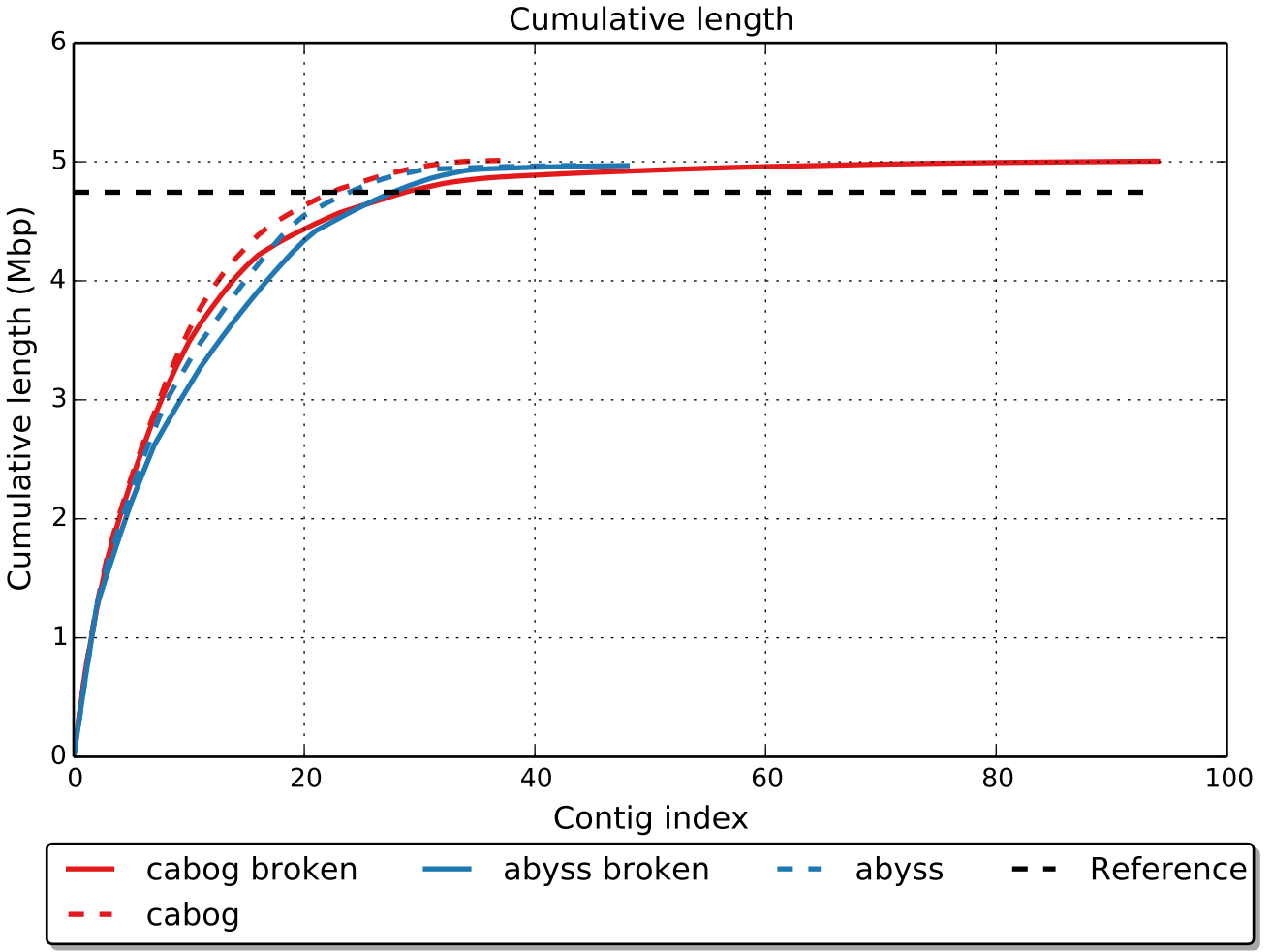
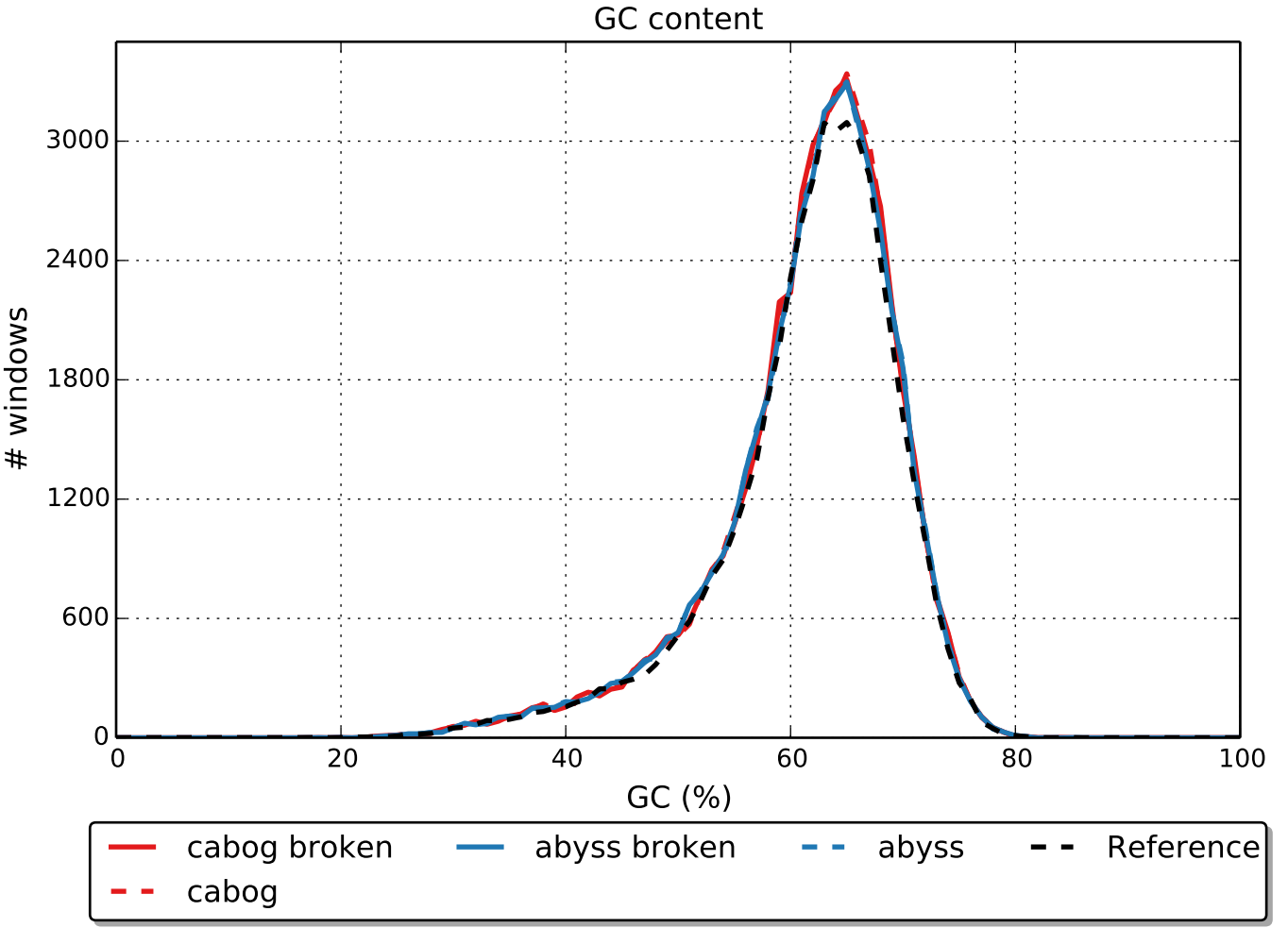
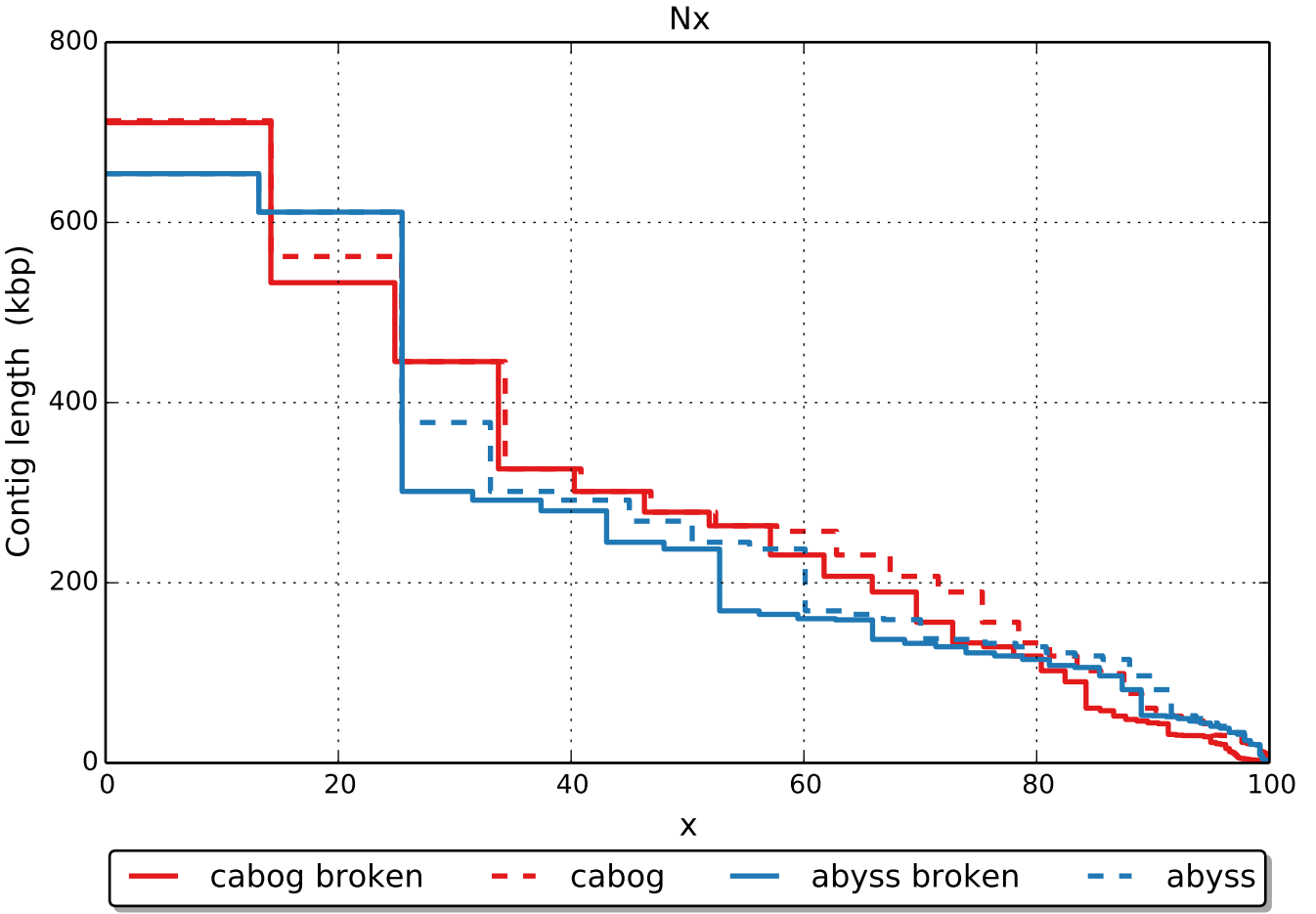
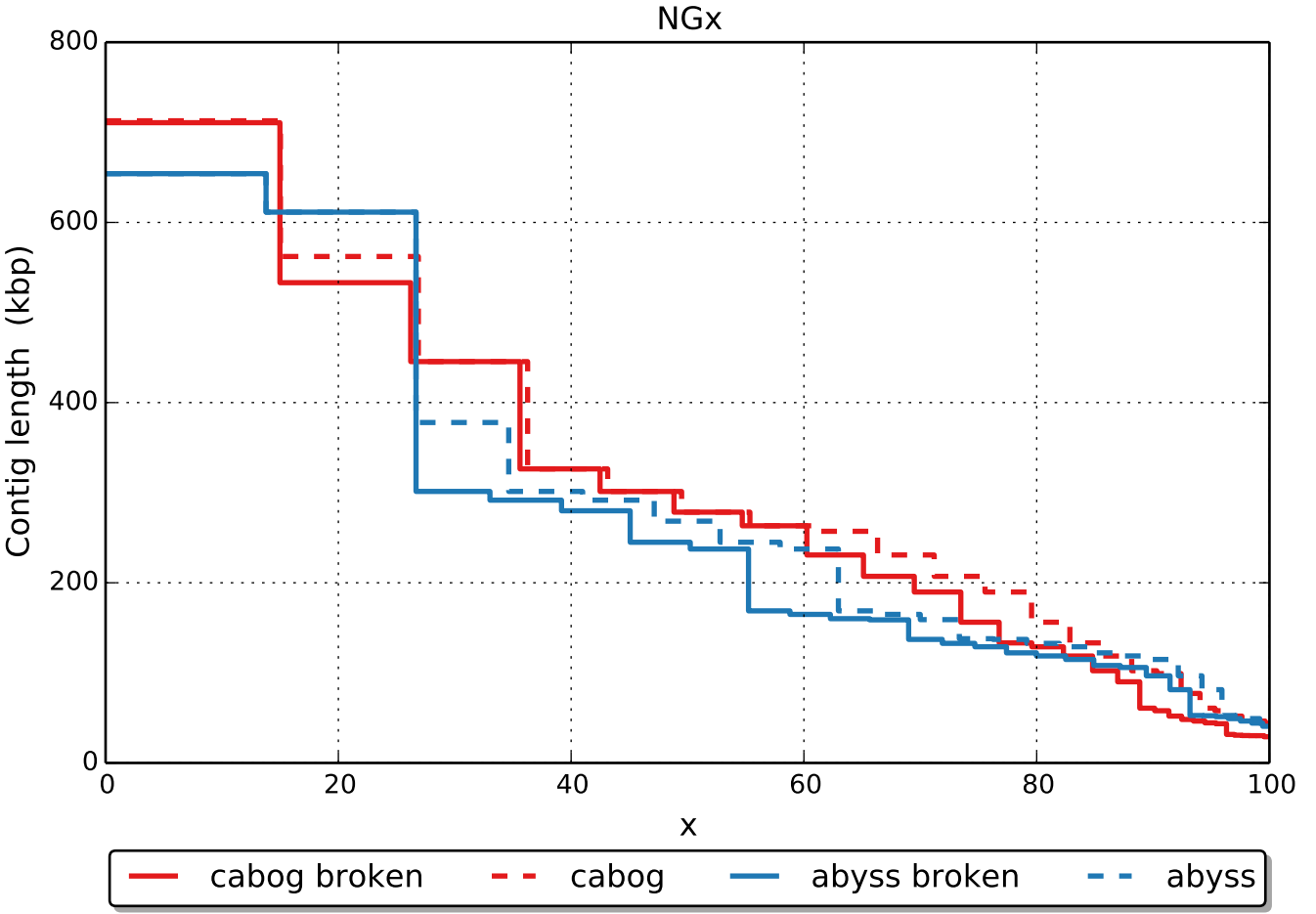
Combined_history

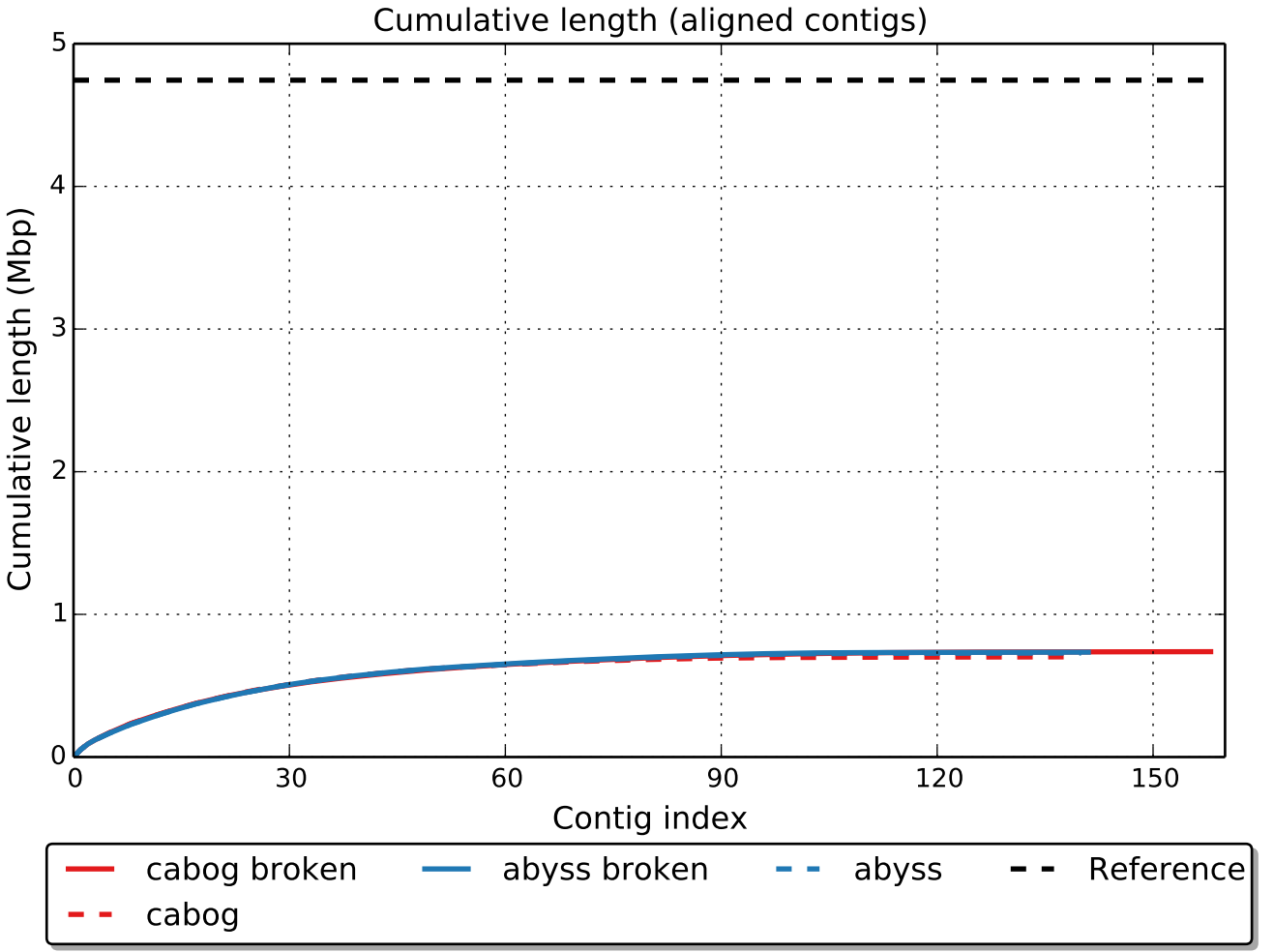
Scaffold

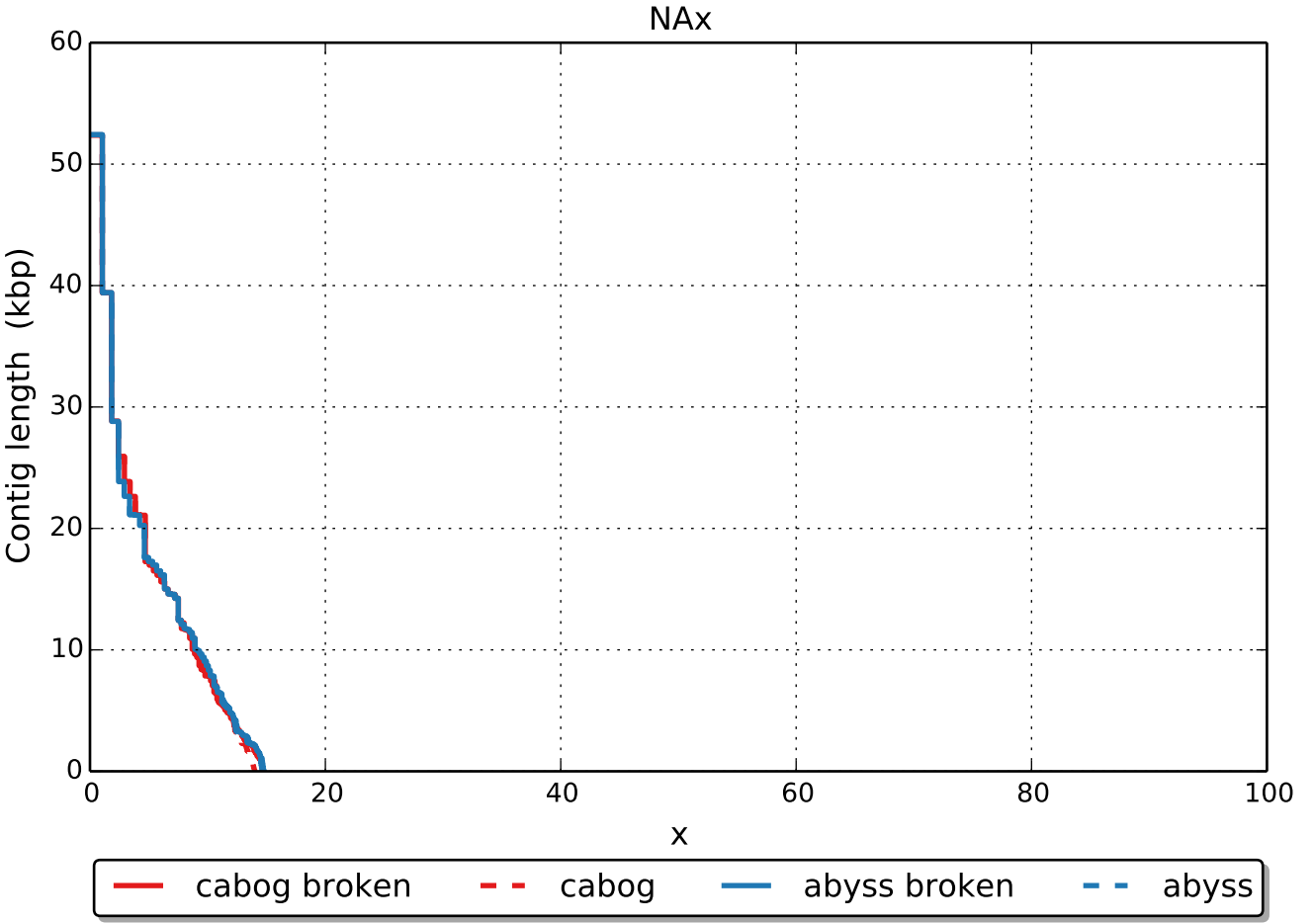

Cumulative length
Cumulative length (Mbp)
Contig index
0
1
2
3
4
5
6
0
20
40
60
80
100
cabog broken
cabog
abyss broken
abyss
Reference

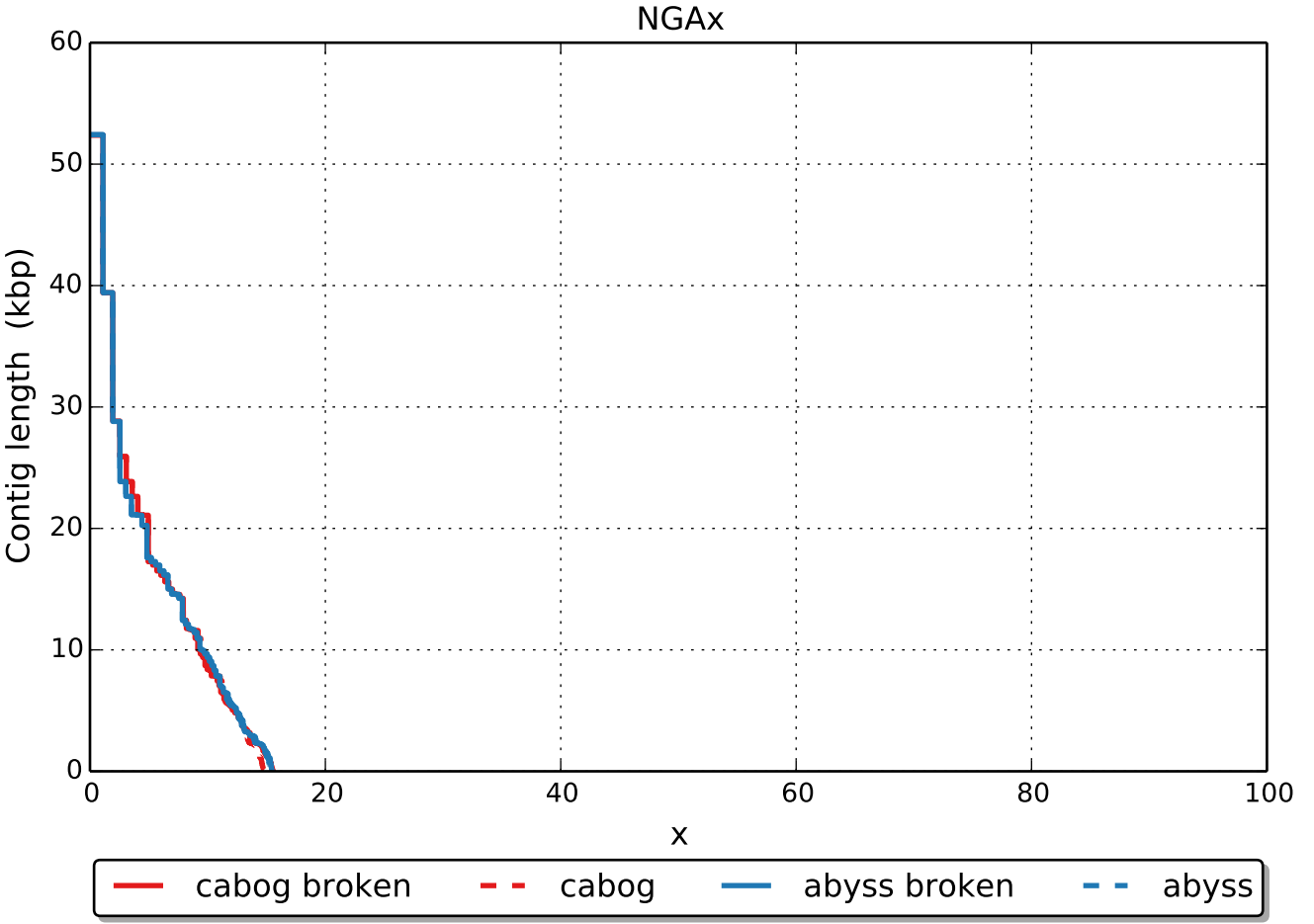

GC content
windows
3000
2400
1800
1200
600
0
0
20
40
60
80
100
GC (%)
cabog broken
abyss broken
abyss
Reference
cabog

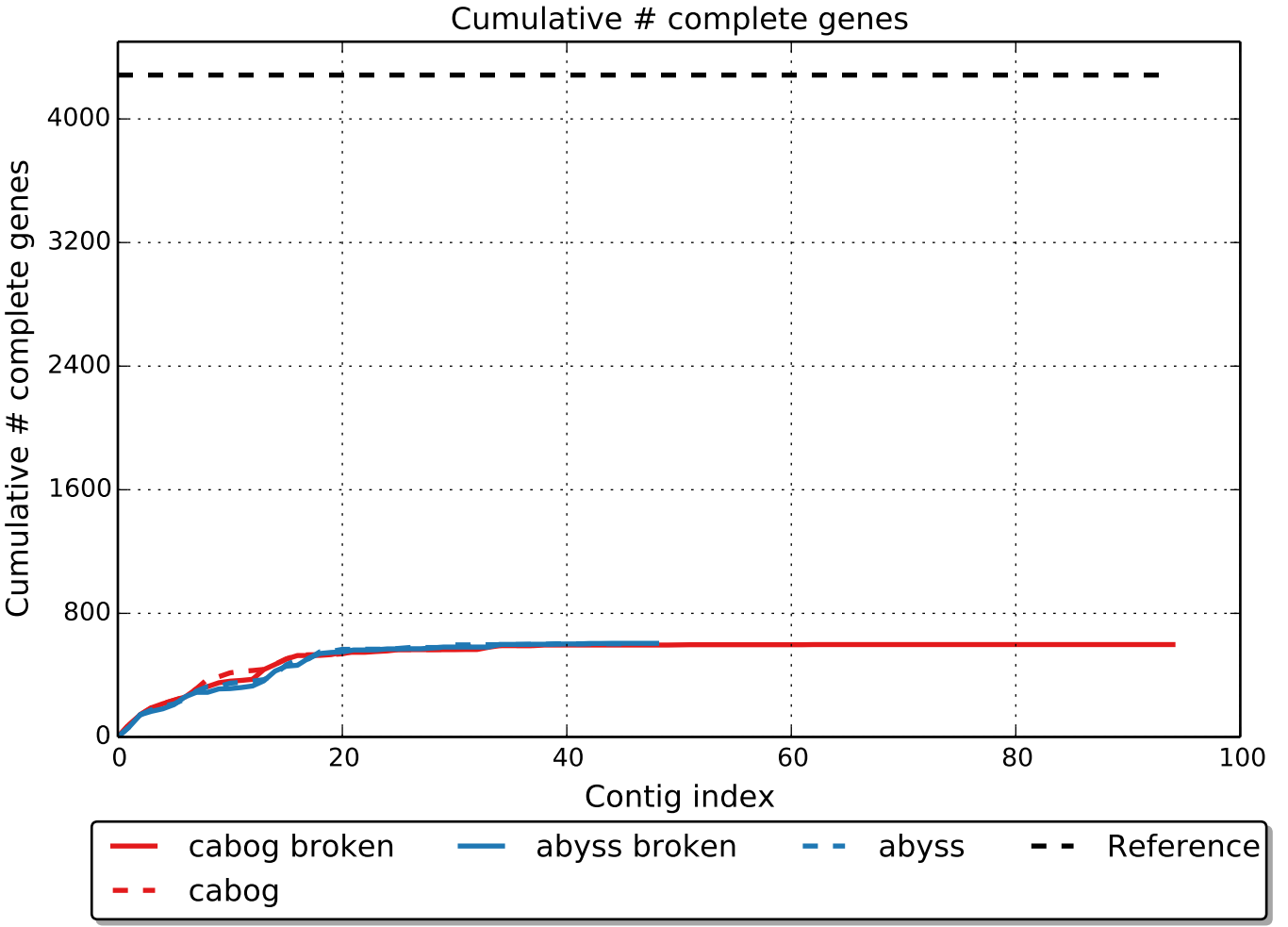

Nx
800
600
400
200
0
Contig length (kbp)
0
20
40
60
80
100
x
cabog broken
cabog
abyss broken
abyss

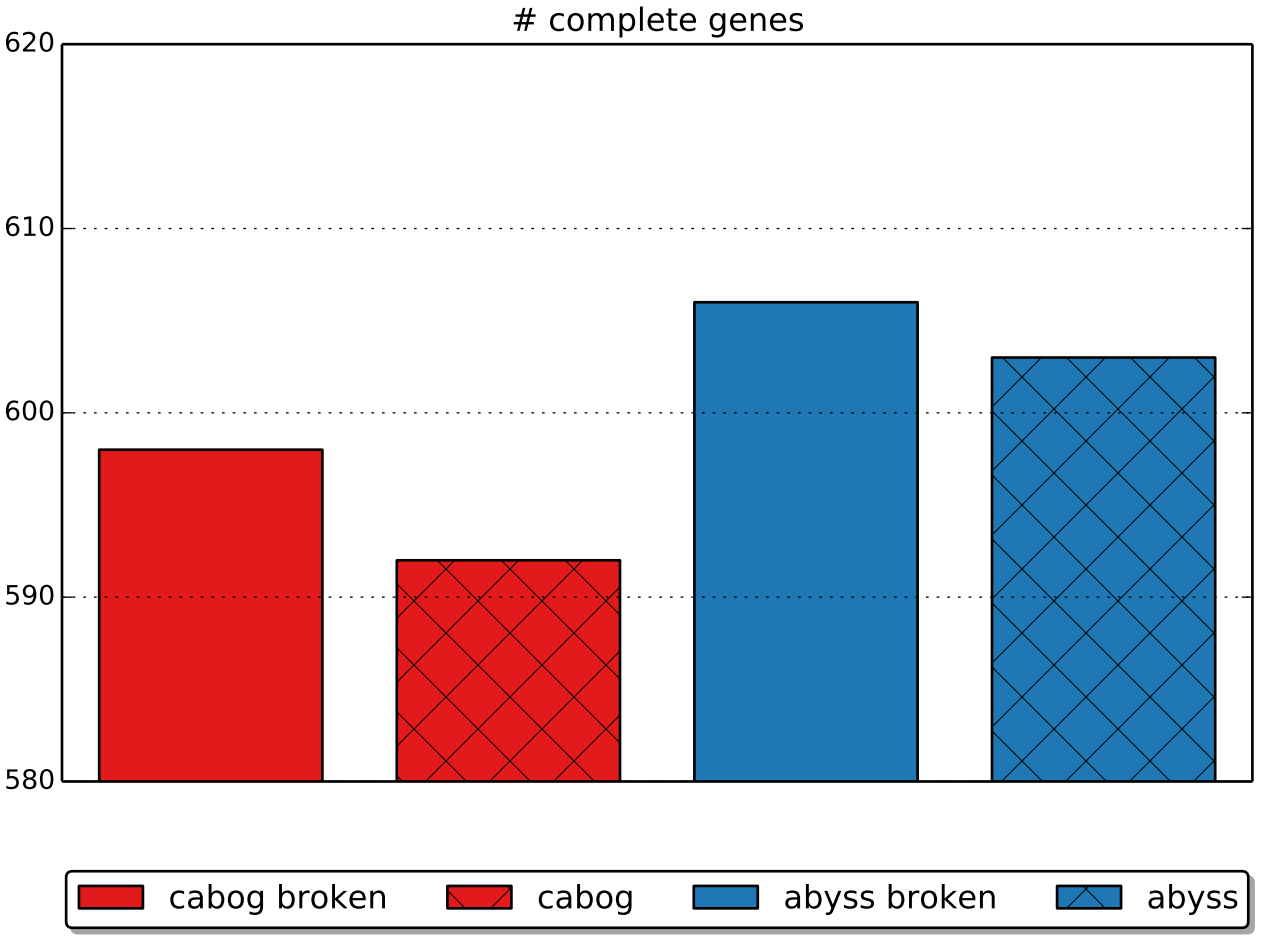

NGx
800
600
400
200
0
Contig length (kbp)
0
20
40
60
80
100
x
cabog broken
cabog
abyss broken
abyss

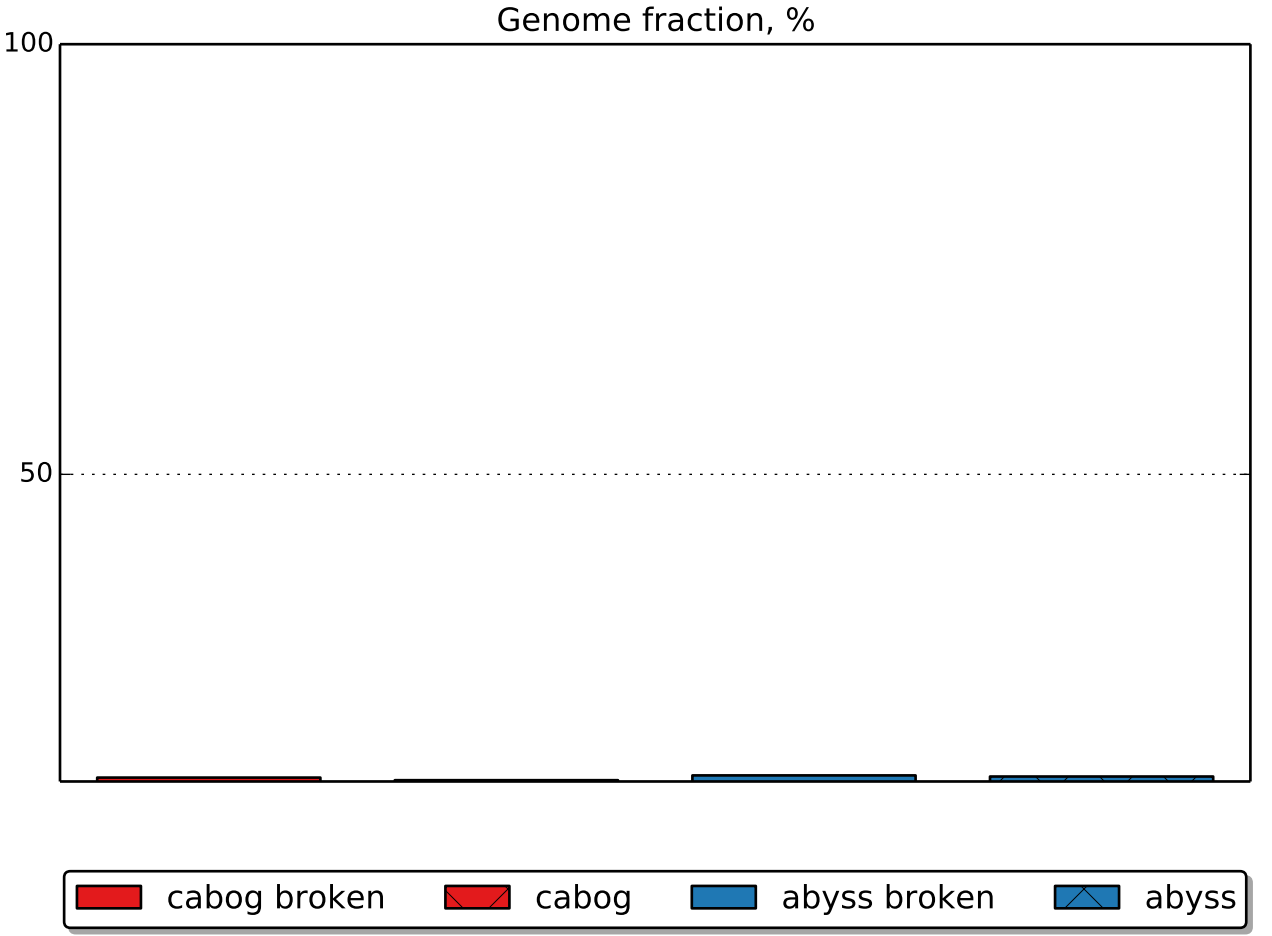

Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
1
2
3
4
5
0
30
60
90
120
150
Contig index
cabog broken
abyss broken
abyss
Reference
cabog


NAx
Contig length (kbp)
60
50
40
30
20
10
0
0
20
40
60
80
100
x
cabog broken
cabog
abyss broken
abyss

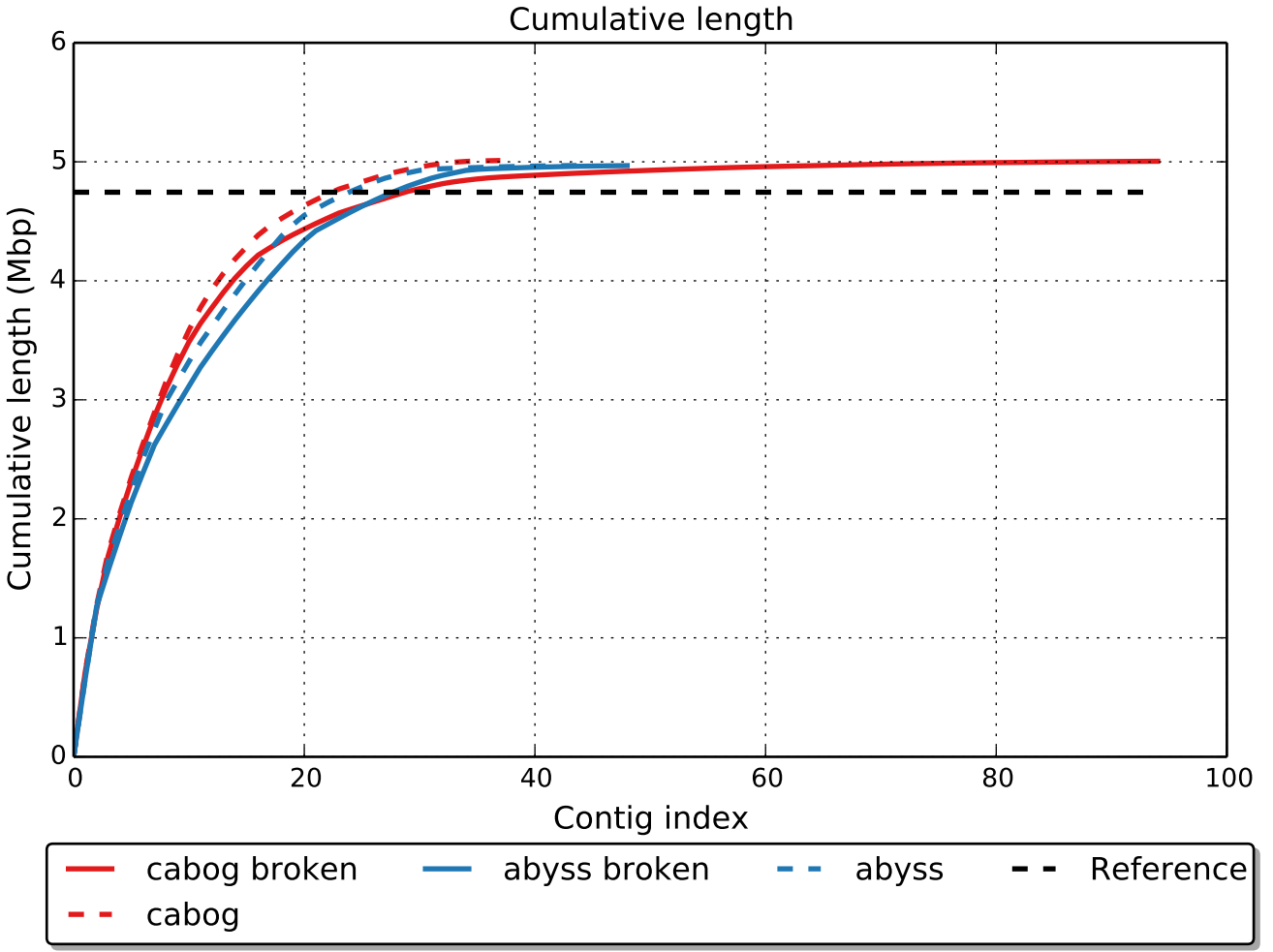

NGAx
Contig length (kbp)
60
50
40
30
20
10
0
0
20
40
60
80
100
x
cabog broken
cabog
abyss broken
abyss

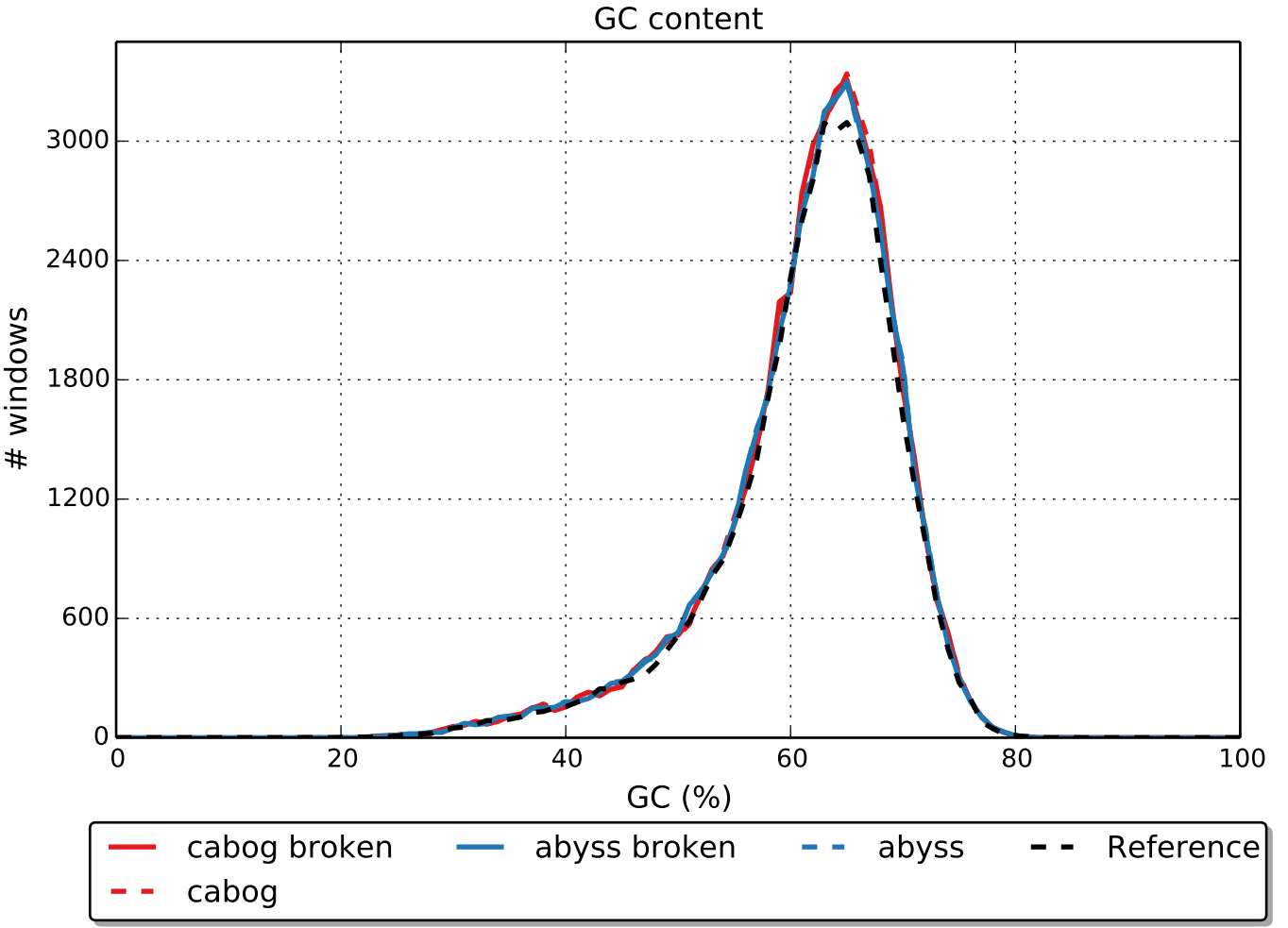

Cumulative # complete genes
Cumulative # complete genes
4000
3200
2400
1600
800
0
0
20
40
60
80
100
Contig index
cabog broken
abyss broken
abyss
Reference
cabog

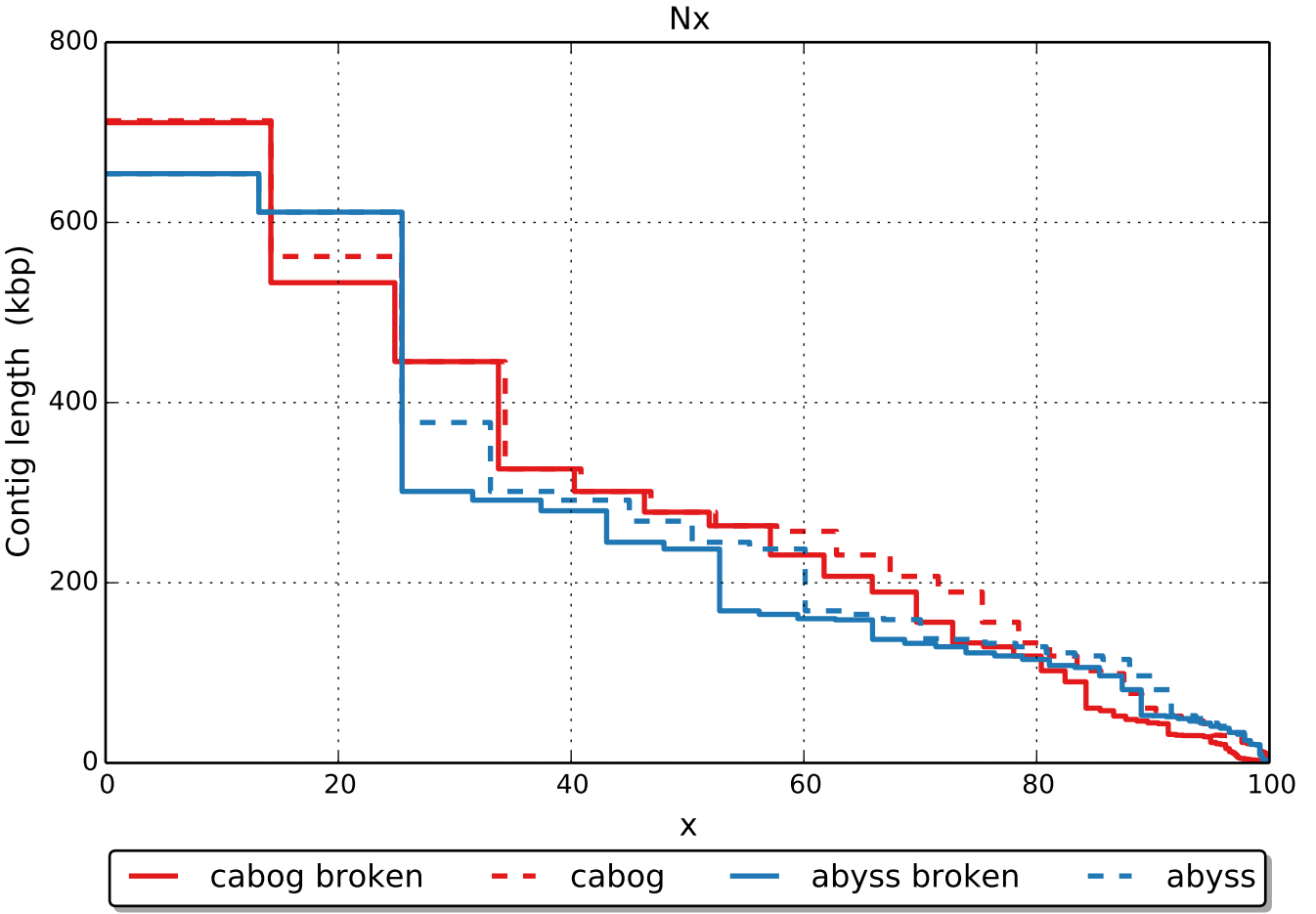

complete genes
620
610
600
590
580
cabog broken
cabog
abyss broken
abyss

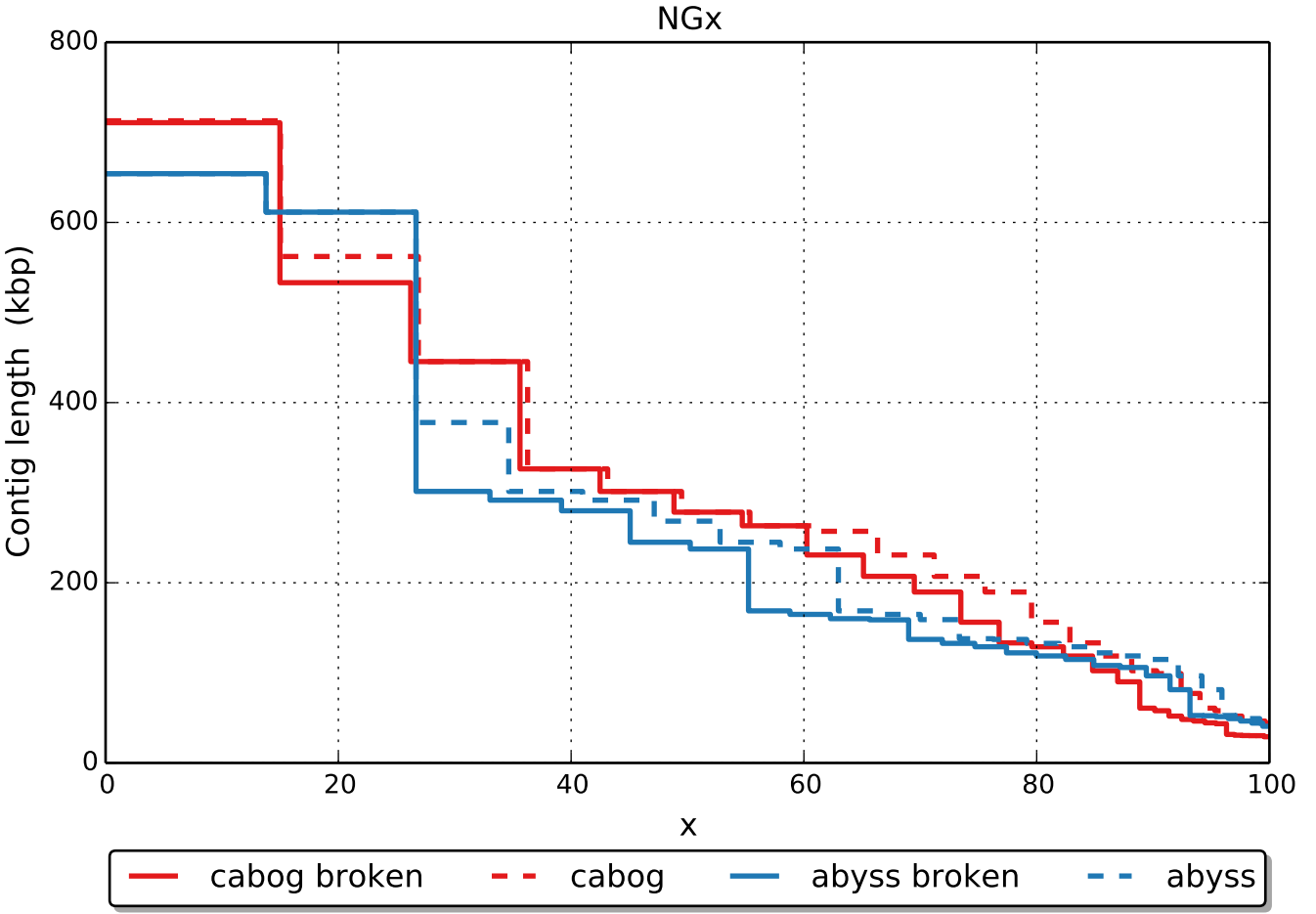

Genome fraction, %
100
50
cabog broken
cabog
abyss broken
abyss

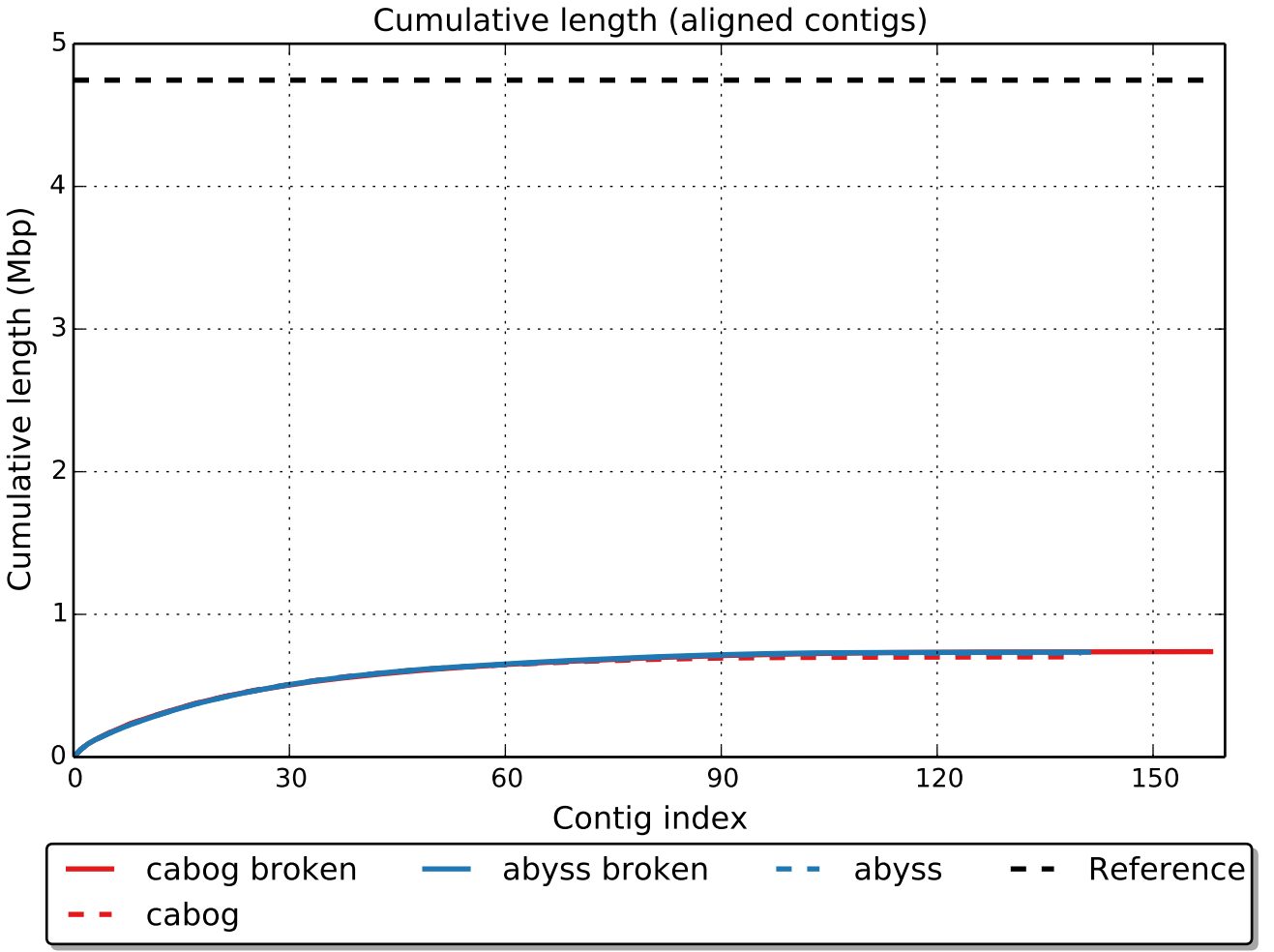
Scaffold

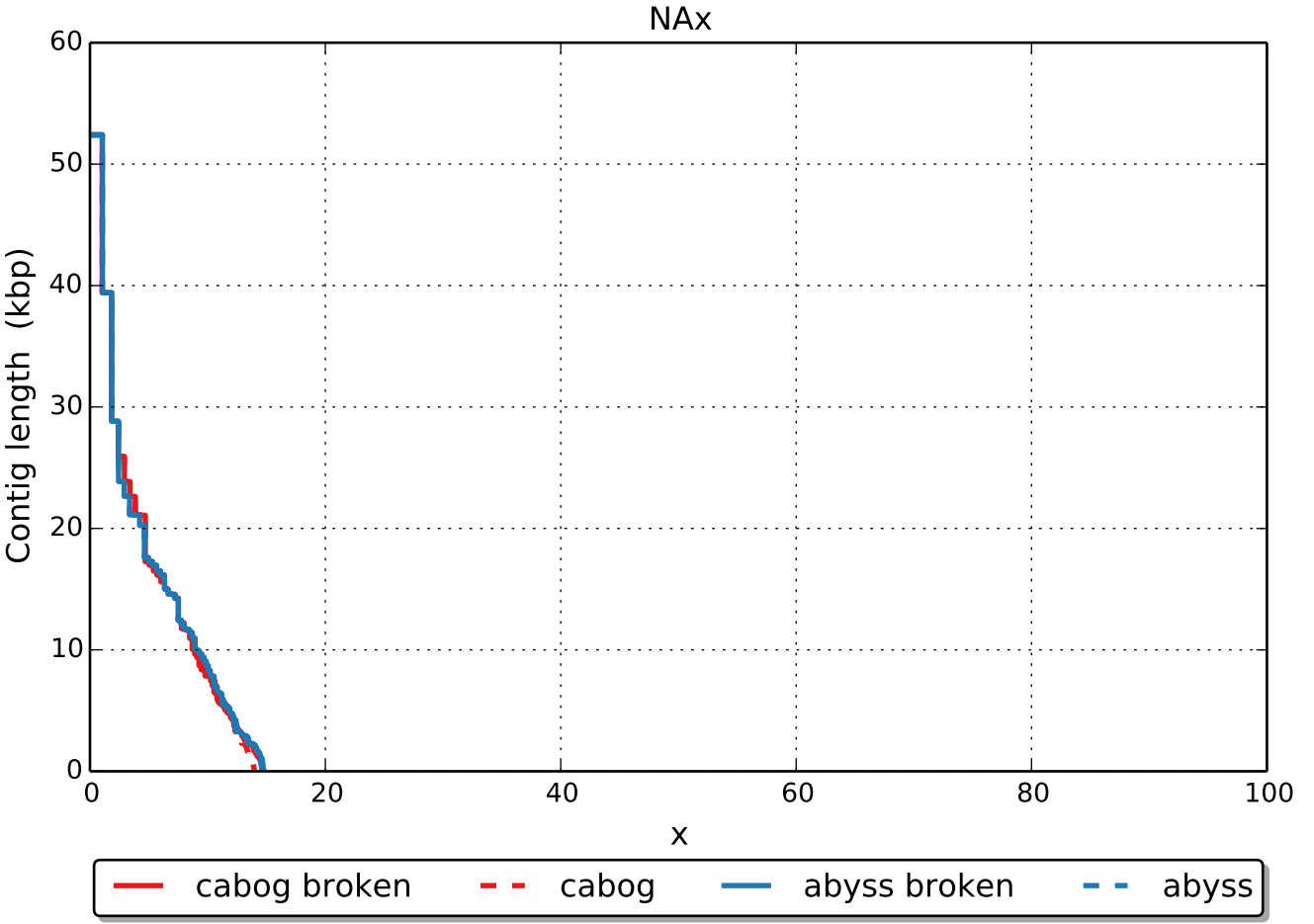

Cumulative length
Cumulative length (Mbp)
Contig index
0
1
2
3
4
5
6
0
20
40
60
80
100
cabog broken
cabog
abyss broken
abyss
Reference

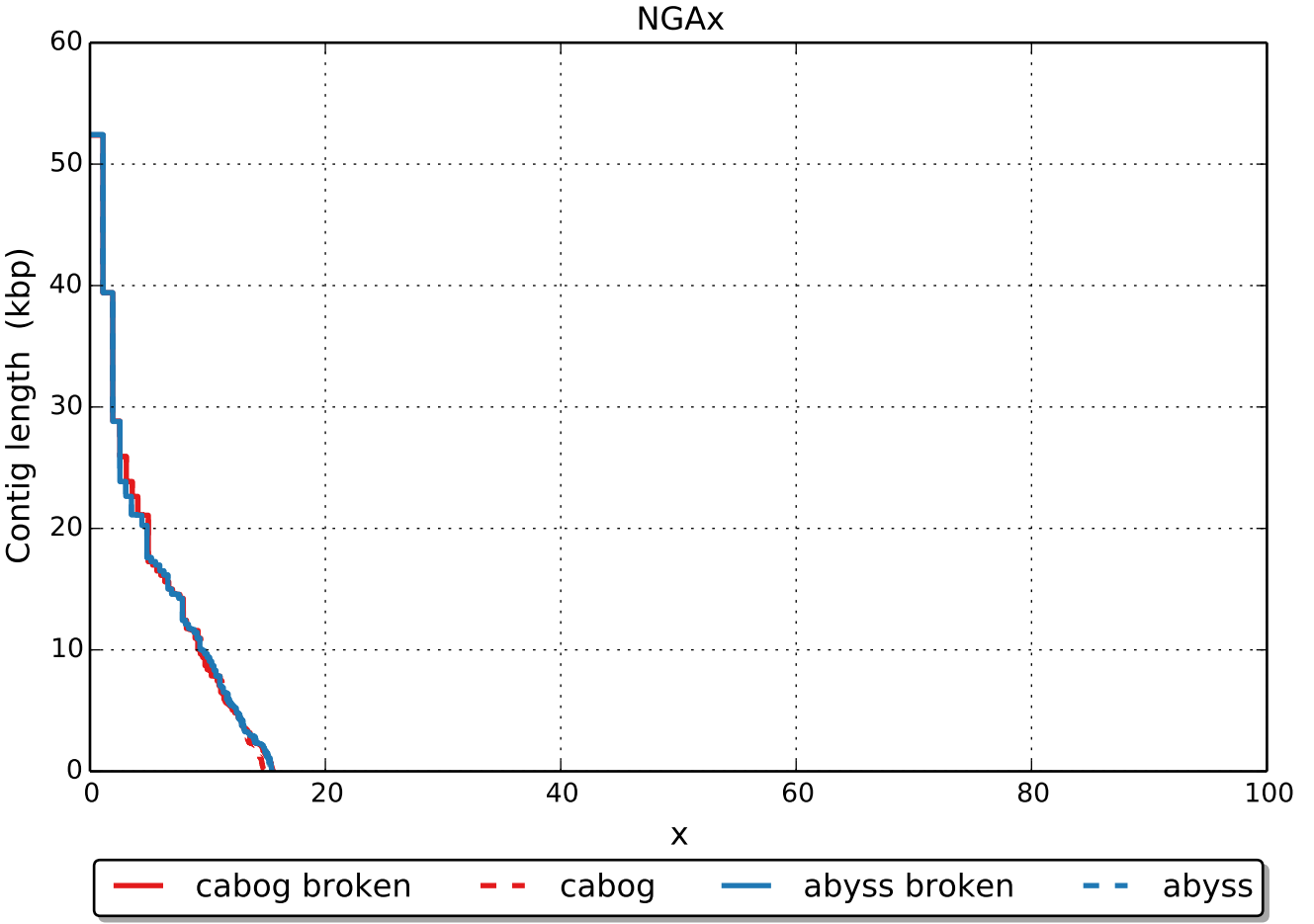

GC content
windows
3000
2400
1800
1200
600
0
0
20
40
60
80
100
GC (%)
cabog broken
abyss broken
abyss
Reference
cabog

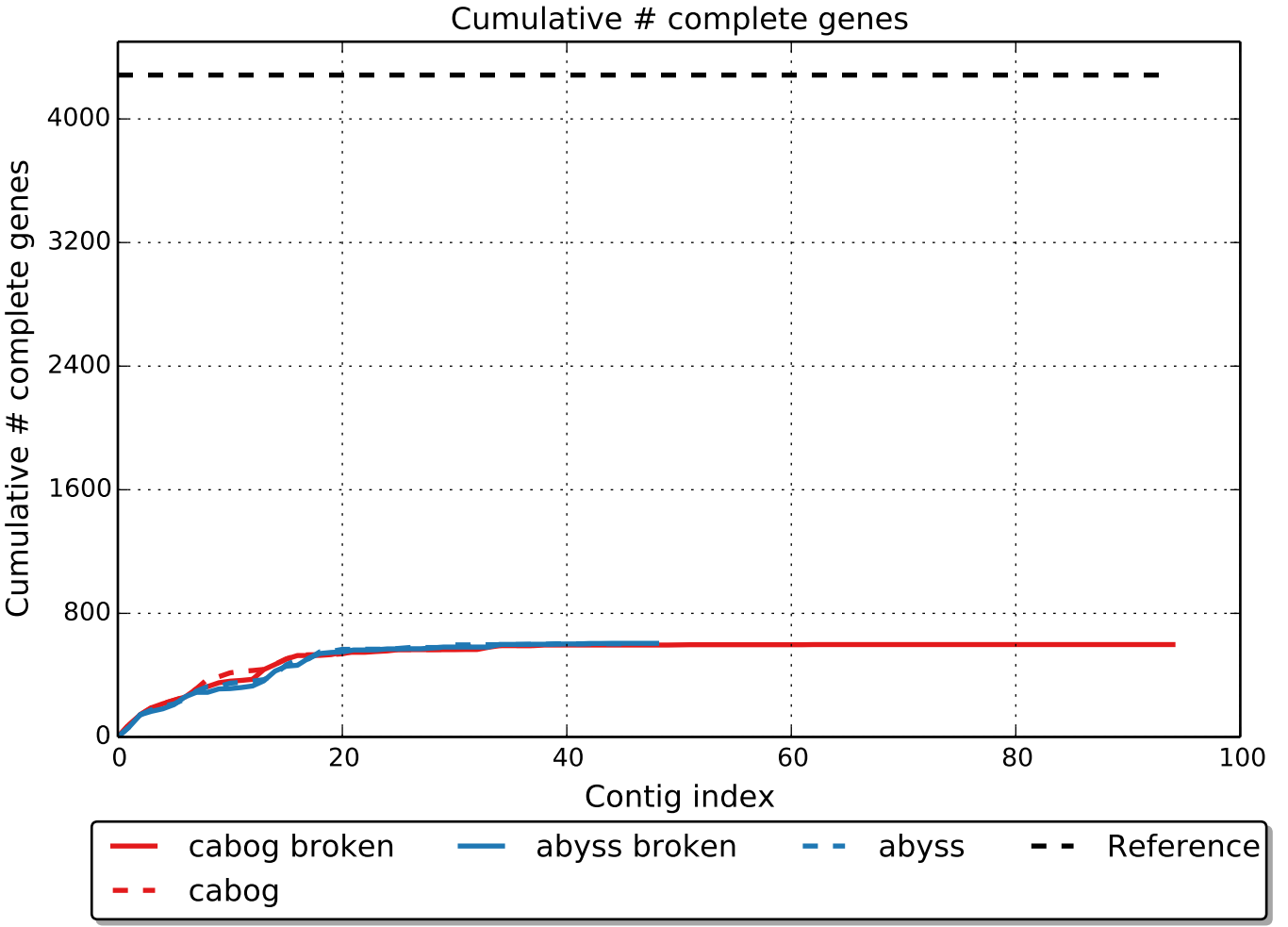

Nx
800
600
400
200
0
Contig length (kbp)
0
20
40
60
80
100
x
cabog broken
cabog
abyss broken
abyss

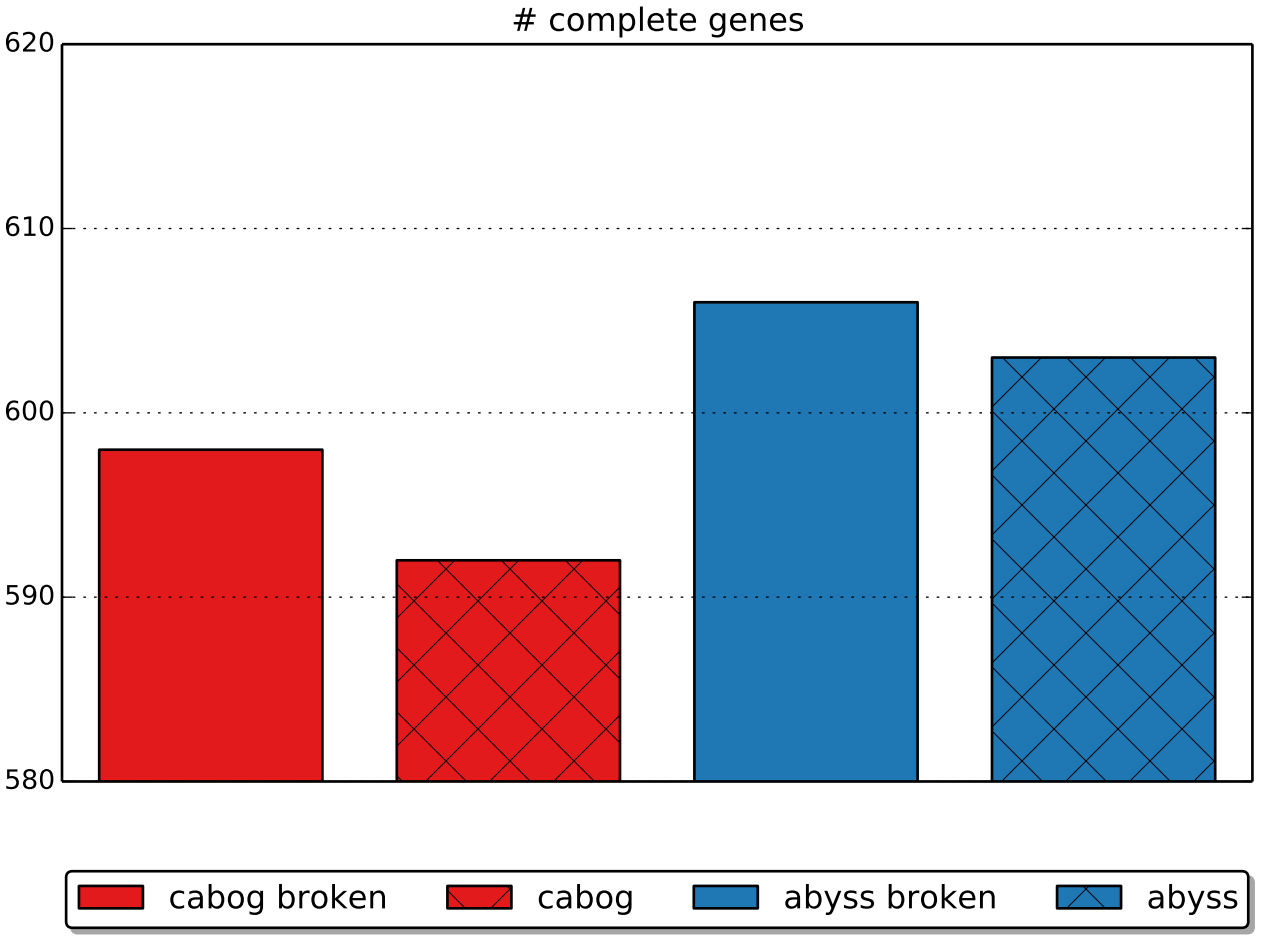

NGx
800
600
400
200
0
Contig length (kbp)
0
20
40
60
80
100
x
cabog broken
cabog
abyss broken
abyss

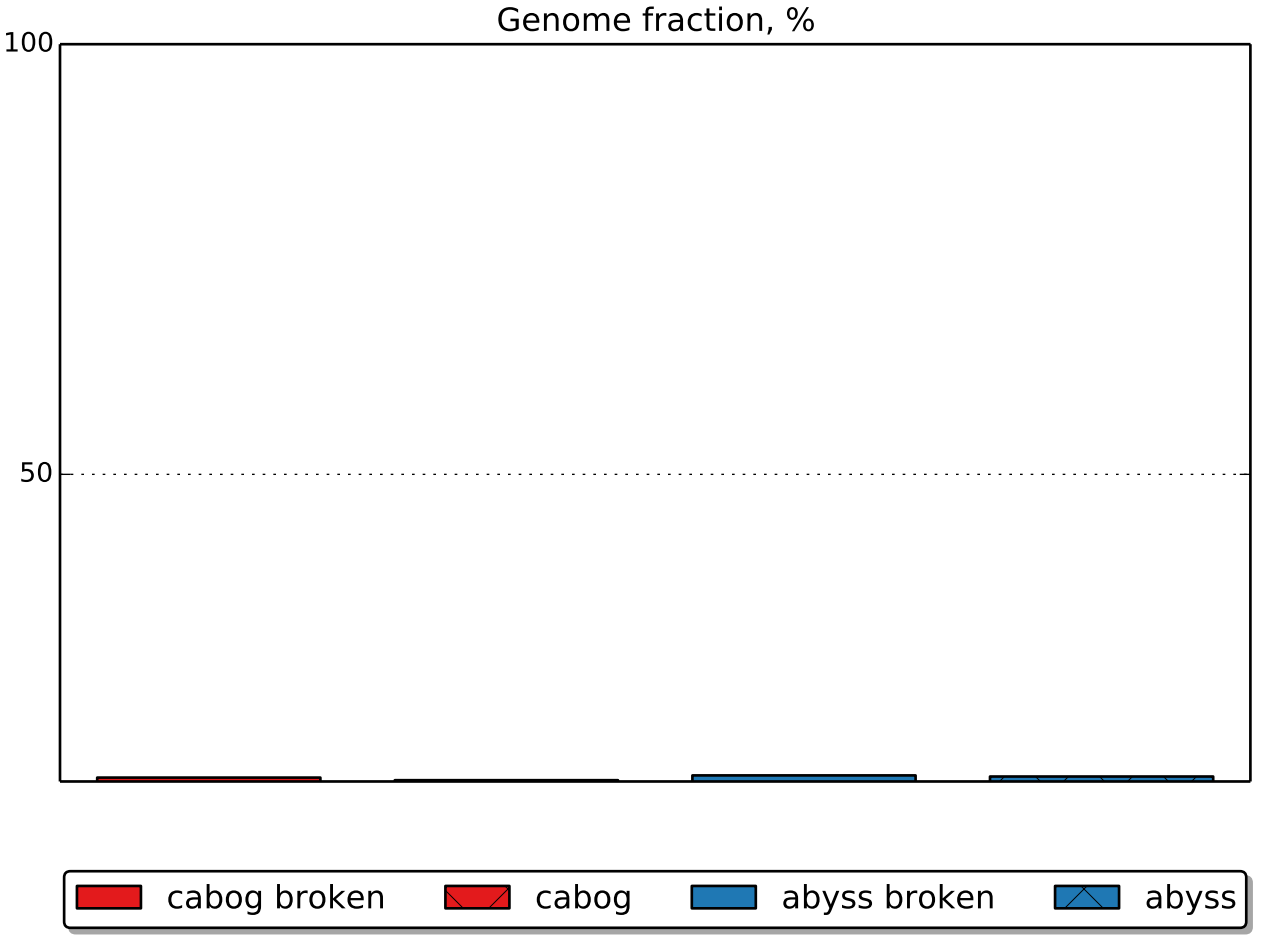

Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
1
2
3
4
5
0
30
60
90
120
150
Contig index
cabog broken
abyss broken
abyss
Reference
cabog


NAx
Contig length (kbp)
60
50
40
30
20
10
0
0
20
40
60
80
100
x
cabog broken
cabog
abyss broken
abyss

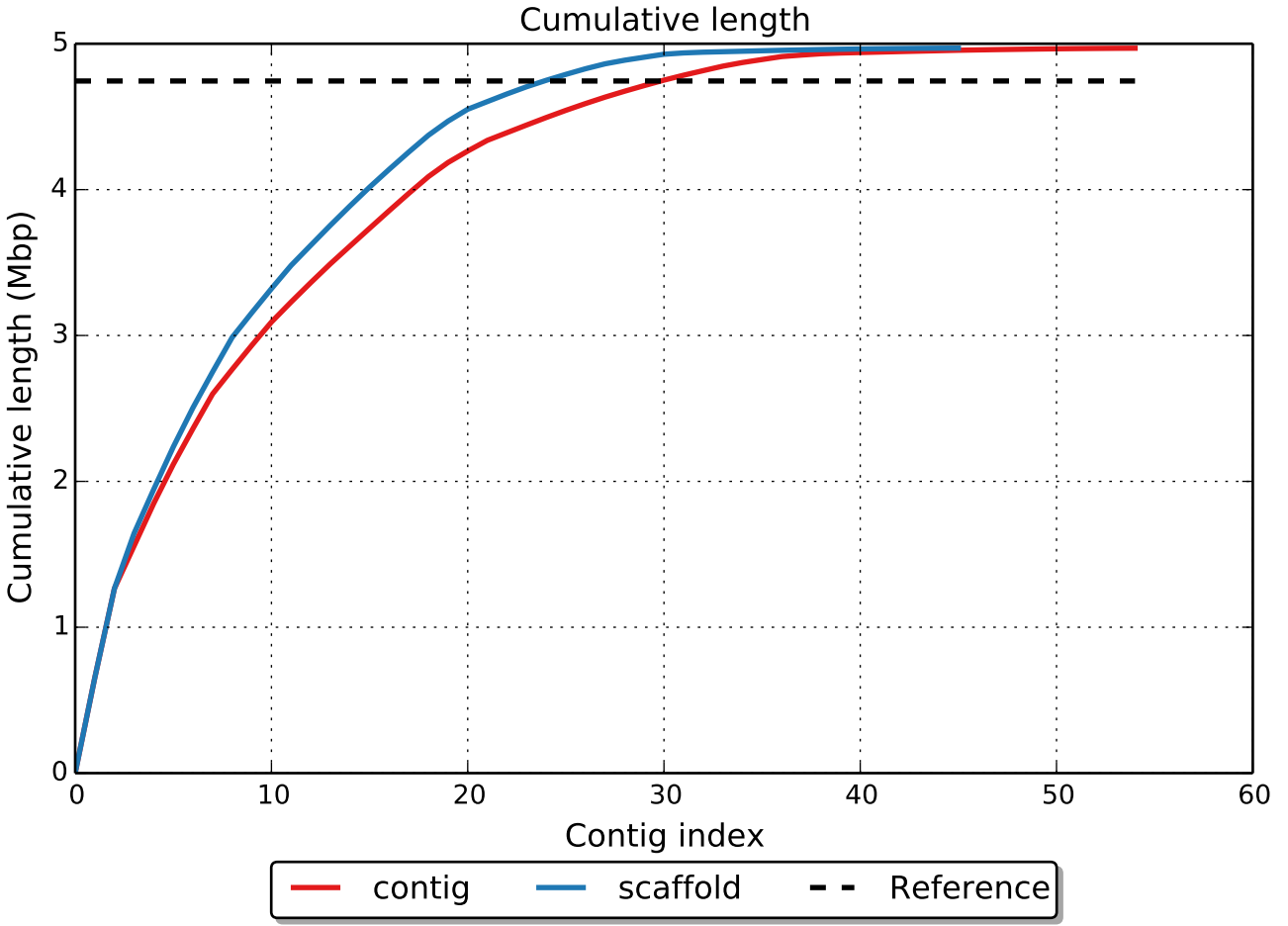

NGAx
Contig length (kbp)
60
50
40
30
20
10
0
0
20
40
60
80
100
x
cabog broken
cabog
abyss broken
abyss

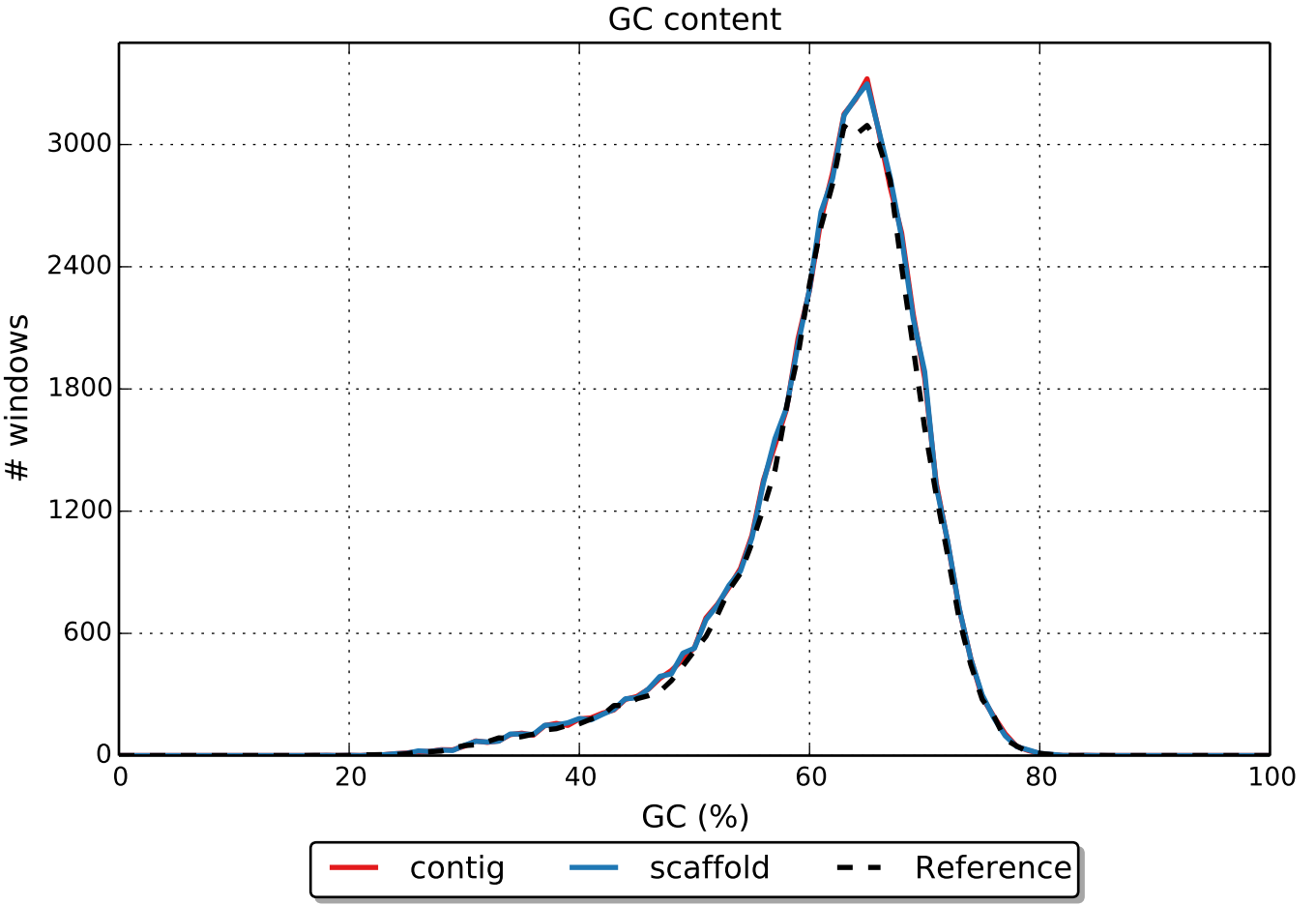

Cumulative # complete genes
Cumulative # complete genes
4000
3200
2400
1600
800
0
0
20
40
60
80
100
Contig index
cabog broken
abyss broken
abyss
Reference
cabog

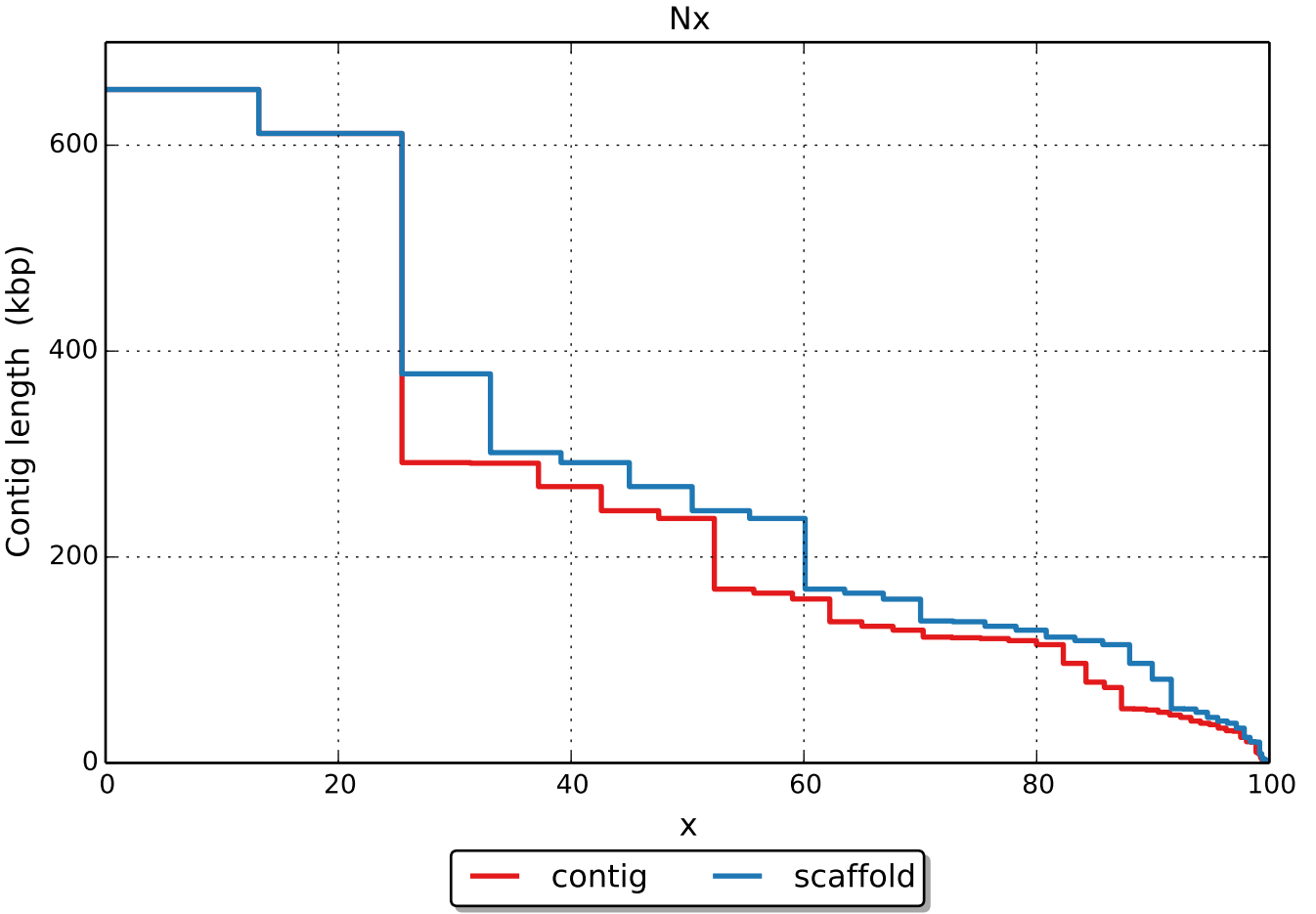

complete genes
620
610
600
590
580
cabog broken
cabog
abyss broken
abyss

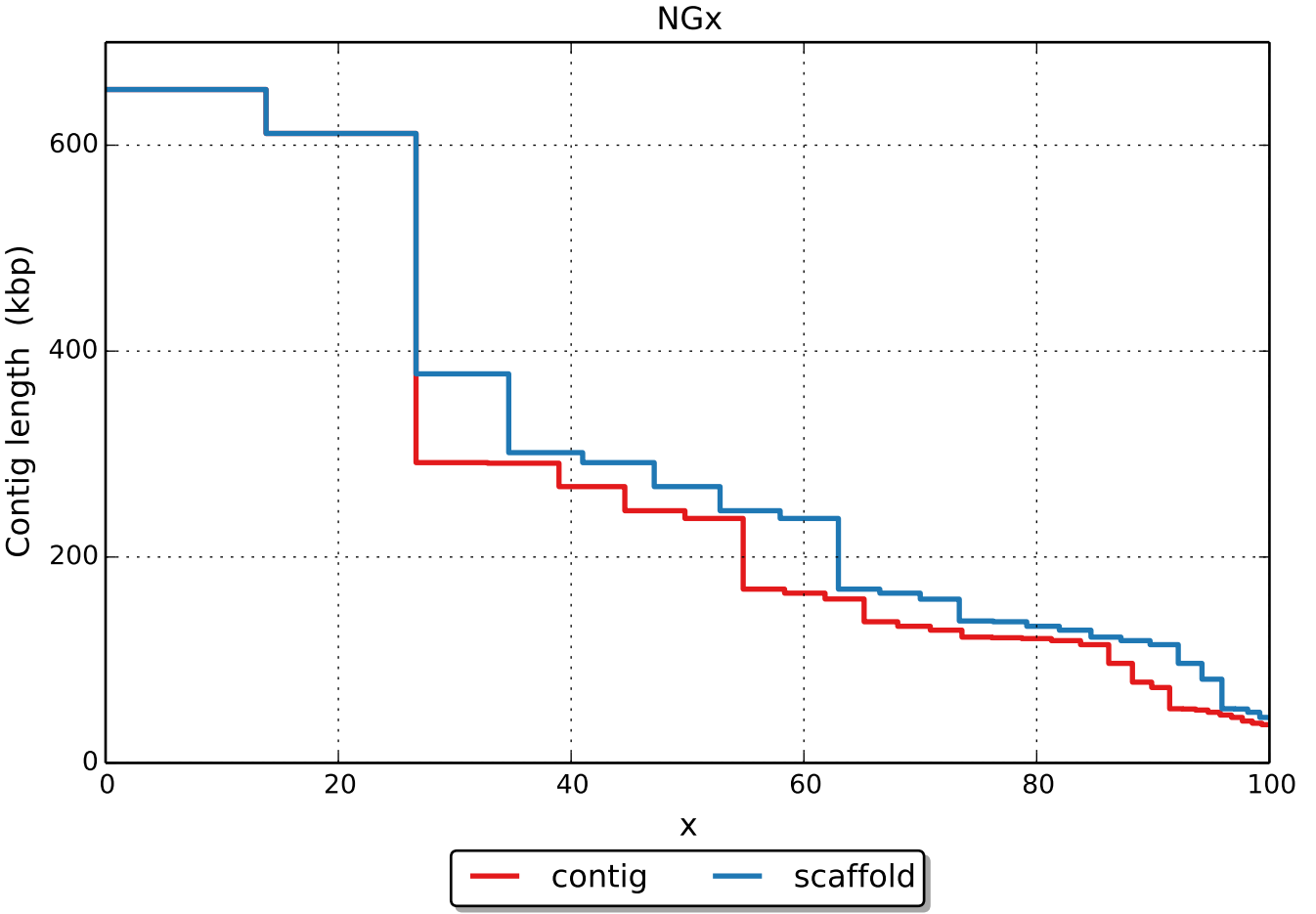

Genome fraction, %
100
50
cabog broken
cabog
abyss broken
abyss

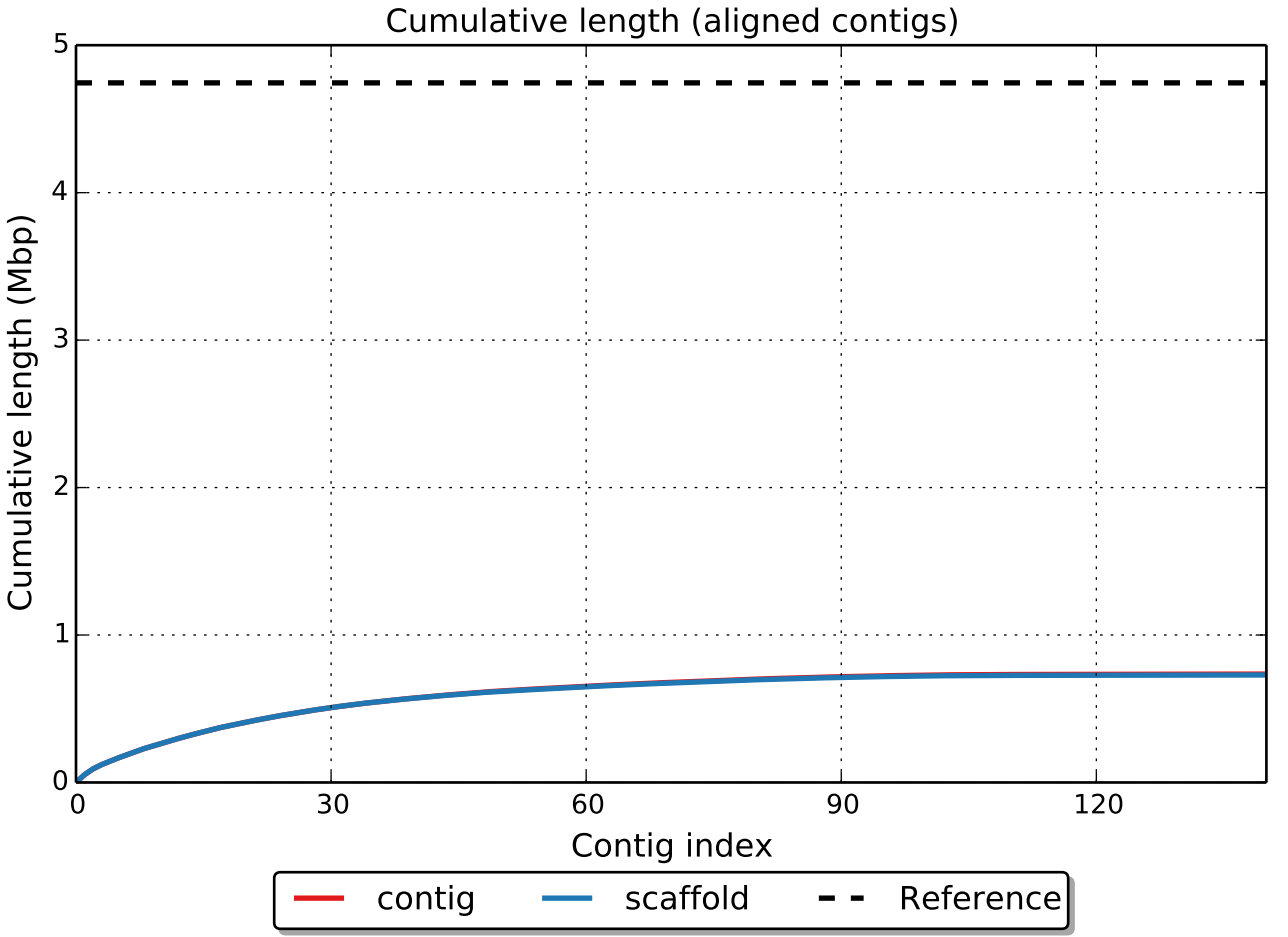
Combined_dataset

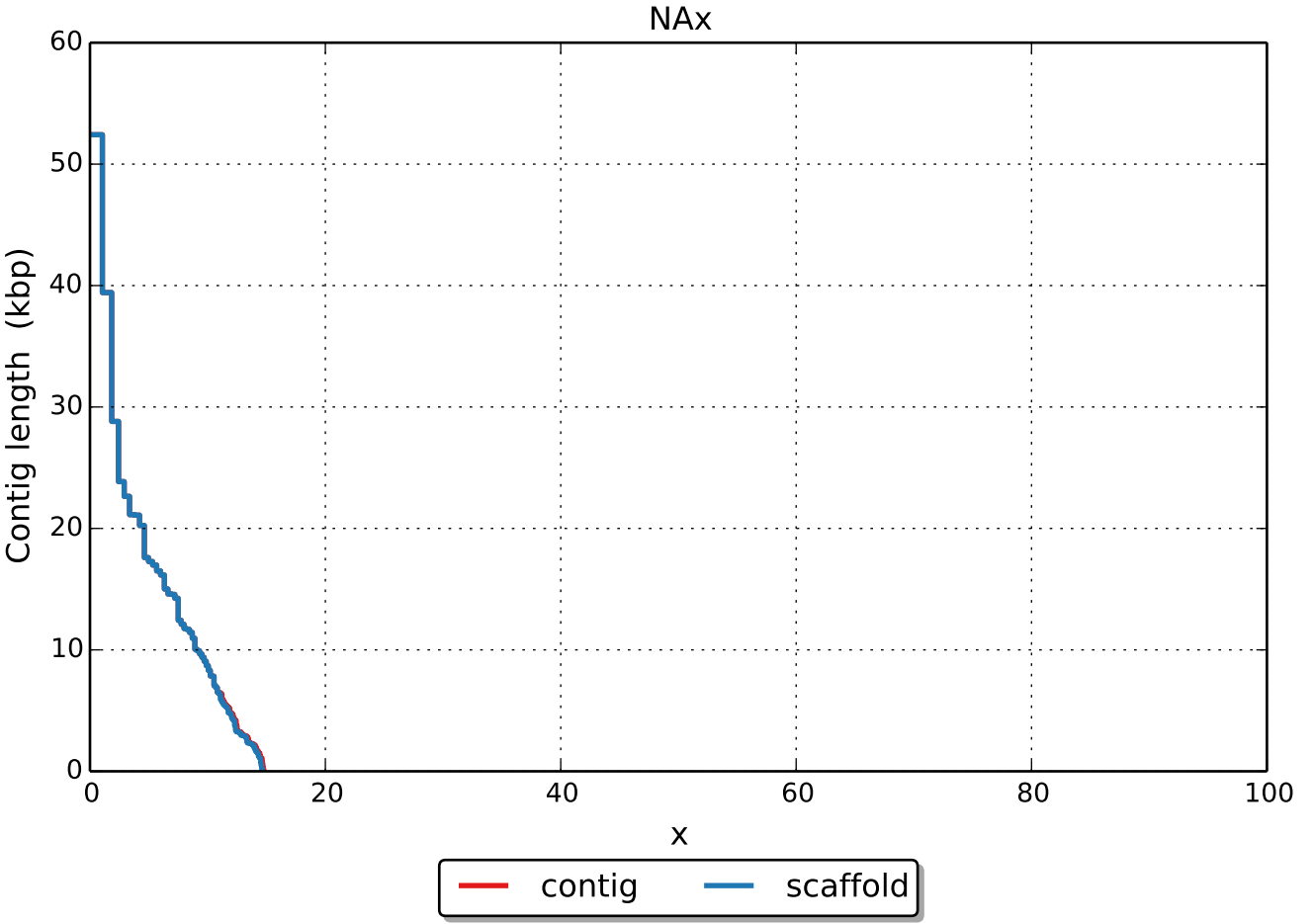

Cumulative length
Cumulative length (Mbp)
Contig index
0
1
2
3
4
5
0
10
20
30
40
50
60
contig
scaffold
Reference

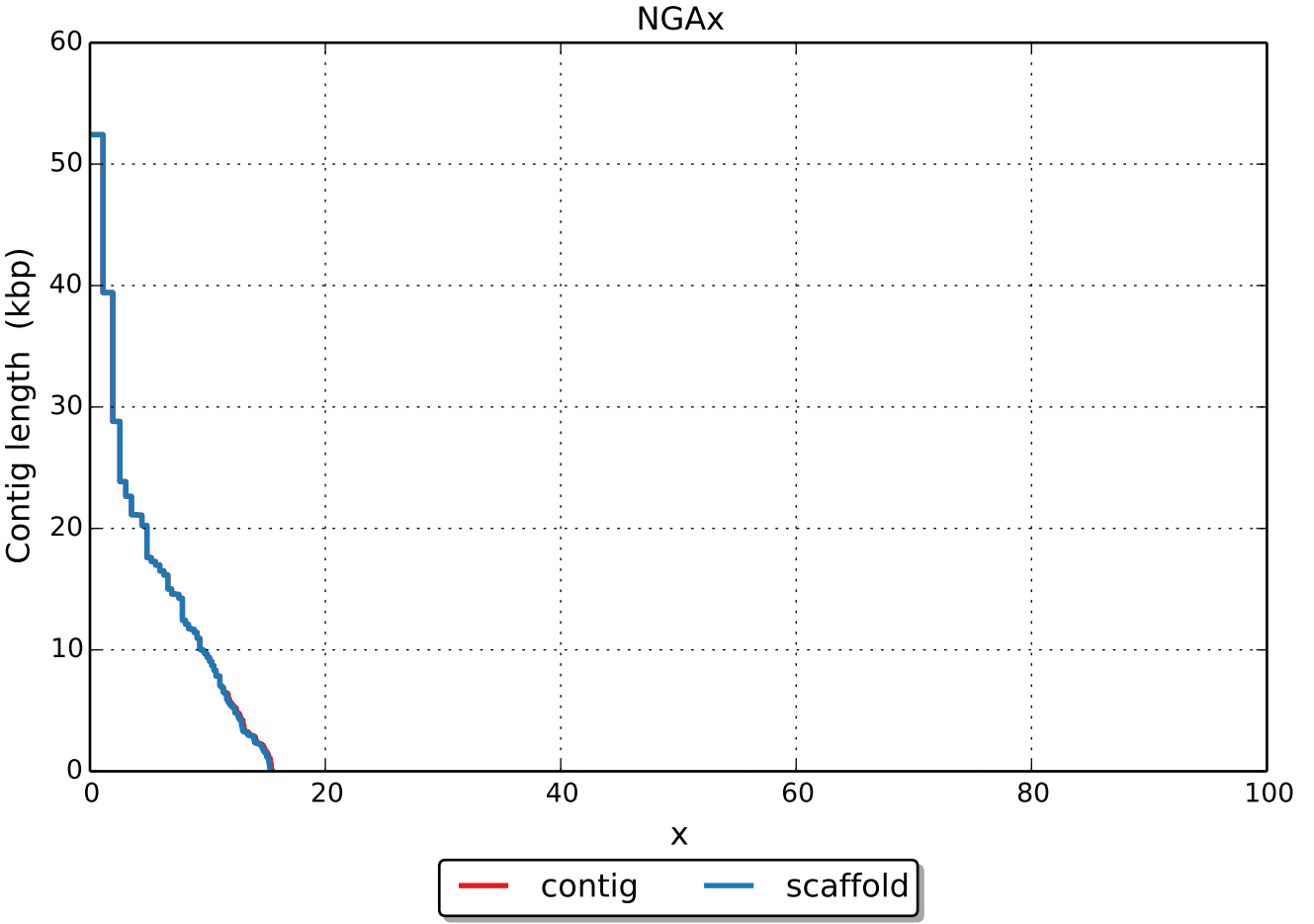

GC content
windows
3000
2400
1800
1200
600
0
0
20
40
60
80
100
GC (%)
contig
scaffold
Reference

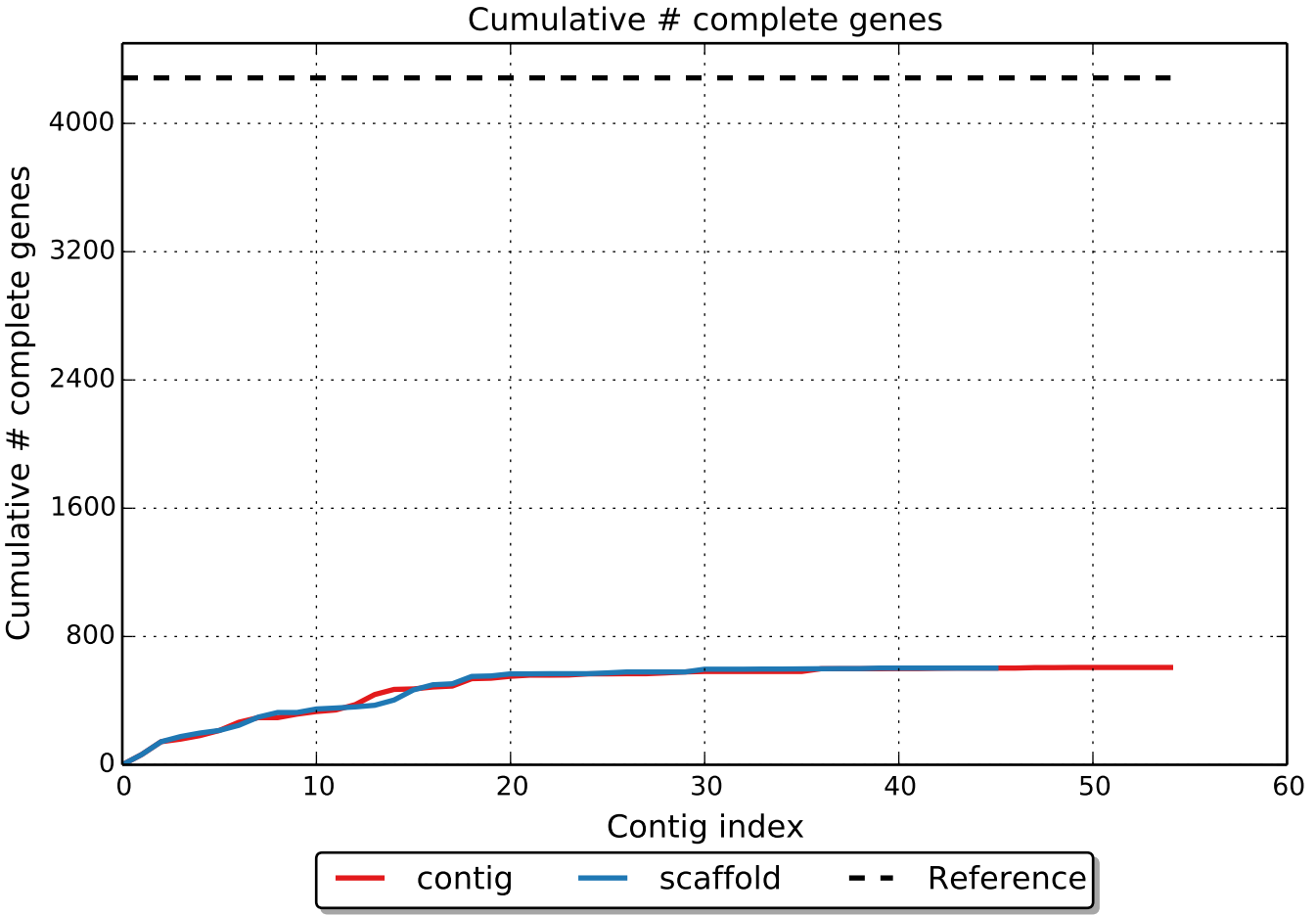

Nx
Contig length (kbp)
600
400
200
0
0
20
40
60
80
100
x
contig
scaffold

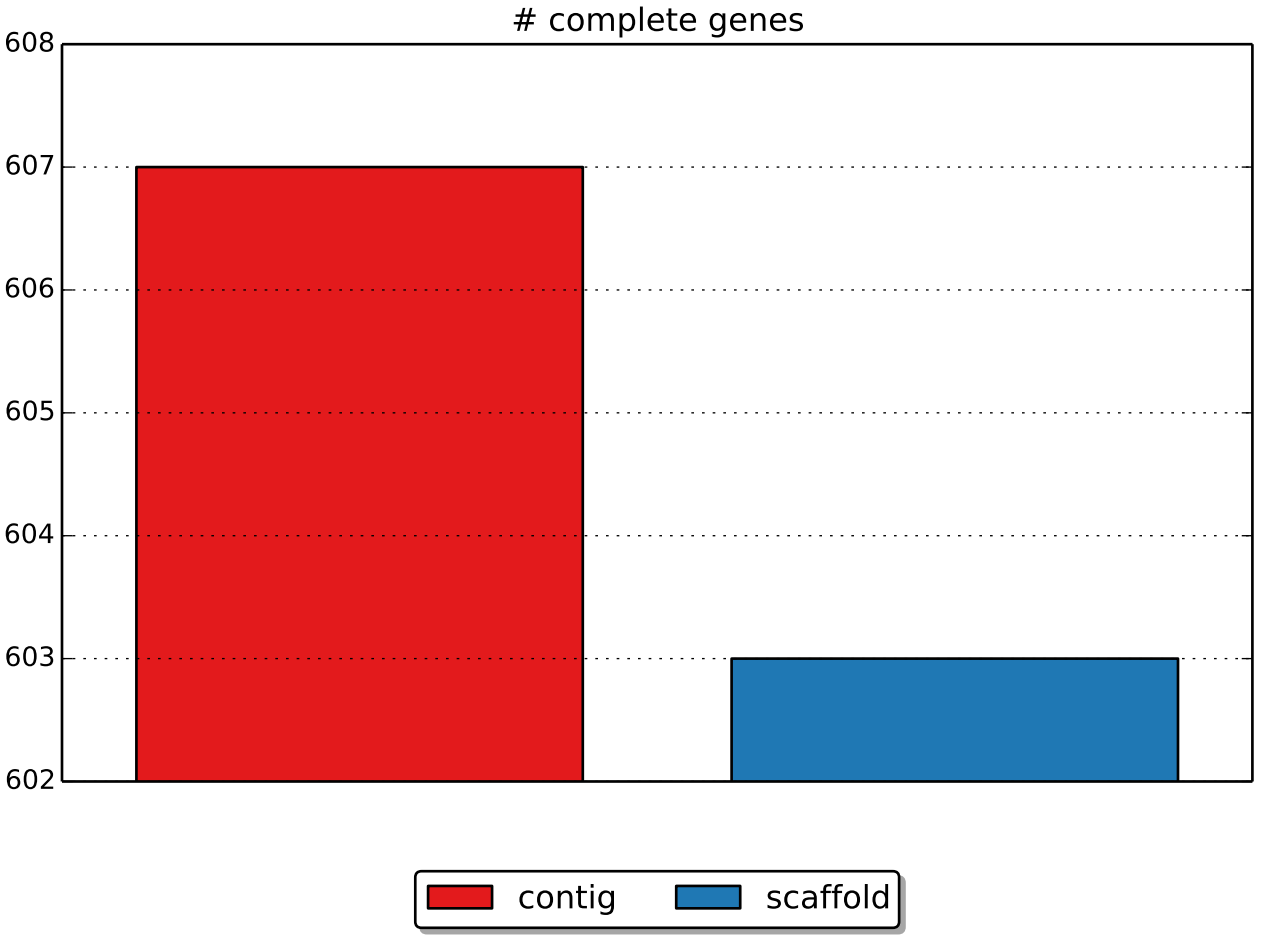

NGx
Contig length (kbp)
600
400
200
0
0
20
40
60
80
100
x
contig
scaffold

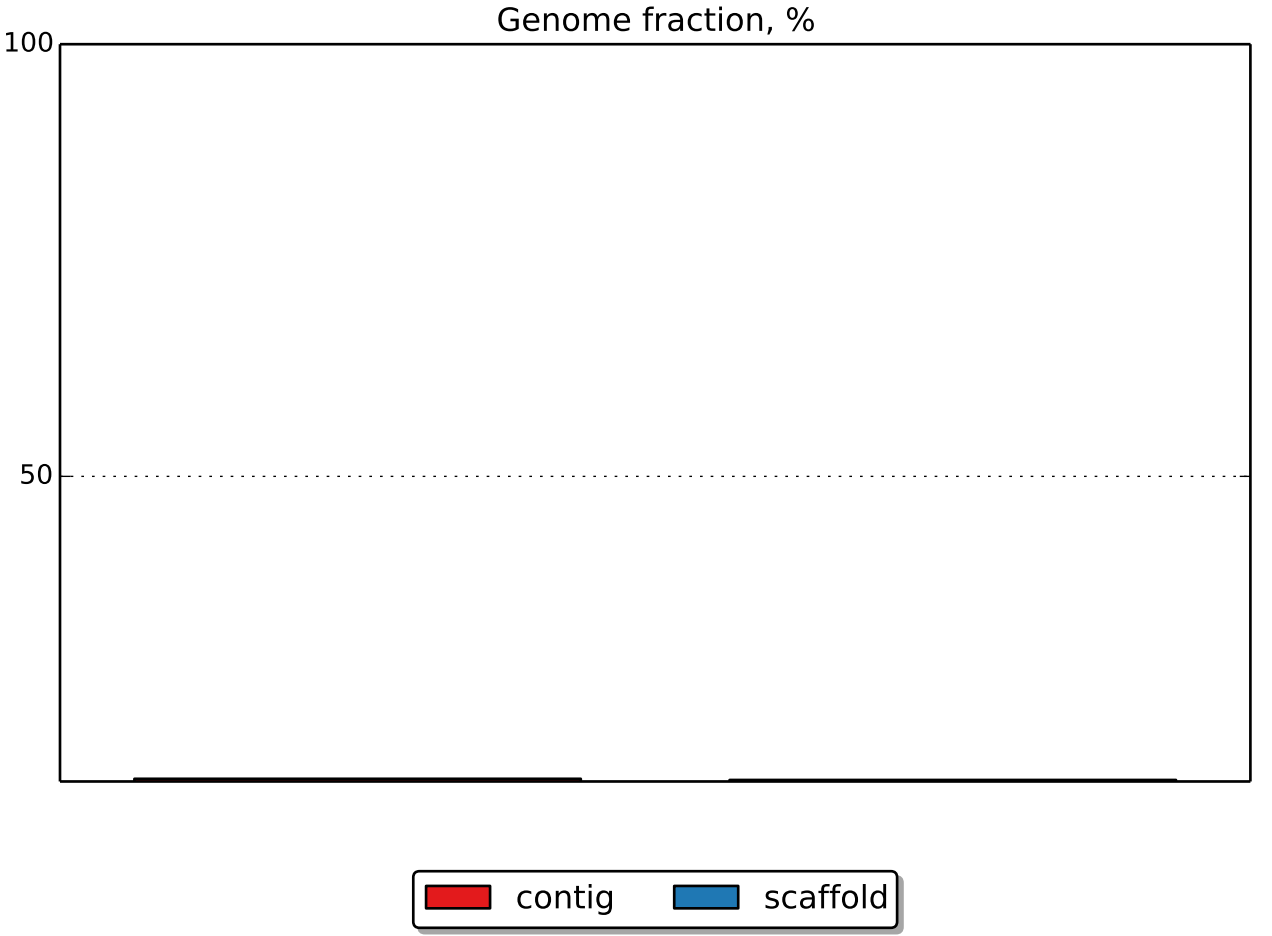

Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
1
2
3
4
5
0
30
60
90
120
Contig index
contig
scaffold
Reference


NAx
Contig length (kbp)
0
10
20
30
40
50
60
0
20
40
60
80
100
x
contig
scaffold


NGAx
Contig length (kbp)
60
50
40
30
20
10
0
0
20
40
60
80
100
x
contig
scaffold


Cumulative # complete genes
Cumulative # complete genes
4000
3200
2400
1600
800
0
0
10
20
30
40
50
60
Contig index
contig
scaffold
Reference


complete genes
608
607
606
605
604
603
602
contig
scaffold


Genome fraction, %
100
50
contig
scaffold