Report

	velvet_contigs	velvetlong_contigs	spades_short_contigs	spades_actual_contigs
# contigs (>= 0 bp)	311	16	1	128
# contigs (>= 1000 bp)	0	7	1	4
# contigs (>= 5000 bp)	0	7	1	0
# contigs (>= 10000 bp)	0	4	1	0
# contigs (>= 25000 bp)	0	1	1	0
# contigs (>= 50000 bp)	0	0	1	0
Total length (>= 0 bp)	58644	100170	100000	49818
Total length (>= 1000 bp)	0	99371	100000	5313
Total length (>= 5000 bp)	0	99371	100000	0
Total length (>= 10000 bp)	0	81014	100000	0
Total length (>= 25000 bp)	0	33205	100000	0
Total length (>= 50000 bp)	0	0	100000	0
# contigs	12	7	1	20
Largest contig	998	33205	100000	1737
Total length	8044	99371	100000	15922
Reference length	4639675	4639675	4639675	4639675
GC (%)	50.31	52.56	52.59	51.21
Reference GC (%)	50.79	50.79	50.79	50.79
N50	679	19876	100000	718
N75	542	13387	100000	635
L50	5	2	1	8
L75	9	4	1	13
# misassemblies	0	0	0	1
# misassembled contigs	0	0	0	1
Misassembled contigs length	0	0	0	1084
# 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 (%)	0.173	2.141	2.155	0.343
Duplication ratio	1.000	1.000	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	0.00	31.40
# indels per 100 kbp	0.00	0.00	0.00	0.00
Largest alignment	998	33205	100000	1737
Total aligned length	8044	99371	100000	15922
NA50	679	19876	100000	715
NGA50	-	-	-	-
NA75	542	13387	100000	587
LA50	5	2	1	8
LA75	9	4	1	14

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

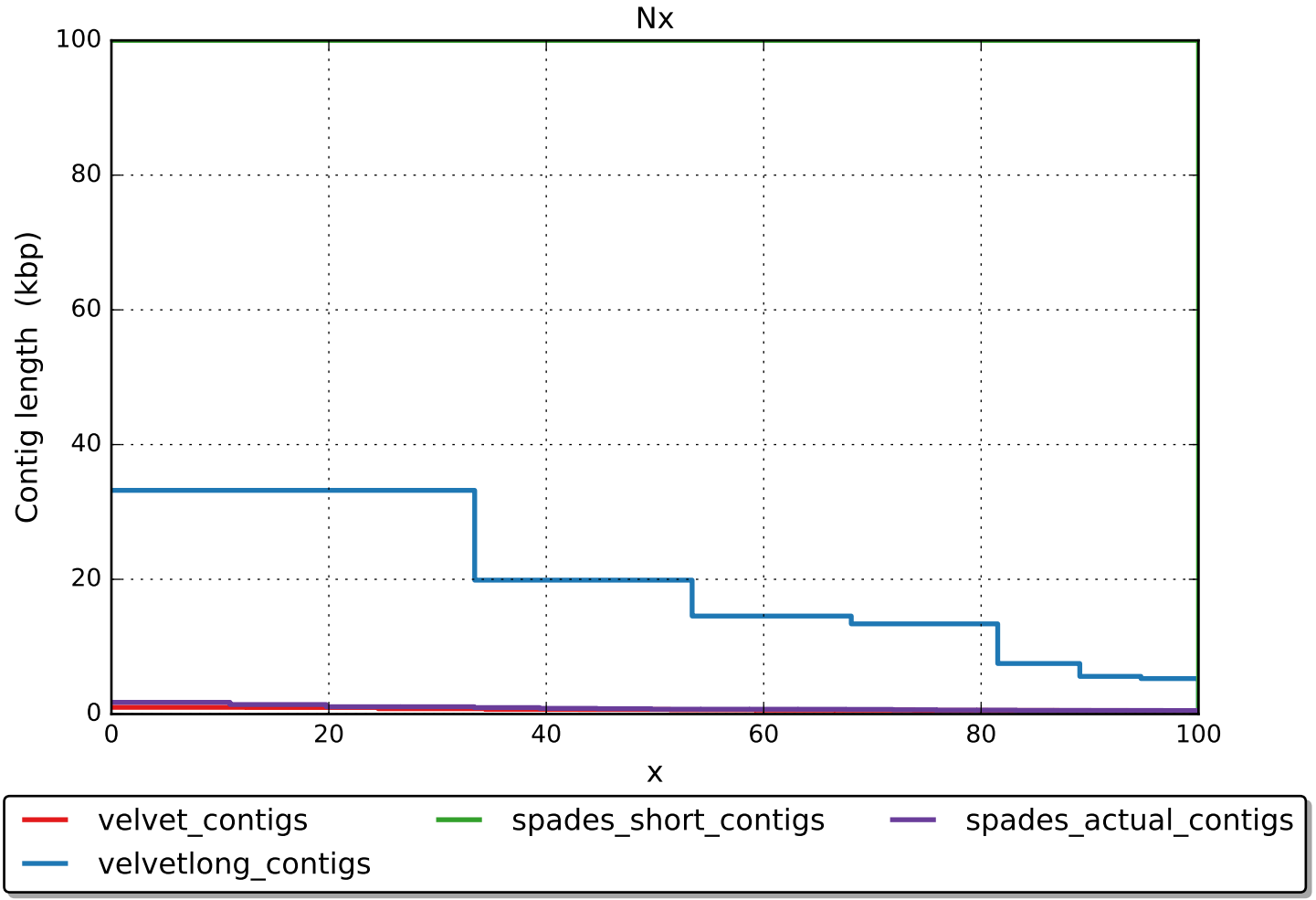
	velvet_contigs	velvetlong_contigs	spades_short_contigs	spades_actual_contigs
# misassemblies	0	0	0	1
# relocations	0	0	0	1
# translocations	0	0	0	0
# inversions	0	0	0	0
# misassembled contigs	0	0	0	1
Misassembled contigs length	0	0	0	1084
# local misassemblies	0	0	0	0
# mismatches	0	0	0	5
# indels	0	0	0	0
# short indels	0	0	0	0
# long indels	0	0	0	0
Indels length	0	0	0	0

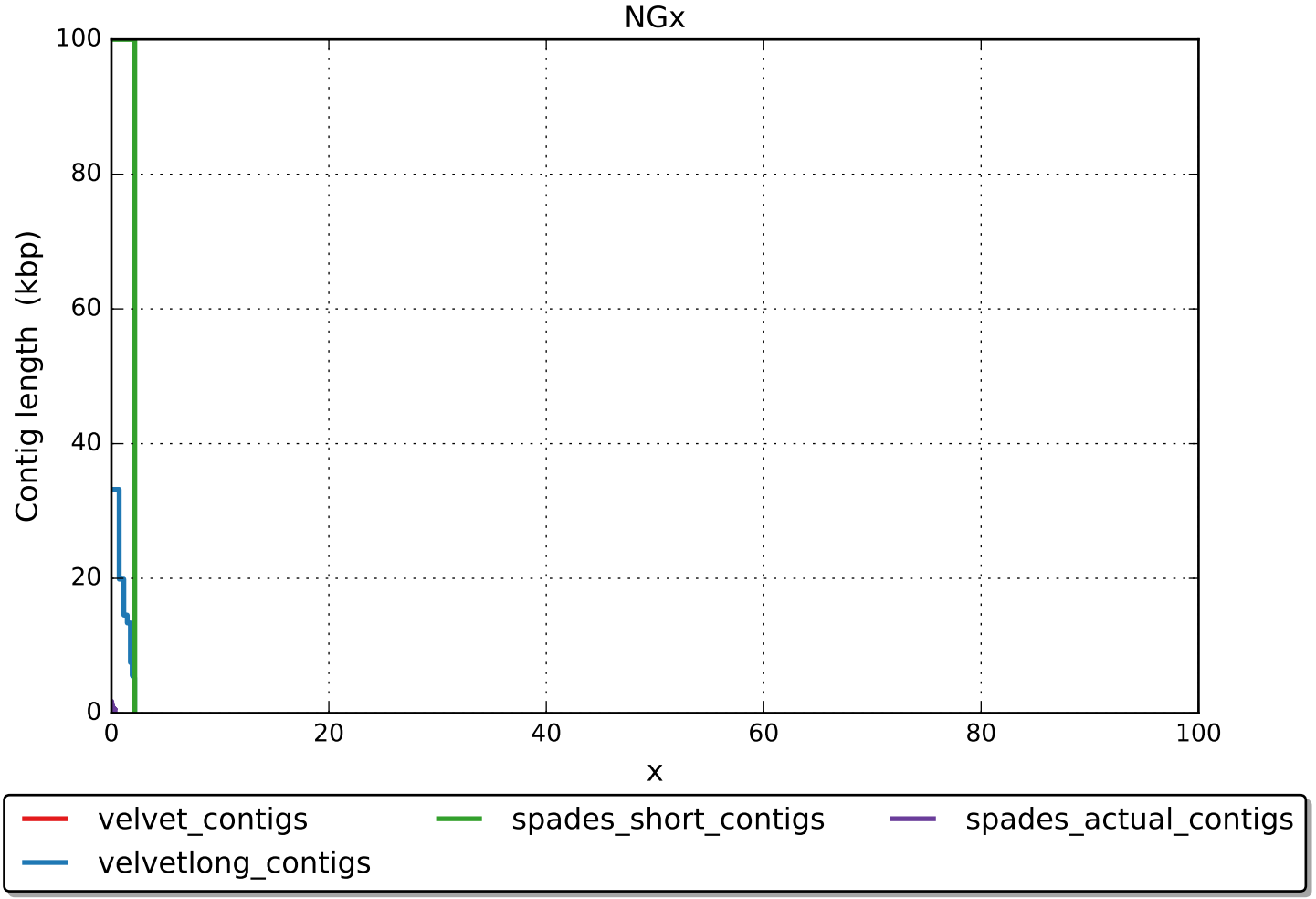
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

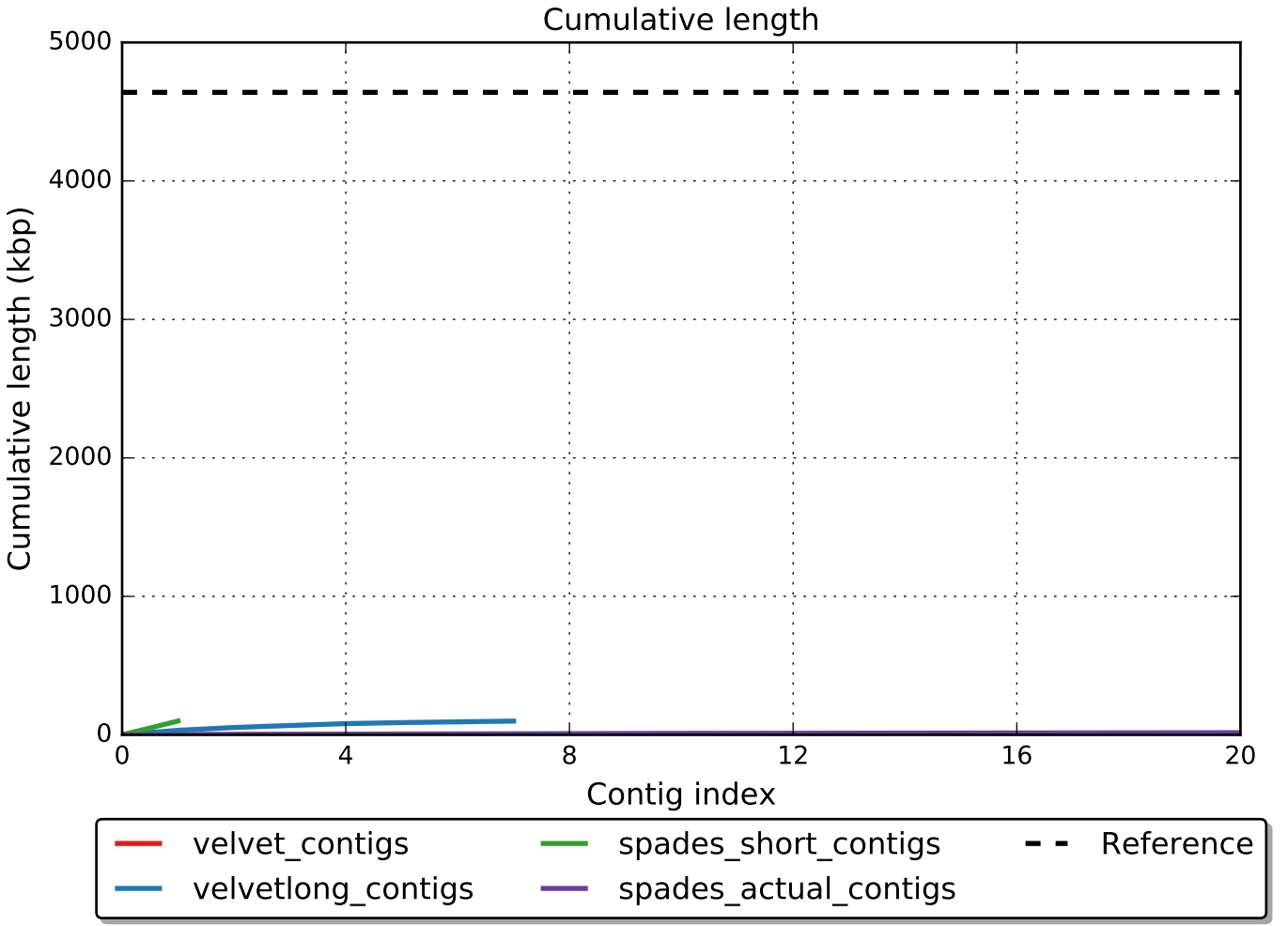
Unaligned report

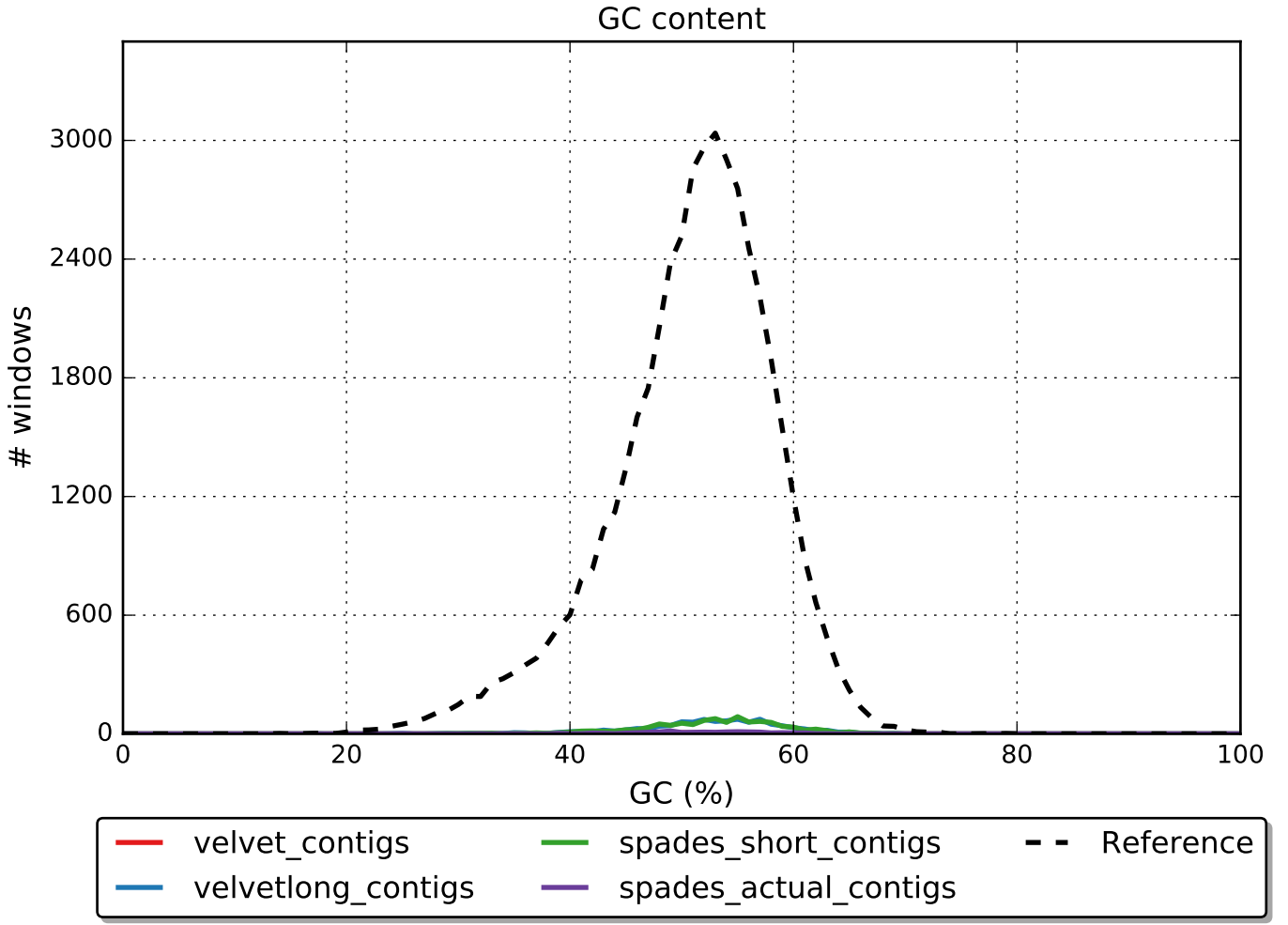
	velvet_contigs	velvetlong_contigs	spades_short_contigs	spades_actual_contigs
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	0	0	0	0
# with misassembly	0	0	0	0
# both parts are significant	0	0	0	0
Partially unaligned length	0	0	0	0
# N's	0	0	0	0

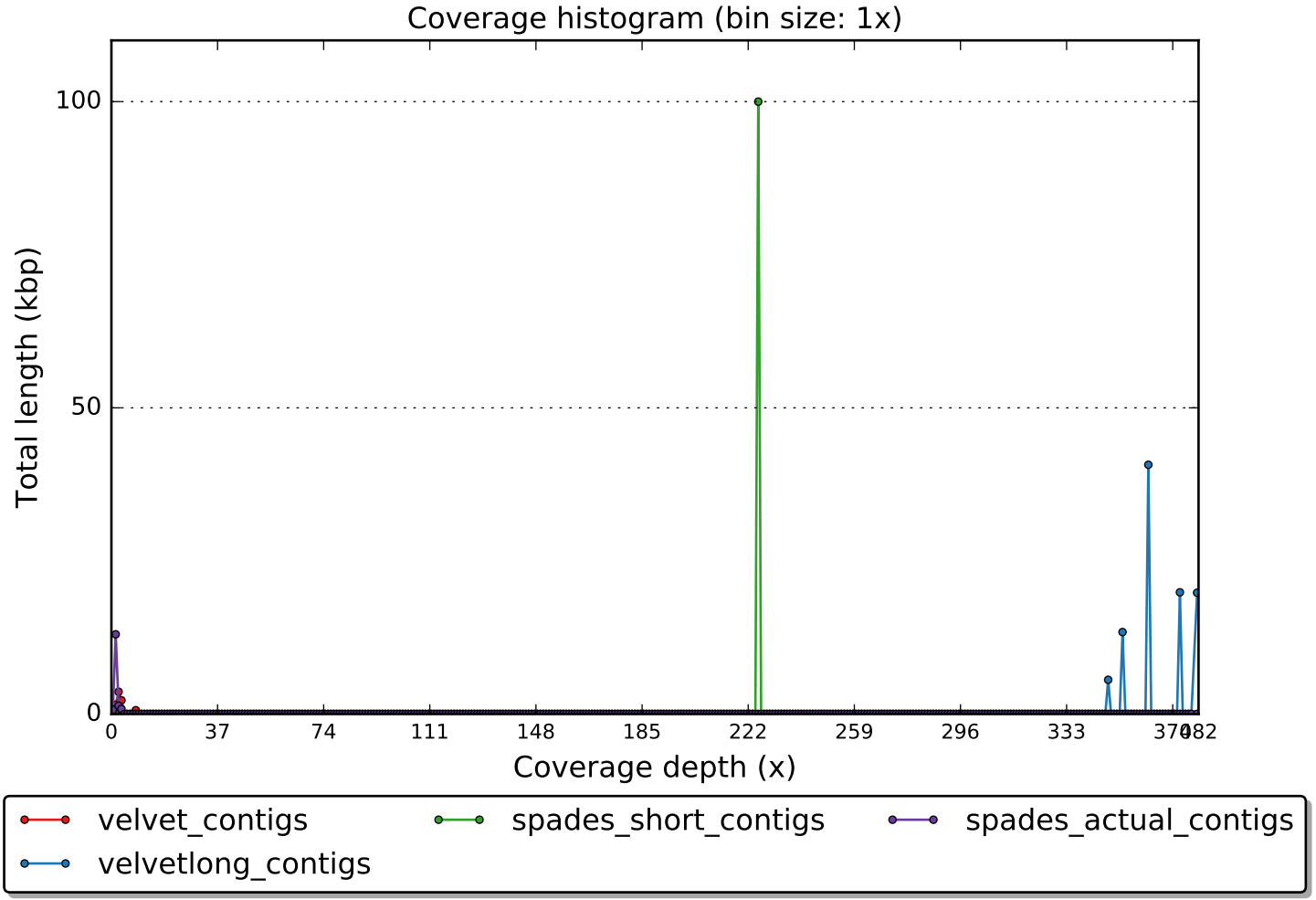
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

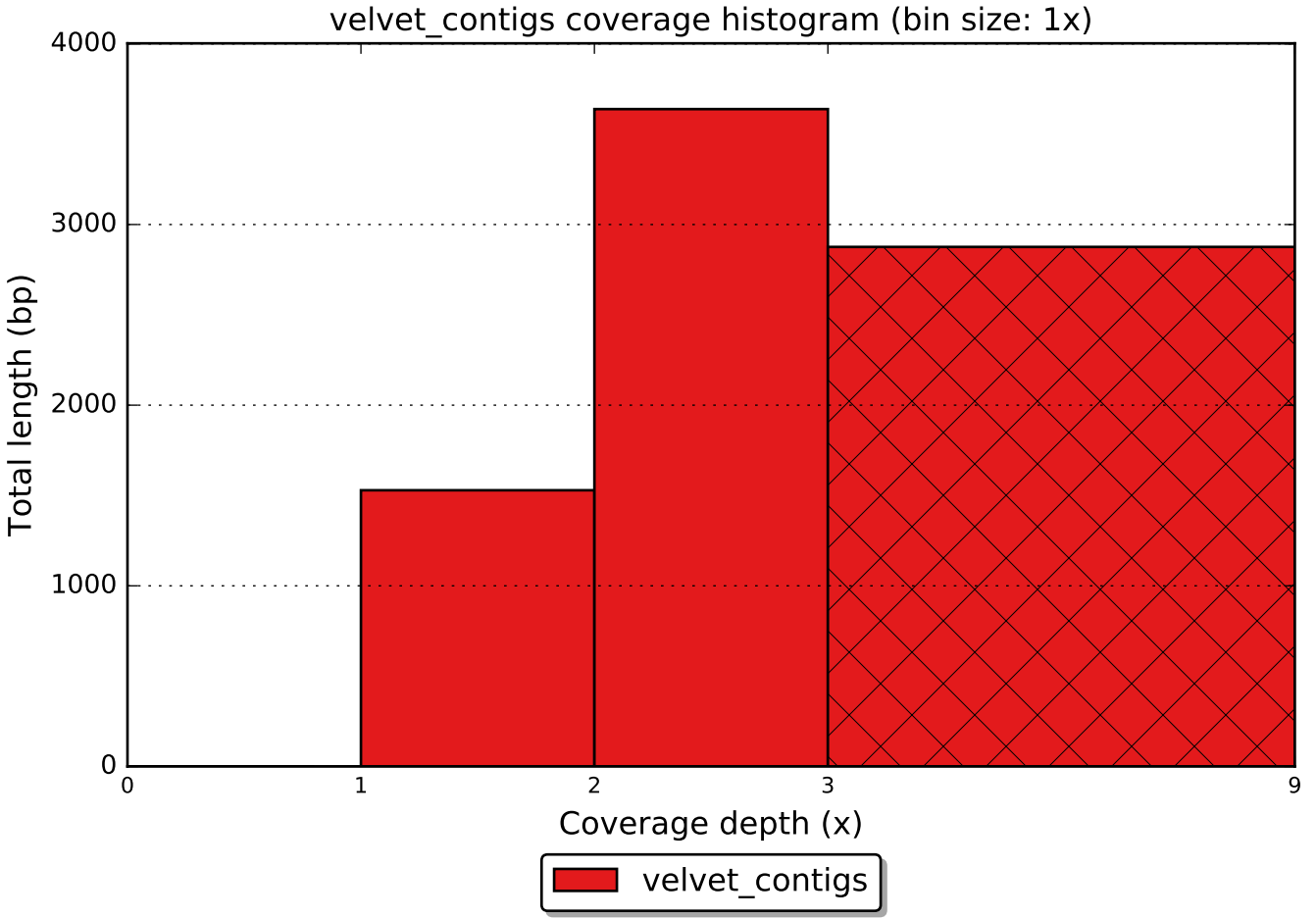

Nx
Contig length (kbp)
x
0
20
40
60
80
100
velvet_contigs
velvetlong_contigs
spades_short_contigs
spades_actual_contigs

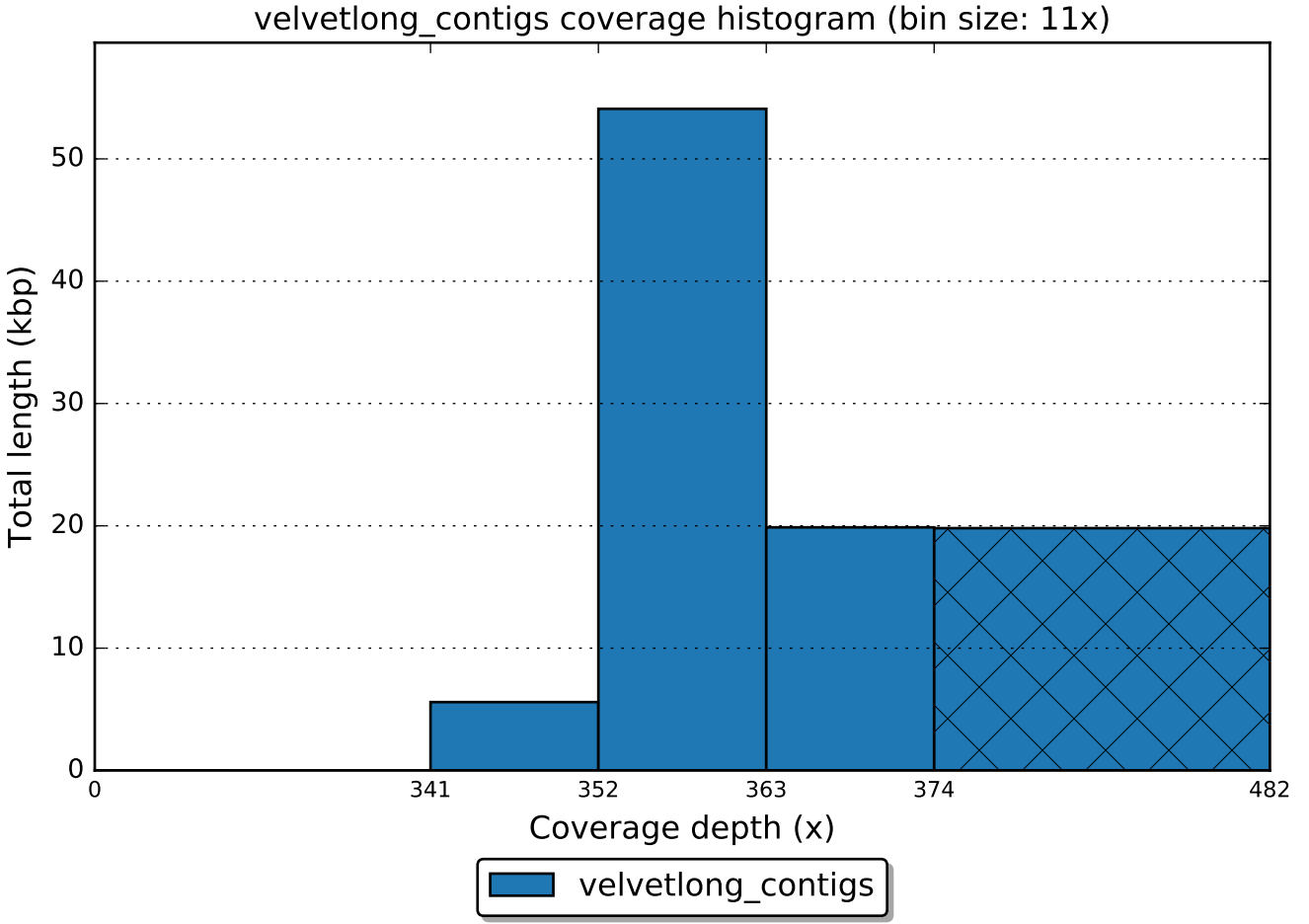

NGx
Contig length (kbp)
x
0
20
40
60
80
100
velvet_contigs
velvetlong_contigs
spades_short_contigs
spades_actual_contigs

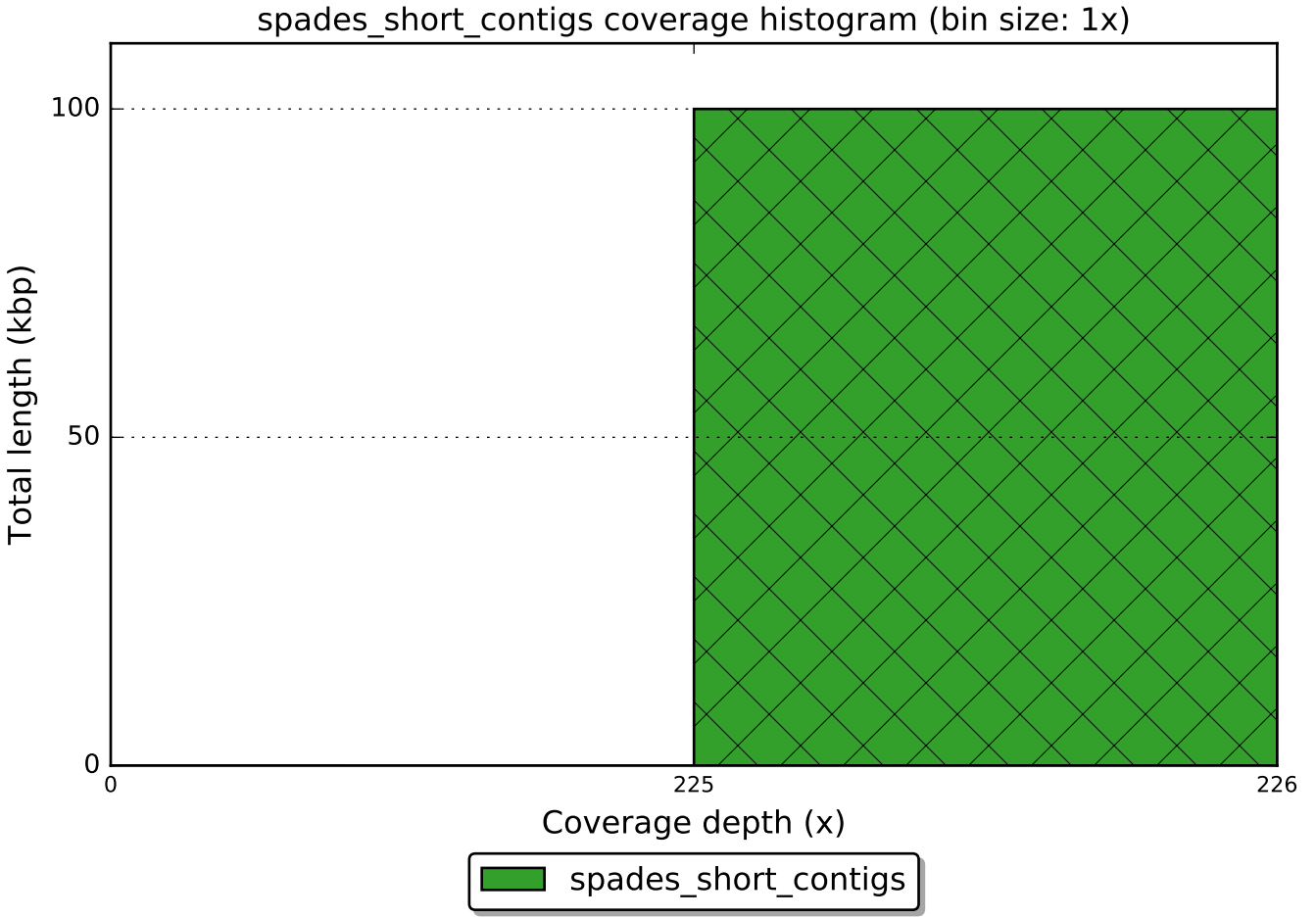

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
4
8
12
16
20
Contig index
velvet_contigs
velvetlong_contigs
spades_short_contigs
spades_actual_contigs
Reference

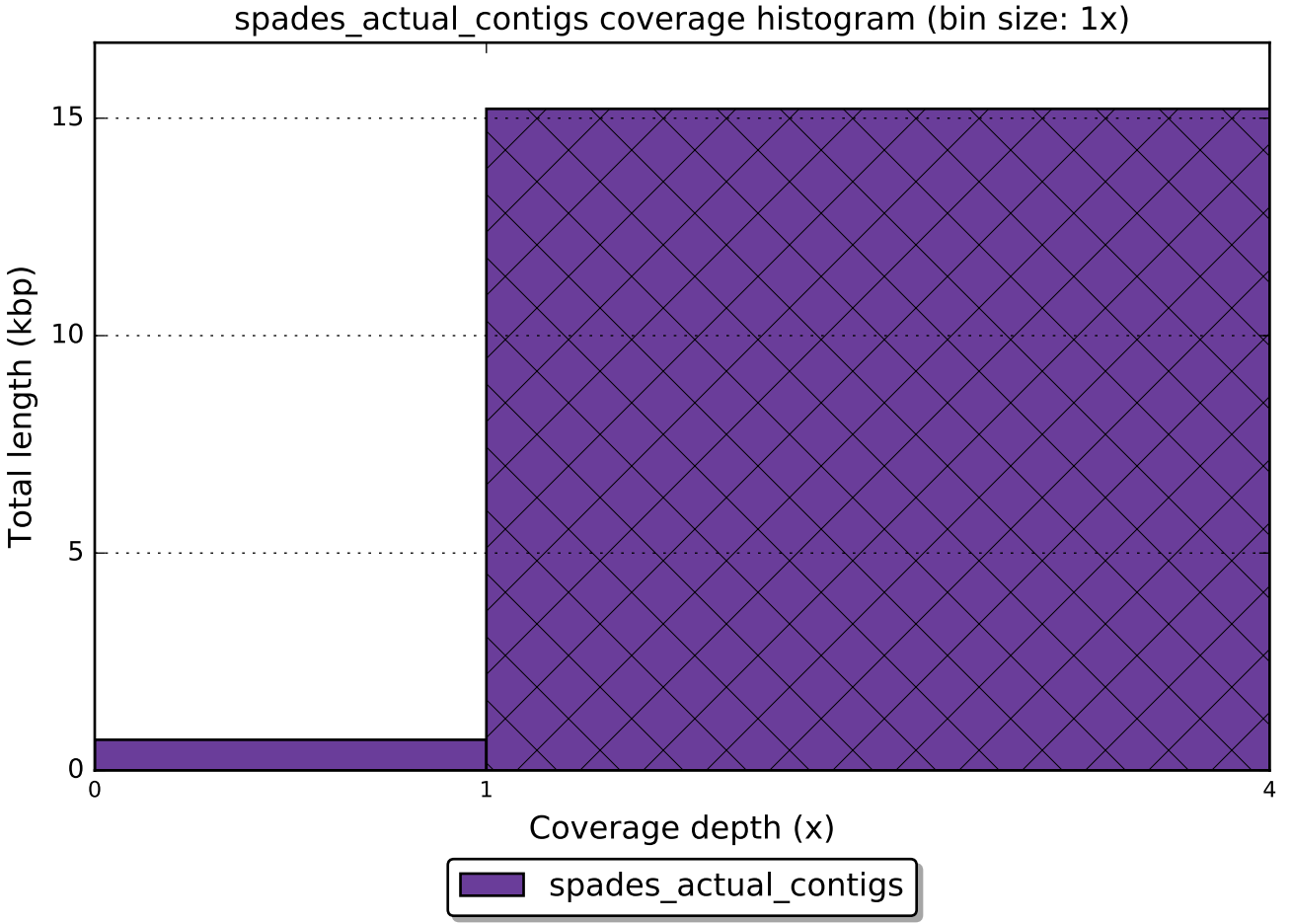

GC content
windows
3000
2400
1800
1200
600
0
0
20
40
60
80
100
GC (%)
velvet_contigs
velvetlong_contigs
spades_short_contigs
spades_actual_contigs
Reference

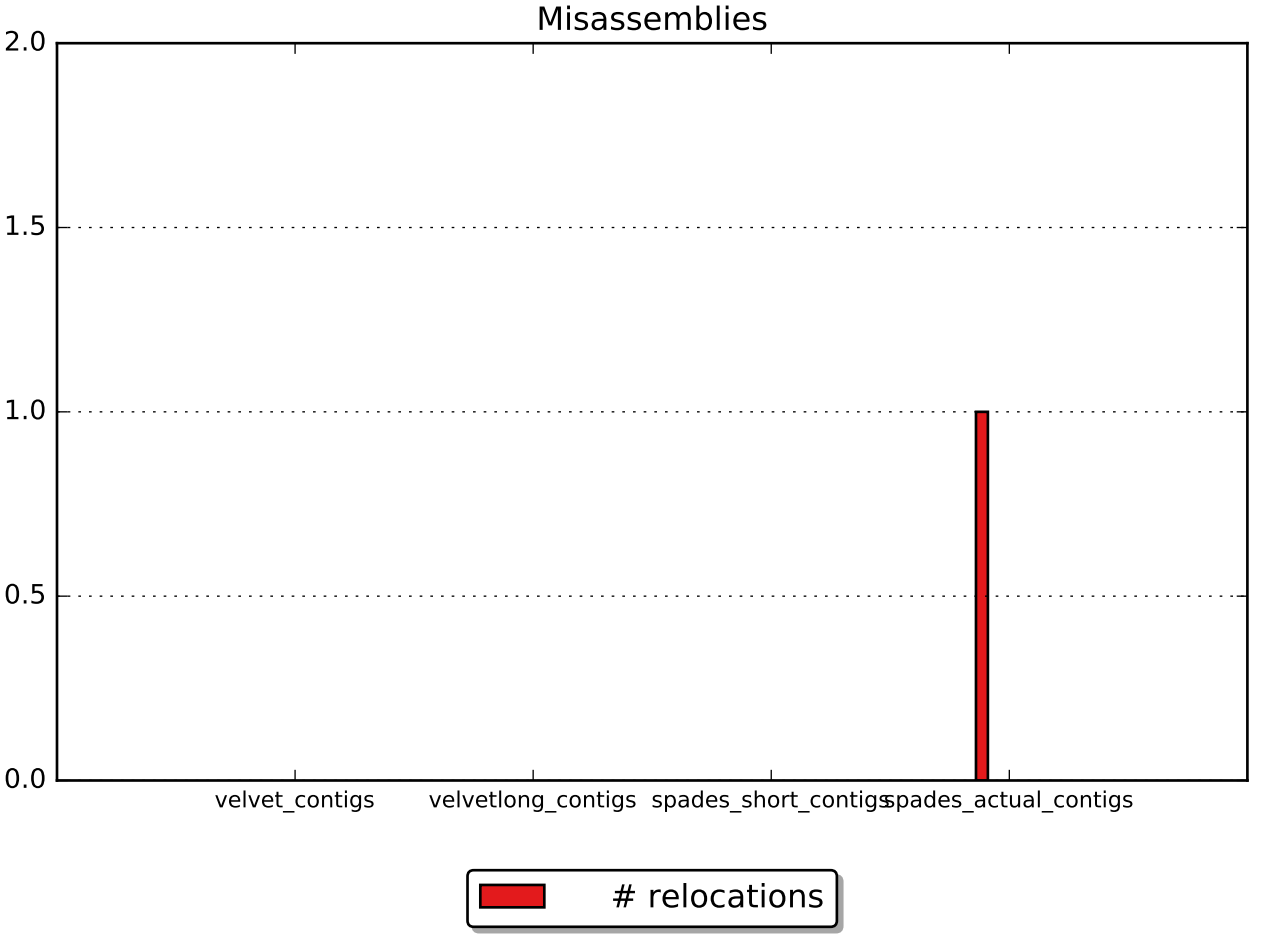

Coverage histogram (bin size: 1x)
Total length (kbp)
100
50
0
0
37
74
111
148
185
222
259
296
333
370
382
Coverage depth (x)
velvet_contigs
spades_short_contigs
spades_actual_contigs
velvetlong_contigs

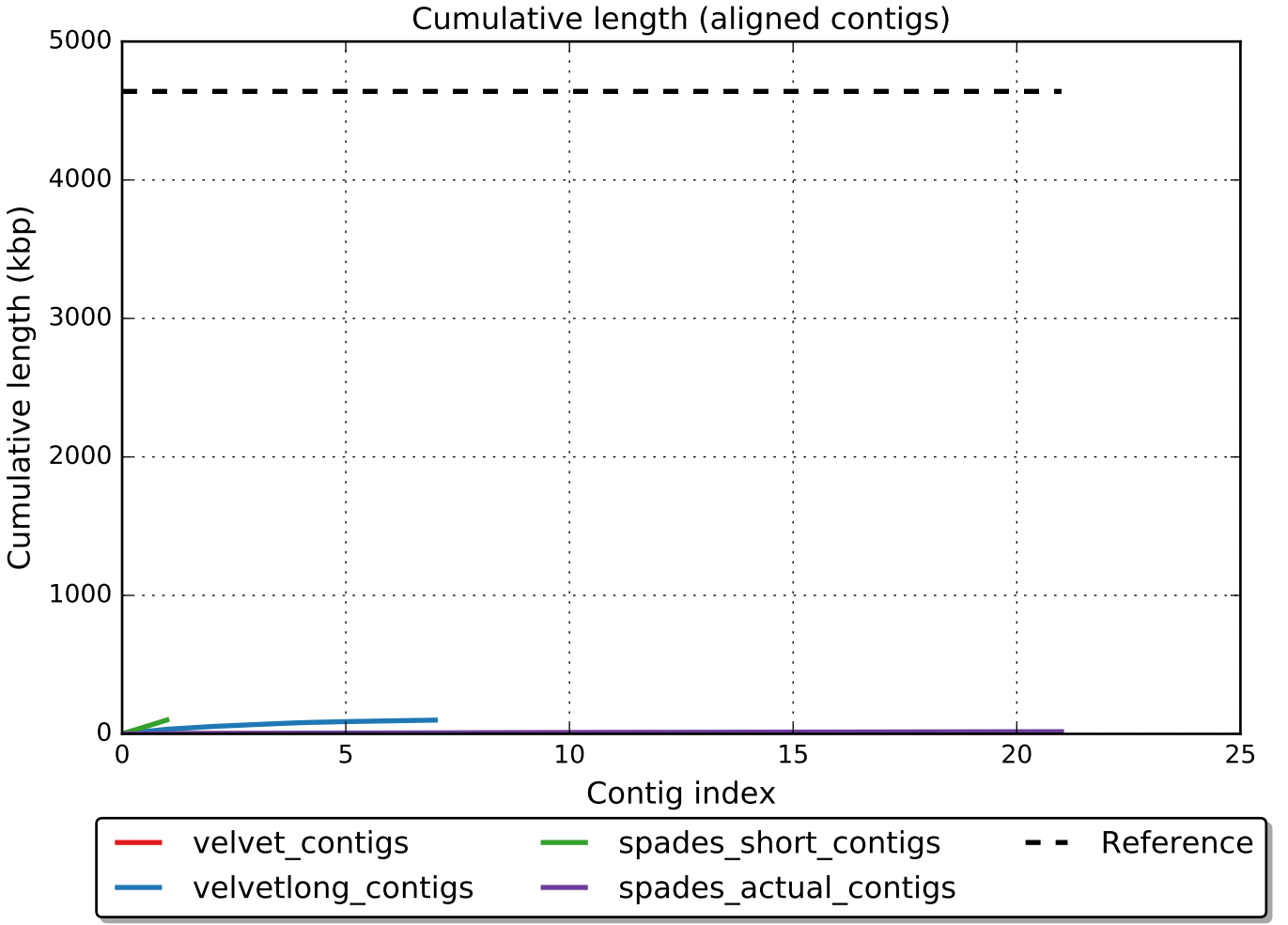

velvet_contigs coverage histogram (bin size: 1x)
4000
3000
2000
1000
0
Total length (bp)
0
1
2
3
9
Coverage depth (x)
velvet_contigs

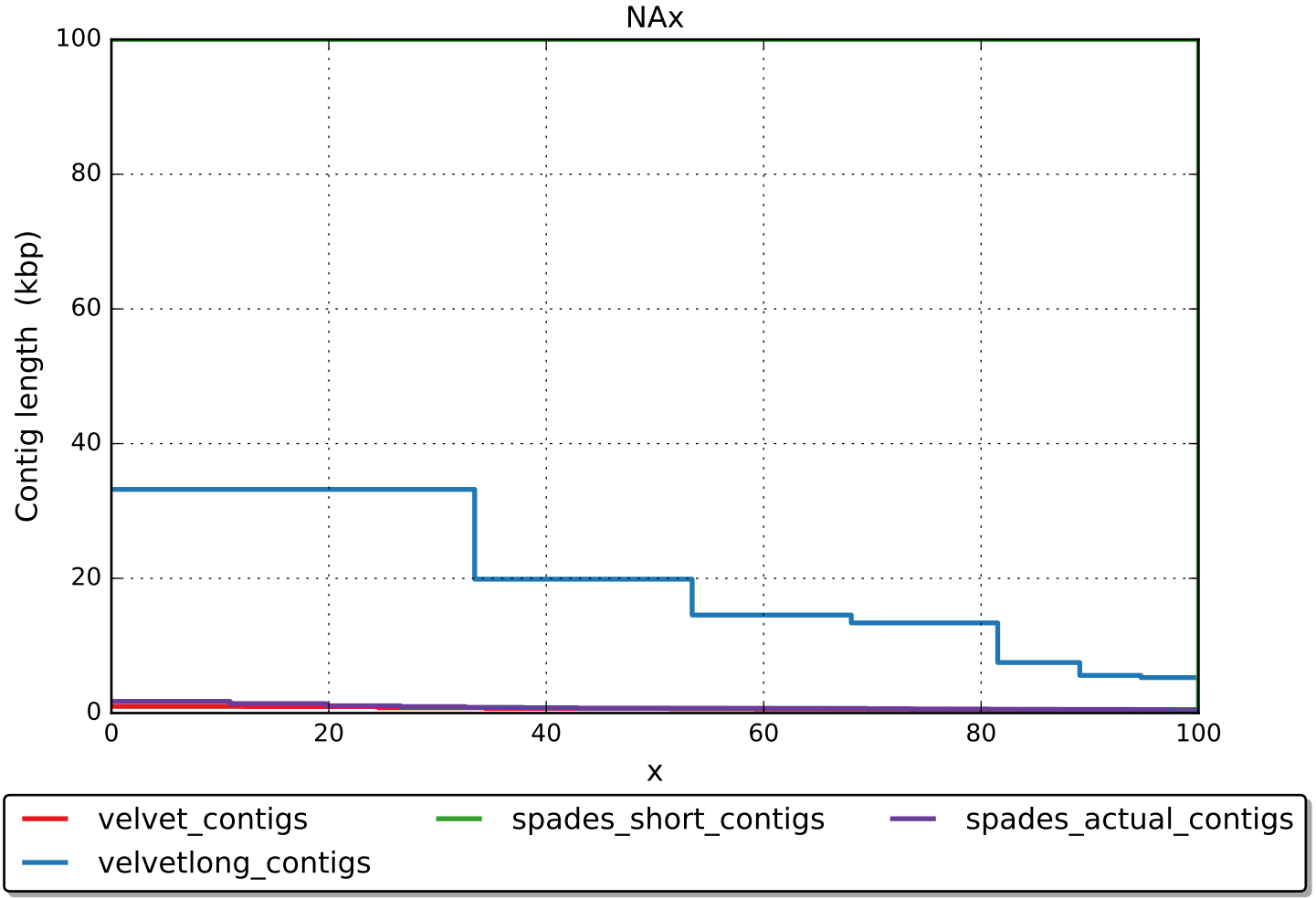

velvetlong_contigs coverage histogram (bin size: 11x)
Total length (kbp)
0
10
20
30
40
50
0
341
352
363
374
482
Coverage depth (x)
velvetlong_contigs

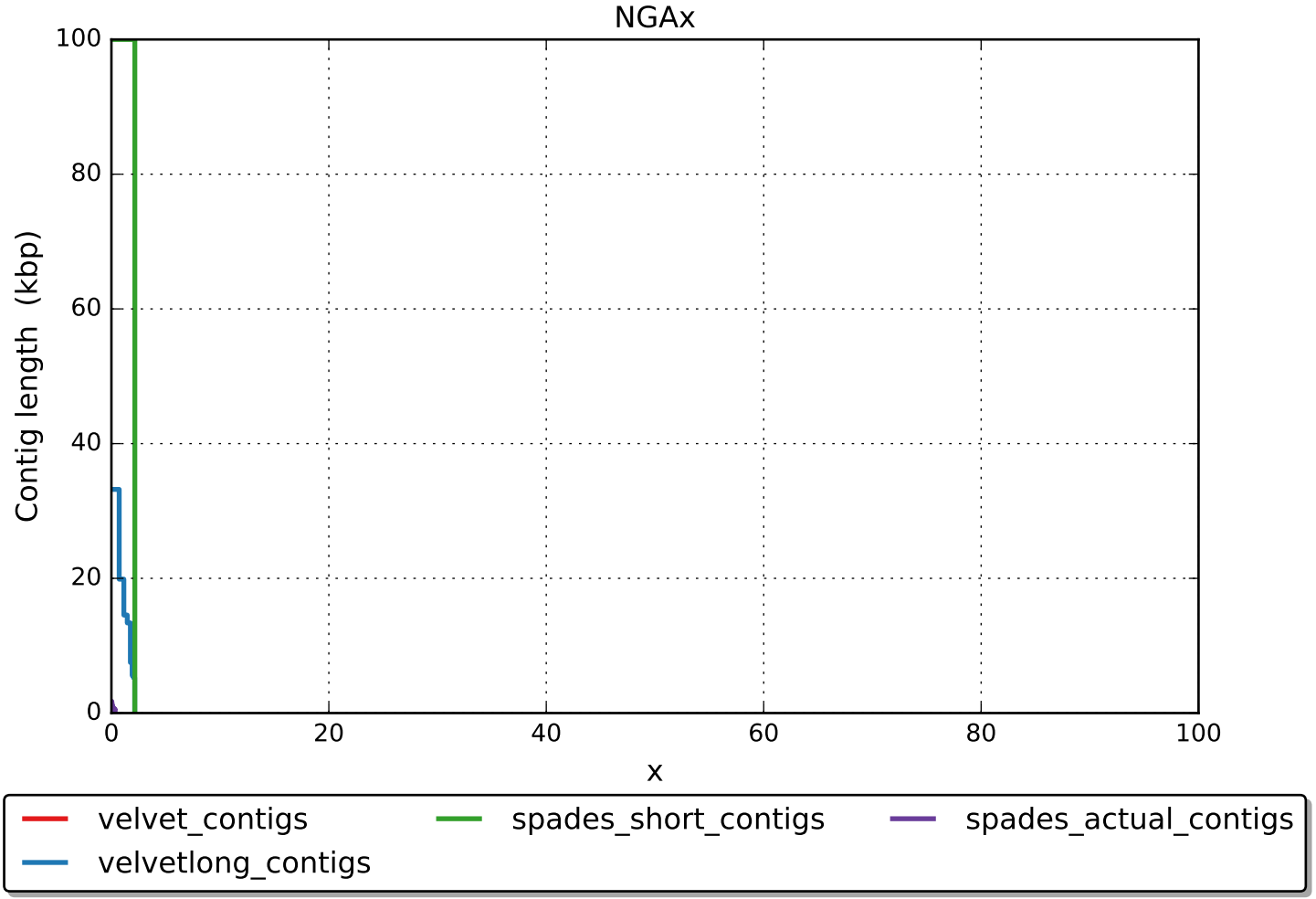

spades_short_contigs coverage histogram (bin size: 1x)
Total length (kbp)
100
50
0
0
225
226
Coverage depth (x)
spades_short_contigs

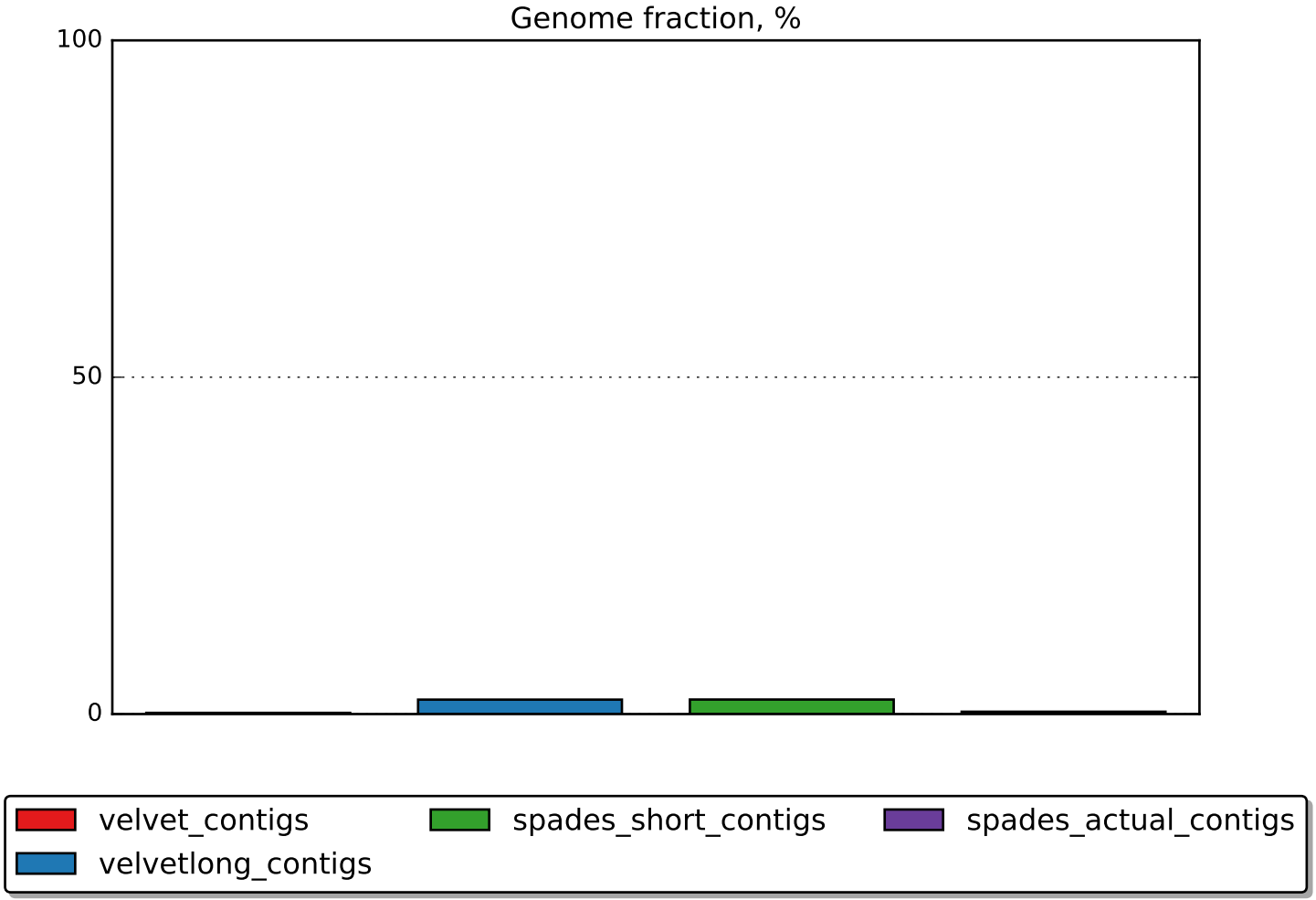

spades_actual_contigs coverage histogram (bin size: 1x)
Total length (kbp)
15
10
5
0
0
1
4
Coverage depth (x)
spades_actual_contigs


Misassemblies
2.0
1.5
1.0
0.5
0.0
velvet_contigs
velvetlong_contigs
spades_short_contigs
spades_actual_contigs
relocations


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
5
10
15
20
25
Contig index
velvet_contigs
velvetlong_contigs
spades_short_contigs
spades_actual_contigs
Reference


NAx
Contig length (kbp)
100
80
60
40
20
0
0
20
40
60
80
100
x
velvet_contigs
velvetlong_contigs
spades_short_contigs
spades_actual_contigs


NGAx
Contig length (kbp)
x
0
20
40
60
80
100
velvet_contigs
velvetlong_contigs
spades_short_contigs
spades_actual_contigs


Genome fraction, %
100
50
0
velvet_contigs
velvetlong_contigs
spades_short_contigs
spades_actual_contigs