

GeneMark

Version 2.5p (09.08.06)

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PROGRAM INFORMATION

Sequence : Mycobacterium phage HenryJackson complete sequence, 69033 bp, circularly permuted, Cluster
Analysis Date : 5/27/18 at 14:57:37
Pages : 34
Sequence Length : 69033 bp
GC Content : 66.51%

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,

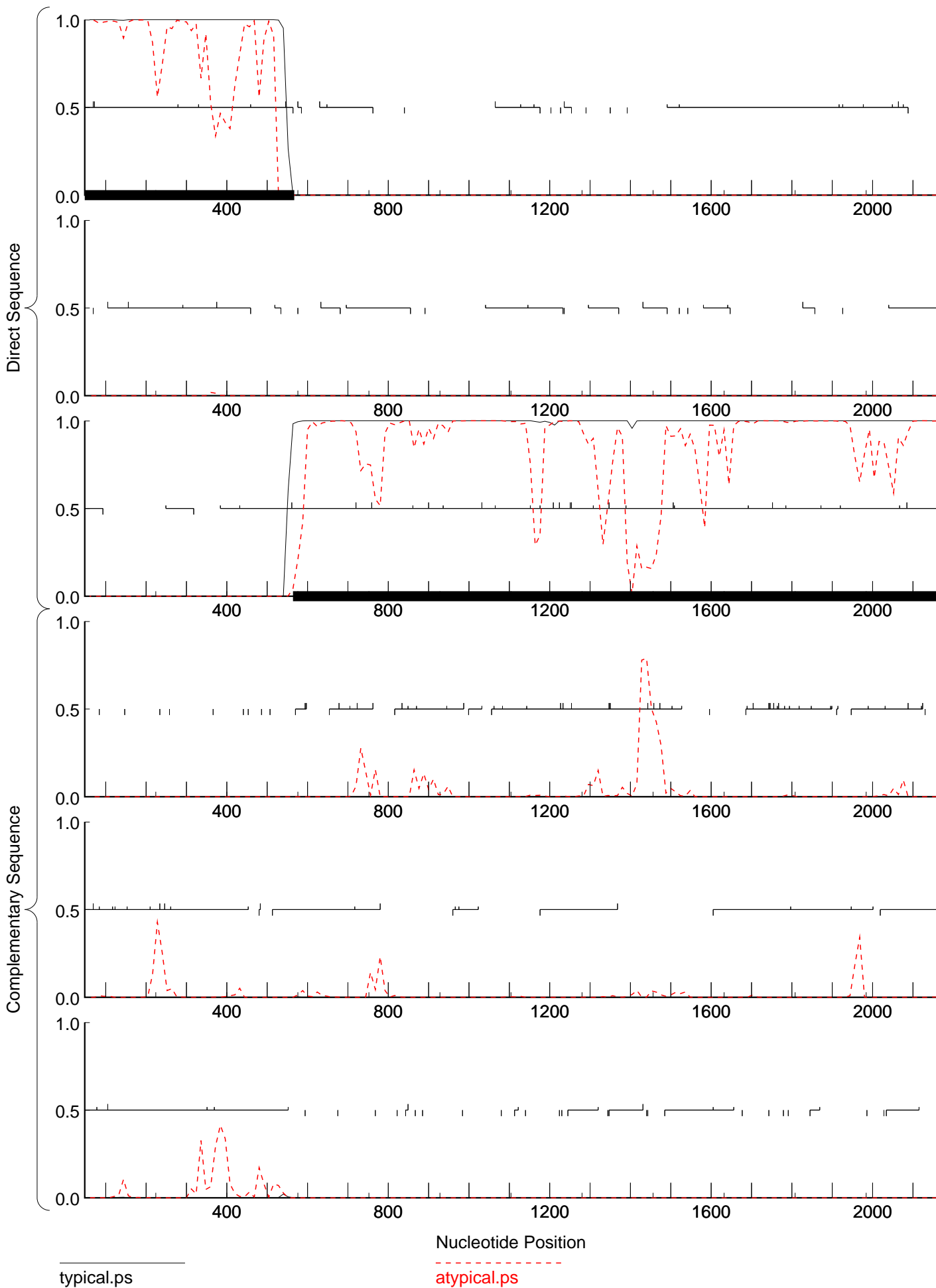
Matrix notes & comments

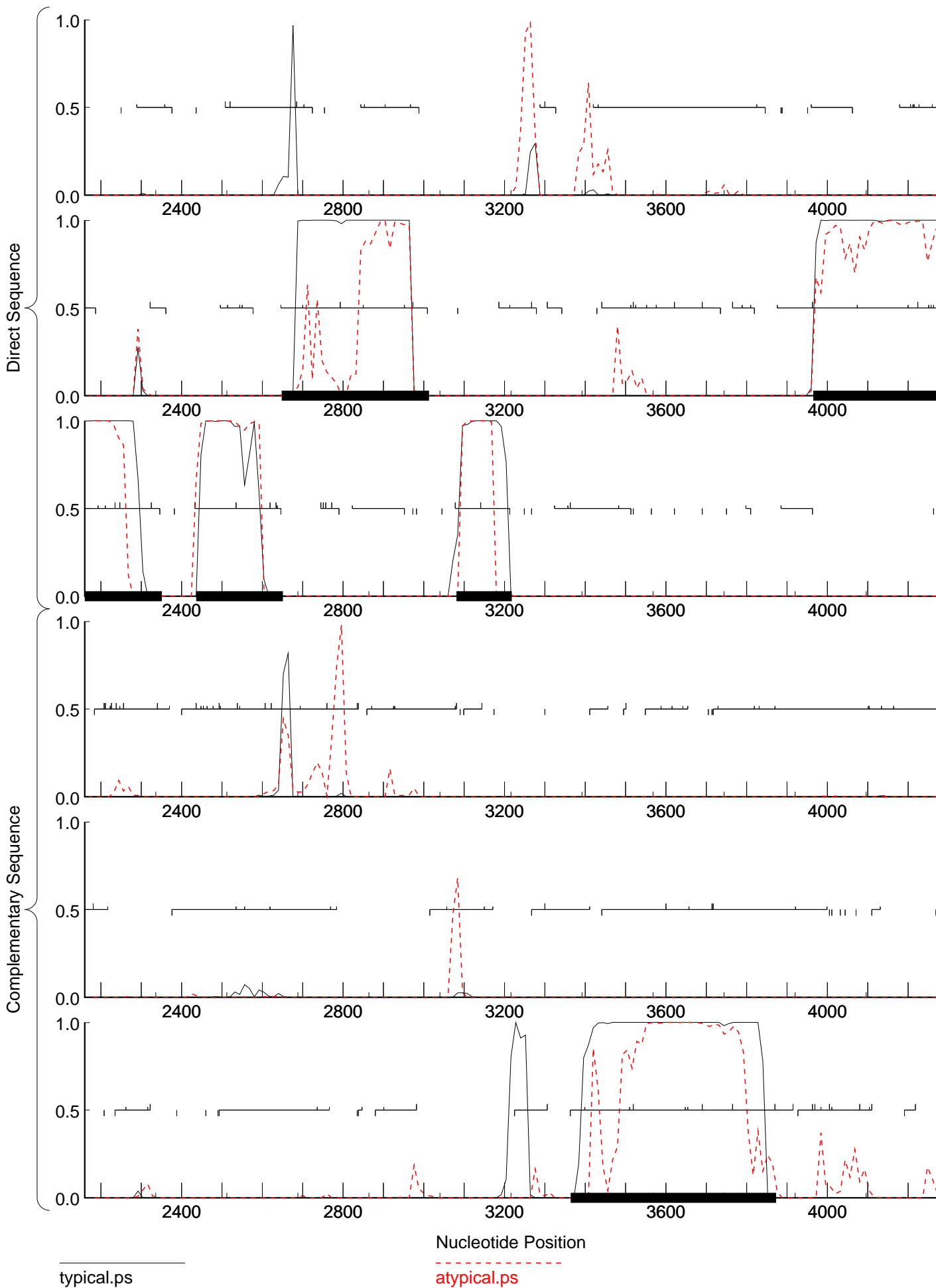
Training set derived by GeneMarkS, 4.30 October 2014
Sun May 27 14:57:37 2018

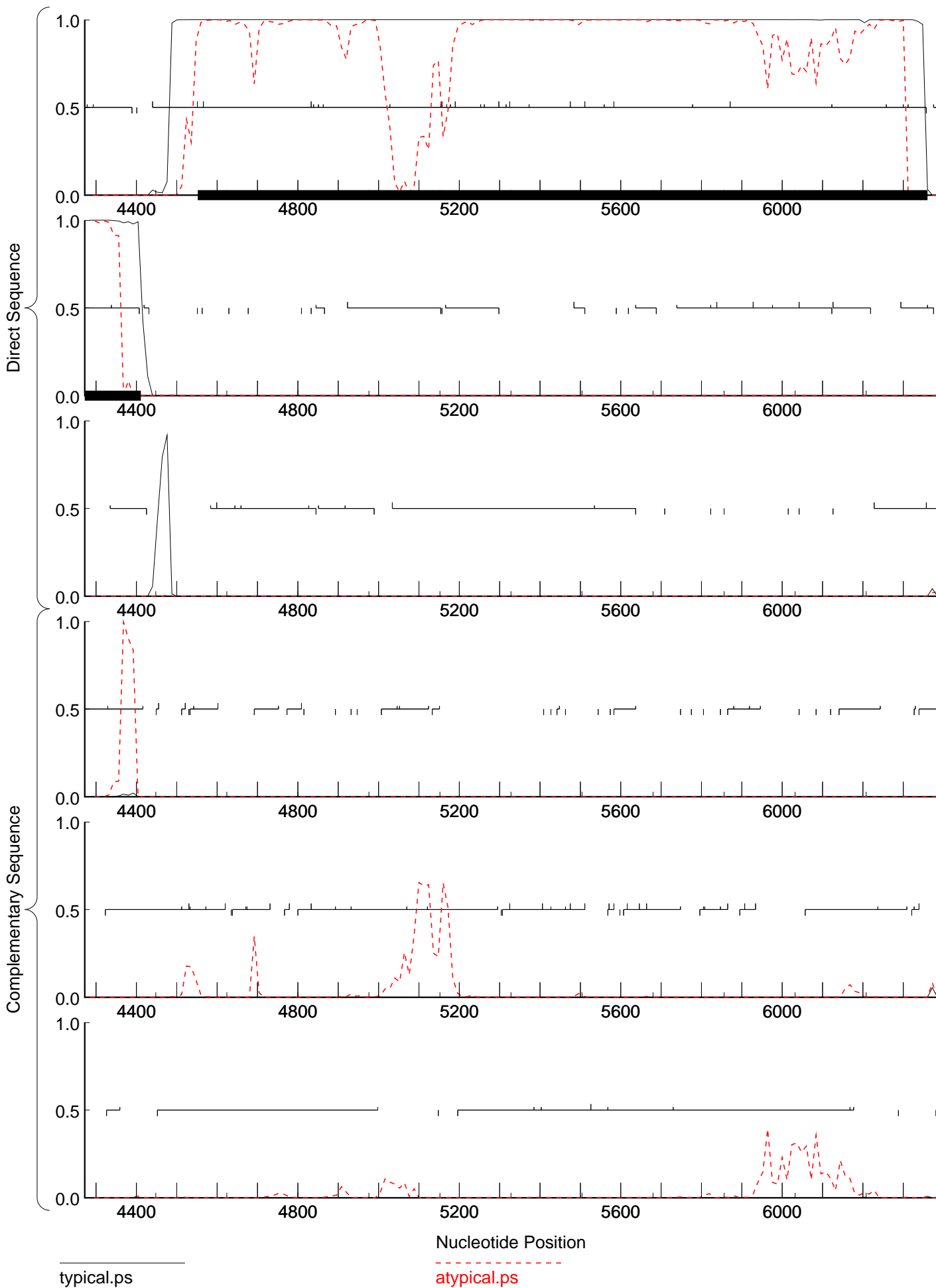
MATRIX INFORMATION

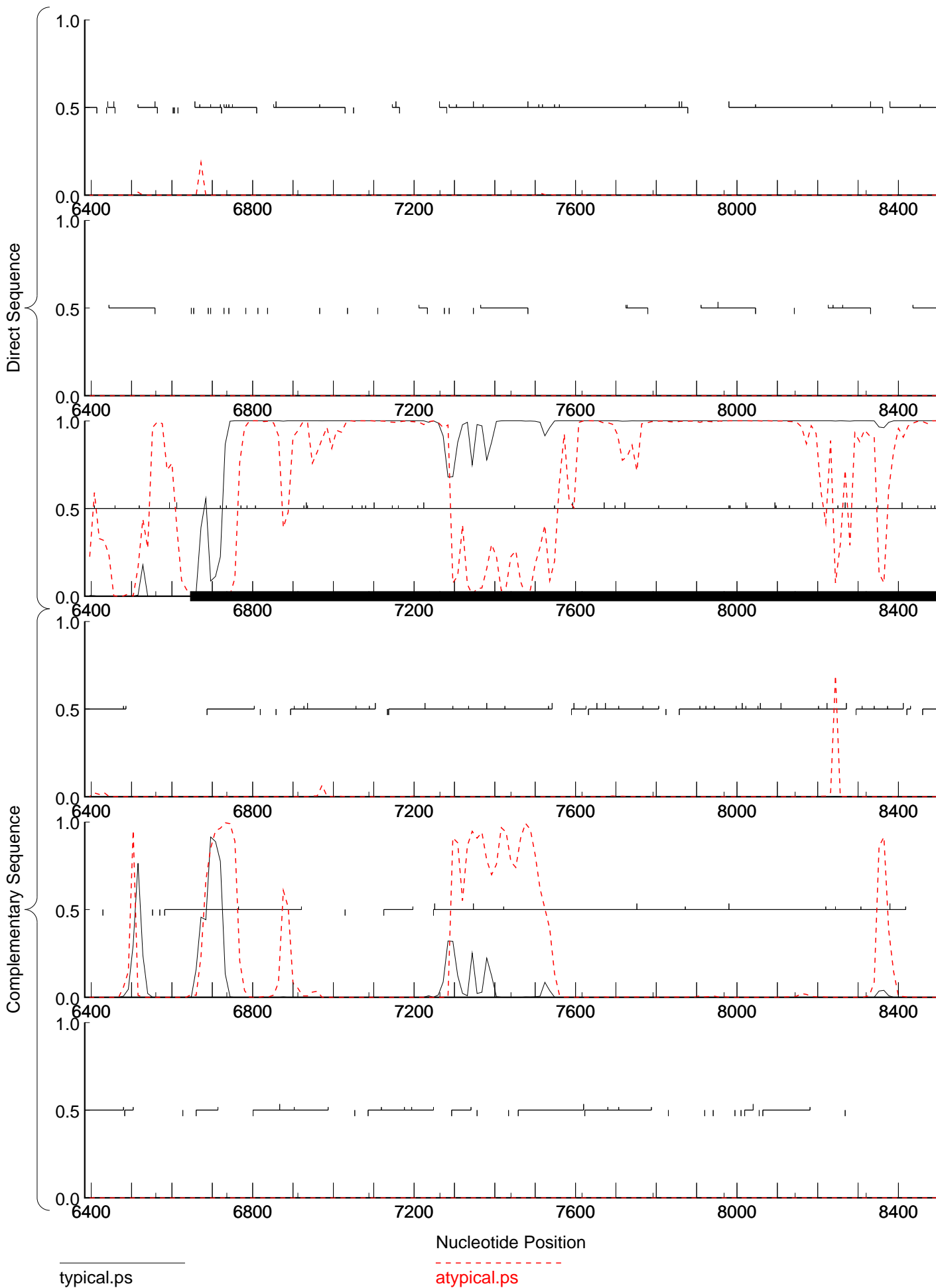
Matrix : -
Author : -
Order : 4

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



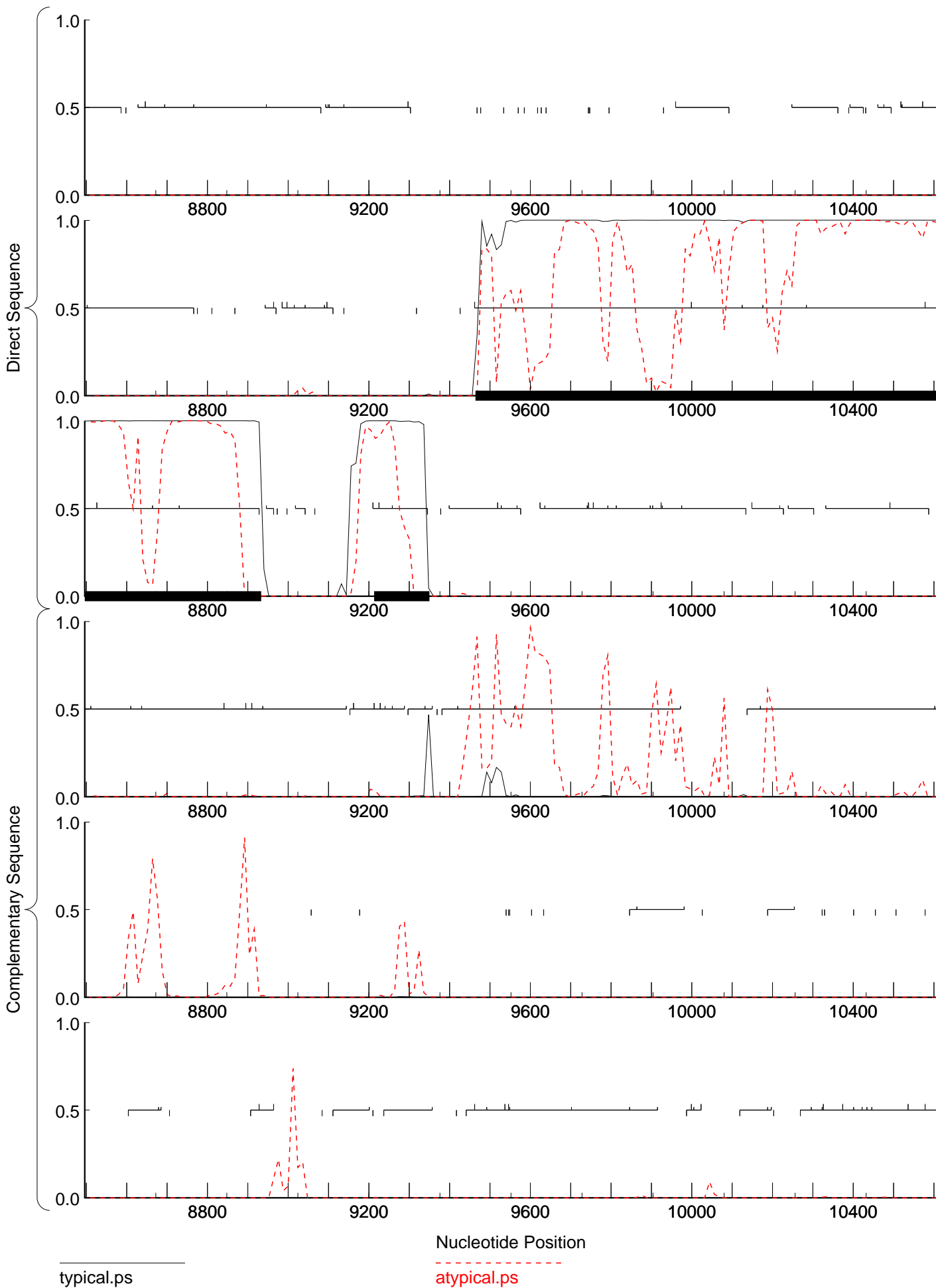


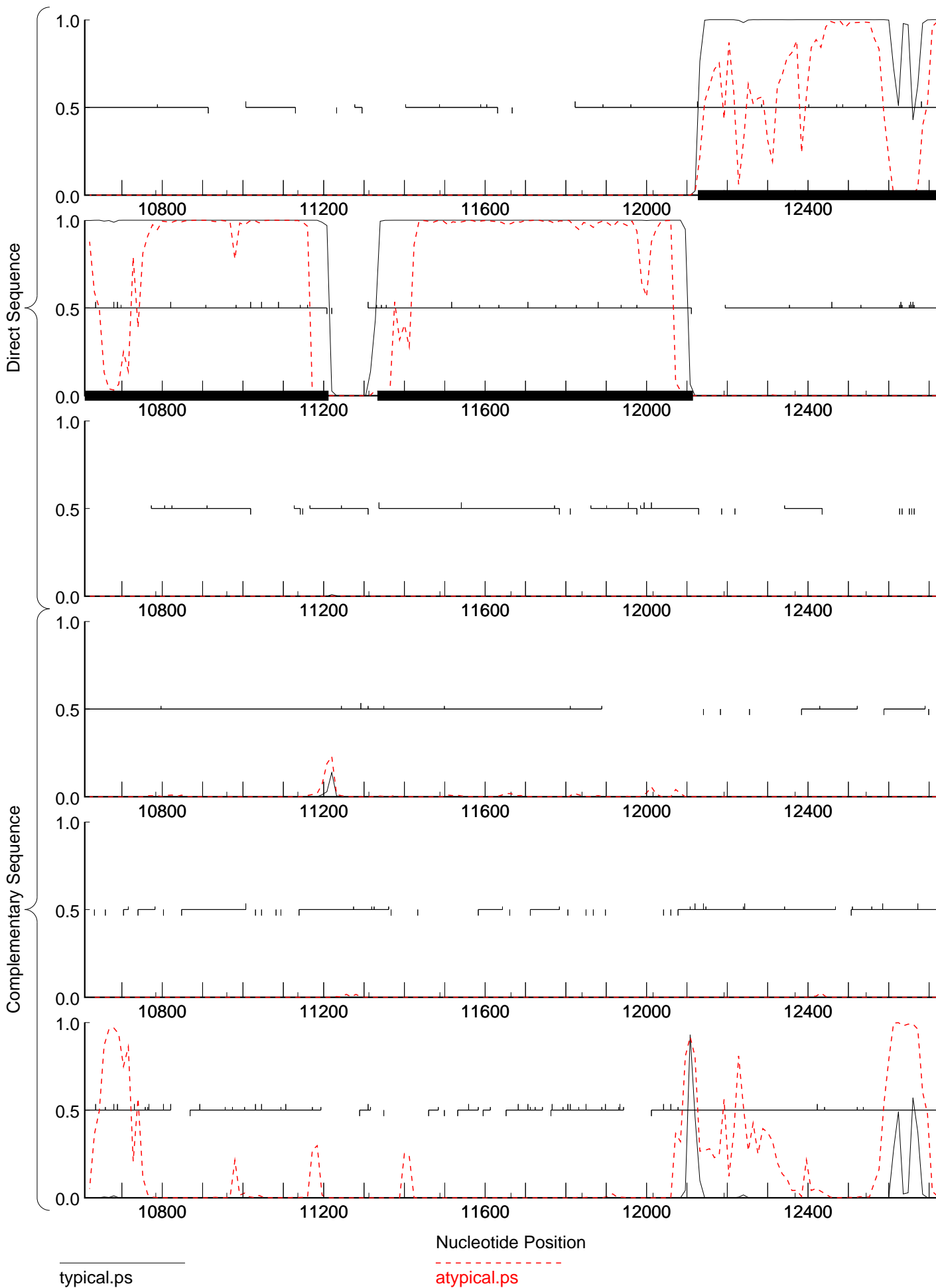


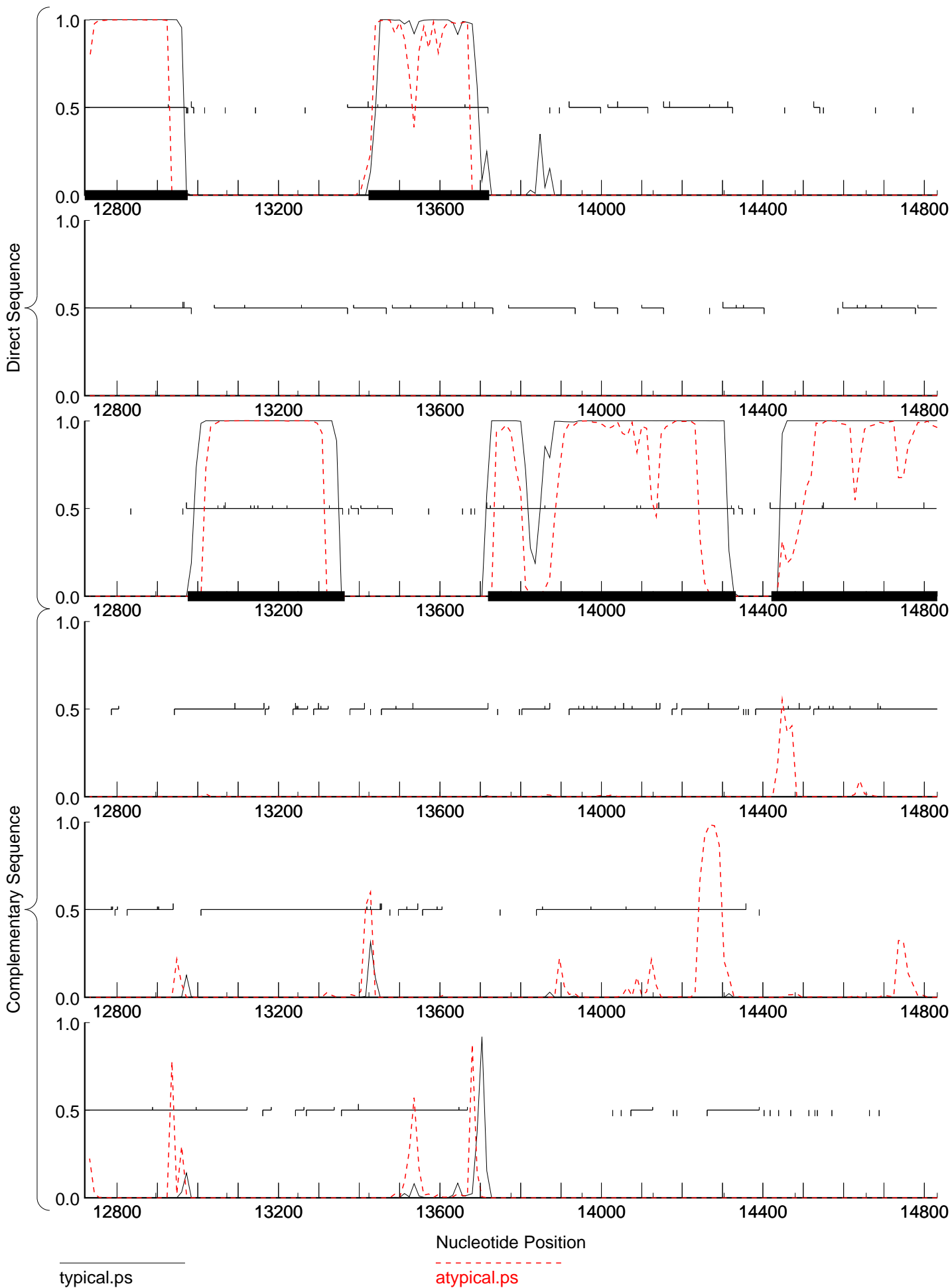


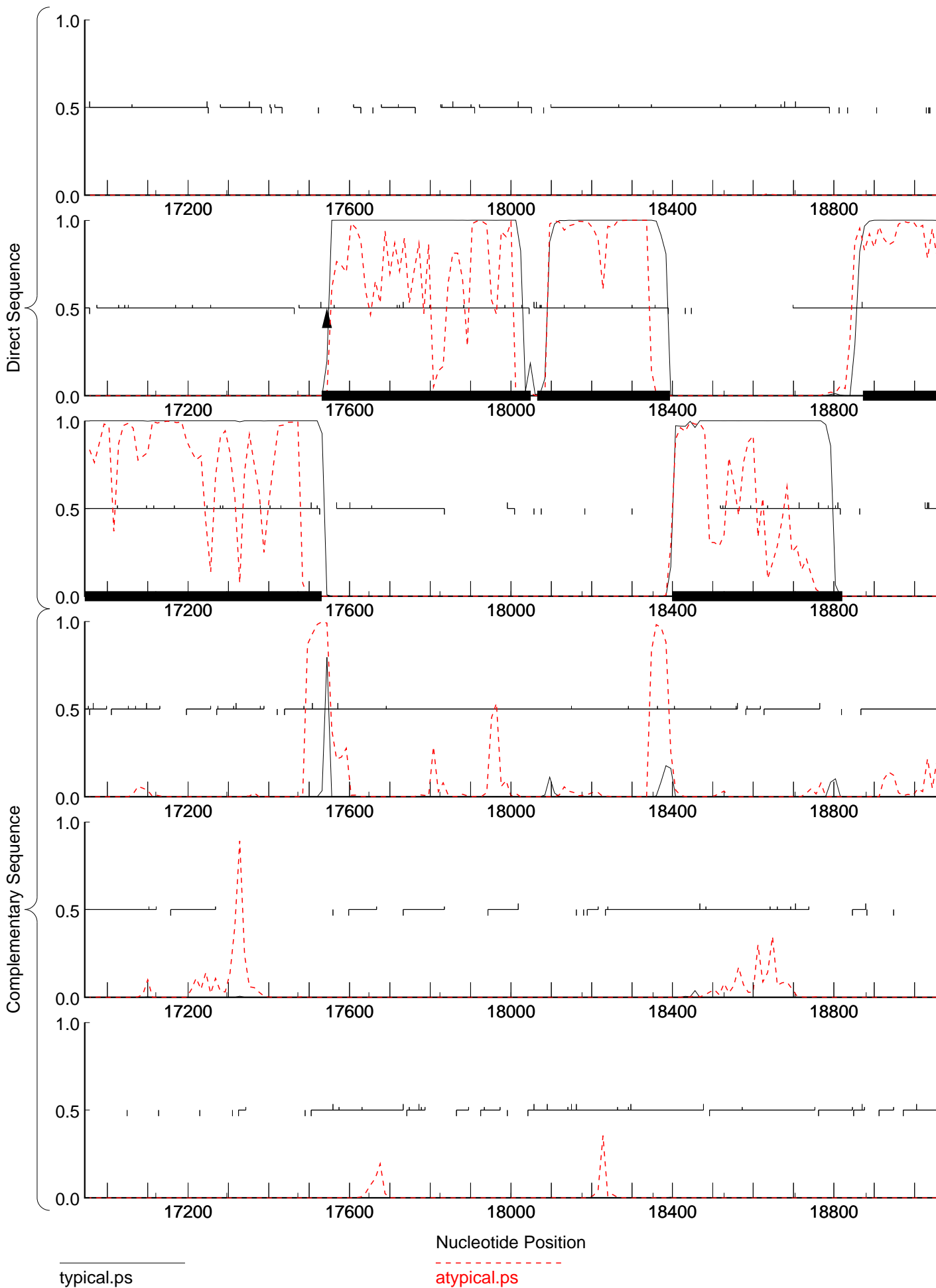
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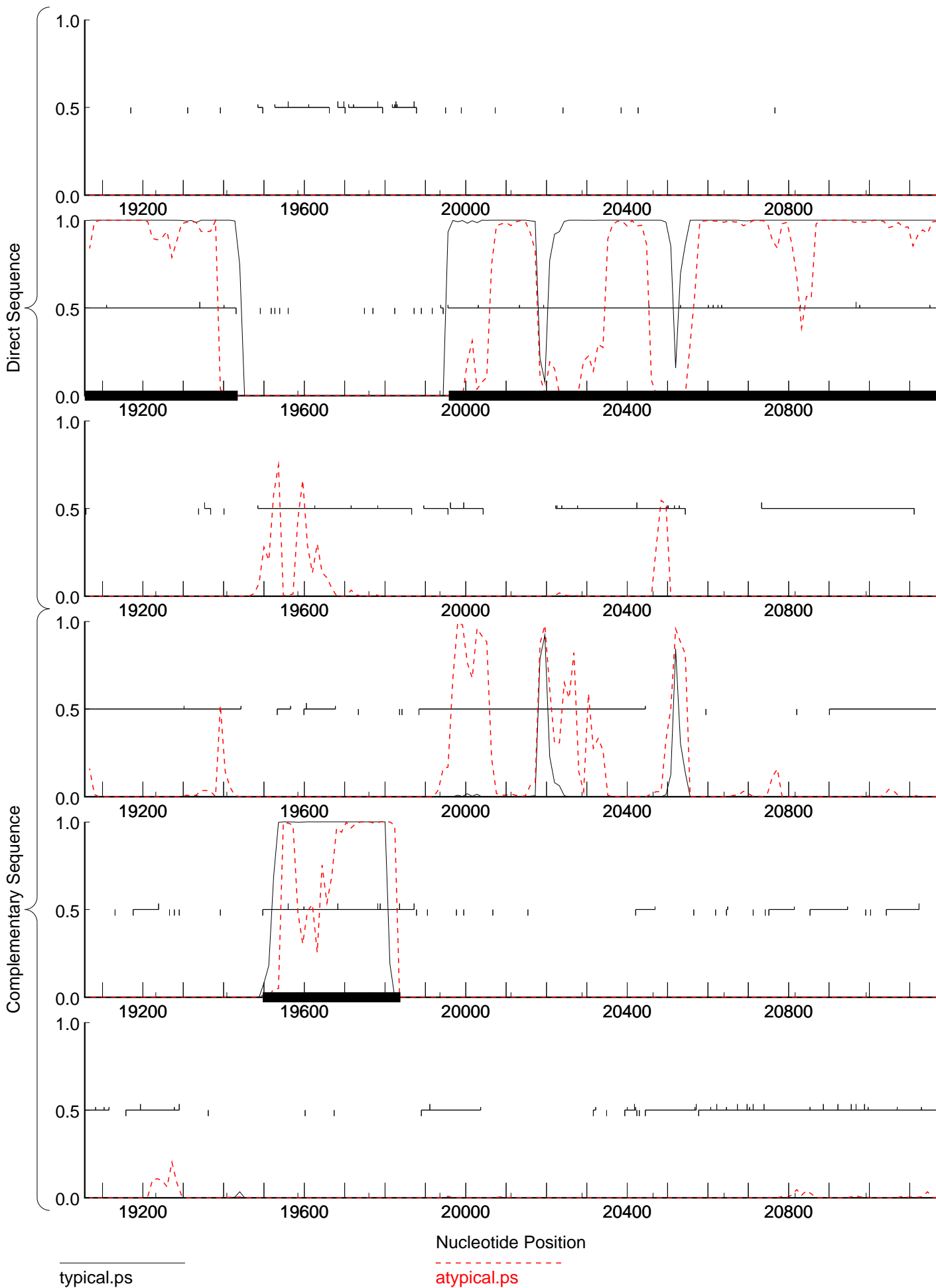
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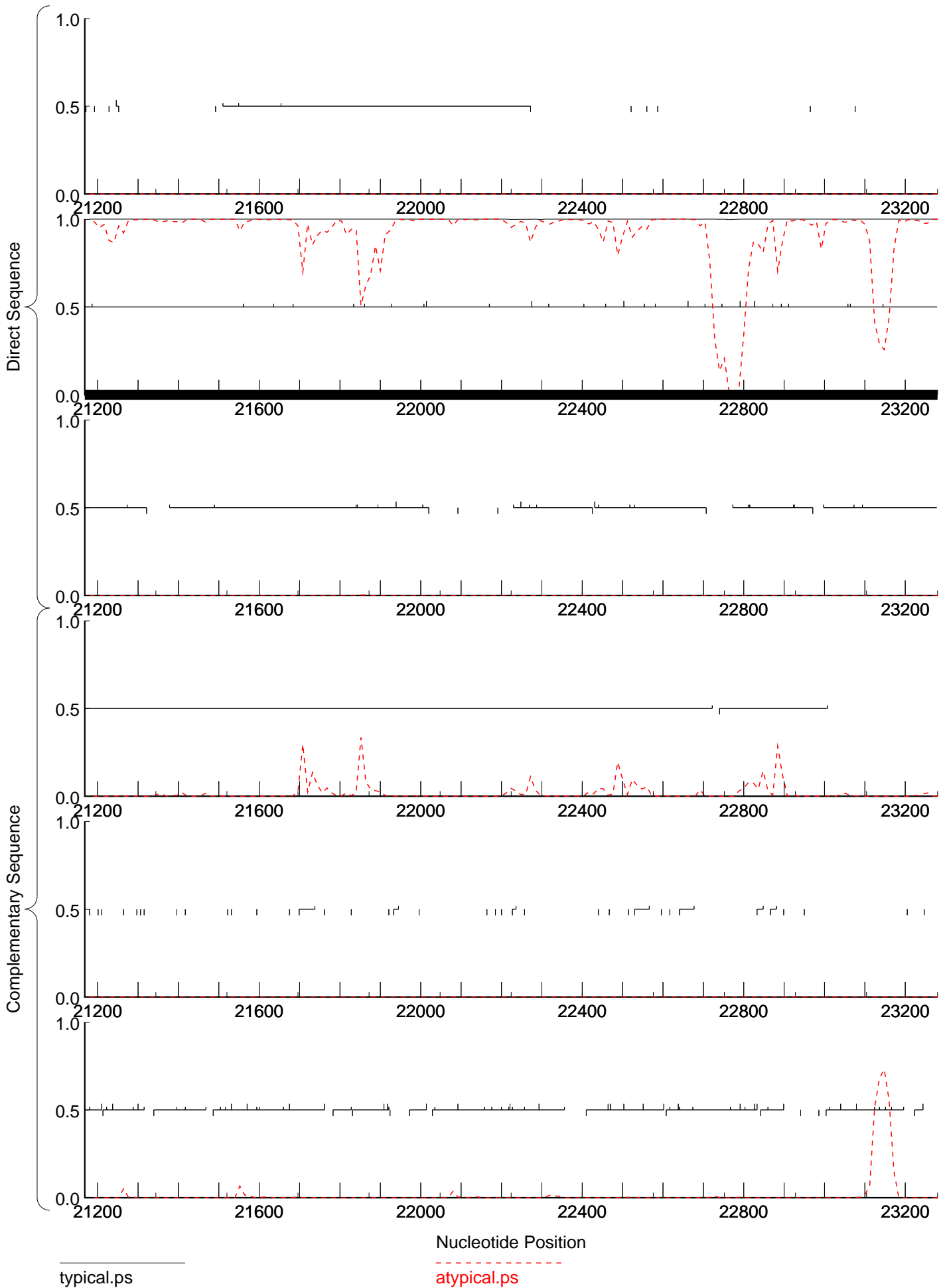


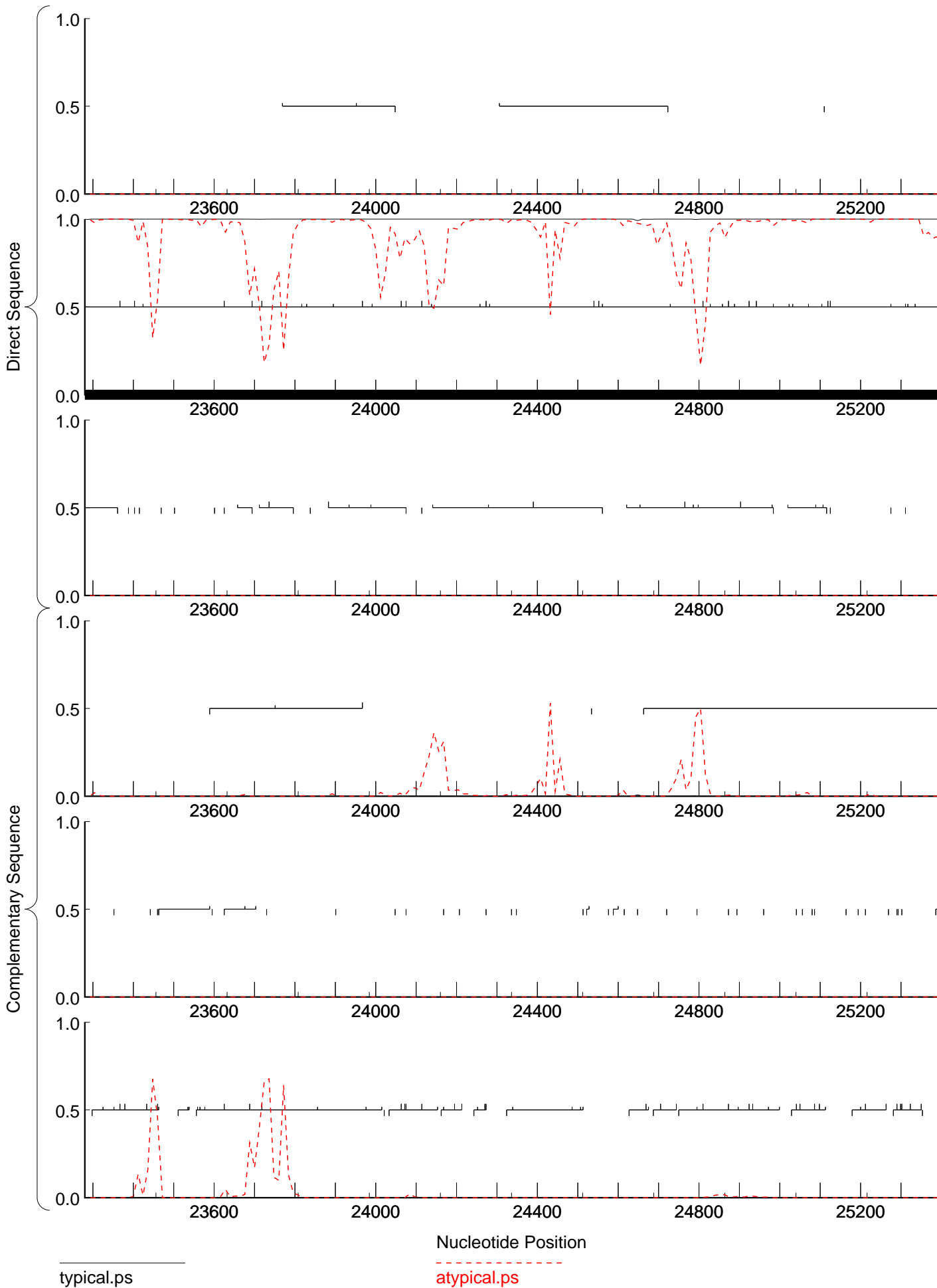






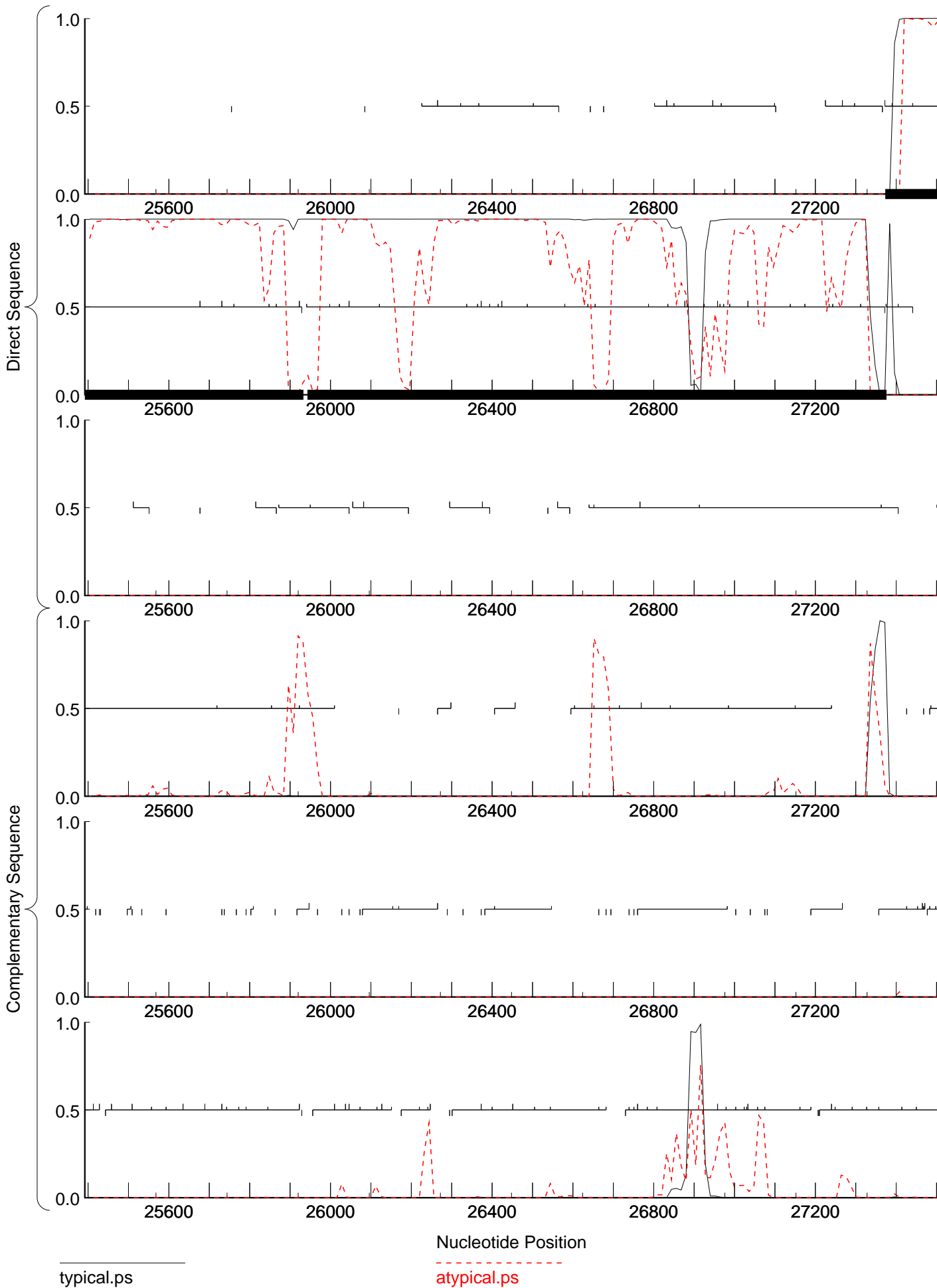


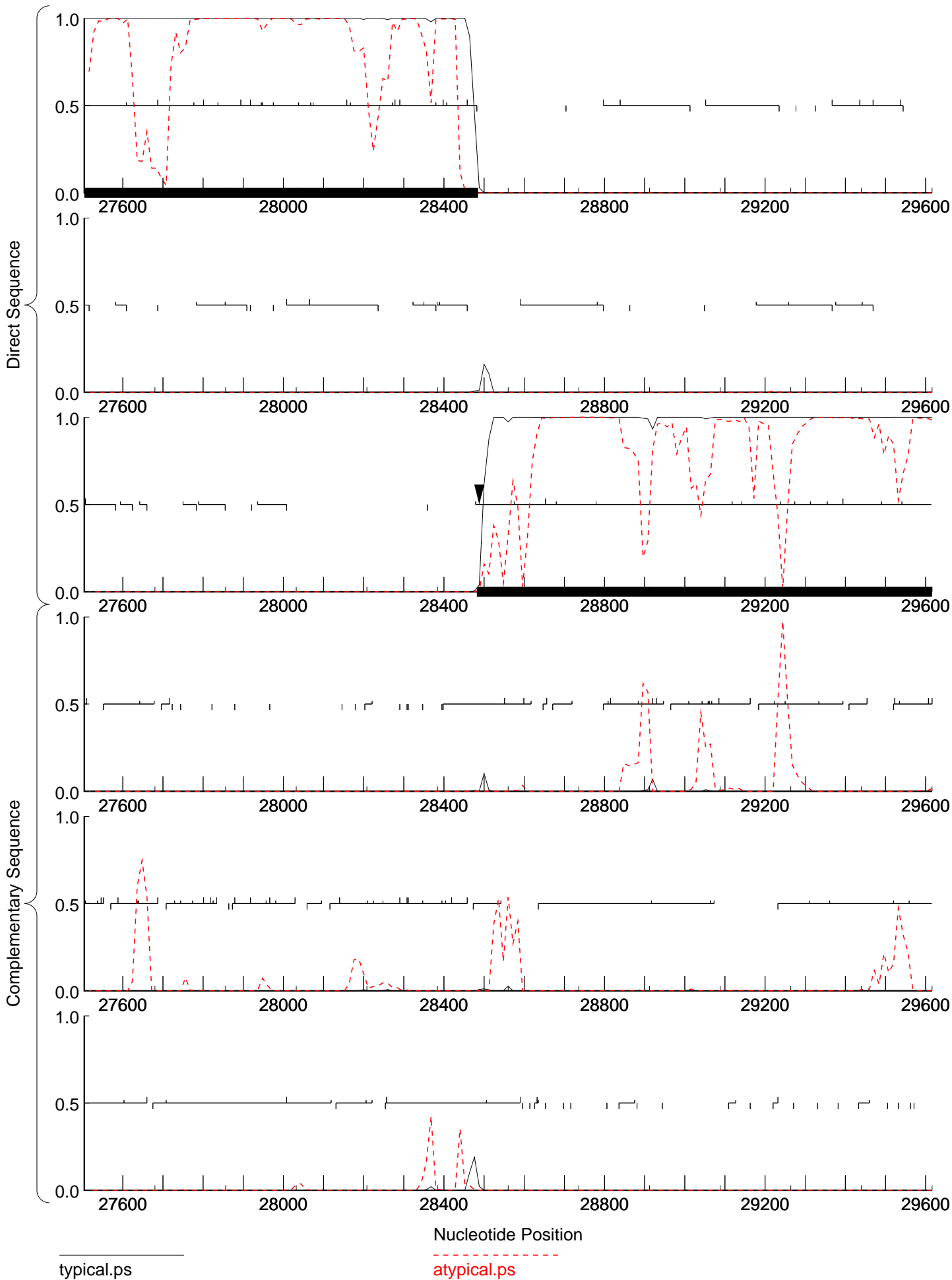




typical.ps

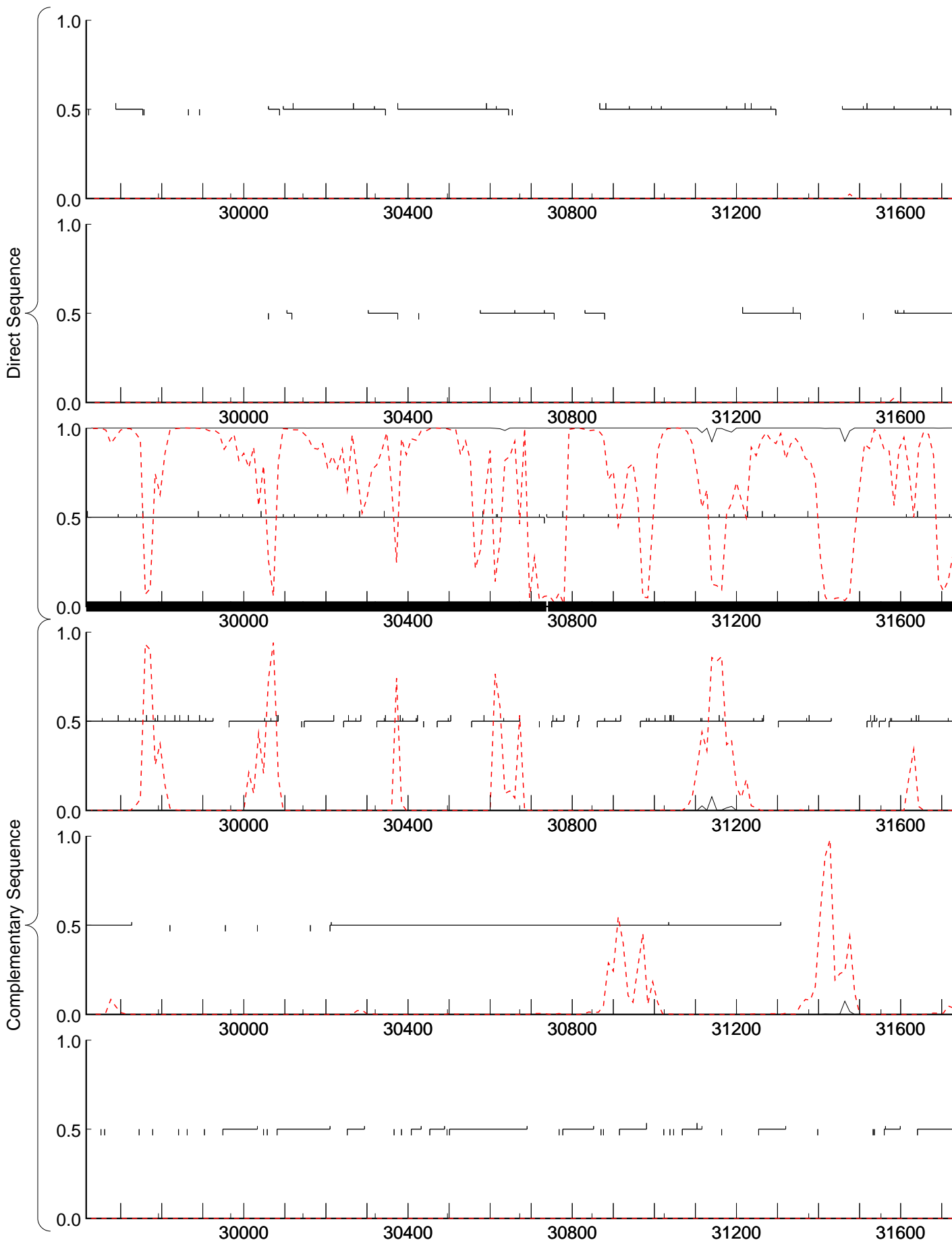
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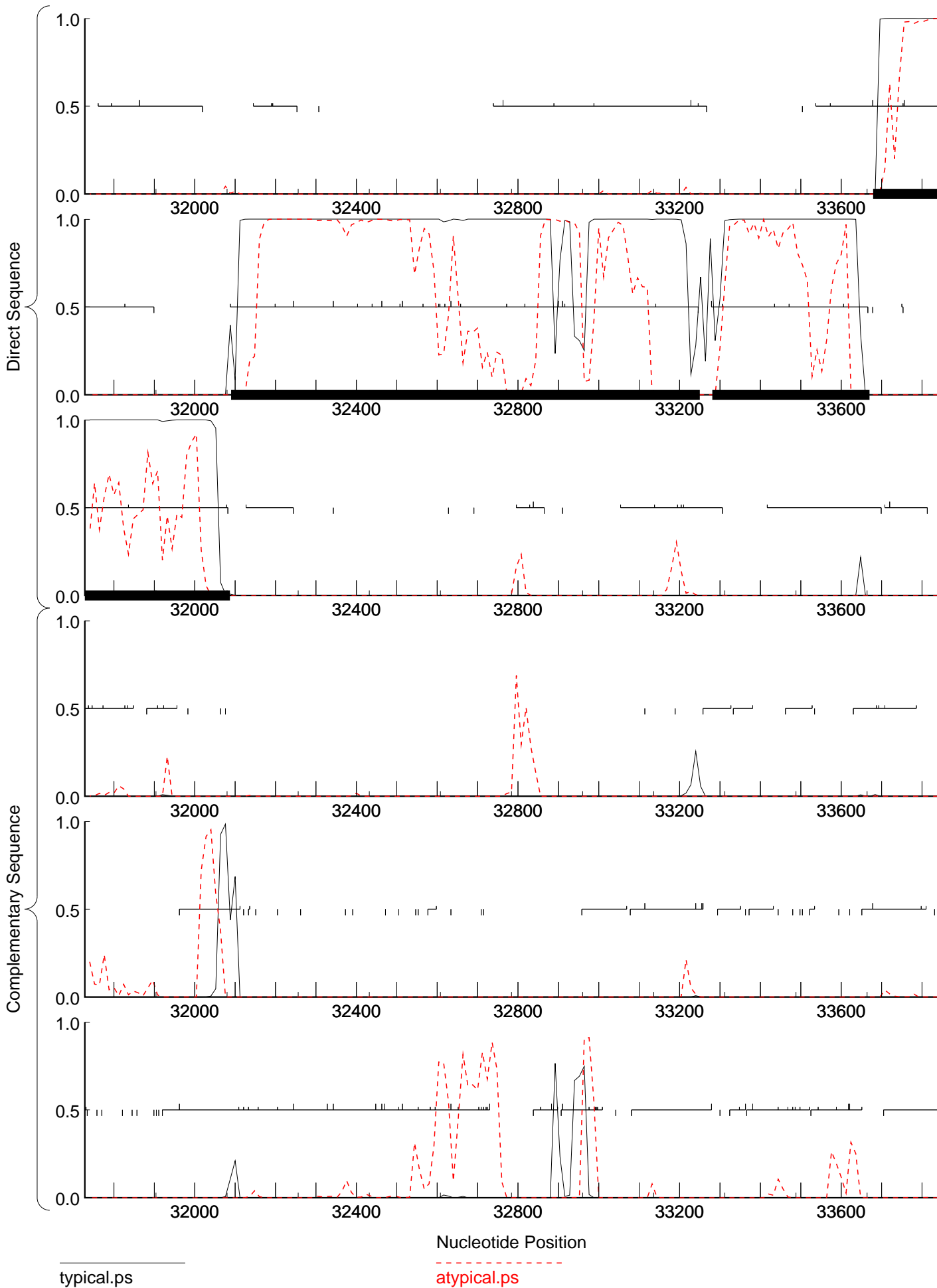
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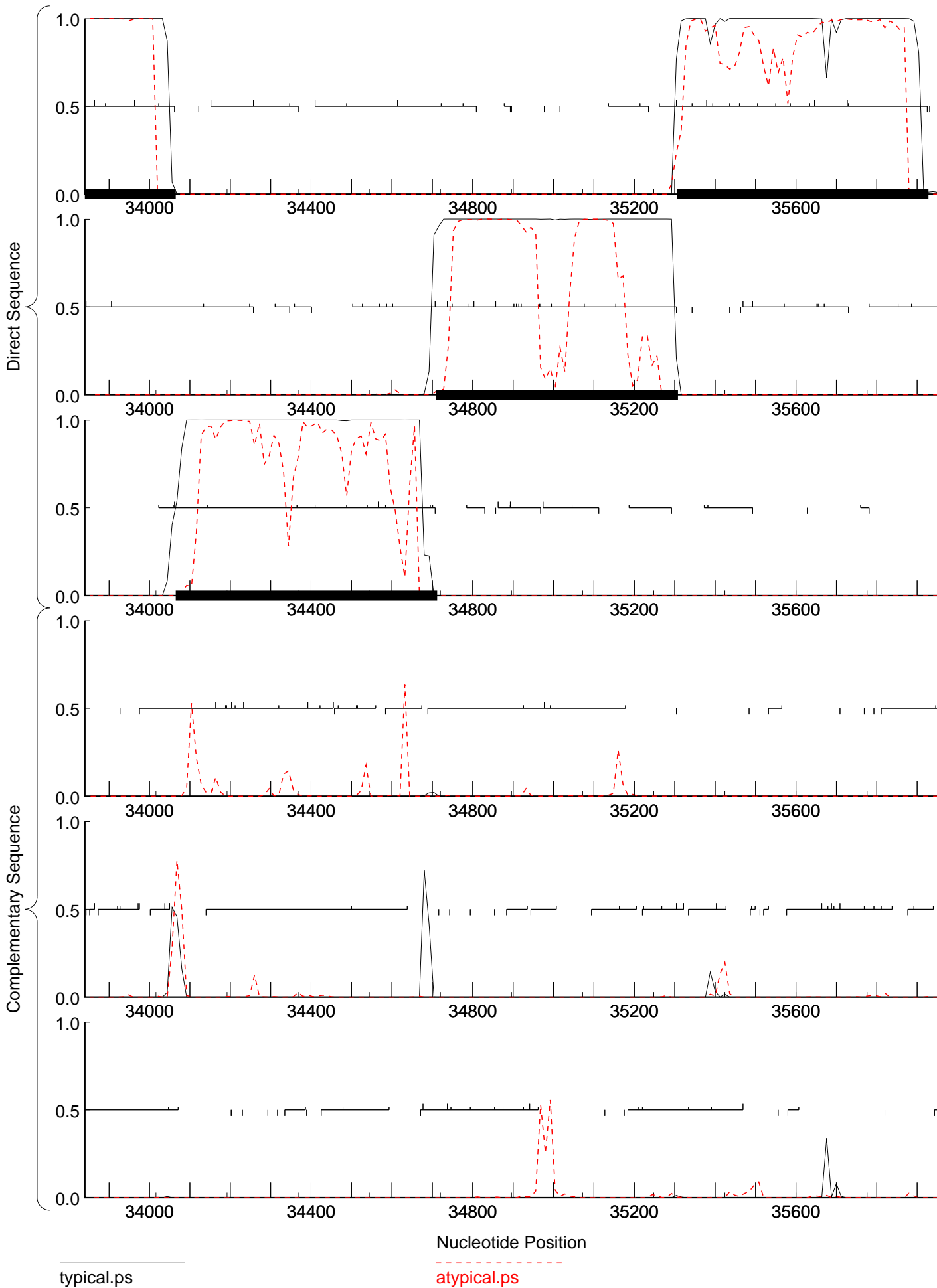
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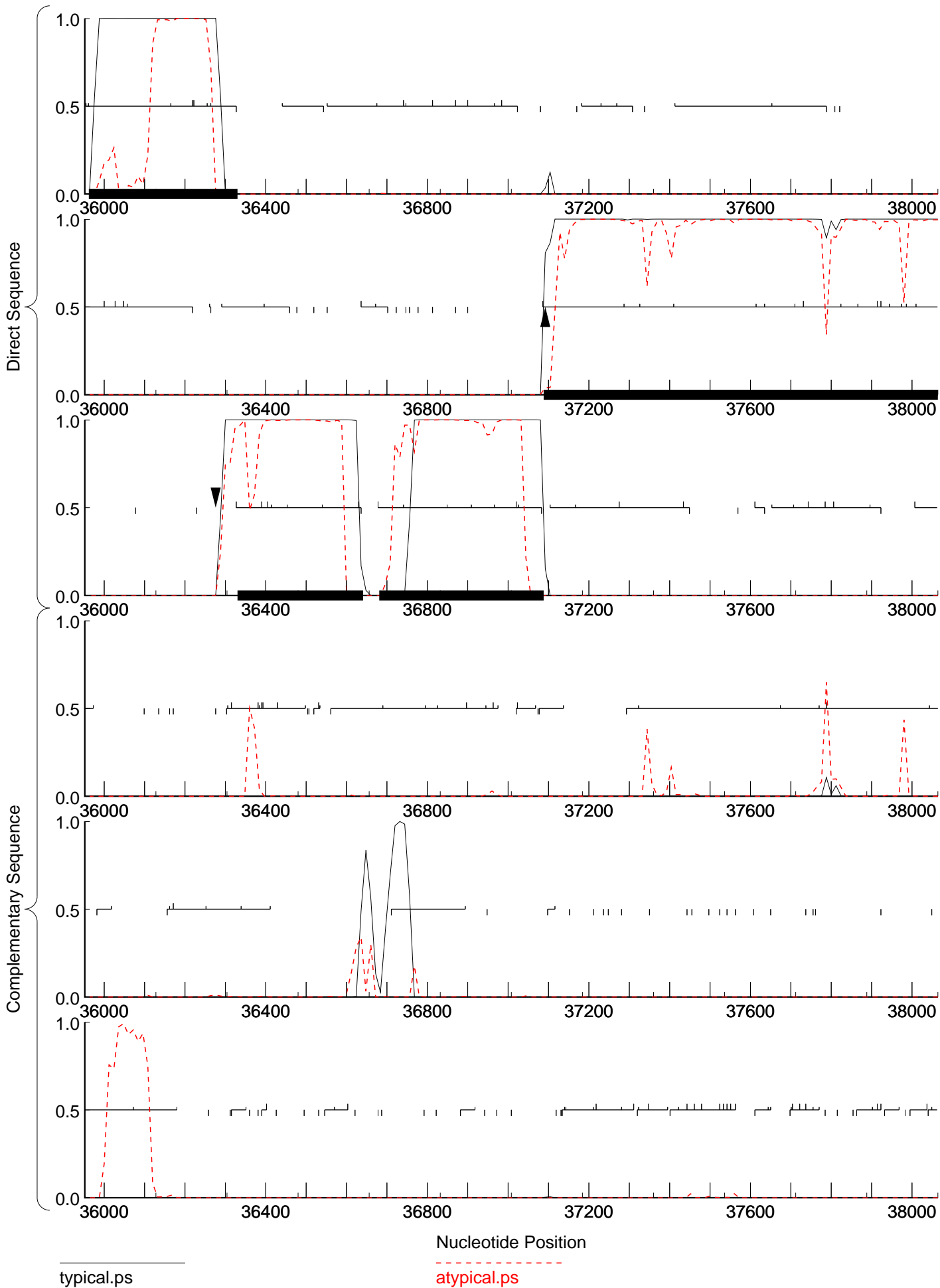


typical.ps

atypical.ps

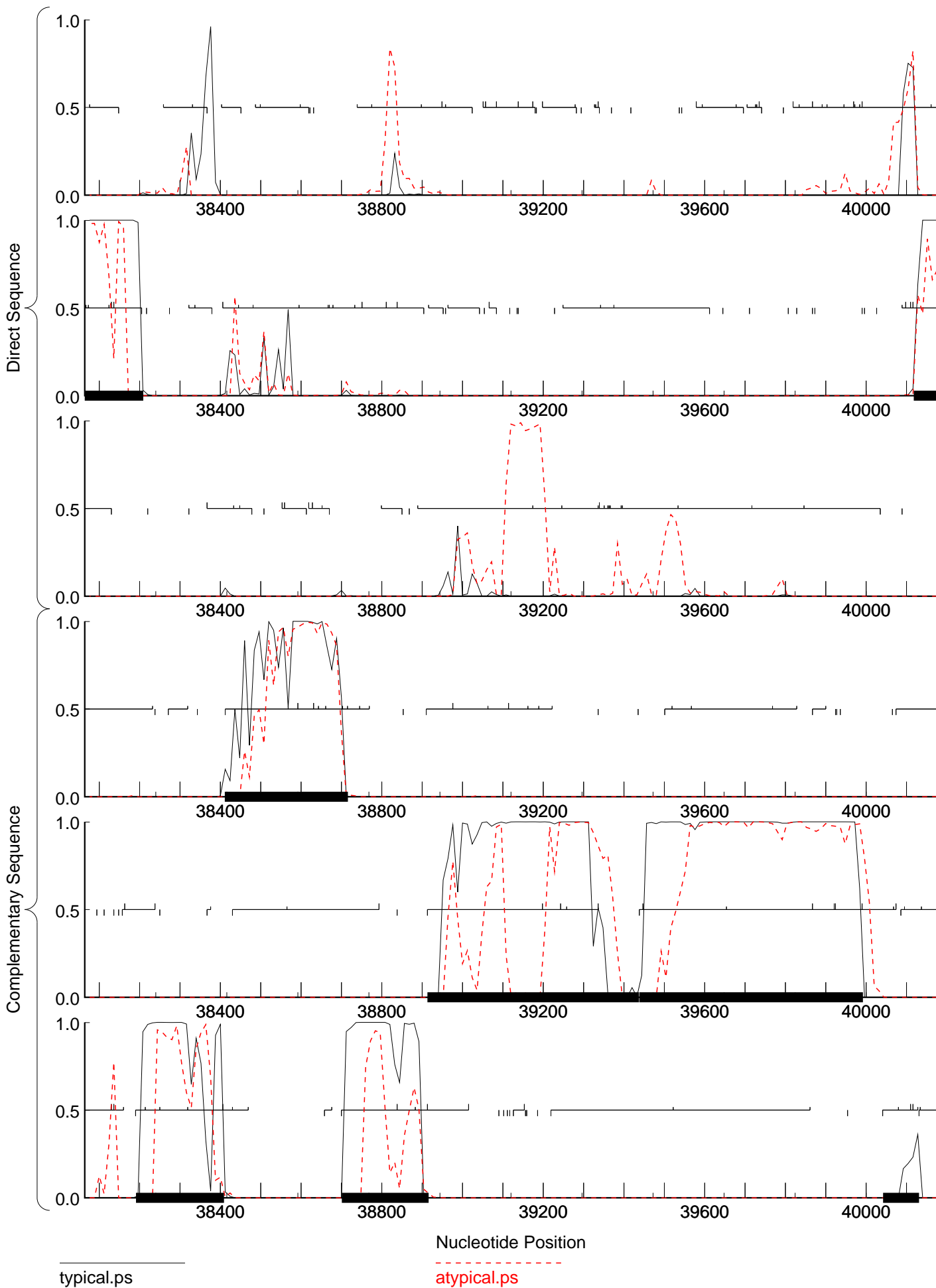






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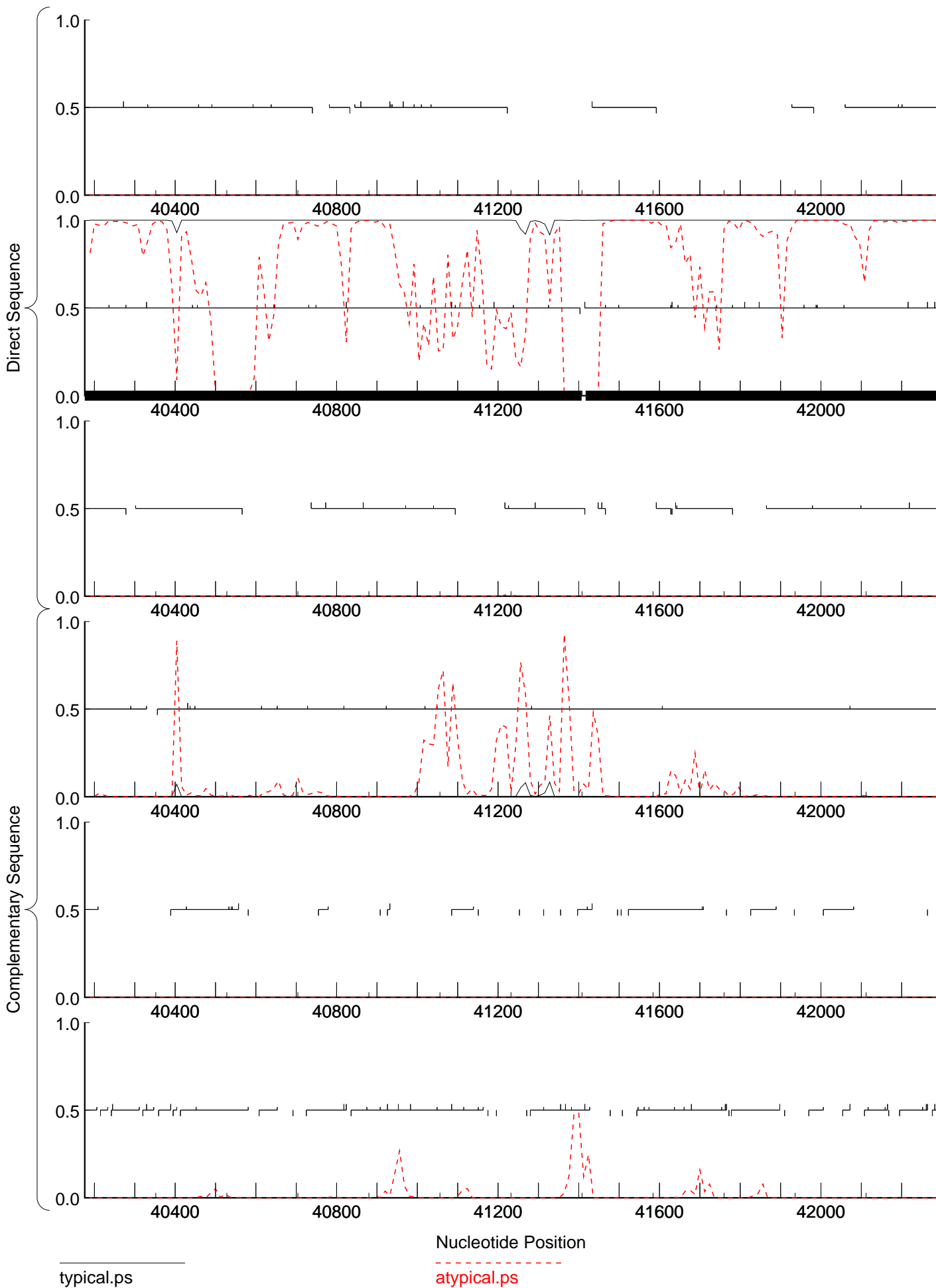
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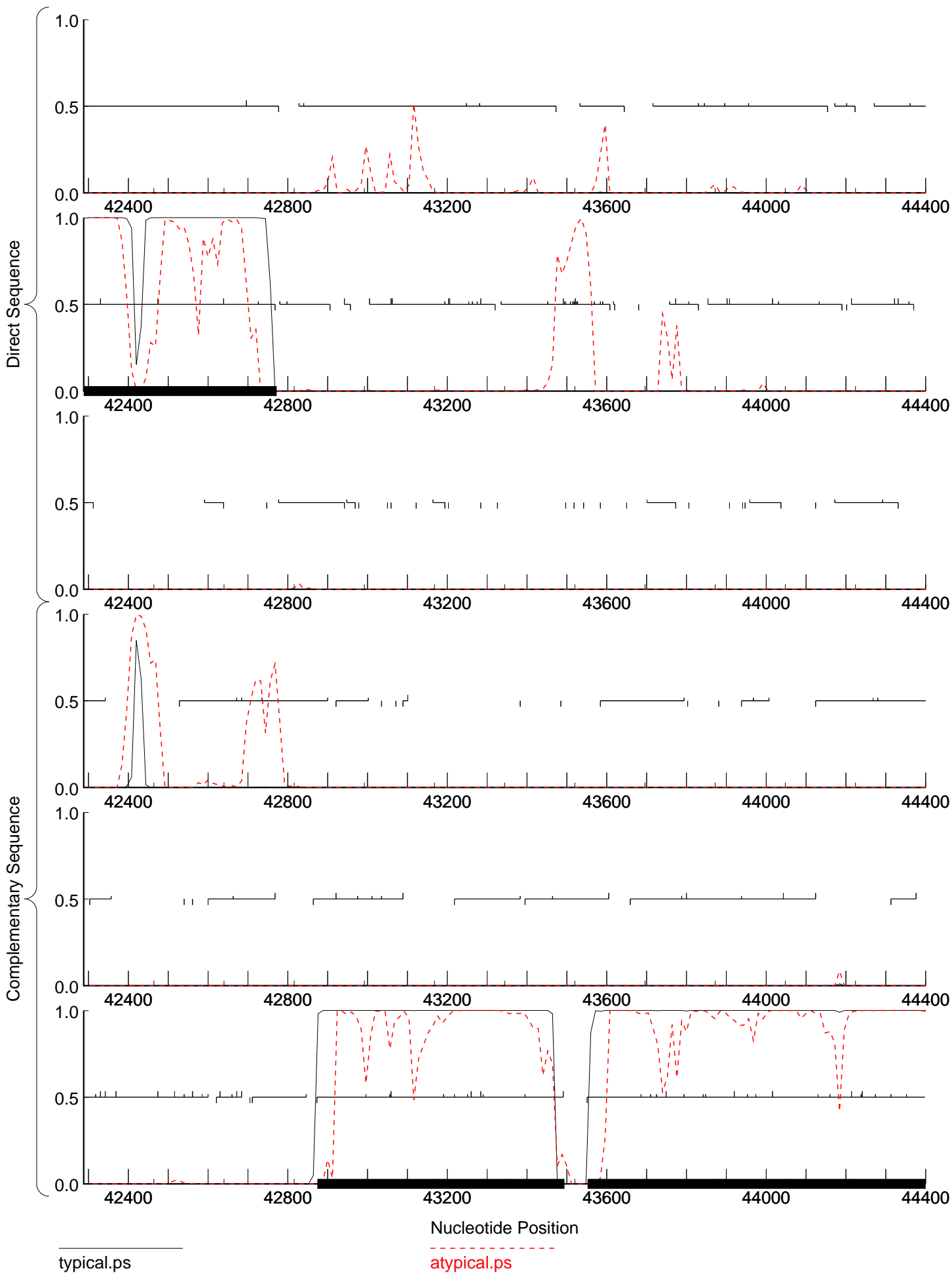


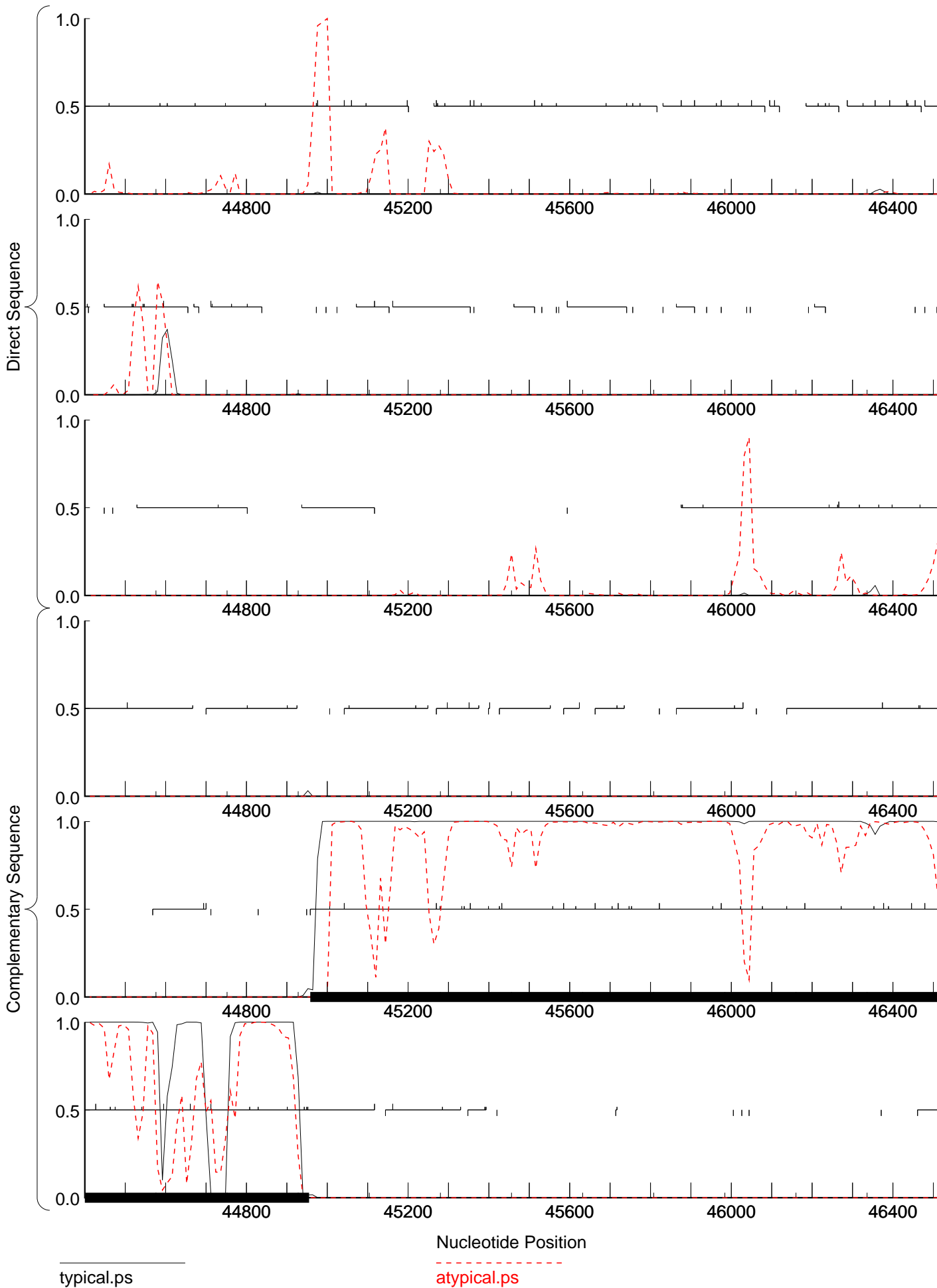
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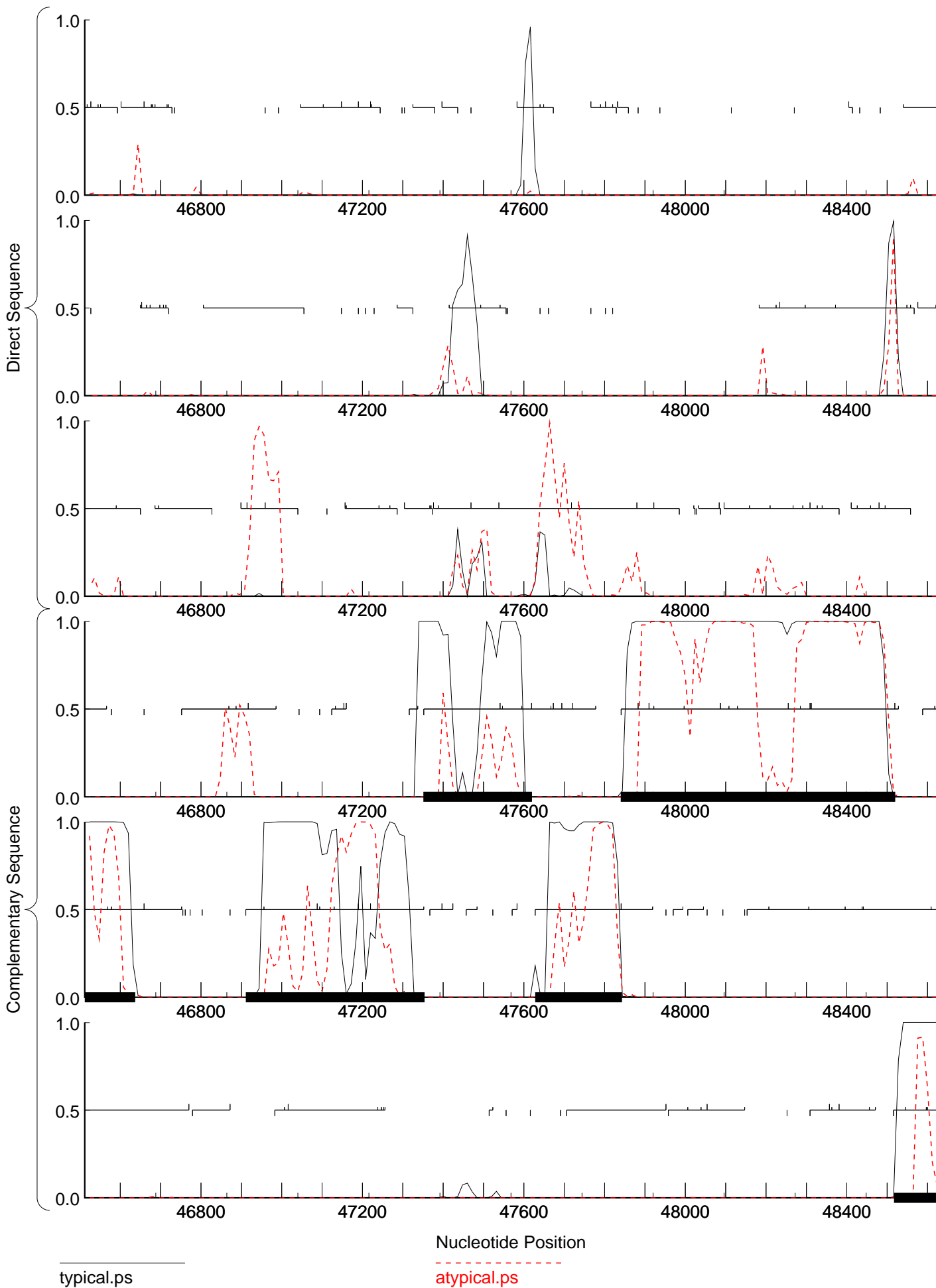
Nucleotide Position

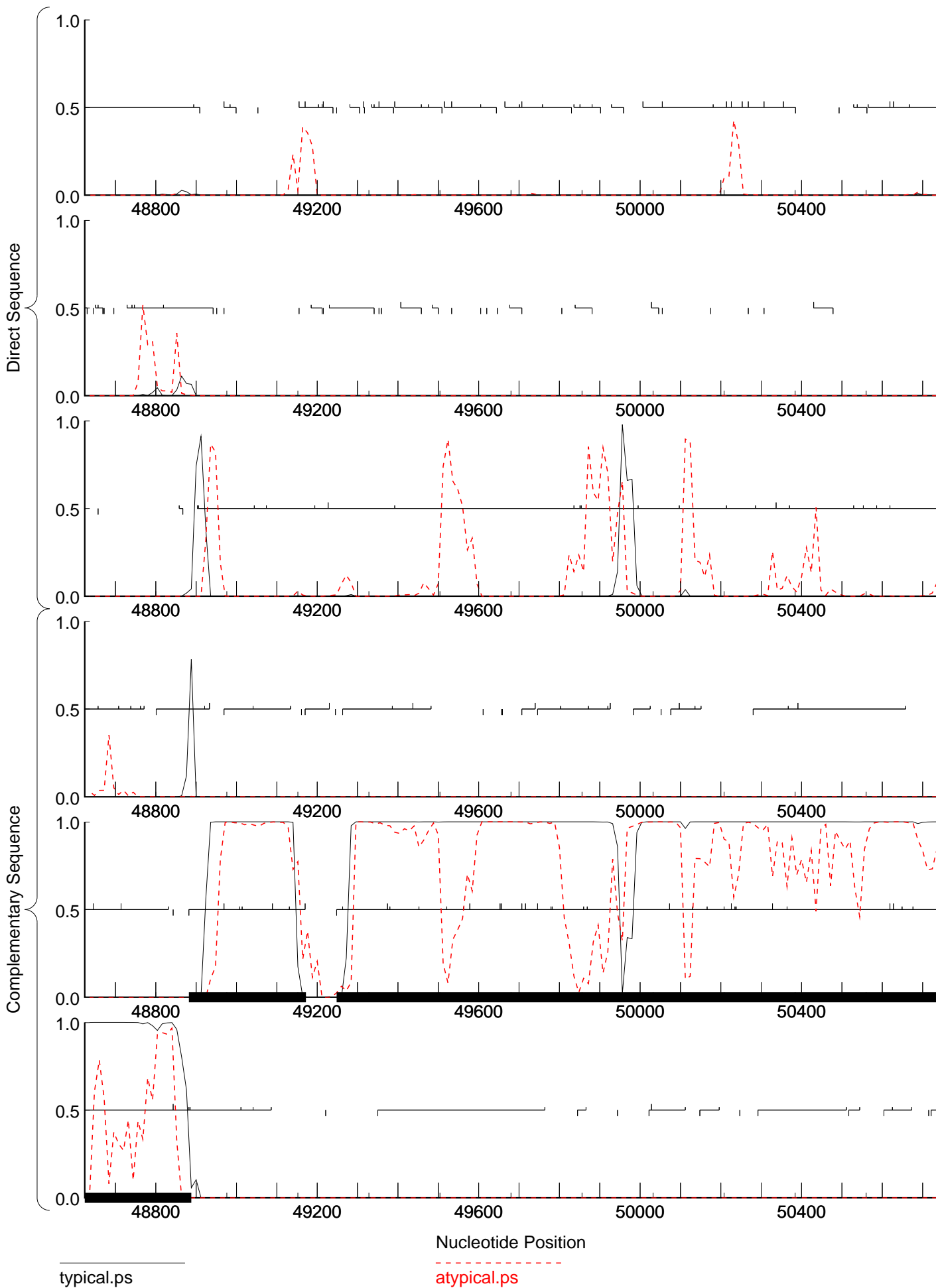
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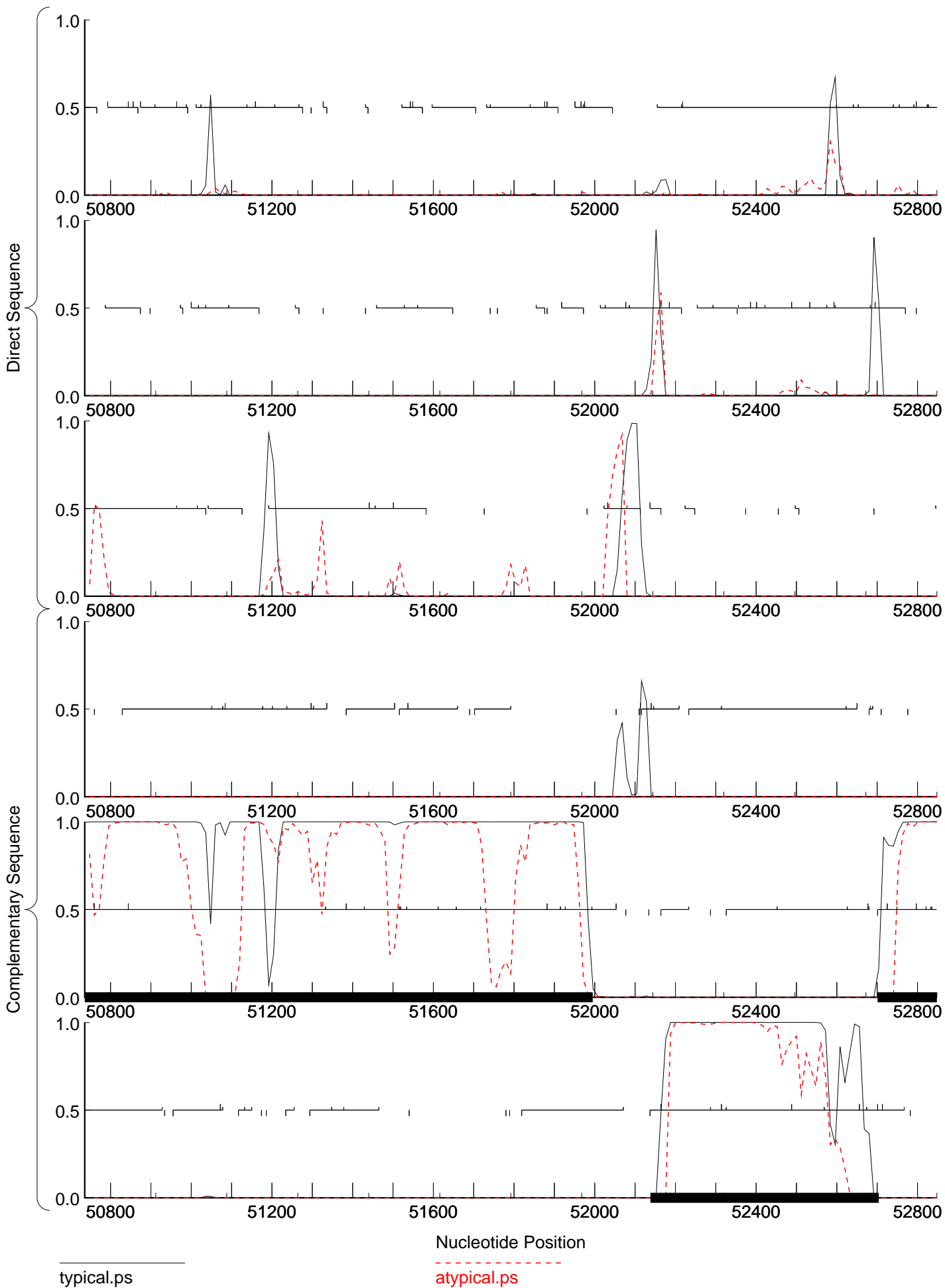






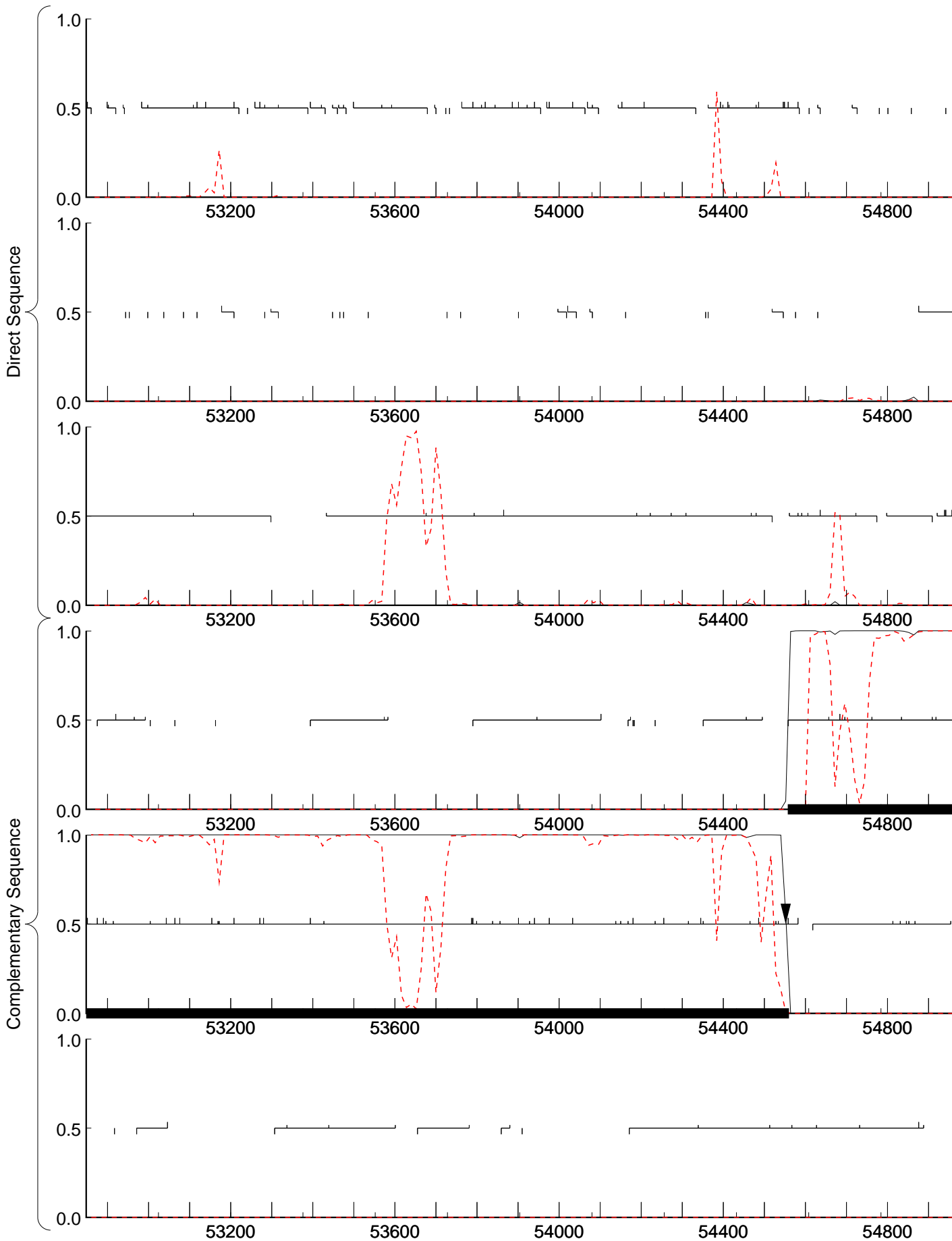
typical.ps

atypical.ps



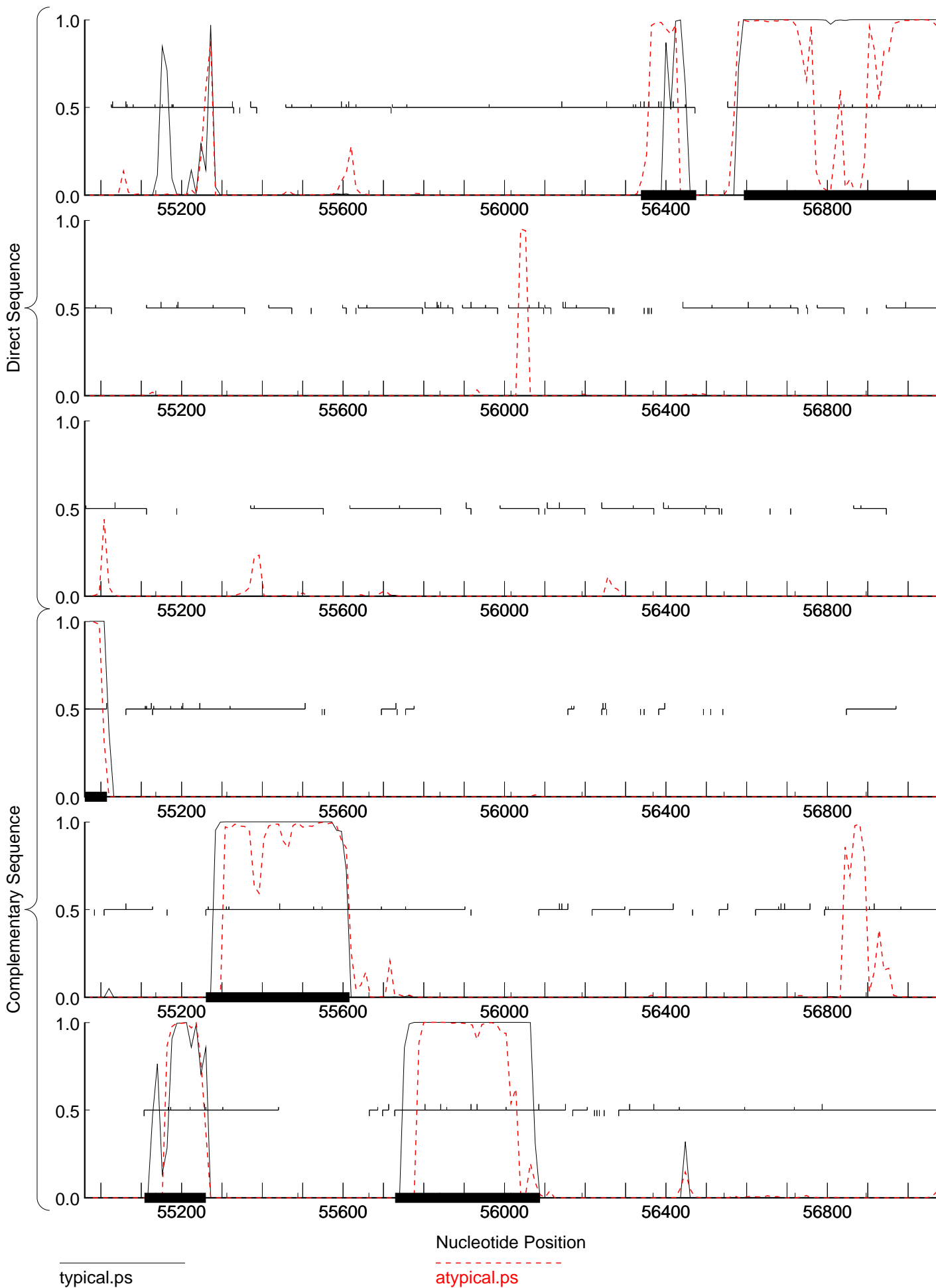
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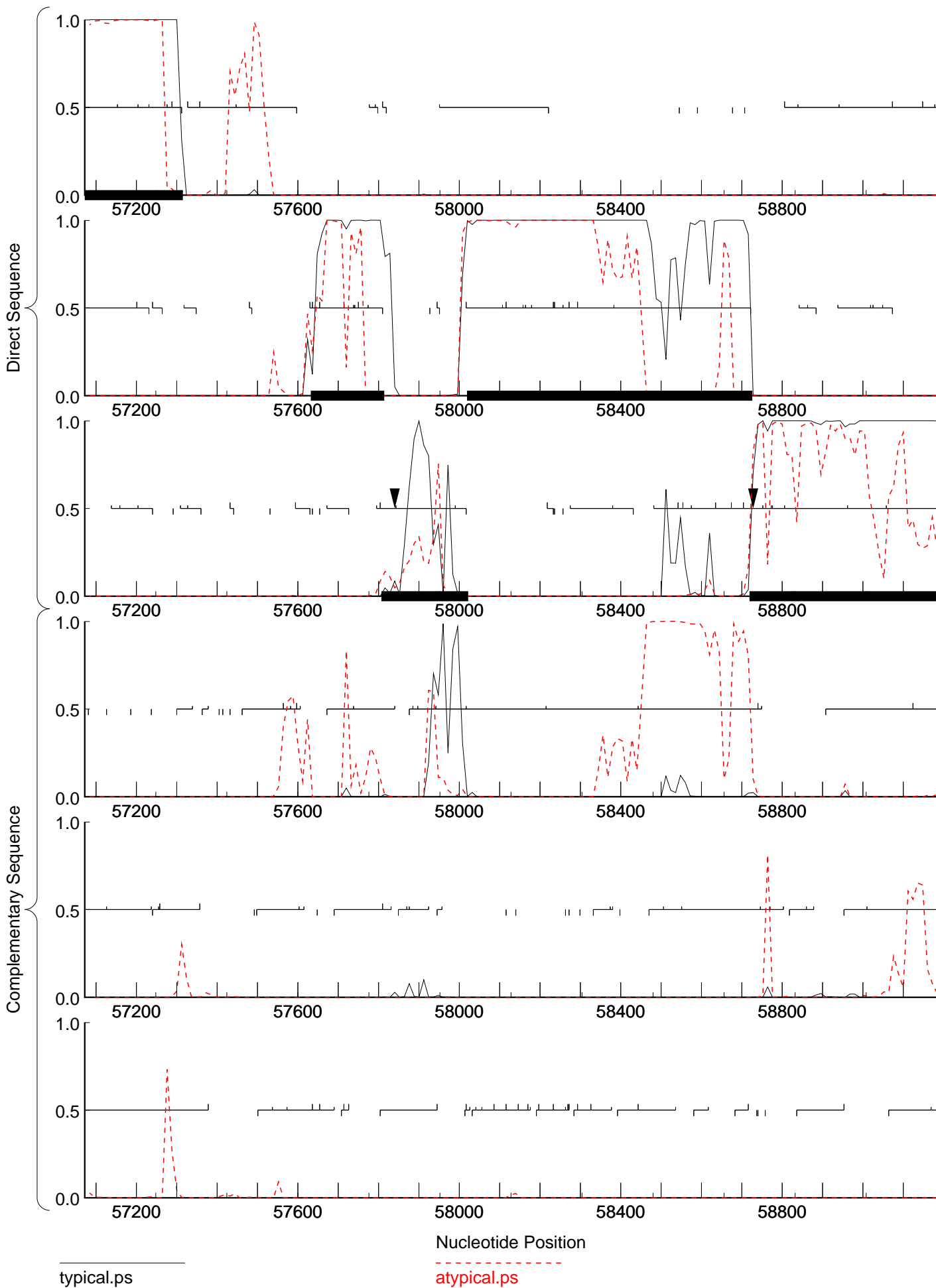
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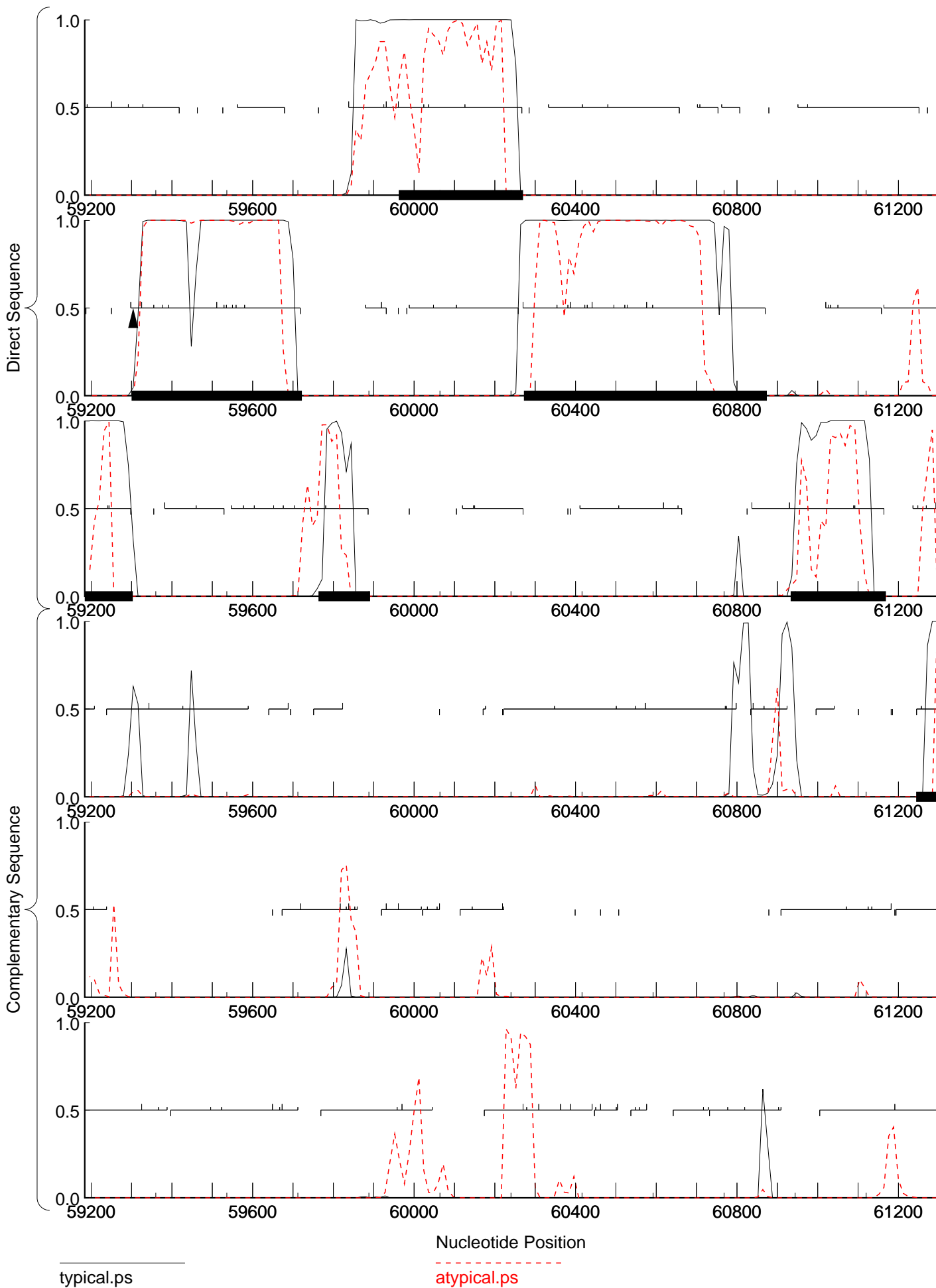
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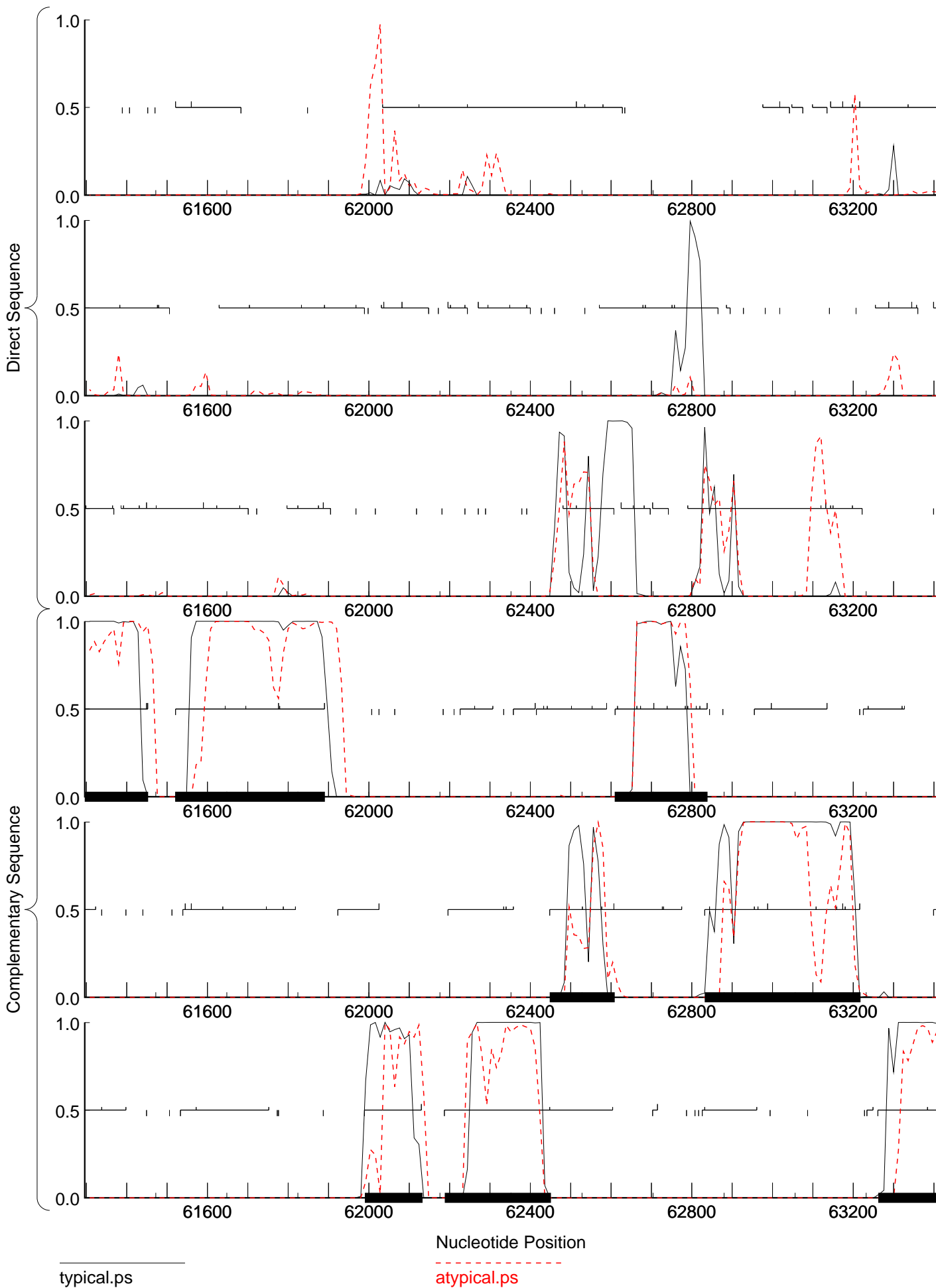


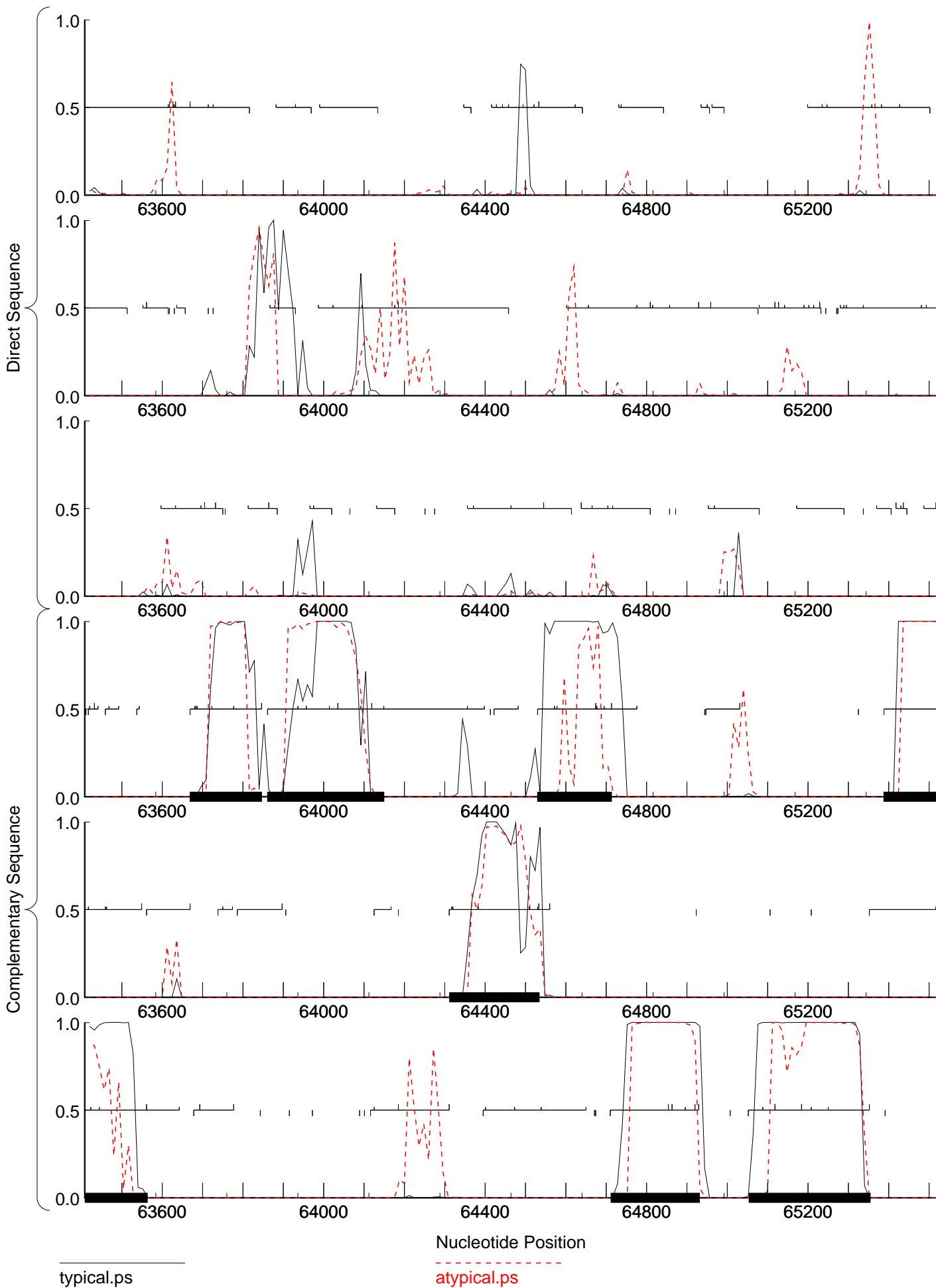
typical.ps

atypical.ps









typical.ps

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