GeneMark

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

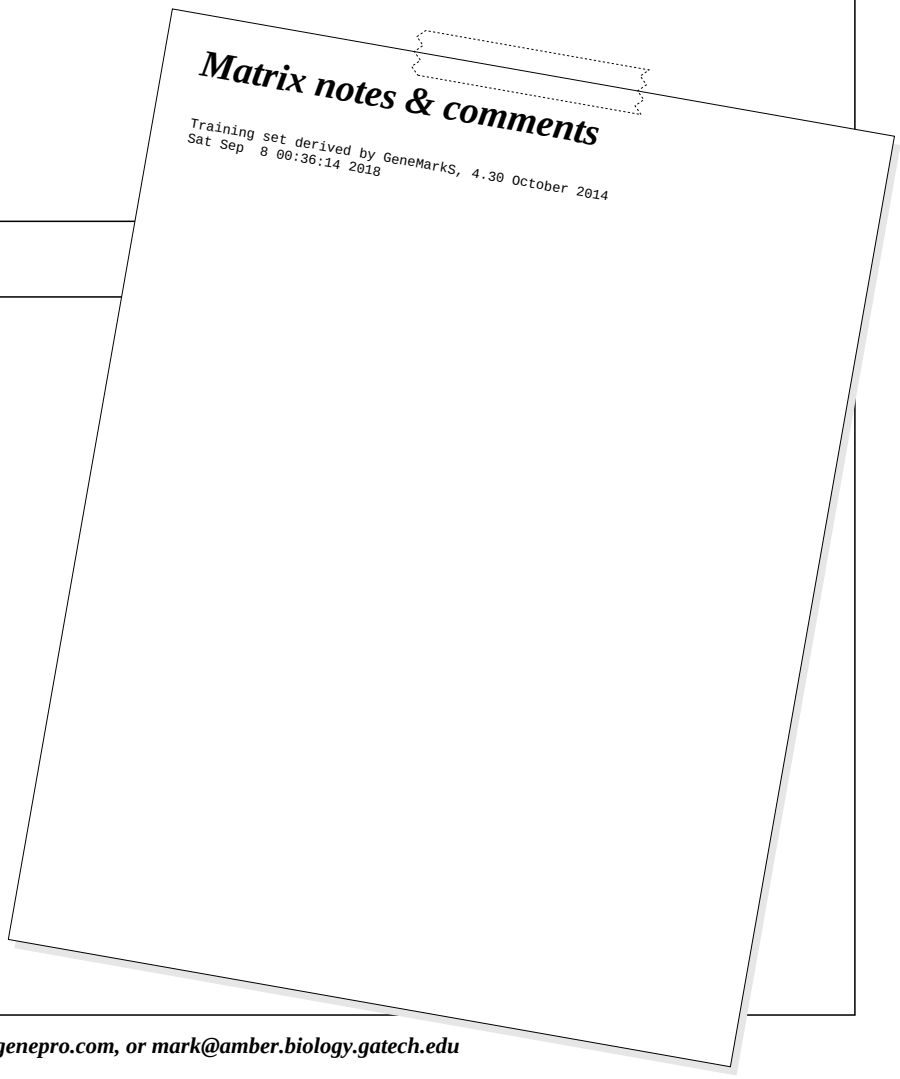
PROGRAM INFORMATION

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Sequence         :  Gordonia phage Tredge complete sequence, 75345 bp including 1173 bp terminal repeat, Cluste
Analysis Date    :  3/29/24 at 2:49:47
Pages            :  37
Sequence Length  :  75345 bp
GC Content       :   59.62%

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,
```



MATRIX INFORMATION

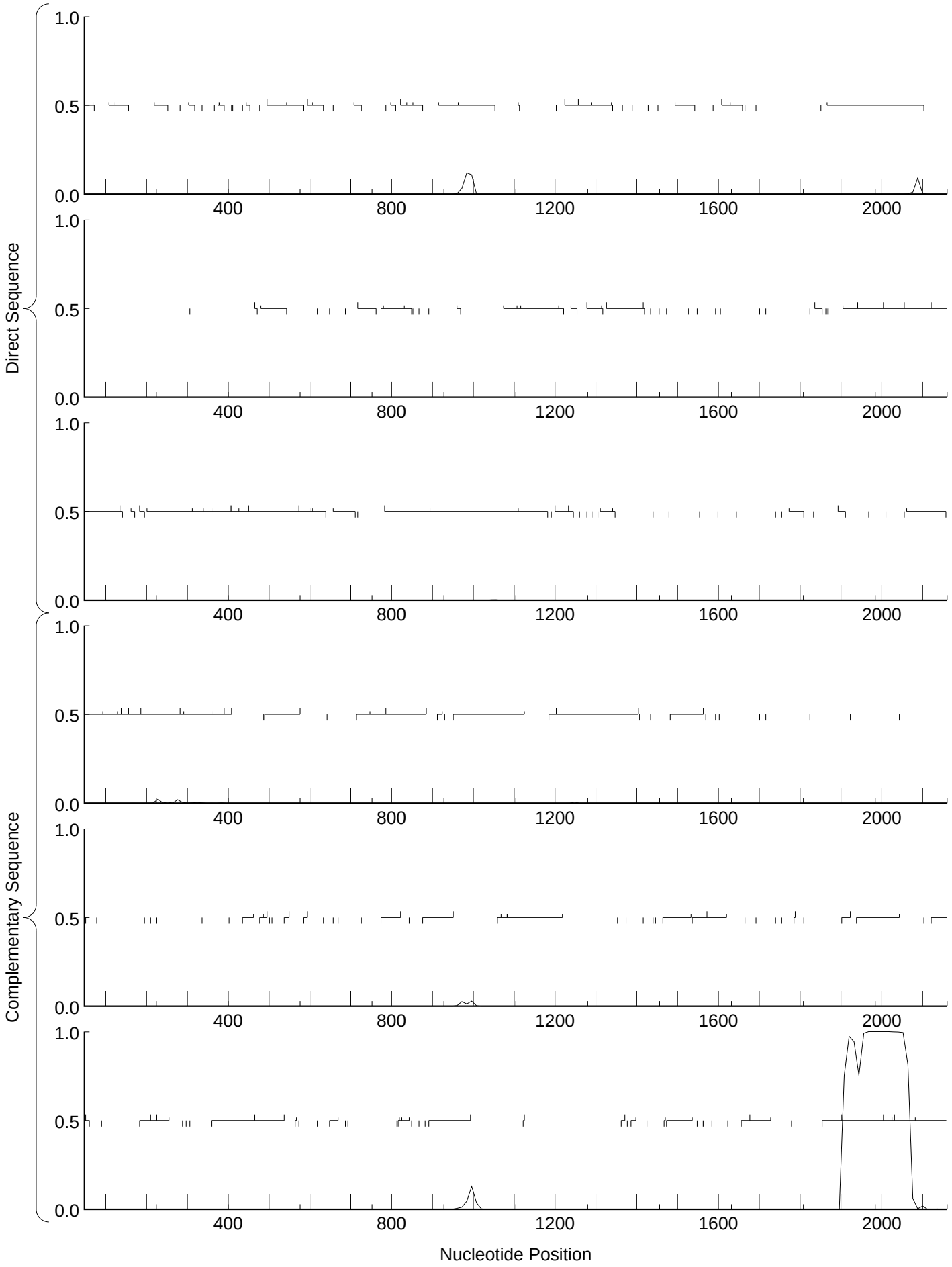
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Matrix     :  -
Author     :  -

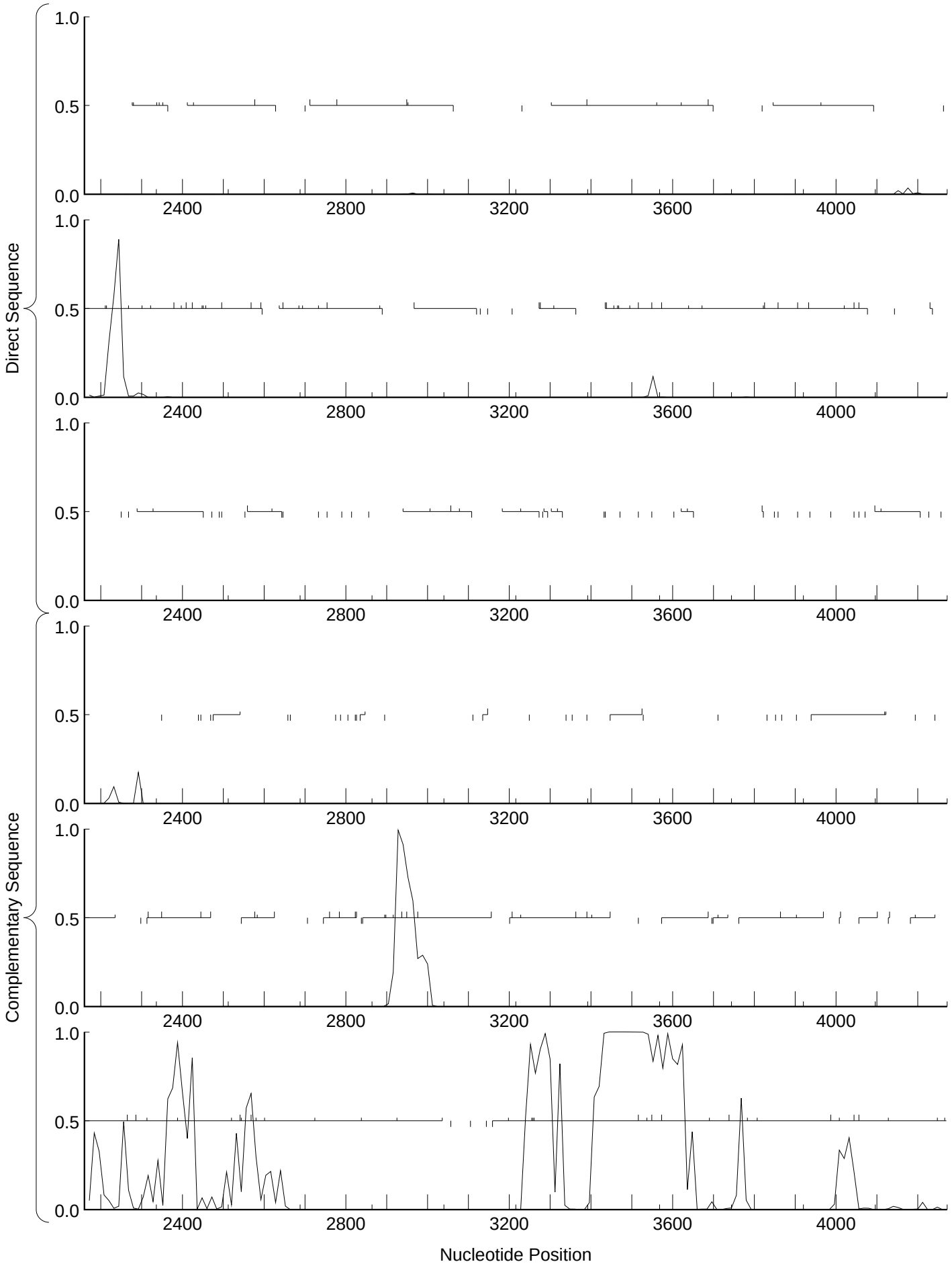
Order      :  4
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  Send questions / comments to:
      Dr. M. Borodovsky
      Georgia Institute of Technology
      School of Biology
      Atlanta, GA  30332-0230
```

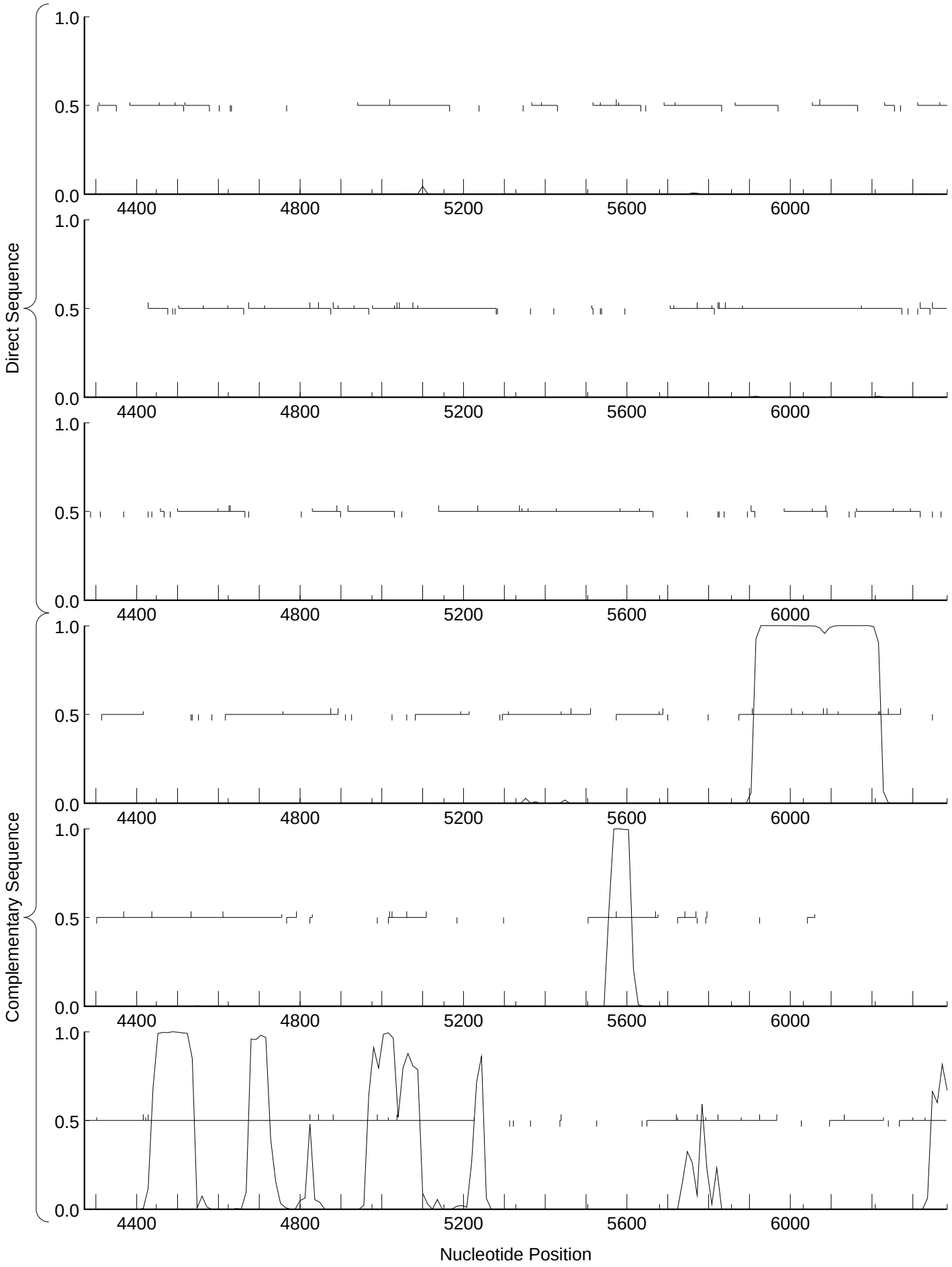

For help or information, send electronic mail to: custserv@genepro.com, or mark@amber.biology.gatech.edu

, phage Tredge complete sequence, 75345 bp including 1173 bp terminal repeat, Cluster CS4, Order 4, Window 96, Step 12, 2/37

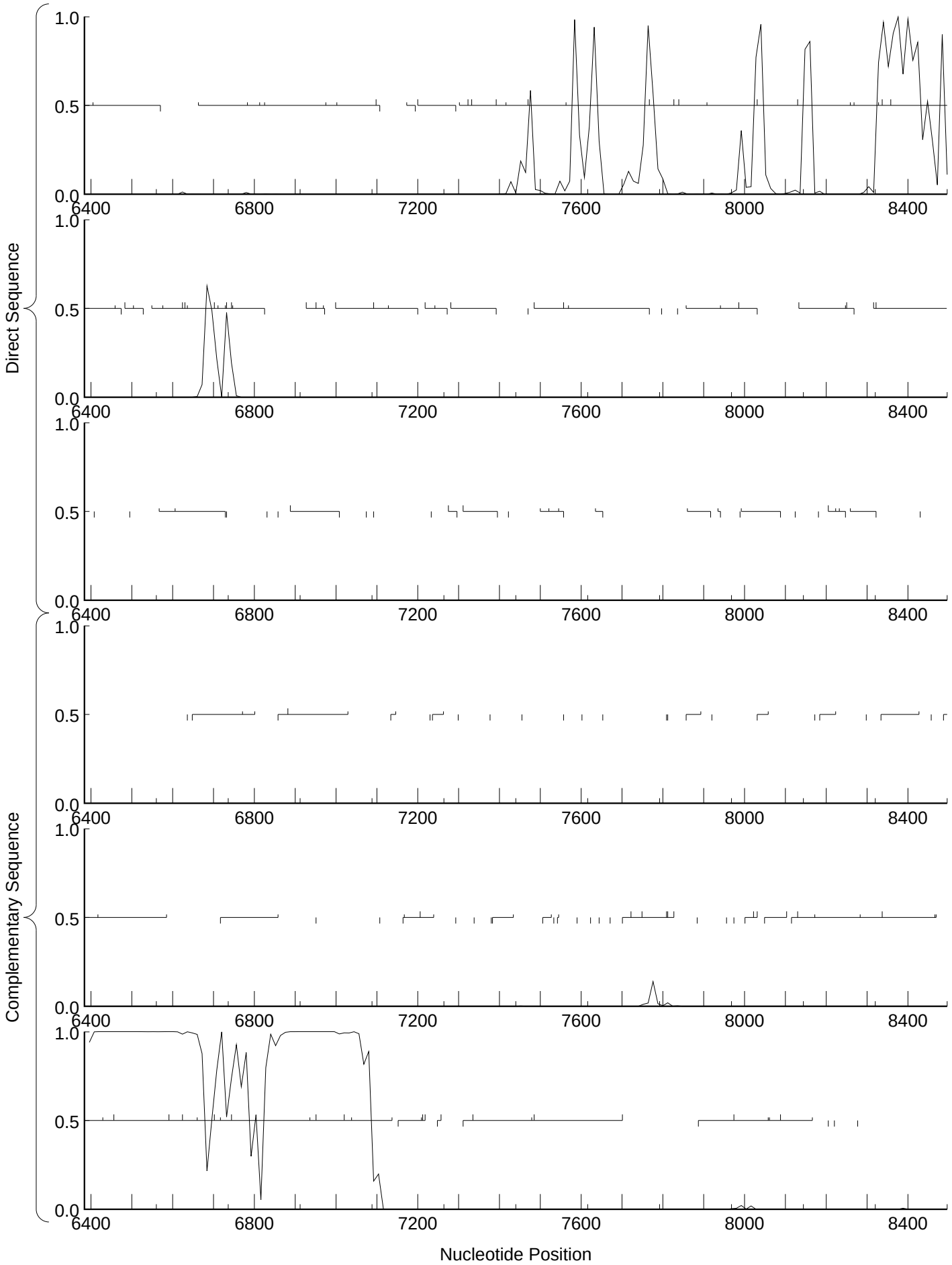



Direct Sequence
Complementary Sequence
1.0
0.5
0.0
2400
2800
3200
3600
4000
Nucleotide Position

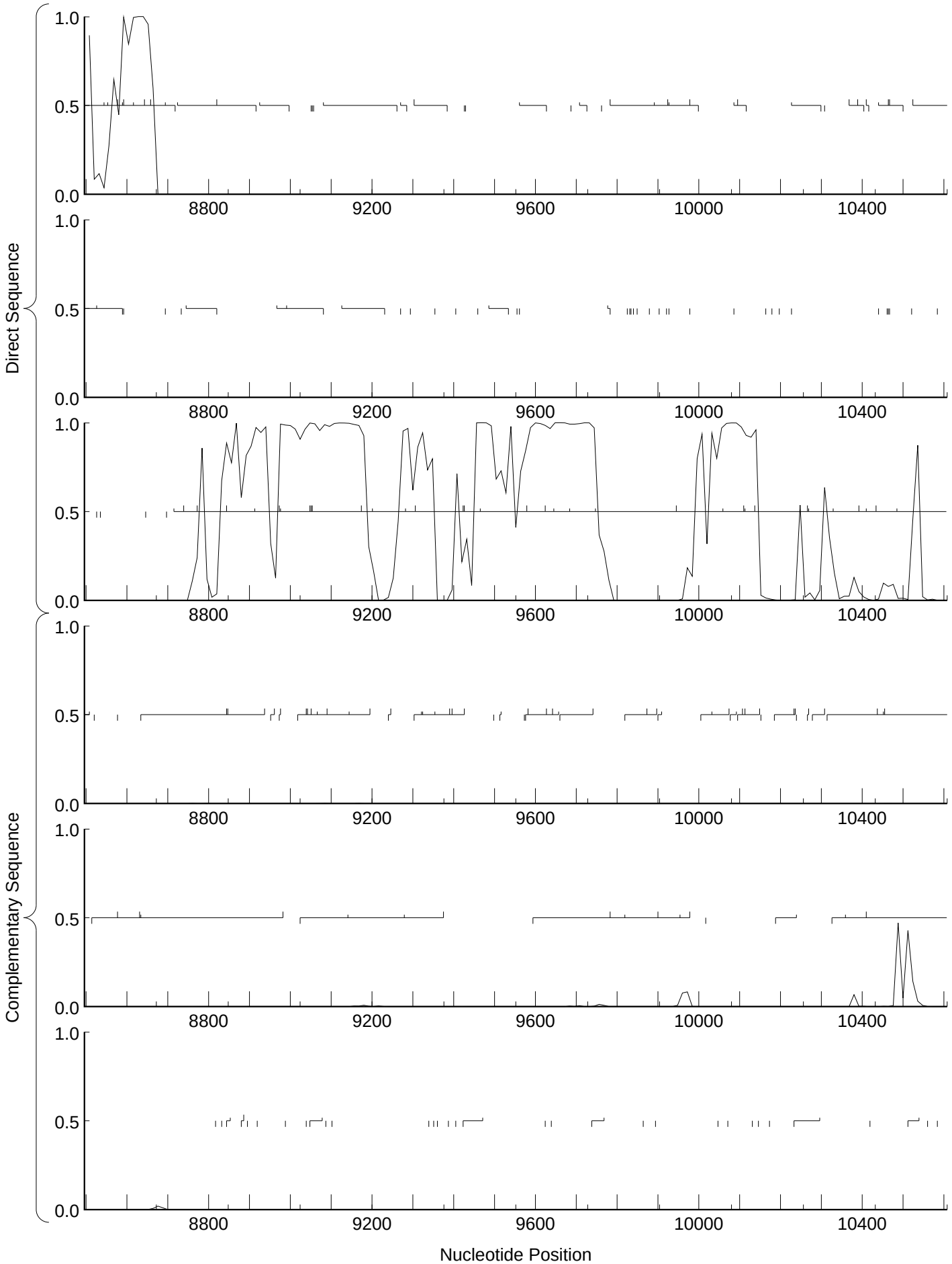
phage Tredge complete sequence, 75345 bp including 1173 bp terminal repeat, Cluster CS4, Order 4, Window 96, Step 12, 4/37



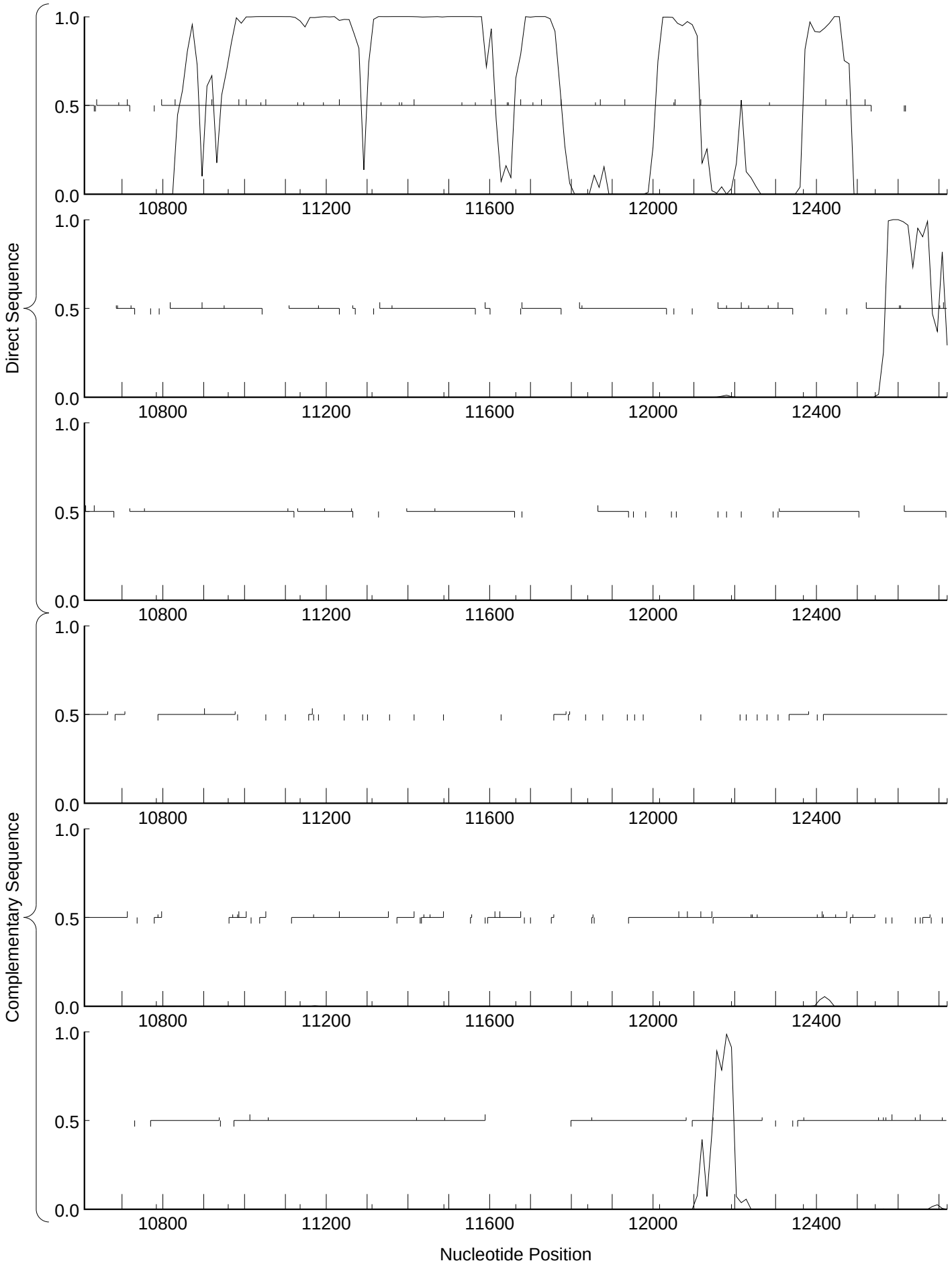
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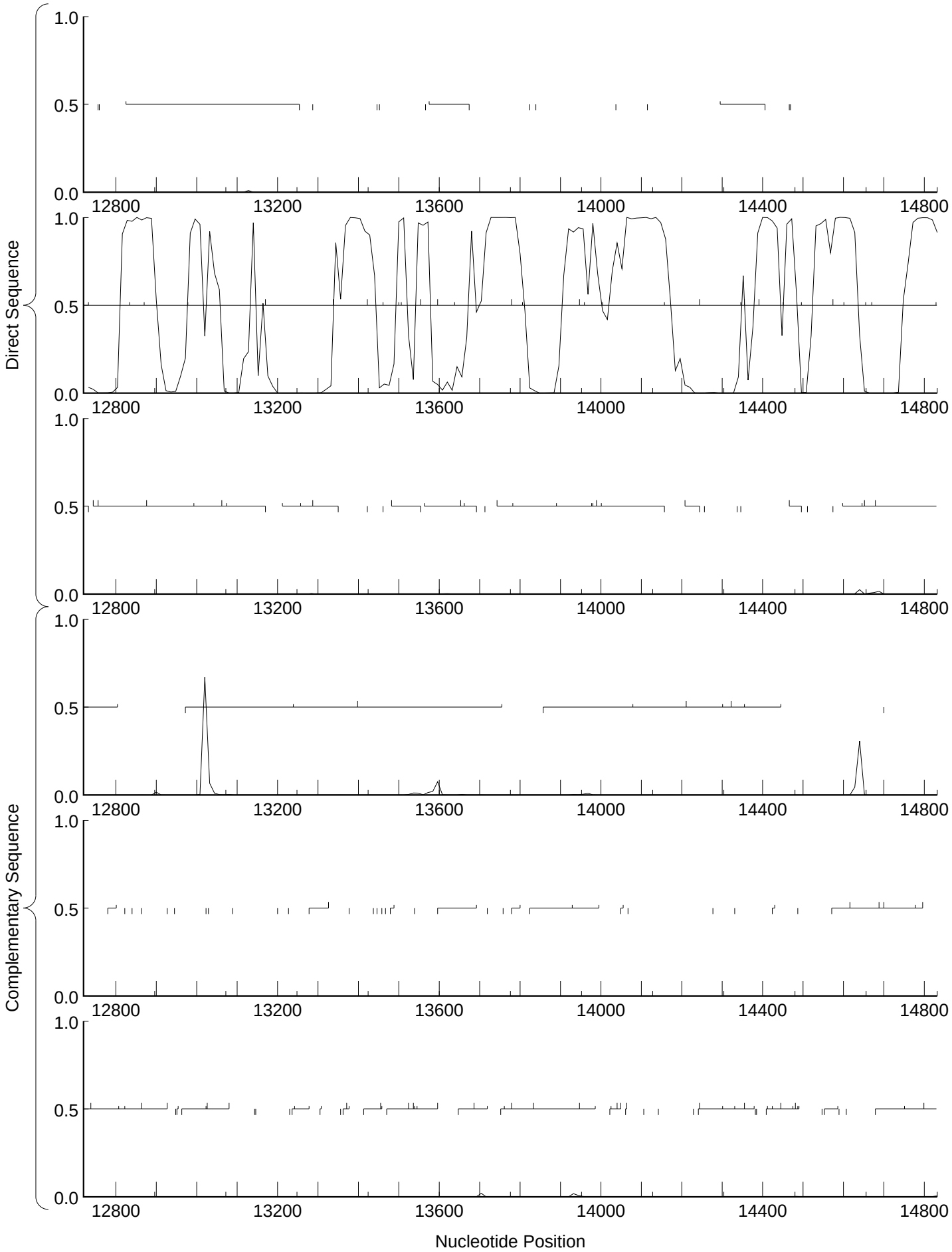
, phage Tredge complete sequence, 75345 bp including 1173 bp terminal repeat, Cluster CS4, Order 4, Window 96, Step 12, 6/37



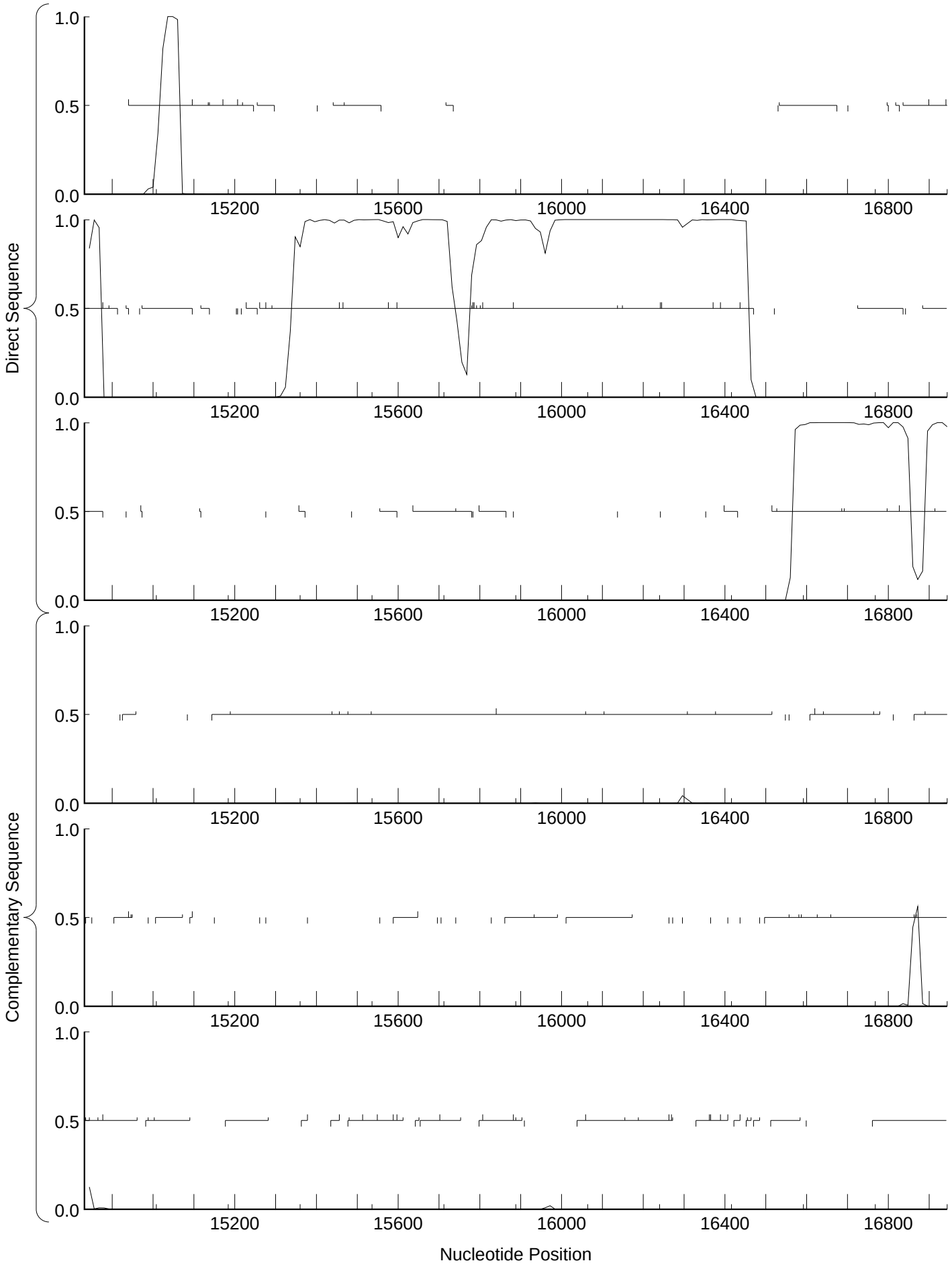
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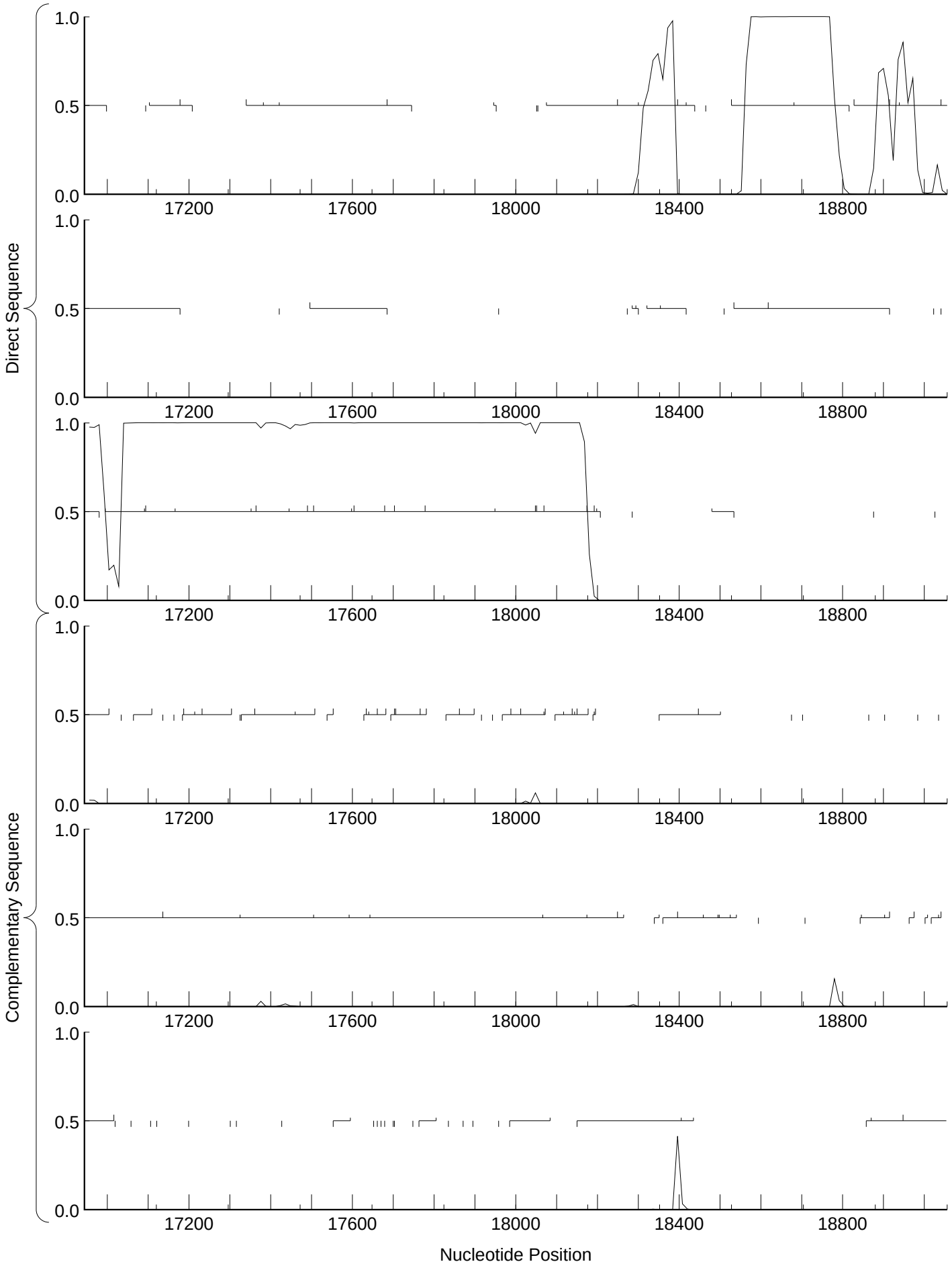


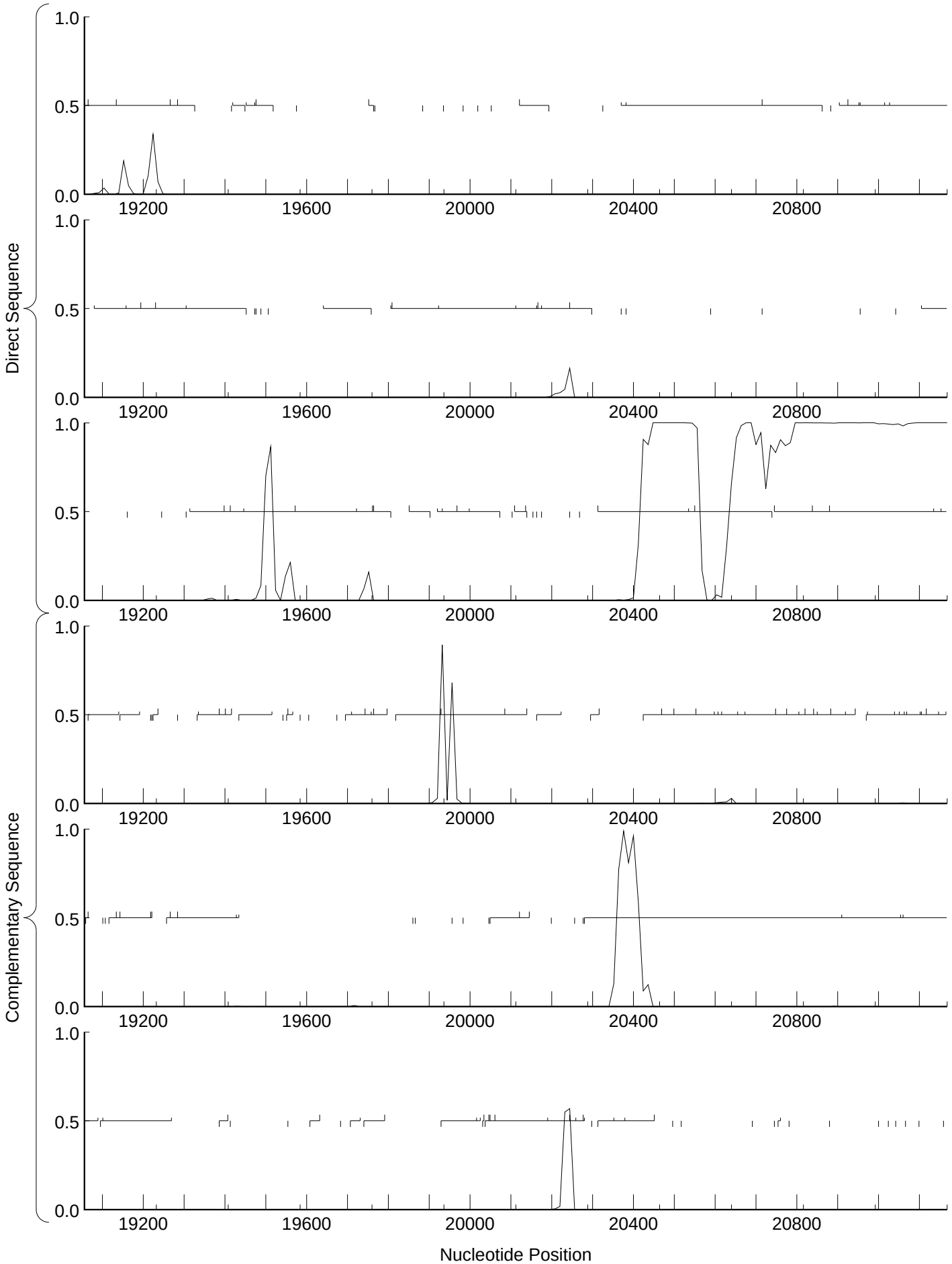
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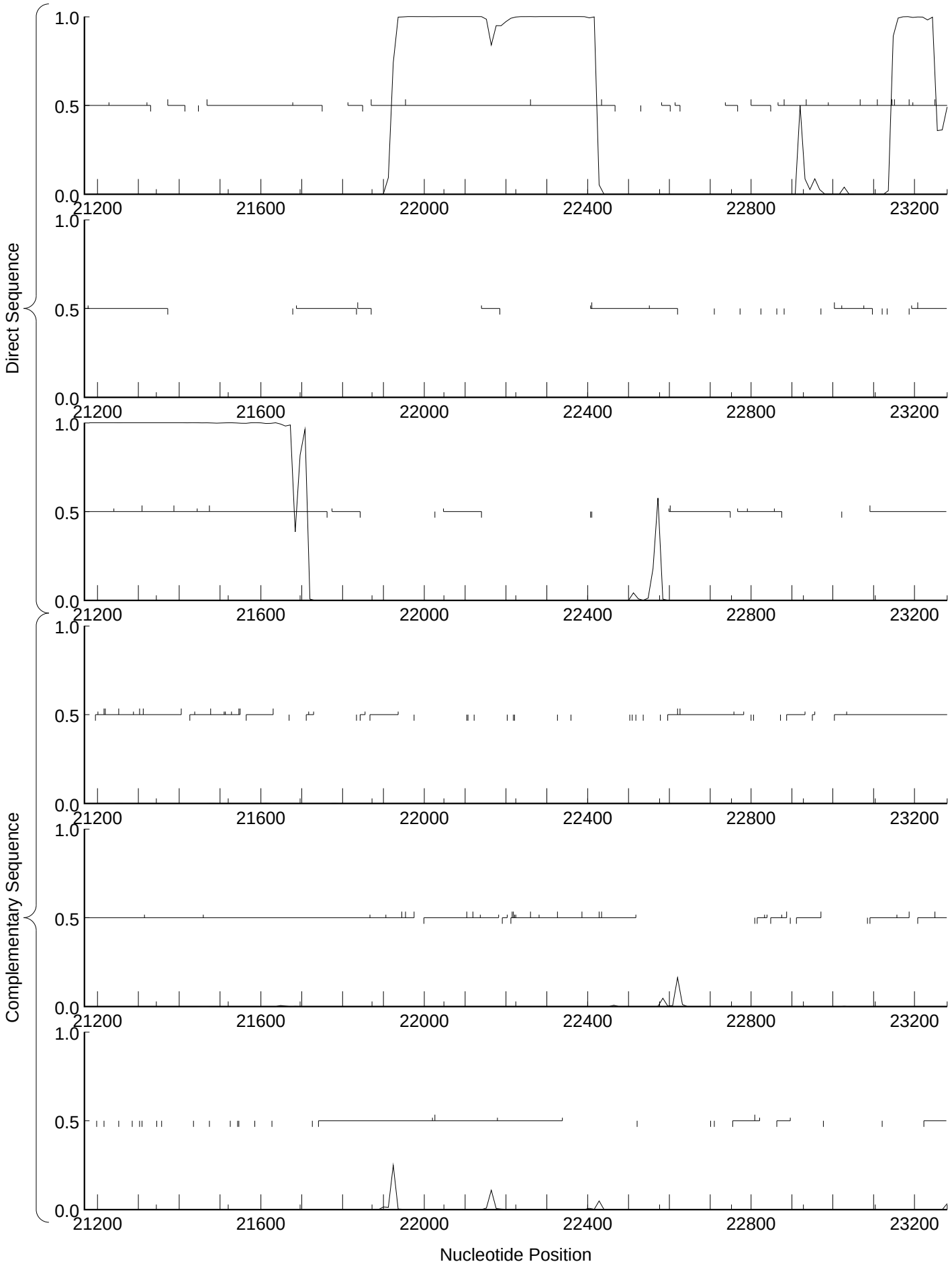


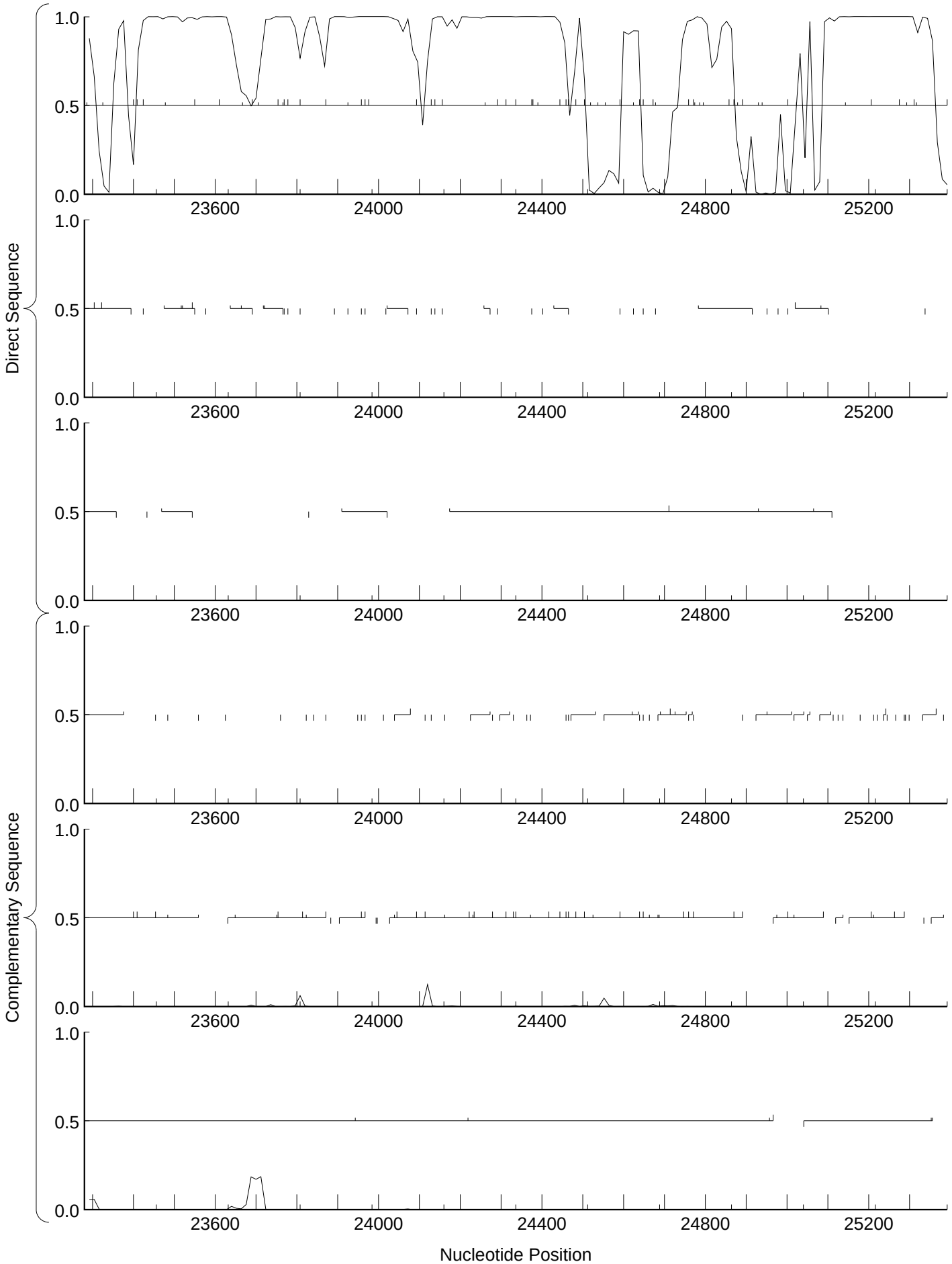
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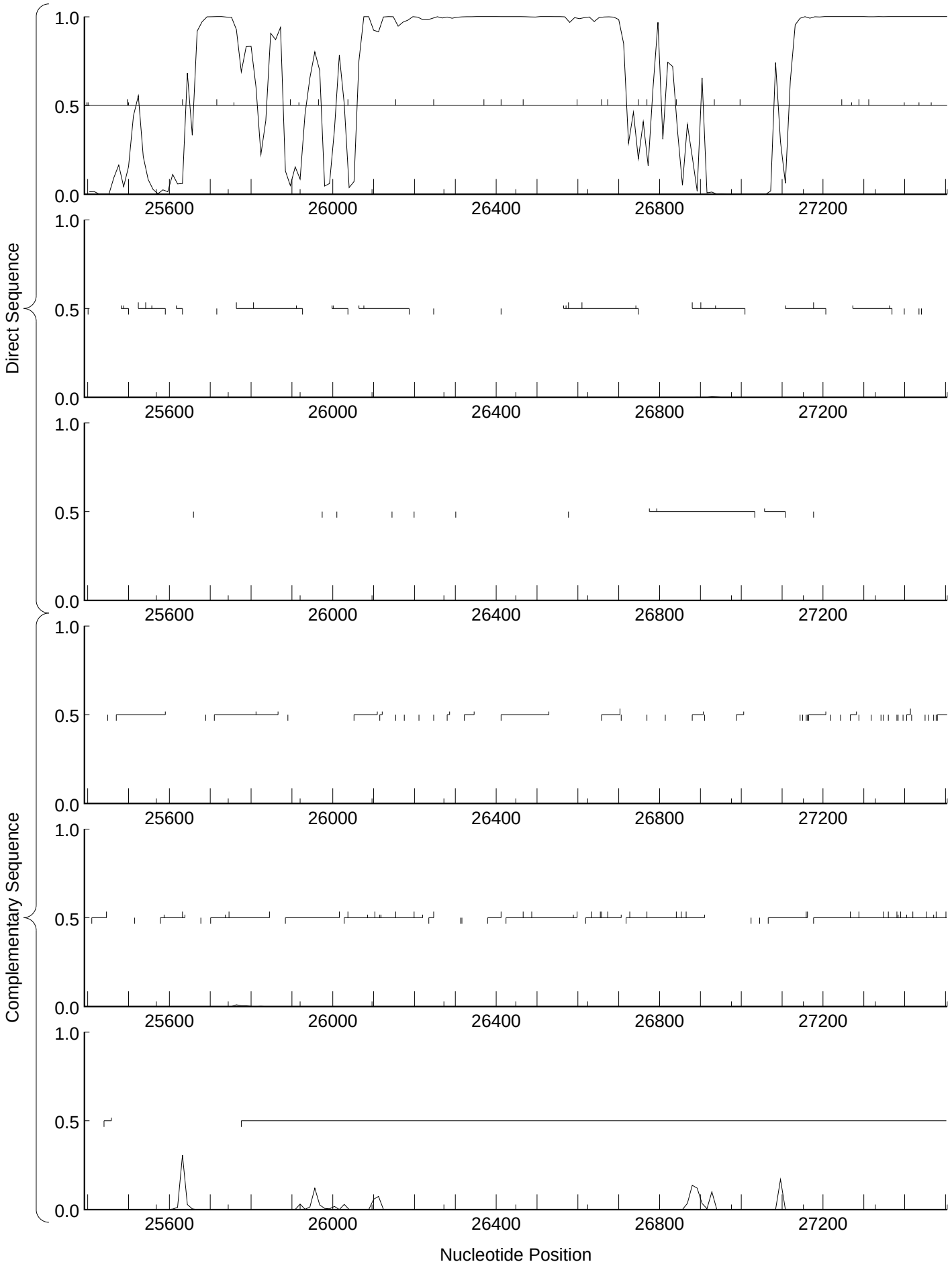


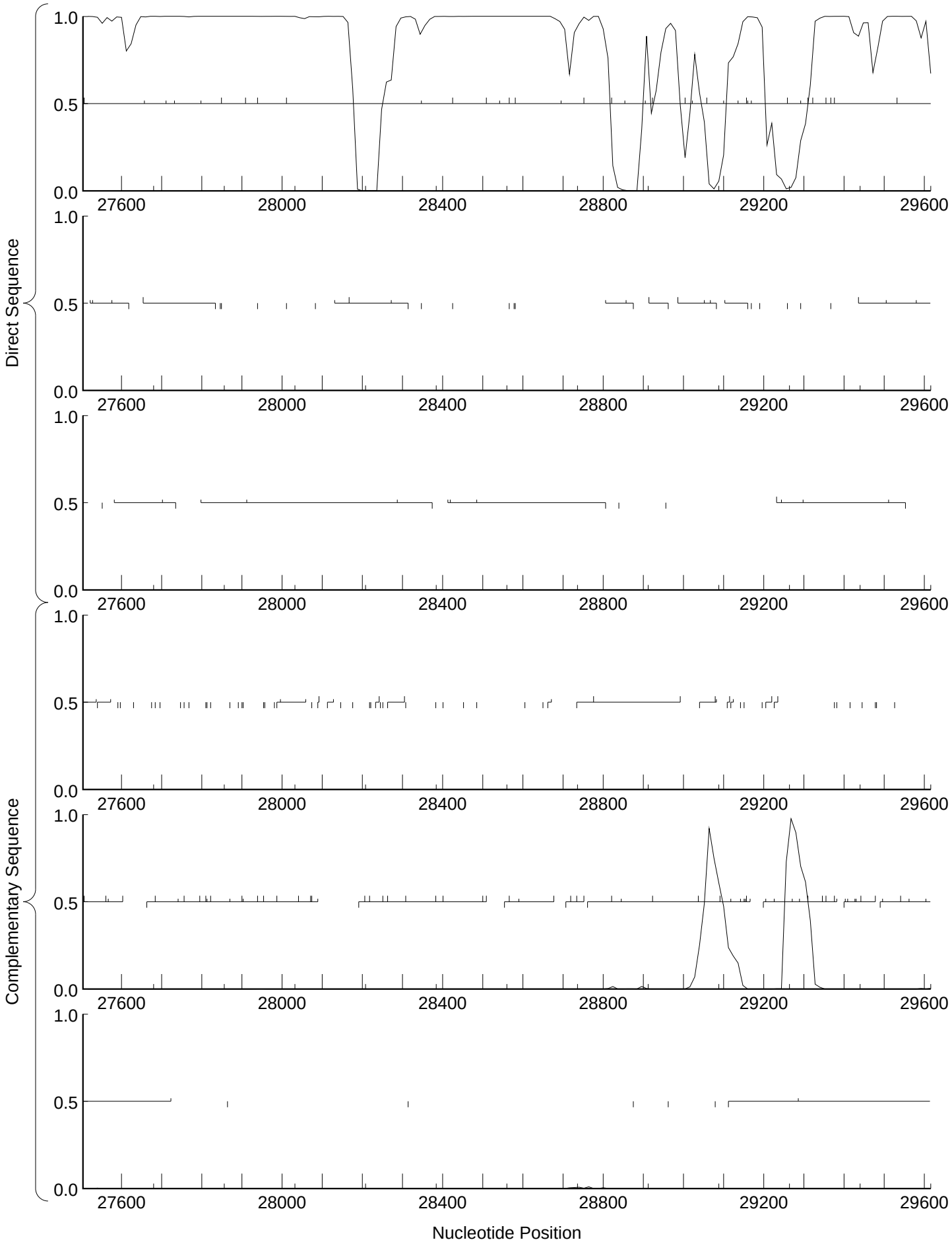

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
17200
17600
18000
18400
18800
Nucleotide Position

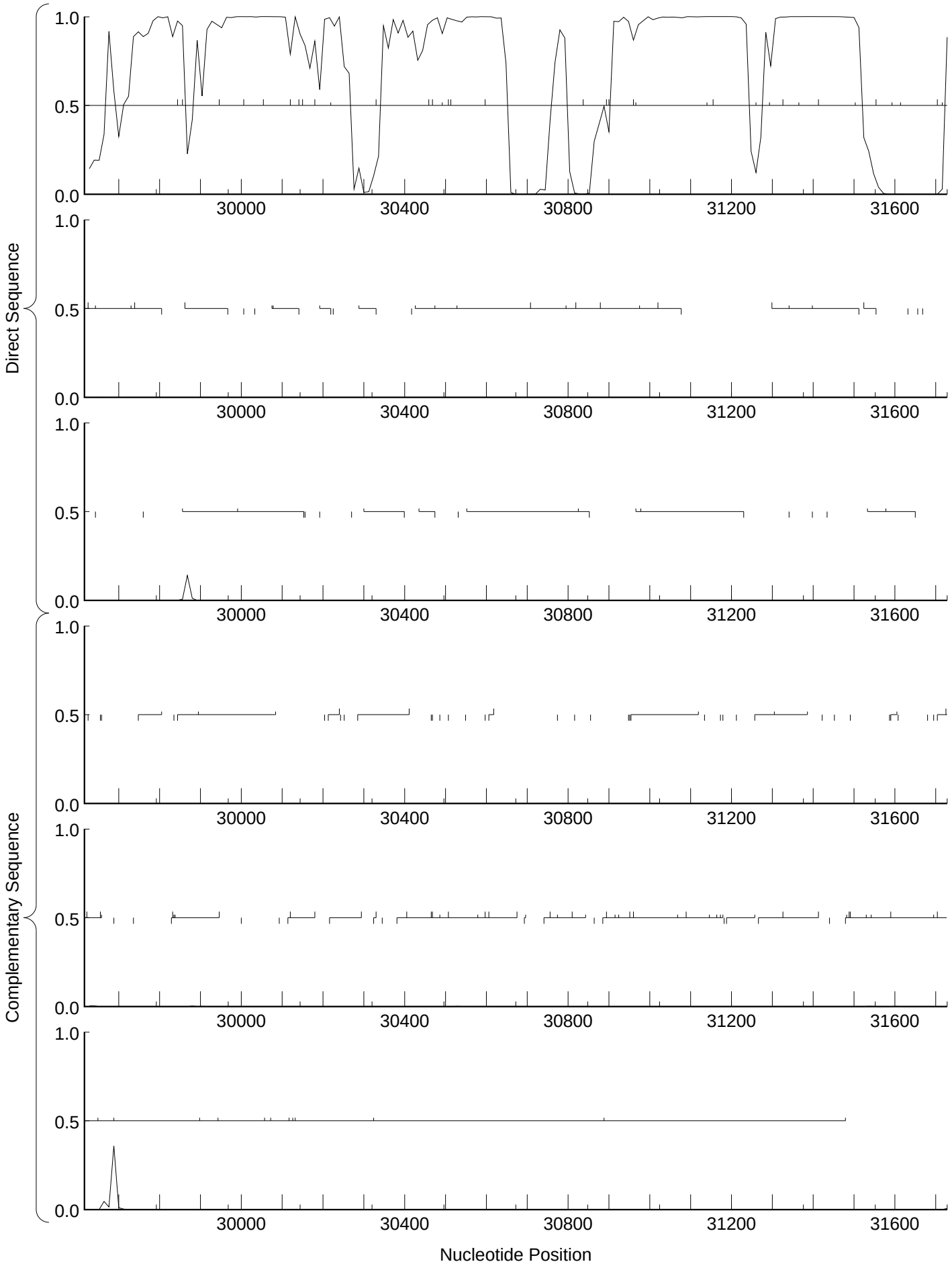

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
19200
19600
20000
20400
20800
Nucleotide Position

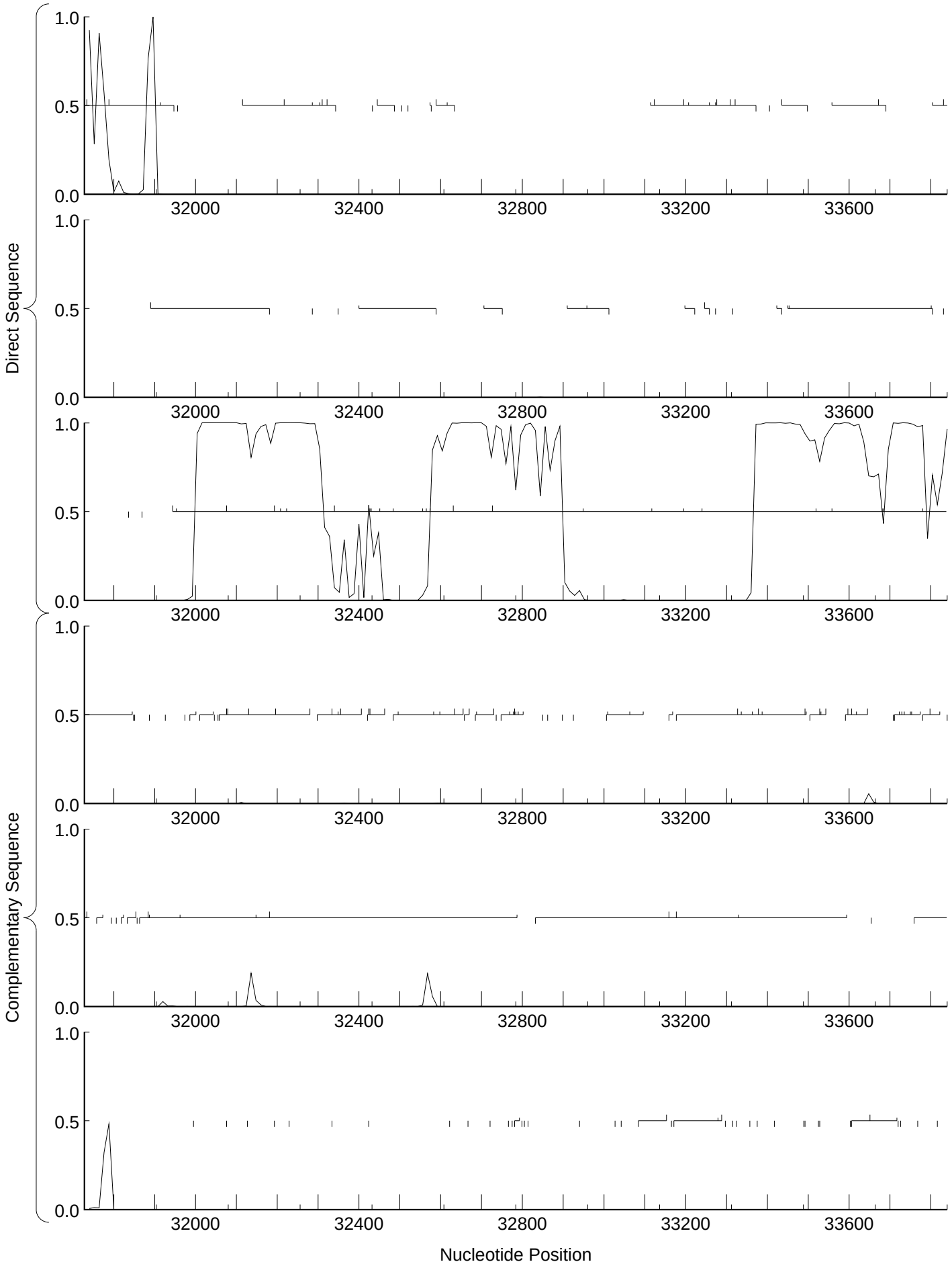

Direct Sequence
Complementary Sequence
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0.5
0.0
21200
21600
22000
22400
22800
23200
Nucleotide Position

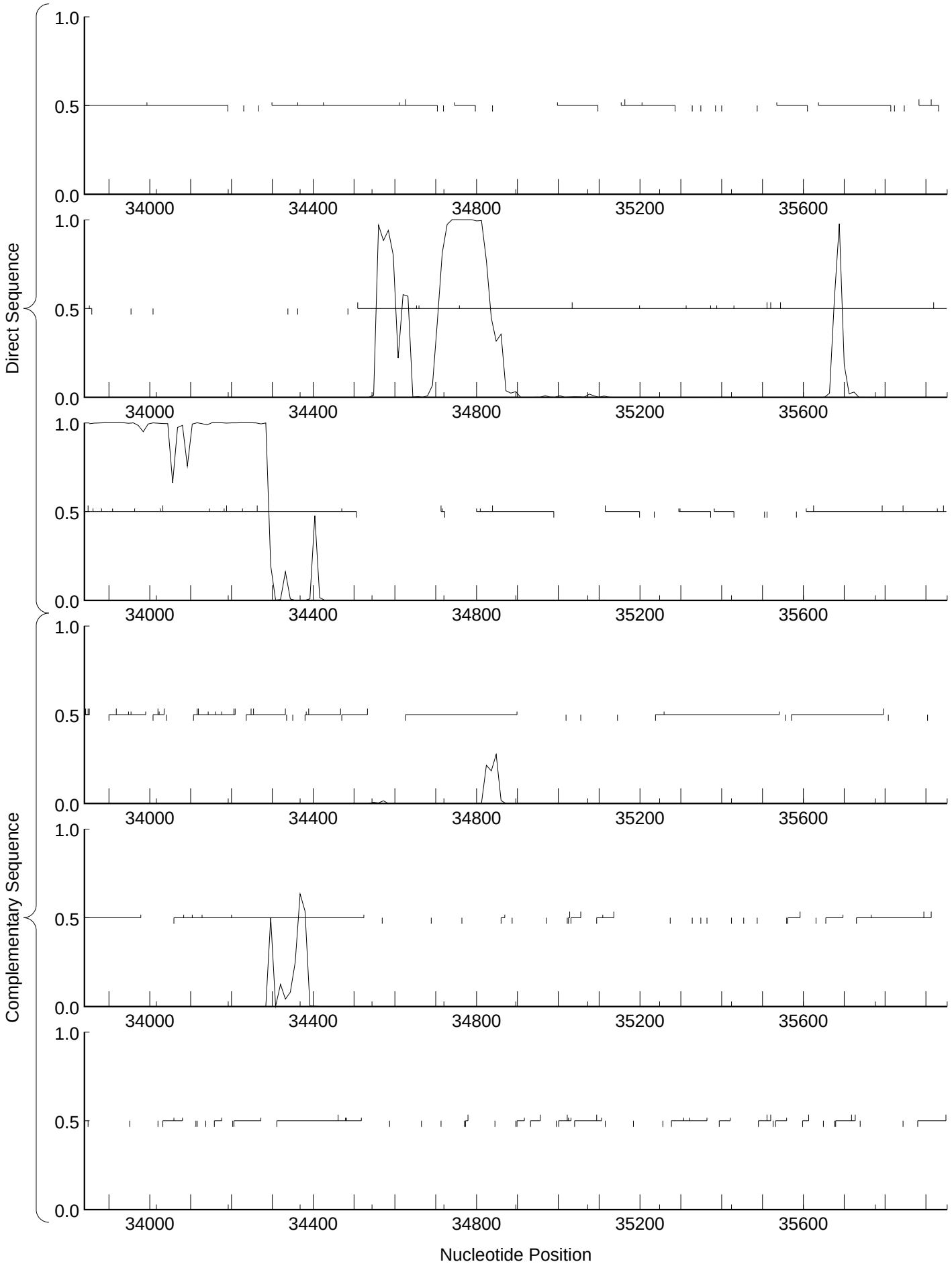

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
23600
24000
24400
24800
25200
Nucleotide Position

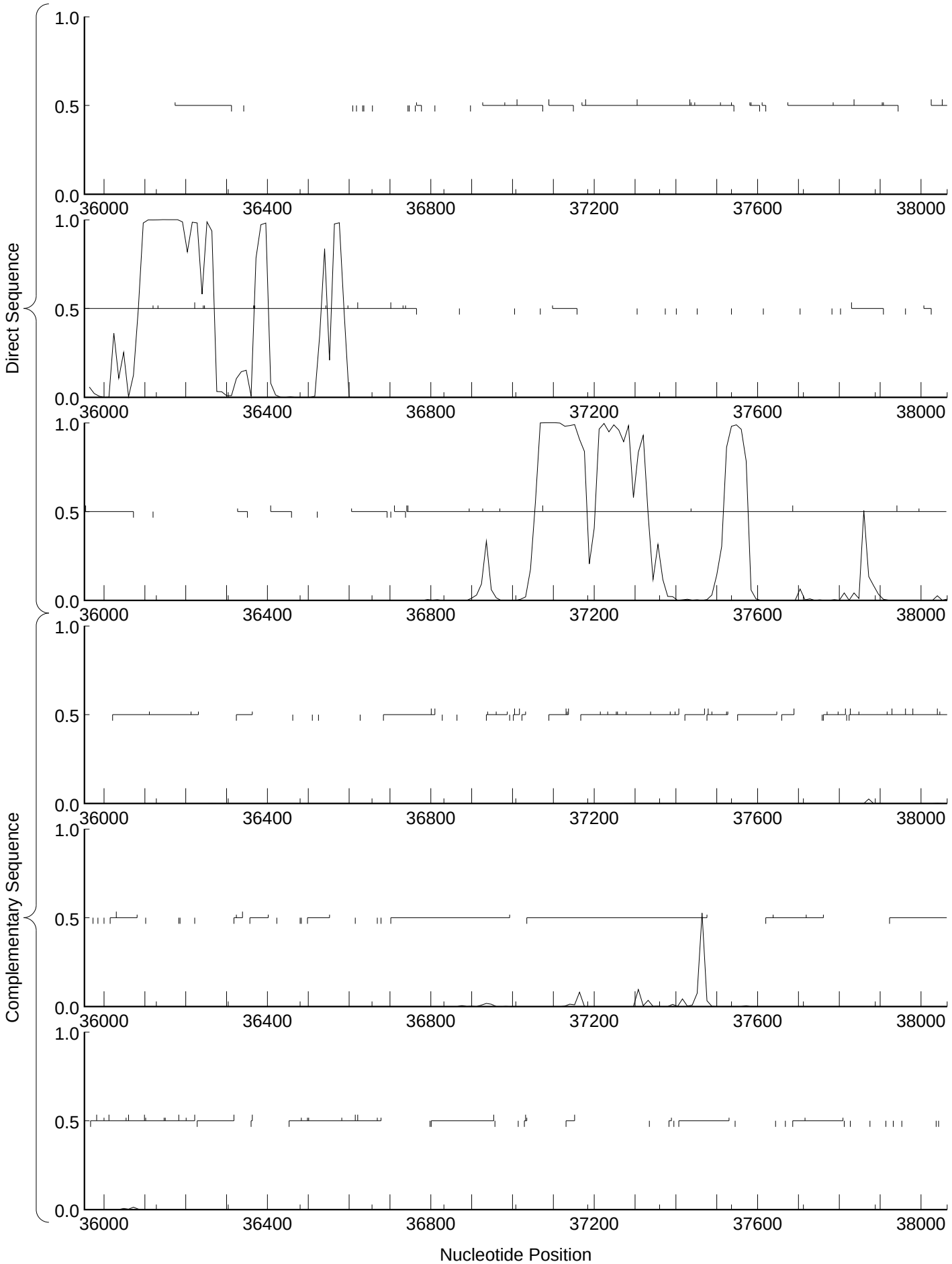

Direct Sequence
Complementary Sequence
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0.0
25600
26000
26400
26800
27200
Nucleotide Position

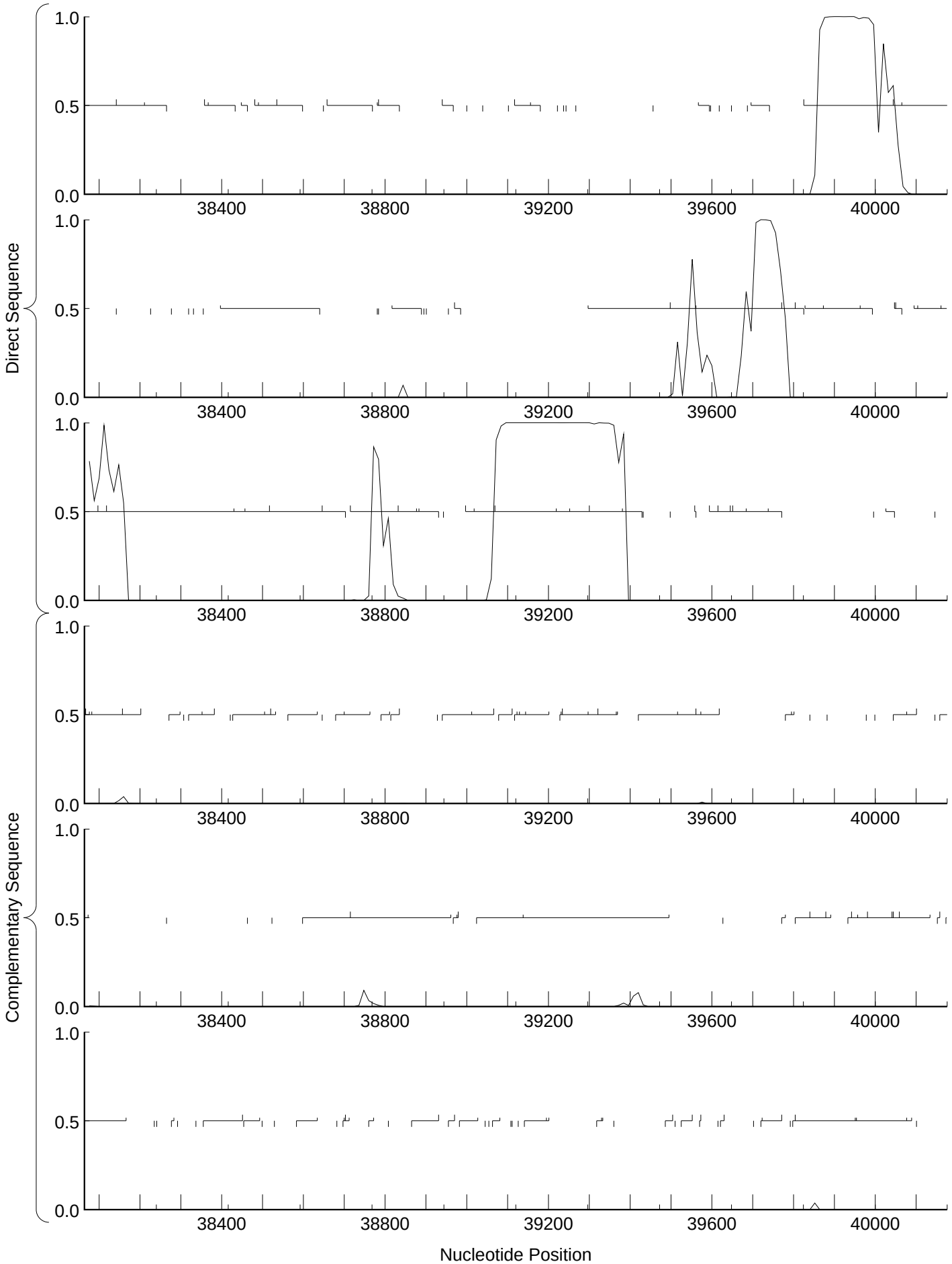

Direct Sequence
Complementary Sequence
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0.0
27600
28000
28400
28800
29200
29600
Nucleotide Position

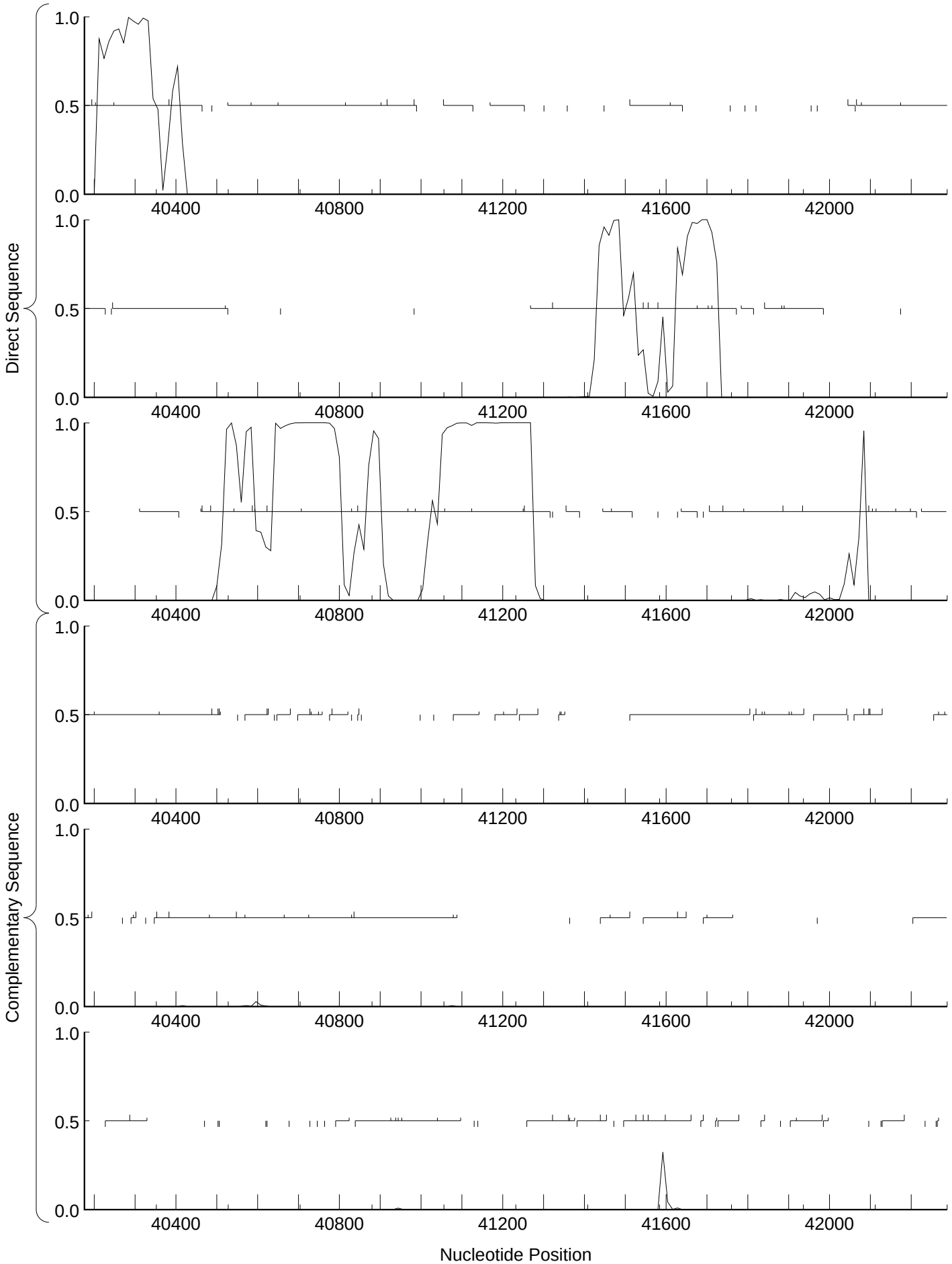

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Complementary Sequence
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0.0
30000
30400
30800
31200
31600
Nucleotide Position

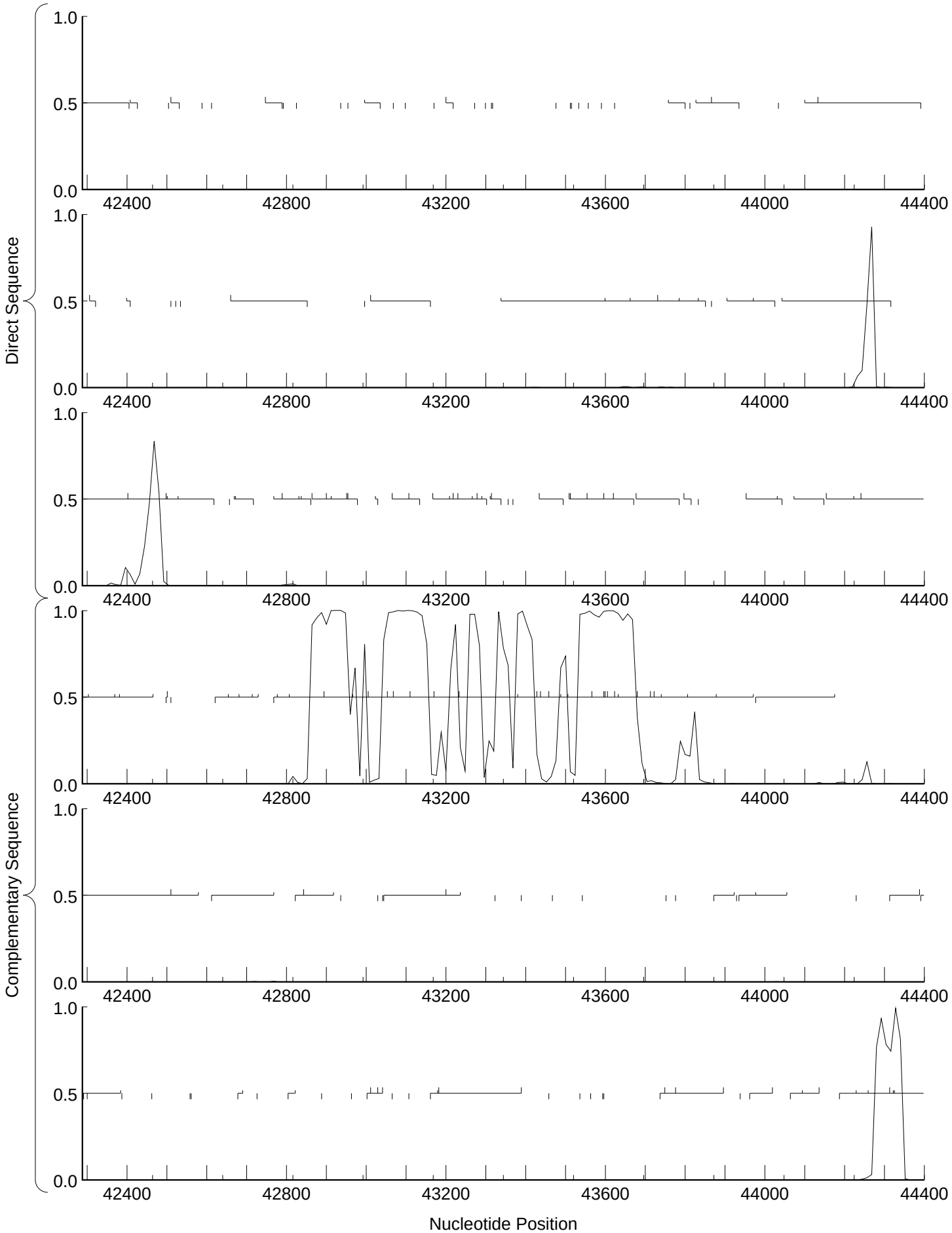

Direct Sequence
Complementary Sequence
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0.5
0.0
32000
32400
32800
33200
33600
Nucleotide Position

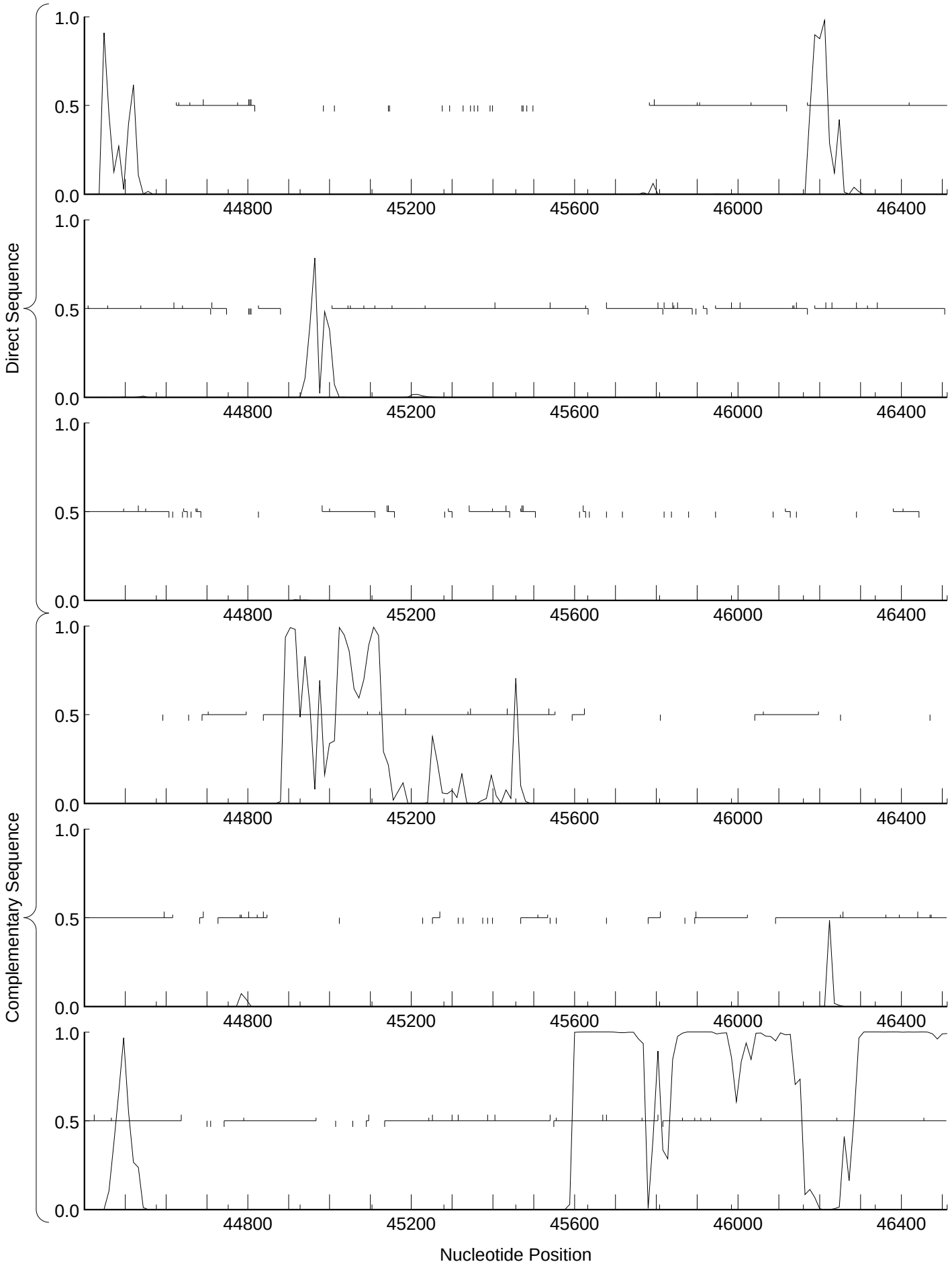

Direct Sequence
Complementary Sequence
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0.5
0.0
34000
34400
34800
35200
35600
Nucleotide Position

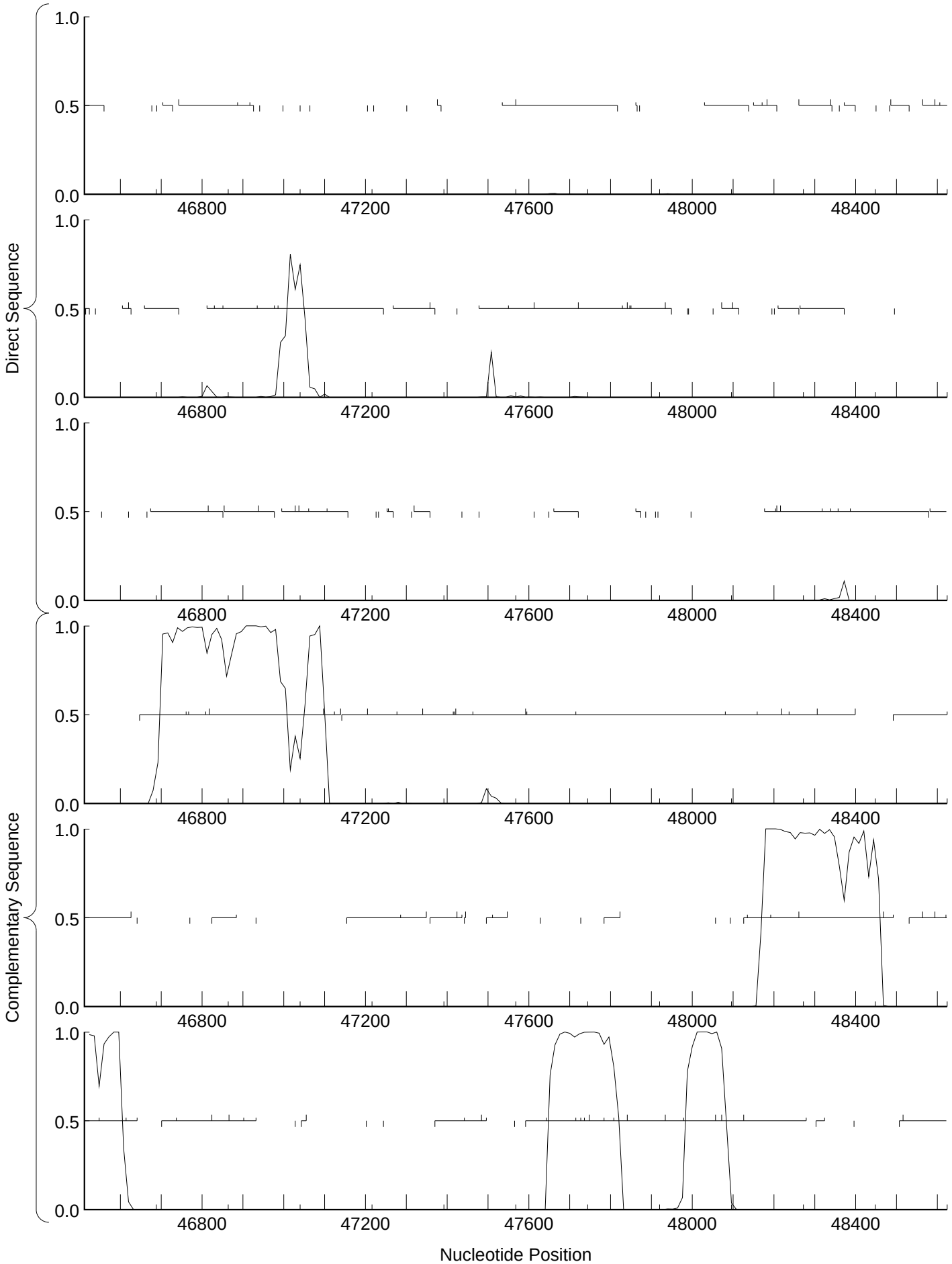

Direct Sequence
Complementary Sequence
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0.5
0.0
36000
36400
36800
37200
37600
38000
Nucleotide Position

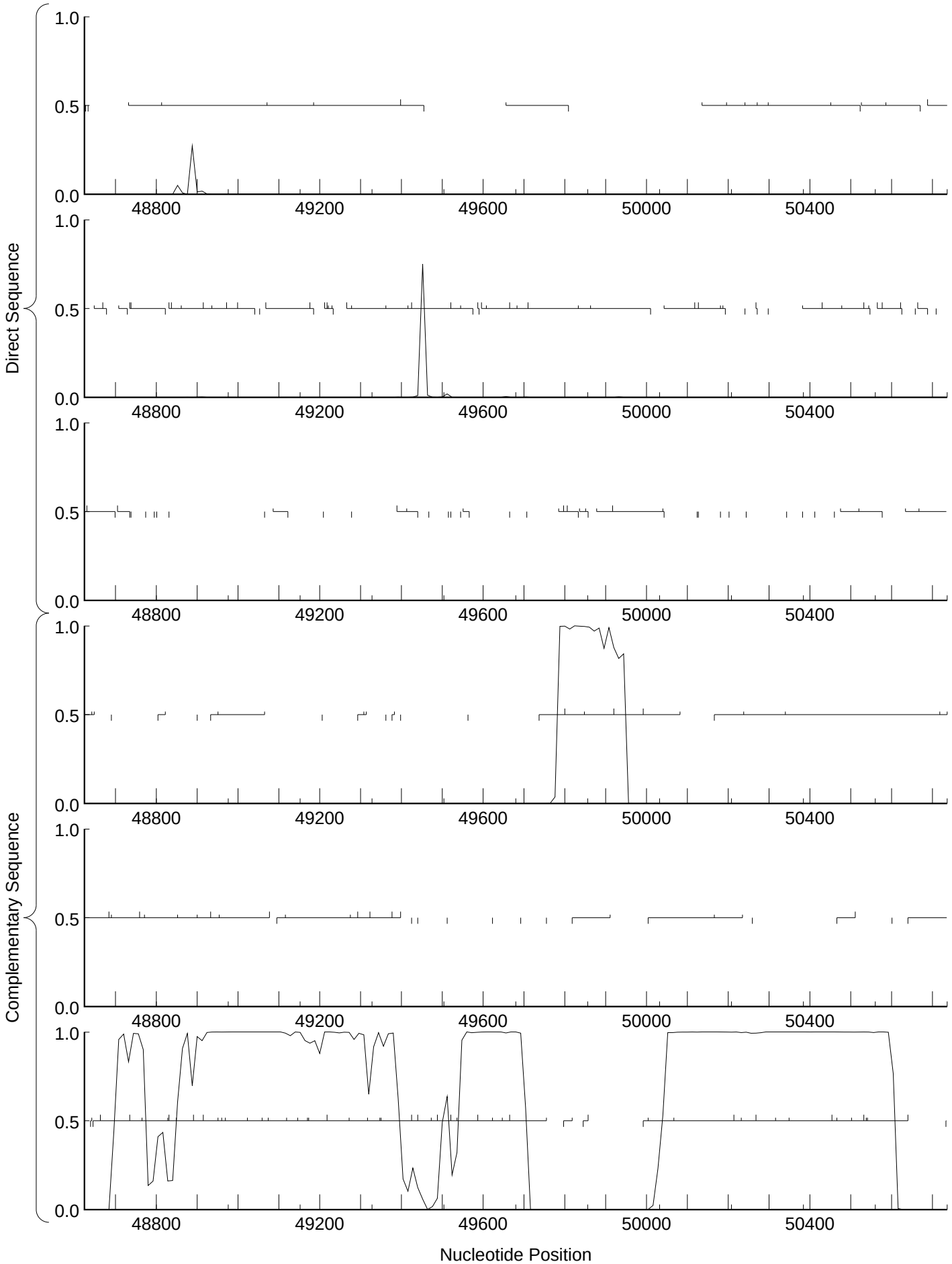

Direct Sequence
Complementary Sequence
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0.0
38400
38800
39200
39600
40000
Nucleotide Position

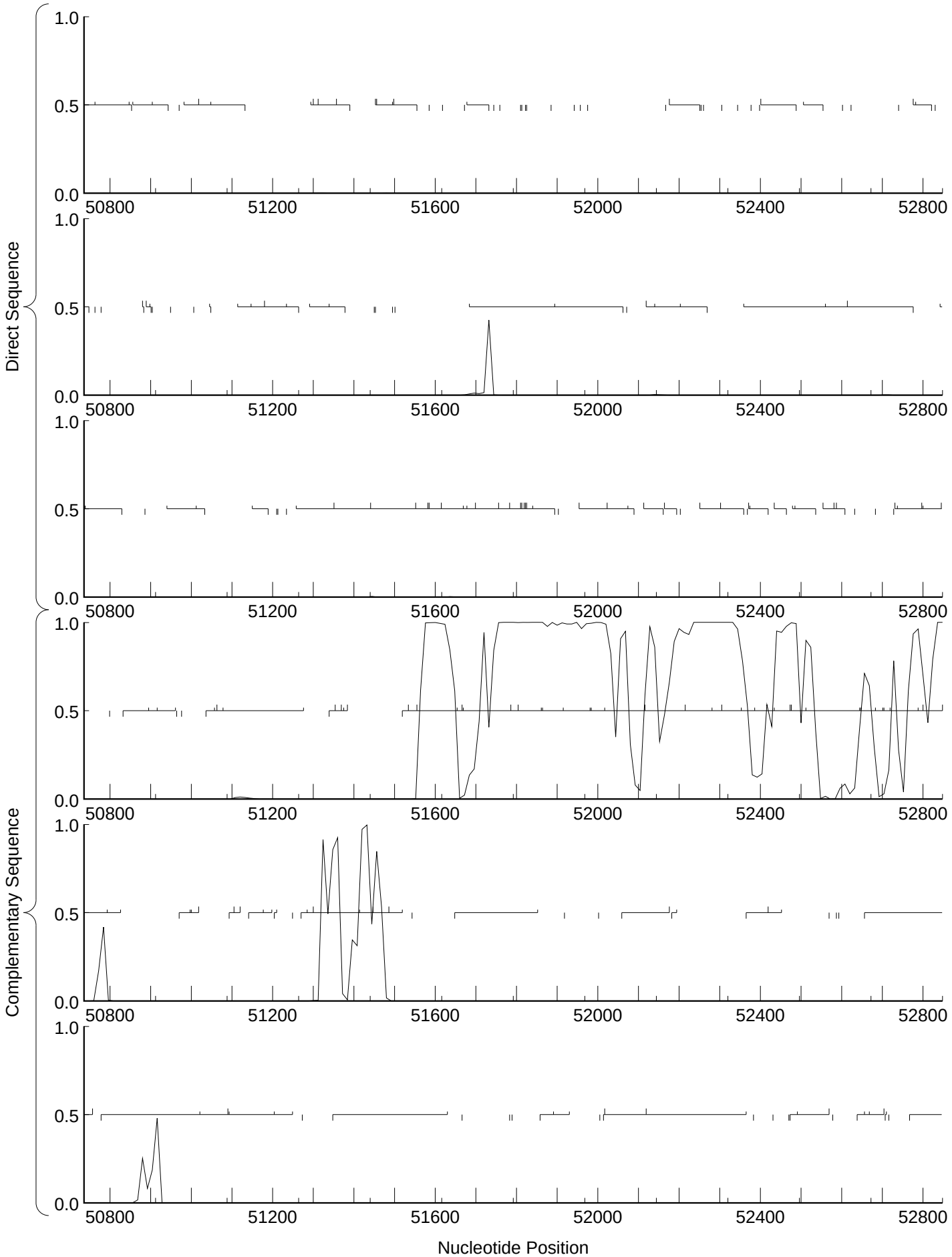

Direct Sequence
Complementary Sequence
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0.0
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41200
41600
42000
Nucleotide Position

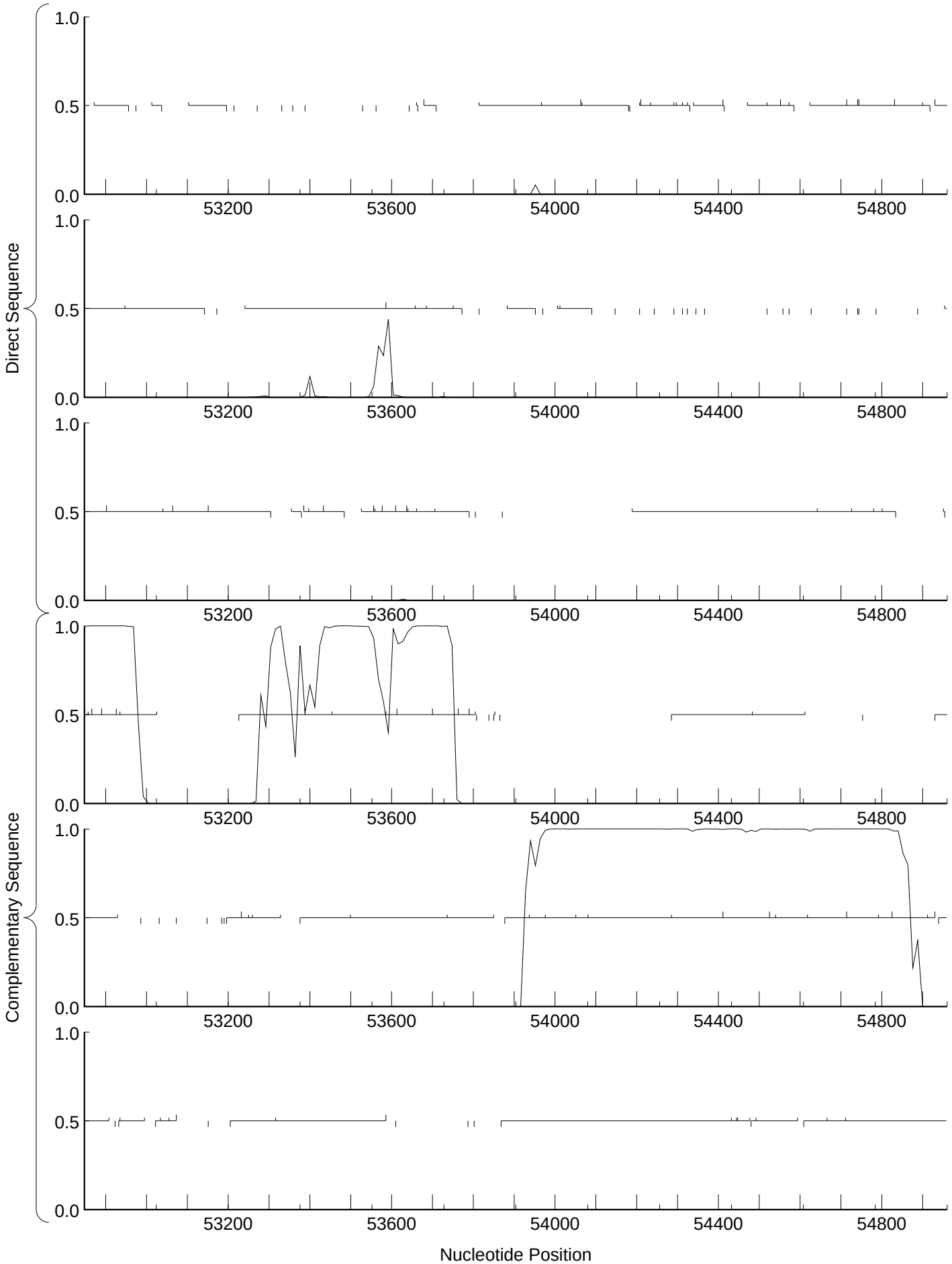

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Complementary Sequence
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0.0
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44000
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Nucleotide Position

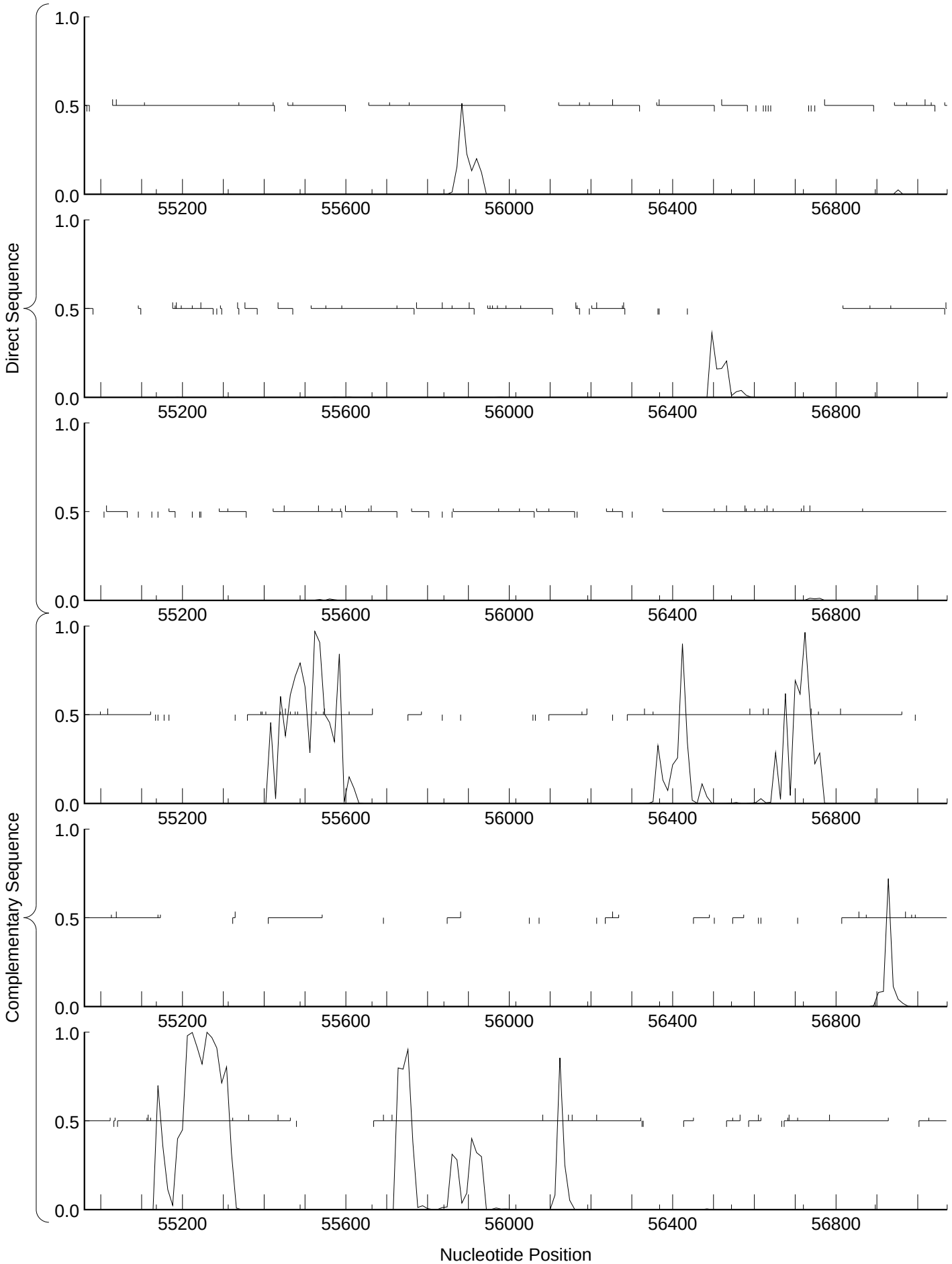

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Complementary Sequence
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45600
46000
46400
Nucleotide Position

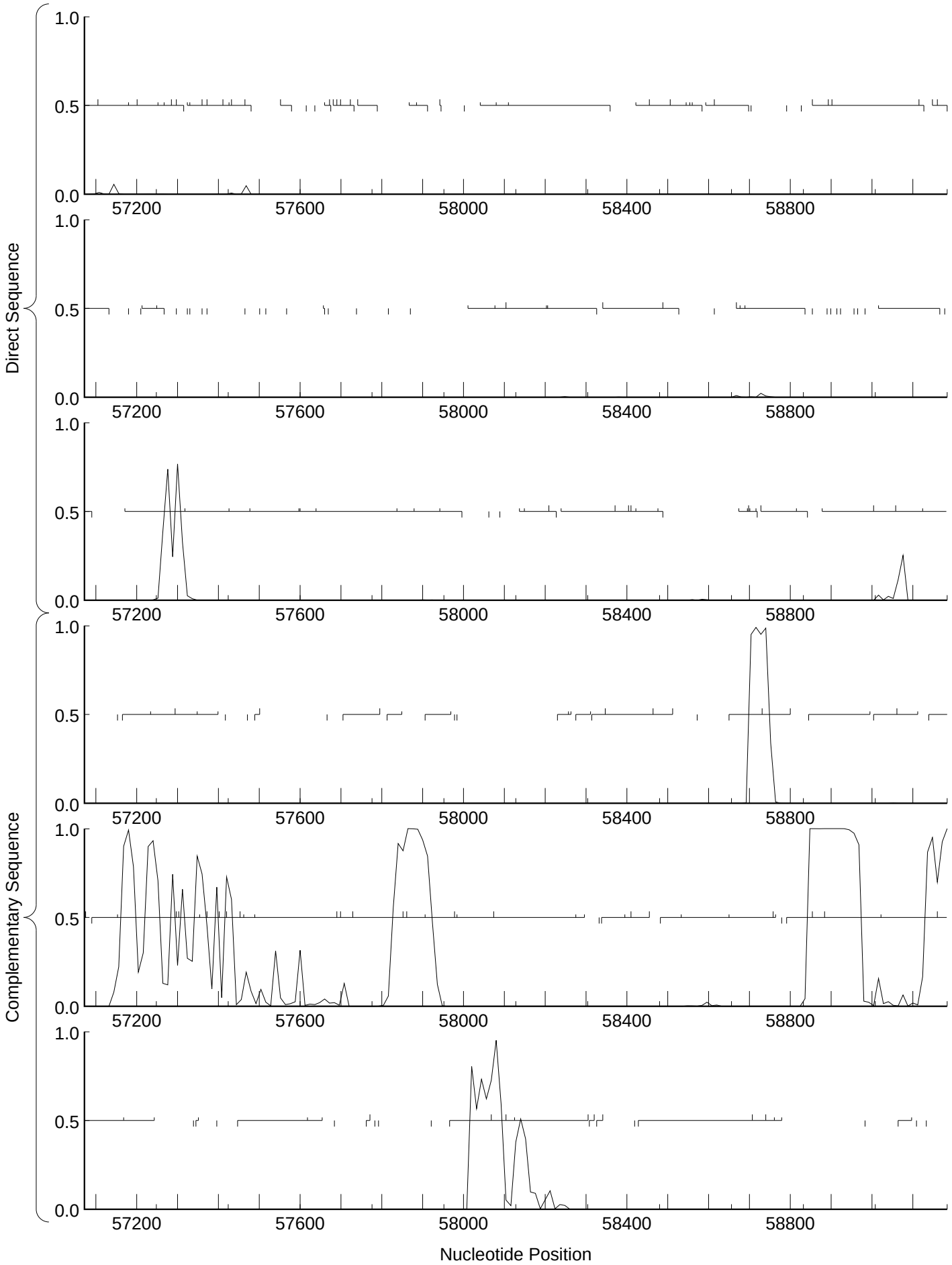

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Complementary Sequence
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0.0
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47200
47600
48000
48400
Nucleotide Position

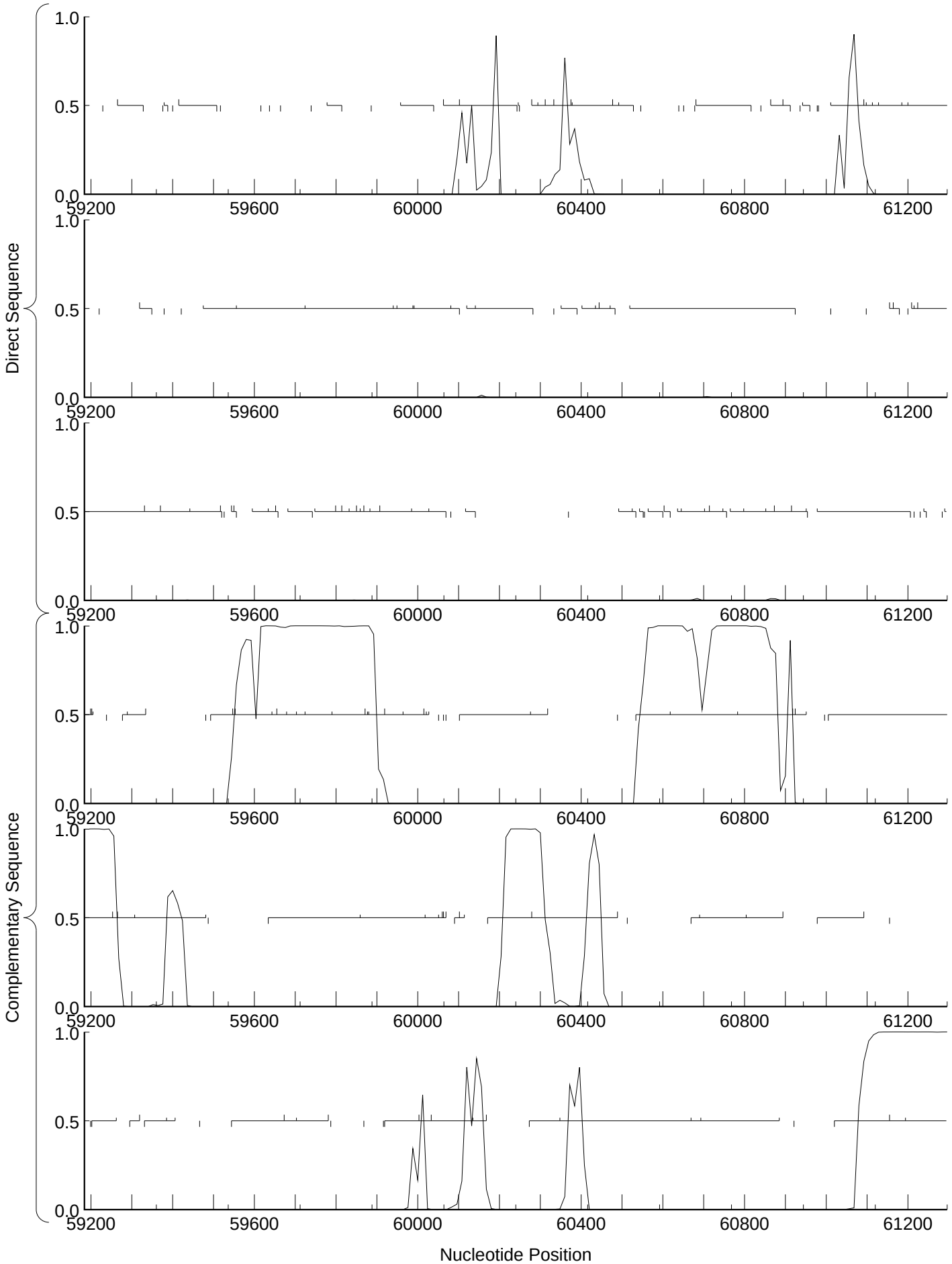

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Complementary Sequence
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0.0
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50000
50400
Nucleotide Position

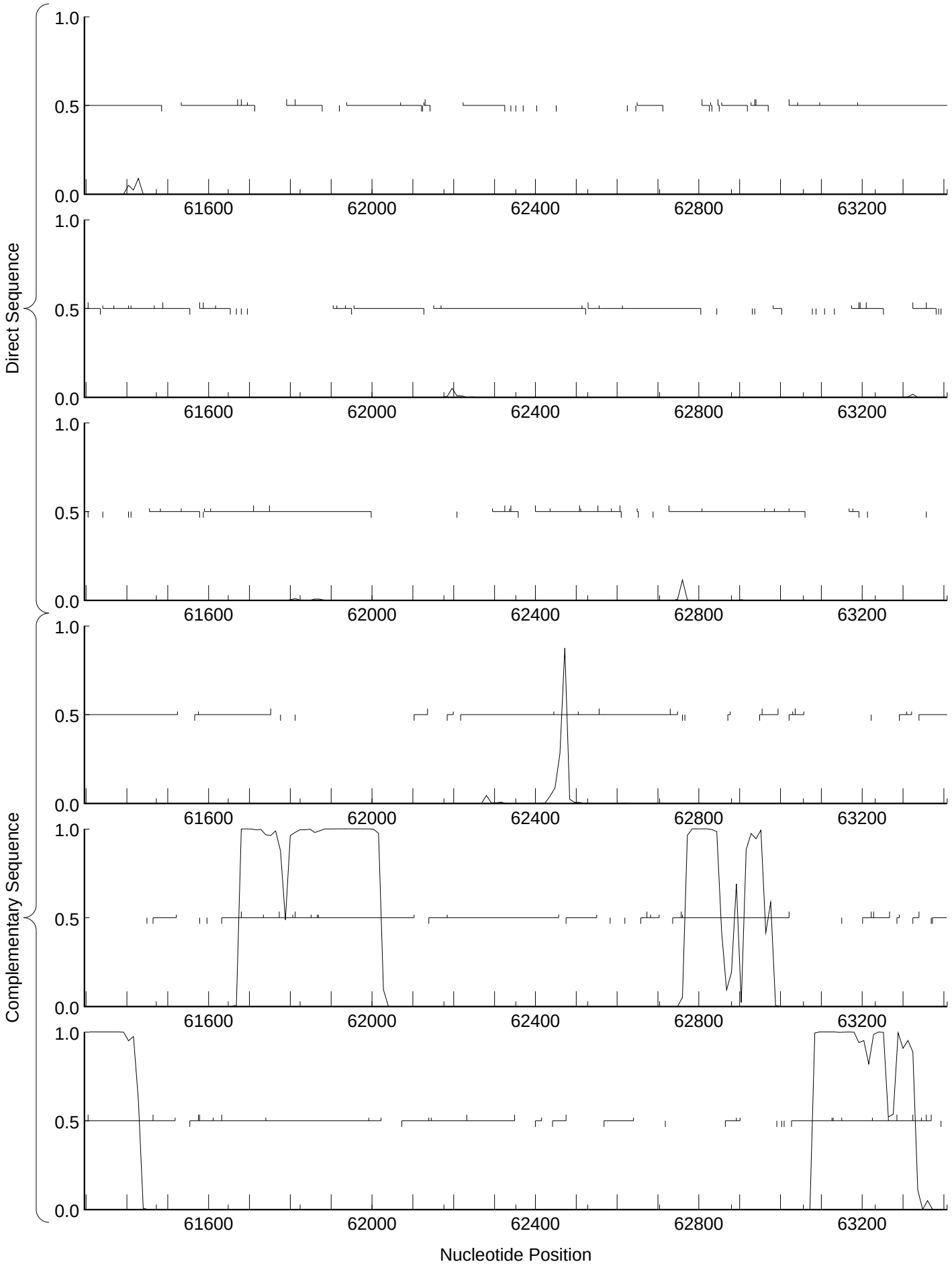

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Complementary Sequence
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0.0
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51200
51600
52000
52400
52800
Nucleotide Position

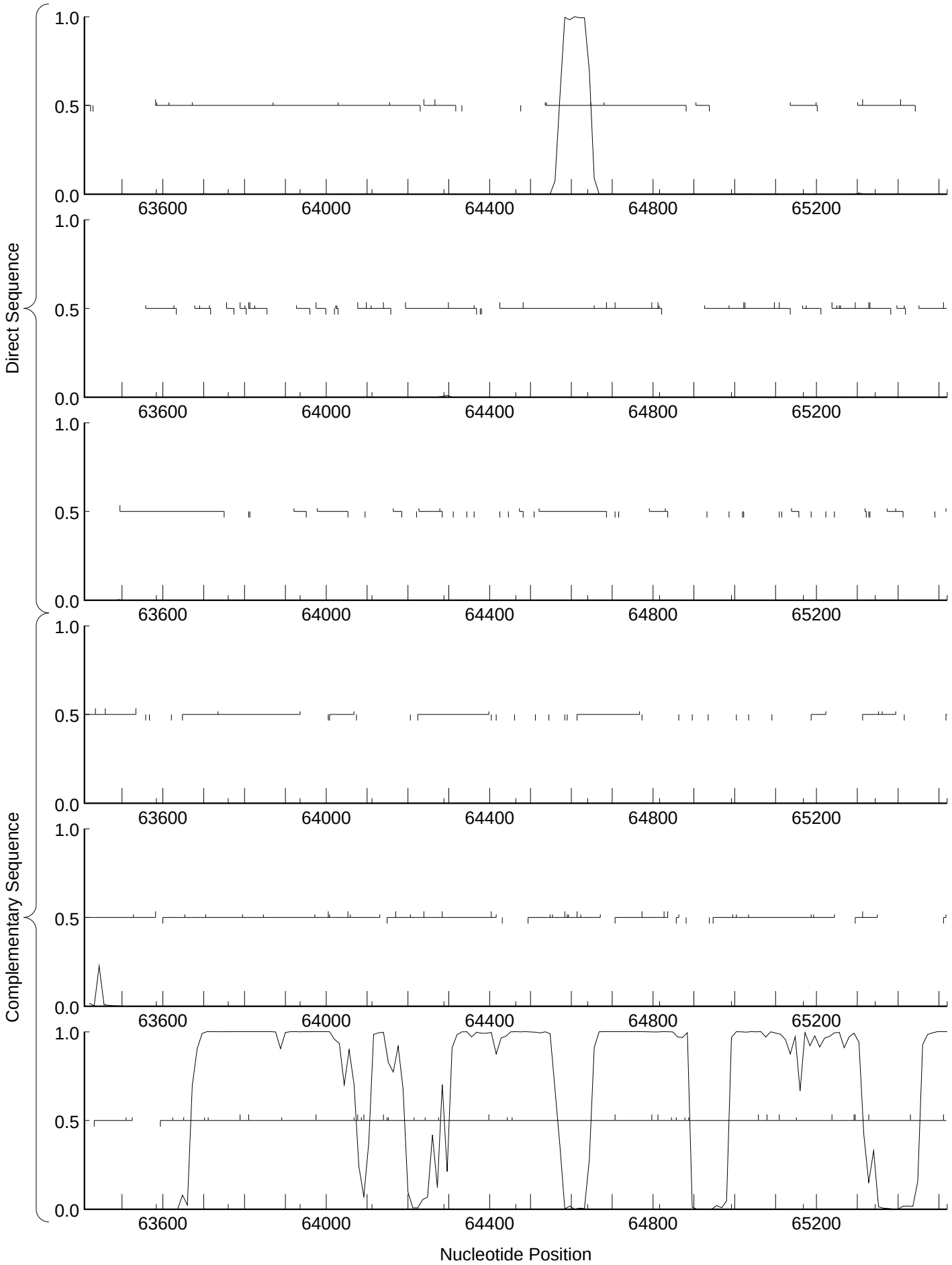

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Complementary Sequence
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54400
54800
Nucleotide Position

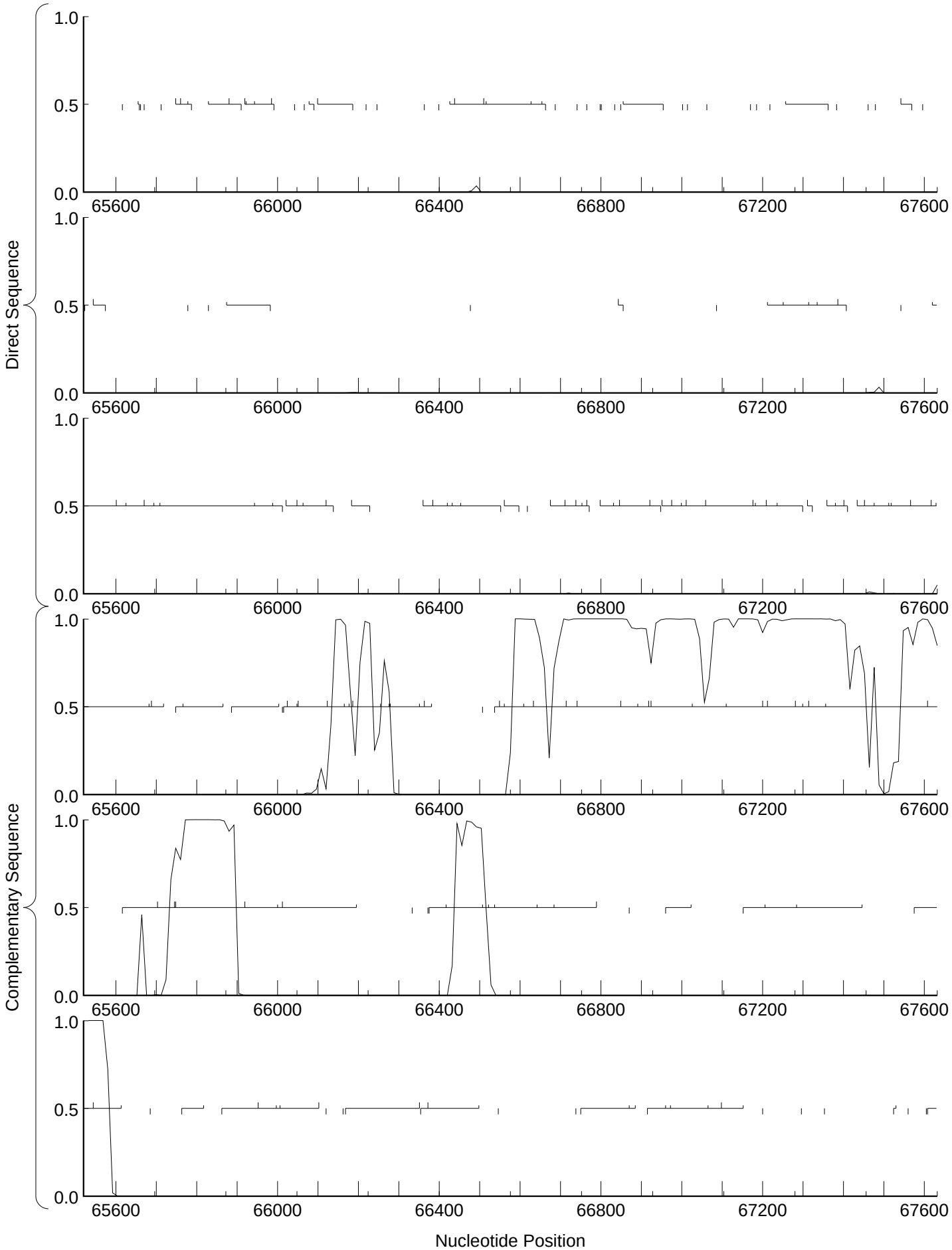

Direct Sequence
Complementary Sequence
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0.0
55200
55600
56000
56400
56800
Nucleotide Position

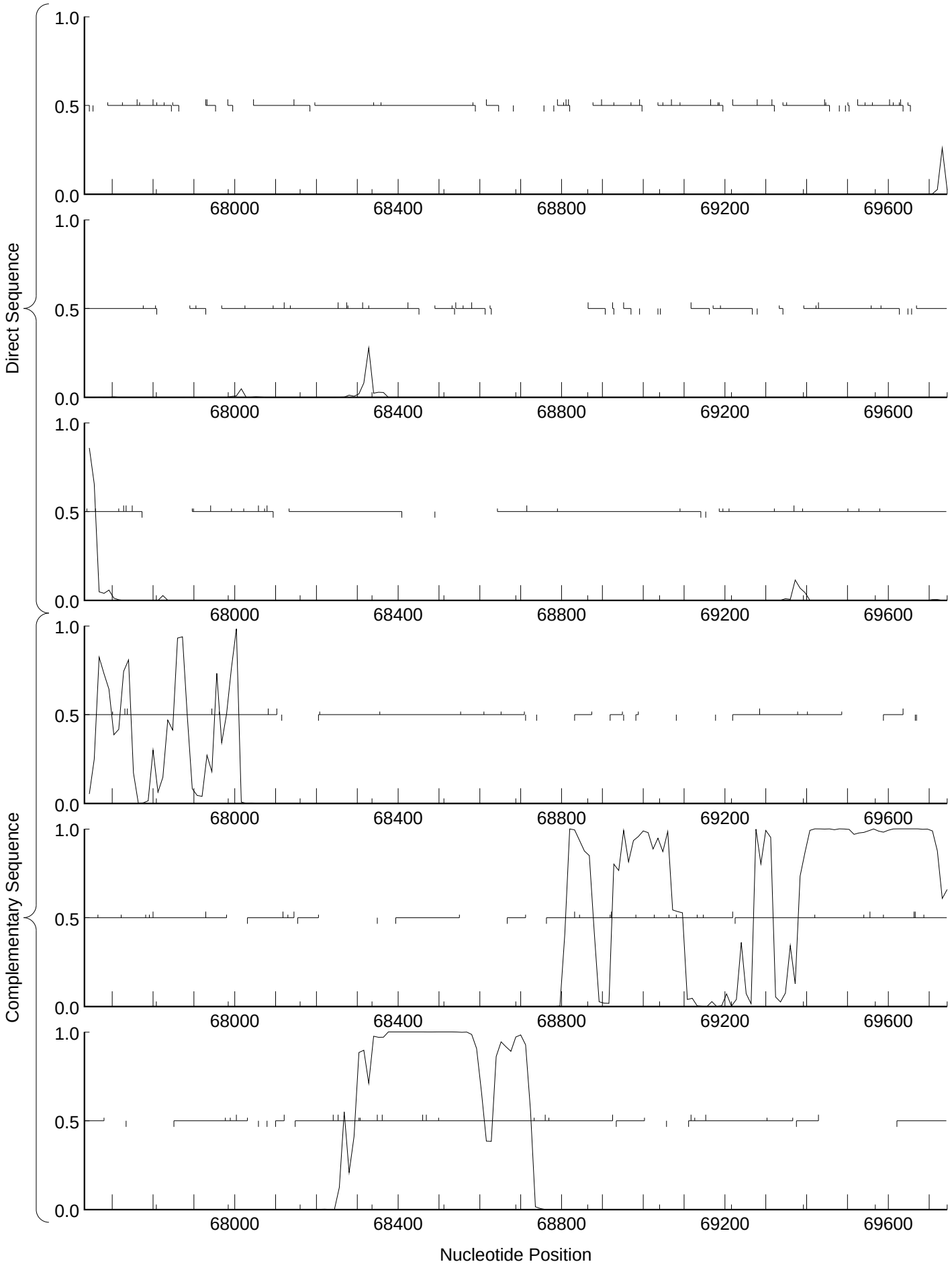

Direct Sequence
Complementary Sequence
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57600
58000
58400
58800
Nucleotide Position

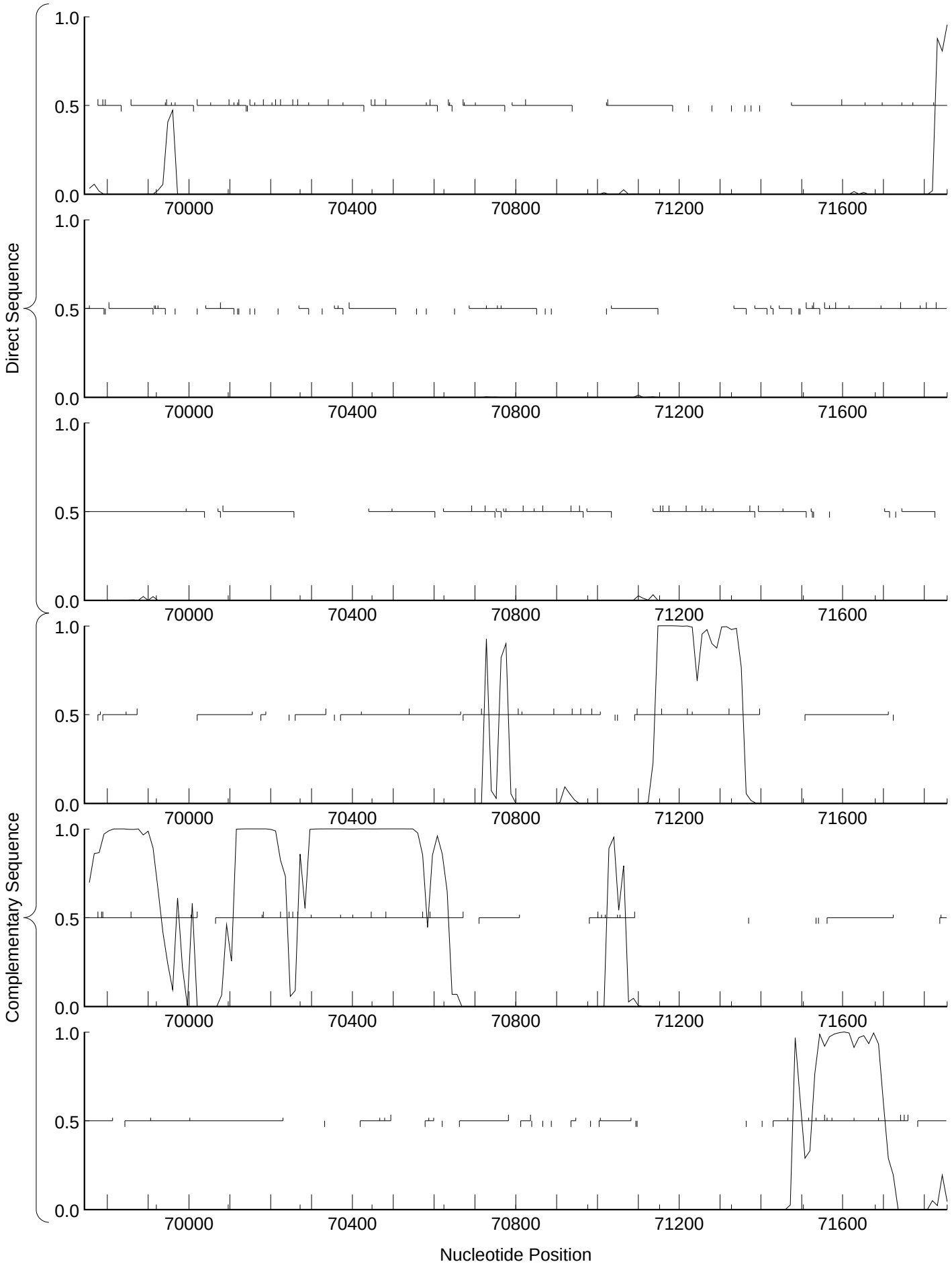

Direct Sequence
Complementary Sequence
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0.5
0.0
59200
59600
60000
60400
60800
61200
Nucleotide Position

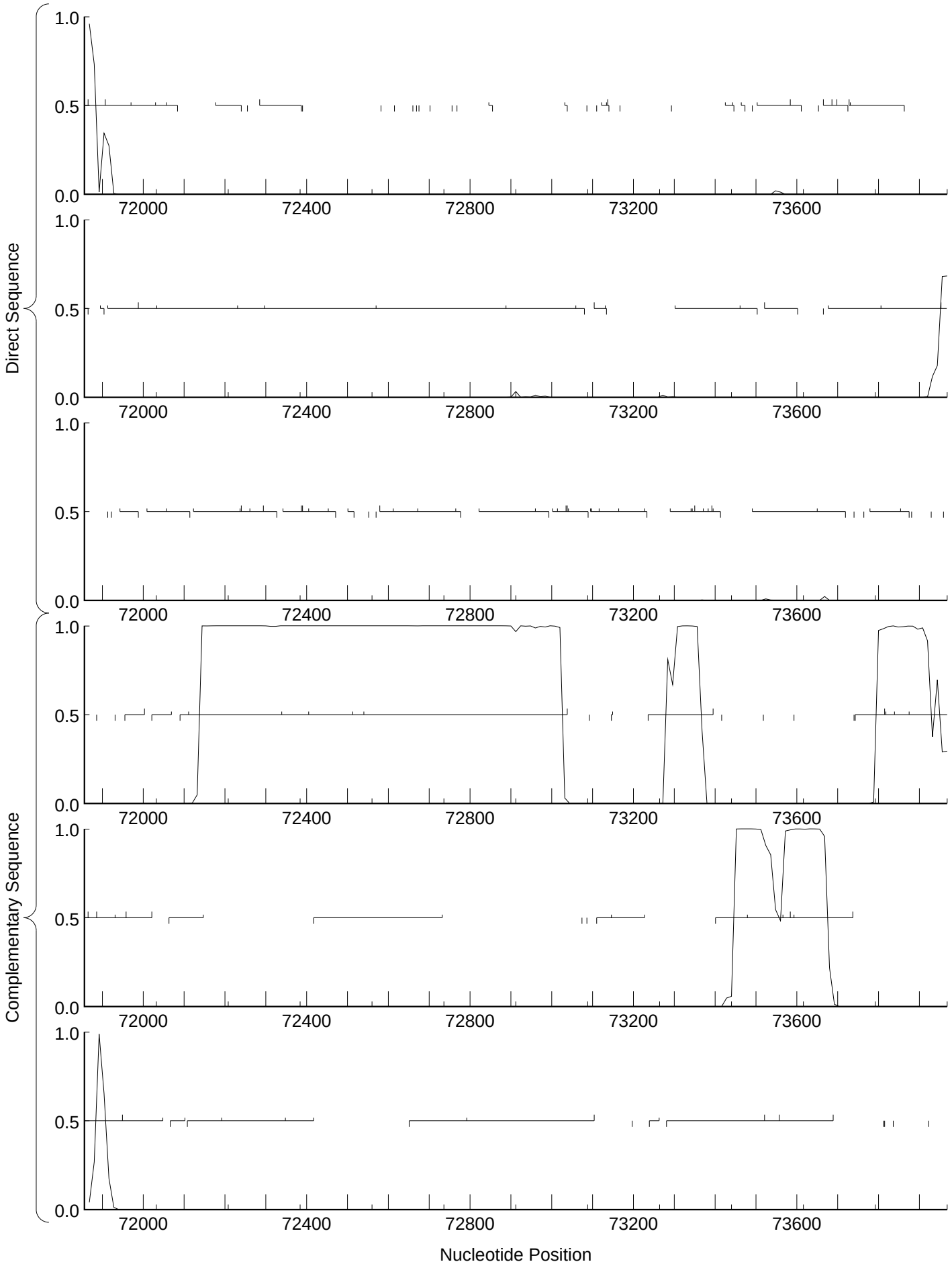

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
61600
62000
62400
62800
63200
Nucleotide Position


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


Direct Sequence
Complementary Sequence
1.0
0.5
0.0
65600
66000
66400
66800
67200
67600
Nucleotide Position


Direct Sequence
Complementary Sequence
1.0
0.5
0.0
68000
68400
68800
69200
69600
Nucleotide Position


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


Direct Sequence
Complementary Sequence
1.0
0.5
0.0
72000
72400
72800
73200
73600
Nucleotide Position

phage Tredge complete sequence, 75345 bp including 1173 bp terminal repeat, Cluster CS4, Order 4, Window 96, Step 12, 37/37
Direct Sequence
Complementary Sequence
1.0
0.5
0.0
74000
74400
74800
75200
75600
76000
Nucleotide Position