Report

	velvet-ctg
# contigs (>= 0 bp)	17510
# contigs (>= 1000 bp)	17510
# contigs (>= 5000 bp)	5897
# contigs (>= 10000 bp)	2278
# contigs (>= 25000 bp)	202
# contigs (>= 50000 bp)	5
Total length (>= 0 bp)	90225299
Total length (>= 1000 bp)	90225299
Total length (>= 5000 bp)	61870406
Total length (>= 10000 bp)	36489743
Total length (>= 25000 bp)	6314356
Total length (>= 50000 bp)	267395
# contigs	17510
Largest contig	58073
Total length	90225299
Reference length	100272607
GC (%)	35.87
Reference GC (%)	35.44
N50	8011
NG50	7000
N75	4081
NG75	3020
L50	3246
LG50	3917
L75	7184
LG75	9325
# misassemblies	342
# misassembled contigs	337
Misassembled contigs length	2228569
# local misassemblies	1080
# unaligned mis. contigs	9
# unaligned contigs	1297 + 194 part
Unaligned length	4028338
Genome fraction (%)	85.620
Duplication ratio	1.004
# N's per 100 kbp	0.00
# mismatches per 100 kbp	49.51
# indels per 100 kbp	23.64
Largest alignment	58073
Total aligned length	85981341
NA50	7730
NGA50	6739
NA75	3720
NGA75	2577
LA50	3303
LGA50	4000
LA75	7487
LGA75	9913

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

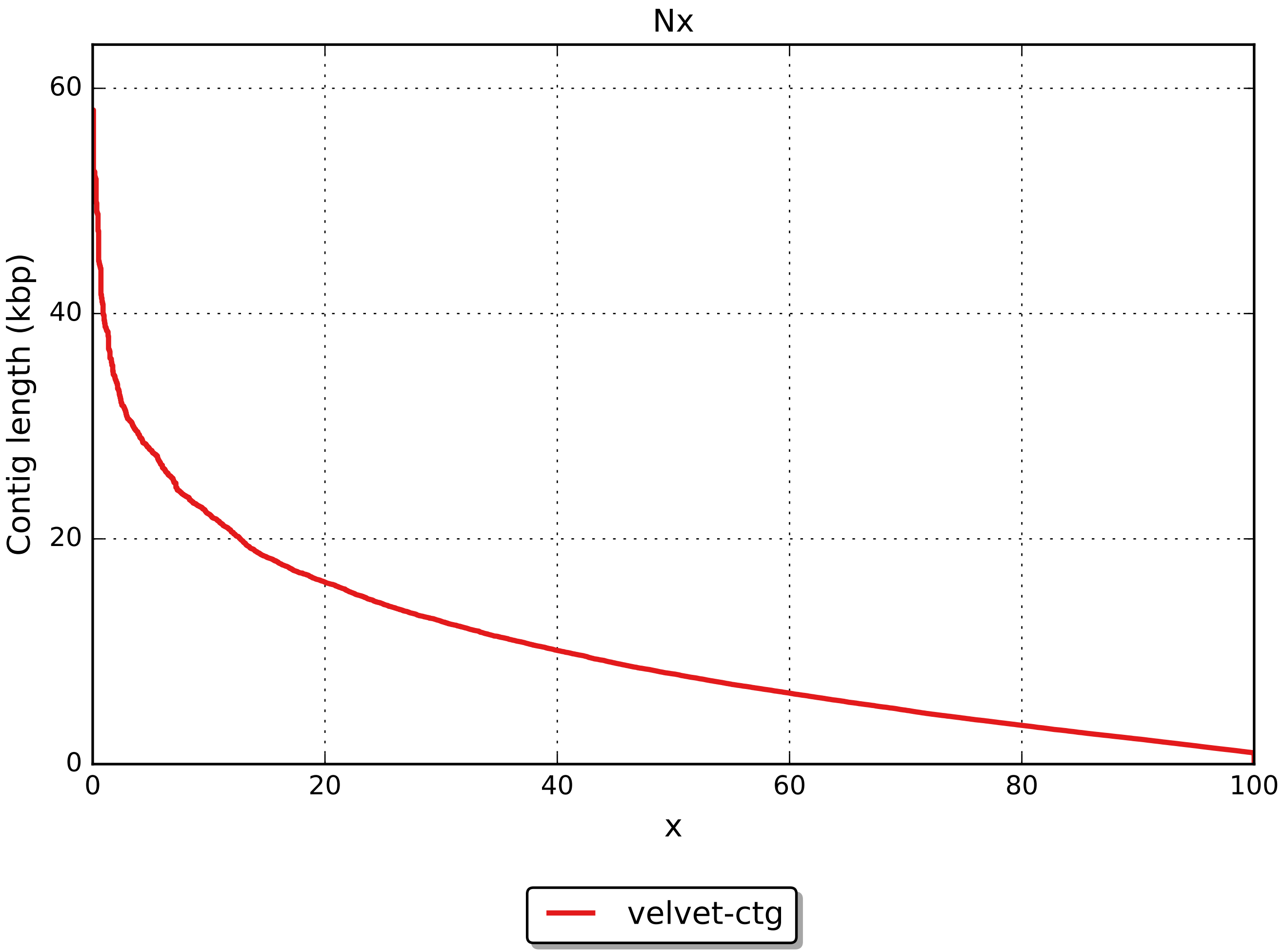
	velvet-ctg
# misassemblies	342
# relocations	197
# translocations	103
# inversions	42
# misassembled contigs	337
Misassembled contigs length	2228569
# local misassemblies	1080
# unaligned mis. contigs	9
# mismatches	42507
# indels	20297
# indels (<= 5 bp)	16121
# indels (> 5 bp)	4176
Indels length	107012

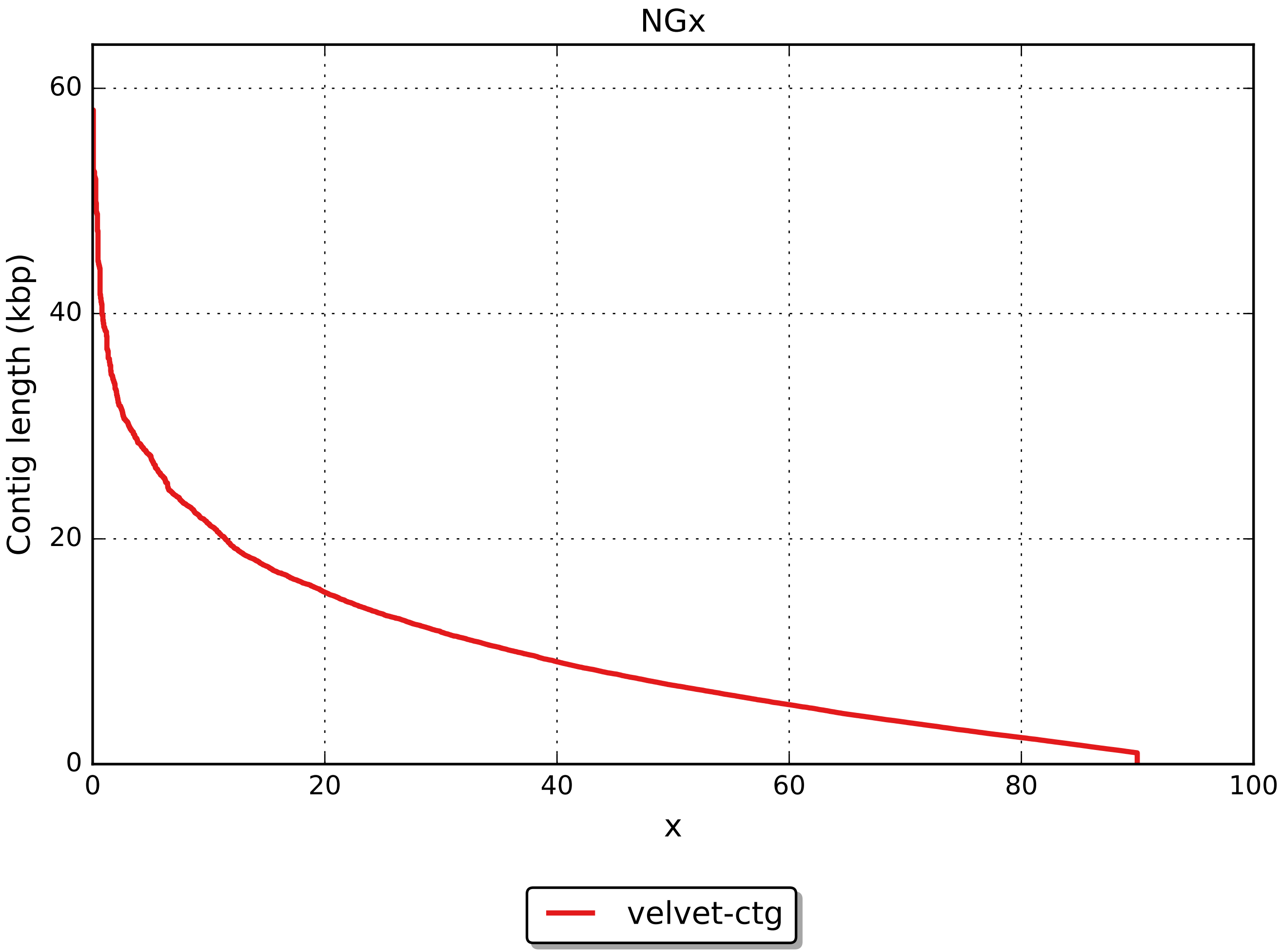
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

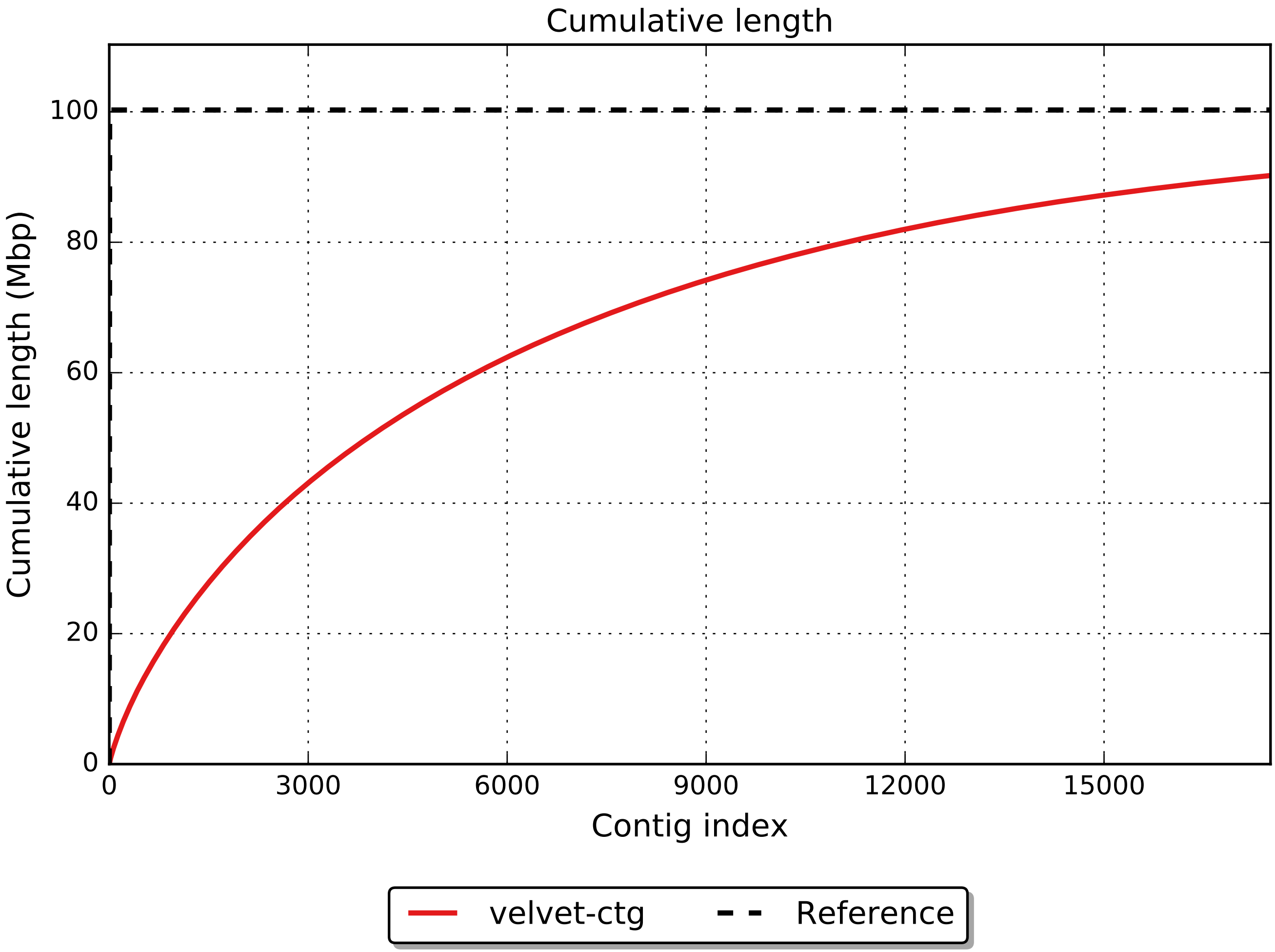
Unaligned report

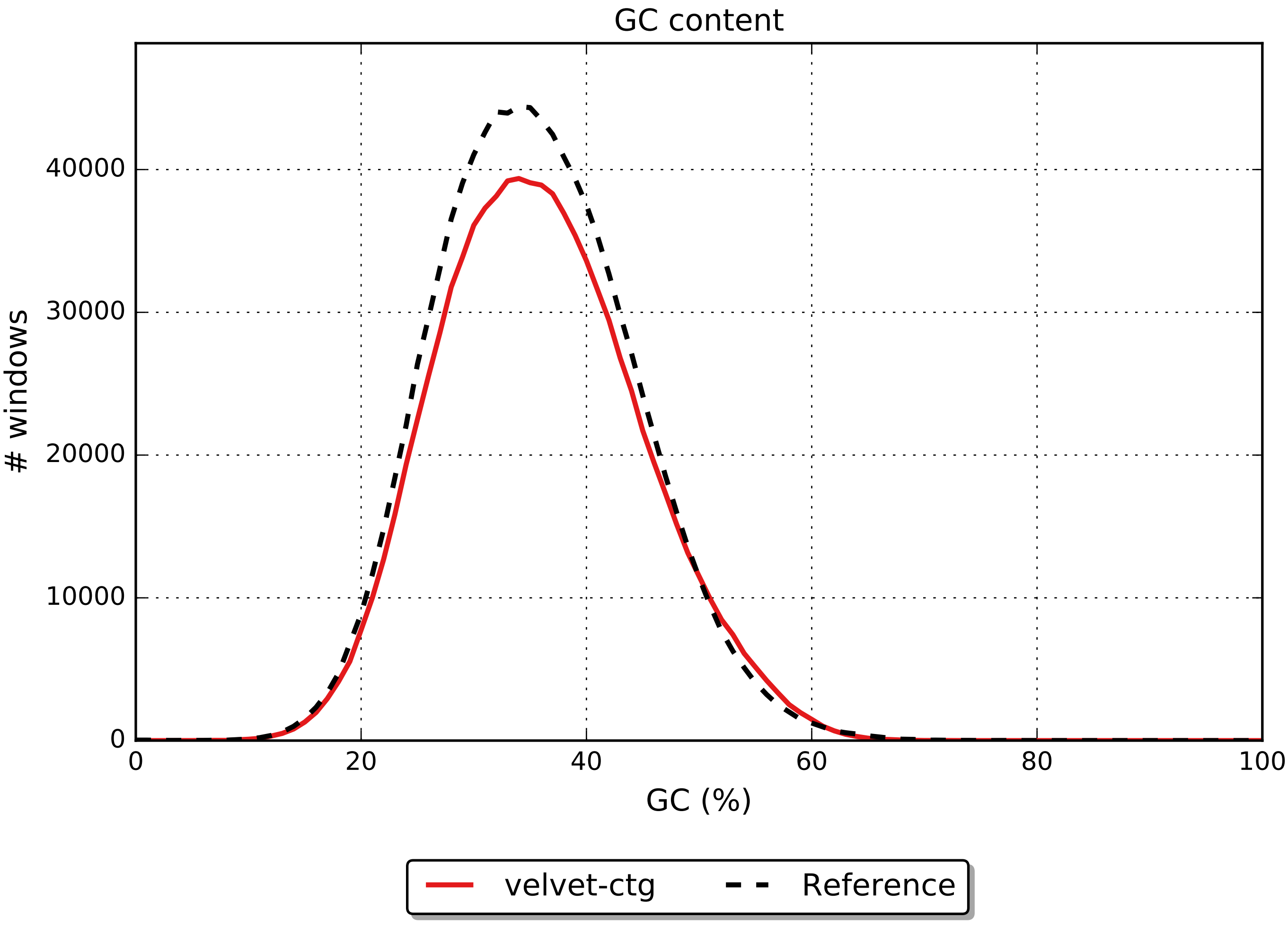
	velvet-ctg
# fully unaligned contigs	1297
Fully unaligned length	3809026
# partially unaligned contigs	194
Partially unaligned length	219312
# N's	0

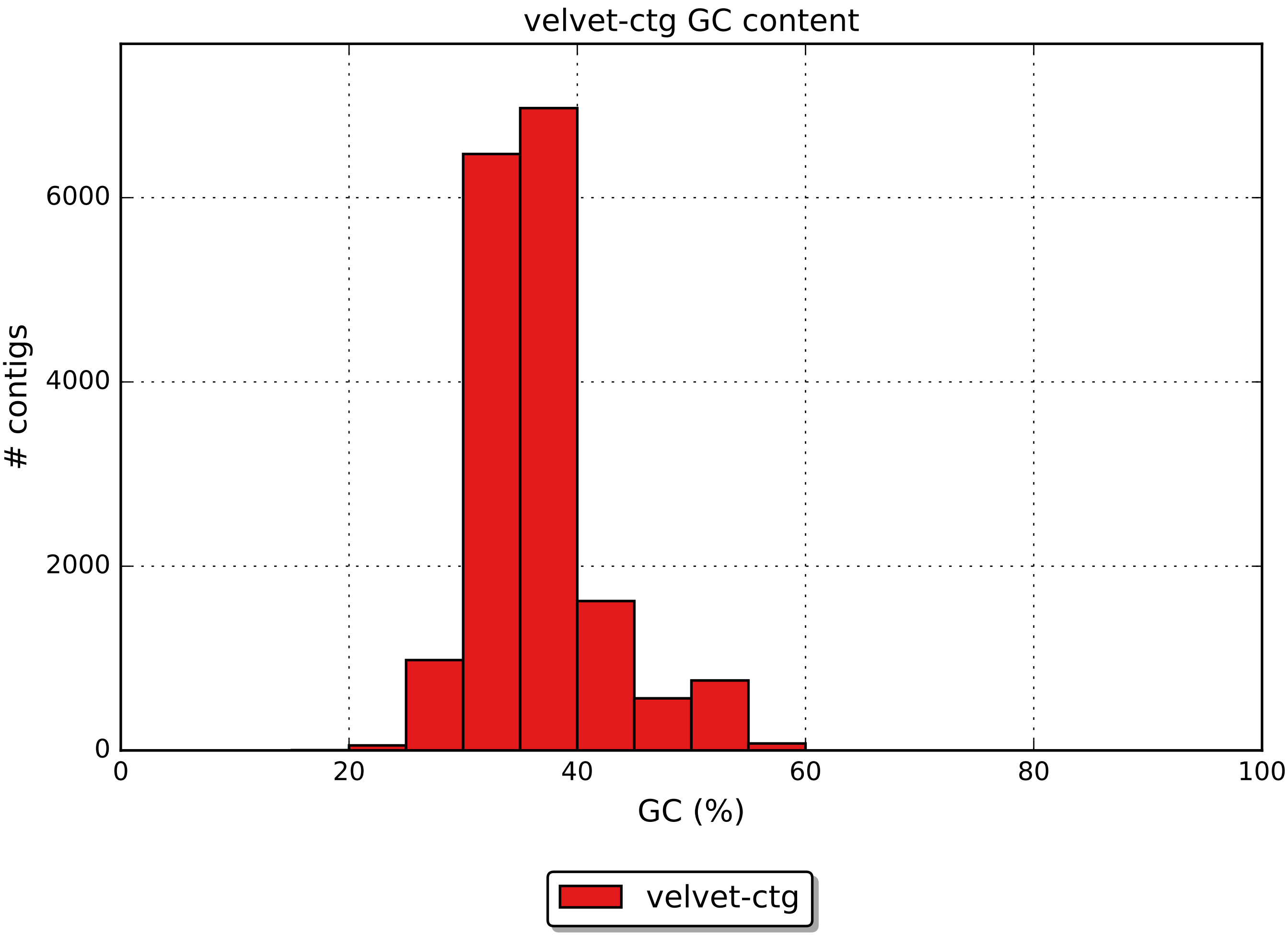
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

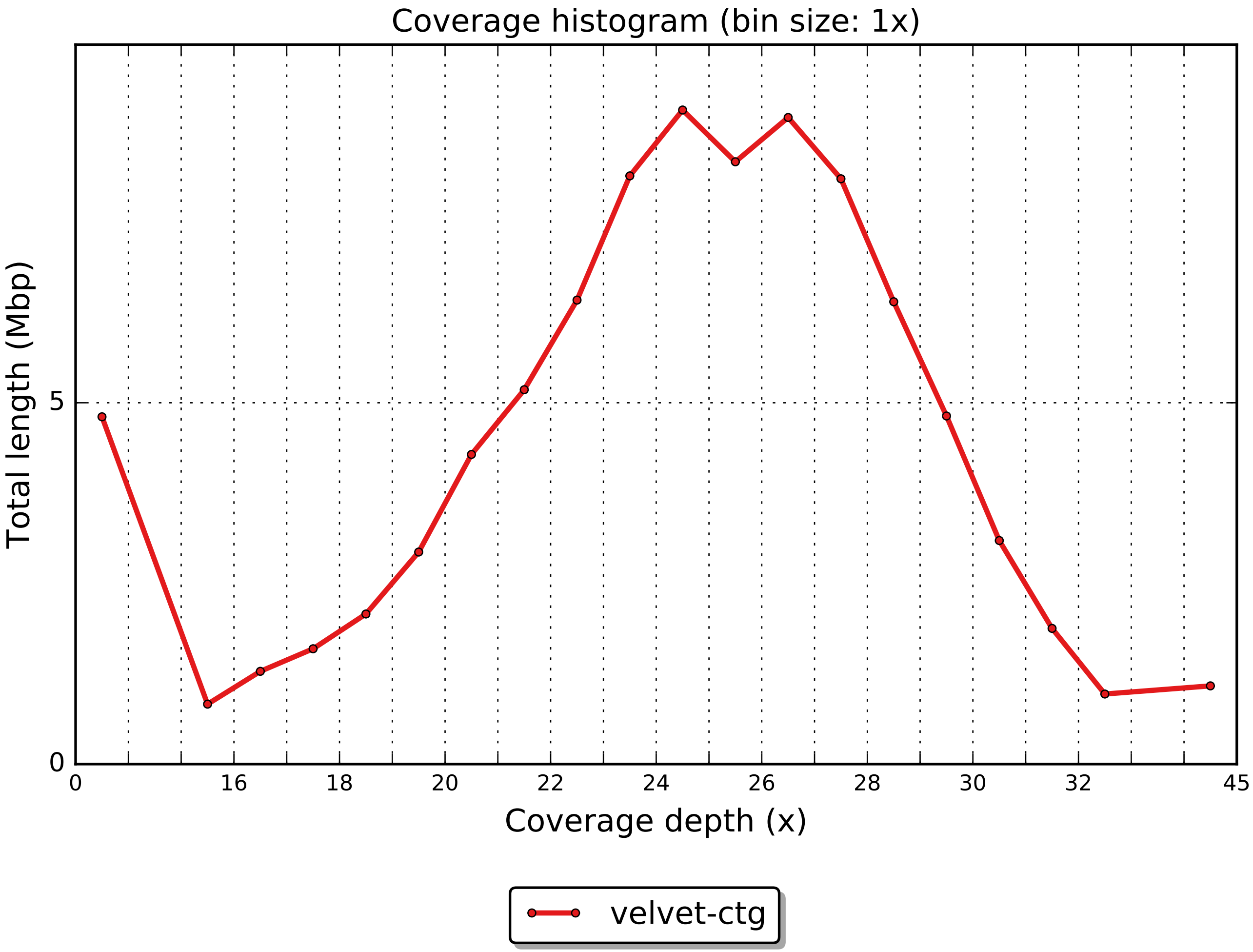

Nx
Contig length (kbp)
60
40
20
0
0
20
40
60
80
100
x
velvet-ctg

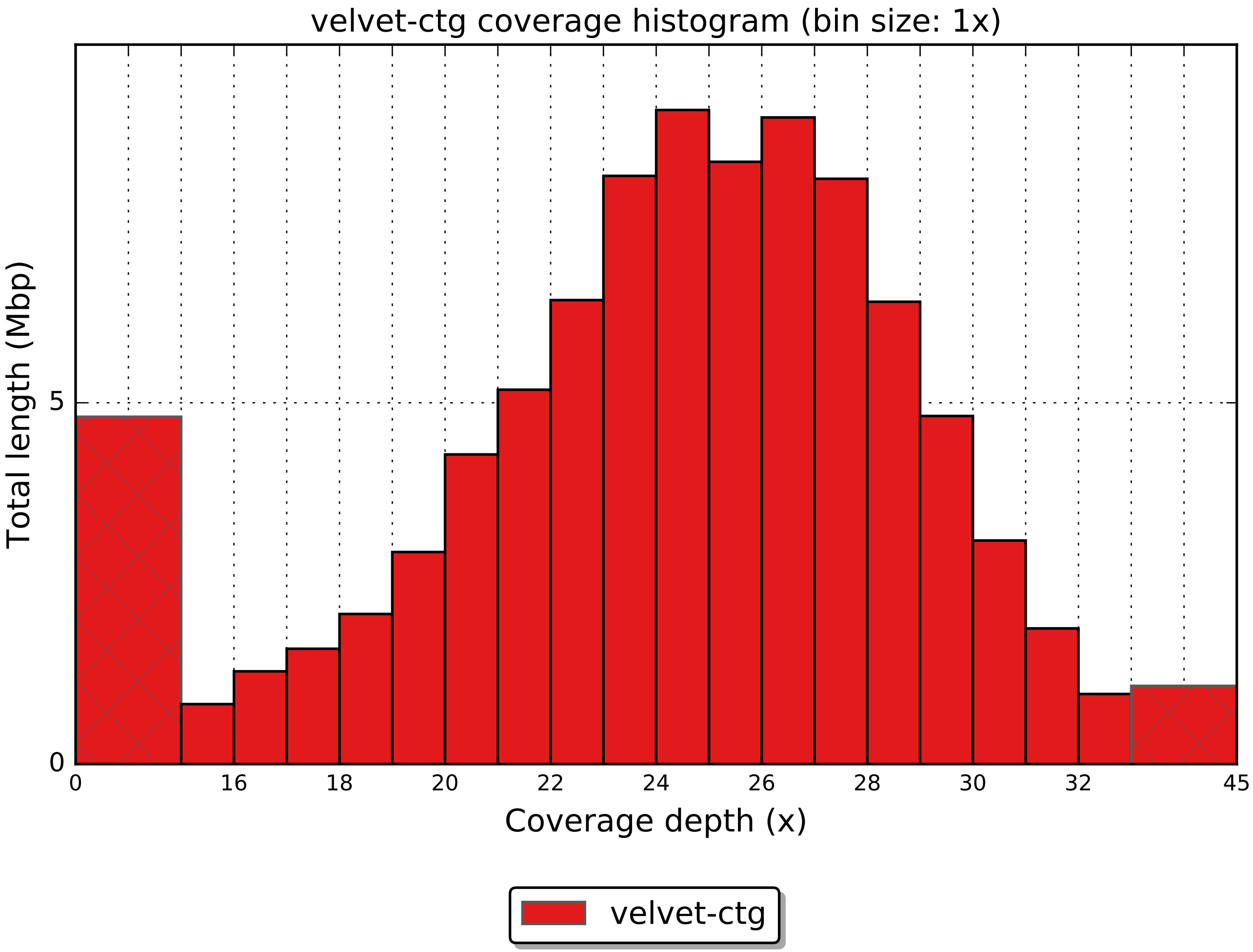

NGx
Contig length (kbp)
60
40
20
0
0
20
40
60
80
100
x
velvet-ctg

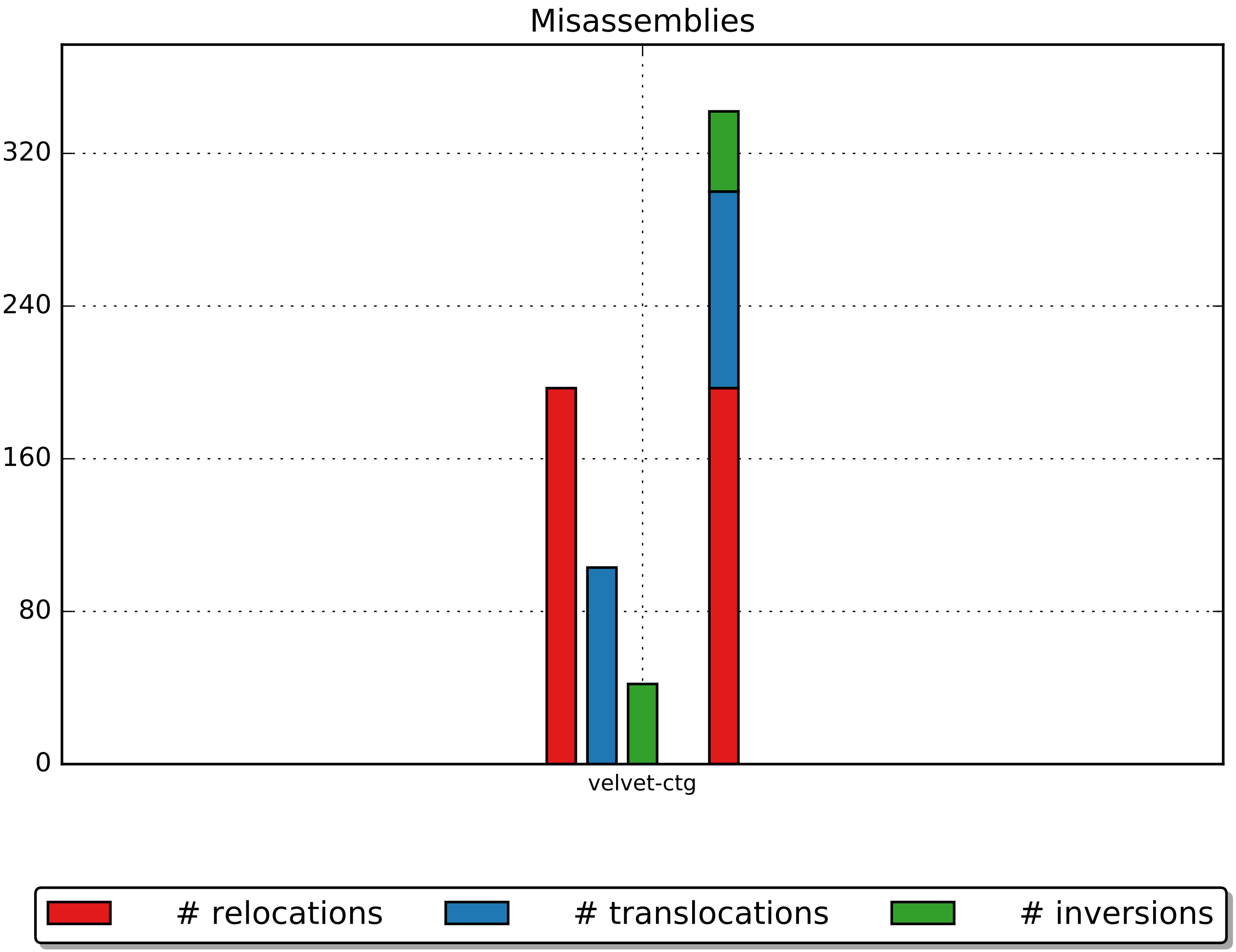

Cumulative length
Cumulative length (Mbp)
0
20
40
60
80
100
0
3000
6000
9000
12000
15000
Contig index
velvet-ctg
Reference

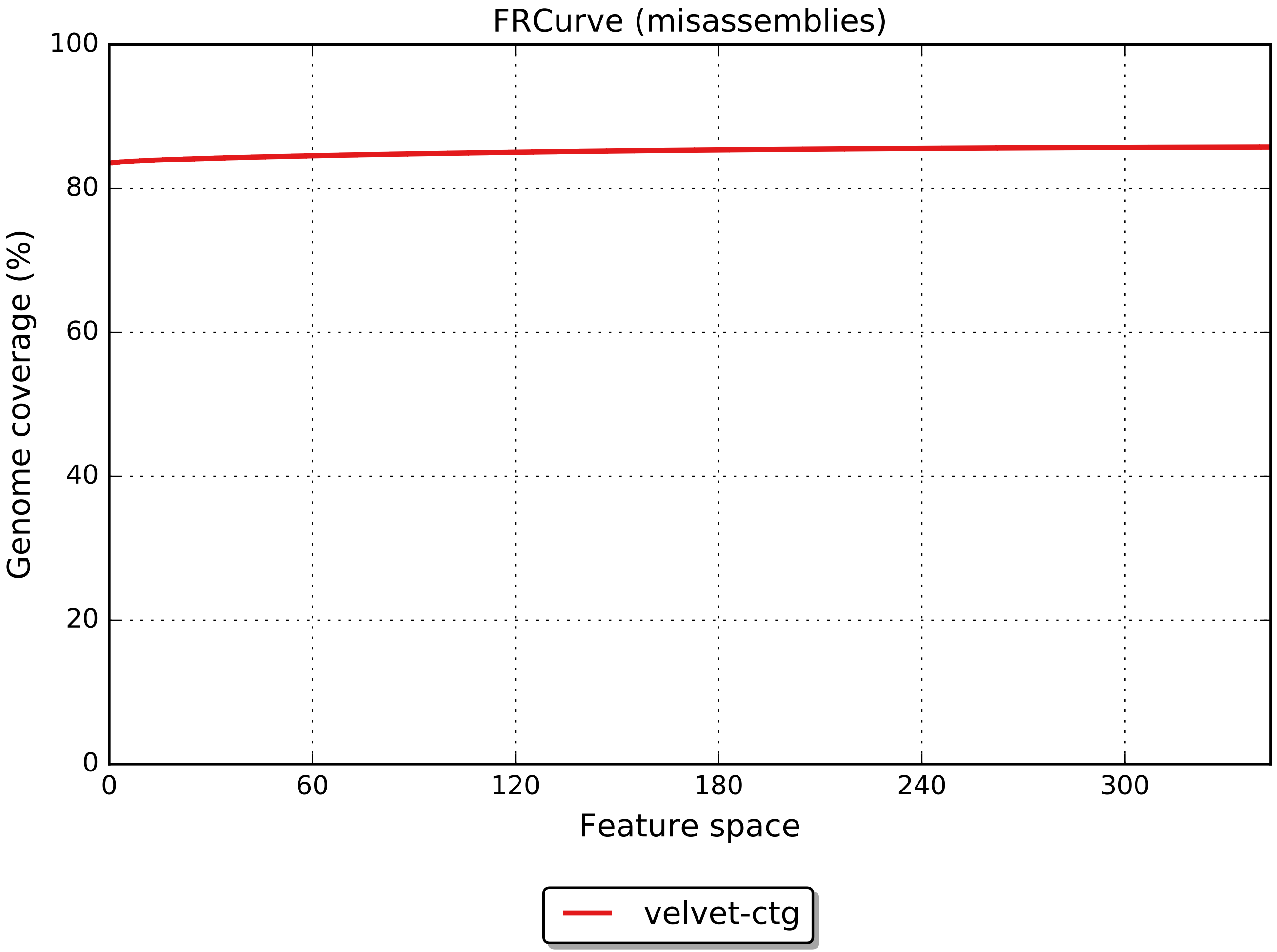

GC content
windows
40000
30000
20000
10000
0
0
20
40
60
80
100
GC (%)
velvet-ctg
Reference

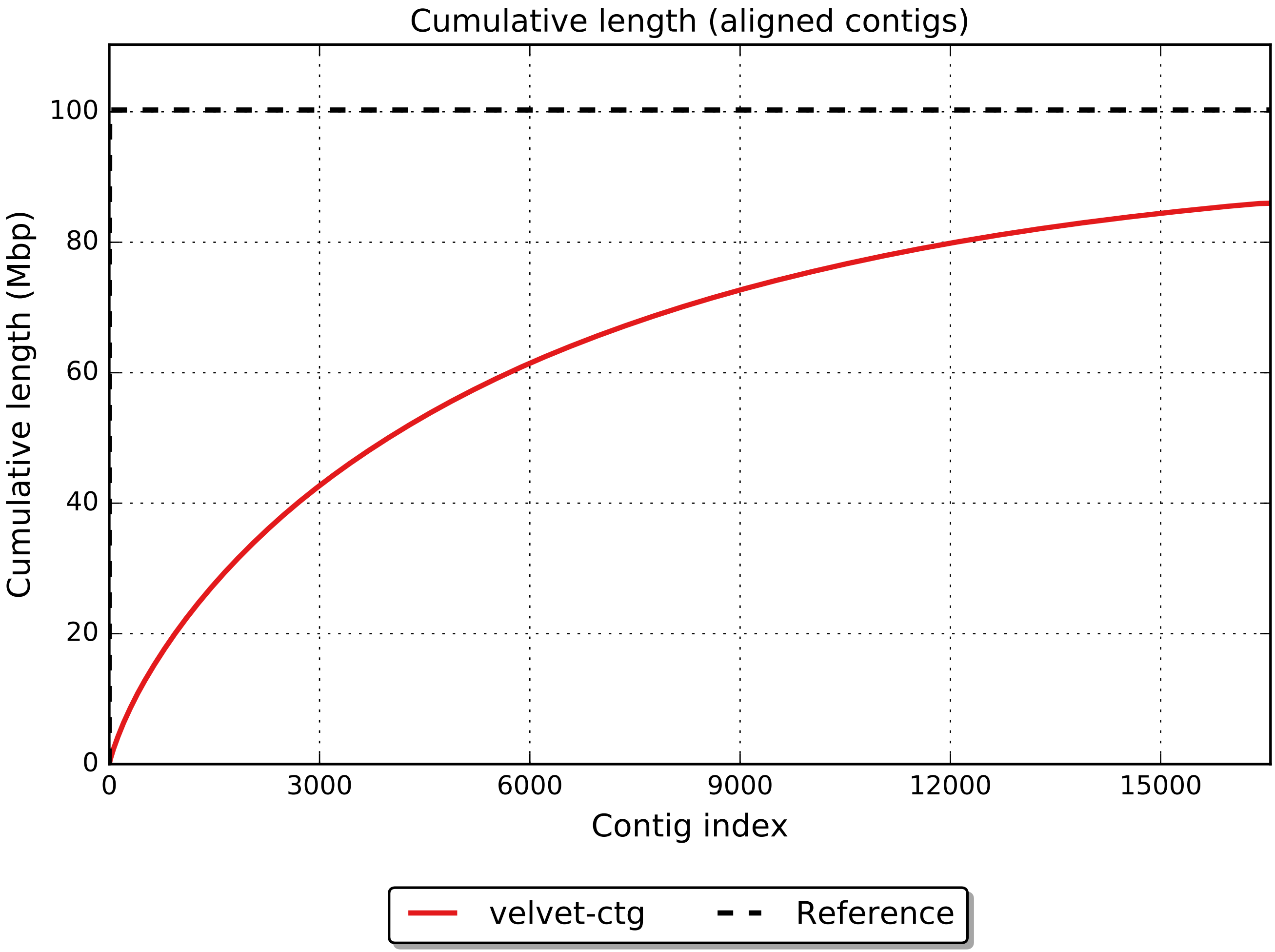

velvet-ctg GC content
contigs
6000
4000
2000
0
0
20
40
60
80
100
GC (%)
velvet-ctg

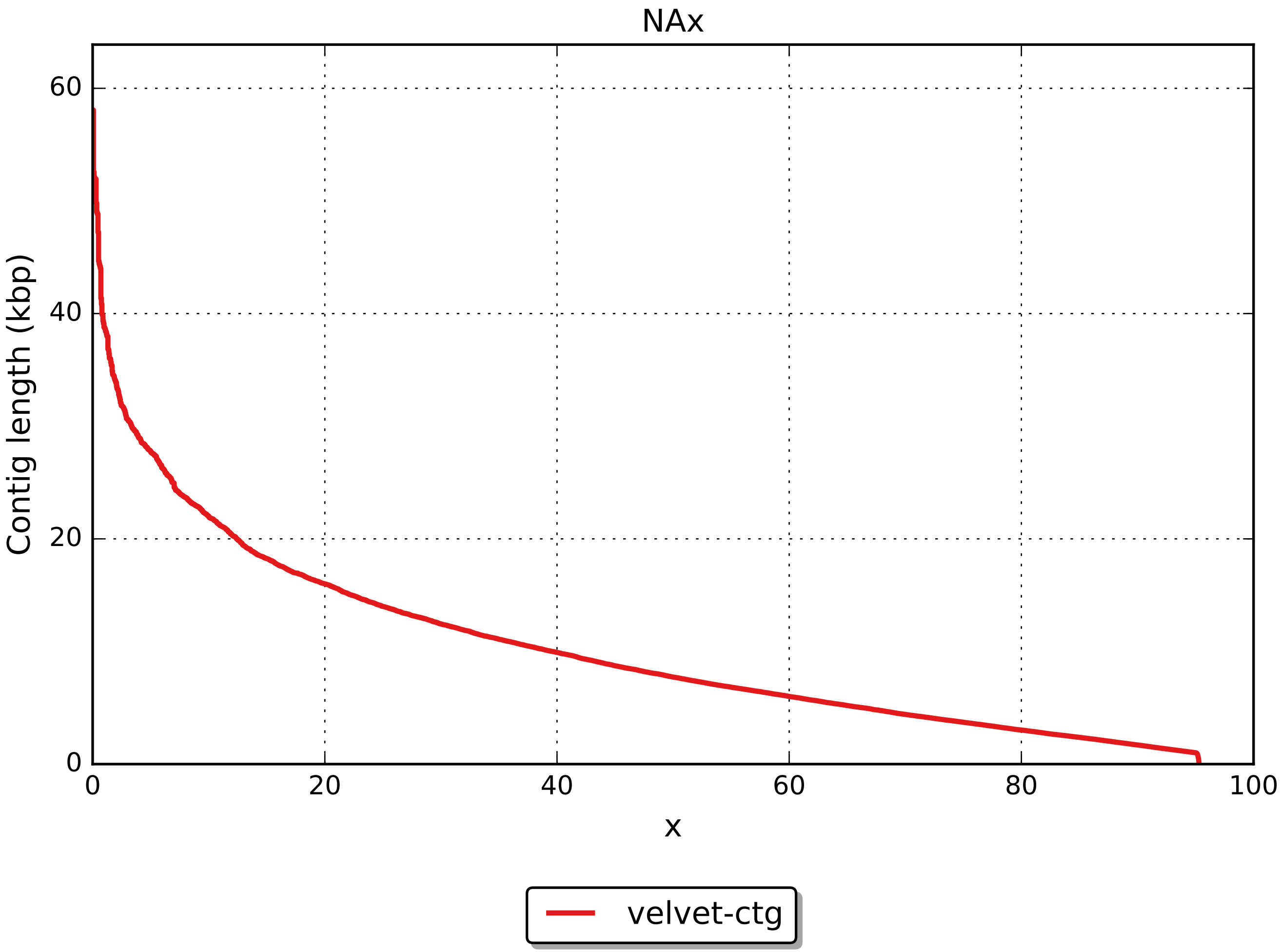

Coverage histogram (bin size: 1x)
Total length (Mbp)
5
0
0
16
18
20
22
24
26
28
30
32
45
Coverage depth (x)
velvet-ctg

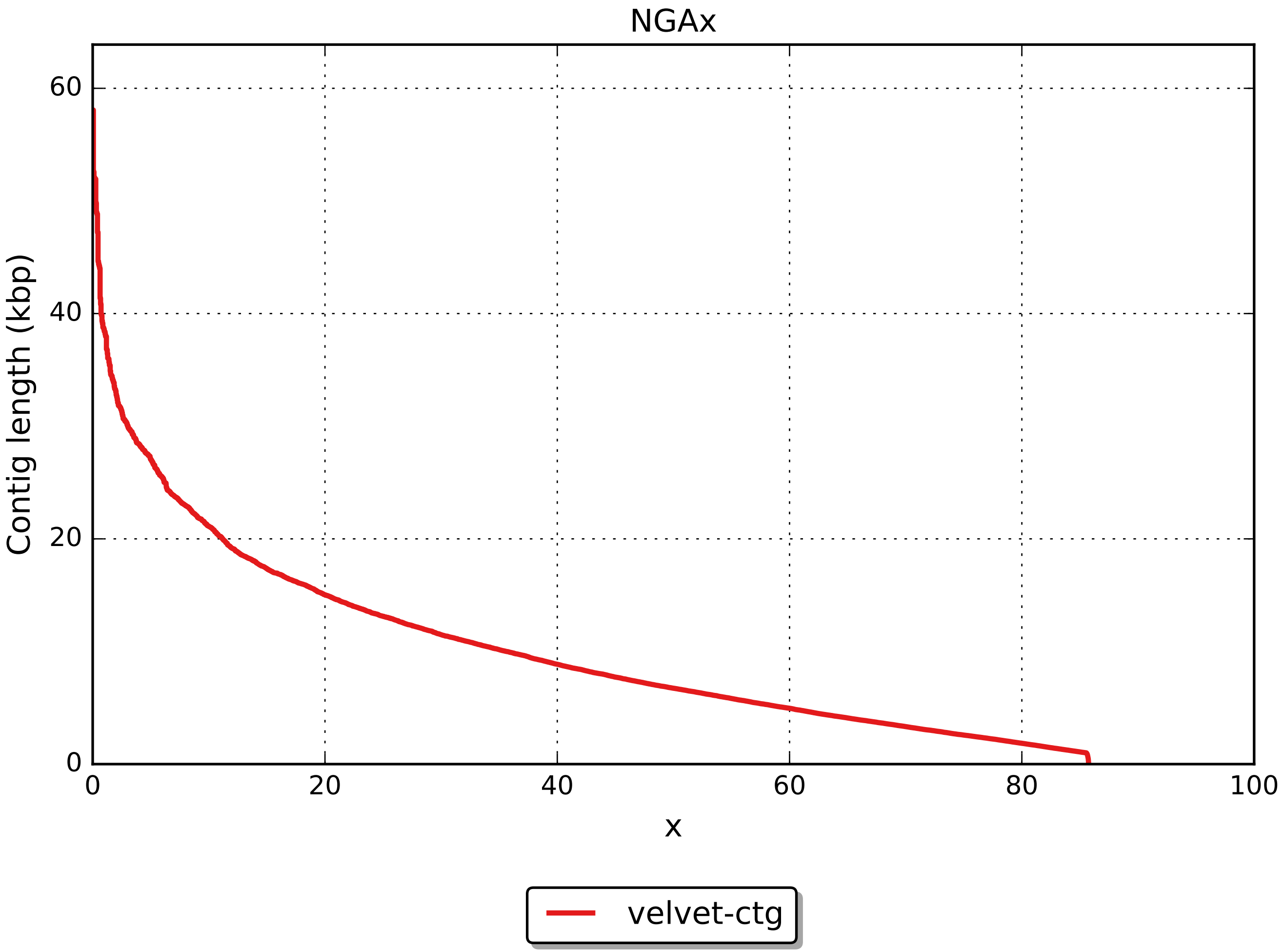

velvet-ctg coverage histogram (bin size: 1x)
Total length (Mbp)
5
0
0
16
18
20
22
24
26
28
30
32
45
Coverage depth (x)
velvet-ctg


Misassemblies
320
240
160
80
0
velvet-ctg
relocations
translocations
inversions


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
60
120
180
240
300
Feature space
velvet-ctg


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
20
40
60
80
100
0
3000
6000
9000
12000
15000
Contig index
velvet-ctg
Reference


NAx
Contig length (kbp)
60
40
20
0
0
20
40
60
80
100
x
velvet-ctg


NGAx
Contig length (kbp)
0
20
40
60
x
0
20
40
60
80
100
velvet-ctg