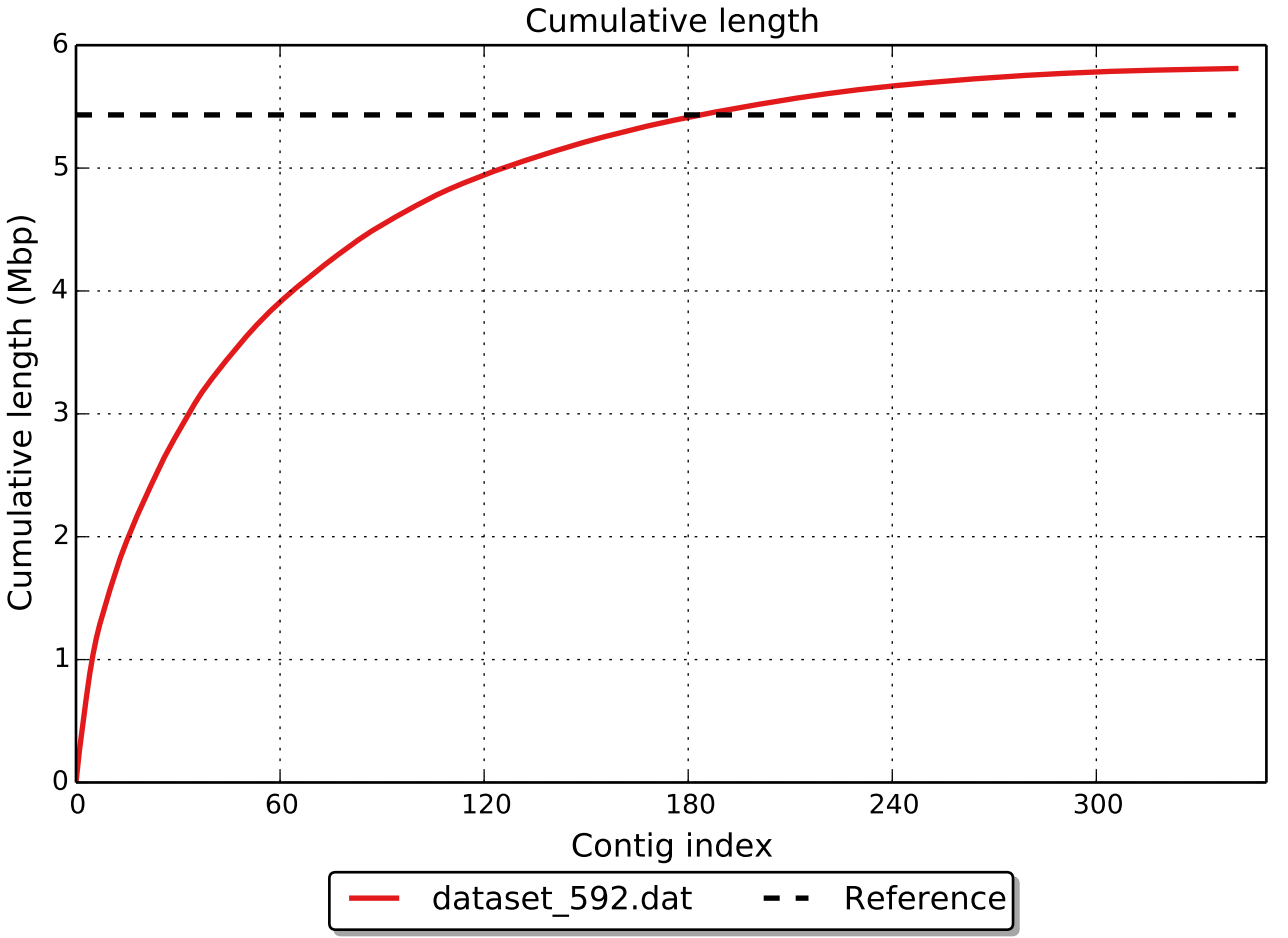
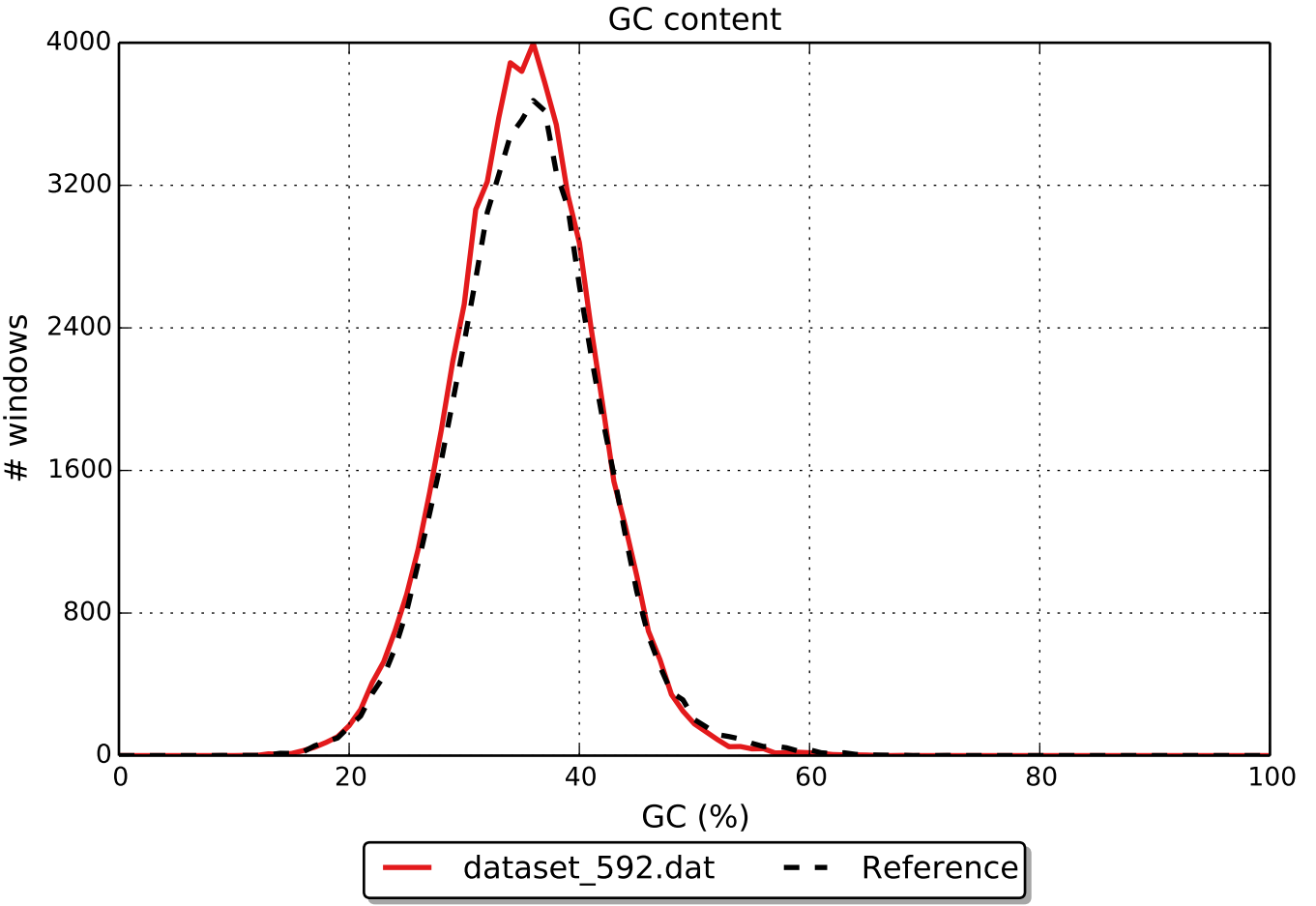
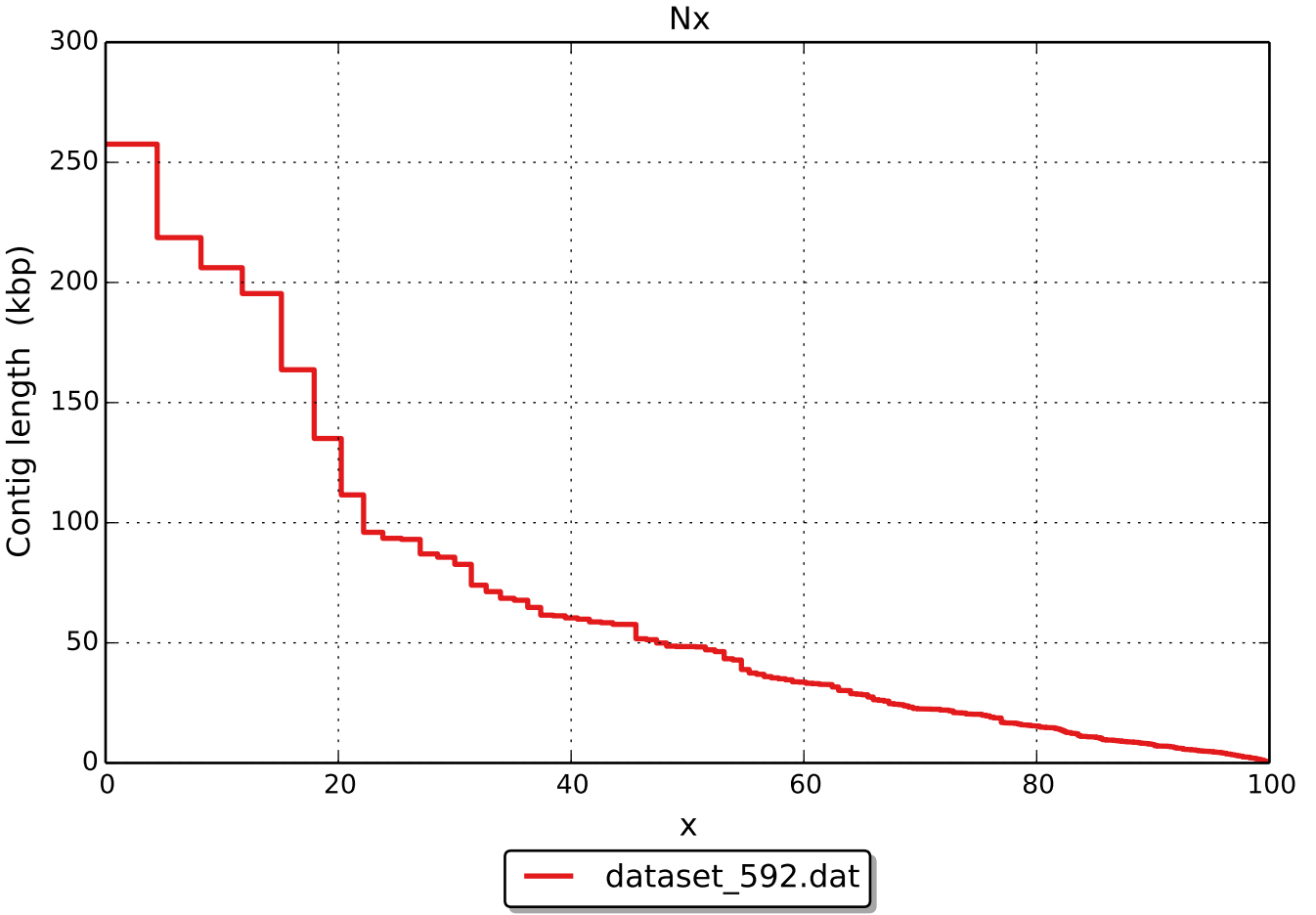
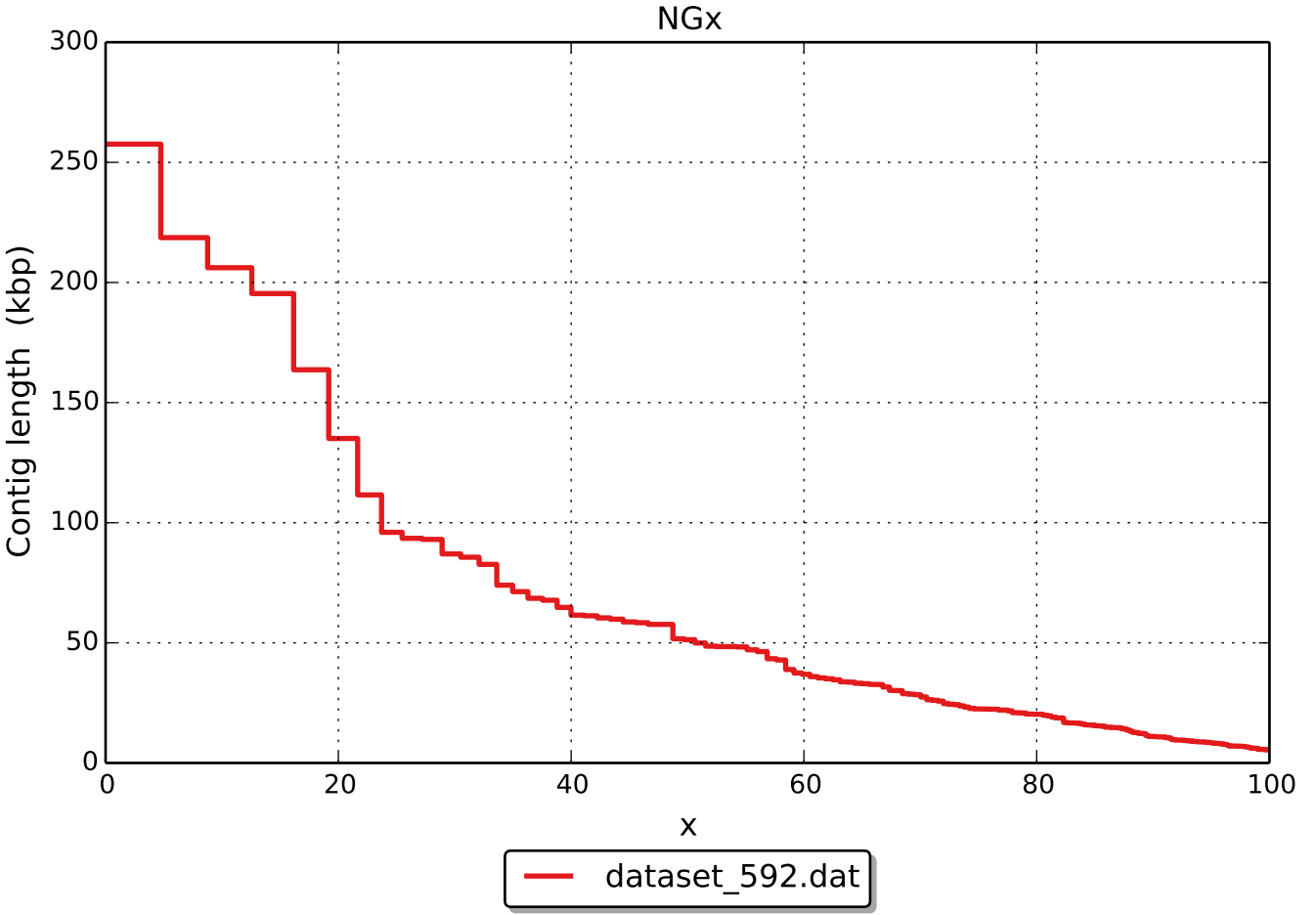
Combined_reference

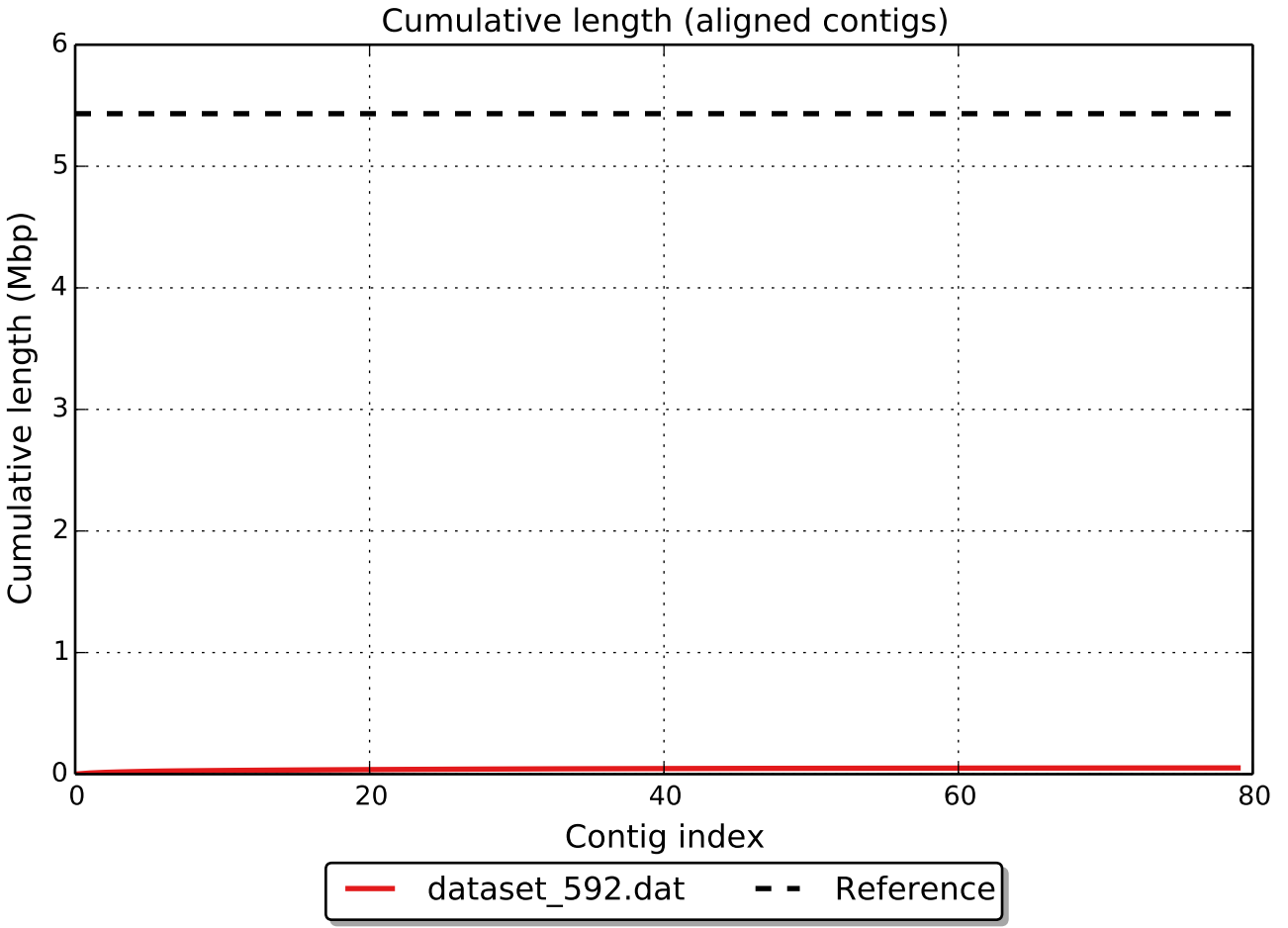
B_cereus_ATCC_1098

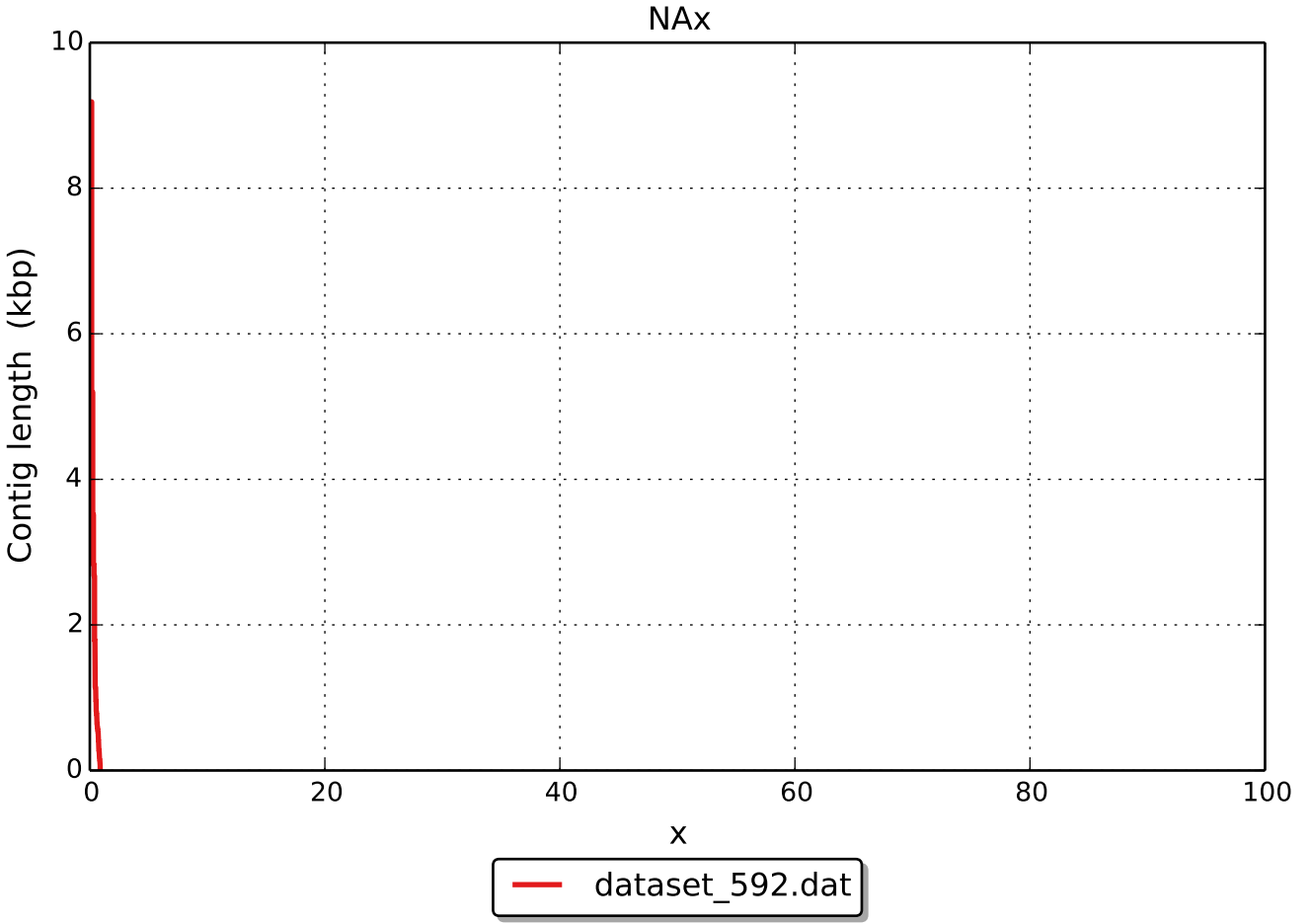

Cumulative length
Cumulative length (Mbp)
0
1
2
3
4
5
6
0
60
120
180
240
300
Contig index
dataset_592.dat
Reference

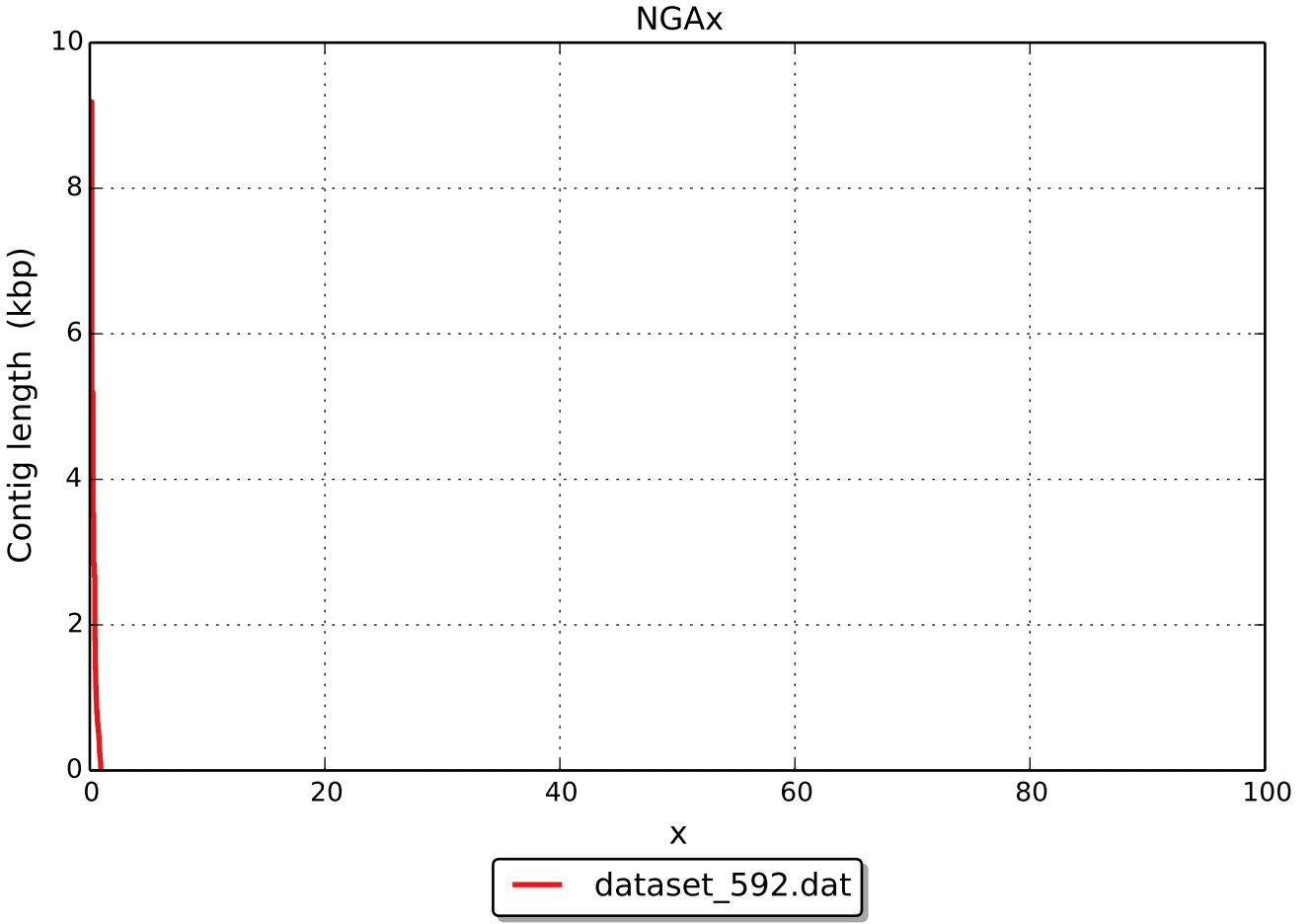

GC content
4000
3200
2400
1600
800
0
windows
0
20
40
60
80
100
GC (%)
dataset_592.dat
Reference

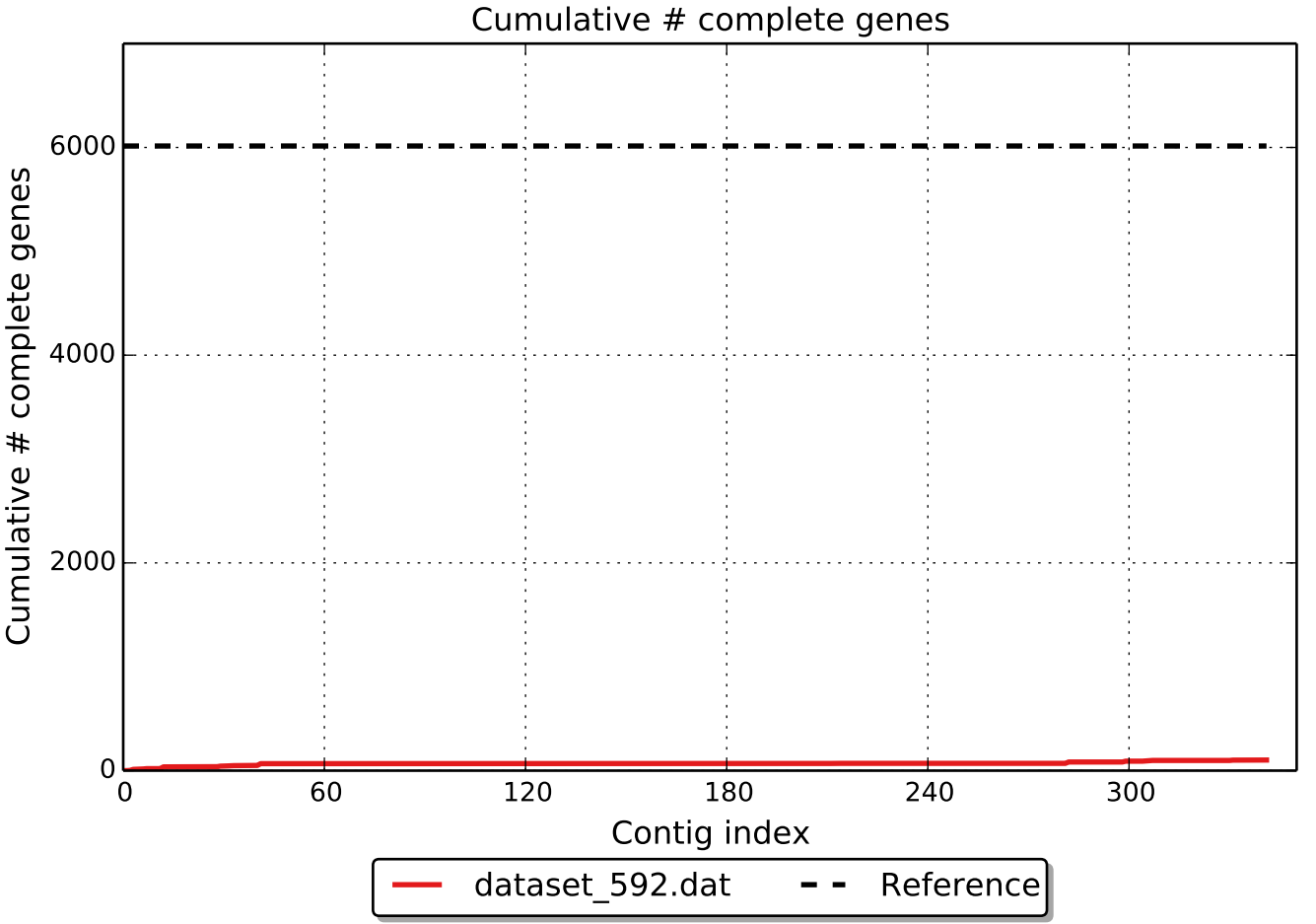

Nx
Contig length (kbp)
300
250
200
150
100
50
0
0
20
40
60
80
100
x
dataset_592.dat

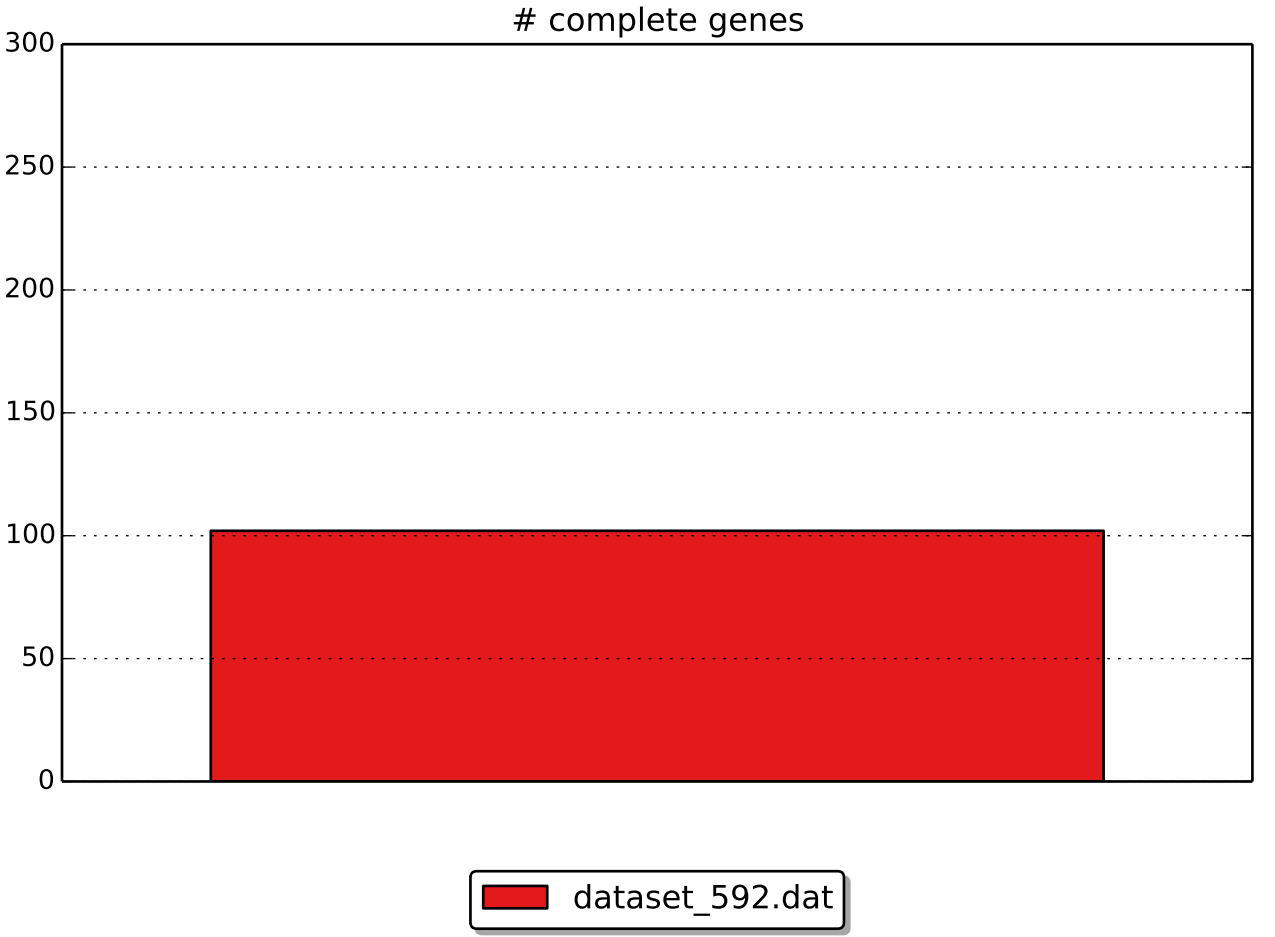

NGx
300
250
200
150
100
50
0
Contig length (kbp)
0
20
40
60
80
100
x
dataset_592.dat

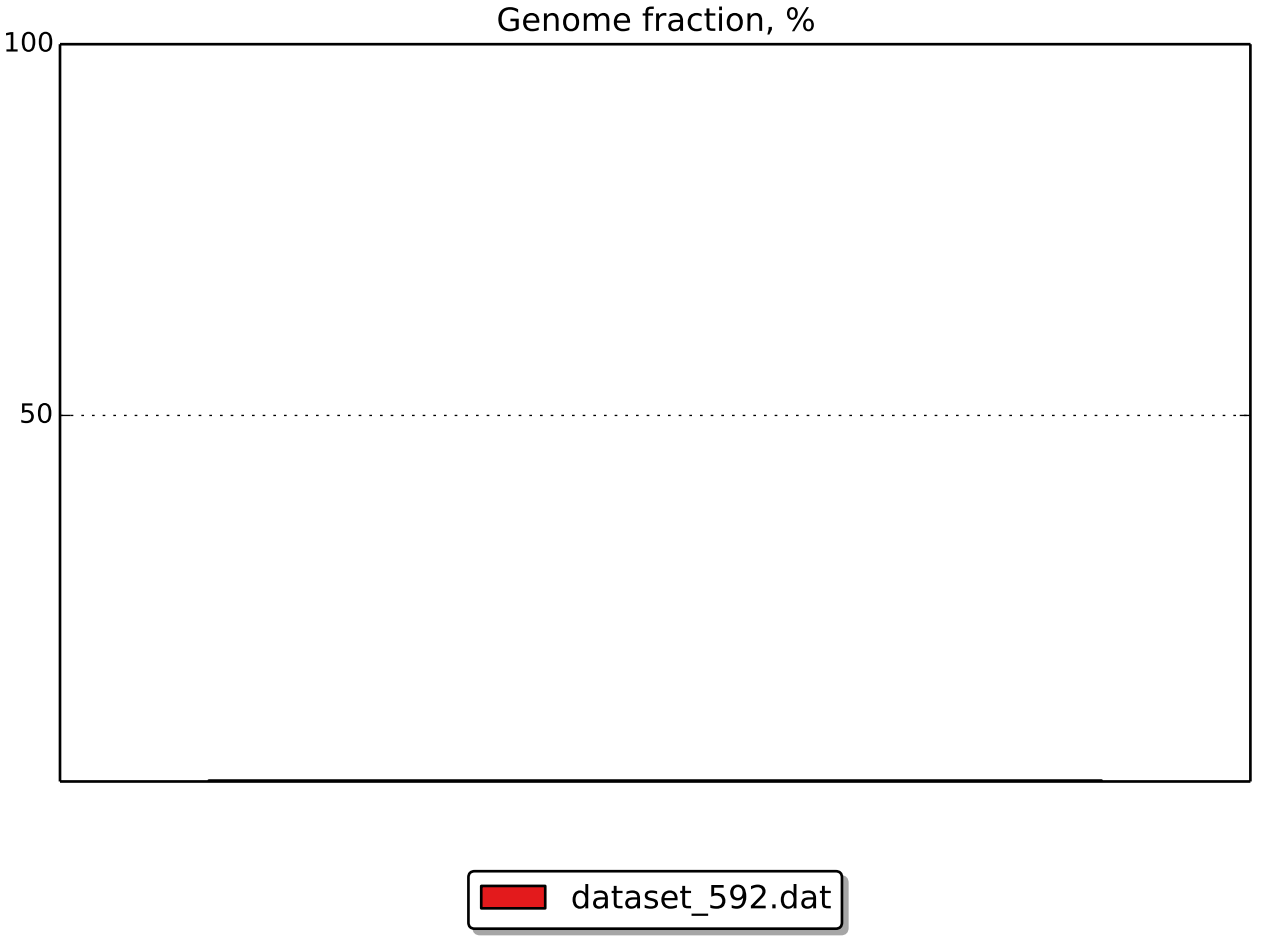

Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
1
2
3
4
5
6
0
20
40
60
80
Contig index
dataset_592.dat
Reference


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

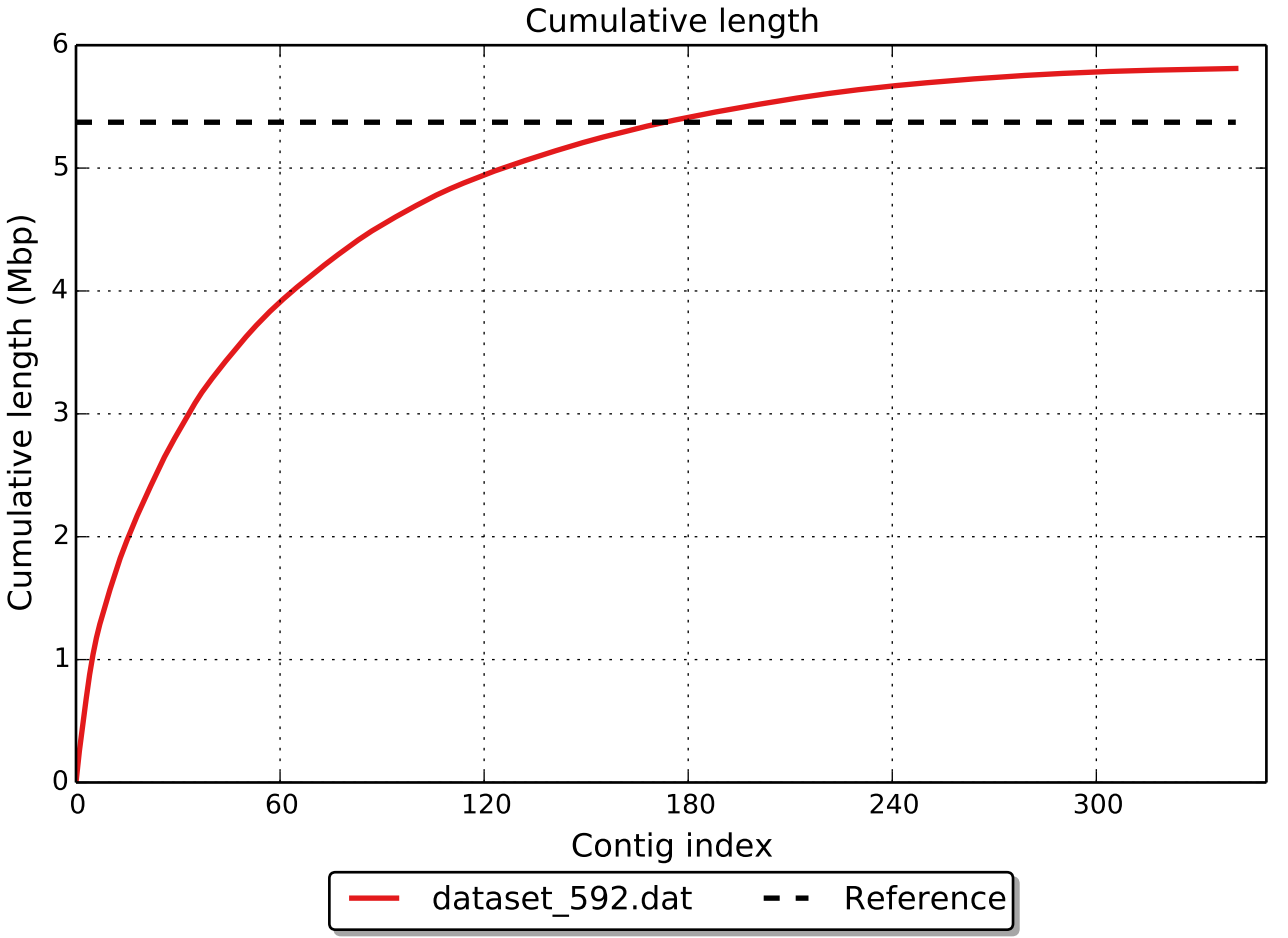

NGAx
Contig length (kbp)
10
8
6
4
2
0
0
20
40
60
80
100
x
dataset_592.dat

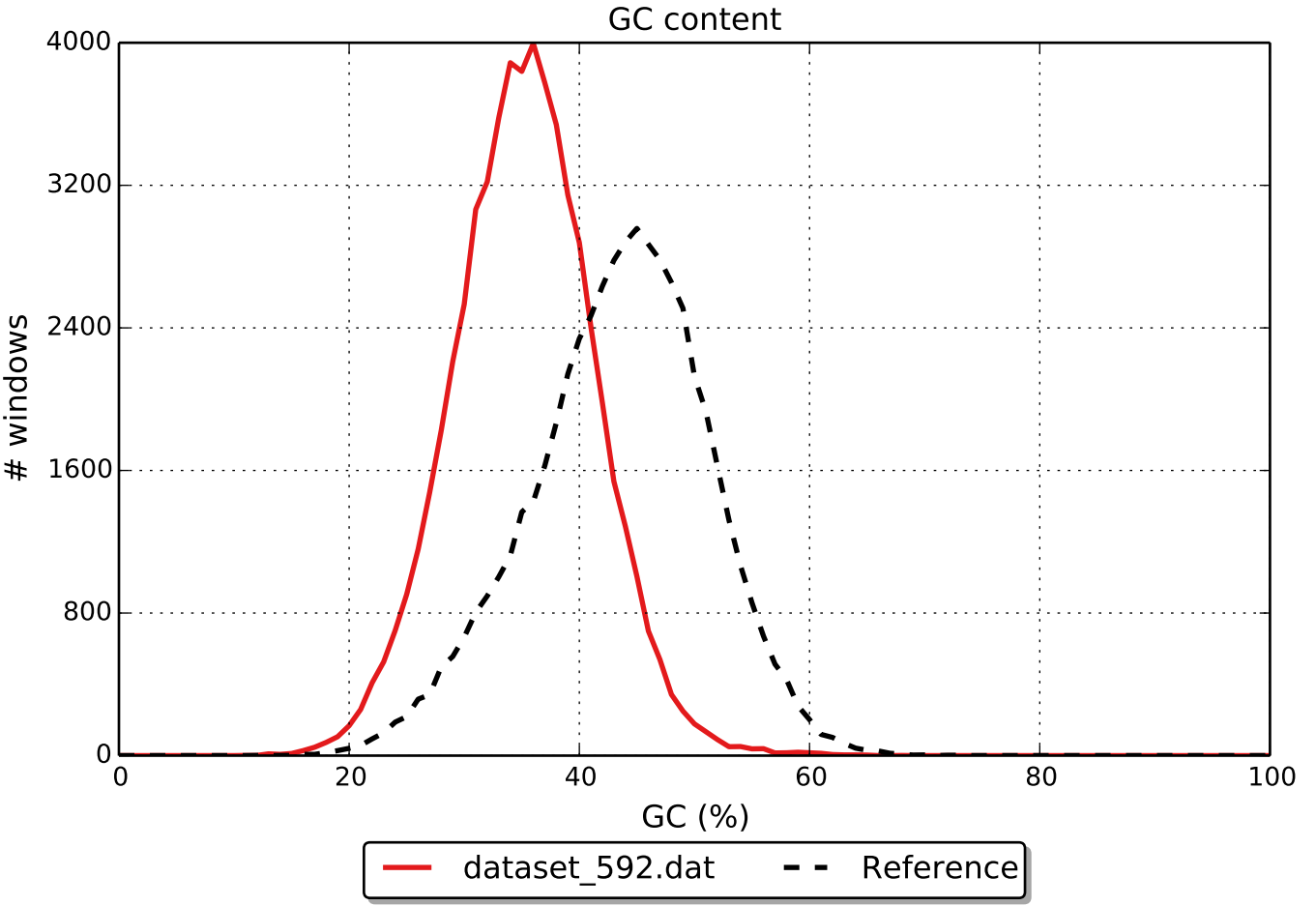

Cumulative # complete genes
Cumulative # complete genes
6000
4000
2000
0
0
60
120
180
240
300
Contig index
dataset_592.dat
Reference

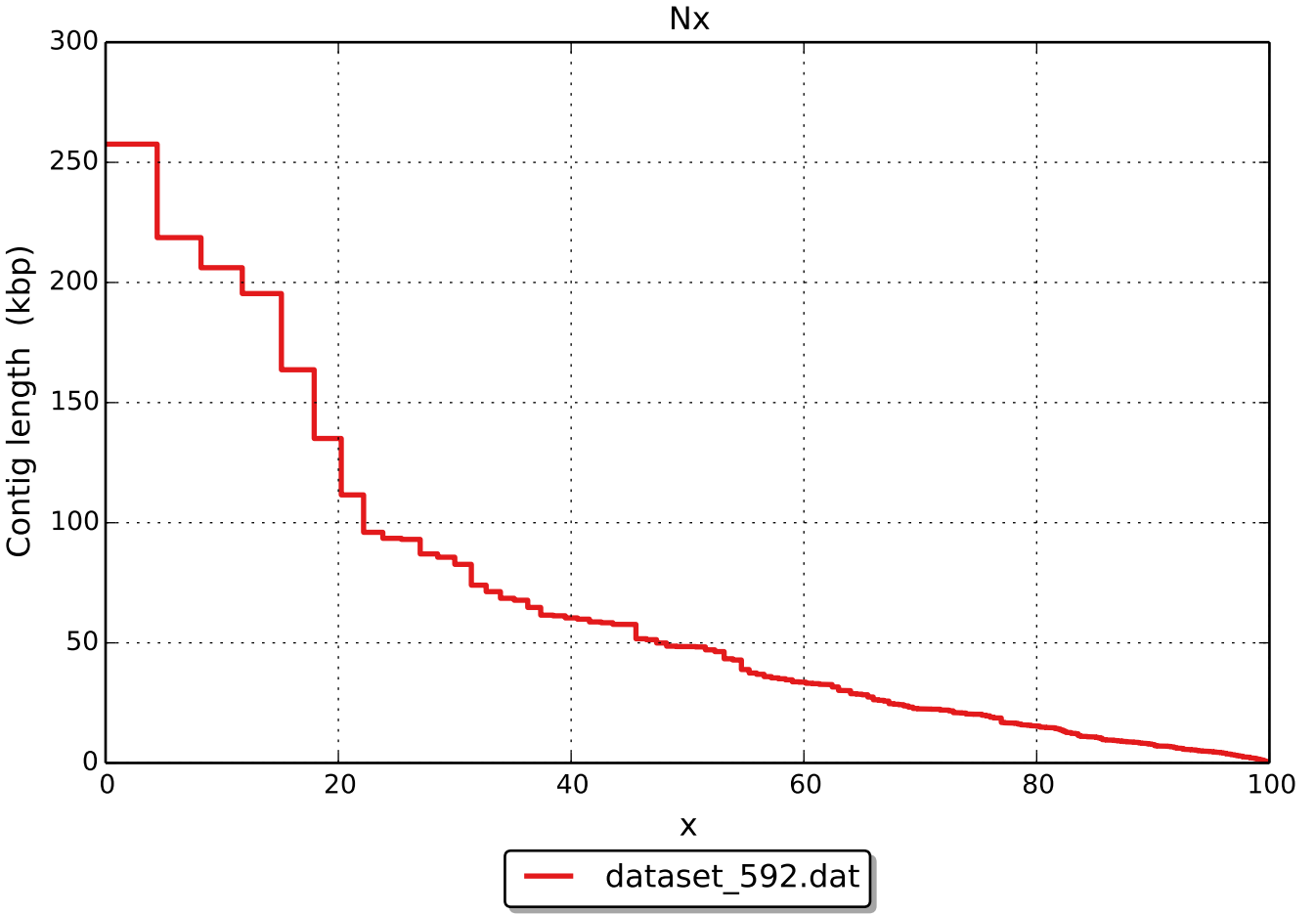

complete genes
300
250
200
150
100
50
0
dataset_592.dat

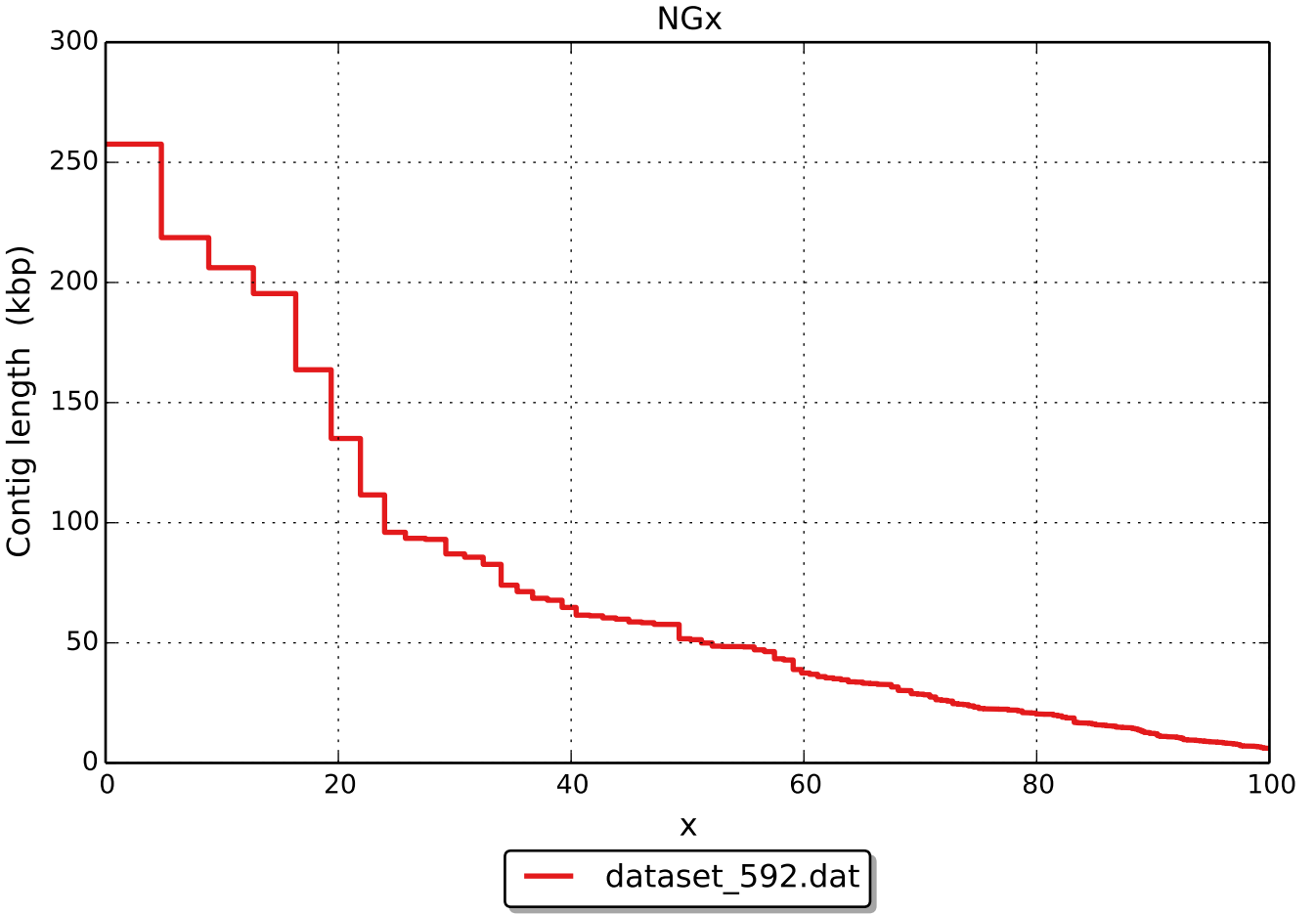

Genome fraction, %
100
50
dataset_592.dat

B_fragilis_638R

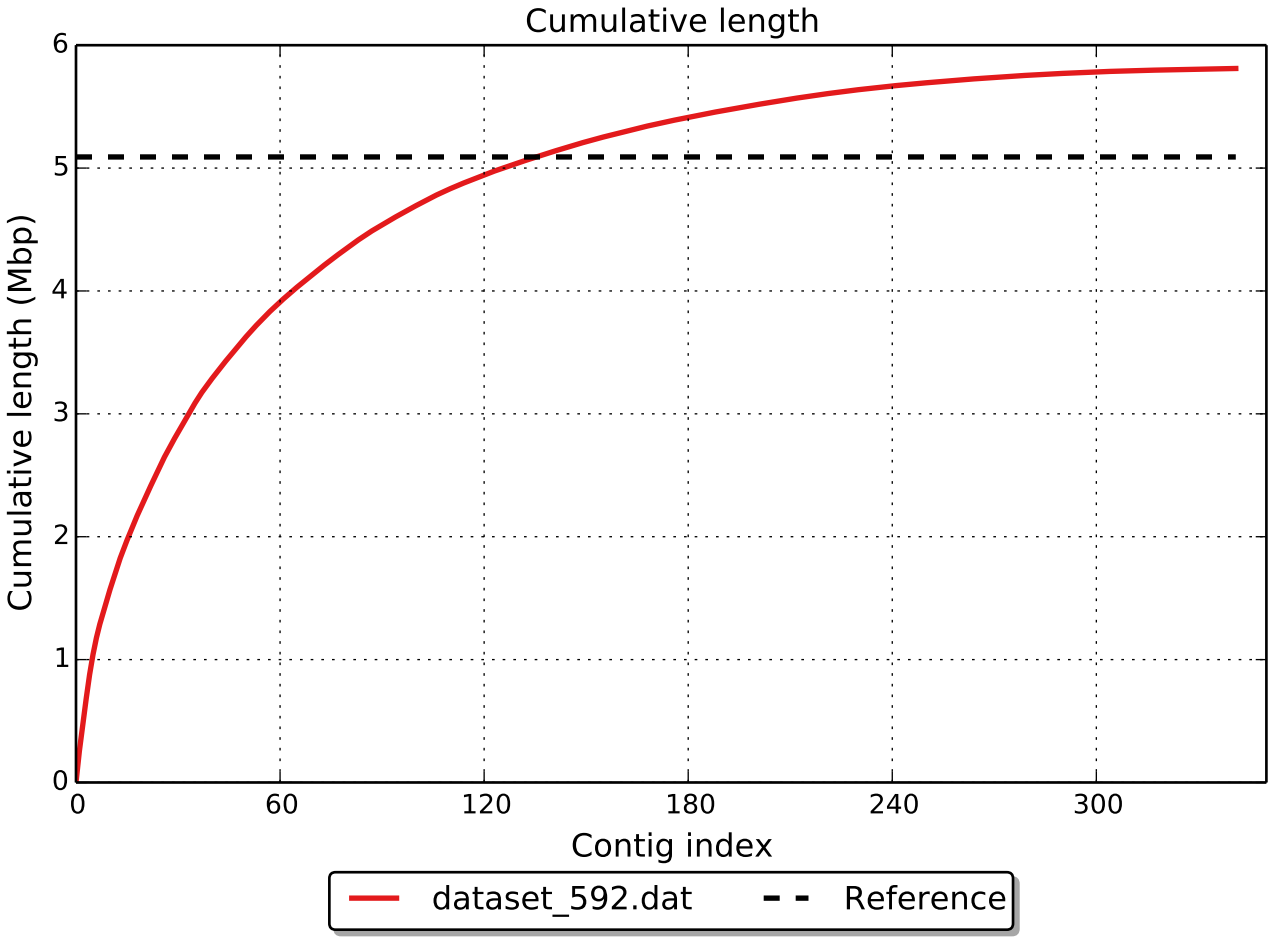

Cumulative length
Cumulative length (Mbp)
0
1
2
3
4
5
6
0
60
120
180
240
300
Contig index
dataset_592.dat
Reference

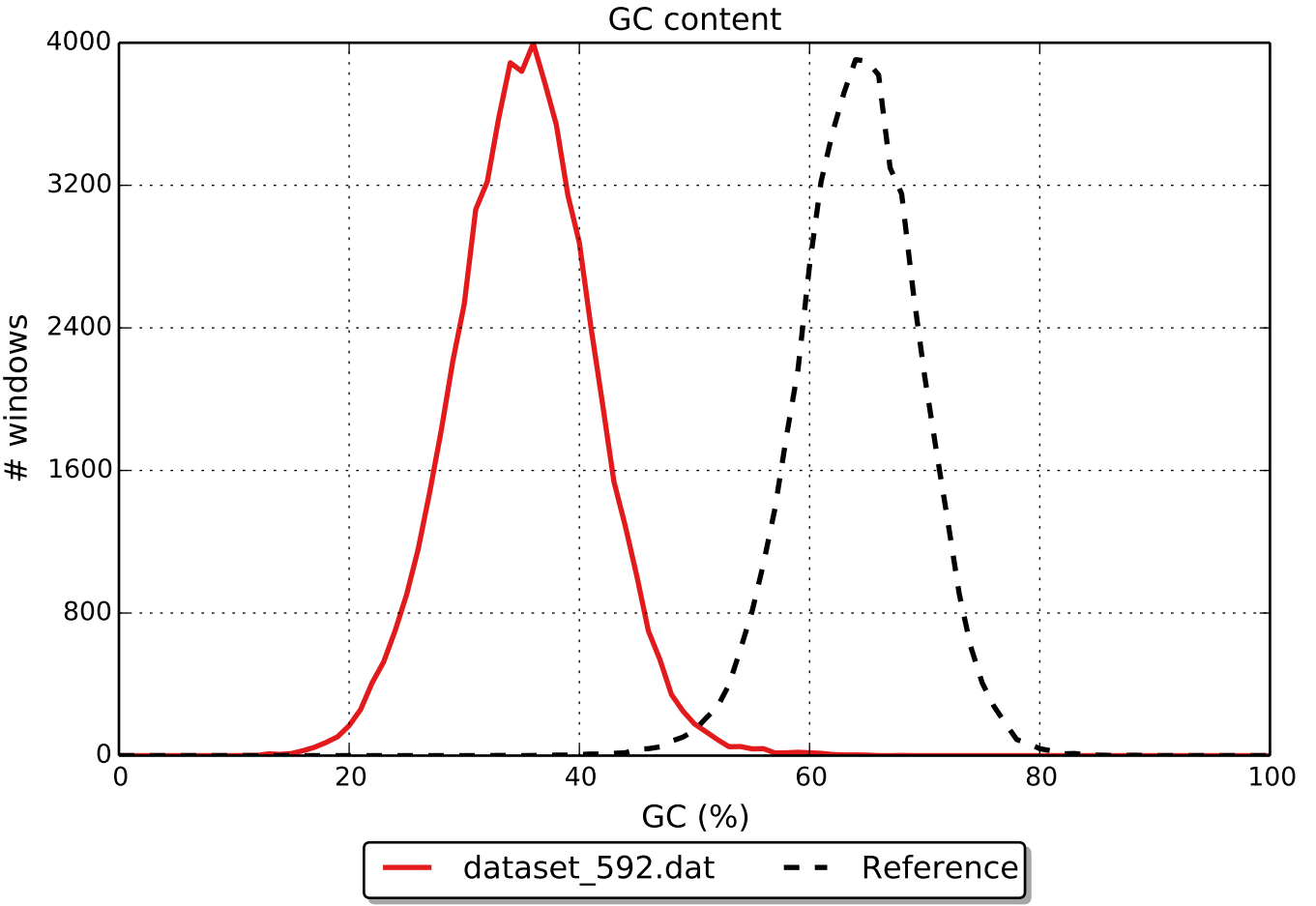

GC content
4000
3200
2400
1600
800
0
windows
0
20
40
60
80
100
GC (%)
dataset_592.dat
Reference

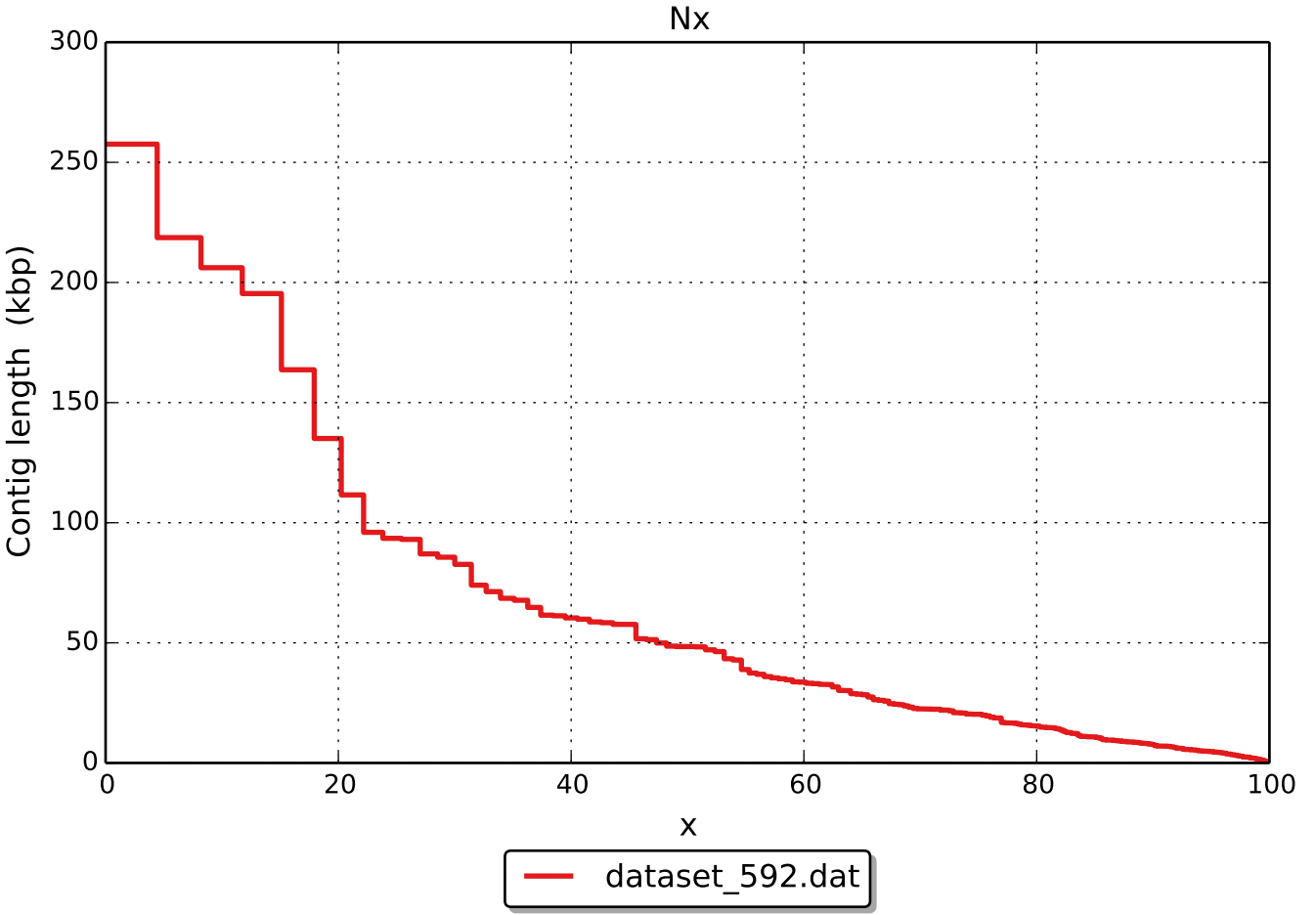

Nx
Contig length (kbp)
300
250
200
150
100
50
0
0
20
40
60
80
100
x
dataset_592.dat

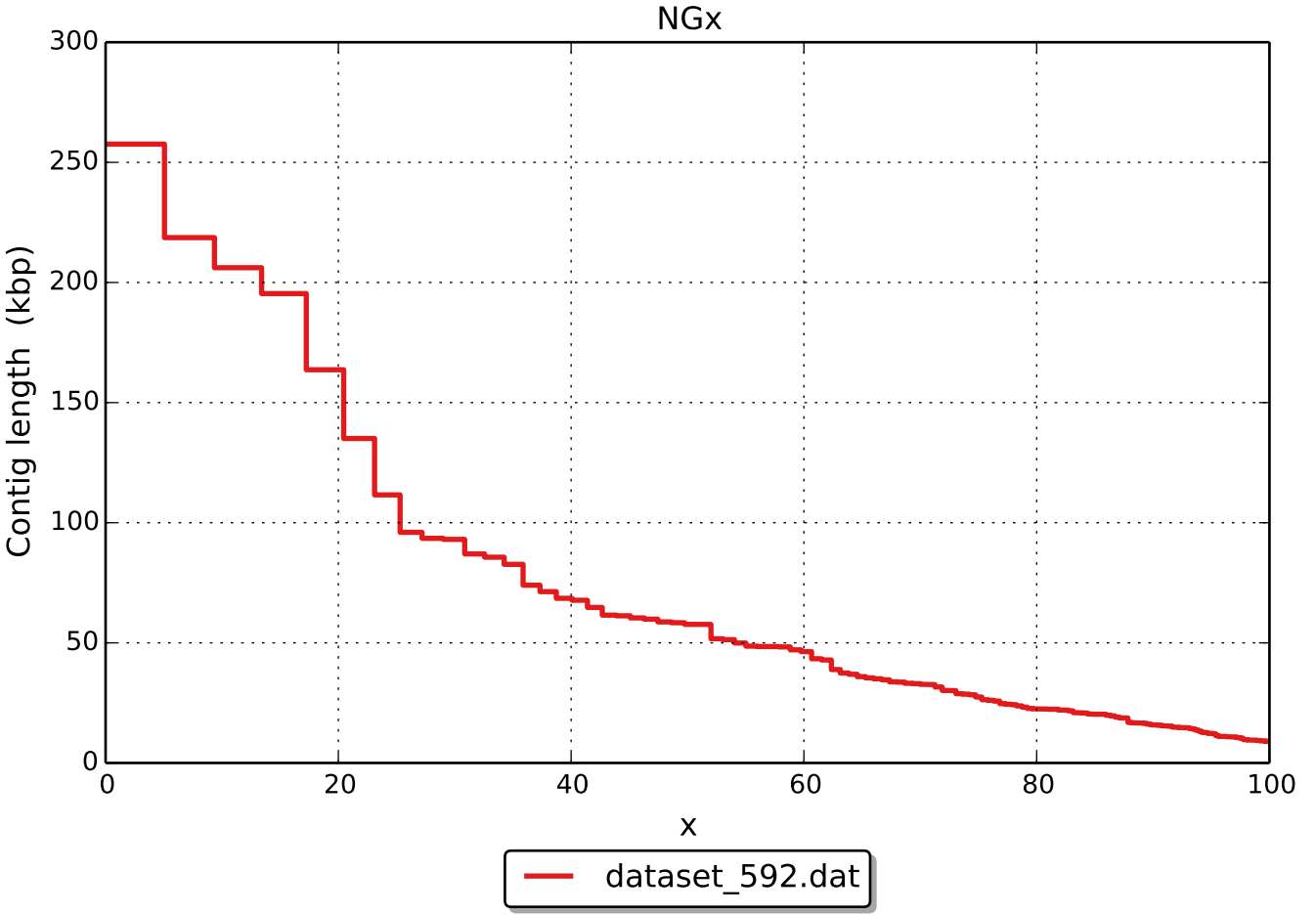

NGx
300
250
200
150
100
50
0
Contig length (kbp)
0
20
40
60
80
100
x
dataset_592.dat

M_abscessus_ATCC_19977


Cumulative length
Cumulative length (Mbp)
0
1
2
3
4
5
6
0
60
120
180
240
300
Contig index
dataset_592.dat
Reference


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

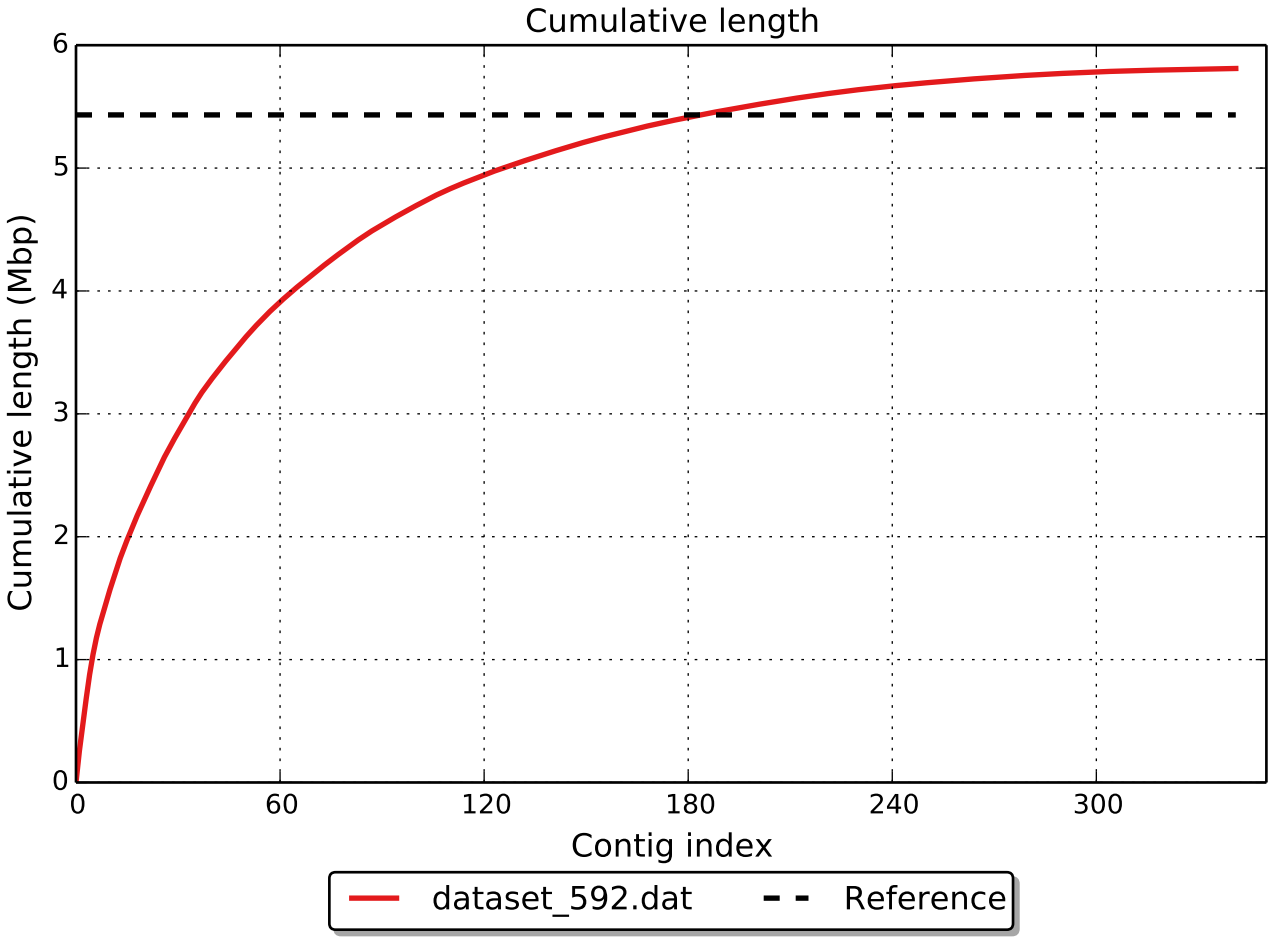

Nx
Contig length (kbp)
300
250
200
150
100
50
0
0
20
40
60
80
100
x
dataset_592.dat

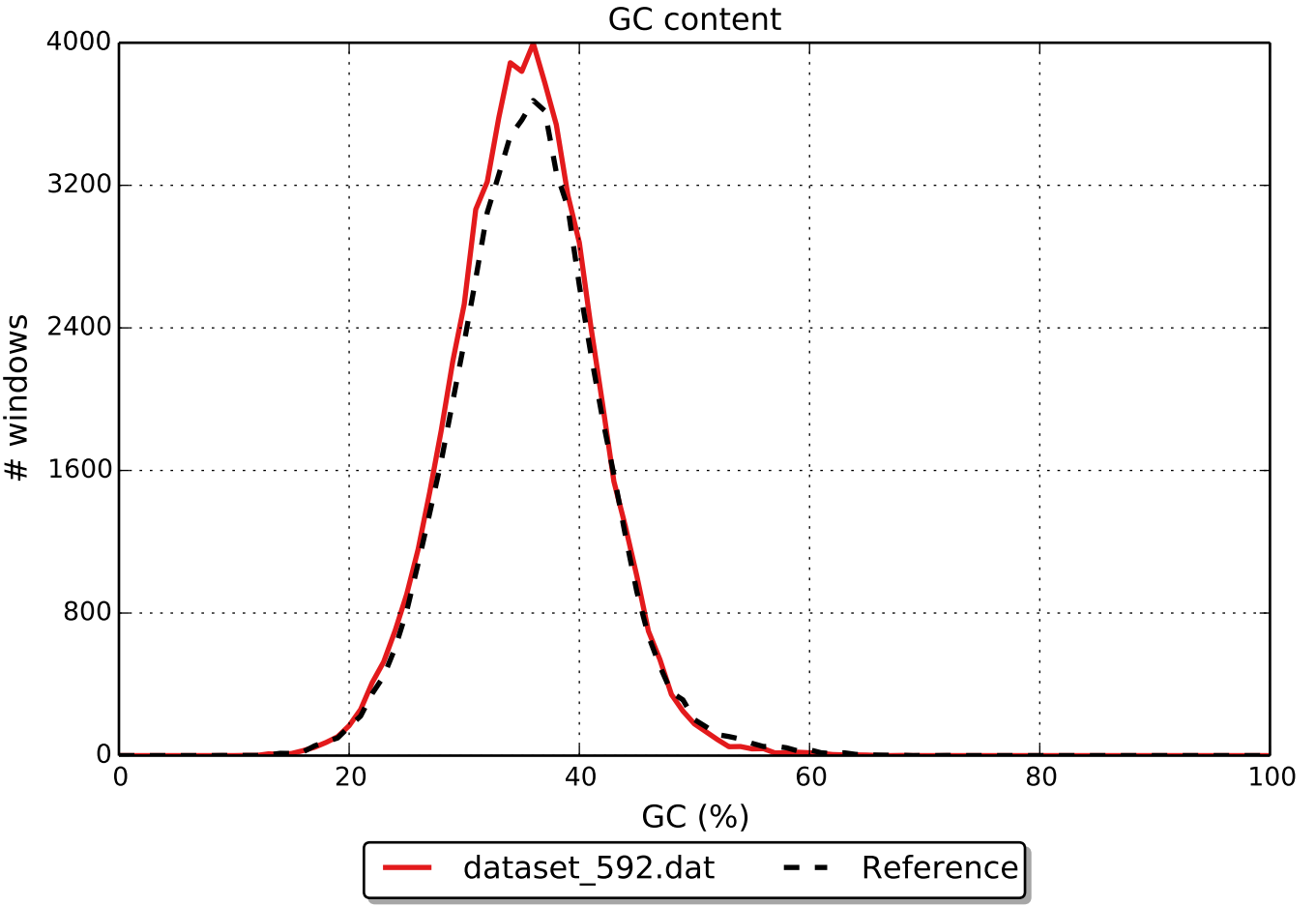

NGx
300
250
200
150
100
50
0
Contig length (kbp)
0
20
40
60
80
100
x
dataset_592.dat

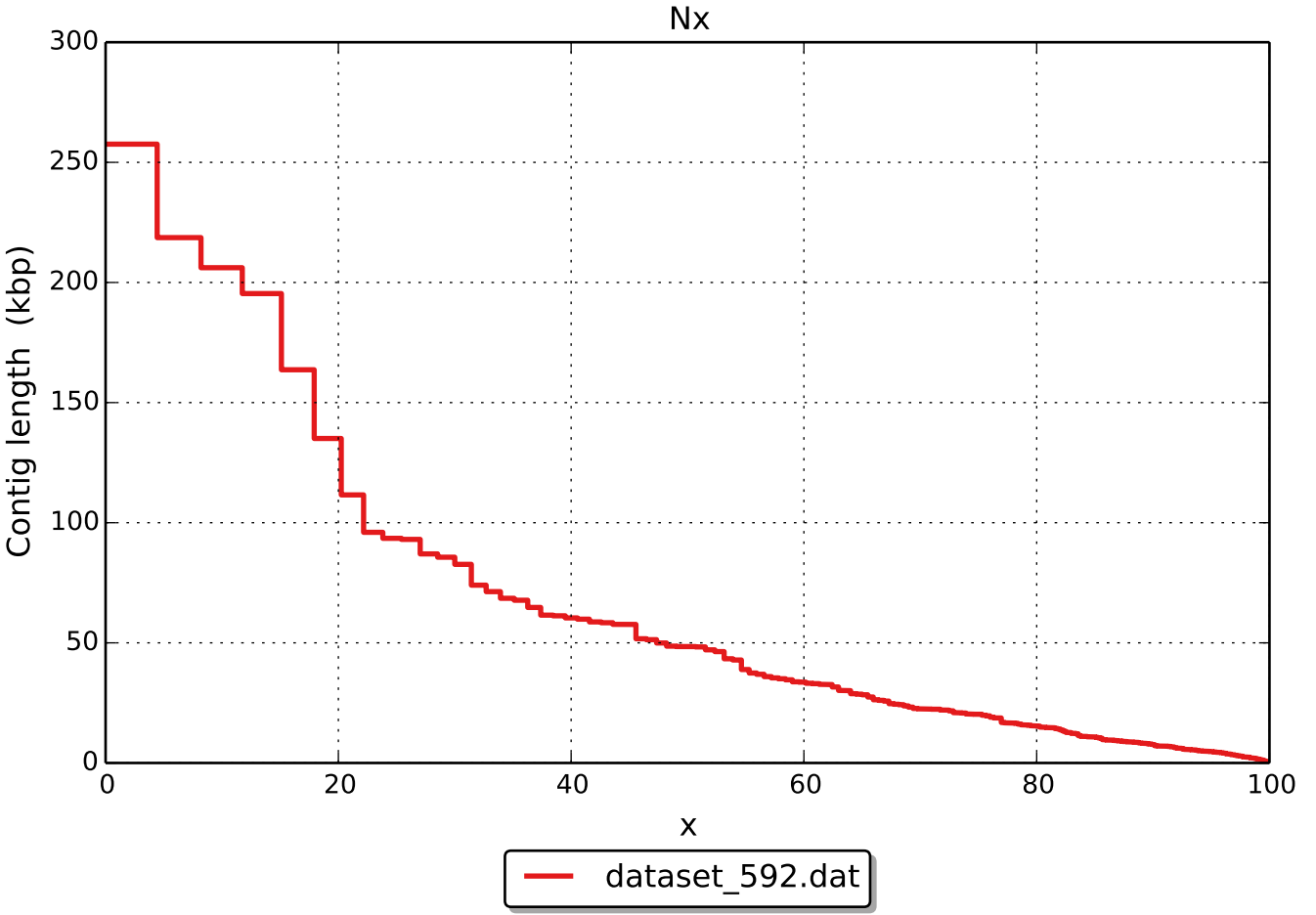
Combined_history

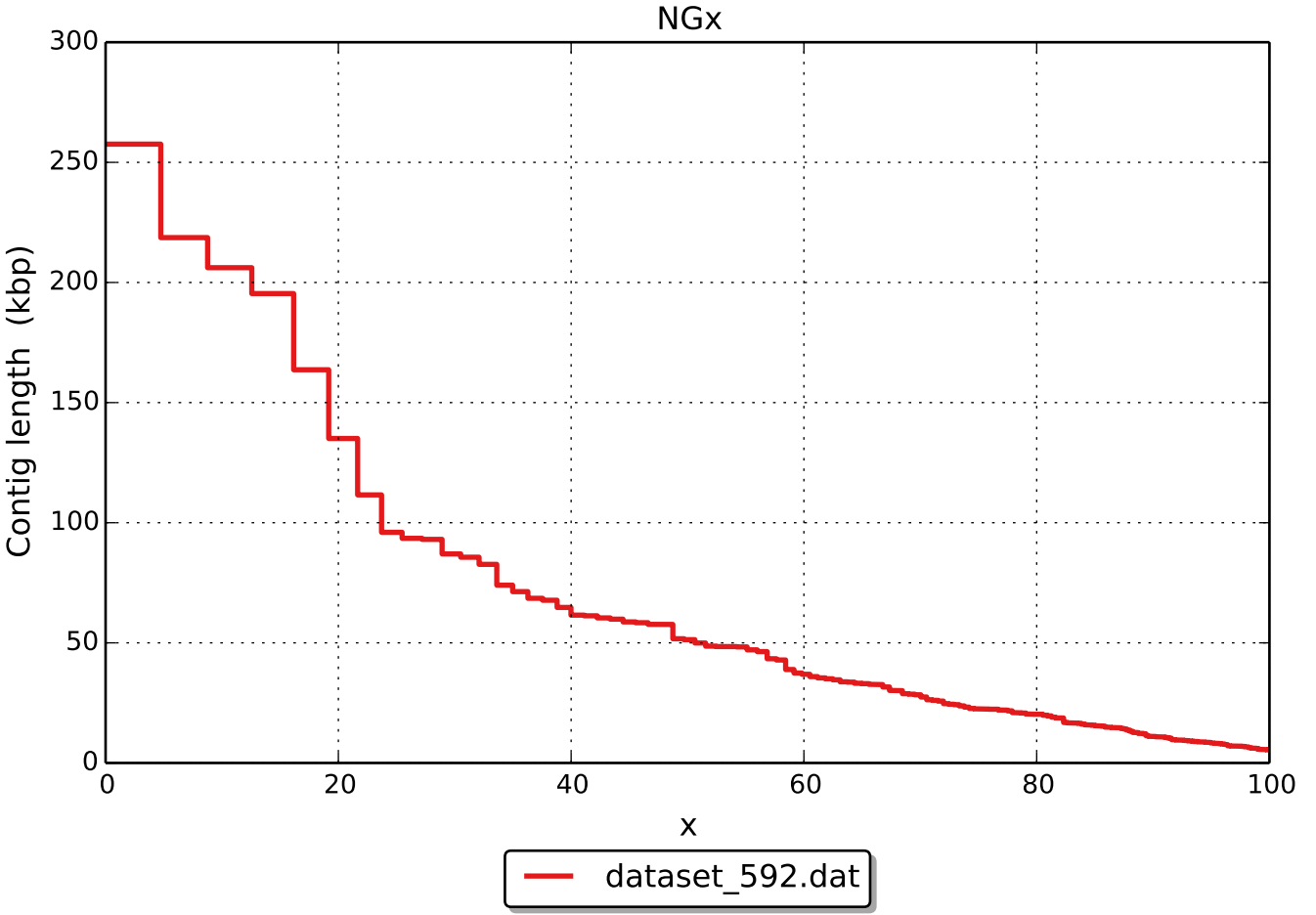
Combined_reference

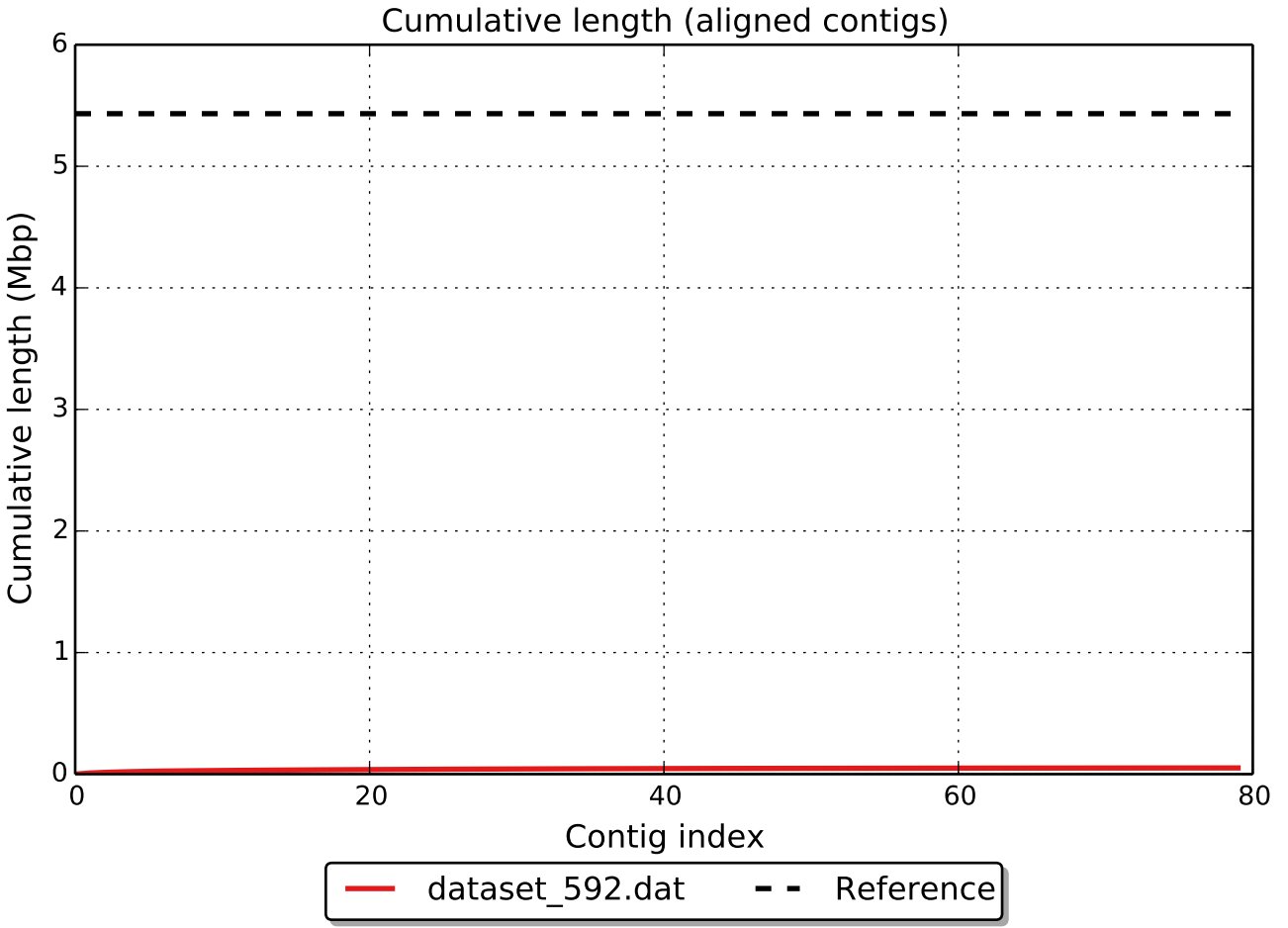
B_cereus_ATCC_1098

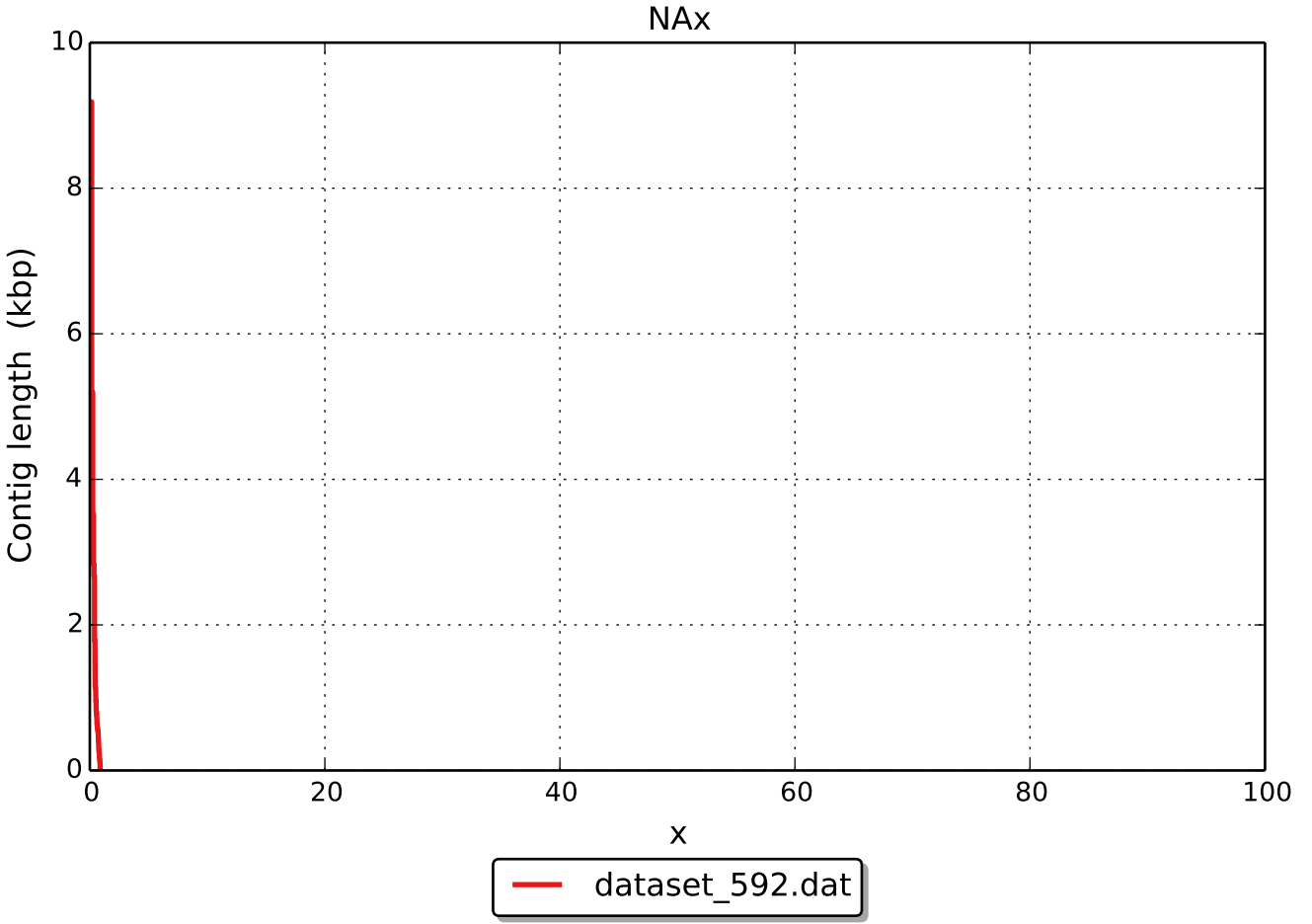

Cumulative length
Cumulative length (Mbp)
0
1
2
3
4
5
6
0
60
120
180
240
300
Contig index
dataset_592.dat
Reference

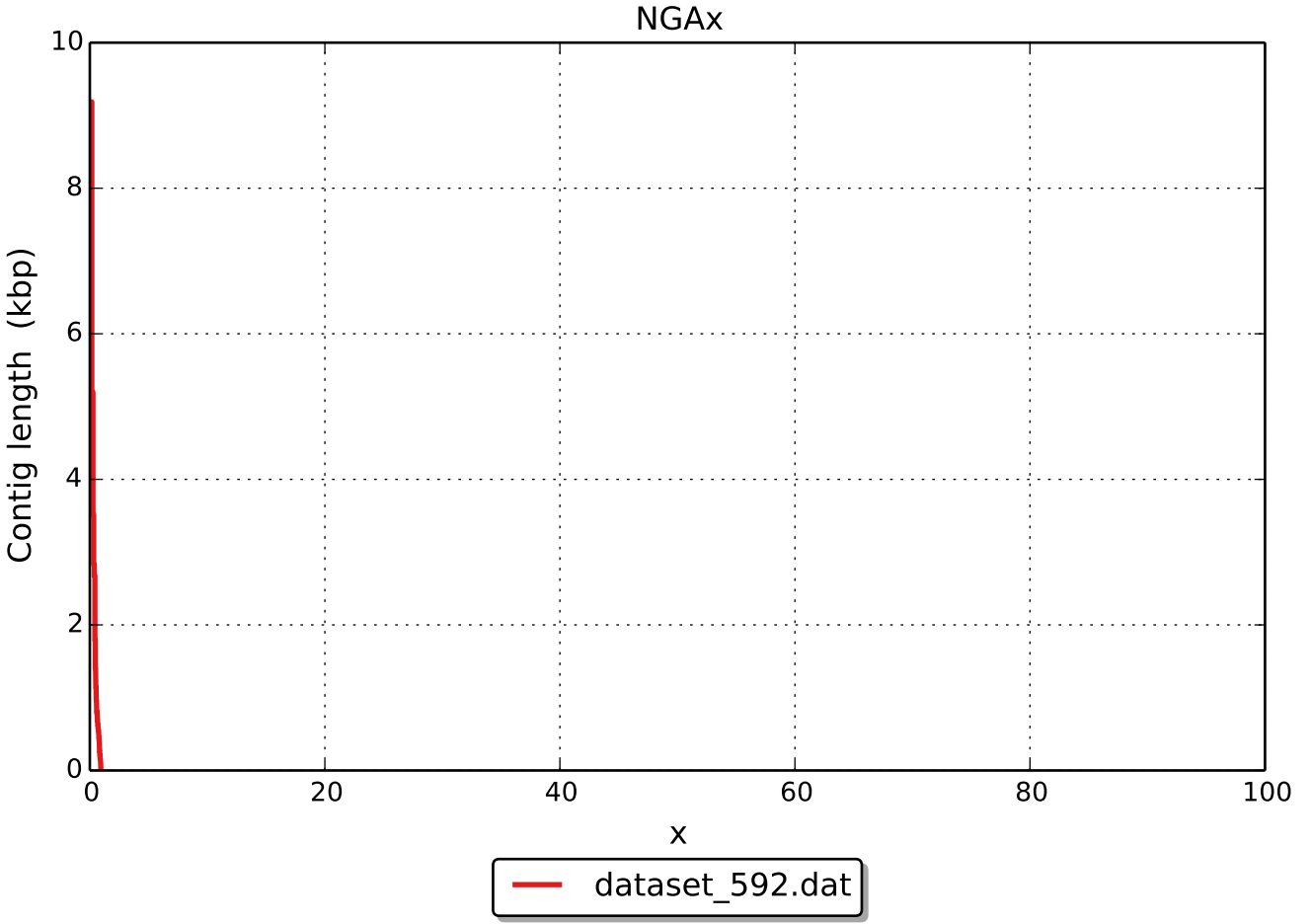

GC content
4000
3200
2400
1600
800
0
windows
0
20
40
60
80
100
GC (%)
dataset_592.dat
Reference

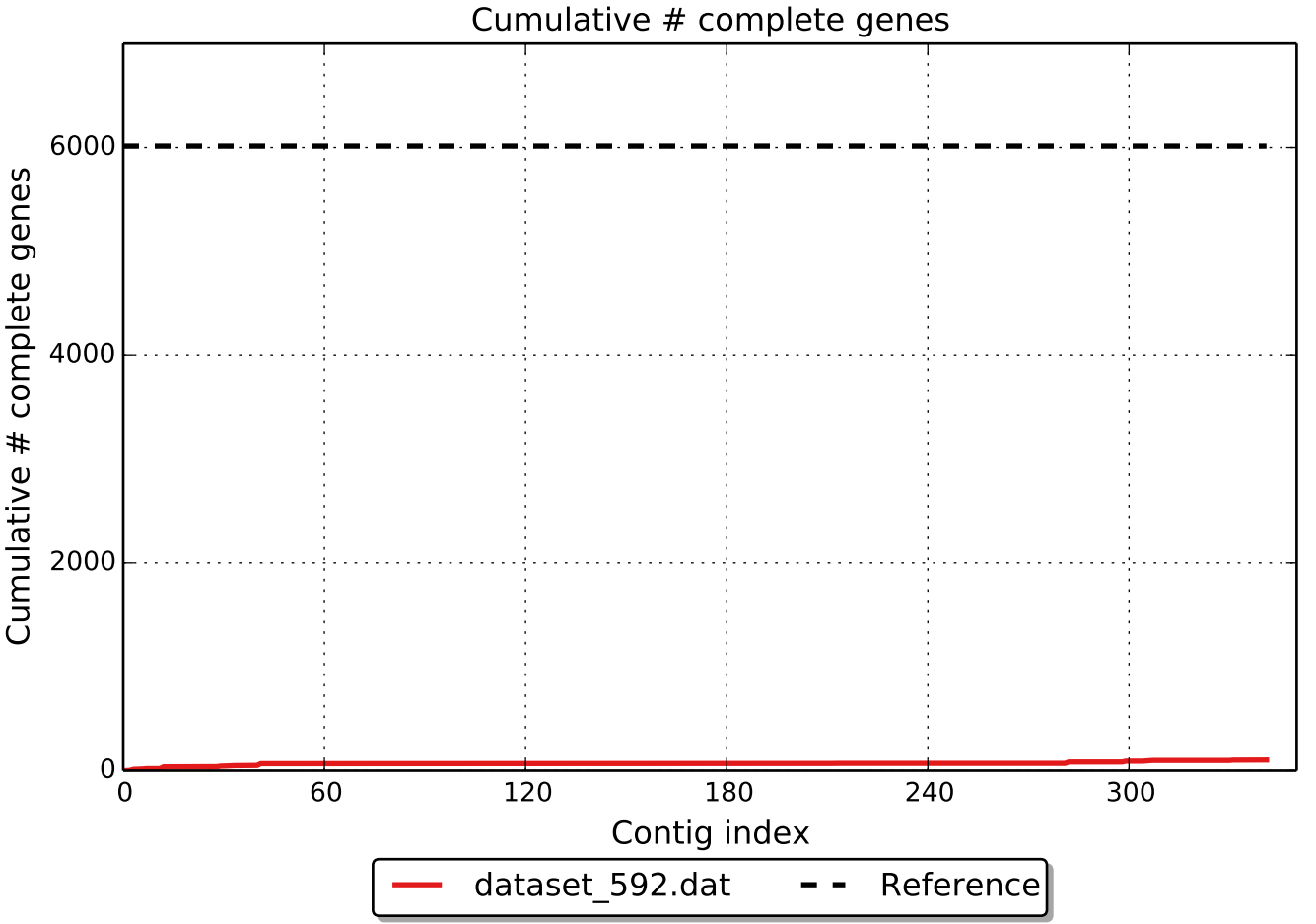

Nx
Contig length (kbp)
300
250
200
150
100
50
0
0
20
40
60
80
100
x
dataset_592.dat

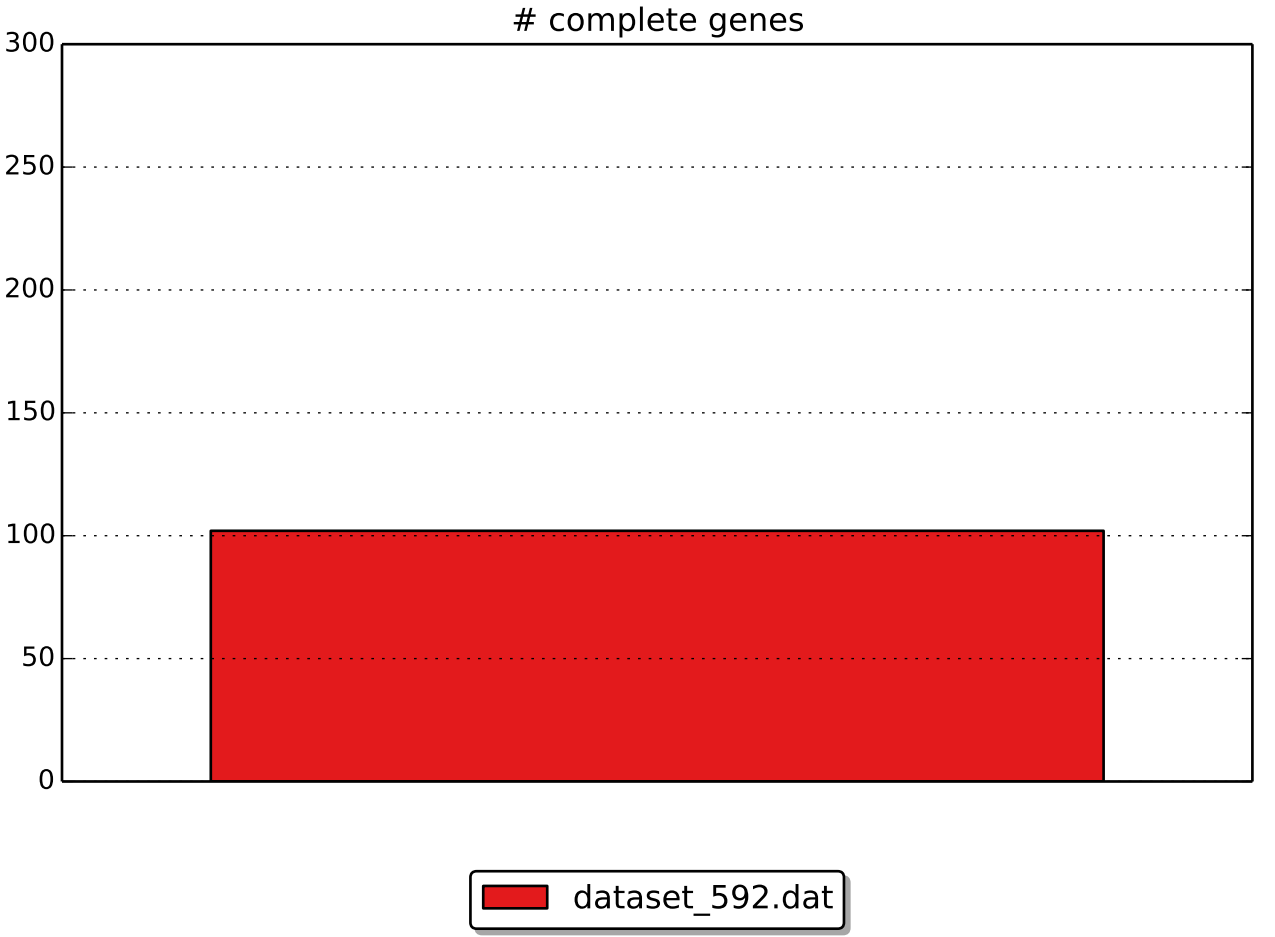

NGx
300
250
200
150
100
50
0
Contig length (kbp)
0
20
40
60
80
100
x
dataset_592.dat

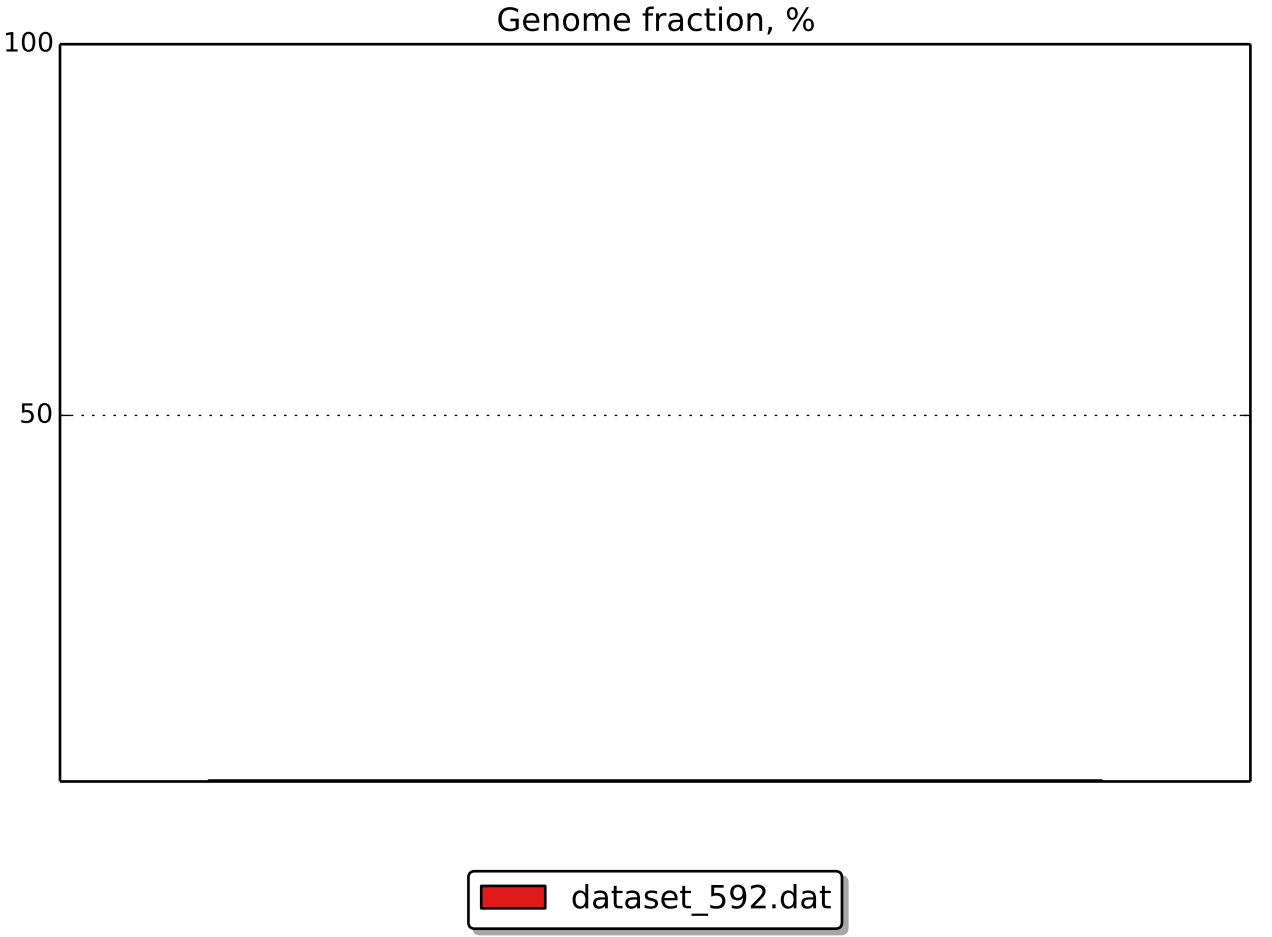

Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
1
2
3
4
5
6
0
20
40
60
80
Contig index
dataset_592.dat
Reference


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

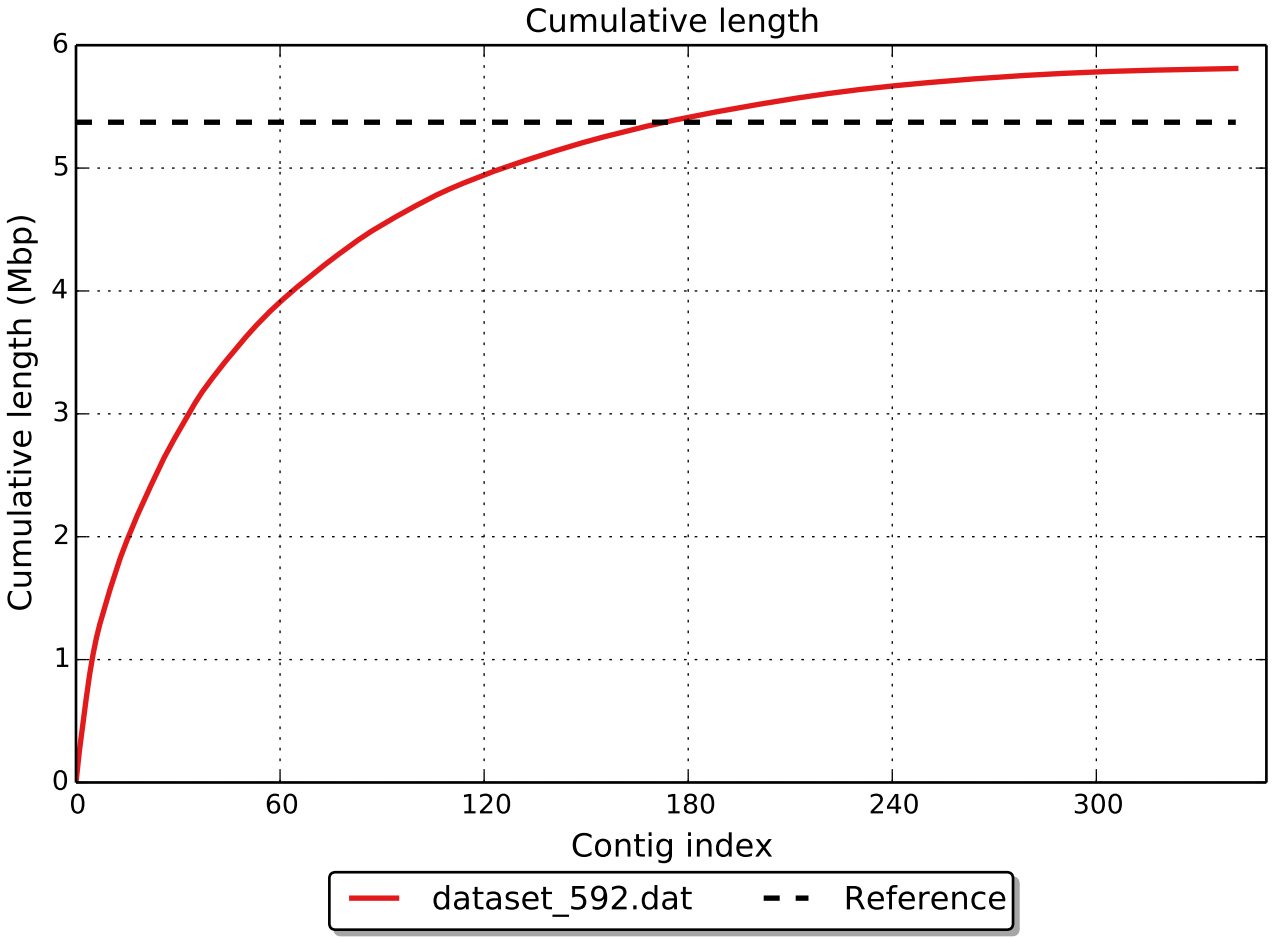

NGAx
Contig length (kbp)
10
8
6
4
2
0
0
20
40
60
80
100
x
dataset_592.dat

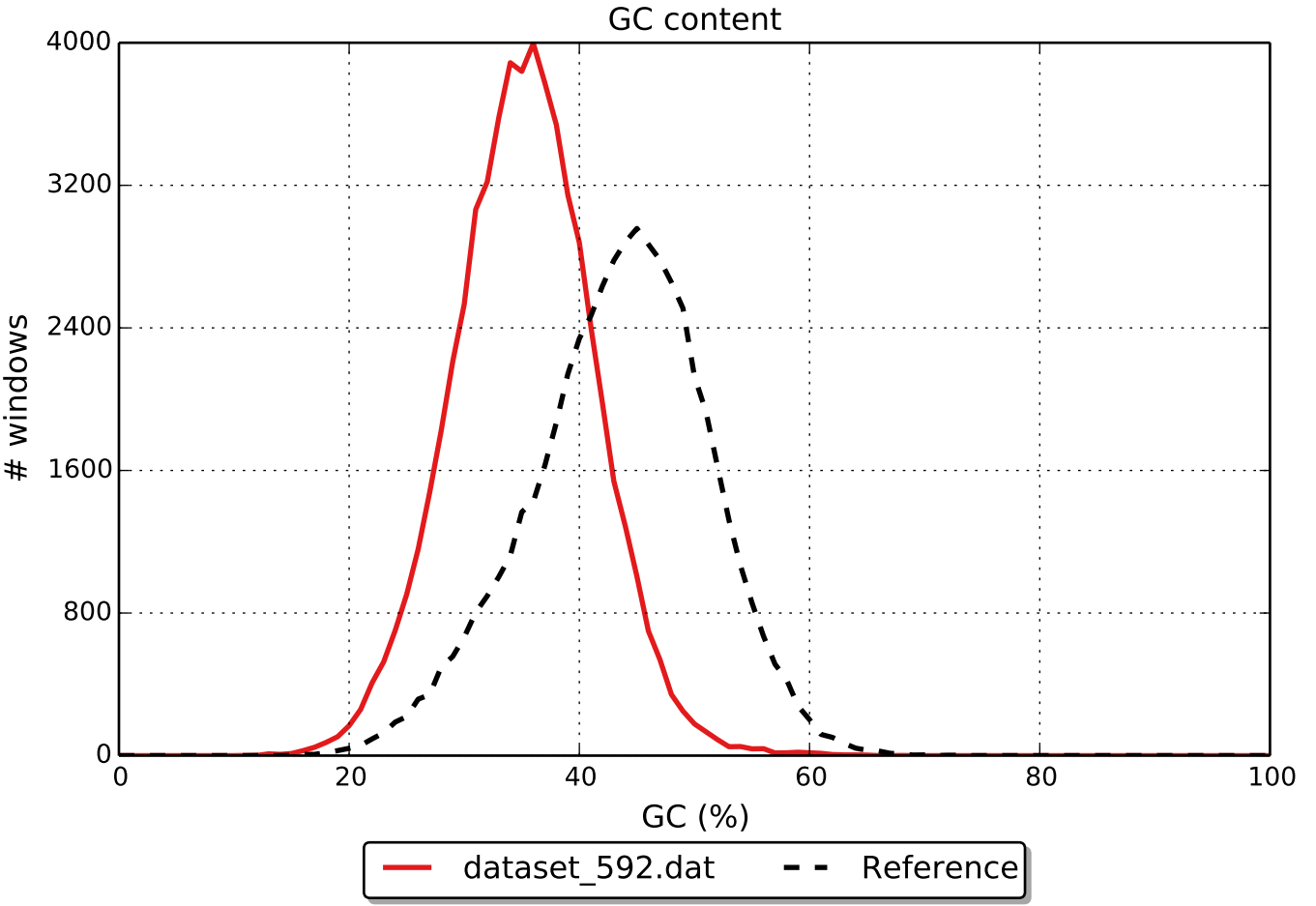

Cumulative # complete genes
Cumulative # complete genes
6000
4000
2000
0
0
60
120
180
240
300
Contig index
dataset_592.dat
Reference

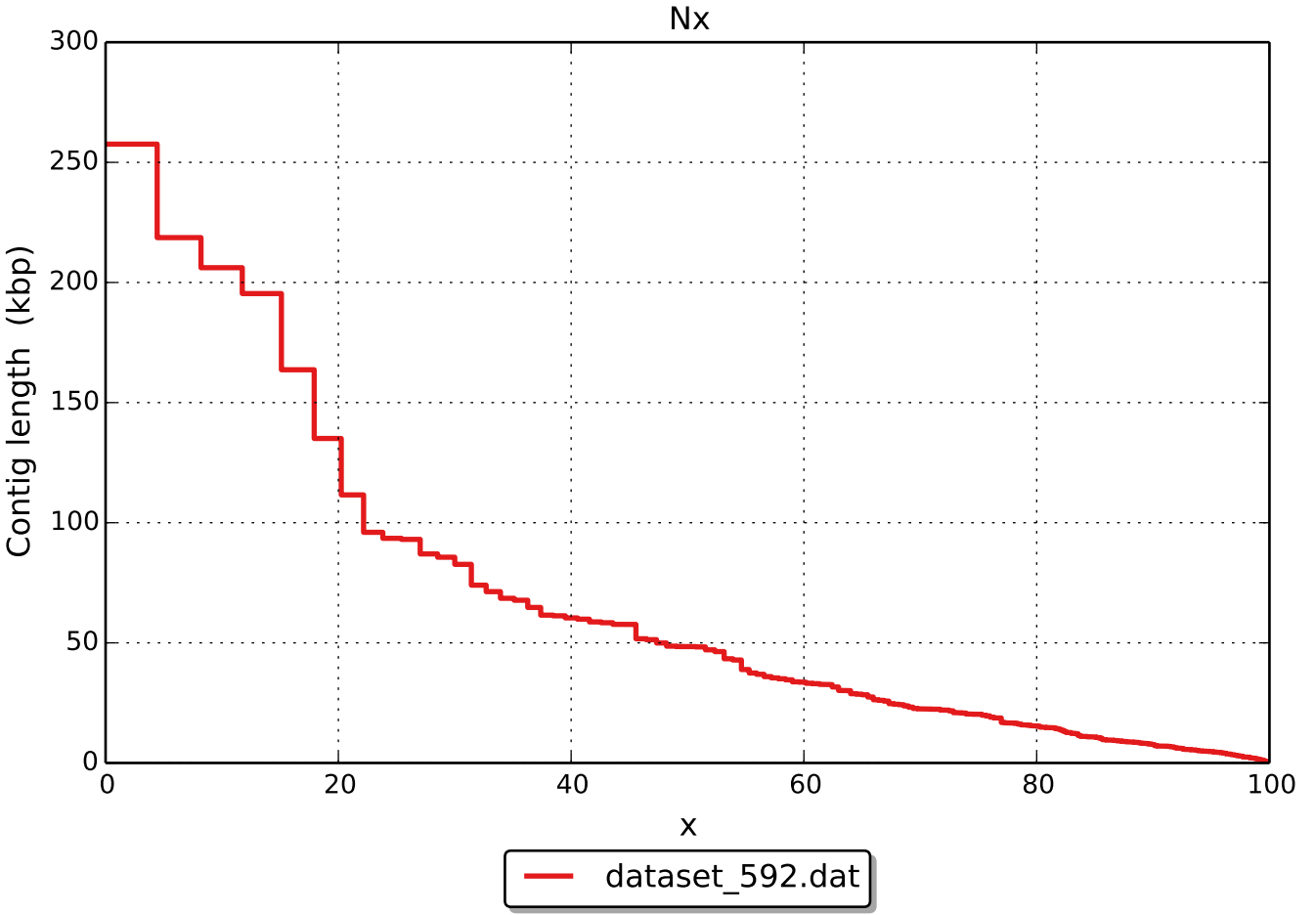

complete genes
300
250
200
150
100
50
0
dataset_592.dat

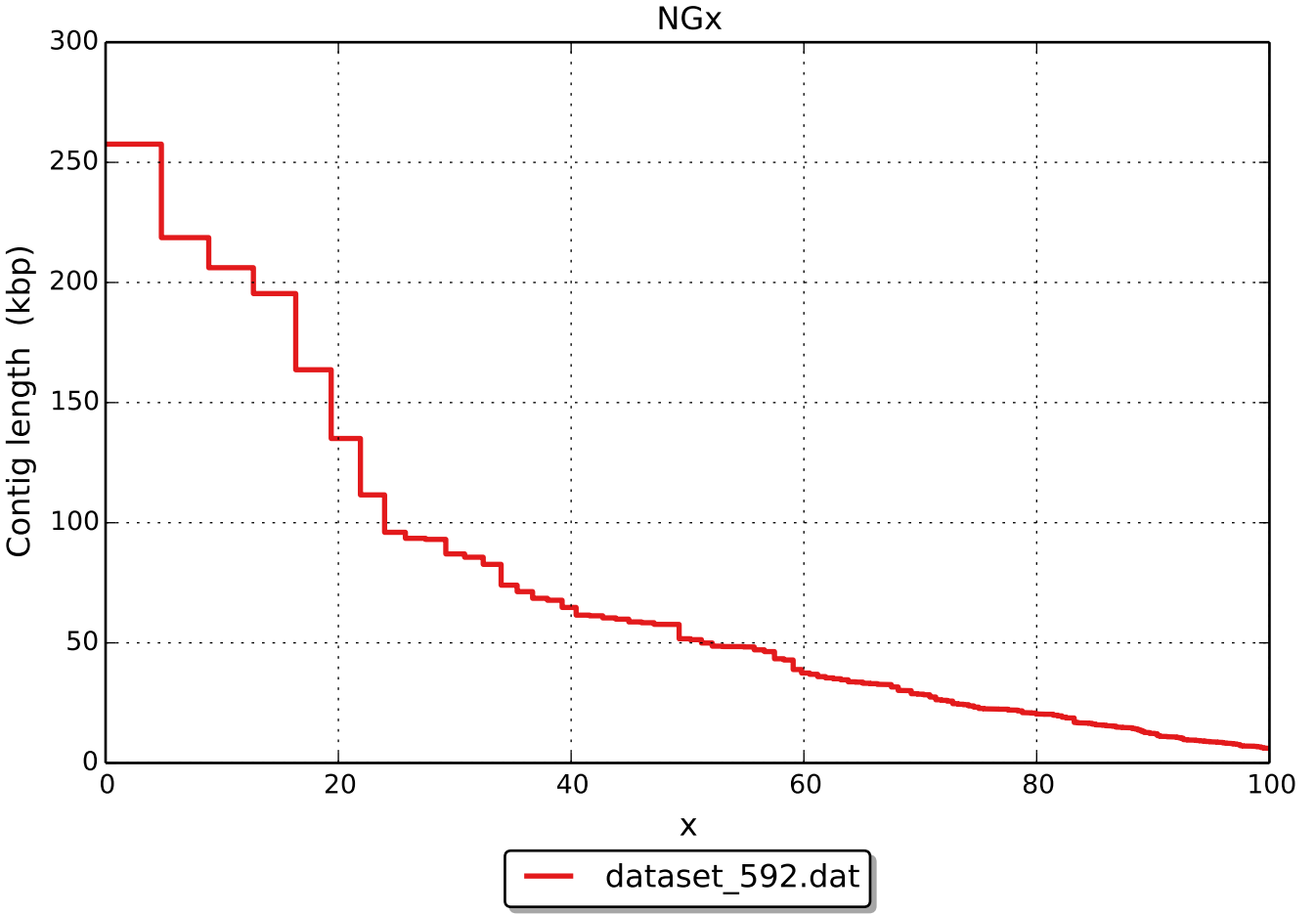

Genome fraction, %
100
50
dataset_592.dat

B_fragilis_638R

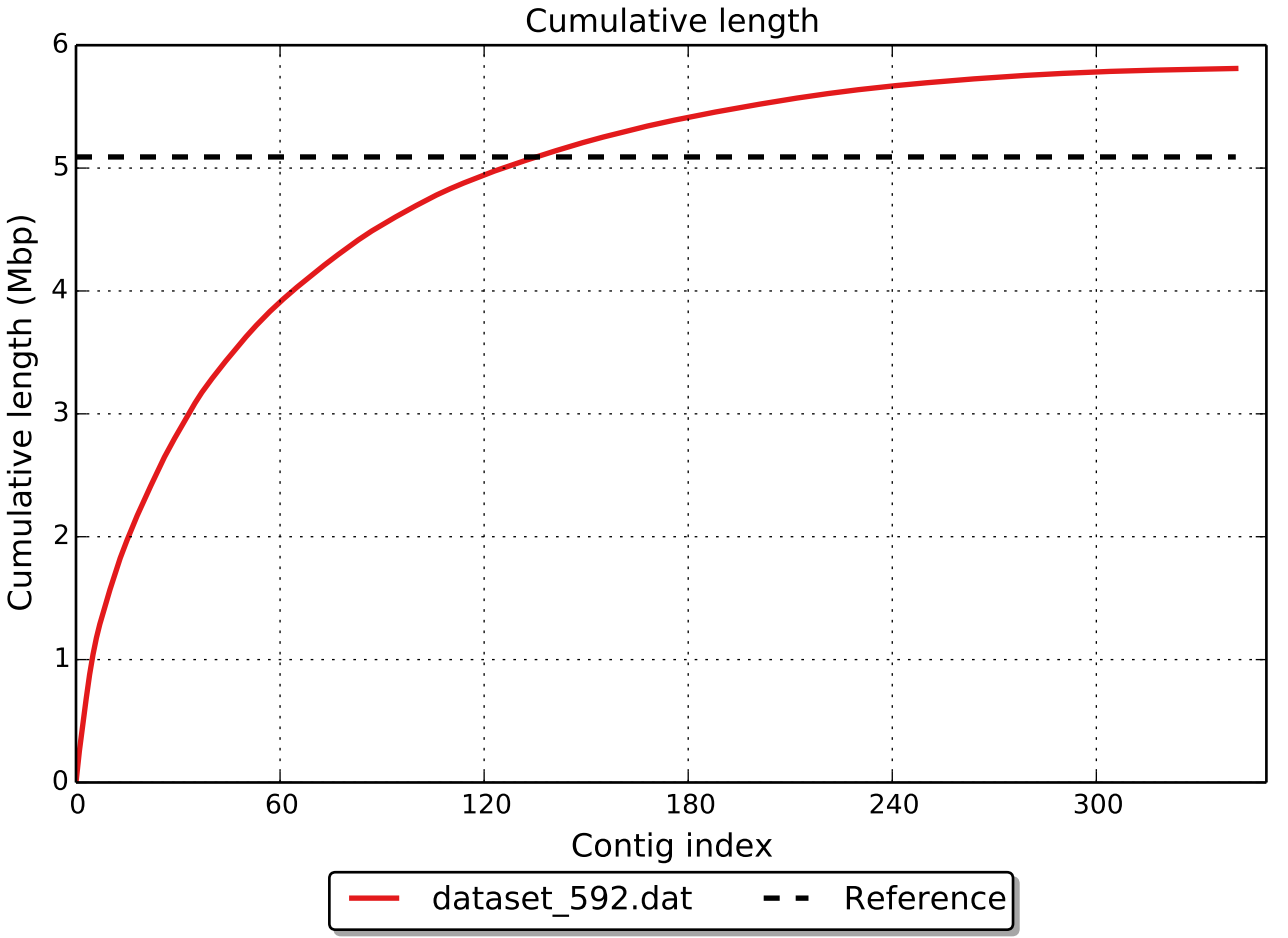

Cumulative length
Cumulative length (Mbp)
0
1
2
3
4
5
6
0
60
120
180
240
300
Contig index
dataset_592.dat
Reference

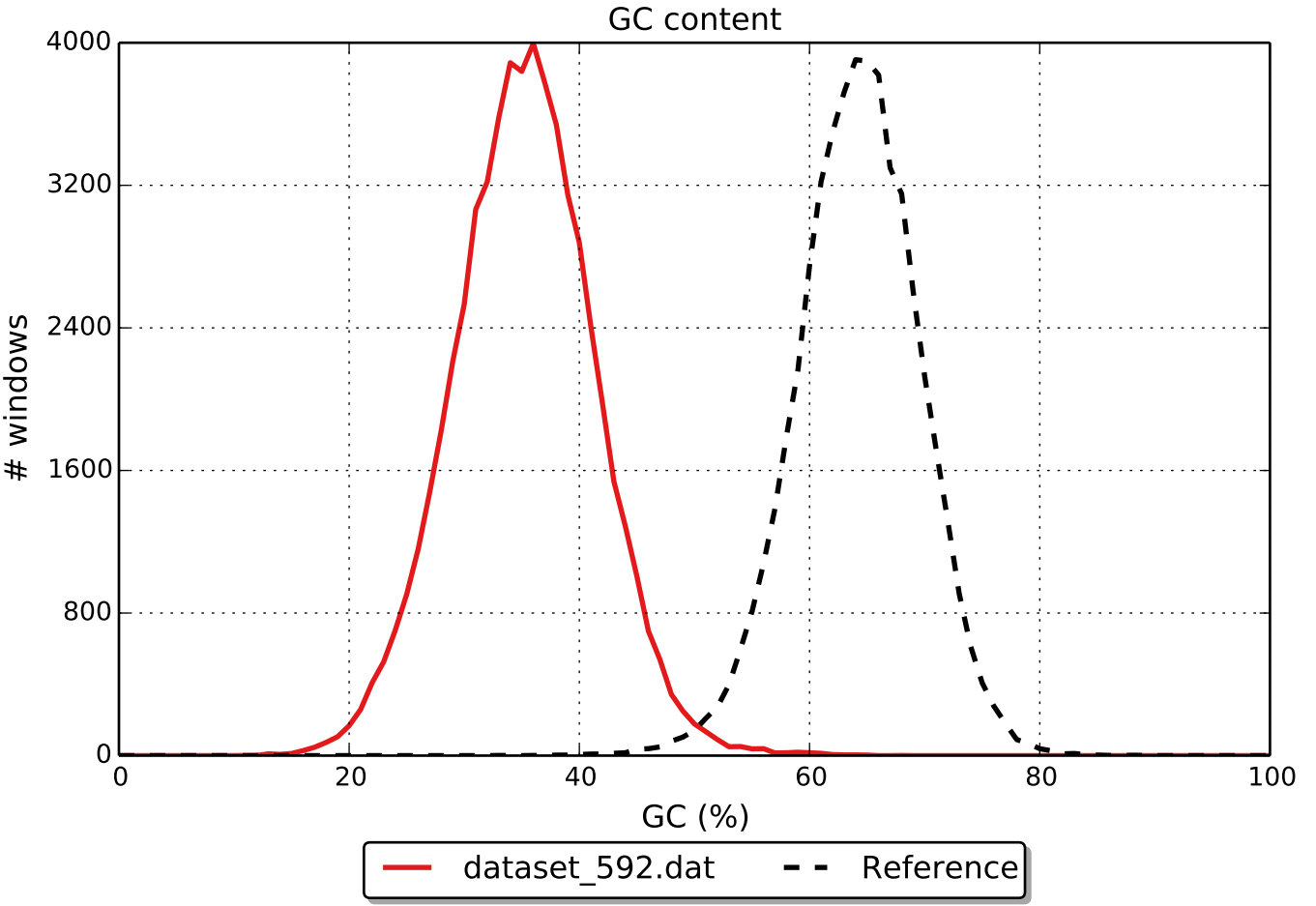

GC content
4000
3200
2400
1600
800
0
windows
0
20
40
60
80
100
GC (%)
dataset_592.dat
Reference

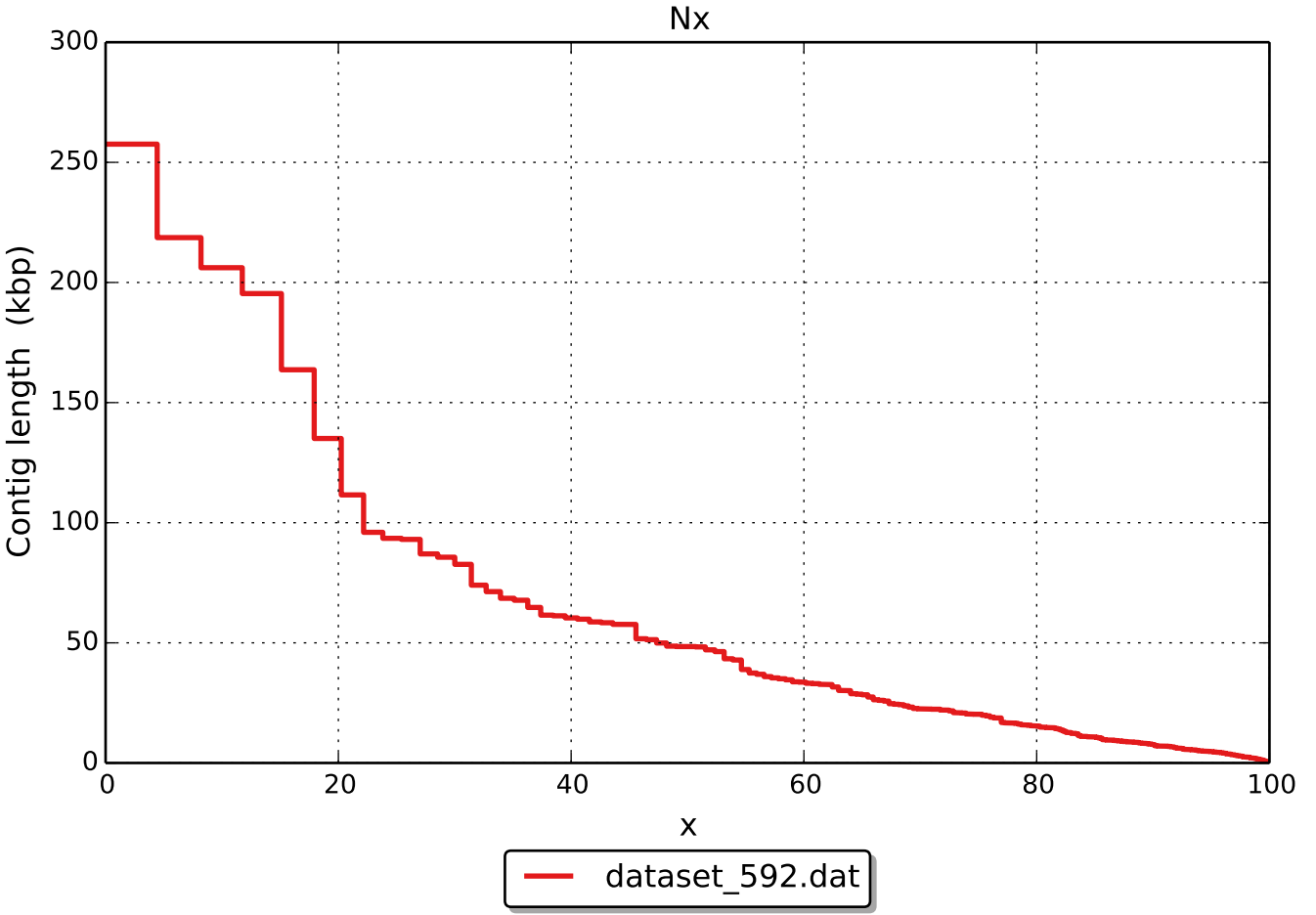

Nx
Contig length (kbp)
300
250
200
150
100
50
0
0
20
40
60
80
100
x
dataset_592.dat

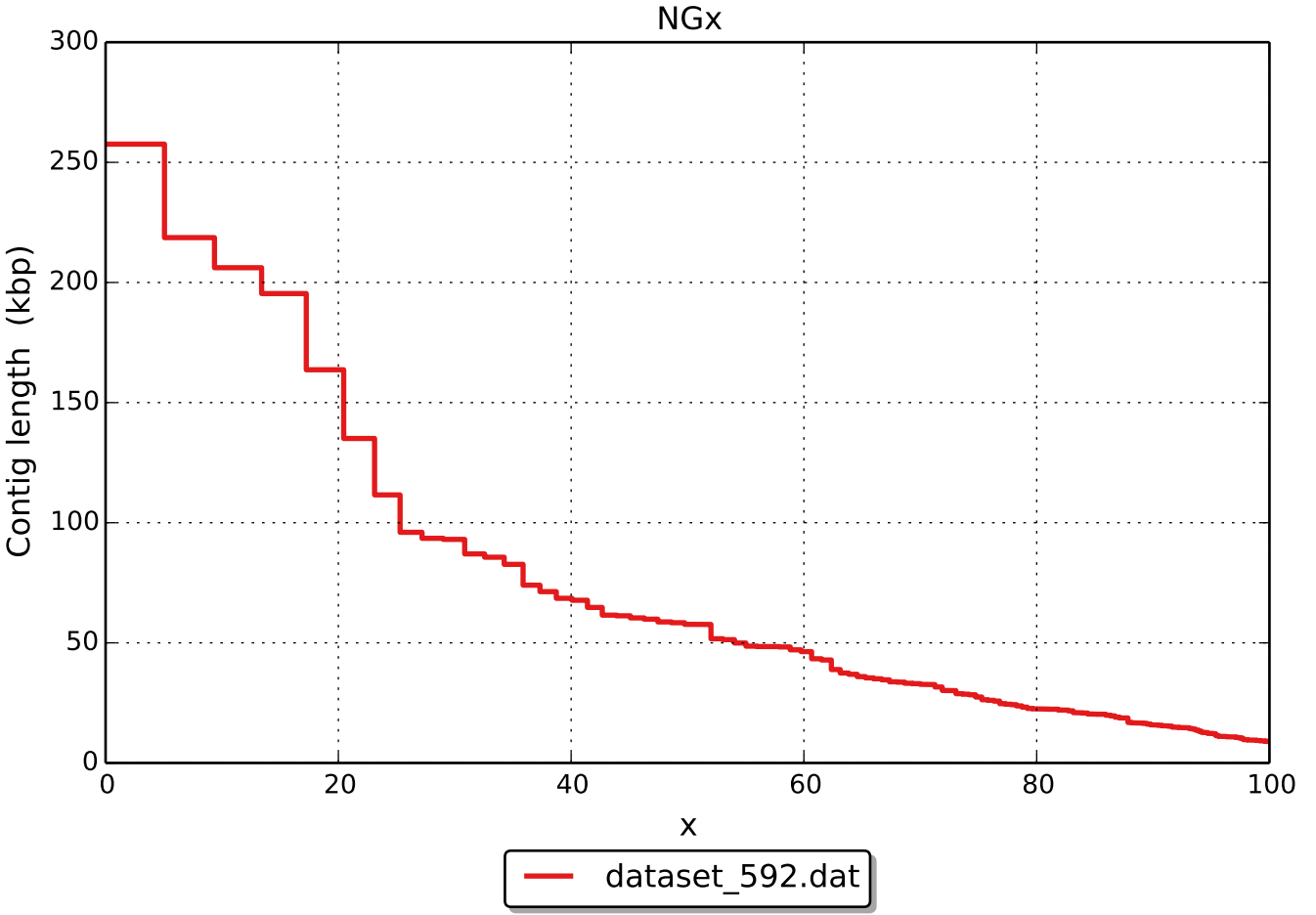

NGx
300
250
200
150
100
50
0
Contig length (kbp)
0
20
40
60
80
100
x
dataset_592.dat

M_abscessus_ATCC_19977


Cumulative length
Cumulative length (Mbp)
0
1
2
3
4
5
6
0
60
120
180
240
300
Contig index
dataset_592.dat
Reference

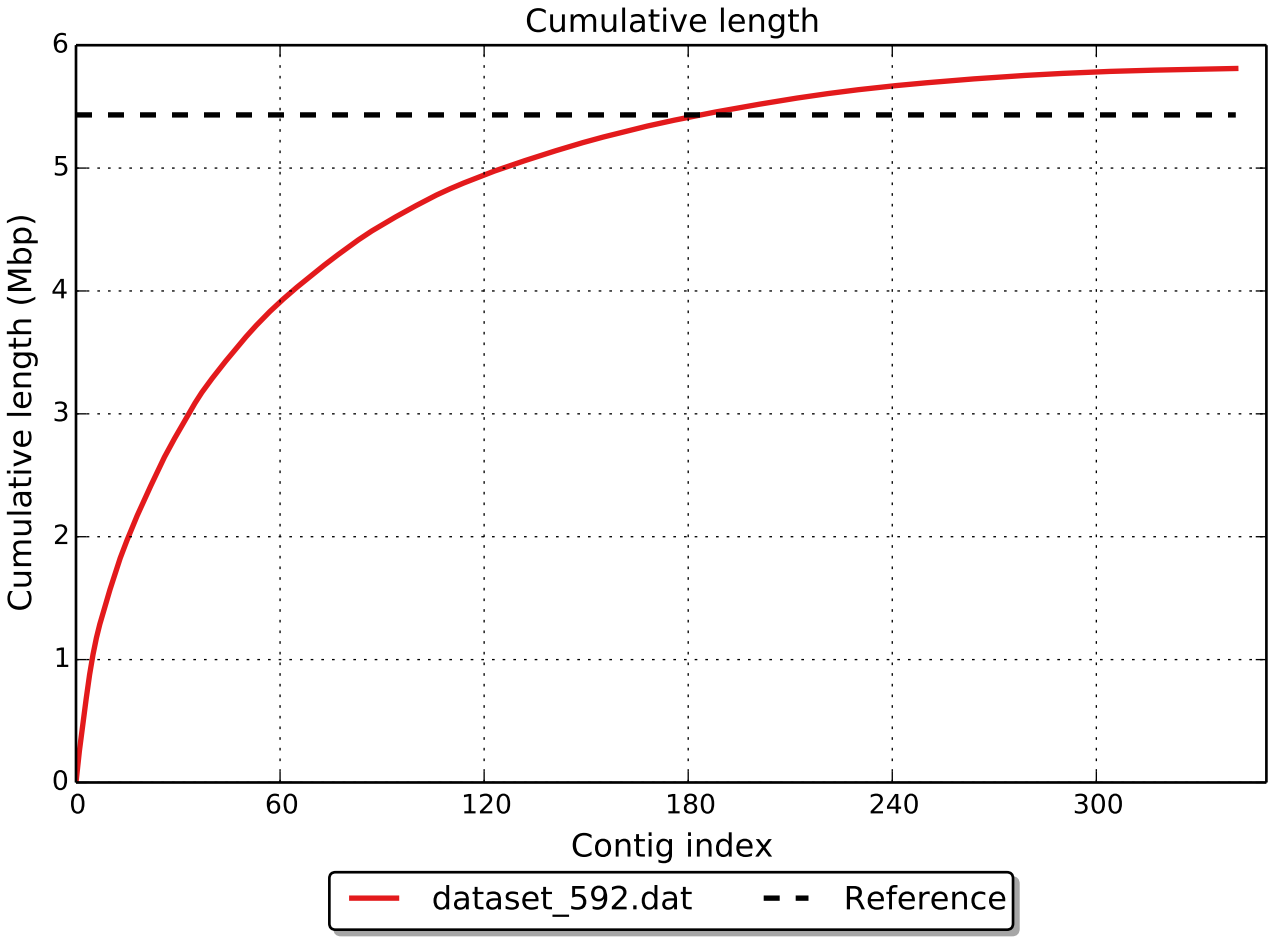

GC content
4000
3200
2400
1600
800
0
windows
0
20
40
60
80
100
GC (%)
dataset_592.dat
Reference

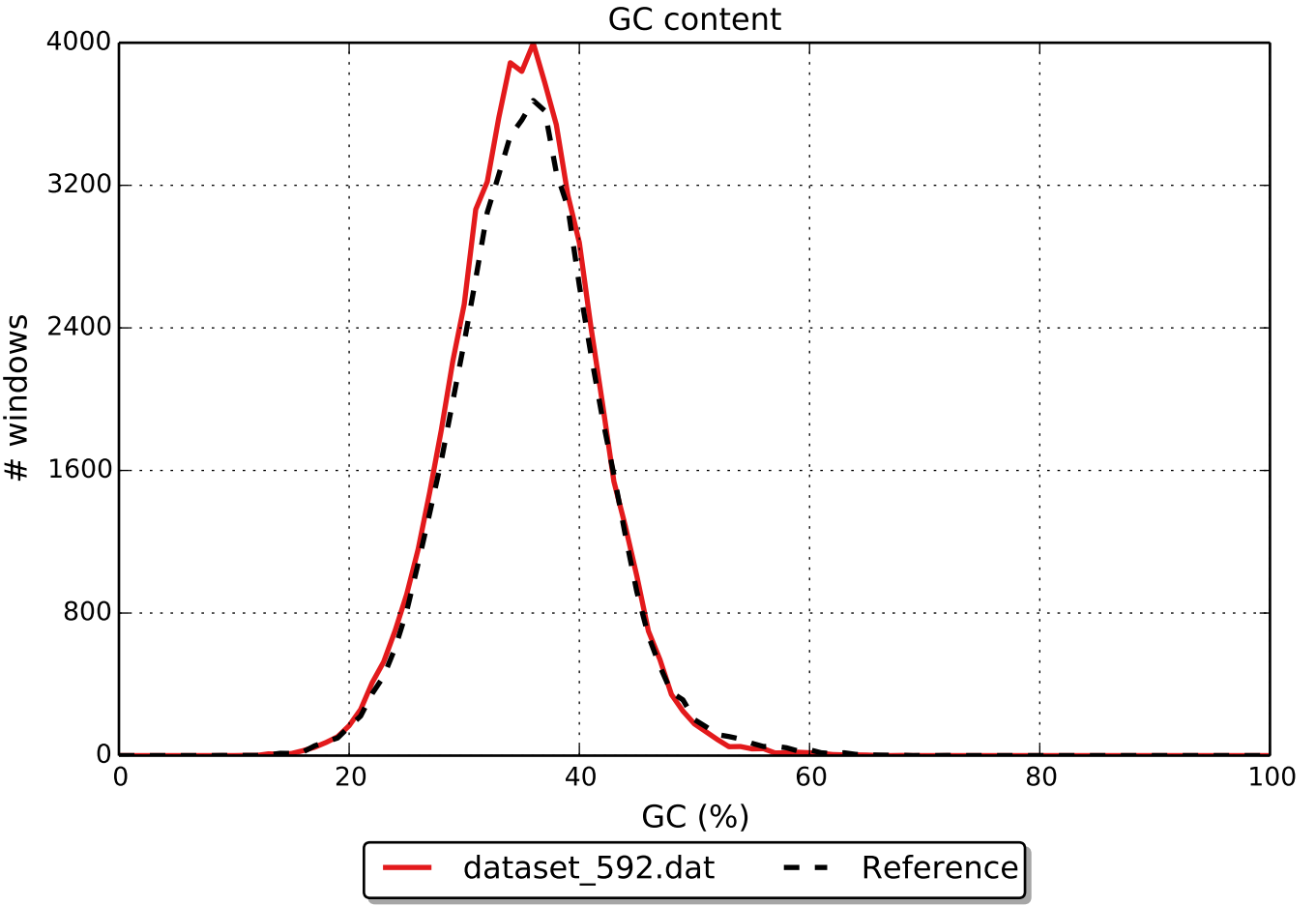

Nx
Contig length (kbp)
300
250
200
150
100
50
0
0
20
40
60
80
100
x
dataset_592.dat

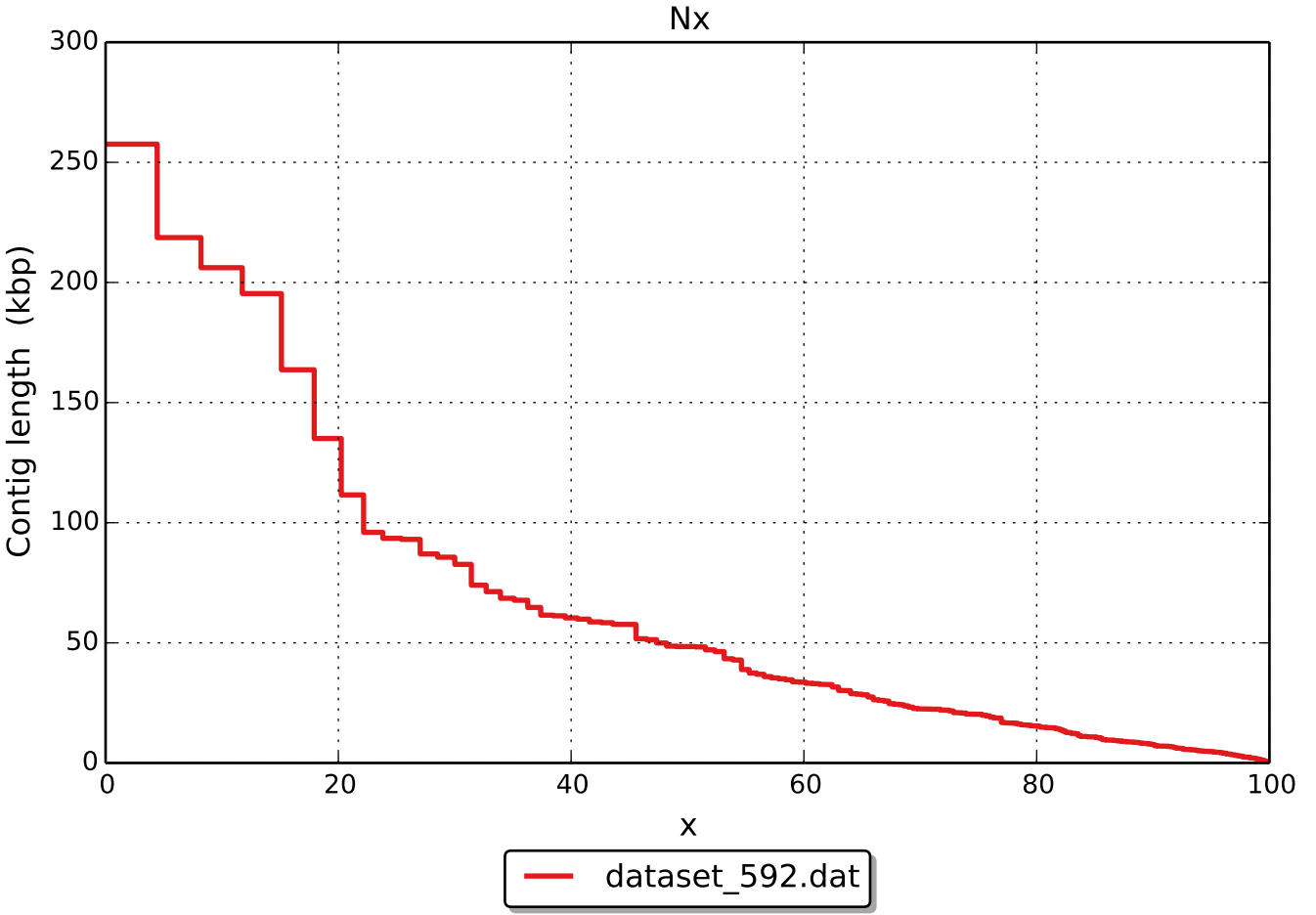

NGx
300
250
200
150
100
50
0
Contig length (kbp)
0
20
40
60
80
100
x
dataset_592.dat

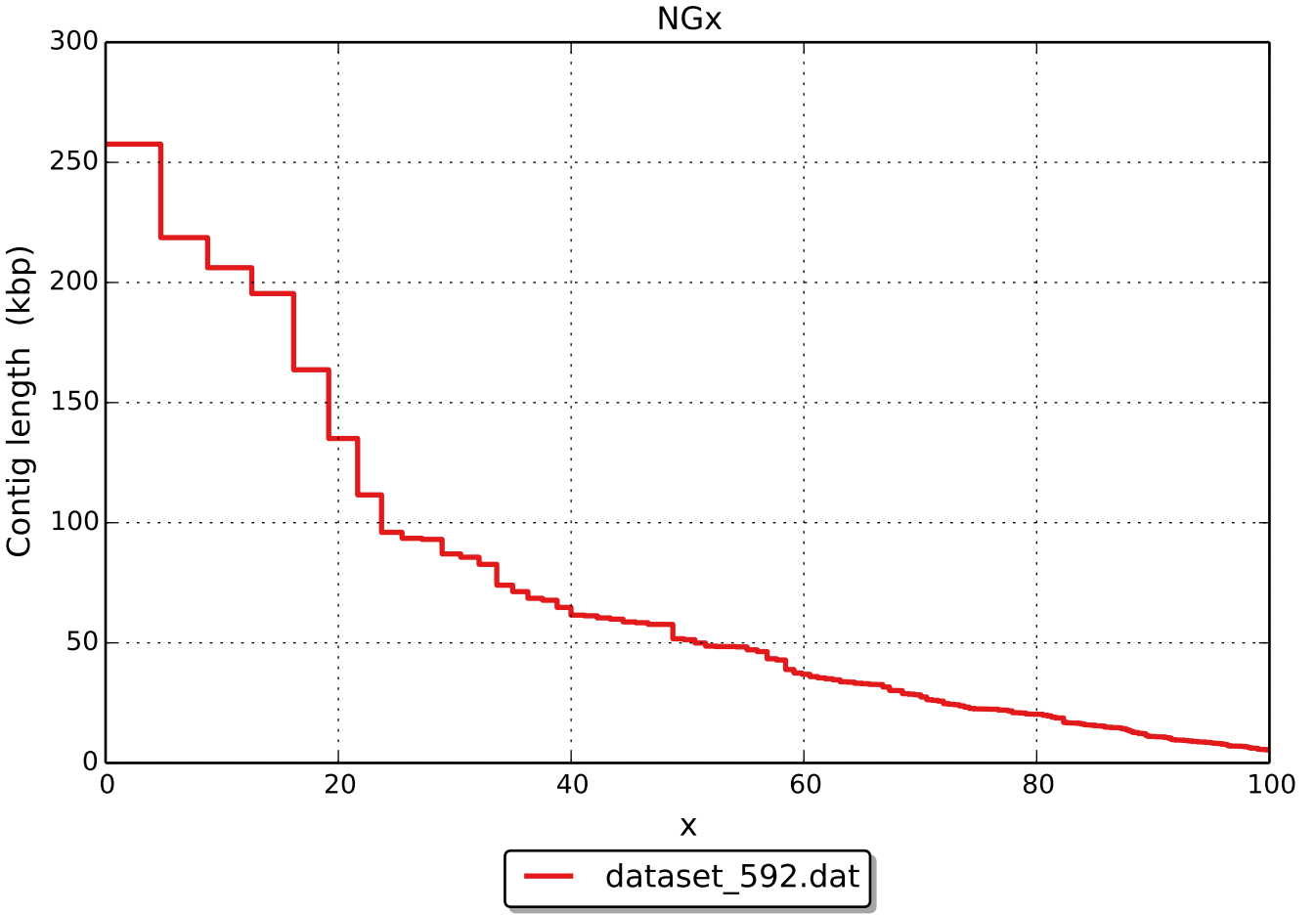
Combined_reference

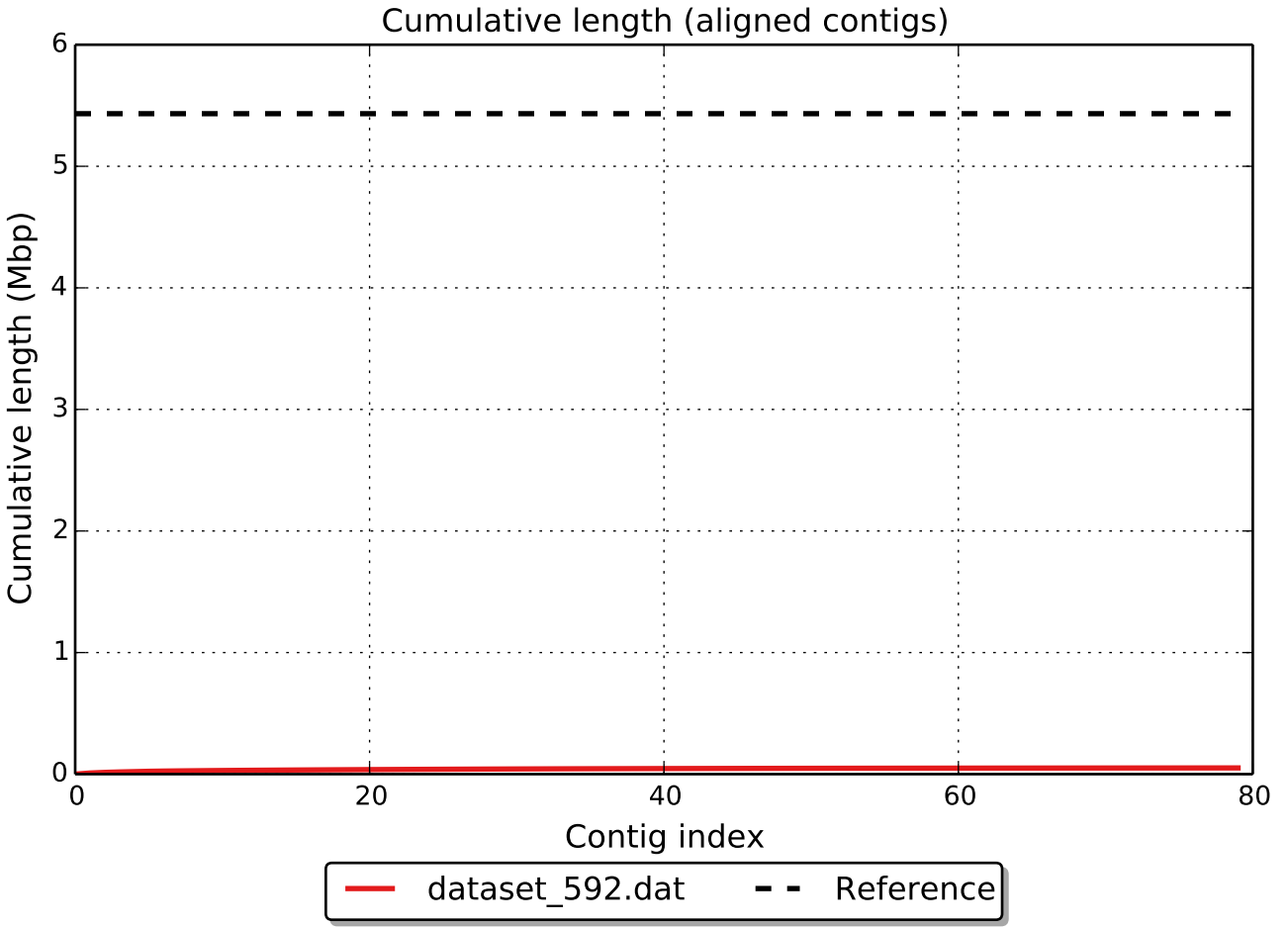
B_cereus_ATCC_1098

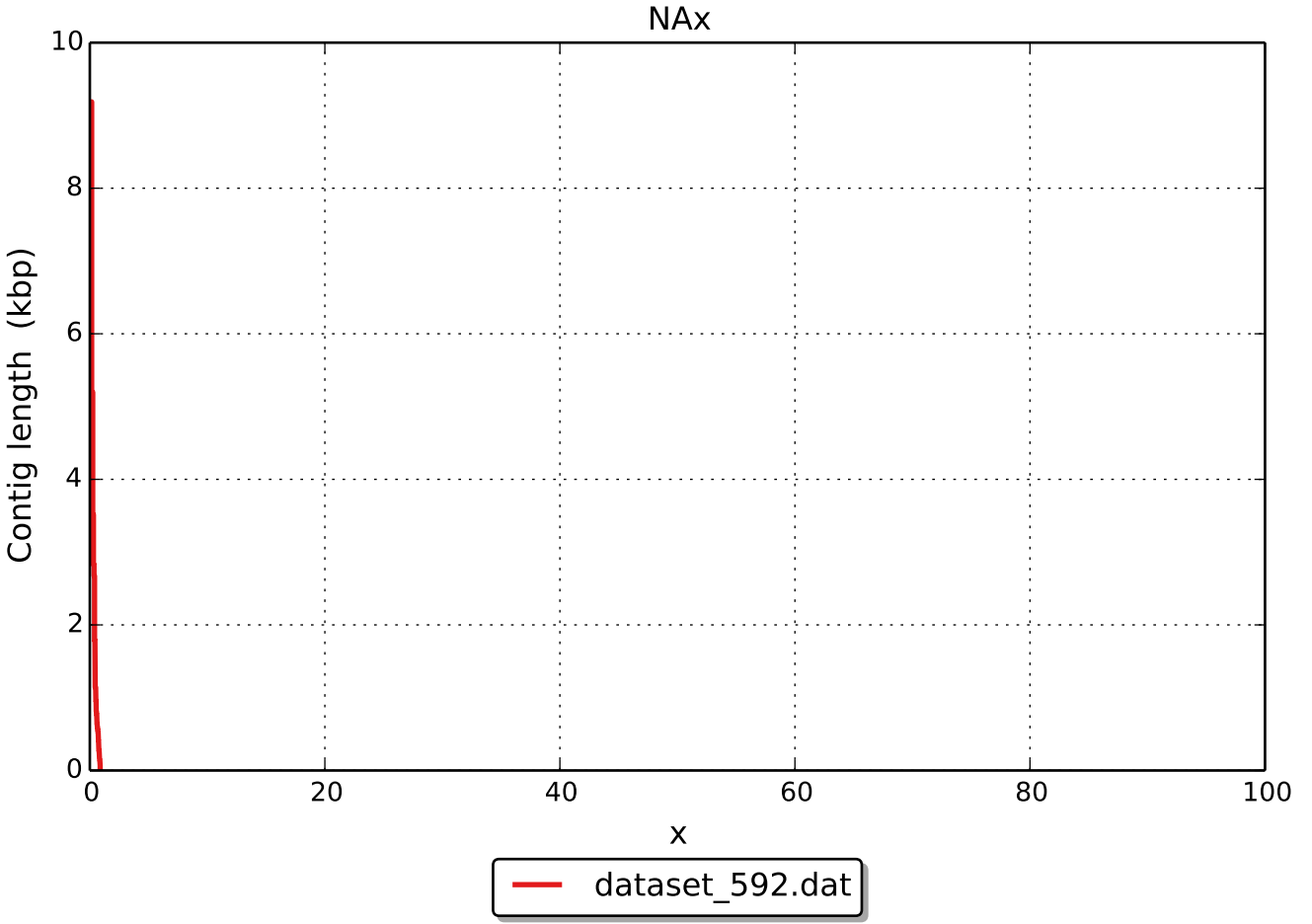

Cumulative length
Cumulative length (Mbp)
0
1
2
3
4
5
6
0
60
120
180
240
300
Contig index
dataset_592.dat
Reference

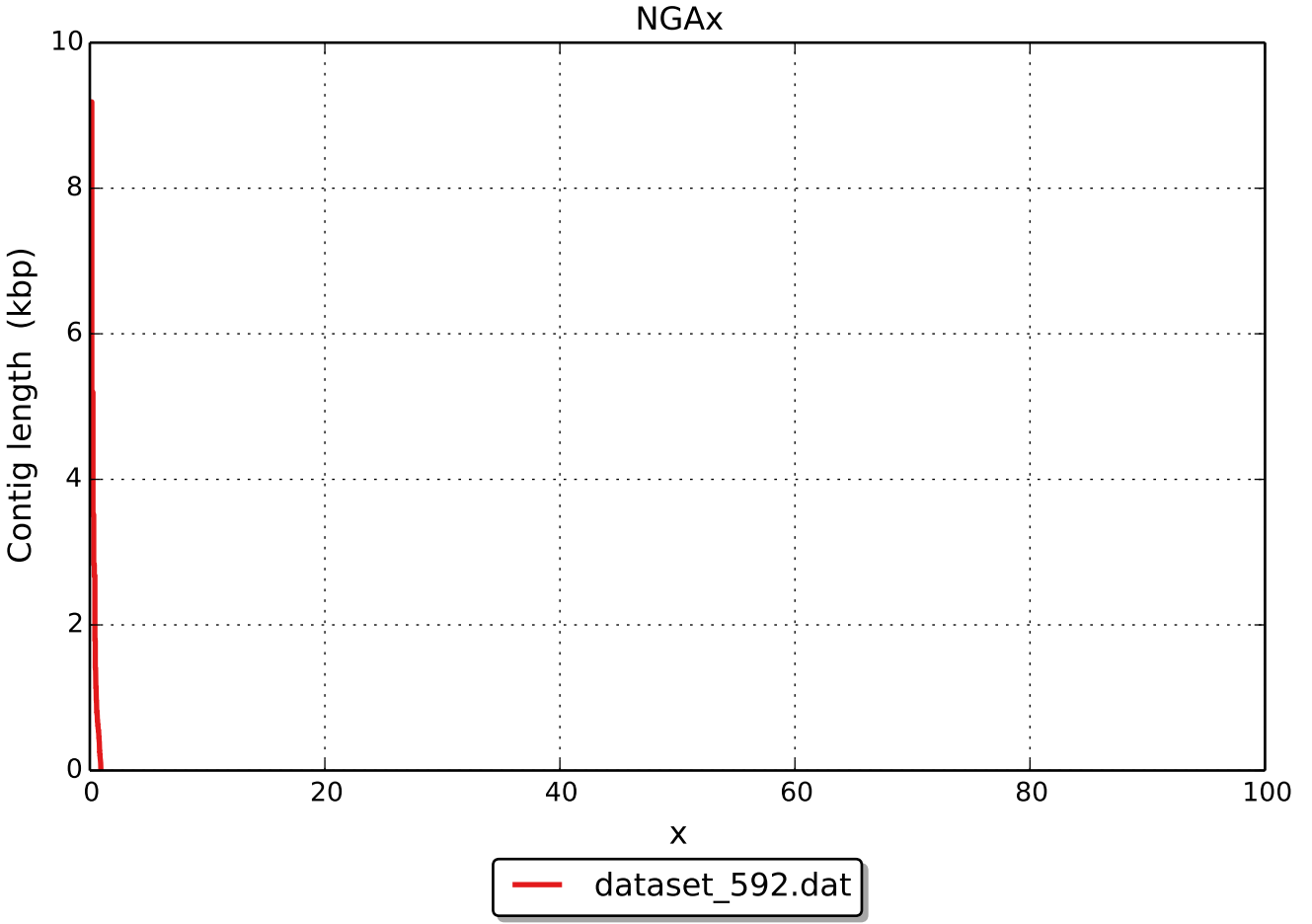

GC content
4000
3200
2400
1600
800
0
windows
0
20
40
60
80
100
GC (%)
dataset_592.dat
Reference

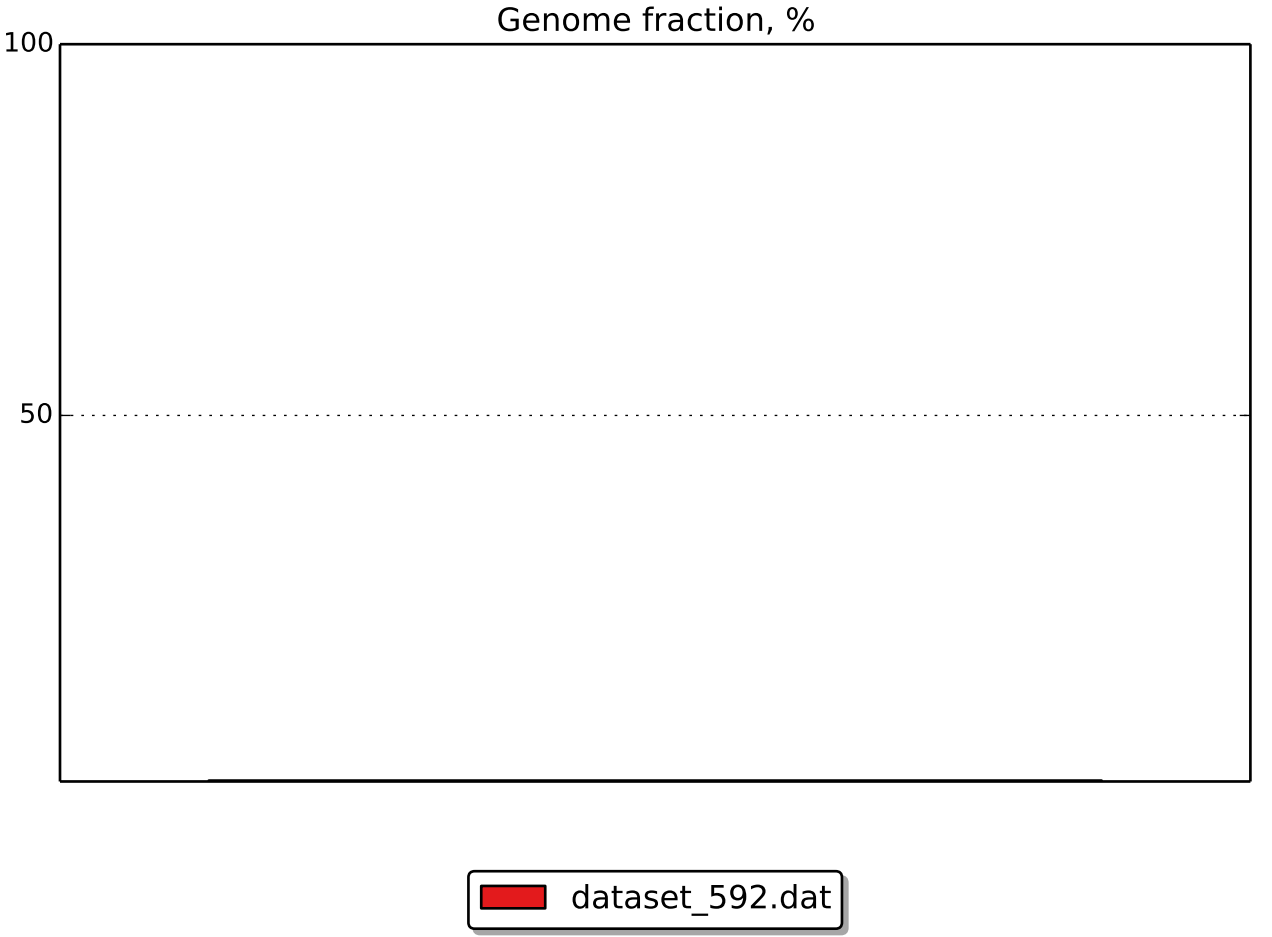

Nx
Contig length (kbp)
300
250
200
150
100
50
0
0
20
40
60
80
100
x
dataset_592.dat


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

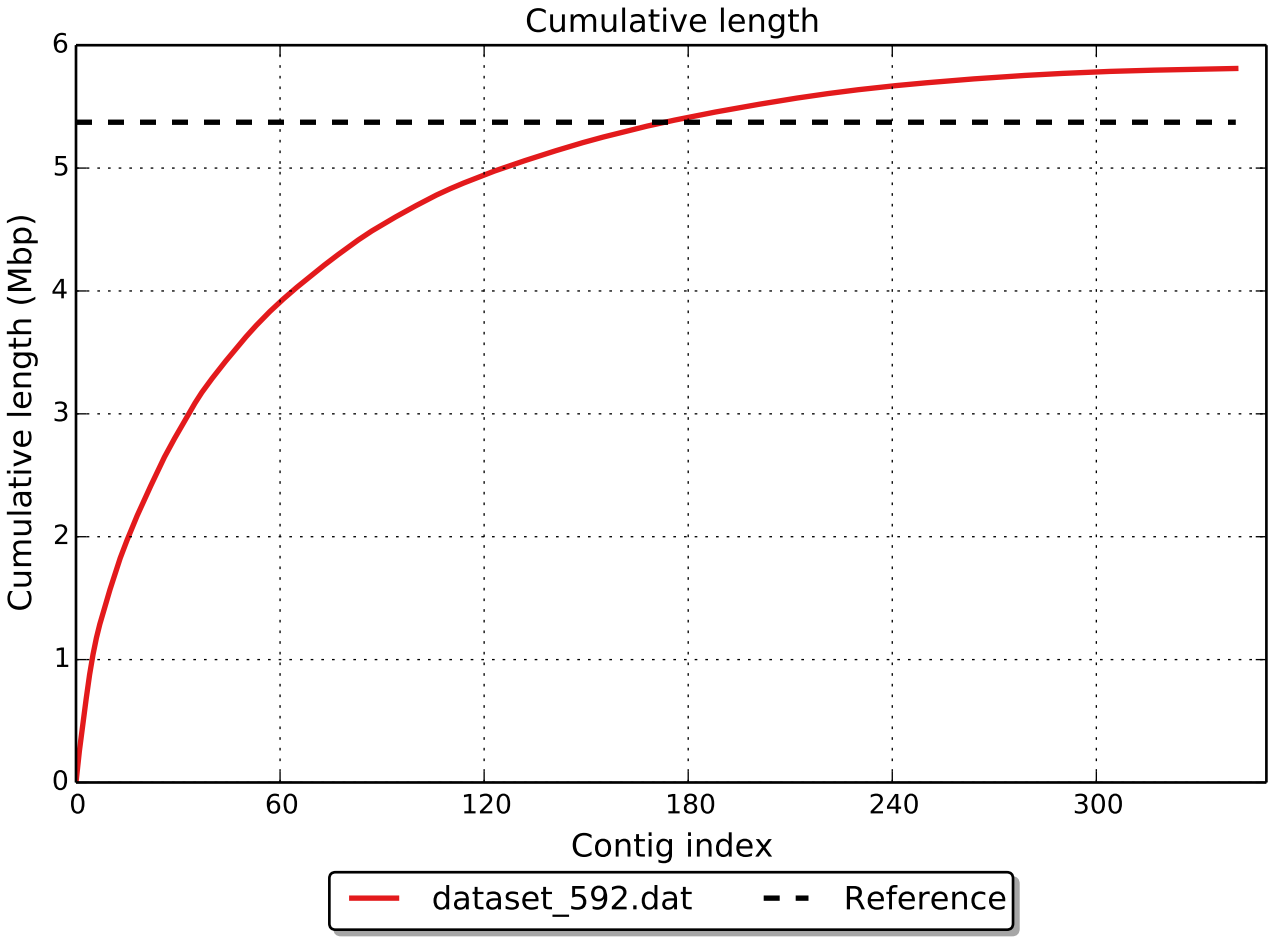

Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
1
2
3
4
5
6
0
20
40
60
80
Contig index
dataset_592.dat
Reference

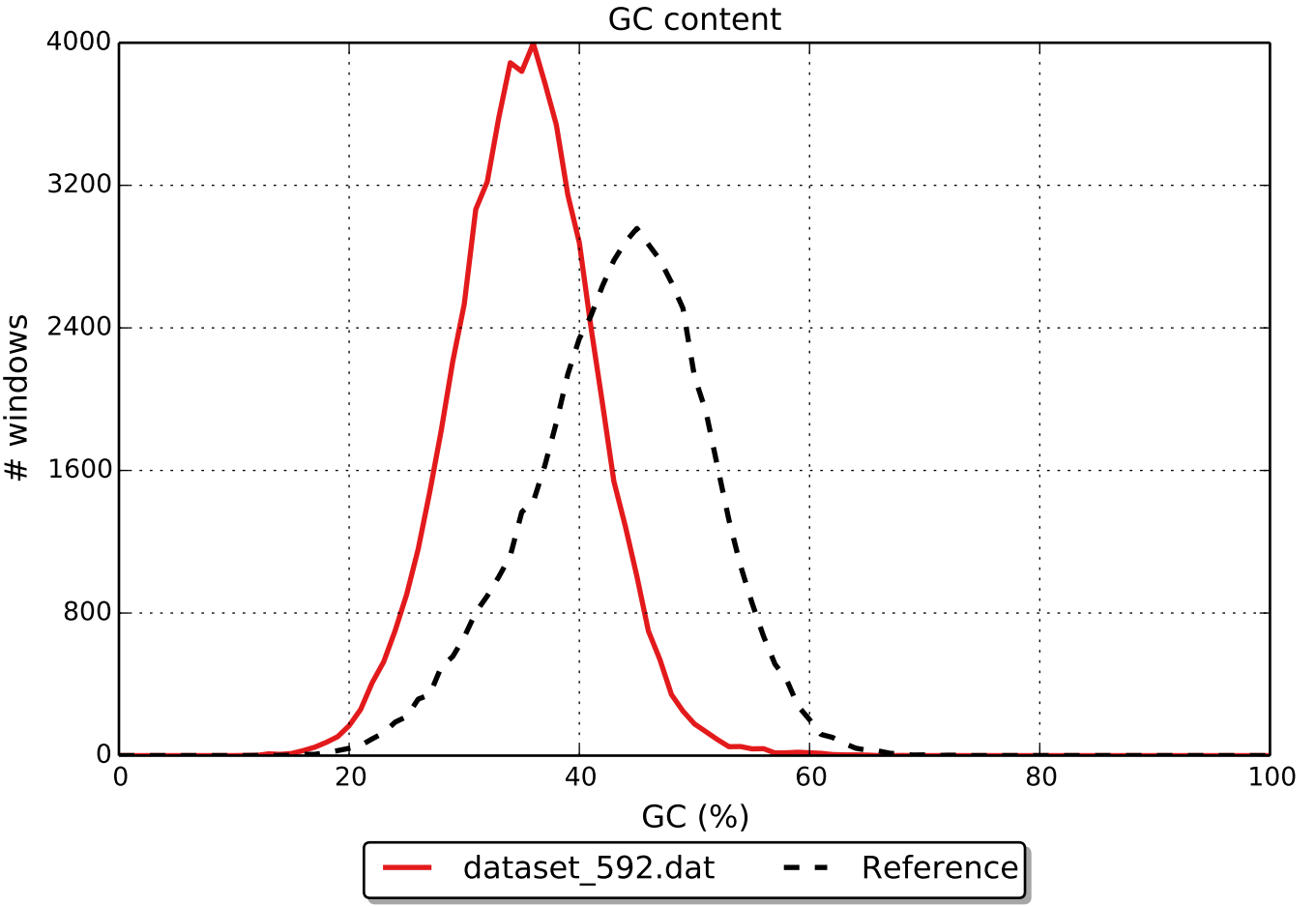

NAx
Contig length (kbp)
10
8
6
4
2
0
0
20
40
60
80
100
x
dataset_592.dat

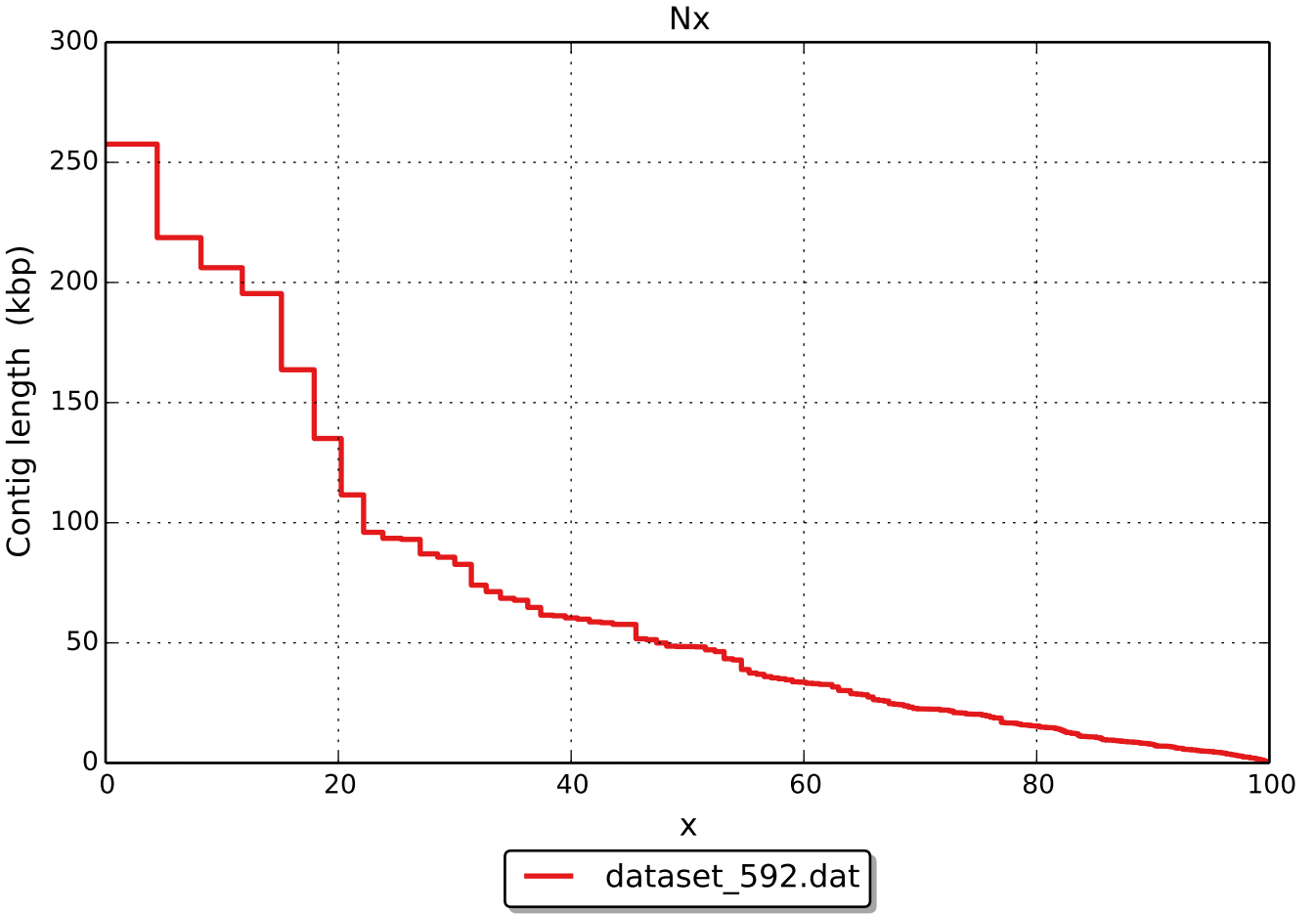

NGAx
Contig length (kbp)
10
8
6
4
2
0
0
20
40
60
80
100
x
dataset_592.dat

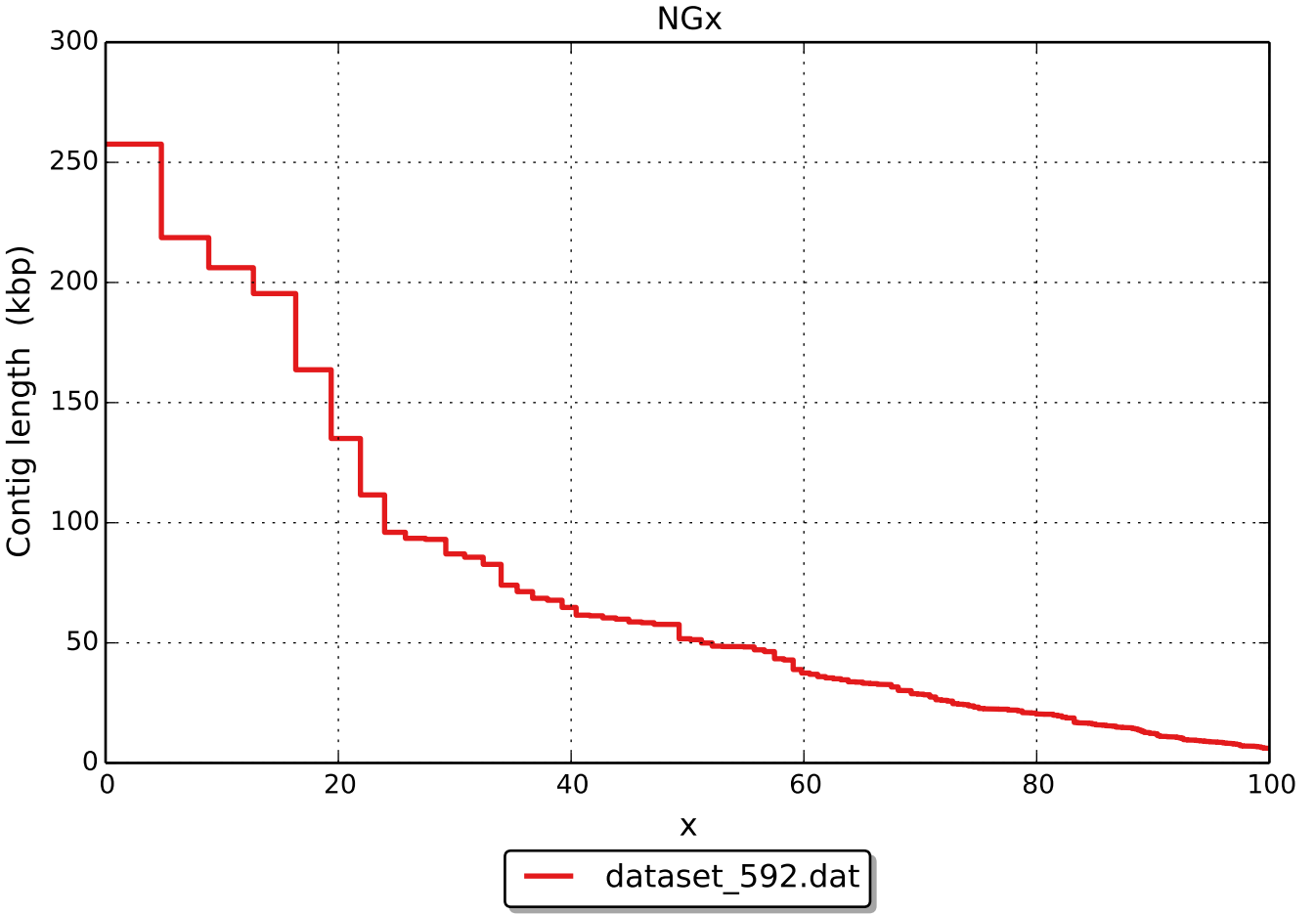

Genome fraction, %
100
50
dataset_592.dat

B_fragilis_638R


Cumulative length
Cumulative length (Mbp)
0
1
2
3
4
5
6
0
60
120
180
240
300
Contig index
dataset_592.dat
Reference


GC content
4000
3200
2400
1600
800
0
windows
0
20
40
60
80
100
GC (%)
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


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