GeneMark

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

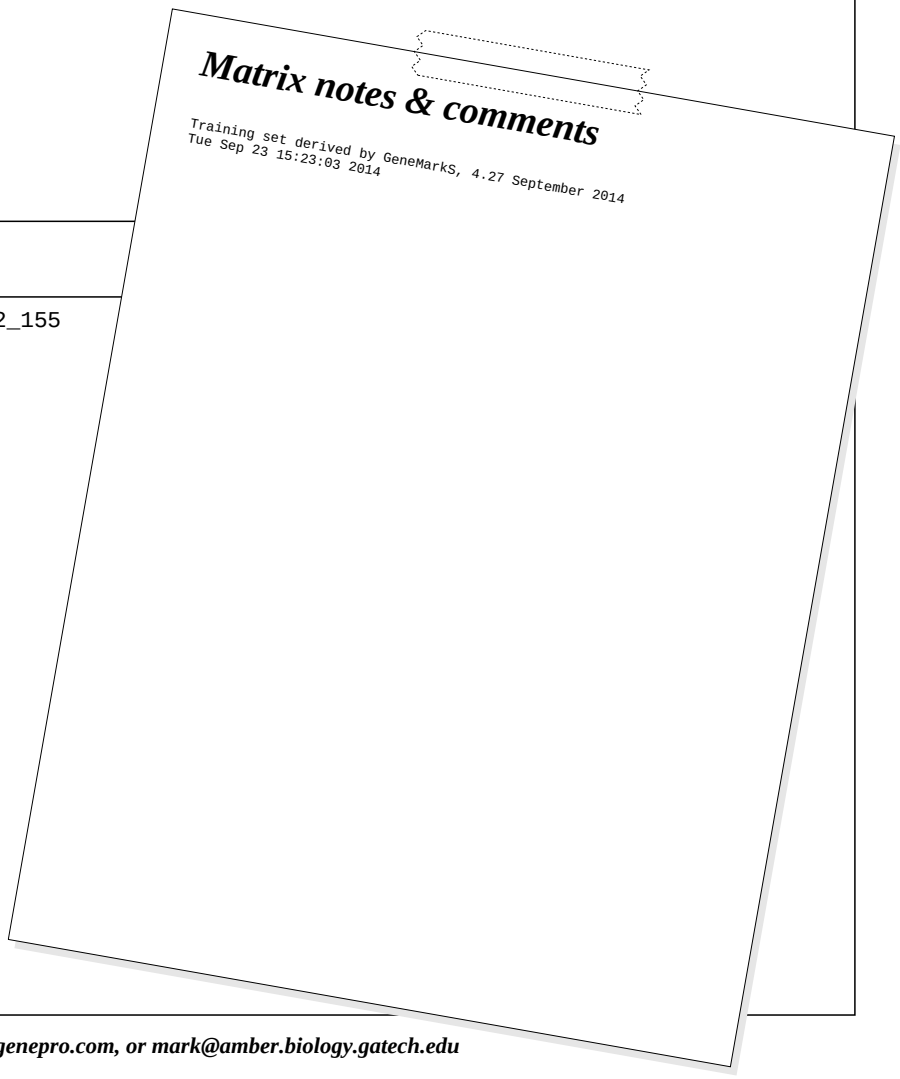
PROGRAM INFORMATION

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Sequence         :  Mycobacterium phage CrimD Final Sequence, 59798 bp including 11-base 3' overhang (CTCGTAGGCA
Analysis Date    :  3/29/24 at 10:28:46
Pages            :  30
Sequence Length  :  59798 bp
GC Content       :   66.88%

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

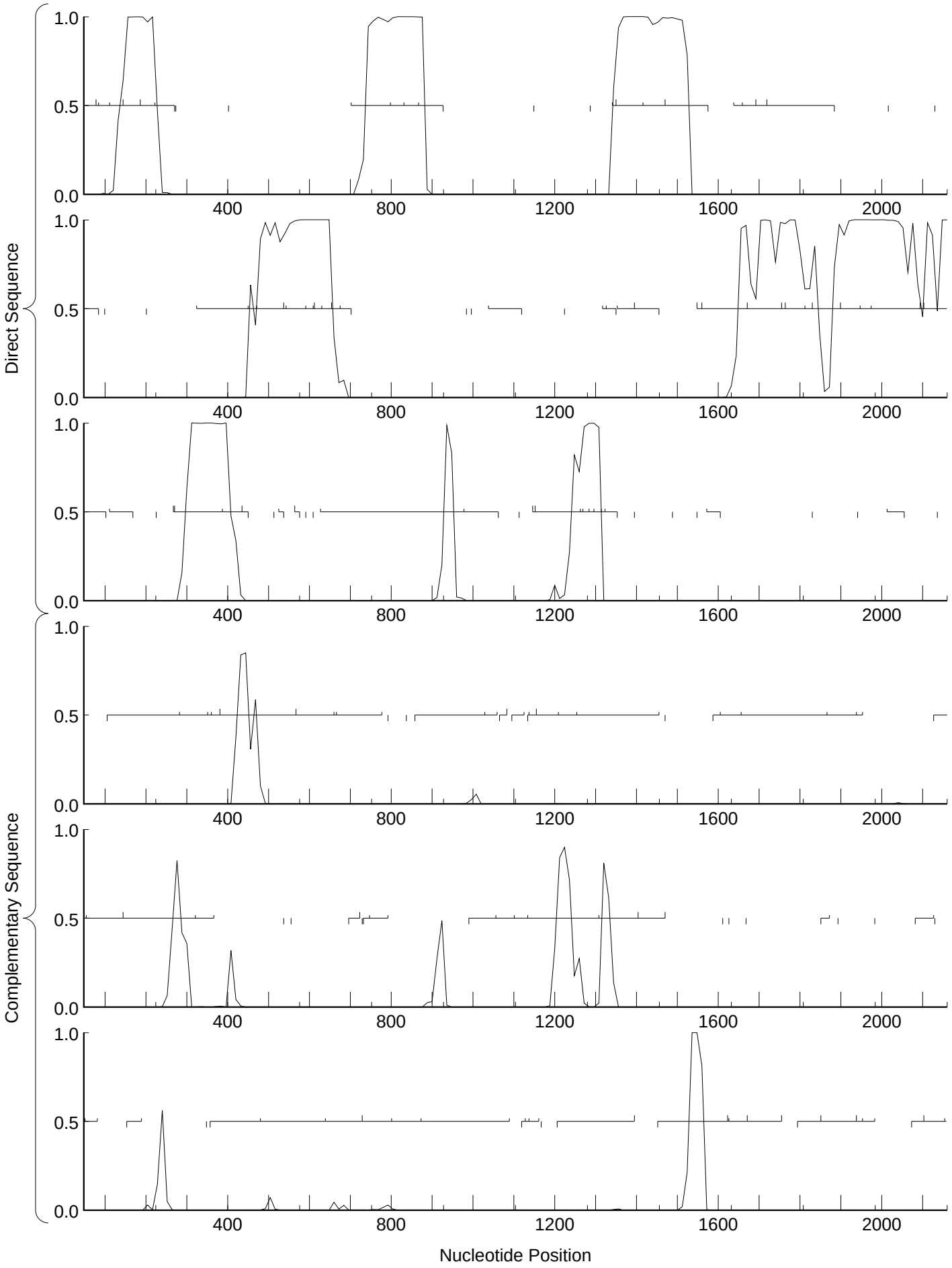
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Matrix     :  Mycobacterium_smegmatis_MC2_155
Author     :  -

Order      :  4
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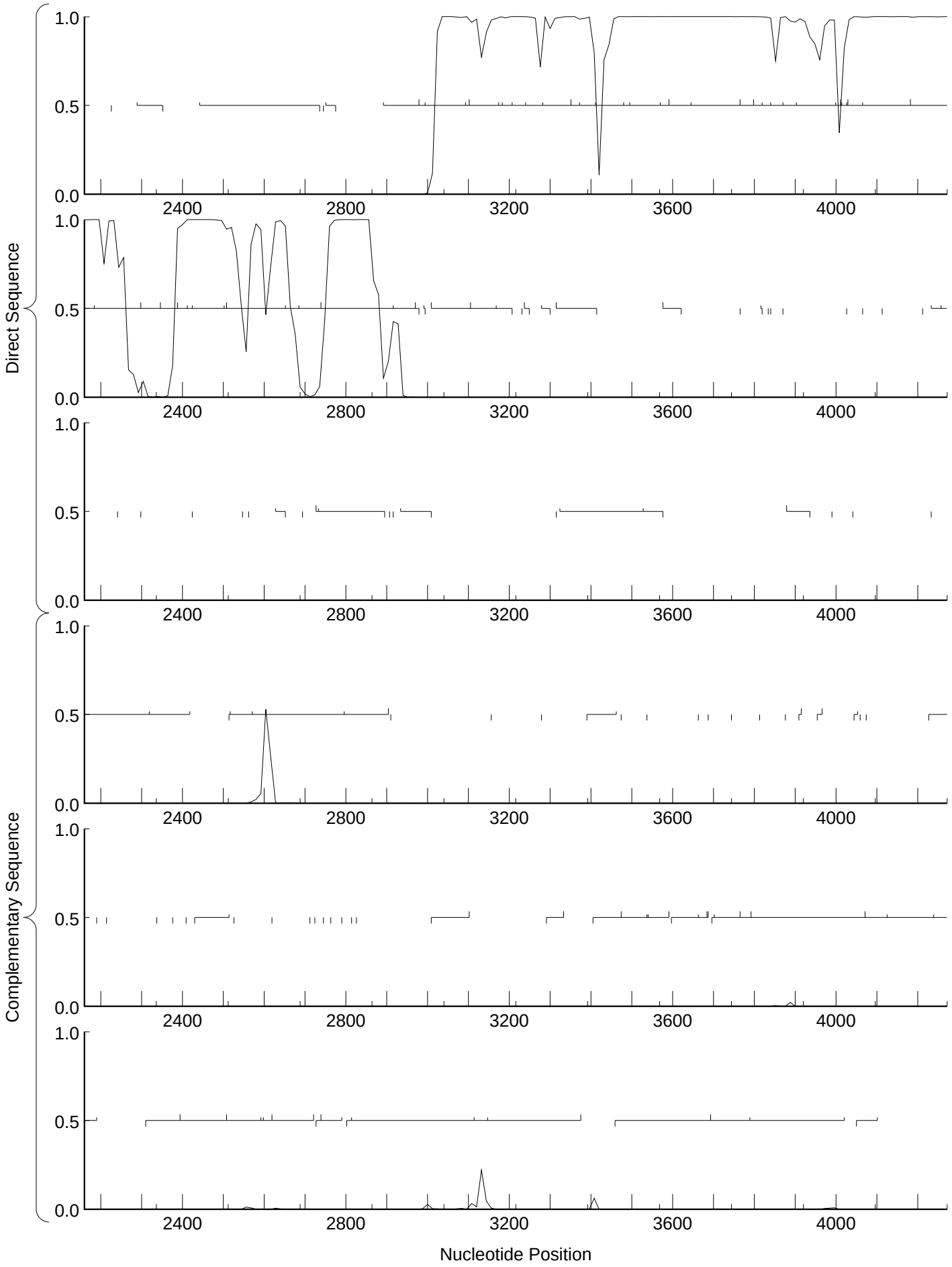

```
  Send questions / comments to:
      Dr. M. Borodovsky
      Georgia Institute of Technology
      School of Biology
      Atlanta, GA  30332-0230
```


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

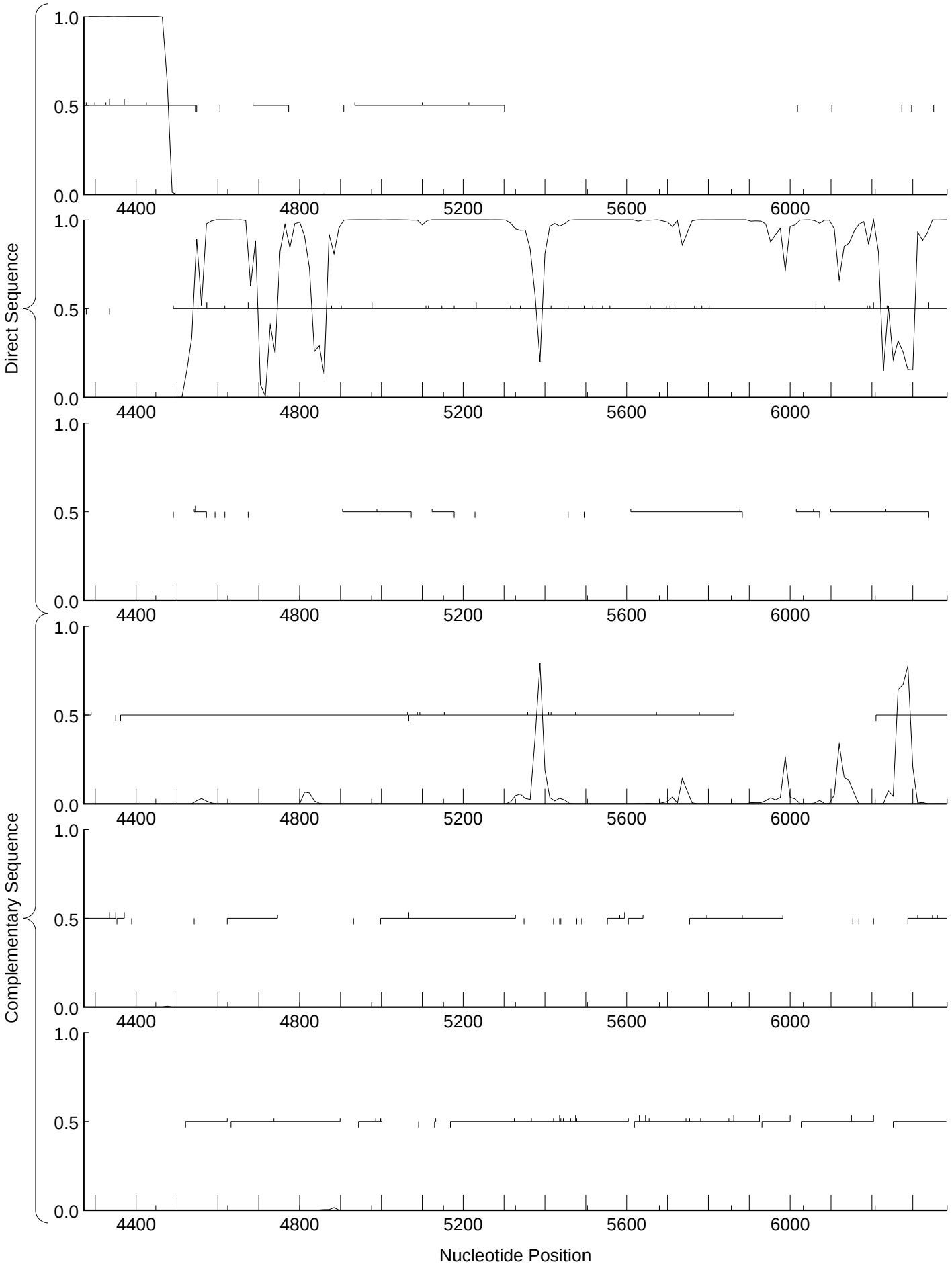
imD Final Sequence, 59798 bp including 11-base 3’ overhang (CTCGTAGGCAT), Cluster K1, Order 4, Window 96, Step 12, 2/30



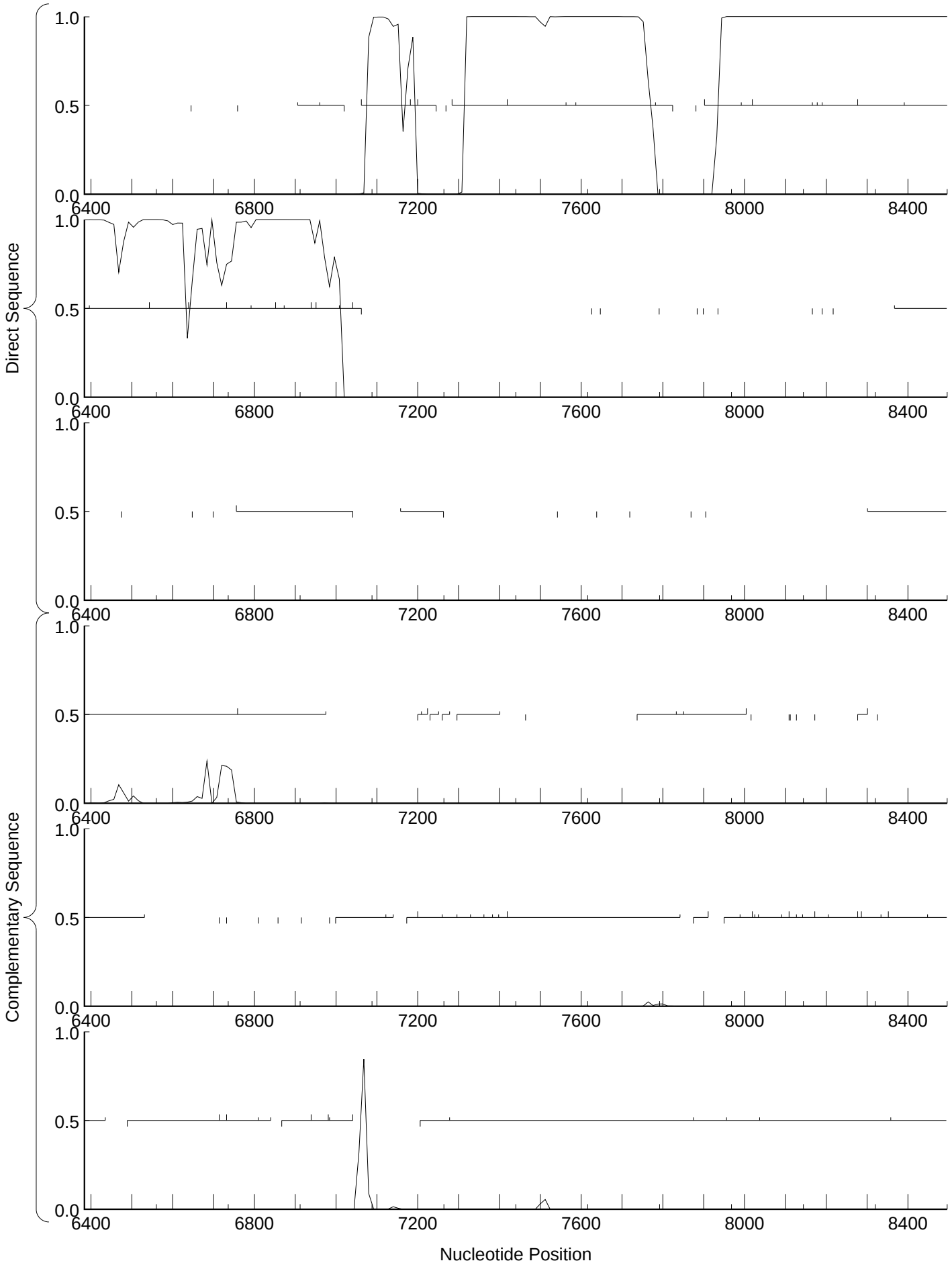
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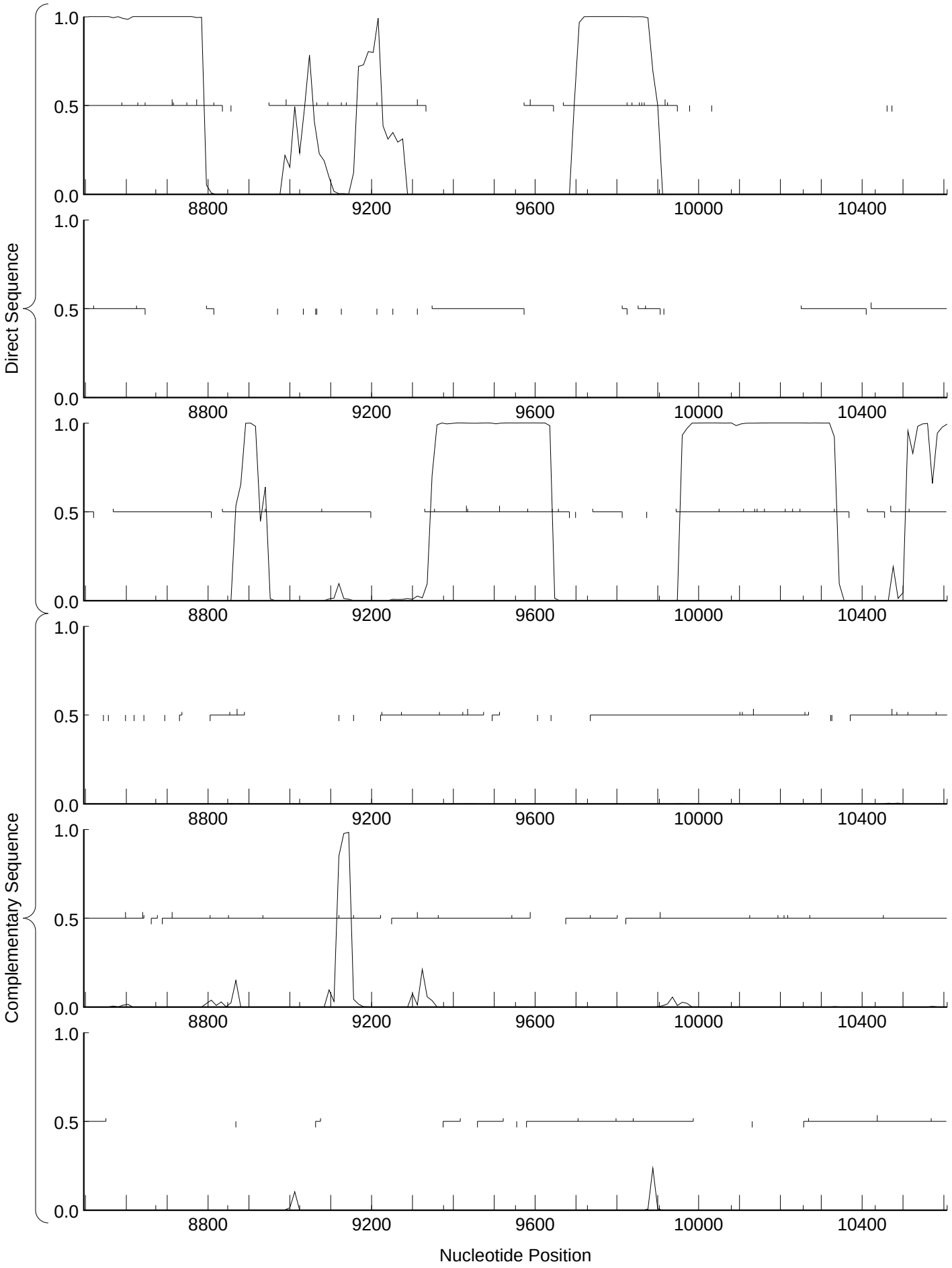
imD Final Sequence, 59798 bp including 11-base 3’ overhang (CTCGTAGGCAT), Cluster K1, Order 4, Window 96, Step 12, 4/30



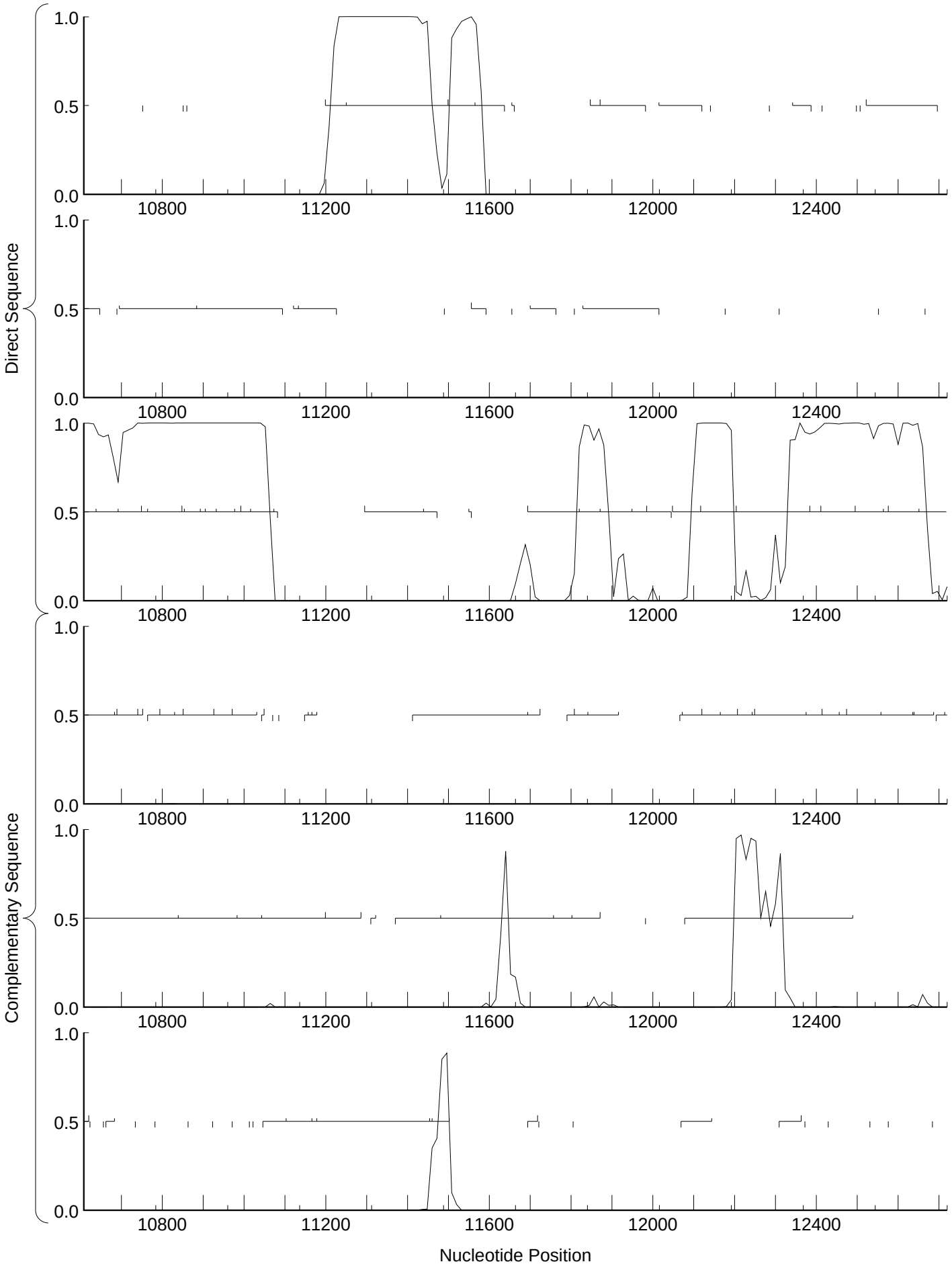
imD Final Sequence, 59798 bp including 11-base 3’ overhang (CTCGTAGGCAT), Cluster K1, Order 4, Window 96, Step 12, 5/30



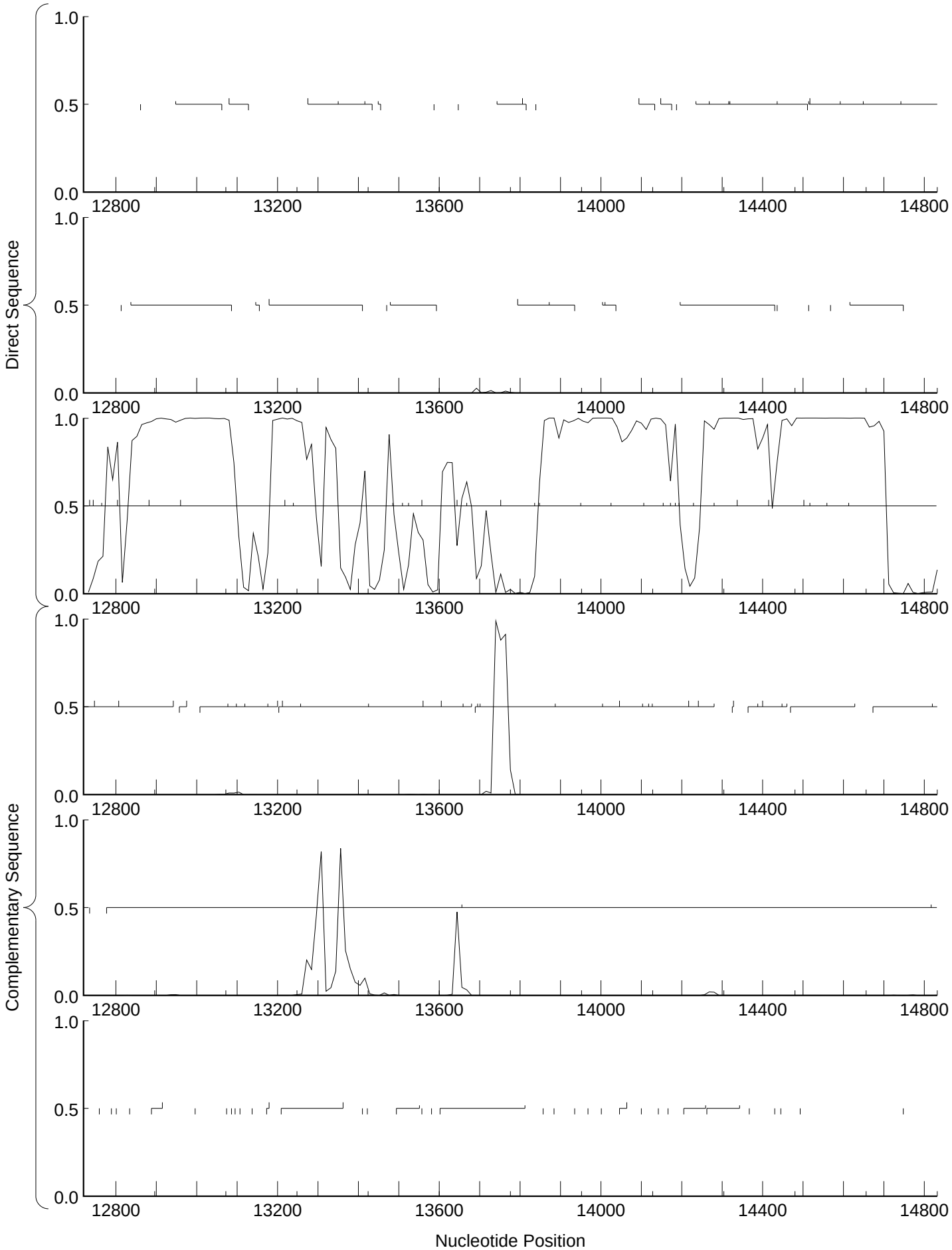
imD Final Sequence, 59798 bp including 11-base 3’ overhang (CTCGTAGGCAT), Cluster K1, Order 4, Window 96, Step 12, 6/30



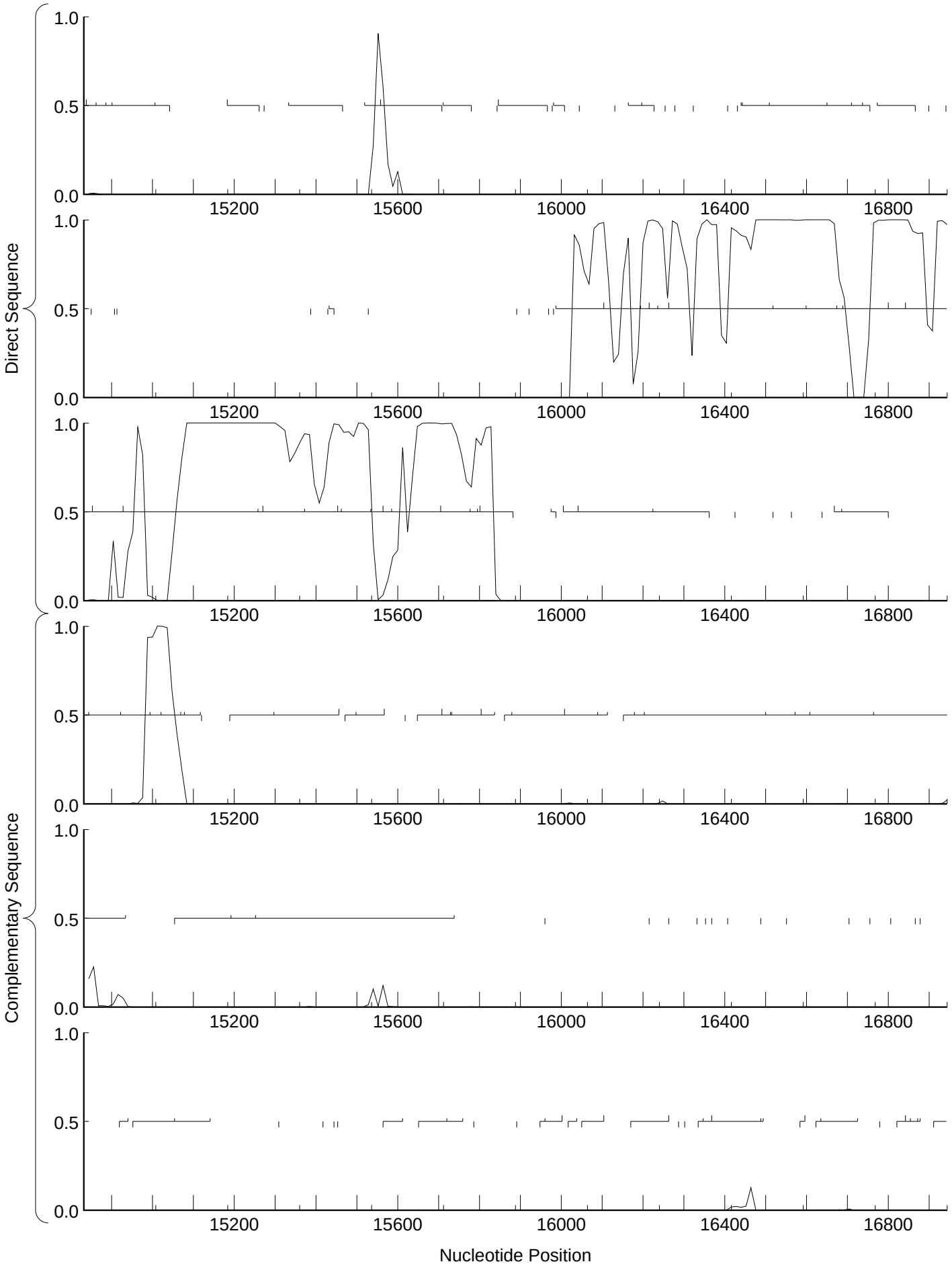
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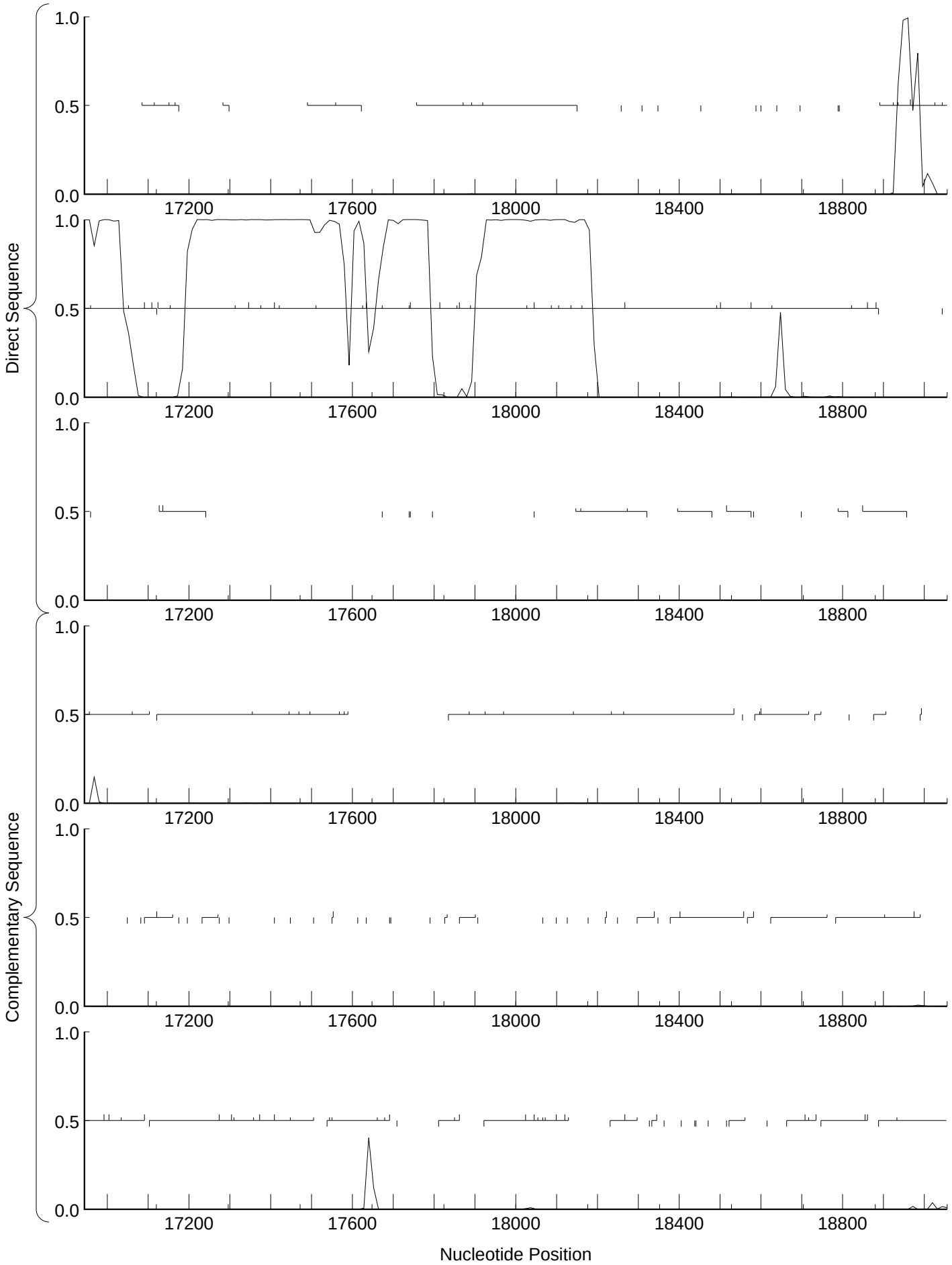
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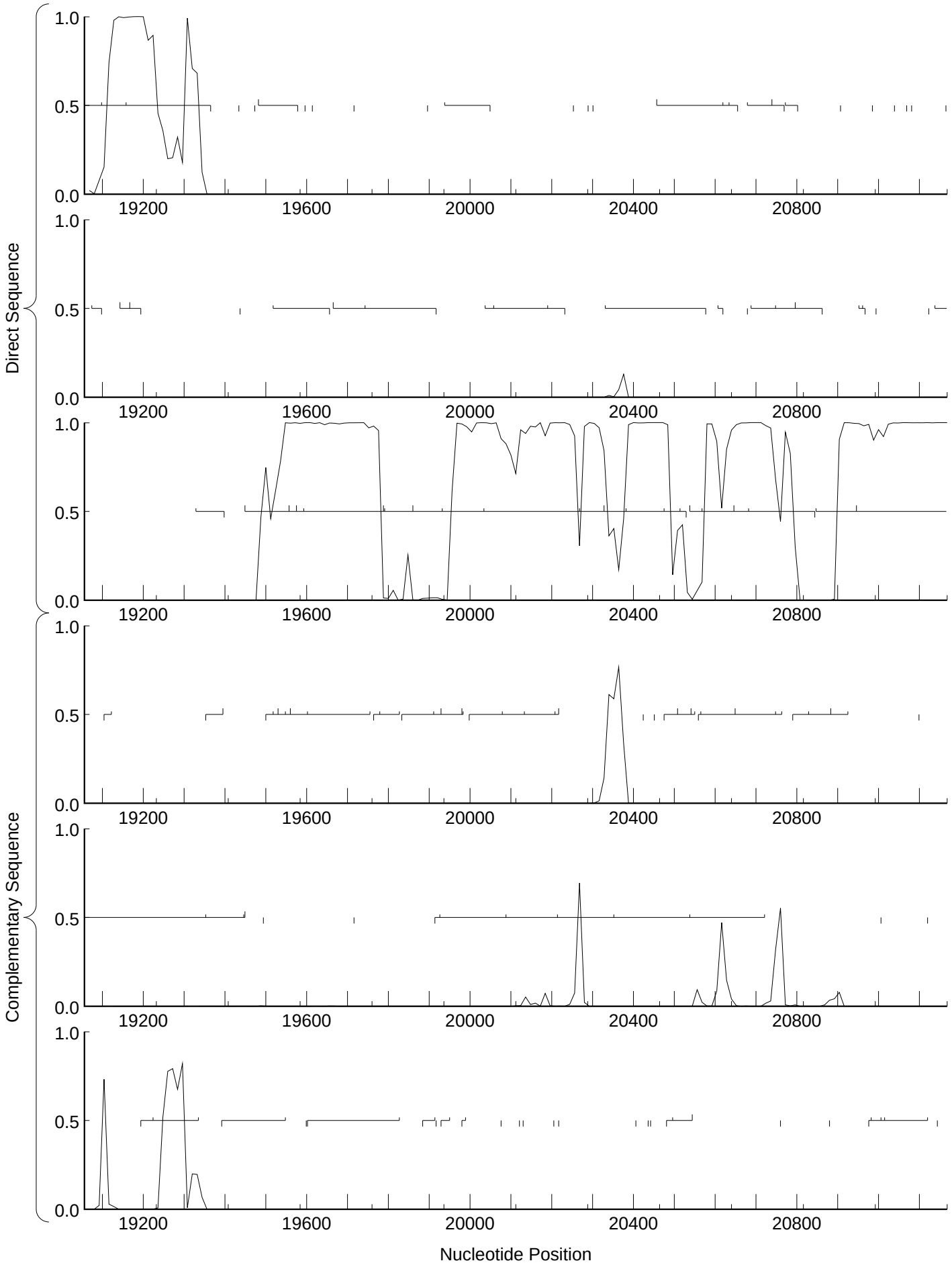
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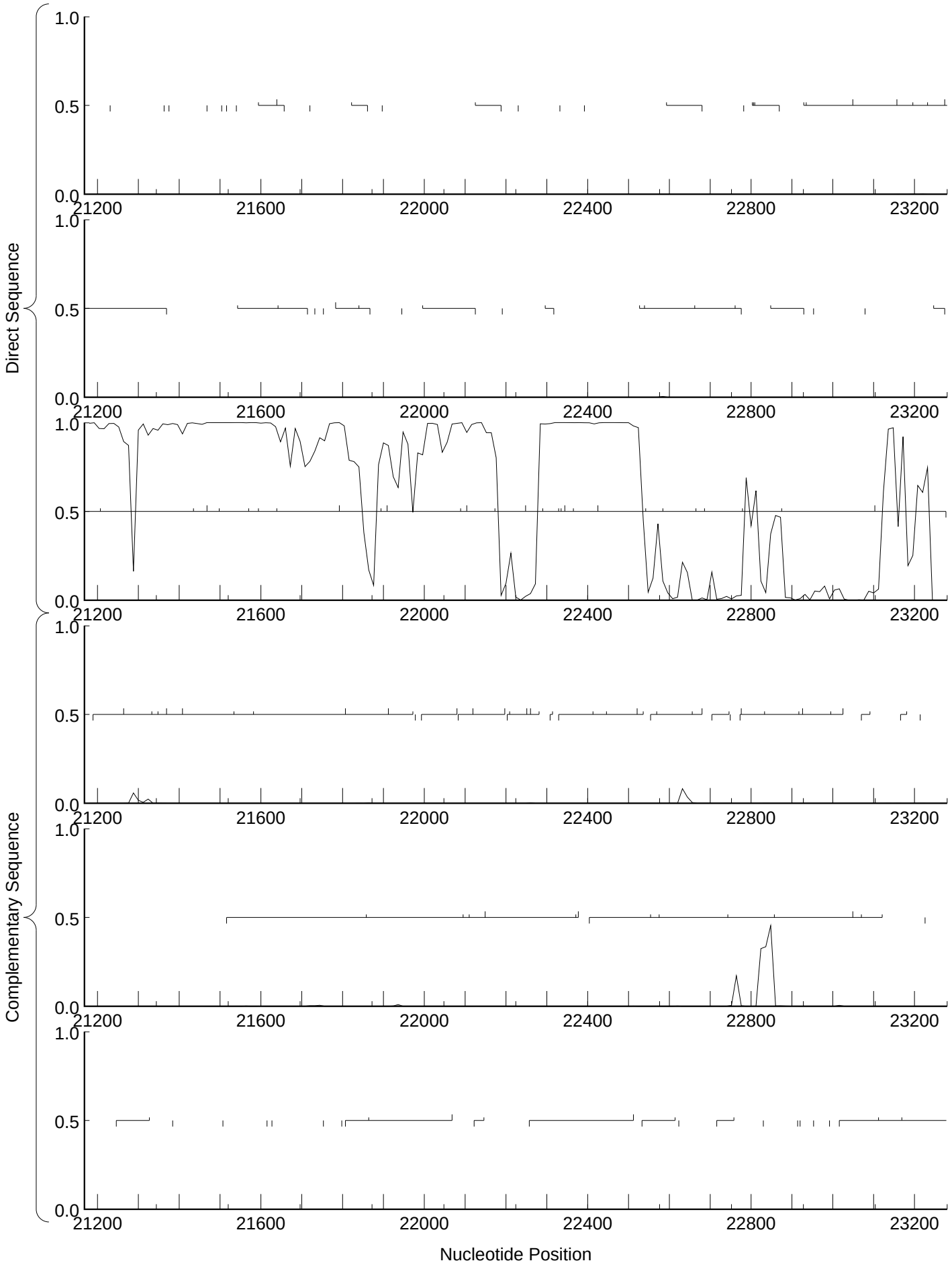
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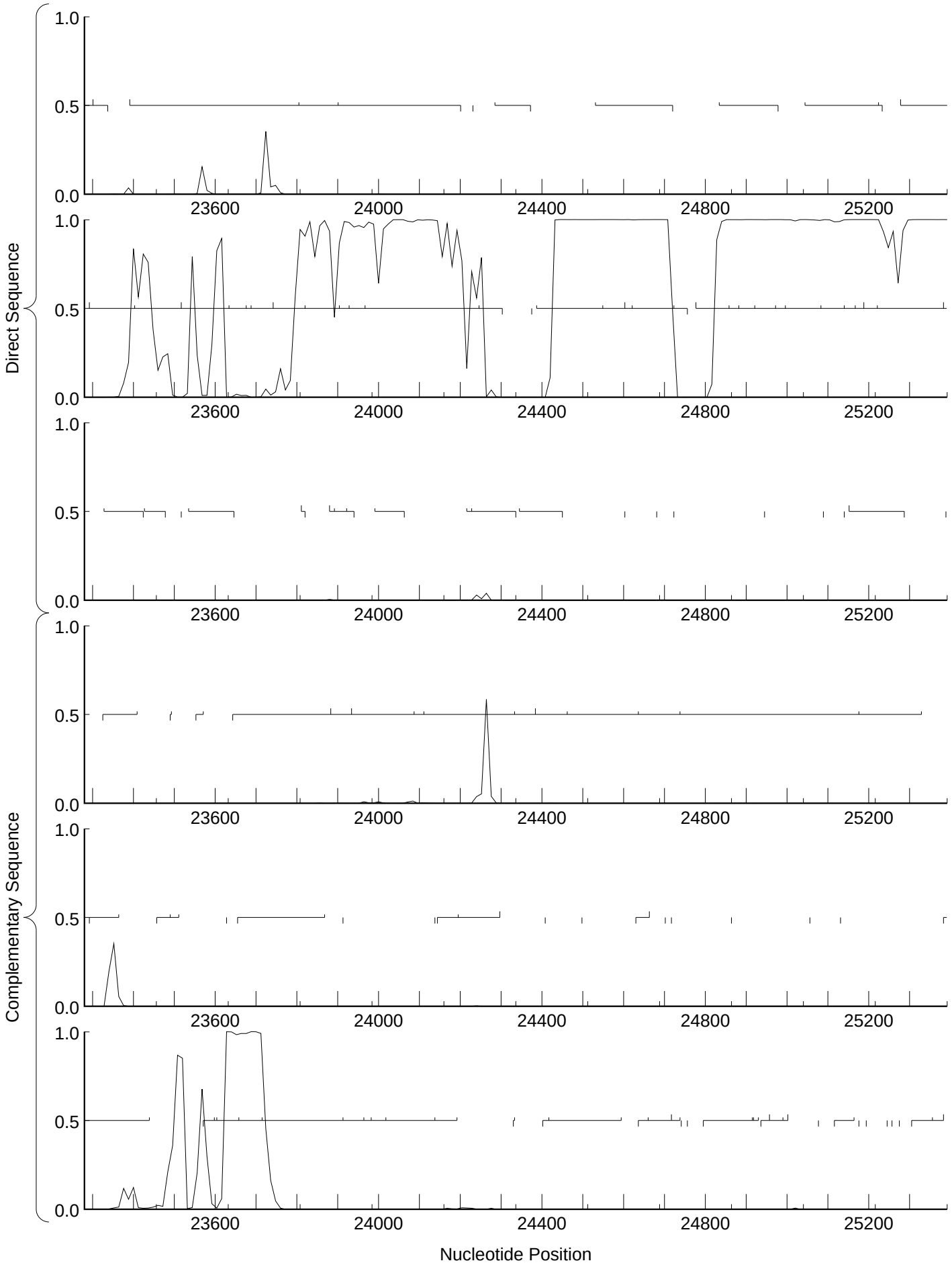


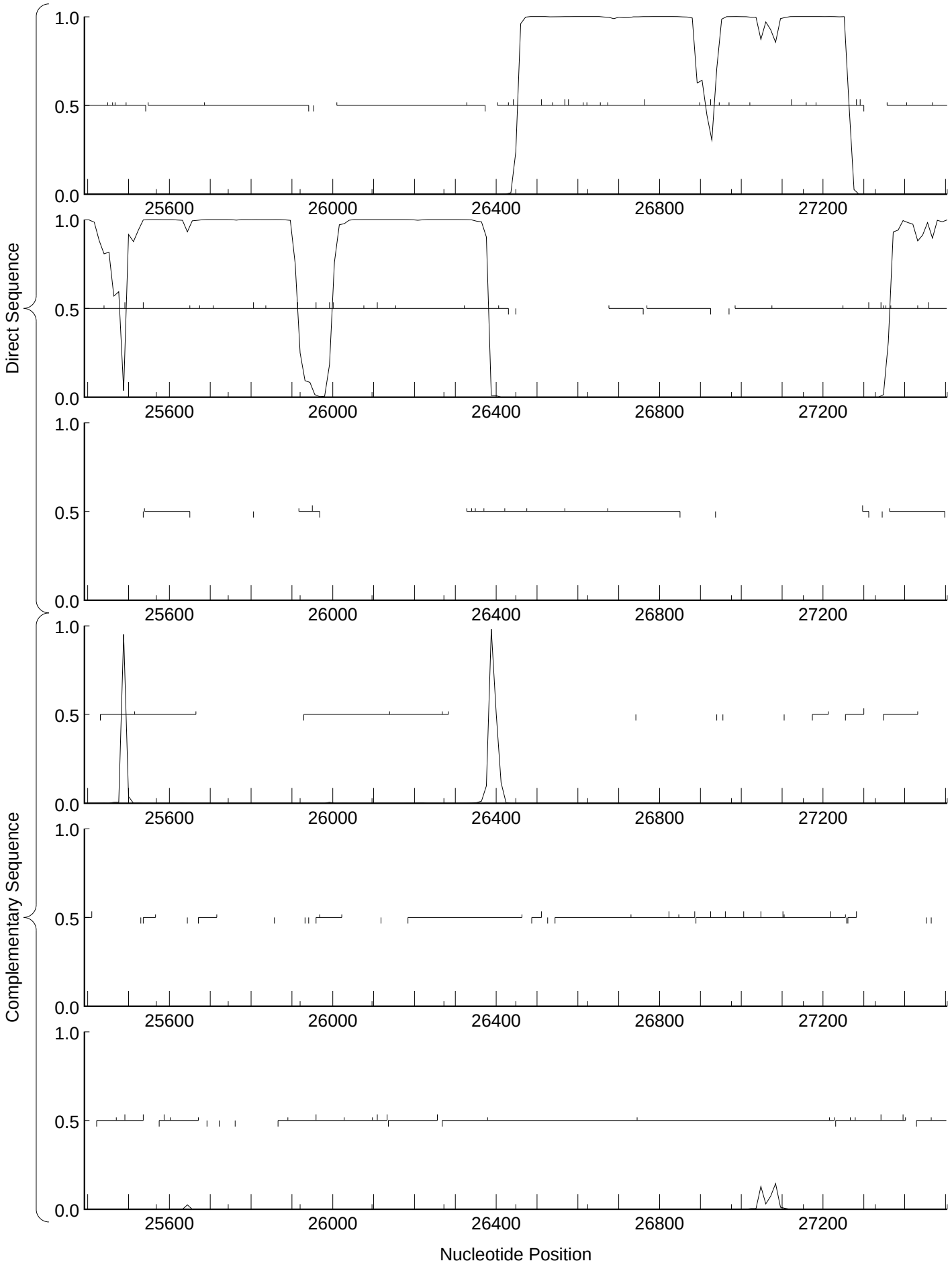
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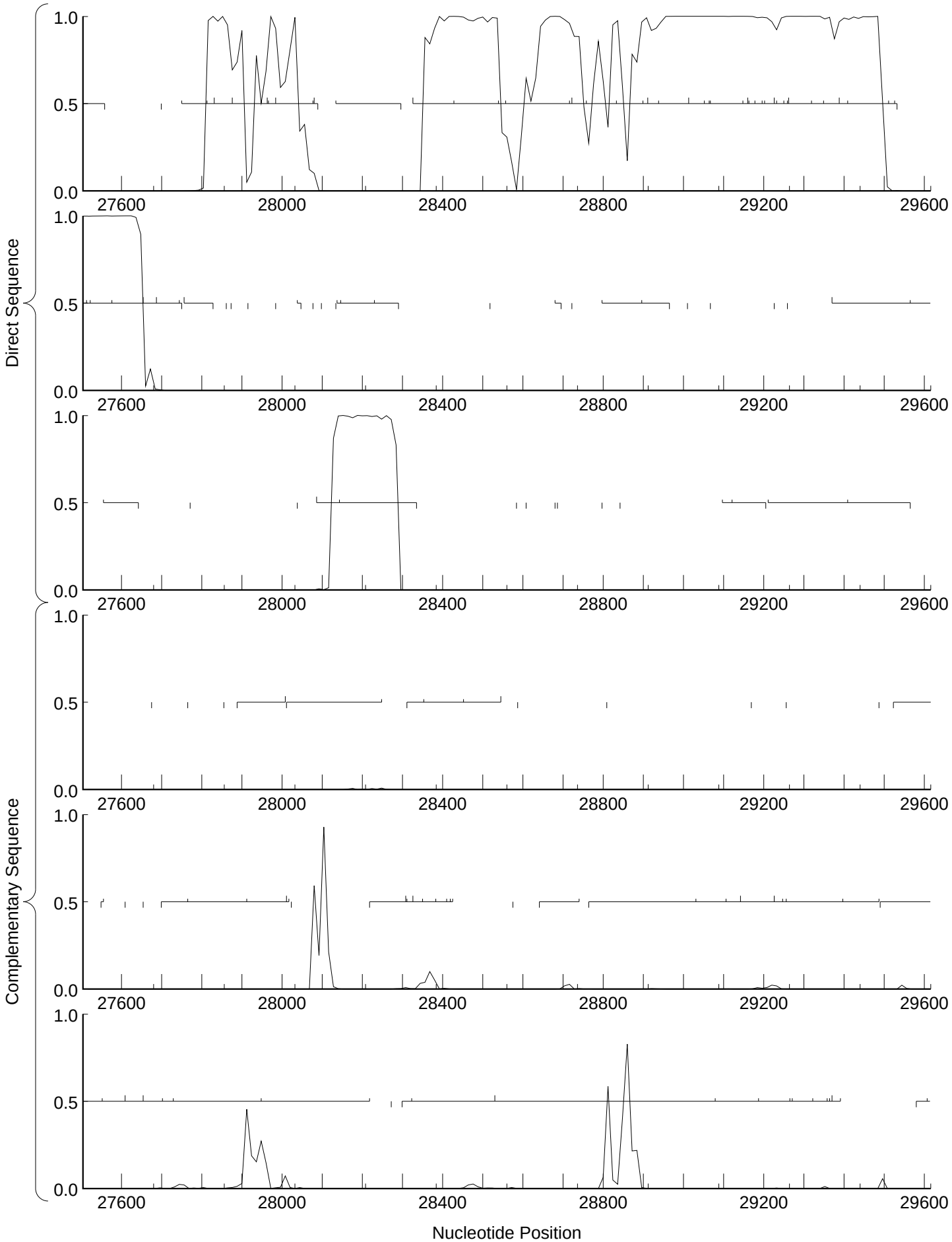
mD Final Sequence, 59798 bp including 11-base 3’ overhang (CTCGTAGGCAT), Cluster K1, Order 4, Window 96, Step 12, 12/30

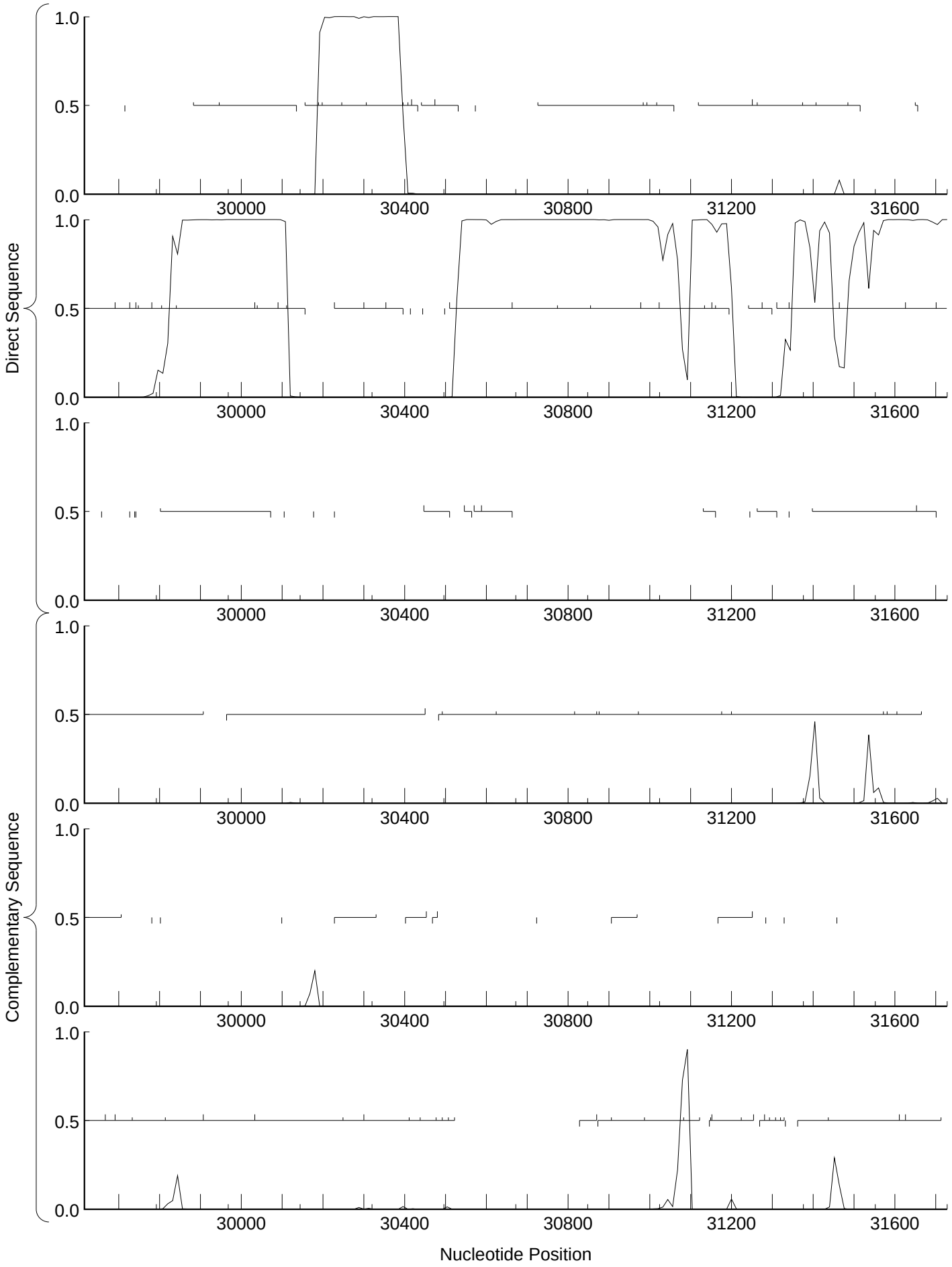


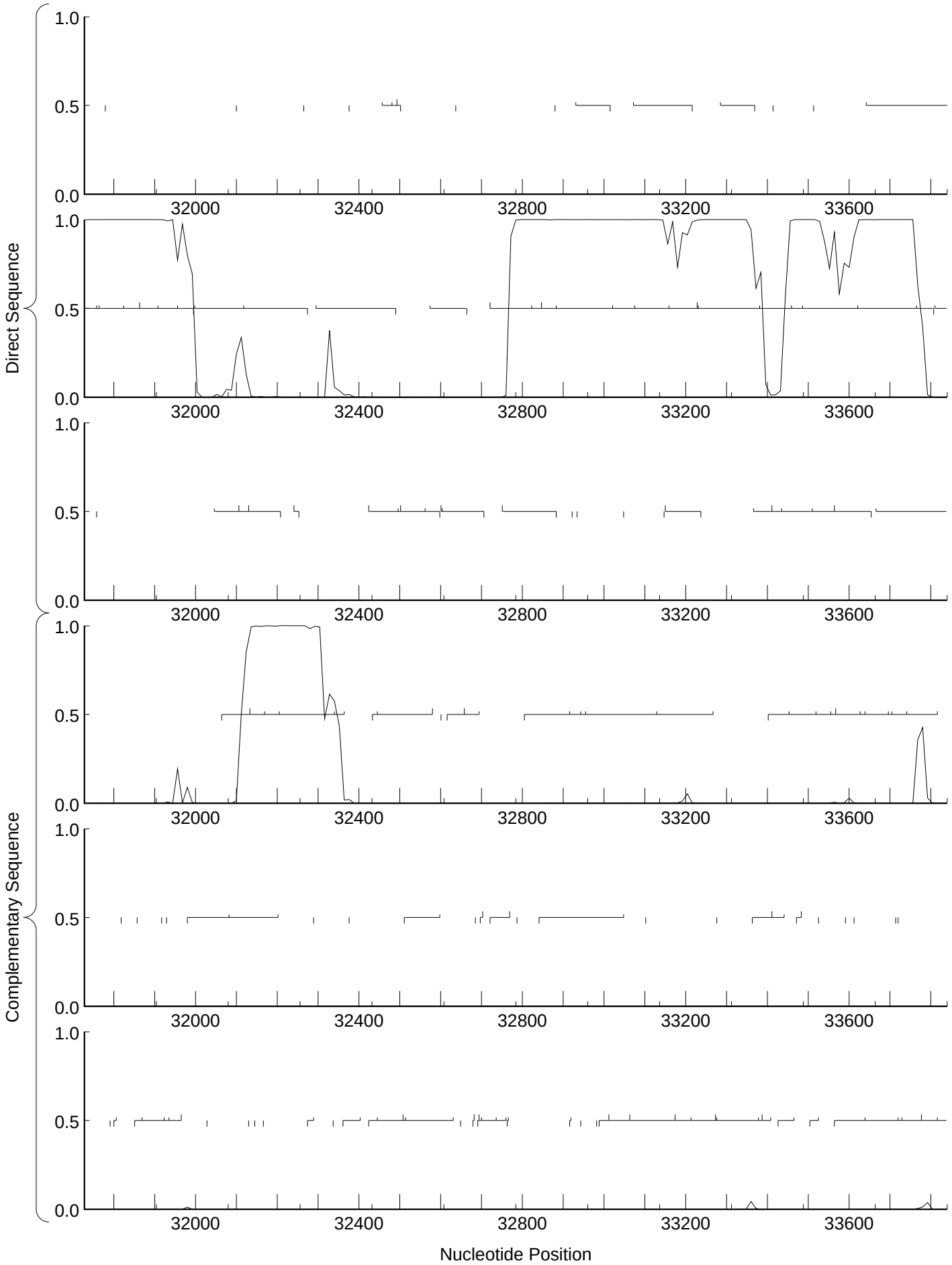

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Complementary Sequence
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0.0
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24000
24400
24800
25200
Nucleotide Position

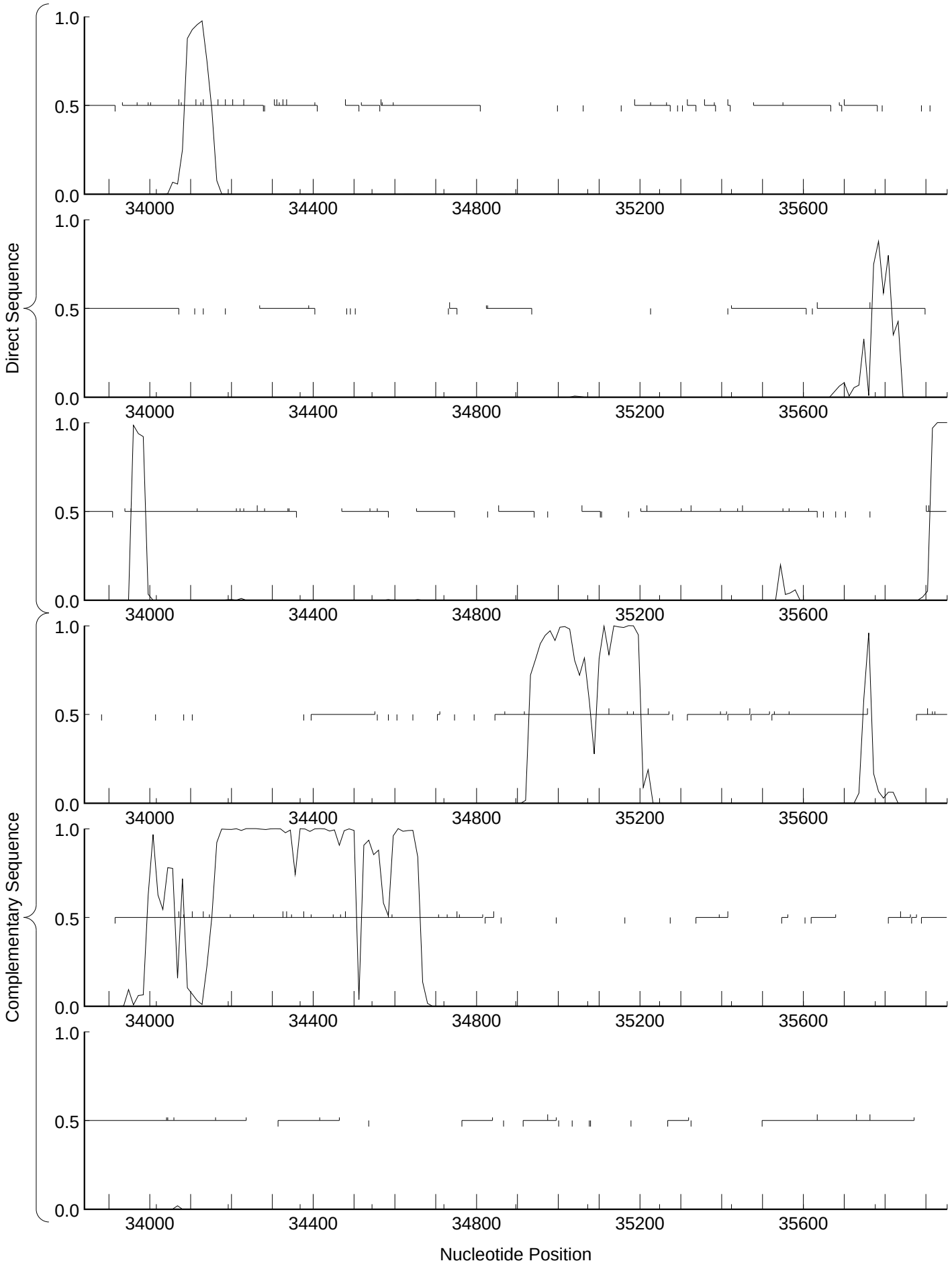

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
25600
26000
26400
26800
27200
Nucleotide Position

mD Final Sequence, 59798 bp including 11-base 3’ overhang (CTCGTAGGCAT), Cluster K1, Order 4, Window 96, Step 12, 15/30

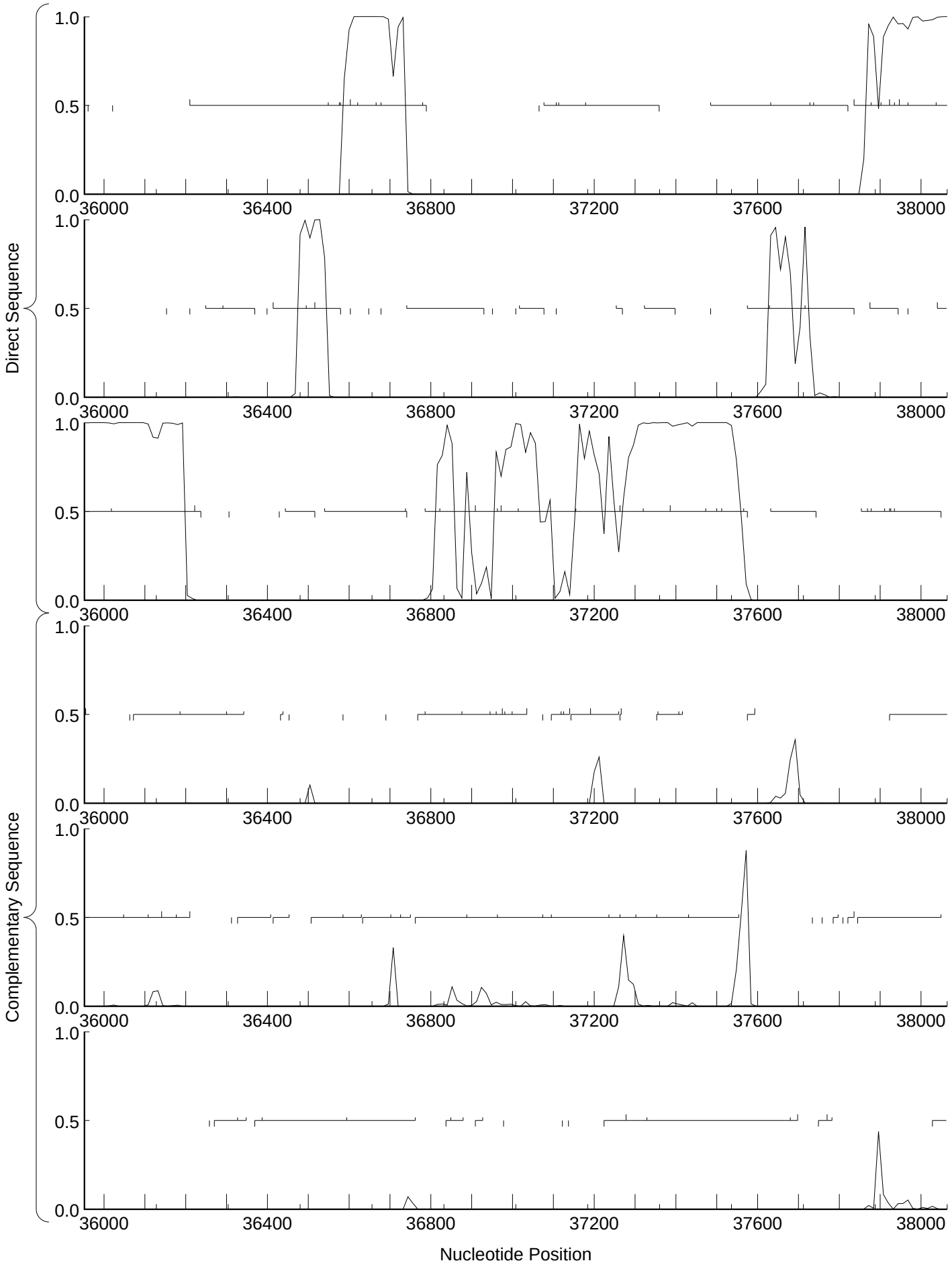


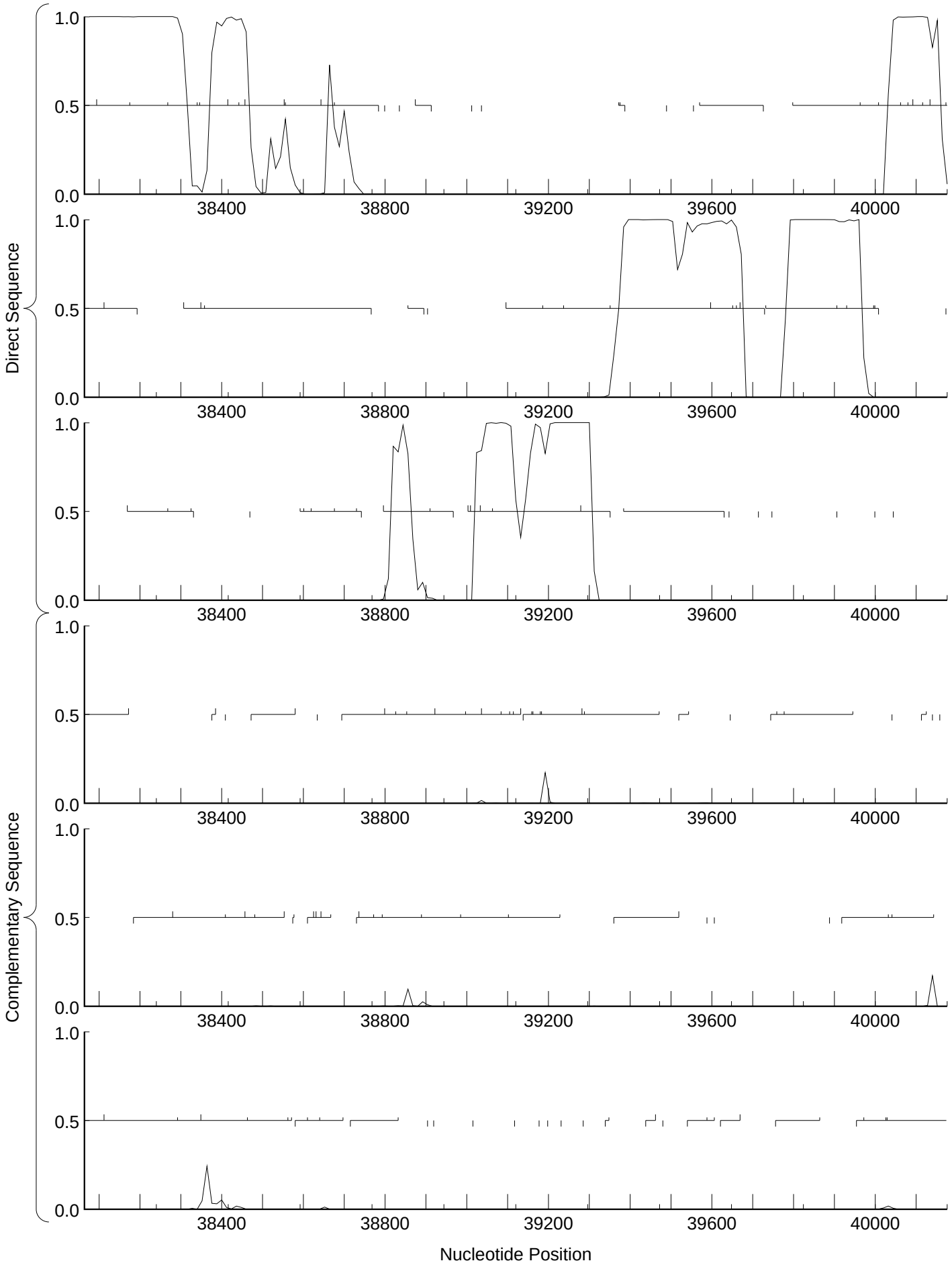

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
30000
30400
30800
31200
31600
Nucleotide Position


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

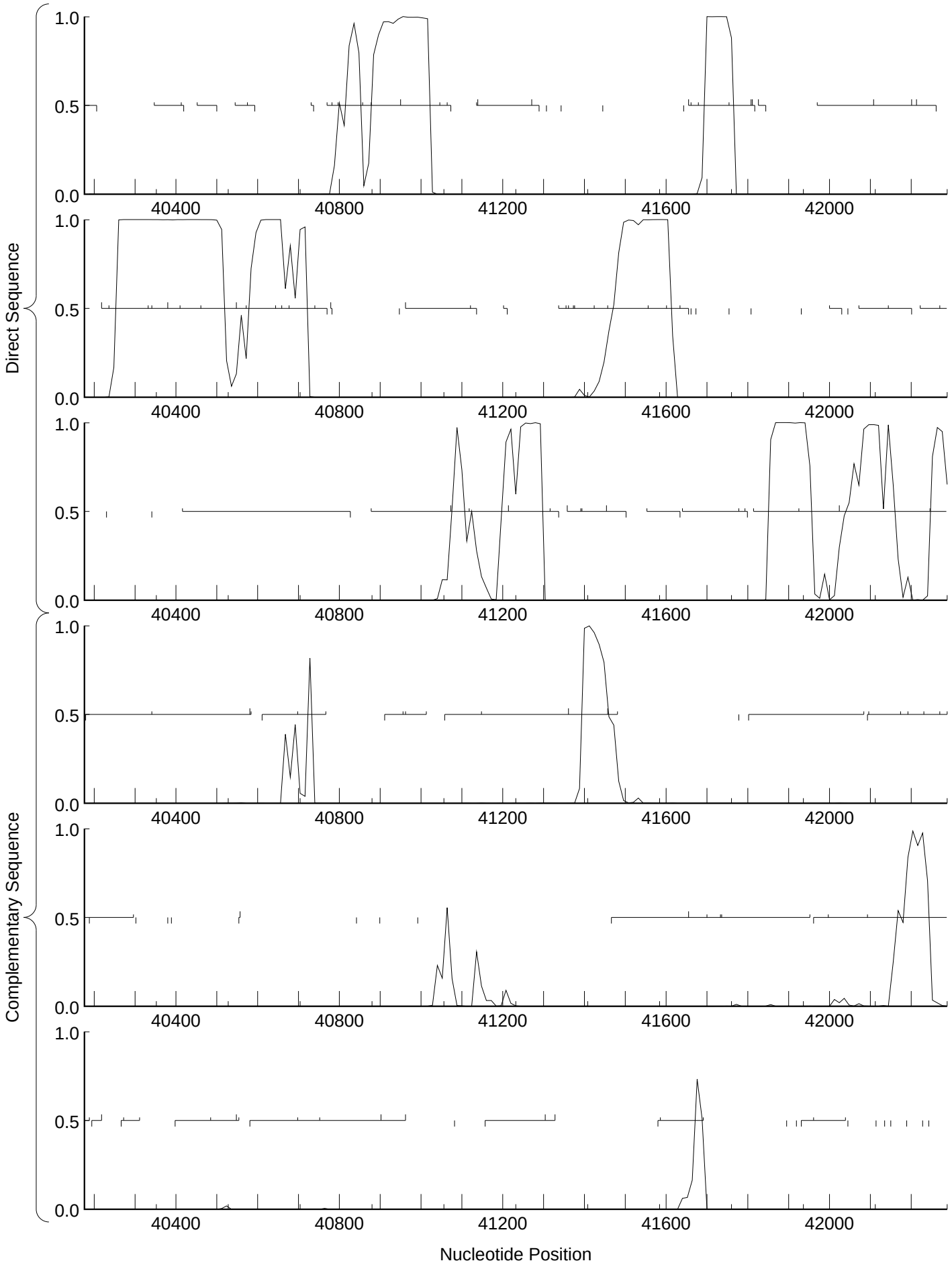

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Complementary Sequence
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0.0
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34400
34800
35200
35600
Nucleotide Position

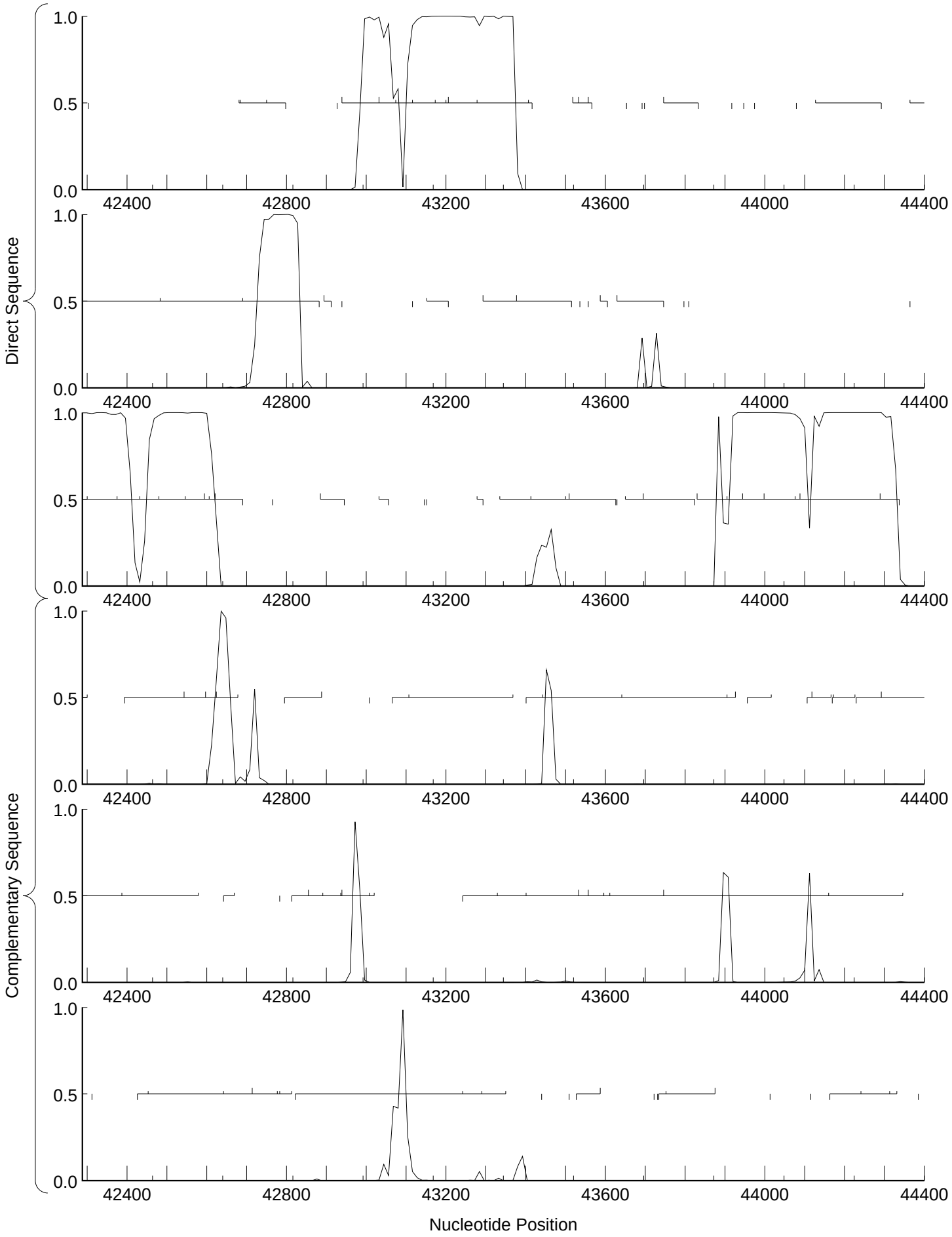
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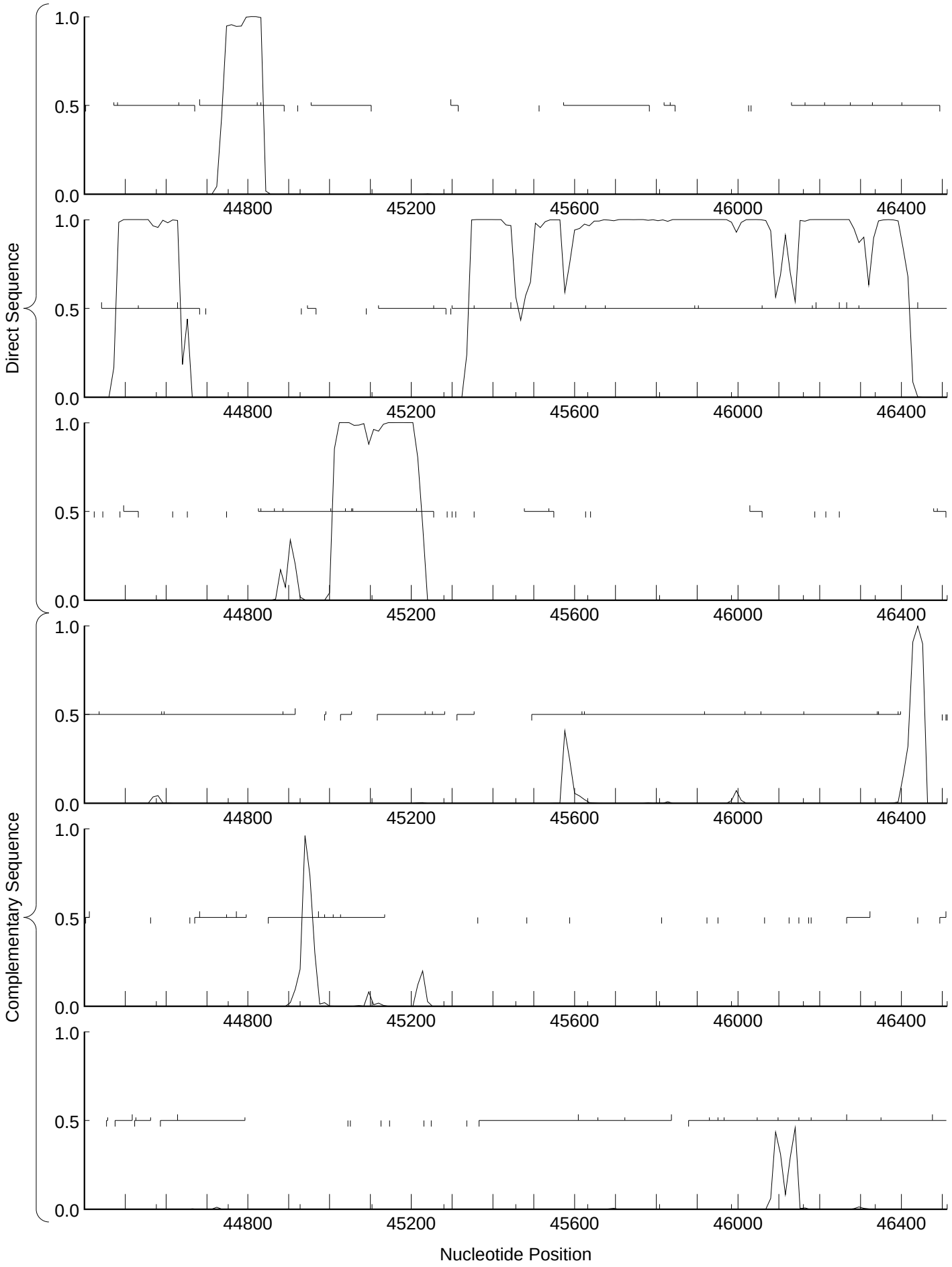

Direct Sequence
Complementary Sequence
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38400
38800
39200
39600
40000
Nucleotide Position

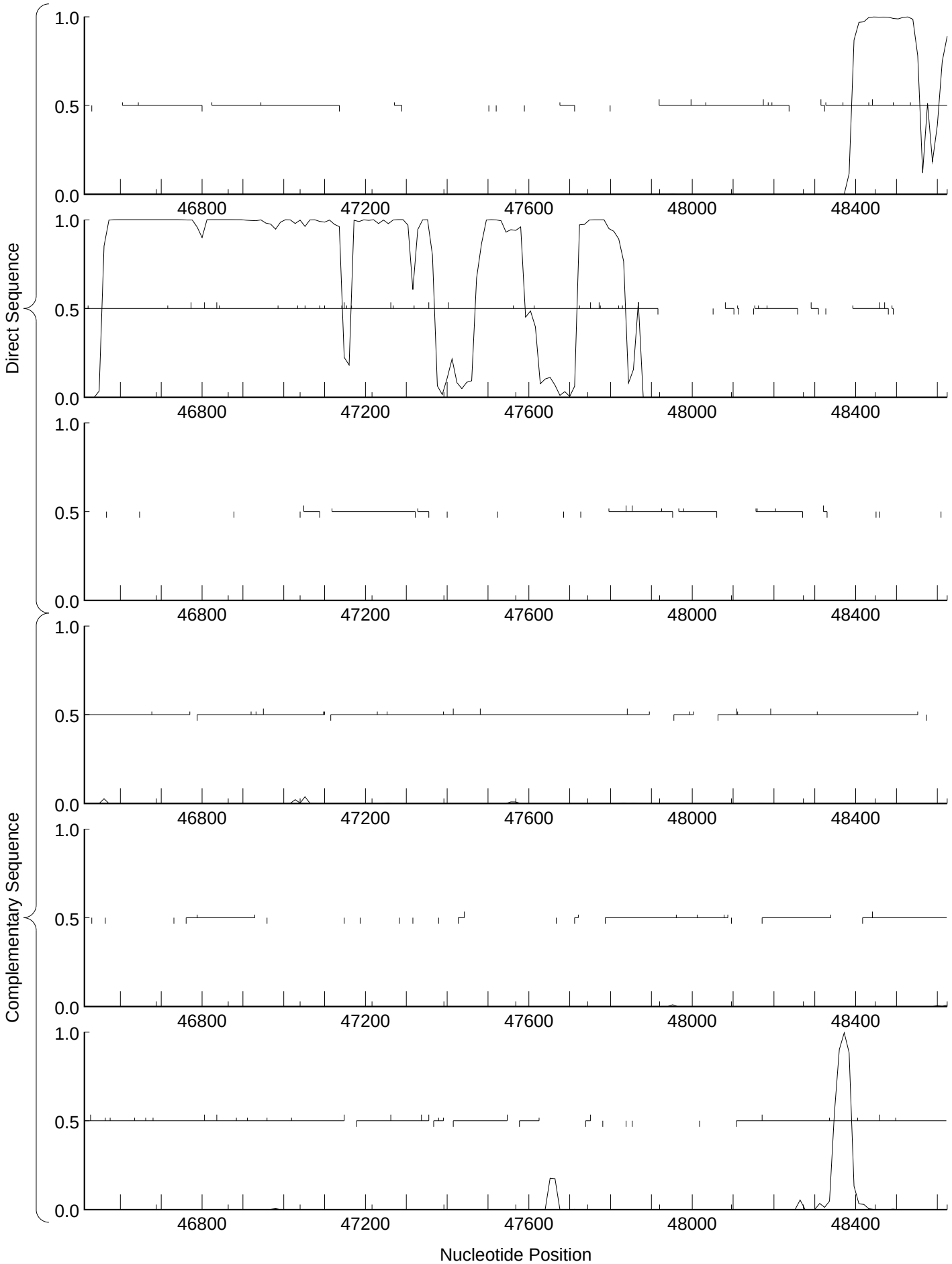
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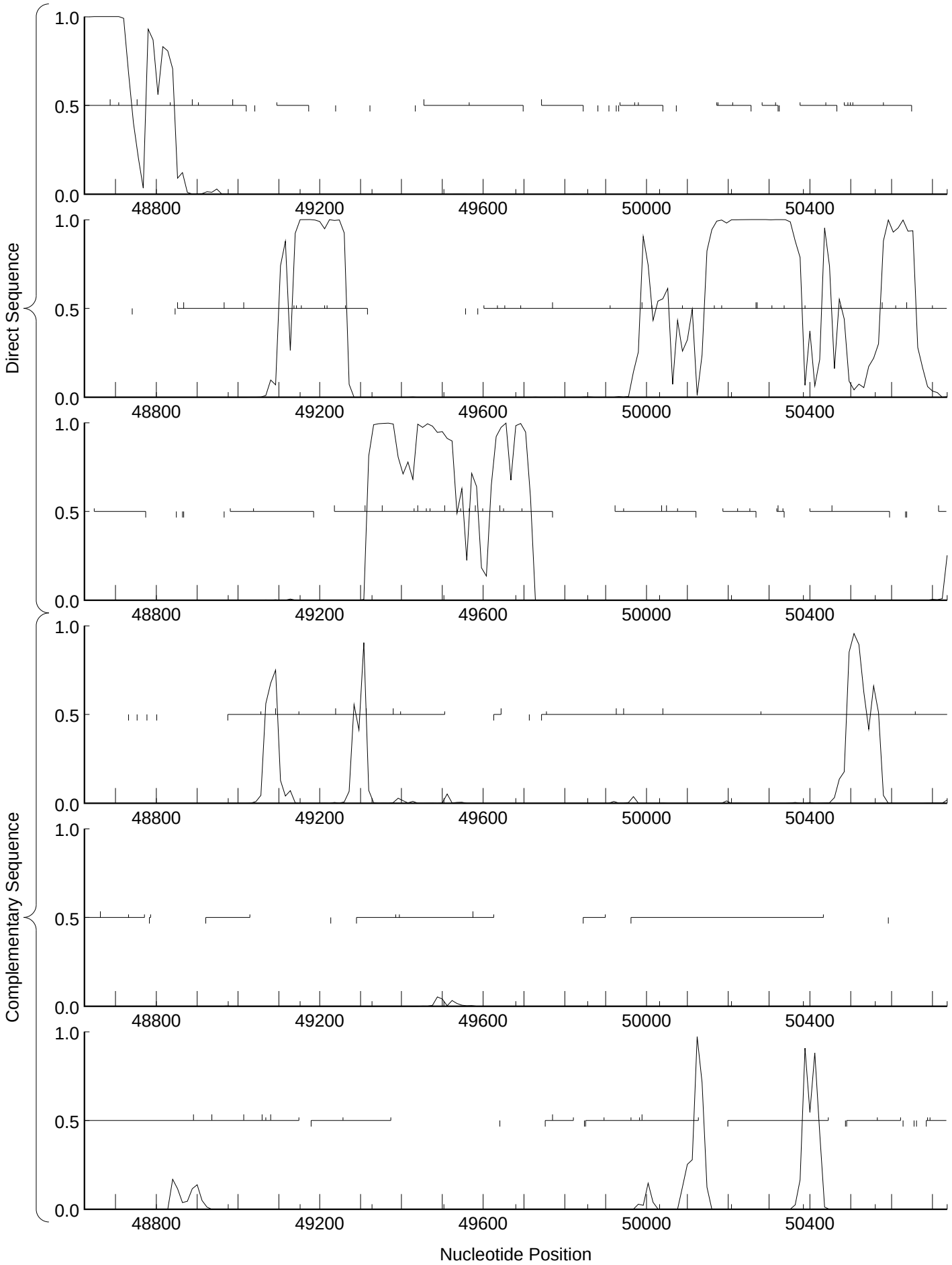


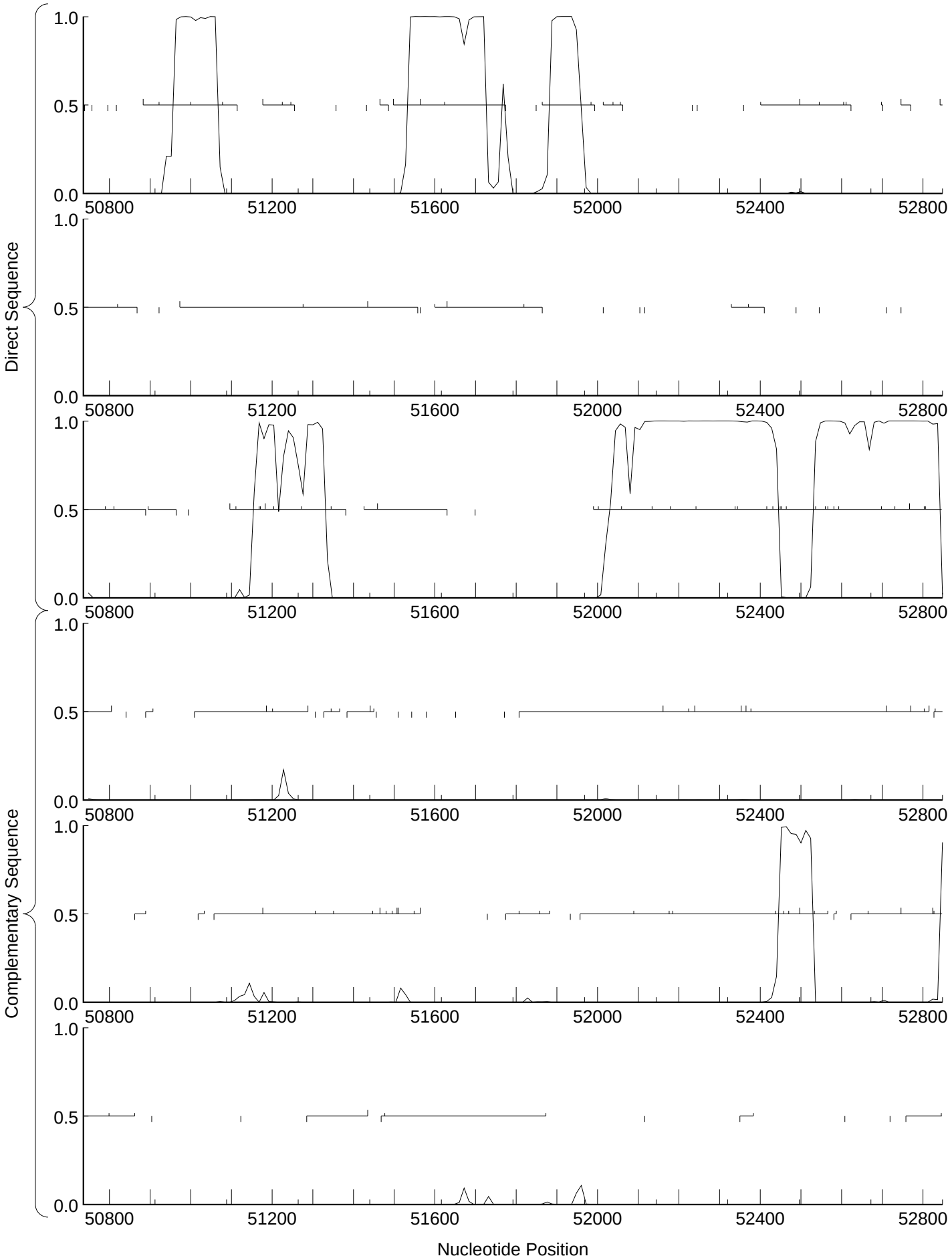

Direct Sequence
Complementary Sequence
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0.5
0.0
42400
42800
43200
43600
44000
44400
Nucleotide Position

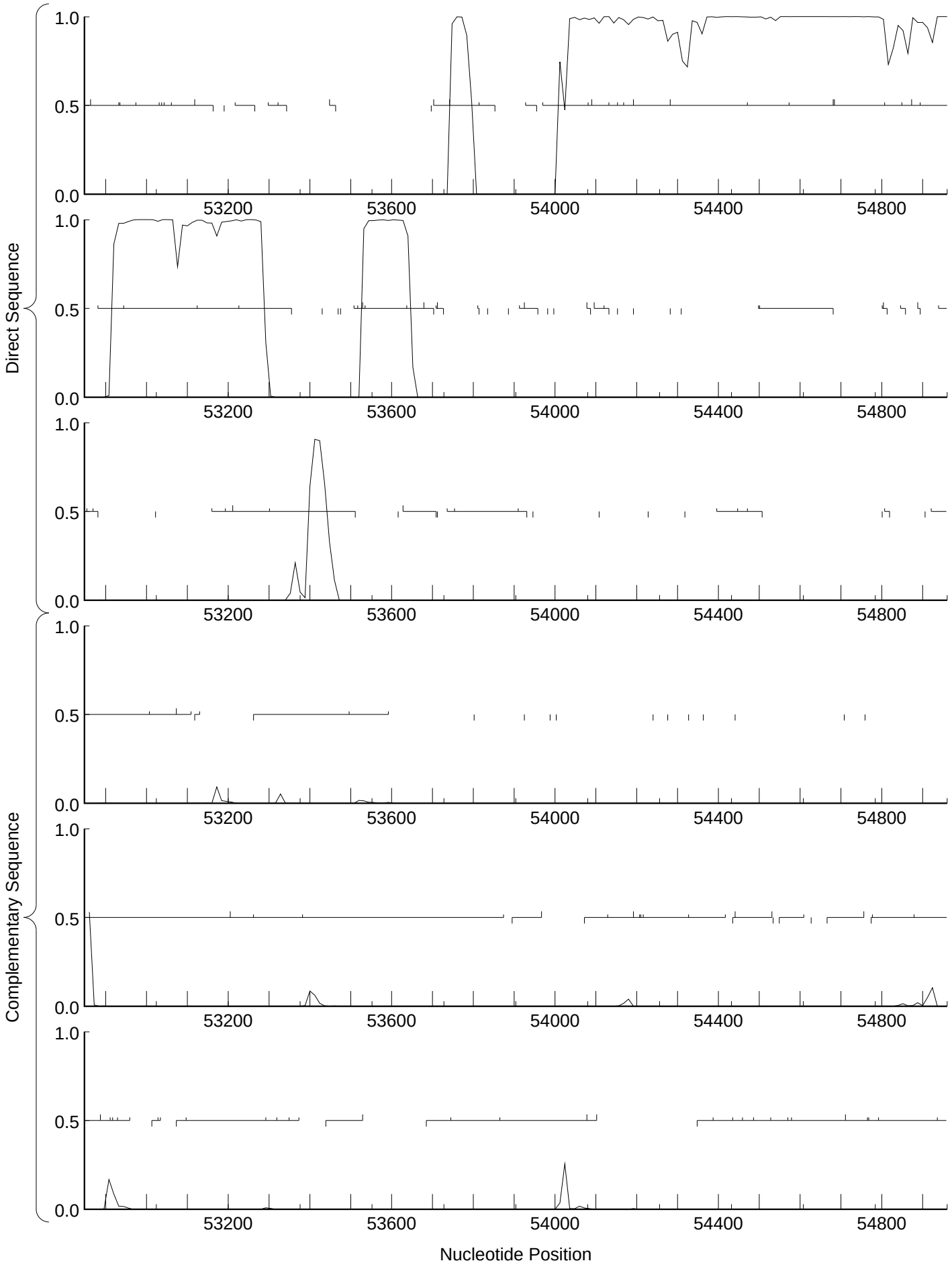
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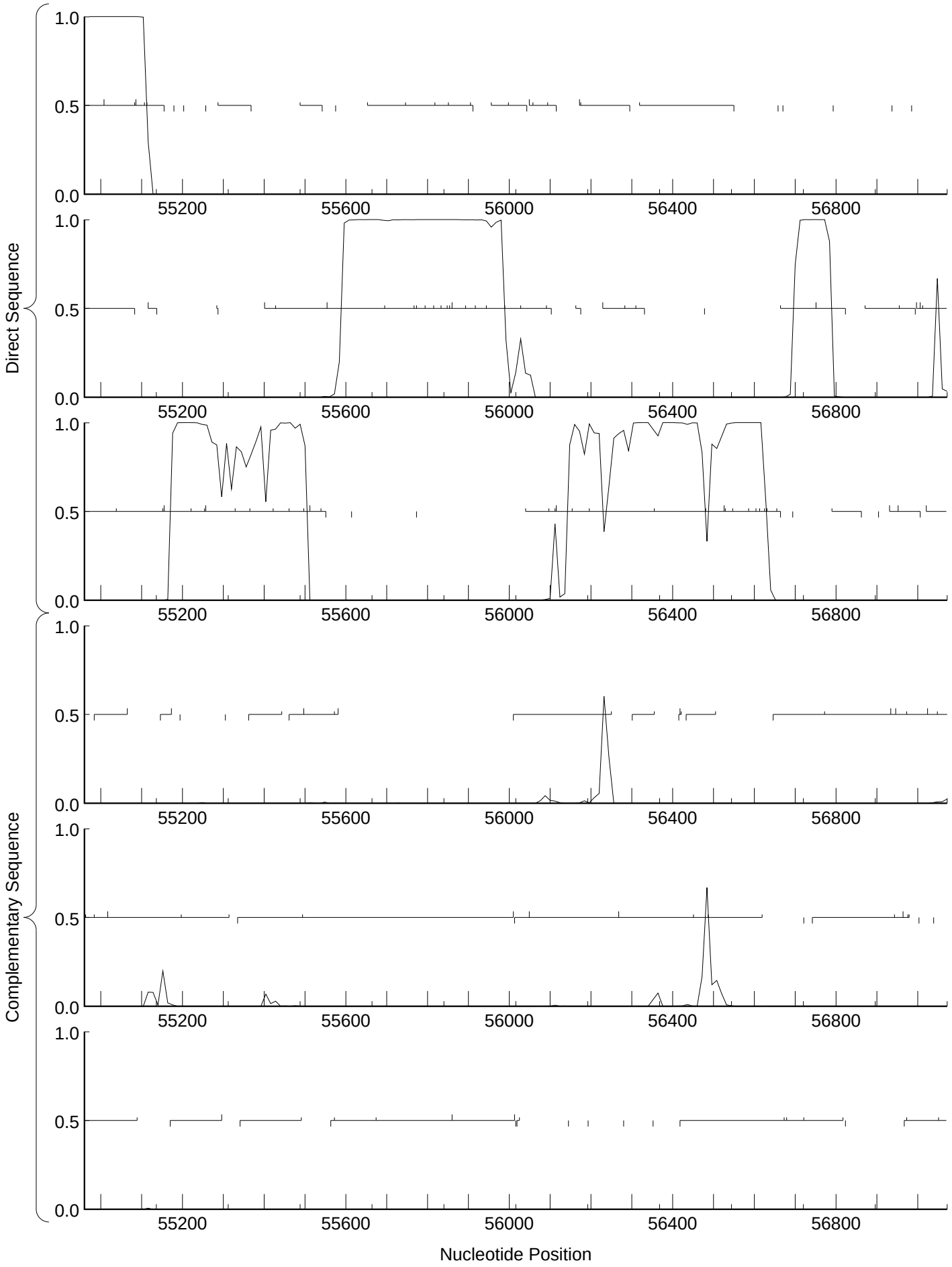


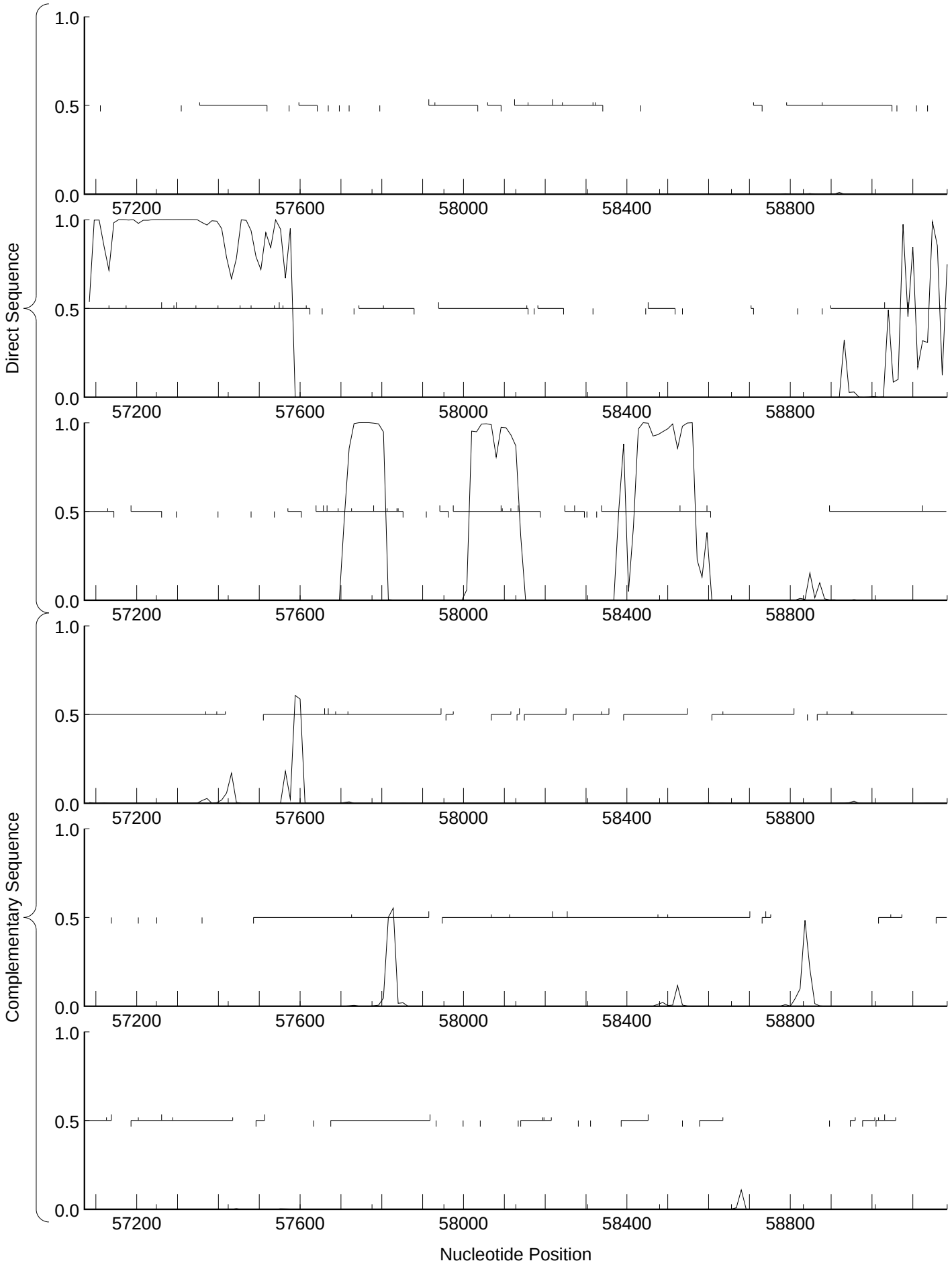

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
46800
47200
47600
48000
48400
Nucleotide Position


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


Direct Sequence
Complementary Sequence
1.0
0.5
0.0
50800
51200
51600
52000
52400
52800
Nucleotide Position


Direct Sequence
Complementary Sequence
1.0
0.5
0.0
53200
53600
54000
54400
54800
Nucleotide Position


Direct Sequence
Complementary Sequence
1.0
0.5
0.0
55200
55600
56000
56400
56800
Nucleotide Position


Direct Sequence
Complementary Sequence
1.0
0.5
0.0
57200
57600
58000
58400
58800
Nucleotide Position

mD Final Sequence, 59798 bp including 11-base 3’ overhang (CTCGTAGGCAT), Cluster K1, Order 4, Window 96, Step 12, 30/30

