Report

	SPAdes	Velvet
# contigs (>= 0 bp)	152	192
# contigs (>= 1000 bp)	80	107
# contigs (>= 5000 bp)	56	82
# contigs (>= 10000 bp)	52	74
# contigs (>= 25000 bp)	45	57
# contigs (>= 50000 bp)	31	33
Total length (>= 0 bp)	4570605	4569214
Total length (>= 1000 bp)	4549301	4546082
Total length (>= 5000 bp)	4496699	4492466
Total length (>= 10000 bp)	4467005	4432370
Total length (>= 25000 bp)	4364167	4147479
Total length (>= 50000 bp)	3878287	3287286
# contigs	93	120
Largest contig	285114	242032
Total length	4558330	4554702
Reference length	4639675	4639675
GC (%)	50.74	50.74
Reference GC (%)	50.79	50.79
N50	132831	82776
NG50	132831	82776
N75	67340	42907
NG75	64399	42783
L50	13	18
LG50	13	18
L75	24	36
LG75	25	38
# misassemblies	0	3
# misassembled contigs	0	2
Misassembled contigs length	0	323967
# local misassemblies	12	11
# unaligned mis. contigs	0	0
# unaligned contigs	4 + 0 part	0 + 0 part
Unaligned length	2947	0
Genome fraction (%)	98.139	98.131
Duplication ratio	1.000	1.000
# N's per 100 kbp	0.00	0.00
# mismatches per 100 kbp	2.72	2.44
# indels per 100 kbp	0.26	0.35
Largest alignment	285114	196677
Total aligned length	4554957	4554351
NA50	132831	78602
NGA50	132831	78602
NA75	67340	42856
NGA75	64399	42783
LA50	13	19
LGA50	13	19
LA75	24	38
LGA75	25	39

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

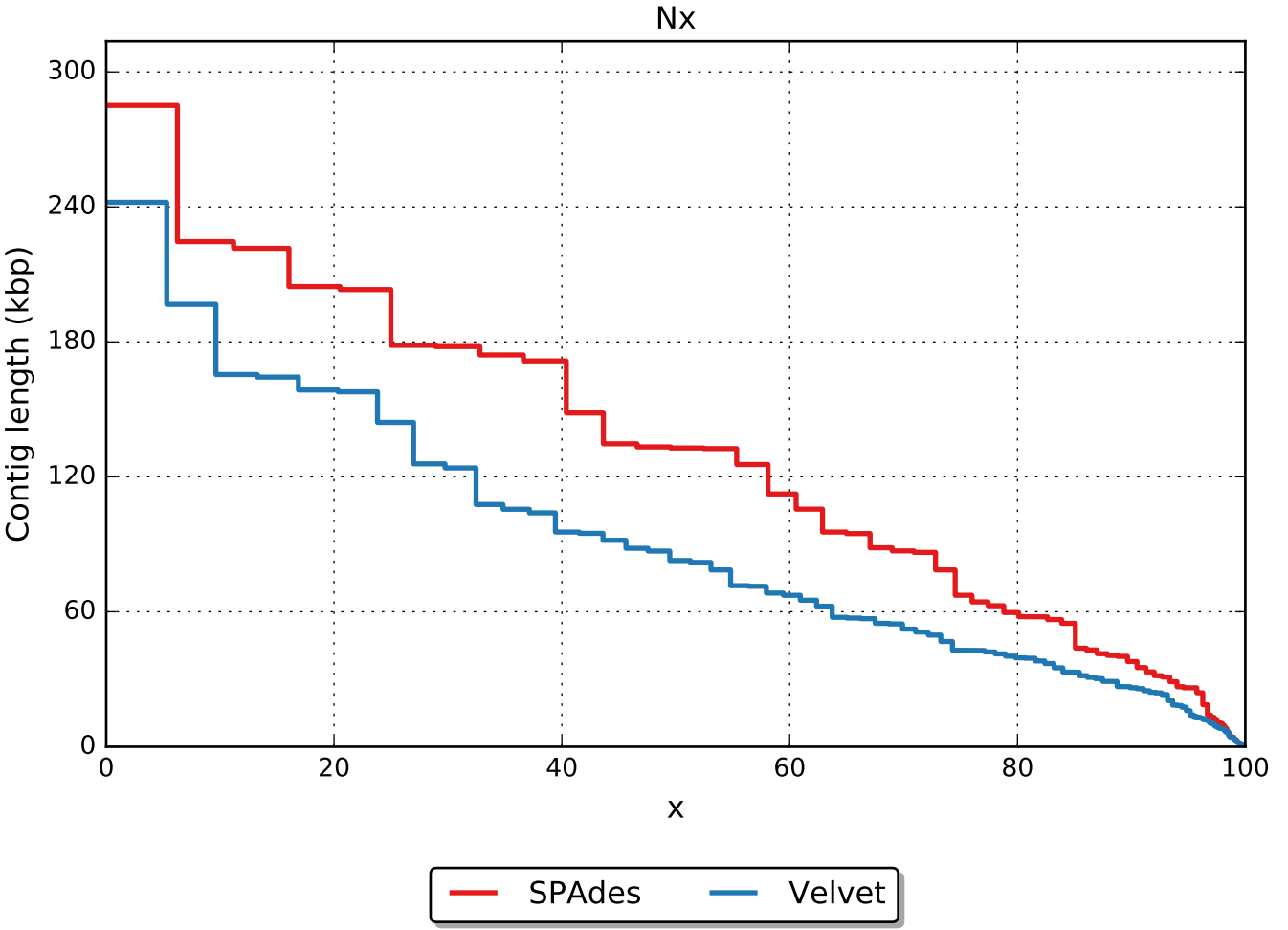
	SPAdes	Velvet
# misassemblies	0	3
# relocations	0	3
# translocations	0	0
# inversions	0	0
# misassembled contigs	0	2
Misassembled contigs length	0	323967
# local misassemblies	12	11
# unaligned mis. contigs	0	0
# mismatches	124	111
# indels	12	16
# indels (<= 5 bp)	12	16
# indels (> 5 bp)	0	0
Indels length	19	20

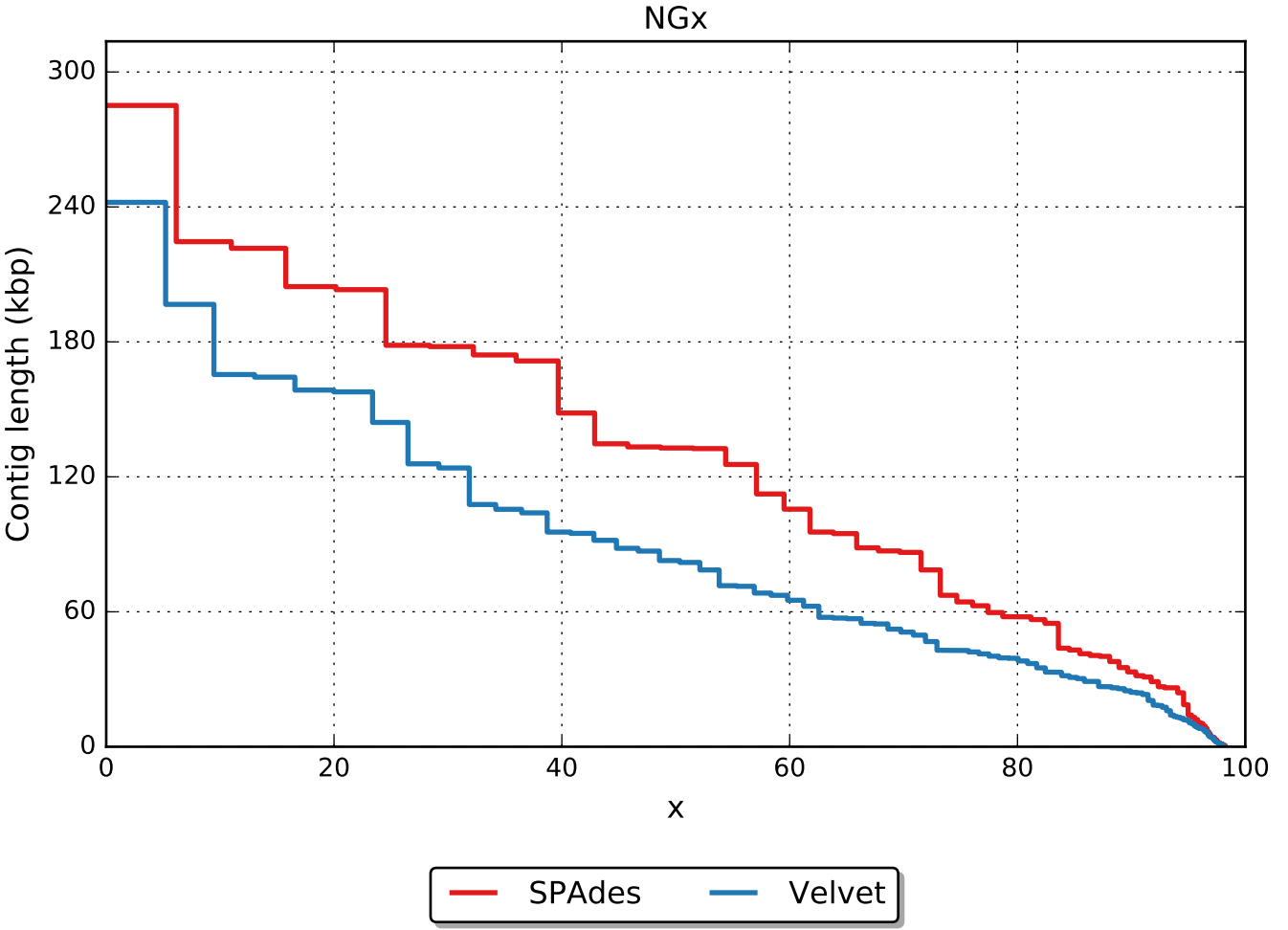
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

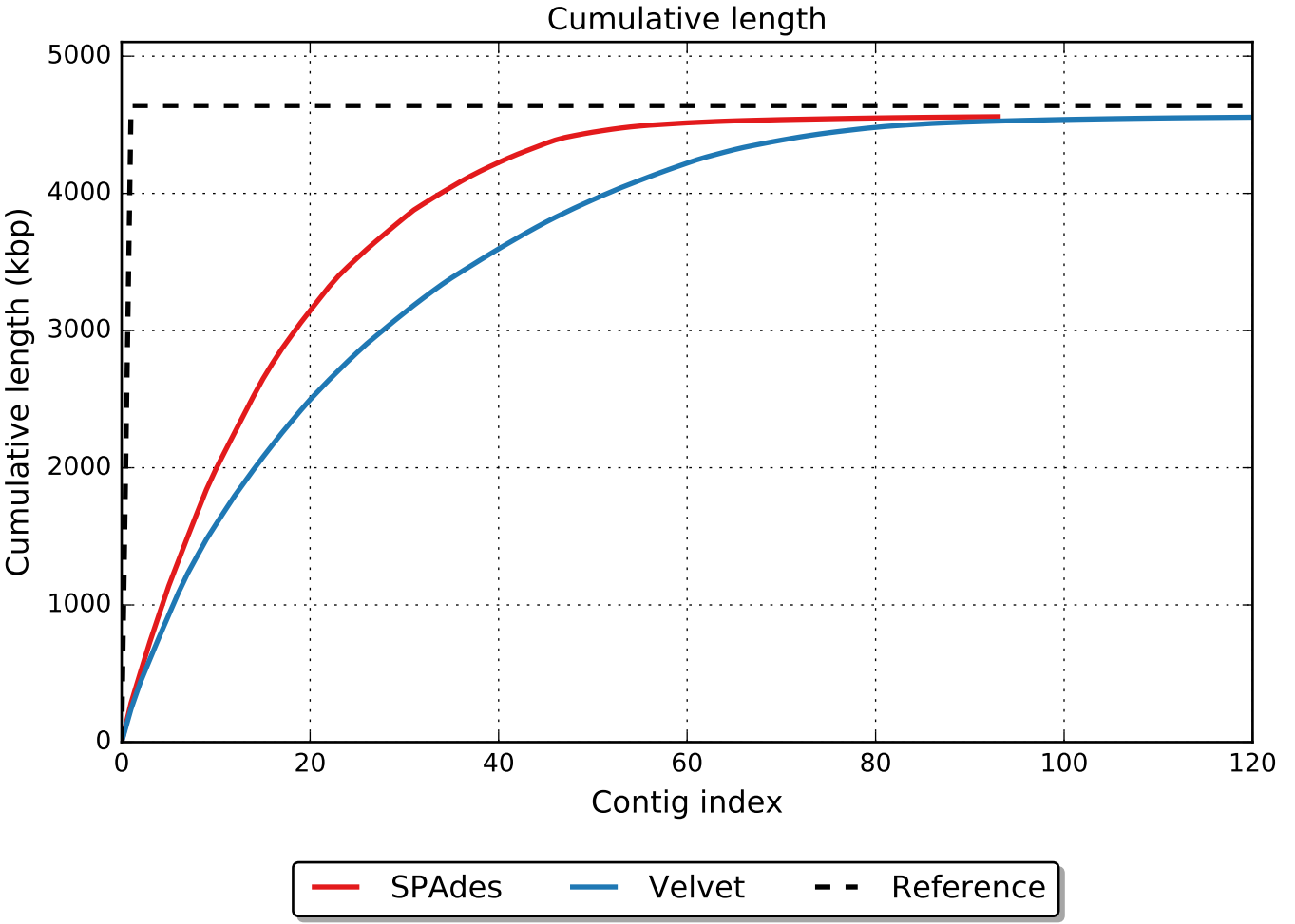
Unaligned report

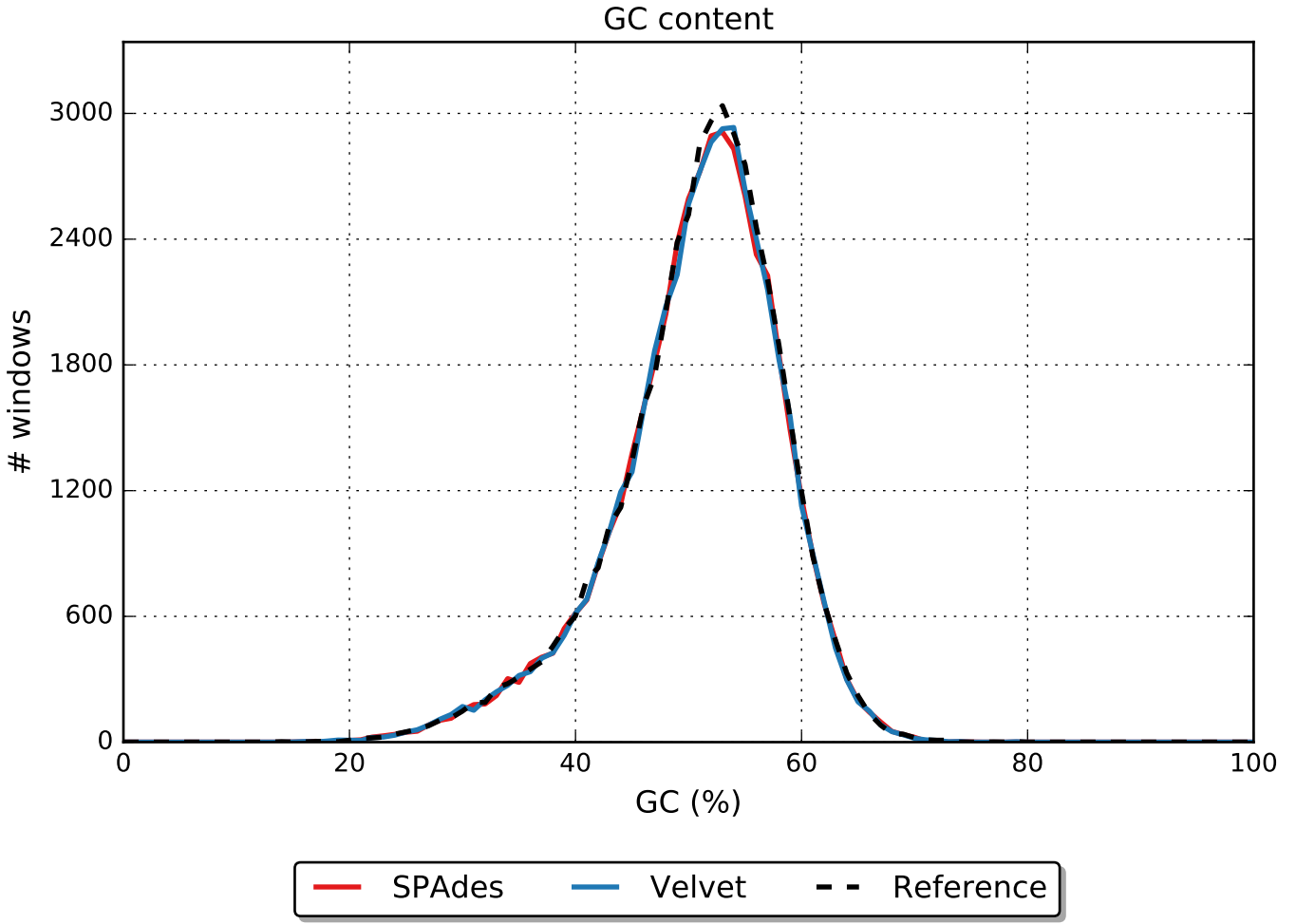
	SPAdes	Velvet
# fully unaligned contigs	4	0
Fully unaligned length	2947	0
# partially unaligned contigs	0	0
Partially unaligned length	0	0
# N's	0	0

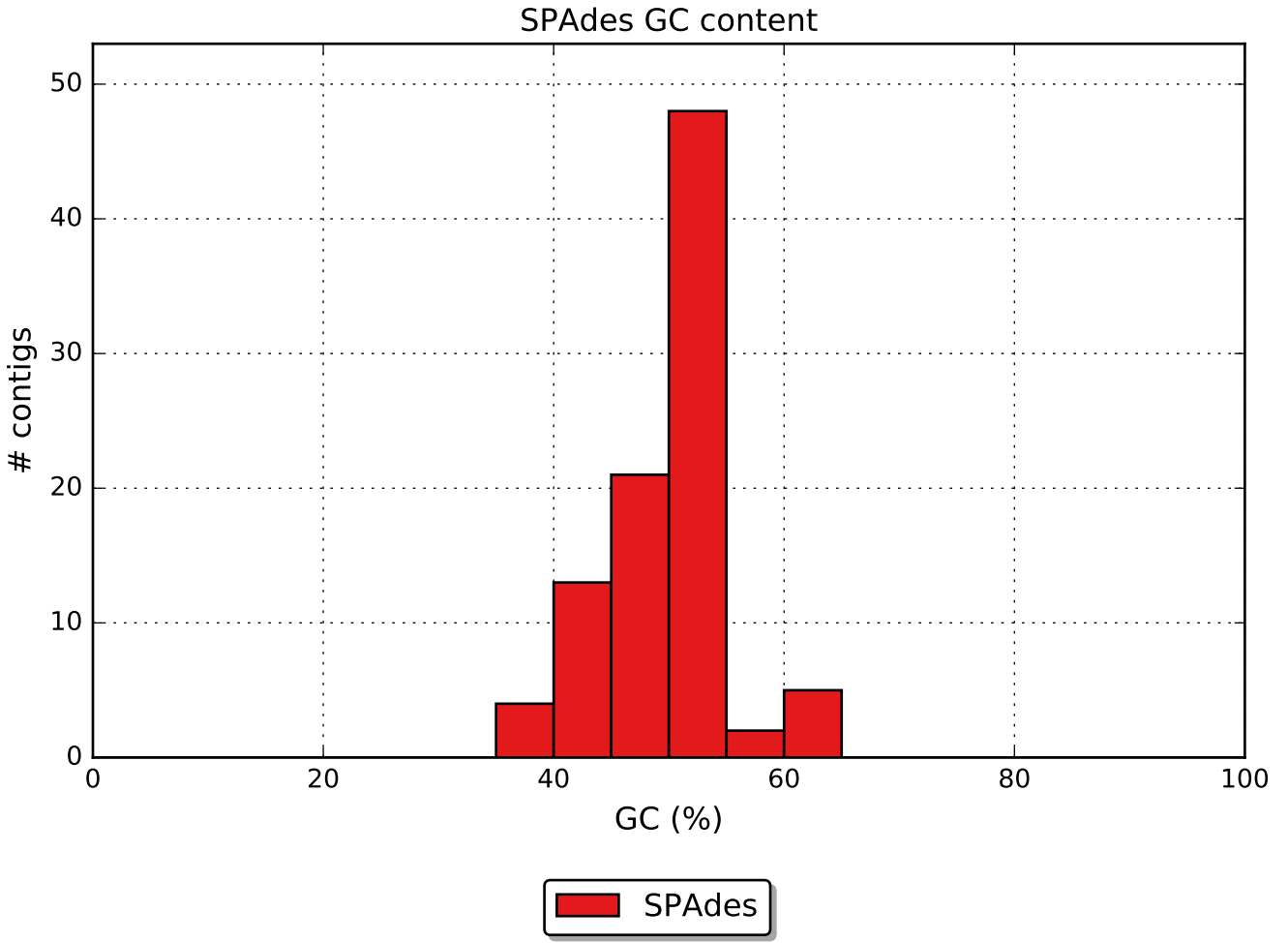
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

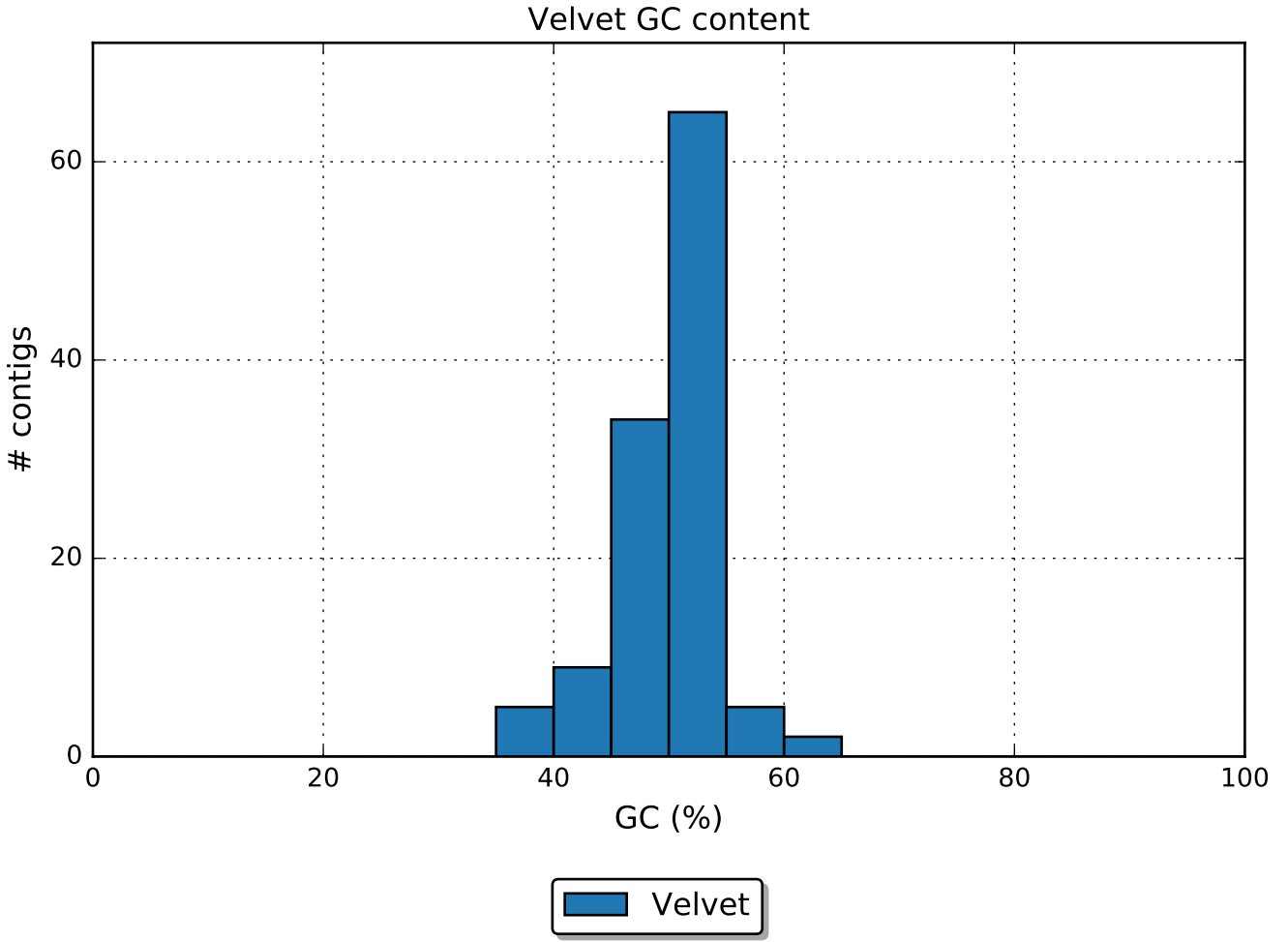

Nx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
SPAdes
Velvet

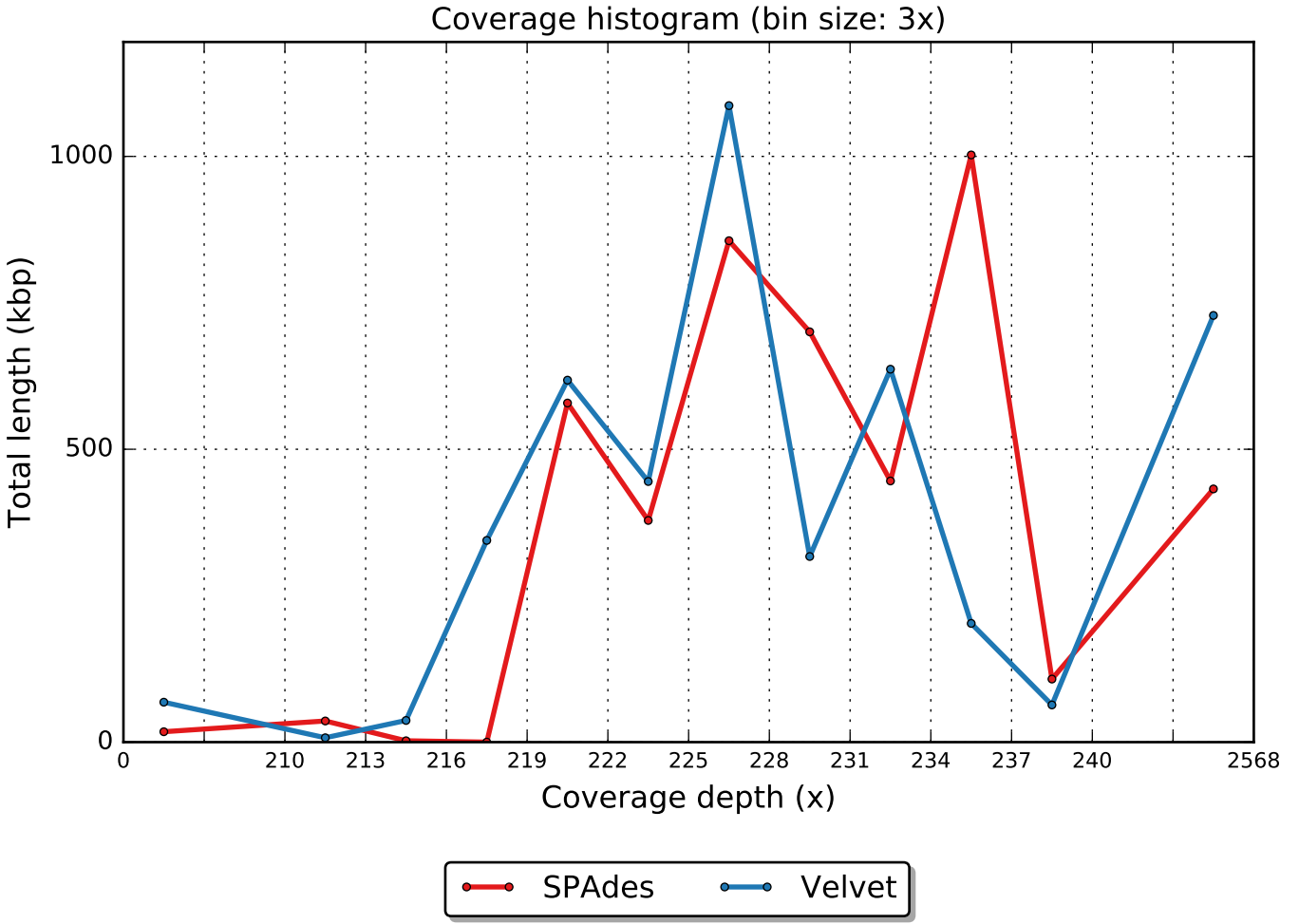

NGx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
SPAdes
Velvet

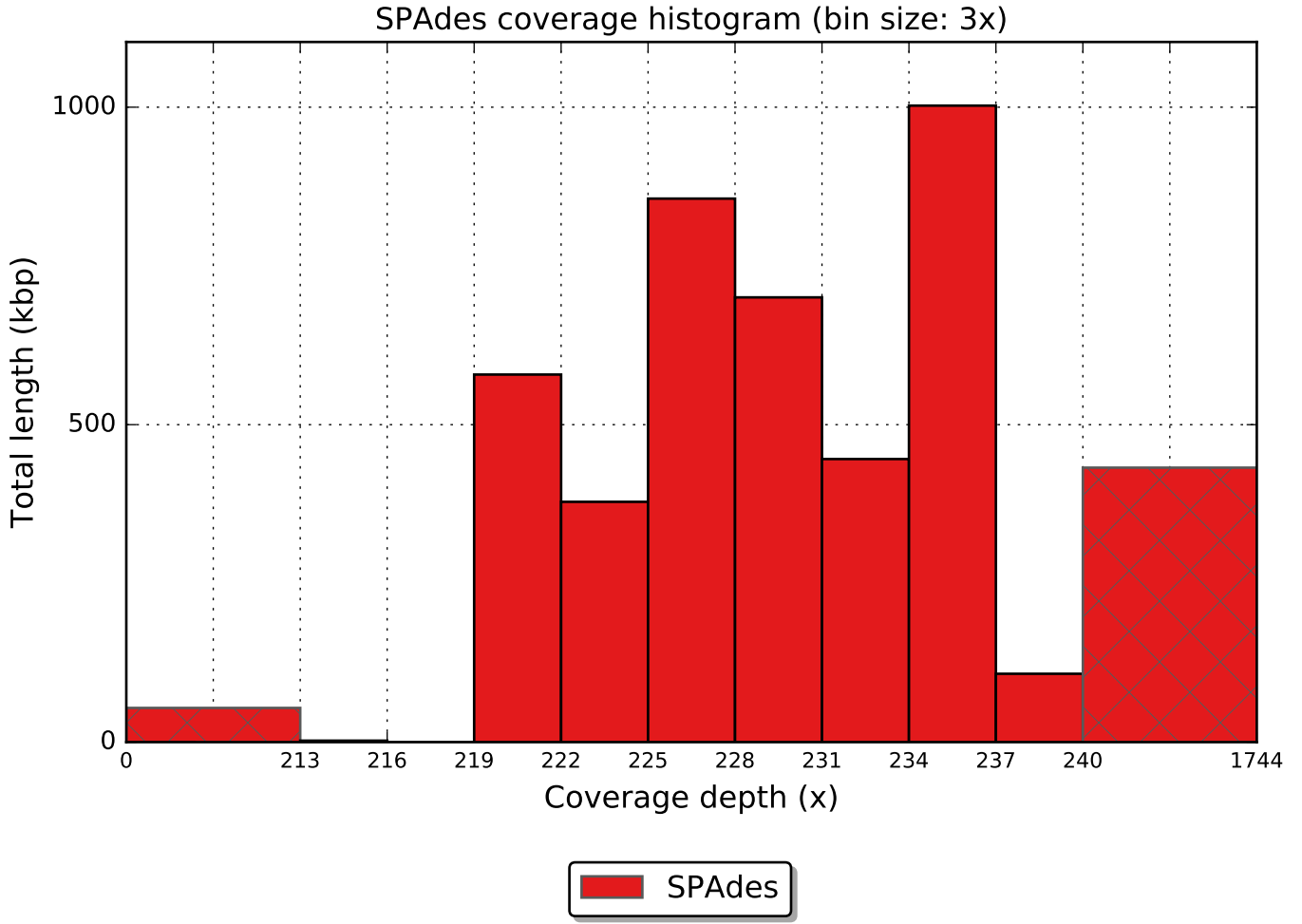

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
100
120
Contig index
SPAdes
Velvet
Reference

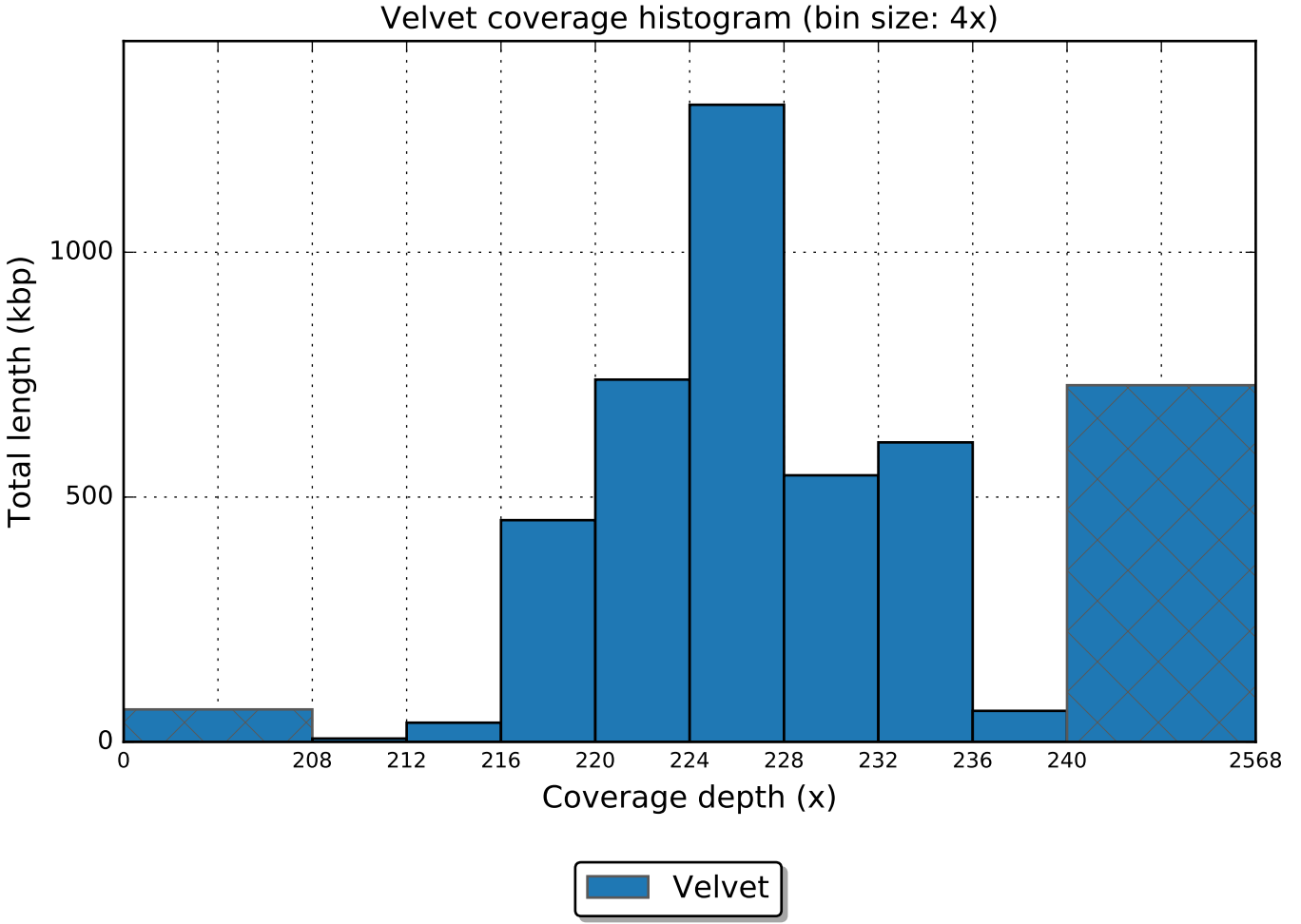

GC content
windows
GC (%)
0
600
1200
1800
2400
3000
0
20
40
60
80
100
SPAdes
Velvet
Reference

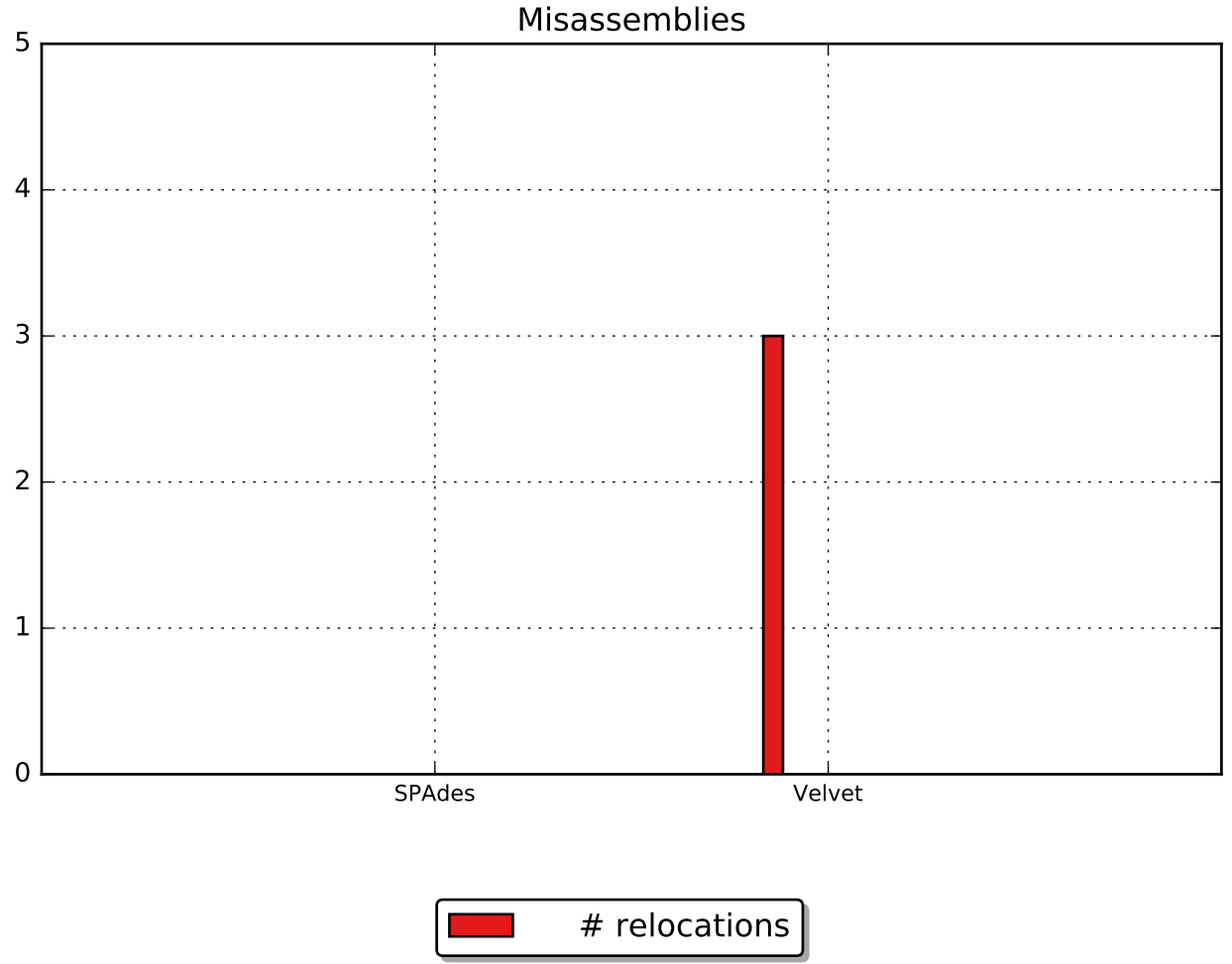

SPAdes GC content
contigs
GC (%)
0
10
20
30
40
50
0
20
40
60
80
100
SPAdes

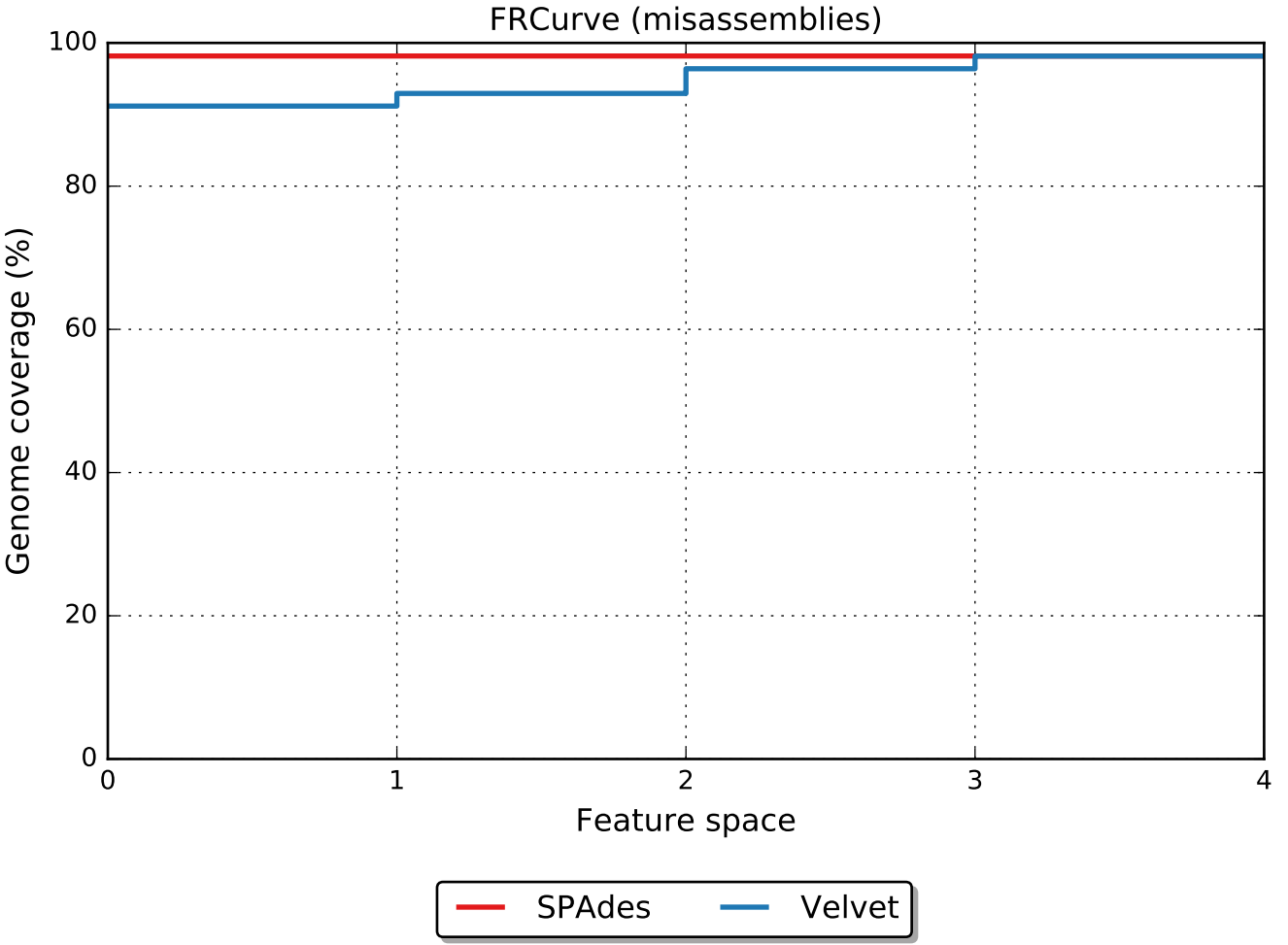

Velvet GC content
contigs
GC (%)
0
20
40
60
80
100
Velvet

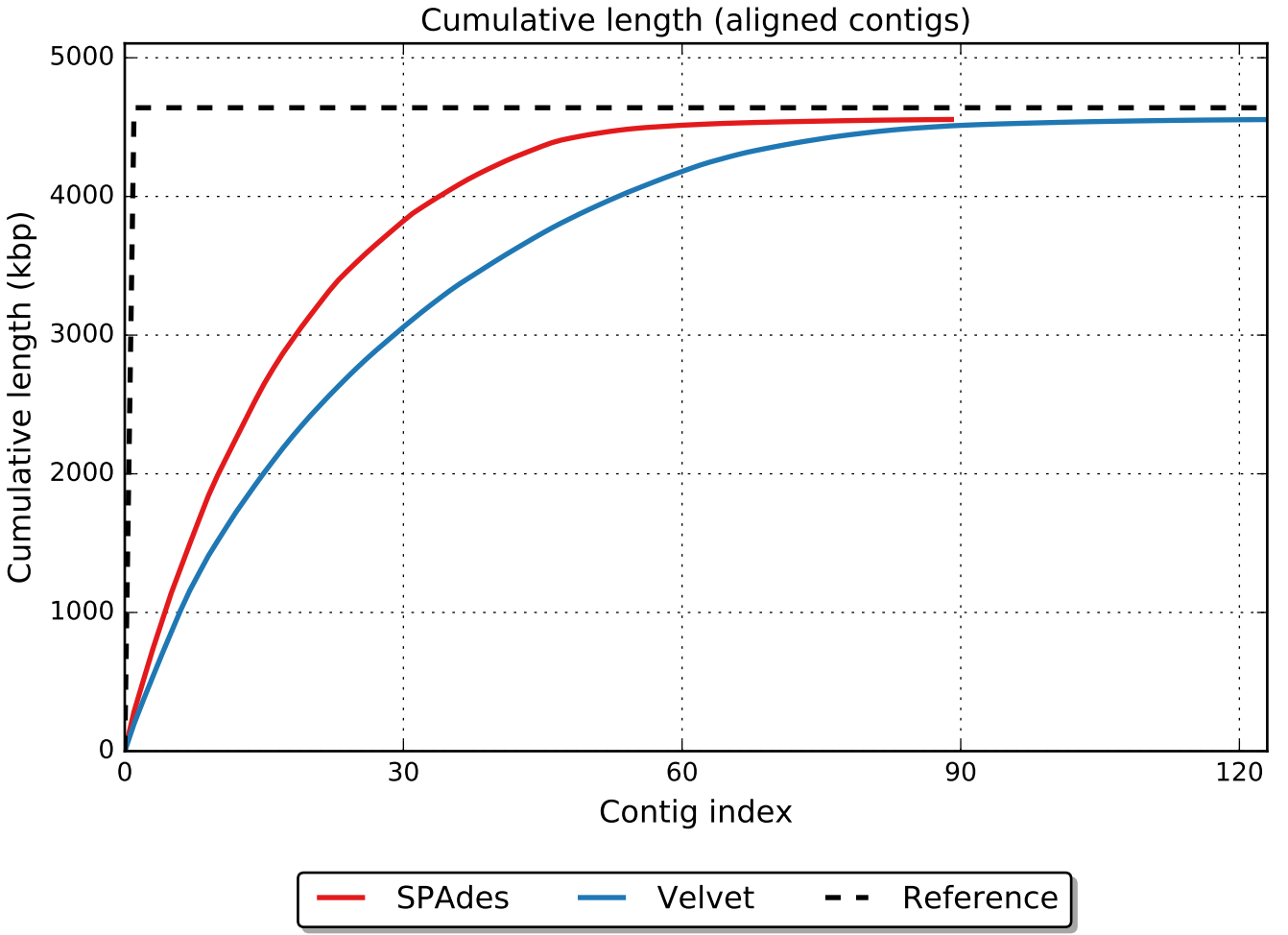

Coverage histogram (bin size: 3x)
Total length (kbp)
1000
500
0
0
210
213
216
219
222
225
228
231
234
237
240
2568
Coverage depth (x)
SPAdes
Velvet

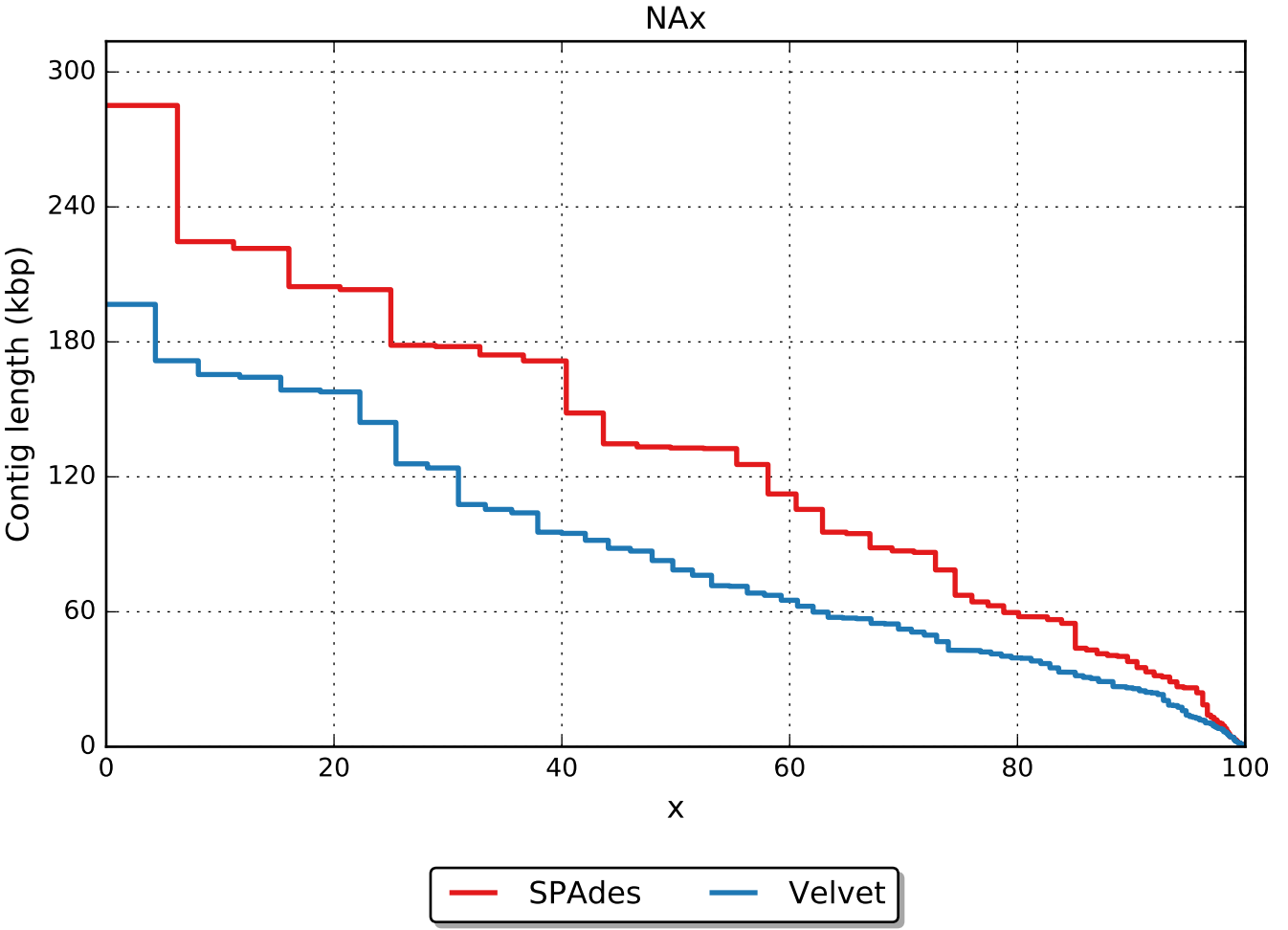

SPAdes coverage histogram (bin size: 3x)
Total length (kbp)
1000
500
0
0
213
216
219
222
225
228
231
234
237
240
1744
Coverage depth (x)
SPAdes

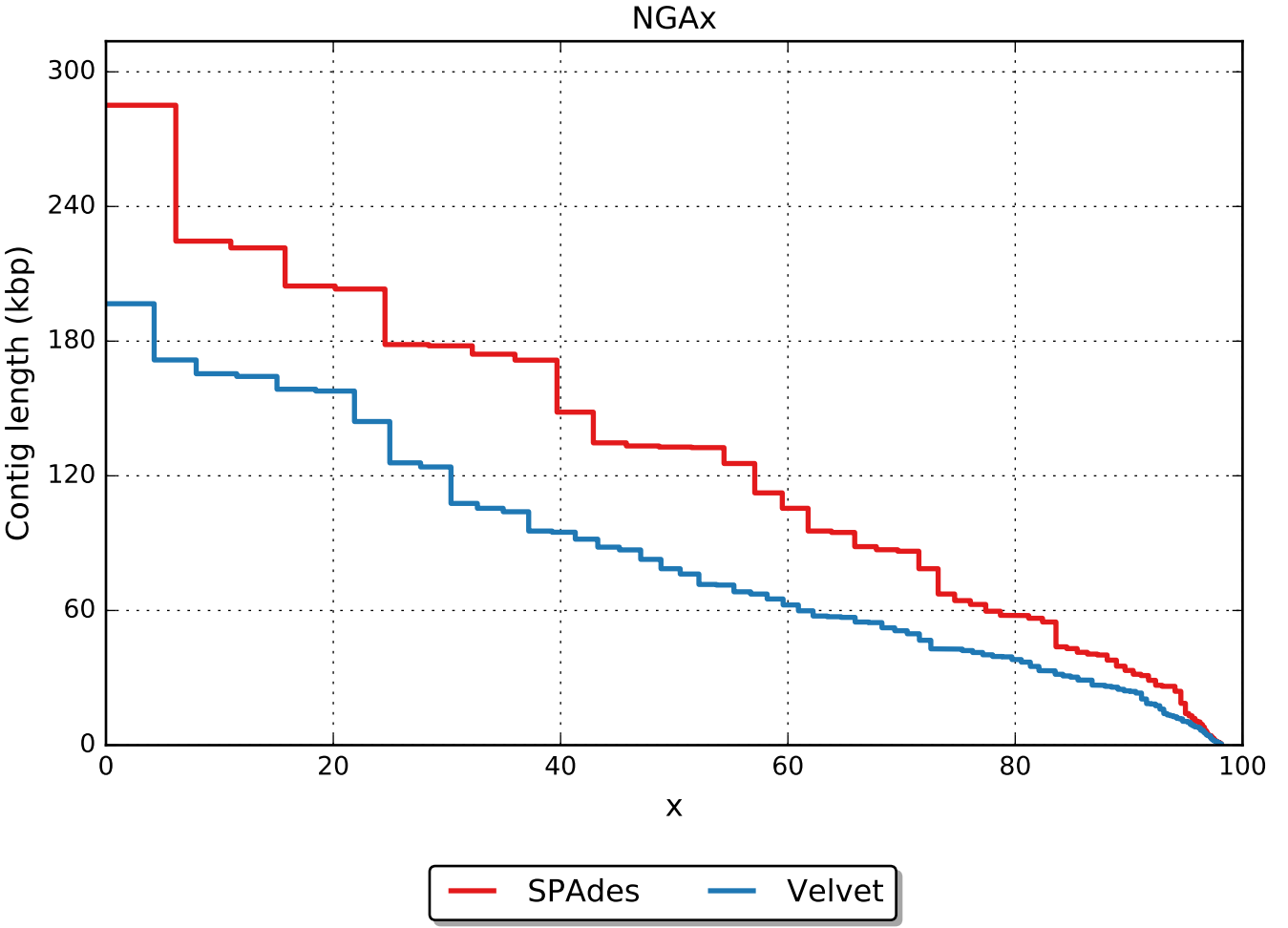

Velvet coverage histogram (bin size: 4x)
Total length (kbp)
1000
500
0
0
208
212
216
220
224
228
232
236
240
2568
Coverage depth (x)
Velvet

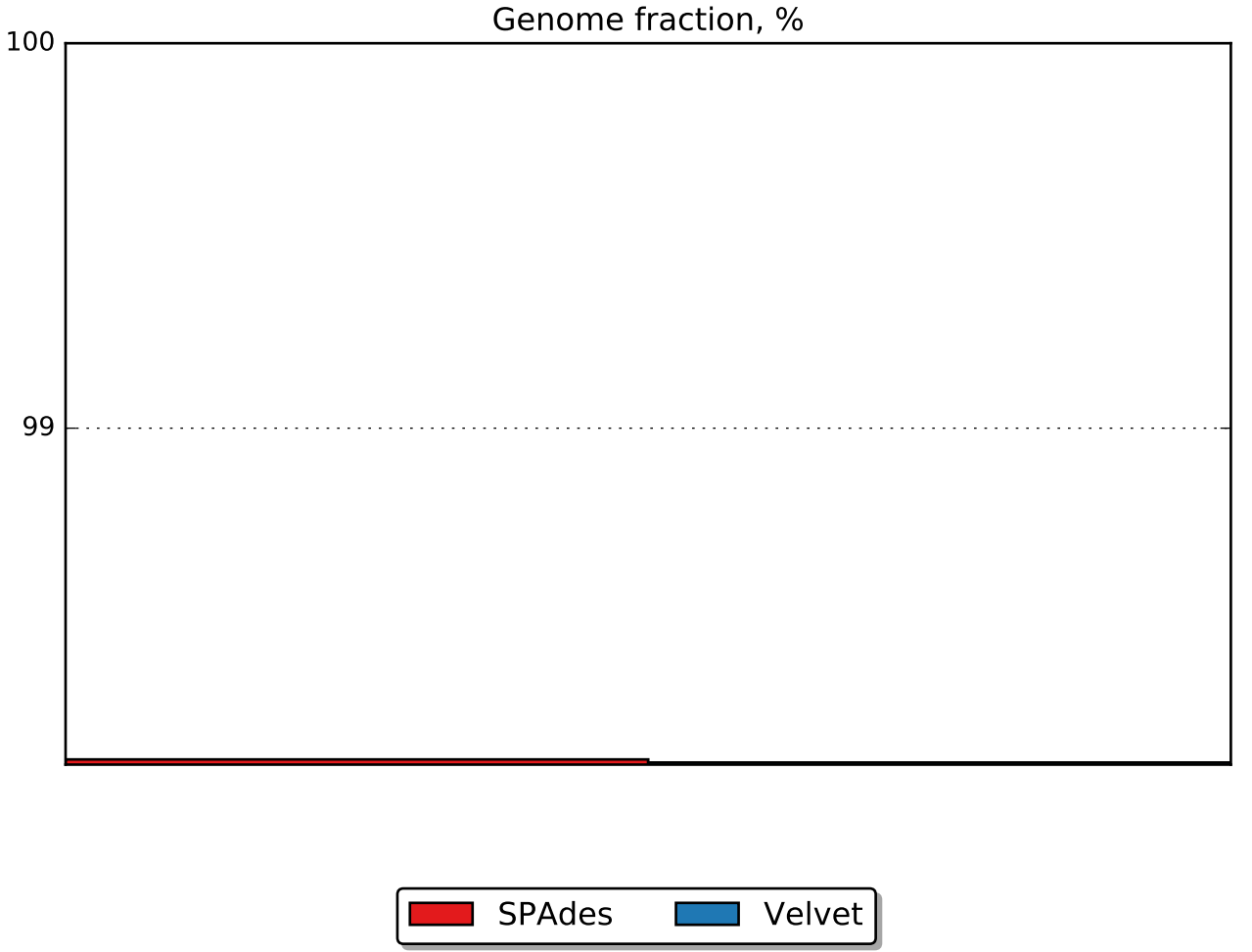

Misassemblies
5
4
3
2
1
0
SPAdes
Velvet
relocations


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
2
3
4
Feature space
SPAdes
Velvet


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
30
60
90
120
Contig index
SPAdes
Velvet
Reference


NAx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
SPAdes
Velvet


NGAx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
SPAdes
Velvet


Genome fraction, %
100
99
SPAdes
Velvet