GeneMark

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

PROGRAM INFORMATION

```
Sequence         :  Mycobacterium phage LittleE
Analysis Date    :  3/28/24 at 18:30:36
Pages            :  53
Sequence Length  :  109086 bp
GC Content       :   61.35%

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

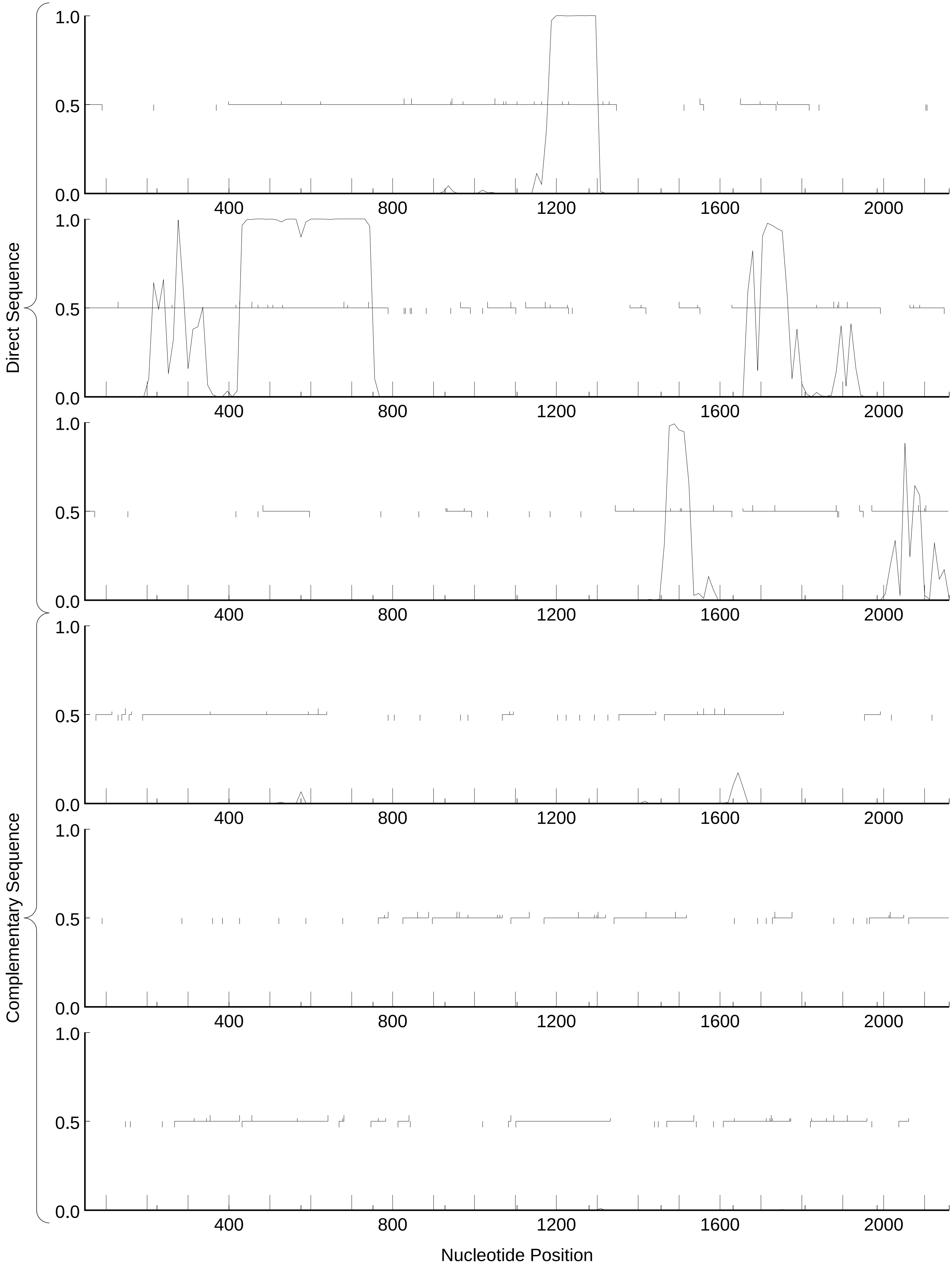
```
Matrix     :  Mycobacterium_smegmatis_MC2_155
Author     :  -

Order      :  4
```


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

Matrix notes & comments

Training set derived by GeneMarkS, 4.27 September 2014
Tue Sep 23 15:23:03 2014

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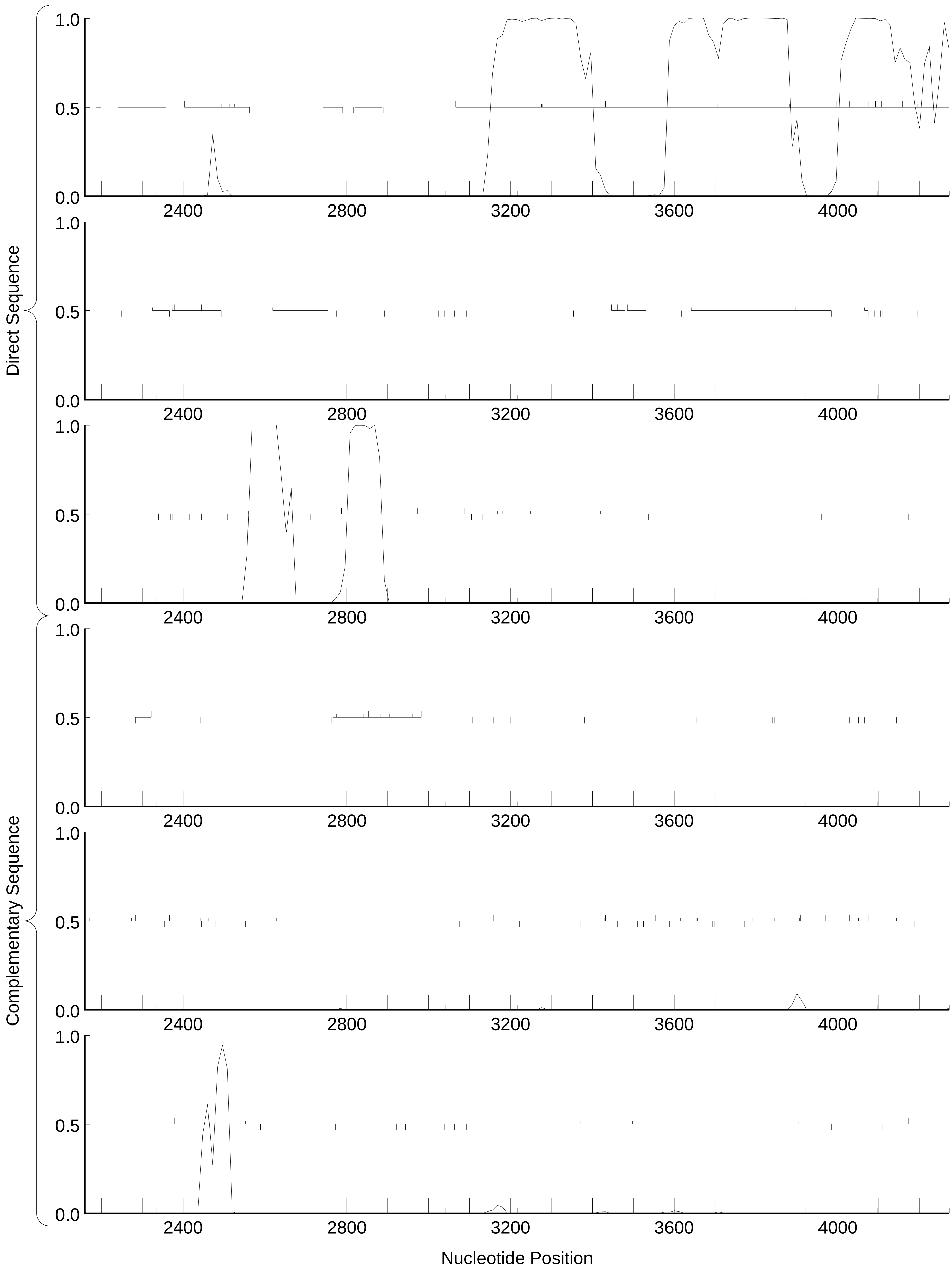
Nucleotide Position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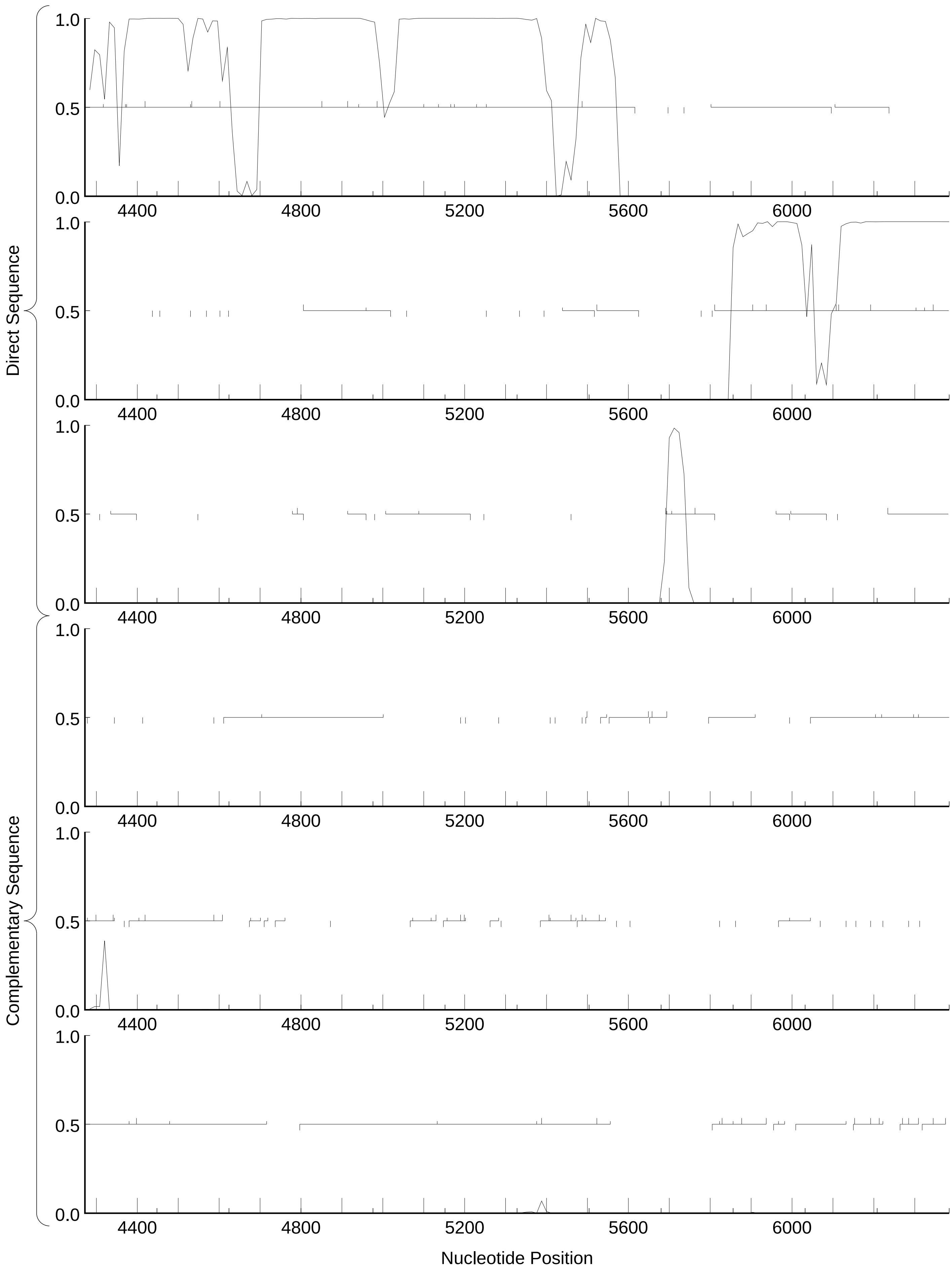
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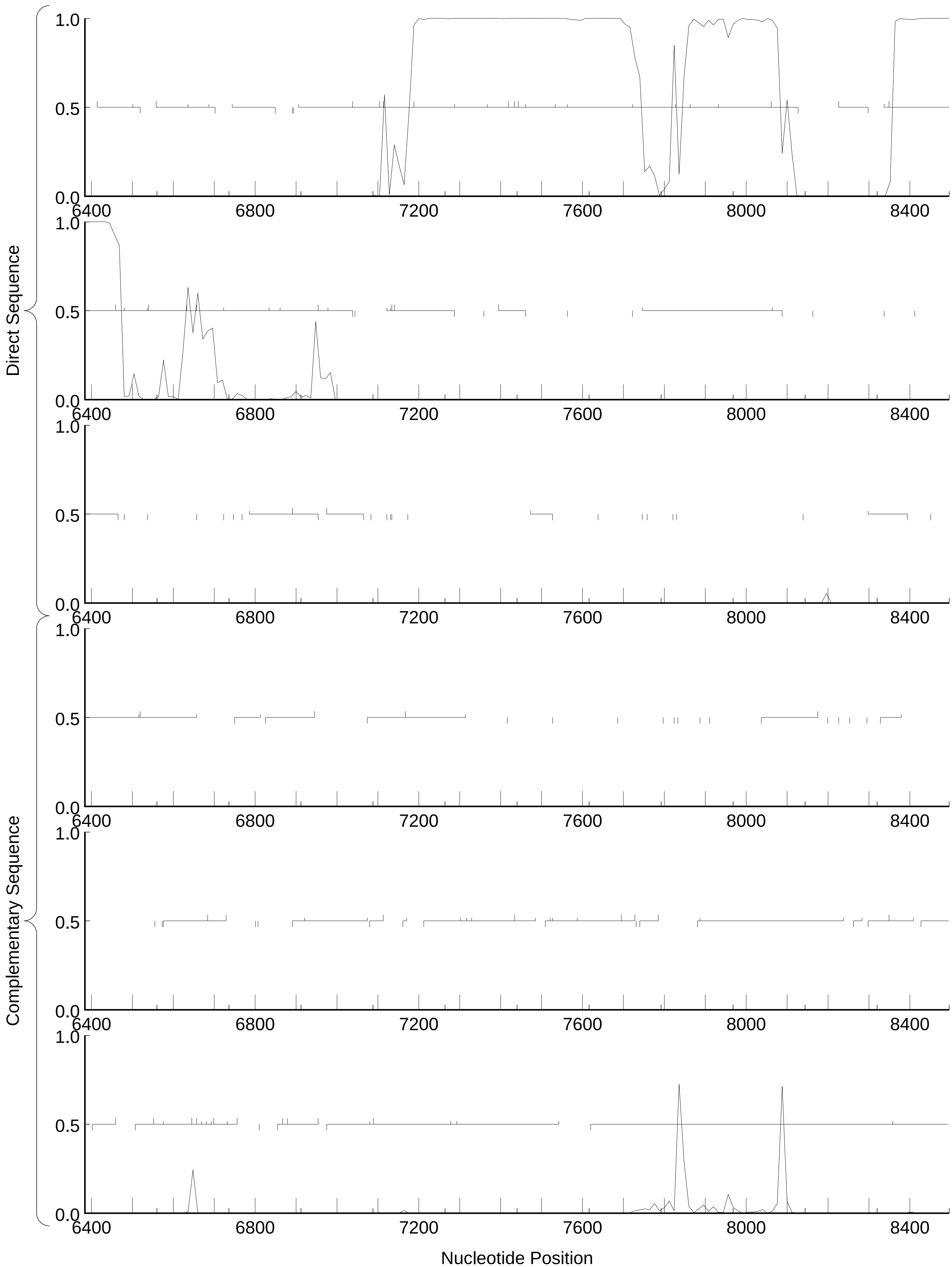

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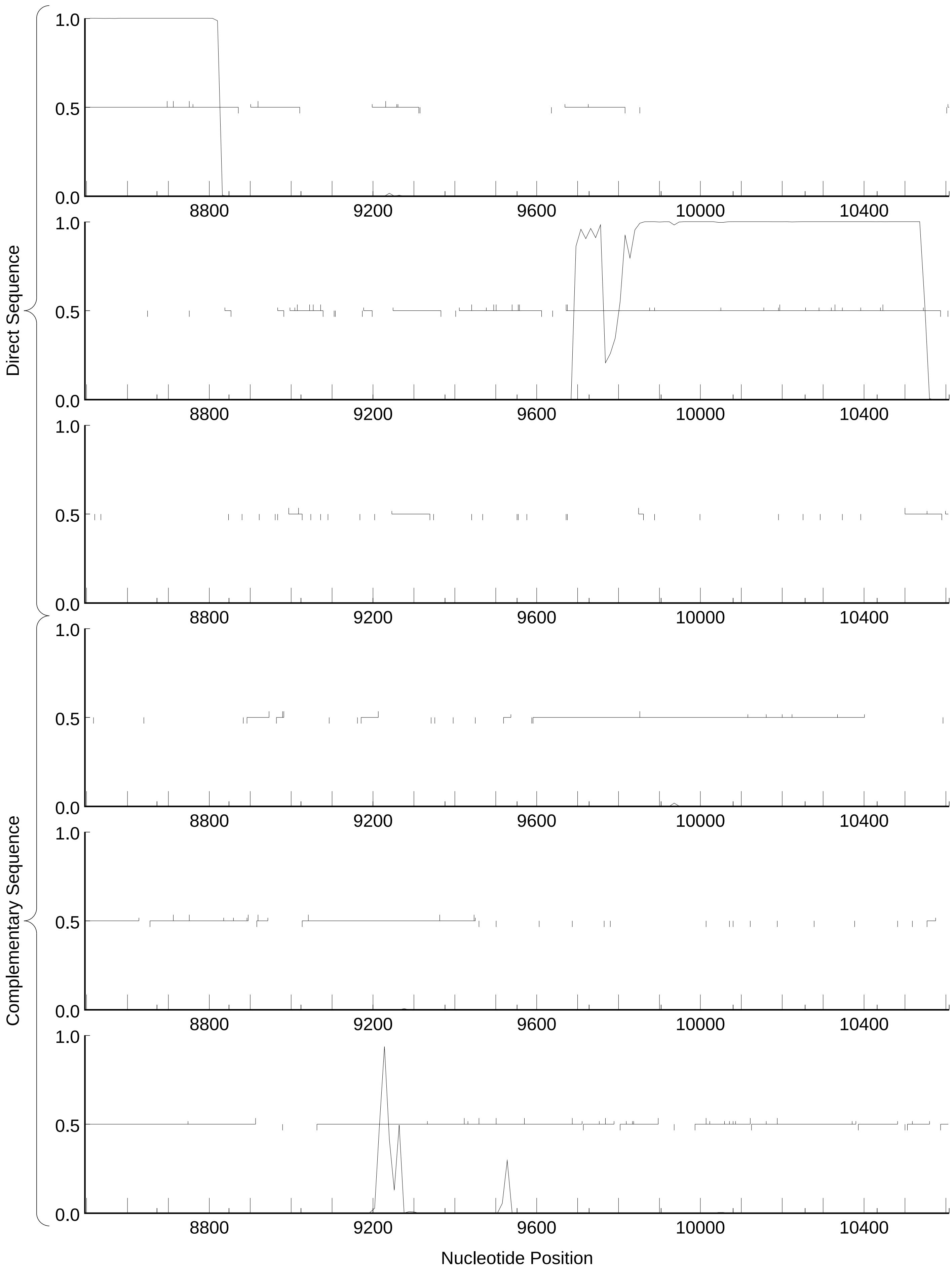
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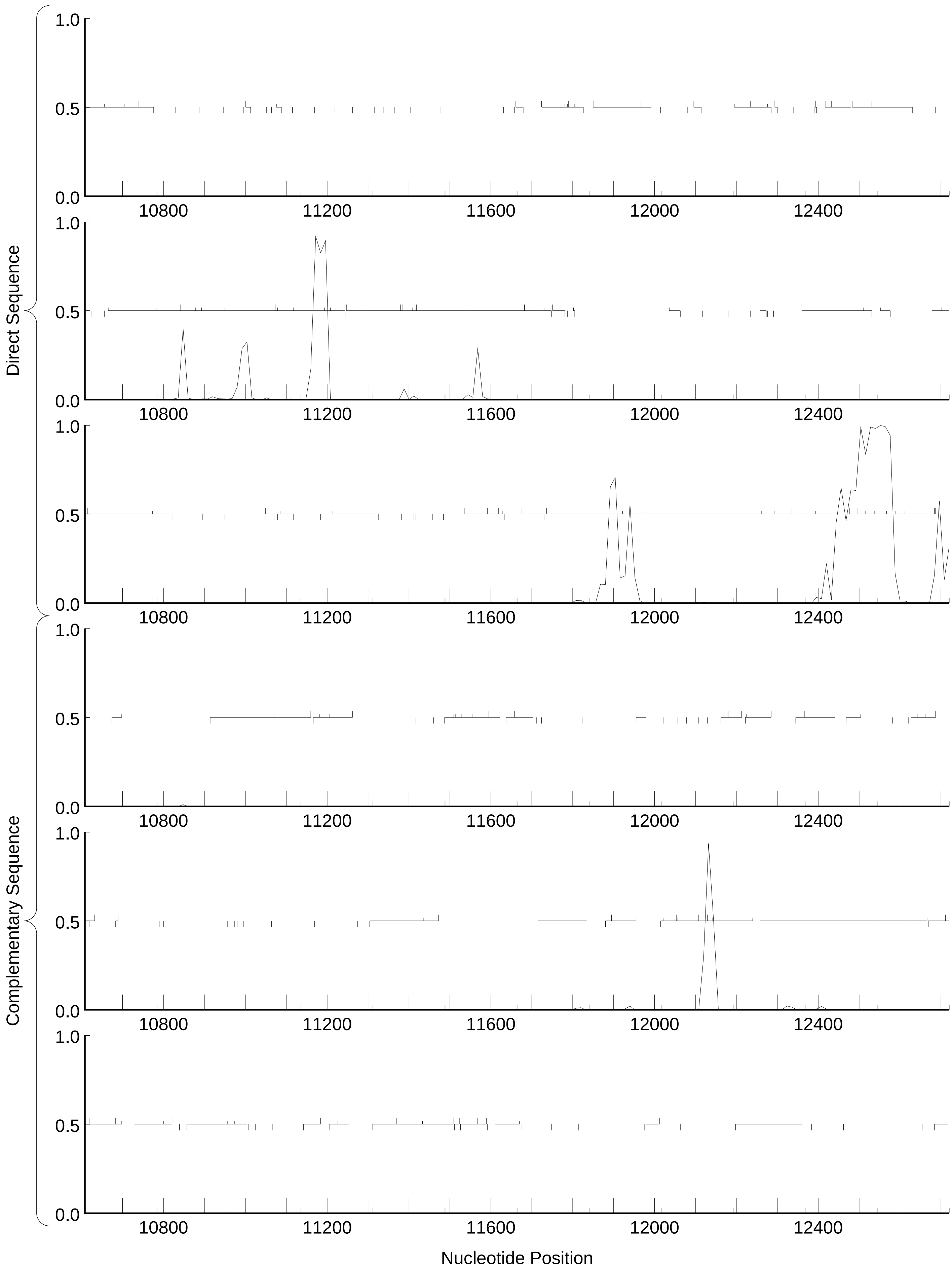
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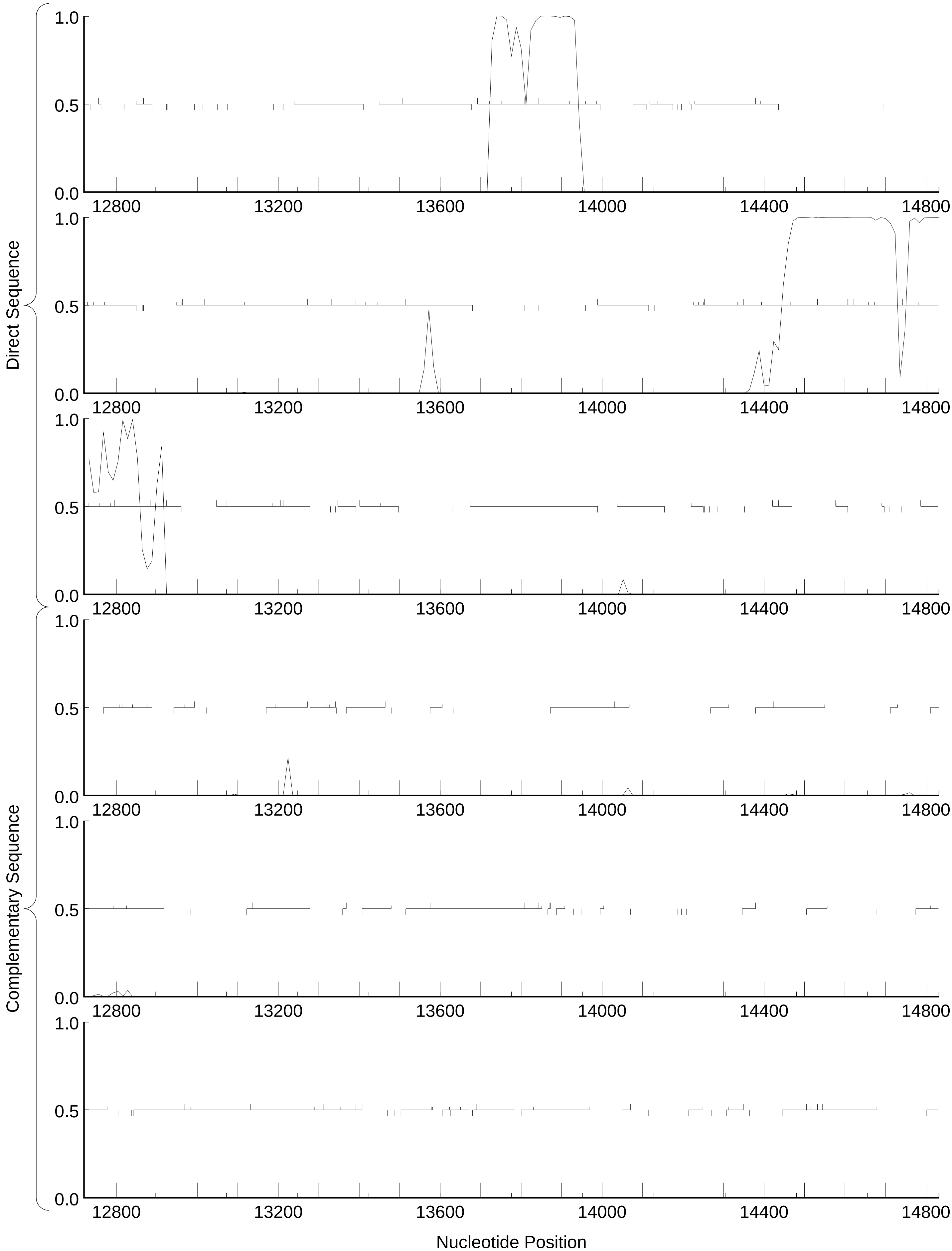
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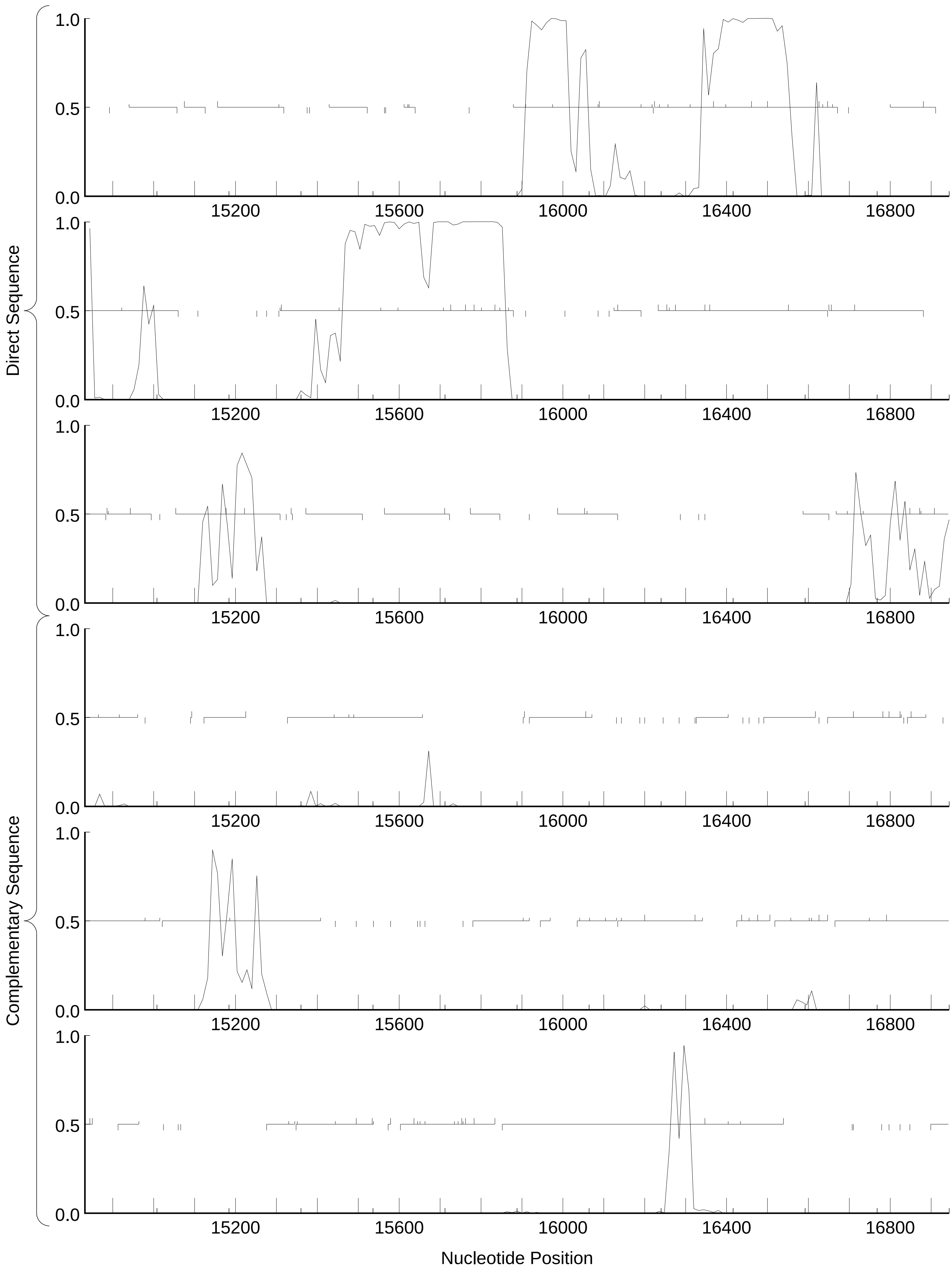
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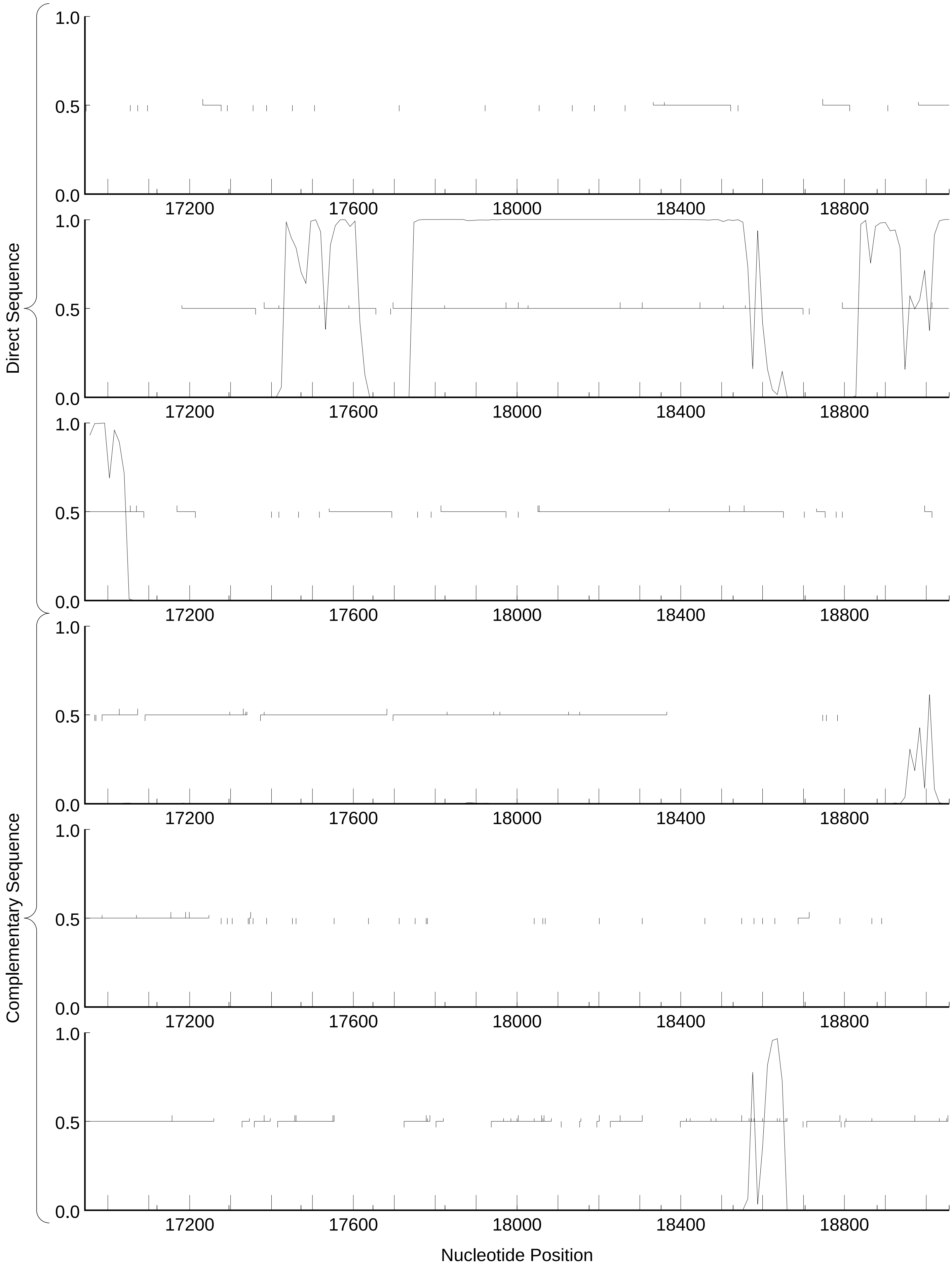
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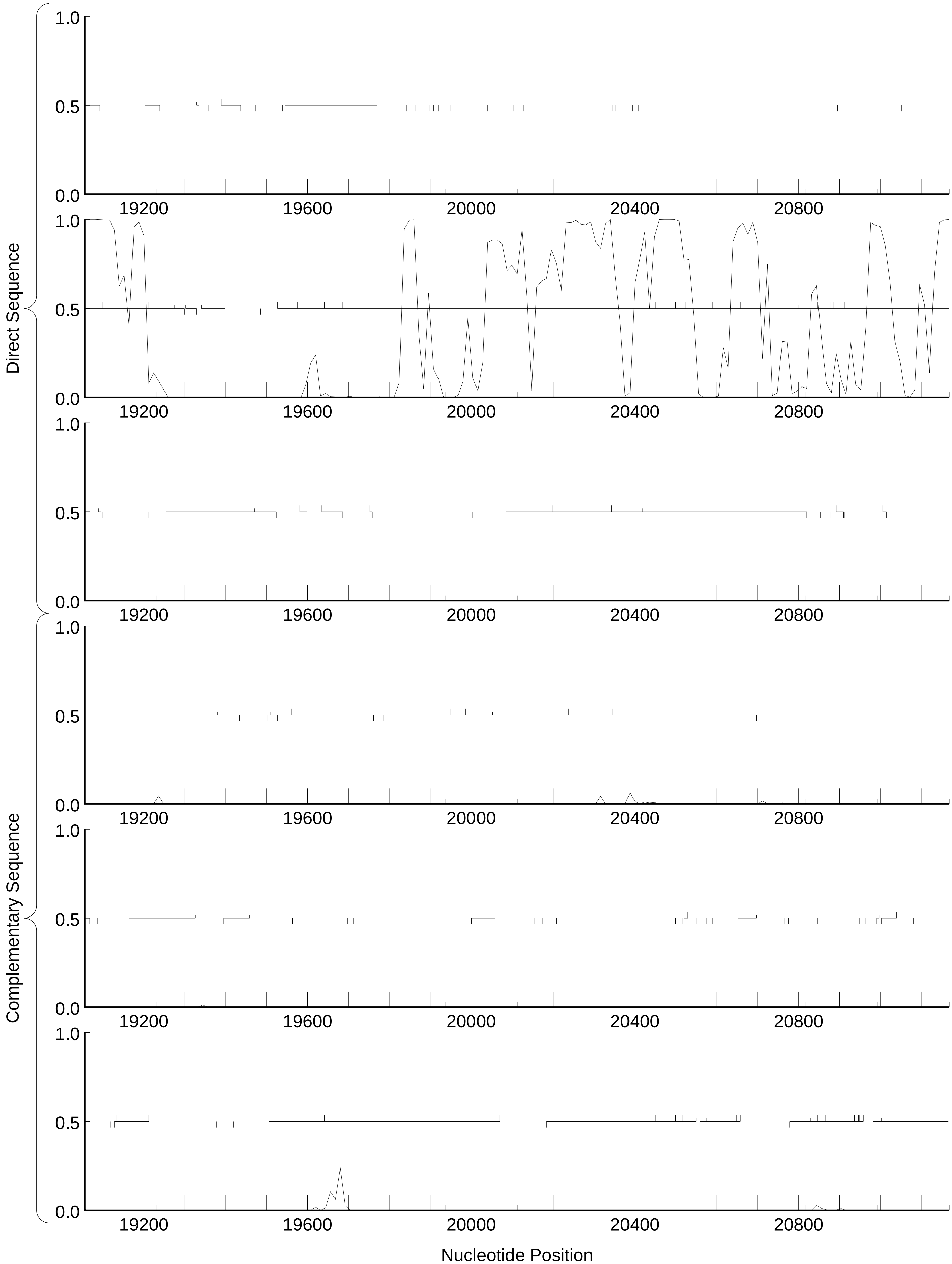

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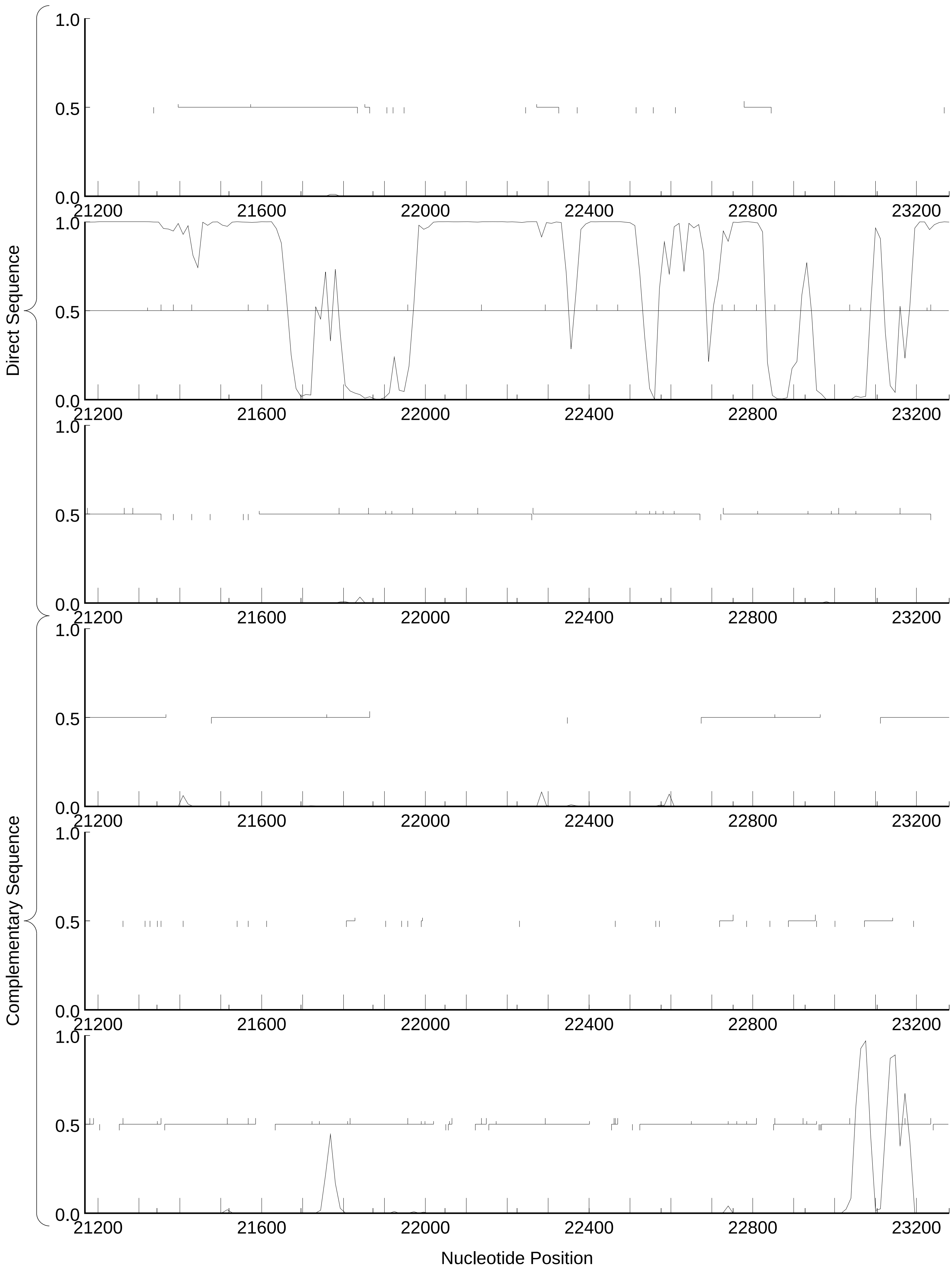
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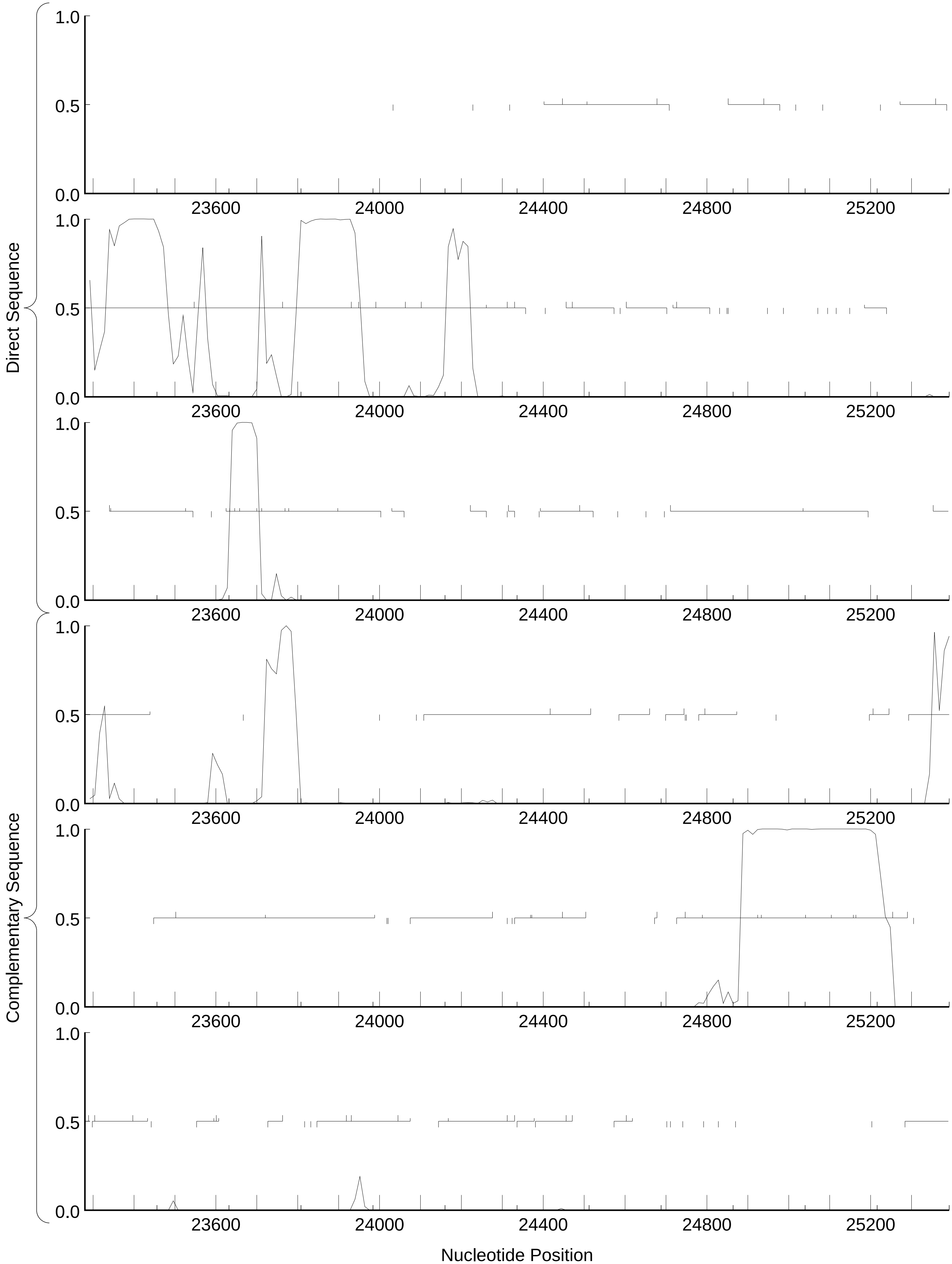

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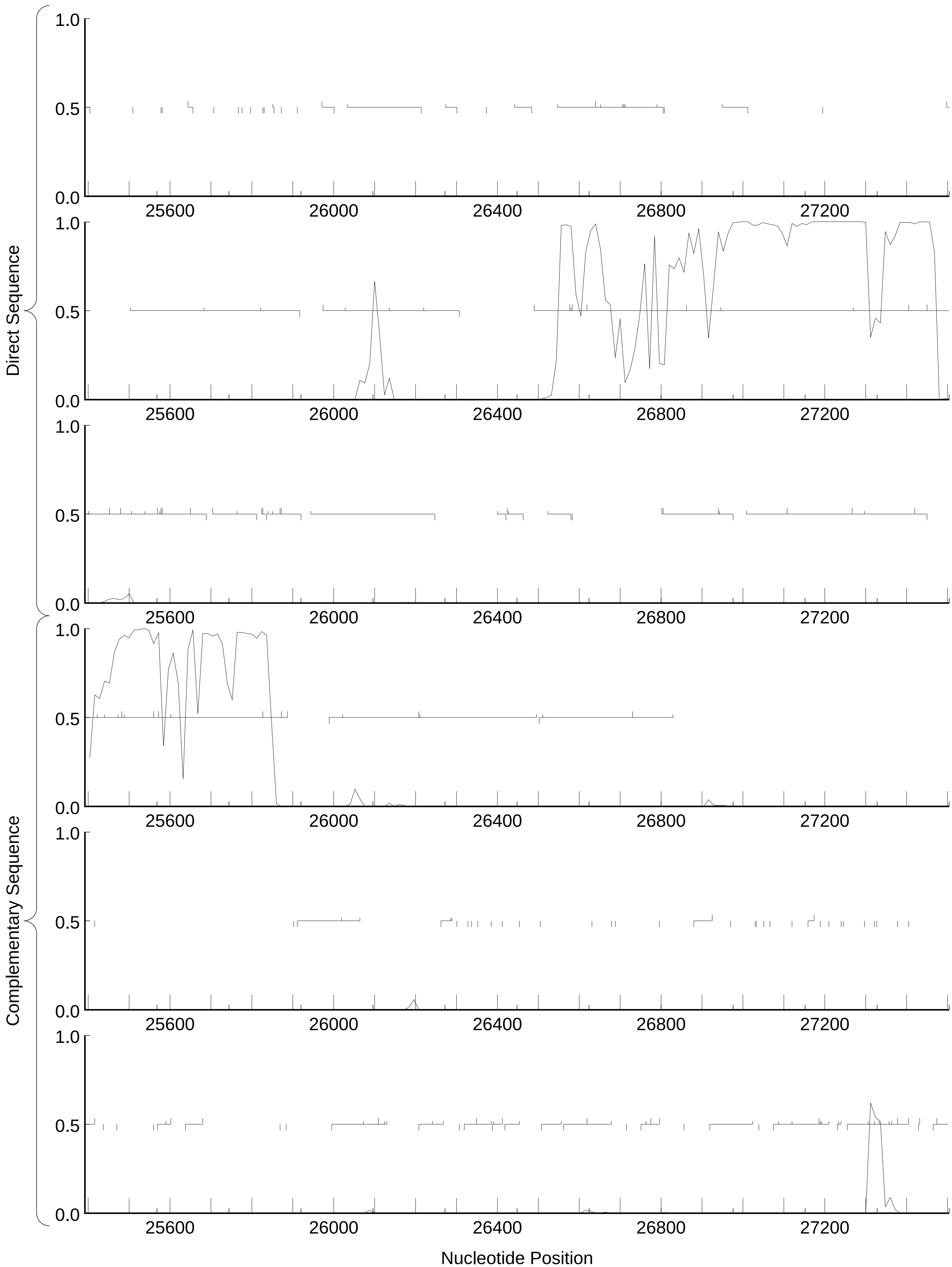
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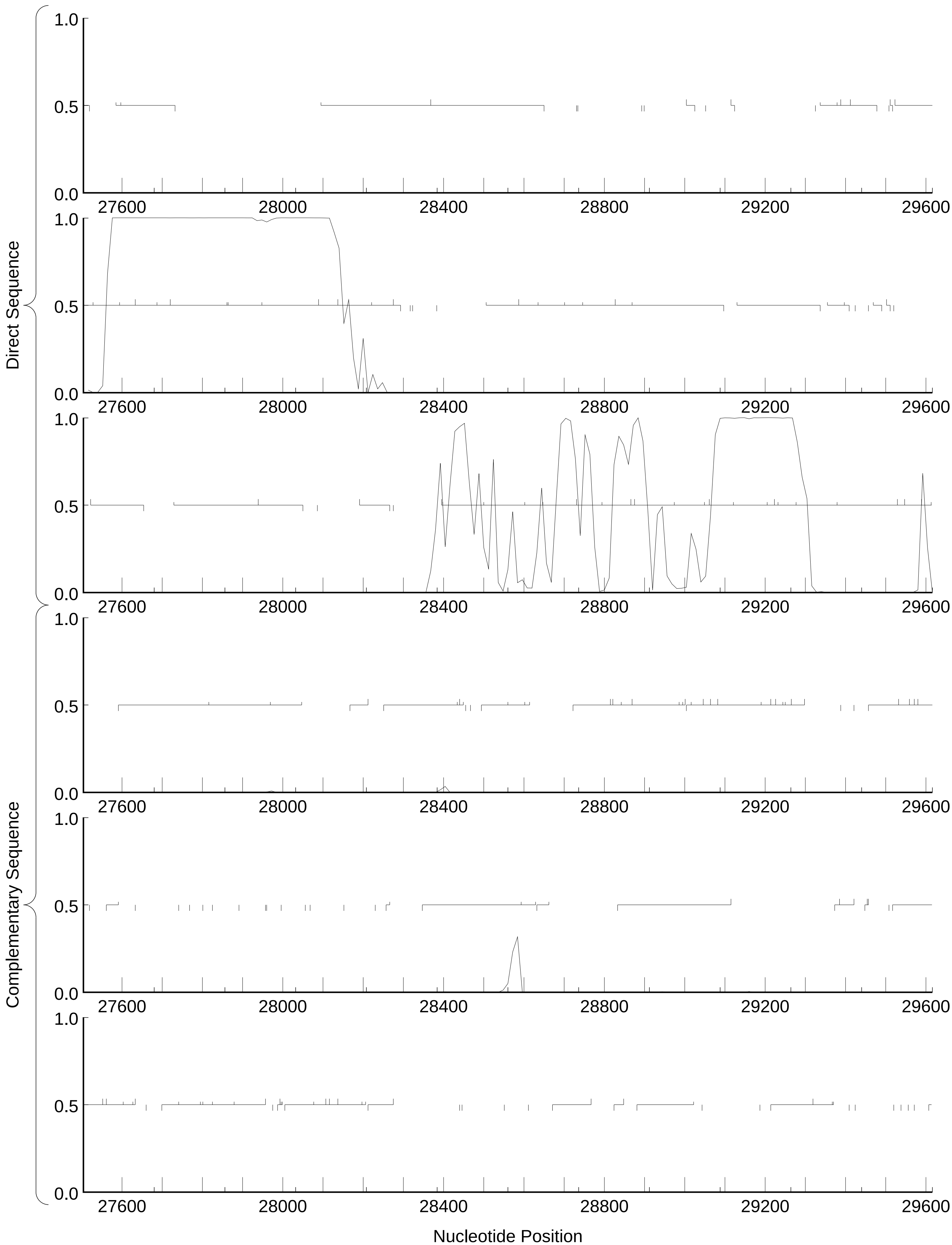
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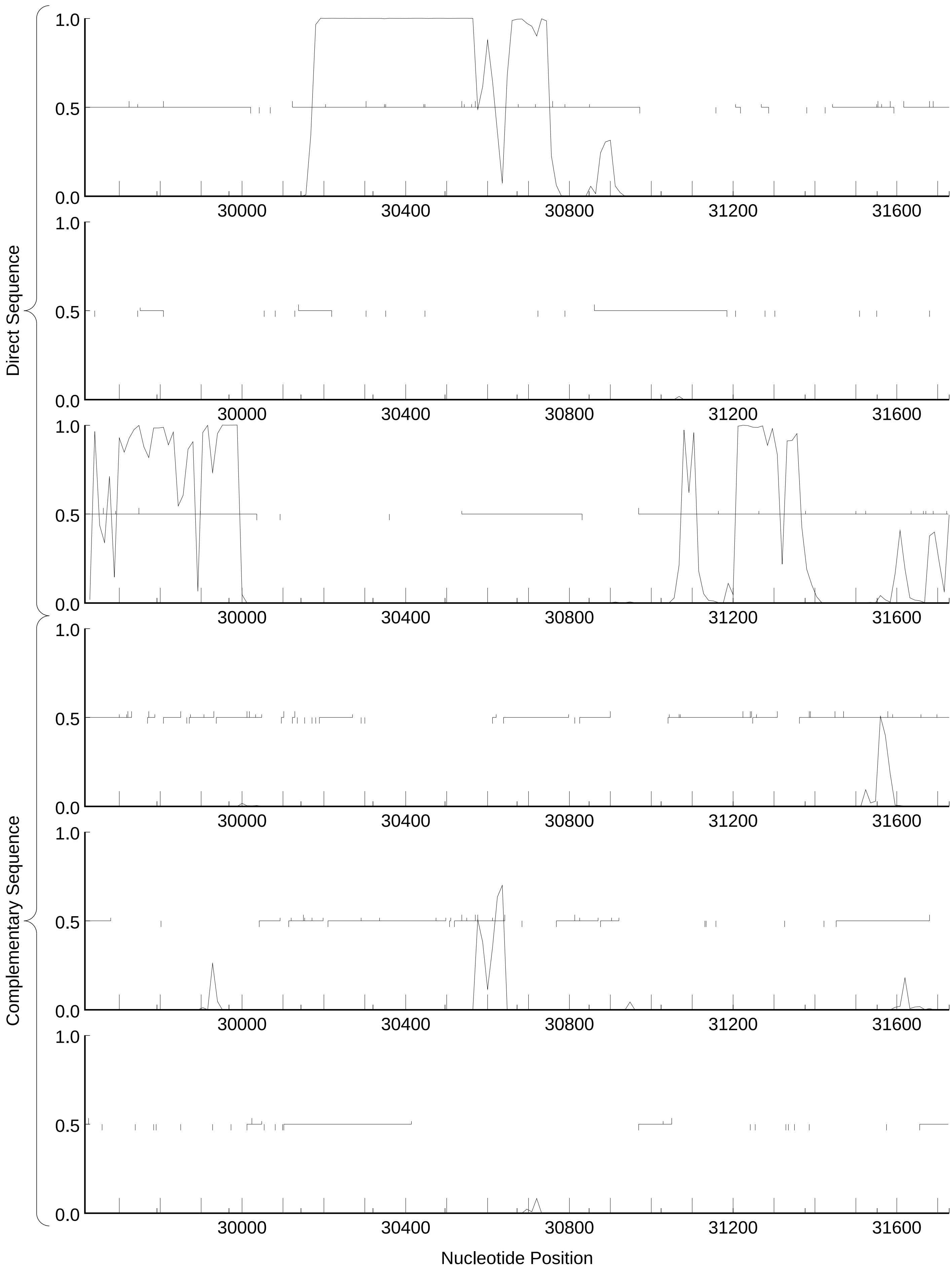
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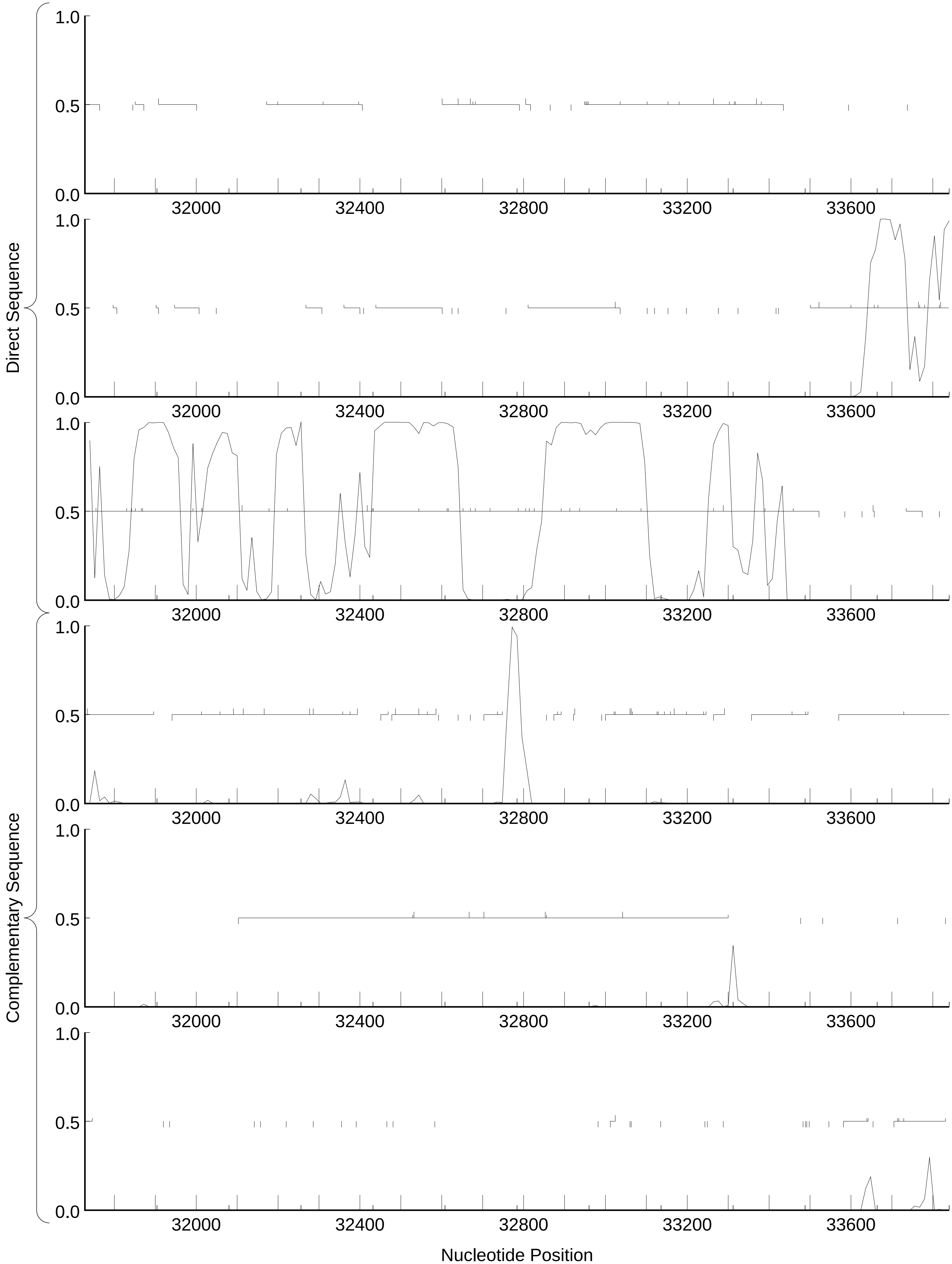

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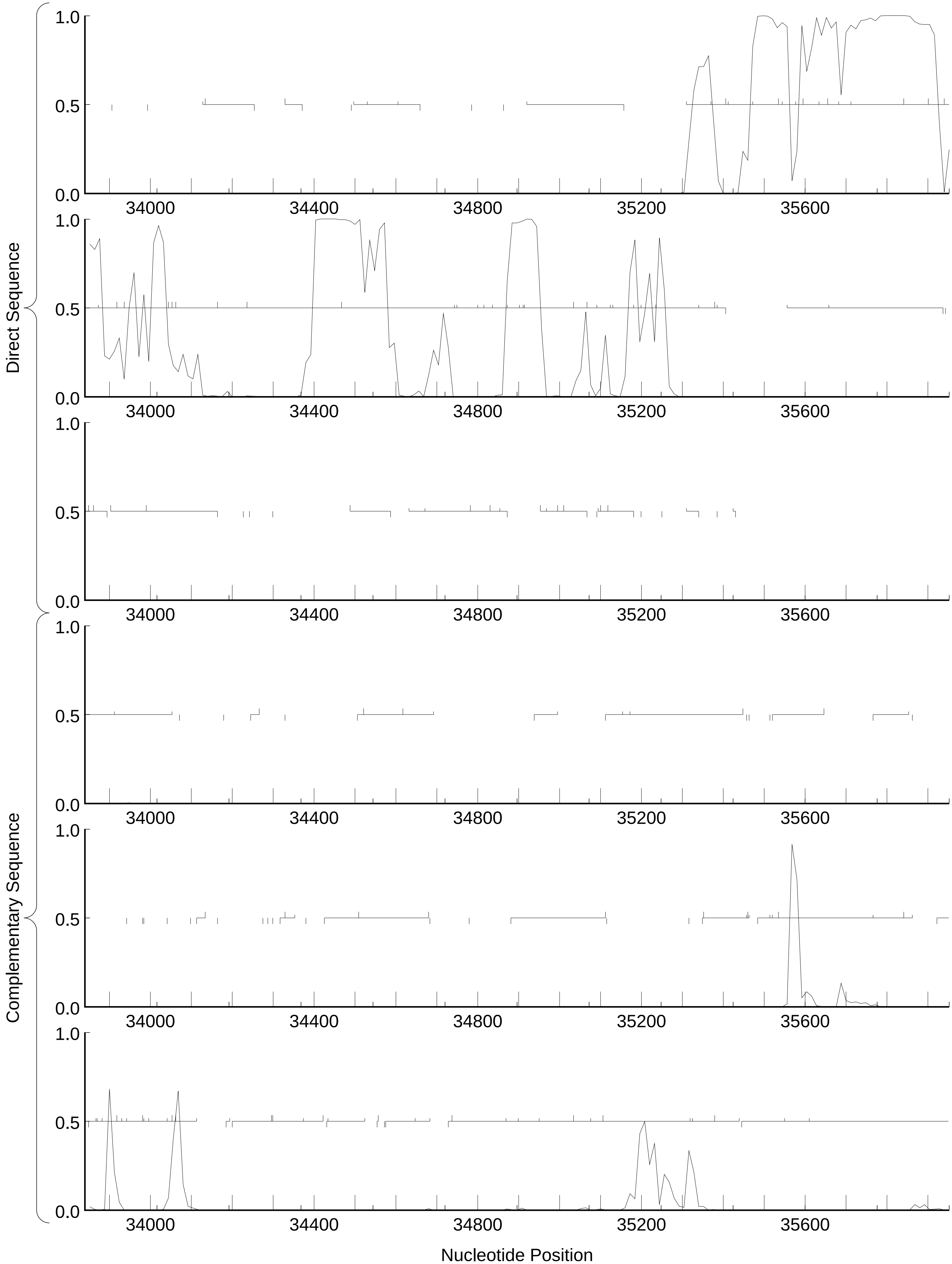

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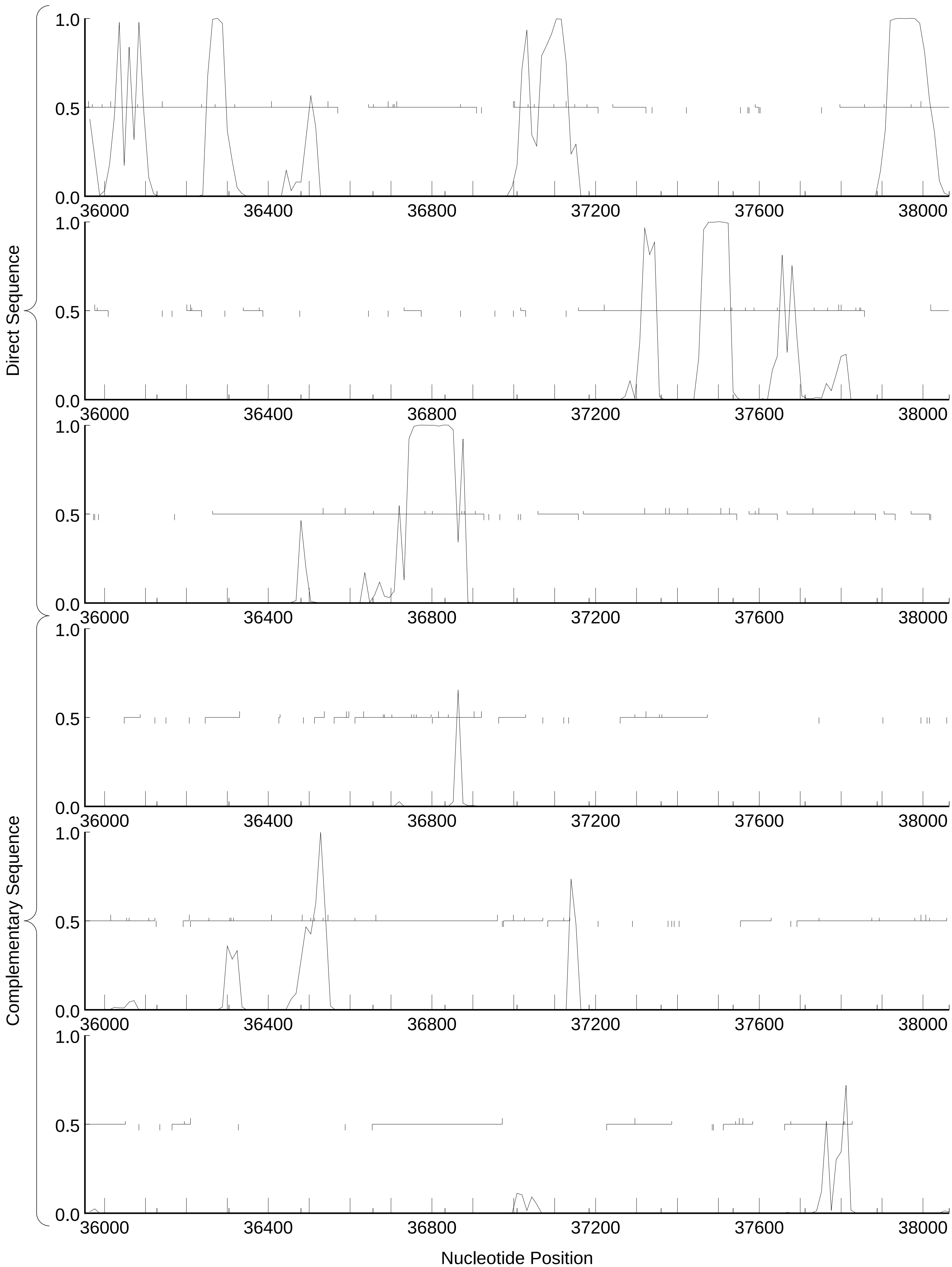
Nucleotide Position



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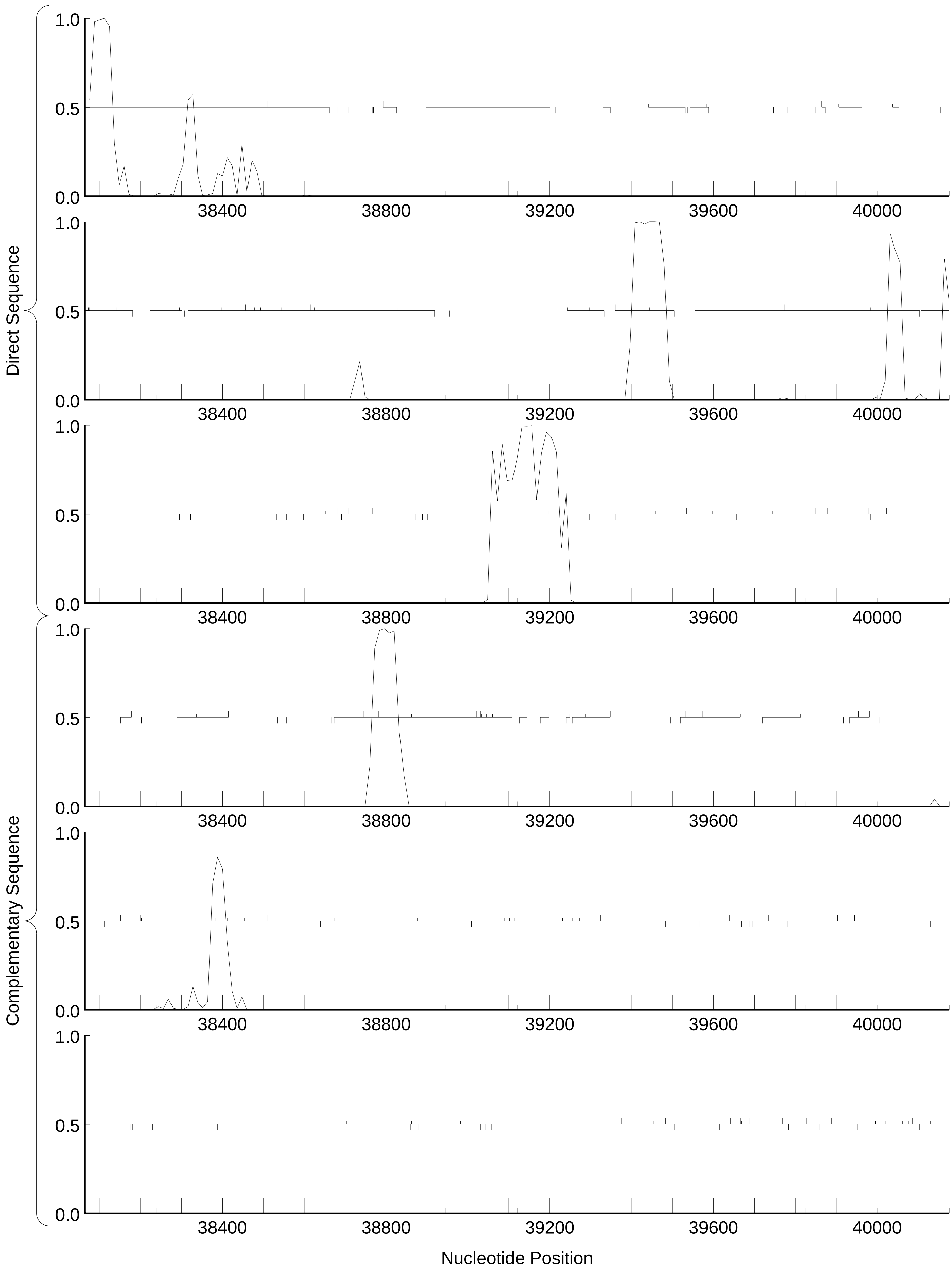
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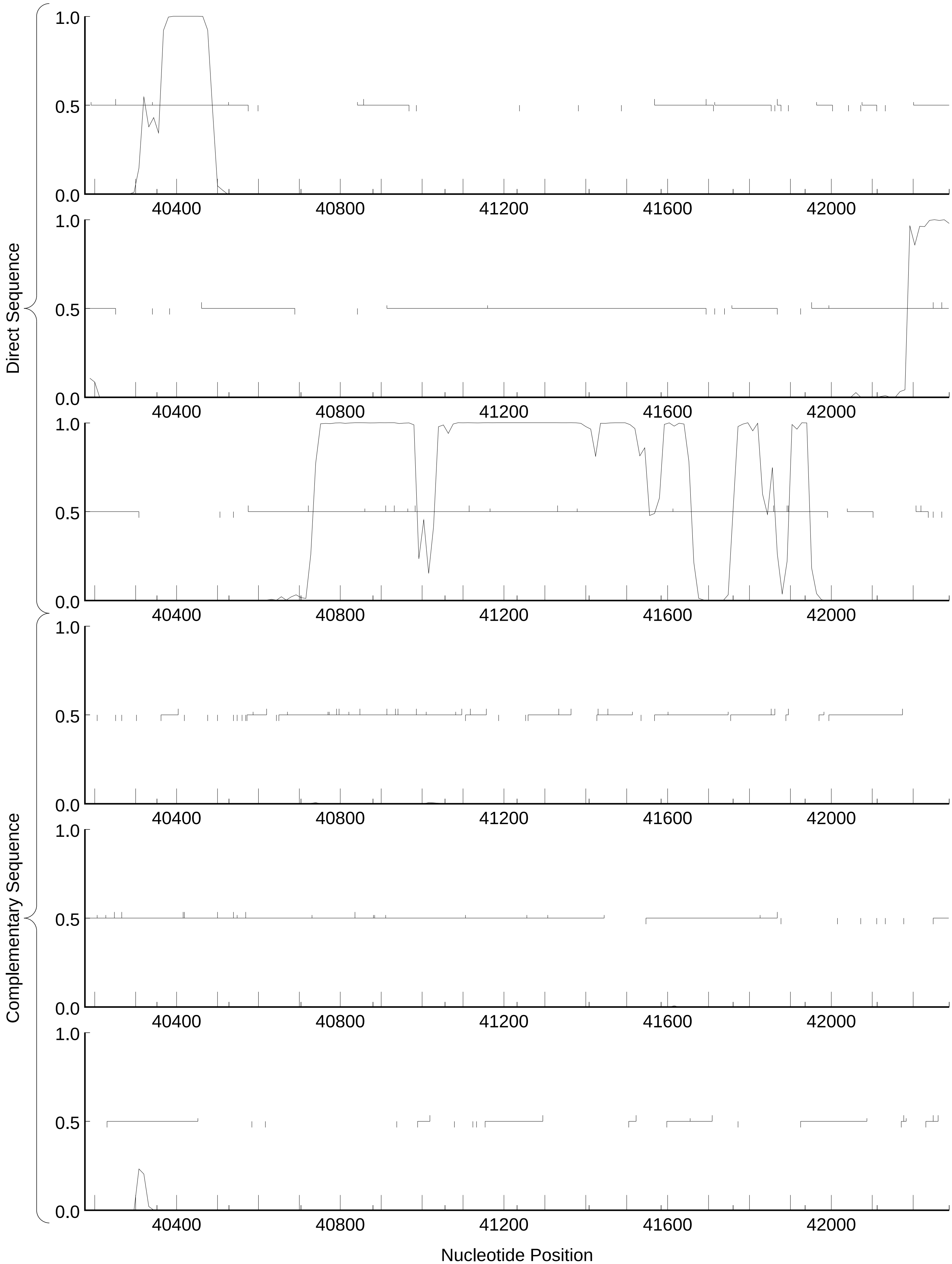
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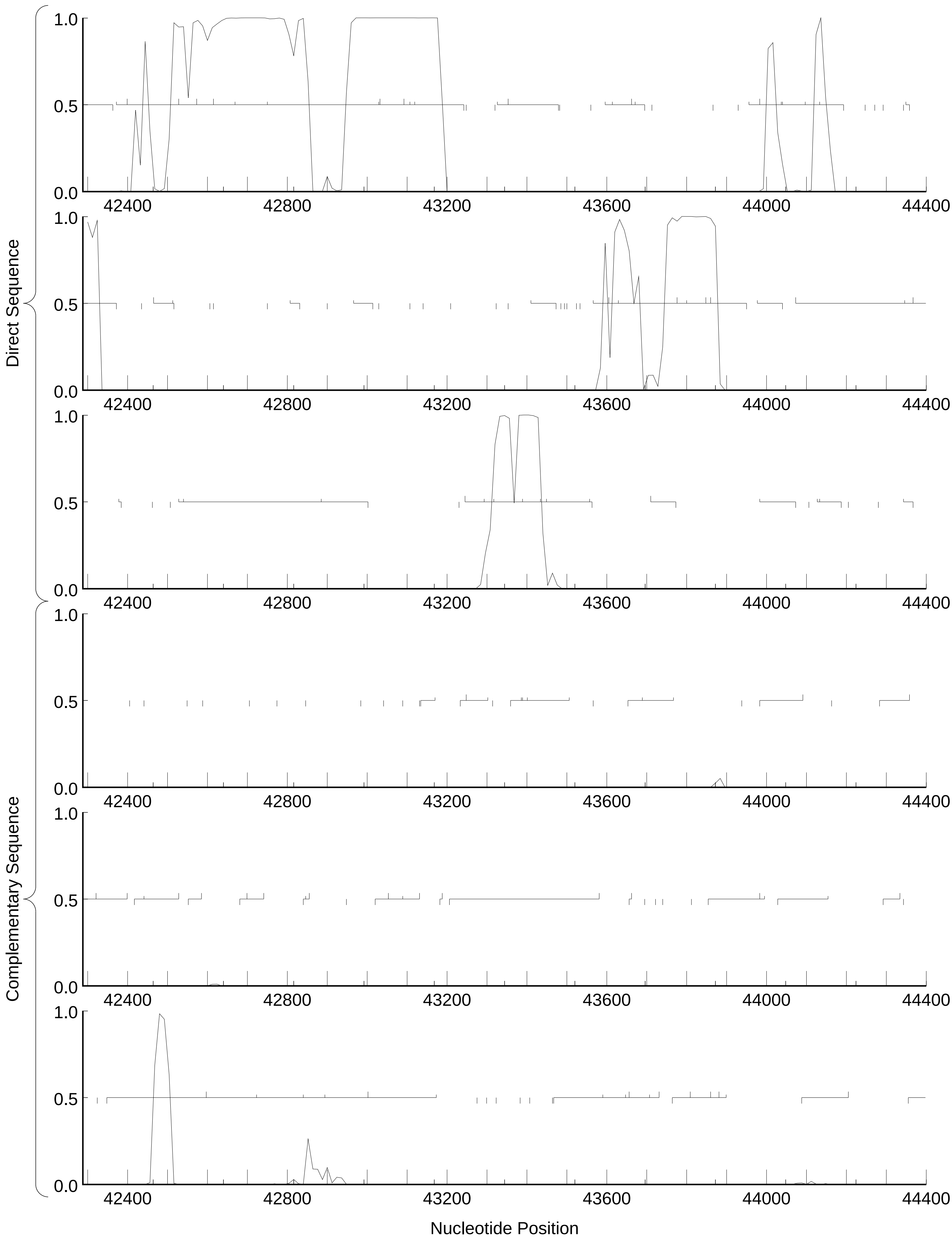

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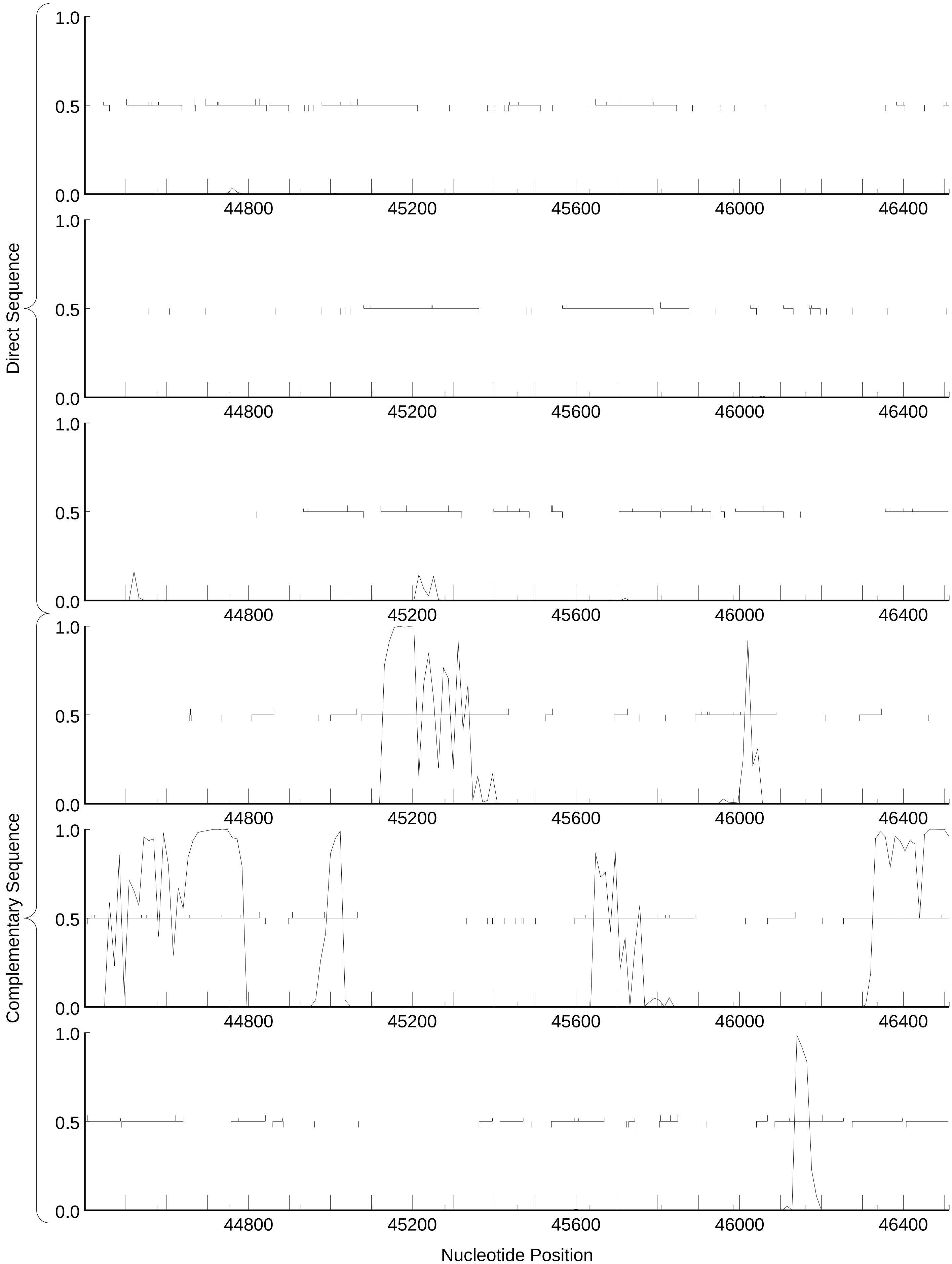
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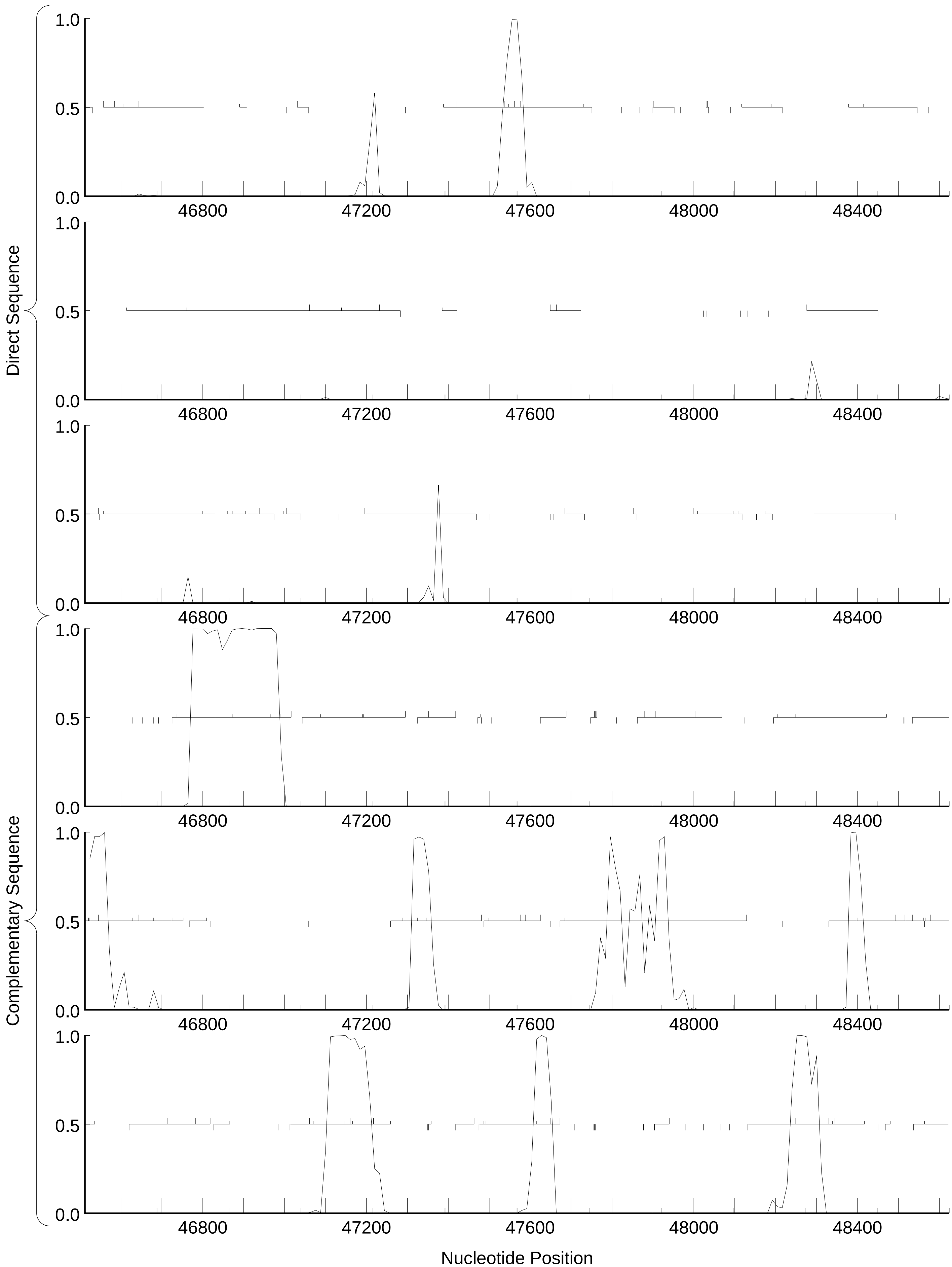
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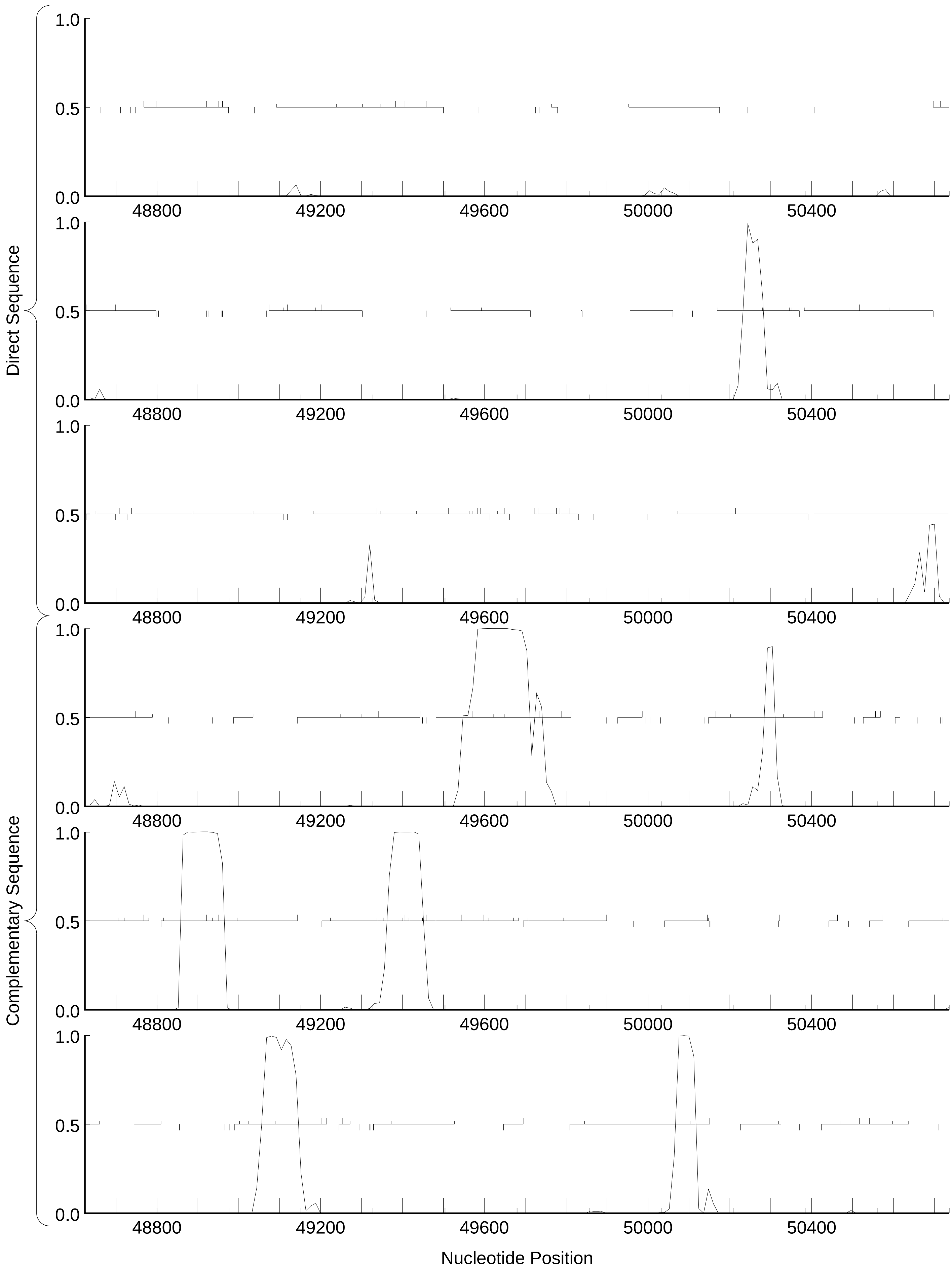
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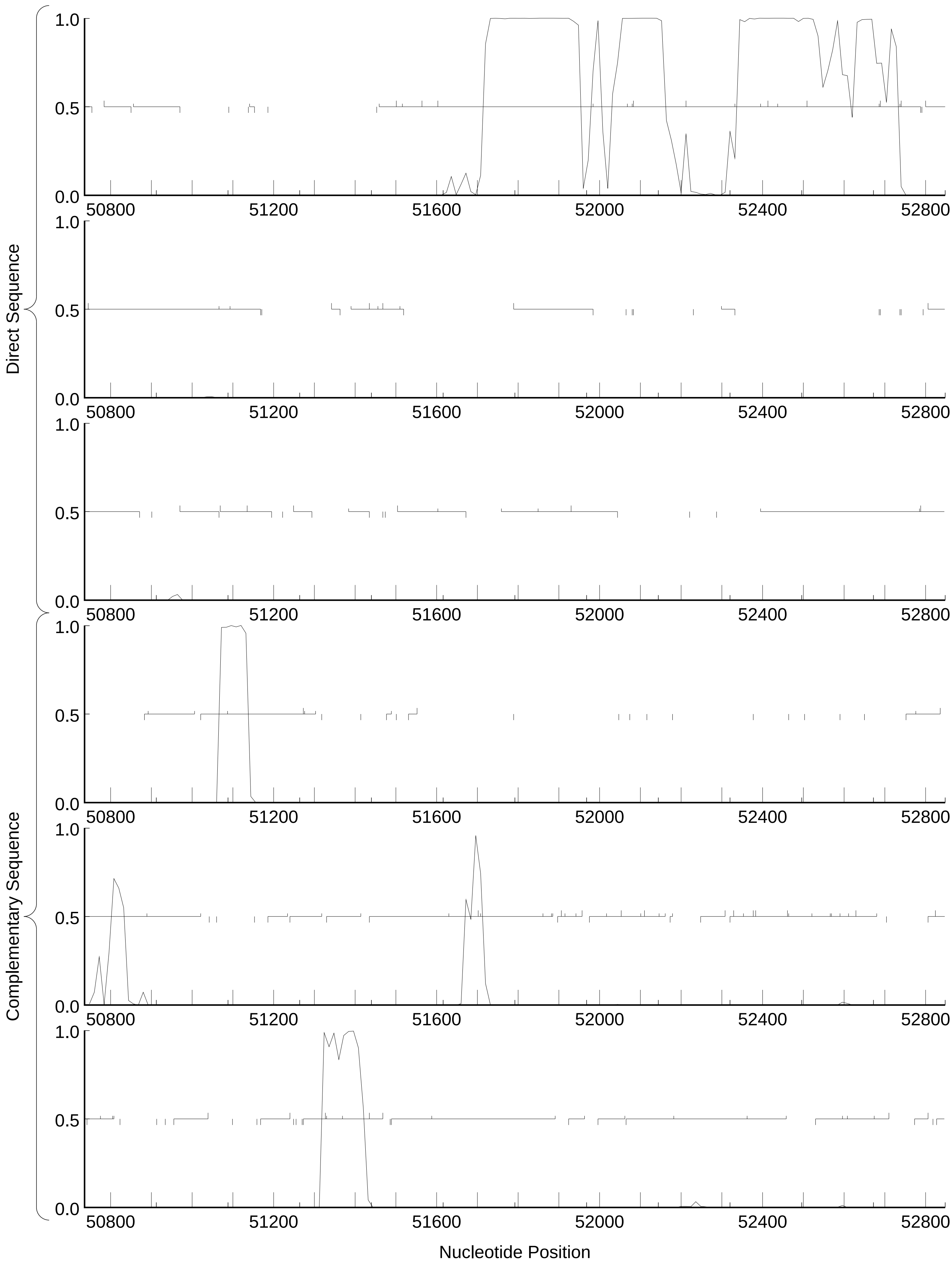
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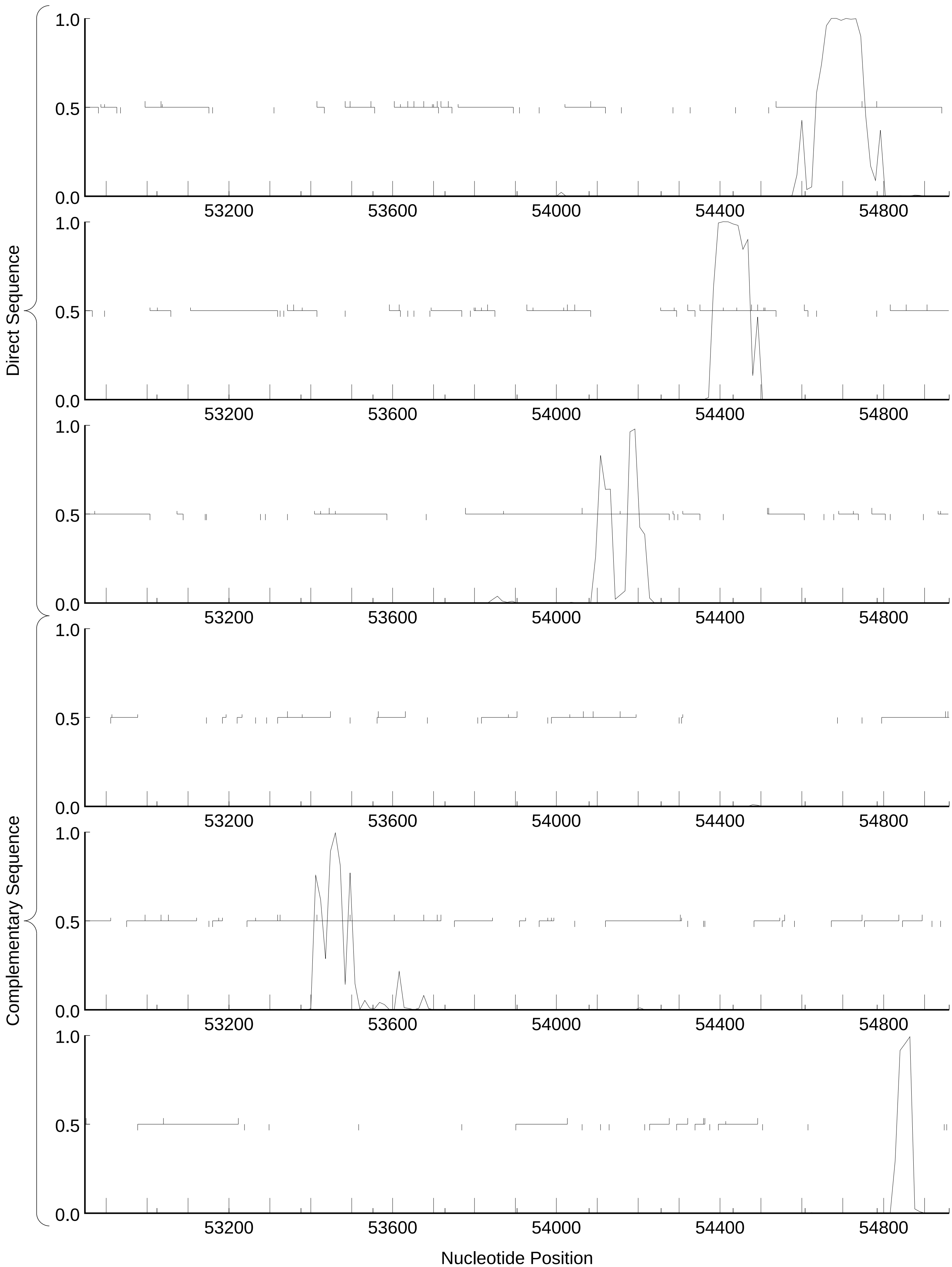
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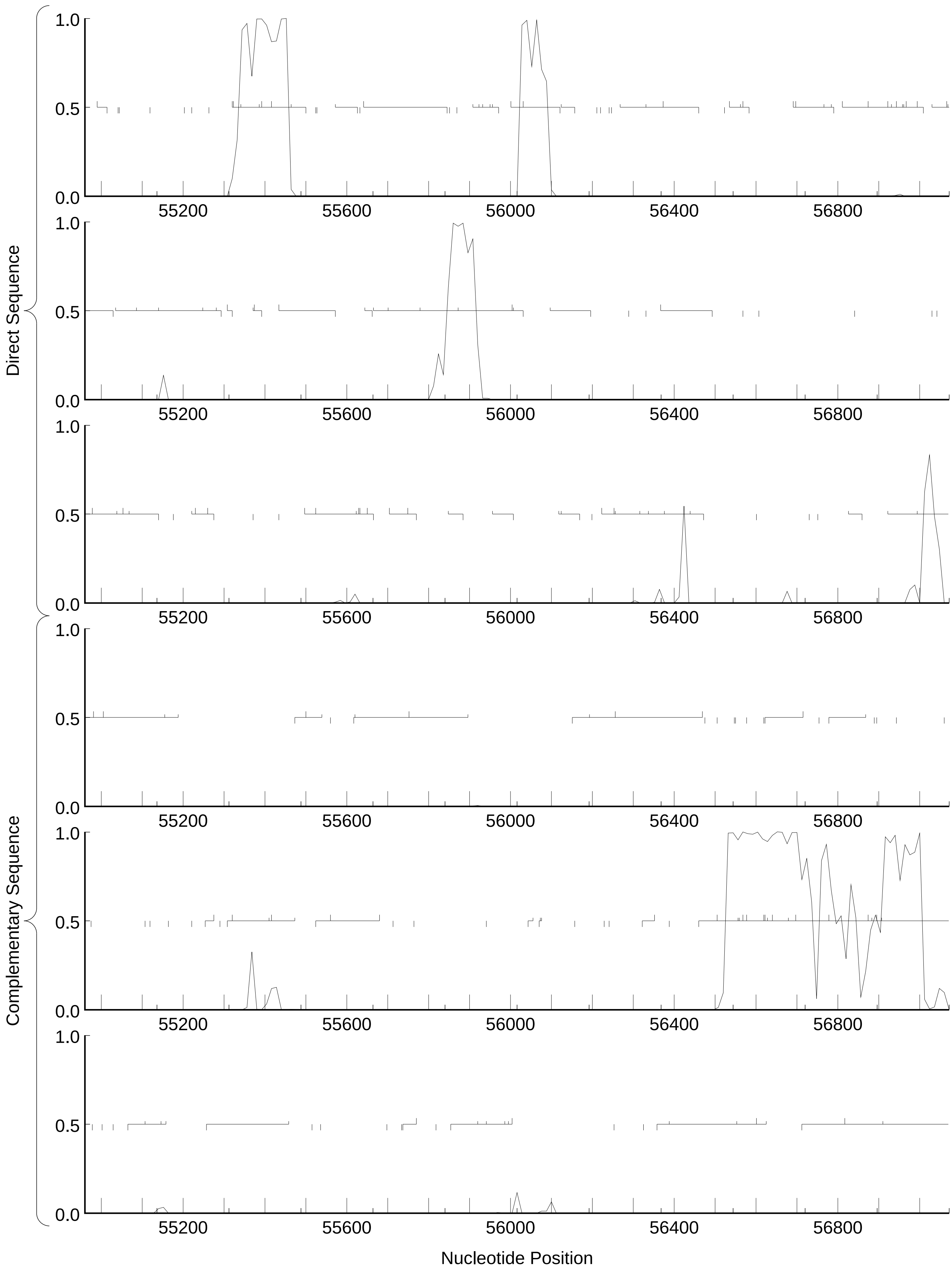

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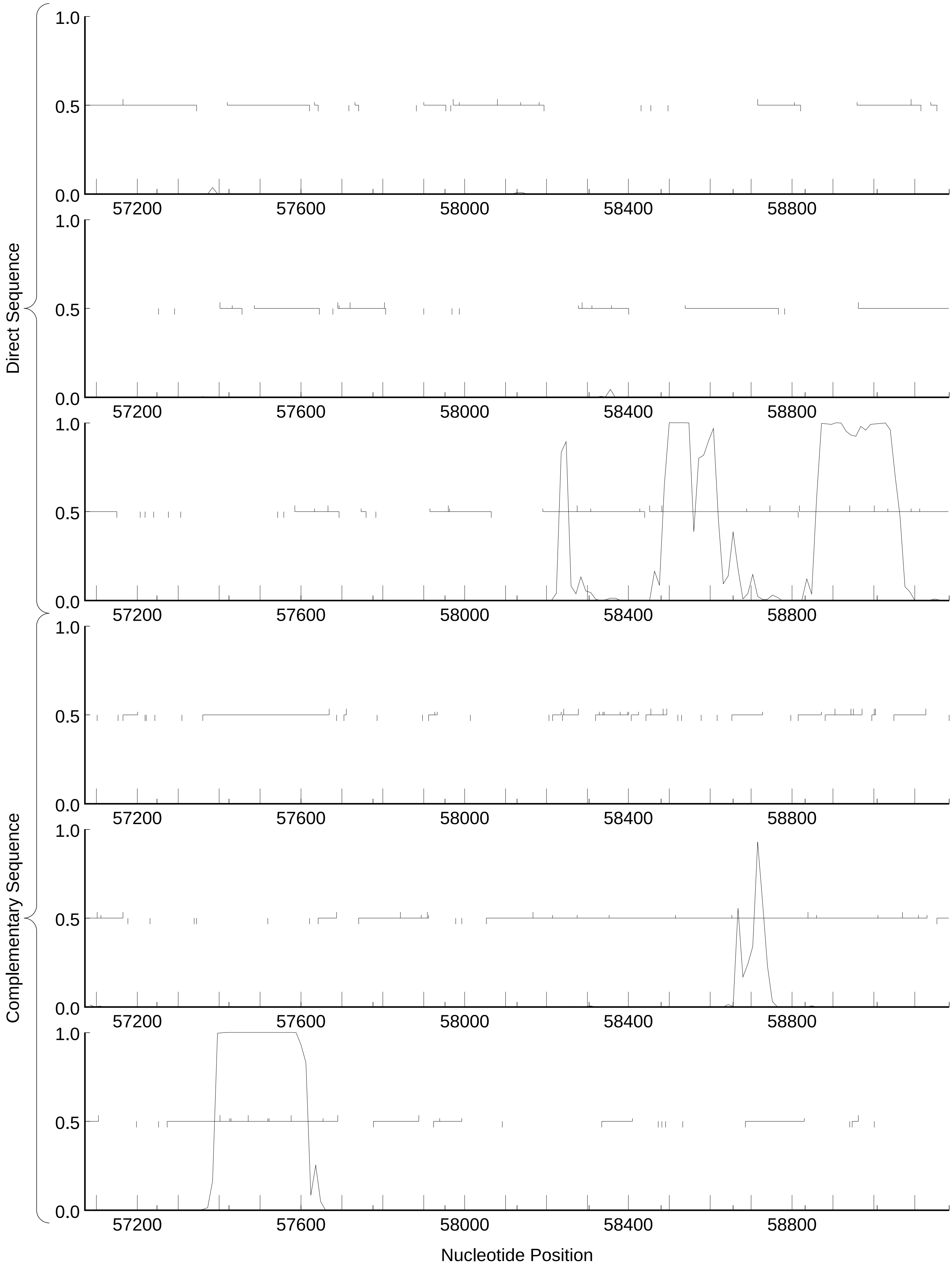
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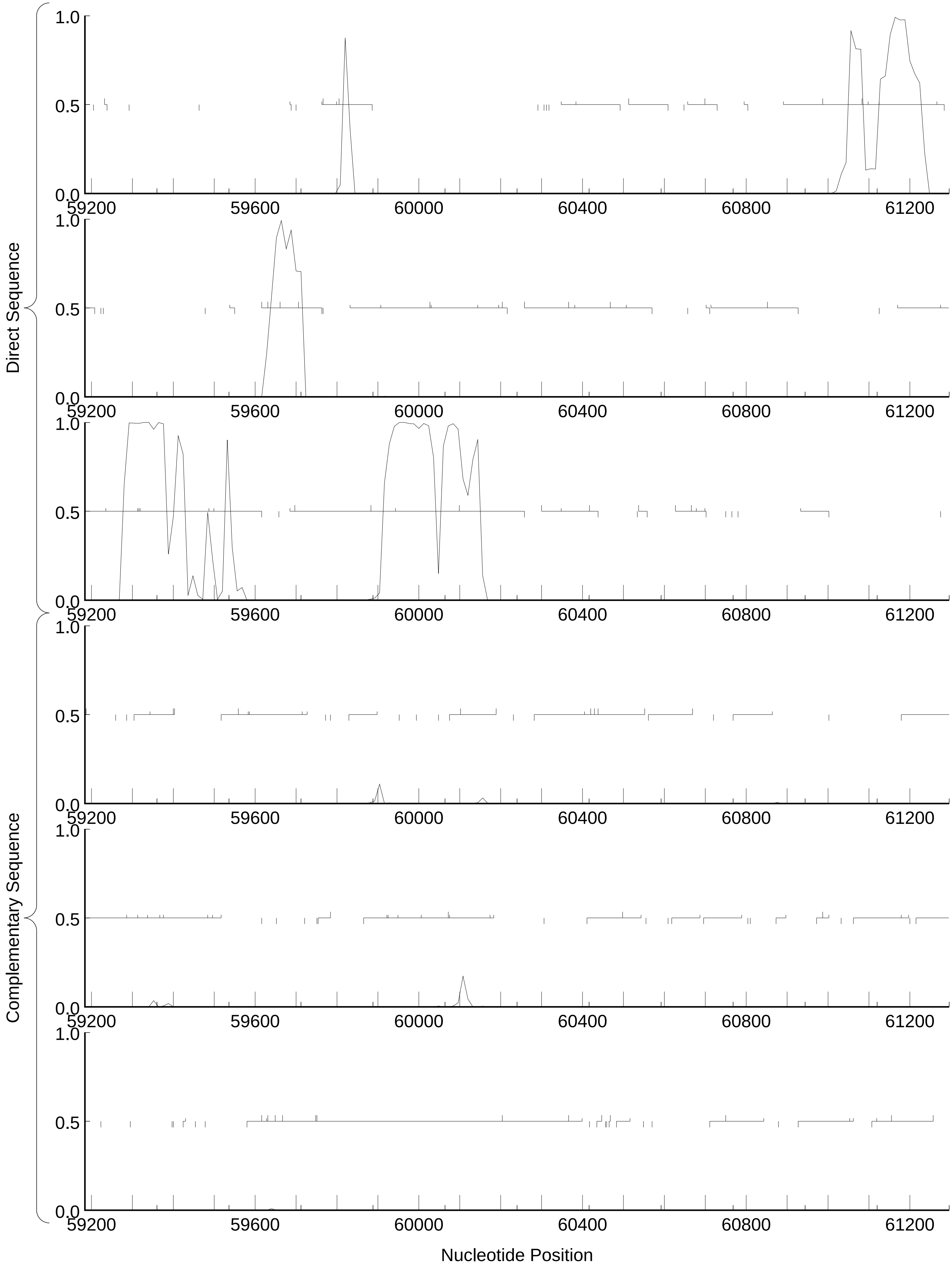
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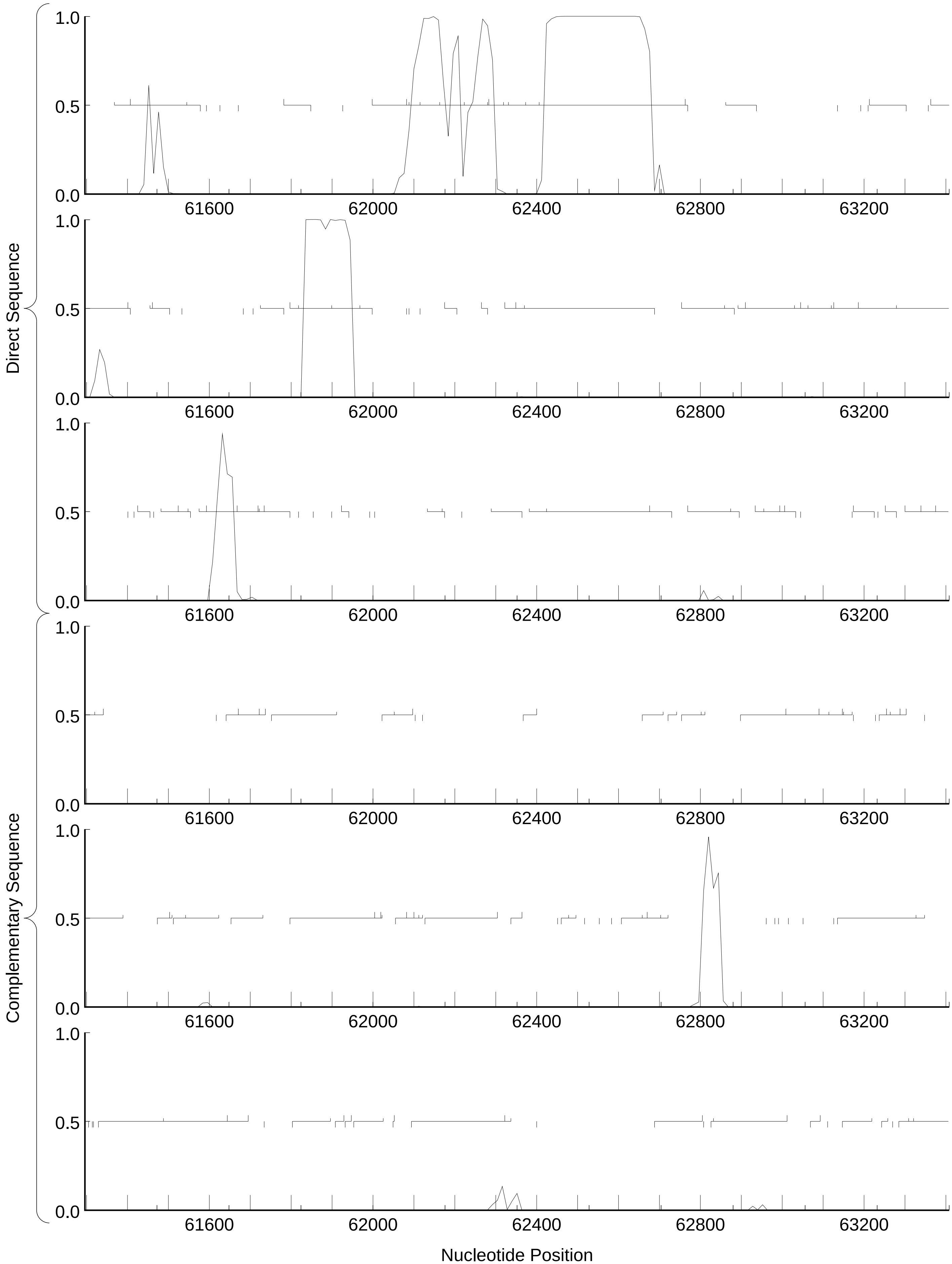
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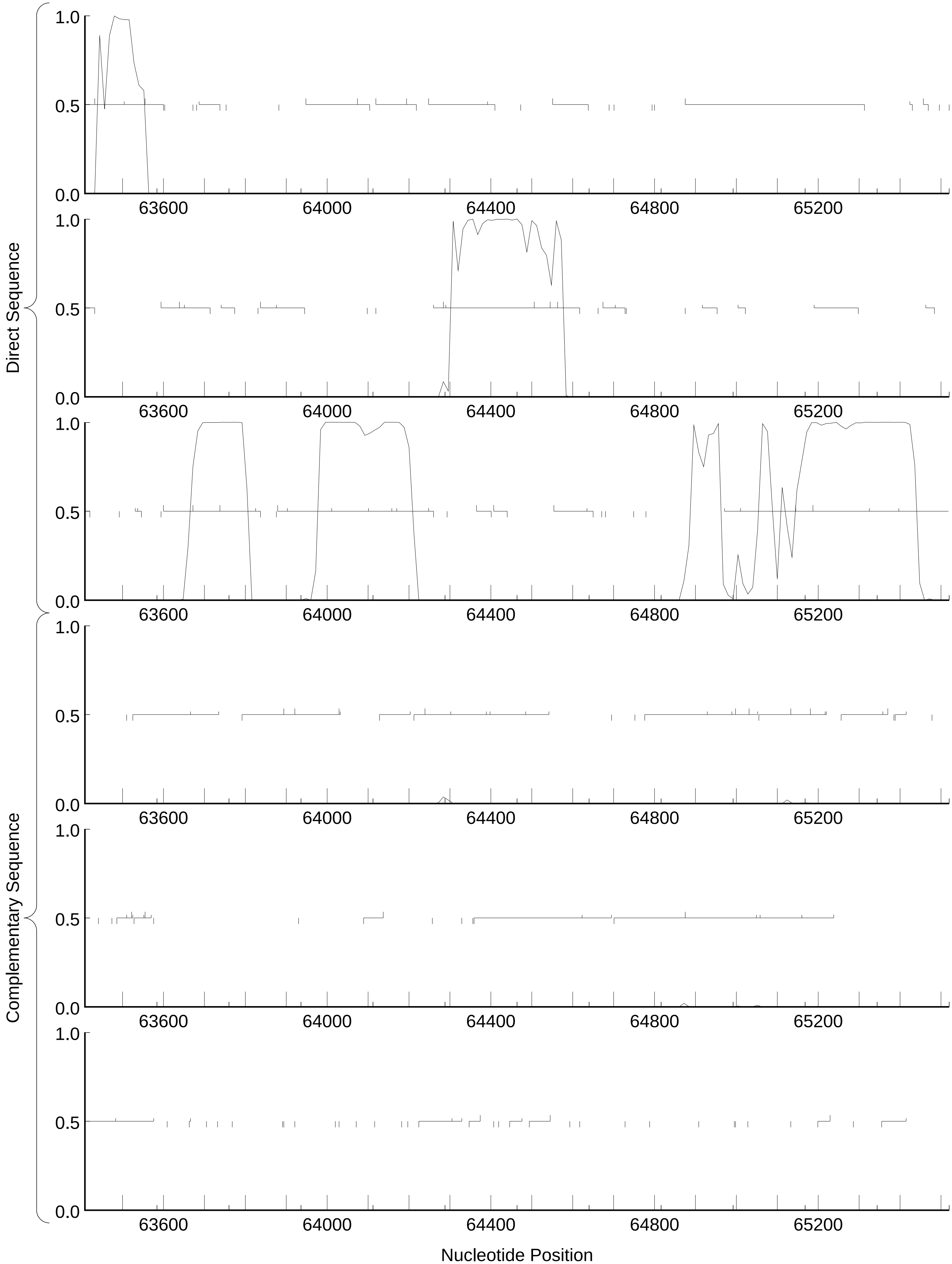
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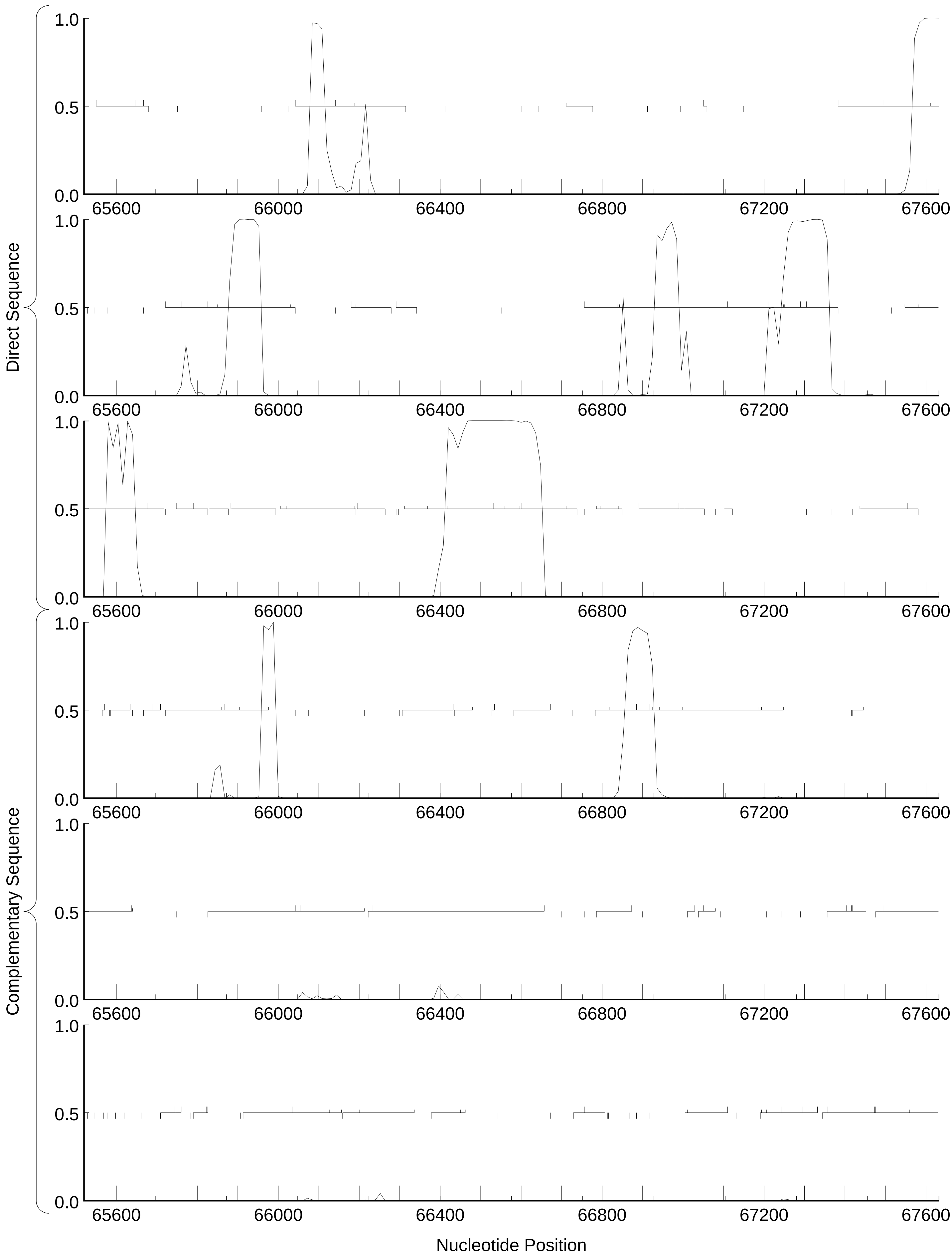
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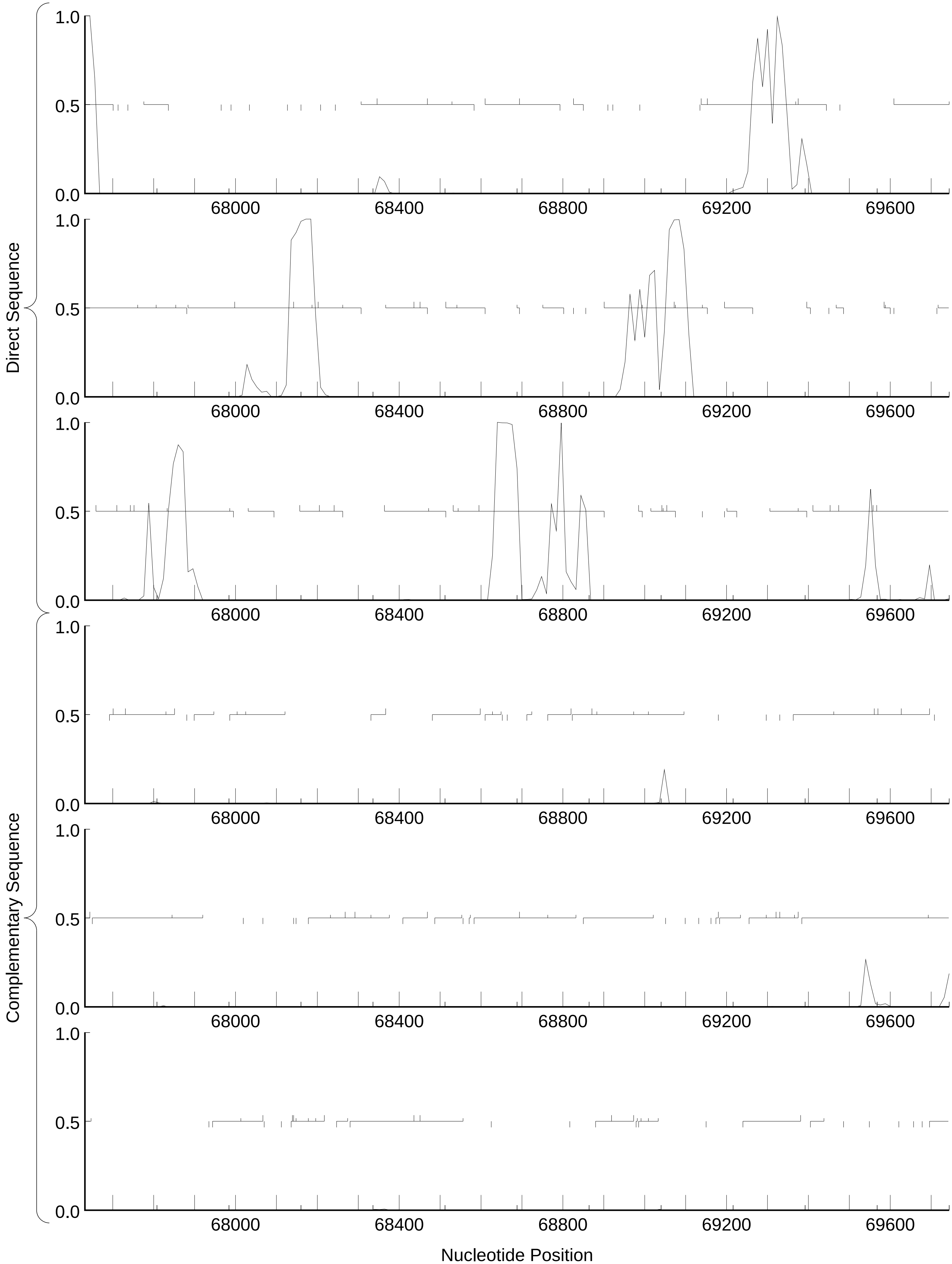
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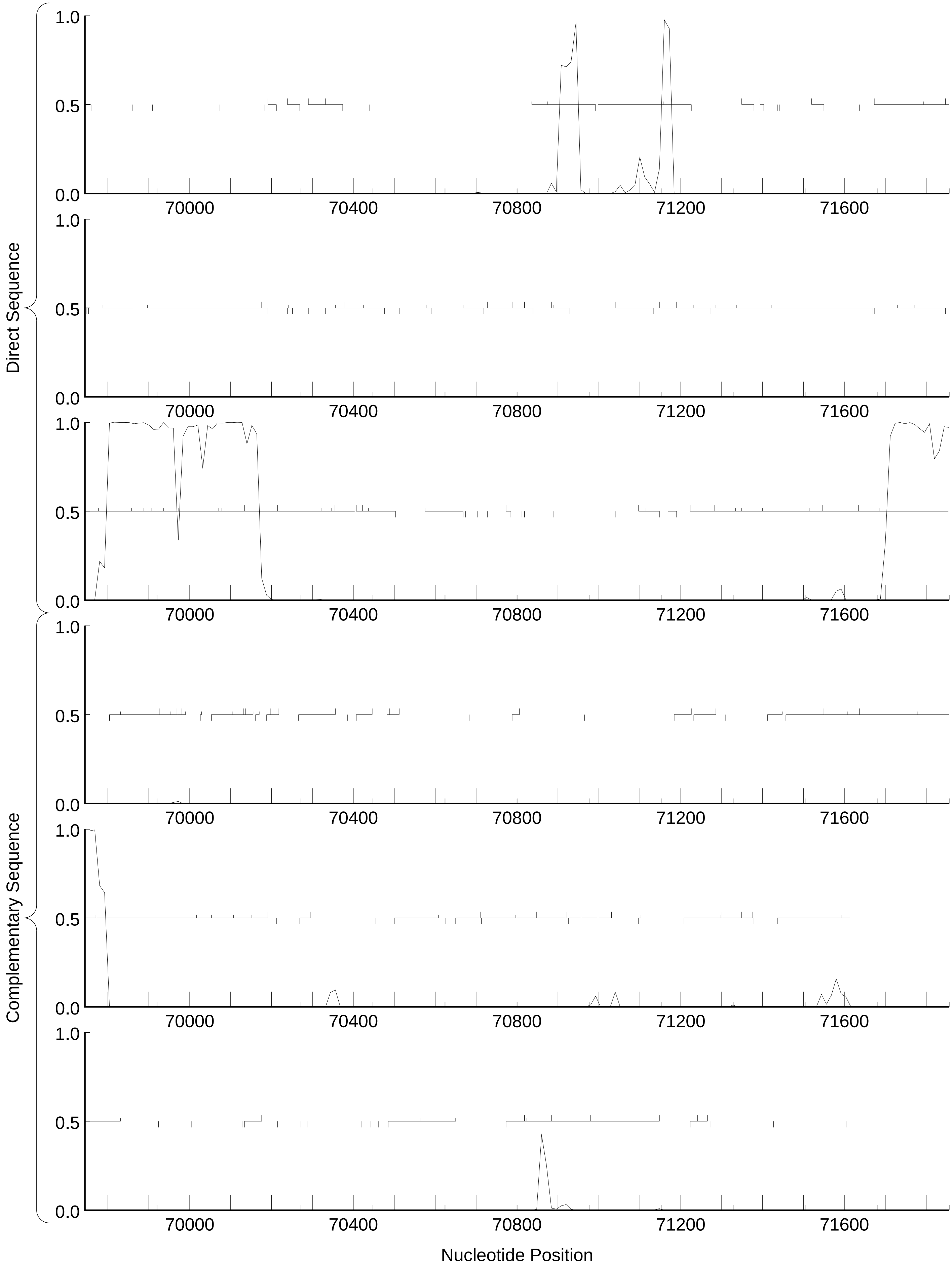

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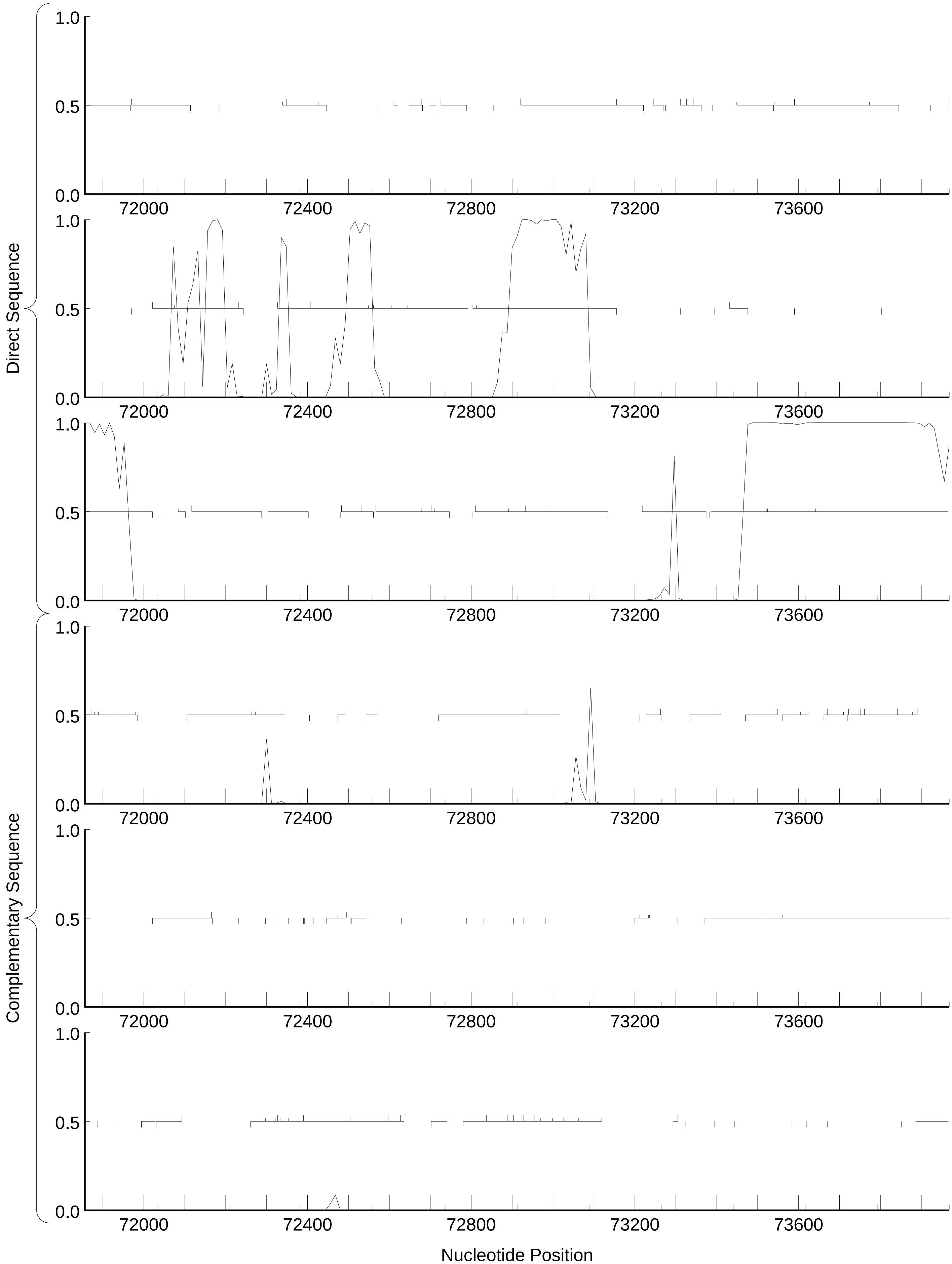
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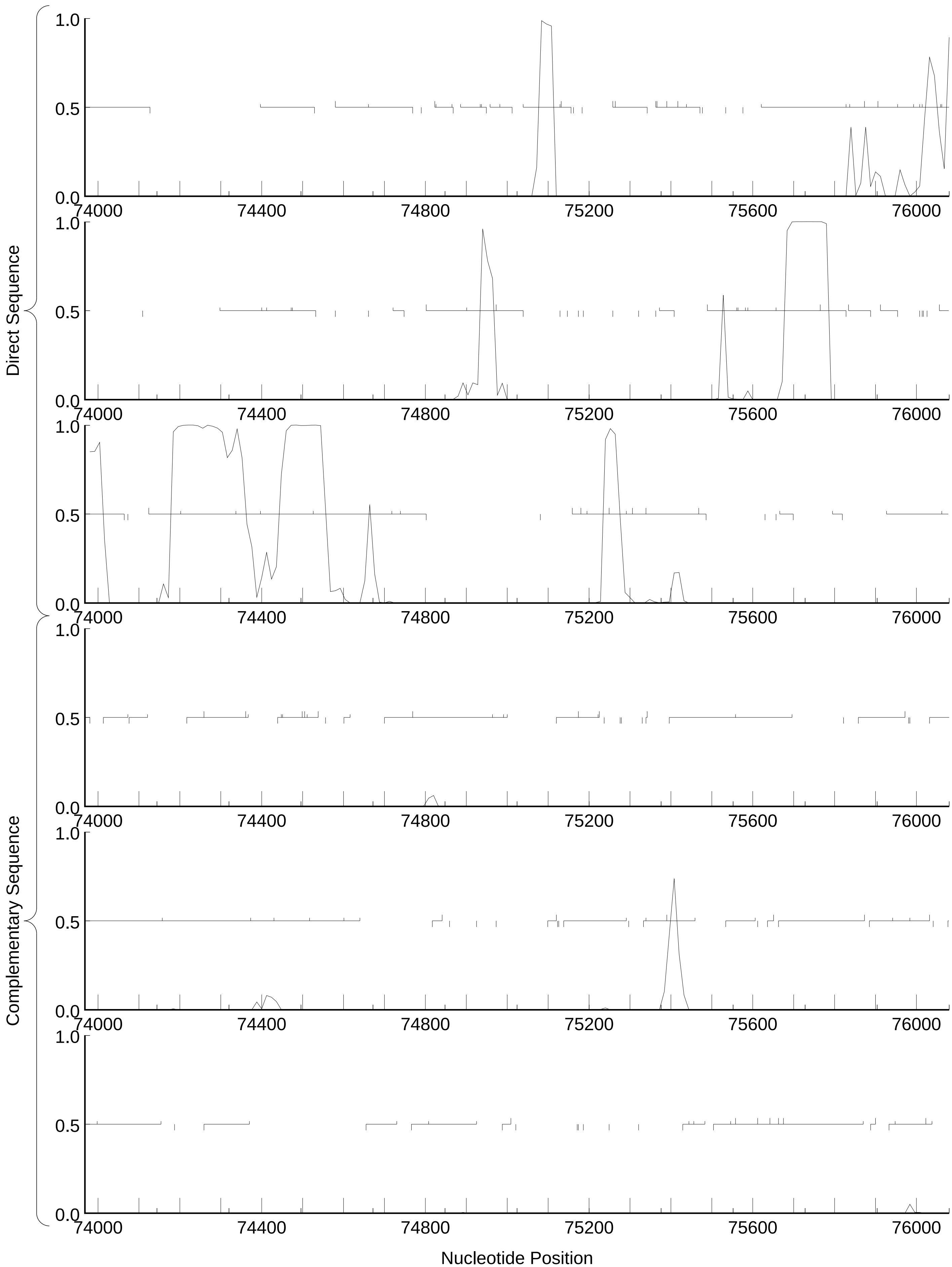
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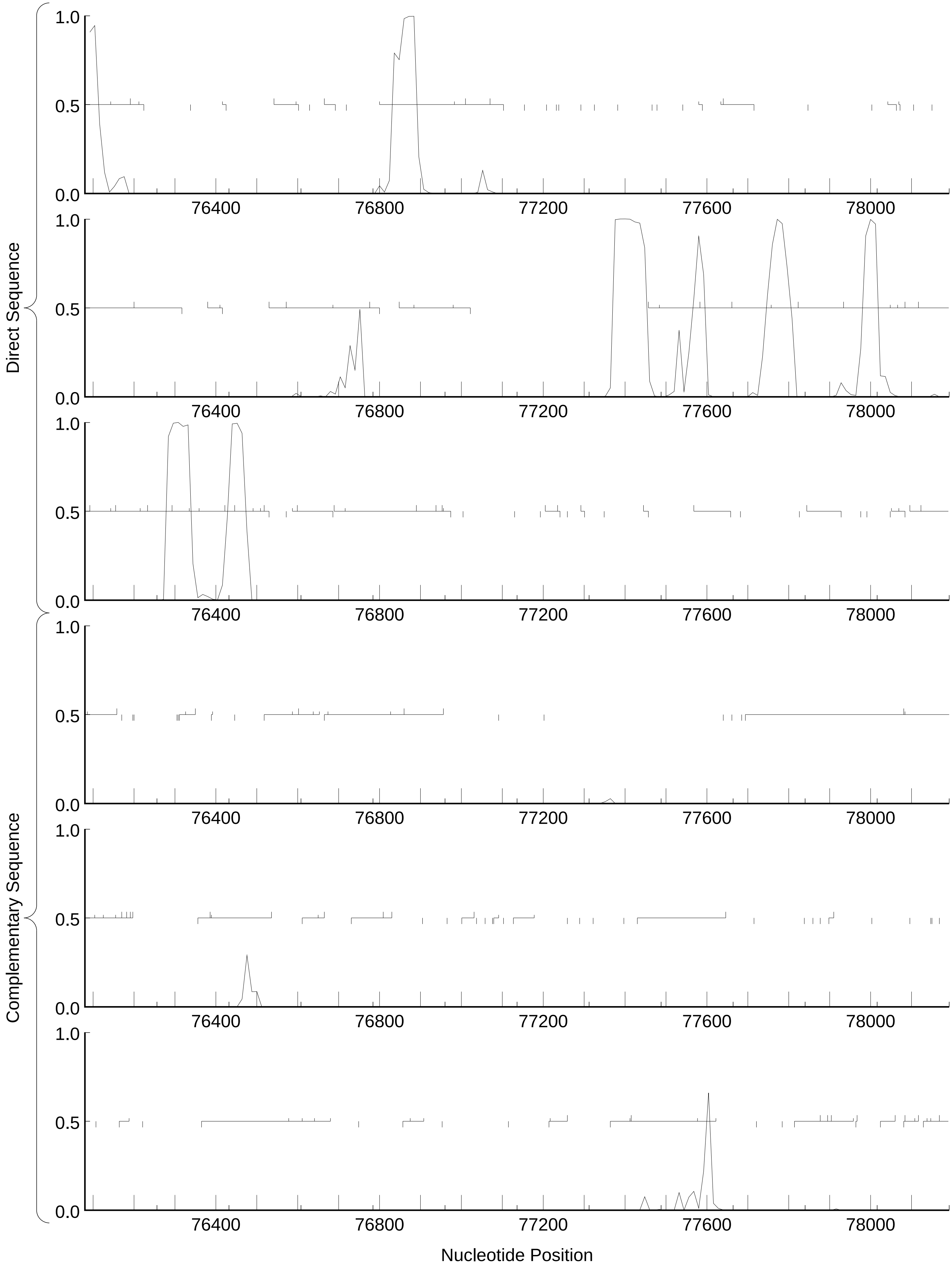

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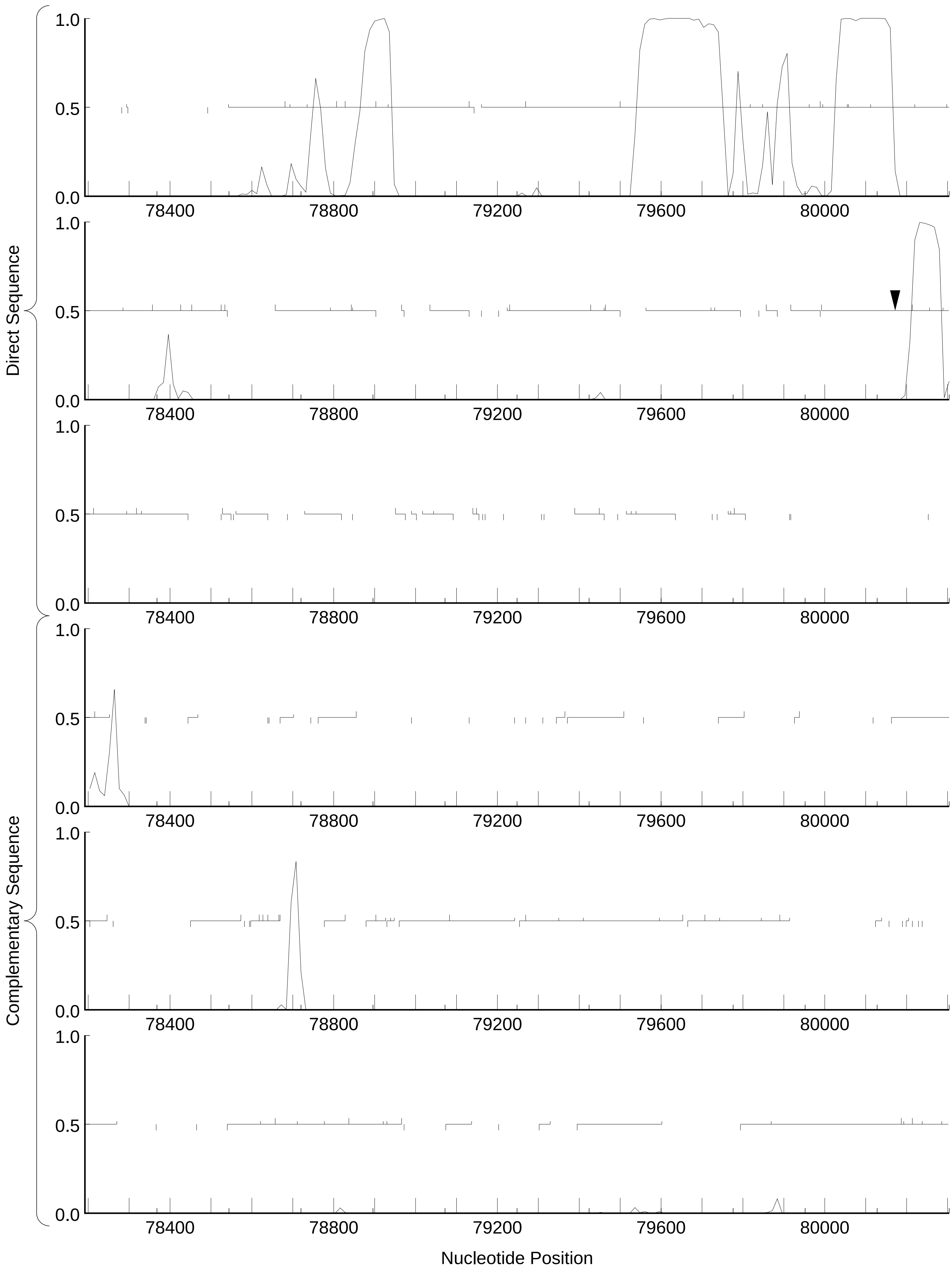

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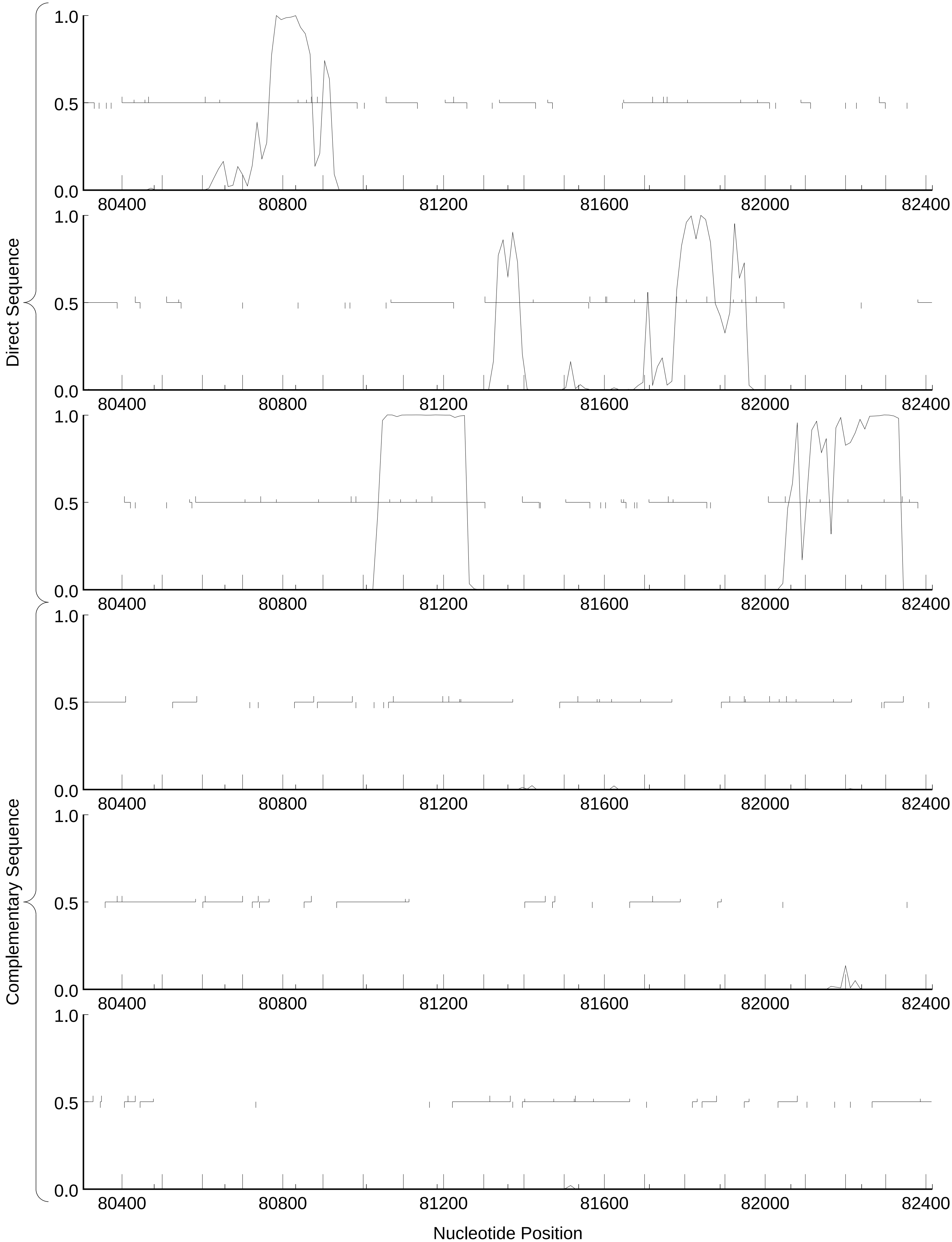

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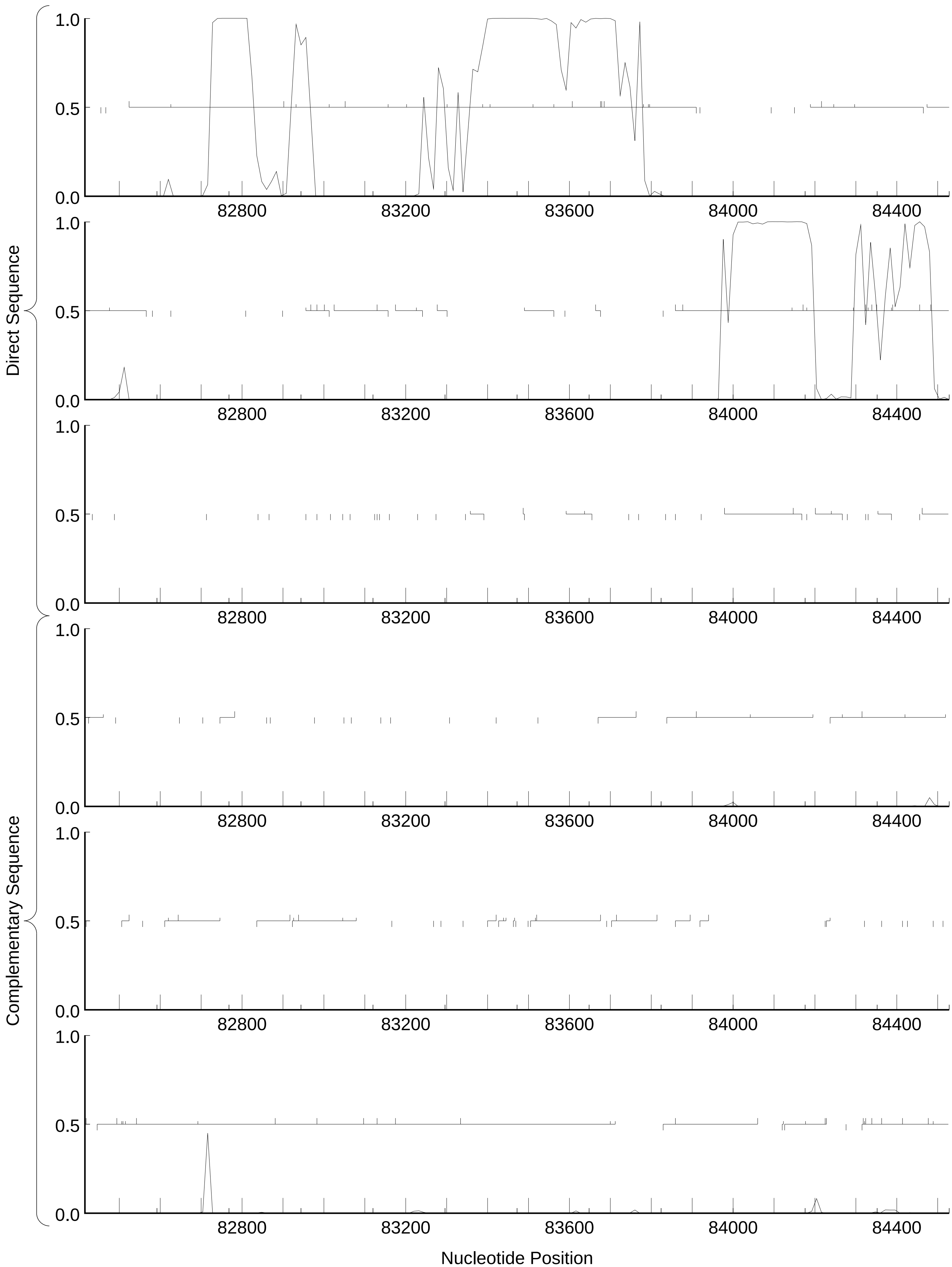
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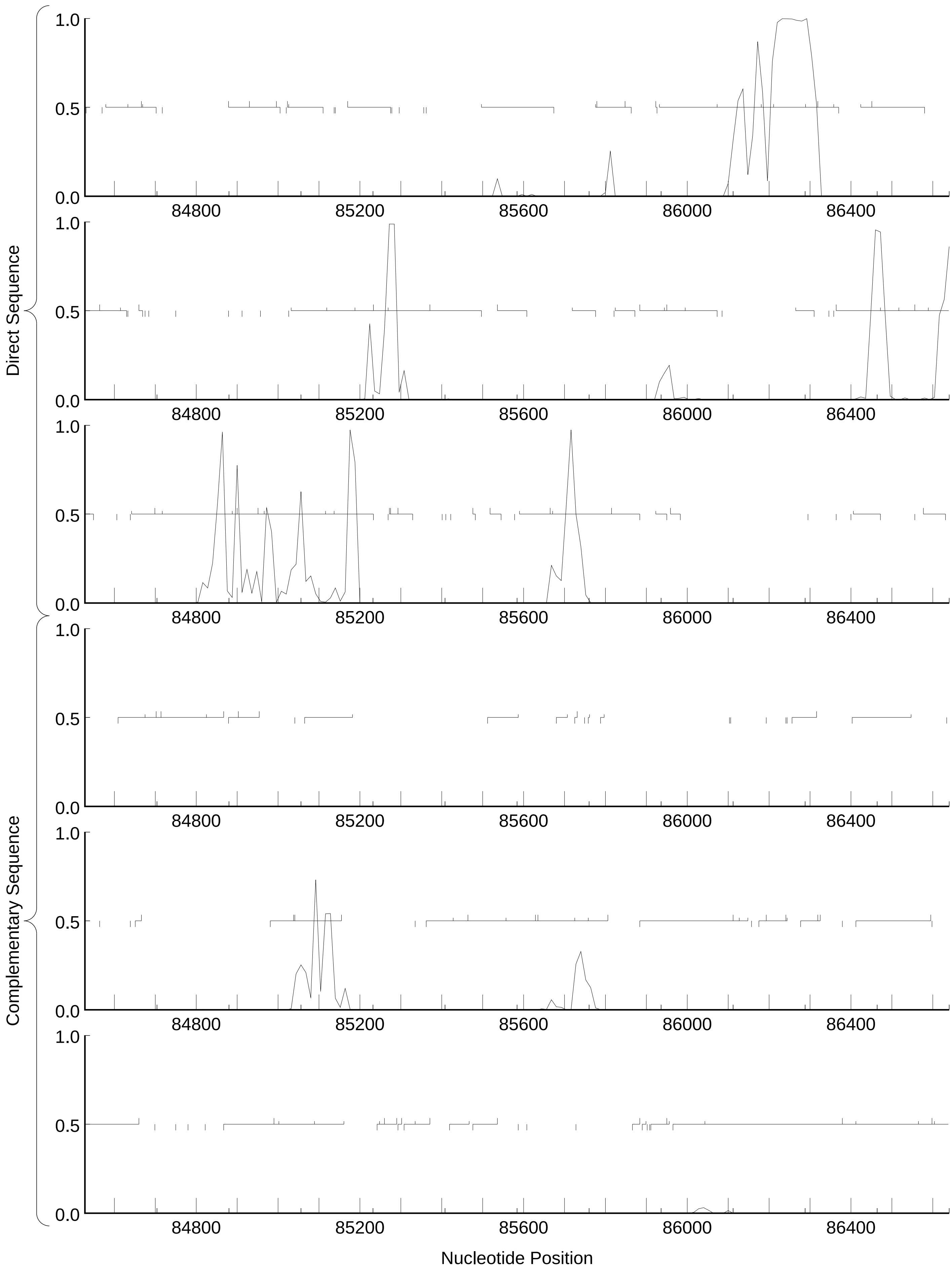
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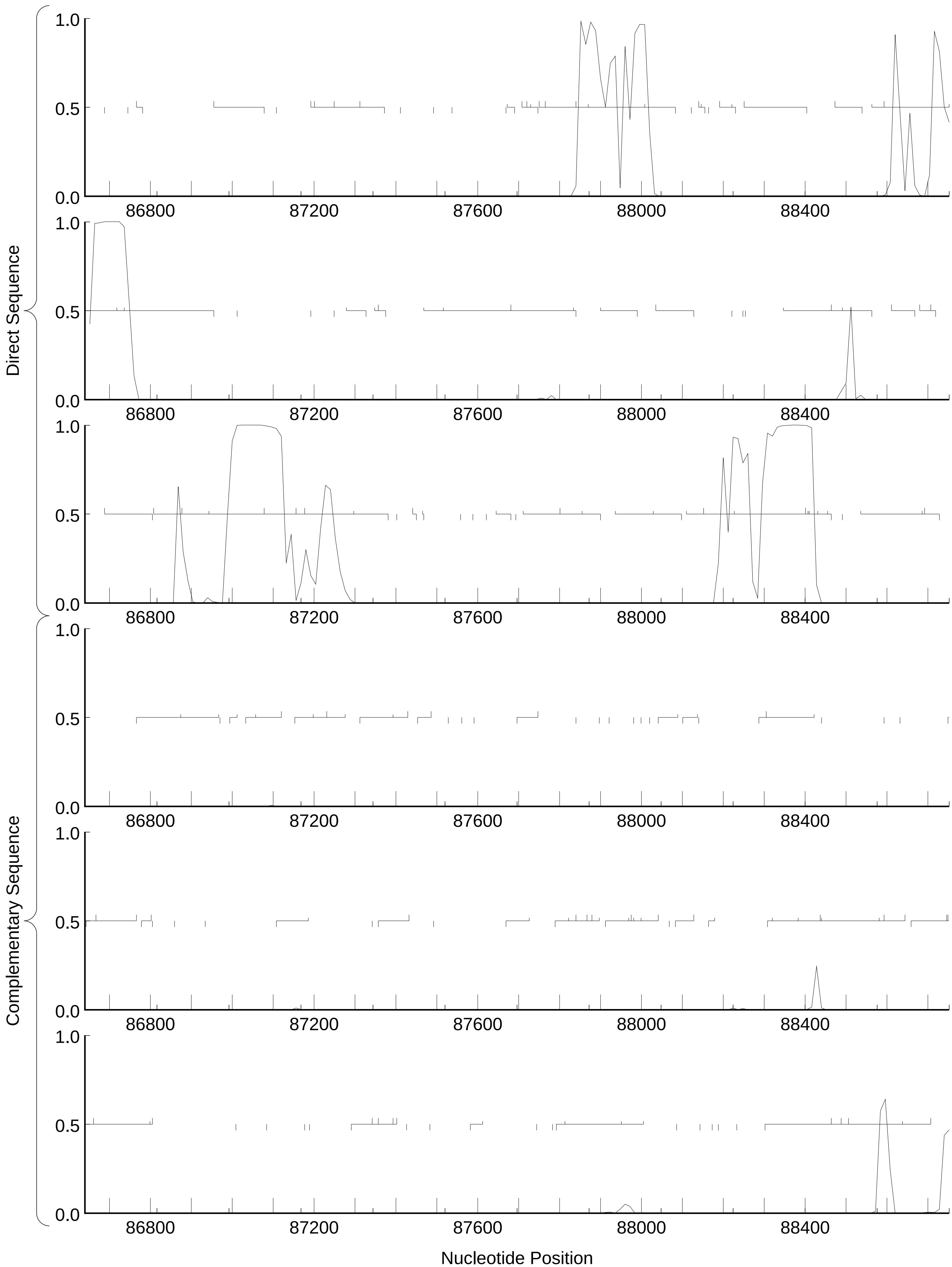
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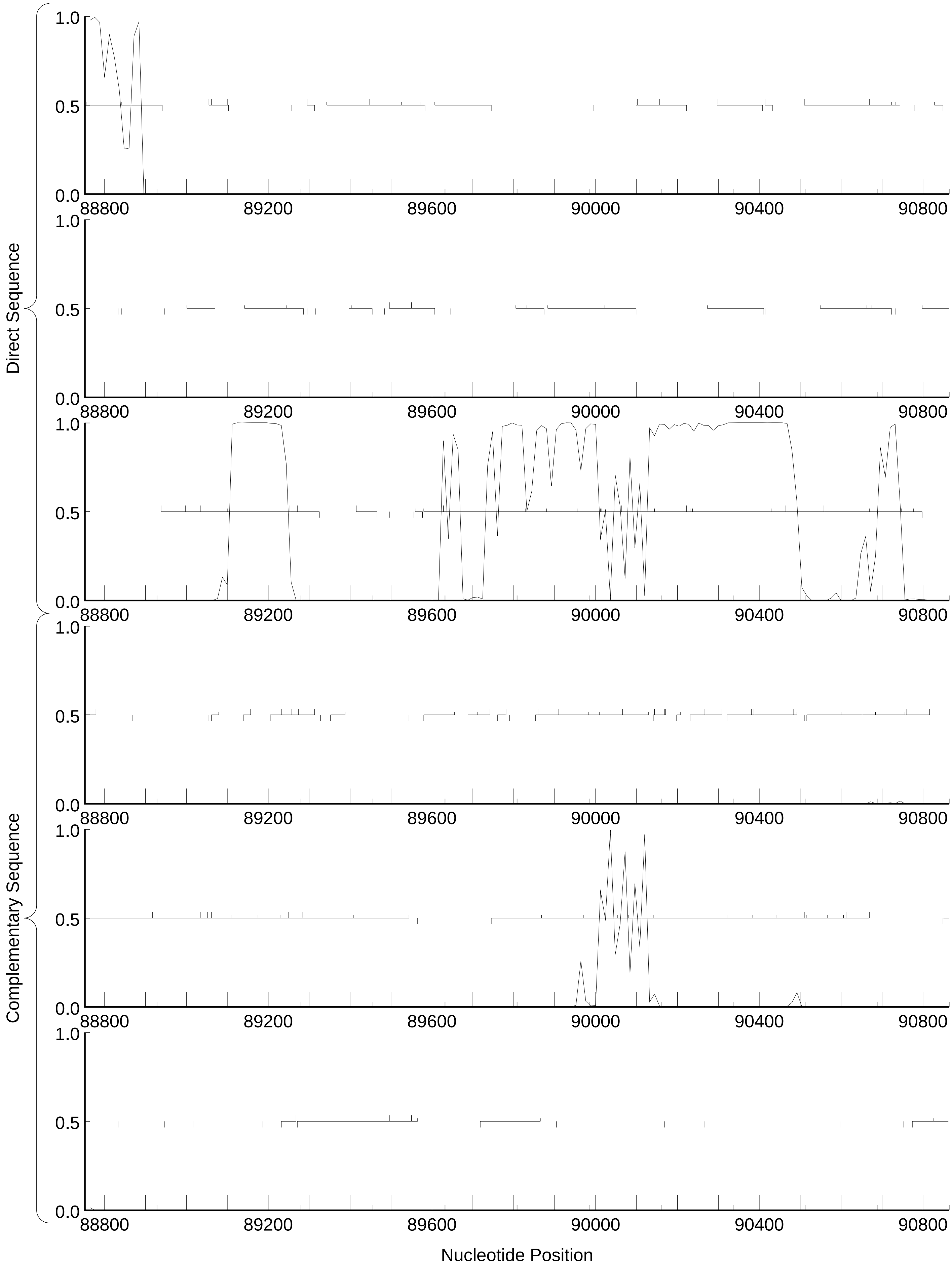
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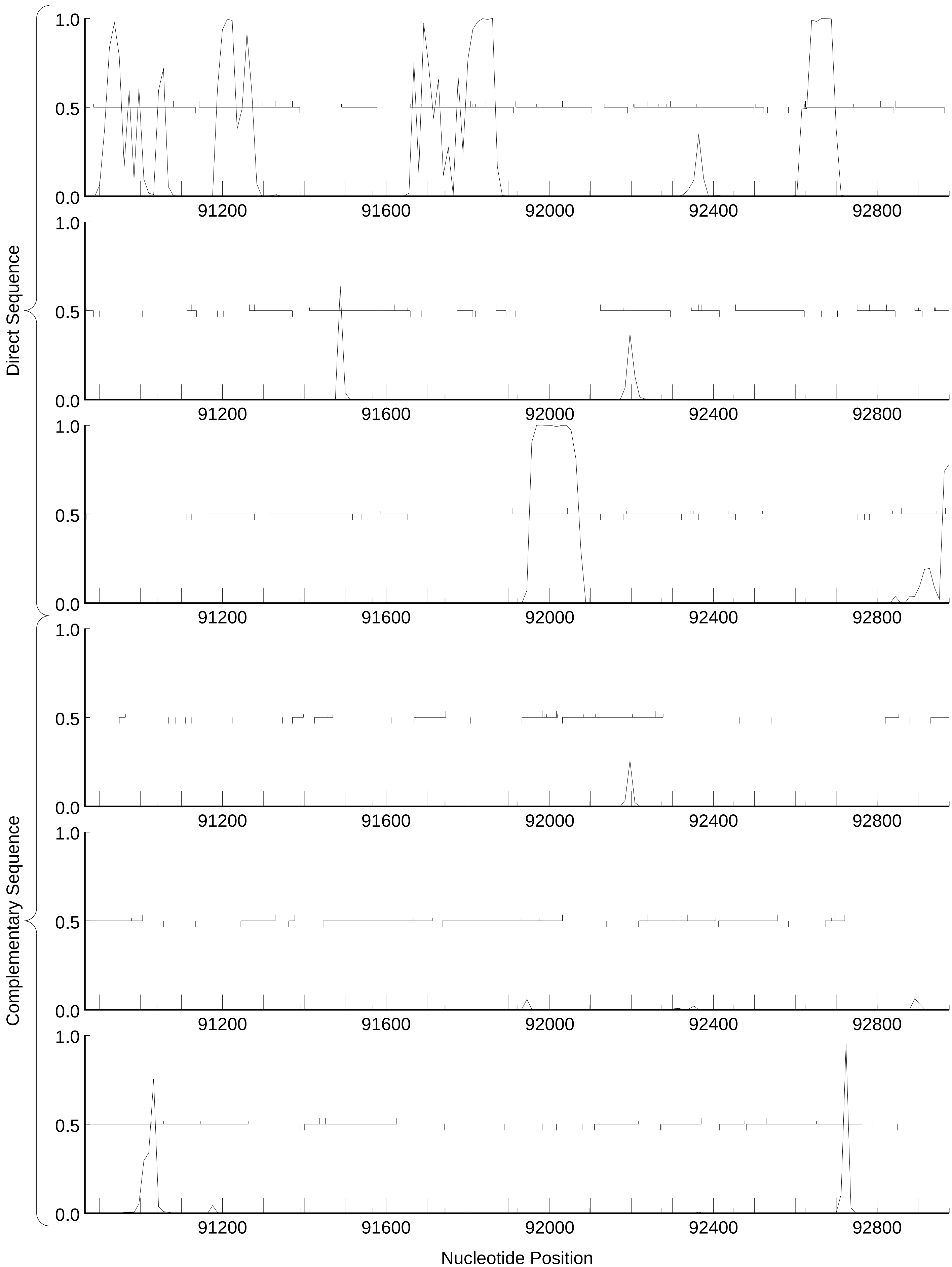
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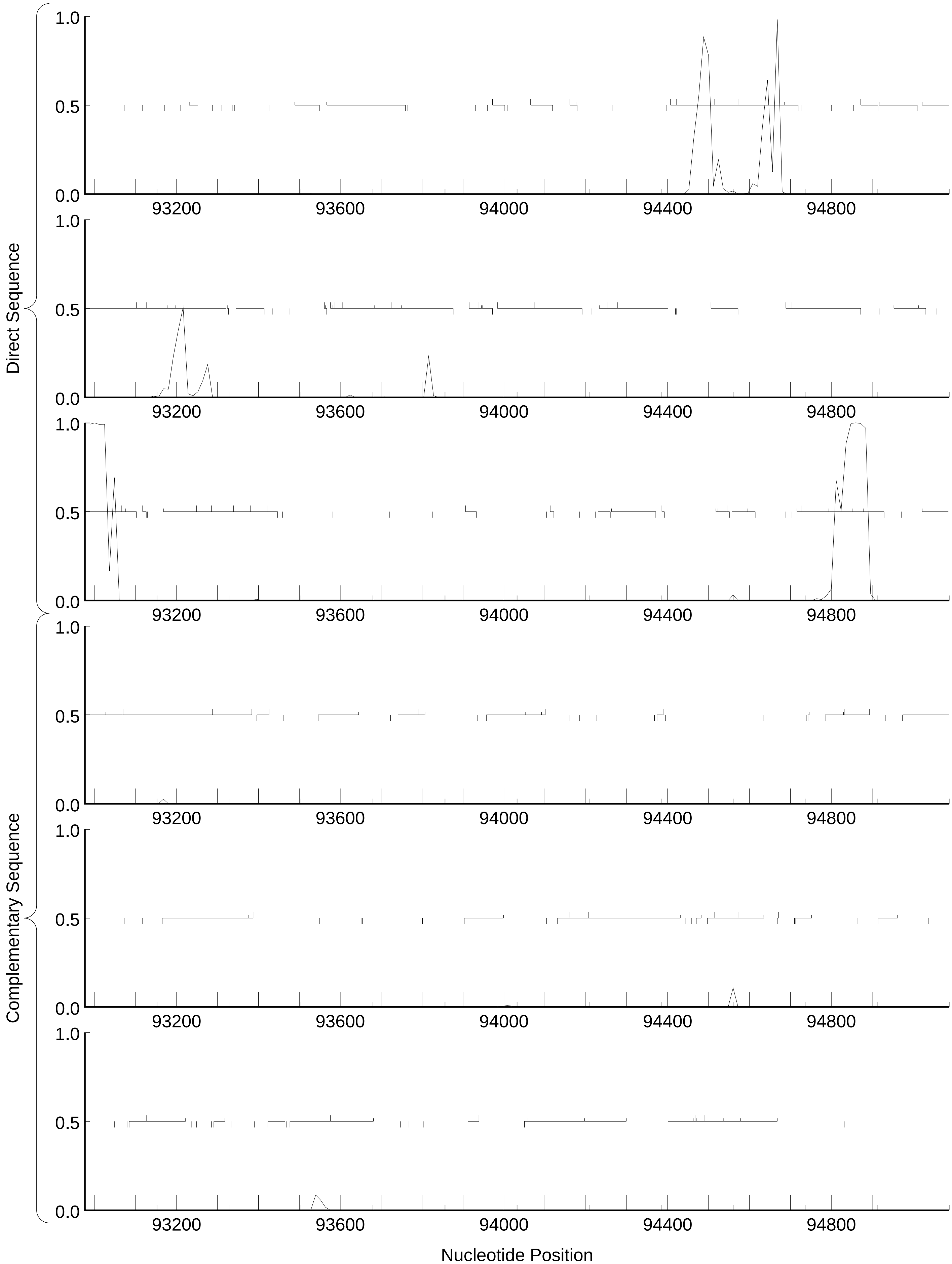
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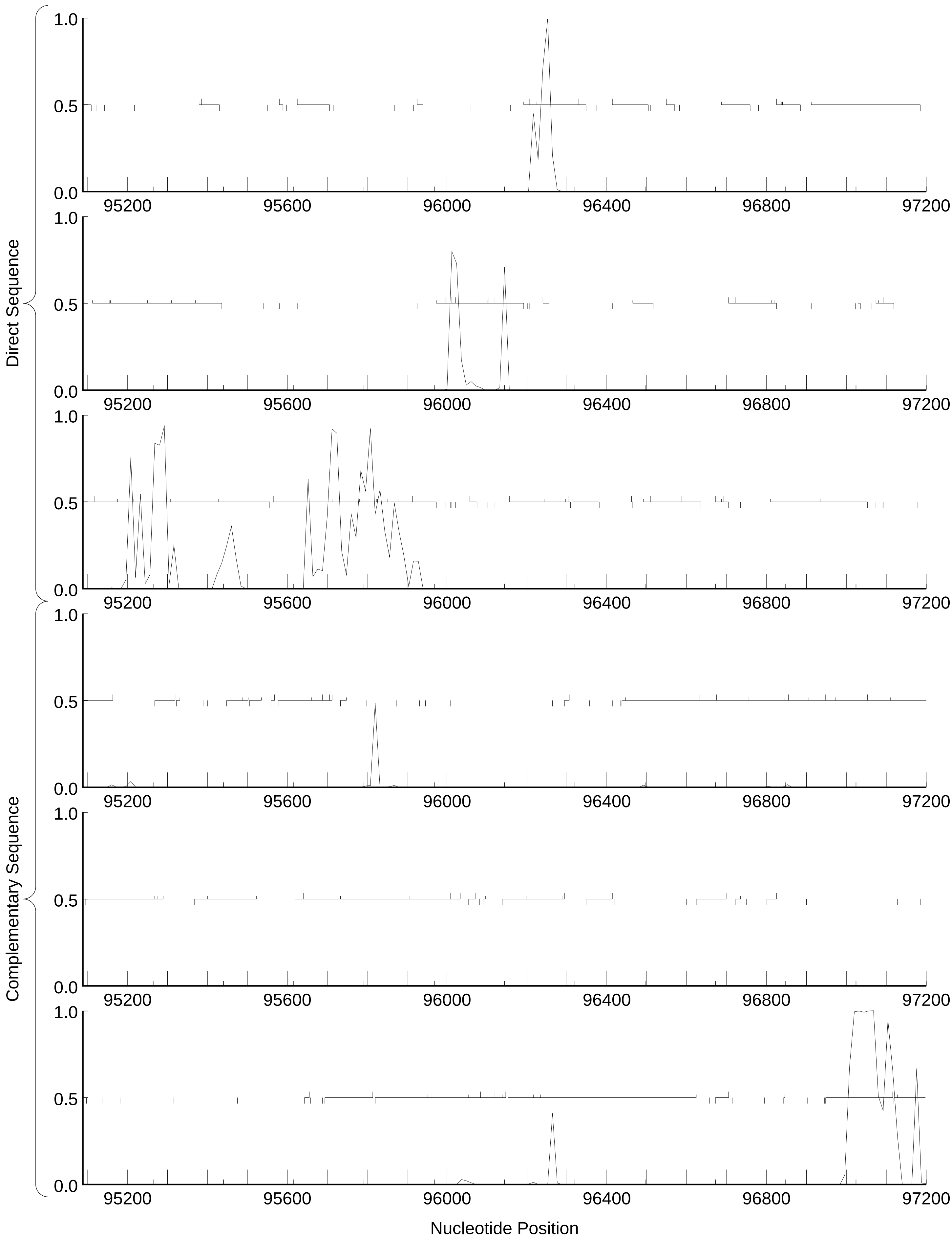
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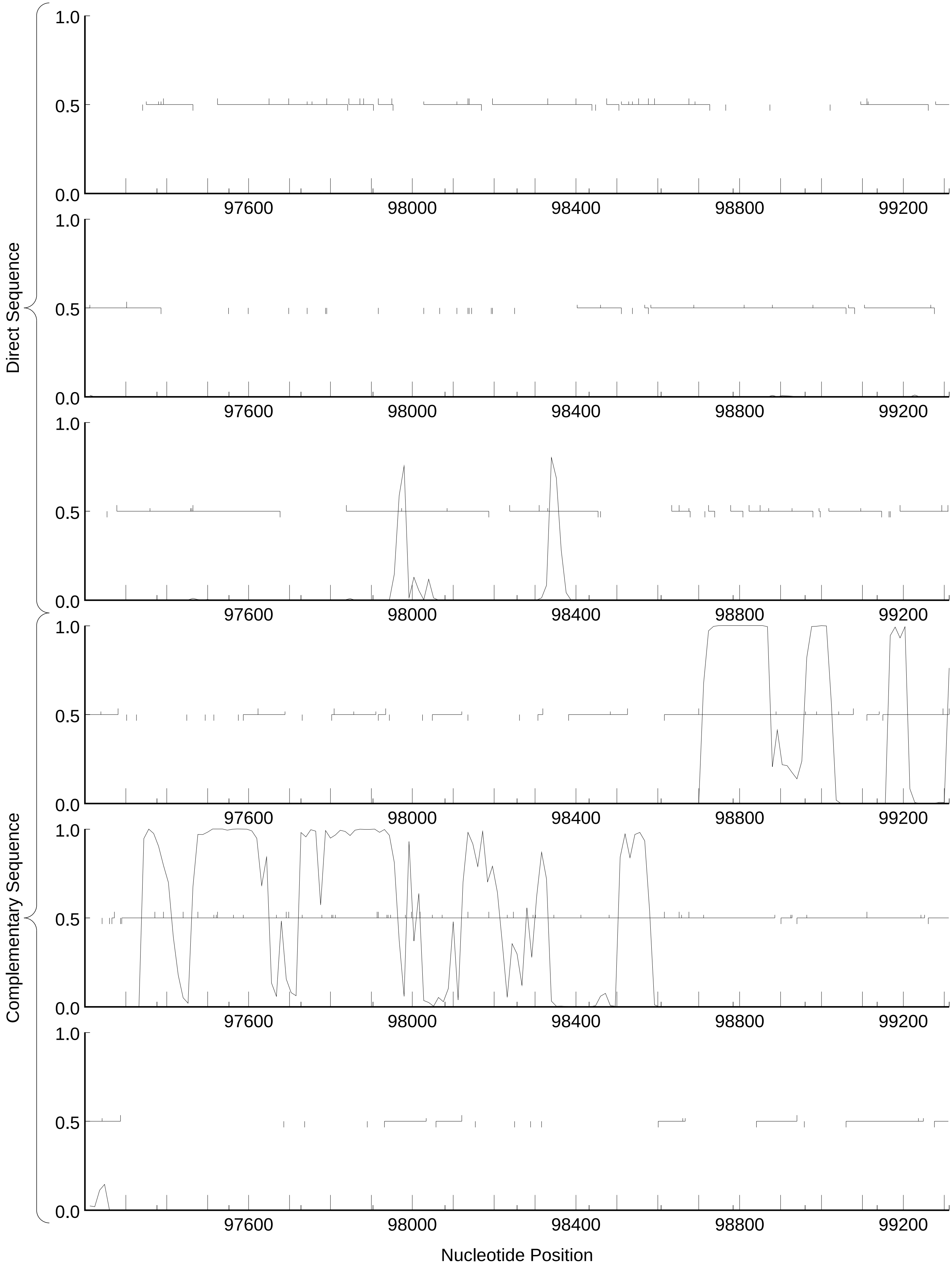
Nucleotide Position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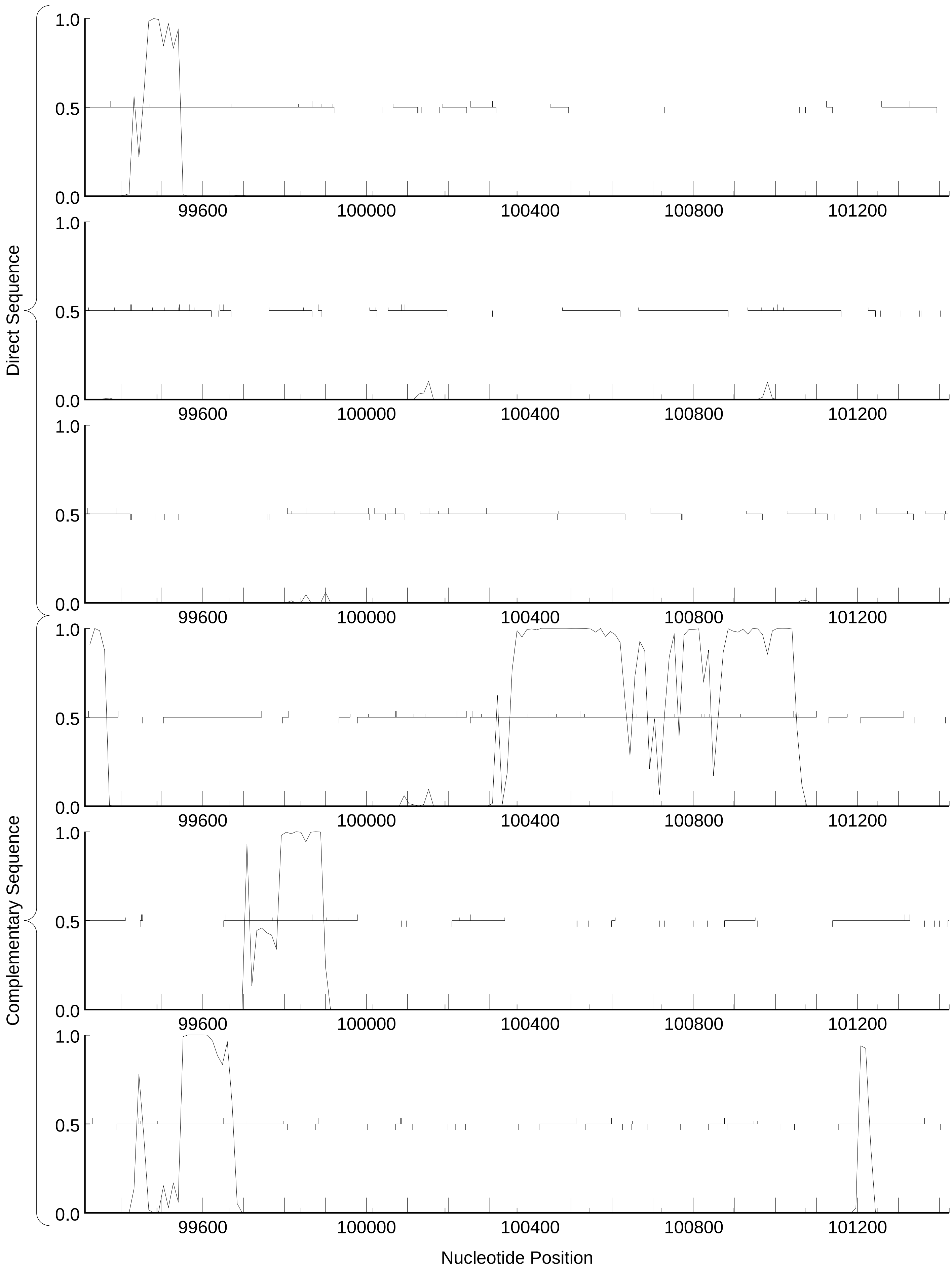

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Complementary Sequence
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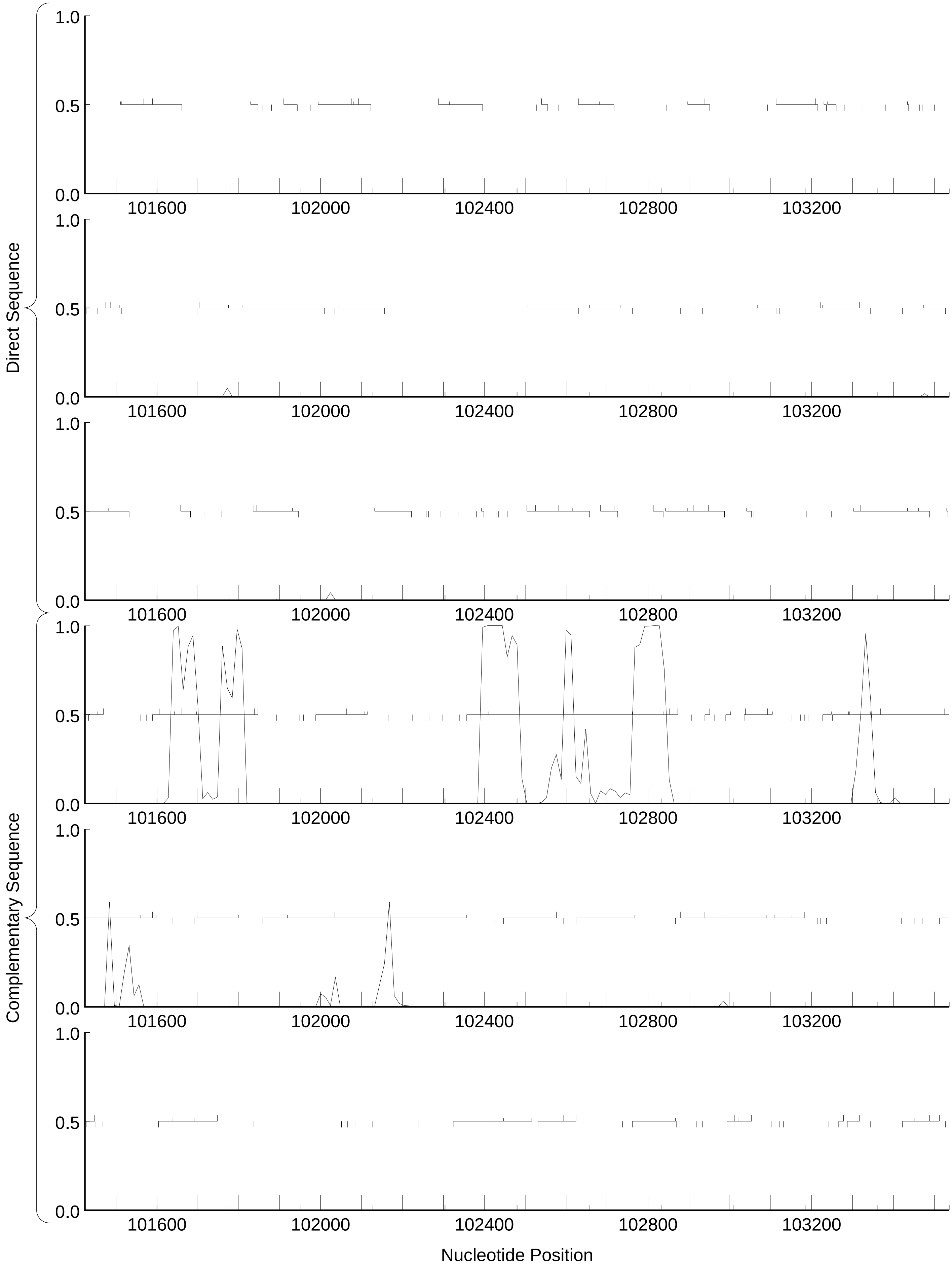
Nucleotide Position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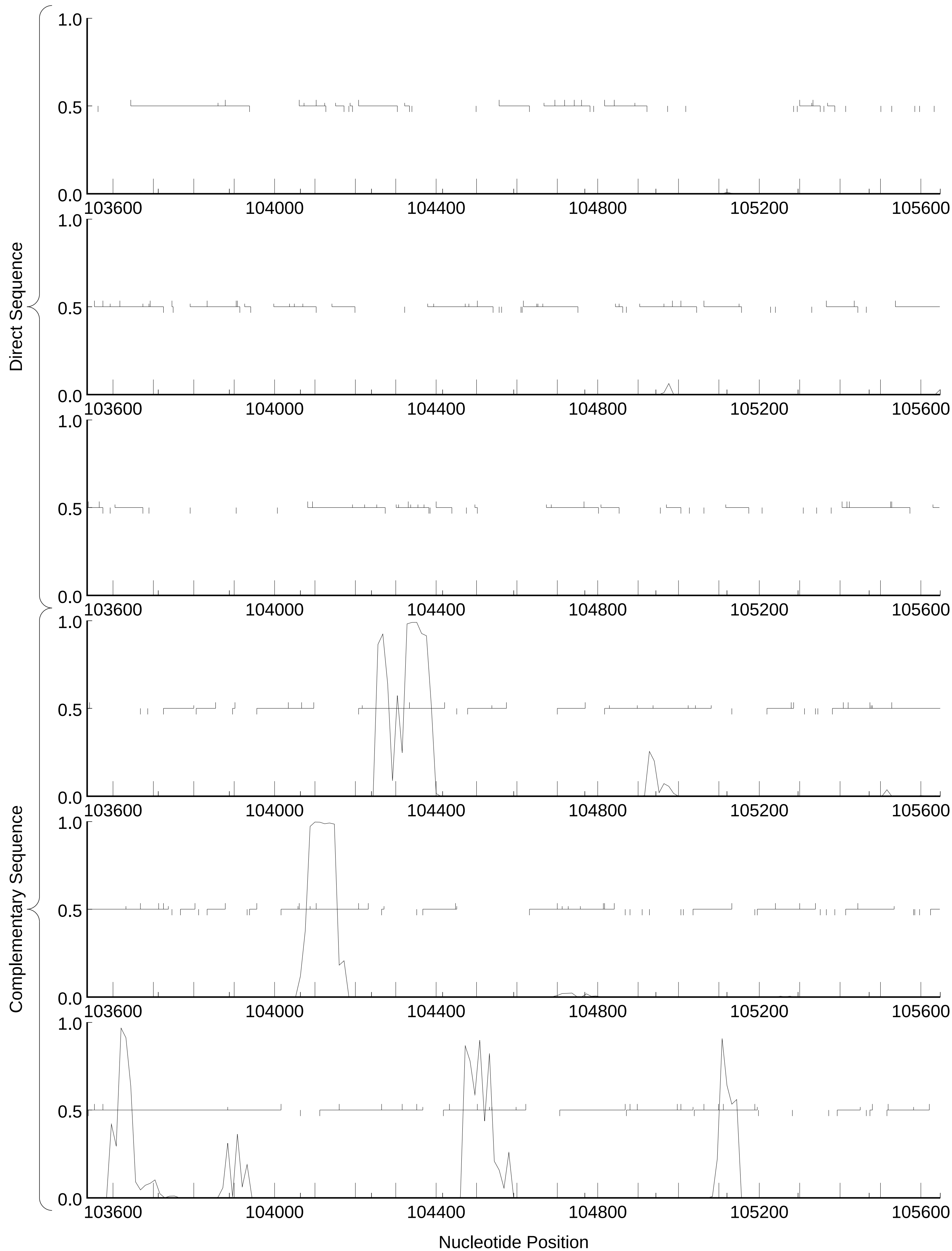
Nucleotide Position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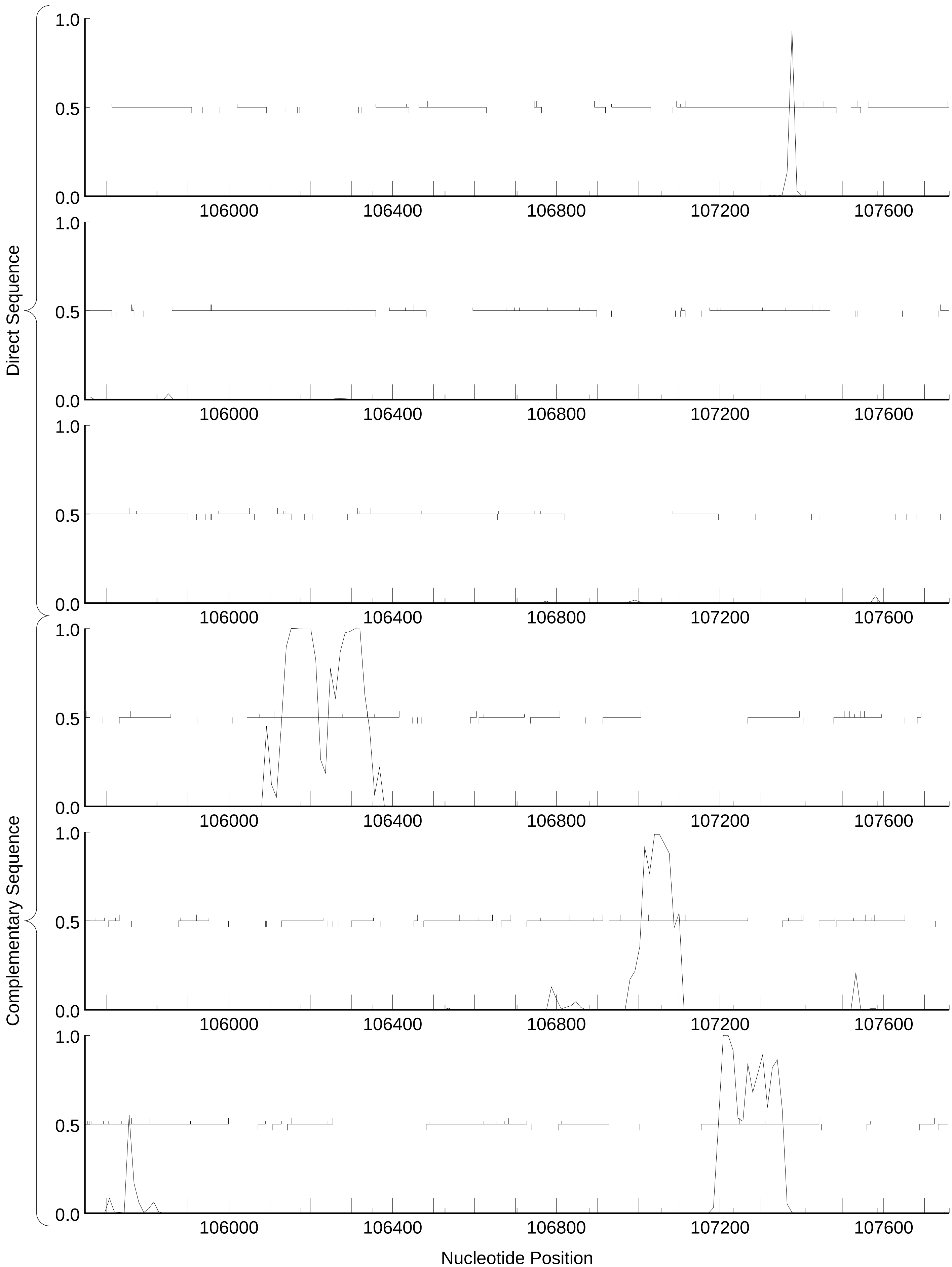
Nucleotide Position


Direct Sequence
Complementary Sequence
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0.5
0.0
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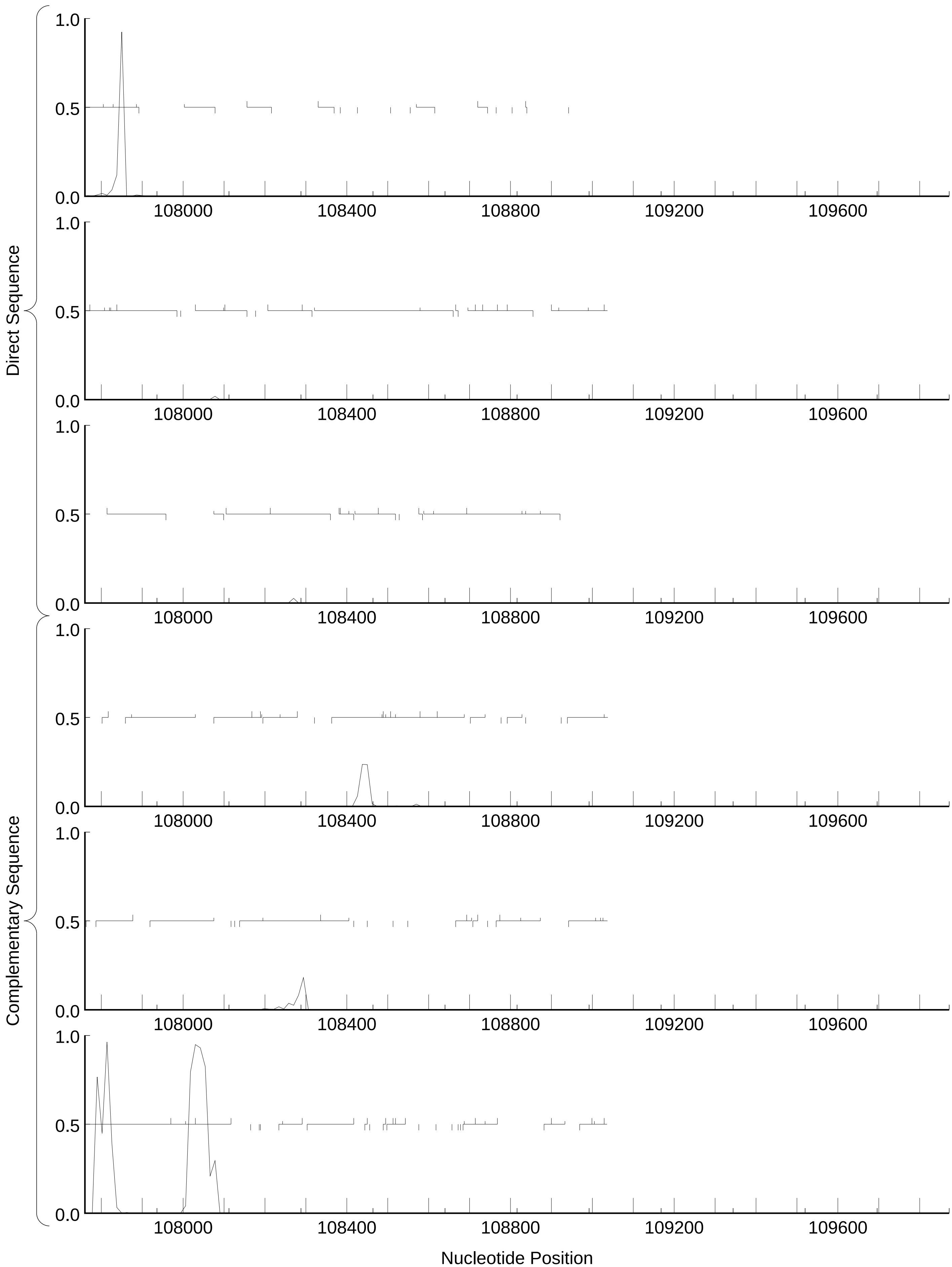
106400
106800
107200
107600
Nucleotide Position


Direct Sequence
Complementary Sequence
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0.5
0.0
108000
108400
108800
109200
109600
Nucleotide Position