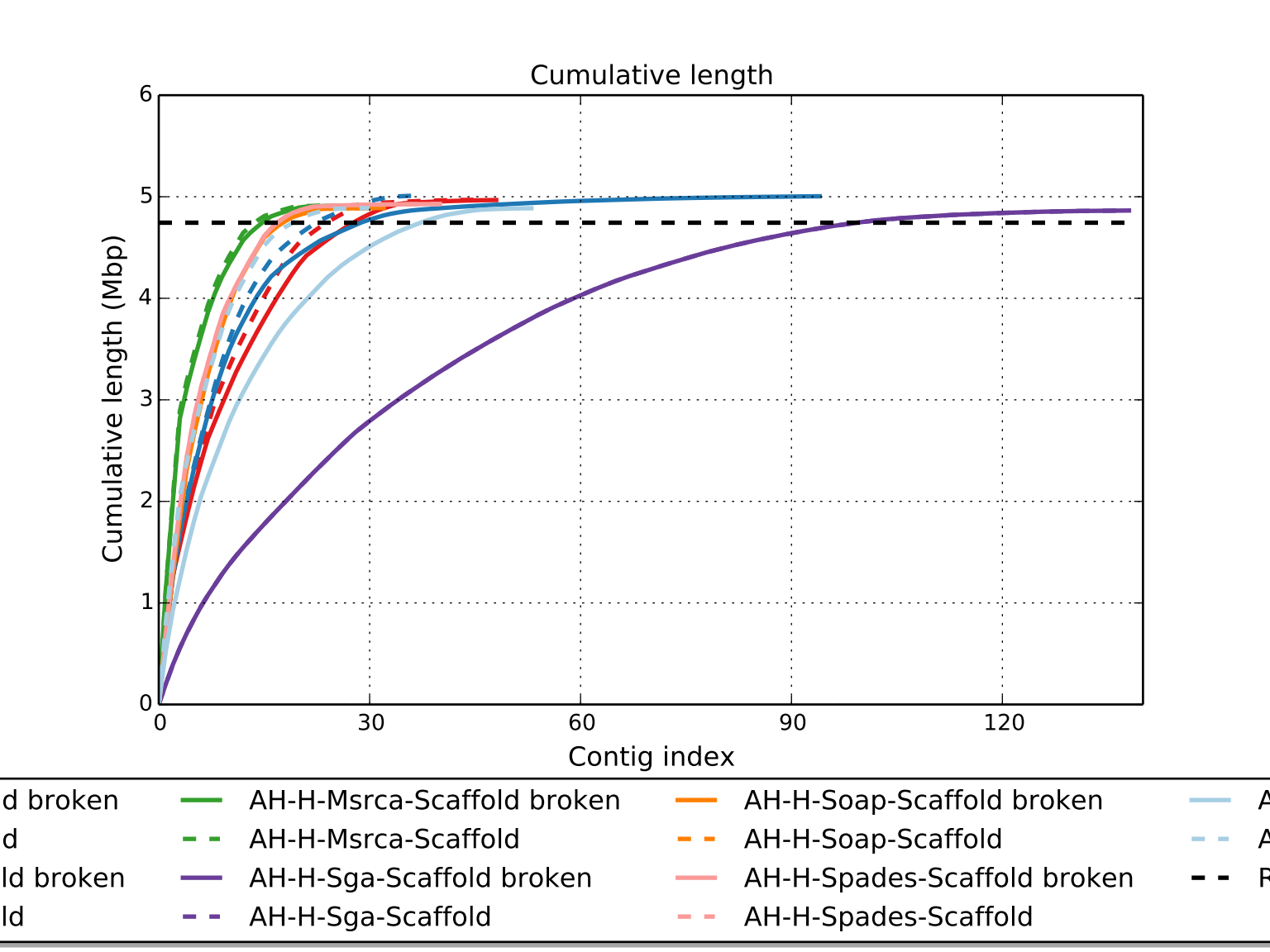
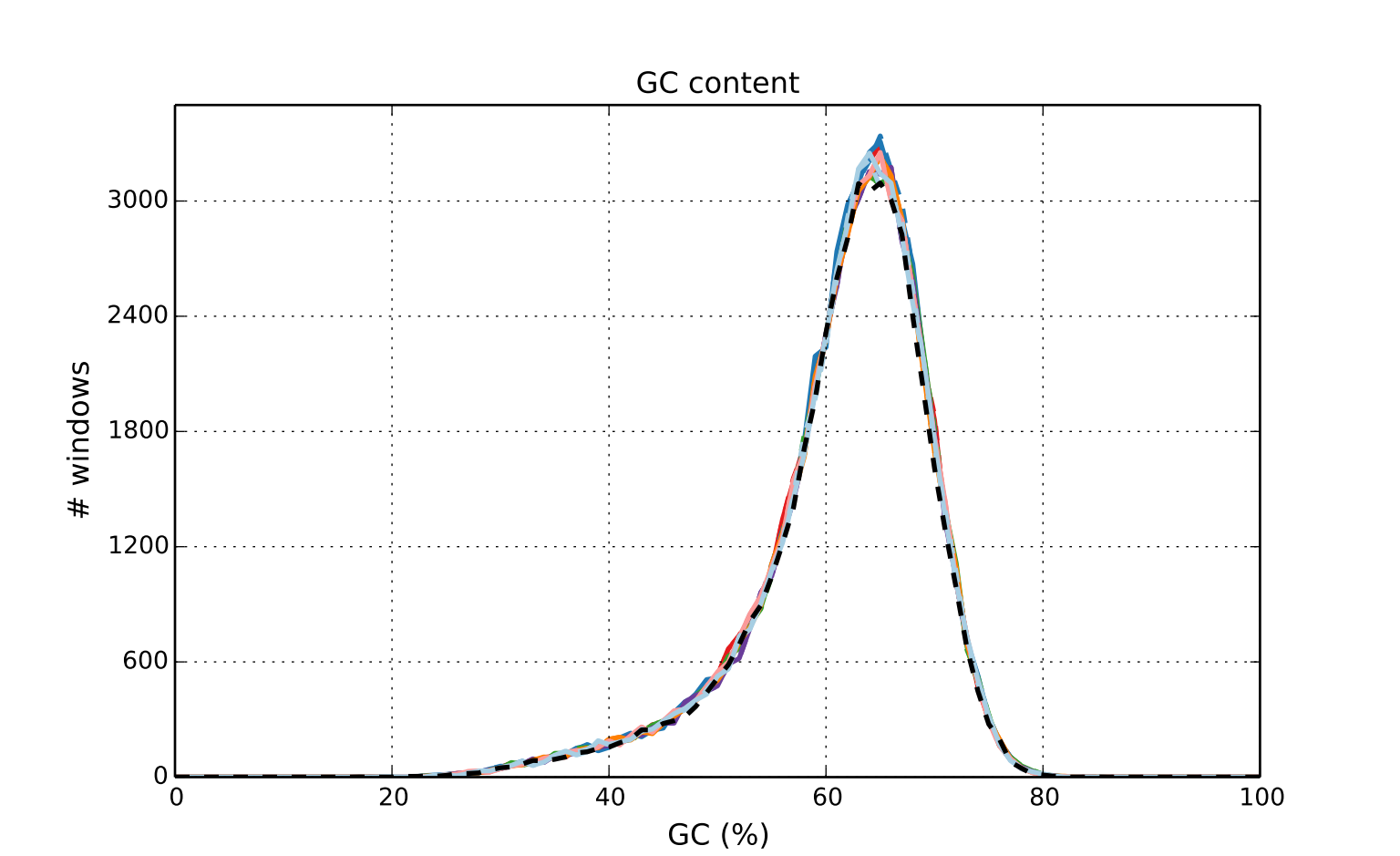
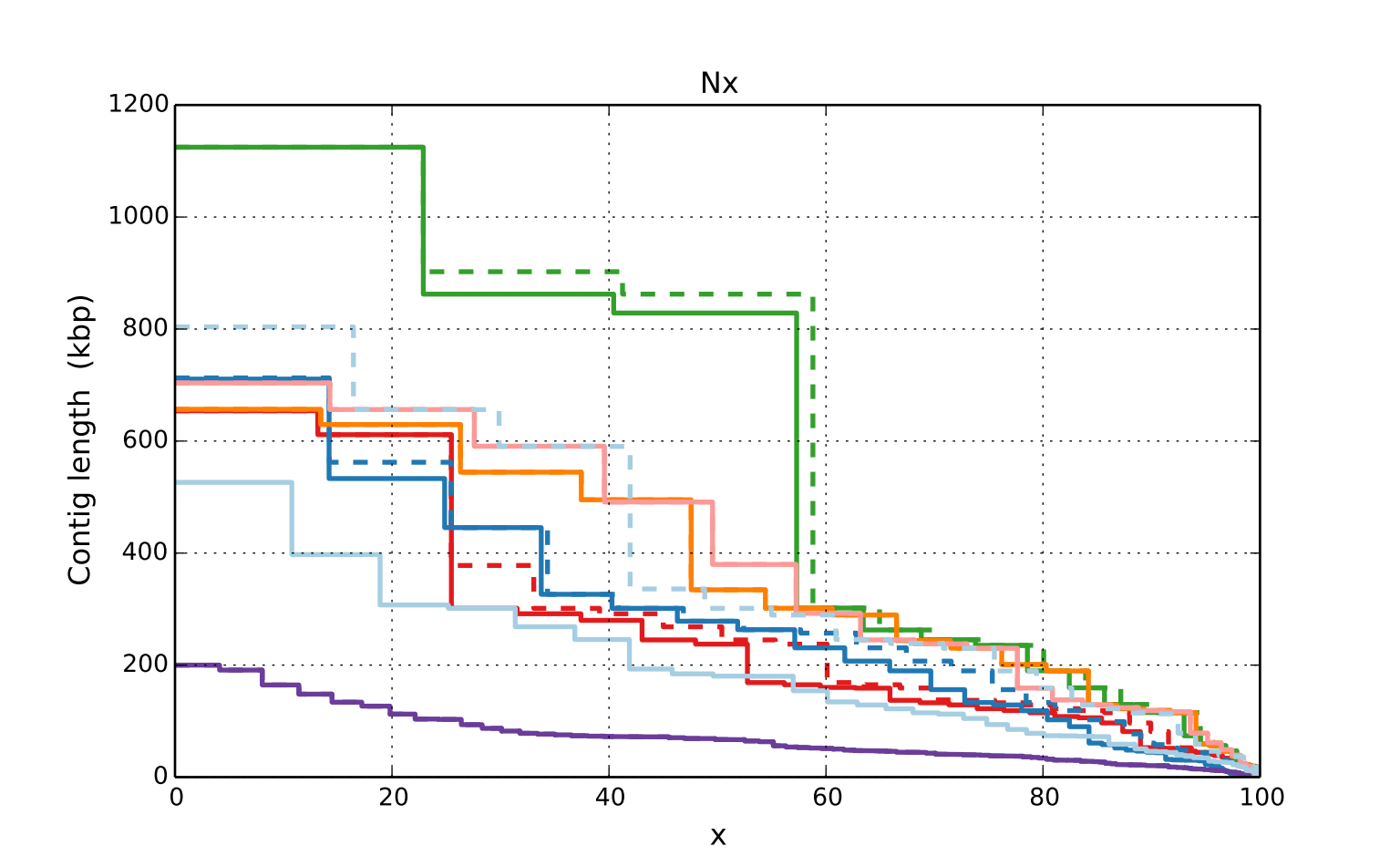
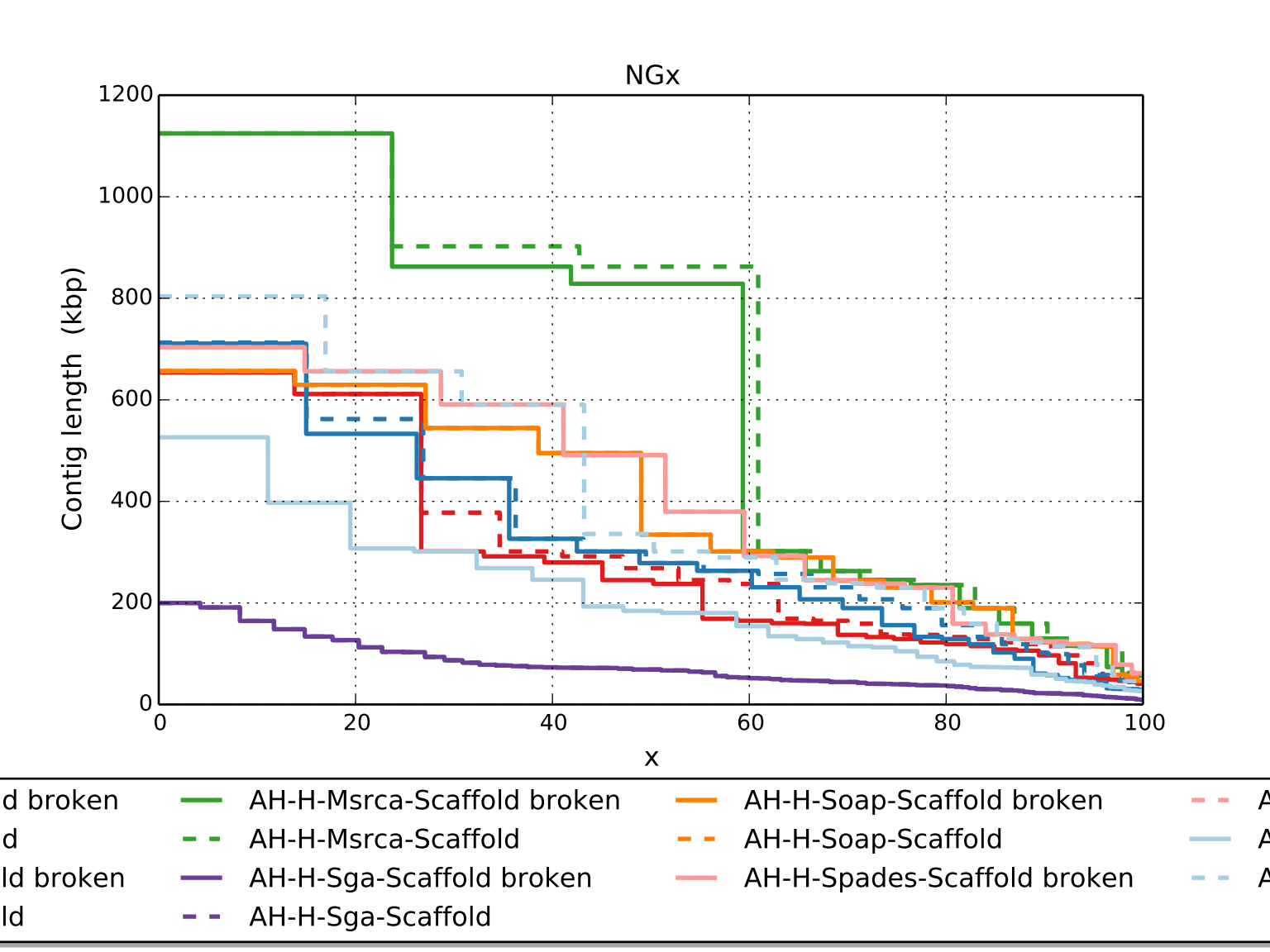
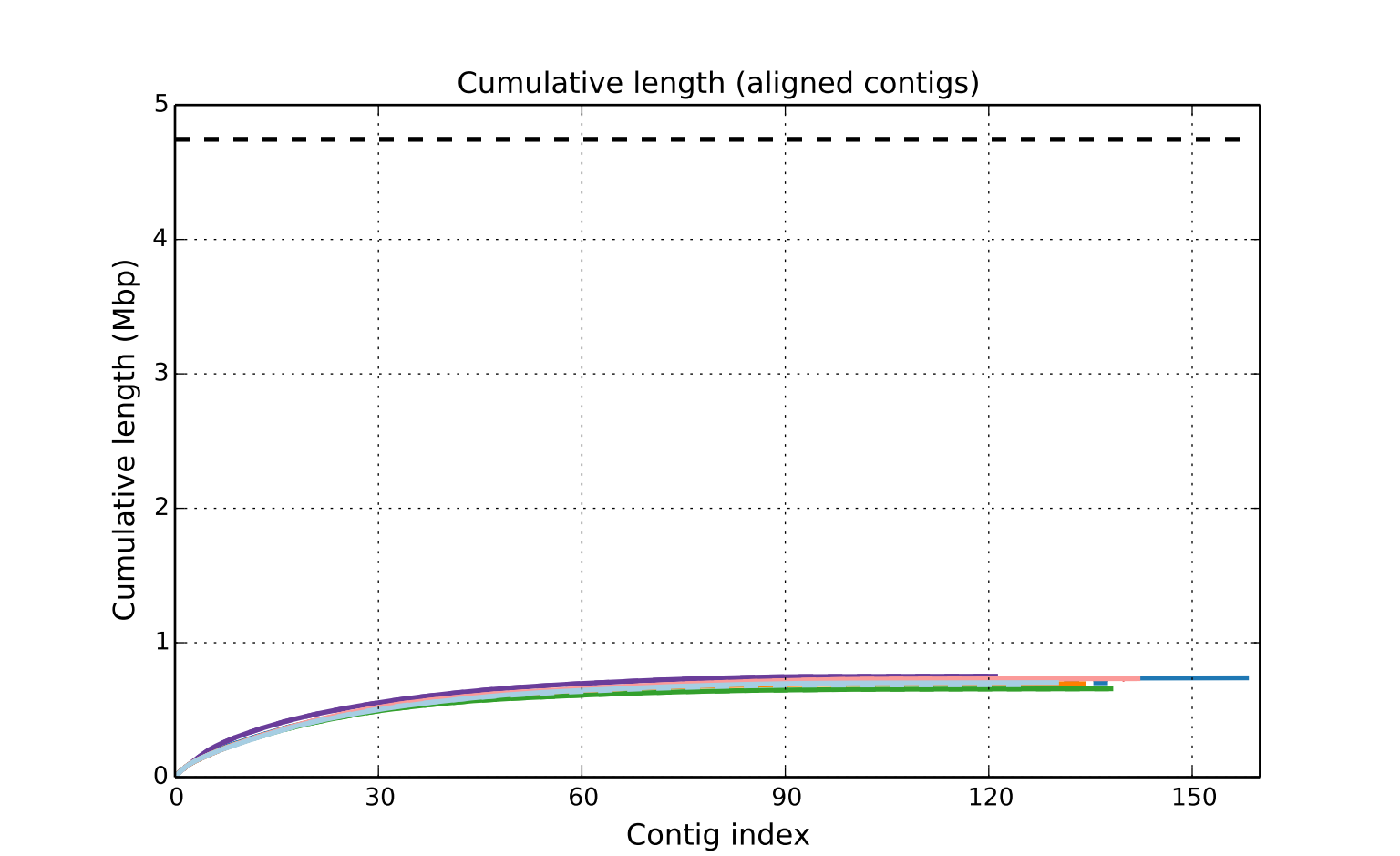
Scaffold

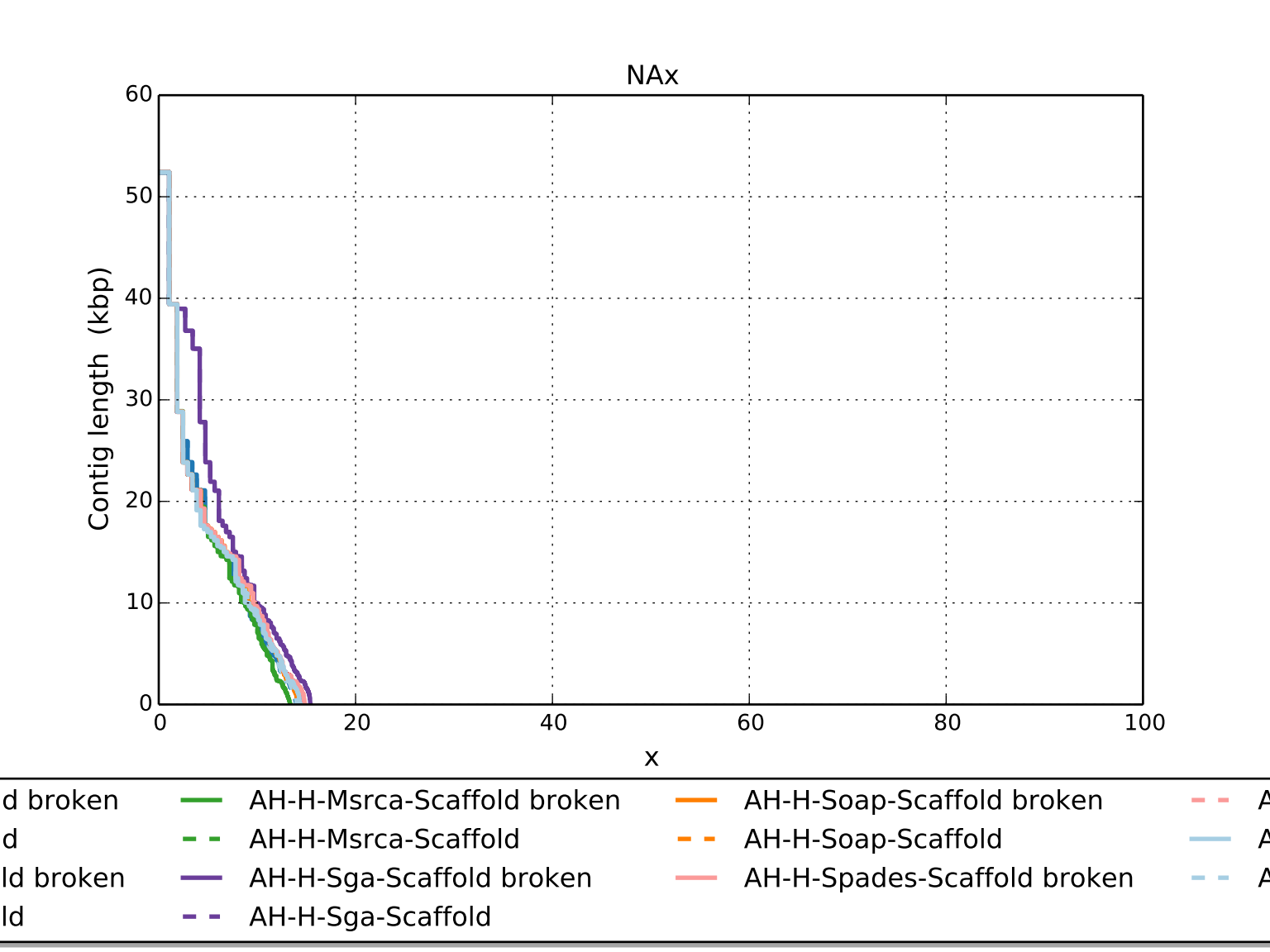

Cumulative length
Cumulative length (Mbp)
Contig index
0
1
2
3
4
5
6
0
30
60
90
120
d broken
d
ld broken
ld
AH-H-Msrca-Scaffold broken
AH-H-Msrca-Scaffold
AH-H-Sga-Scaffold broken
AH-H-Sga-Scaffold
AH-H-Soap-Scaffold broken
AH-H-Soap-Scaffold
AH-H-Spades-Scaffold broken
AH-H-Spades-Scaffold
A
A
R

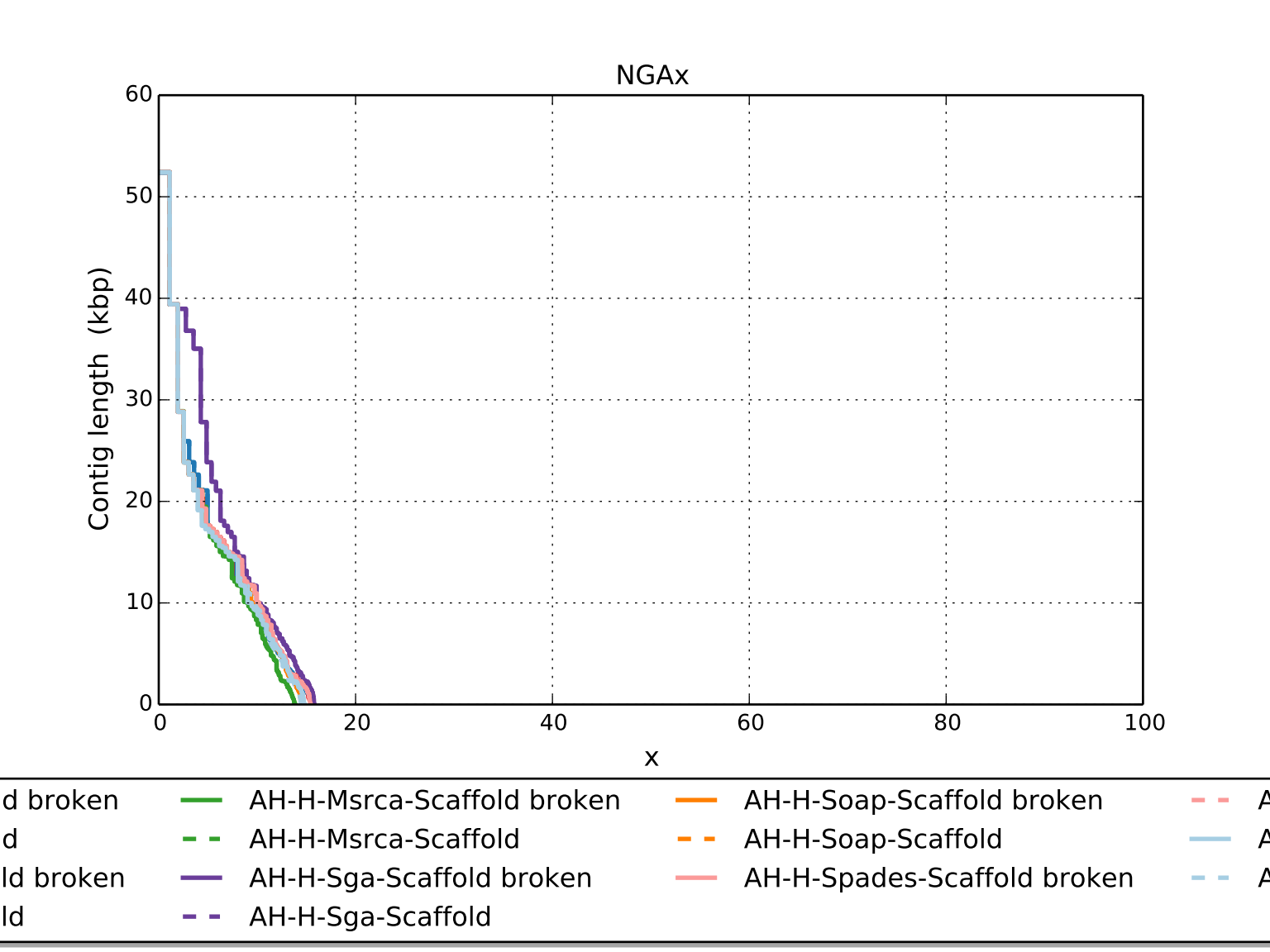

GC content
windows
GC (%)
0
600
1200
1800
2400
3000
0
20
40
60
80
100
d broken
d
ld broken
ld
AH-H-Msrca-Scaffold broken
AH-H-Msrca-Scaffold
AH-H-Sga-Scaffold broken
AH-H-Sga-Scaffold
AH-H-Soap-Scaffold broken
AH-H-Soap-Scaffold
AH-H-Spades-Scaffold broken
AH-H-Spades-Scaffold

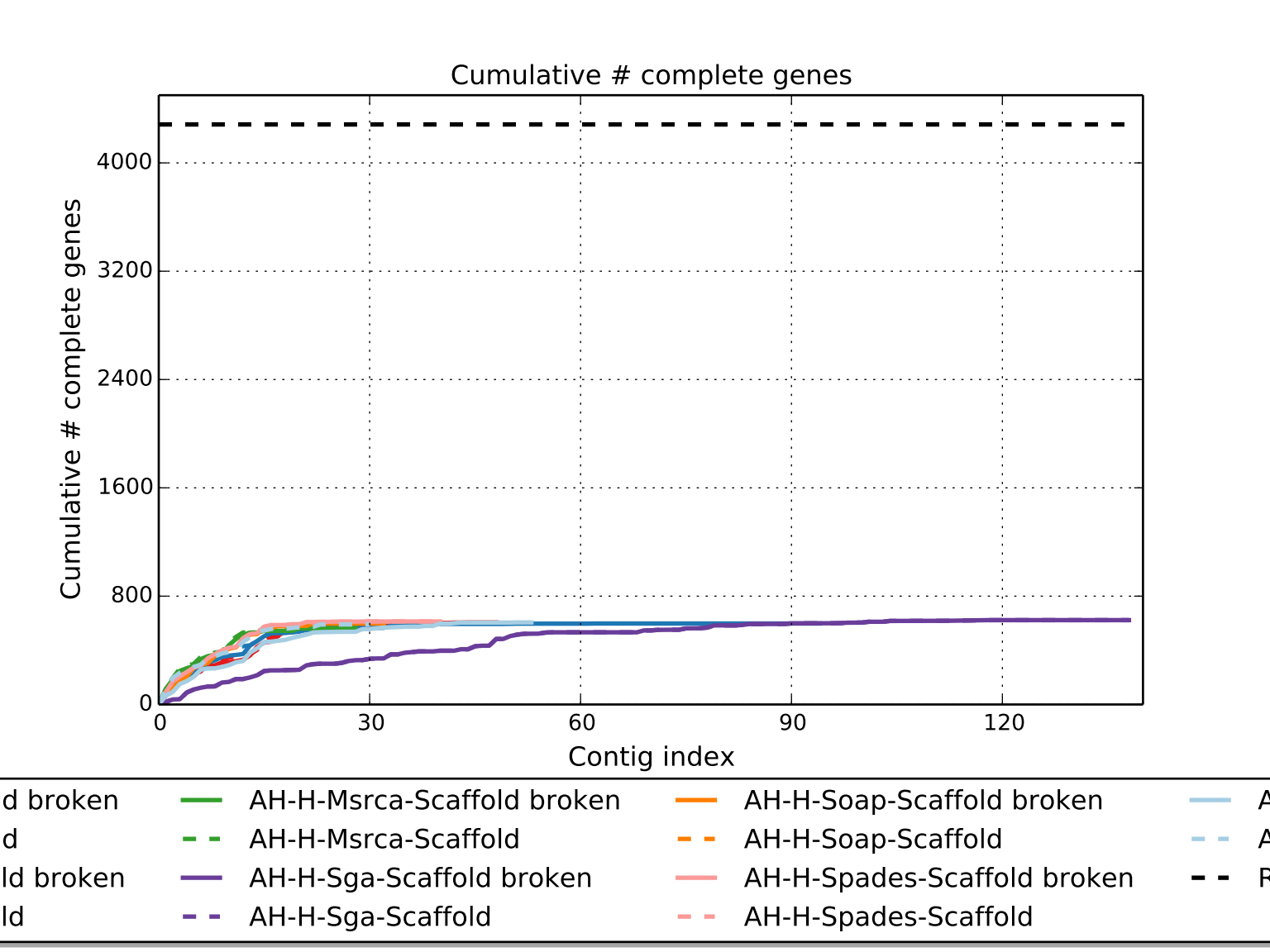

Nx
Contig length (kbp)
x
0
200
400
600
800
1000
1200
0
20
40
60
80
100
d broken
d
ld broken
ld
AH-H-Msrca-Scaffold broken
AH-H-Msrca-Scaffold
AH-H-Sga-Scaffold broken
AH-H-Sga-Scaffold
AH-H-Soap-Scaffold broken
AH-H-Soap-Scaffold
AH-H-Spades-Scaffold broken

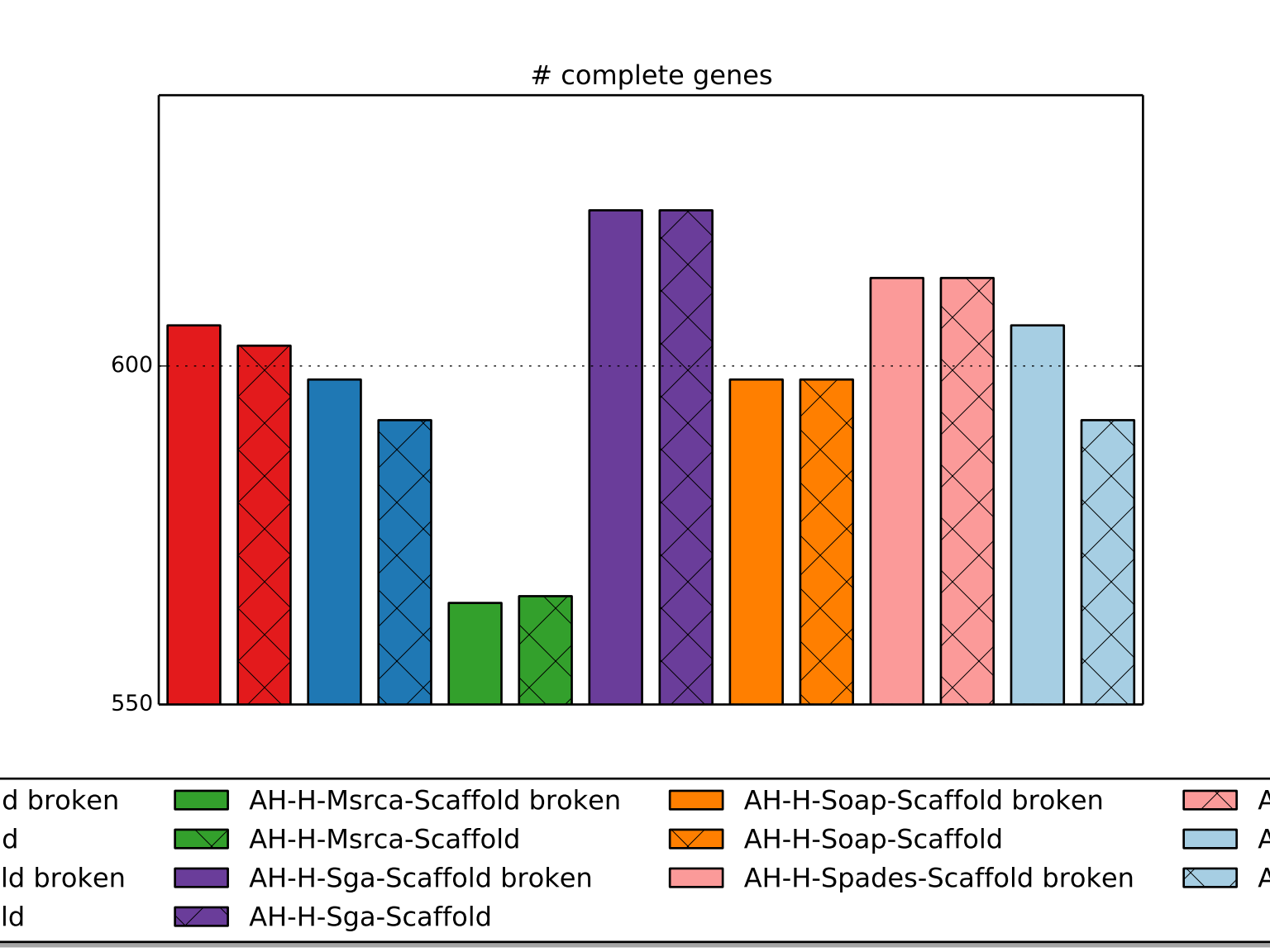

NGx
Contig length (kbp)
x
0
200
400
600
800
1000
1200
0
20
40
60
80
100
d broken
d
ld broken
ld
AH-H-Msrca-Scaffold broken
AH-H-Msrca-Scaffold
AH-H-Sga-Scaffold broken
AH-H-Sga-Scaffold
AH-H-Soap-Scaffold broken
AH-H-Soap-Scaffold
AH-H-Spades-Scaffold broken

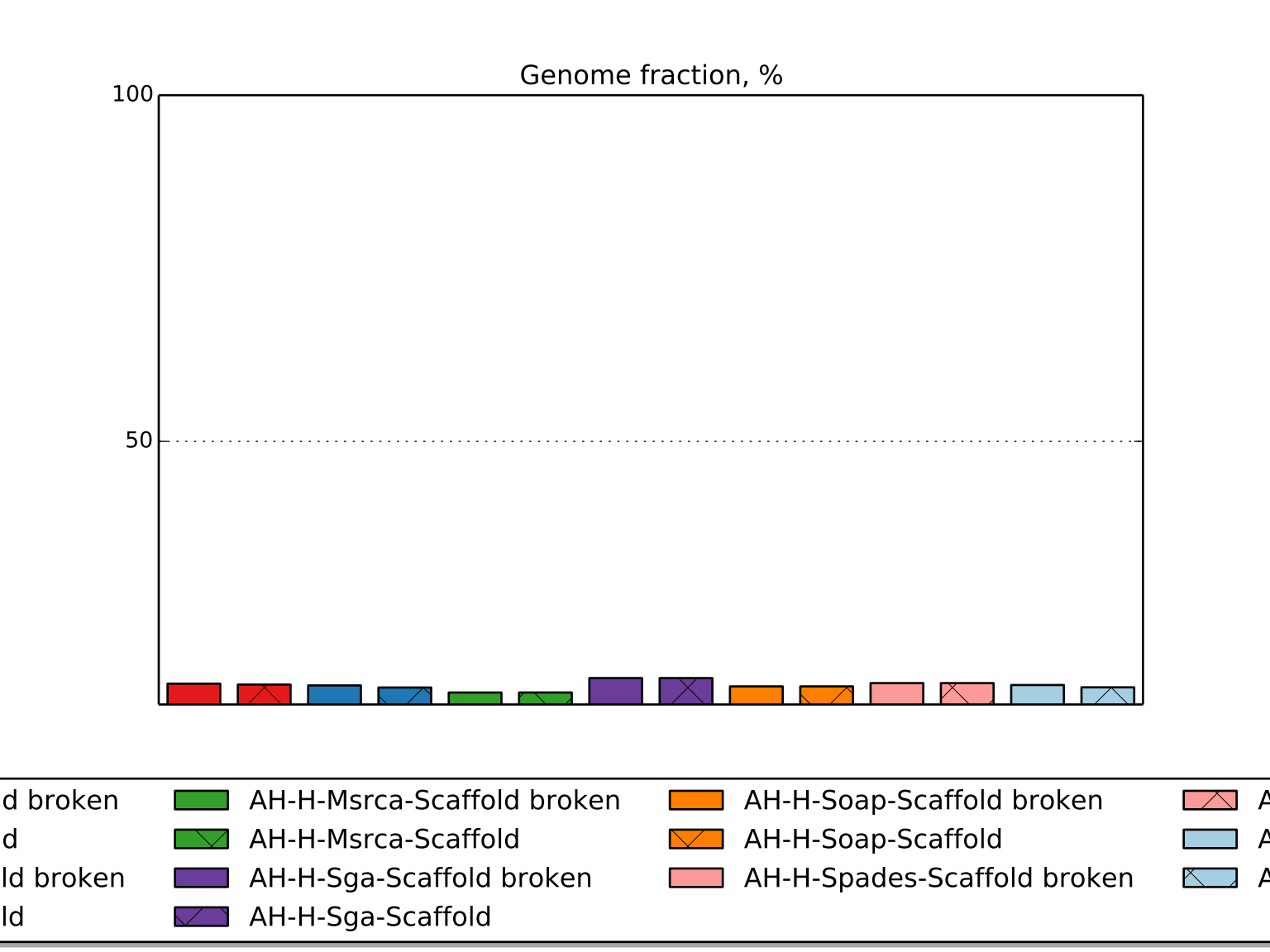

Cumulative length (aligned contigs)
Cumulative length (Mbp)
Contig index
0
1
2
3
4
5
0
30
60
90
120
150
d broken
d
ld broken
ld
AH-H-Msrca-Scaffold broken
AH-H-Msrca-Scaffold
AH-H-Sga-Scaffold broken
AH-H-Sga-Scaffold
AH-H-Soap-Scaffold broken
AH-H-Soap-Scaffold
AH-H-Spades-Scaffold broken
AH-H-Spades-Scaffold
A
A
R


NAx
Contig length (kbp)
x
0
10
20
30
40
50
60
0
20
40
60
80
100
d broken
d
ld broken
ld
AH-H-Msrca-Scaffold broken
AH-H-Msrca-Scaffold
AH-H-Sga-Scaffold broken
AH-H-Sga-Scaffold
AH-H-Soap-Scaffold broken
AH-H-Soap-Scaffold
AH-H-Spades-Scaffold broken

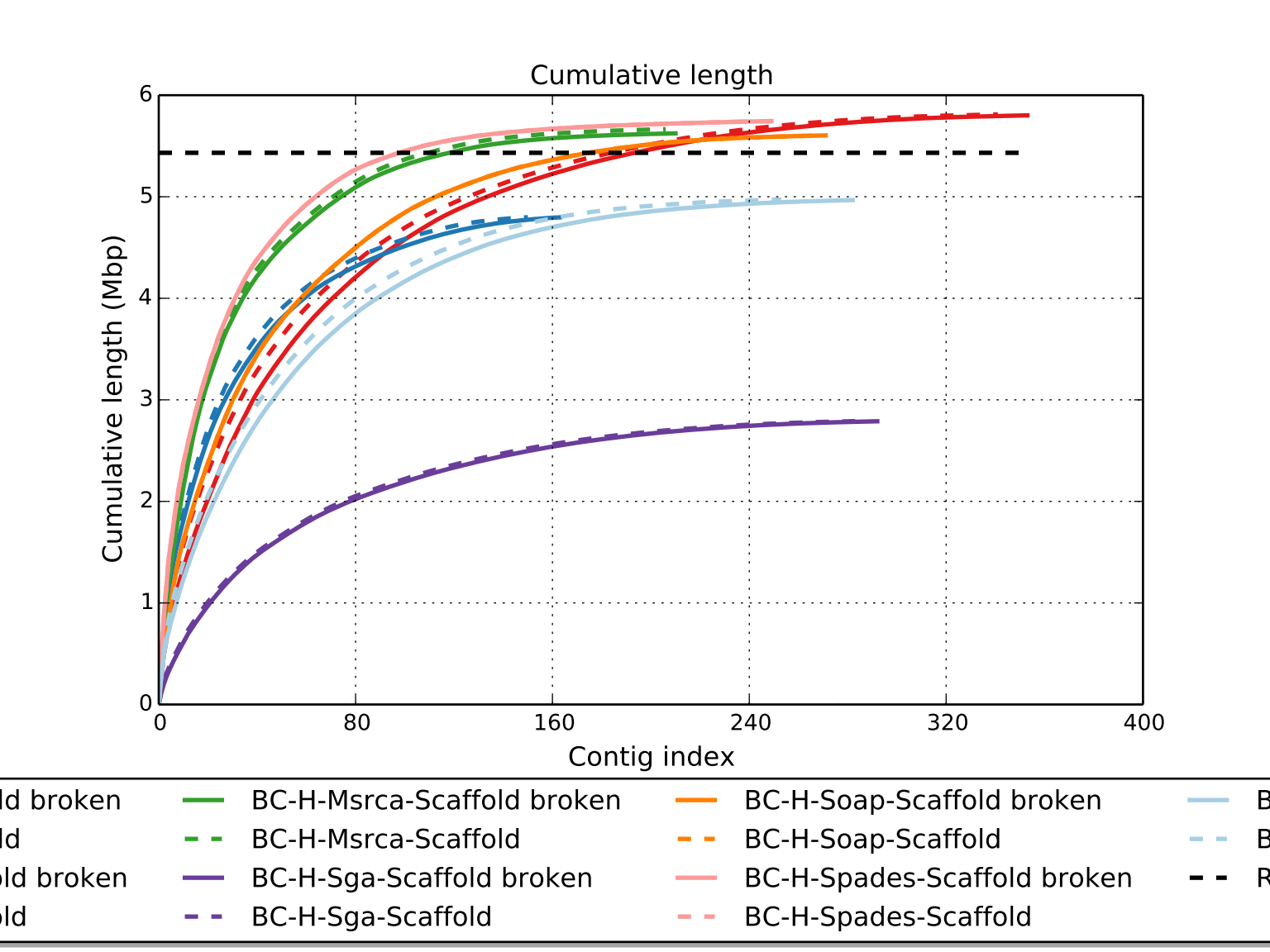

NGAx
Contig length (kbp)
x
0
10
20
30
40
50
60
0
20
40
60
80
100
d broken
d
ld broken
ld
AH-H-Msrca-Scaffold broken
AH-H-Msrca-Scaffold
AH-H-Sga-Scaffold broken
AH-H-Sga-Scaffold
AH-H-Soap-Scaffold broken
AH-H-Soap-Scaffold
AH-H-Spades-Scaffold broken

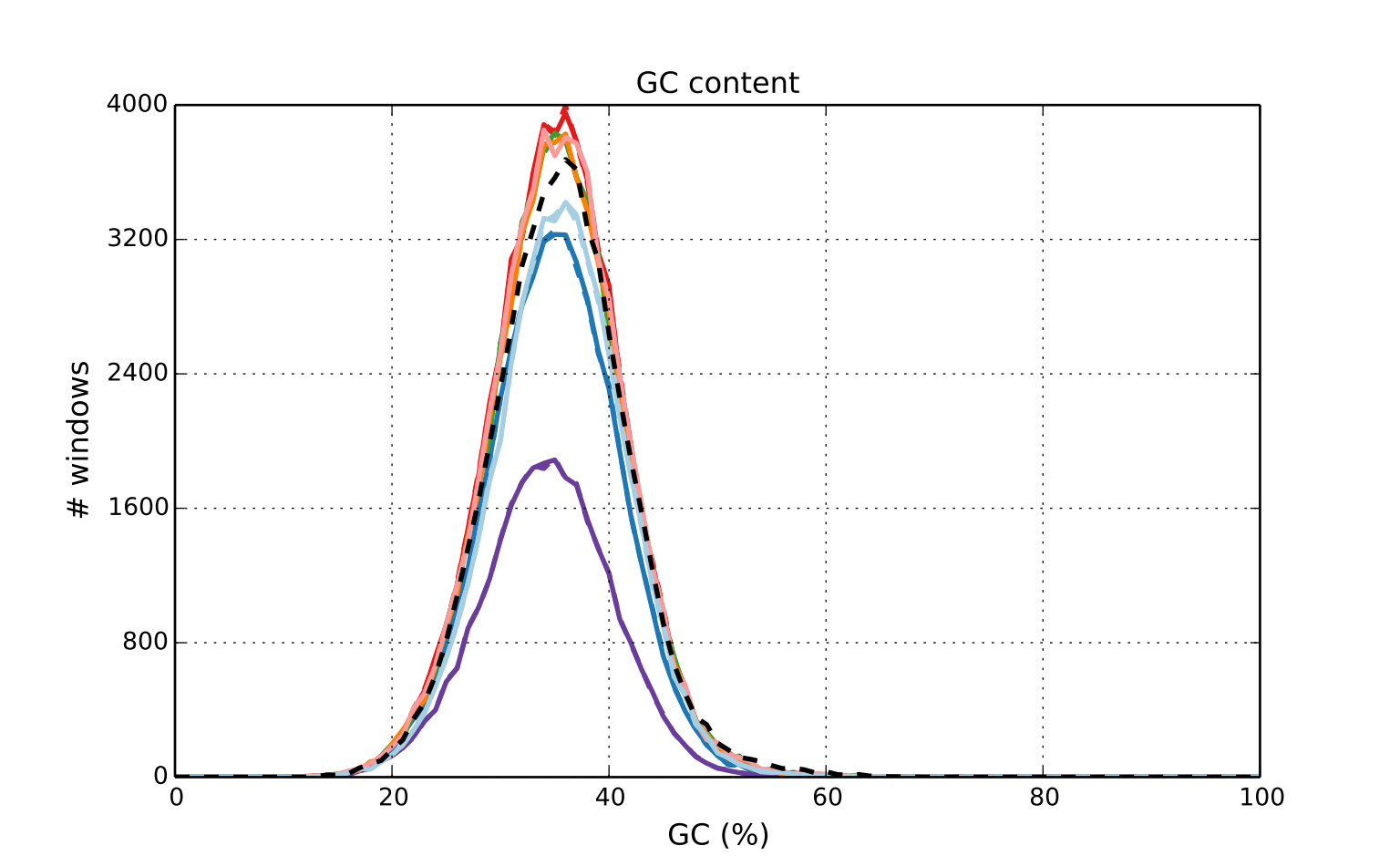

Cumulative # complete genes
Cumulative # complete genes
4000
3200
2400
1600
800
0
0
30
60
90
120
Contig index
d broken
d
ld broken
ld
AH-H-Msrca-Scaffold broken
AH-H-Msrca-Scaffold
AH-H-Sga-Scaffold broken
AH-H-Sga-Scaffold
AH-H-Soap-Scaffold broken
AH-H-Soap-Scaffold
AH-H-Spades-Scaffold broken
AH-H-Spades-Scaffold

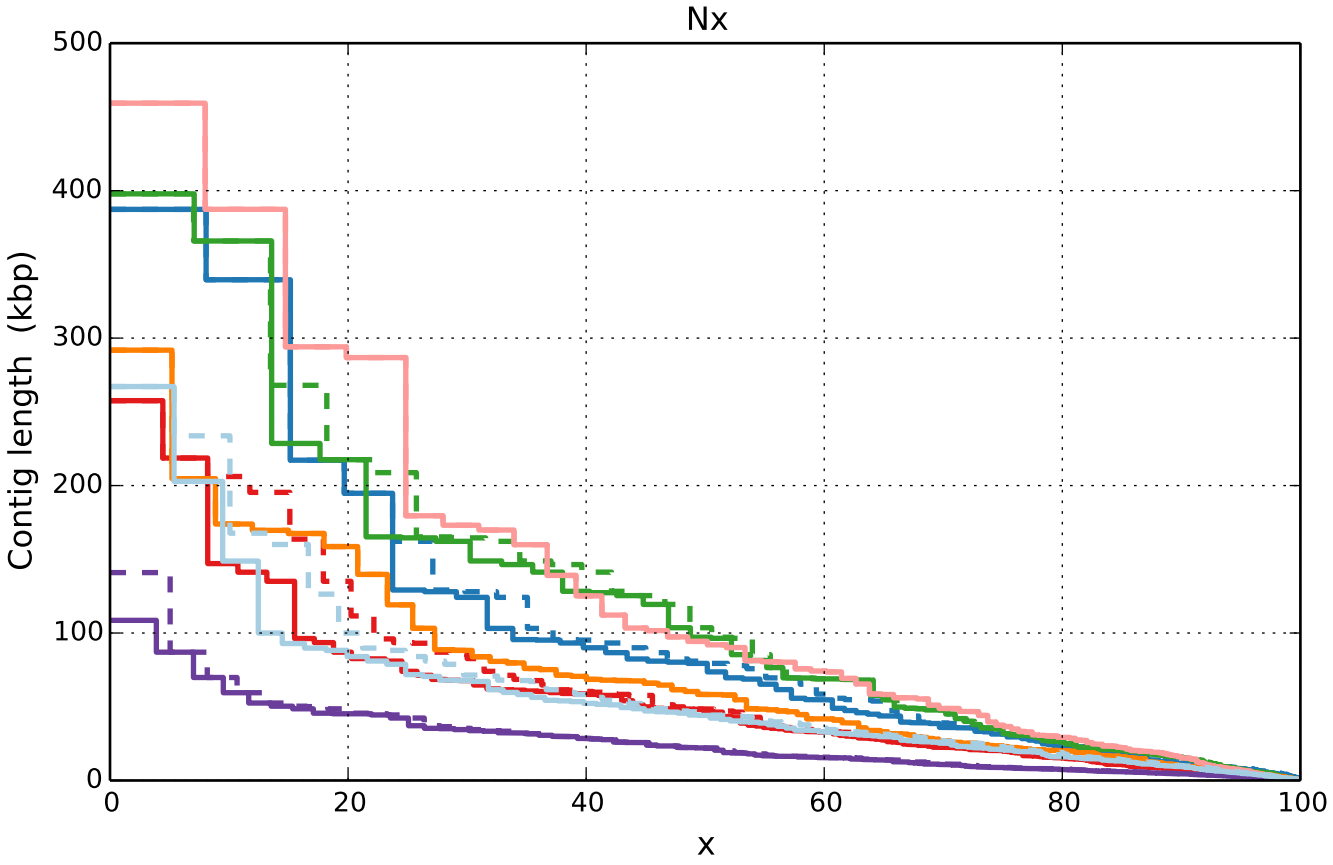

complete genes
600
550
d broken
d
ld broken
ld
AH-H-Msrca-Scaffold broken
AH-H-Msrca-Scaffold
AH-H-Sga-Scaffold broken
AH-H-Sga-Scaffold
AH-H-Soap-Scaffold broken
AH-H-Soap-Scaffold
AH-H-Spades-Scaffold broken


Genome fraction, %
100
50
d broken
d
ld broken
ld
AH-H-Msrca-Scaffold broken
AH-H-Msrca-Scaffold
AH-H-Sga-Scaffold broken
AH-H-Sga-Scaffold
AH-H-Soap-Scaffold broken
AH-H-Soap-Scaffold
AH-H-Spades-Scaffold broken

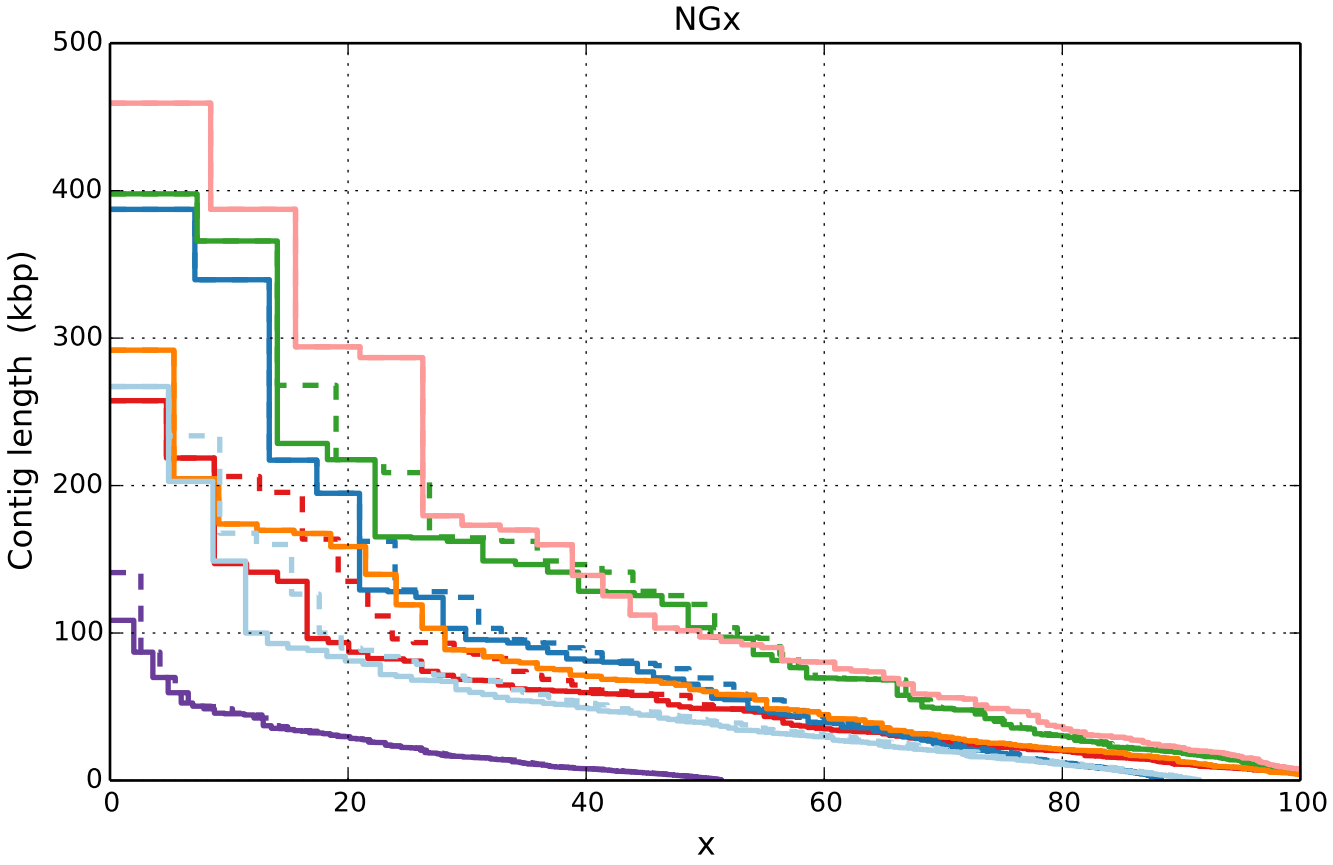
Scaffold

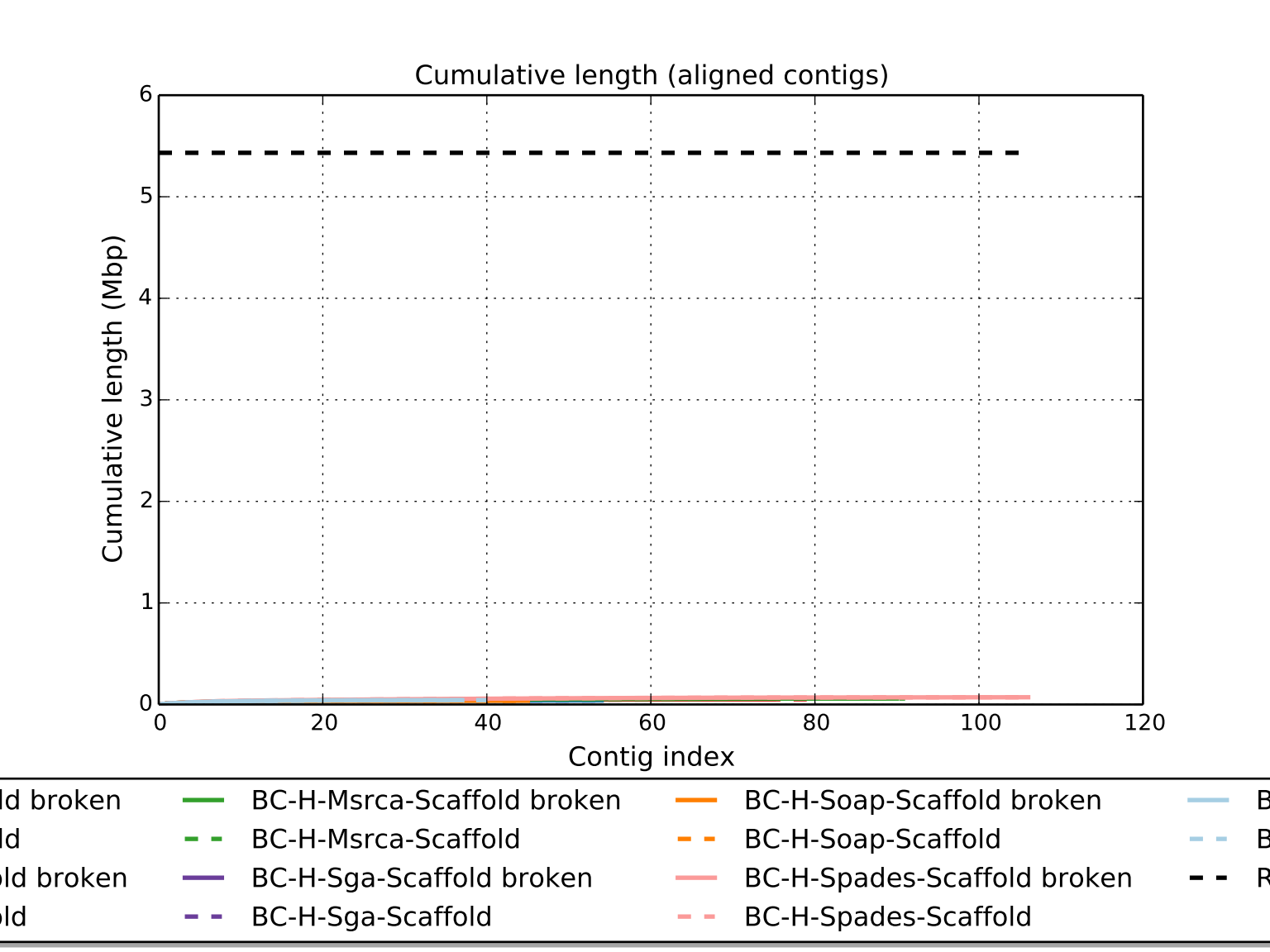

Cumulative length
Cumulative length (Mbp)
Contig index
0
1
2
3
4
5
6
0
80
160
240
320
400
ld broken
ld
old broken
old
BC-H-Msrca-Scaffold broken
BC-H-Msrca-Scaffold
BC-H-Sga-Scaffold broken
BC-H-Sga-Scaffold
BC-H-Soap-Scaffold broken
BC-H-Soap-Scaffold
BC-H-Spades-Scaffold broken
BC-H-Spades-Scaffold
B
B
R

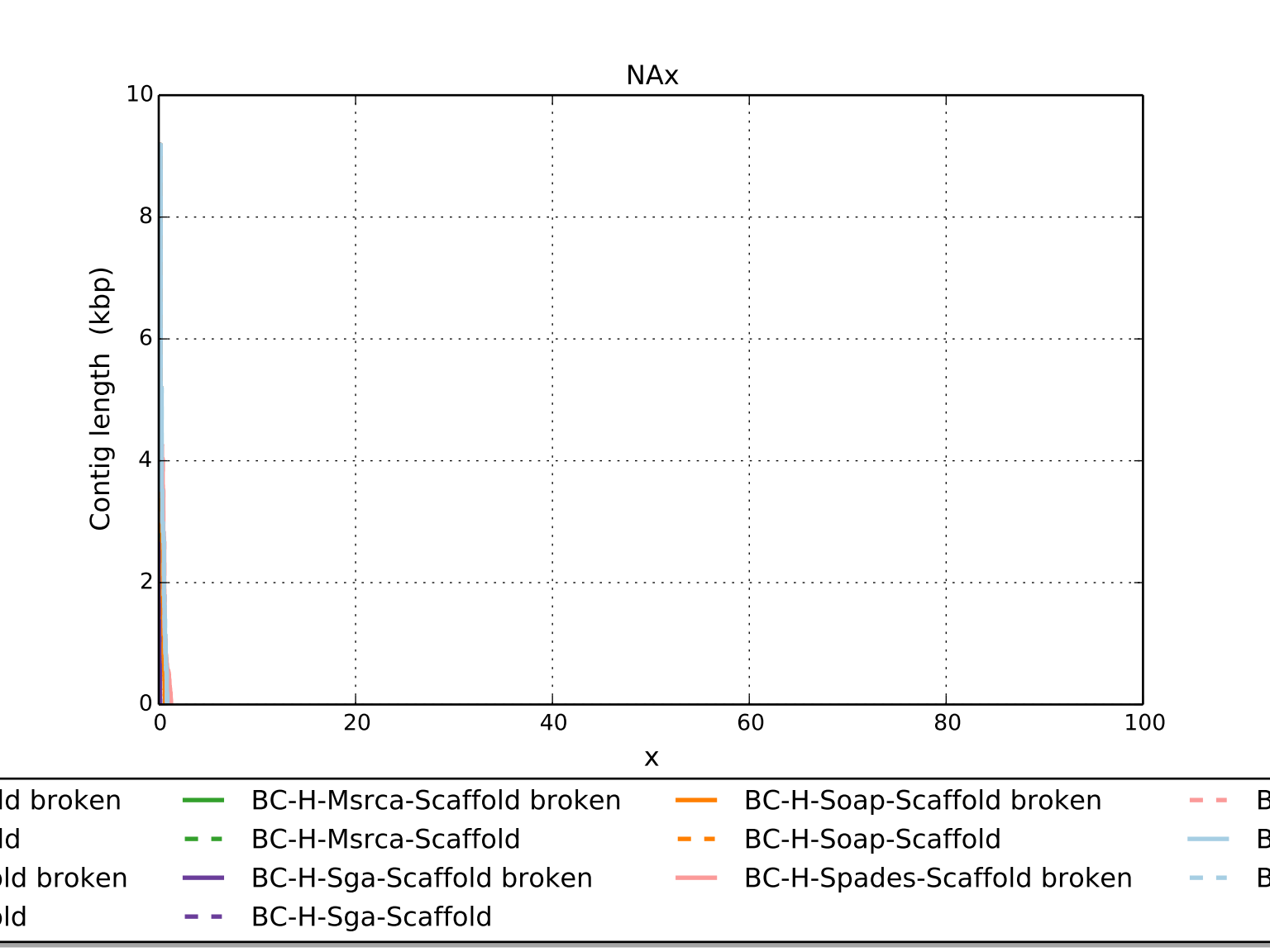

GC content
windows
GC (%)
0
800
1600
2400
3200
4000
0
20
40
60
80
100
ld broken
ld
old broken
old
BC-H-Msrca-Scaffold broken
BC-H-Msrca-Scaffold
BC-H-Sga-Scaffold broken
BC-H-Sga-Scaffold
BC-H-Soap-Scaffold broken
BC-H-Soap-Scaffold
BC-H-Spades-Scaffold broken
BC-H-Spades-Scaffold
B
B
R

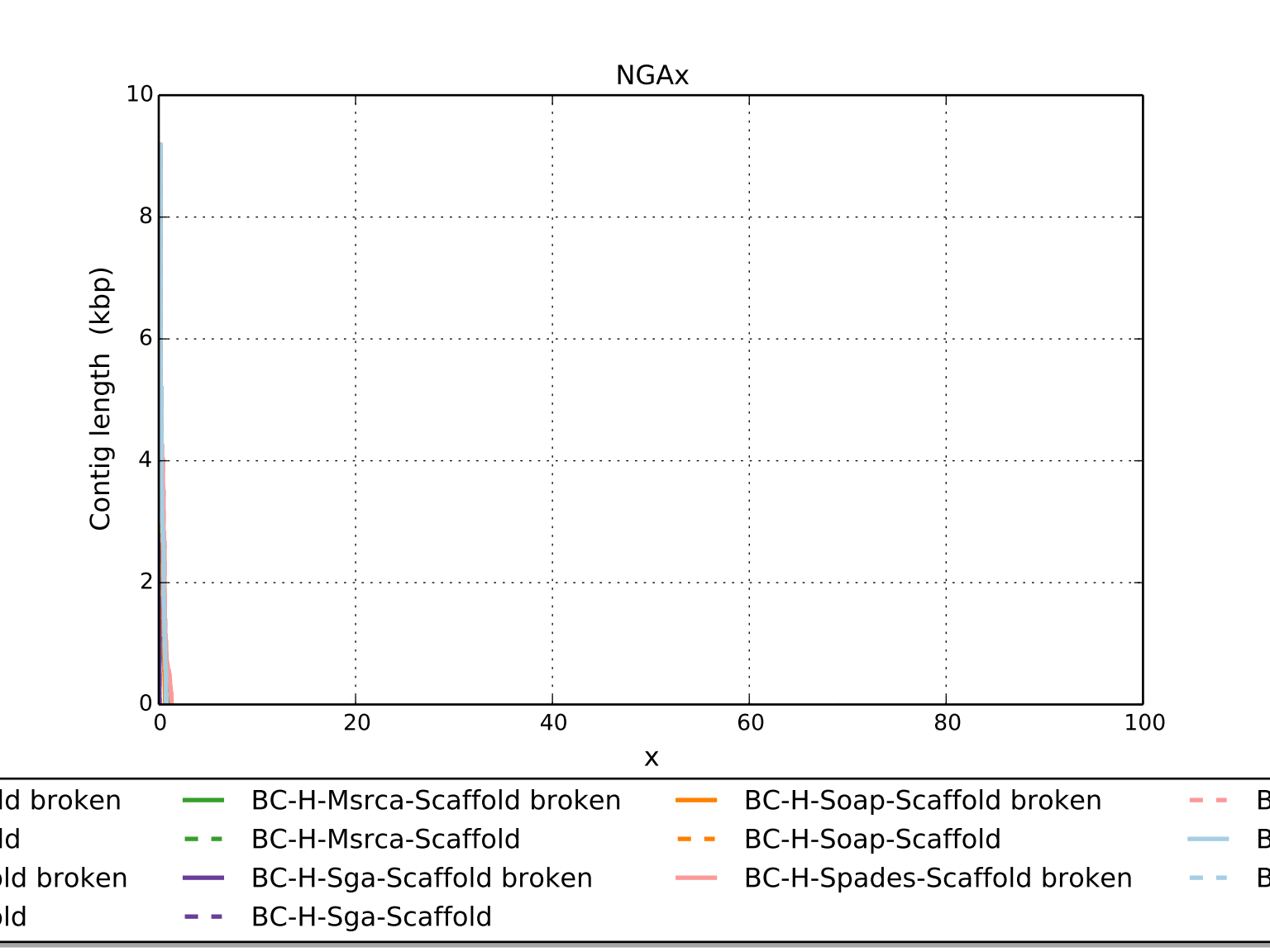


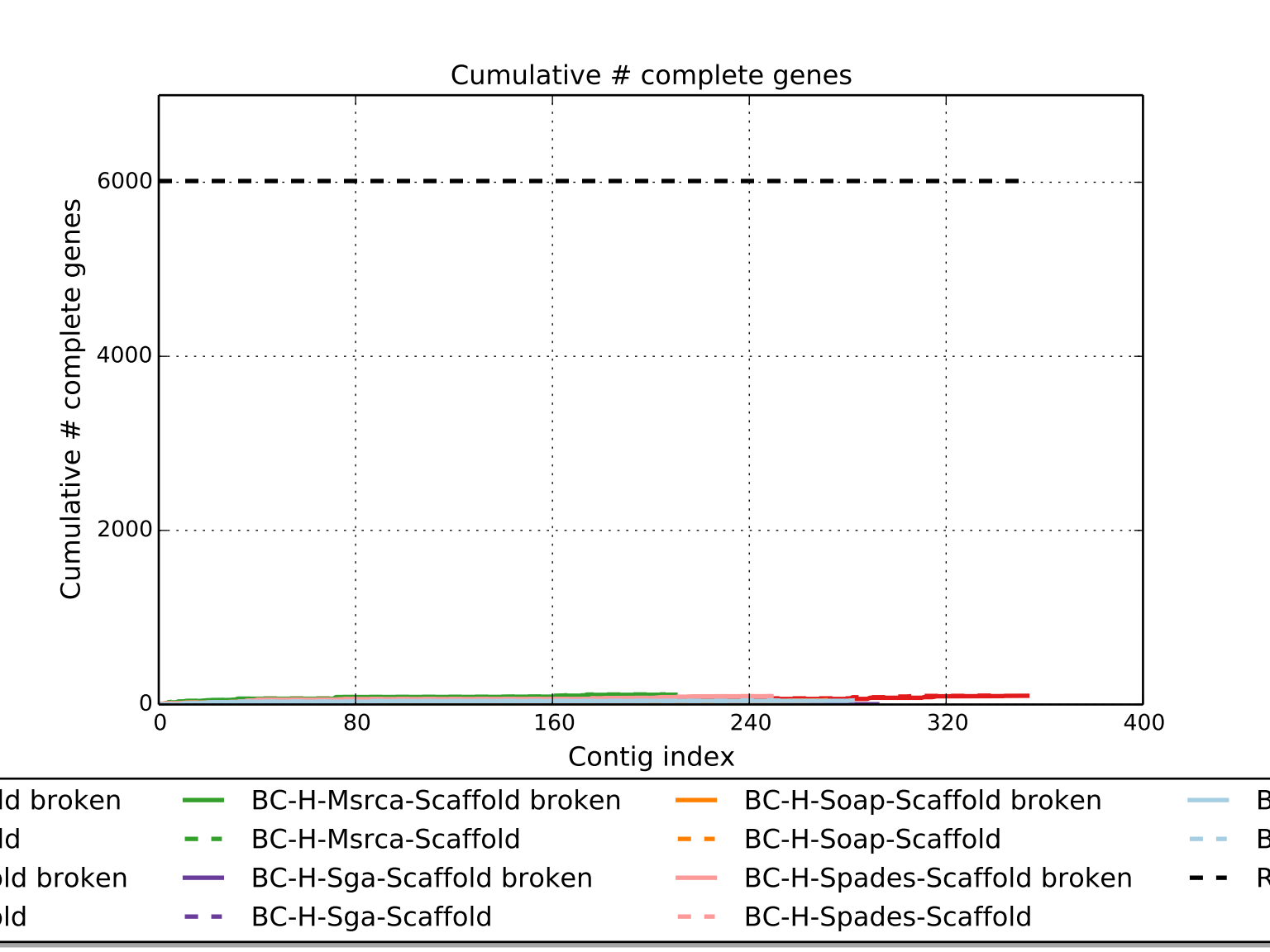
ld broken
ld
old broken
old
BC-H-Msrca-Scaffold broken
BC-H-Msrca-Scaffold
BC-H-Sga-Scaffold broken
BC-H-Sga-Scaffold
BC-H-Soap-Scaffold broken
BC-H-Soap-Scaffold
BC-H-Spades-Scaffold broken
B
B
B

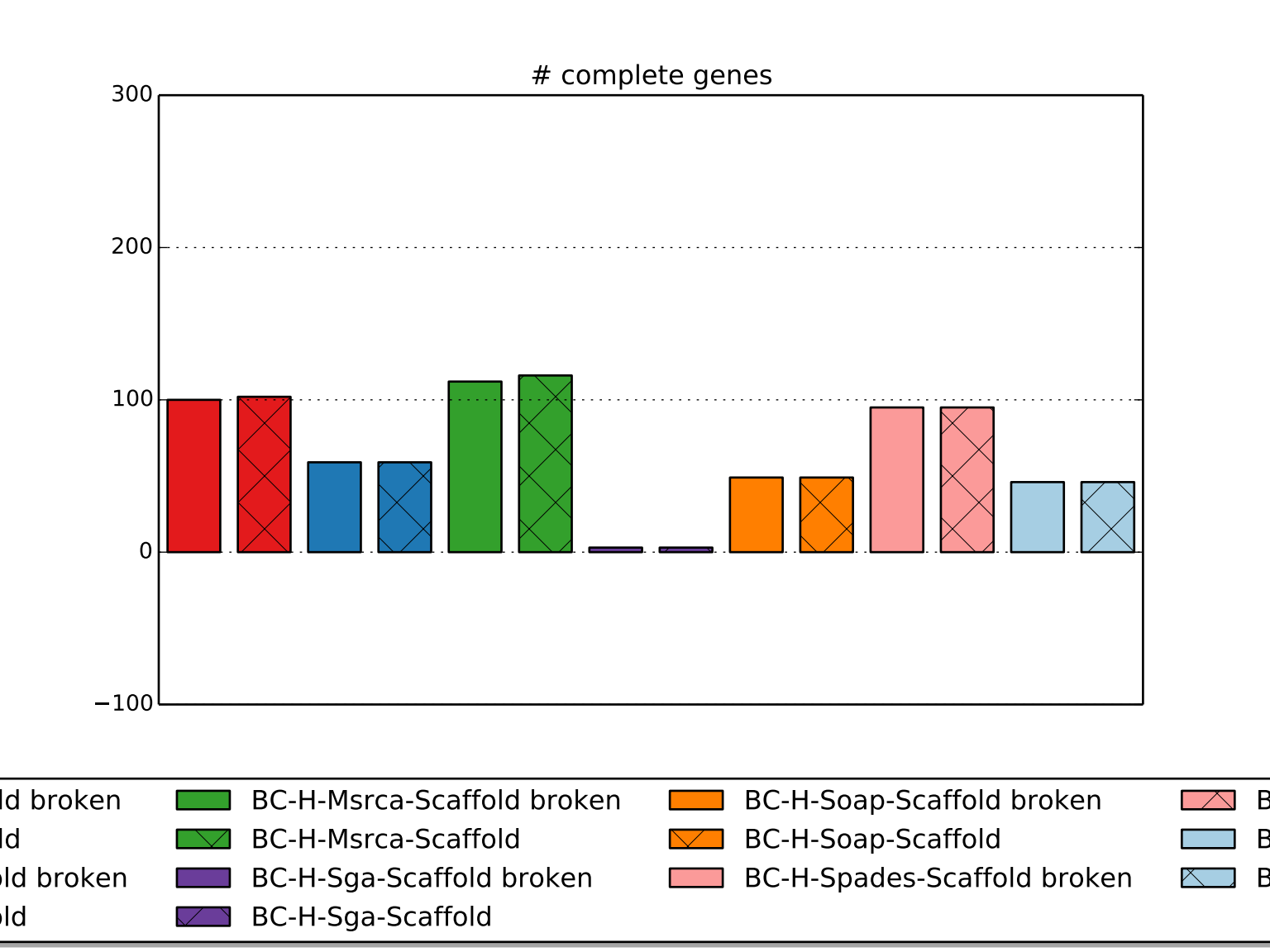

NGx
Contig length (kbp)
500
400
300
200
100
0
0
20
40
60
80
100
x
ld broken
ld
old broken
old
BC-H-Msrca-Scaffold broken
BC-H-Msrca-Scaffold
BC-H-Sga-Scaffold broken
BC-H-Sga-Scaffold
BC-H-Soap-Scaffold broken
BC-H-Soap-Scaffold
BC-H-Spades-Scaffold broken
B
B
B

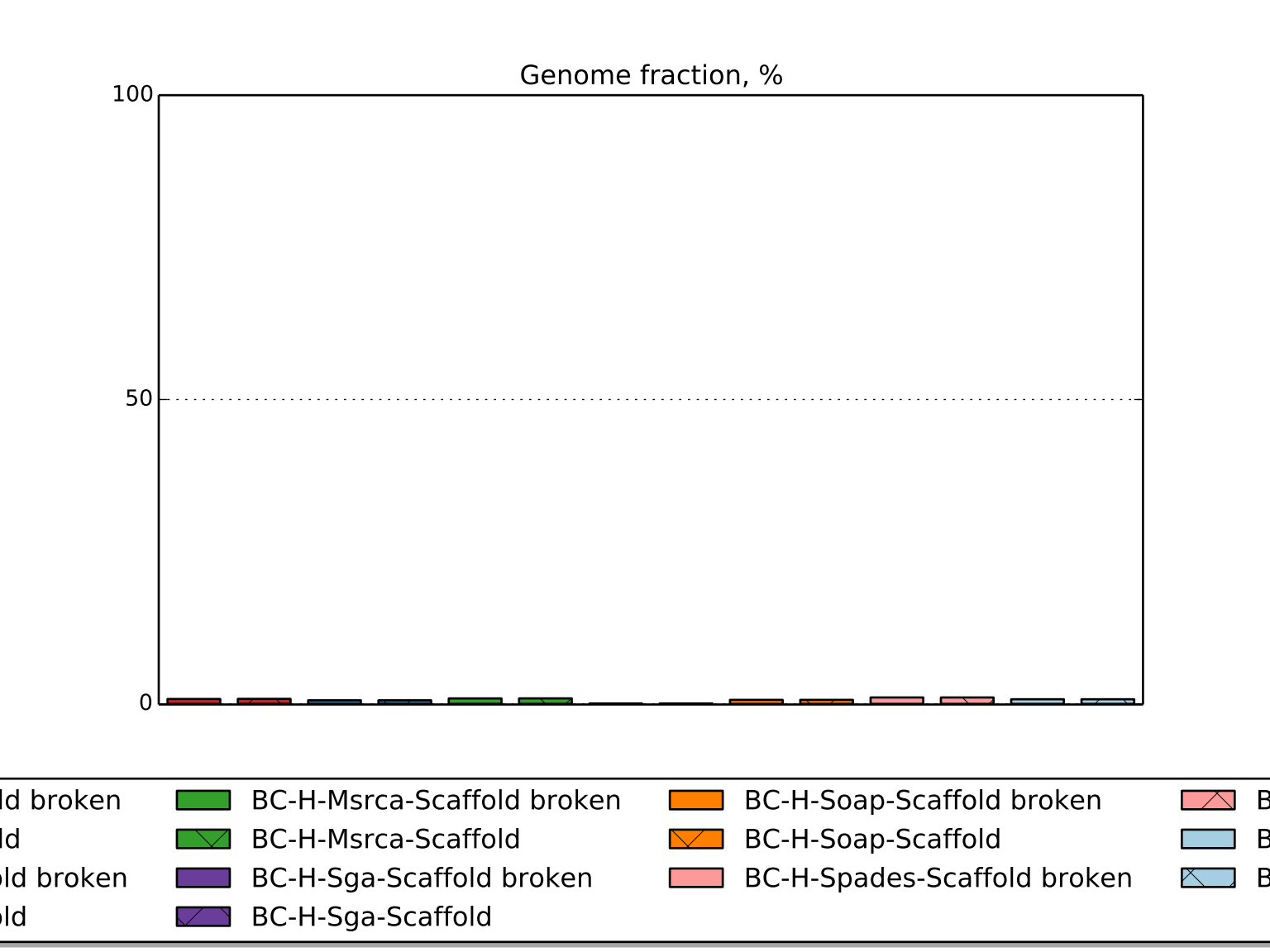

Cumulative length (aligned contigs)
Cumulative length (Mbp)
Contig index
0
1
2
3
4
5
6
0
20
40
60
80
100
120
ld broken
ld
old broken
old
BC-H-Msrca-Scaffold broken
BC-H-Msrca-Scaffold
BC-H-Sga-Scaffold broken
BC-H-Sga-Scaffold
BC-H-Soap-Scaffold broken
BC-H-Soap-Scaffold
BC-H-Spades-Scaffold broken
BC-H-Spades-Scaffold
B
B
R


NAx
Contig length (kbp)
x
0
2
4
6
8
10
0
20
40
60
80
100
ld broken
ld
old broken
old
BC-H-Msrca-Scaffold broken
BC-H-Msrca-Scaffold
BC-H-Sga-Scaffold broken
BC-H-Sga-Scaffold
BC-H-Soap-Scaffold broken
BC-H-Soap-Scaffold
BC-H-Spades-Scaffold broken
B
B
B

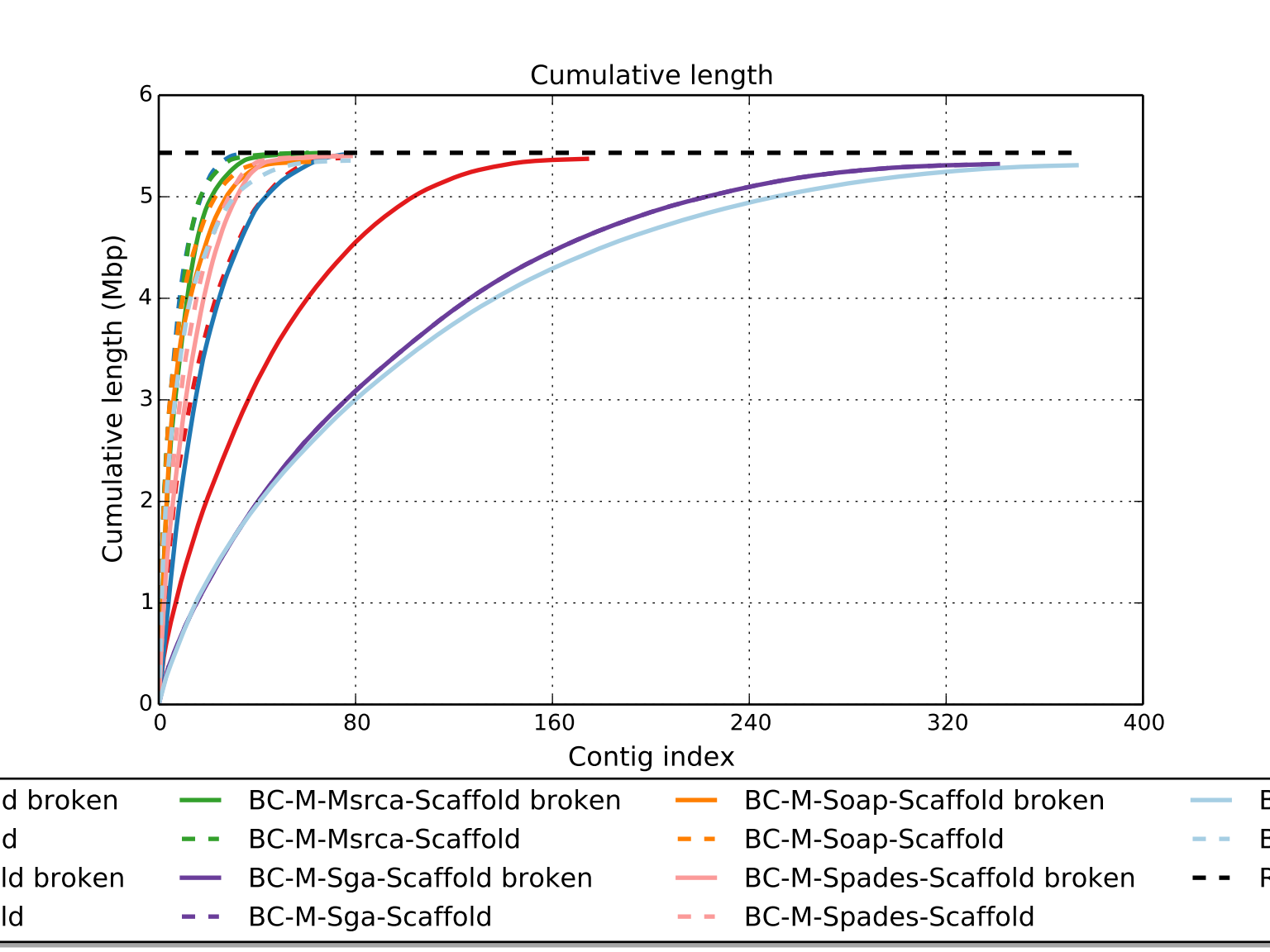

NGAx
Contig length (kbp)
x
0
2
4
6
8
10
0
20
40
60
80
100
ld broken
ld
old broken
old
BC-H-Msrca-Scaffold broken
BC-H-Msrca-Scaffold
BC-H-Sga-Scaffold broken
BC-H-Sga-Scaffold
BC-H-Soap-Scaffold broken
BC-H-Soap-Scaffold
BC-H-Spades-Scaffold broken
B
B
B

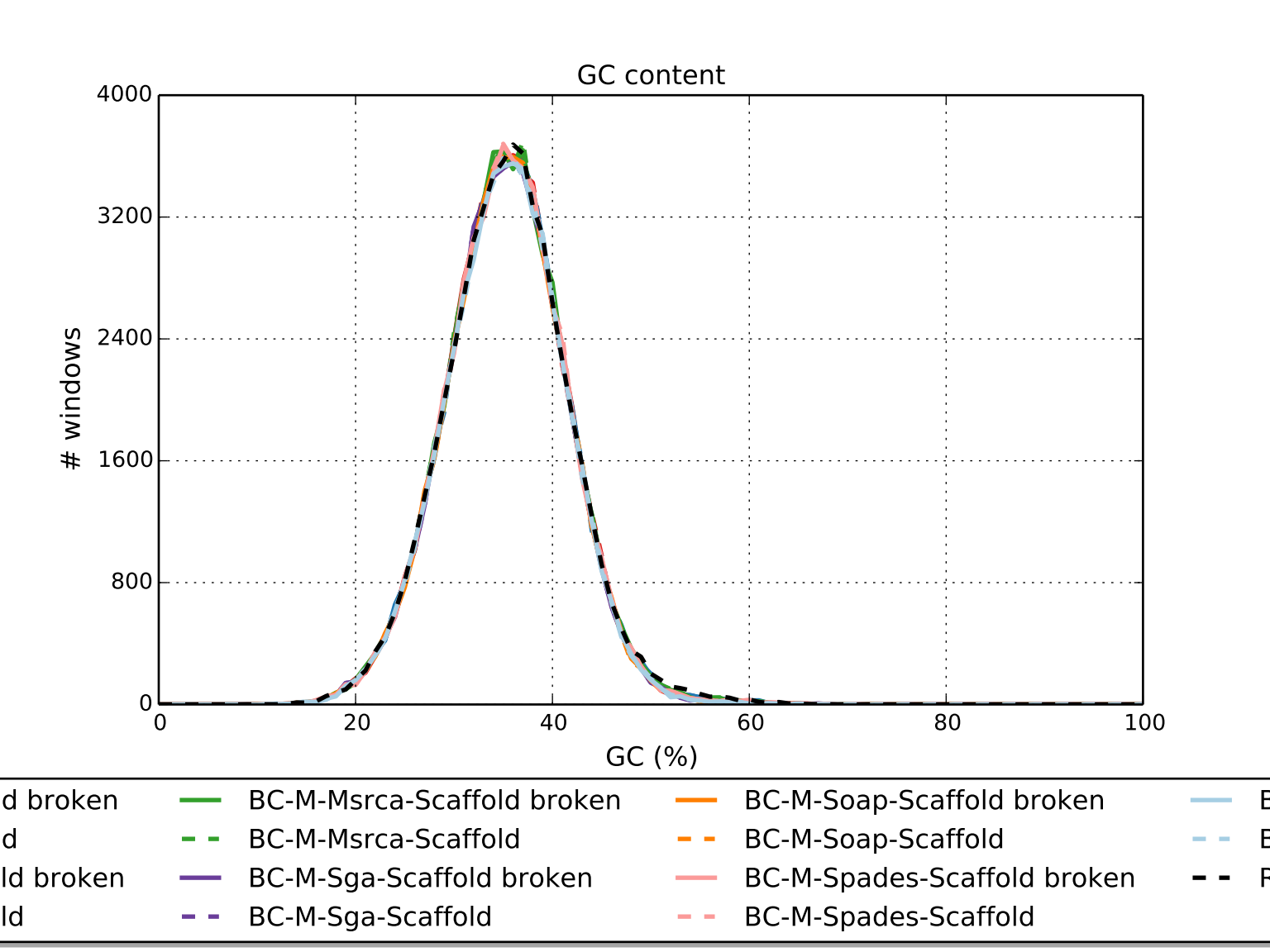

Cumulative # complete genes
Cumulative # complete genes
6000
4000
2000
0
0
80
160
240
320
400
Contig index
ld broken
ld
old broken
old
BC-H-Msrca-Scaffold broken
BC-H-Msrca-Scaffold
BC-H-Sga-Scaffold broken
BC-H-Sga-Scaffold
BC-H-Soap-Scaffold broken
BC-H-Soap-Scaffold
BC-H-Spades-Scaffold broken
BC-H-Spades-Scaffold
B
B
R

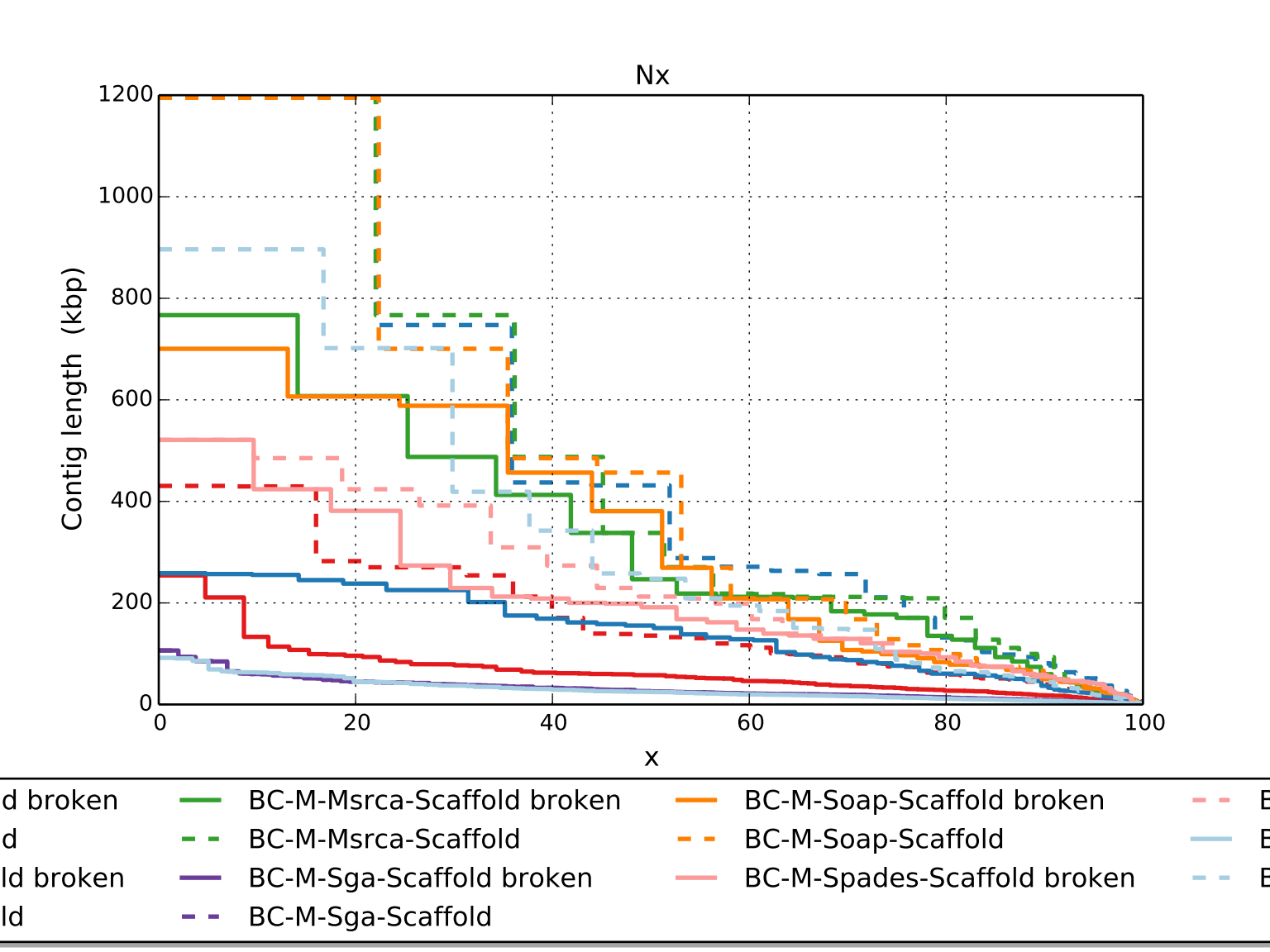

complete genes
300
200
100
0
−100
ld broken
ld
old broken
old
BC-H-Msrca-Scaffold broken
BC-H-Msrca-Scaffold
BC-H-Sga-Scaffold broken
BC-H-Sga-Scaffold
BC-H-Soap-Scaffold broken
BC-H-Soap-Scaffold
BC-H-Spades-Scaffold broken
B
B
B

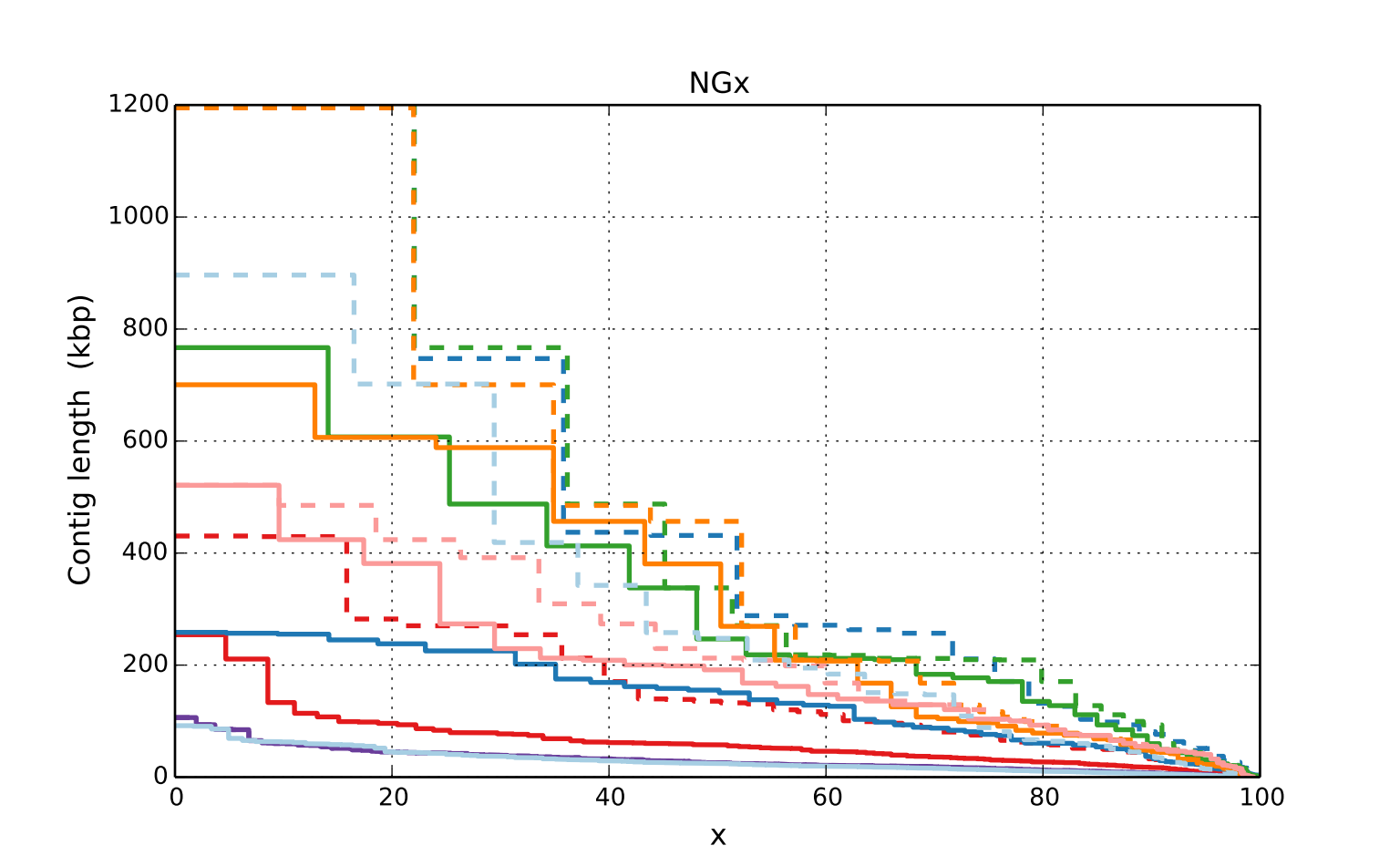

Genome fraction, %
100
50
0
ld broken
ld
old broken
old
BC-H-Msrca-Scaffold broken
BC-H-Msrca-Scaffold
BC-H-Sga-Scaffold broken
BC-H-Sga-Scaffold
BC-H-Soap-Scaffold broken
BC-H-Soap-Scaffold
BC-H-Spades-Scaffold broken
B
B
B

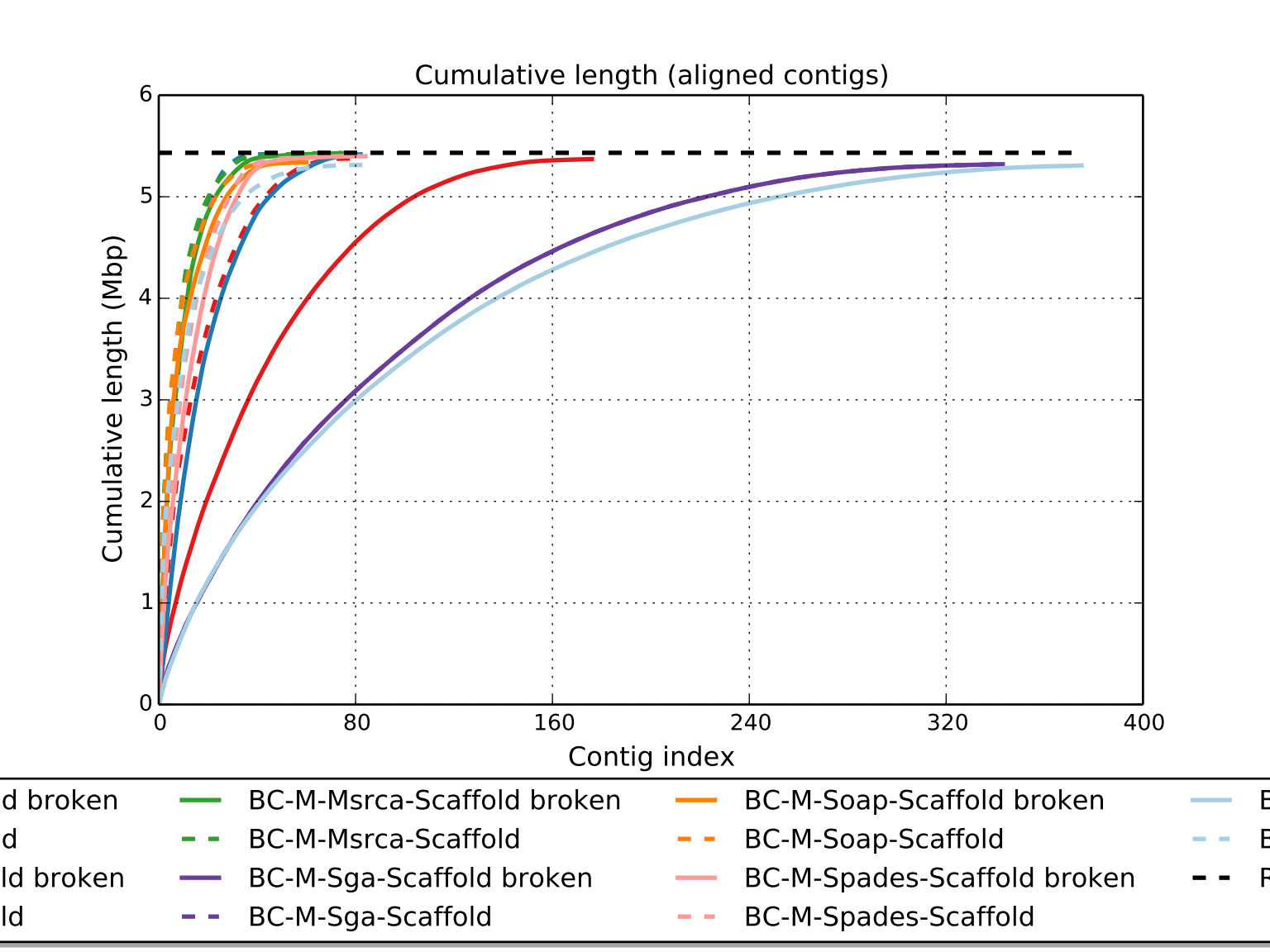
Scaffold

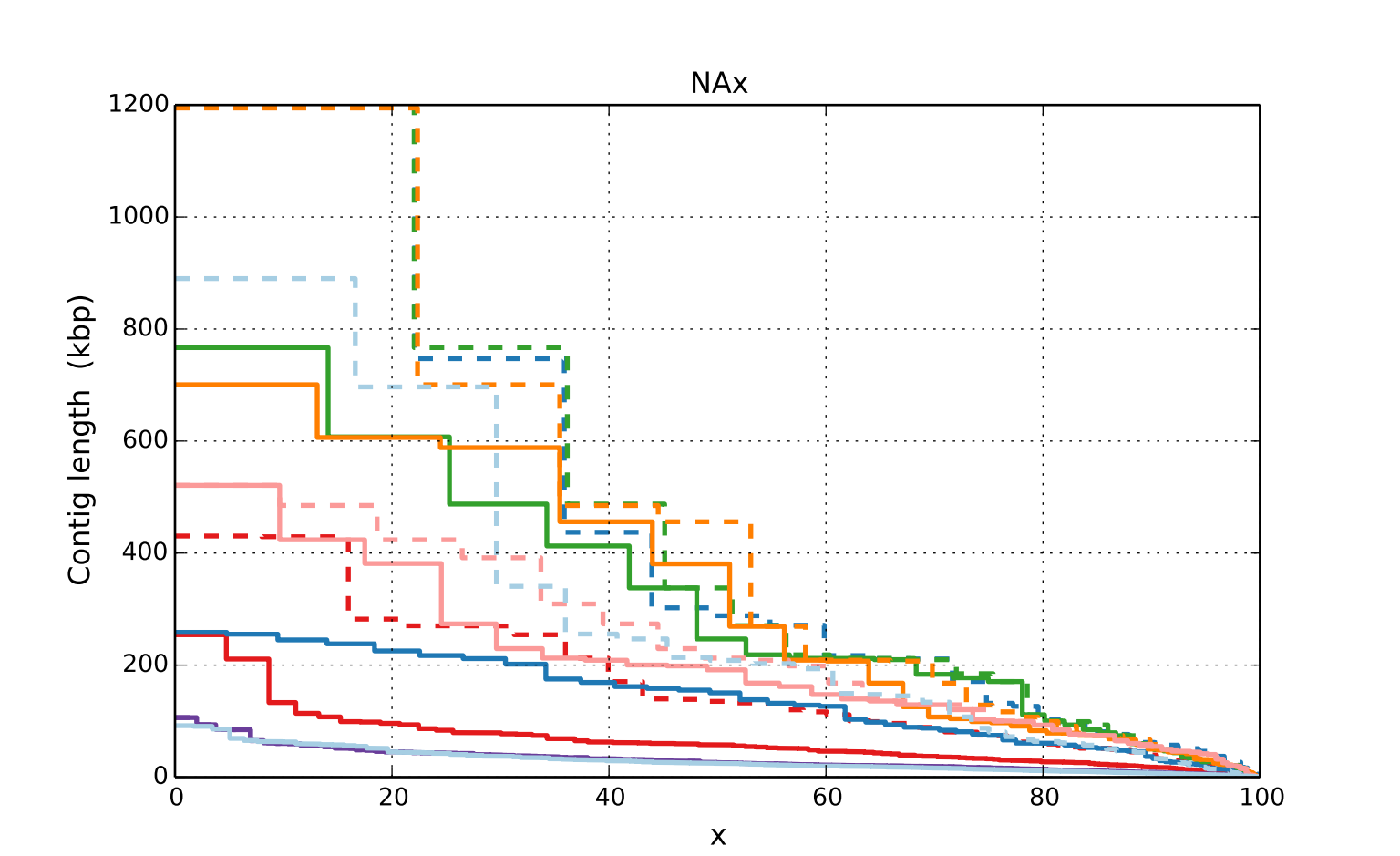

Cumulative length
Cumulative length (Mbp)
Contig index
0
1
2
3
4
5
6
0
80
160
240
320
400
d broken
d
ld broken
ld
BC-M-Msrca-Scaffold broken
BC-M-Msrca-Scaffold
BC-M-Sga-Scaffold broken
BC-M-Sga-Scaffold
BC-M-Soap-Scaffold broken
BC-M-Soap-Scaffold
BC-M-Spades-Scaffold broken
BC-M-Spades-Scaffold

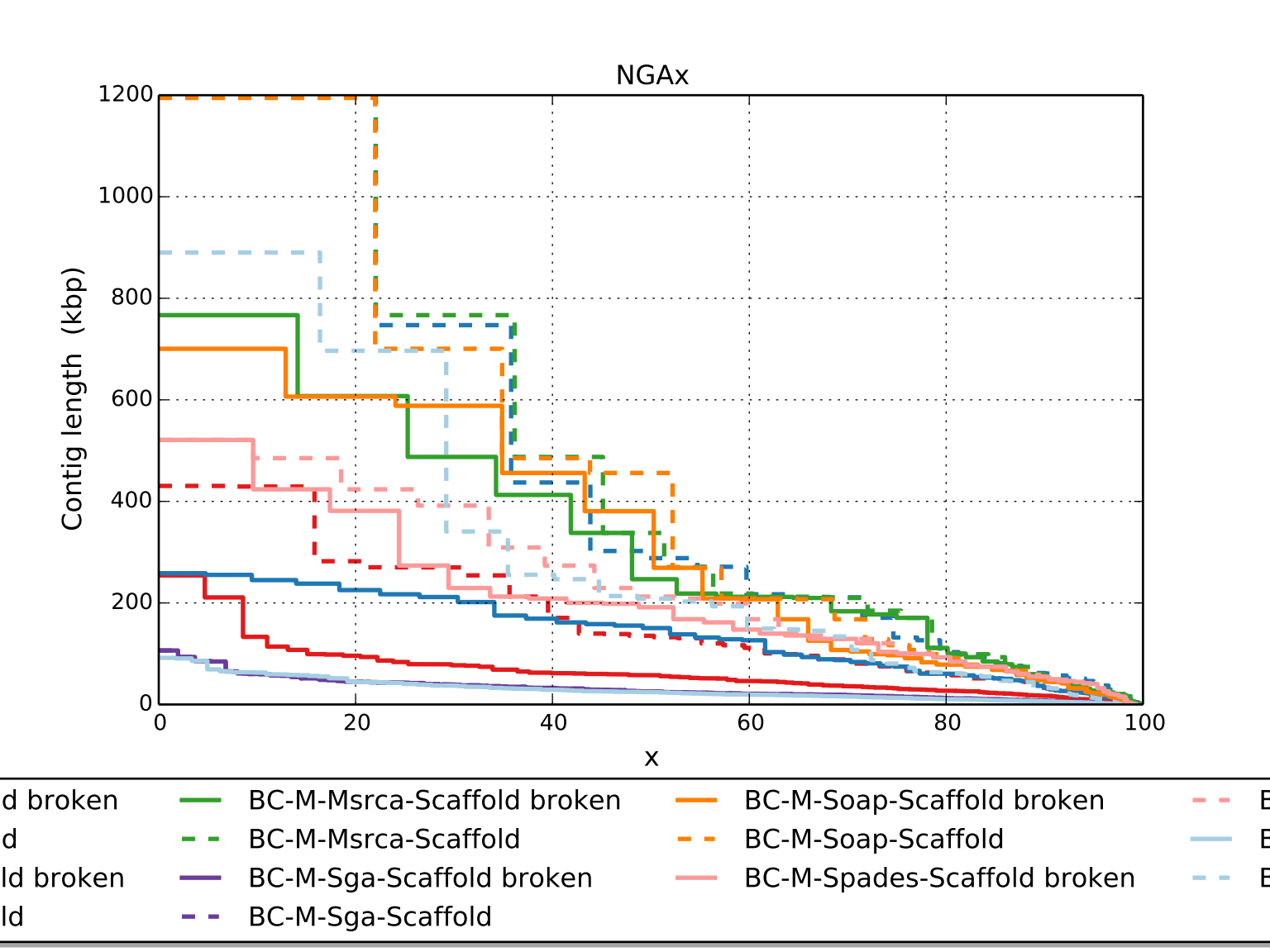

GC content
windows
GC (%)
0
800
1600
2400
3200
4000
0
20
40
60
80
100
d broken
d
ld broken
ld
BC-M-Msrca-Scaffold broken
BC-M-Msrca-Scaffold
BC-M-Sga-Scaffold broken
BC-M-Sga-Scaffold
BC-M-Soap-Scaffold broken
BC-M-Soap-Scaffold
BC-M-Spades-Scaffold broken
BC-M-Spades-Scaffold

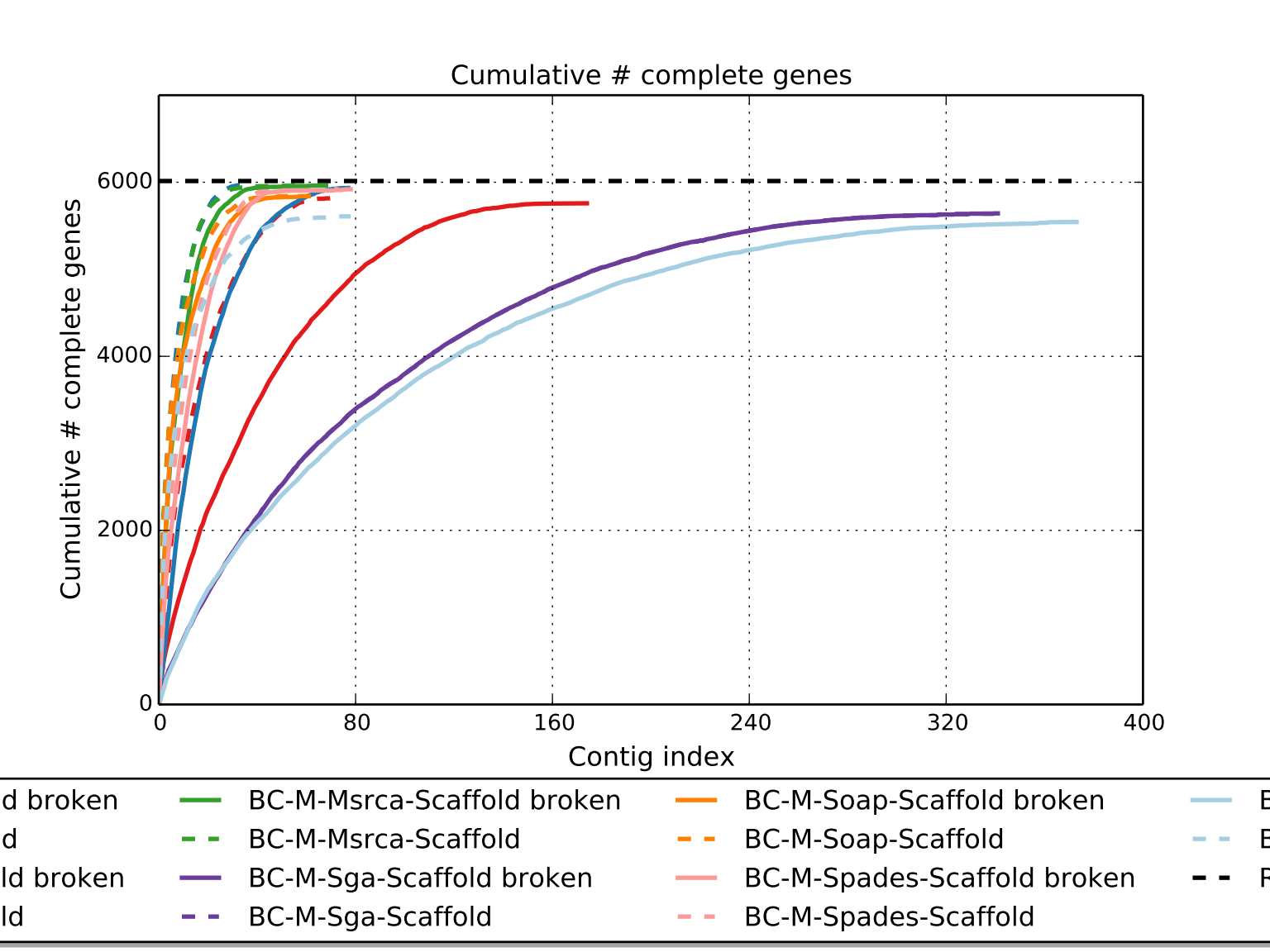

Nx
Contig length (kbp)
x
0
200
400
600
800
1000
1200
0
20
40
60
80
100
d broken
d
ld broken
ld
BC-M-Msrca-Scaffold broken
BC-M-Msrca-Scaffold
BC-M-Sga-Scaffold broken
BC-M-Sga-Scaffold
BC-M-Soap-Scaffold broken
BC-M-Soap-Scaffold
BC-M-Spades-Scaffold broken

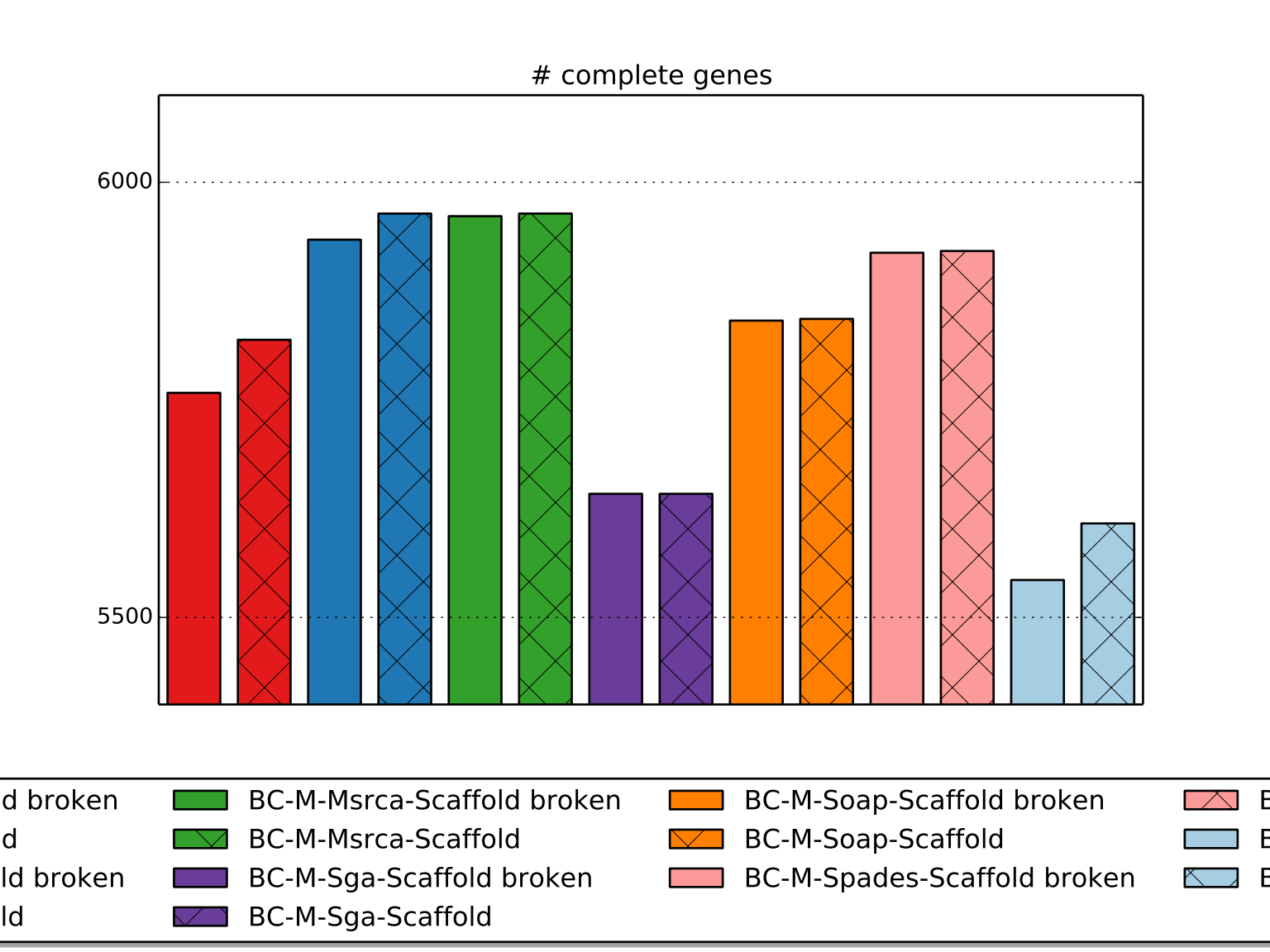

NGx
Contig length (kbp)
x
0
200
400
600
800
1000
1200
0
20
40
60
80
100
d broken
d
ld broken
ld
BC-M-Msrca-Scaffold broken
BC-M-Msrca-Scaffold
BC-M-Sga-Scaffold broken
BC-M-Sga-Scaffold
BC-M-Soap-Scaffold broken
BC-M-Soap-Scaffold
BC-M-Spades-Scaffold broken

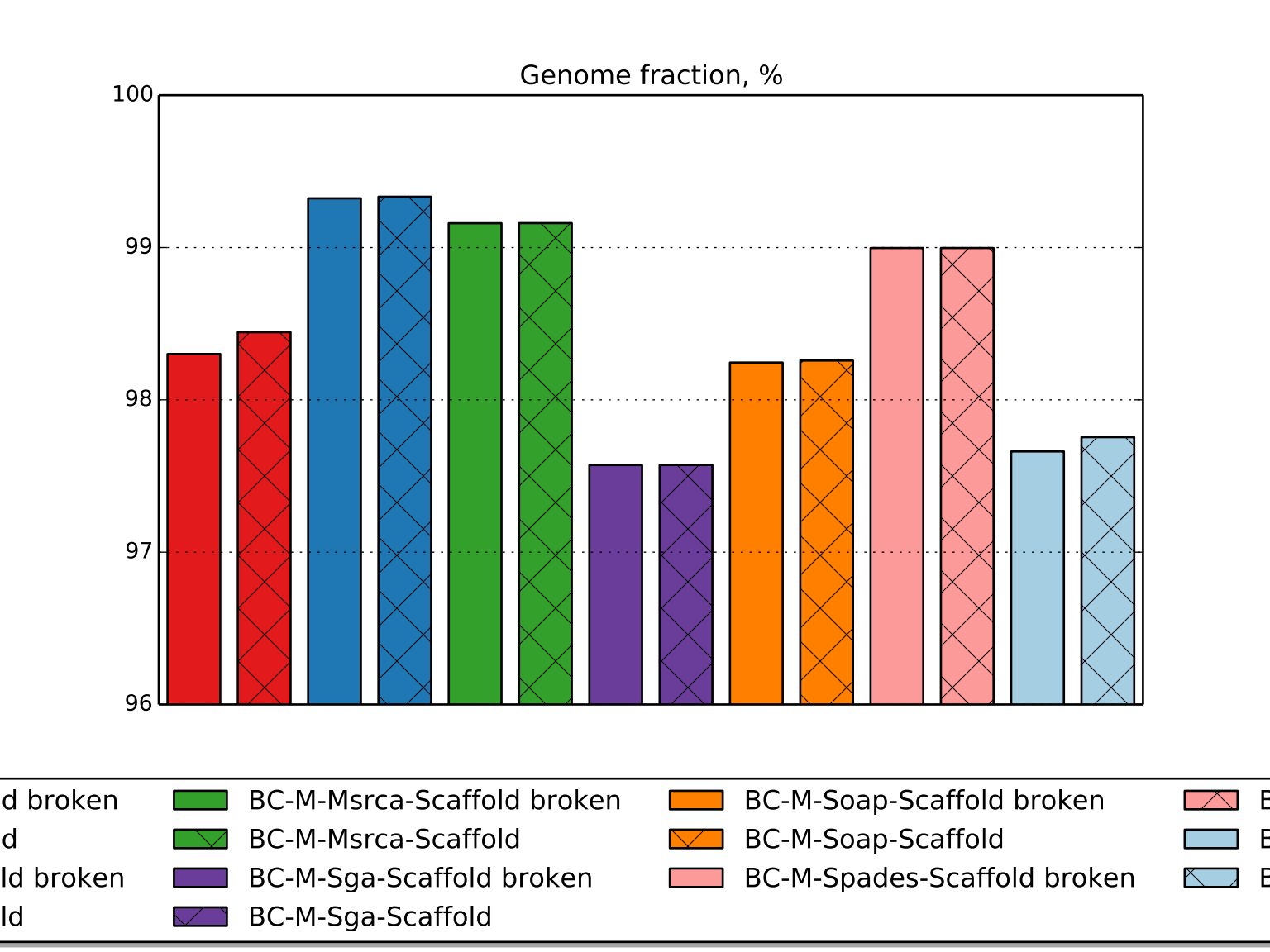

Cumulative length (aligned contigs)
Cumulative length (Mbp)
Contig index
0
1
2
3
4
5
6
0
80
160
240
320
400
d broken
d
ld broken
ld
BC-M-Msrca-Scaffold broken
BC-M-Msrca-Scaffold
BC-M-Sga-Scaffold broken
BC-M-Sga-Scaffold
BC-M-Soap-Scaffold broken
BC-M-Soap-Scaffold
BC-M-Spades-Scaffold broken
BC-M-Spades-Scaffold


NAx
Contig length (kbp)
x
0
200
400
600
800
1000
1200
0
20
40
60
80
100
d broken
d
ld broken
ld
BC-M-Msrca-Scaffold broken
BC-M-Msrca-Scaffold
BC-M-Sga-Scaffold broken
BC-M-Sga-Scaffold
BC-M-Soap-Scaffold broken
BC-M-Soap-Scaffold
BC-M-Spades-Scaffold broken

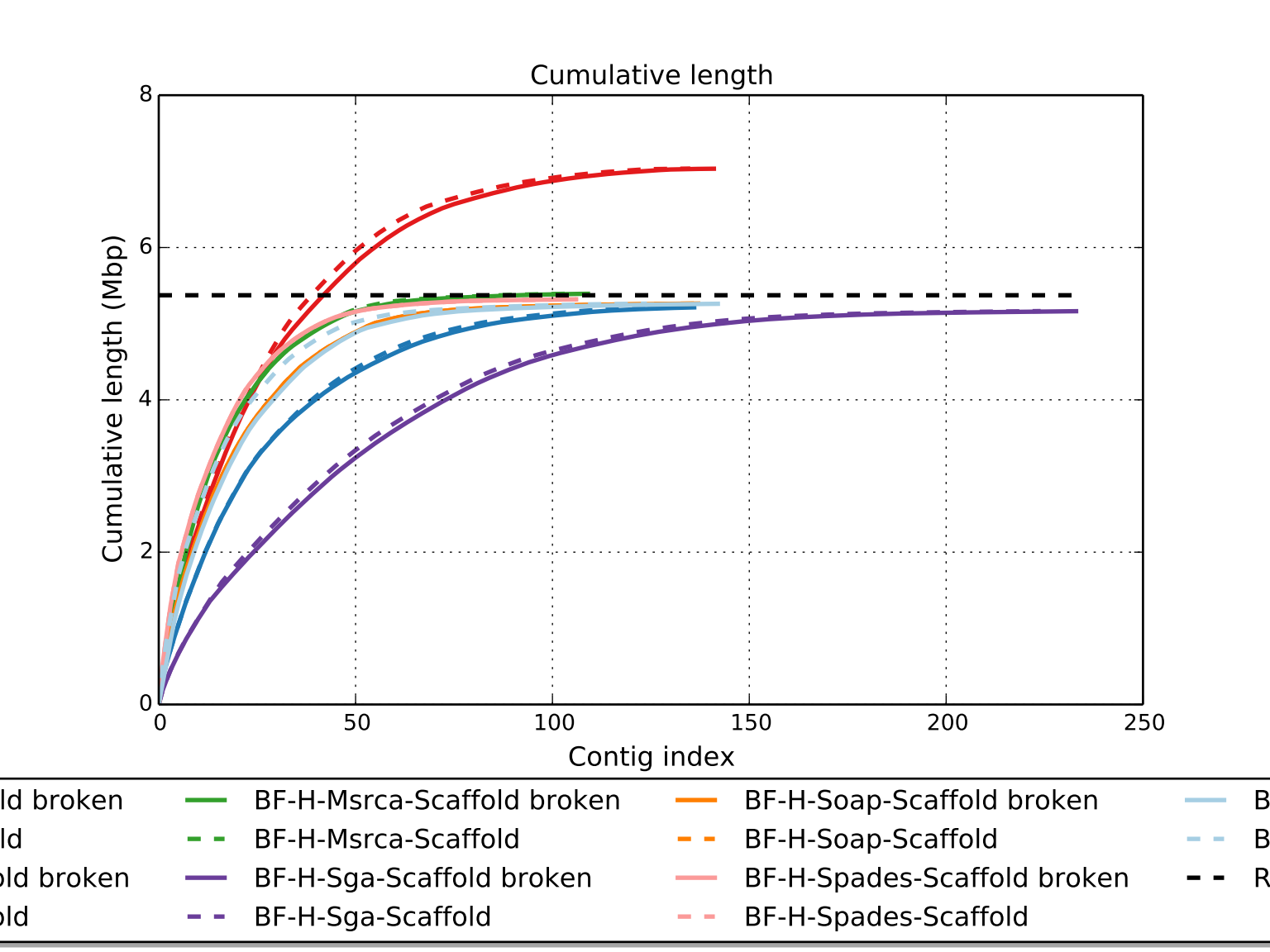

NGAx
Contig length (kbp)
x
0
200
400
600
800
1000
1200
0
20
40
60
80
100
d broken
d
ld broken
ld
BC-M-Msrca-Scaffold broken
BC-M-Msrca-Scaffold
BC-M-Sga-Scaffold broken
BC-M-Sga-Scaffold
BC-M-Soap-Scaffold broken
BC-M-Soap-Scaffold
BC-M-Spades-Scaffold broken

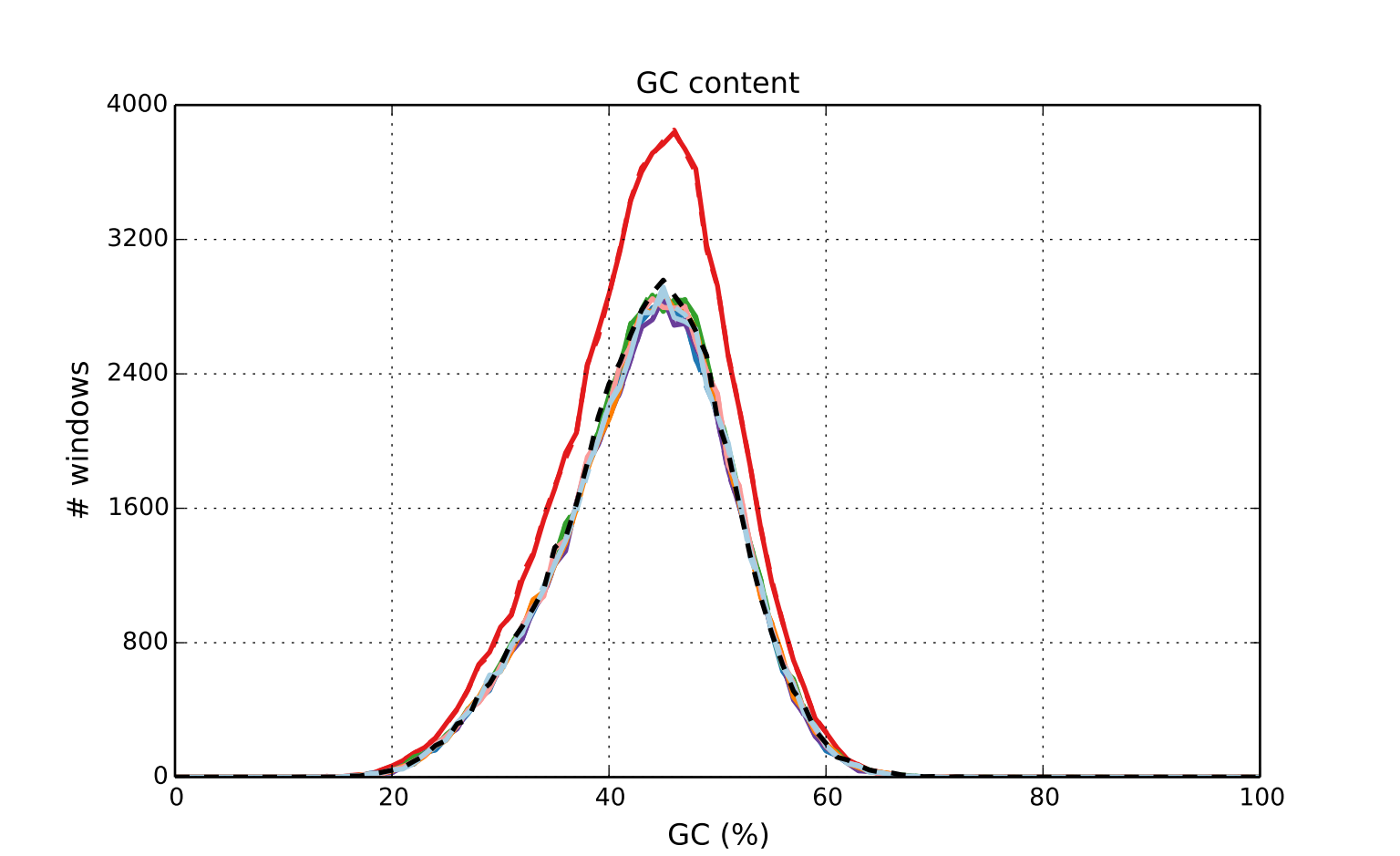

Cumulative # complete genes
Cumulative # complete genes
Contig index
0
2000
4000
6000
0
80
160
240
320
400
d broken
d
ld broken
ld
BC-M-Msrca-Scaffold broken
BC-M-Msrca-Scaffold
BC-M-Sga-Scaffold broken
BC-M-Sga-Scaffold
BC-M-Soap-Scaffold broken
BC-M-Soap-Scaffold
BC-M-Spades-Scaffold broken
BC-M-Spades-Scaffold

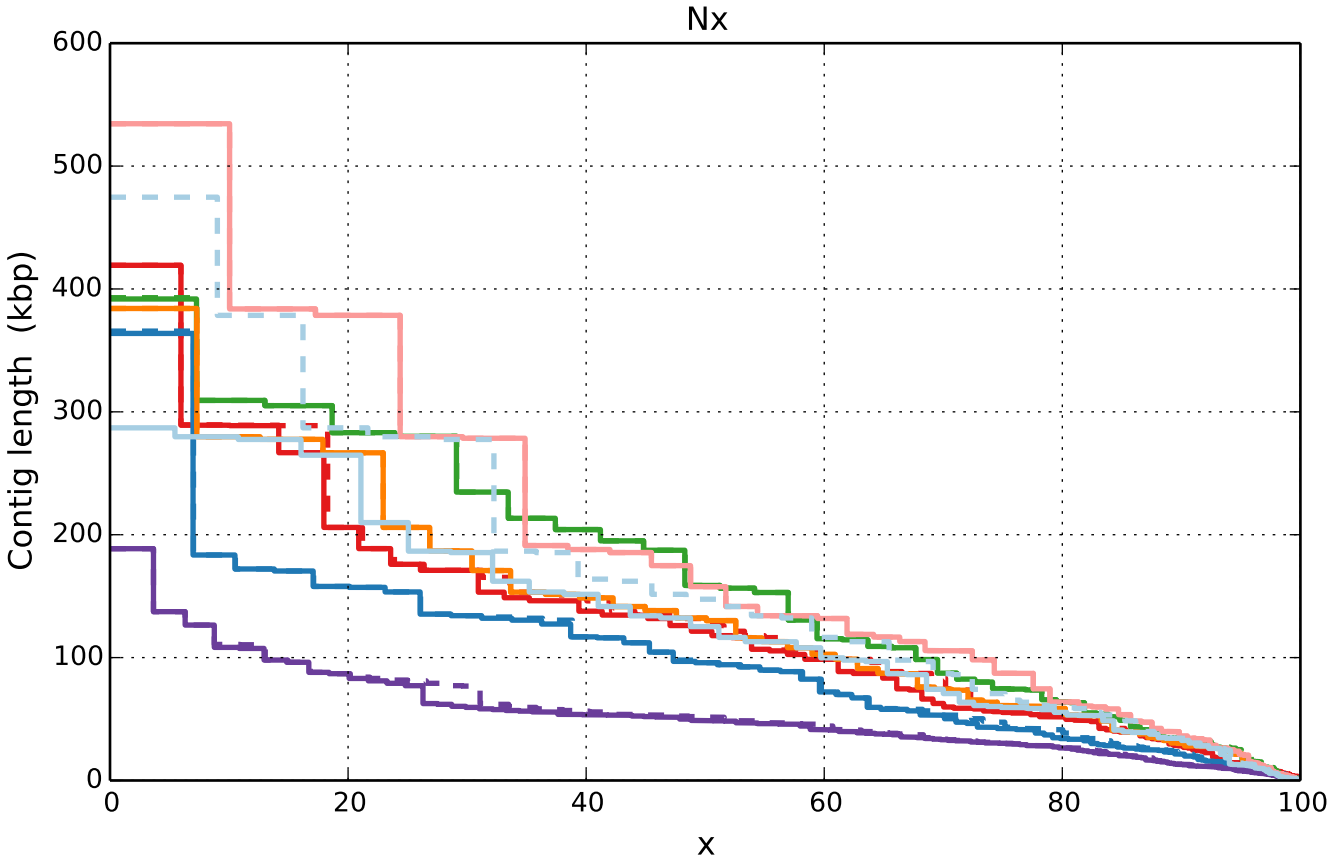

complete genes
6000
5500
d broken
d
ld broken
ld
BC-M-Msrca-Scaffold broken
BC-M-Msrca-Scaffold
BC-M-Sga-Scaffold broken
BC-M-Sga-Scaffold
BC-M-Soap-Scaffold broken
BC-M-Soap-Scaffold
BC-M-Spades-Scaffold broken


Genome fraction, %
100
99
98
97
96
d broken
d
ld broken
ld
BC-M-Msrca-Scaffold broken
BC-M-Msrca-Scaffold
BC-M-Sga-Scaffold broken
BC-M-Sga-Scaffold
BC-M-Soap-Scaffold broken
BC-M-Soap-Scaffold
BC-M-Spades-Scaffold broken

Scaffold


Cumulative length
Cumulative length (Mbp)
Contig index
0
2
4
6
8
0
50
100
150
200
250
ld broken
ld
old broken
old
BF-H-Msrca-Scaffold broken
BF-H-Msrca-Scaffold
BF-H-Sga-Scaffold broken
BF-H-Sga-Scaffold
BF-H-Soap-Scaffold broken
BF-H-Soap-Scaffold
BF-H-Spades-Scaffold broken
BF-H-Spades-Scaffold
B
B
R


GC content
windows
GC (%)
0
800
1600
2400
3200
4000
0
20
40
60
80
100
ld broken
ld
old broken
old
BF-H-Msrca-Scaffold broken
BF-H-Msrca-Scaffold
BF-H-Sga-Scaffold broken
BF-H-Sga-Scaffold
BF-H-Soap-Scaffold broken
BF-H-Soap-Scaffold
BF-H-Spades-Scaffold broken
BF-H-Spades-Scaffold
B
B
R

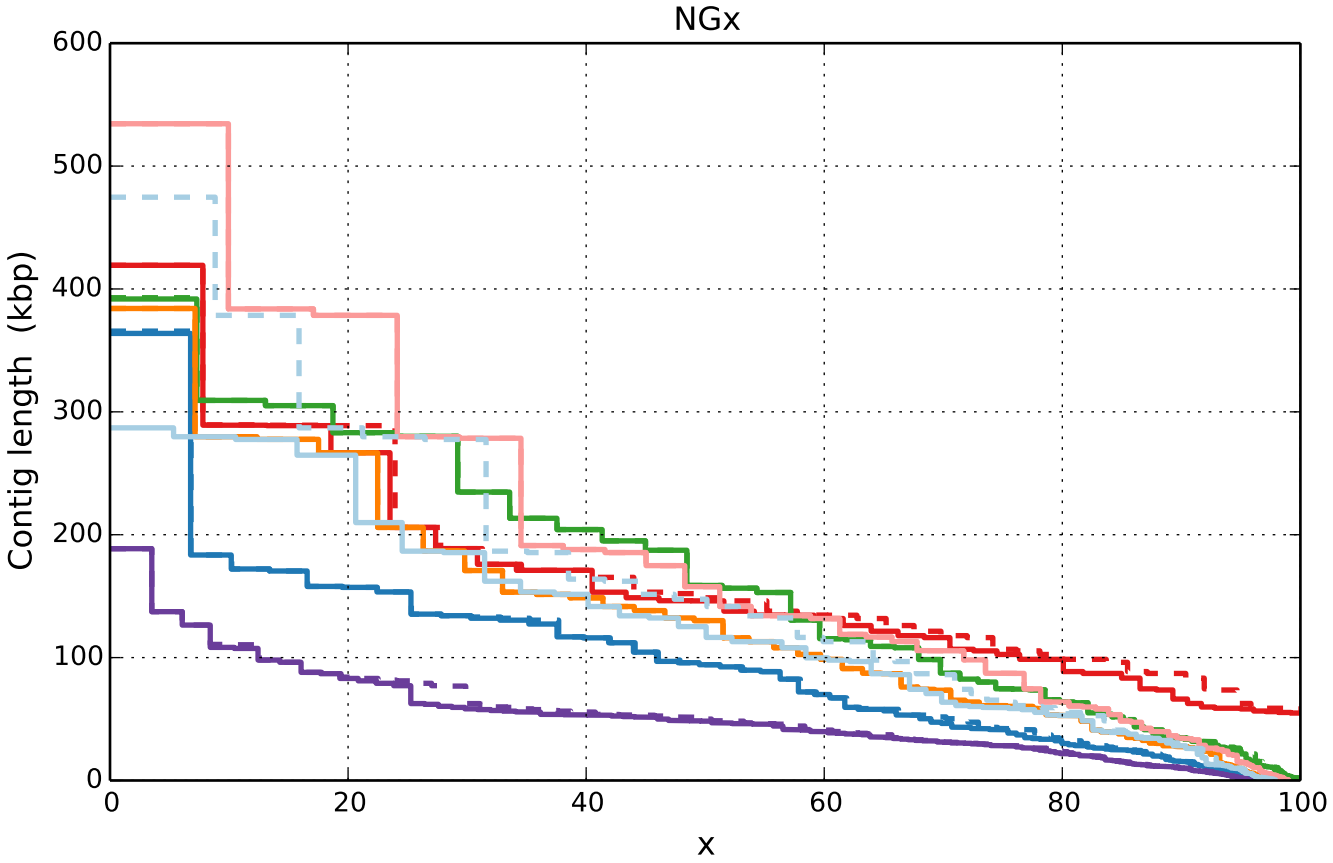


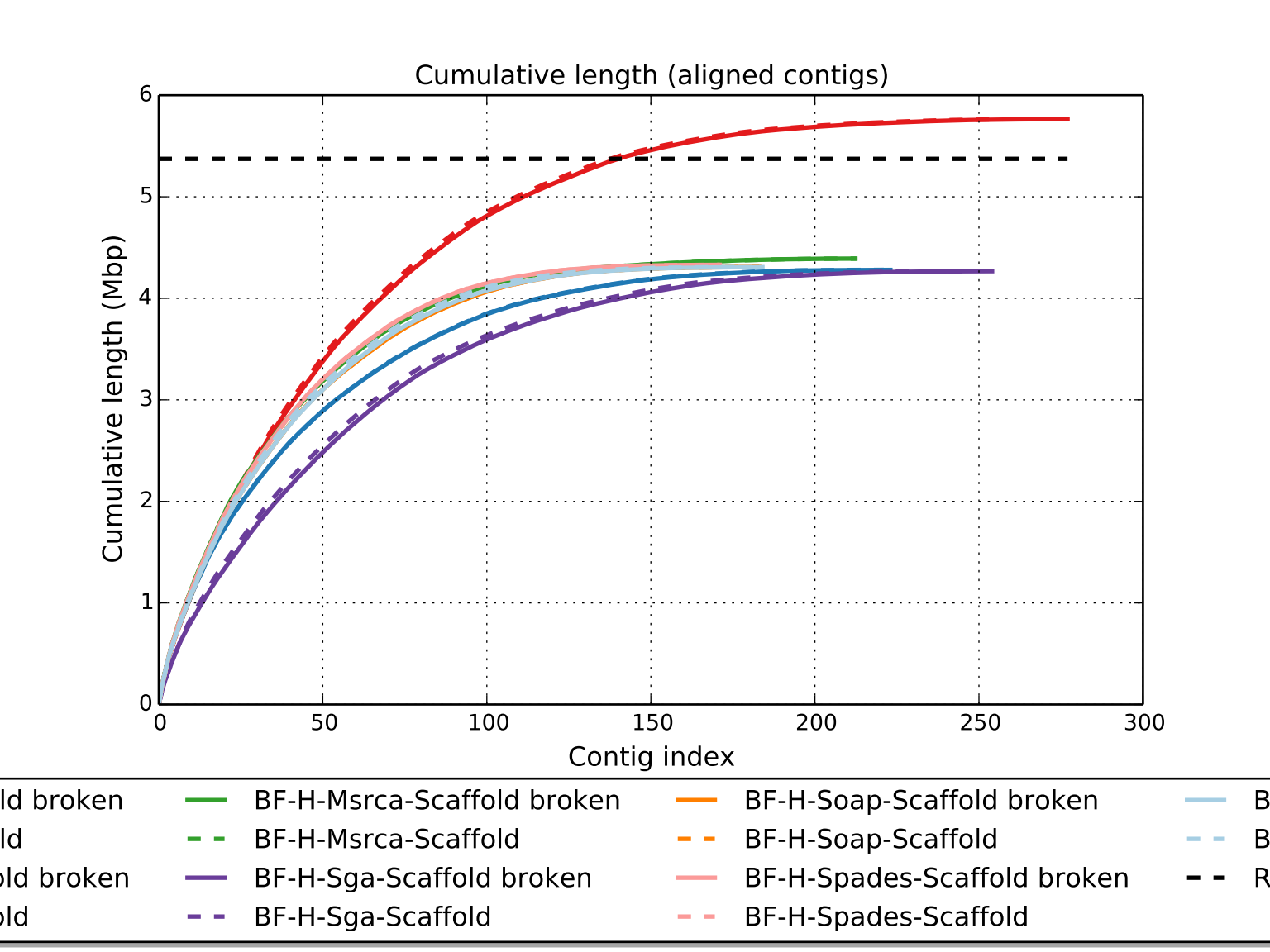
ld broken
ld
old broken
old

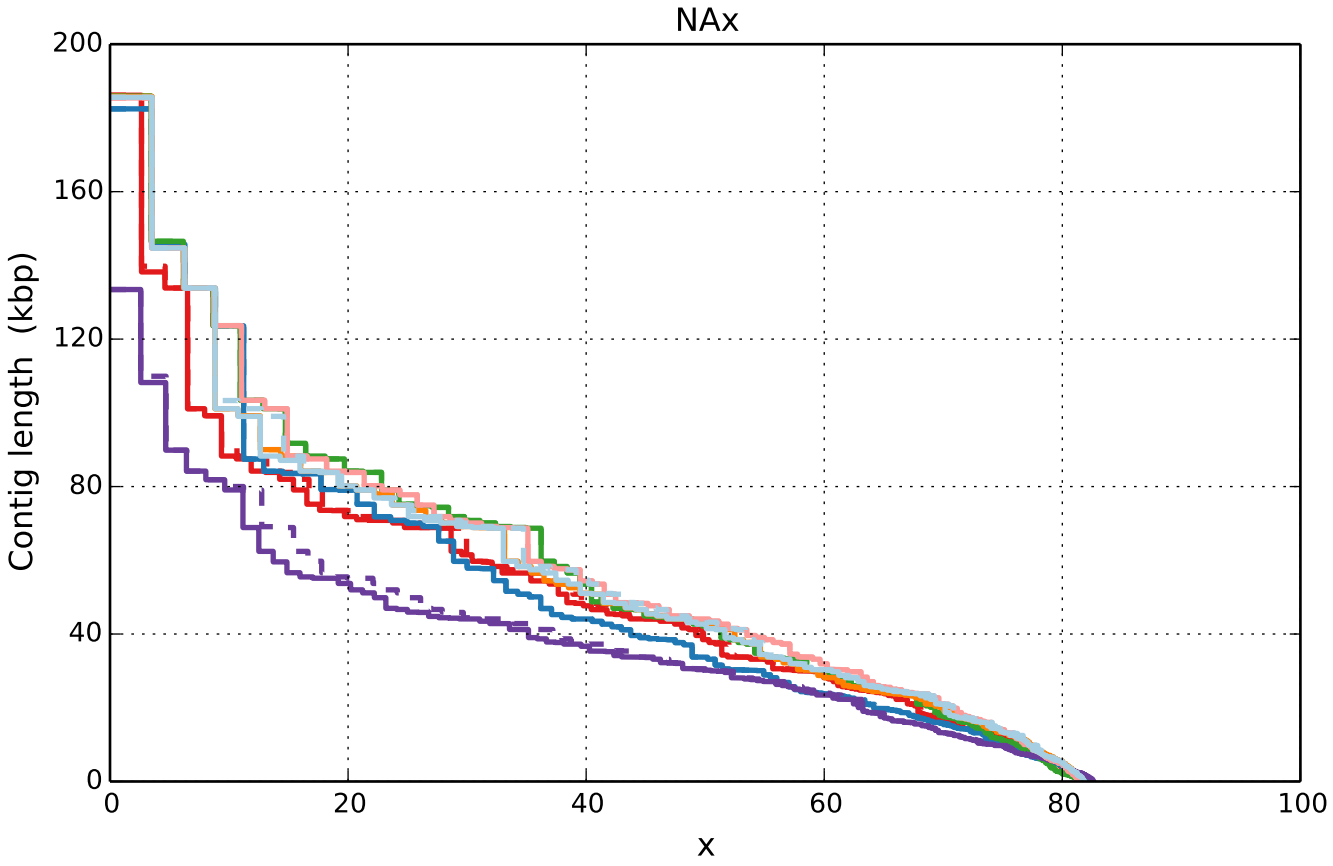
BF-H-Msrca-Scaffold broken
BF-H-Msrca-Scaffold
BF-H-Sga-Scaffold broken
BF-H-Sga-Scaffold

BF-H-Soap-Scaffold broken
BF-H-Soap-Scaffold
BF-H-Spades-Scaffold broken

B
B
B


NGx
Contig length (kbp)
600
500
400
300
200
100
0
0
20
40
60
80
100
x
ld broken
ld
old broken
old
BF-H-Msrca-Scaffold broken
BF-H-Msrca-Scaffold
BF-H-Sga-Scaffold broken
BF-H-Sga-Scaffold
BF-H-Soap-Scaffold broken
BF-H-Soap-Scaffold
BF-H-Spades-Scaffold broken
B
B
B


Cumulative length (aligned contigs)
Cumulative length (Mbp)
Contig index
0
1
2
3
4
5
6
0
50
100
150
200
250
300
ld broken
ld
old broken
old
BF-H-Msrca-Scaffold broken
BF-H-Msrca-Scaffold
BF-H-Sga-Scaffold broken
BF-H-Sga-Scaffold
BF-H-Soap-Scaffold broken
BF-H-Soap-Scaffold
BF-H-Spades-Scaffold broken
BF-H-Spades-Scaffold
B
B
R

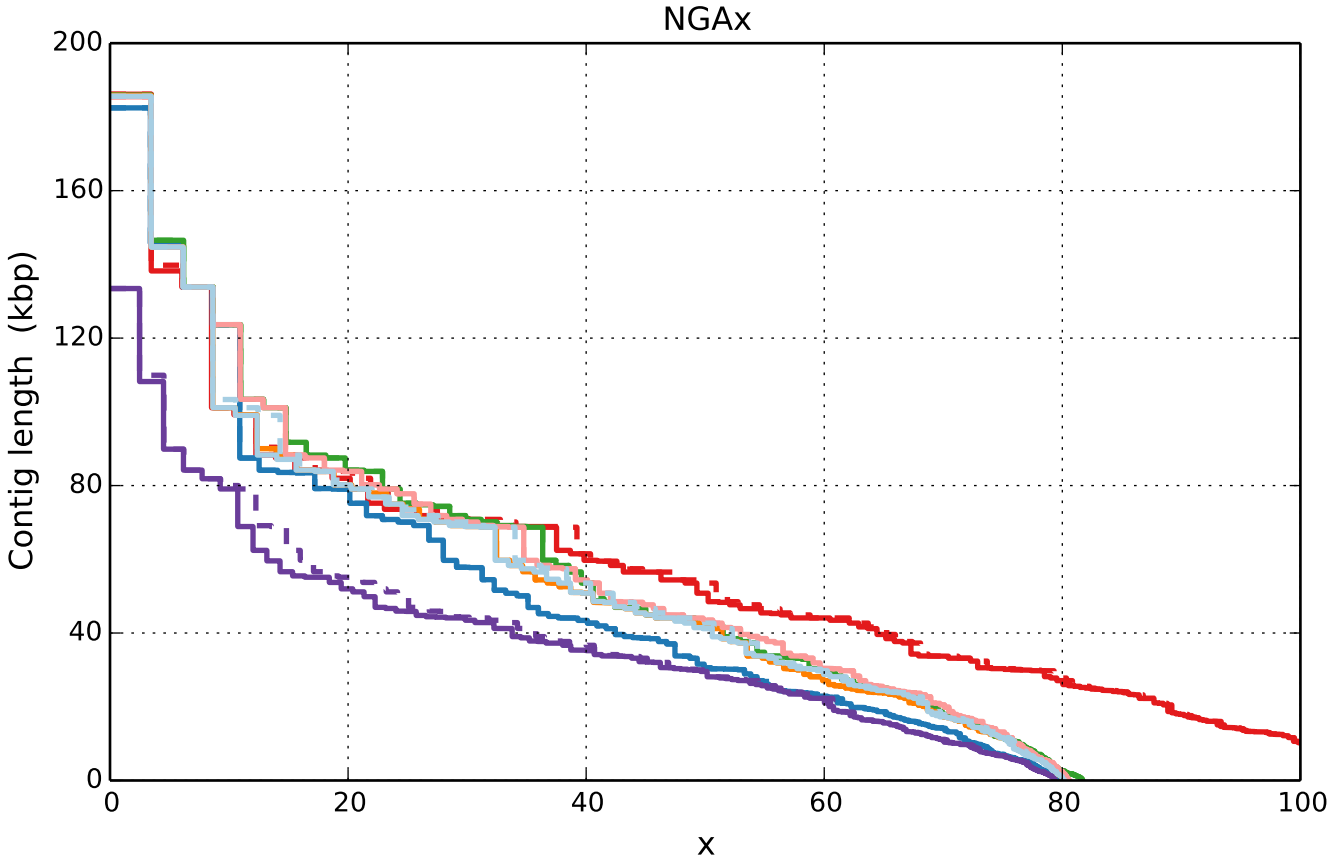


ld broken
ld
old broken
old

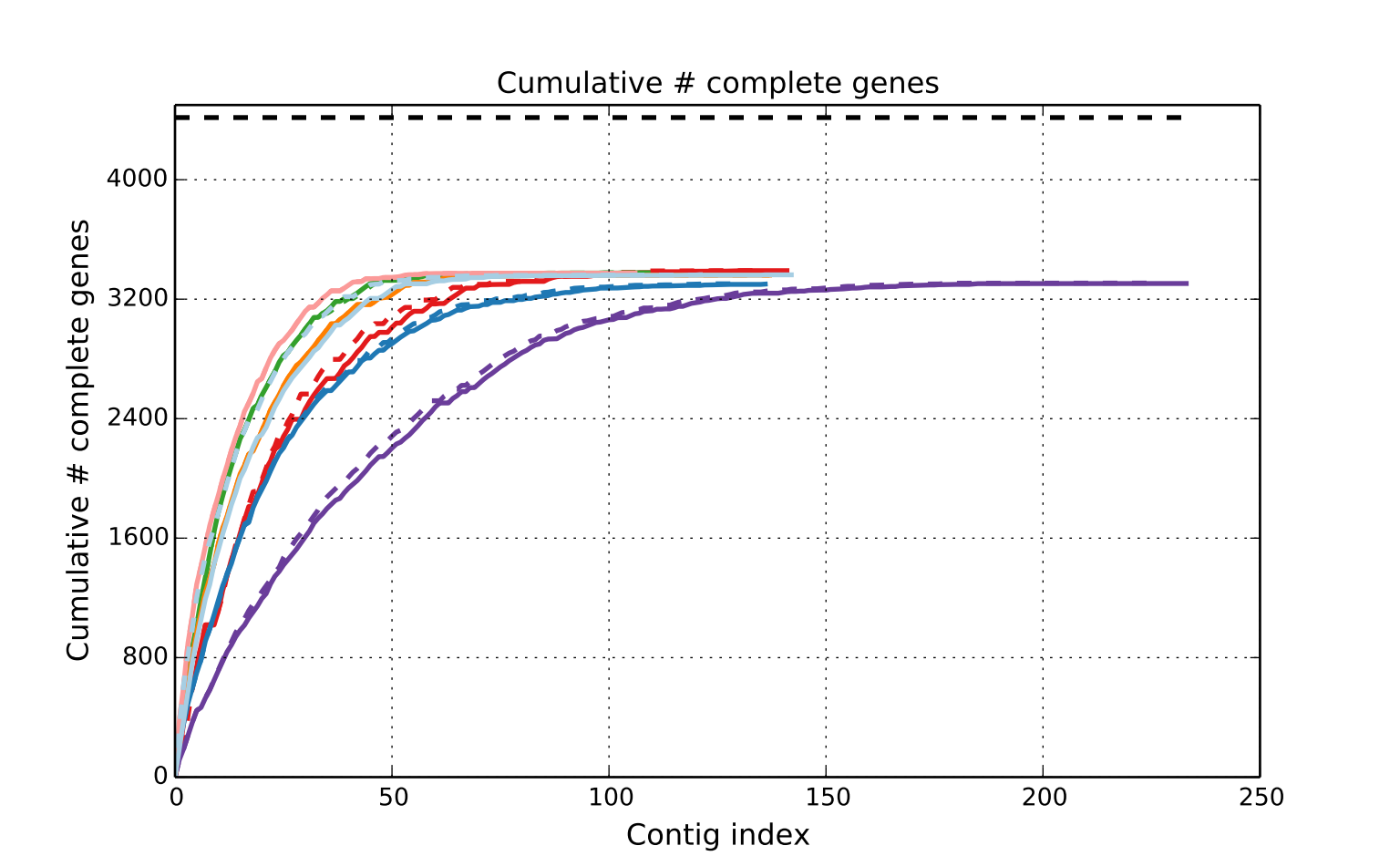
BF-H-Msrca-Scaffold broken
BF-H-Msrca-Scaffold
BF-H-Sga-Scaffold broken
BF-H-Sga-Scaffold

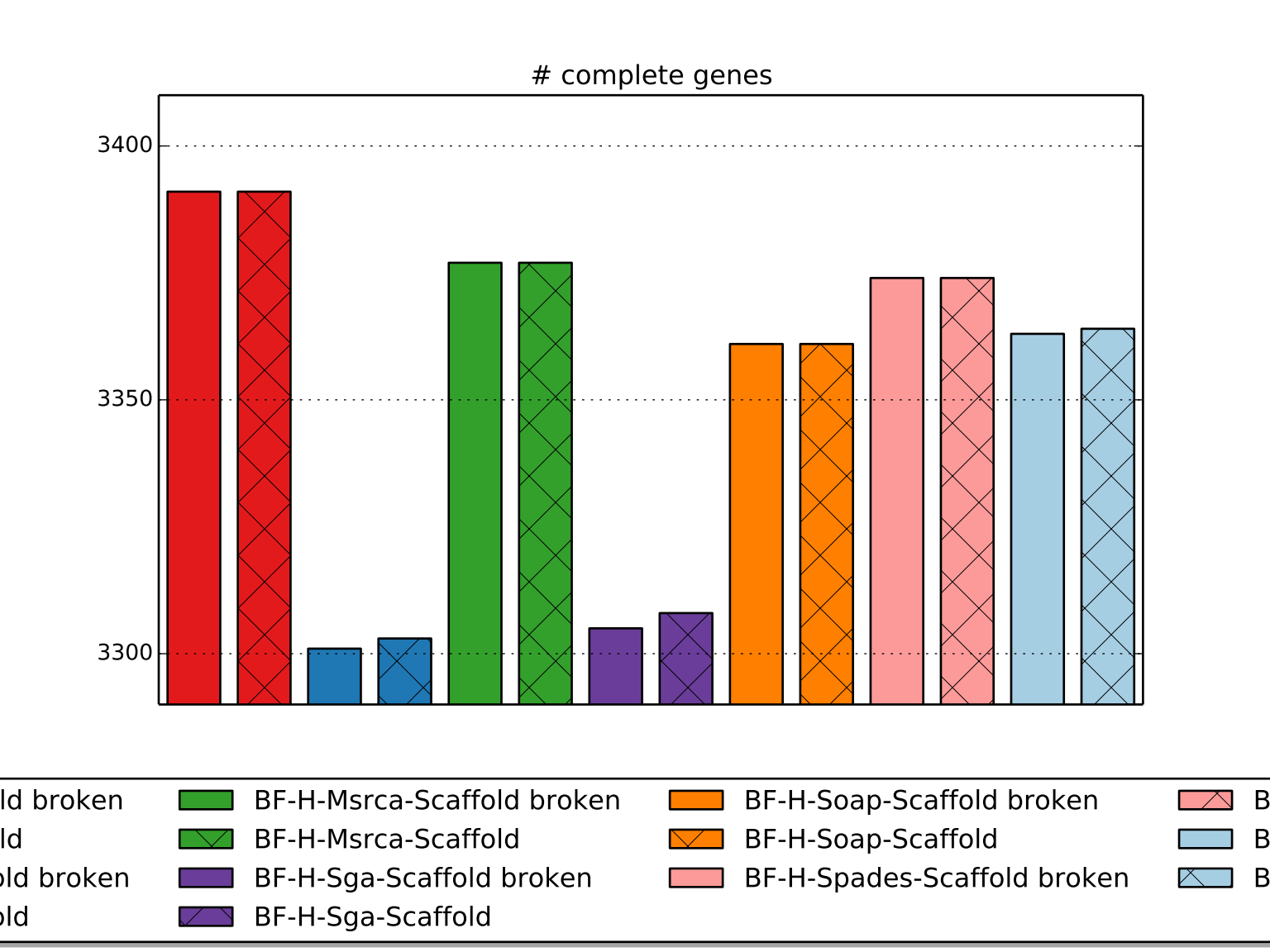
BF-H-Soap-Scaffold broken
BF-H-Soap-Scaffold
BF-H-Spades-Scaffold broken

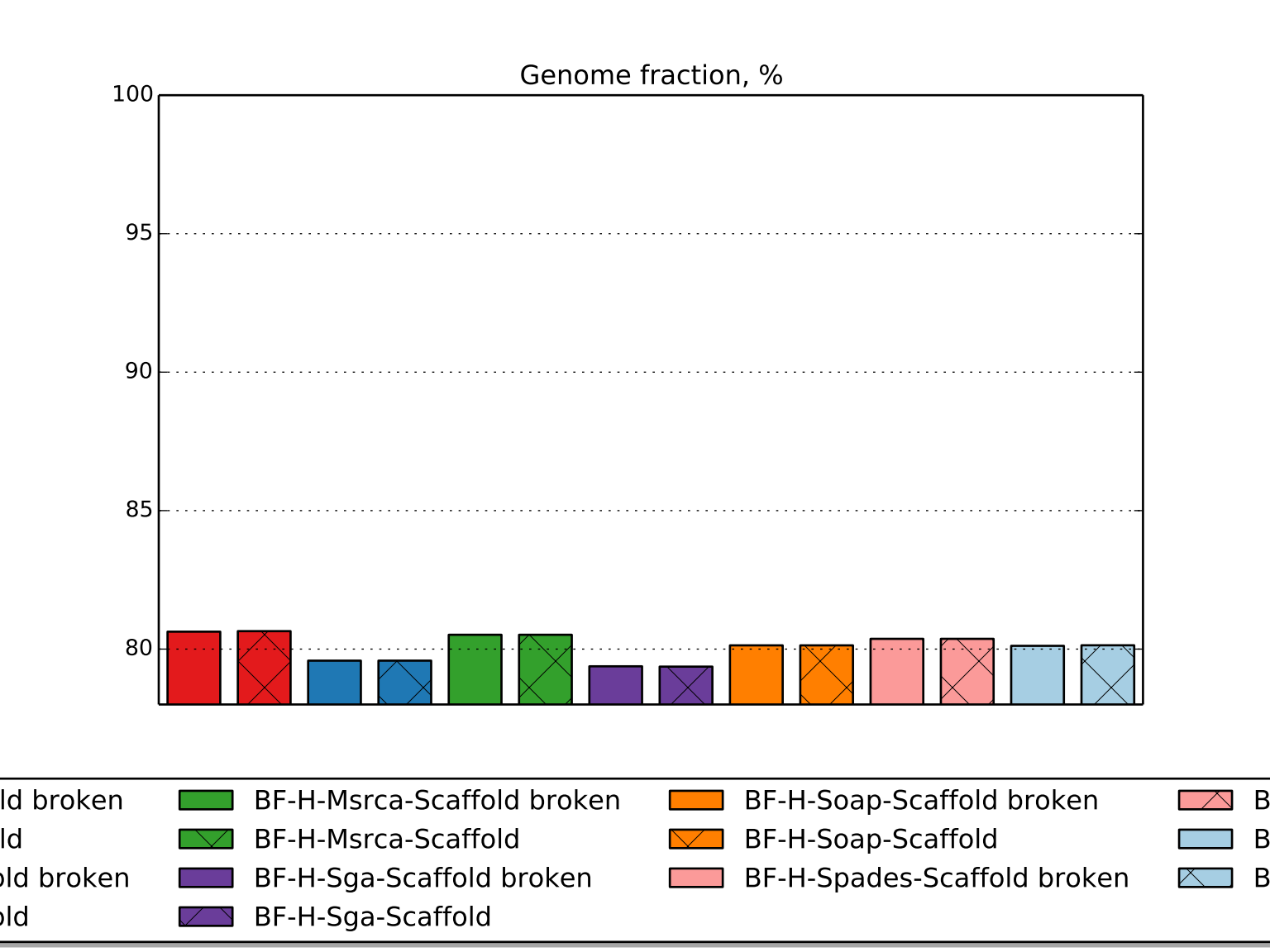
B
B
B



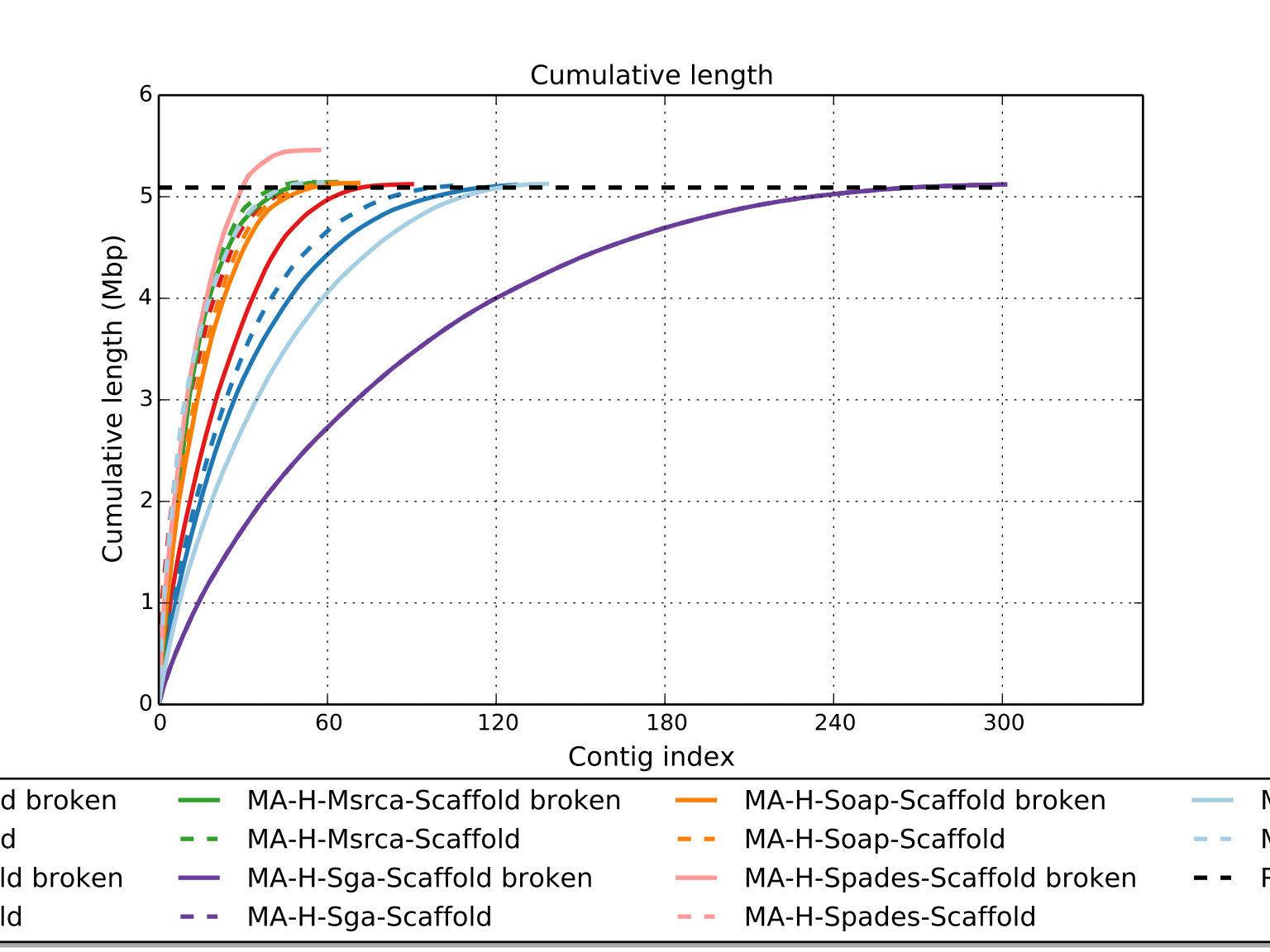
ld broken
ld
old broken
old
BF-H-Msrca-Scaffold broken
BF-H-Msrca-Scaffold
BF-H-Sga-Scaffold broken
BF-H-Sga-Scaffold
BF-H-Soap-Scaffold broken
BF-H-Soap-Scaffold
BF-H-Spades-Scaffold broken
B
B
B

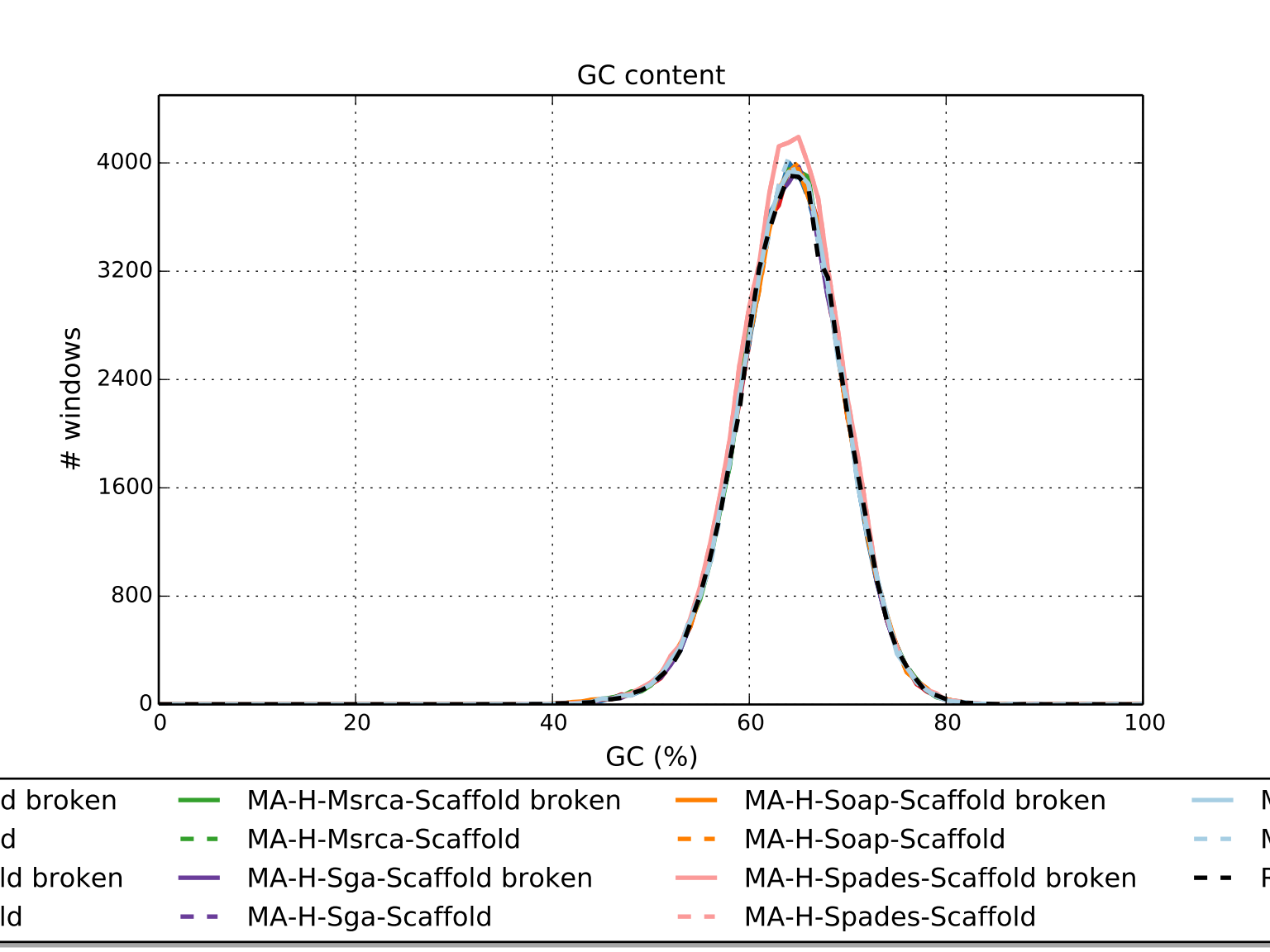

Cumulative # complete genes
Cumulative # complete genes
Contig index
0
800
1600
2400
3200
4000
0
50
100
150
200
250
ld broken
ld
old broken
old
BF-H-Msrca-Scaffold broken
BF-H-Msrca-Scaffold
BF-H-Sga-Scaffold broken
BF-H-Sga-Scaffold
BF-H-Soap-Scaffold broken
BF-H-Soap-Scaffold
BF-H-Spades-Scaffold broken
BF-H-Spades-Scaffold
B
B
R

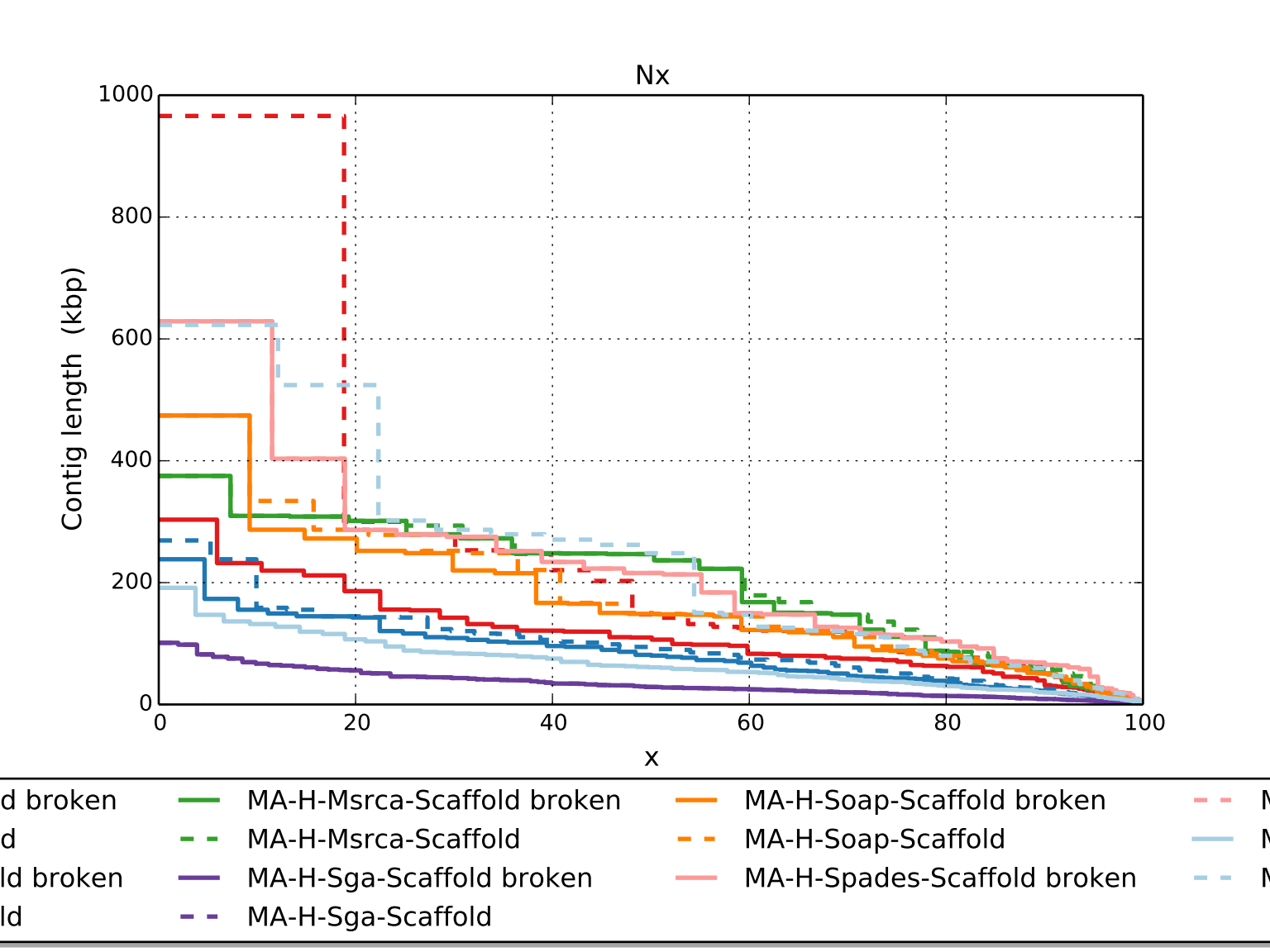

complete genes
3400
3350
3300
ld broken
ld
old broken
old
BF-H-Msrca-Scaffold broken
BF-H-Msrca-Scaffold
BF-H-Sga-Scaffold broken
BF-H-Sga-Scaffold
BF-H-Soap-Scaffold broken
BF-H-Soap-Scaffold
BF-H-Spades-Scaffold broken
B
B
B

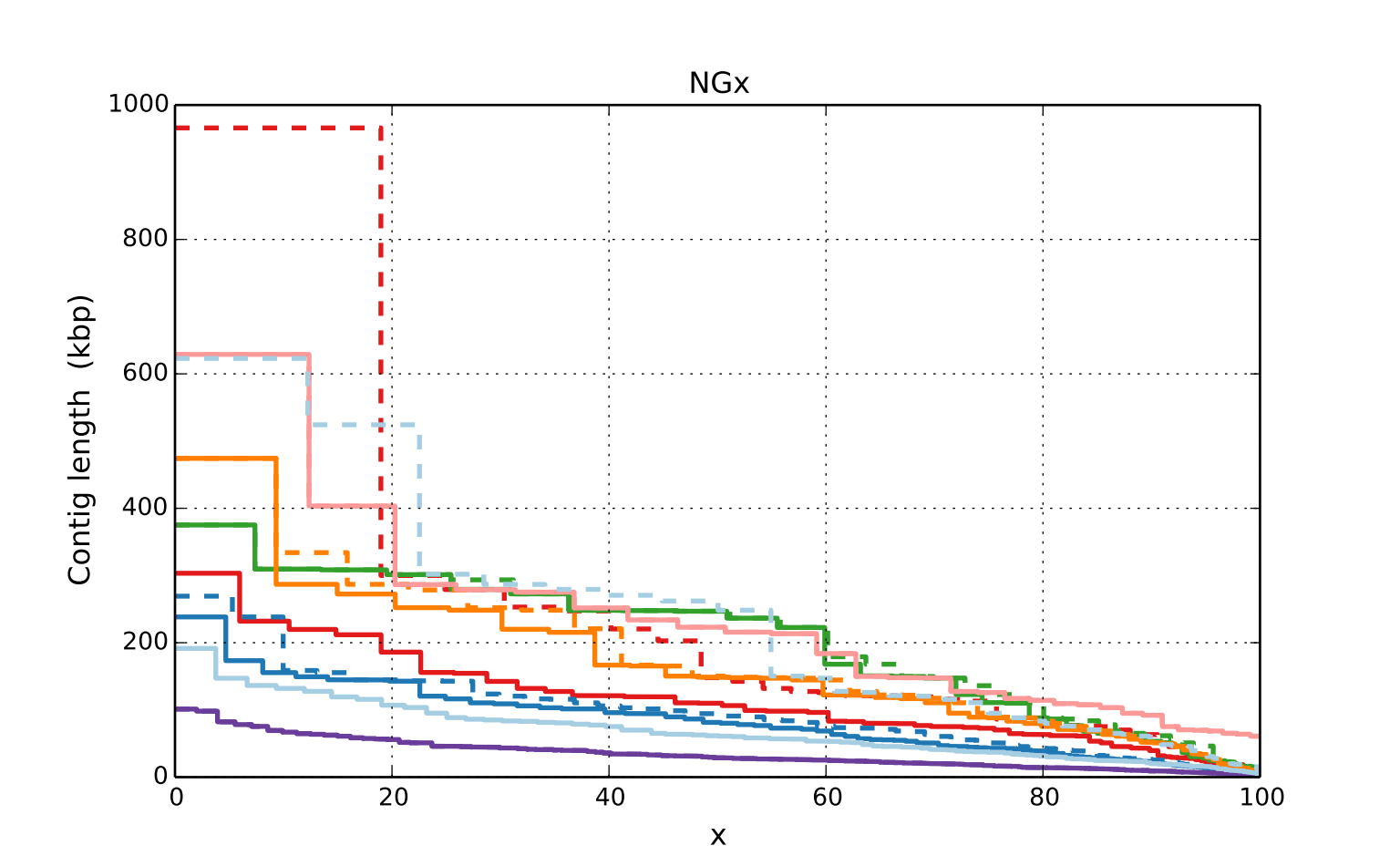

Genome fraction, %
100
95
90
85
80
ld broken
ld
old broken
old
BF-H-Msrca-Scaffold broken
BF-H-Msrca-Scaffold
BF-H-Sga-Scaffold broken
BF-H-Sga-Scaffold
BF-H-Soap-Scaffold broken
BF-H-Soap-Scaffold
BF-H-Spades-Scaffold broken
B
B
B

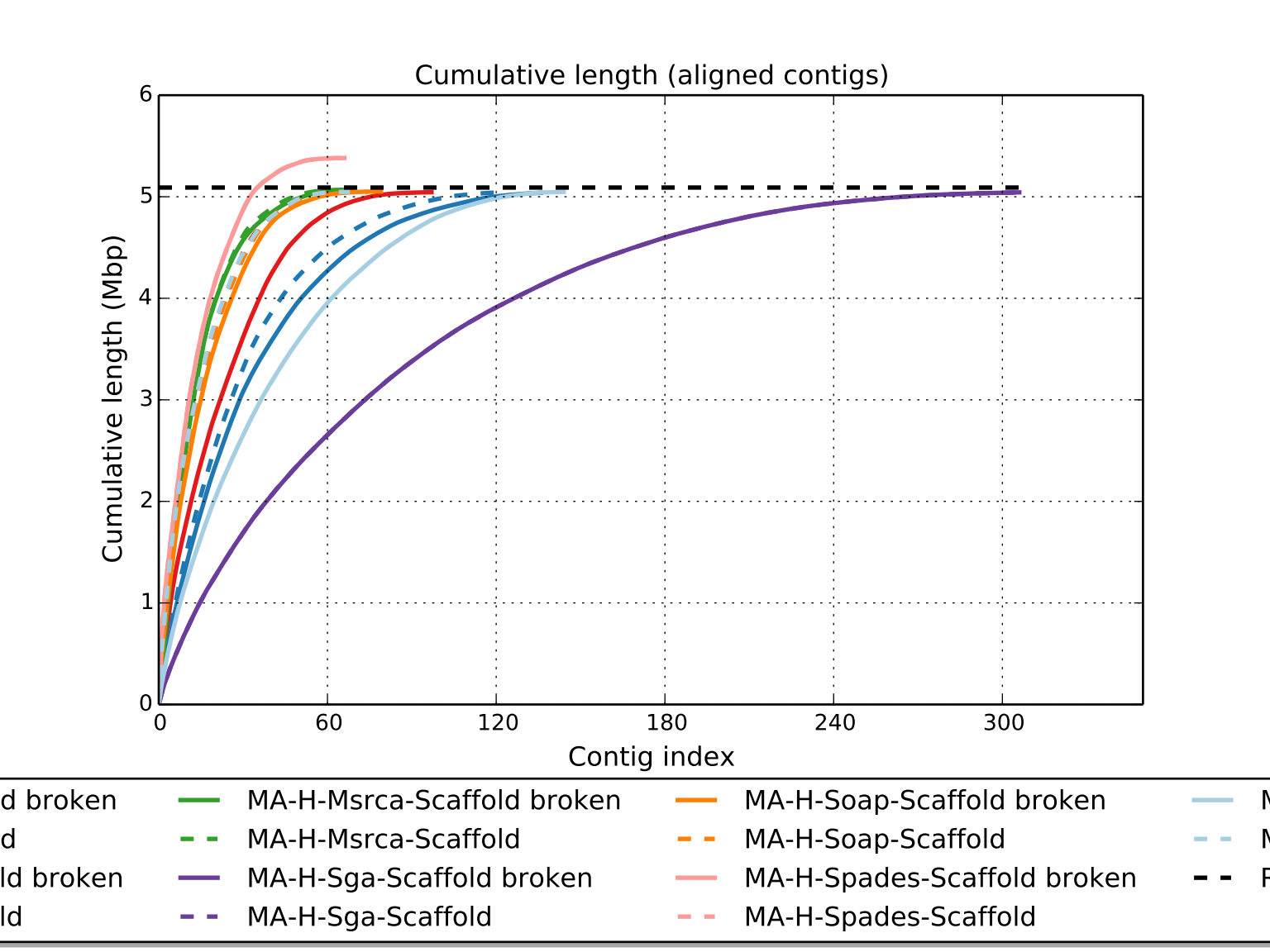
Scaffold

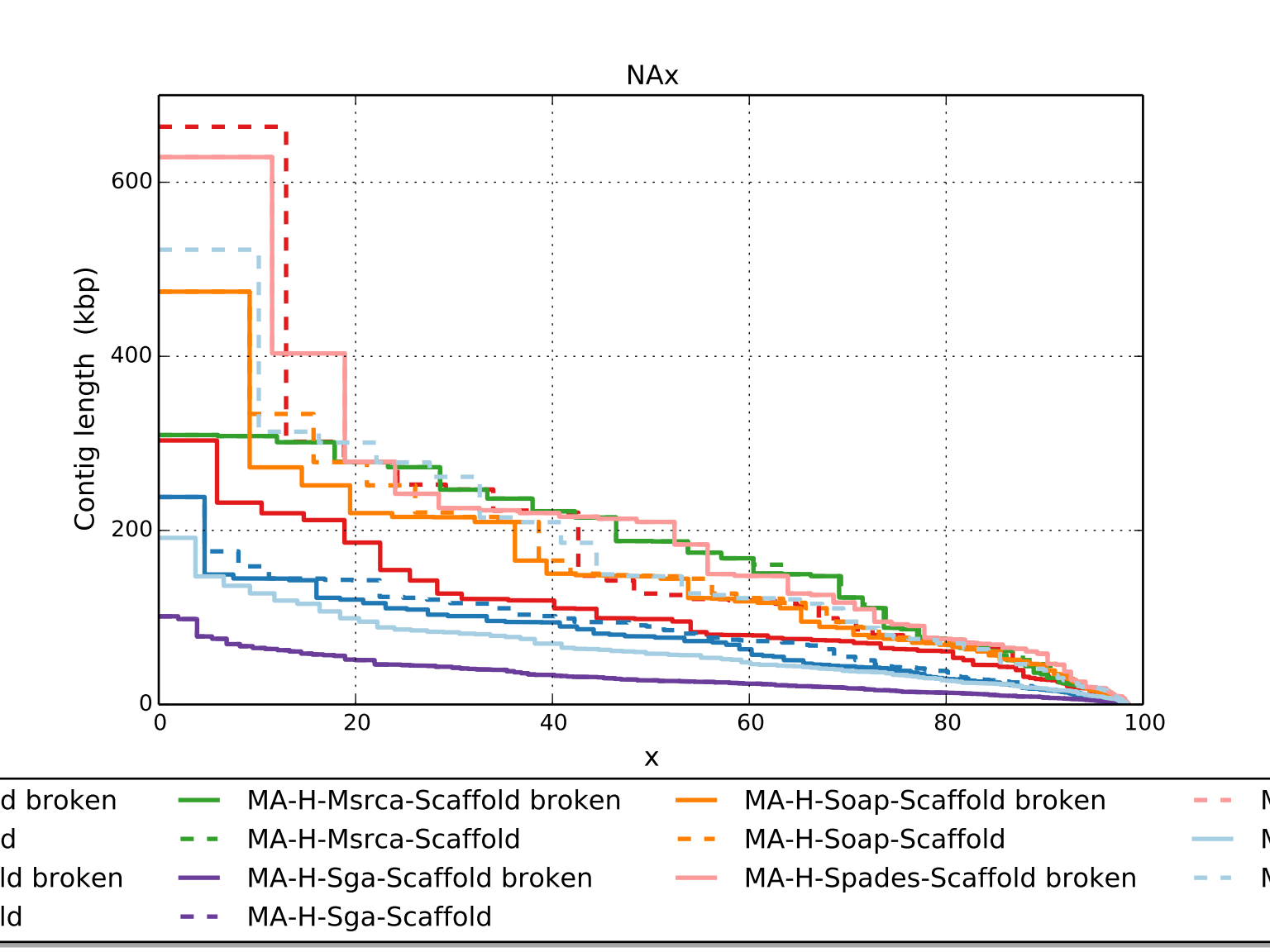

Cumulative length
Cumulative length (Mbp)
Contig index
0
1
2
3
4
5
6
0
60
120
180
240
300
d broken
d
ld broken
ld
MA-H-Msrca-Scaffold broken
MA-H-Msrca-Scaffold
MA-H-Sga-Scaffold broken
MA-H-Sga-Scaffold
MA-H-Soap-Scaffold broken
MA-H-Soap-Scaffold
MA-H-Spades-Scaffold broken
MA-H-Spades-Scaffold

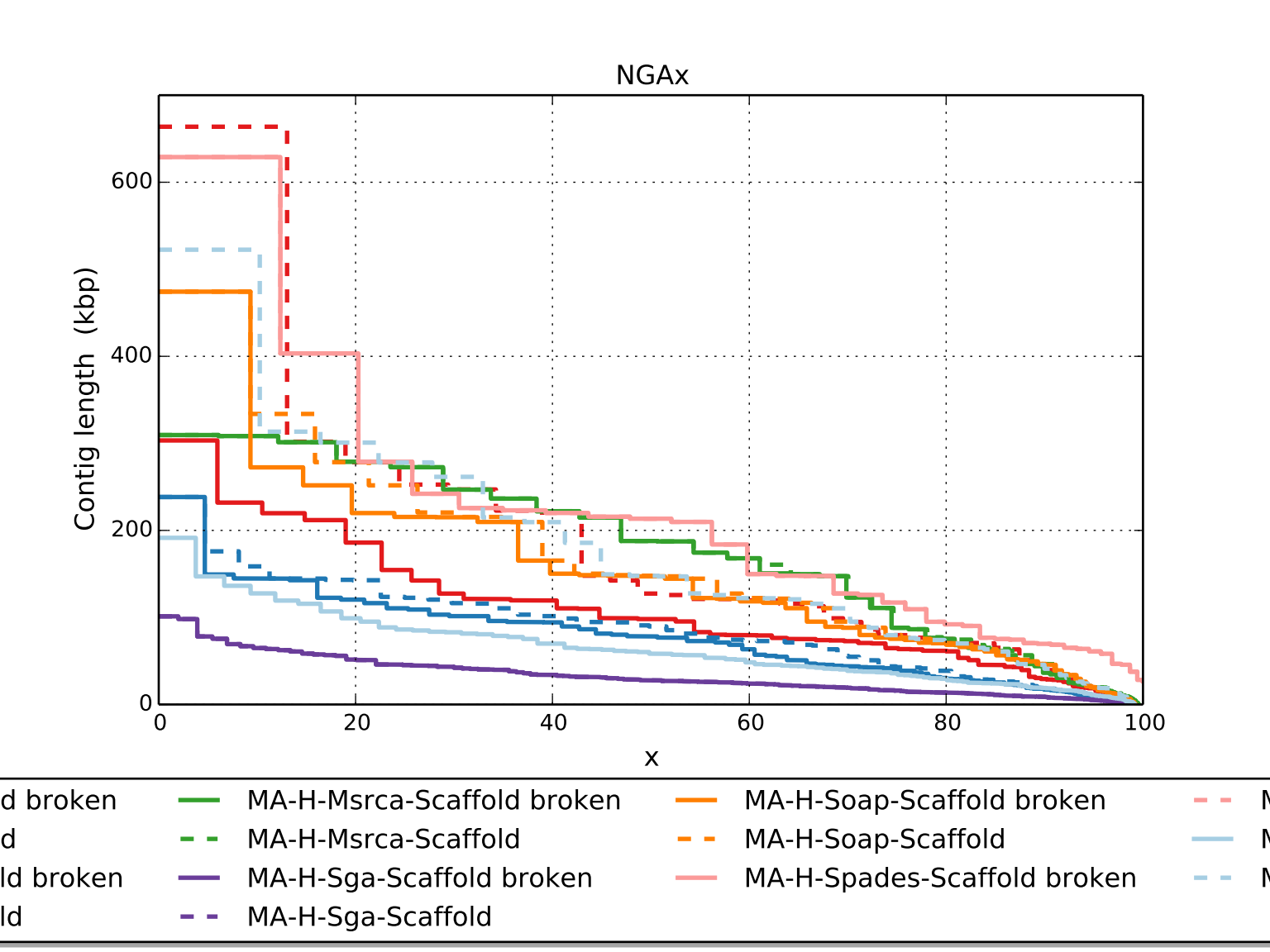

GC content
windows
GC (%)
0
800
1600
2400
3200
4000
0
20
40
60
80
100
d broken
d
ld broken
ld
MA-H-Msrca-Scaffold broken
MA-H-Msrca-Scaffold
MA-H-Sga-Scaffold broken
MA-H-Sga-Scaffold
MA-H-Soap-Scaffold broken
MA-H-Soap-Scaffold
MA-H-Spades-Scaffold broken
MA-H-Spades-Scaffold

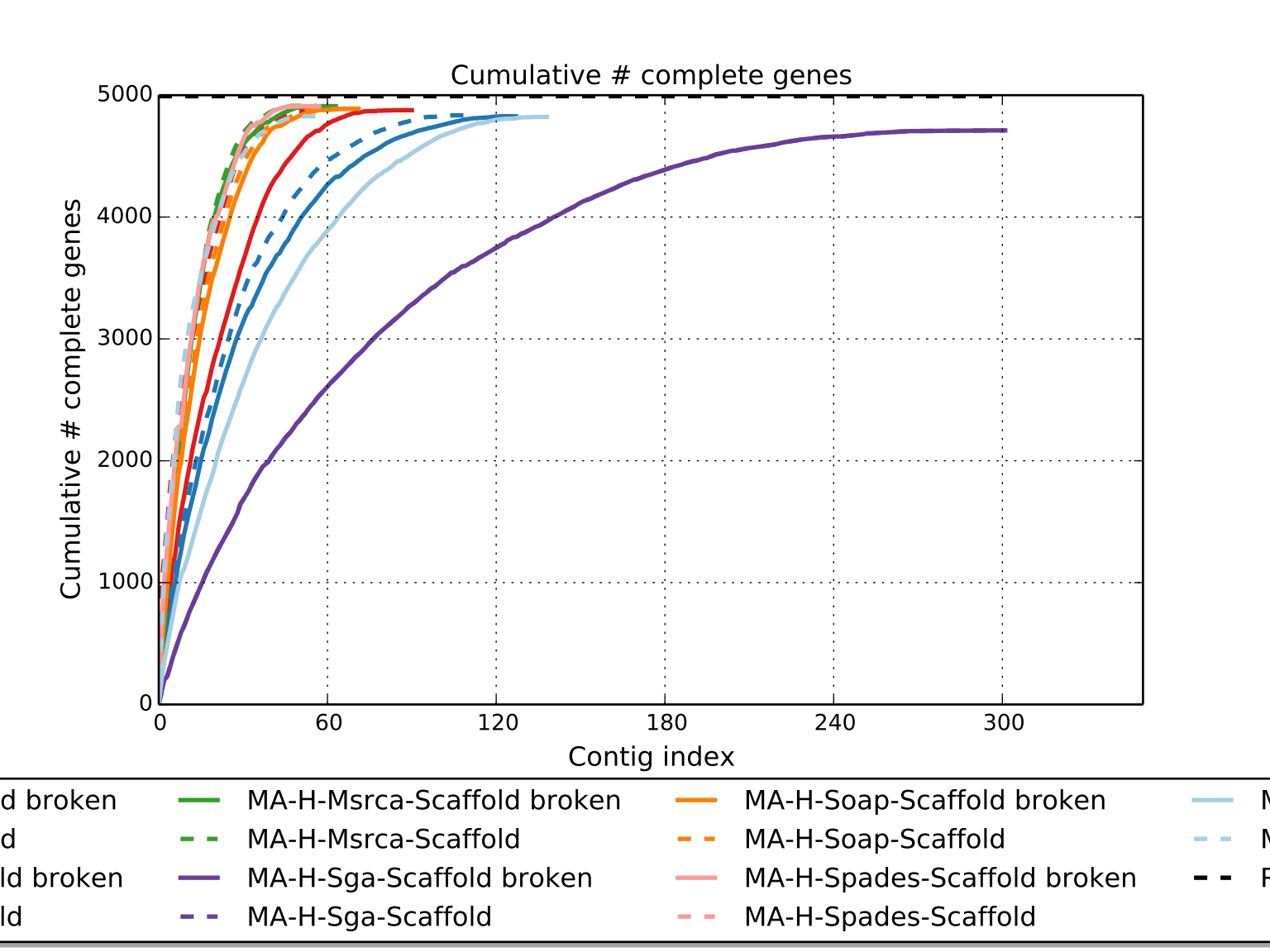

Nx
Contig length (kbp)
x
0
200
400
600
800
1000
0
20
40
60
80
100
d broken
d
ld broken
ld
MA-H-Msrca-Scaffold broken
MA-H-Msrca-Scaffold
MA-H-Sga-Scaffold broken
MA-H-Sga-Scaffold
MA-H-Soap-Scaffold broken
MA-H-Soap-Scaffold
MA-H-Spades-Scaffold broken

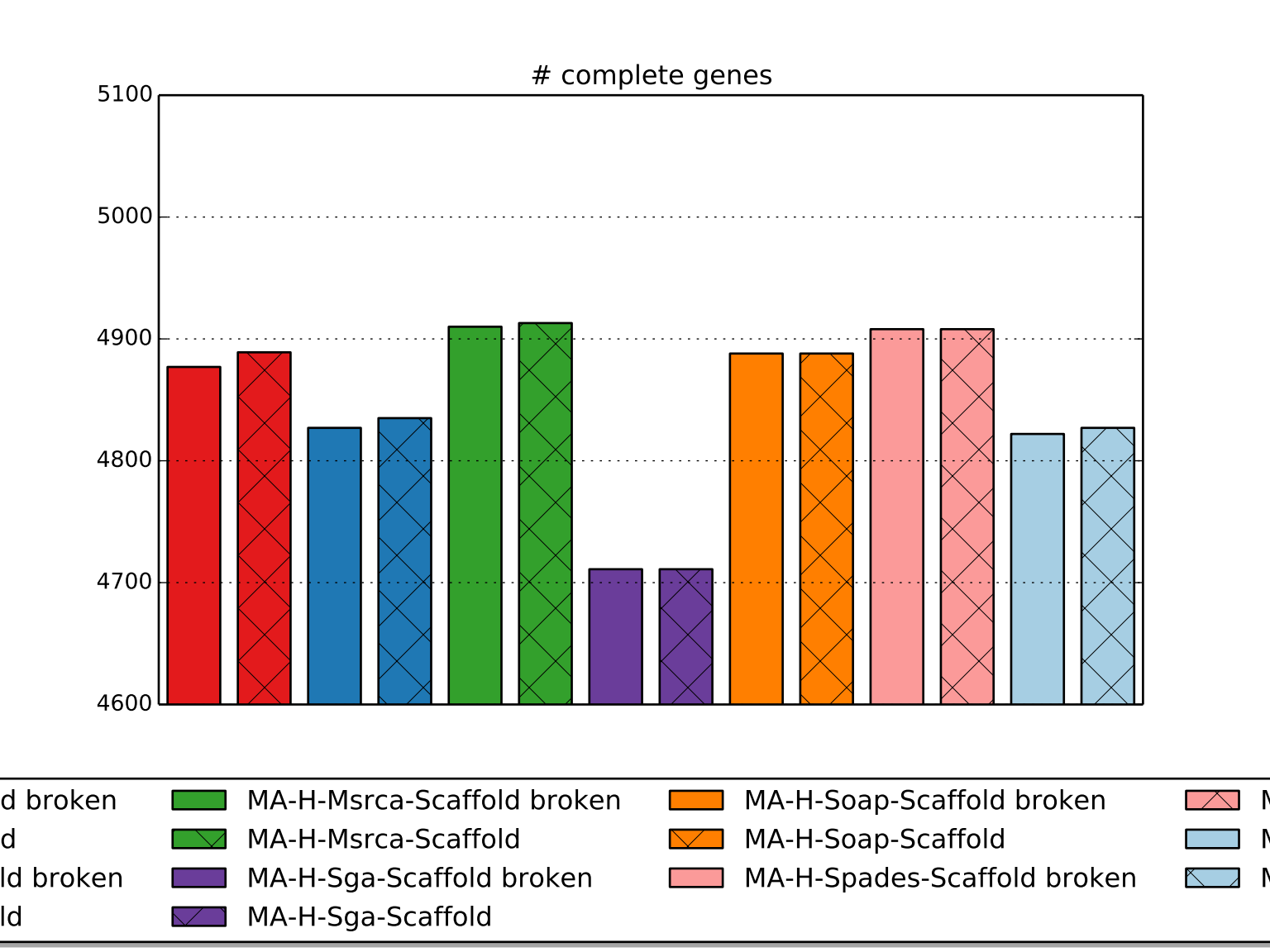

NGx
Contig length (kbp)
x
0
200
400
600
800
1000
0
20
40
60
80
100
d broken
d
ld broken
ld
MA-H-Msrca-Scaffold broken
MA-H-Msrca-Scaffold
MA-H-Sga-Scaffold broken
MA-H-Sga-Scaffold
MA-H-Soap-Scaffold broken
MA-H-Soap-Scaffold
MA-H-Spades-Scaffold broken

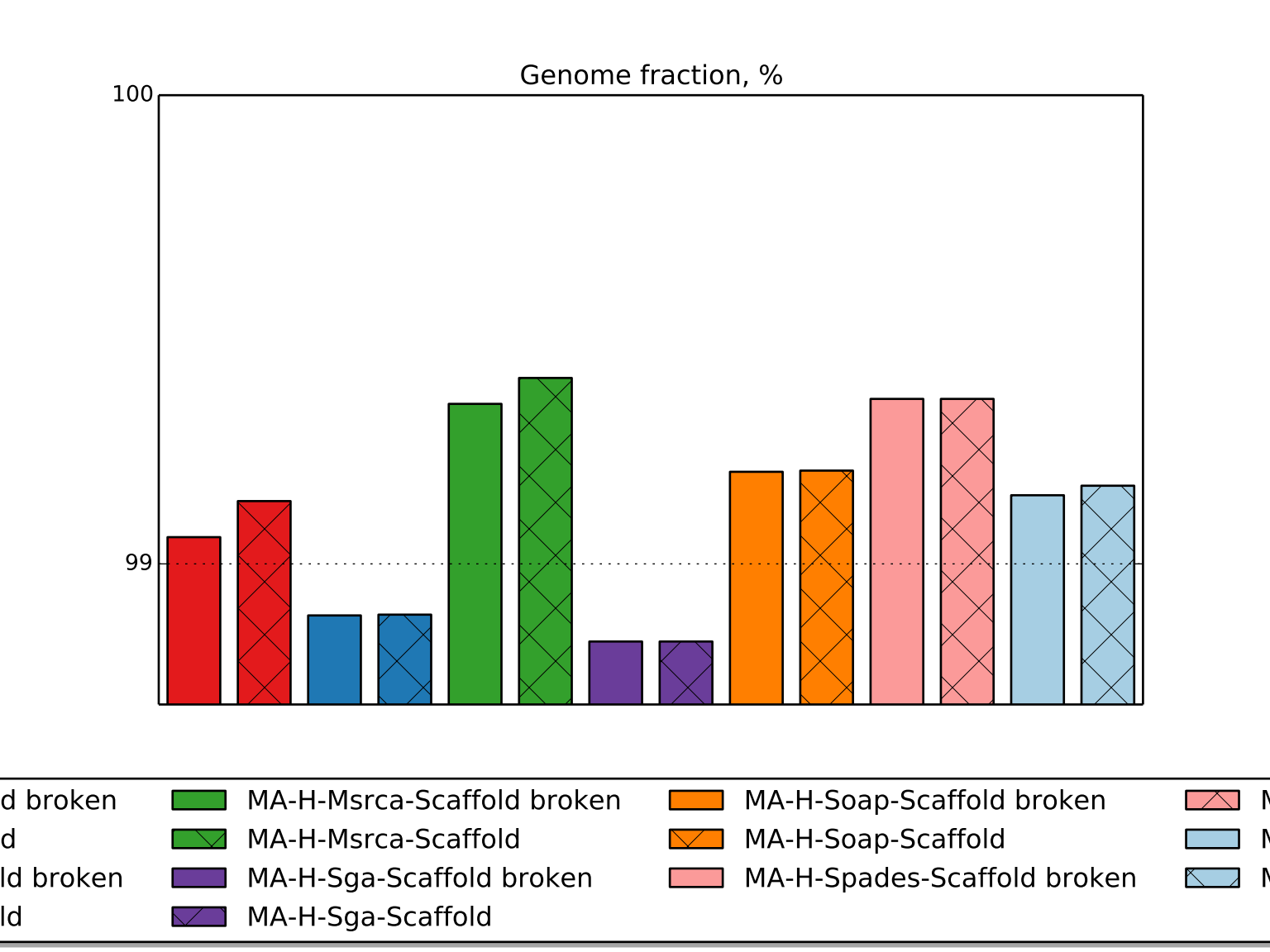

Cumulative length (aligned contigs)
Cumulative length (Mbp)
Contig index
0
1
2
3
4
5
6
0
60
120
180
240
300
d broken
d
ld broken
ld
MA-H-Msrca-Scaffold broken
MA-H-Msrca-Scaffold
MA-H-Sga-Scaffold broken
MA-H-Sga-Scaffold
MA-H-Soap-Scaffold broken
MA-H-Soap-Scaffold
MA-H-Spades-Scaffold broken
MA-H-Spades-Scaffold


NAx
Contig length (kbp)
600
400
200
0
0
20
40
60
80
100
x
d broken
d
ld broken
ld
MA-H-Msrca-Scaffold broken
MA-H-Msrca-Scaffold
MA-H-Sga-Scaffold broken
MA-H-Sga-Scaffold
MA-H-Soap-Scaffold broken
MA-H-Soap-Scaffold
MA-H-Spades-Scaffold broken

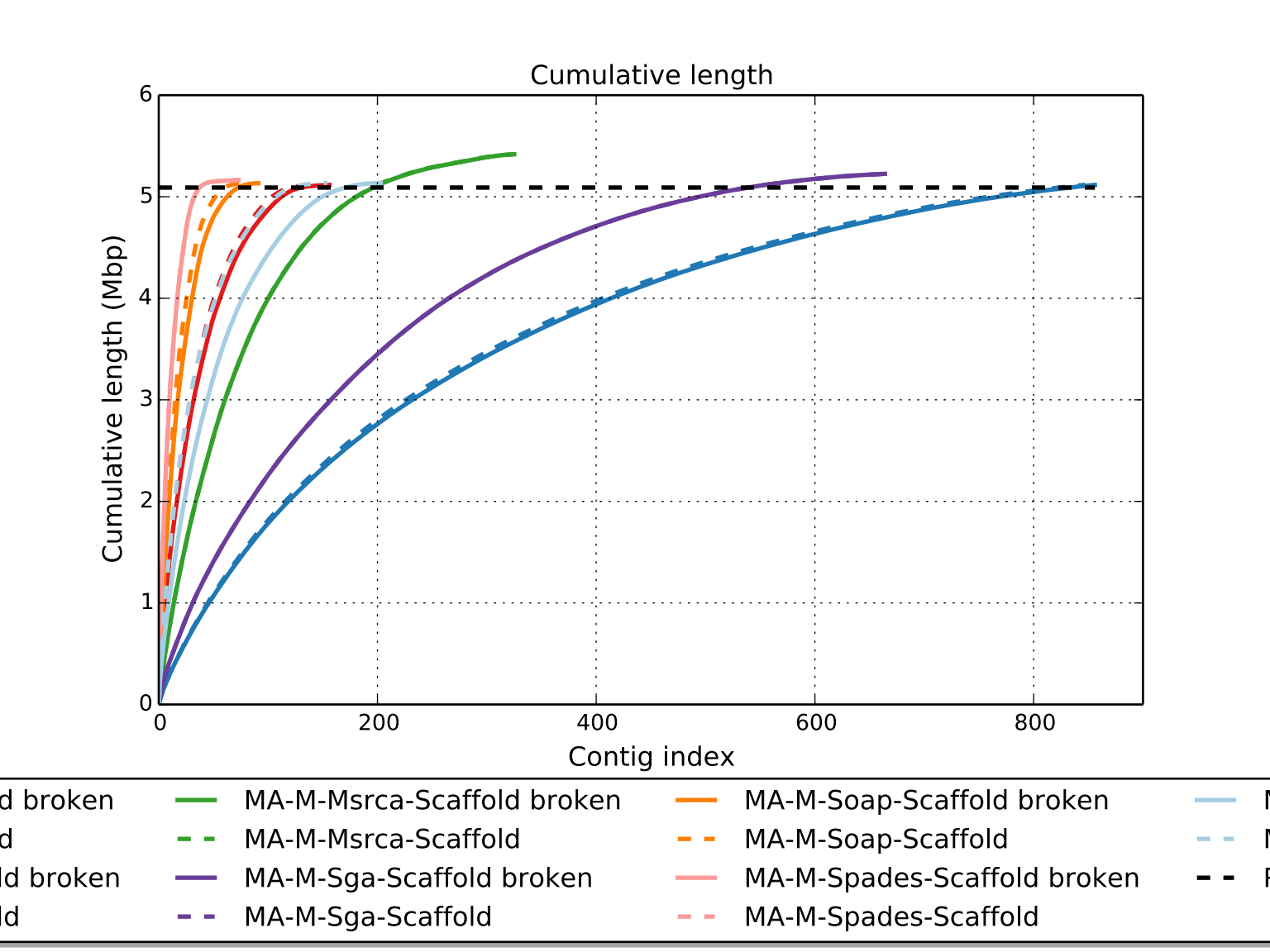

NGAx
Contig length (kbp)
0
200
400
600
0
20
40
60
80
100
x
d broken
d
ld broken
ld
MA-H-Msrca-Scaffold broken
MA-H-Msrca-Scaffold
MA-H-Sga-Scaffold broken
MA-H-Sga-Scaffold
MA-H-Soap-Scaffold broken
MA-H-Soap-Scaffold
MA-H-Spades-Scaffold broken

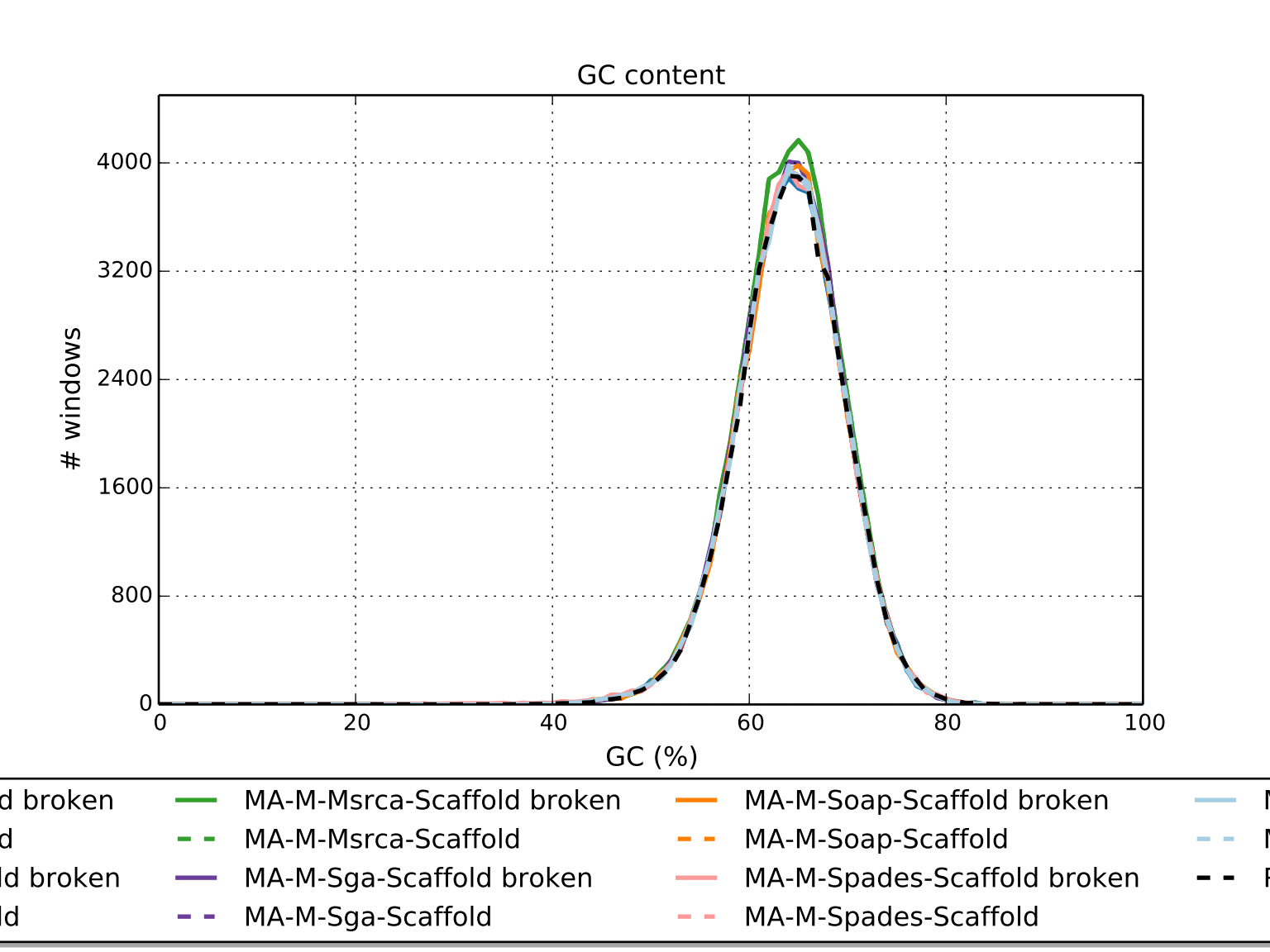

Cumulative # complete genes
Cumulative # complete genes
Contig index
0
1000
2000
3000
4000
5000
0
60
120
180
240
300
d broken
d
ld broken
ld
MA-H-Msrca-Scaffold broken
MA-H-Msrca-Scaffold
MA-H-Sga-Scaffold broken
MA-H-Sga-Scaffold
MA-H-Soap-Scaffold broken
MA-H-Soap-Scaffold
MA-H-Spades-Scaffold broken
MA-H-Spades-Scaffold

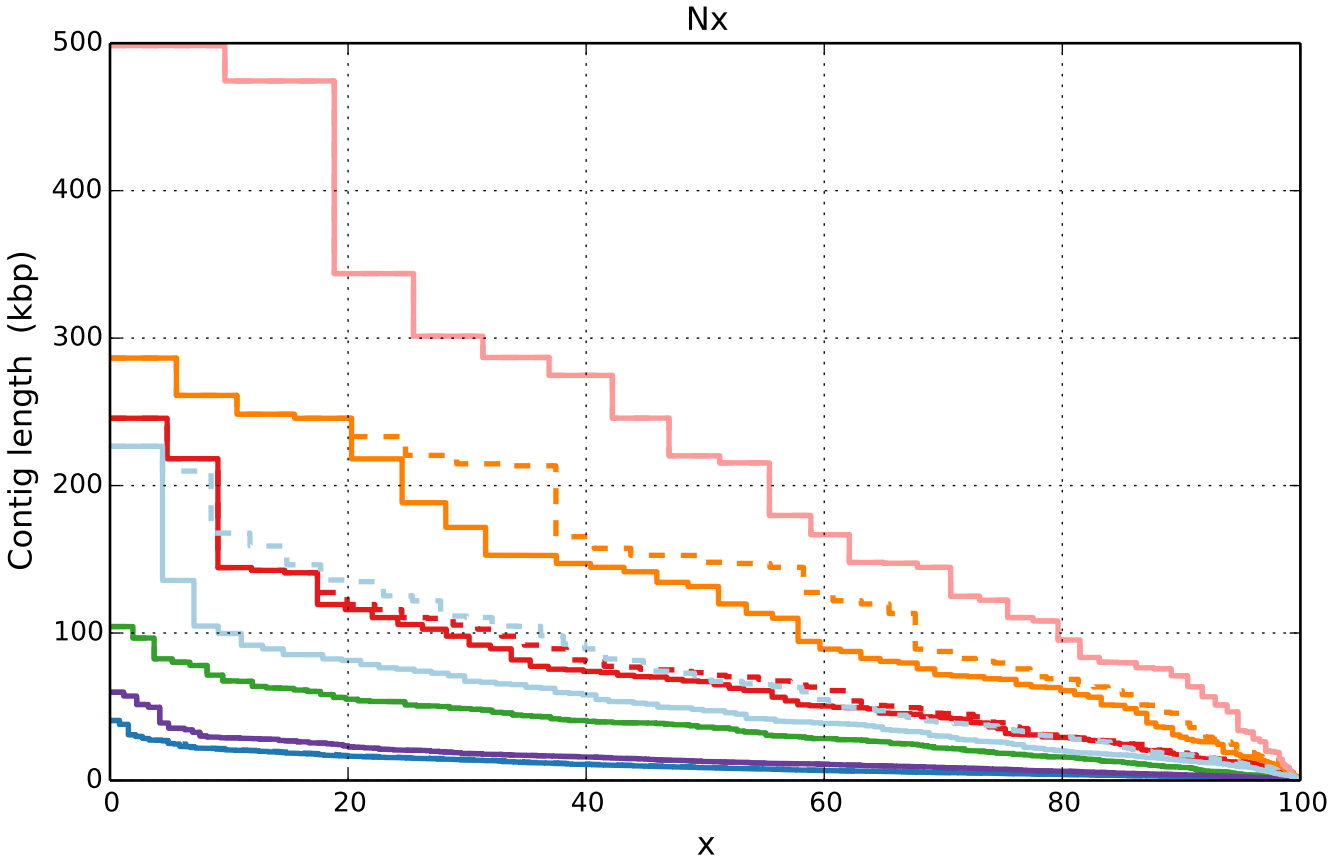

complete genes
5100
5000
4900
4800
4700
4600
d broken
d
ld broken
ld
MA-H-Msrca-Scaffold broken
MA-H-Msrca-Scaffold
MA-H-Sga-Scaffold broken
MA-H-Sga-Scaffold
MA-H-Soap-Scaffold broken
MA-H-Soap-Scaffold
MA-H-Spades-Scaffold broken

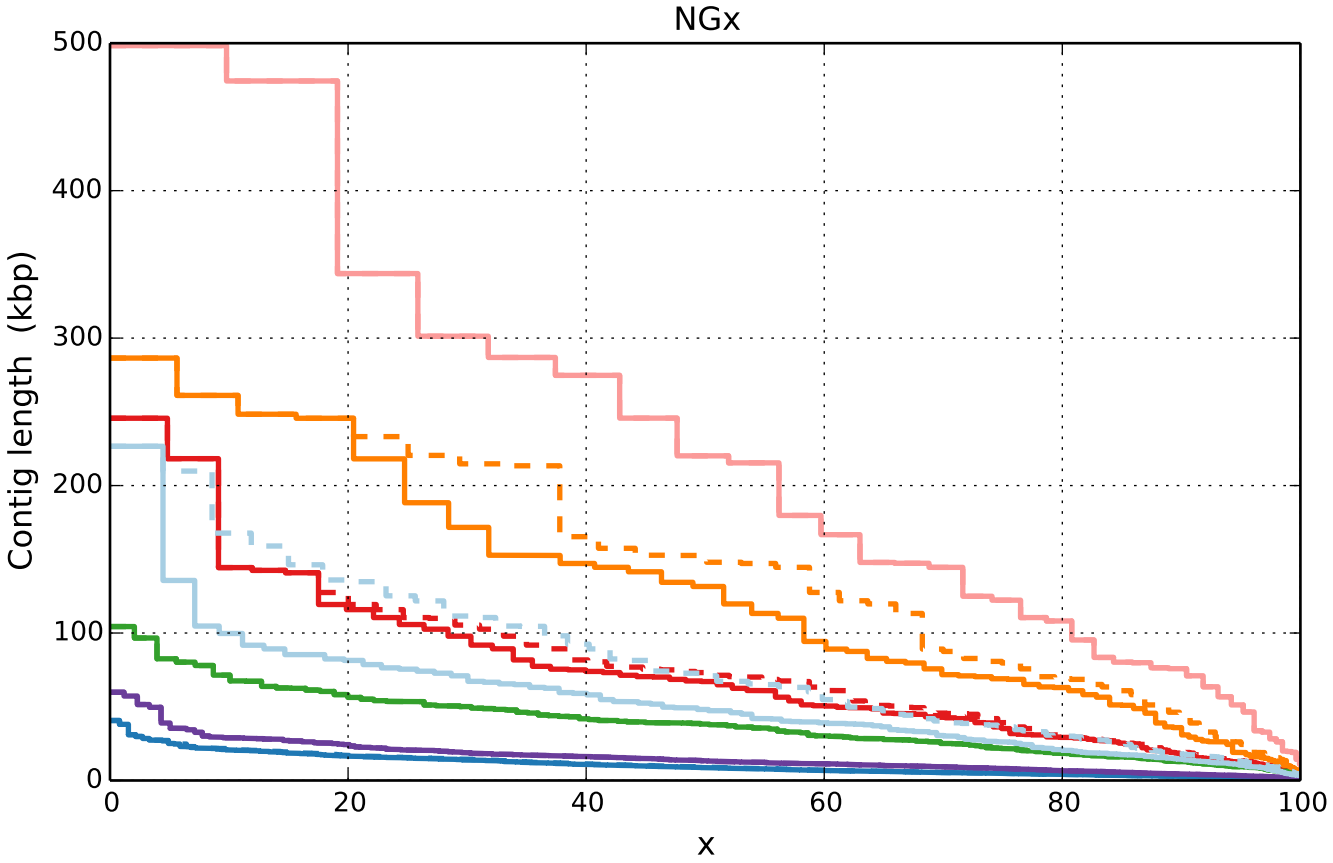

Genome fraction, %
100
99
d broken
d
ld broken
ld
MA-H-Msrca-Scaffold broken
MA-H-Msrca-Scaffold
MA-H-Sga-Scaffold broken
MA-H-Sga-Scaffold
MA-H-Soap-Scaffold broken
MA-H-Soap-Scaffold
MA-H-Spades-Scaffold broken

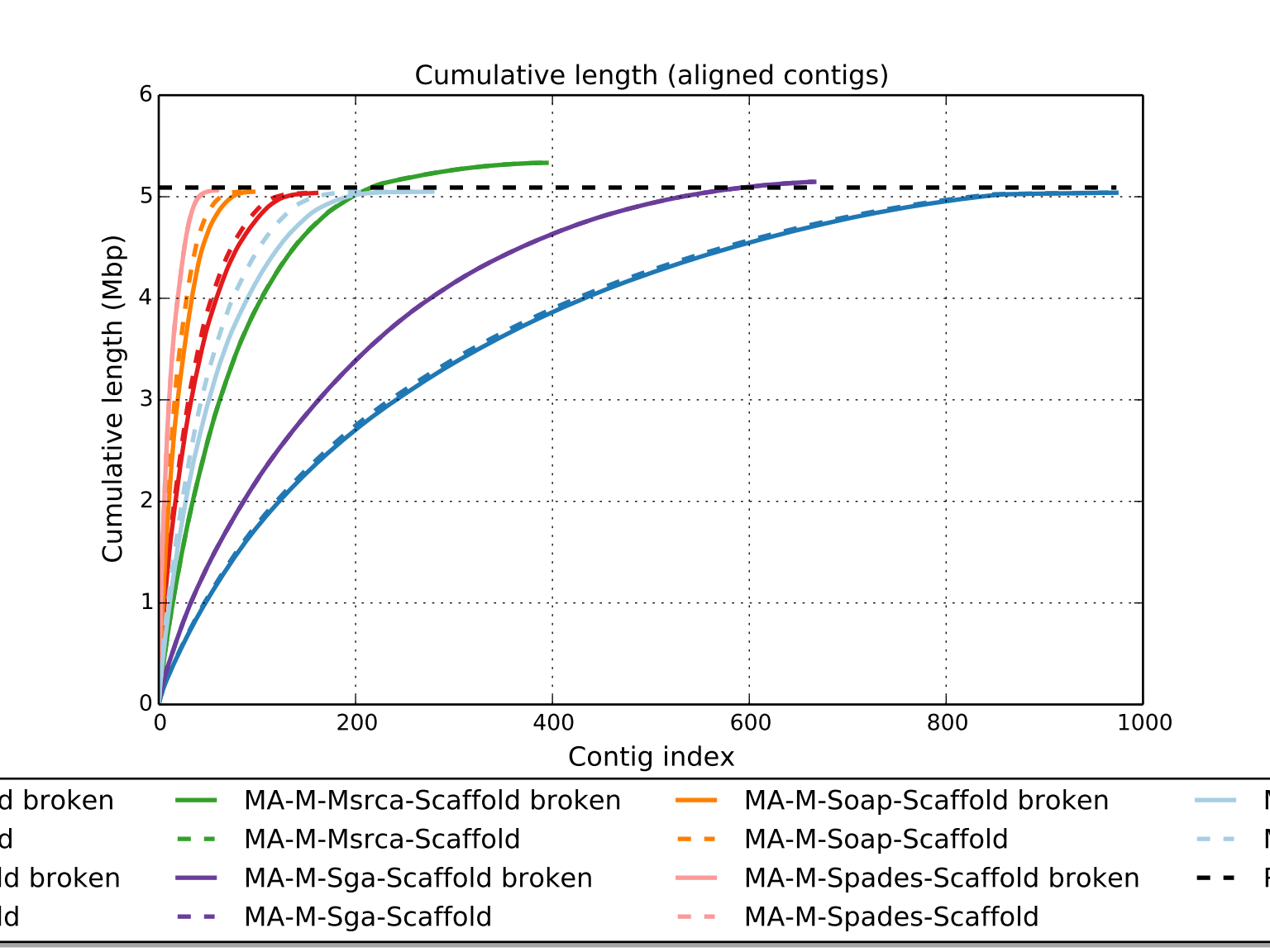
Scaffold

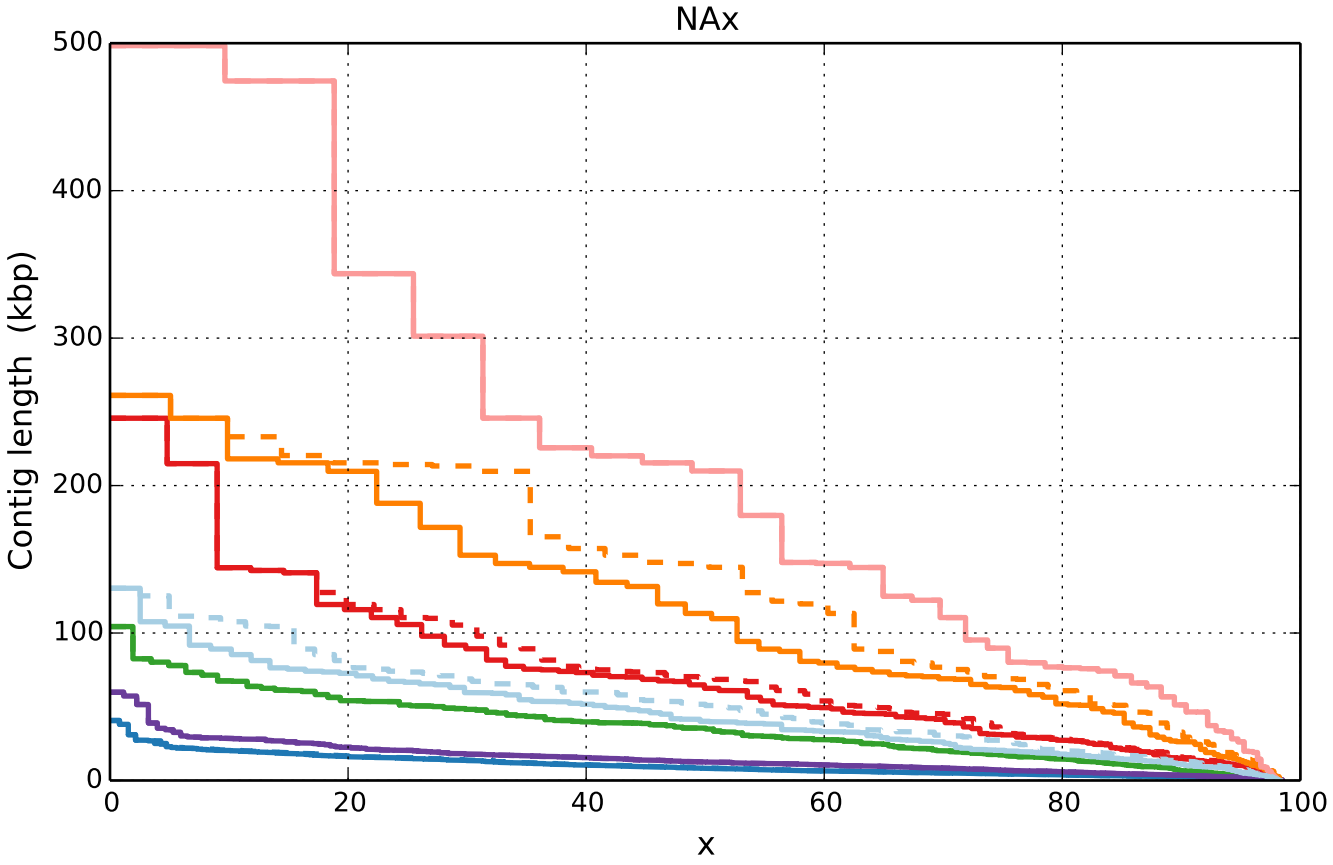

Cumulative length
Cumulative length (Mbp)
Contig index
0
1
2
3
4
5
6
0
200
400
600
800
d broken
d
ld broken
ld
MA-M-Msrca-Scaffold broken
MA-M-Msrca-Scaffold
MA-M-Sga-Scaffold broken
MA-M-Sga-Scaffold
MA-M-Soap-Scaffold broken
MA-M-Soap-Scaffold
MA-M-Spades-Scaffold broken
MA-M-Spades-Scaffold

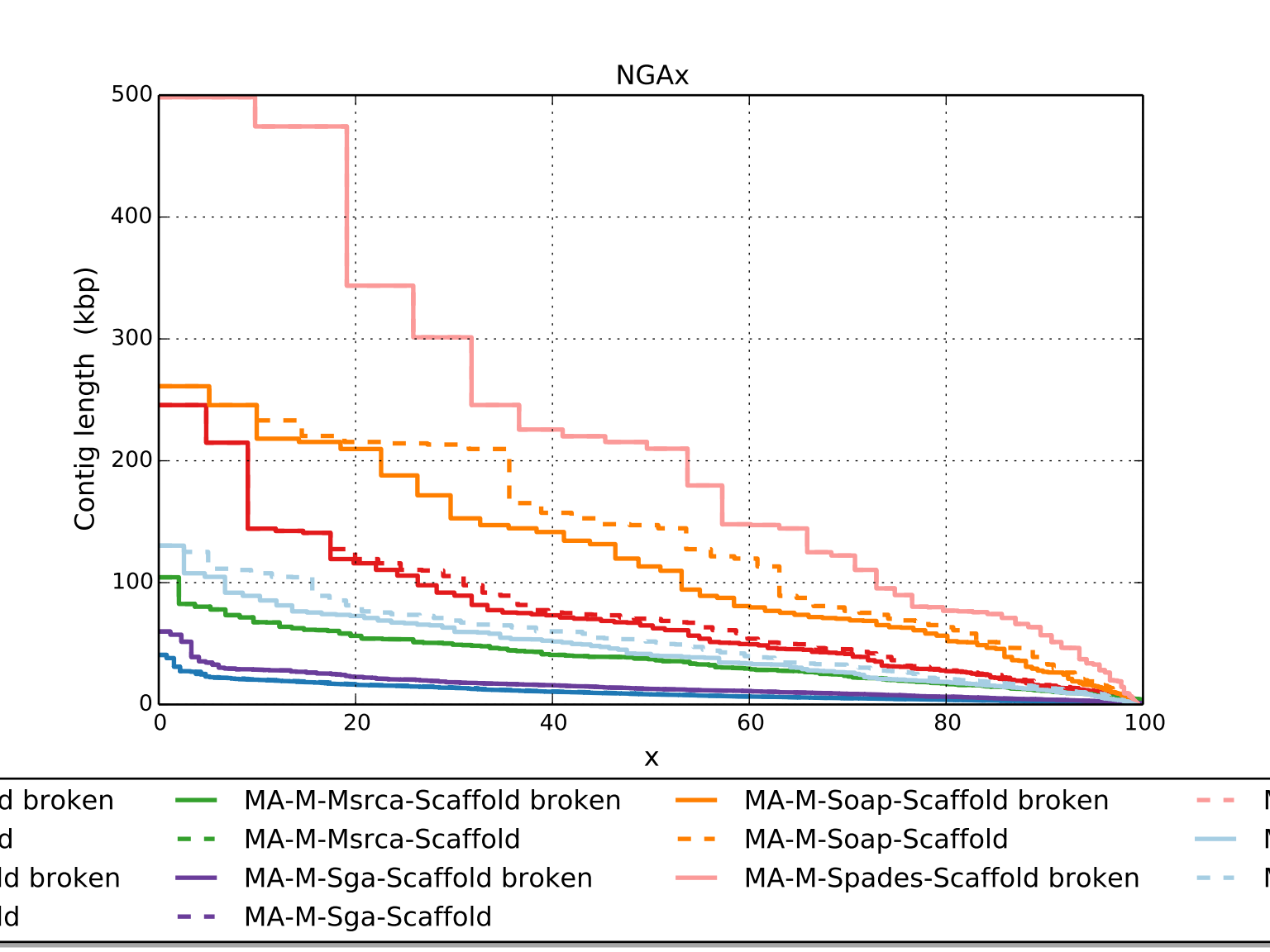

GC content
windows
GC (%)
0
800
1600
2400
3200
4000
0
20
40
60
80
100
d broken
d
ld broken
ld
MA-M-Msrca-Scaffold broken
MA-M-Msrca-Scaffold
MA-M-Sga-Scaffold broken
MA-M-Sga-Scaffold
MA-M-Soap-Scaffold broken
MA-M-Soap-Scaffold
MA-M-Spades-Scaffold broken
MA-M-Spades-Scaffold

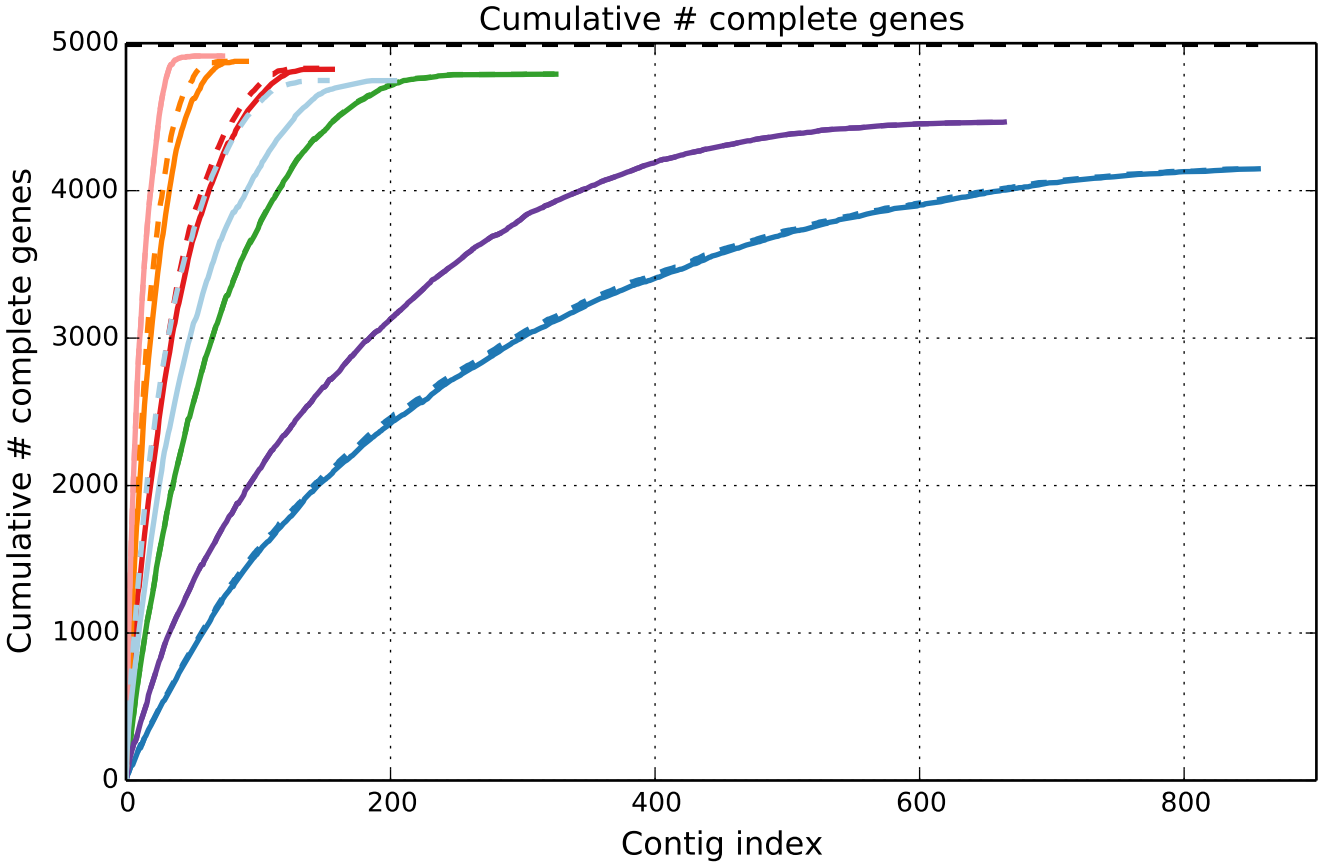

Nx
Contig length (kbp)
500
400
300
200
100
0
0
20
40
60
80
100
x
d broken
d
ld broken
ld
MA-M-Msrca-Scaffold broken
MA-M-Msrca-Scaffold
MA-M-Sga-Scaffold broken
MA-M-Sga-Scaffold
MA-M-Soap-Scaffold broken
MA-M-Soap-Scaffold
MA-M-Spades-Scaffold broken

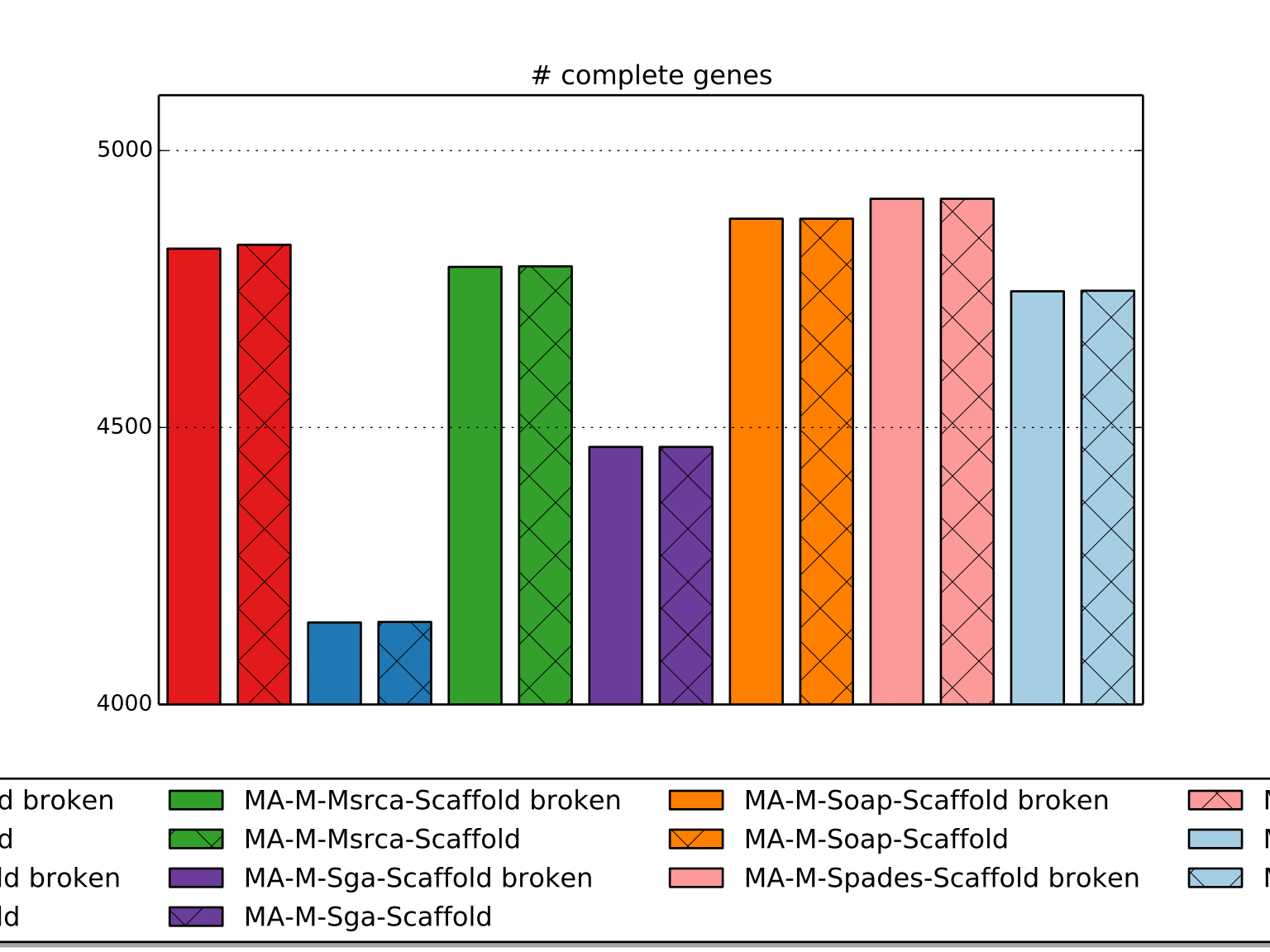

NGx
Contig length (kbp)
500
400
300
200
100
0
0
20
40
60
80
100
x
d broken
d
ld broken
ld
MA-M-Msrca-Scaffold broken
MA-M-Msrca-Scaffold
MA-M-Sga-Scaffold broken
MA-M-Sga-Scaffold
MA-M-Soap-Scaffold broken
MA-M-Soap-Scaffold
MA-M-Spades-Scaffold broken

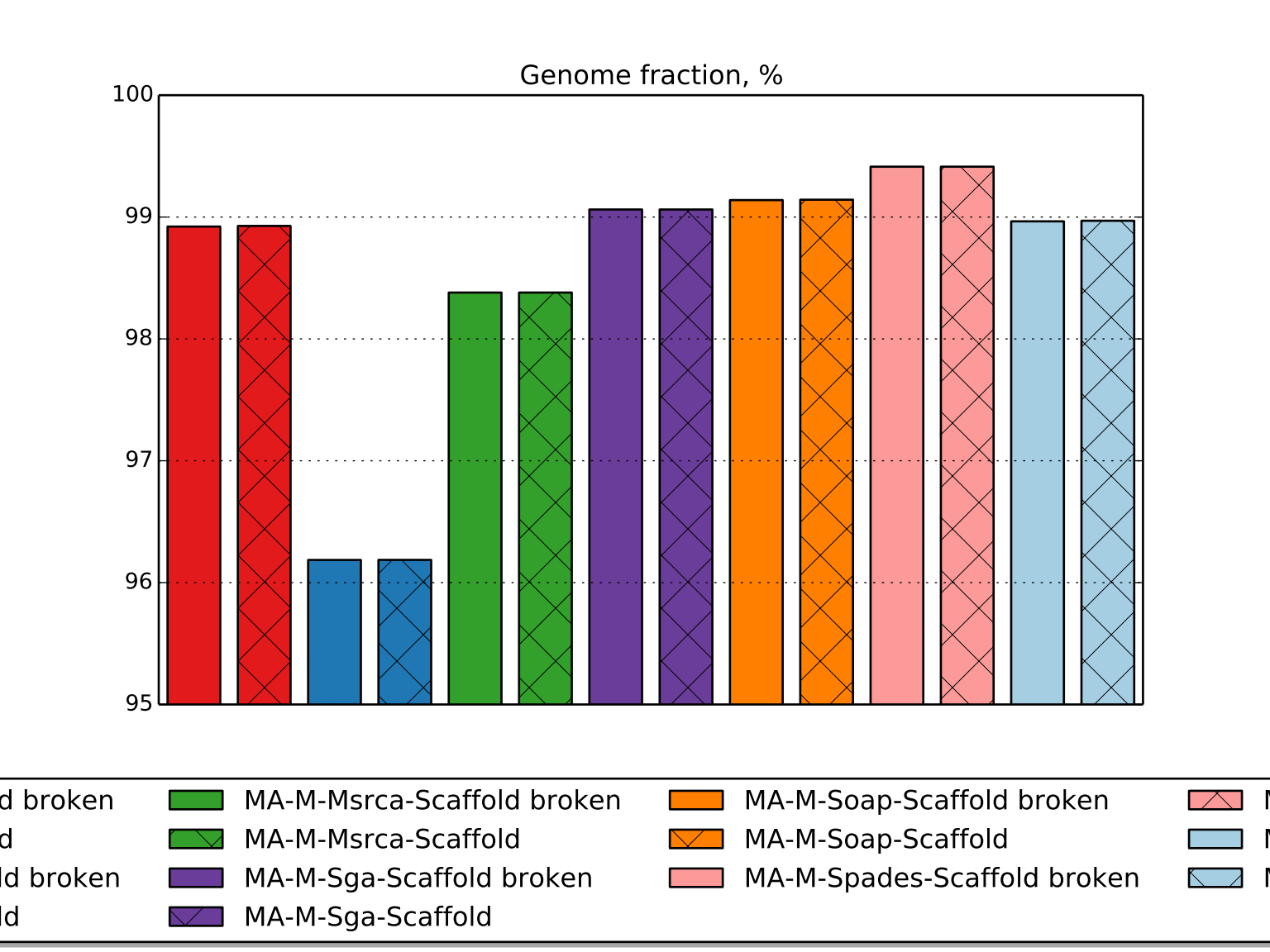

Cumulative length (aligned contigs)
Cumulative length (Mbp)
Contig index
0
1
2
3
4
5
6
0
200
400
600
800
1000
d broken
d
ld broken
ld
MA-M-Msrca-Scaffold broken
MA-M-Msrca-Scaffold
MA-M-Sga-Scaffold broken
MA-M-Sga-Scaffold
MA-M-Soap-Scaffold broken
MA-M-Soap-Scaffold
MA-M-Spades-Scaffold broken
MA-M-Spades-Scaffold


NAx
Contig length (kbp)
500
400
300
200
100
0
0
20
40
60
80
100
x
d broken
d
ld broken
ld
MA-M-Msrca-Scaffold broken
MA-M-Msrca-Scaffold
MA-M-Sga-Scaffold broken
MA-M-Sga-Scaffold
MA-M-Soap-Scaffold broken
MA-M-Soap-Scaffold
MA-M-Spades-Scaffold broken

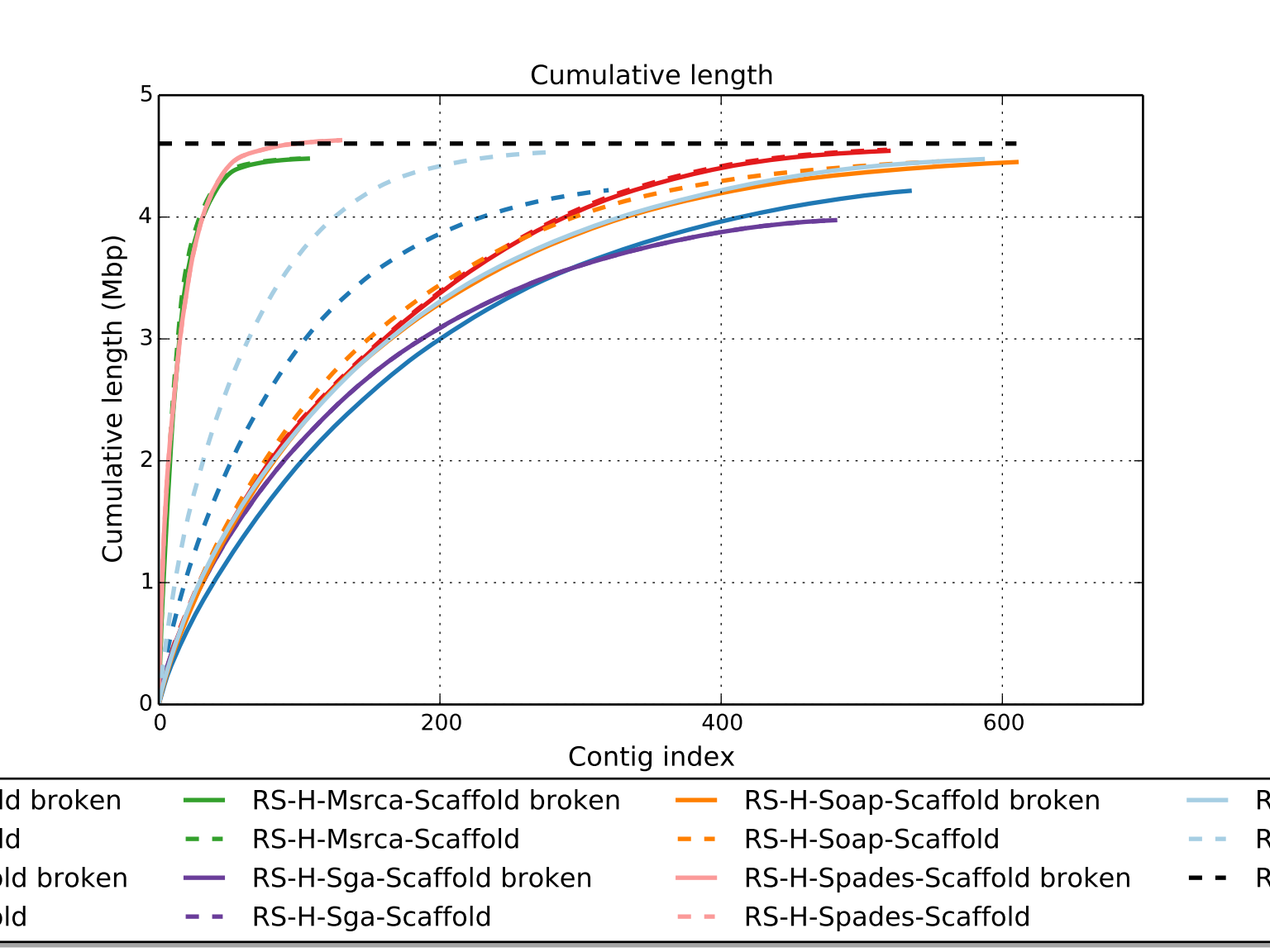

NGAx
Contig length (kbp)
500
400
300
200
100
0
0
20
40
60
80
100
x
d broken
d
ld broken
ld
MA-M-Msrca-Scaffold broken
MA-M-Msrca-Scaffold
MA-M-Sga-Scaffold broken
MA-M-Sga-Scaffold
MA-M-Soap-Scaffold broken
MA-M-Soap-Scaffold
MA-M-Spades-Scaffold broken

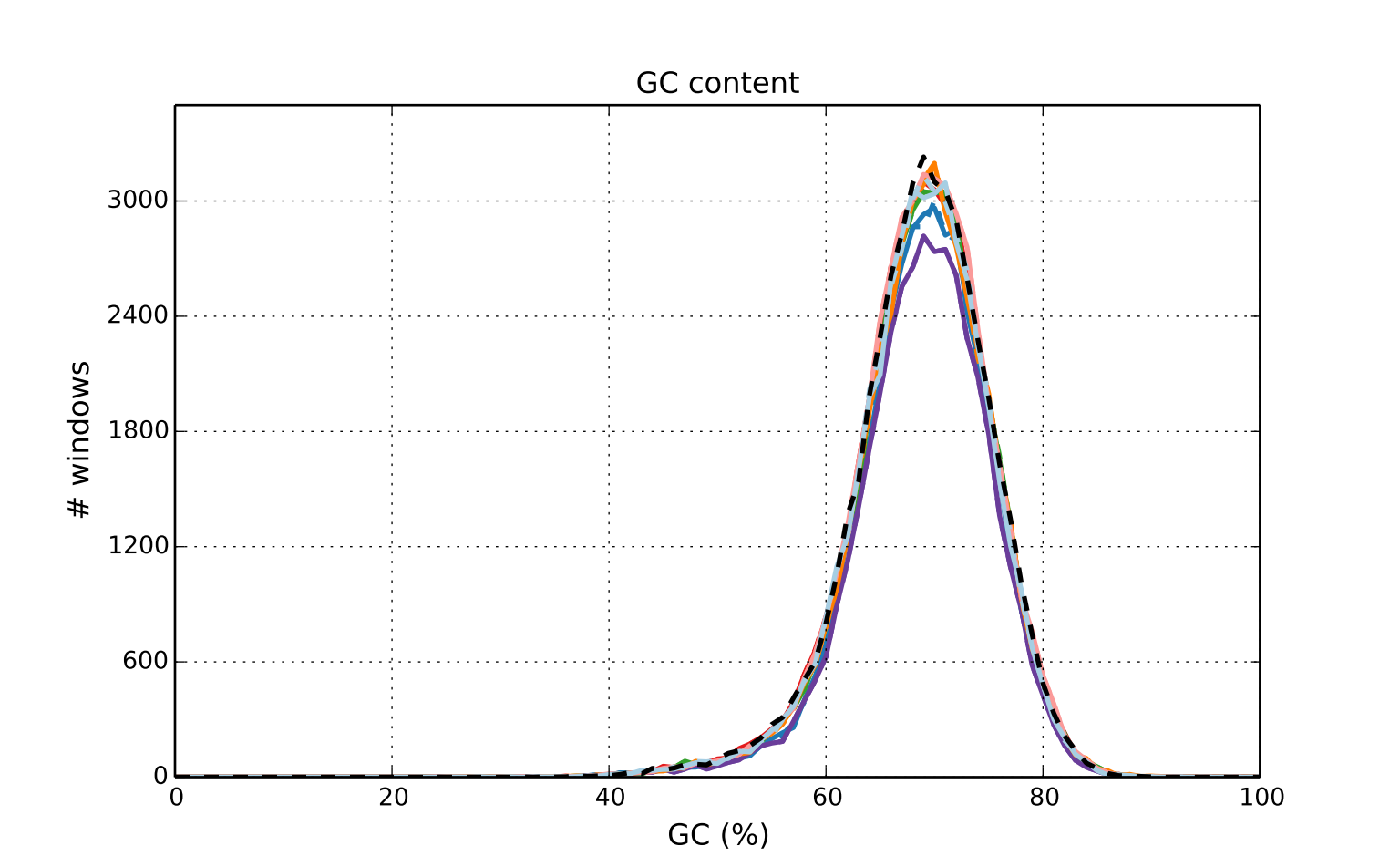

Cumulative # complete genes
Cumulative # complete genes
Contig index
0
1000
2000
3000
4000
5000
0
200
400
600
800
d broken
d
ld broken
ld
MA-M-Msrca-Scaffold broken
MA-M-Msrca-Scaffold
MA-M-Sga-Scaffold broken
MA-M-Sga-Scaffold
MA-M-Soap-Scaffold broken
MA-M-Soap-Scaffold
MA-M-Spades-Scaffold broken
MA-M-Spades-Scaffold

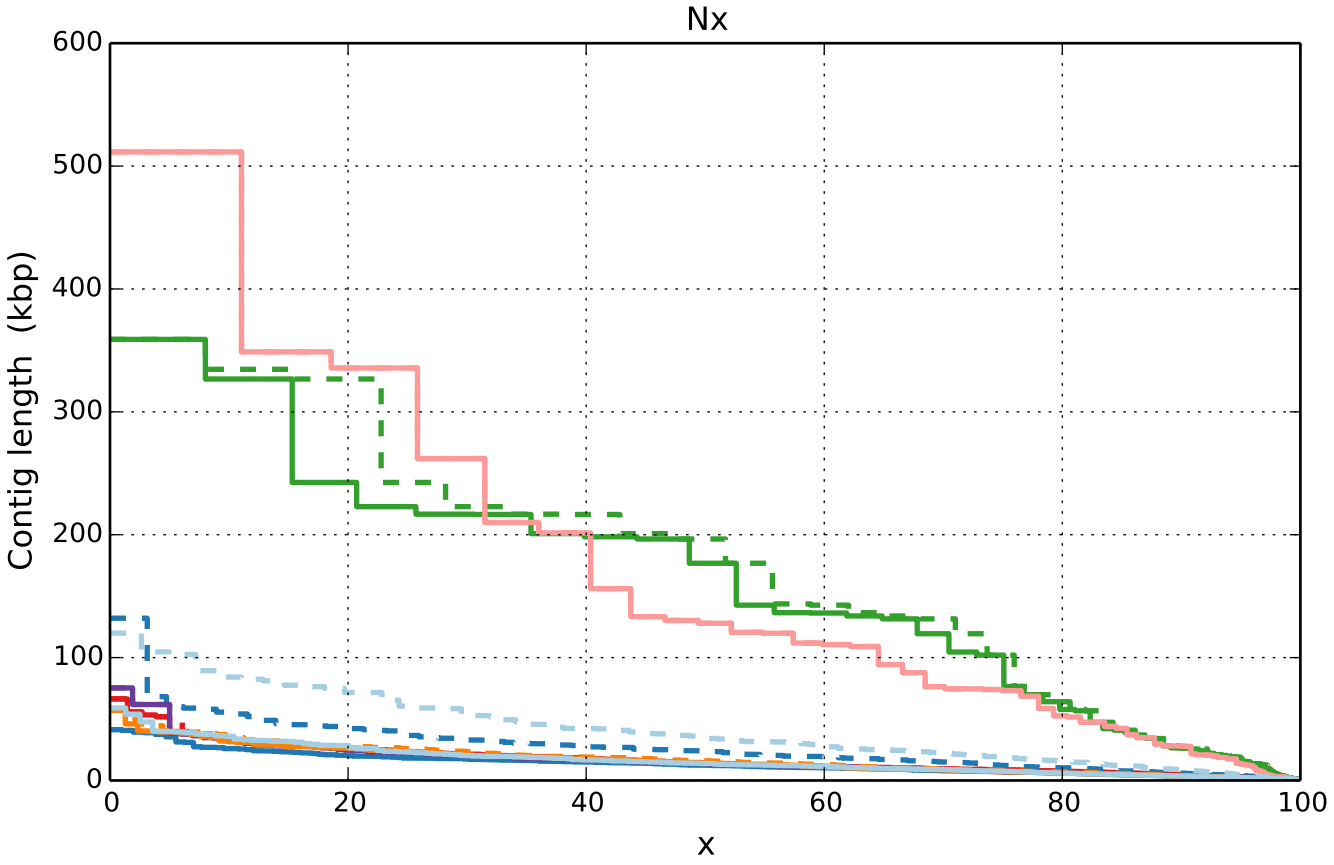

complete genes
5000
4500
4000
d broken
d
ld broken
ld
MA-M-Msrca-Scaffold broken
MA-M-Msrca-Scaffold
MA-M-Sga-Scaffold broken
MA-M-Sga-Scaffold
MA-M-Soap-Scaffold broken
MA-M-Soap-Scaffold
MA-M-Spades-Scaffold broken

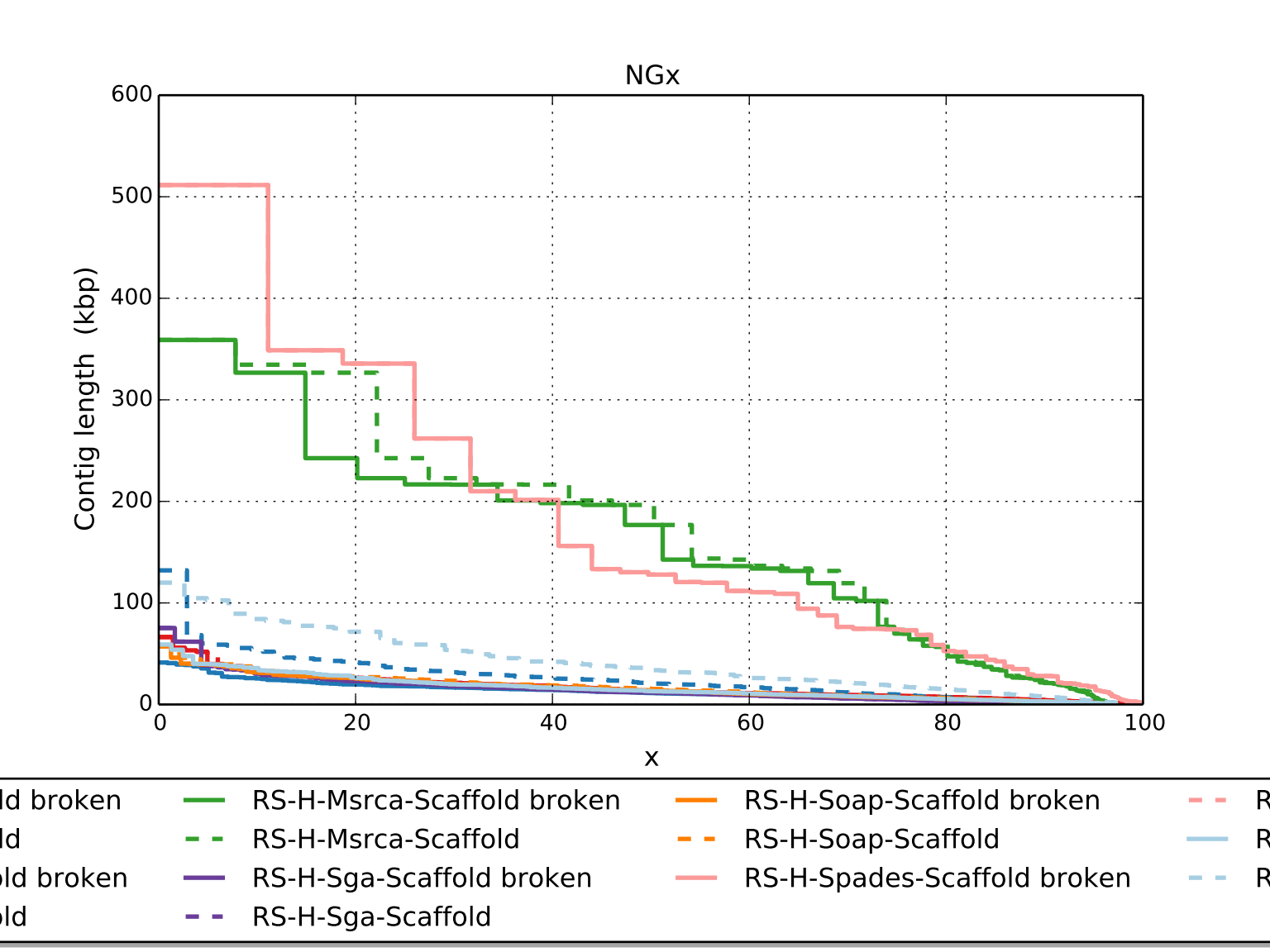

Genome fraction, %
100
99
98
97
96
95
d broken
d
ld broken
ld
MA-M-Msrca-Scaffold broken
MA-M-Msrca-Scaffold
MA-M-Sga-Scaffold broken
MA-M-Sga-Scaffold
MA-M-Soap-Scaffold broken
MA-M-Soap-Scaffold
MA-M-Spades-Scaffold broken

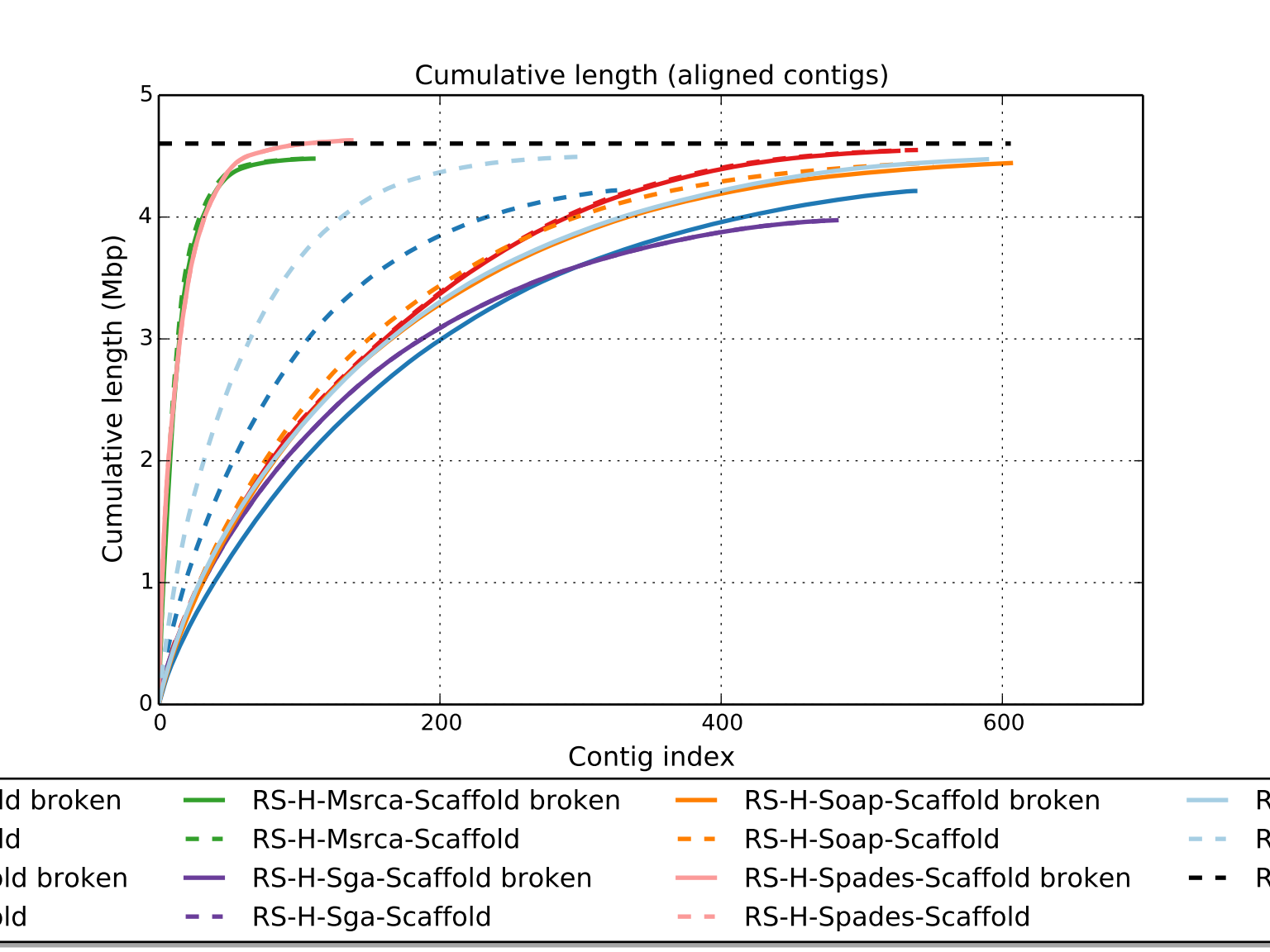
Scaffold

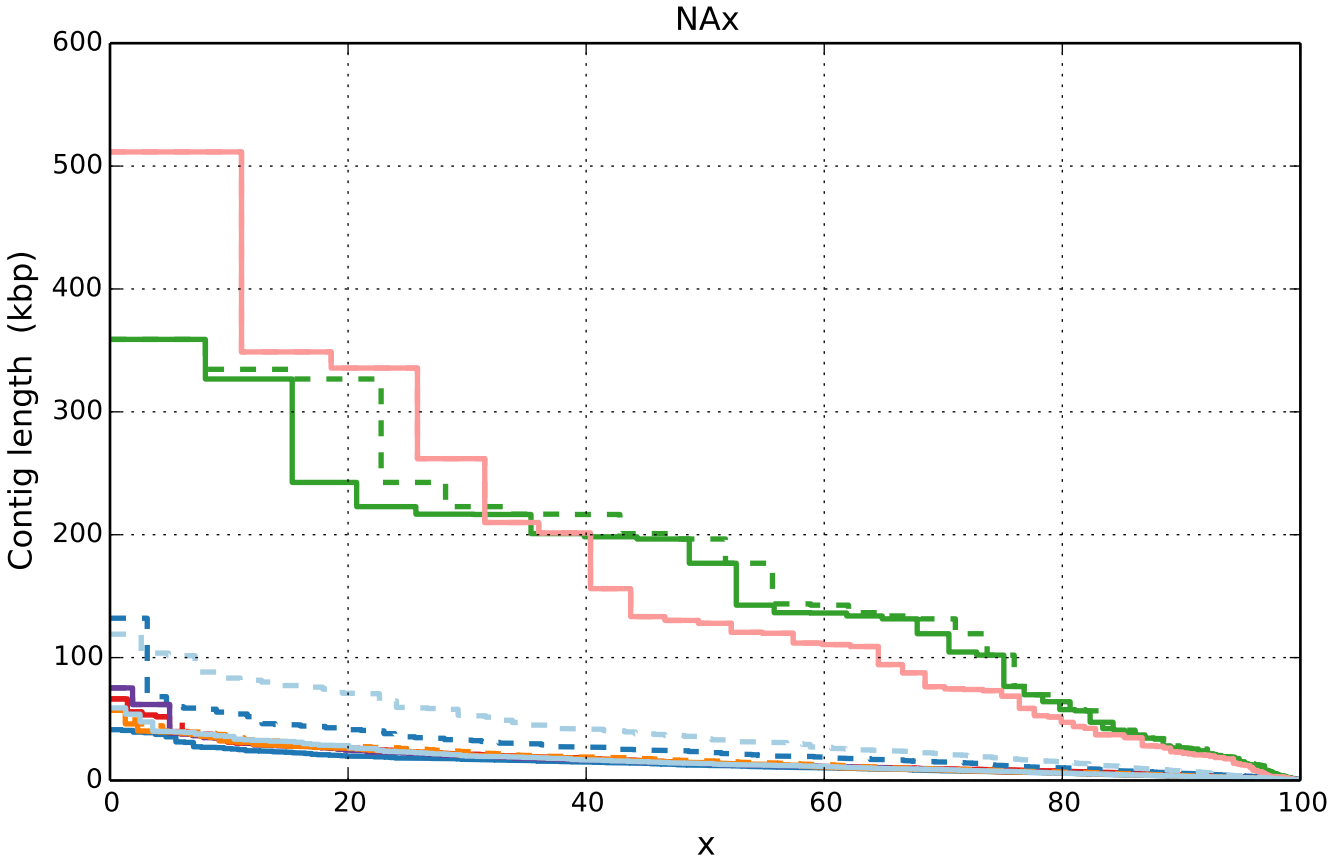

Cumulative length
Cumulative length (Mbp)
Contig index
0
1
2
3
4
5
0
200
400
600
ld broken
ld
old broken
old
RS-H-Msrca-Scaffold broken
RS-H-Msrca-Scaffold
RS-H-Sga-Scaffold broken
RS-H-Sga-Scaffold
RS-H-Soap-Scaffold broken
RS-H-Soap-Scaffold
RS-H-Spades-Scaffold broken
RS-H-Spades-Scaffold
R
R
R

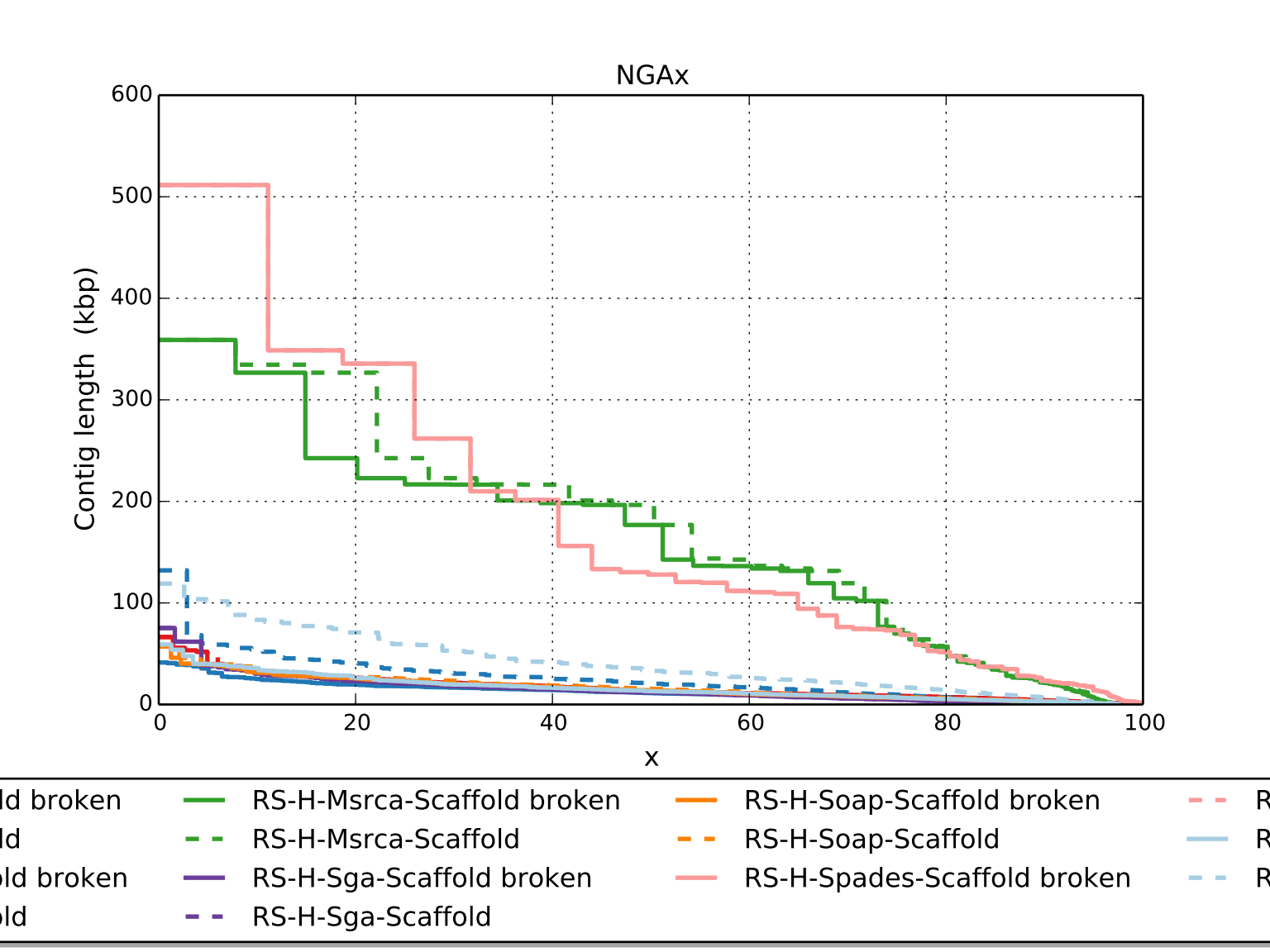

GC content
windows
GC (%)
0
600
1200
1800
2400
3000
0
20
40
60
80
100
ld broken
RS-H-Msrca-Scaffold broken
RS-H-Soap-Scaffold broken
ld
RS-H-Msrca-Scaffold
RS-H-Soap-Scaffold
old broken
RS-H-Sga-Scaffold broken
RS-H-Spades-Scaffold broken
old
RS-H-Sga-Scaffold
RS-H-Spades-Scaffold

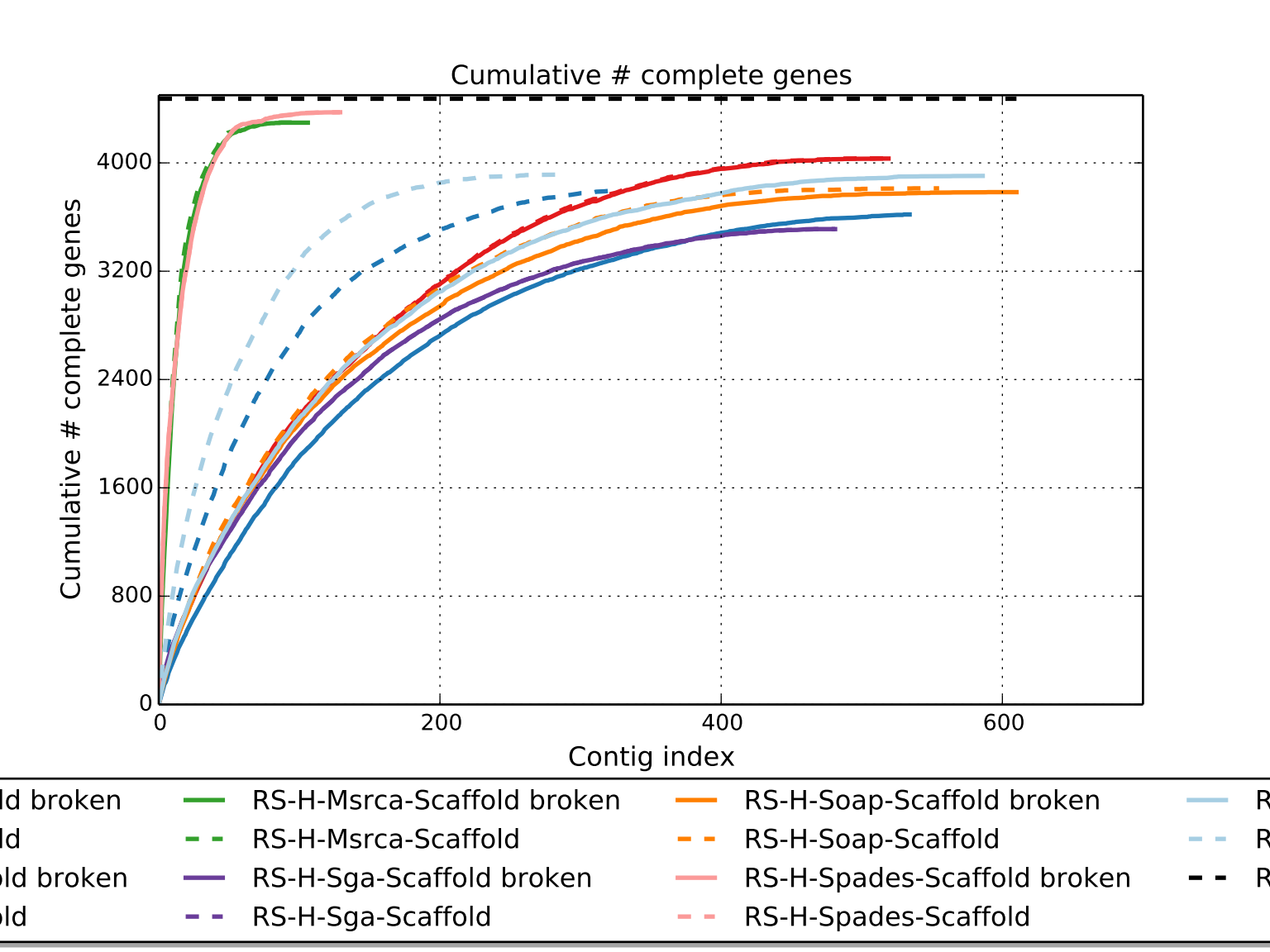

Nx
Contig length (kbp)
600
500
400
300
200
100
0
0
20
40
60
80
100
x
ld broken
ld
old broken
old
RS-H-Msrca-Scaffold broken
RS-H-Msrca-Scaffold
RS-H-Sga-Scaffold broken
RS-H-Sga-Scaffold
RS-H-Soap-Scaffold broken
RS-H-Soap-Scaffold
RS-H-Spades-Scaffold broken
R
R
R

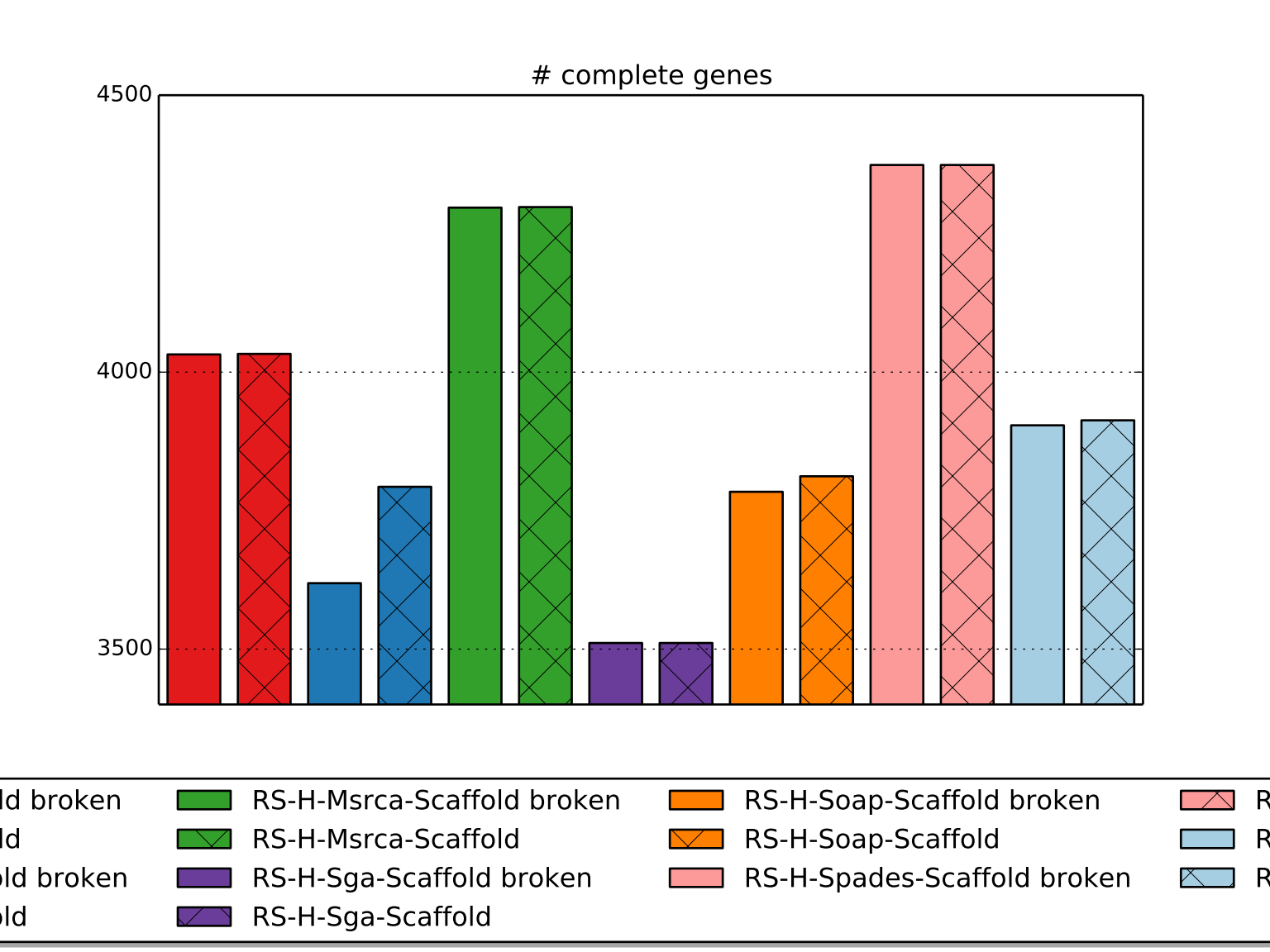

NGx
Contig length (kbp)
x
0
100
200
300
400
500
600
0
20
40
60
80
100
ld broken
ld
old broken
old
RS-H-Msrca-Scaffold broken
RS-H-Msrca-Scaffold
RS-H-Sga-Scaffold broken
RS-H-Sga-Scaffold
RS-H-Soap-Scaffold broken
RS-H-Soap-Scaffold
RS-H-Spades-Scaffold broken
R
R
R

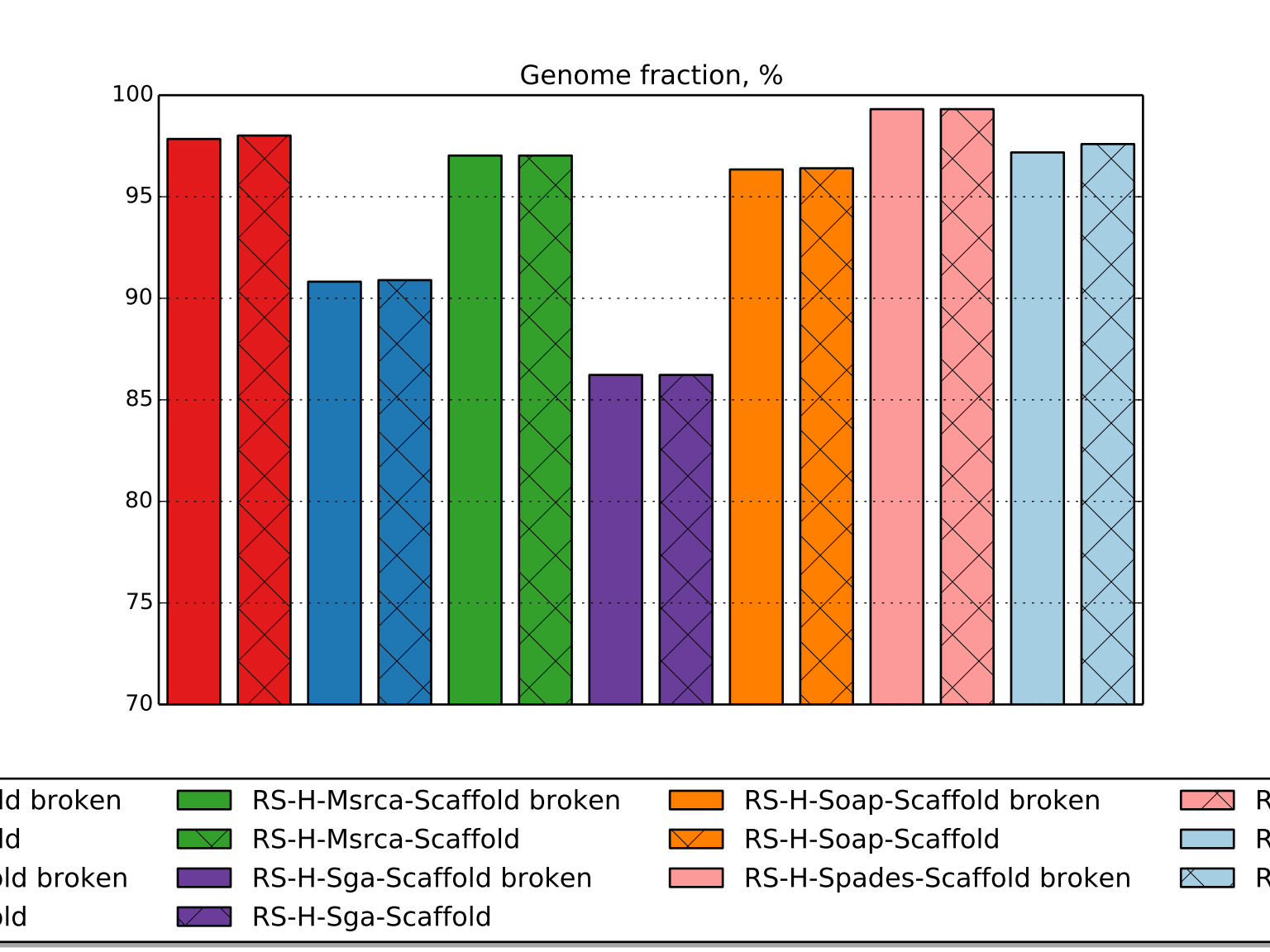

Cumulative length (aligned contigs)
Cumulative length (Mbp)
Contig index
0
1
2
3
4
5
0
200
400
600
ld broken
RS-H-Msrca-Scaffold broken
RS-H-Soap-Scaffold broken
ld
RS-H-Msrca-Scaffold
RS-H-Soap-Scaffold
old broken
RS-H-Sga-Scaffold broken
RS-H-Spades-Scaffold broken
old
RS-H-Sga-Scaffold
RS-H-Spades-Scaffold


NAx
Contig length (kbp)
600
500
400
300
200
100
0
0
20
40
60
80
100
x
ld broken
ld
old broken
old
RS-H-Msrca-Scaffold broken
RS-H-Msrca-Scaffold
RS-H-Sga-Scaffold broken
RS-H-Sga-Scaffold
RS-H-Soap-Scaffold broken
RS-H-Soap-Scaffold
RS-H-Spades-Scaffold broken
R
R
R

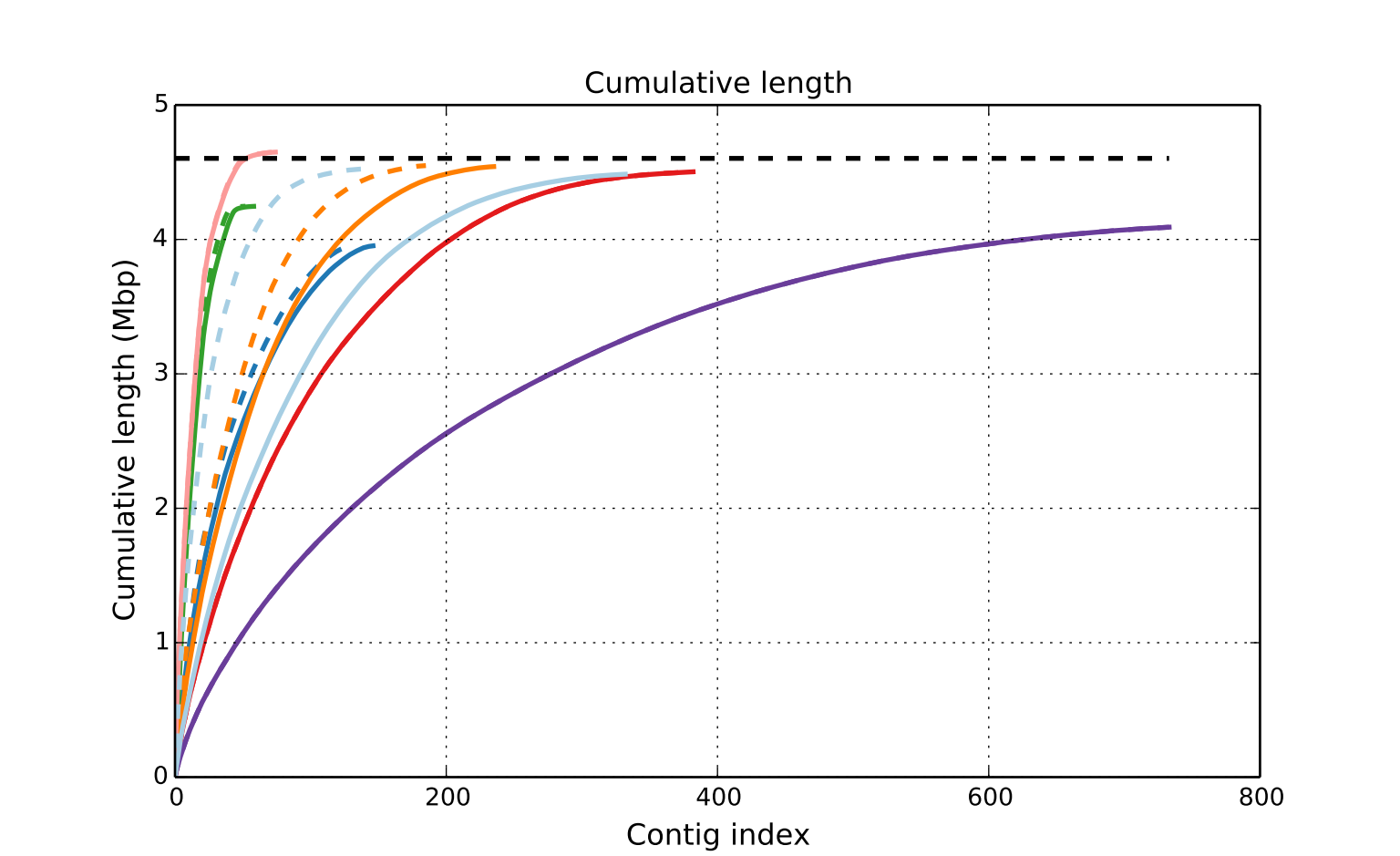

NGAx
Contig length (kbp)
x
0
100
200
300
400
500
600
0
20
40
60
80
100
ld broken
ld
old broken
old
RS-H-Msrca-Scaffold broken
RS-H-Msrca-Scaffold
RS-H-Sga-Scaffold broken
RS-H-Sga-Scaffold
RS-H-Soap-Scaffold broken
RS-H-Soap-Scaffold
RS-H-Spades-Scaffold broken
R
R
R

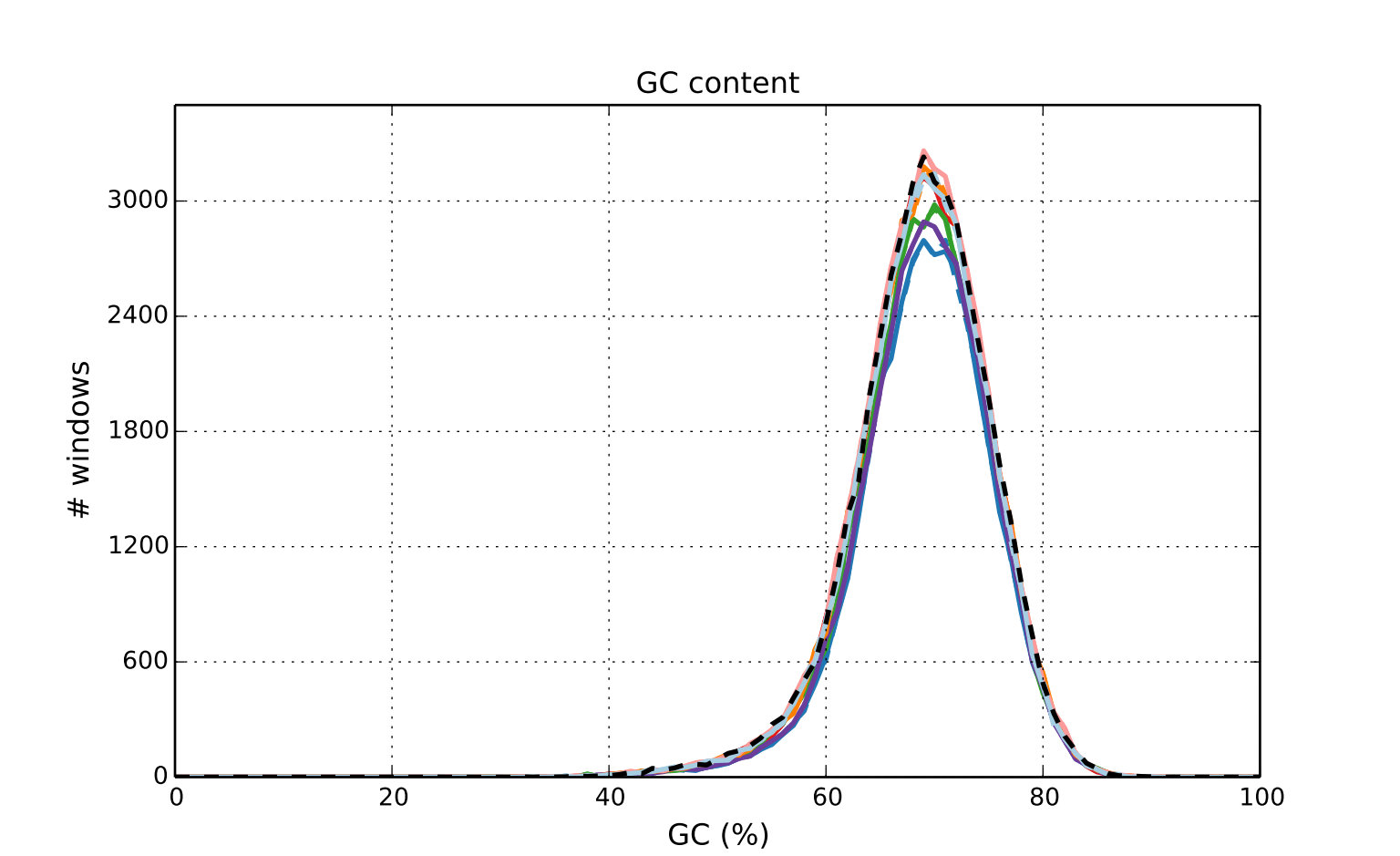

Cumulative # complete genes
Cumulative # complete genes
4000
3200
2400
1600
800
0
0
200
400
600
Contig index
ld broken
RS-H-Msrca-Scaffold broken
RS-H-Soap-Scaffold broken
ld
RS-H-Msrca-Scaffold
RS-H-Soap-Scaffold
old broken
RS-H-Sga-Scaffold broken
RS-H-Spades-Scaffold broken
old
RS-H-Sga-Scaffold
RS-H-Spades-Scaffold

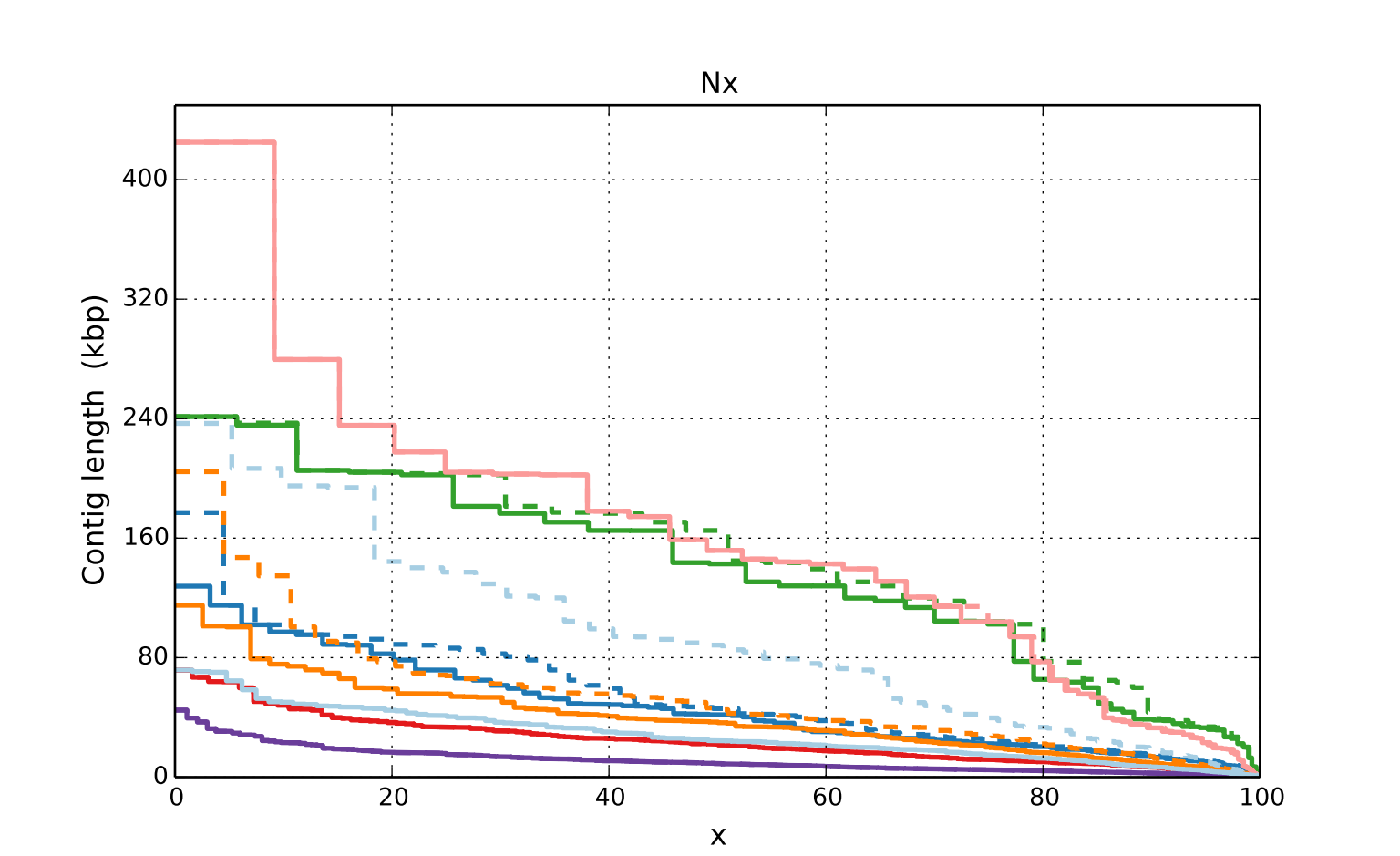

complete genes
4500
4000
3500
ld broken
ld
old broken
old
RS-H-Msrca-Scaffold broken
RS-H-Msrca-Scaffold
RS-H-Sga-Scaffold broken
RS-H-Sga-Scaffold
RS-H-Soap-Scaffold broken
RS-H-Soap-Scaffold
RS-H-Spades-Scaffold broken
R
R
R

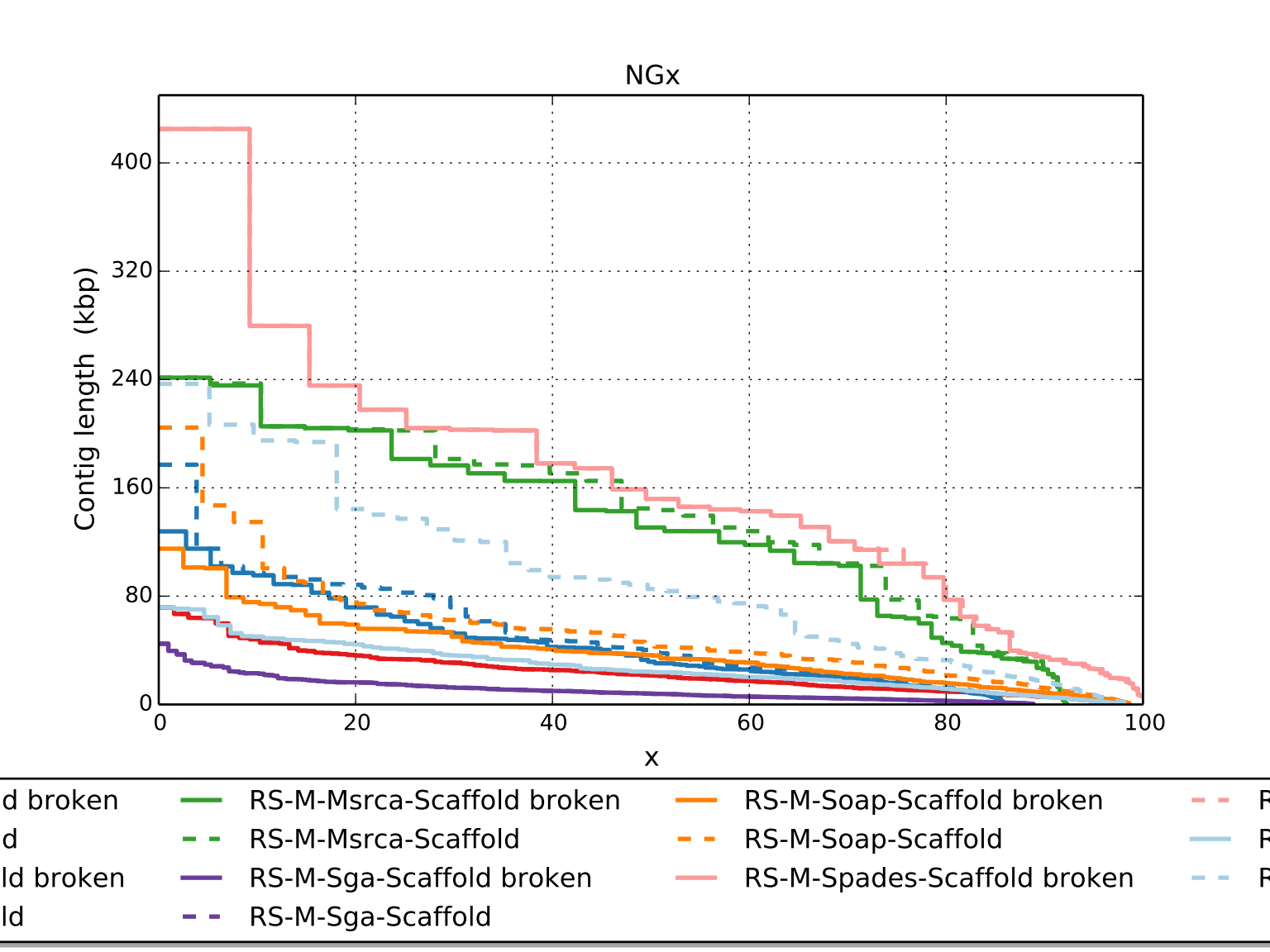

Genome fraction, %
100
95
90
85
80
75
70
ld broken
ld
old broken
old
RS-H-Msrca-Scaffold broken
RS-H-Msrca-Scaffold
RS-H-Sga-Scaffold broken
RS-H-Sga-Scaffold
RS-H-Soap-Scaffold broken
RS-H-Soap-Scaffold
RS-H-Spades-Scaffold broken
R
R
R

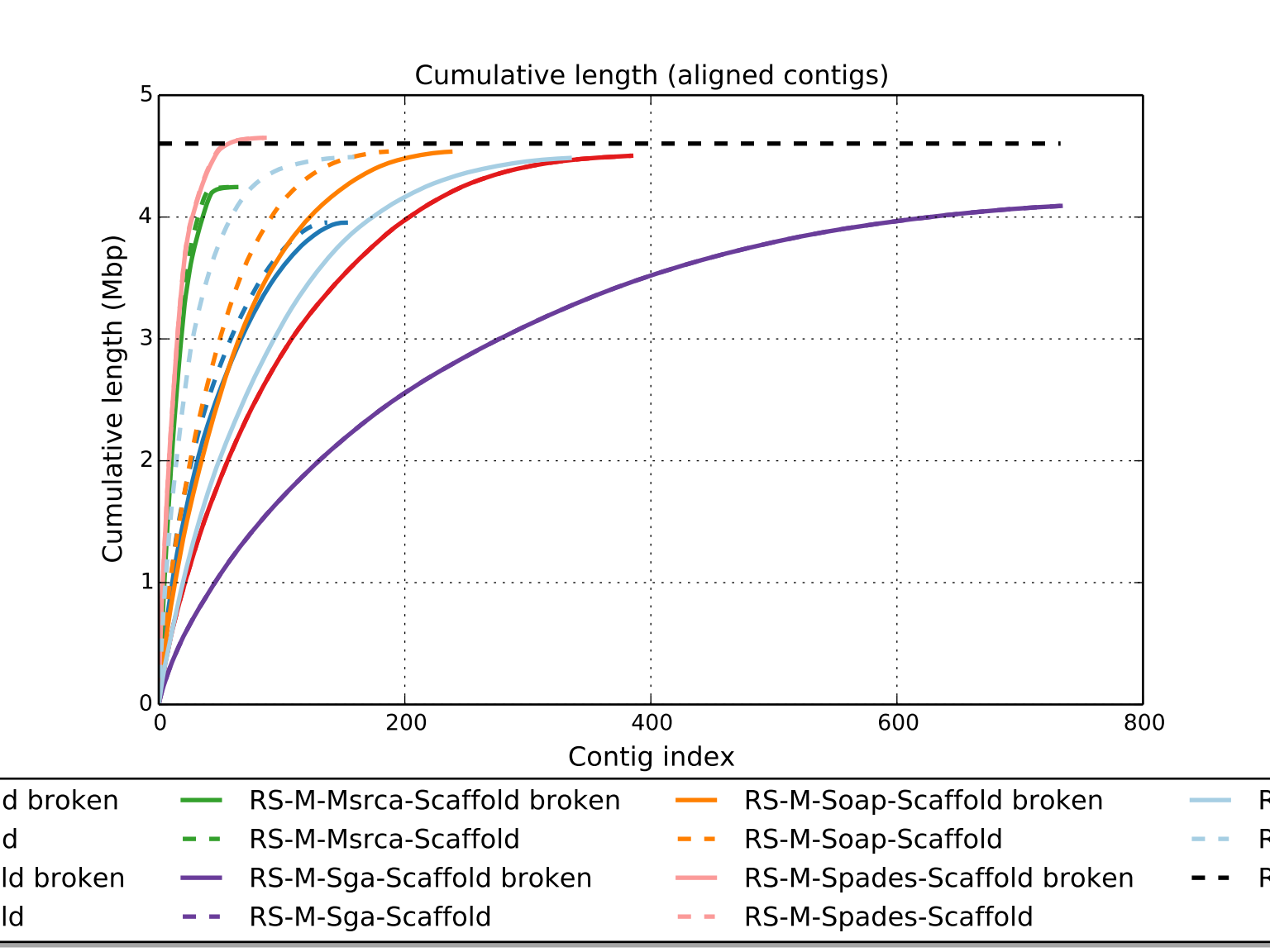
Scaffold

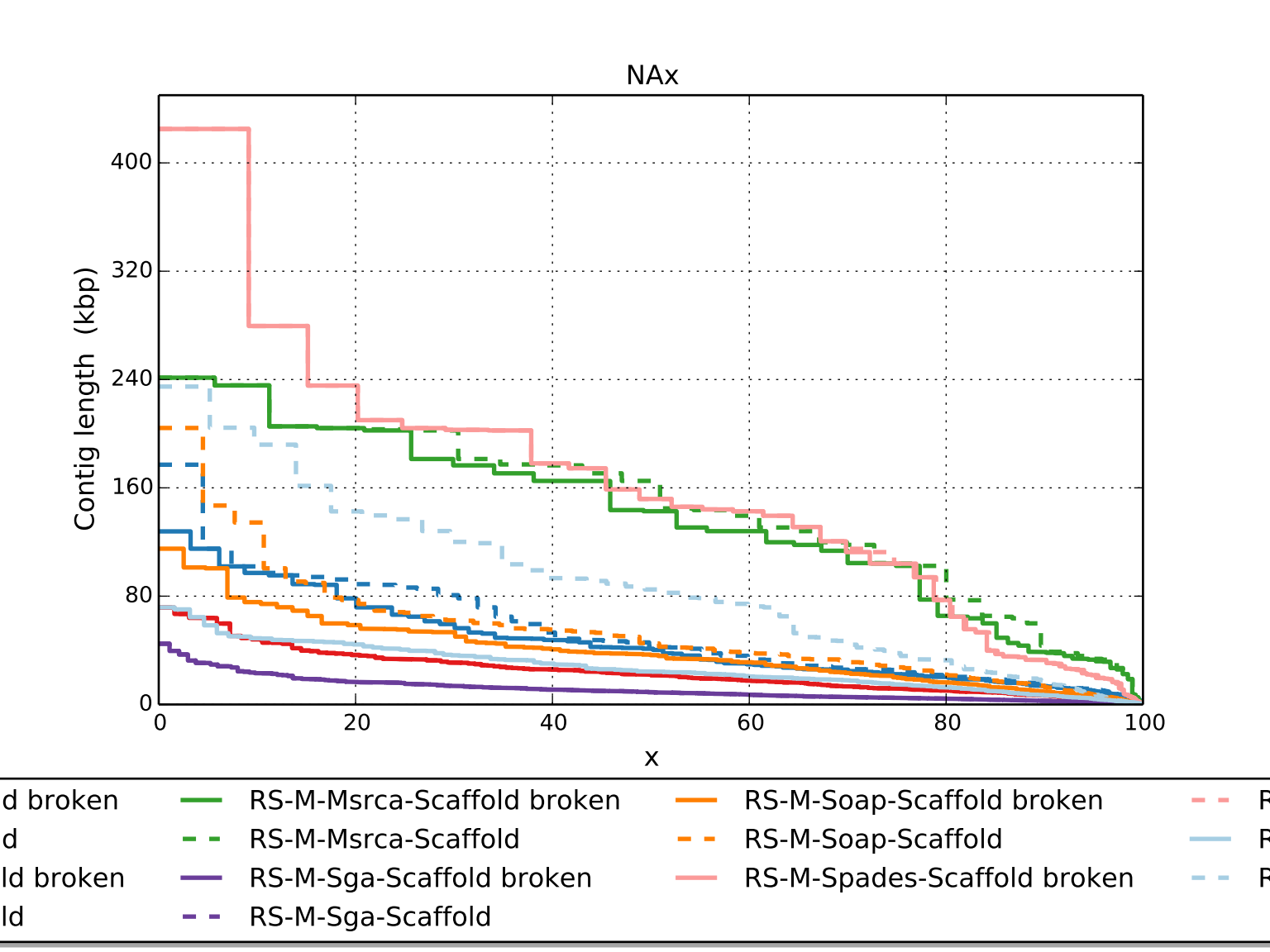

Cumulative length
Cumulative length (Mbp)
Contig index
0
1
2
3
4
5
0
200
400
600
800
d broken
d
ld broken
ld
RS-M-Msrca-Scaffold broken
RS-M-Msrca-Scaffold
RS-M-Sga-Scaffold broken
RS-M-Sga-Scaffold
RS-M-Soap-Scaffold broken
RS-M-Soap-Scaffold
RS-M-Spades-Scaffold broken
RS-M-Spades-Scaffold

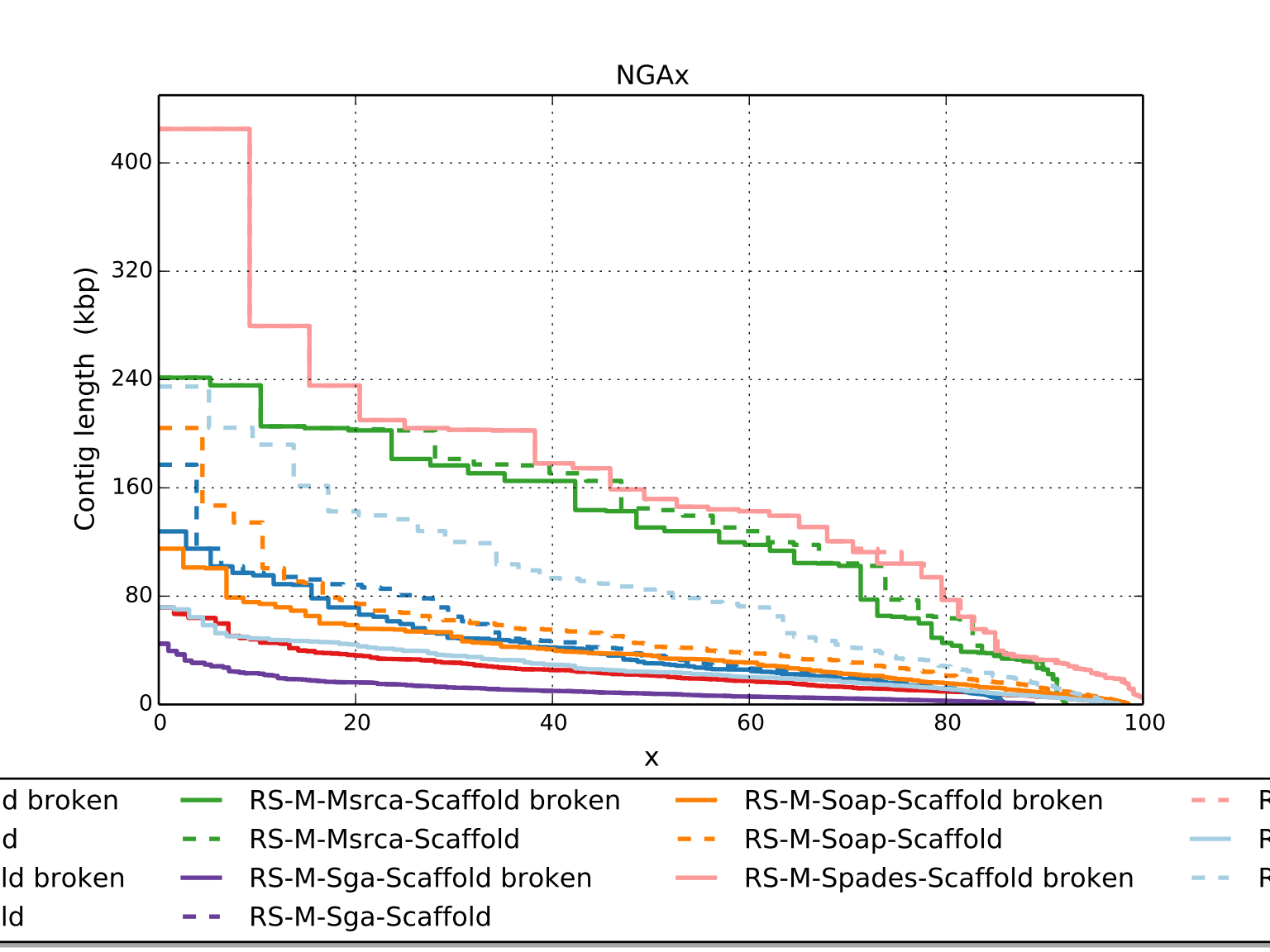

GC content
windows
GC (%)
0
600
1200
1800
2400
3000
0
20
40
60
80
100
d broken
d
ld broken
ld
RS-M-Msrca-Scaffold broken
RS-M-Msrca-Scaffold
RS-M-Sga-Scaffold broken
RS-M-Sga-Scaffold
RS-M-Soap-Scaffold broken
RS-M-Soap-Scaffold
RS-M-Spades-Scaffold broken
RS-M-Spades-Scaffold

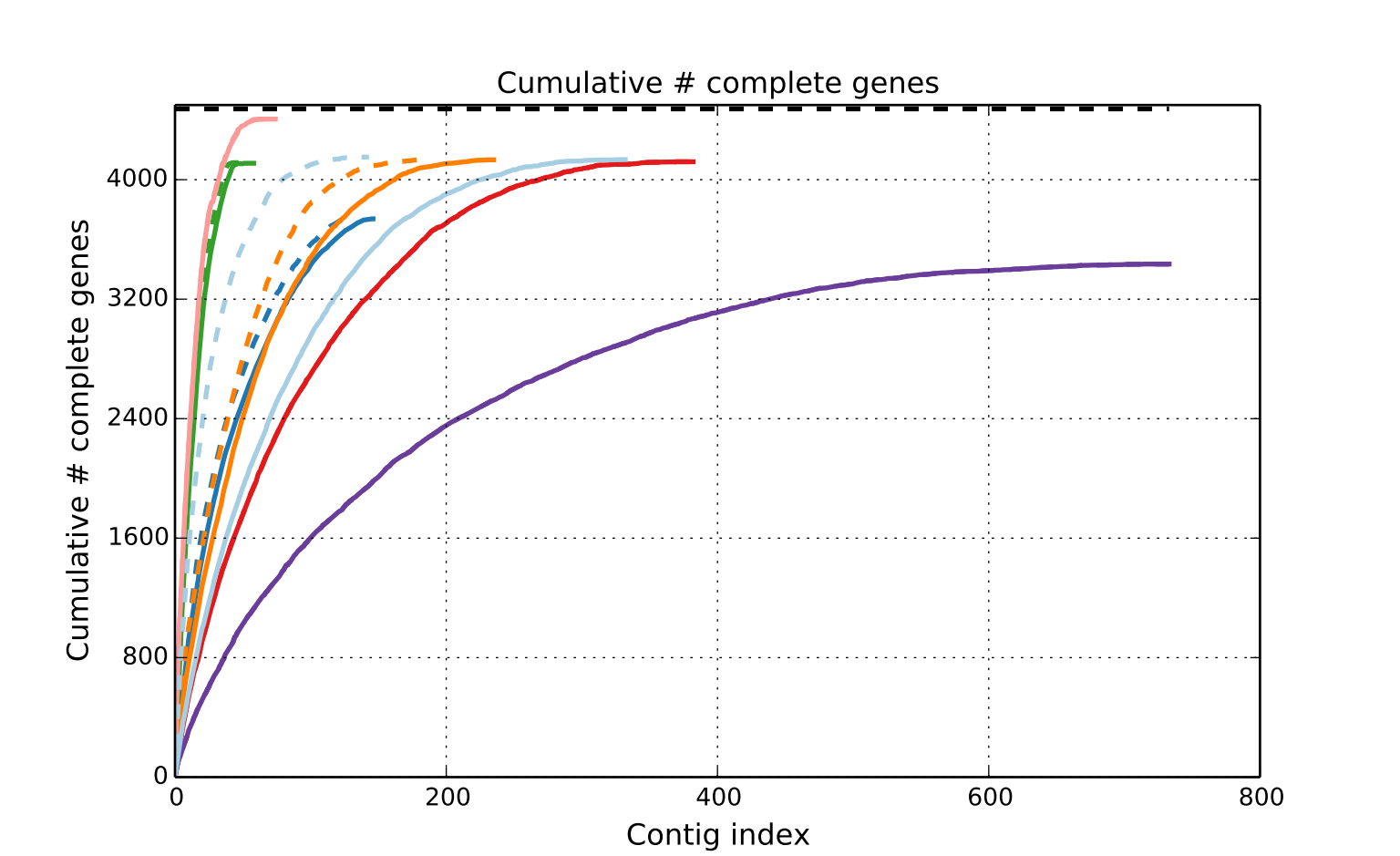

Nx
Contig length (kbp)
400
320
240
160
80
0
0
20
40
60
80
100
x
d broken
d
ld broken
ld
RS-M-Msrca-Scaffold broken
RS-M-Msrca-Scaffold
RS-M-Sga-Scaffold broken
RS-M-Sga-Scaffold
RS-M-Soap-Scaffold broken
RS-M-Soap-Scaffold
RS-M-Spades-Scaffold broken
R
R
R

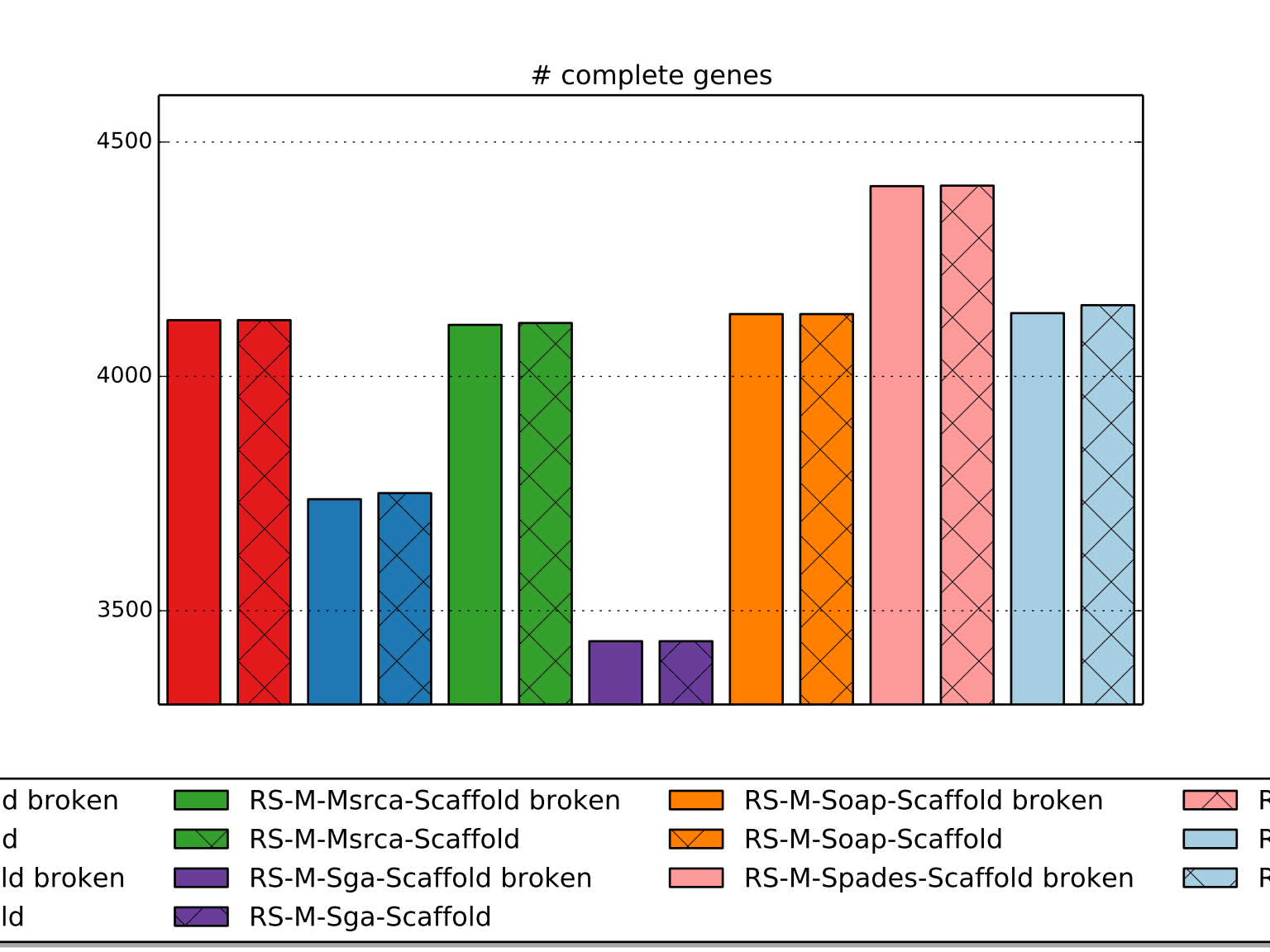

NGx
Contig length (kbp)
400
320
240
160
80
0
0
20
40
60
80
100
x
d broken
d
ld broken
ld
RS-M-Msrca-Scaffold broken
RS-M-Msrca-Scaffold
RS-M-Sga-Scaffold broken
RS-M-Sga-Scaffold
RS-M-Soap-Scaffold broken
RS-M-Soap-Scaffold
RS-M-Spades-Scaffold broken
R
R
R

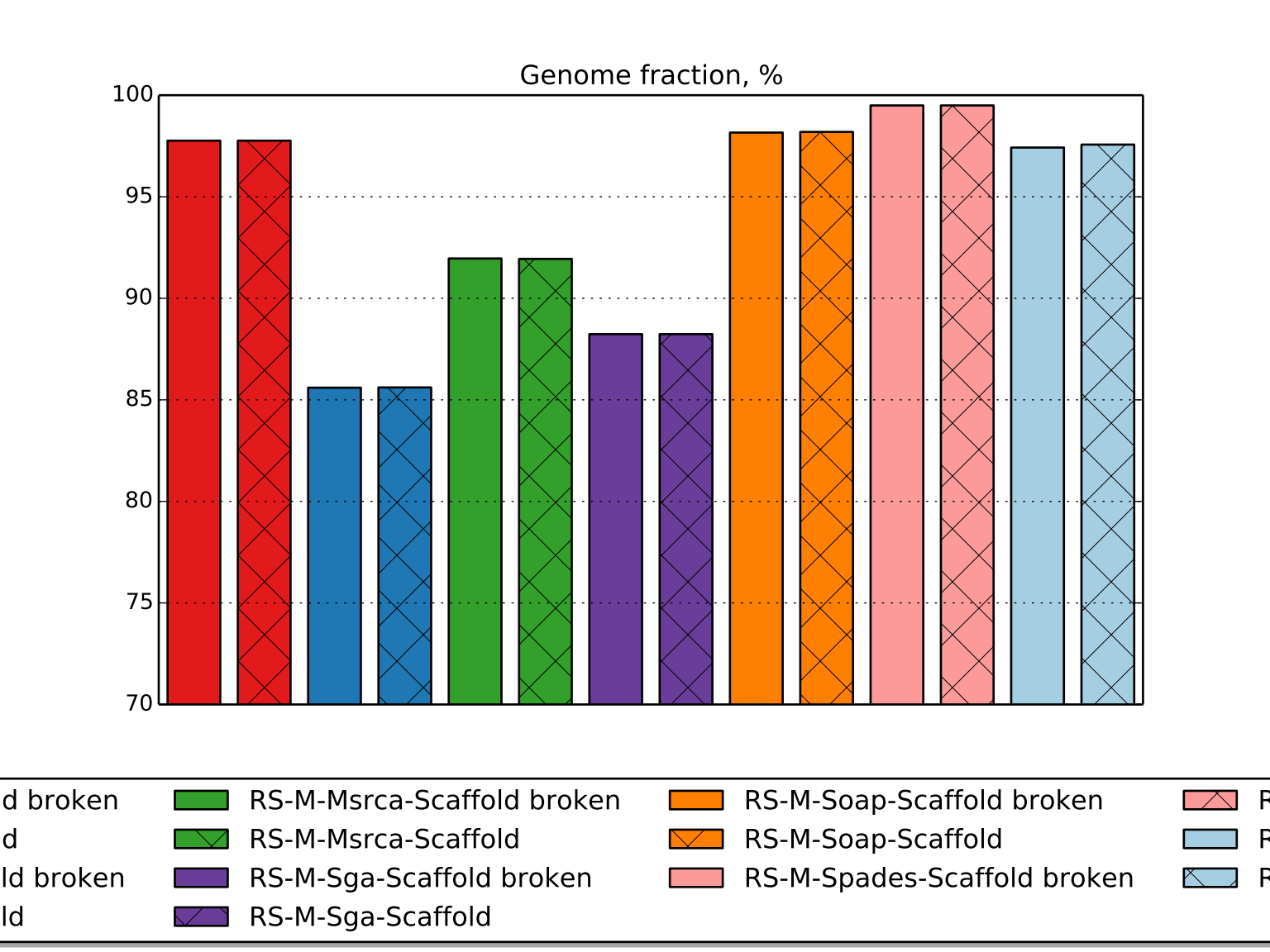

Cumulative length (aligned contigs)
Cumulative length (Mbp)
Contig index
0
1
2
3
4
5
0
200
400
600
800
d broken
d
ld broken
ld
RS-M-Msrca-Scaffold broken
RS-M-Msrca-Scaffold
RS-M-Sga-Scaffold broken
RS-M-Sga-Scaffold
RS-M-Soap-Scaffold broken
RS-M-Soap-Scaffold
RS-M-Spades-Scaffold broken
RS-M-Spades-Scaffold


NAx
Contig length (kbp)
400
320
240
160
80
0
0
20
40
60
80
100
x
d broken
d
ld broken
ld
RS-M-Msrca-Scaffold broken
RS-M-Msrca-Scaffold
RS-M-Sga-Scaffold broken
RS-M-Sga-Scaffold
RS-M-Soap-Scaffold broken
RS-M-Soap-Scaffold
RS-M-Spades-Scaffold broken
R
R
R

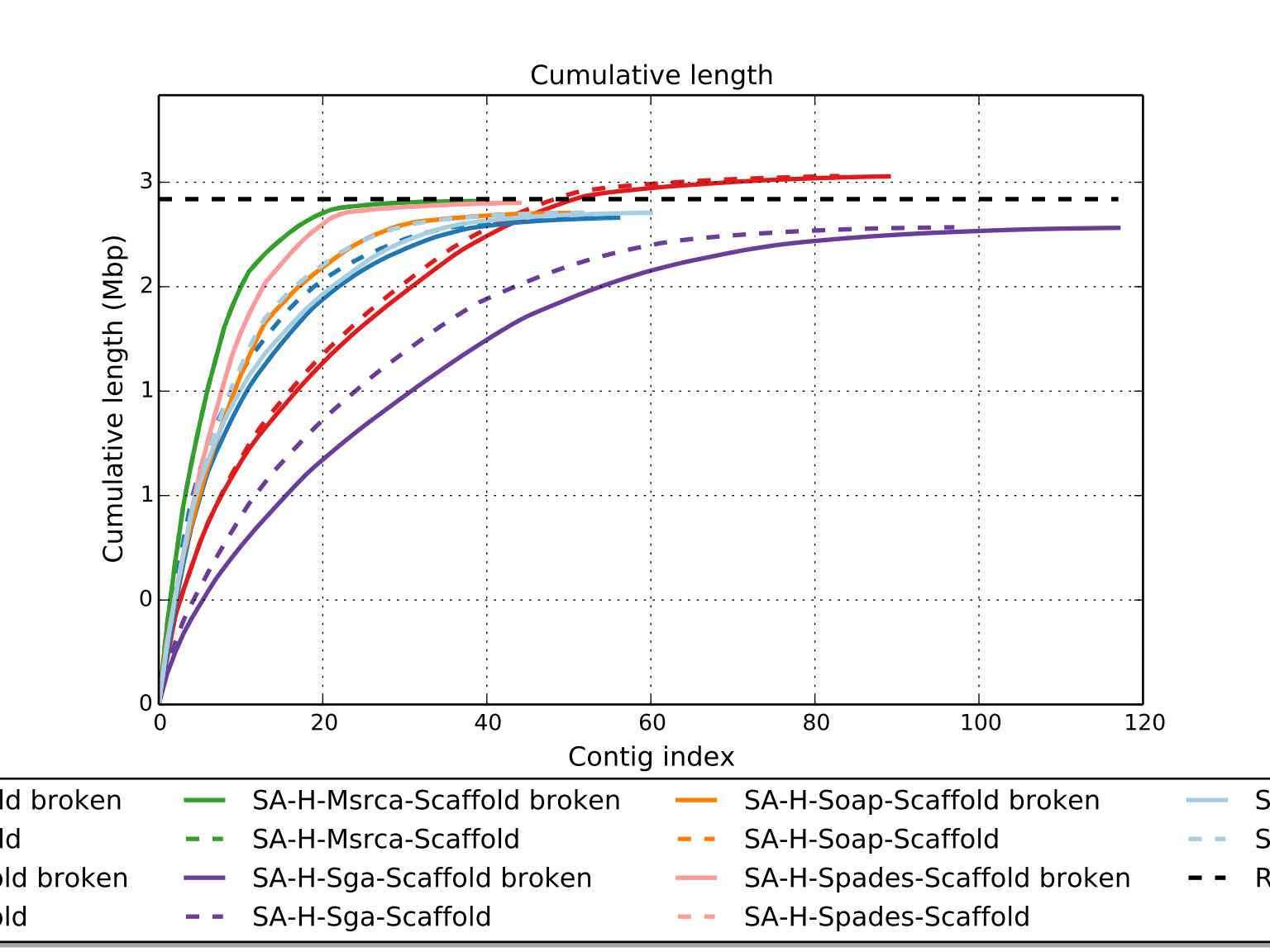

NGAx
Contig length (kbp)
400
320
240
160
80
0
0
20
40
60
80
100
x
d broken
d
ld broken
ld
RS-M-Msrca-Scaffold broken
RS-M-Msrca-Scaffold
RS-M-Sga-Scaffold broken
RS-M-Sga-Scaffold
RS-M-Soap-Scaffold broken
RS-M-Soap-Scaffold
RS-M-Spades-Scaffold broken

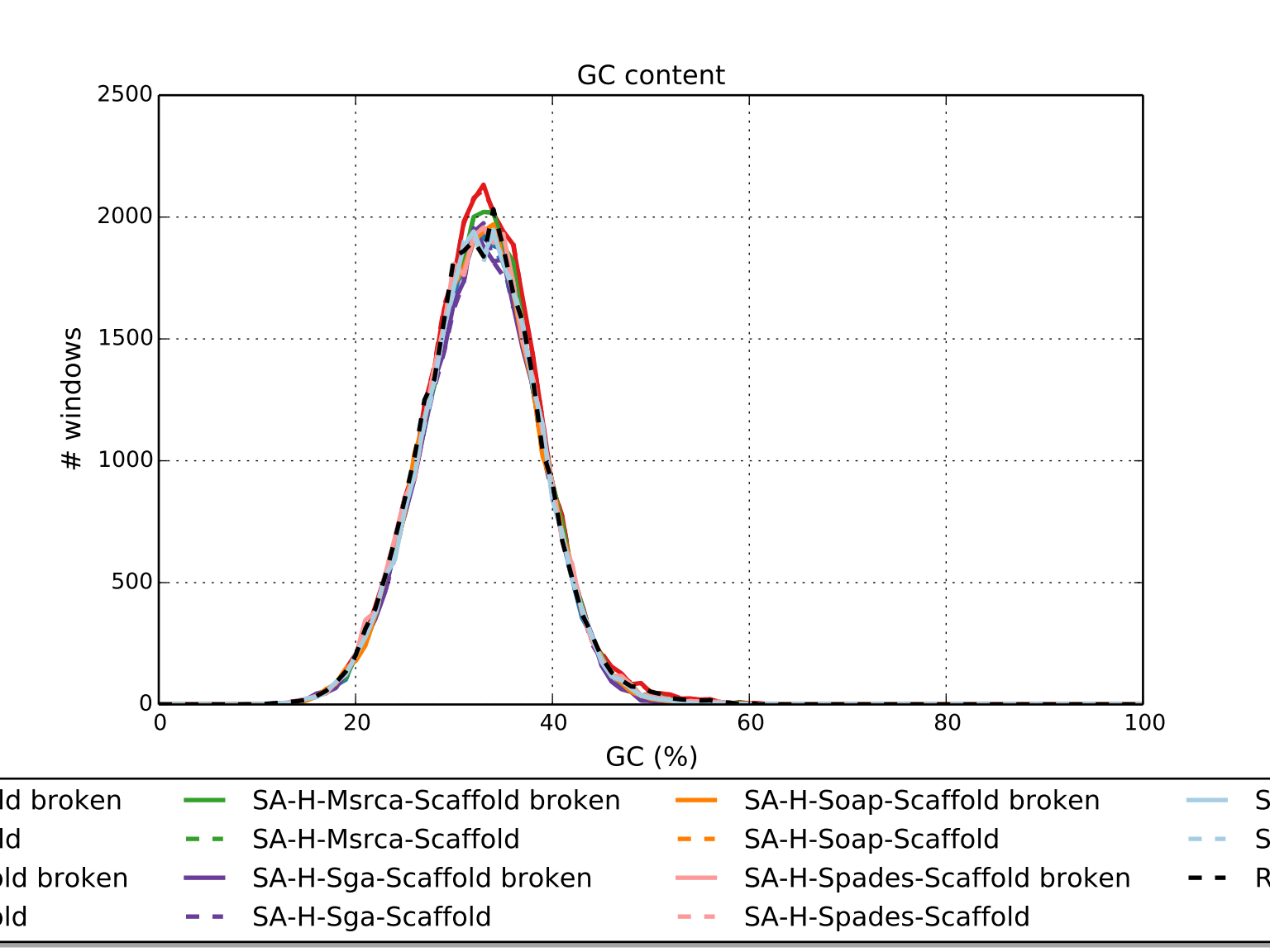

Cumulative # complete genes
Cumulative # complete genes
Contig index
0
800
1600
2400
3200
4000
0
200
400
600
800
d broken
d
ld broken
ld
RS-M-Msrca-Scaffold broken
RS-M-Msrca-Scaffold
RS-M-Sga-Scaffold broken
RS-M-Sga-Scaffold
RS-M-Soap-Scaffold broken
RS-M-Soap-Scaffold
RS-M-Spades-Scaffold broken
RS-M-Spades-Scaffold
R
R
R

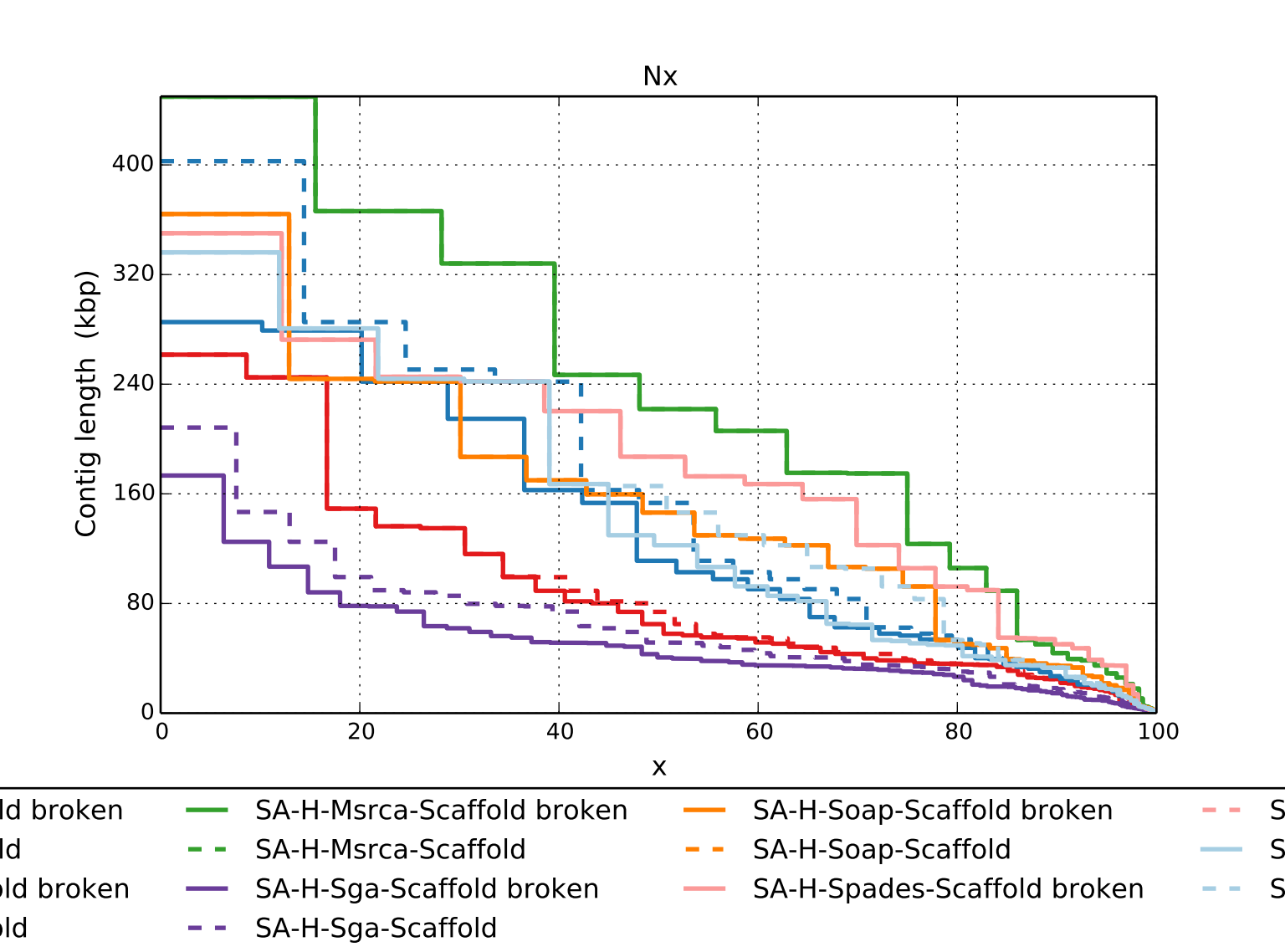

complete genes
4500
4000
3500
d broken
d
ld broken
ld
RS-M-Msrca-Scaffold broken
RS-M-Msrca-Scaffold
RS-M-Sga-Scaffold broken
RS-M-Sga-Scaffold
RS-M-Soap-Scaffold broken
RS-M-Soap-Scaffold
RS-M-Spades-Scaffold broken

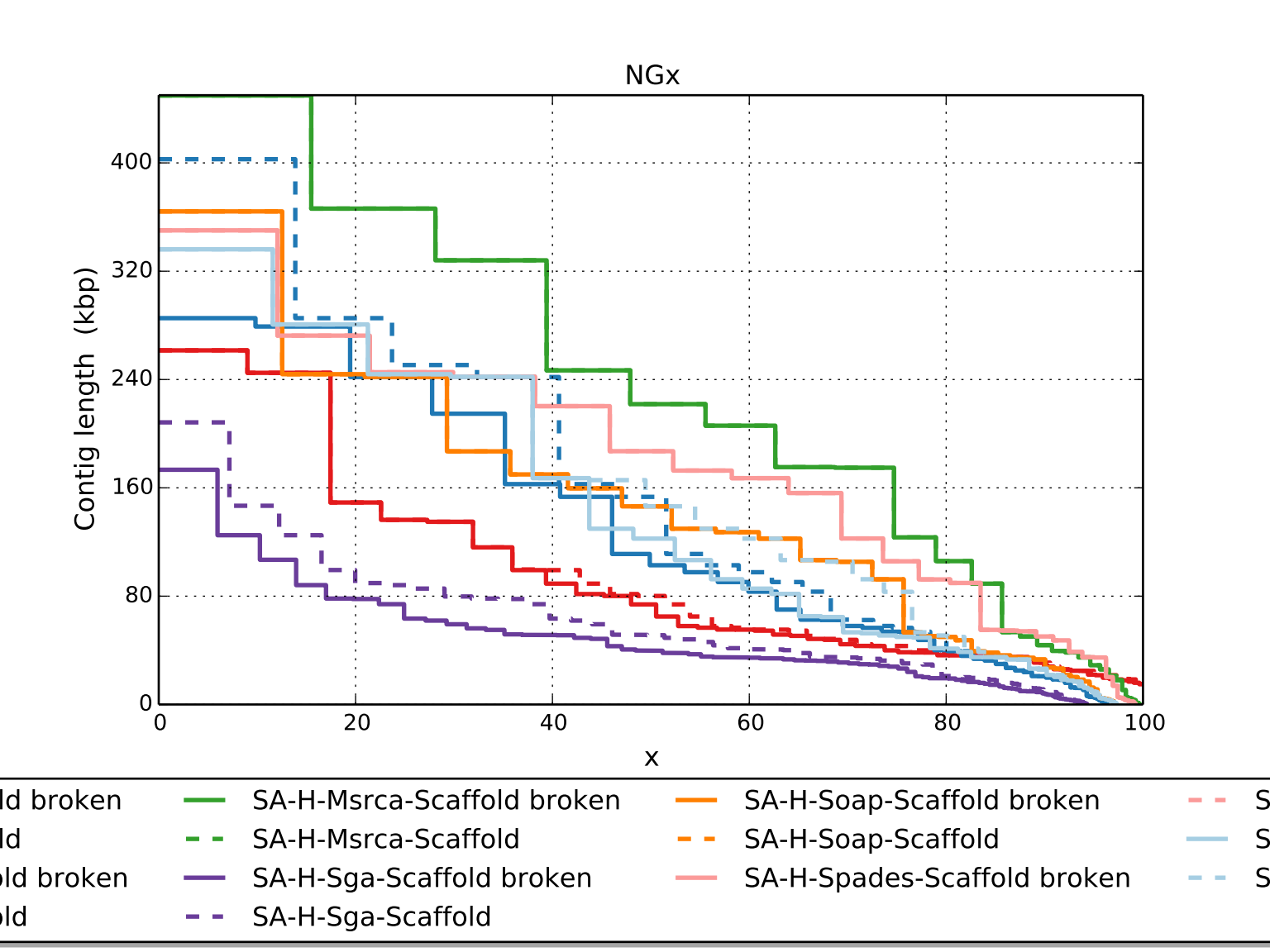

Genome fraction, %
100
95
90
85
80
75
70
d broken
d
ld broken
ld
RS-M-Msrca-Scaffold broken
RS-M-Msrca-Scaffold
RS-M-Sga-Scaffold broken
RS-M-Sga-Scaffold
RS-M-Soap-Scaffold broken
RS-M-Soap-Scaffold
RS-M-Spades-Scaffold broken
R
R
R

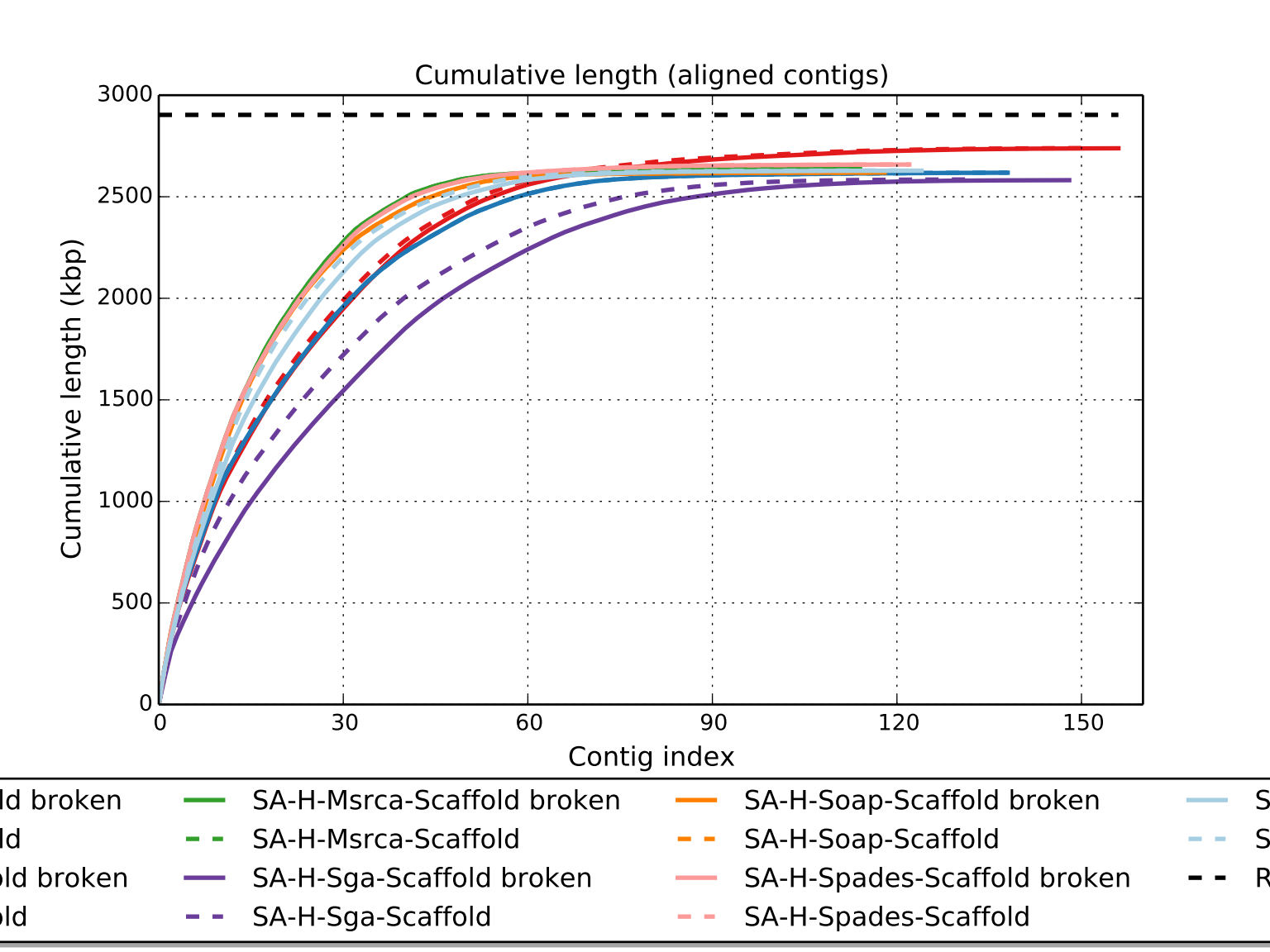
Scaffold

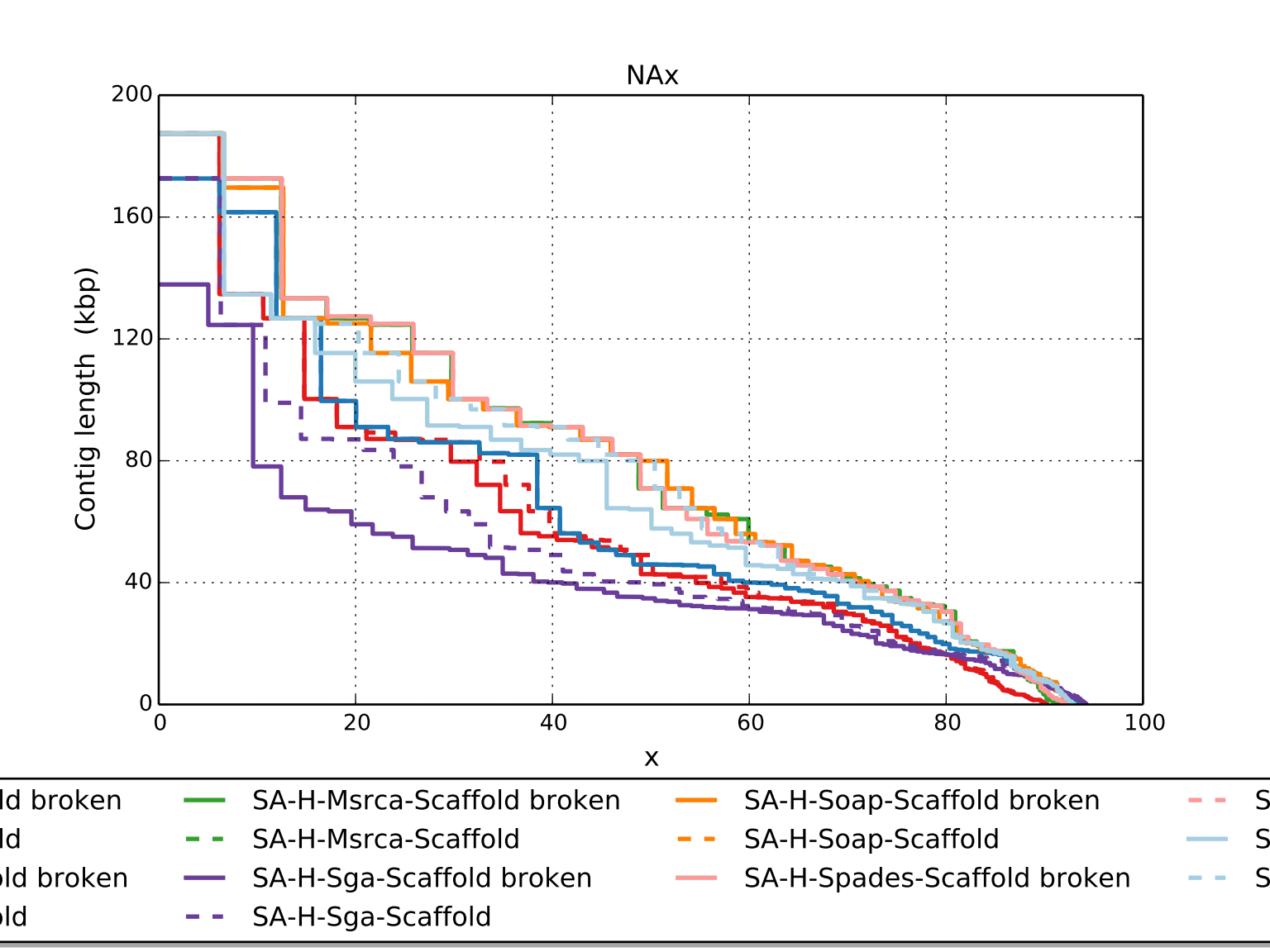

Cumulative length
Cumulative length (Mbp)
Contig index
0
20
40
60
80
100
120
0
1
2
3
ld broken
SA-H-Msrca-Scaffold broken
SA-H-Soap-Scaffold broken
S
ld
SA-H-Msrca-Scaffold
SA-H-Soap-Scaffold
S
old broken
SA-H-Sga-Scaffold broken
SA-H-Spades-Scaffold broken
R
old
SA-H-Sga-Scaffold
SA-H-Spades-Scaffold

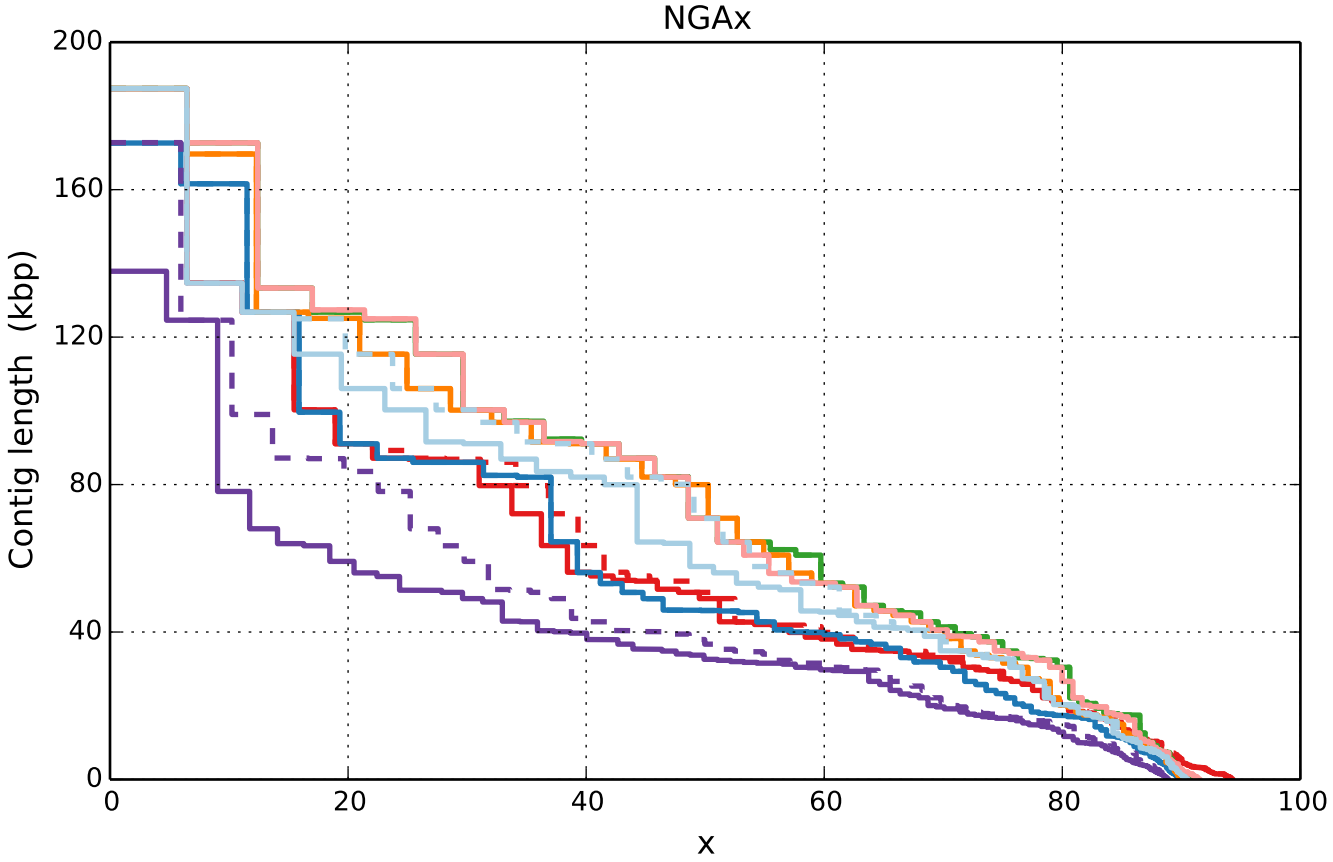

GC content
windows
GC (%)
0
500
1000
1500
2000
2500
0
20
40
60
80
100
ld broken
ld
old broken
old
SA-H-Msrca-Scaffold broken
SA-H-Msrca-Scaffold
SA-H-Sga-Scaffold broken
SA-H-Sga-Scaffold
SA-H-Soap-Scaffold broken
SA-H-Soap-Scaffold
SA-H-Spades-Scaffold broken
SA-H-Spades-Scaffold
S
S
R


Nx
Contig length (kbp)
400
320
240
160
80
0
0
20
40
60
80
100
x
ld broken
ld
old broken
old
SA-H-Msrca-Scaffold broken
SA-H-Msrca-Scaffold
SA-H-Sga-Scaffold broken
SA-H-Sga-Scaffold
SA-H-Soap-Scaffold broken
SA-H-Soap-Scaffold
SA-H-Spades-Scaffold broken
S
S
S


NGx
Contig length (kbp)
400
320
240
160
80
0
0
20
40
60
80
100
x
ld broken
ld
old broken
old
SA-H-Msrca-Scaffold broken
SA-H-Msrca-Scaffold
SA-H-Sga-Scaffold broken
SA-H-Sga-Scaffold
SA-H-Soap-Scaffold broken
SA-H-Soap-Scaffold
SA-H-Spades-Scaffold broken
S
S
S


Cumulative length (aligned contigs)
Cumulative length (kbp)
Contig index
0
500
1000
1500
2000
2500
3000
0
30
60
90
120
150
ld broken
ld
old broken
old
SA-H-Msrca-Scaffold broken
SA-H-Msrca-Scaffold
SA-H-Sga-Scaffold broken
SA-H-Sga-Scaffold
SA-H-Soap-Scaffold broken
SA-H-Soap-Scaffold
SA-H-Spades-Scaffold broken
SA-H-Spades-Scaffold
S
S
R


NAx
Contig length (kbp)
x
0
40
80
120
160
200
0
20
40
60
80
100
ld broken
ld
old broken
old
SA-H-Msrca-Scaffold broken
SA-H-Msrca-Scaffold
SA-H-Sga-Scaffold broken
SA-H-Sga-Scaffold
SA-H-Soap-Scaffold broken
SA-H-Soap-Scaffold
SA-H-Spades-Scaffold broken
S
S
S

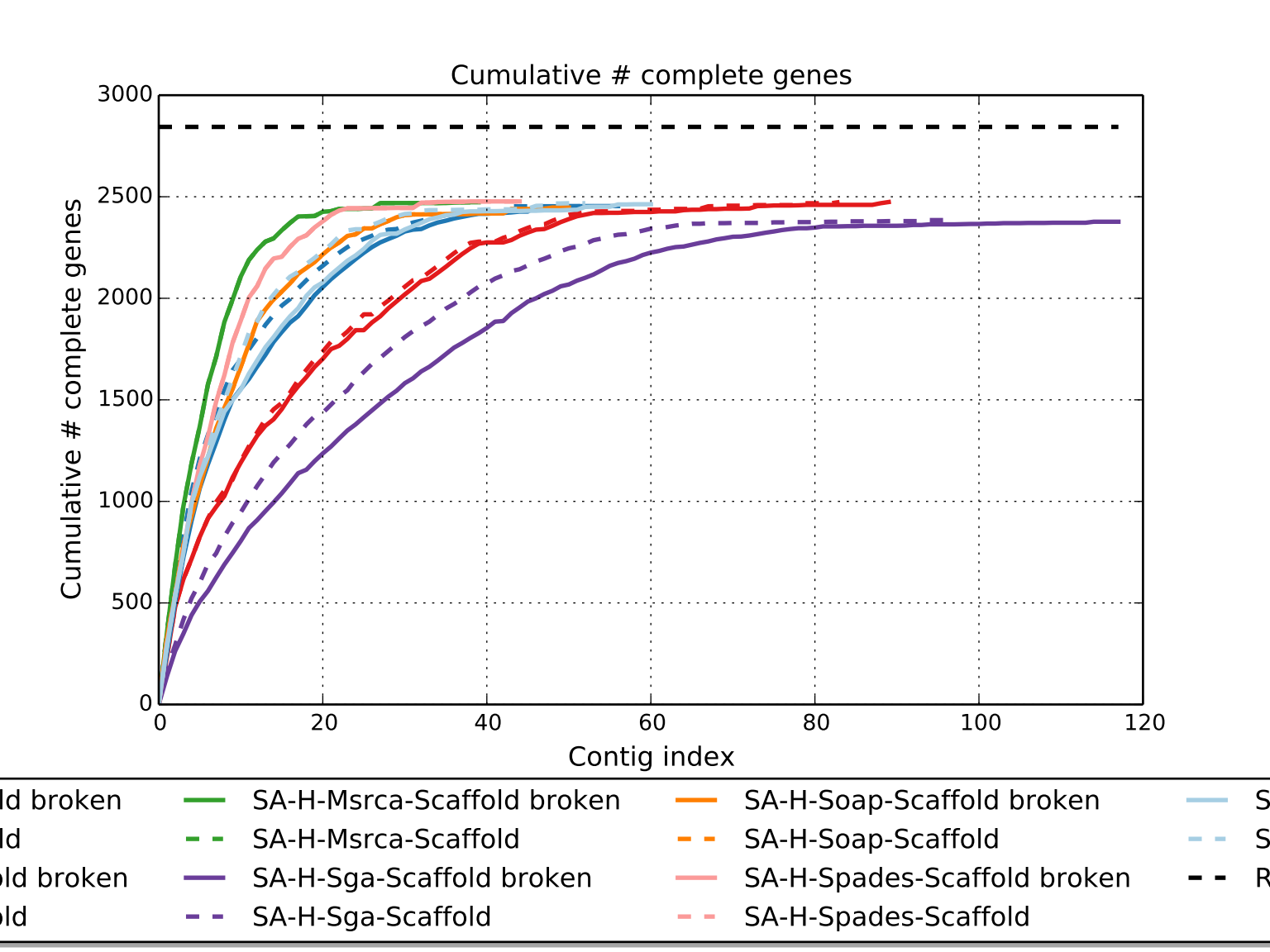


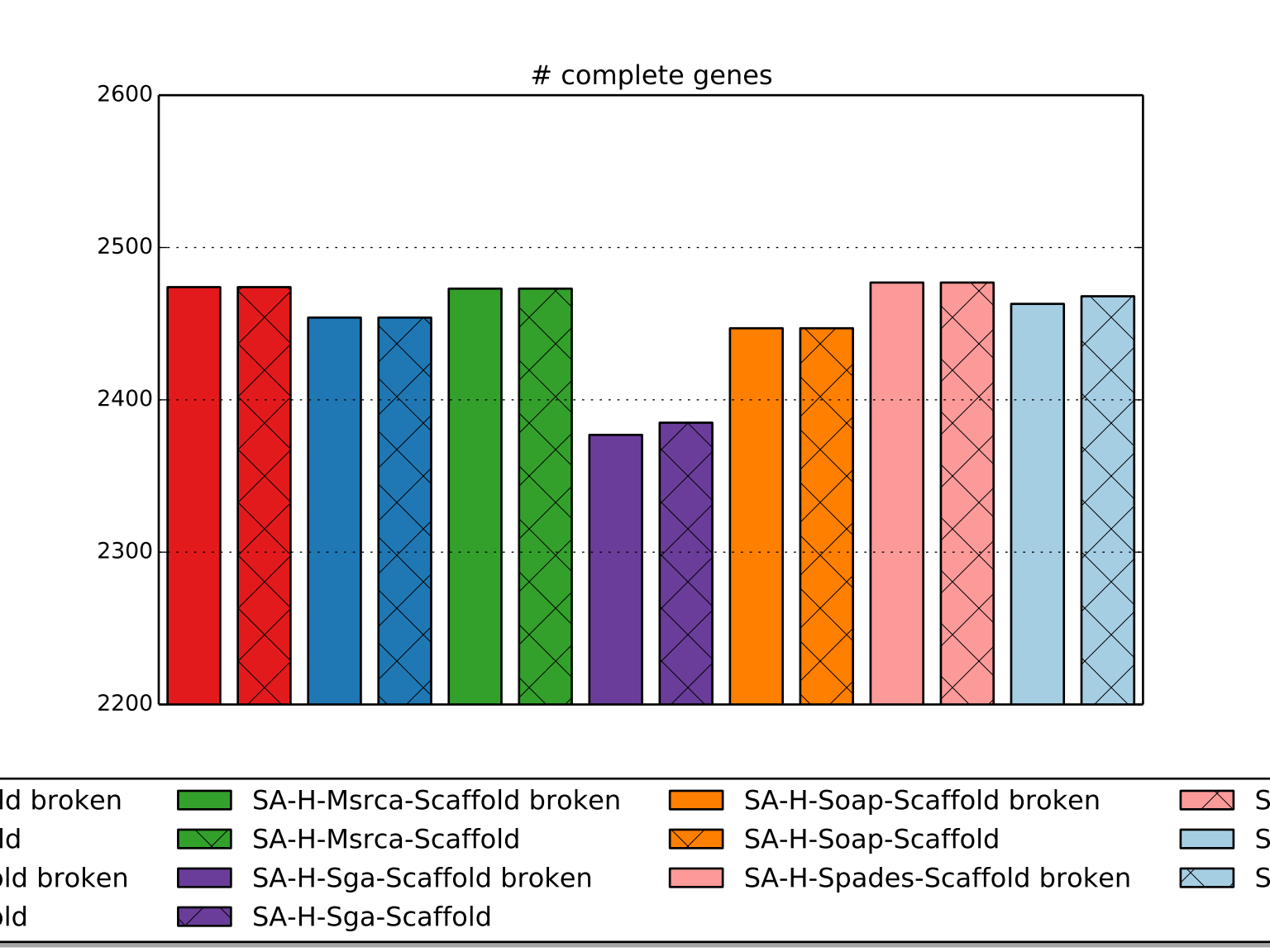
ld broken
ld
old broken
old

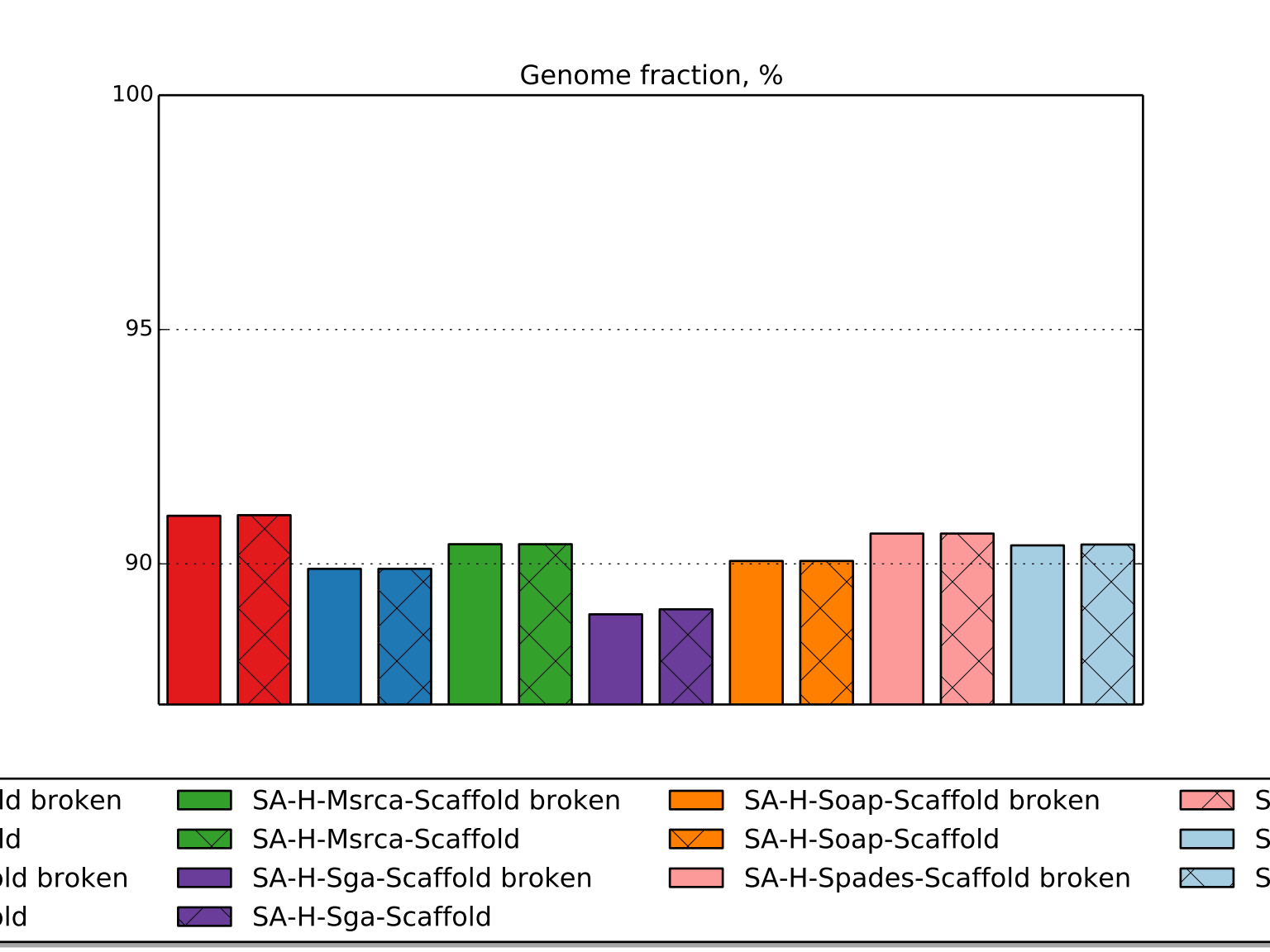
SA-H-Msrca-Scaffold broken
SA-H-Msrca-Scaffold
SA-H-Sga-Scaffold broken
SA-H-Sga-Scaffold

SA-H-Soap-Scaffold broken
SA-H-Soap-Scaffold
SA-H-Spades-Scaffold broken

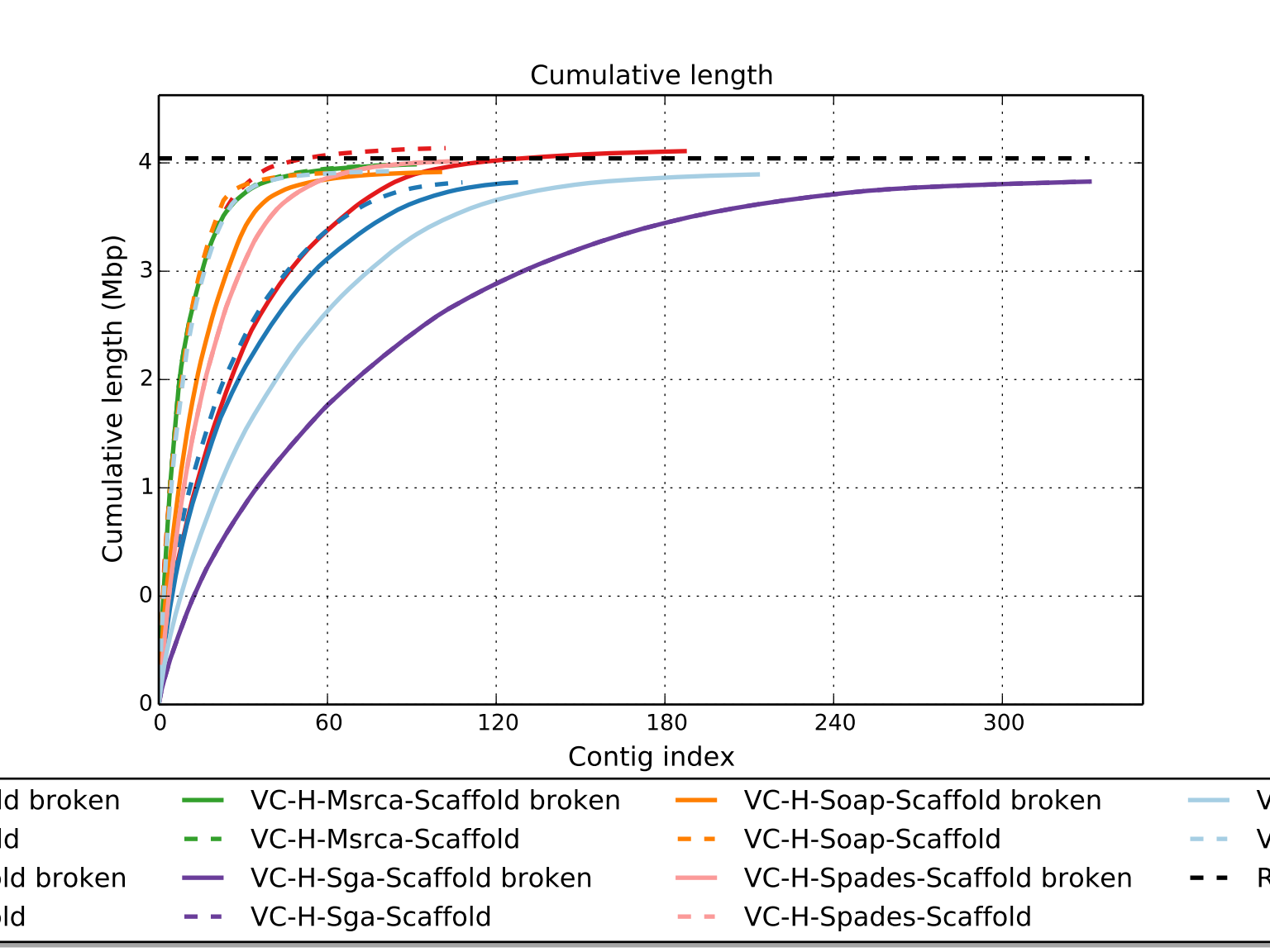
S
S
S

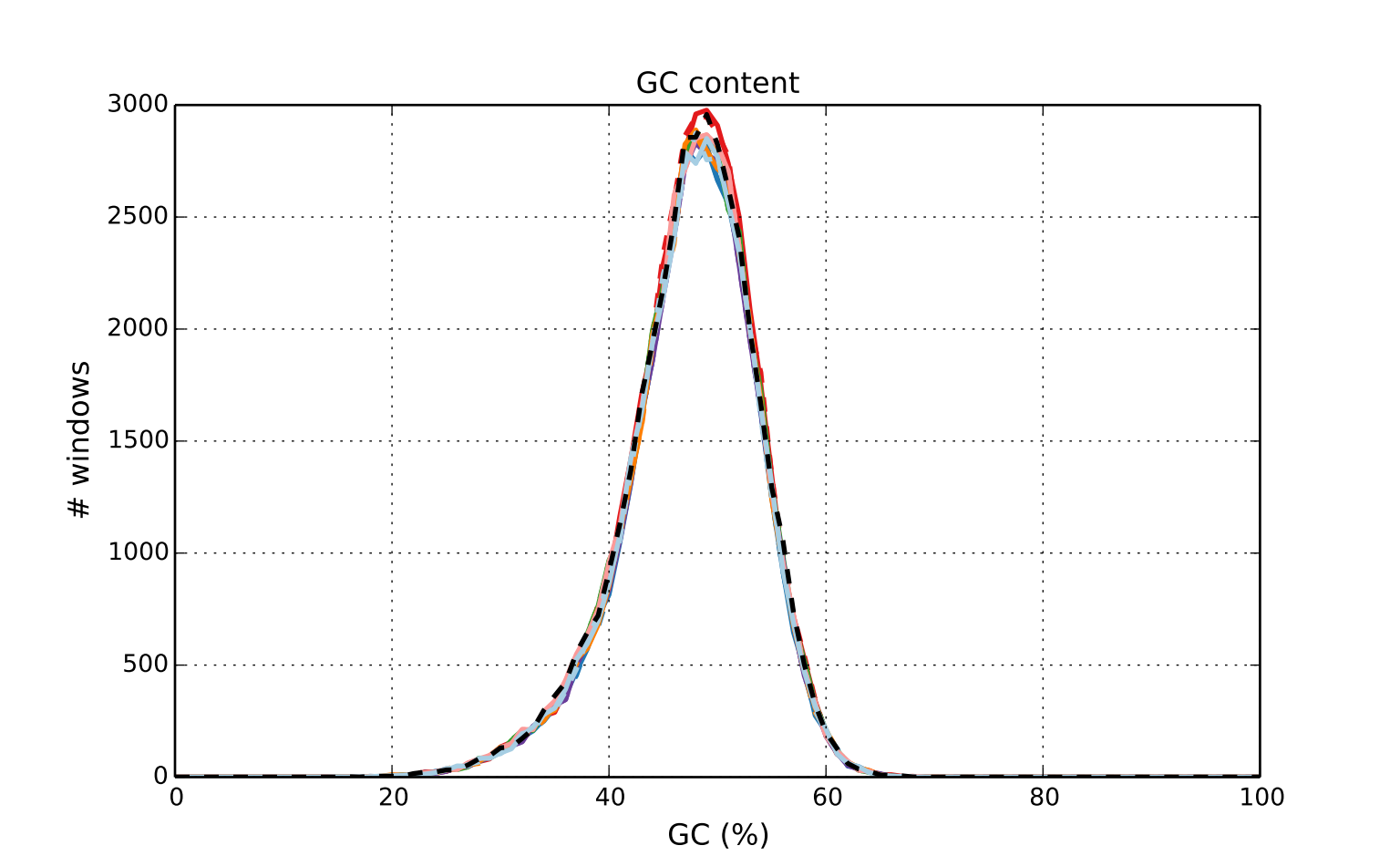

Cumulative # complete genes
Cumulative # complete genes
Contig index
0
500
1000
1500
2000
2500
3000
0
20
40
60
80
100
120
ld broken
ld
old broken
old
SA-H-Msrca-Scaffold broken
SA-H-Msrca-Scaffold
SA-H-Sga-Scaffold broken
SA-H-Sga-Scaffold
SA-H-Soap-Scaffold broken
SA-H-Soap-Scaffold
SA-H-Spades-Scaffold broken
SA-H-Spades-Scaffold
S
S
R

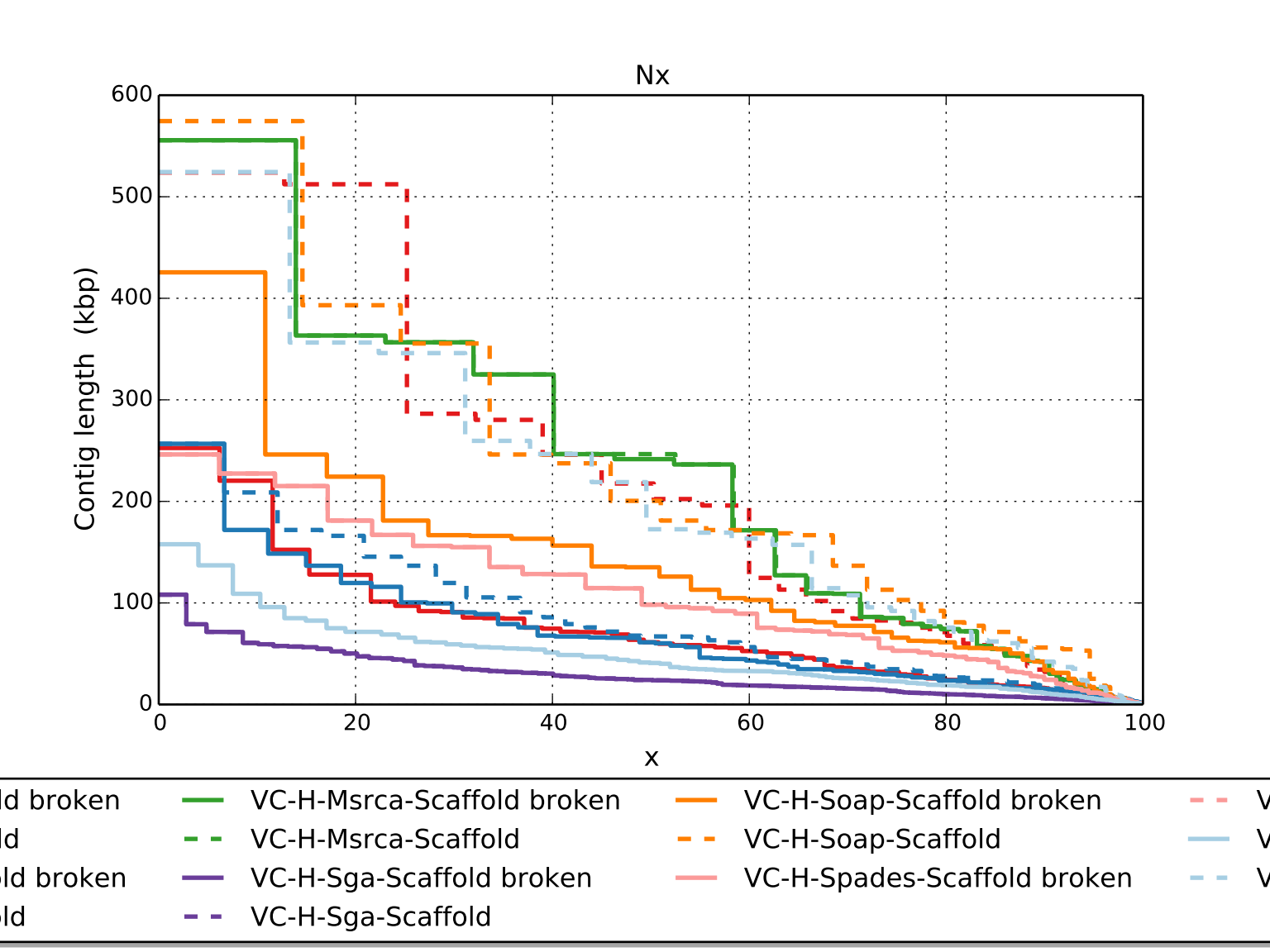

complete genes
2600
2500
2400
2300
2200
ld broken
ld
old broken
old
SA-H-Msrca-Scaffold broken
SA-H-Msrca-Scaffold
SA-H-Sga-Scaffold broken
SA-H-Sga-Scaffold
SA-H-Soap-Scaffold broken
SA-H-Soap-Scaffold
SA-H-Spades-Scaffold broken
S
S
S

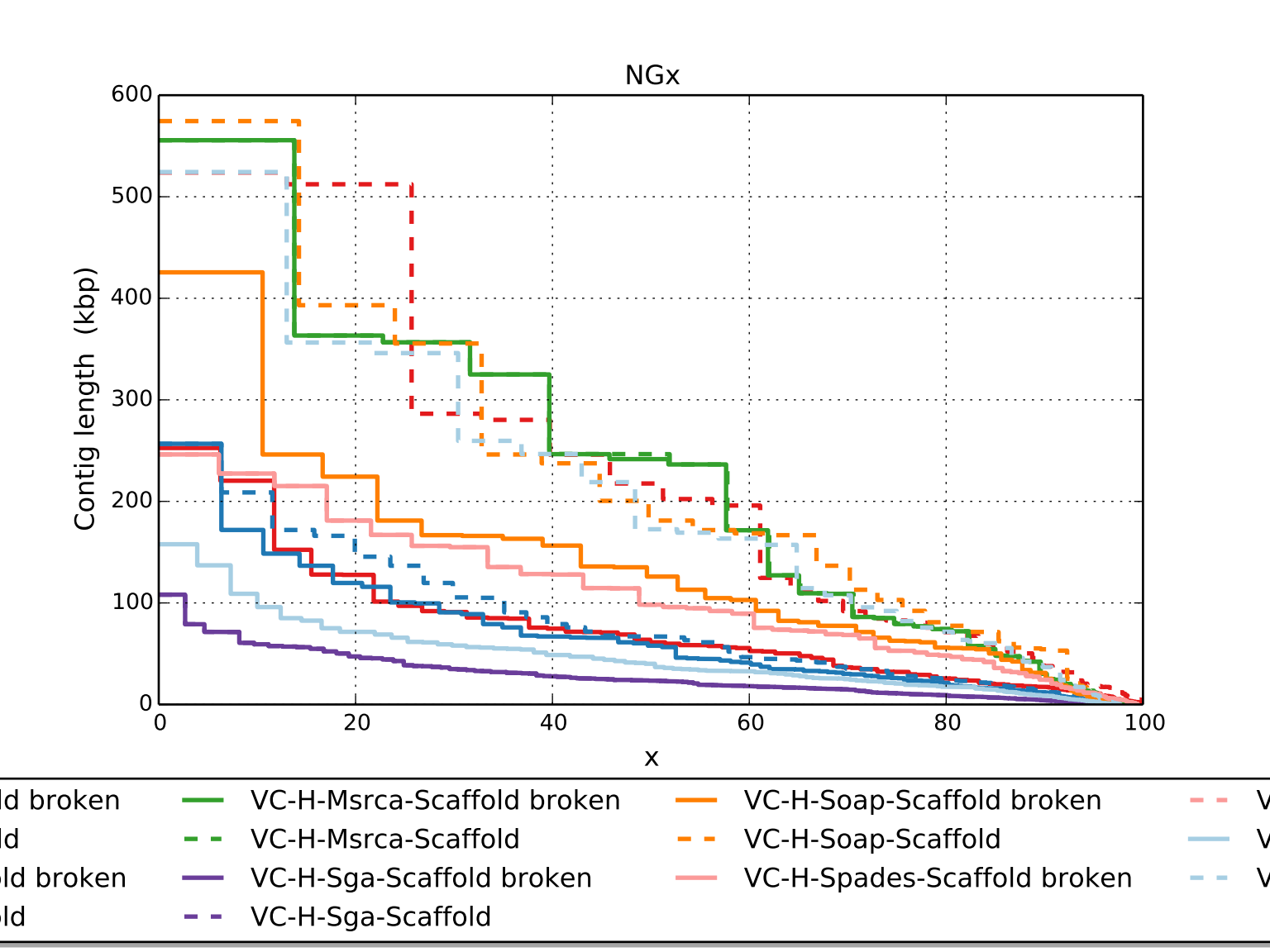

Genome fraction, %
100
95
90
ld broken
ld
old broken
old
SA-H-Msrca-Scaffold broken
SA-H-Msrca-Scaffold
SA-H-Sga-Scaffold broken
SA-H-Sga-Scaffold
SA-H-Soap-Scaffold broken
SA-H-Soap-Scaffold
SA-H-Spades-Scaffold broken
S
S
S

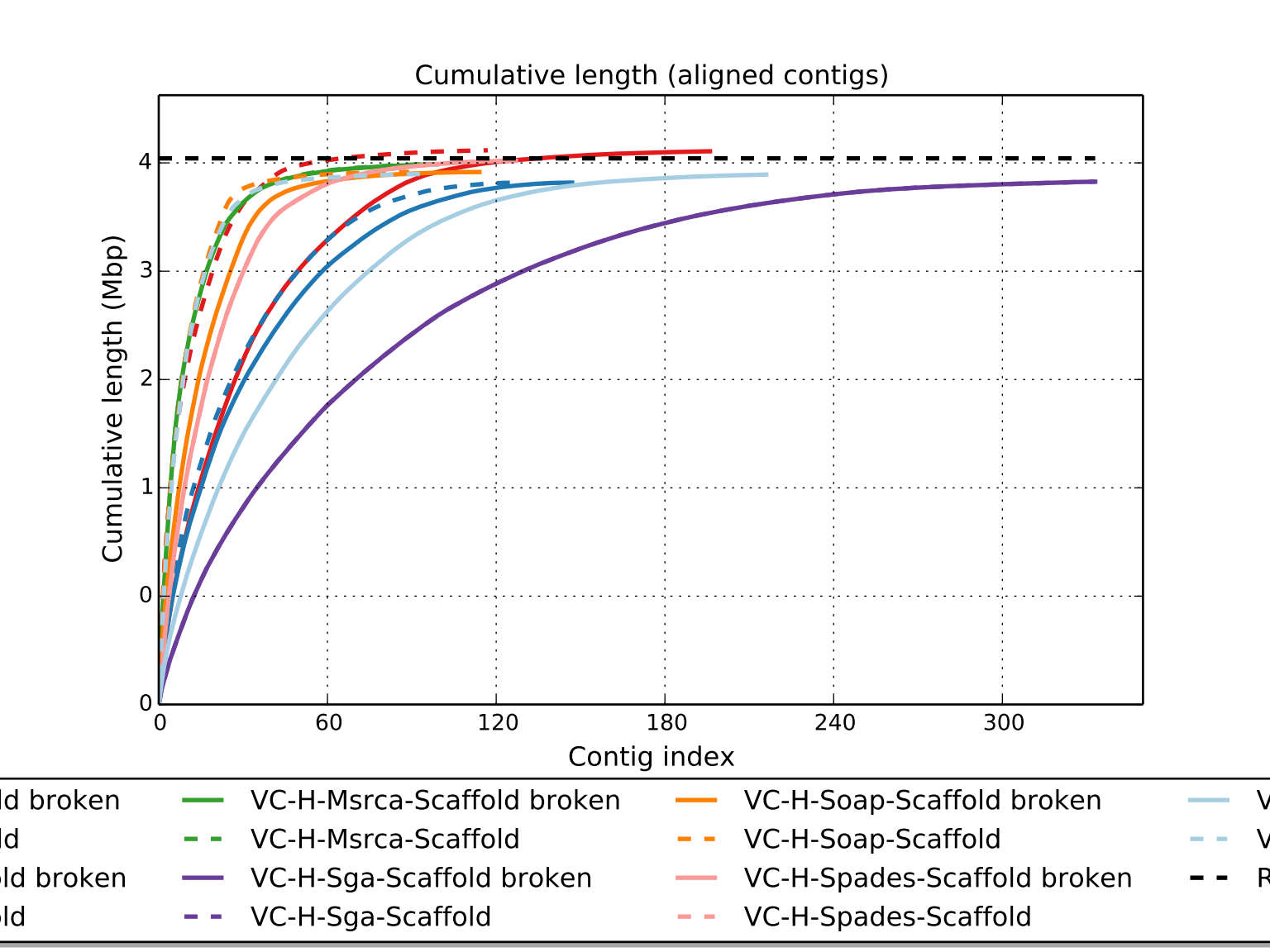
Scaffold

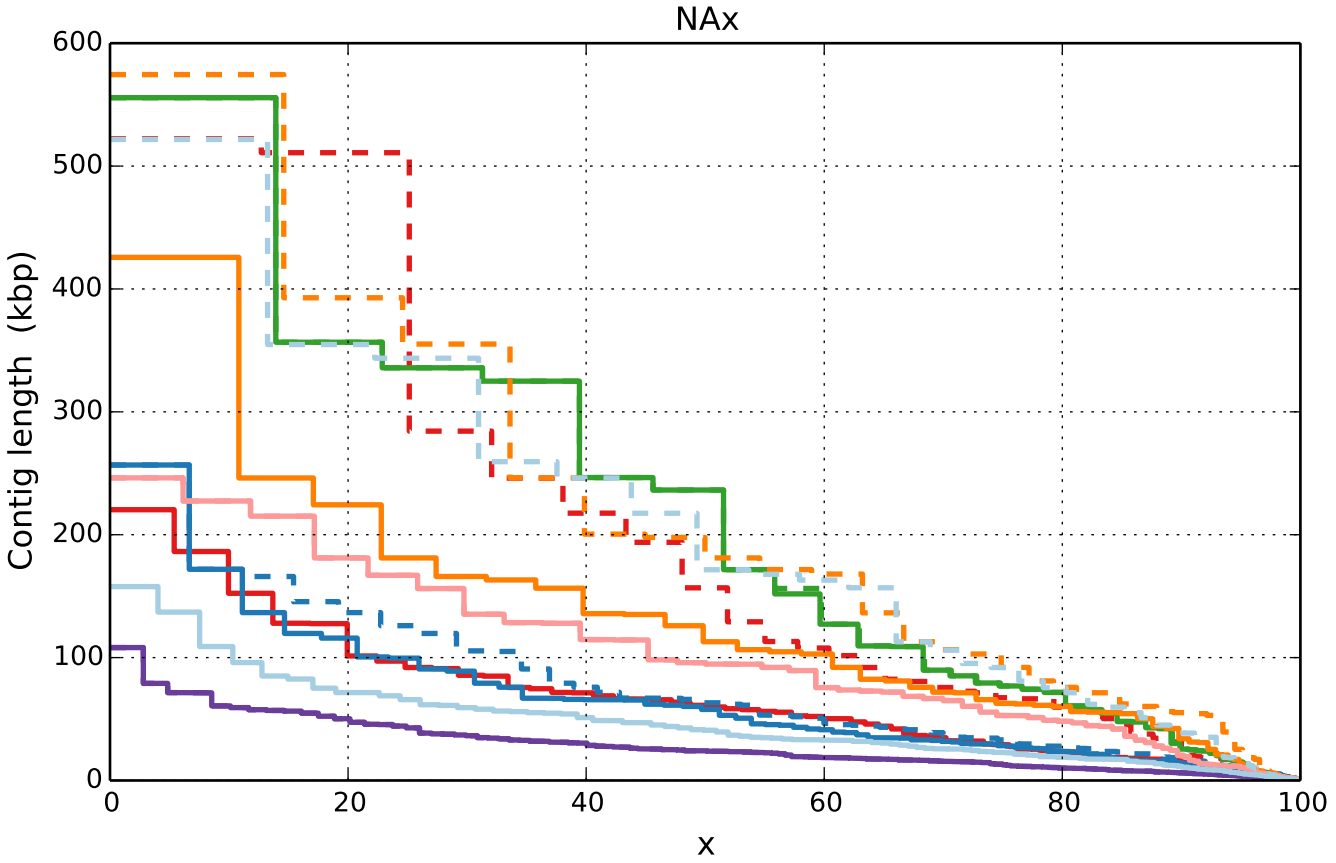

Cumulative length
Cumulative length (Mbp)
Contig index
0
1
2
3
4
0
60
120
180
240
300
ld broken
ld
old broken
old
VC-H-Msrca-Scaffold broken
VC-H-Msrca-Scaffold
VC-H-Sga-Scaffold broken
VC-H-Sga-Scaffold
VC-H-Soap-Scaffold broken
VC-H-Soap-Scaffold
VC-H-Spades-Scaffold broken
VC-H-Spades-Scaffold
V
V
R

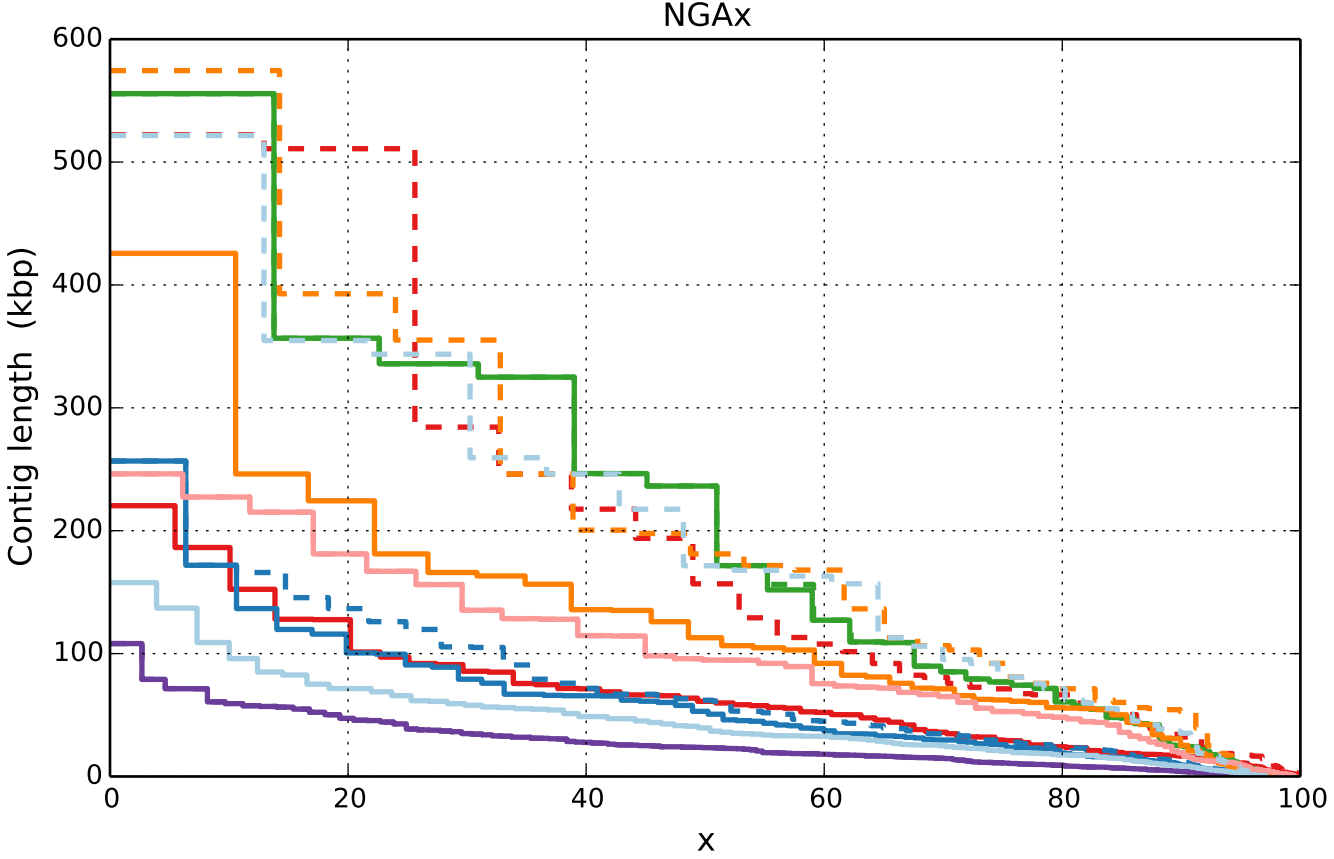

GC content
windows
GC (%)
0
500
1000
1500
2000
2500
3000
0
20
40
60
80
100
ld broken
ld
old broken
old
VC-H-Msrca-Scaffold broken
VC-H-Msrca-Scaffold
VC-H-Sga-Scaffold broken
VC-H-Sga-Scaffold
VC-H-Soap-Scaffold broken
VC-H-Soap-Scaffold
VC-H-Spades-Scaffold broken
VC-H-Spades-Scaffold
V
V
R

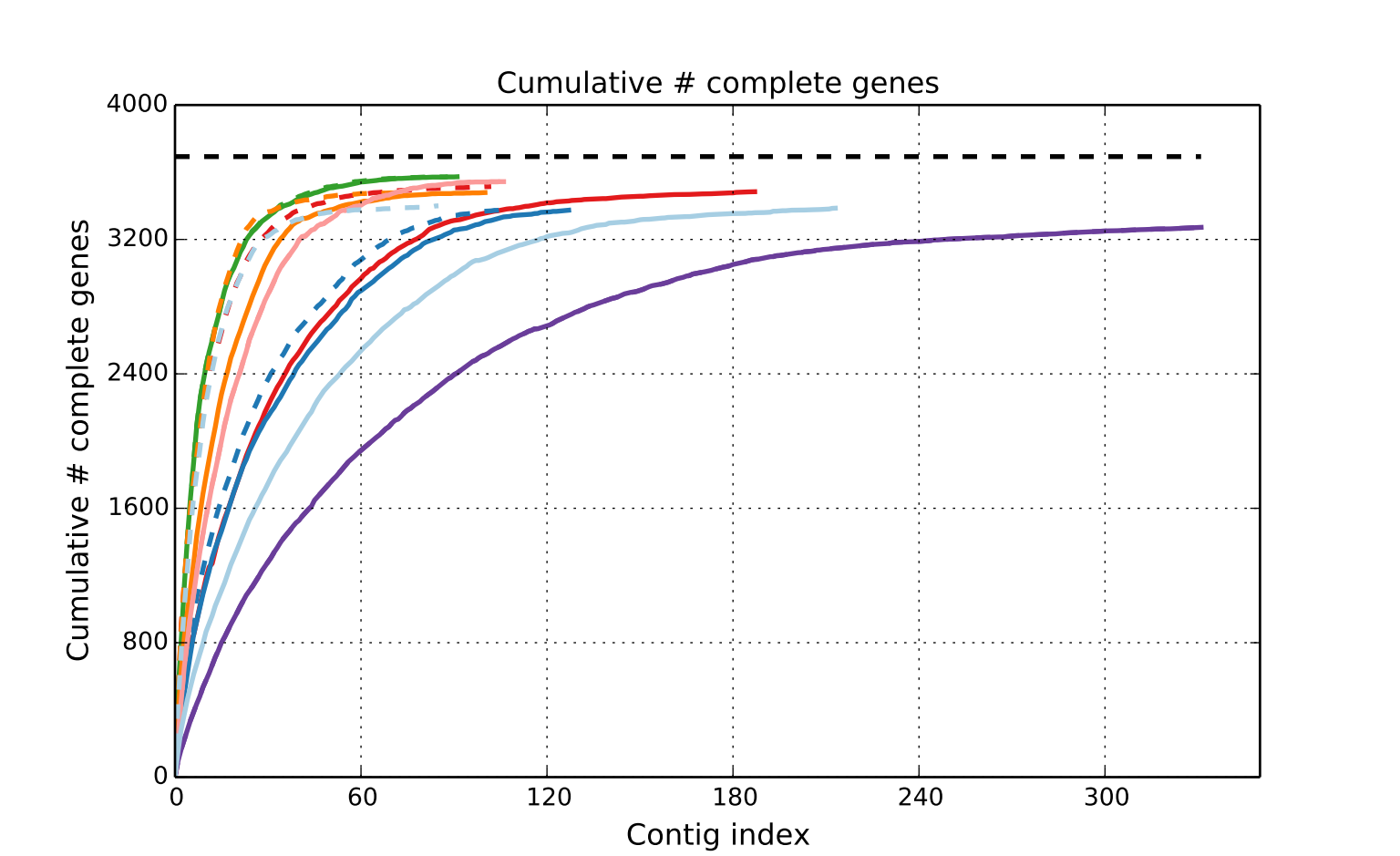

Nx
Contig length (kbp)
x
0
100
200
300
400
500
600
0
20
40
60
80
100
ld broken
ld
old broken
old
VC-H-Msrca-Scaffold broken
VC-H-Msrca-Scaffold
VC-H-Sga-Scaffold broken
VC-H-Sga-Scaffold
VC-H-Soap-Scaffold broken
VC-H-Soap-Scaffold
VC-H-Spades-Scaffold broken

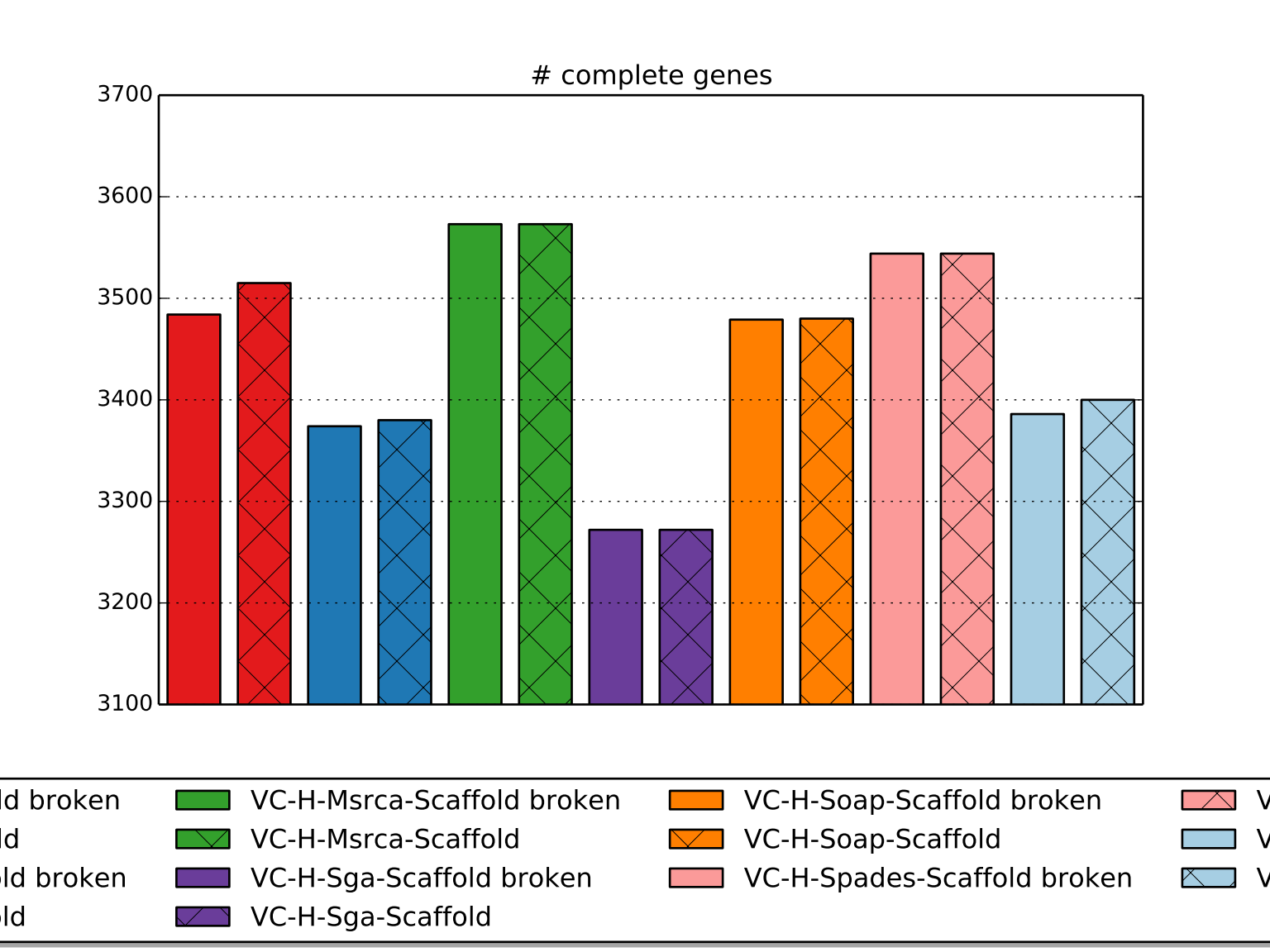

NGx
Contig length (kbp)
600
500
400
300
200
100
0
0
20
40
60
80
100
x
ld broken
ld
old broken
old
VC-H-Msrca-Scaffold broken
VC-H-Msrca-Scaffold
VC-H-Sga-Scaffold broken
VC-H-Sga-Scaffold
VC-H-Soap-Scaffold broken
VC-H-Soap-Scaffold
VC-H-Spades-Scaffold broken
V
V
V

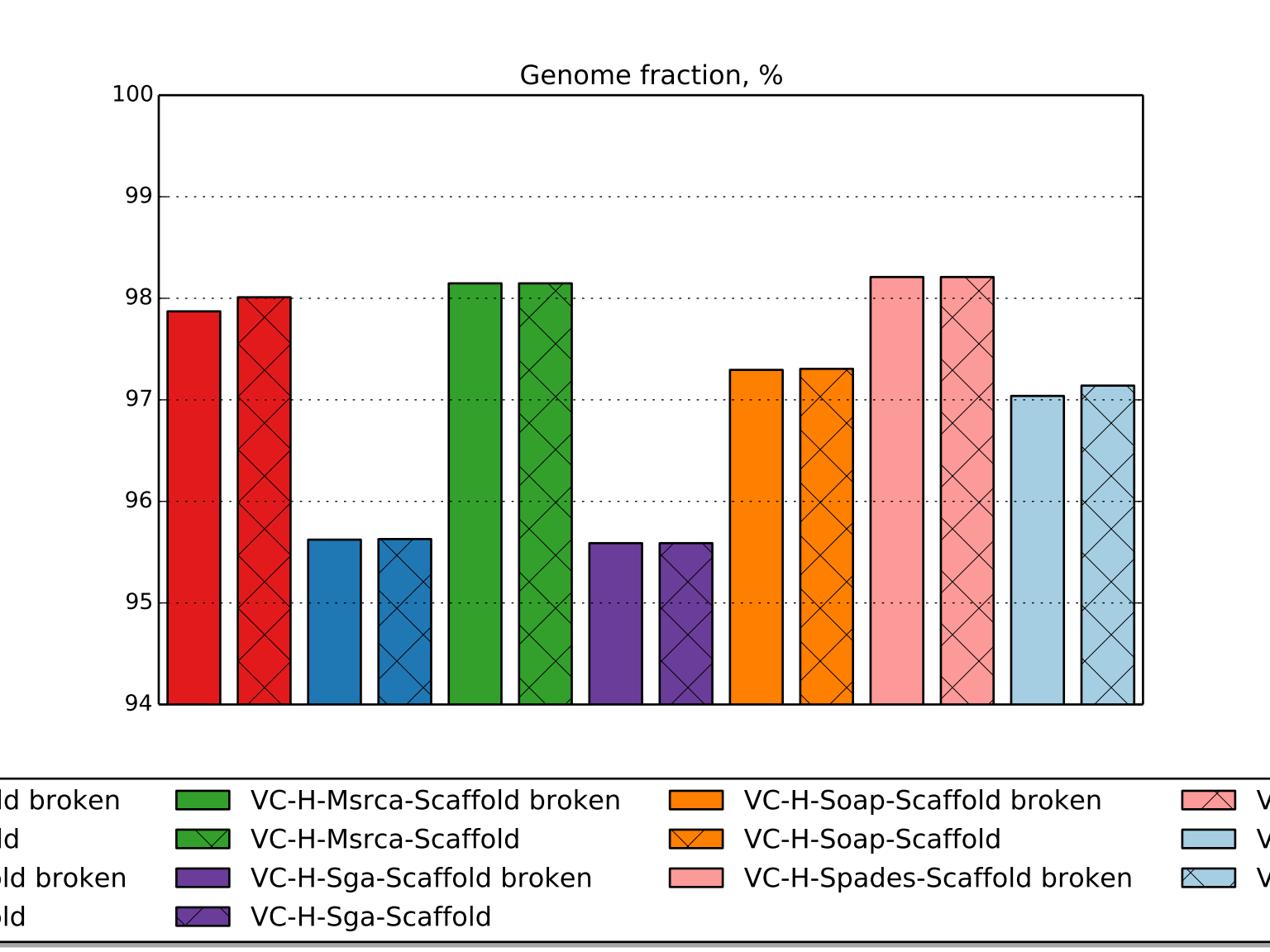

Cumulative length (aligned contigs)
Cumulative length (Mbp)
Contig index
0
1
2
3
4
0
60
120
180
240
300
ld broken
ld
old broken
old
VC-H-Msrca-Scaffold broken
VC-H-Msrca-Scaffold
VC-H-Sga-Scaffold broken
VC-H-Sga-Scaffold
VC-H-Soap-Scaffold broken
VC-H-Soap-Scaffold
VC-H-Spades-Scaffold broken
VC-H-Spades-Scaffold
V
V
R


NAx
Contig length (kbp)
600
500
400
300
200
100
0
0
20
40
60
80
100
x
ld broken
ld
old broken
old
VC-H-Msrca-Scaffold broken
VC-H-Msrca-Scaffold
VC-H-Sga-Scaffold broken
VC-H-Sga-Scaffold
VC-H-Soap-Scaffold broken
VC-H-Soap-Scaffold
VC-H-Spades-Scaffold broken
V
V
V

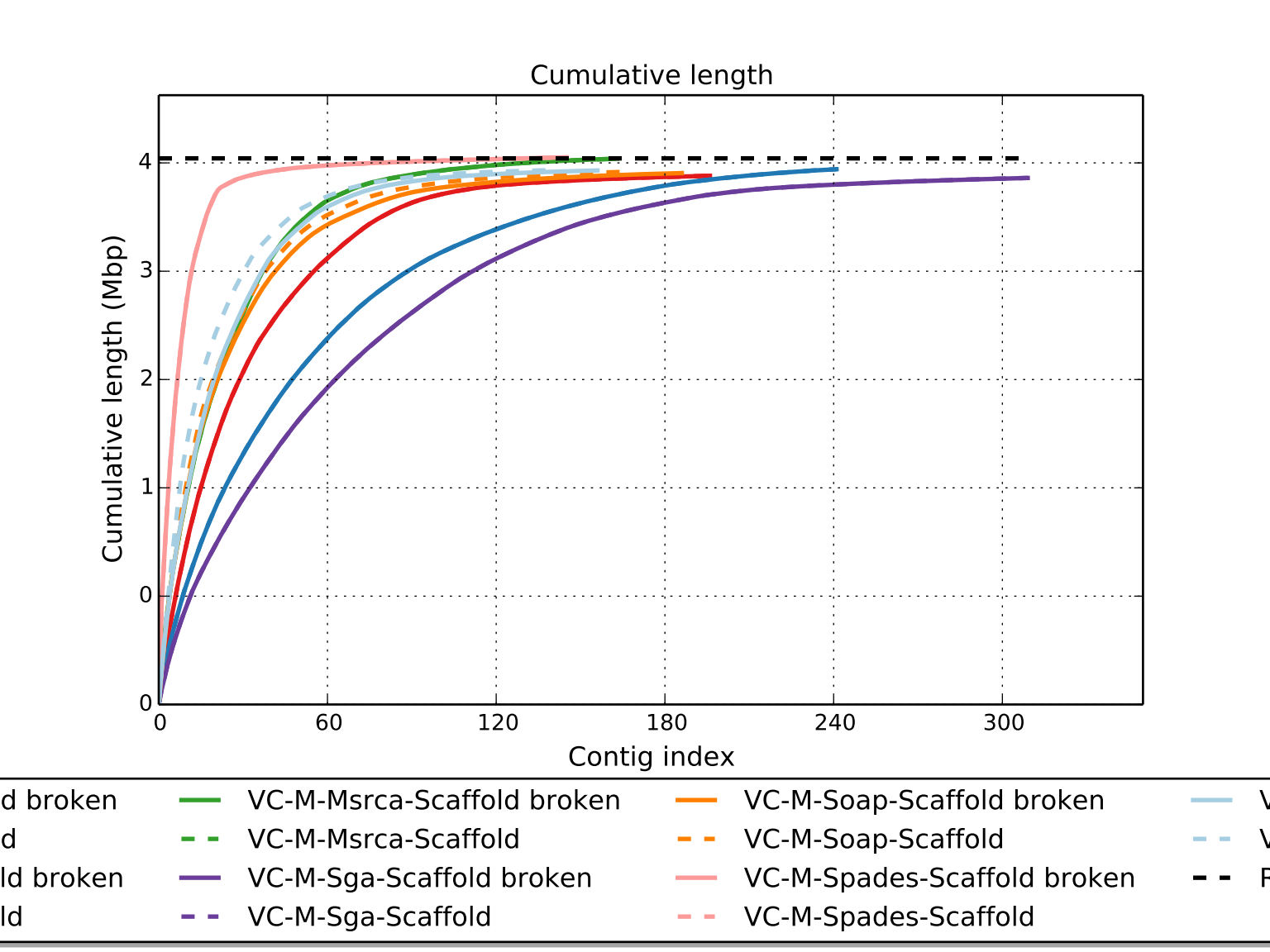

NGAx
Contig length (kbp)
600
500
400
300
200
100
0
0
20
40
60
80
100
x
ld broken
ld
old broken
old
VC-H-Msrca-Scaffold broken
VC-H-Msrca-Scaffold
VC-H-Sga-Scaffold broken
VC-H-Sga-Scaffold
VC-H-Soap-Scaffold broken
VC-H-Soap-Scaffold
VC-H-Spades-Scaffold broken
V
V
V

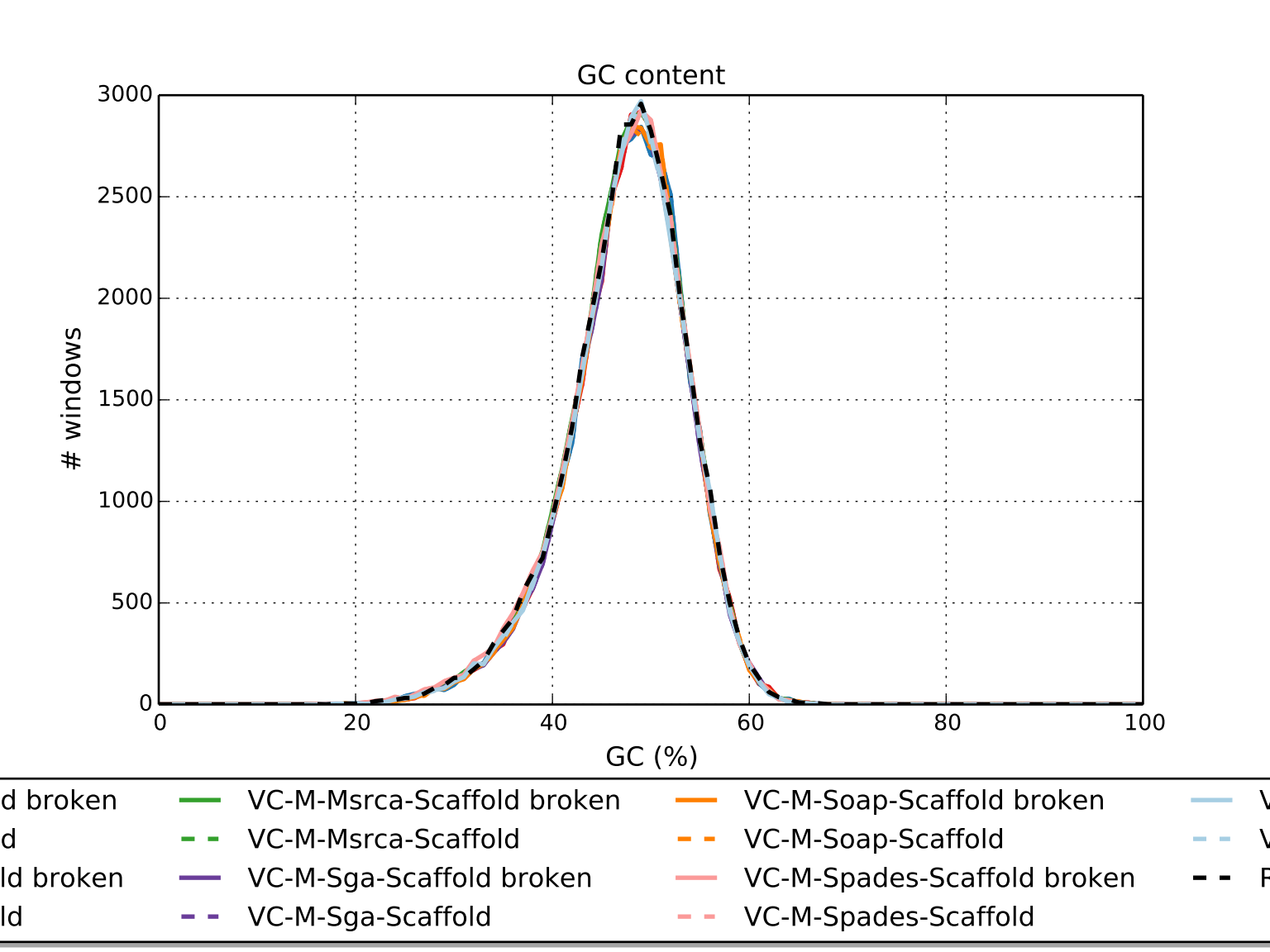

Cumulative # complete genes
Cumulative # complete genes
Contig index
0
800
1600
2400
3200
4000
0
60
120
180
240
300
ld broken
ld
old broken
old
VC-H-Msrca-Scaffold broken
VC-H-Msrca-Scaffold
VC-H-Sga-Scaffold broken
VC-H-Sga-Scaffold
VC-H-Soap-Scaffold broken
VC-H-Soap-Scaffold
VC-H-Spades-Scaffold broken
VC-H-Spades-Scaffold
V
V
R

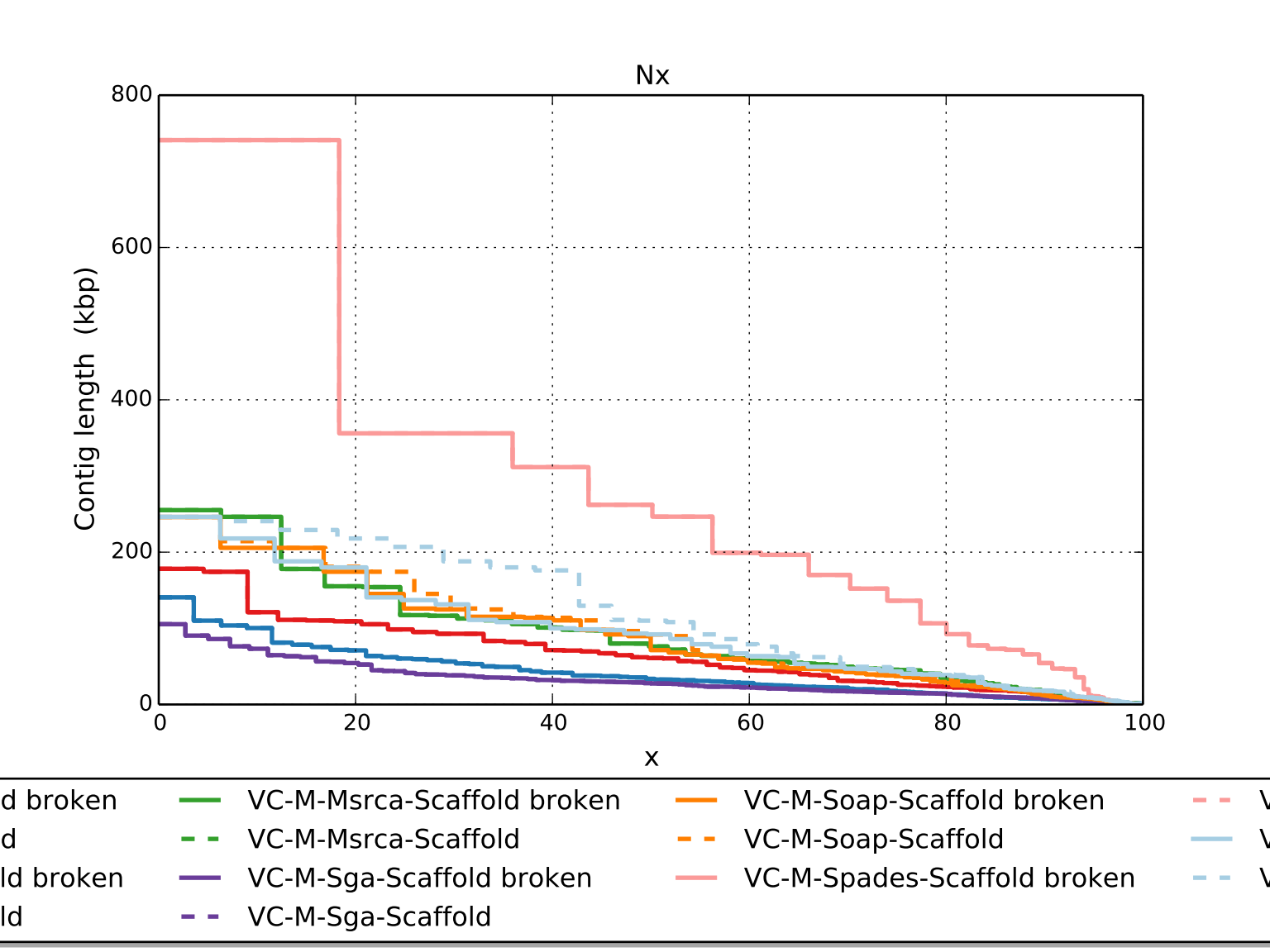

complete genes
3700
3600
3500
3400
3300
3200
3100
ld broken
ld
old broken
old
VC-H-Msrca-Scaffold broken
VC-H-Msrca-Scaffold
VC-H-Sga-Scaffold broken
VC-H-Sga-Scaffold
VC-H-Soap-Scaffold broken
VC-H-Soap-Scaffold
VC-H-Spades-Scaffold broken
V
V
V

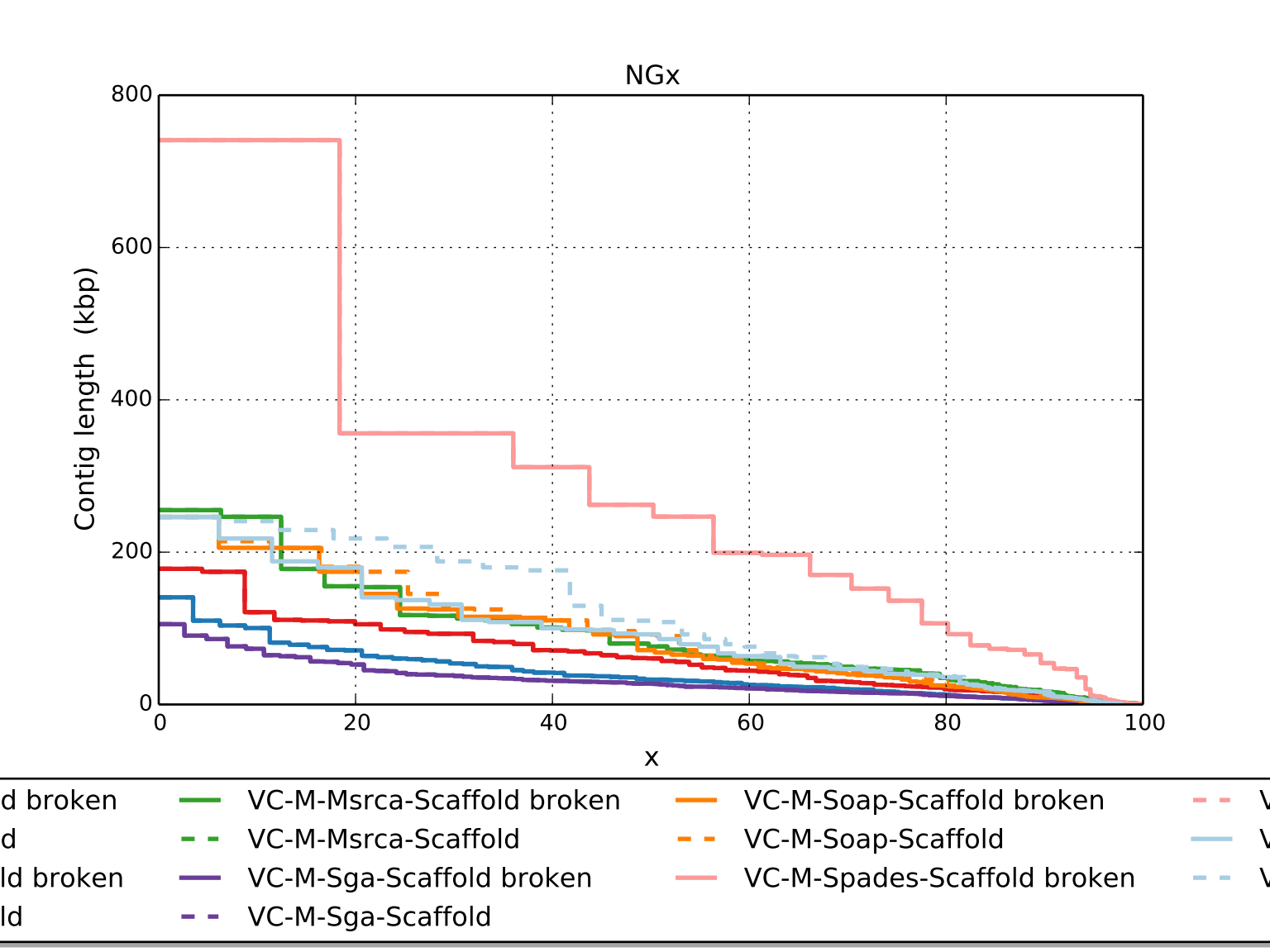

Genome fraction, %
100
99
98
97
96
95
94
ld broken
ld
old broken
old
VC-H-Msrca-Scaffold broken
VC-H-Msrca-Scaffold
VC-H-Sga-Scaffold broken
VC-H-Sga-Scaffold
VC-H-Soap-Scaffold broken
VC-H-Soap-Scaffold
VC-H-Spades-Scaffold broken
V
V
V

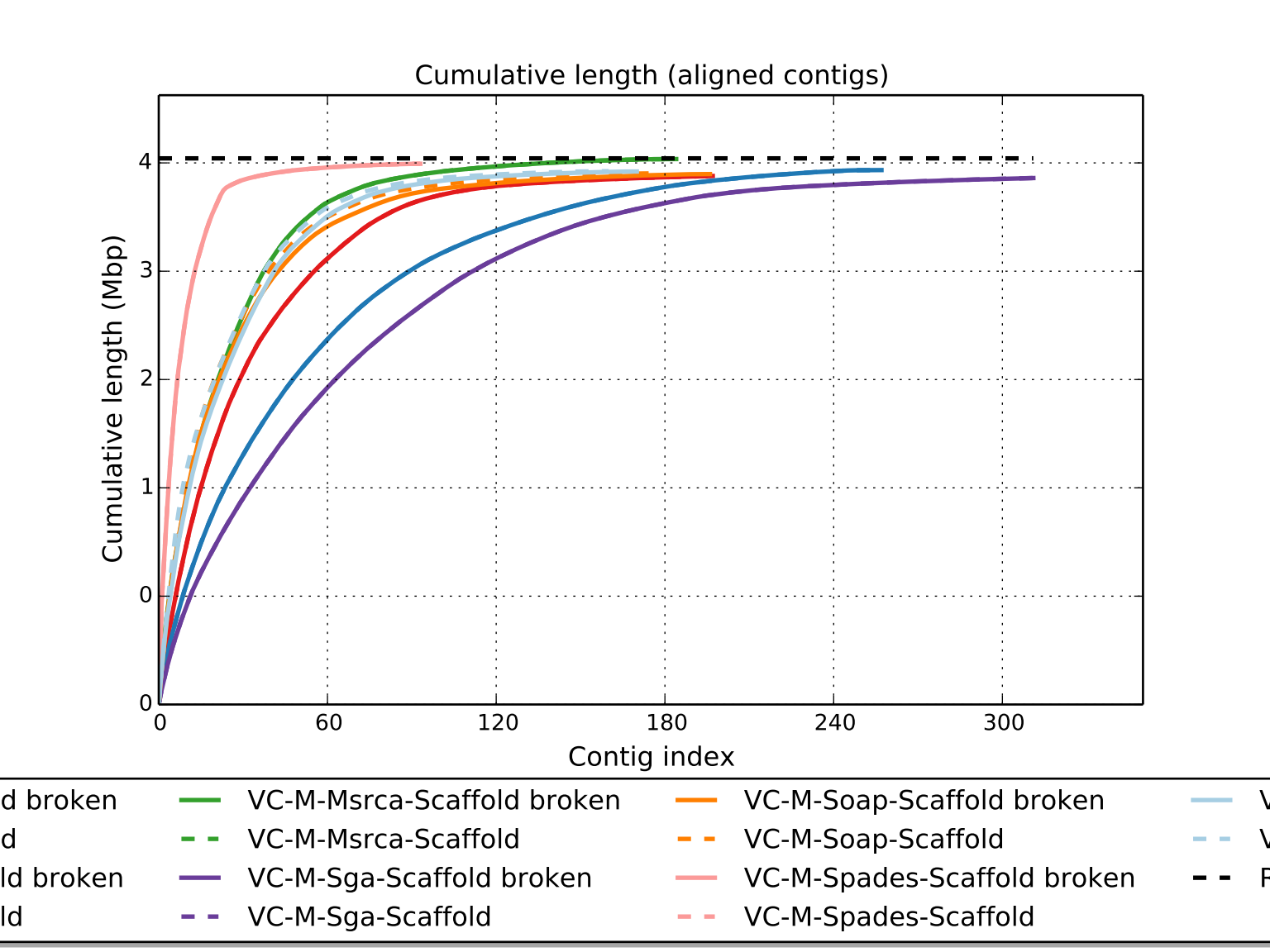
Scaffold

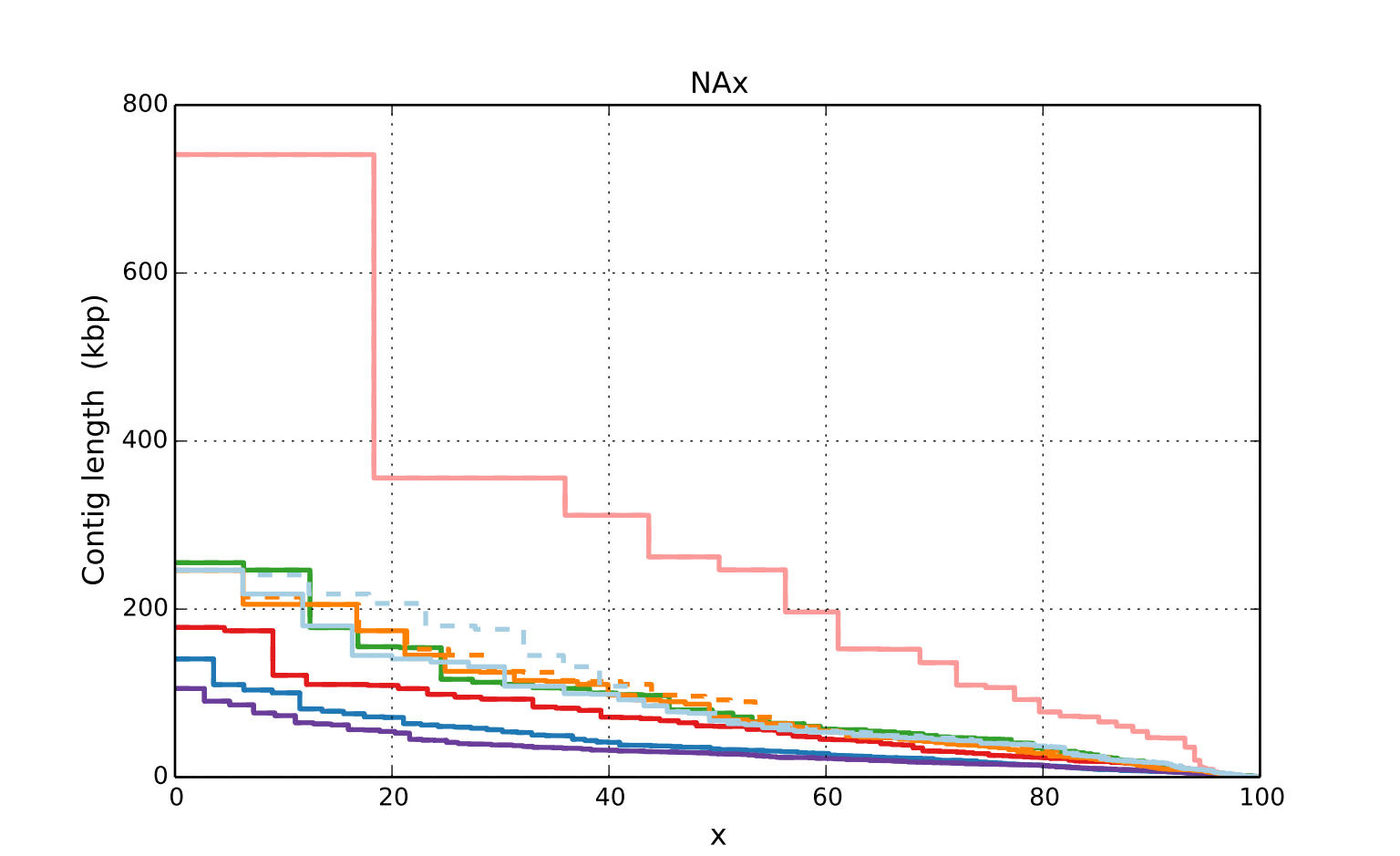

Cumulative length
Cumulative length (Mbp)
Contig index
0
1
2
3
4
0
60
120
180
240
300
d broken
d
ld broken
ld
VC-M-Msrca-Scaffold broken
VC-M-Msrca-Scaffold
VC-M-Sga-Scaffold broken
VC-M-Sga-Scaffold
VC-M-Soap-Scaffold broken
VC-M-Soap-Scaffold
VC-M-Spades-Scaffold broken
VC-M-Spades-Scaffold

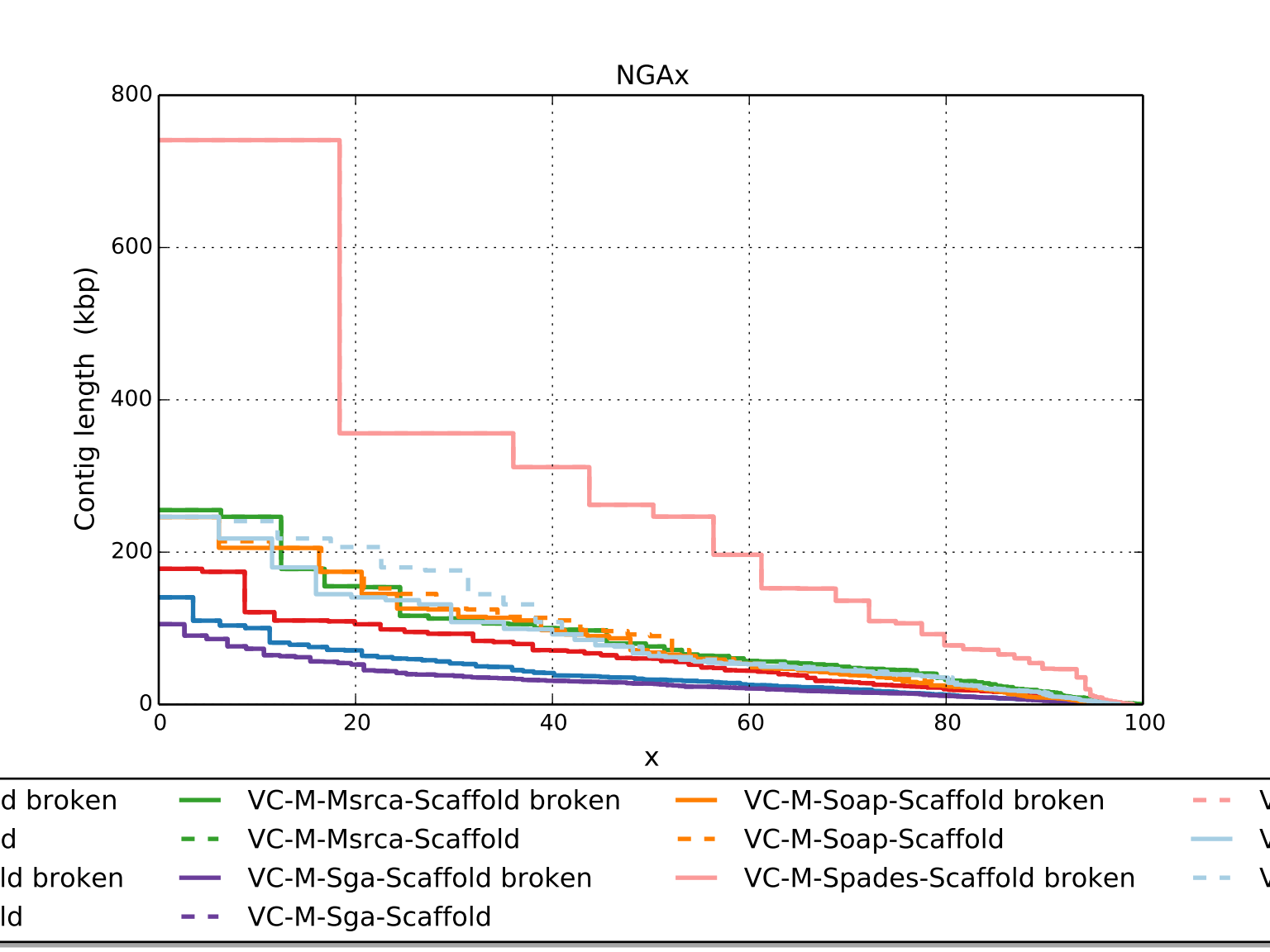

GC content
windows
GC (%)
0
500
1000
1500
2000
2500
3000
0
20
40
60
80
100
d broken
d
ld broken
ld
VC-M-Msrca-Scaffold broken
VC-M-Msrca-Scaffold
VC-M-Sga-Scaffold broken
VC-M-Sga-Scaffold
VC-M-Soap-Scaffold broken
VC-M-Soap-Scaffold
VC-M-Spades-Scaffold broken
VC-M-Spades-Scaffold

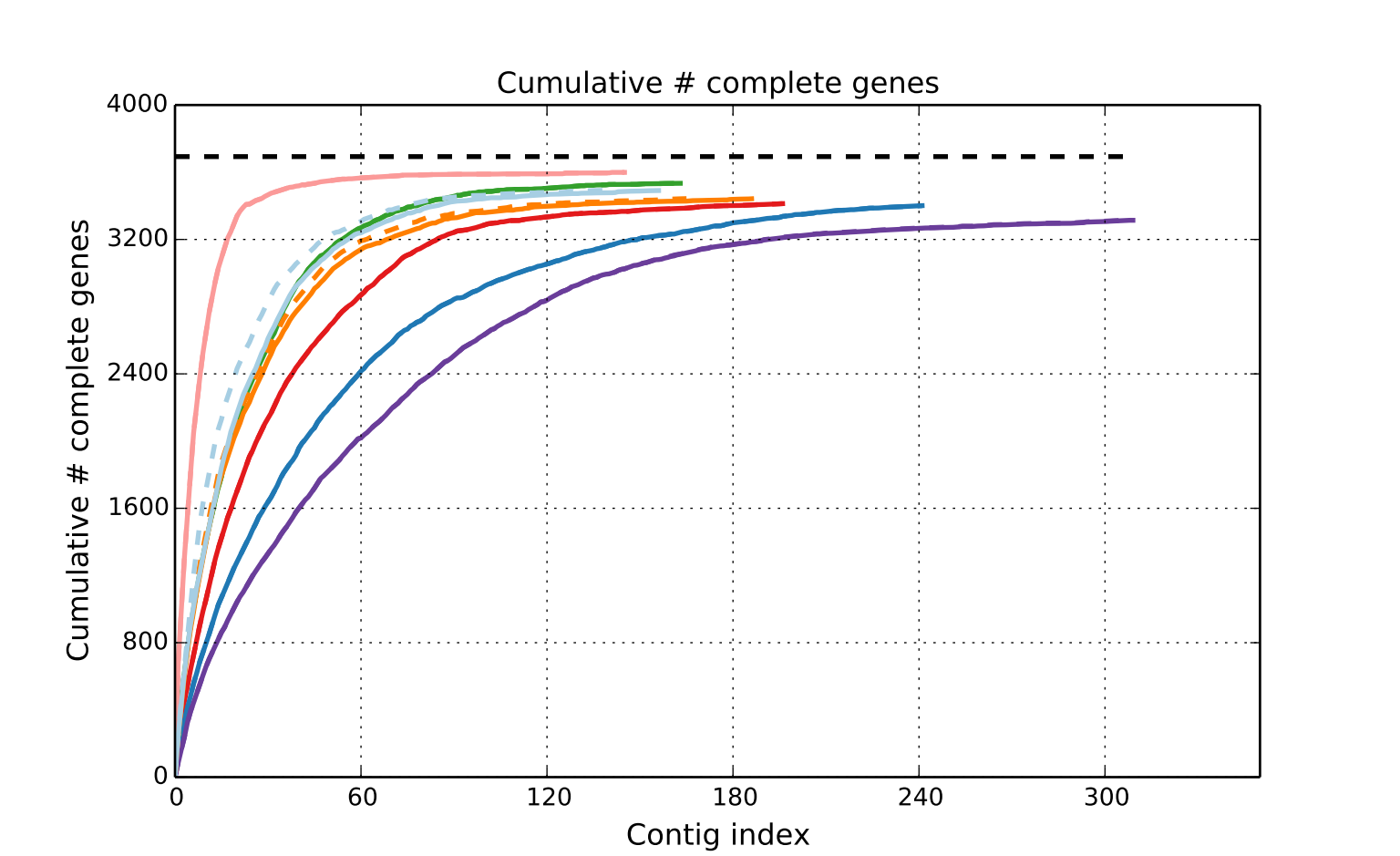

Nx
Contig length (kbp)
x
0
200
400
600
800
0
20
40
60
80
100
d broken
d
ld broken
ld
VC-M-Msrca-Scaffold broken
VC-M-Msrca-Scaffold
VC-M-Sga-Scaffold broken
VC-M-Sga-Scaffold
VC-M-Soap-Scaffold broken
VC-M-Soap-Scaffold
VC-M-Spades-Scaffold broken

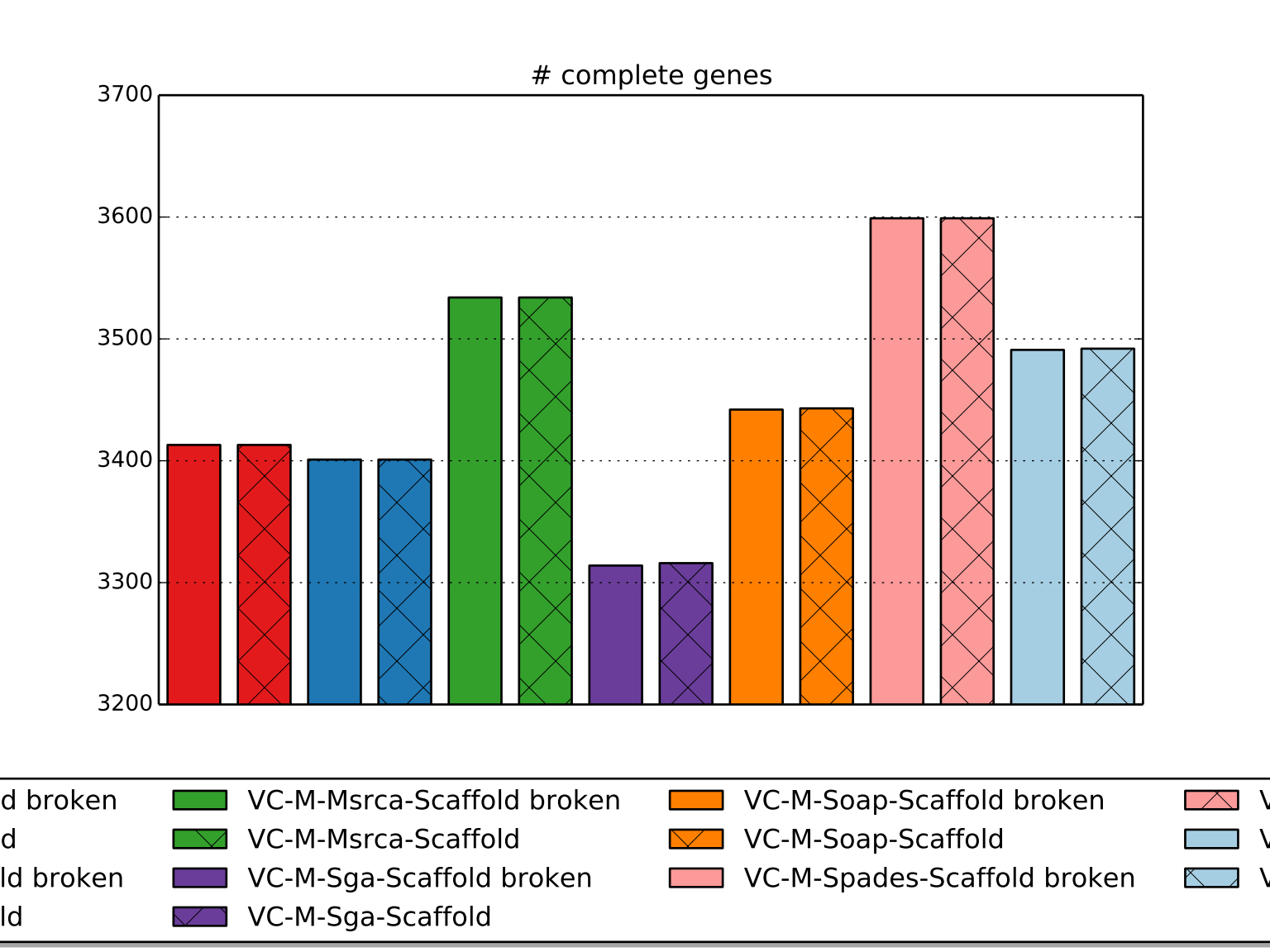

NGx
Contig length (kbp)
x
0
200
400
600
800
0
20
40
60
80
100
d broken
d
ld broken
ld
VC-M-Msrca-Scaffold broken
VC-M-Msrca-Scaffold
VC-M-Sga-Scaffold broken
VC-M-Sga-Scaffold
VC-M-Soap-Scaffold broken
VC-M-Soap-Scaffold
VC-M-Spades-Scaffold broken

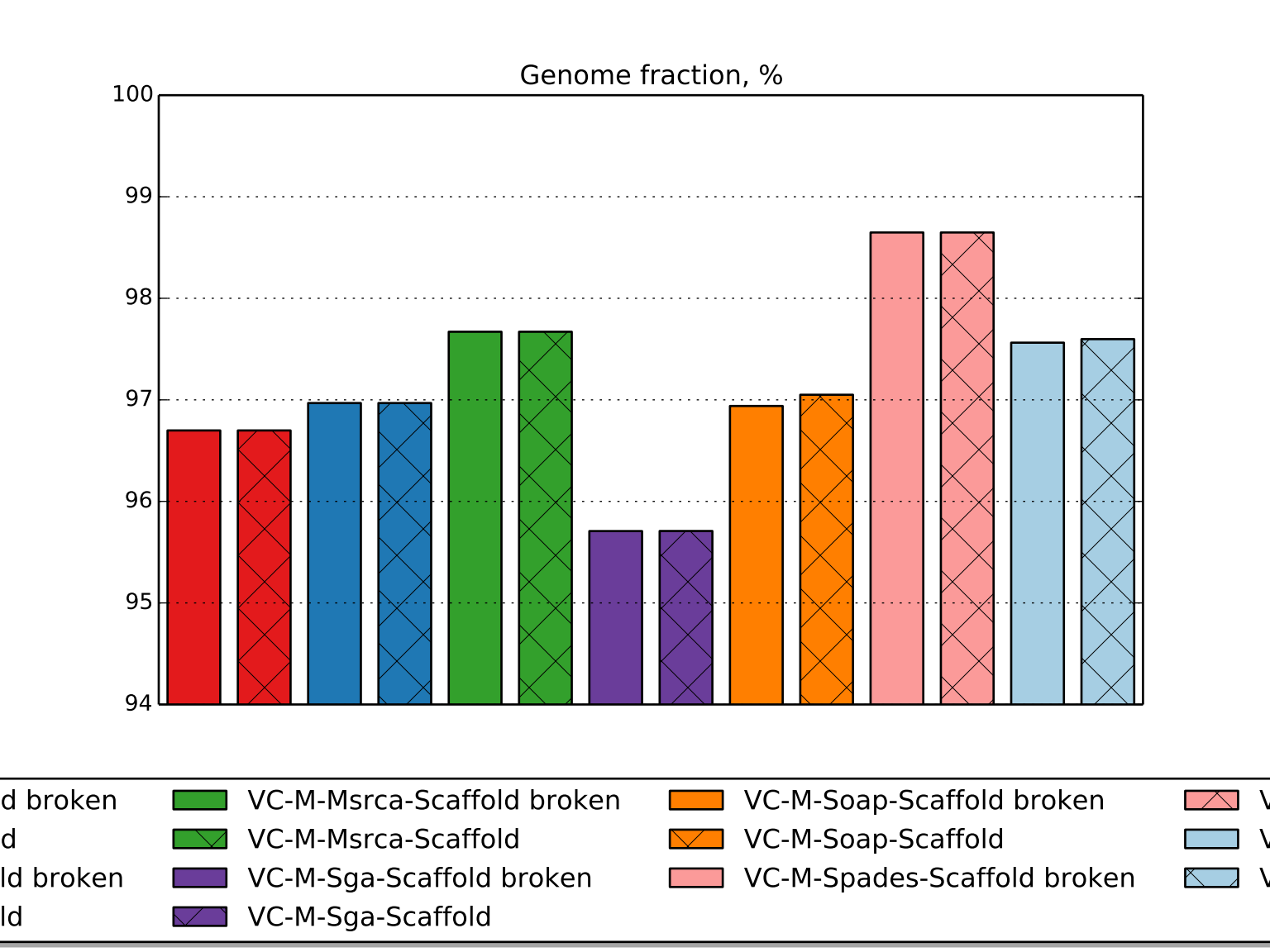

Cumulative length (aligned contigs)
Cumulative length (Mbp)
Contig index
0
1
2
3
4
0
60
120
180
240
300
d broken
d
ld broken
ld
VC-M-Msrca-Scaffold broken
VC-M-Msrca-Scaffold
VC-M-Sga-Scaffold broken
VC-M-Sga-Scaffold
VC-M-Soap-Scaffold broken
VC-M-Soap-Scaffold
VC-M-Spades-Scaffold broken
VC-M-Spades-Scaffold


NAx
Contig length (kbp)
x
0
200
400
600
800
0
20
40
60
80
100
d broken
d
ld broken
ld
VC-M-Msrca-Scaffold broken
VC-M-Msrca-Scaffold
VC-M-Sga-Scaffold broken
VC-M-Sga-Scaffold
VC-M-Soap-Scaffold broken
VC-M-Soap-Scaffold
VC-M-Spades-Scaffold broken

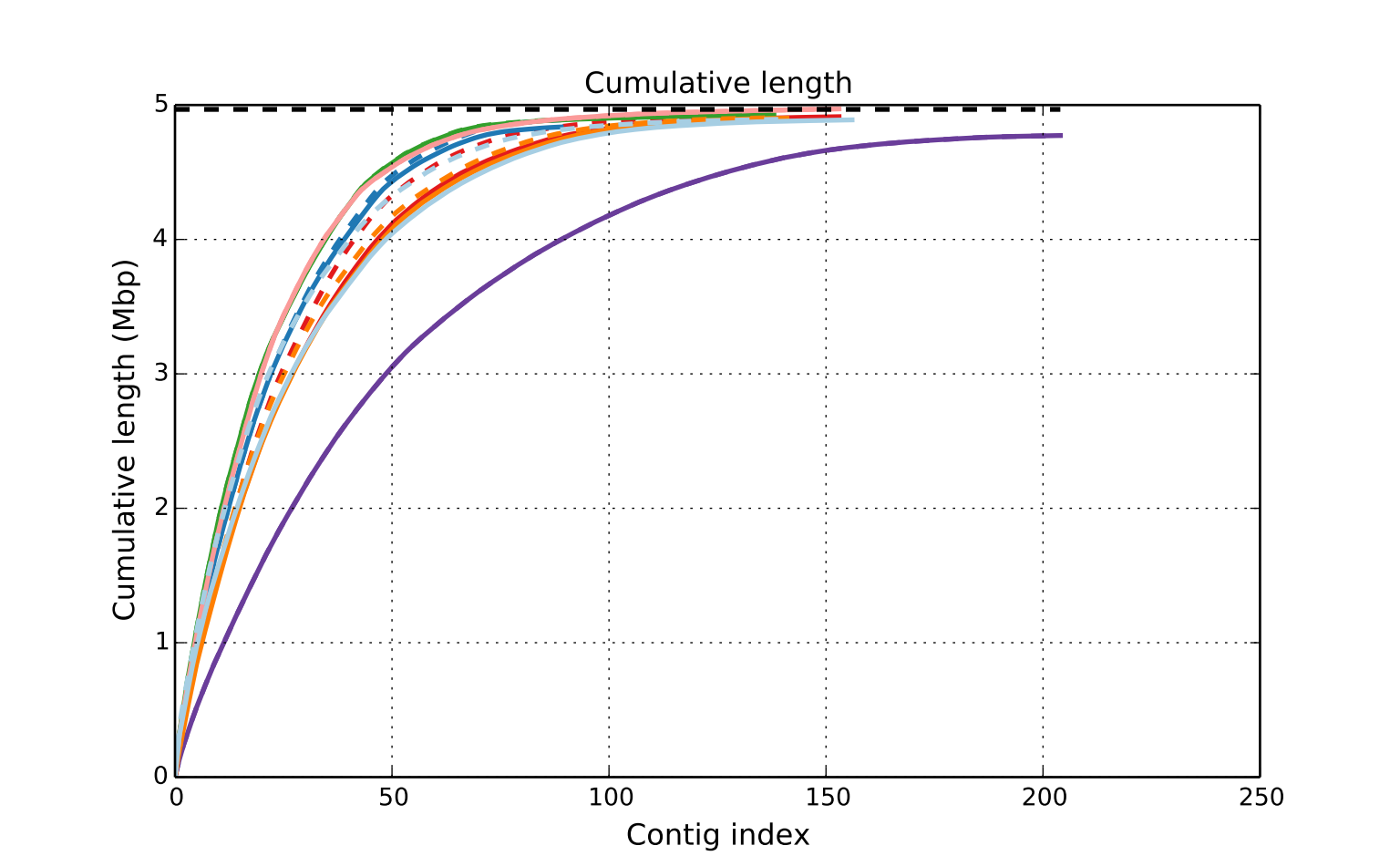

NGAx
Contig length (kbp)
x
0
200
400
600
800
0
20
40
60
80
100
d broken
d
ld broken
ld
VC-M-Msrca-Scaffold broken
VC-M-Msrca-Scaffold
VC-M-Sga-Scaffold broken
VC-M-Sga-Scaffold
VC-M-Soap-Scaffold broken
VC-M-Soap-Scaffold
VC-M-Spades-Scaffold broken

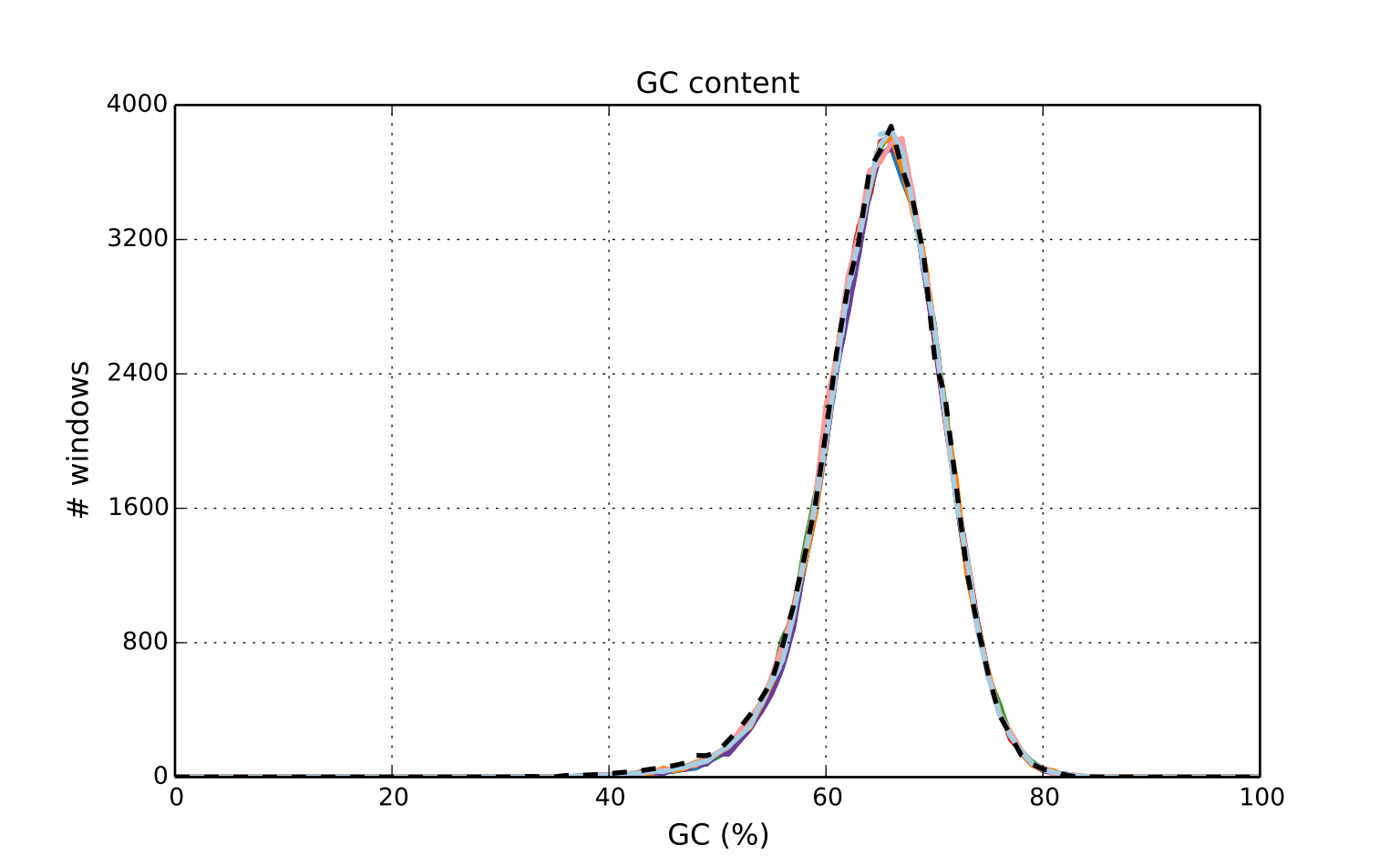

Cumulative # complete genes
Cumulative # complete genes
Contig index
0
800
1600
2400
3200
4000
0
60
120
180
240
300
d broken
d
ld broken
ld
VC-M-Msrca-Scaffold broken
VC-M-Msrca-Scaffold
VC-M-Sga-Scaffold broken
VC-M-Sga-Scaffold
VC-M-Soap-Scaffold broken
VC-M-Soap-Scaffold
VC-M-Spades-Scaffold broken
VC-M-Spades-Scaffold

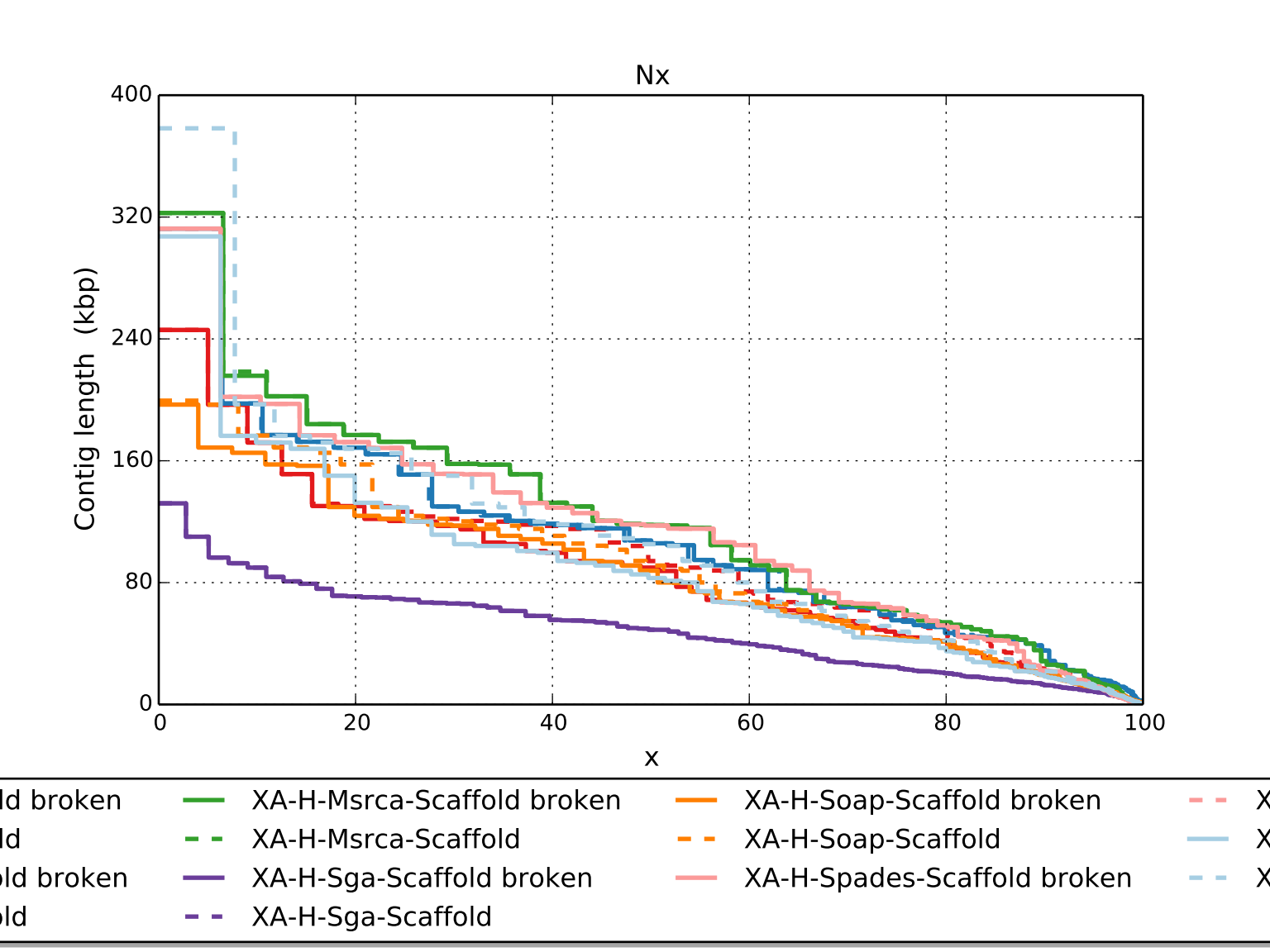

complete genes
3700
3600
3500
3400
3300
3200
d broken
d
ld broken
ld
VC-M-Msrca-Scaffold broken
VC-M-Msrca-Scaffold
VC-M-Sga-Scaffold broken
VC-M-Sga-Scaffold
VC-M-Soap-Scaffold broken
VC-M-Soap-Scaffold
VC-M-Spades-Scaffold broken

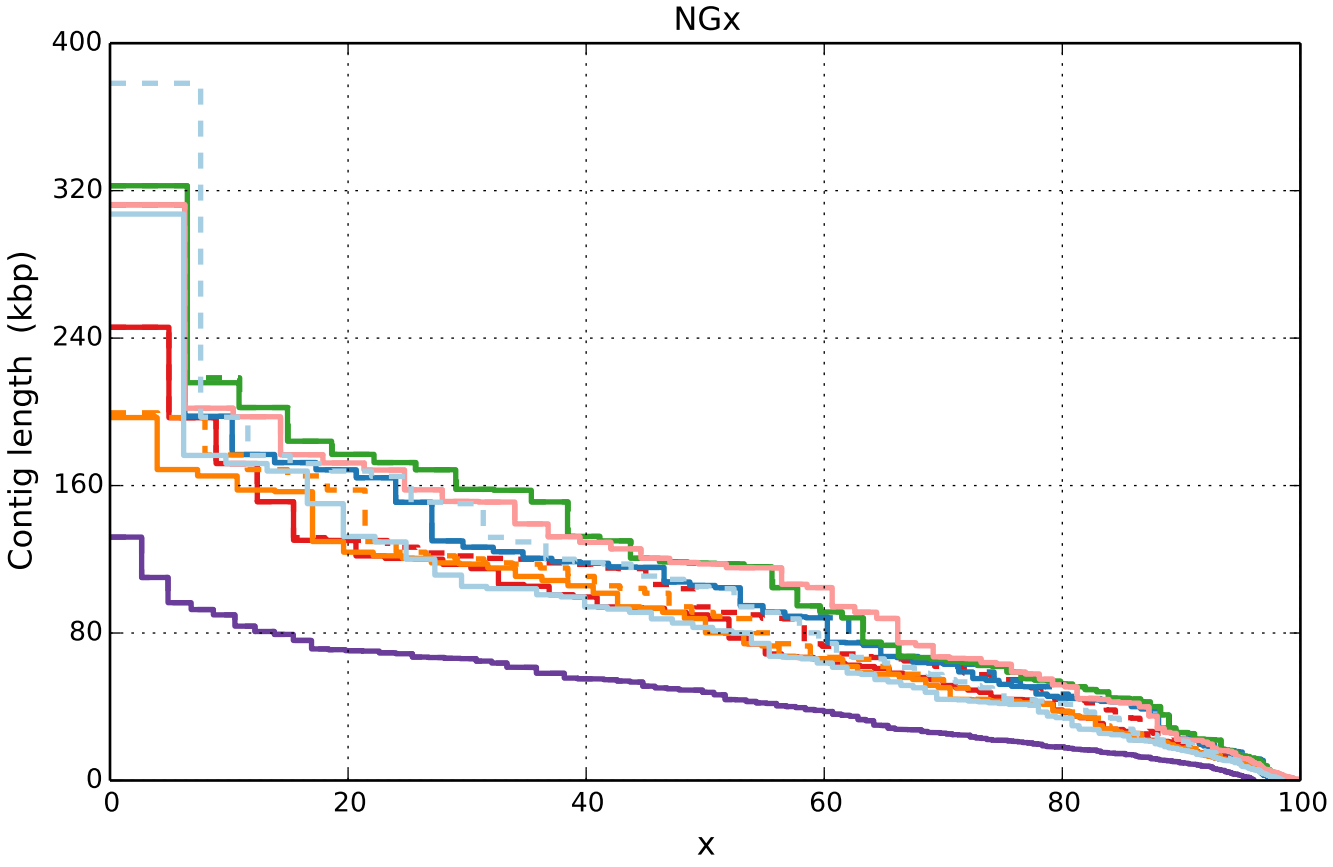

Genome fraction, %
100
99
98
97
96
95
94
d broken
d
ld broken
ld
VC-M-Msrca-Scaffold broken
VC-M-Msrca-Scaffold
VC-M-Sga-Scaffold broken
VC-M-Sga-Scaffold
VC-M-Soap-Scaffold broken
VC-M-Soap-Scaffold
VC-M-Spades-Scaffold broken
V
V
V

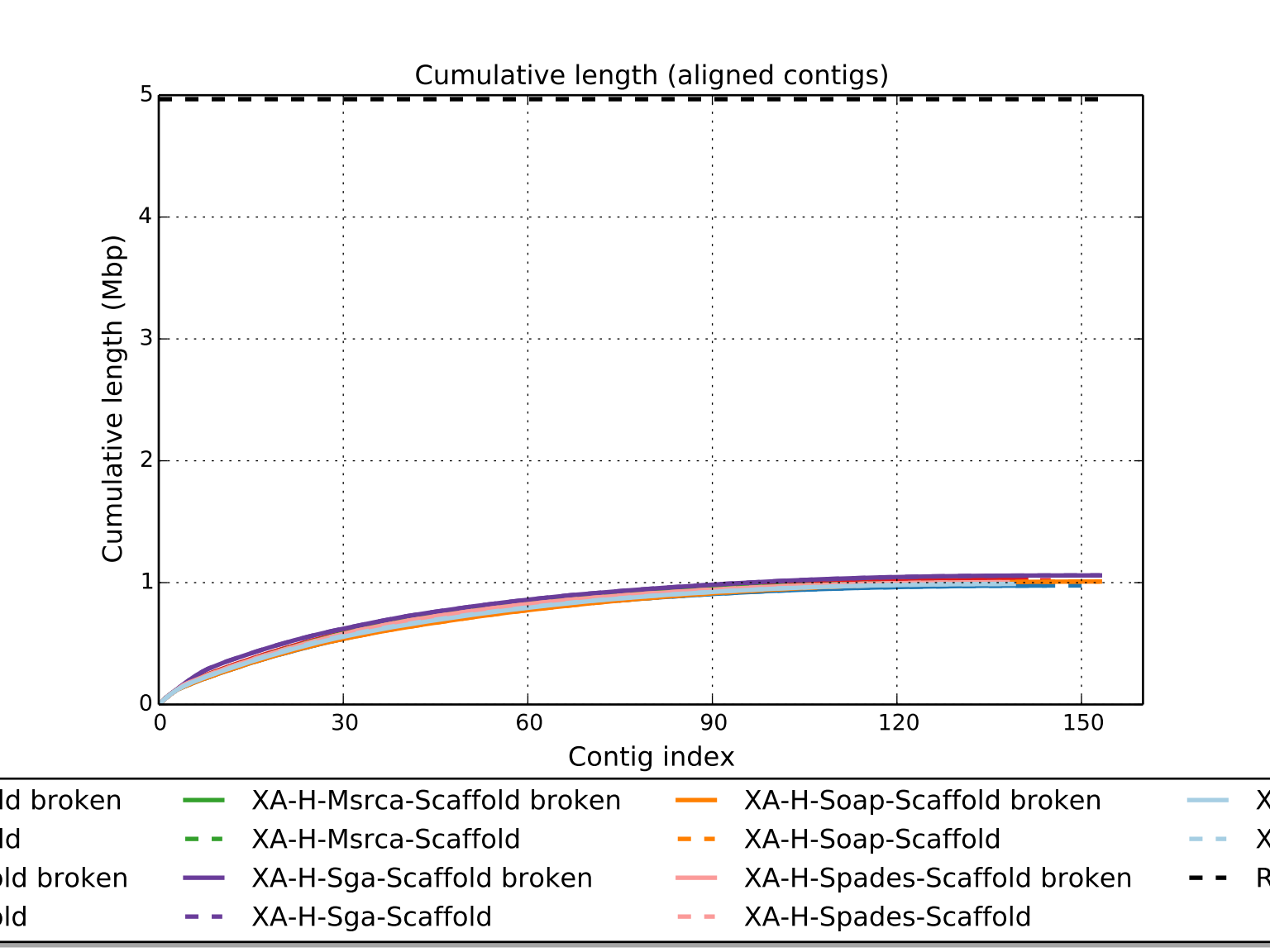
Scaffold

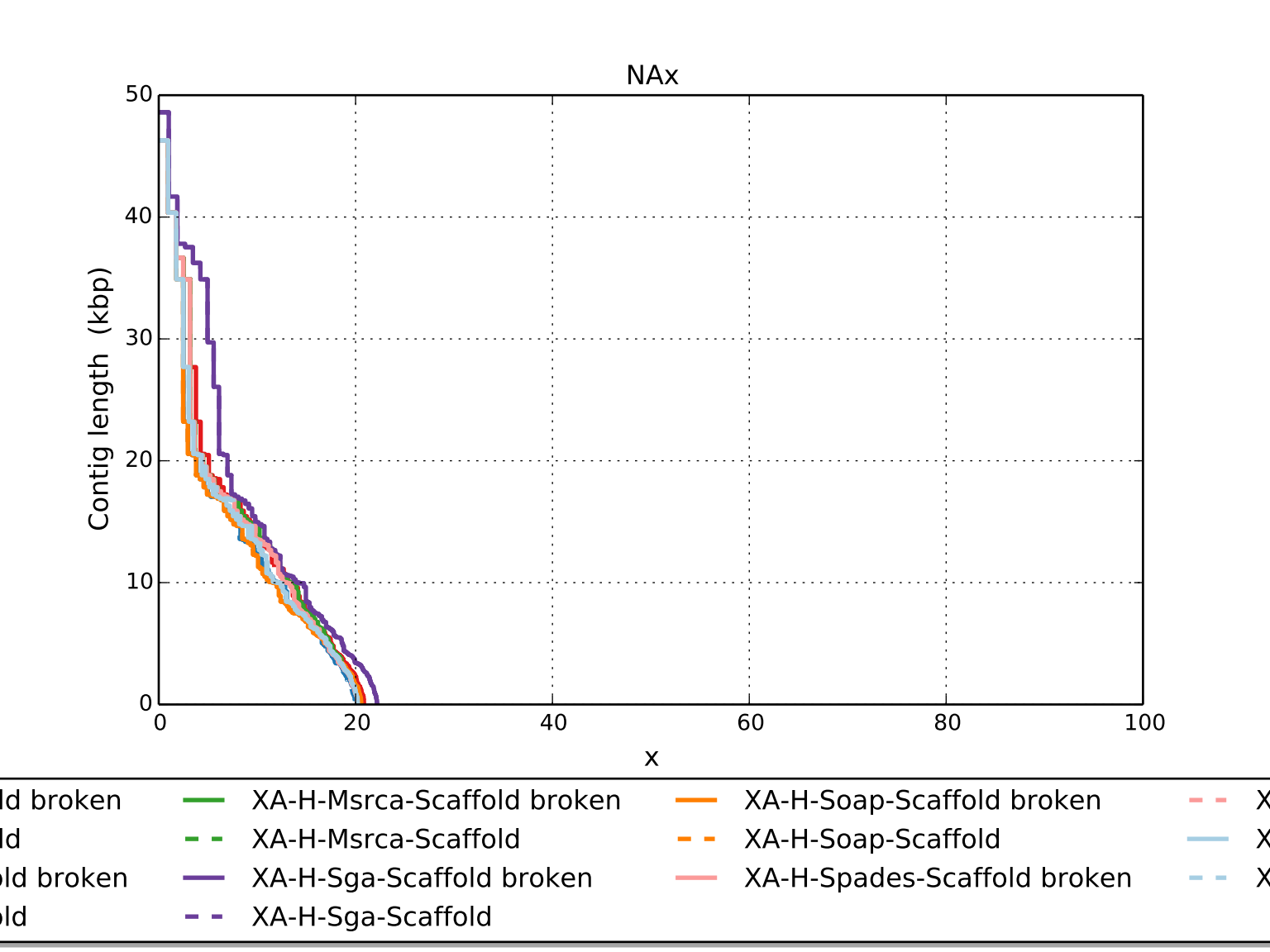

Cumulative length
Cumulative length (Mbp)
Contig index
0
1
2
3
4
5
0
50
100
150
200
250
ld broken
ld
old broken
old
XA-H-Msrca-Scaffold broken
XA-H-Msrca-Scaffold
XA-H-Sga-Scaffold broken
XA-H-Sga-Scaffold
XA-H-Soap-Scaffold broken
XA-H-Soap-Scaffold
XA-H-Spades-Scaffold broken
XA-H-Spades-Scaffold
X
X
R

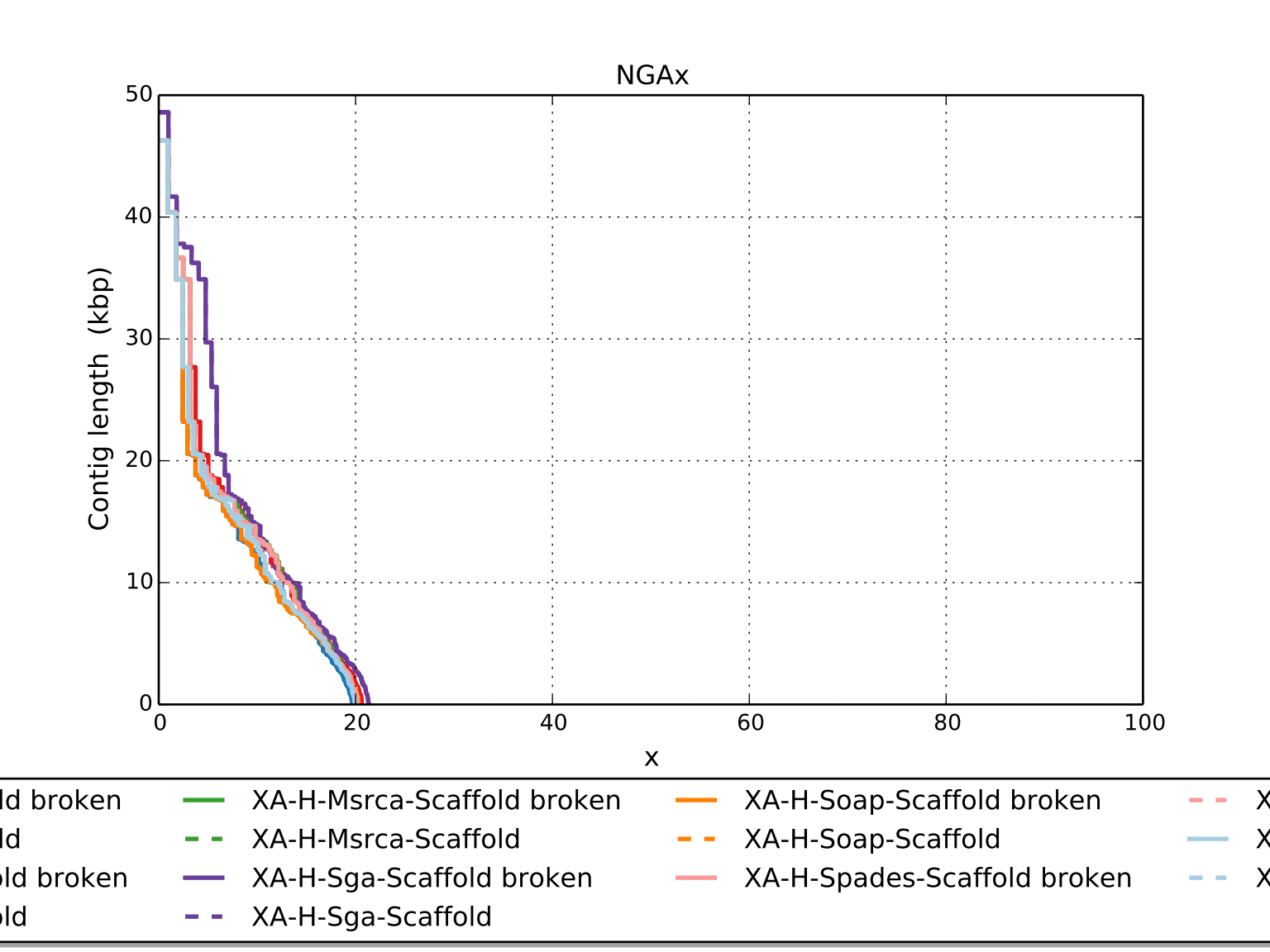

GC content
windows
GC (%)
0
800
1600
2400
3200
4000
0
20
40
60
80
100
ld broken
ld
old broken
old
XA-H-Msrca-Scaffold broken
XA-H-Msrca-Scaffold
XA-H-Sga-Scaffold broken
XA-H-Sga-Scaffold
XA-H-Soap-Scaffold broken
XA-H-Soap-Scaffold
XA-H-Spades-Scaffold broken
XA-H-Spades-Scaffold
X
X
R

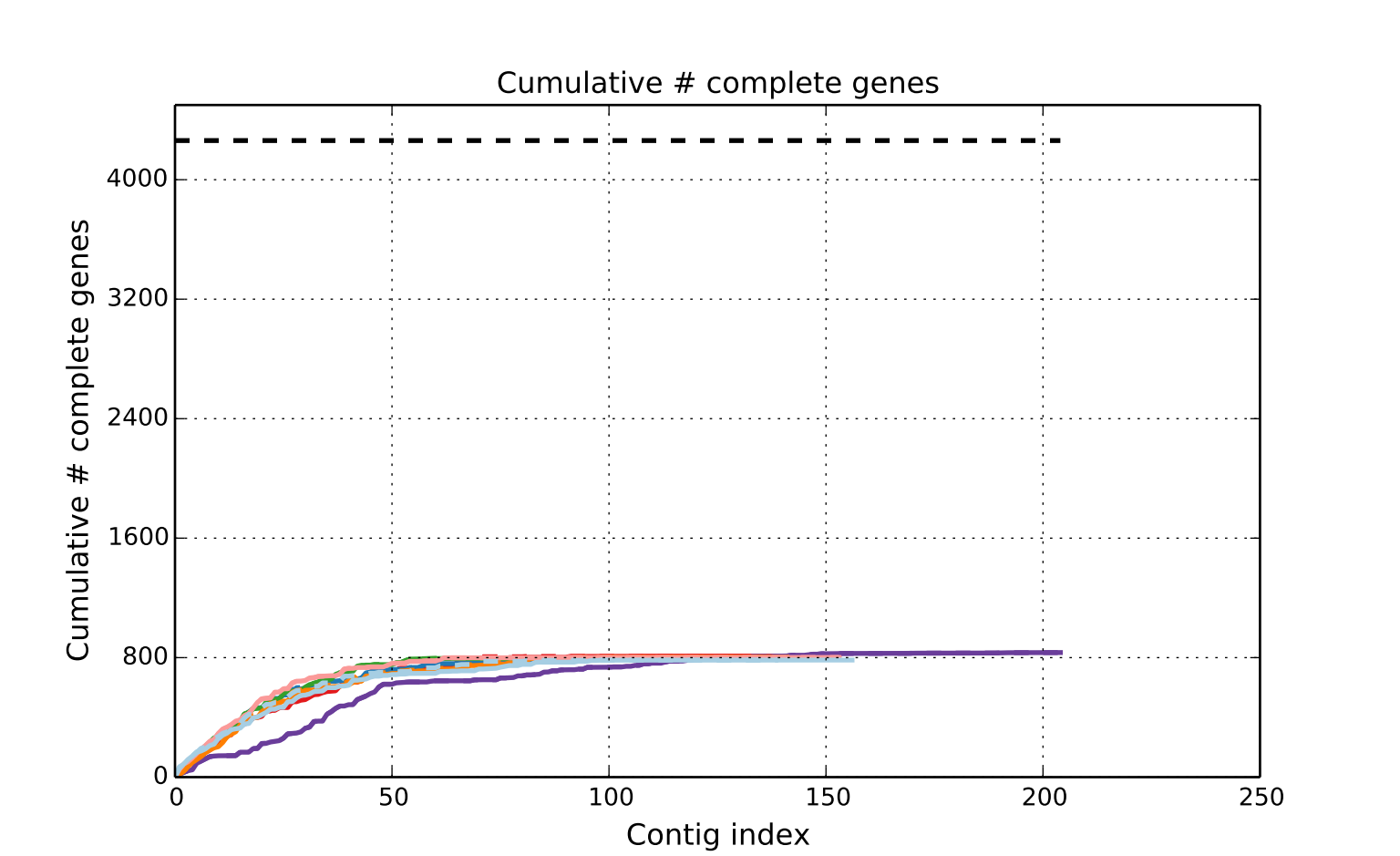

Nx
Contig length (kbp)
x
0
80
160
240
320
400
0
20
40
60
80
100
ld broken
ld
old broken
old
XA-H-Msrca-Scaffold broken
XA-H-Msrca-Scaffold
XA-H-Sga-Scaffold broken
XA-H-Sga-Scaffold
XA-H-Soap-Scaffold broken
XA-H-Soap-Scaffold
XA-H-Spades-Scaffold broken
X
X
X

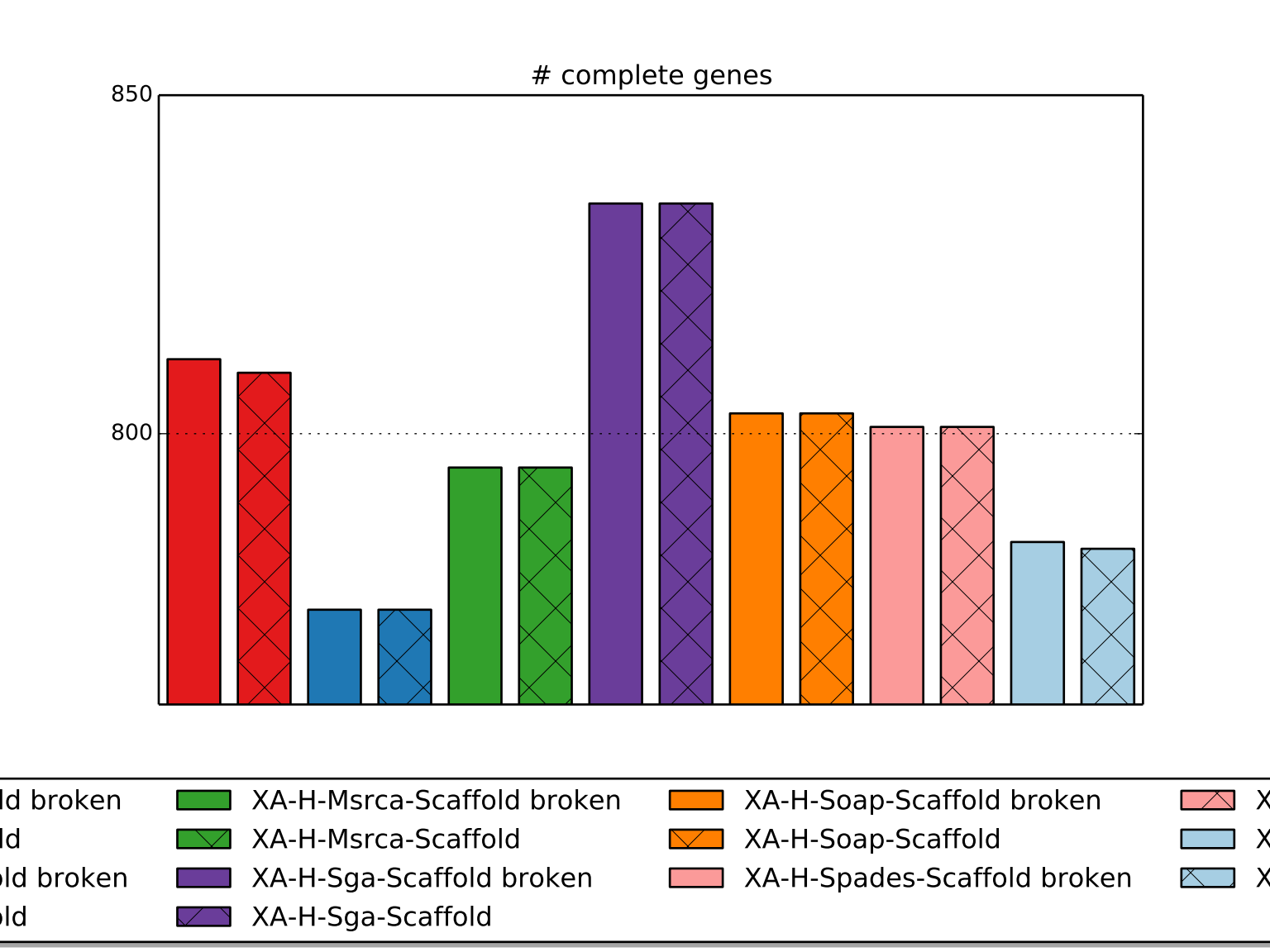

NGx
Contig length (kbp)
400
320
240
160
80
0
0
20
40
60
80
100
x
ld broken
ld
old broken
old
XA-H-Msrca-Scaffold broken
XA-H-Msrca-Scaffold
XA-H-Sga-Scaffold broken
XA-H-Sga-Scaffold
XA-H-Soap-Scaffold broken
XA-H-Soap-Scaffold
XA-H-Spades-Scaffold broken
X
X
X

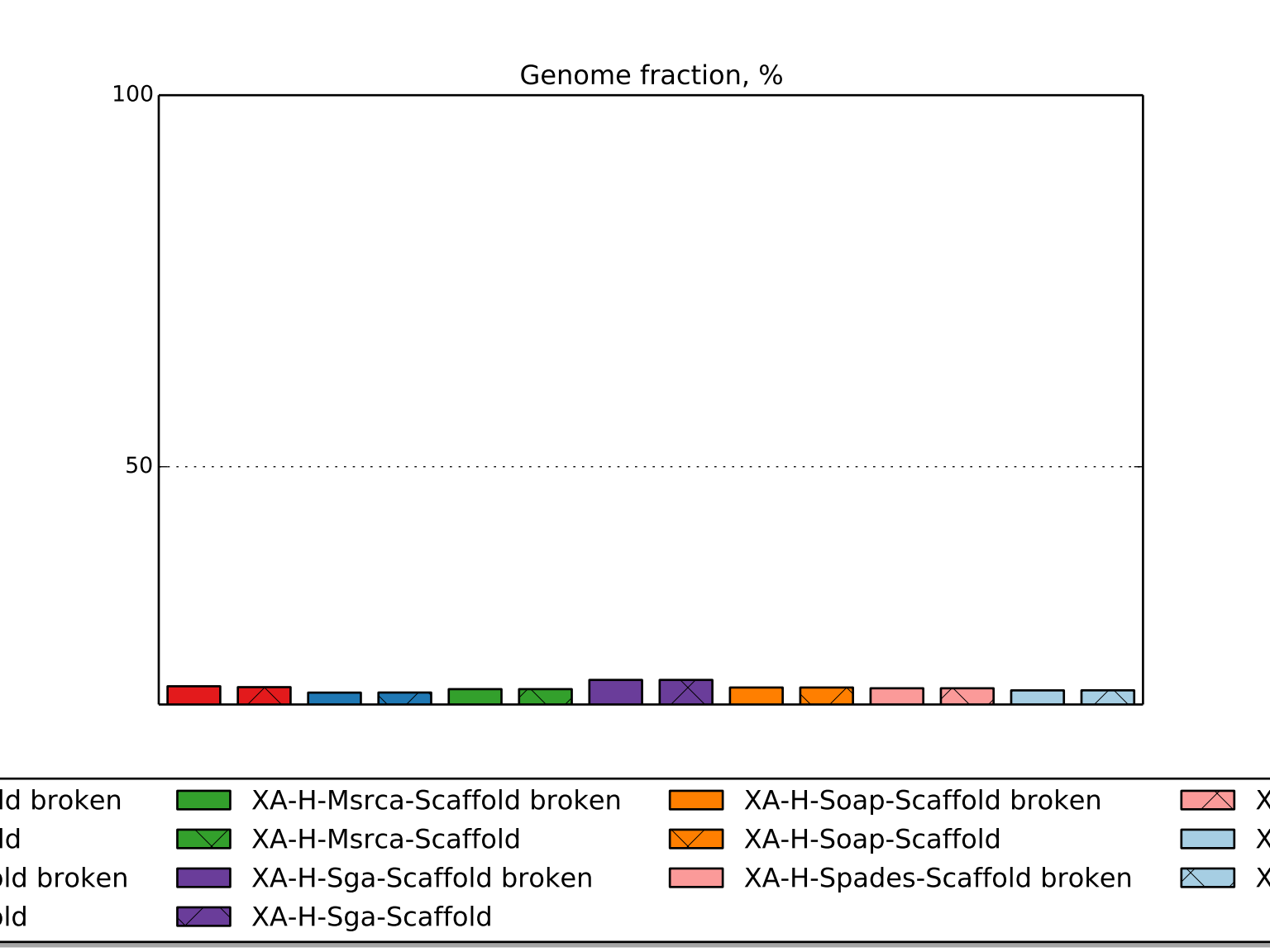

Cumulative length (aligned contigs)
Cumulative length (Mbp)
Contig index
0
1
2
3
4
5
0
30
60
90
120
150
ld broken
ld
old broken
old
XA-H-Msrca-Scaffold broken
XA-H-Msrca-Scaffold
XA-H-Sga-Scaffold broken
XA-H-Sga-Scaffold
XA-H-Soap-Scaffold broken
XA-H-Soap-Scaffold
XA-H-Spades-Scaffold broken
XA-H-Spades-Scaffold
X
X
R


NAx
Contig length (kbp)
x
0
10
20
30
40
50
0
20
40
60
80
100
ld broken
ld
old broken
old
XA-H-Msrca-Scaffold broken
XA-H-Msrca-Scaffold
XA-H-Sga-Scaffold broken
XA-H-Sga-Scaffold
XA-H-Soap-Scaffold broken
XA-H-Soap-Scaffold
XA-H-Spades-Scaffold broken
X
X
X


NGAx
Contig length (kbp)
x
0
10
20
30
40
50
0
20
40
60
80
100
ld broken
ld
old broken
old
XA-H-Msrca-Scaffold broken
XA-H-Msrca-Scaffold
XA-H-Sga-Scaffold broken
XA-H-Sga-Scaffold
XA-H-Soap-Scaffold broken
XA-H-Soap-Scaffold
XA-H-Spades-Scaffold broken
X
X
X


Cumulative # complete genes
Cumulative # complete genes
4000
3200
2400
1600
800
0
0
50
100
150
200
250
Contig index
ld broken
ld
old broken
old
XA-H-Msrca-Scaffold broken
XA-H-Msrca-Scaffold
XA-H-Sga-Scaffold broken
XA-H-Sga-Scaffold
XA-H-Soap-Scaffold broken
XA-H-Soap-Scaffold
XA-H-Spades-Scaffold broken
XA-H-Spades-Scaffold
X
X
R


complete genes
850
800
ld broken
ld
old broken
old
XA-H-Msrca-Scaffold broken
XA-H-Msrca-Scaffold
XA-H-Sga-Scaffold broken
XA-H-Sga-Scaffold
XA-H-Soap-Scaffold broken
XA-H-Soap-Scaffold
XA-H-Spades-Scaffold broken


Genome fraction, %
100
50
ld broken
ld
old broken
old
XA-H-Msrca-Scaffold broken
XA-H-Msrca-Scaffold
XA-H-Sga-Scaffold broken
XA-H-Sga-Scaffold
XA-H-Soap-Scaffold broken
XA-H-Soap-Scaffold
XA-H-Spades-Scaffold broken