GeneMark

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

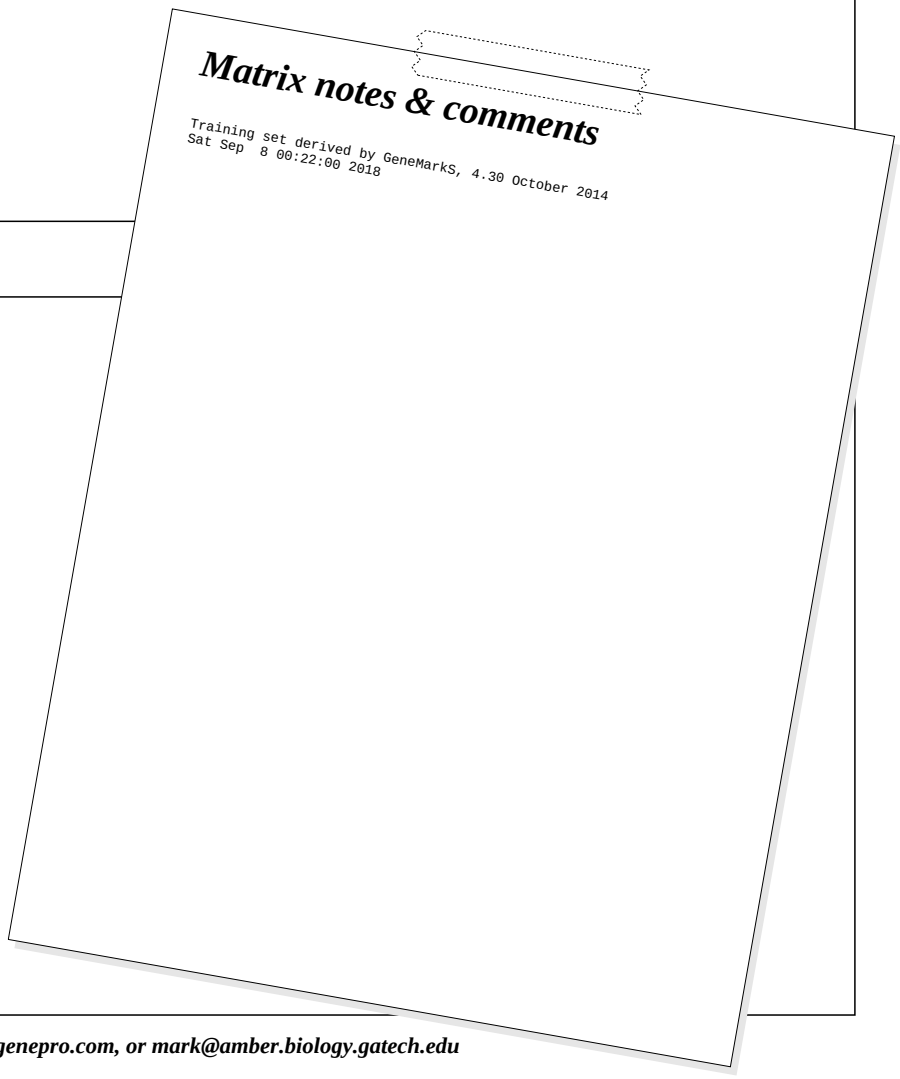
PROGRAM INFORMATION

```
Sequence         :  Arthrobacter phage Lasagna complete sequence, 42602 bp including 13-base 3' overhang (GGTAA
Analysis Date    :  3/29/24 at 3:47:02
Pages            :  22
Sequence Length  :  42602 bp
GC Content       :   60.80%

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

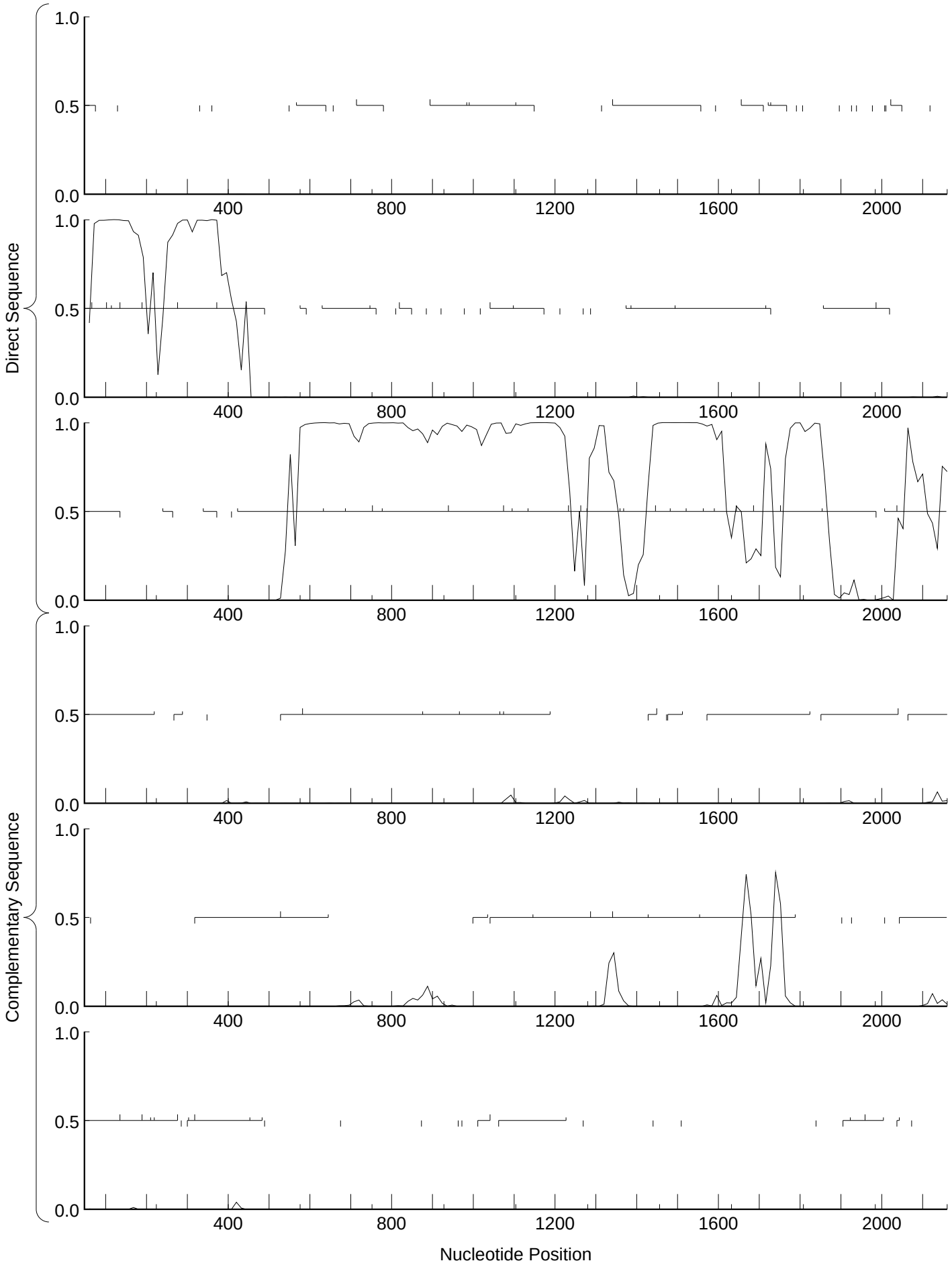
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Matrix     :  -
Author     :  -

Order      :  4
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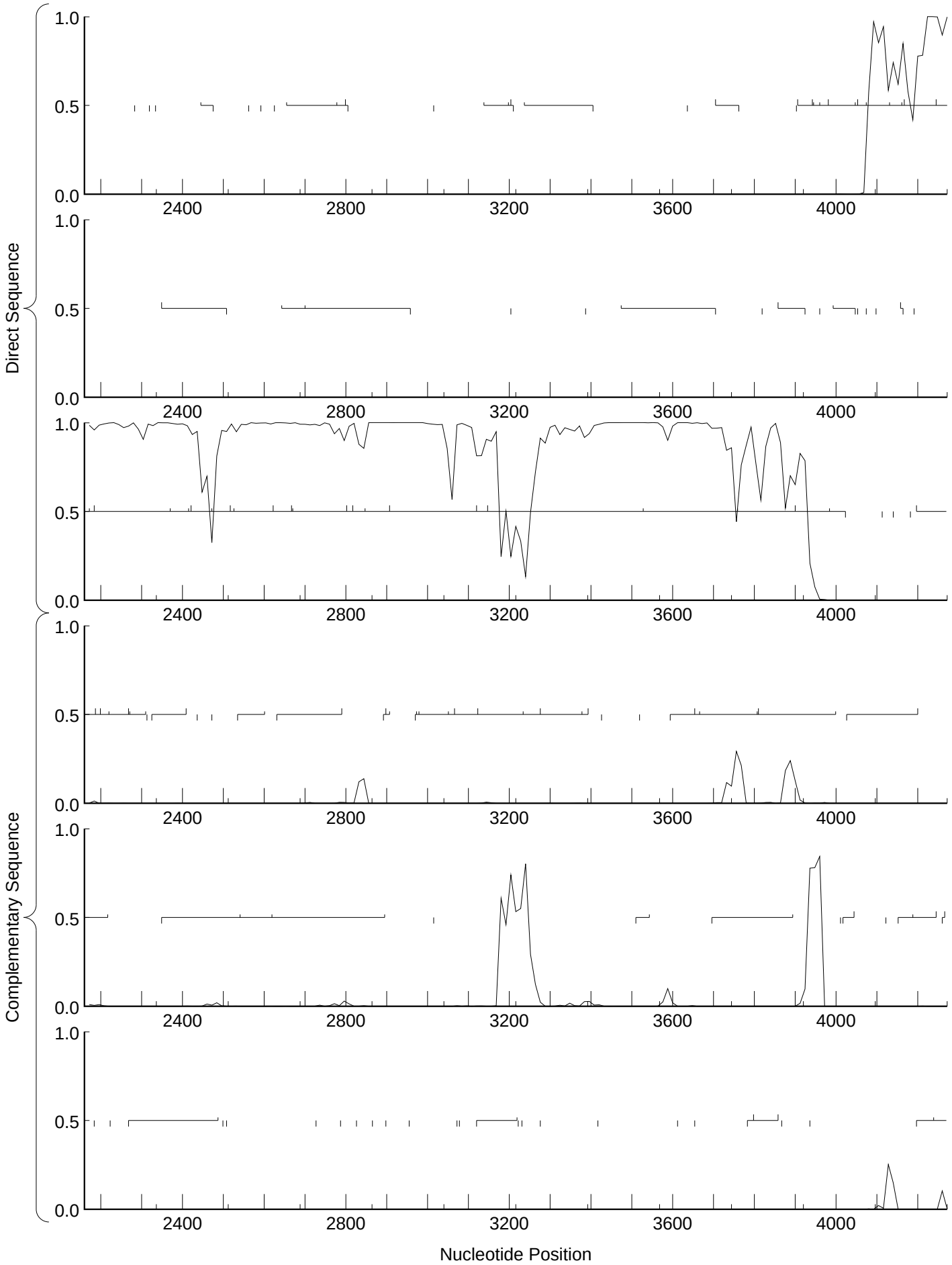

```
  Send questions / comments to:
      Dr. M. Borodovsky
      Georgia Institute of Technology
      School of Biology
      Atlanta, GA  30332-0230
```


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

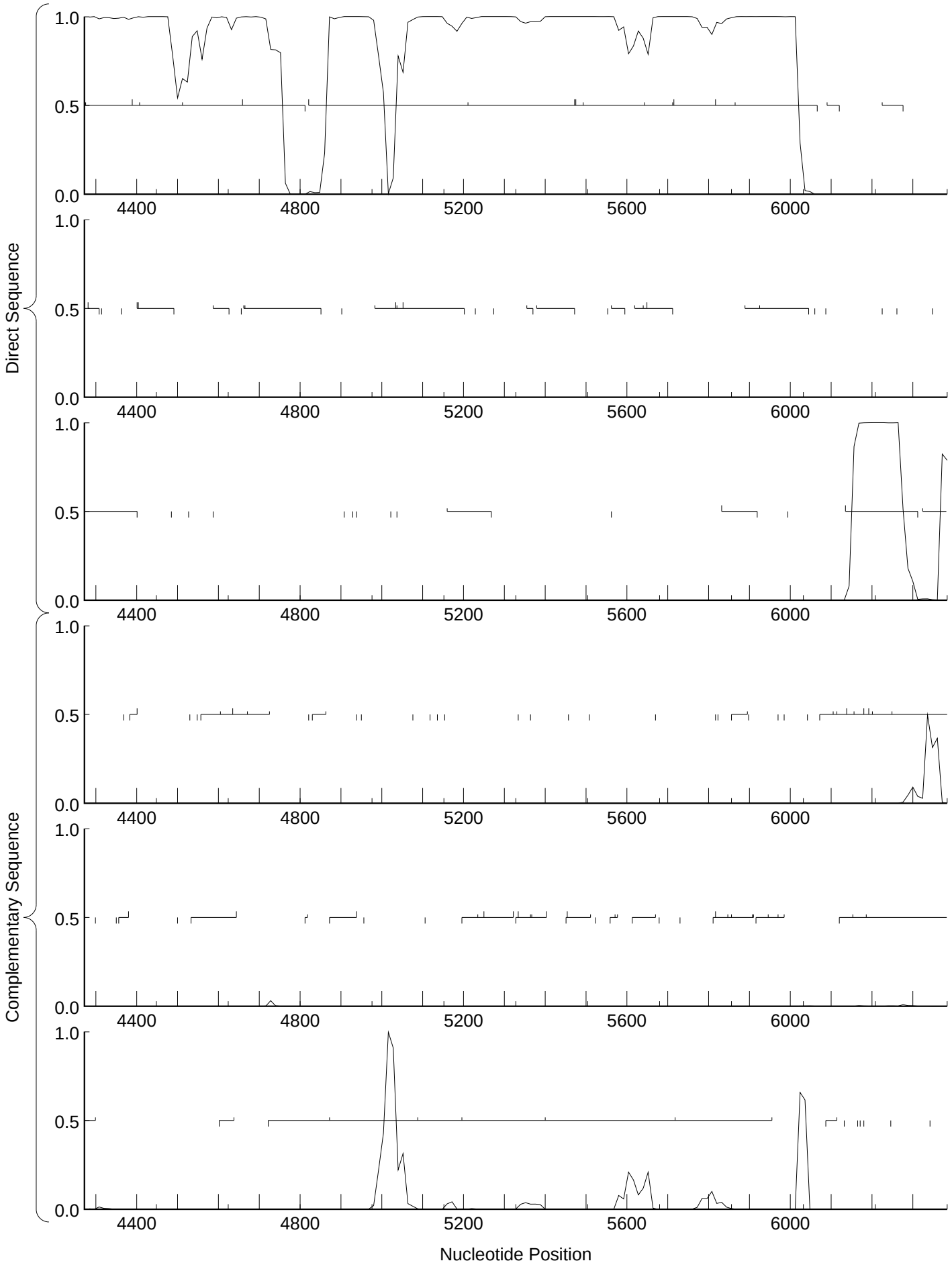
mplete sequence, 42602 bp including 13-base 3’ overhang (GGTAACCGTGATA), Cluster AK, Order 4, Window 96, Step 12, 2/22



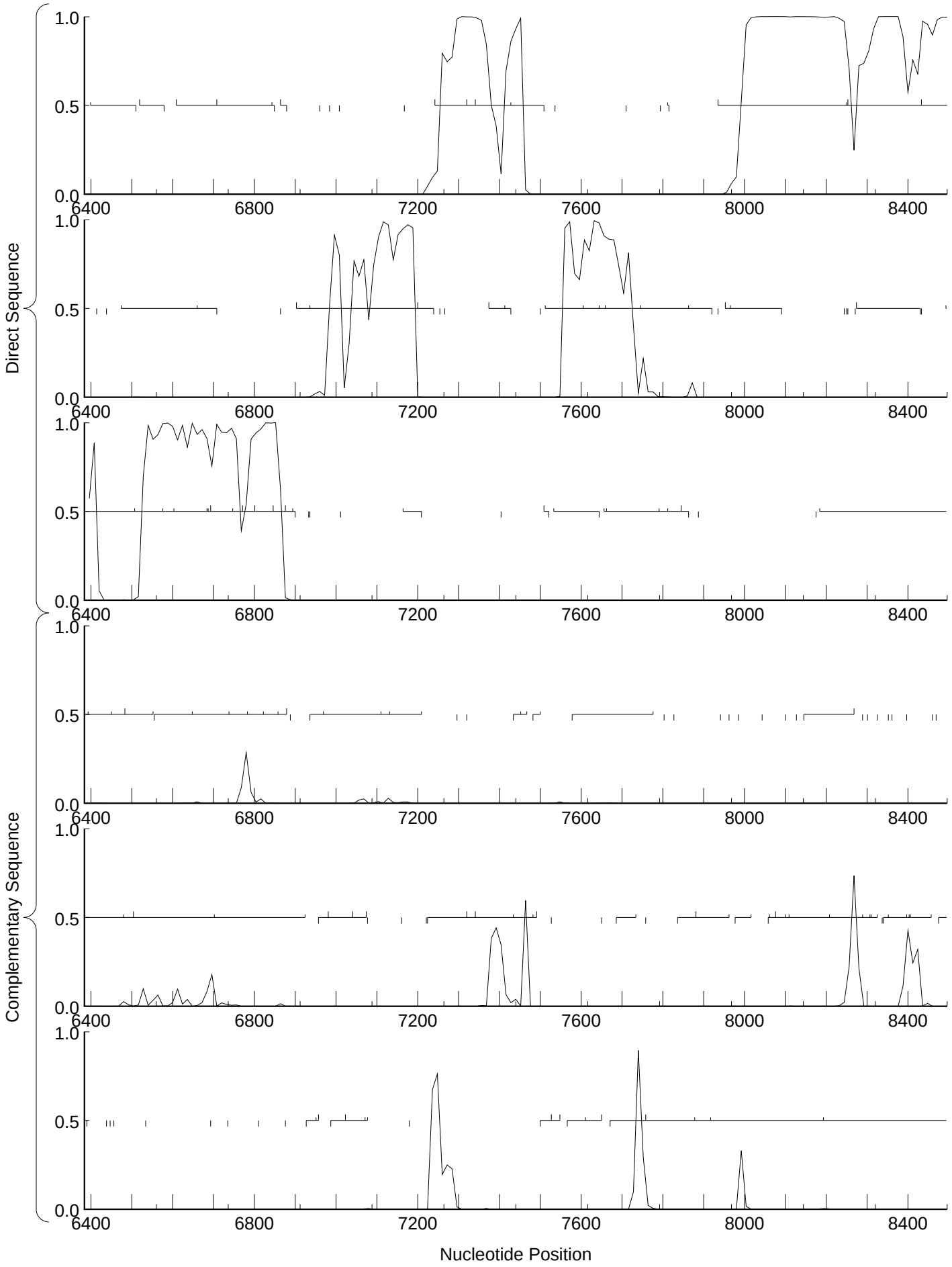
mplete sequence, 42602 bp including 13-base 3’ overhang (GGTAACCGTGATA), Cluster AK, Order 4, Window 96, Step 12, 3/22



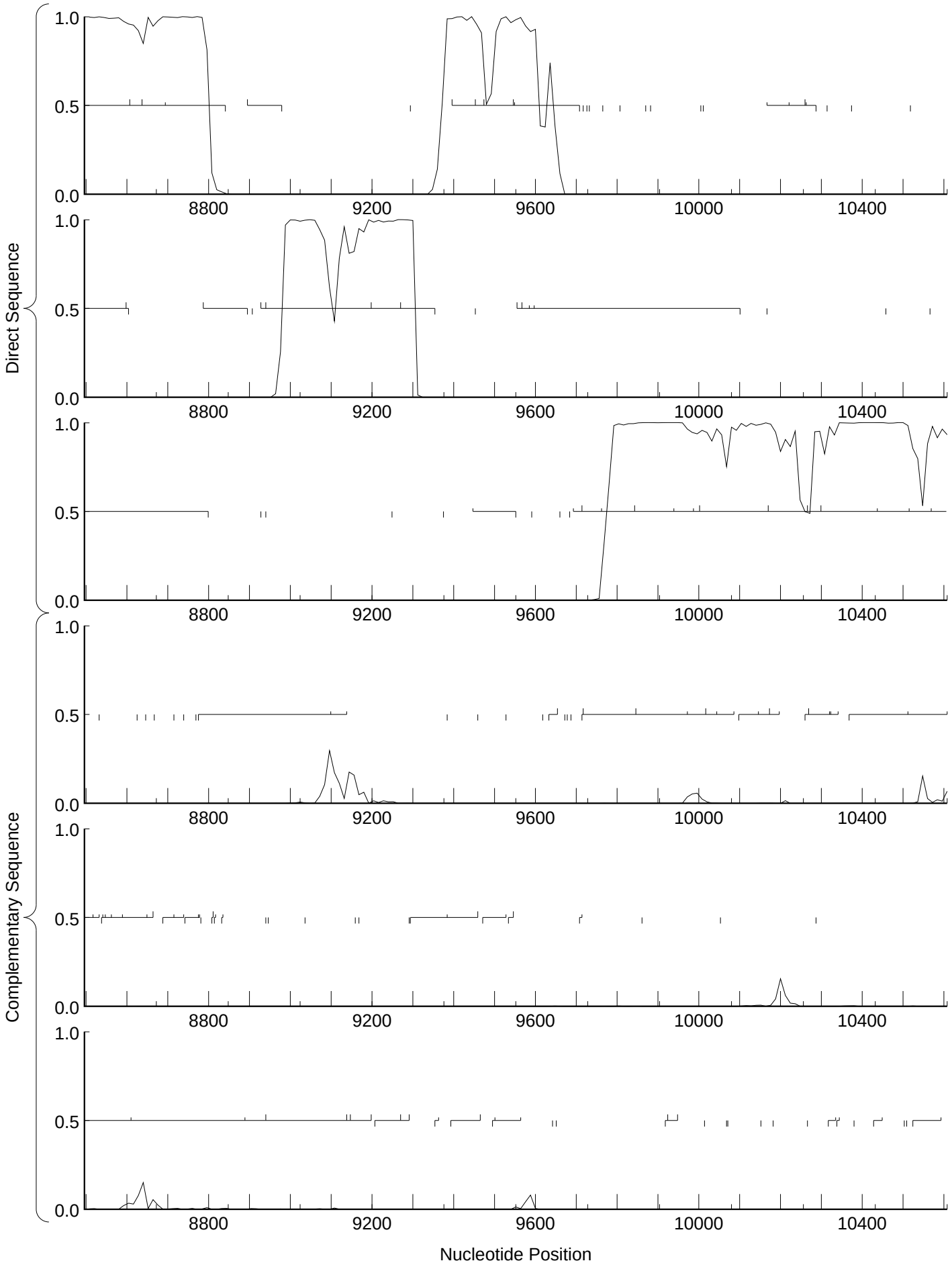
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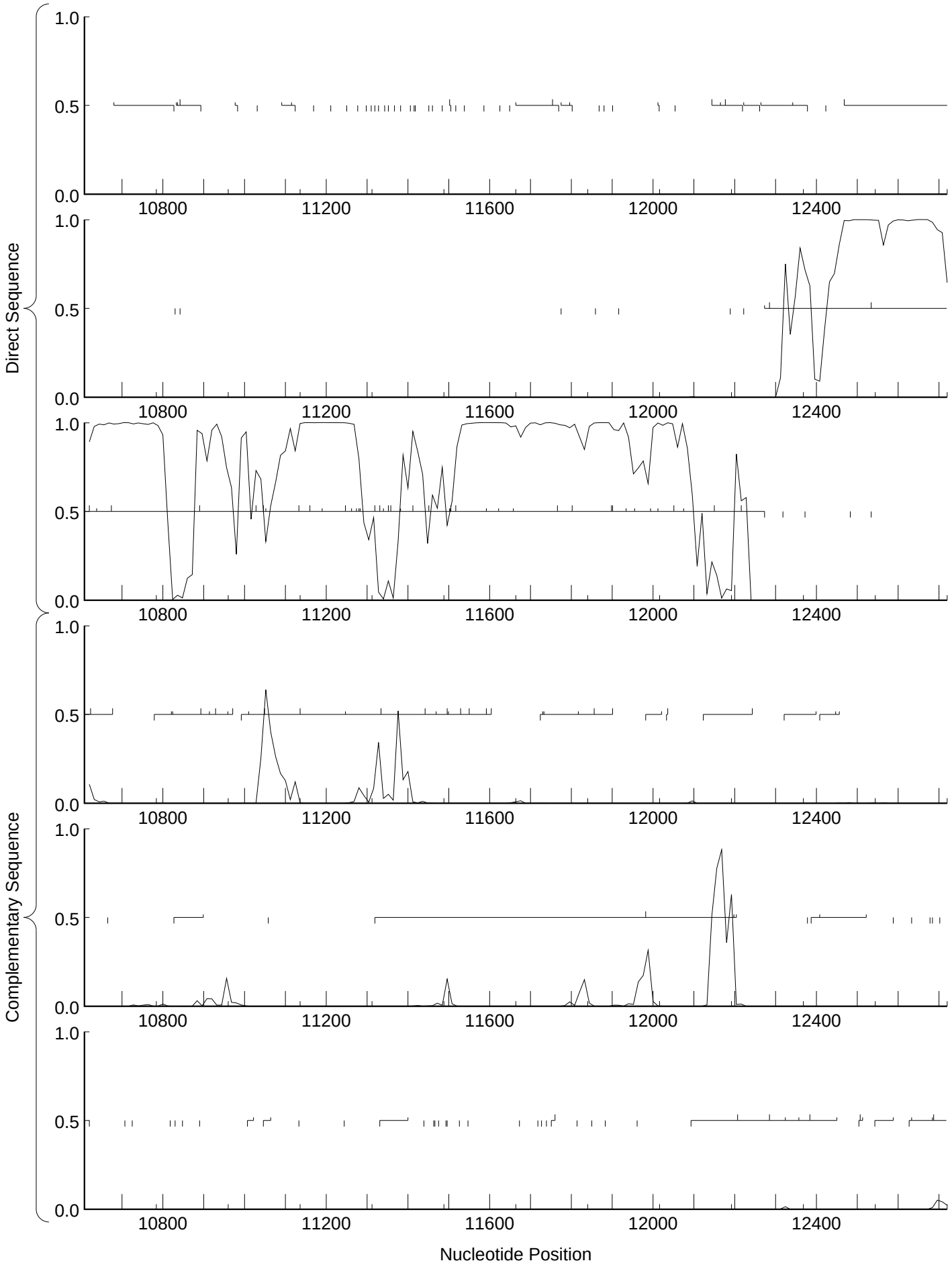
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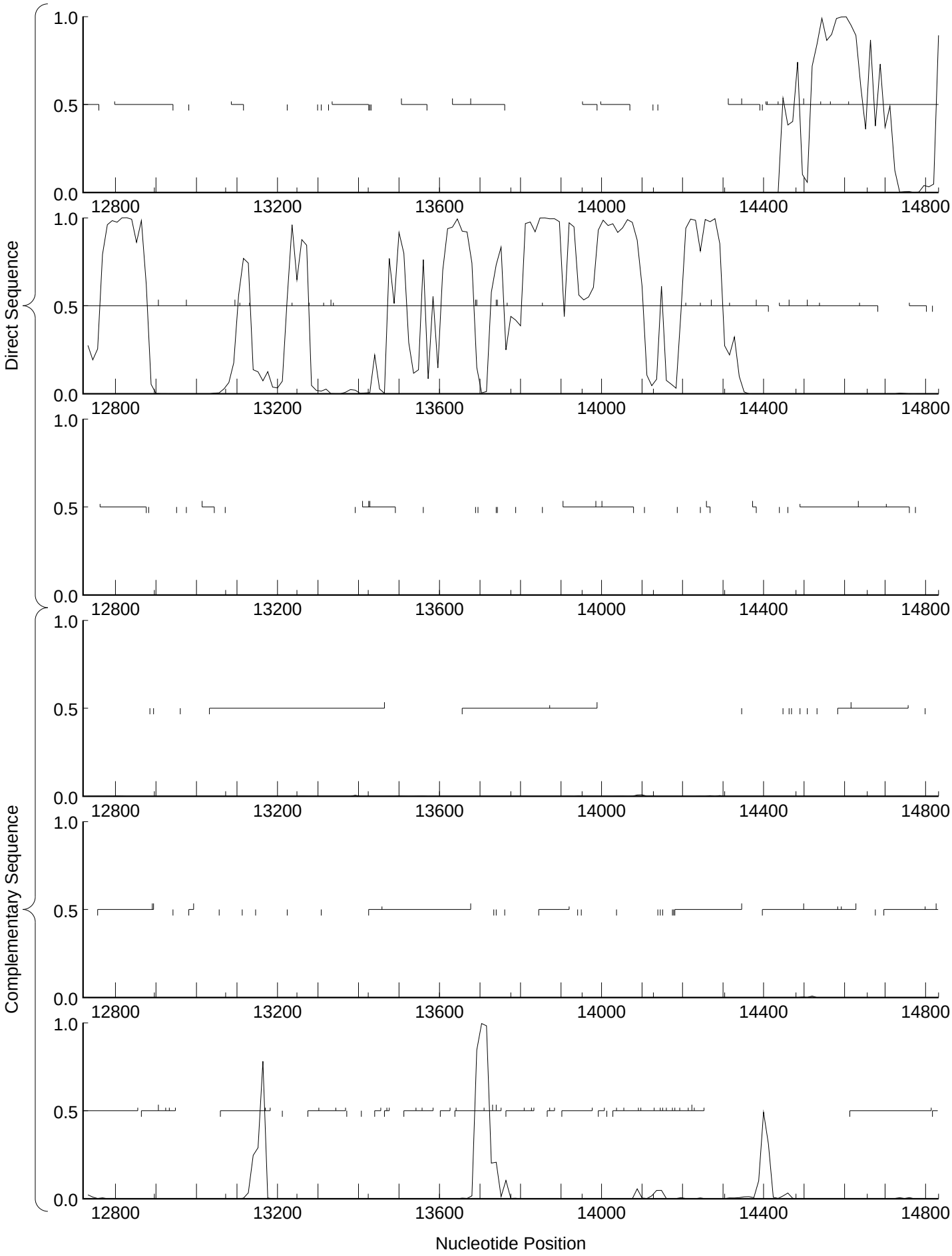
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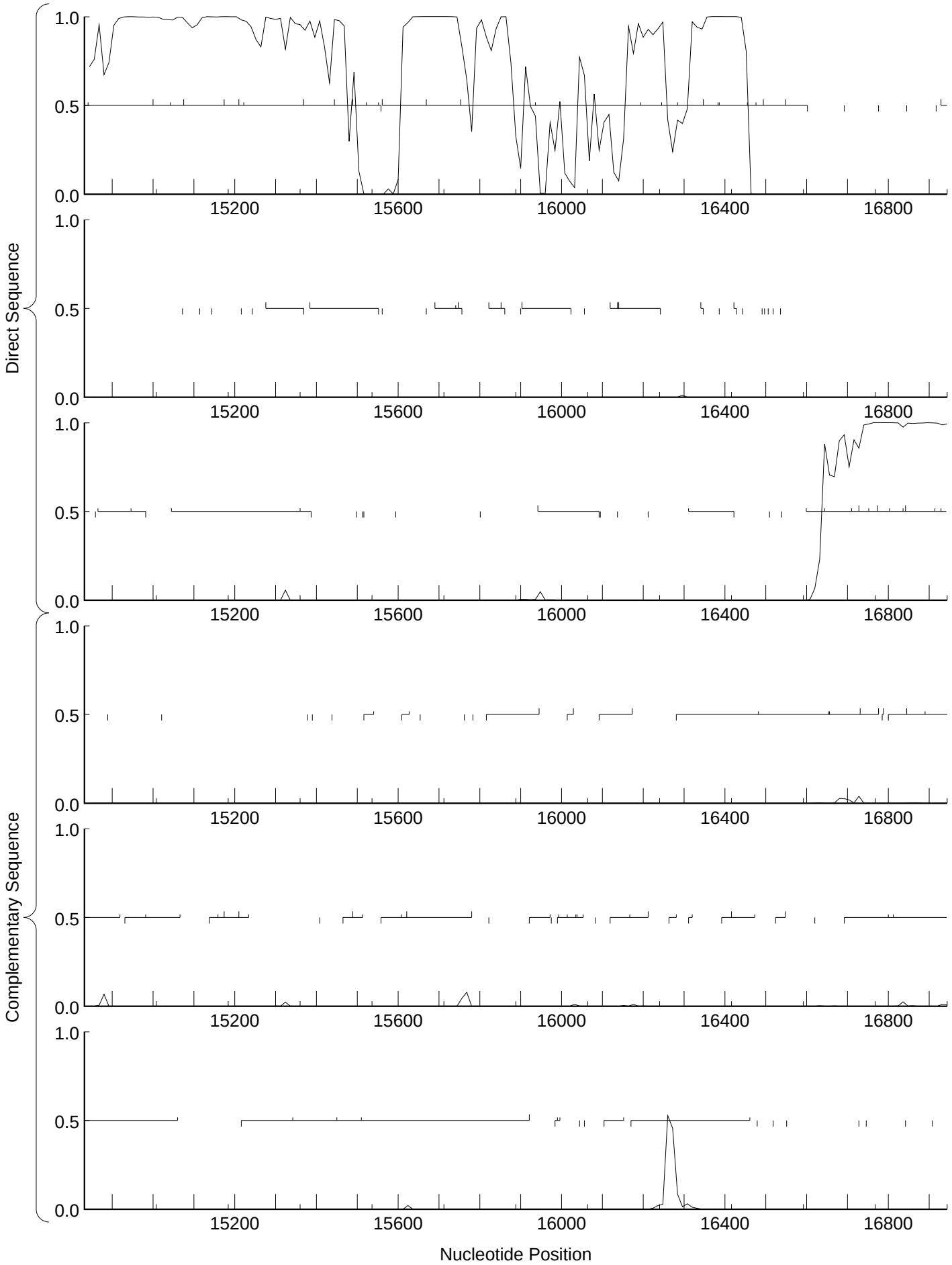
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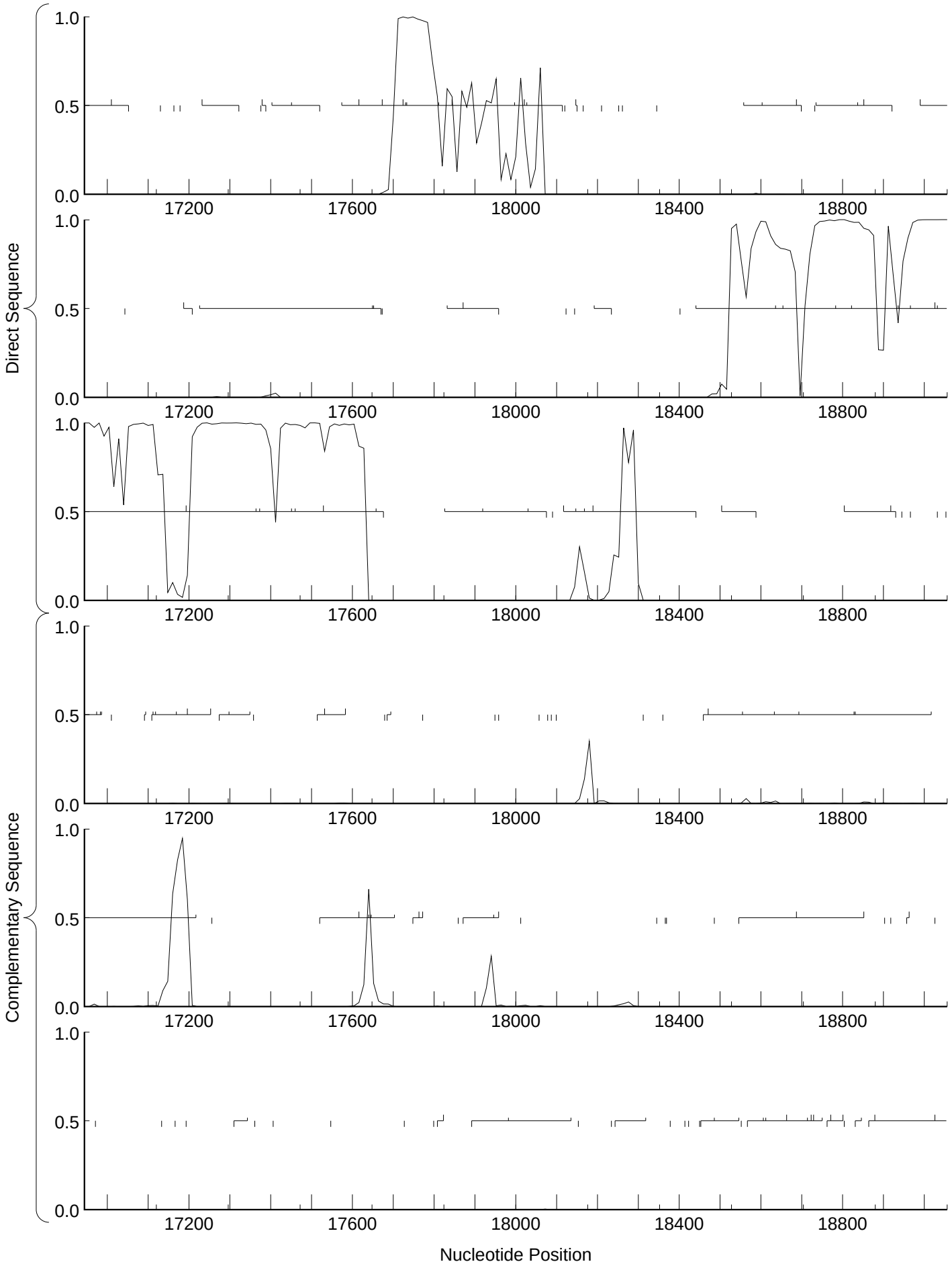
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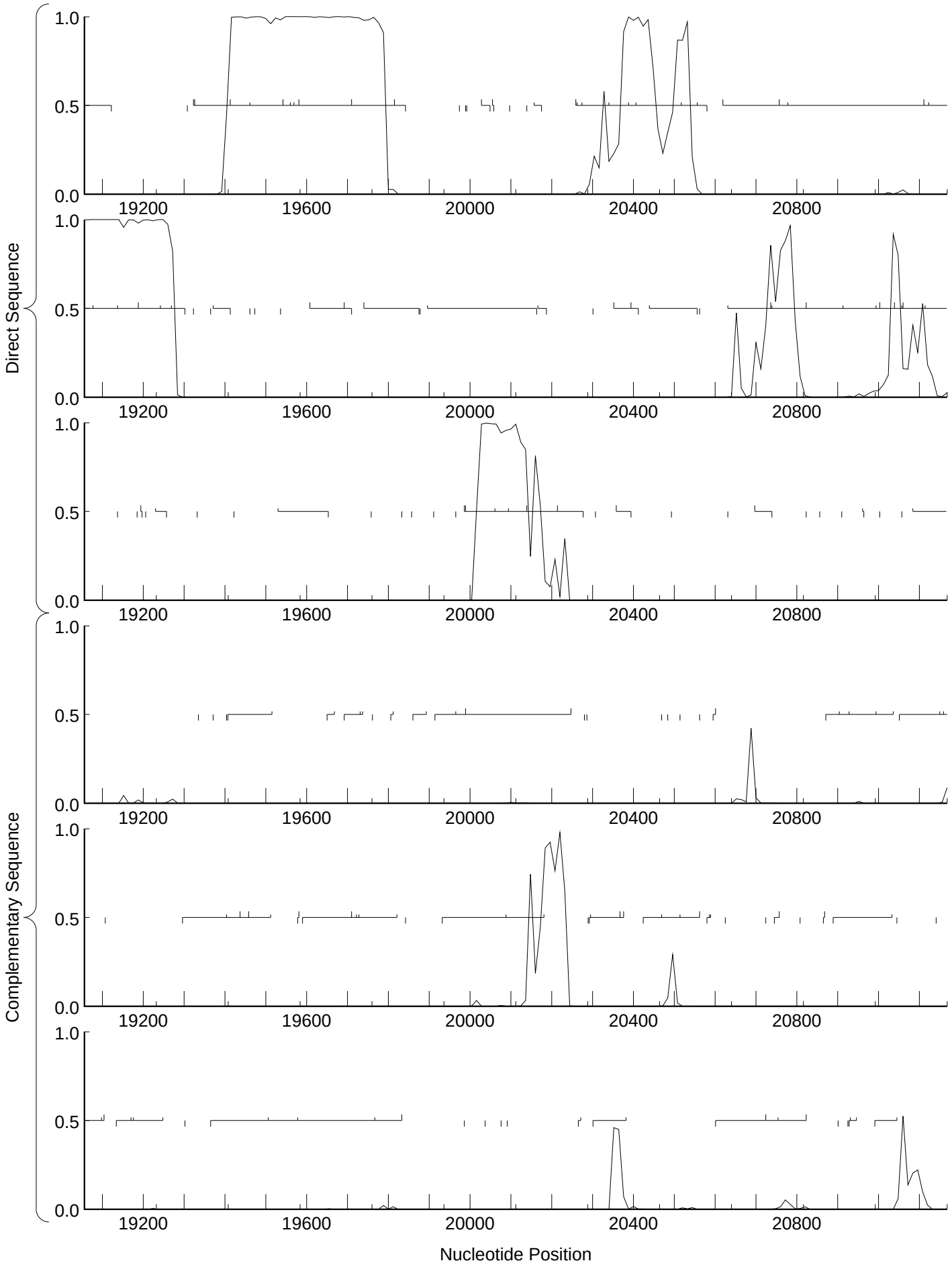
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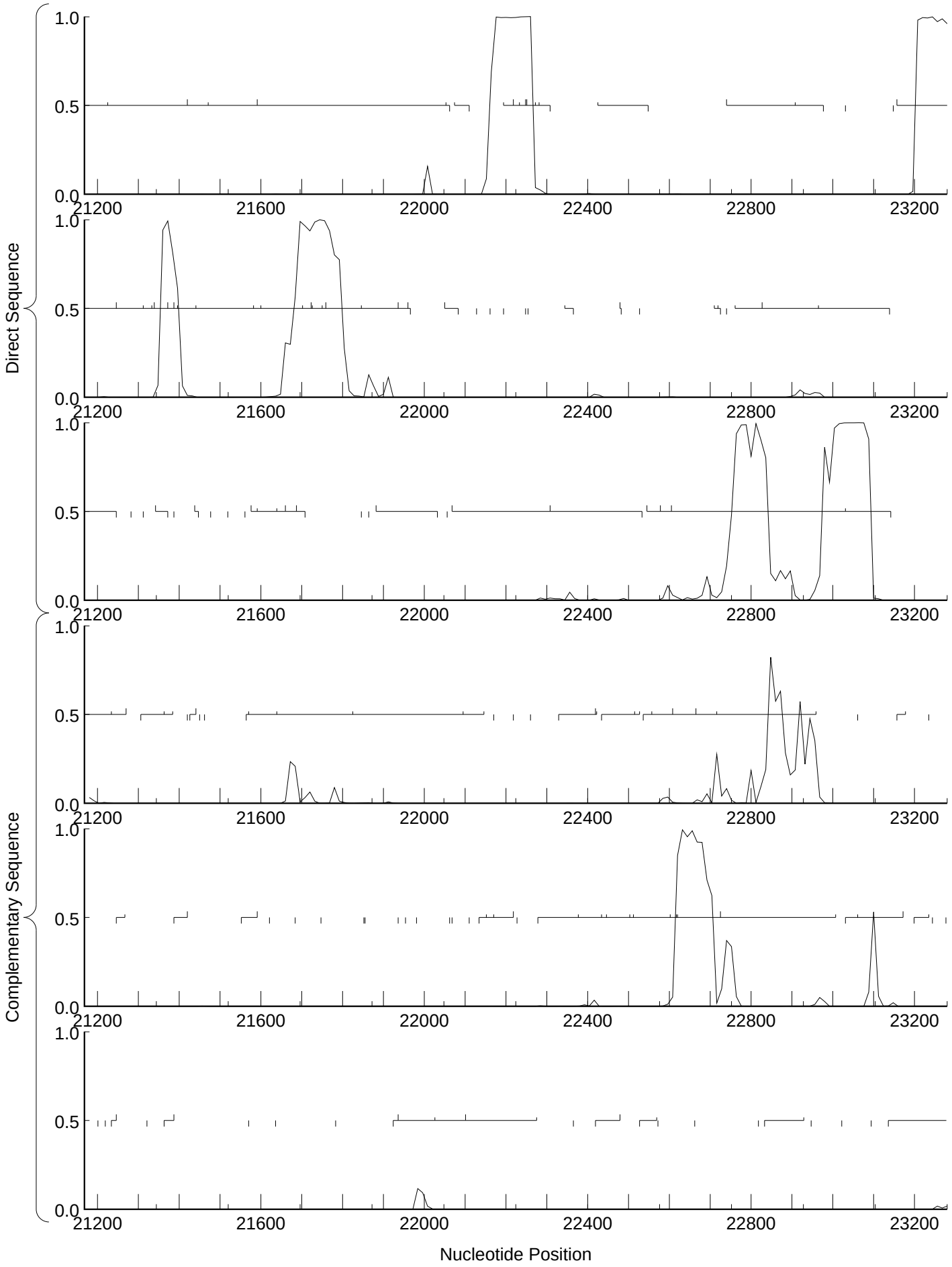
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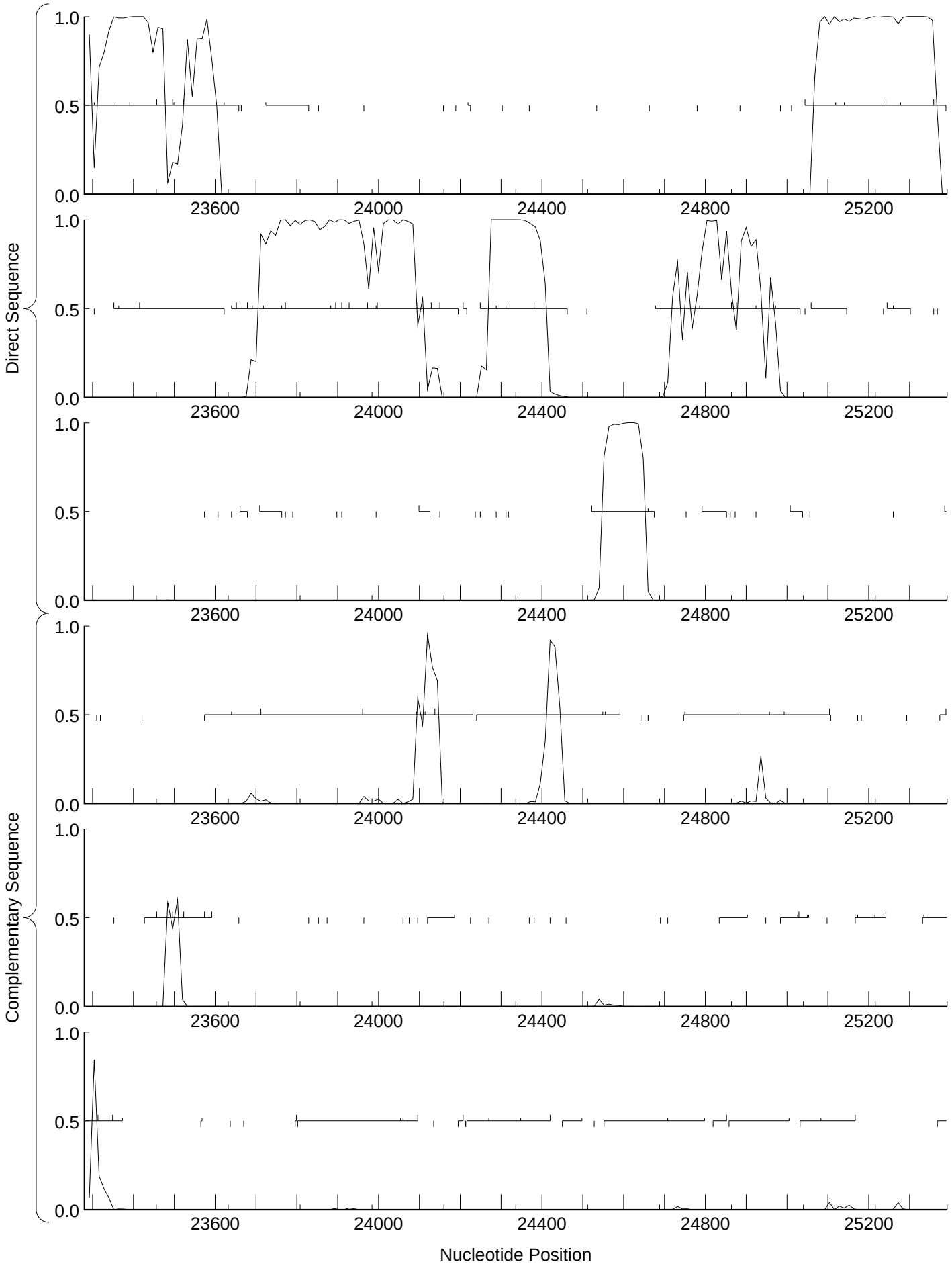
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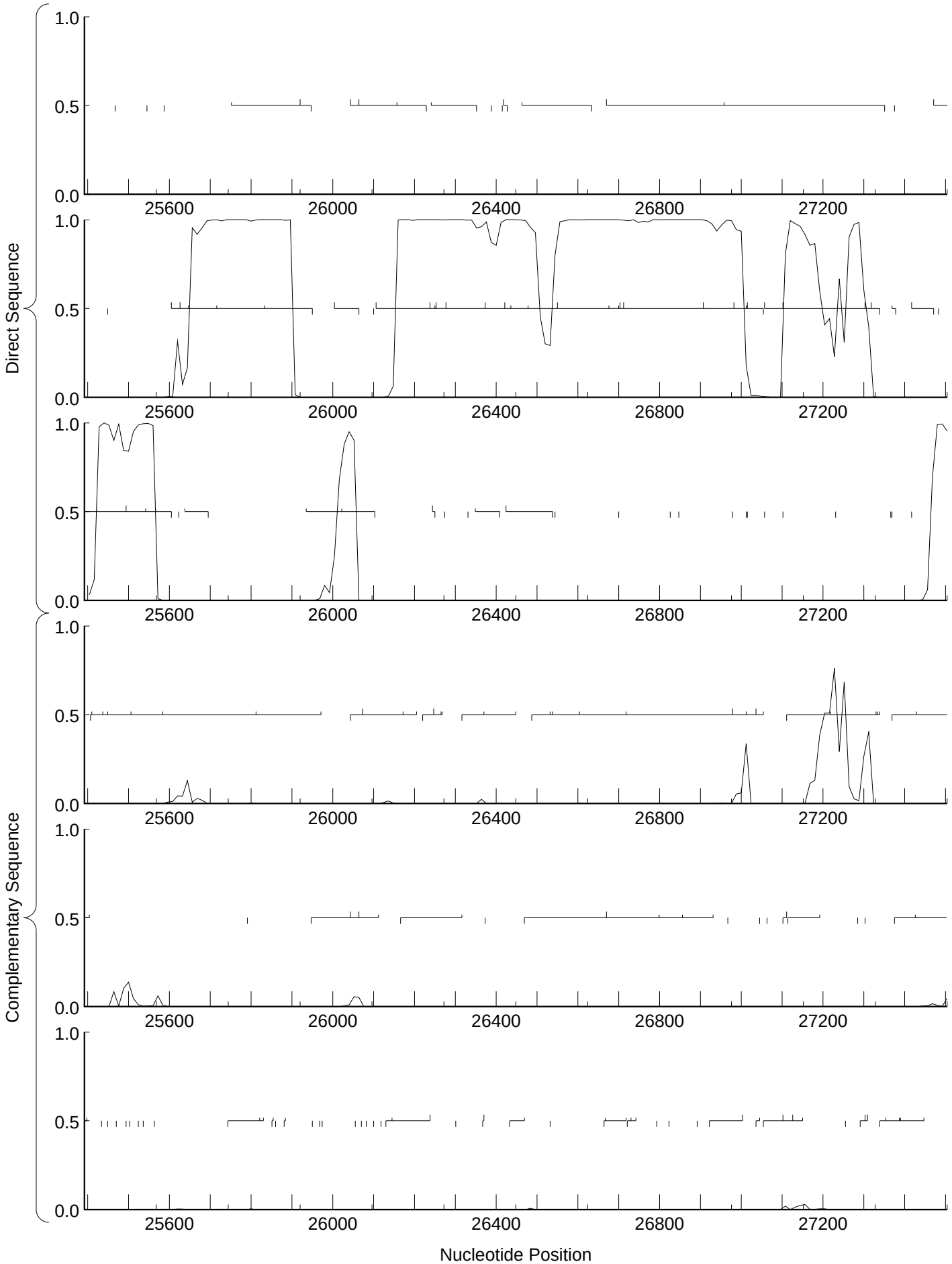


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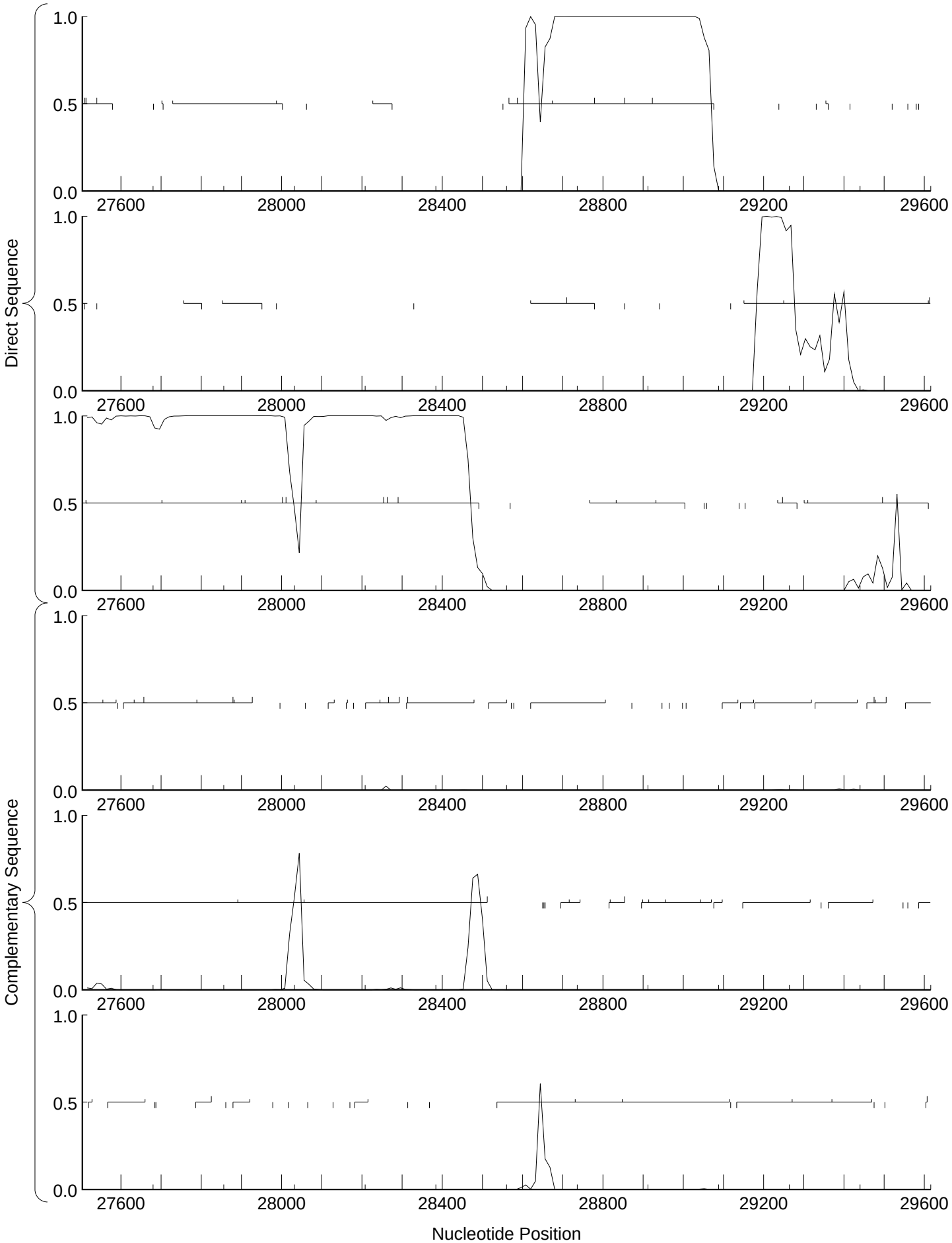


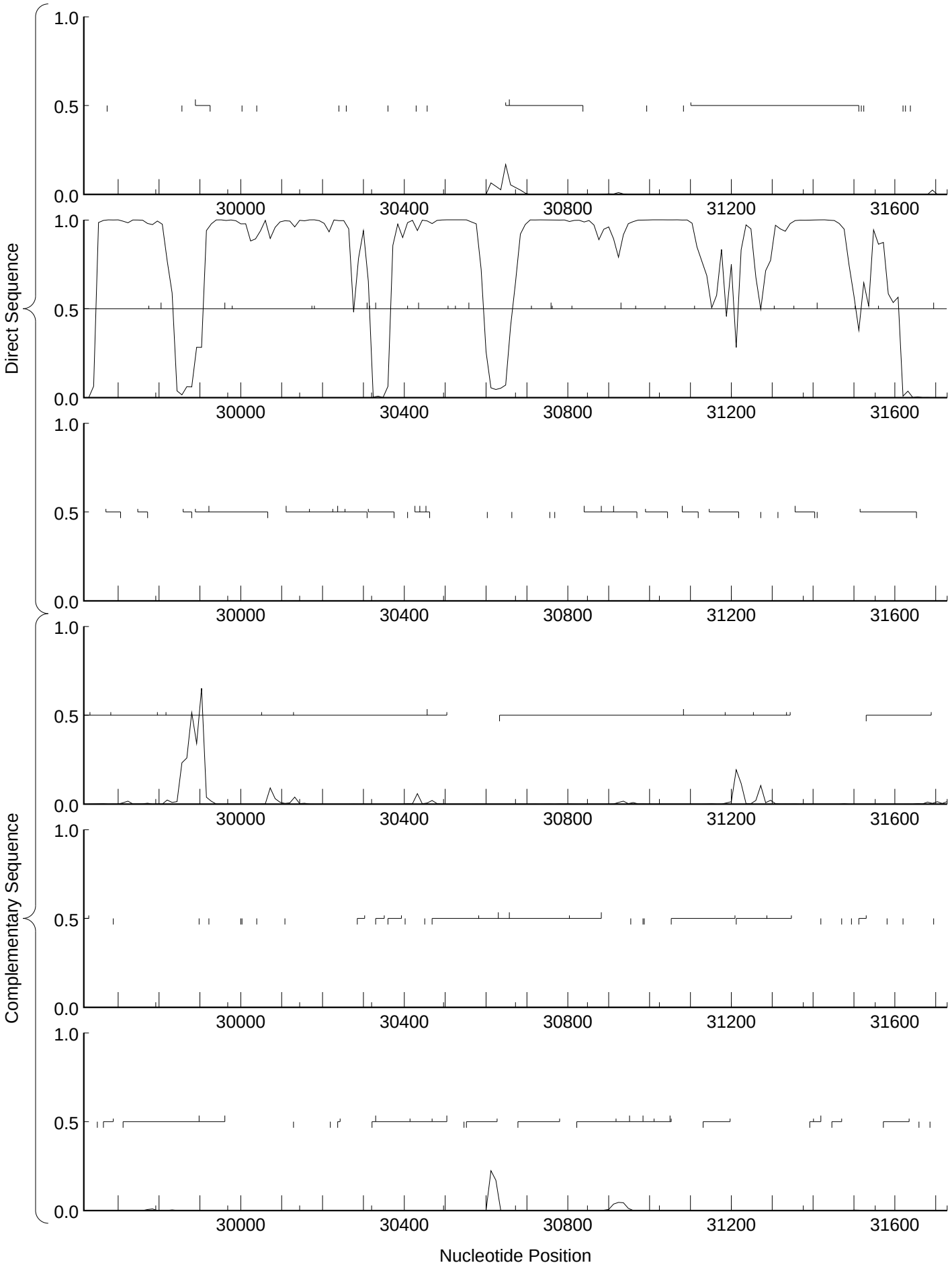
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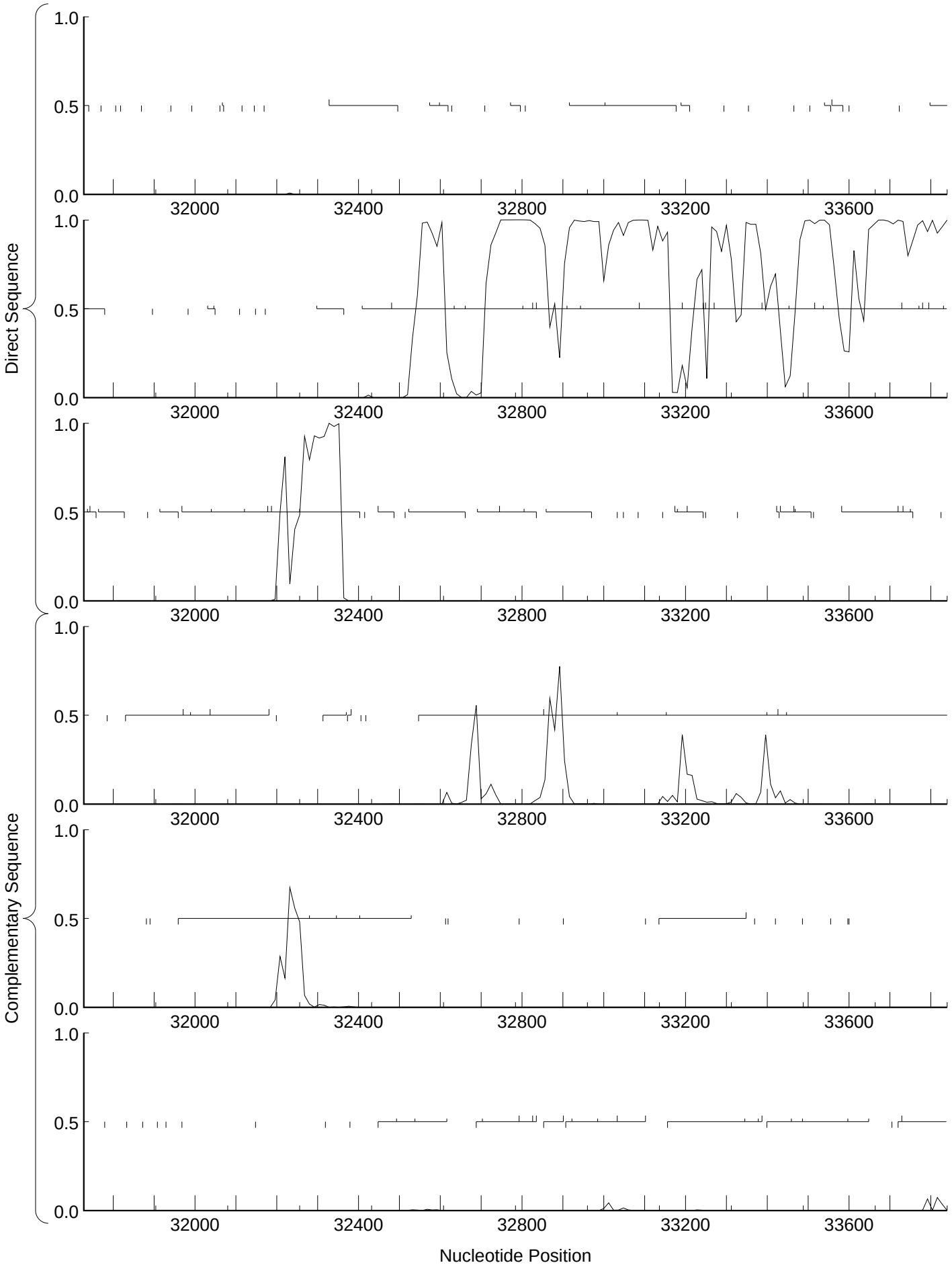


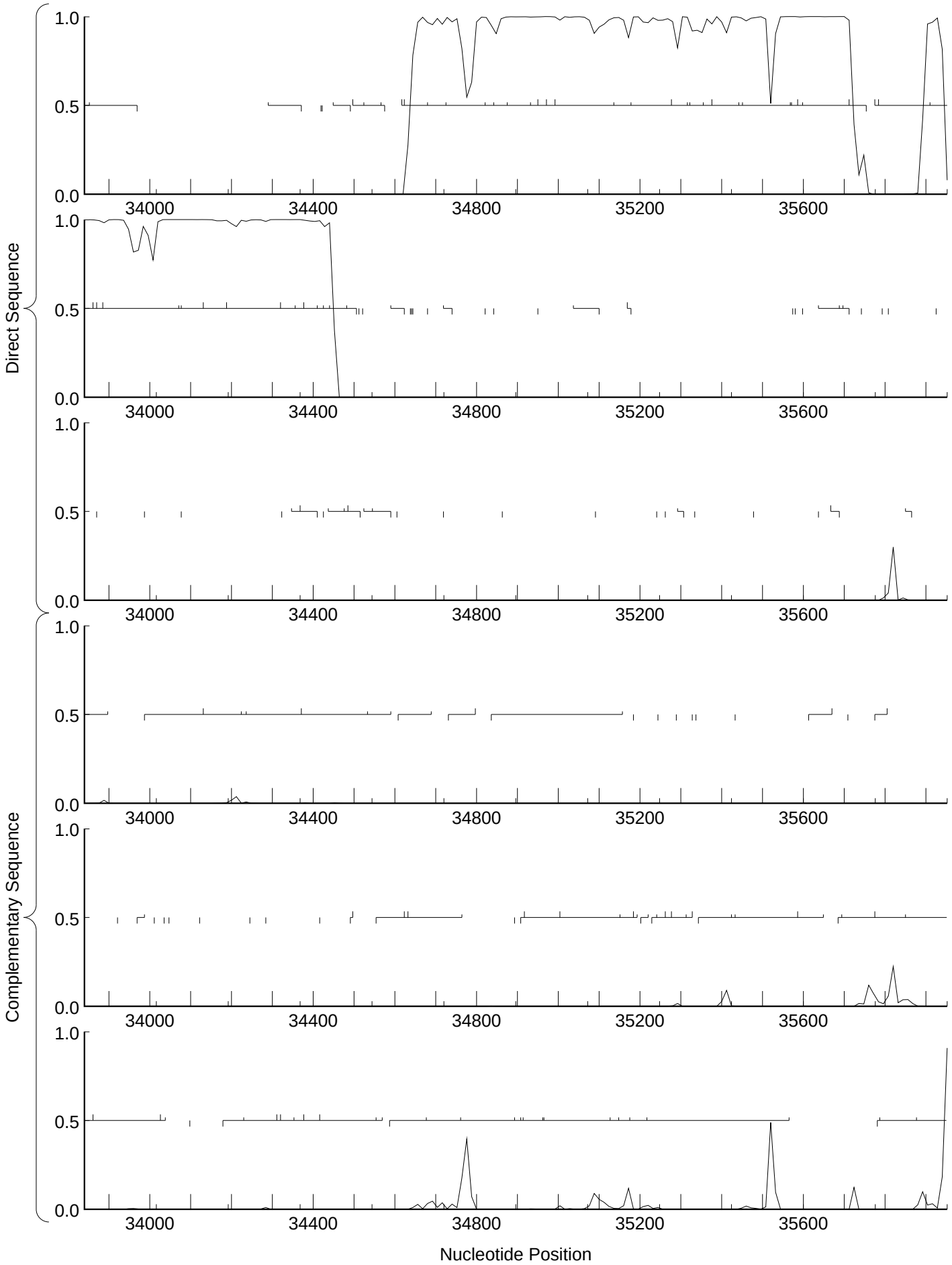

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
25600
26000
26400
26800
27200
Nucleotide Position

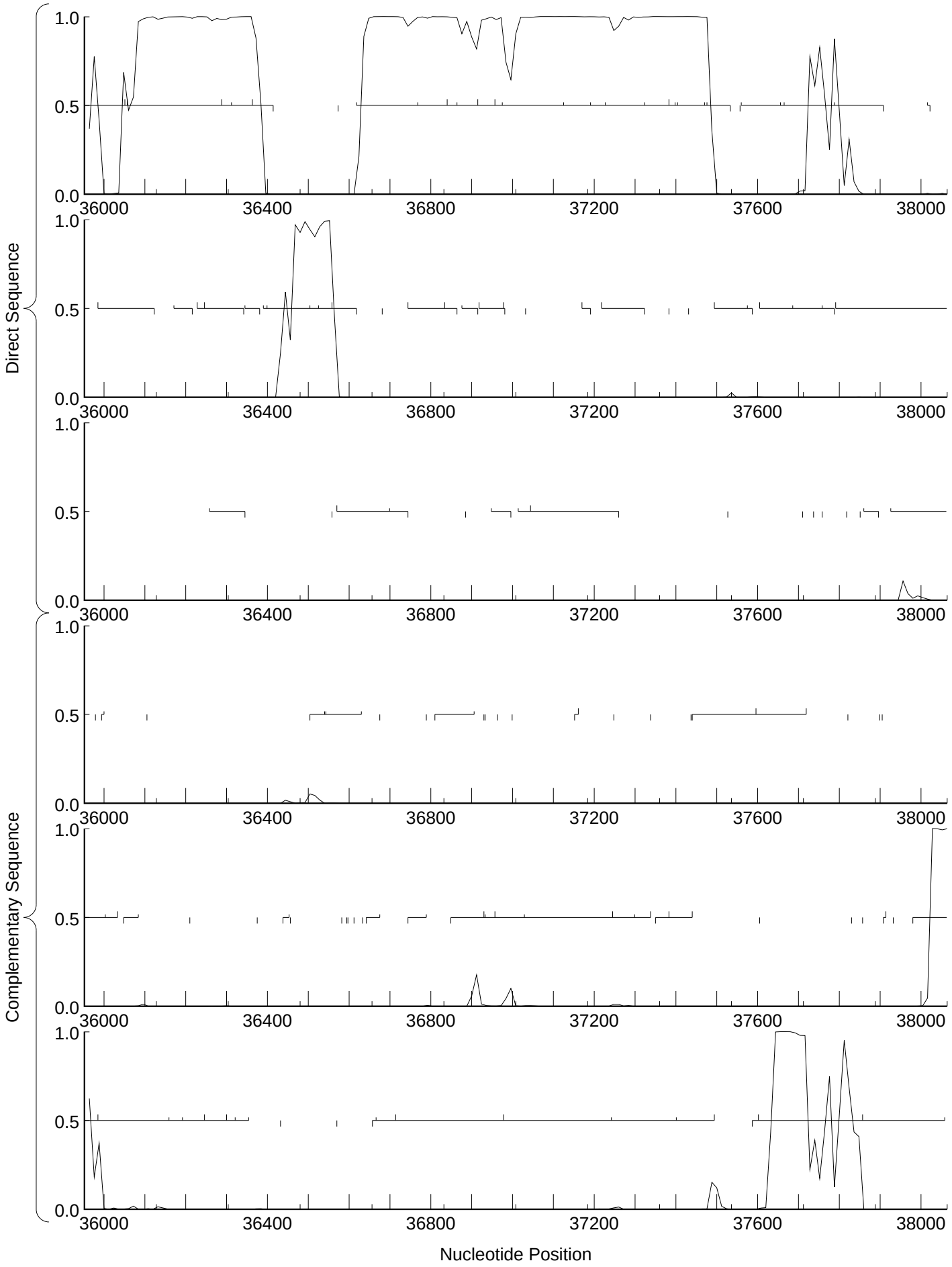
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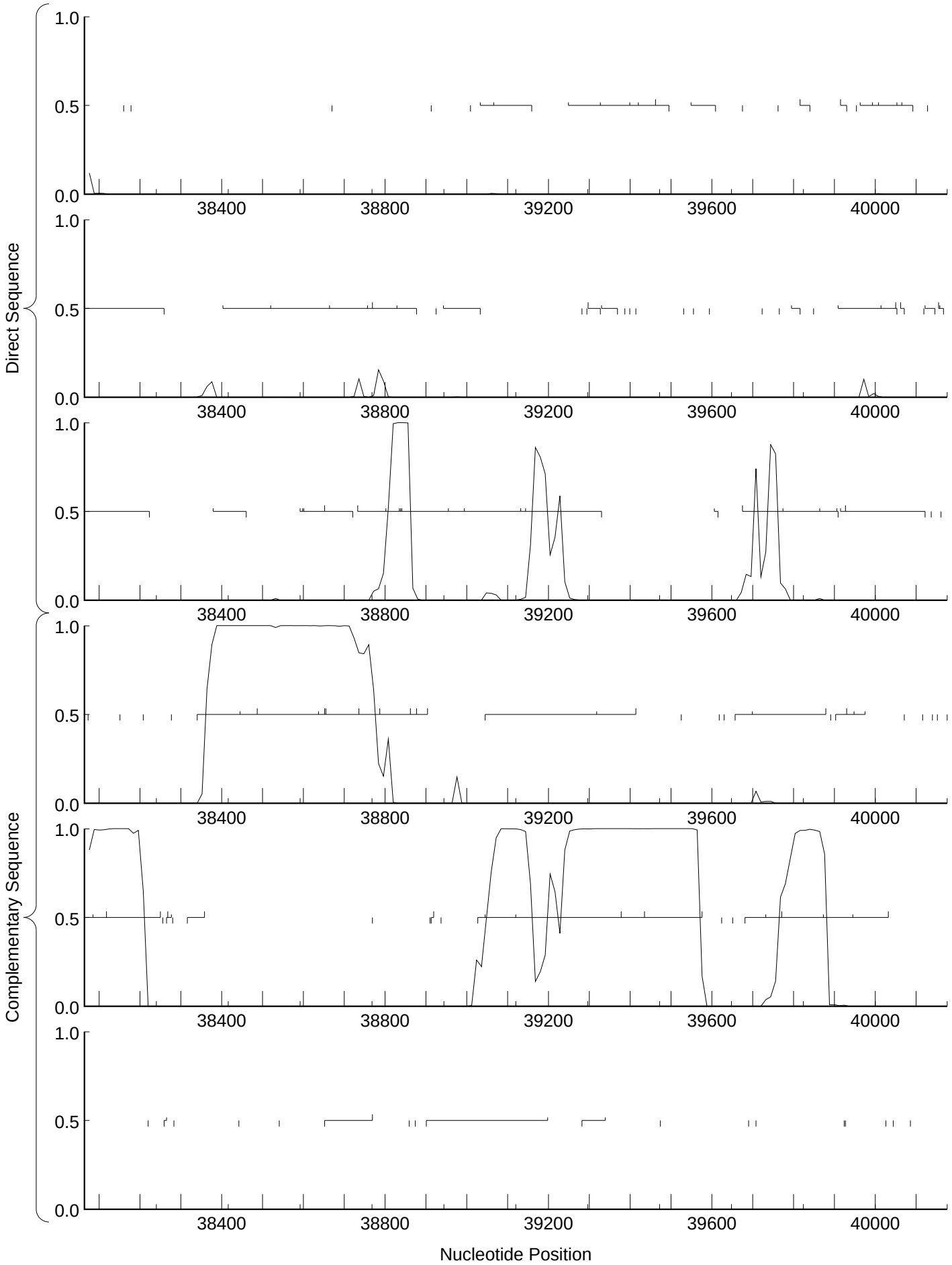

Direct Sequence
Complementary Sequence
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0.5
0.0
30000
30400
30800
31200
31600
Nucleotide Position

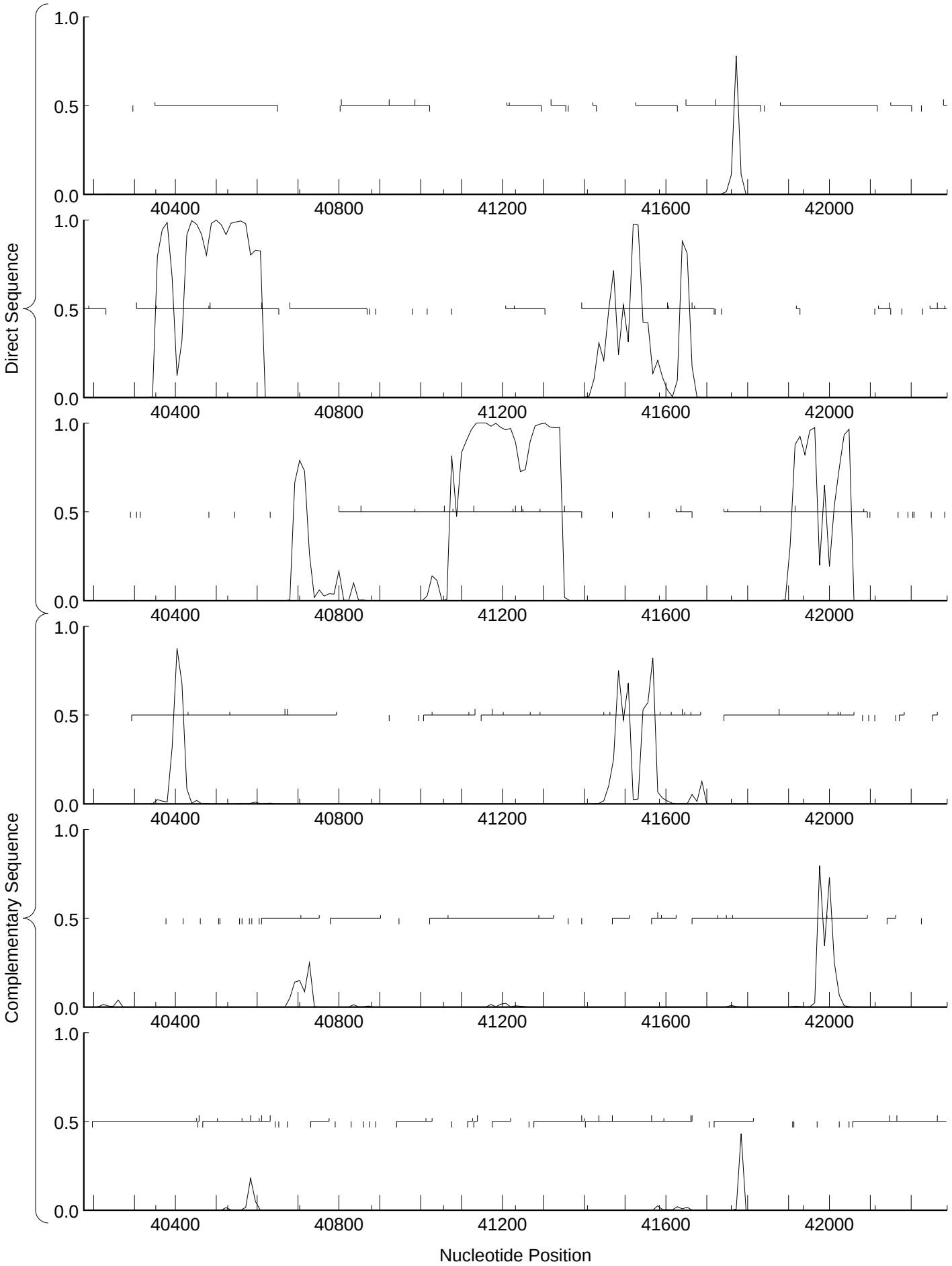

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
32000
32400
32800
33200
33600
Nucleotide Position


Direct Sequence
Complementary Sequence
1.0
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

mplete sequence, 42602 bp including 13-base 3’ overhang (GGTAACCGTGATA), Cluster AK, Order 4, Window 96, Step 12, 20/22




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

mplete sequence, 42602 bp including 13-base 3’ overhang (GGTAACCGTGATA), Cluster AK, Order 4, Window 96, Step 12, 22/22

