Report

	spades_default	spades_kmers_careful	megahit_default	megahit_min_count_3
# contigs (>= 0 bp)	288	239	195	198
# contigs (>= 1000 bp)	132	91	156	158
# contigs (>= 5000 bp)	94	74	118	121
# contigs (>= 10000 bp)	87	67	104	108
# contigs (>= 25000 bp)	67	58	72	75
# contigs (>= 50000 bp)	51	43	49	51
Total length (>= 0 bp)	8490011	8510655	8510860	8511217
Total length (>= 1000 bp)	8447218	8472540	8492975	8493797
Total length (>= 5000 bp)	8371775	8438829	8406233	8408960
Total length (>= 10000 bp)	8324069	8384754	8296360	8308919
Total length (>= 25000 bp)	8010950	8245120	7760464	7762256
Total length (>= 50000 bp)	7438644	7723080	6917725	6910273
# contigs	132	91	156	158
Largest contig	754490	961949	539126	539126
Total length	8447218	8472540	8492975	8493797
Reference length	8605945	8605945	8605945	8605945
GC (%)	66.67	66.67	66.66	66.66
Reference GC (%)	66.61	66.61	66.61	66.61
N50	151907	217699	144335	131456
NG50	143914	217699	144335	131456
N75	85907	107910	66469	64244
NG75	79029	98944	64299	62113
L50	16	12	19	20
LG50	17	12	19	20
L75	35	26	40	42
LG75	36	27	41	43
# misassemblies	5	6	9	8
# misassembled contigs	5	6	9	8
Misassembled contigs length	1454524	1719134	1200775	1050989
# local misassemblies	10	9	6	5
# unaligned mis. contigs	0	0	0	0
# unaligned contigs	0 + 0 part	1 + 0 part	0 + 0 part	0 + 0 part
Unaligned length	0	1080	0	0
Genome fraction (%)	98.133	98.425	98.596	98.601
Duplication ratio	1.000	1.000	1.001	1.001
# N's per 100 kbp	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	5.16	3.57	2.58	2.52
# indels per 100 kbp	1.04	0.72	0.41	0.47
# genes	7529 + 85 part	7559 + 67 part	7539 + 105 part	7540 + 103 part
Largest alignment	445563	505920	350746	350746
Total aligned length	8447074	8471293	8492537	8493253
NA50	143914	198969	144083	125159
NGA50	143431	198969	144083	125159
NA75	85907	103468	61973	61722
NGA75	78885	98938	61722	57545
LA50	17	13	20	21
LGA50	18	13	20	21
LA75	36	28	42	44
LGA75	38	29	43	45

All statistics are based on contigs of size >= 1000 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

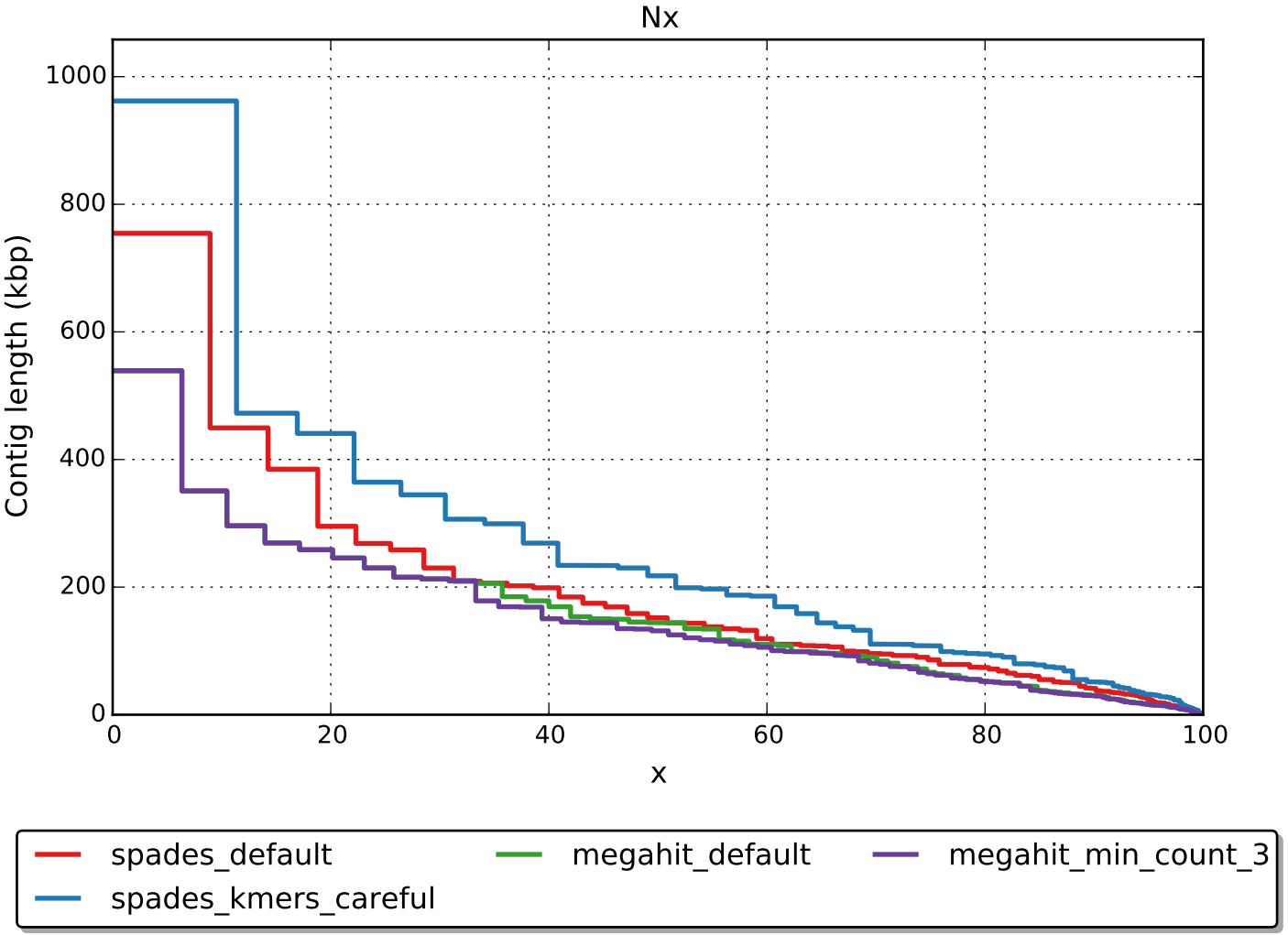
	spades_default	spades_kmers_careful	megahit_default	megahit_min_count_3
# misassemblies	5	6	9	8
# relocations	5	5	5	4
# translocations	0	1	4	4
# inversions	0	0	0	0
# misassembled contigs	5	6	9	8
Misassembled contigs length	1454524	1719134	1200775	1050989
# local misassemblies	10	9	6	5
# unaligned mis. contigs	0	0	0	0
# mismatches	436	302	219	214
# indels	88	61	35	40
# indels (<= 5 bp)	55	42	25	29
# indels (> 5 bp)	33	19	10	11
Indels length	772	538	213	237

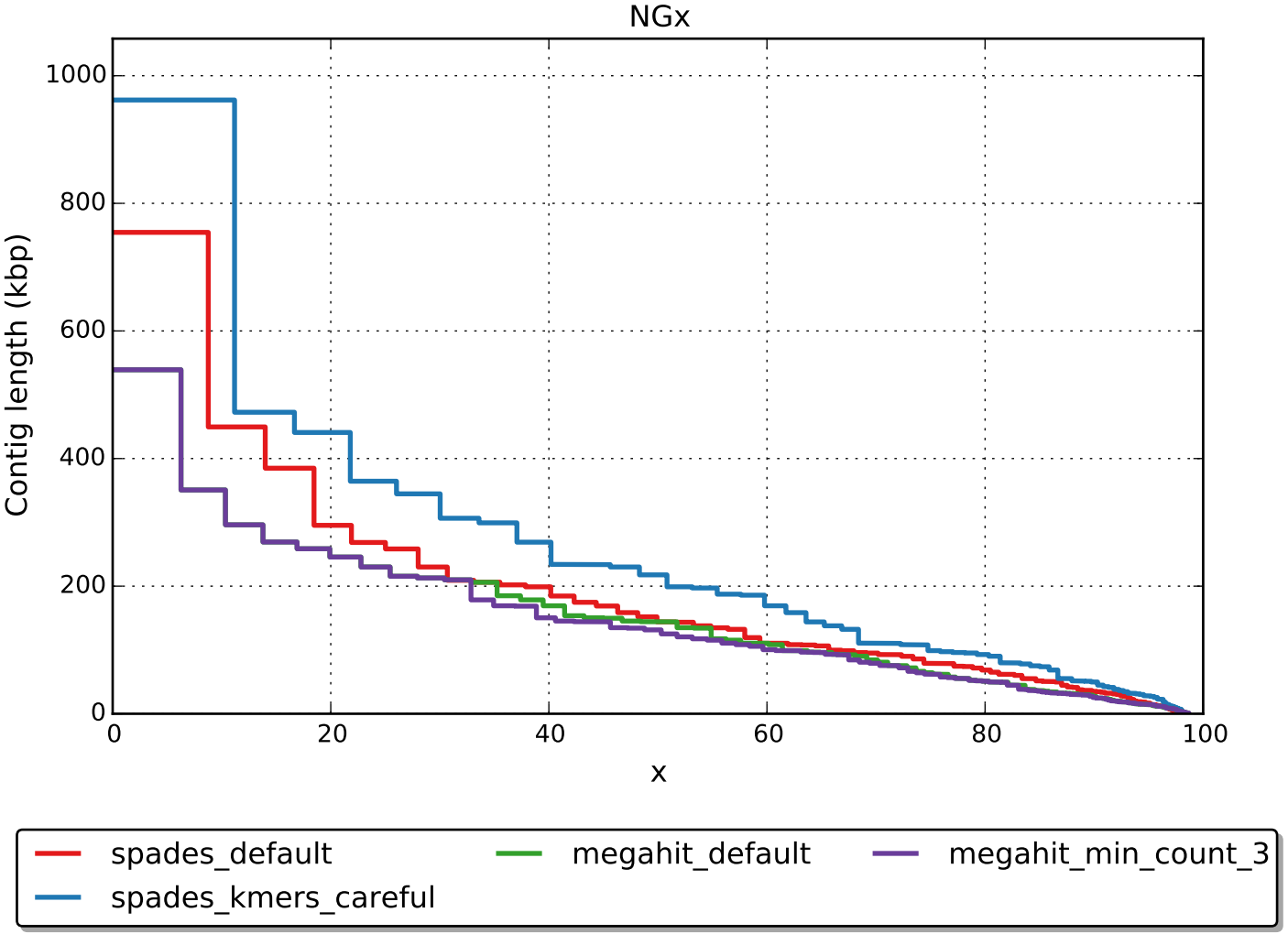
All statistics are based on contigs of size >= 1000 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

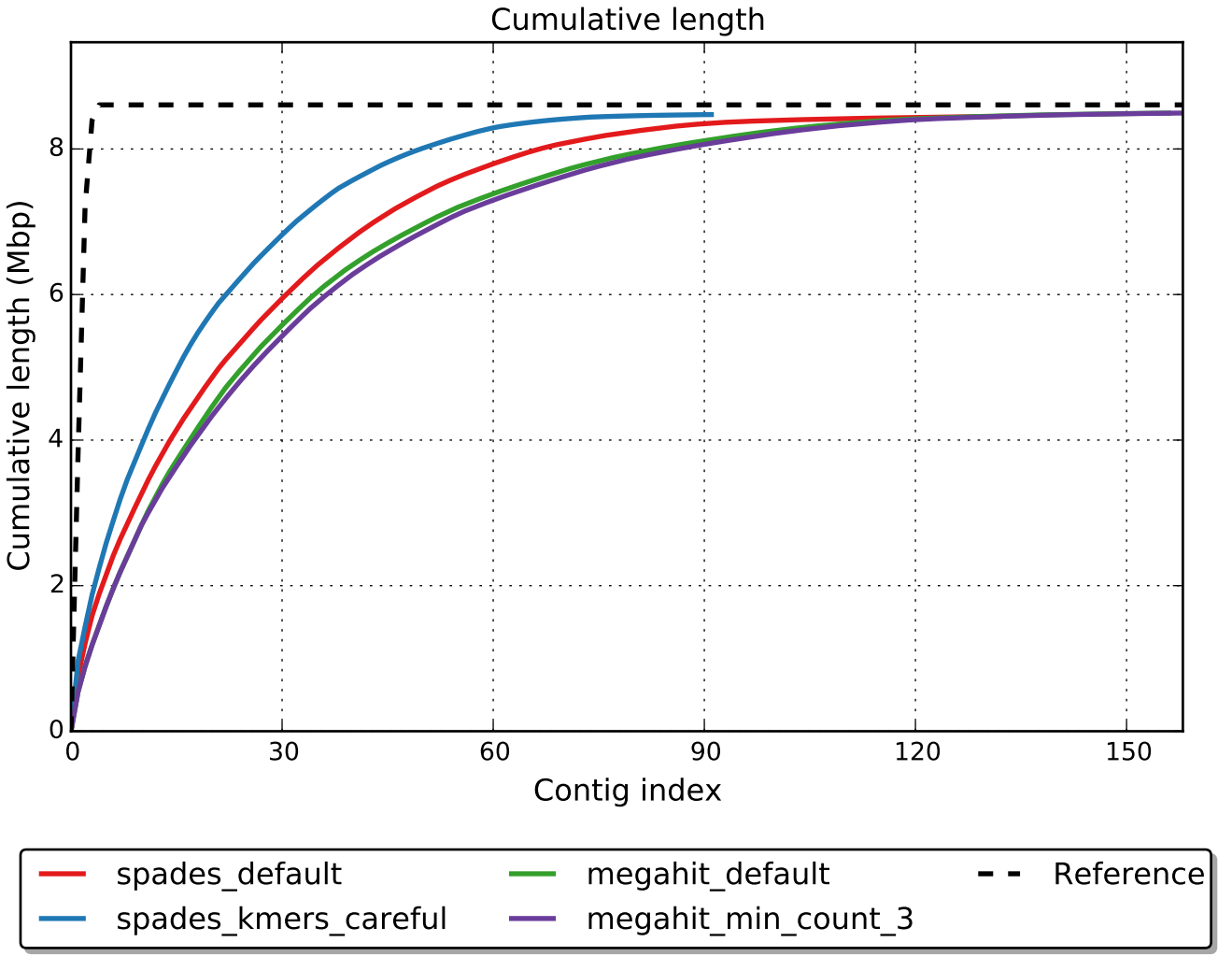
Unaligned report

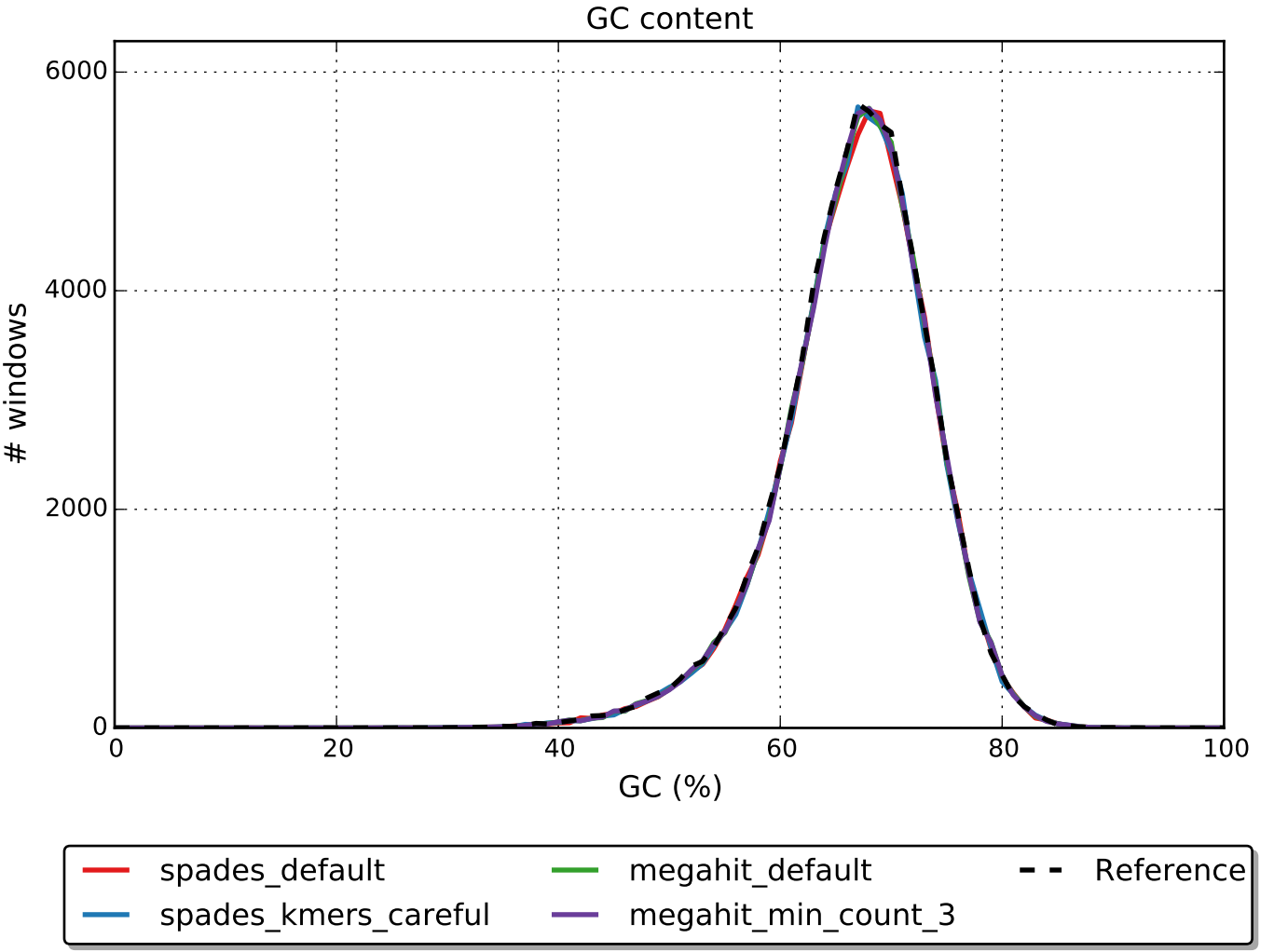
	spades_default	spades_kmers_careful	megahit_default	megahit_min_count_3
# fully unaligned contigs	0	1	0	0
Fully unaligned length	0	1080	0	0
# partially unaligned contigs	0	0	0	0
Partially unaligned length	0	0	0	0
# N's	0	0	0	0

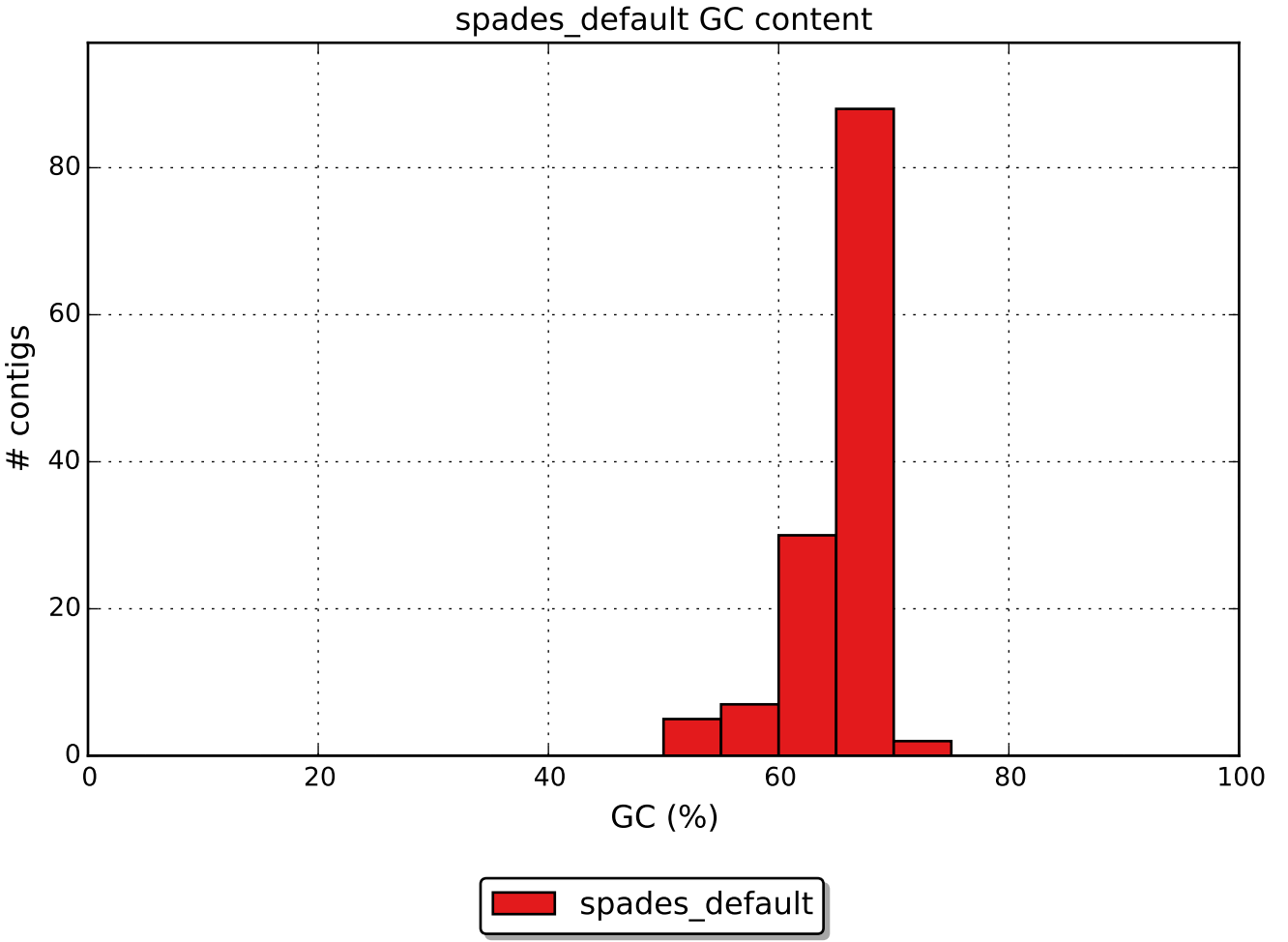
All statistics are based on contigs of size >= 1000 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

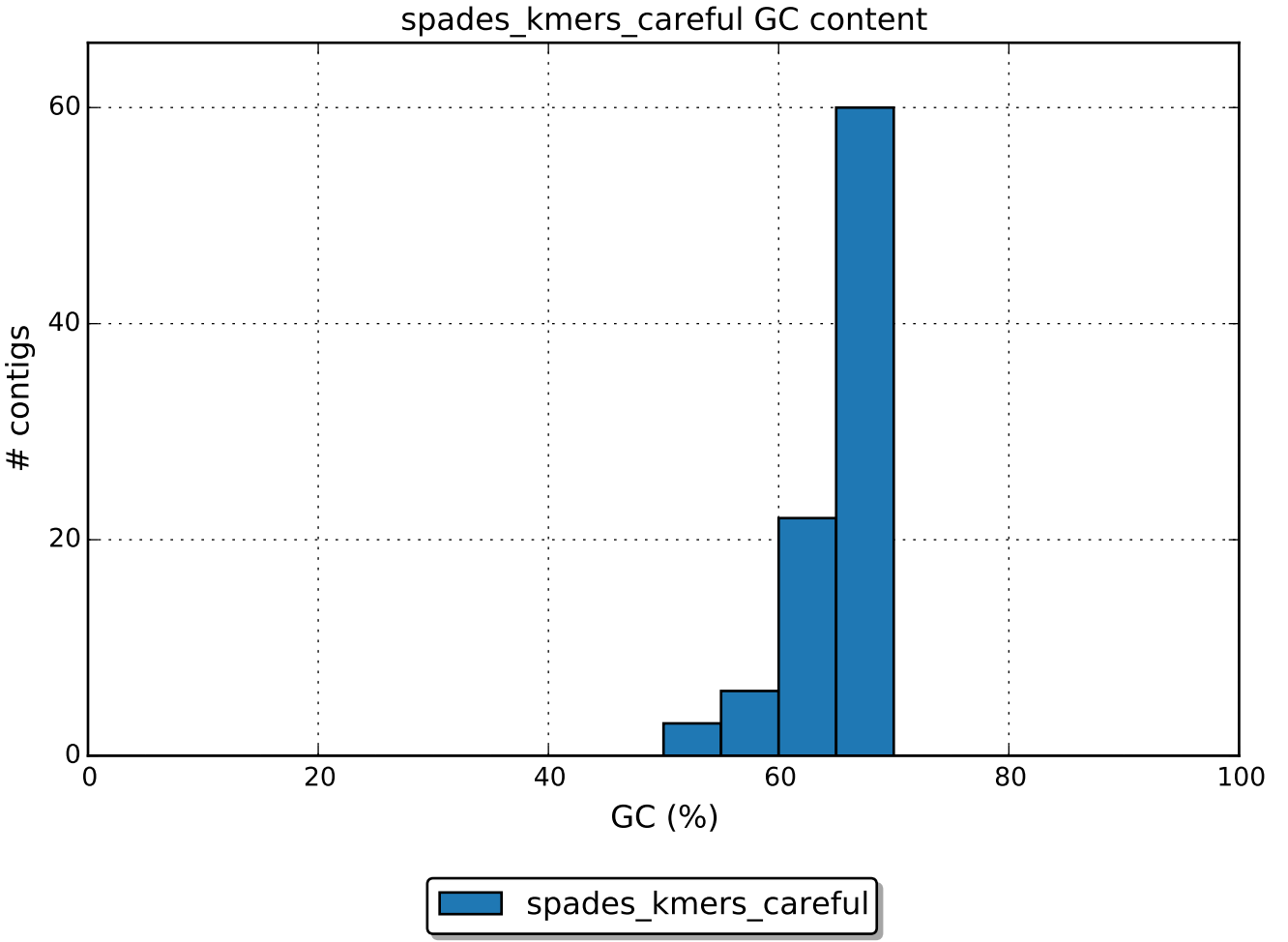

Nx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
spades_default
spades_kmers_careful
megahit_default
megahit_min_count_3

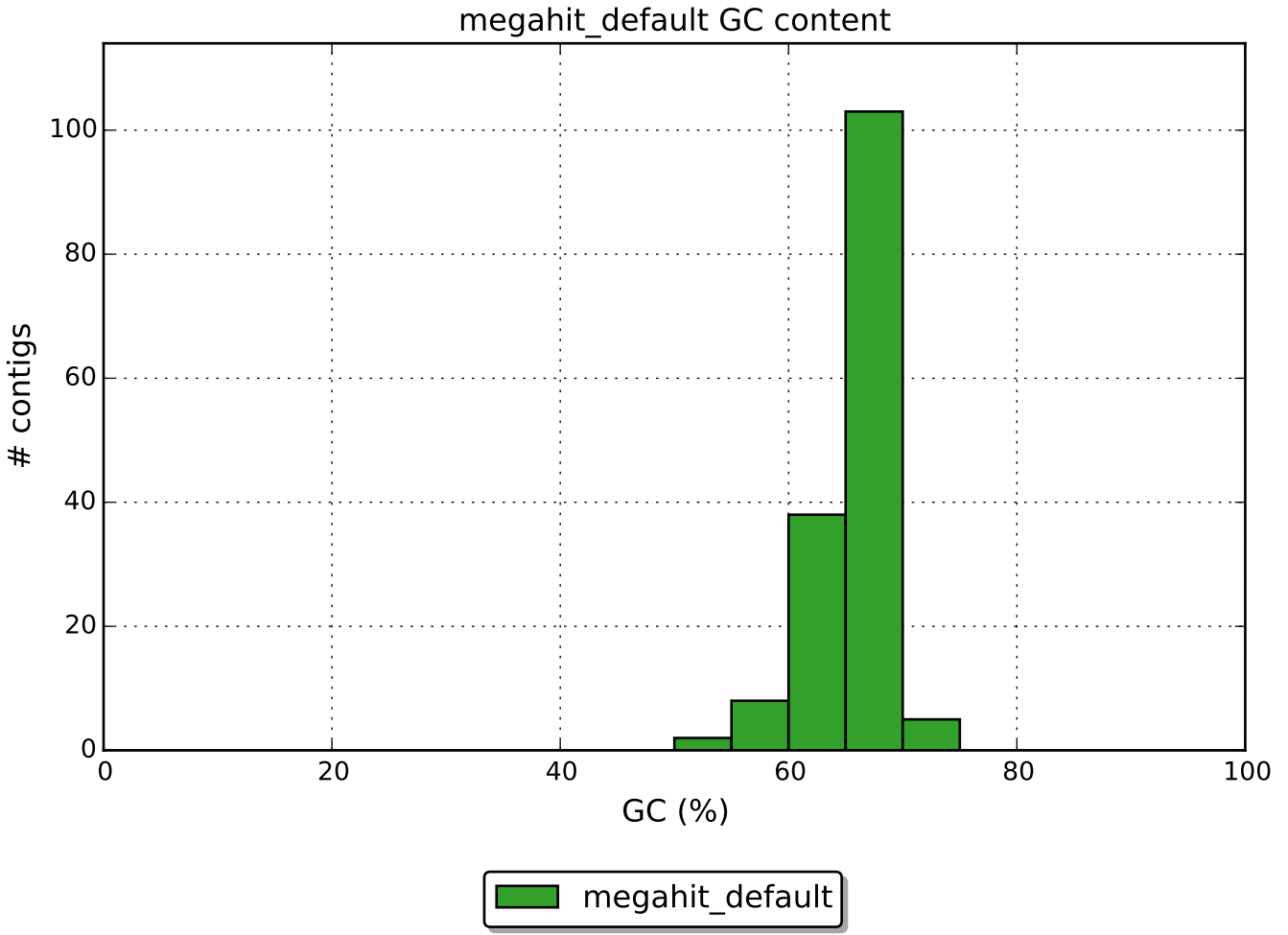

NGx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
spades_default
spades_kmers_careful
megahit_default
megahit_min_count_3

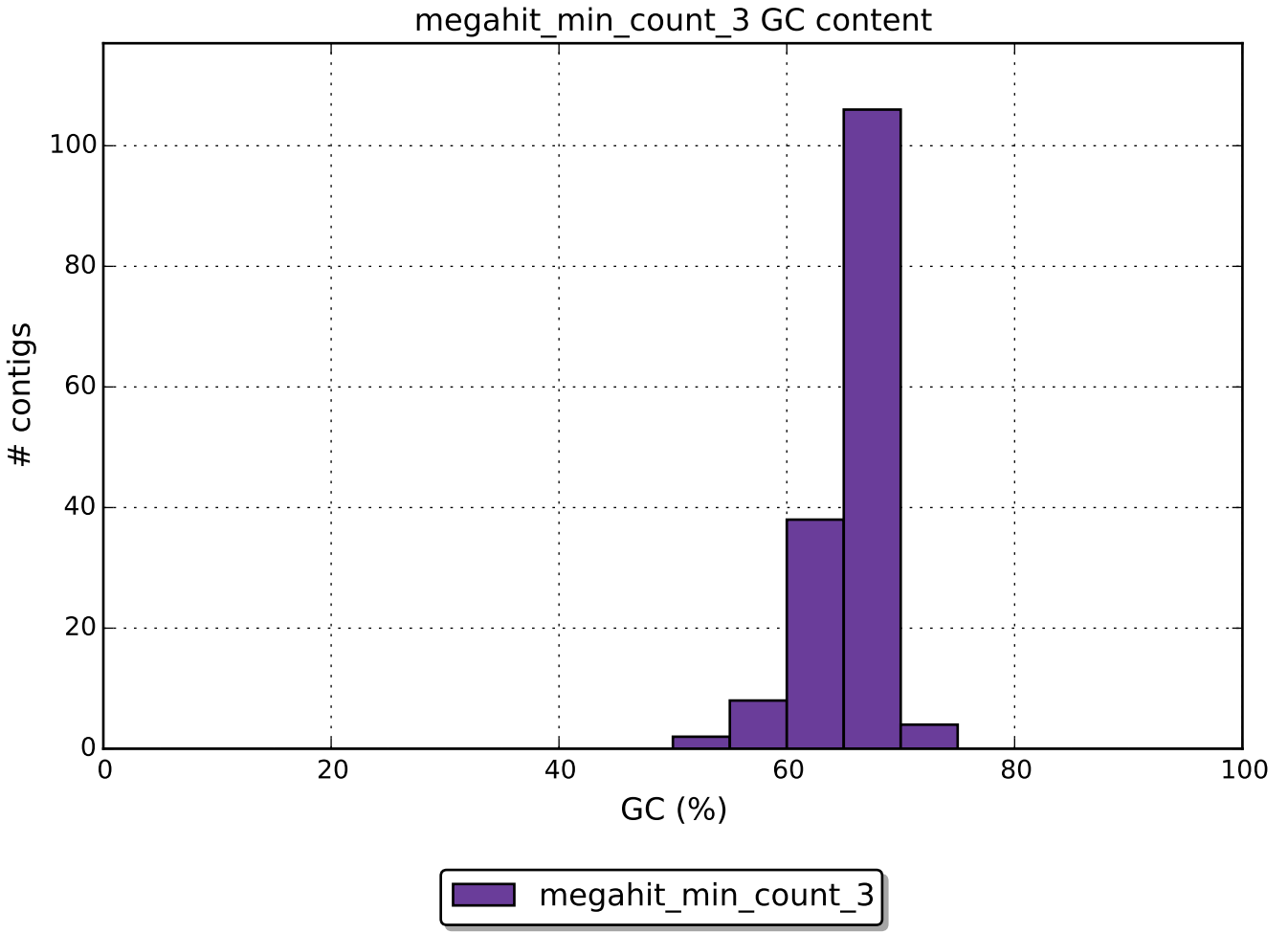

Cumulative length
Cumulative length (Mbp)
0
2
4
6
8
0
30
60
90
120
150
Contig index
spades_default
spades_kmers_careful
megahit_default
megahit_min_count_3
Reference

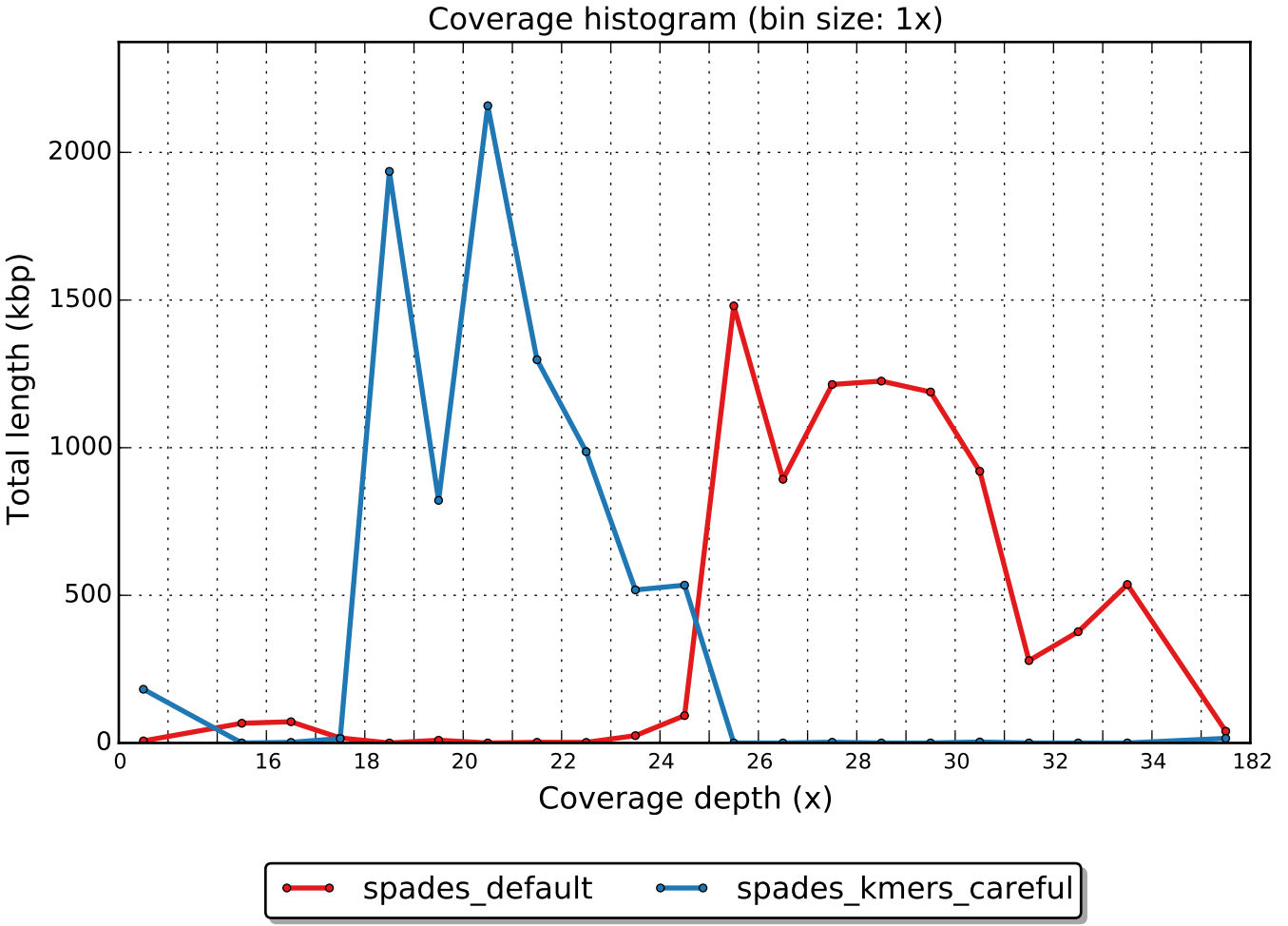

GC content
6000
4000
2000
0
windows
0
20
40
60
80
100
GC (%)
spades_default
spades_kmers_careful
megahit_default
megahit_min_count_3
Reference

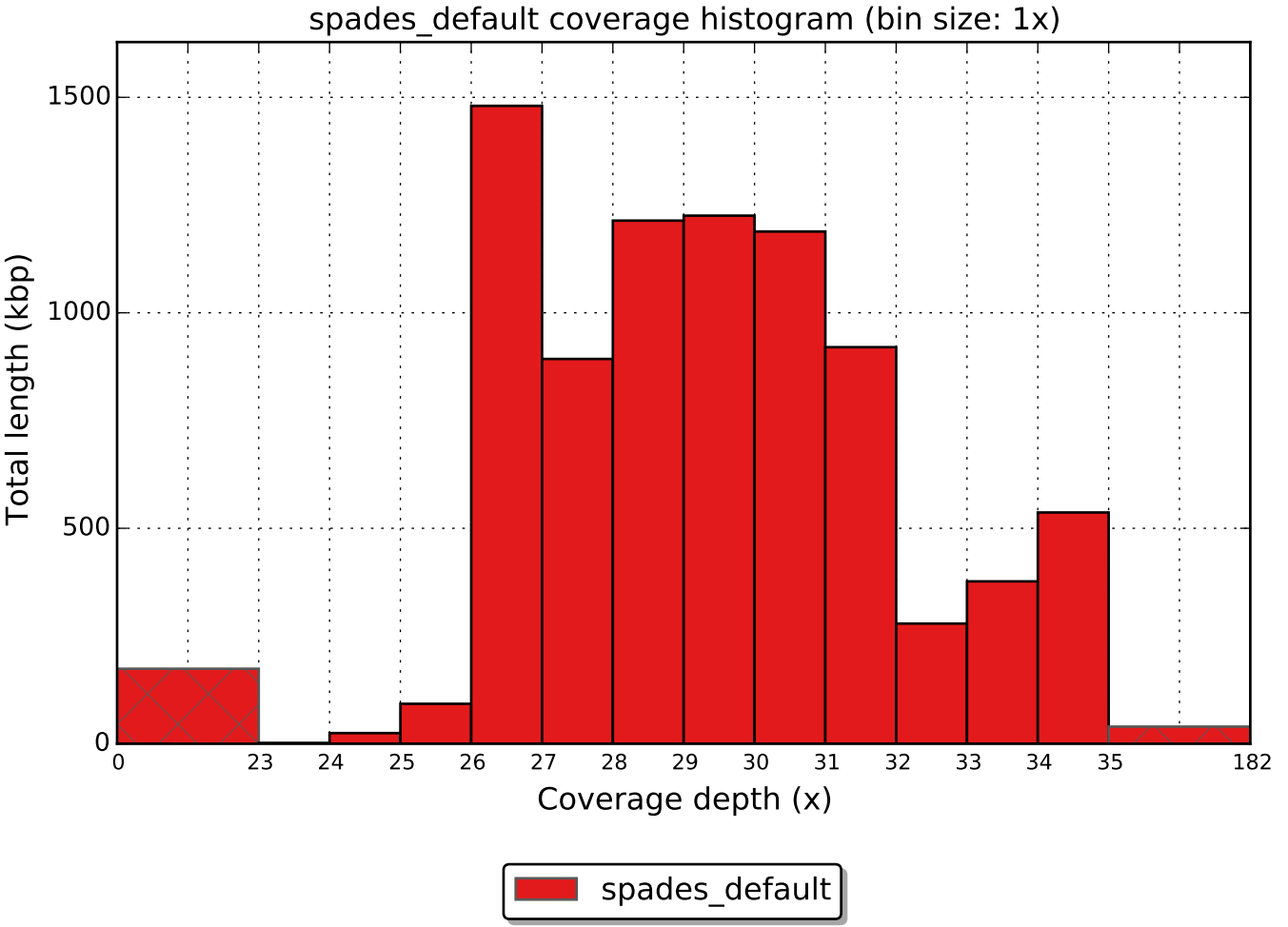

spades_default GC content
contigs
GC (%)
0
20
40
60
80
100
spades_default

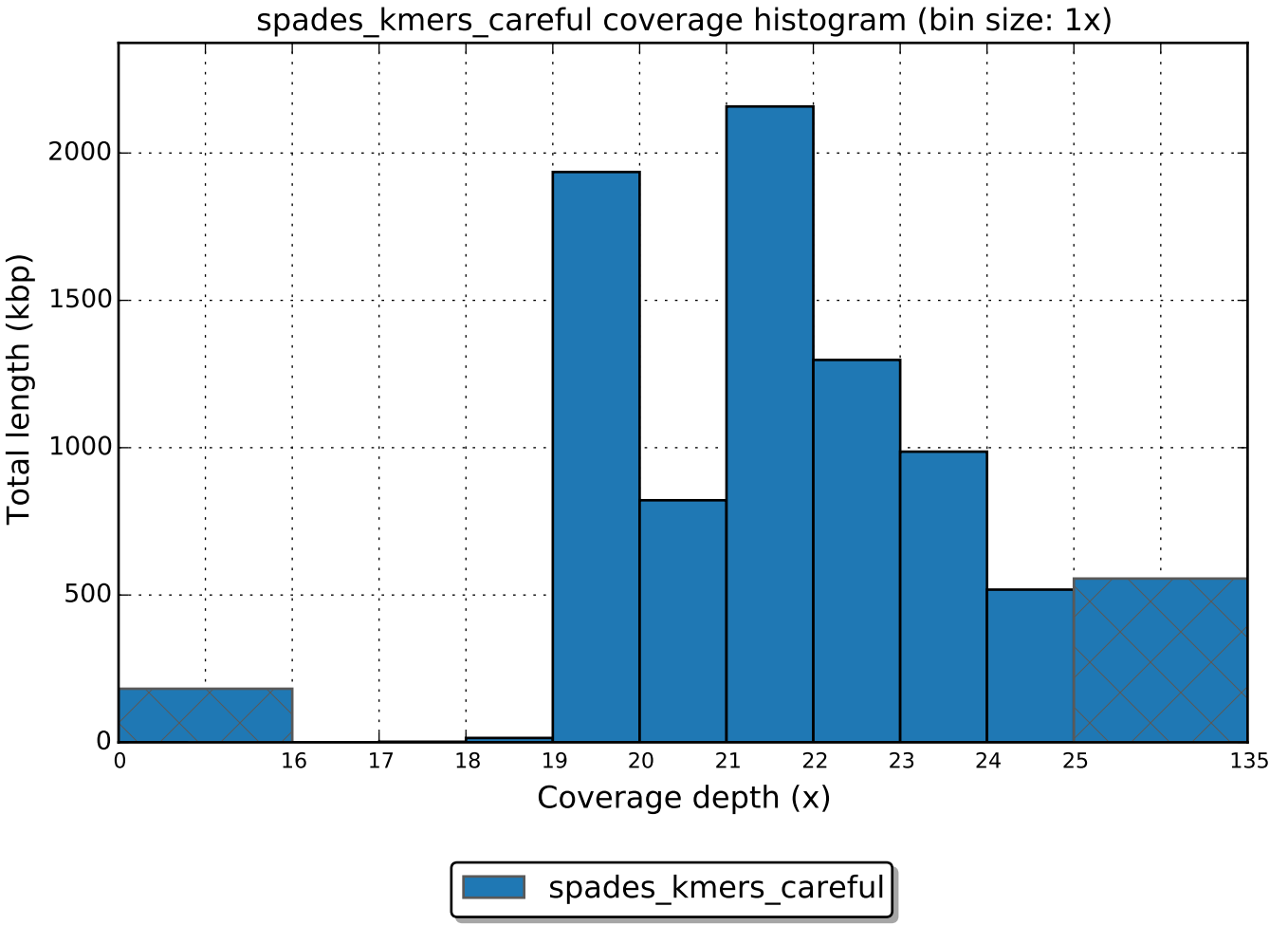

spades_kmers_careful GC content
contigs
GC (%)
0
20
40
60
80
100
spades_kmers_careful

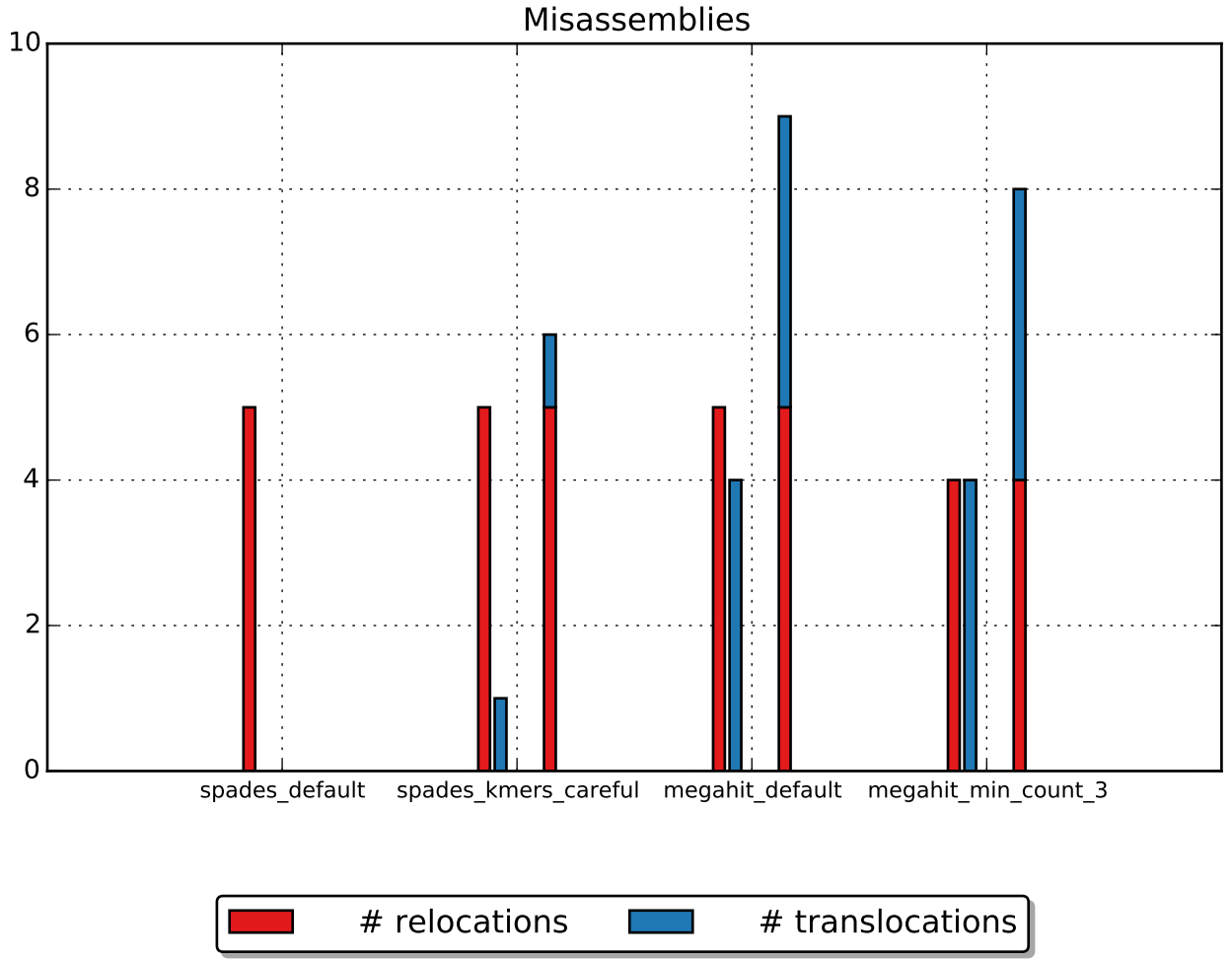

megahit_default GC content
contigs
GC (%)
0
20
40
60
80
100
megahit_default

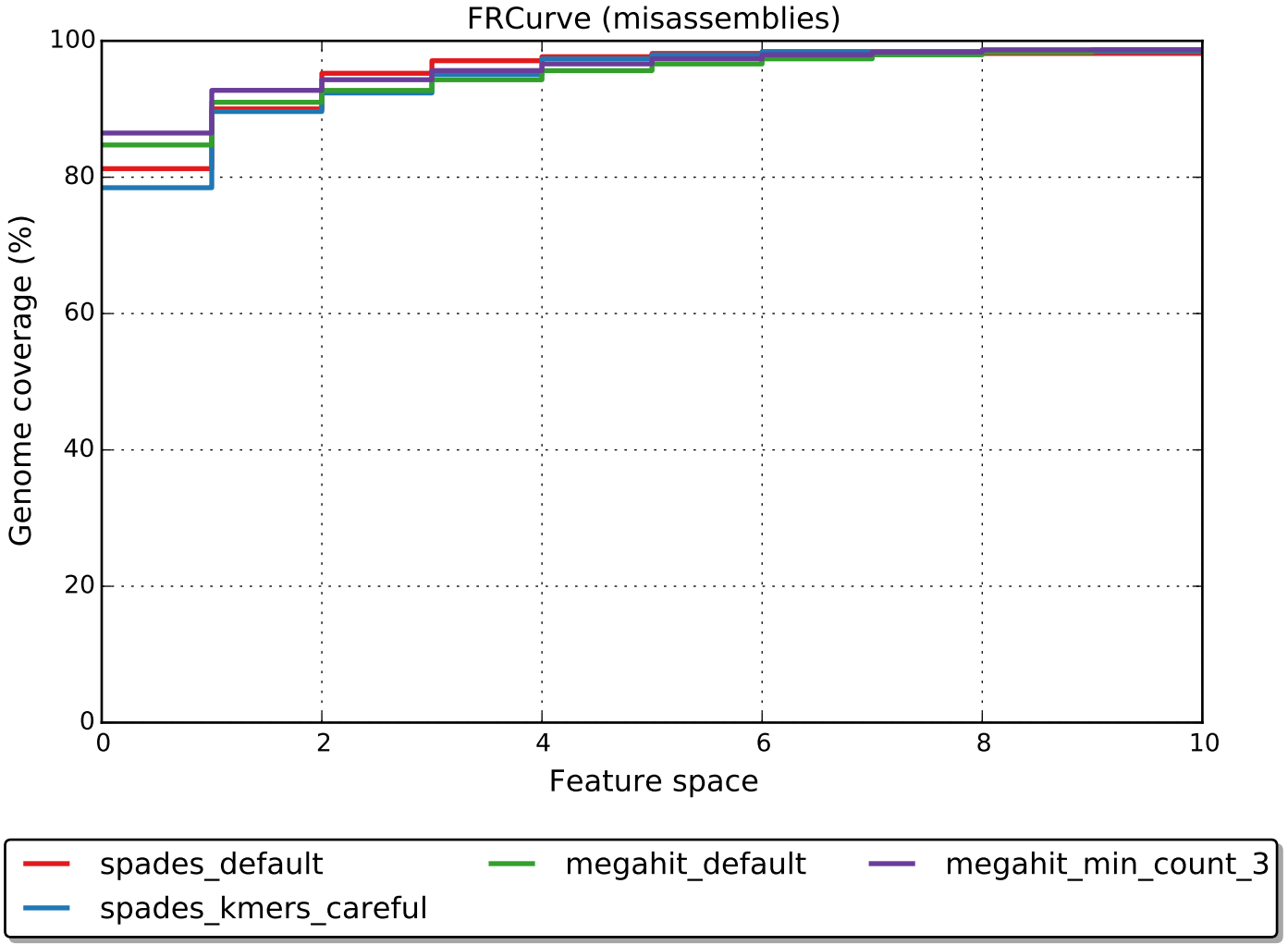

megahit_min_count_3 GC content
contigs
GC (%)
0
20
40
60
80
100
megahit_min_count_3

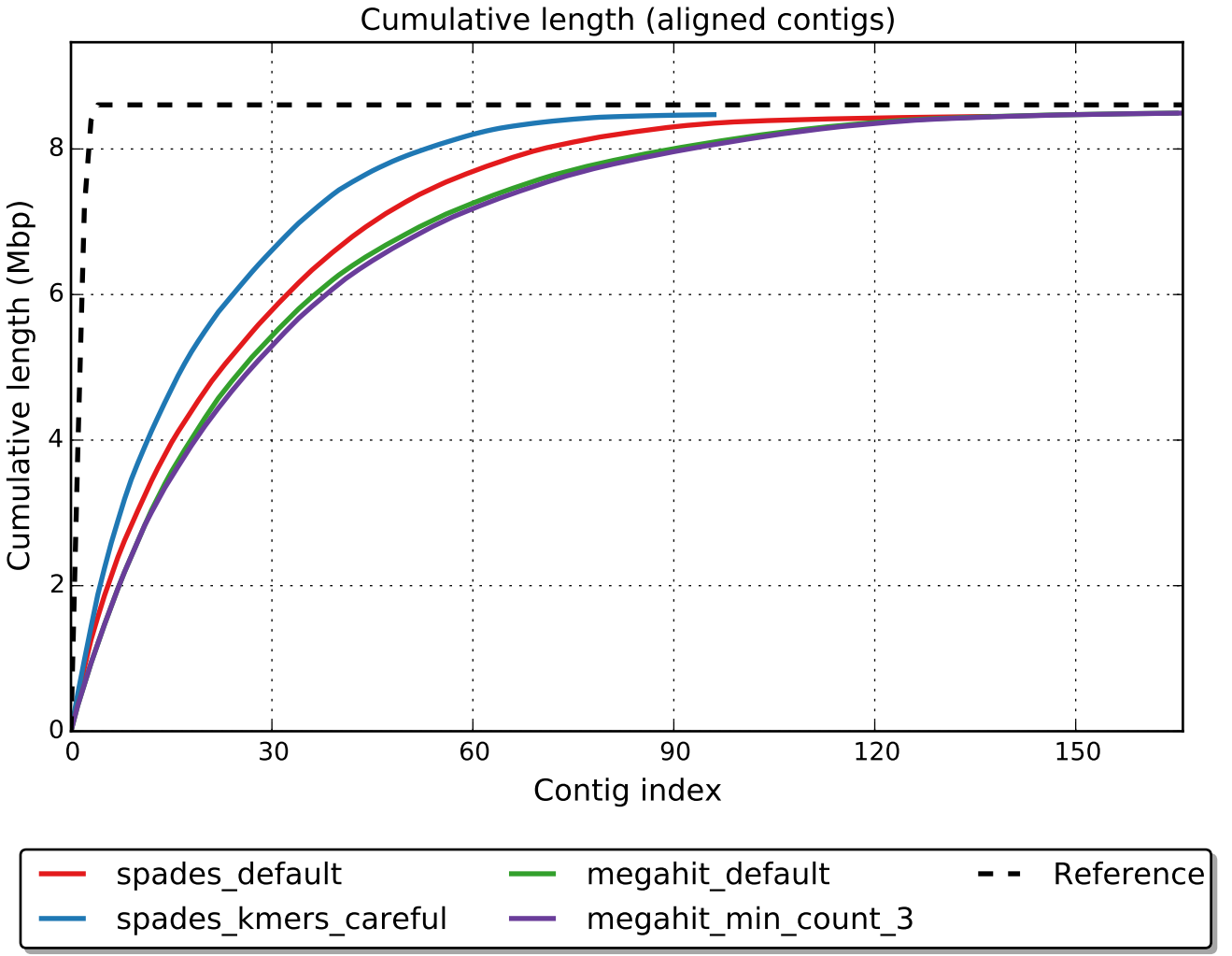

Coverage histogram (bin size: 1x)
Total length (kbp)
2000
1500
1000
500
0
0
16
18
20
22
24
26
28
30
32
34
182
Coverage depth (x)
spades_default
spades_kmers_careful

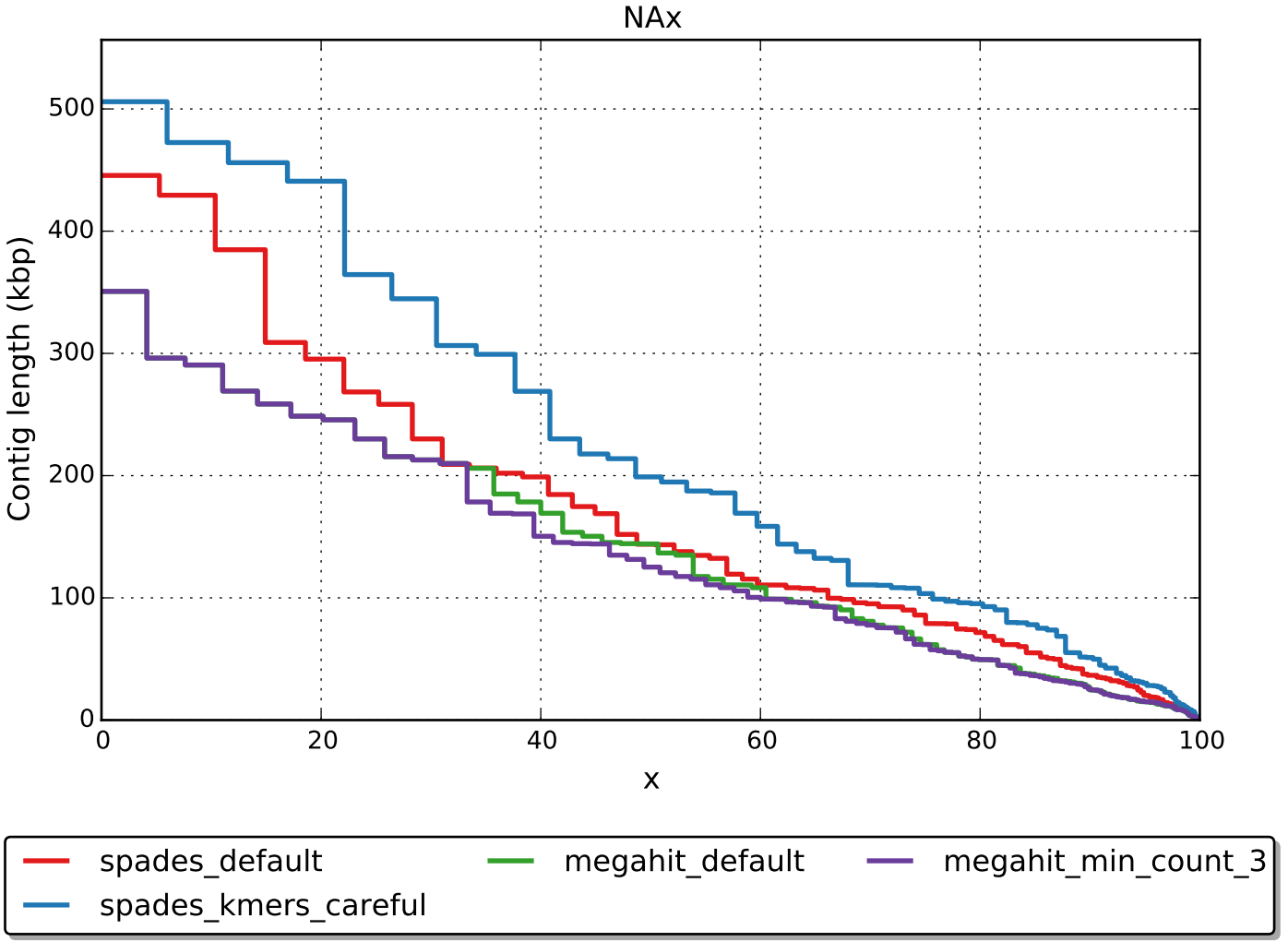

spades_default coverage histogram (bin size: 1x)
Total length (kbp)
1500
1000
500
0
0
23
24
25
26
27
28
29
30
31
32
33
34
35
182
Coverage depth (x)
spades_default

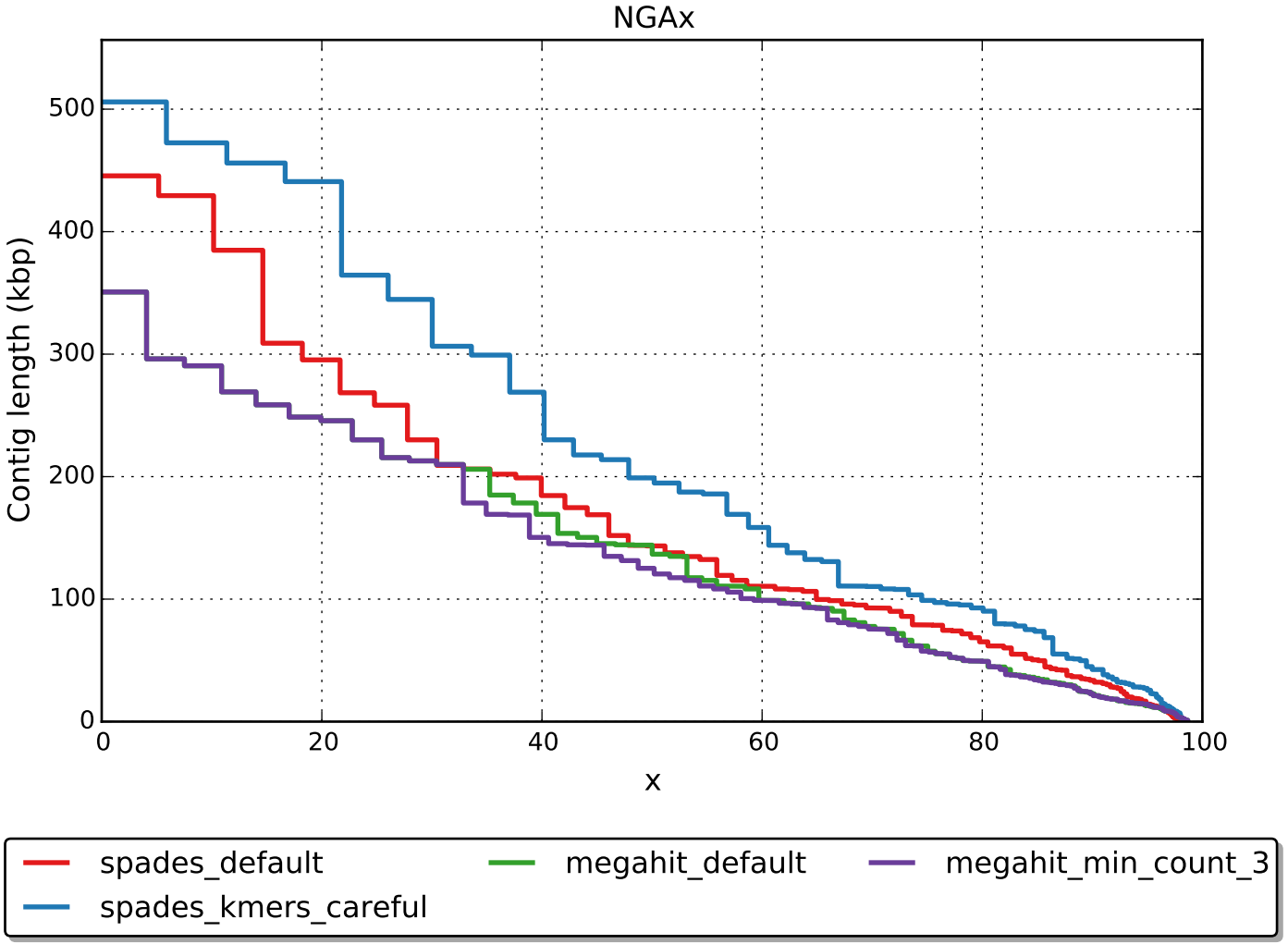

spades_kmers_careful coverage histogram (bin size: 1x)
Total length (kbp)
2000
1500
1000
500
0
0
16
17
18
19
20
21
22
23
24
25
135
Coverage depth (x)
spades_kmers_careful

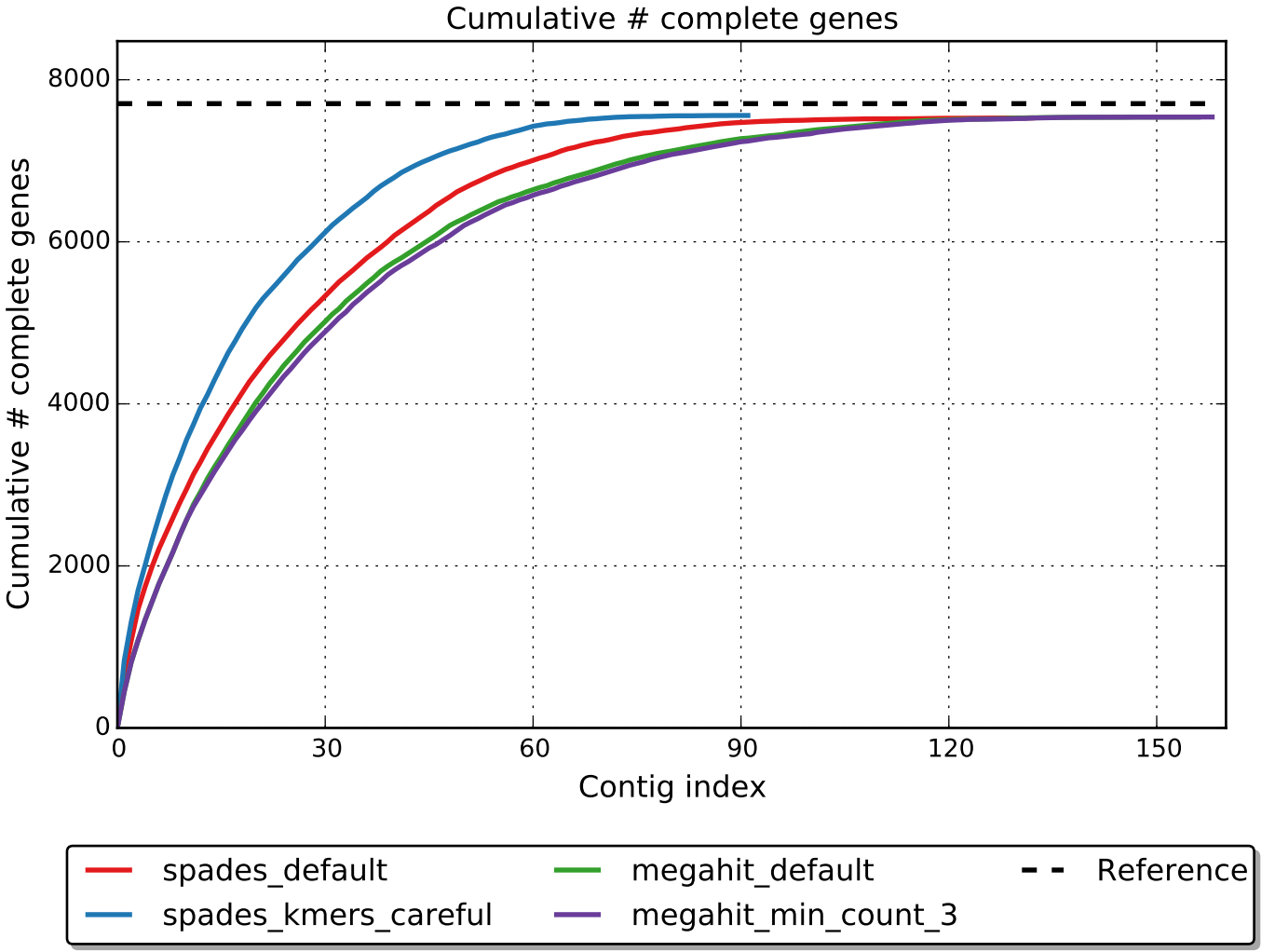

Misassemblies
10
8
6
4
2
0
spades_default
spades_kmers_careful
megahit_default
megahit_min_count_3
relocations
translocations

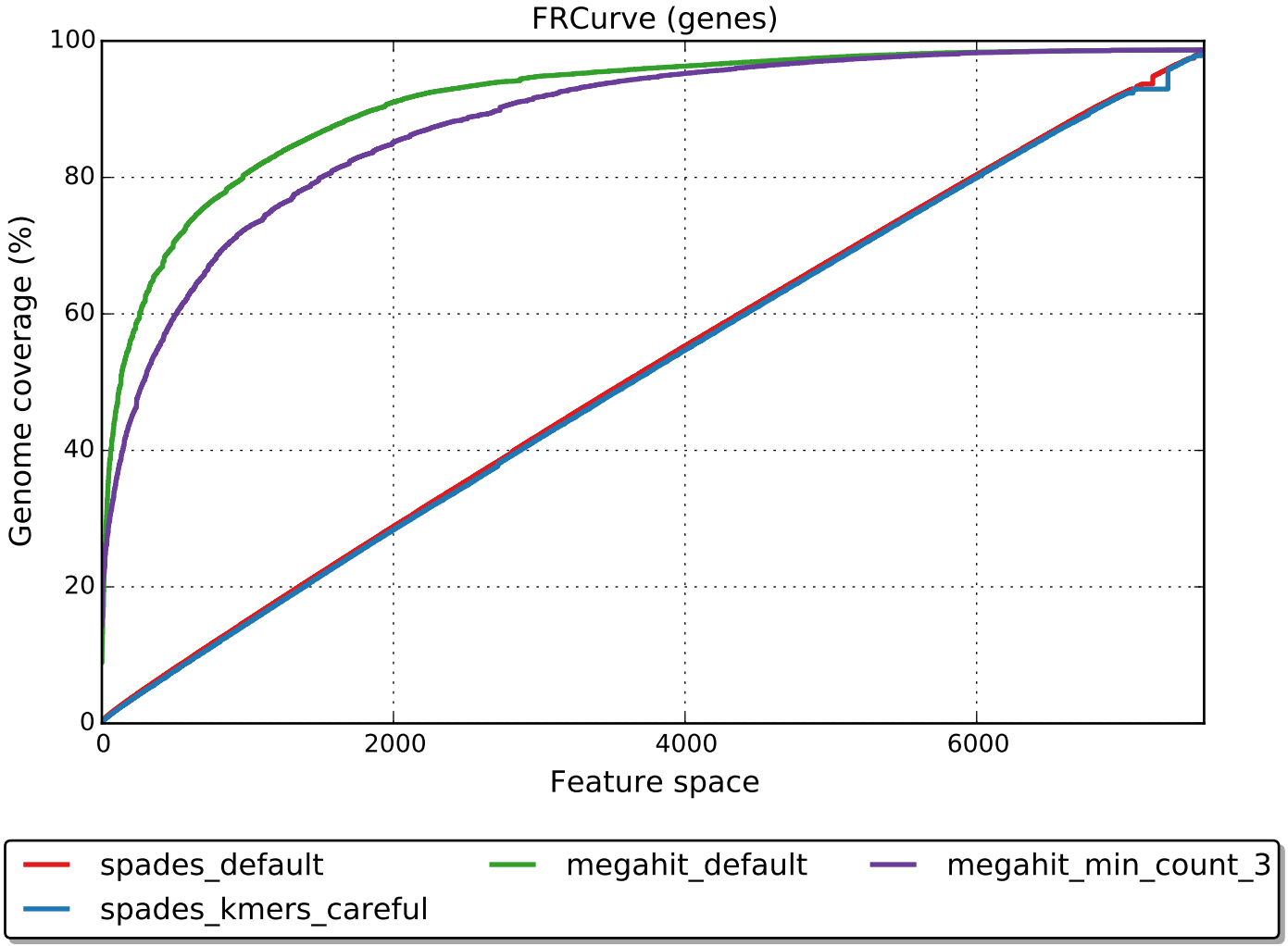

FRCurve (misassemblies)
Genome coverage (%)
Feature space
0
20
40
60
80
100
0
2
4
6
8
10
spades_default
spades_kmers_careful
megahit_default
megahit_min_count_3

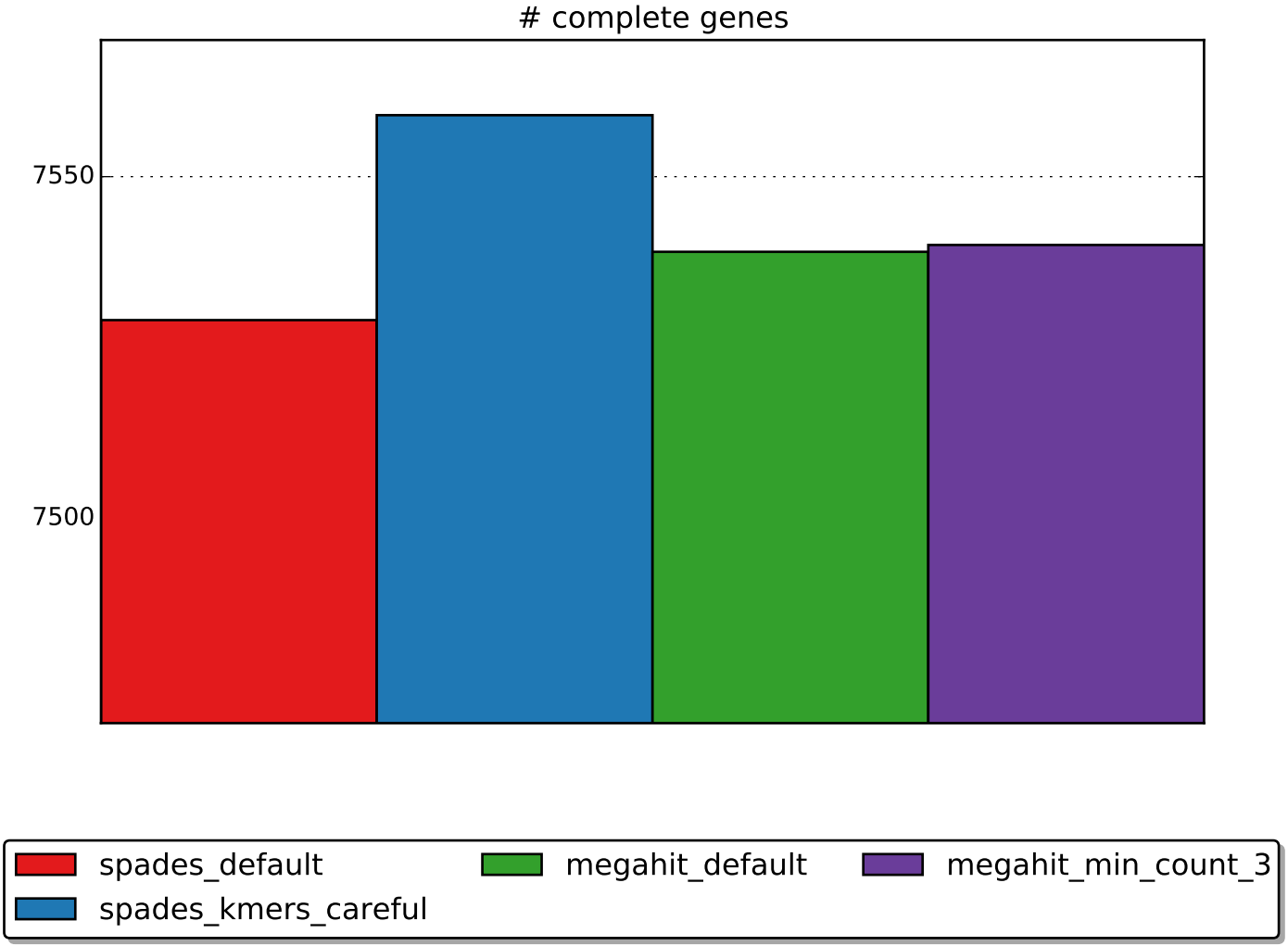

Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
2
4
6
8
0
30
60
90
120
150
Contig index
spades_default
spades_kmers_careful
megahit_default
megahit_min_count_3
Reference

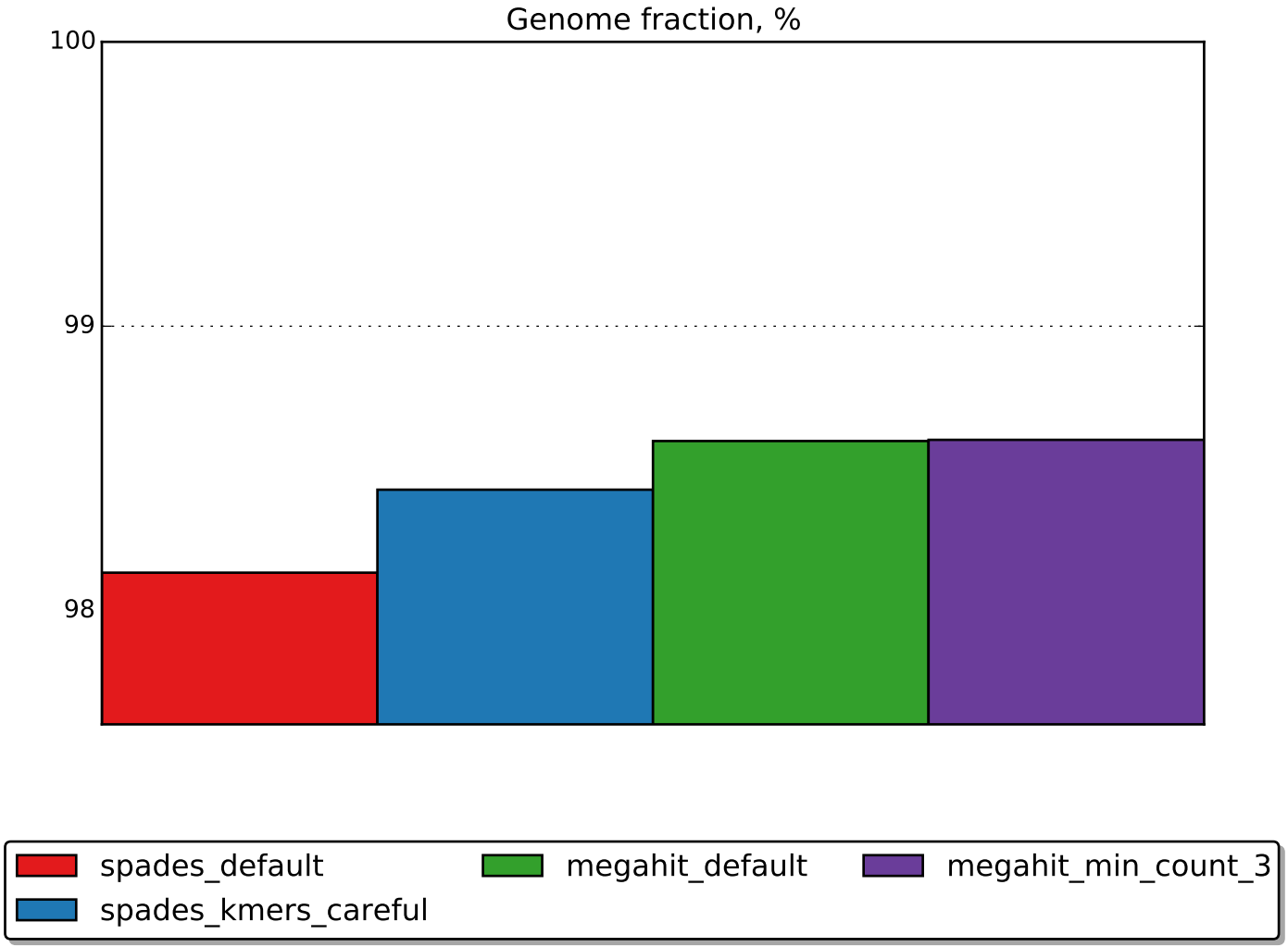

NAx
Contig length (kbp)
x
0
100
200
300
400
500
0
20
40
60
80
100
spades_default
spades_kmers_careful
megahit_default
megahit_min_count_3


NGAx
Contig length (kbp)
0
100
200
300
400
500
0
20
40
60
80
100
x
spades_default
spades_kmers_careful
megahit_default
megahit_min_count_3


Cumulative # complete genes
Cumulative # complete genes
8000
6000
4000
2000
0
0
30
60
90
120
150
Contig index
spades_default
spades_kmers_careful
megahit_default
megahit_min_count_3
Reference


FRCurve (genes)
Genome coverage (%)
Feature space
0
20
40
60
80
100
0
2000
4000
6000
spades_default
spades_kmers_careful
megahit_default
megahit_min_count_3


complete genes
7550
7500
spades_default
spades_kmers_careful
megahit_default
megahit_min_count_3


Genome fraction, %
100
99
98
spades_default
spades_kmers_careful
megahit_default
megahit_min_count_3