Report

	contigs_velvet_high	contigs_spades_high	contigs_spades_low	contigs_velvet_low
# contigs (>= 0 bp)	18	1	128	306
# contigs (>= 1000 bp)	9	1	4	0
# contigs (>= 5000 bp)	7	1	0	0
# contigs (>= 10000 bp)	3	1	0	0
# contigs (>= 25000 bp)	1	1	0	0
# contigs (>= 50000 bp)	0	1	0	0
Total length (>= 0 bp)	100179	100000	49819	59682
Total length (>= 1000 bp)	99404	100000	5313	0
Total length (>= 5000 bp)	94645	100000	0	0
Total length (>= 10000 bp)	66455	100000	0	0
Total length (>= 25000 bp)	33205	100000	0	0
Total length (>= 50000 bp)	0	100000	0	0
# contigs	10	1	128	261
Largest contig	33205	100000	1737	998
Total length	99720	100000	49819	55774
Reference length	4639675	4639675	4639675	4639675
GC (%)	52.57	52.59	51.87	51.66
Reference GC (%)	50.79	50.79	50.79	50.79
N50	19863	100000	372	272
N75	9837	100000	292	138
L50	2	1	42	68
L75	4	1	79	136
# 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 (%)	2.148	2.155	1.072	1.192
Duplication ratio	1.001	1.000	1.002	1.008
# N's per 100 kbp	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	0.00	0.00	10.05	0.00
# indels per 100 kbp	0.00	0.00	0.00	0.00
Largest alignment	33205	100000	1737	998
Total aligned length	99720	100000	49819	55774
NA50	19863	100000	372	272
NGA50	-	-	-	-
NA75	9837	100000	292	138
LA50	2	1	43	68
LA75	4	1	80	136

All statistics are based on contigs of size >= 100 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

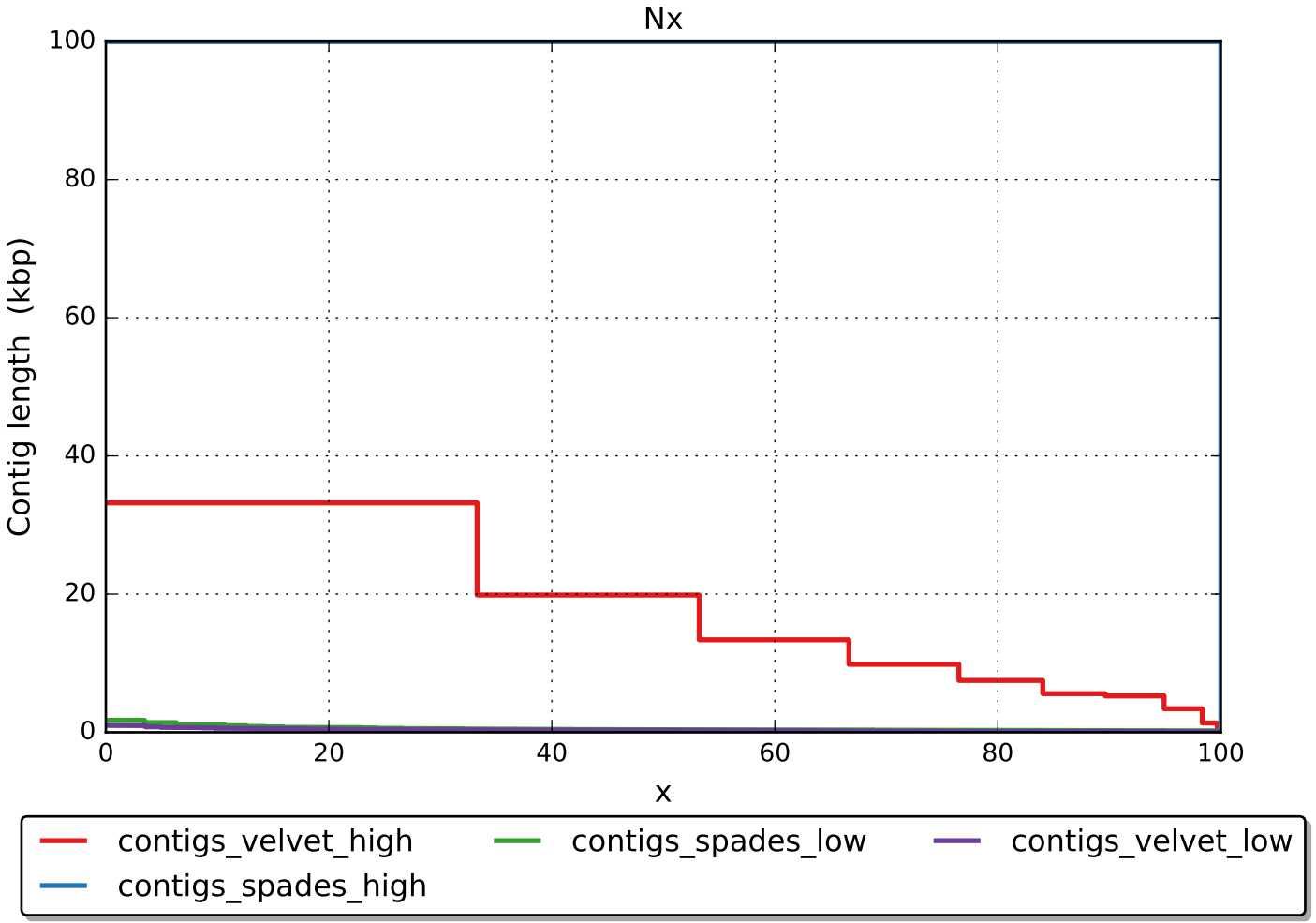
	contigs_velvet_high	contigs_spades_high	contigs_spades_low	contigs_velvet_low
# misassemblies	0	0	1	0
# relocations	0	0	1	0
# translocations	0	0	0	0
# inversions	0	0	0	0
# misassembled contigs	0	0	1	0
Misassembled contigs length	0	0	1084	0
# local misassemblies	0	0	0	0
# mismatches	0	0	5	0
# indels	0	0	0	0
# short indels	0	0	0	0
# long indels	0	0	0	0
Indels length	0	0	0	0

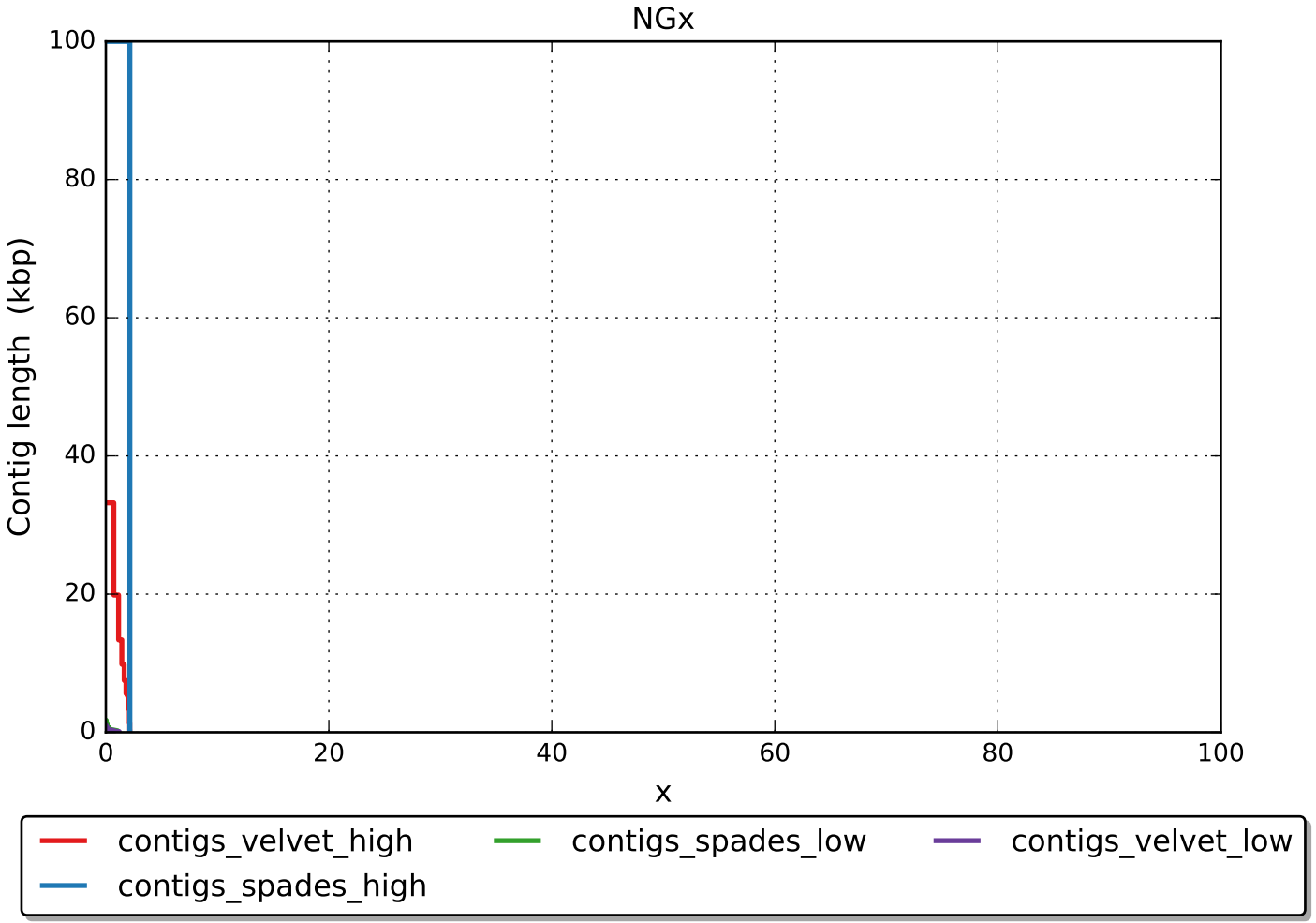
All statistics are based on contigs of size >= 100 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

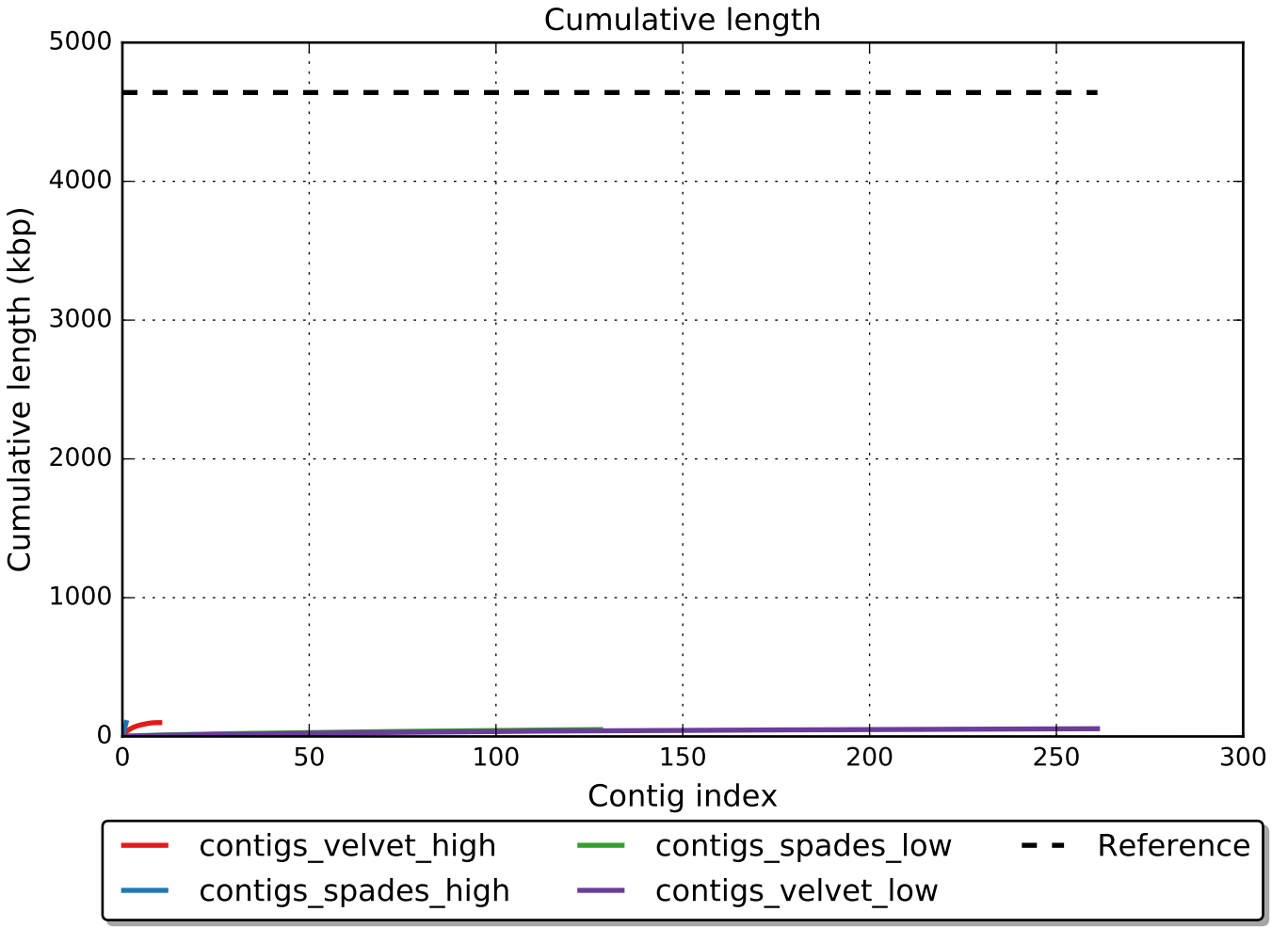
Unaligned report

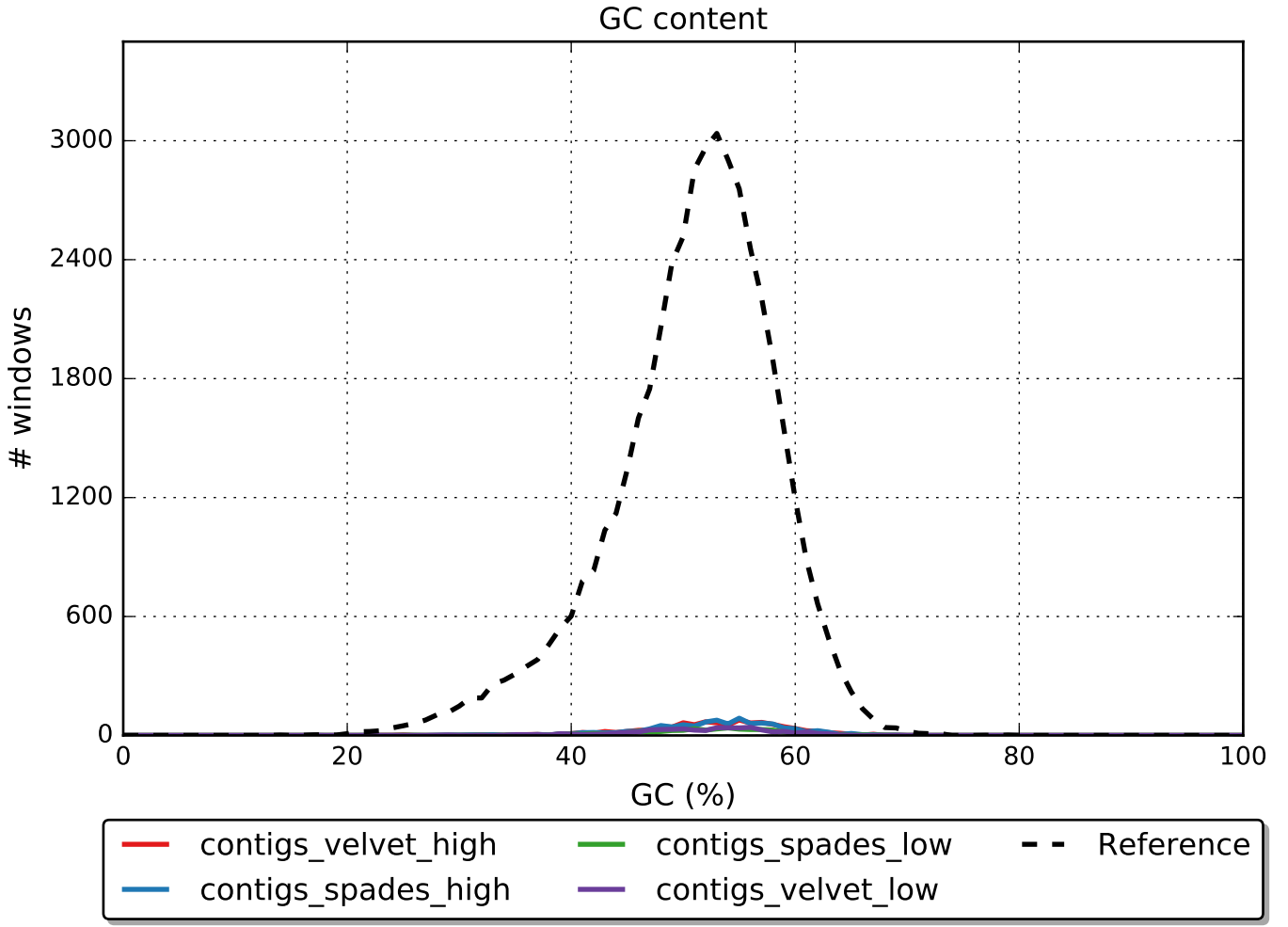
	contigs_velvet_high	contigs_spades_high	contigs_spades_low	contigs_velvet_low
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	0	0	0	0
# with misassembly	0	0	0	0
# both parts are significant	0	0	0	0
Partially unaligned length	0	0	0	0
# N's	0	0	0	0

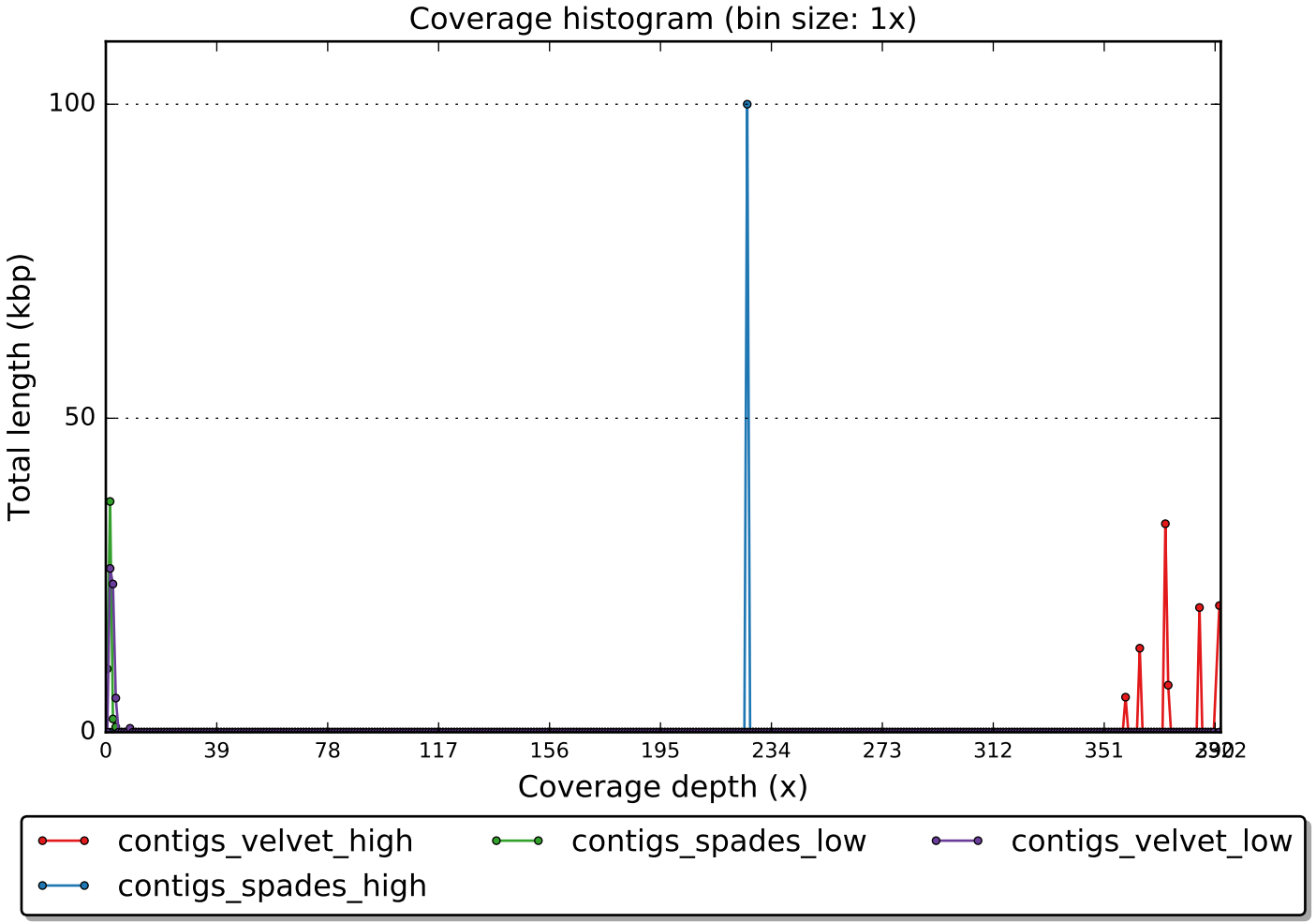
All statistics are based on contigs of size >= 100 bp, unless otherwise noted
(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

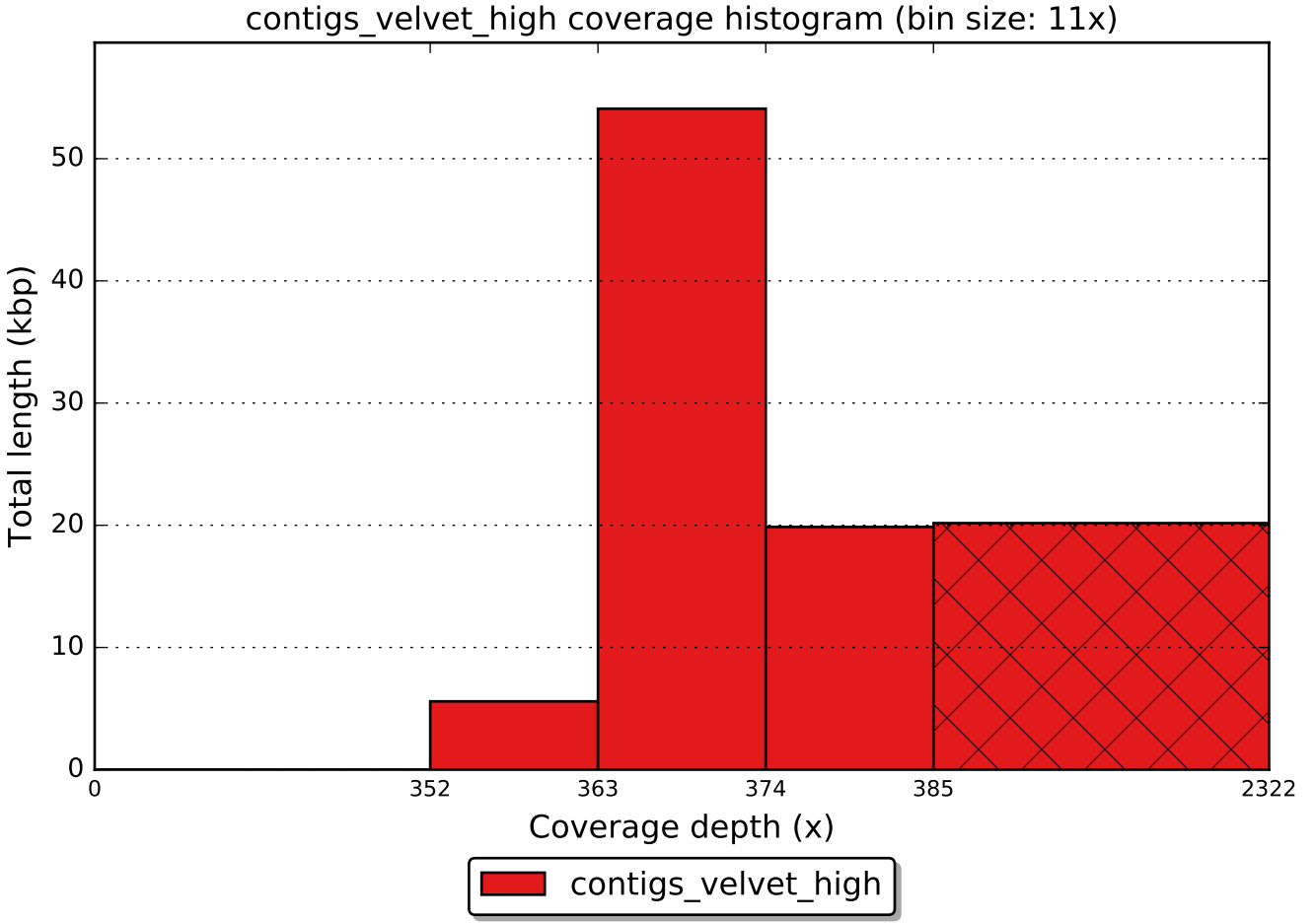

Nx
Contig length (kbp)
x
0
20
40
60
80
100
contigs_velvet_high
contigs_spades_high
contigs_spades_low
contigs_velvet_low

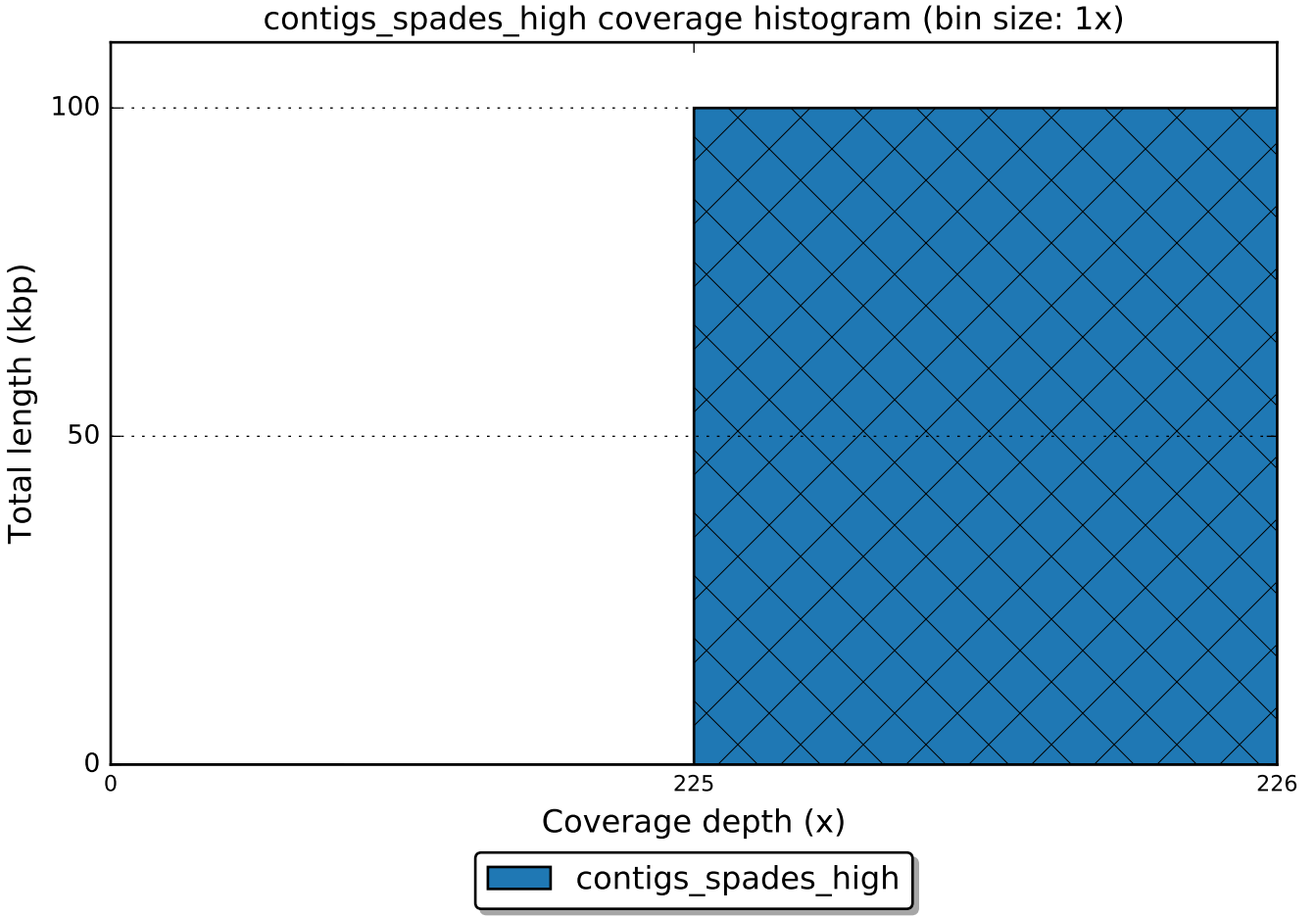

NGx
Contig length (kbp)
x
0
20
40
60
80
100
contigs_velvet_high
contigs_spades_high
contigs_spades_low
contigs_velvet_low

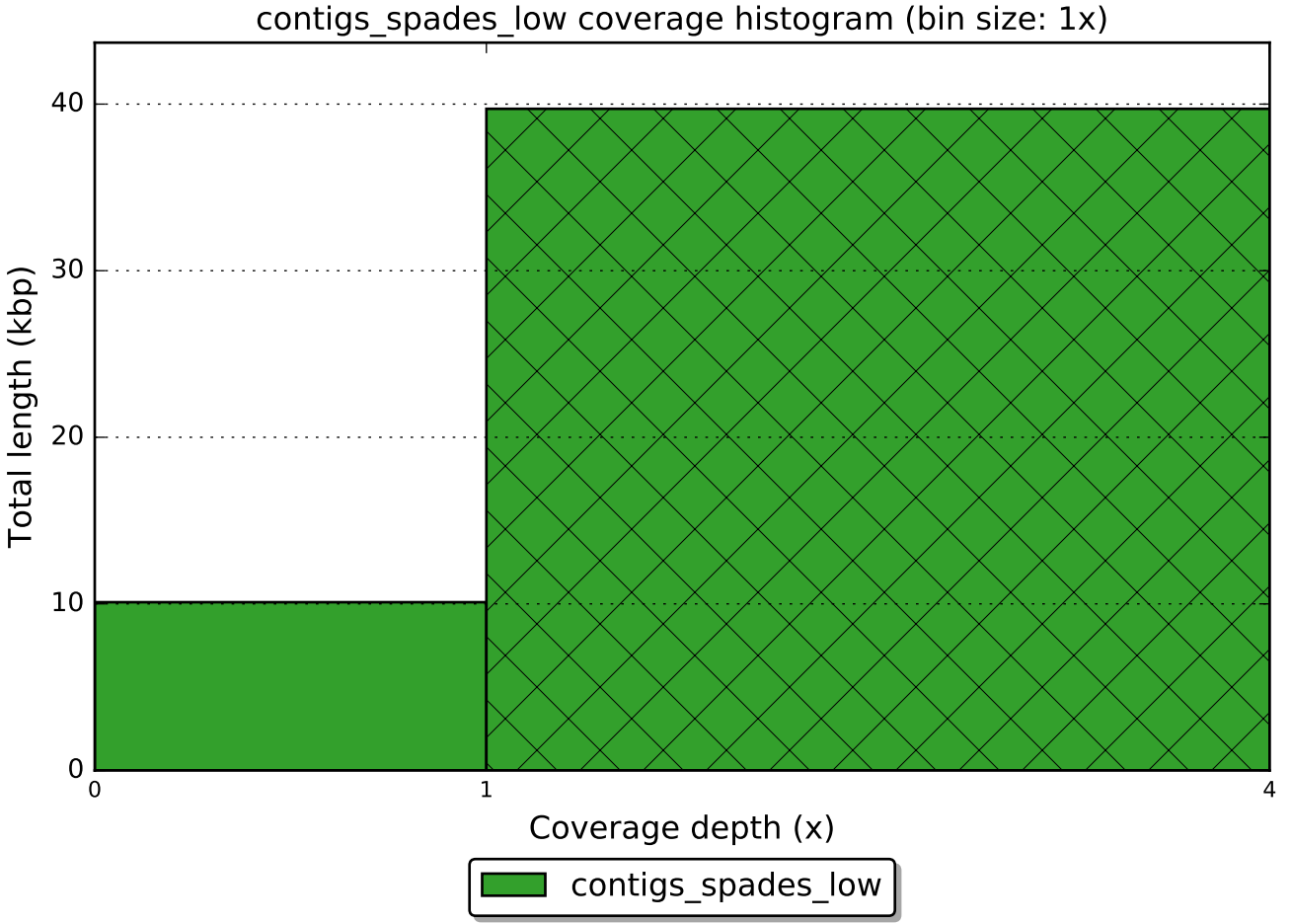

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
50
100
150
200
250
300
Contig index
contigs_velvet_high
contigs_spades_high
contigs_spades_low
contigs_velvet_low
Reference

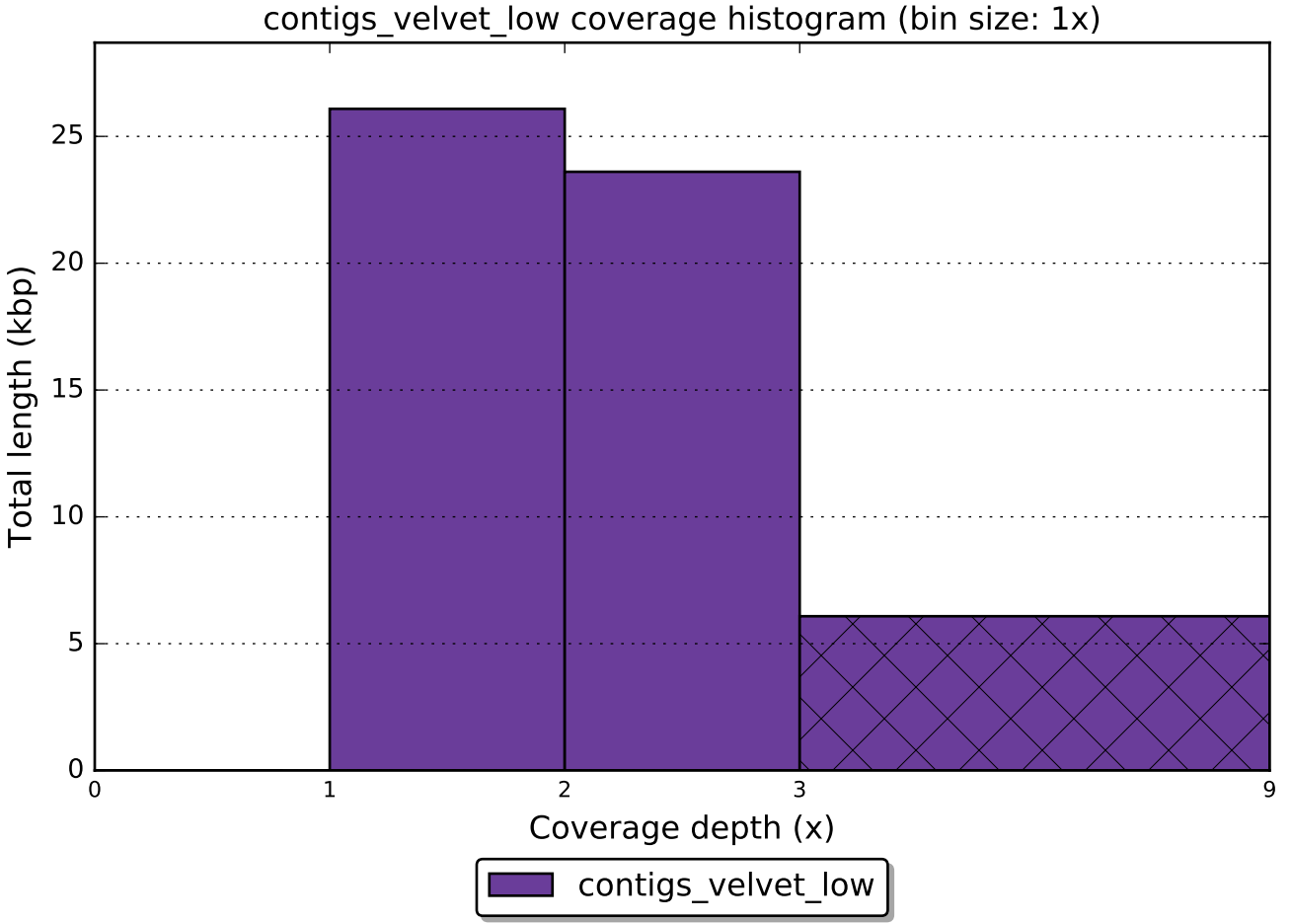

GC content
windows
3000
2400
1800
1200
600
0
0
20
40
60
80
100
GC (%)
contigs_velvet_high
contigs_spades_high
contigs_spades_low
contigs_velvet_low
Reference

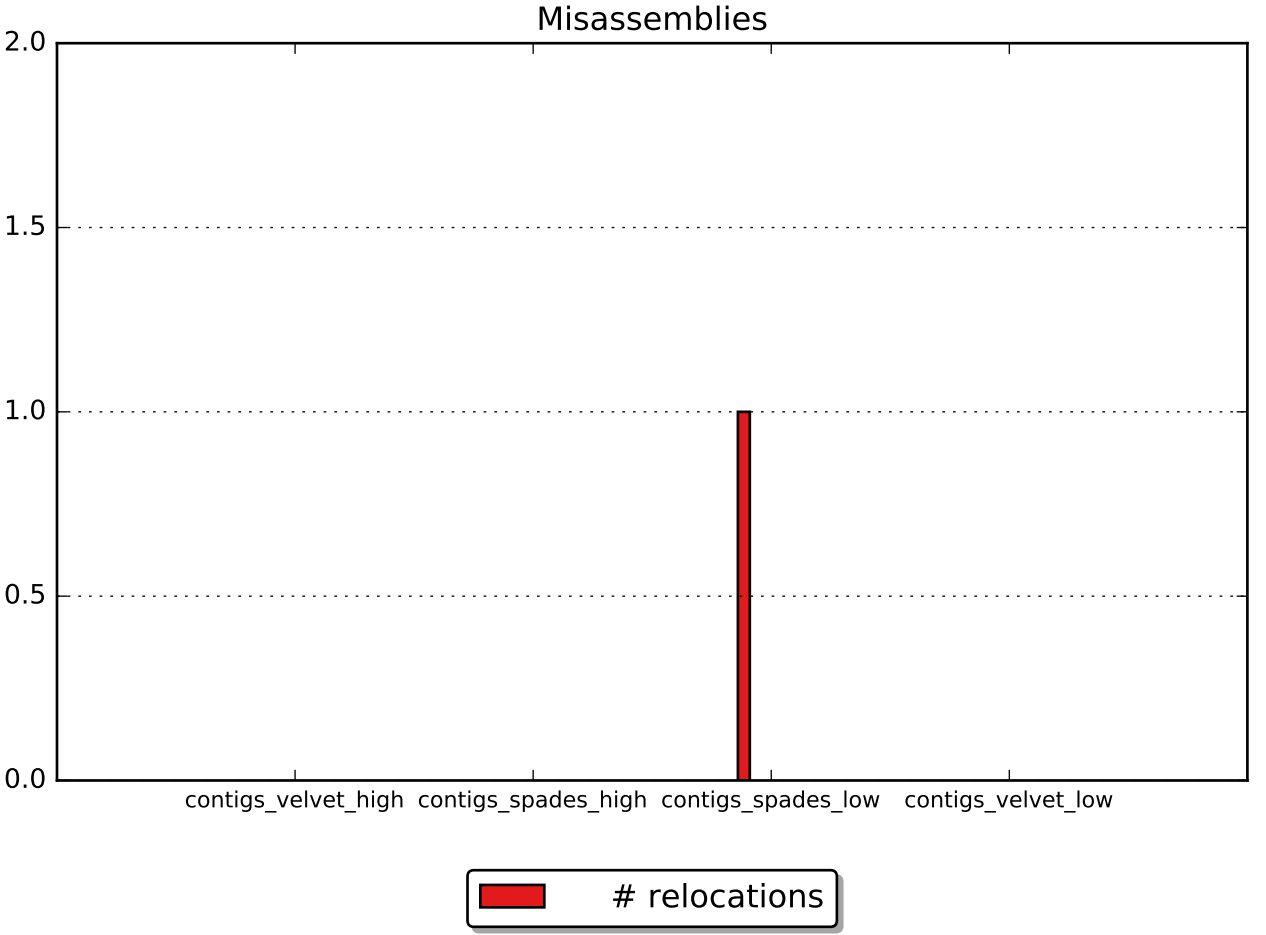

Coverage histogram (bin size: 1x)
Total length (kbp)
100
50
0
0
39
78
117
156
195
234
273
312
351
390
Coverage depth (x)
contigs_velvet_high
contigs_spades_low
contigs_velvet_low
contigs_spades_high

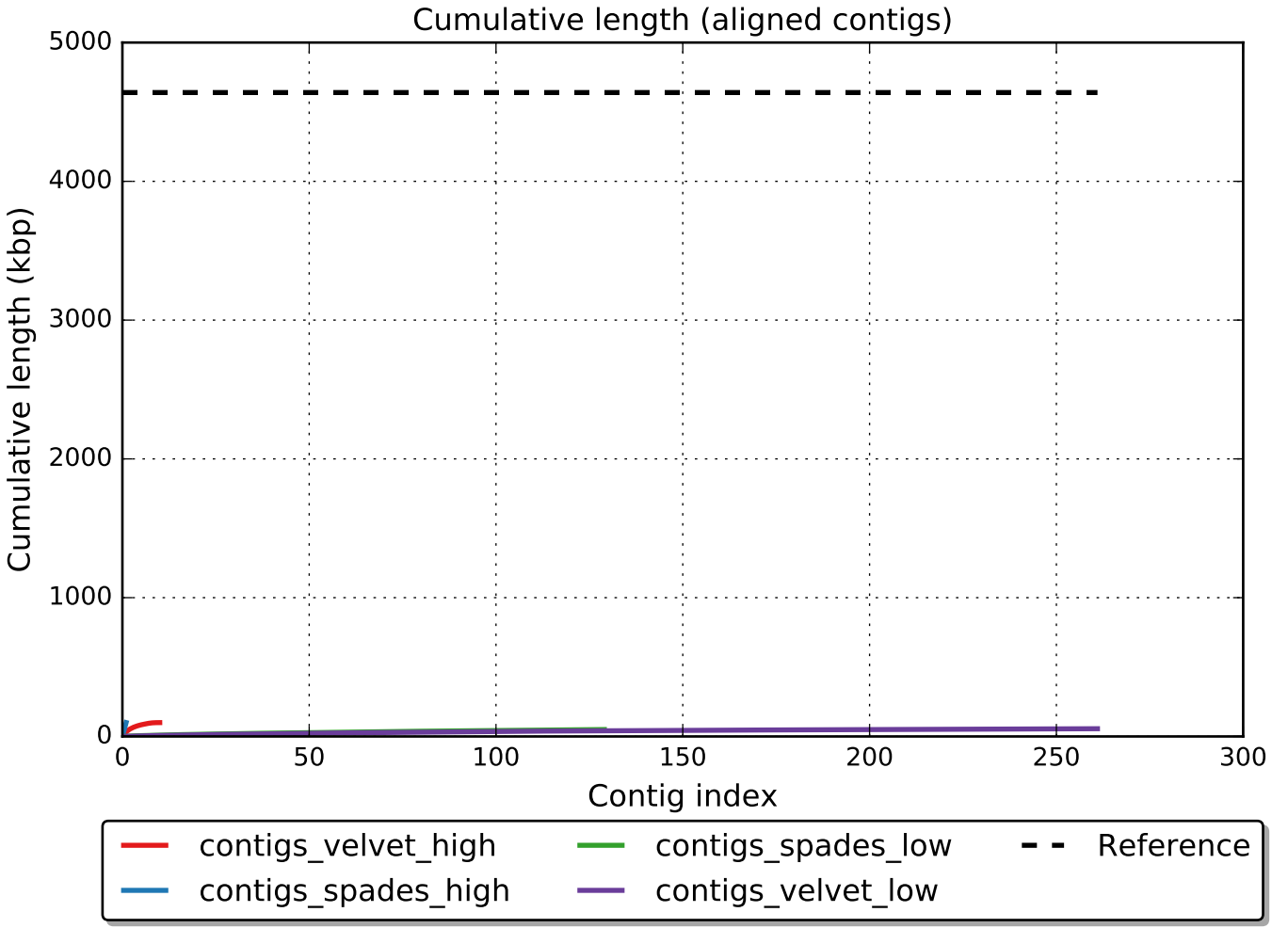

contigs_velvet_high coverage histogram (bin size: 11x)
Total length (kbp)
0
10
20
30
40
50
0
352
363
374
385
2322
Coverage depth (x)
contigs_velvet_high

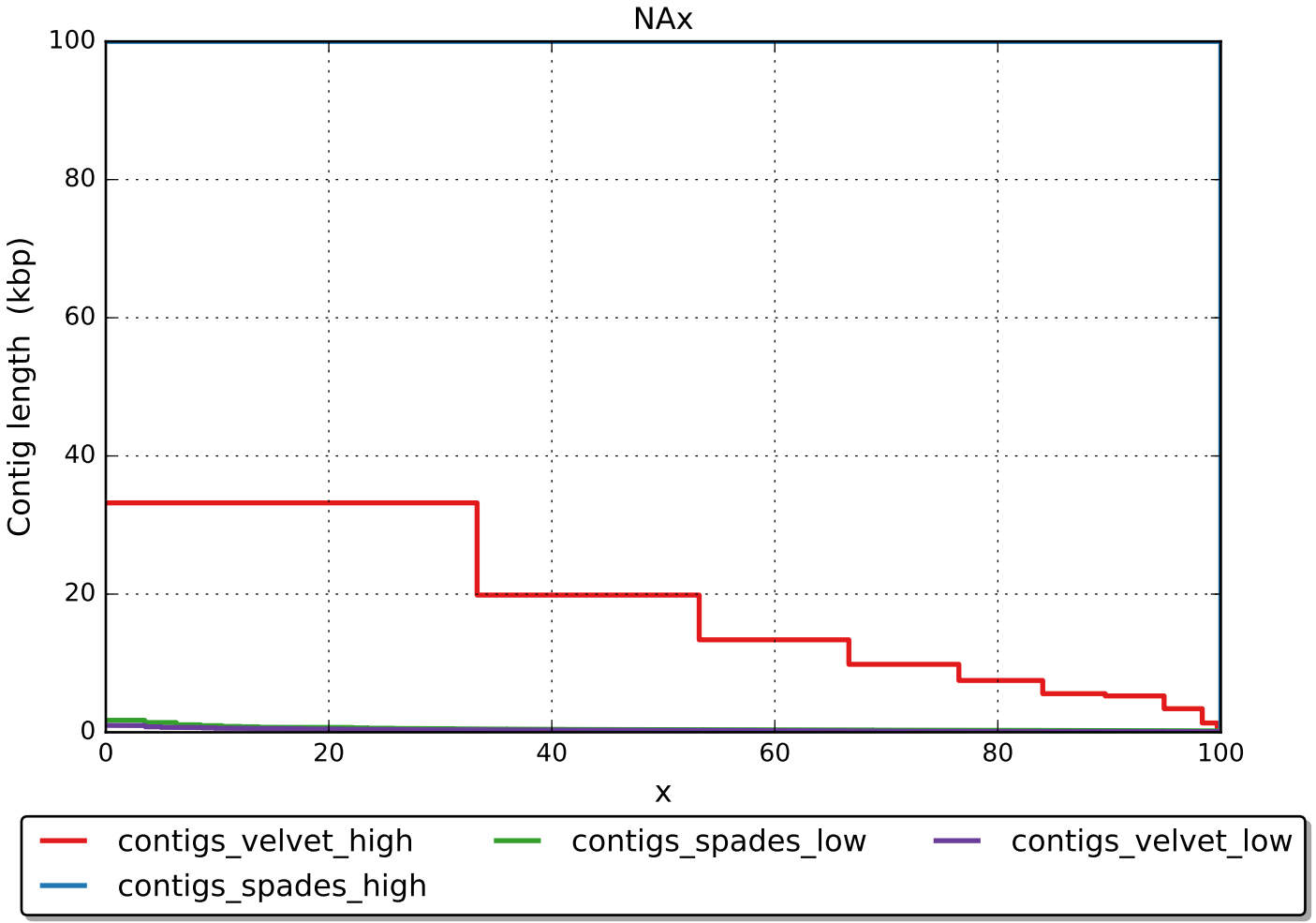

contigs_spades_high coverage histogram (bin size: 1x)
Total length (kbp)
100
50
0
0
225
226
Coverage depth (x)
contigs_spades_high

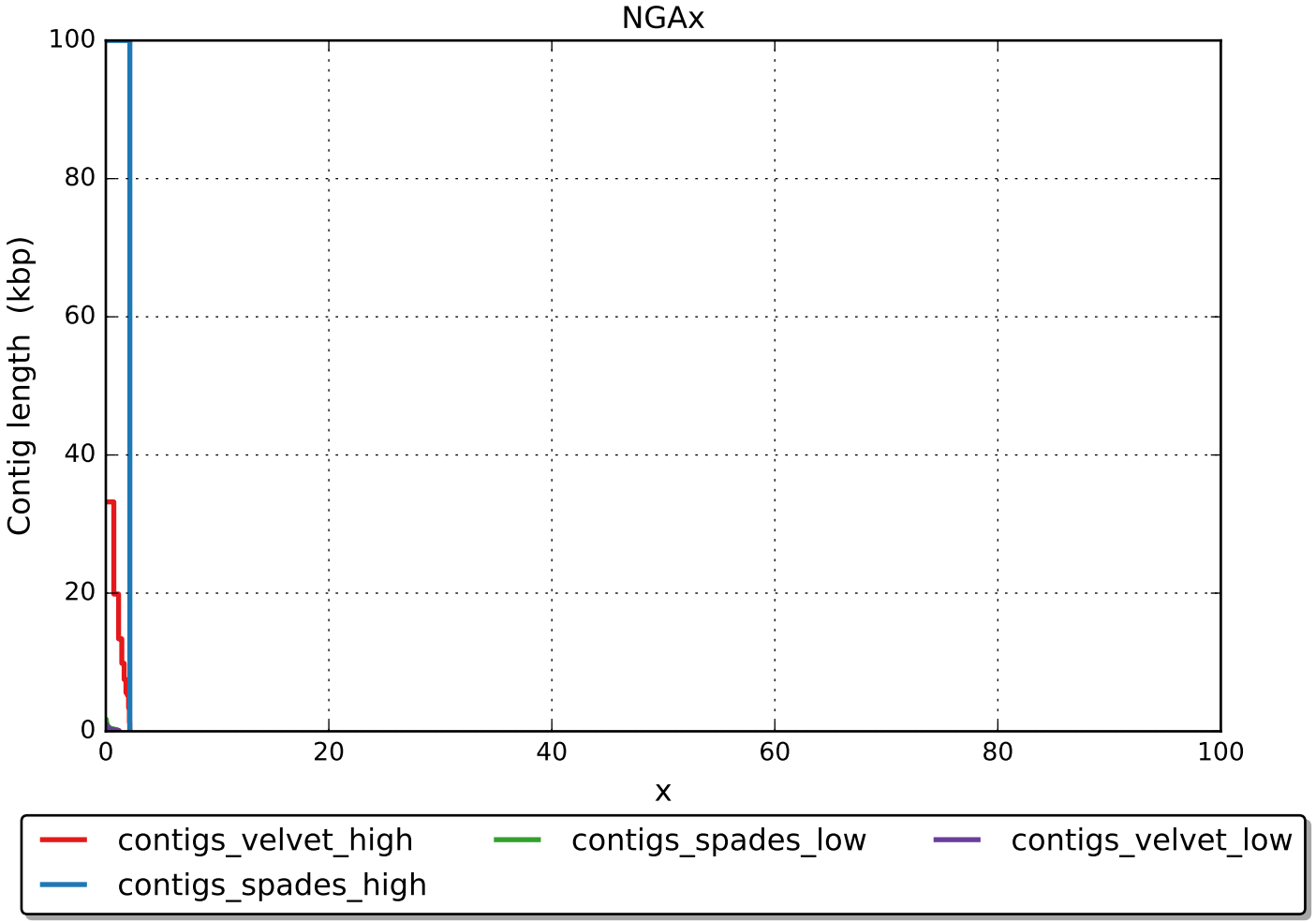

contigs_spades_low coverage histogram (bin size: 1x)
Total length (kbp)
40
30
20
10
0
0
1
4
Coverage depth (x)
contigs_spades_low

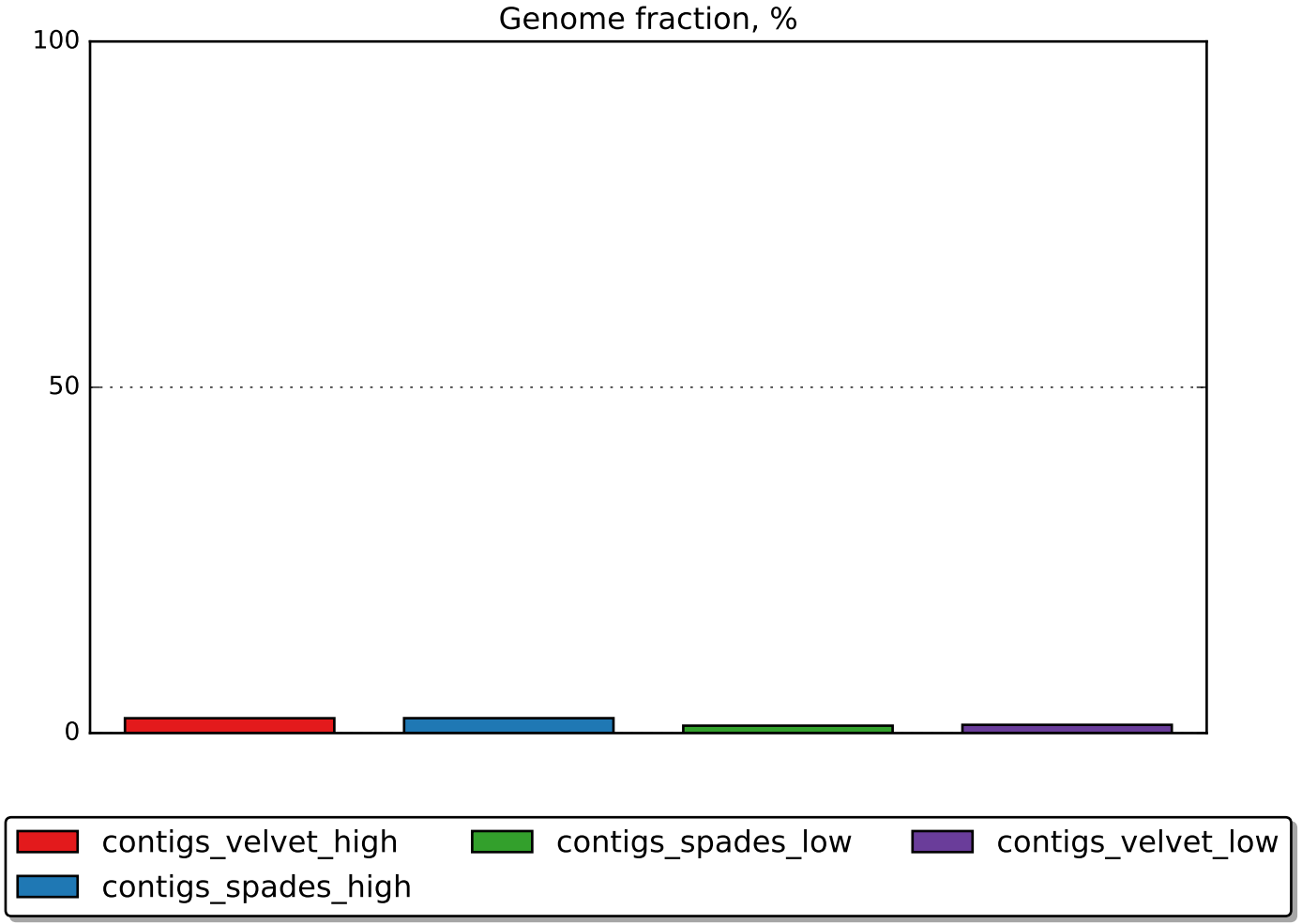

contigs_velvet_low coverage histogram (bin size: 1x)
Total length (kbp)
0
5
10
15
20
25
0
1
2
3
9
Coverage depth (x)
contigs_velvet_low


Misassemblies
2.0
1.5
1.0
0.5
0.0
contigs_velvet_high
contigs_spades_high
contigs_spades_low
contigs_velvet_low
relocations


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
50
100
150
200
250
300
Contig index
contigs_velvet_high
contigs_spades_high
contigs_spades_low
contigs_velvet_low
Reference


NAx
Contig length (kbp)
100
80
60
40
20
0
0
20
40
60
80
100
x
contigs_velvet_high
contigs_spades_low
contigs_velvet_low
contigs_spades_high


NGAx
Contig length (kbp)
x
0
20
40
60
80
100
contigs_velvet_high
contigs_spades_high
contigs_spades_low
contigs_velvet_low


Genome fraction, %
100
50
0
contigs_velvet_high
contigs_spades_high
contigs_spades_low
contigs_velvet_low