GeneMark

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

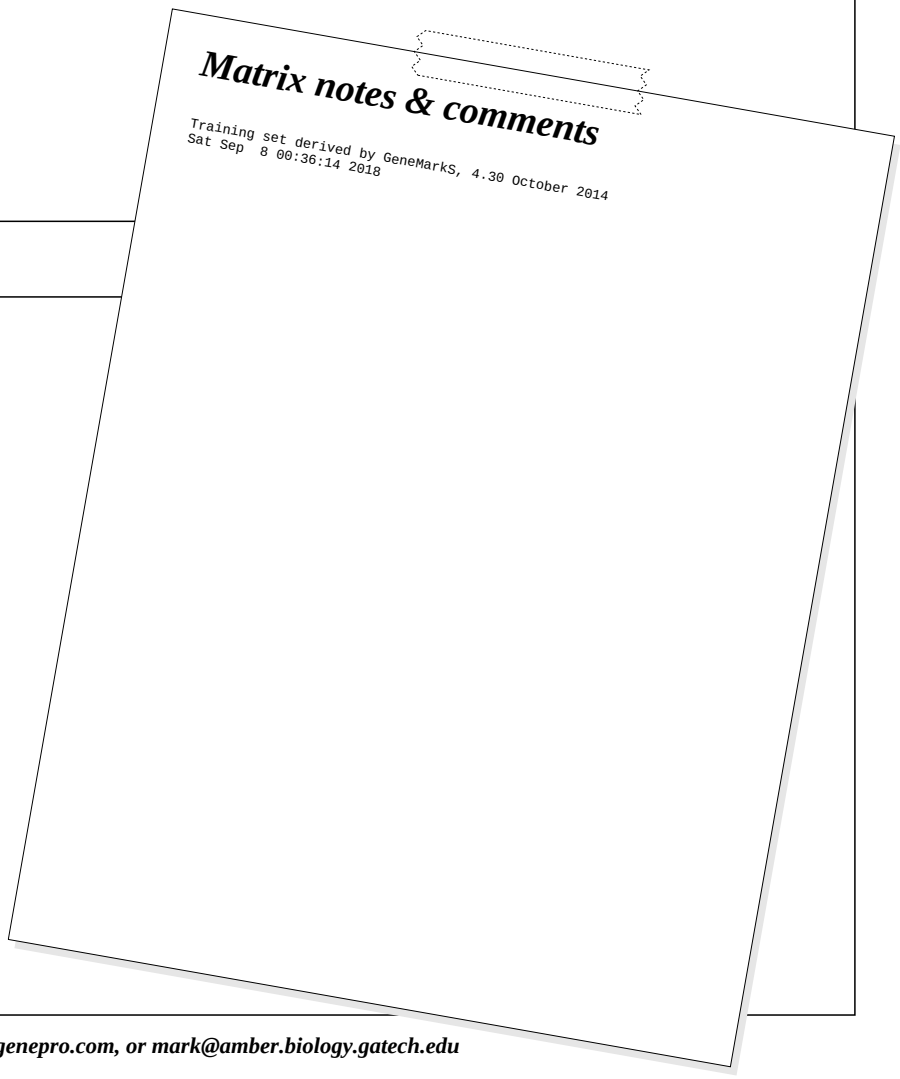
PROGRAM INFORMATION

```
Sequence         :  Gordonia phage Kvothe complete sequence, 75462 bp including 1172 bp terminal repeat, Cluste
Analysis Date    :  3/29/24 at 0:41:18
Pages            :  37
Sequence Length  :  75462 bp
GC Content       :   59.48%

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

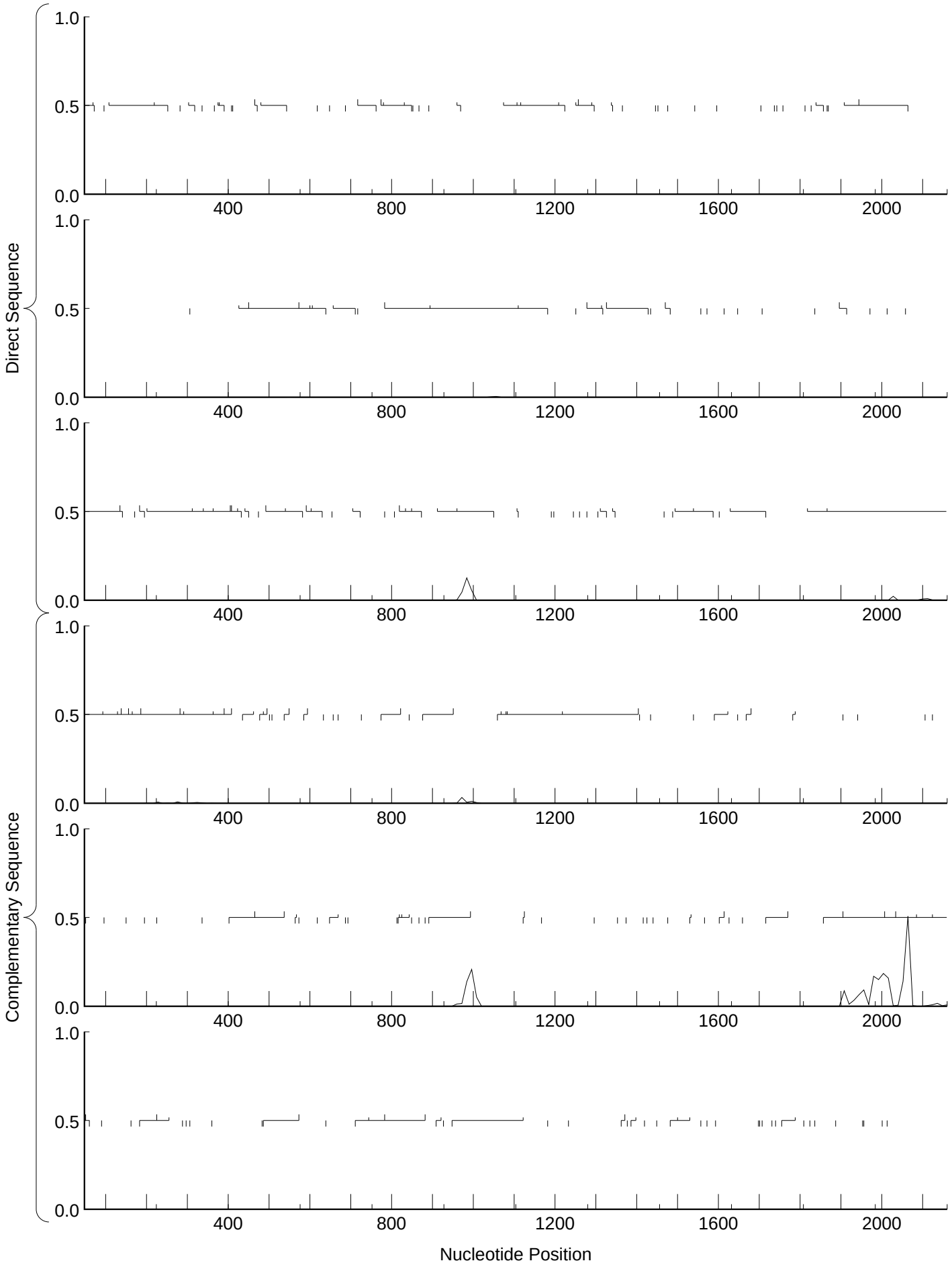
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Matrix     :  -
Author     :  -

Order      :  4
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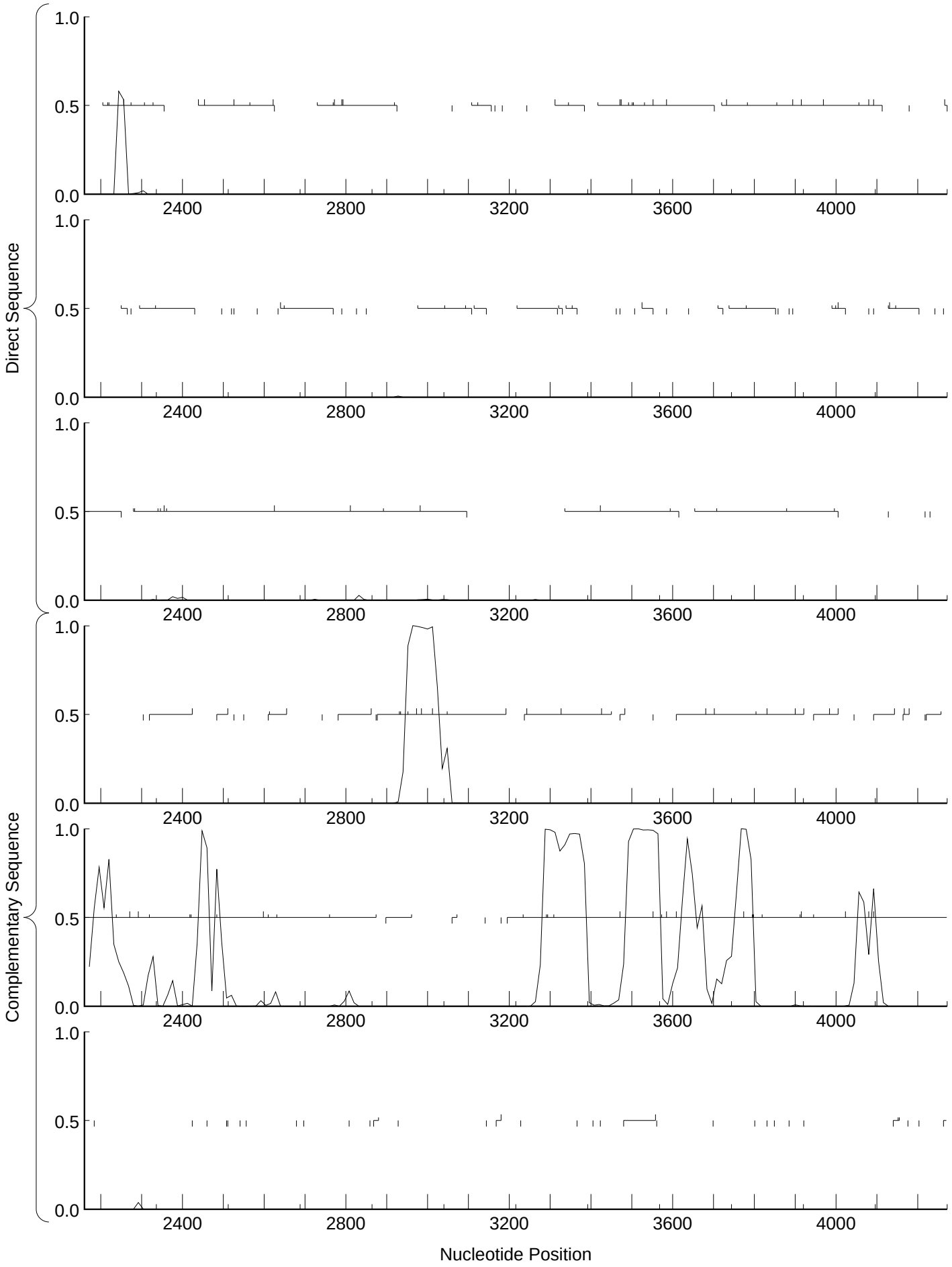

```
  Send questions / comments to:
      Dr. M. Borodovsky
      Georgia Institute of Technology
      School of Biology
      Atlanta, GA  30332-0230
```


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

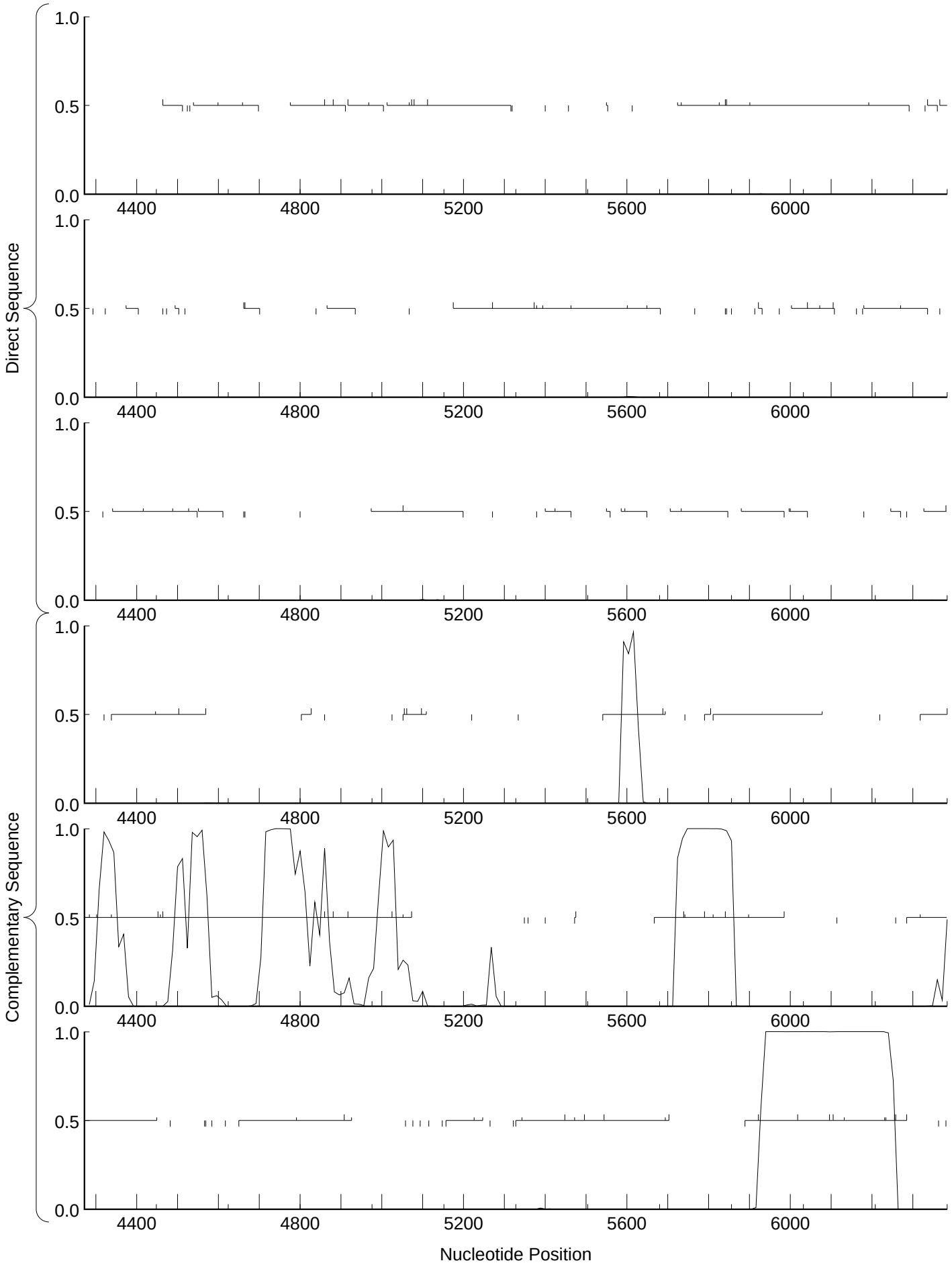
, phage Kvothe complete sequence, 75462 bp including 1172 bp terminal repeat, Cluster CS4, Order 4, Window 96, Step 12, 2/37

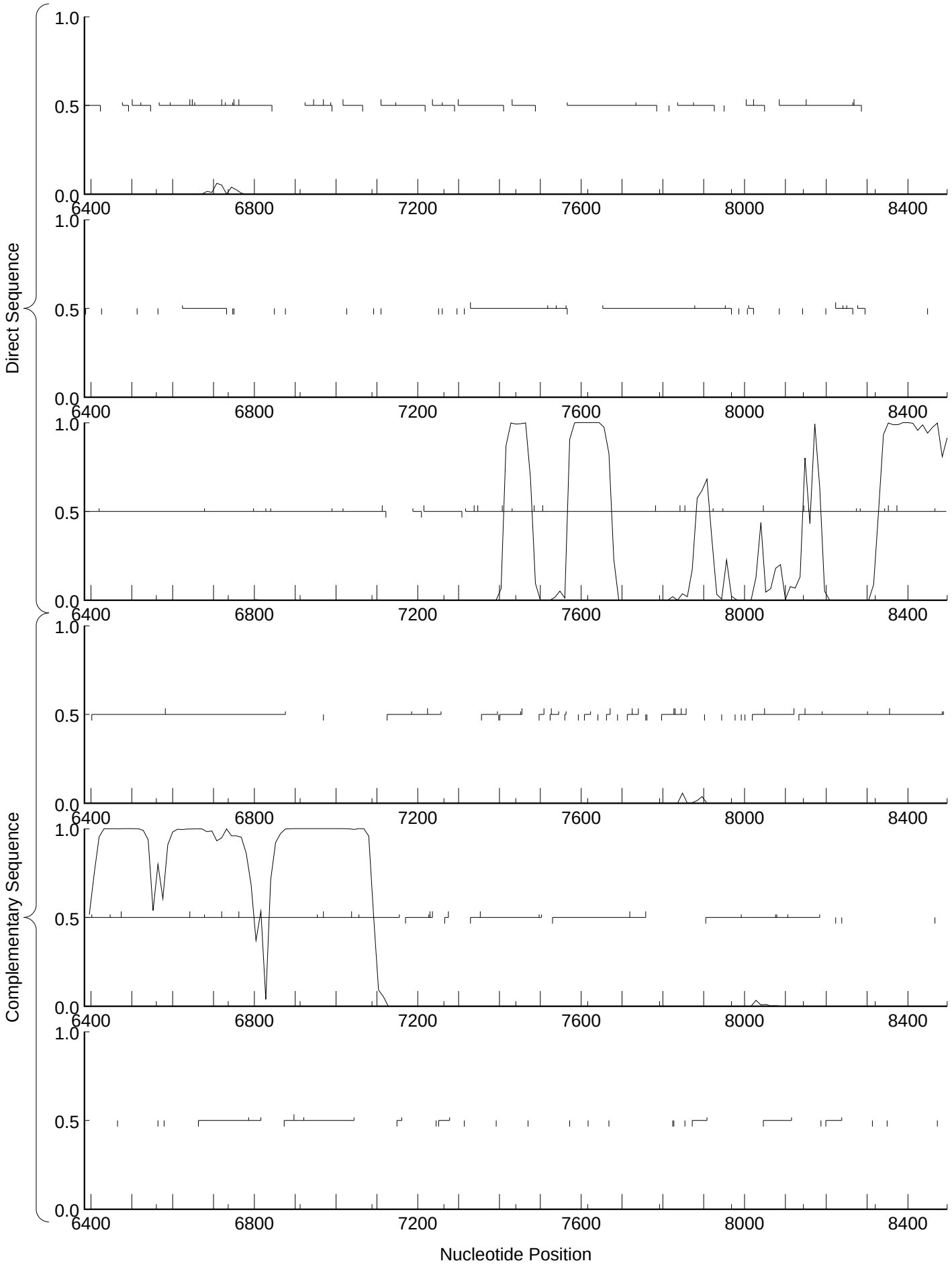


, phage Kvothe complete sequence, 75462 bp including 1172 bp terminal repeat, Cluster CS4, Order 4, Window 96, Step 12, 3/37

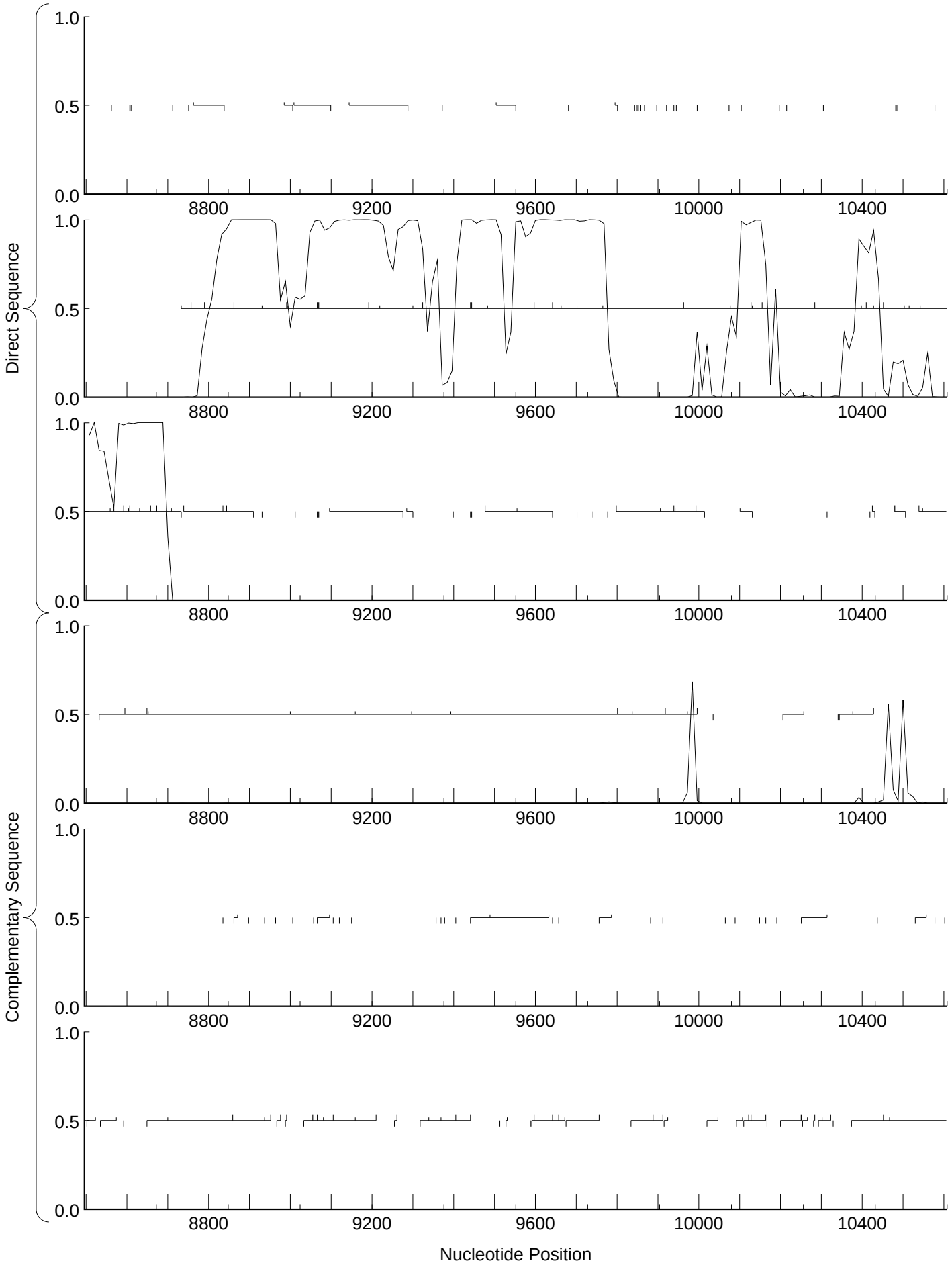


phage Kvothe complete sequence, 75462 bp including 1172 bp terminal repeat, Cluster CS4, Order 4, Window 96, Step 12, 4/37

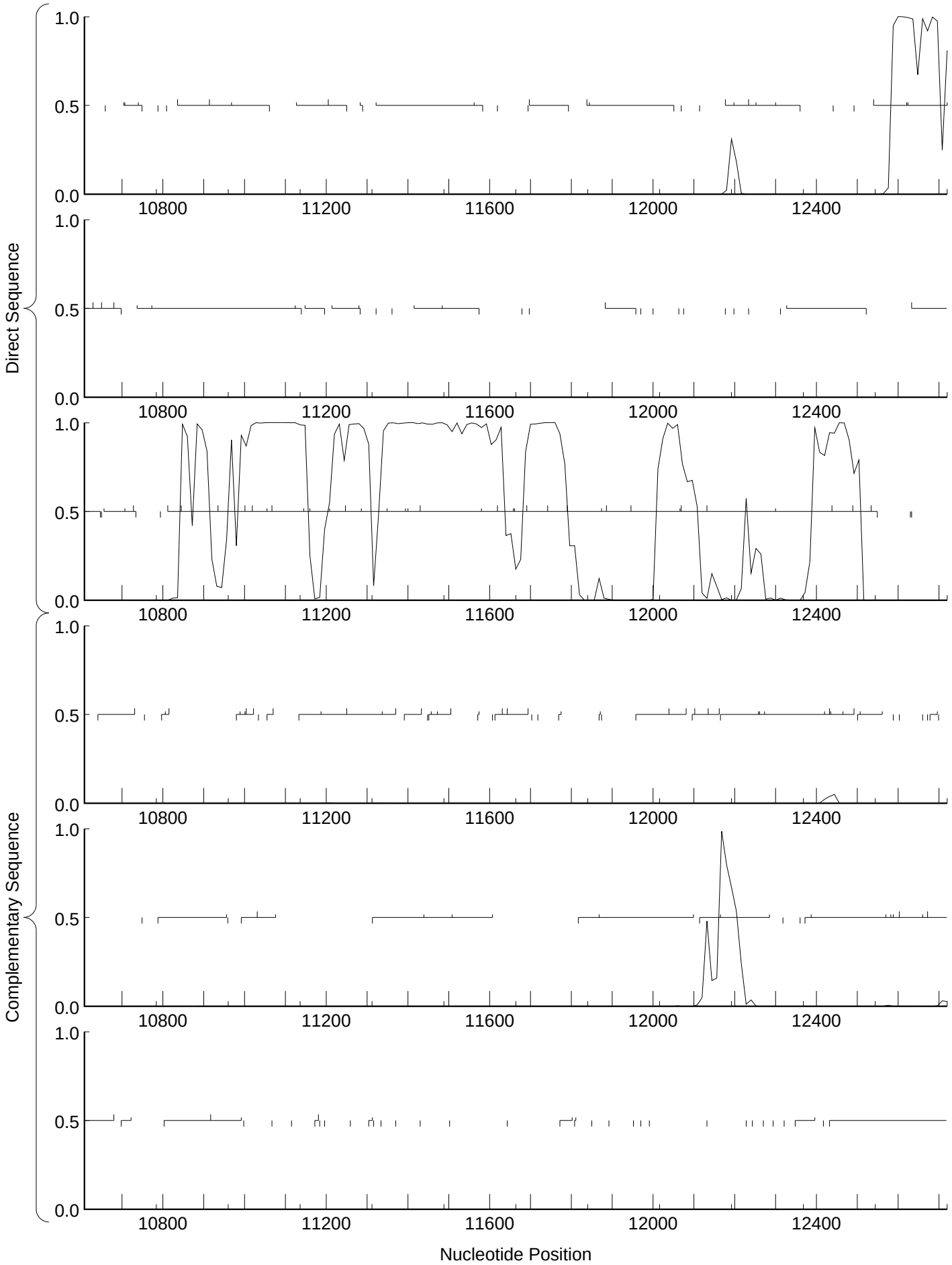


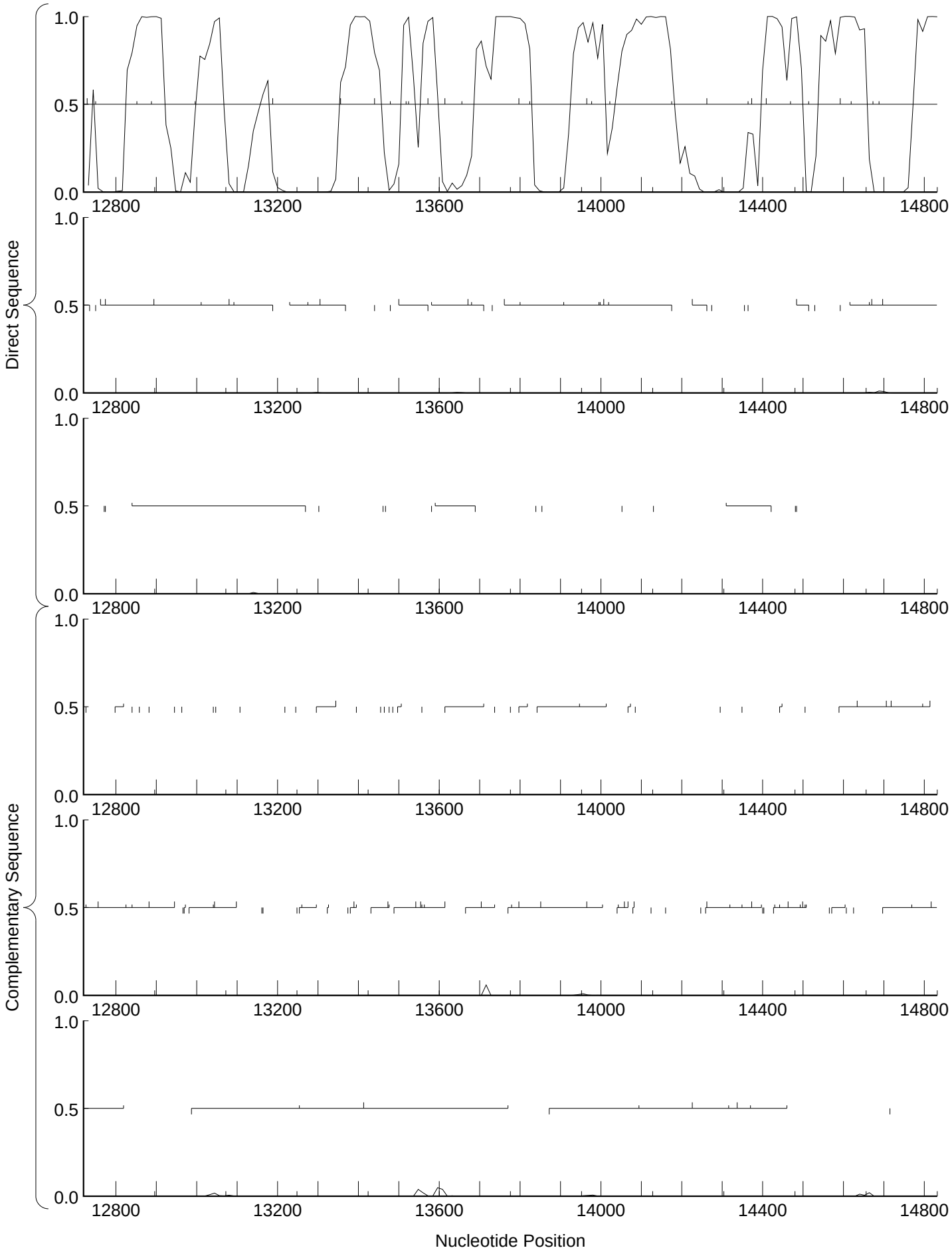

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
6400
6800
7200
7600
8000
8400
Nucleotide Position

phage Kvothe complete sequence, 75462 bp including 1172 bp terminal repeat, Cluster CS4, Order 4, Window 96, Step 12, 6/37

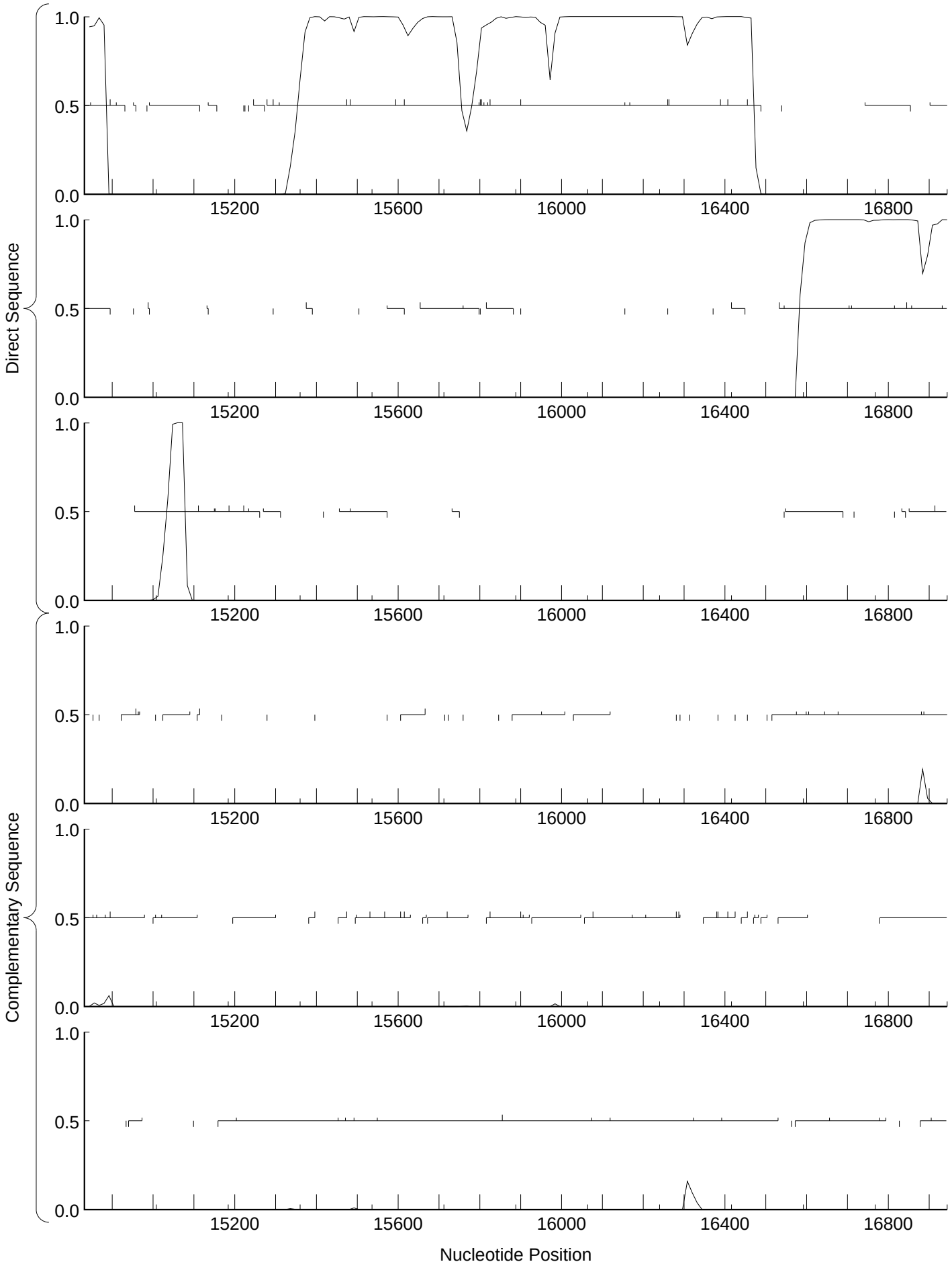


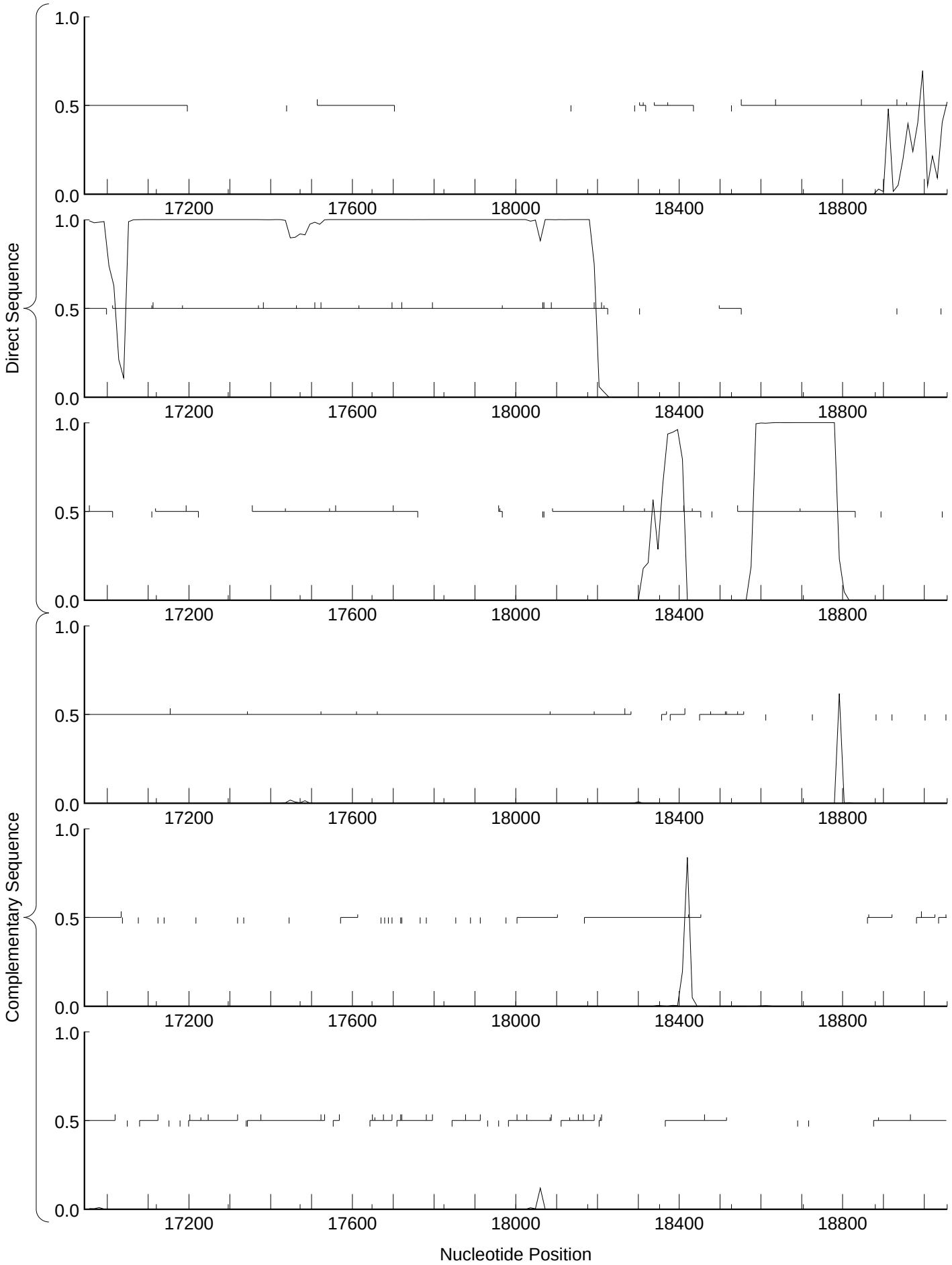
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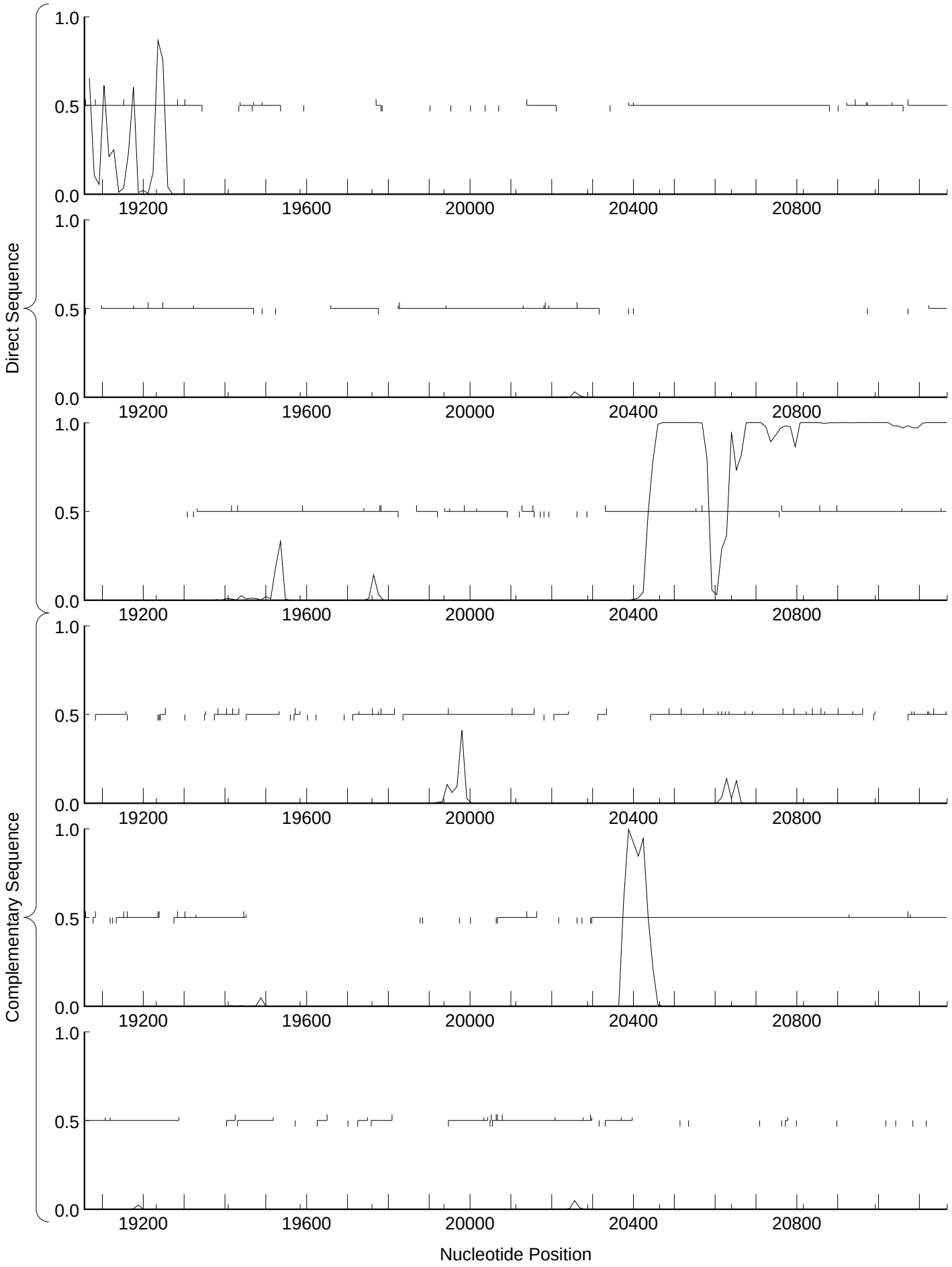


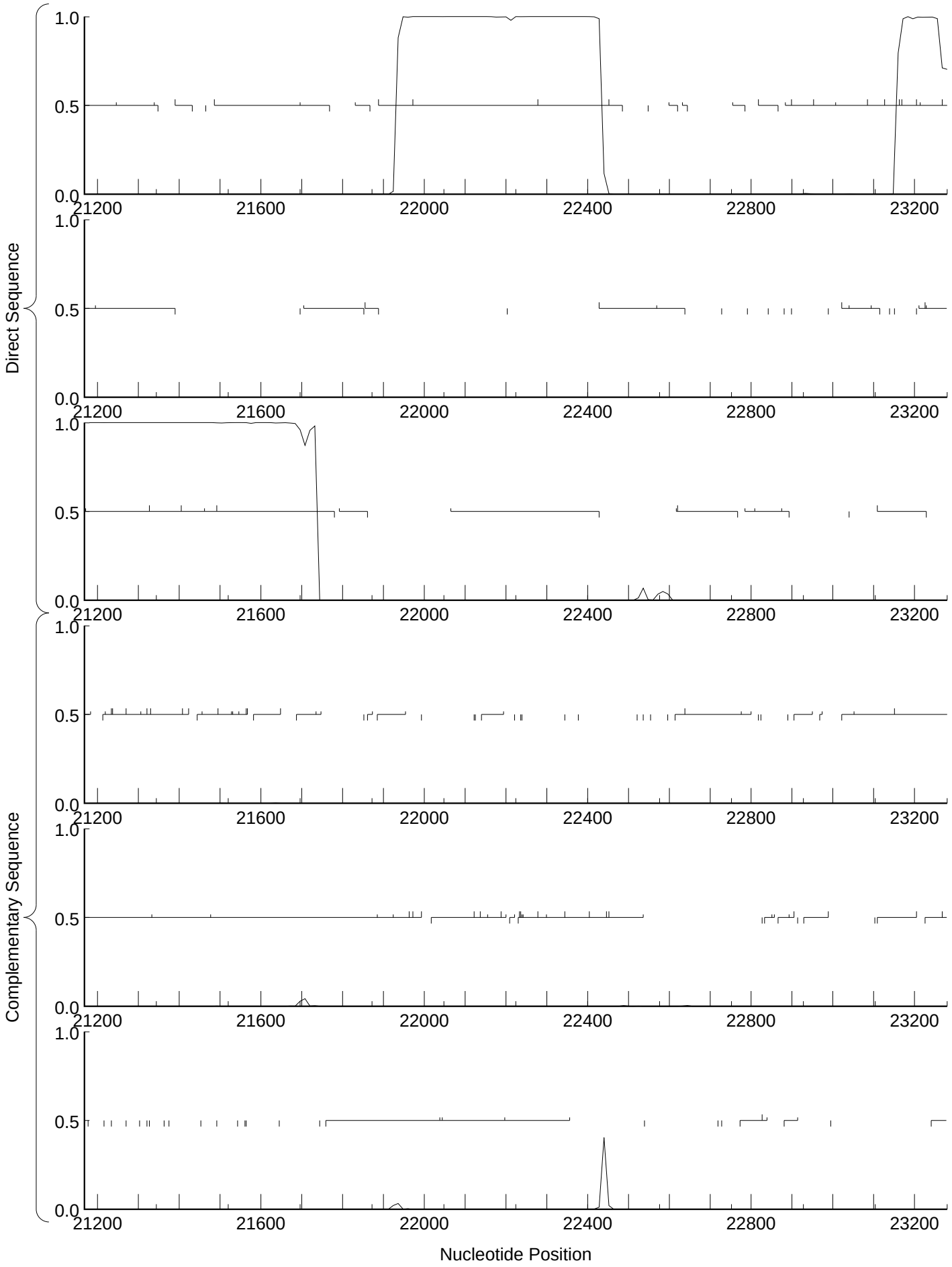

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Complementary Sequence
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0.0
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14000
14400
14800
Nucleotide Position

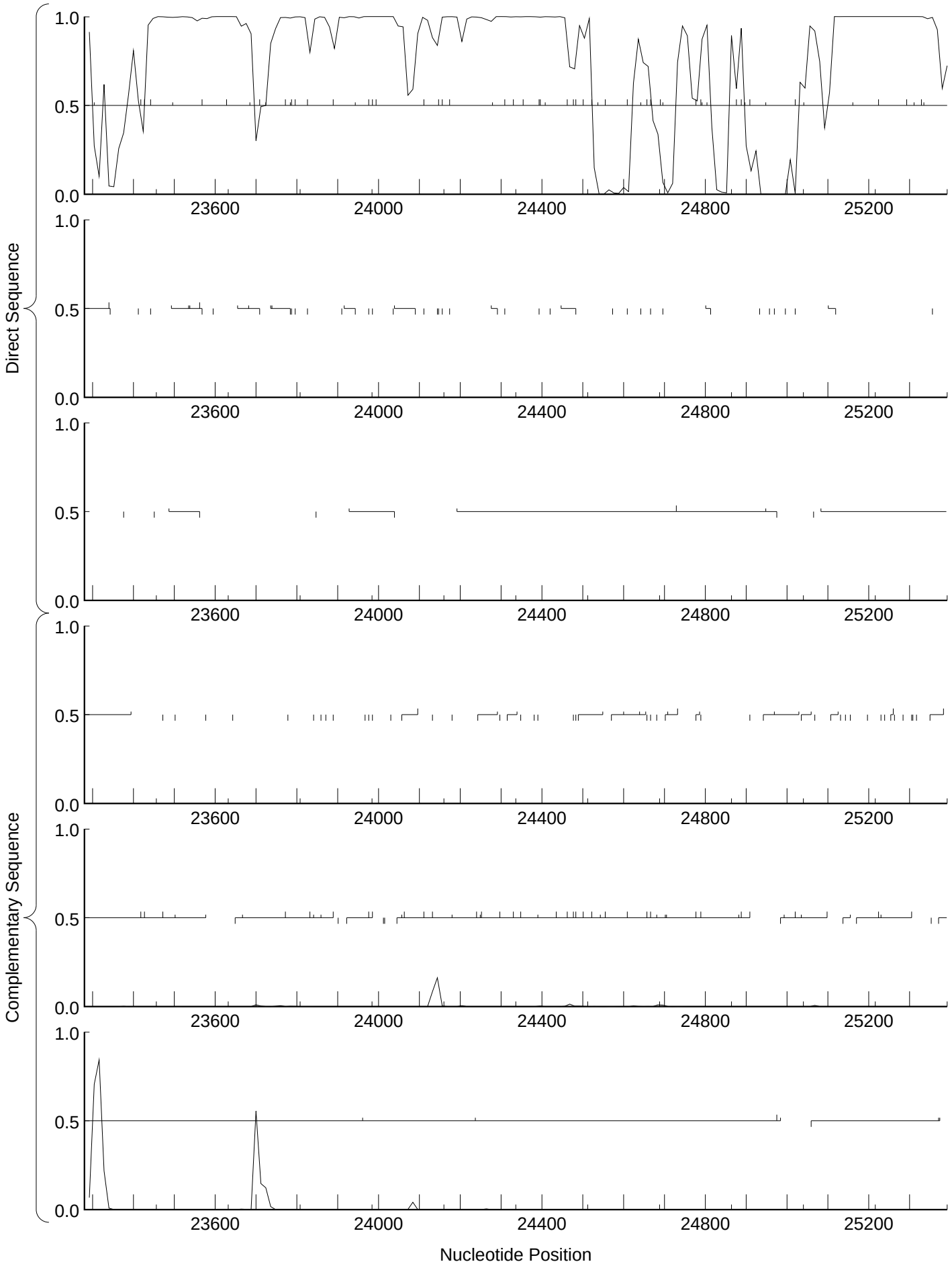
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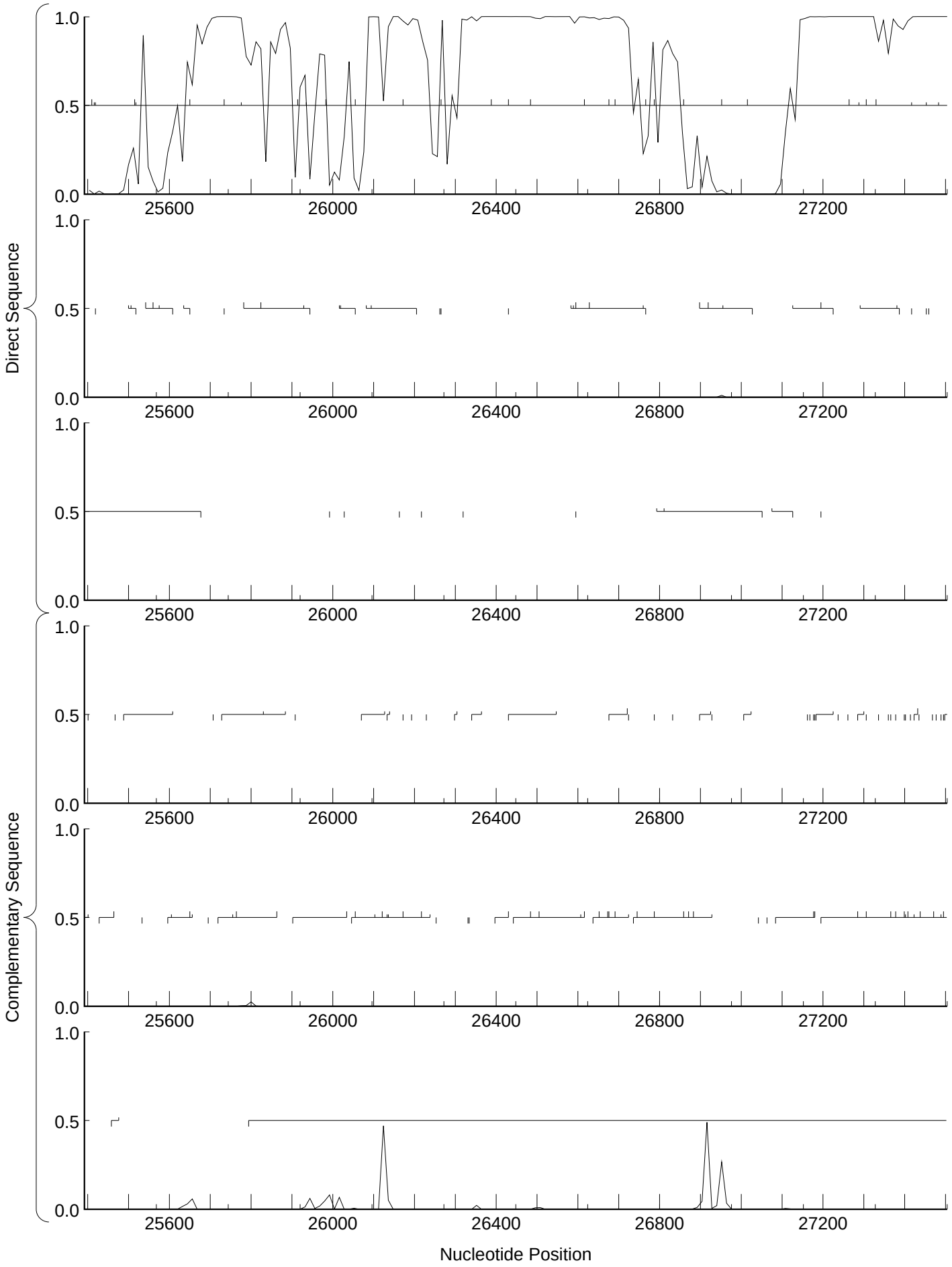


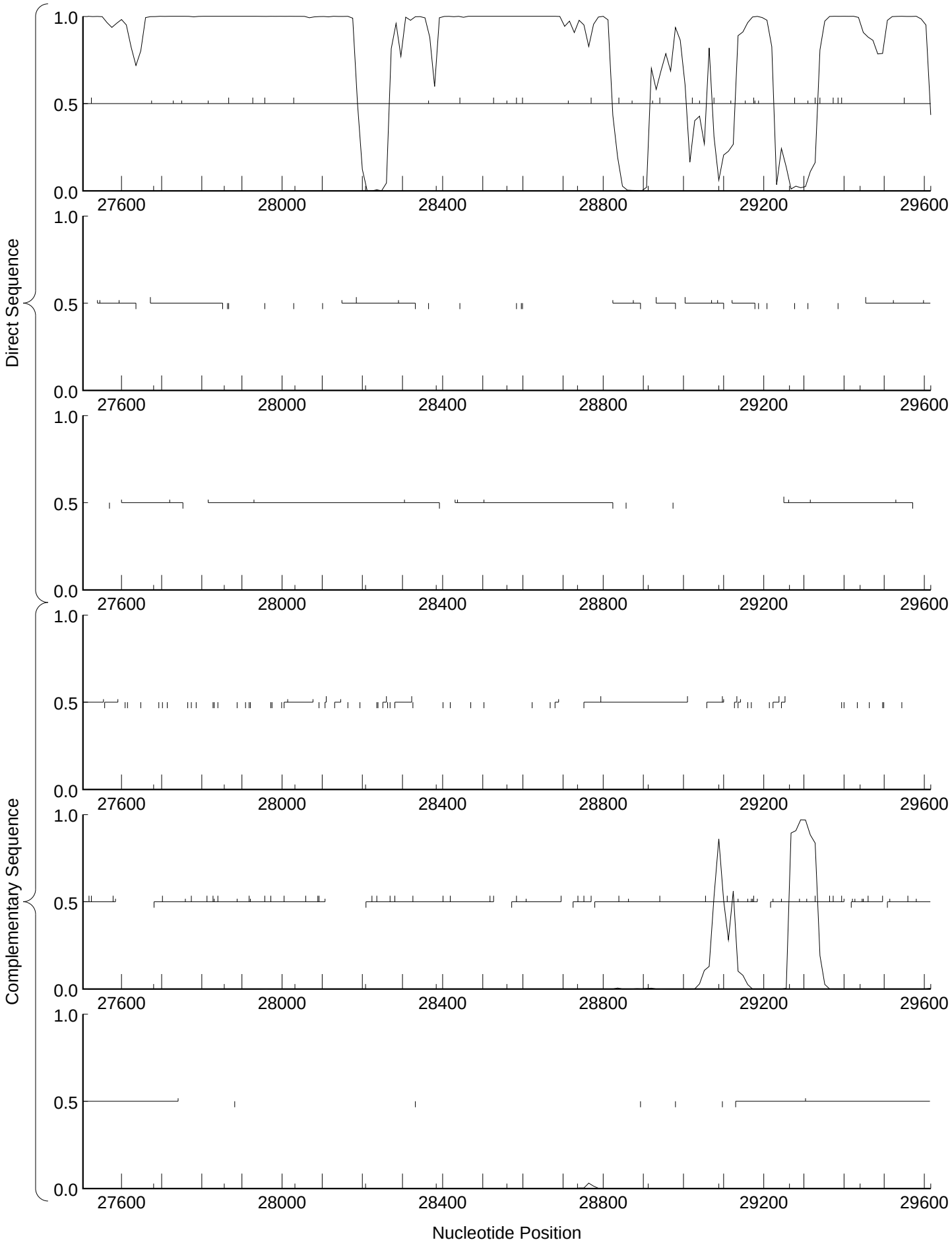

Direct Sequence
Complementary Sequence
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0.5
0.0
17200
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18000
18400
18800
Nucleotide Position

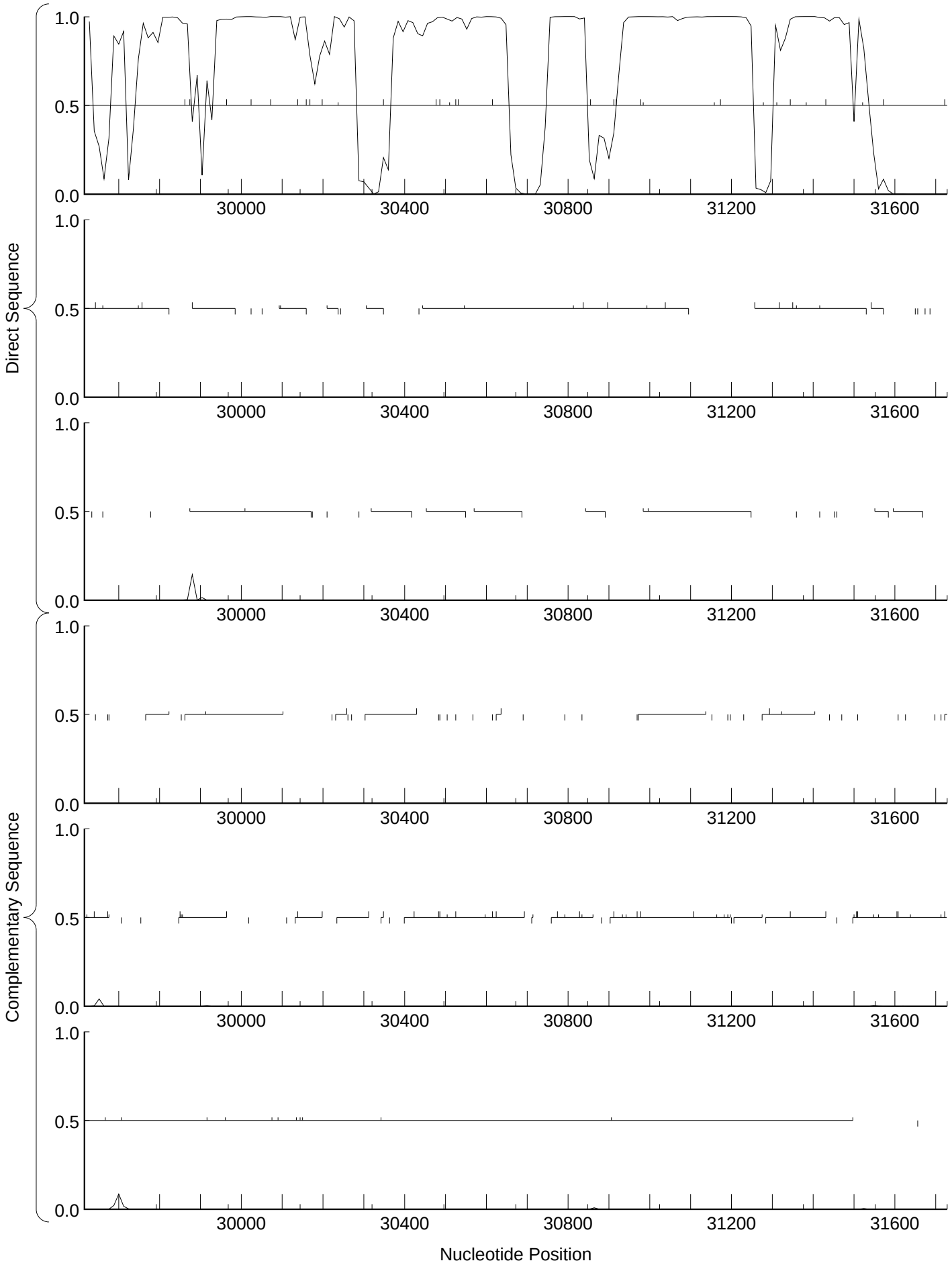

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Complementary Sequence
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Nucleotide Position

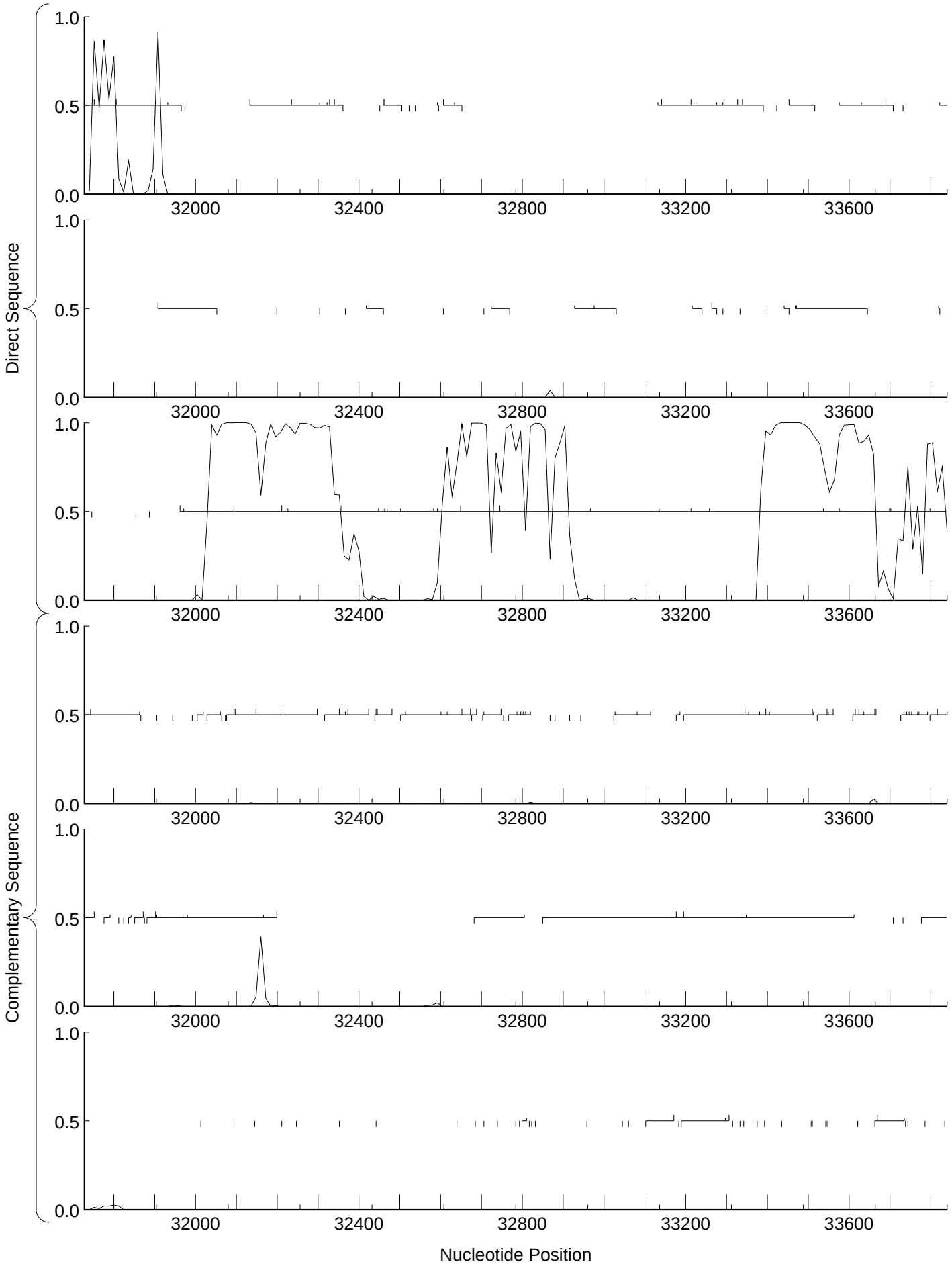

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Complementary Sequence
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Nucleotide Position

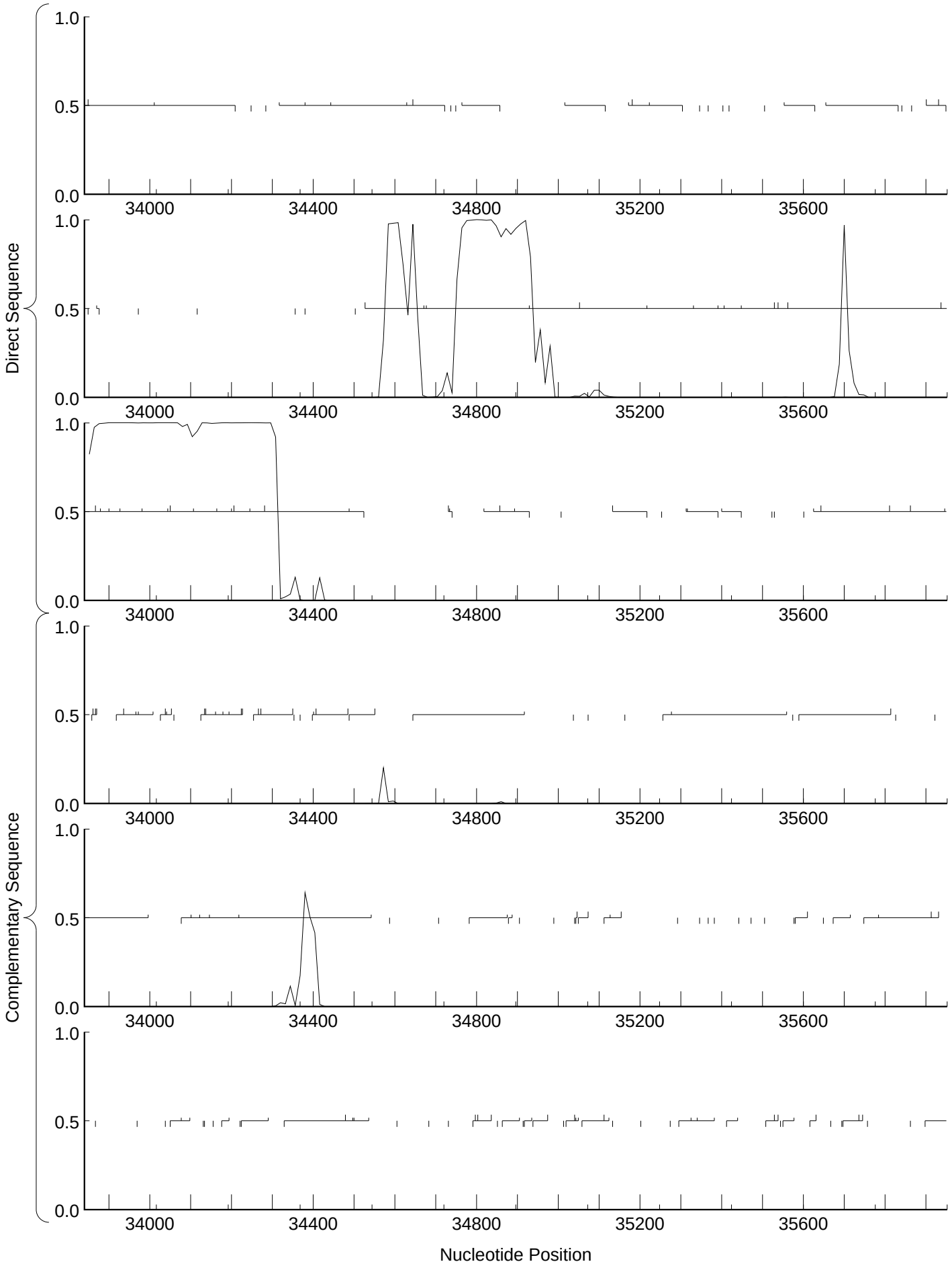

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Complementary Sequence
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24800
25200
Nucleotide Position

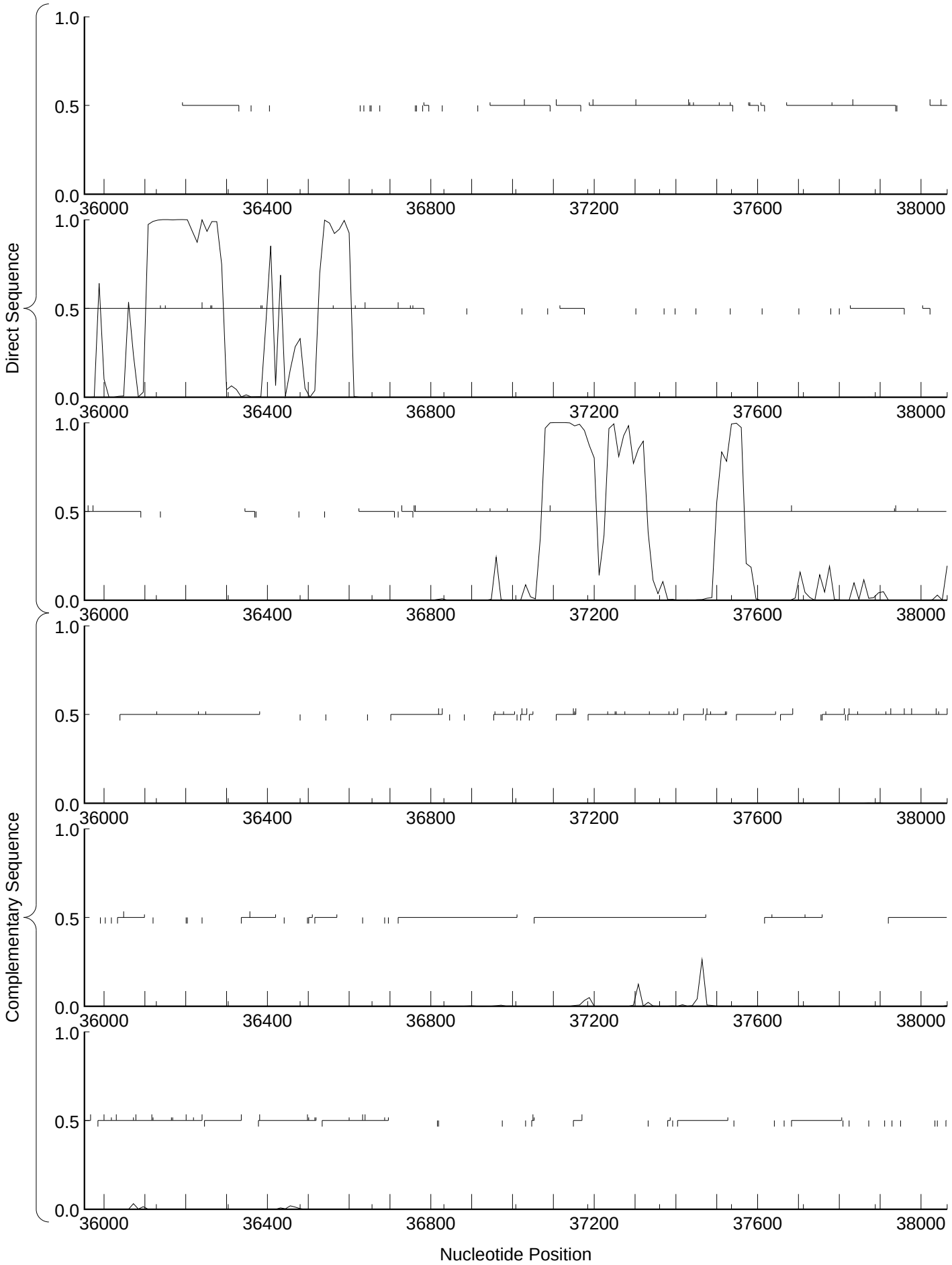

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Complementary Sequence
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Nucleotide Position

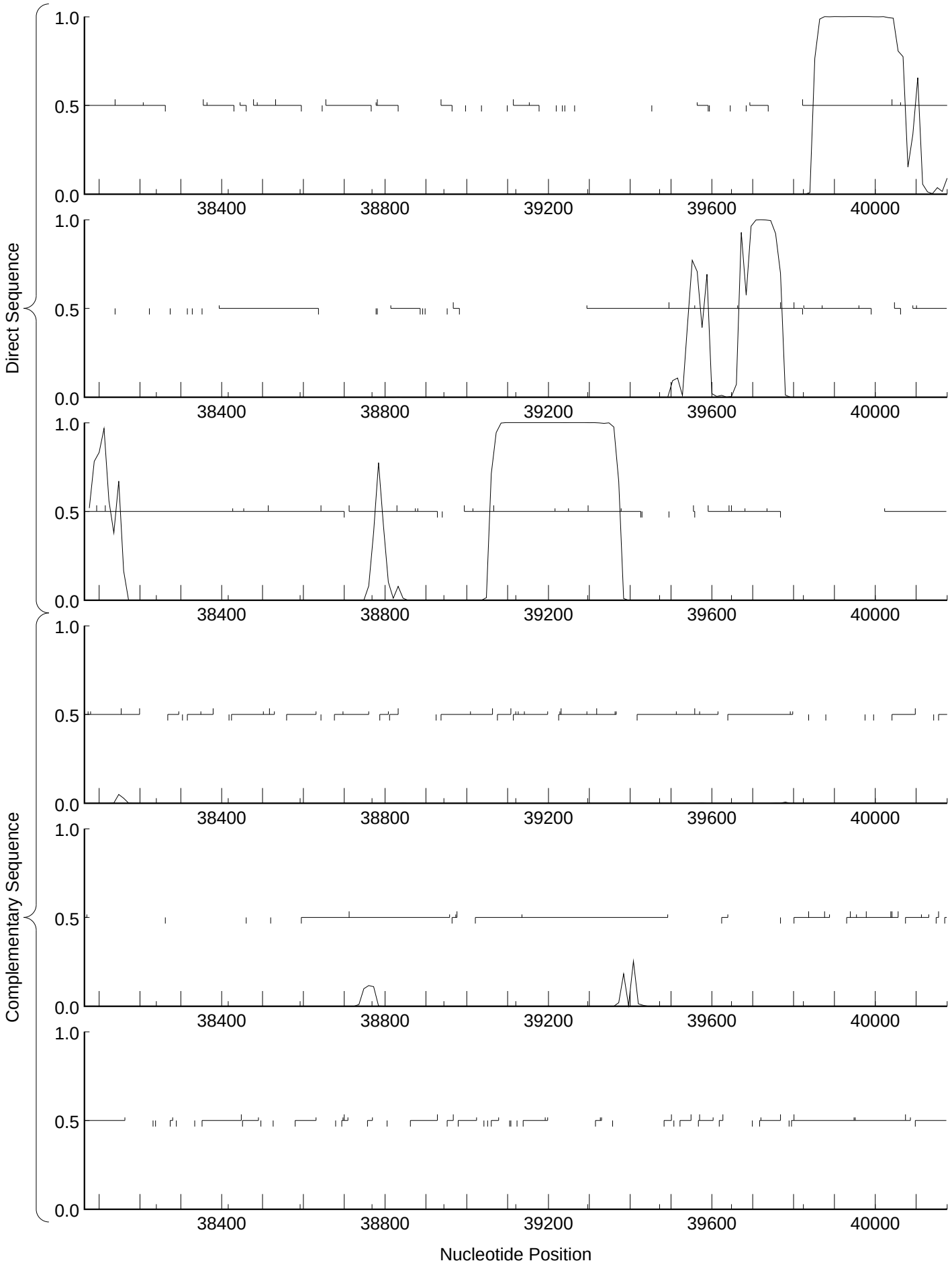

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Complementary Sequence
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Nucleotide Position

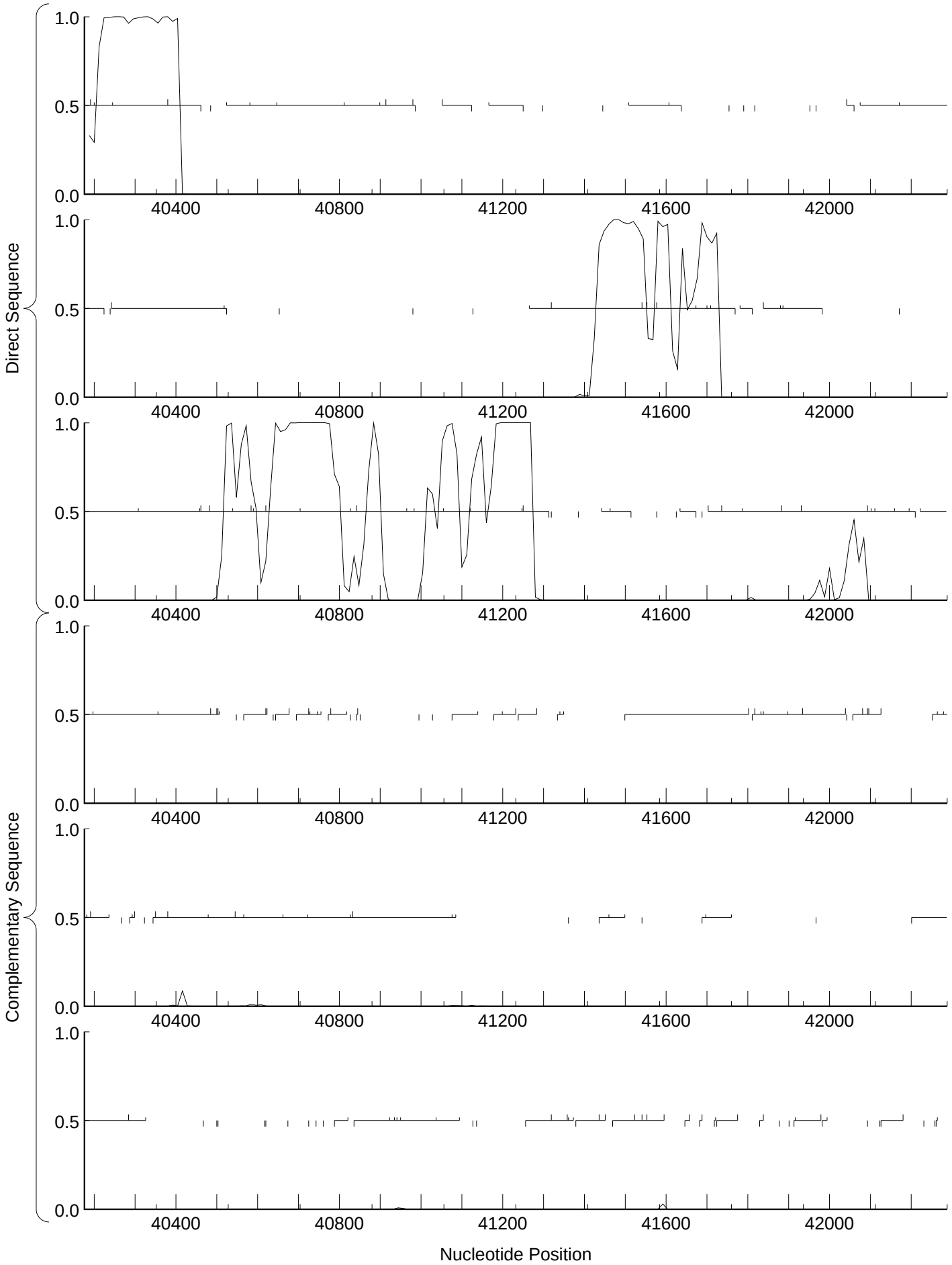

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31600
Nucleotide Position

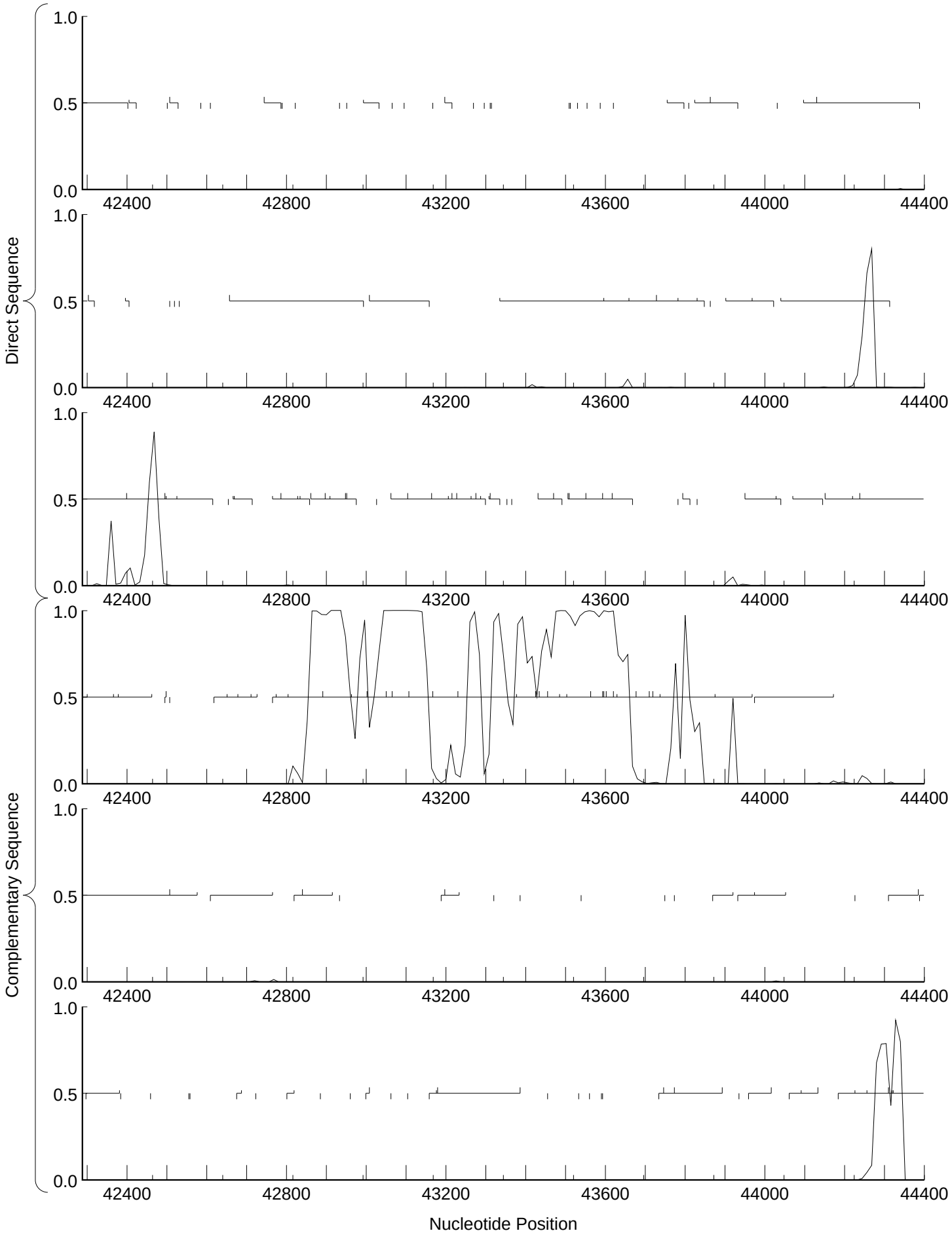

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Nucleotide Position

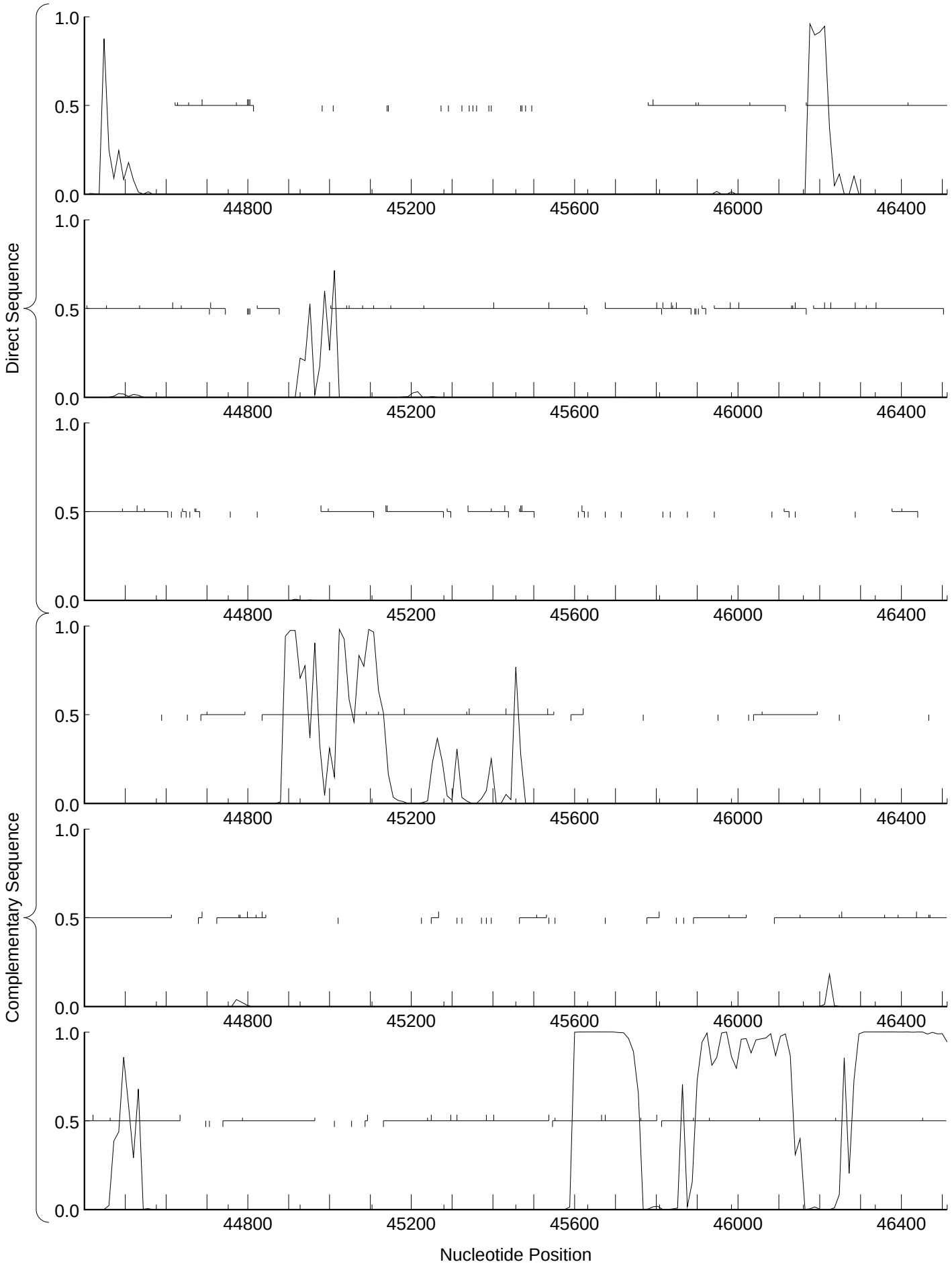

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Complementary Sequence
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Nucleotide Position

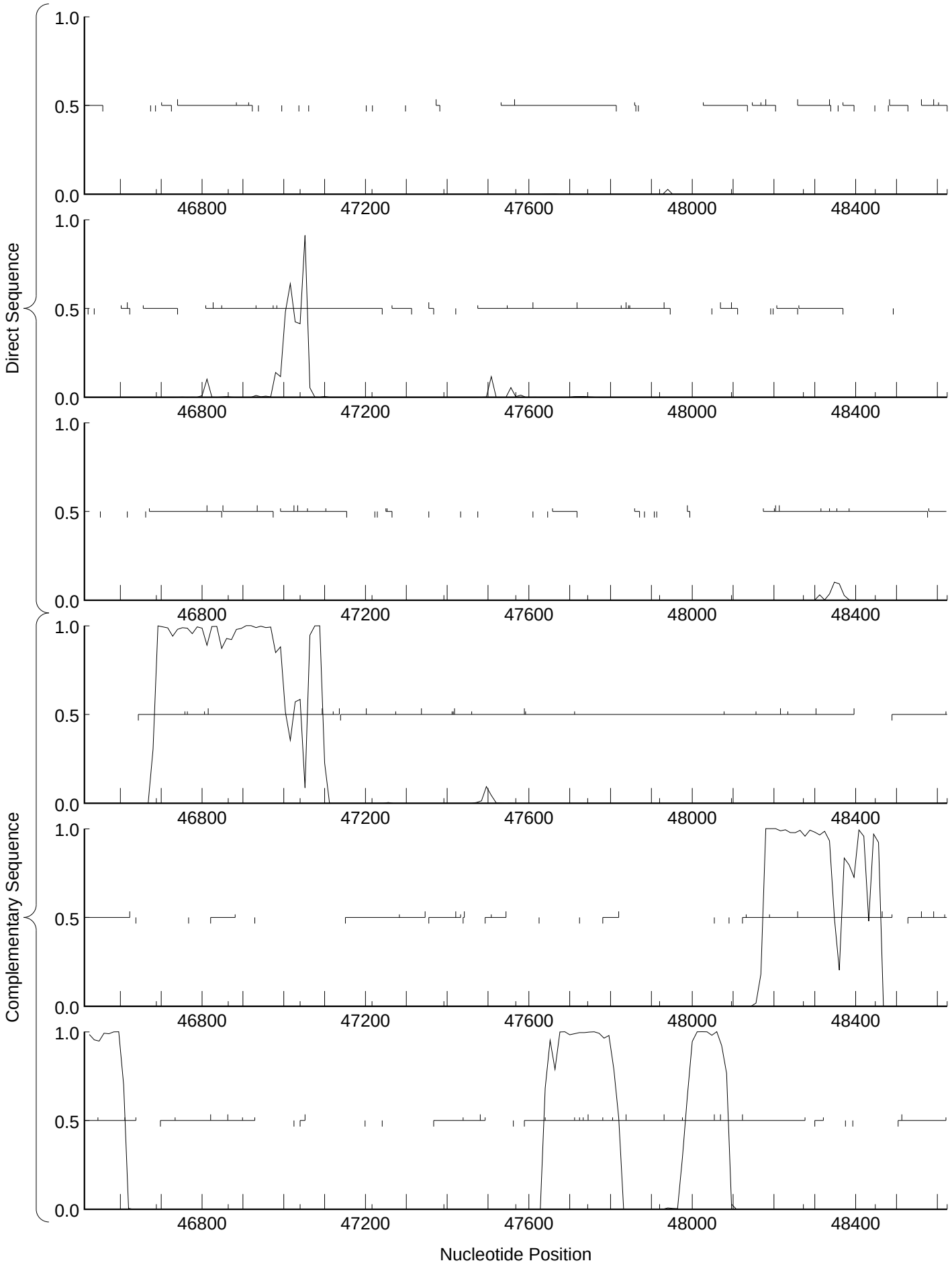

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Nucleotide Position

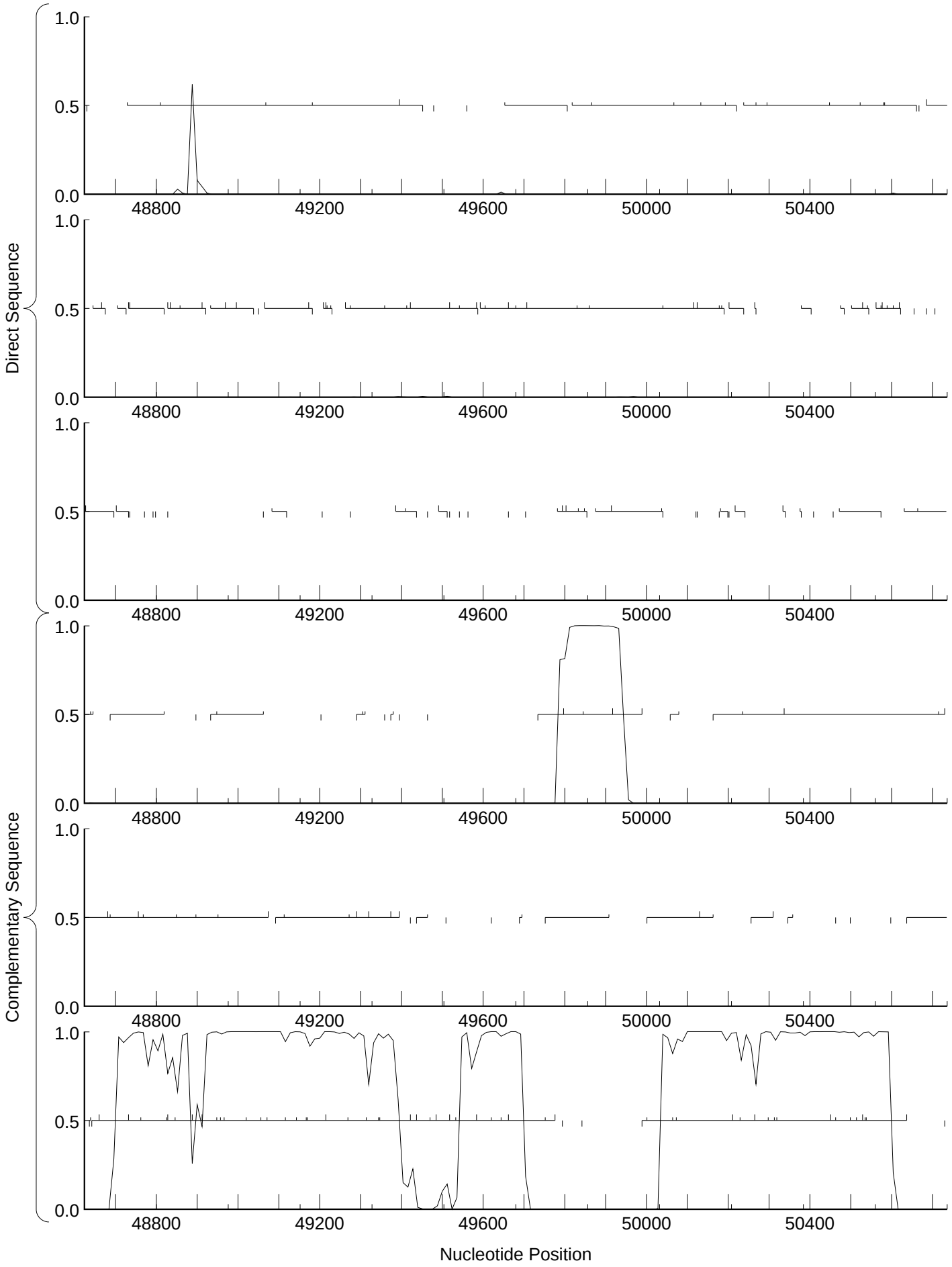

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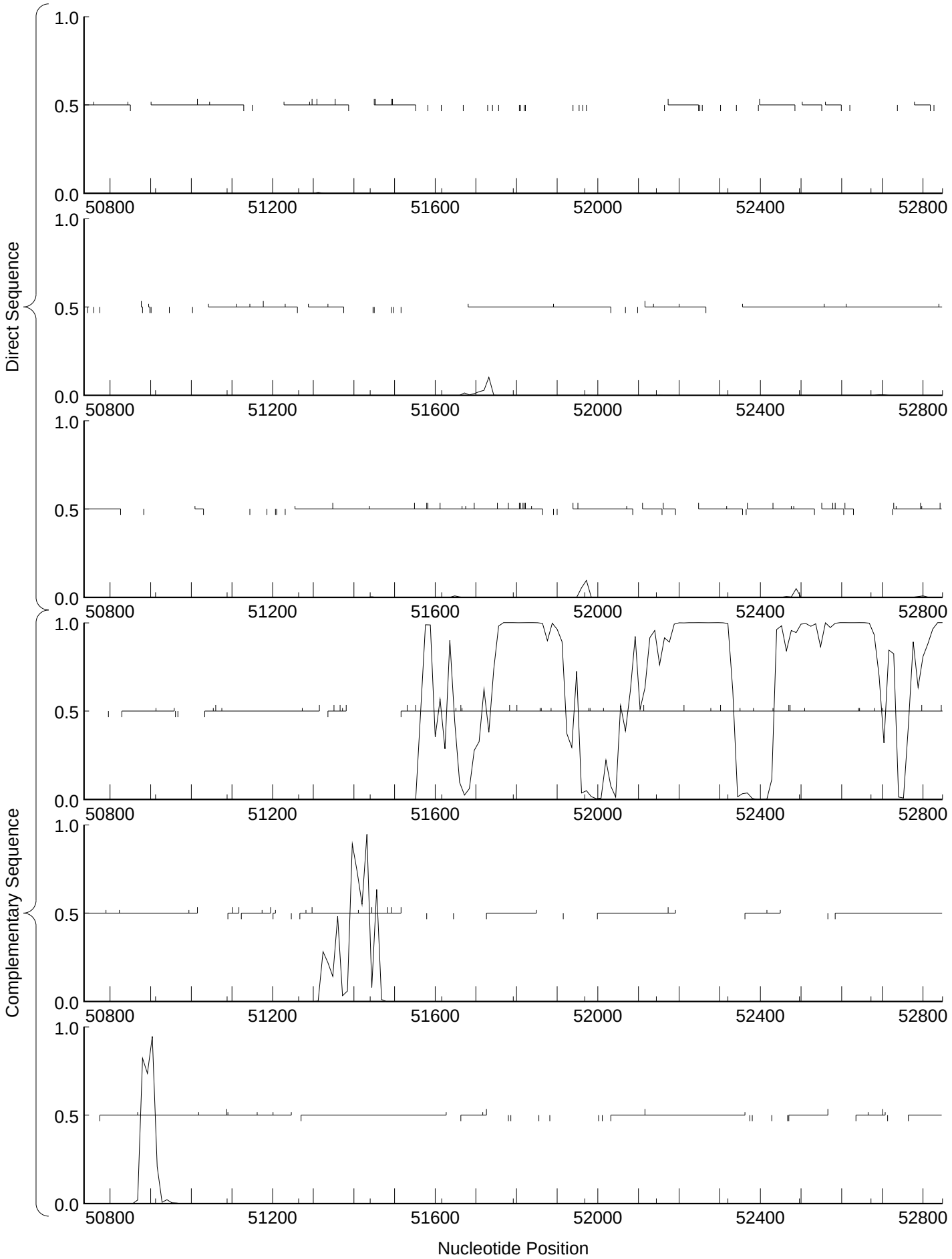

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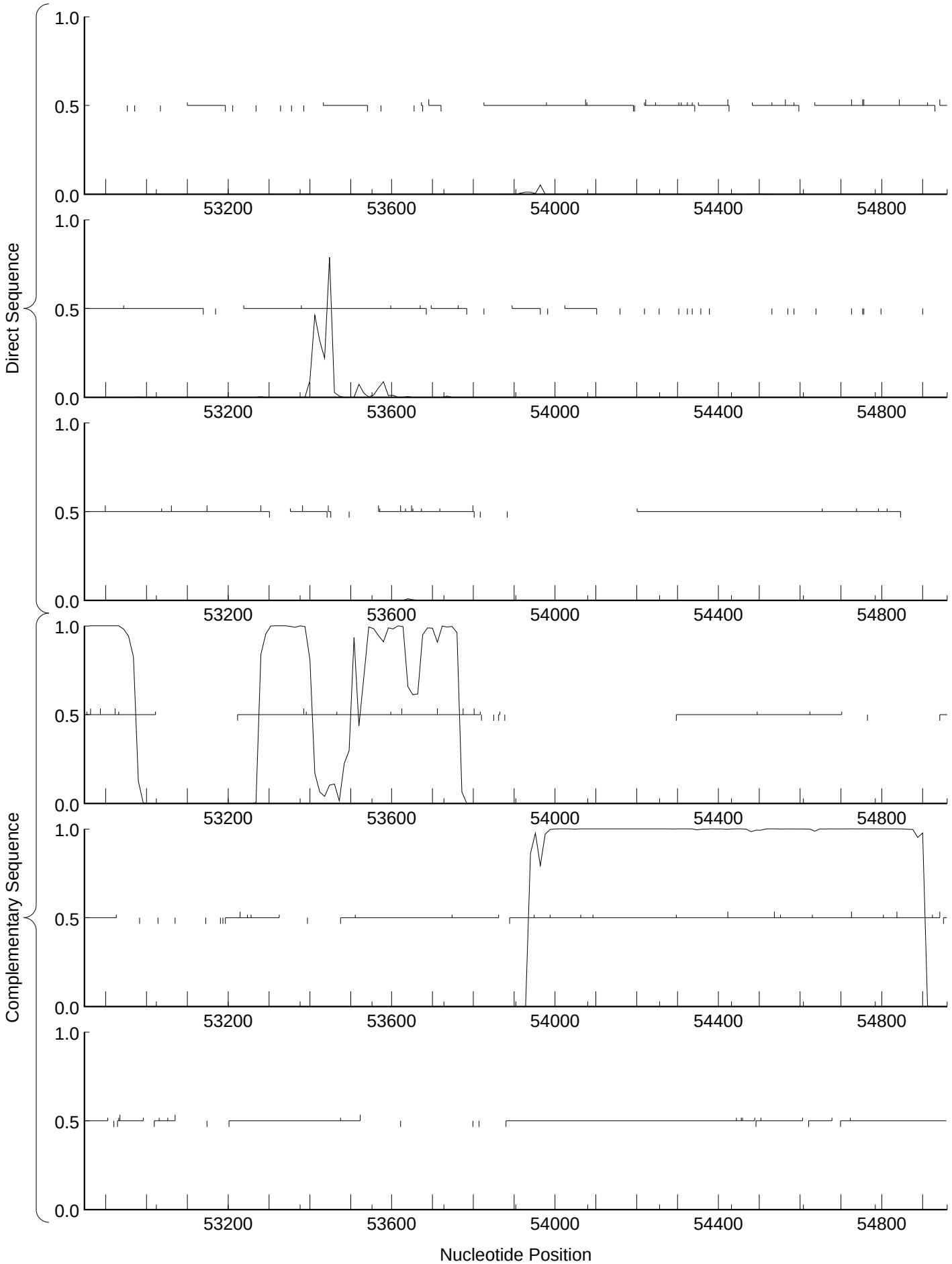

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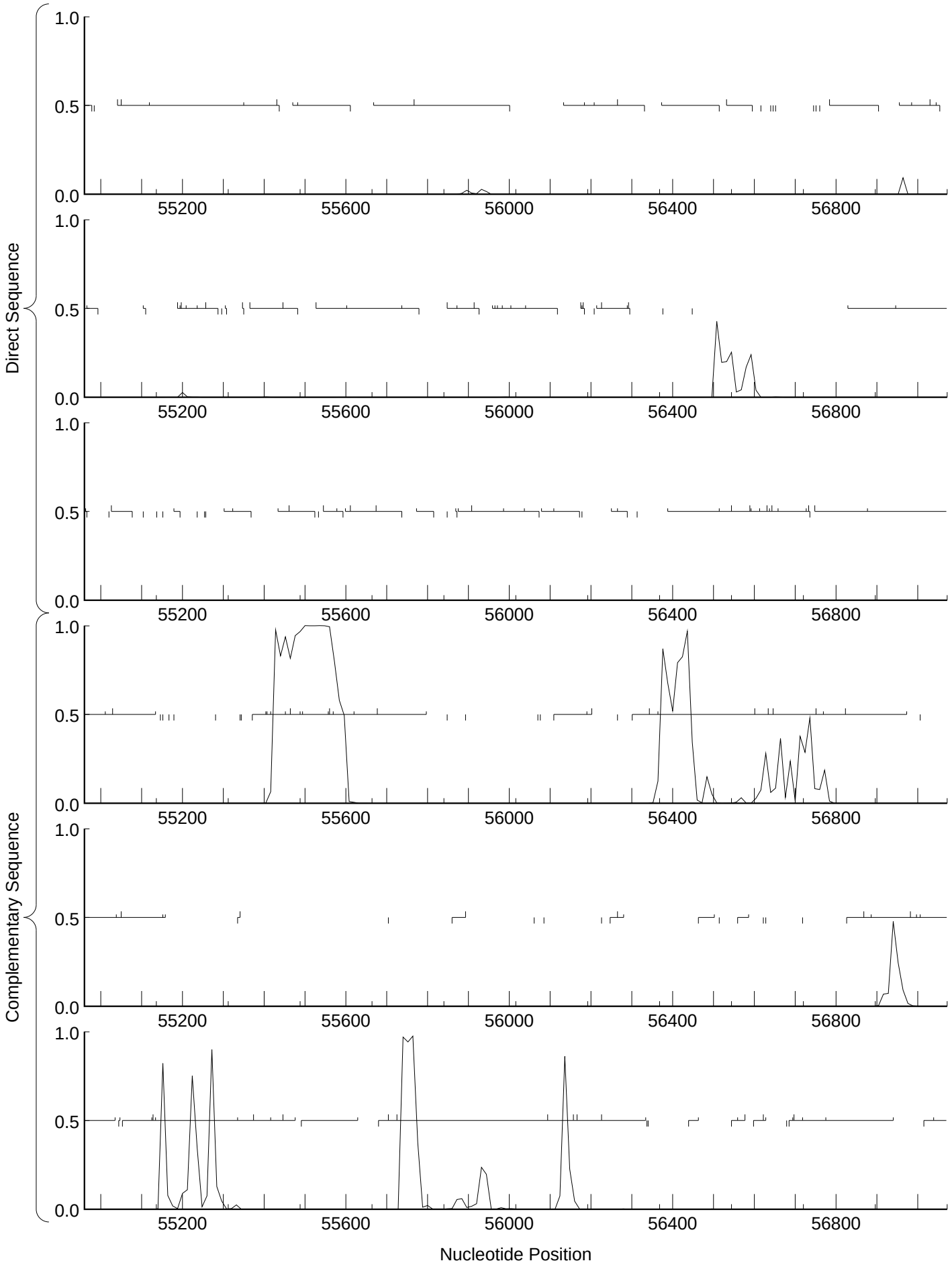

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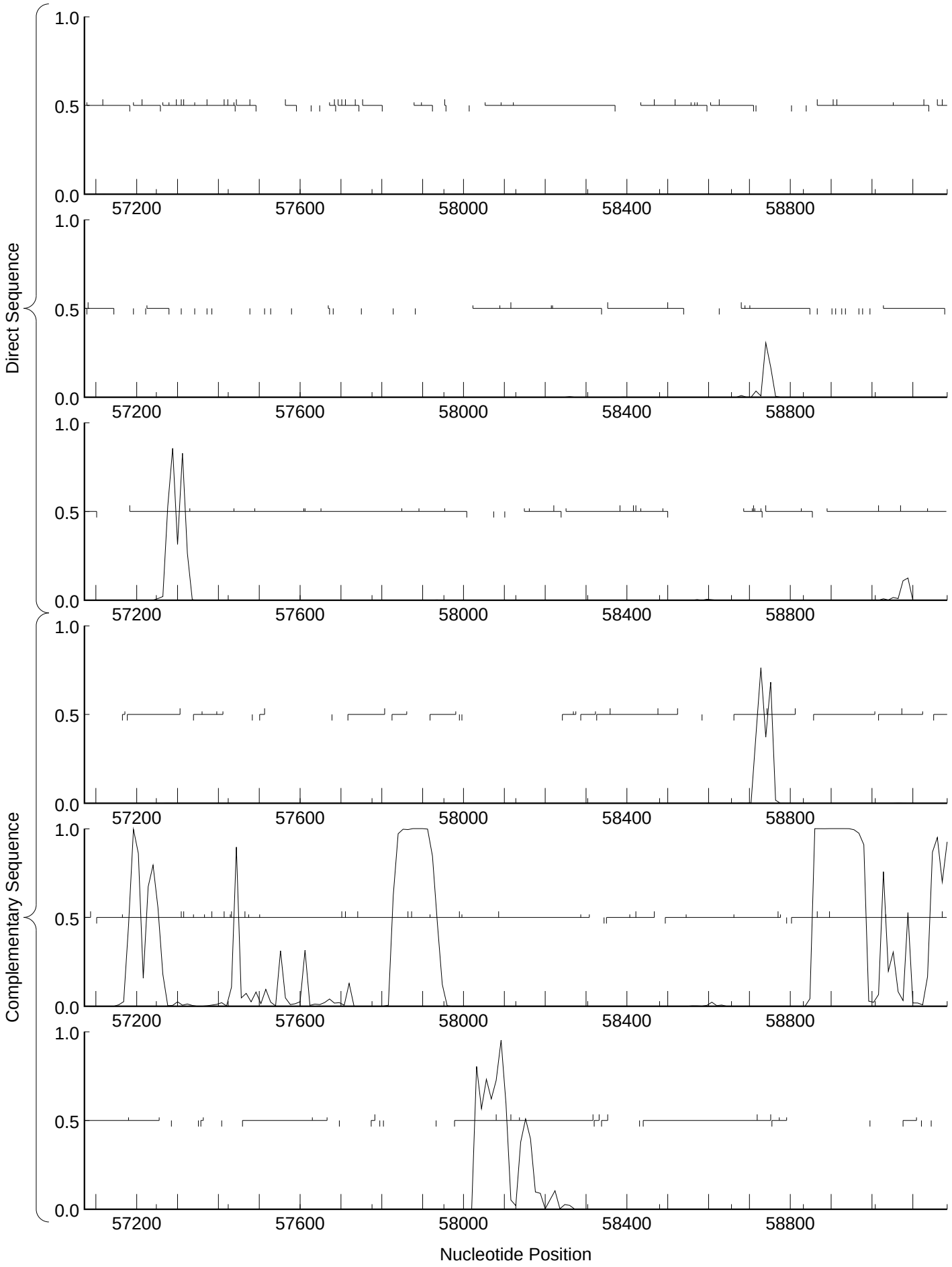

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Nucleotide Position

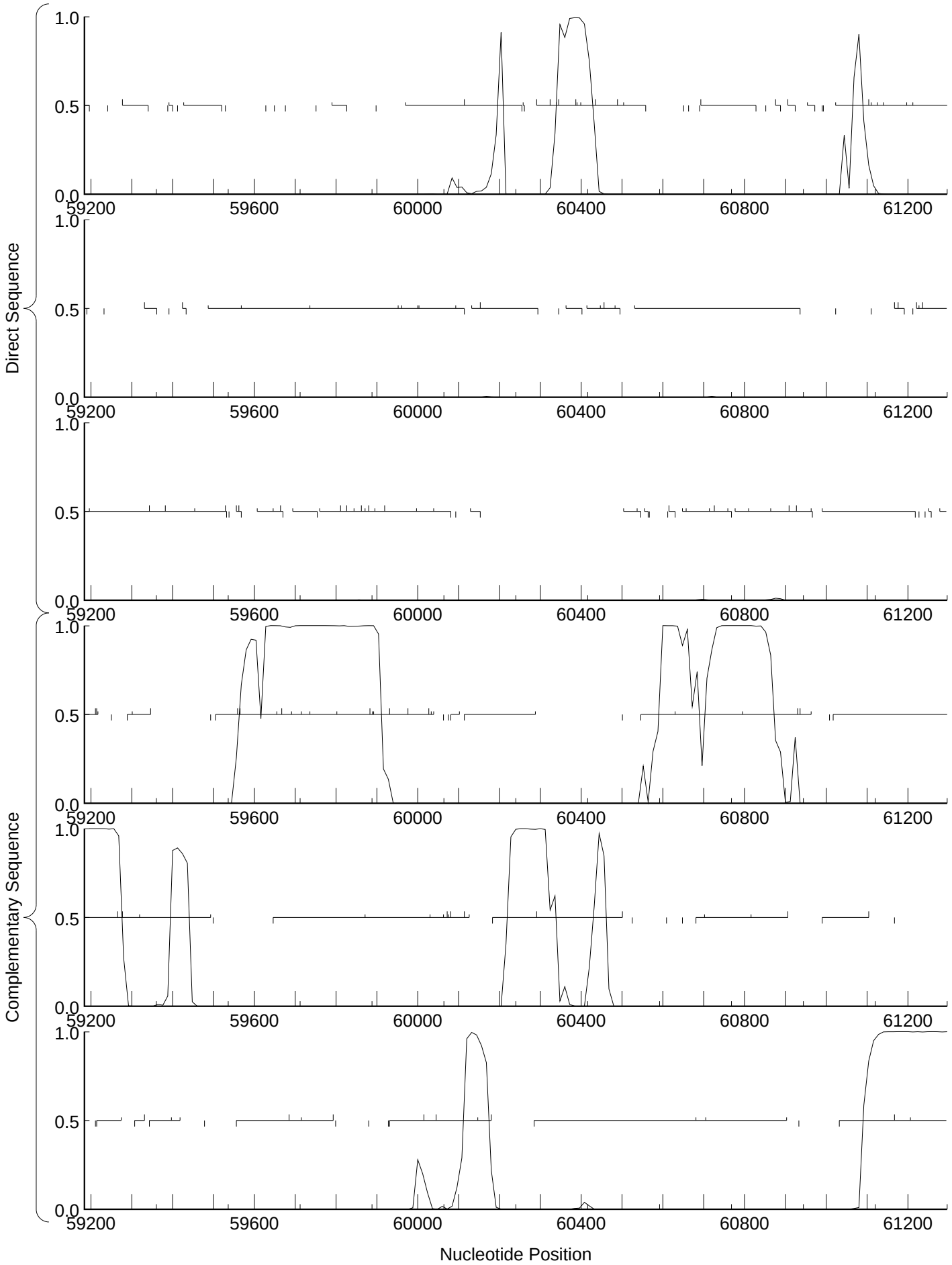

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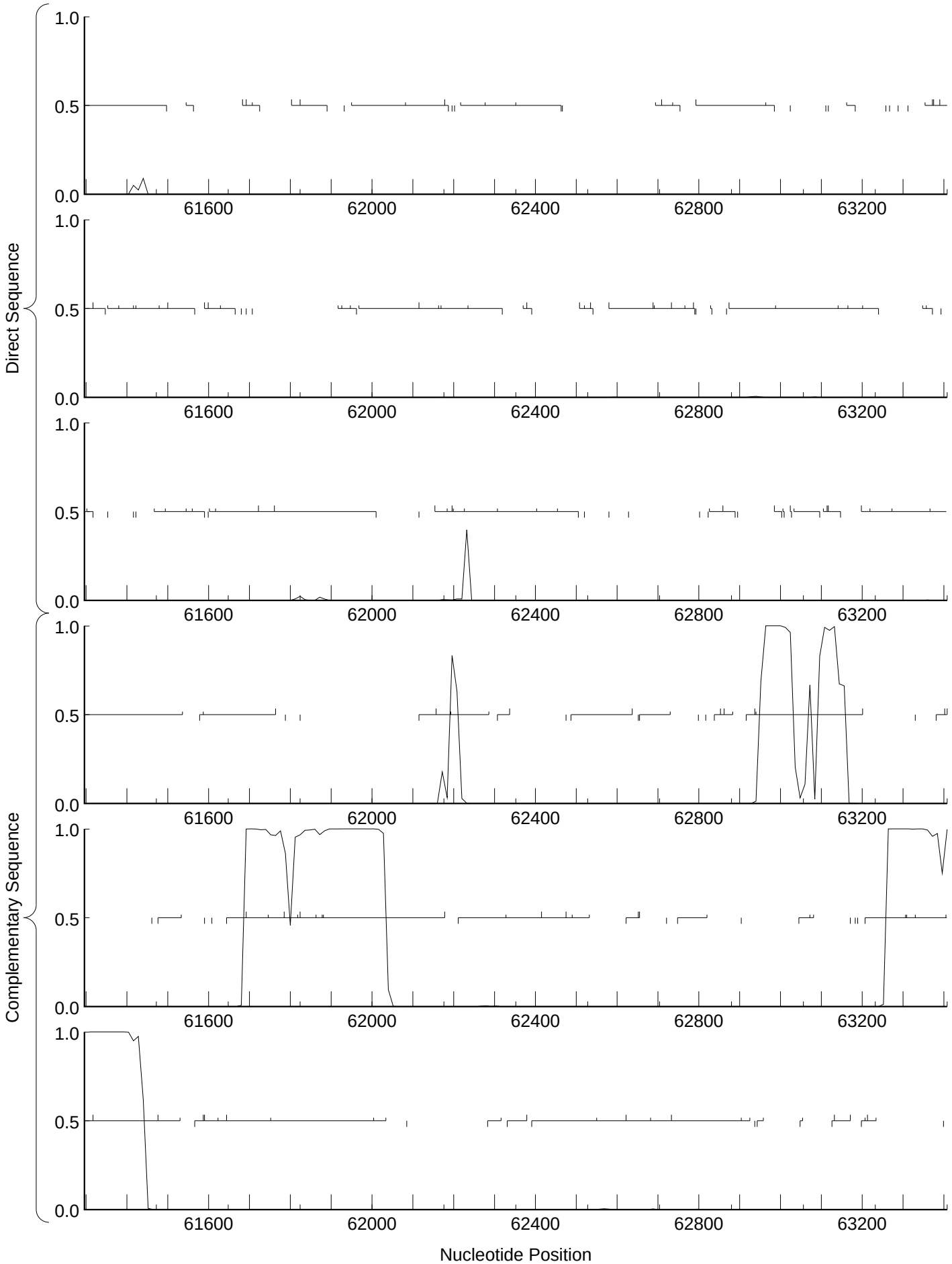

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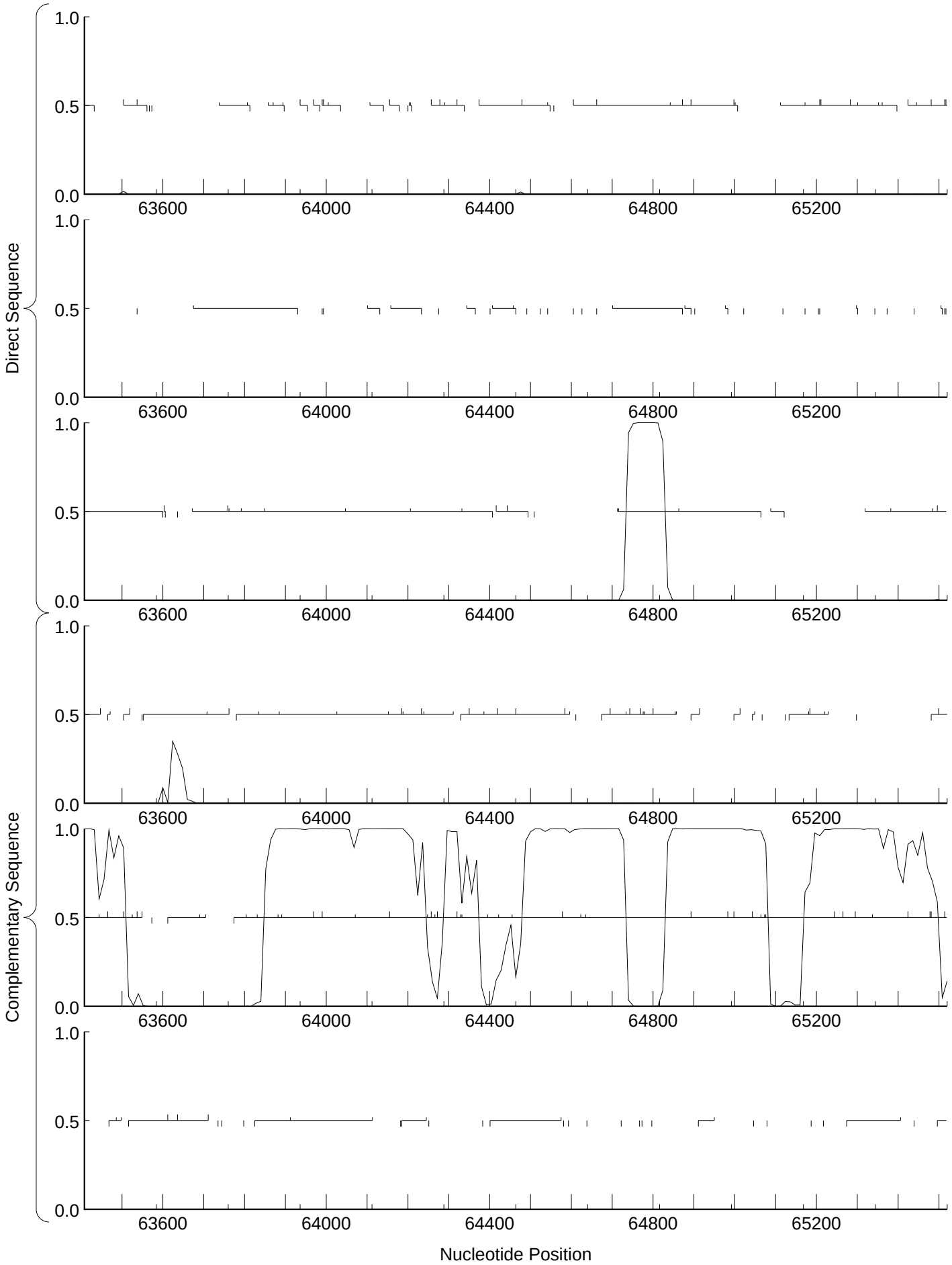

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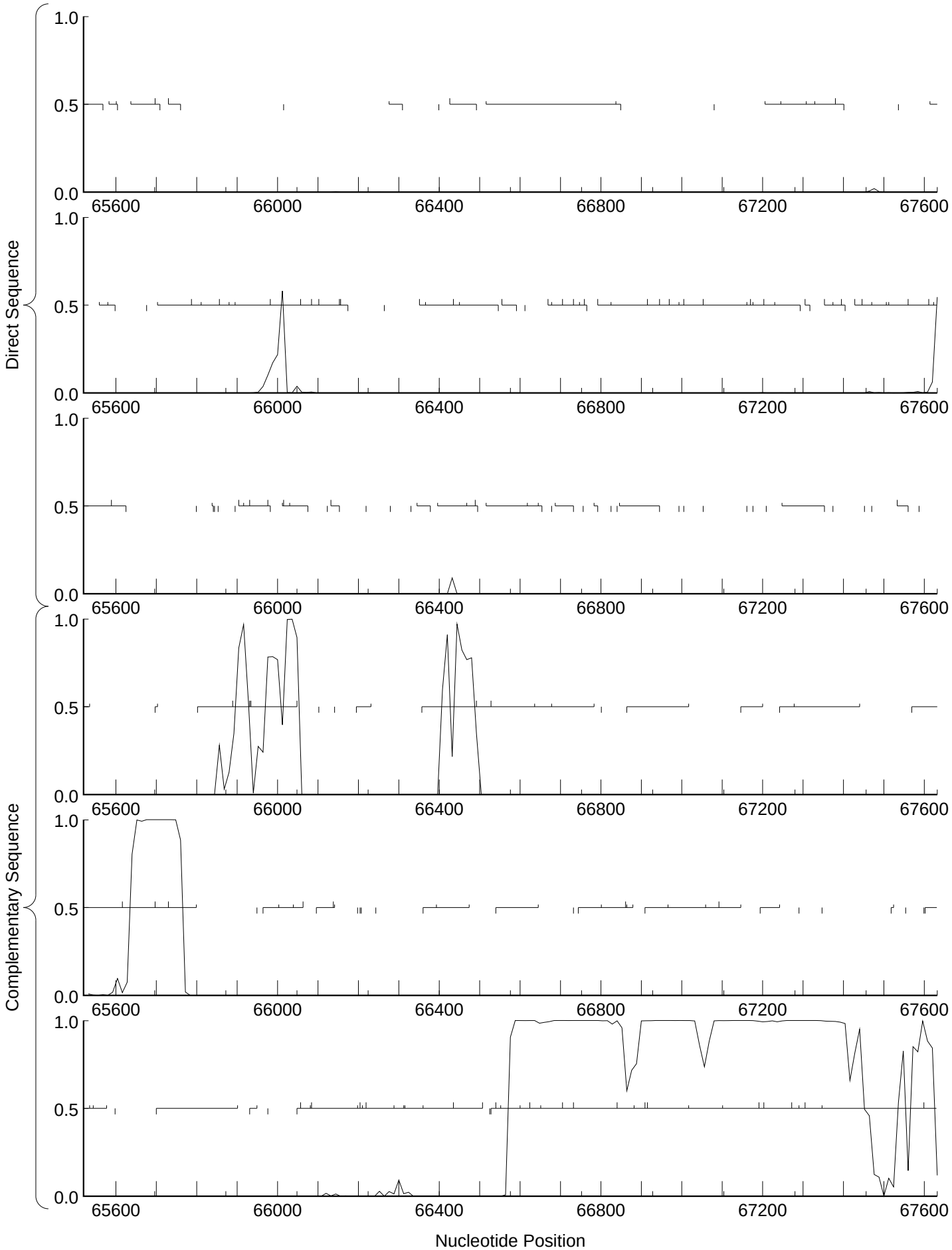

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Nucleotide Position

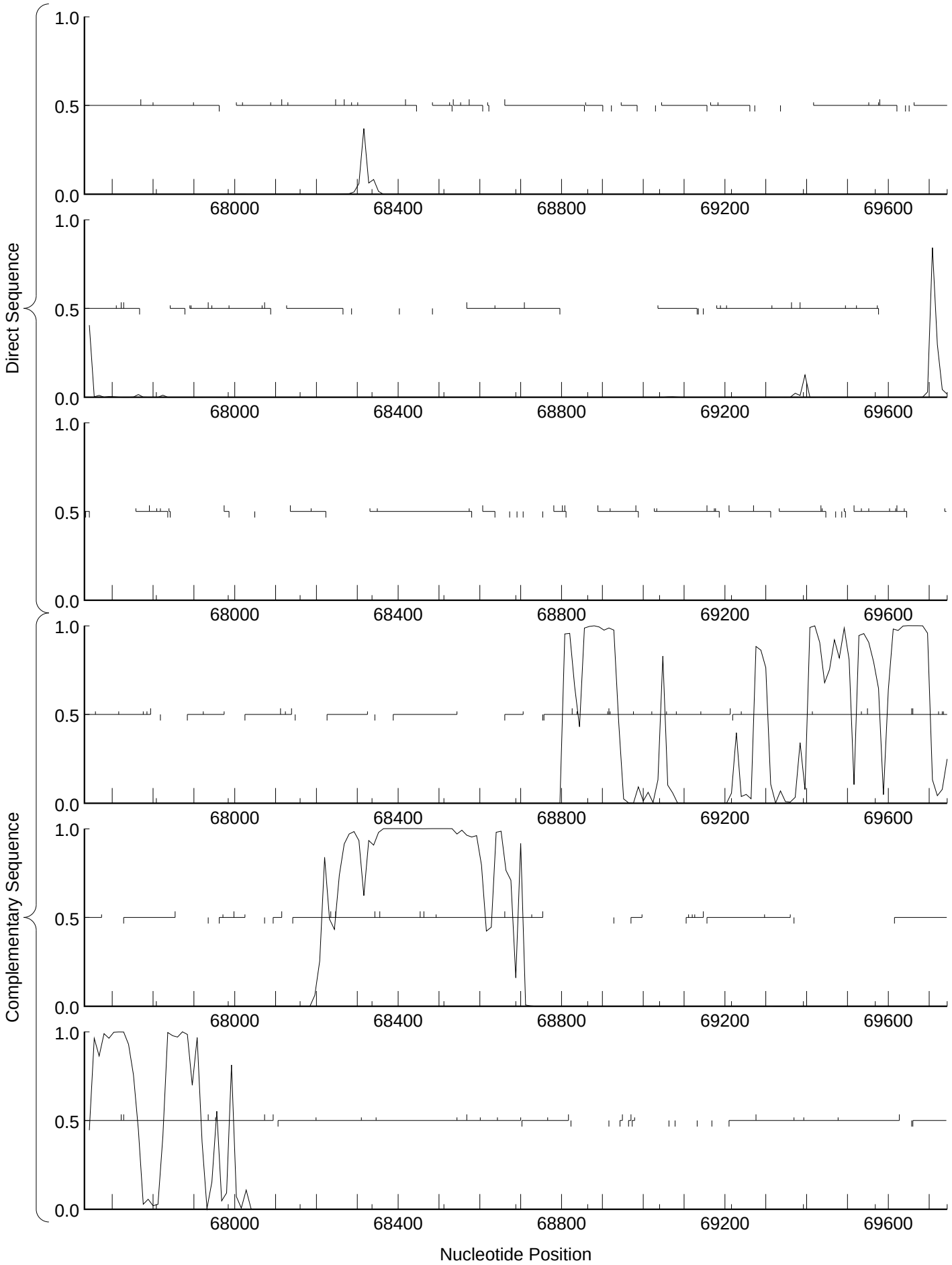

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Nucleotide Position

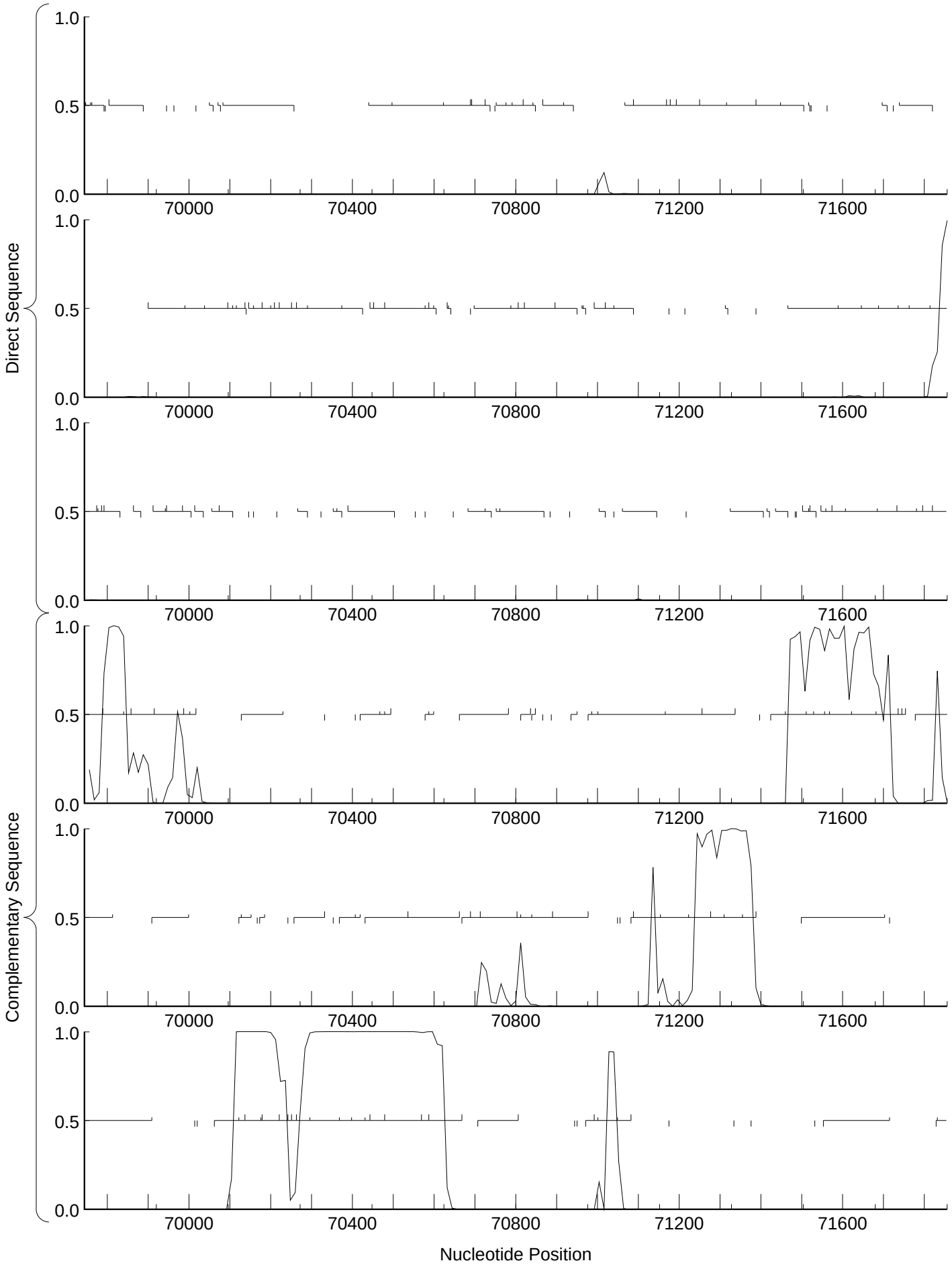

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Nucleotide Position

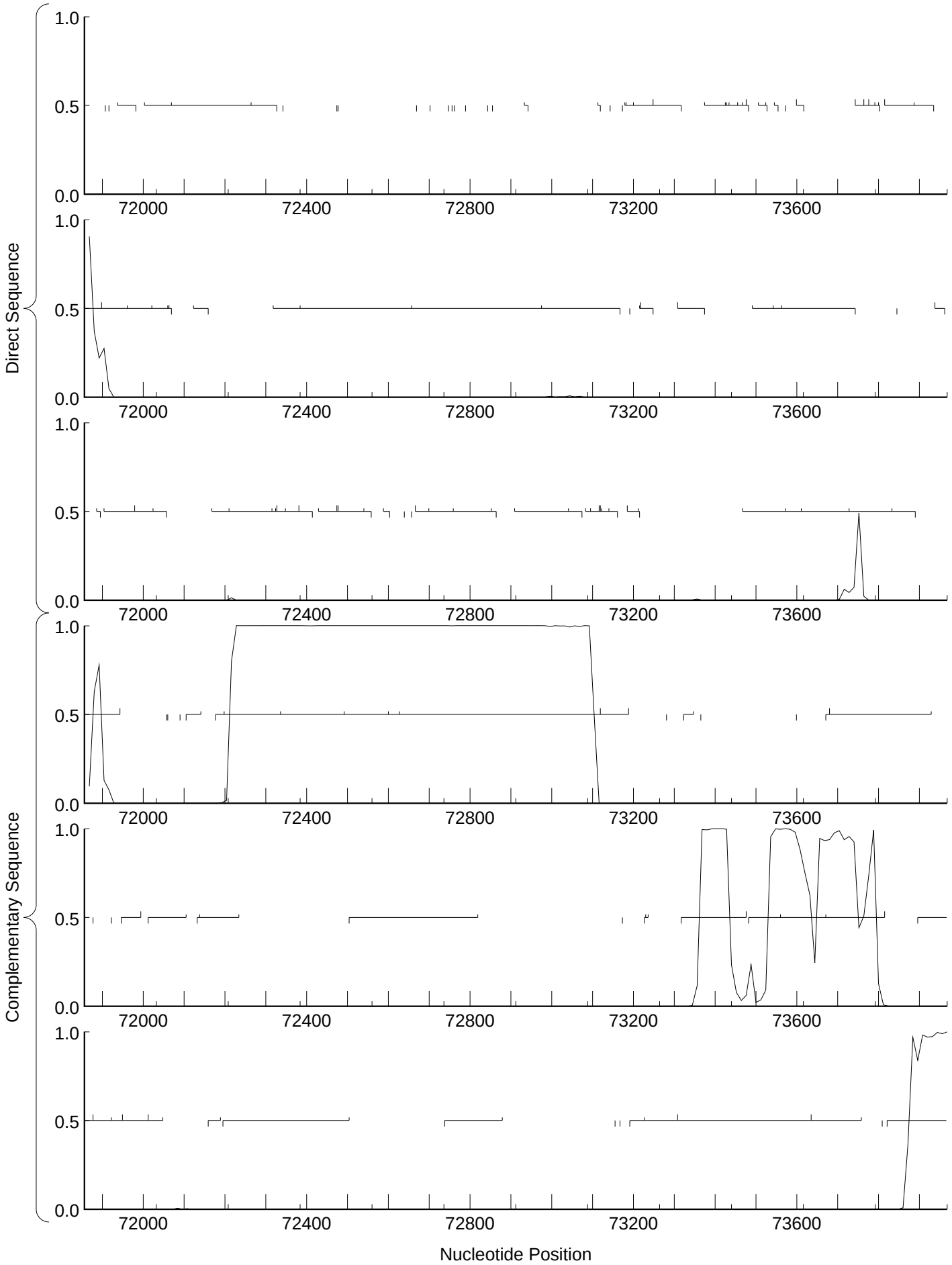

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Nucleotide Position

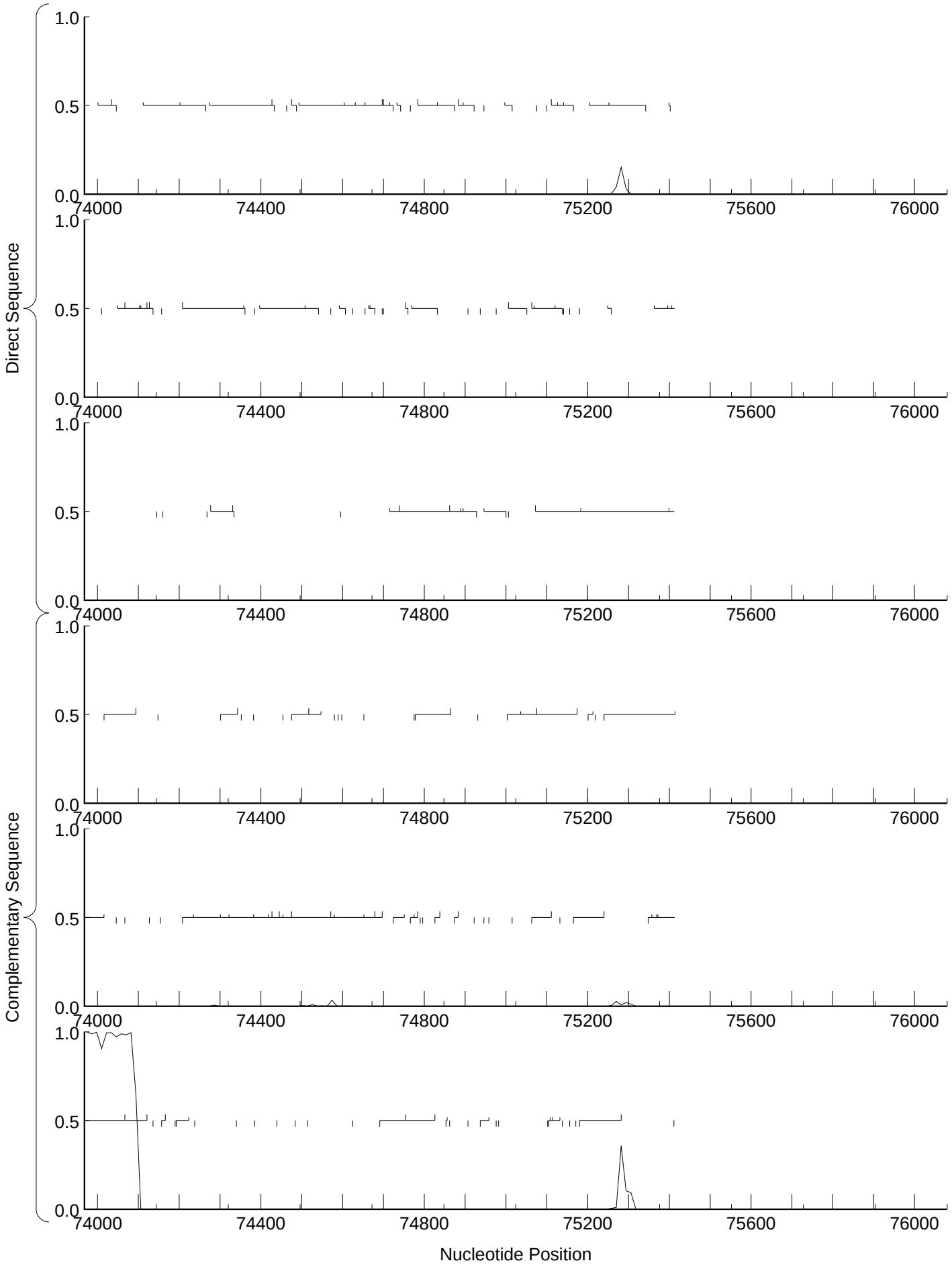

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64800
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Direct Sequence
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66000
66400
66800
67200
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Nucleotide Position


Direct Sequence
Complementary Sequence
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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


Direct Sequence
Complementary Sequence
1.0
0.5
0.0
74000
74400
74800
75200
75600
76000
Nucleotide Position