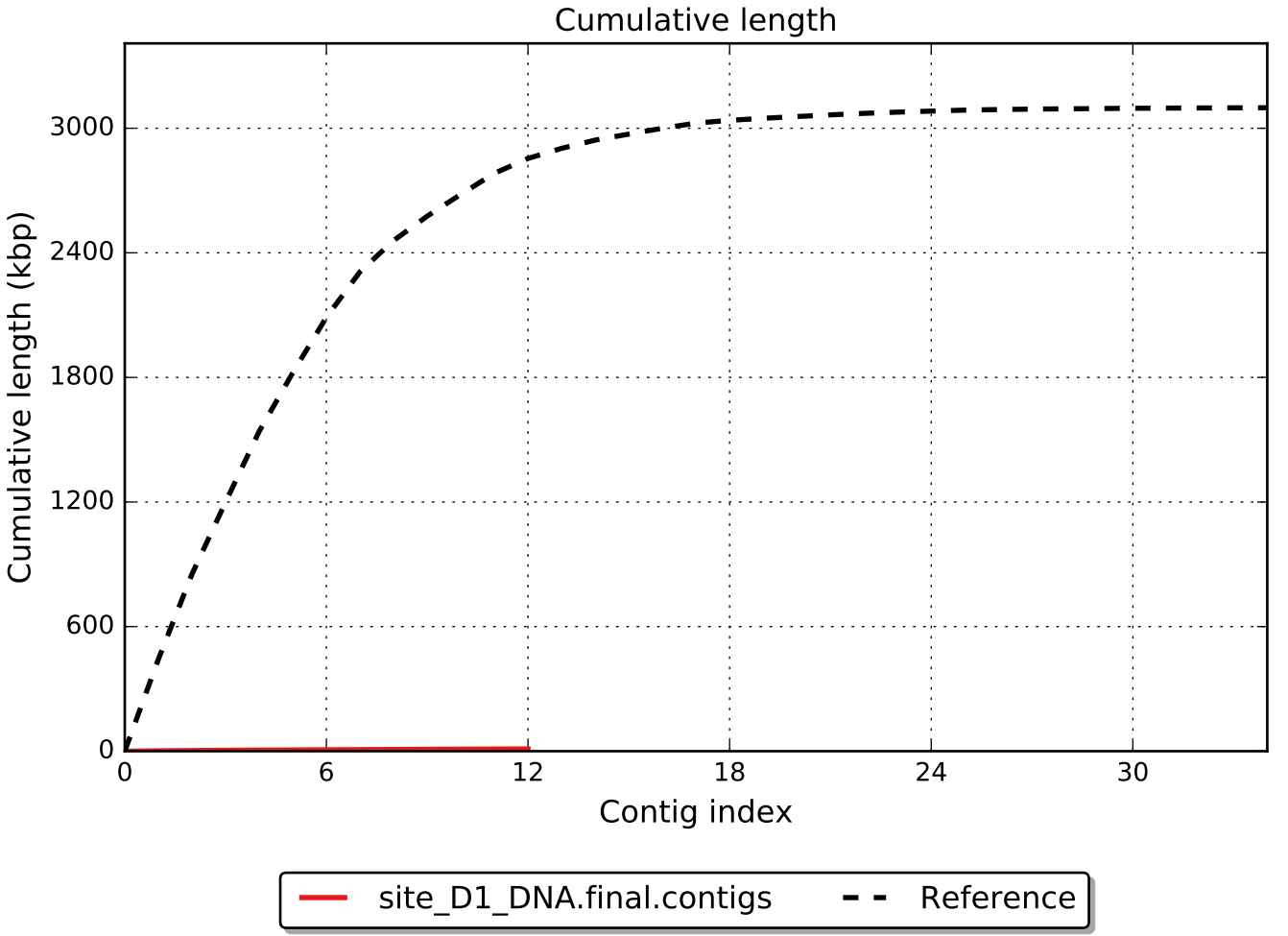
Unaligned report

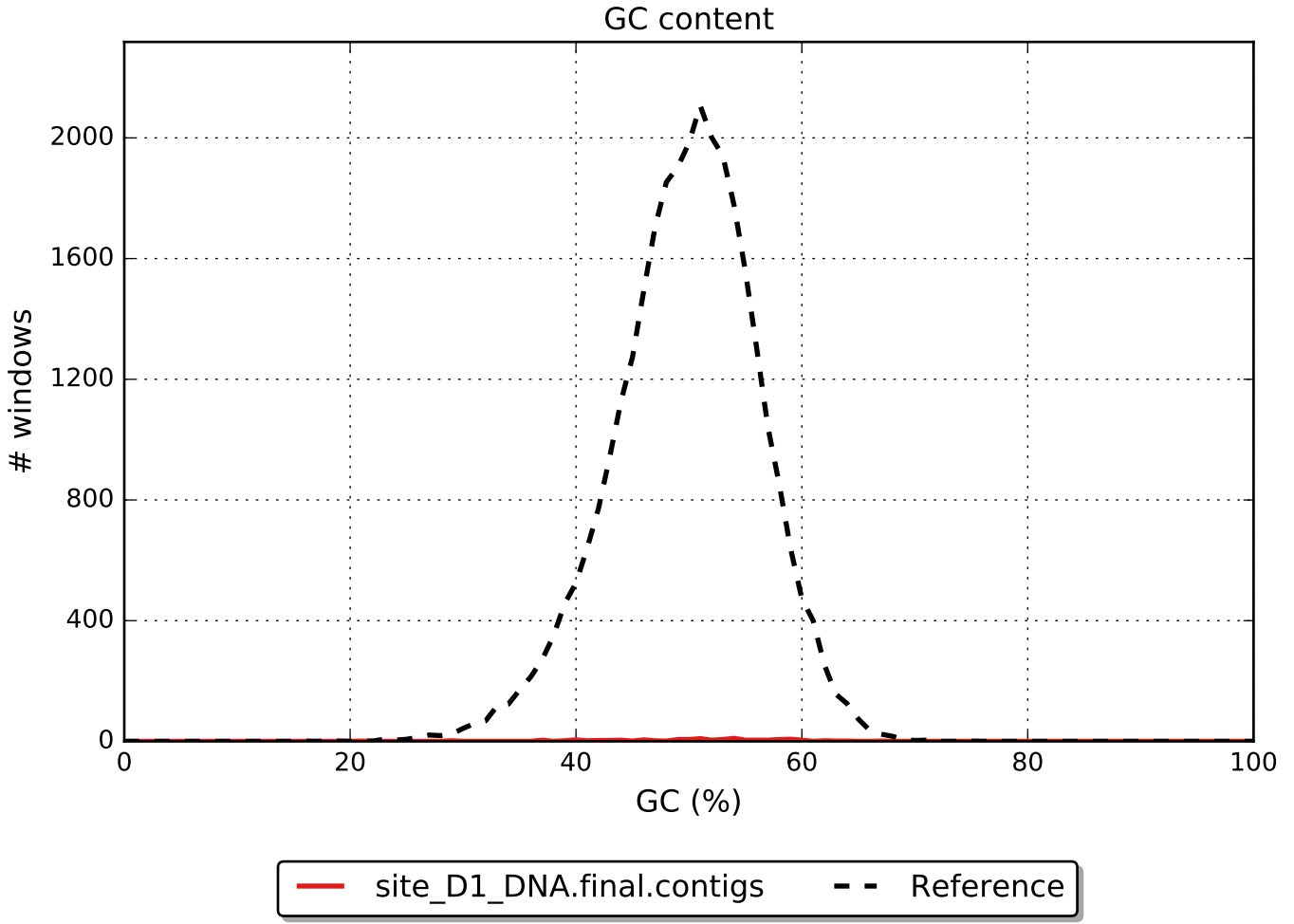
	site_D1_DNA.final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	5
Partially unaligned length	4458
# N's	0

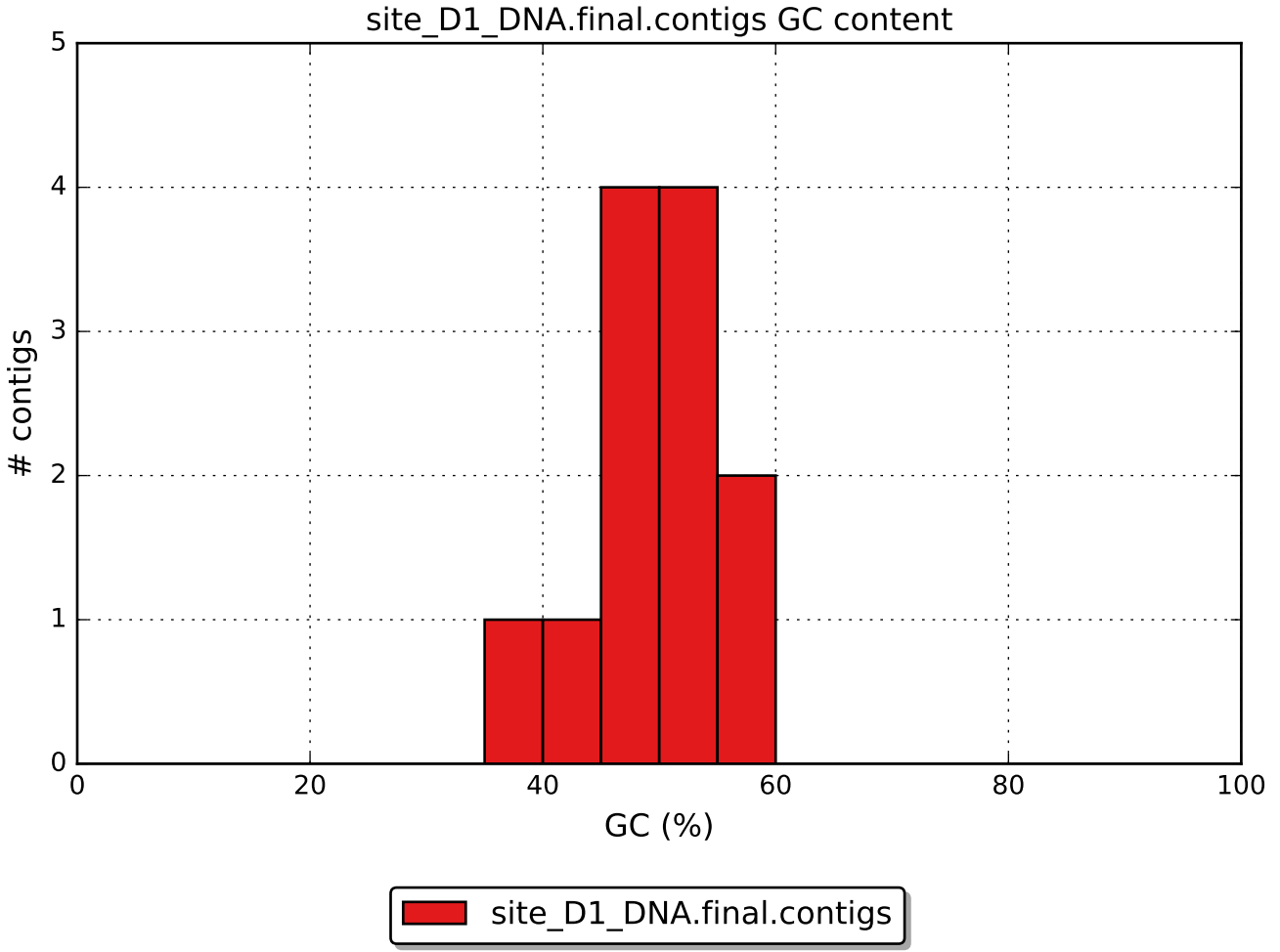
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

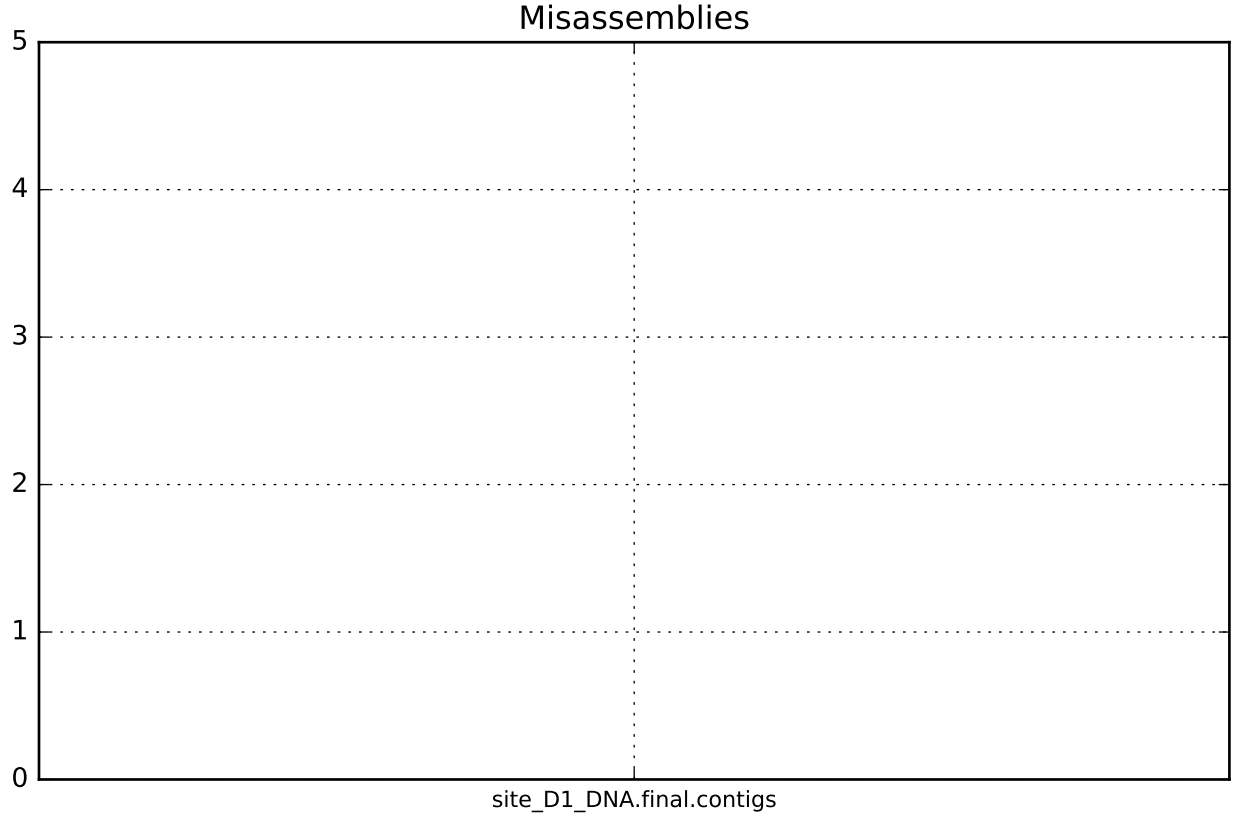

Nx
Contig length (bp)
0
400
800
1200
1600
0
20
40
60
80
100
x
site_D1_DNA.final.contigs

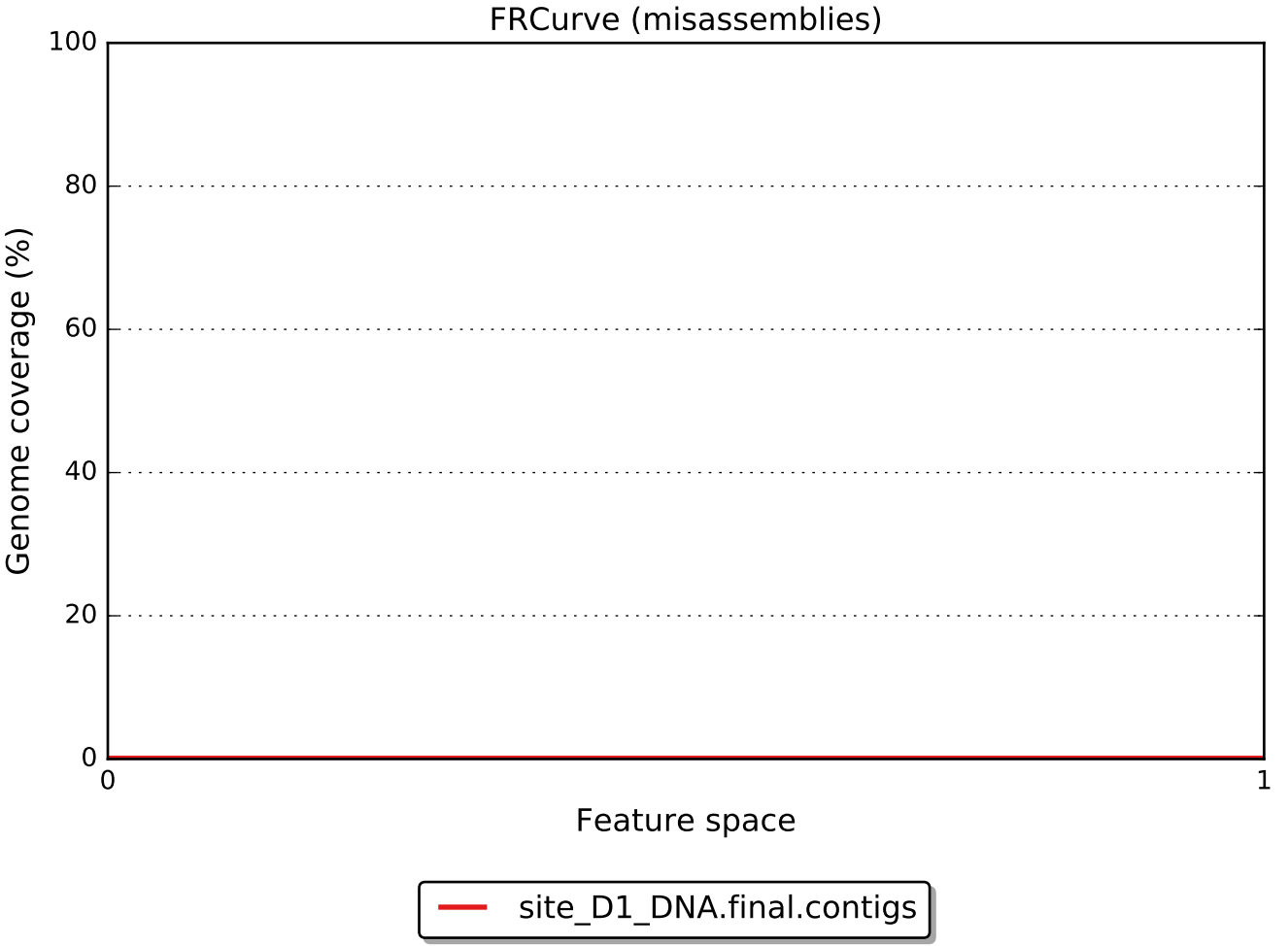

NGx
Contig length (bp)
0
400
800
1200
1600
0
20
40
60
80
100
x
site_D1_DNA.final.contigs

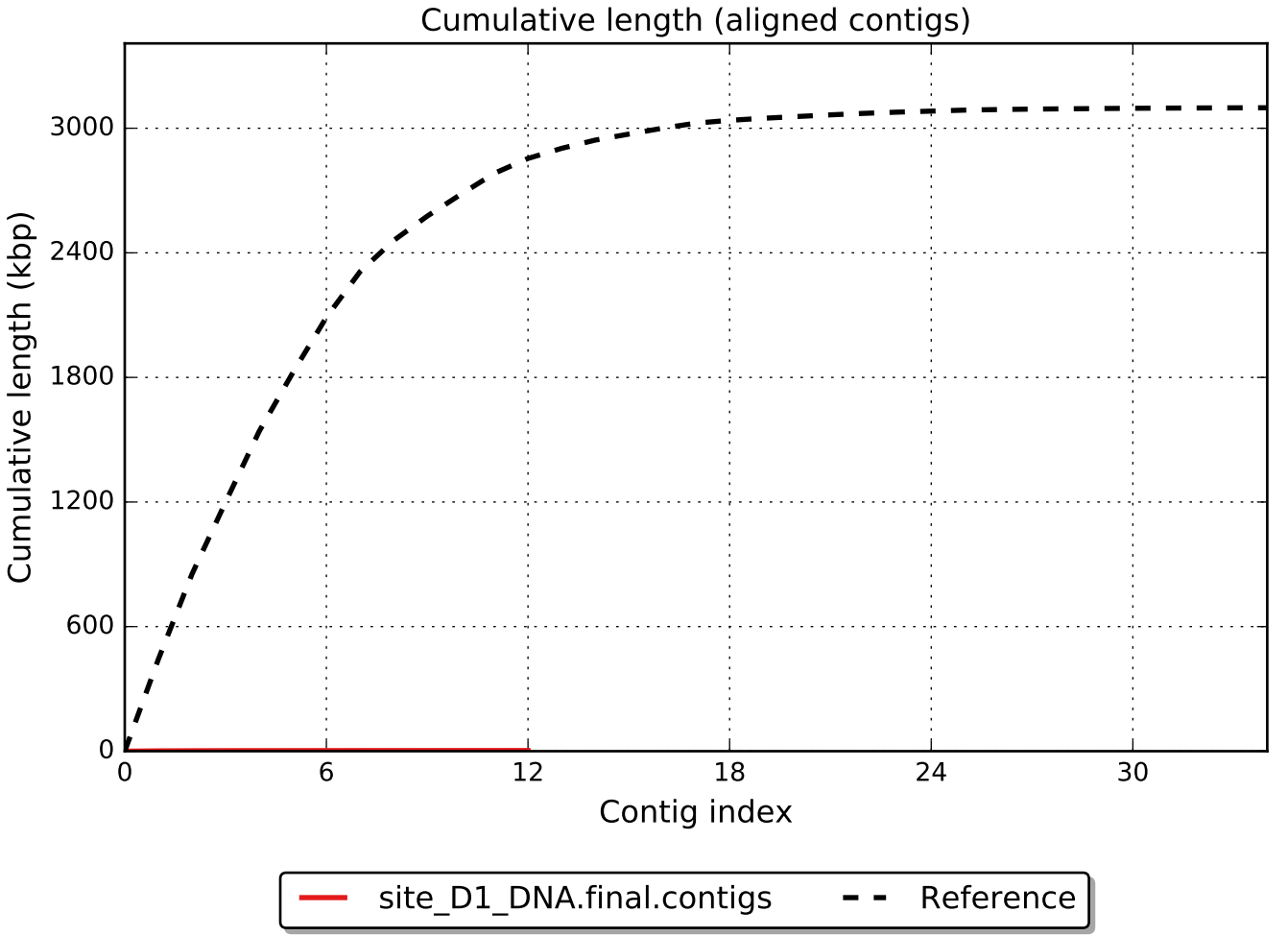

Cumulative length
Cumulative length (kbp)
3000
2400
1800
1200
600
0
0
6
12
18
24
30
Contig index
site_D1_DNA.final.contigs
Reference

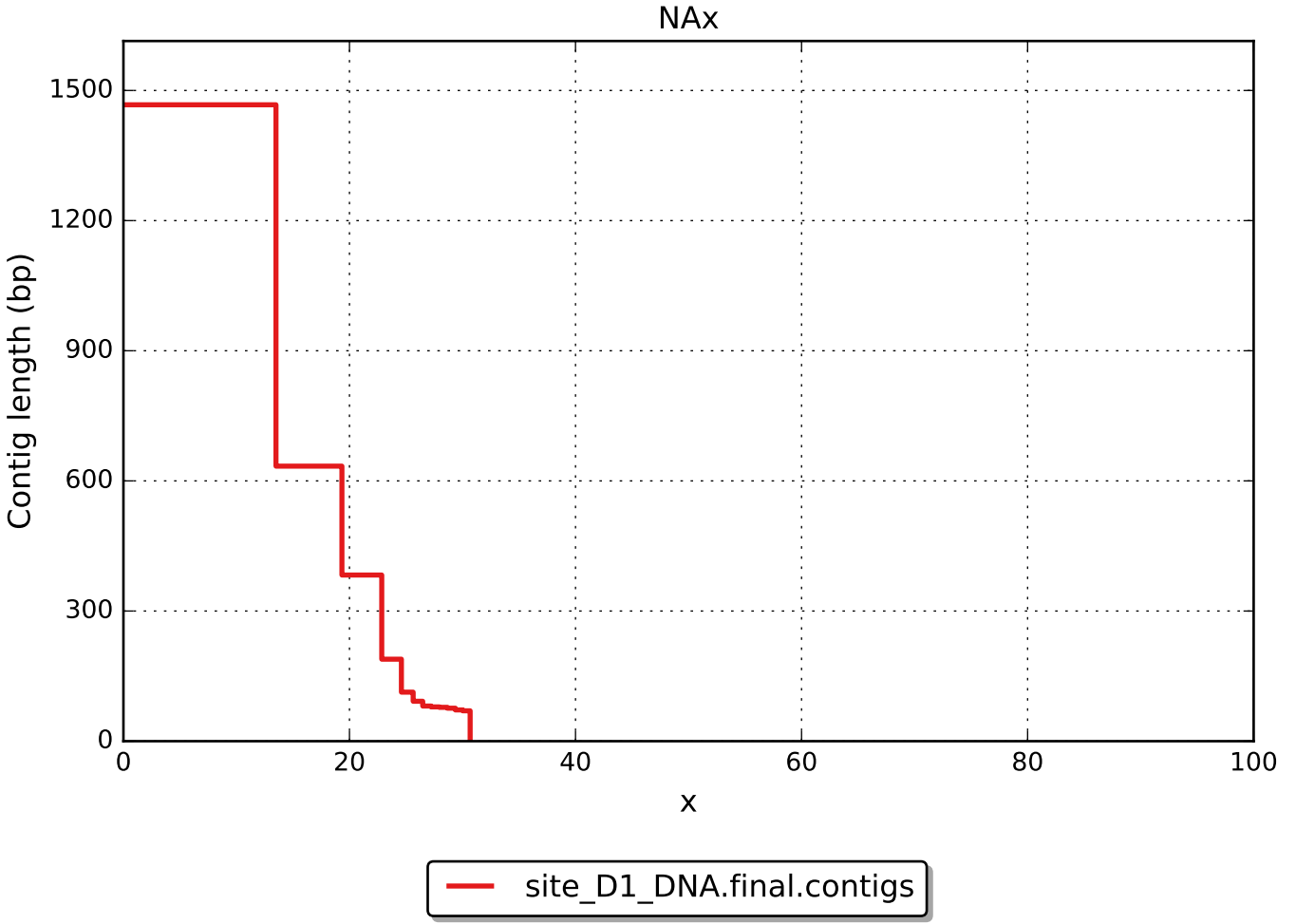

GC content
windows
GC (%)
0
400
800
1200
1600
2000
0
20
40
60
80
100
site_D1_DNA.final.contigs
Reference

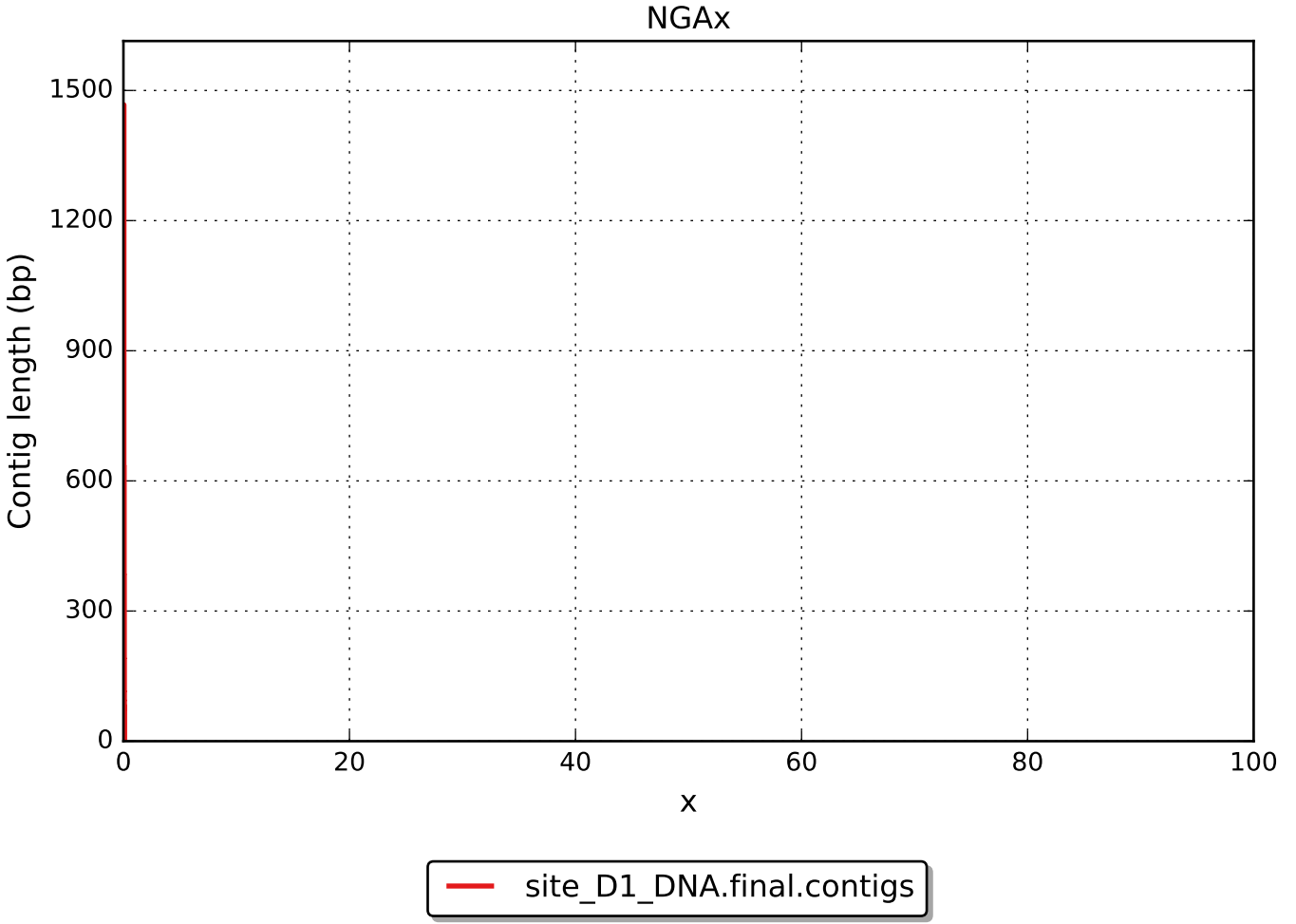

site_D1_DNA.final.contigs GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
site_D1_DNA.final.contigs


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)
3000
2400
1800
1200
600
0
0
6
12
18
24
30
Contig index
site_D1_DNA.final.contigs
Reference


NAx
Contig length (bp)
1500
1200
900
600
300
0
0
20
40
60
80
100
x
site_D1_DNA.final.contigs


NGAx
Contig length (bp)
1500
1200
900
600
300
0
0
20
40
60
80
100
x
site_D1_DNA.final.contigs