Report

	site_D1_DNA.final.contigs
# contigs (>= 0 bp)	159944
# contigs (>= 1000 bp)	23722
# contigs (>= 5000 bp)	1070
# contigs (>= 10000 bp)	226
# contigs (>= 25000 bp)	30
# contigs (>= 50000 bp)	12
Total length (>= 0 bp)	118996402
Total length (>= 1000 bp)	48247005
Total length (>= 5000 bp)	9786216
Total length (>= 10000 bp)	4144053
Total length (>= 25000 bp)	1395140
Total length (>= 50000 bp)	822203
# contigs	85351
Largest contig	128464
Total length	90052867
Reference length	78837296
N50	1078
N75	701
L50	20616
L75	47141
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# structural variations	0
# unaligned mis. contigs	0
# unaligned contigs	85246 + 49 part
Unaligned length	90003621
Genome fraction (%)	0.043
Duplication ratio	1.653
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2380.53
# indels per 100 kbp	166.85
Largest alignment	2489
Total aligned length	32641

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

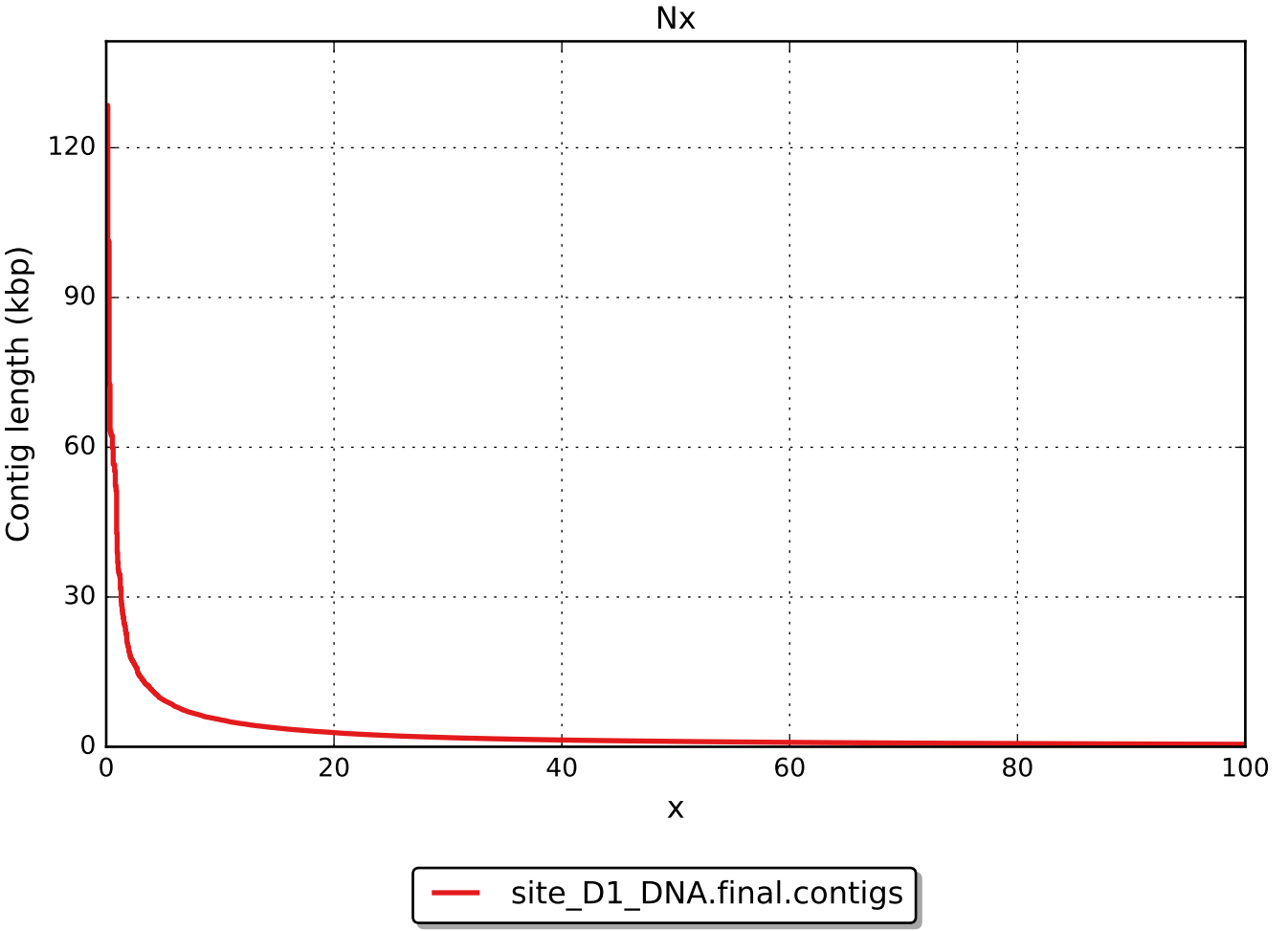
	site_D1_DNA.final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	2
# possible misassemblies	2
# local misassemblies	0
# structural variations	0
# unaligned mis. contigs	0
# mismatches	799
# indels	56
# indels (<= 5 bp)	56
# indels (> 5 bp)	0
Indels length	61

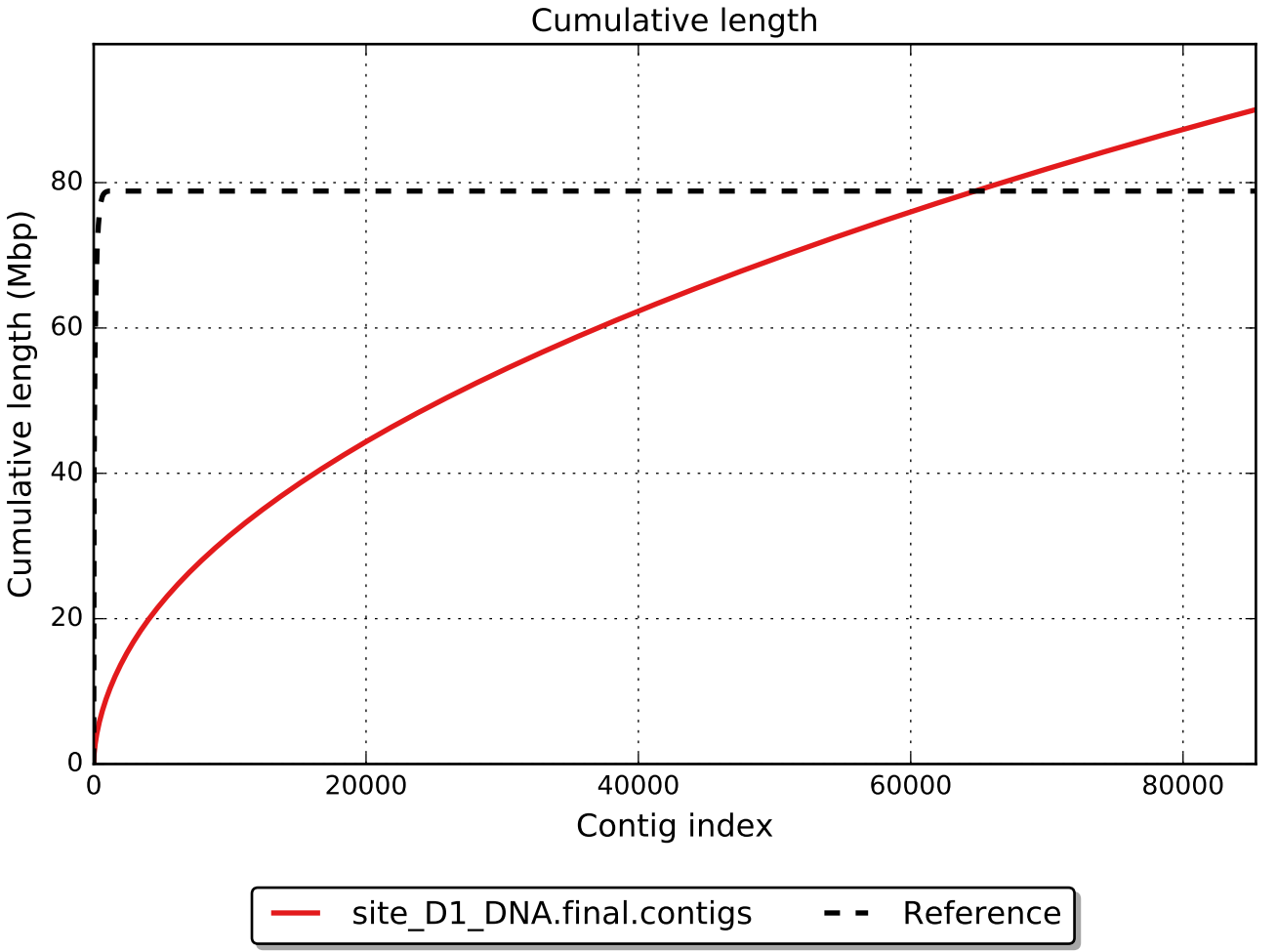
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

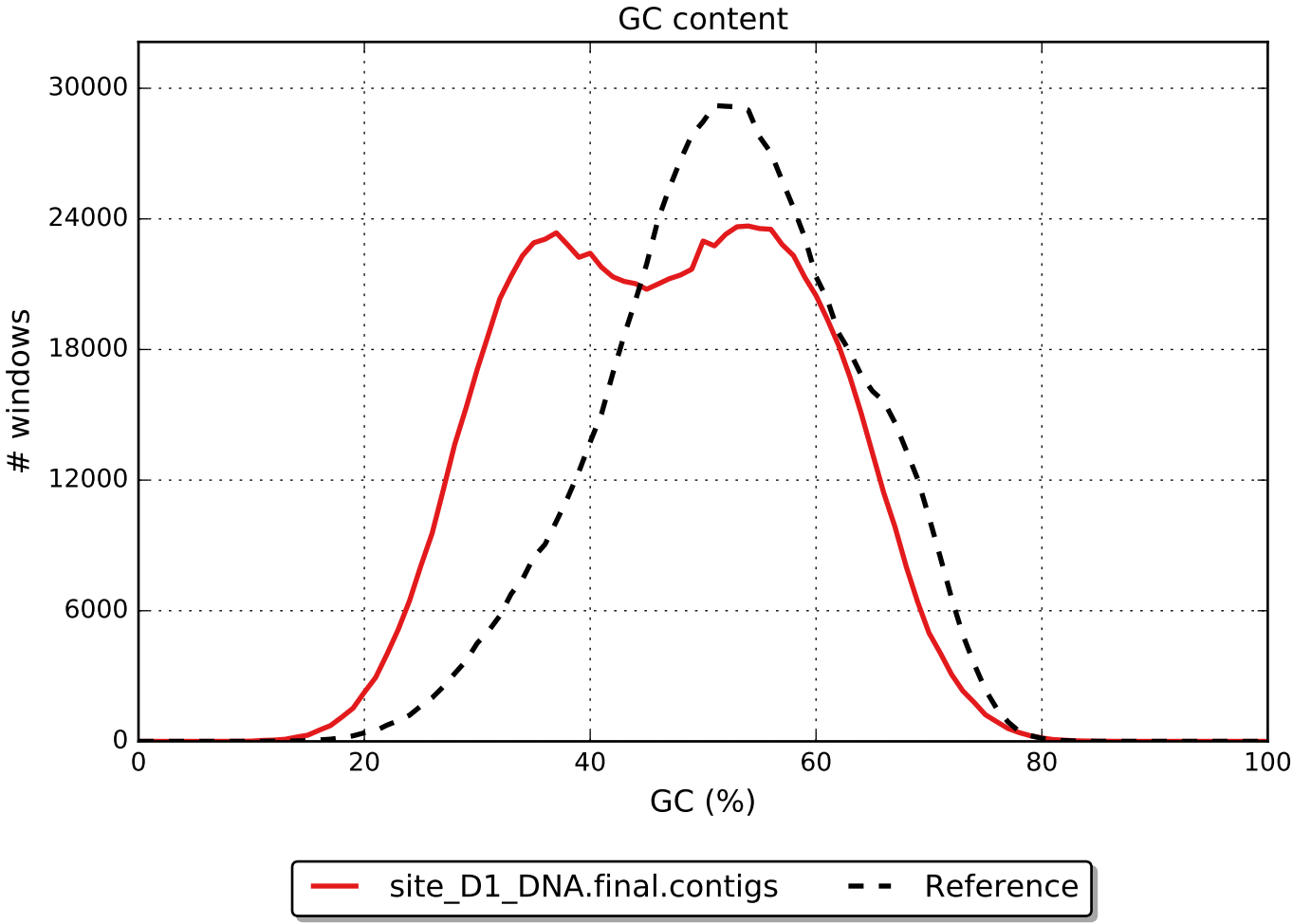
Unaligned report

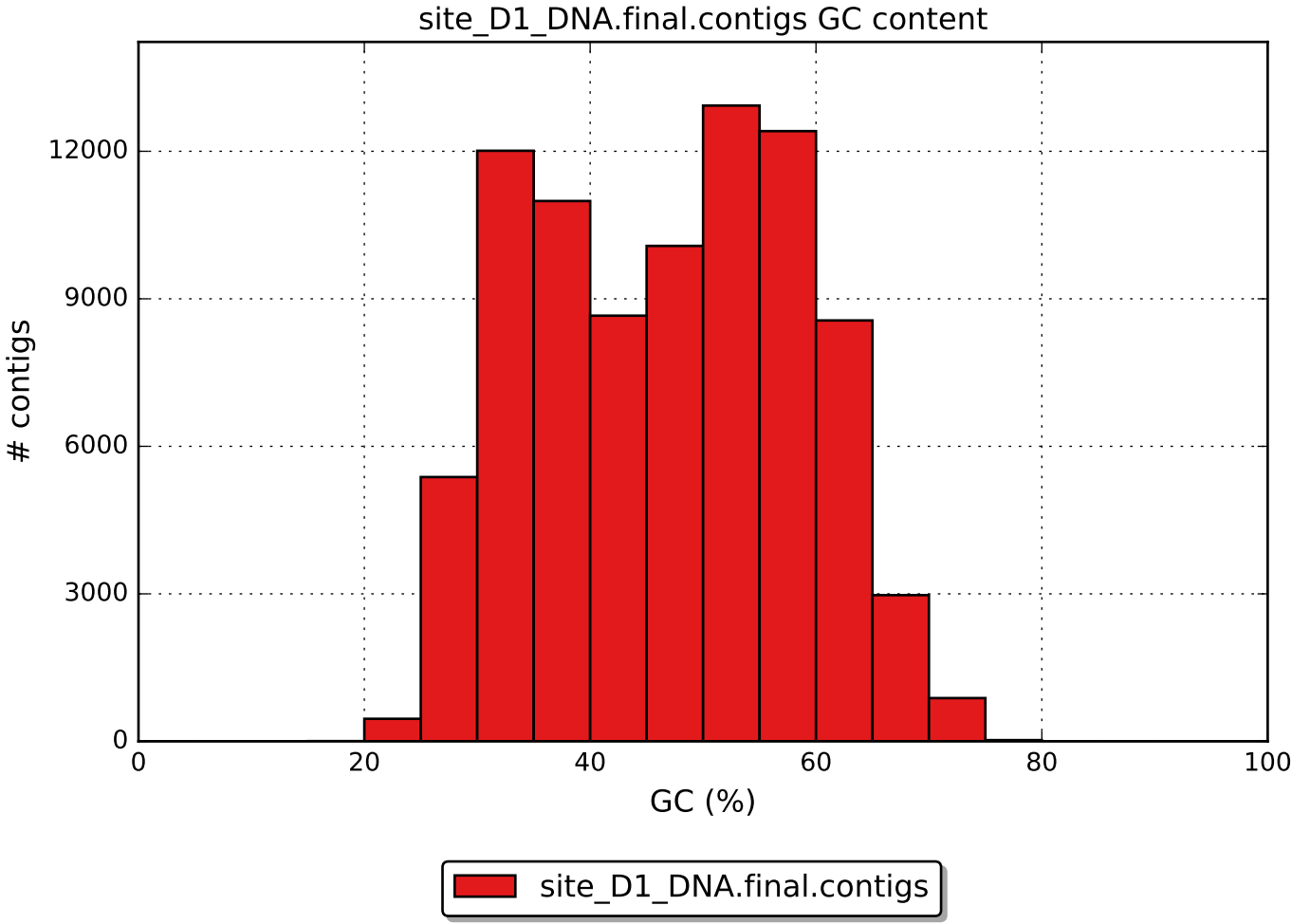
	site_D1_DNA.final.contigs
# fully unaligned contigs	85246
Fully unaligned length	89931485
# partially unaligned contigs	49
Partially unaligned length	72136
# N's	0

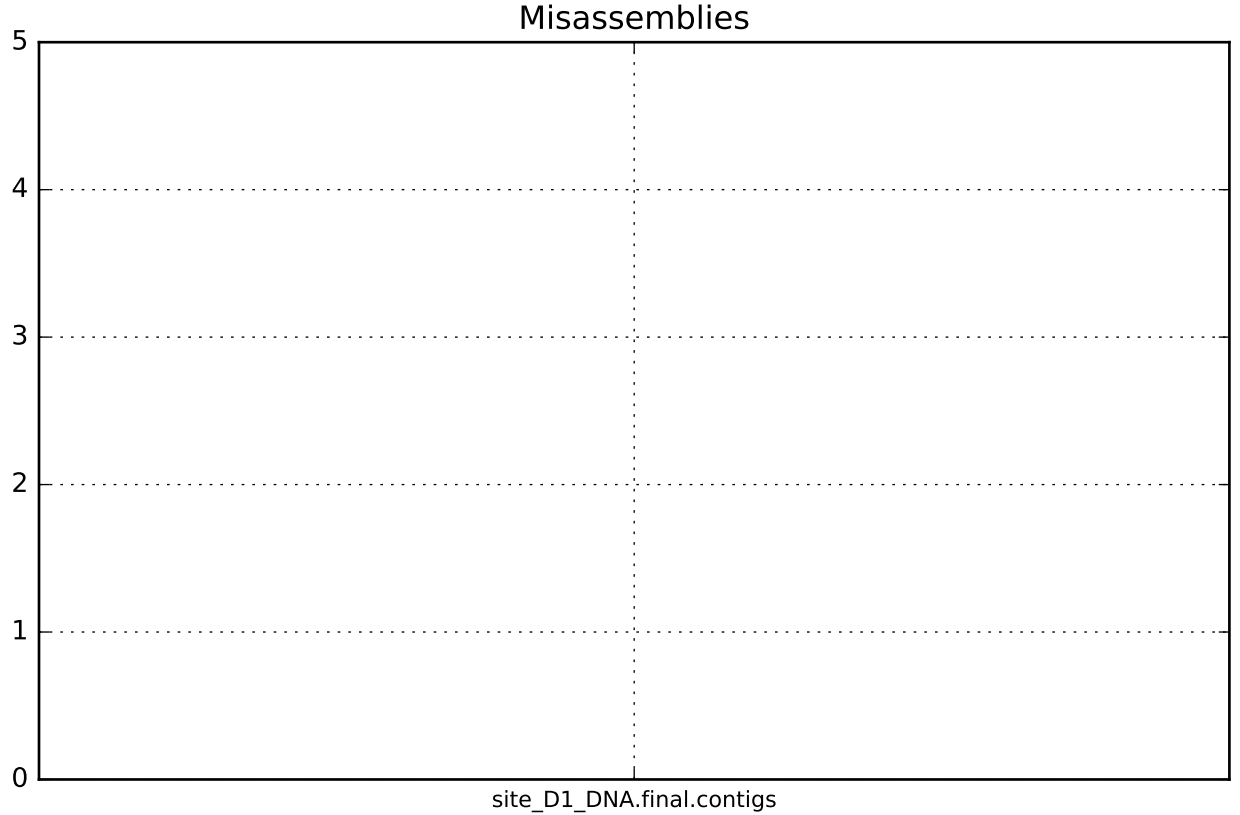
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

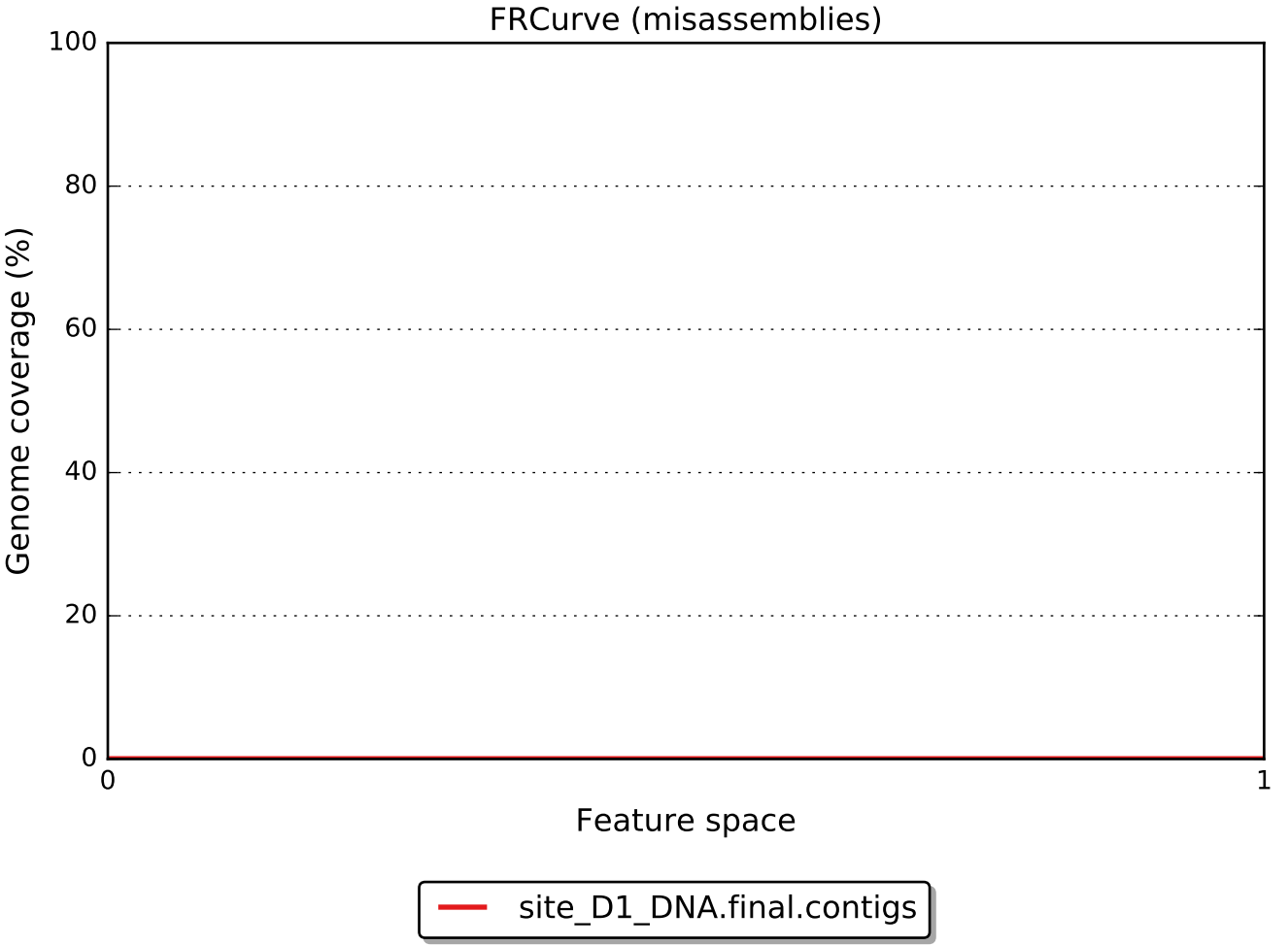

Nx
Contig length (kbp)
120
90
60
30
0
0
20
40
60
80
100
x
site_D1_DNA.final.contigs

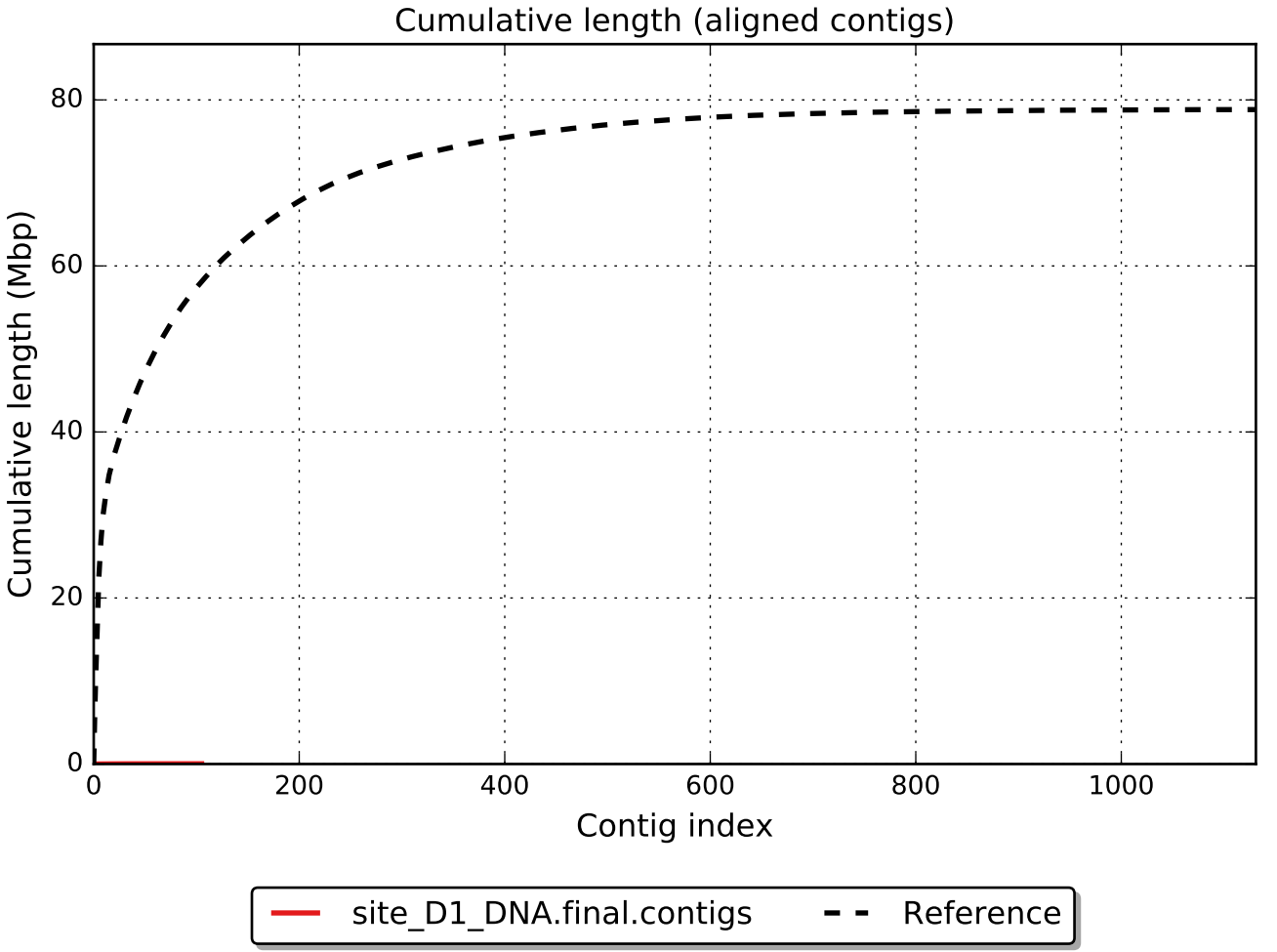

Cumulative length
Cumulative length (Mbp)
0
20
40
60
80
0
20000
40000
60000
80000
Contig index
site_D1_DNA.final.contigs
Reference

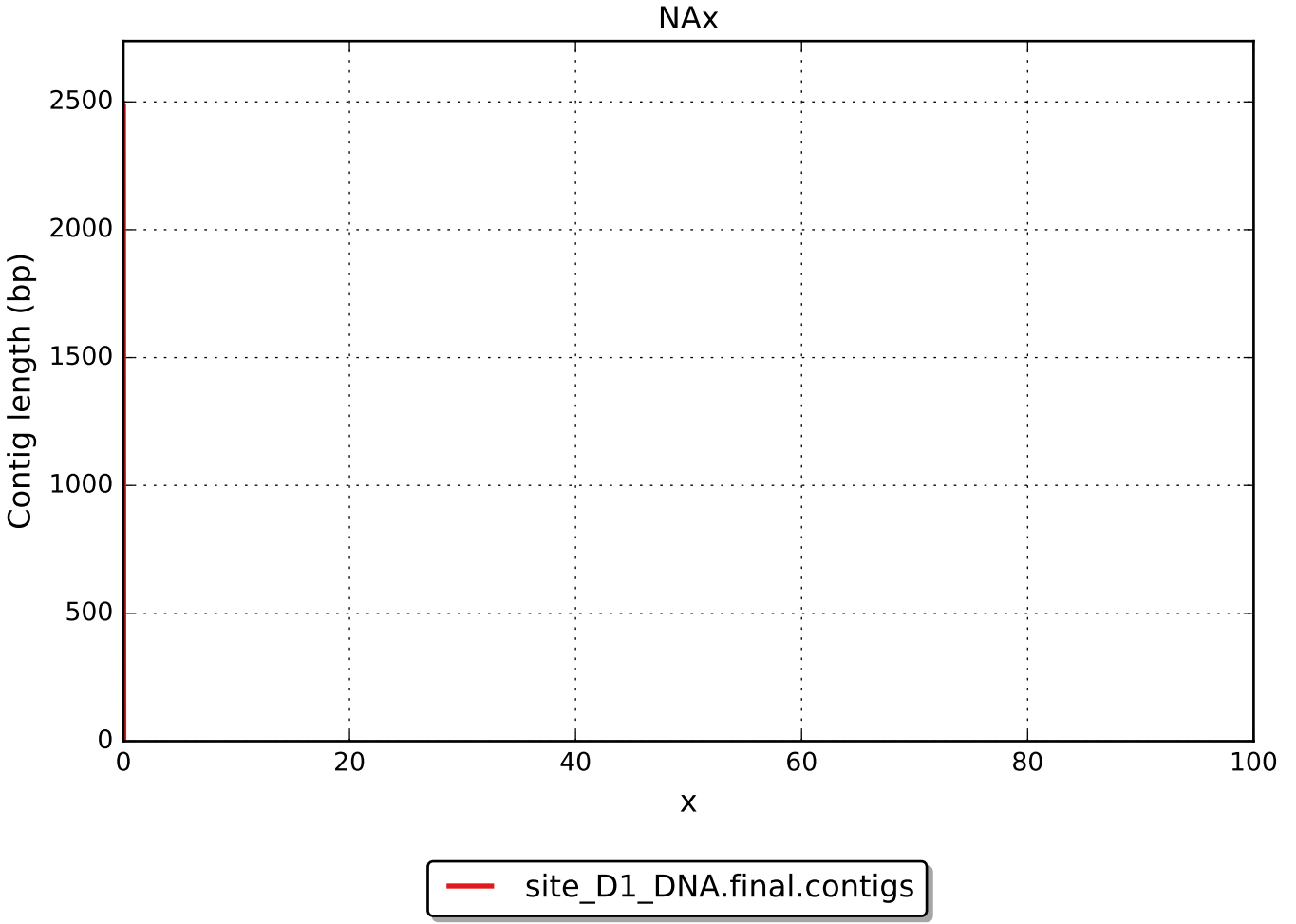

GC content
30000
24000
18000
12000
6000
0
windows
0
20
40
60
80
100
GC (%)
site_D1_DNA.final.contigs
Reference


site_D1_DNA.final.contigs GC content
contigs
GC (%)
0
3000
6000
9000
12000
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 (Mbp)
0
20
40
60
80
0
200
400
600
800
1000
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