GeneMark

Version 2.5p (09.08.06) *Copyright 1993 - M. Borodovsky, J. McIninch*

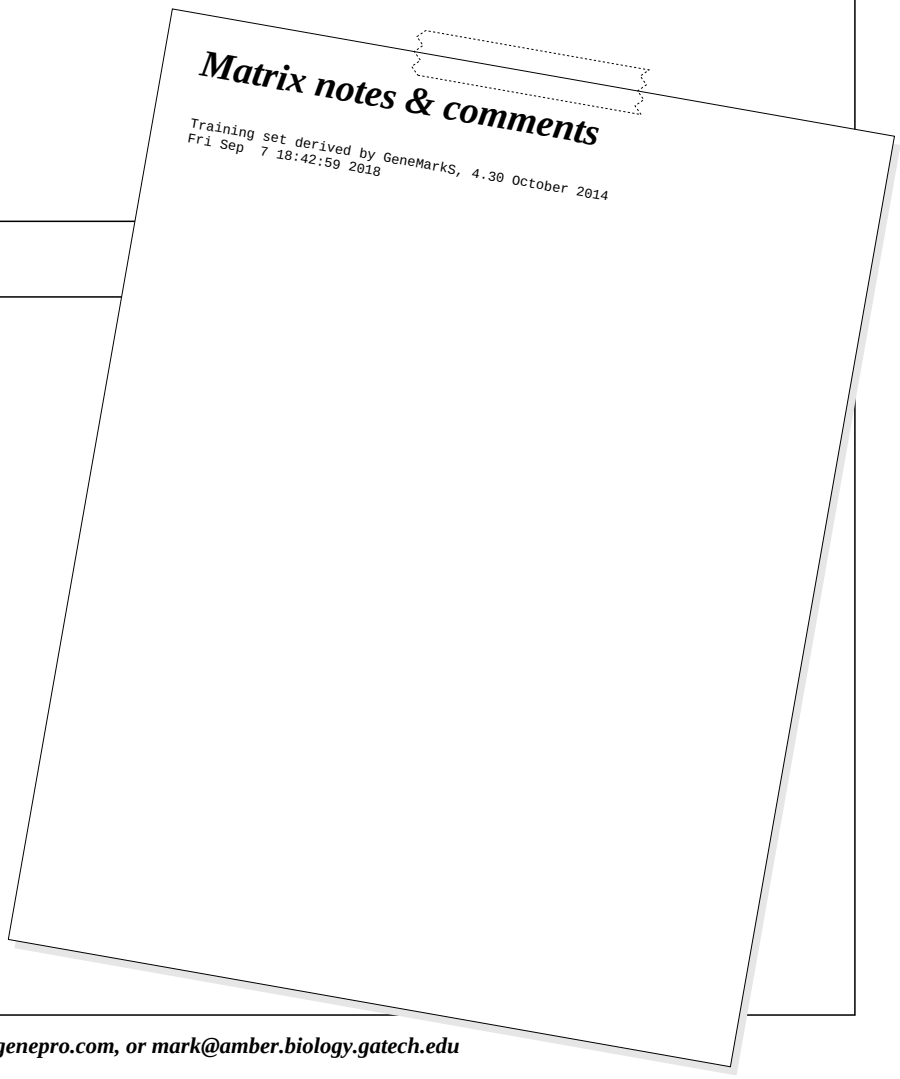
PROGRAM INFORMATION

```
Sequence         :  Microbacterium phage Stromboli complete sequence, 41594 bp including 10-base 3' overhang (T
Analysis Date    :  3/28/24 at 5:38:37
Pages            :  21
Sequence Length  :  41594 bp
GC Content       :   68.80%

Window Length    :  96 bp
Window Step      :  12 bp
Threshold Value  :  0.500

PS-Version       :  1.2

GeneMark Options :  PostScript graph,
                    Mark ORFs / splice sites,
                    List ORFs,
                    List regions and/or splice sites,
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MATRIX INFORMATION

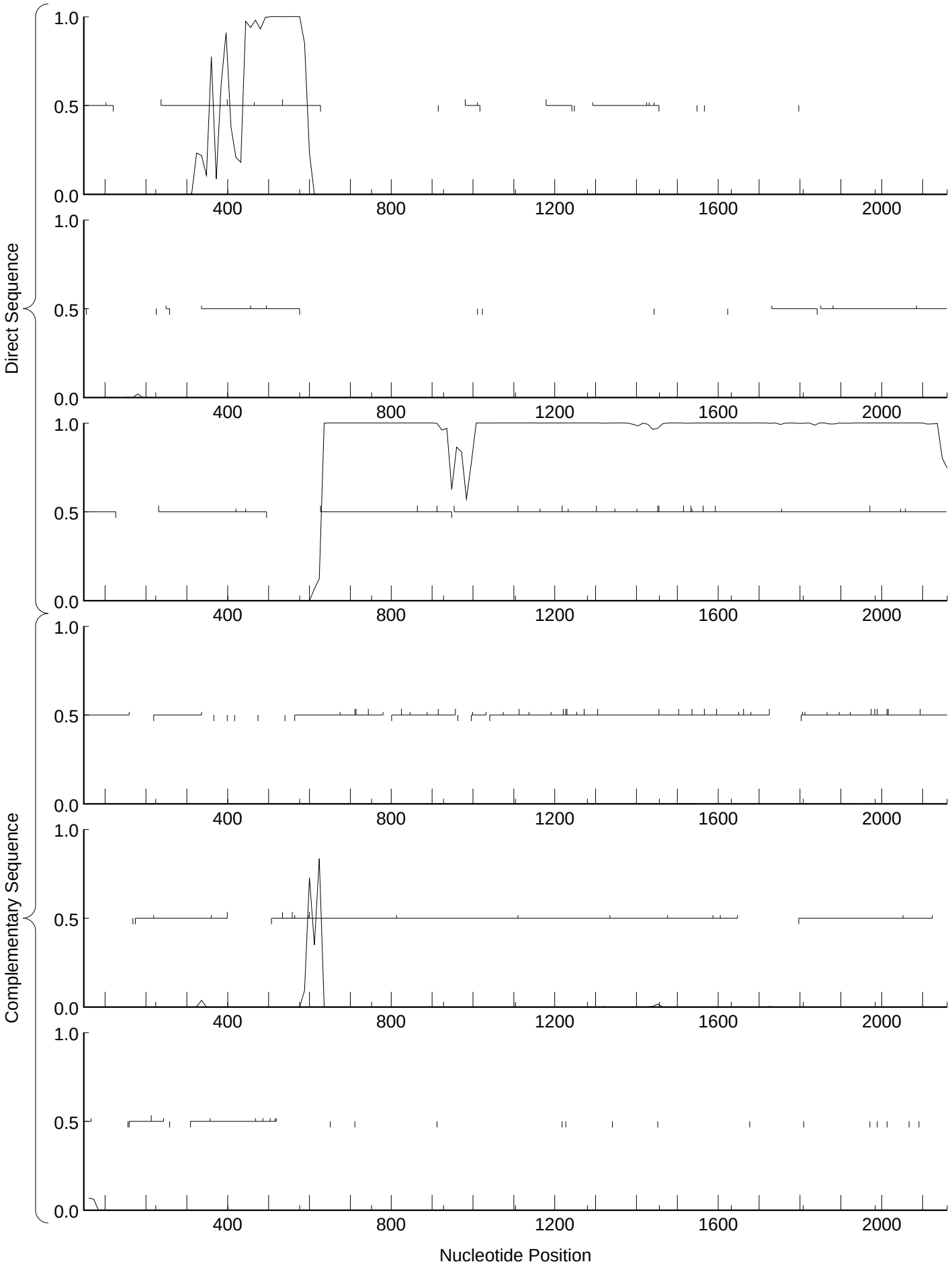
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Matrix     :  -
Author     :  -

Order      :  4
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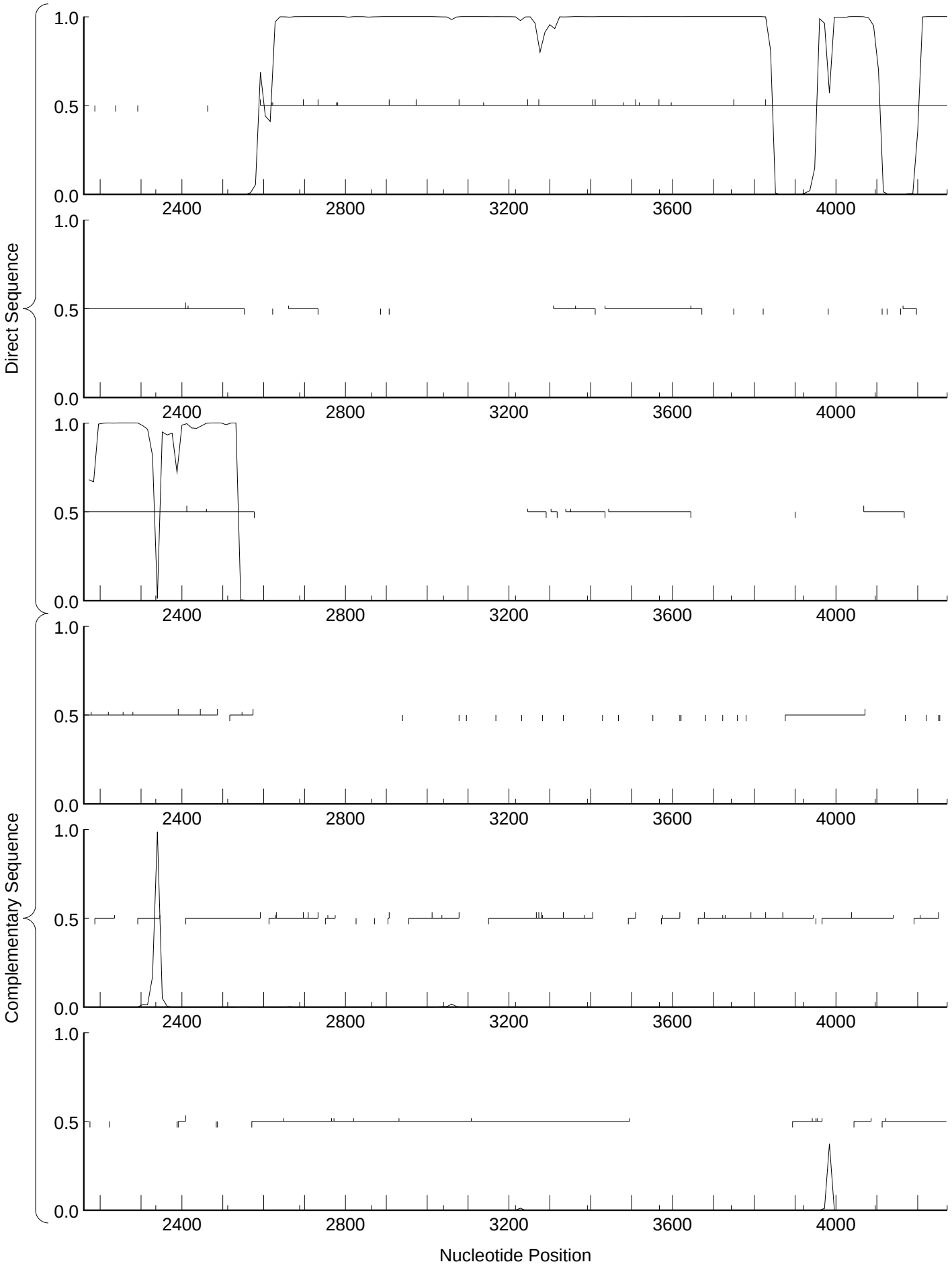

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  Send questions / comments to:
      Dr. M. Borodovsky
      Georgia Institute of Technology
      School of Biology
      Atlanta, GA  30332-0230
```

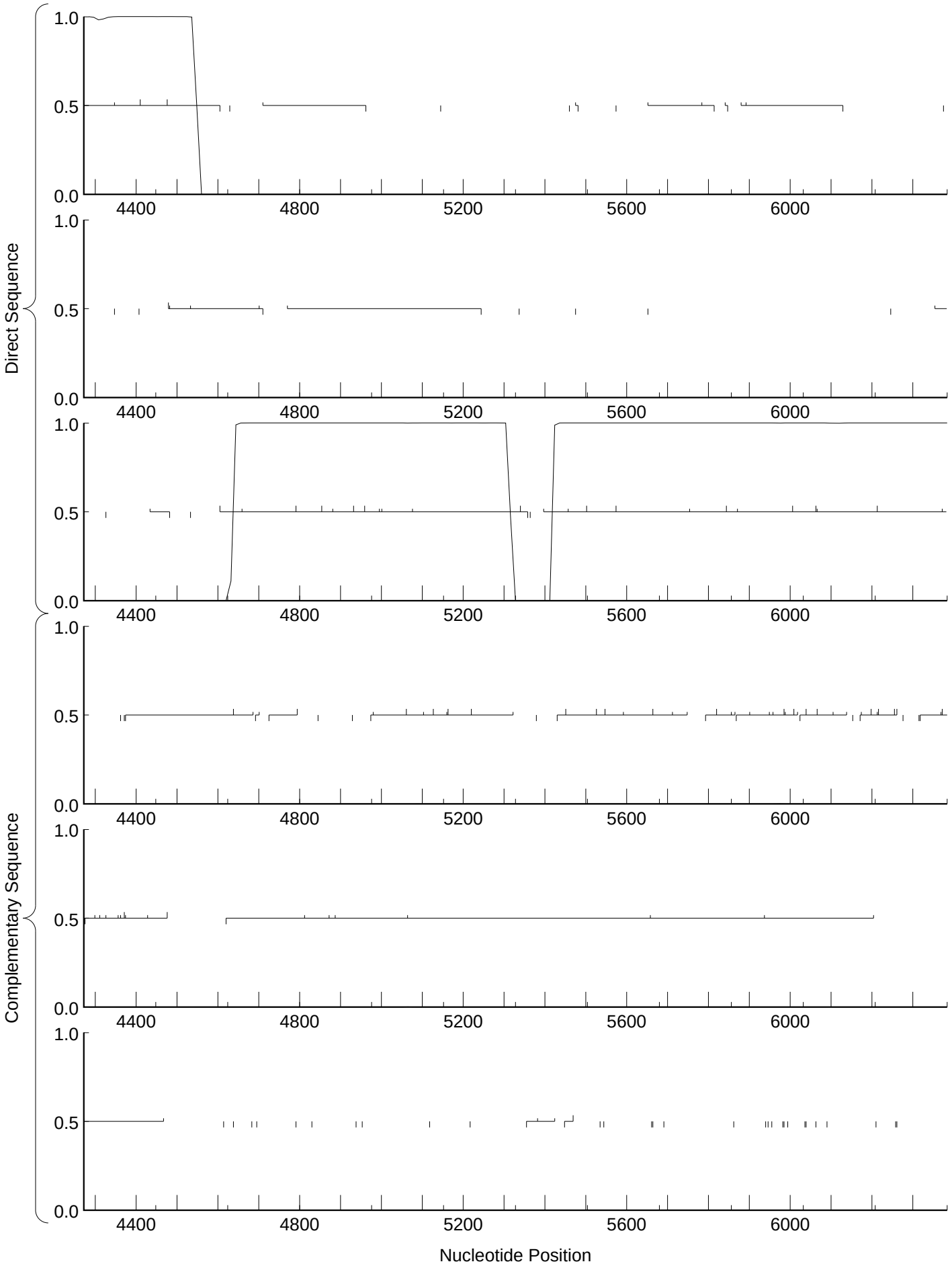

For help or information, send electronic mail to: custserv@genepro.com, or mark@amber.biology.gatech.edu

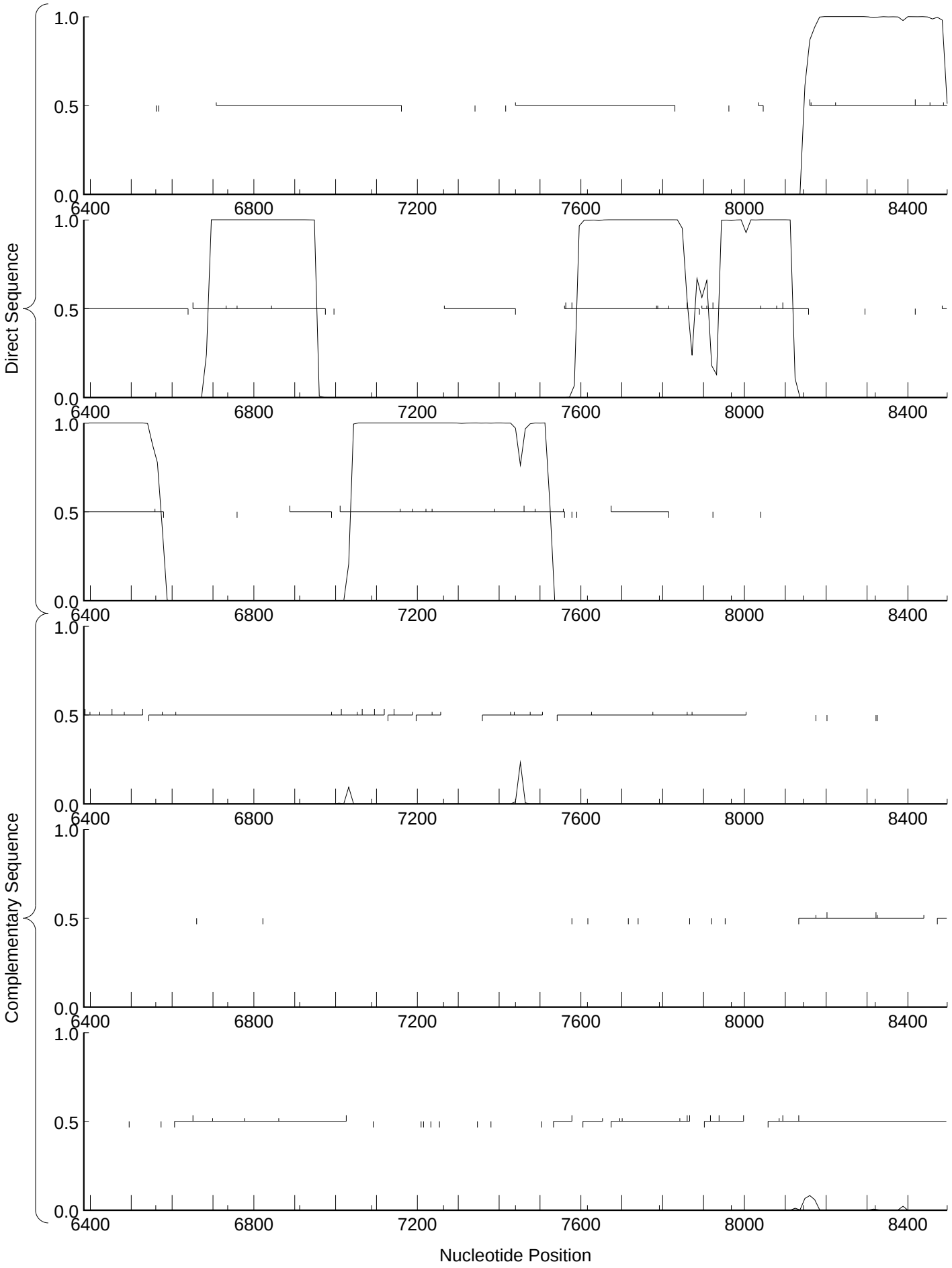
oli complete sequence, 41594 bp including 10-base 3’ overhang (TCTCCCGGCA), Cluster EB, Order 4, Window 96, Step 12, 2/21



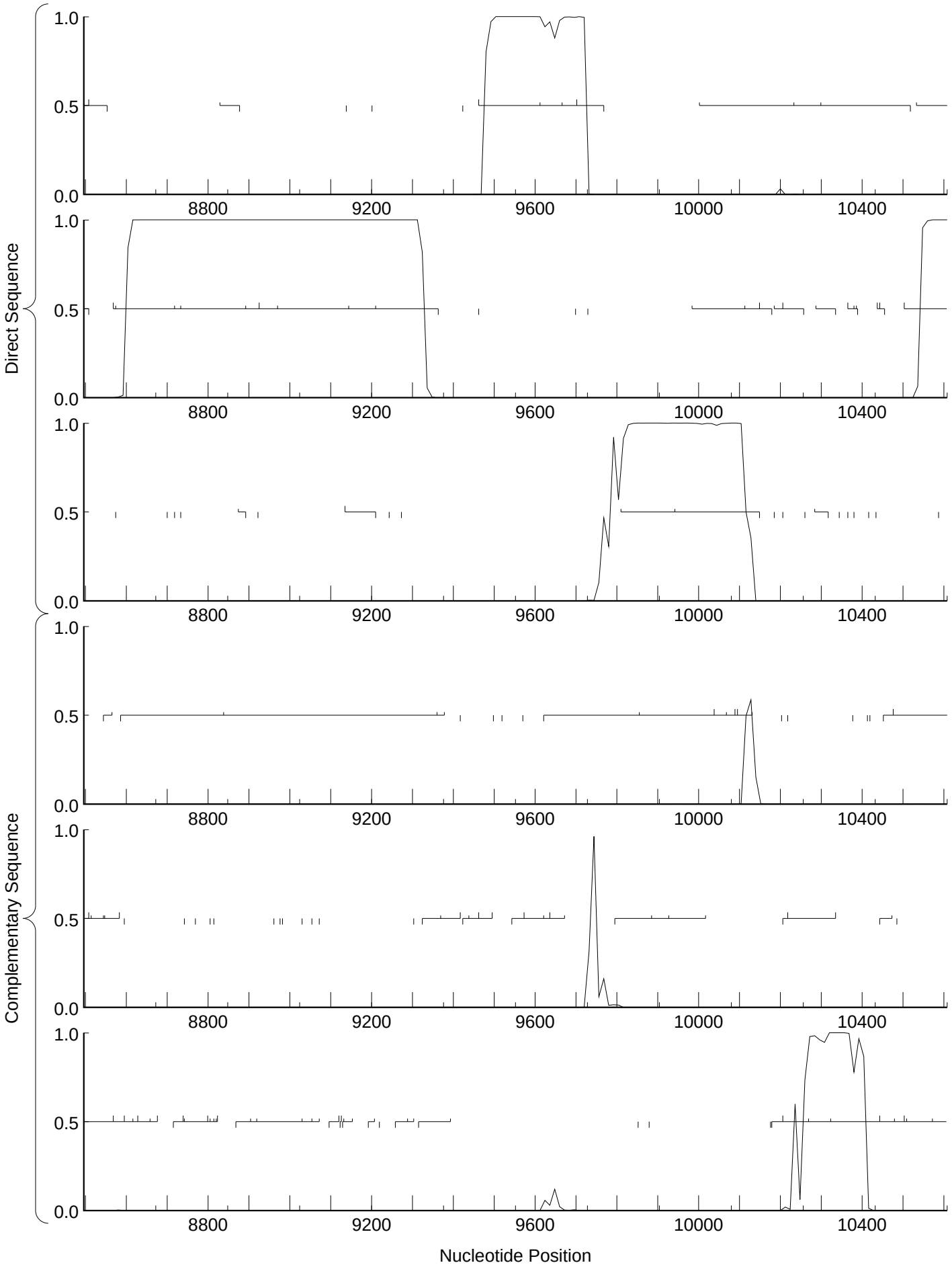
oli complete sequence, 41594 bp including 10-base 3’ overhang (TCTCCCGGCA), Cluster EB, Order 4, Window 96, Step 12, 3/21

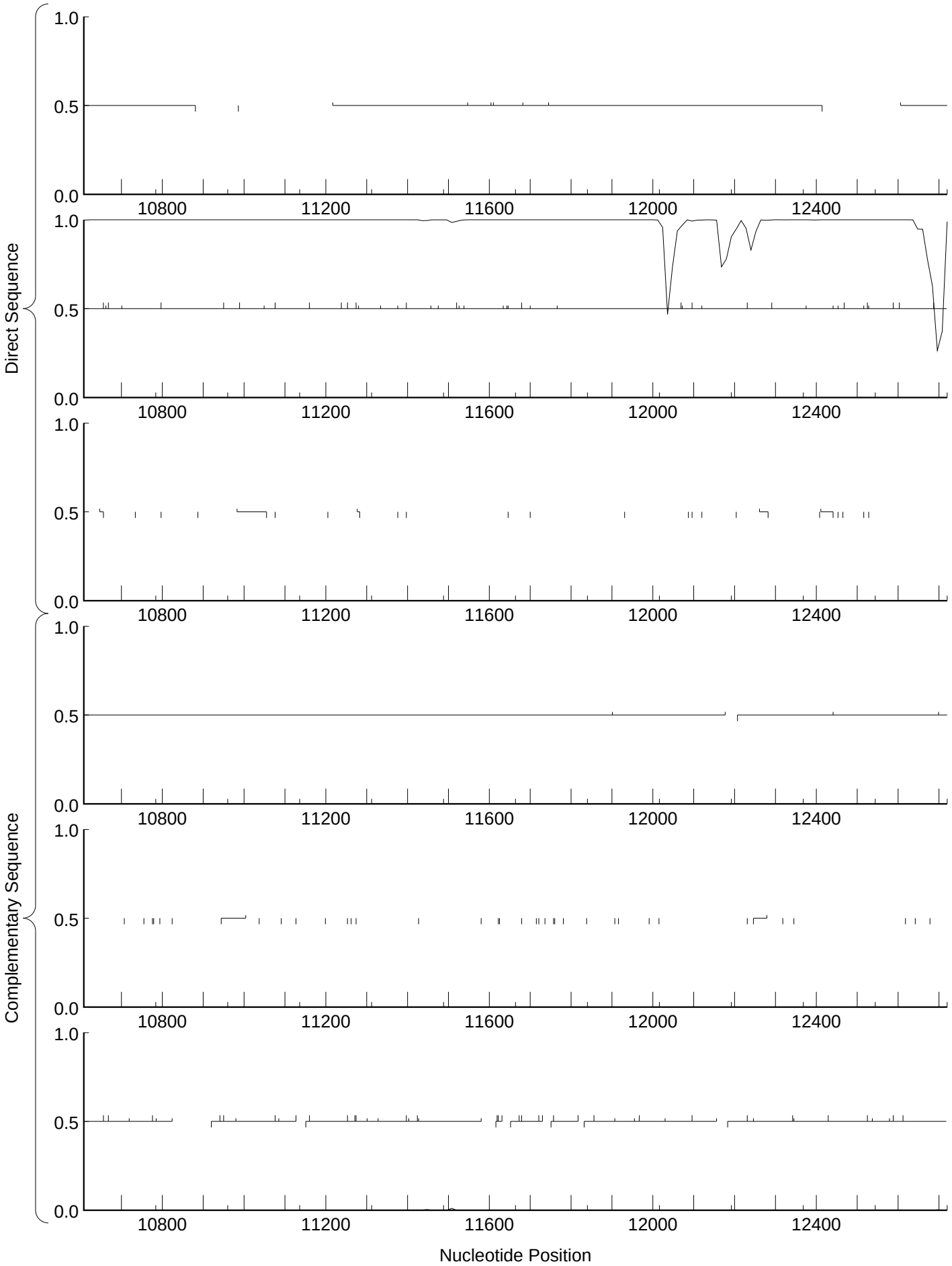


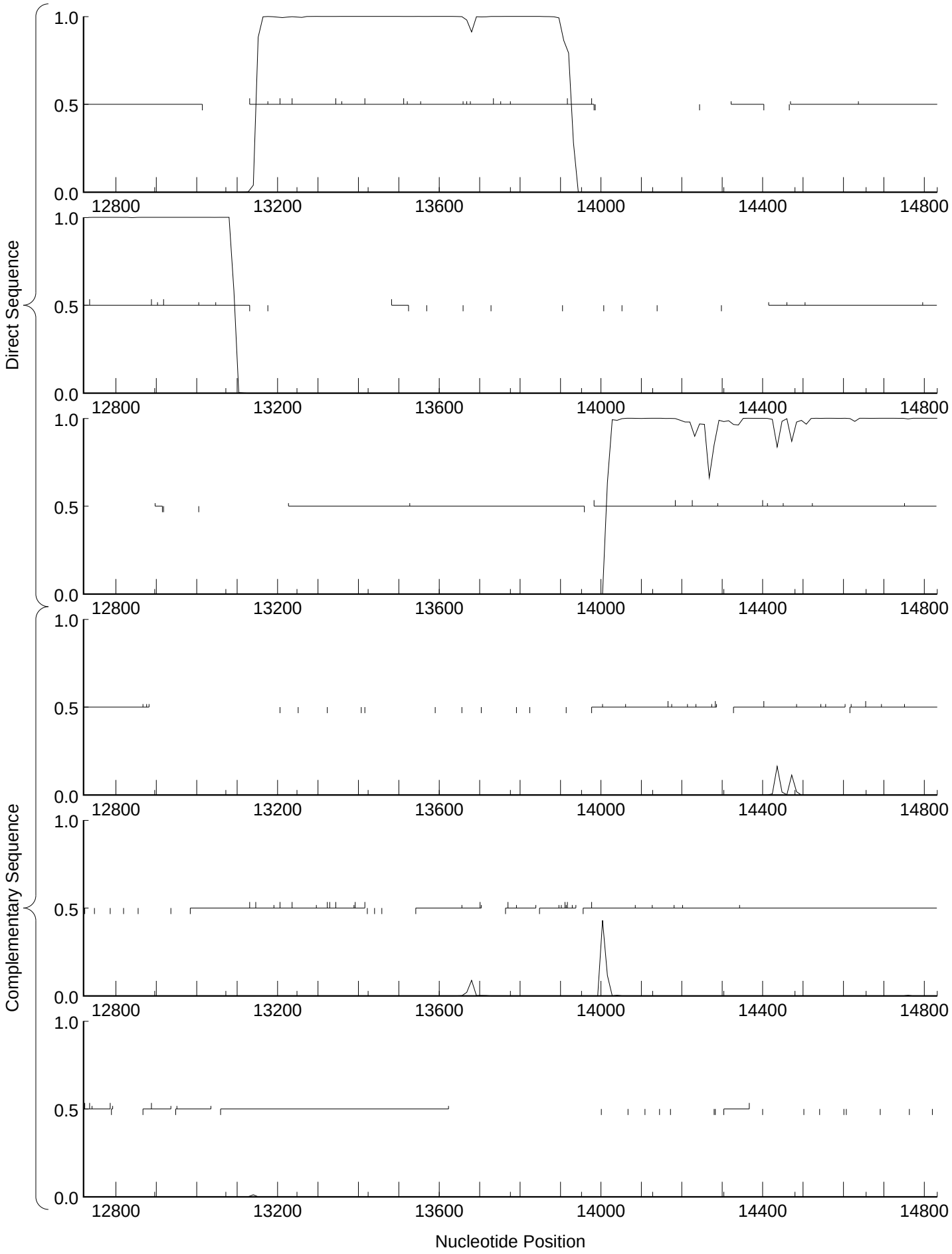

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
4400
4800
5200
5600
6000
Nucleotide Position


Direct Sequence
Complementary Sequence
1.0
0.5
0.0
6400
6800
7200
7600
8000
8400
Nucleotide Position

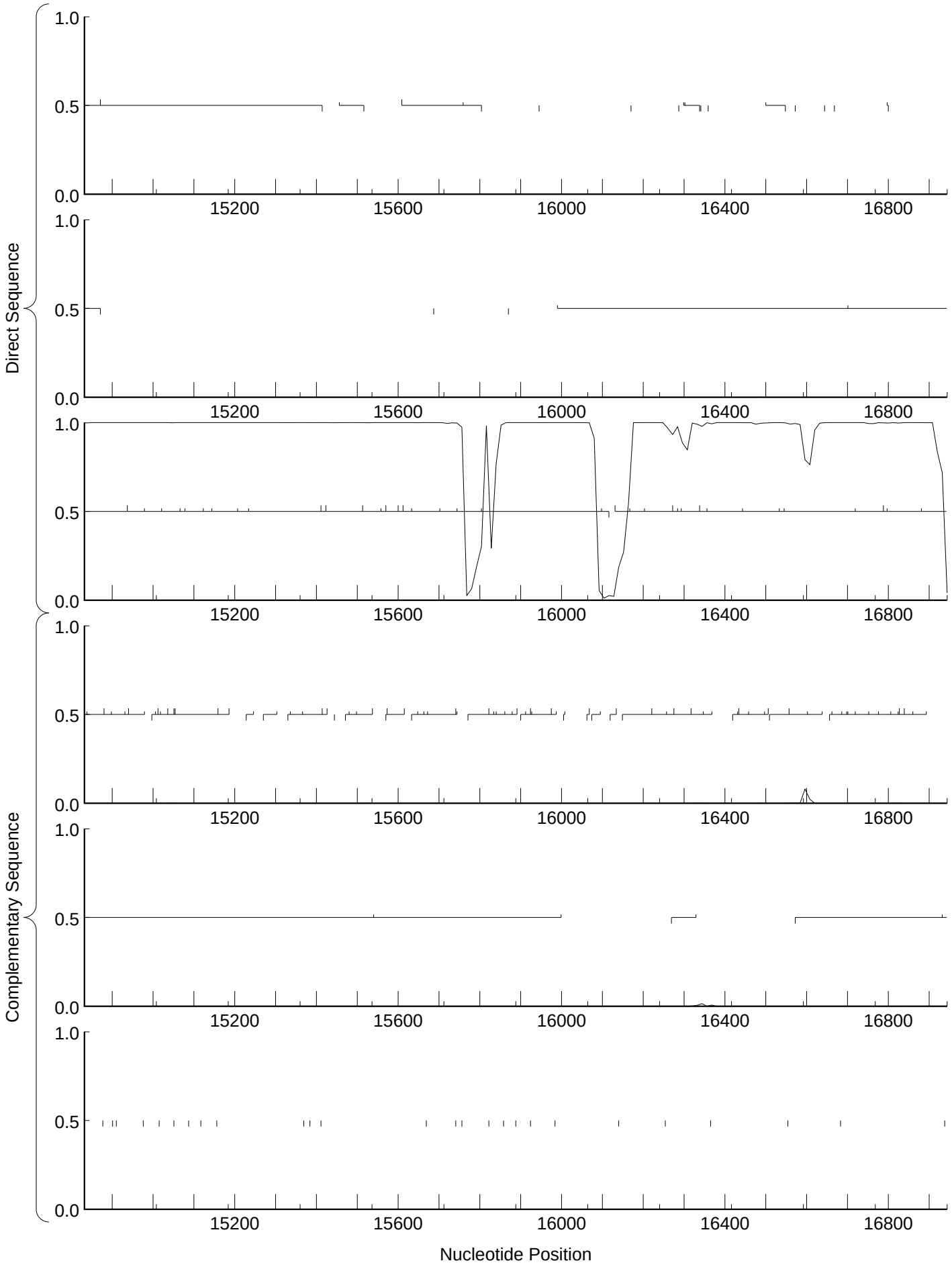
oli complete sequence, 41594 bp including 10-base 3’ overhang (TCTCCCGGCA), Cluster EB, Order 4, Window 96, Step 12, 6/21



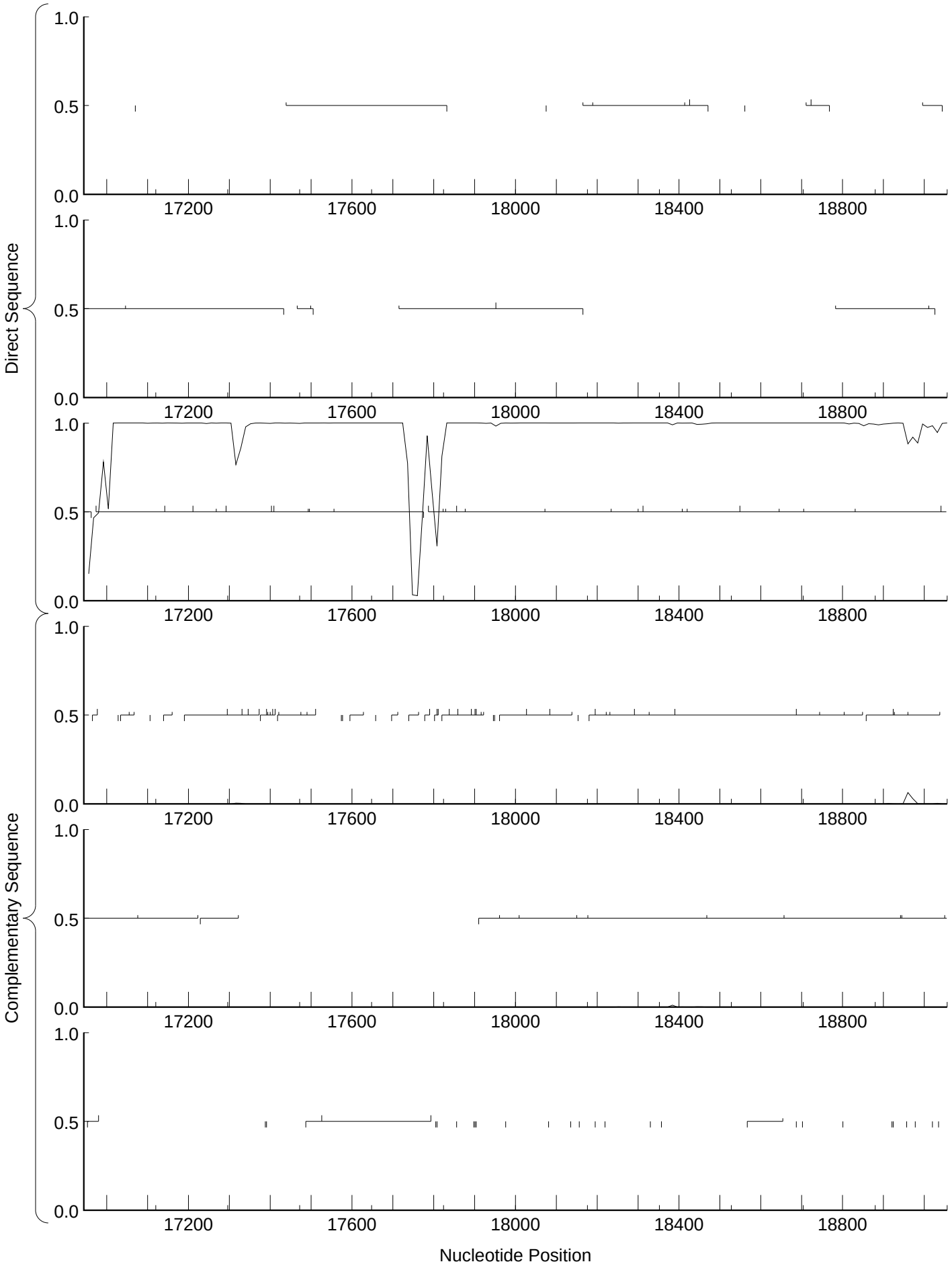

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
10800
11200
11600
12000
12400
Nucleotide Position


Direct Sequence
Complementary Sequence
1.0
0.5
0.0
12800
13200
13600
14000
14400
14800
Nucleotide Position

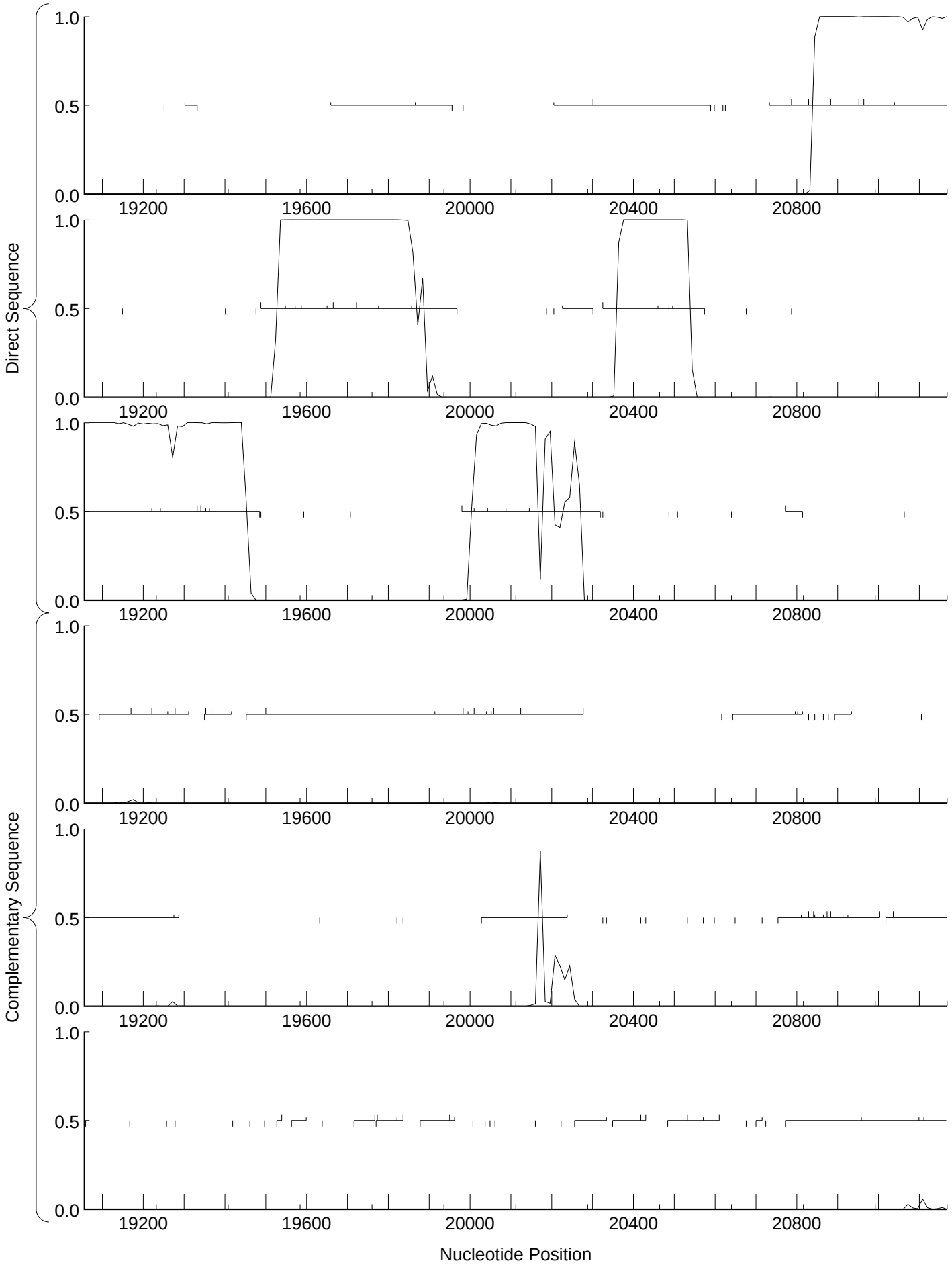
oli complete sequence, 41594 bp including 10-base 3’ overhang (TCTCCCGGCA), Cluster EB, Order 4, Window 96, Step 12, 9/21



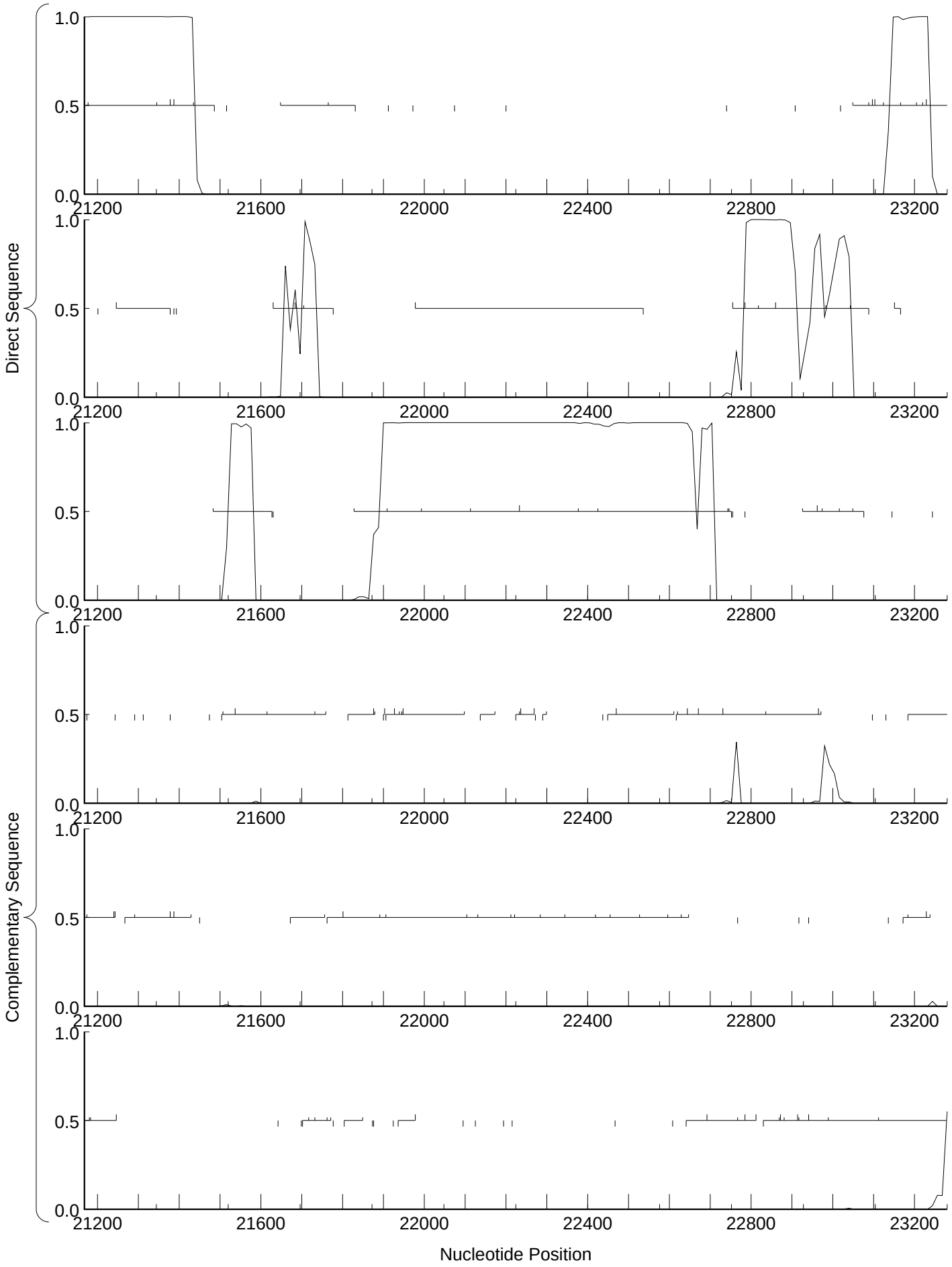
complete sequence, 41594 bp including 10-base 3’ overhang (TCTCCCGGCA), Cluster EB, Order 4, Window 96, Step 12, 10/21



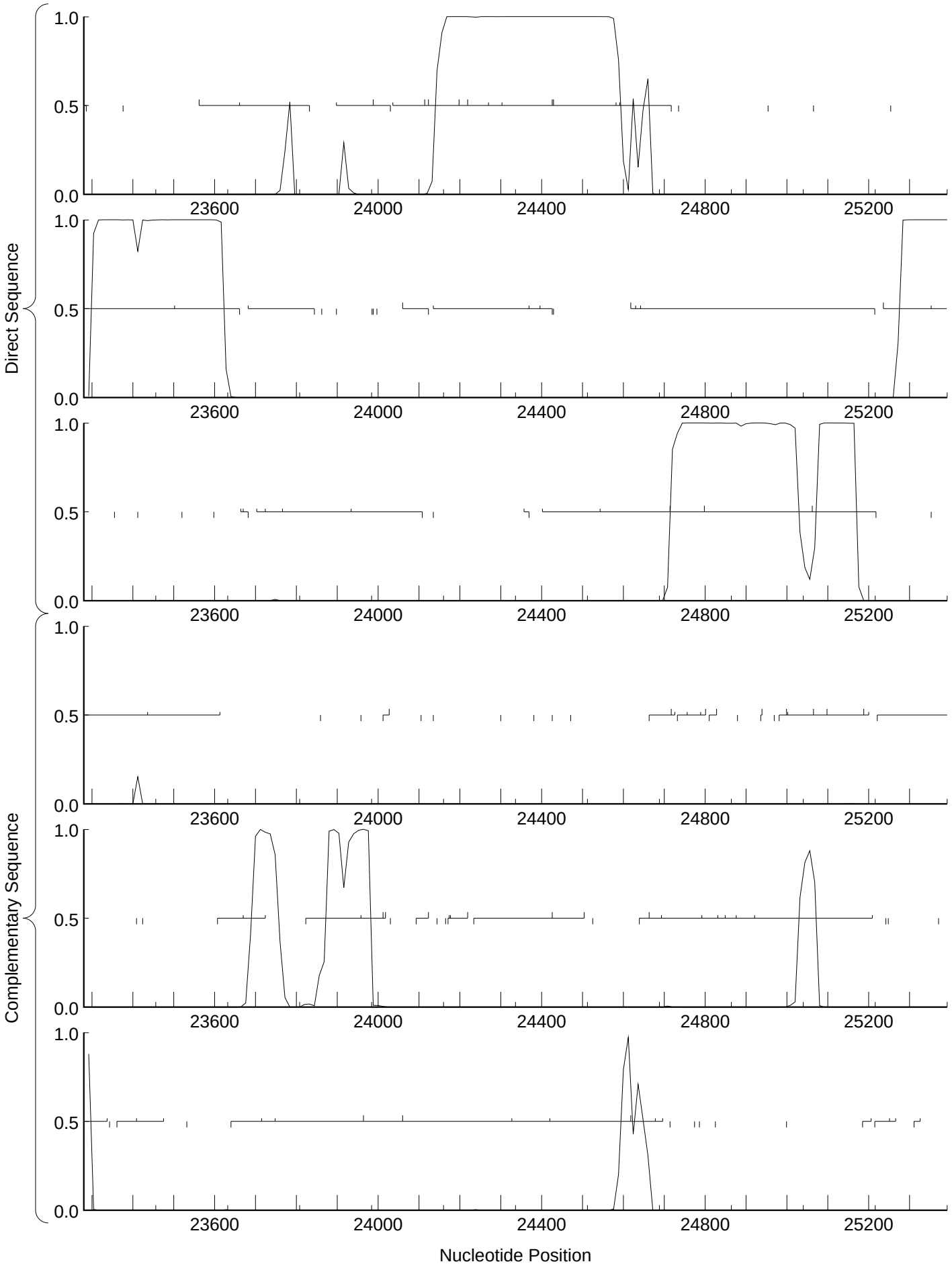
complete sequence, 41594 bp including 10-base 3’ overhang (TCTCCCGGCA), Cluster EB, Order 4, Window 96, Step 12, 11/21



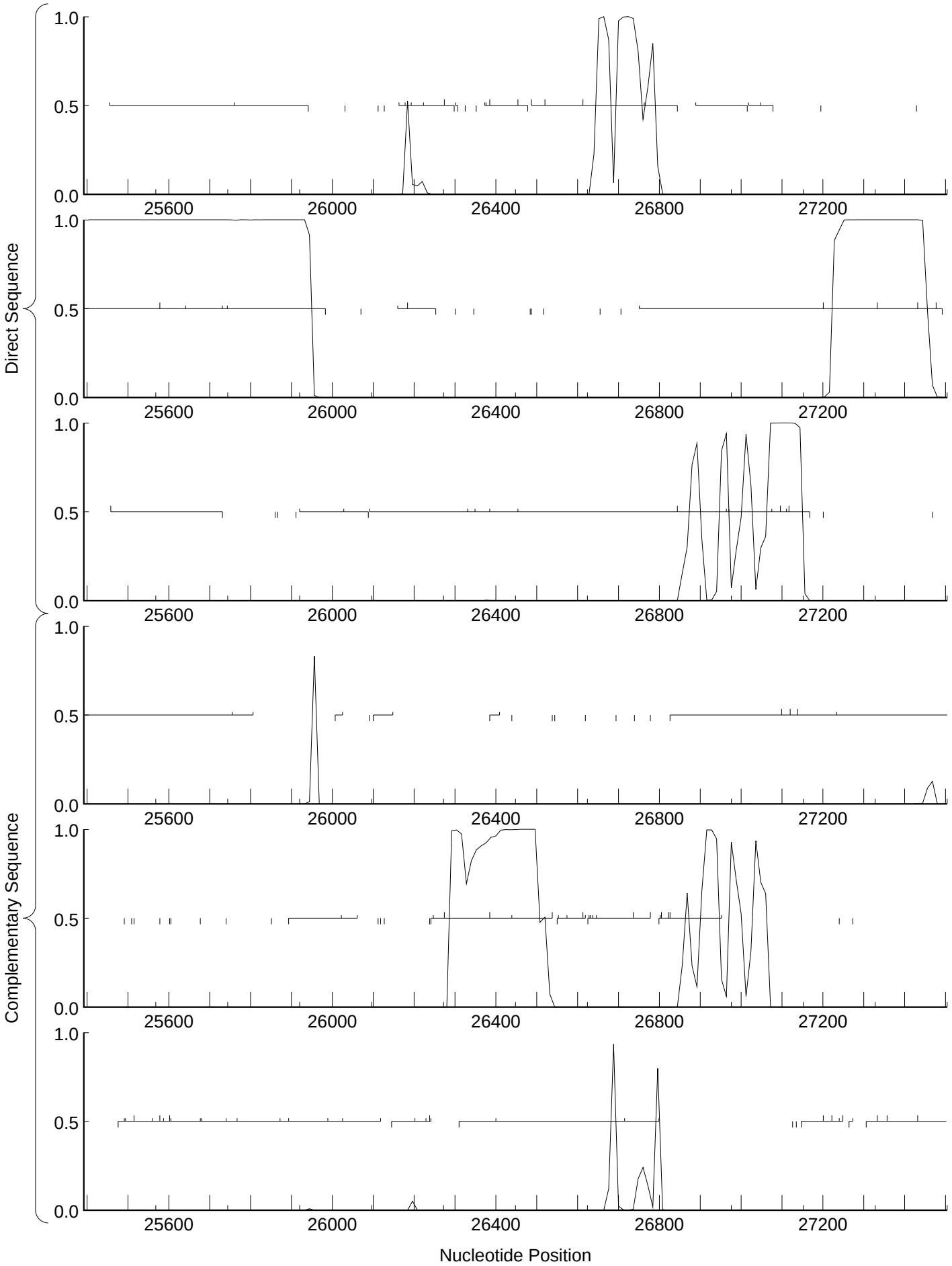
complete sequence, 41594 bp including 10-base 3’ overhang (TCTCCCGGCA), Cluster EB, Order 4, Window 96, Step 12, 12/21



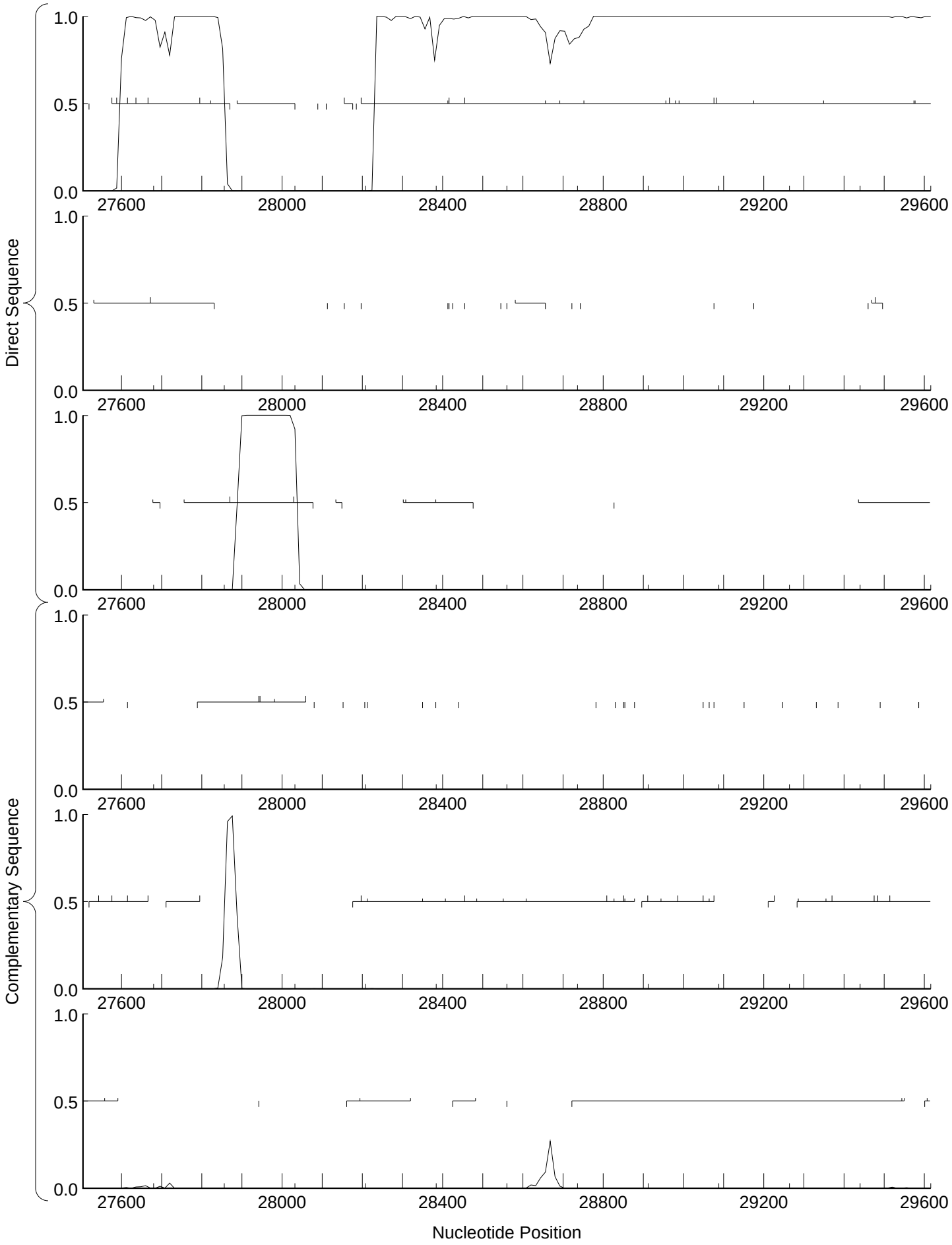
complete sequence, 41594 bp including 10-base 3’ overhang (TCTCCCGGCA), Cluster EB, Order 4, Window 96, Step 12, 13/21



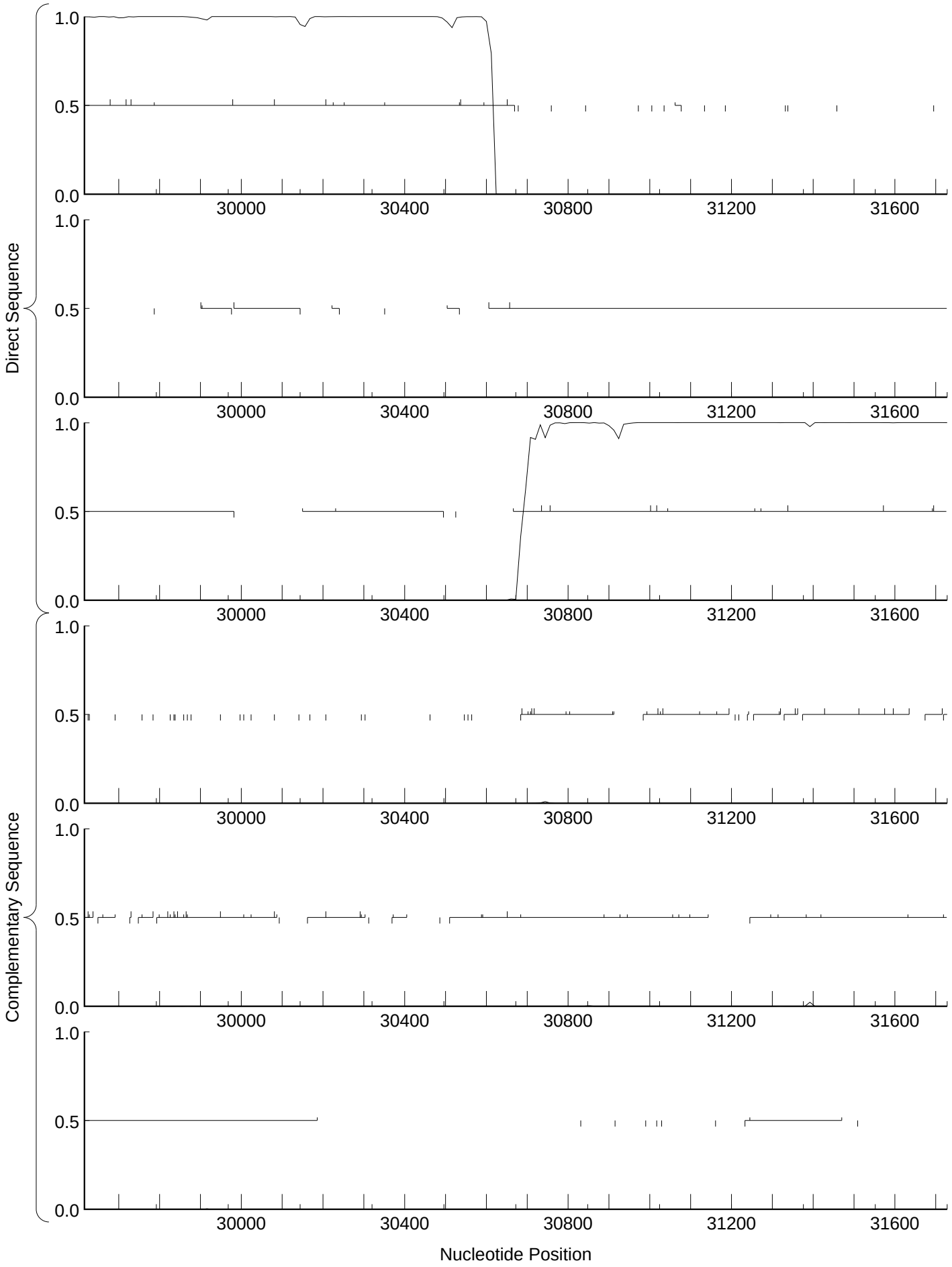
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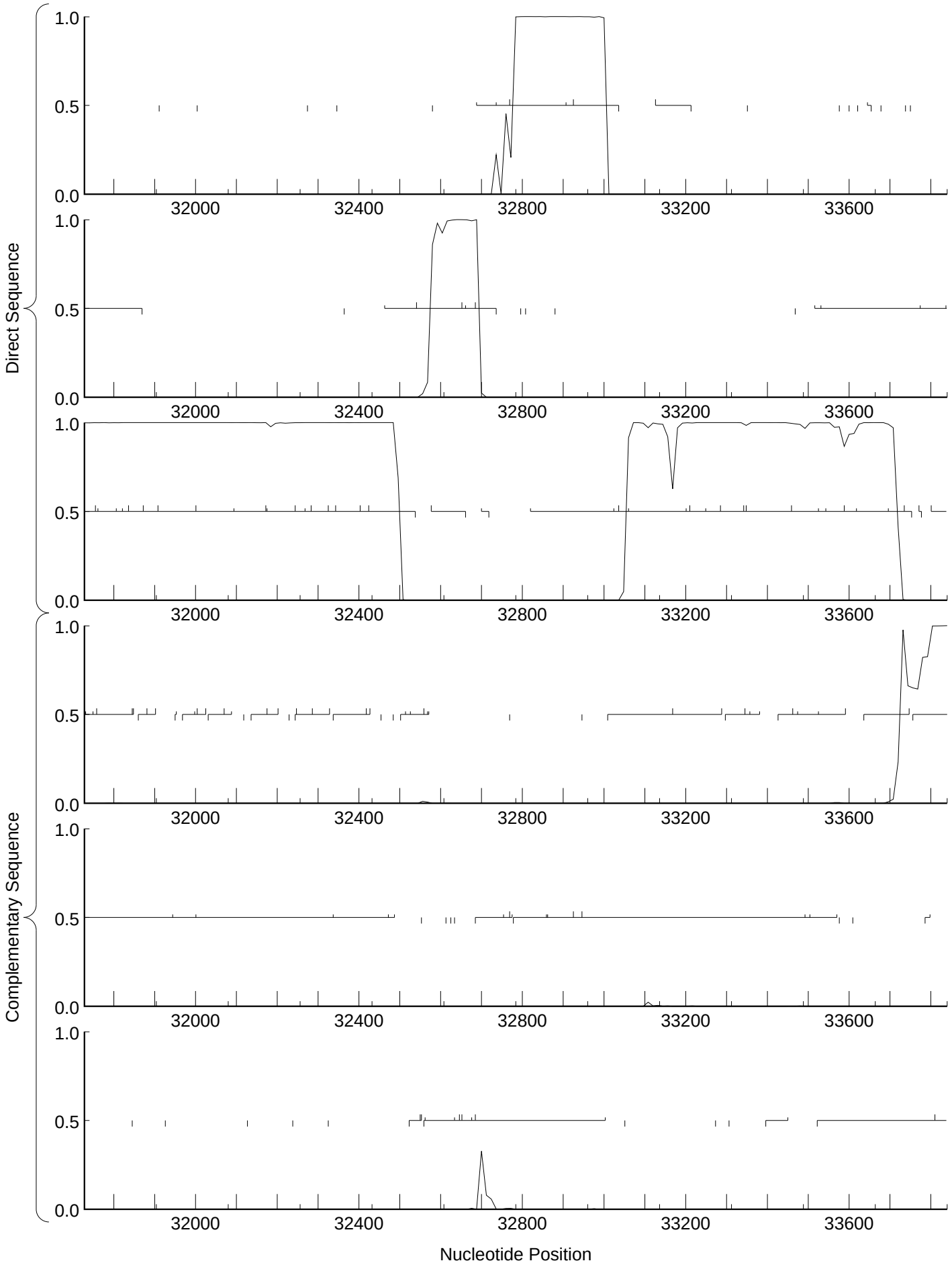
complete sequence, 41594 bp including 10-base 3’ overhang (TCTCCCGGCA), Cluster EB, Order 4, Window 96, Step 12, 15/21



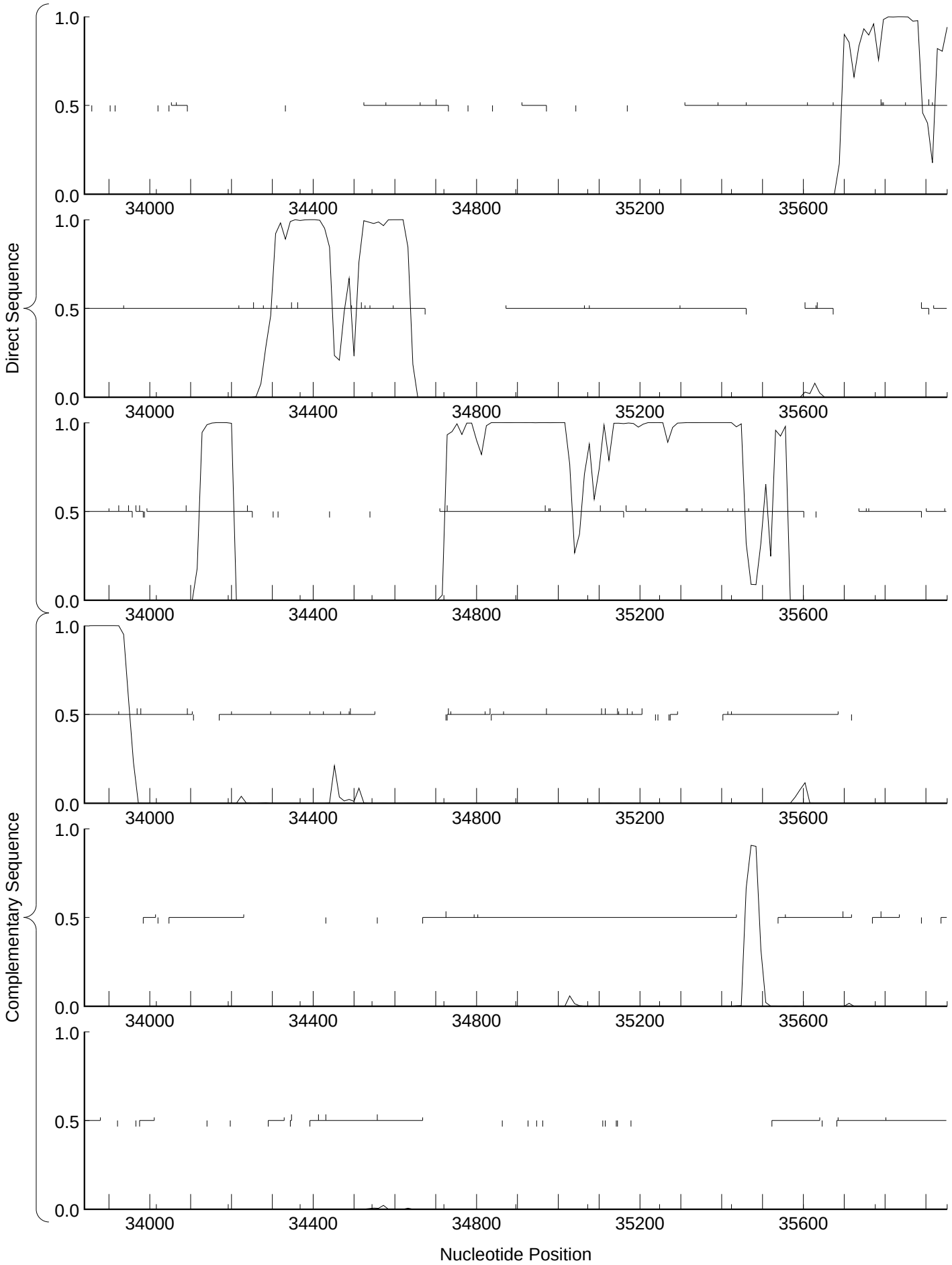
complete sequence, 41594 bp including 10-base 3’ overhang (TCTCCCGGCA), Cluster EB, Order 4, Window 96, Step 12, 16/21



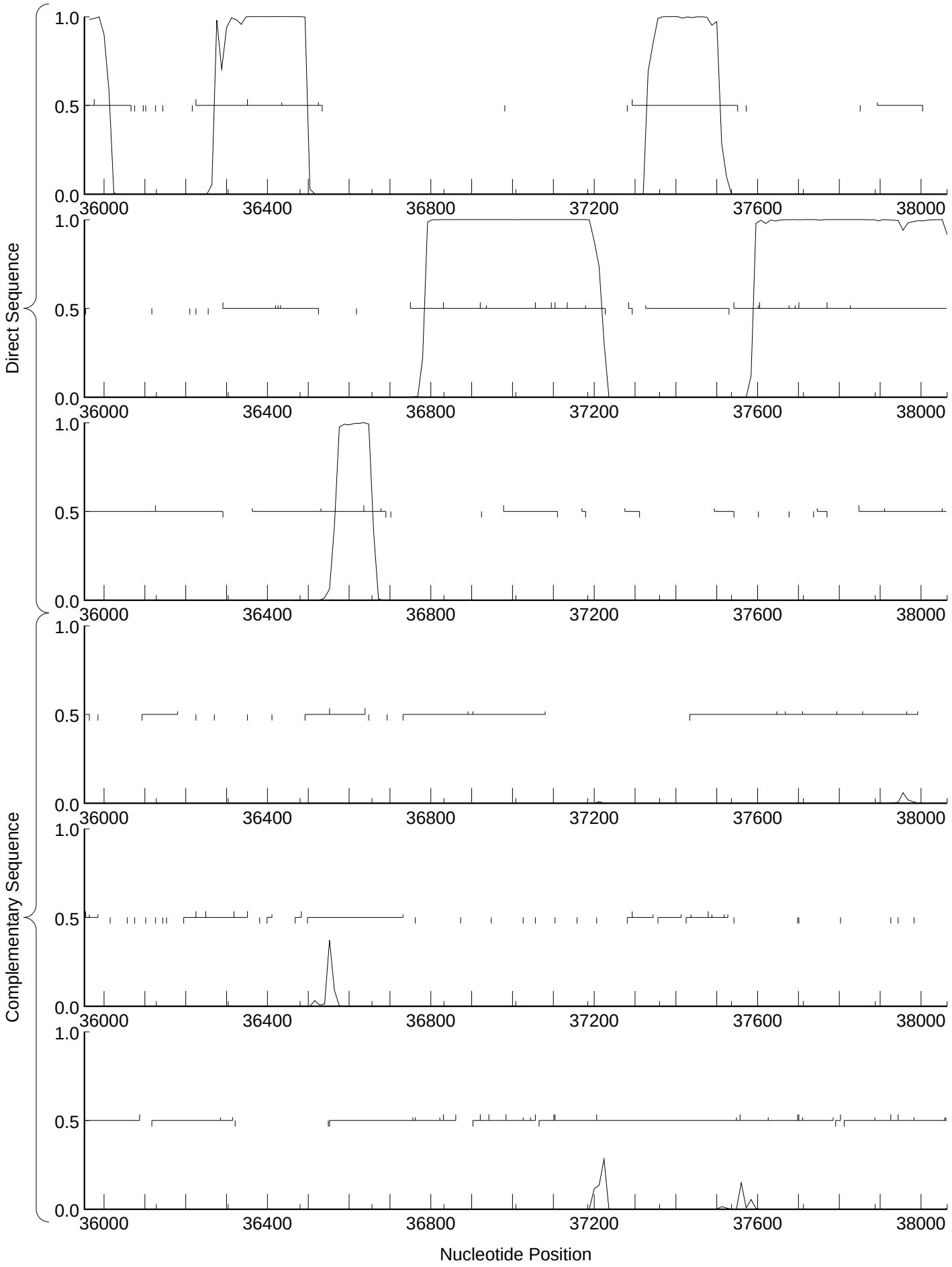
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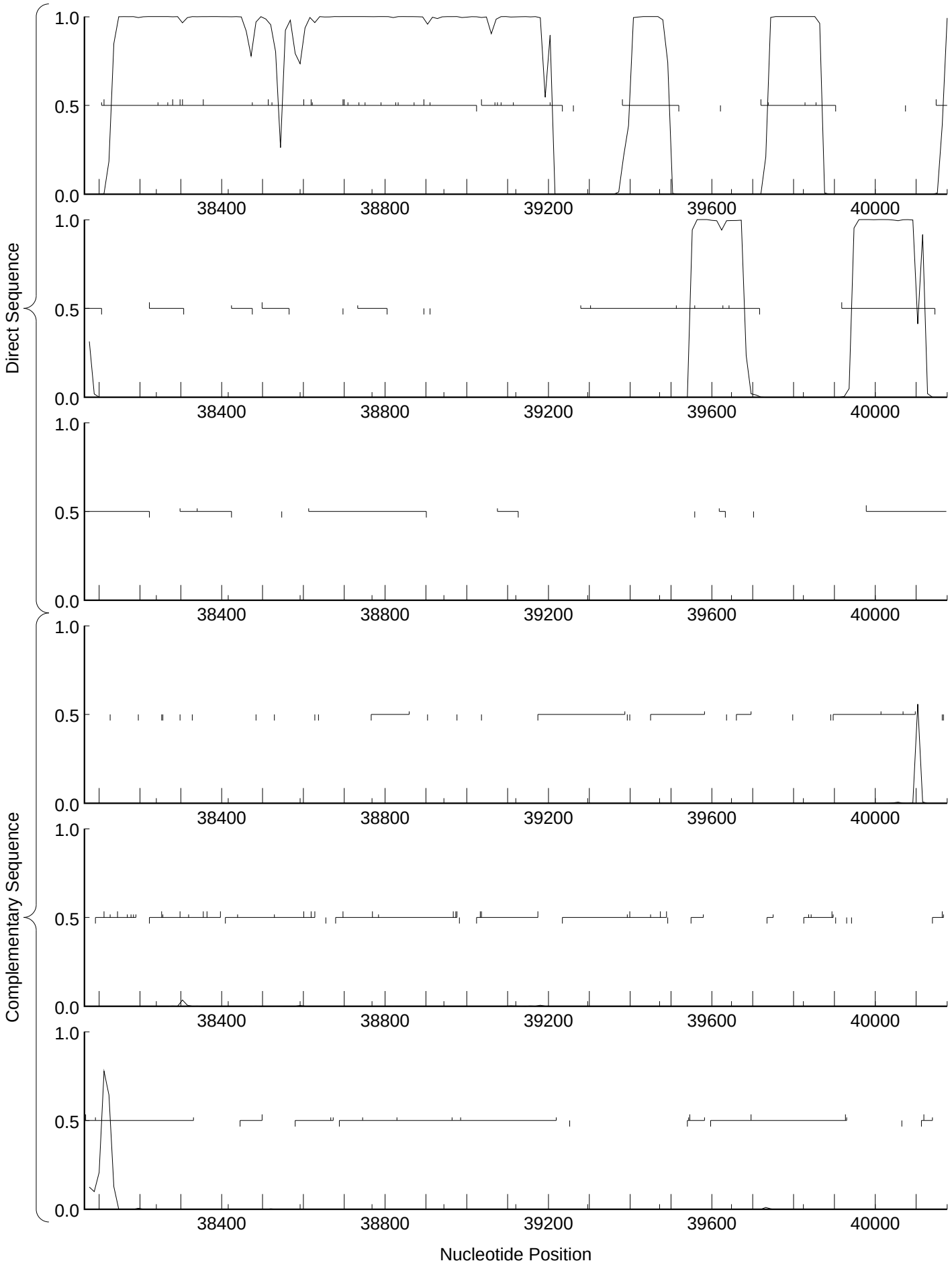
complete sequence, 41594 bp including 10-base 3’ overhang (TCTCCCGGCA), Cluster EB, Order 4, Window 96, Step 12, 18/21



complete sequence, 41594 bp including 10-base 3’ overhang (TCTCCCGGCA), Cluster EB, Order 4, Window 96, Step 12, 19/21



complete sequence, 41594 bp including 10-base 3’ overhang (TCTCCCGGCA), Cluster EB, Order 4, Window 96, Step 12, 20/21



complete sequence, 41594 bp including 10-base 3’ overhang (TCTCCCGGCA), Cluster EB, Order 4, Window 96, Step 12, 21/21

