GeneMark

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

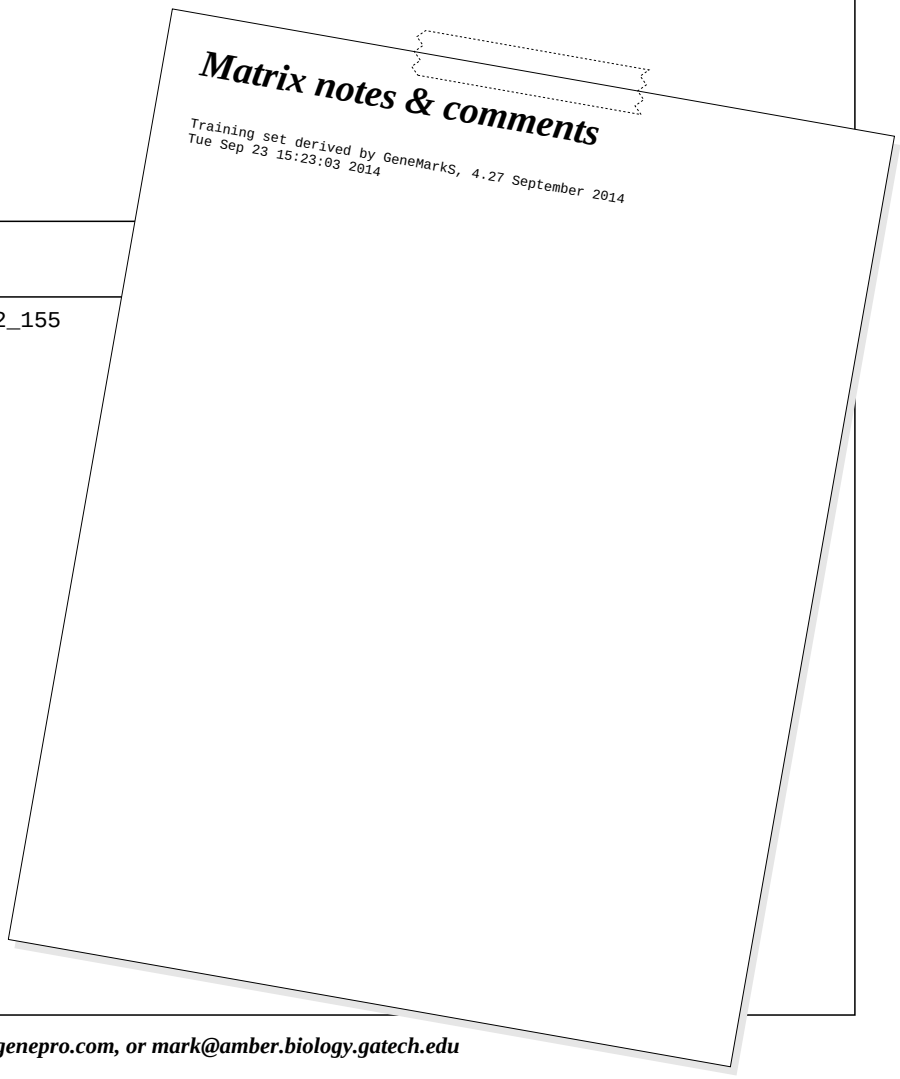
PROGRAM INFORMATION

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Sequence         :  Mycobacterium phage Saints25 complete sequence, 73415 bp including 9-base 3’ overhang (CGCT
Analysis Date    :  3/28/24 at 5:24:43
Pages            :  36
Sequence Length  :  73415 bp
GC Content       :   62.95%

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

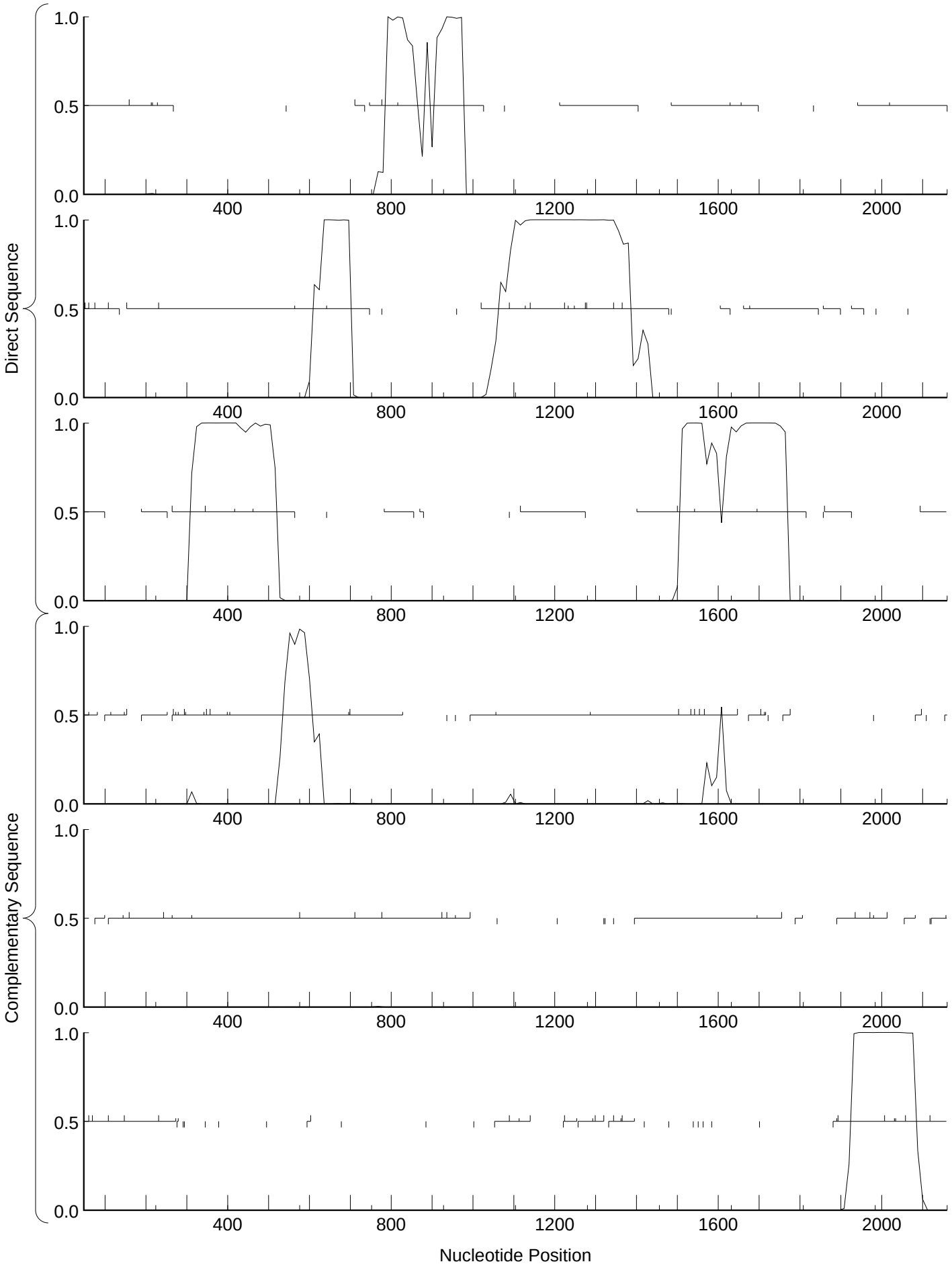
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Author     :  -

Order      :  4
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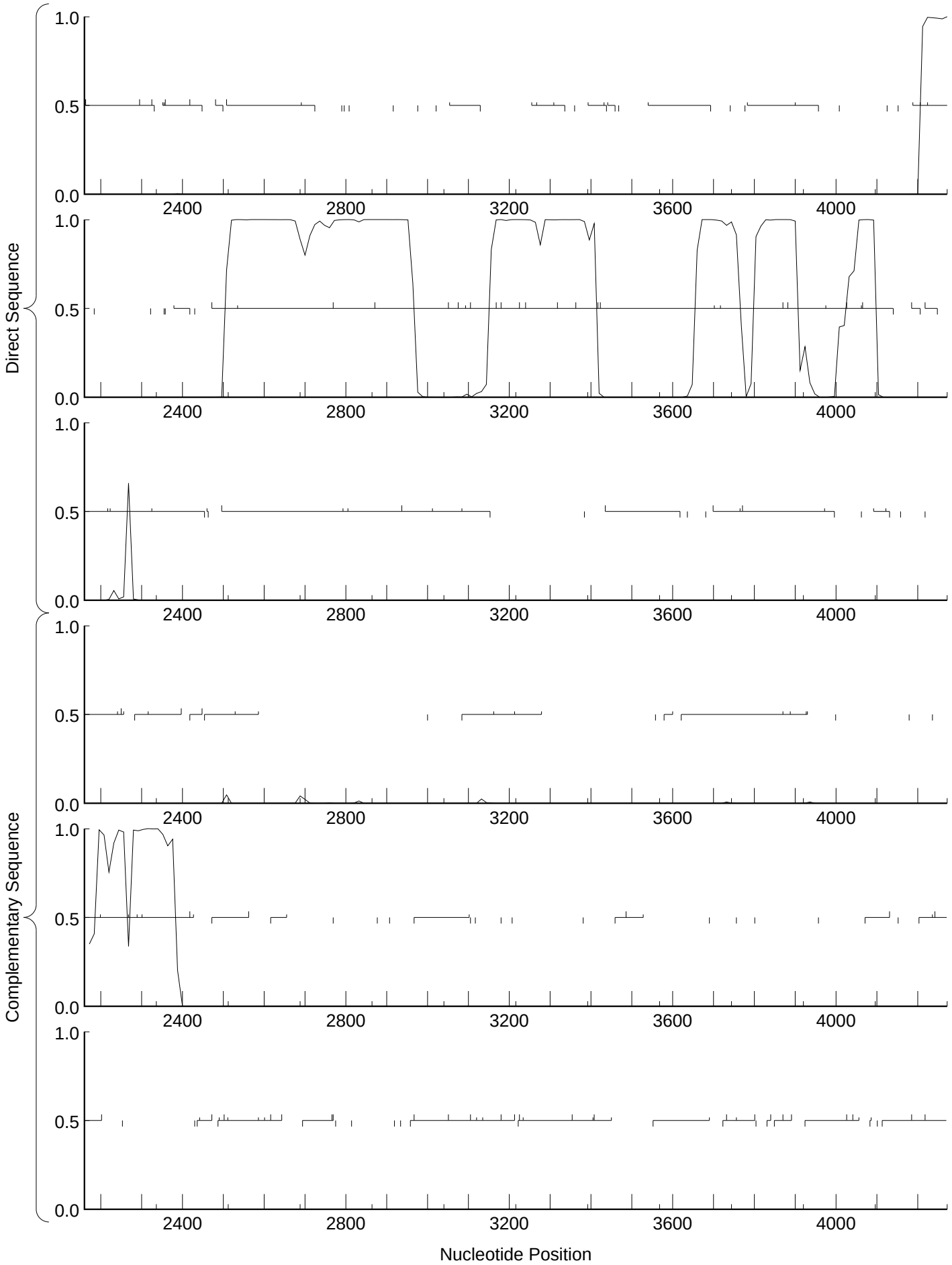

```
  Send questions / comments to:
      Dr. M. Borodovsky
      Georgia Institute of Technology
      School of Biology
      Atlanta, GA  30332-0230
```


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

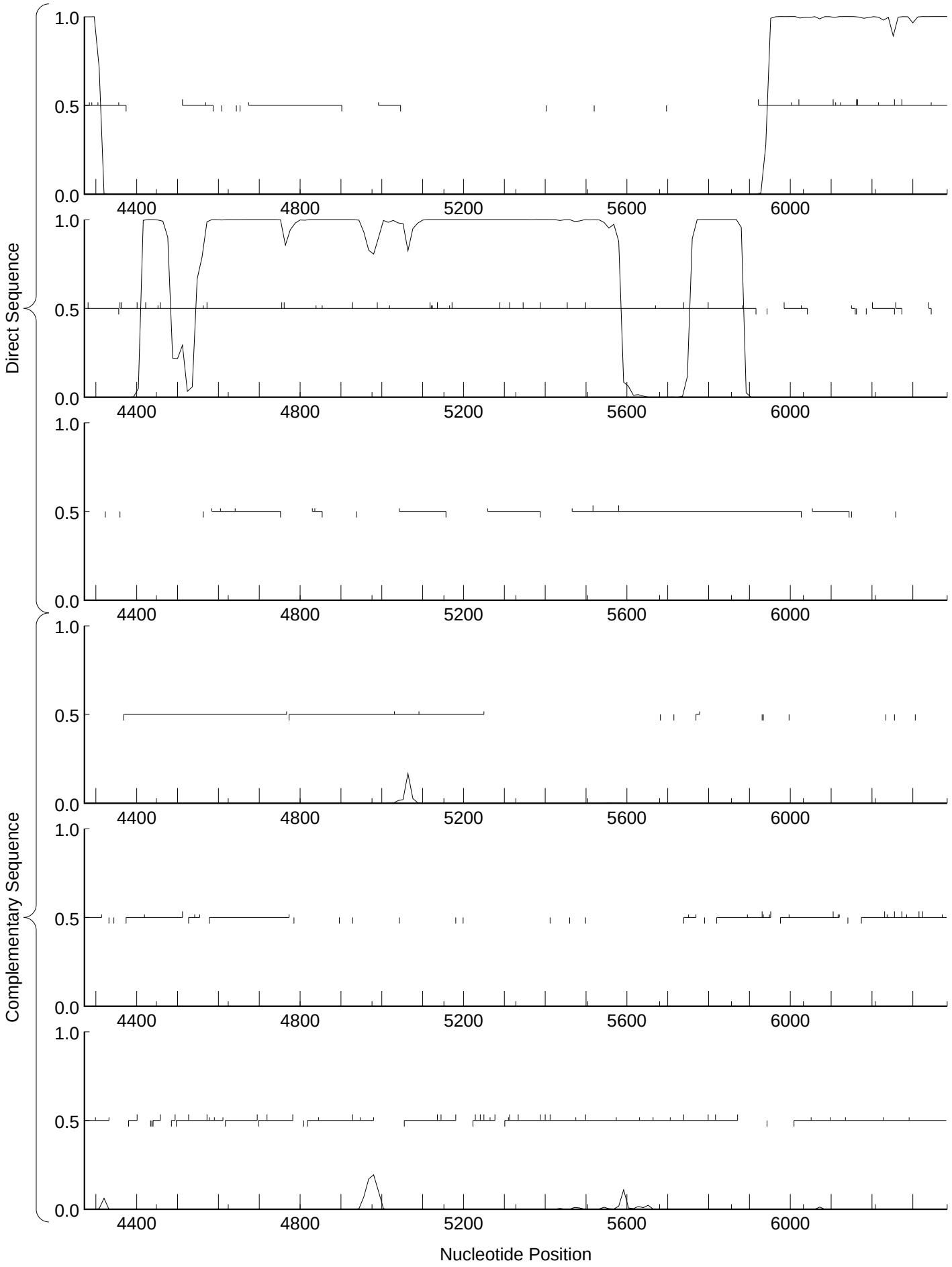
ints25 complete sequence, 73415 bp including 9-base 3’ overhang (CGCTTGTCA), Cluster E, Order 4, Window 96, Step 12, 2/36



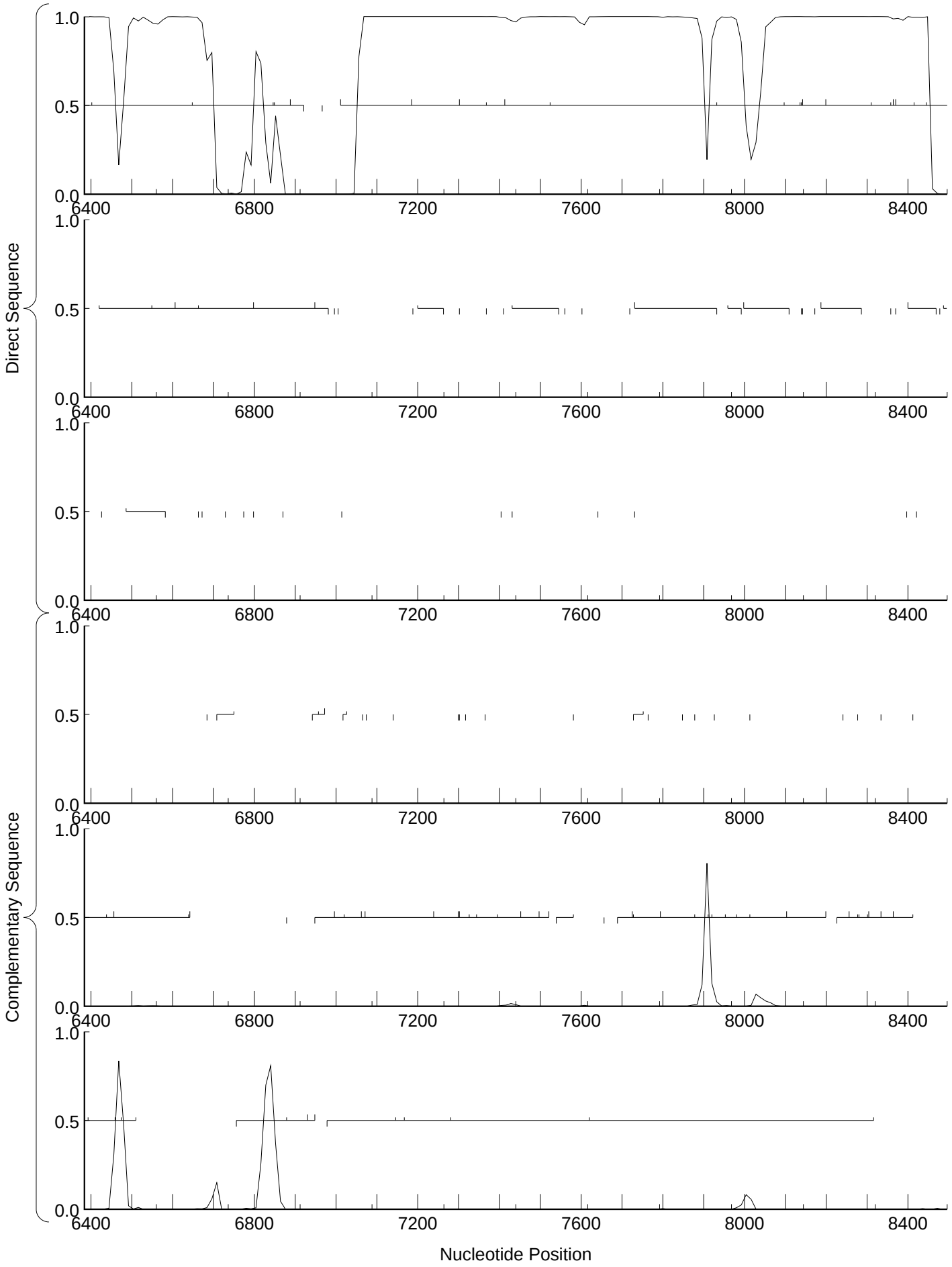
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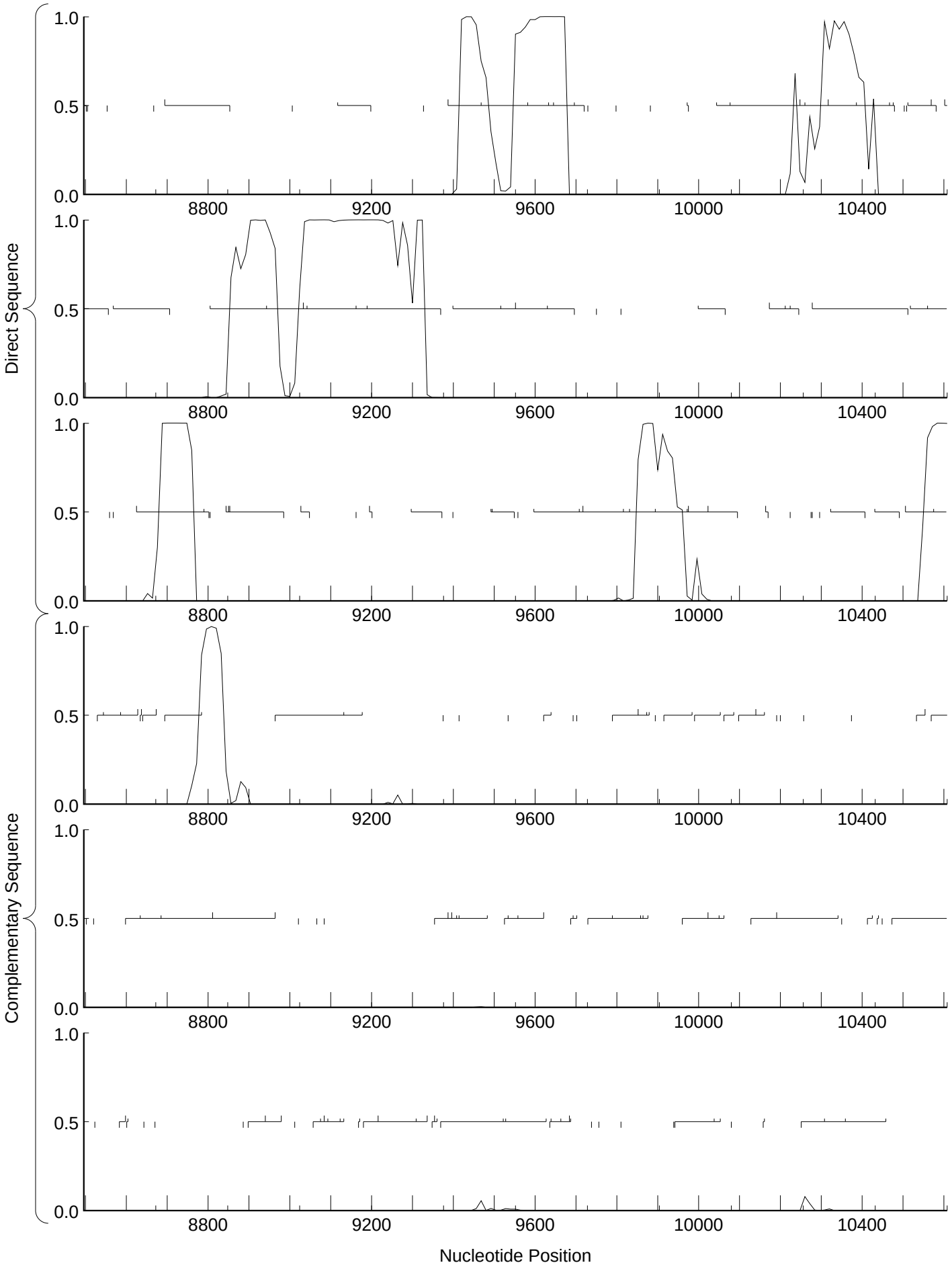
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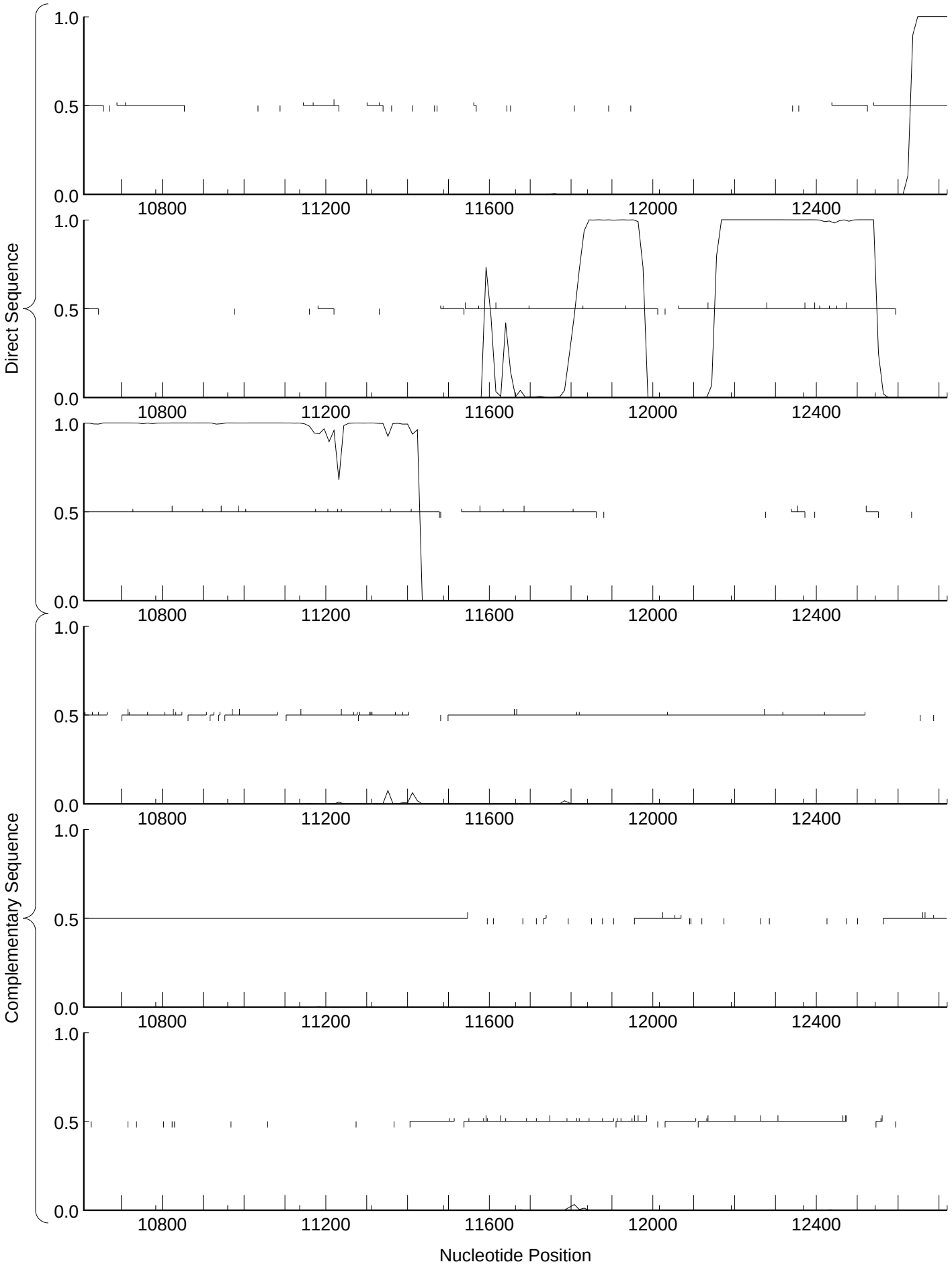
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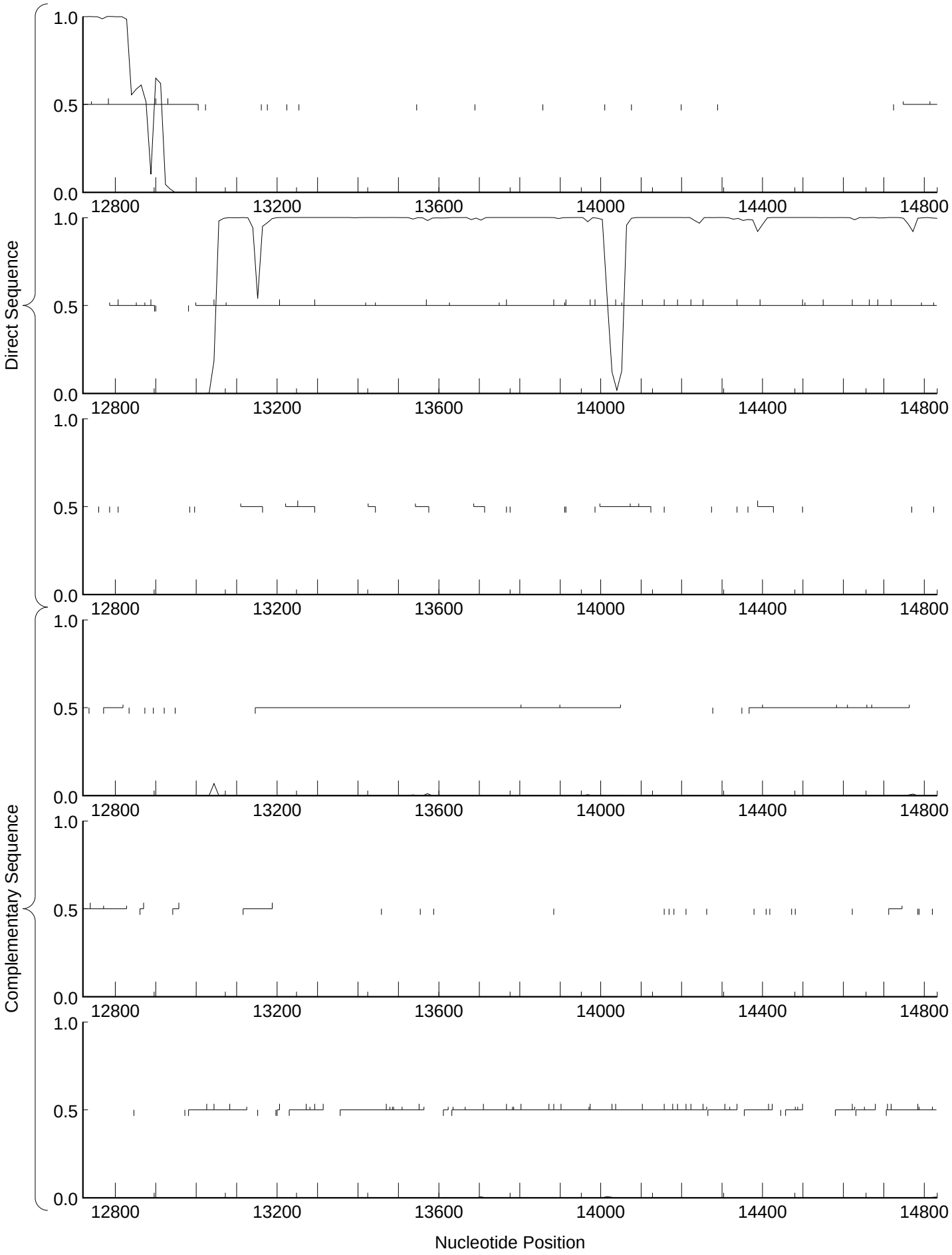
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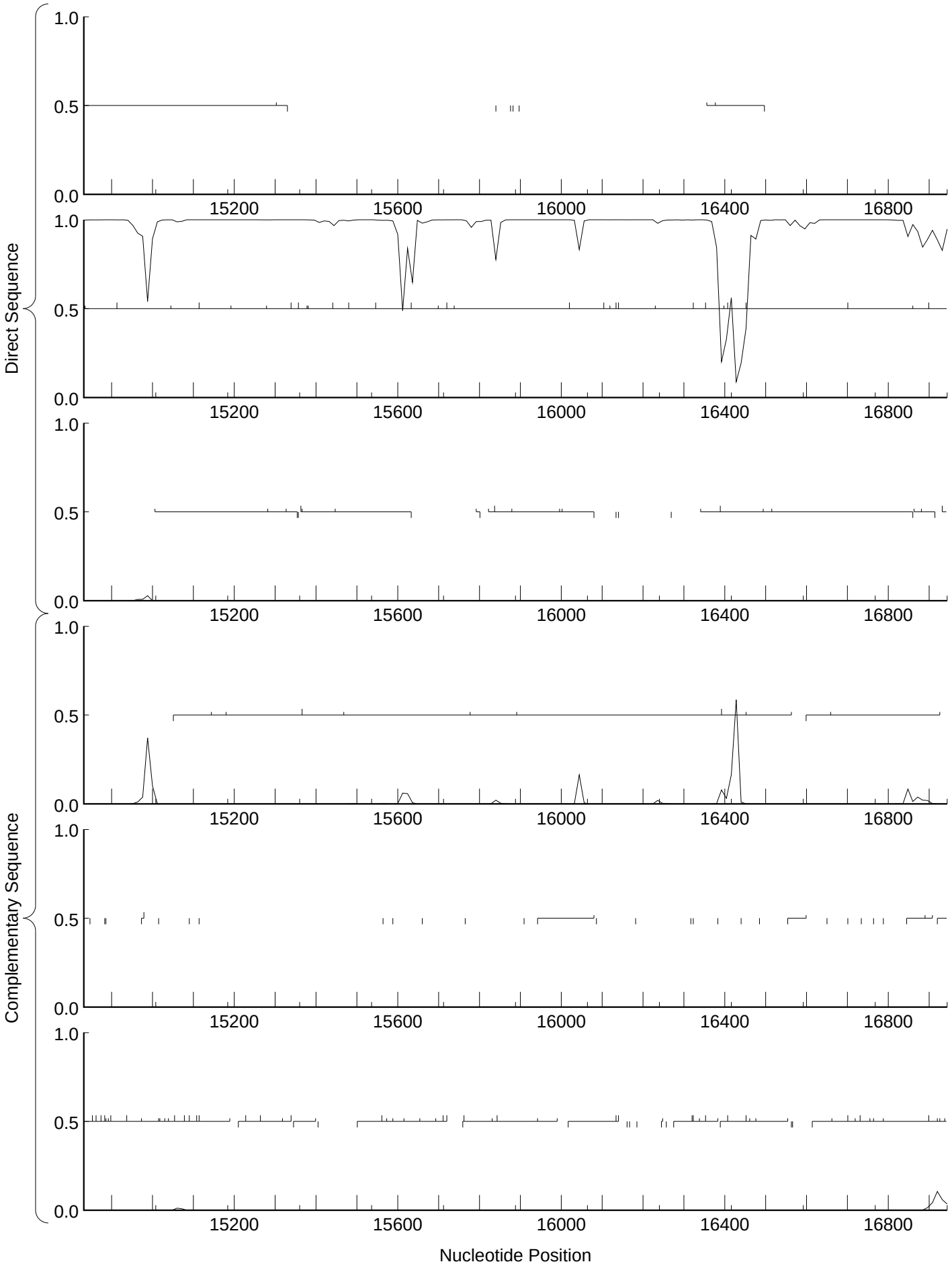
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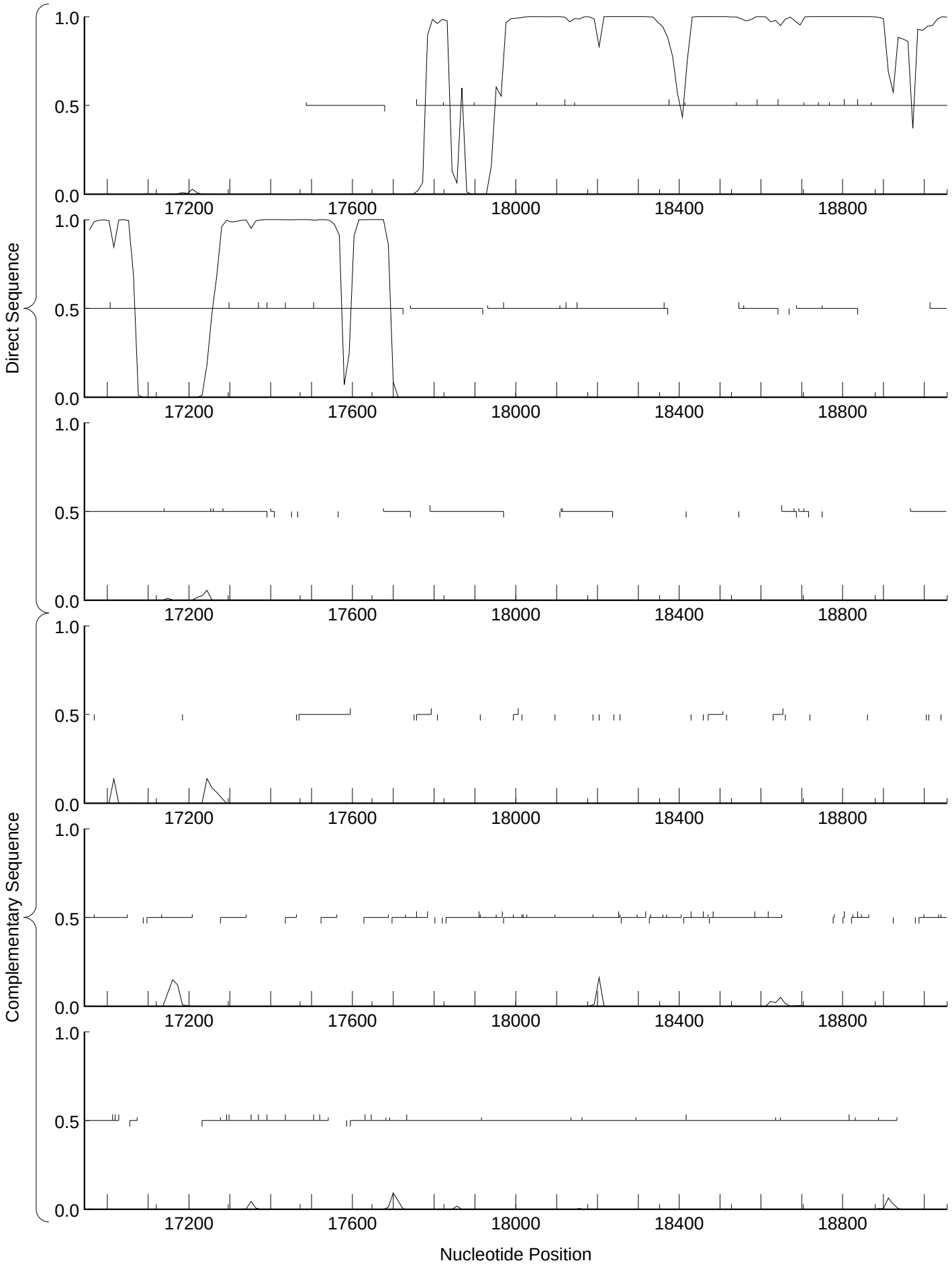


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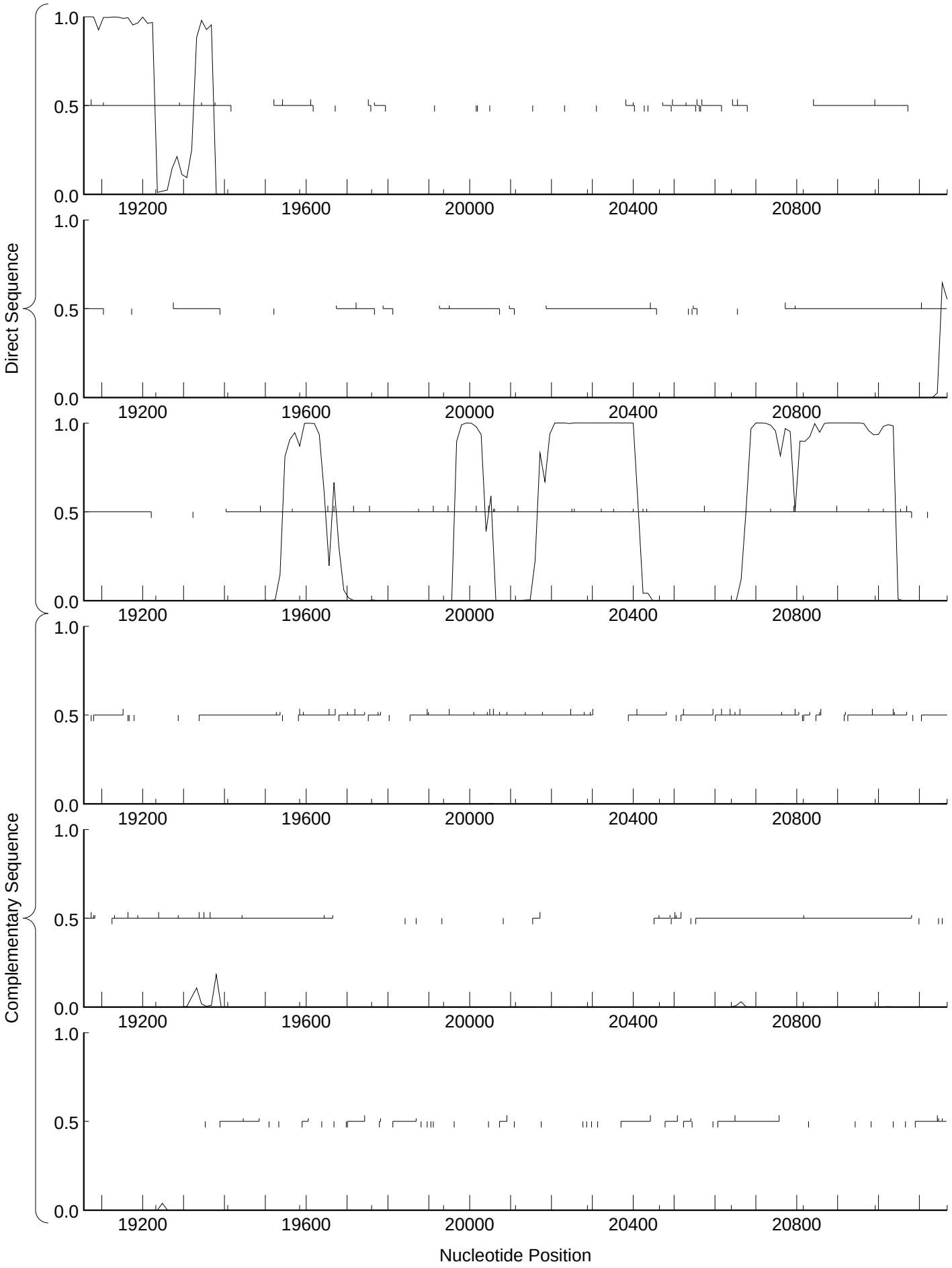


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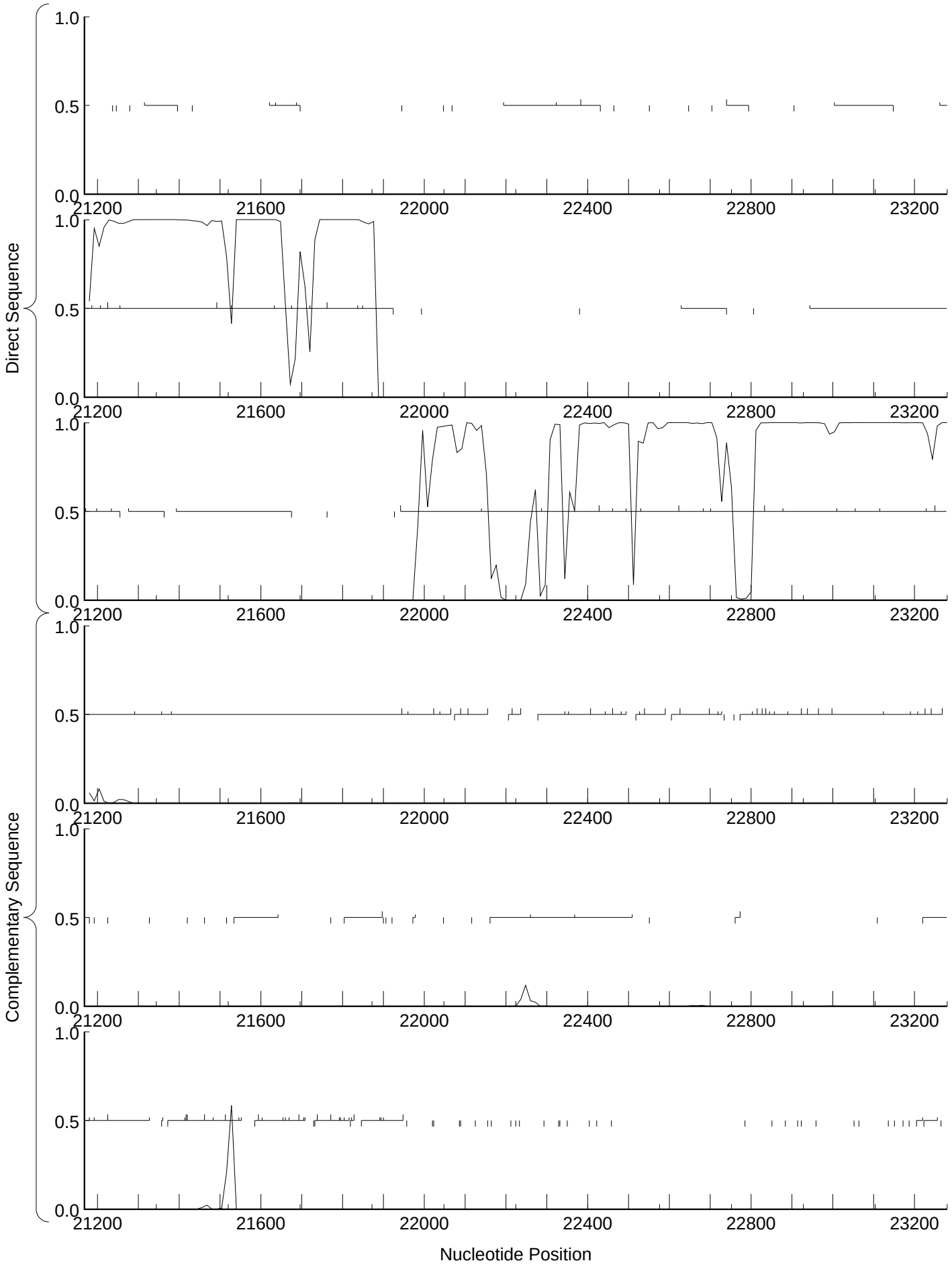


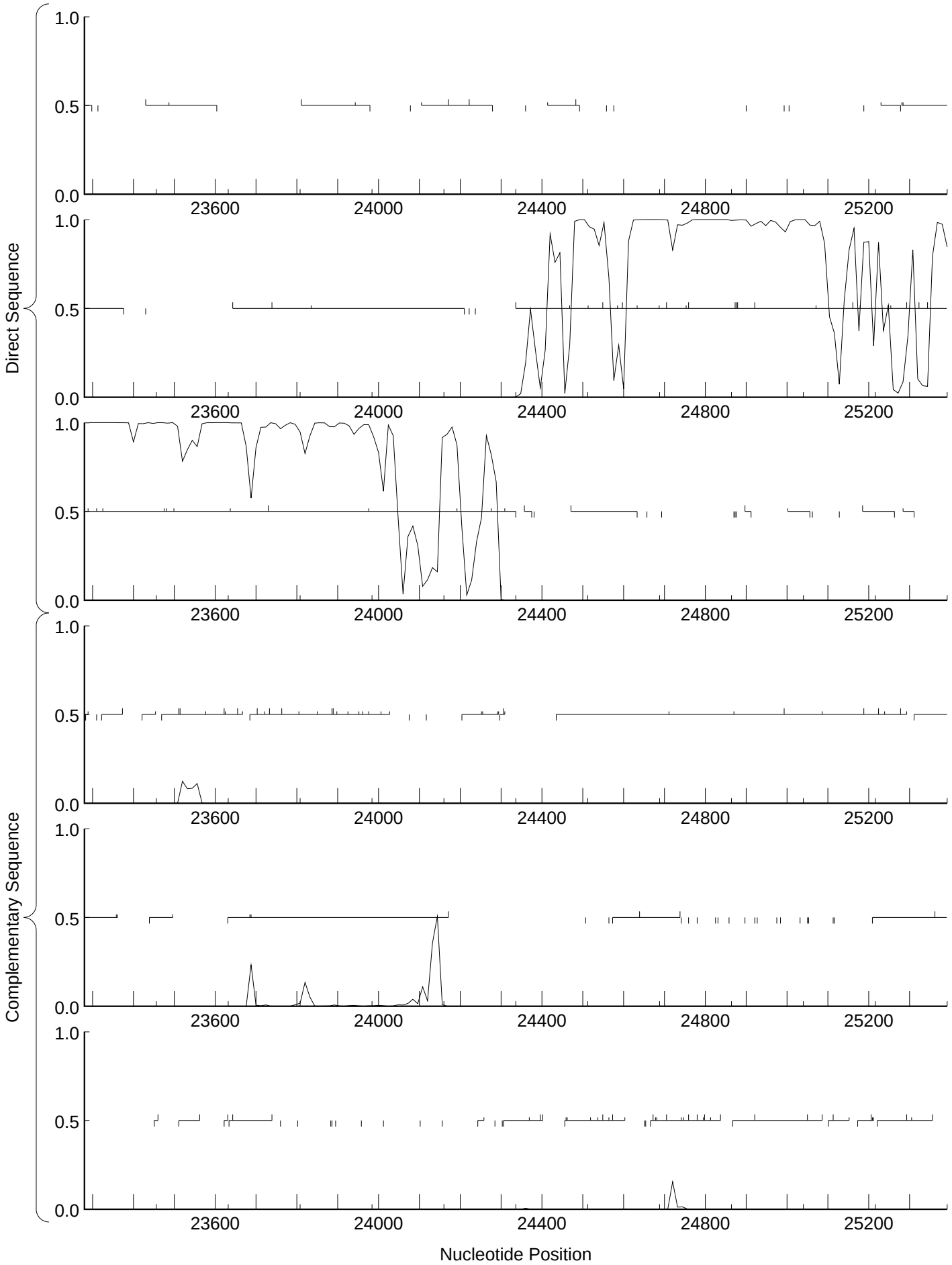

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Complementary Sequence
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0.0
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17600
18000
18400
18800
Nucleotide Position

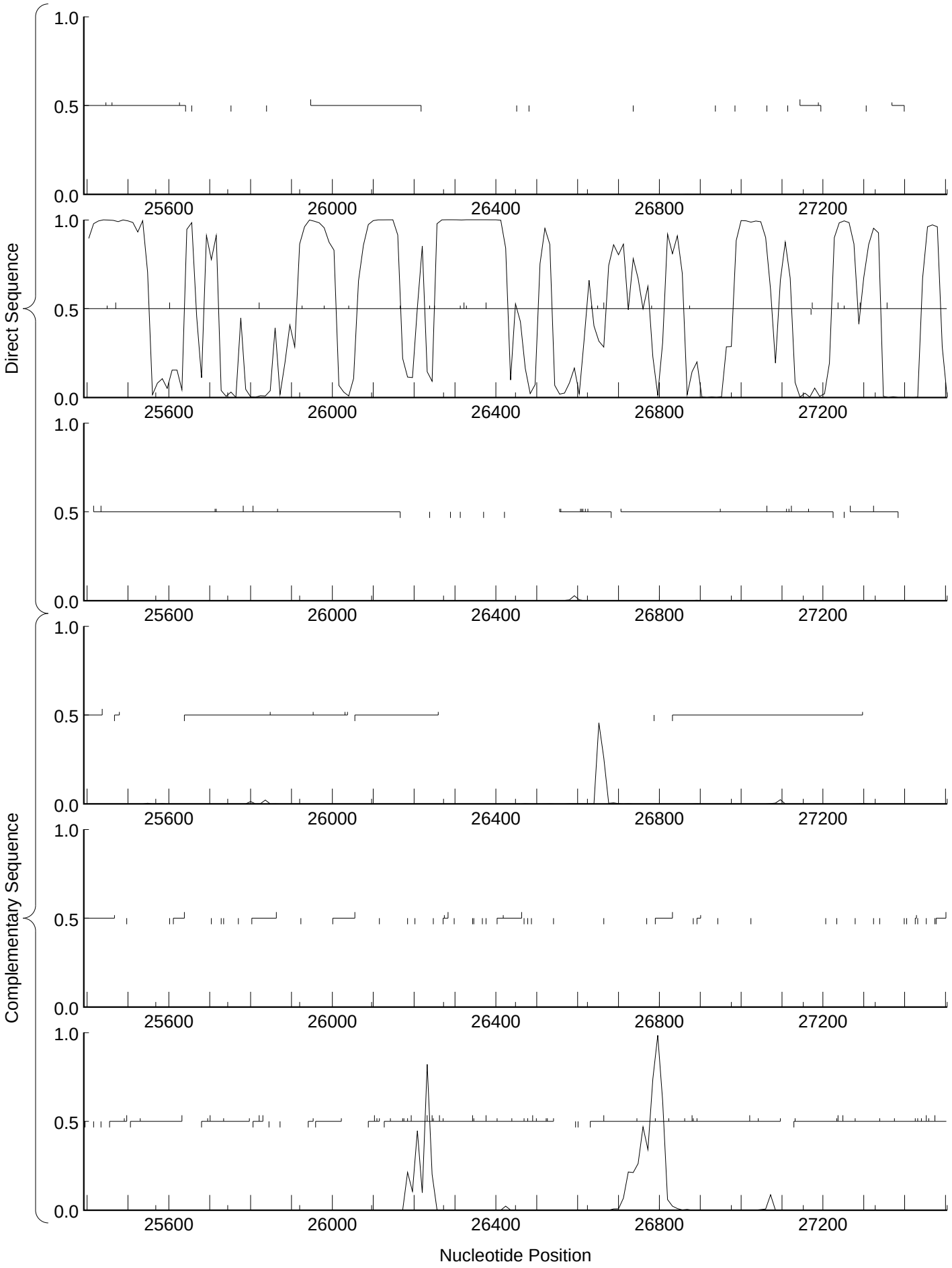
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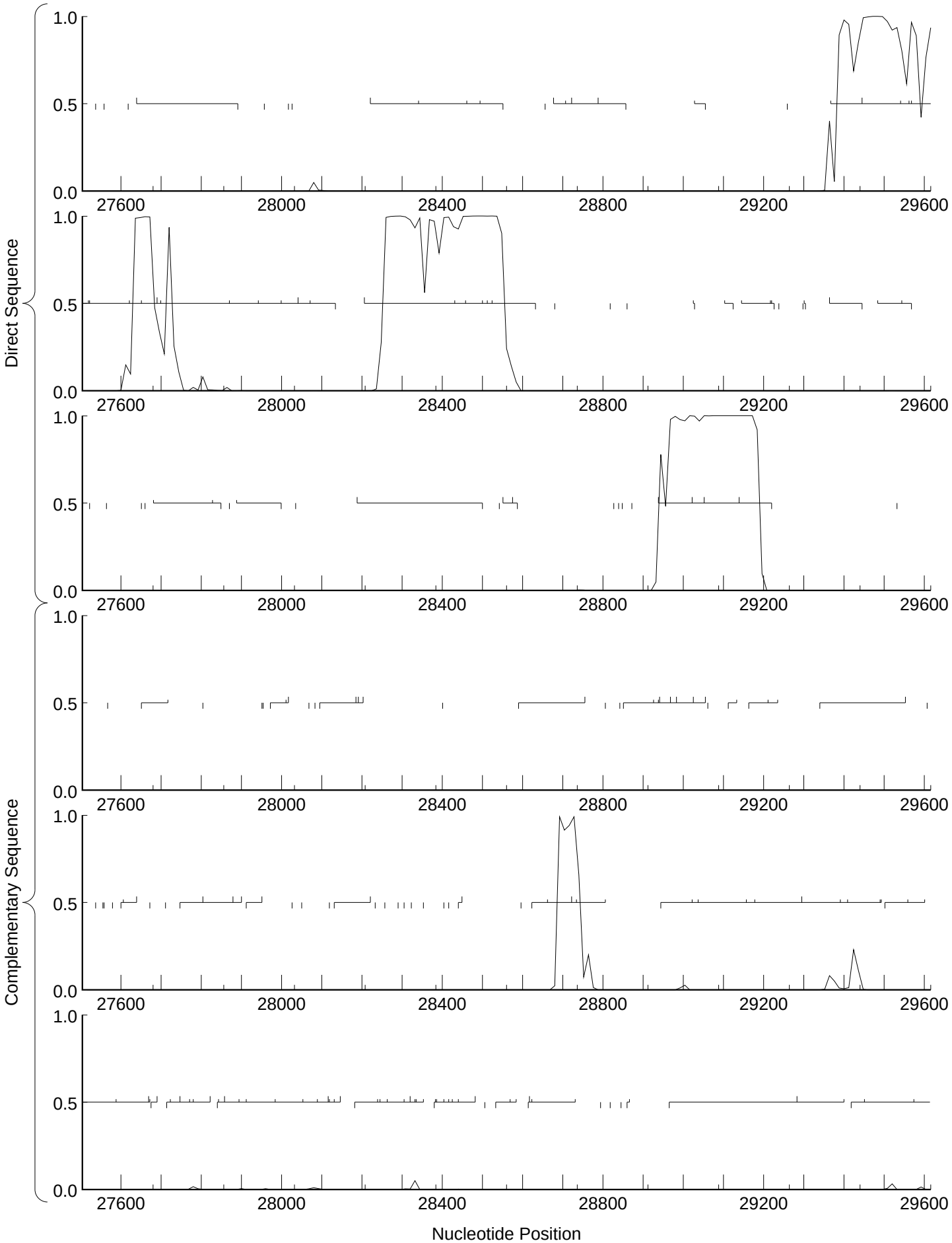
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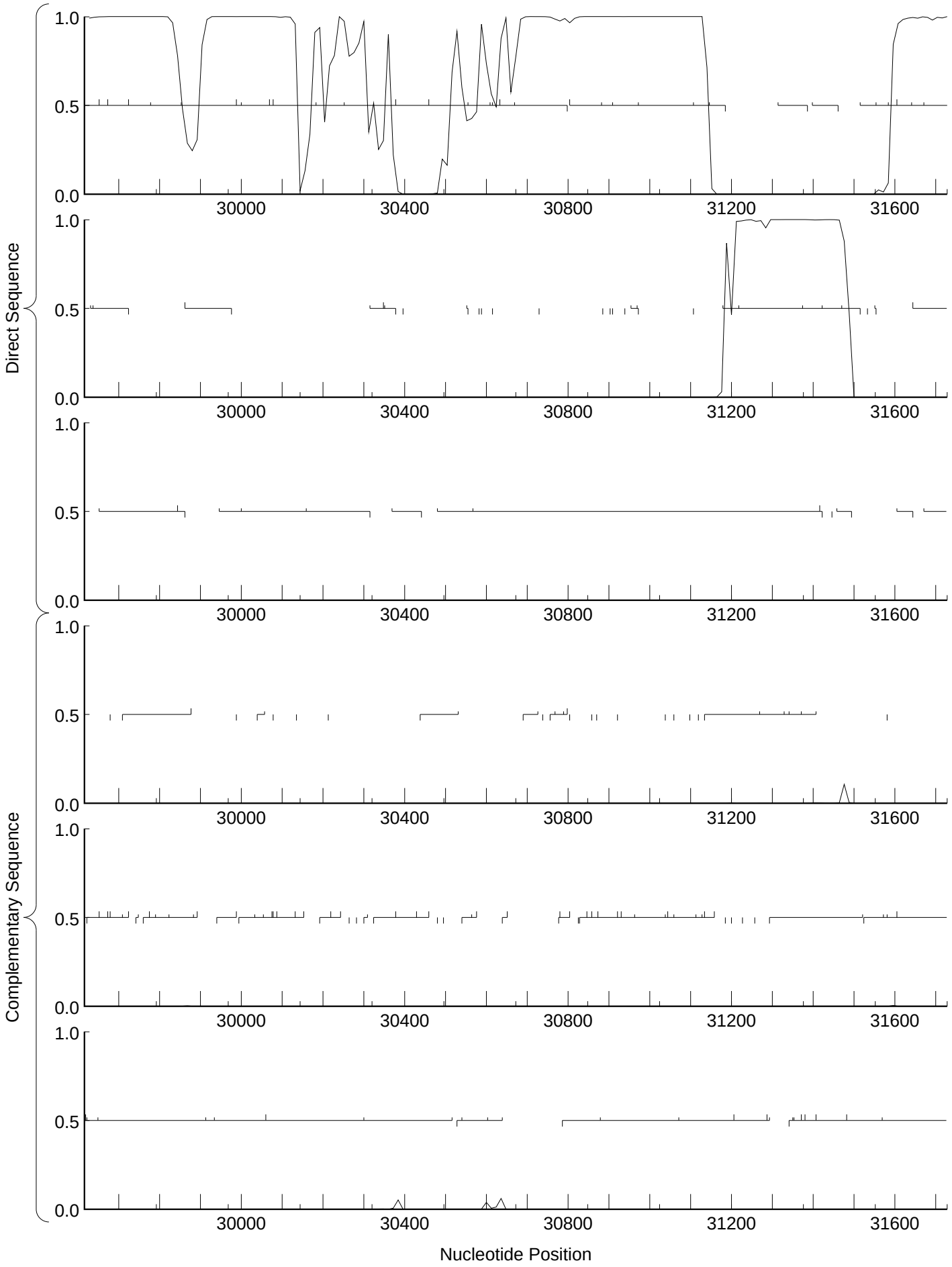



Direct Sequence
Complementary Sequence
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0.5
0.0
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24400
24800
25200
Nucleotide Position

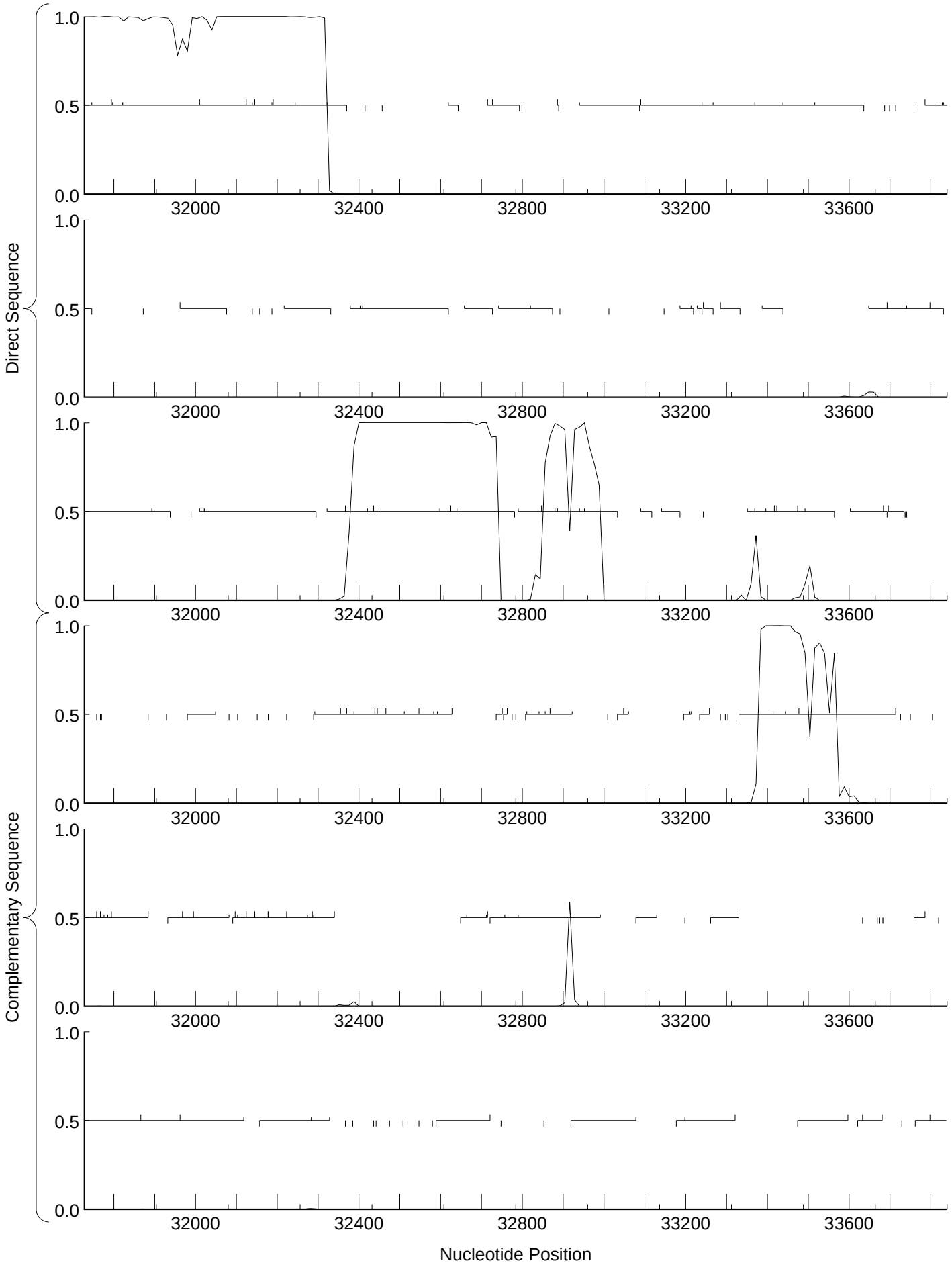

Direct Sequence
Complementary Sequence
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0.0
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26400
26800
27200
Nucleotide Position

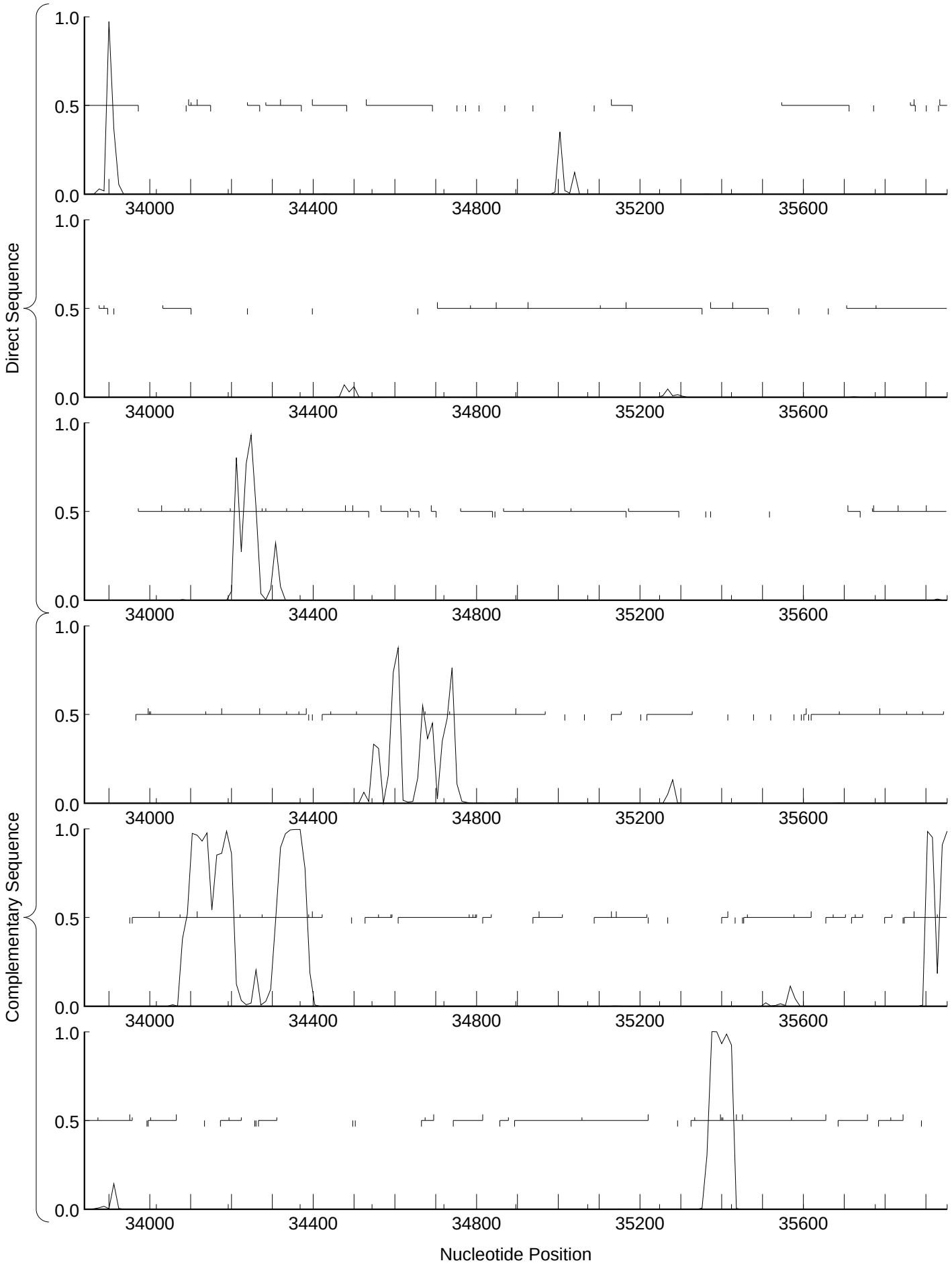
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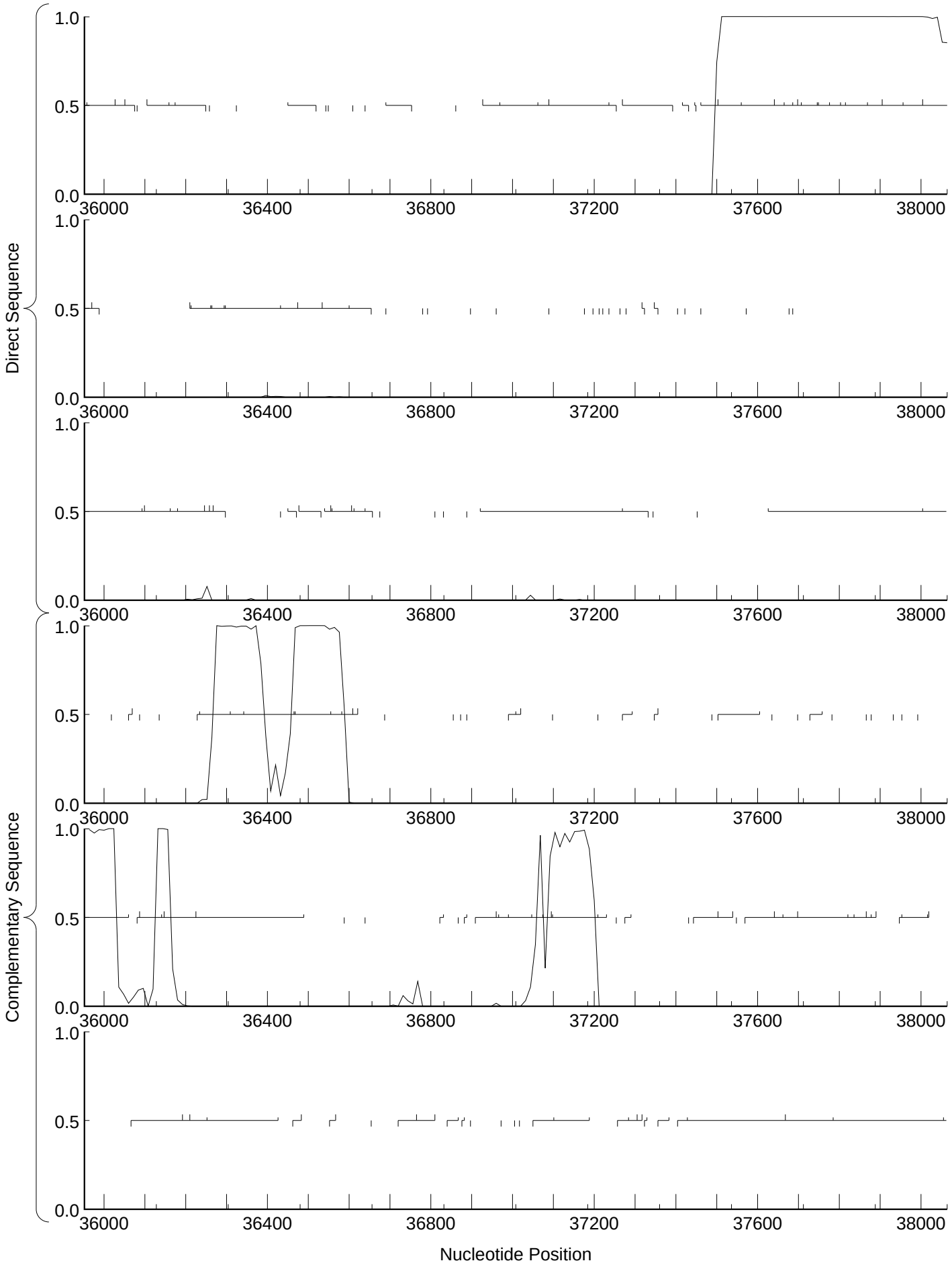

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
30000
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31200
31600
Nucleotide Position

nts25 complete sequence, 73415 bp including 9-base 3' overhang (CGCTTGTCA), Cluster E, Order 4, Window 96, Step 12, 17/36

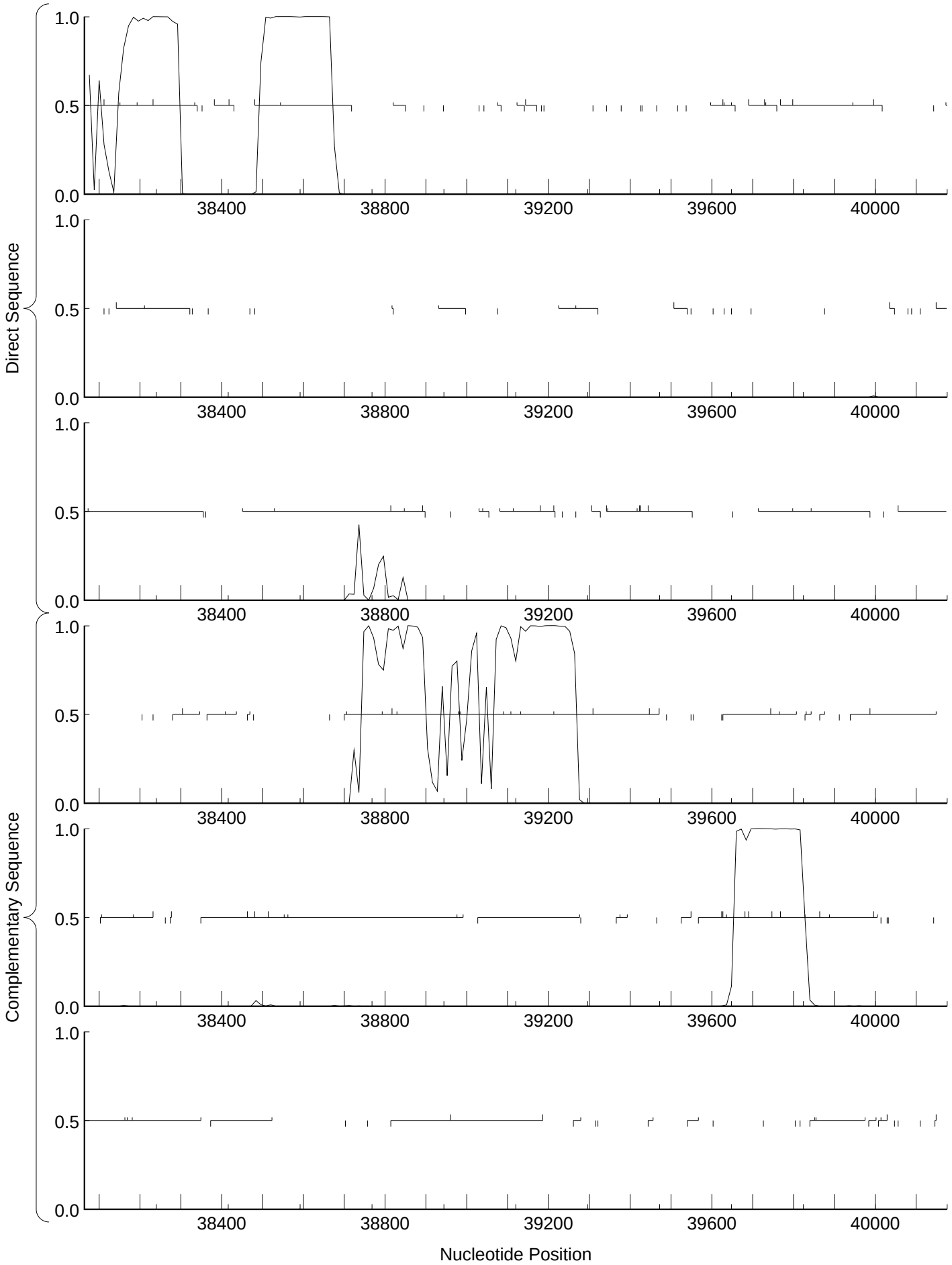


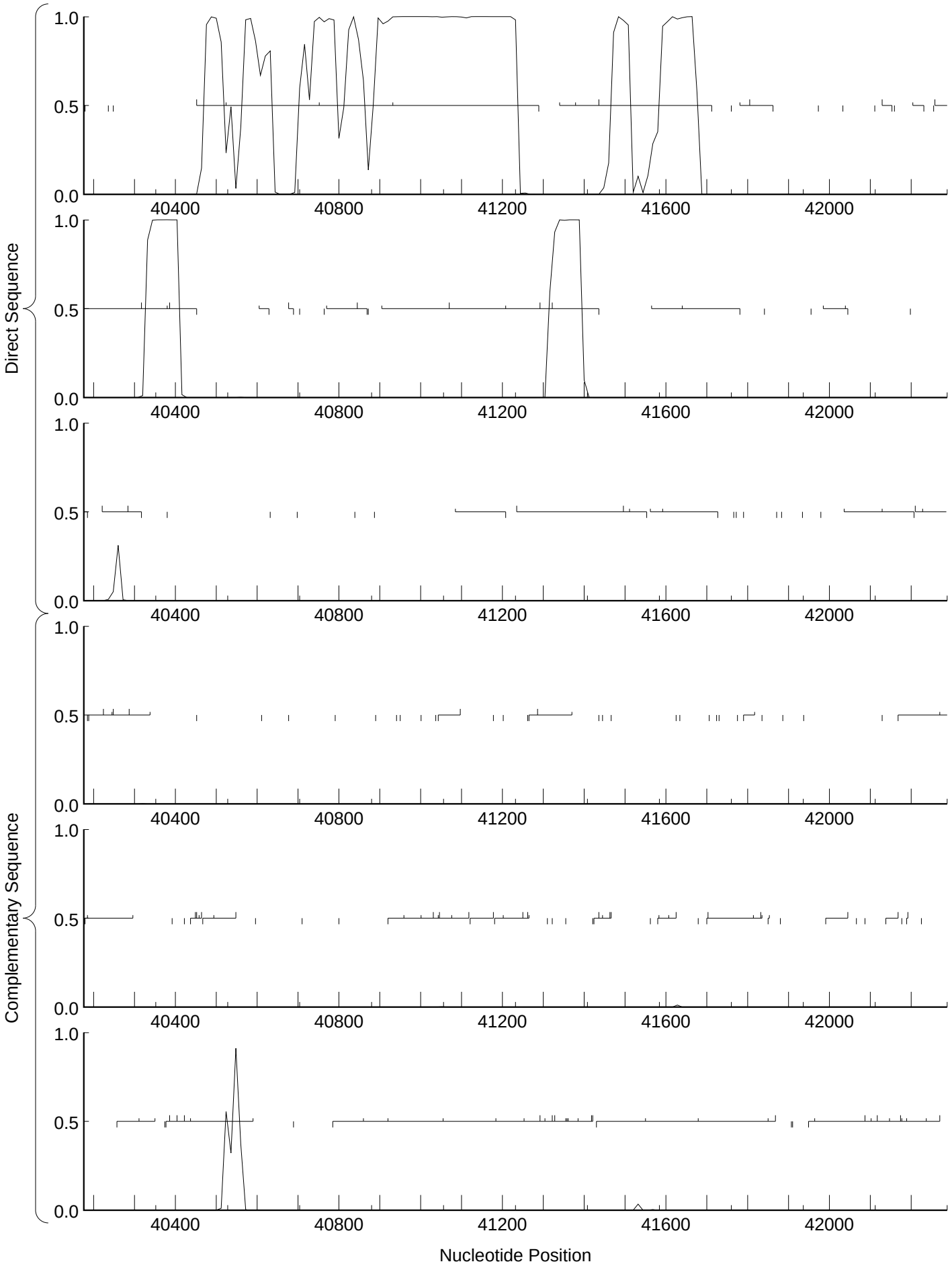

Direct Sequence
Complementary Sequence
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0.5
0.0
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34400
34800
35200
35600
Nucleotide Position

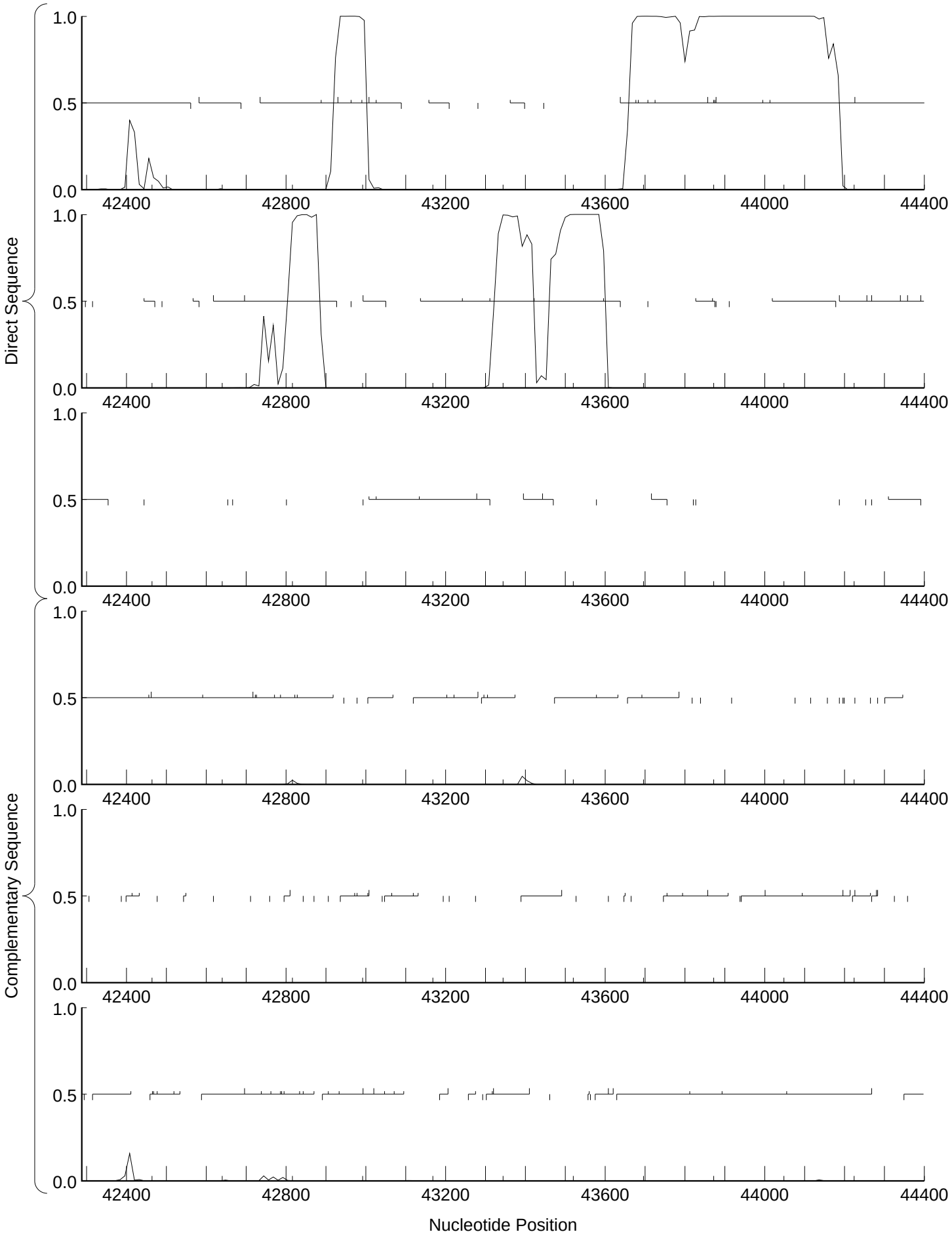
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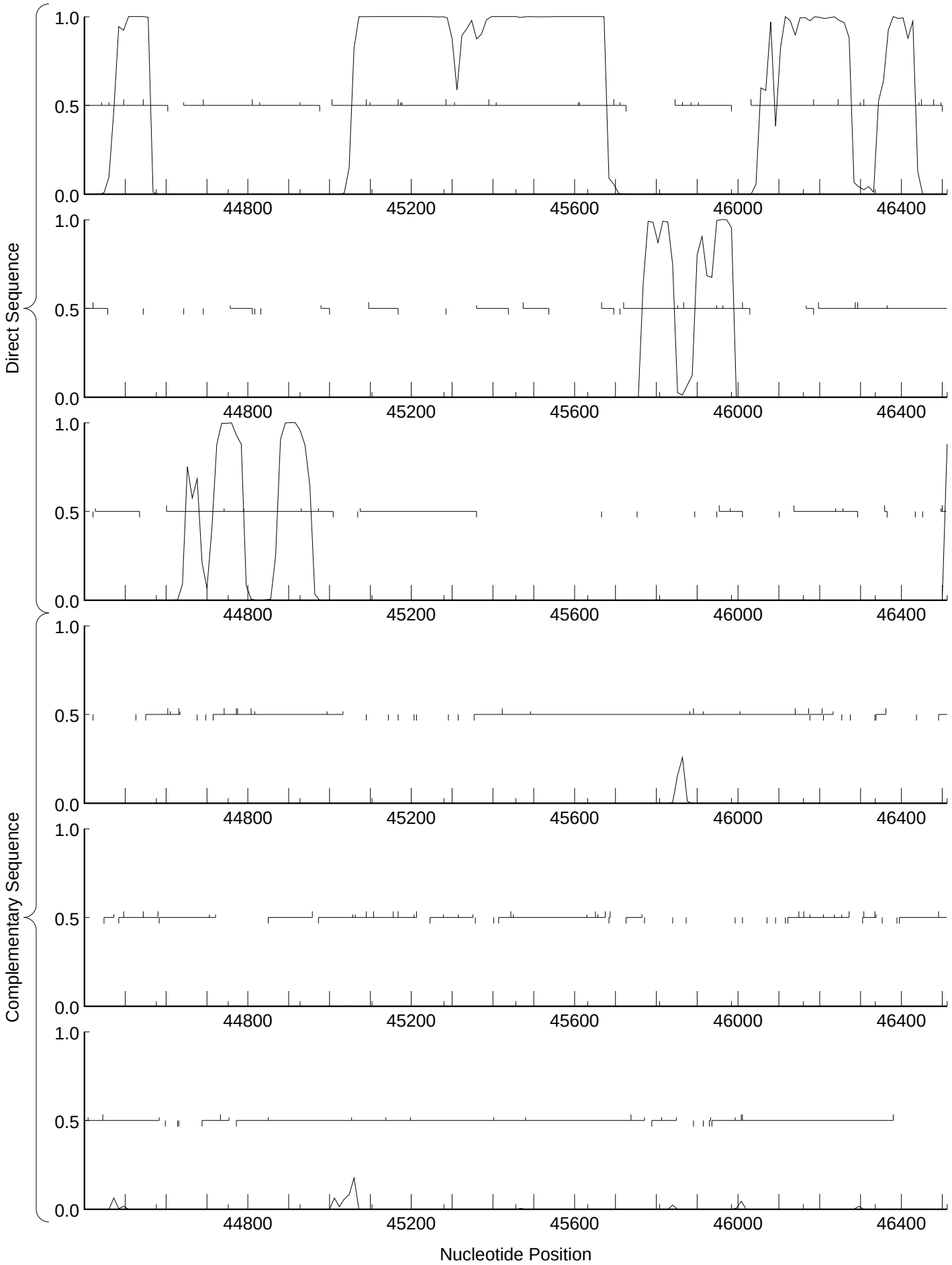


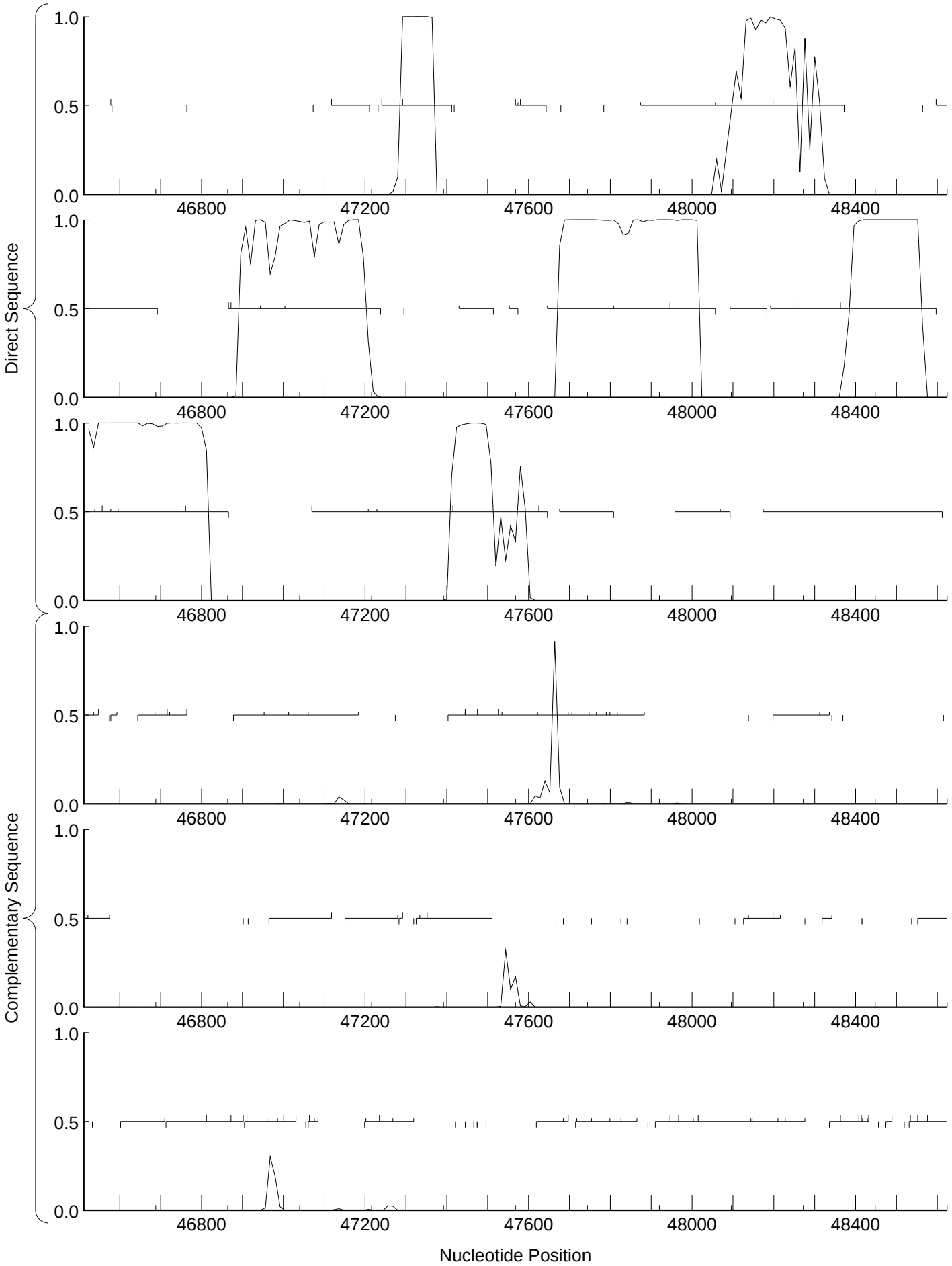
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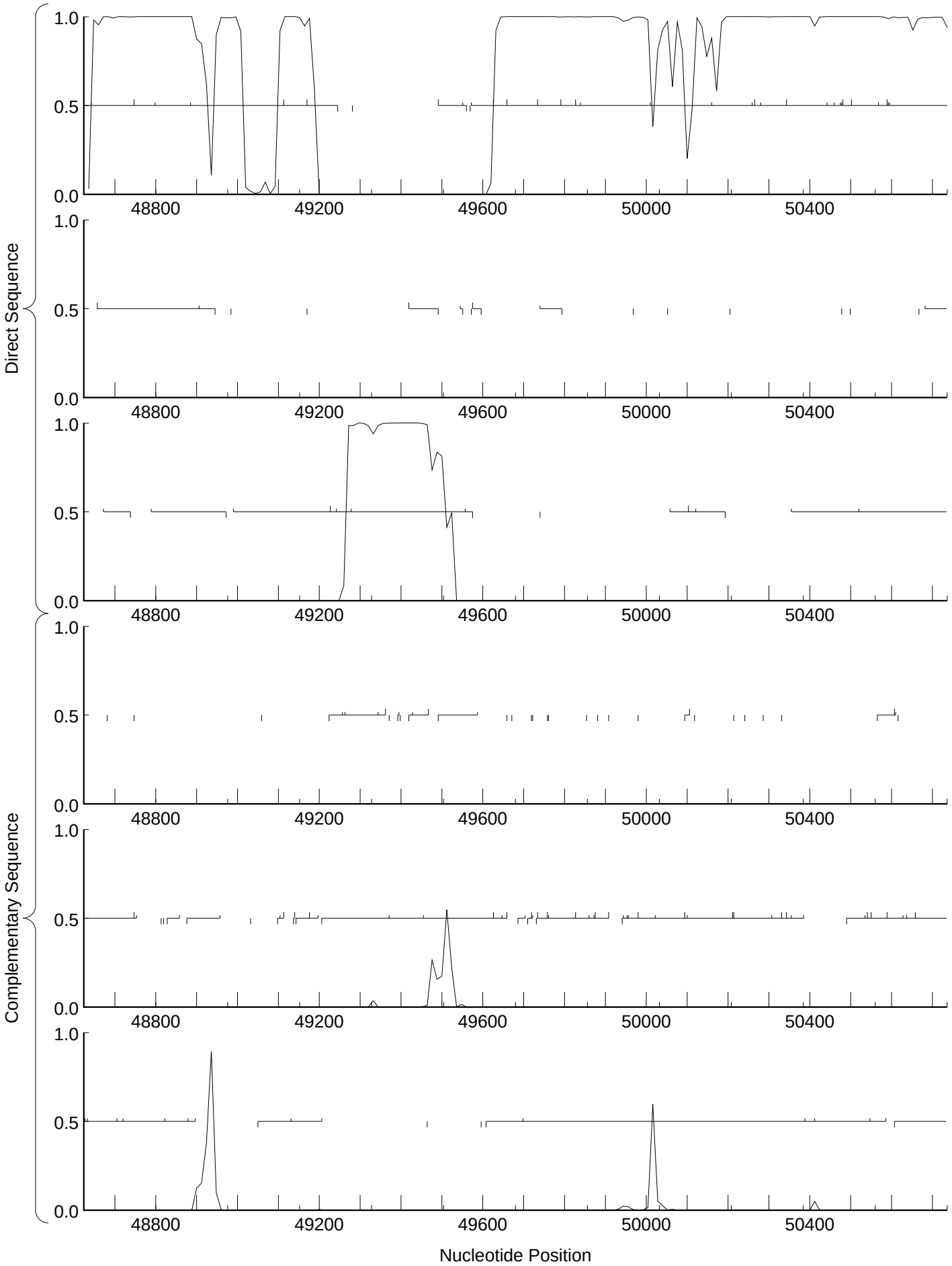

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Complementary Sequence
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0.5
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41200
41600
42000
Nucleotide Position

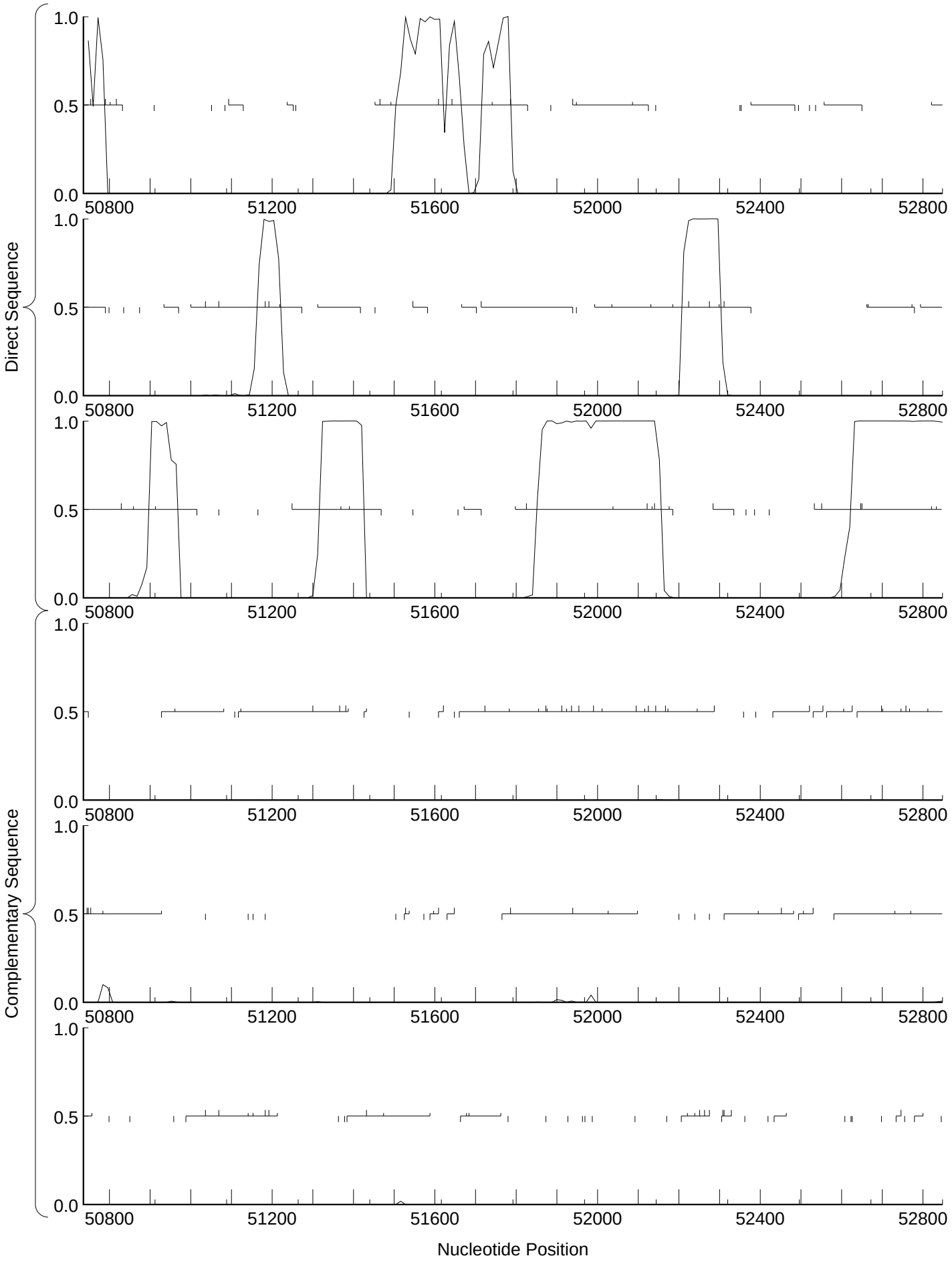

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
42400
42800
43200
43600
44000
44400
Nucleotide Position


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

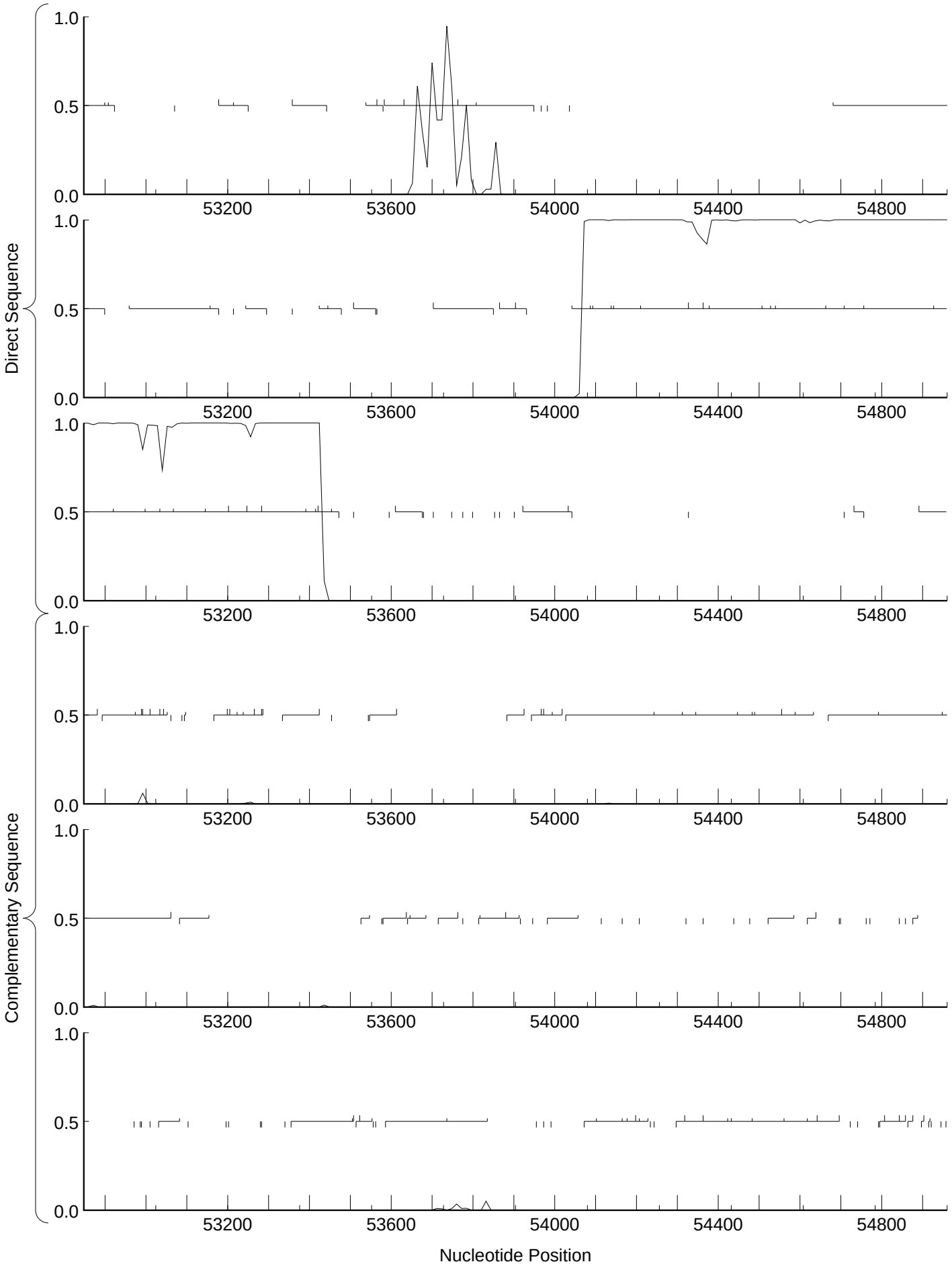

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Complementary Sequence
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47600
48000
48400
Nucleotide Position

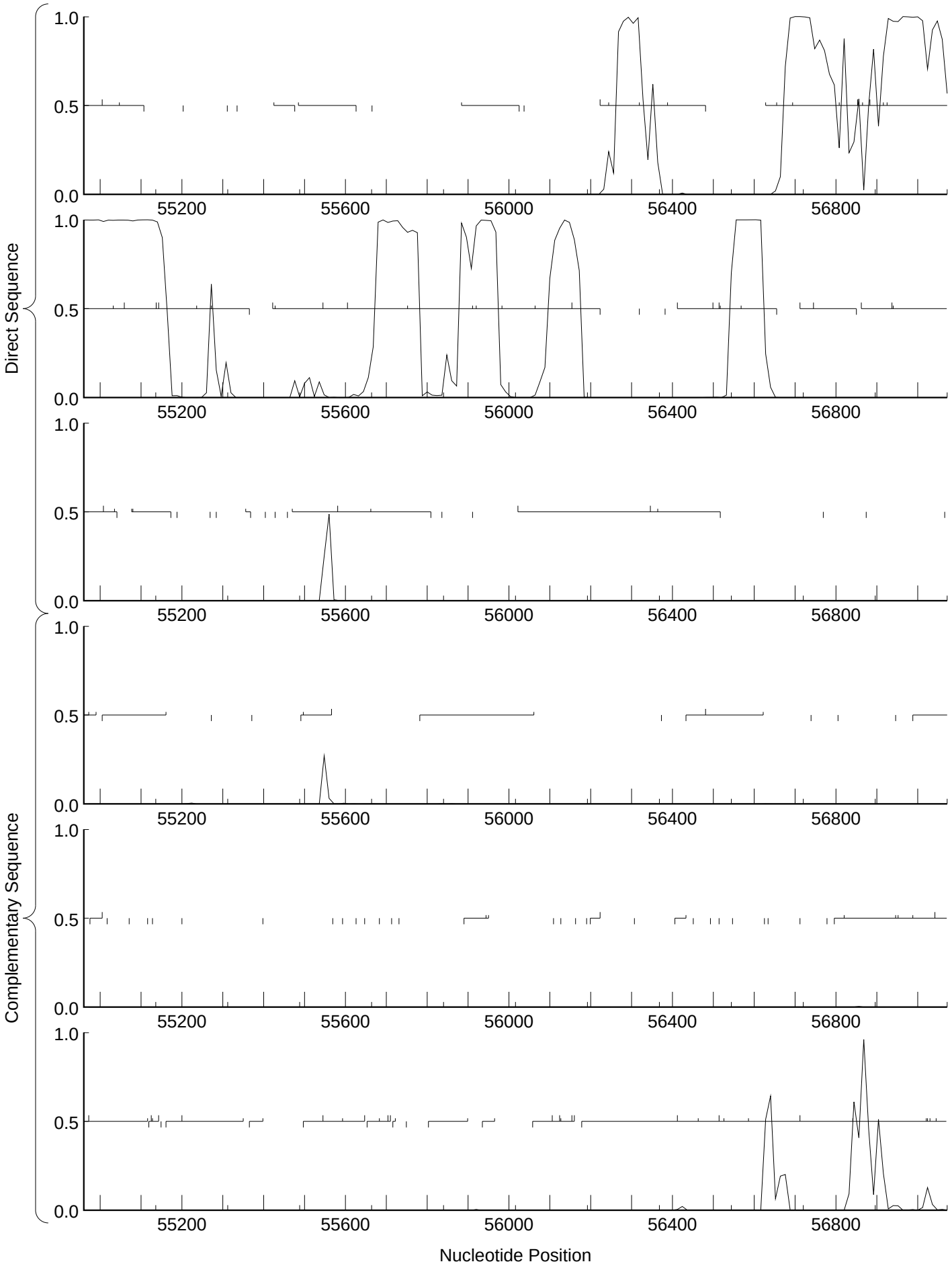
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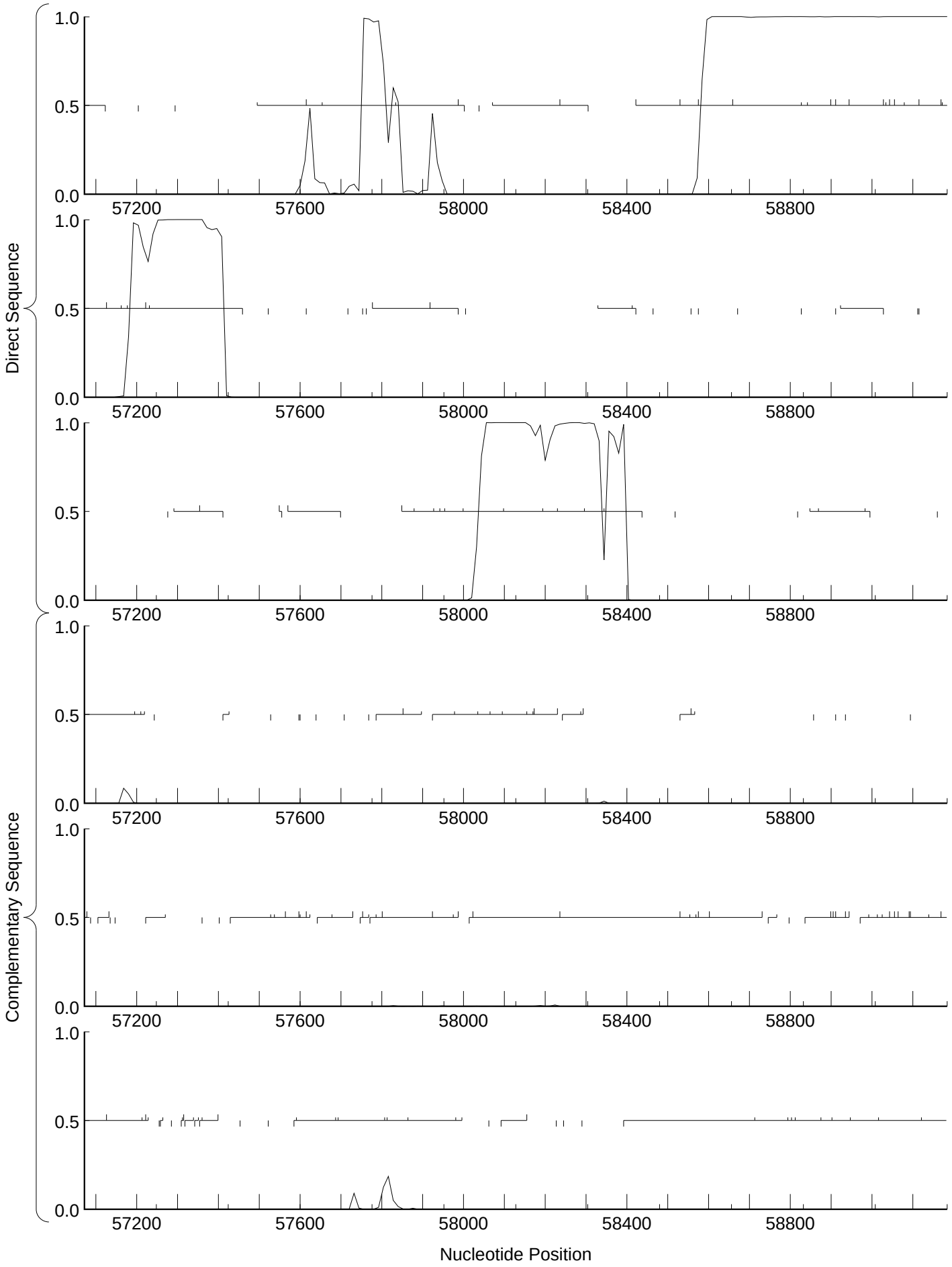



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Complementary Sequence
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51200
51600
52000
52400
52800
Nucleotide Position

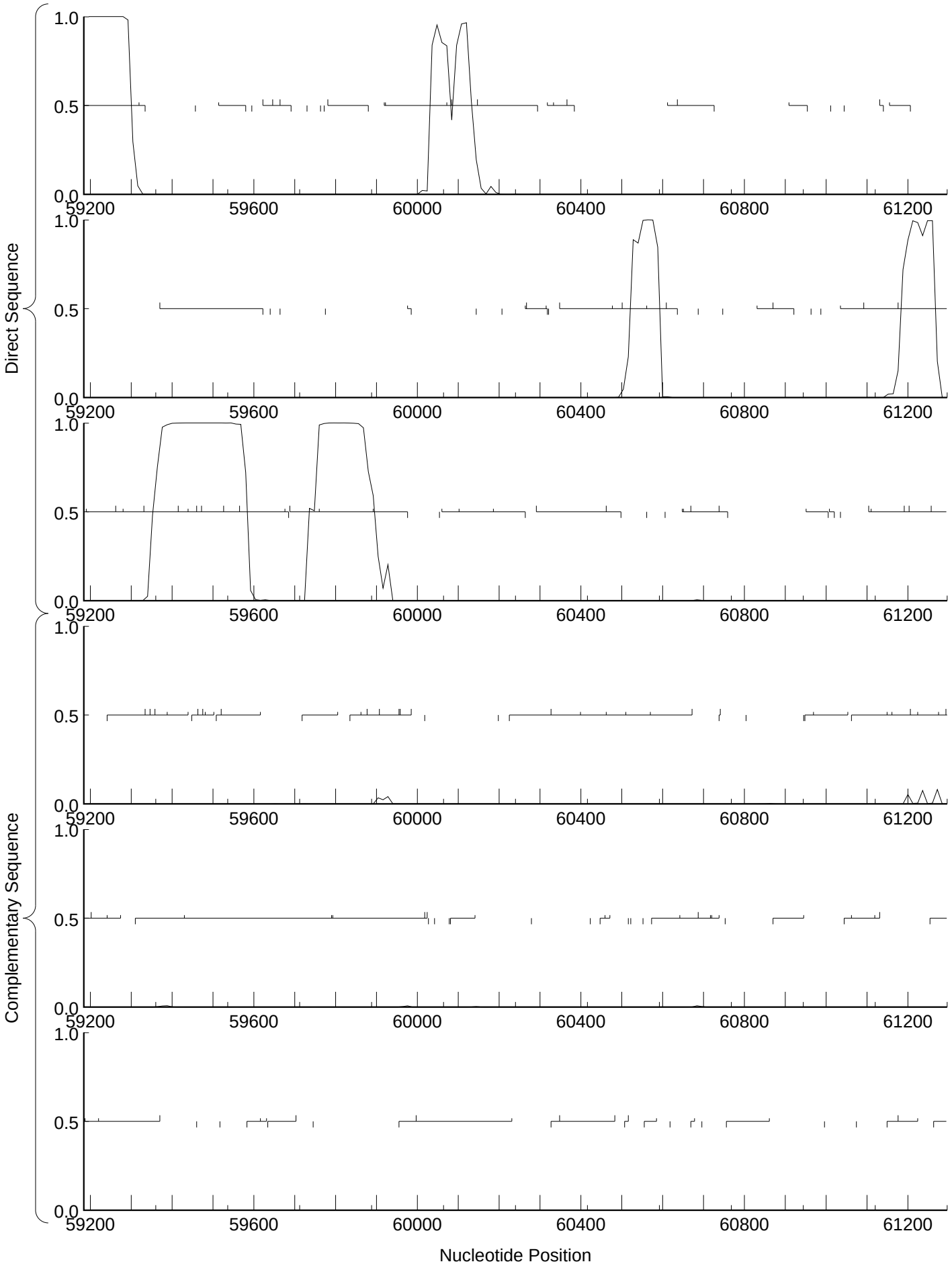
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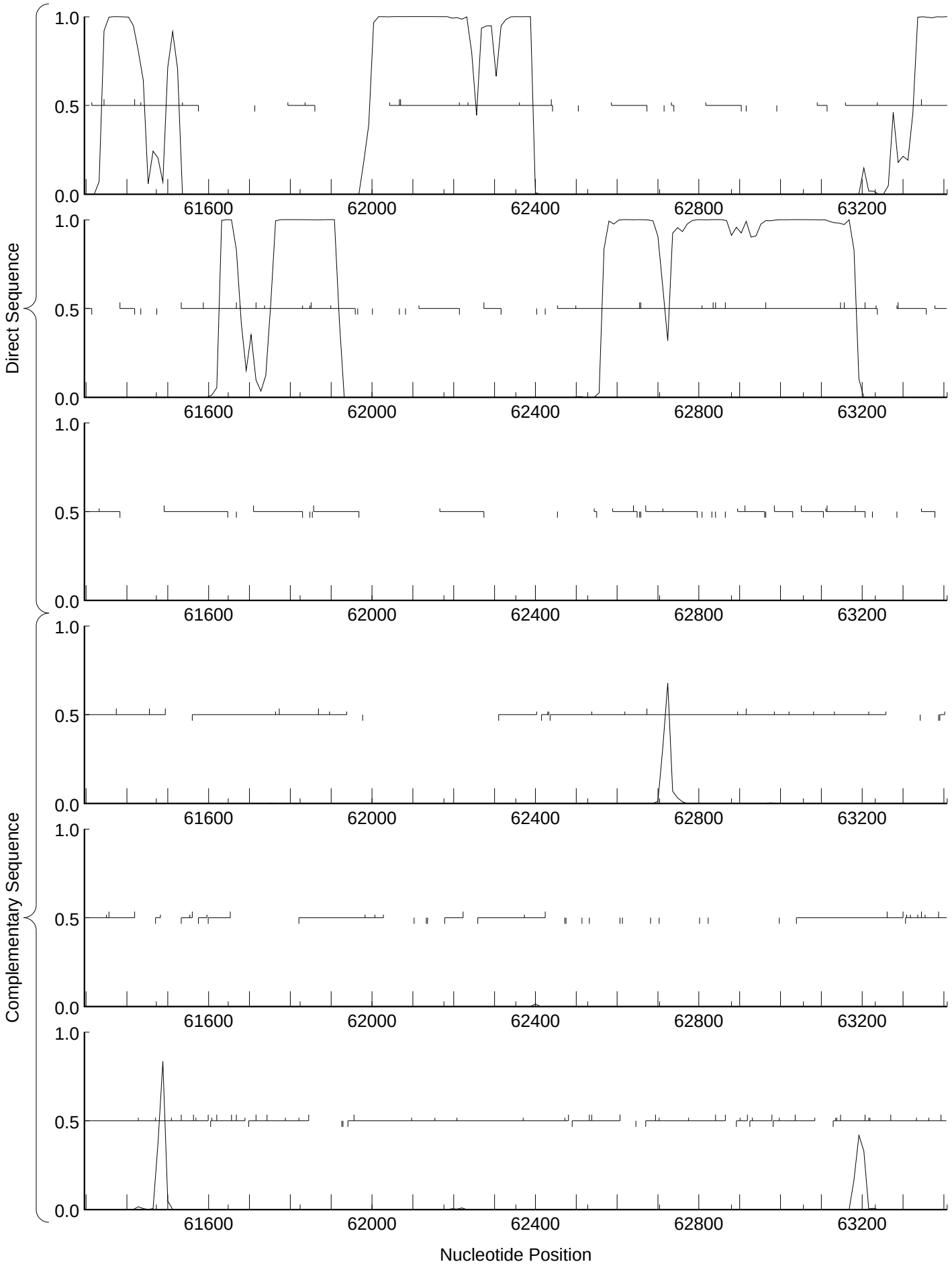

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Complementary Sequence
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0.5
0.0
55200
55600
56000
56400
56800
Nucleotide Position


Direct Sequence
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0.5
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57200
57600
58000
58400
58800
Nucleotide Position

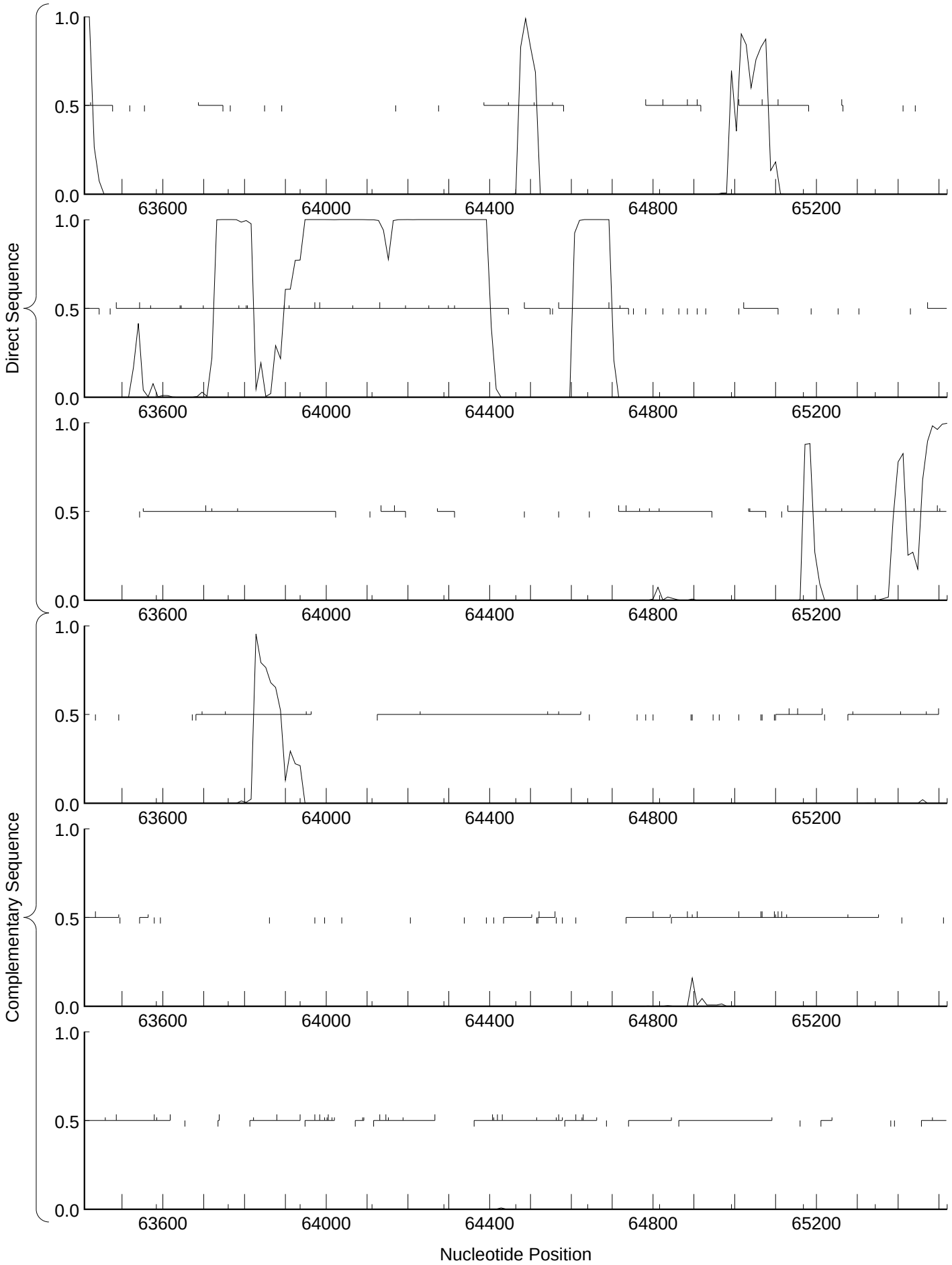
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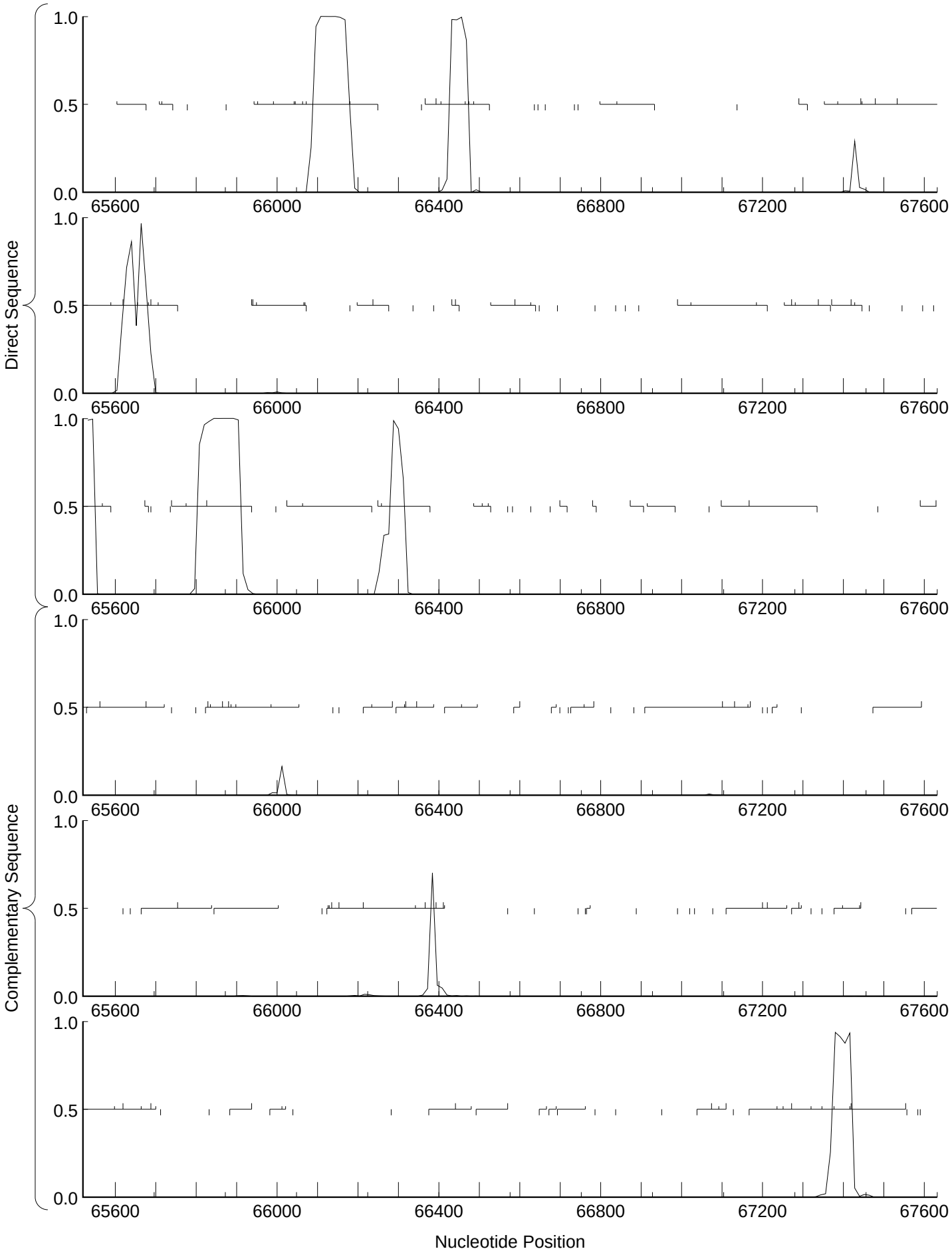
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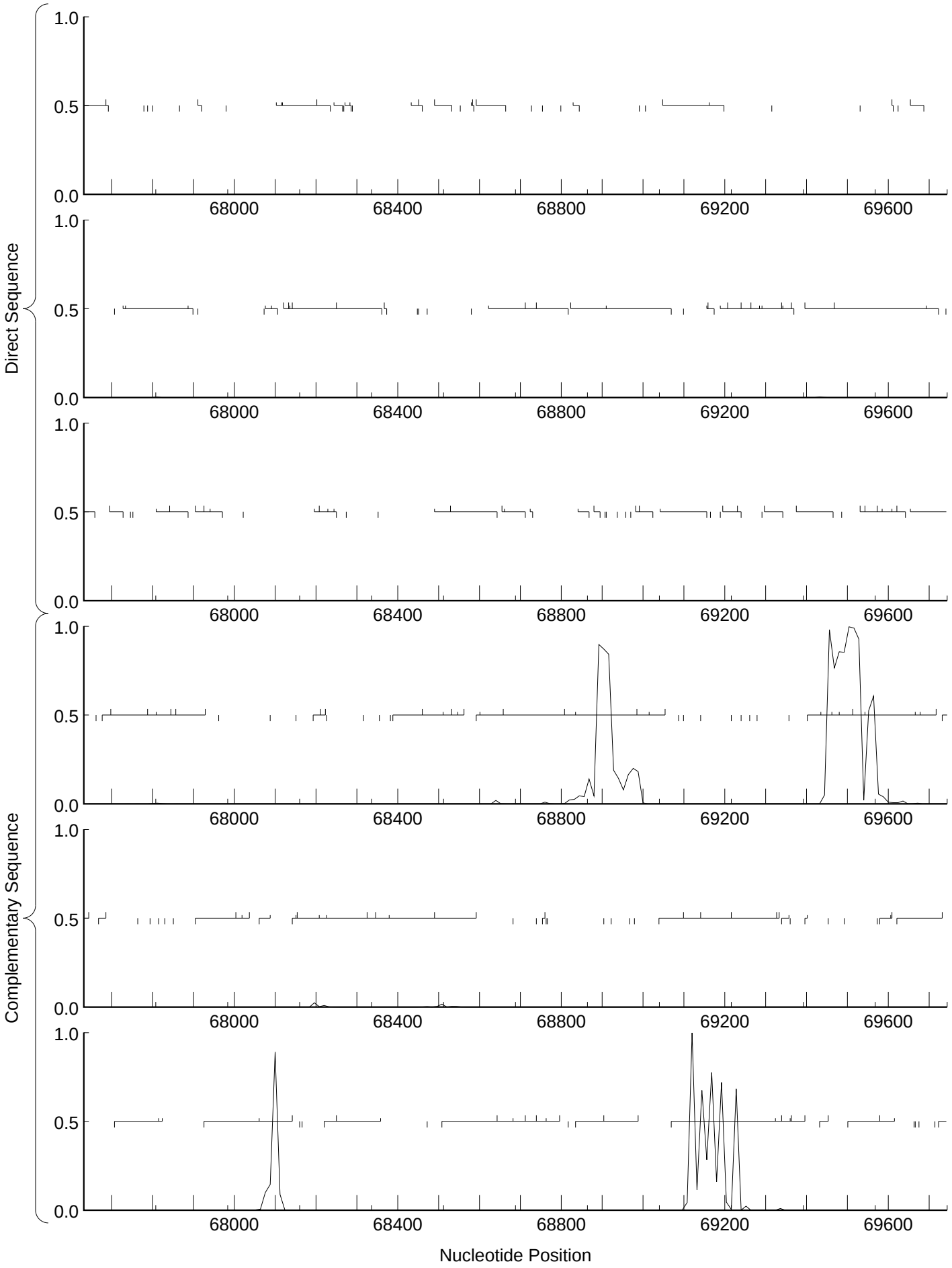
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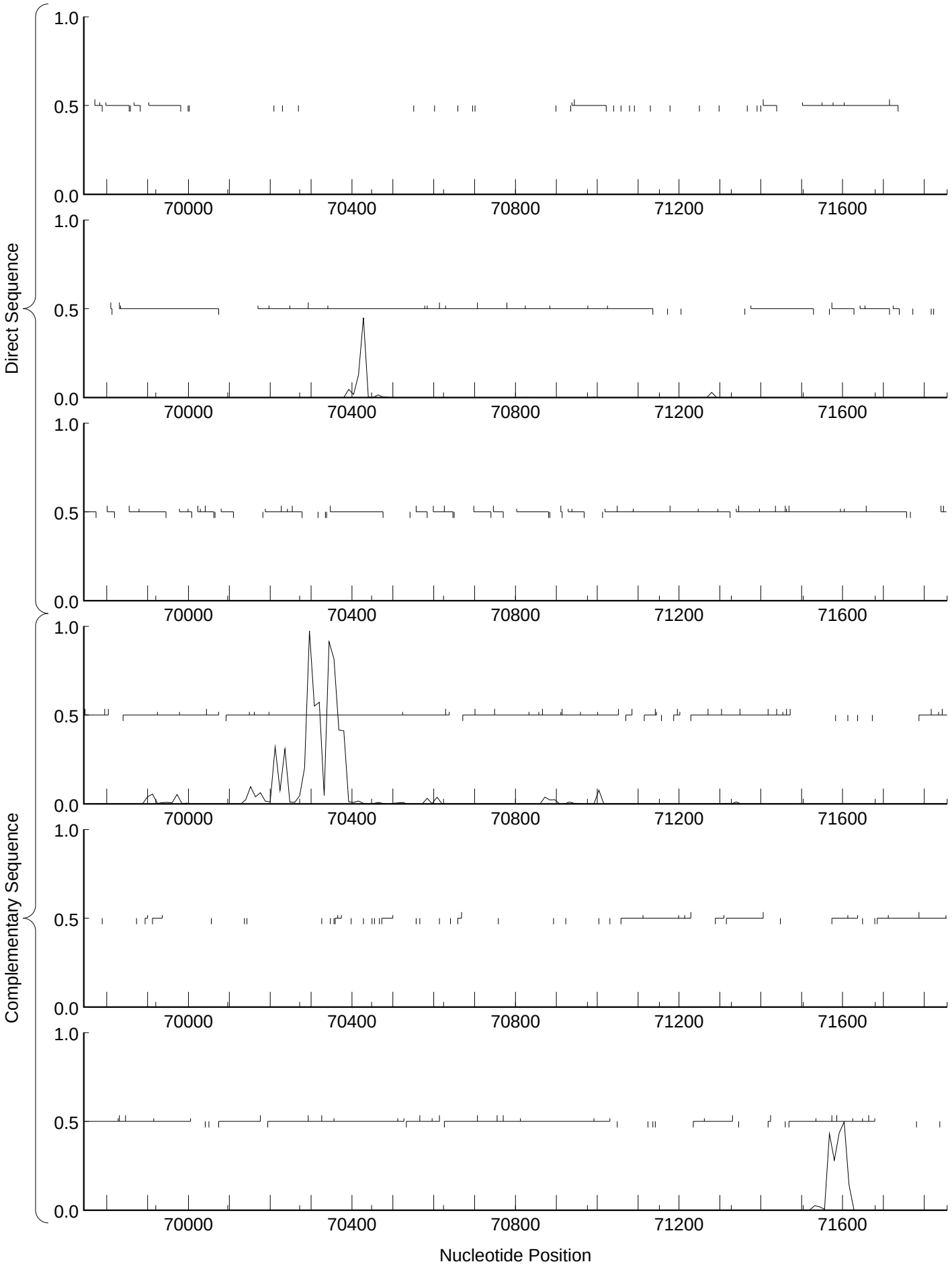


nts25 complete sequence, 73415 bp including 9-base 3' overhang (CGCTTGTCA), Cluster E, Order 4, Window 96, Step 12, 33/36



nts25 complete sequence, 73415 bp including 9-base 3' overhang (CGCTTGTCA), Cluster E, Order 4, Window 96, Step 12, 34/36




Direct Sequence
Complementary Sequence
1.0
0.5
0.0
70000
70400
70800
71200
71600
Nucleotide Position

nts25 complete sequence, 73415 bp including 9-base 3' overhang (CGCTTGTCA), Cluster E, Order 4, Window 96, Step 12, 36/36

