GeneMark

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

PROGRAM INFORMATION

```
Sequence         :  Mycobacterium phage Rabbs complete sequence, 42430 bp including 10-base 3' overhang (CCCATG
Analysis Date    :  3/28/24 at 19:45:52
Pages            :  22
Sequence Length  :  42430 bp
GC Content       :   66.43%

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

PS-Version       :  1.2

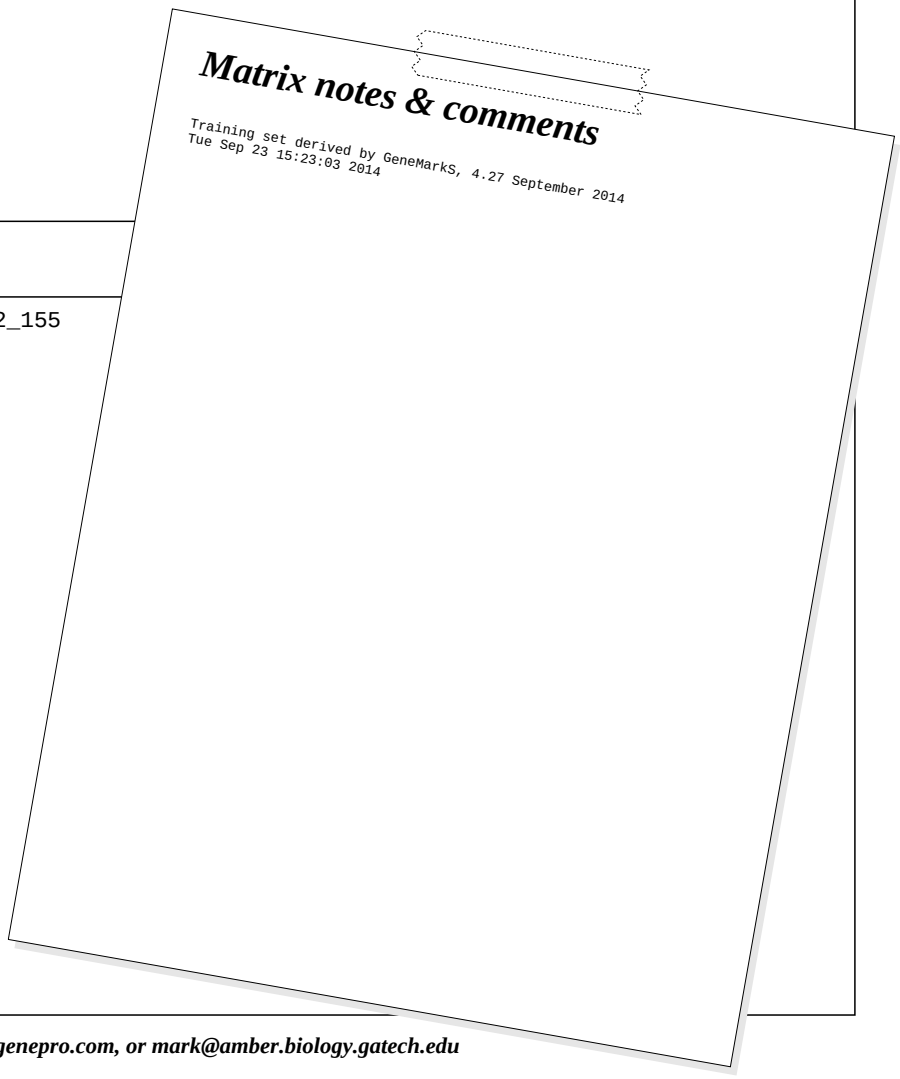
GeneMark Options :  PostScript graph,
                    Mark ORFs / splice sites,
                    List ORFs,
                    List regions and/or splice sites,
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MATRIX INFORMATION

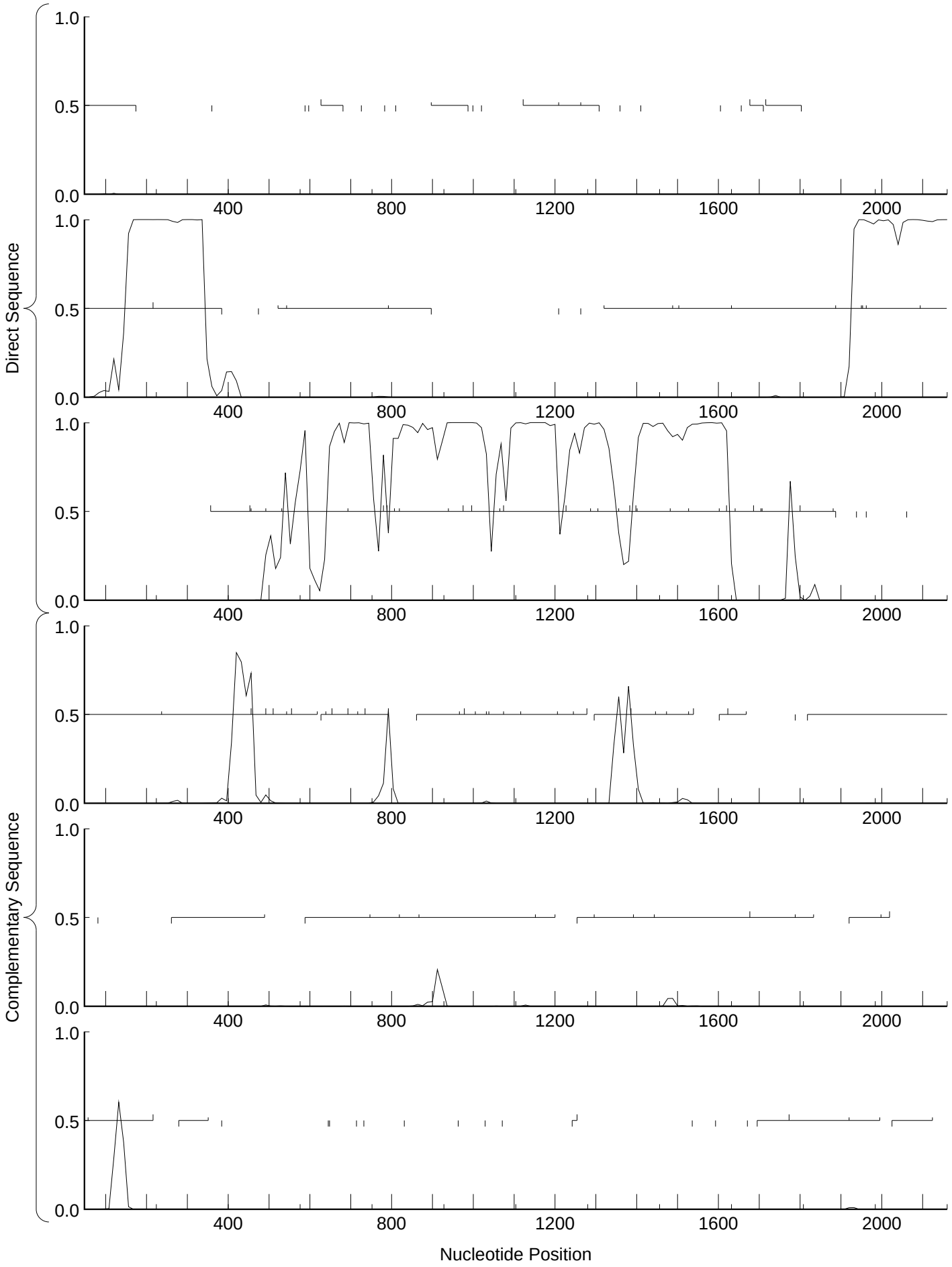
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Matrix     :  Mycobacterium_smegmatis_MC2_155
Author     :  -

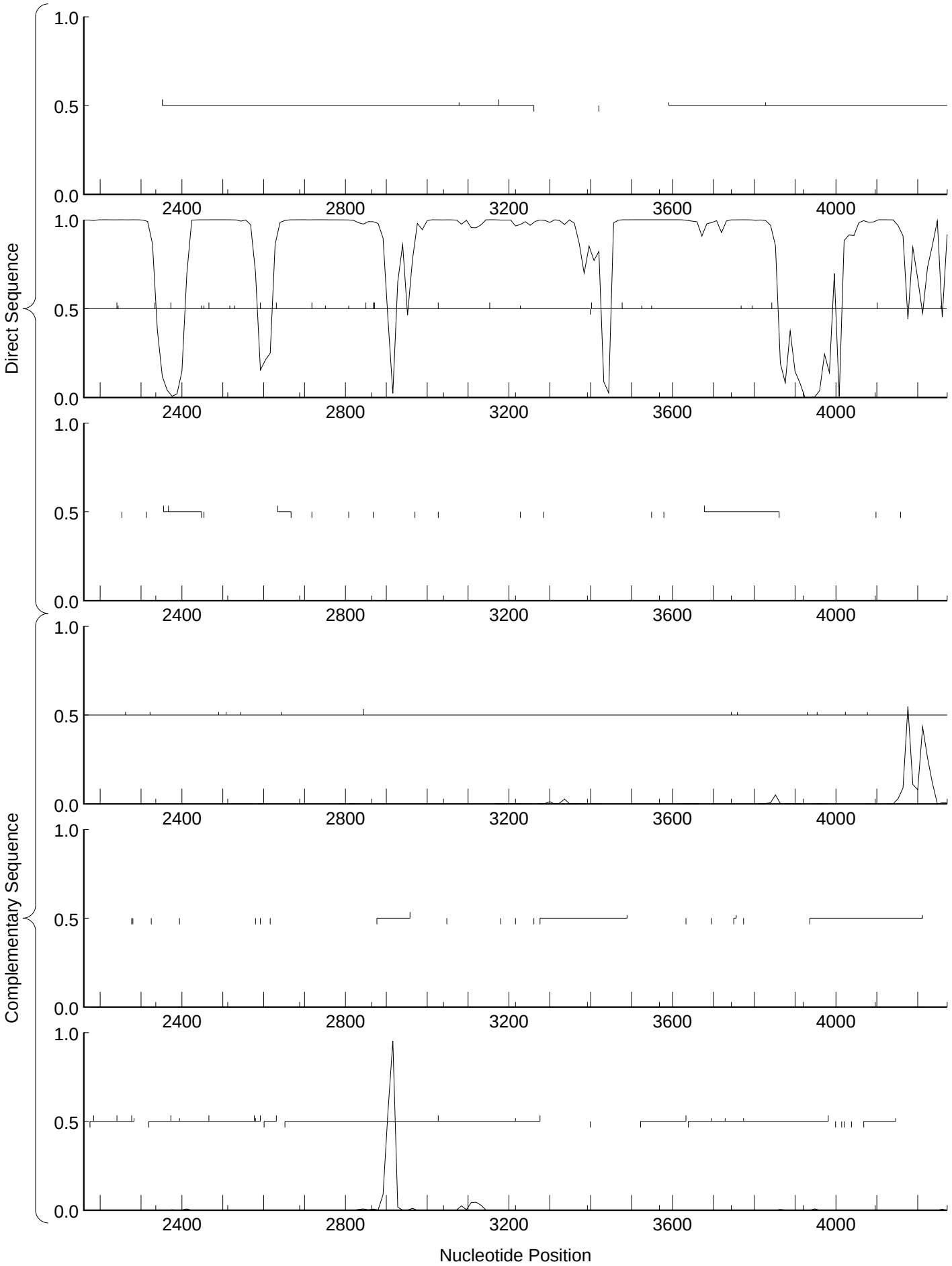
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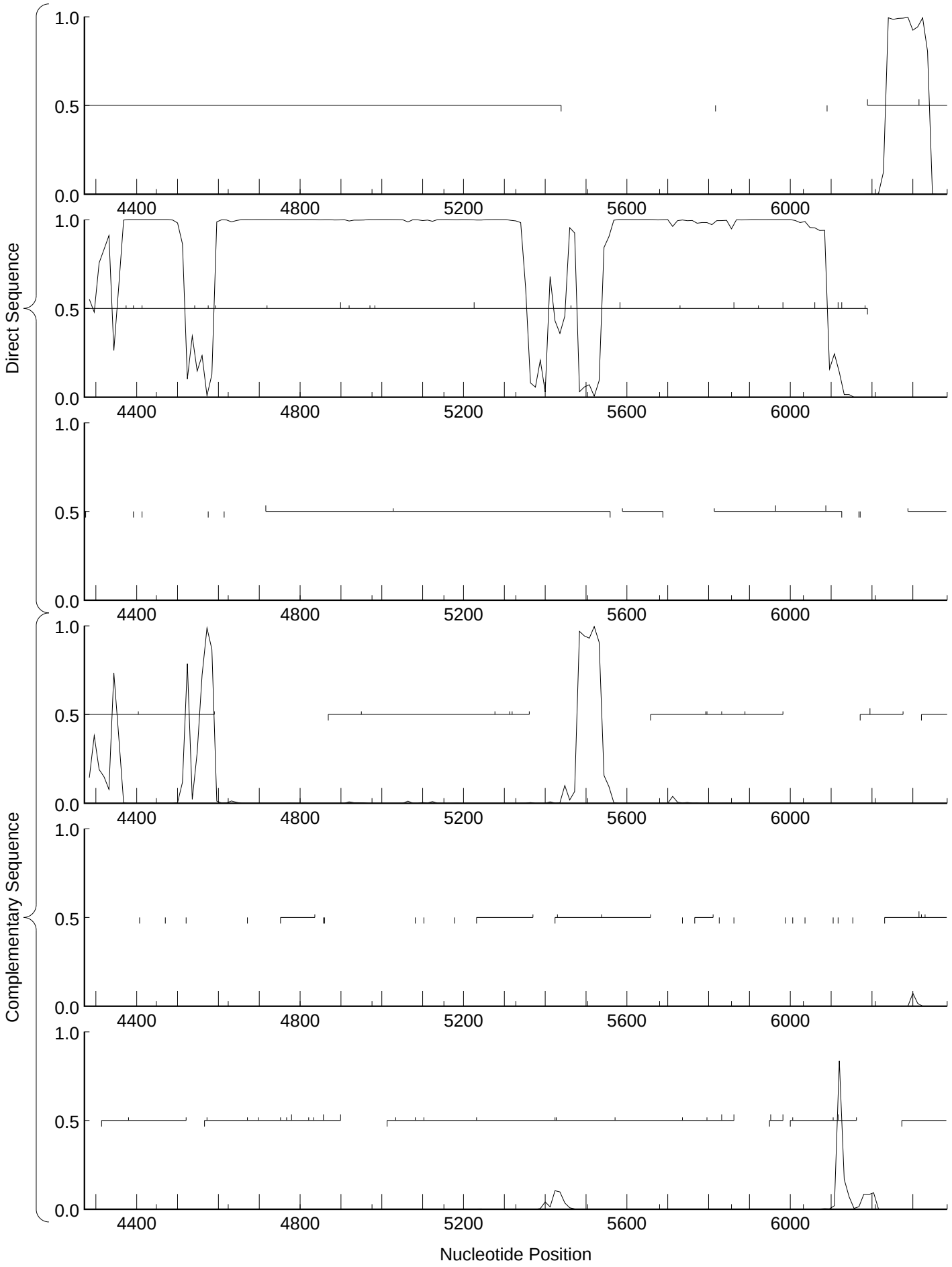

  Send questions / comments to:
      Dr. M. Borodovsky
      Georgia Institute of Technology
      School of Biology
      Atlanta, GA  30332-0230
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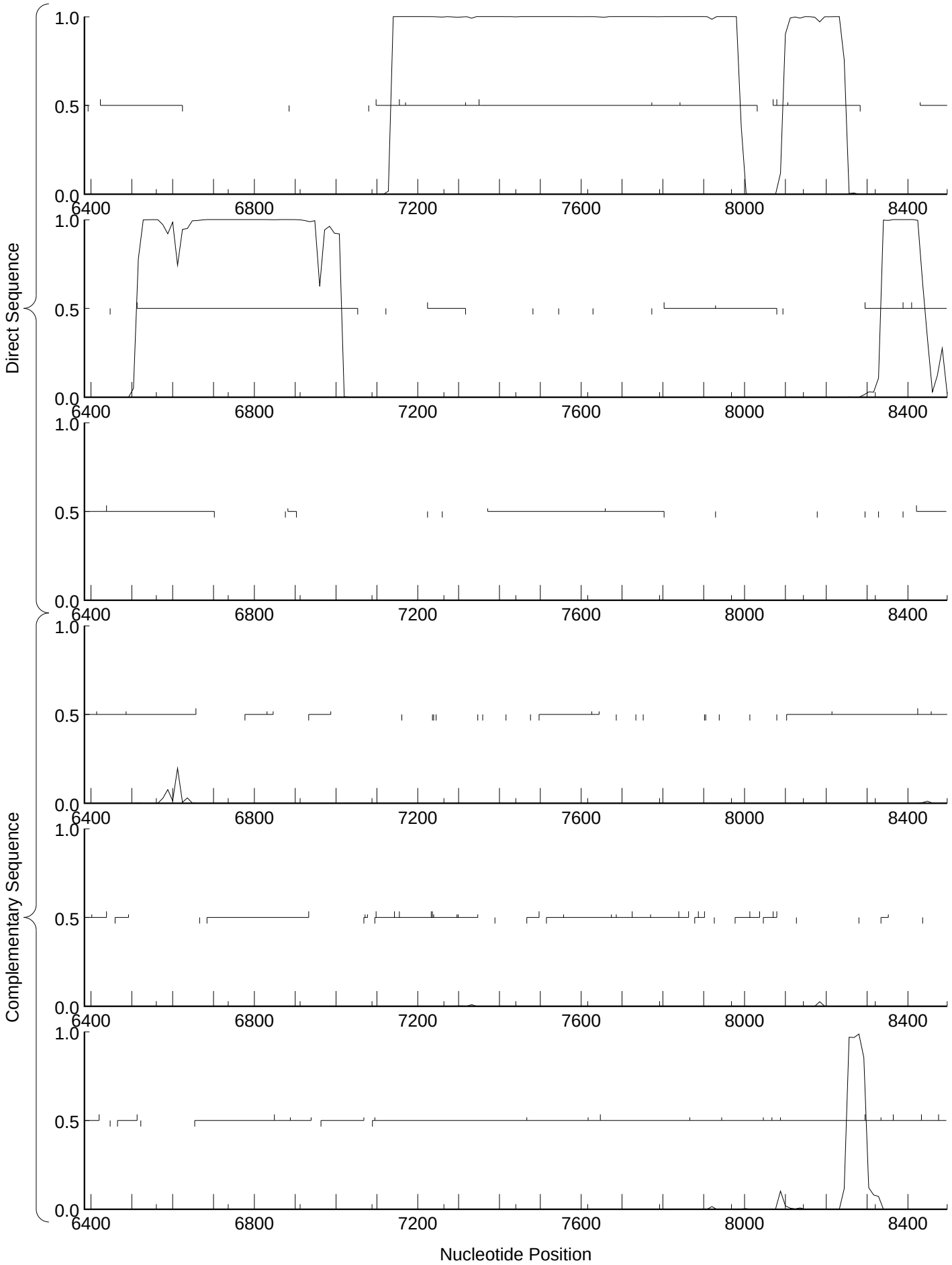


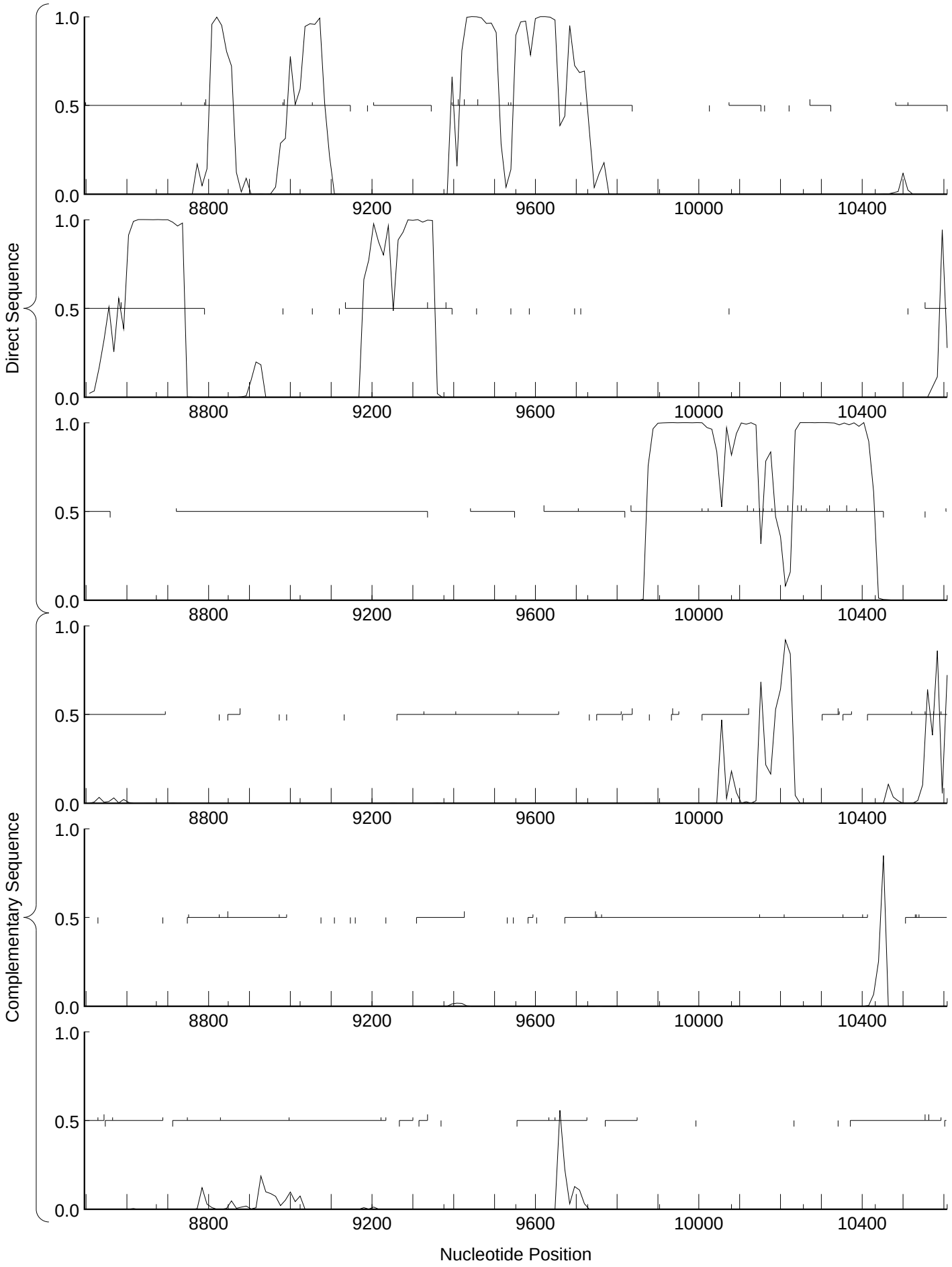
For help or information, send electronic mail to: custserv@genepro.com, or mark@amber.biology.gatech.edu

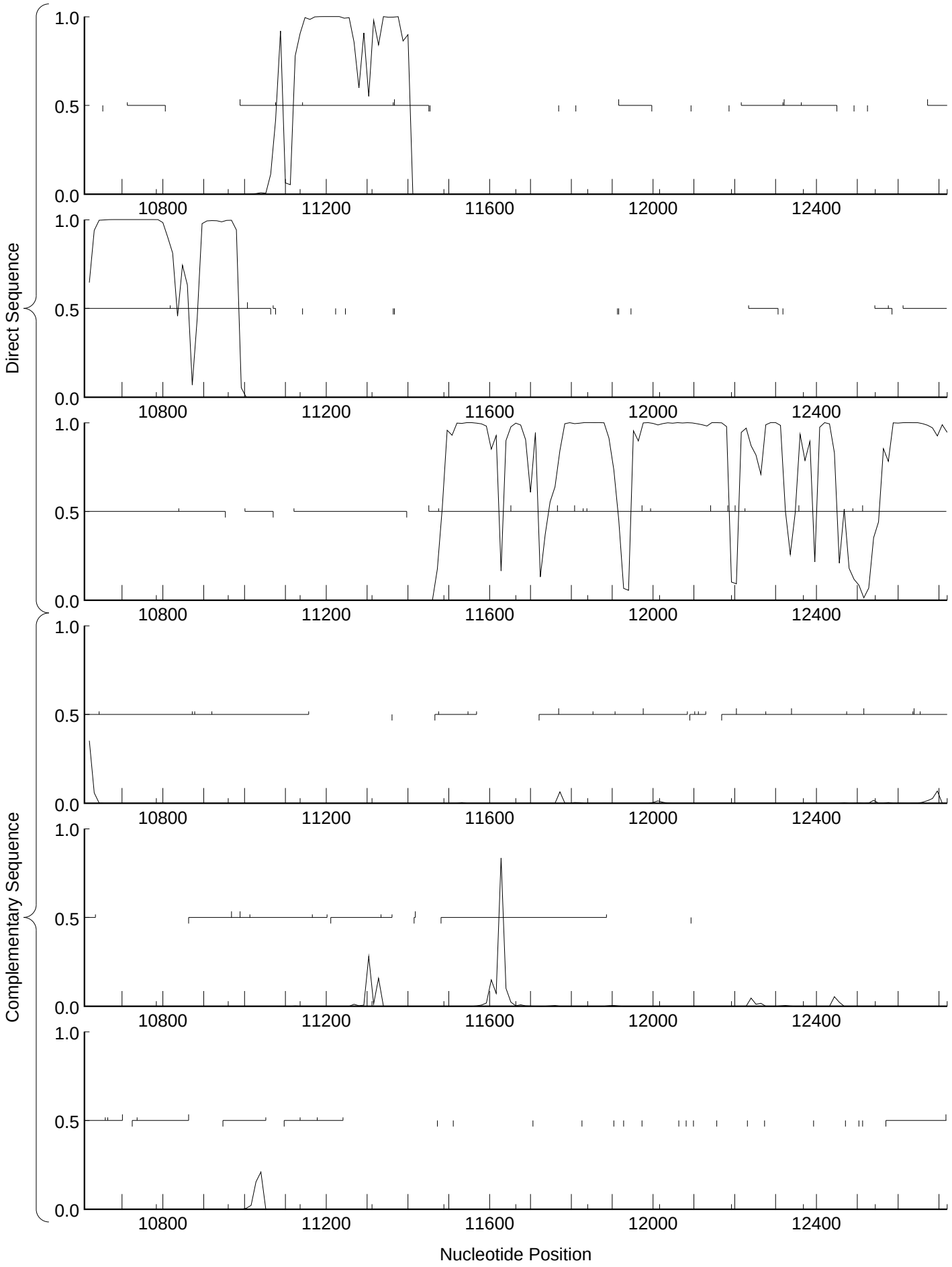

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
400
800
1200
1600
2000
Nucleotide Position

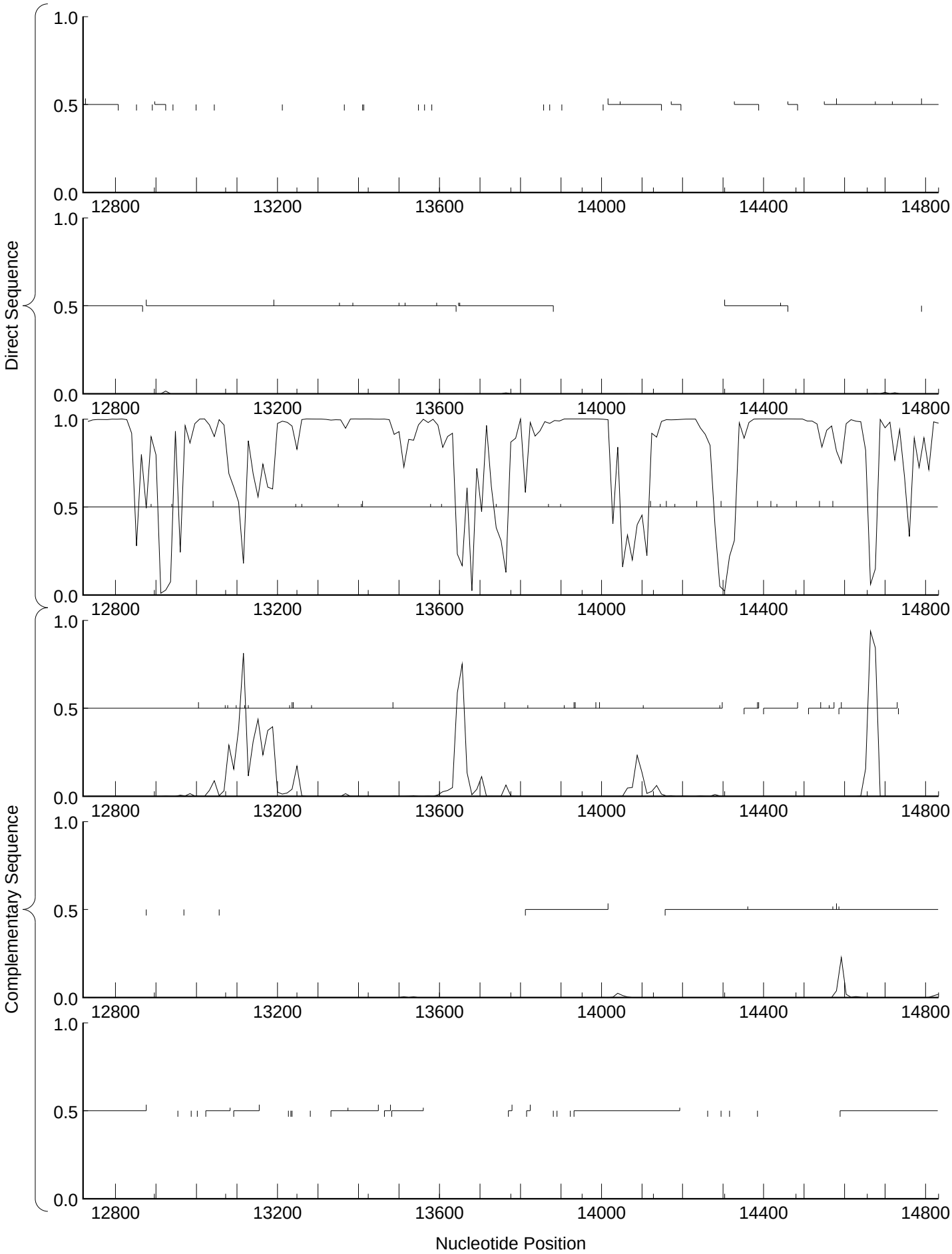

Direct Sequence
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0.0
2400
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3200
3600
4000
Nucleotide Position

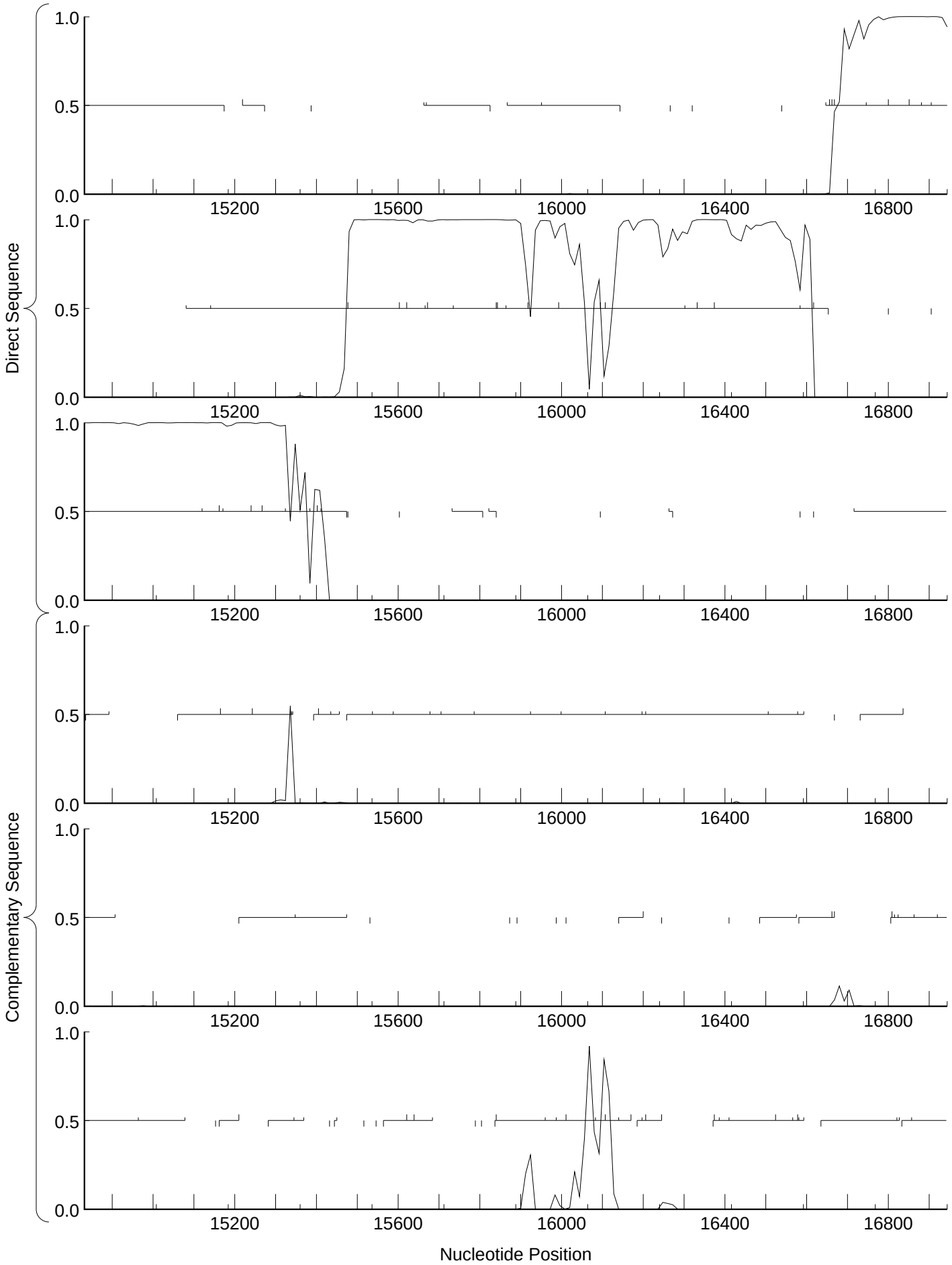

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
4400
4800
5200
5600
6000
Nucleotide Position


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

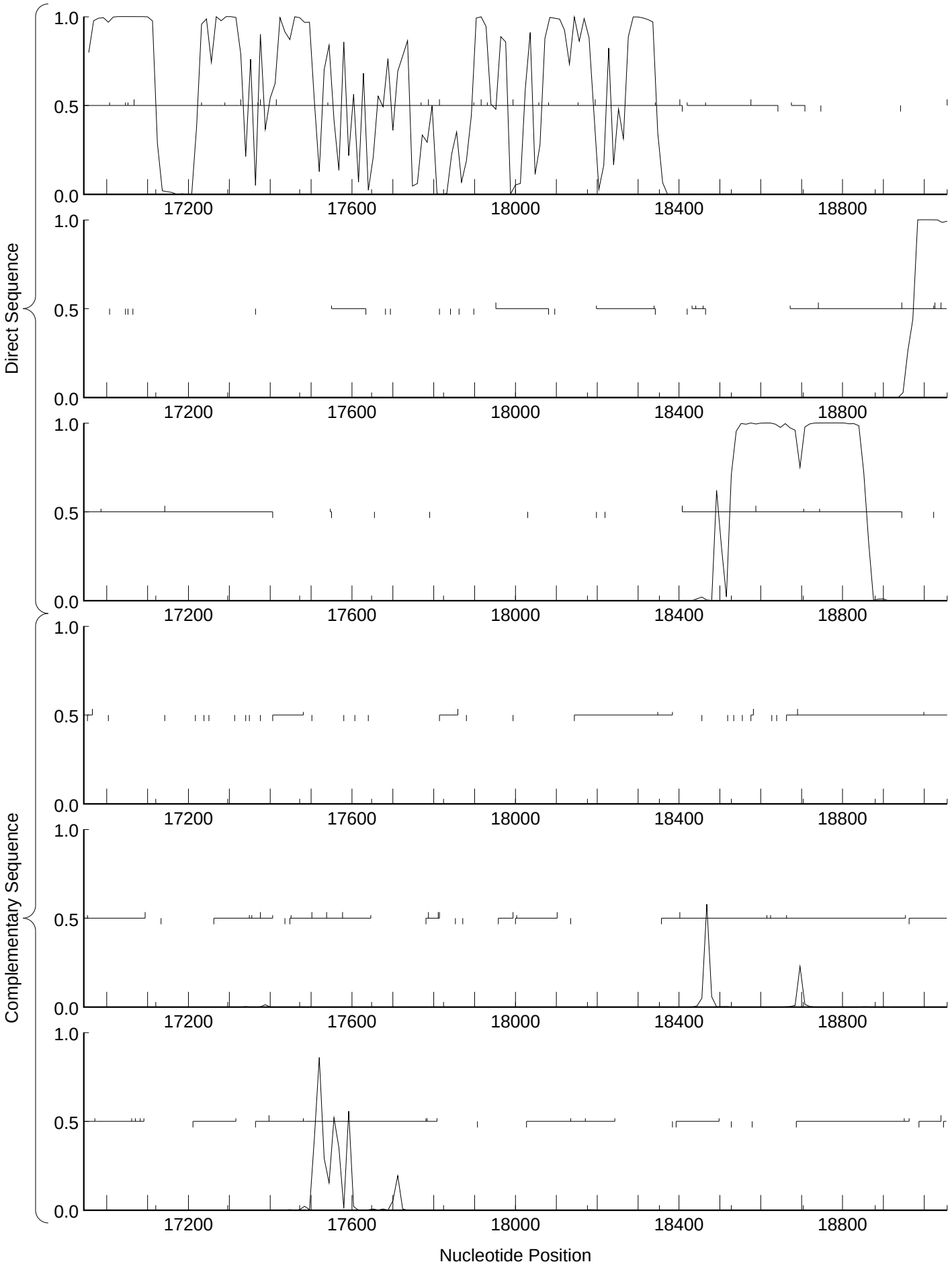

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
8800
9200
9600
10000
10400
Nucleotide Position


Direct Sequence
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0.0
10800
11200
11600
12000
12400
Nucleotide Position

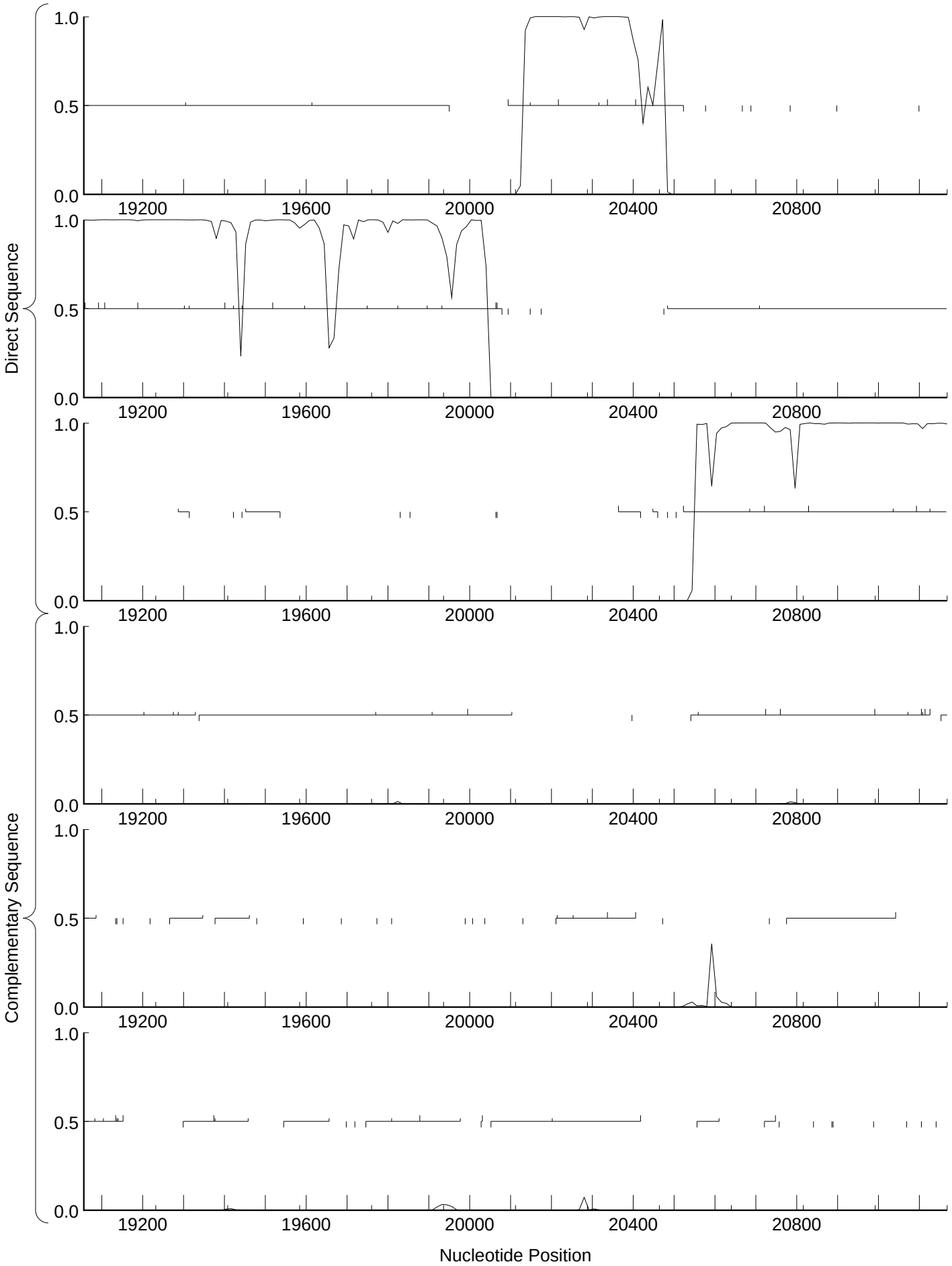

Direct Sequence
Complementary Sequence
1.0
0.5
0.0
12800
13200
13600
14000
14400
14800
Nucleotide Position


Direct Sequence
Complementary Sequence
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0.5
0.0
15200
15600
16000
16400
16800
Nucleotide Position

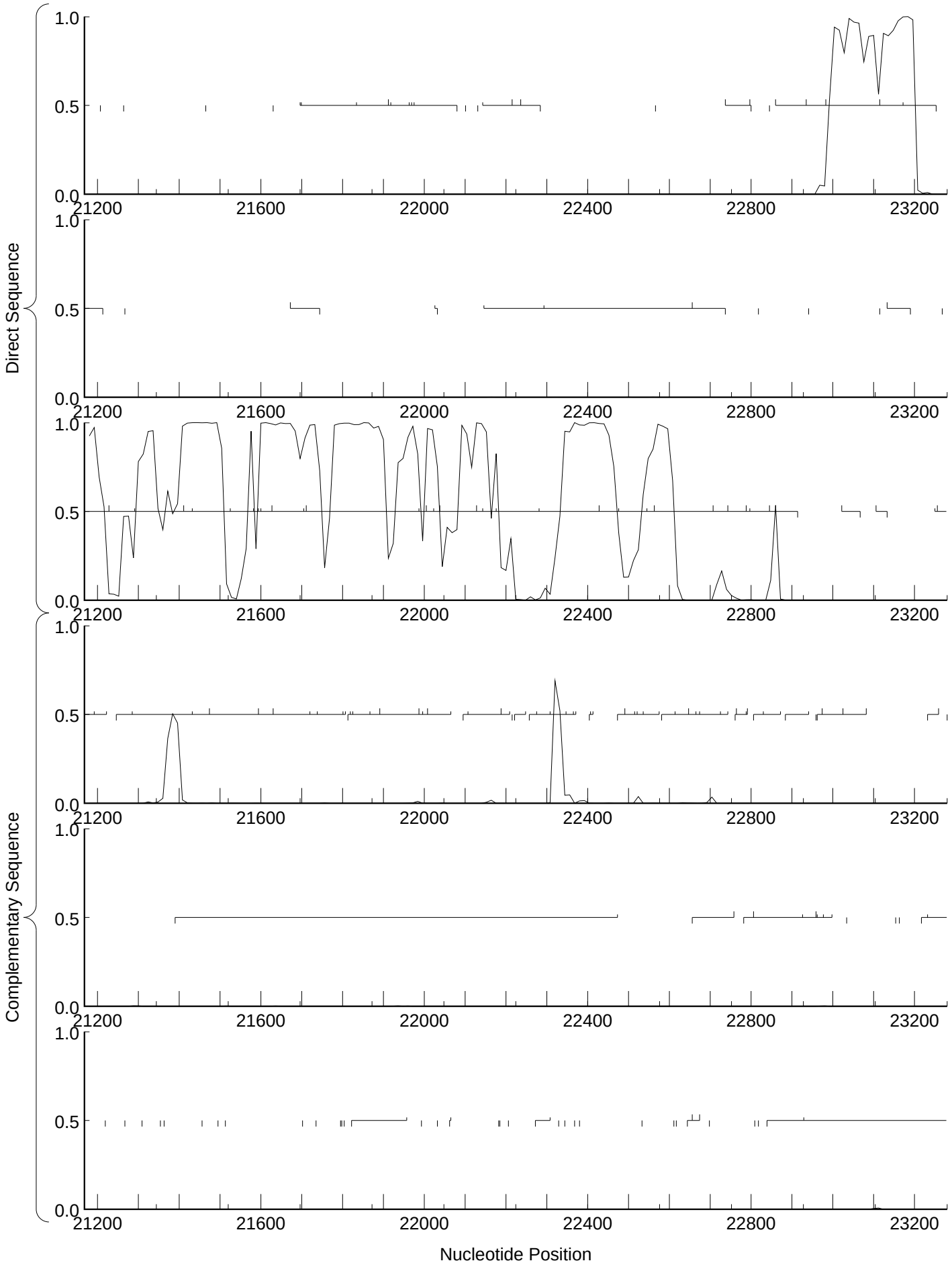
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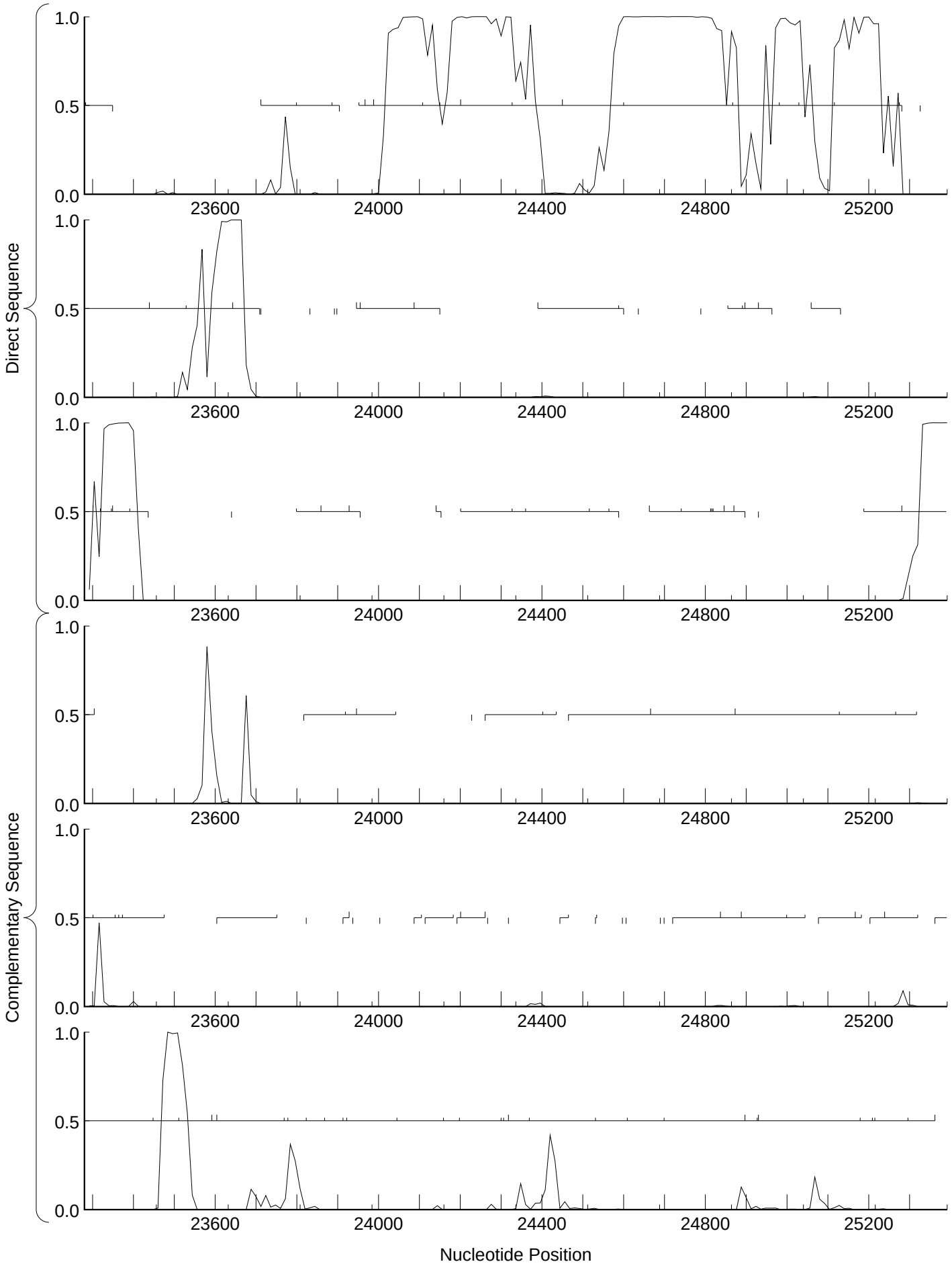
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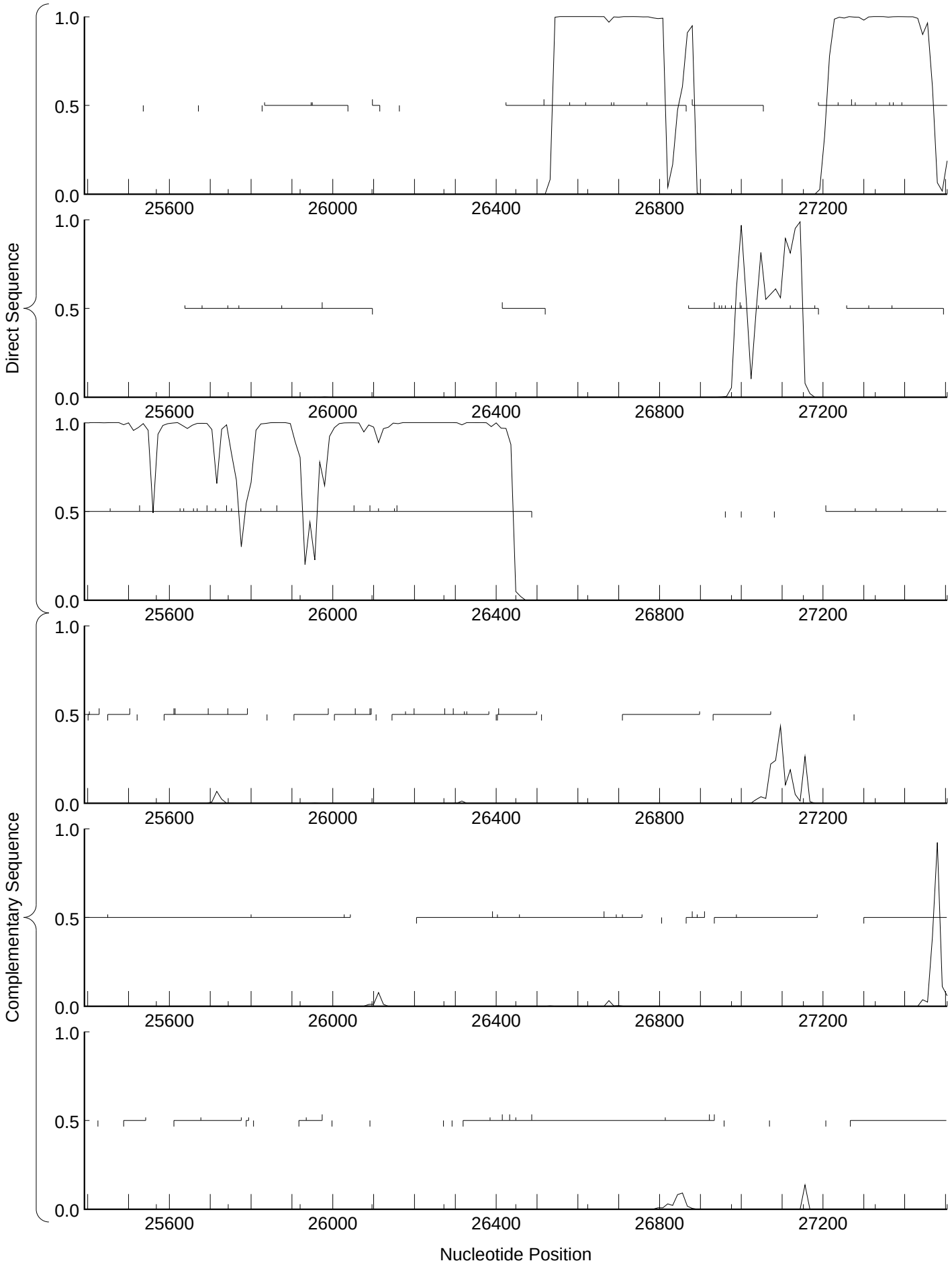
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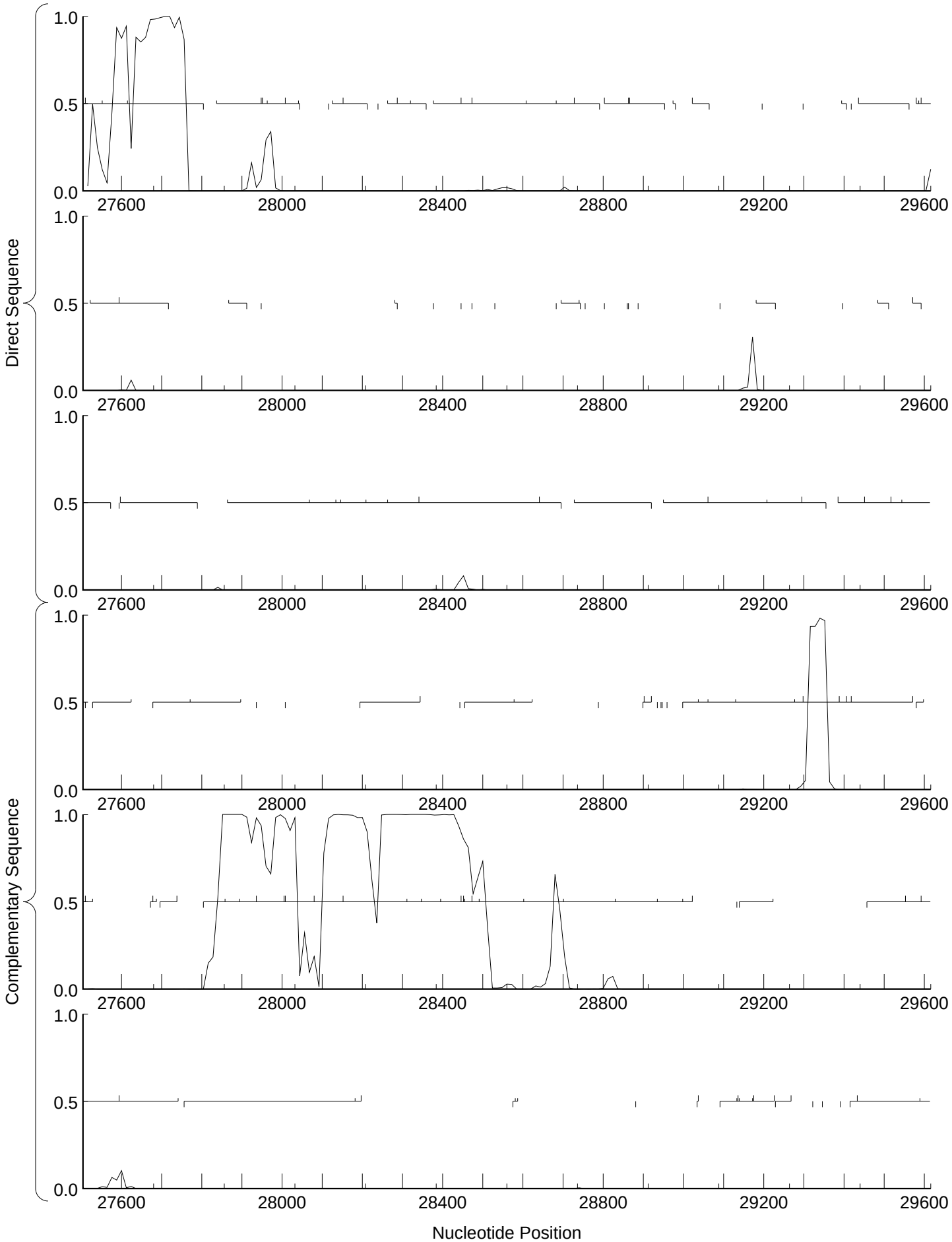
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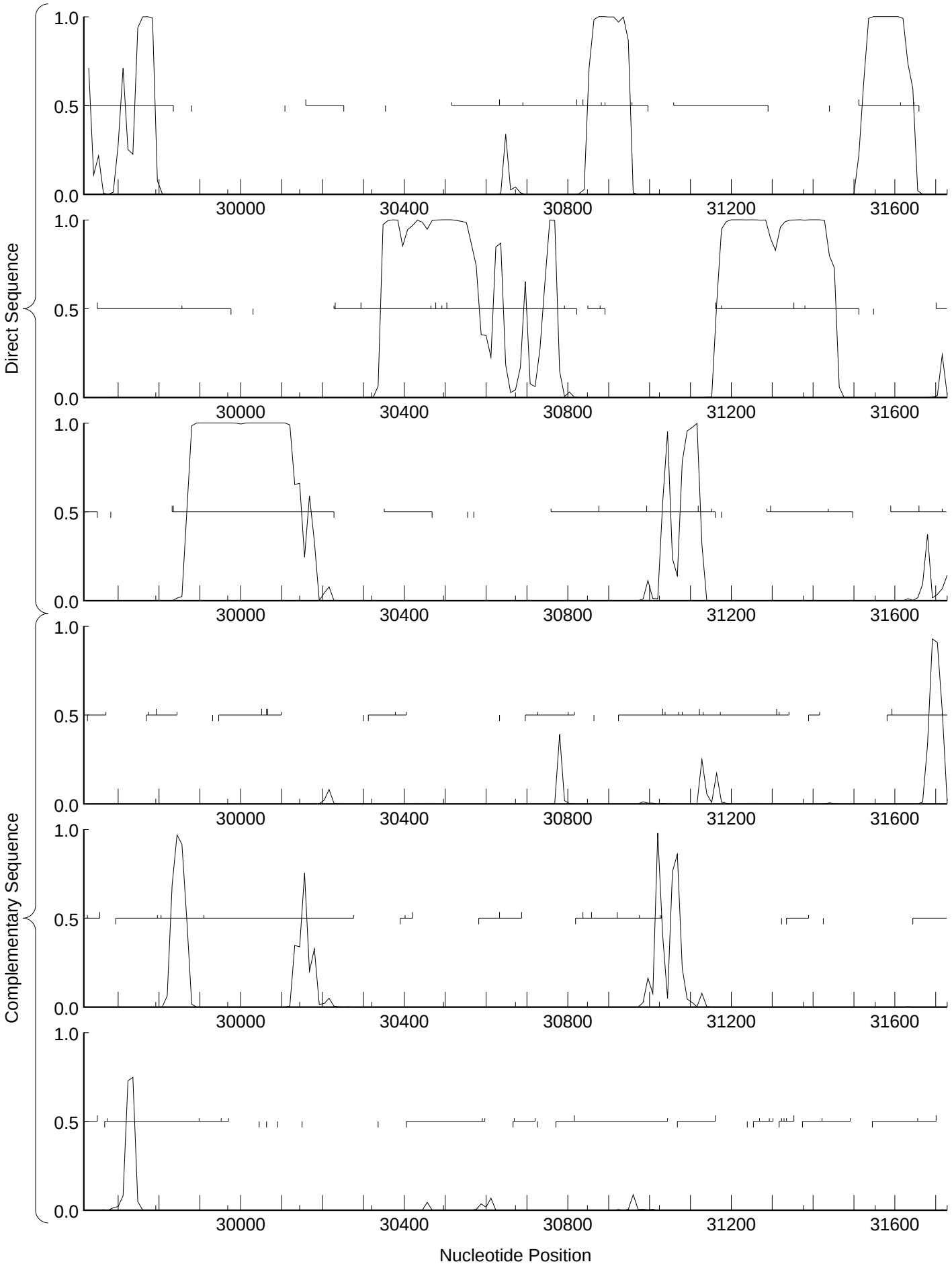
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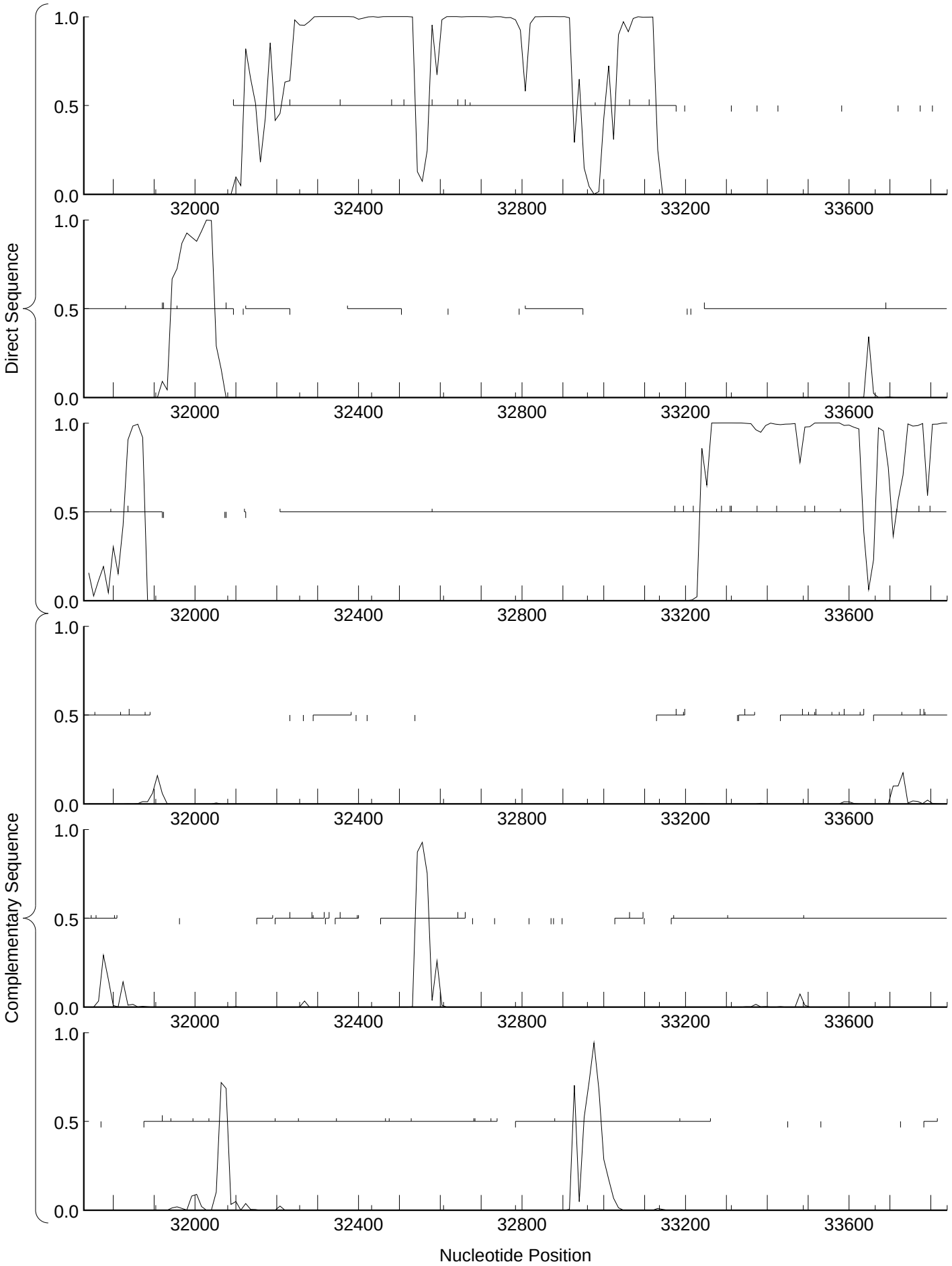
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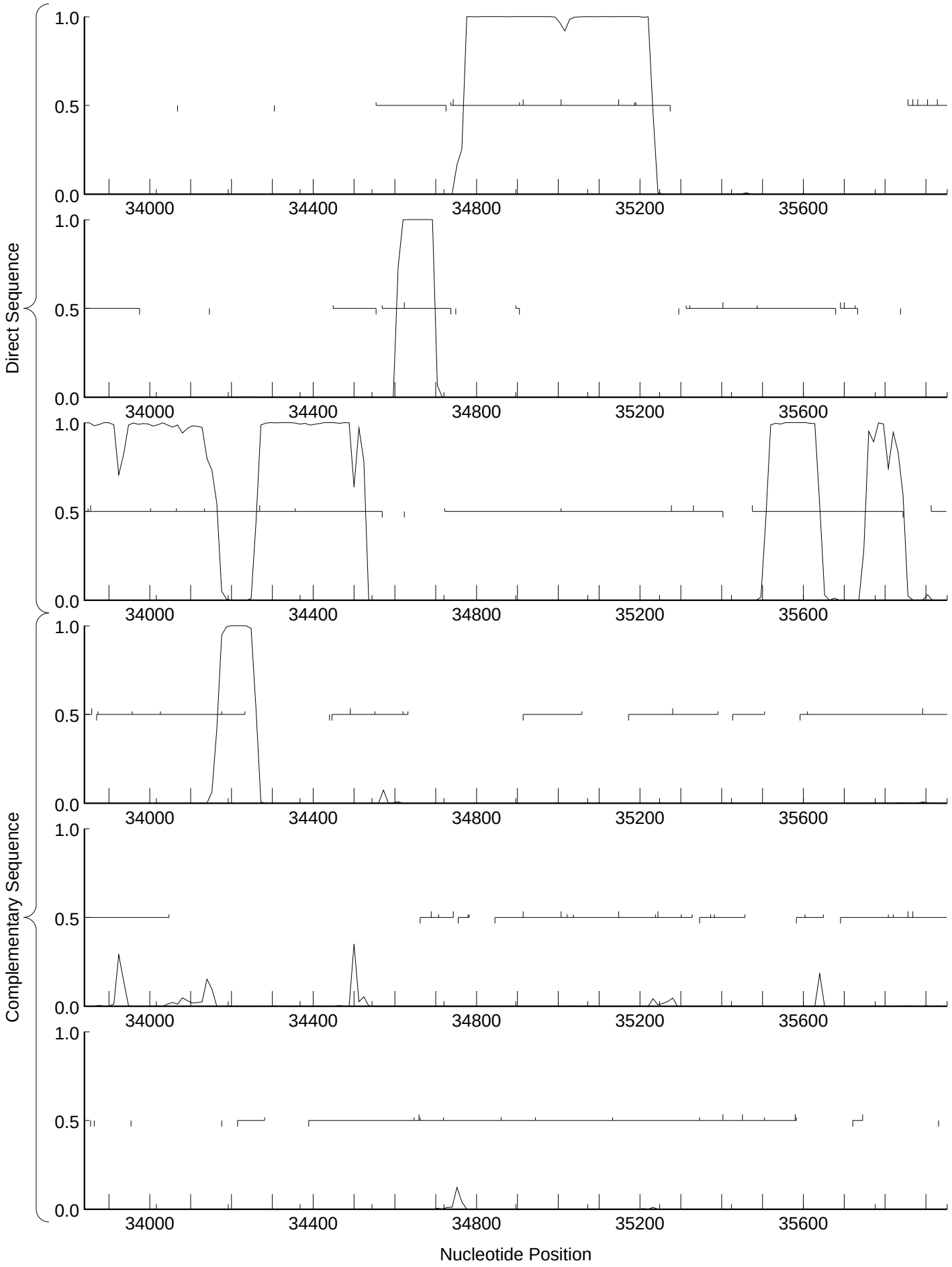
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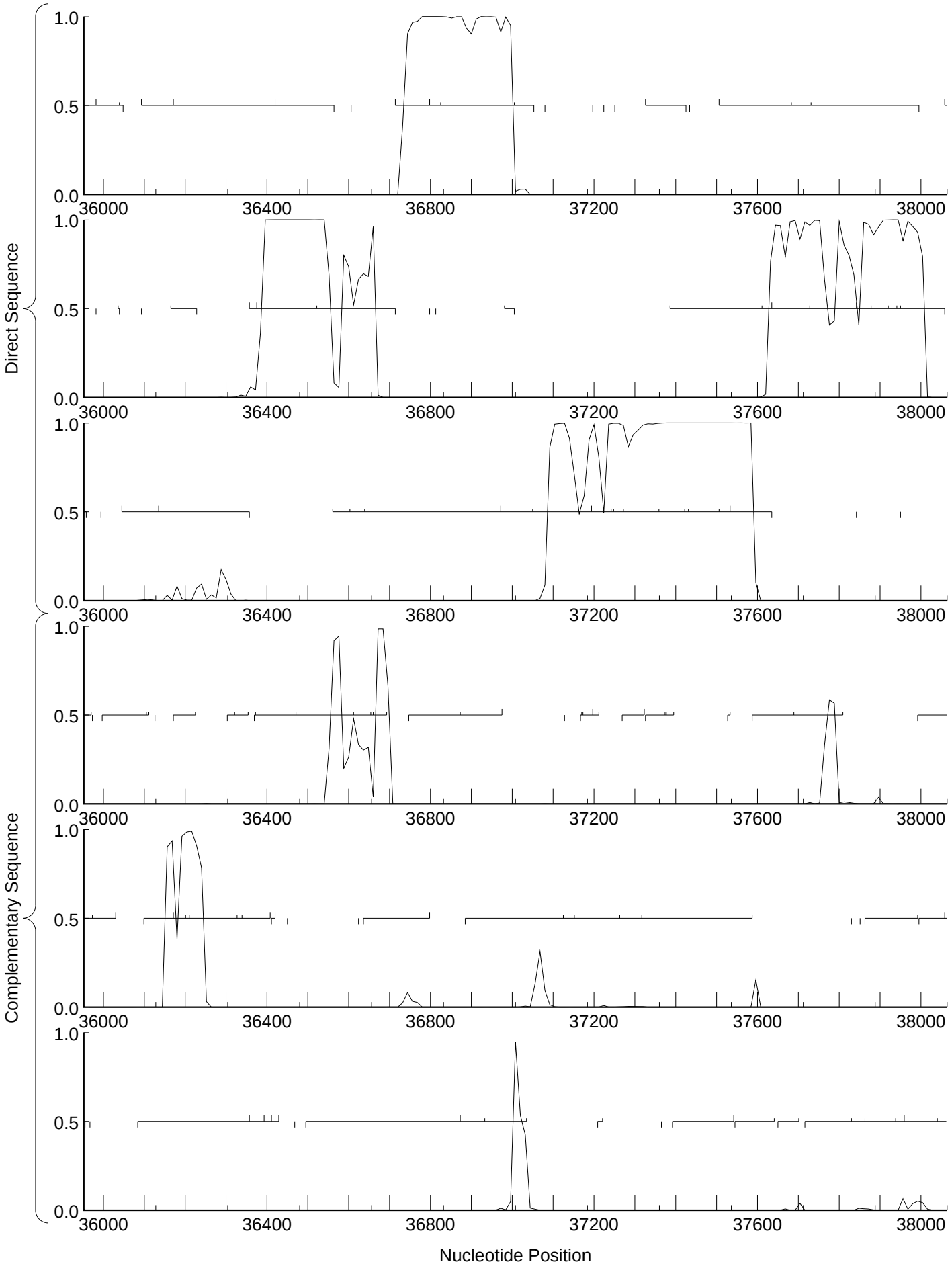
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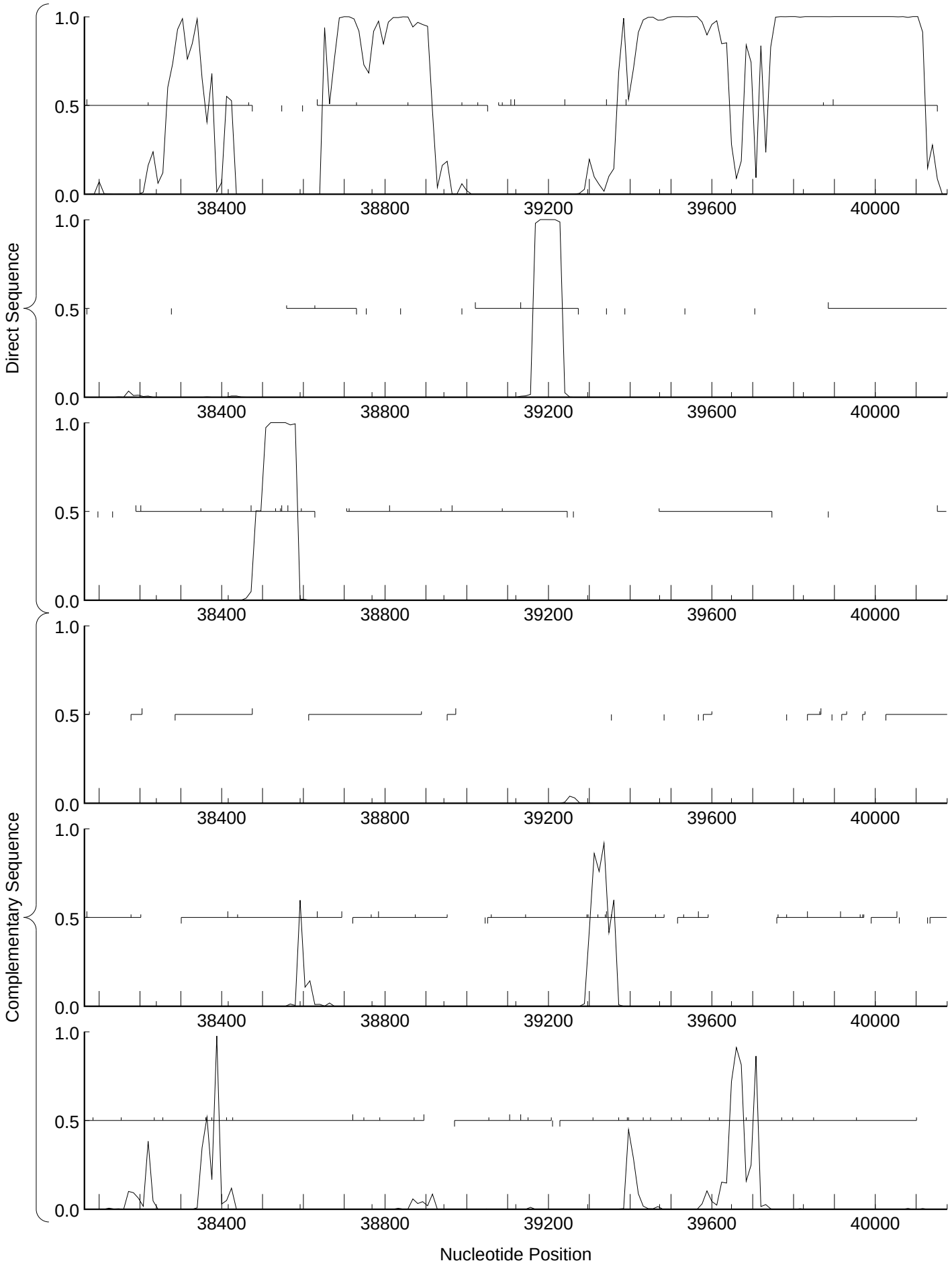
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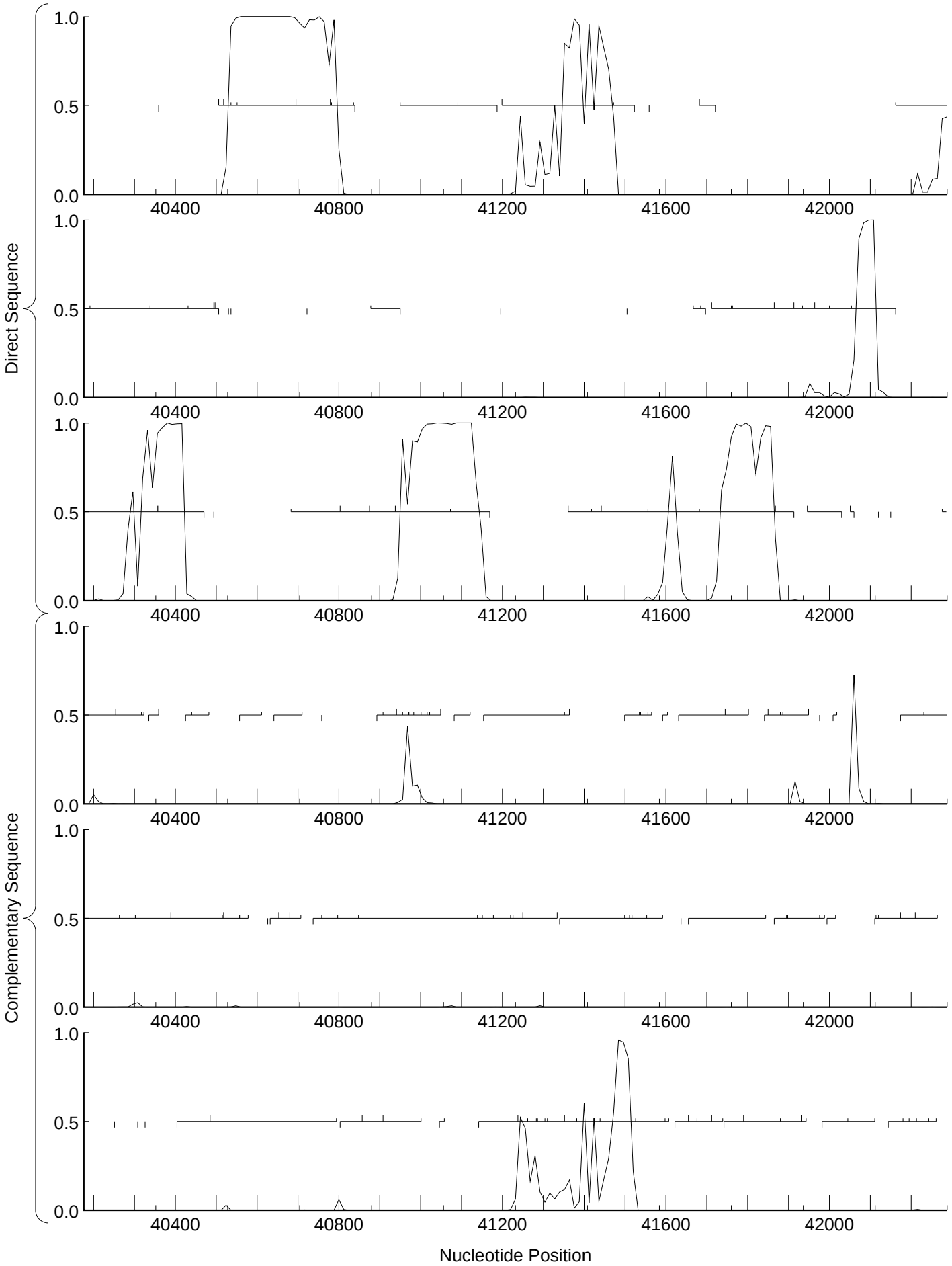
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s complete sequence, 42430 bp including 10-base 3’ overhang (CCCATGGCAT), Cluster G1, Order 4, Window 96, Step 12, 20/22



s complete sequence, 42430 bp including 10-base 3’ overhang (CCCATGGCAT), Cluster G1, Order 4, Window 96, Step 12, 21/22



s complete sequence, 42430 bp including 10-base 3’ overhang (CCCATGGCAT), Cluster G1, Order 4, Window 96, Step 12, 22/22

