GeneMark

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

PROGRAM INFORMATION

```
Sequence         :  Arthrobacter phage Supakev complete sequence, 43764 bp including 13-base 3' overhang (GCTTA
Analysis Date    :  3/29/24 at 4:05:39
Pages            :  22
Sequence Length  :  43764 bp
GC Content       :   61.70%

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,
```

MATRIX INFORMATION

```
Matrix     :  -
Author     :  -

Order      :  4

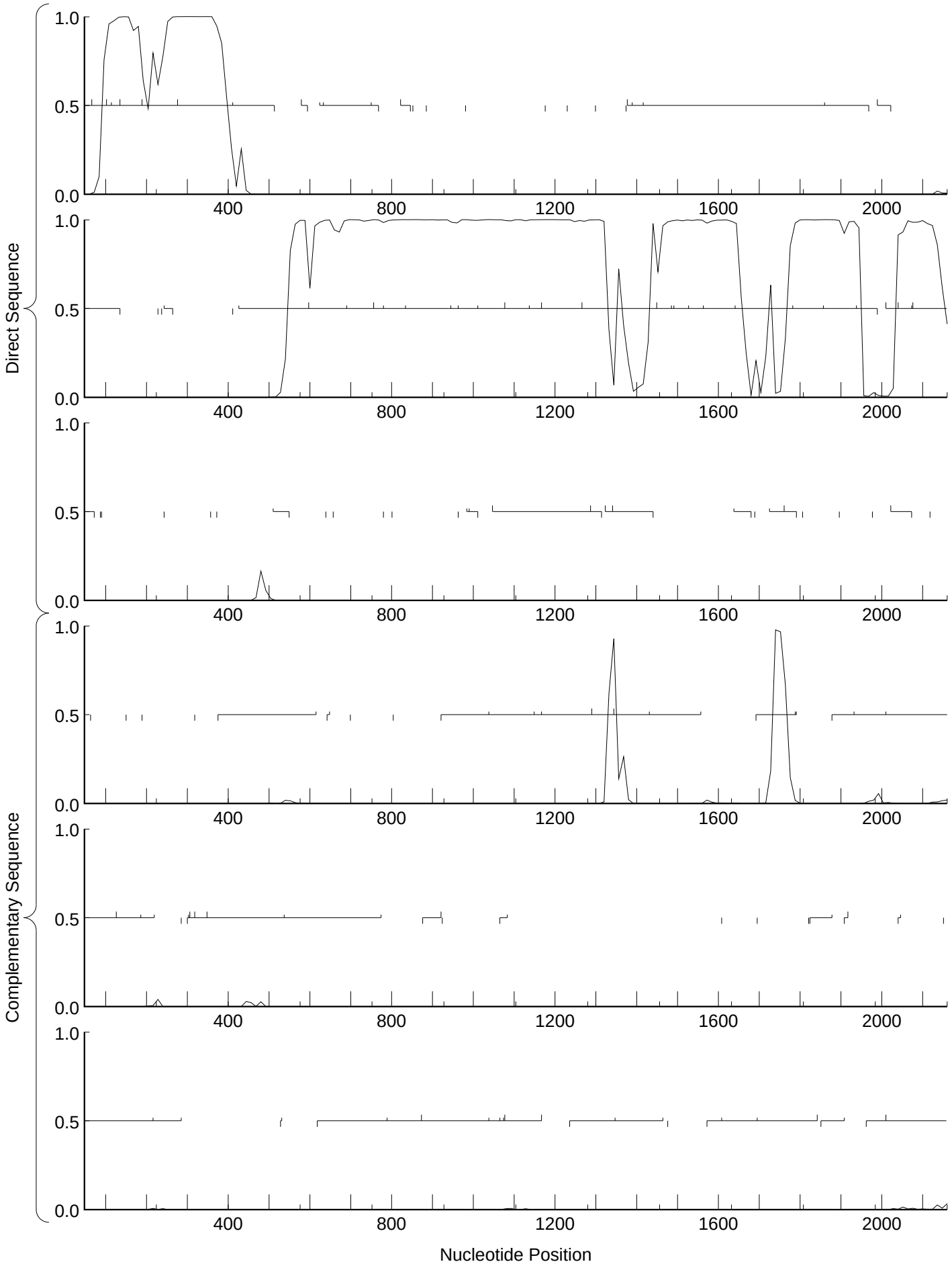

  Send questions / comments to:
      Dr. M. Borodovsky
      Georgia Institute of Technology
      School of Biology
      Atlanta, GA  30332-0230
```

Matrix notes & comments

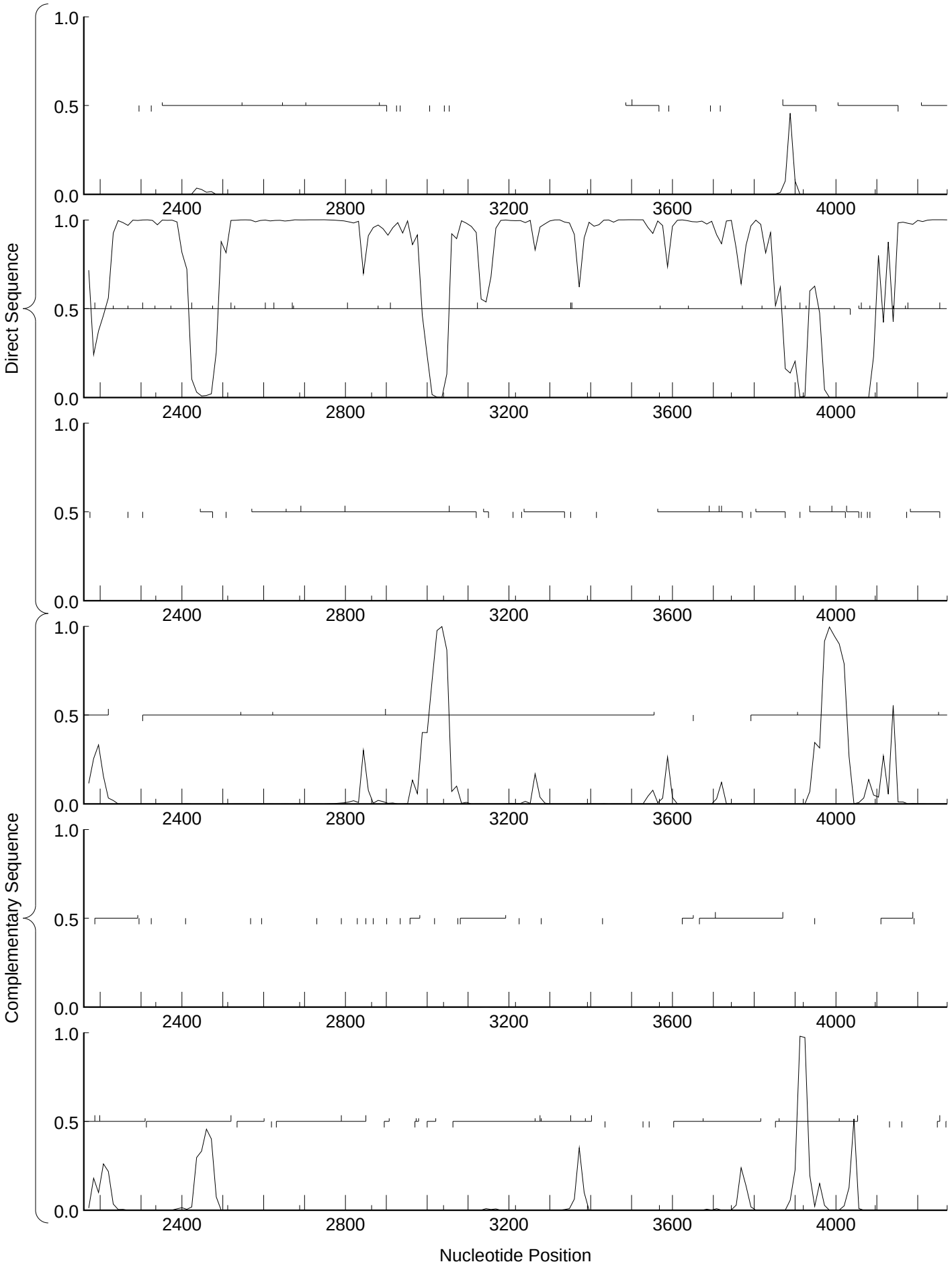
Training set derived by GeneMarkS, 4.30 October 2014
Sat Sep 8 00:22:00 2018

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

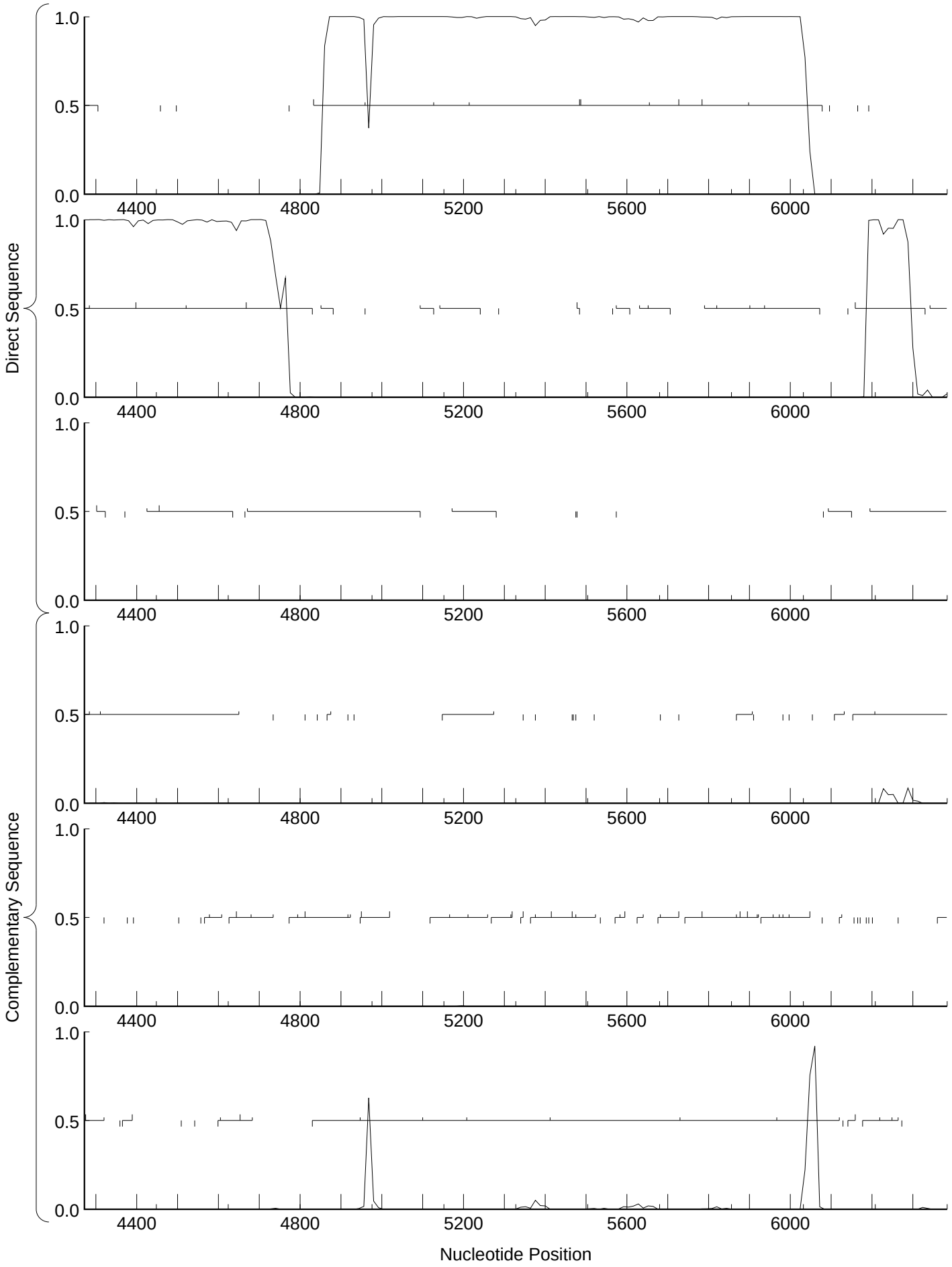
mplete sequence, 43764 bp including 13-base 3’ overhang (GCTTACCGTGATA), Cluster AK, Order 4, Window 96, Step 12, 2/22



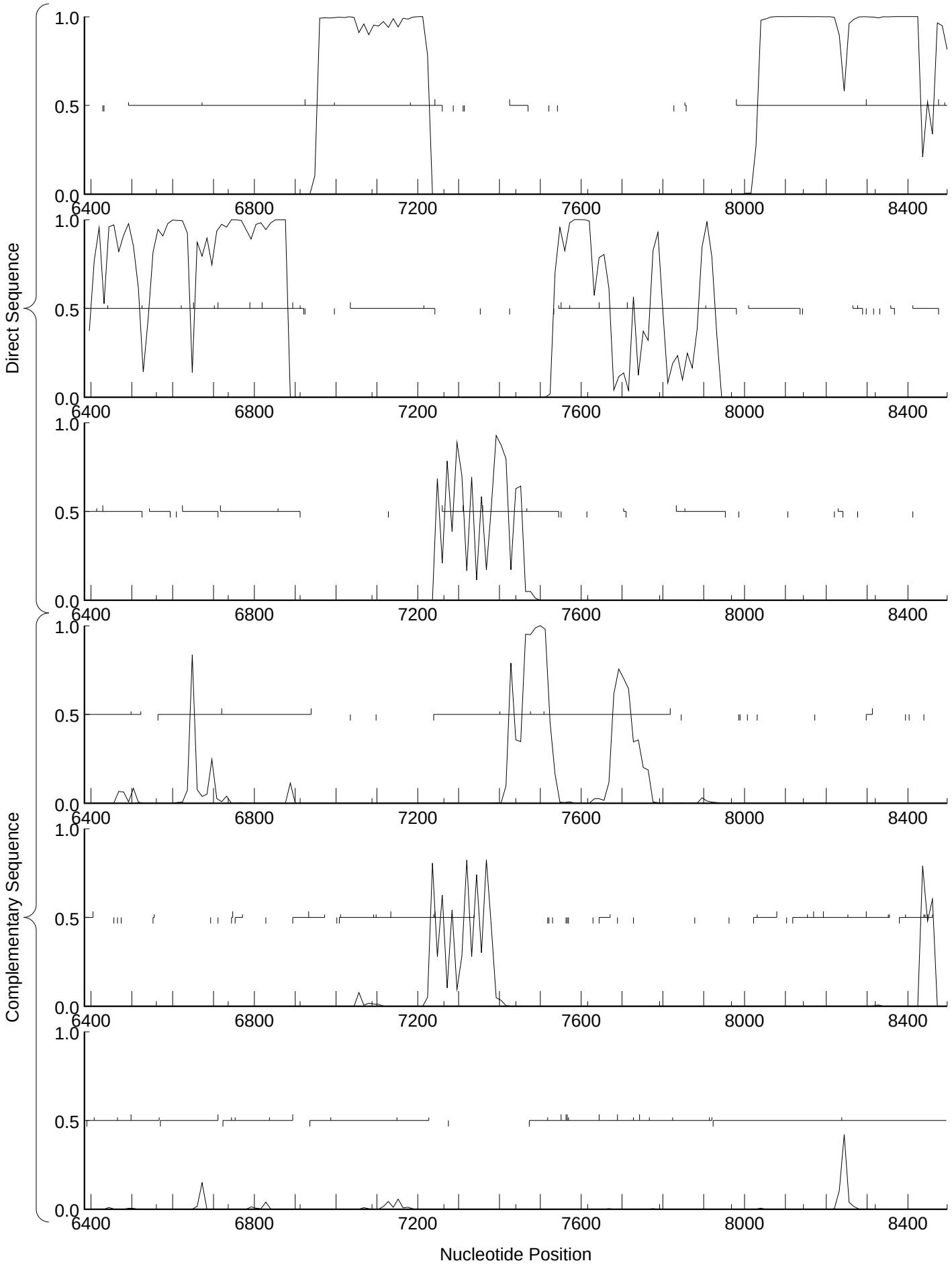
mplete sequence, 43764 bp including 13-base 3’ overhang (GCTTACCGTGATA), Cluster AK, Order 4, Window 96, Step 12, 3/22



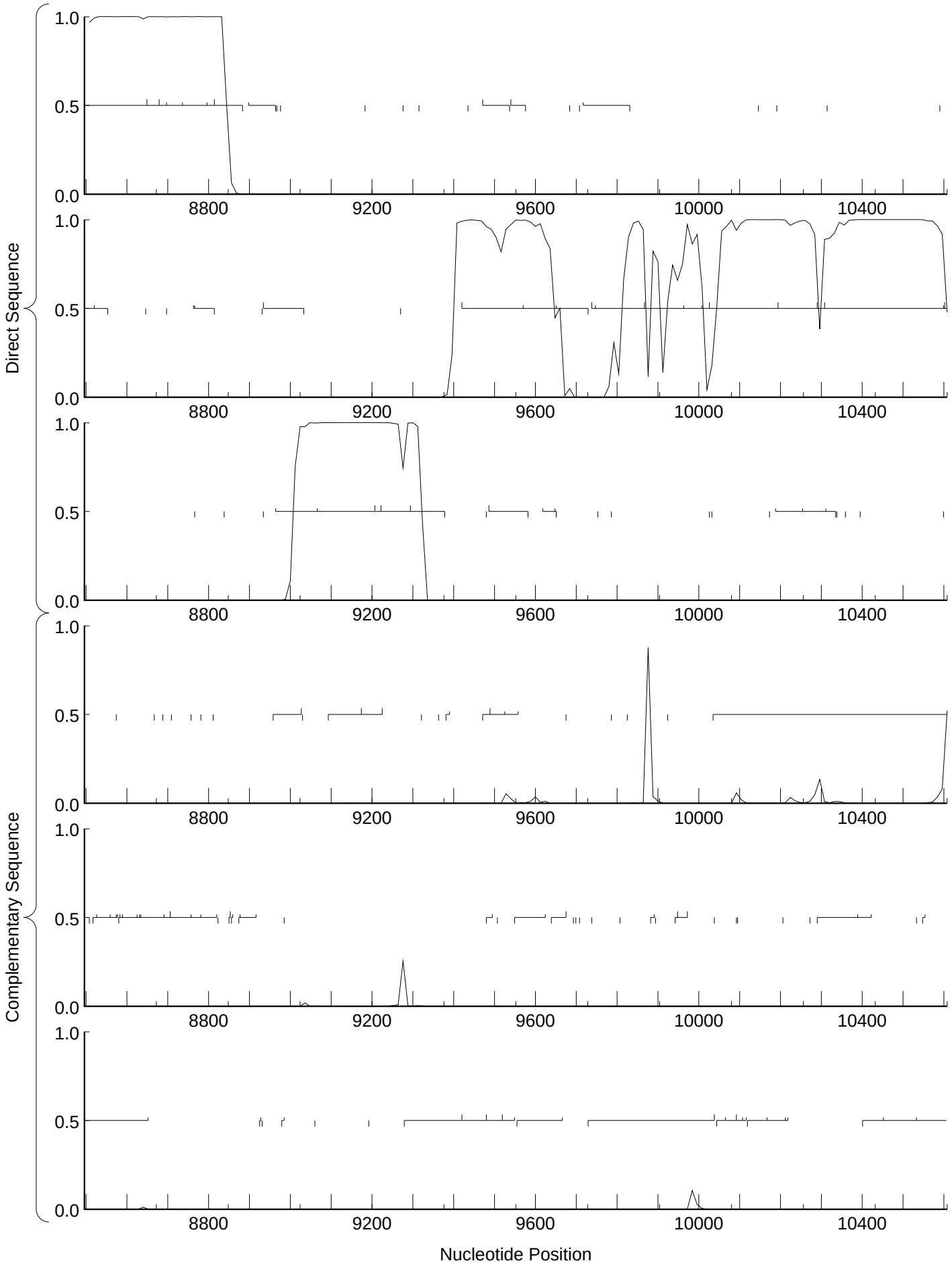
mplete sequence, 43764 bp including 13-base 3’ overhang (GCTTACCGTGATA), Cluster AK, Order 4, Window 96, Step 12, 4/22



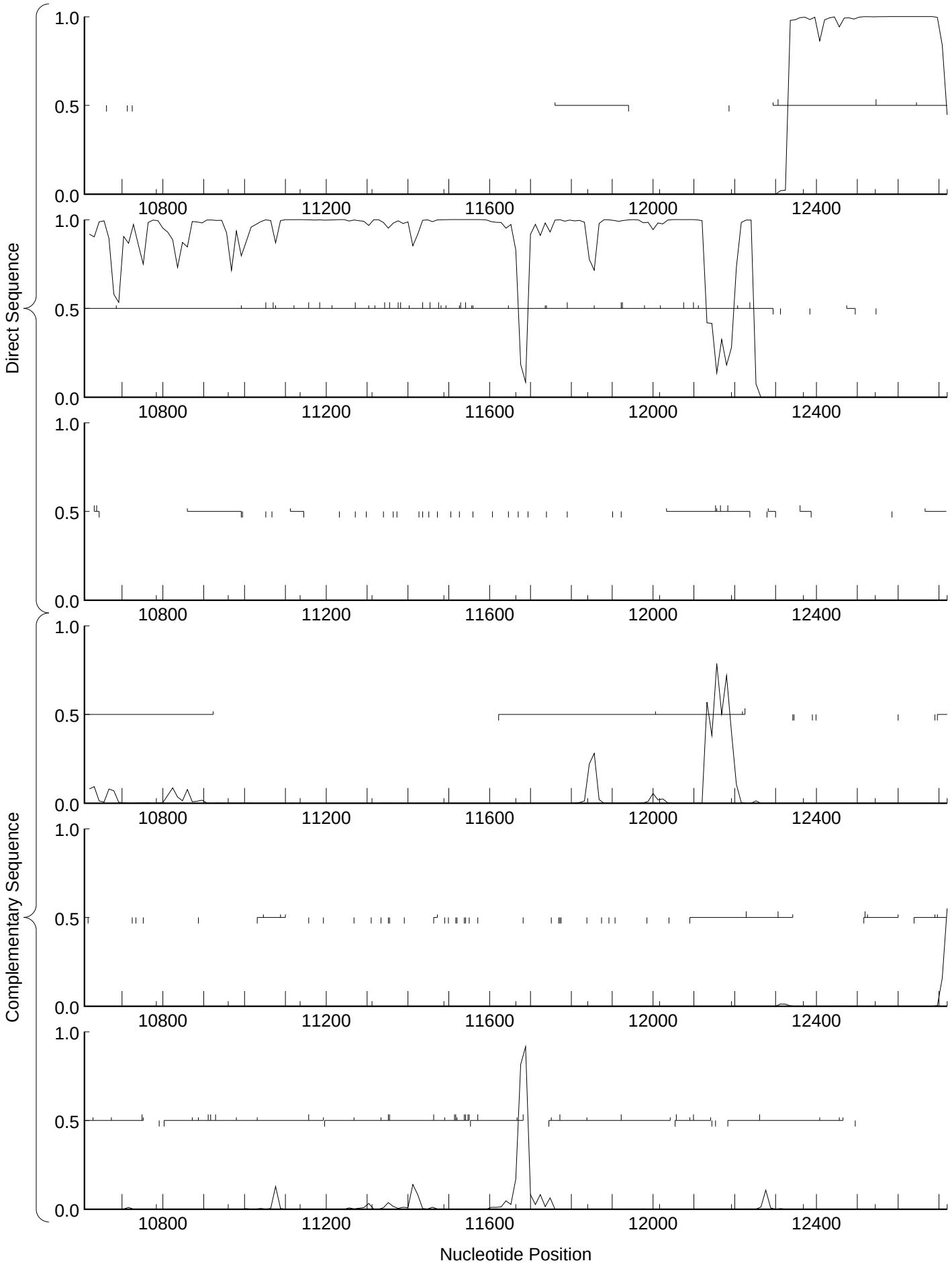
mplete sequence, 43764 bp including 13-base 3’ overhang (GCTTACCGTGATA), Cluster AK, Order 4, Window 96, Step 12, 5/22



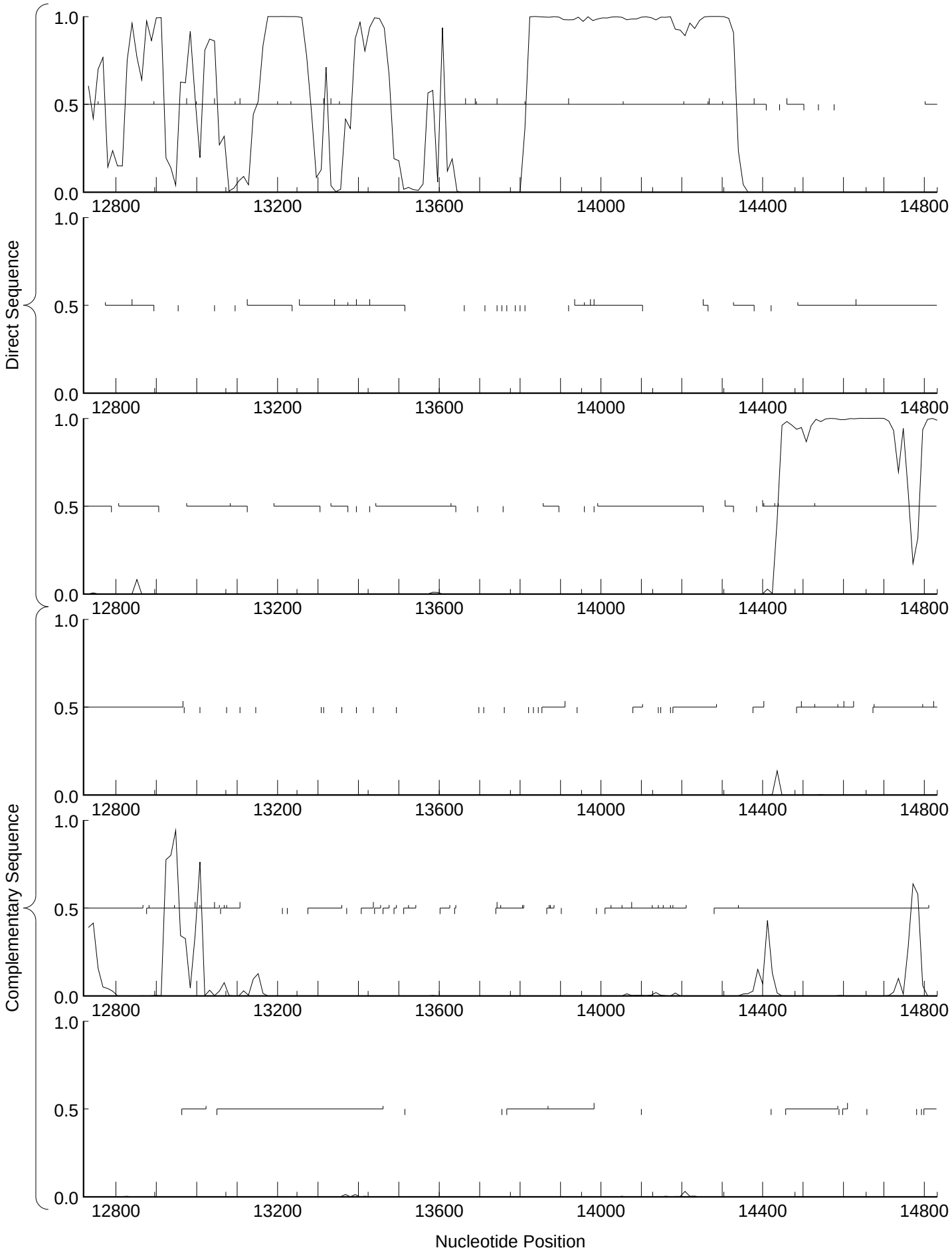
mplete sequence, 43764 bp including 13-base 3’ overhang (GCTTACCGTGATA), Cluster AK, Order 4, Window 96, Step 12, 6/22



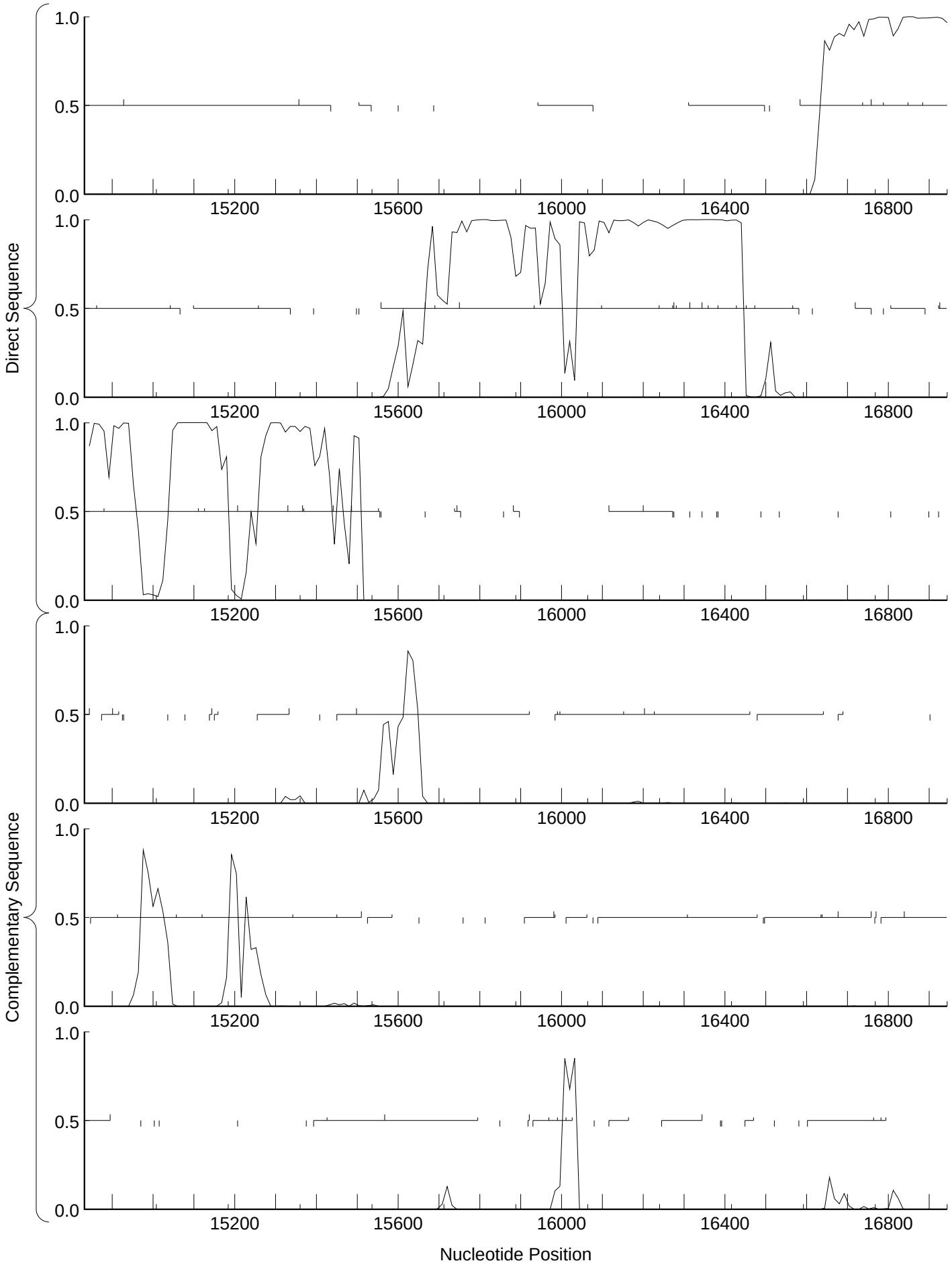
mplete sequence, 43764 bp including 13-base 3’ overhang (GCTTACCGTGATA), Cluster AK, Order 4, Window 96, Step 12, 7/22



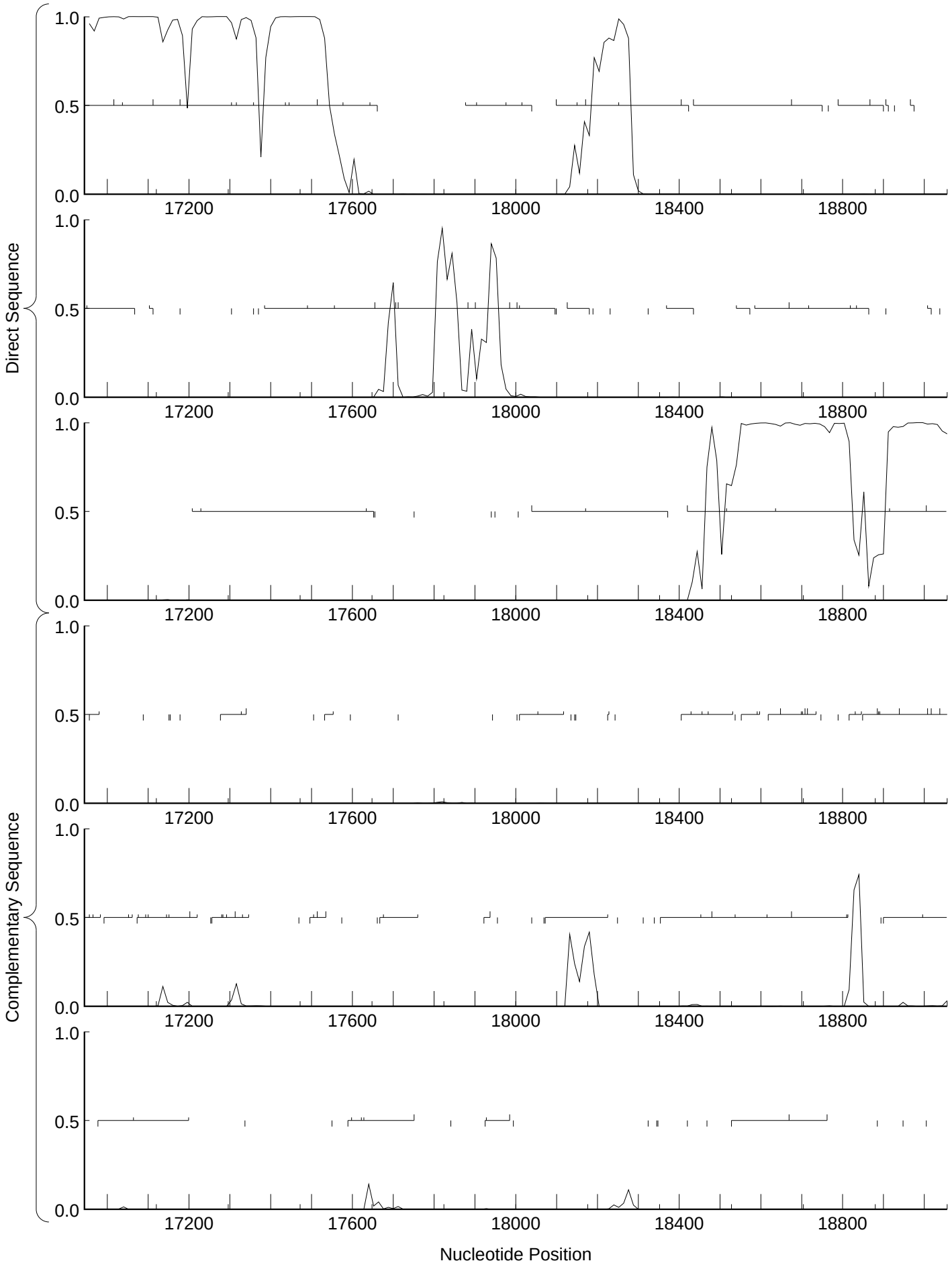
mplete sequence, 43764 bp including 13-base 3’ overhang (GCTTACCGTGATA), Cluster AK, Order 4, Window 96, Step 12, 8/22



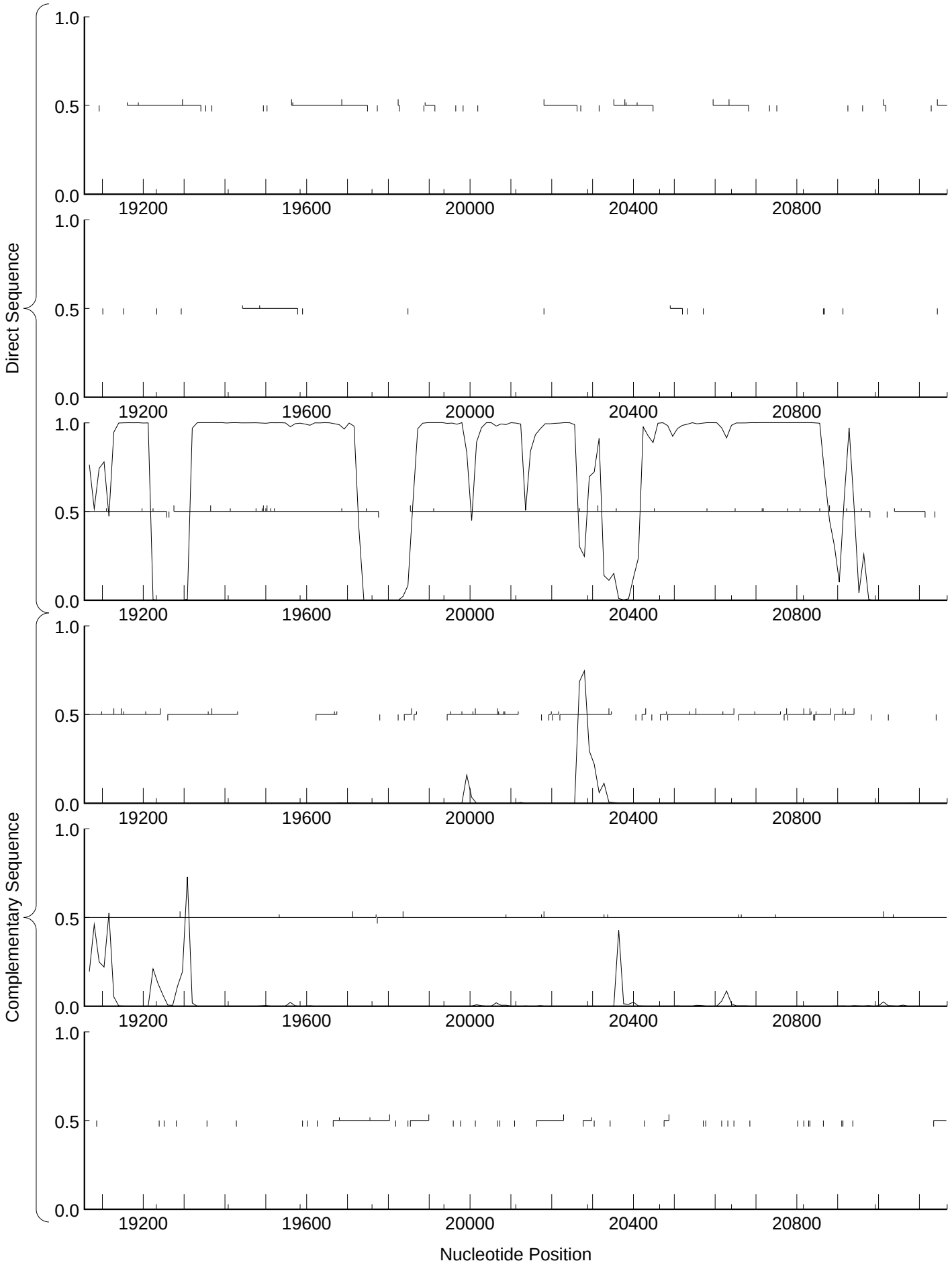
mplete sequence, 43764 bp including 13-base 3’ overhang (GCTTACCGTGATA), Cluster AK, Order 4, Window 96, Step 12, 9/22



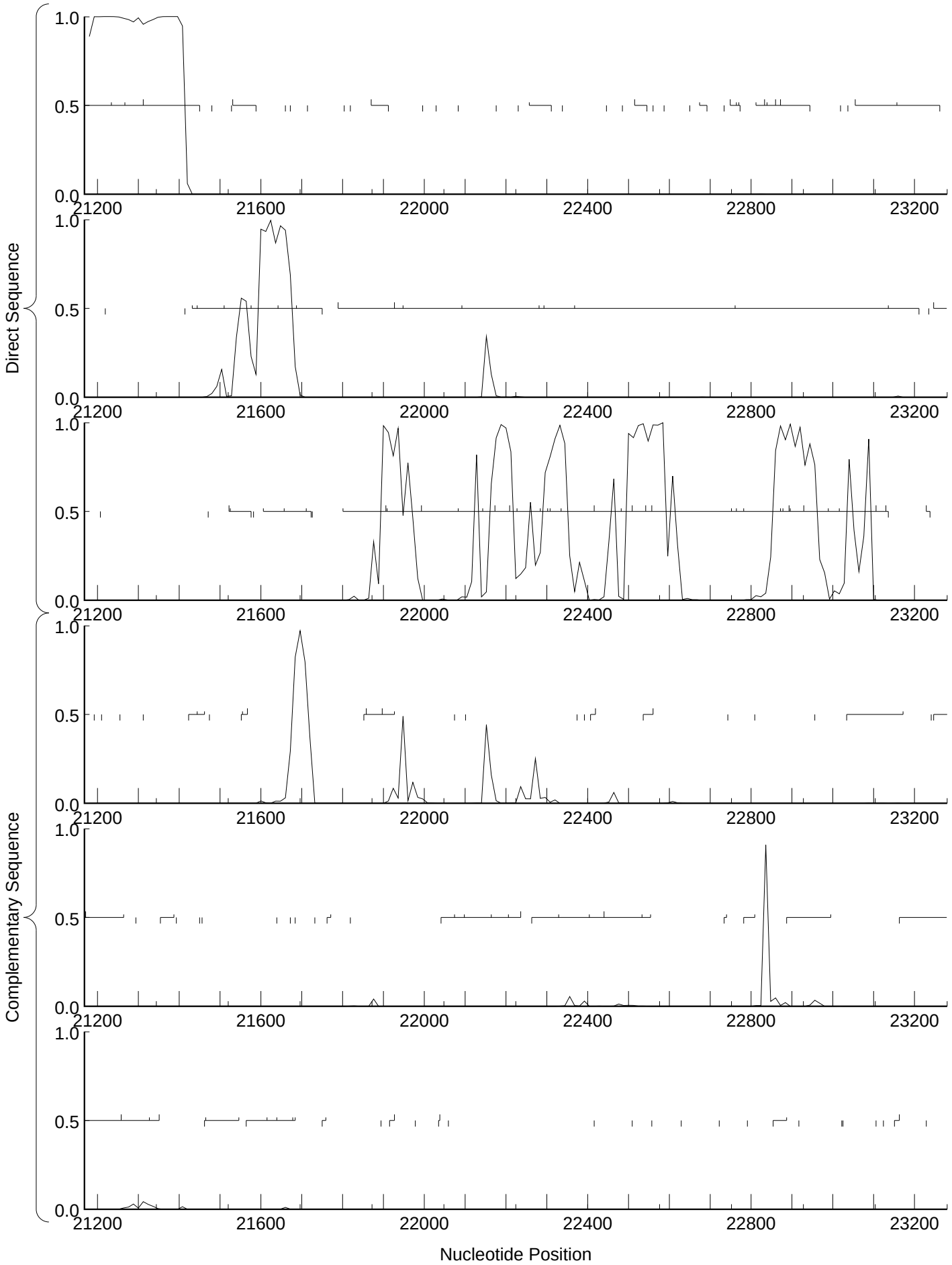
nplete sequence, 43764 bp including 13-base 3' overhang (GCTTACCGTGATA), Cluster AK, Order 4, Window 96, Step 12, 10/22



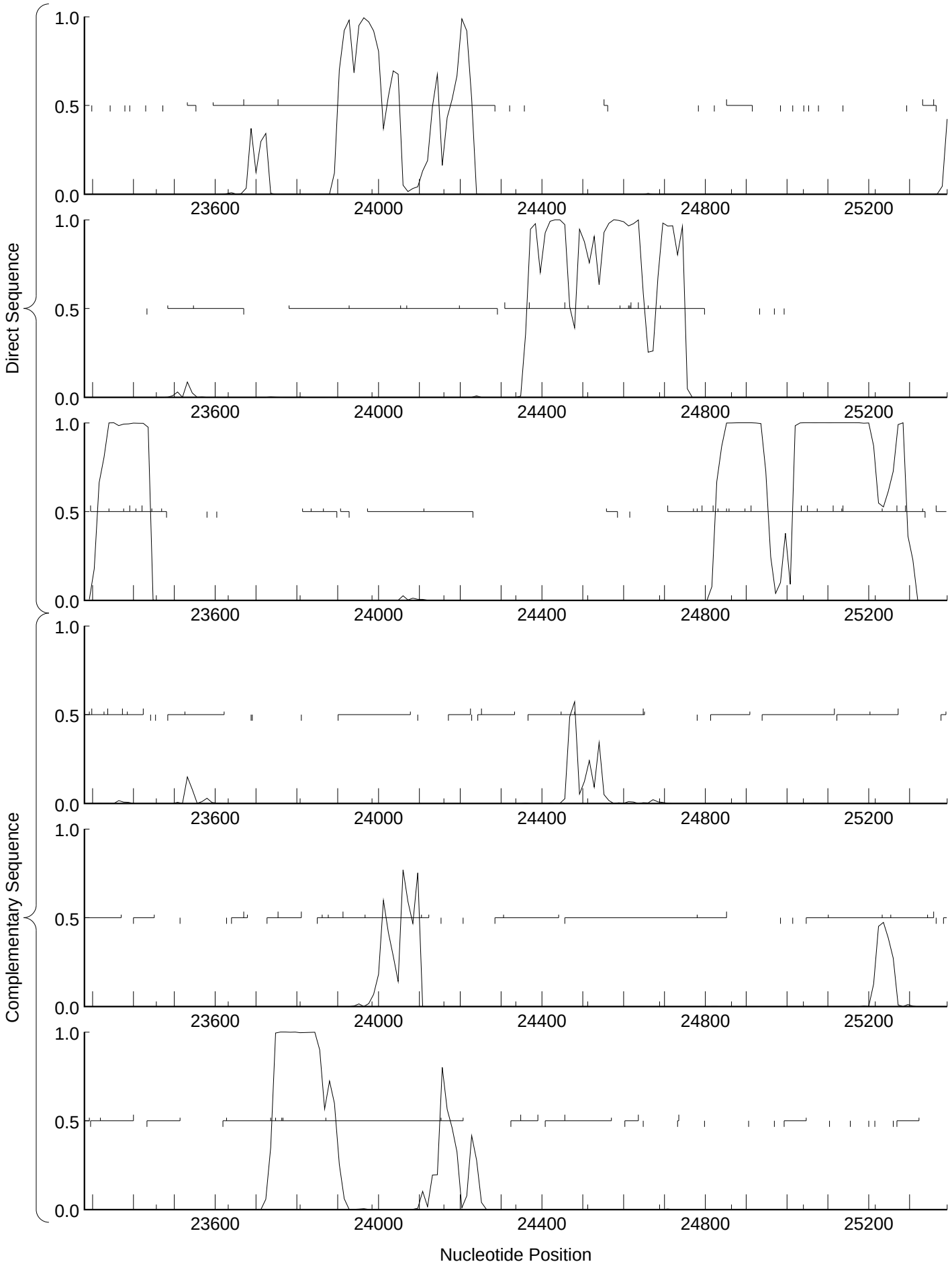
nplete sequence, 43764 bp including 13-base 3’ overhang (GCTTACCGTGATA), Cluster AK, Order 4, Window 96, Step 12, 11/22



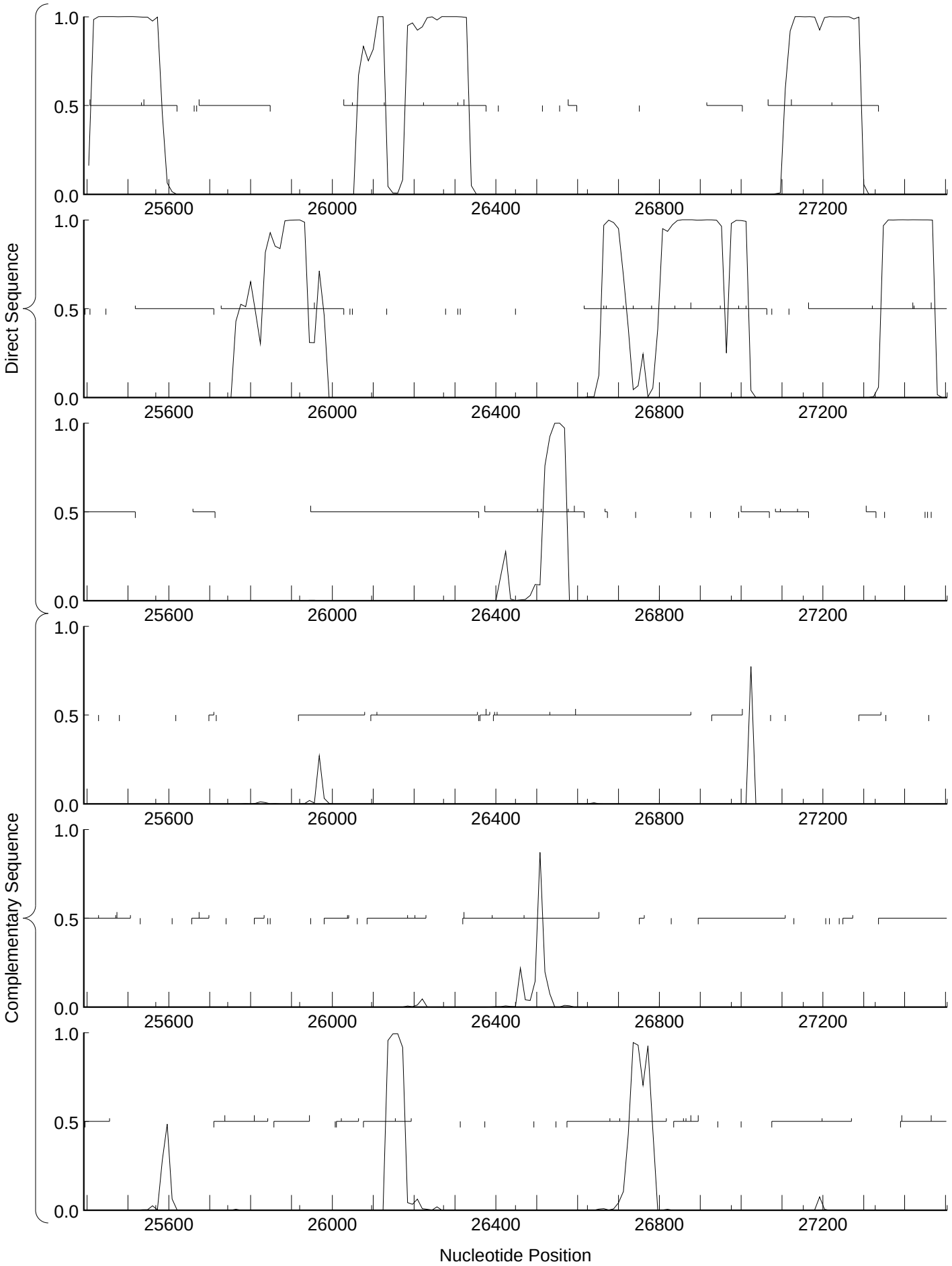
nplete sequence, 43764 bp including 13-base 3’ overhang (GCTTACCGTGATA), Cluster AK, Order 4, Window 96, Step 12, 12/22



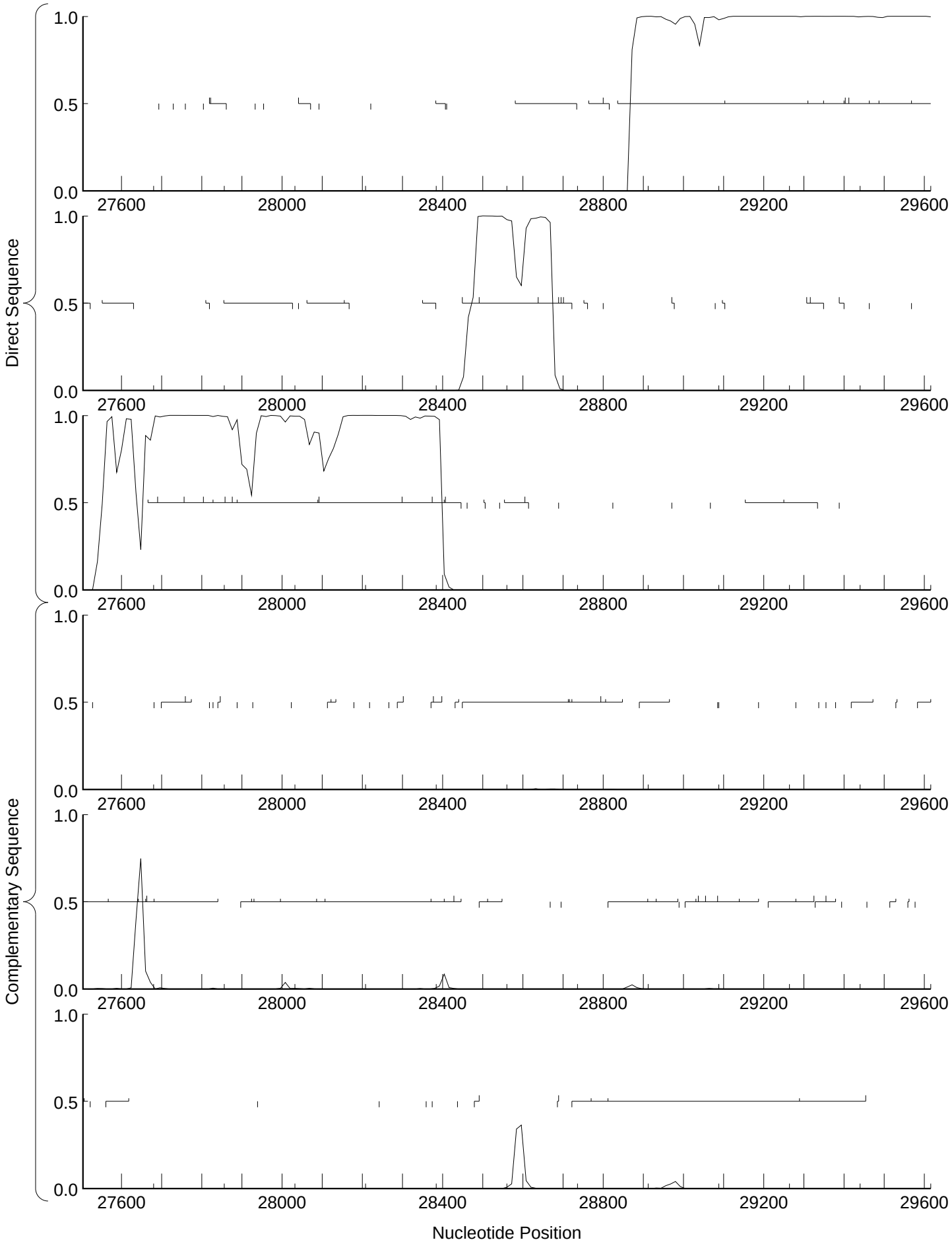
nplete sequence, 43764 bp including 13-base 3’ overhang (GCTTACCGTGATA), Cluster AK, Order 4, Window 96, Step 12, 13/22



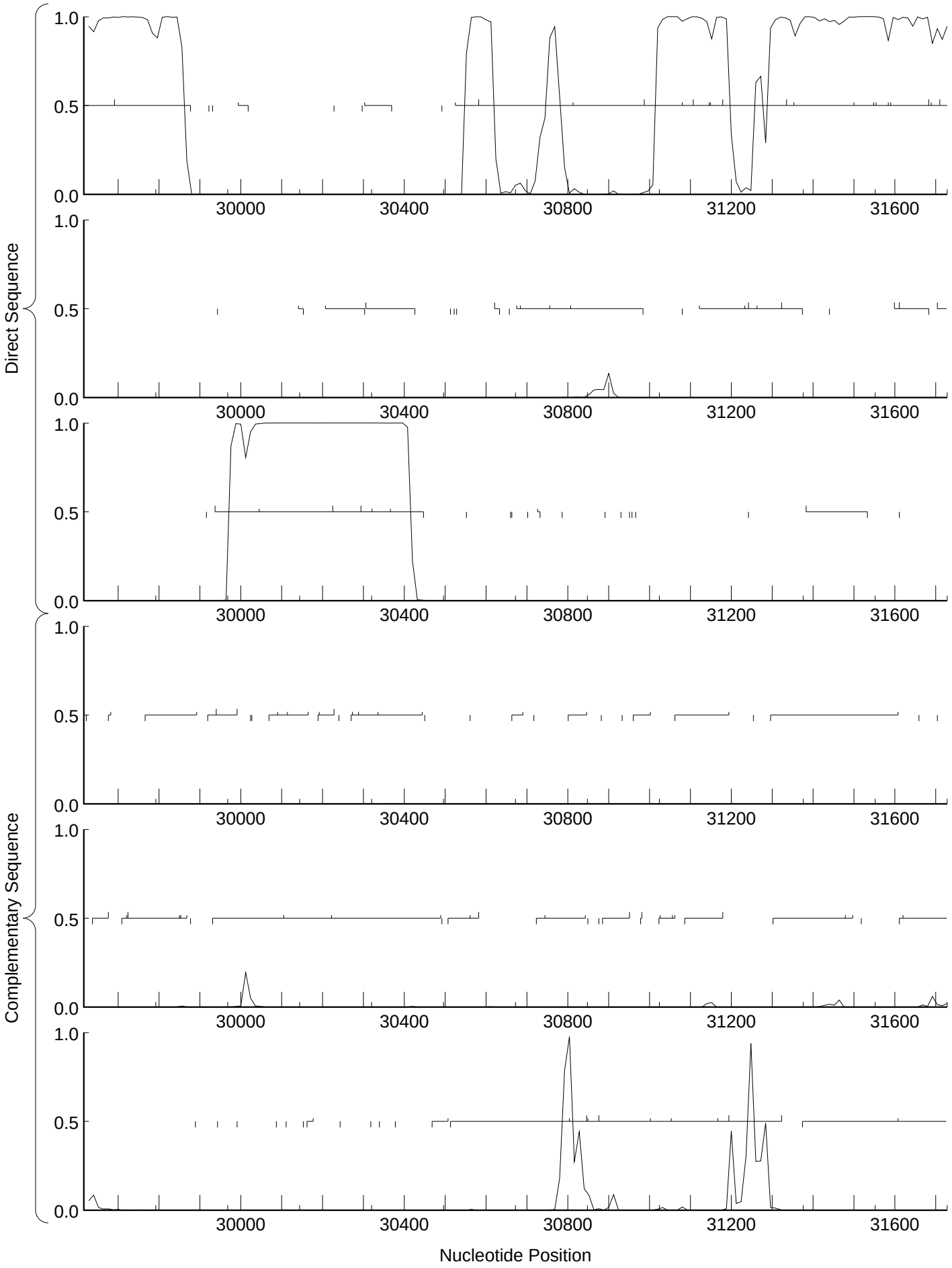
nplete sequence, 43764 bp including 13-base 3' overhang (GCTTACCGTGATA), Cluster AK, Order 4, Window 96, Step 12, 14/22



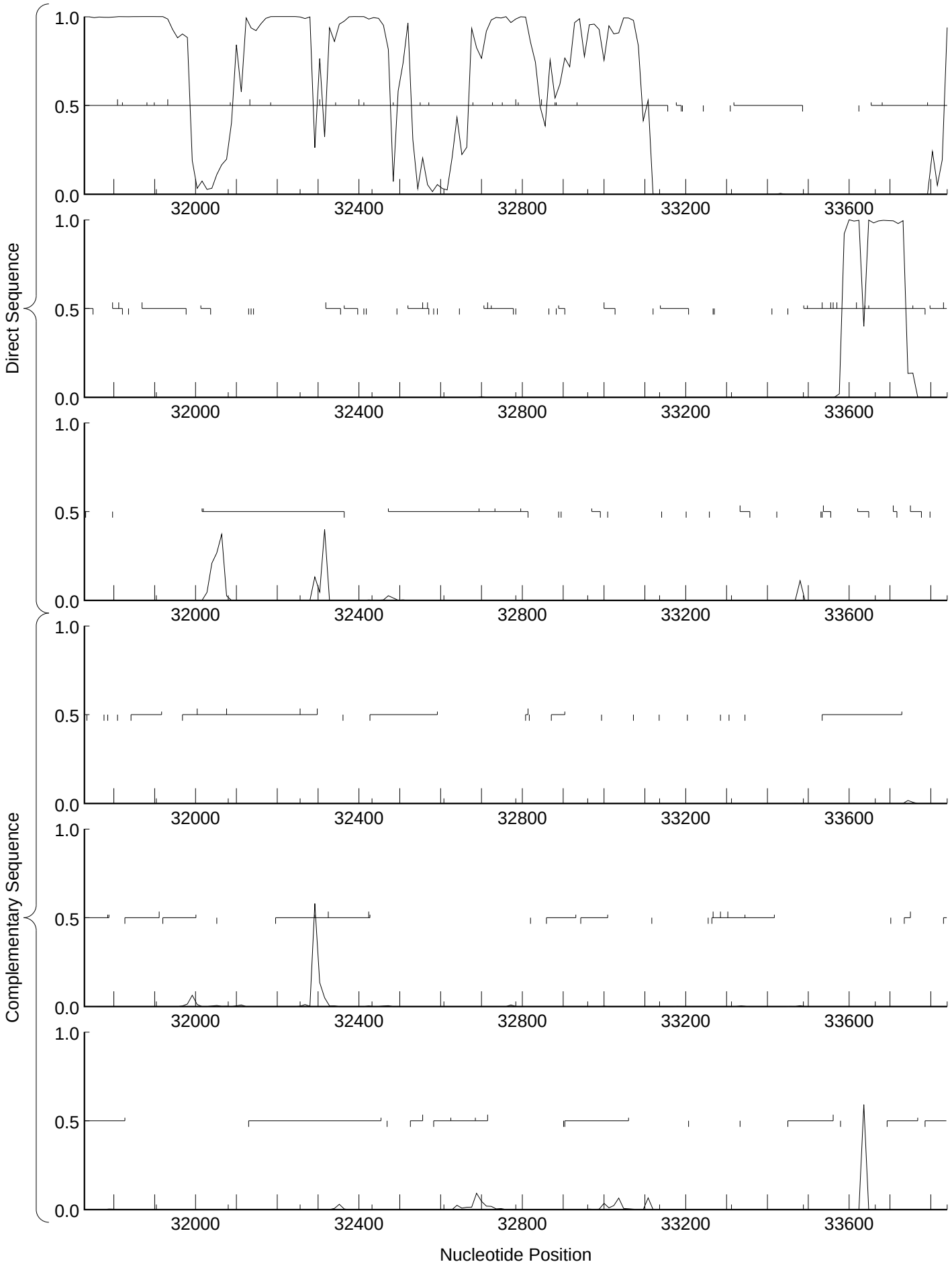
nplete sequence, 43764 bp including 13-base 3’ overhang (GCTTACCGTGATA), Cluster AK, Order 4, Window 96, Step 12, 15/22

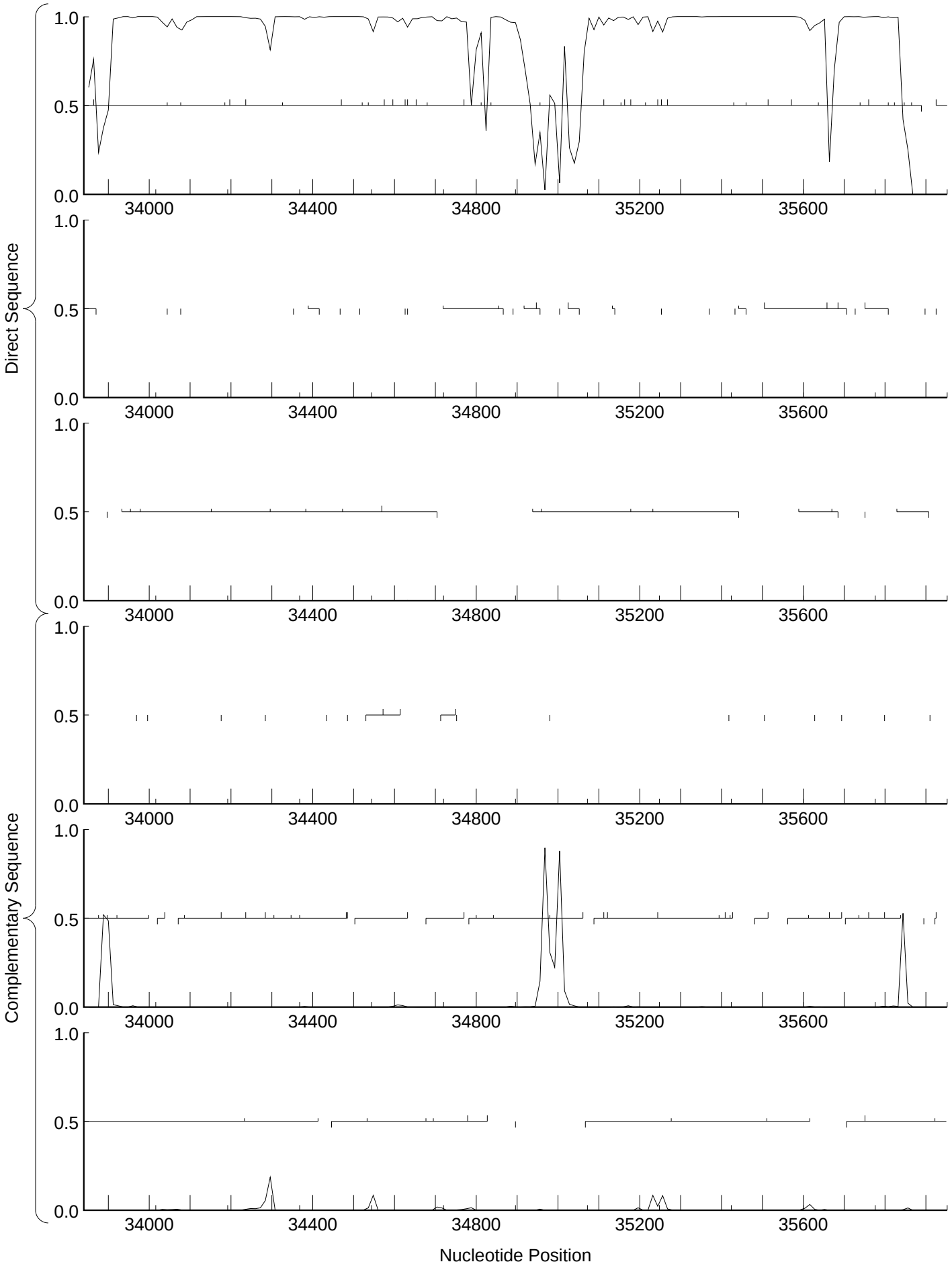


nplete sequence, 43764 bp including 13-base 3’ overhang (GCTTACCGTGATA), Cluster AK, Order 4, Window 96, Step 12, 16/22

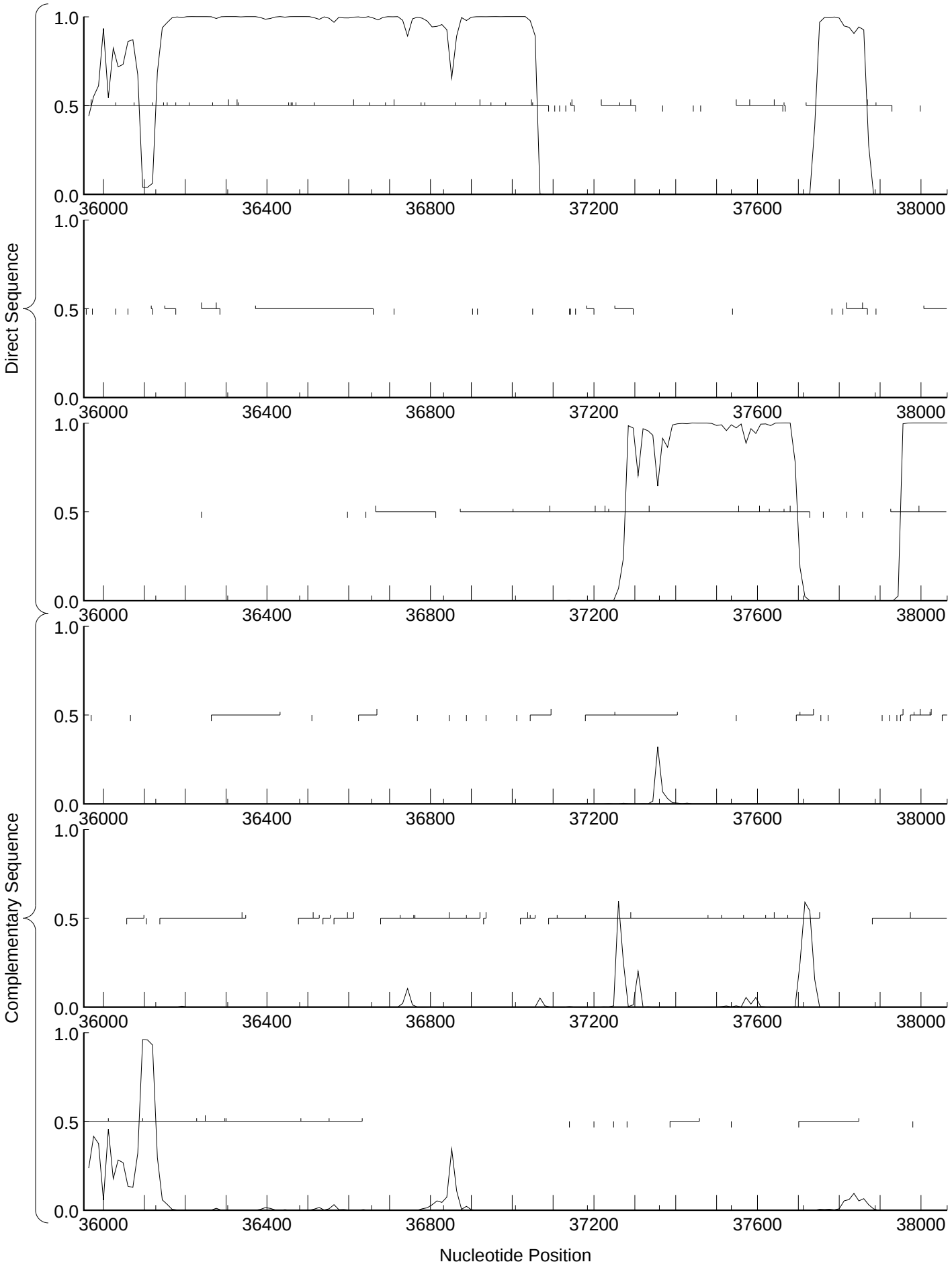


nplete sequence, 43764 bp including 13-base 3' overhang (GCTTACCGTGATA), Cluster AK, Order 4, Window 96, Step 12, 17/22

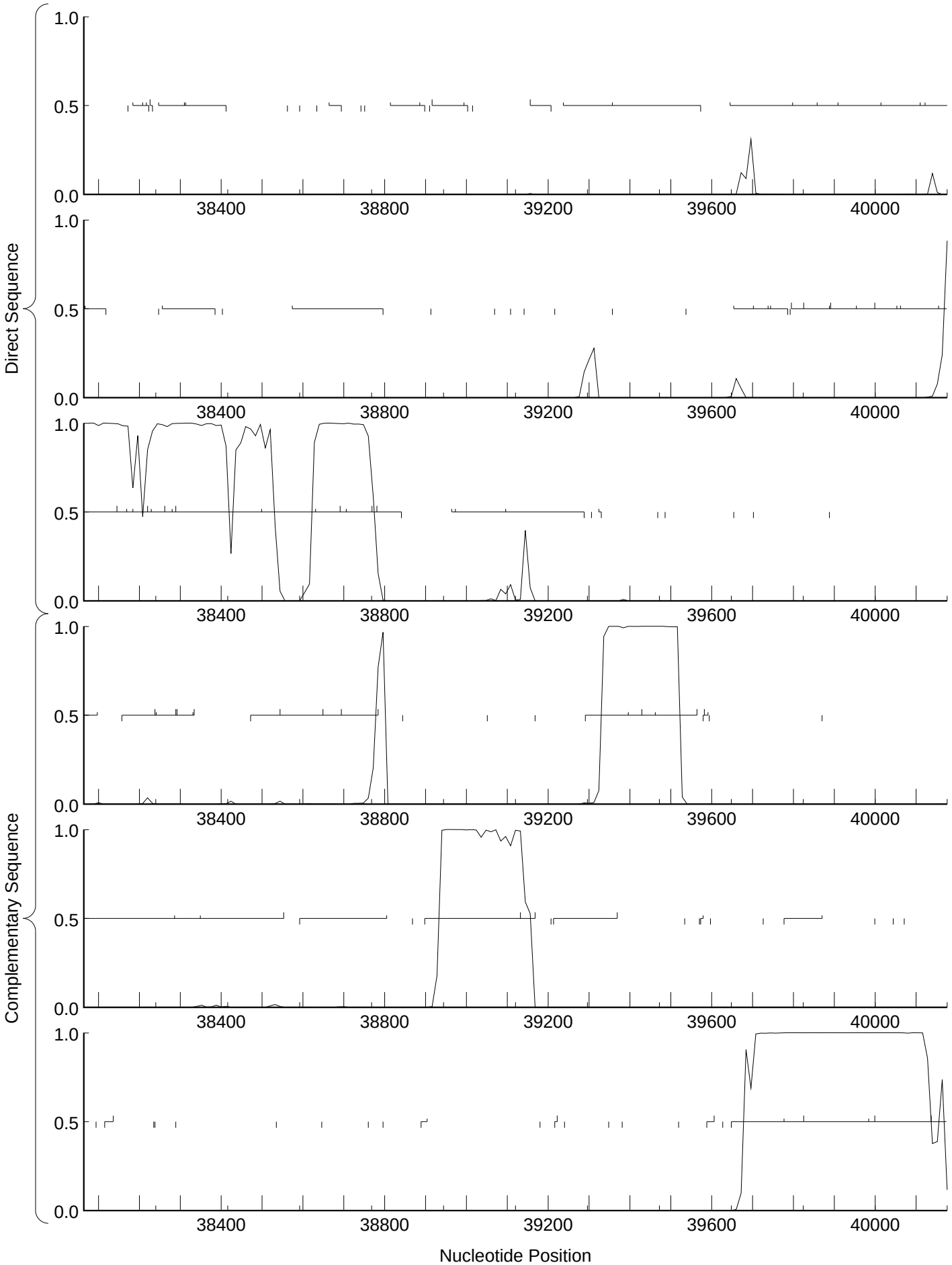



Direct Sequence
Complementary Sequence
1.0
0.5
0.0
34000
34400
34800
35200
35600
Nucleotide Position

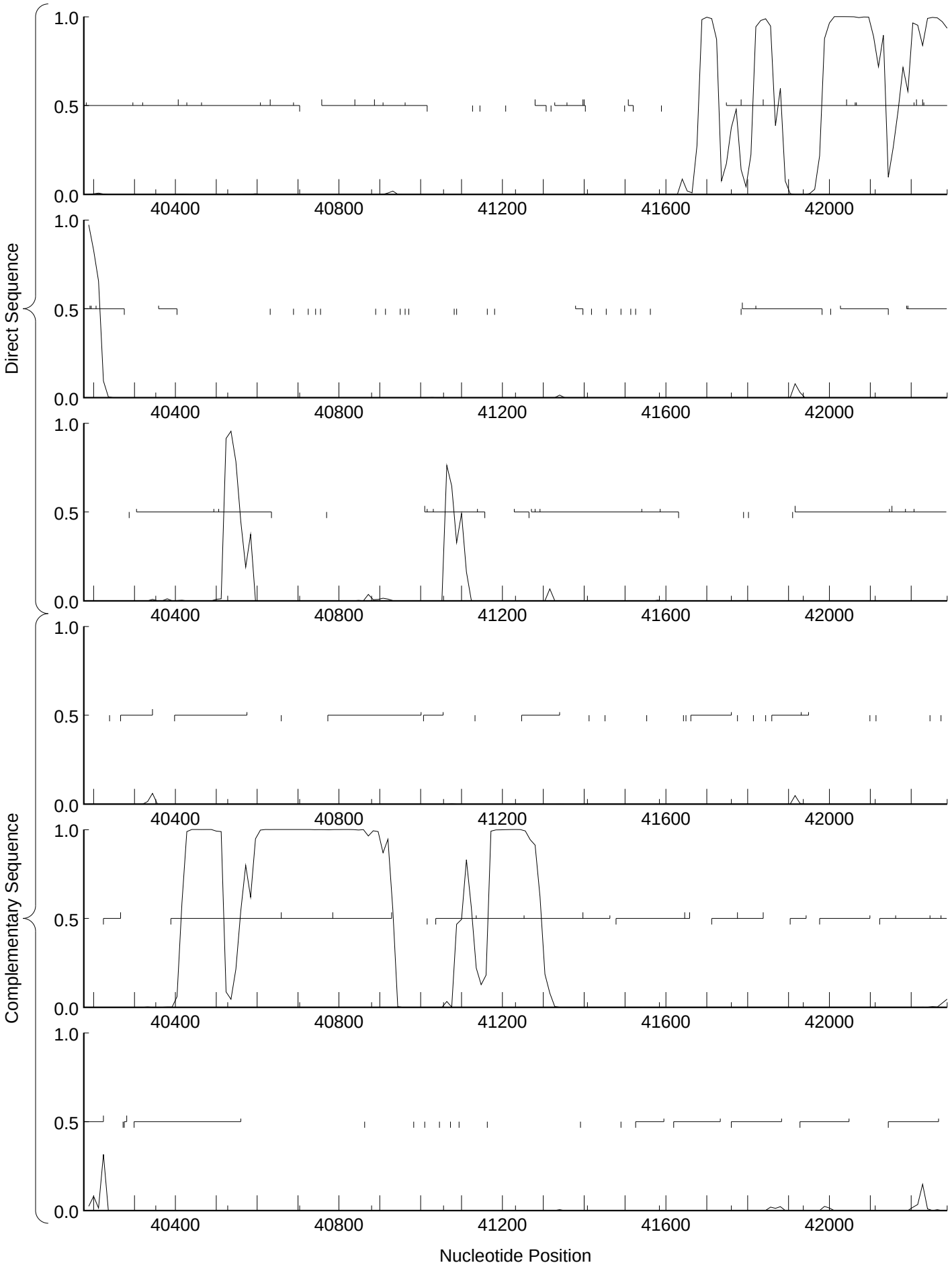
nplete sequence, 43764 bp including 13-base 3' overhang (GCTTACCGTGATA), Cluster AK, Order 4, Window 96, Step 12, 19/22



nplete sequence, 43764 bp including 13-base 3’ overhang (GCTTACCGTGATA), Cluster AK, Order 4, Window 96, Step 12, 20/22



nplete sequence, 43764 bp including 13-base 3’ overhang (GCTTACCGTGATA), Cluster AK, Order 4, Window 96, Step 12, 21/22



nplete sequence, 43764 bp including 13-base 3’ overhang (GCTTACCGTGATA), Cluster AK, Order 4, Window 96, Step 12, 22/22

