Report

	spades2_contigs	Assem_contigs	spades_contigs	Assem_contigs 1
# contigs (>= 0 bp)	1	16	128	305
# contigs (>= 1000 bp)	1	7	4	0
# contigs (>= 5000 bp)	1	7	0	0
# contigs (>= 10000 bp)	1	4	0	0
# contigs (>= 25000 bp)	1	1	0	0
# contigs (>= 50000 bp)	1	0	0	0
Total length (>= 0 bp)	100000	100309	49818	56973
Total length (>= 1000 bp)	100000	99584	5313	0
Total length (>= 5000 bp)	100000	99584	0	0
Total length (>= 10000 bp)	100000	81134	0	0
Total length (>= 25000 bp)	100000	33235	0	0
Total length (>= 50000 bp)	100000	0	0	0
# contigs	1	7	20	11
Largest contig	100000	33235	1737	998
Total length	100000	99584	15922	7243
Reference length	4639675	4639675	4639675	4639675
GC (%)	52.59	52.58	51.21	50.71
Reference GC (%)	50.79	50.79	50.79	50.79
N50	100000	19911	718	632
N75	100000	13440	635	542
L50	1	2	8	5
L75	1	4	13	8
# misassemblies	0	0	1	0
# misassembled contigs	0	0	1	0
Misassembled contigs length	0	0	1084	0
# local misassemblies	0	0	0	0
# unaligned contigs	0 + 0 part	0 + 0 part	0 + 0 part	0 + 0 part
Unaligned length	0	0	0	0
Genome fraction (%)	2.155	2.145	0.343	0.156
Duplication ratio	1.000	1.001	1.000	1.000
# N's per 100 kbp	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	0.00	0.00	31.40	0.00
# indels per 100 kbp	0.00	0.00	0.00	0.00
Largest alignment	100000	33235	1737	998
Total aligned length	100000	99584	15922	7243
NA50	100000	19911	715	632
NGA50	-	-	-	-
NA75	100000	13440	587	542
LA50	1	2	8	5
LA75	1	4	14	8

All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

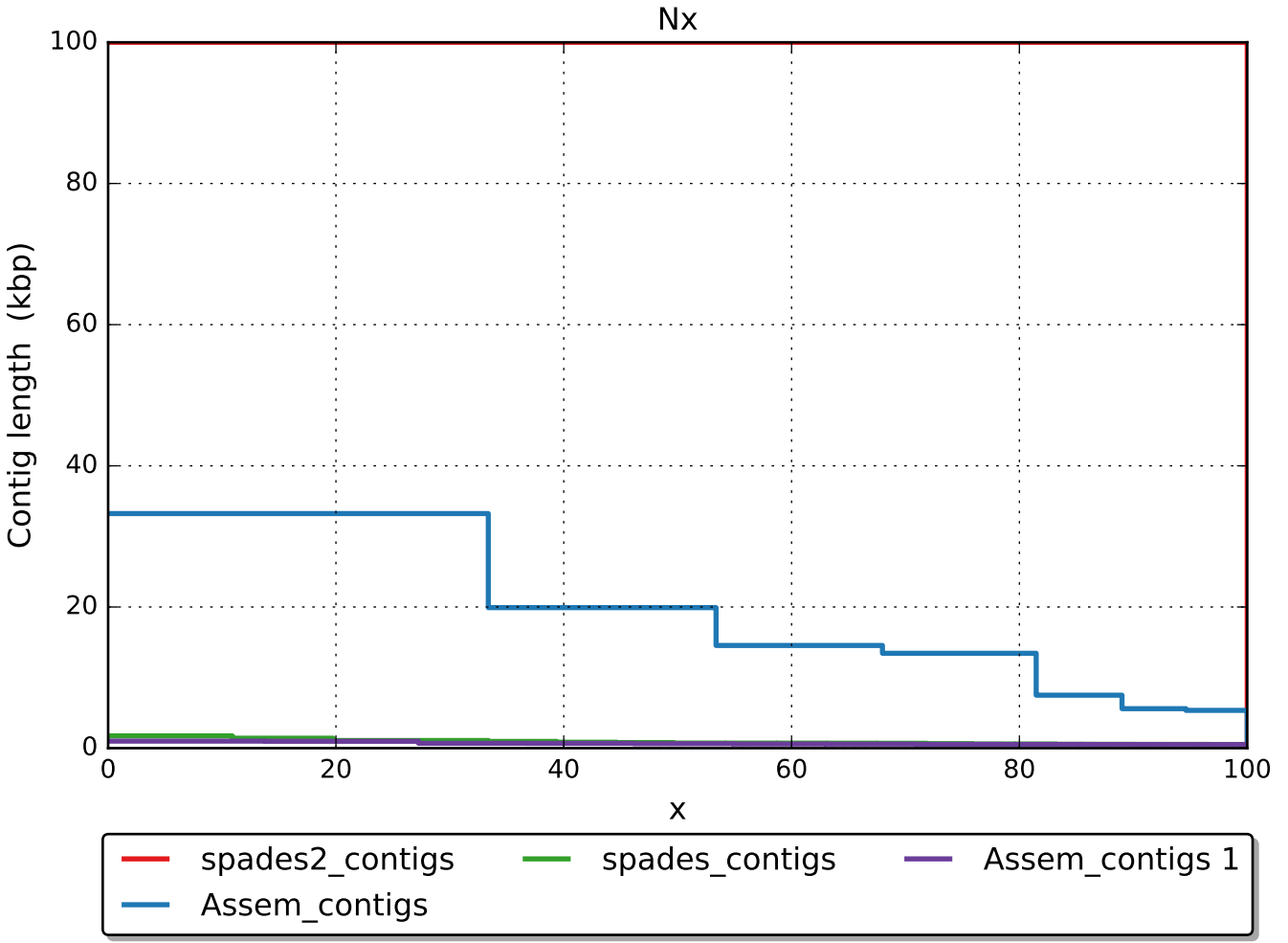
	spades2_contigs	Assem_contigs	spades_contigs	Assem_contigs 1
# misassemblies	0	0	1	0
# relocations	0	0	1	0
# translocations	0	0	0	0
# inversions	0	0	0	0
# misassembled contigs	0	0	1	0
Misassembled contigs length	0	0	1084	0
# local misassemblies	0	0	0	0
# mismatches	0	0	5	0
# indels	0	0	0	0
# short indels	0	0	0	0
# long indels	0	0	0	0
Indels length	0	0	0	0

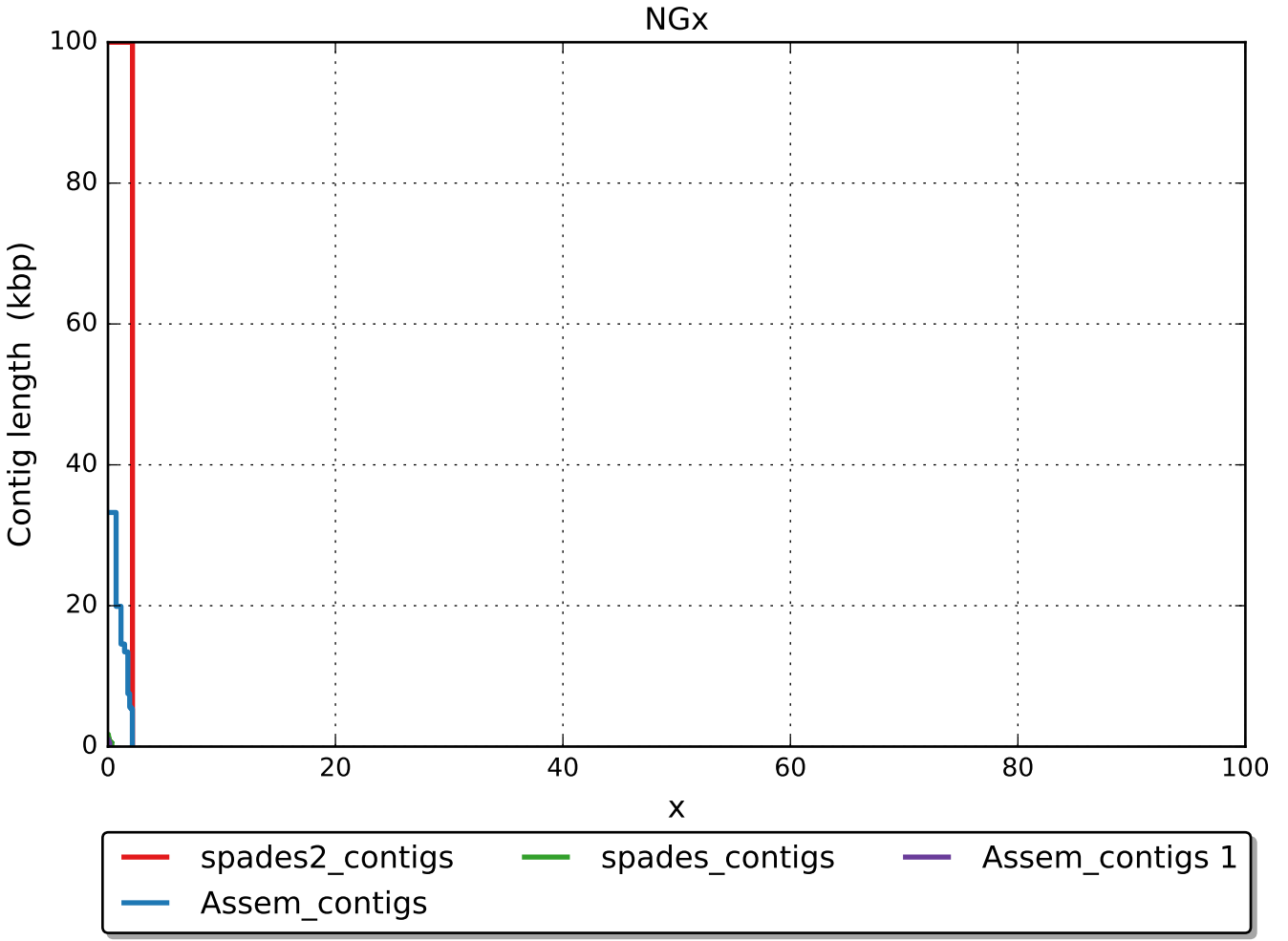
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

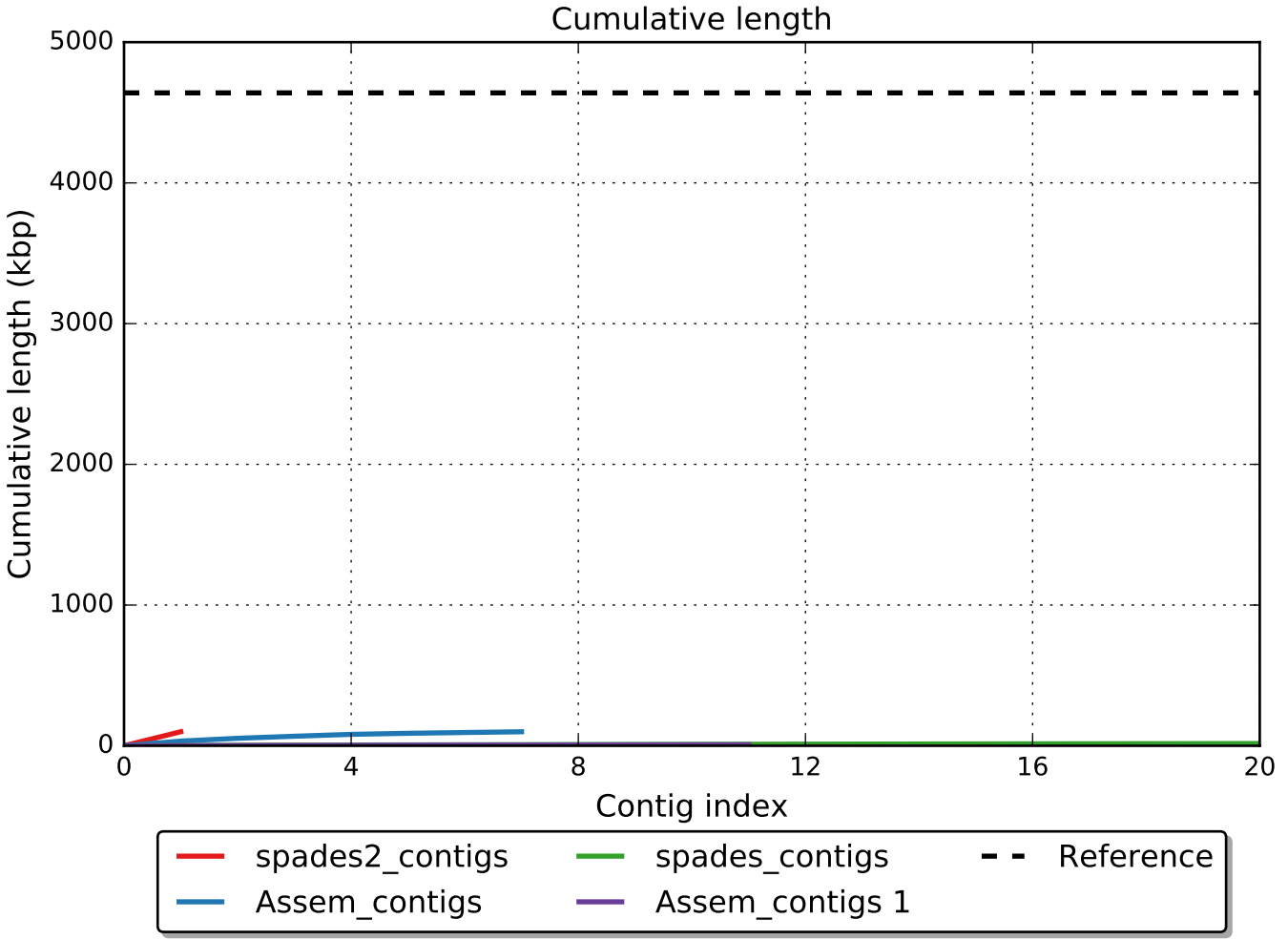
Unaligned report

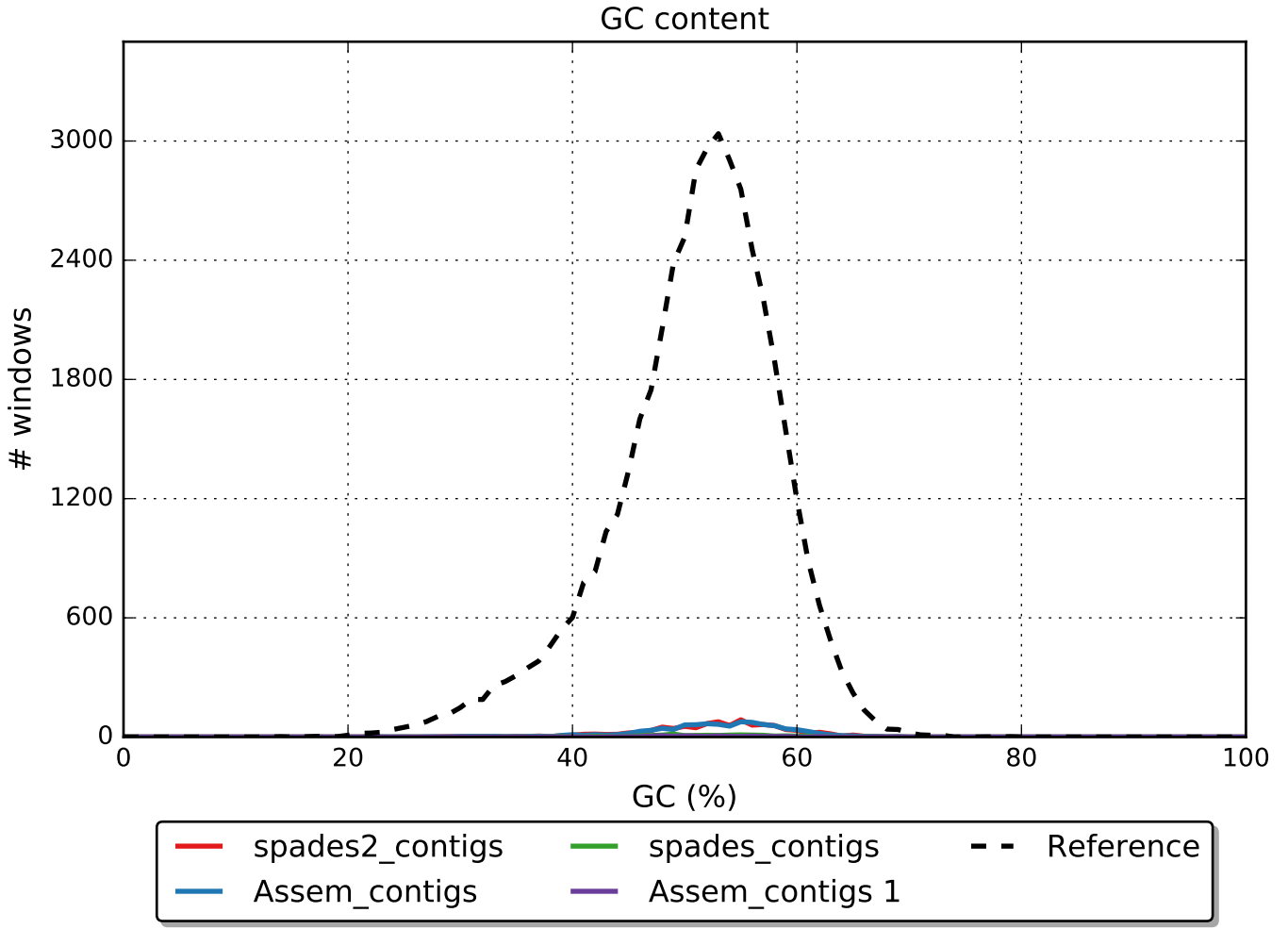
	spades2_contigs	Assem_contigs	spades_contigs	Assem_contigs 1
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	0	0	0	0
# with misassembly	0	0	0	0
# both parts are significant	0	0	0	0
Partially unaligned length	0	0	0	0
# N's	0	0	0	0

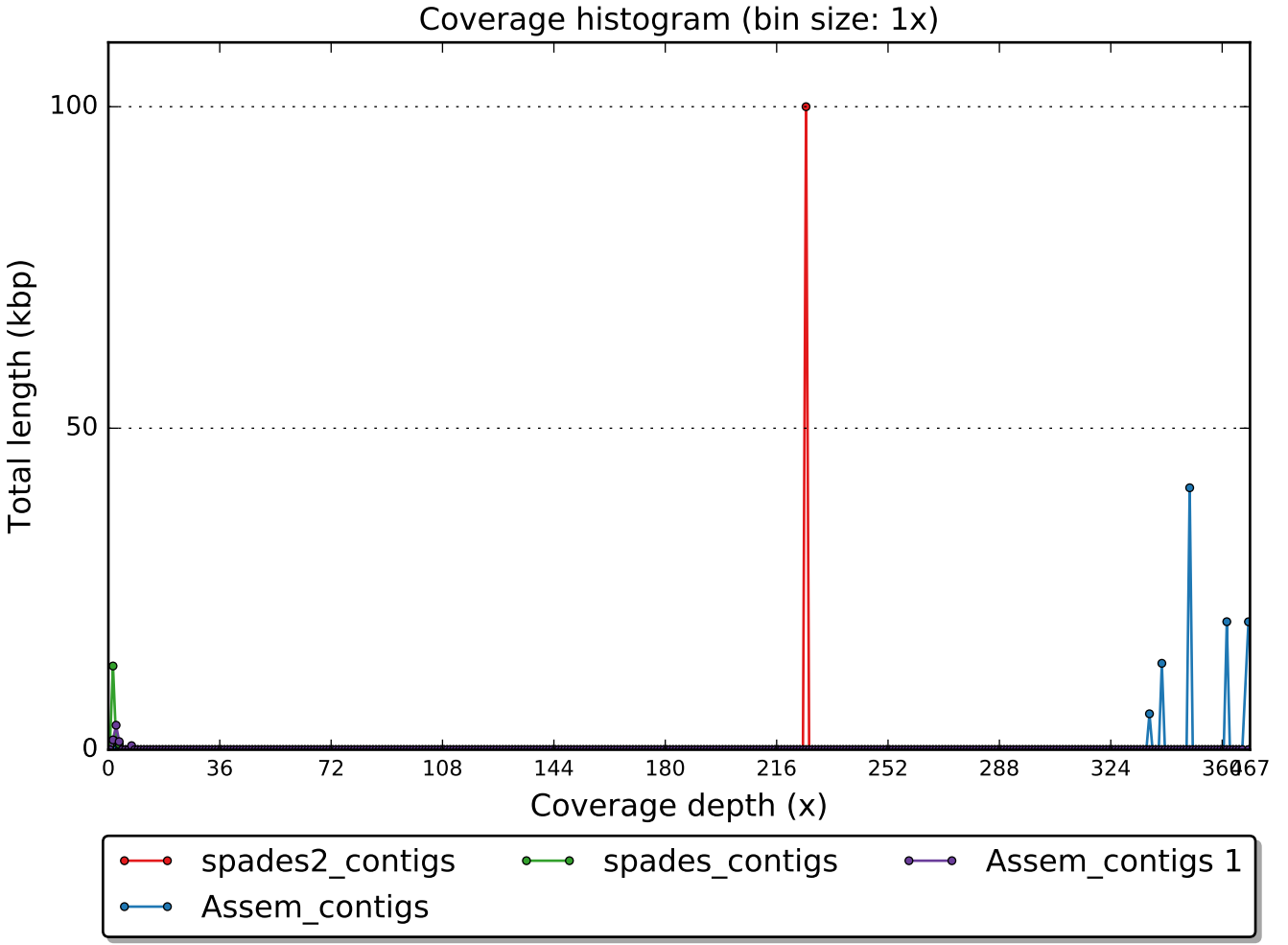
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

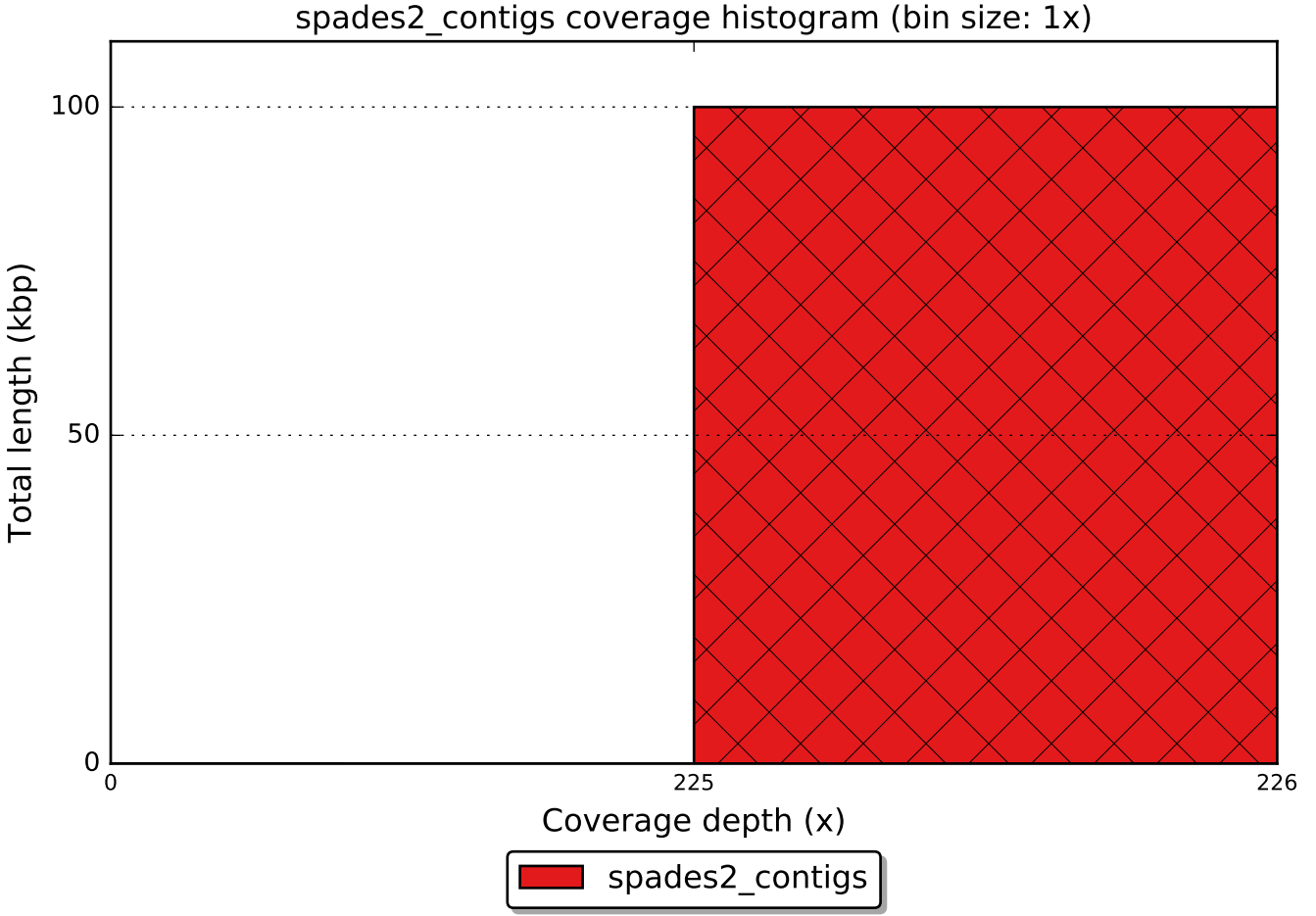

Nx
Contig length (kbp)
100
80
60
40
20
0
0
20
40
60
80
100
x
spades2_contigs
spades_contigs
Assem_contigs 1
Assem_contigs

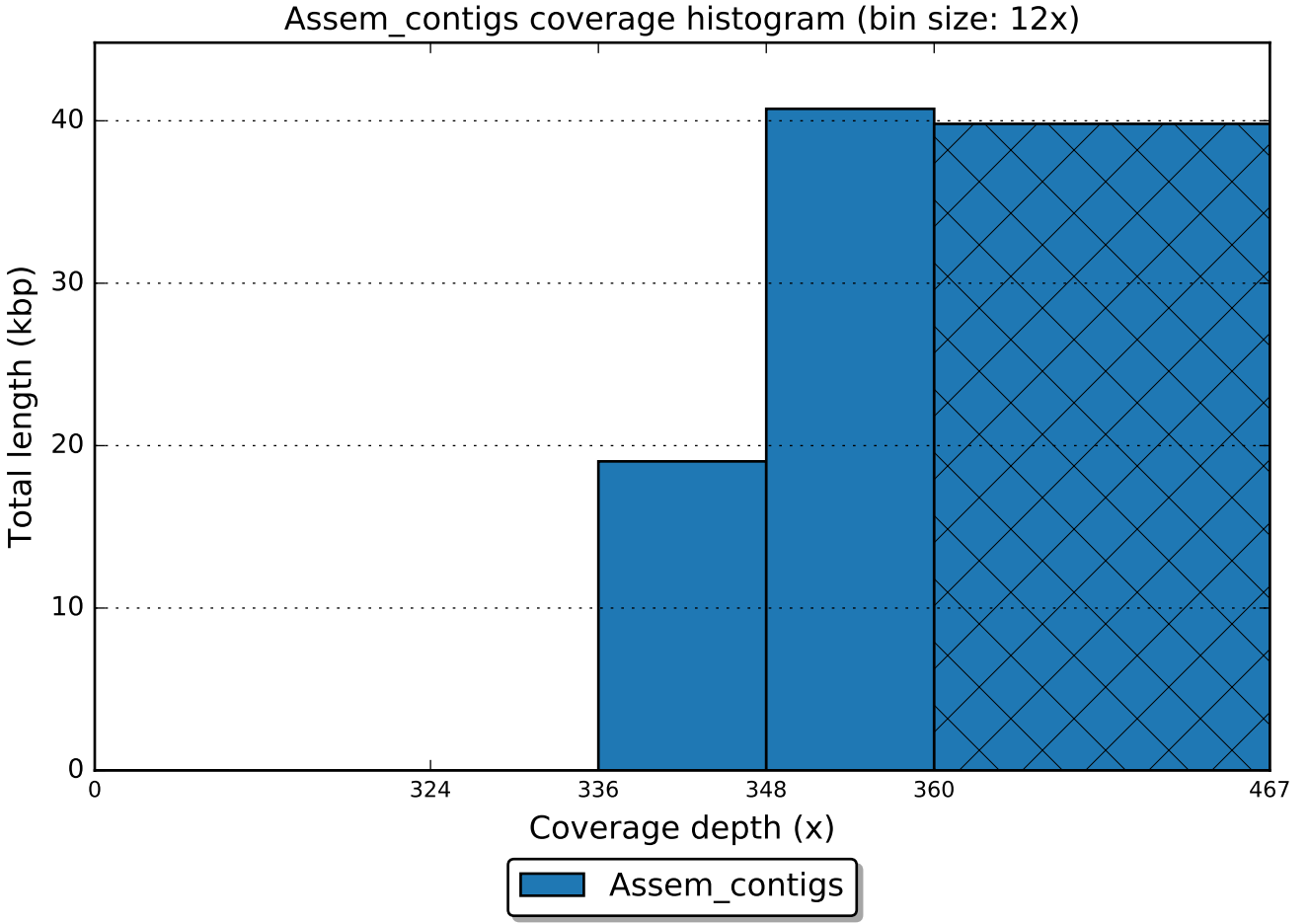

NGx
Contig length (kbp)
x
0
20
40
60
80
100
spades2_contigs
spades_contigs
Assem_contigs 1
Assem_contigs

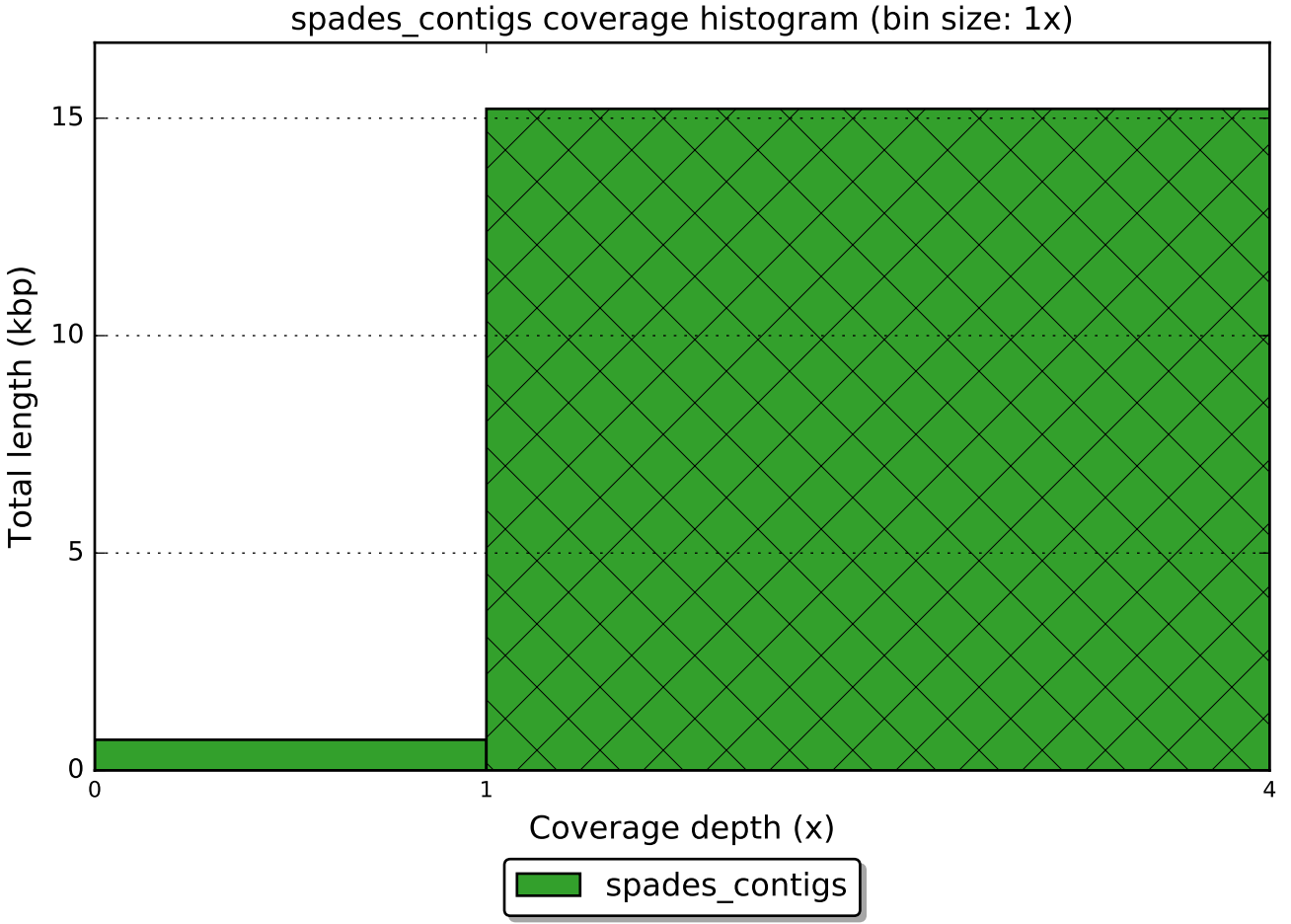

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
4
8
12
16
20
Contig index
spades2_contigs
Assem_contigs
spades_contigs
Assem_contigs 1
Reference

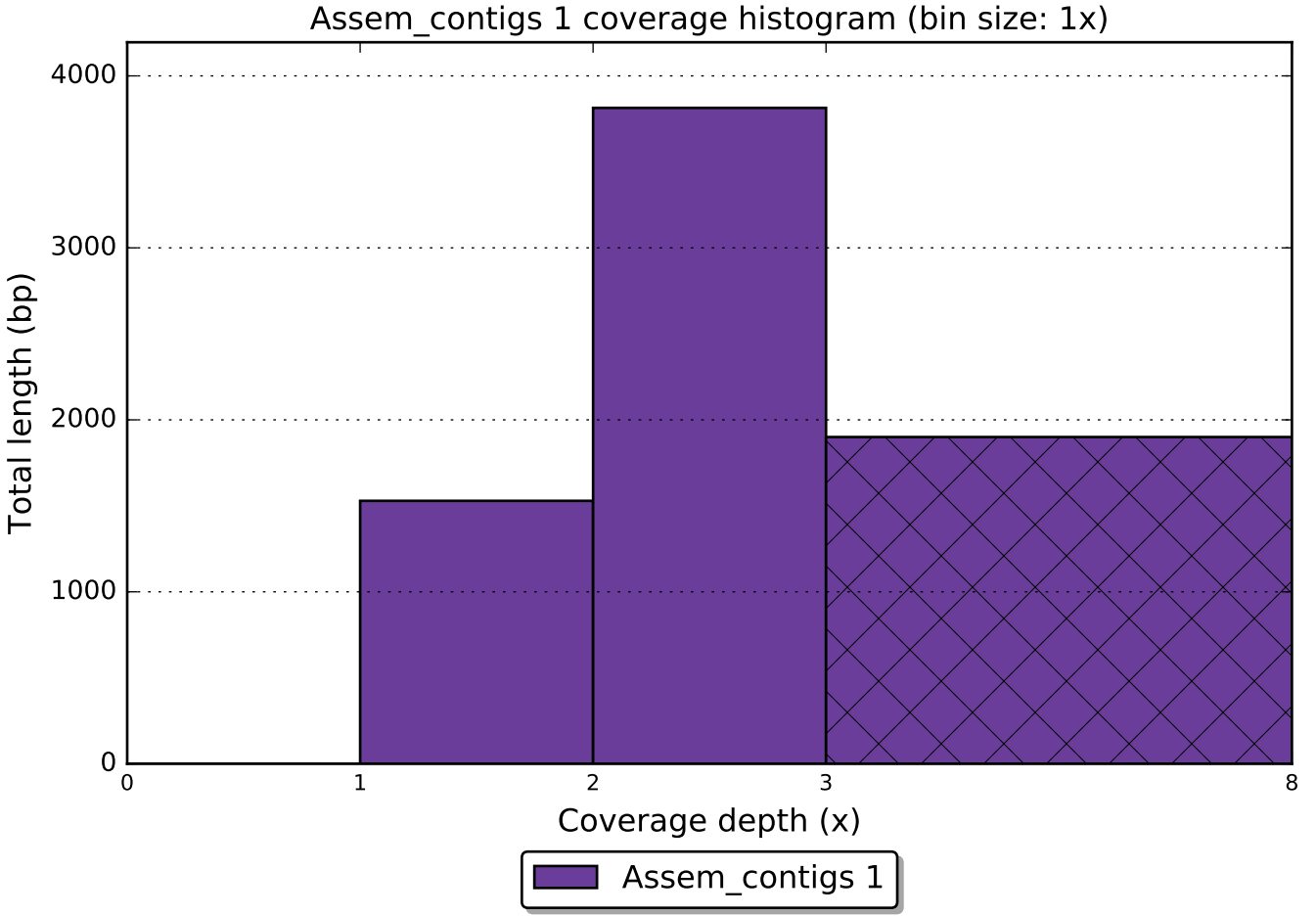

GC content
windows
3000
2400
1800
1200
600
0
0
20
40
60
80
100
GC (%)
spades2_contigs
Assem_contigs
spades_contigs
Assem_contigs 1
Reference

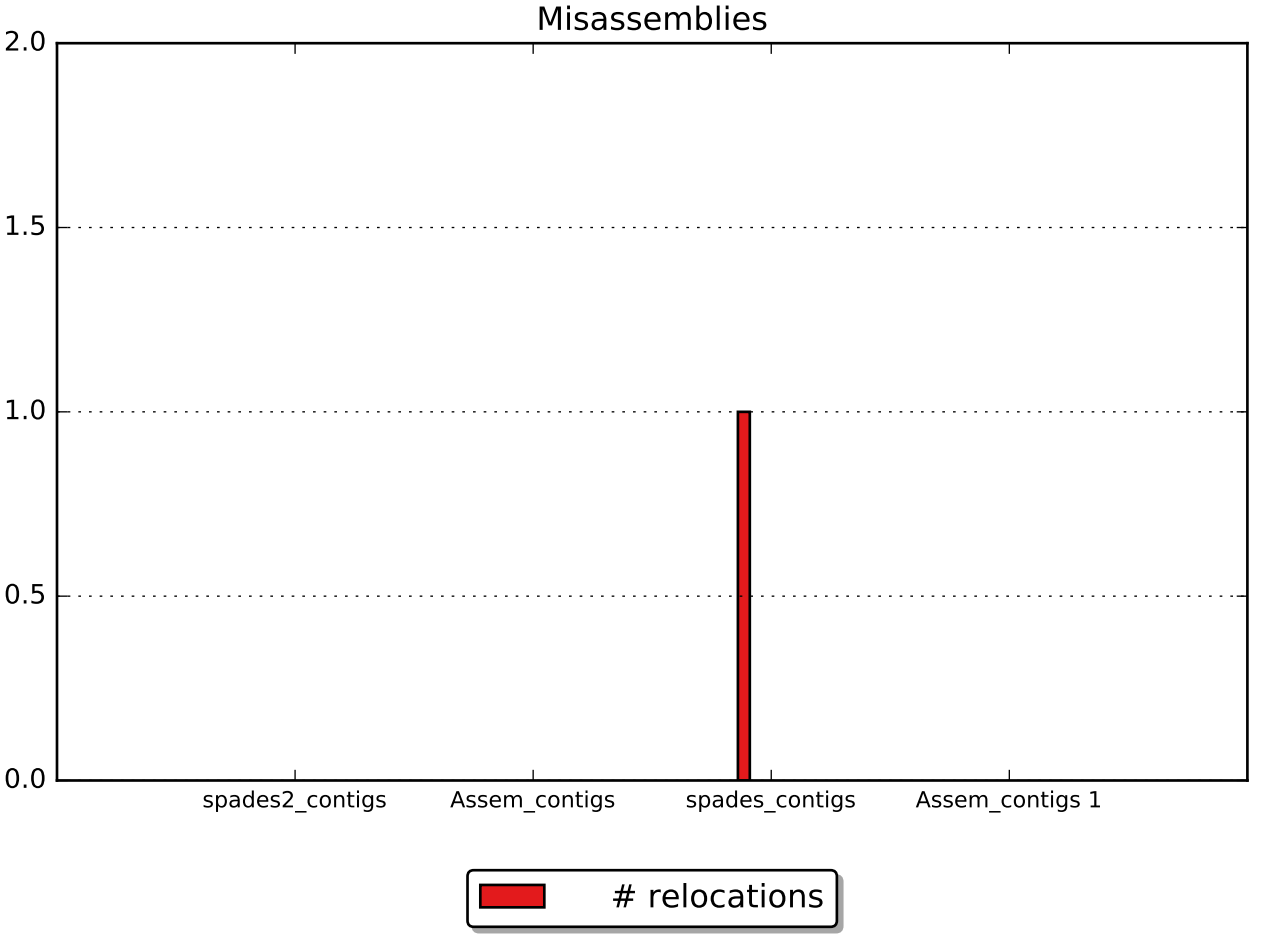

Coverage histogram (bin size: 1x)
Total length (kbp)
100
50
0
0
36
72
108
144
180
216
252
288
324
360
367
Coverage depth (x)
spades2_contigs
spades_contigs
Assem_contigs 1
Assem_contigs

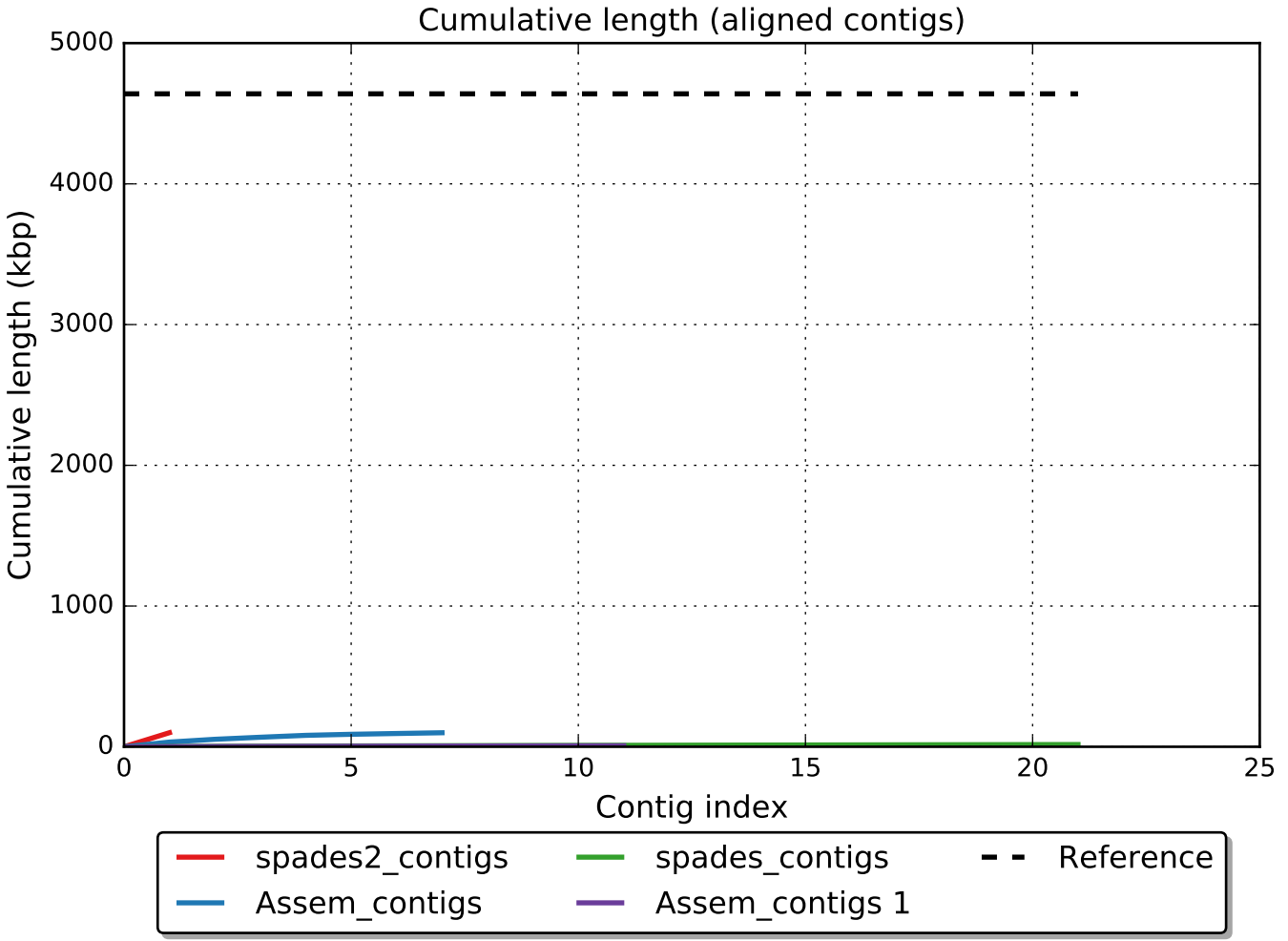

spades2_contigs coverage histogram (bin size: 1x)
100
50
0
Total length (kbp)
0
225
226
Coverage depth (x)
spades2_contigs

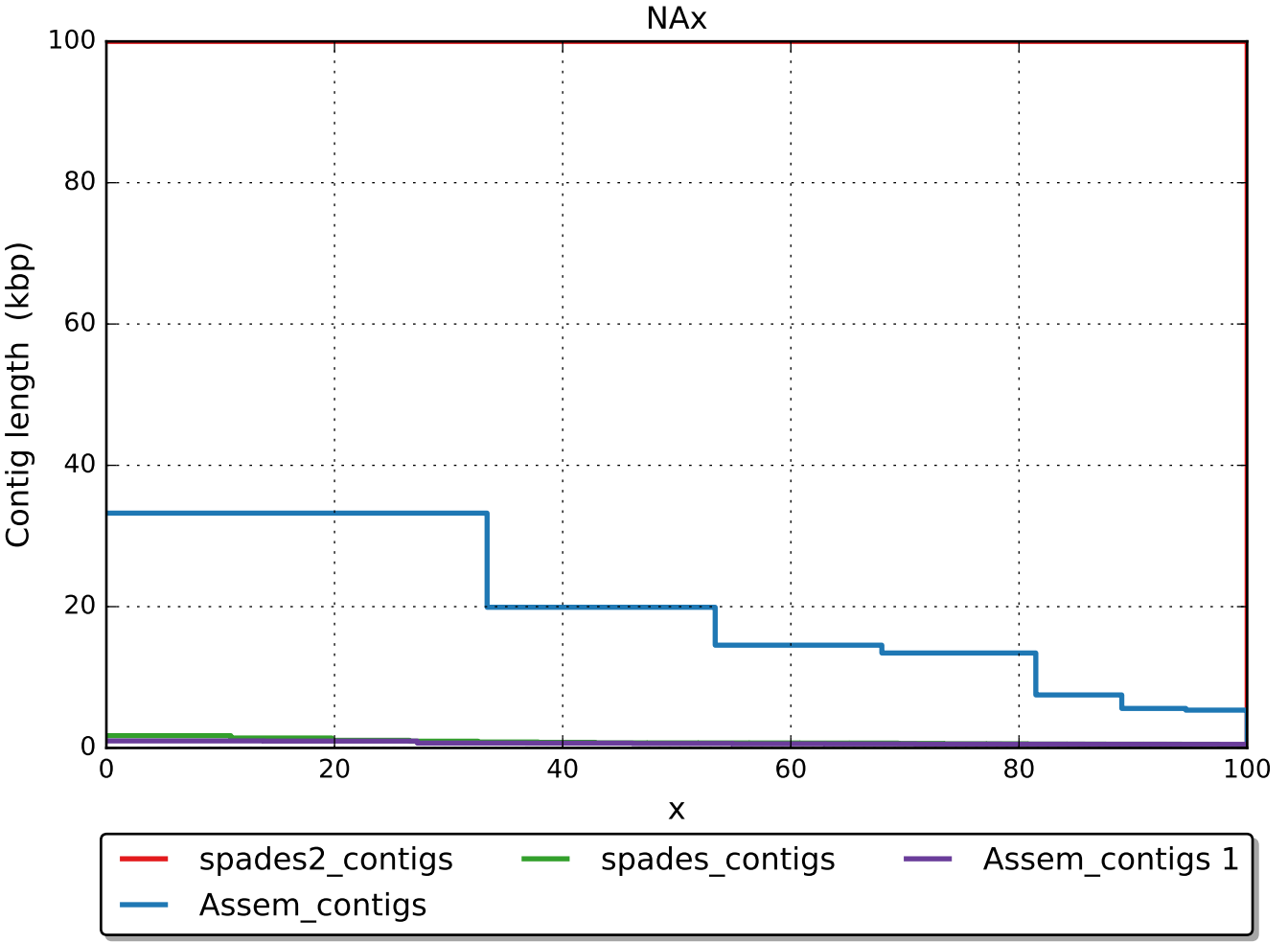

Assem_contigs coverage histogram (bin size: 12x)
Total length (kbp)
0
10
20
30
40
0
324
336
348
360
467
Coverage depth (x)
Assem_contigs

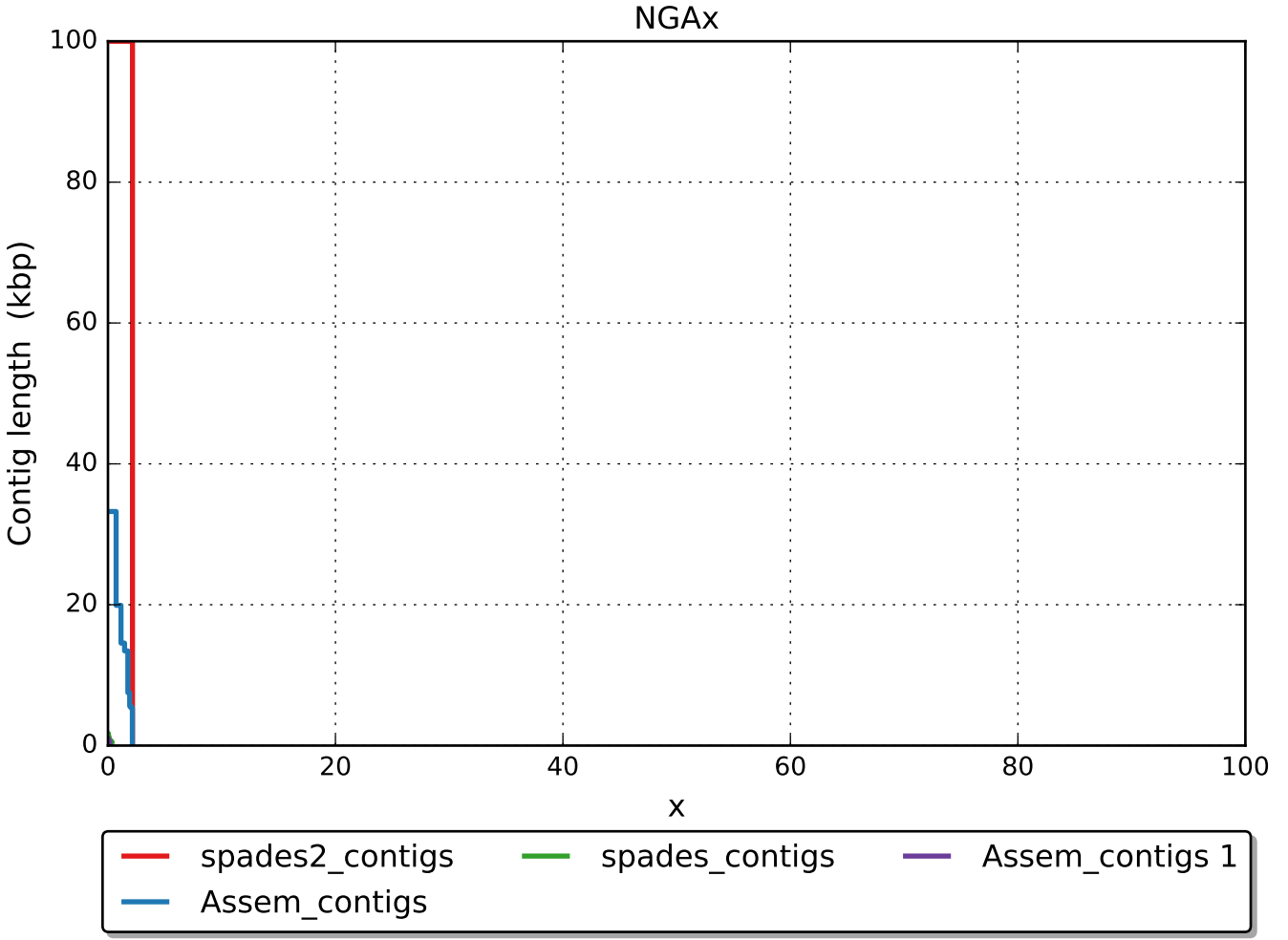

spades_contigs coverage histogram (bin size: 1x)
Total length (kbp)
15
10
5
0
0
1
4
Coverage depth (x)
spades_contigs

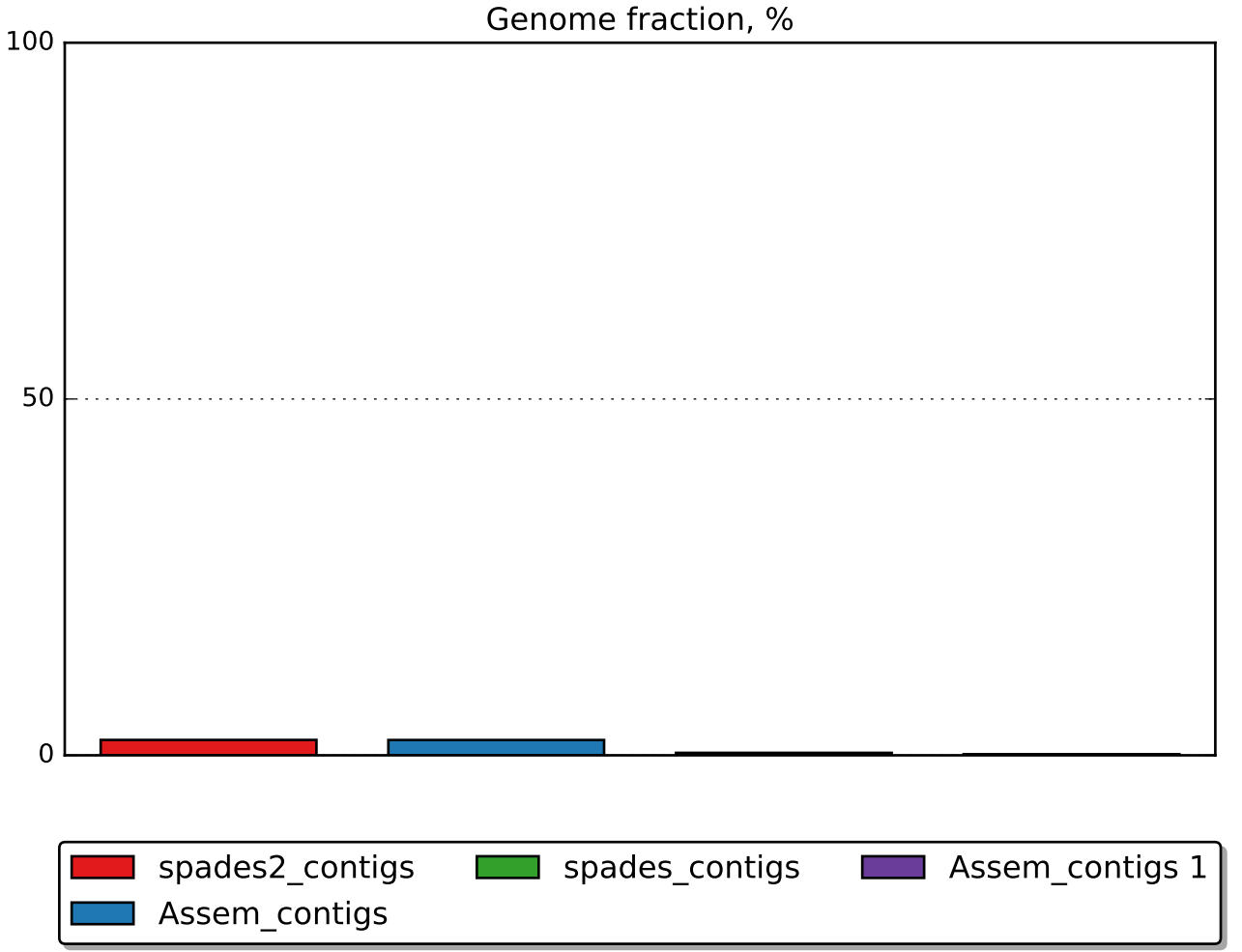

Assem_contigs 1 coverage histogram (bin size: 1x)
Total length (bp)
4000
3000
2000
1000
0
0
1
2
3
8
Coverage depth (x)
Assem_contigs 1


Misassemblies
2.0
1.5
1.0
0.5
0.0
spades2_contigs
Assem_contigs
spades_contigs
Assem_contigs 1
relocations


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
5
10
15
20
25
Contig index
spades2_contigs
Assem_contigs
spades_contigs
Assem_contigs 1
Reference


NAx
Contig length (kbp)
100
80
60
40
20
0
0
20
40
60
80
100
x
spades2_contigs
spades_contigs
Assem_contigs 1
Assem_contigs


NGAx
Contig length (kbp)
100
80
60
40
20
0
0
20
40
60
80
100
x
spades2_contigs
spades_contigs
Assem_contigs 1
Assem_contigs


Genome fraction, %
100
50
0
spades2_contigs
spades_contigs
Assem_contigs 1
Assem_contigs