GeneMark

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

PROGRAM INFORMATION

```
Sequence         :  Mycobacterium phage Familton complete sequence, 71807 bp including 4-base 3’ overhang (GTGT
Analysis Date    :  3/28/24 at 20:55:40
Pages            :  35
Sequence Length  :  71807 bp
GC Content       :   65.44%

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

PS-Version       :  1.2

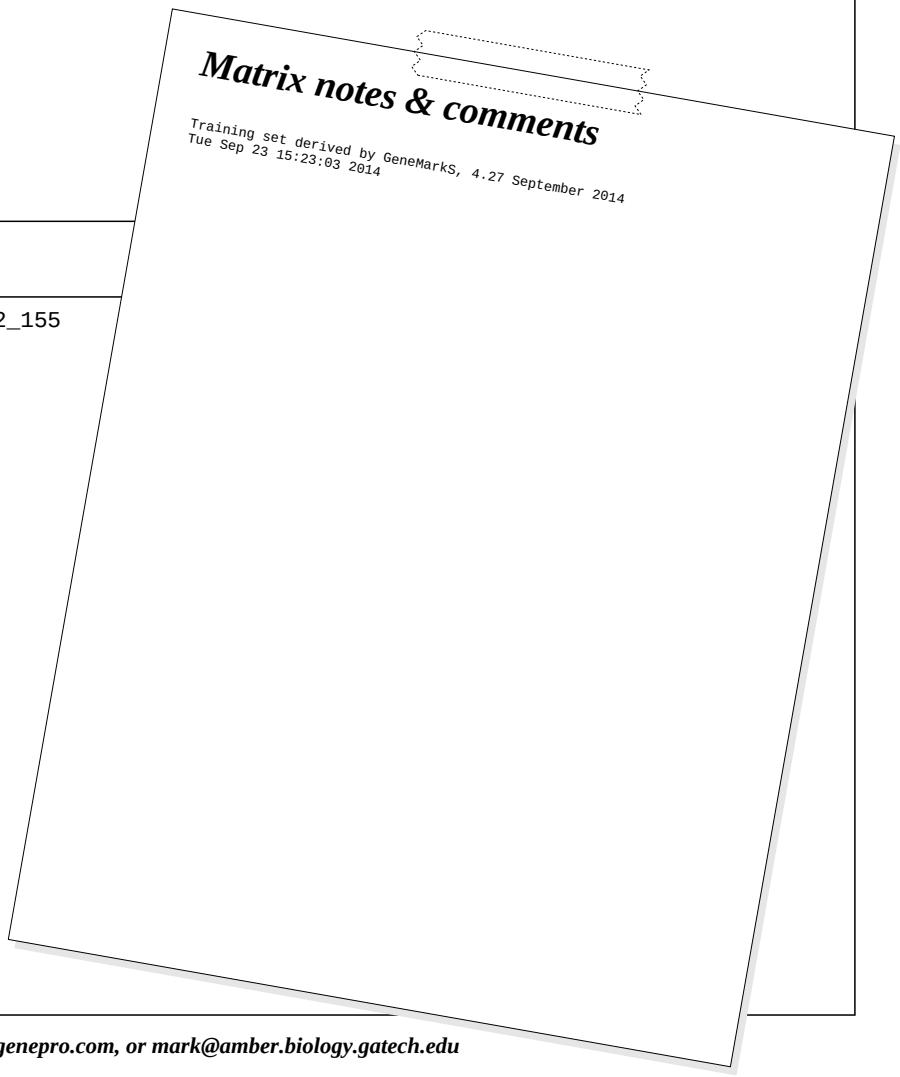
GeneMark Options :  PostScript graph,
                    Mark ORFs / splice sites,
                    List ORFs,
                    List regions and/or splice sites,
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MATRIX INFORMATION

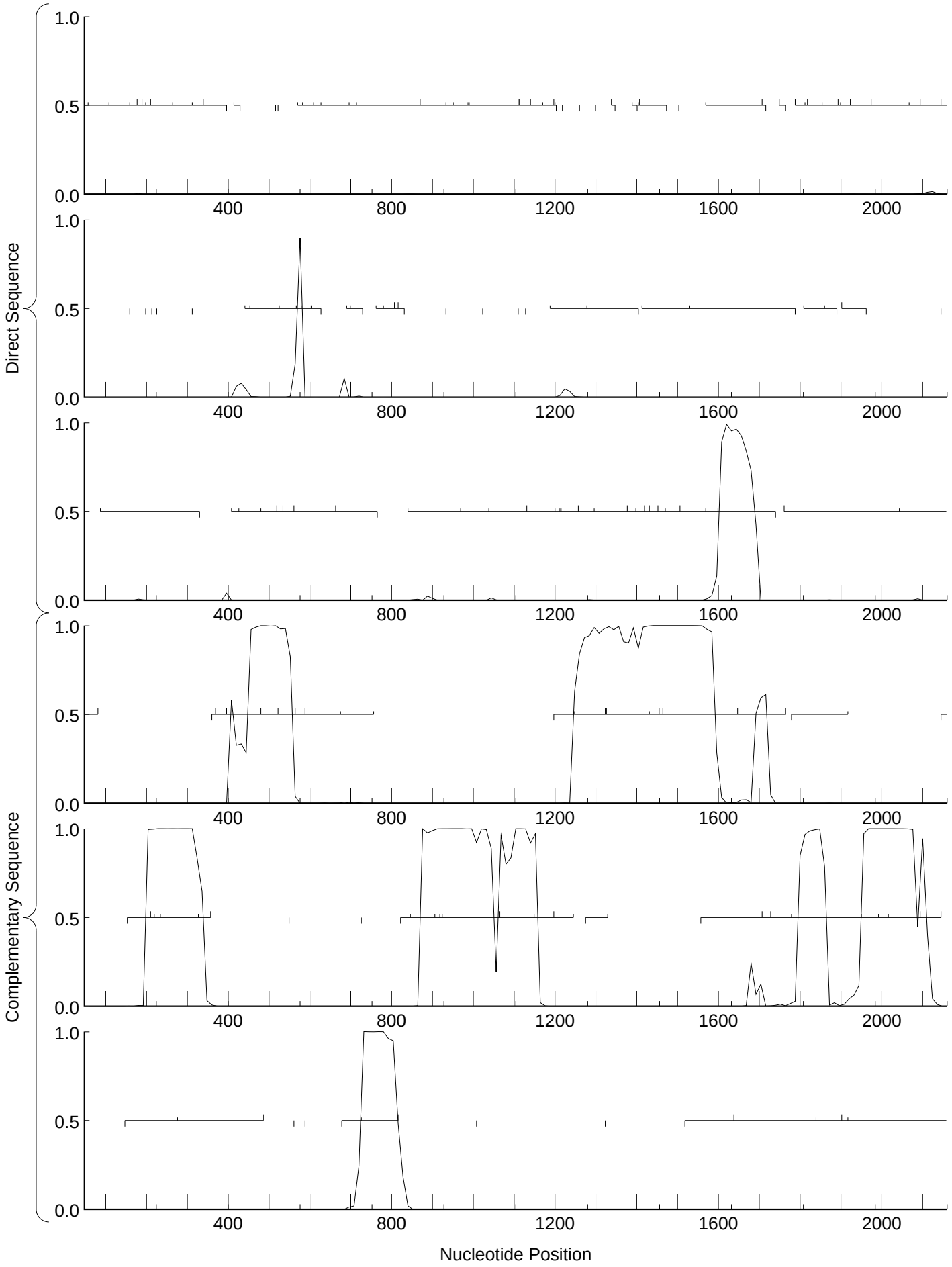
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Matrix     :  Mycobacterium_smegmatis_MC2_155
Author     :  -

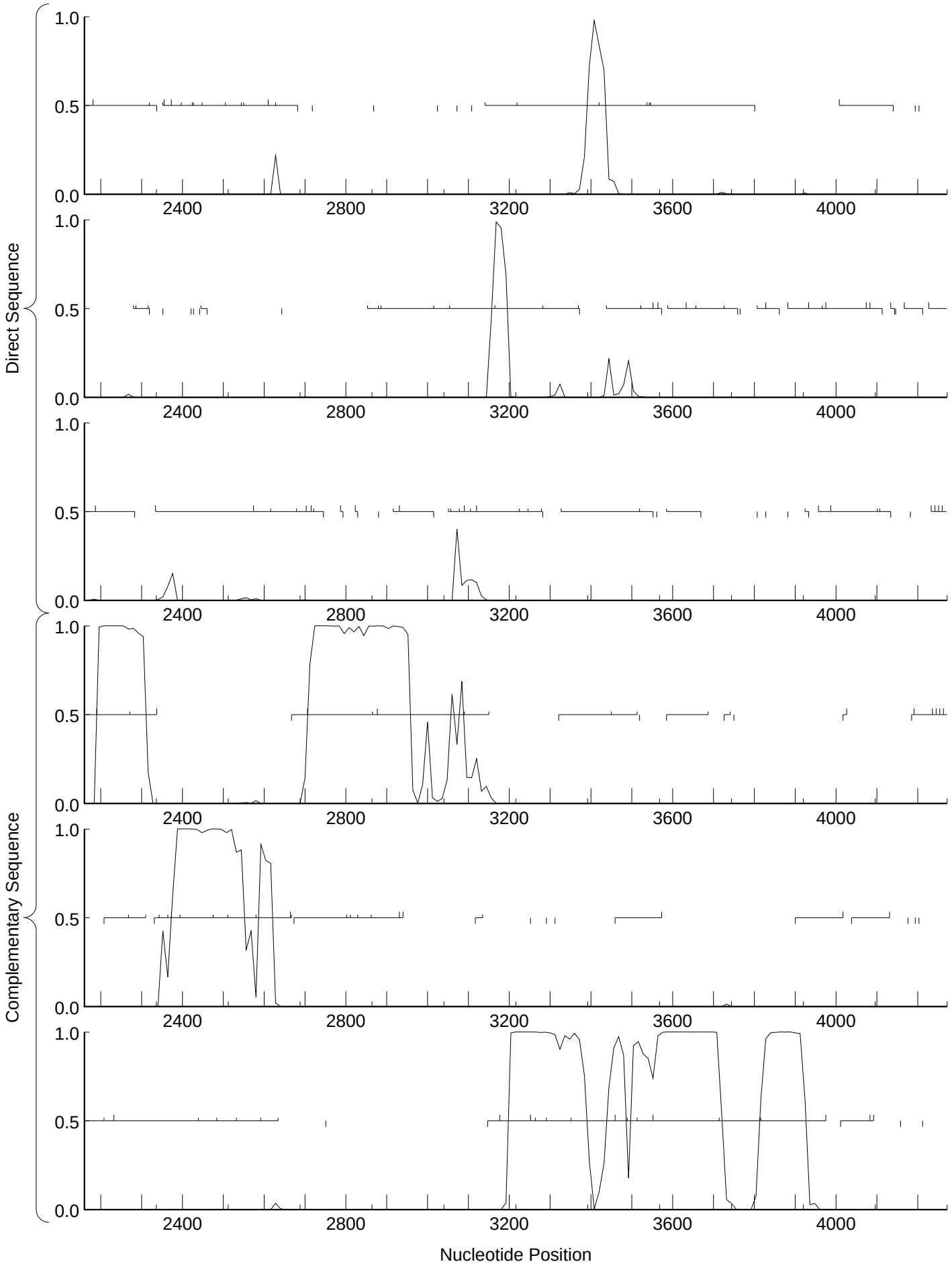
Order      :  4

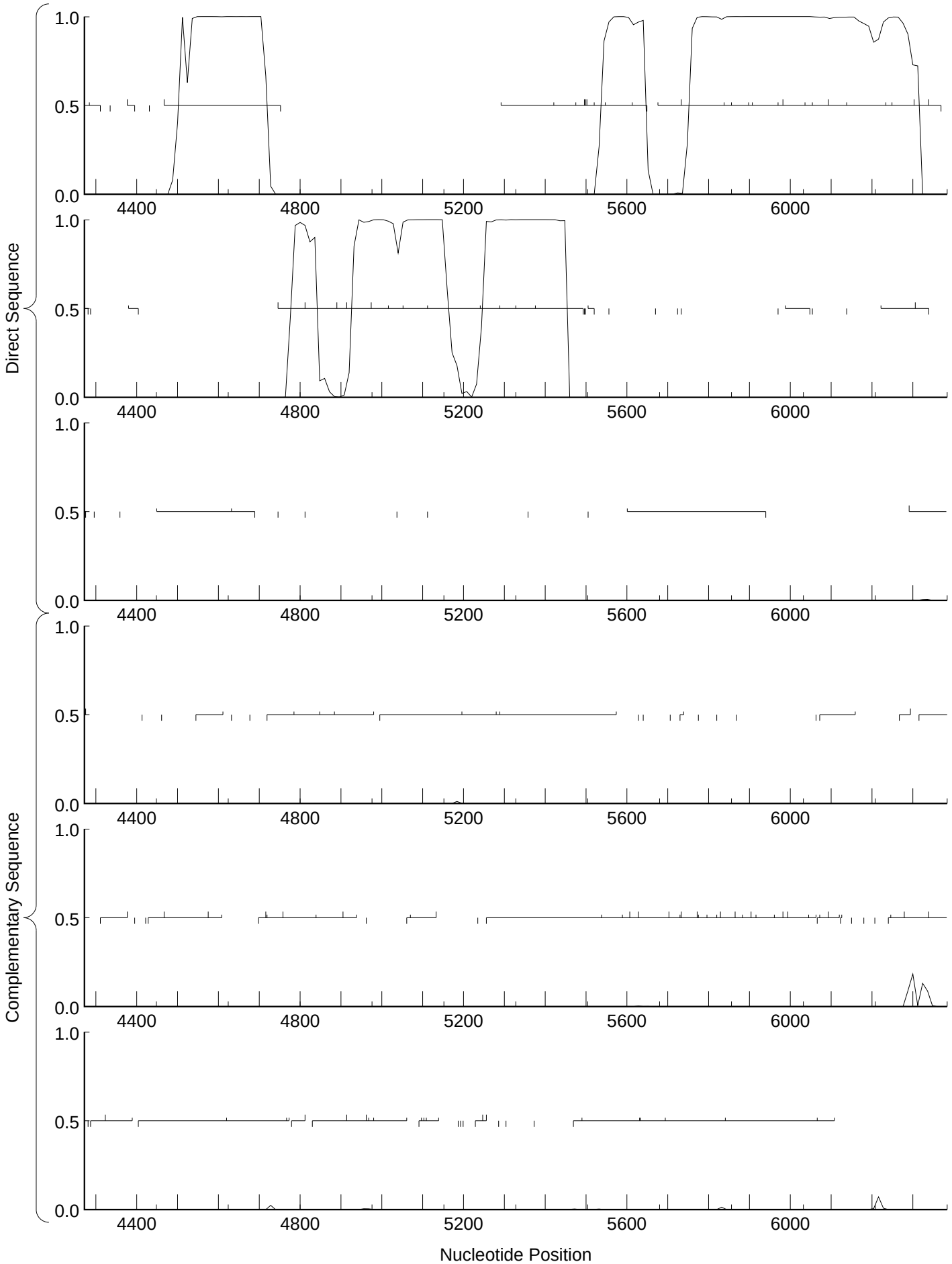

  Send questions / comments to:
      Dr. M. Borodovsky
      Georgia Institute of Technology
      School of Biology
      Atlanta, GA  30332-0230
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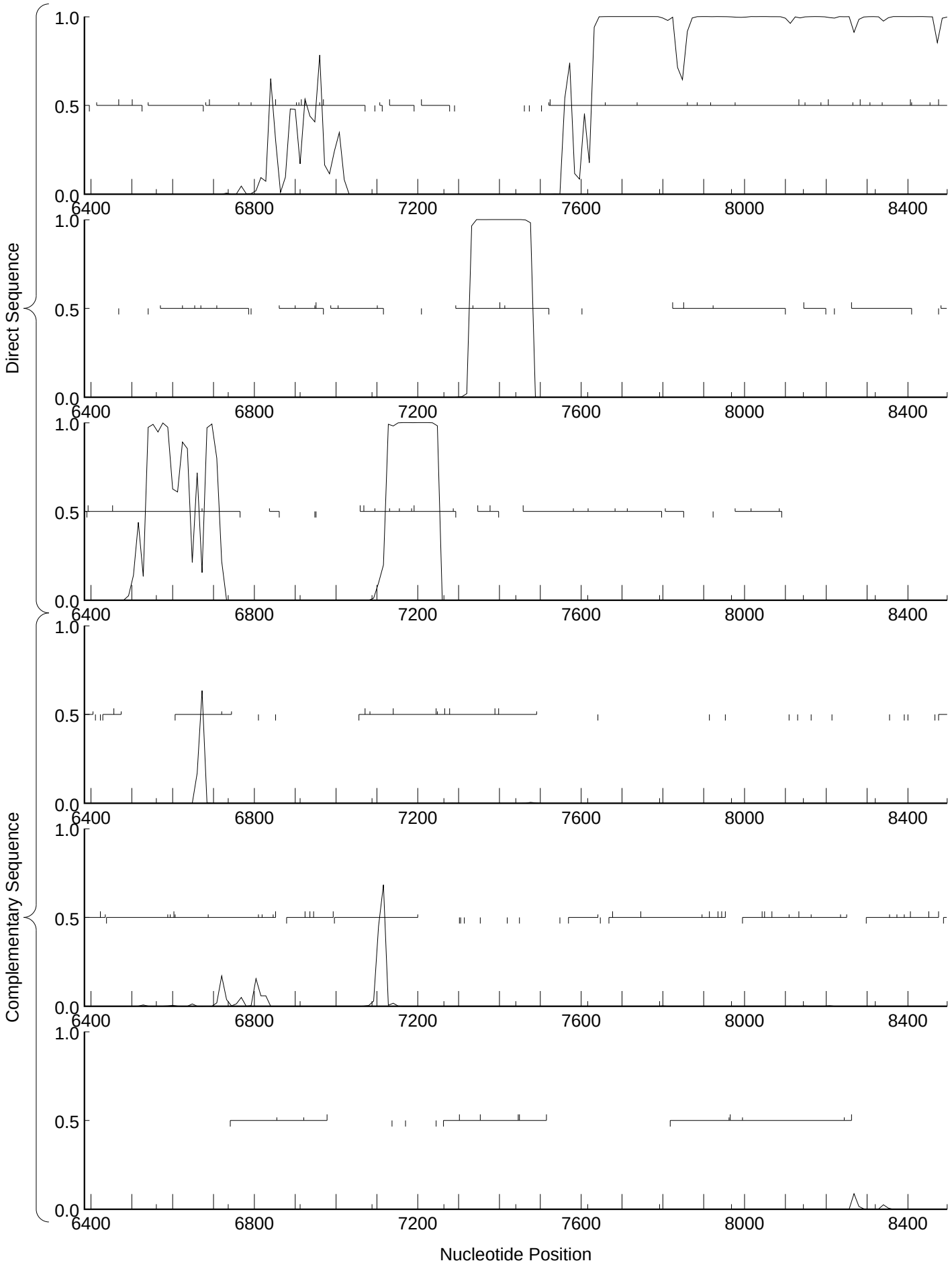


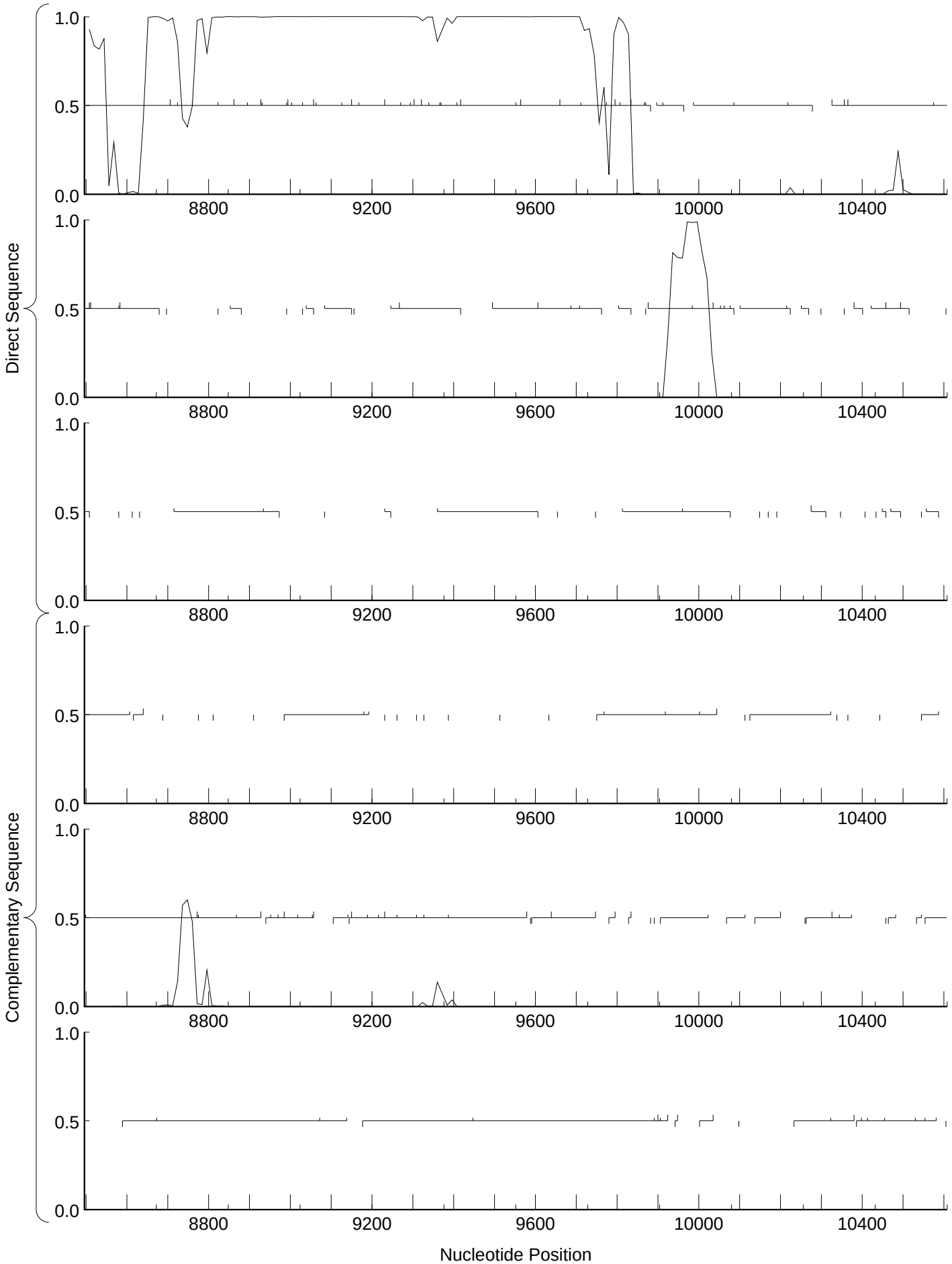
For help or information, send electronic mail to: custserv@genepro.com, or mark@amber.biology.gatech.edu


Direct Sequence
Complementary Sequence
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800
1200
1600
2000
Nucleotide Position

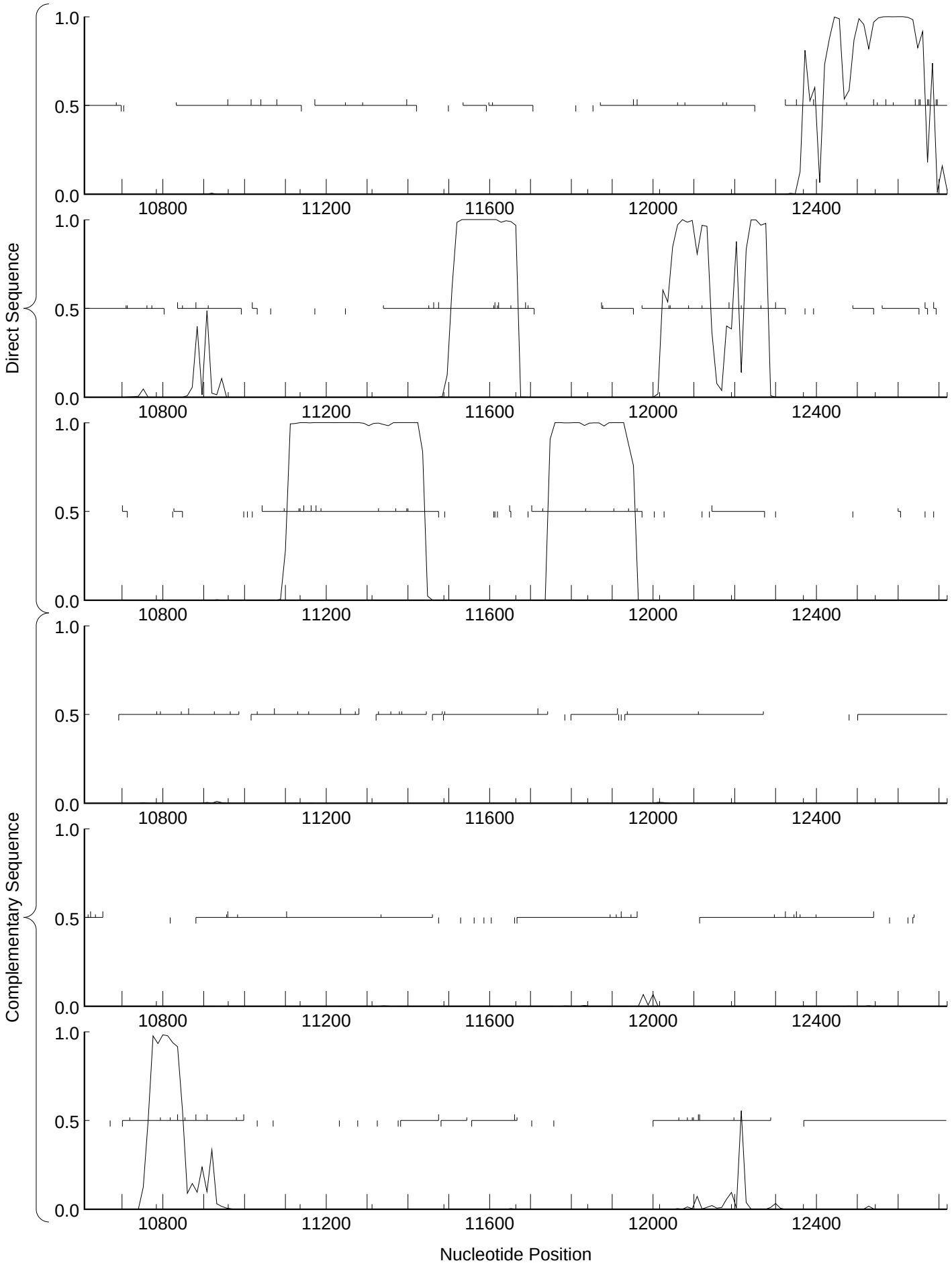

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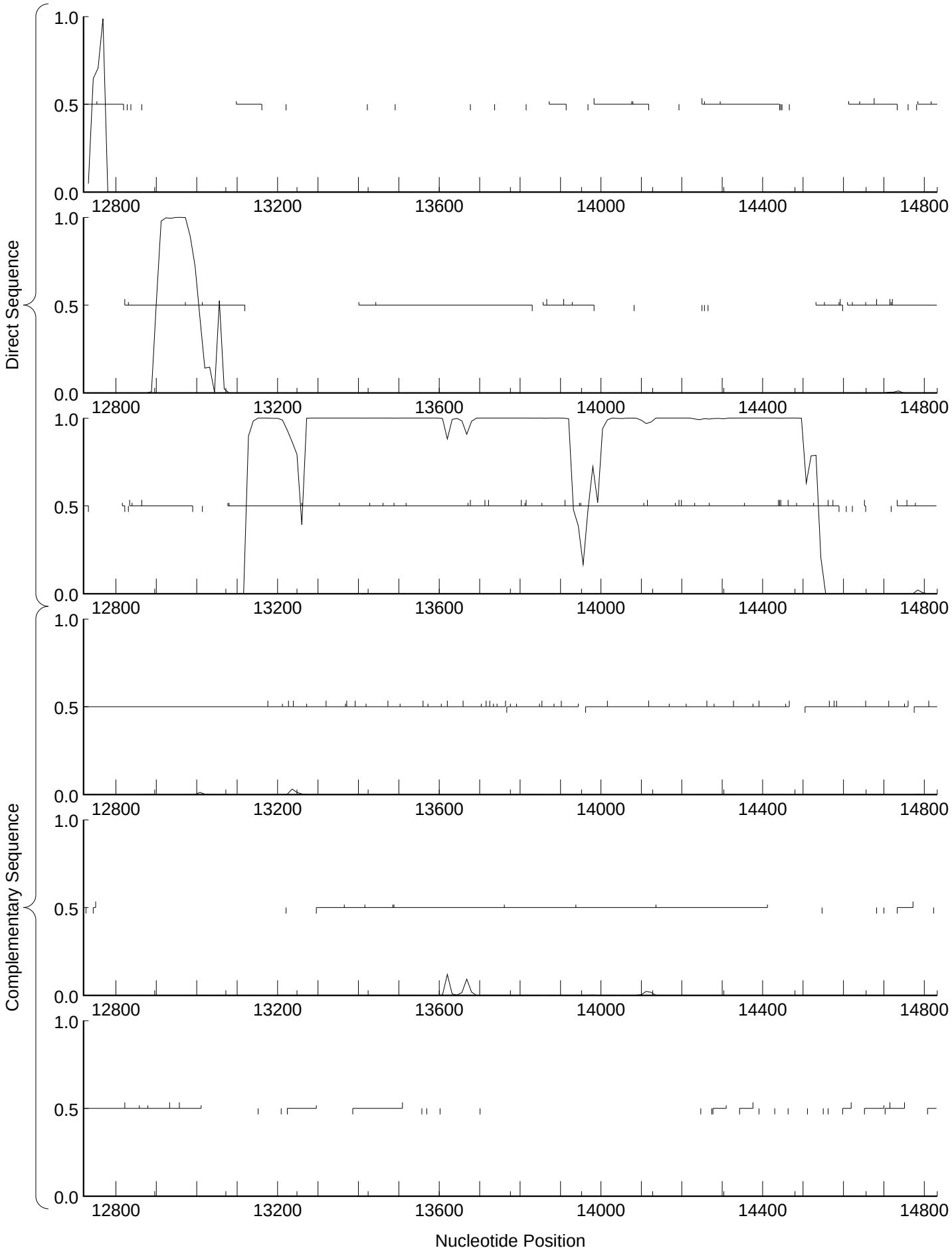

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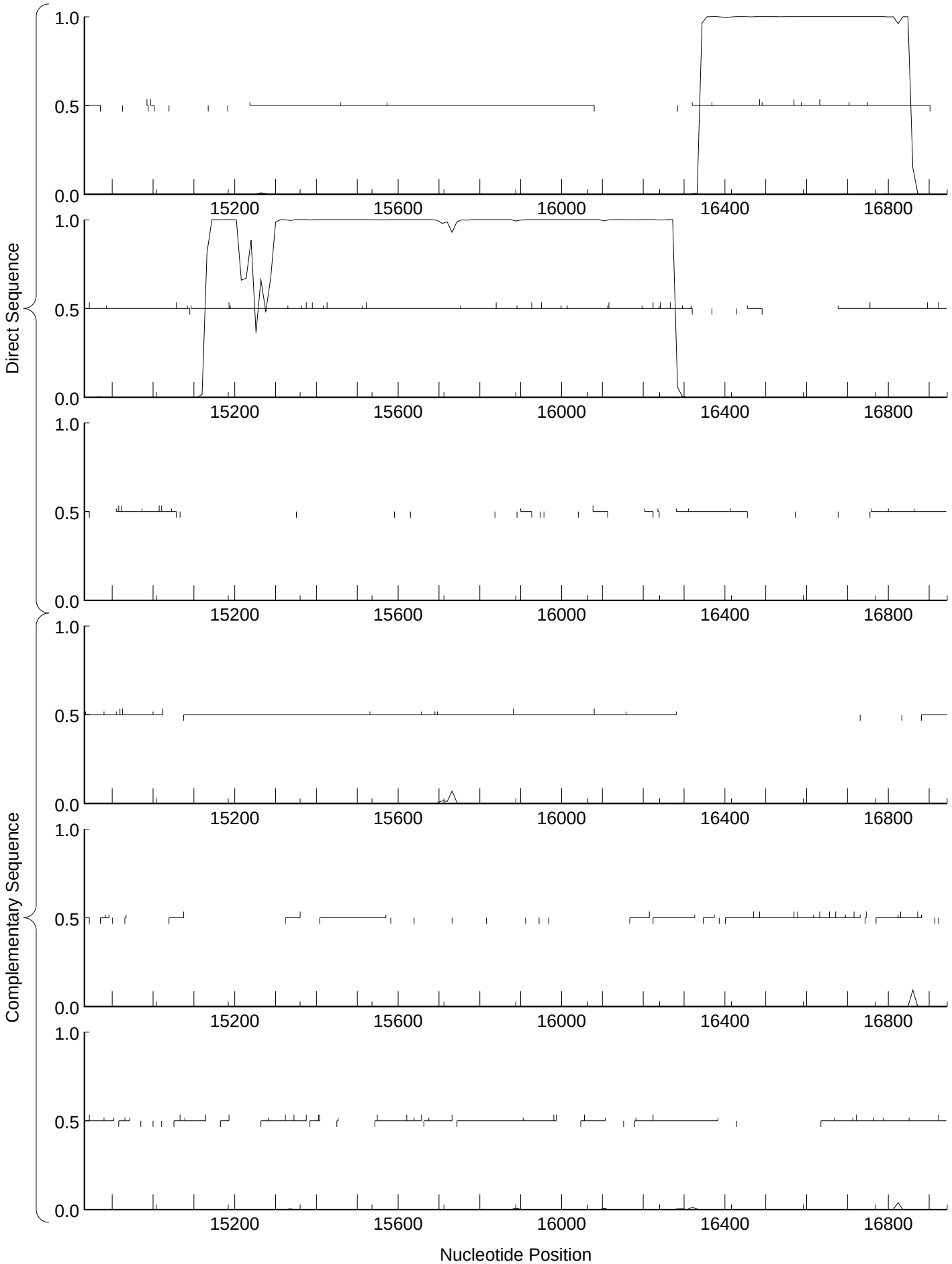

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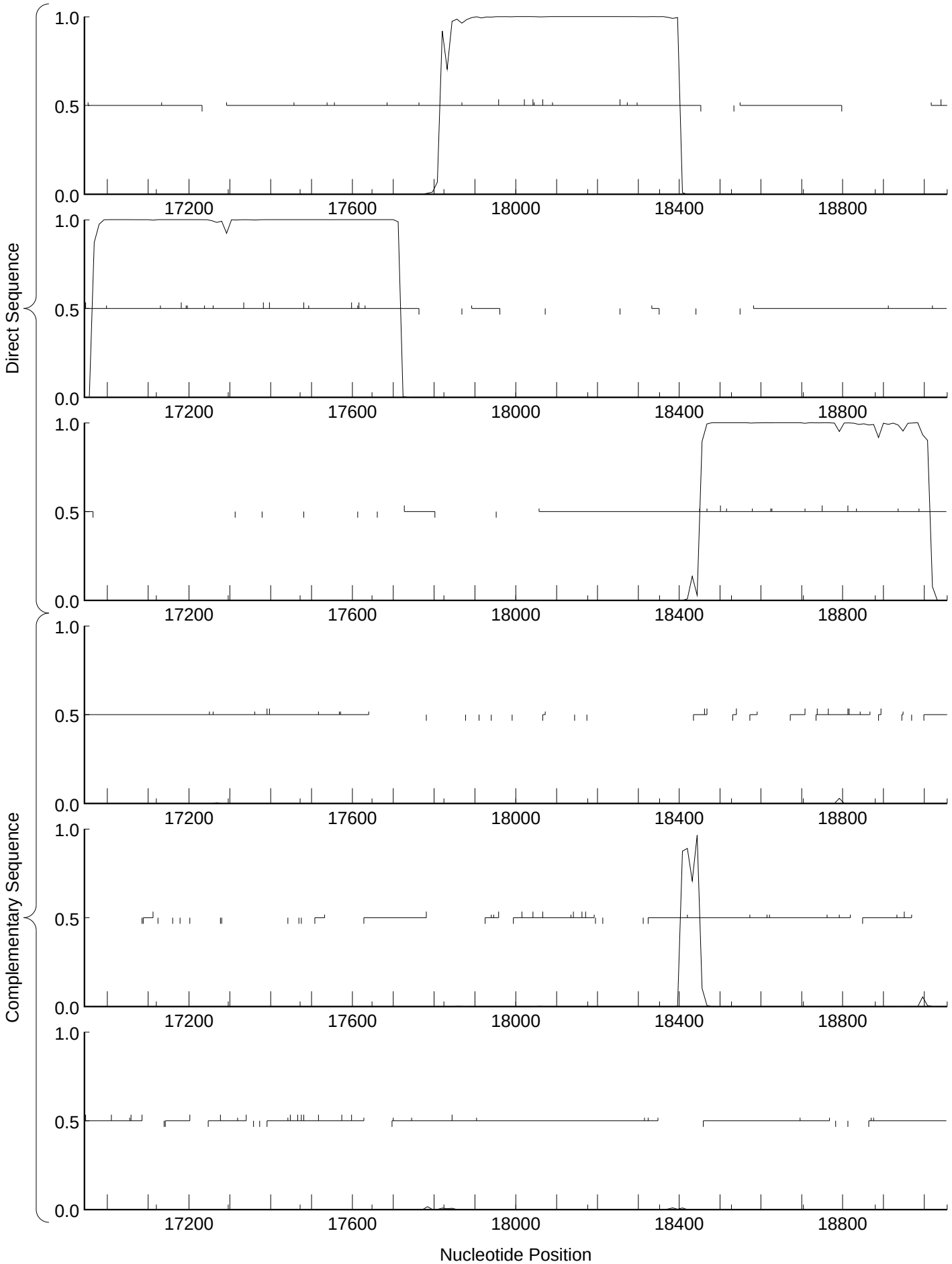

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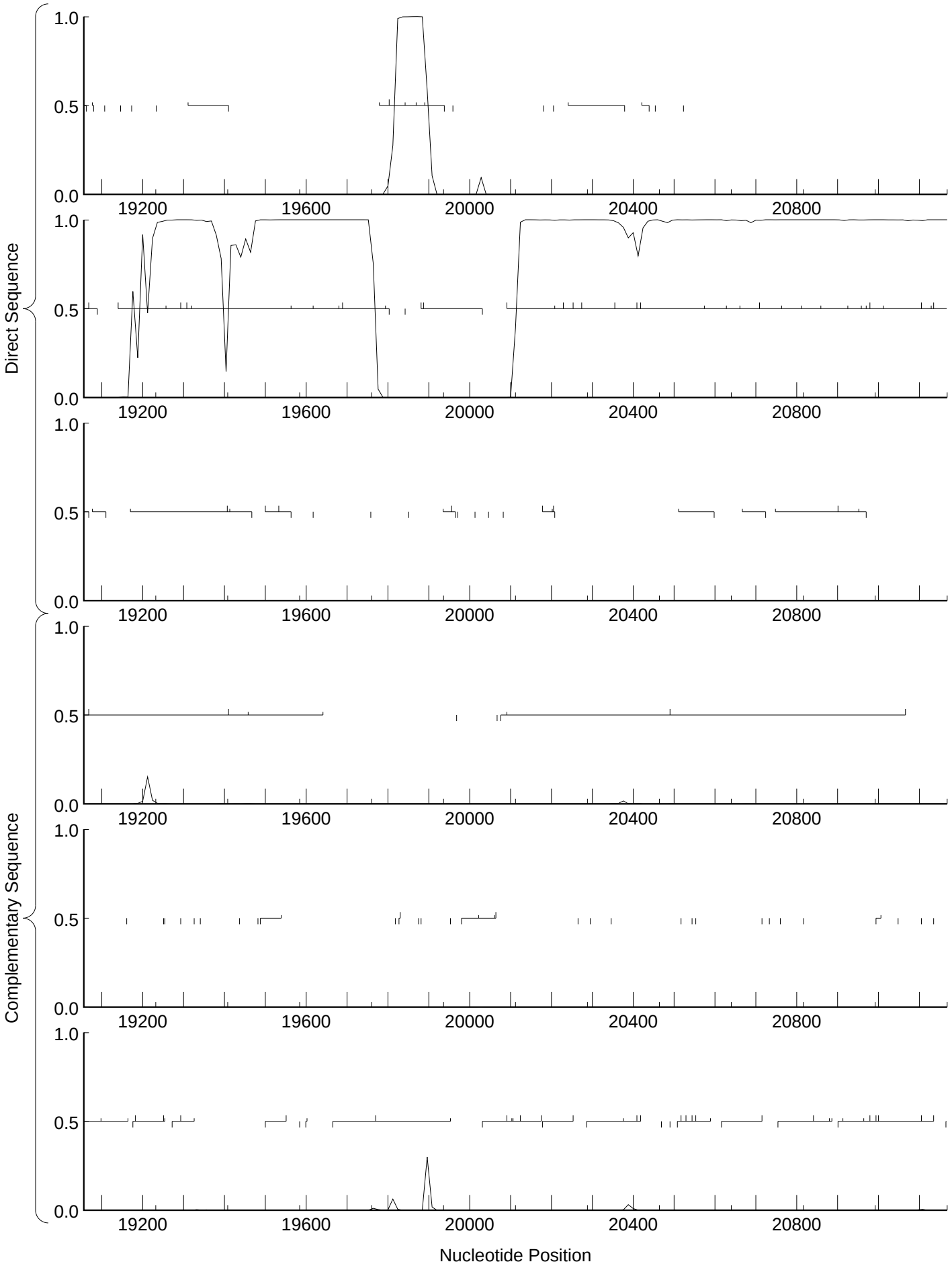
nage Familton complete sequence, 71807 bp including 4-base 3' overhang (GTGT), Cluster O, Order 4, Window 96, Step 12, 7/35

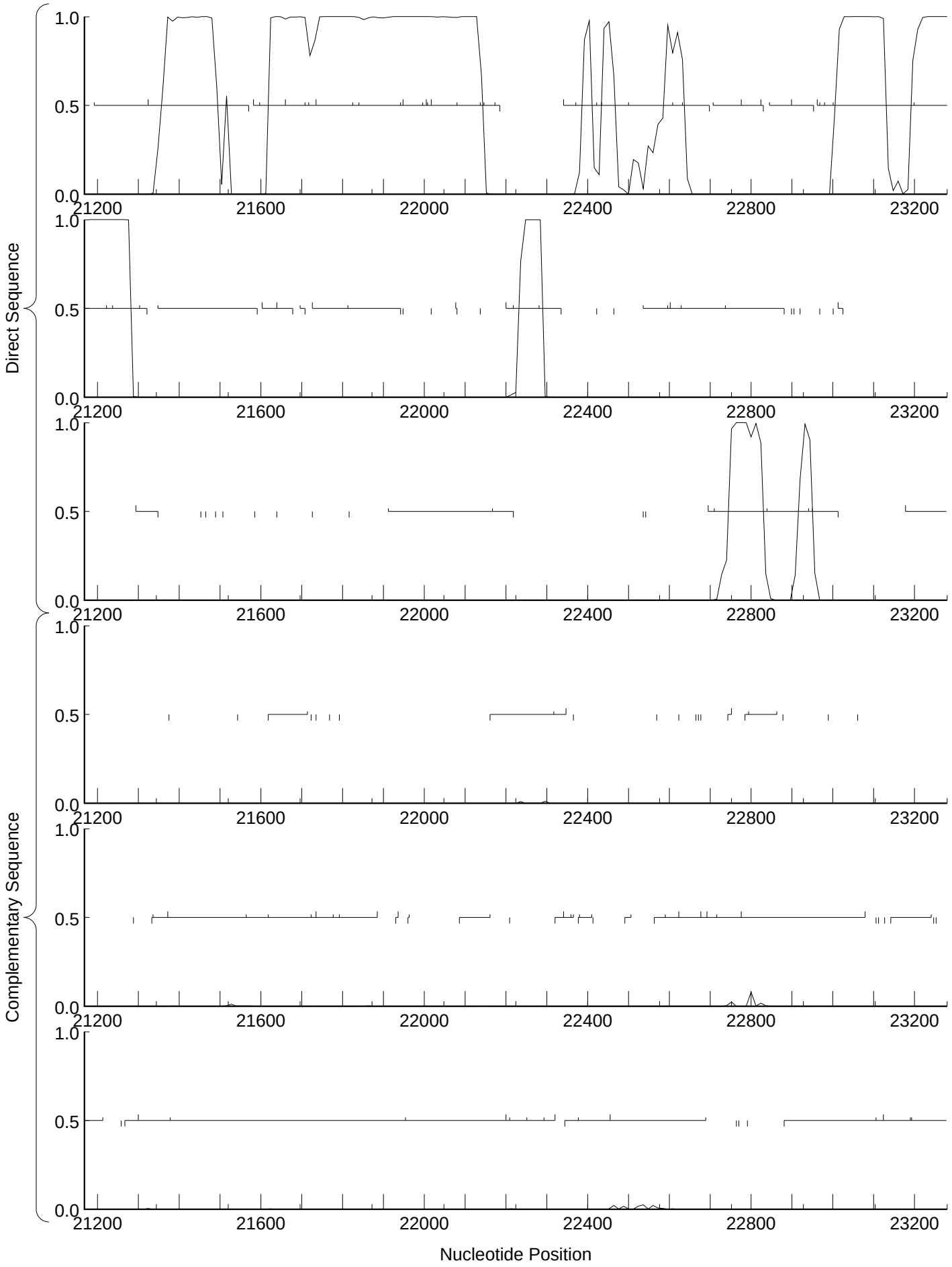


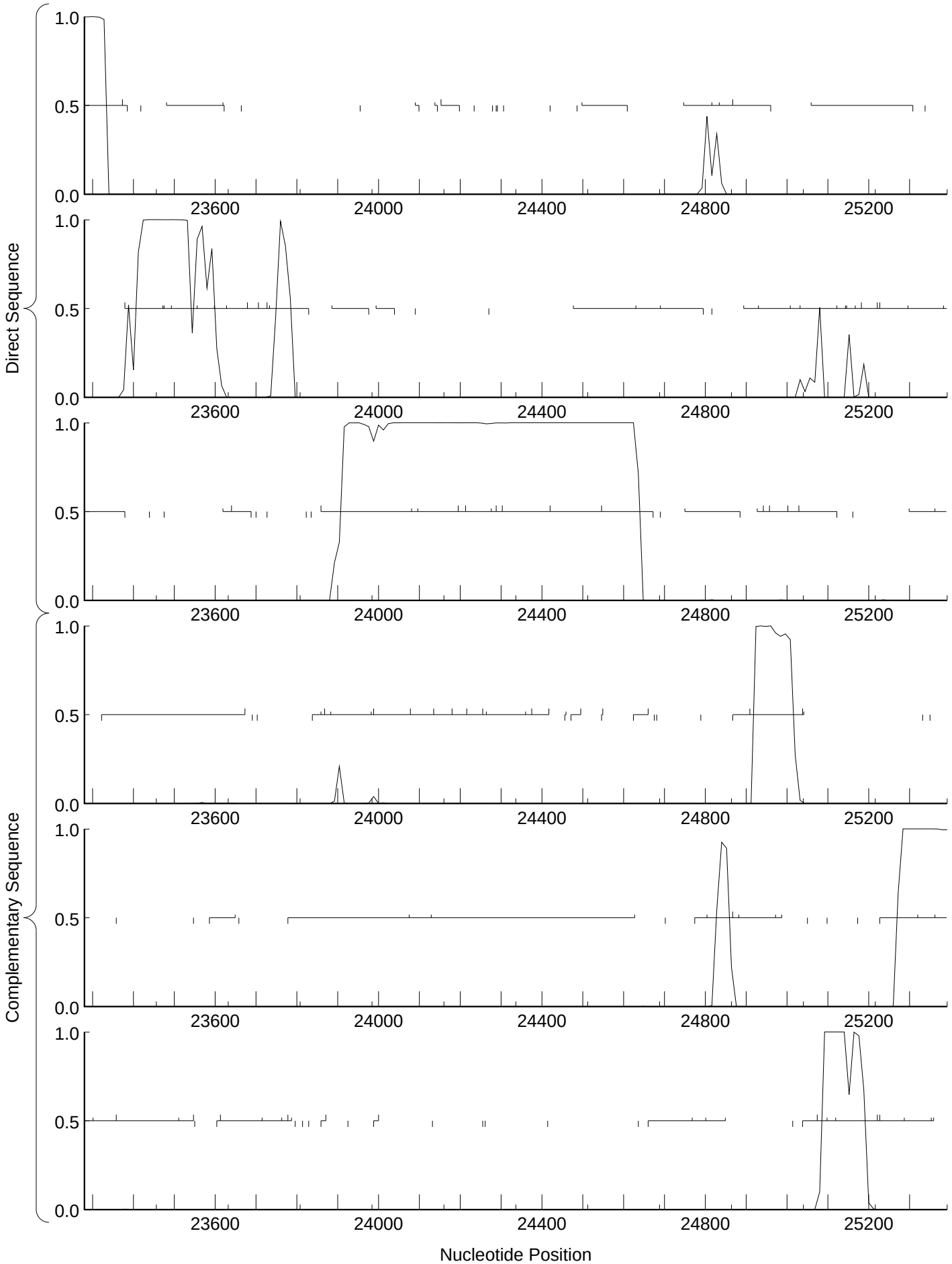

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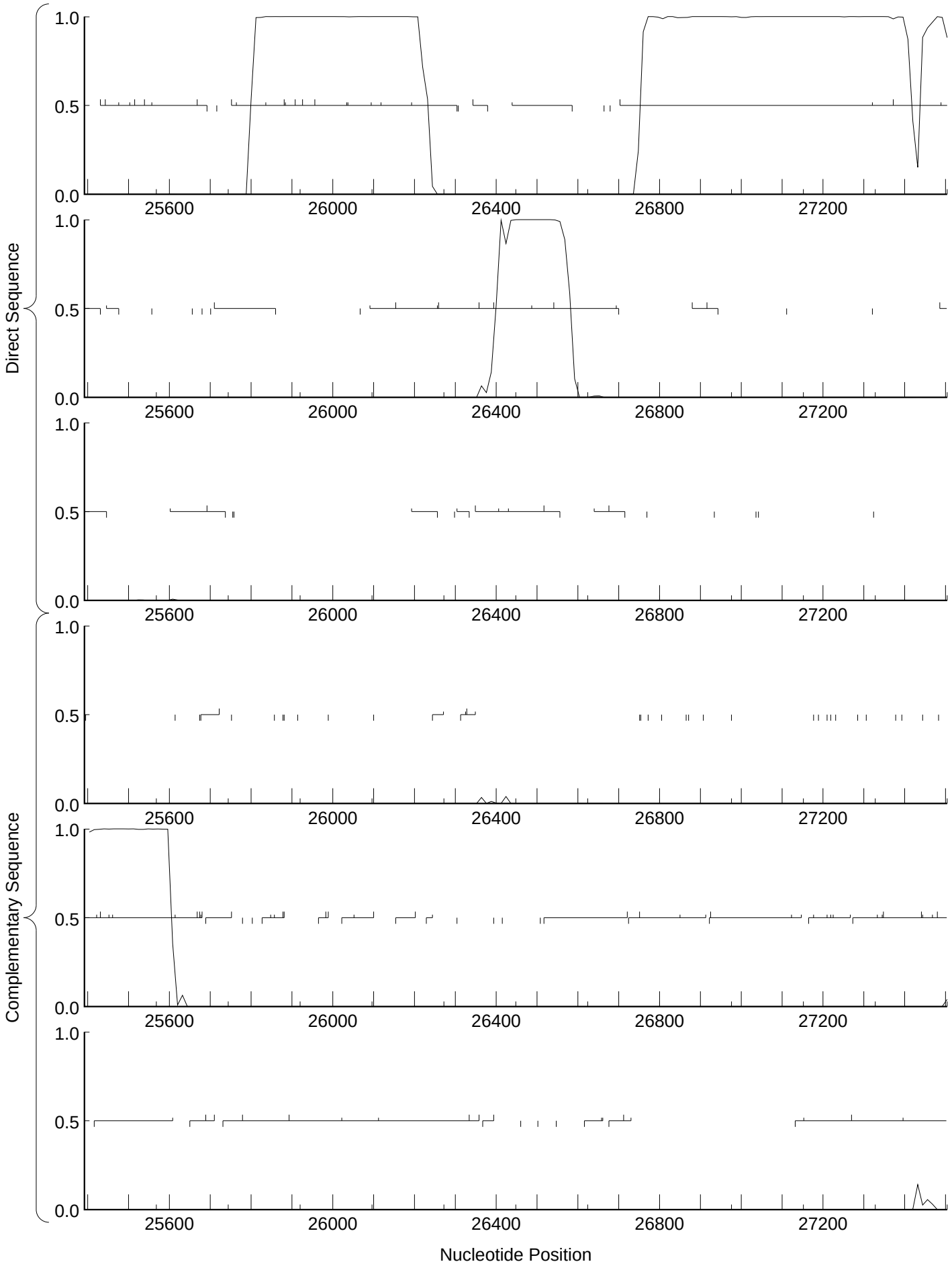

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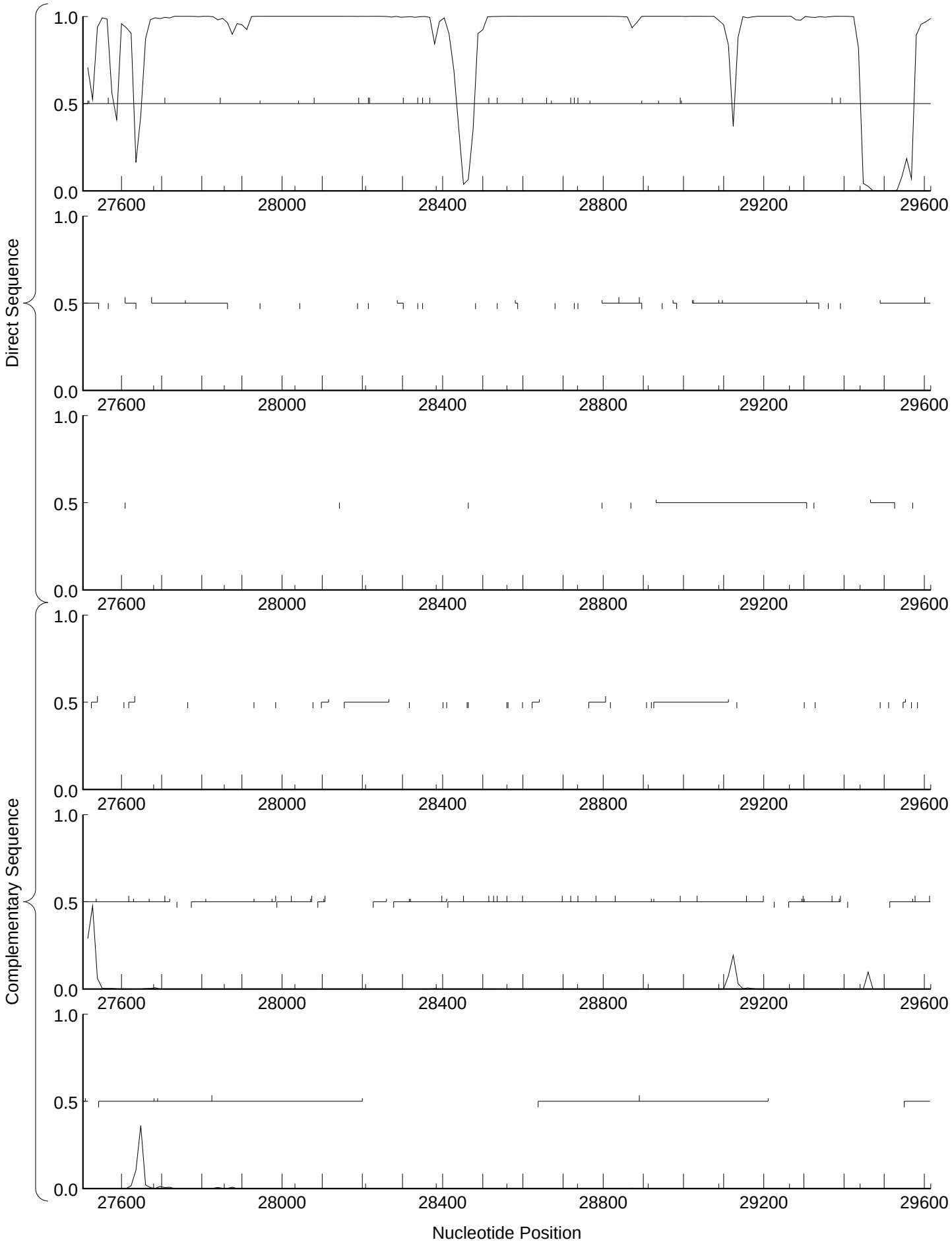

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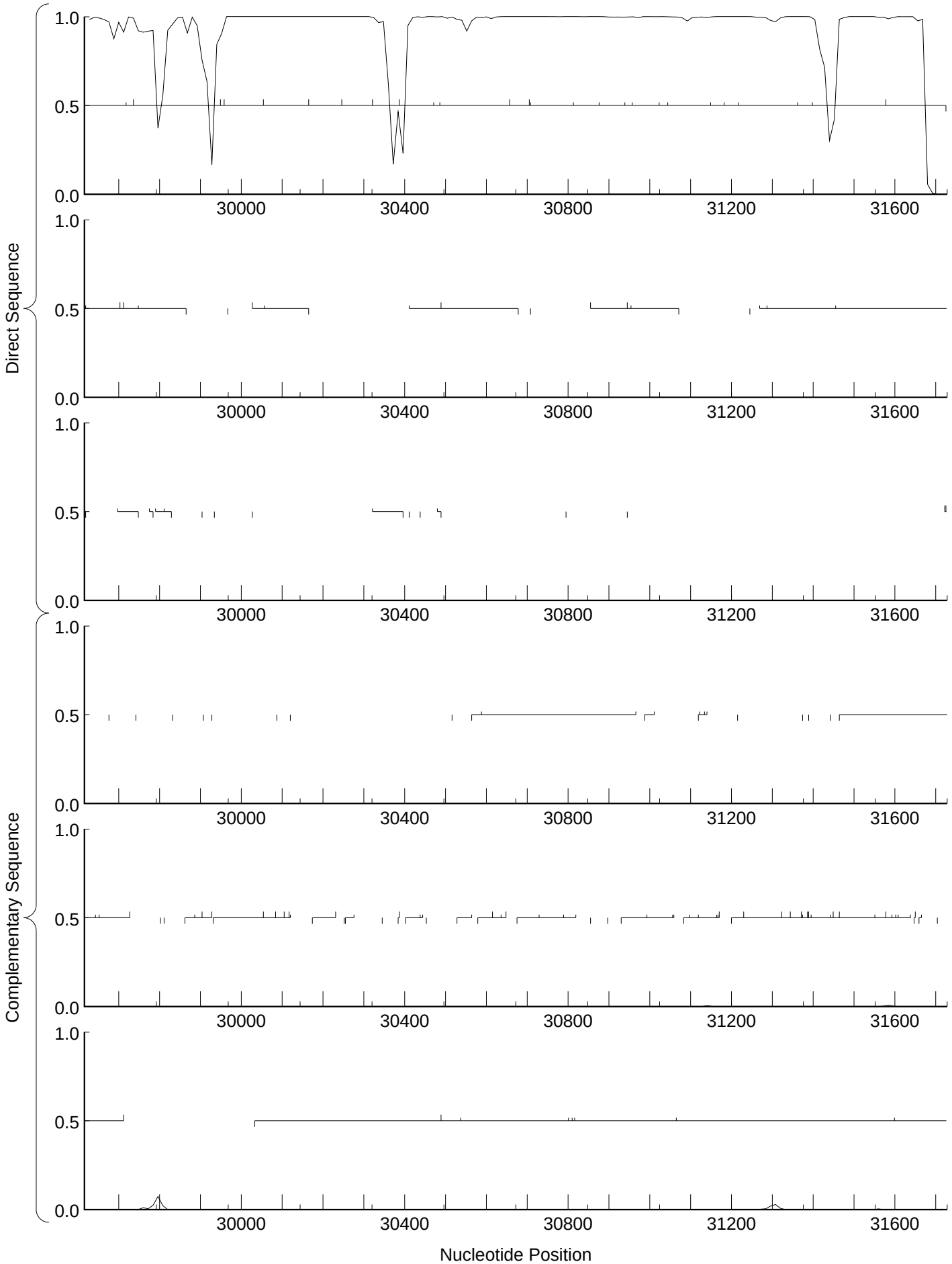

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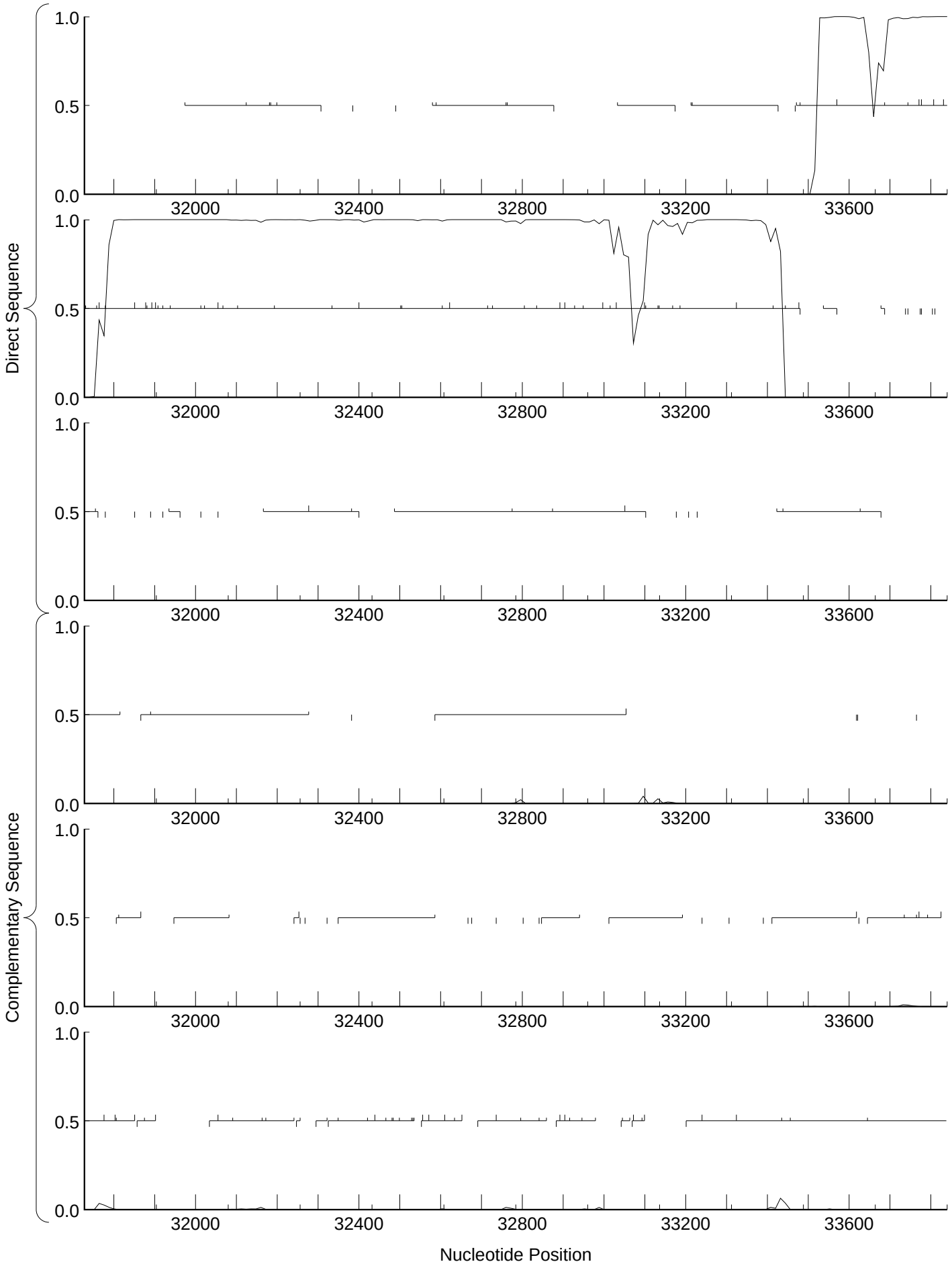

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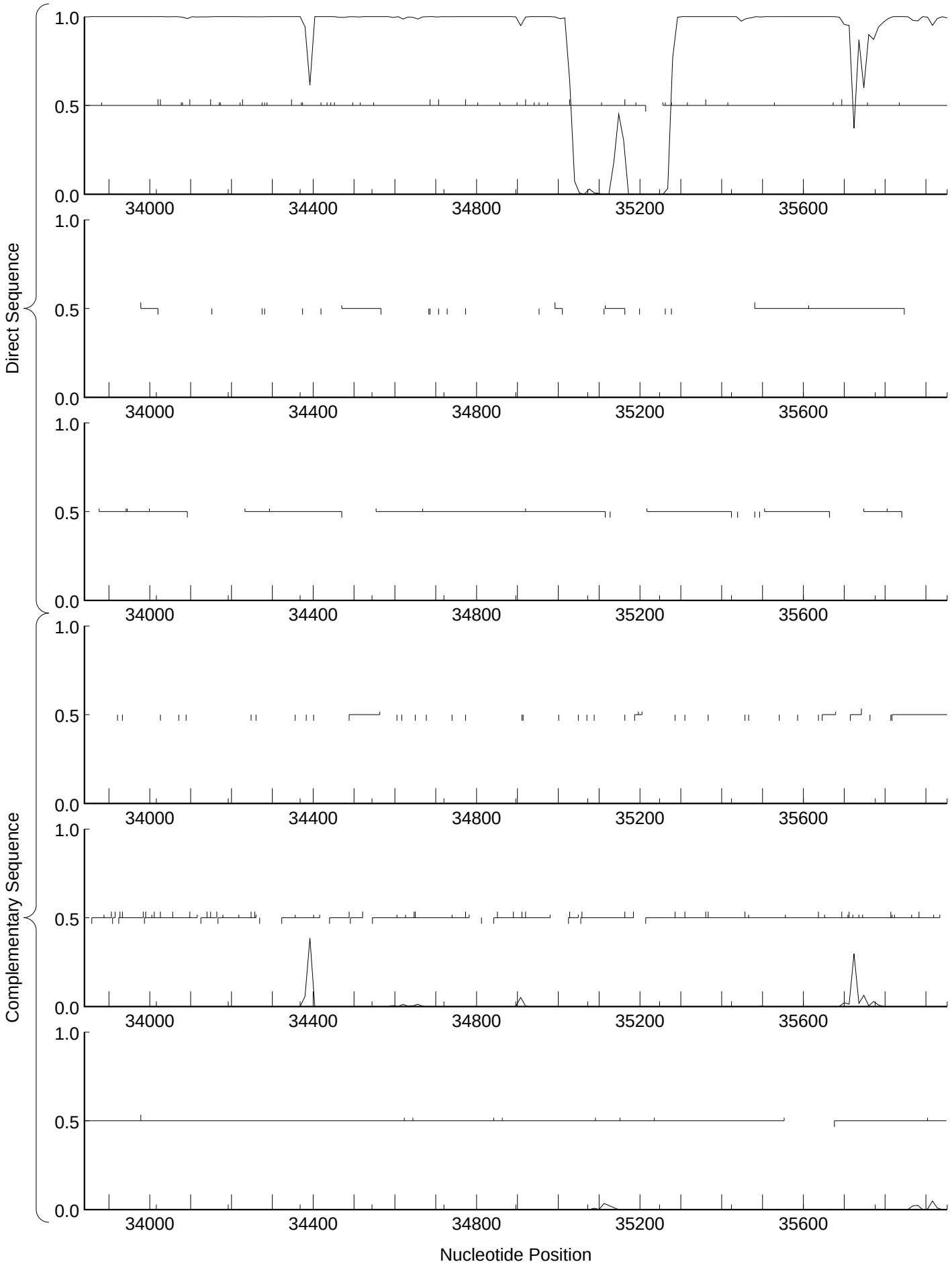

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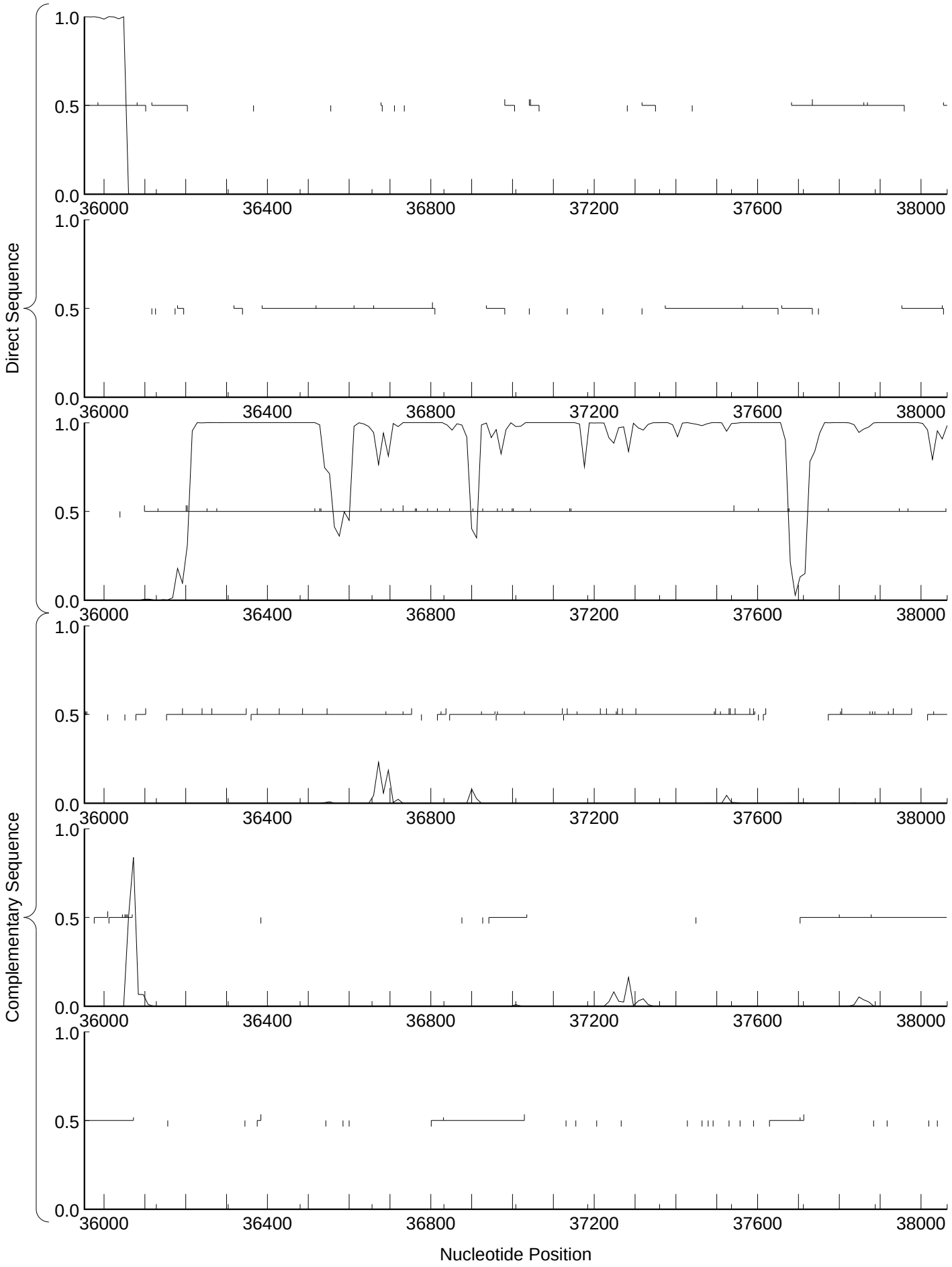

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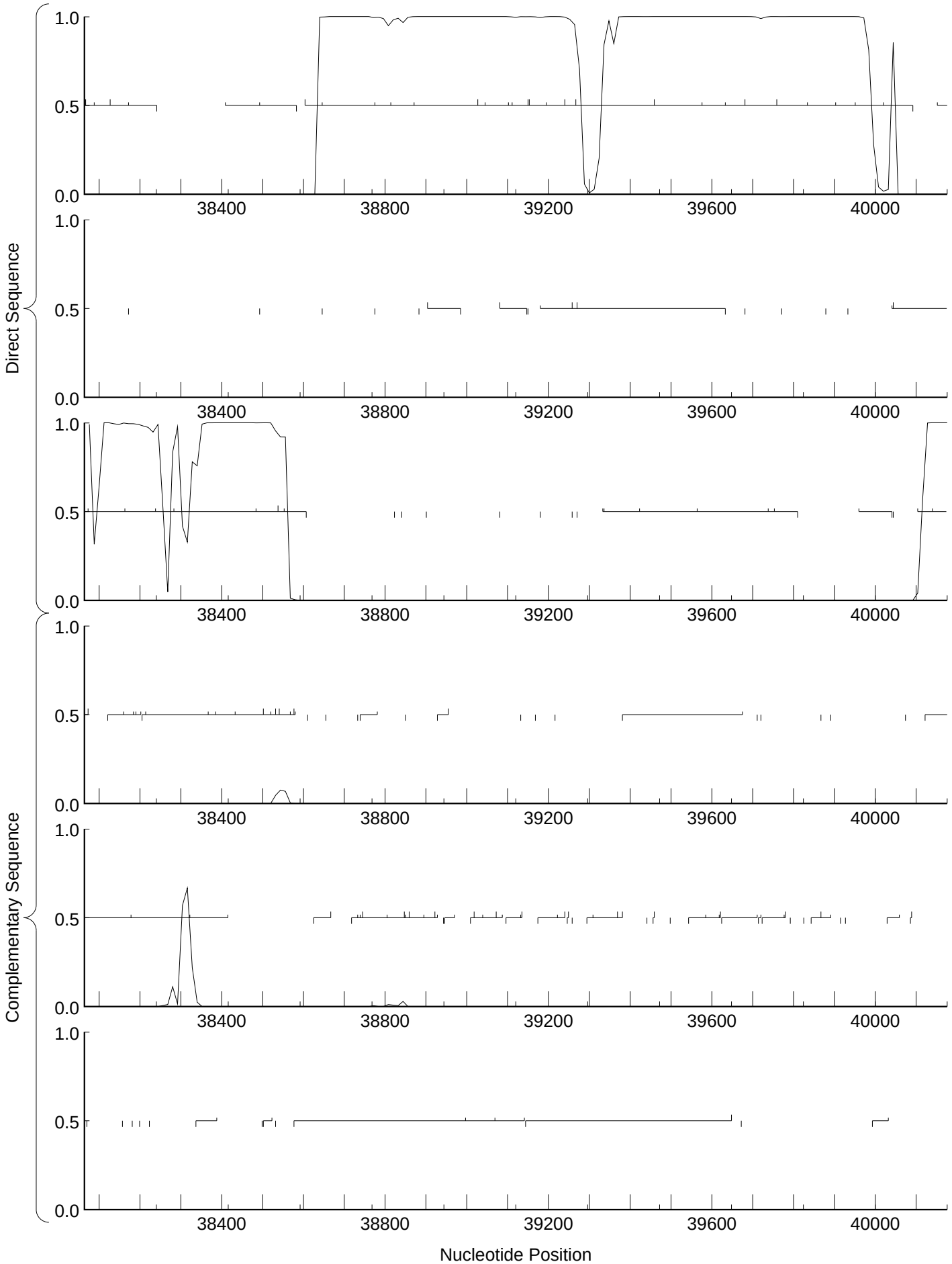

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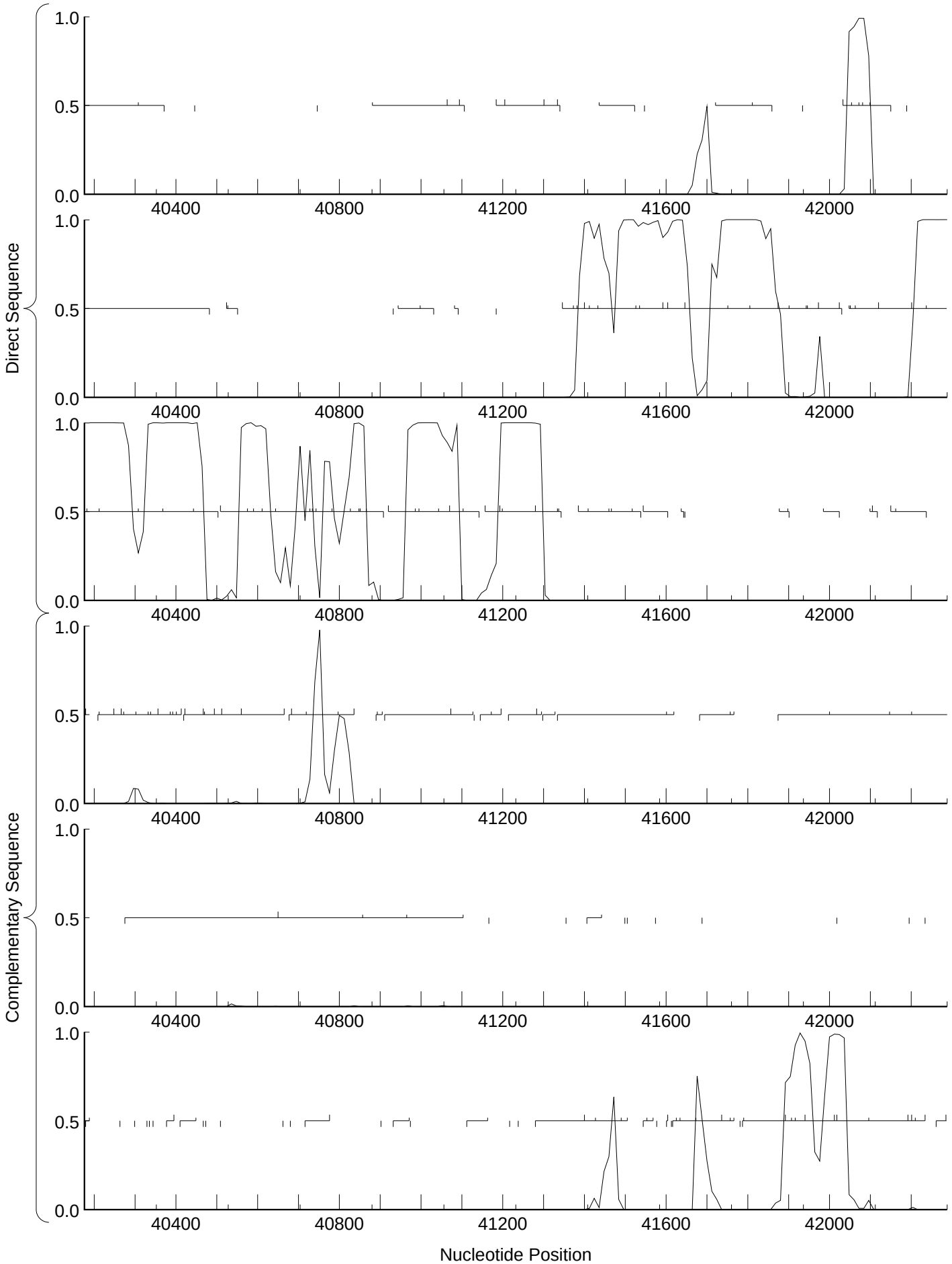

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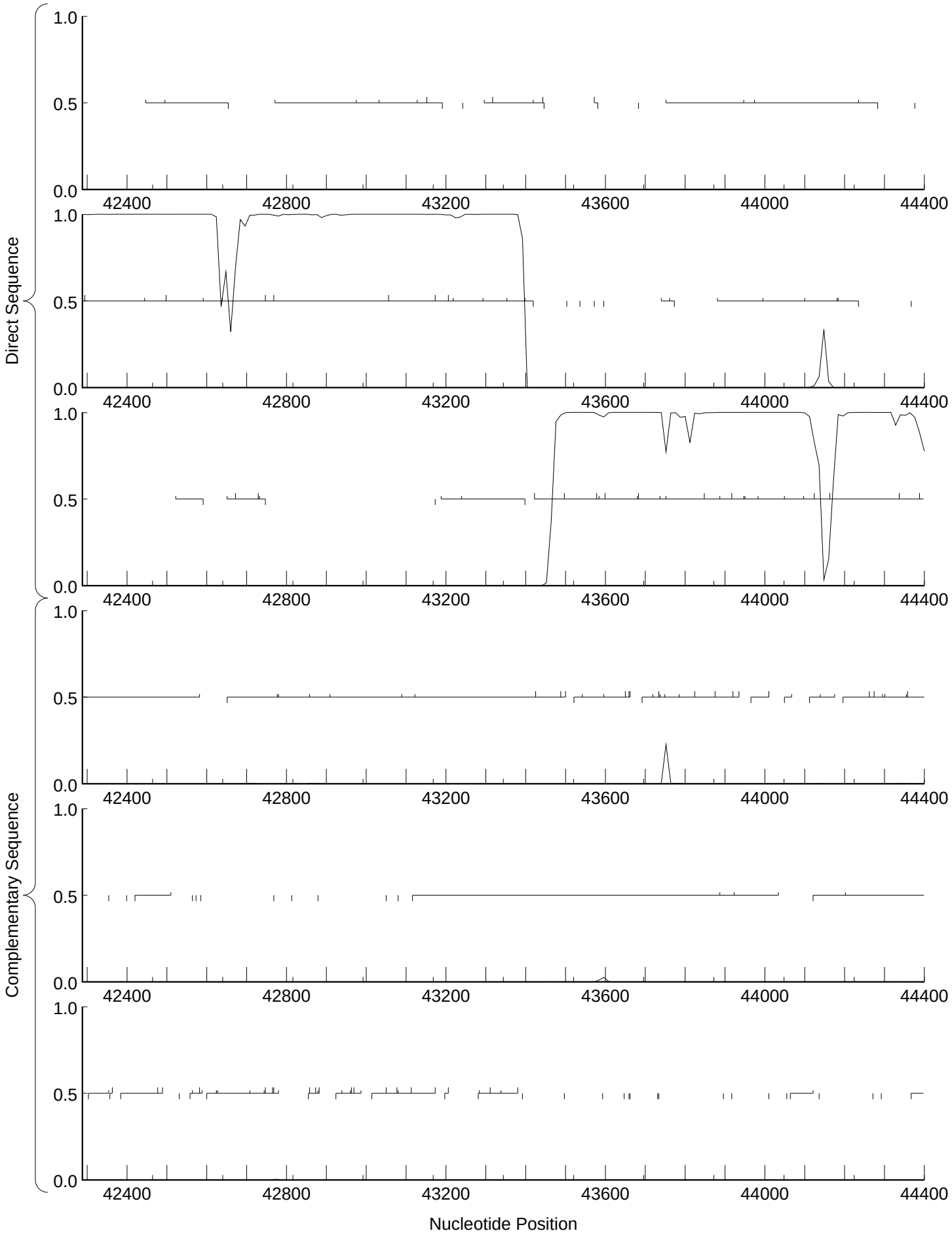

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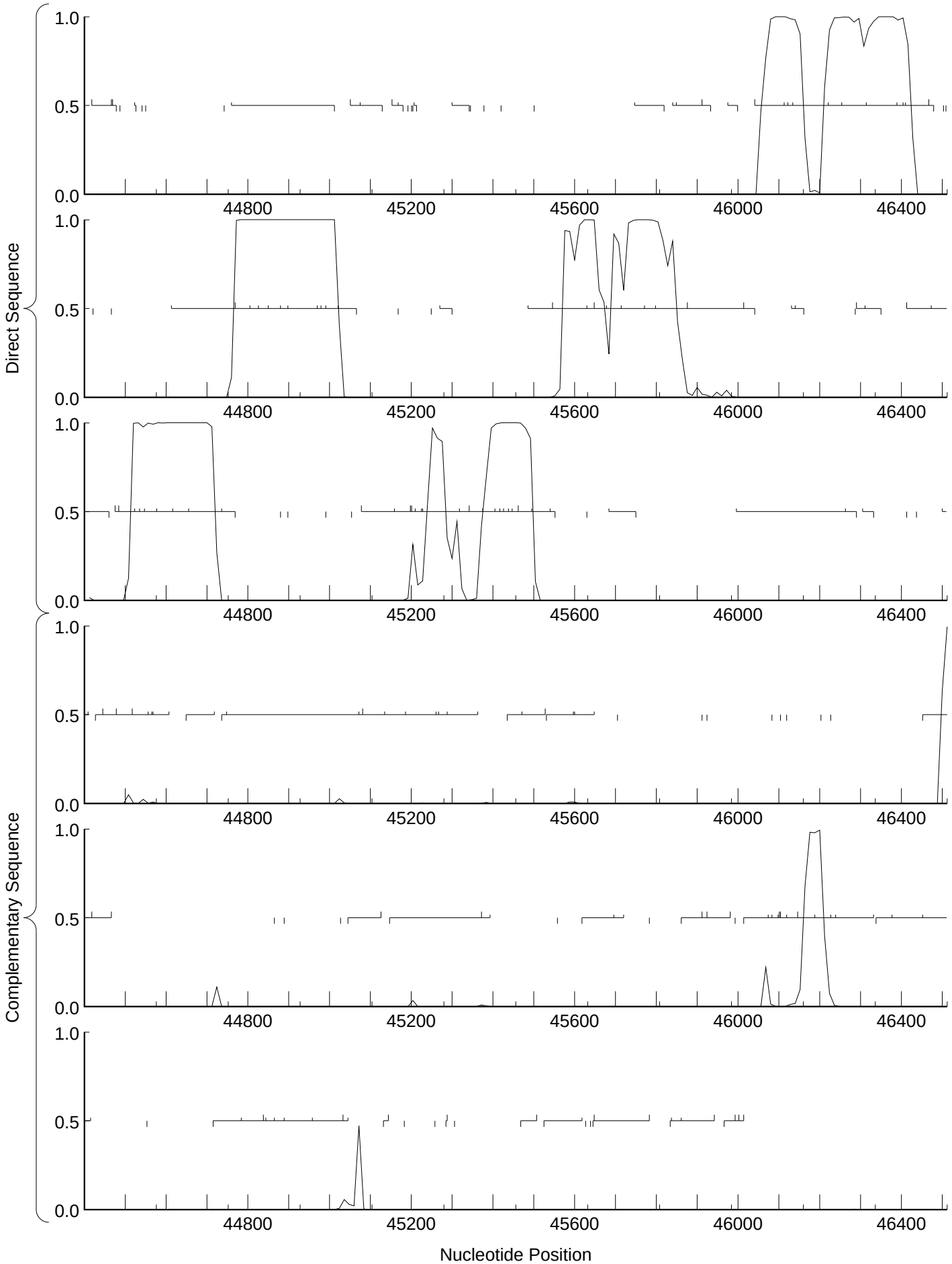

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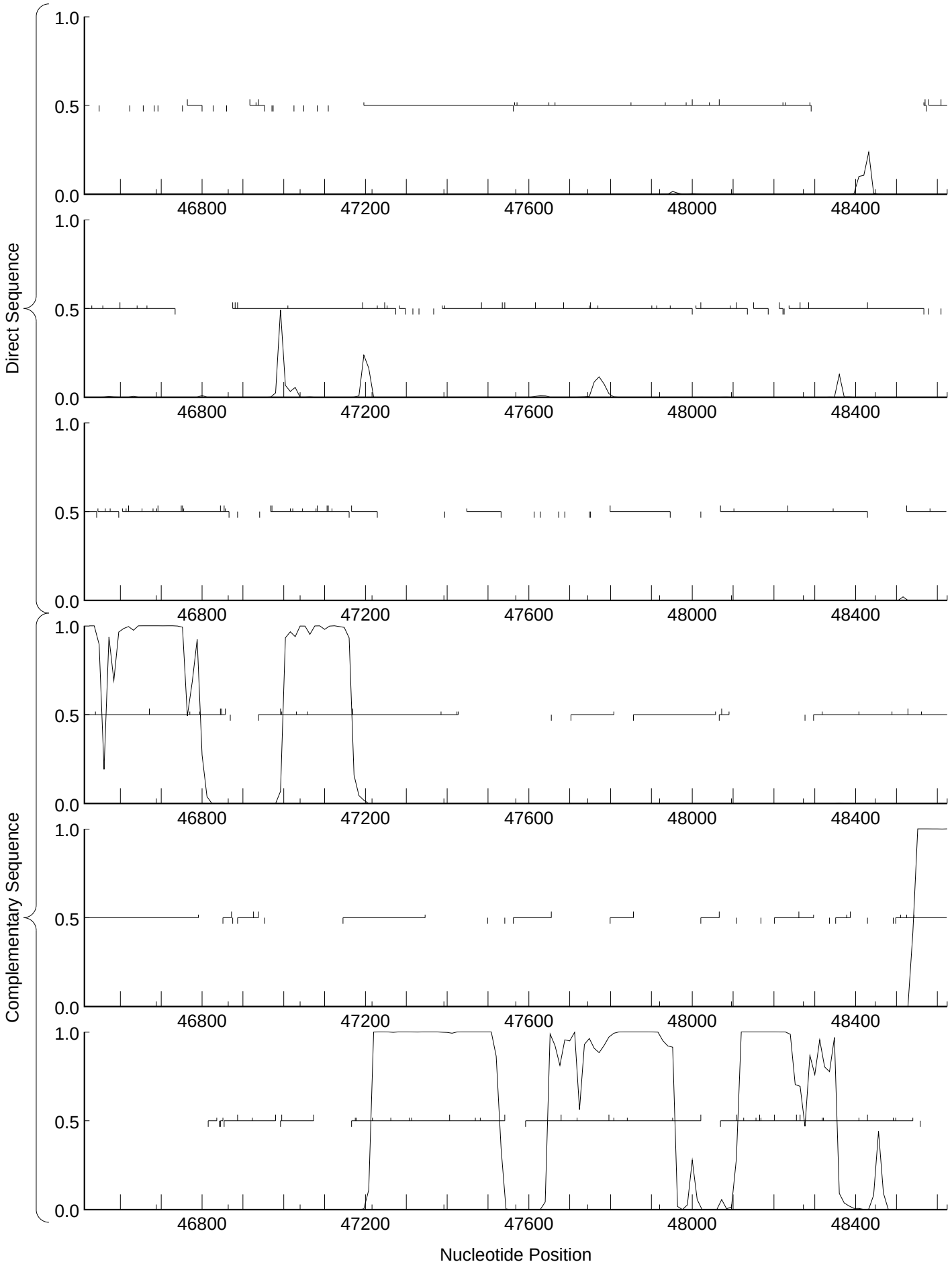

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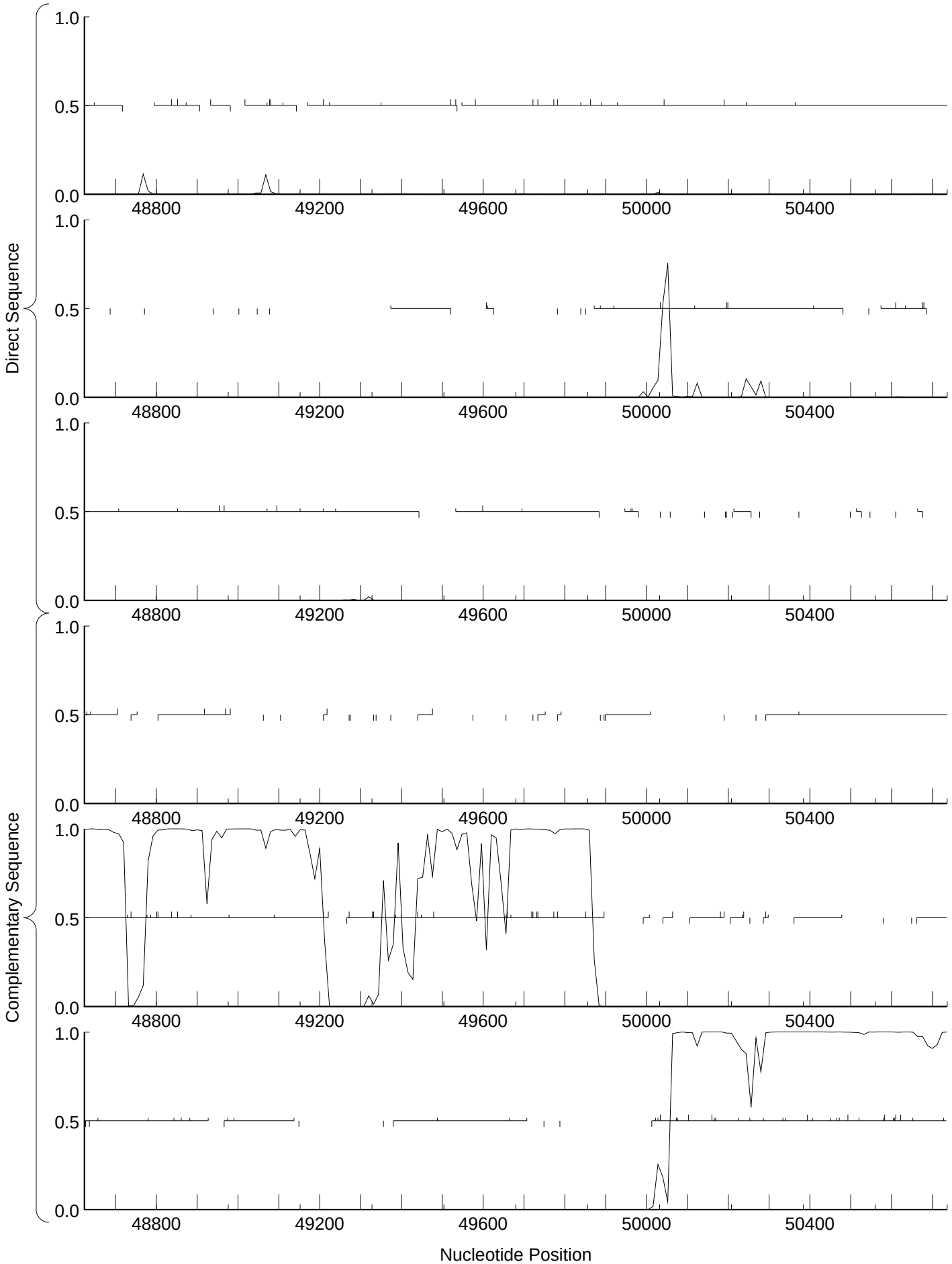

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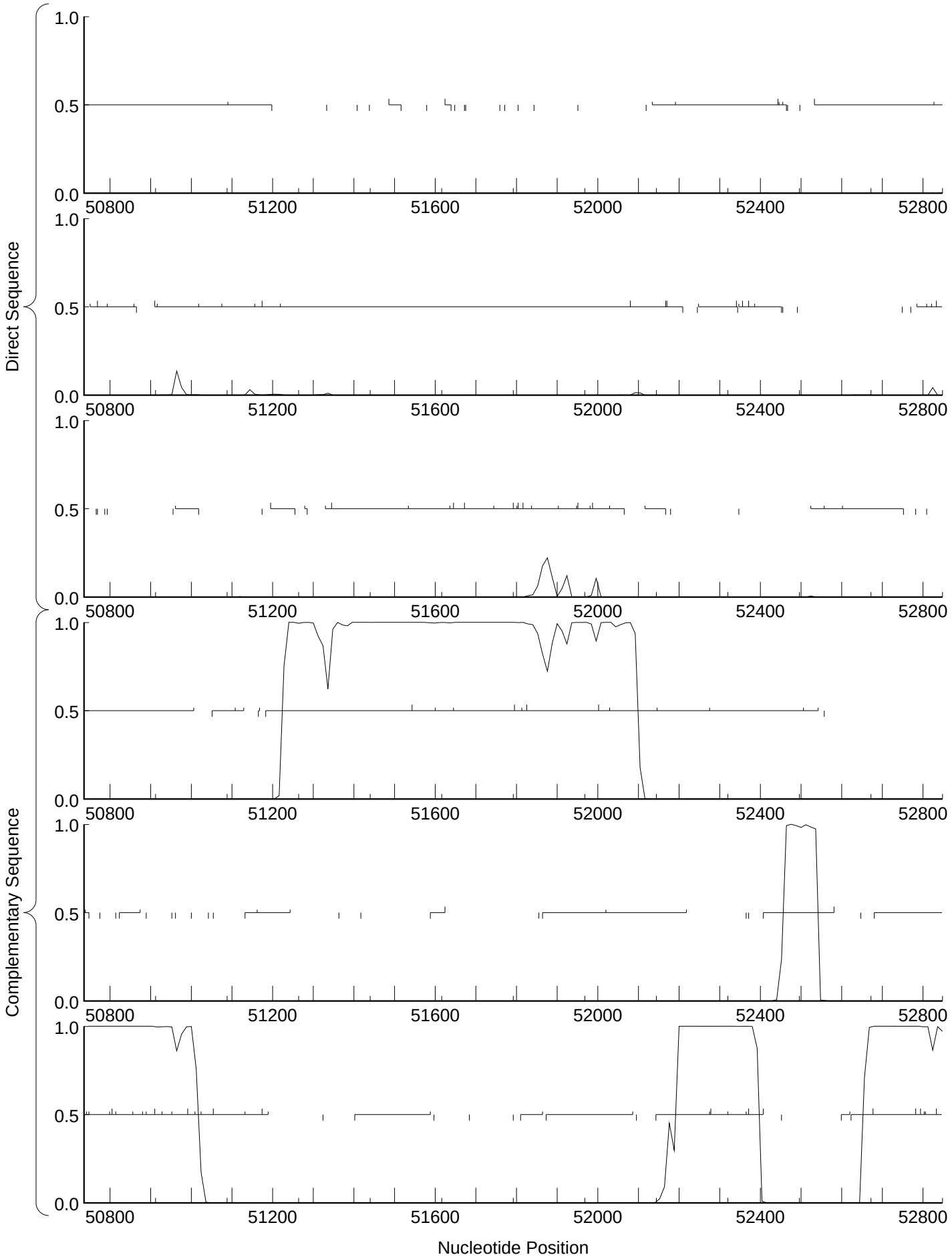

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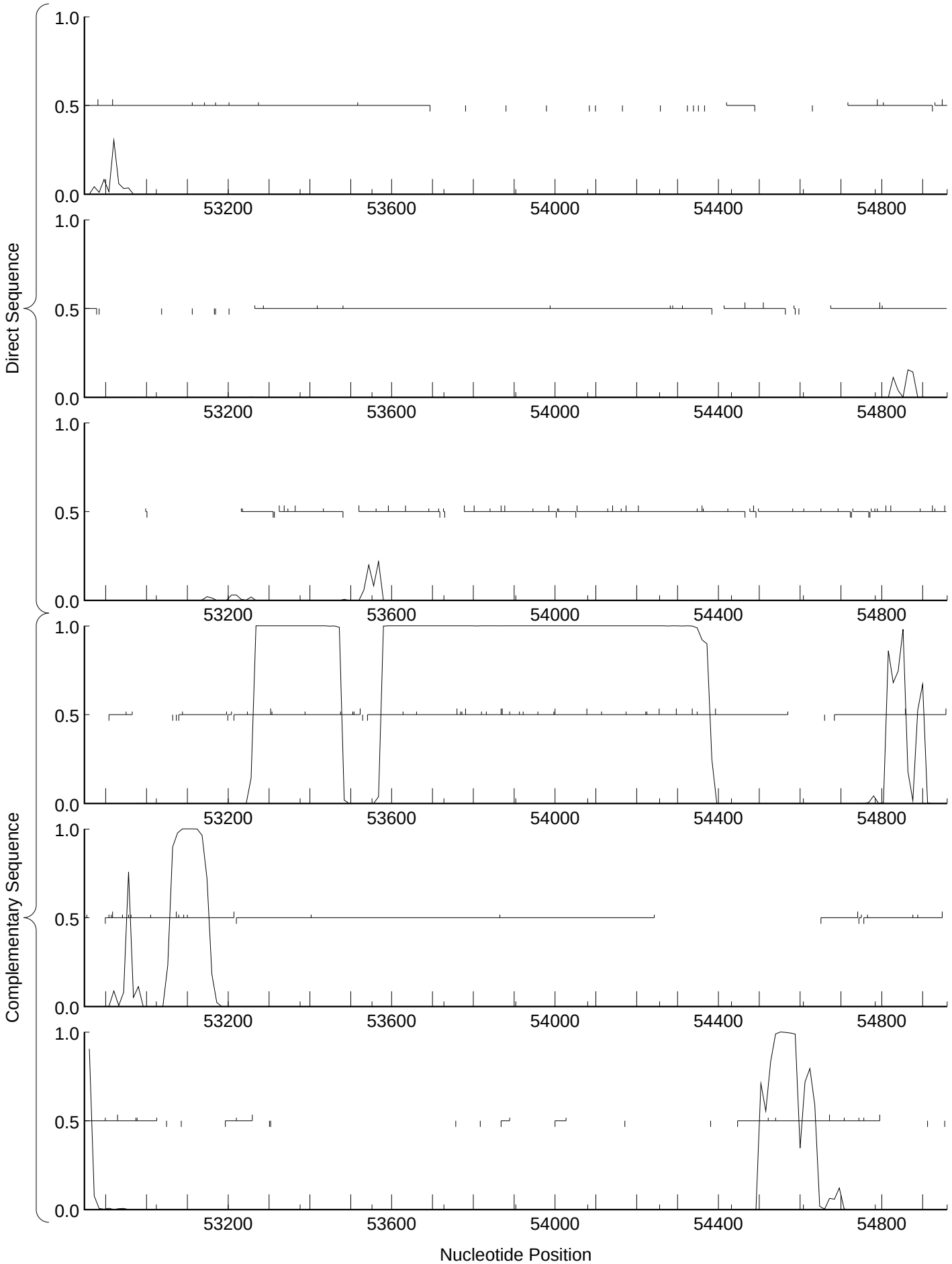

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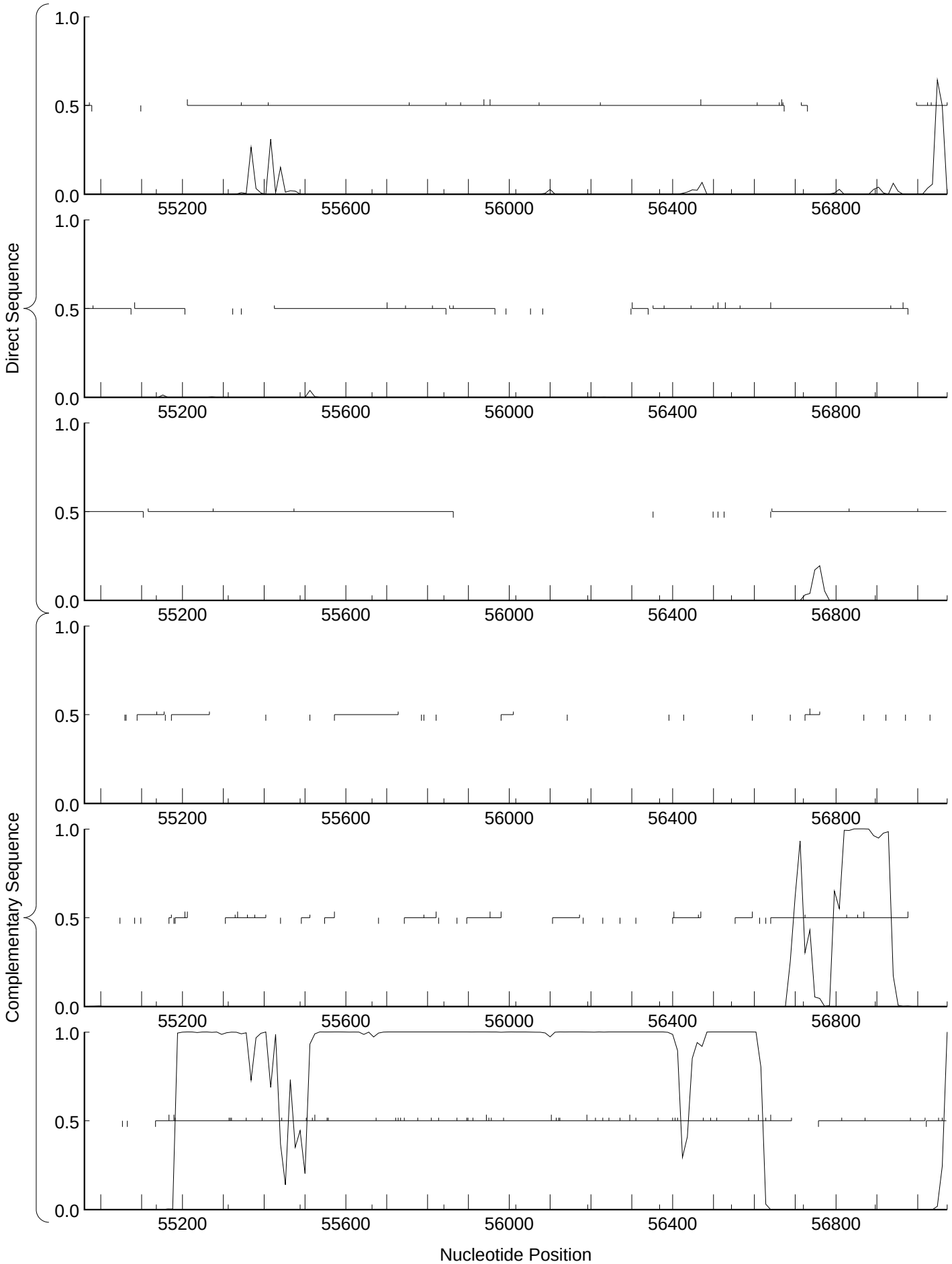

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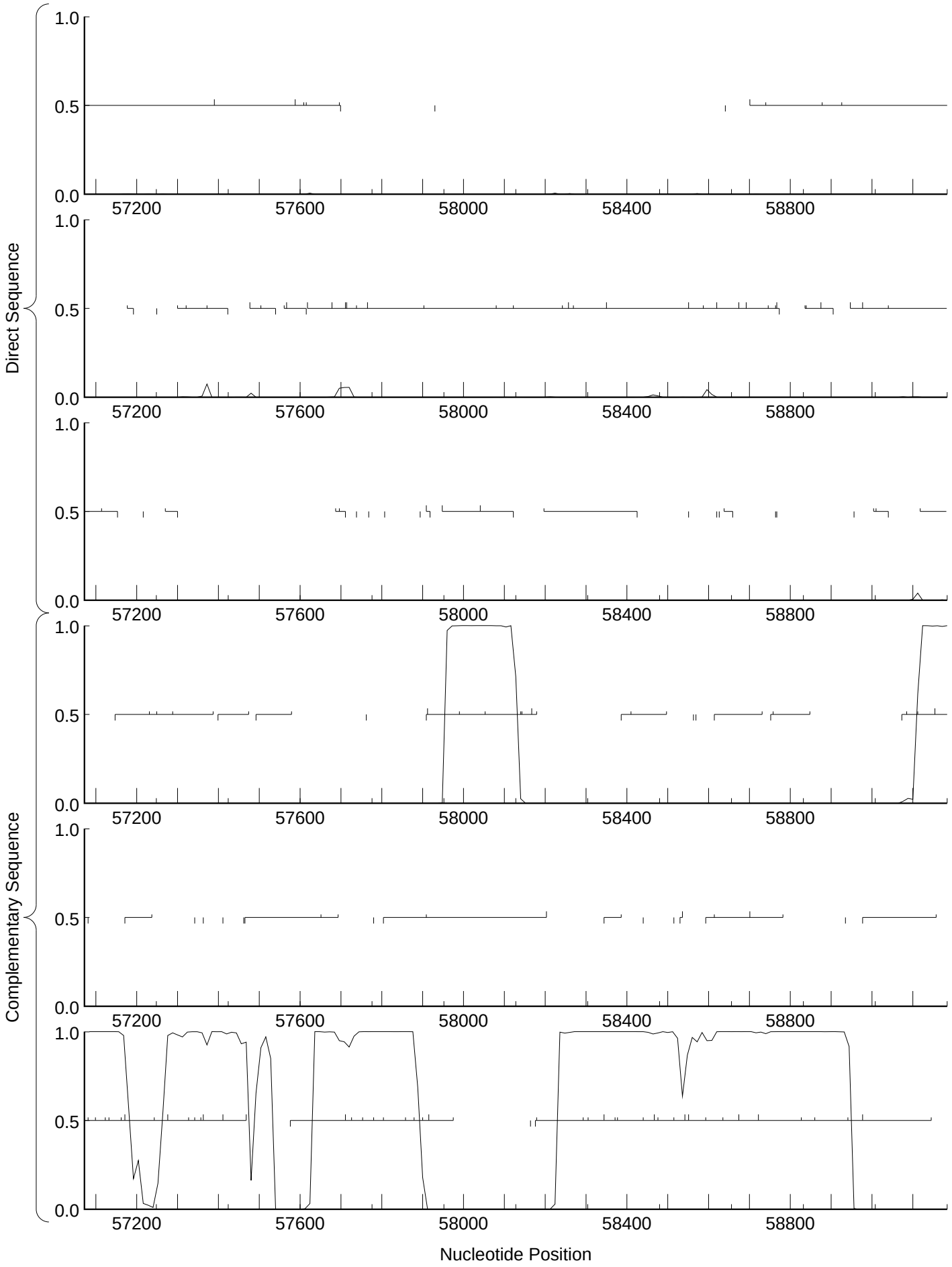

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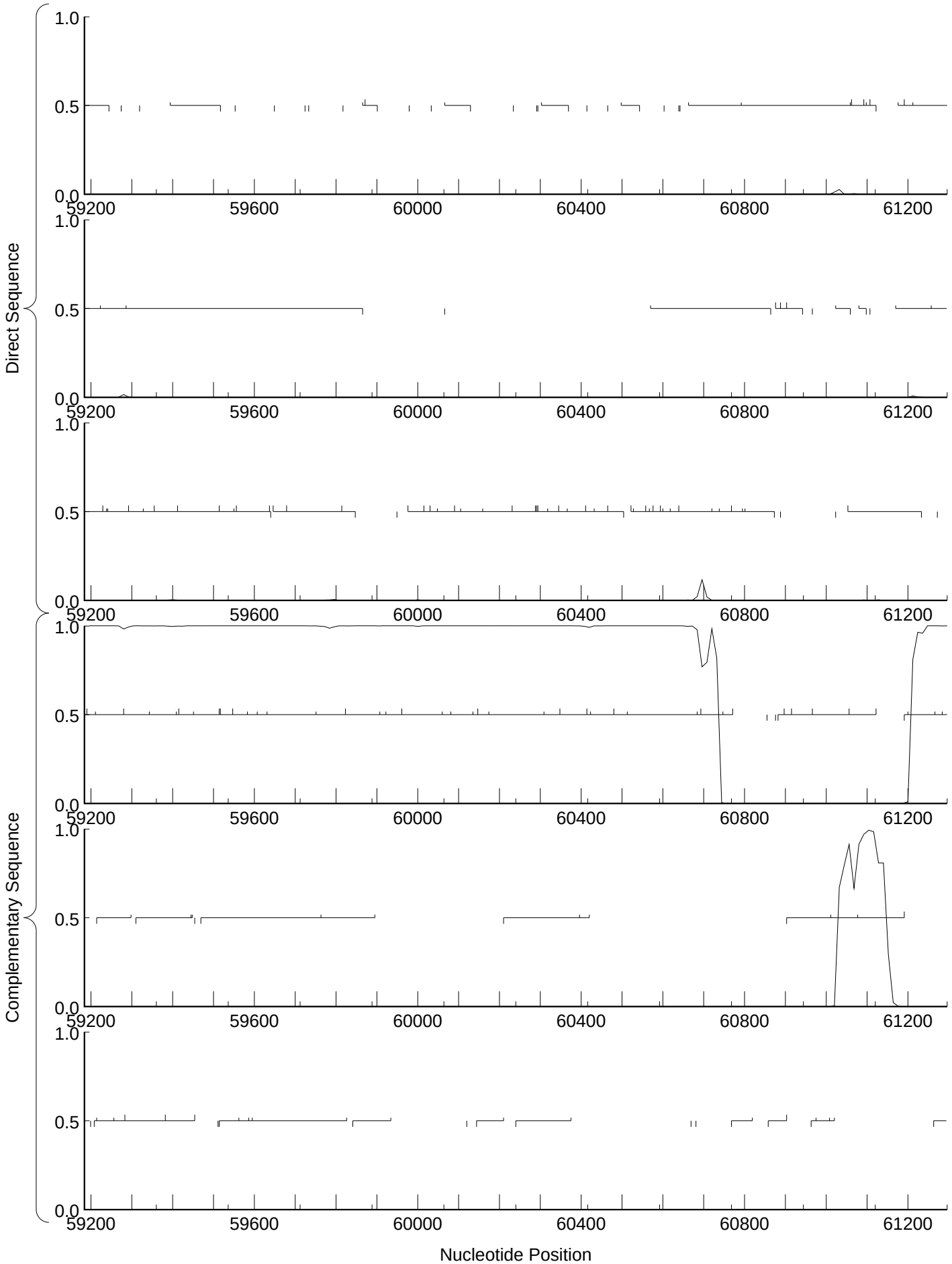

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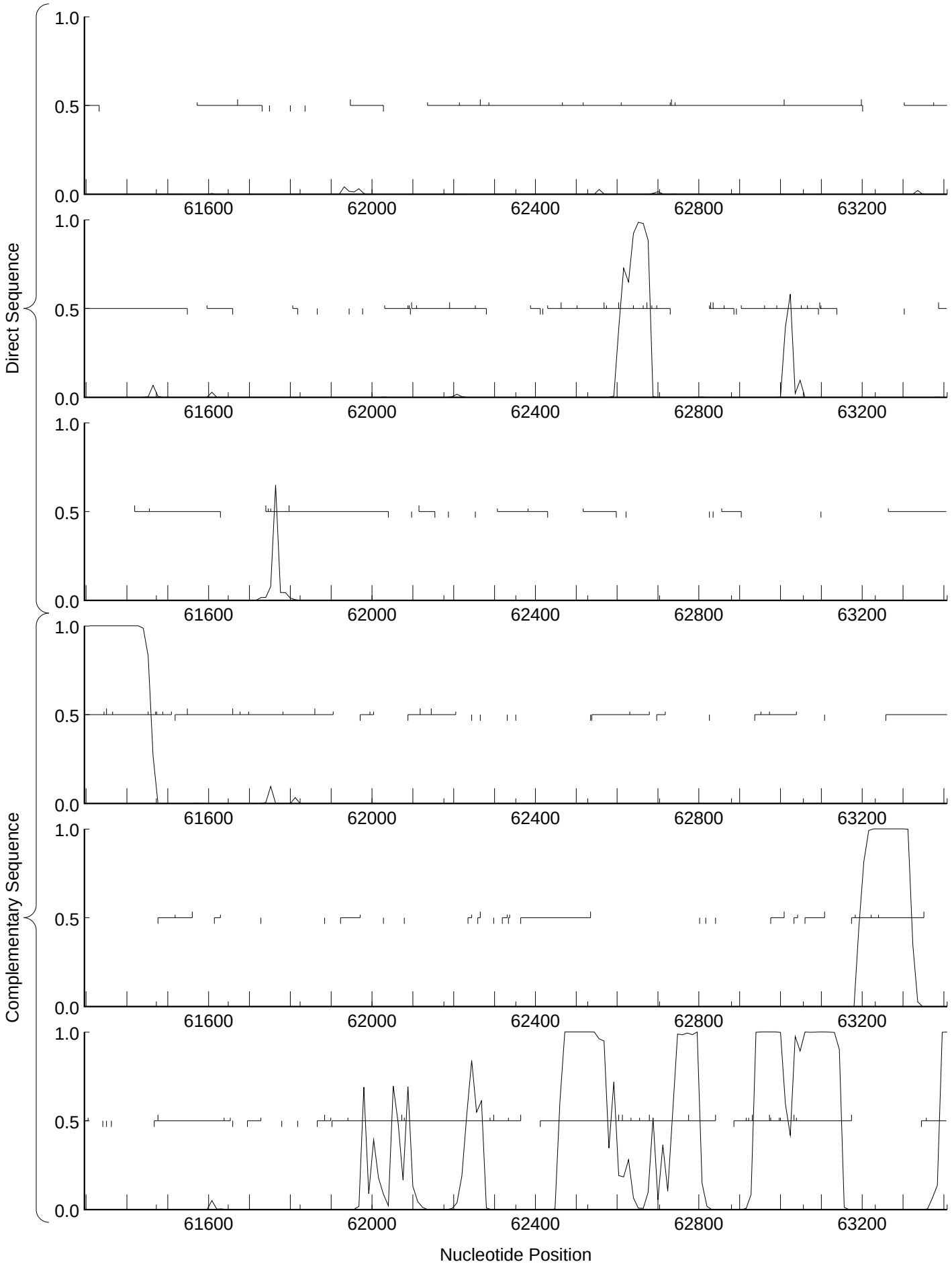

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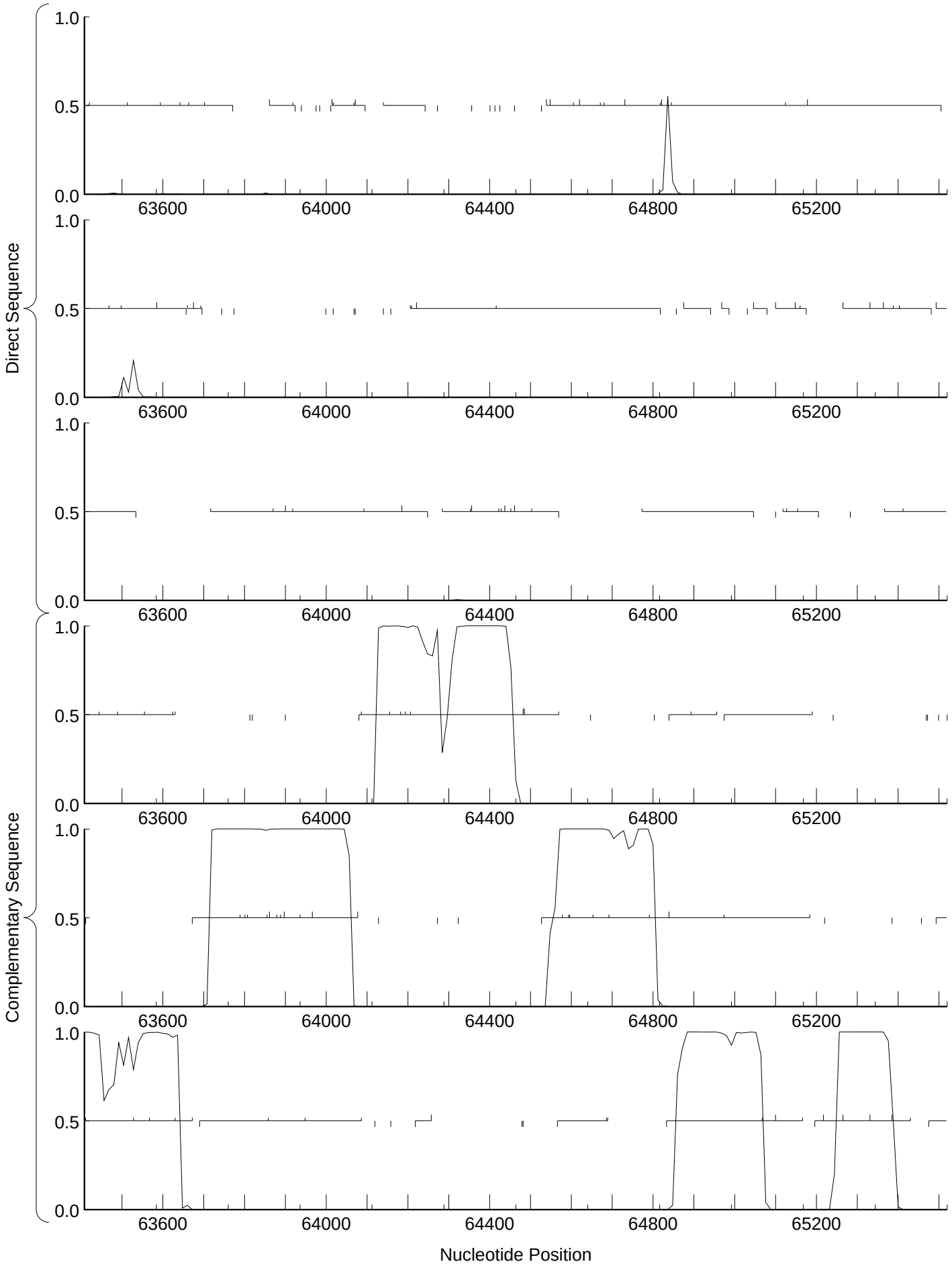

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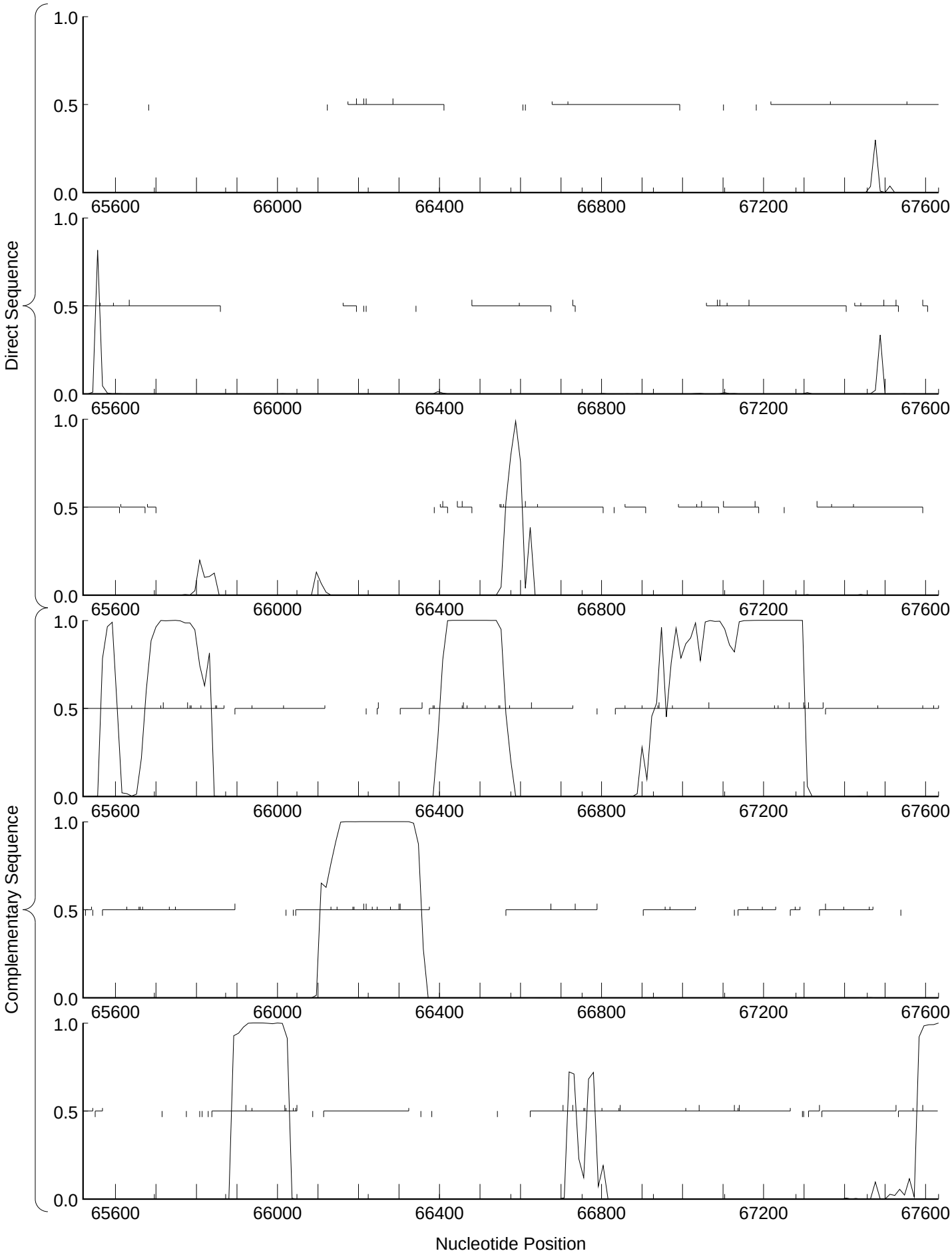

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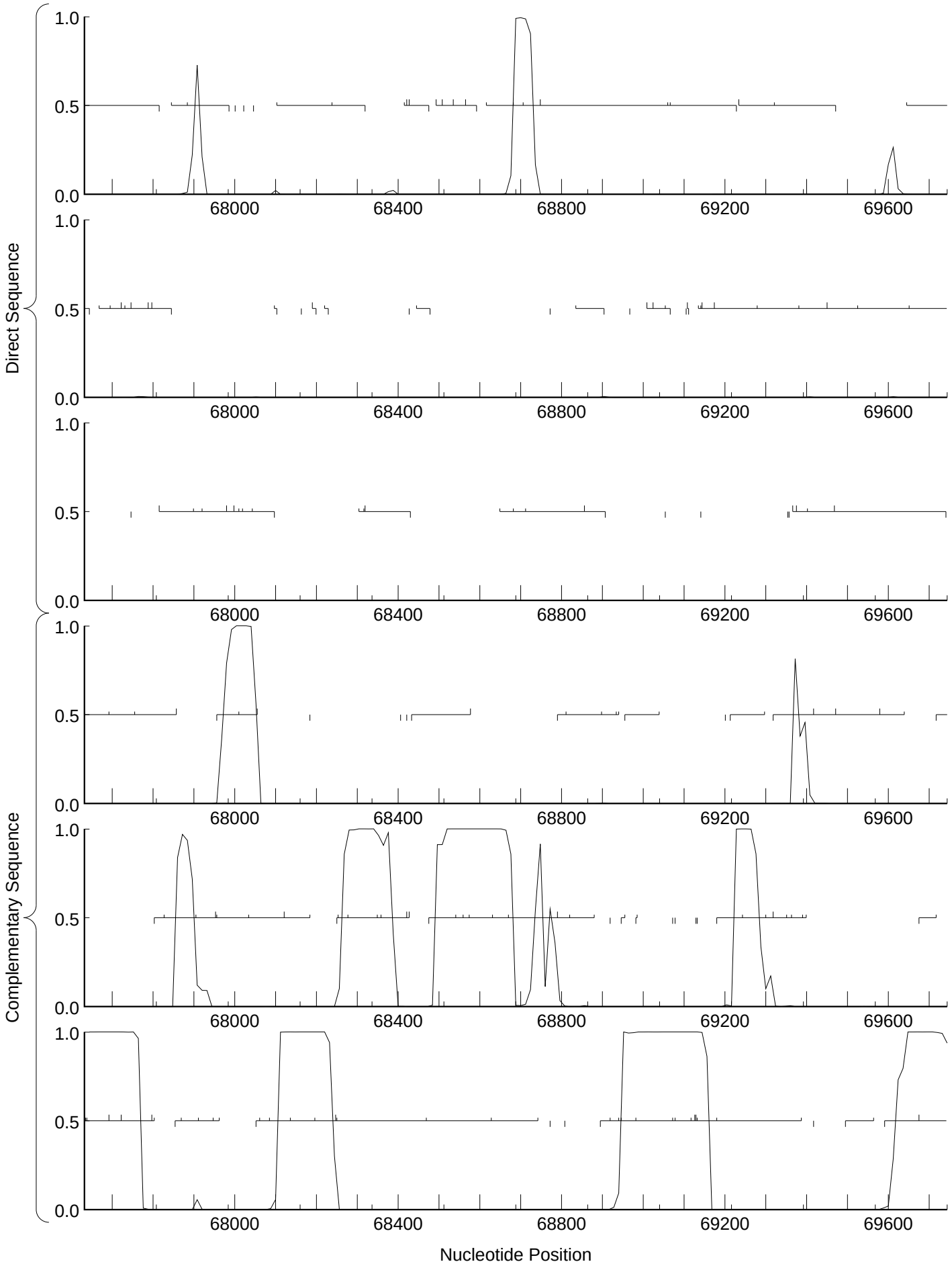

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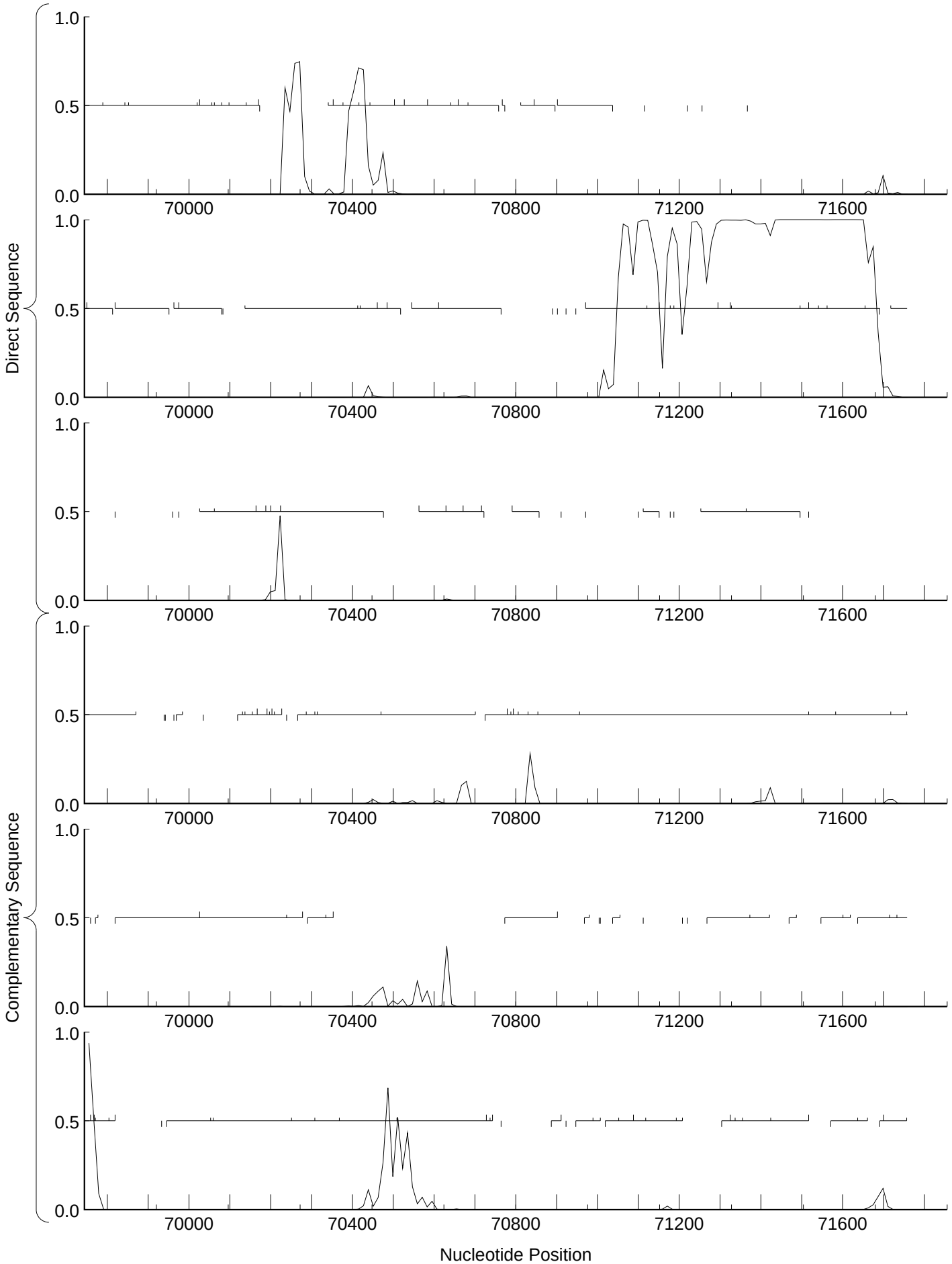

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63200
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Complementary Sequence
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Direct Sequence
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Nucleotide Position


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Nucleotide Position


Direct Sequence
Complementary Sequence
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