# GeneMark

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

## PROGRAM INFORMATION

```
Sequence         :  Streptomyces phage Daudau complete sequence, 50602 bp including 11-base 3' overhang (CGCCGA
Analysis Date    :  3/29/24 at 4:28:48
Pages            :  25
Sequence Length  :  50602 bp
GC Content       :   67.12%

Window Length    :  96 bp
Window Step      :  12 bp
Threshold Value  :  0.500

PS-Version       :  1.2

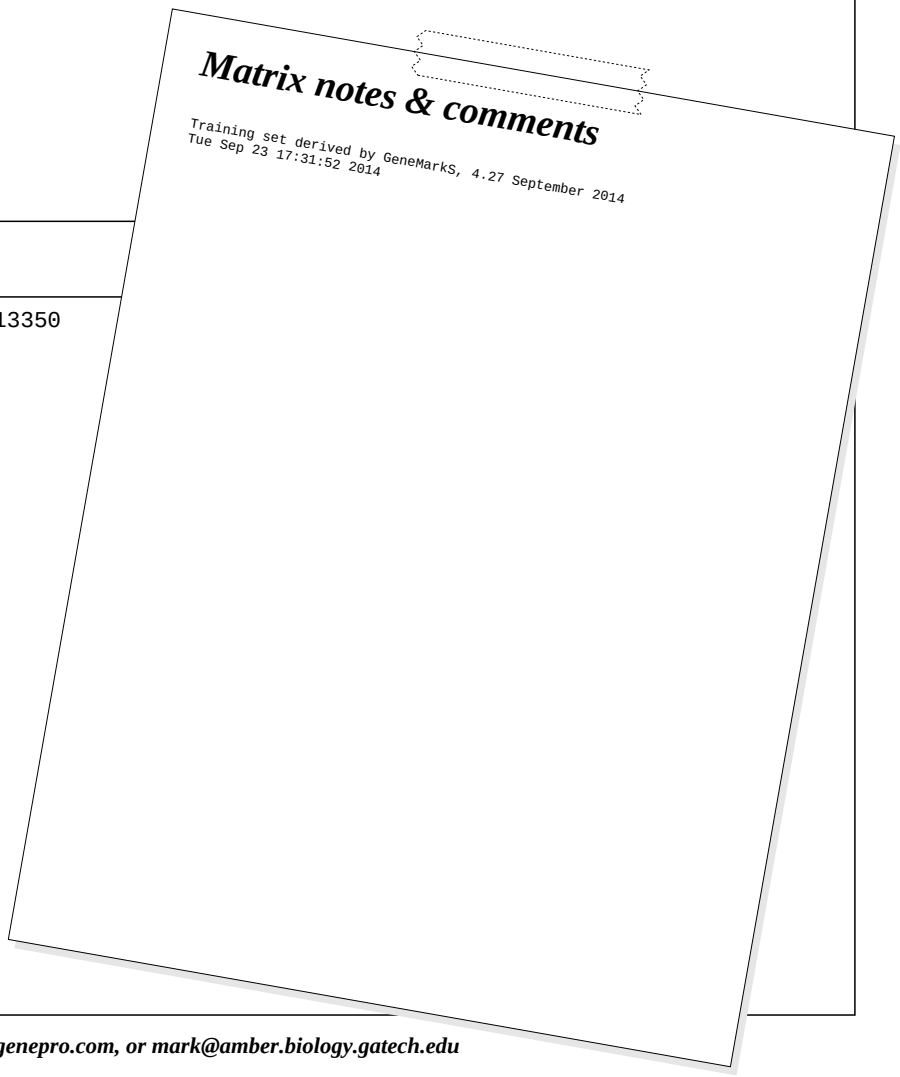
GeneMark Options :  PostScript graph,
                    Mark ORFs / splice sites,
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                    List regions and/or splice sites,
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## MATRIX INFORMATION

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Matrix     :  Streptomyces_griseus_NBRC_13350
Author     :  -

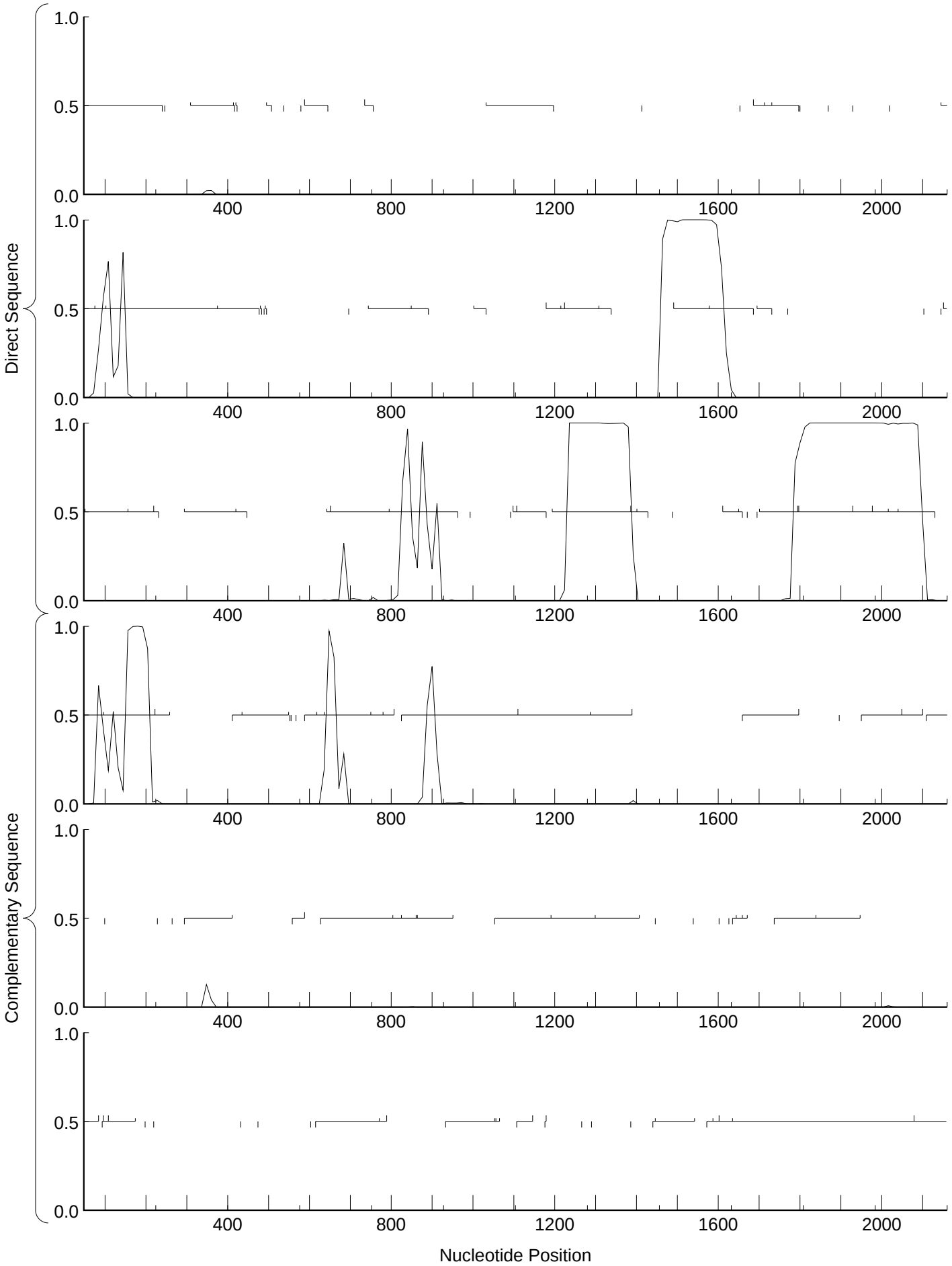
Order      :  4


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

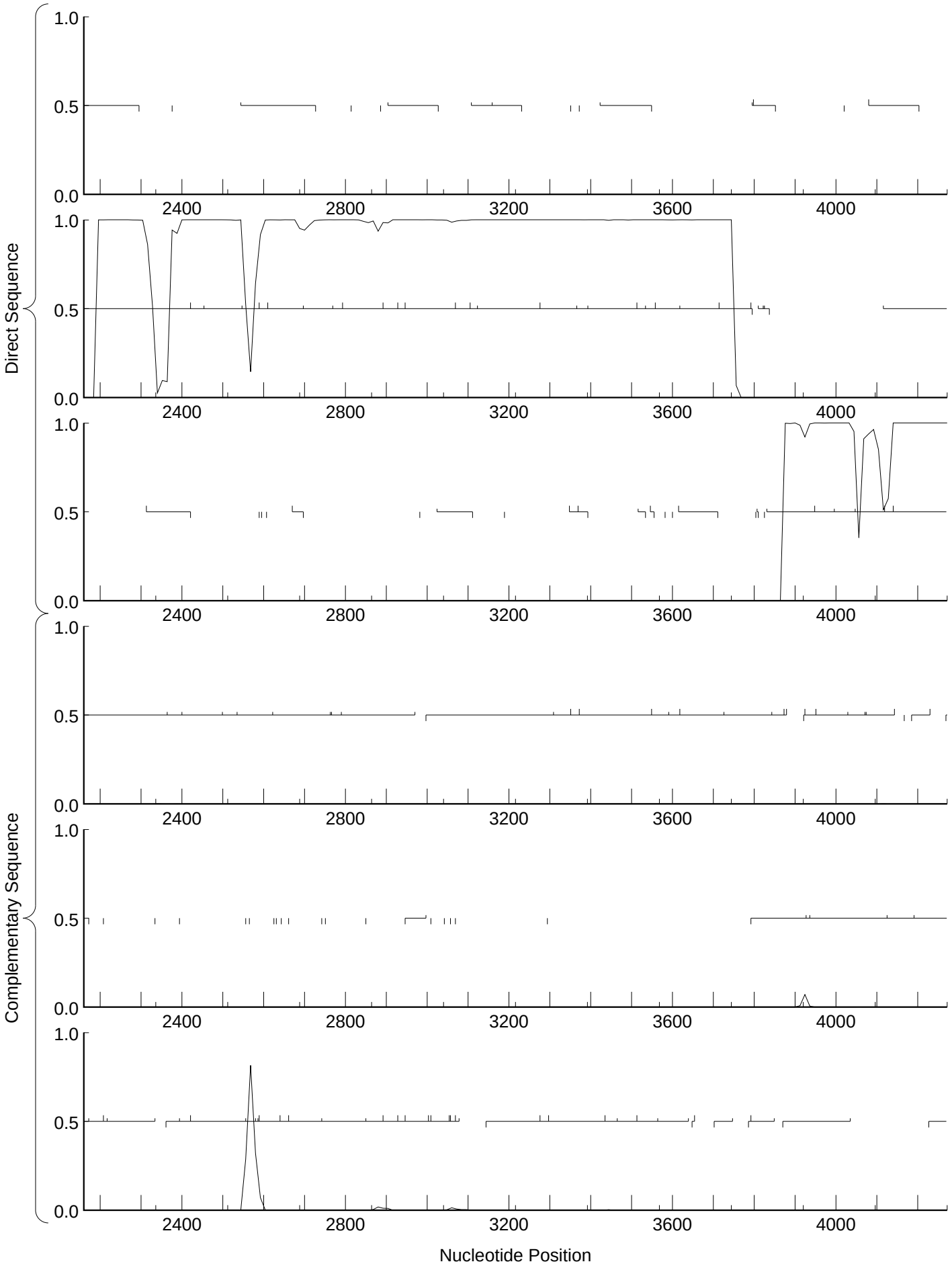



*For help or information, send electronic mail to: custserv@genepro.com, or mark@amber.biology.gatech.edu*

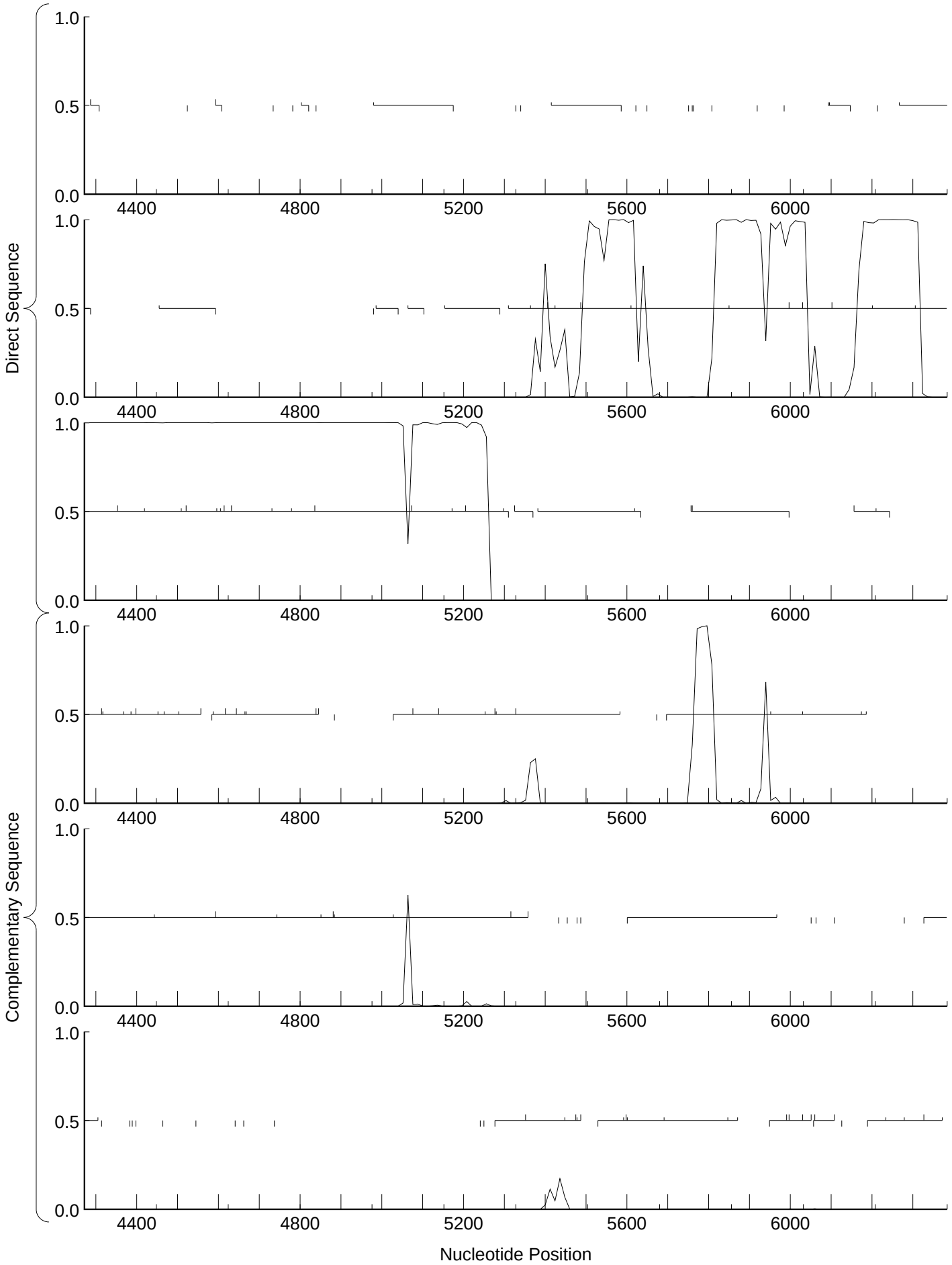
complete sequence, 50602 bp including 11-base 3' overhang (CGCCGAGTCTT), Cluster BD2, Order 4, Window 96, Step 12, 2/25



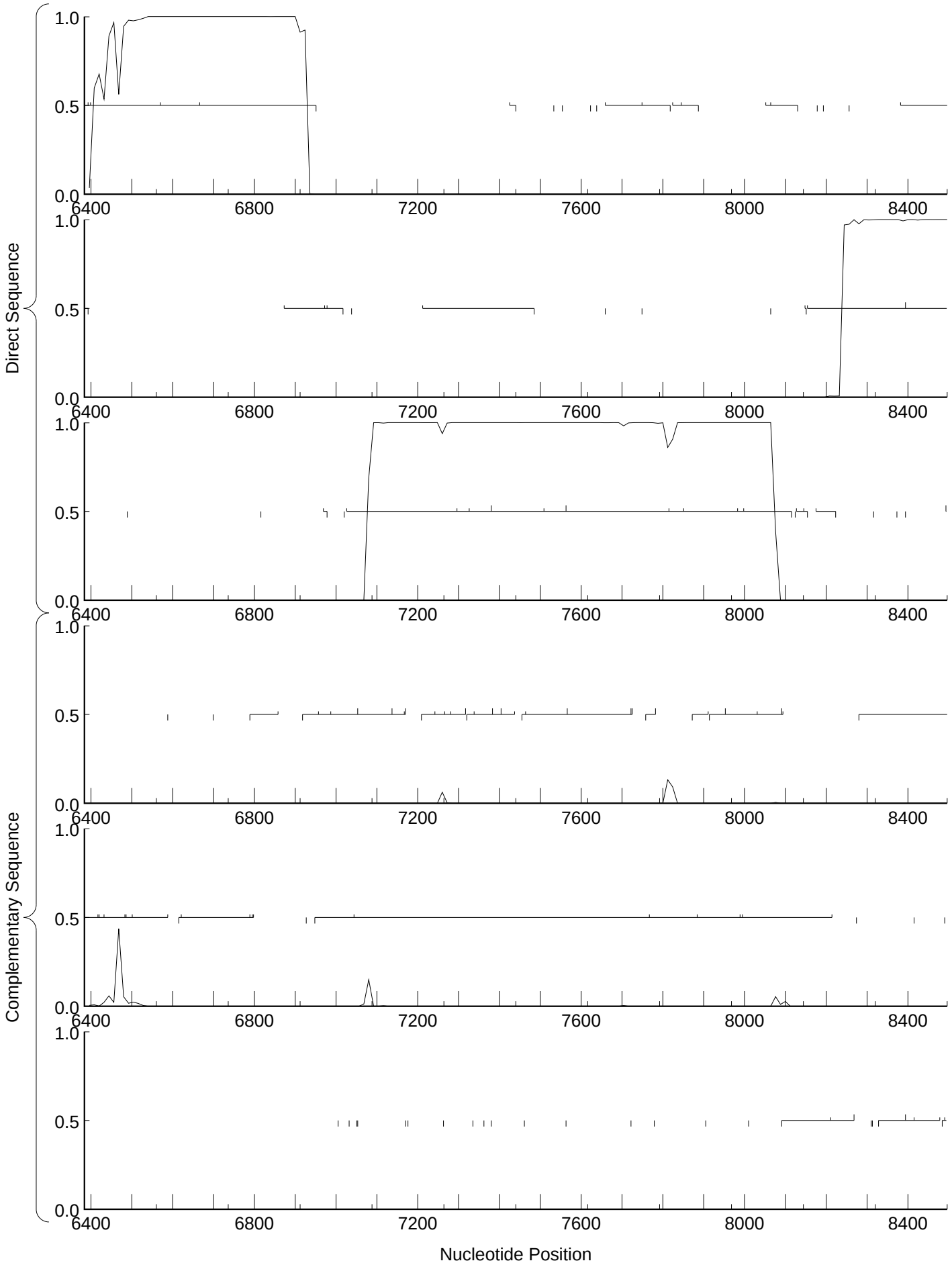
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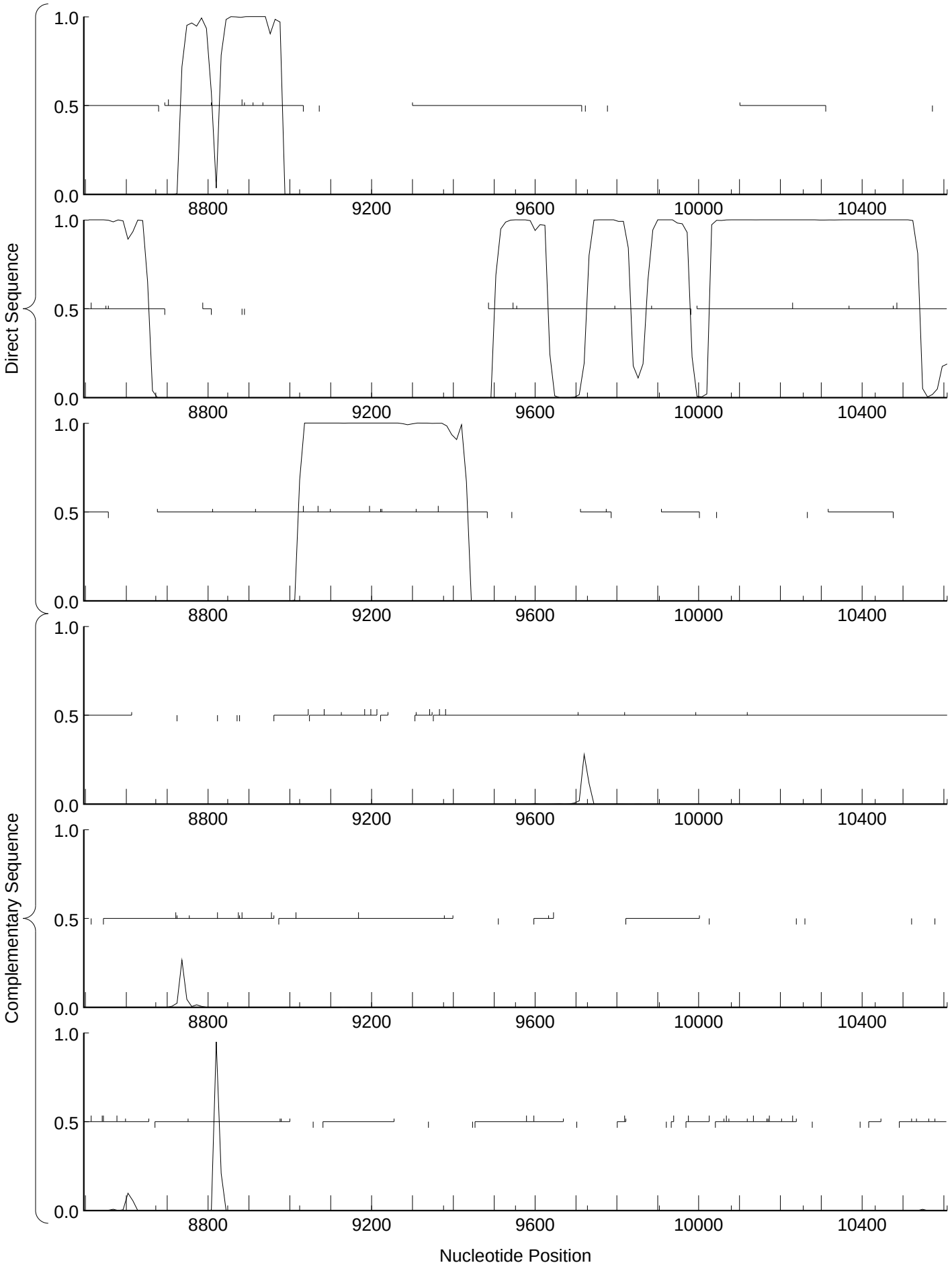
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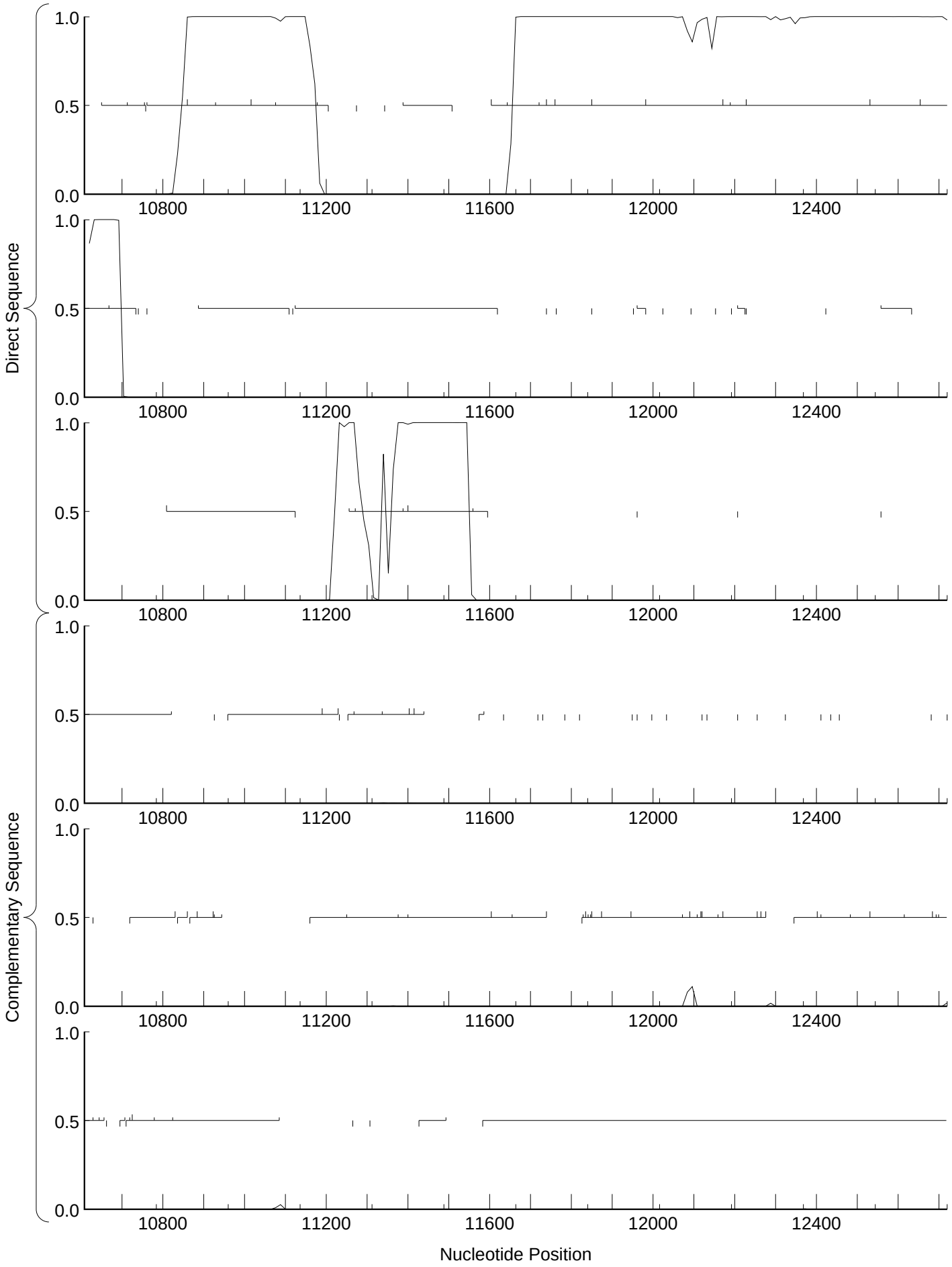
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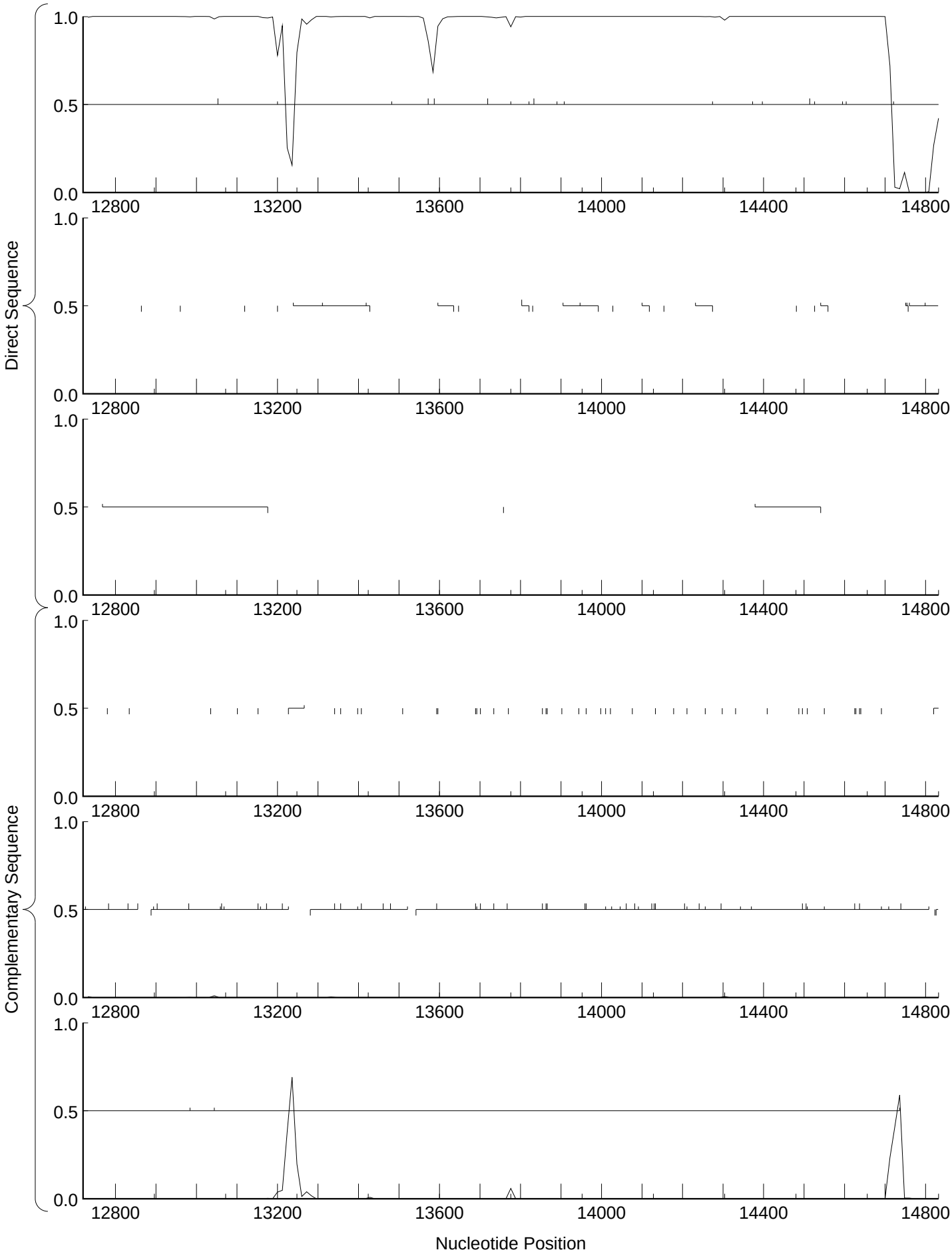
complete sequence, 50602 bp including 11-base 3' overhang (CGCCGAGTCTT), Cluster BD2, Order 4, Window 96, Step 12, 6/25



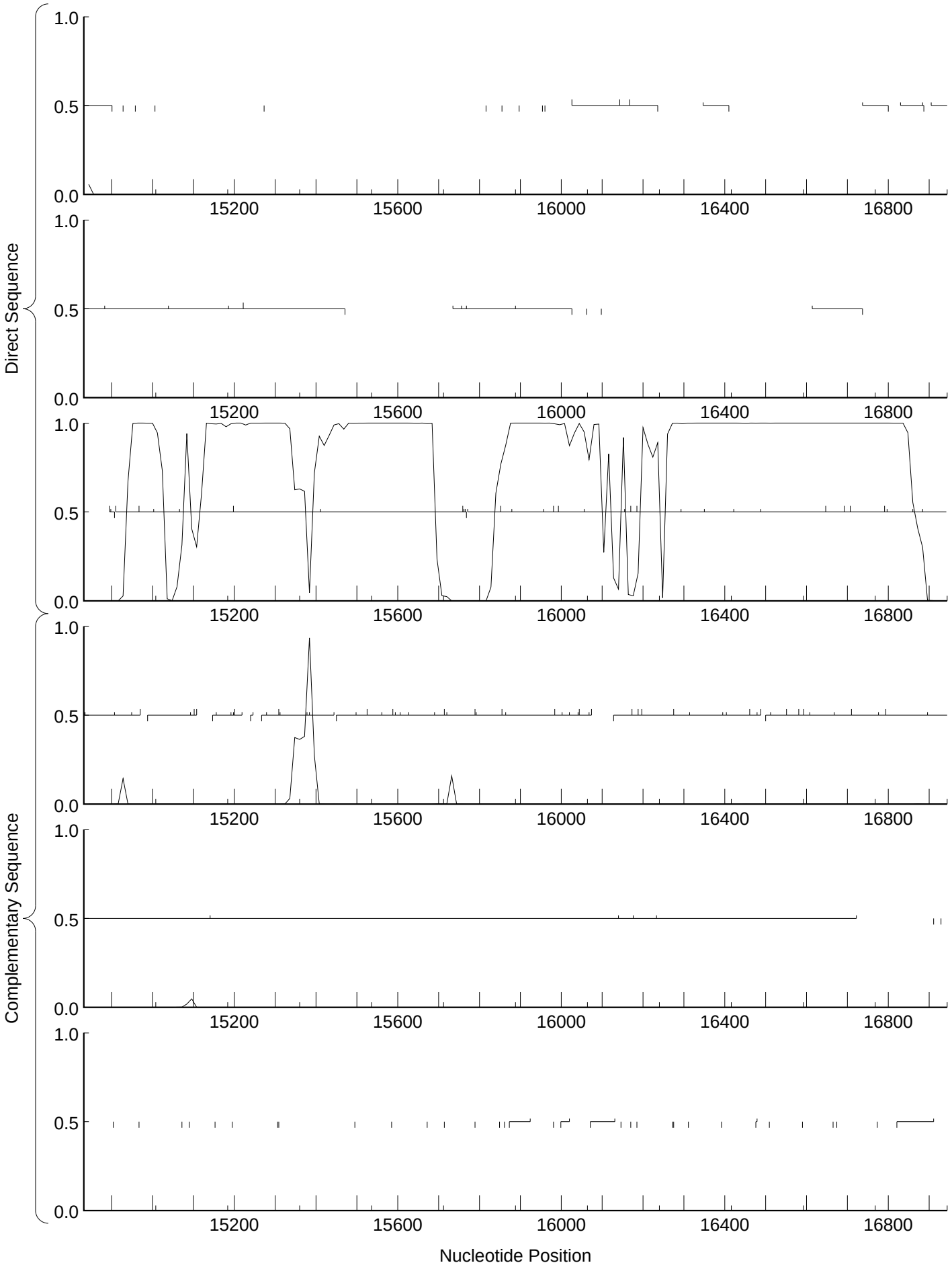
complete sequence, 50602 bp including 11-base 3’ overhang (CGCCGAGTCTT), Cluster BD2, Order 4, Window 96, Step 12, 7/25

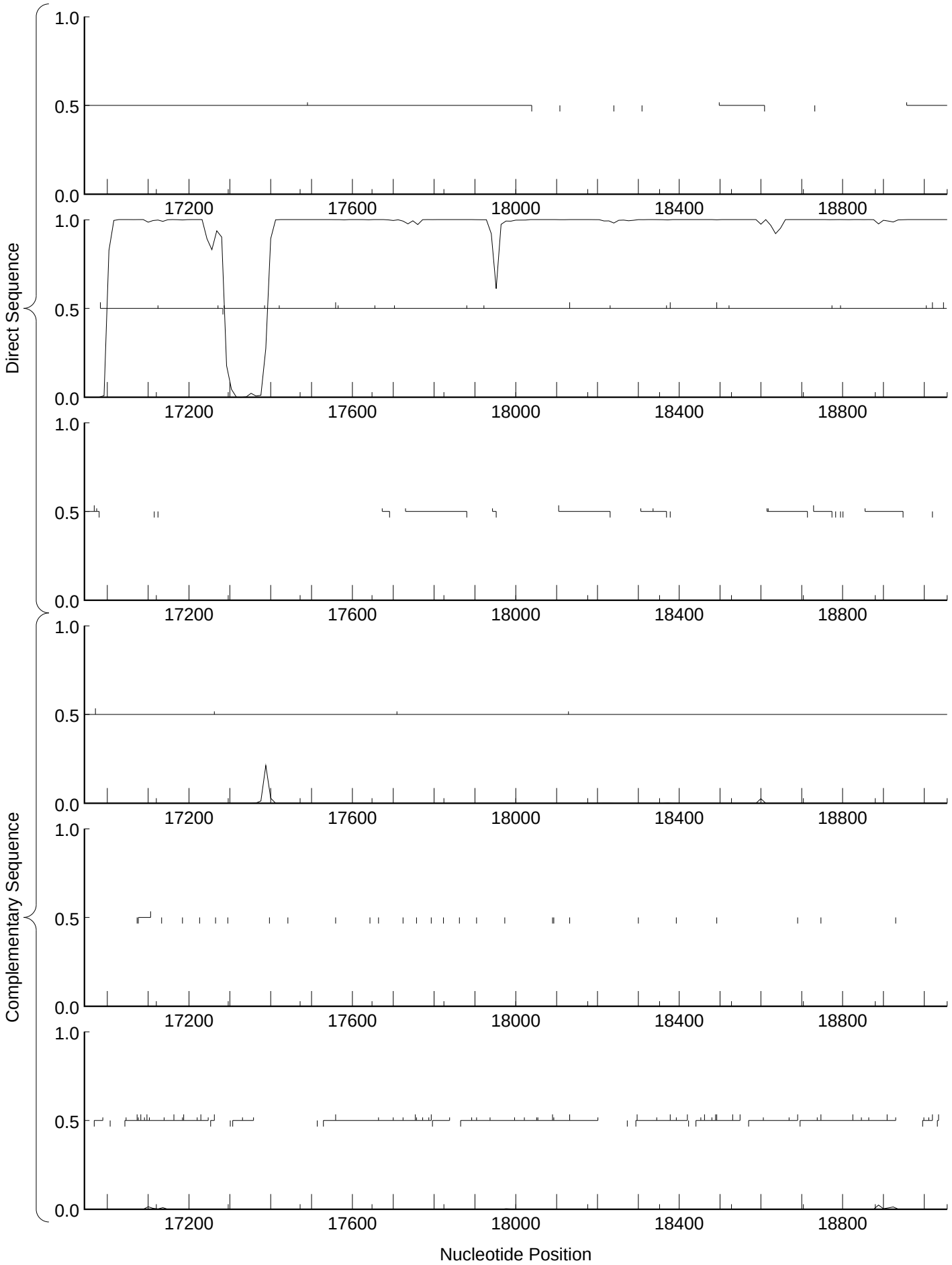


complete sequence, 50602 bp including 11-base 3' overhang (CGCCGAGTCTT), Cluster BD2, Order 4, Window 96, Step 12, 8/25

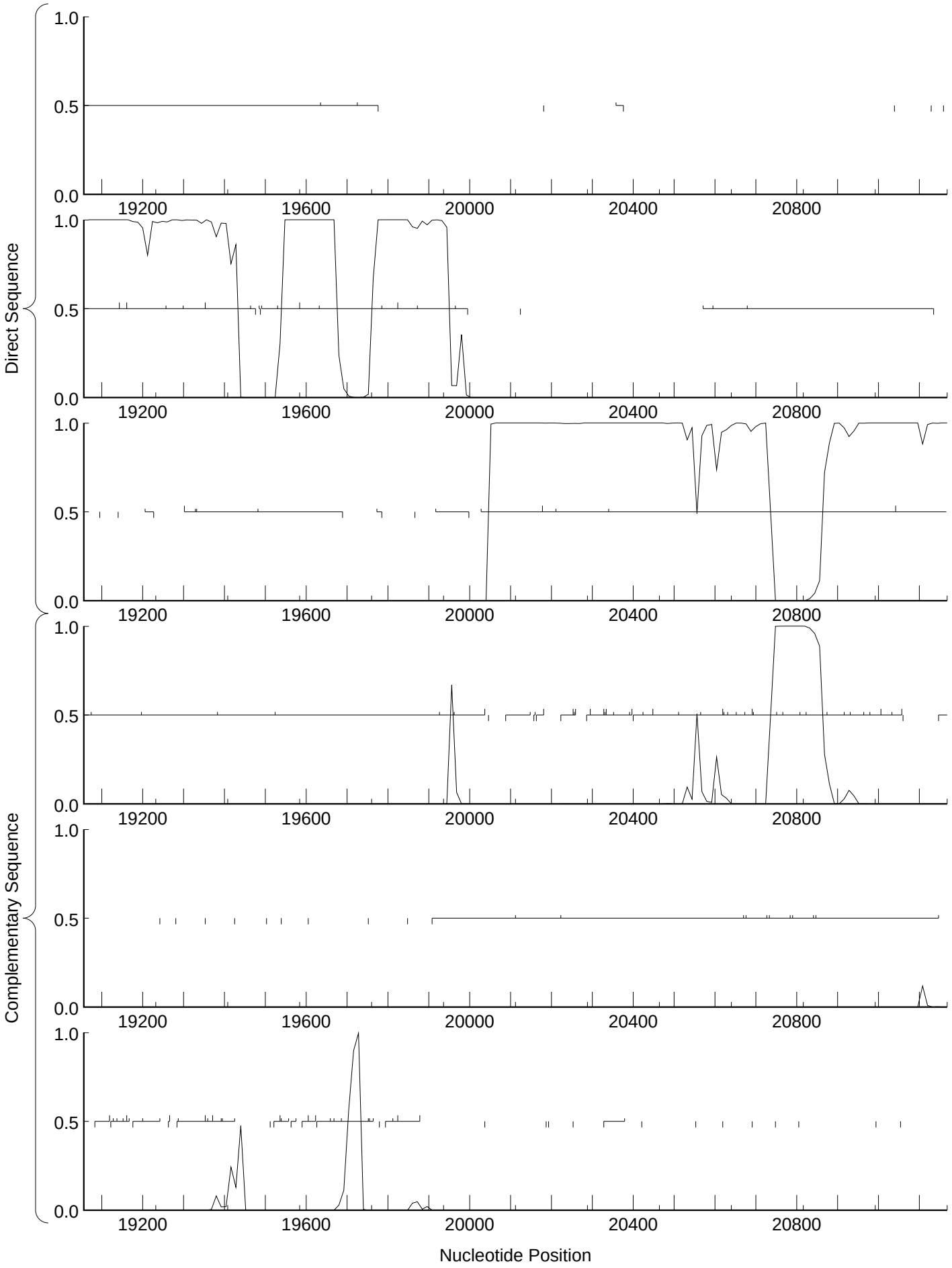


complete sequence, 50602 bp including 11-base 3' overhang (CGCCGAGTCTT), Cluster BD2, Order 4, Window 96, Step 12, 9/25

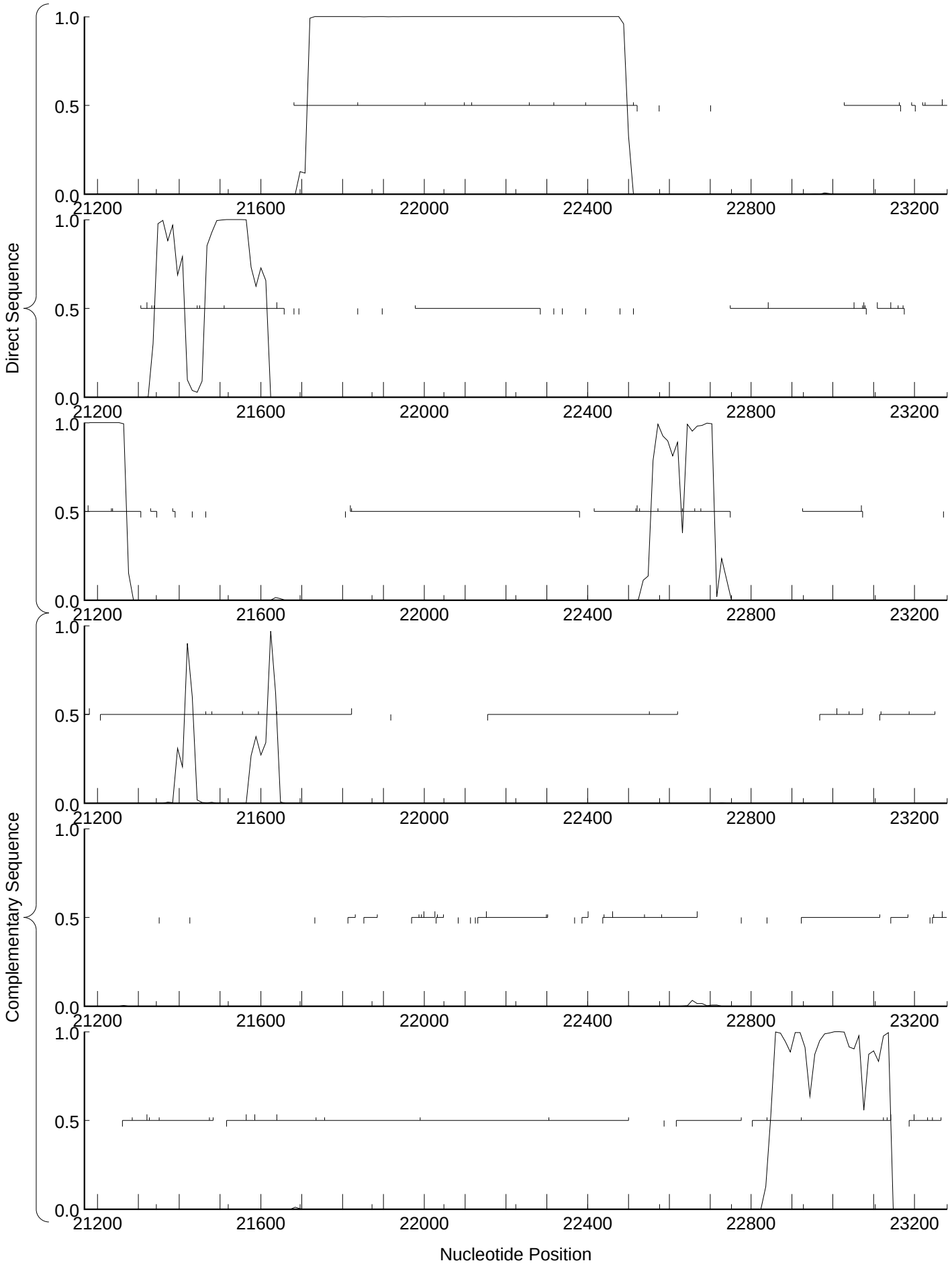


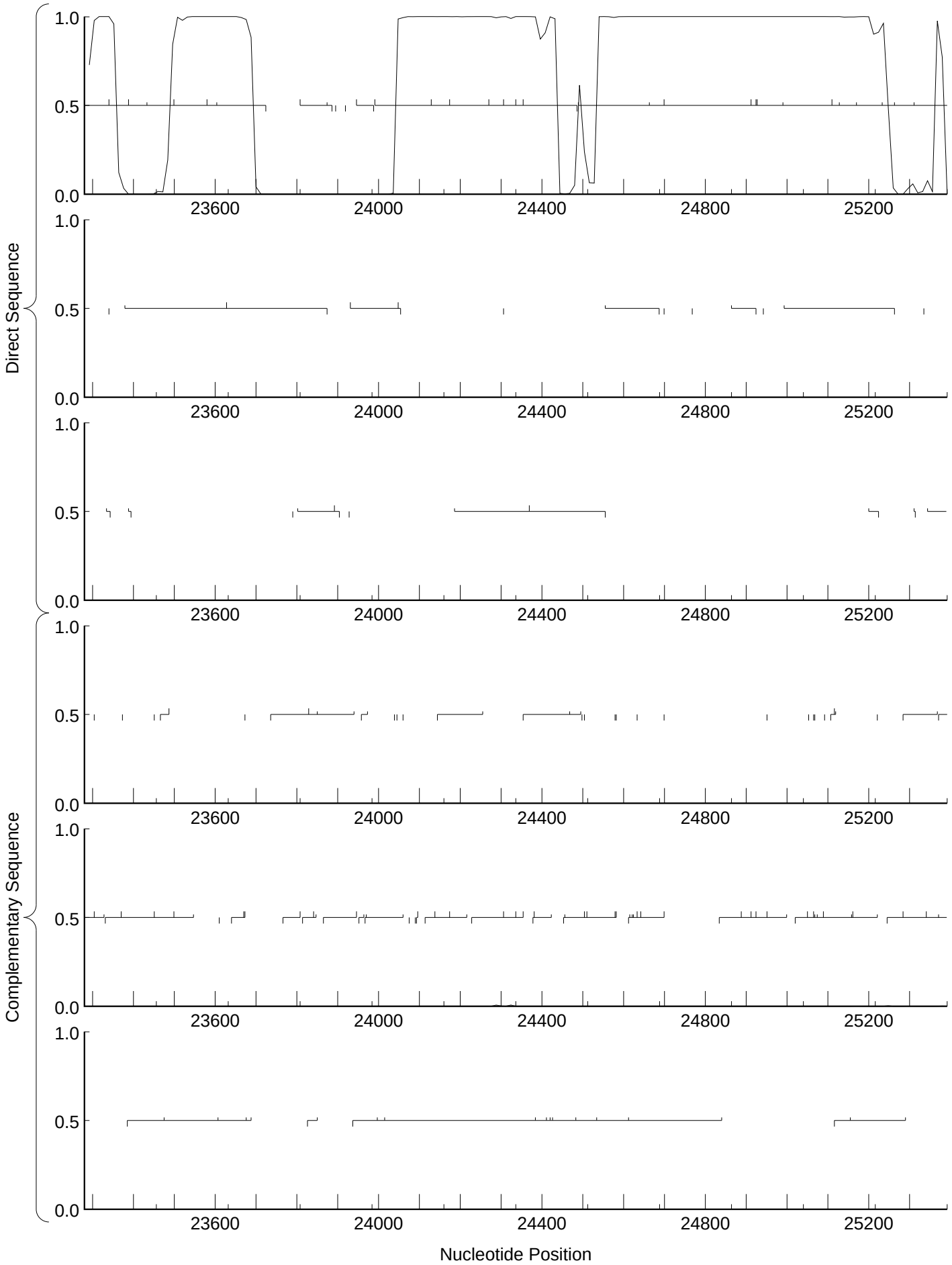

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
17200
17600
18000
18400
18800
Nucleotide Position

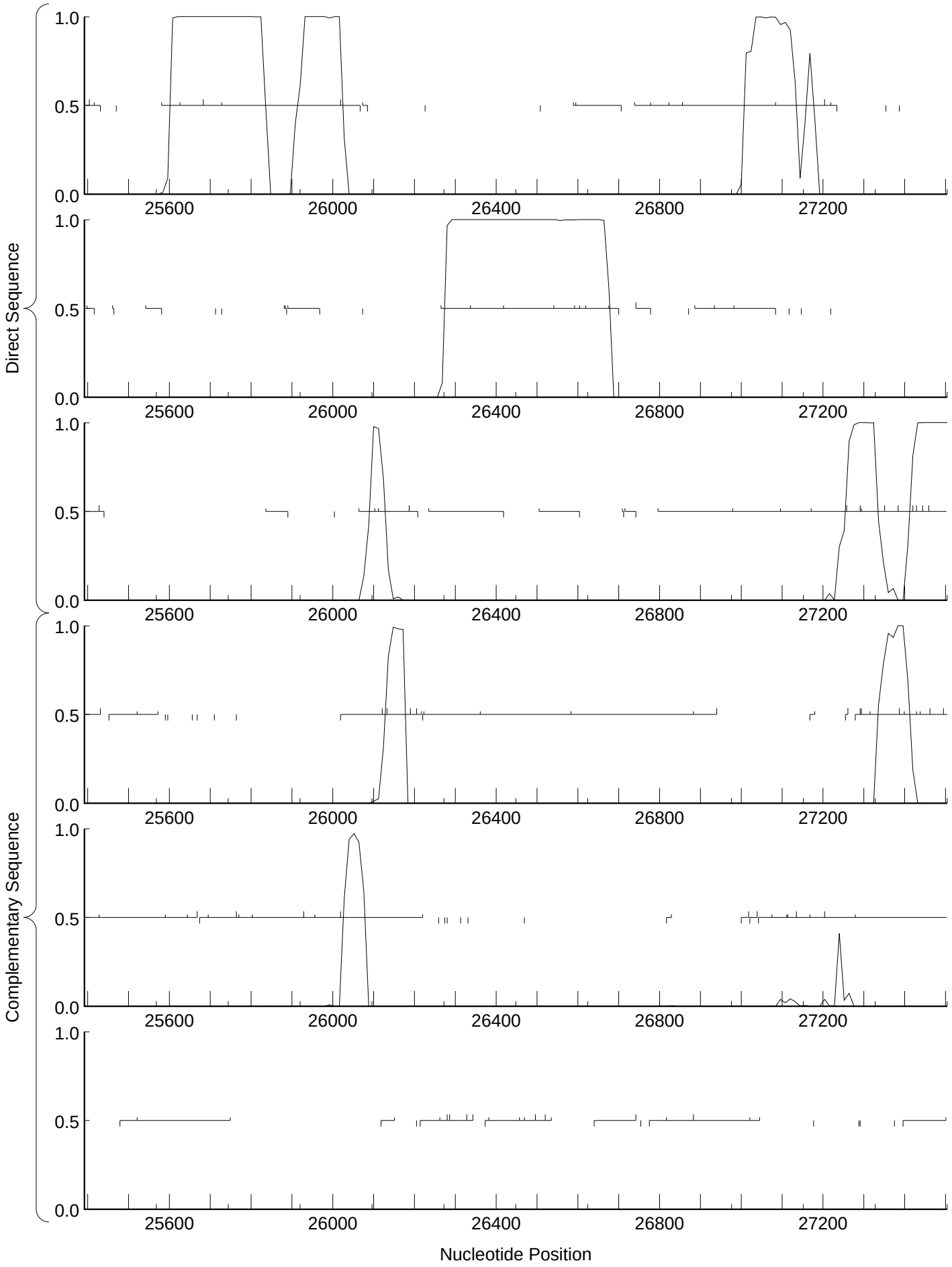
mplete sequence, 50602 bp including 11-base 3’ overhang (CGCCGAGTCTT), Cluster BD2, Order 4, Window 96, Step 12, 11/25

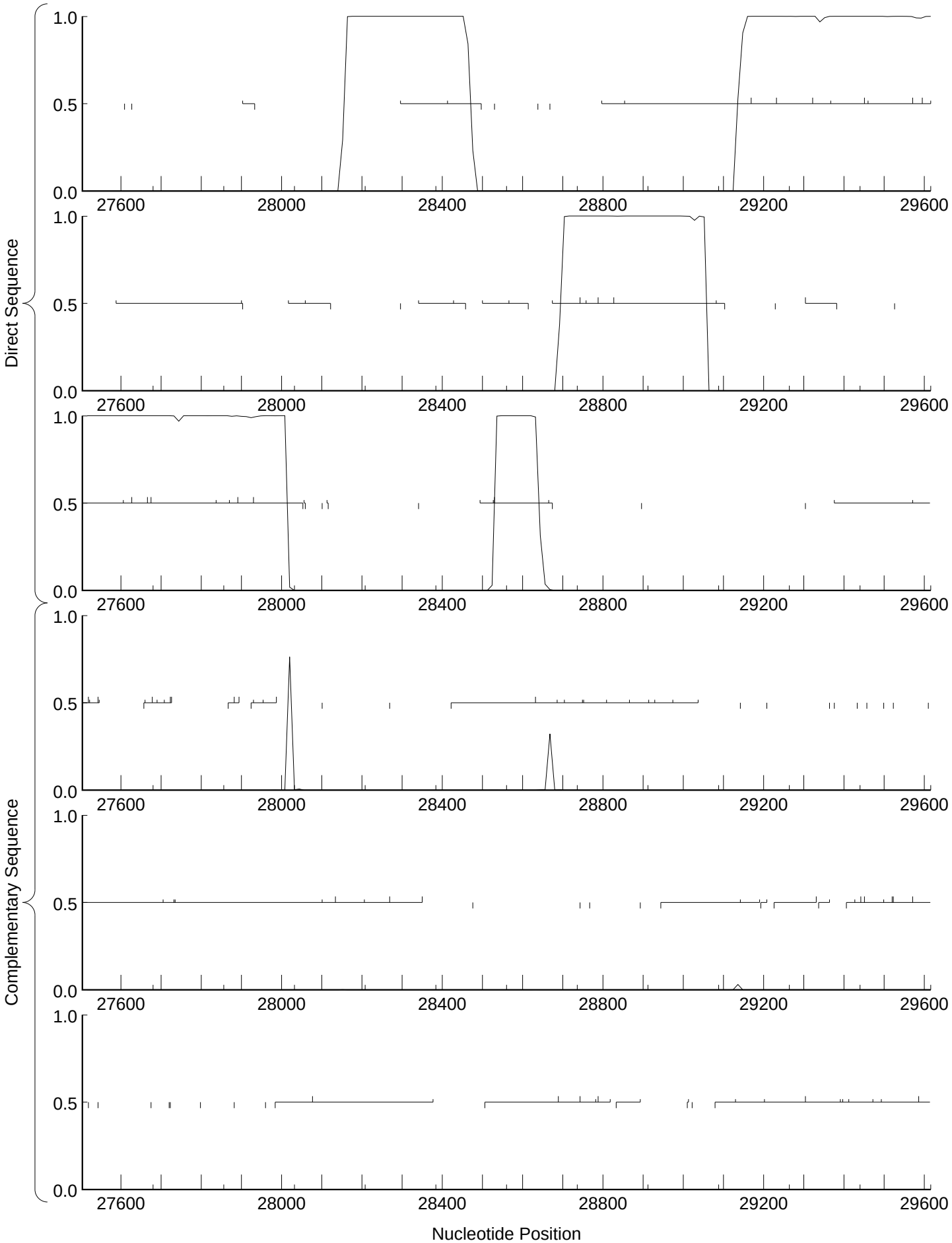


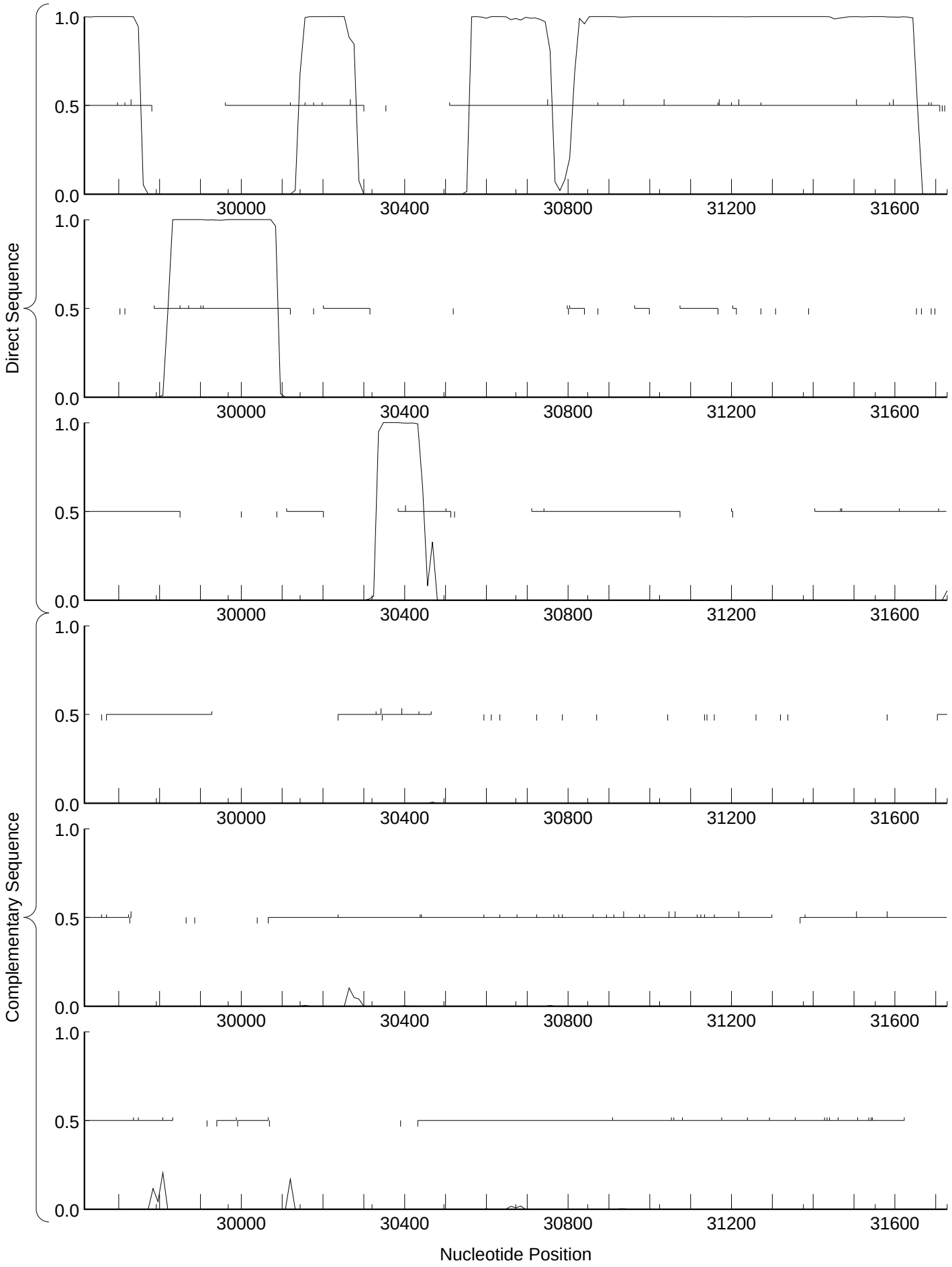
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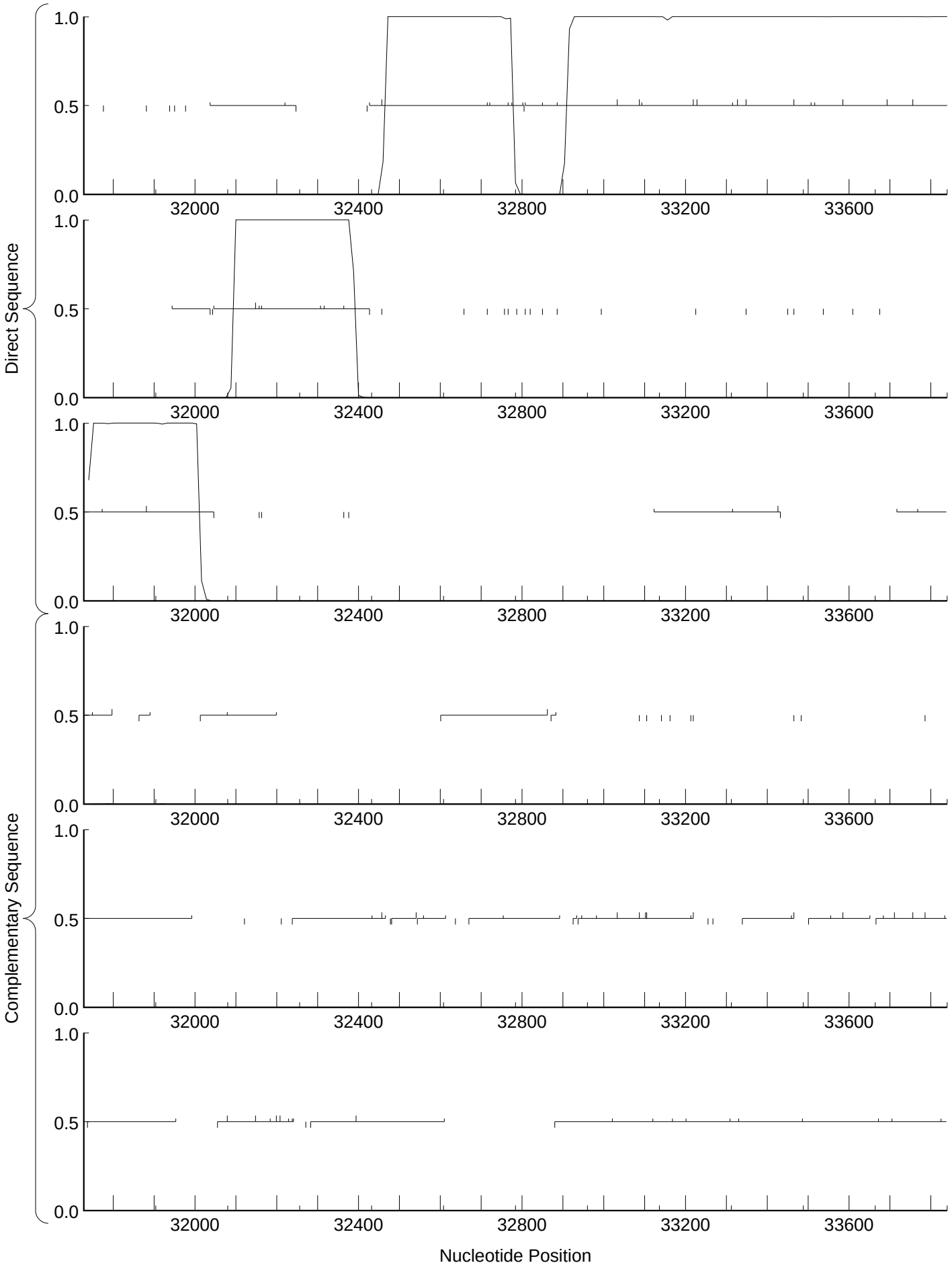


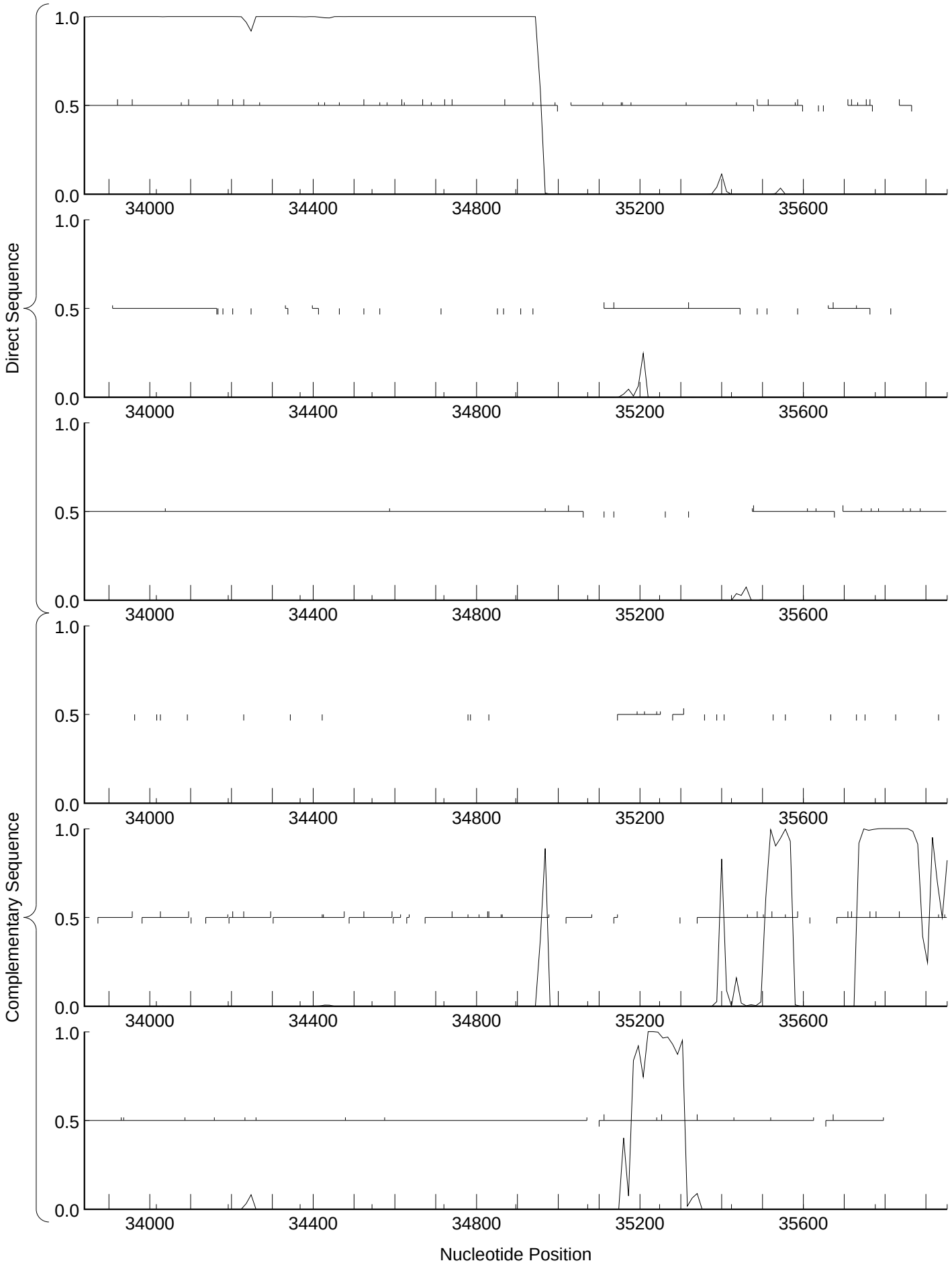

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
23600
24000
24400
24800
25200
Nucleotide Position

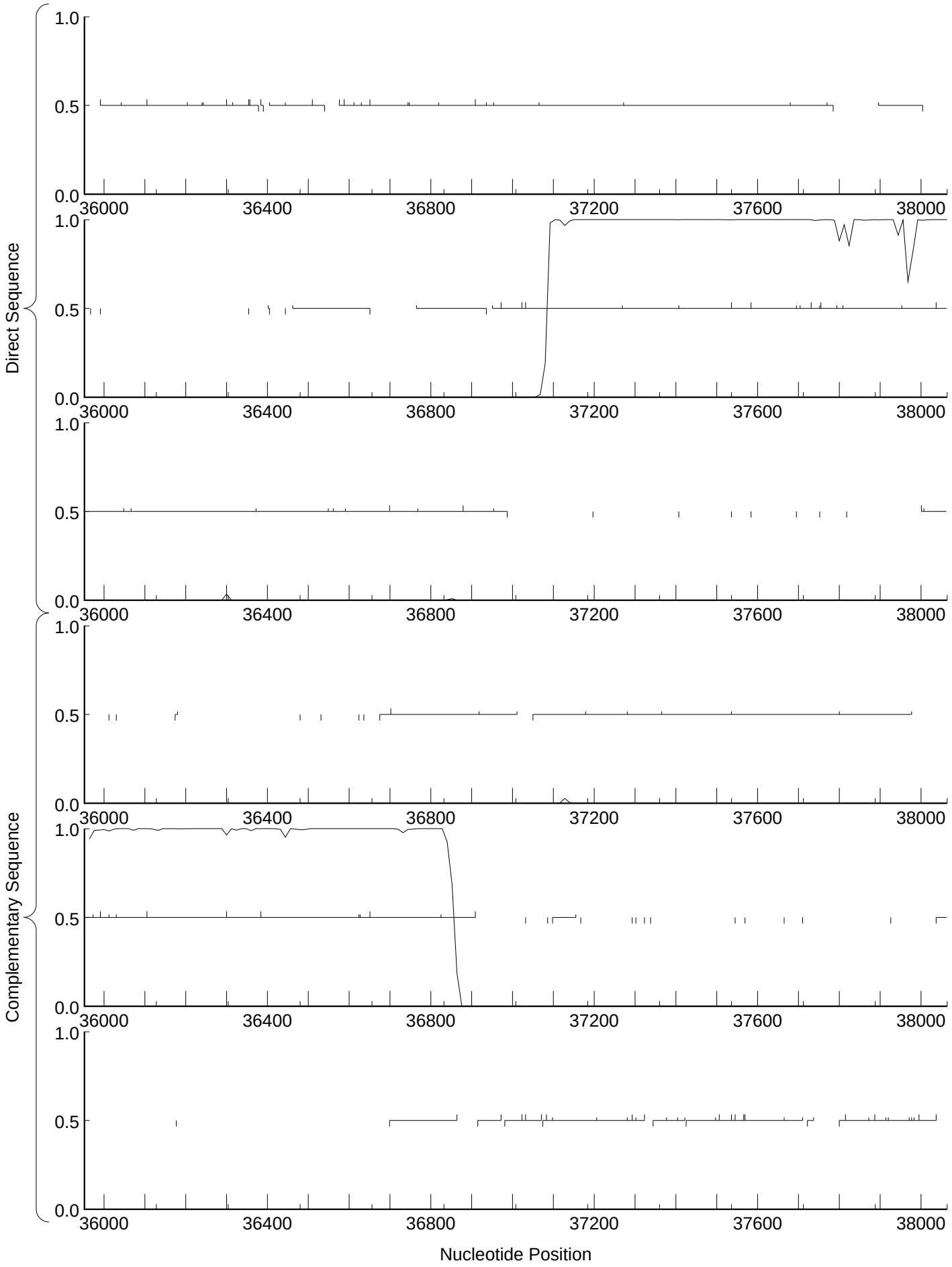

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
25600
26000
26400
26800
27200
Nucleotide Position

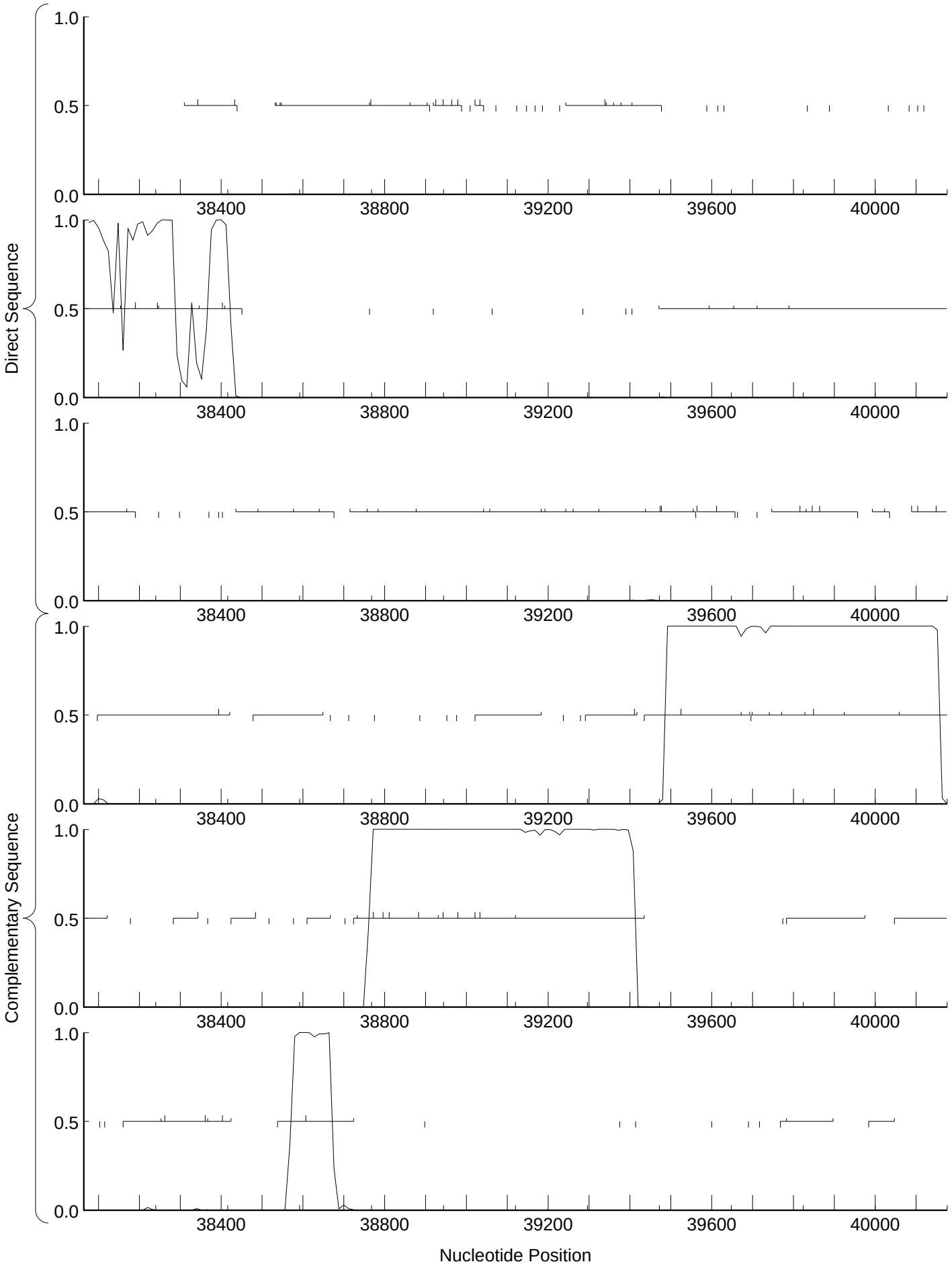

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
27600
28000
28400
28800
29200
29600
Nucleotide Position

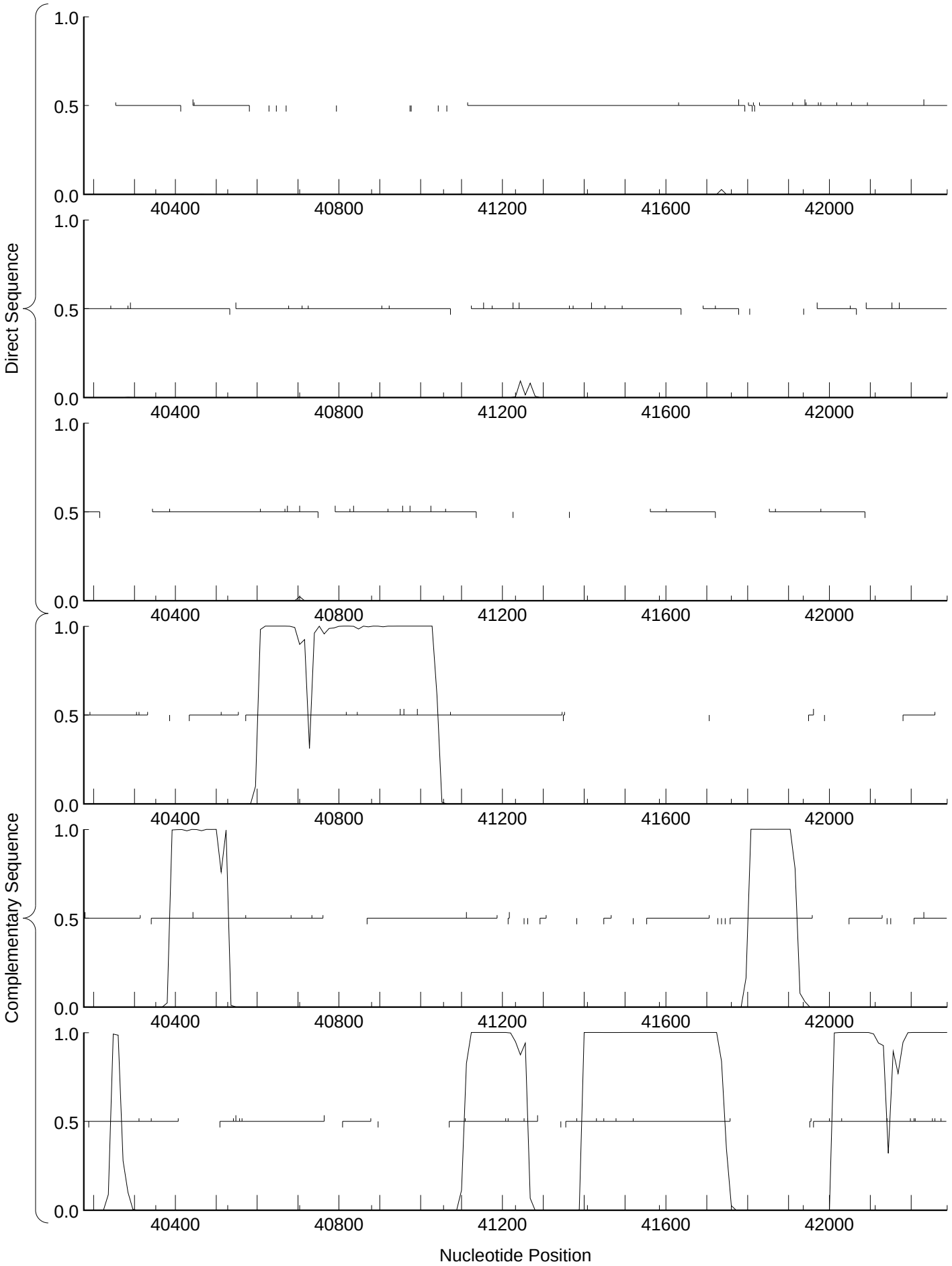

Direct Sequence
Complementary Sequence
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0.0
30000
30400
30800
31200
31600
Nucleotide Position

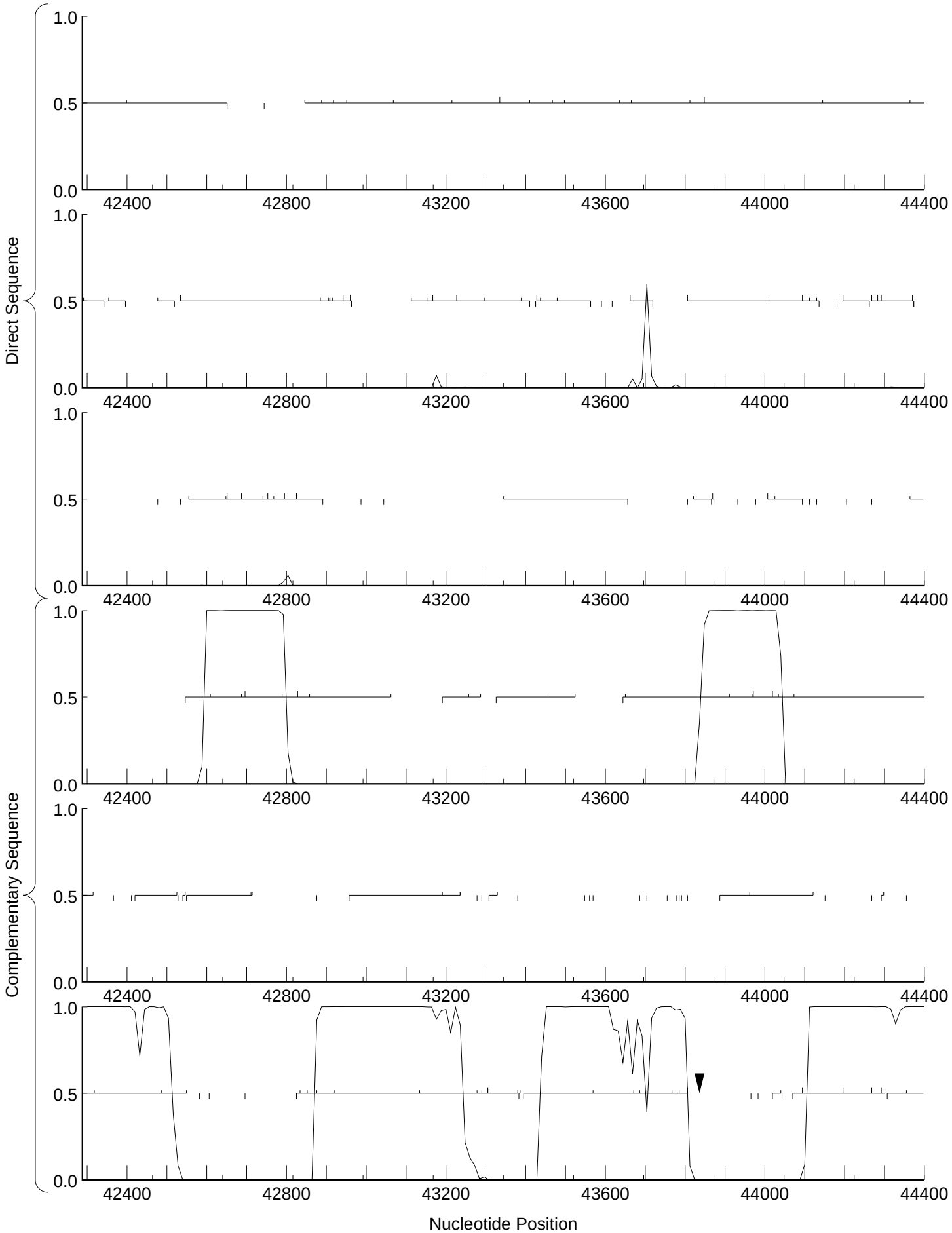

Direct Sequence
Complementary Sequence
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0.5
0.0
32000
32400
32800
33200
33600
Nucleotide Position

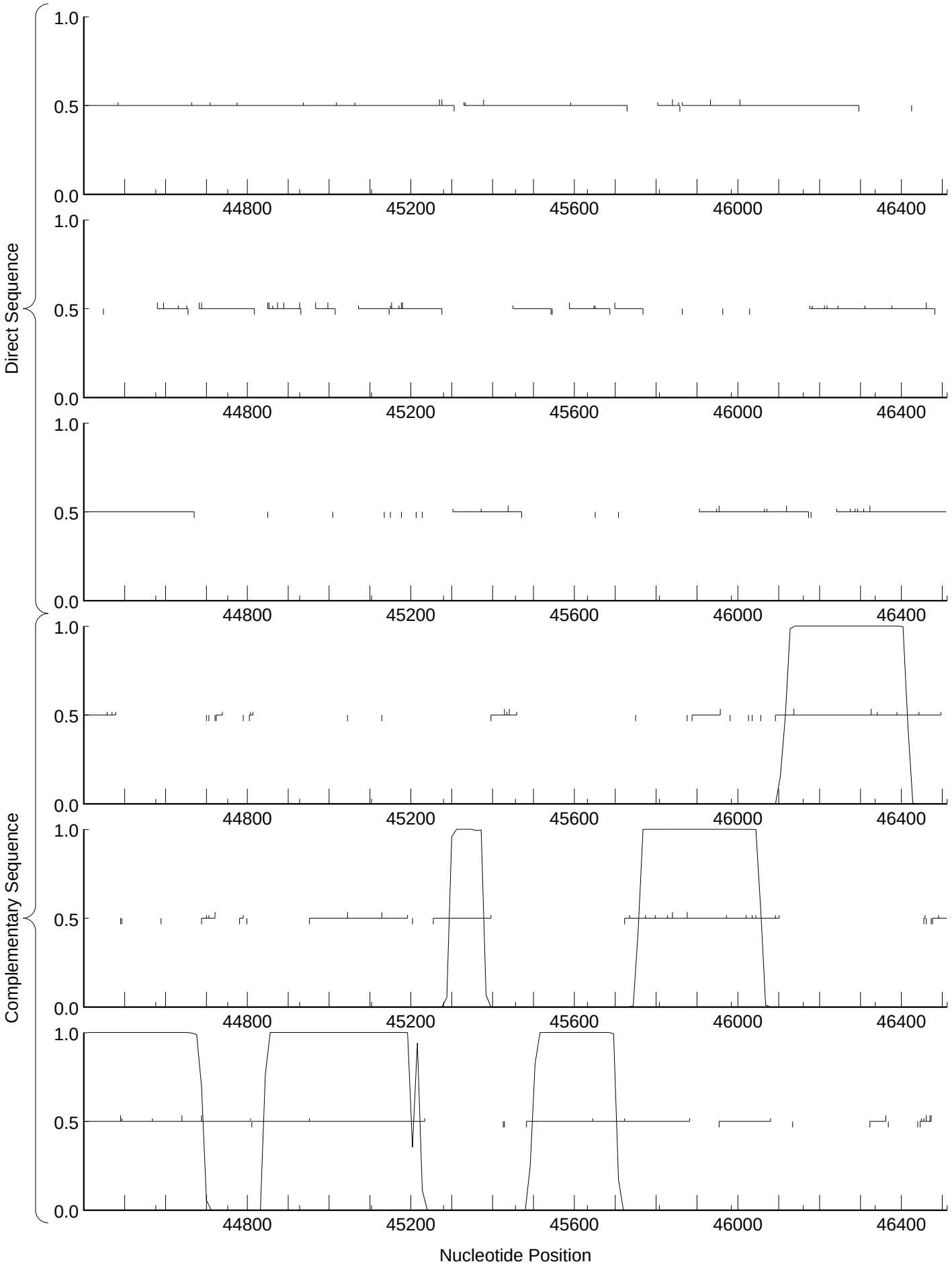

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
34000
34400
34800
35200
35600
Nucleotide Position

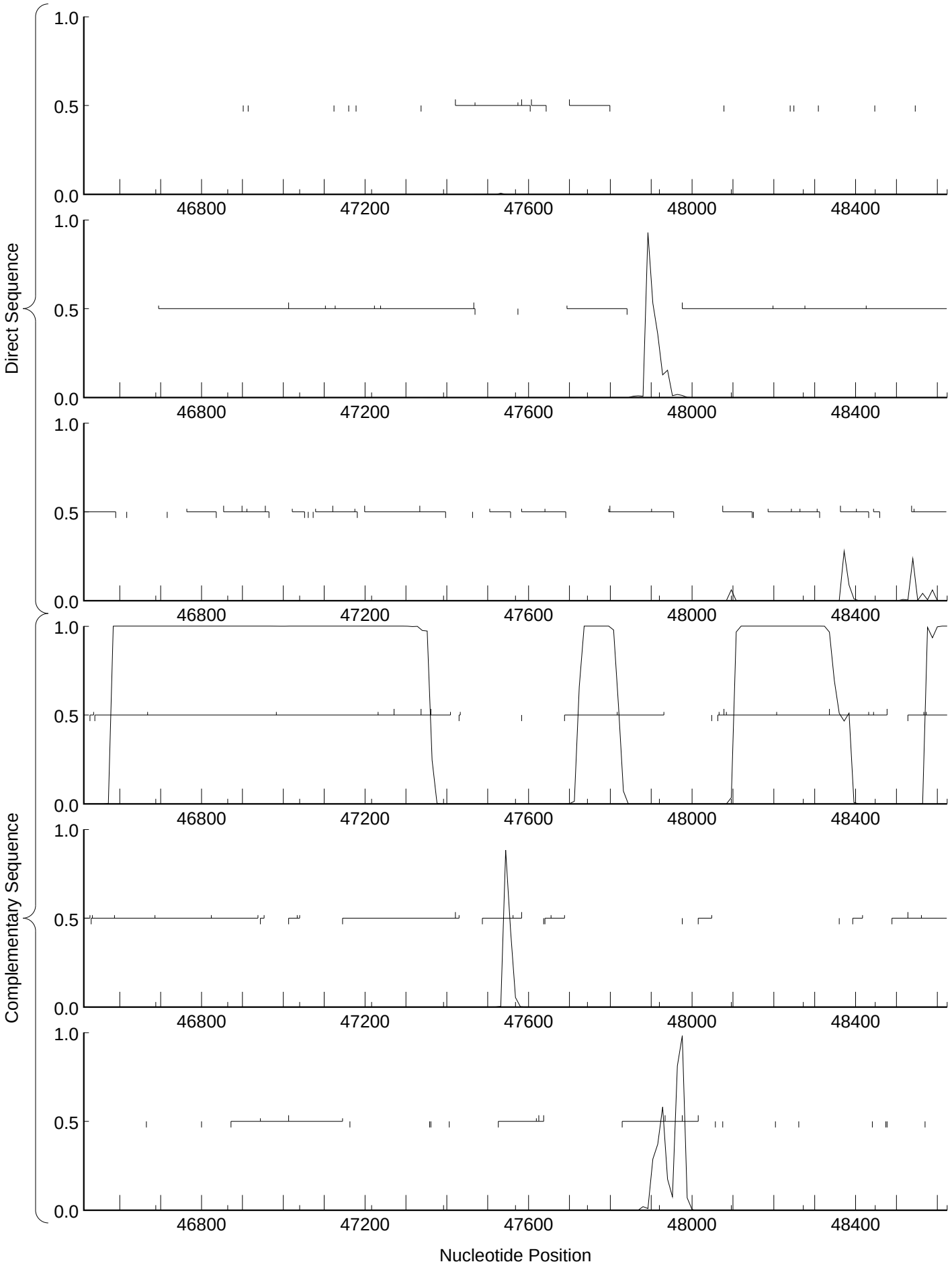

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
36000
36400
36800
37200
37600
38000
Nucleotide Position

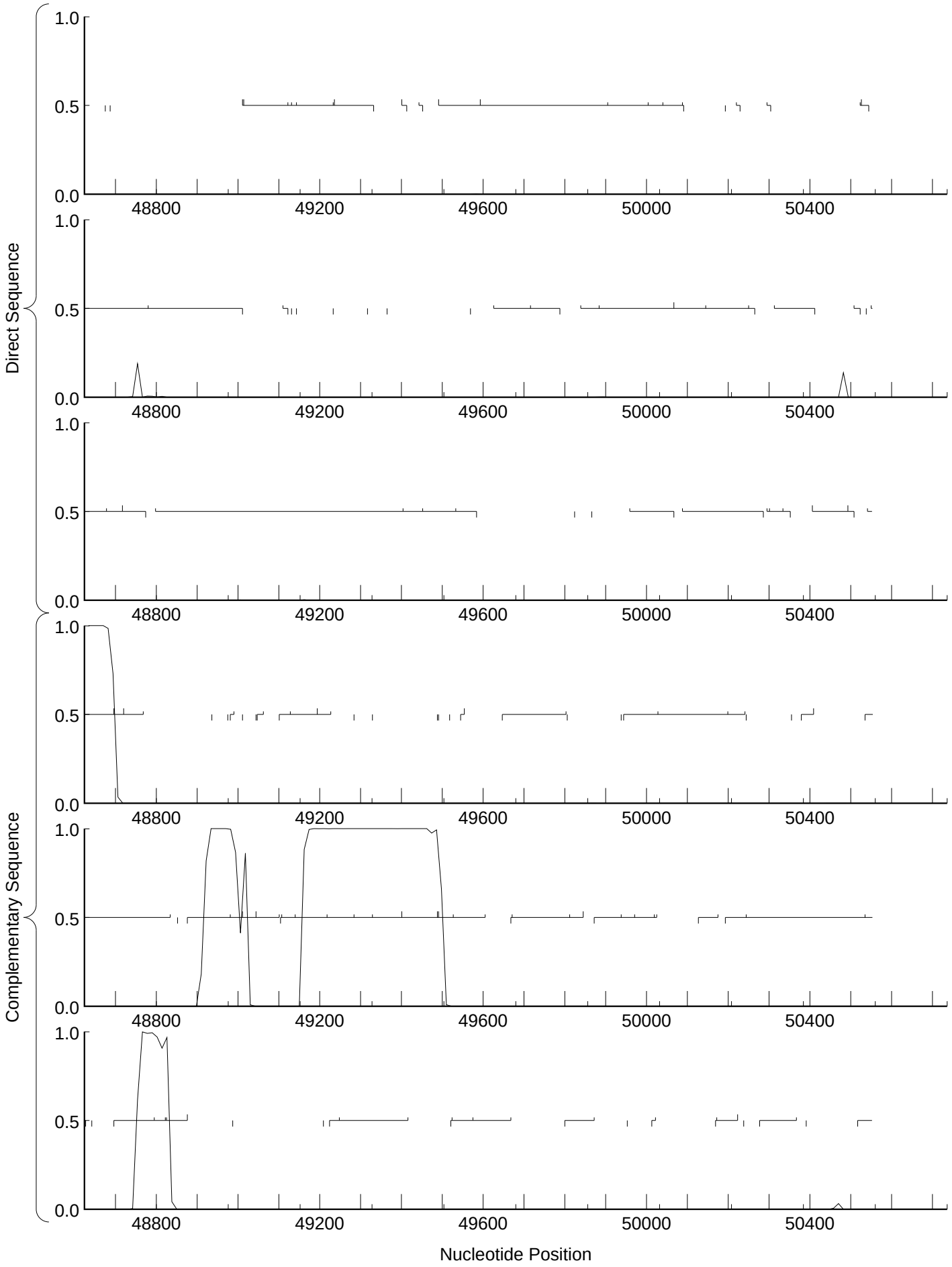

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
38400
38800
39200
39600
40000
Nucleotide Position


Direct Sequence
Complementary Sequence
1.0
0.5
0.0
40400
40800
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
1.0
0.5
0.0
44800
45200
45600
46000
46400
Nucleotide Position


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


Direct Sequence
Complementary Sequence
1.0
0.5
0.0
48800
49200
49600
50000
50400
Nucleotide Position