

GeneMark

Version 2.5p (09.08.06)

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PROGRAM INFORMATION

Sequence : Arthrobacter phage Racecar complete sequence, 173709 bp, circularly permuted, Cluster FC
Analysis Date : 9/22/17 at 5:55:39
Pages : 84
Sequence Length : 173709 bp
GC Content : 53.07%

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,

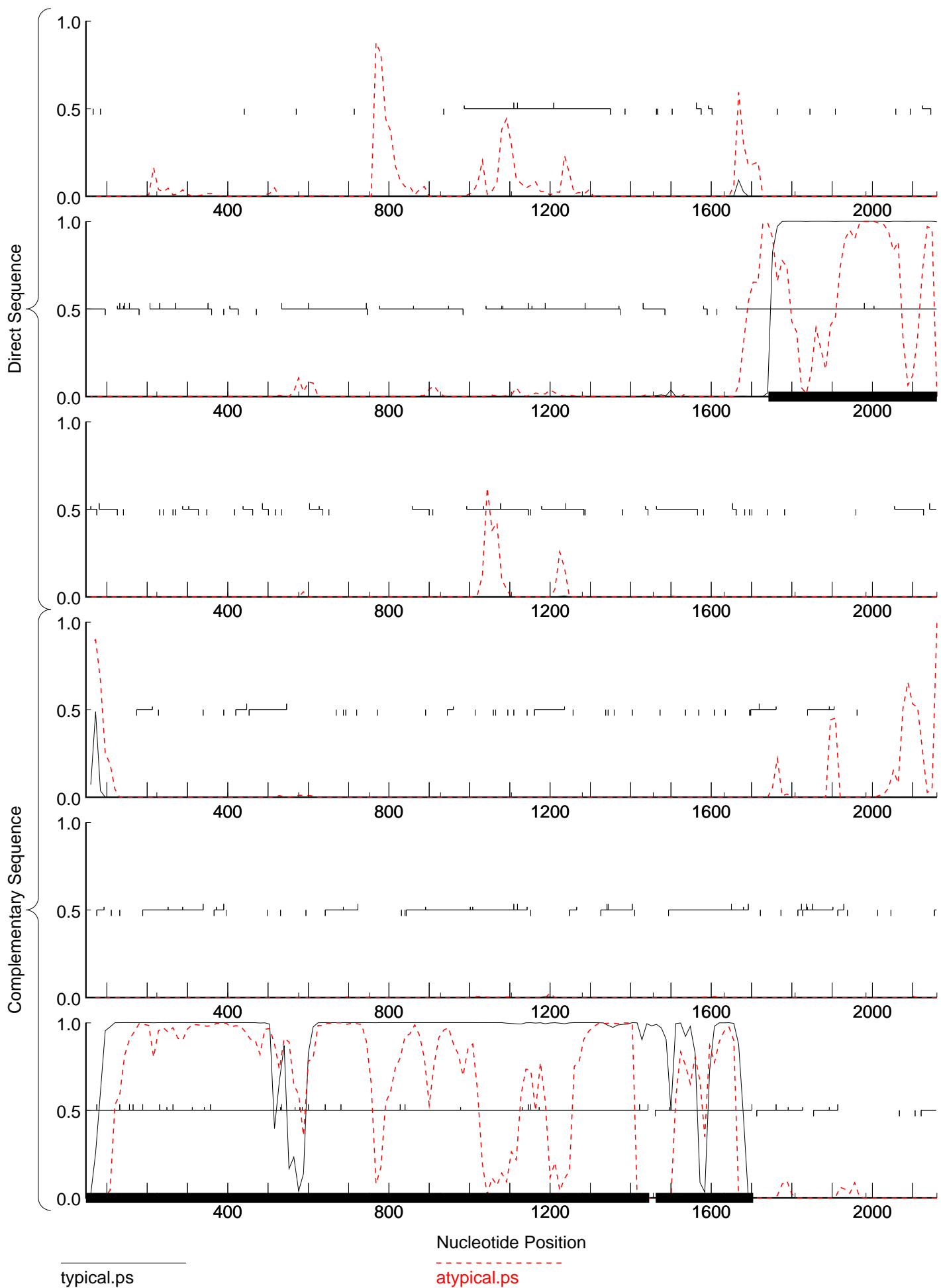
MATRIX INFORMATION

Matrix : -
Author : -
Order : 4

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

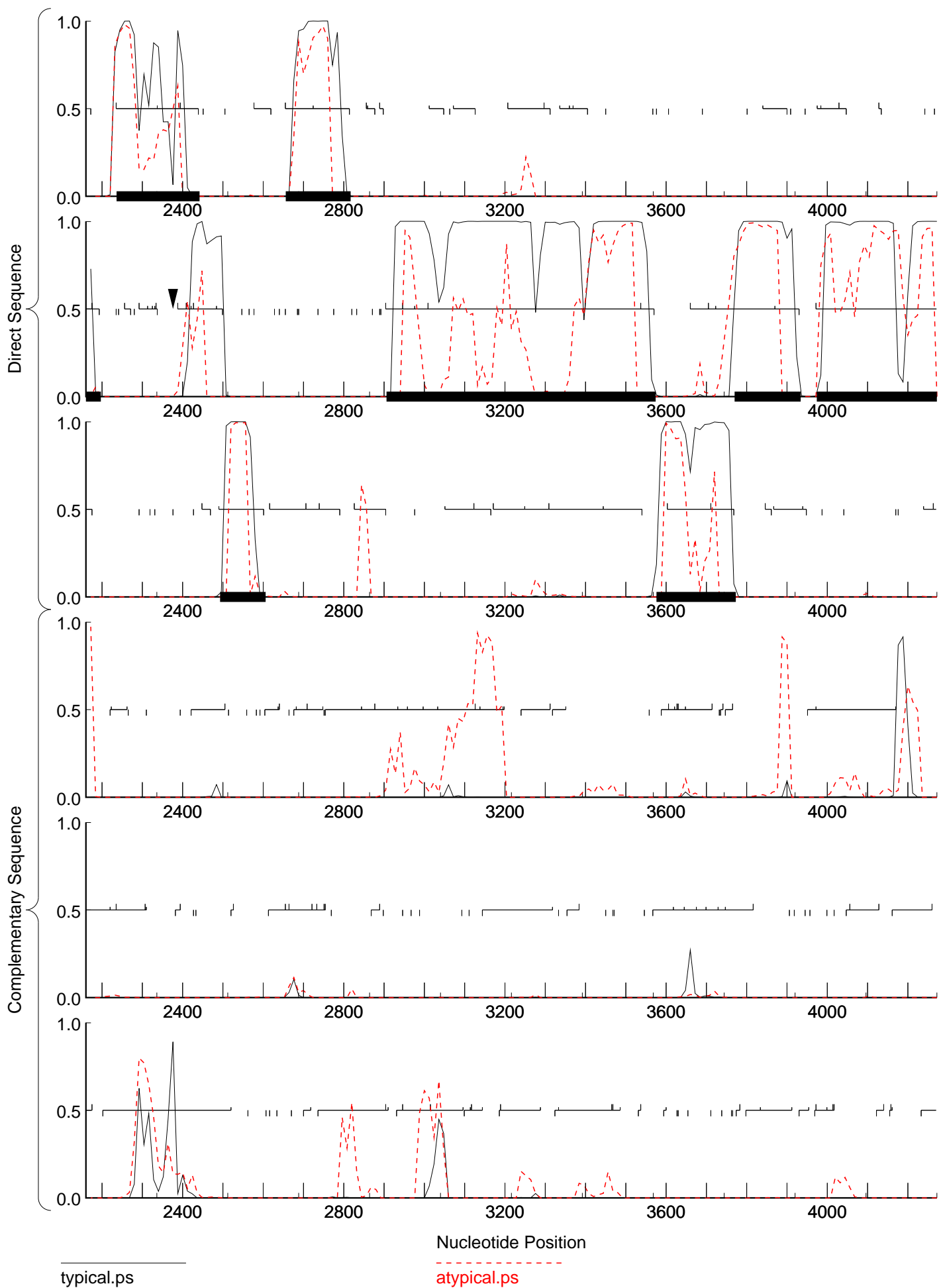
Matrix notes & comments

Training set derived by GeneMarkS, 4.30 October 2014
Fri Sep 22 05:55:39 2017



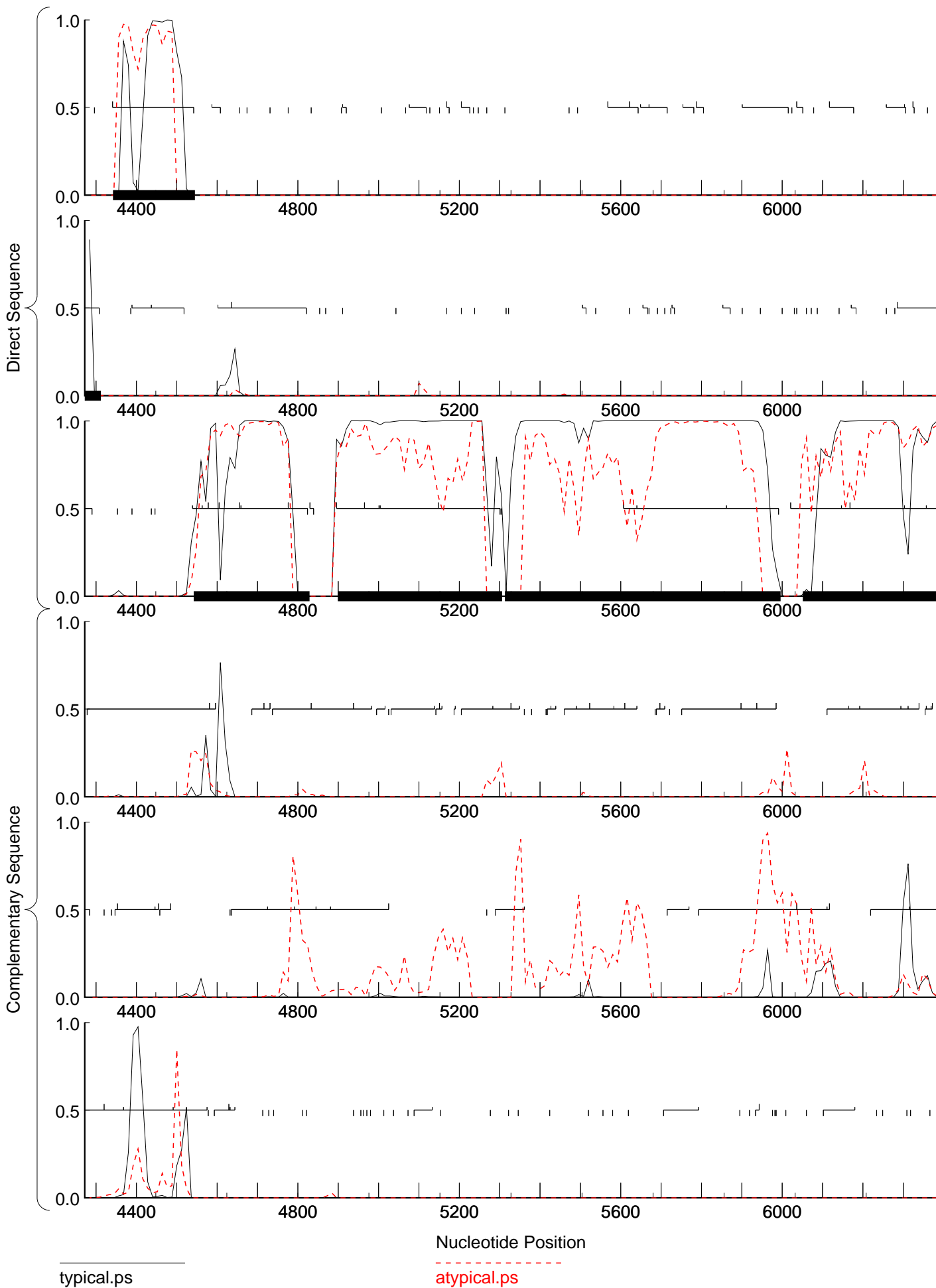
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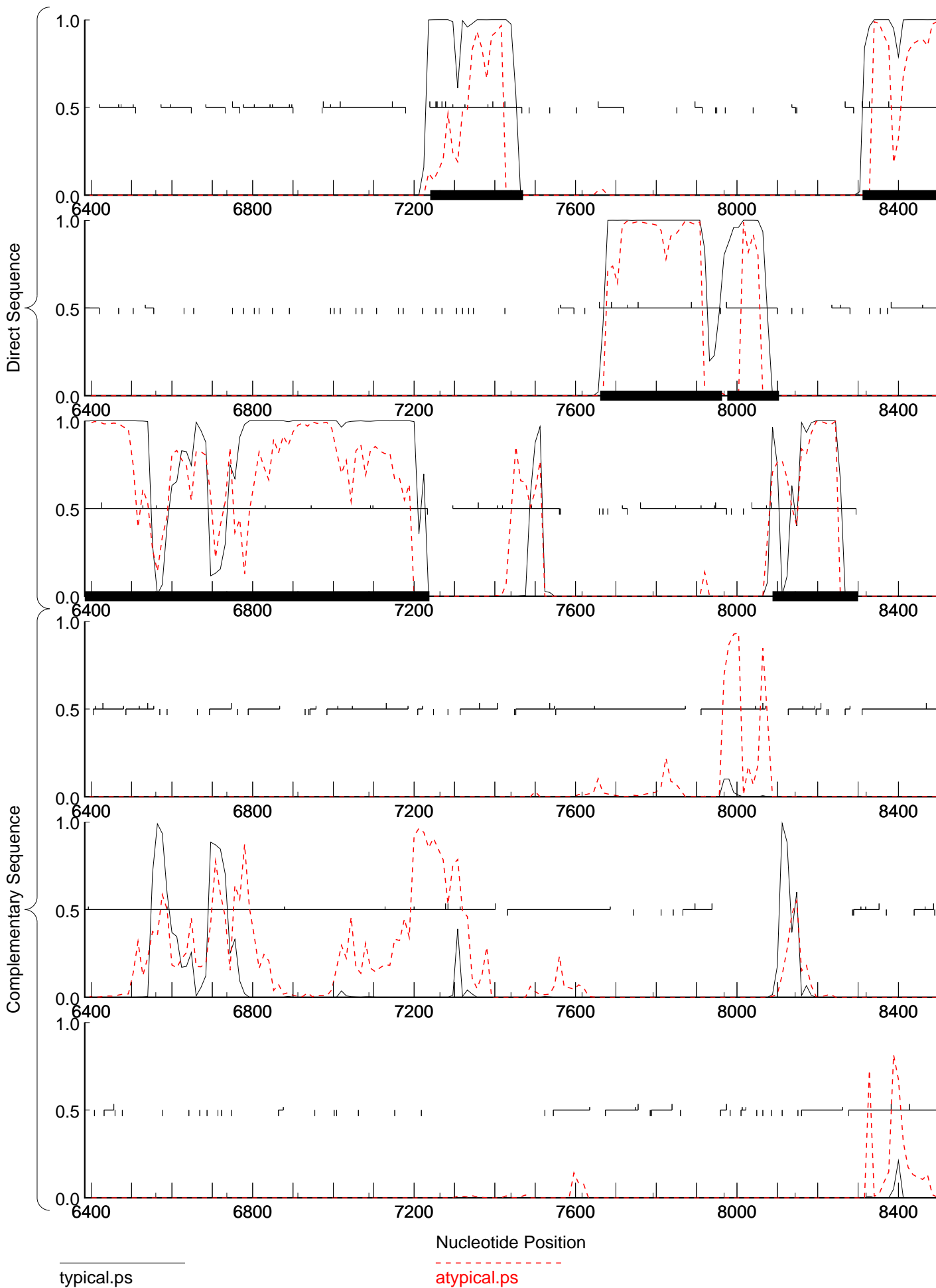
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typical.ps

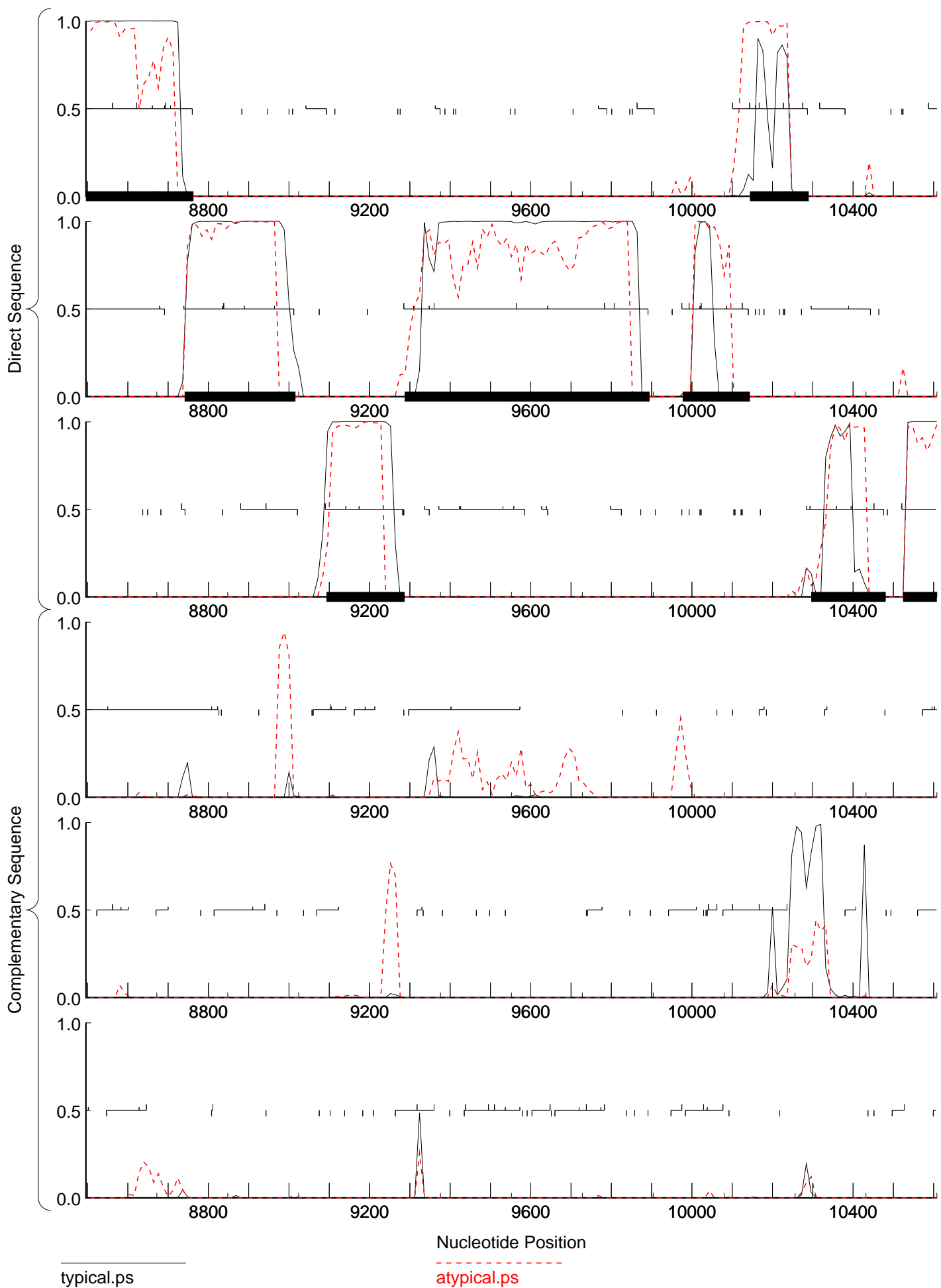
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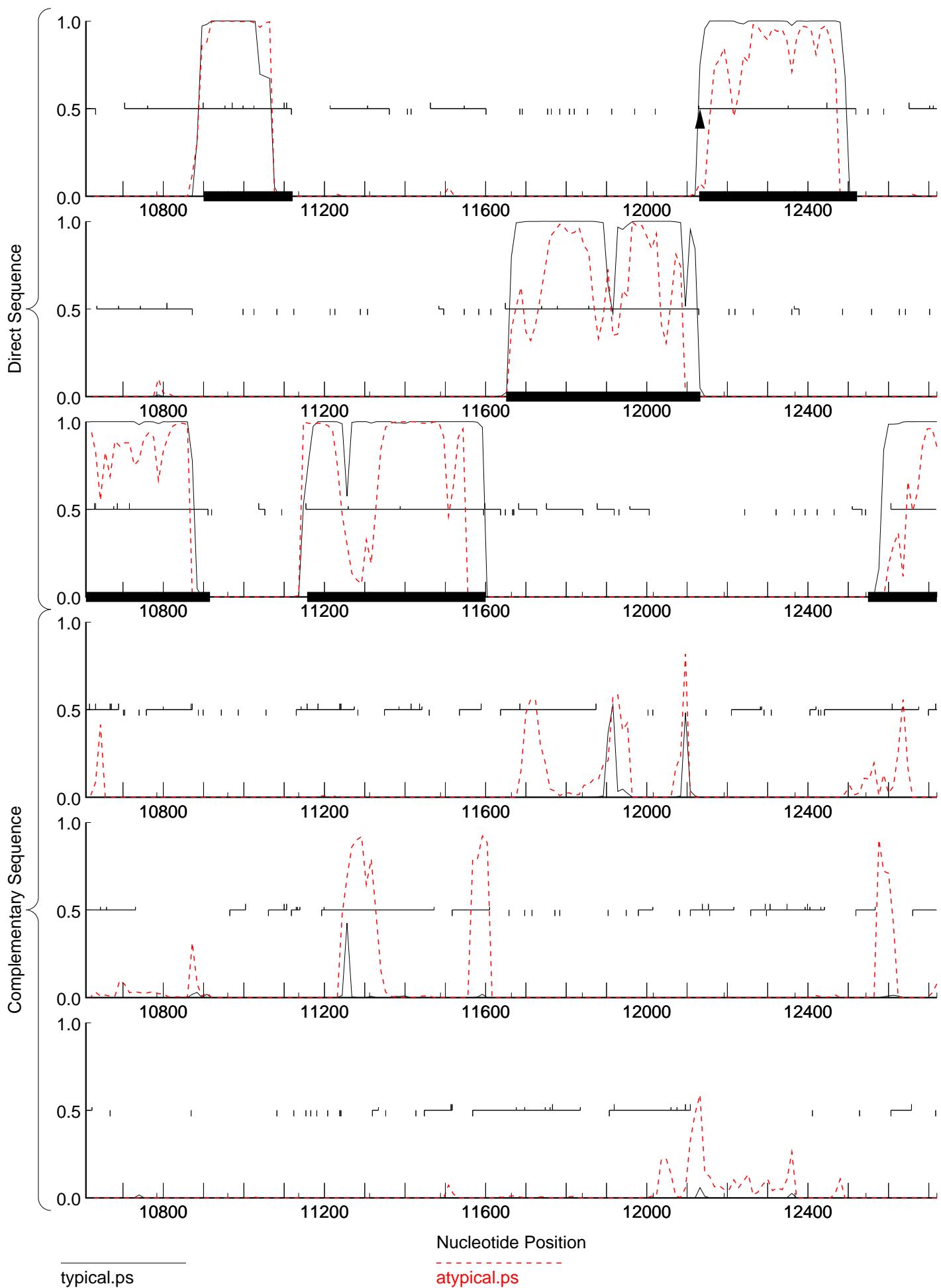




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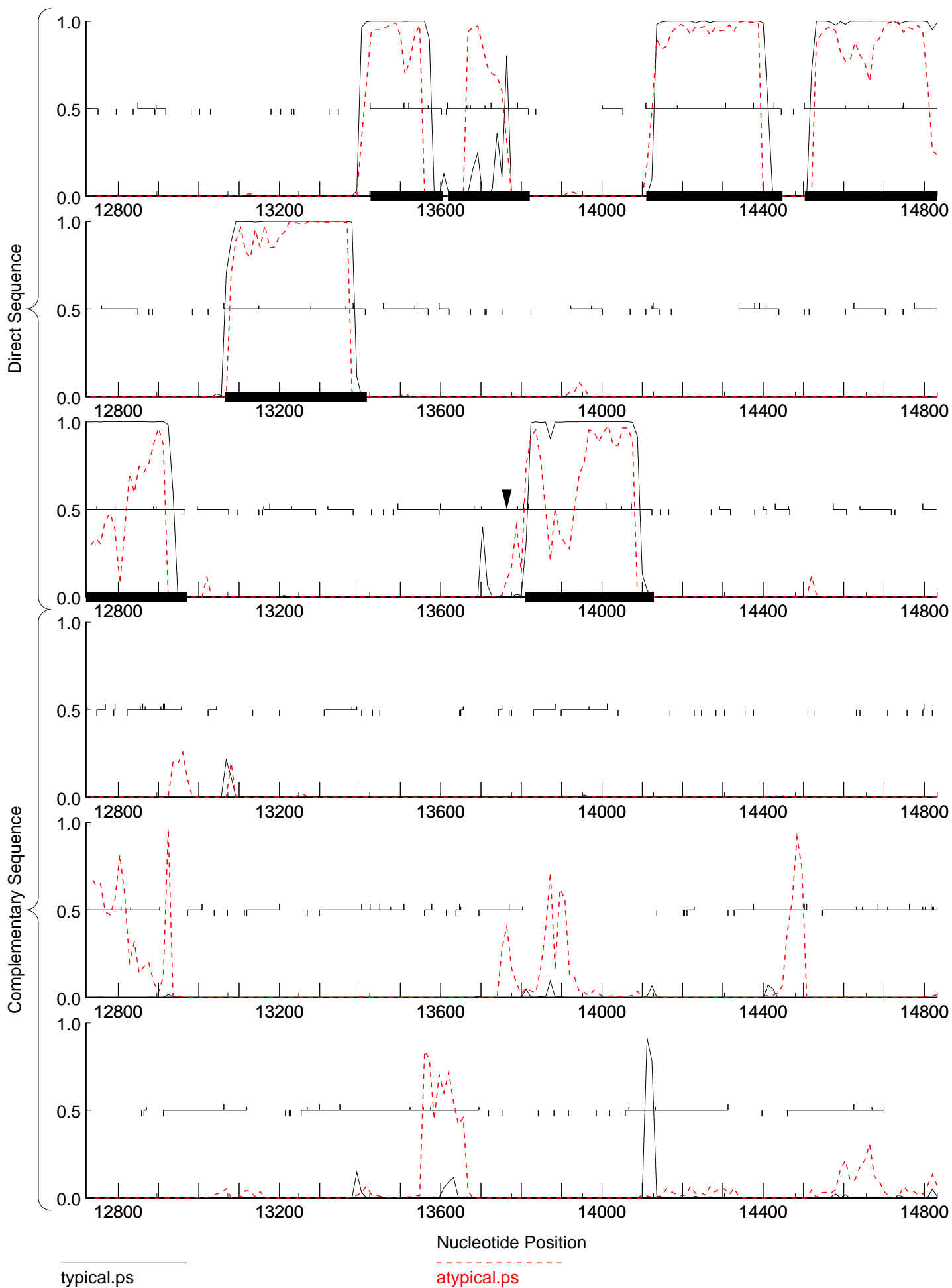
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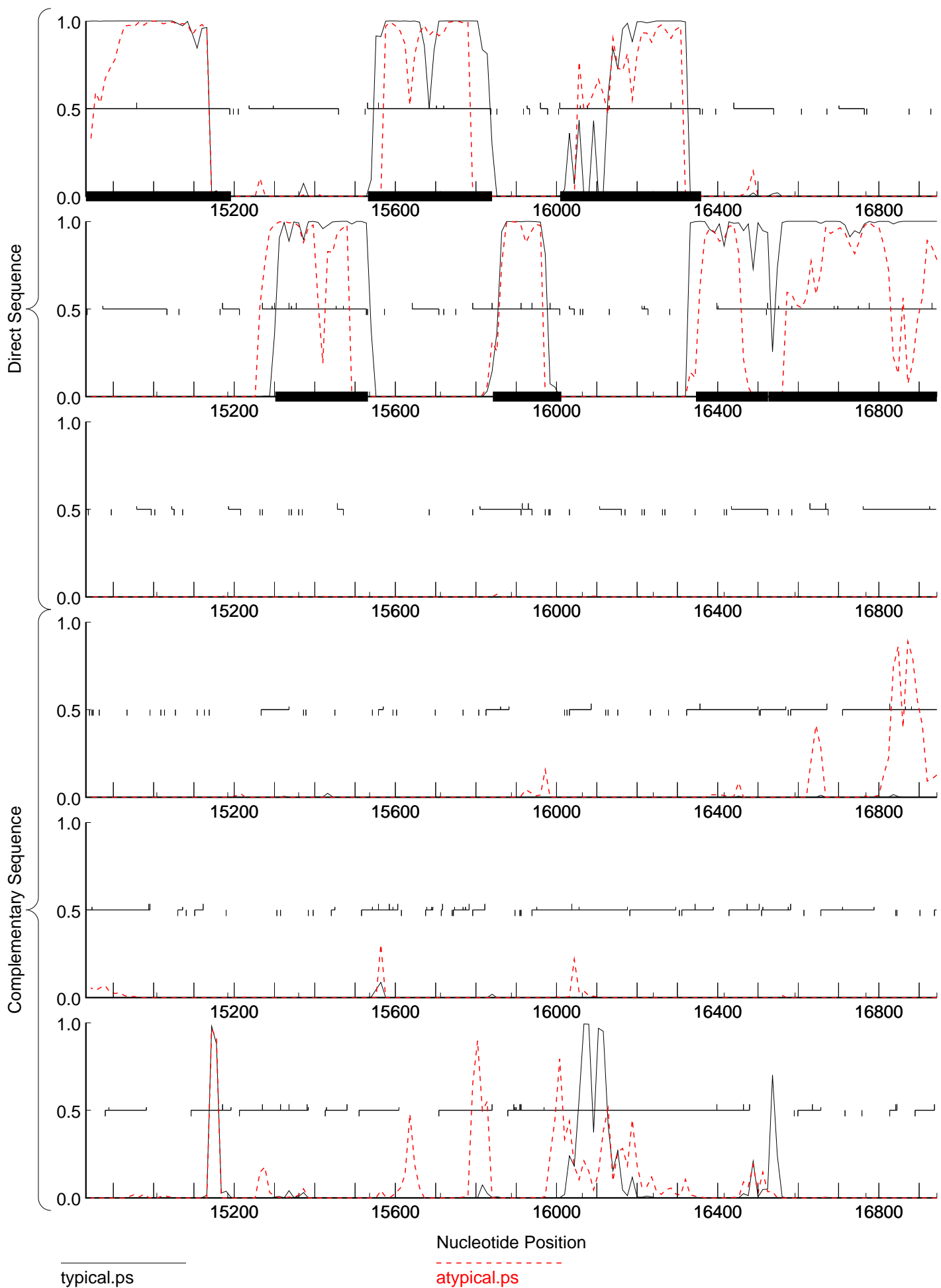




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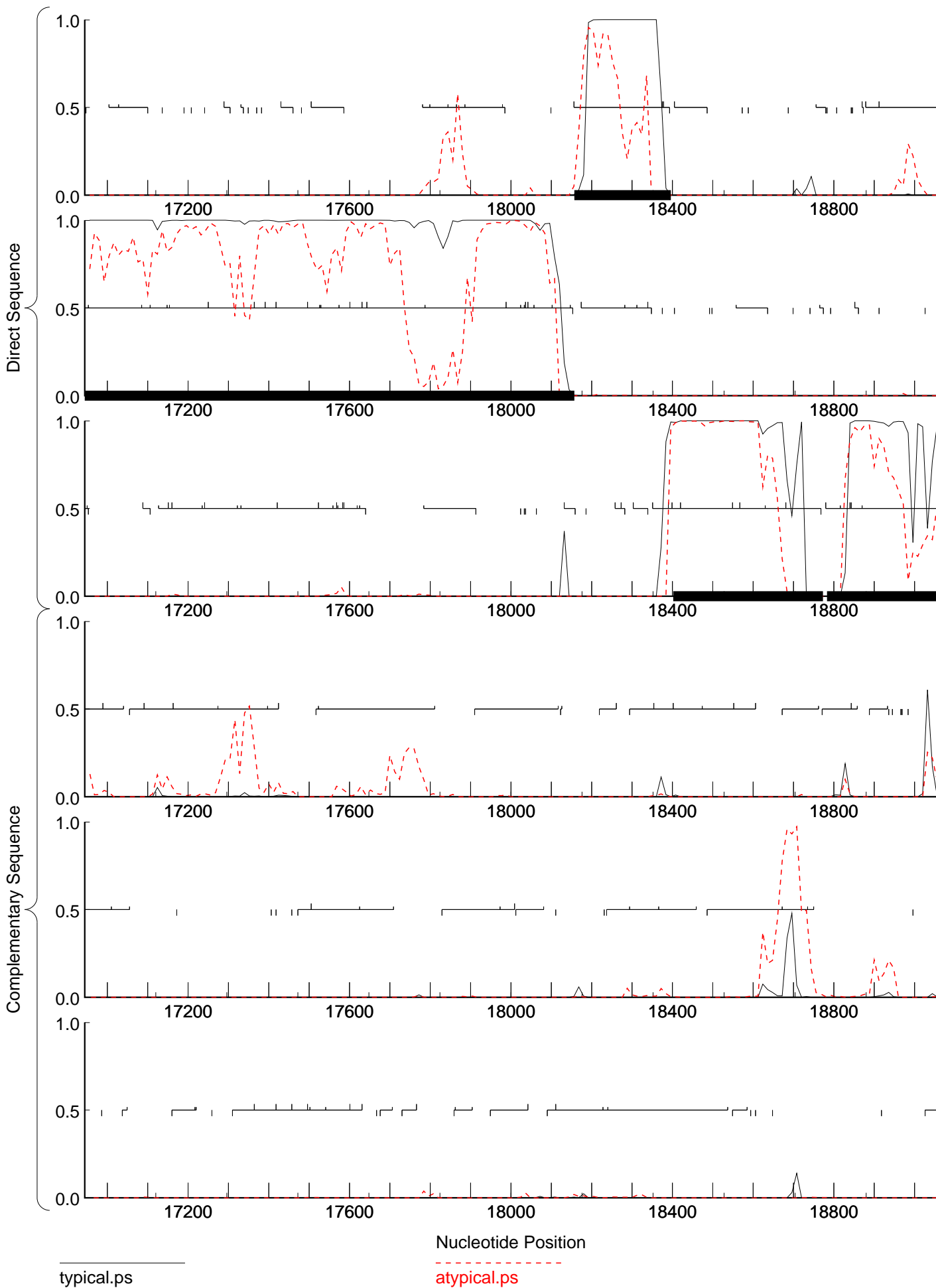
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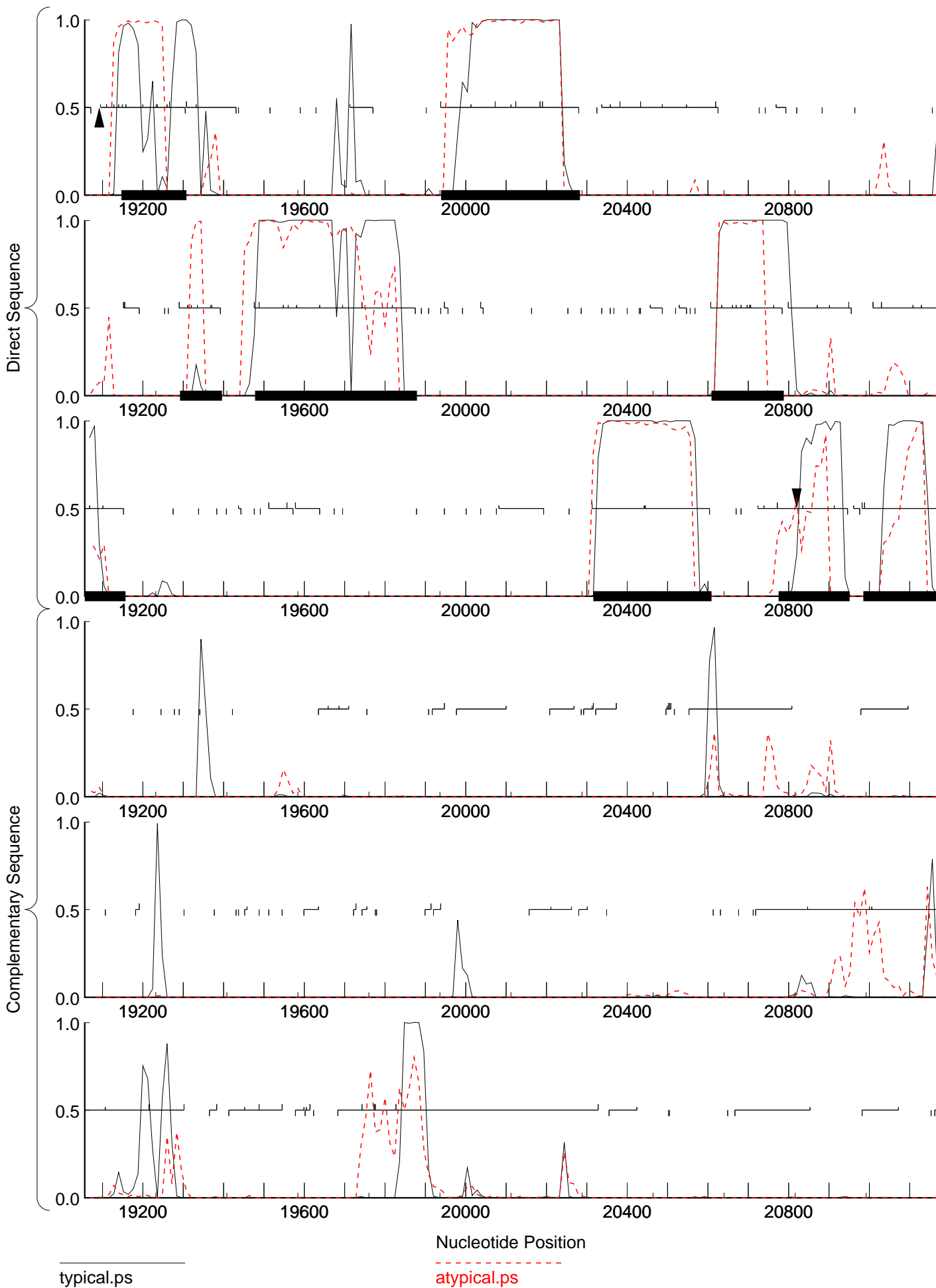
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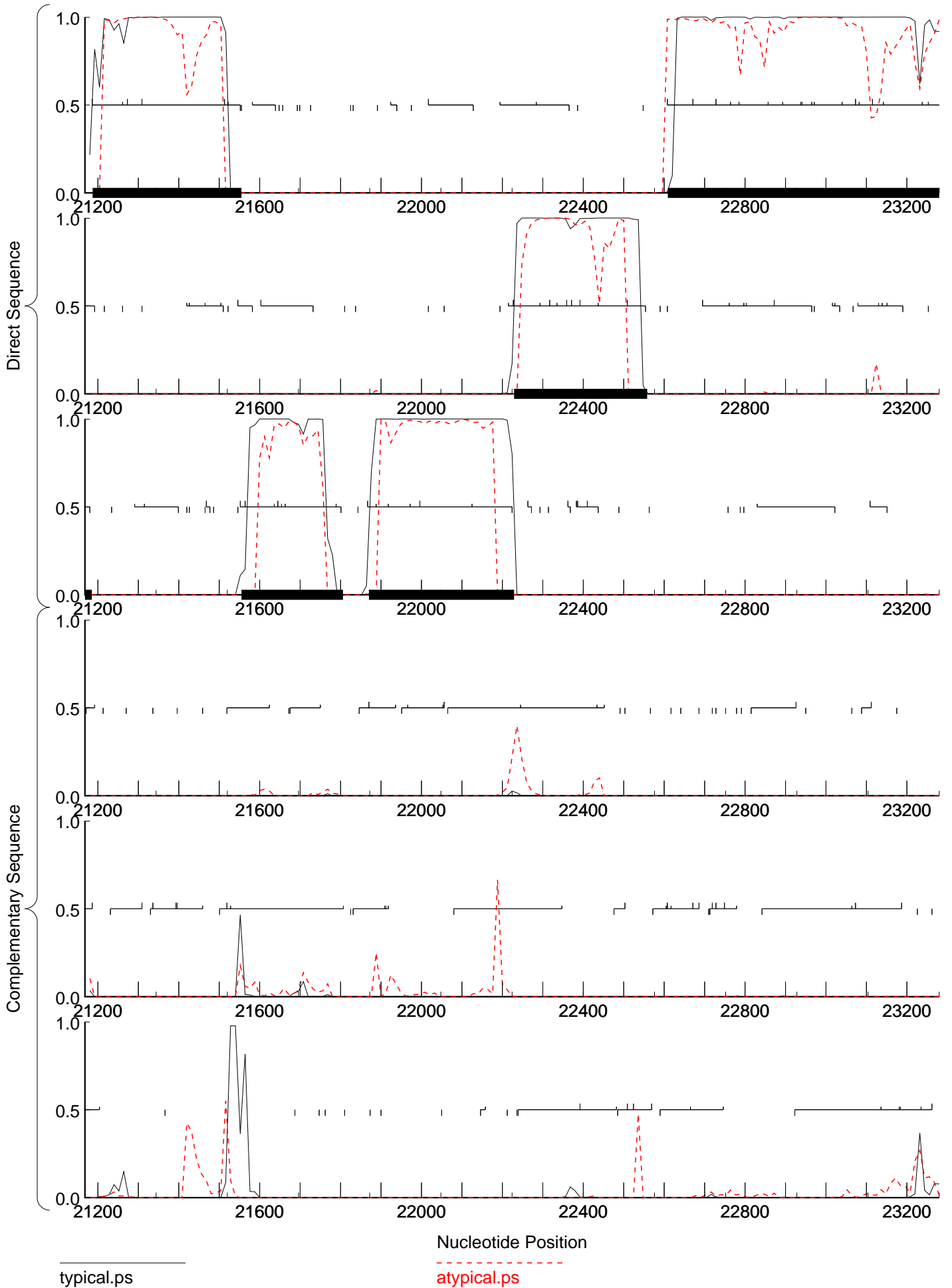
Nucleotide Position

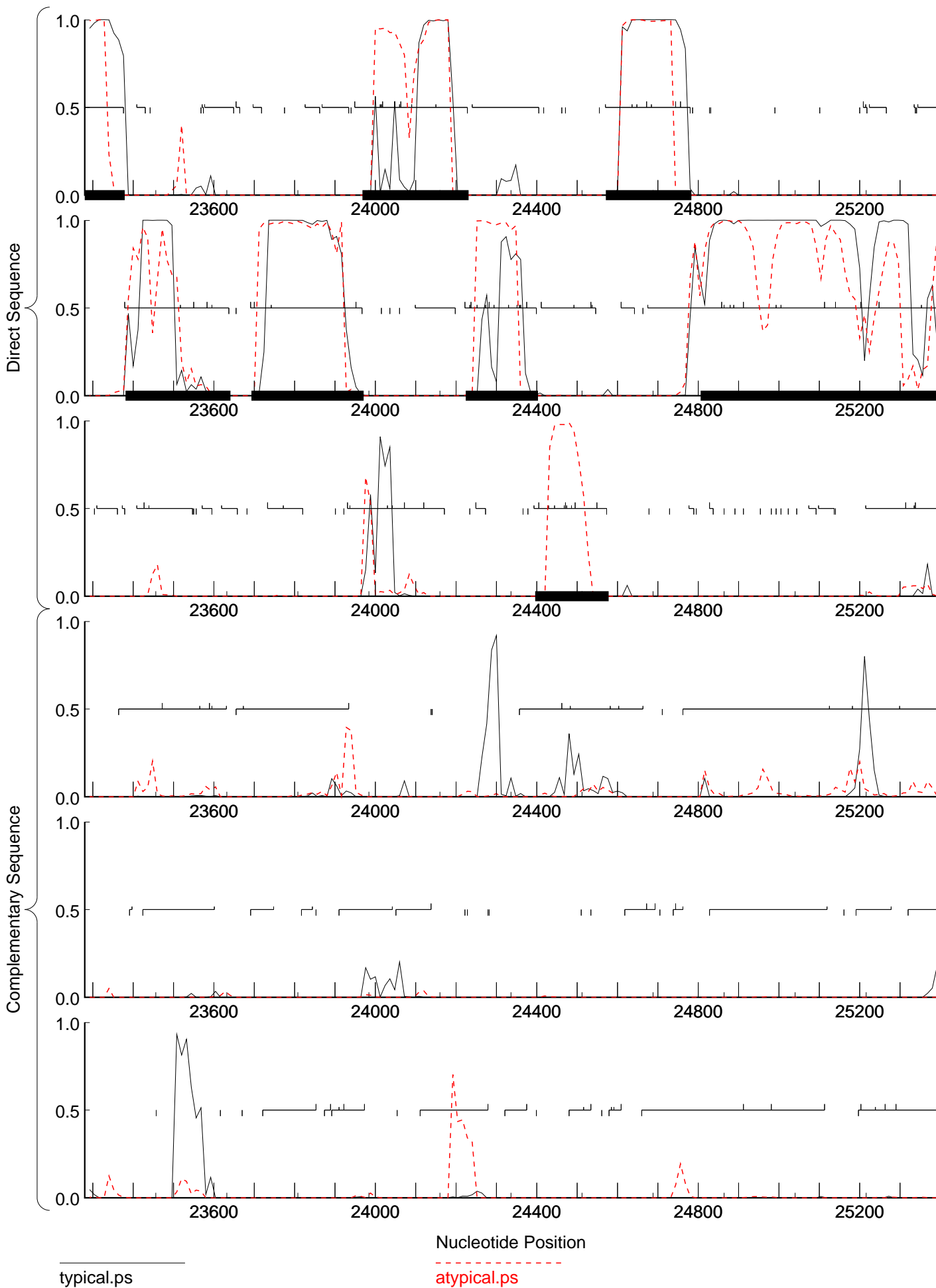
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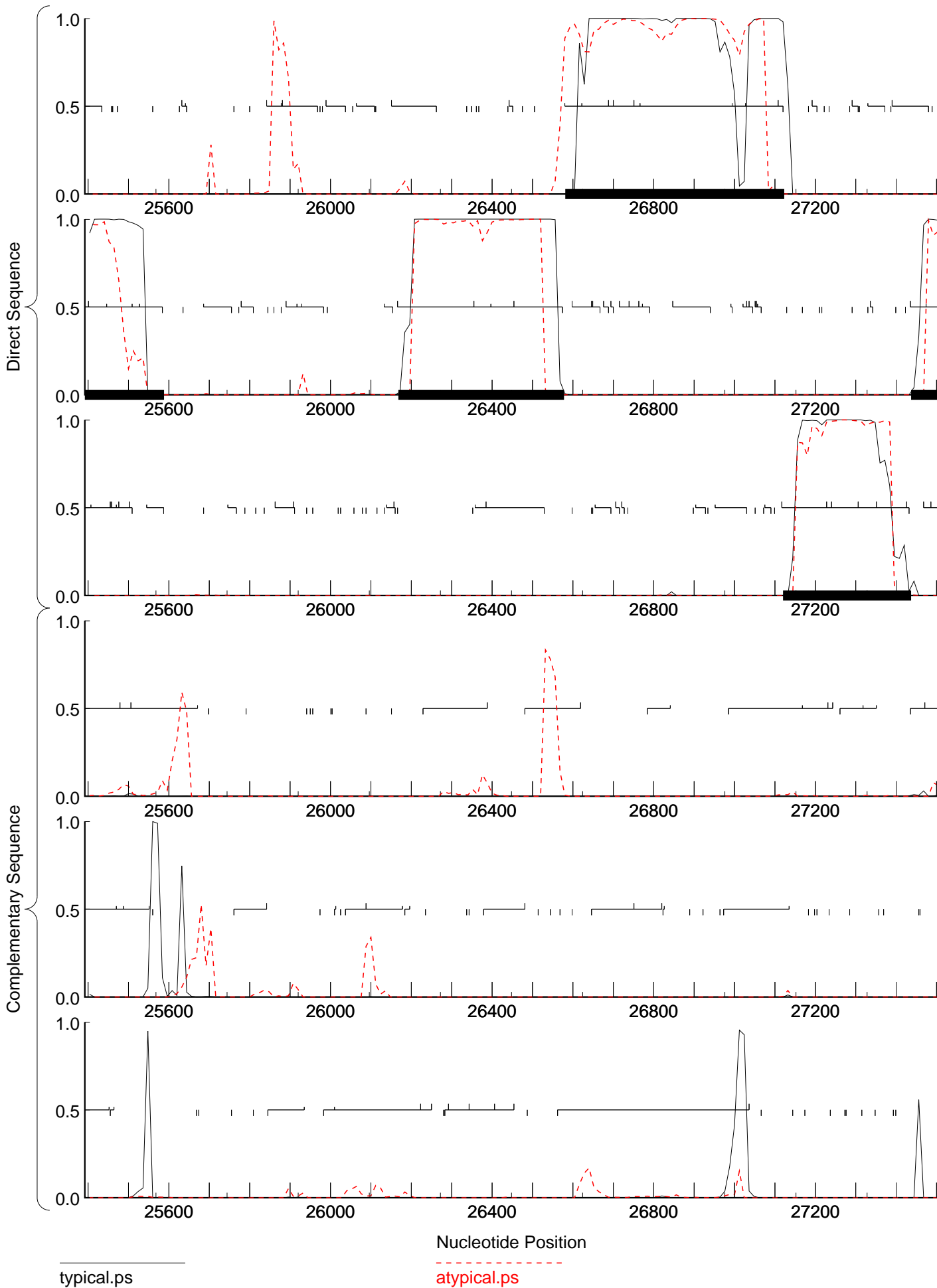


typical.ps

atypical.ps

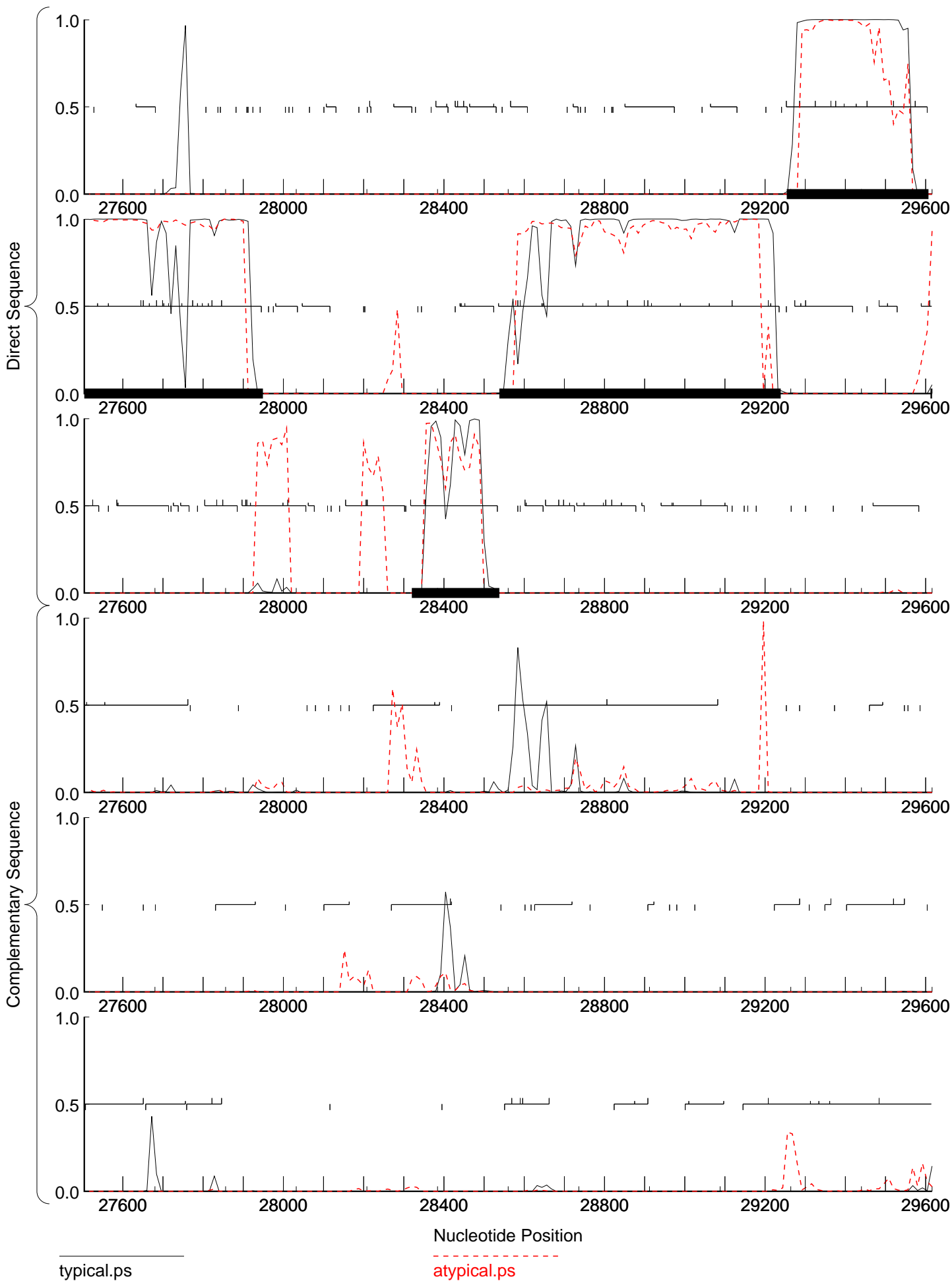


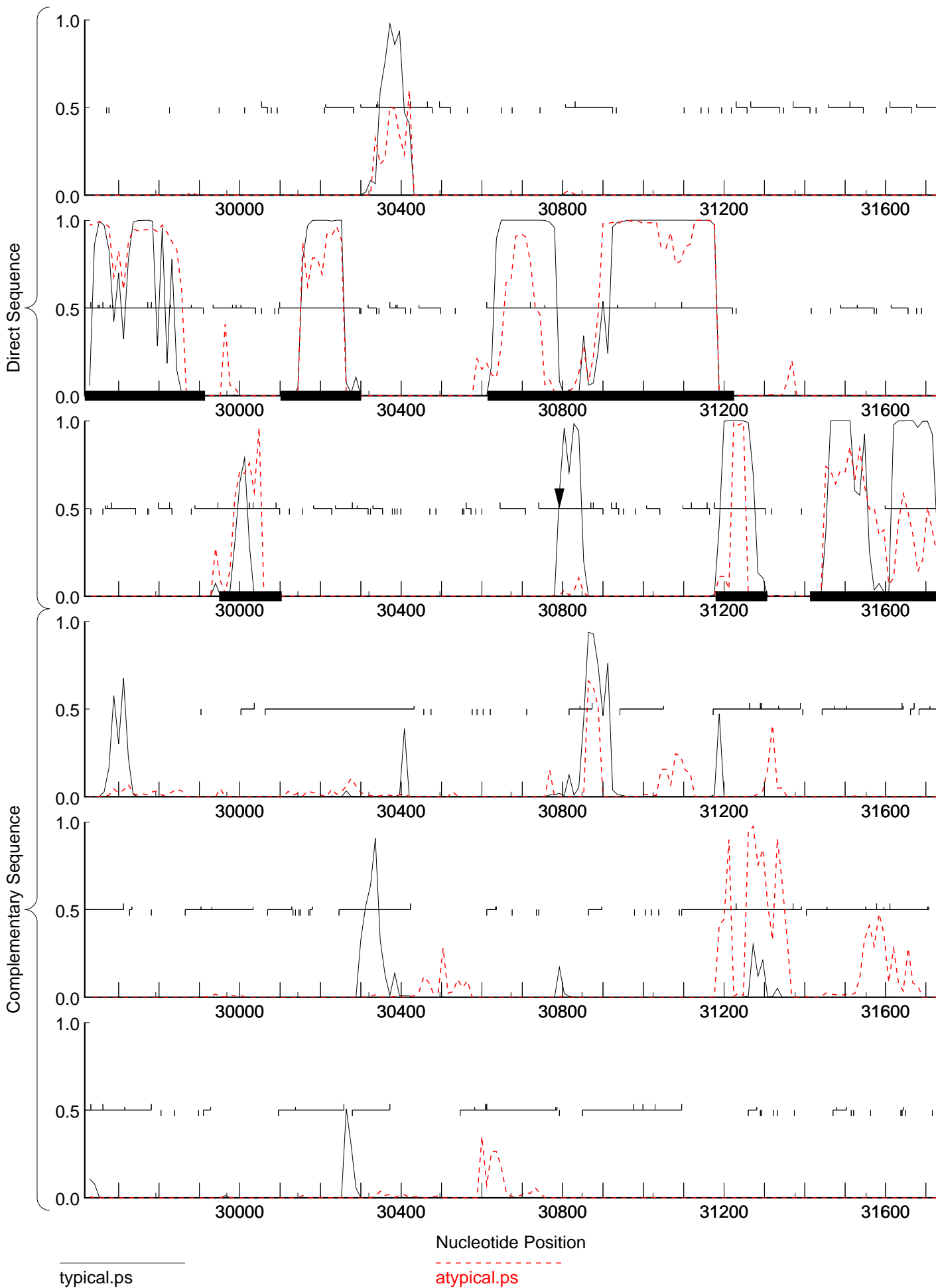


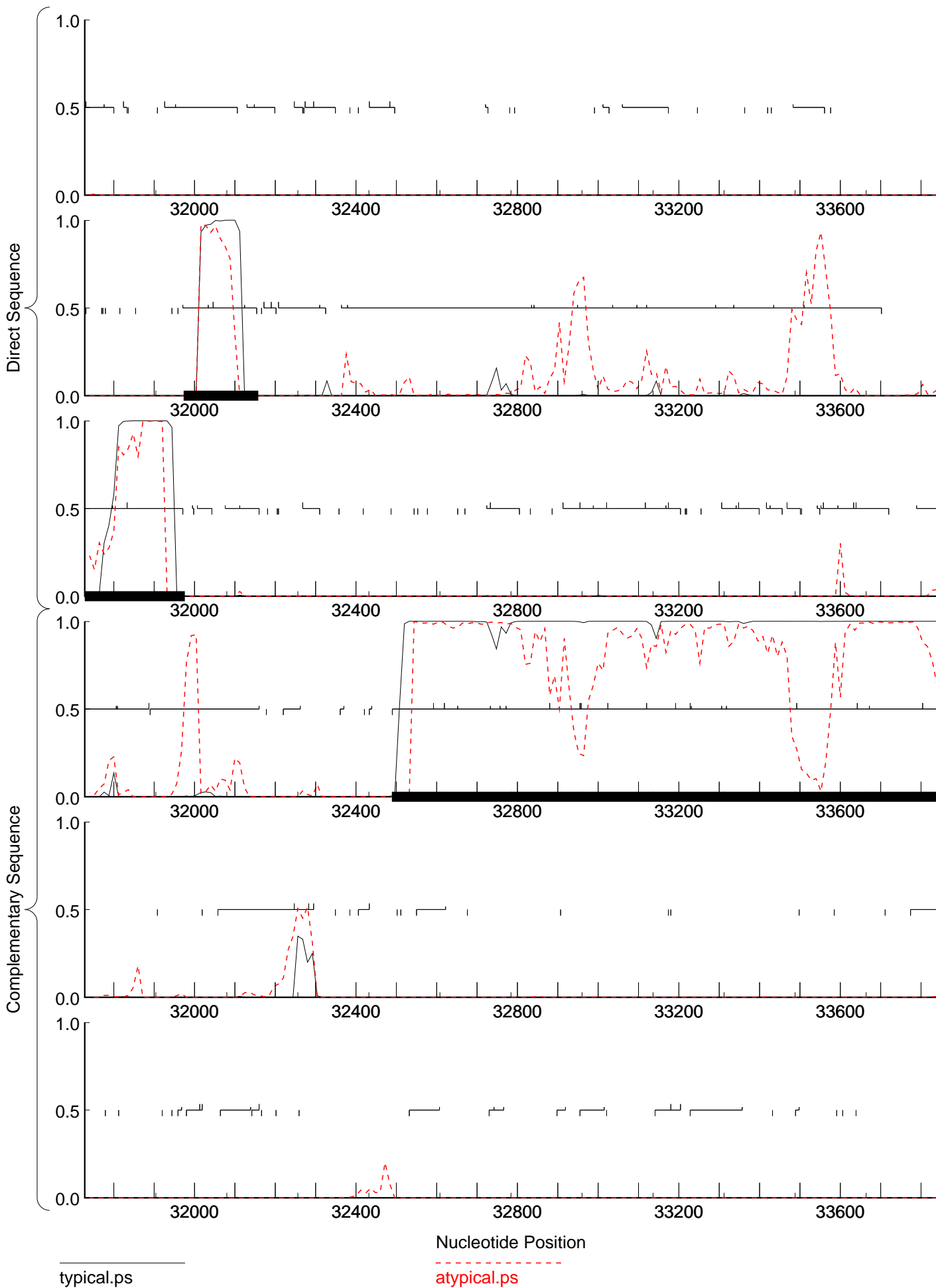


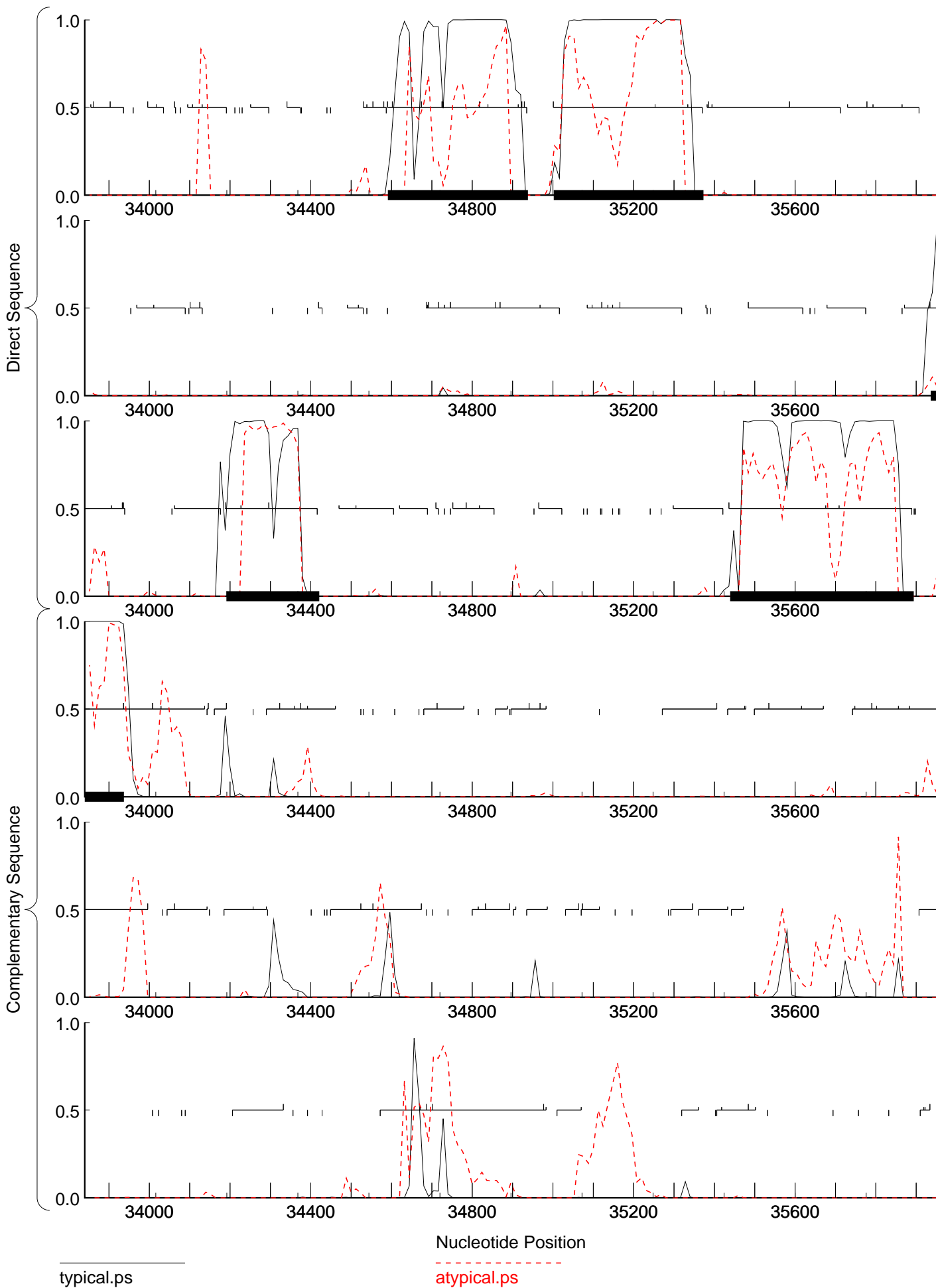
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atypical.ps



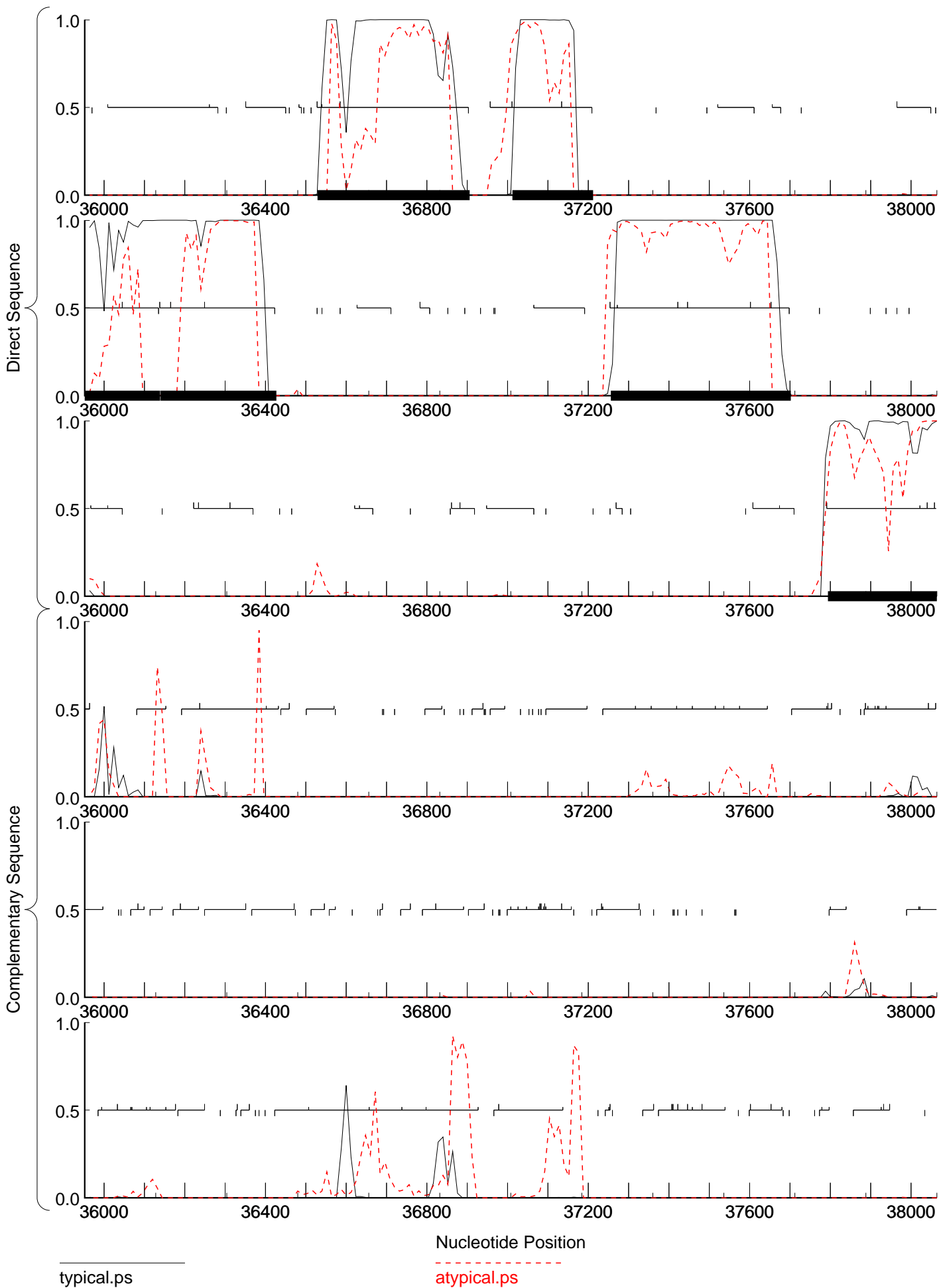


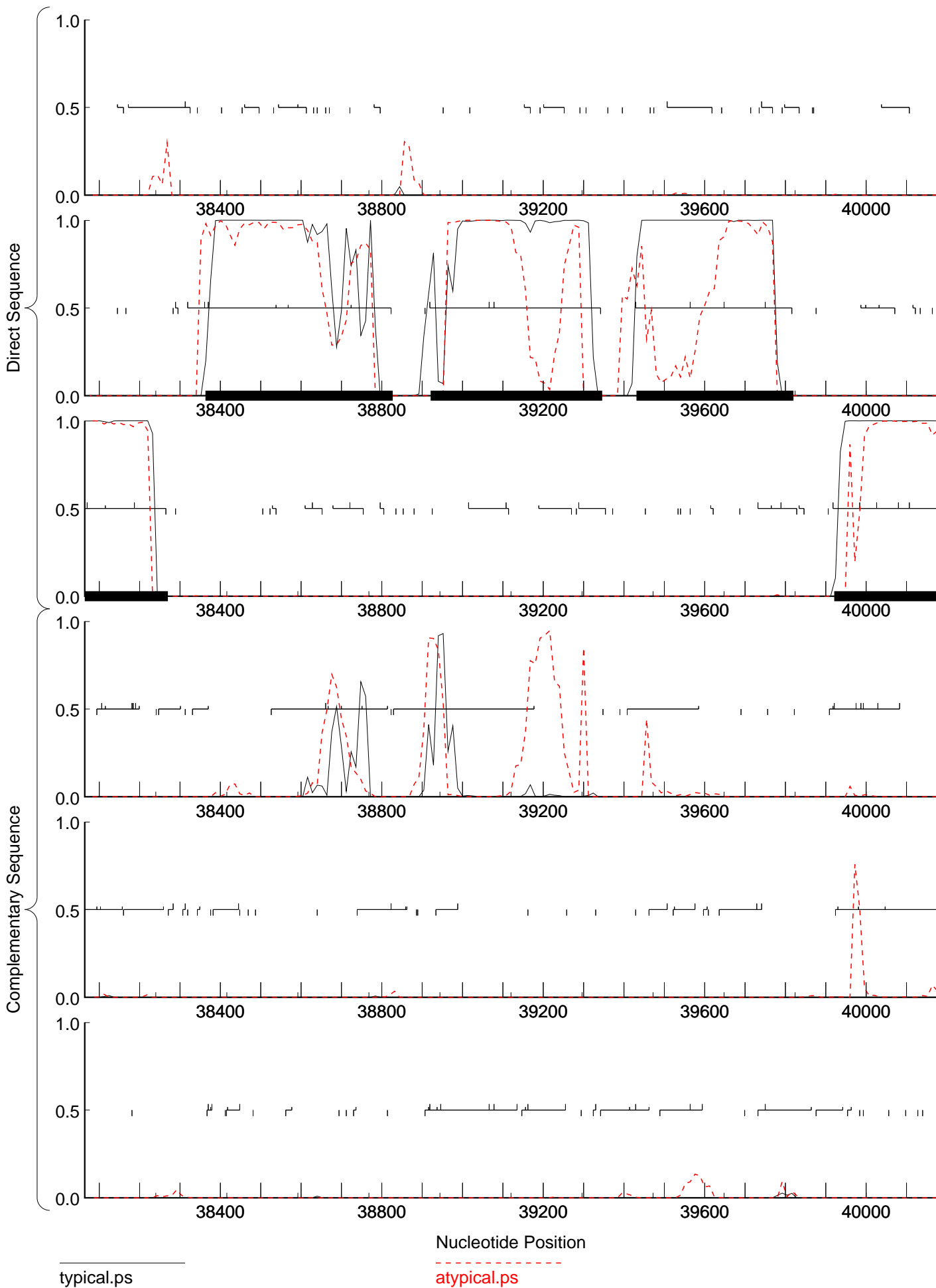


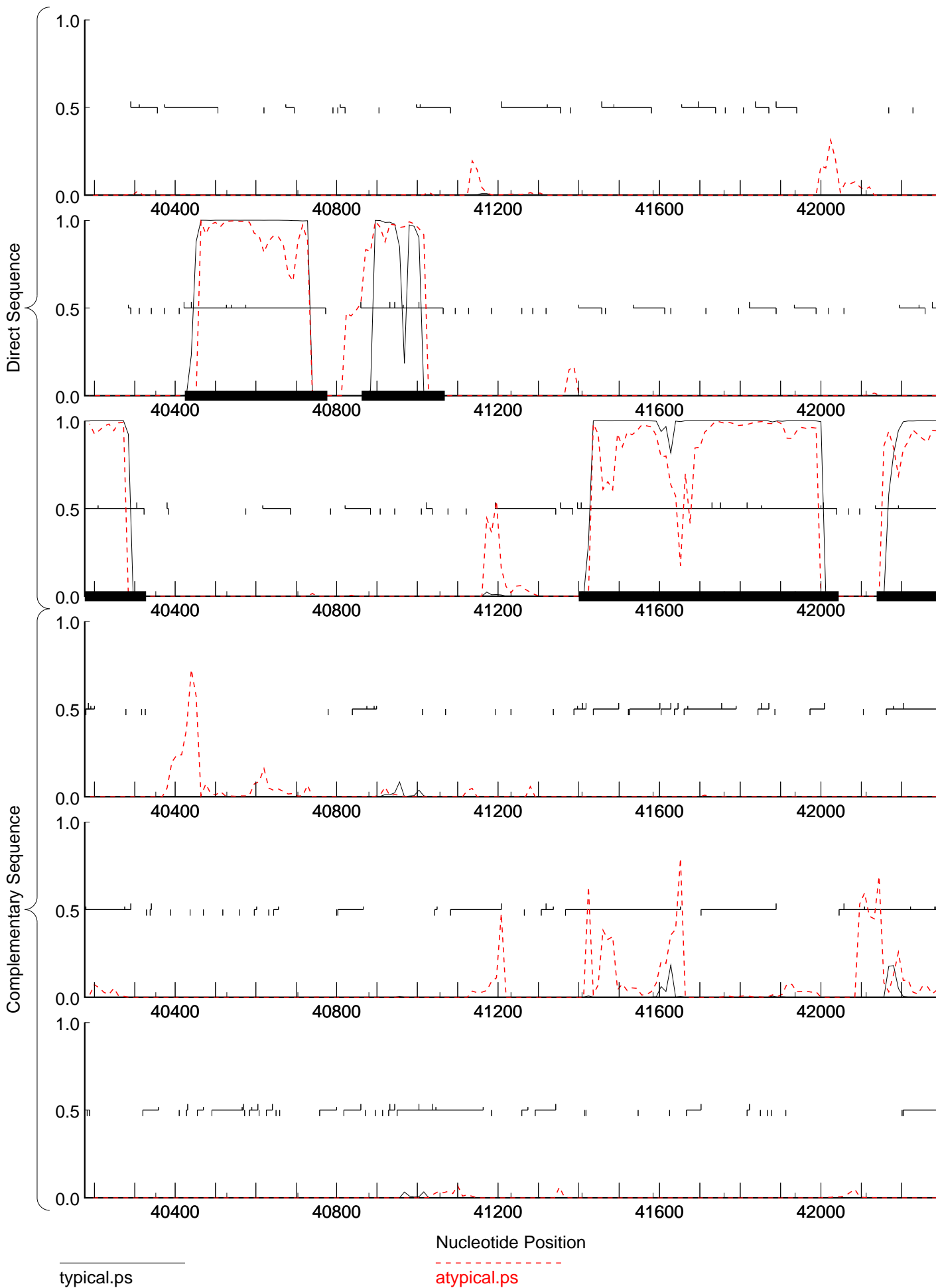


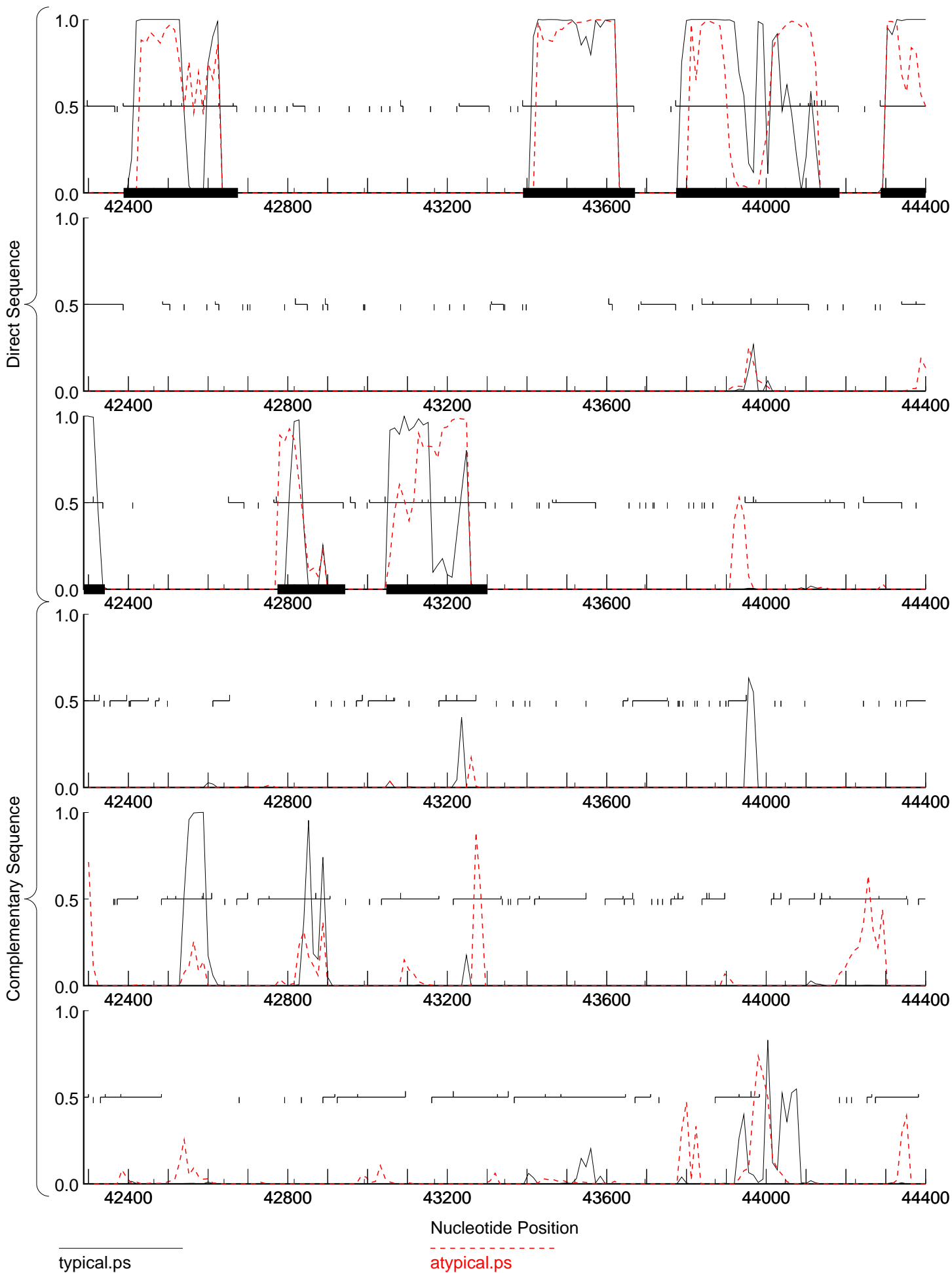
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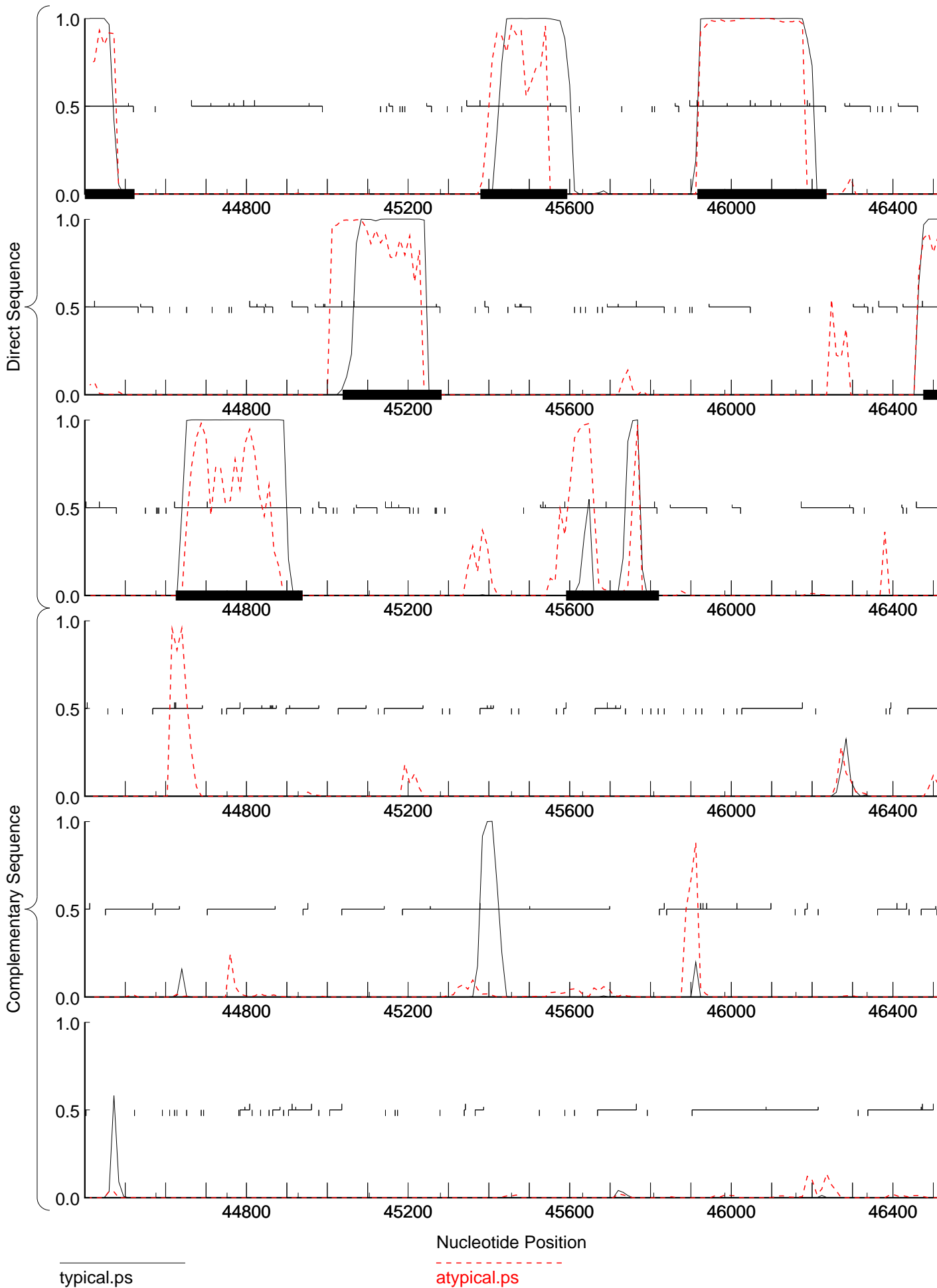






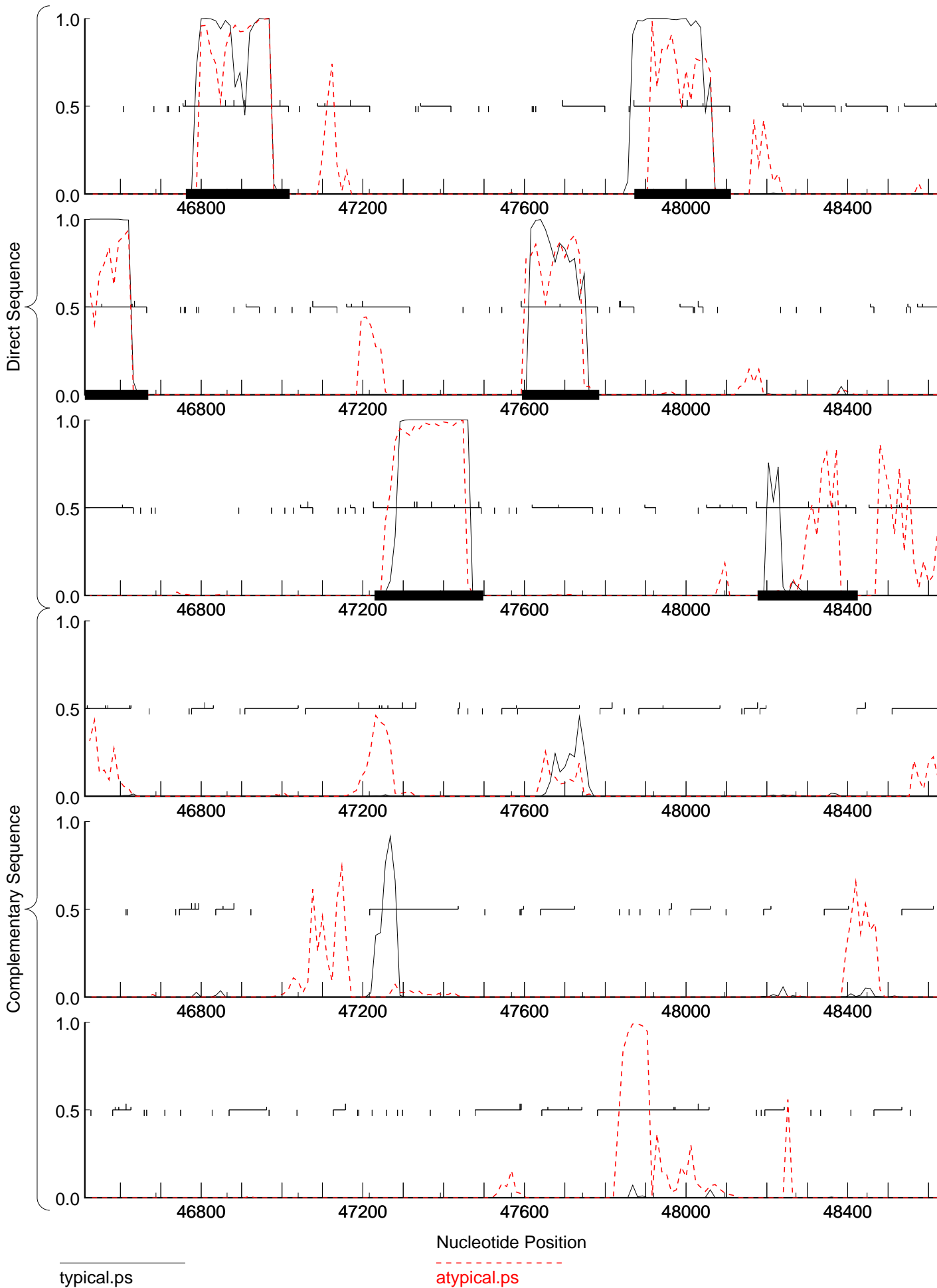
typical.ps

atypical.ps



typical.ps

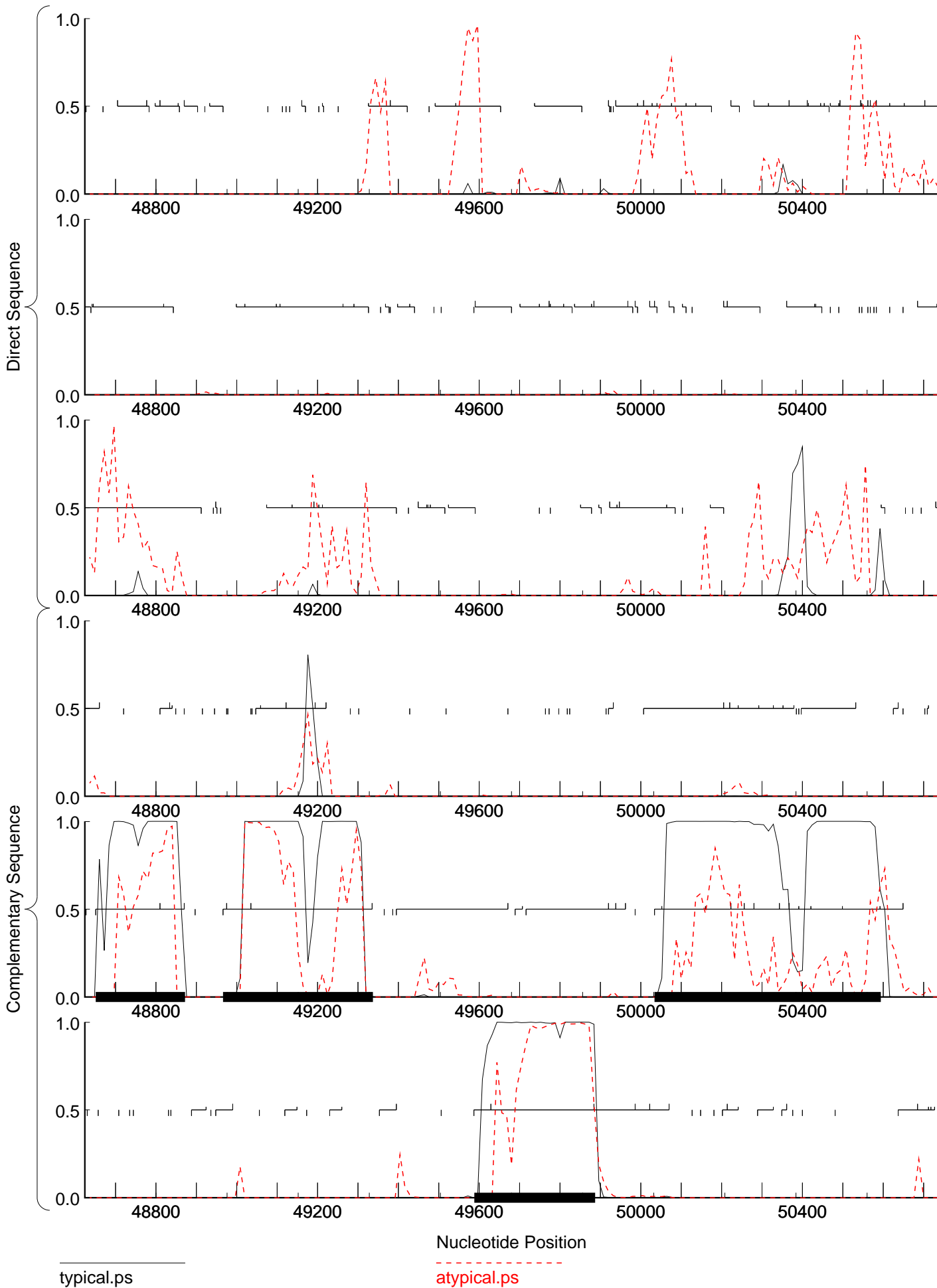
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typical.ps

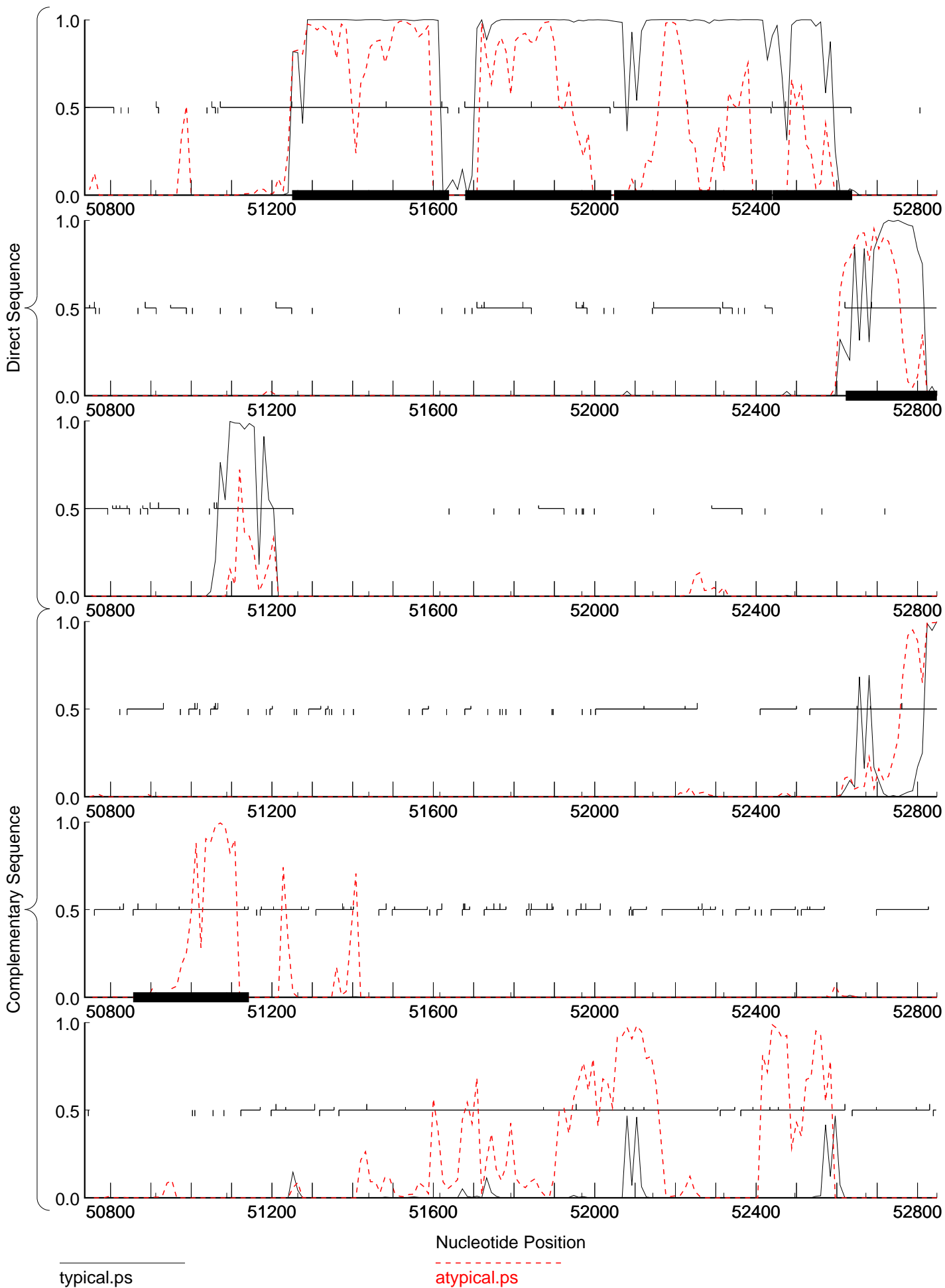
Nucleotide Position

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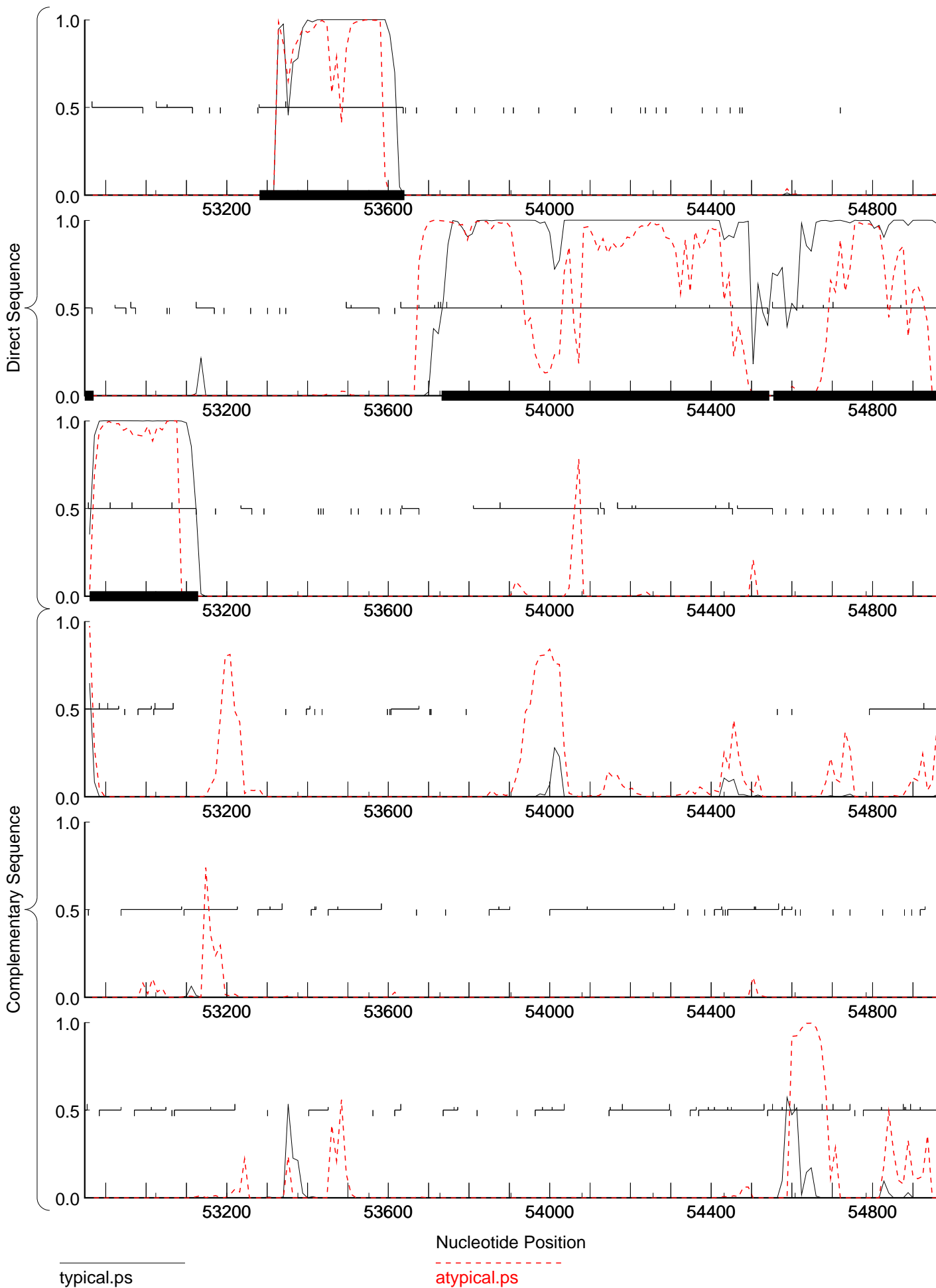
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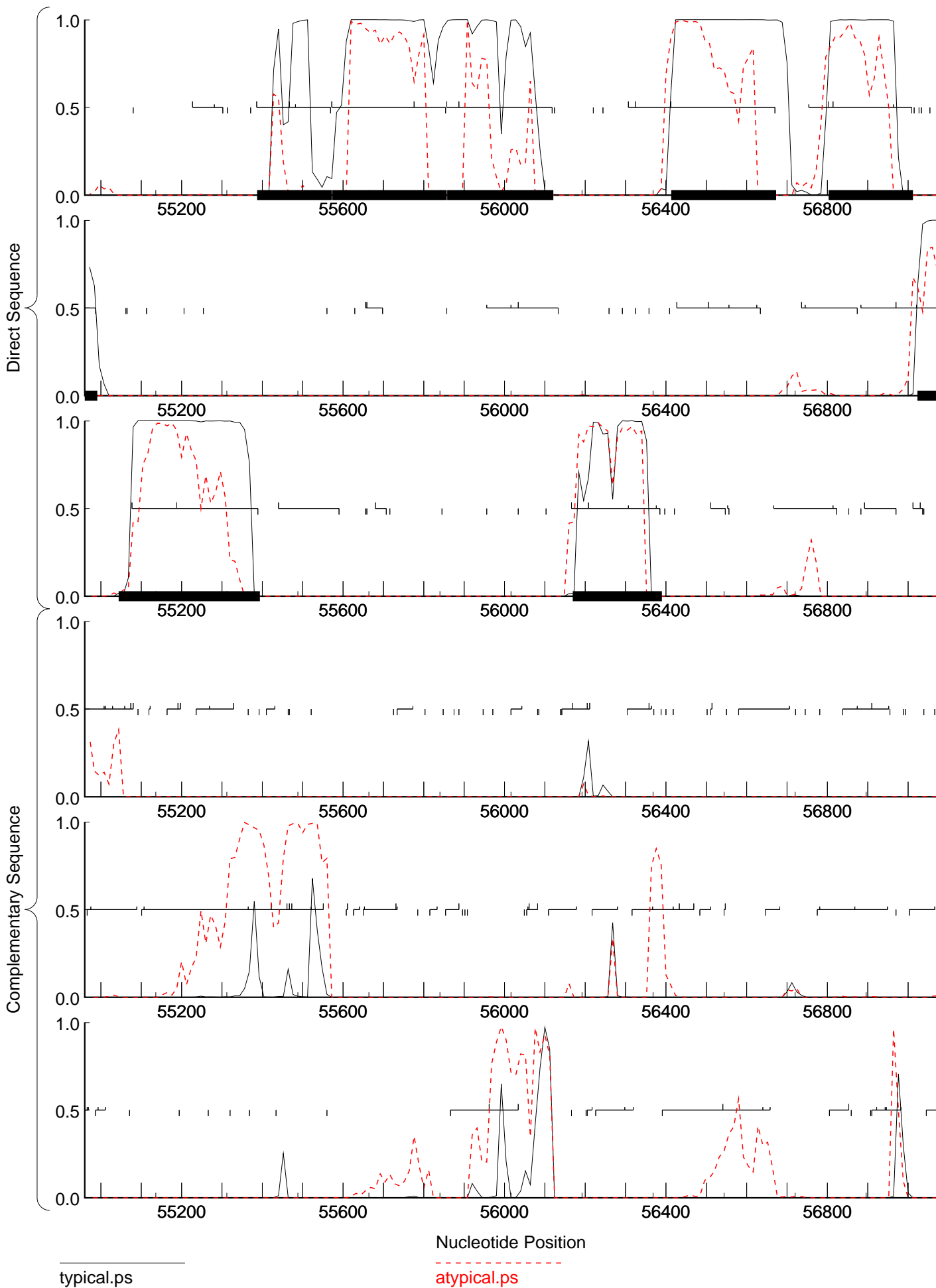
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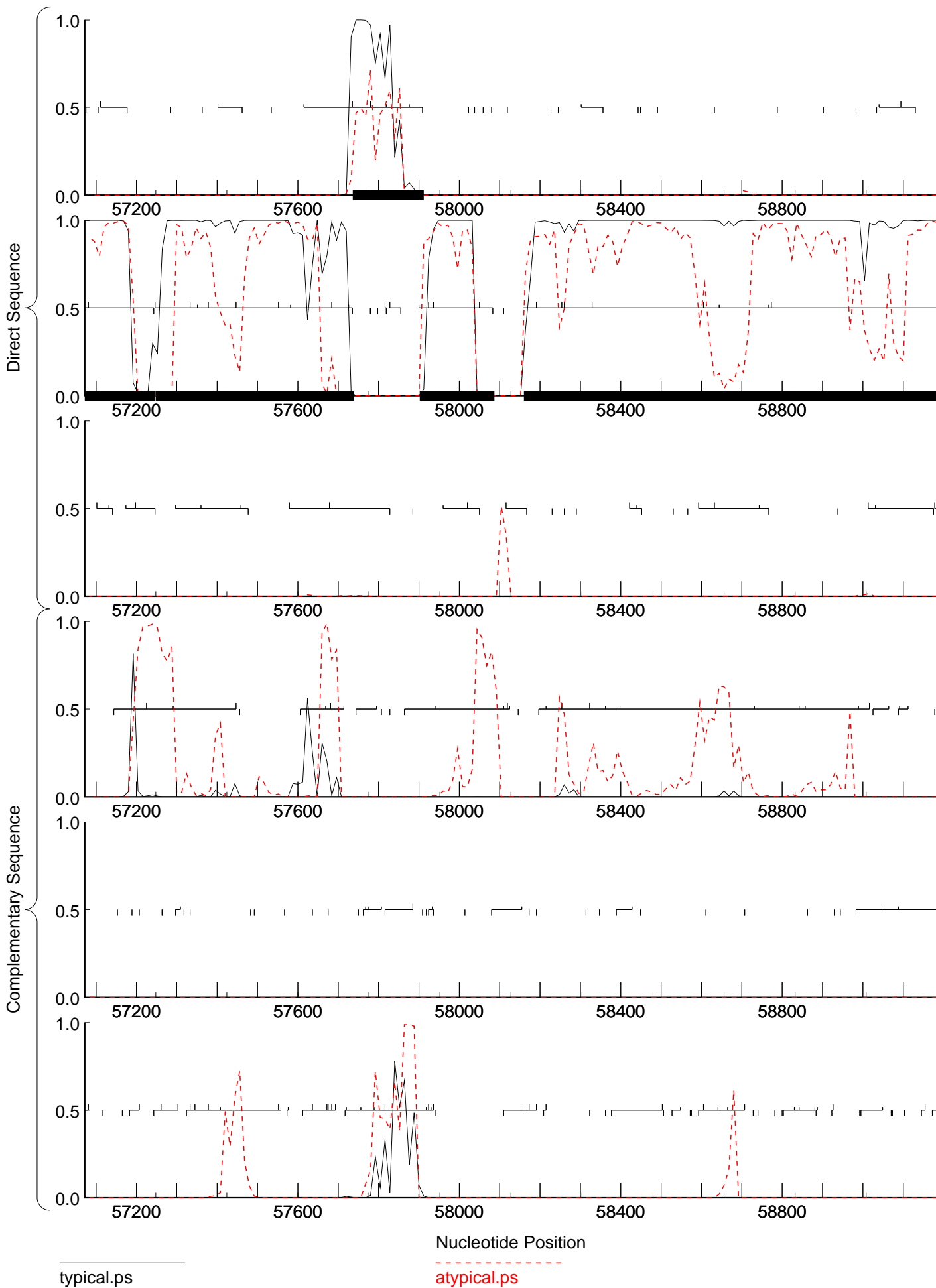


typical.ps

atypical.ps

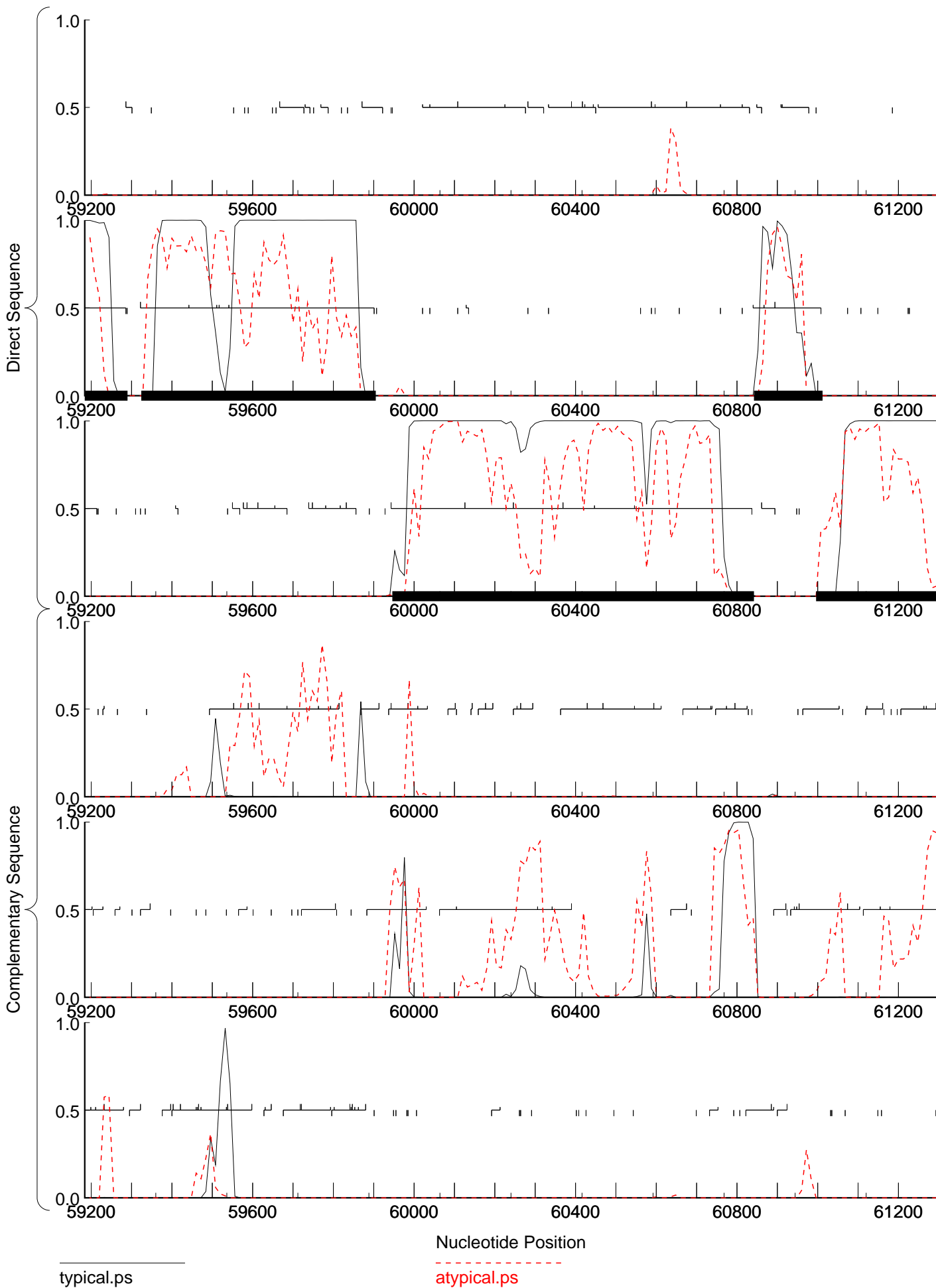






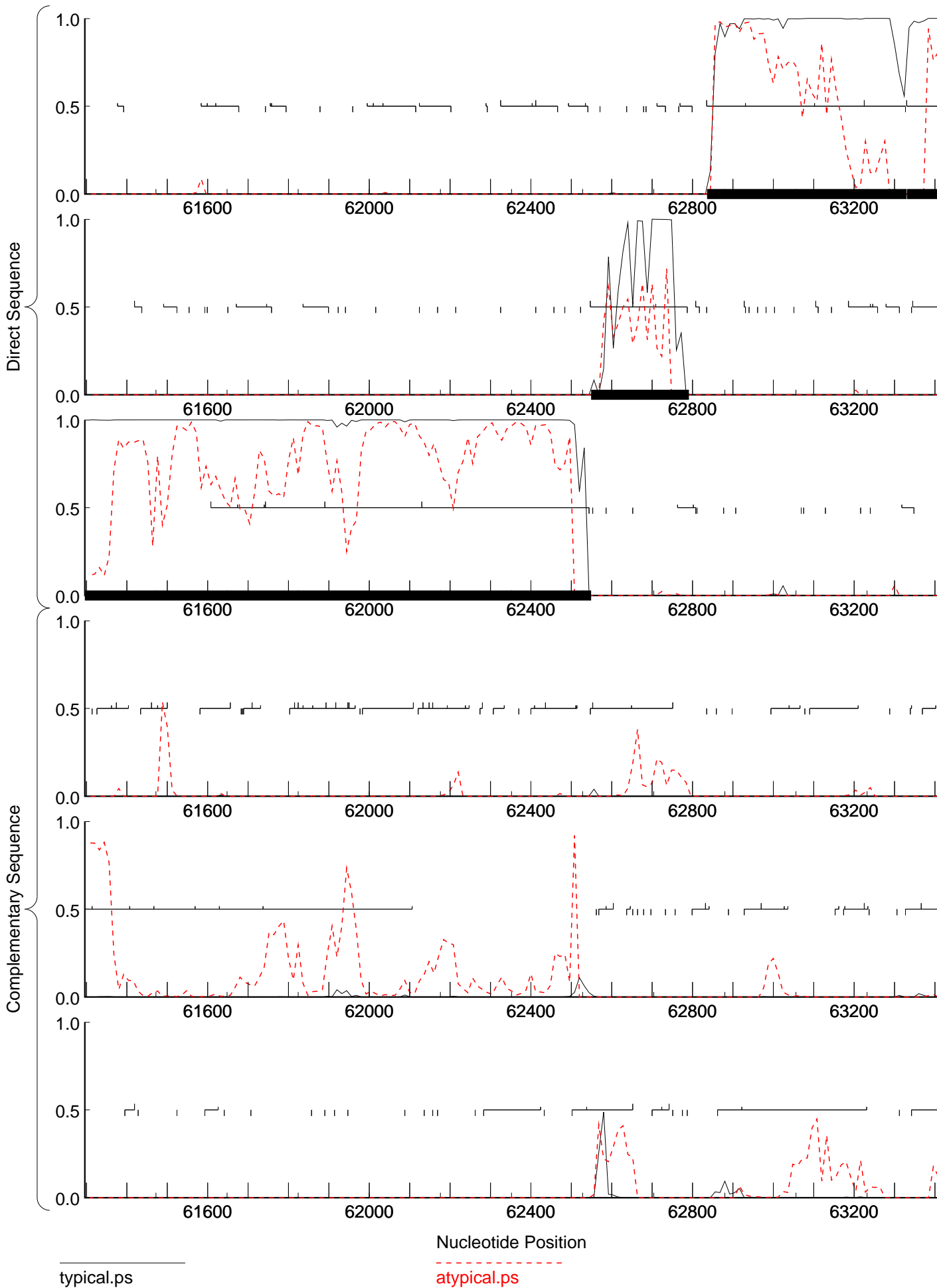
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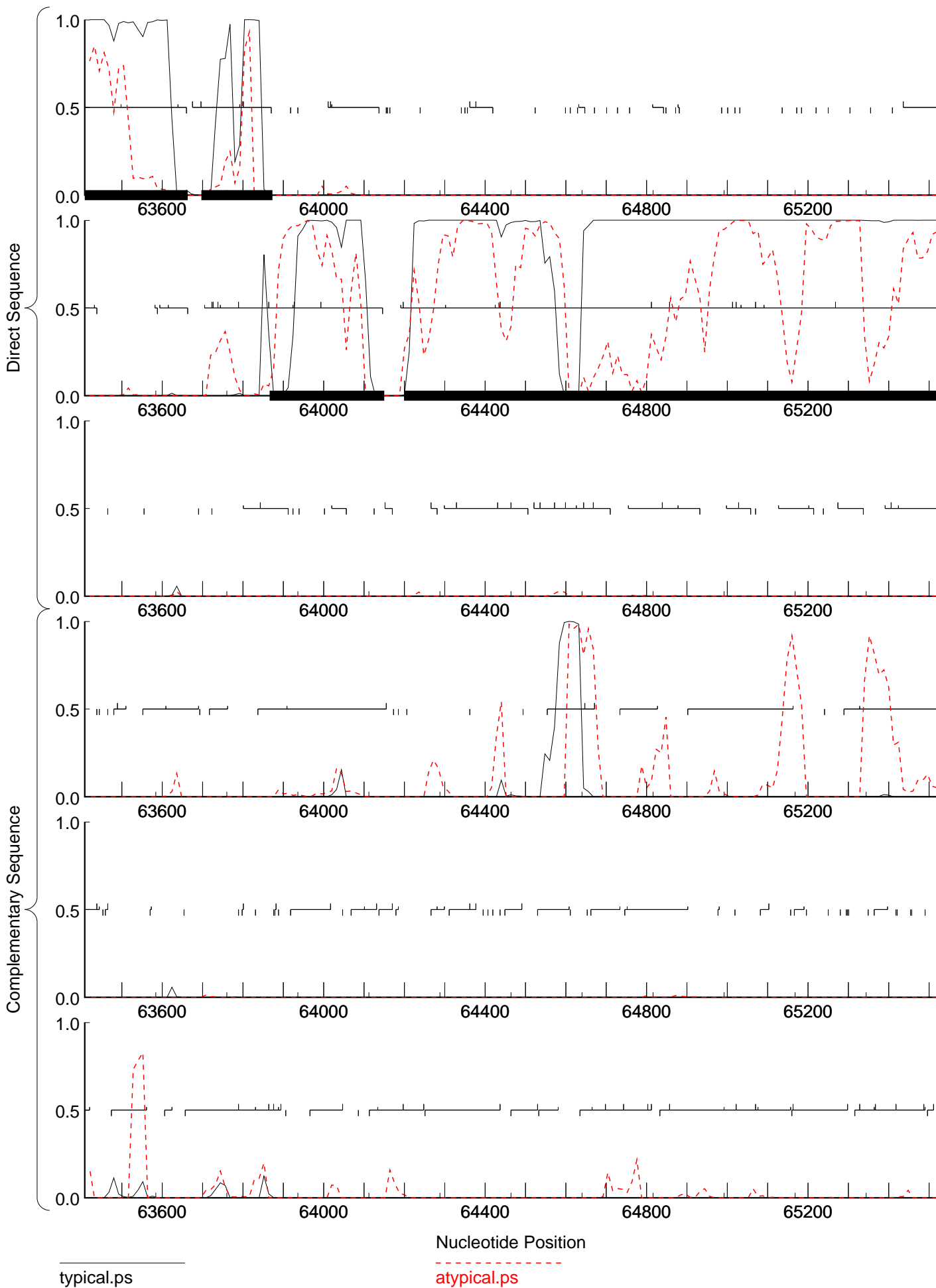
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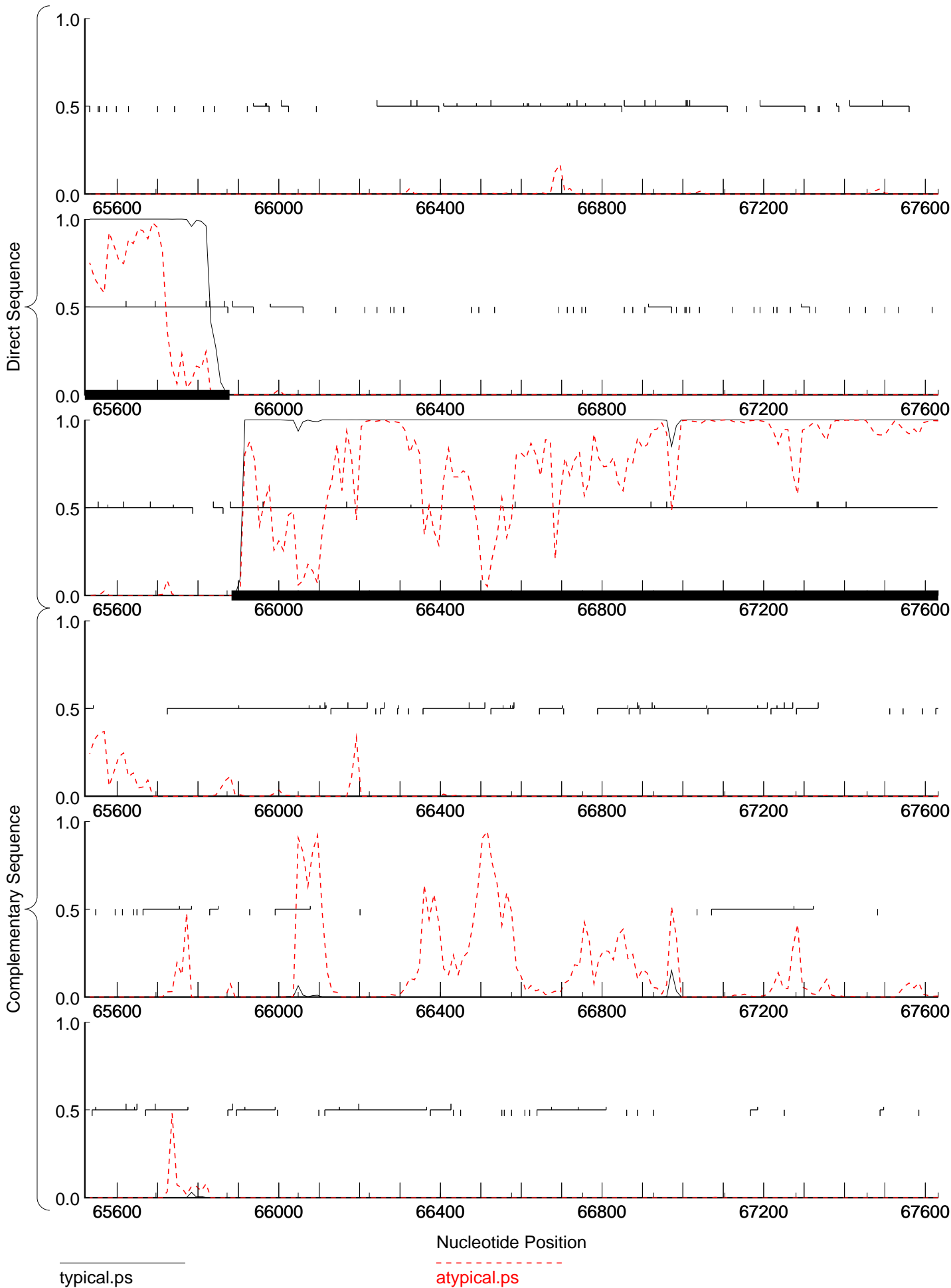
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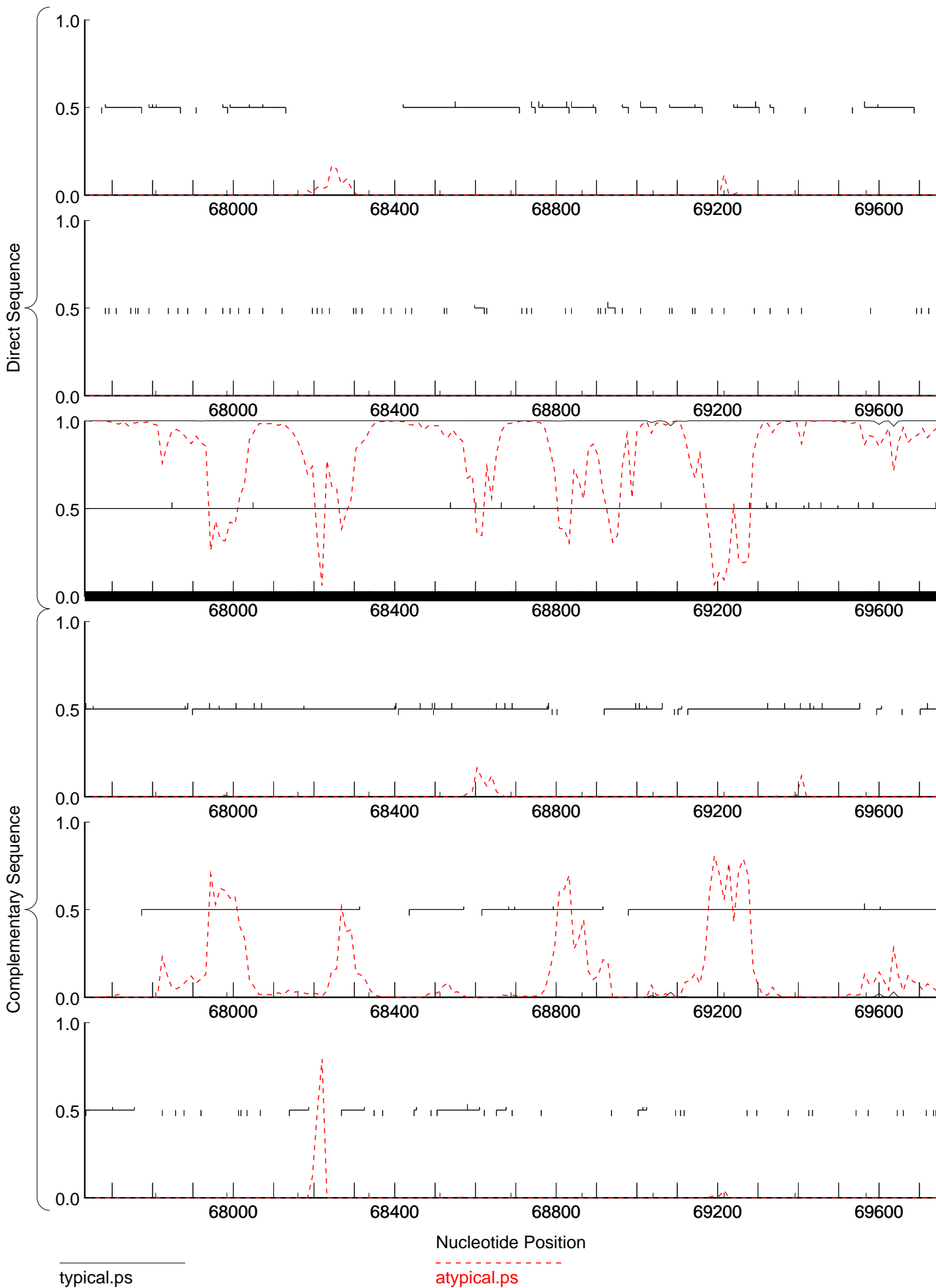
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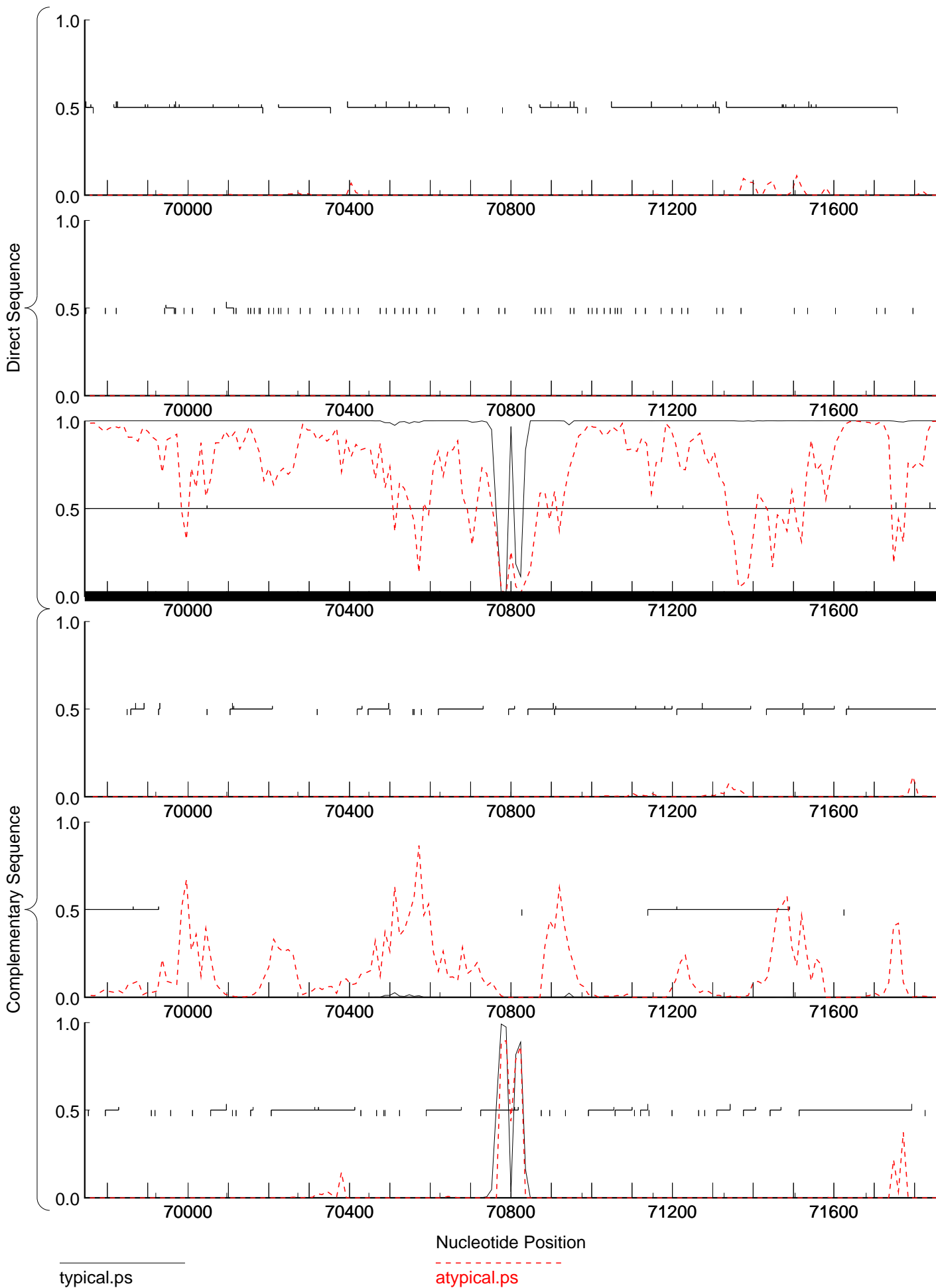
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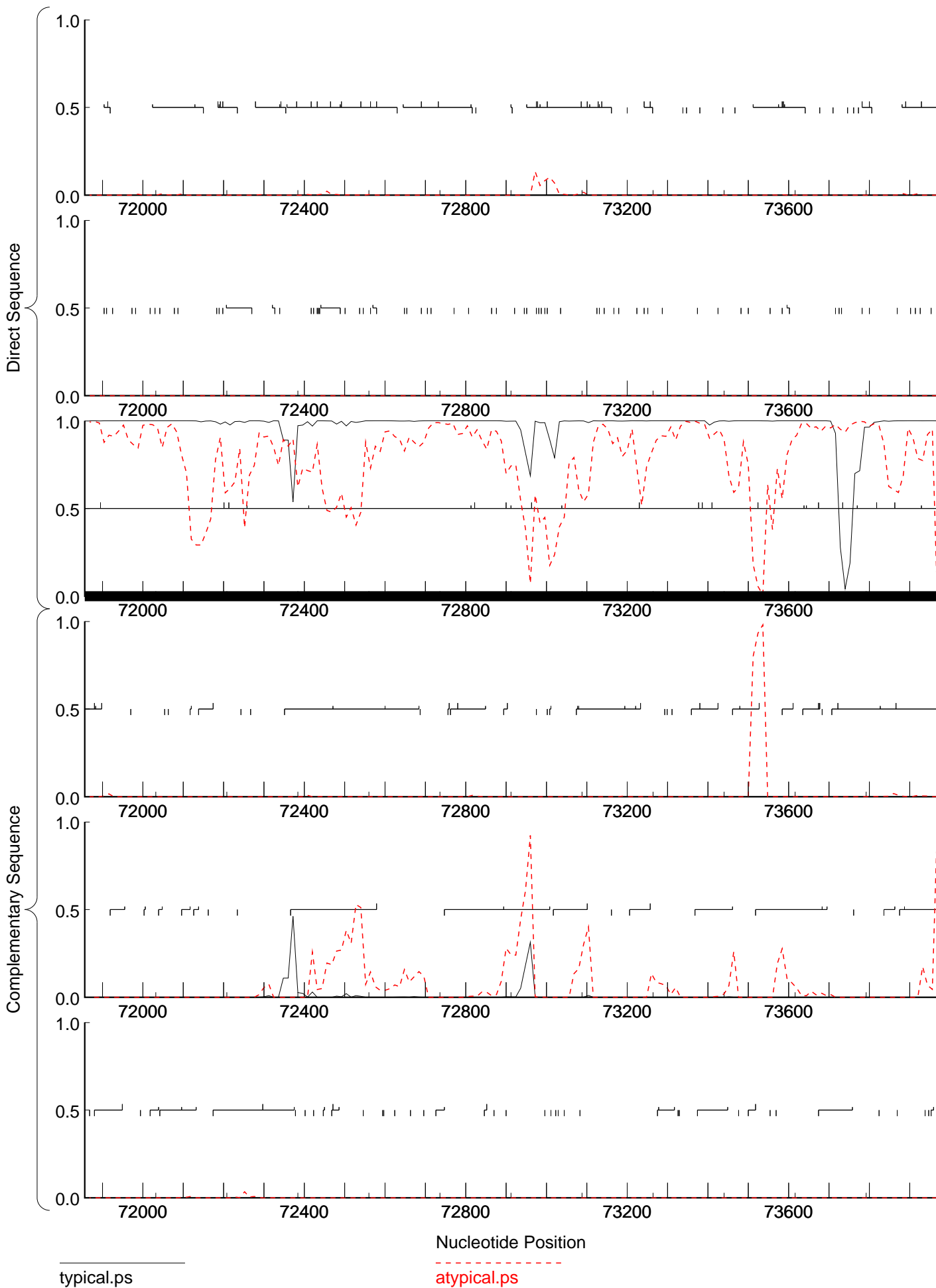
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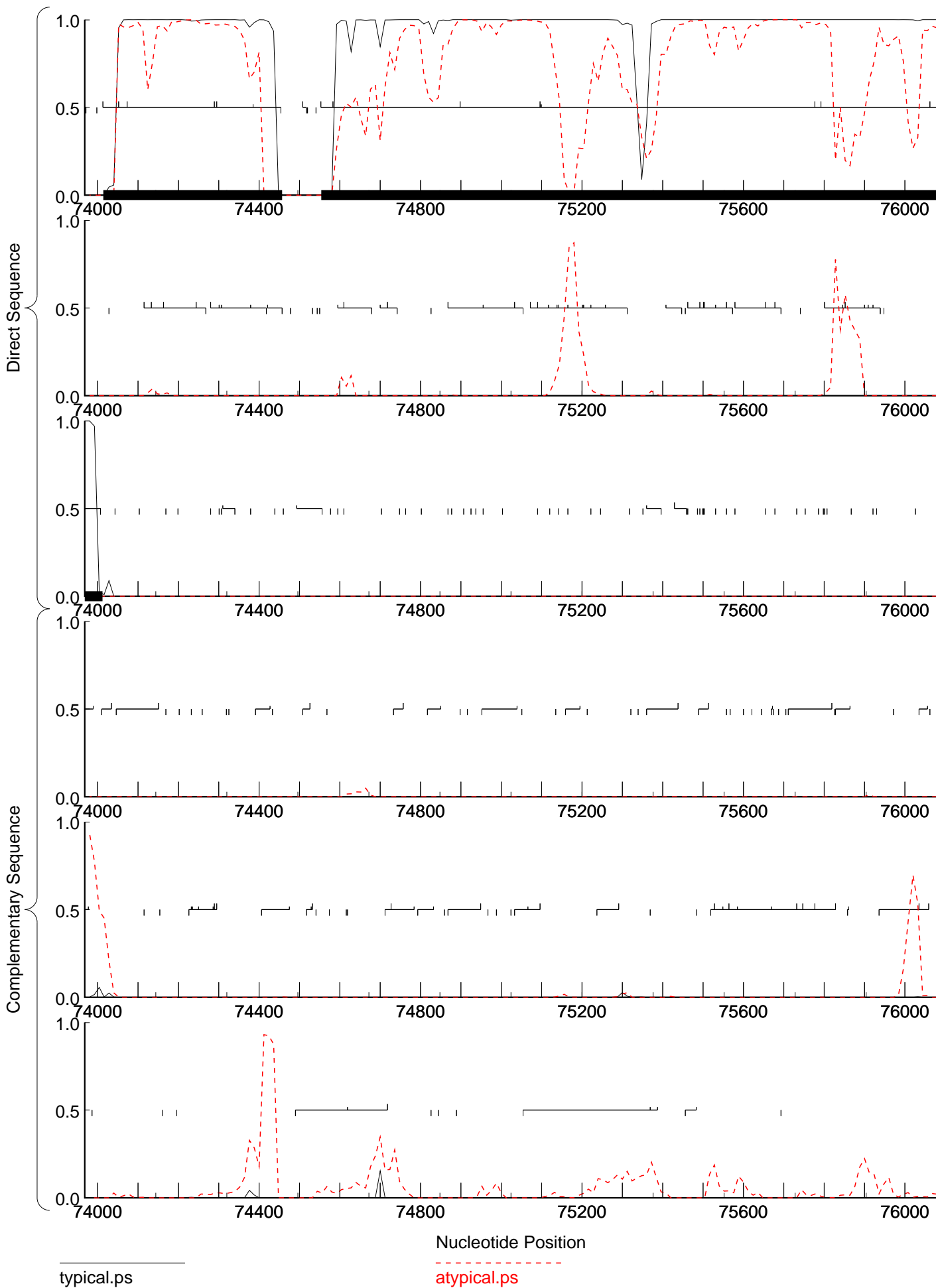
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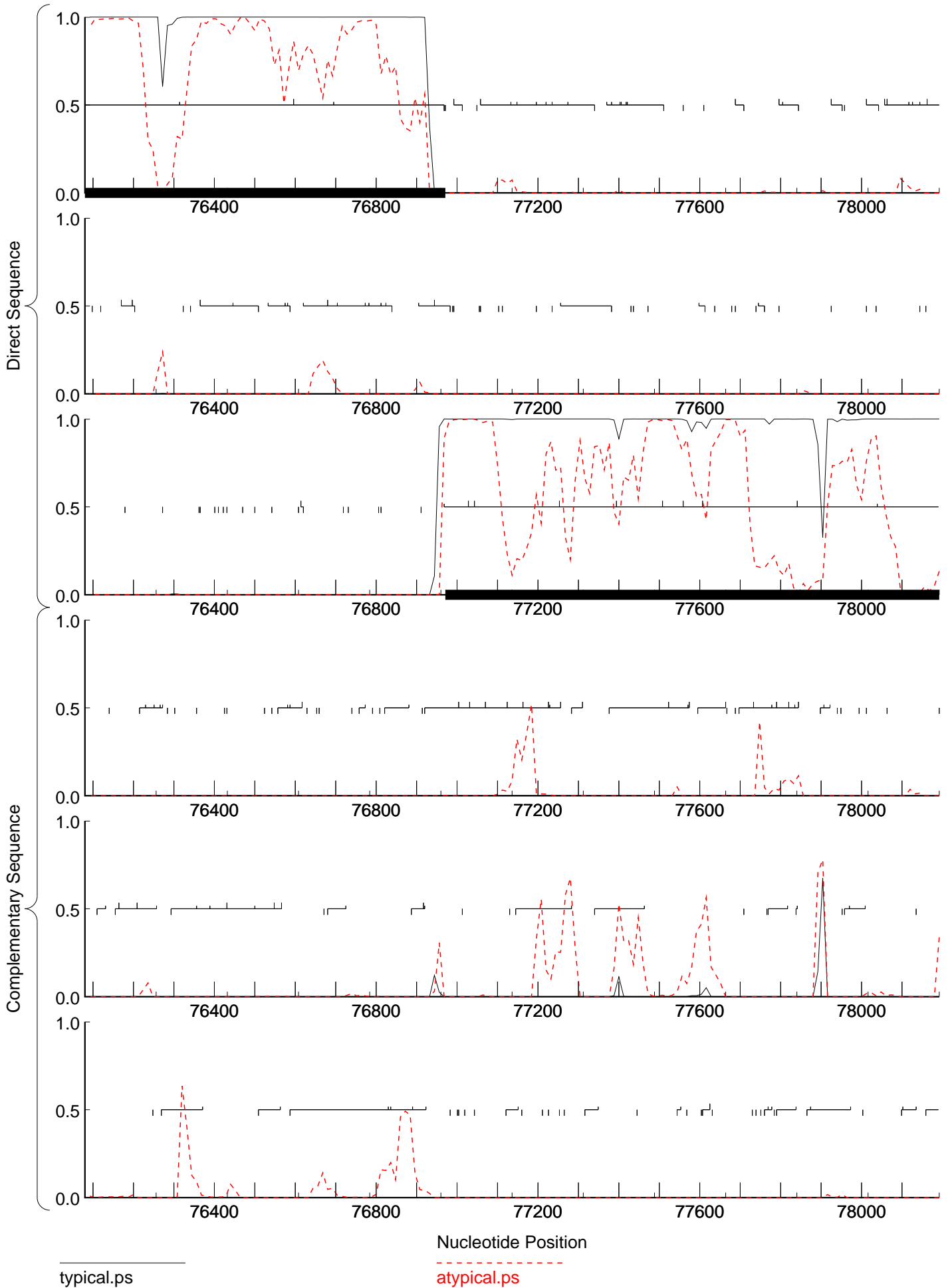
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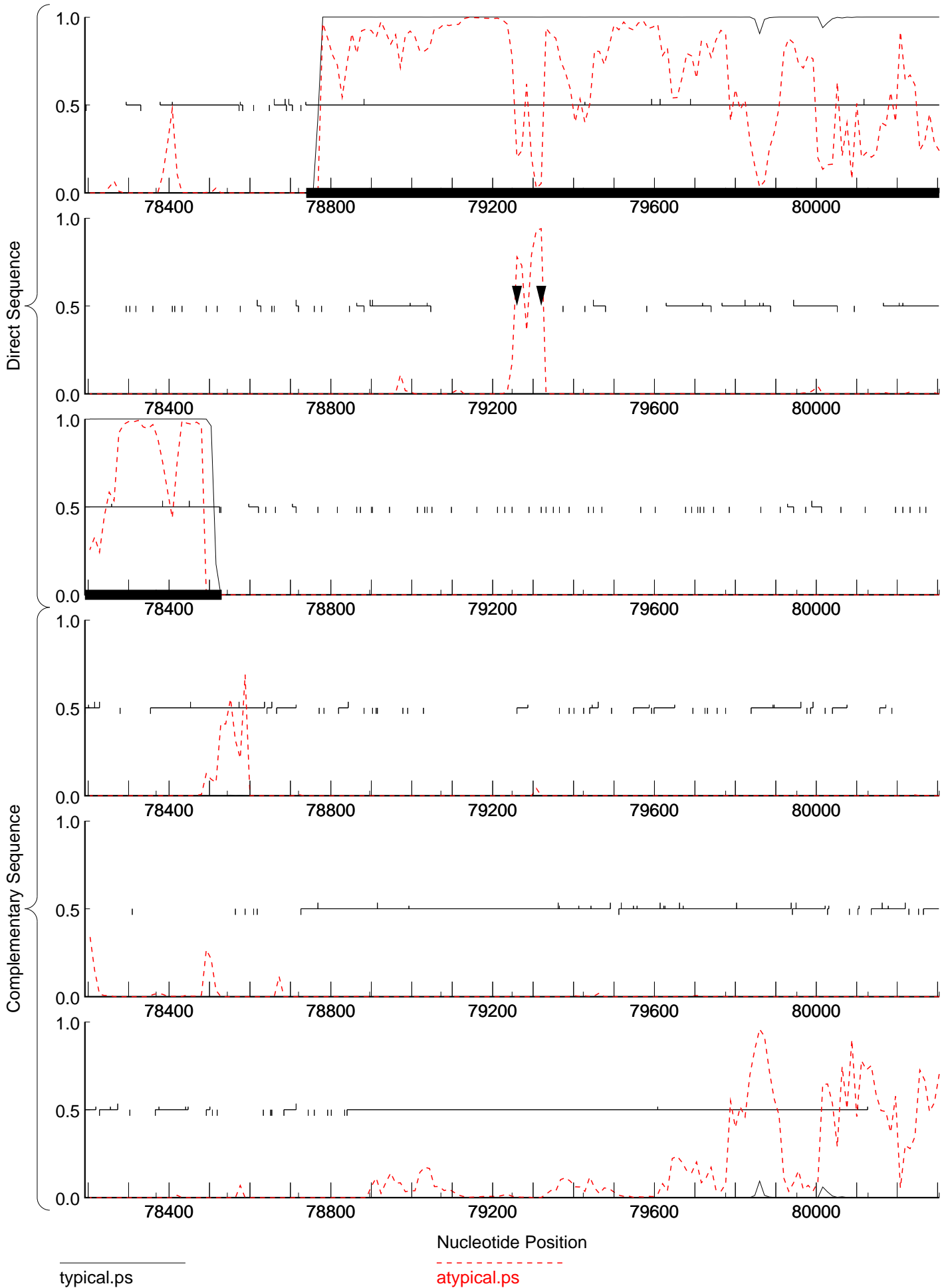
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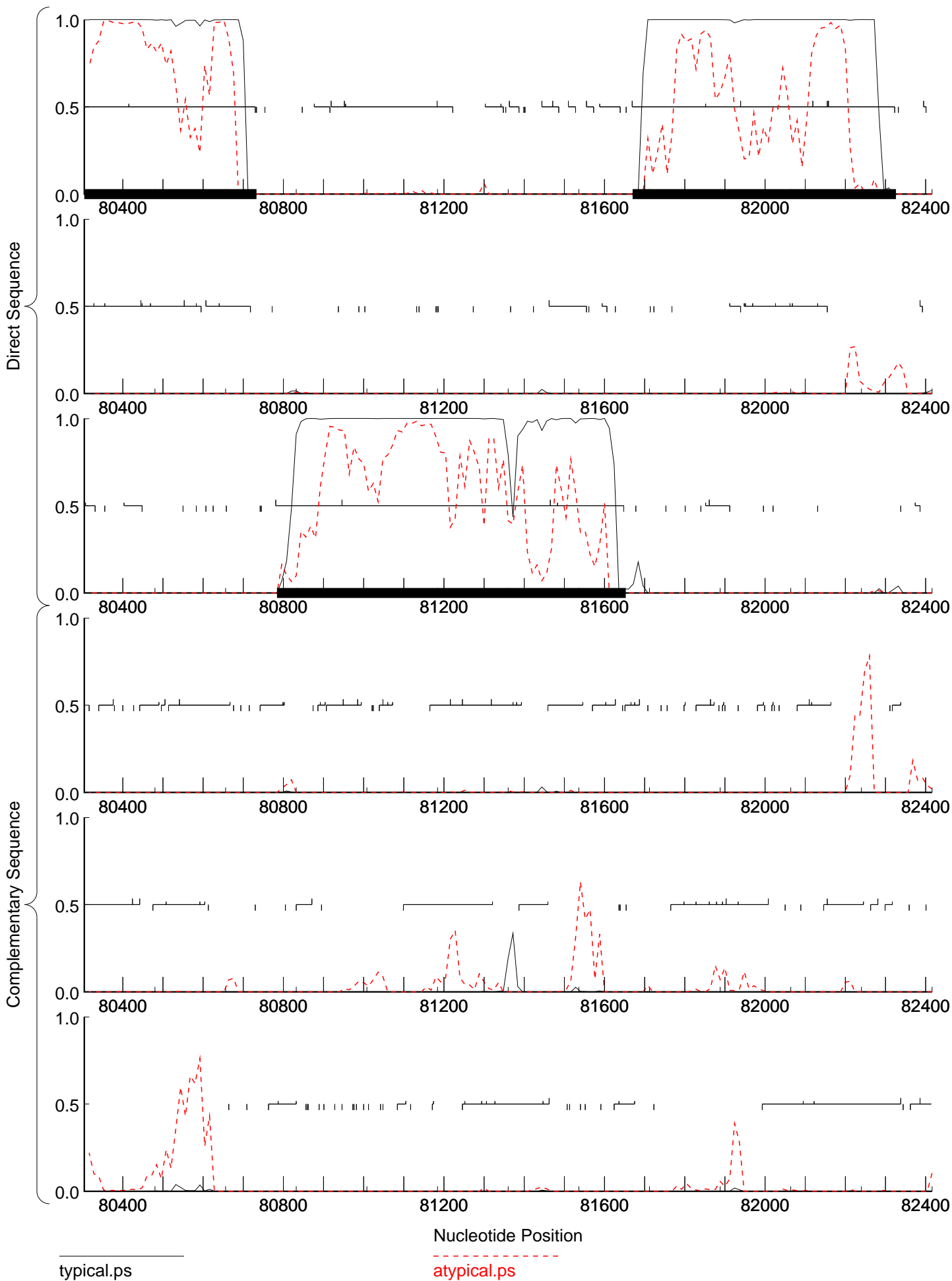


typical.ps

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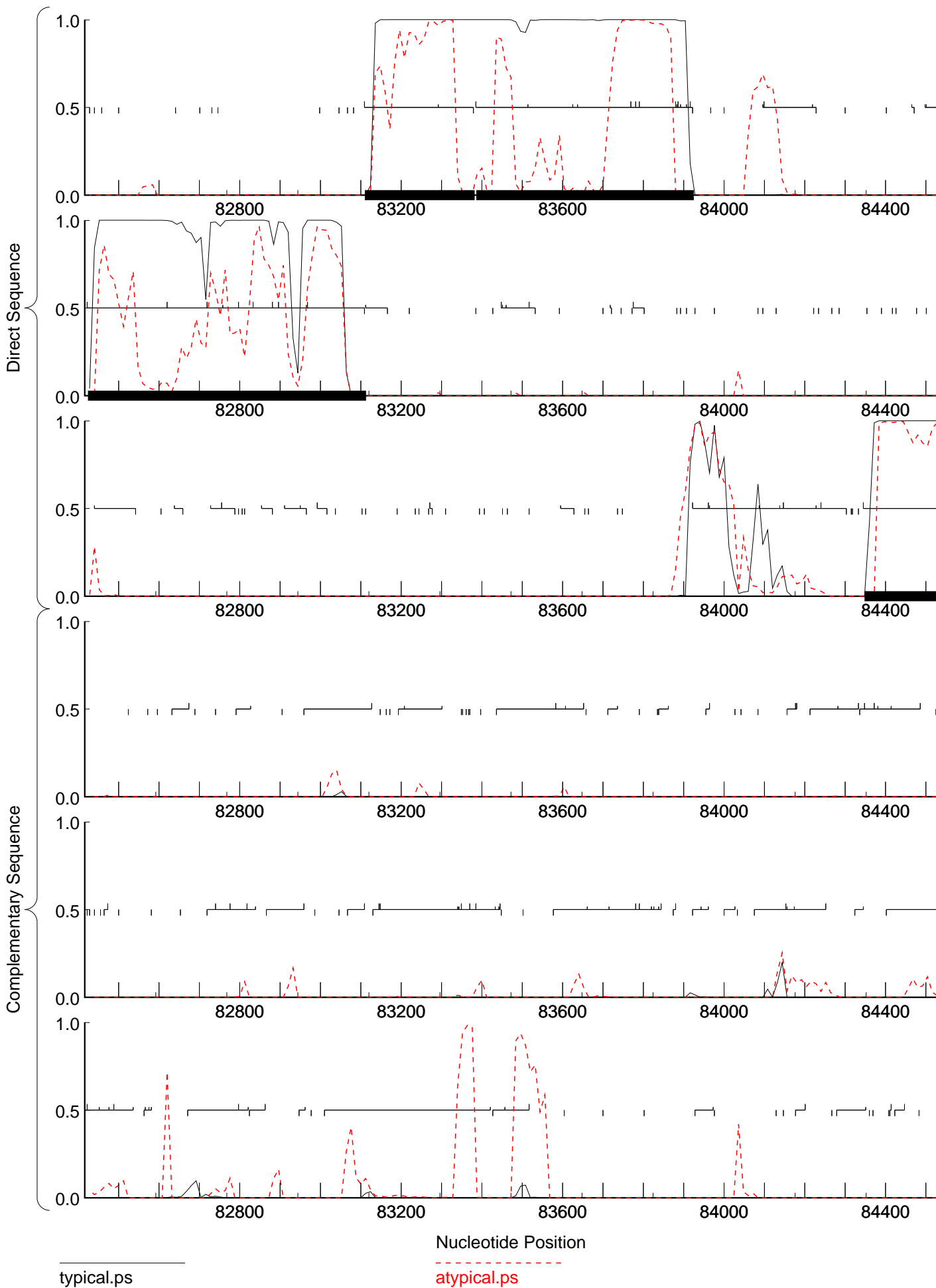






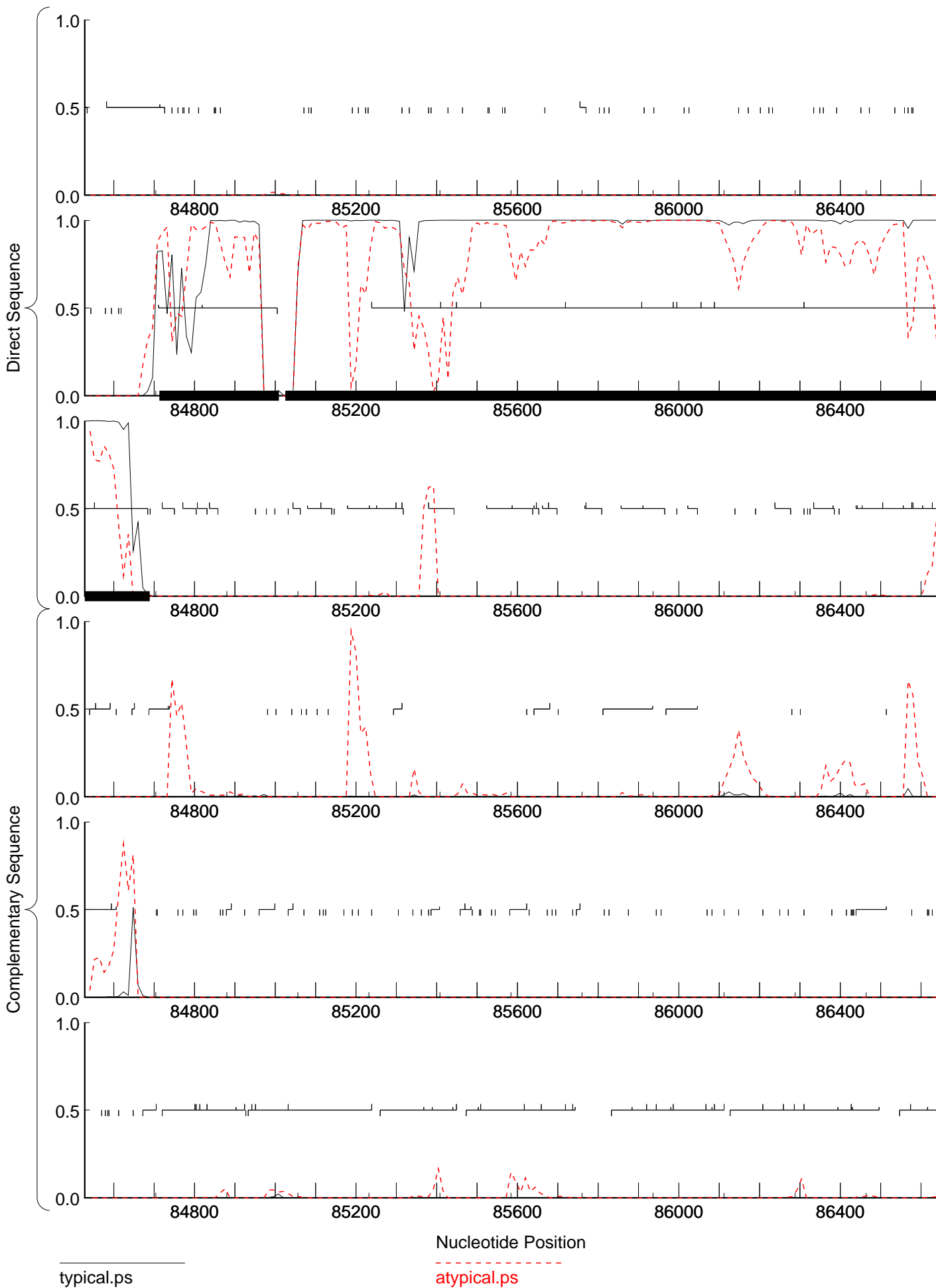
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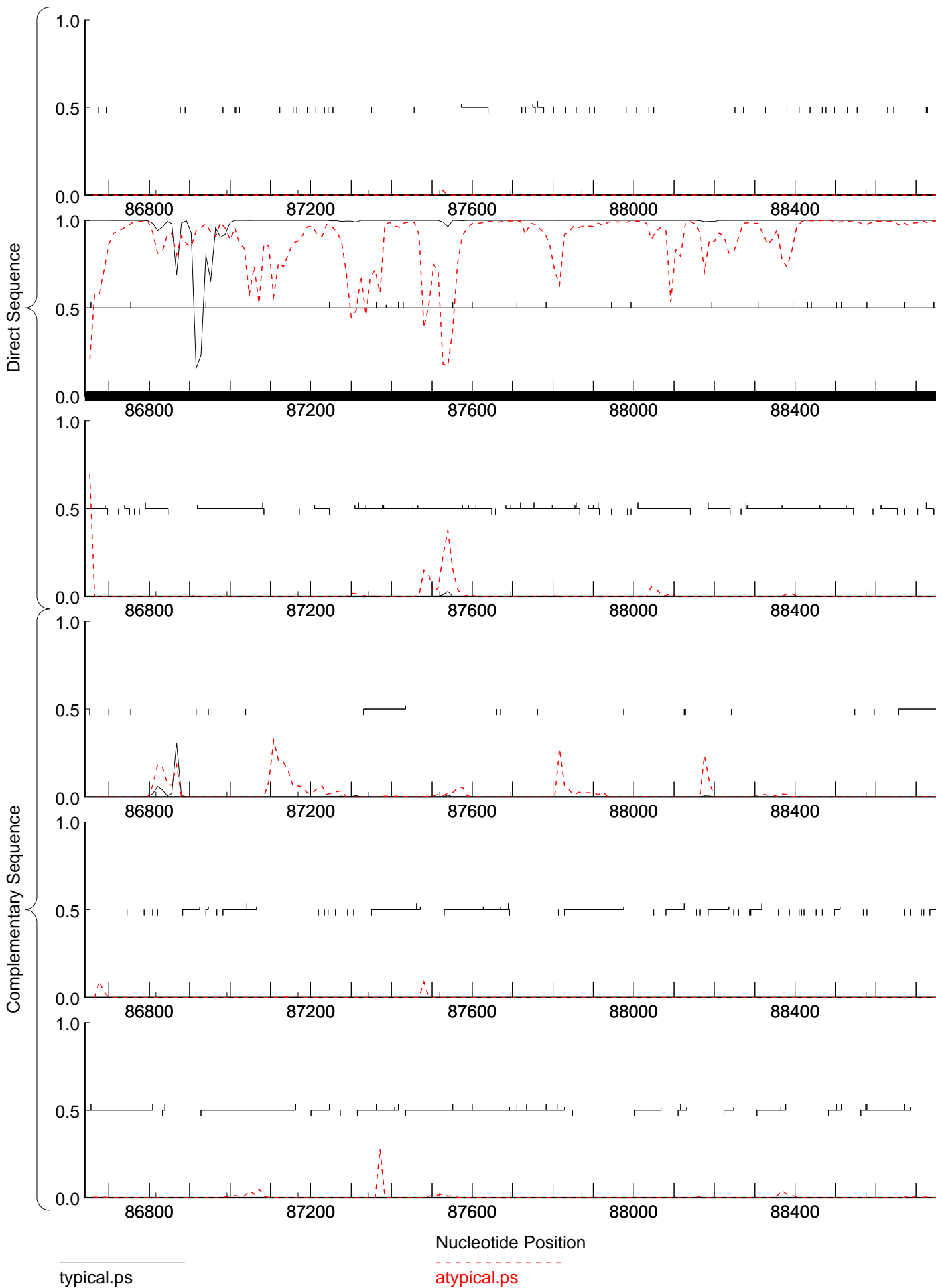
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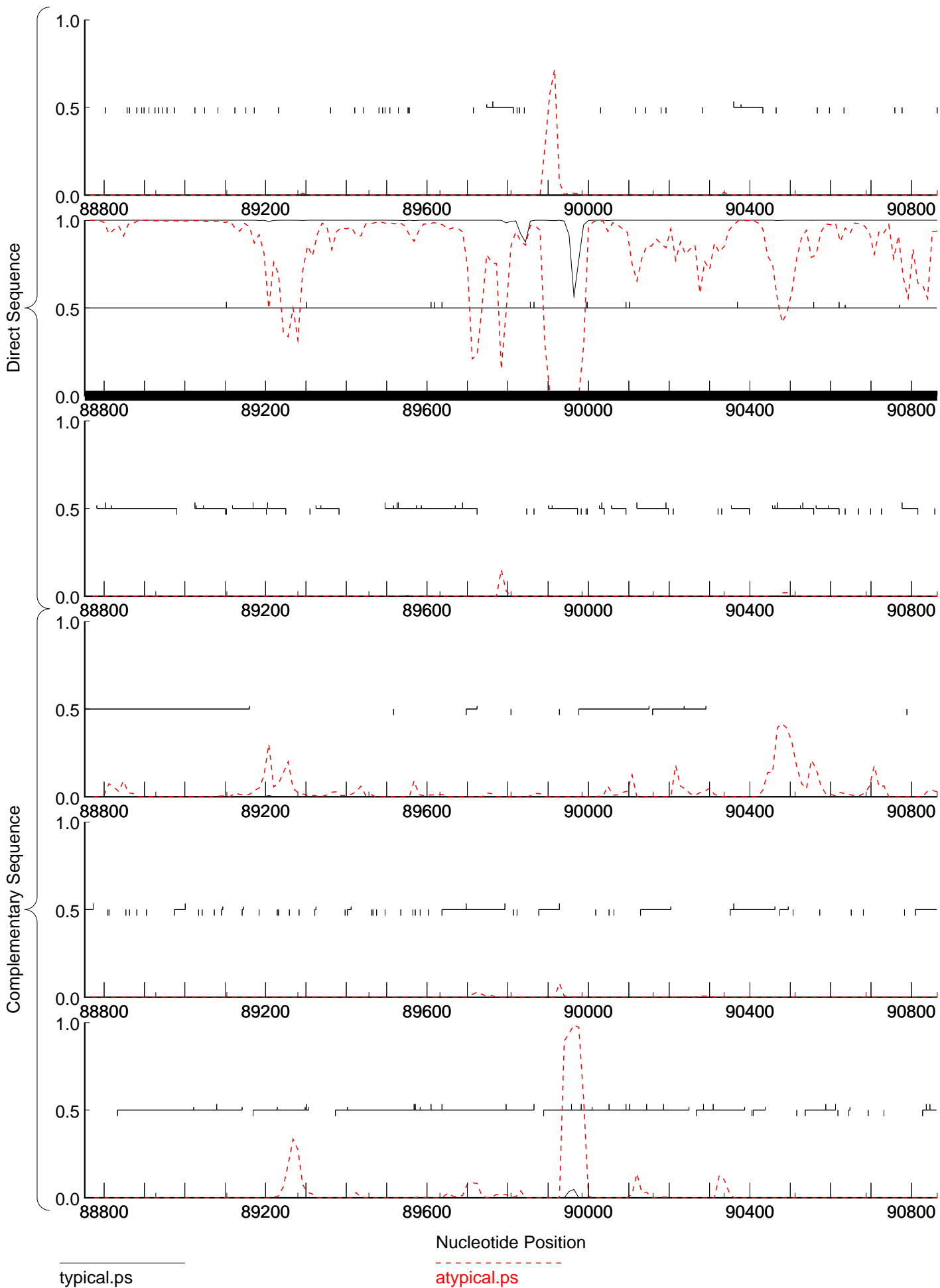
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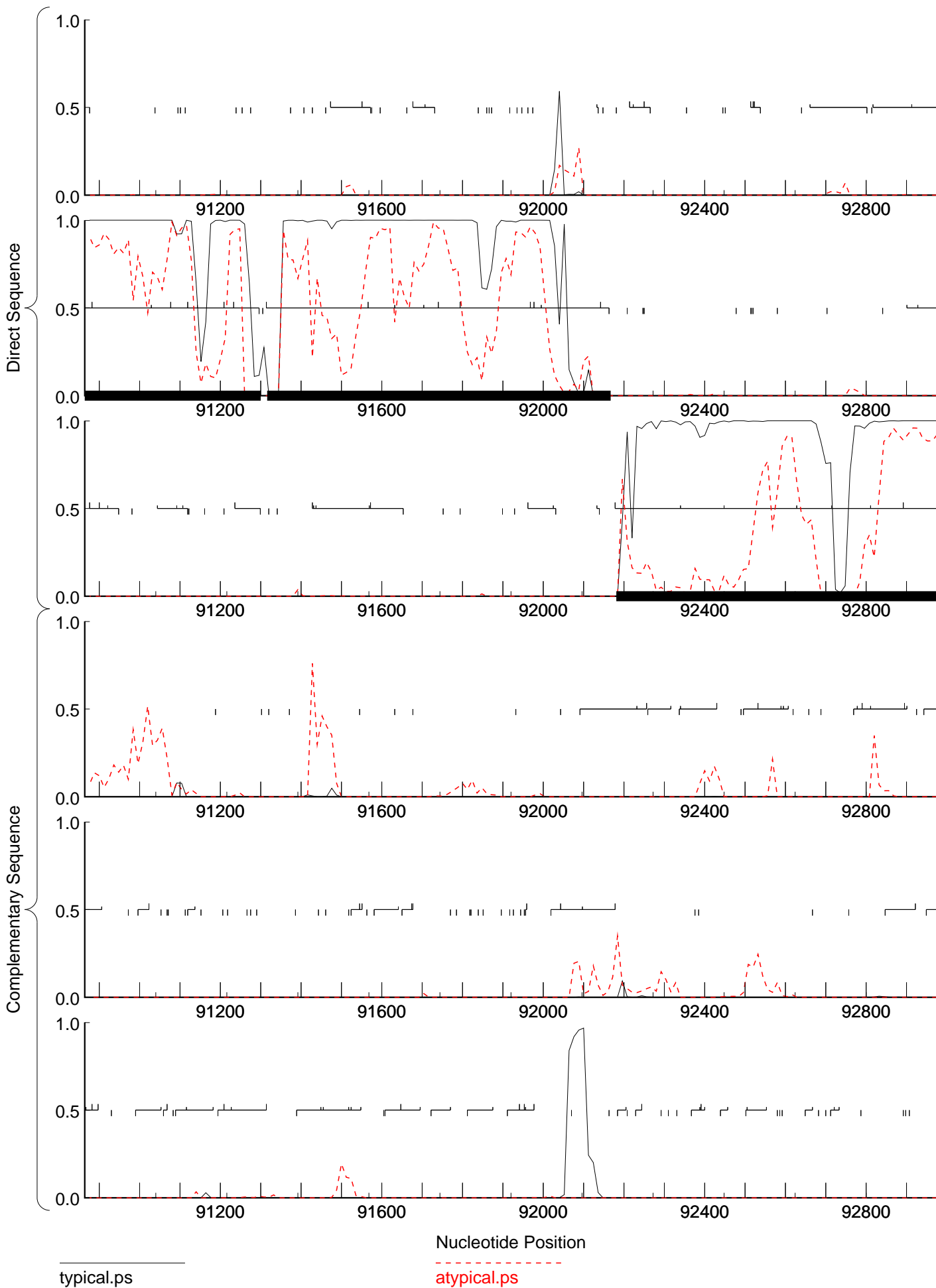


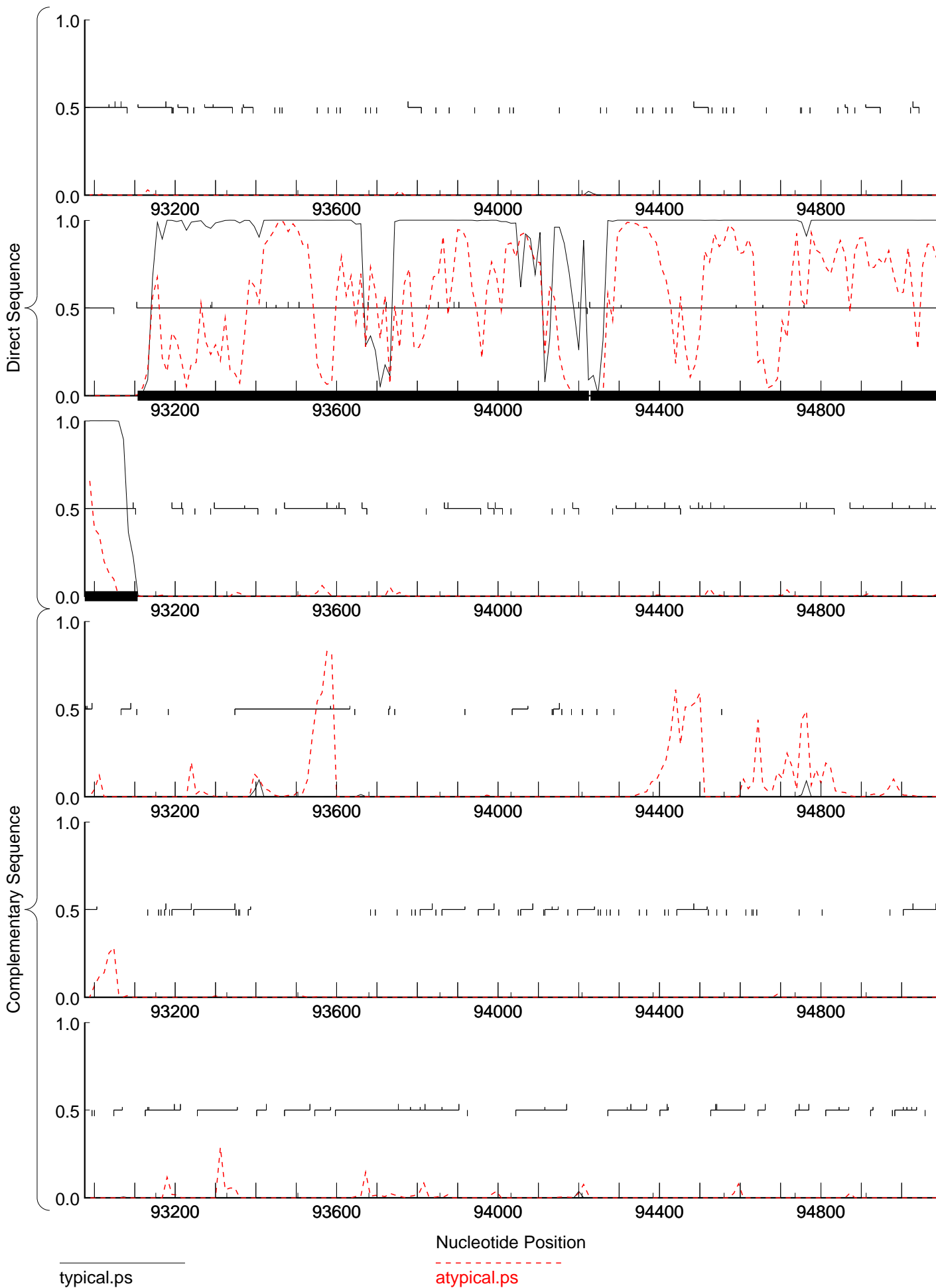


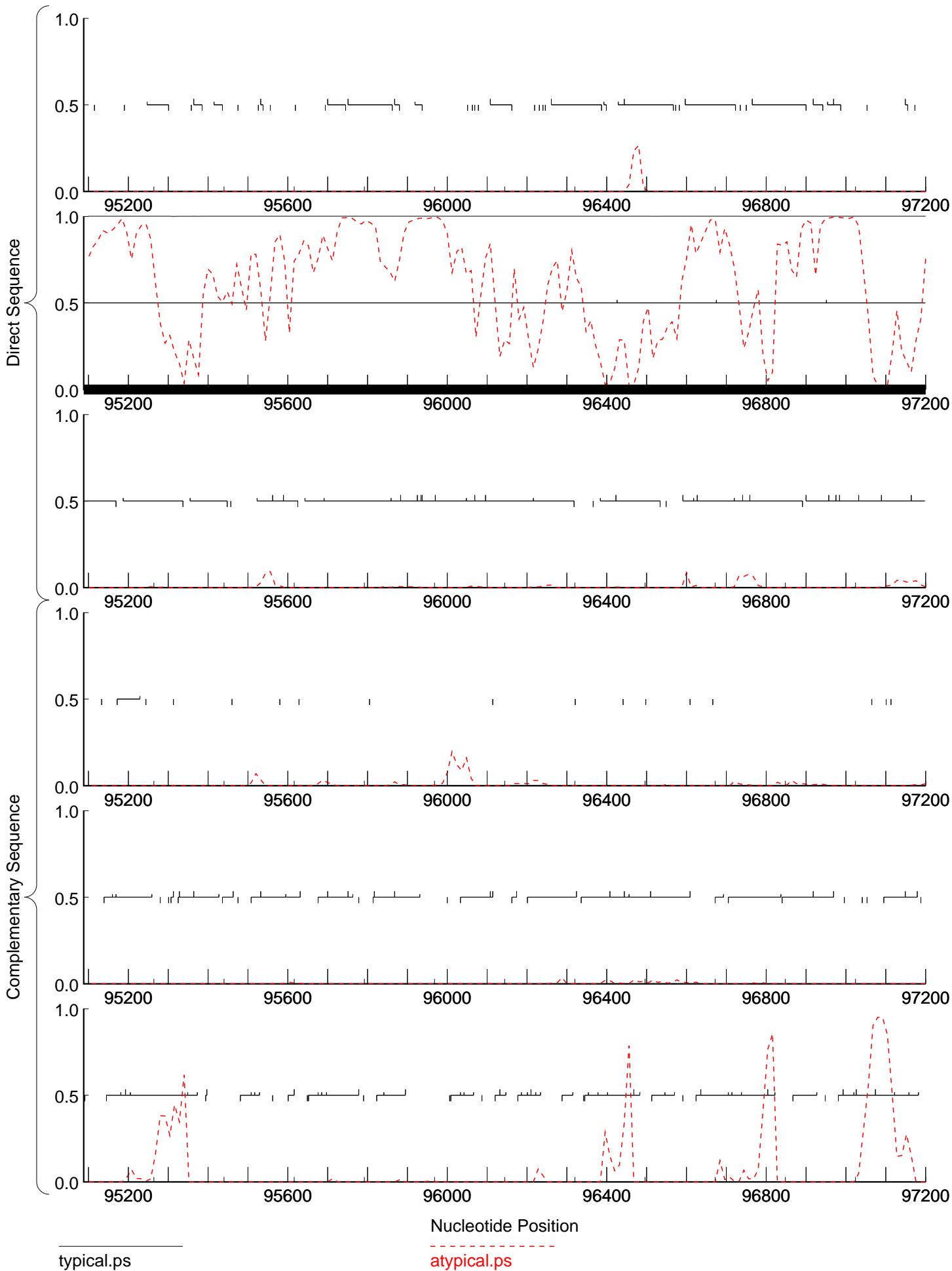
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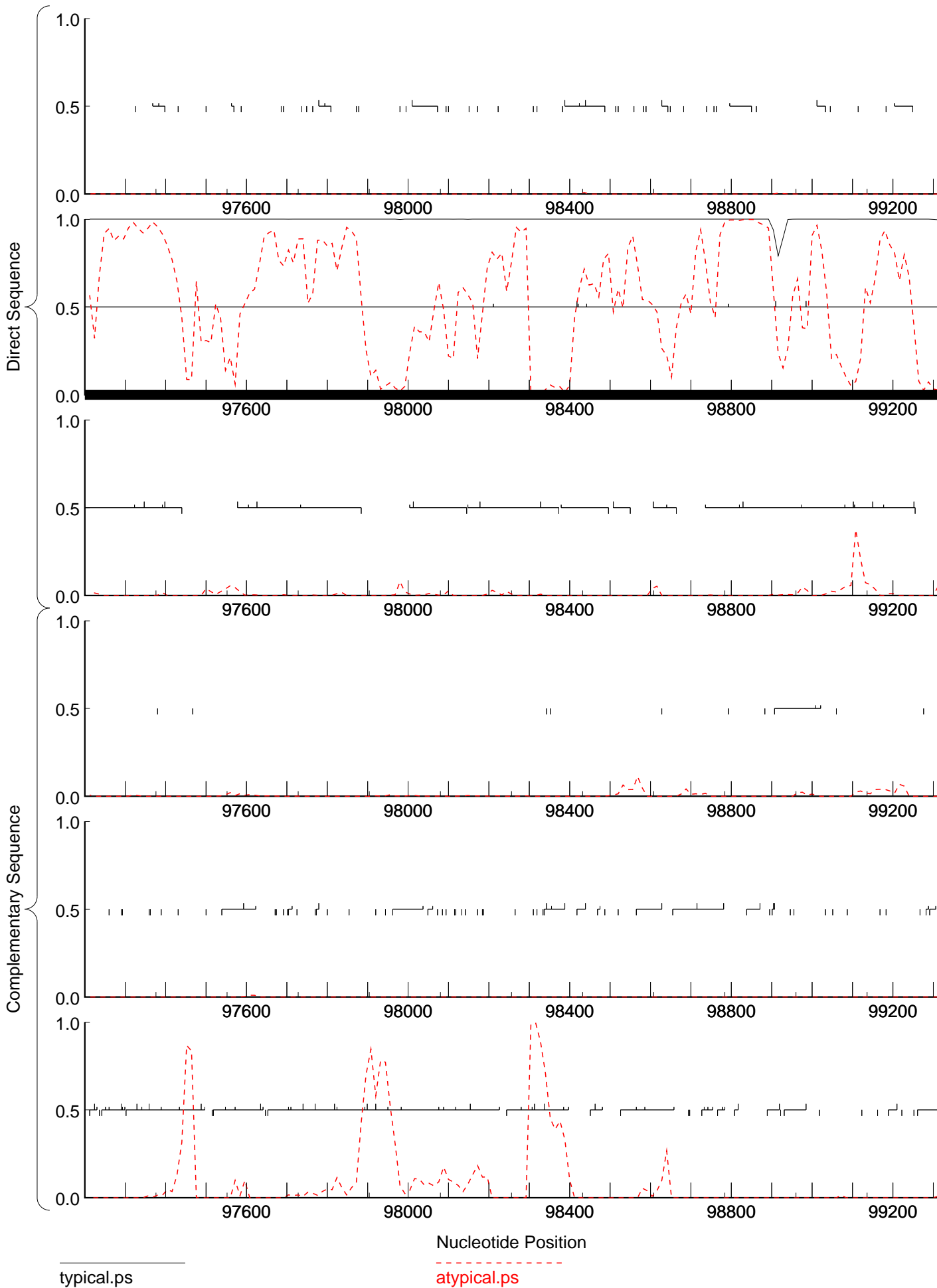


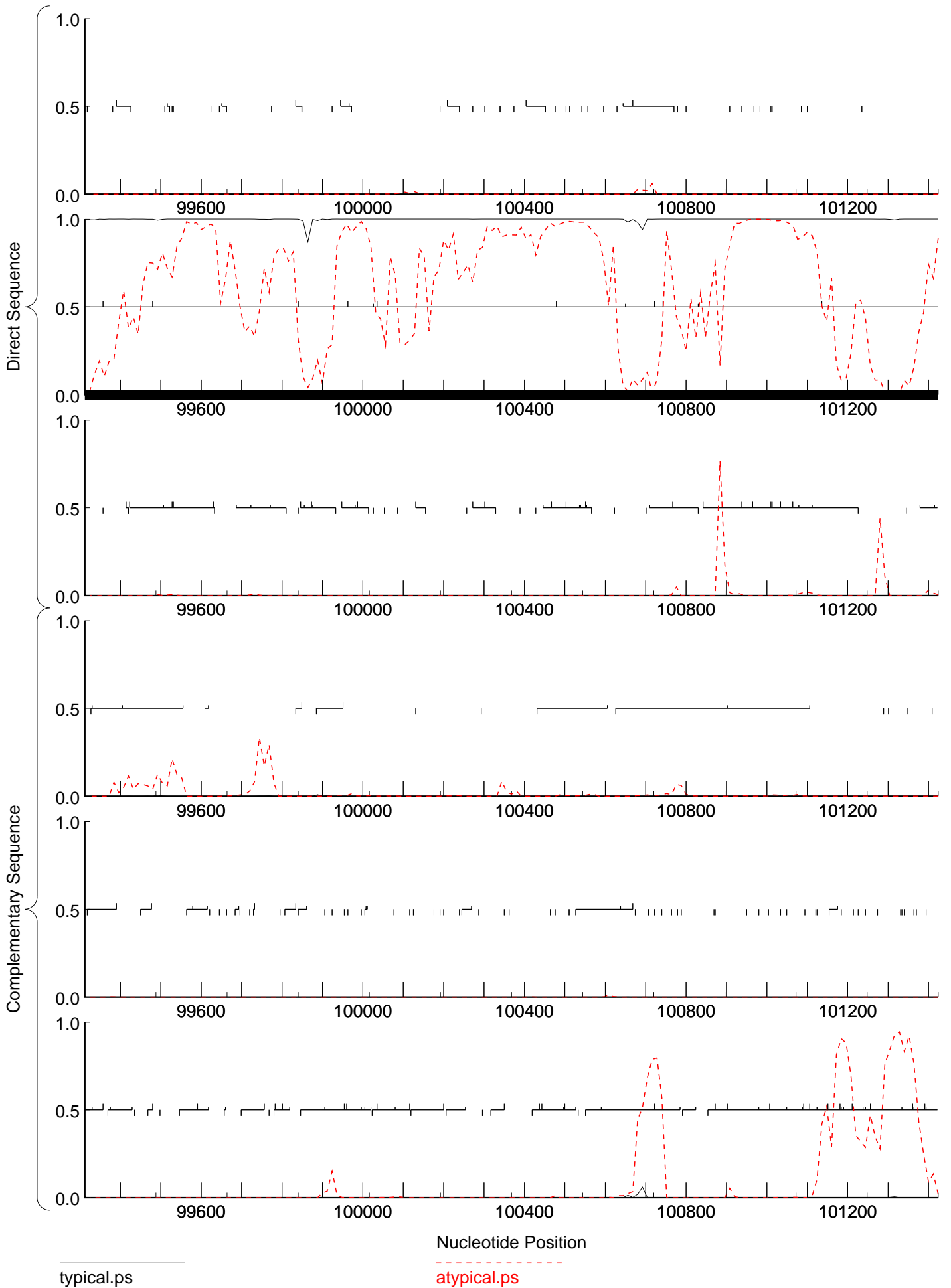


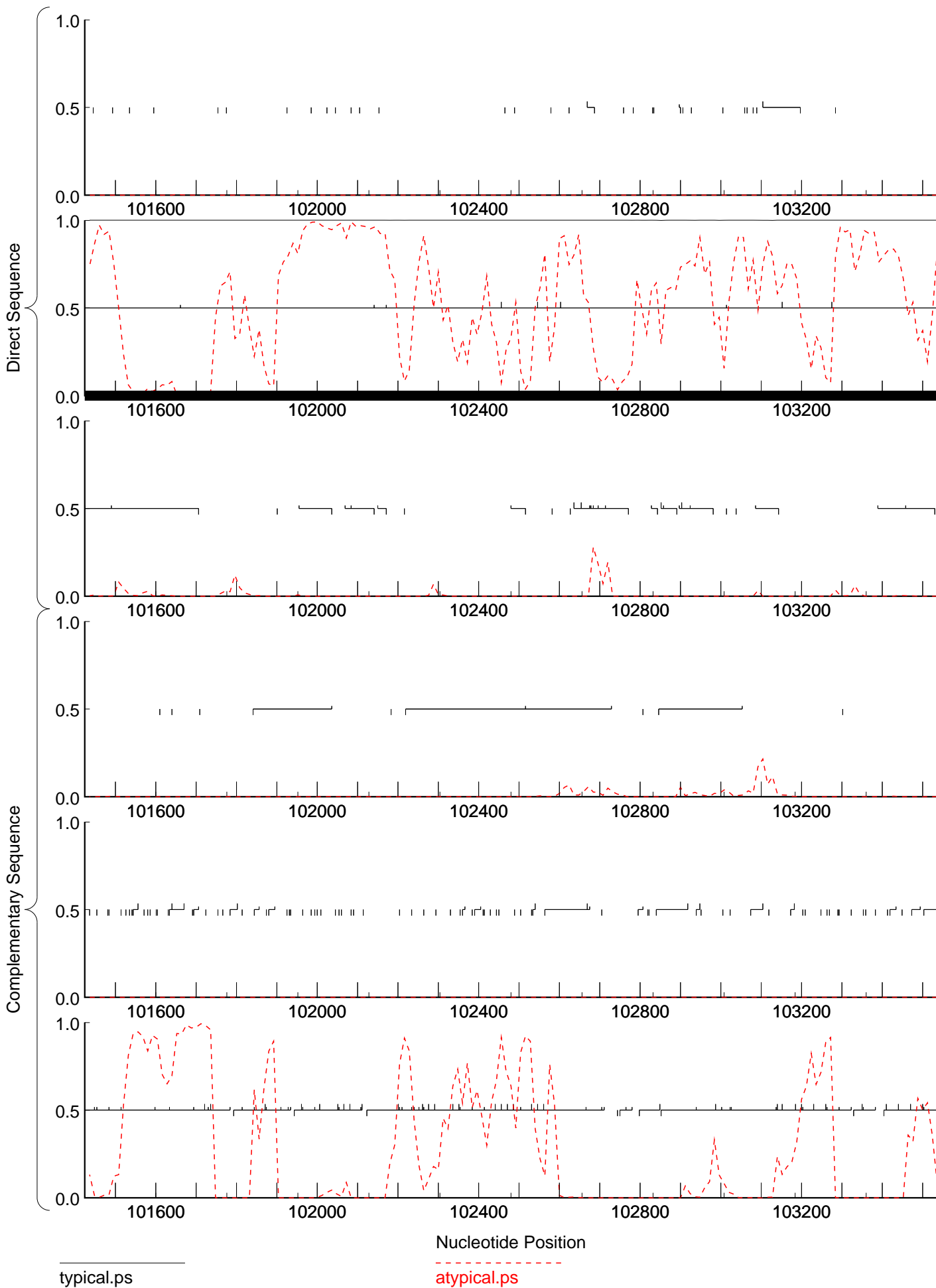


typical.ps

atypical.ps

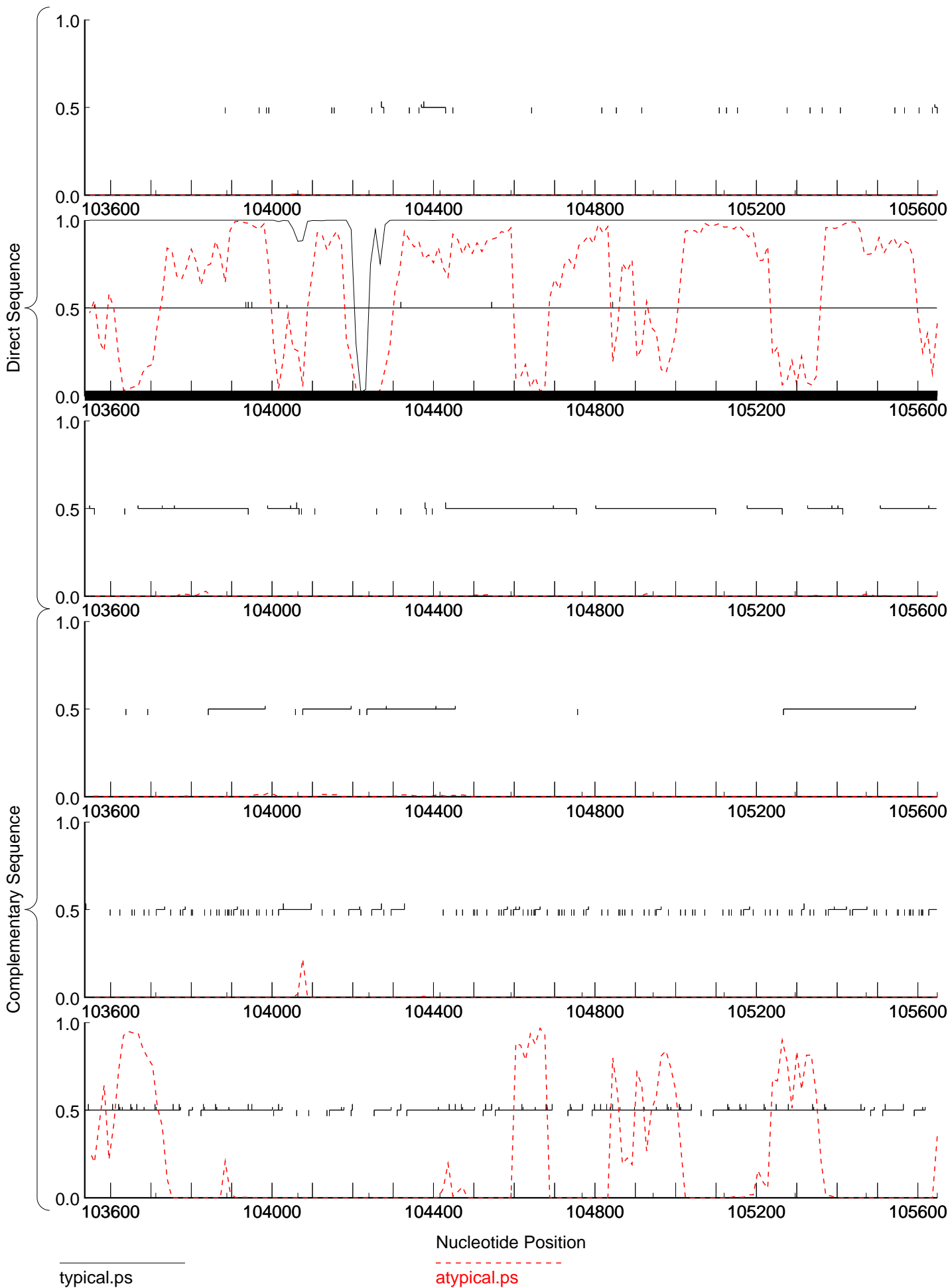


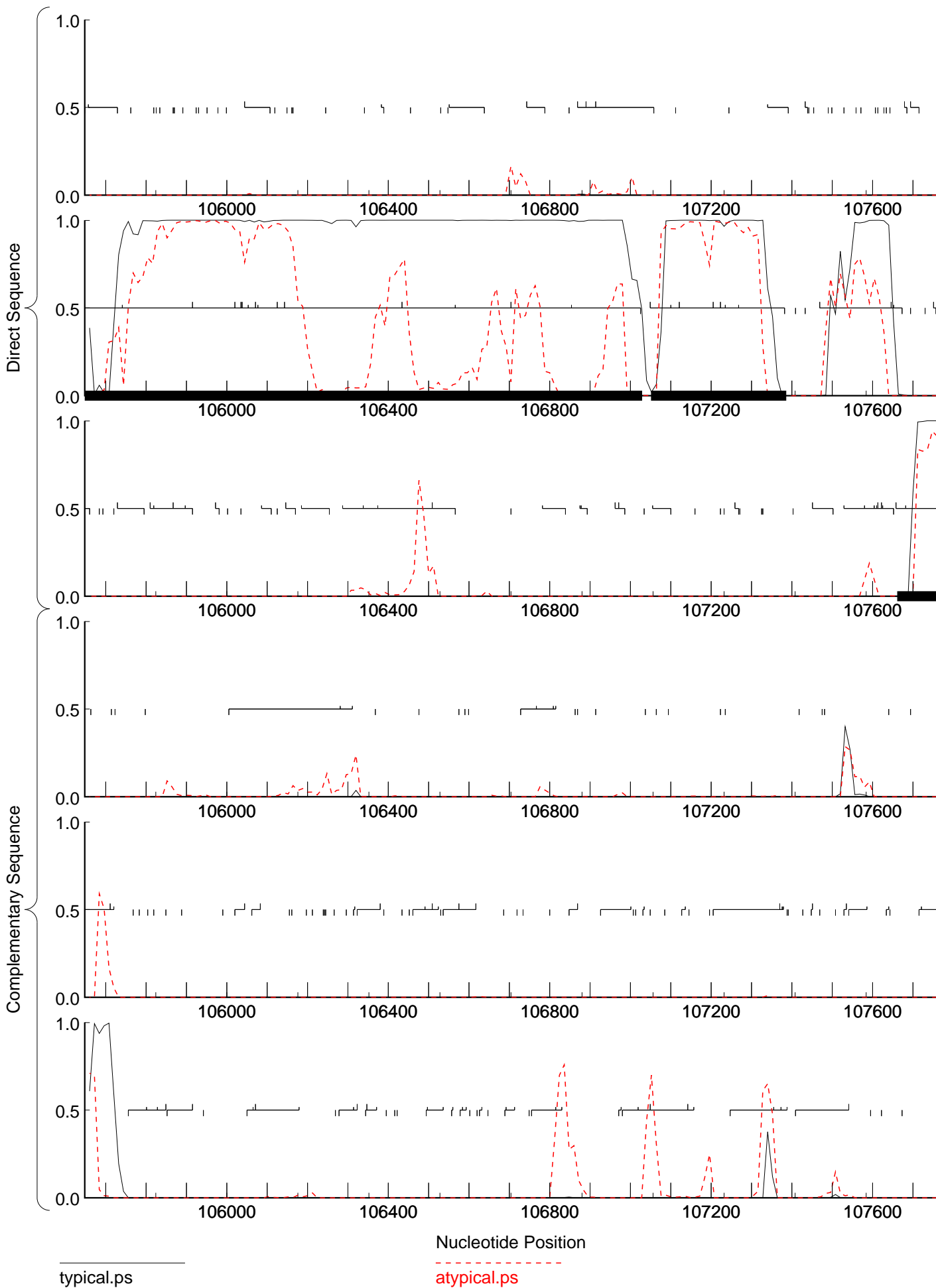


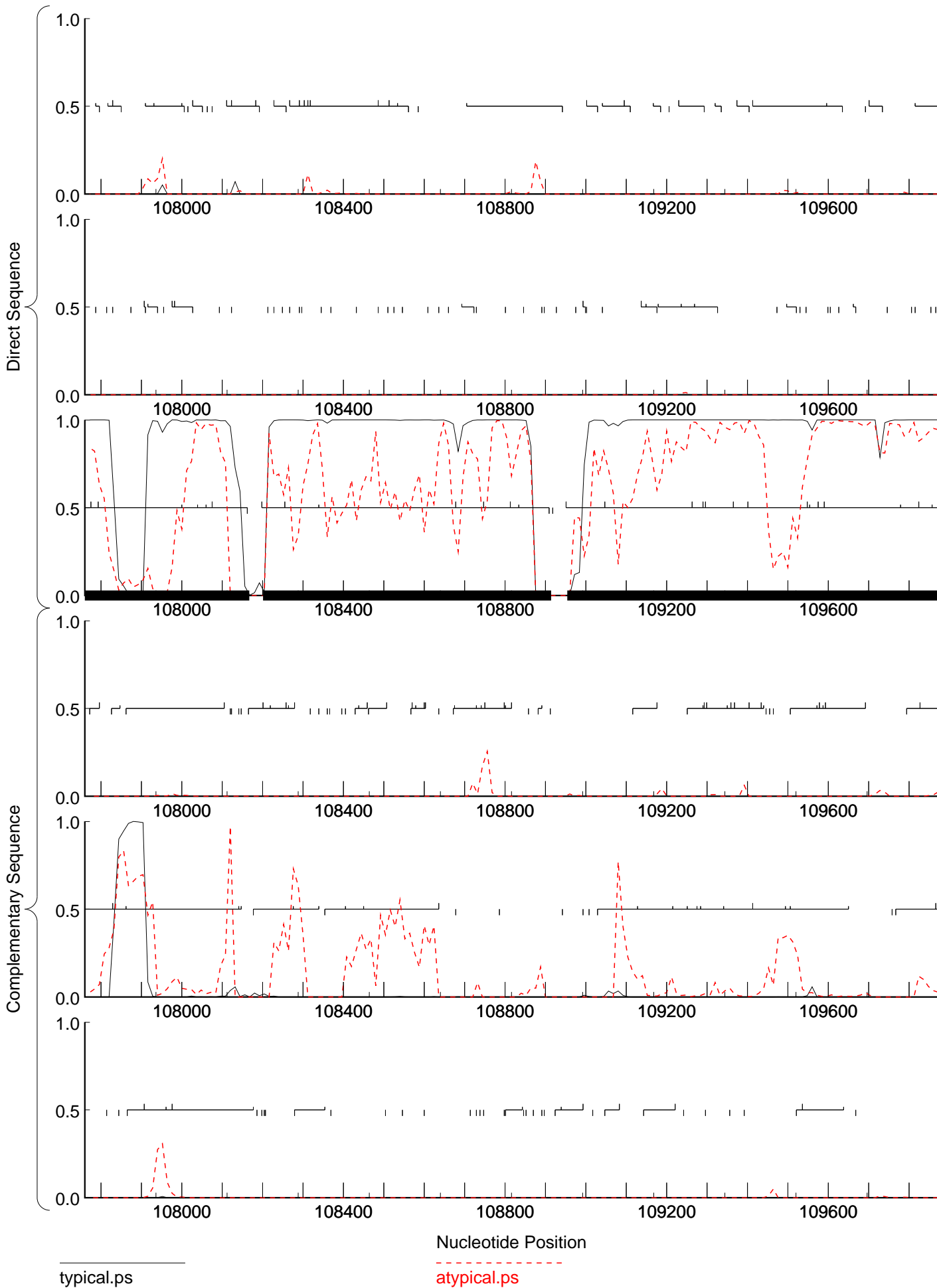


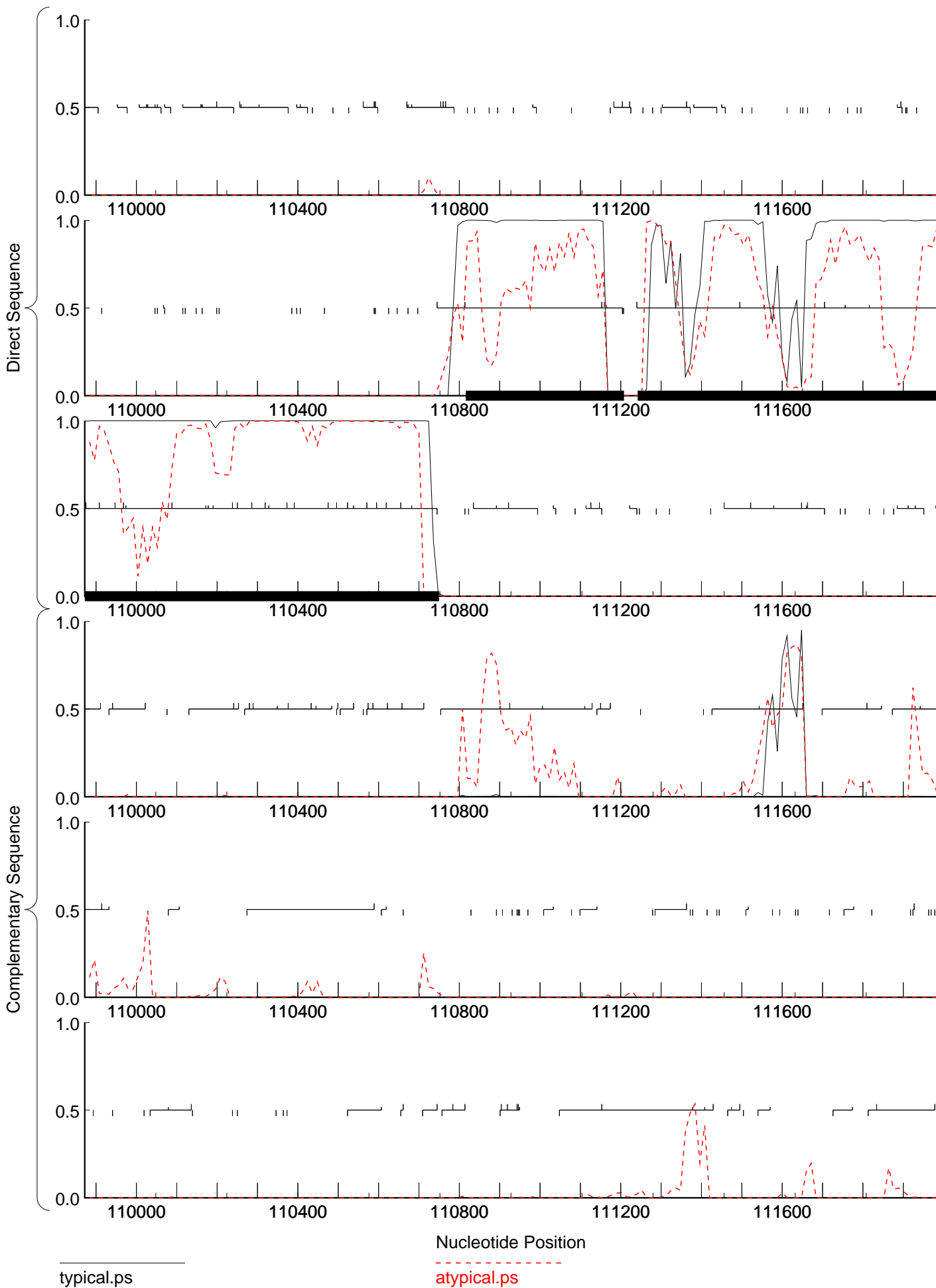
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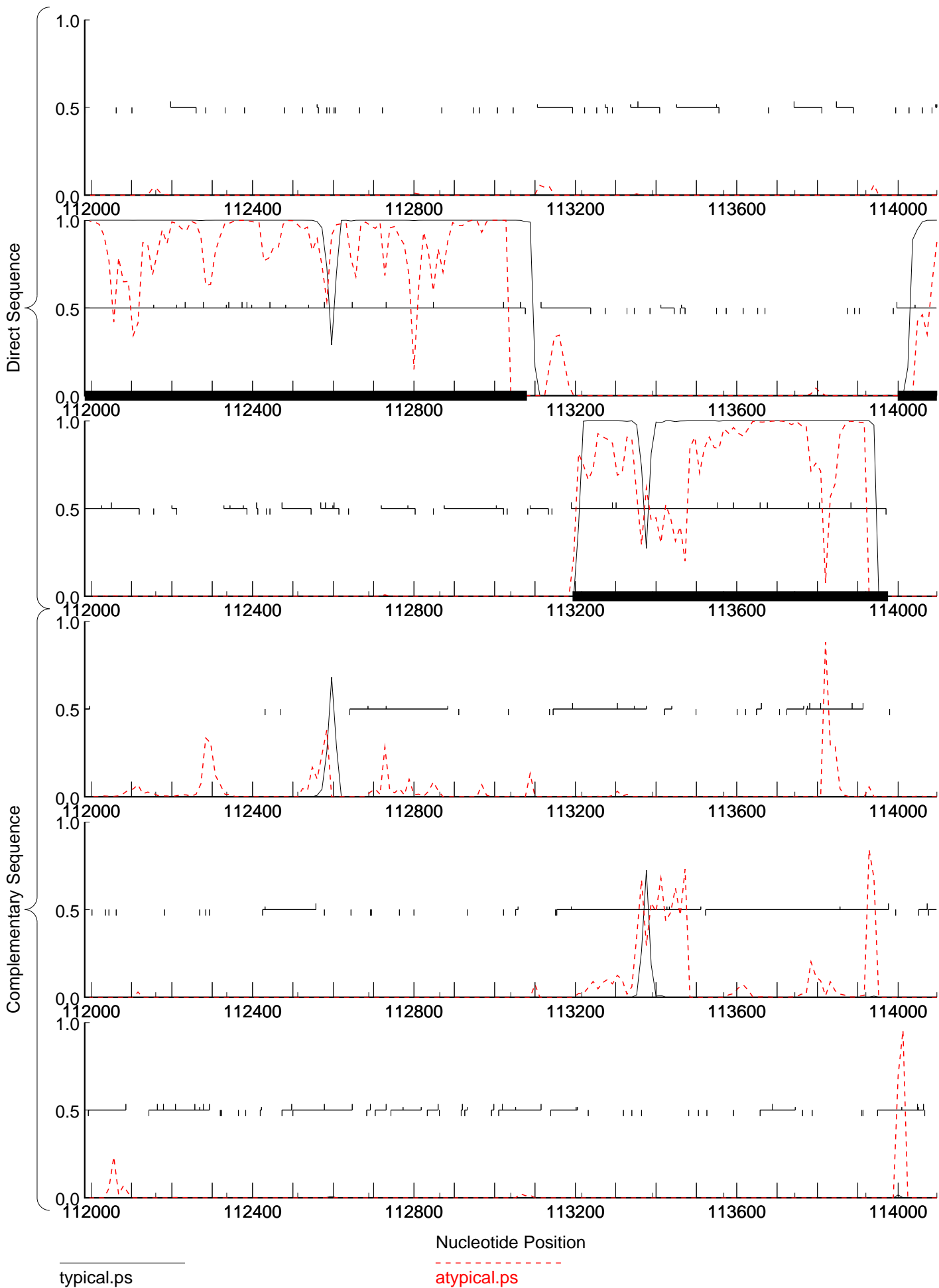
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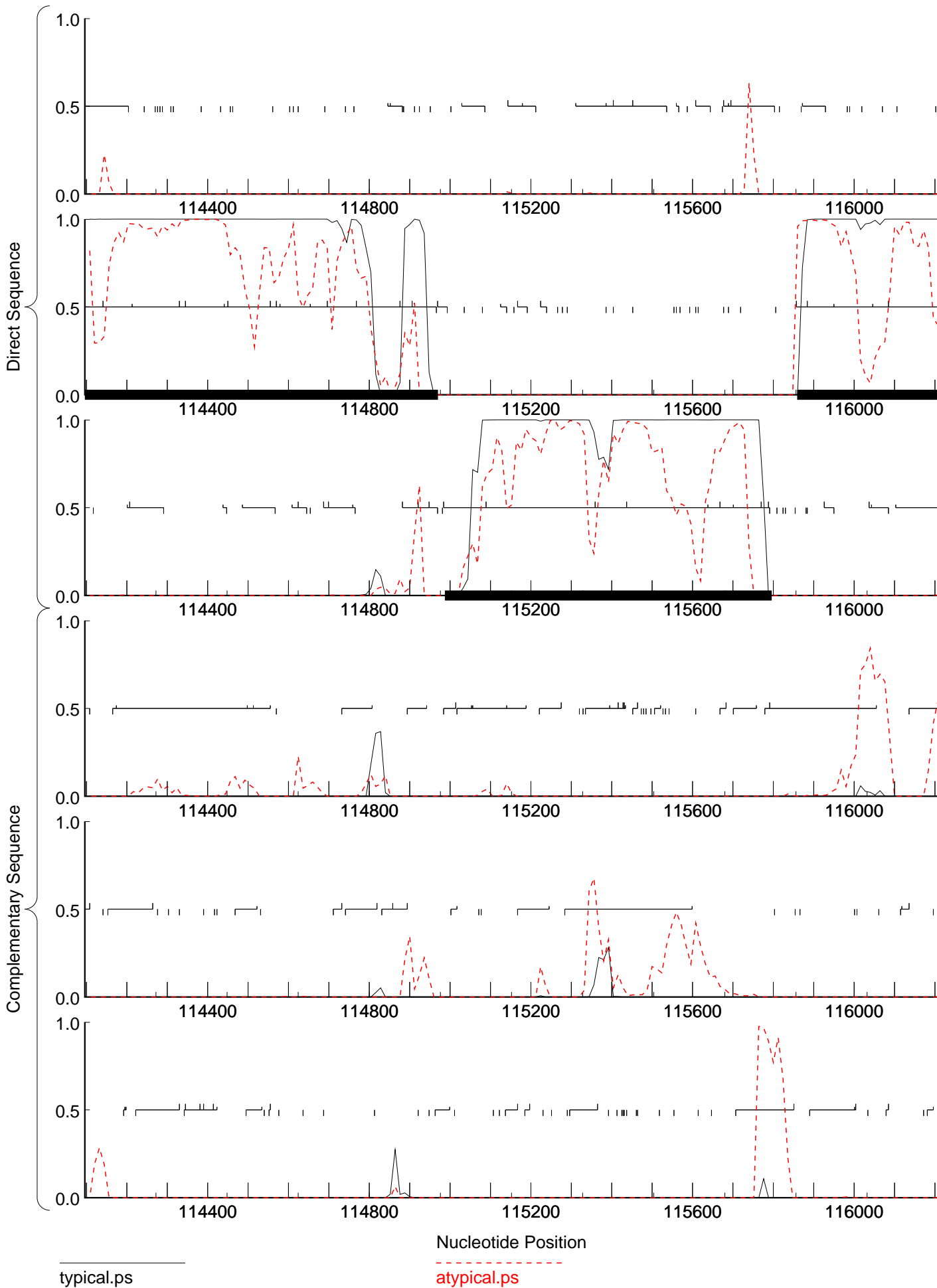






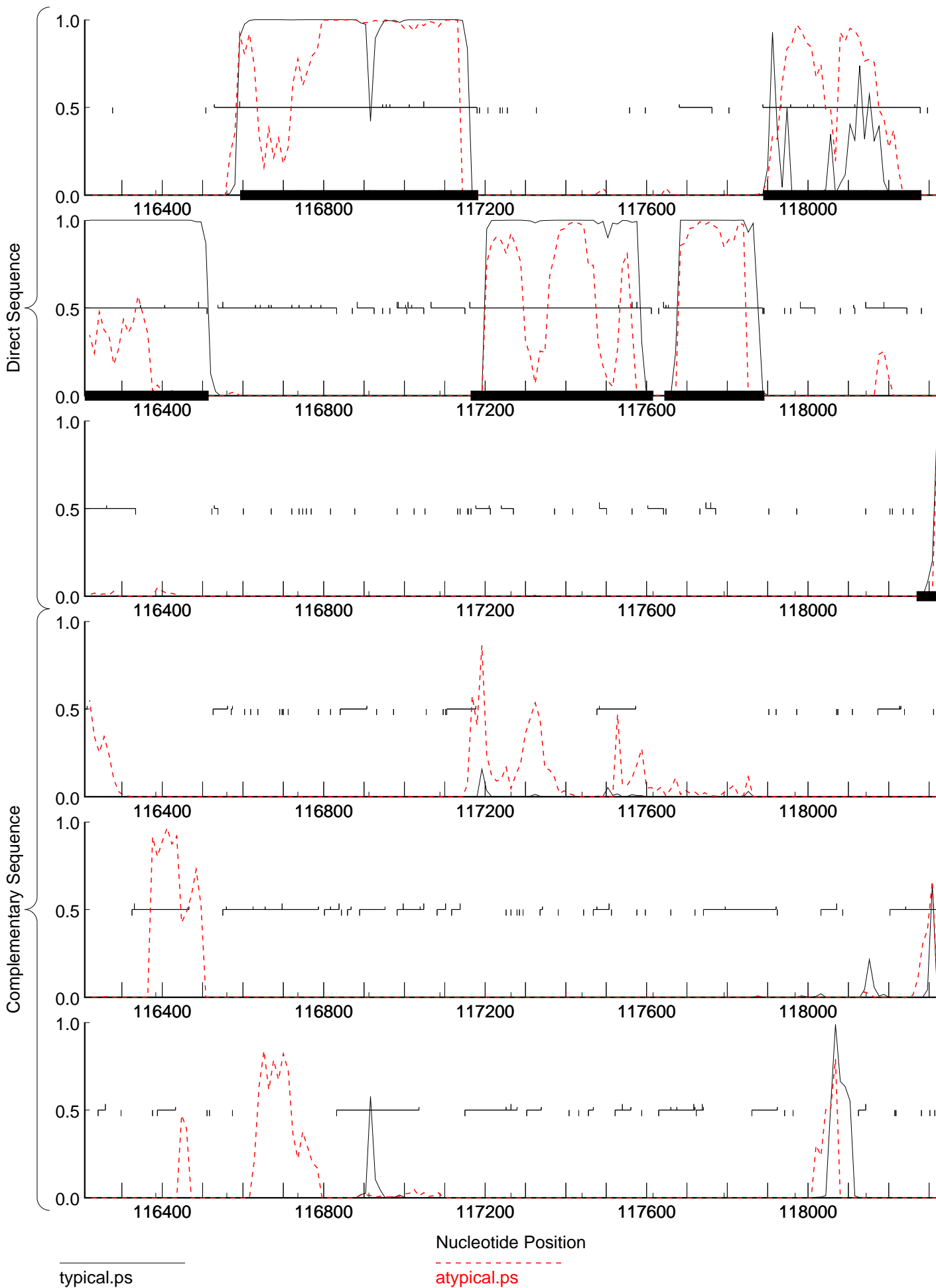


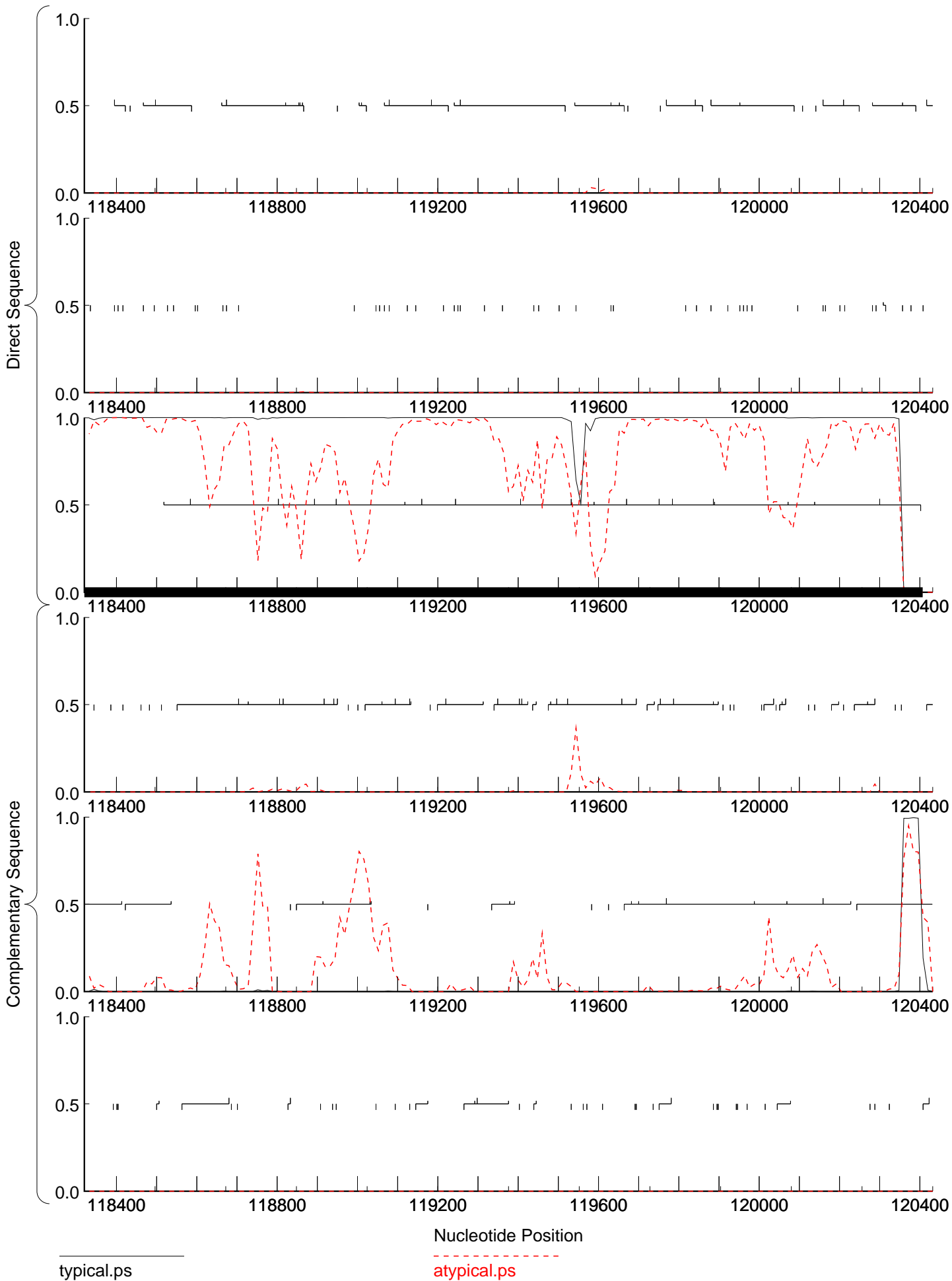


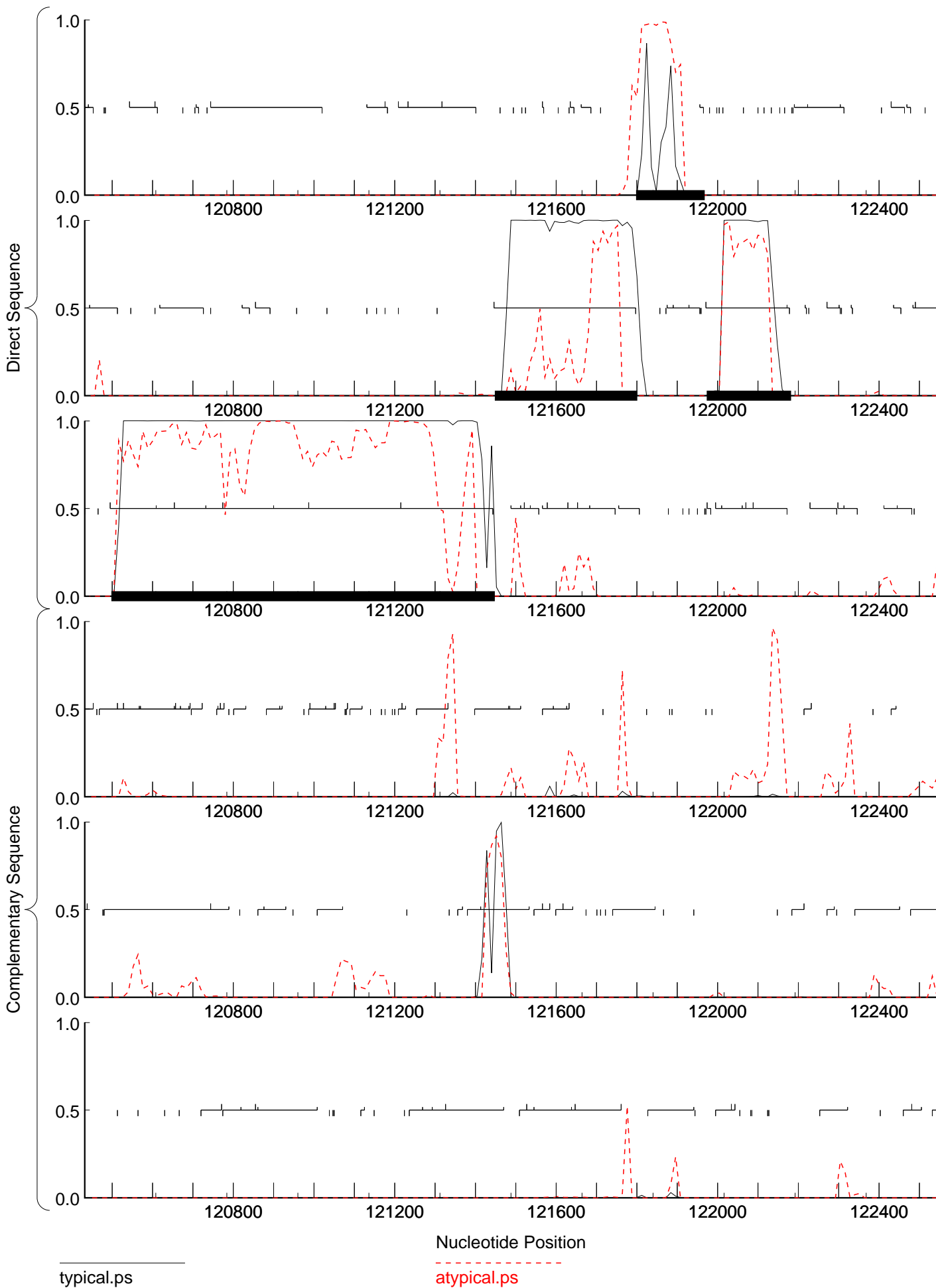


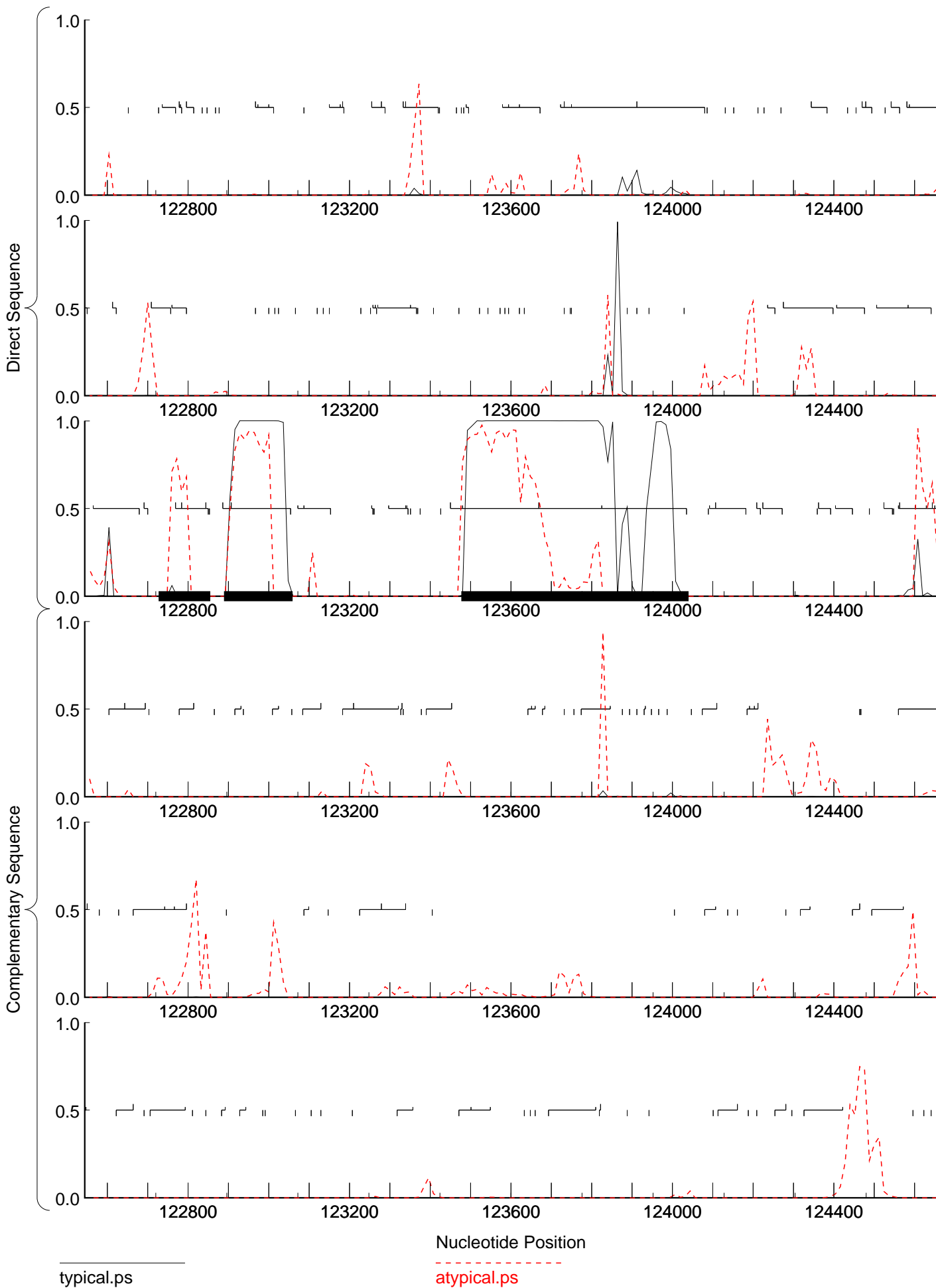
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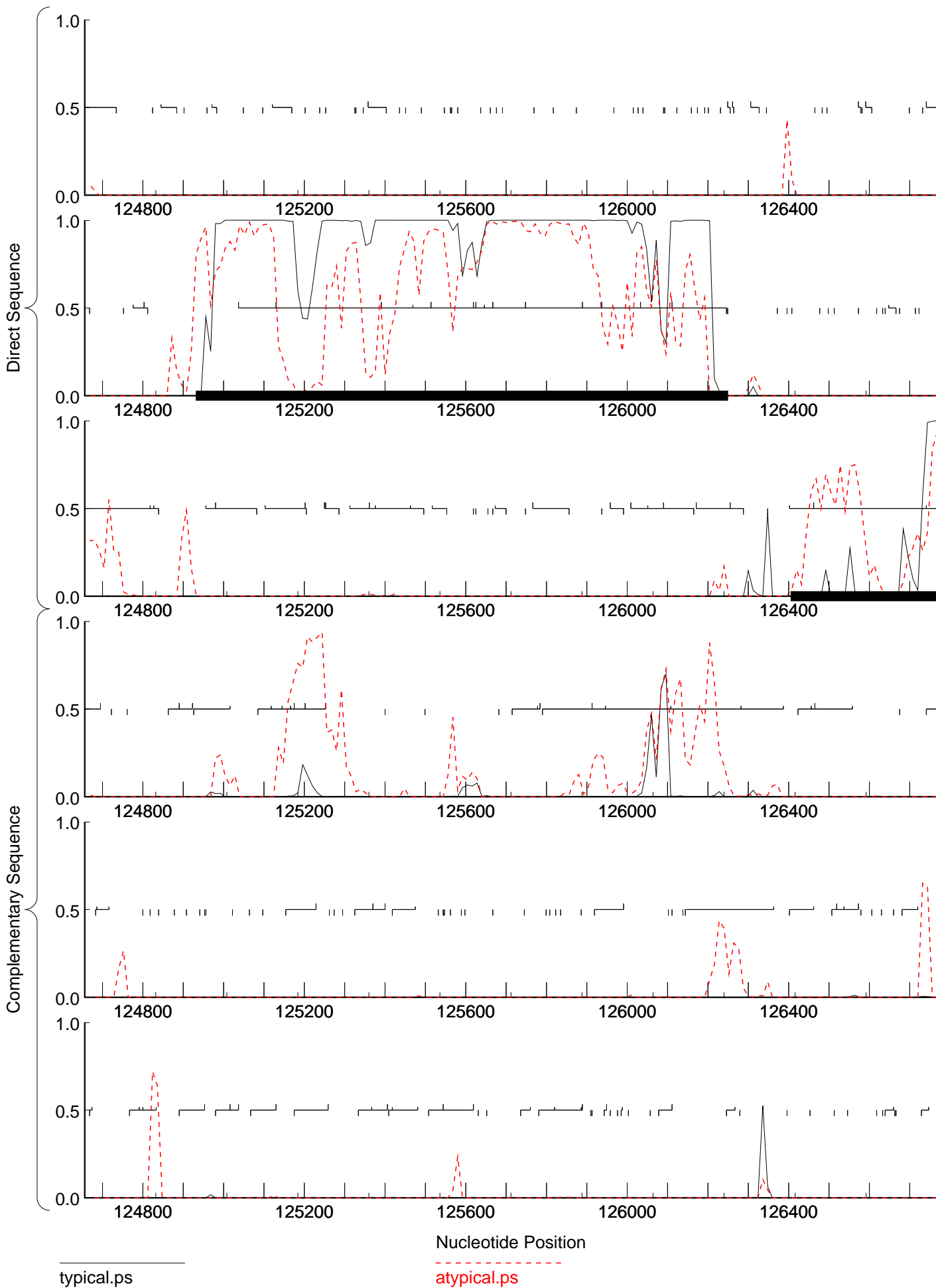
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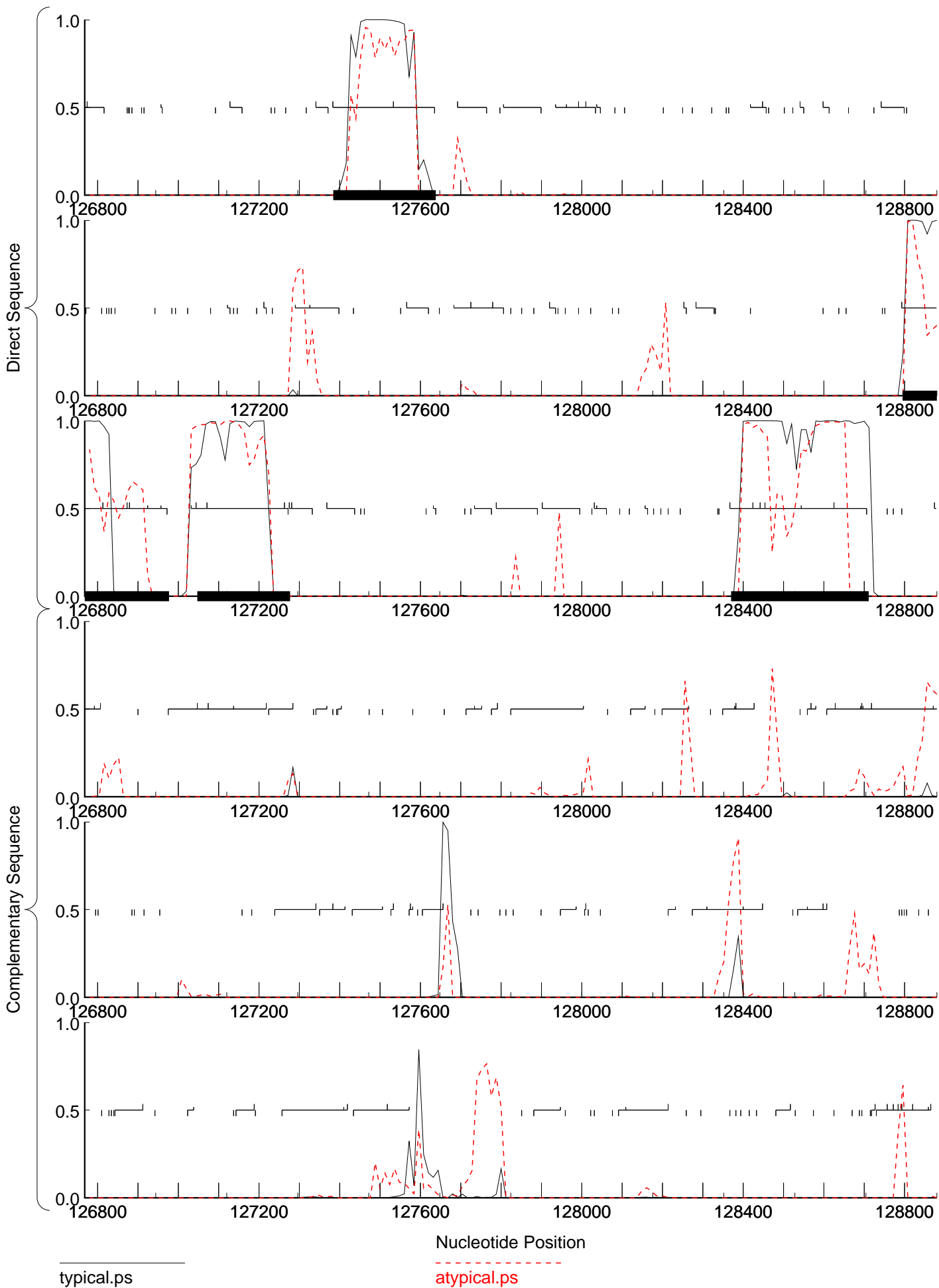


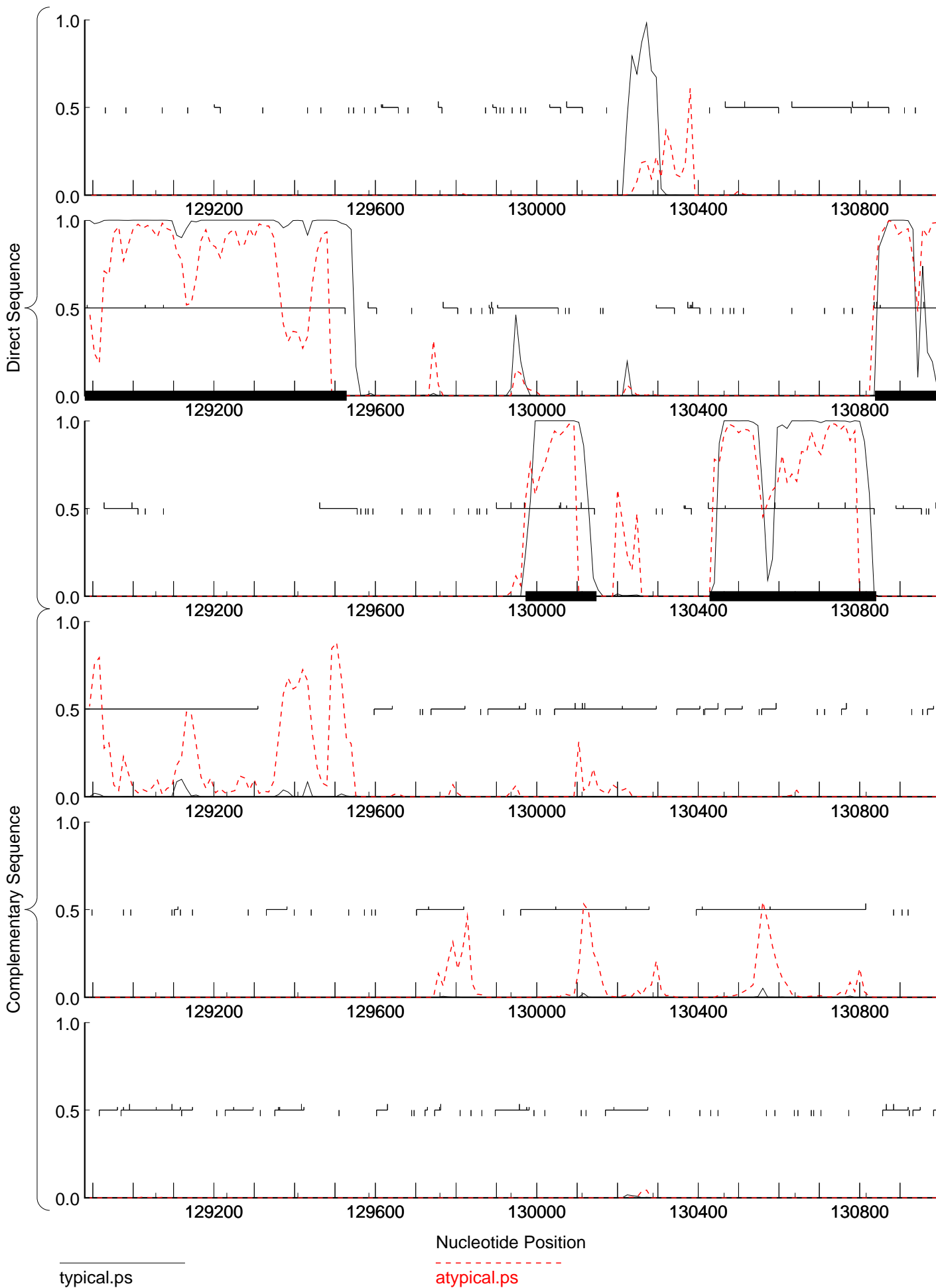




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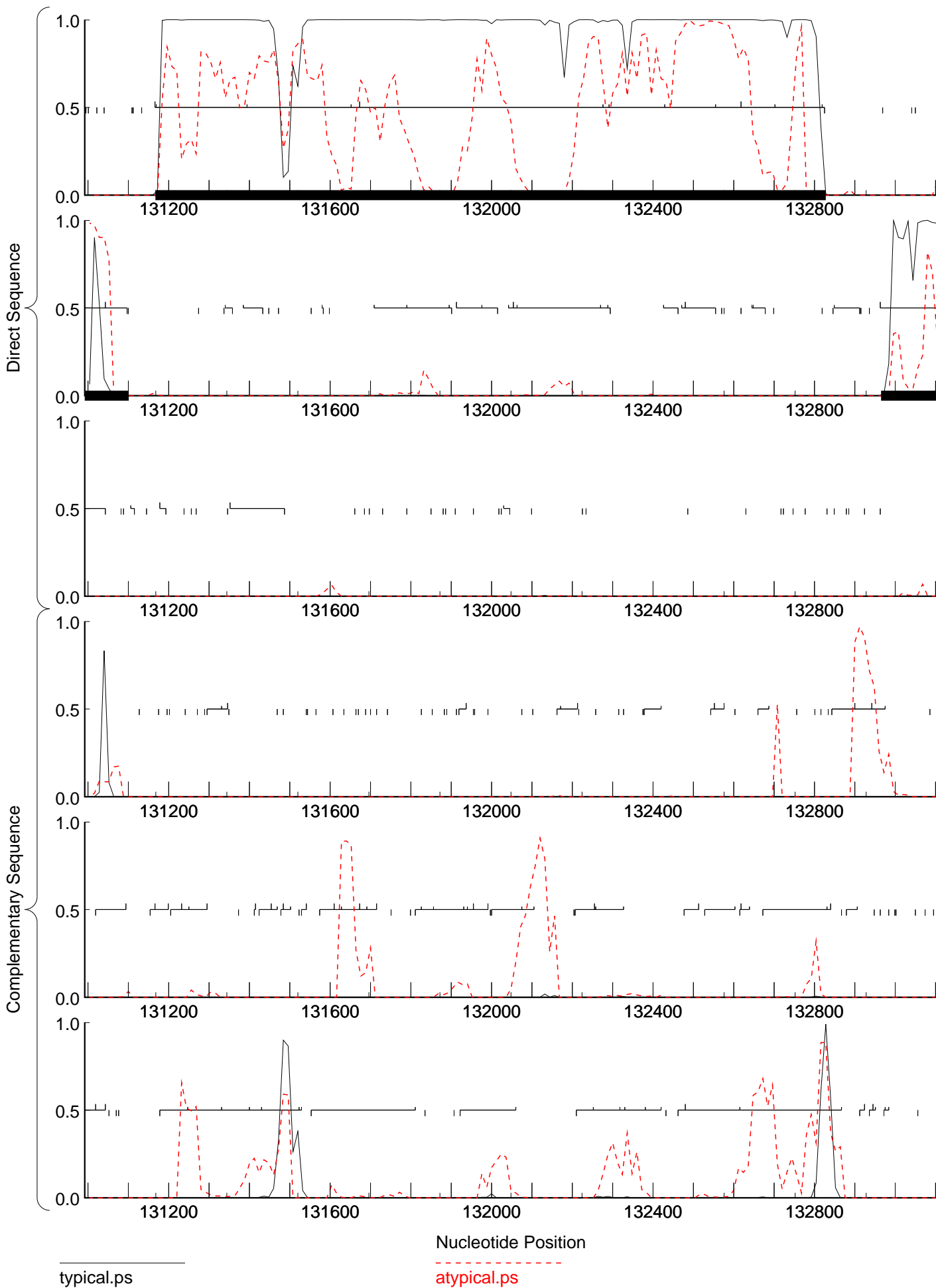
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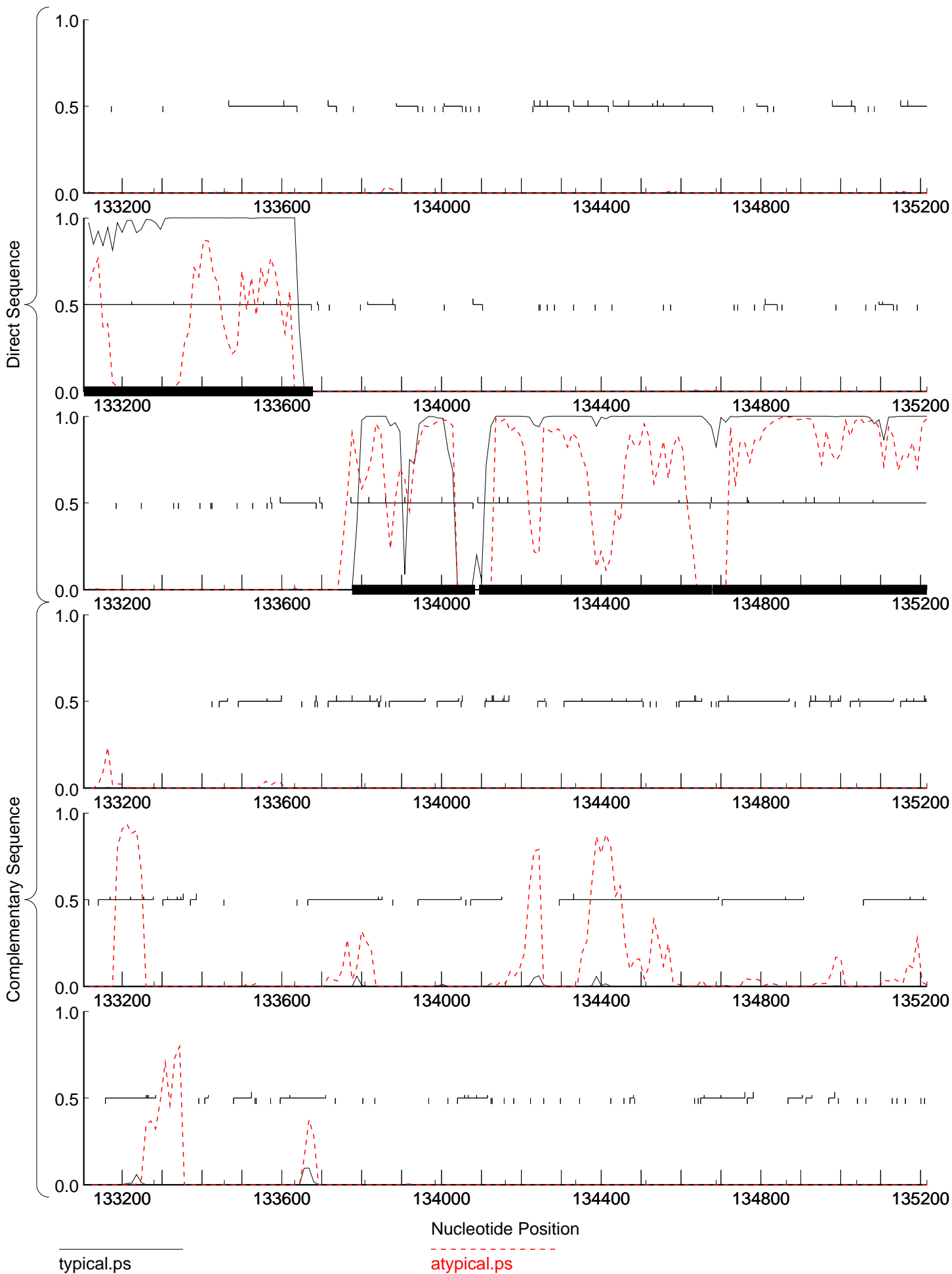


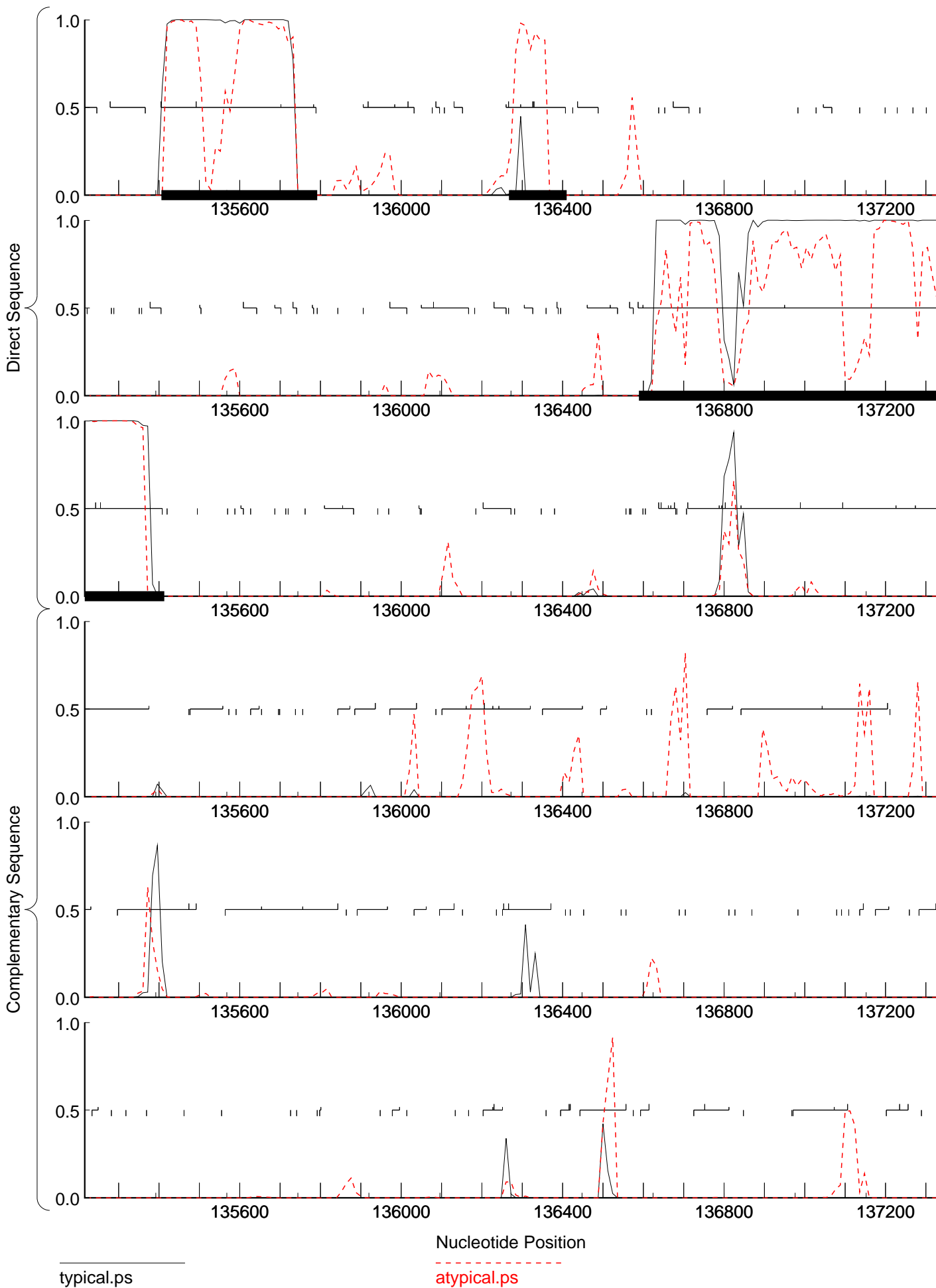


typical.ps

atypical.ps

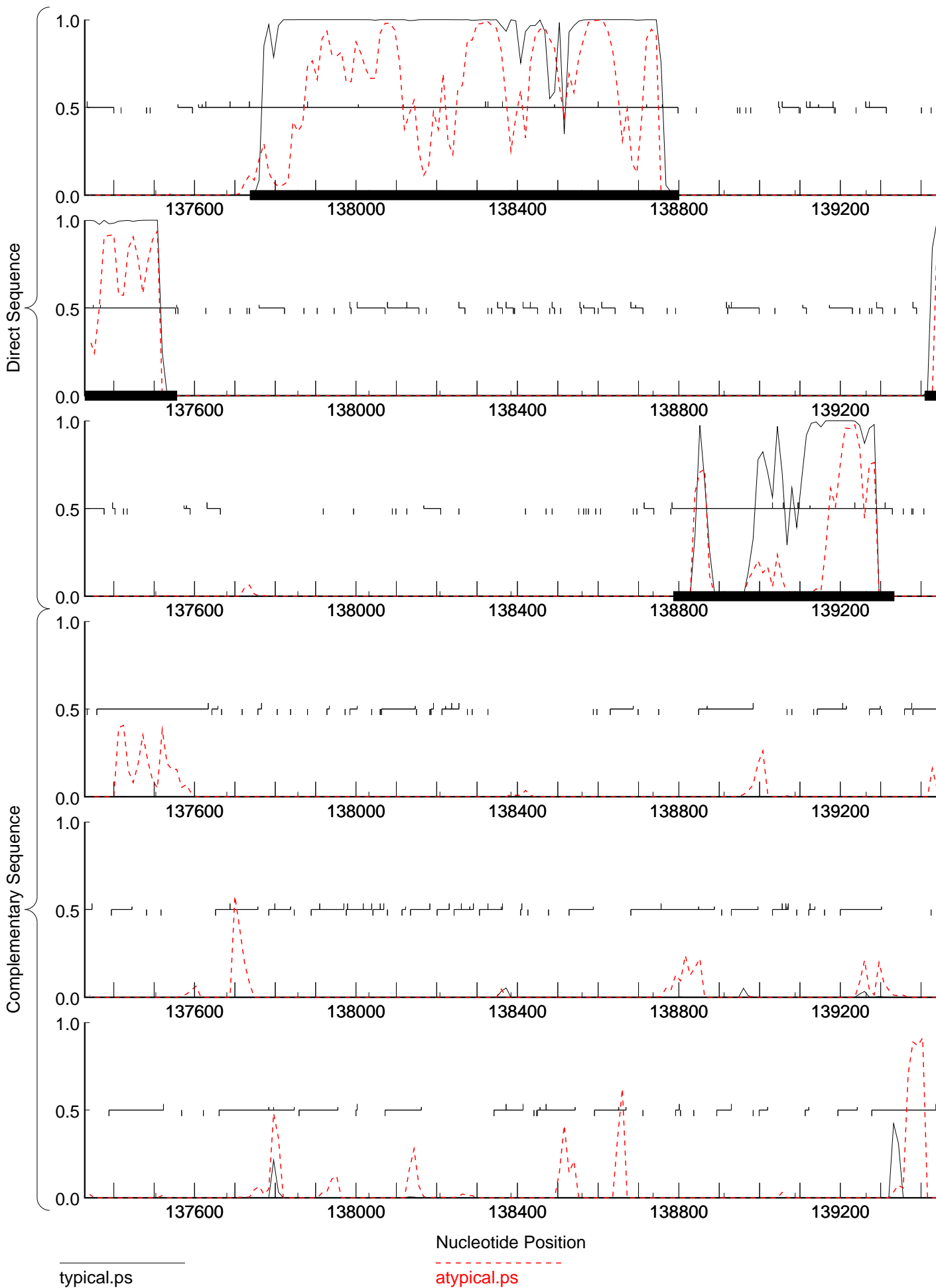






typical.ps

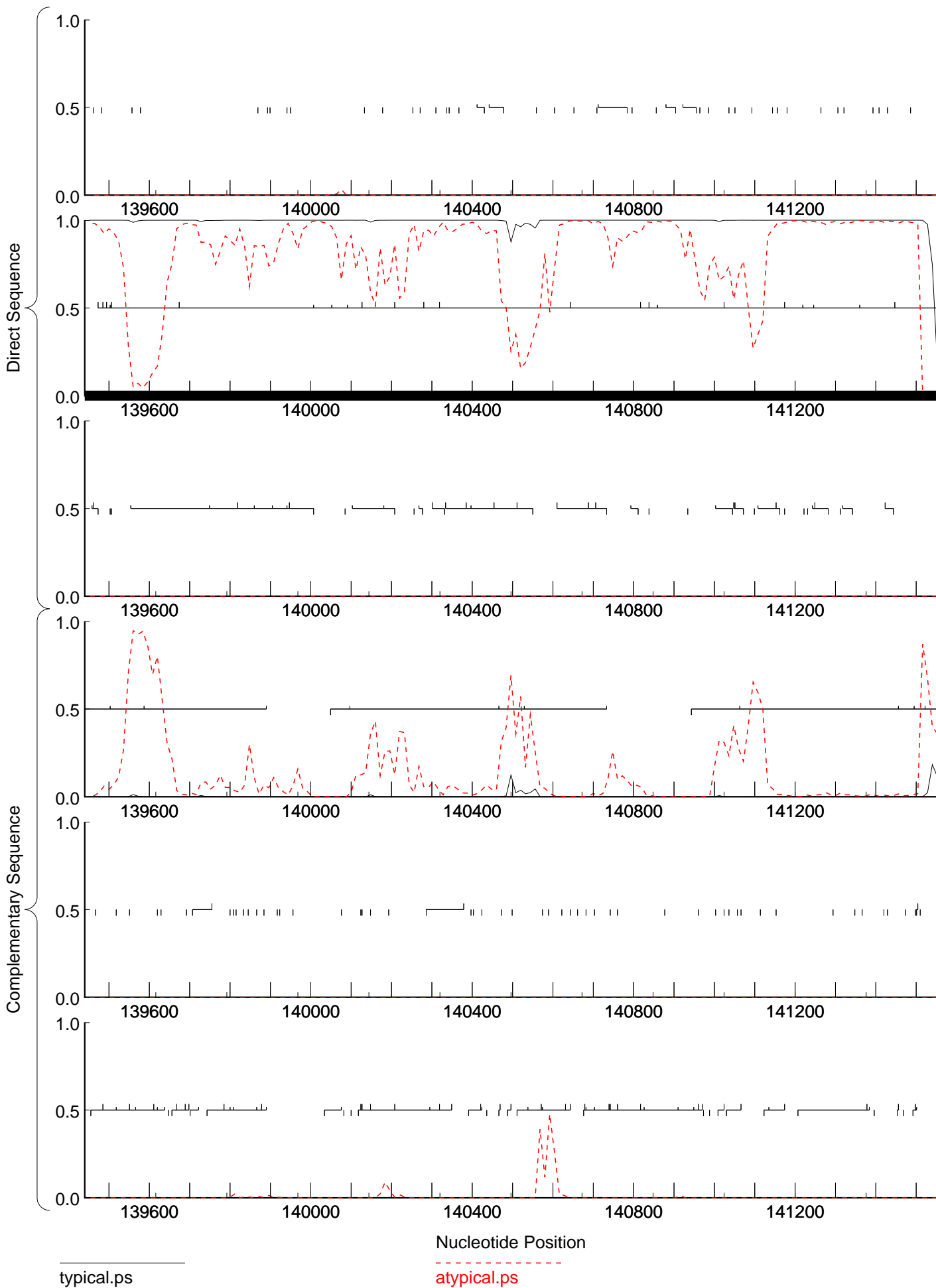
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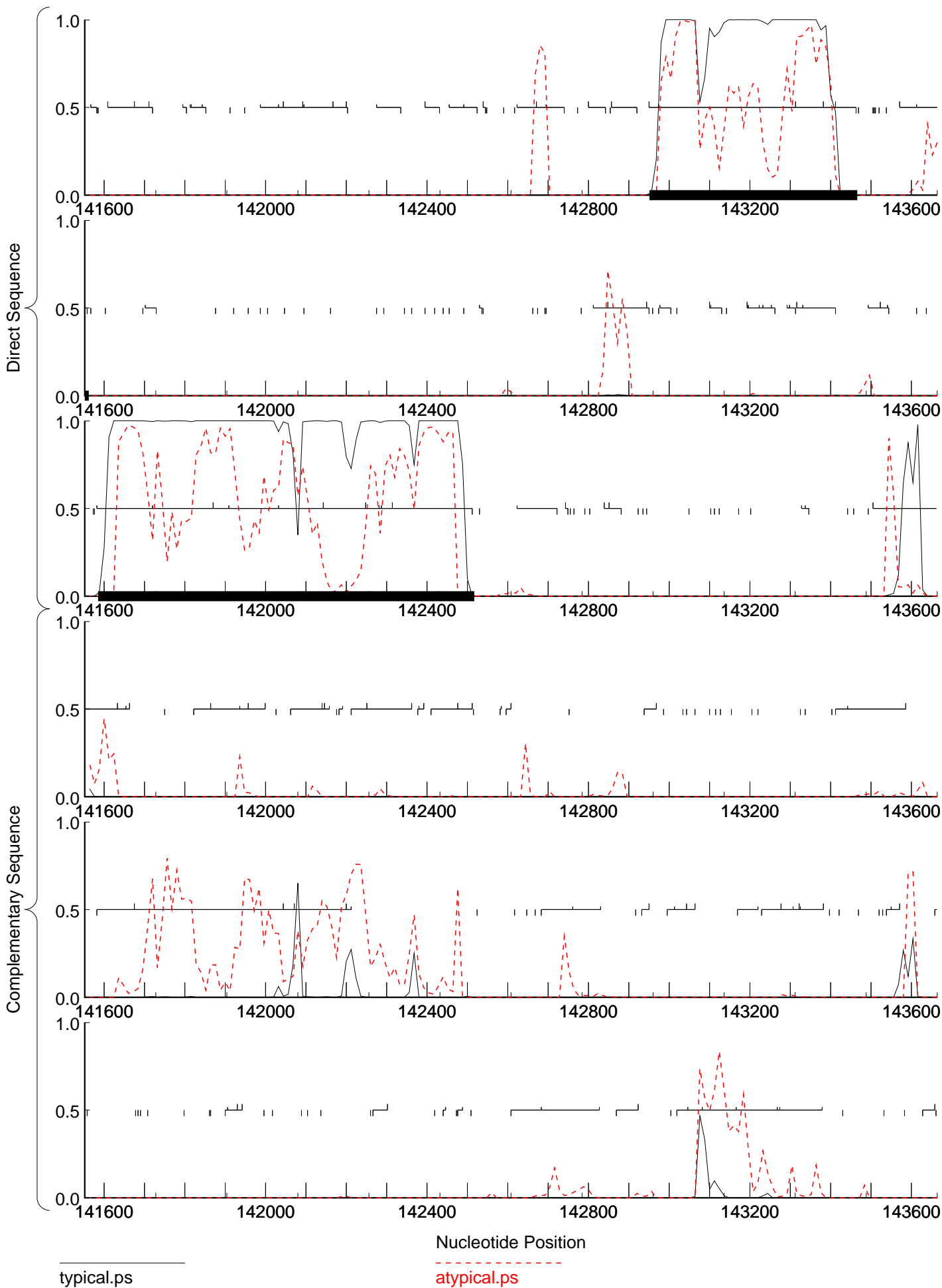
Nucleotide Position

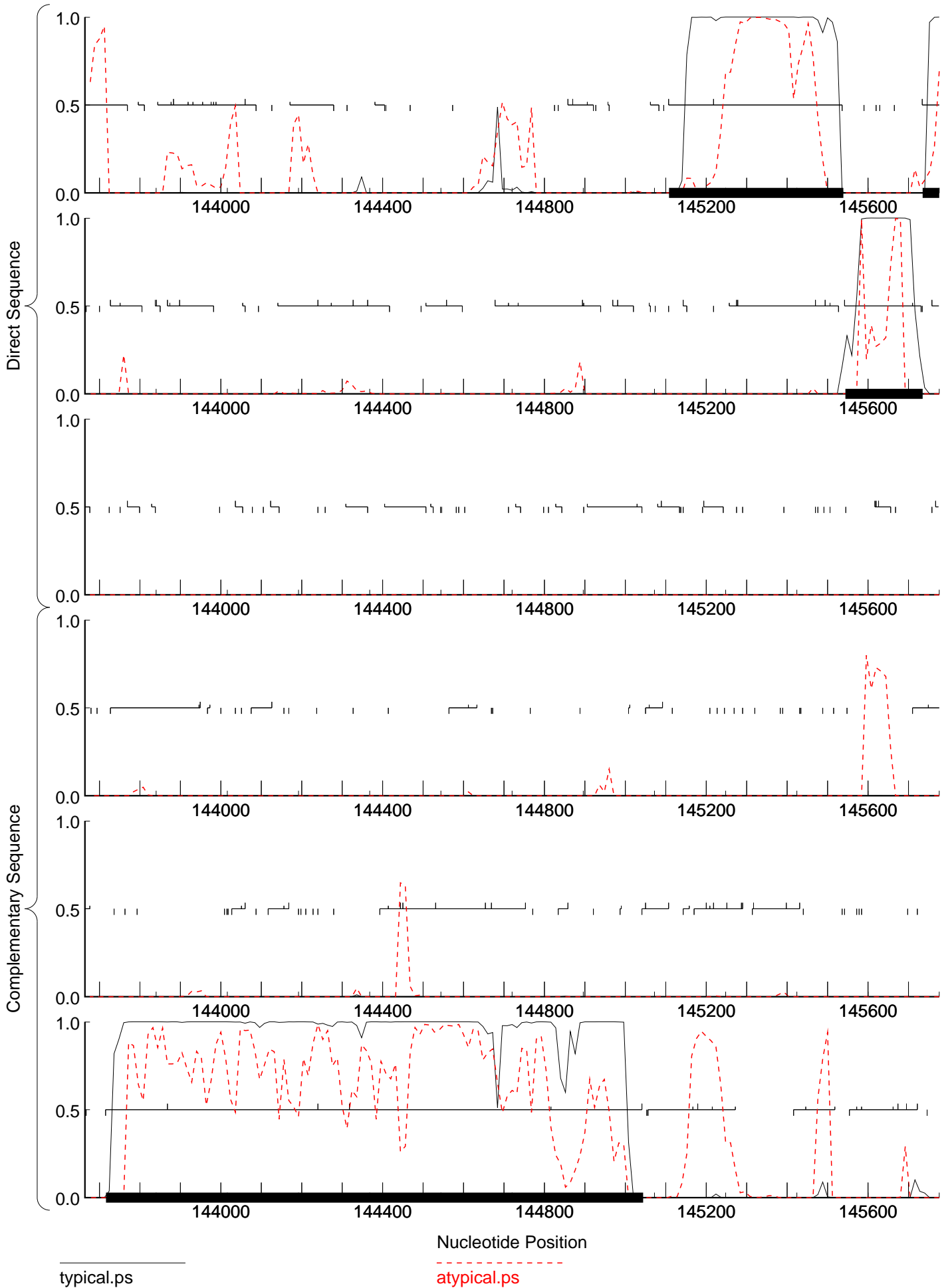
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typical.ps

atypical.ps

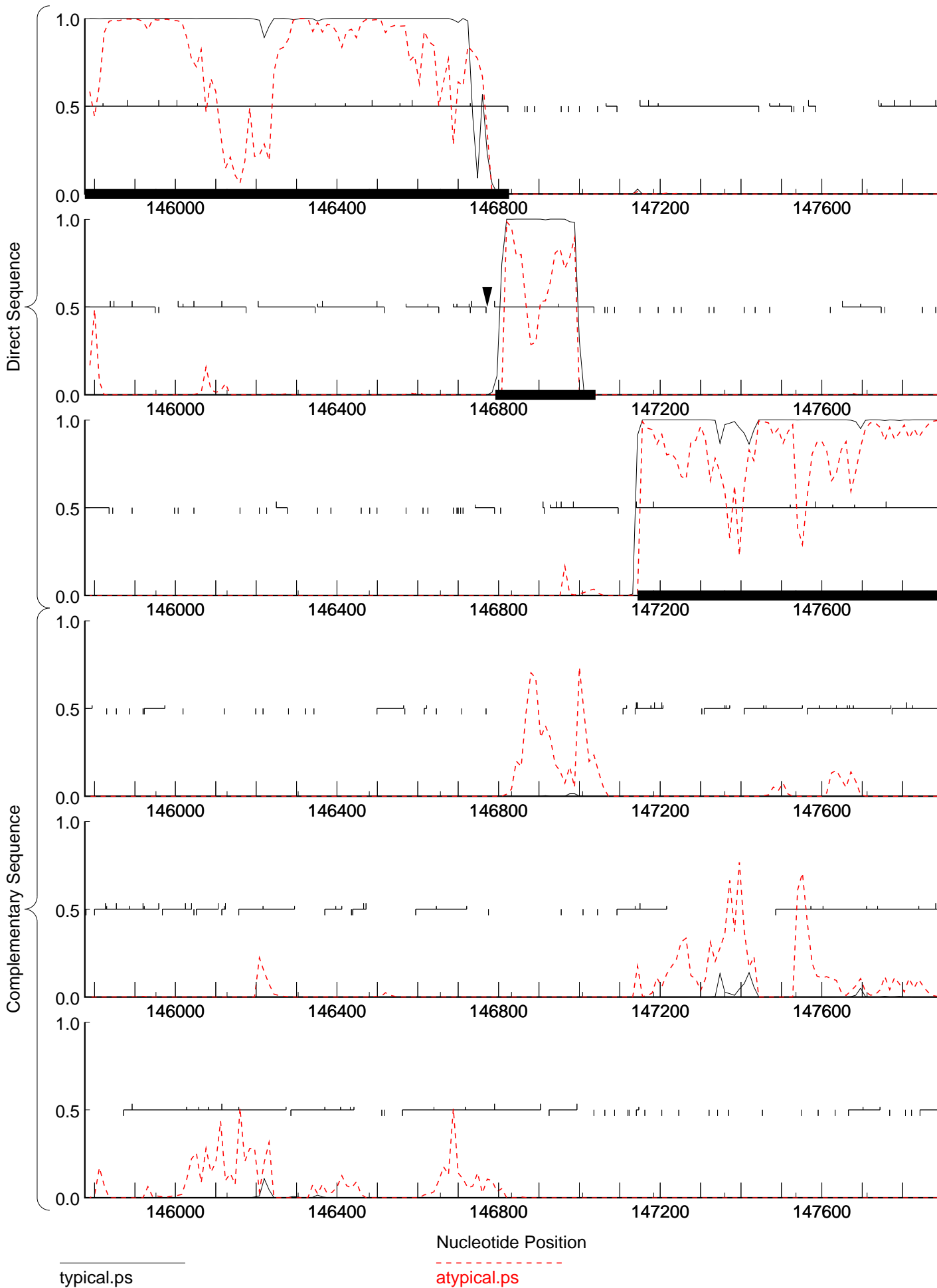




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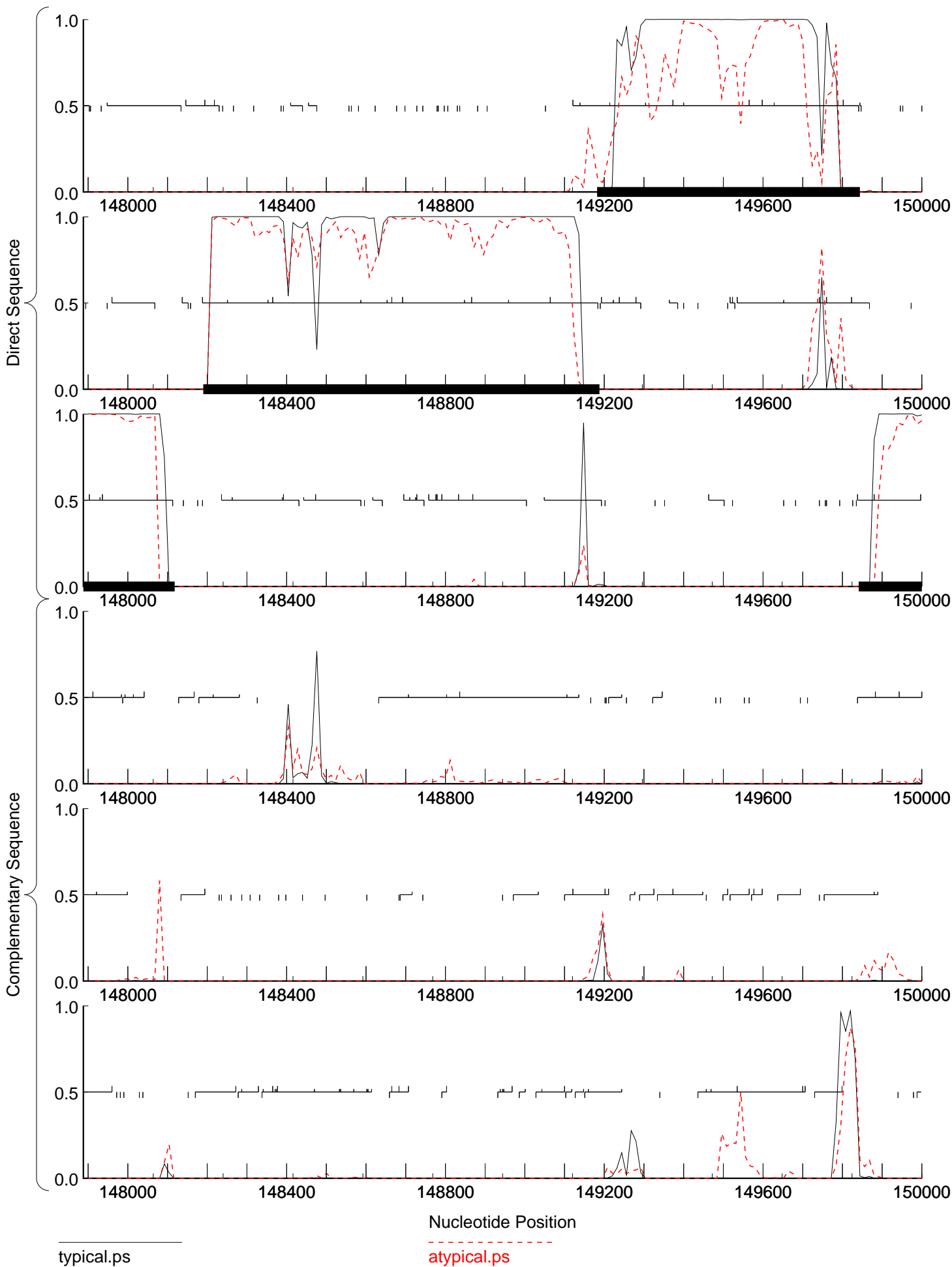
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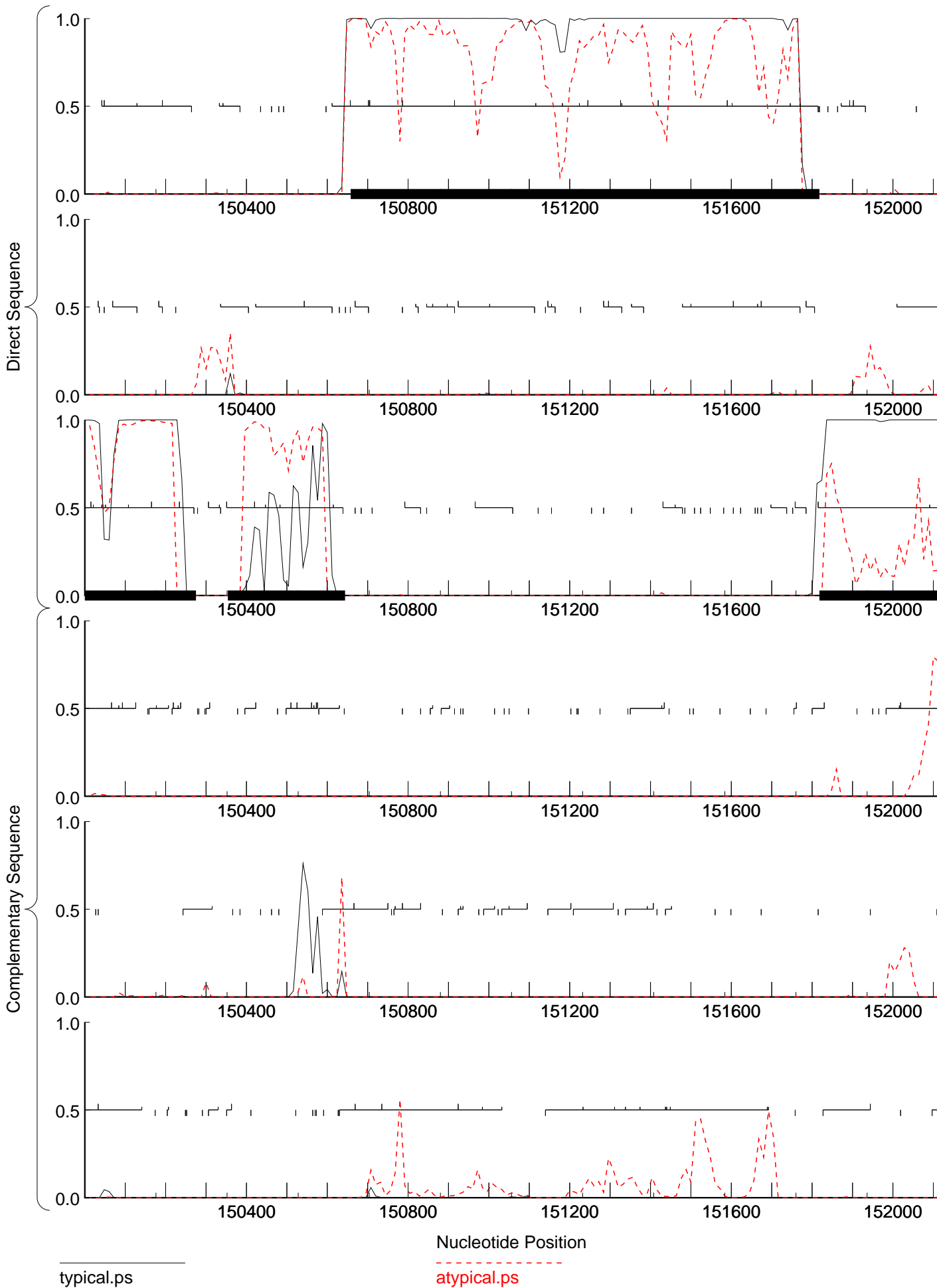
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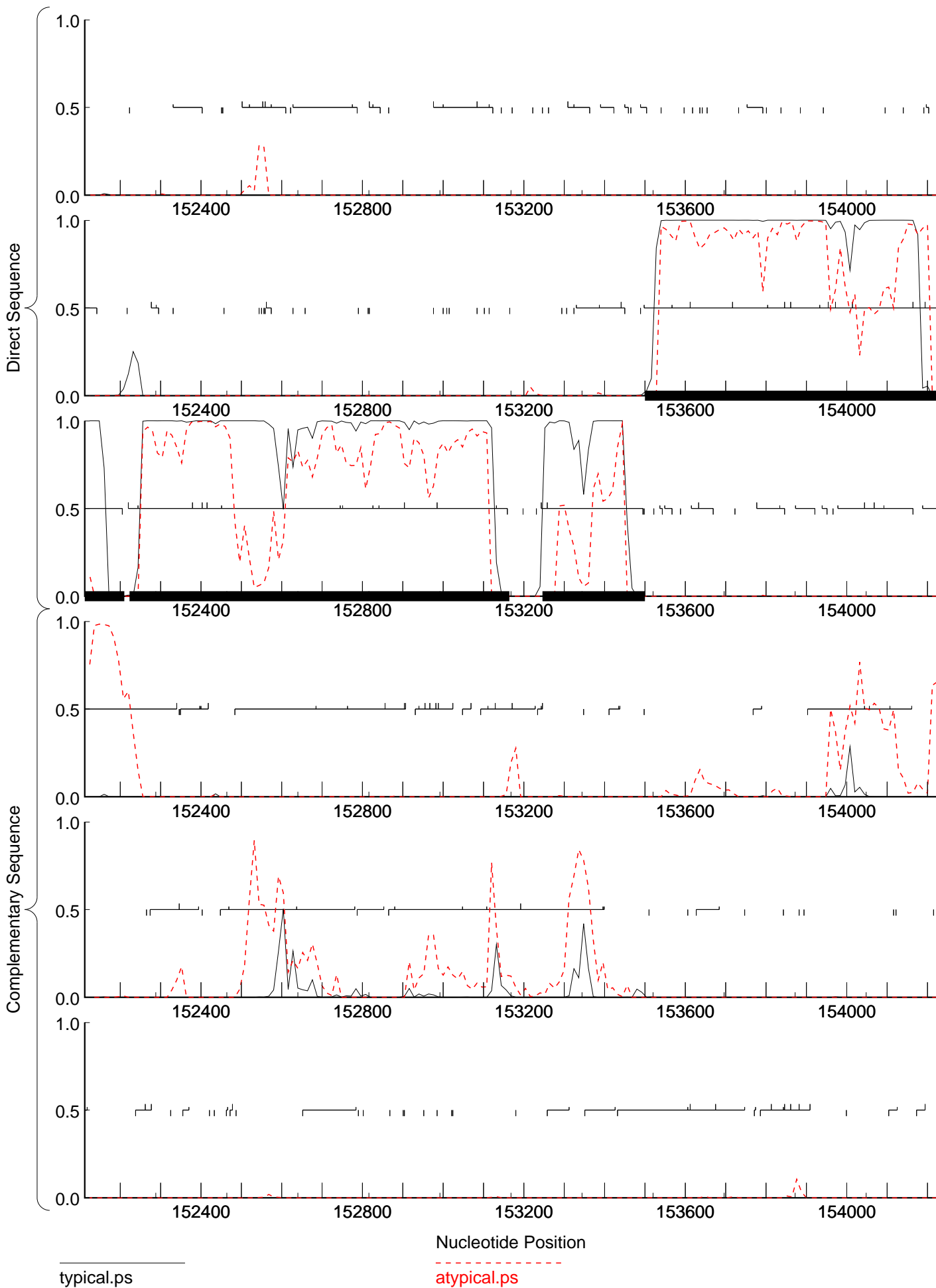


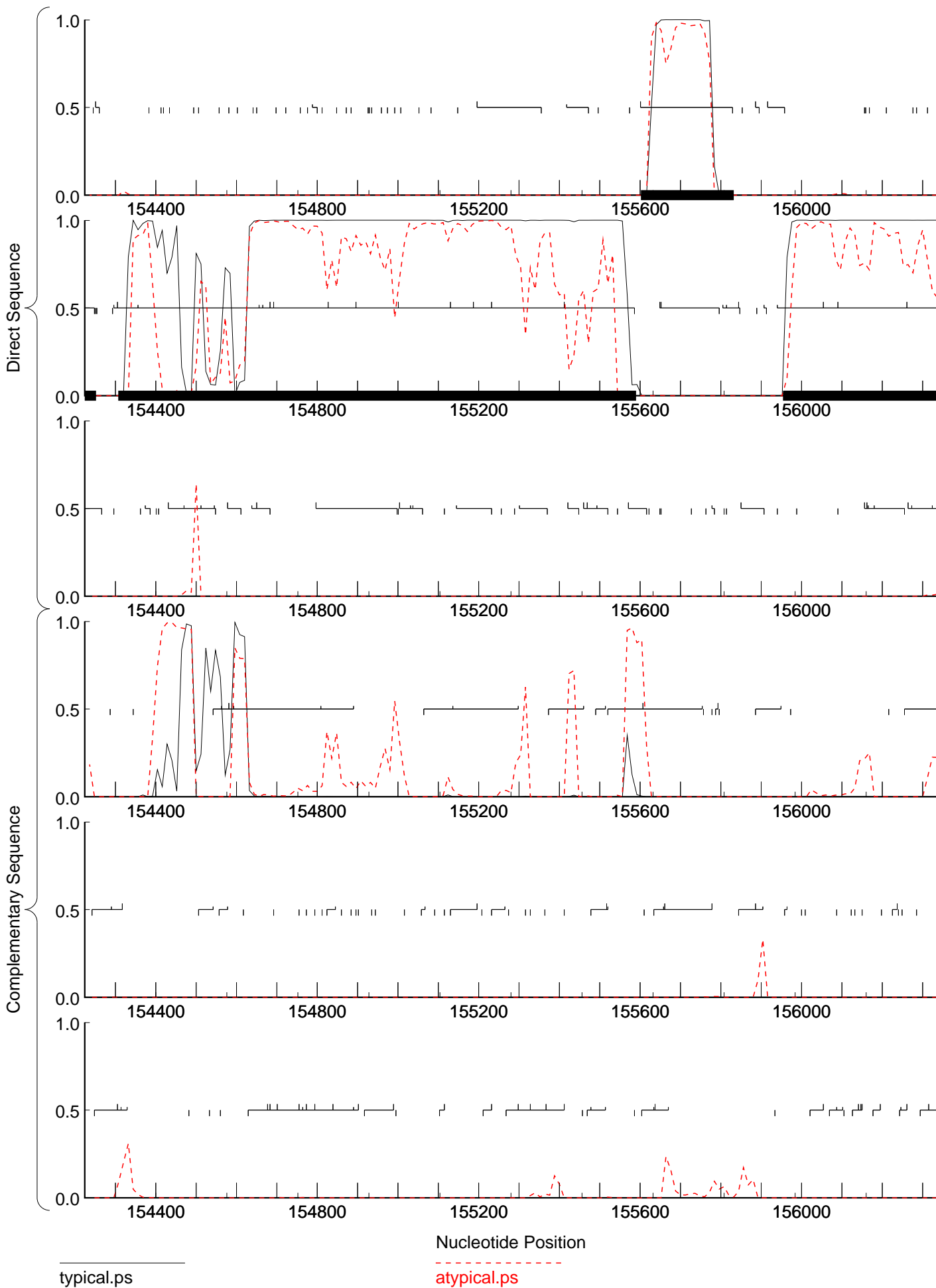
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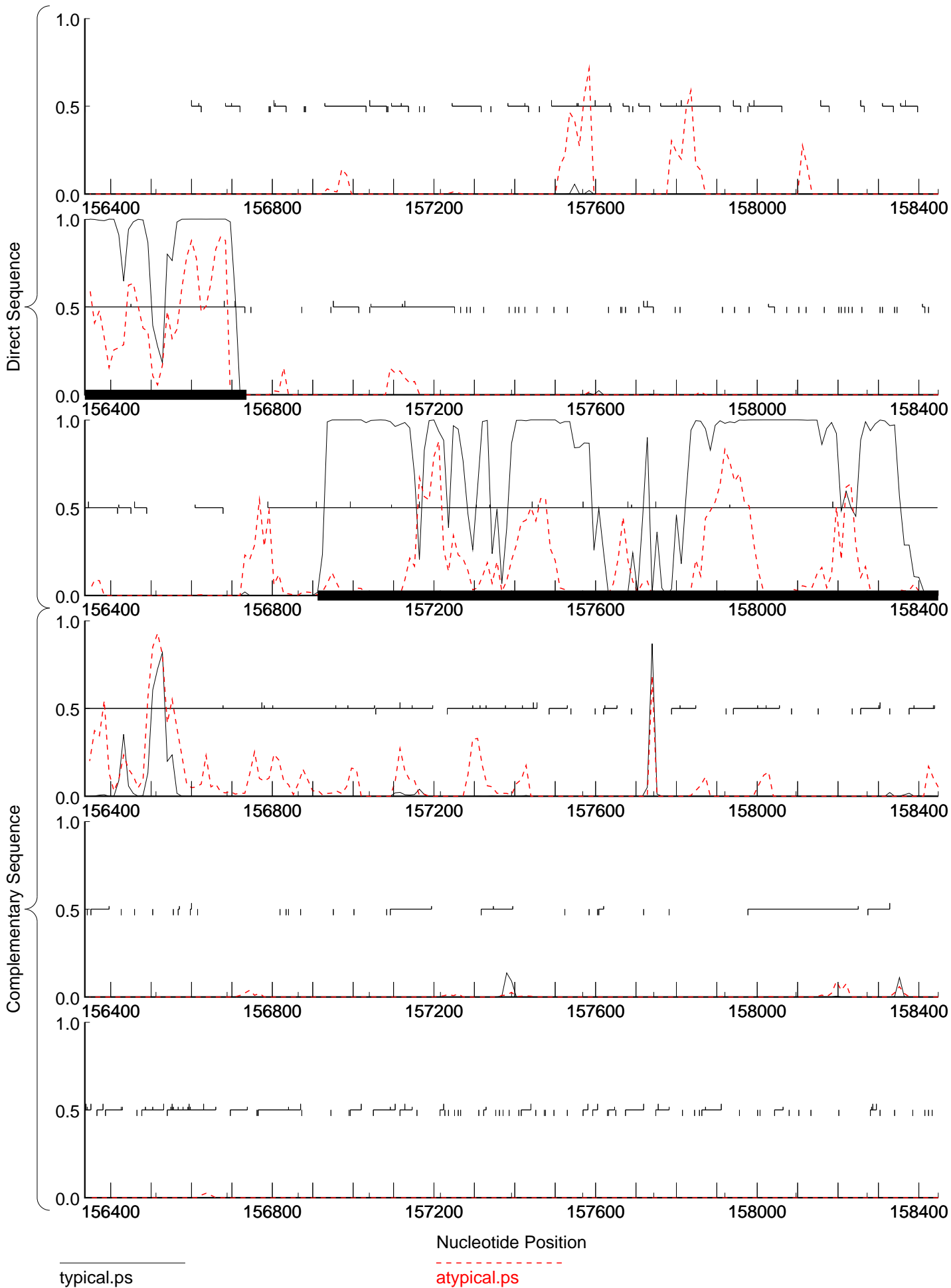


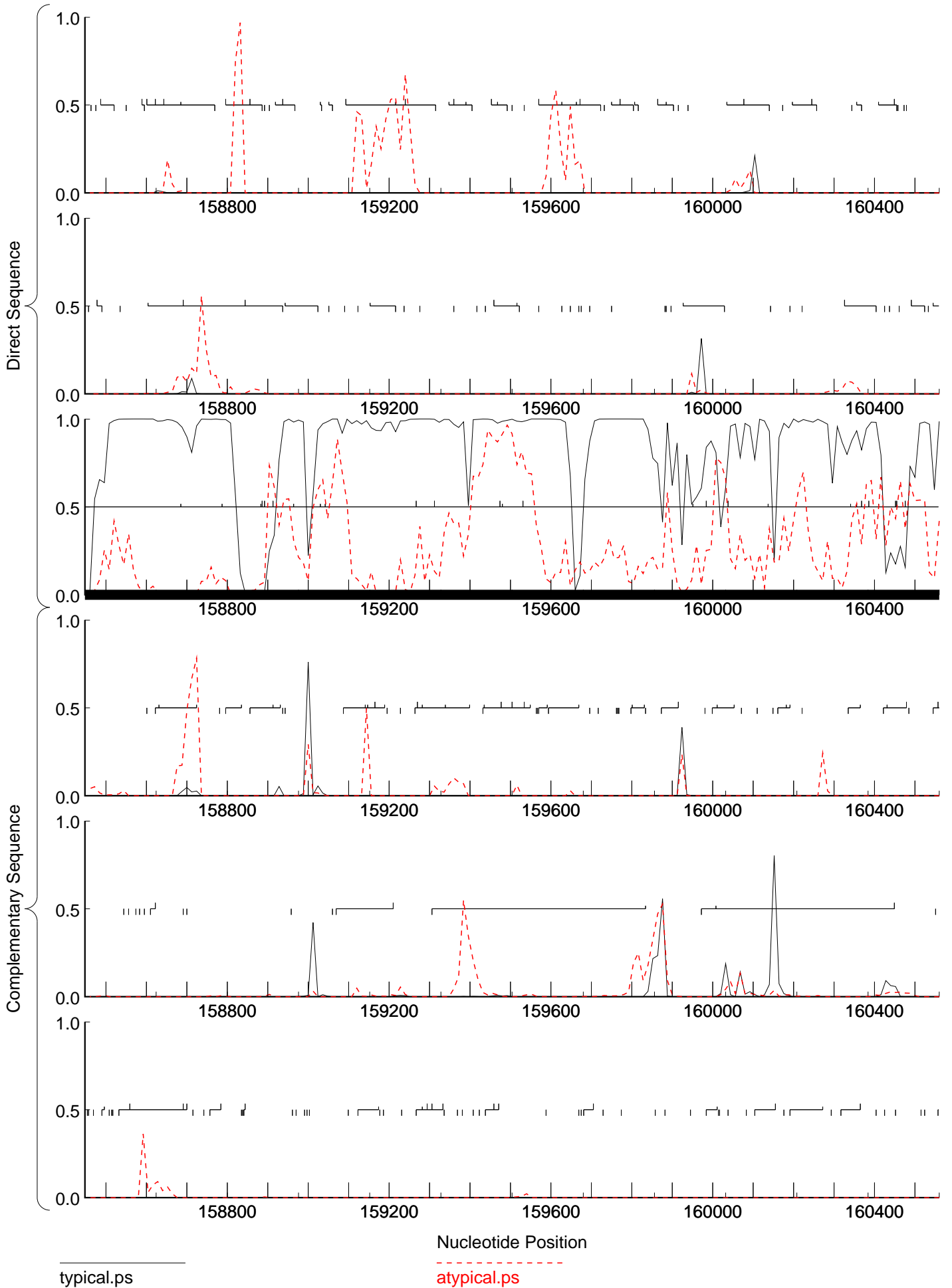


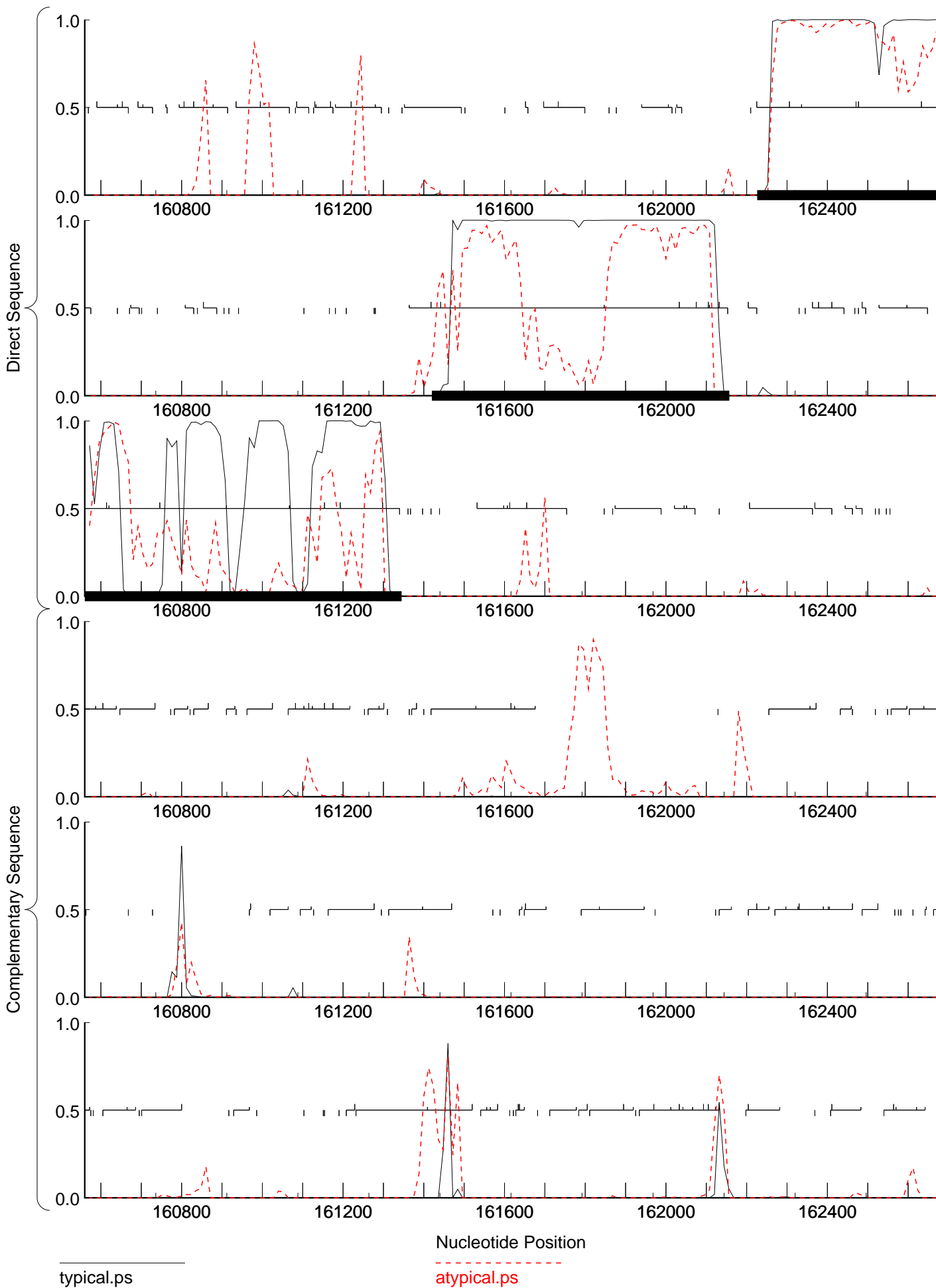


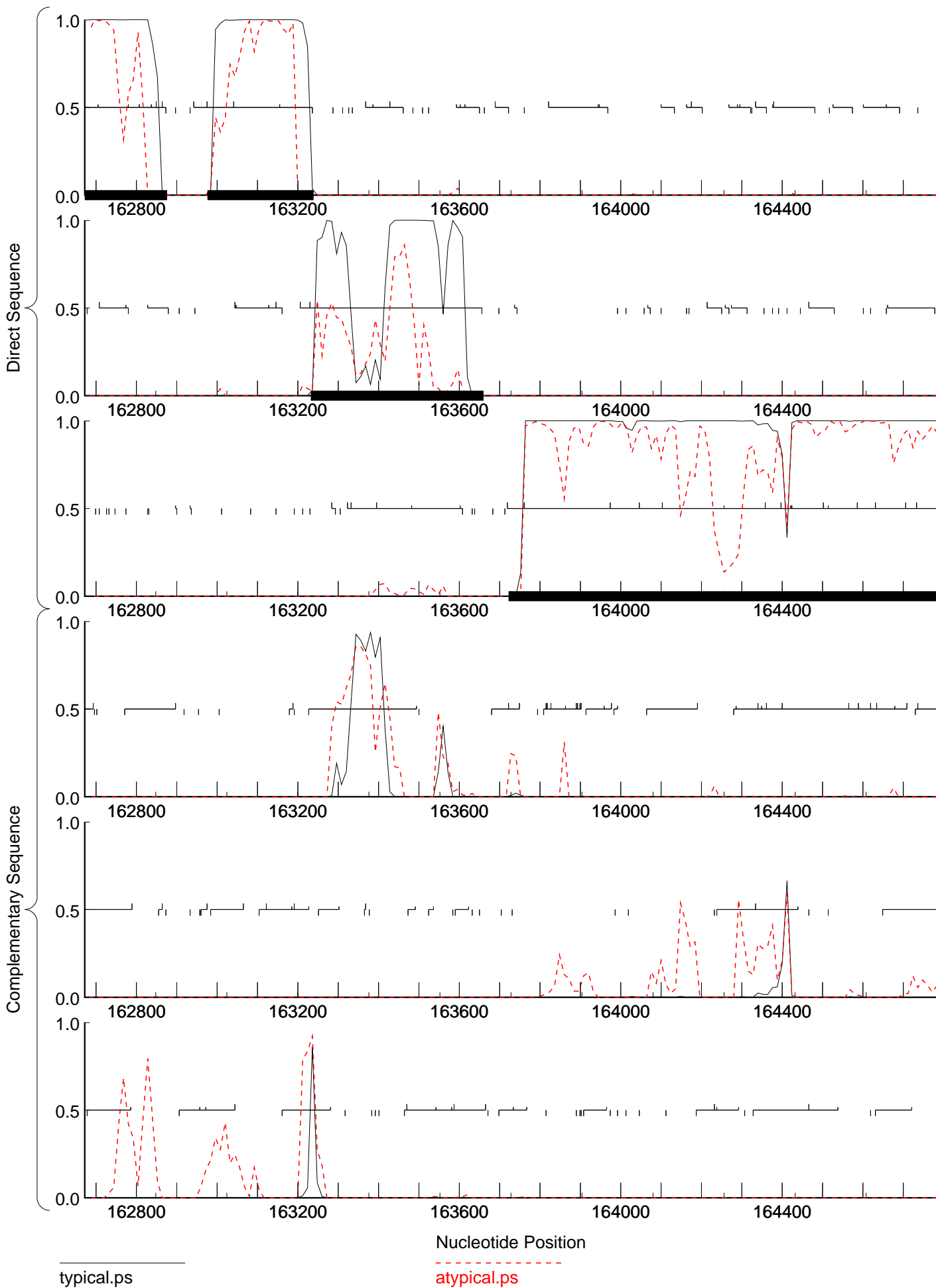
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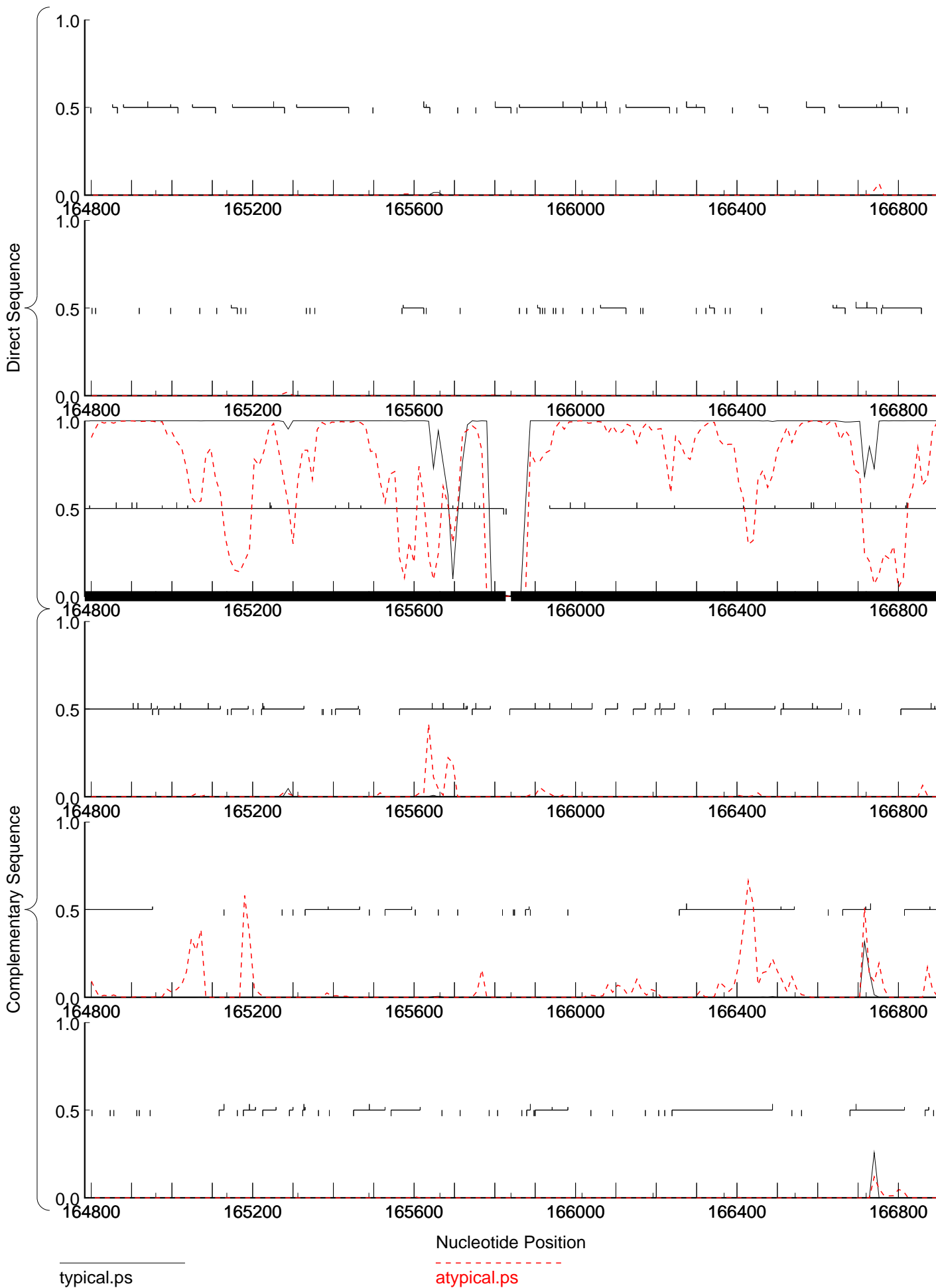
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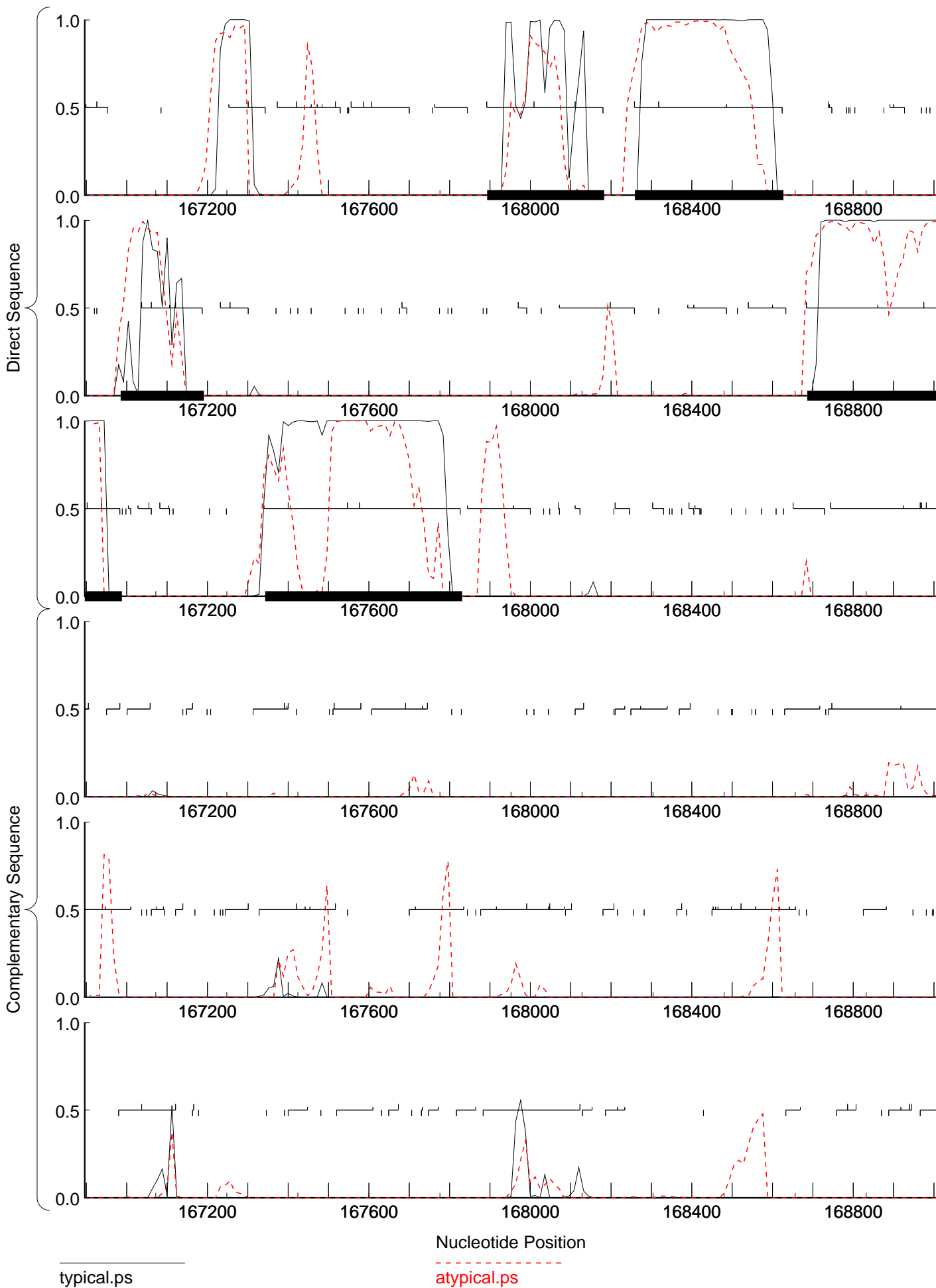


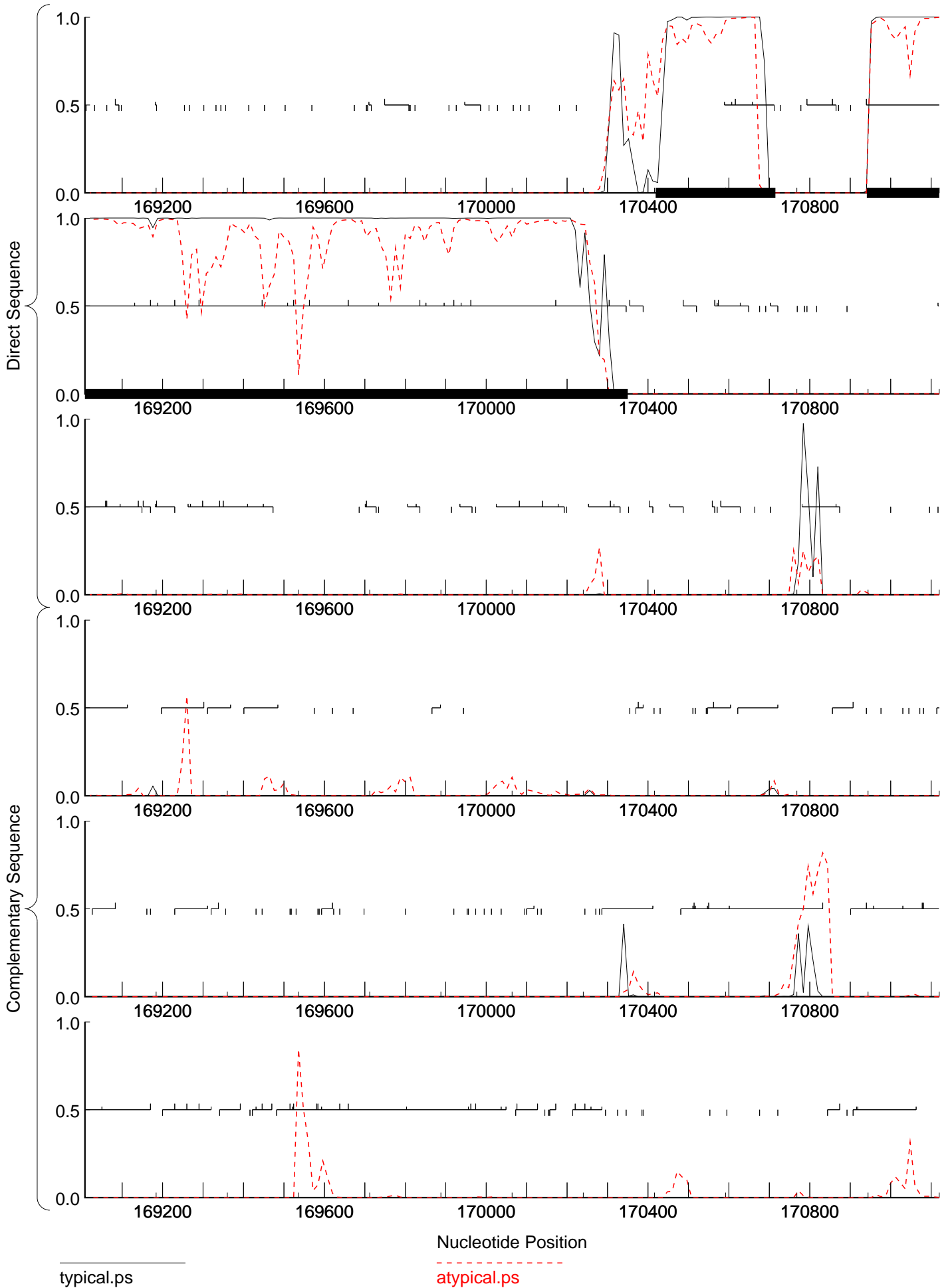


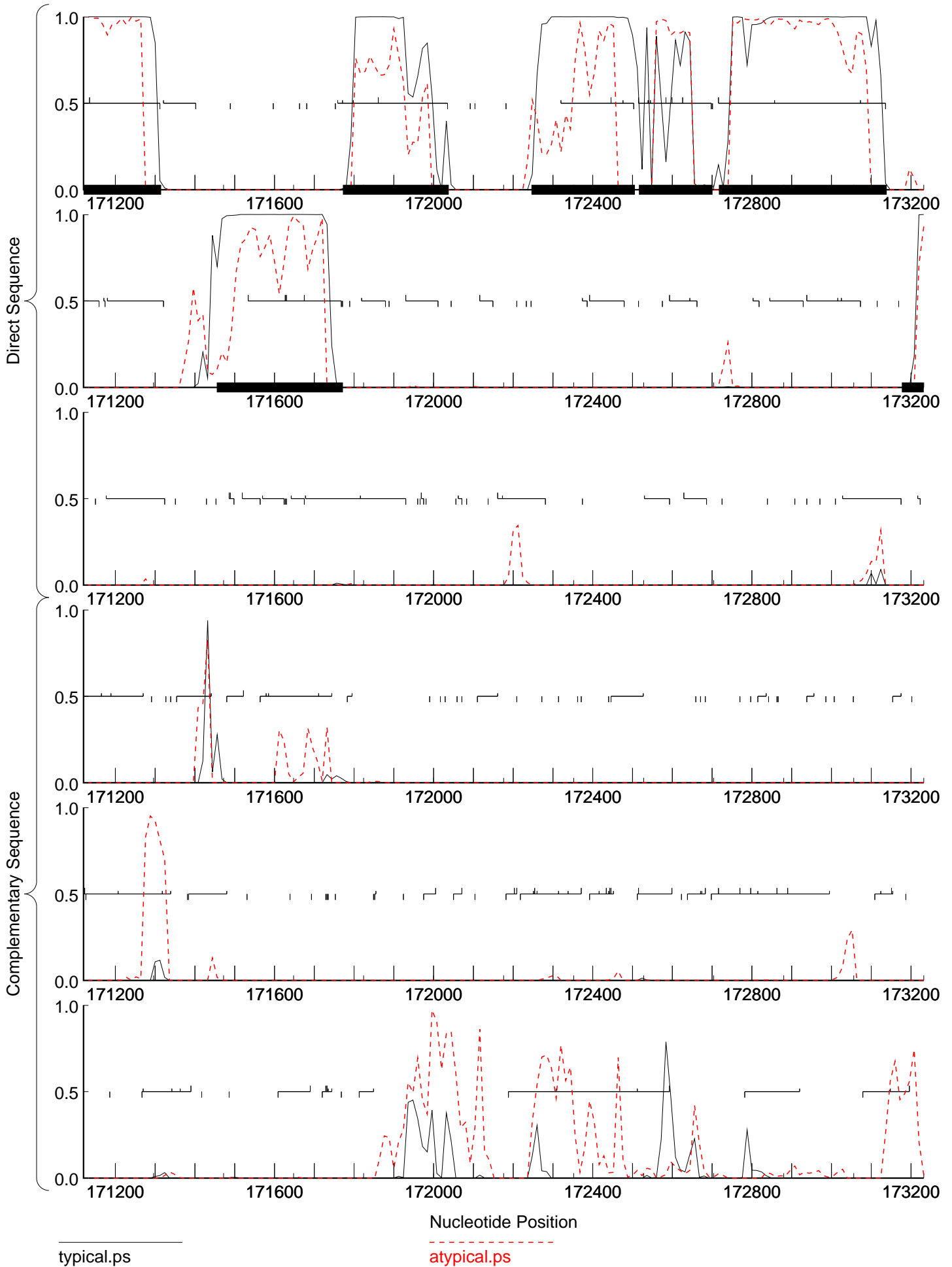












typical.ps

atypical.ps

