Report

	Short-Velvet_contigs	Long-Velvet_contigs	Short-Spades_contigs	Long-Spades_contigs
# contigs (>= 0 bp)	311	12	128	1
# contigs (>= 1000 bp)	0	7	4	1
# contigs (>= 5000 bp)	0	7	0	1
# contigs (>= 10000 bp)	0	4	0	1
# contigs (>= 25000 bp)	0	1	0	1
# contigs (>= 50000 bp)	0	0	0	1
Total length (>= 0 bp)	58644	100000	49818	100000
Total length (>= 1000 bp)	0	99448	5313	100000
Total length (>= 5000 bp)	0	99448	0	100000
Total length (>= 10000 bp)	0	81025	0	100000
Total length (>= 25000 bp)	0	33205	0	100000
Total length (>= 50000 bp)	0	0	0	100000
# contigs	12	7	20	1
Largest contig	998	33205	1737	100000
Total length	8044	99448	15922	100000
Reference length	4639675	4639675	4639675	4639675
GC (%)	50.31	52.57	51.21	52.59
Reference GC (%)	50.79	50.79	50.79	50.79
N50	679	19876	718	100000
N75	542	13398	635	100000
L50	5	2	8	1
L75	9	4	13	1
# 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 (%)	0.173	2.143	0.343	2.155
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	31.40	0.00
# indels per 100 kbp	0.00	0.00	0.00	0.00
Largest alignment	998	33205	1737	100000
Total aligned length	8044	99448	15922	100000
NA50	679	19876	715	100000
NGA50	-	-	-	-
NA75	542	13398	587	100000
LA50	5	2	8	1
LA75	9	4	14	1

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

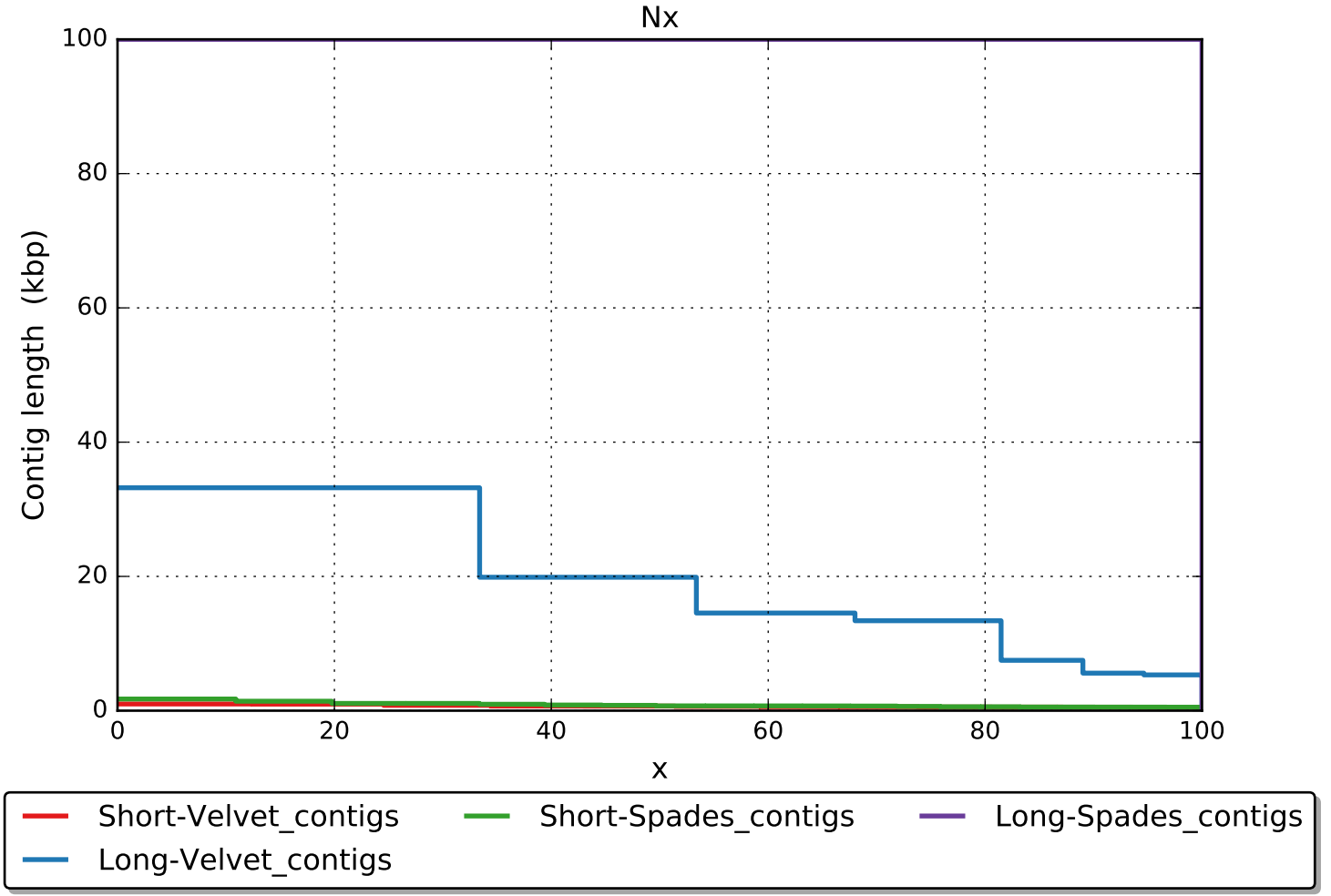
	Short-Velvet_contigs	Long-Velvet_contigs	Short-Spades_contigs	Long-Spades_contigs
# misassemblies	0	0	1	0
# relocations	0	0	1	0
# translocations	0	0	0	0
# inversions	0	0	0	0
# misassembled contigs	0	0	1	0
Misassembled contigs length	0	0	1084	0
# local misassemblies	0	0	0	0
# mismatches	0	0	5	0
# indels	0	0	0	0
# short indels	0	0	0	0
# long indels	0	0	0	0
Indels length	0	0	0	0

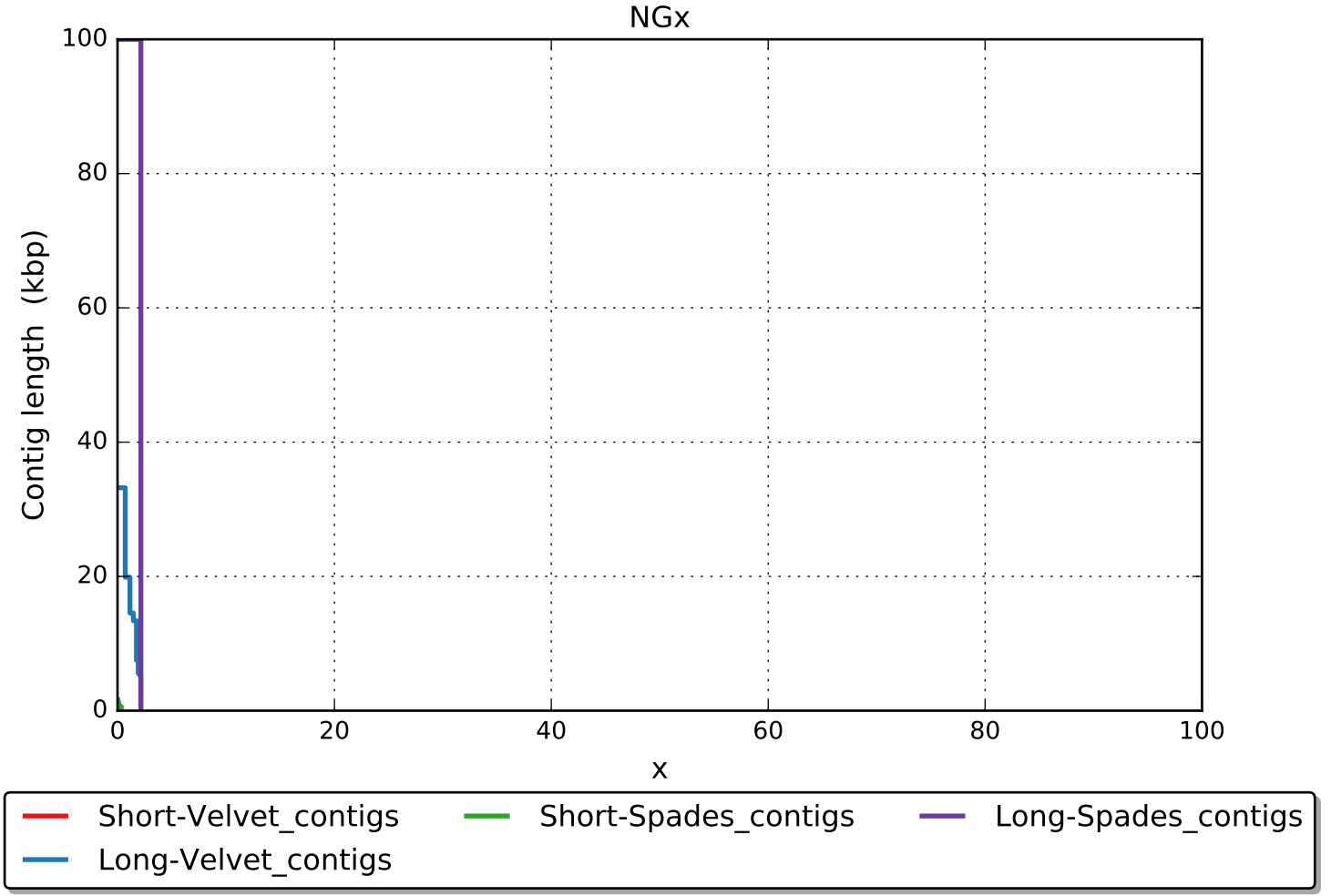
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

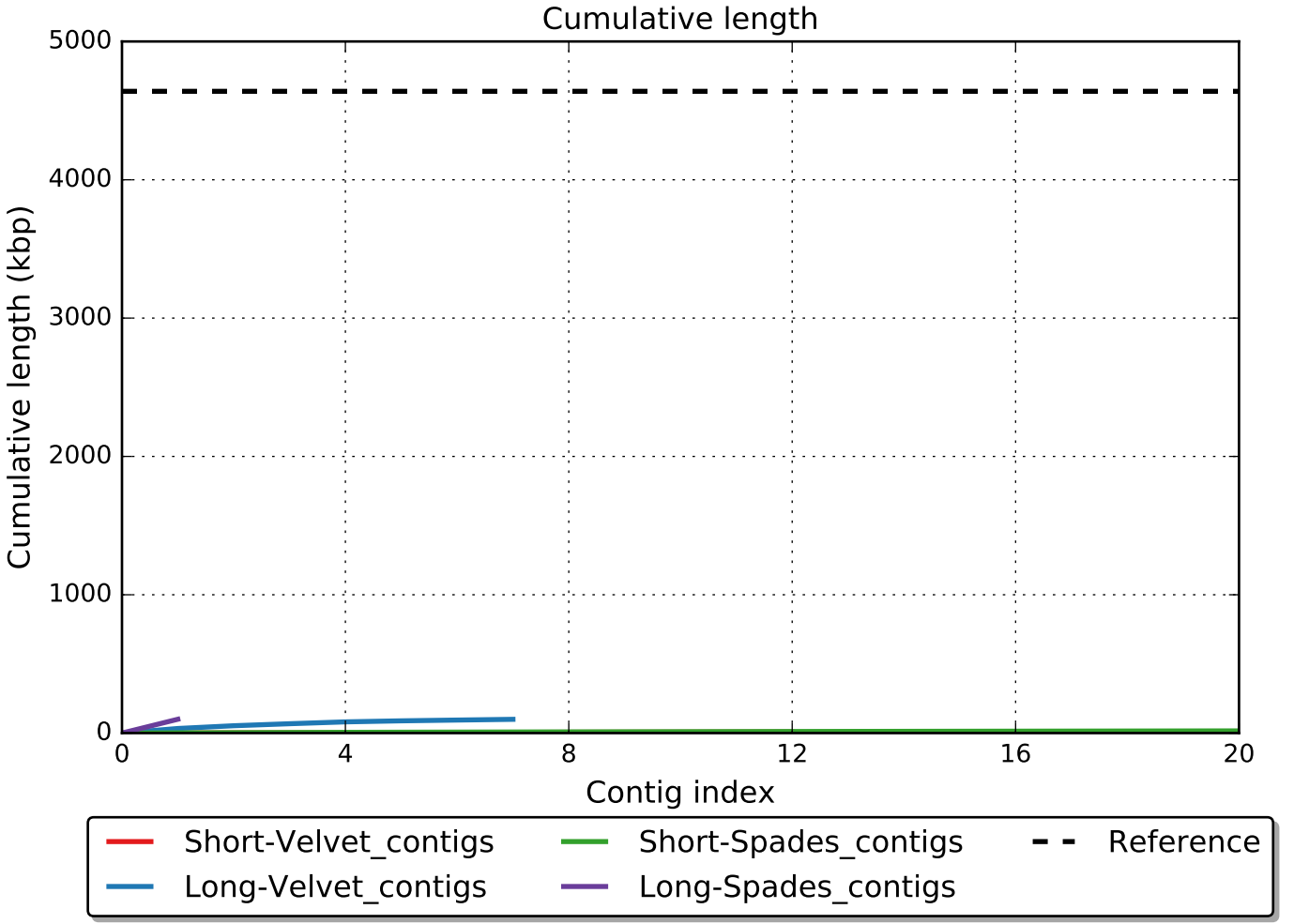
Unaligned report

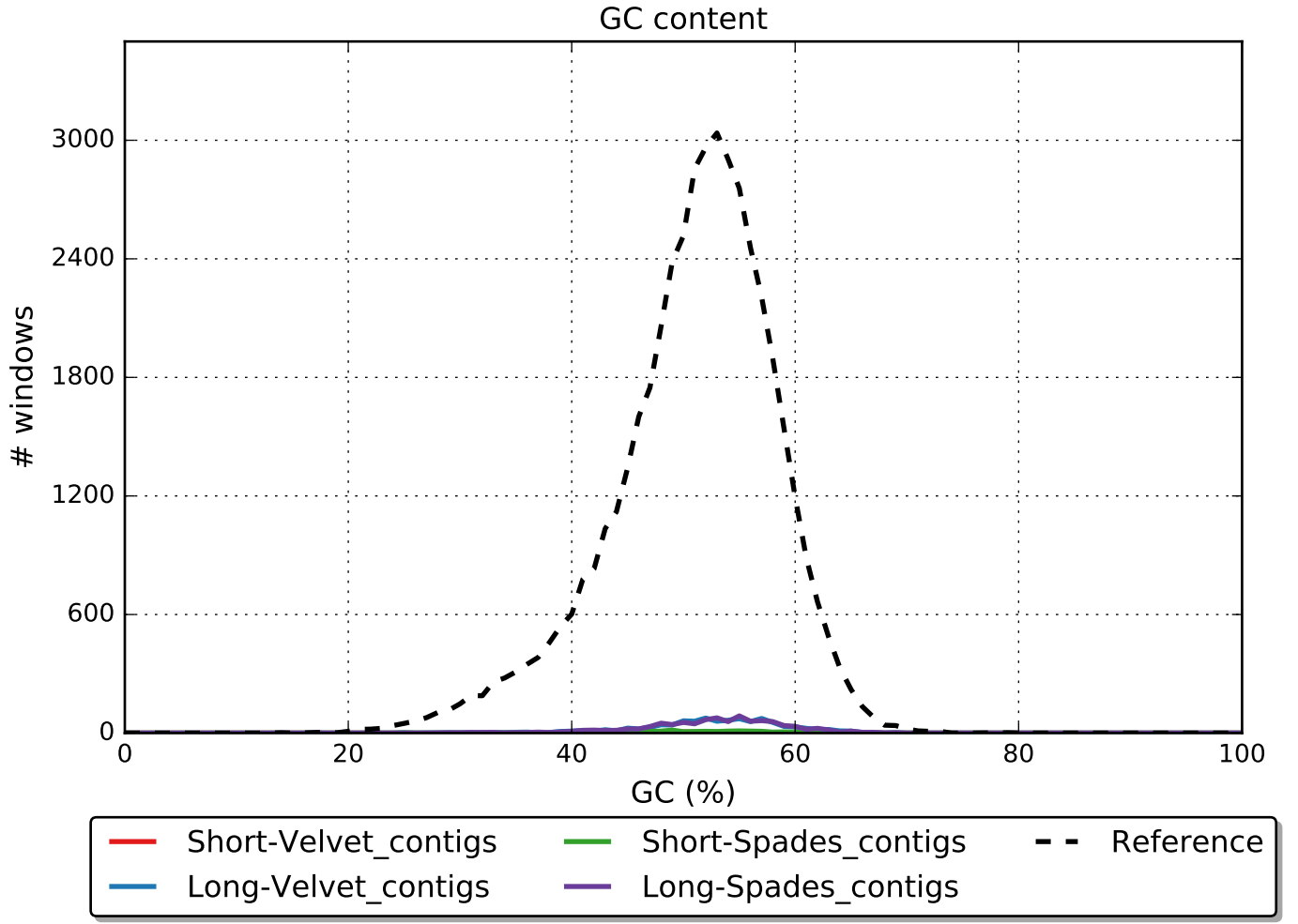
	Short-Velvet_contigs	Long-Velvet_contigs	Short-Spades_contigs	Long-Spades_contigs
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	0	0	0	0
# with misassembly	0	0	0	0
# both parts are significant	0	0	0	0
Partially unaligned length	0	0	0	0
# N's	0	0	0	0

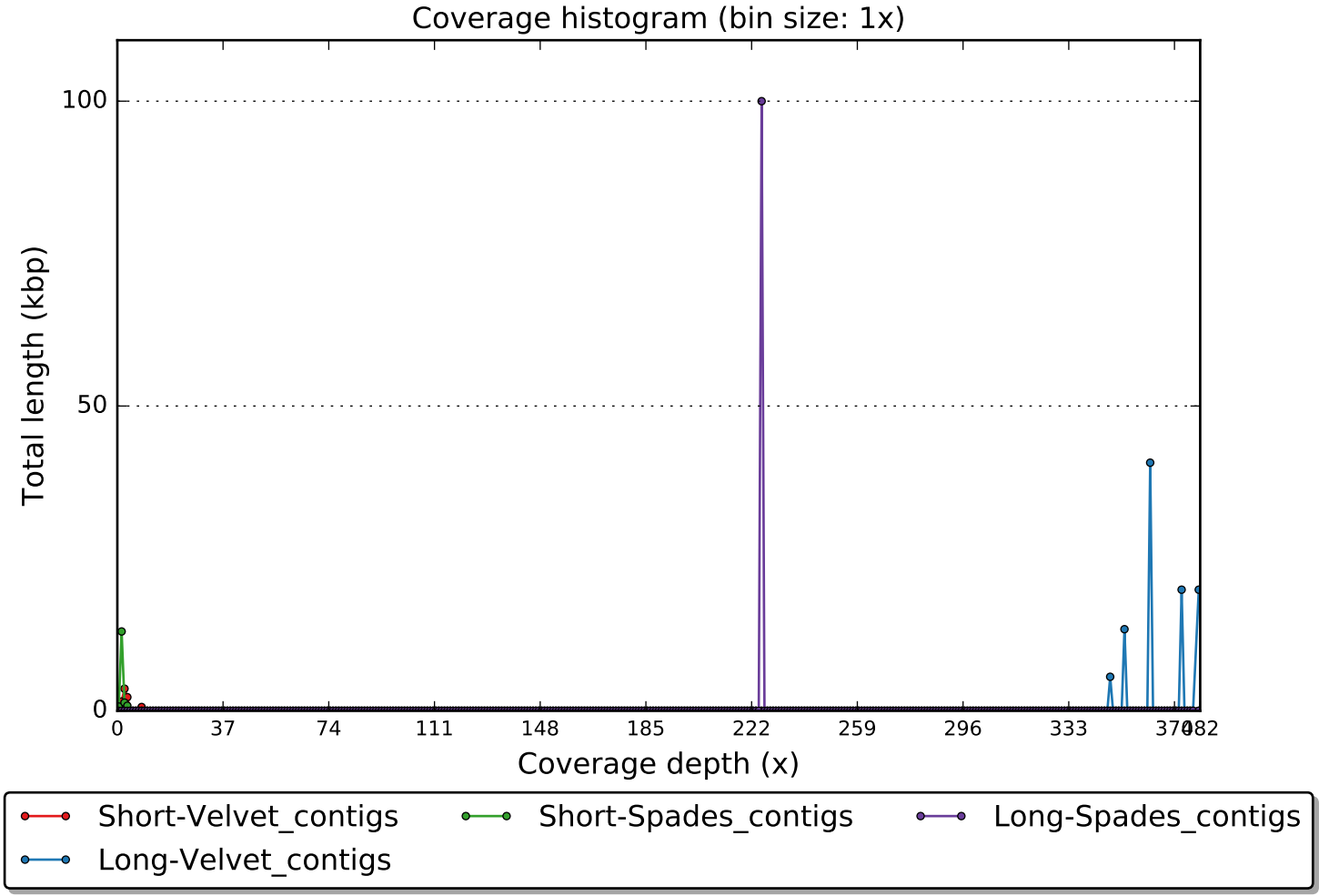
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

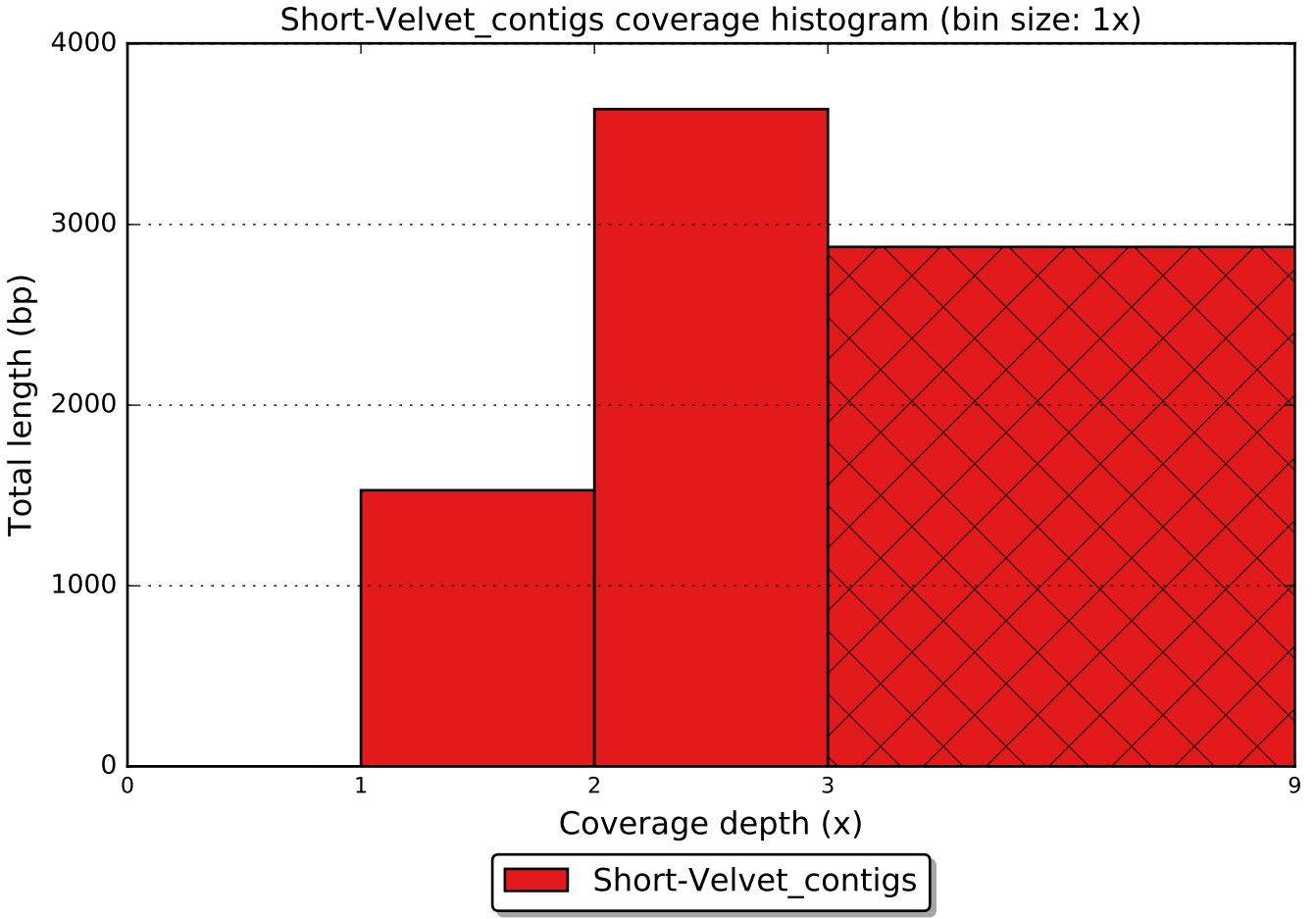

Nx
Contig length (kbp)
100
80
60
40
20
0
0
20
40
60
80
100
x
Short-Velvet_contigs
Short-Spades_contigs
Long-Spades_contigs
Long-Velvet_contigs

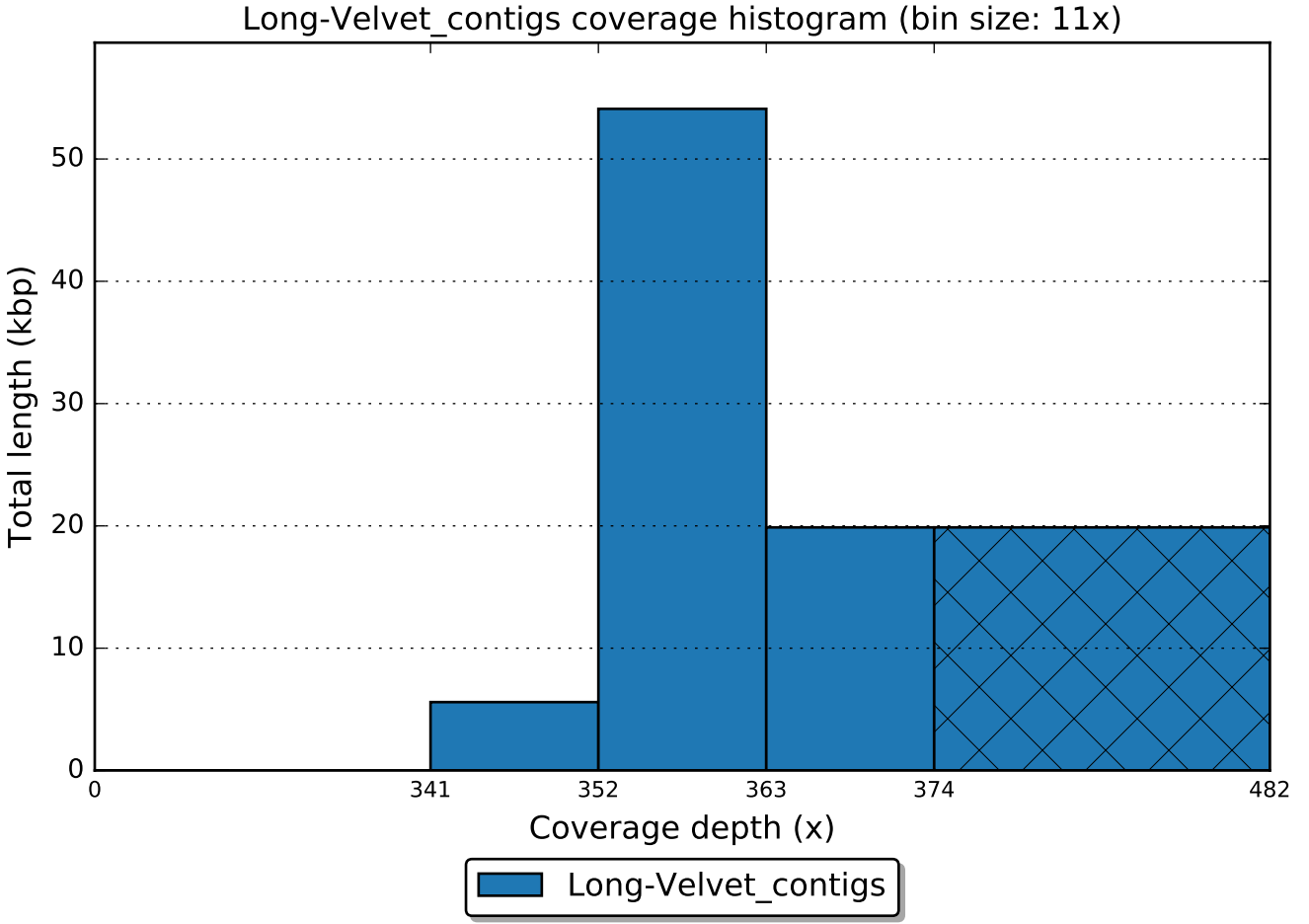

NGx
Contig length (kbp)
x
0
20
40
60
80
100
Short-Velvet_contigs
Short-Spades_contigs
Long-Spades_contigs
Long-Velvet_contigs

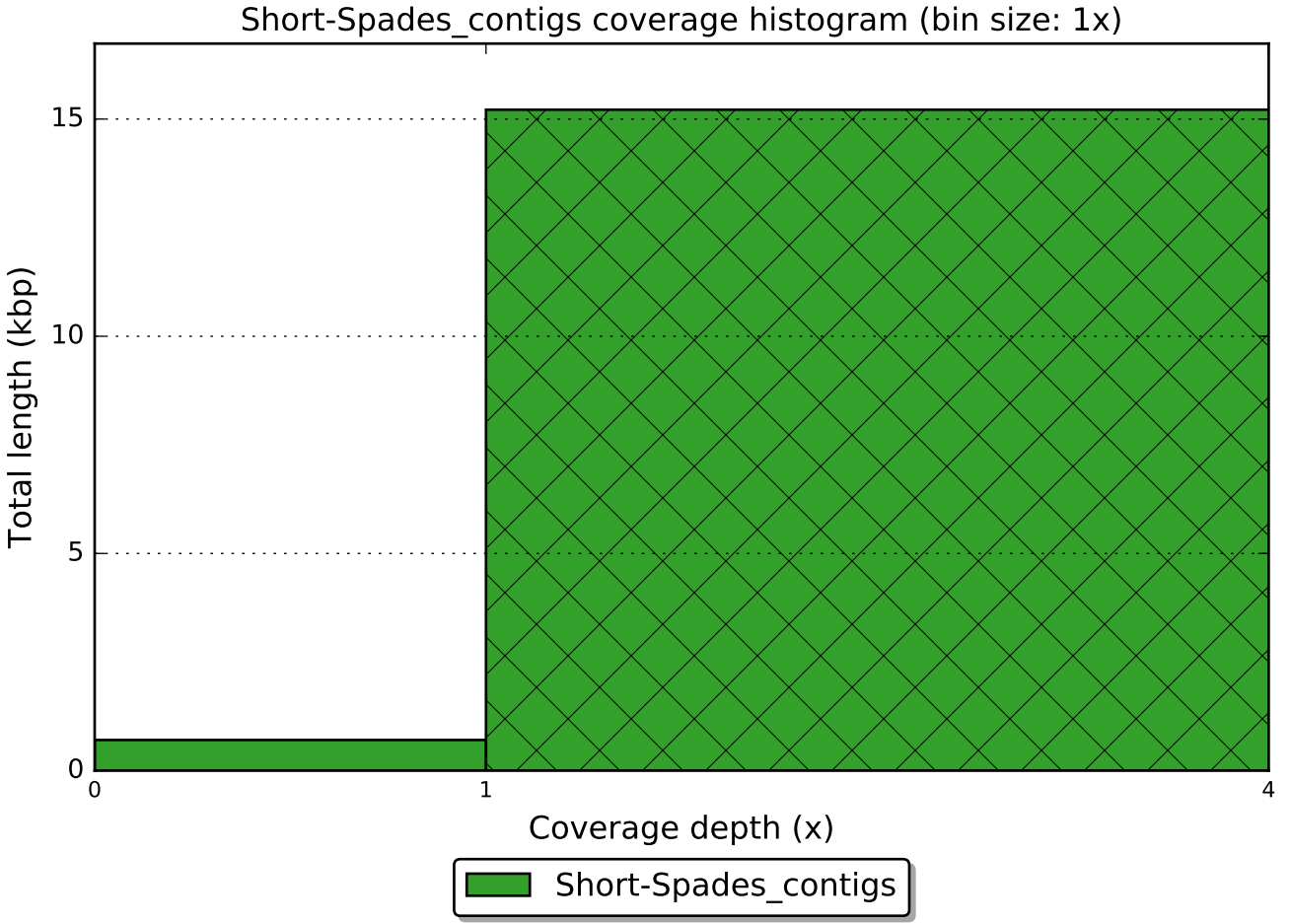

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
4
8
12
16
20
Contig index
Short-Velvet_contigs
Long-Velvet_contigs
Short-Spades_contigs
Long-Spades_contigs
Reference

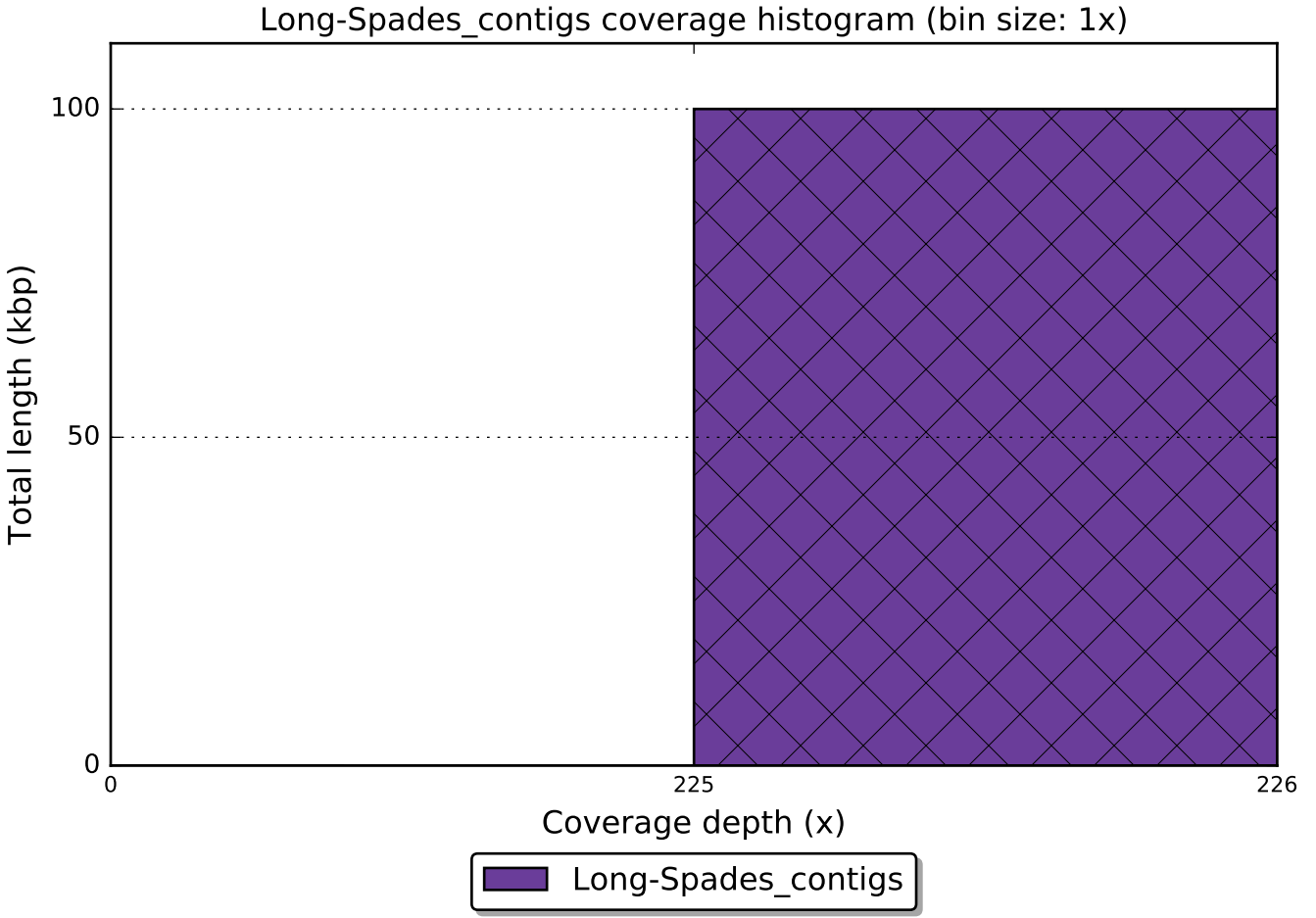

GC content
windows
3000
2400
1800
1200
600
0
0
20
40
60
80
100
GC (%)
Short-Velvet_contigs
Long-Velvet_contigs
Short-Spades_contigs
Long-Spades_contigs
Reference

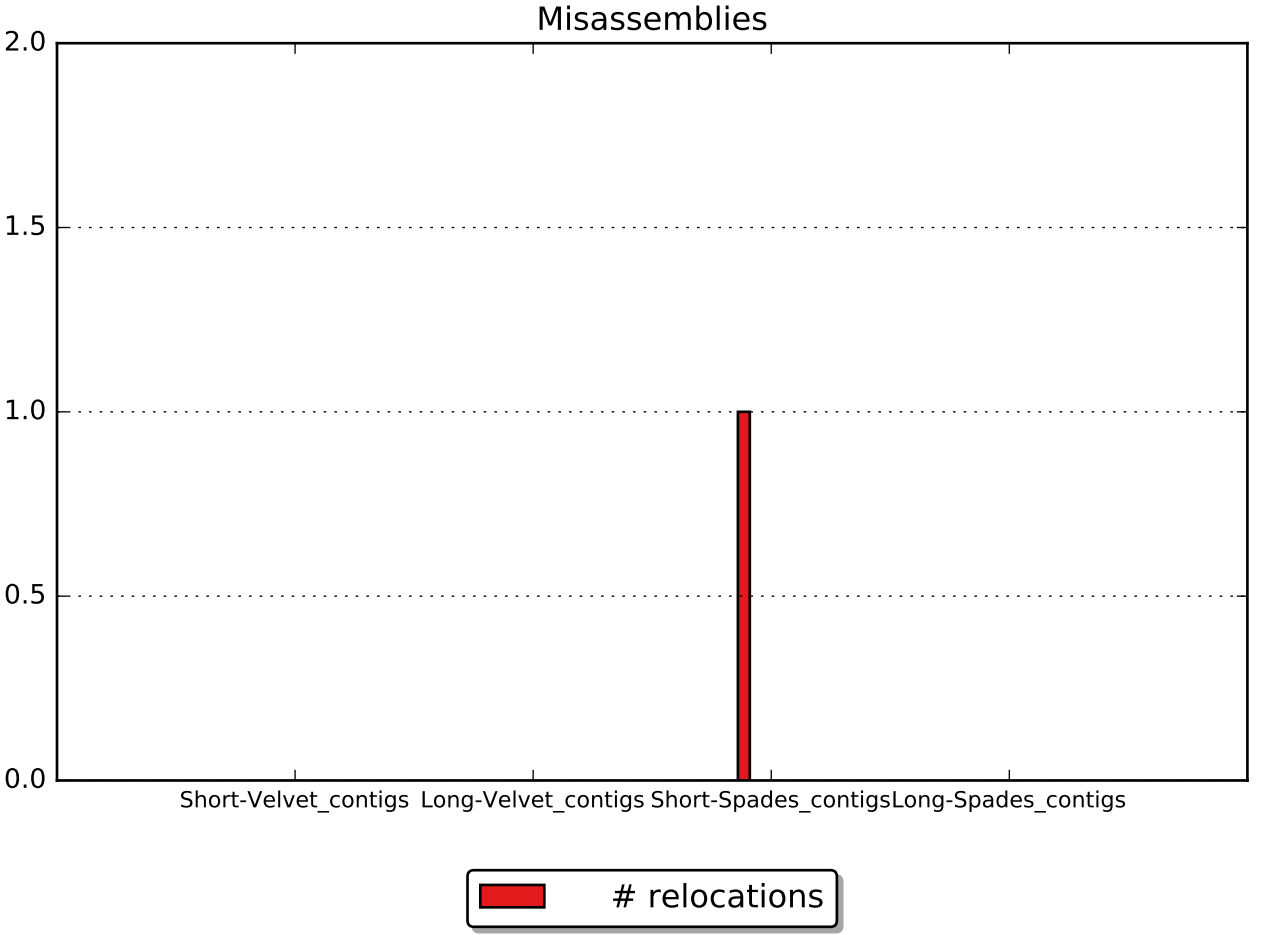

Coverage histogram (bin size: 1x)
Total length (kbp)
100
50
0
0
37
74
111
148
185
222
259
296
333
370
382
Coverage depth (x)
Short-Velvet_contigs
Short-Spades_contigs
Long-Spades_contigs
Long-Velvet_contigs

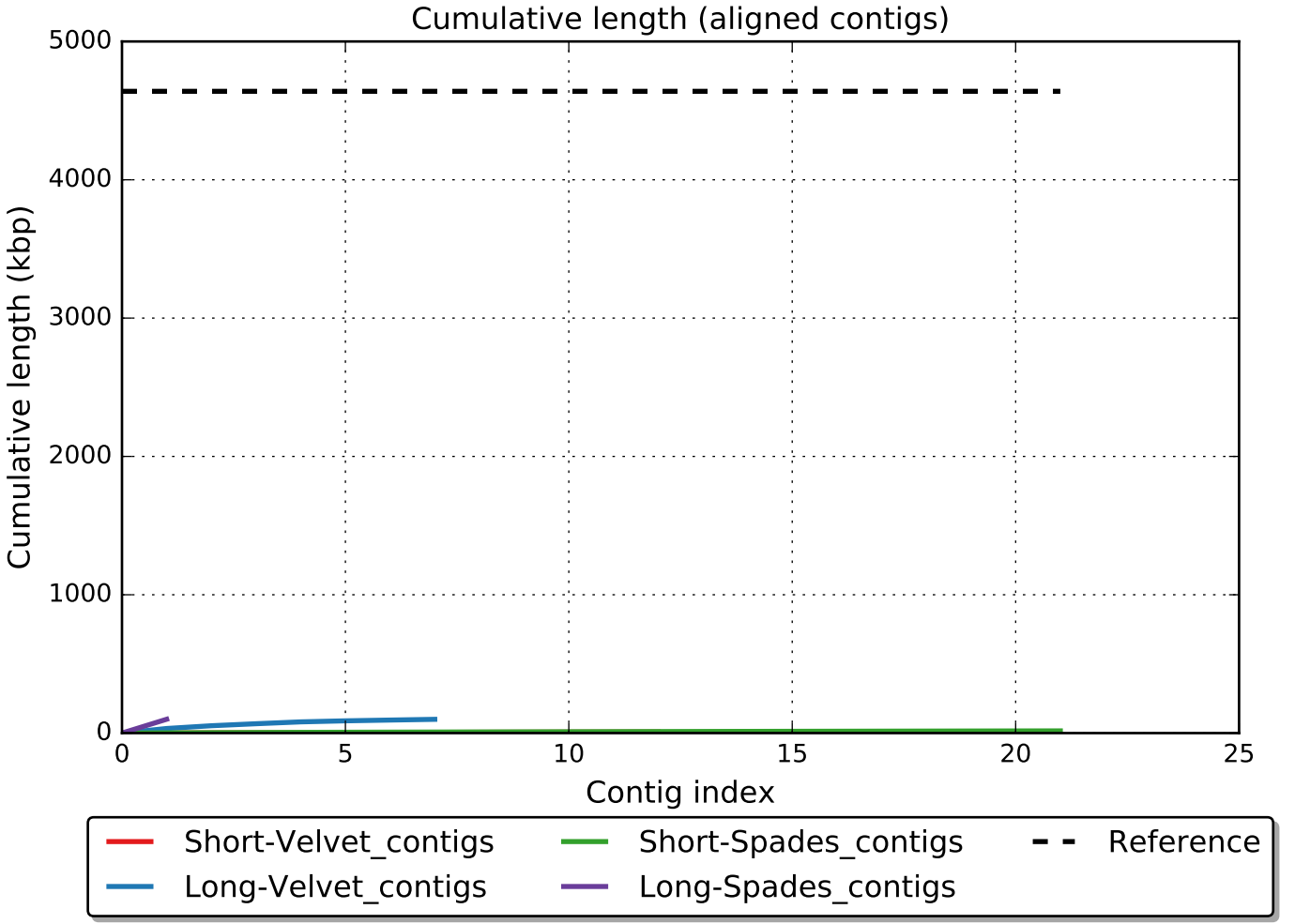

Short-Velvet_contigs coverage histogram (bin size: 1x)
Total length (bp)
4000
3000
2000
1000
0
0
1
2
3
9
Coverage depth (x)
Short-Velvet_contigs

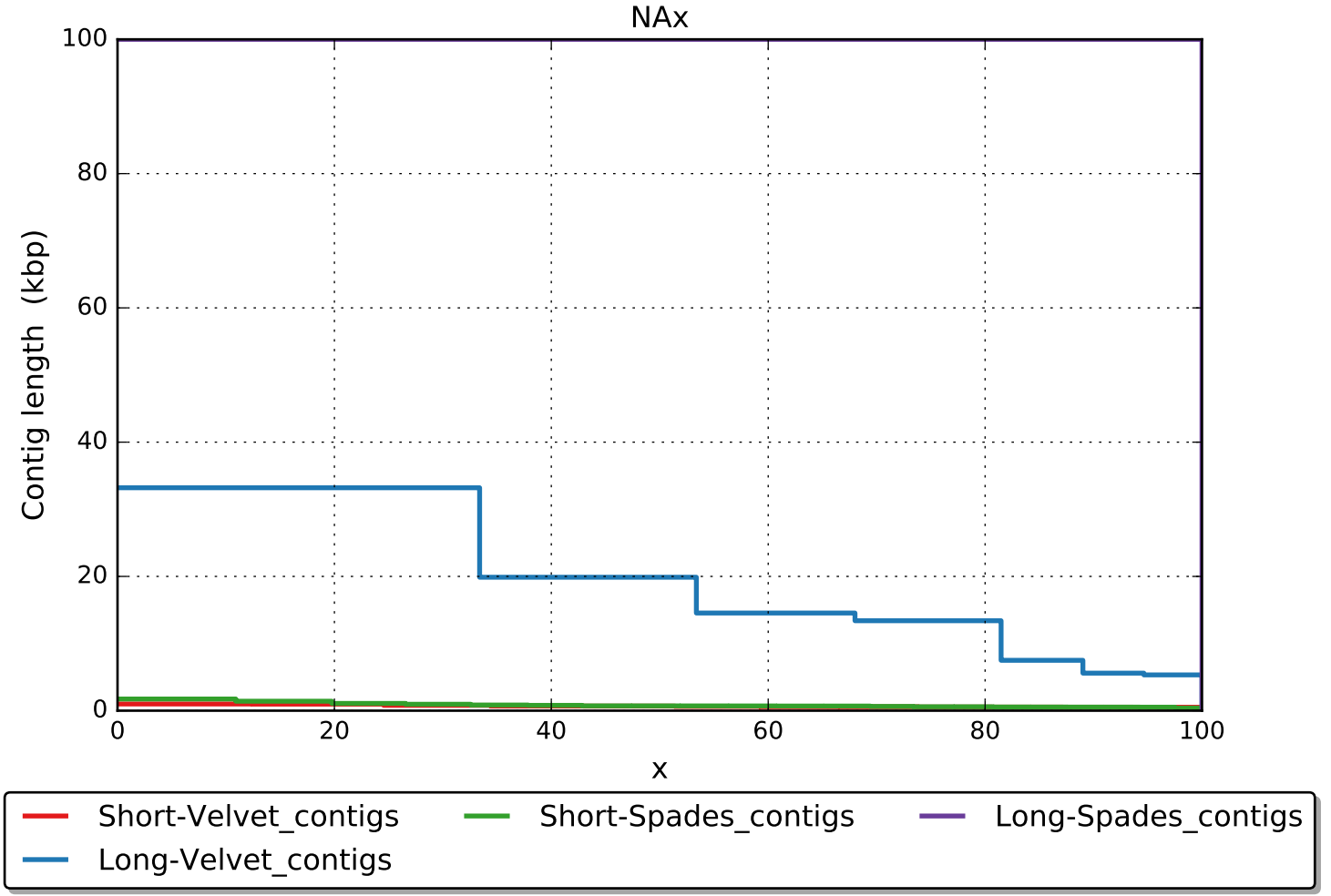

Long-Velvet_contigs coverage histogram (bin size: 11x)
Total length (kbp)
0
10
20
30
40
50
0
341
352
363
374
482
Coverage depth (x)
Long-Velvet_contigs

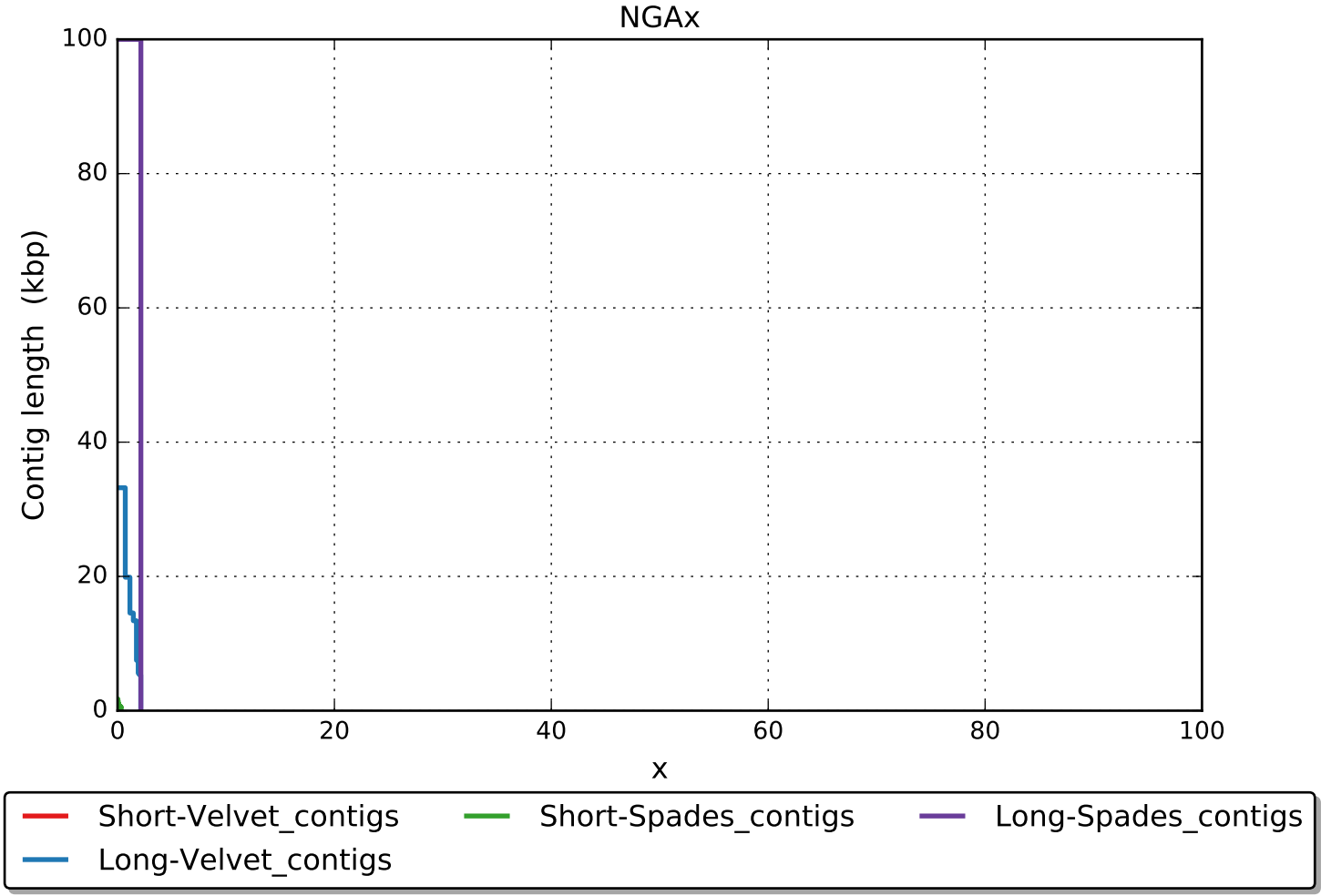

Short-Spades_contigs coverage histogram (bin size: 1x)
Total length (kbp)
15
10
5
0
0
1
4
Coverage depth (x)
Short-Spades_contigs

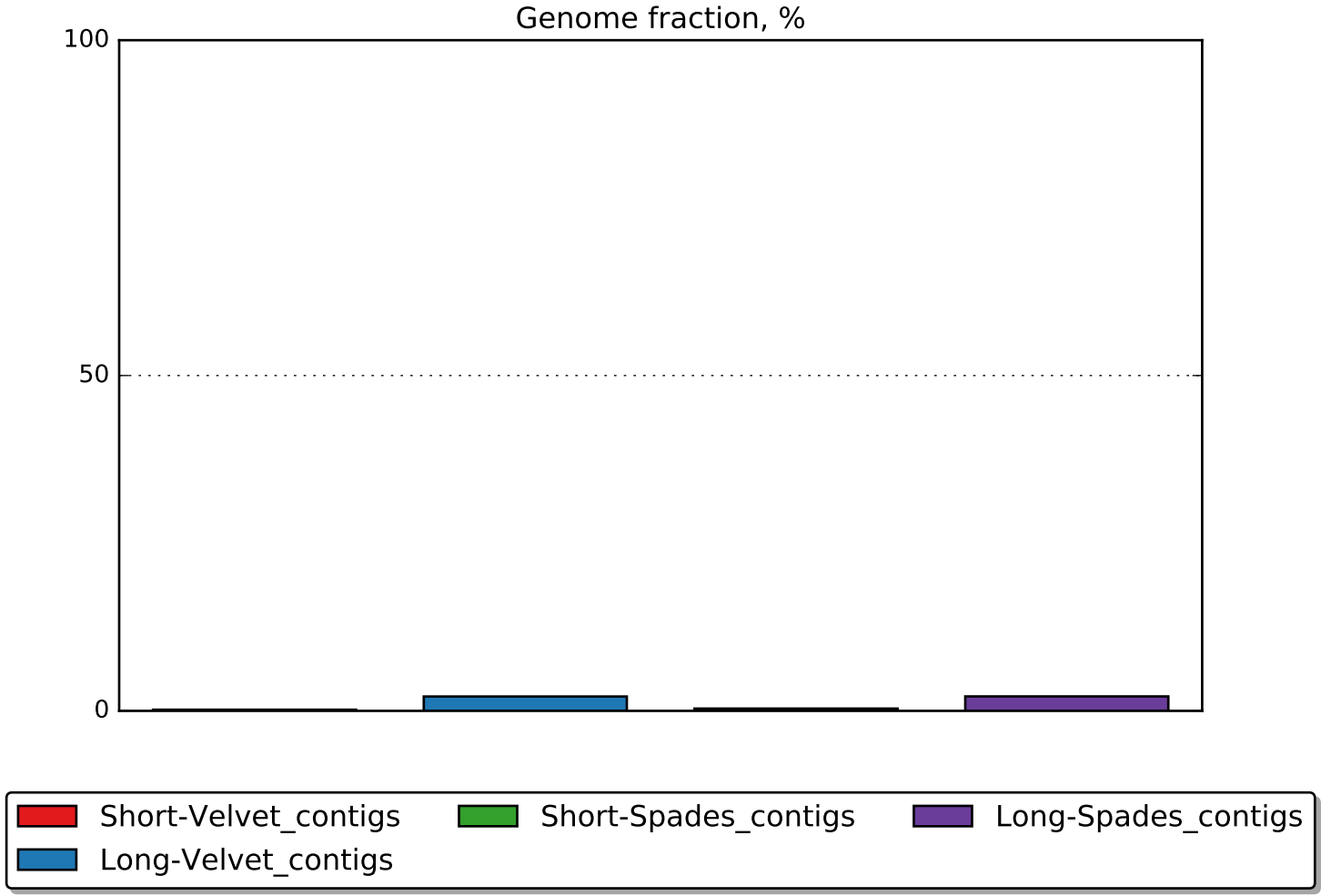

Long-Spades_contigs coverage histogram (bin size: 1x)
Total length (kbp)
100
50
0
0
225
226
Coverage depth (x)
Long-Spades_contigs


Misassemblies
2.0
1.5
1.0
0.5
0.0
Short-Velvet_contigs
Long-Velvet_contigs
Short-Spades_contigs
Long-Spades_contigs
relocations


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
5
10
15
20
25
Contig index
Short-Velvet_contigs
Long-Velvet_contigs
Short-Spades_contigs
Long-Spades_contigs
Reference


NAx
Contig length (kbp)
100
80
60
40
20
0
0
20
40
60
80
100
x
Short-Velvet_contigs
Short-Spades_contigs
Long-Spades_contigs
Long-Velvet_contigs


NGAx
Contig length (kbp)
100
80
60
40
20
0
0
20
40
60
80
100
x
Short-Velvet_contigs
Short-Spades_contigs
Long-Spades_contigs
Long-Velvet_contigs


Genome fraction, %
100
50
0
Short-Velvet_contigs
Short-Spades_contigs
Long-Spades_contigs
Long-Velvet_contigs