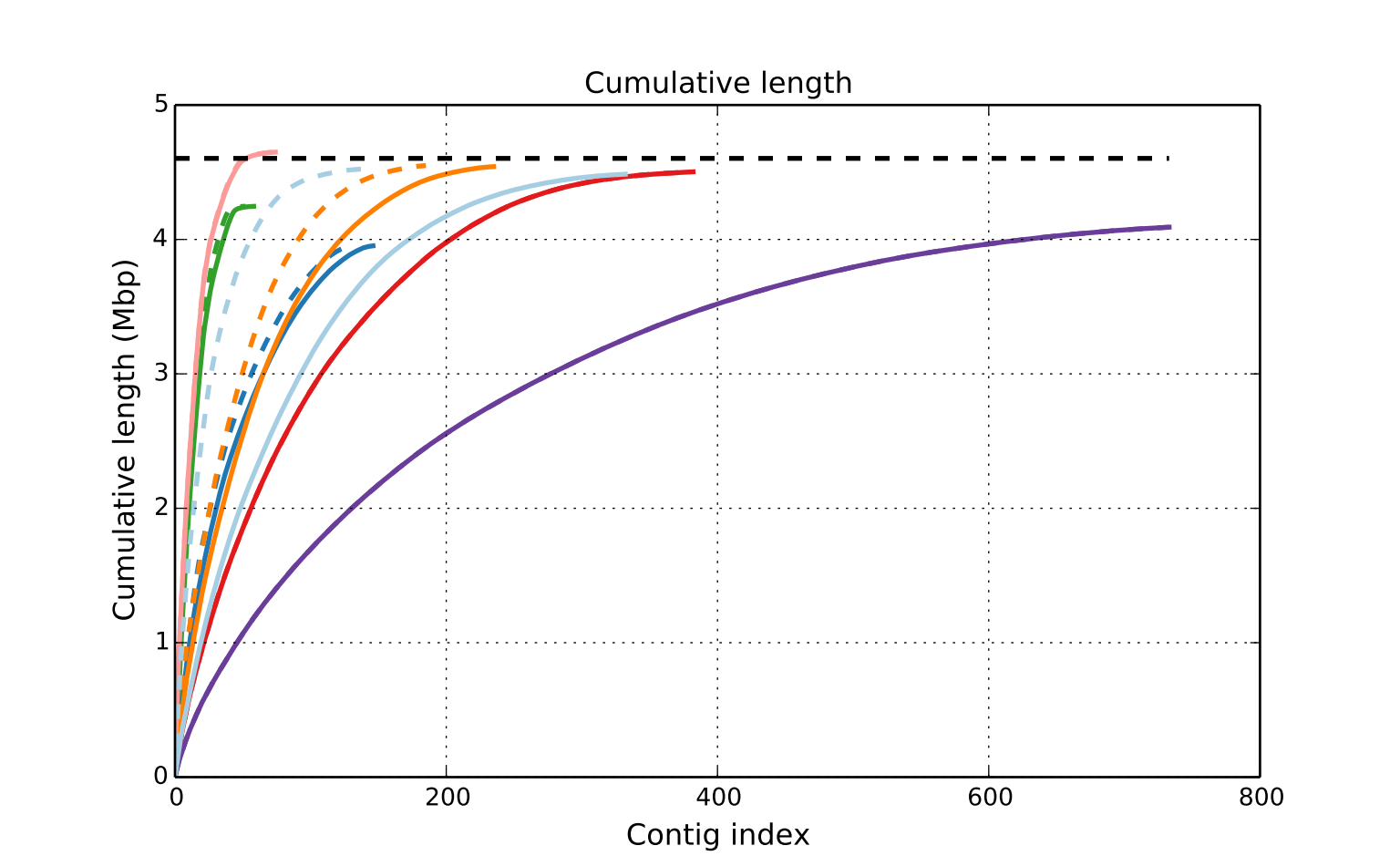
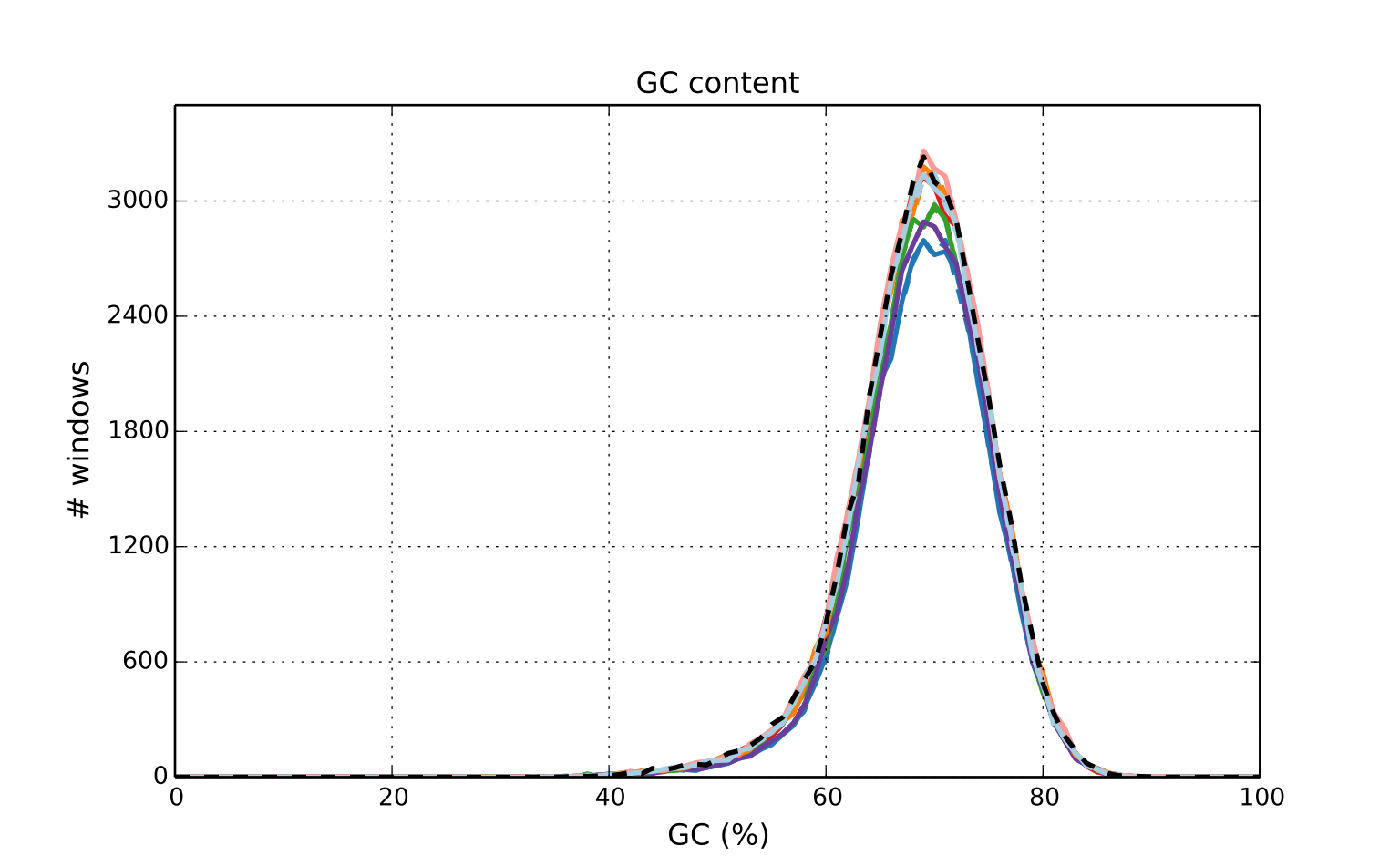
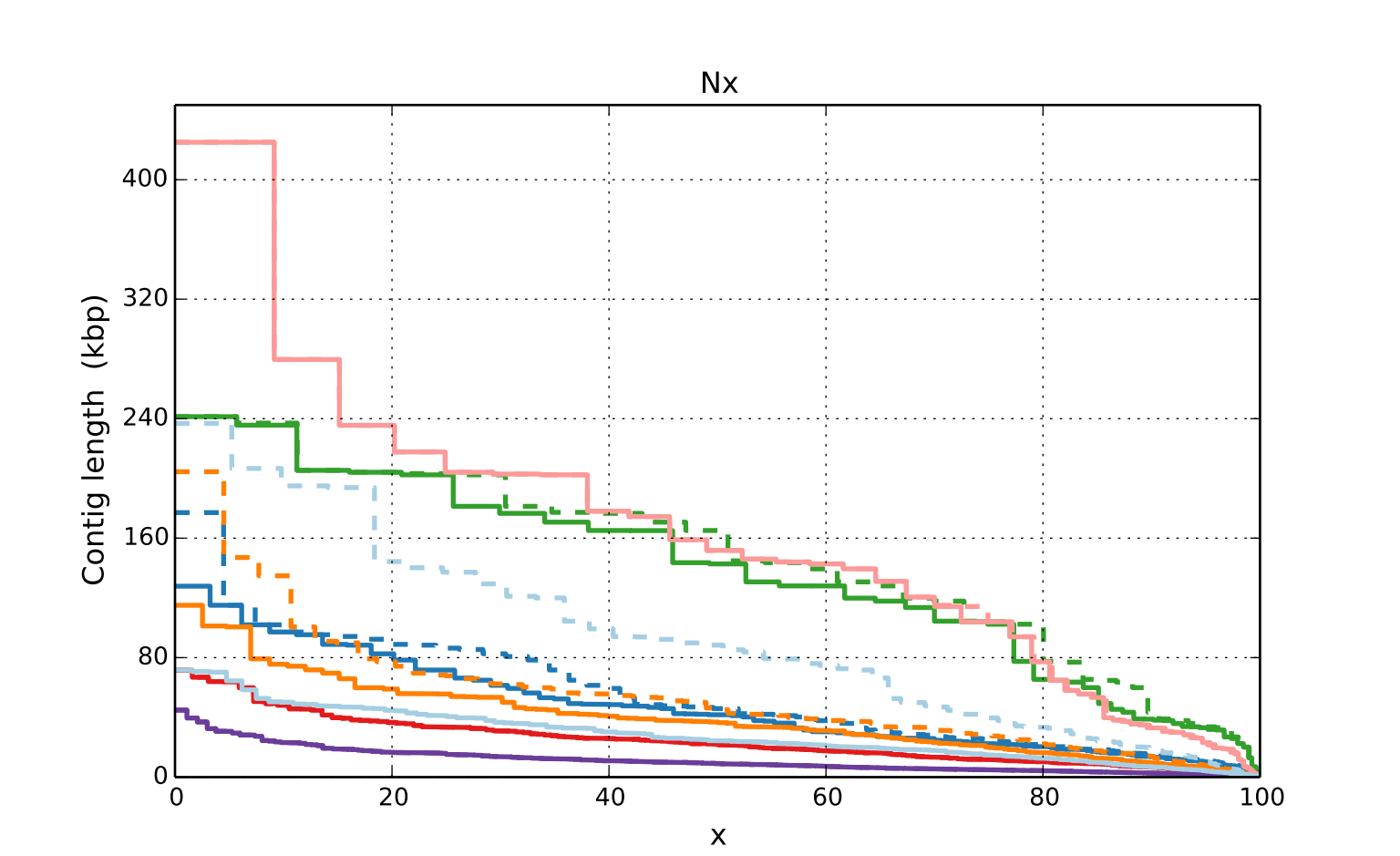
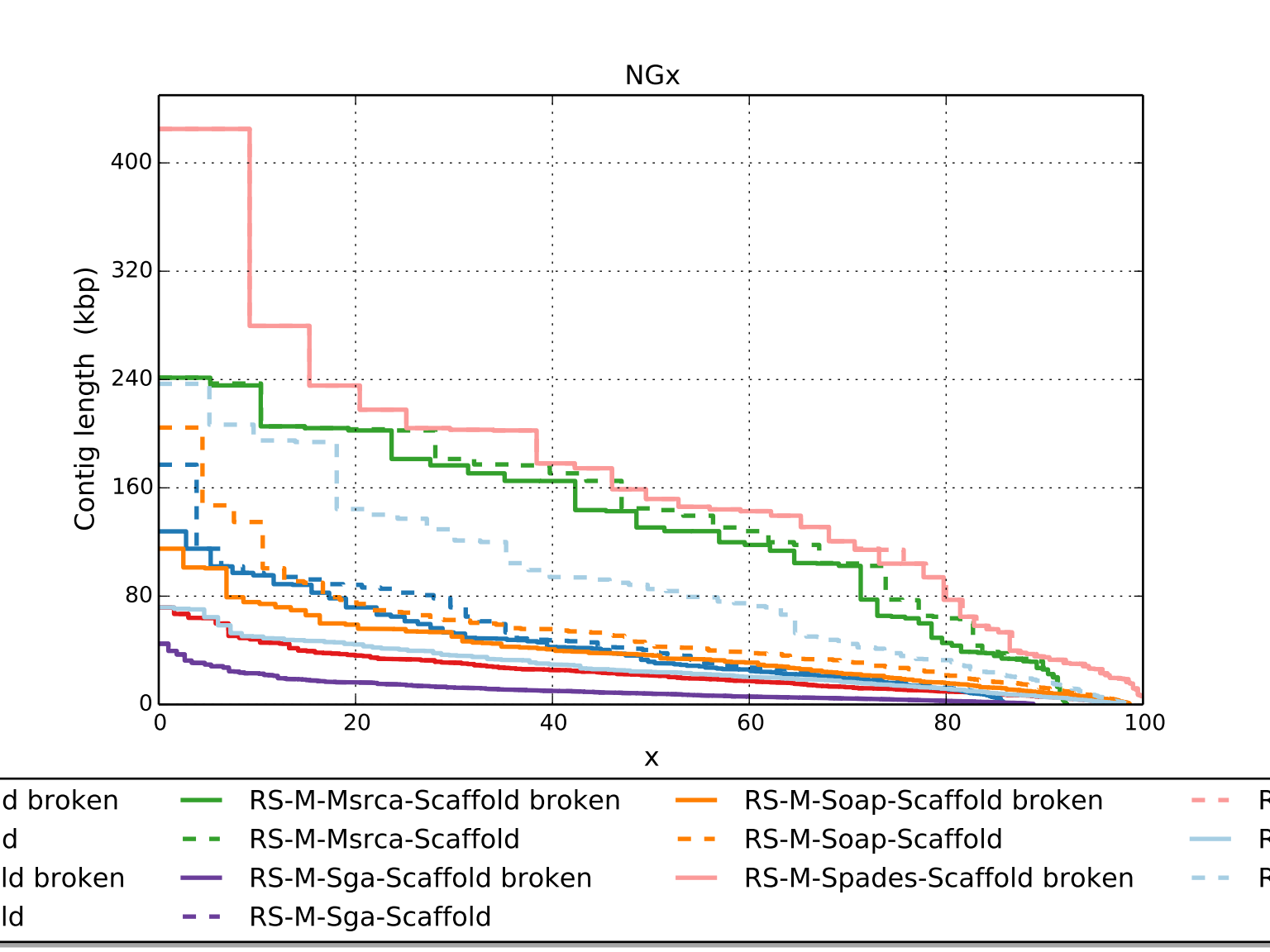
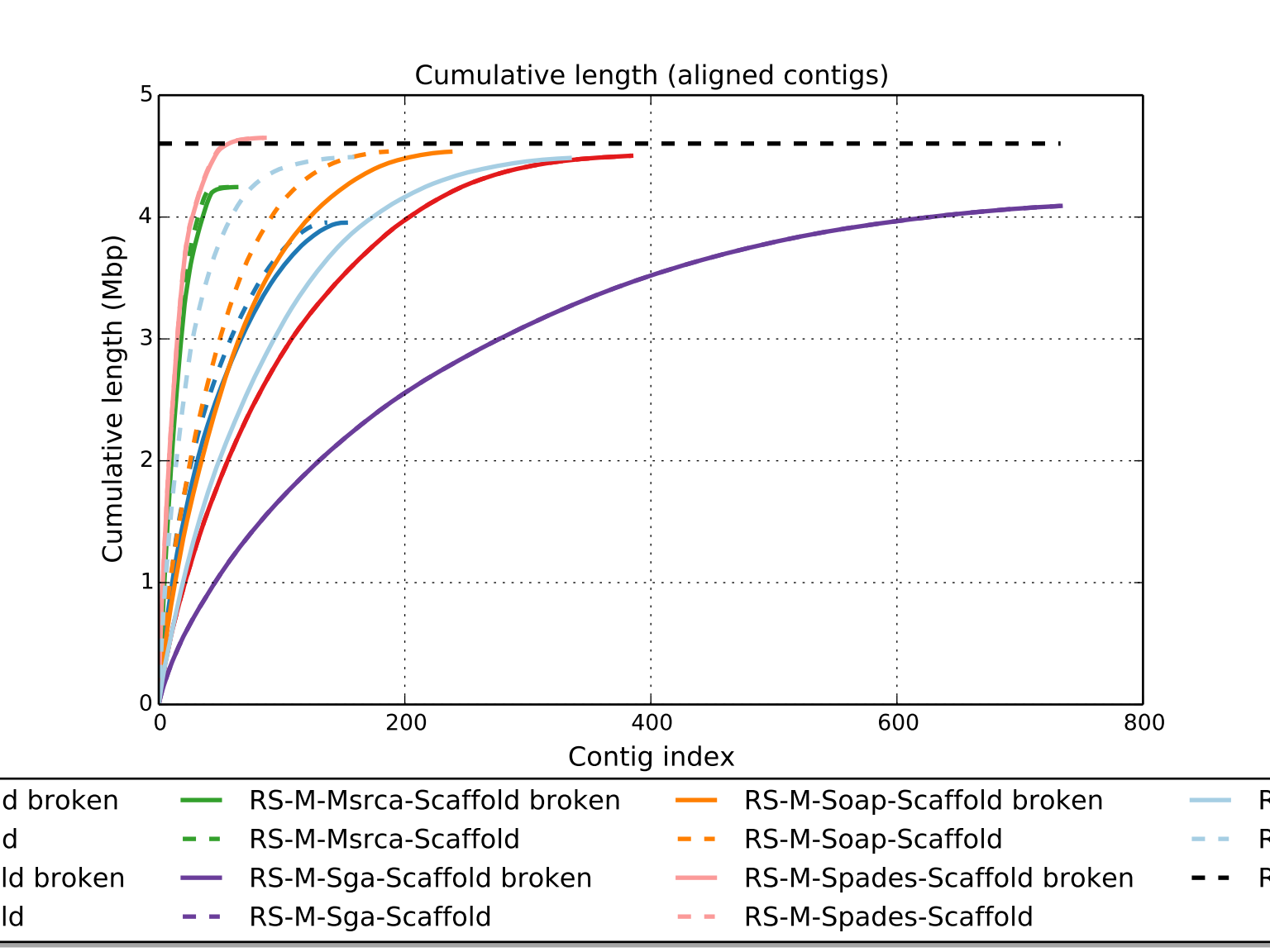
Scaffold

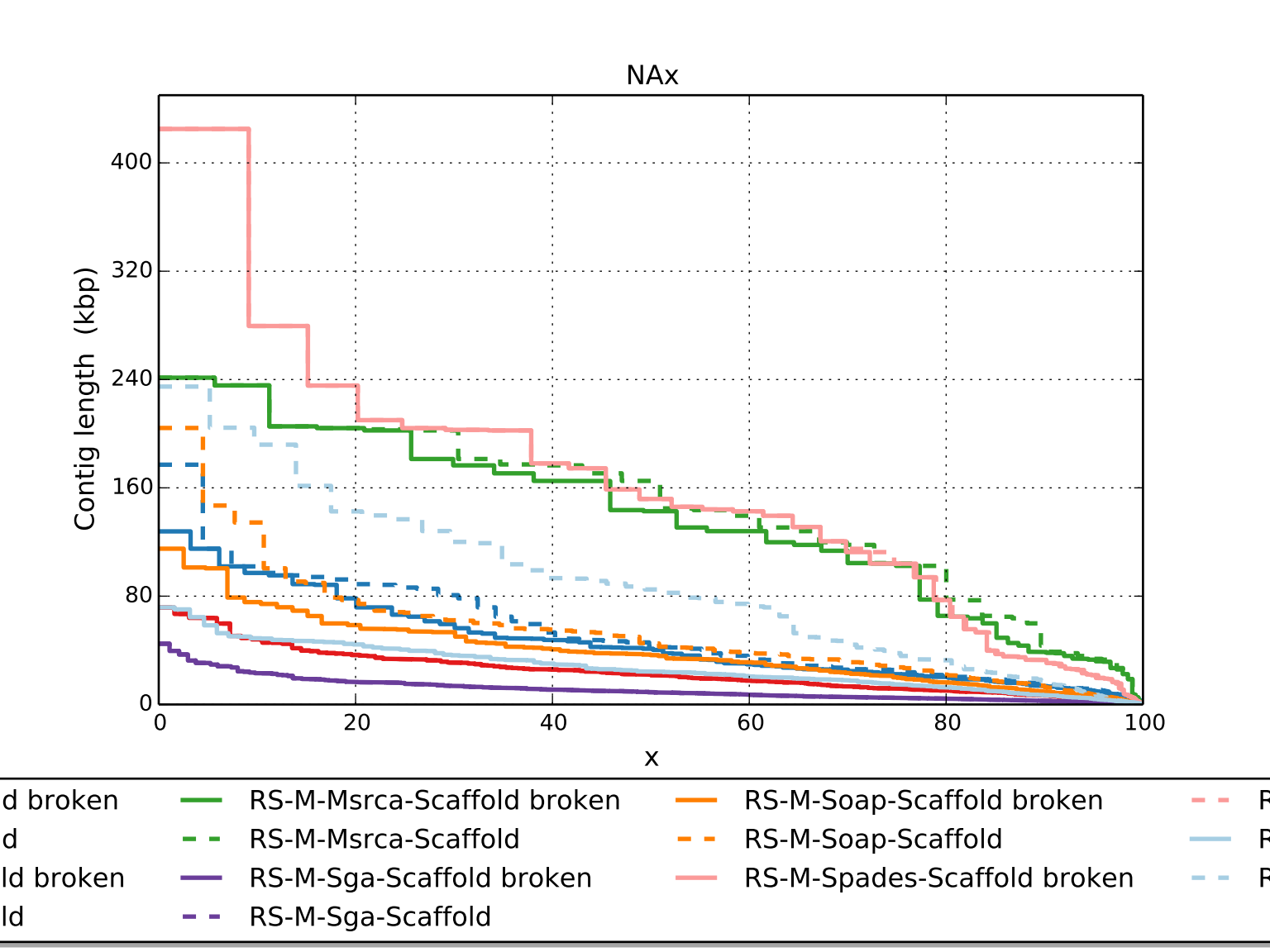

Cumulative length
Cumulative length (Mbp)
Contig index
0
1
2
3
4
5
0
200
400
600
800
d broken
d
ld broken
ld
RS-M-Msrca-Scaffold broken
RS-M-Msrca-Scaffold
RS-M-Sga-Scaffold broken
RS-M-Sga-Scaffold
RS-M-Soap-Scaffold broken
RS-M-Soap-Scaffold
RS-M-Spades-Scaffold broken
RS-M-Spades-Scaffold

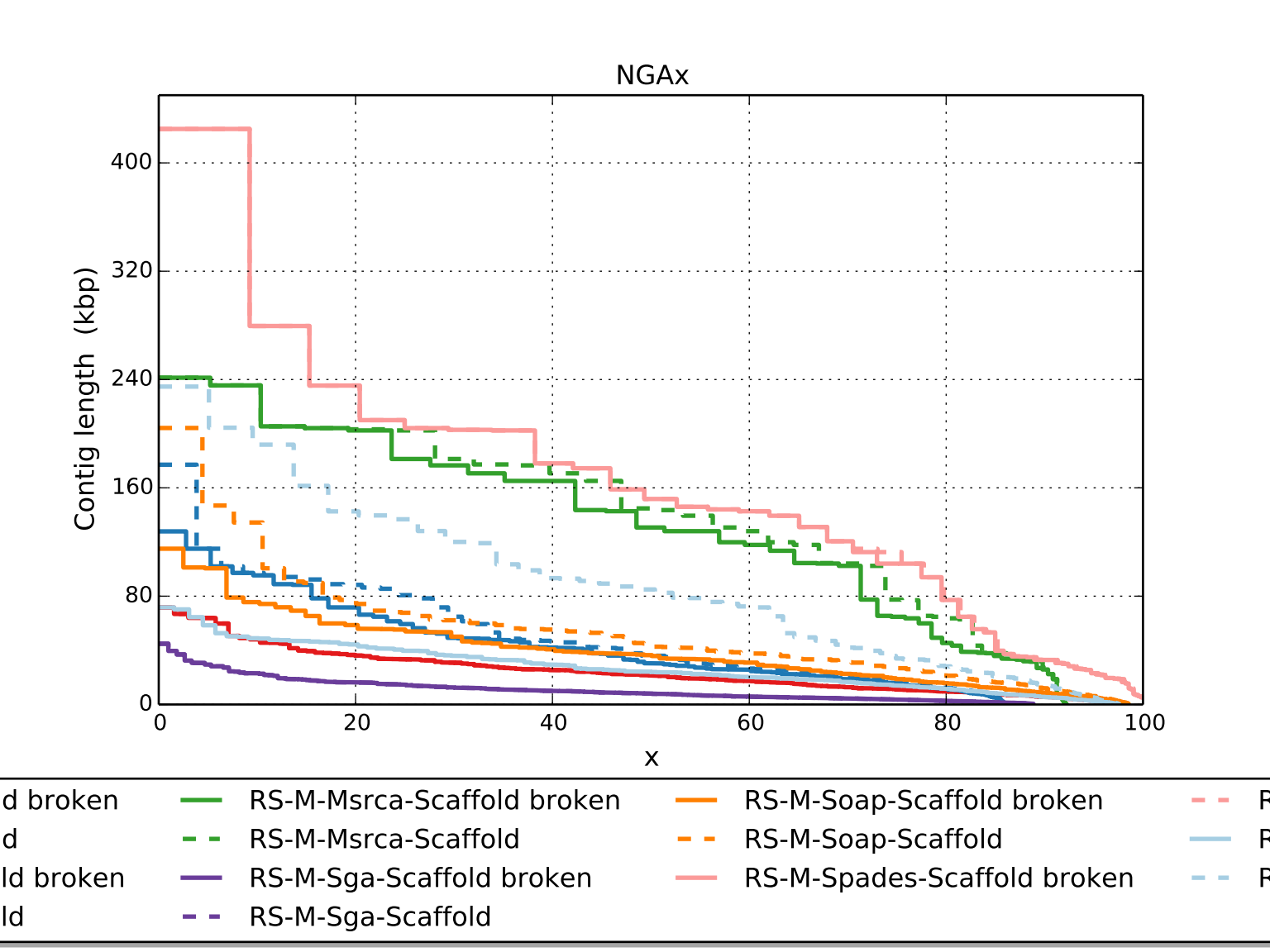

GC content
windows
GC (%)
0
600
1200
1800
2400
3000
0
20
40
60
80
100
d broken
d
ld broken
ld
RS-M-Msrca-Scaffold broken
RS-M-Msrca-Scaffold
RS-M-Sga-Scaffold broken
RS-M-Sga-Scaffold
RS-M-Soap-Scaffold broken
RS-M-Soap-Scaffold
RS-M-Spades-Scaffold broken
RS-M-Spades-Scaffold

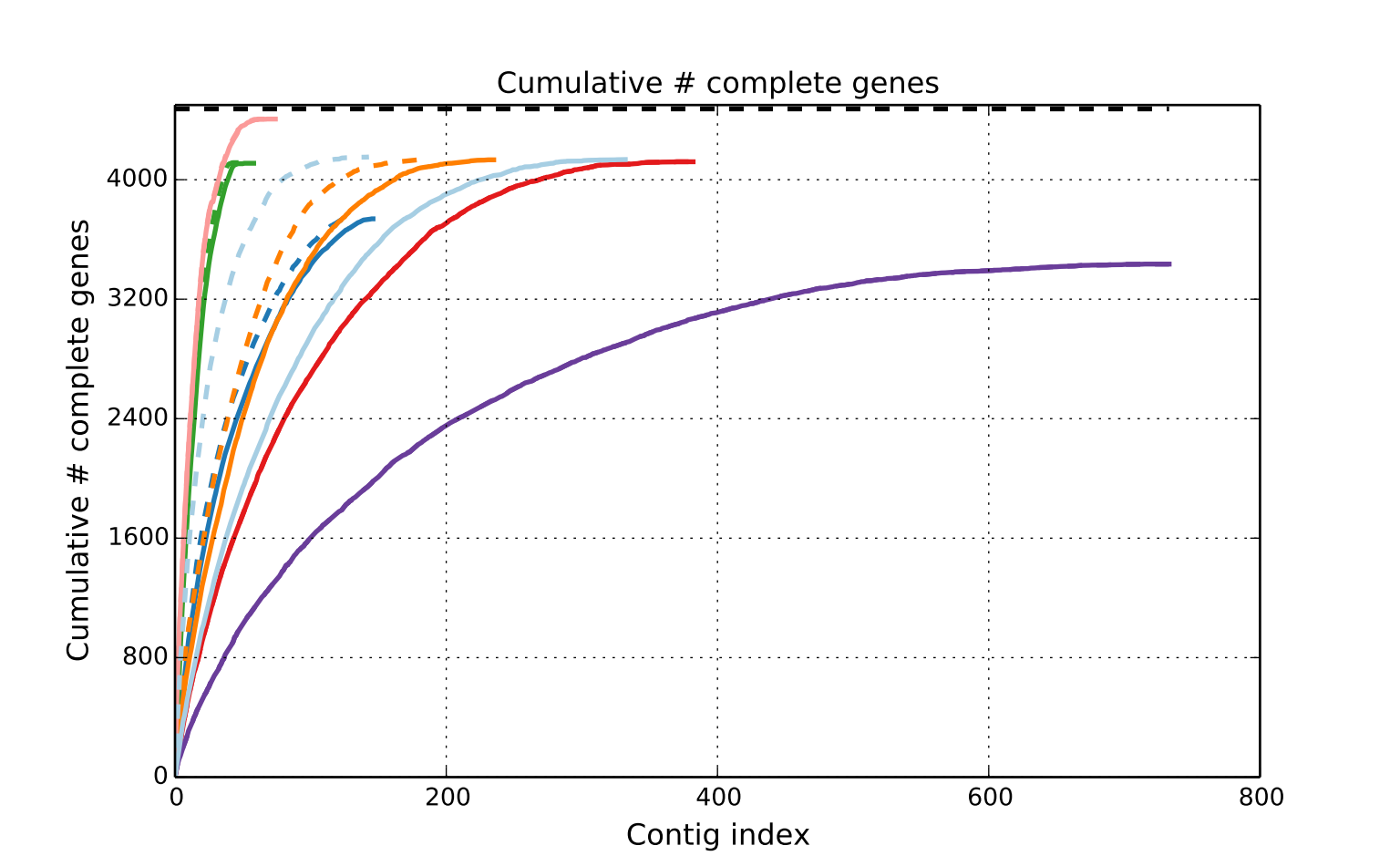

Nx
Contig length (kbp)
400
320
240
160
80
0
0
20
40
60
80
100
x
d broken
d
ld broken
ld
RS-M-Msrca-Scaffold broken
RS-M-Msrca-Scaffold
RS-M-Sga-Scaffold broken
RS-M-Sga-Scaffold
RS-M-Soap-Scaffold broken
RS-M-Soap-Scaffold
RS-M-Spades-Scaffold broken
R
R
R

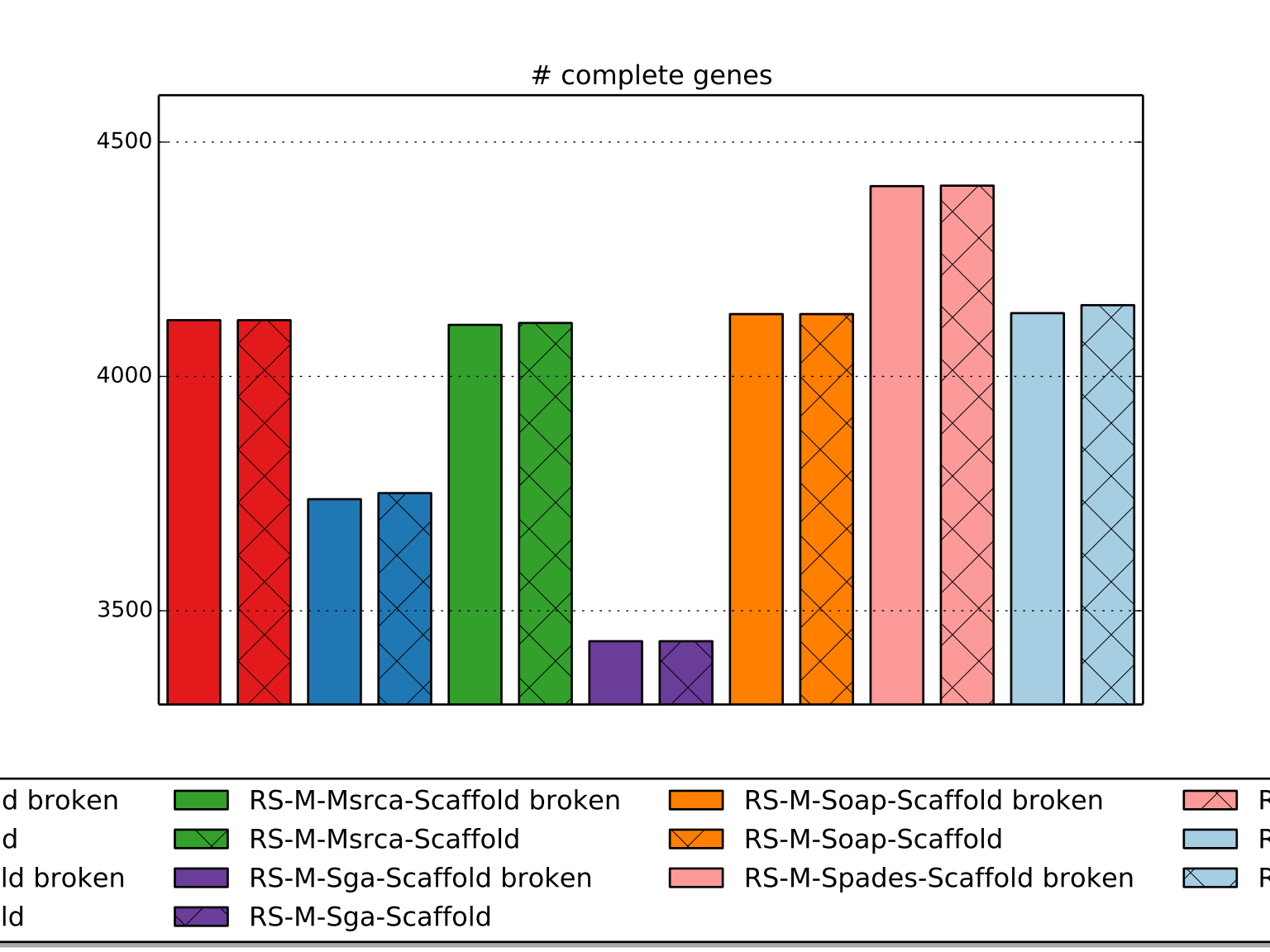

NGx
Contig length (kbp)
400
320
240
160
80
0
0
20
40
60
80
100
x
d broken
d
ld broken
ld
RS-M-Msrca-Scaffold broken
RS-M-Msrca-Scaffold
RS-M-Sga-Scaffold broken
RS-M-Sga-Scaffold
RS-M-Soap-Scaffold broken
RS-M-Soap-Scaffold
RS-M-Spades-Scaffold broken
R
R
R

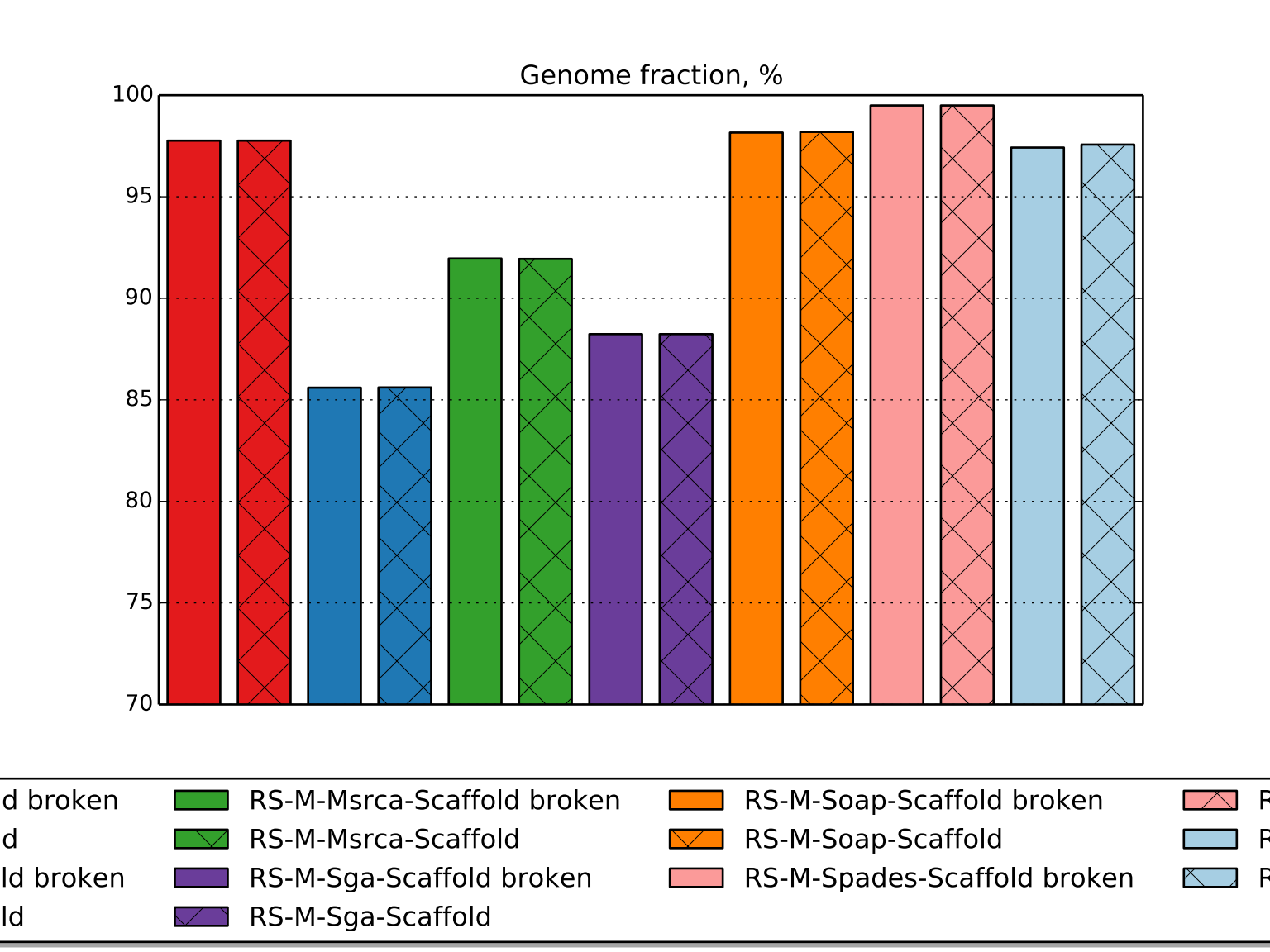

Cumulative length (aligned contigs)
Cumulative length (Mbp)
Contig index
0
1
2
3
4
5
0
200
400
600
800
d broken
d
ld broken
ld
RS-M-Msrca-Scaffold broken
RS-M-Msrca-Scaffold
RS-M-Sga-Scaffold broken
RS-M-Sga-Scaffold
RS-M-Soap-Scaffold broken
RS-M-Soap-Scaffold
RS-M-Spades-Scaffold broken
RS-M-Spades-Scaffold


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

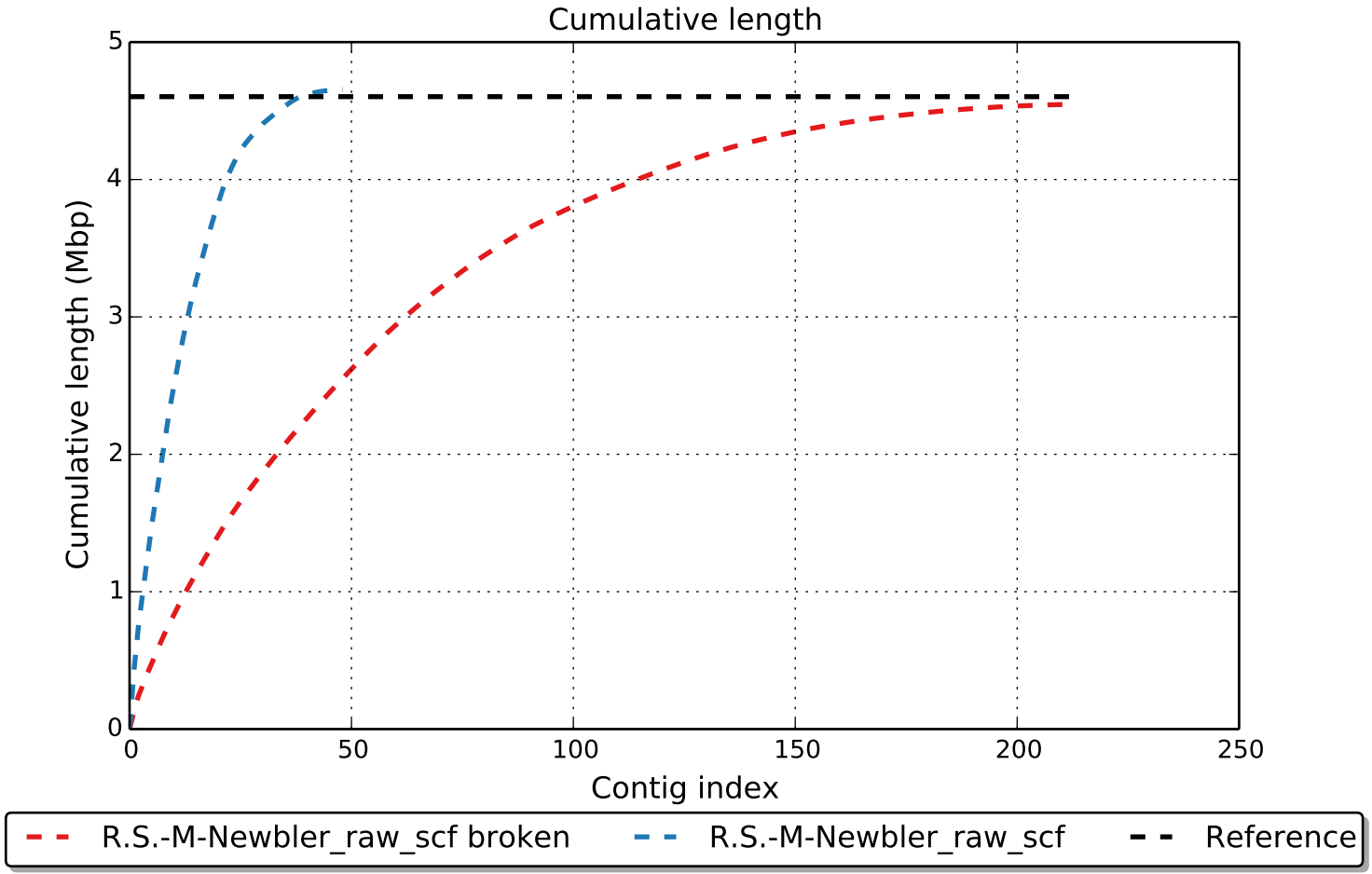

NGAx
Contig length (kbp)
400
320
240
160
80
0
0
20
40
60
80
100
x
d broken
d
ld broken
ld
RS-M-Msrca-Scaffold broken
RS-M-Msrca-Scaffold
RS-M-Sga-Scaffold broken
RS-M-Sga-Scaffold
RS-M-Soap-Scaffold broken
RS-M-Soap-Scaffold
RS-M-Spades-Scaffold broken

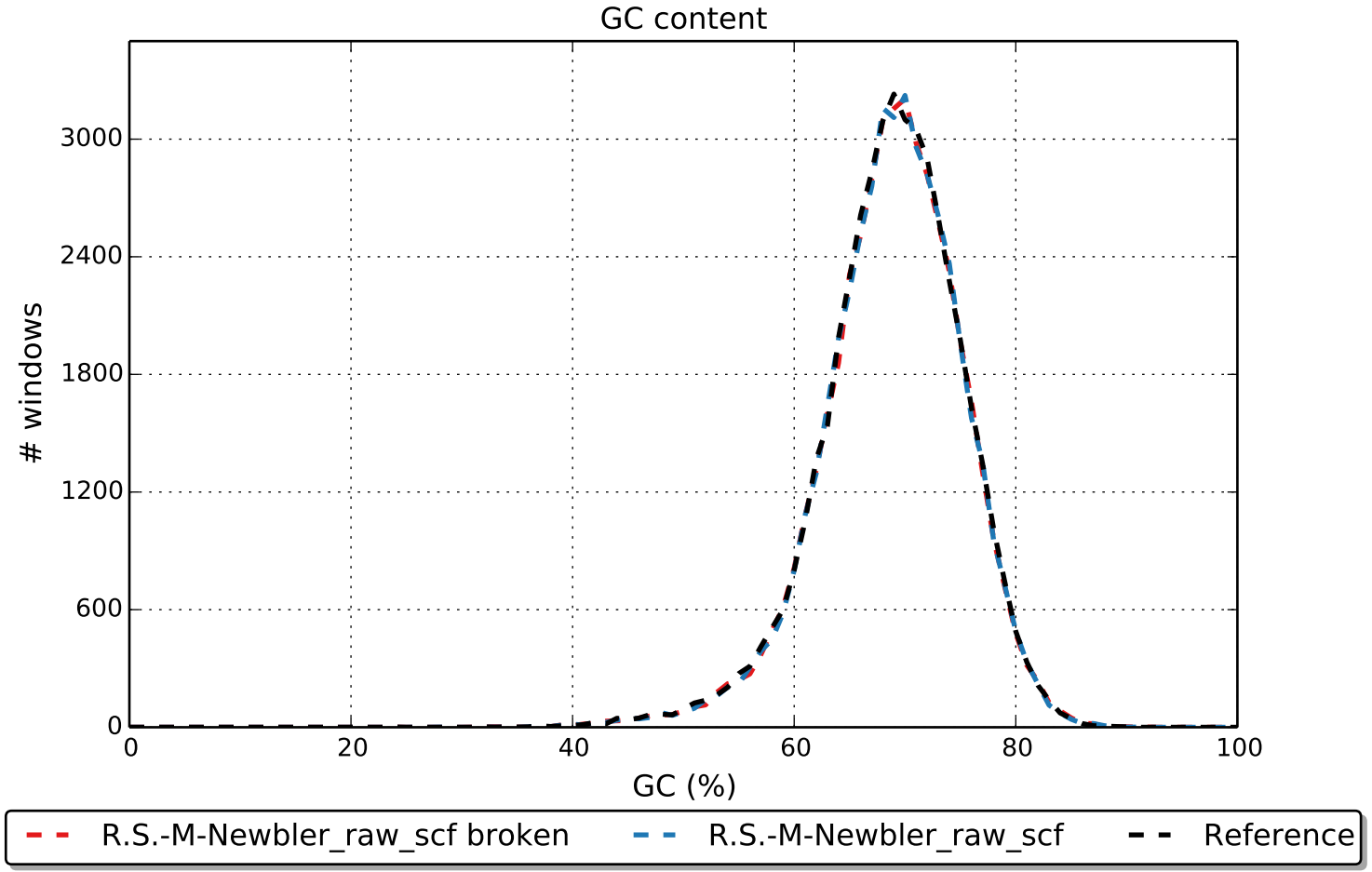

Cumulative # complete genes
Cumulative # complete genes
Contig index
0
800
1600
2400
3200
4000
0
200
400
600
800
d broken
d
ld broken
ld
RS-M-Msrca-Scaffold broken
RS-M-Msrca-Scaffold
RS-M-Sga-Scaffold broken
RS-M-Sga-Scaffold
RS-M-Soap-Scaffold broken
RS-M-Soap-Scaffold
RS-M-Spades-Scaffold broken
RS-M-Spades-Scaffold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

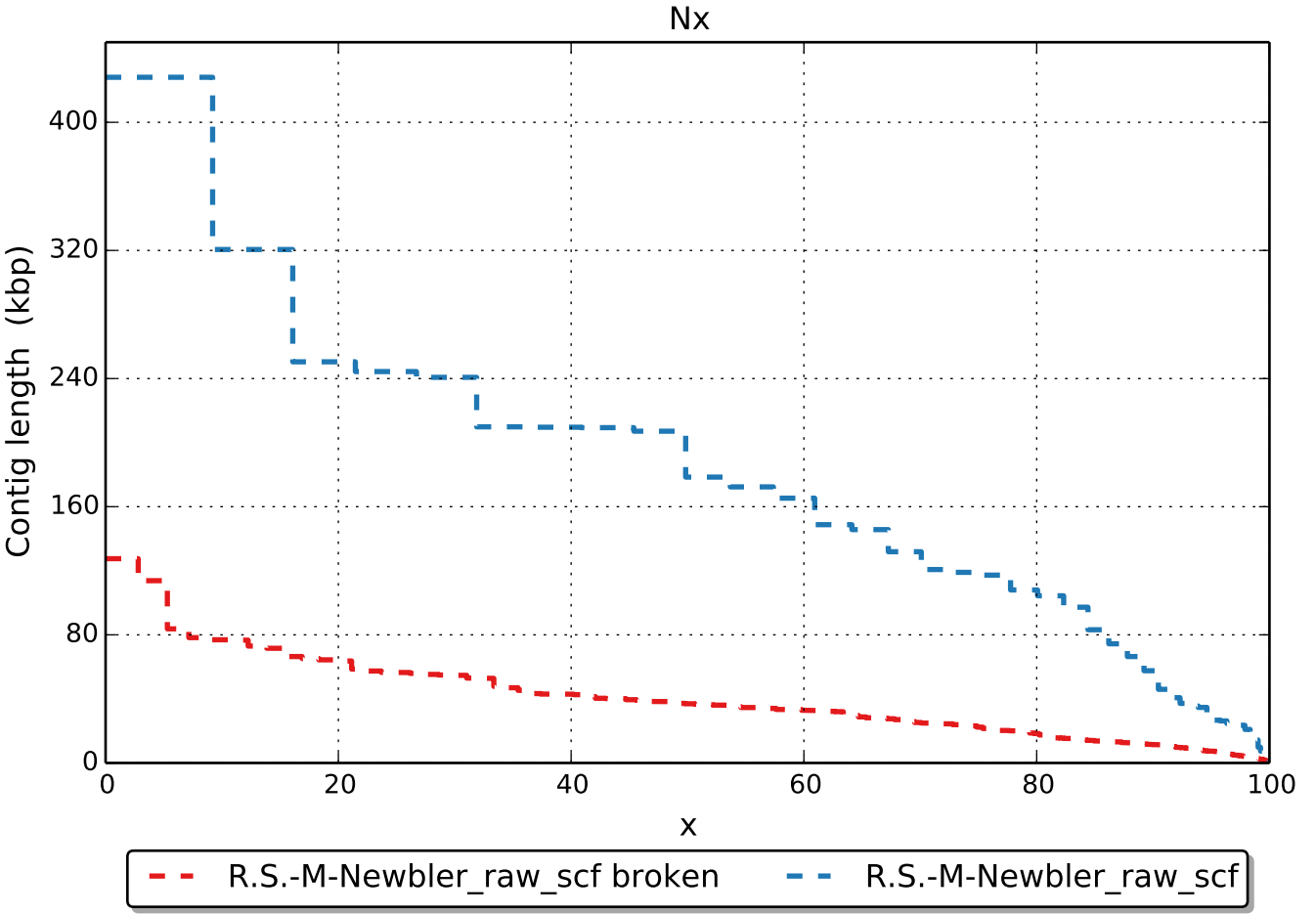

complete genes
4500
4000
3500
d broken
d
ld broken
ld
RS-M-Msrca-Scaffold broken
RS-M-Msrca-Scaffold
RS-M-Sga-Scaffold broken
RS-M-Sga-Scaffold
RS-M-Soap-Scaffold broken
RS-M-Soap-Scaffold
RS-M-Spades-Scaffold broken

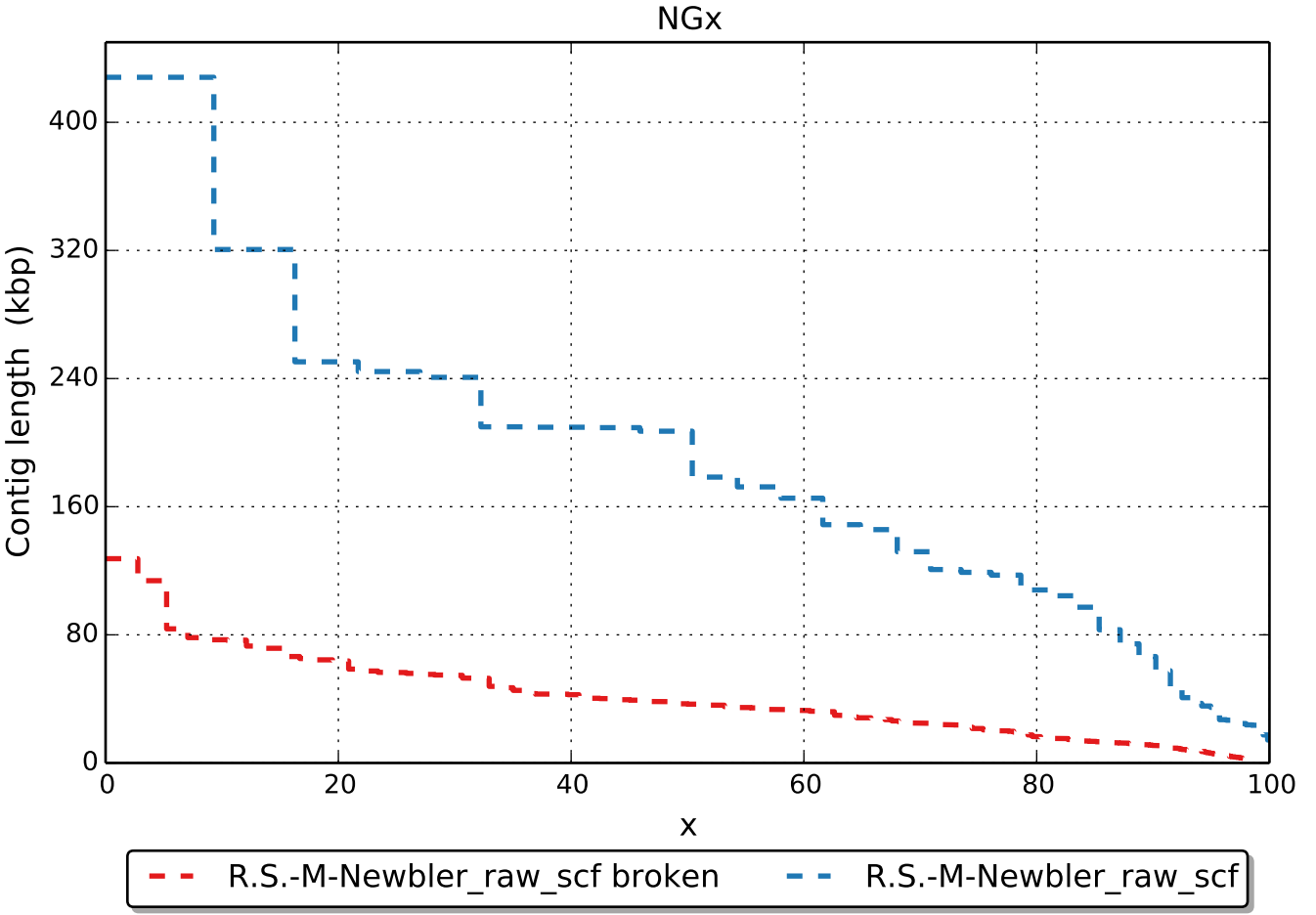

Genome fraction, %
100
95
90
85
80
75
70
d broken
d
ld broken
ld
RS-M-Msrca-Scaffold broken
RS-M-Msrca-Scaffold
RS-M-Sga-Scaffold broken
RS-M-Sga-Scaffold
RS-M-Soap-Scaffold broken
RS-M-Soap-Scaffold
RS-M-Spades-Scaffold broken
R
R
R

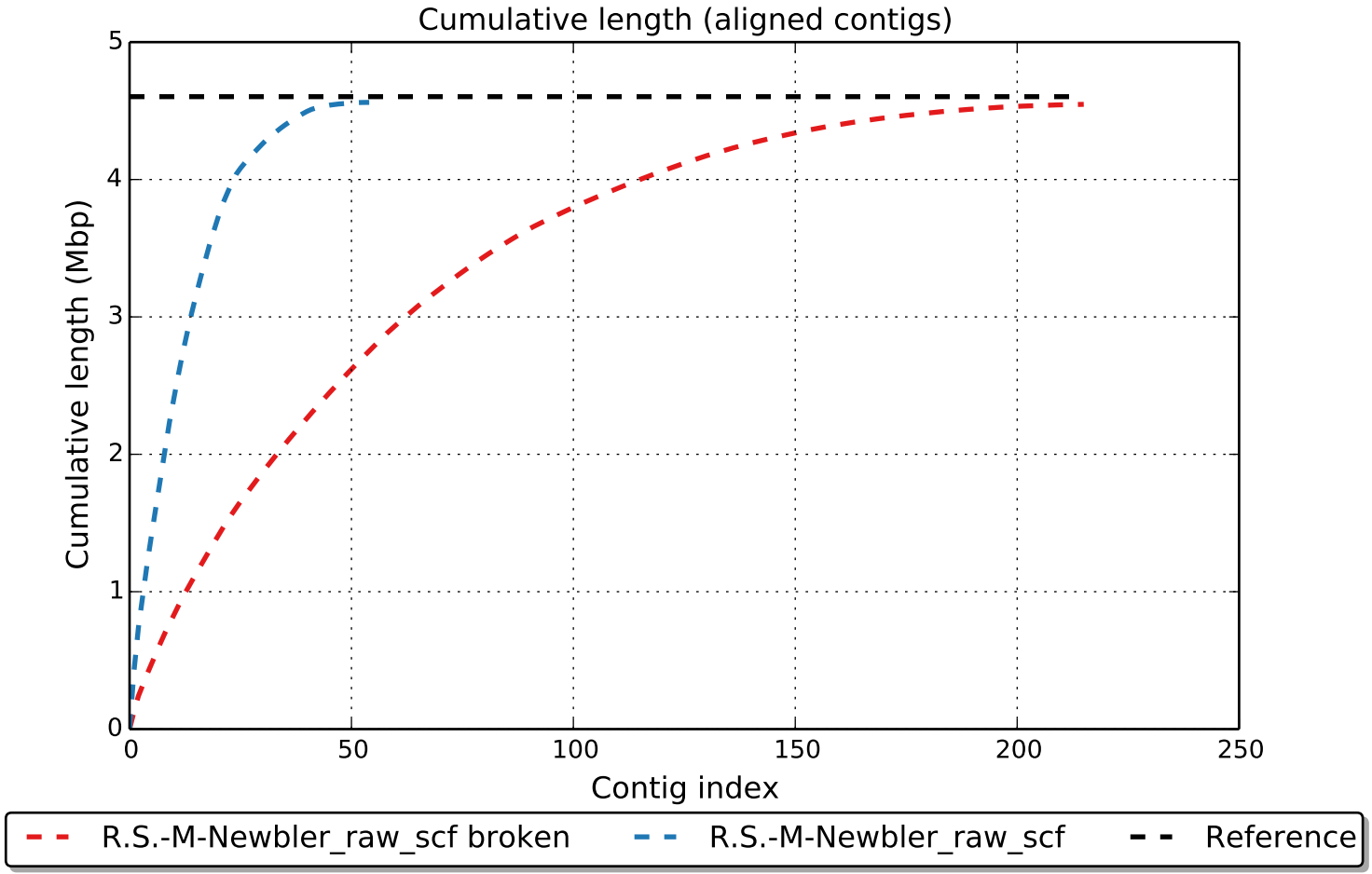
Scaffold

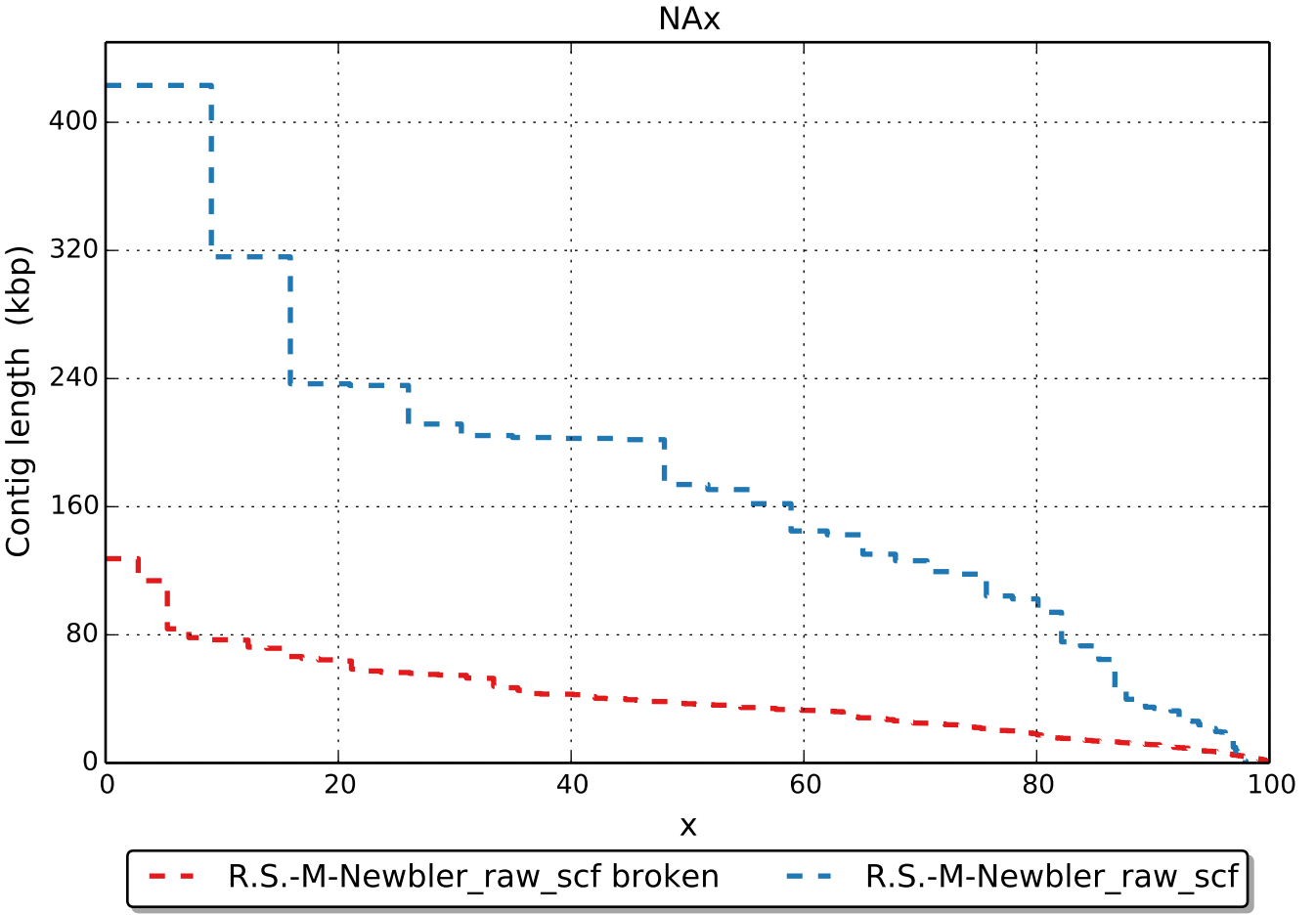

Cumulative length
Cumulative length (Mbp)
Contig index
0
1
2
3
4
5
0
50
100
150
200
250
R.S.-M-Newbler_raw_scf broken
R.S.-M-Newbler_raw_scf
Reference

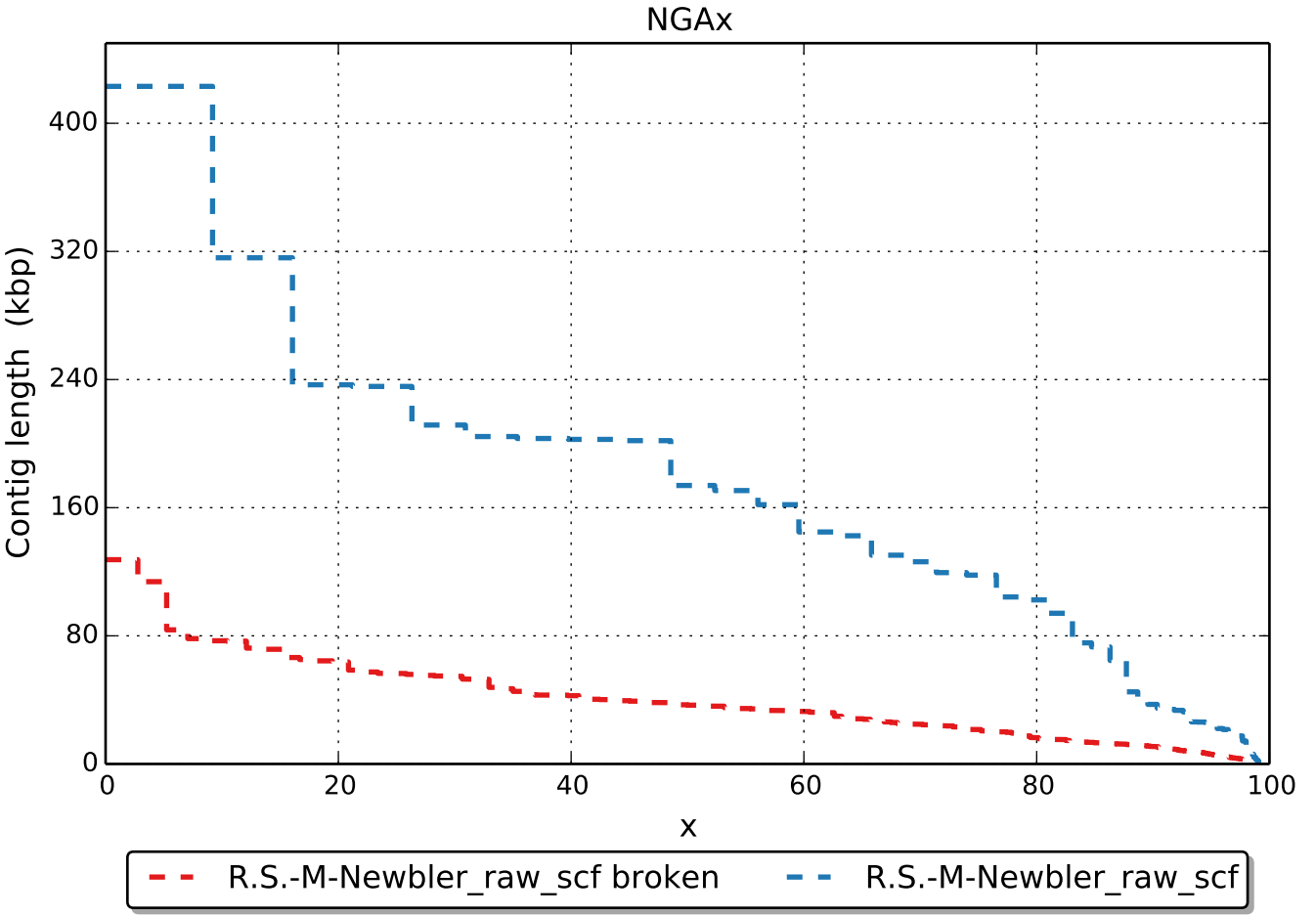

GC content
windows
GC (%)
0
600
1200
1800
2400
3000
0
20
40
60
80
100
R.S.-M-Newbler_raw_scf broken
R.S.-M-Newbler_raw_scf
Reference

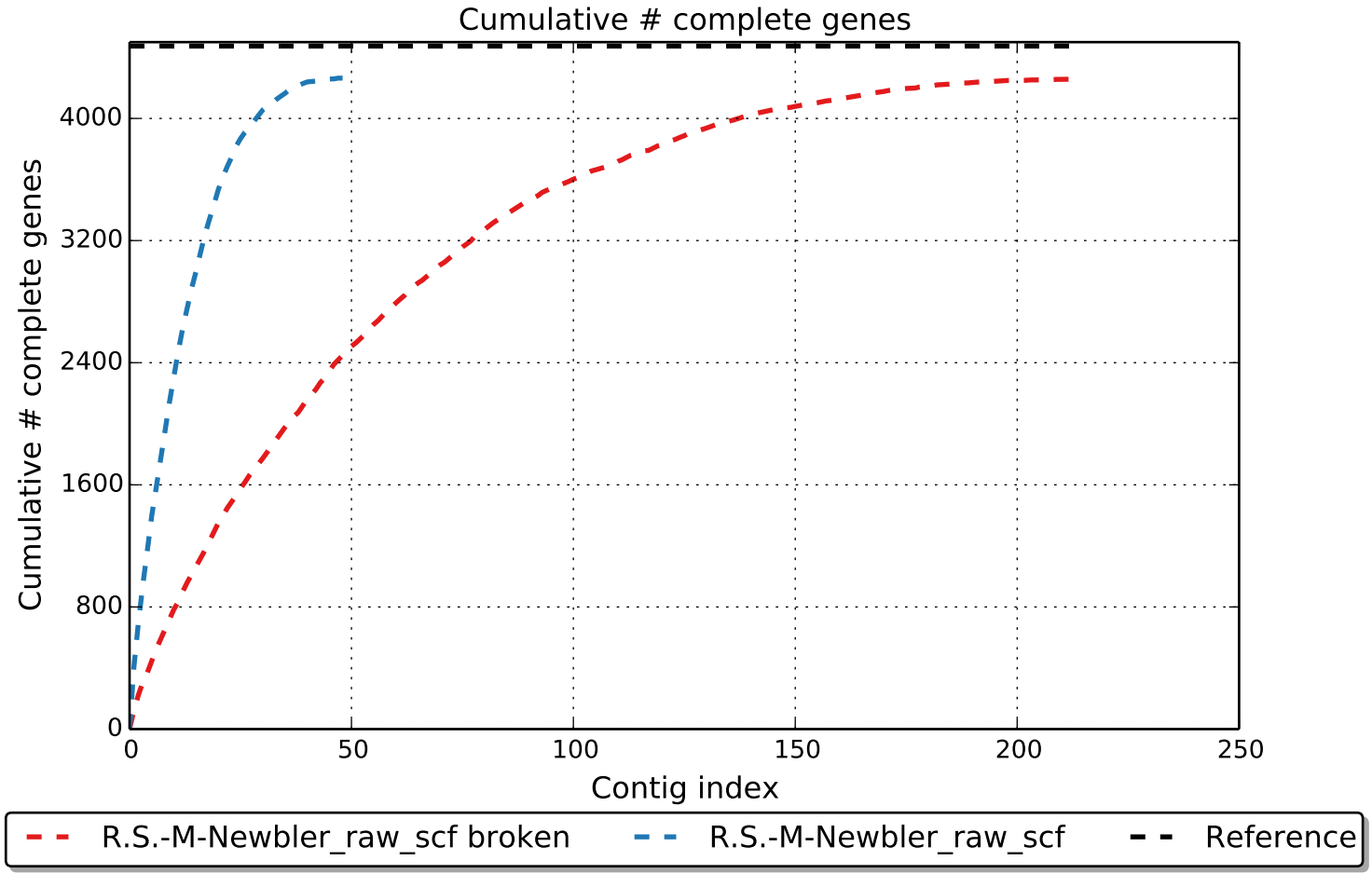

Nx
Contig length (kbp)
400
320
240
160
80
0
0
20
40
60
80
100
x
R.S.-M-Newbler_raw_scf broken
R.S.-M-Newbler_raw_scf

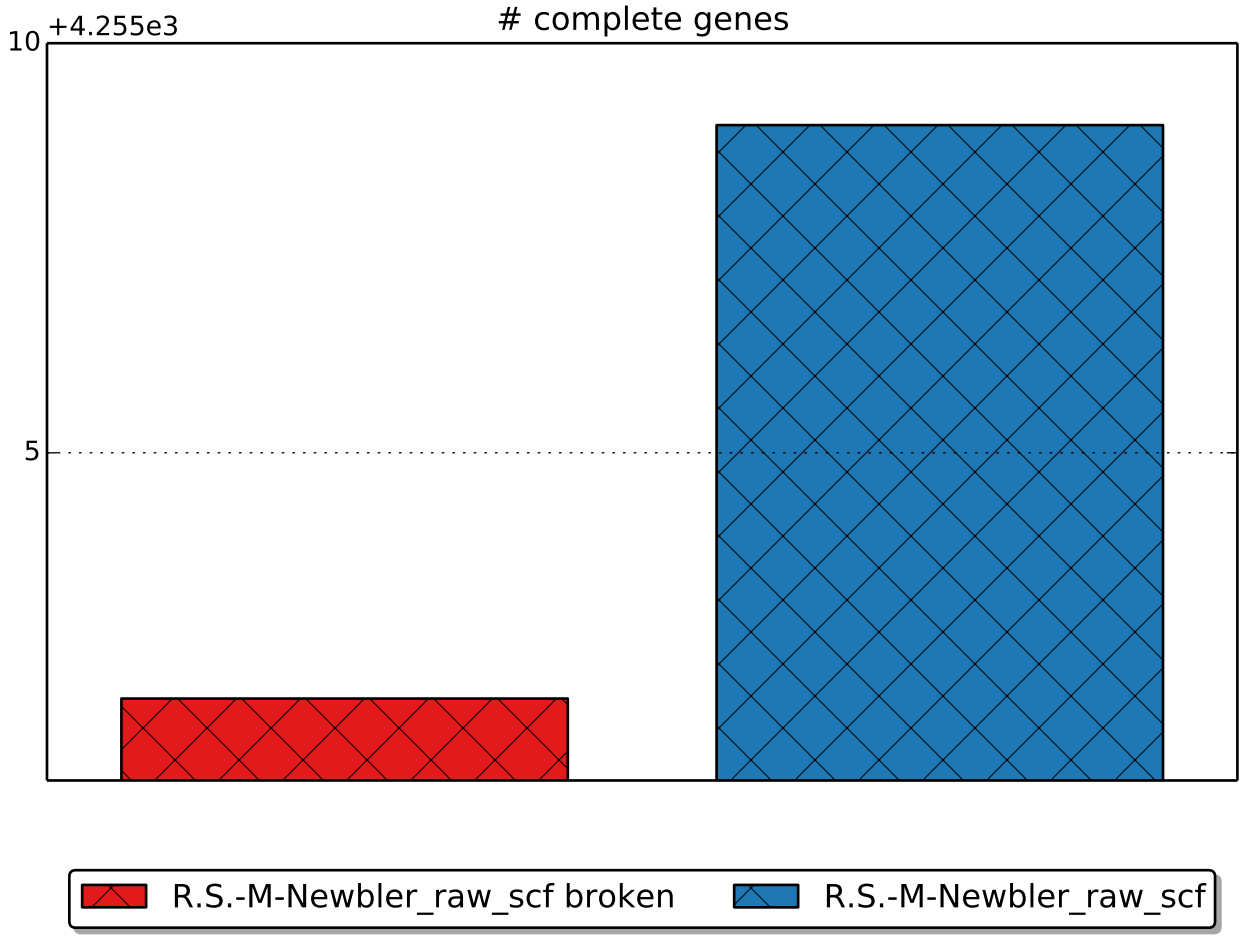

NGx
Contig length (kbp)
400
320
240
160
80
0
0
20
40
60
80
100
x
R.S.-M-Newbler_raw_scf broken
R.S.-M-Newbler_raw_scf

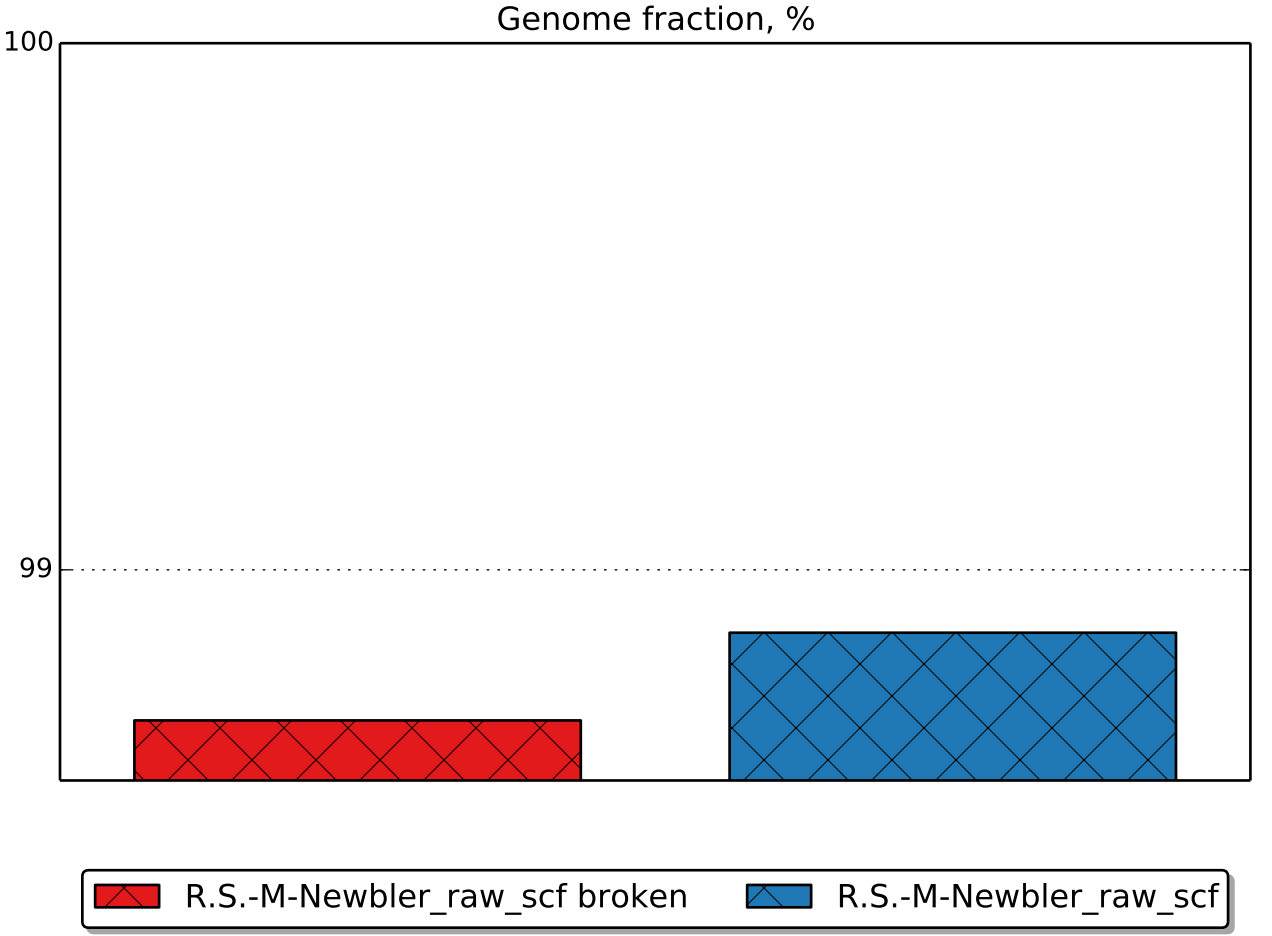

Cumulative length (aligned contigs)
Cumulative length (Mbp)
Contig index
0
1
2
3
4
5
0
50
100
150
200
250
R.S.-M-Newbler_raw_scf broken
R.S.-M-Newbler_raw_scf
Reference


NAx
Contig length (kbp)
400
320
240
160
80
0
0
20
40
60
80
100
x
R.S.-M-Newbler_raw_scf broken
R.S.-M-Newbler_raw_scf


NGAx
Contig length (kbp)
400
320
240
160
80
0
0
20
40
60
80
100
x
R.S.-M-Newbler_raw_scf broken
R.S.-M-Newbler_raw_scf


Cumulative # complete genes
Cumulative # complete genes
4000
3200
2400
1600
800
0
0
50
100
150
200
250
Contig index
R.S.-M-Newbler_raw_scf broken
R.S.-M-Newbler_raw_scf
Reference


complete genes
+4.255e3
10
5
R.S.-M-Newbler_raw_scf broken
R.S.-M-Newbler_raw_scf


Genome fraction, %
100
99
R.S.-M-Newbler_raw_scf broken
R.S.-M-Newbler_raw_scf