GeneMark

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

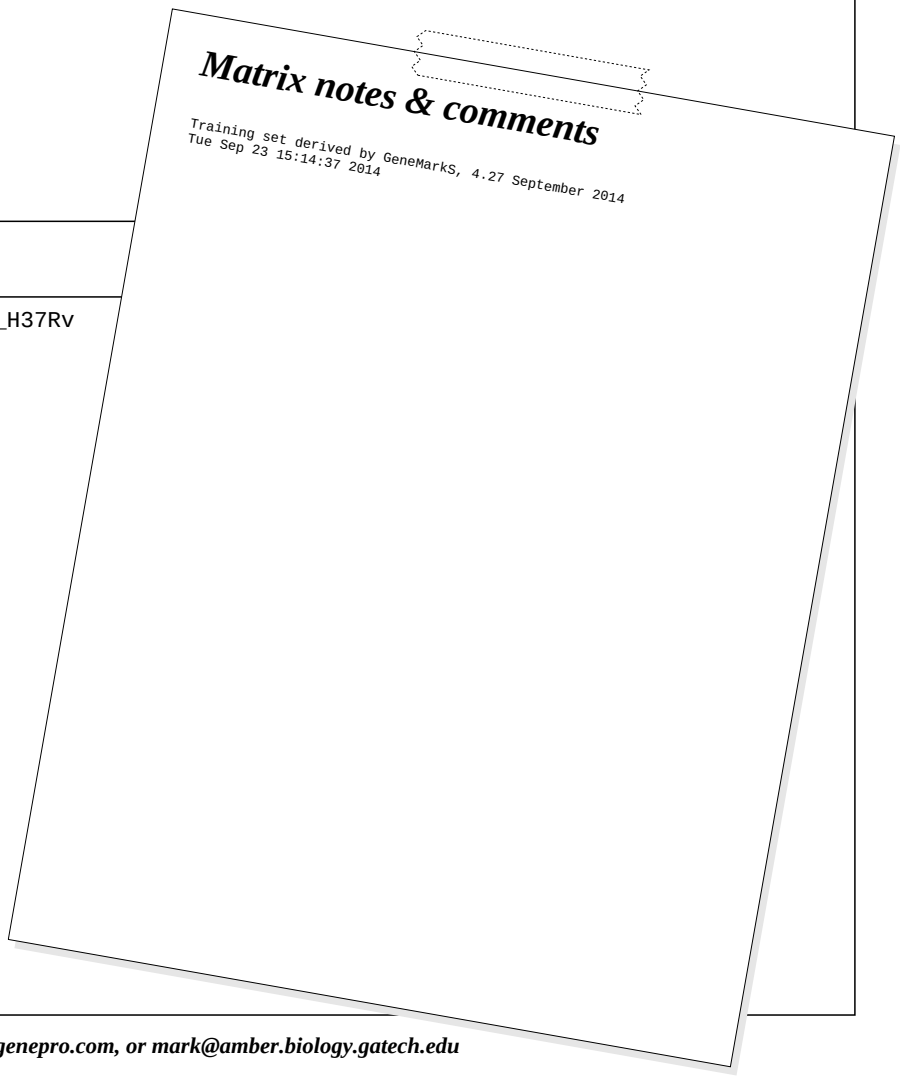
PROGRAM INFORMATION

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Sequence         :  Mycobacterium phage SimranZ1 complete sequence, 56335 bp including 10-base 3' overhang (CCG
Analysis Date    :  3/28/24 at 19:11:09
Pages            :  28
Sequence Length  :  56335 bp
GC Content       :   61.26%

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

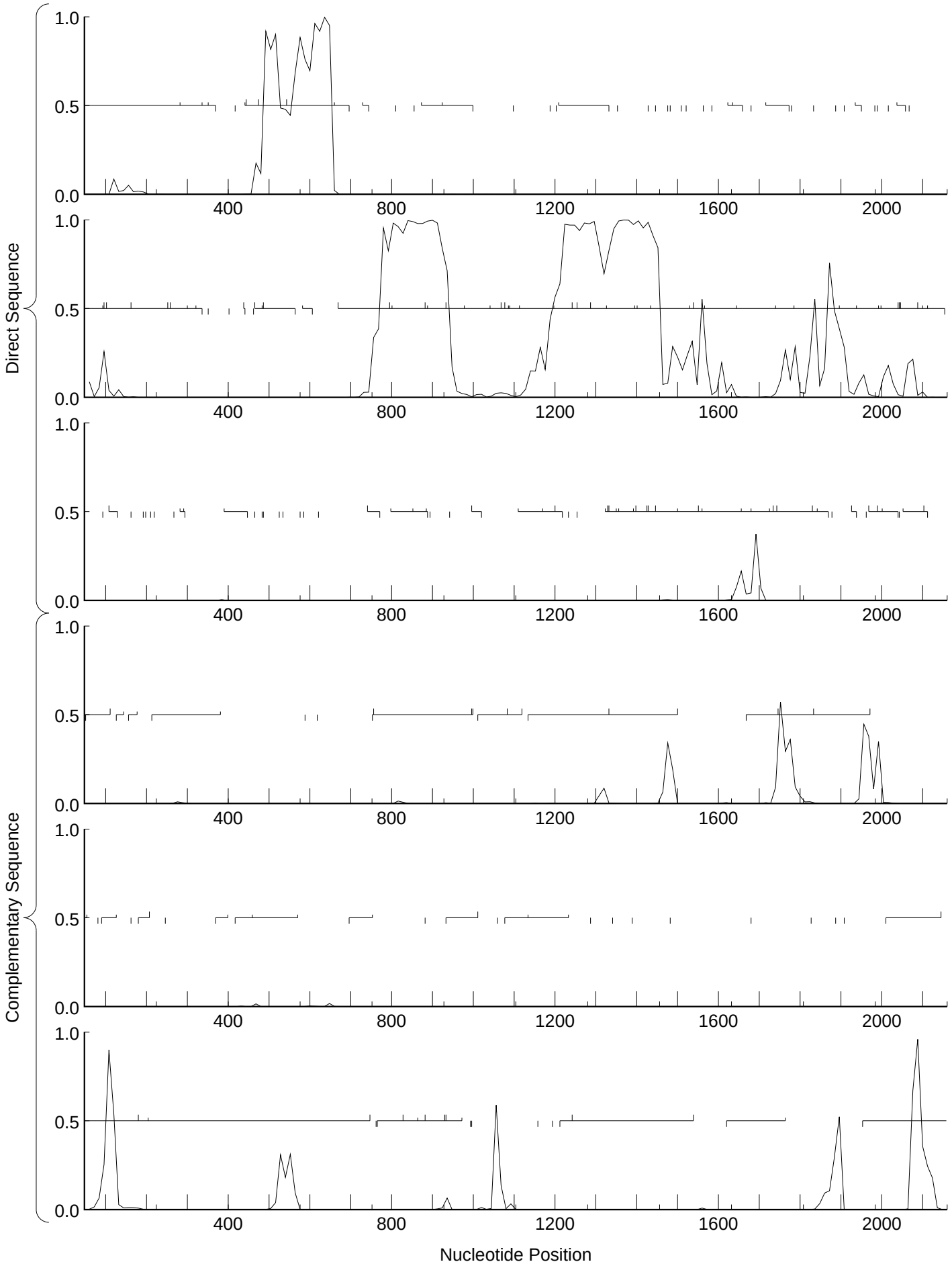
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Matrix     :  Mycobacterium_tuberculosis_H37Rv
Author     :  -

Order      :  4
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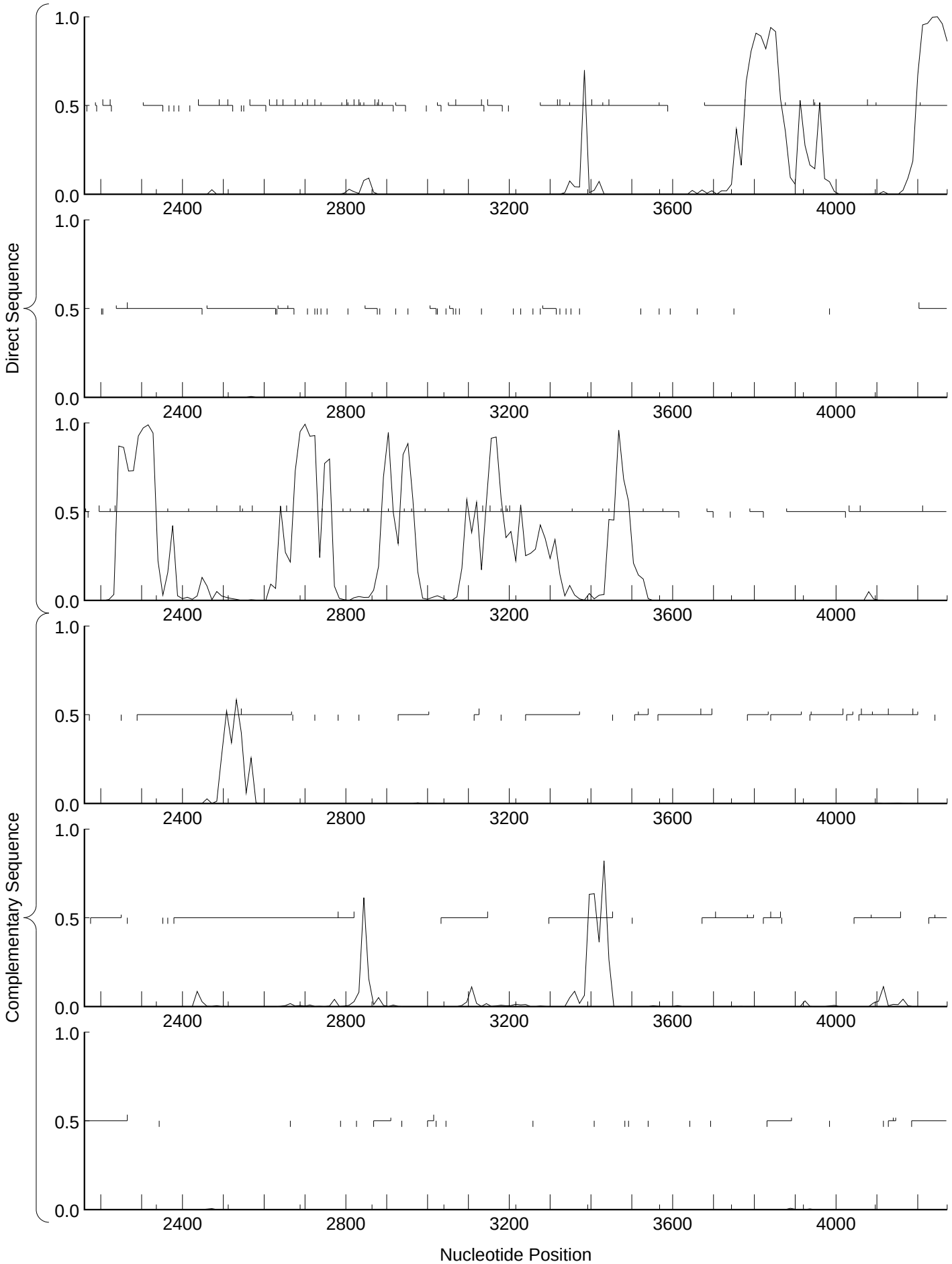

```
  Send questions / comments to:
      Dr. M. Borodovsky
      Georgia Institute of Technology
      School of Biology
      Atlanta, GA  30332-0230
```


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

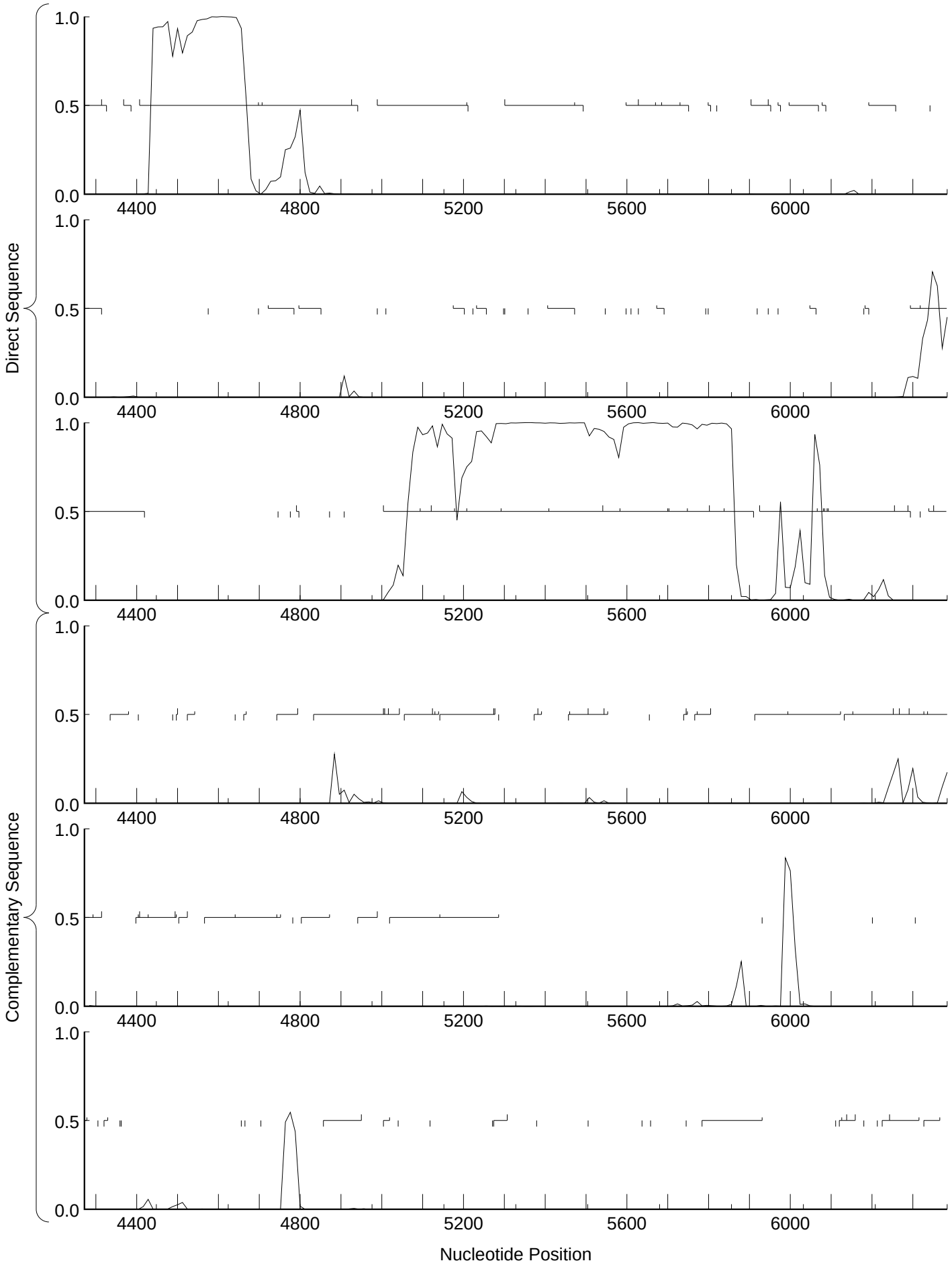
Z1 complete sequence, 56335 bp including 10-base 3’ overhang (CCGAAGGCAT), Cluster F1, Order 4, Window 96, Step 12, 2/28



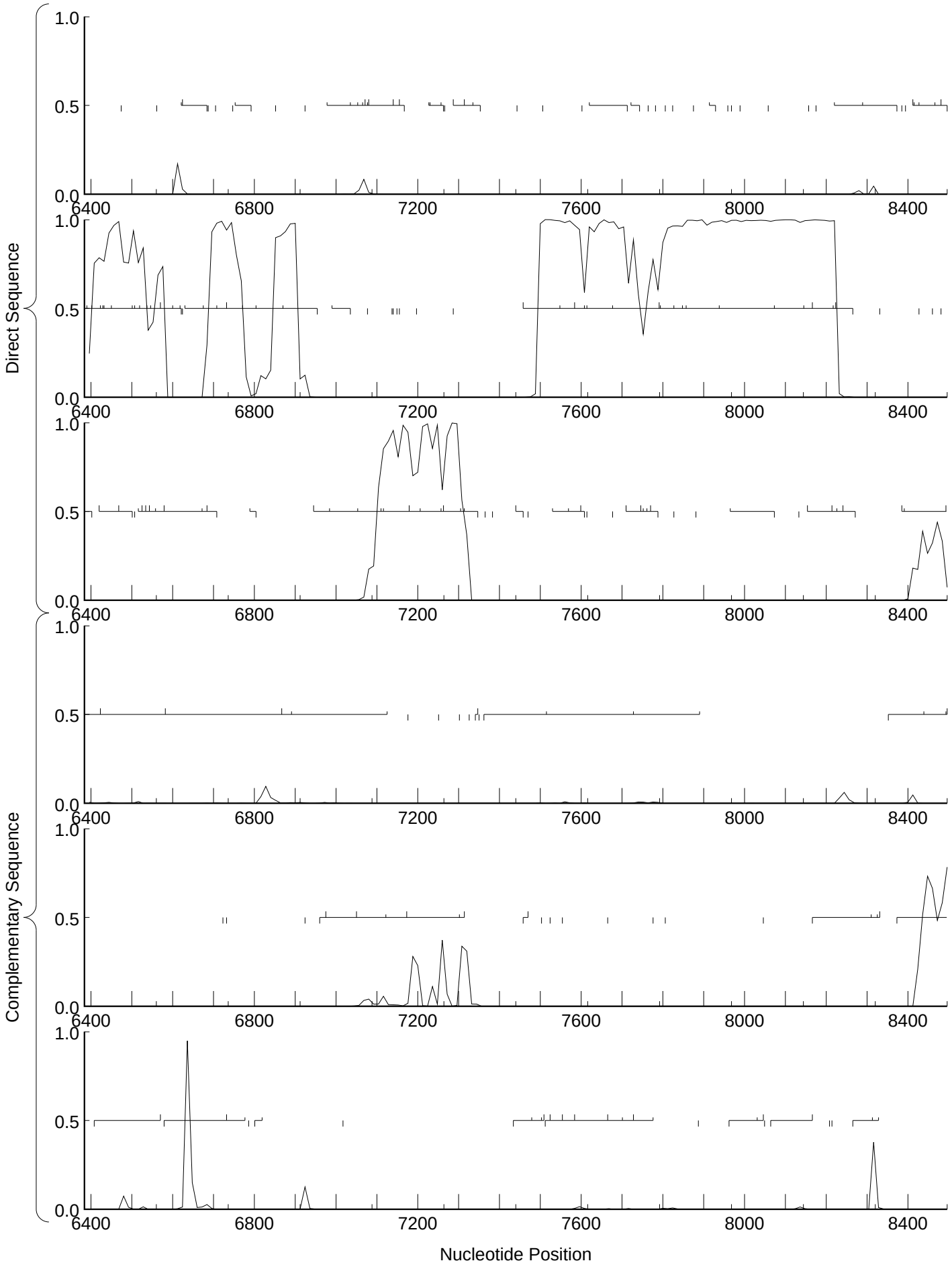
Z1 complete sequence, 56335 bp including 10-base 3’ overhang (CCGAAGGCAT), Cluster F1, Order 4, Window 96, Step 12, 3/28



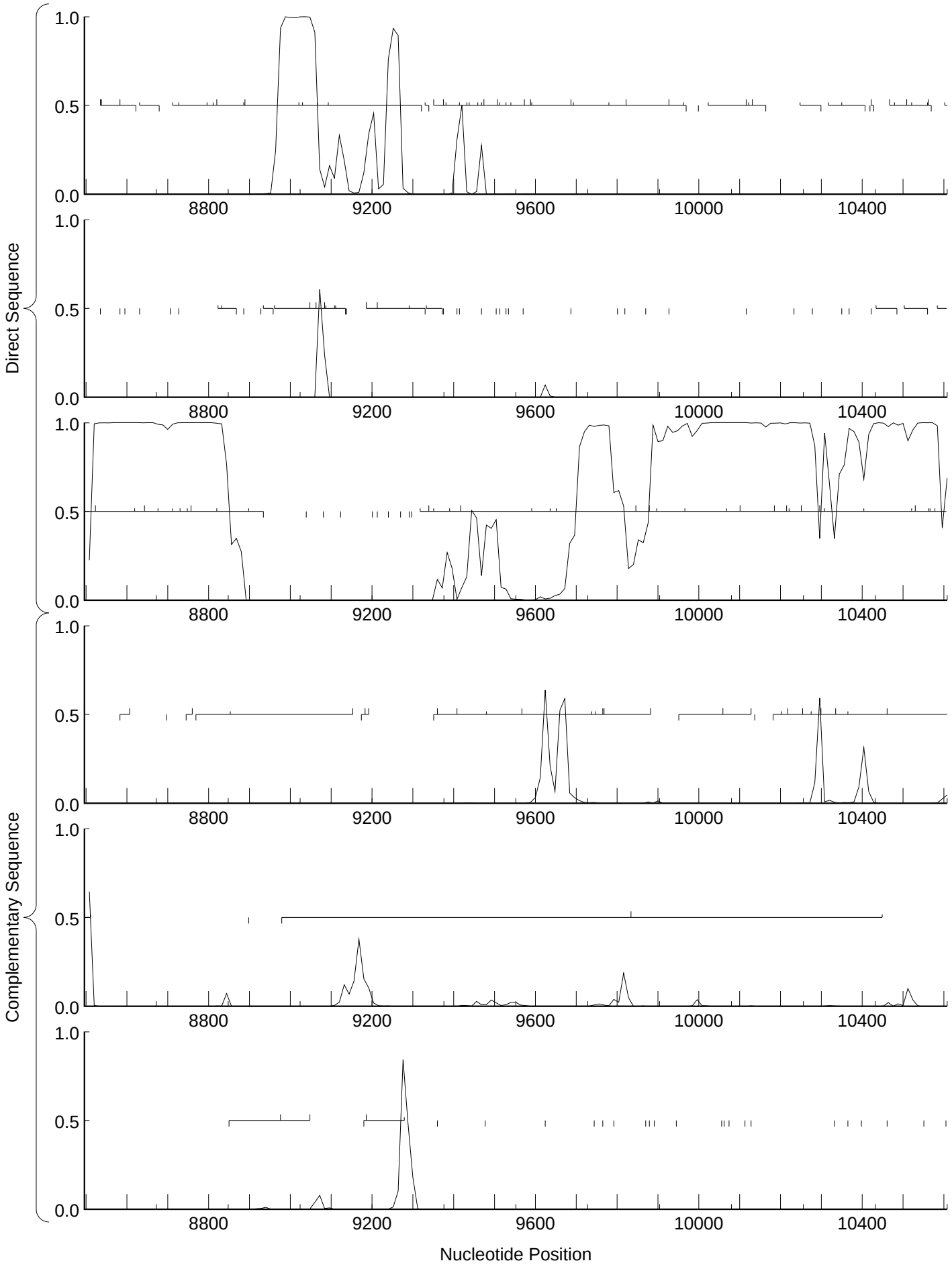
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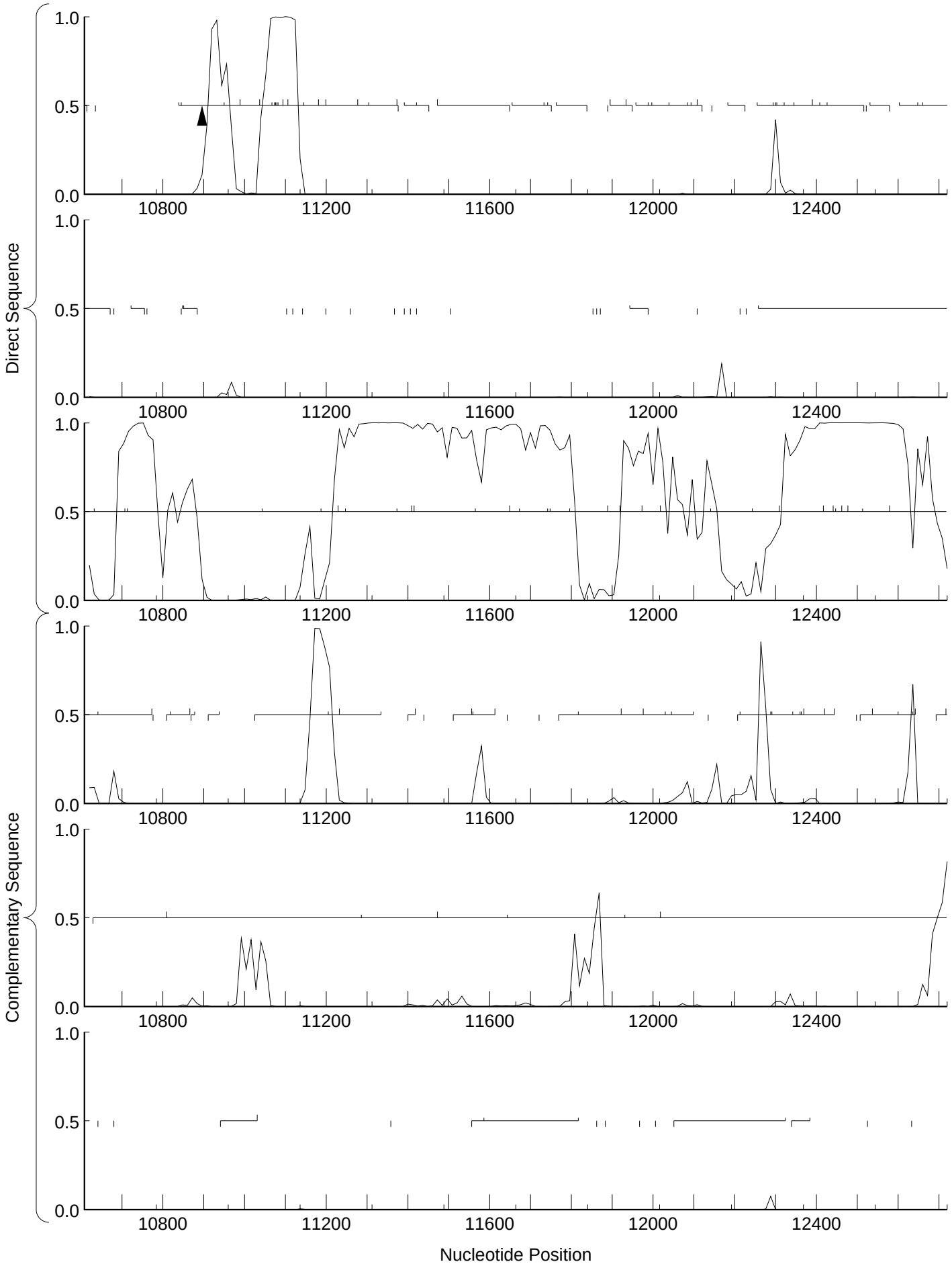
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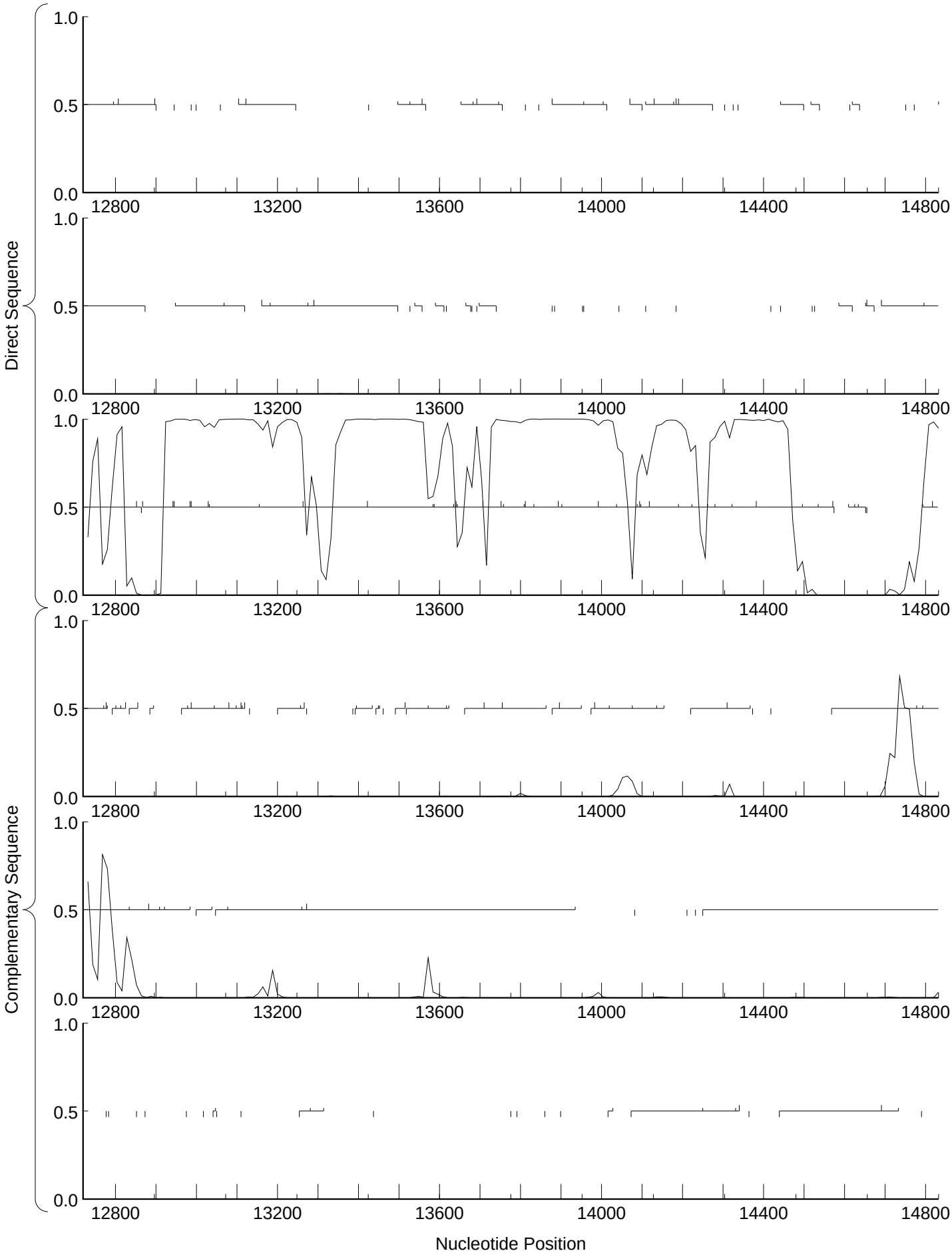
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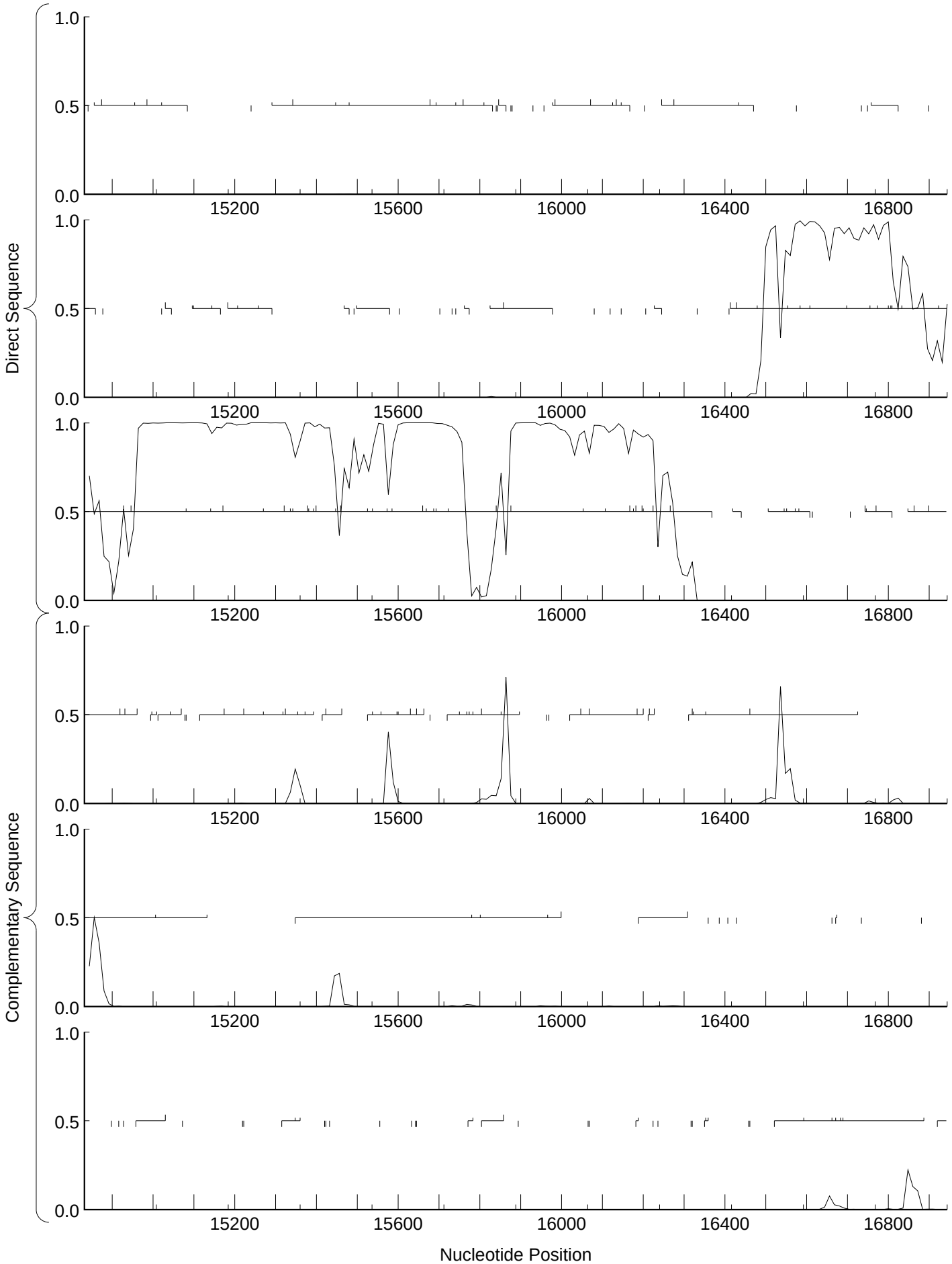
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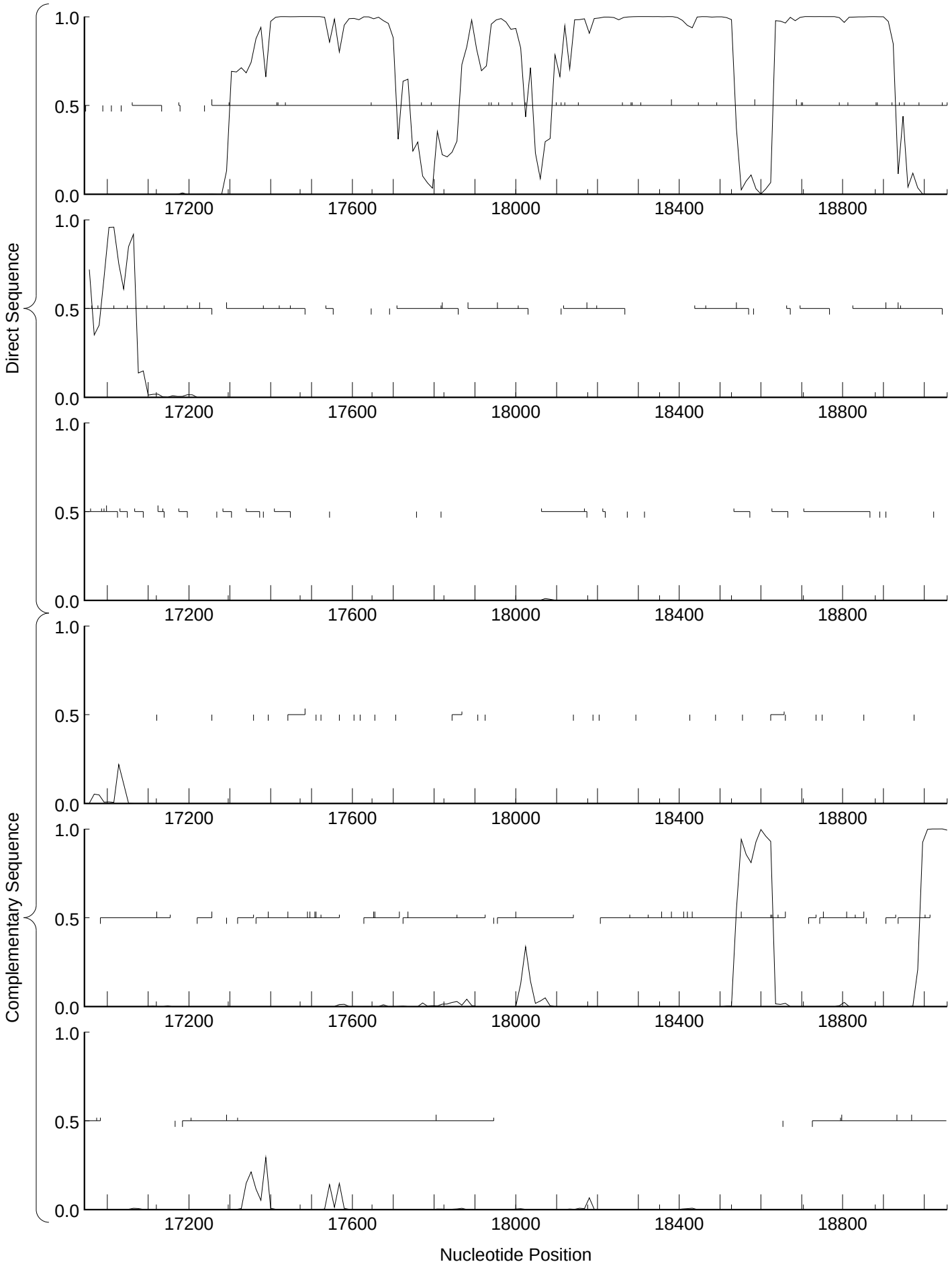


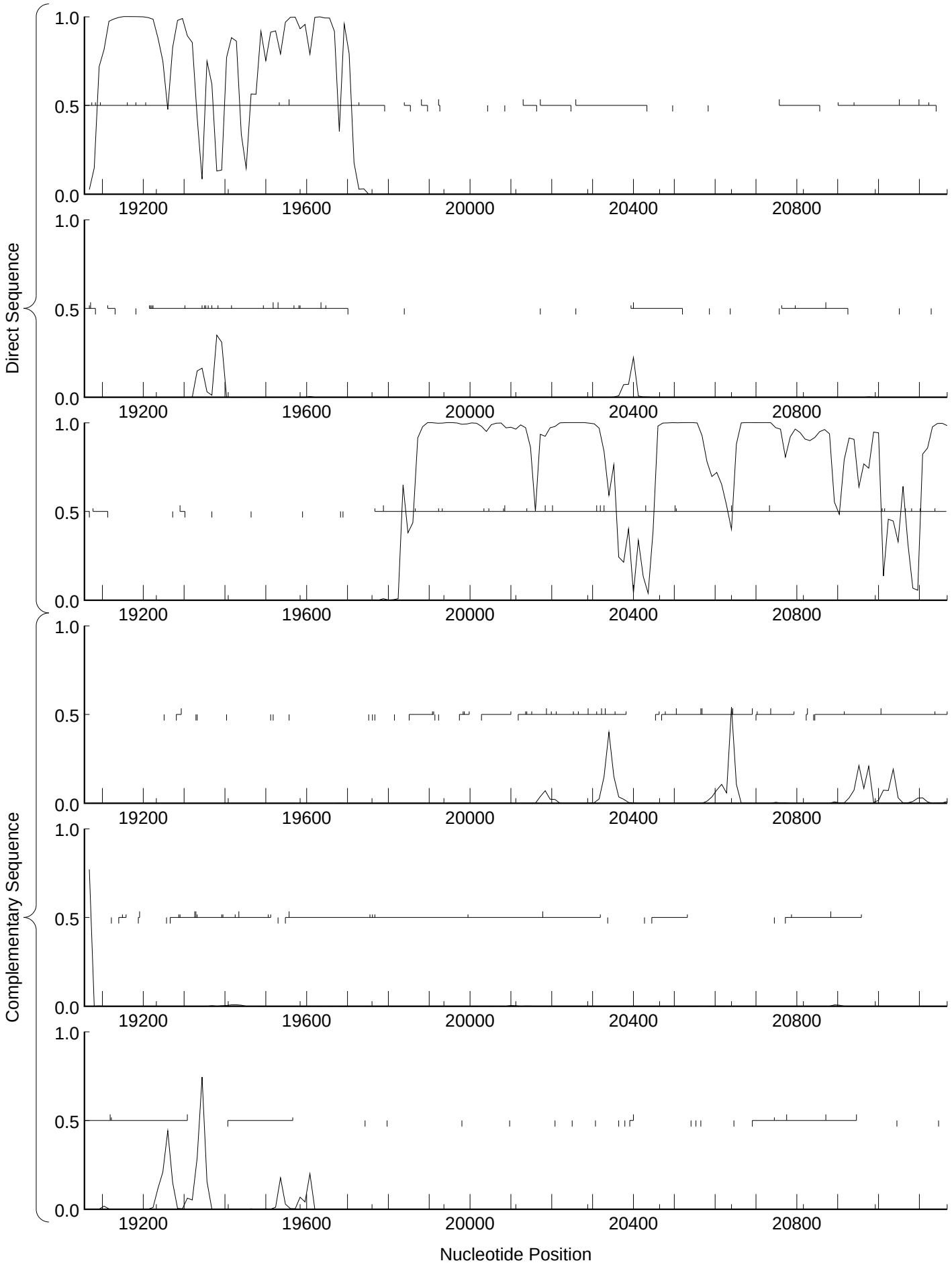
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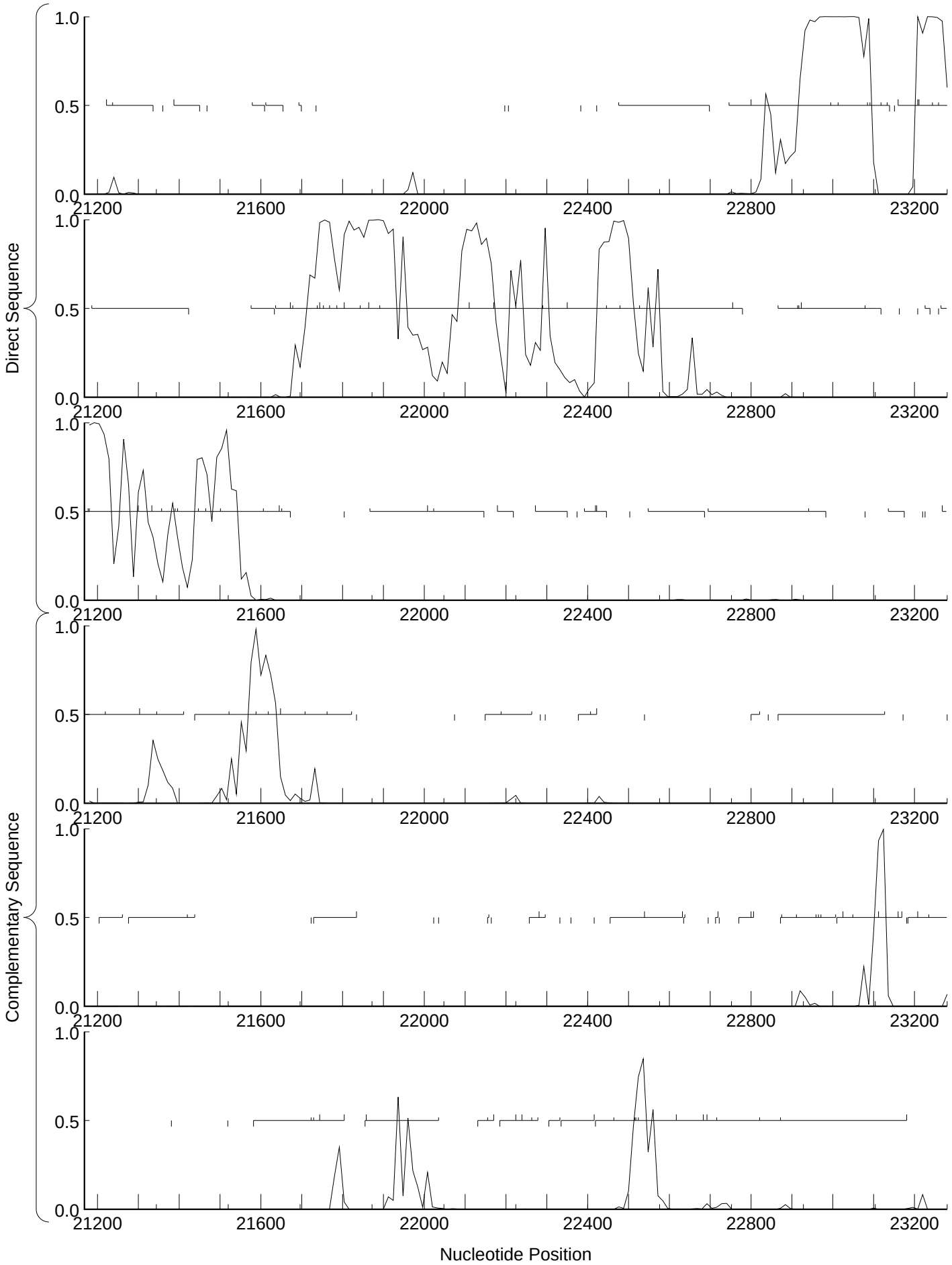


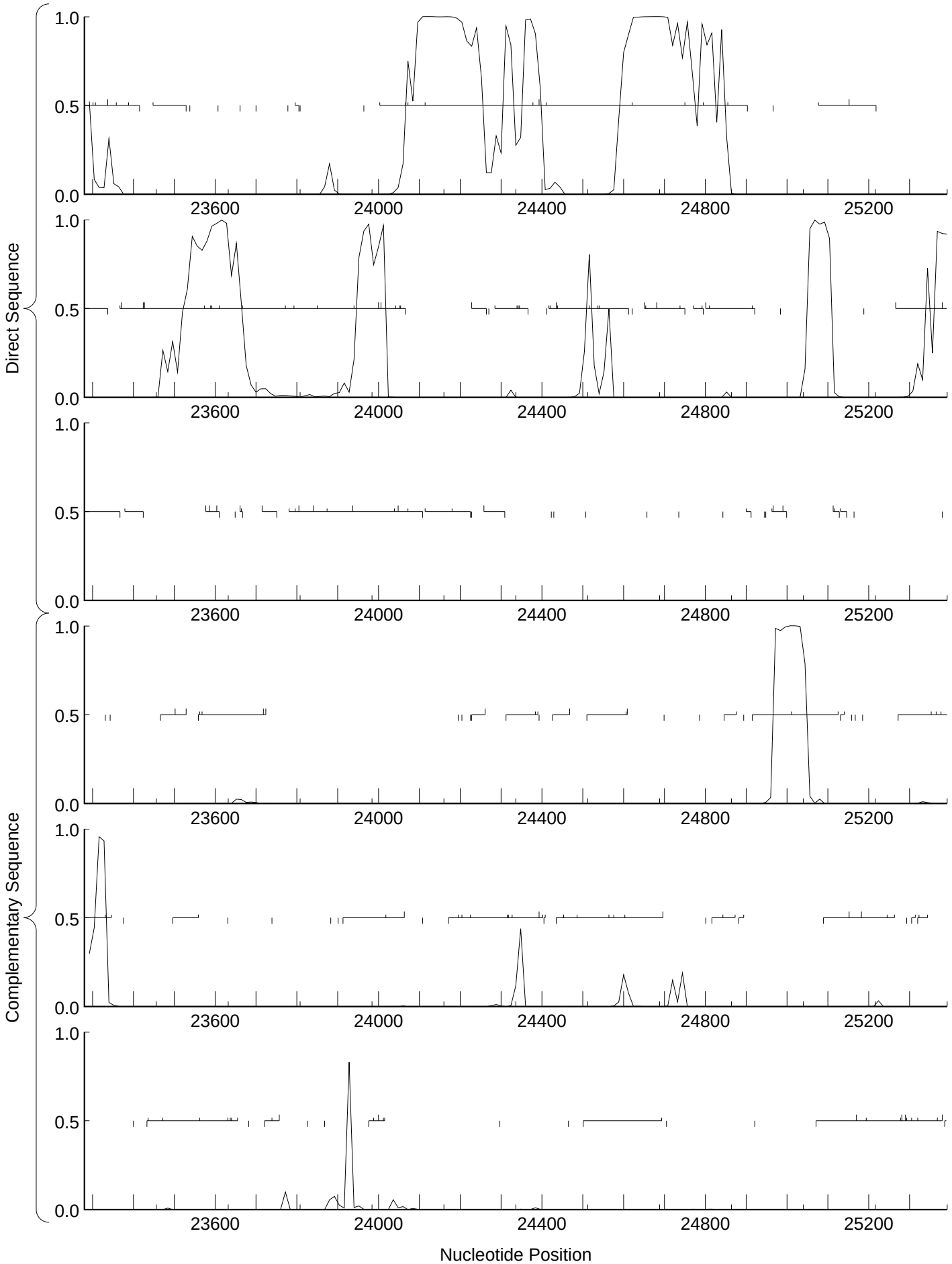
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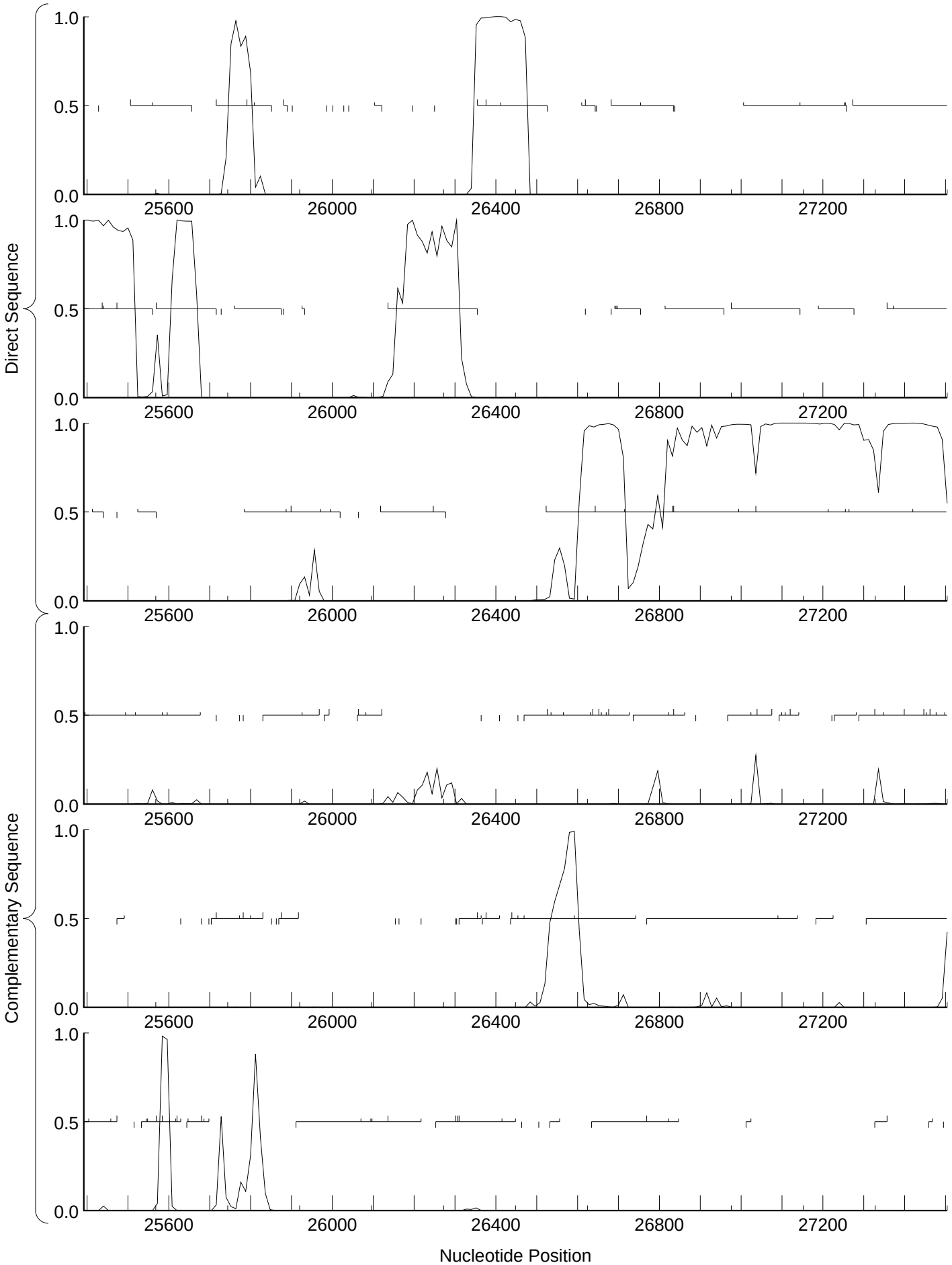


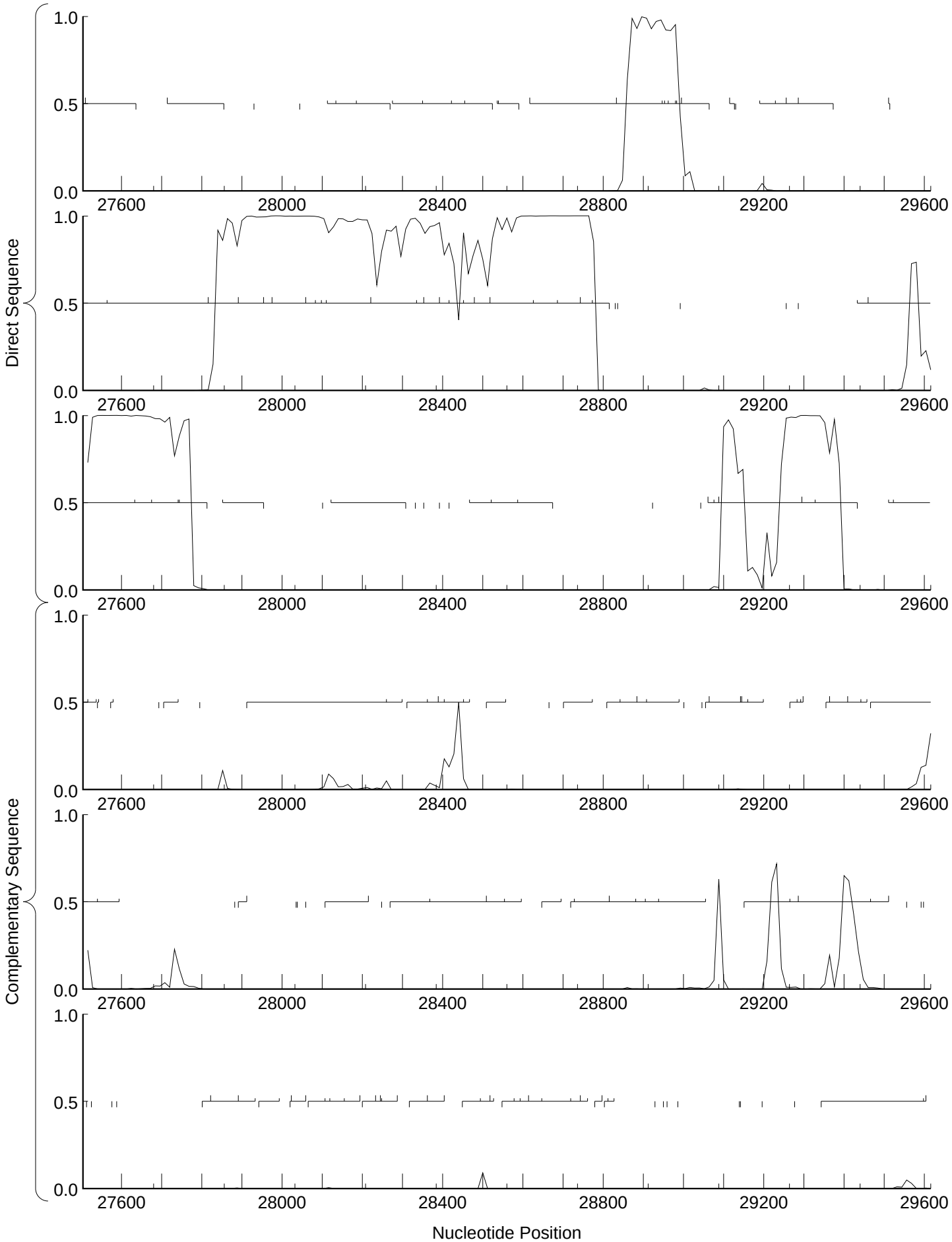

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Complementary Sequence
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0.5
0.0
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17600
18000
18400
18800
Nucleotide Position

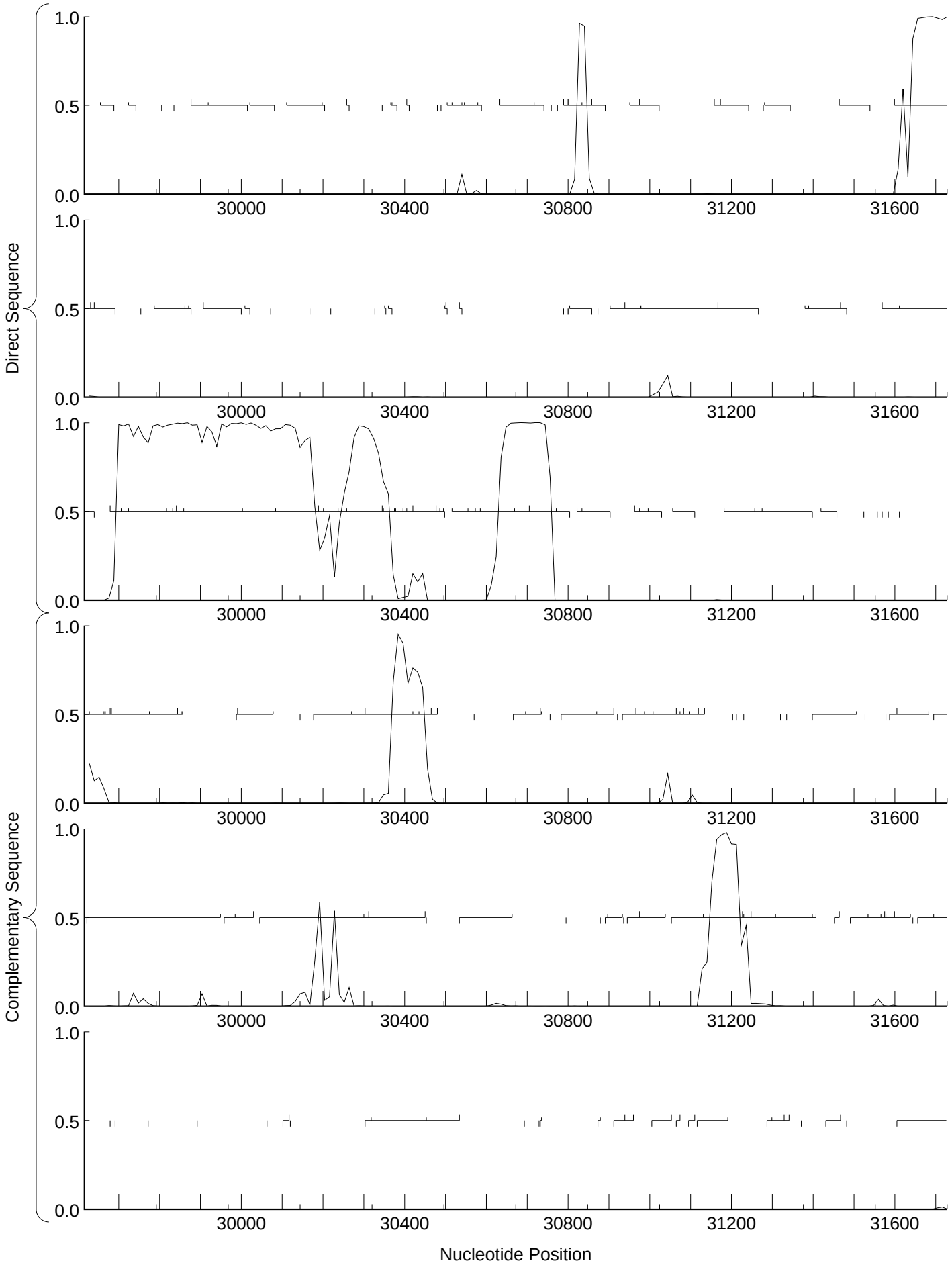

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Complementary Sequence
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20000
20400
20800
Nucleotide Position

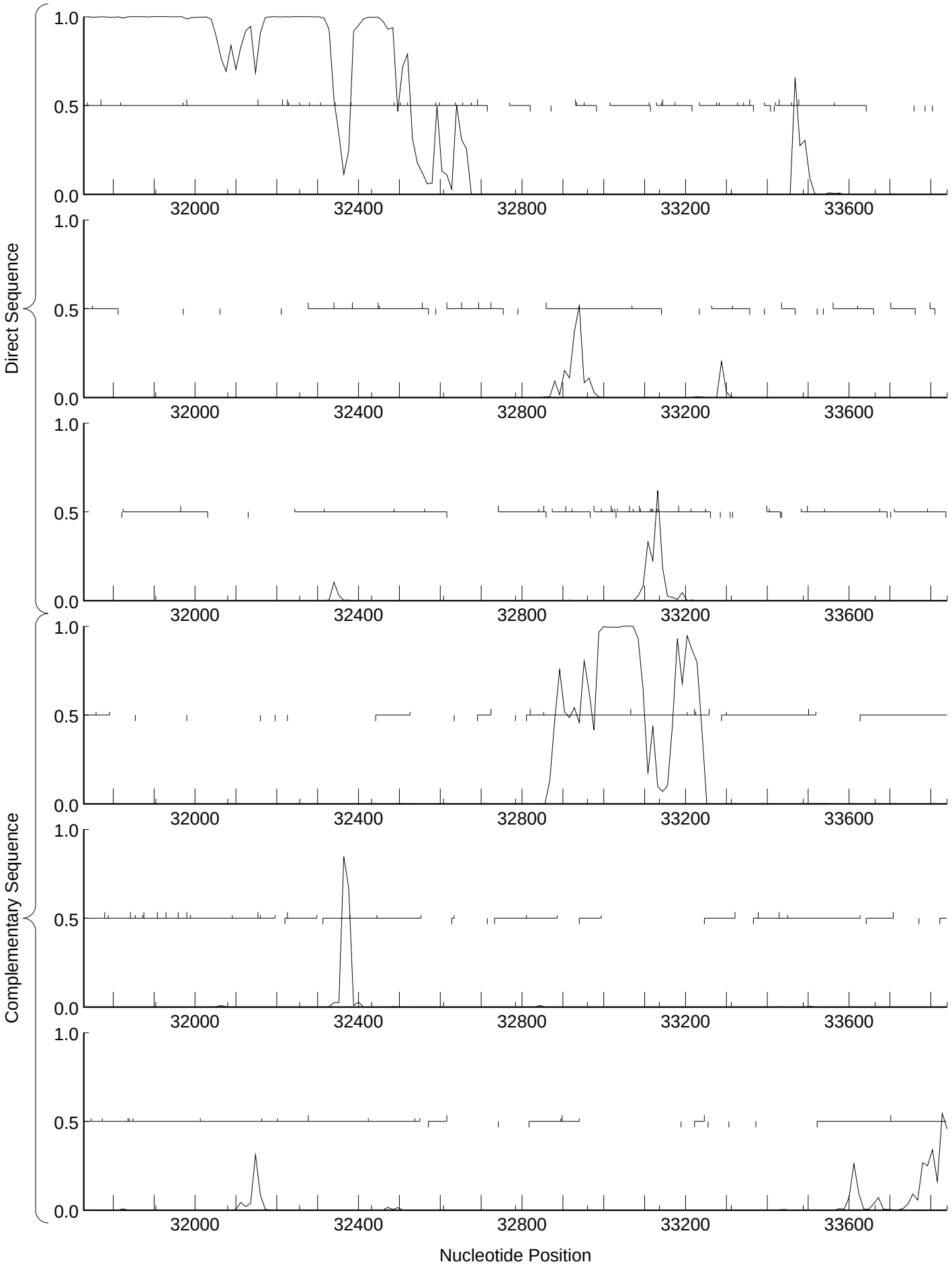

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21600
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22400
22800
23200
Nucleotide Position

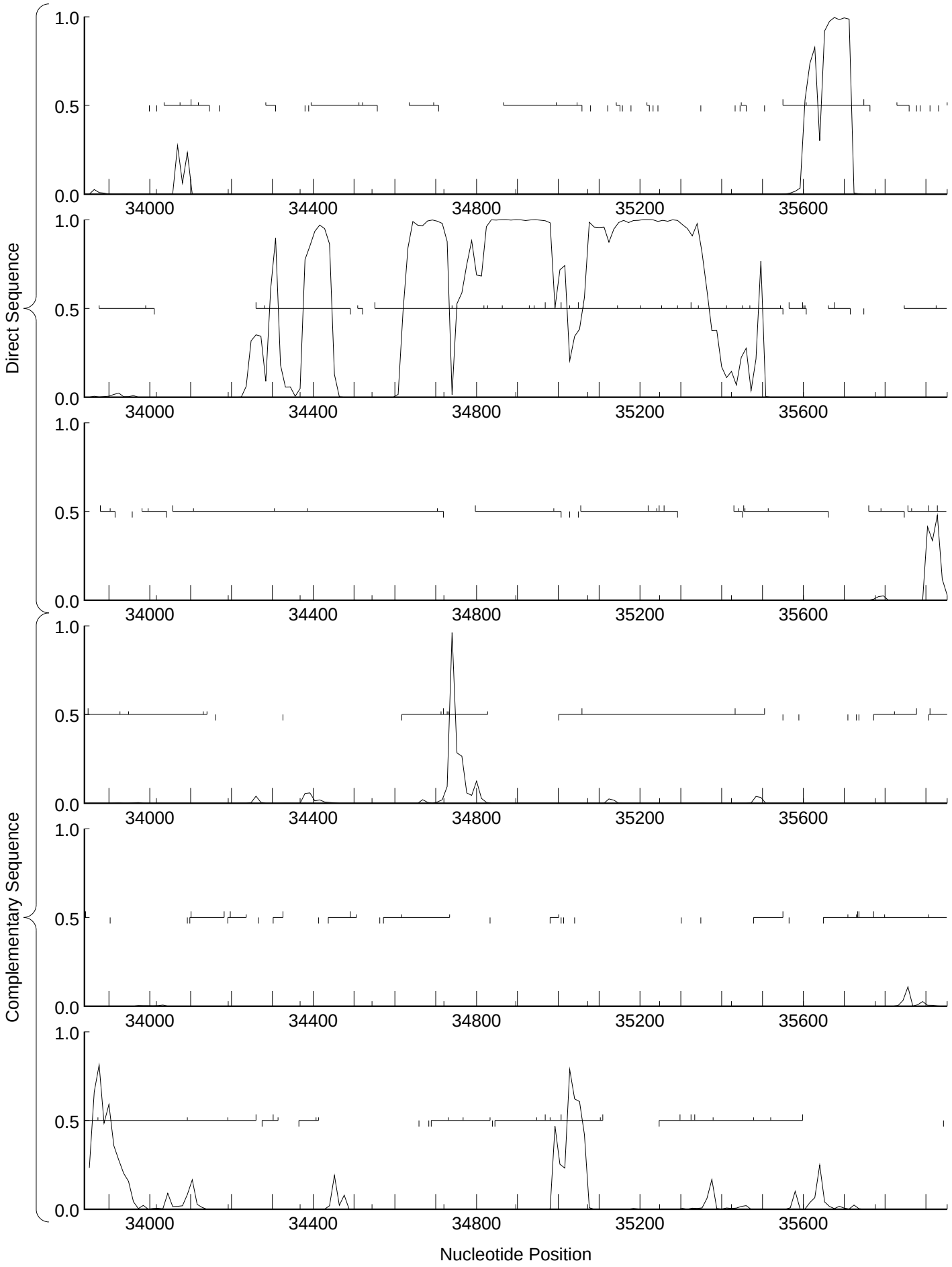

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Complementary Sequence
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0.0
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24400
24800
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Nucleotide Position

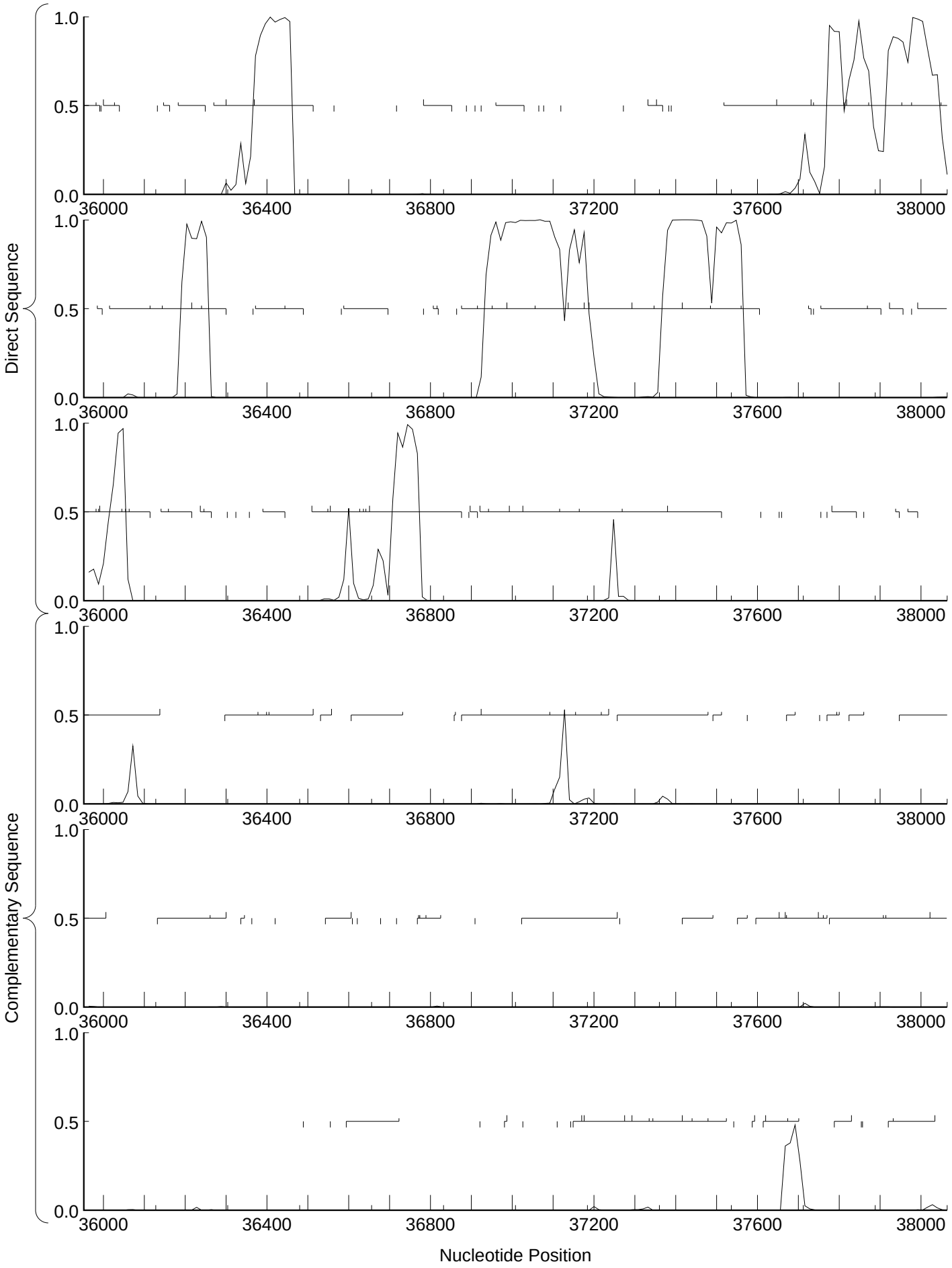

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Complementary Sequence
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Nucleotide Position

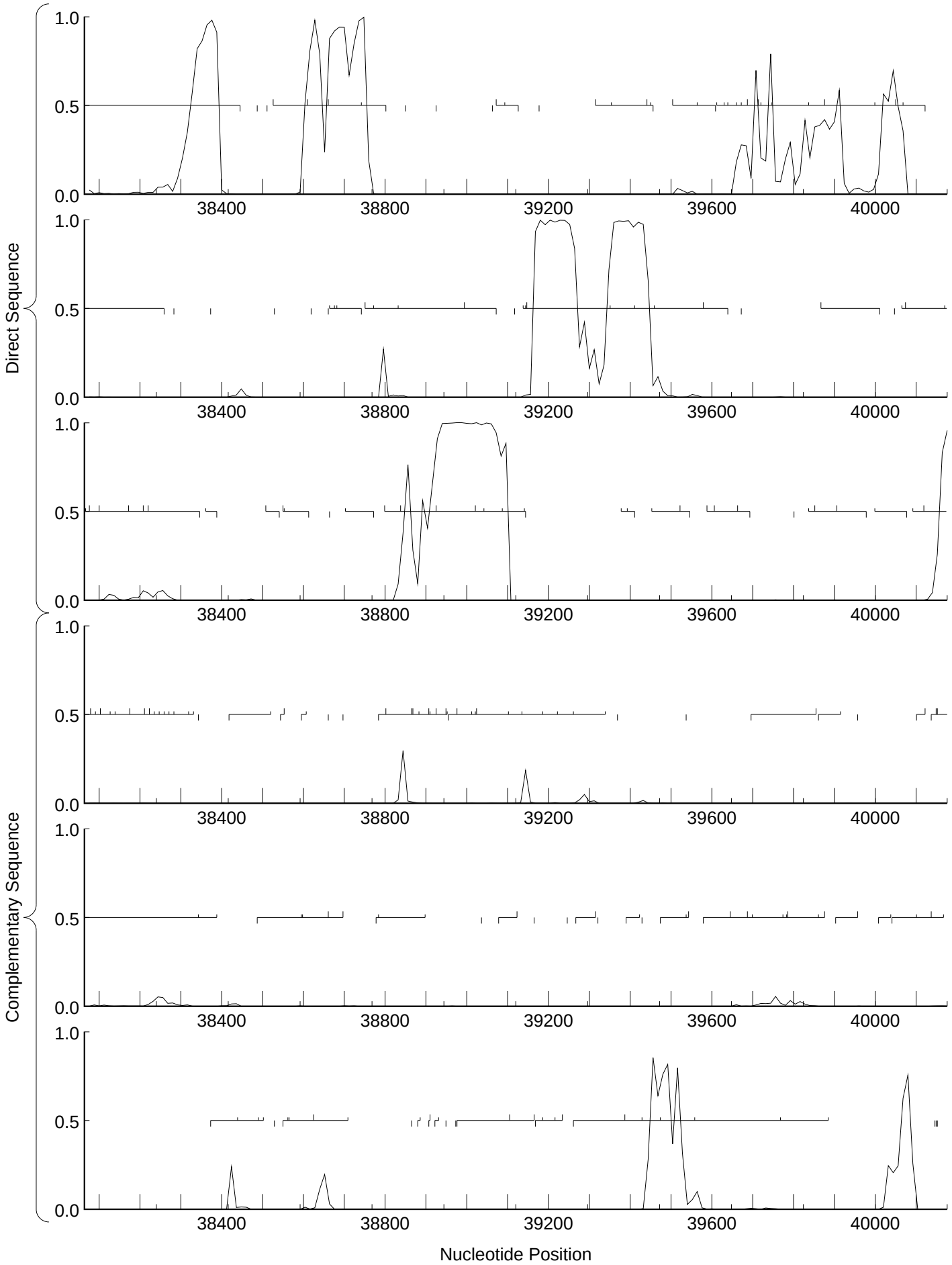

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Complementary Sequence
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29200
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Nucleotide Position

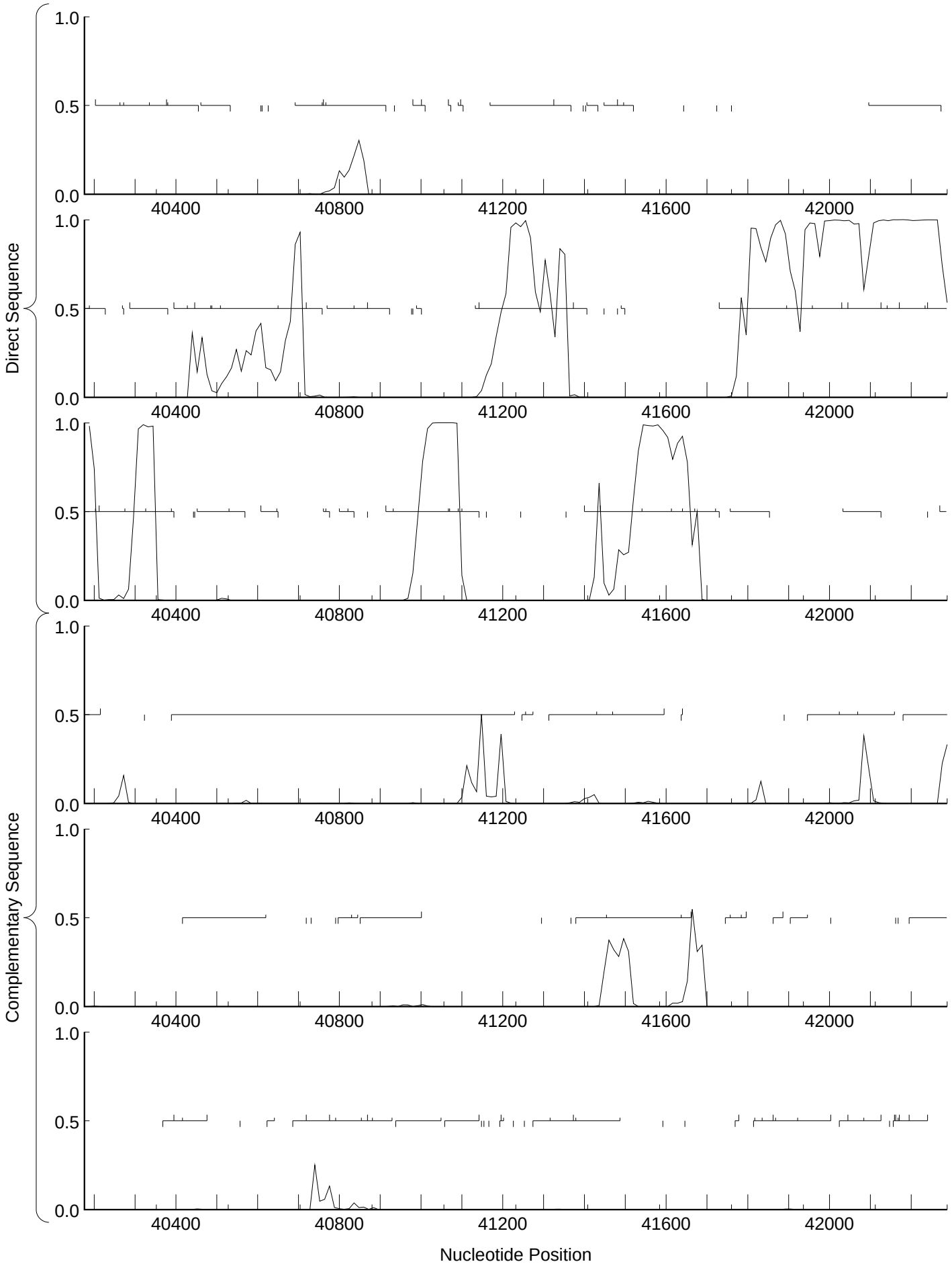

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Complementary Sequence
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31200
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Nucleotide Position

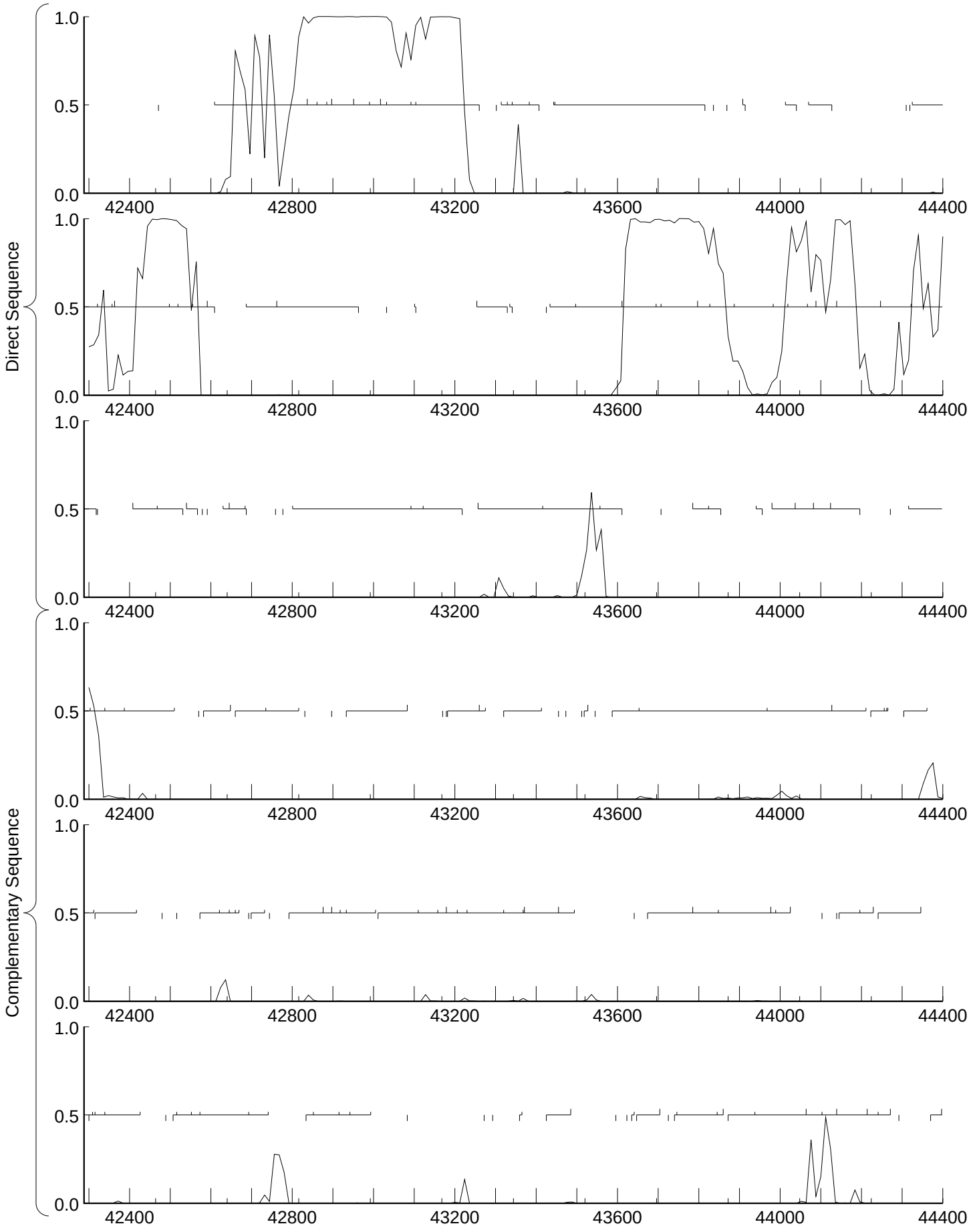

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33200
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Nucleotide Position

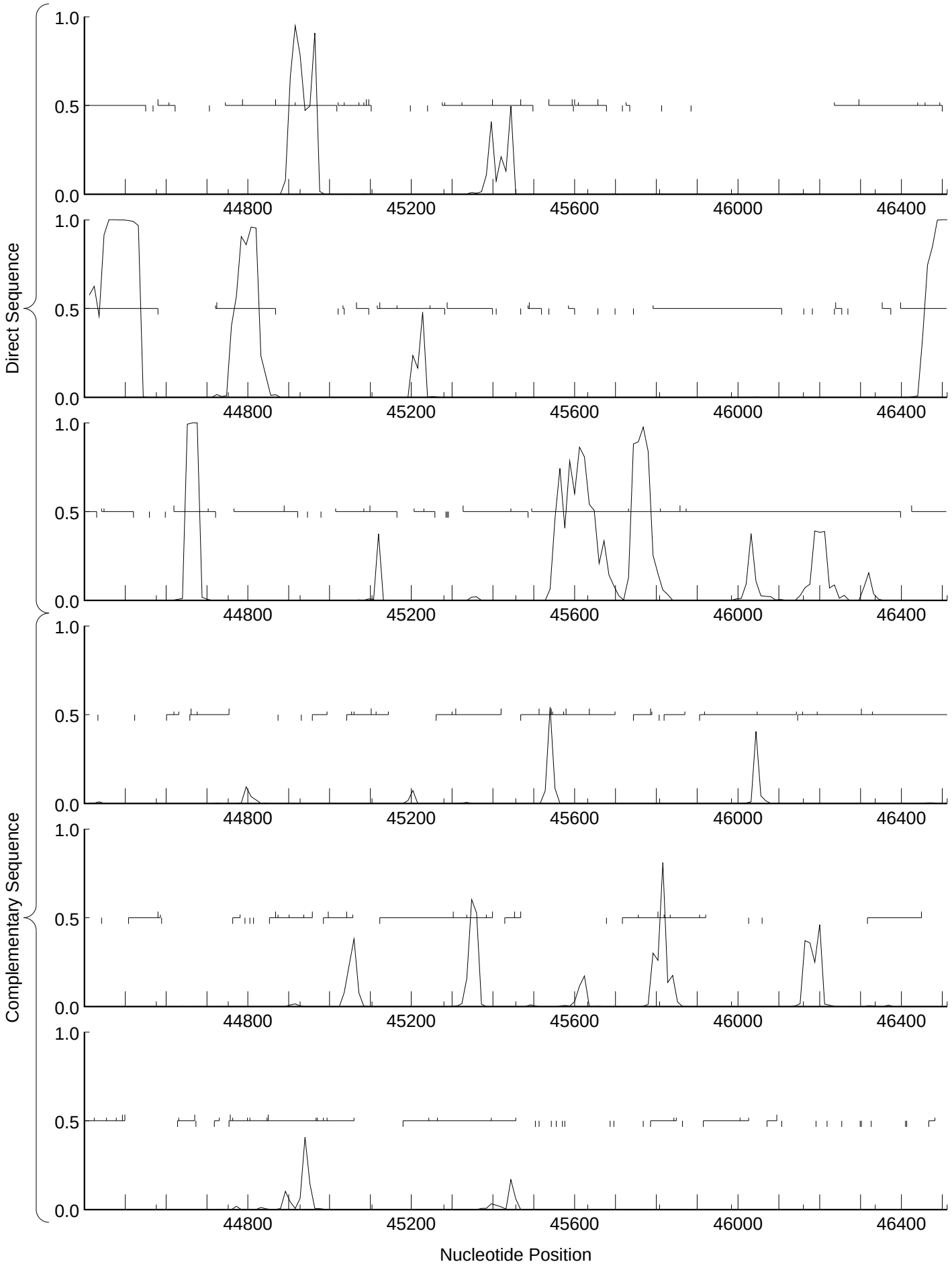

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Complementary Sequence
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Nucleotide Position

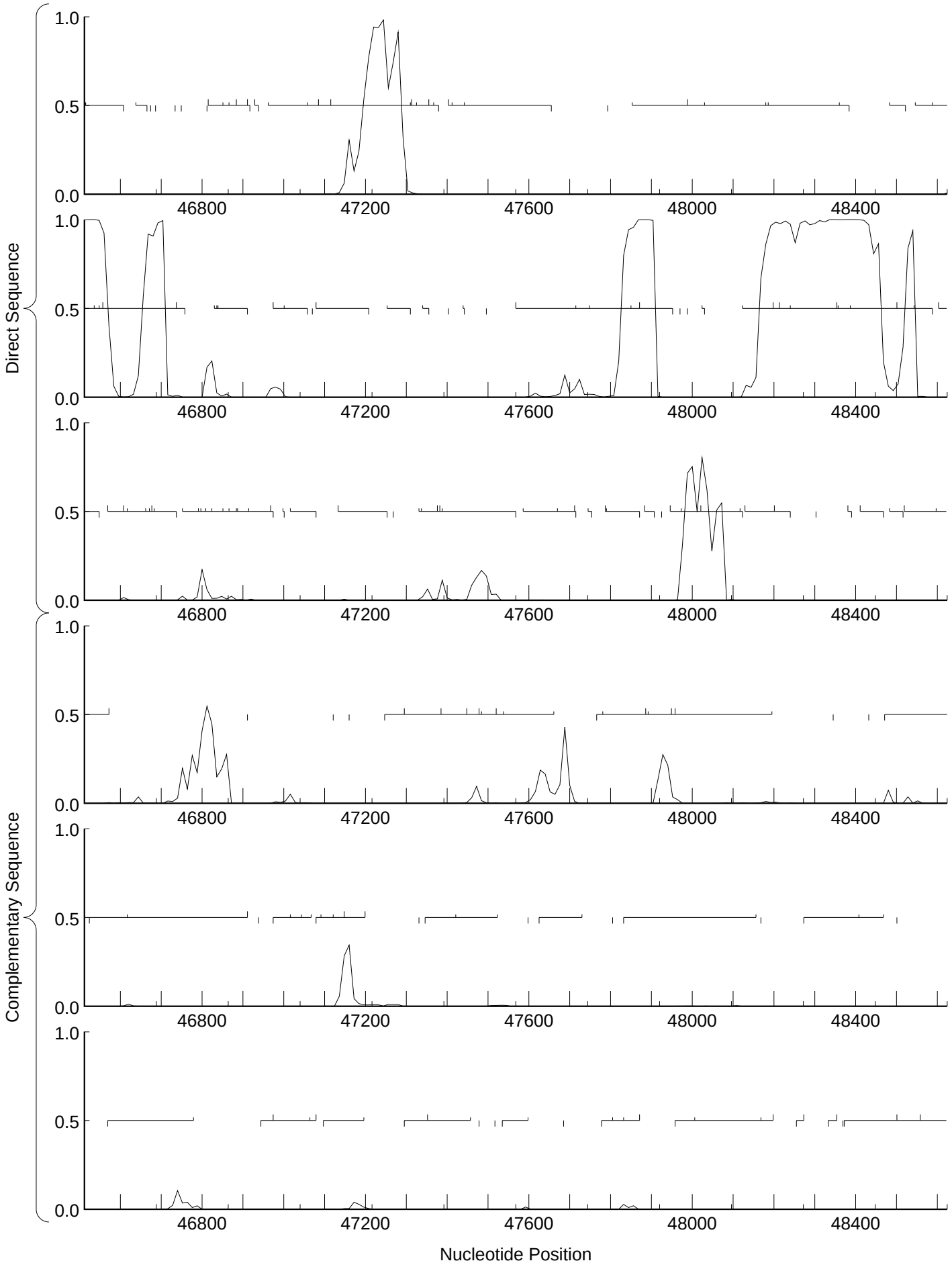

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Complementary Sequence
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37600
38000
Nucleotide Position

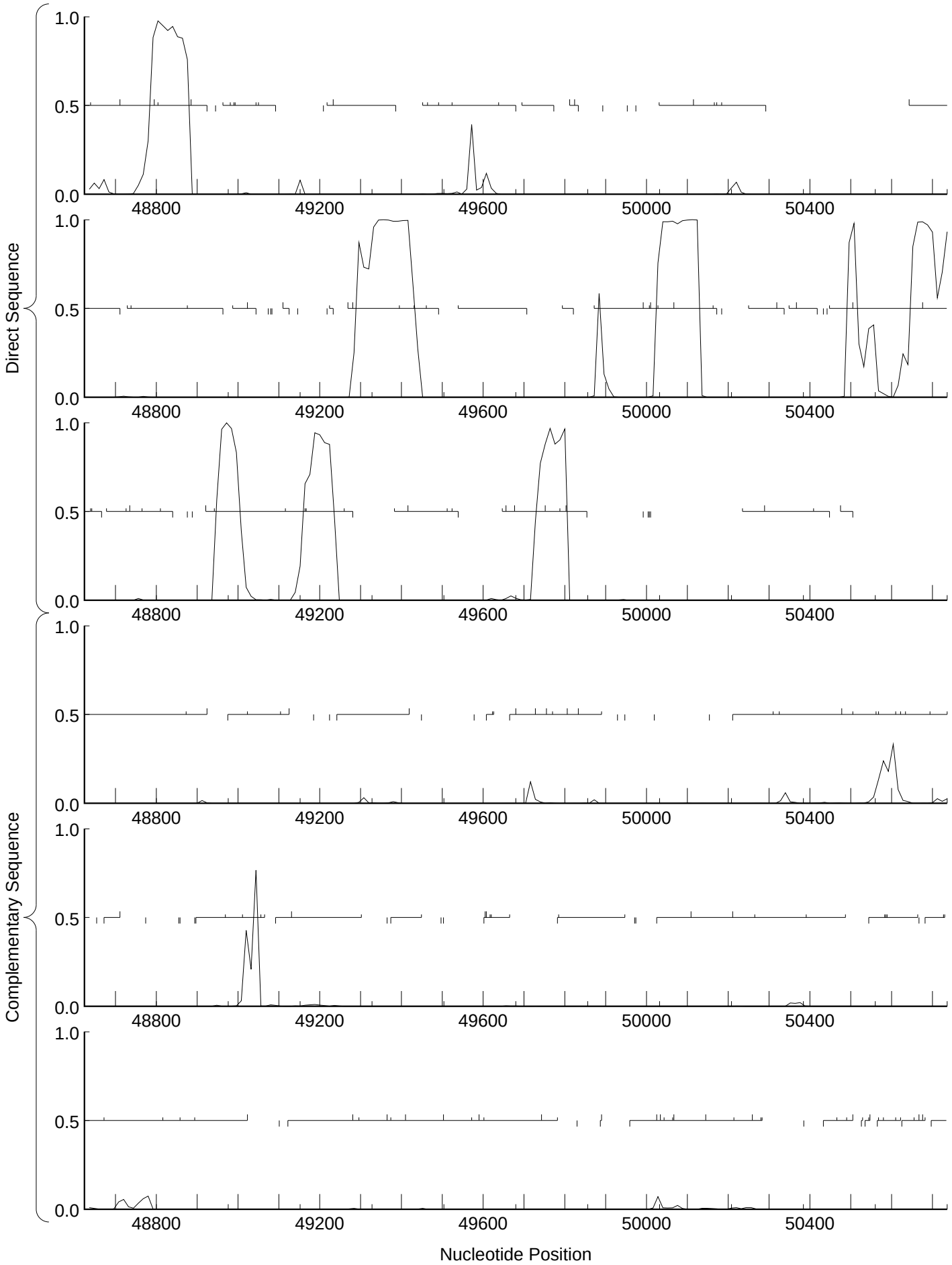

Direct Sequence
Complementary Sequence
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38800
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39600
40000
Nucleotide Position

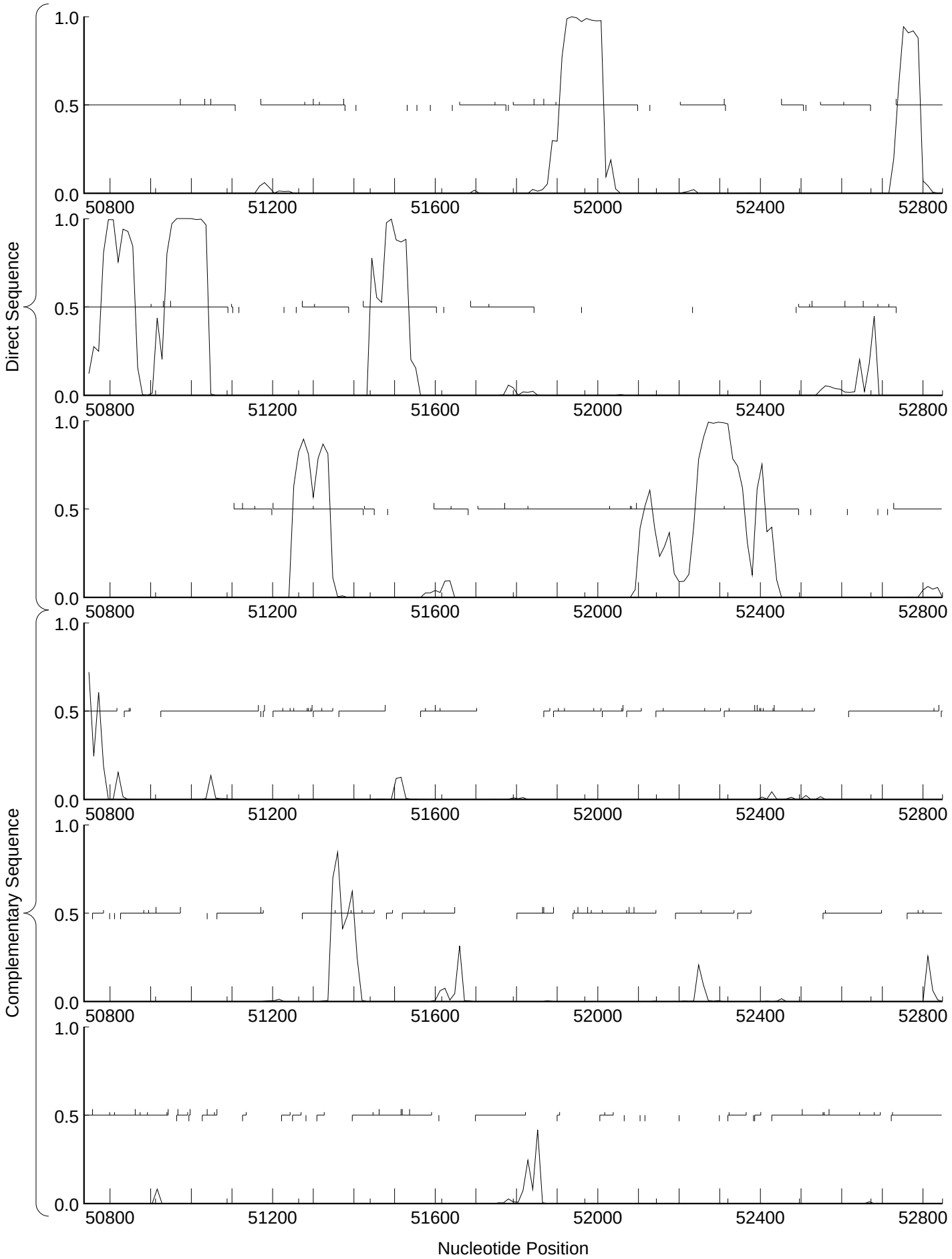

Direct Sequence
Complementary Sequence
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40800
41200
41600
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Nucleotide Position

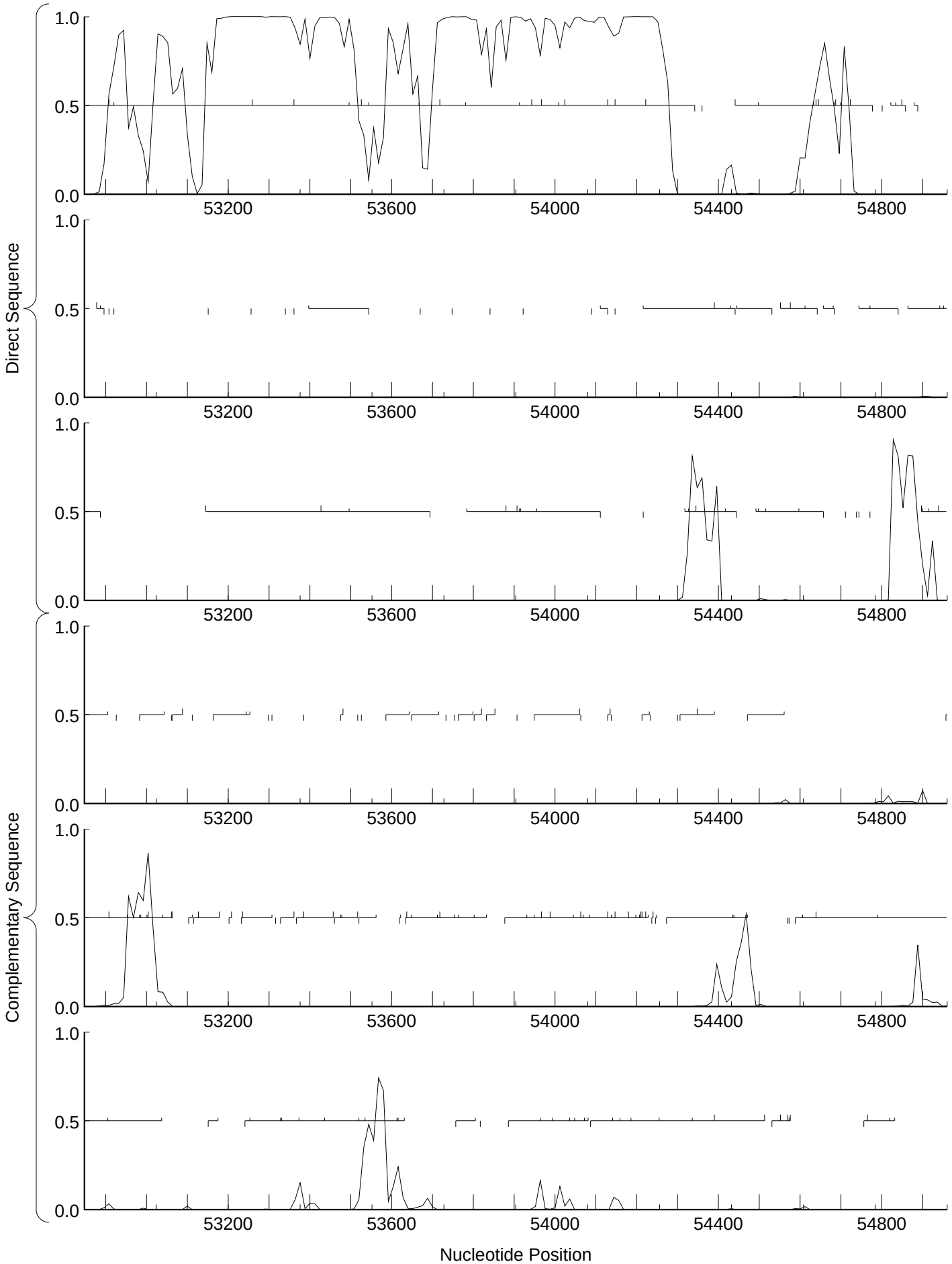

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44000
44400
Nucleotide Position

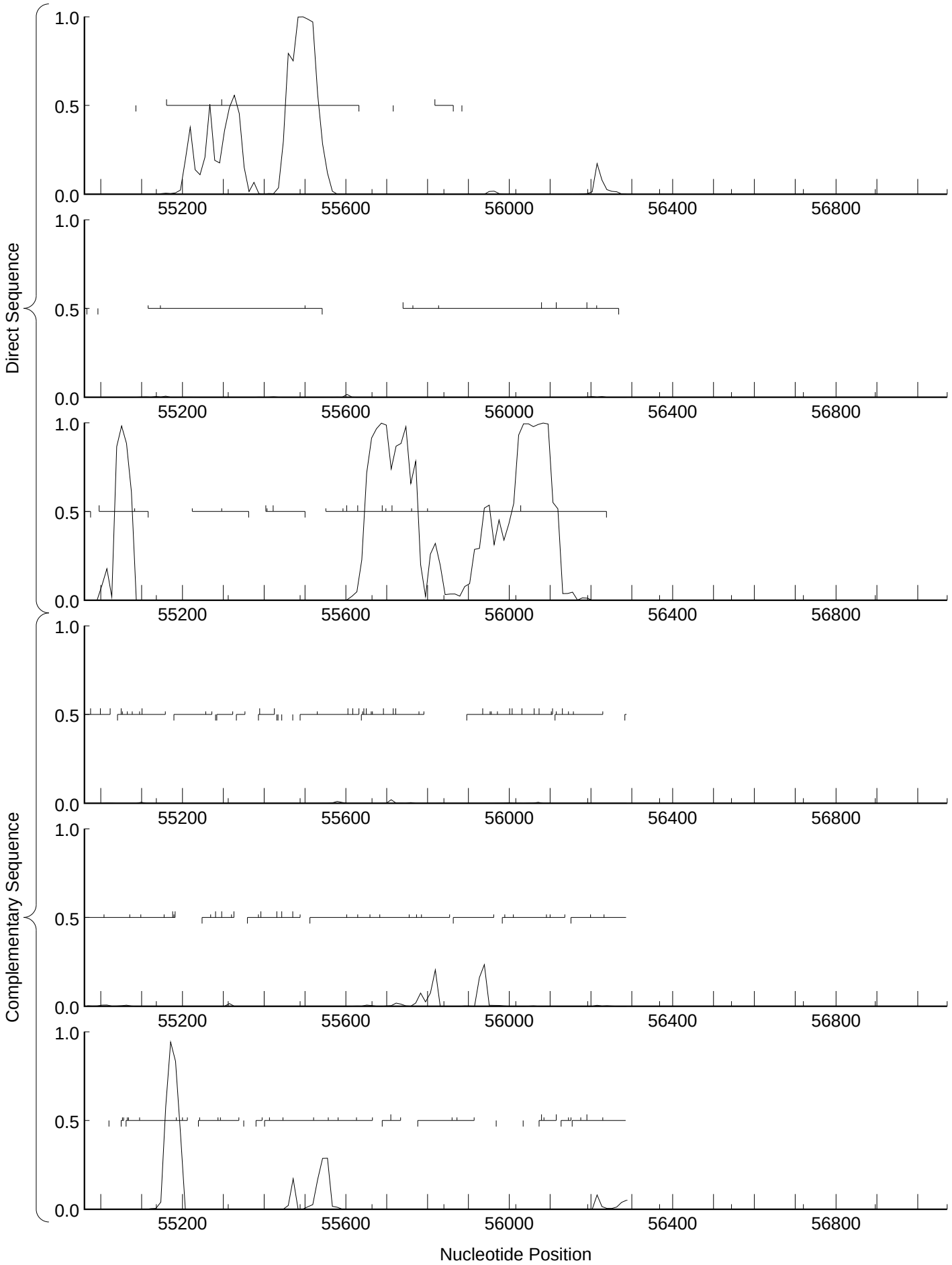

Direct Sequence
Complementary Sequence
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0.0
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45600
46000
46400
Nucleotide Position


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


Direct Sequence
Complementary Sequence
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0.5
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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