GeneMark

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

PROGRAM INFORMATION

```
Sequence         :  Mycobacterium phage ChipMunk complete sequence, 53932 bp including 10-base 3’ overhang (CGG
Analysis Date    :  3/29/24 at 7:43:25
Pages            :  27
Sequence Length  :  53932 bp
GC Content       :   63.06%

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

PS-Version       :  1.2

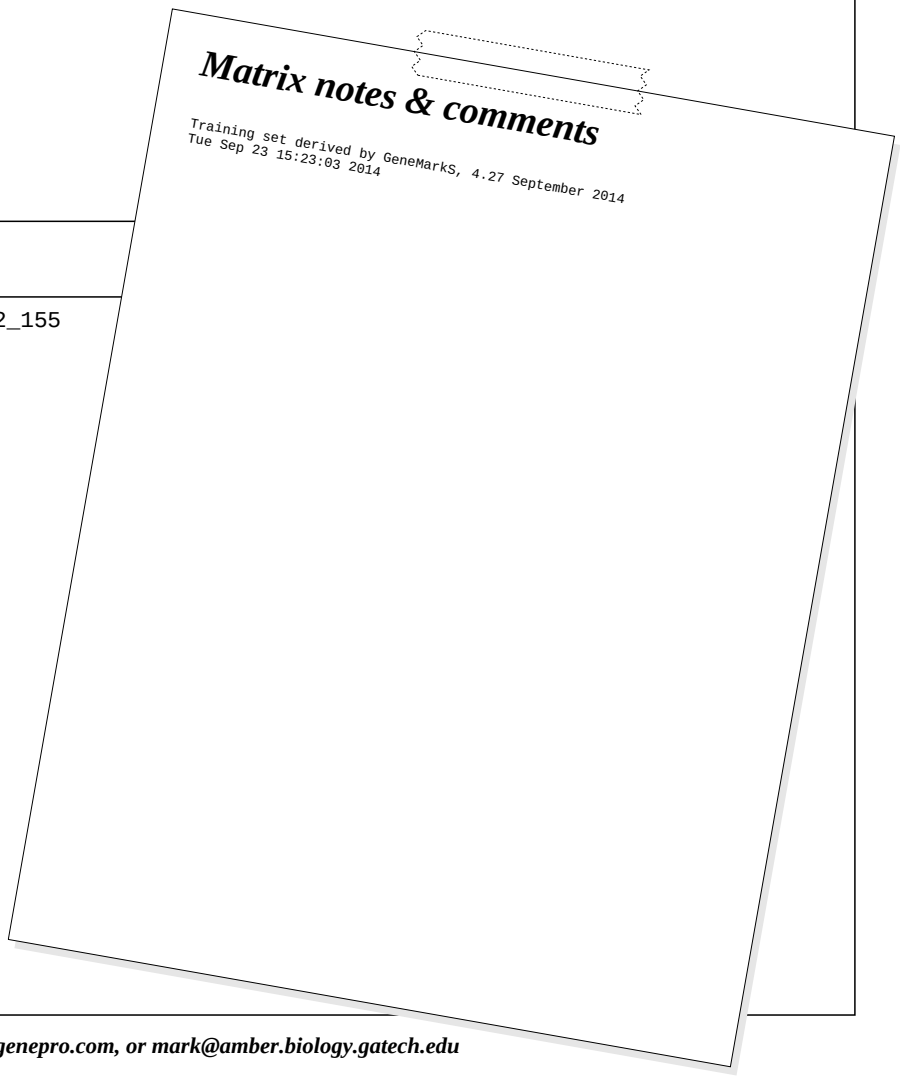
GeneMark Options :  PostScript graph,
                    Mark ORFs / splice sites,
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                    List regions and/or splice sites,
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MATRIX INFORMATION

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Matrix     :  Mycobacterium_smegmatis_MC2_155
Author     :  -

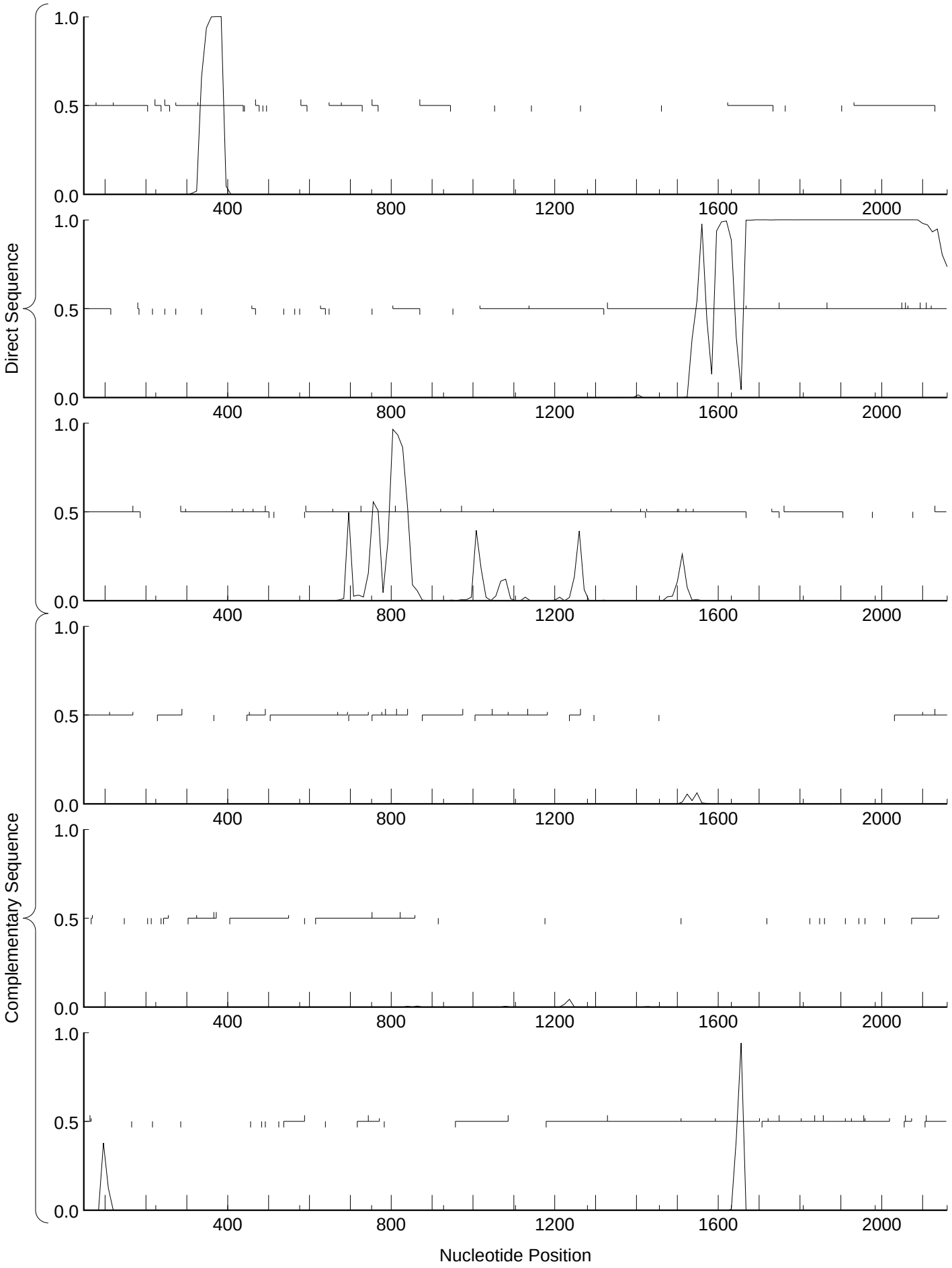
Order      :  4


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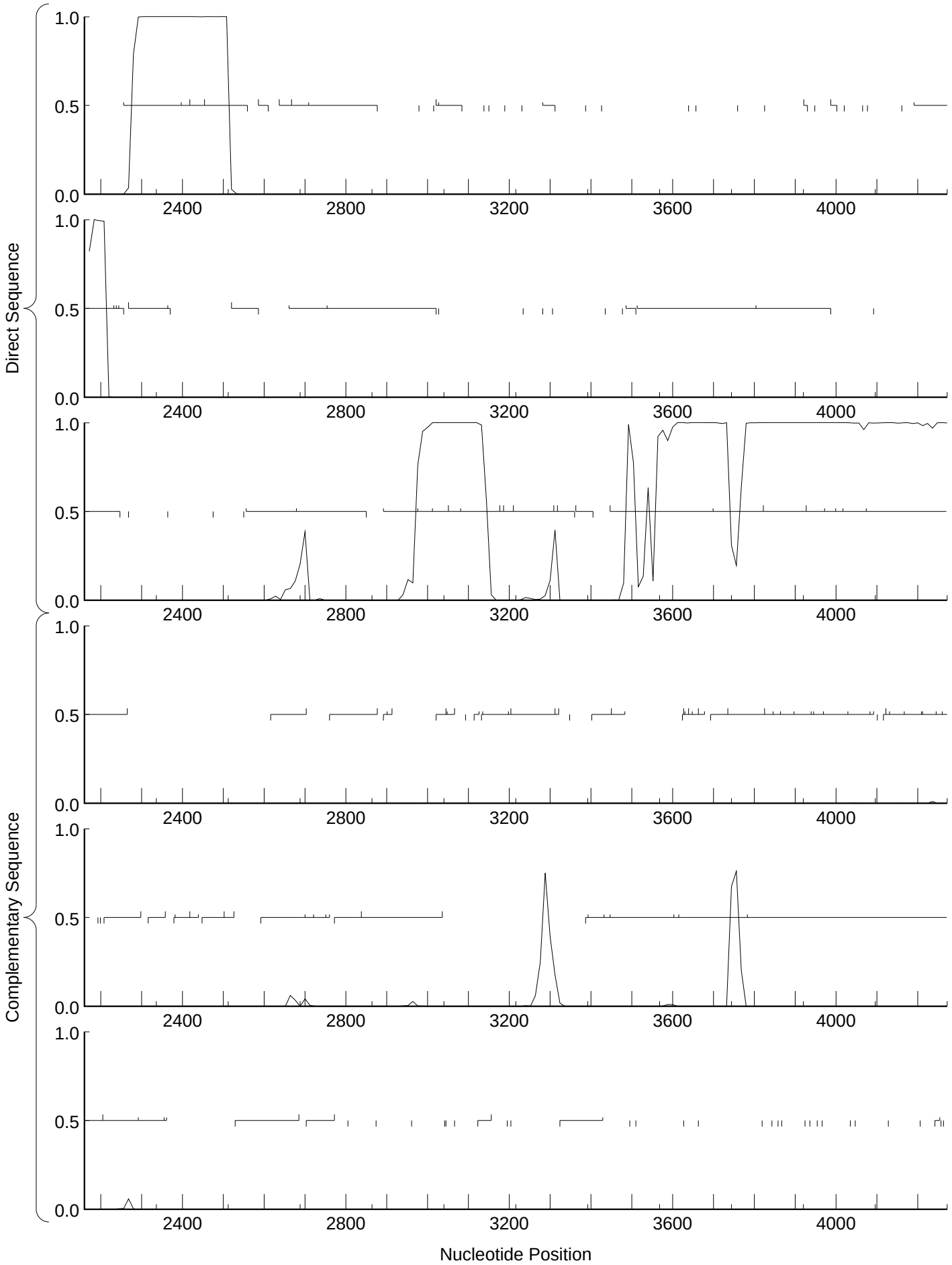


For help or information, send electronic mail to: custserv@genepro.com, or mark@amber.biology.gatech.edu

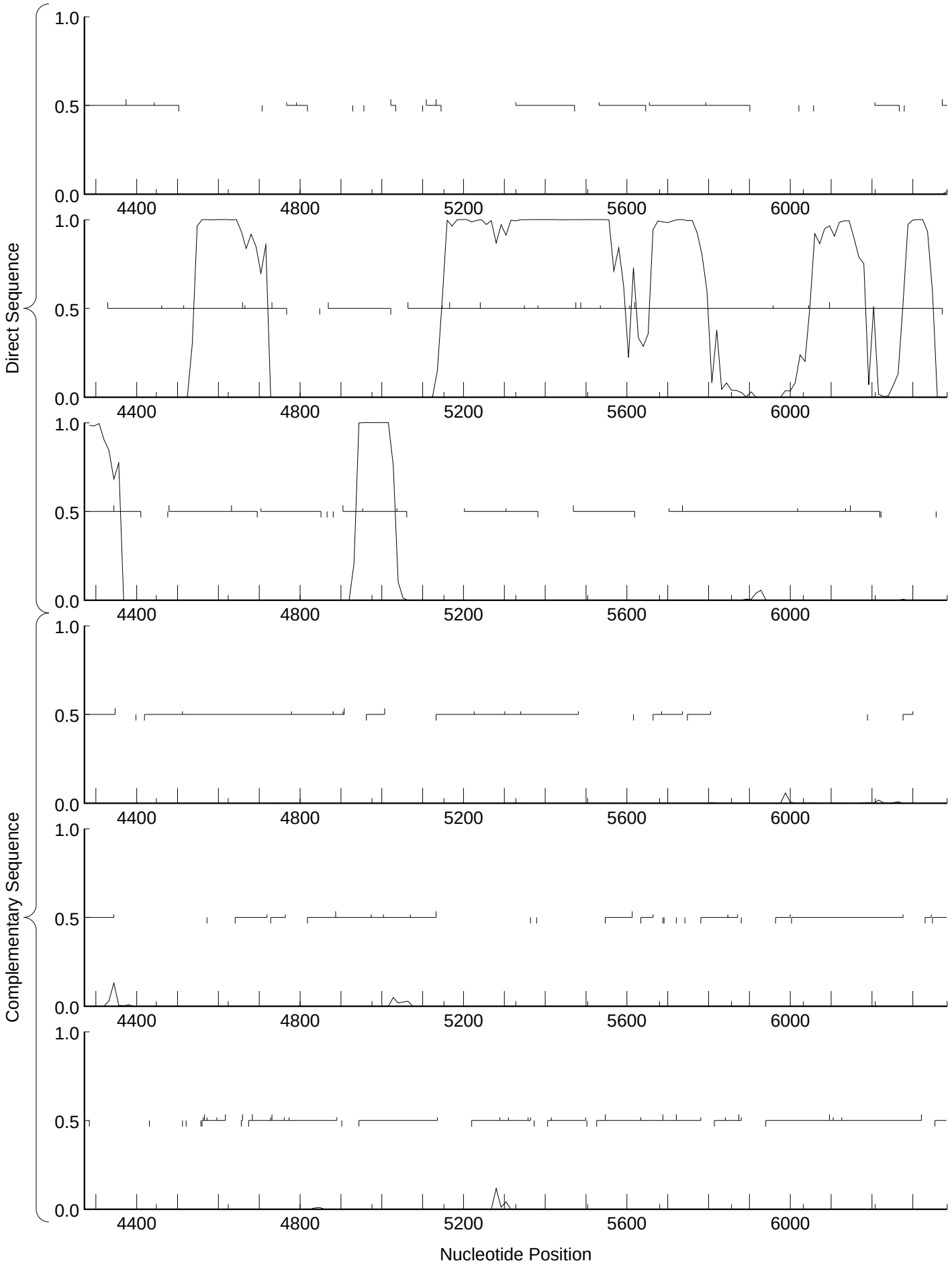
nk complete sequence, 53932 bp including 10-base 3’ overhang (CGGTCGGTTA), Cluster A2, Order 4, Window 96, Step 12, 2/27



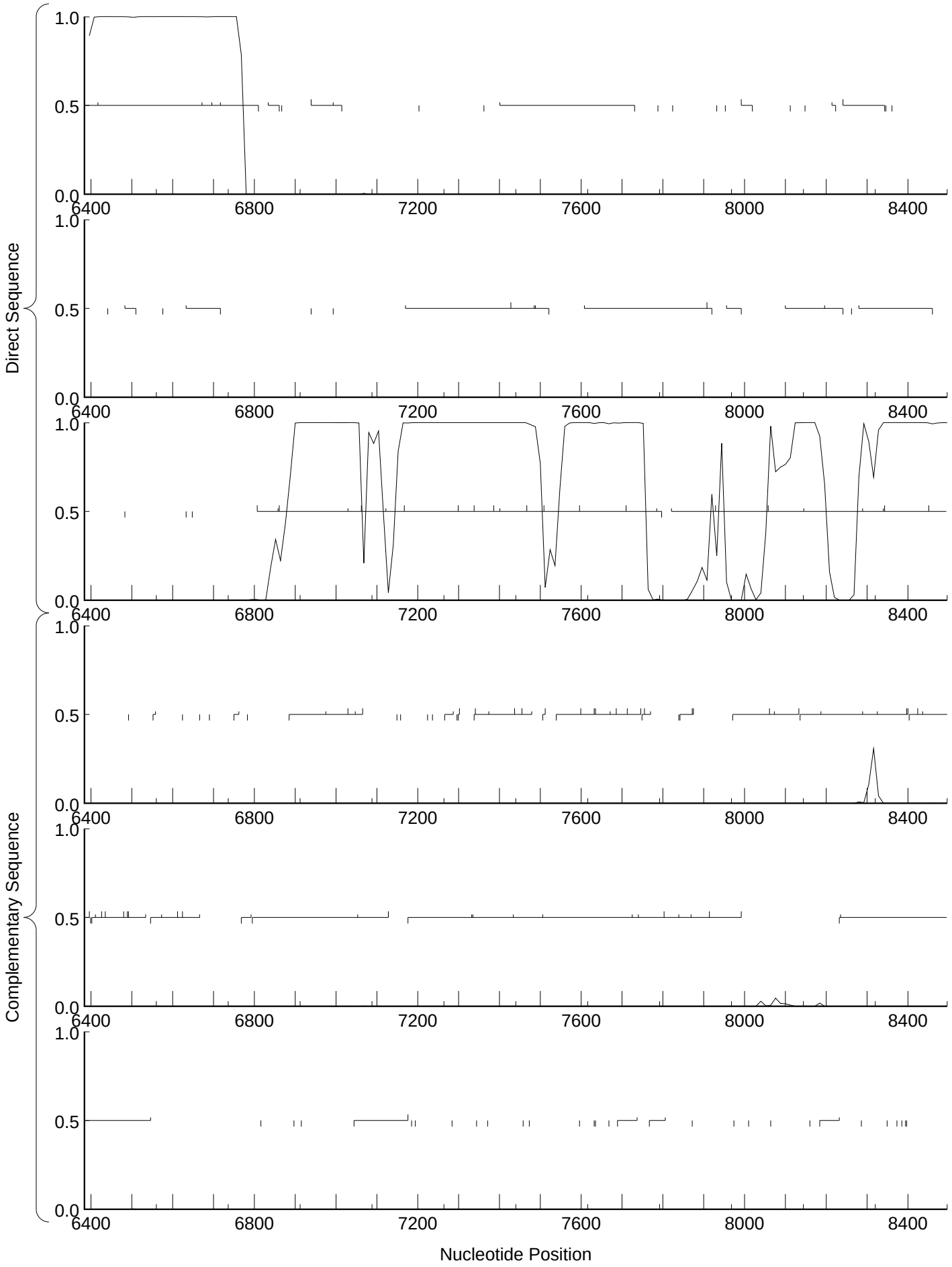
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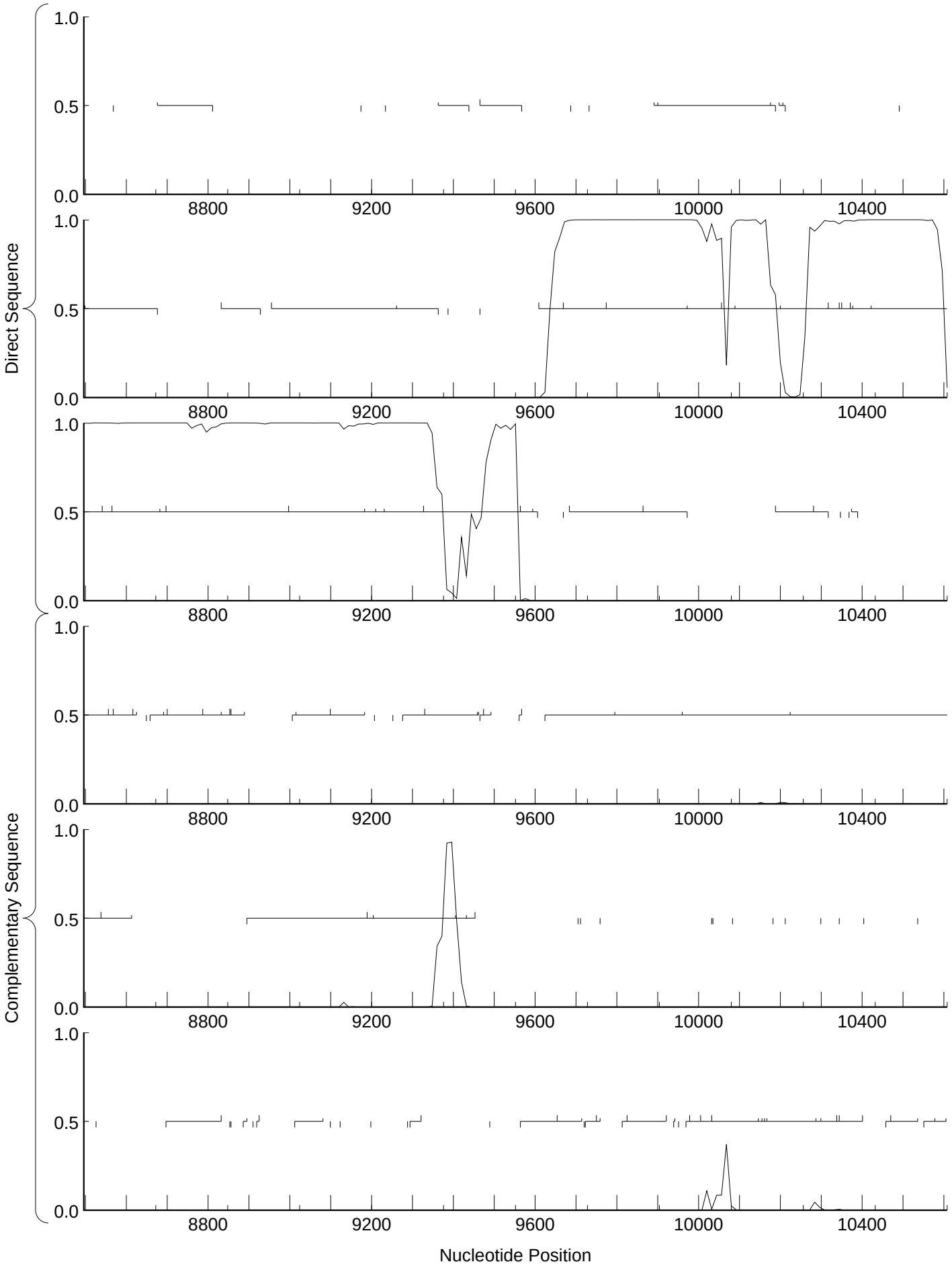
nk complete sequence, 53932 bp including 10-base 3’ overhang (CGGTCGGTTA), Cluster A2, Order 4, Window 96, Step 12, 4/27



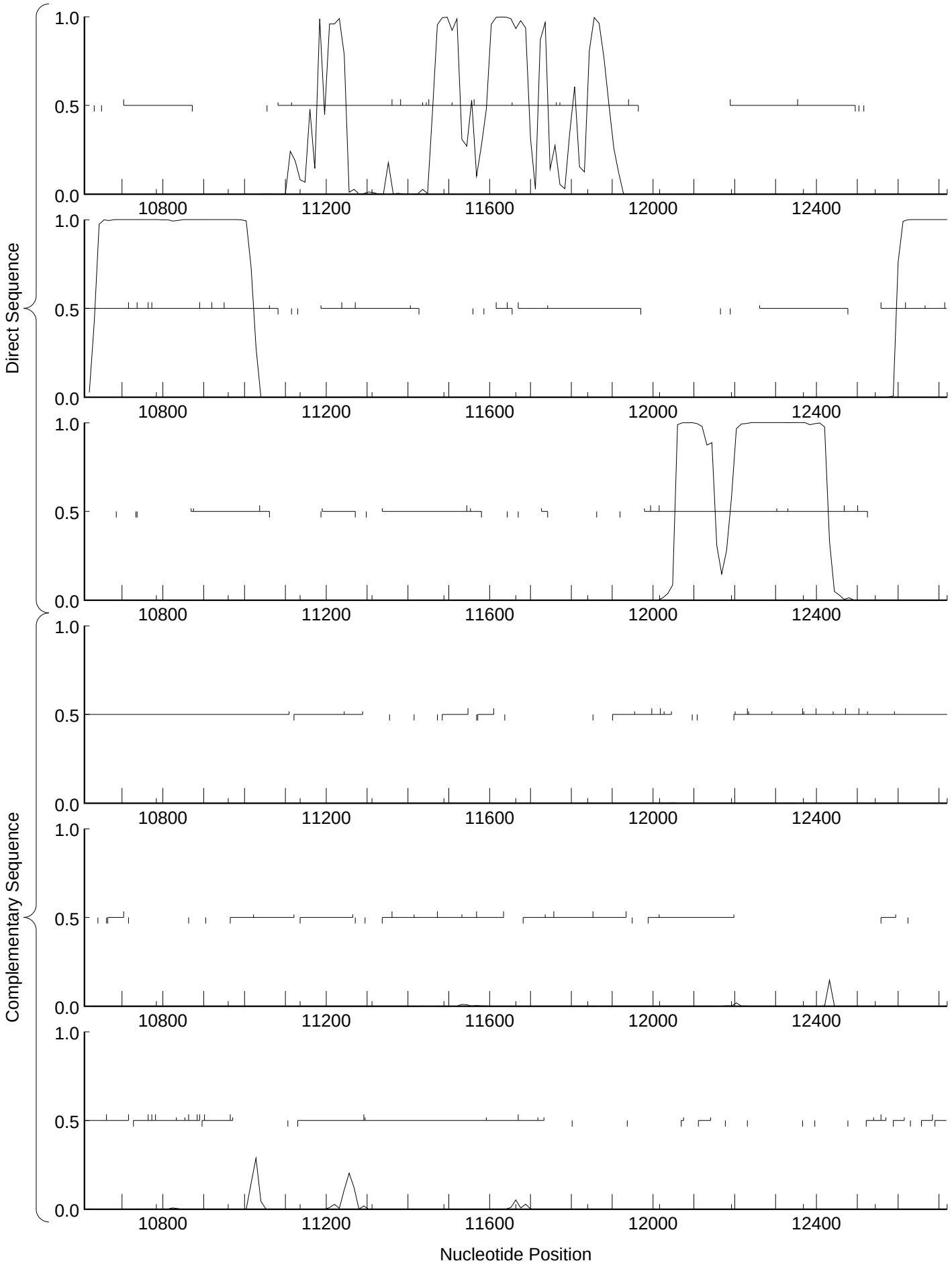
nk complete sequence, 53932 bp including 10-base 3’ overhang (CGGTCGGTTA), Cluster A2, Order 4, Window 96, Step 12, 5/27



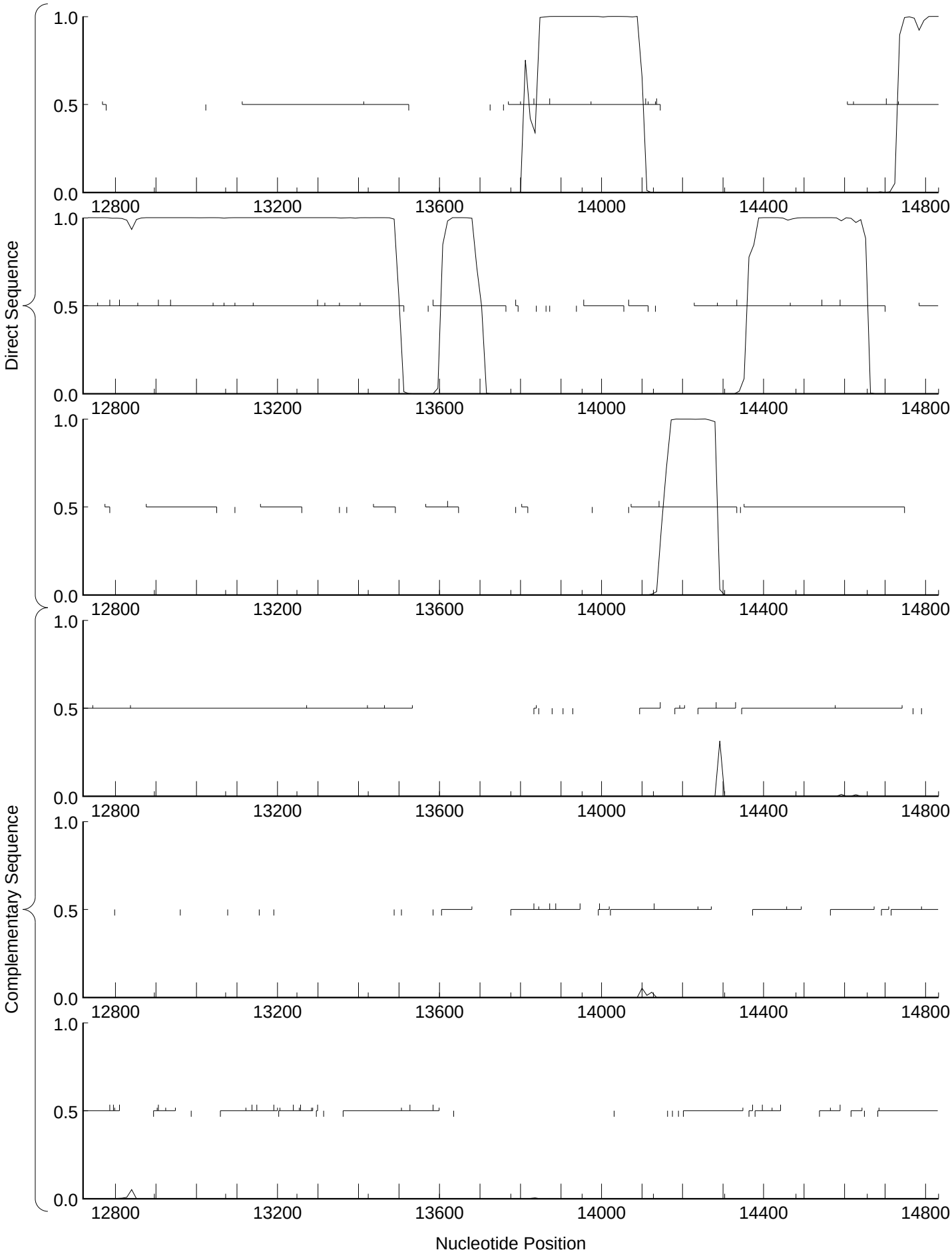
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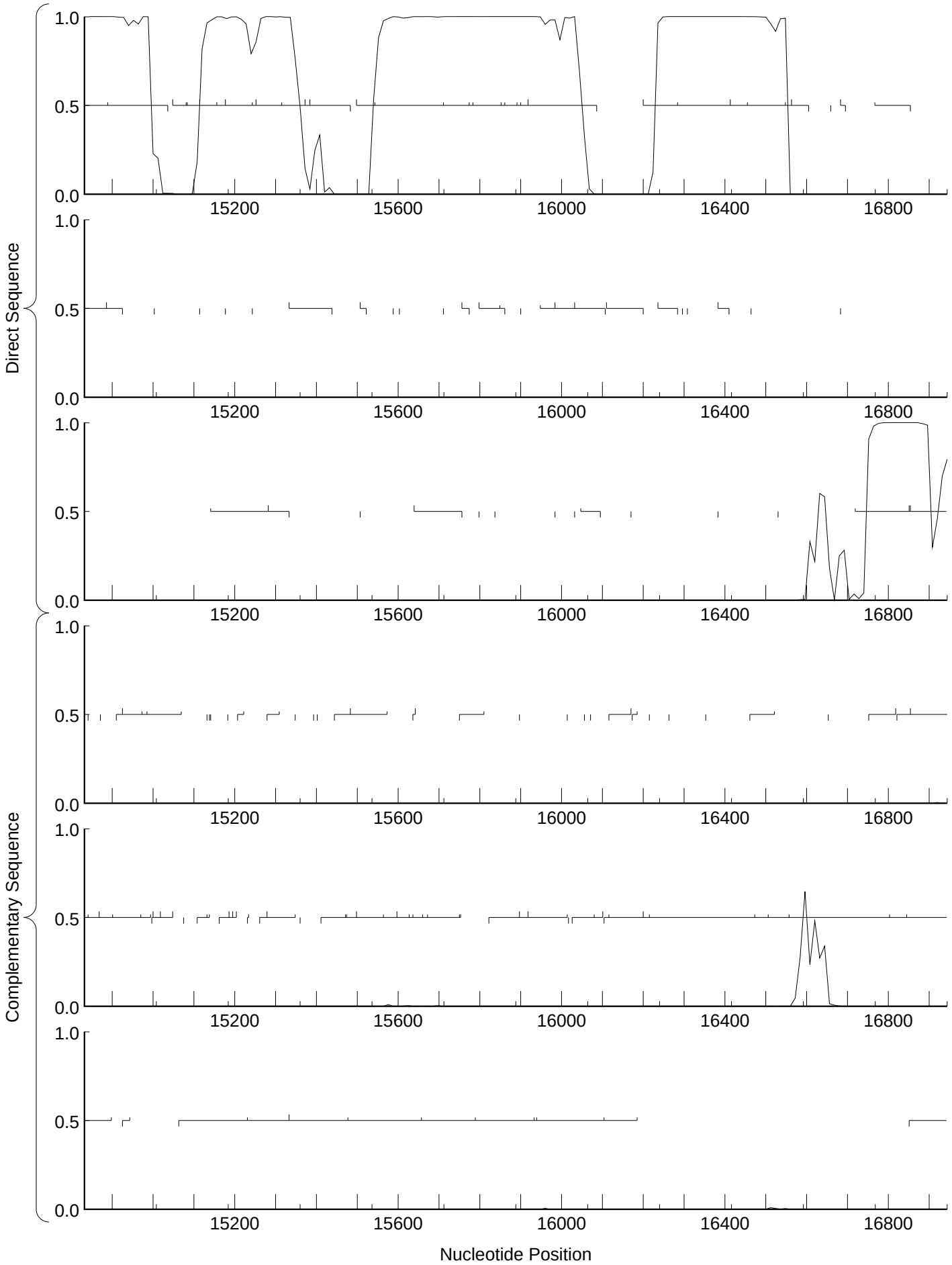
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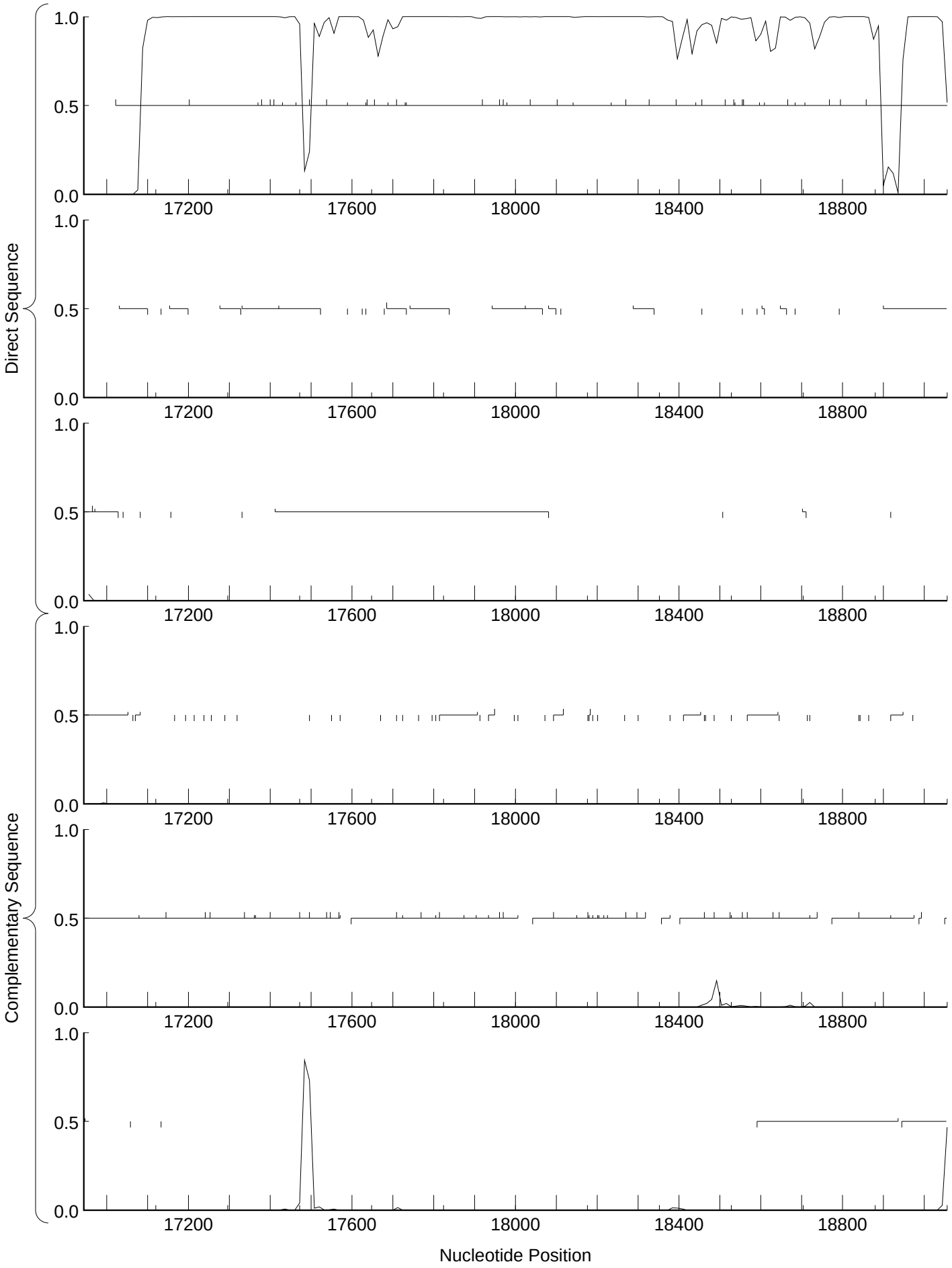


nk complete sequence, 53932 bp including 10-base 3’ overhang (CGGTCGGTTA), Cluster A2, Order 4, Window 96, Step 12, 8/27

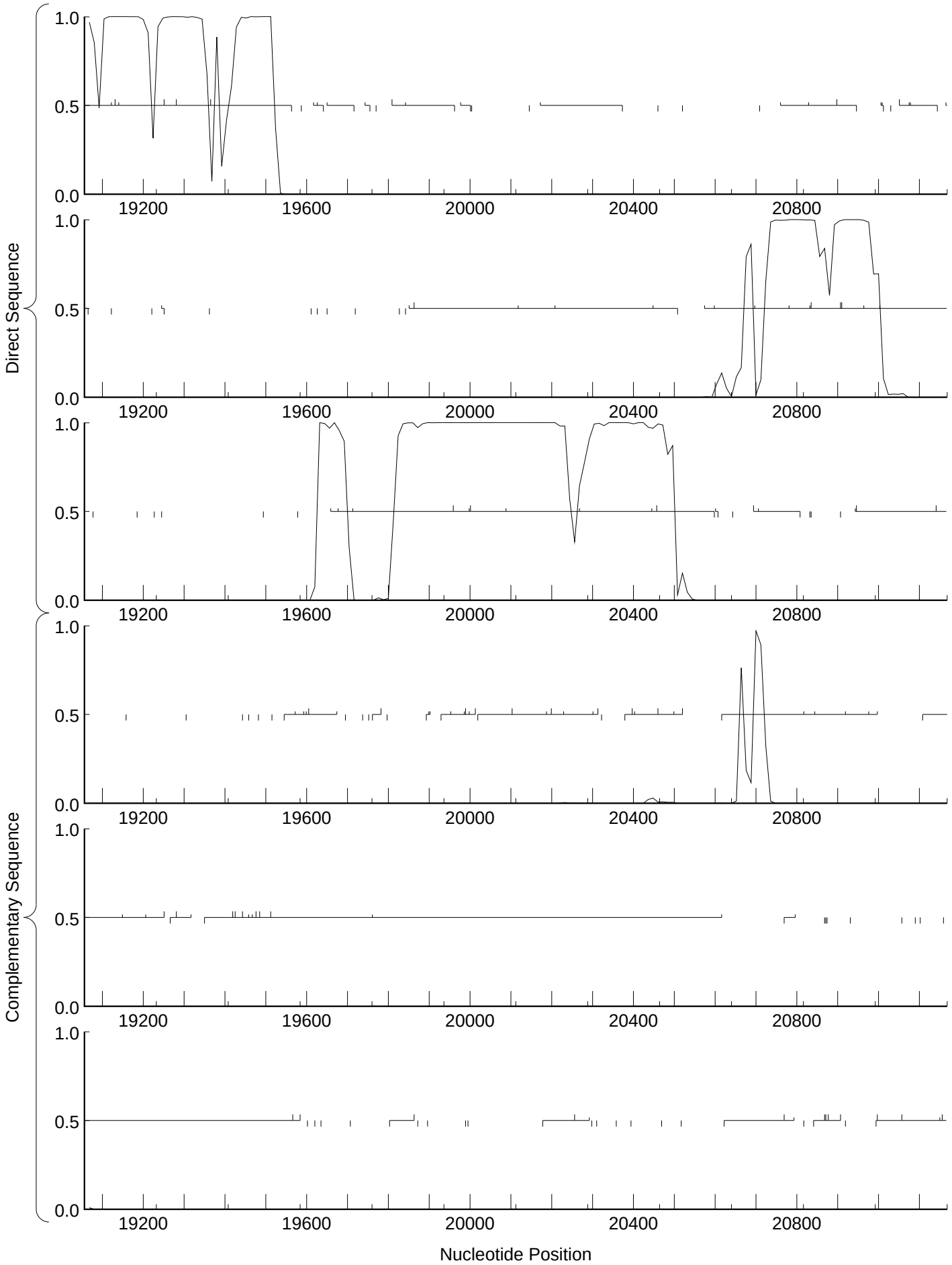


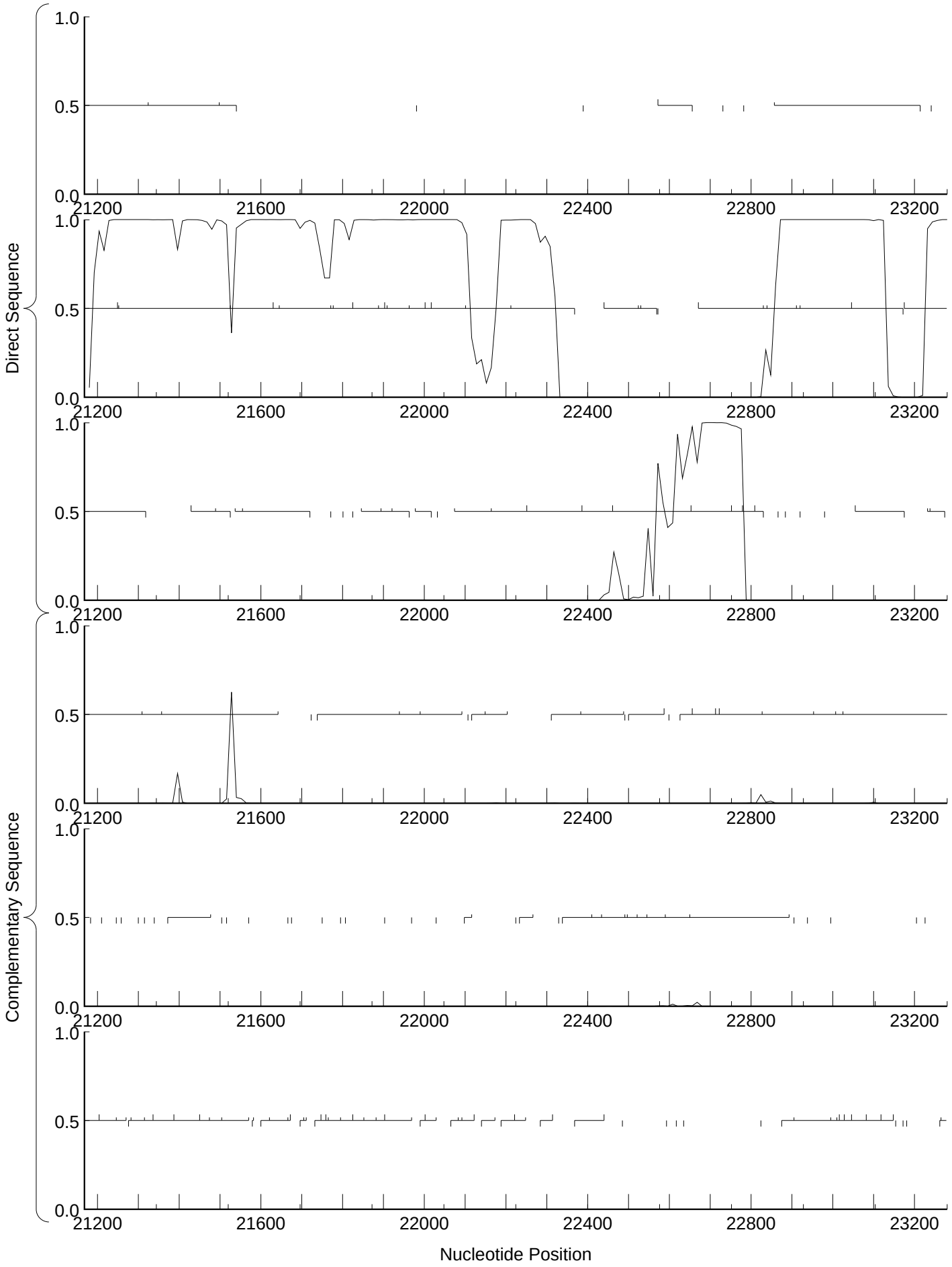
nk complete sequence, 53932 bp including 10-base 3’ overhang (CGGTCGGTTA), Cluster A2, Order 4, Window 96, Step 12, 9/27

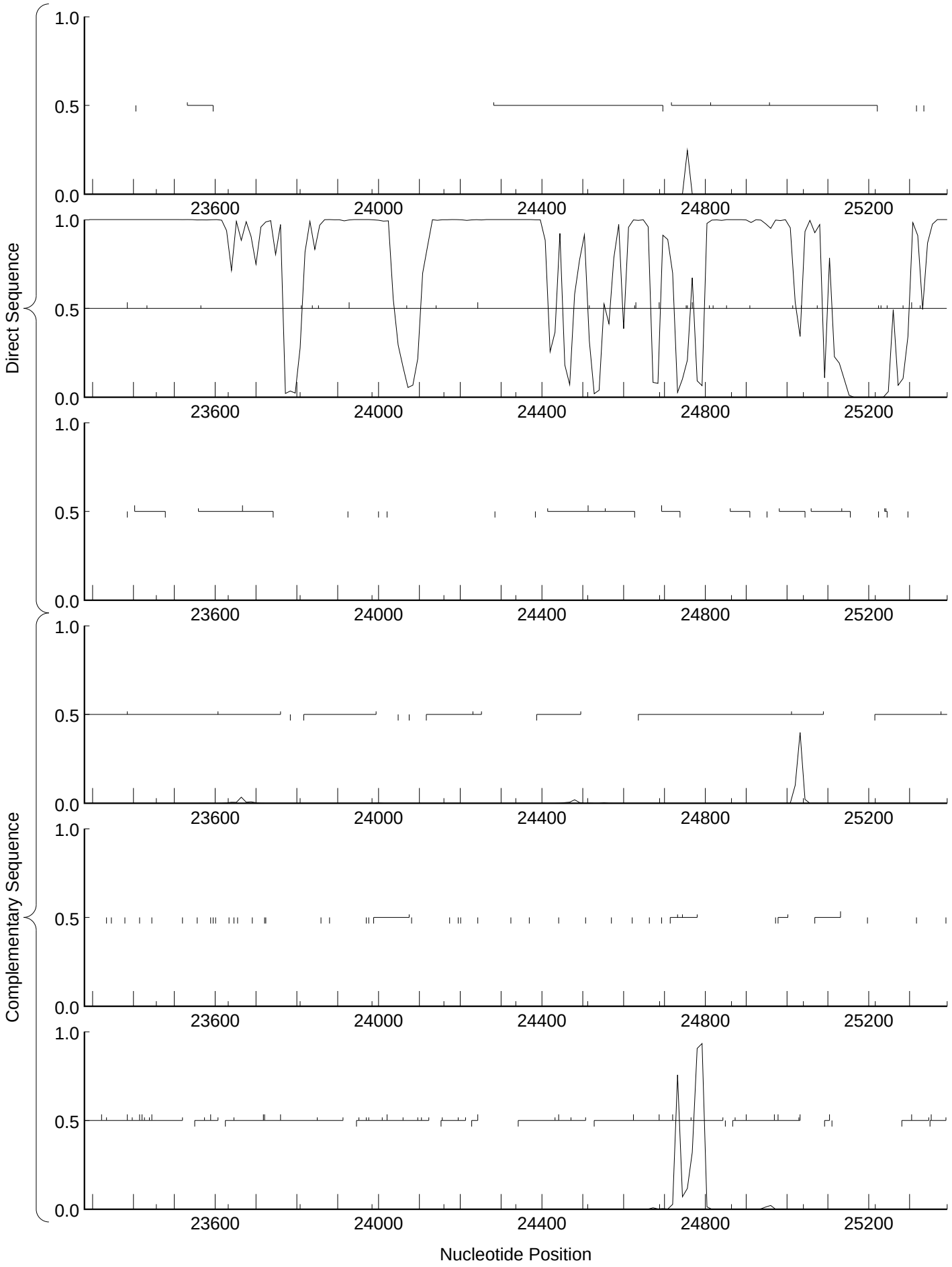



Direct Sequence
Complementary Sequence
1.0
0.5
0.0
17200
17600
18000
18400
18800
Nucleotide Position

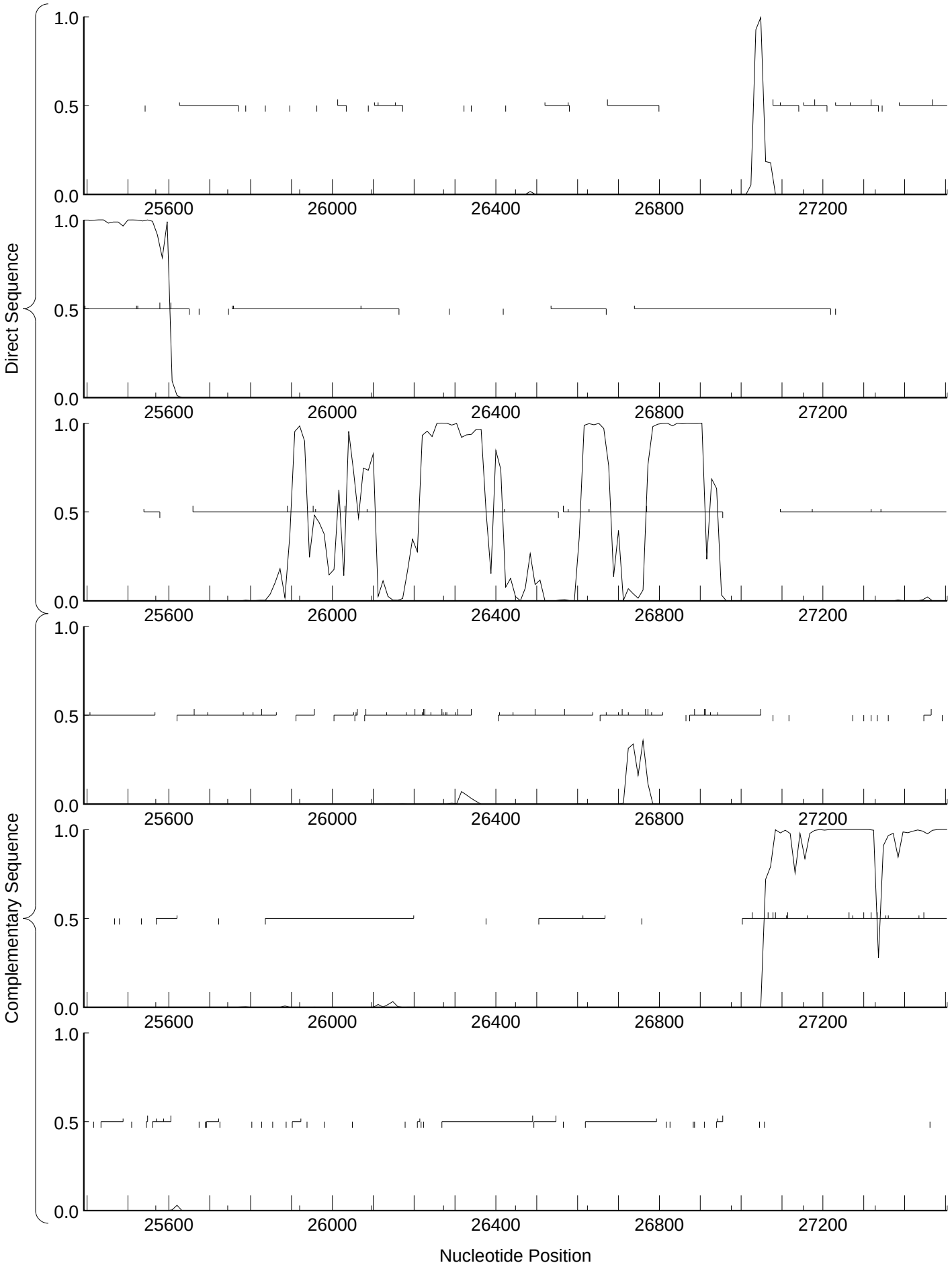
k complete sequence, 53932 bp including 10-base 3’ overhang (CGGTCGGTTA), Cluster A2, Order 4, Window 96, Step 12, 11/27



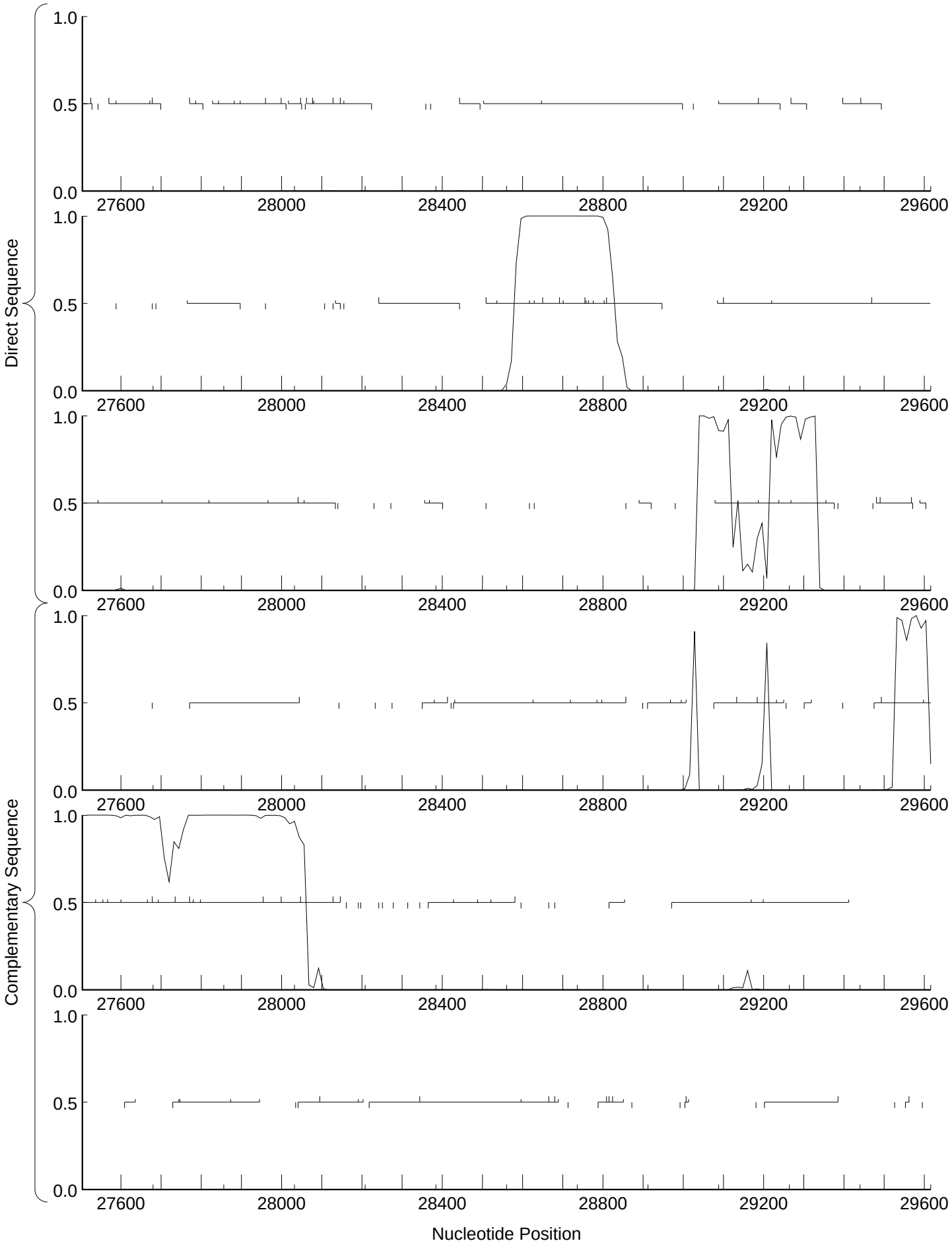

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
21200
21600
22000
22400
22800
23200
Nucleotide Position


Direct Sequence
Complementary Sequence
1.0
0.5
0.0
23600
24000
24400
24800
25200
Nucleotide Position

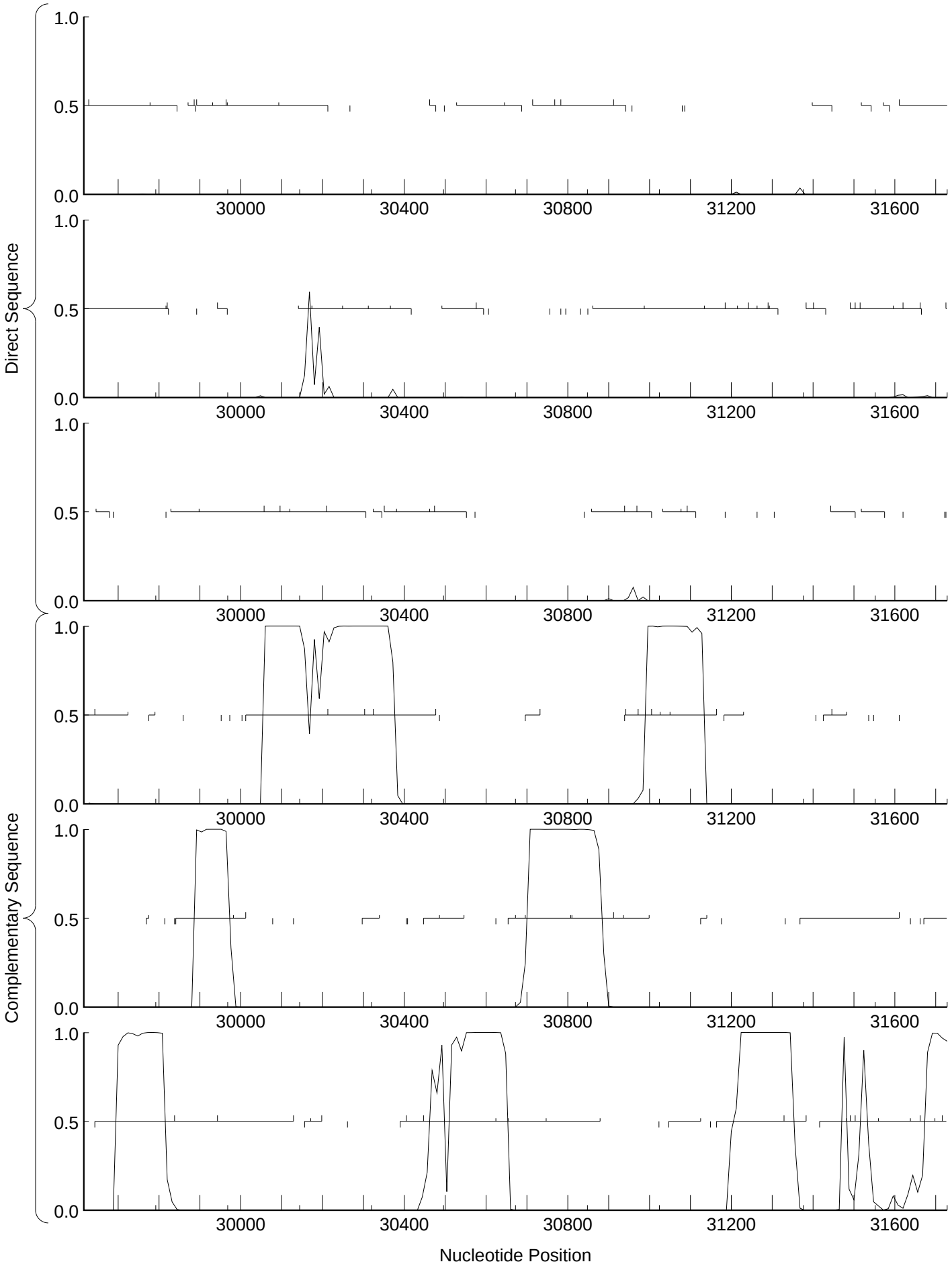
k complete sequence, 53932 bp including 10-base 3’ overhang (CGGTCGGTTA), Cluster A2, Order 4, Window 96, Step 12, 14/27

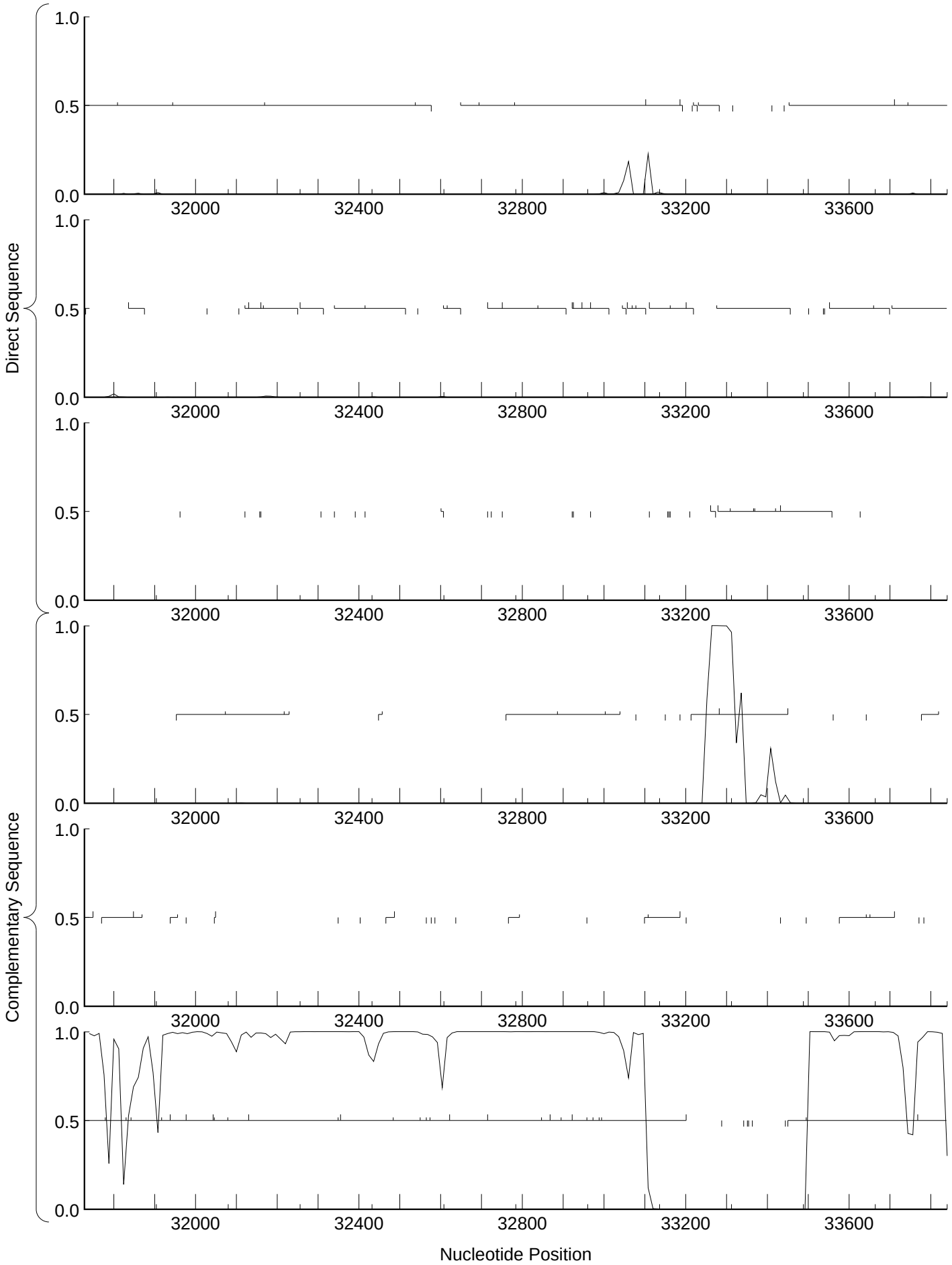


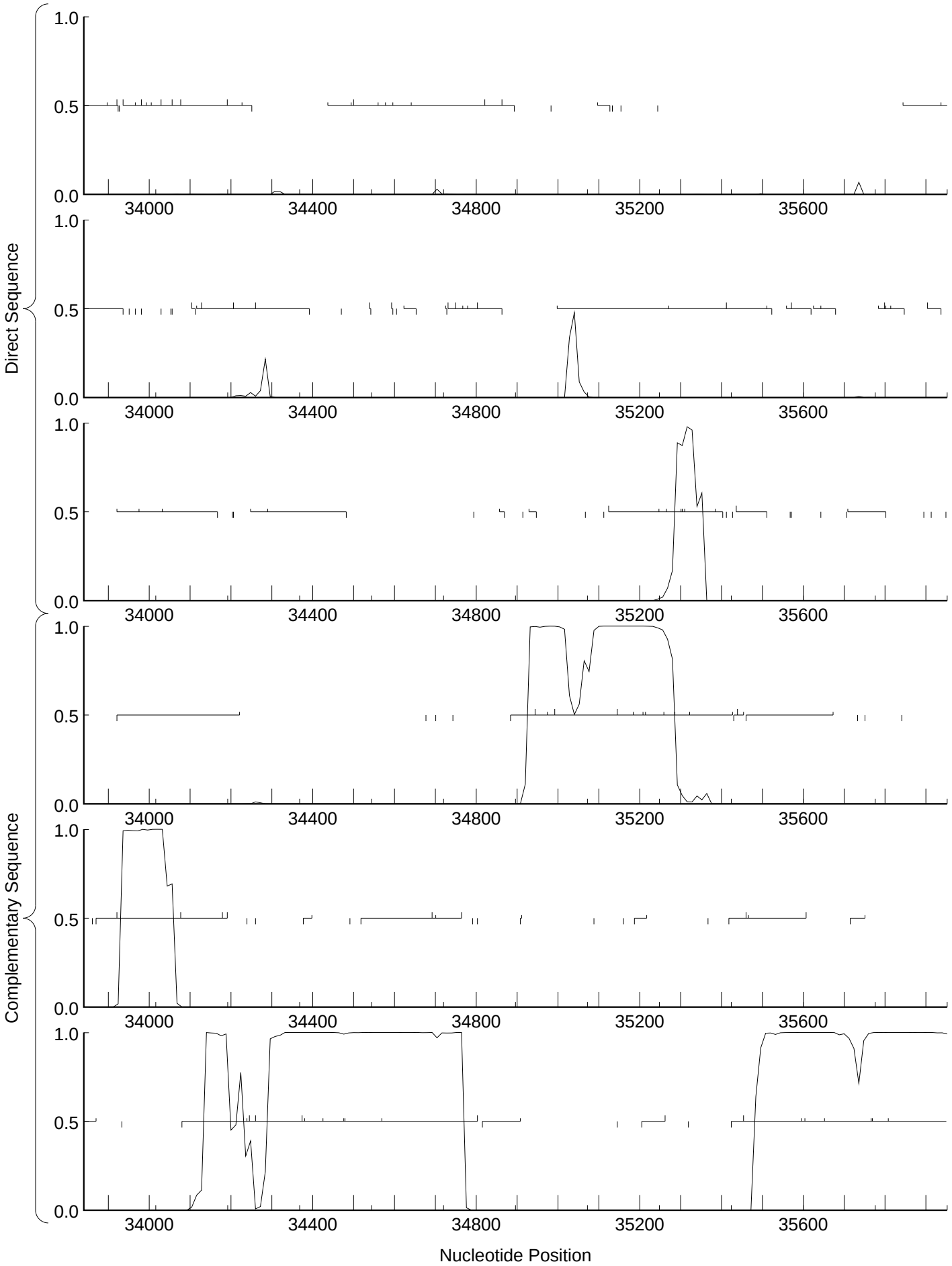
k complete sequence, 53932 bp including 10-base 3' overhang (CGGTCGGTTA), Cluster A2, Order 4, Window 96, Step 12, 15/27

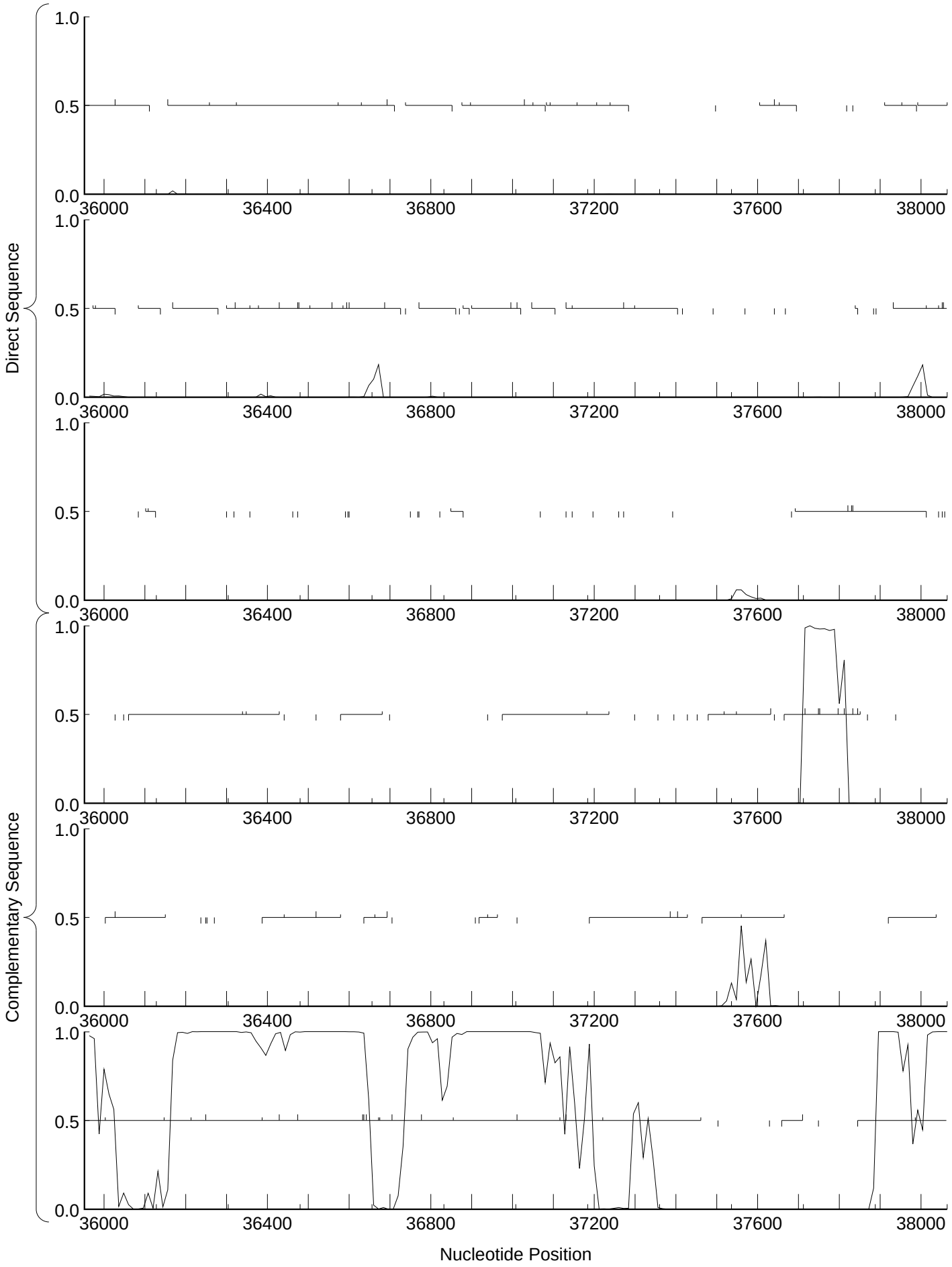


k complete sequence, 53932 bp including 10-base 3’ overhang (CGGTCGGTTA), Cluster A2, Order 4, Window 96, Step 12, 16/27

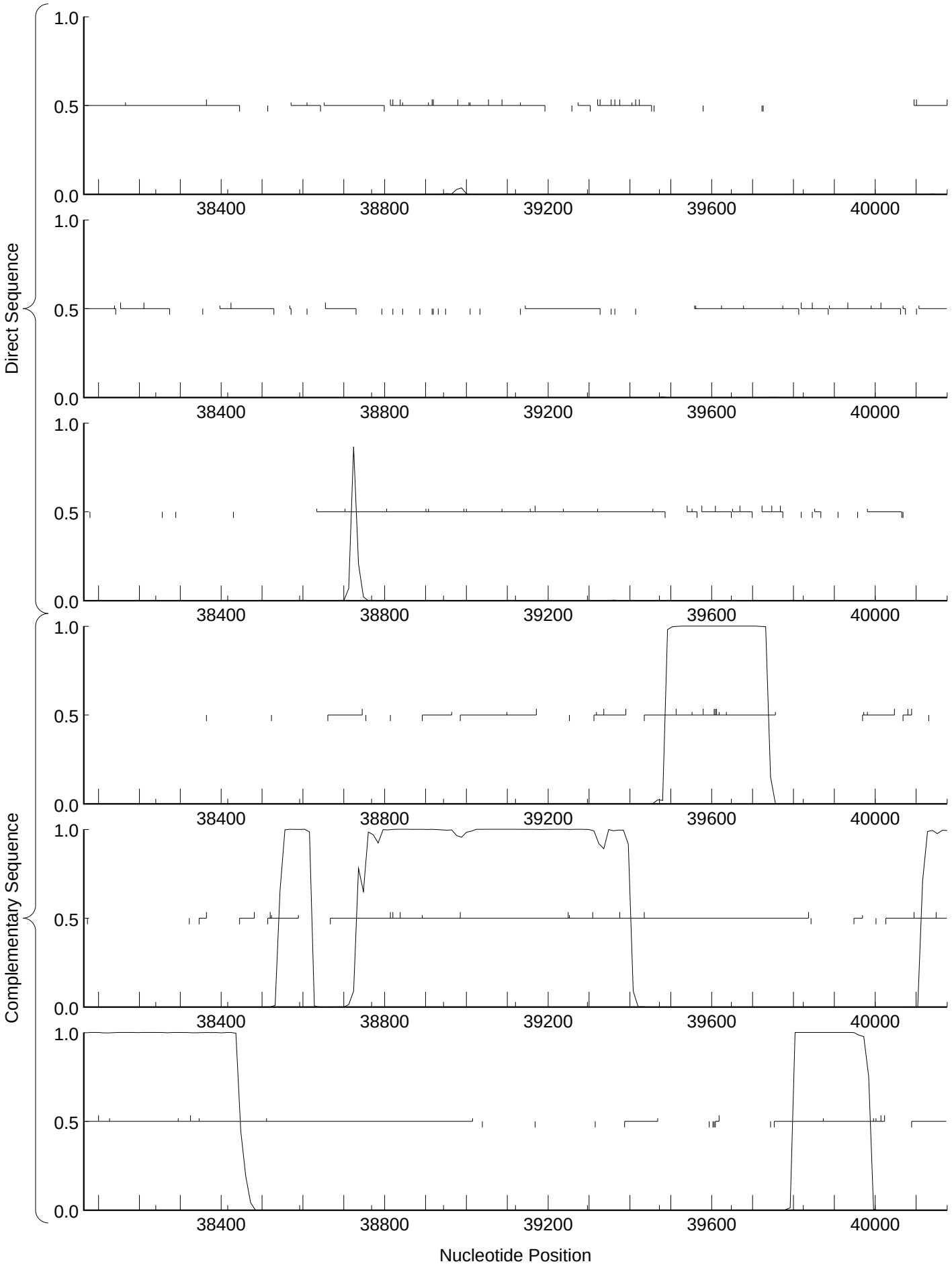


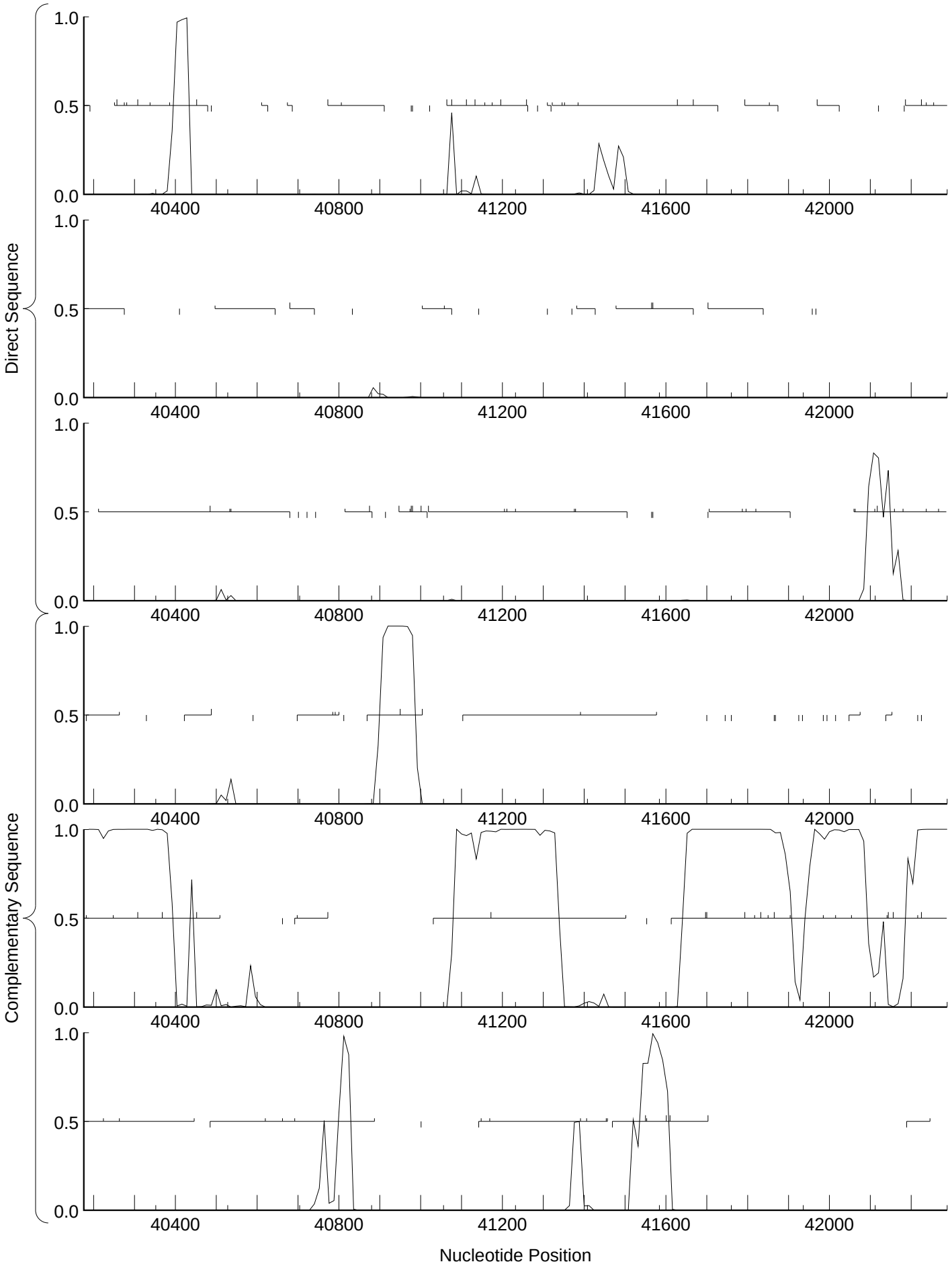

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
32000
32400
32800
33200
33600
Nucleotide Position

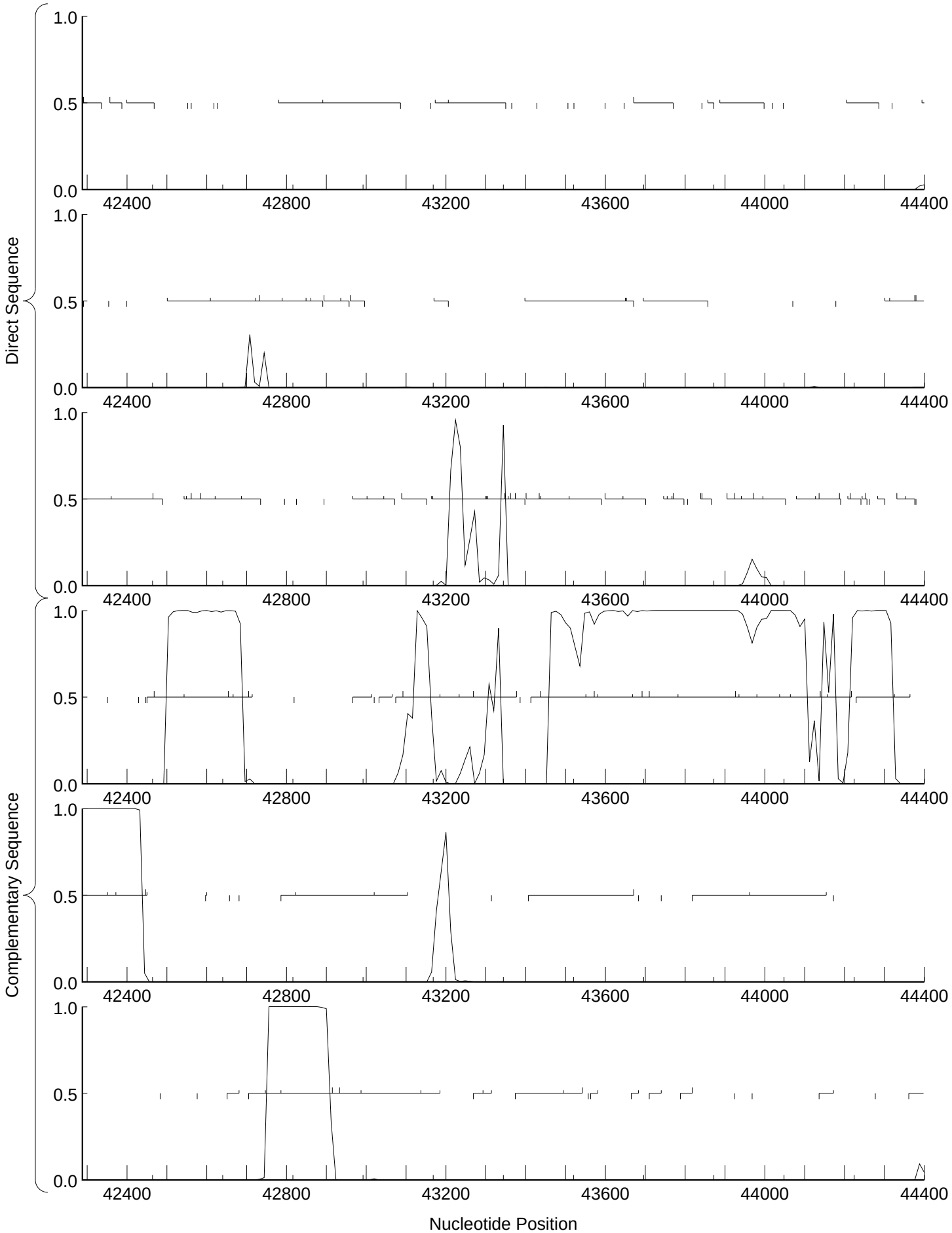

Direct Sequence
Complementary Sequence
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0.5
0.0
34000
34400
34800
35200
35600
Nucleotide Position

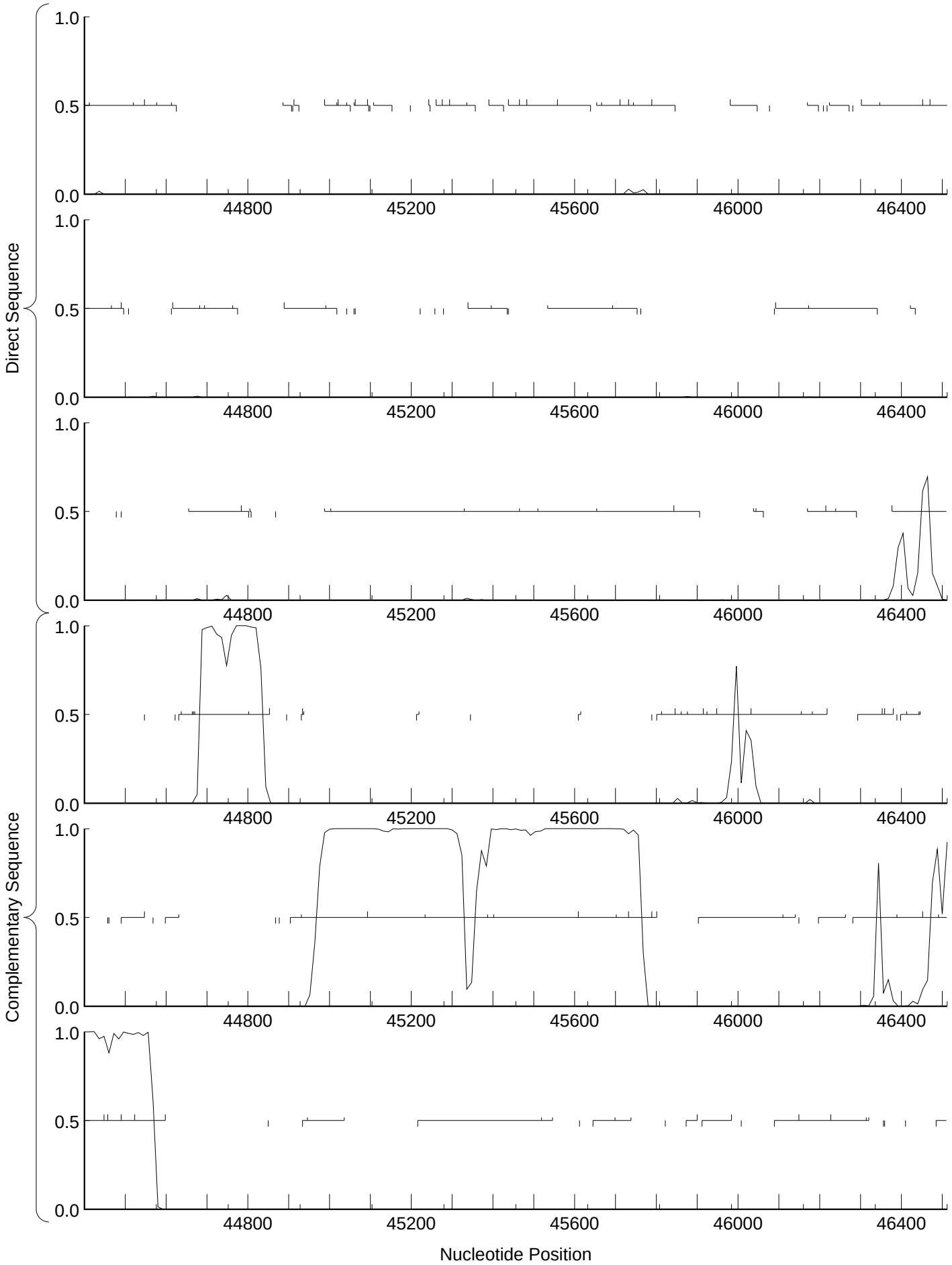

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
36000
36400
36800
37200
37600
38000
Nucleotide Position

k complete sequence, 53932 bp including 10-base 3' overhang (CGGTCGGTTA), Cluster A2, Order 4, Window 96, Step 12, 20/27

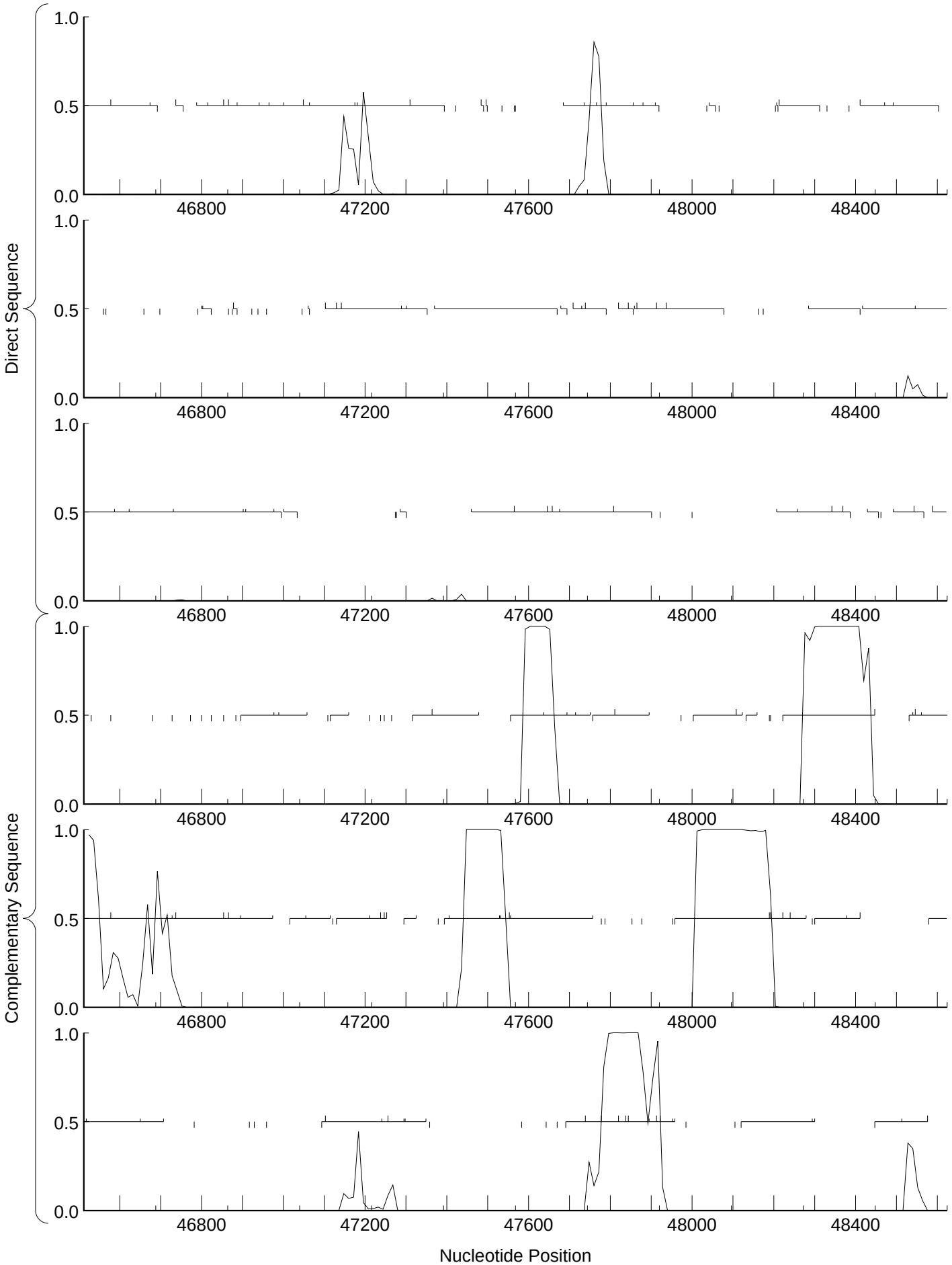


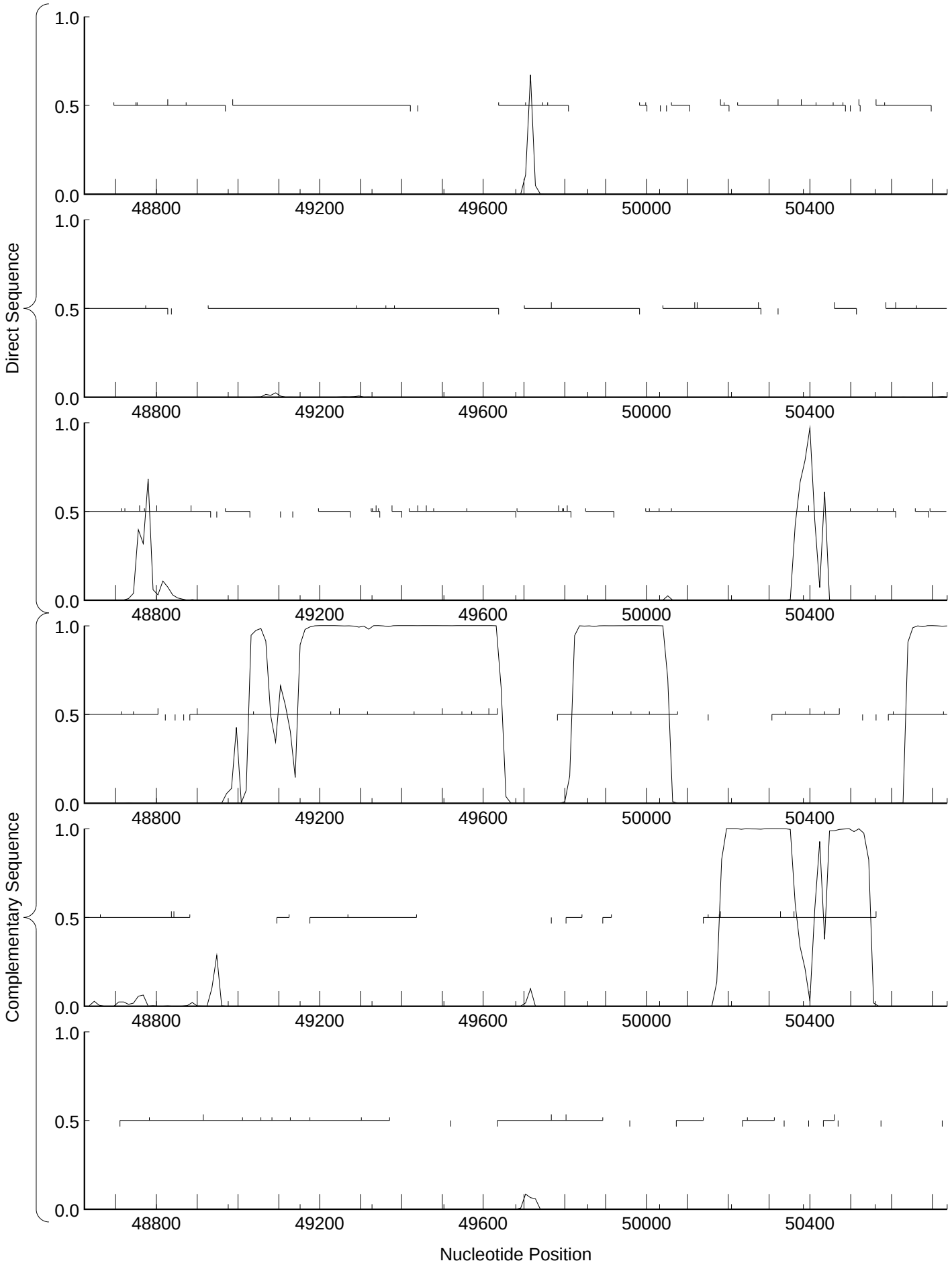

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
40400
40800
41200
41600
42000
Nucleotide Position


Direct Sequence
Complementary Sequence
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0.5
0.0
42400
42800
43200
43600
44000
44400
Nucleotide Position

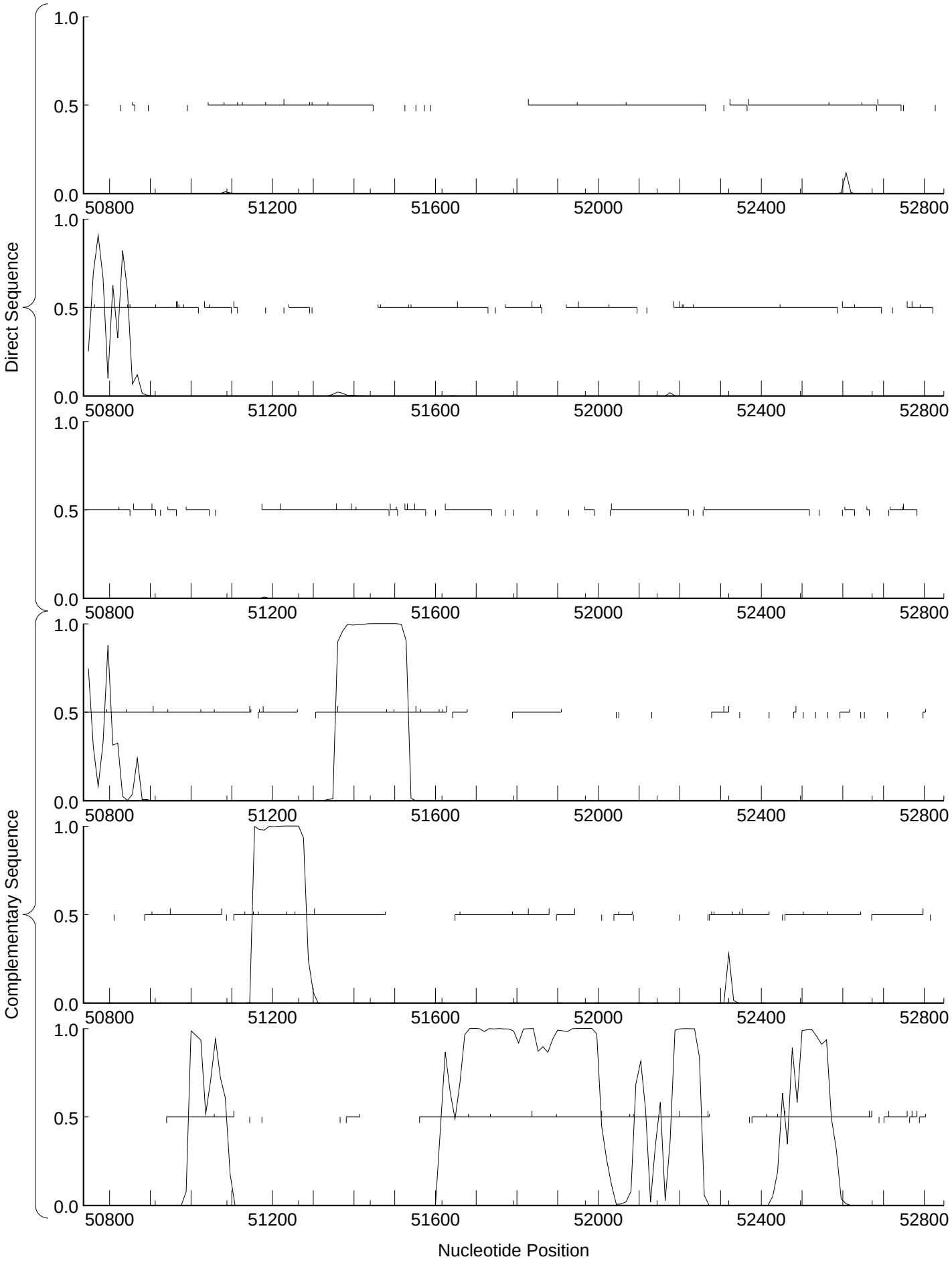

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
44800
45200
45600
46000
46400
Nucleotide Position

k complete sequence, 53932 bp including 10-base 3’ overhang (CGGTCGGTTA), Cluster A2, Order 4, Window 96, Step 12, 24/27




Direct Sequence
Complementary Sequence
1.0
0.5
0.0
48800
49200
49600
50000
50400
Nucleotide Position

k complete sequence, 53932 bp including 10-base 3' overhang (CGGTCGGTTA), Cluster A2, Order 4, Window 96, Step 12, 26/27



k complete sequence, 53932 bp including 10-base 3’ overhang (CGGTCGGTTA), Cluster A2, Order 4, Window 96, Step 12, 27/27

