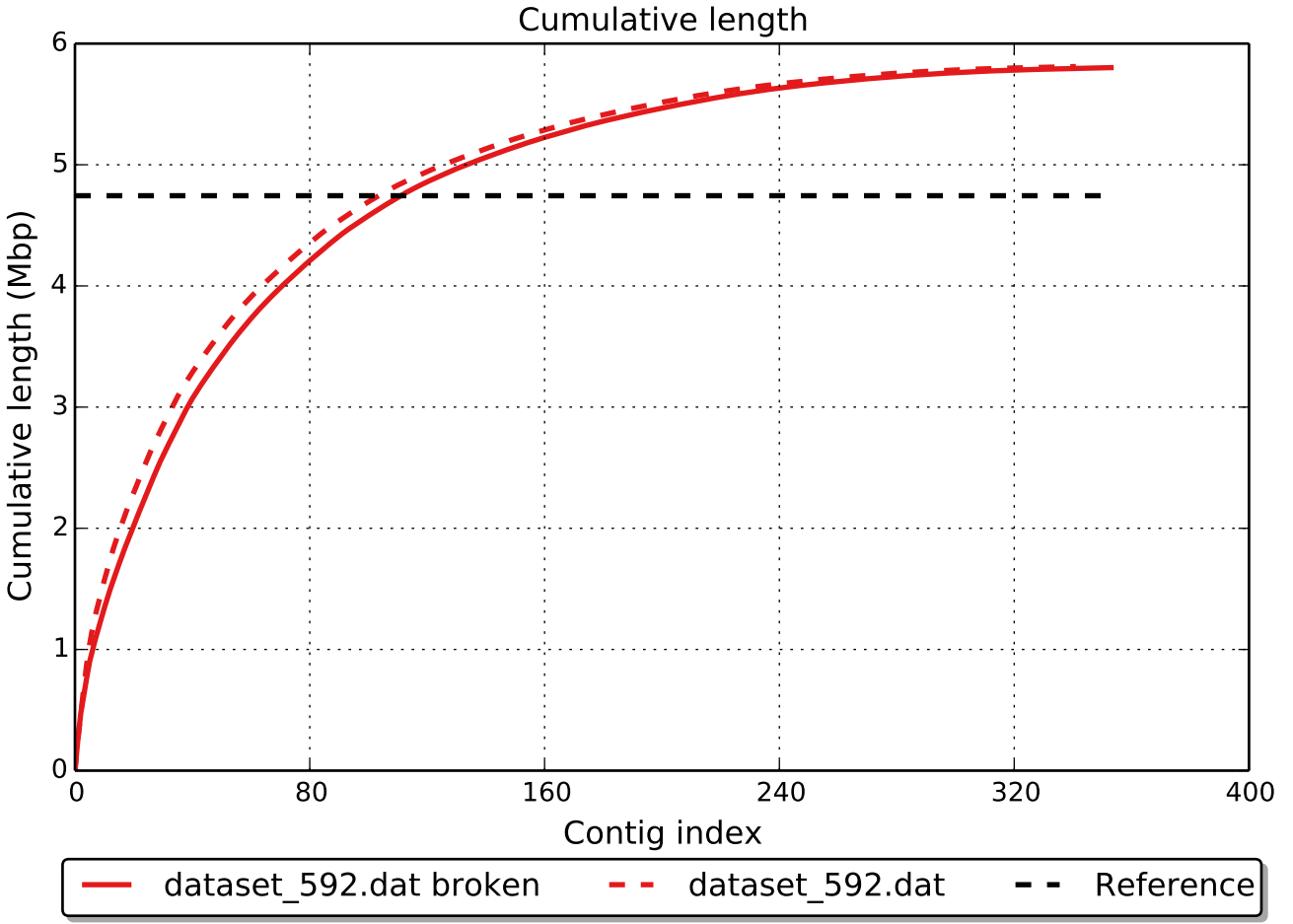
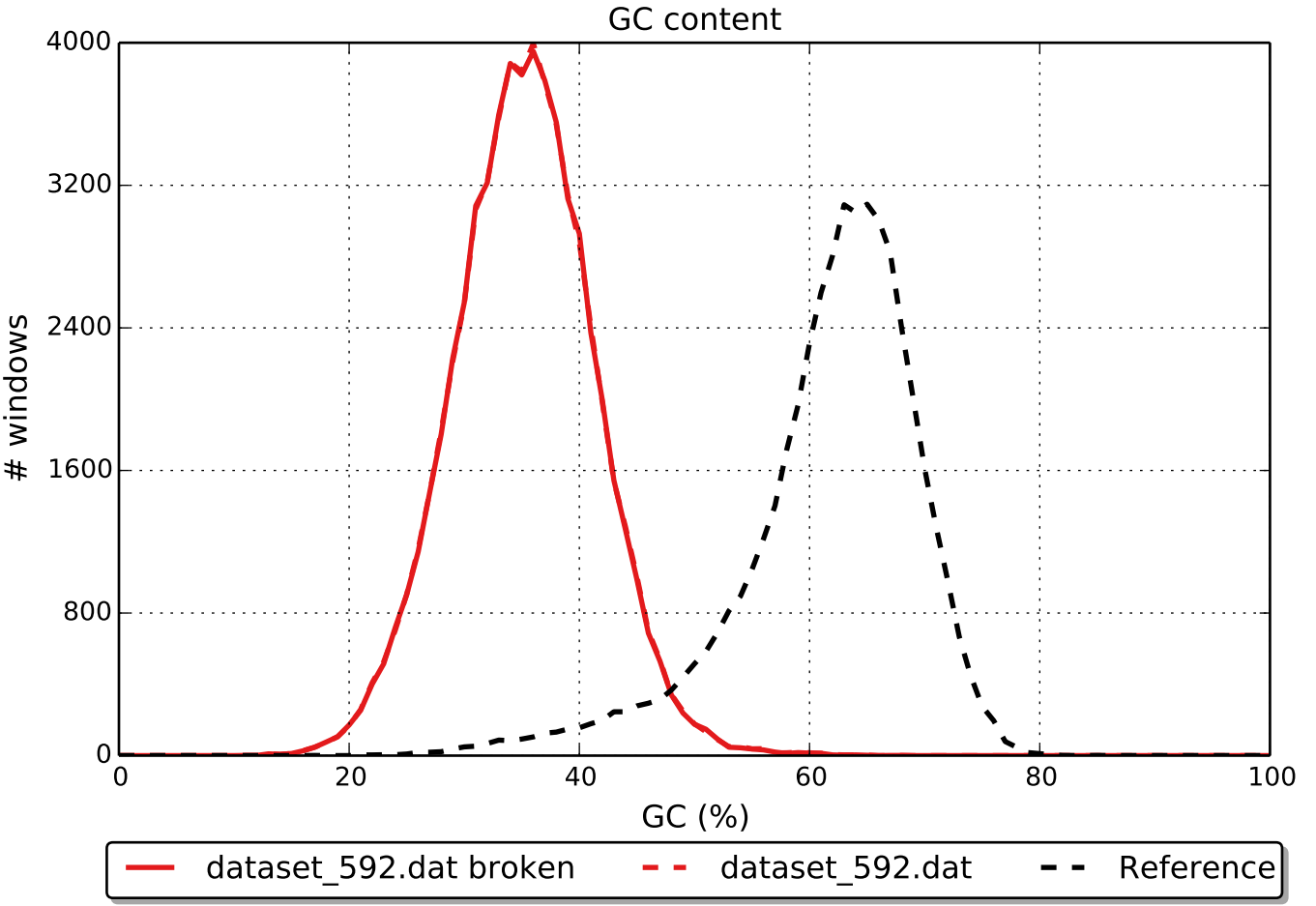
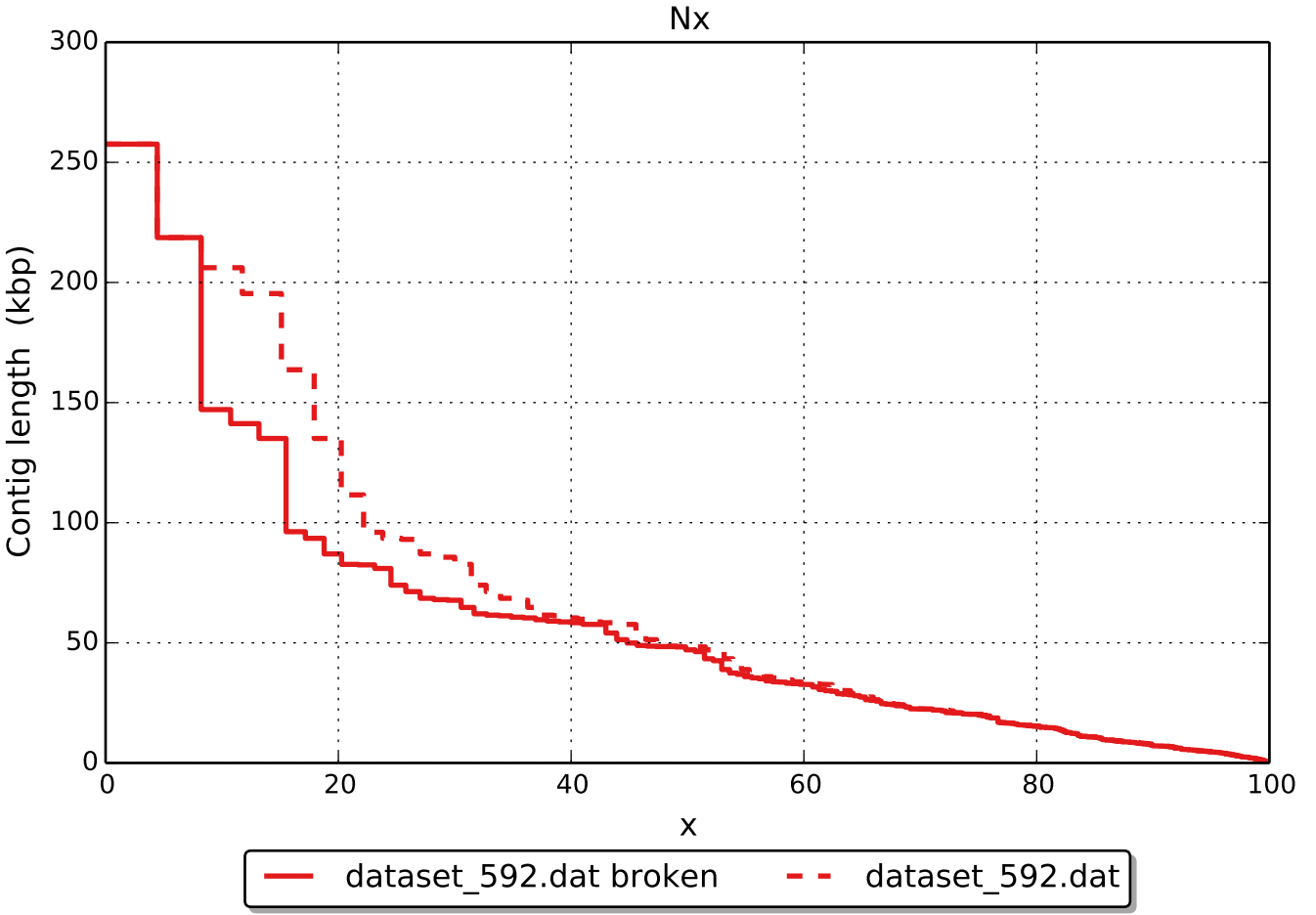
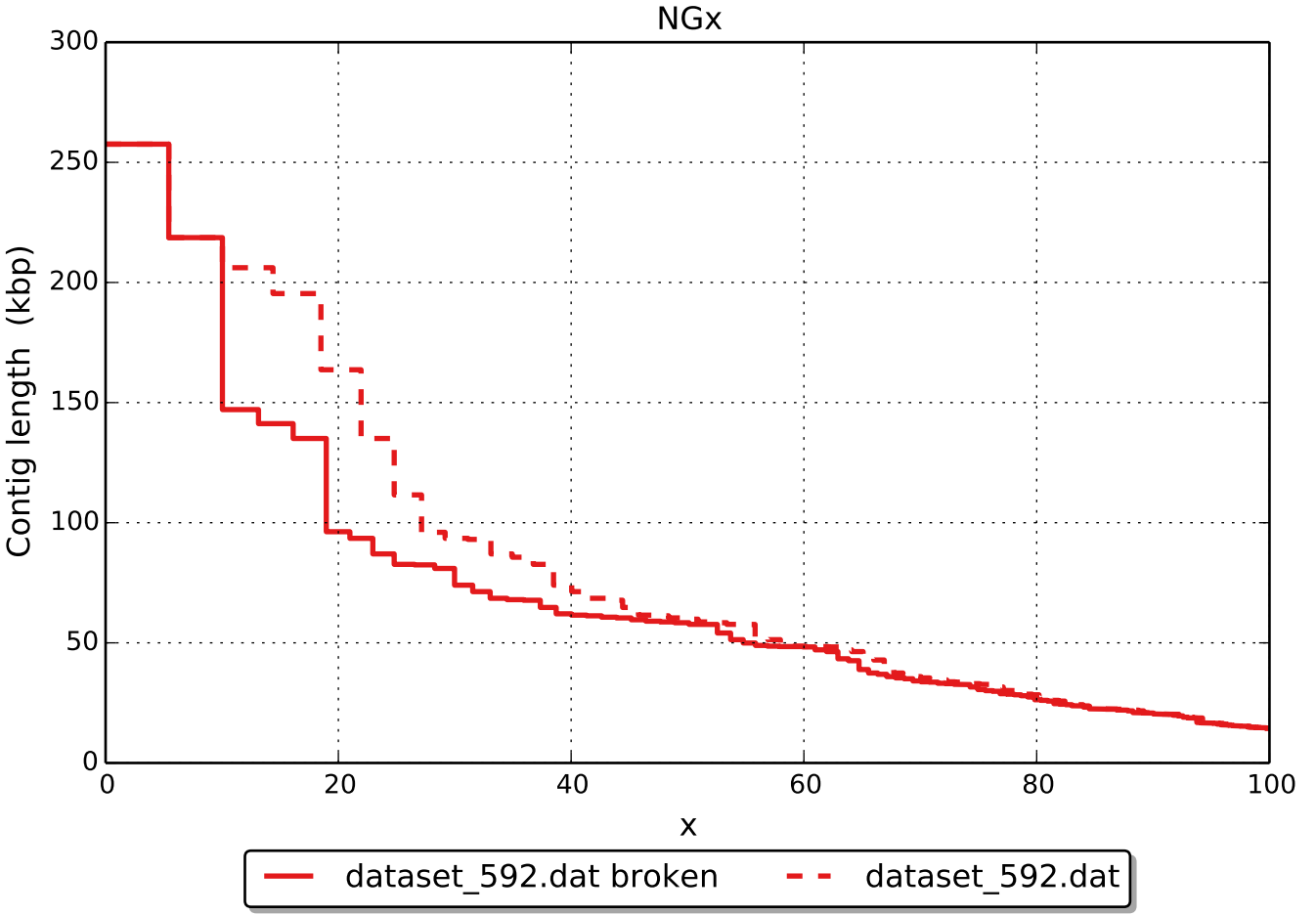
A_hydrophila_ATCC_7966

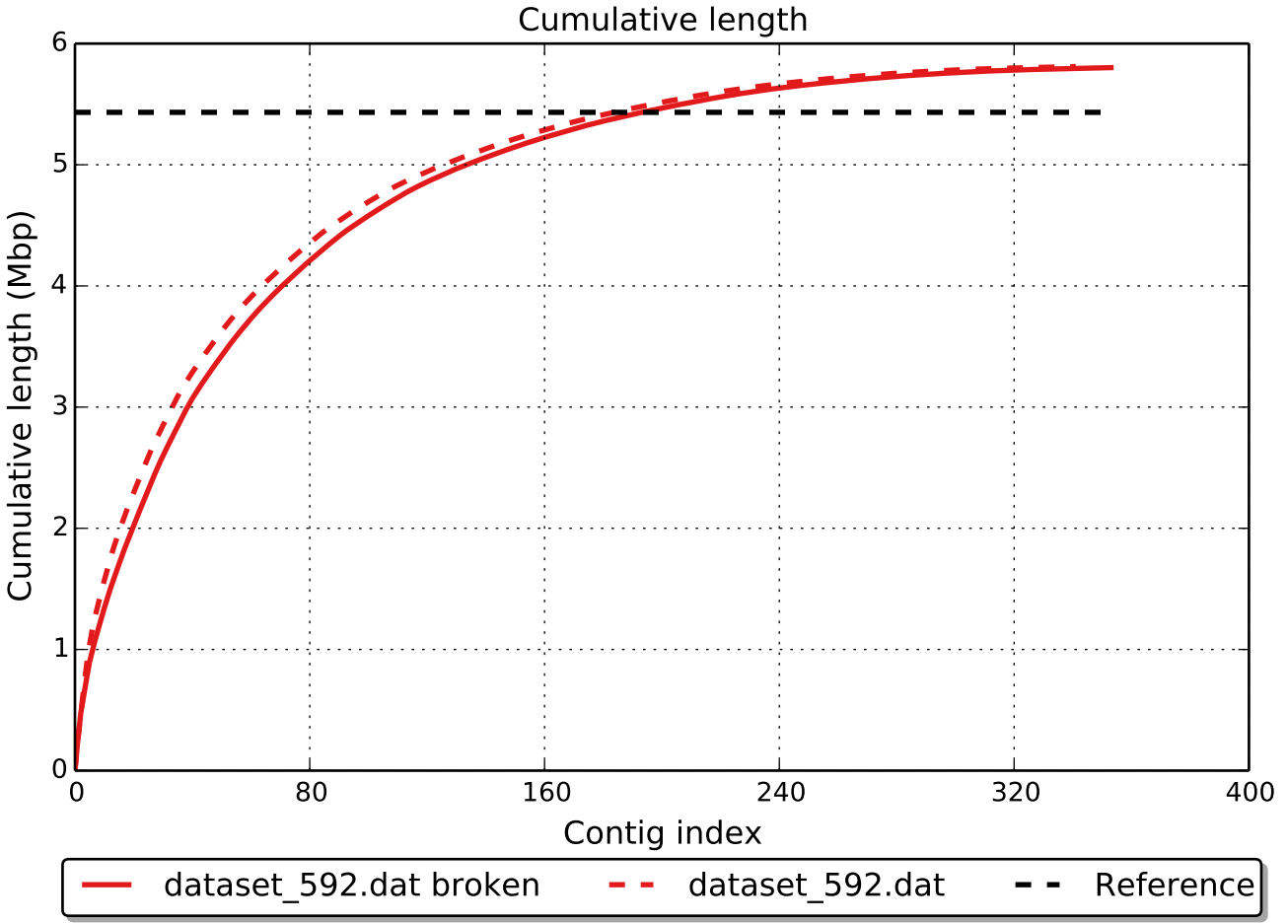

Cumulative length
Cumulative length (Mbp)
0
1
2
3
4
5
6
0
80
160
240
320
400
Contig index
dataset_592.dat broken
dataset_592.dat
Reference

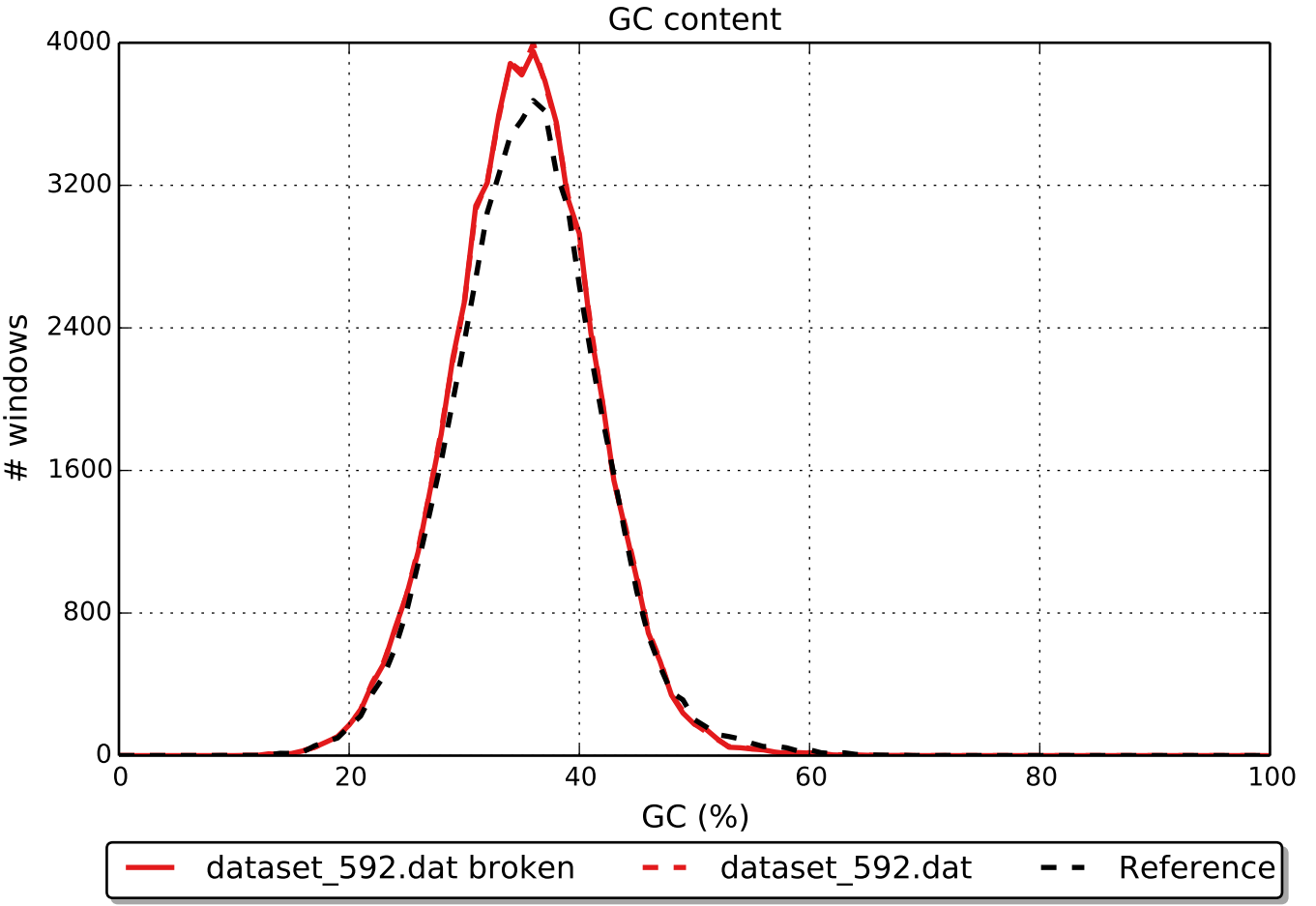

GC content
4000
3200
2400
1600
800
0
# windows
0
20
40
60
80
100
GC (%)
dataset_592.dat broken
dataset_592.dat
Reference

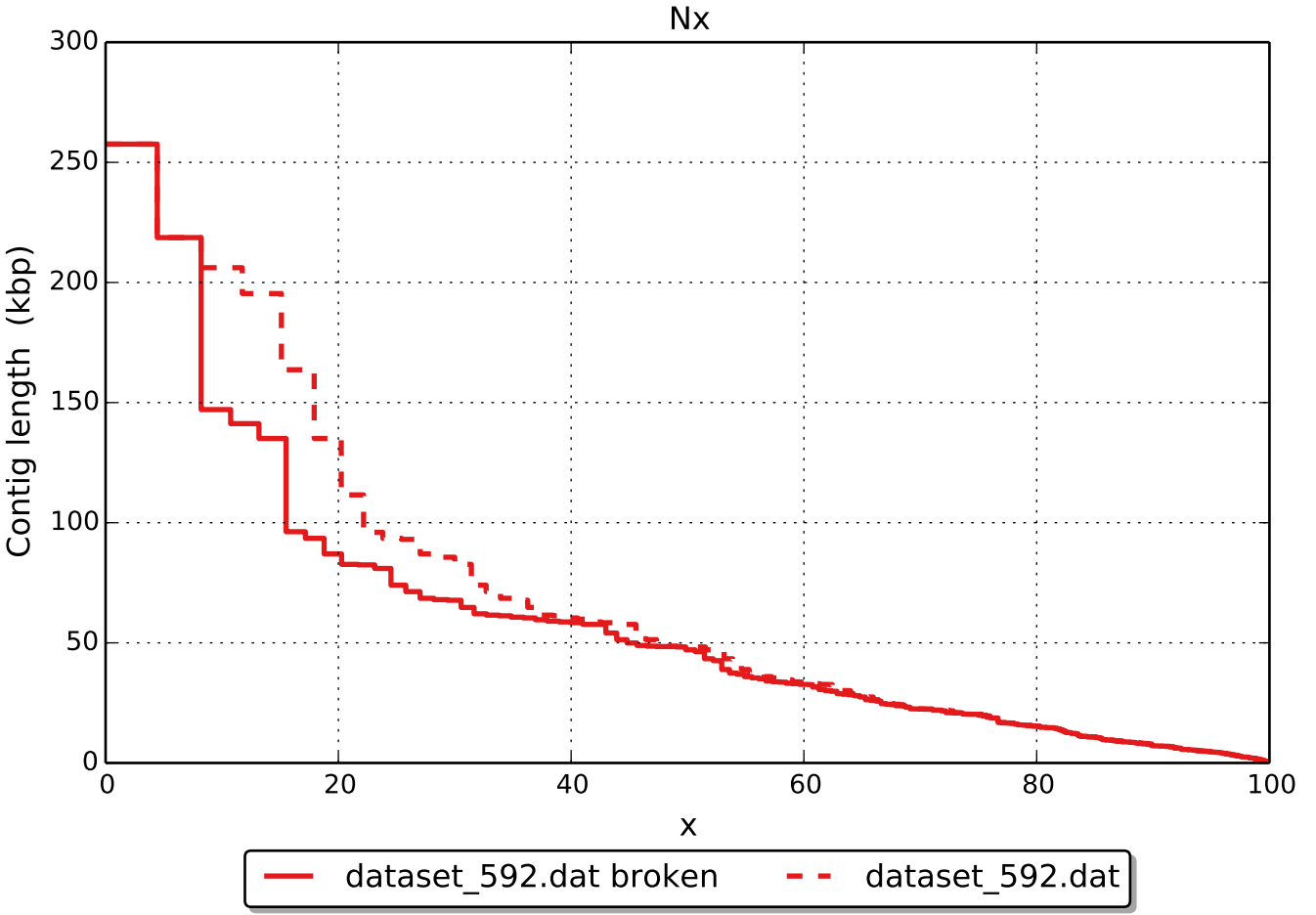

Nx
Contig length (kbp)
300
250
200
150
100
50
0
0
20
40
60
80
100
x
dataset_592.dat broken
dataset_592.dat

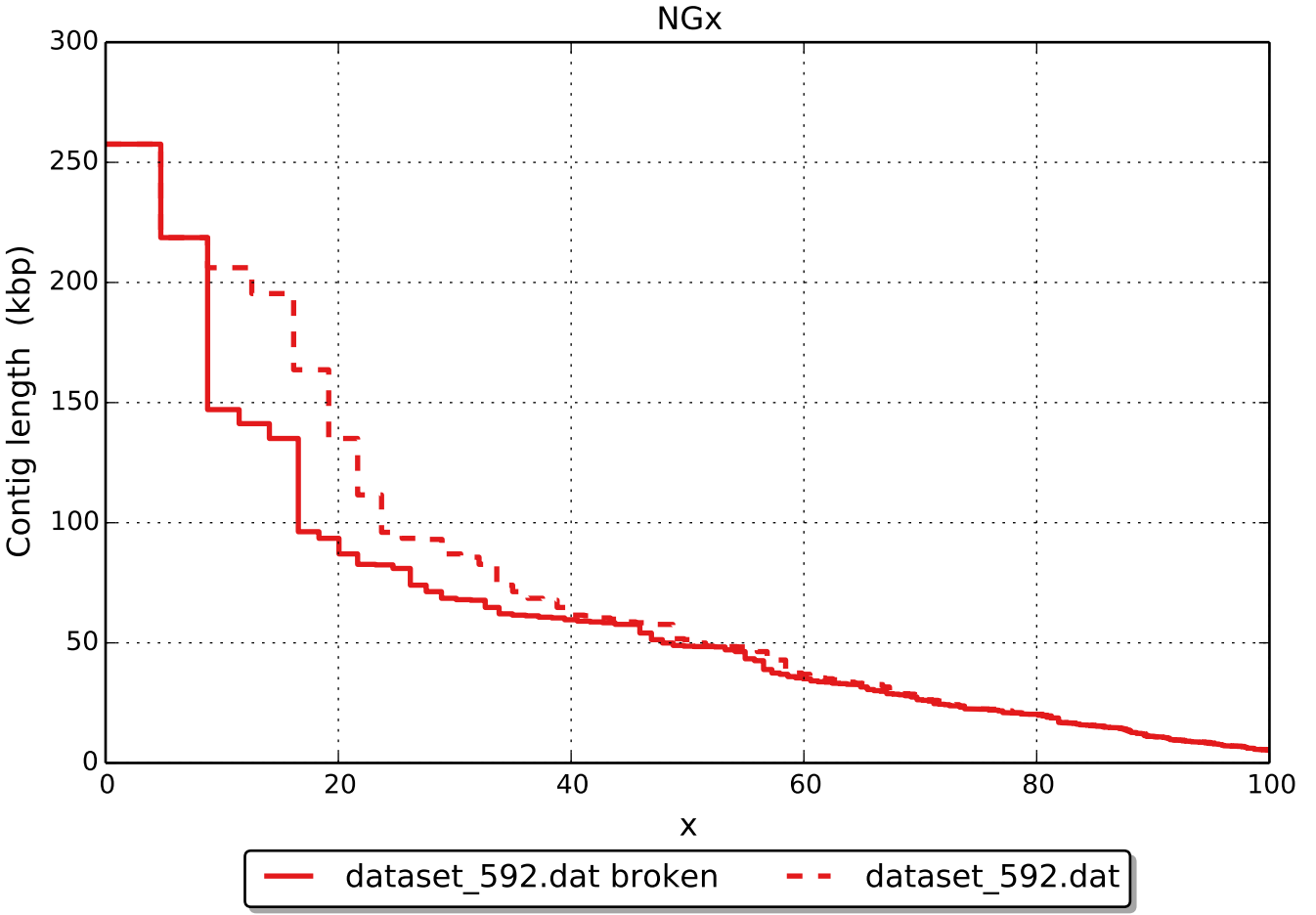

NGx
Contig length (kbp)
300
250
200
150
100
50
0
0
20
40
60
80
100
x
dataset_592.dat broken
dataset_592.dat

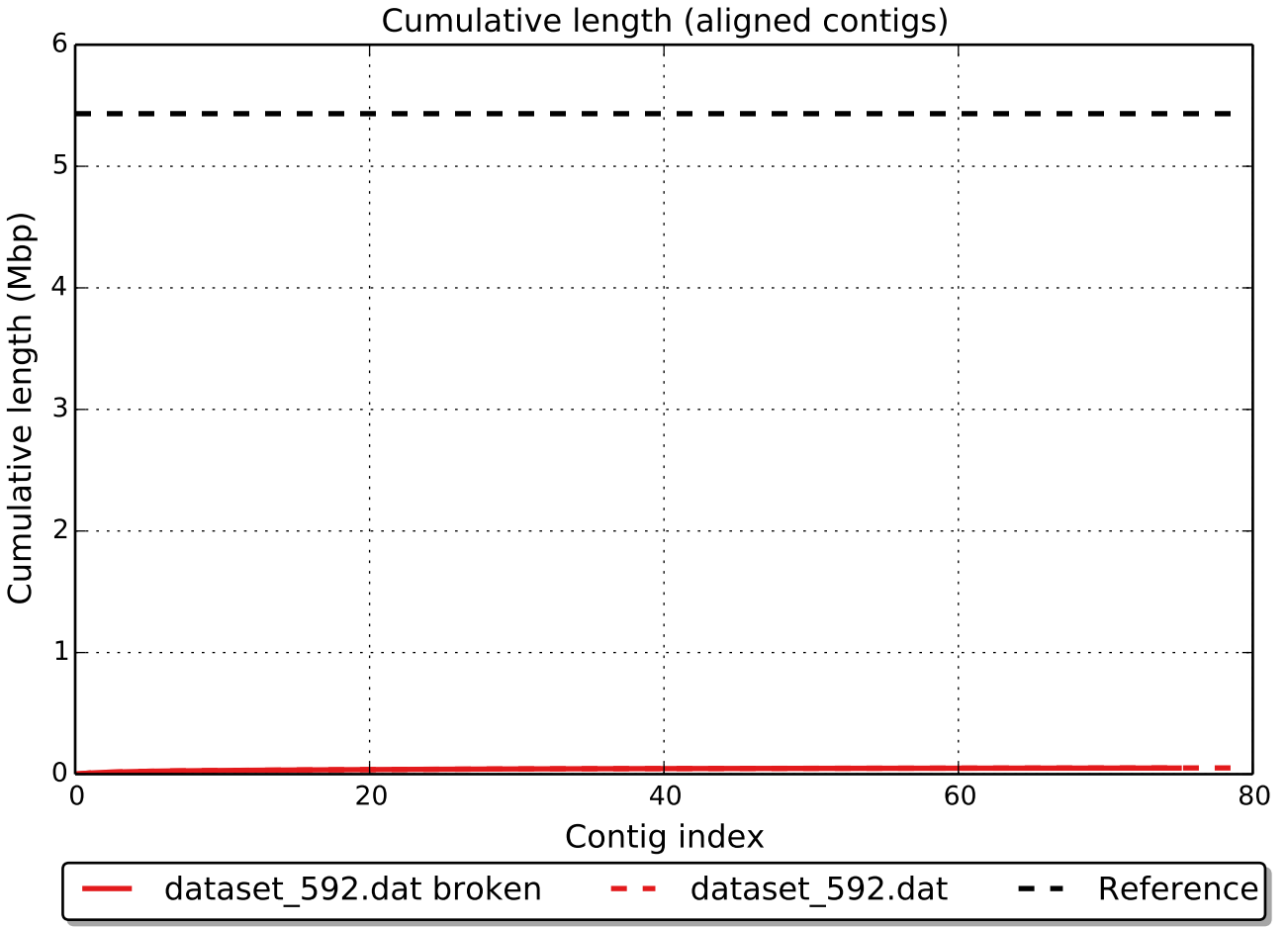
B_cereus_ATCC_1098

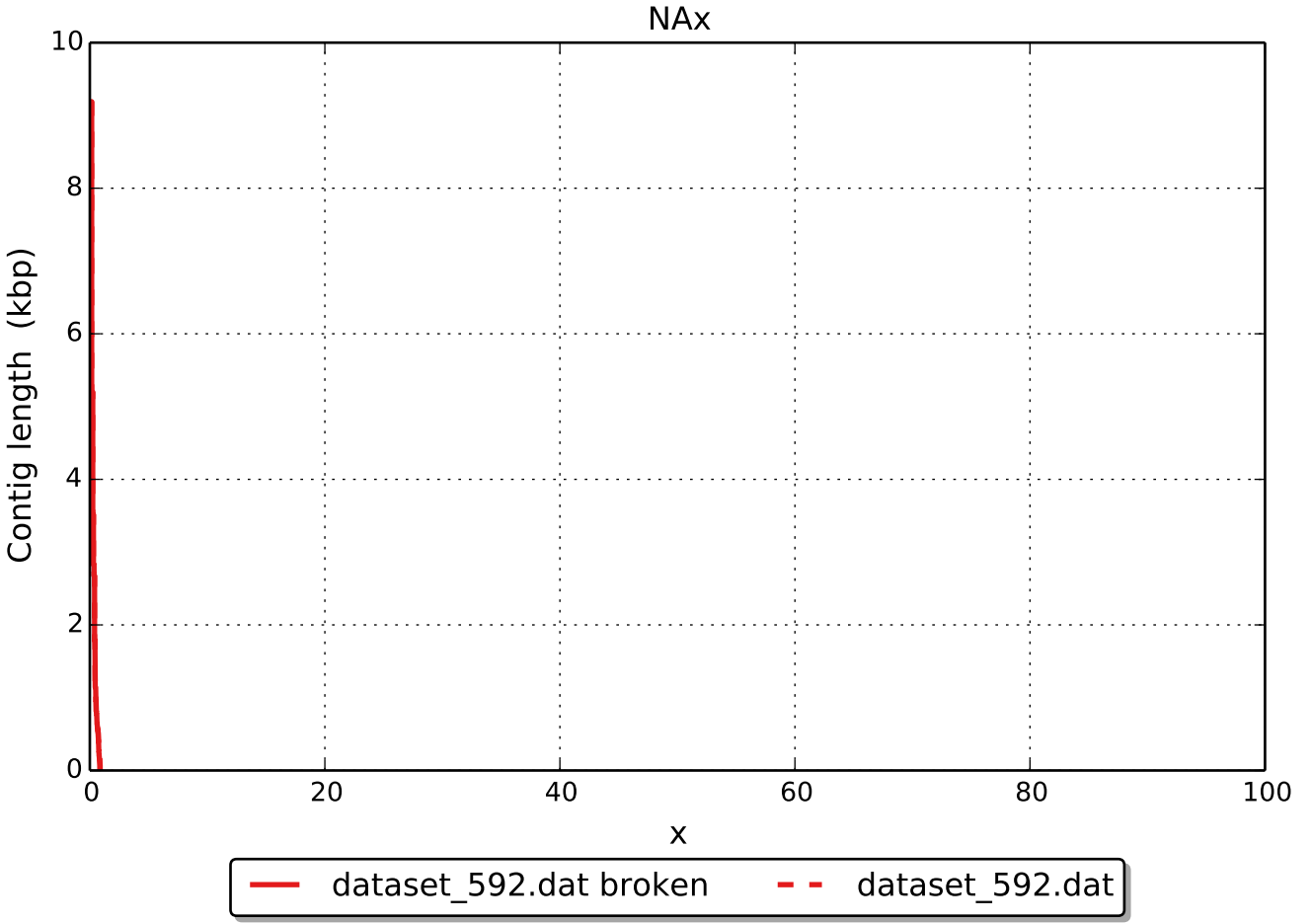

Cumulative length
Cumulative length (Mbp)
0
1
2
3
4
5
6
0
80
160
240
320
400
Contig index
dataset_592.dat broken
dataset_592.dat
Reference

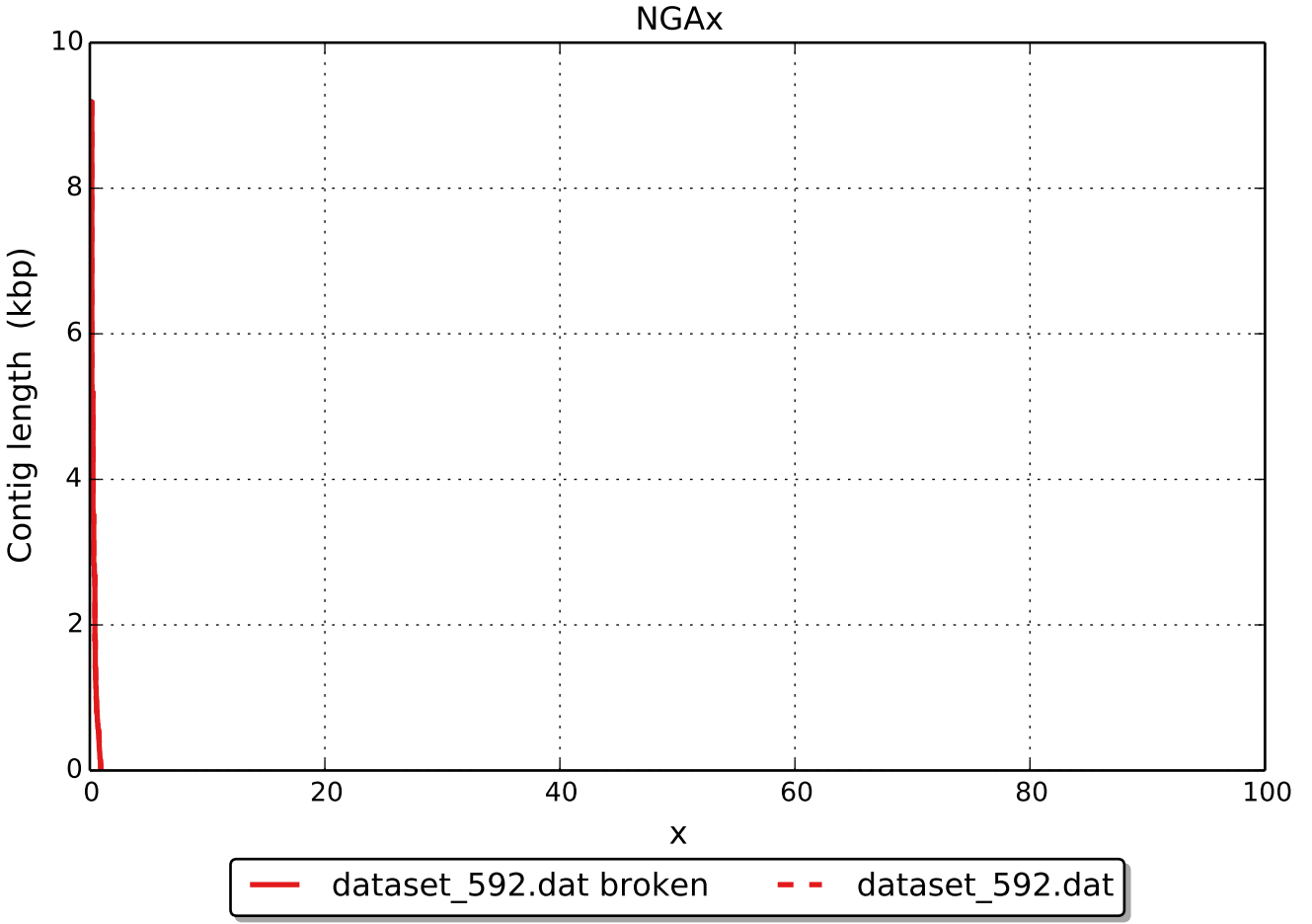

GC content
4000
3200
2400
1600
800
0
# windows
0
20
40
60
80
100
GC (%)
dataset_592.dat broken
dataset_592.dat
Reference

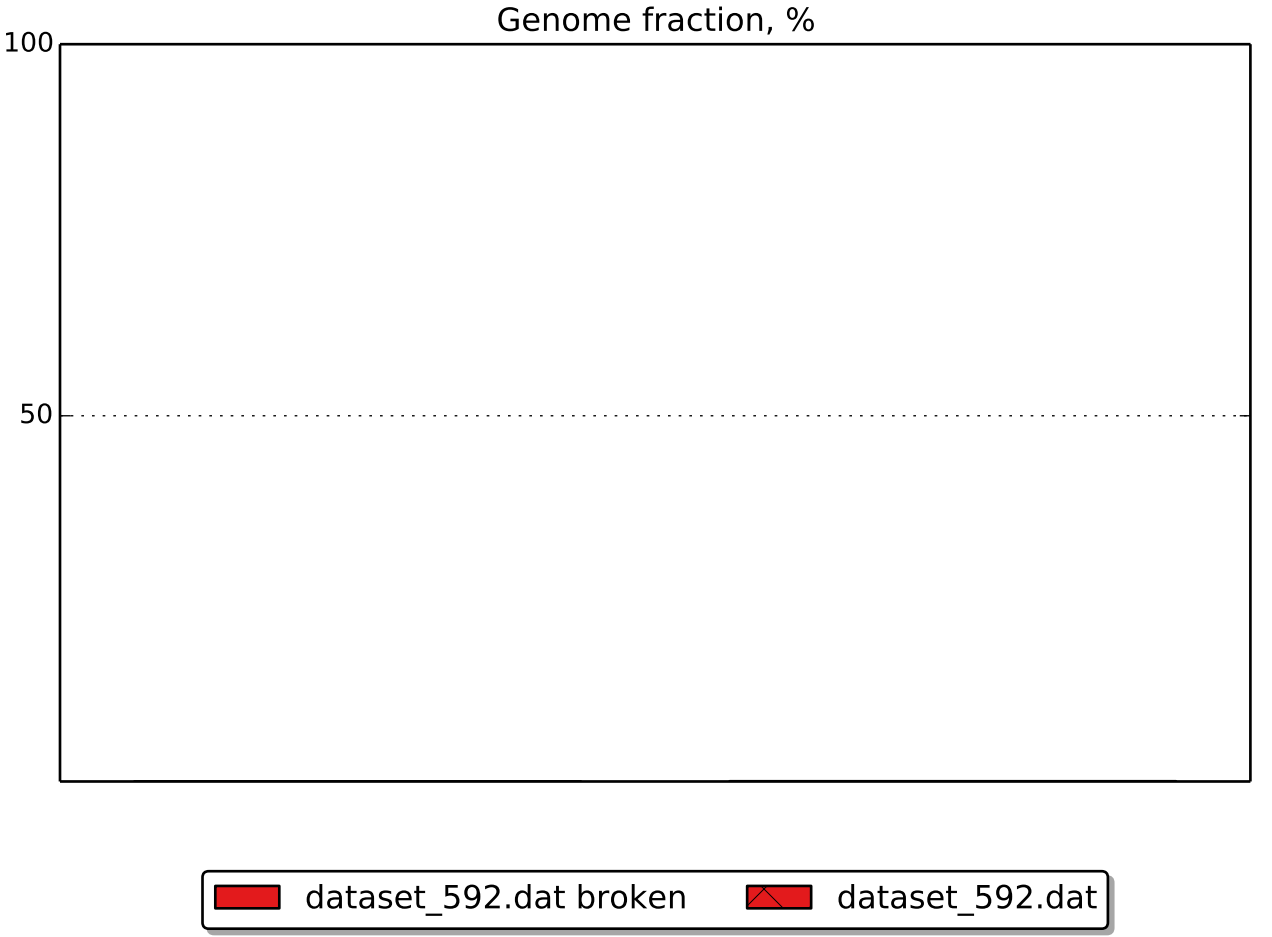

Nx
Contig length (kbp)
300
250
200
150
100
50
0
0
20
40
60
80
100
x
dataset_592.dat broken
dataset_592.dat


NGx
Contig length (kbp)
300
250
200
150
100
50
0
0
20
40
60
80
100
x
dataset_592.dat broken
dataset_592.dat


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
1
2
3
4
5
6
0
20
40
60
80
Contig index
dataset_592.dat broken
dataset_592.dat
Reference


NAx
Contig length (kbp)
0
2
4
6
8
10
0
20
40
60
80
100
x
dataset_592.dat broken
dataset_592.dat


NGAx
Contig length (kbp)
10
8
6
4
2
0
0
20
40
60
80
100
x
dataset_592.dat broken
dataset_592.dat


Genome fraction, %
100
50
dataset_592.dat broken
dataset_592.dat