Report

	site_D1_DNA.final.contigs
# contigs (>= 1000 bp)	1
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	3052
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	4
Largest contig	3052
Total length	5209
Reference length	4537917
GC (%)	52.49
Reference GC (%)	46.17
N50	3052
N75	778
L50	1
L75	3
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# structural variations	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 1 part
Unaligned length	2947
Genome fraction (%)	0.045
Duplication ratio	1.119
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2226.62
# indels per 100 kbp	197.92
Largest alignment	777
Total aligned length	2099
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

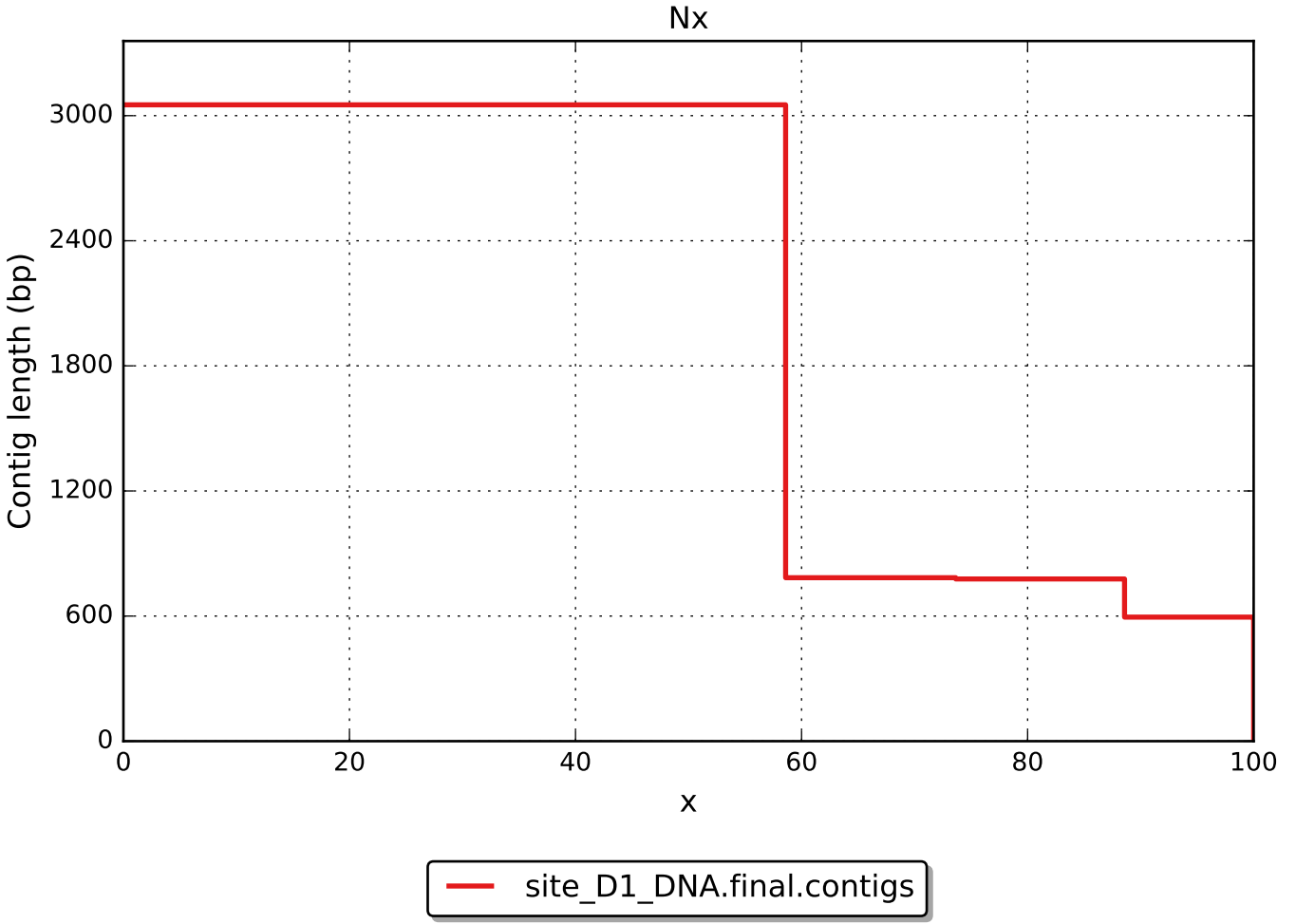
	site_D1_DNA.final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# structural variations	0
# unaligned mis. contigs	0
# mismatches	45
# indels	4
# indels (<= 5 bp)	4
# indels (> 5 bp)	0
Indels length	4

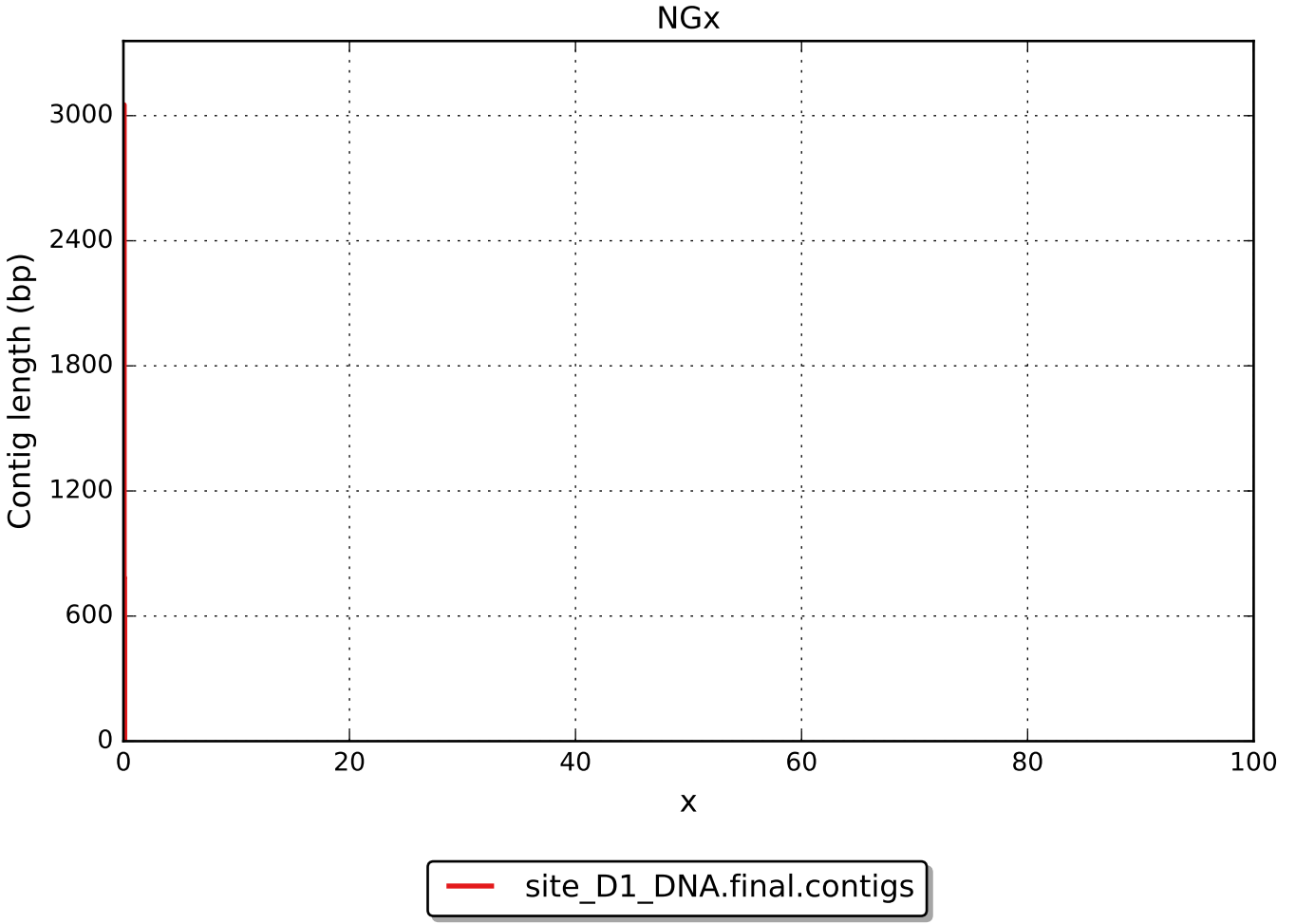
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

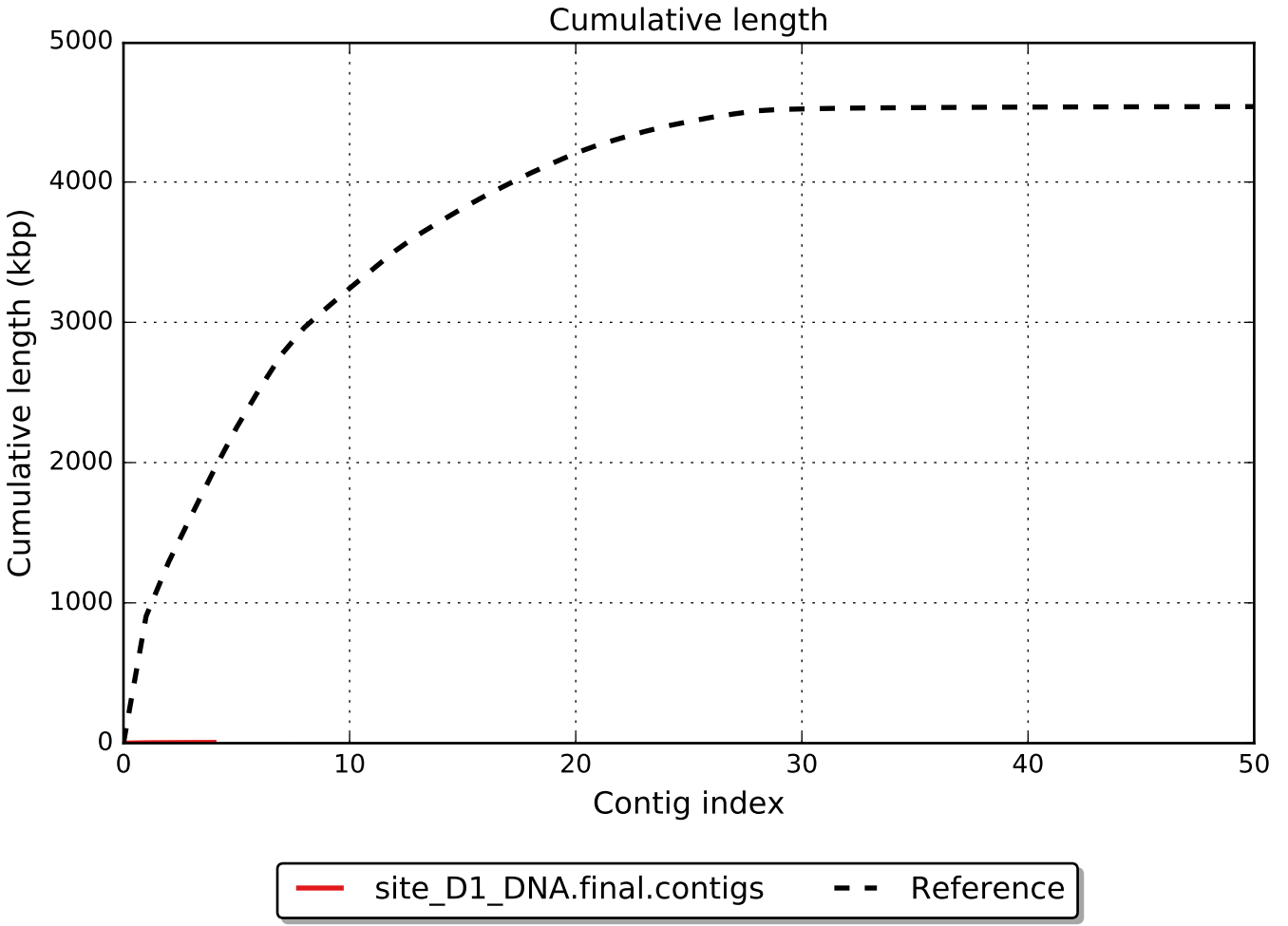
Unaligned report

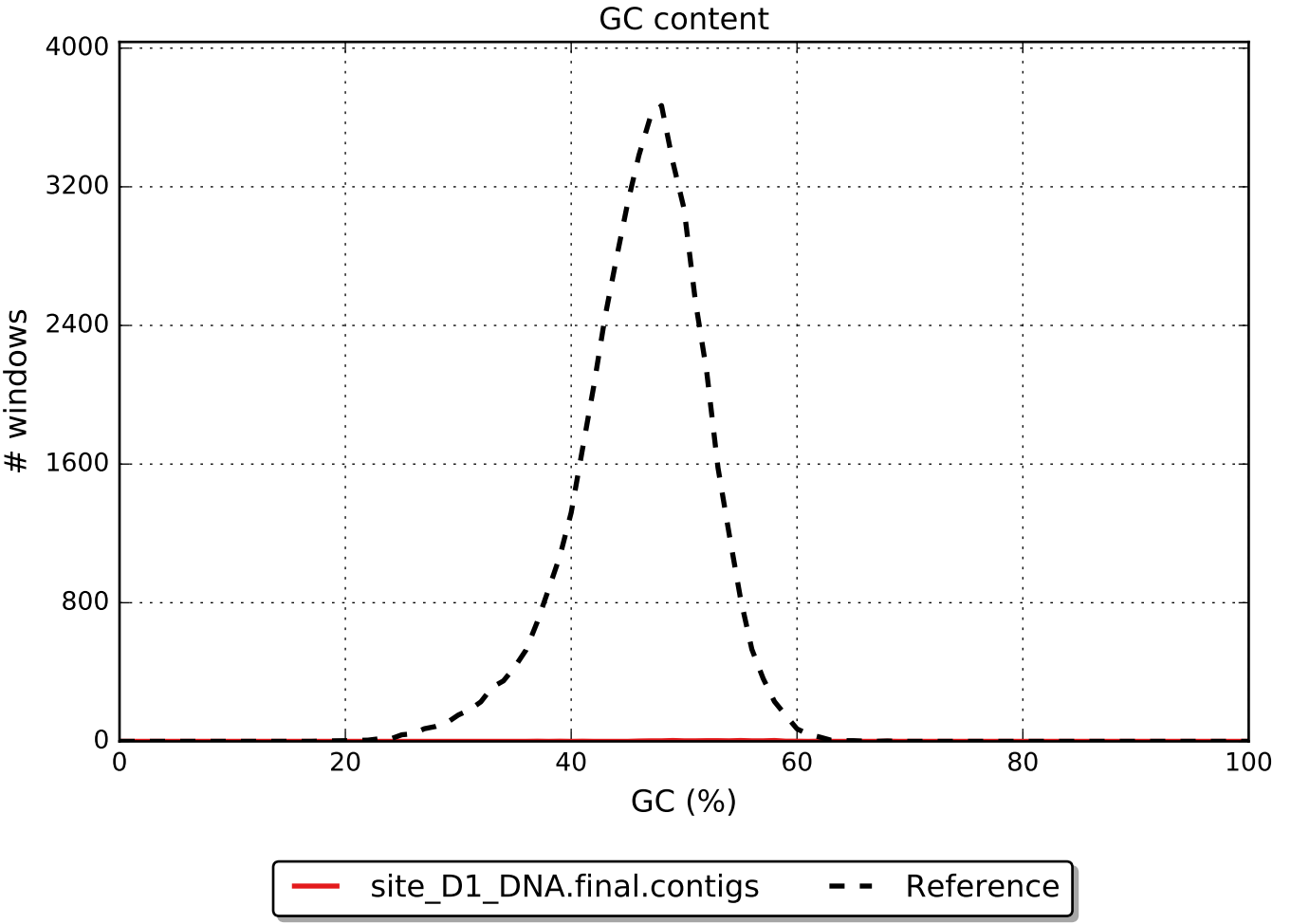
	site_D1_DNA.final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
Partially unaligned length	2947
# N's	0

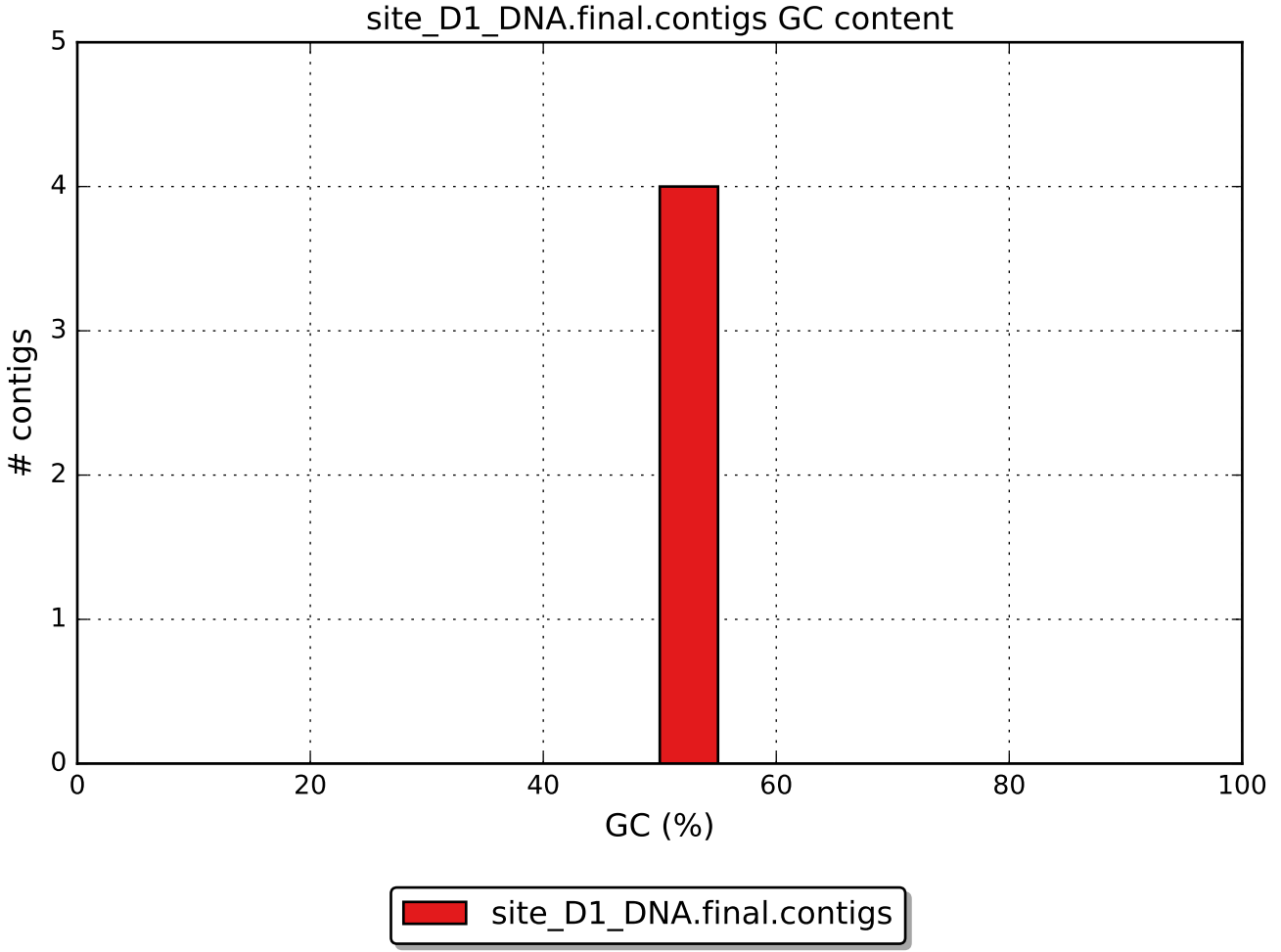
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

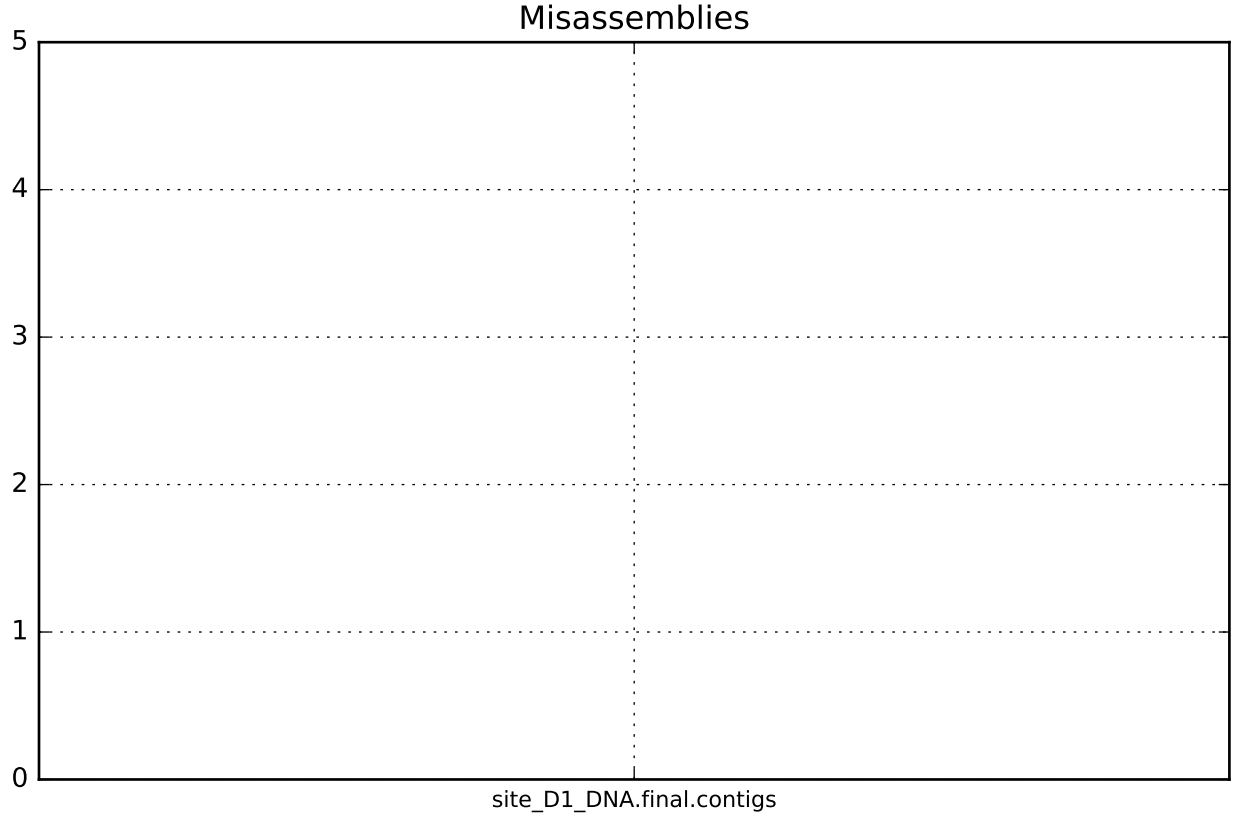

Nx
Contig length (bp)
3000
2400
1800
1200
600
0
0
20
40
60
80
100
x
site_D1_DNA.final.contigs

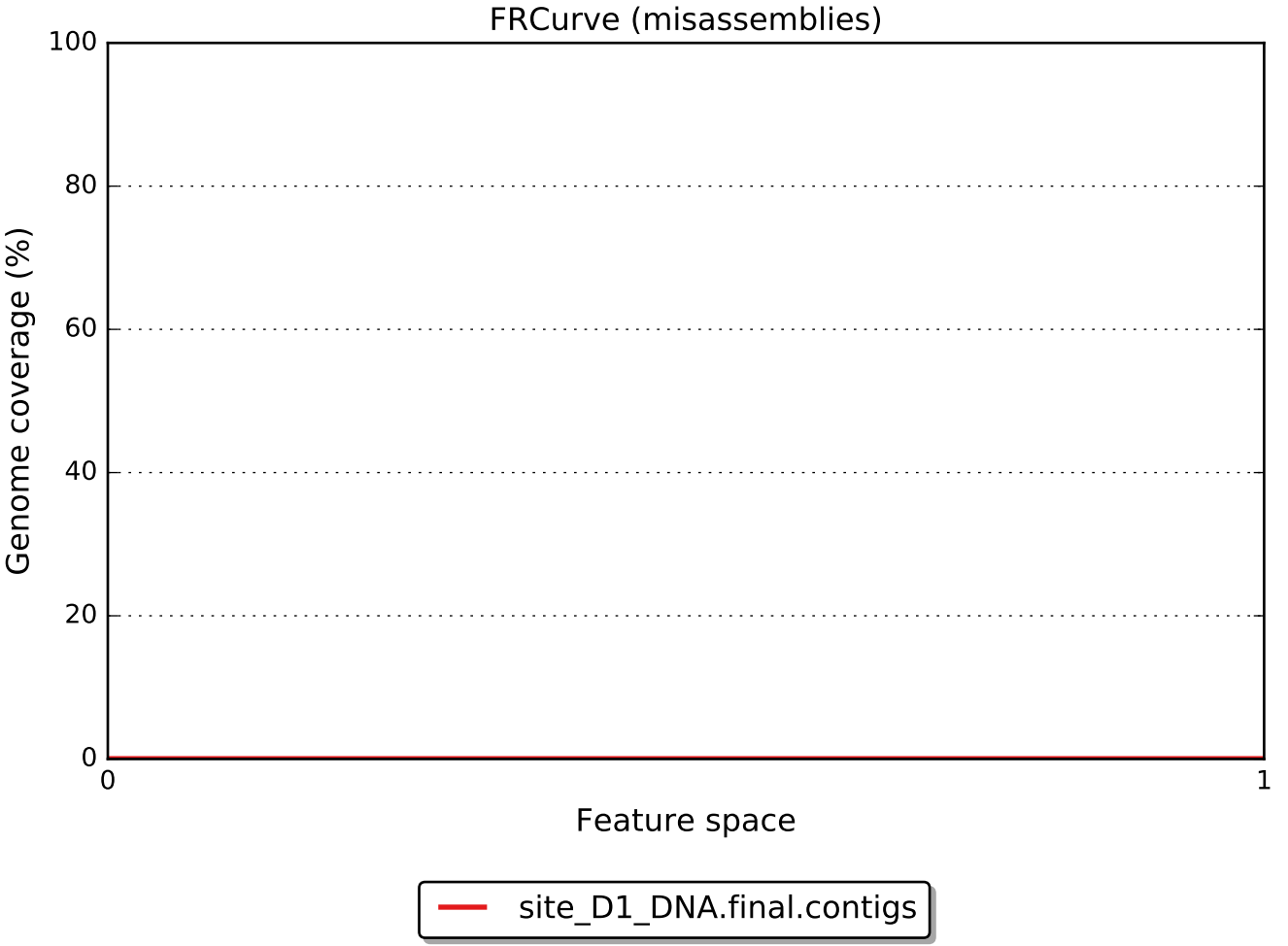

NGx
Contig length (bp)
3000
2400
1800
1200
600
0
0
20
40
60
80
100
x
site_D1_DNA.final.contigs

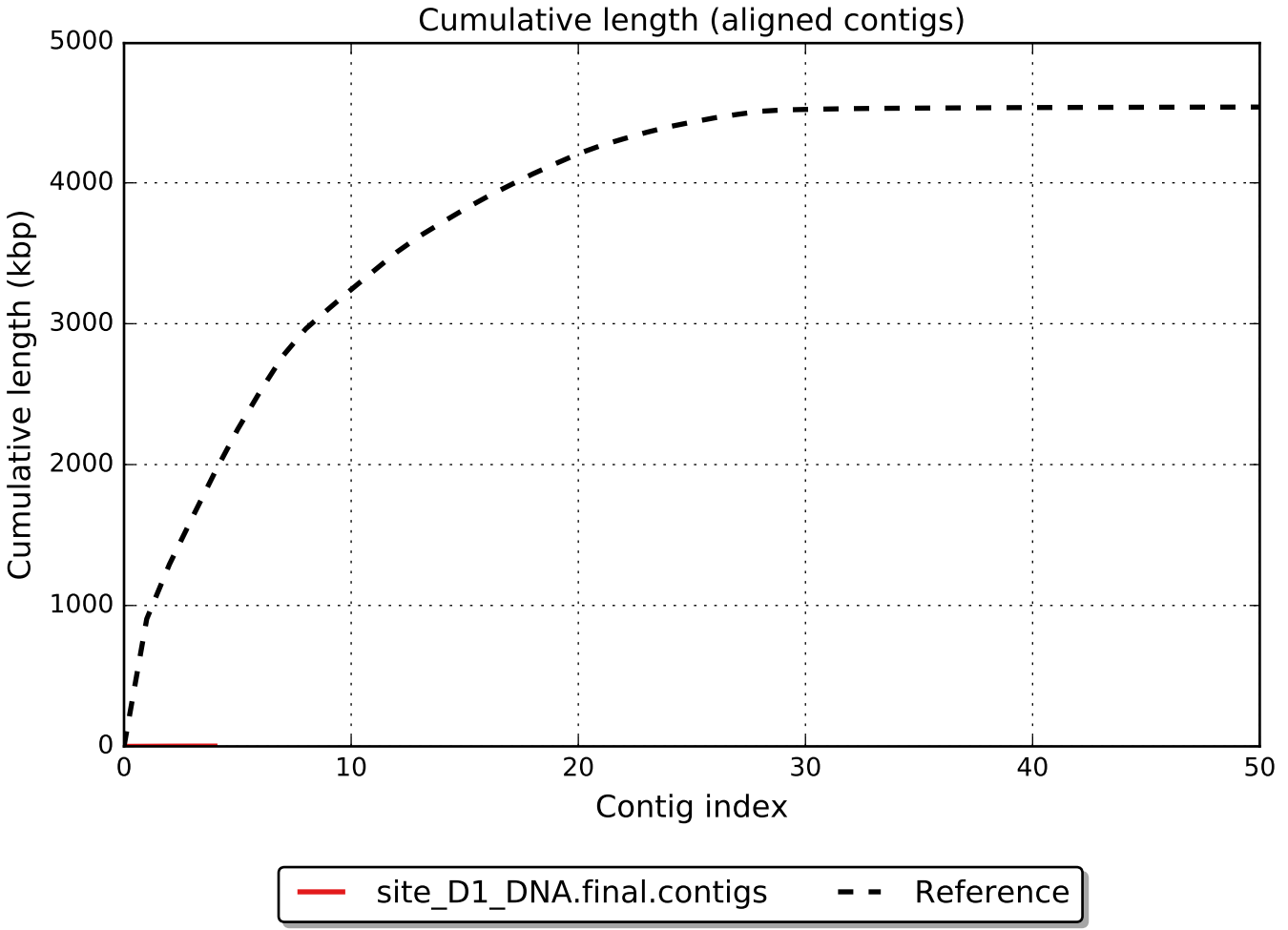

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
10
20
30
40
50
Contig index
site_D1_DNA.final.contigs
Reference

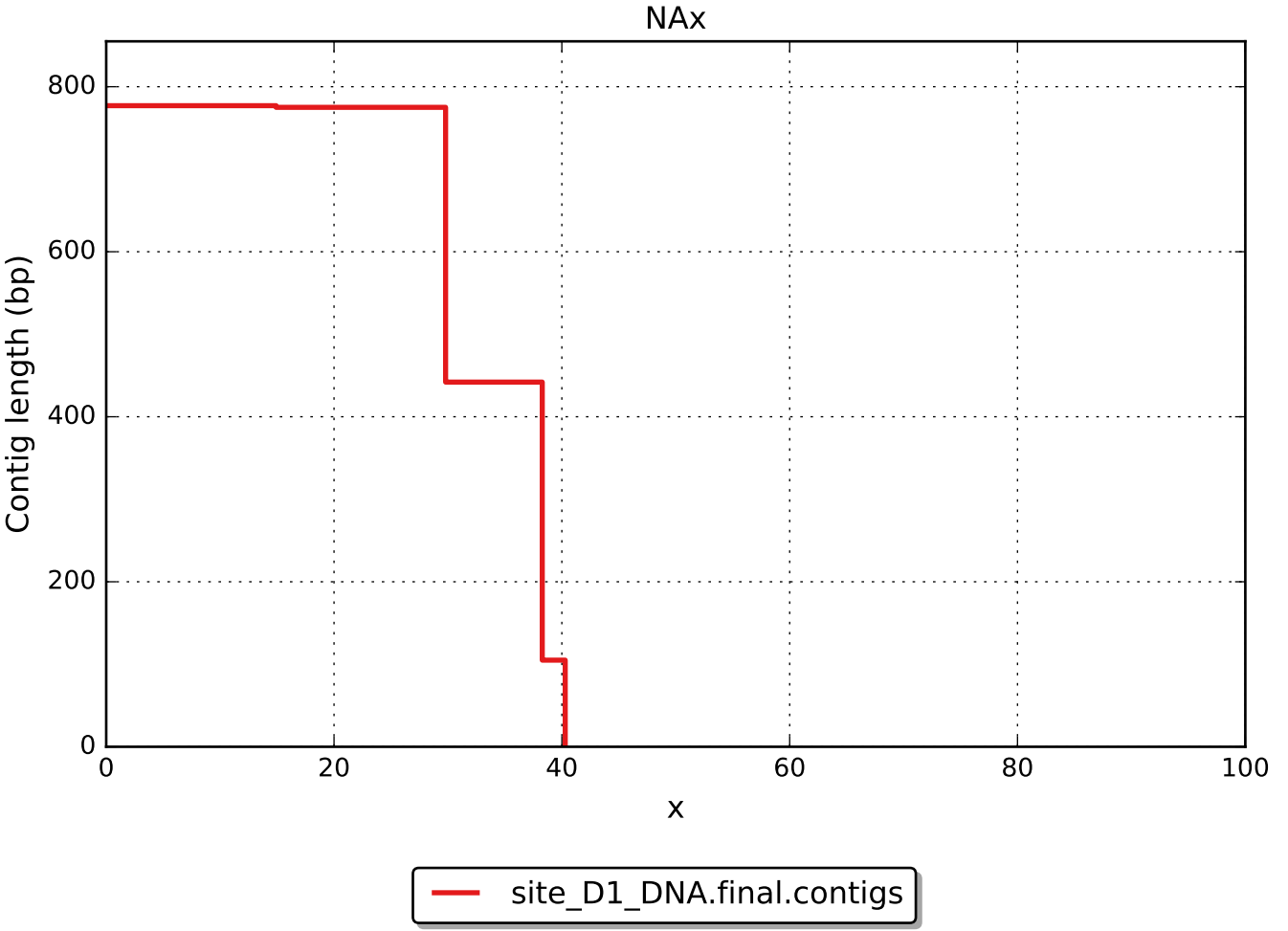

GC content
4000
3200
2400
1600
800
0
windows
0
20
40
60
80
100
GC (%)
site_D1_DNA.final.contigs
Reference

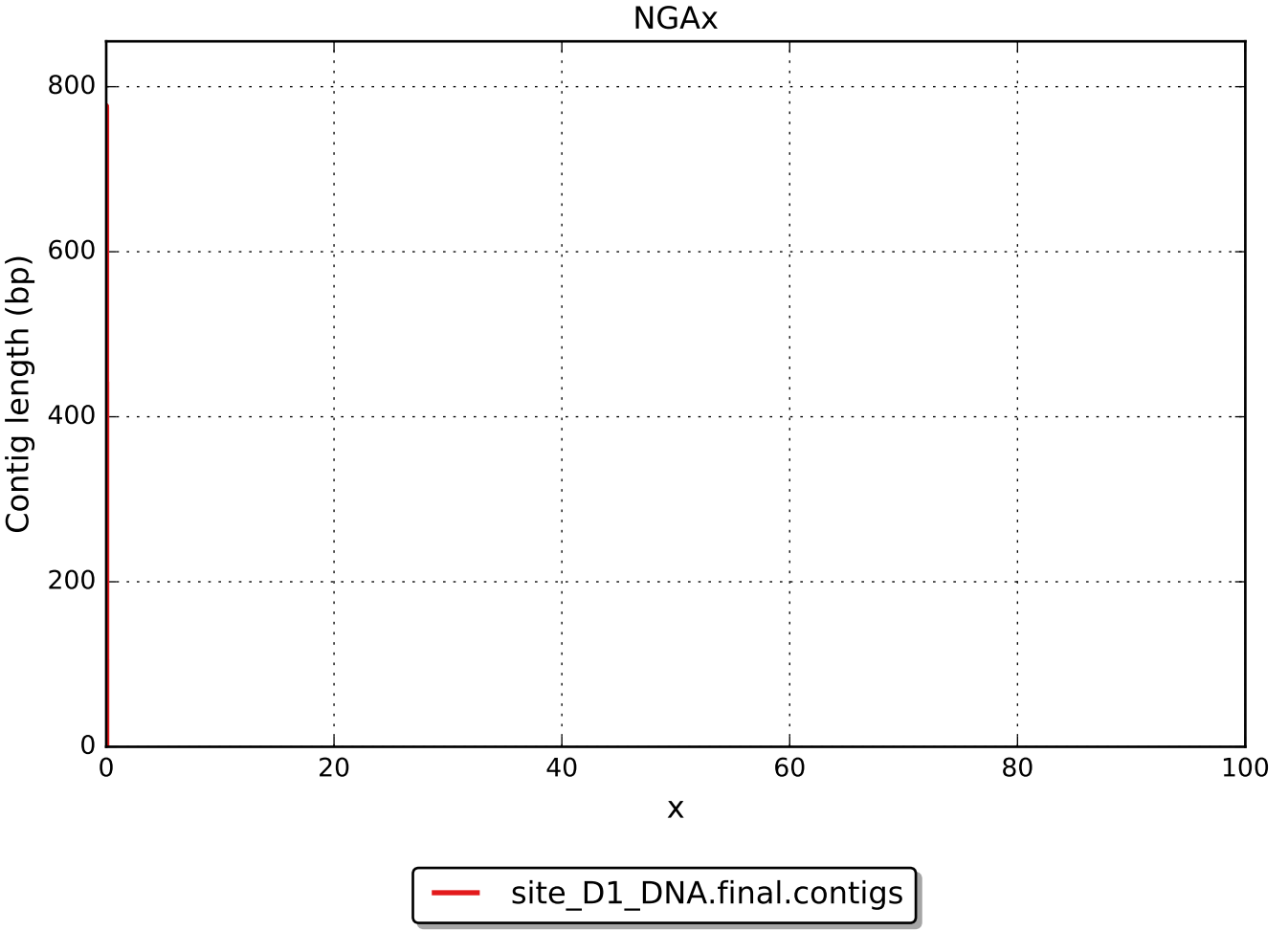

site_D1_DNA.final.contigs GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
site_D1_DNA.final.contigs


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)
5000
4000
3000
2000
1000
0
0
10
20
30
40
50
Contig index
site_D1_DNA.final.contigs
Reference


NAx
Contig length (bp)
800
600
400
200
0
0
20
40
60
80
100
x
site_D1_DNA.final.contigs


NGAx
Contig length (bp)
800
600
400
200
0
0
20
40
60
80
100
x
site_D1_DNA.final.contigs