GeneMark

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

PROGRAM INFORMATION

```
Sequence         :  Arthrobacter phage Tank complete sequence, 67592 bp including ~589 bp terminal repeat, Clus
Analysis Date    :  3/28/24 at 22:19:08
Pages            :  34
Sequence Length  :  67592 bp
GC Content       :   62.87%

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     :  -

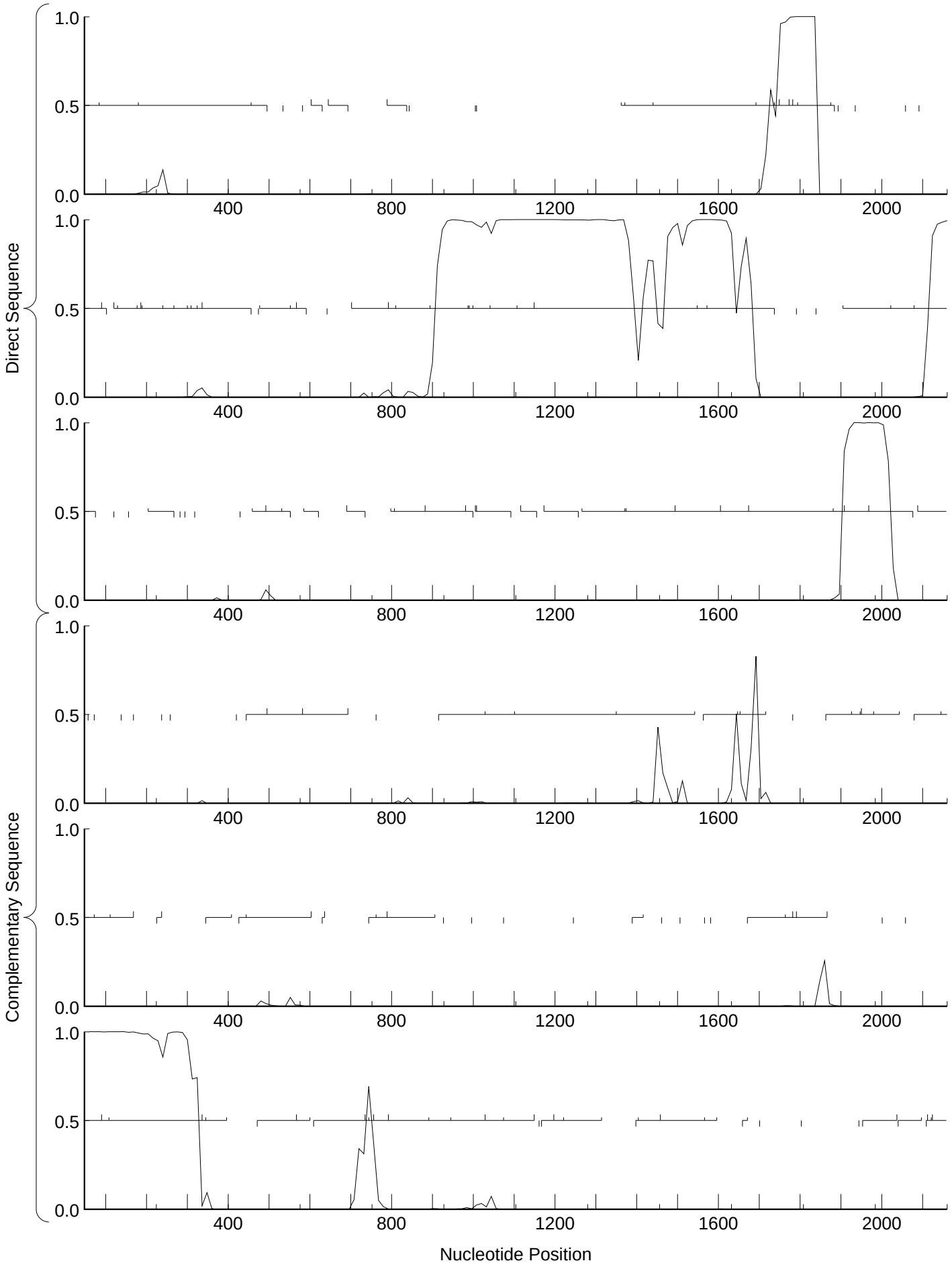
Order      :  4


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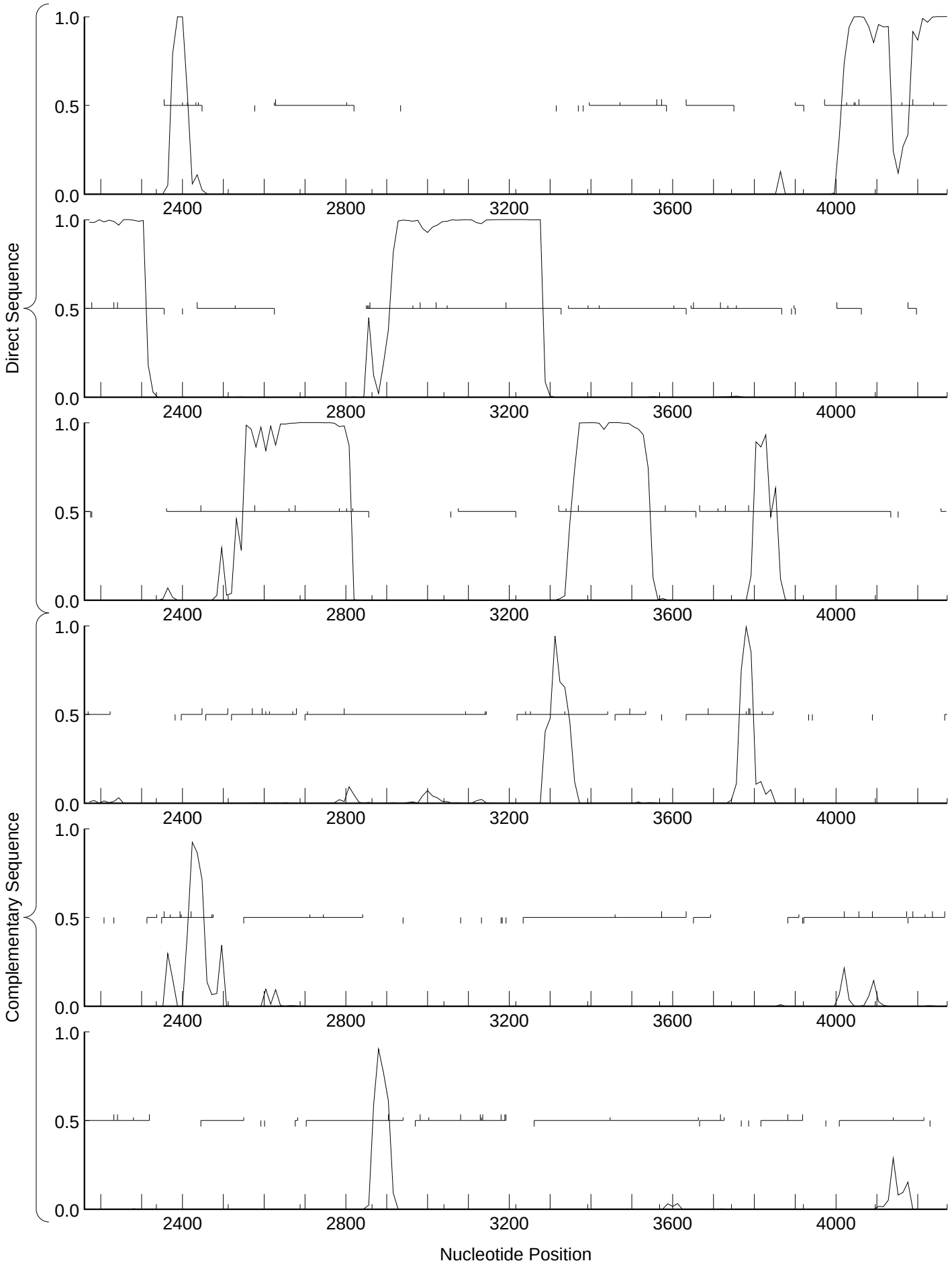


For help or information, send electronic mail to: custserv@genepro.com, or mark@amber.biology.gatech.edu

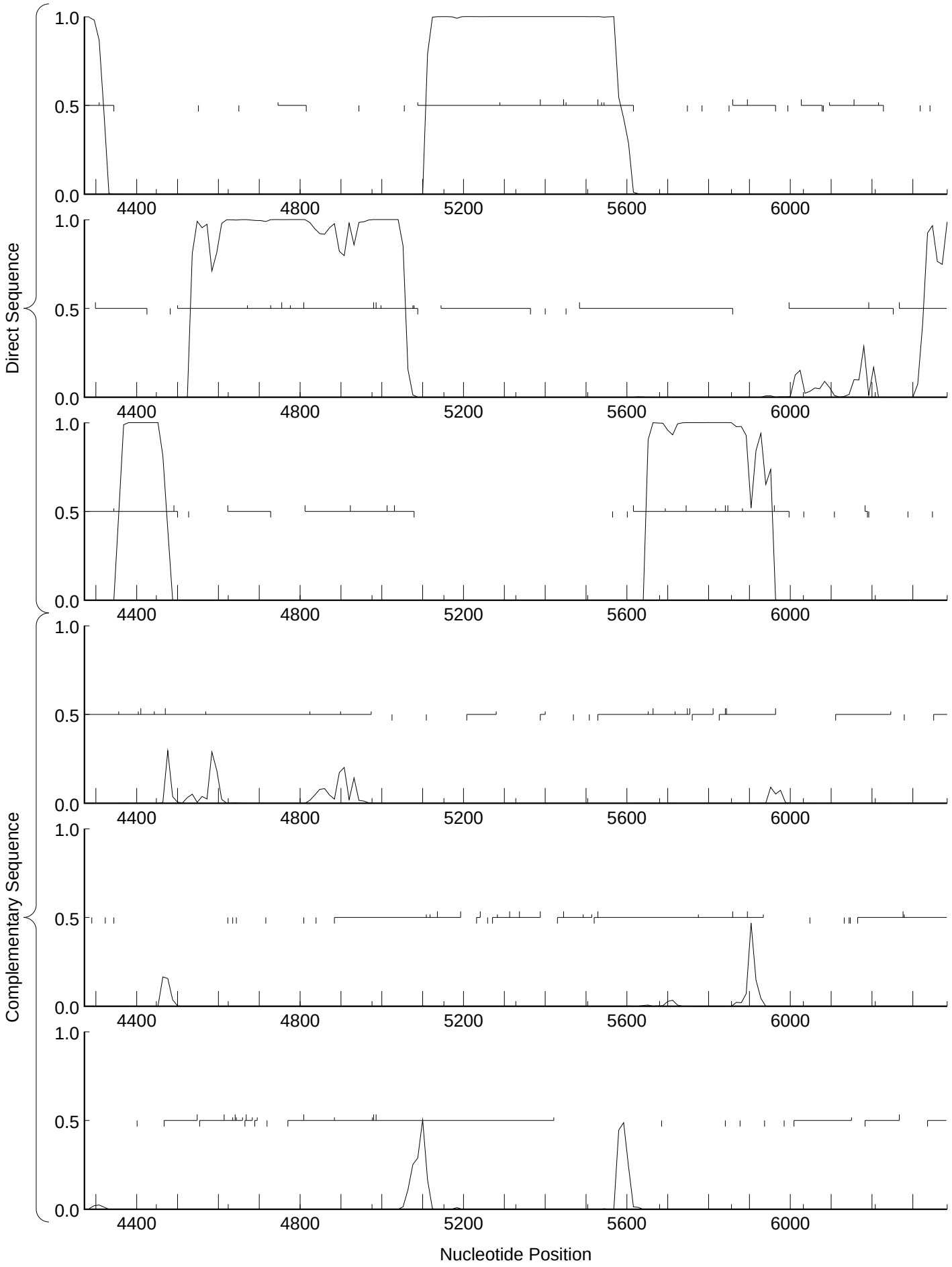
ter phage Tank complete sequence, 67592 bp including ~589 bp terminal repeat, Cluster AP1, Order 4, Window 96, Step 12, 2/34



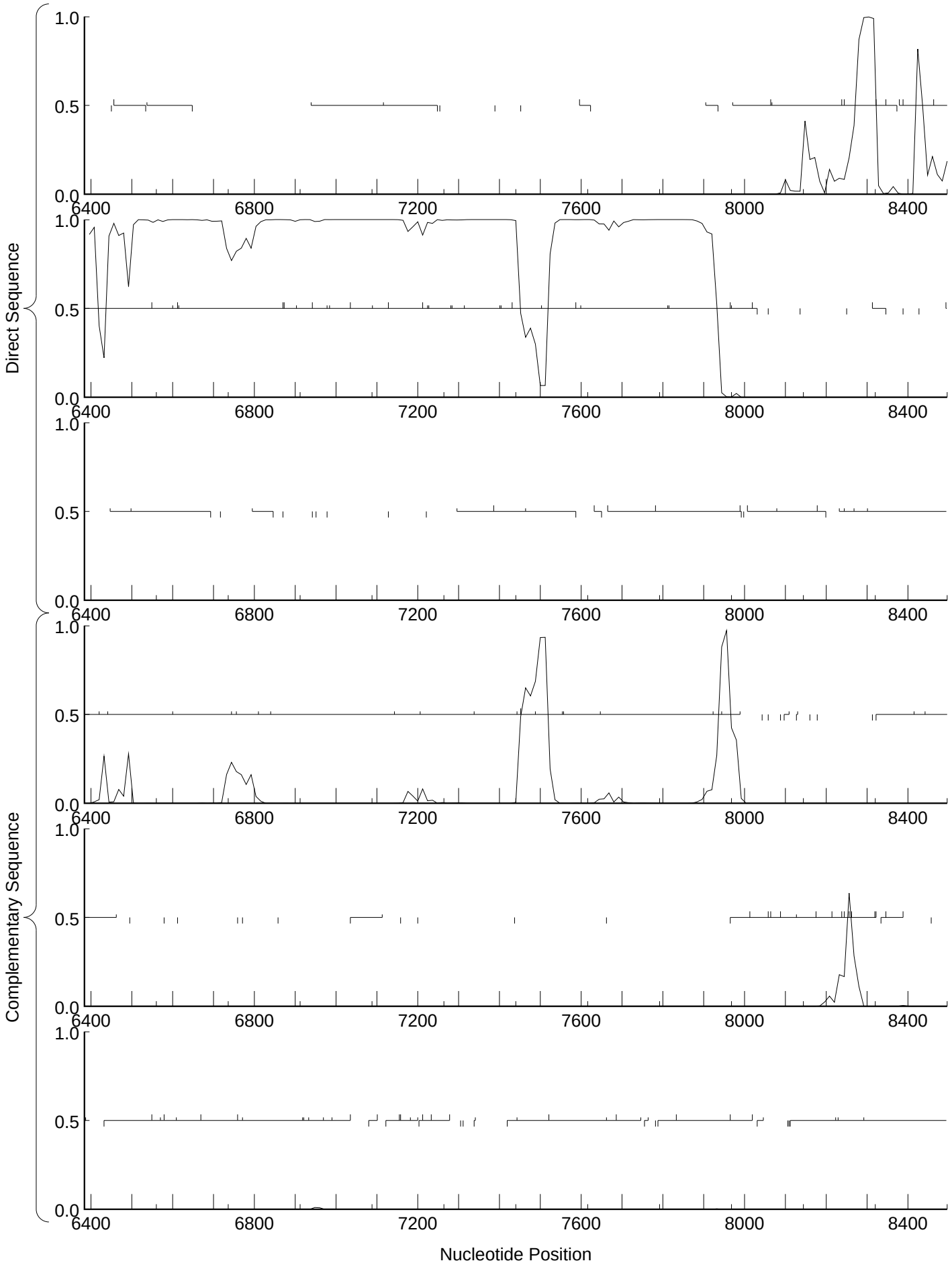
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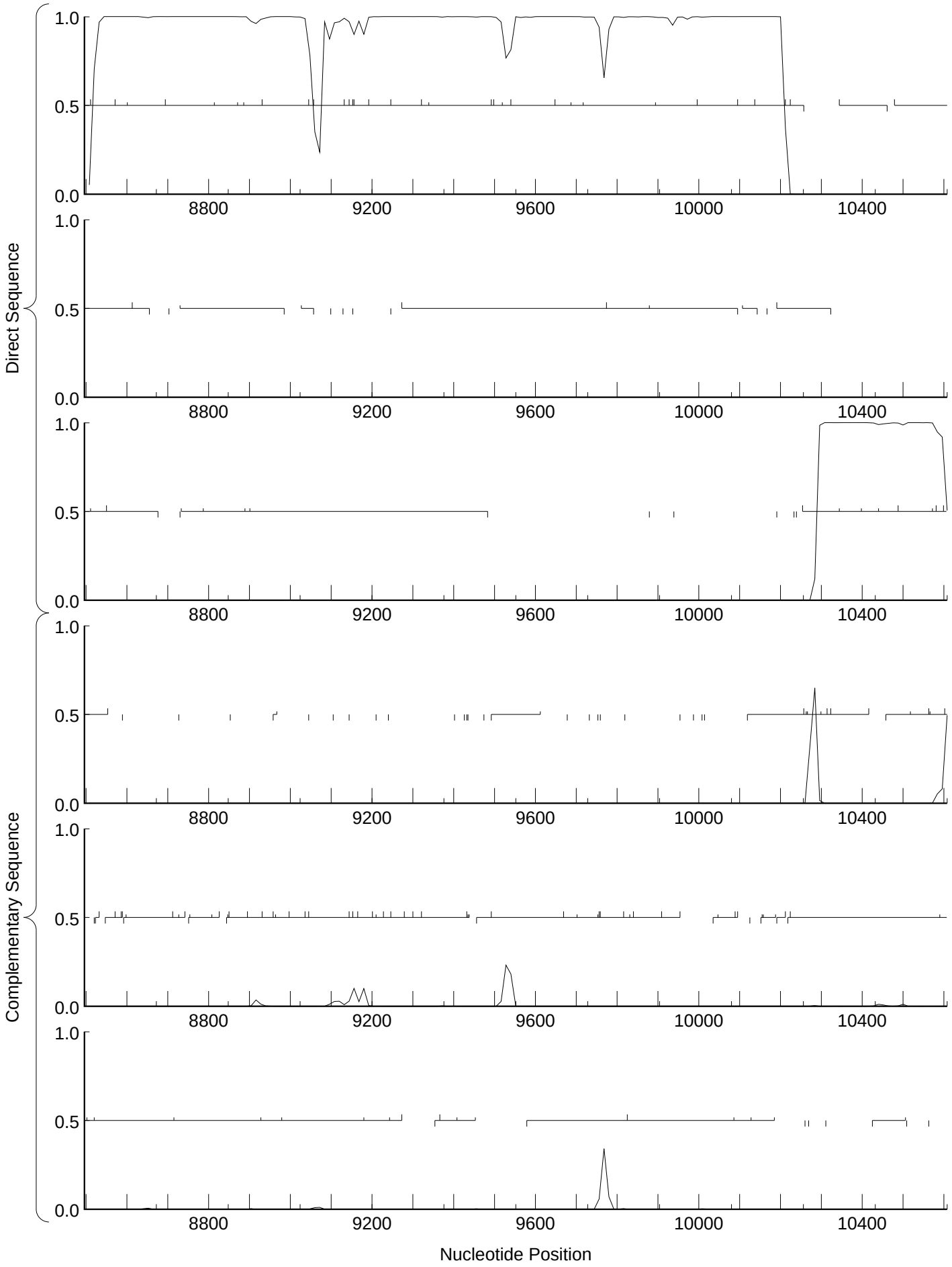
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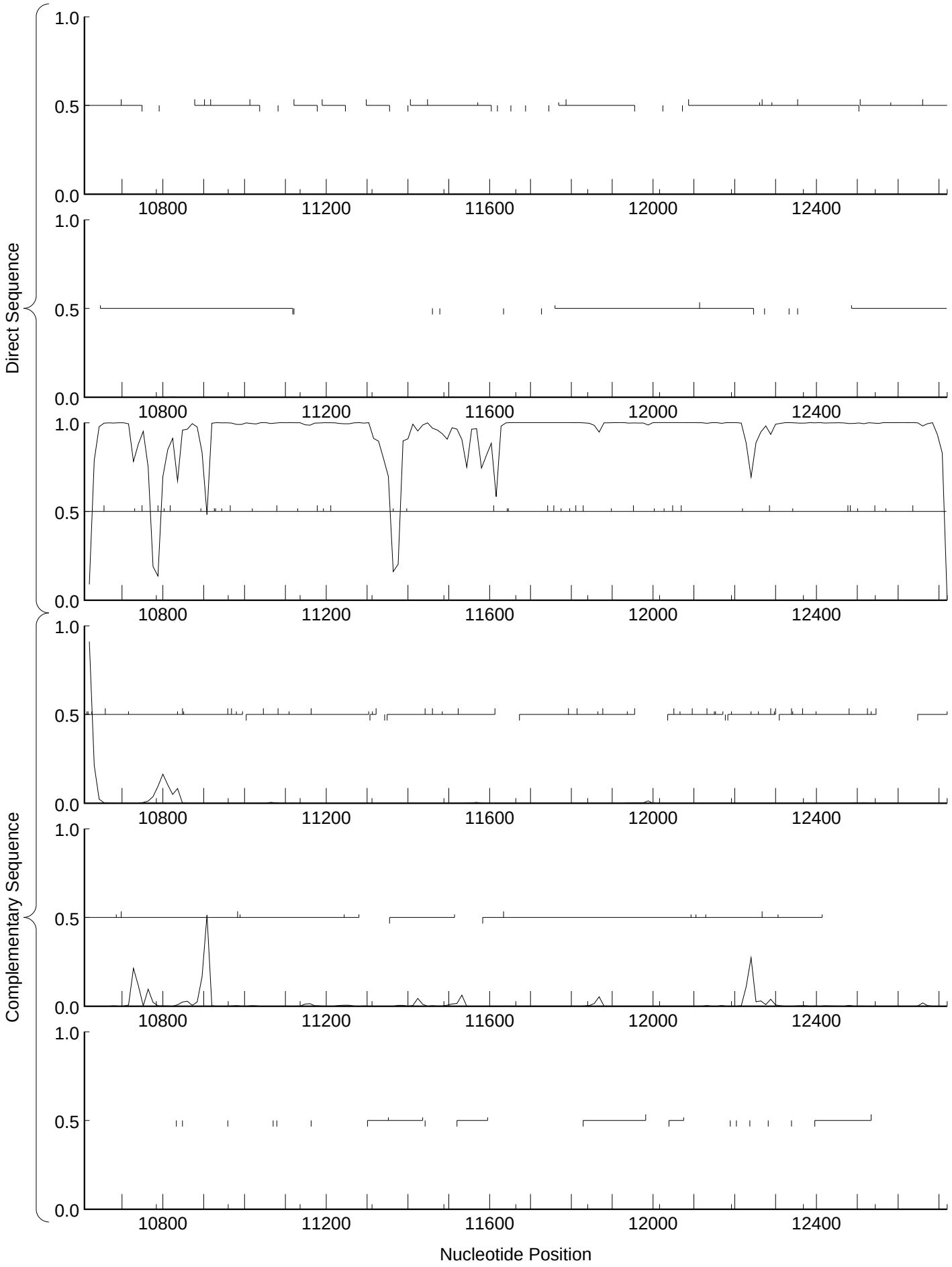
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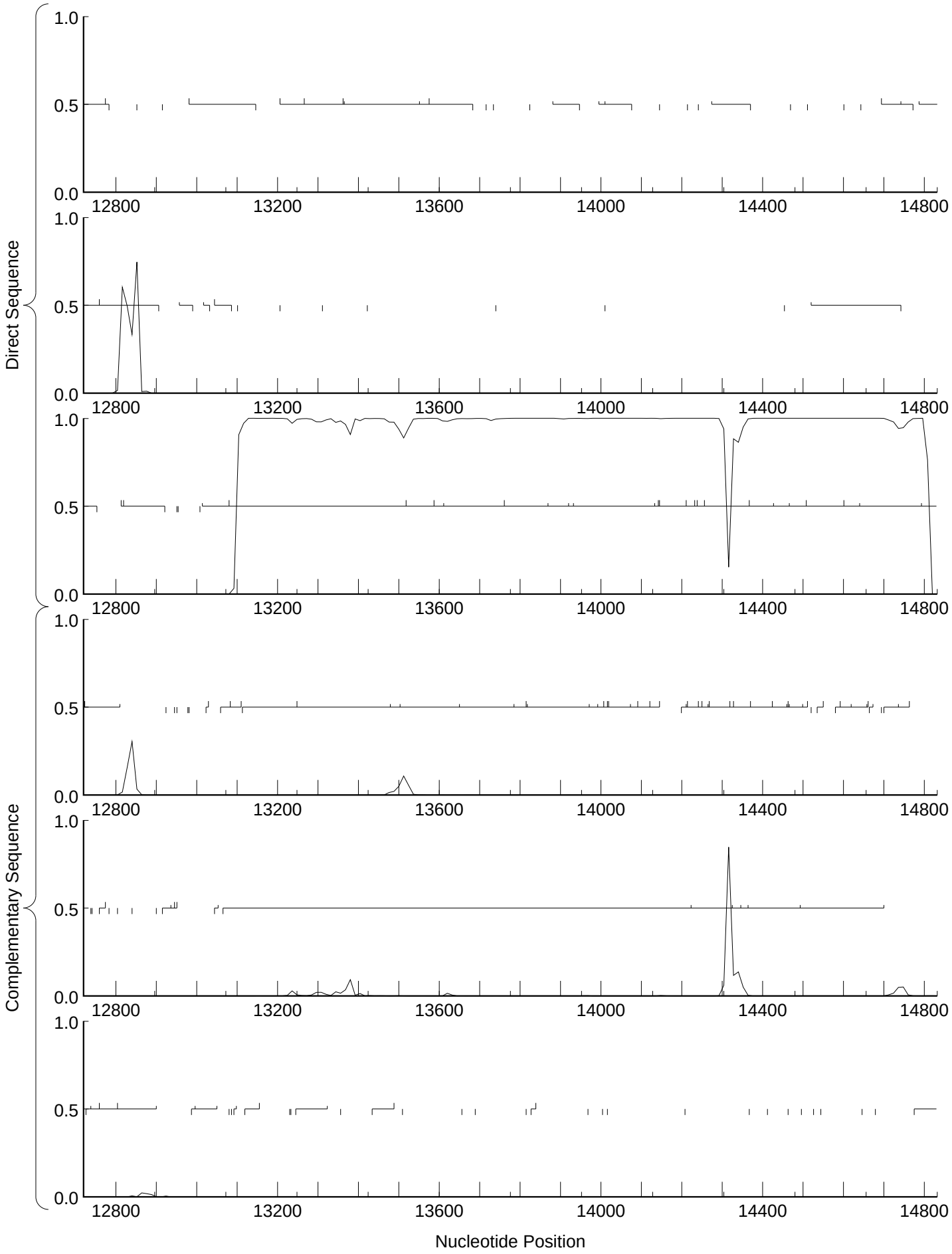
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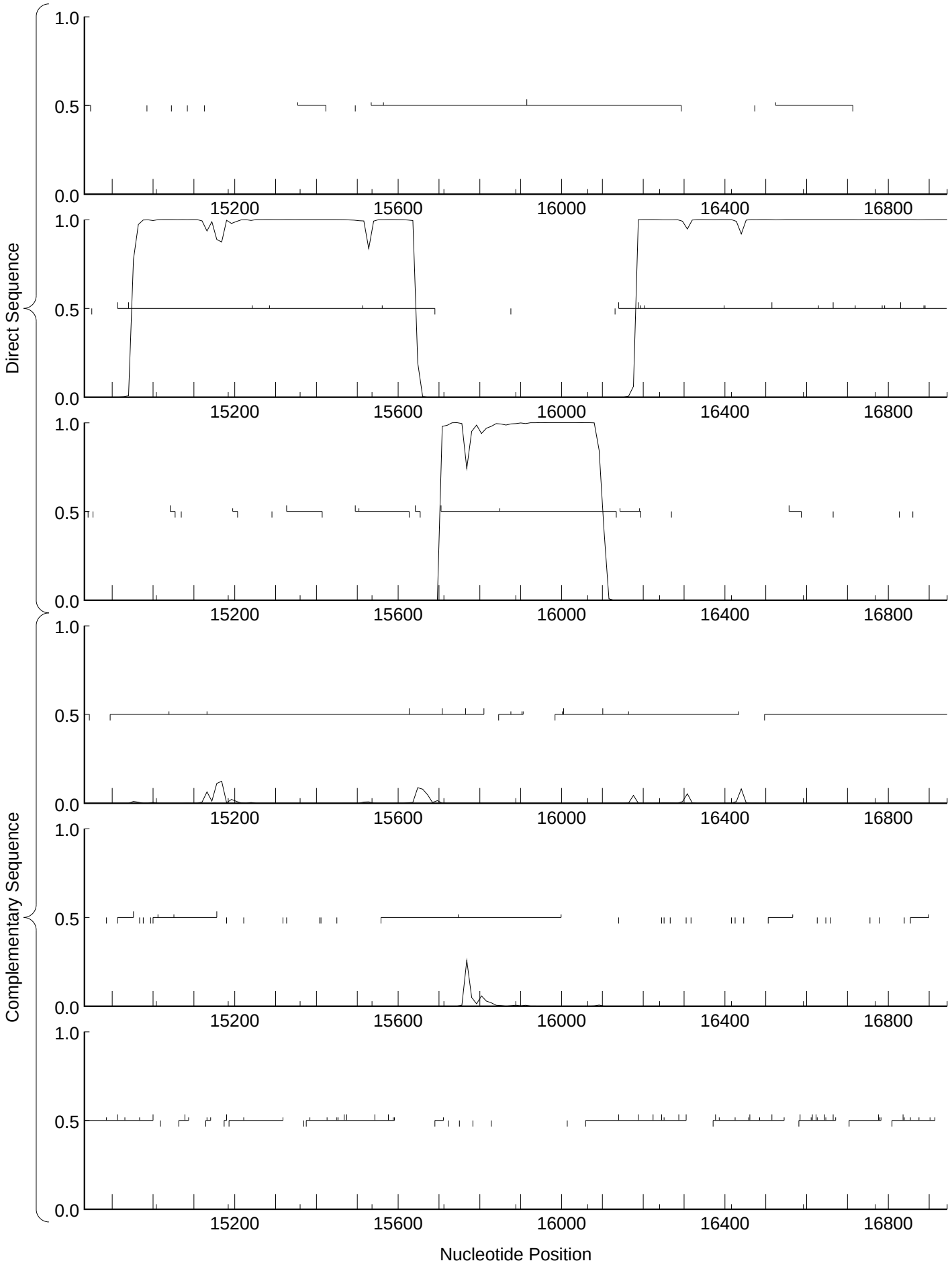
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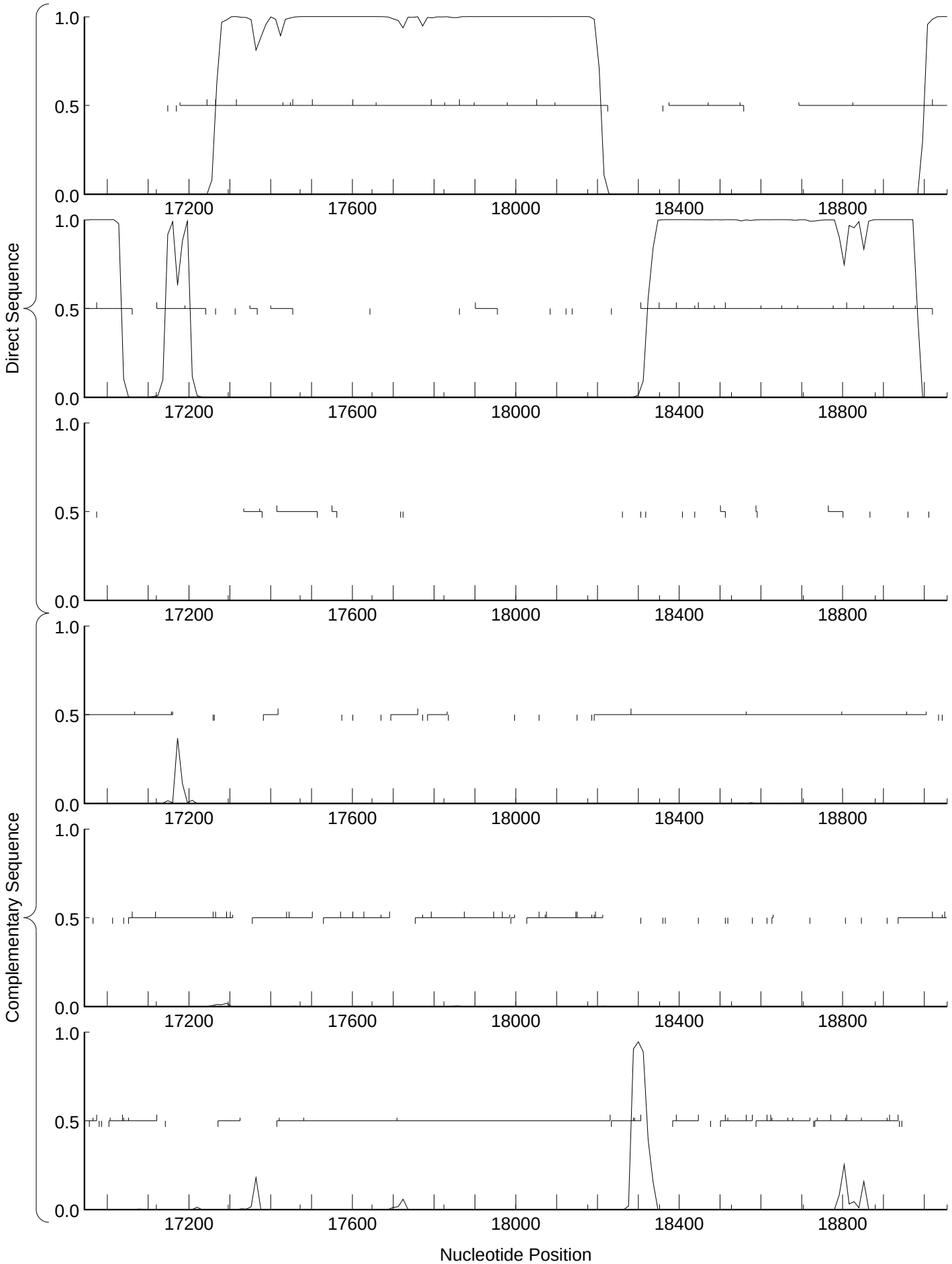


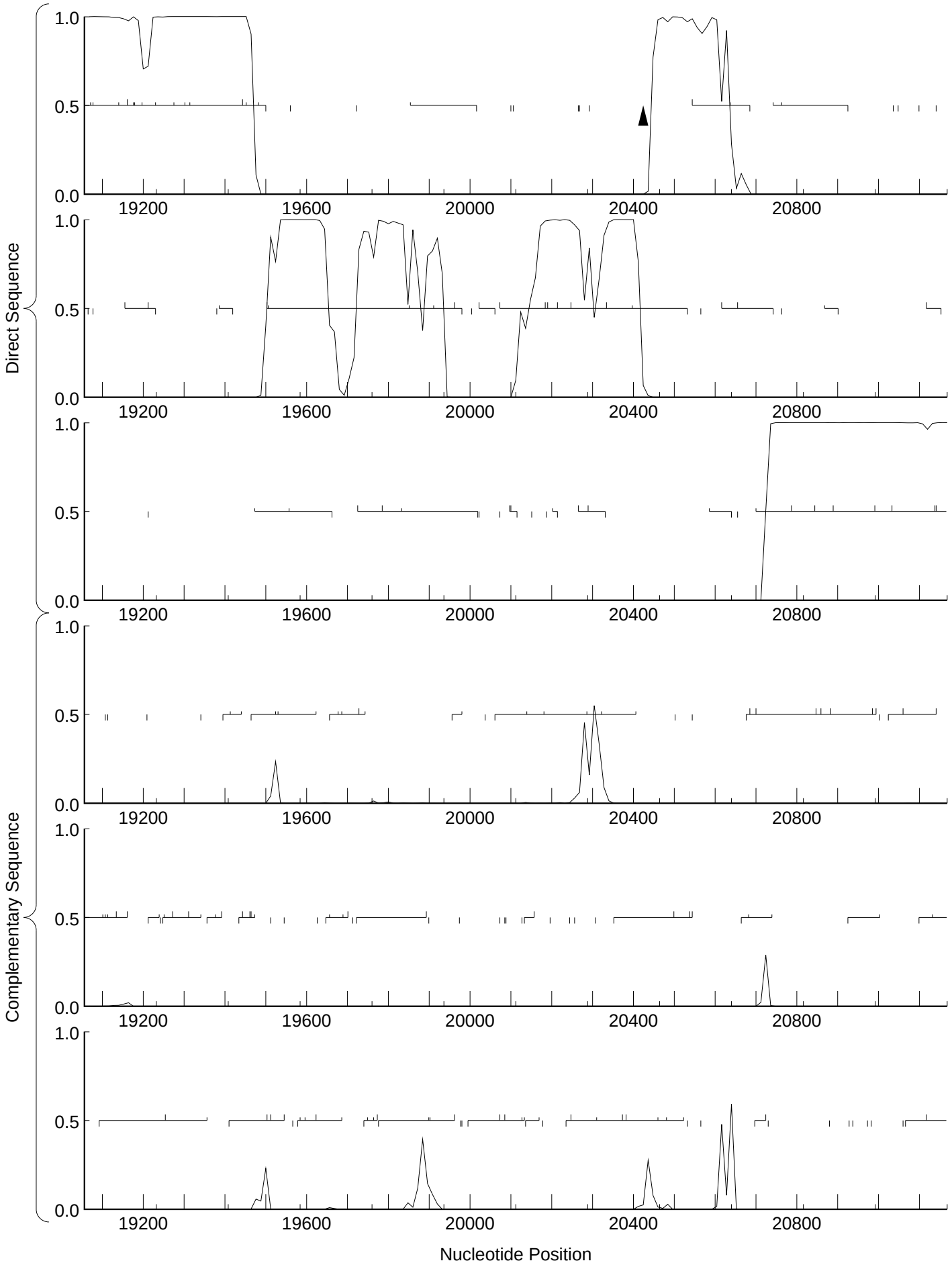
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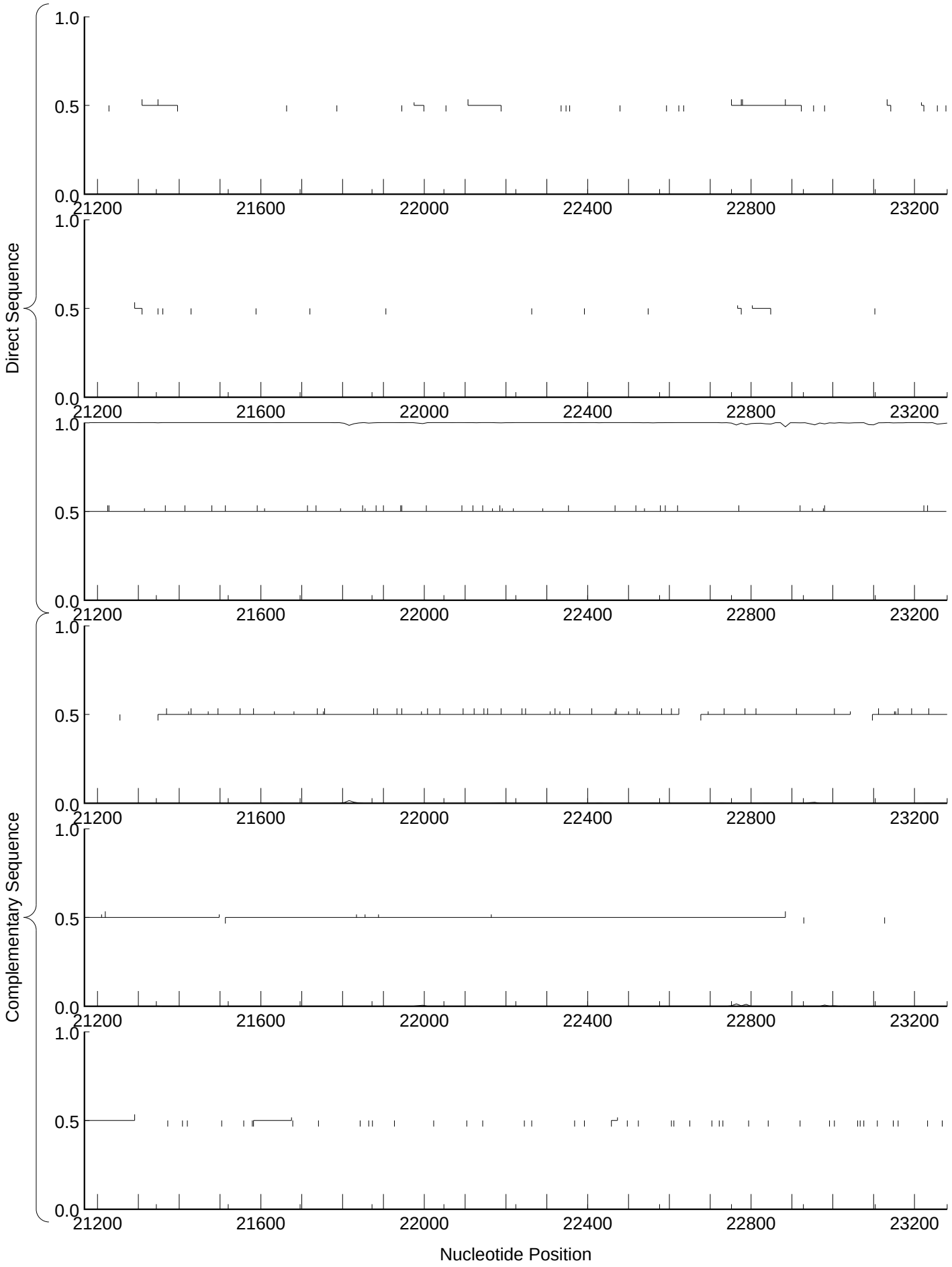
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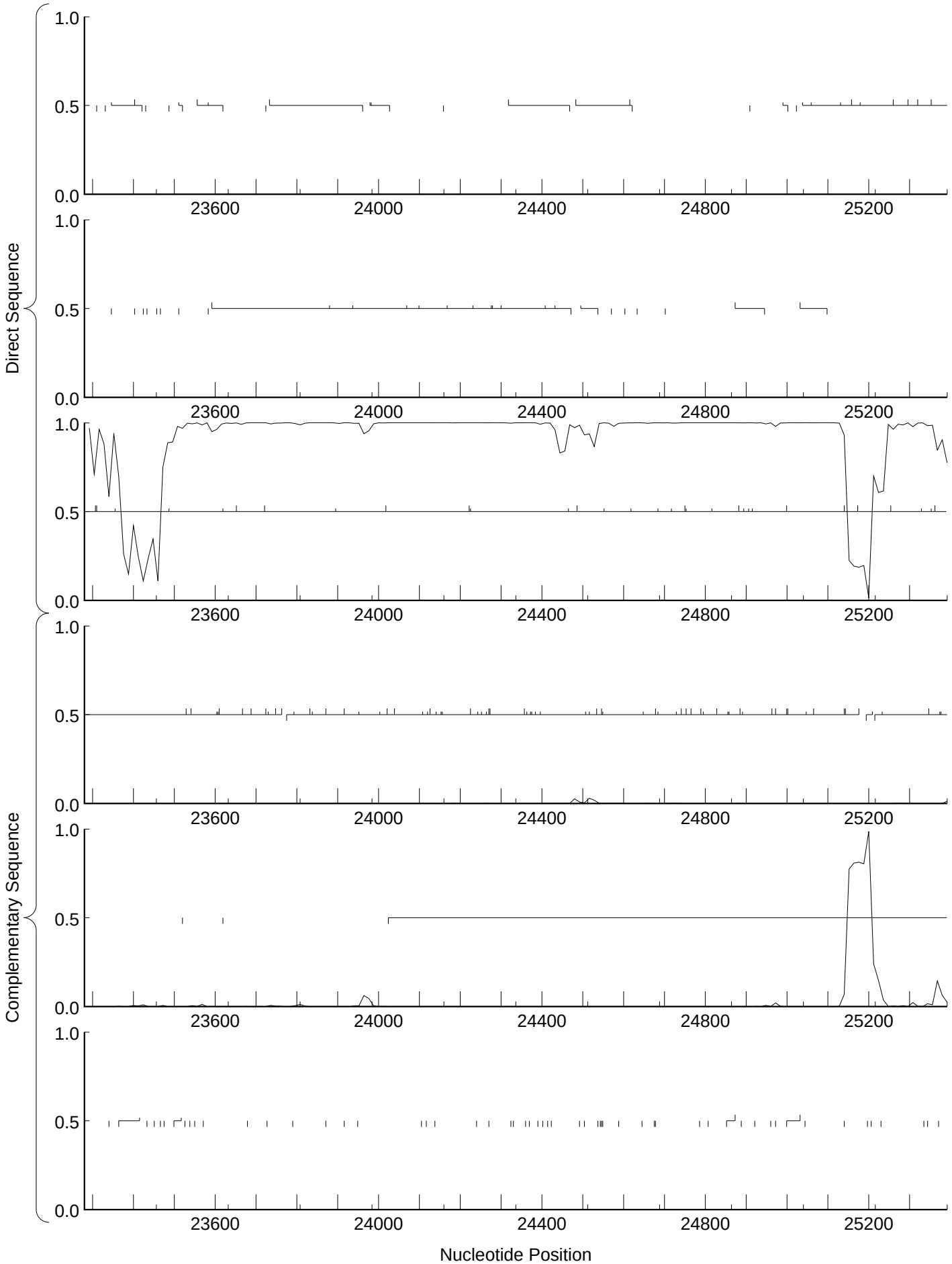


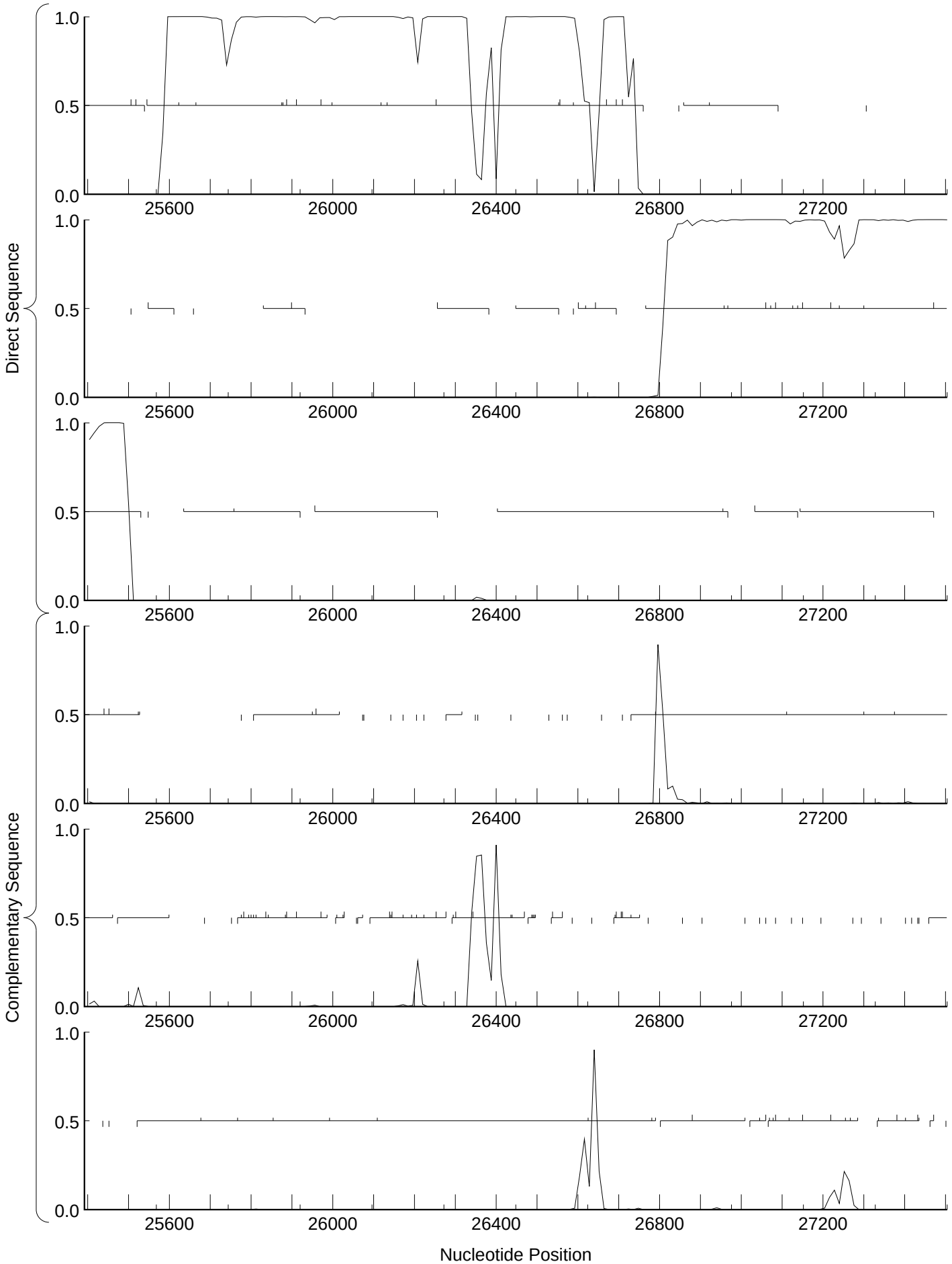

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
17200
17600
18000
18400
18800
Nucleotide Position

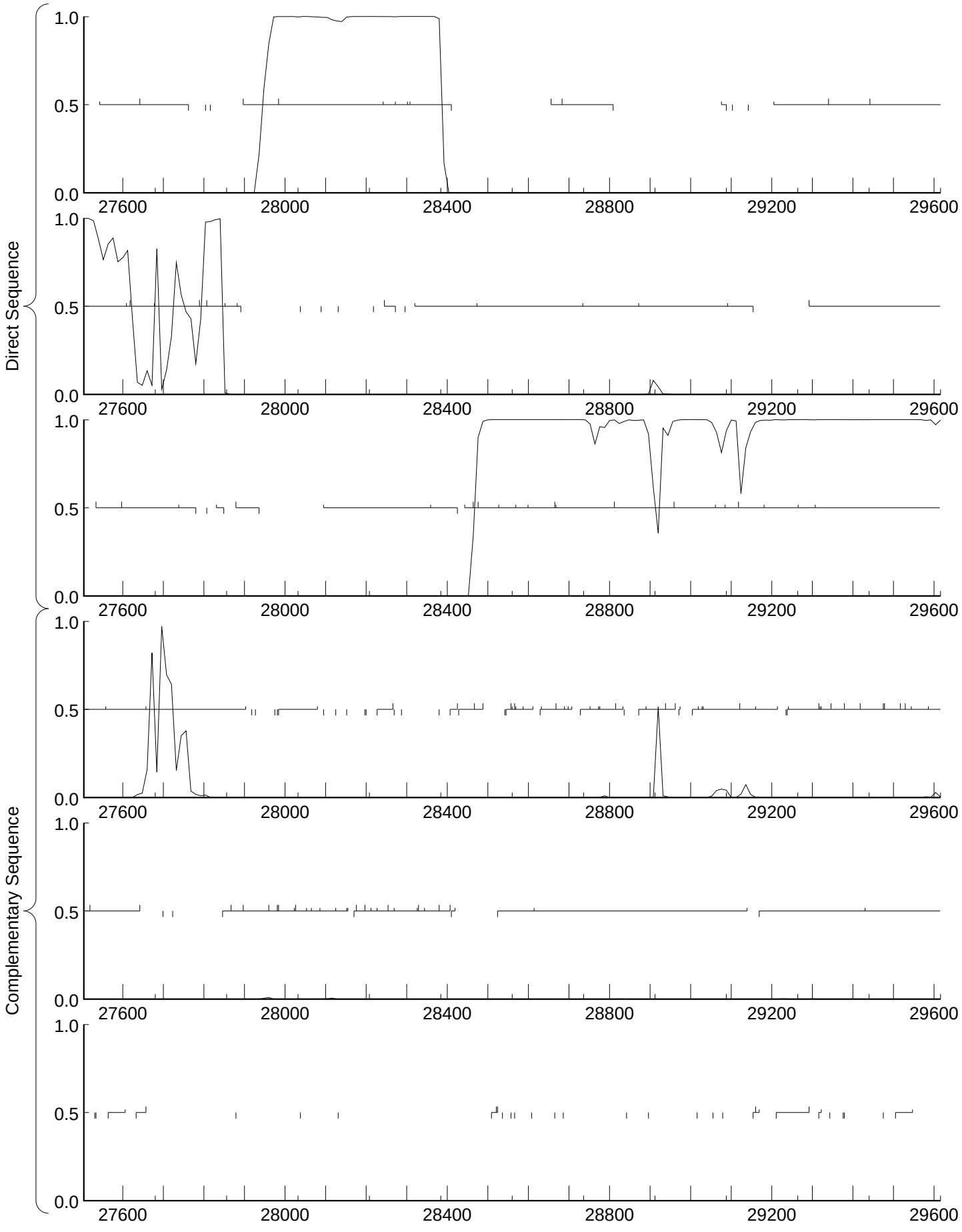

Direct Sequence
Complementary Sequence
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0.5
0.0
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19600
20000
20400
20800
Nucleotide Position

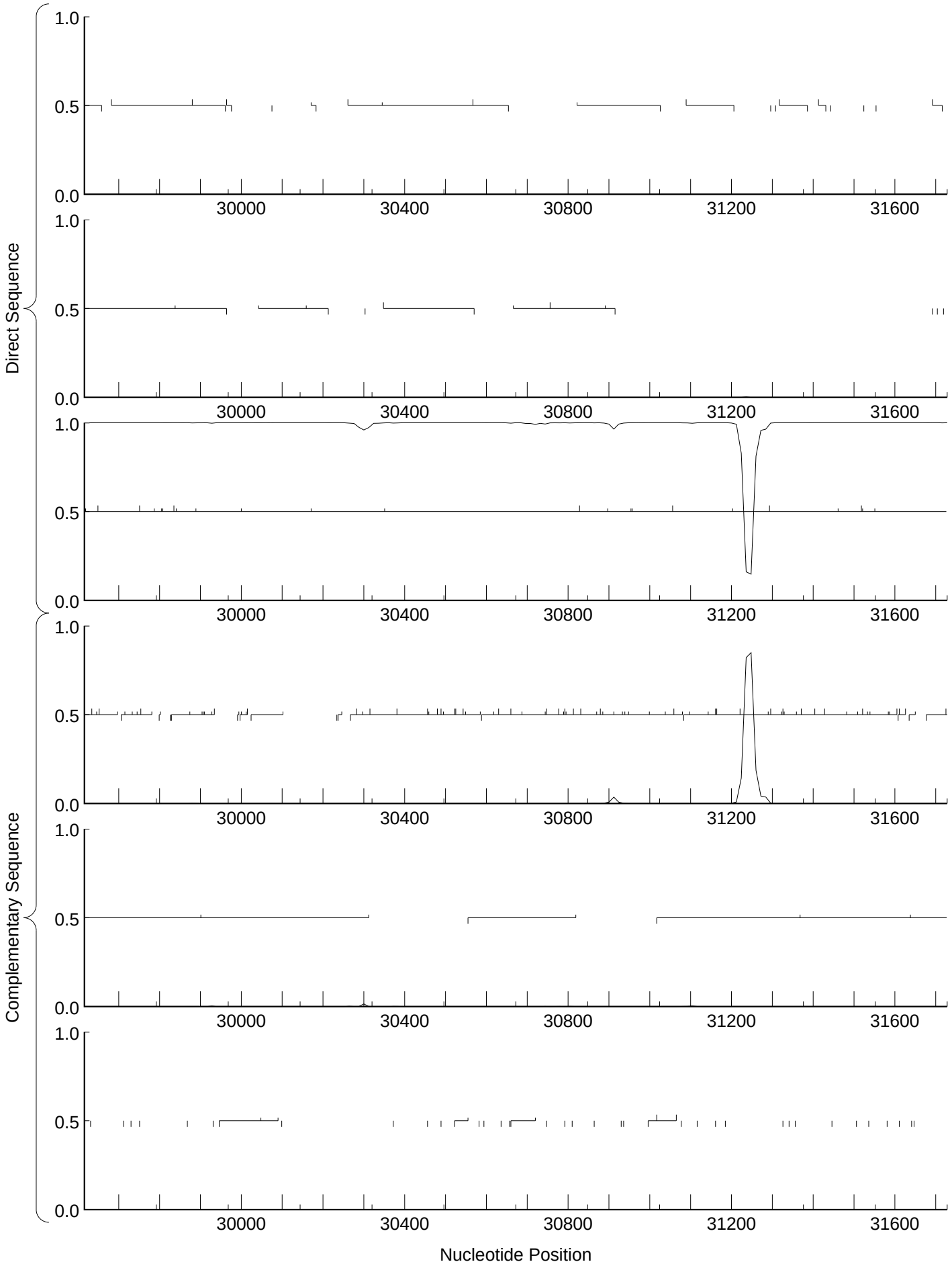
er phage Tank complete sequence, 67592 bp including ~589 bp terminal repeat, Cluster AP1, Order 4, Window 96, Step 12, 12/34



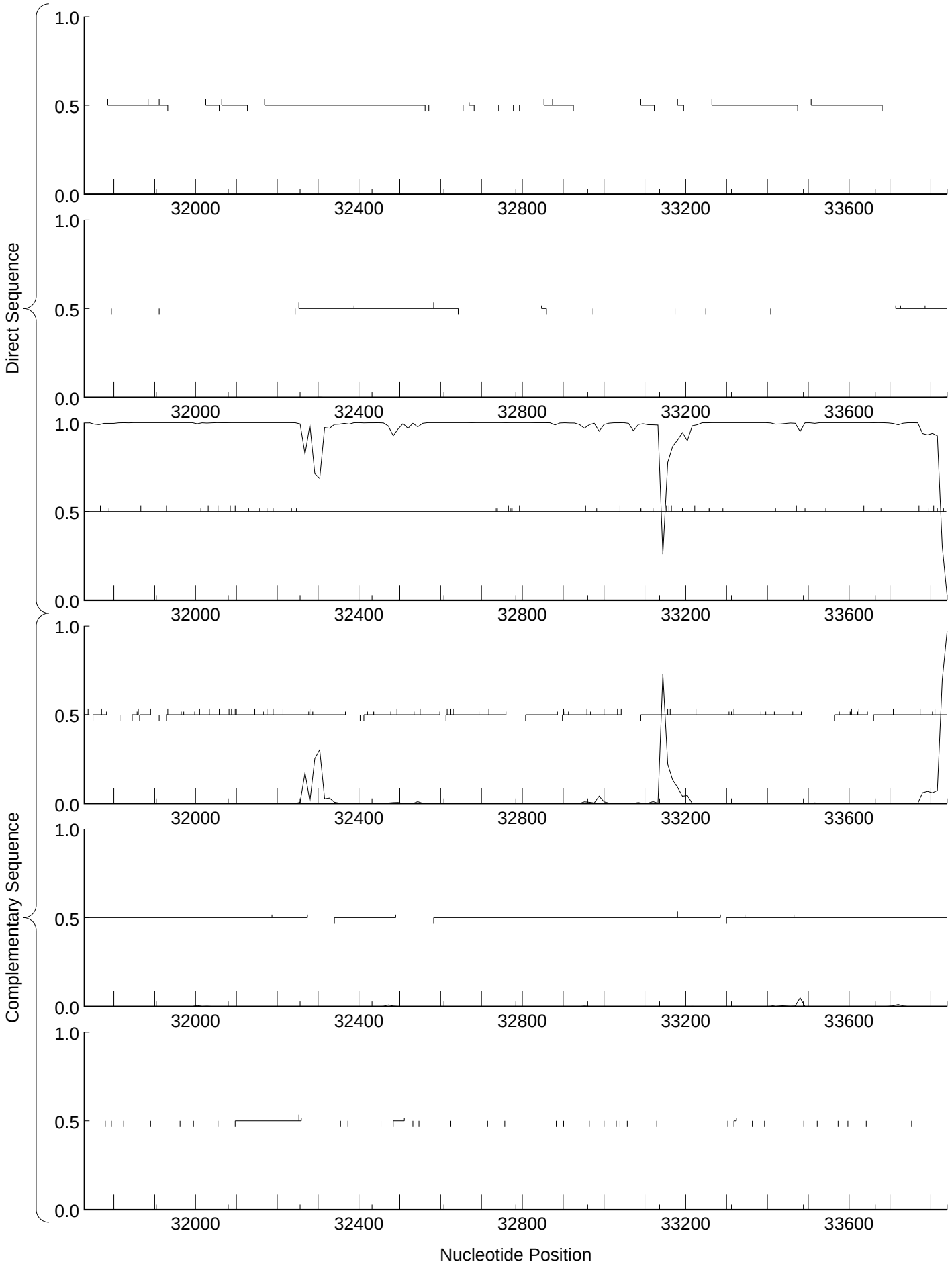

Direct Sequence
Complementary Sequence
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0.5
0.0
23600
24000
24400
24800
25200
Nucleotide Position

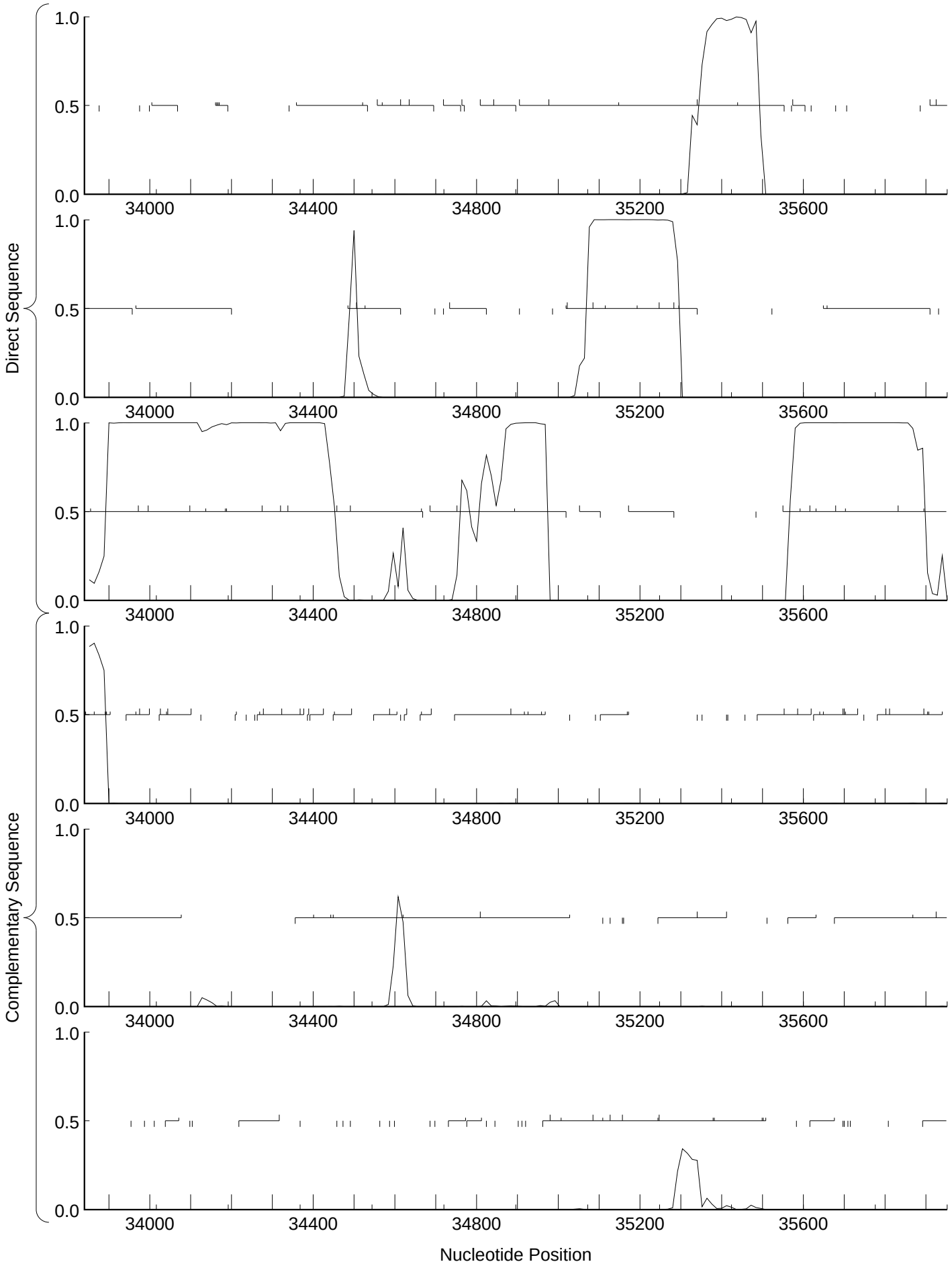

Direct Sequence
Complementary Sequence
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0.5
0.0
25600
26000
26400
26800
27200
Nucleotide Position

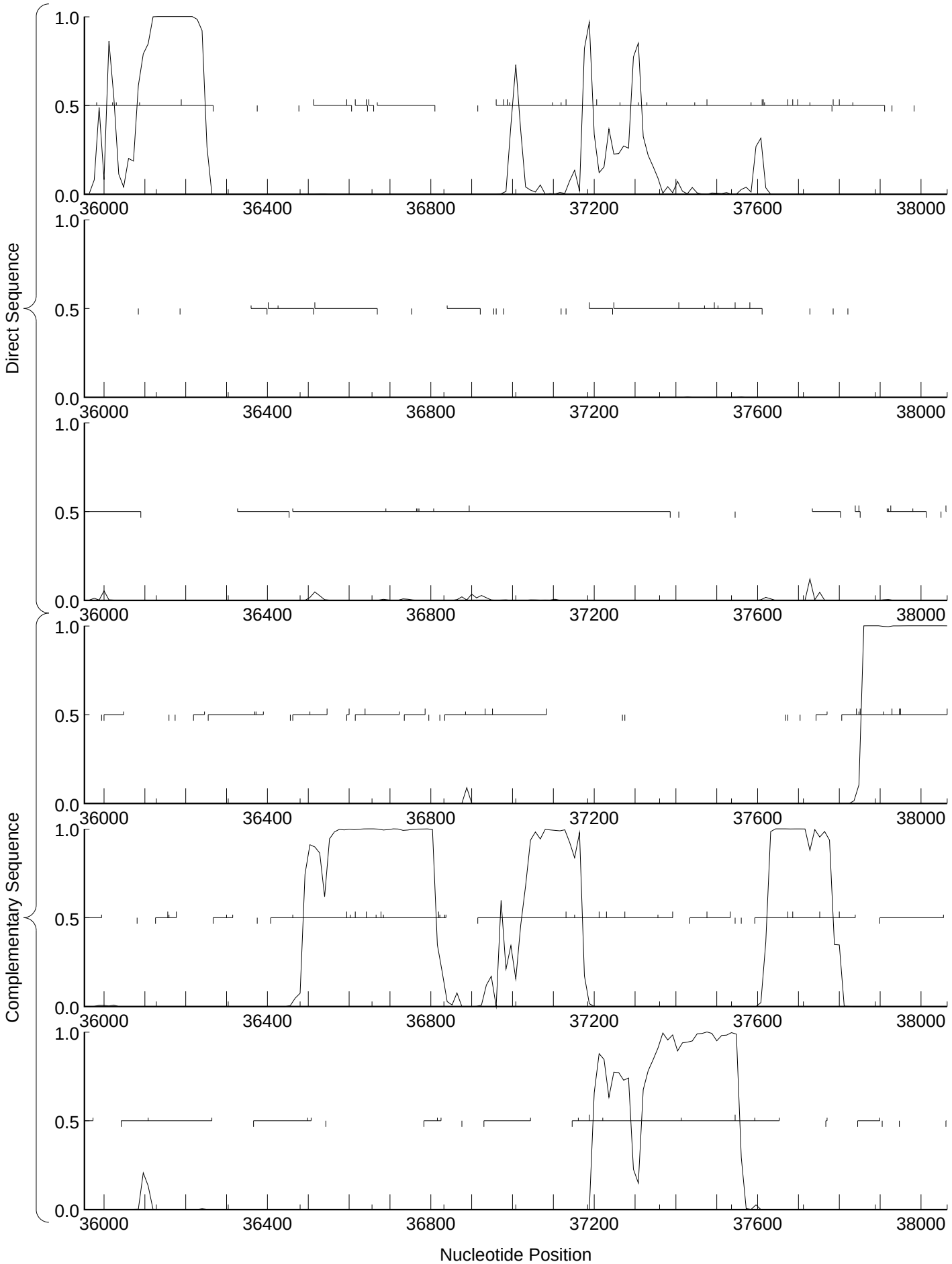

Direct Sequence
Complementary Sequence
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0.0
27600
28000
28400
28800
29200
29600
Nucleotide Position

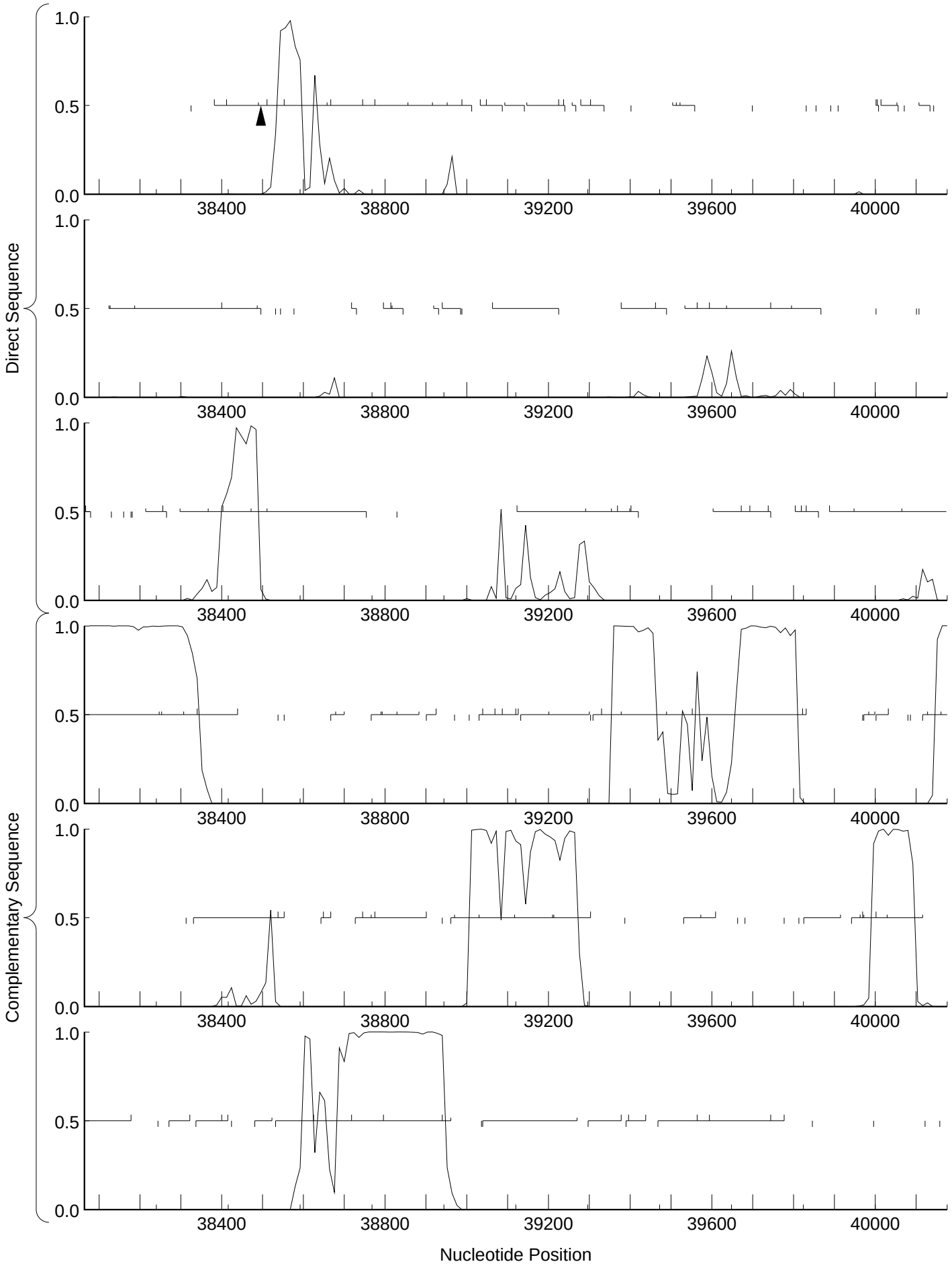

Direct Sequence
Complementary Sequence
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0.5
0.0
30000
30400
30800
31200
31600
Nucleotide Position

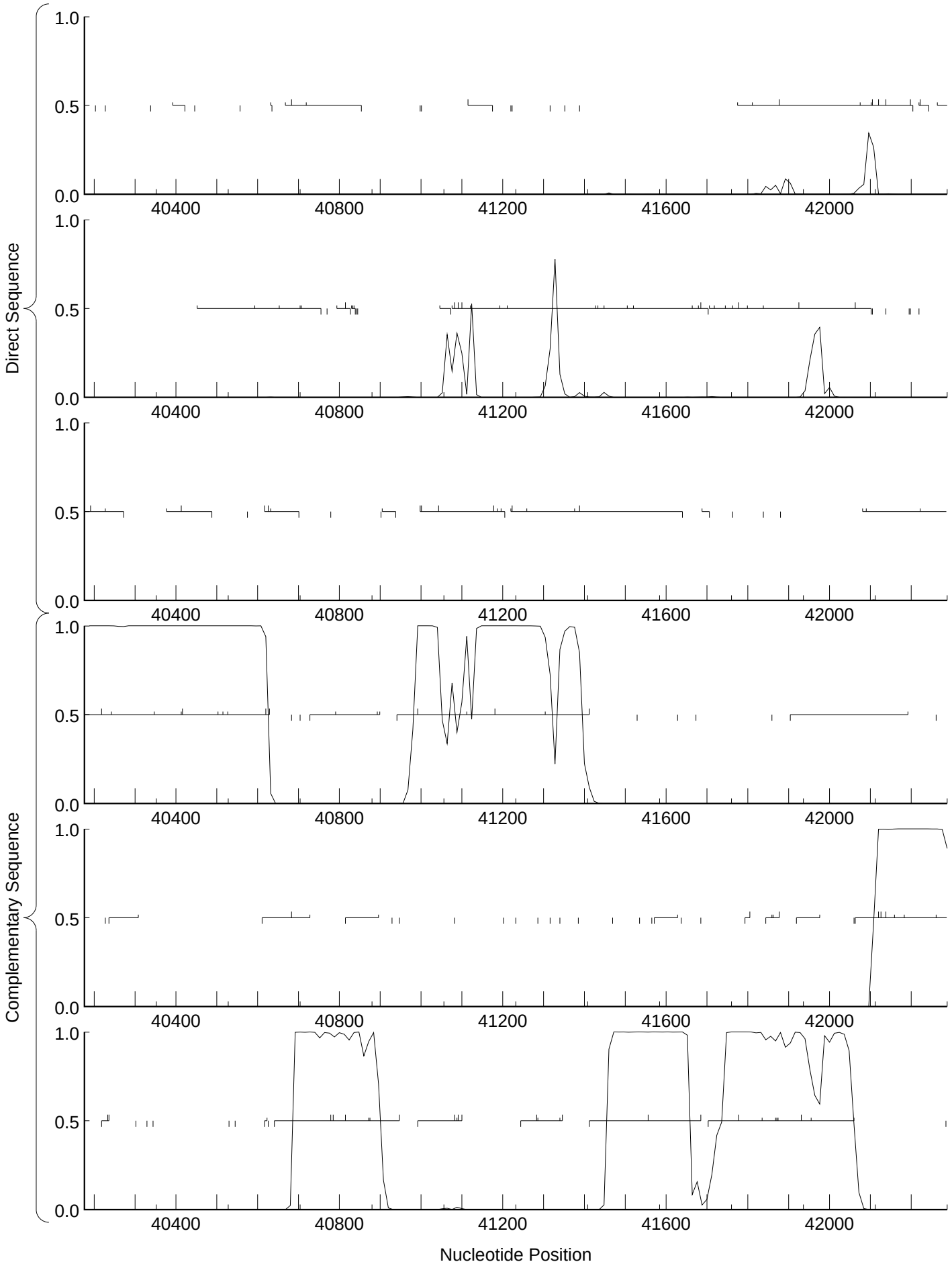
er phage Tank complete sequence, 67592 bp including ~589 bp terminal repeat, Cluster AP1, Order 4, Window 96, Step 12, 17/34

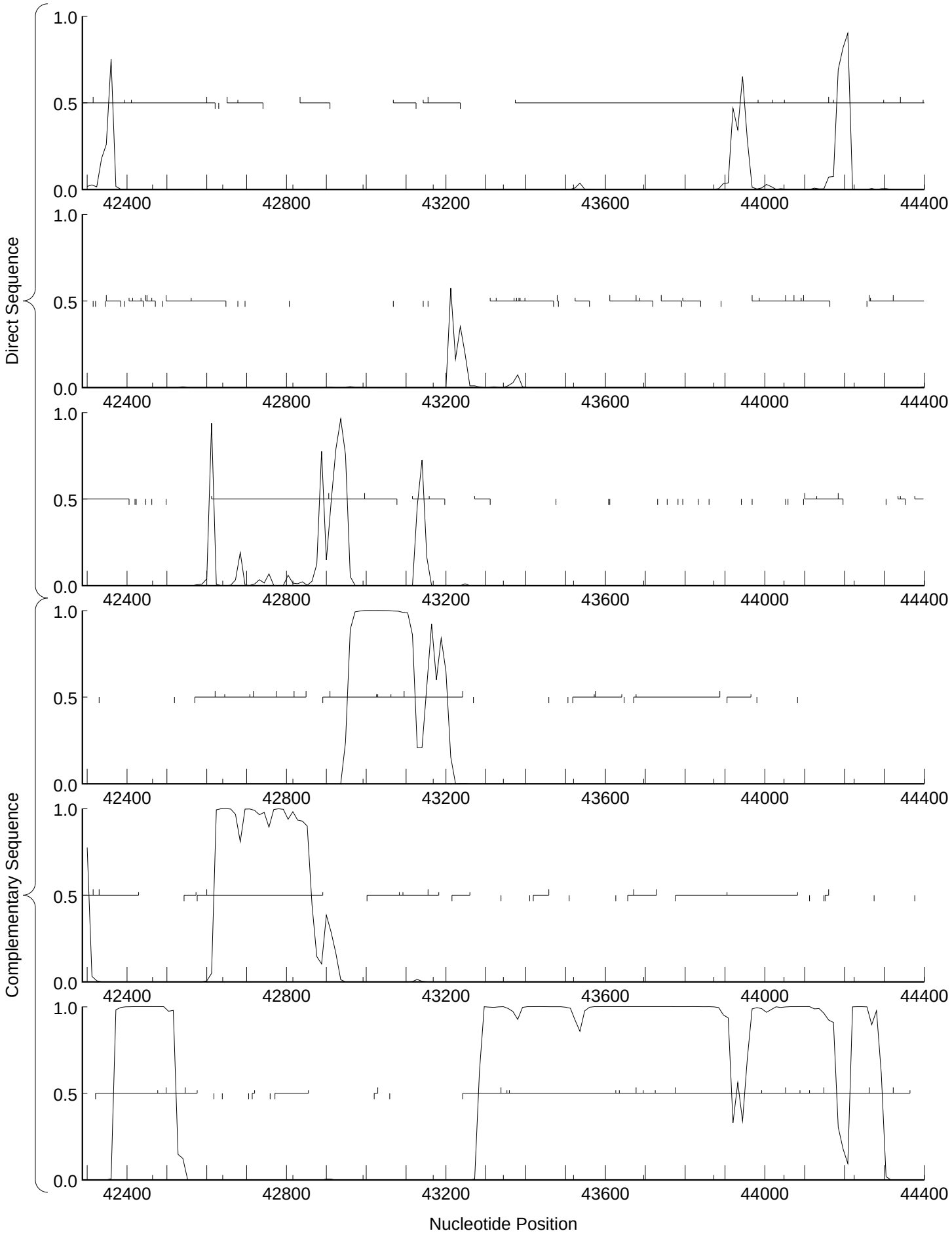


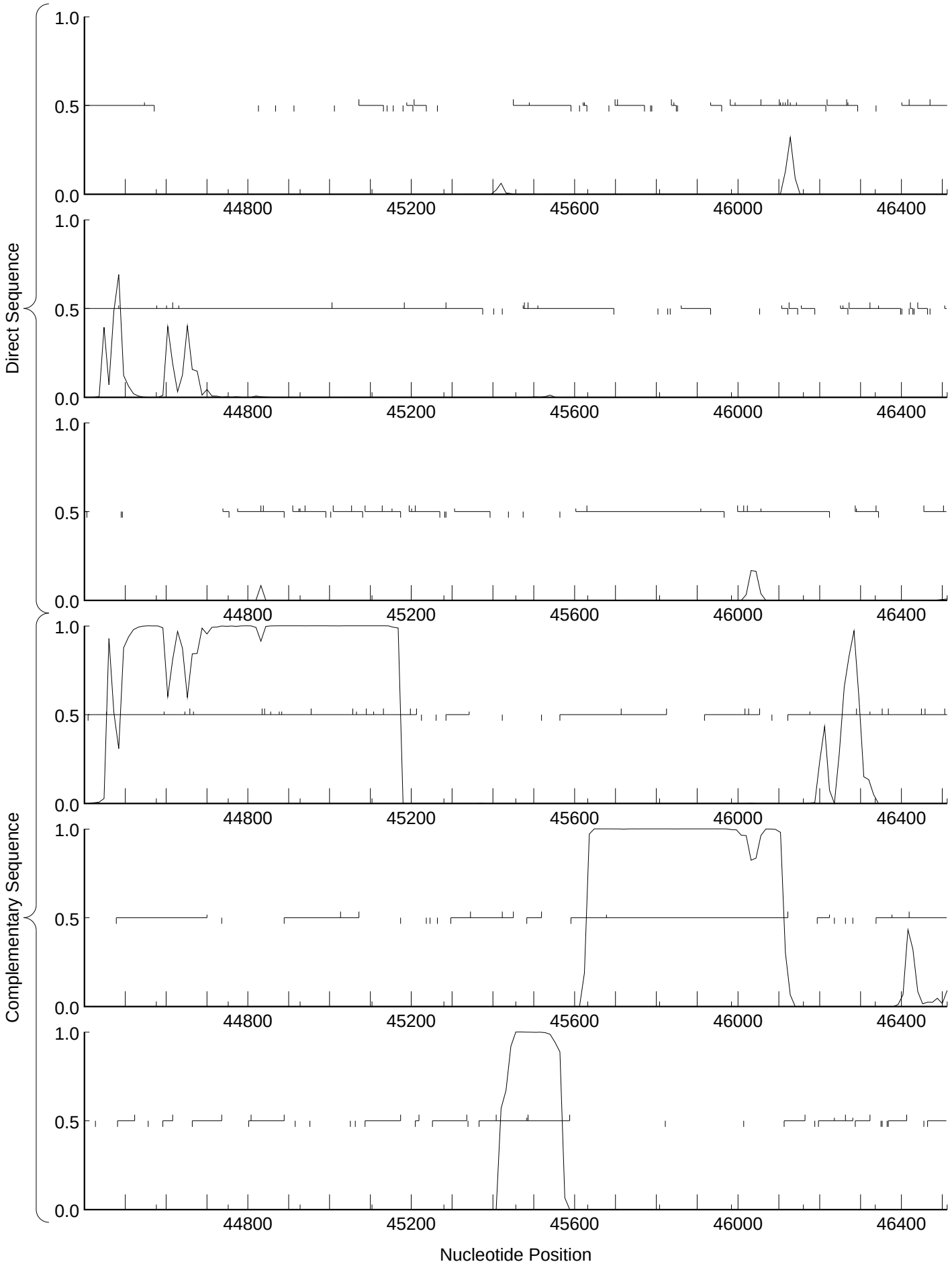

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
34000
34400
34800
35200
35600
Nucleotide Position


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

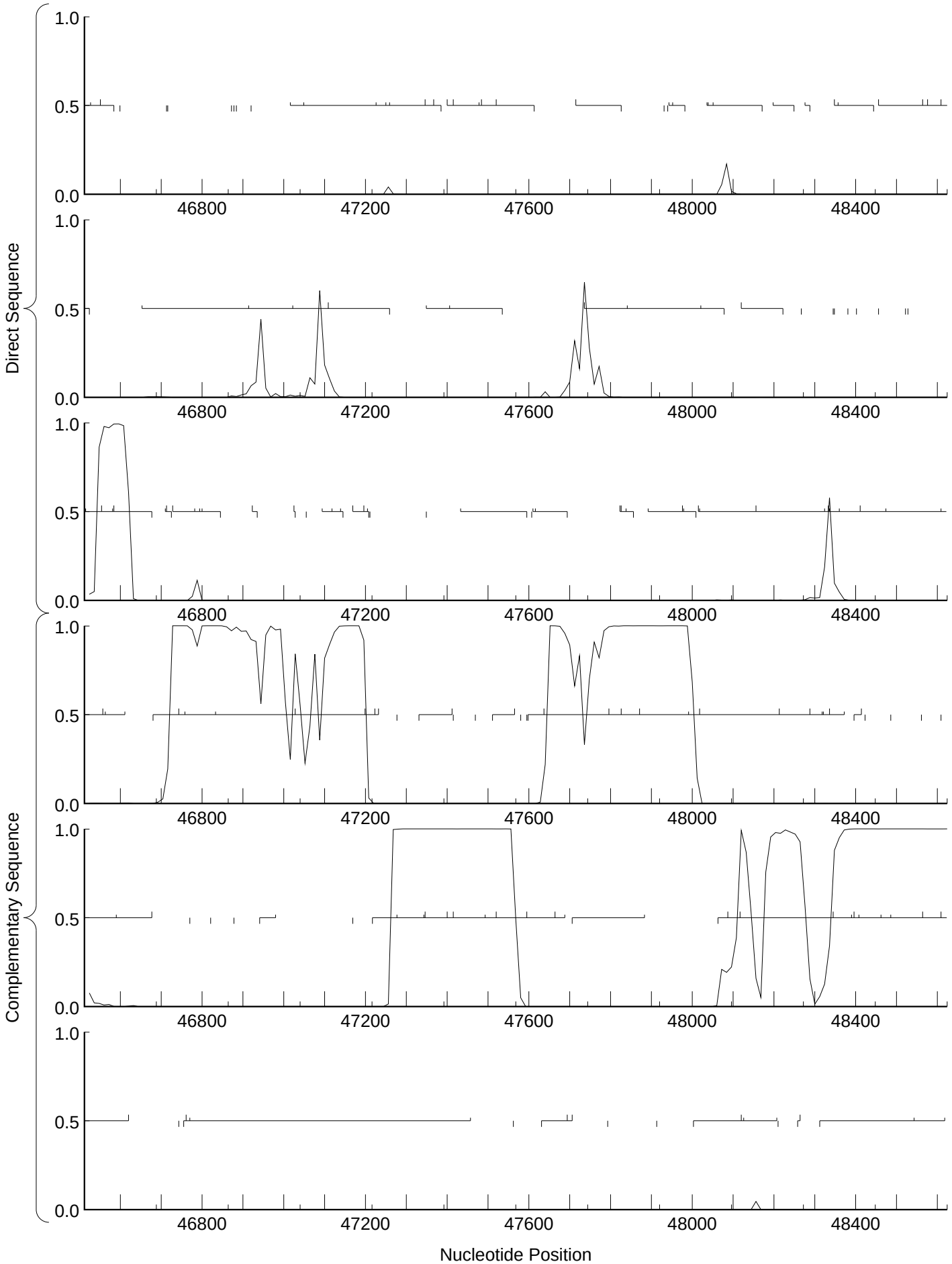

Direct Sequence
Complementary Sequence
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38800
39200
39600
40000
Nucleotide Position

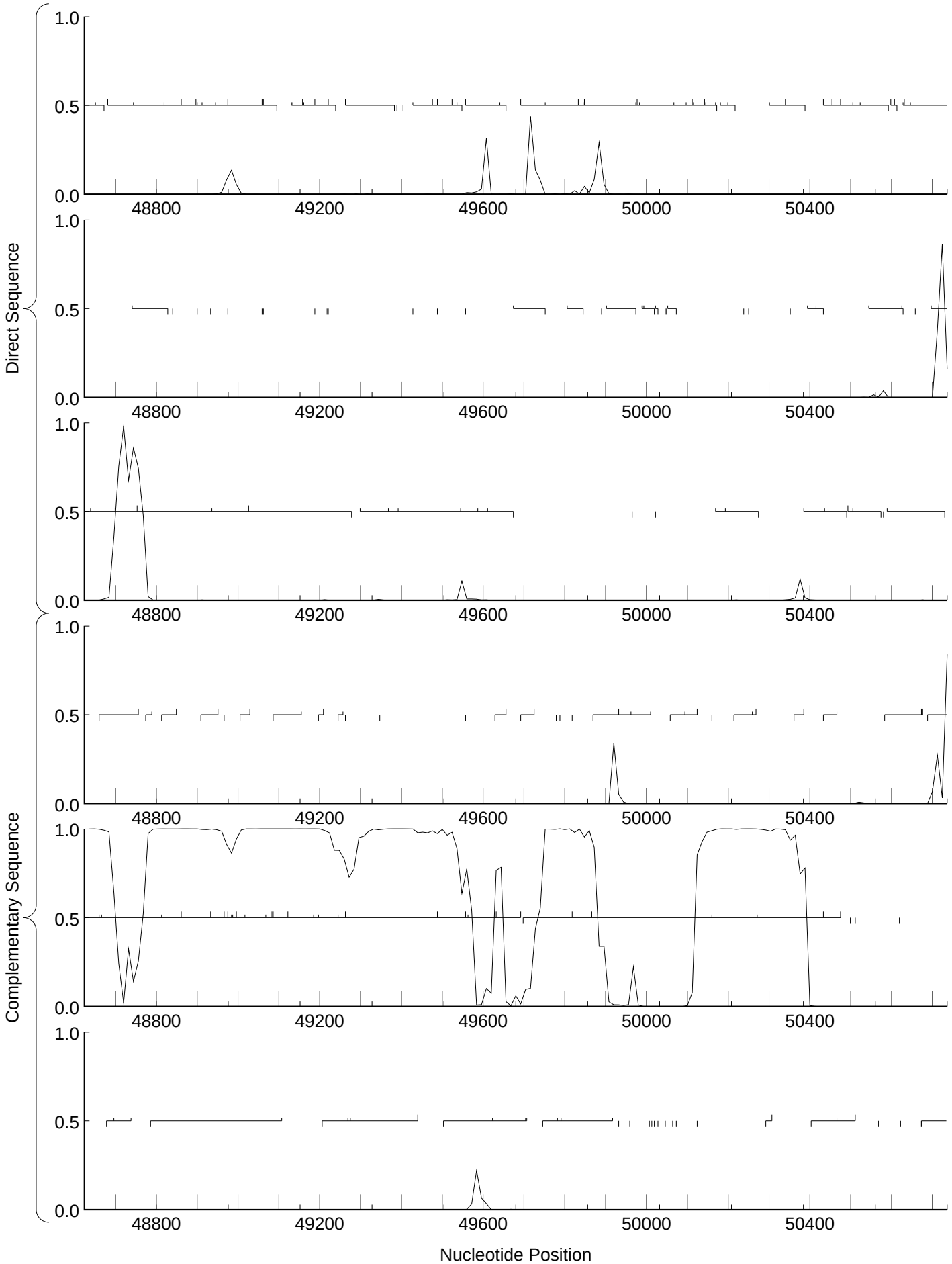

Direct Sequence
Complementary Sequence
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41600
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Nucleotide Position

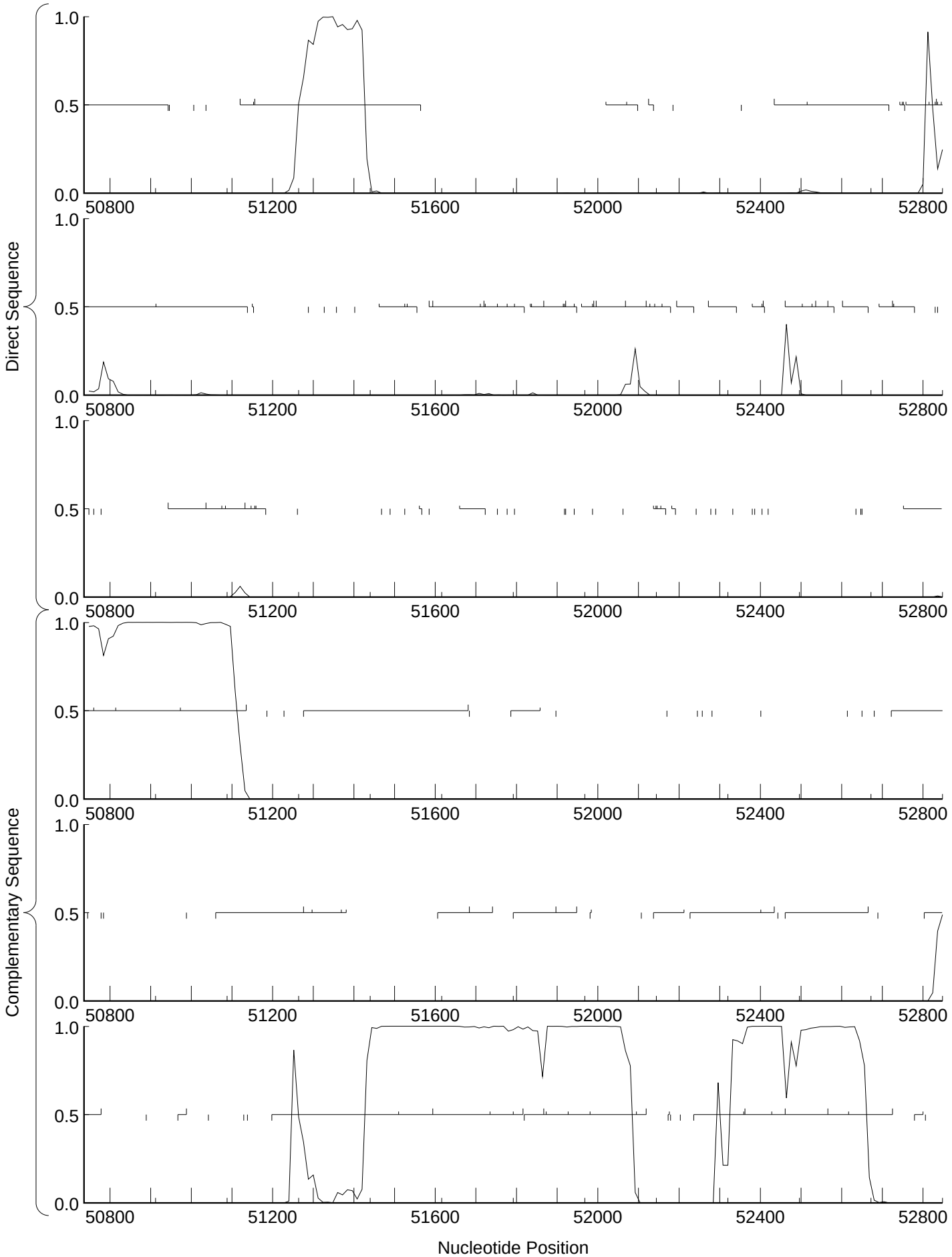

Direct Sequence
Complementary Sequence
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0.0
42400
42800
43200
43600
44000
44400
Nucleotide Position

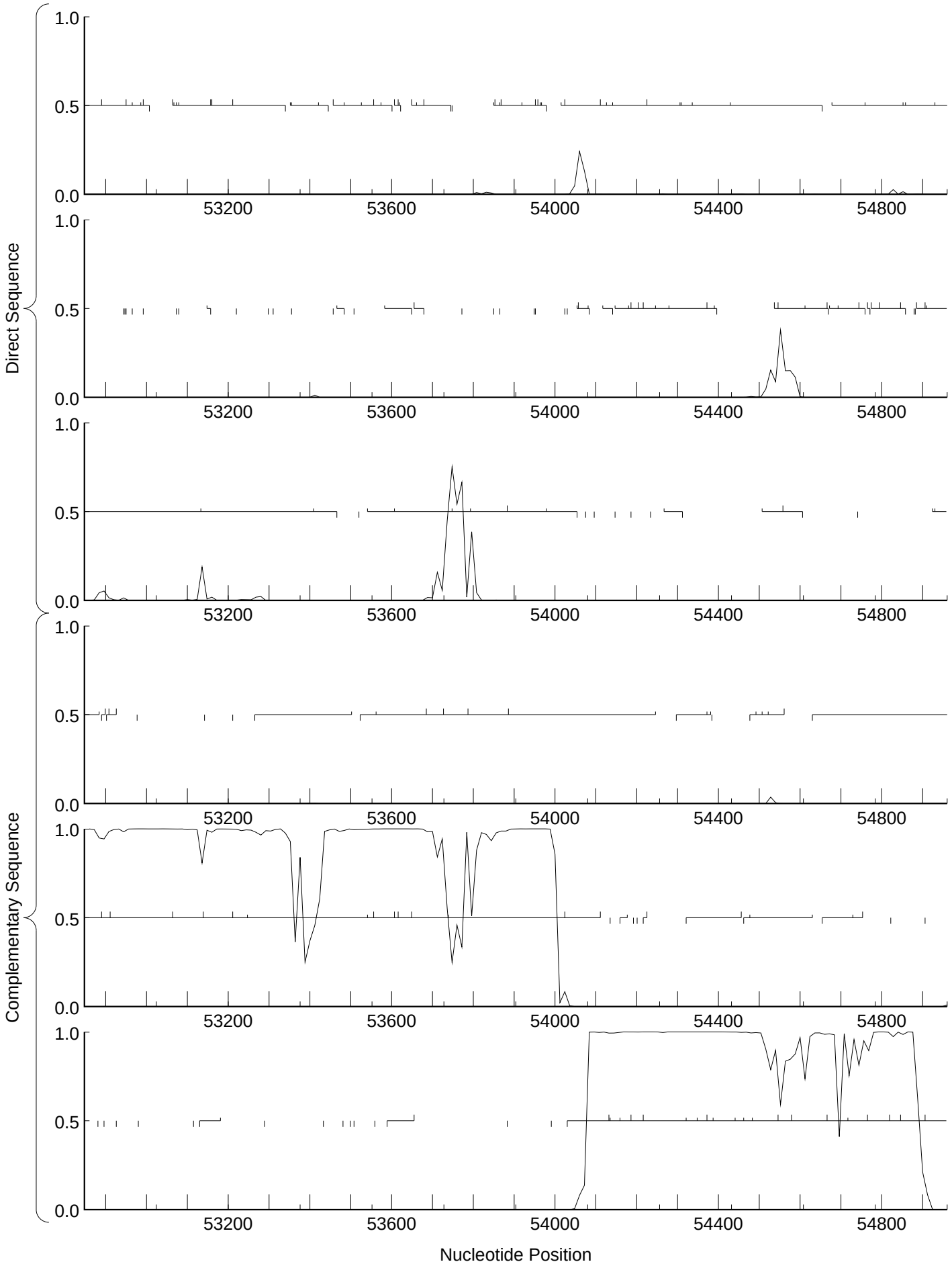

Direct Sequence
Complementary Sequence
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0.0
44800
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45600
46000
46400
Nucleotide Position

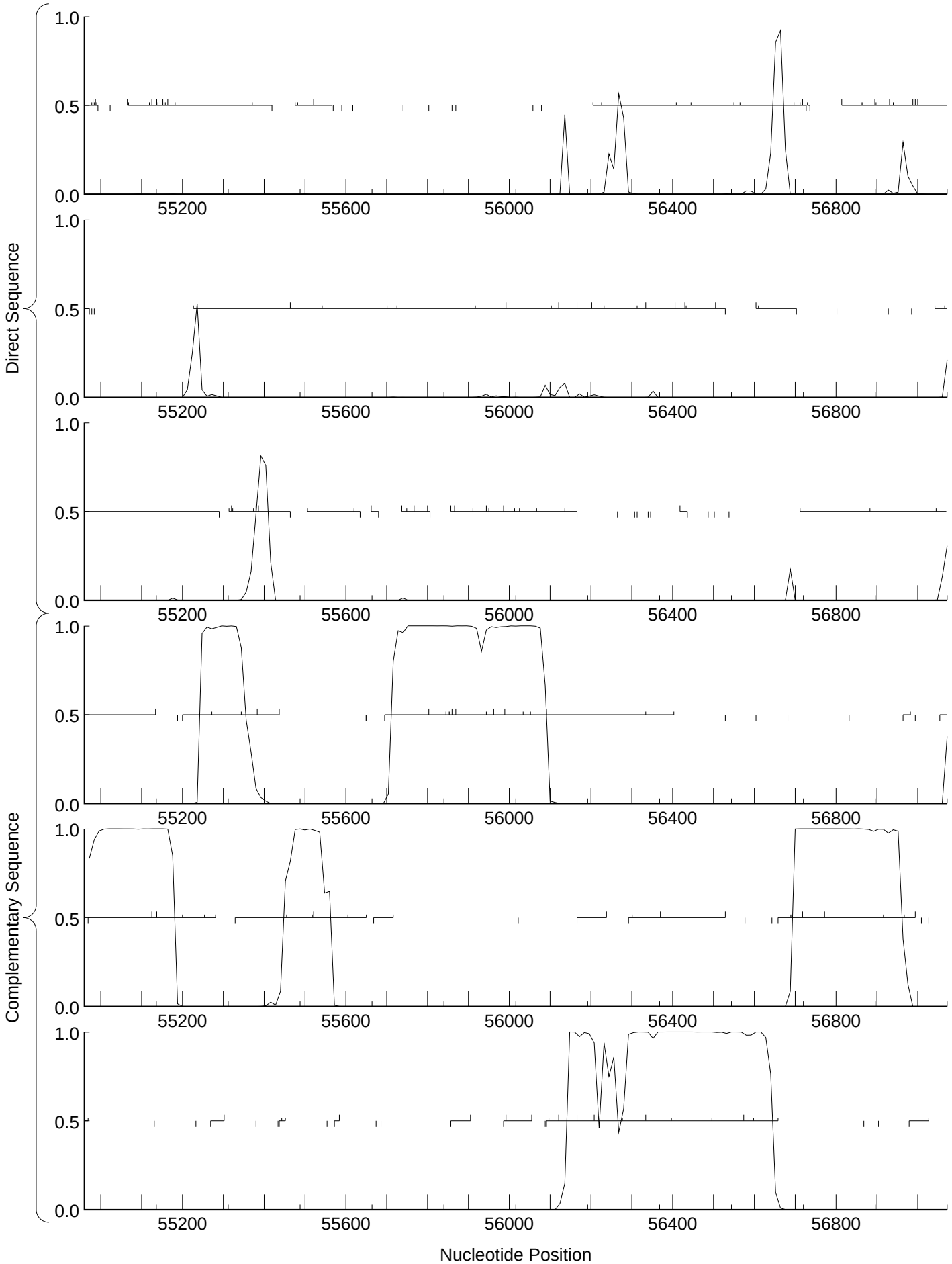
r phage Tank complete sequence, 67592 bp including ~589 bp terminal repeat, Cluster AP1, Order 4, Window 96, Step 12, 24/34



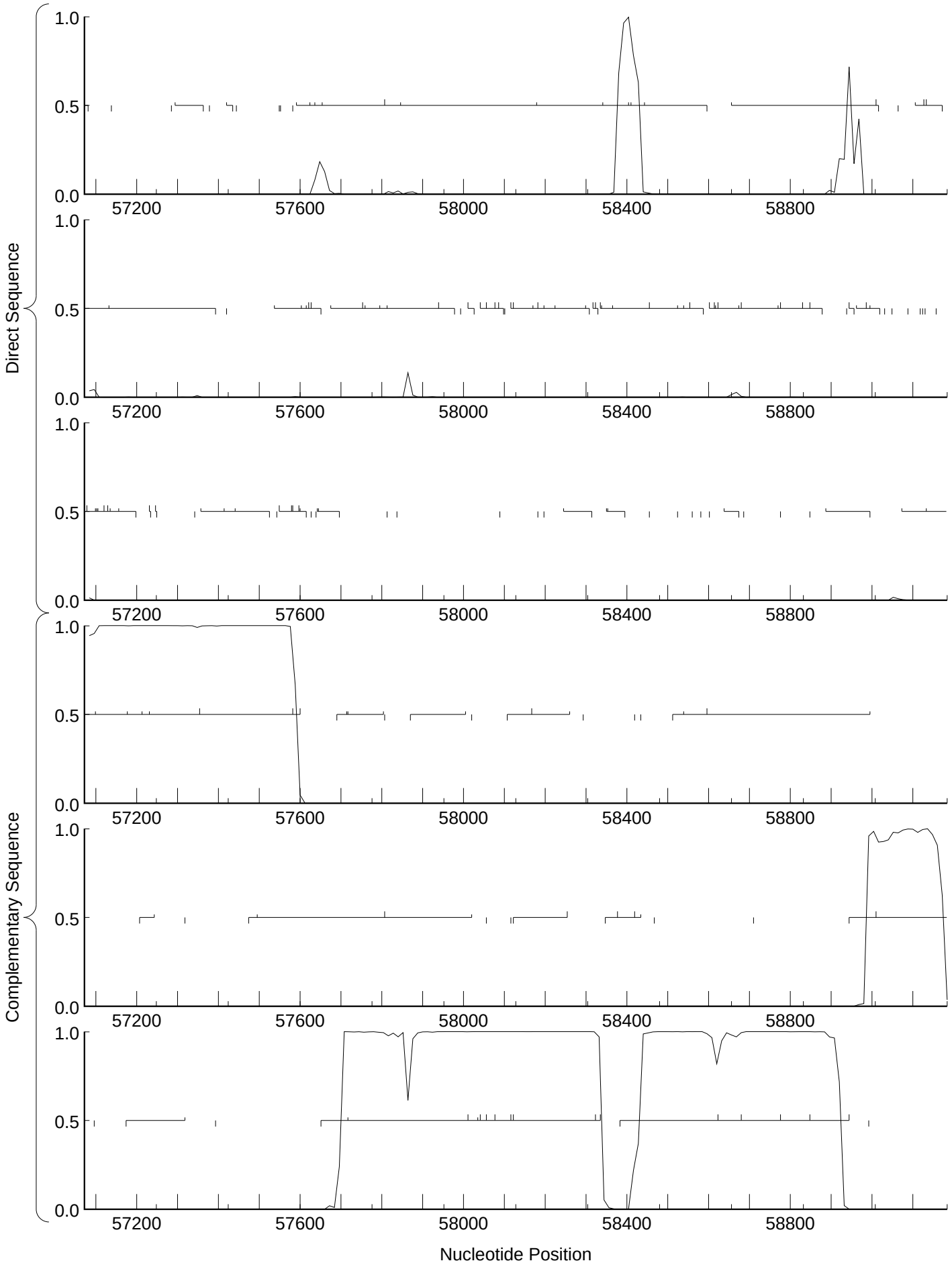

Direct Sequence
Complementary Sequence
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49600
50000
50400
Nucleotide Position

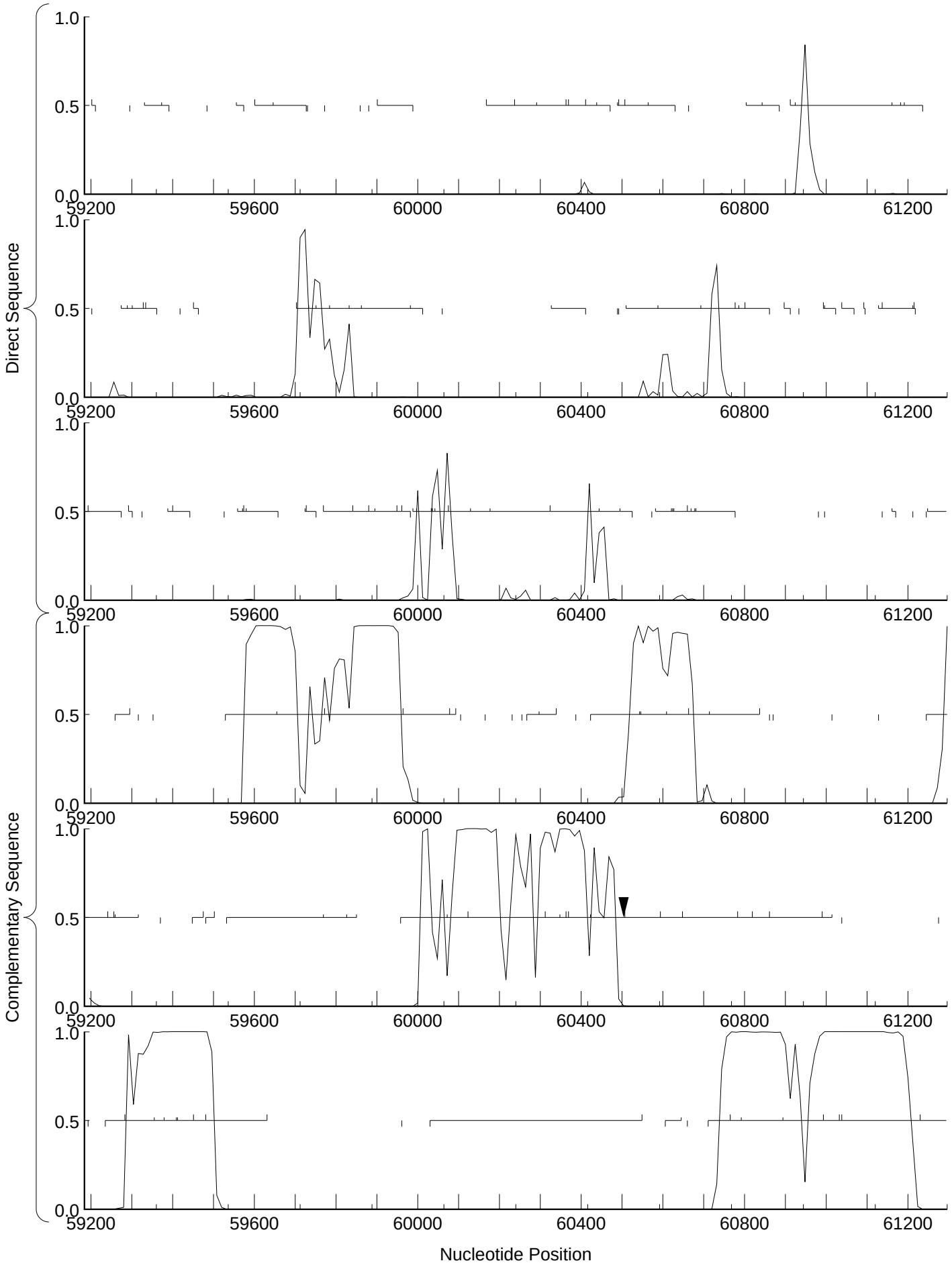

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Complementary Sequence
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50800
51200
51600
52000
52400
52800
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54400
54800
Nucleotide Position

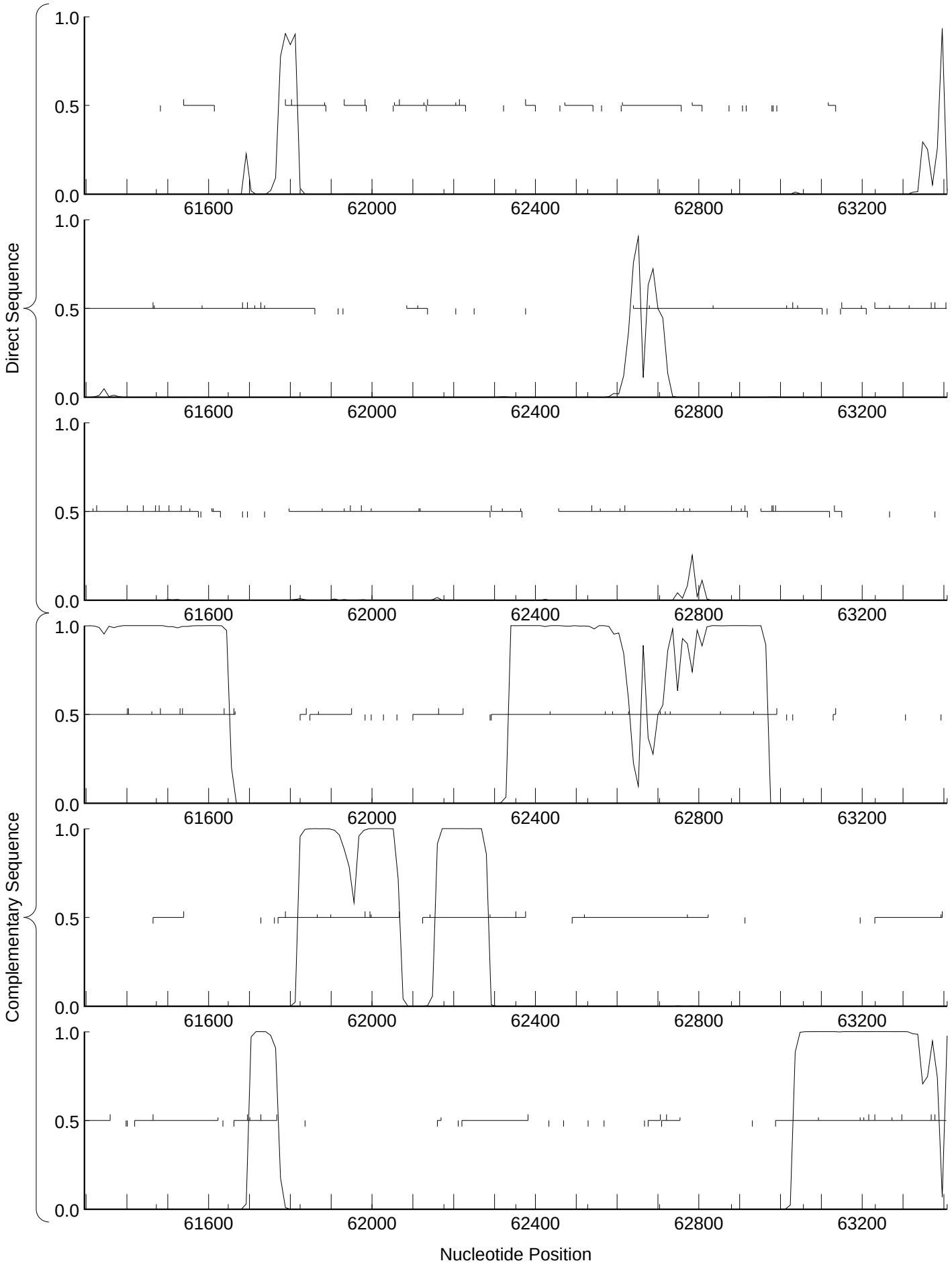

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Complementary Sequence
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56400
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Nucleotide Position

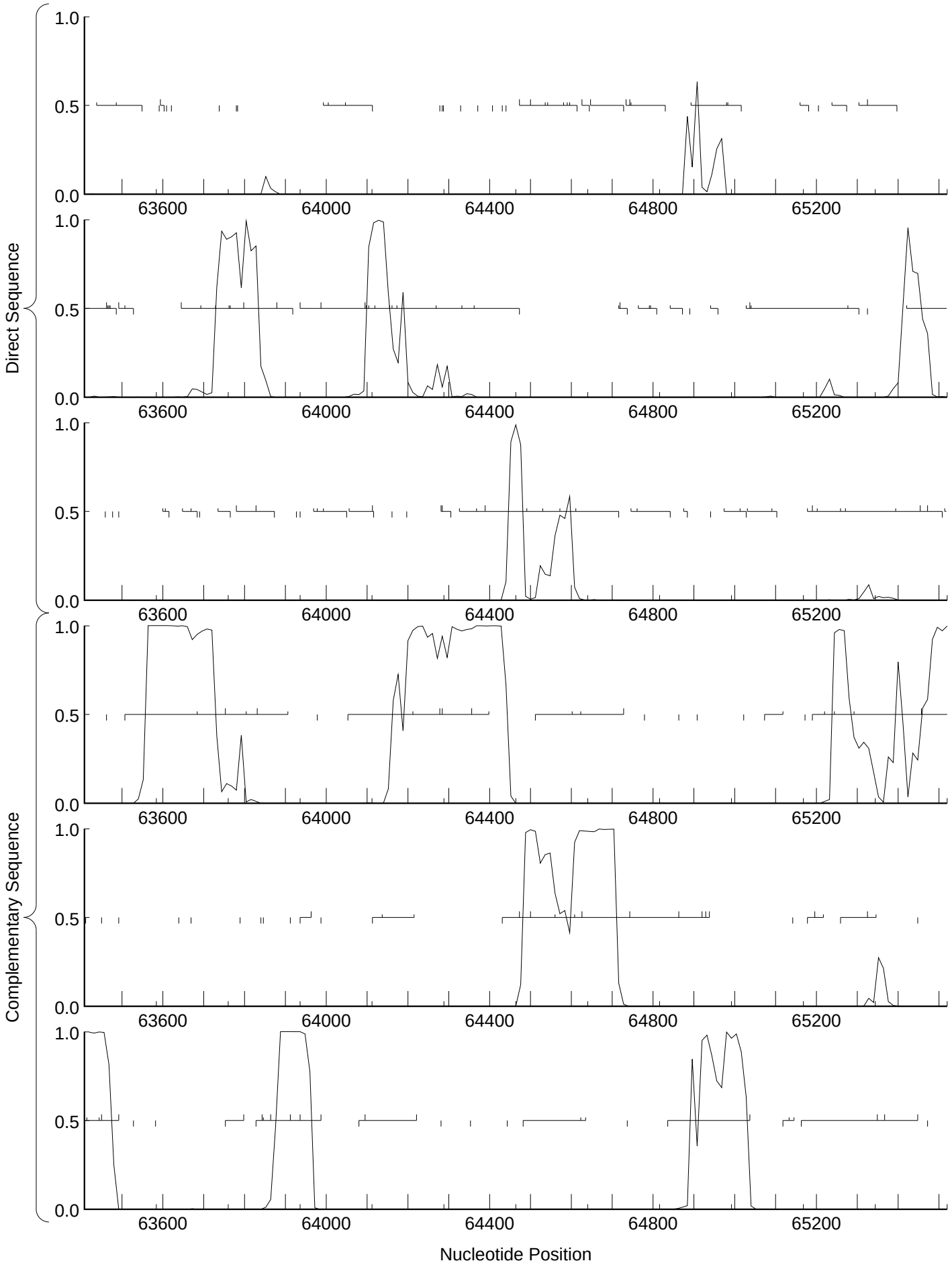
r phage Tank complete sequence, 67592 bp including ~589 bp terminal repeat, Cluster AP1, Order 4, Window 96, Step 12, 29/34




Direct Sequence
Complementary Sequence
1.0
0.5
0.0
59200
59600
60000
60400
60800
61200
Nucleotide Position

er phage Tank complete sequence, 67592 bp including ~589 bp terminal repeat, Cluster AP1, Order 4, Window 96, Step 12, 31/34




Direct Sequence
Complementary Sequence
1.0
0.5
0.0
63600
64000
64400
64800
65200
Nucleotide Position

er phage Tank complete sequence, 67592 bp including ~589 bp terminal repeat, Cluster AP1, Order 4, Window 96, Step 12, 33/34

