

# GeneMark

Version 2.5p (09.08.06)

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## PROGRAM INFORMATION

Sequence : Mycobacterium phage Beaglebox complete sequence, 68418 bp, circularly permuted, Cluster B1  
Analysis Date : 3/18/18 at 19:27:12  
Pages : 34  
Sequence Length : 68418 bp  
GC Content : 66.53%

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,

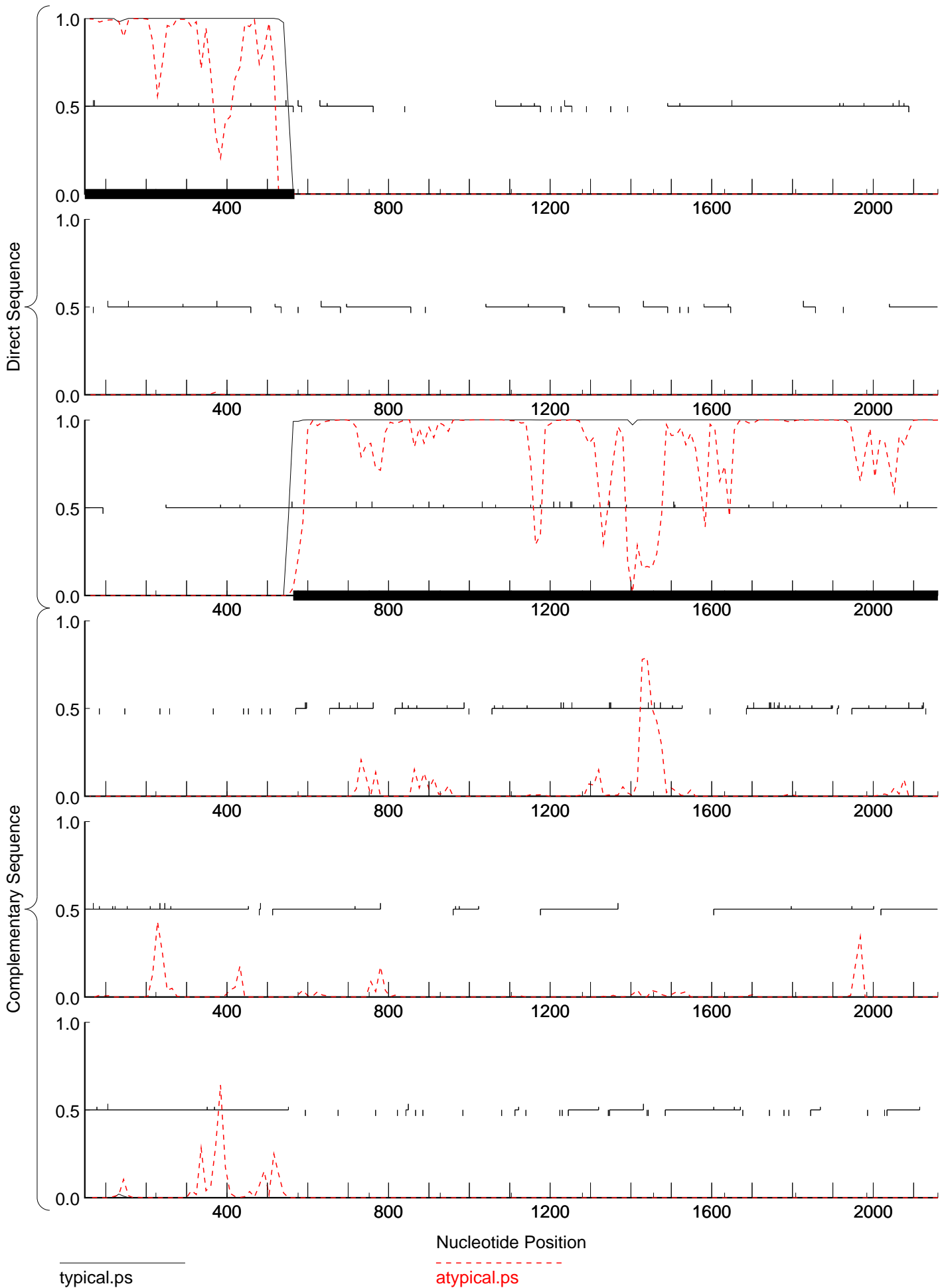
## MATRIX INFORMATION

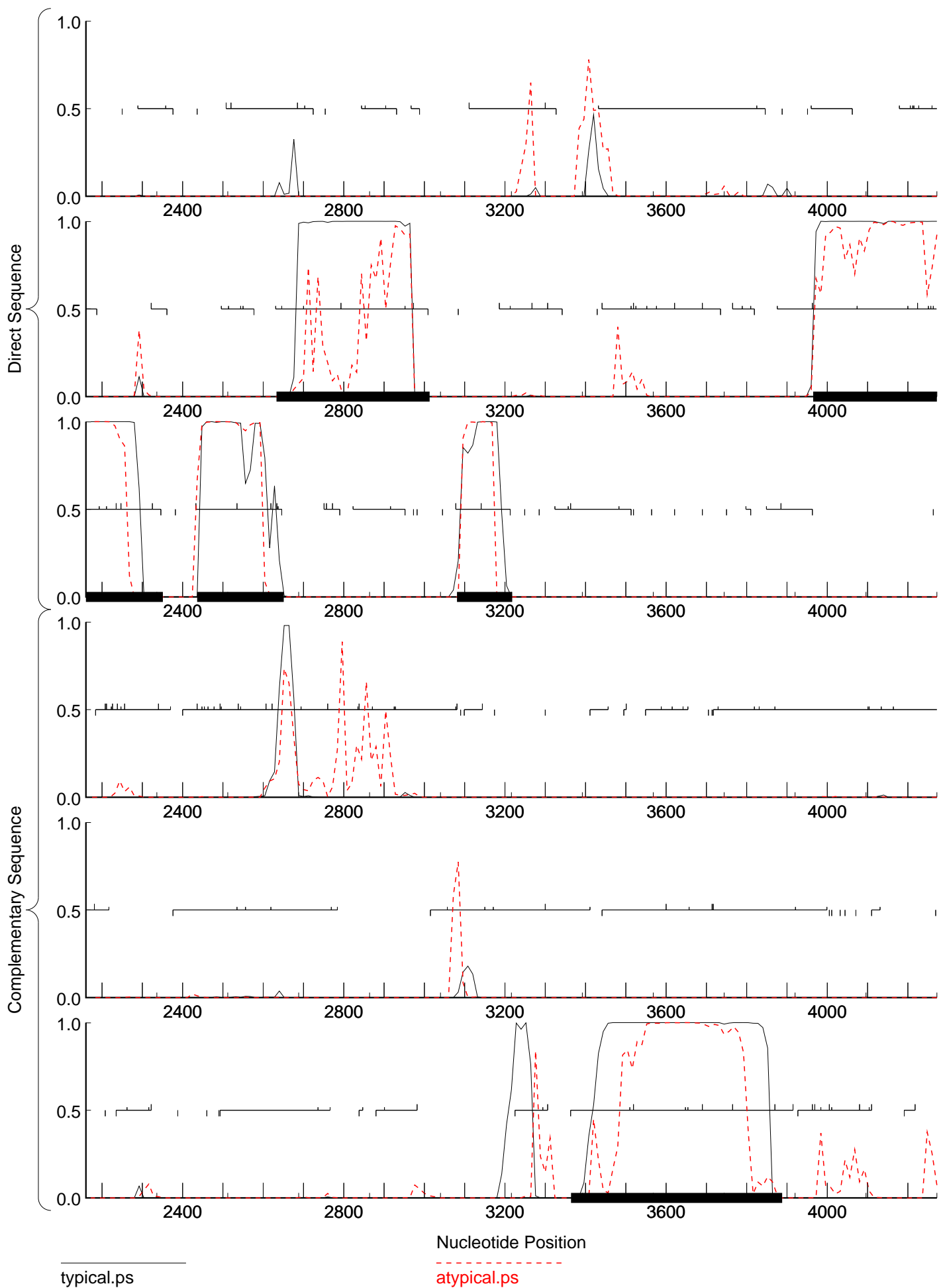
Matrix : -  
Author : -  
Order : 4

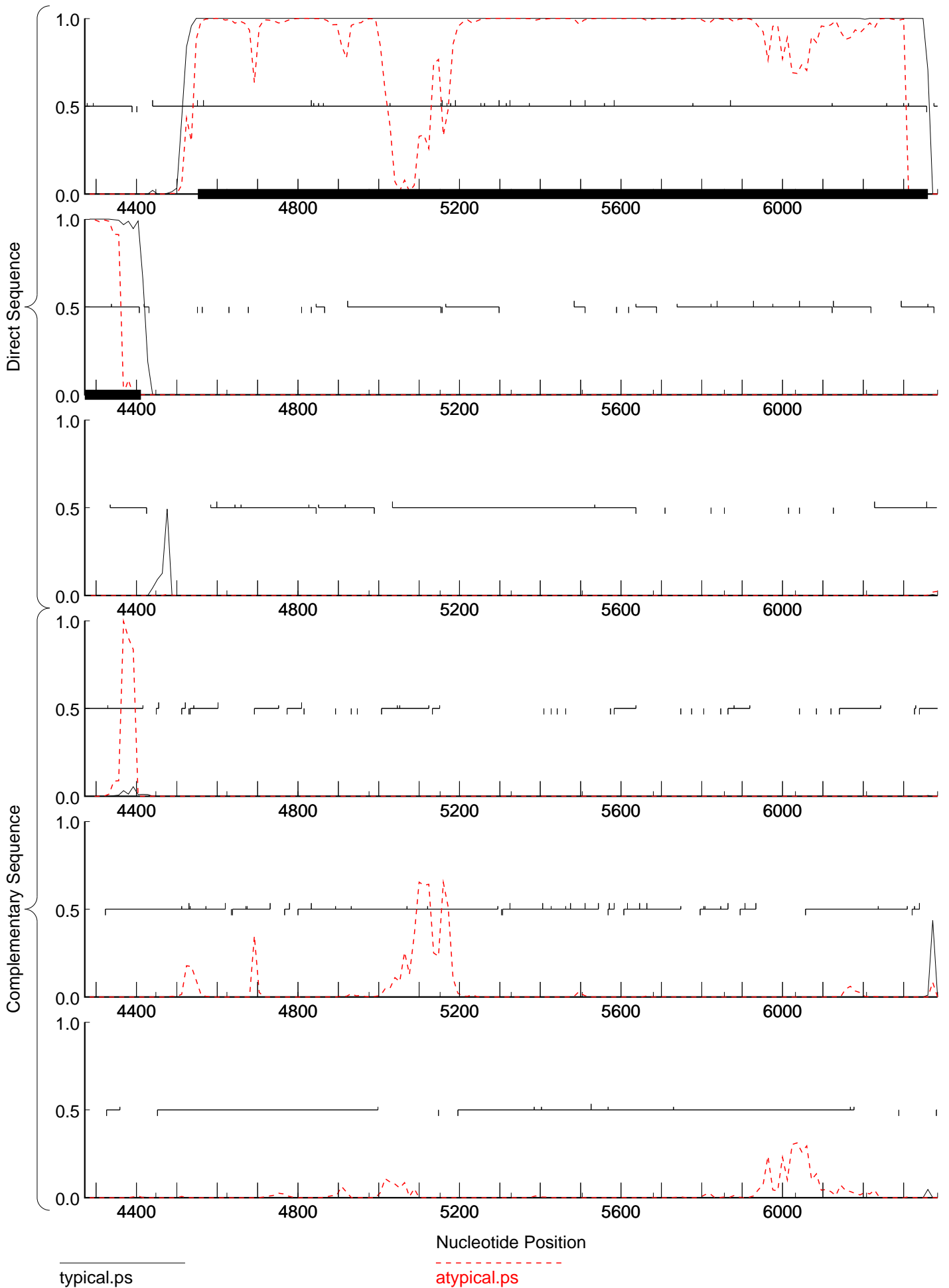
Send questions / comments to:  
Dr. M. Borodovsky  
Georgia Institute of Technology  
School of Biology  
Atlanta, GA 30332-0230

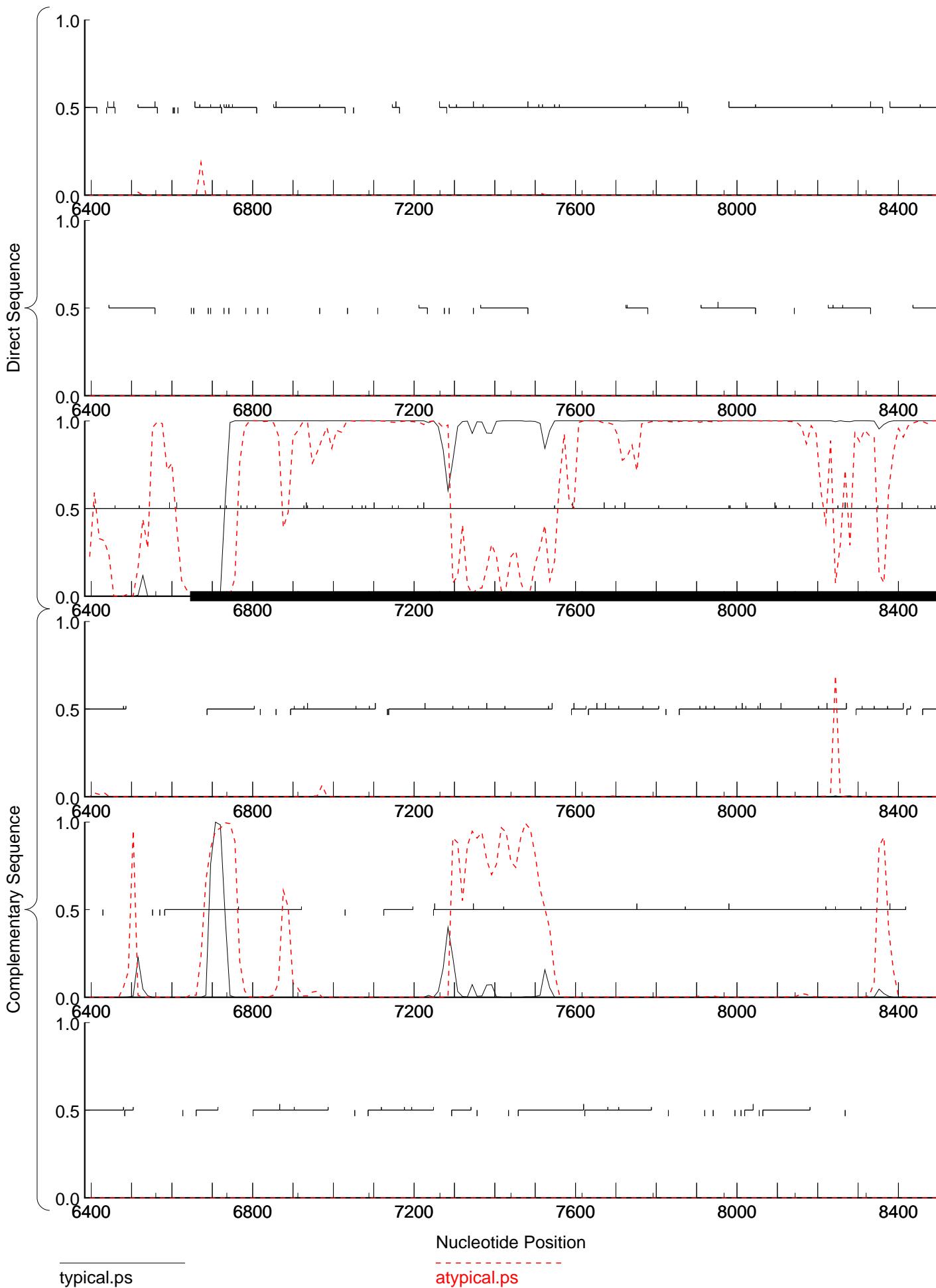
### Matrix notes & comments

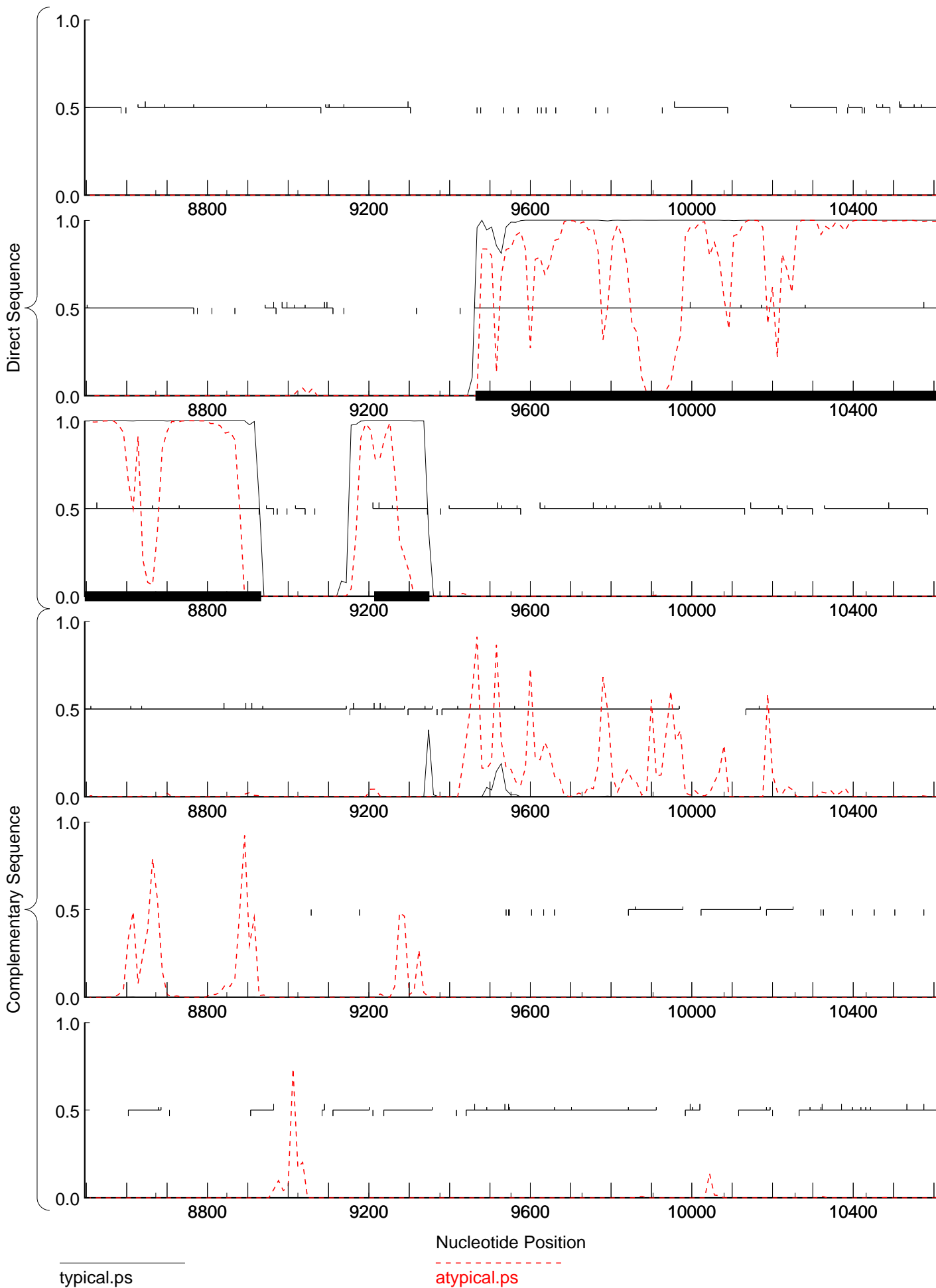
Training set derived by GeneMarkS, 4.30 October 2014  
Sun Mar 18 19:27:12 2018

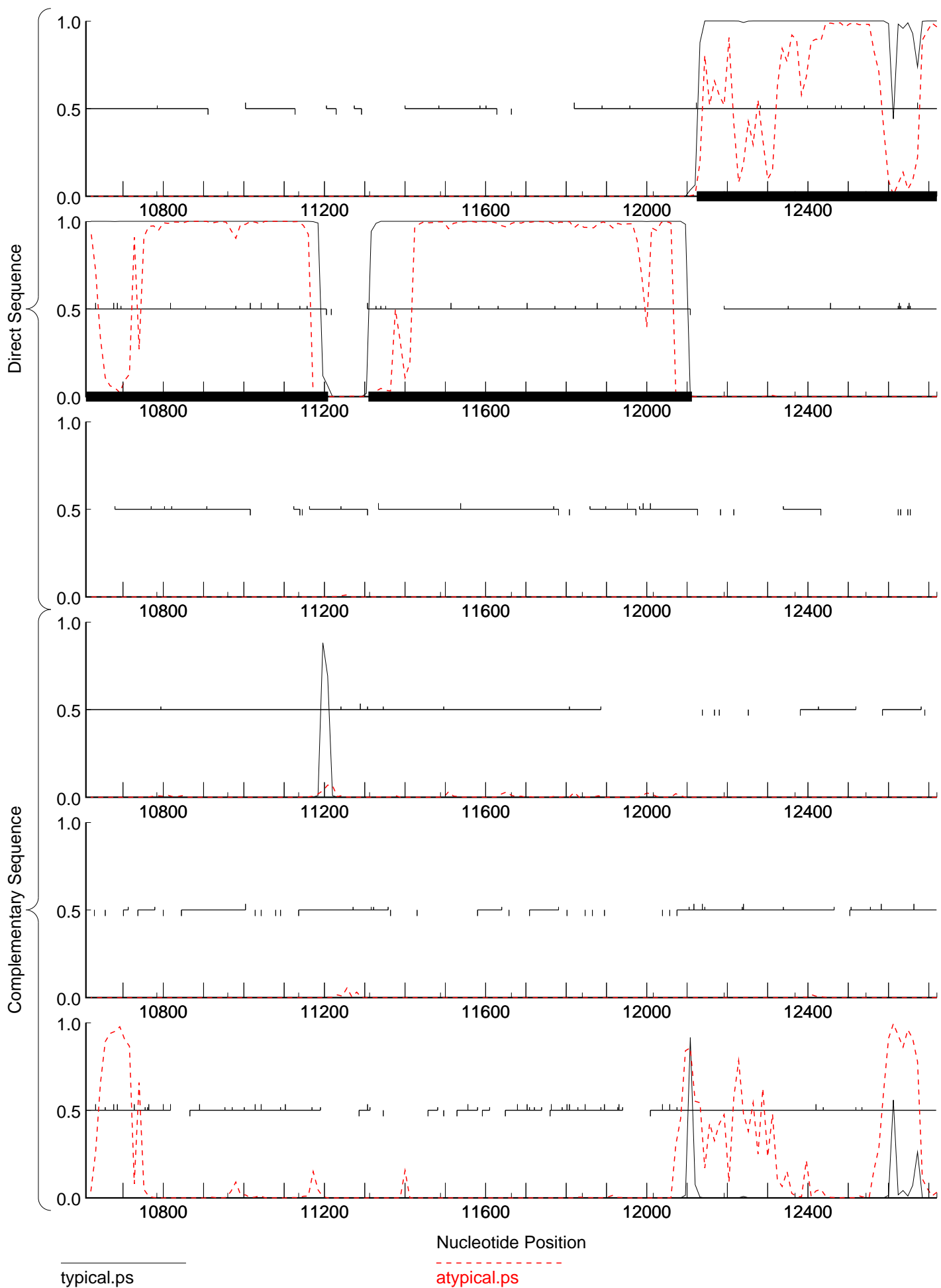


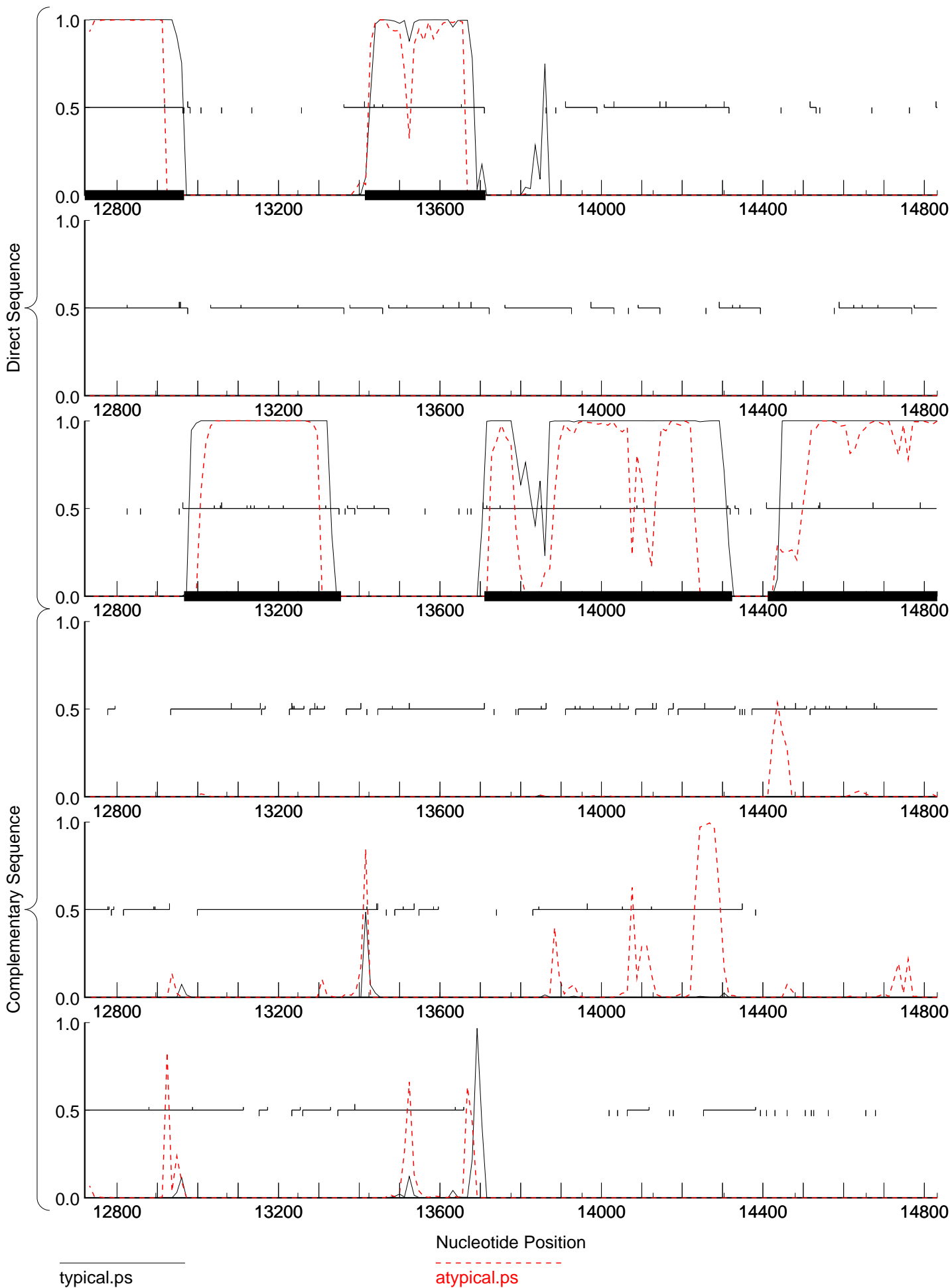




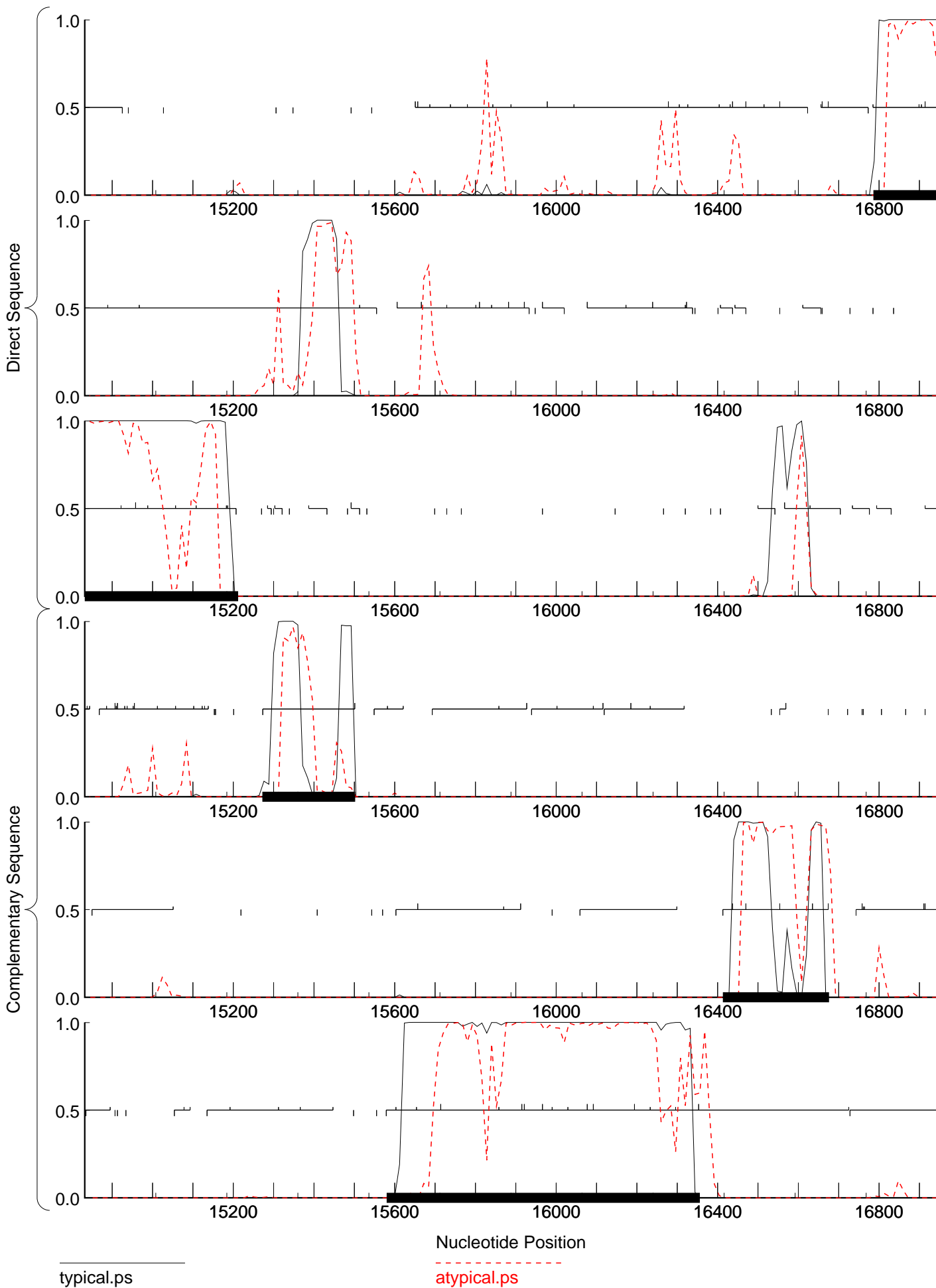






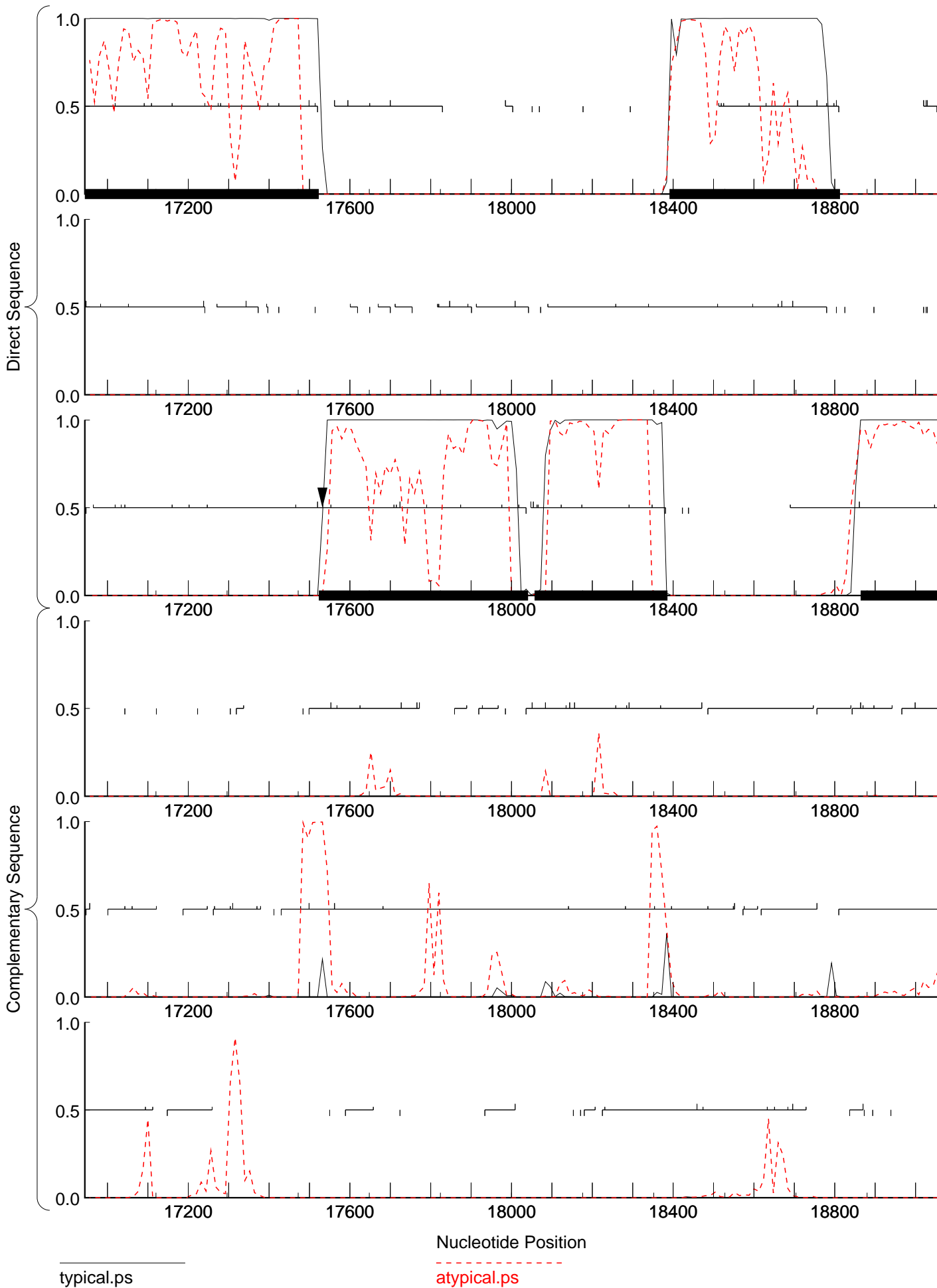






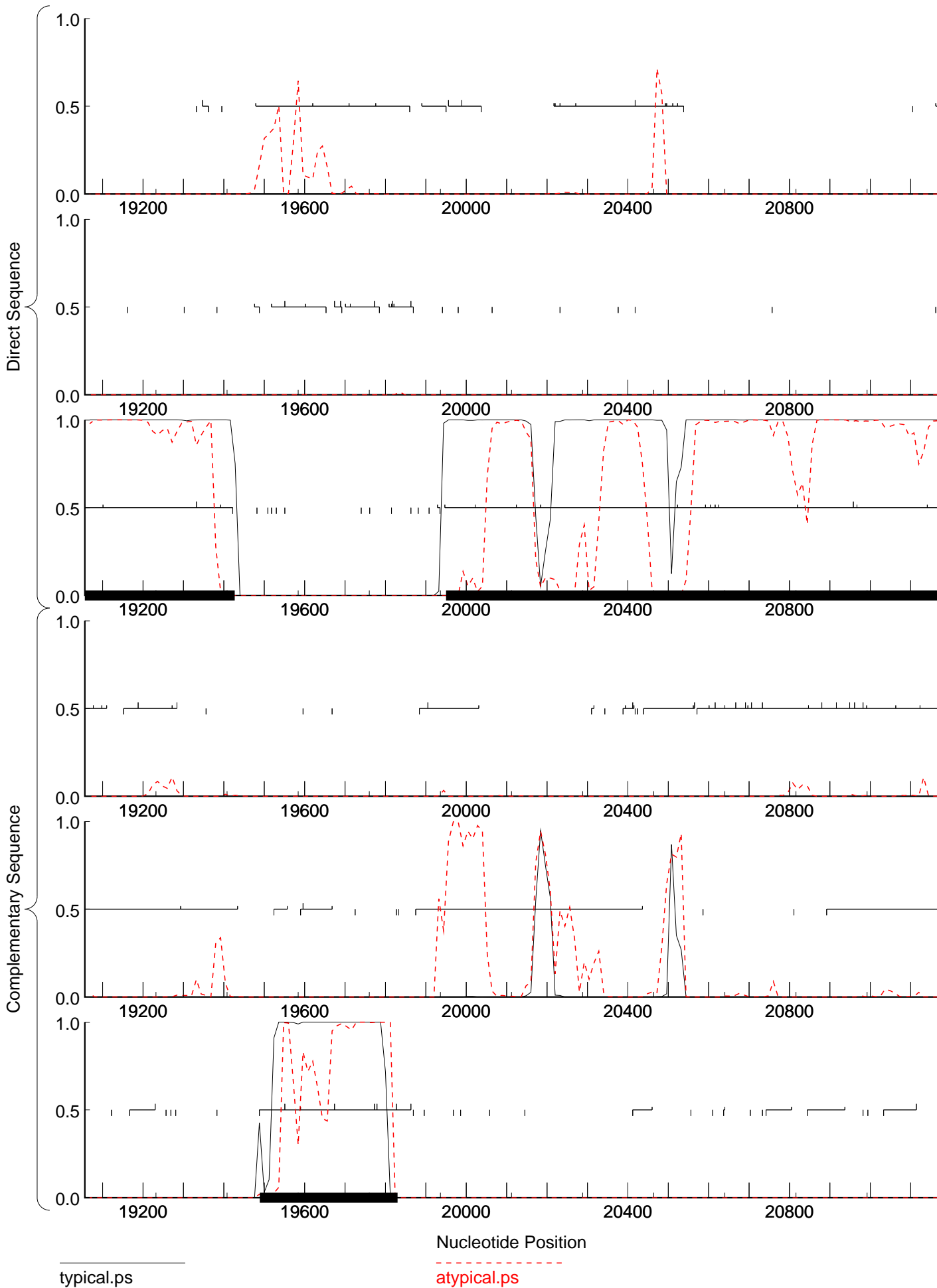
typical.ps

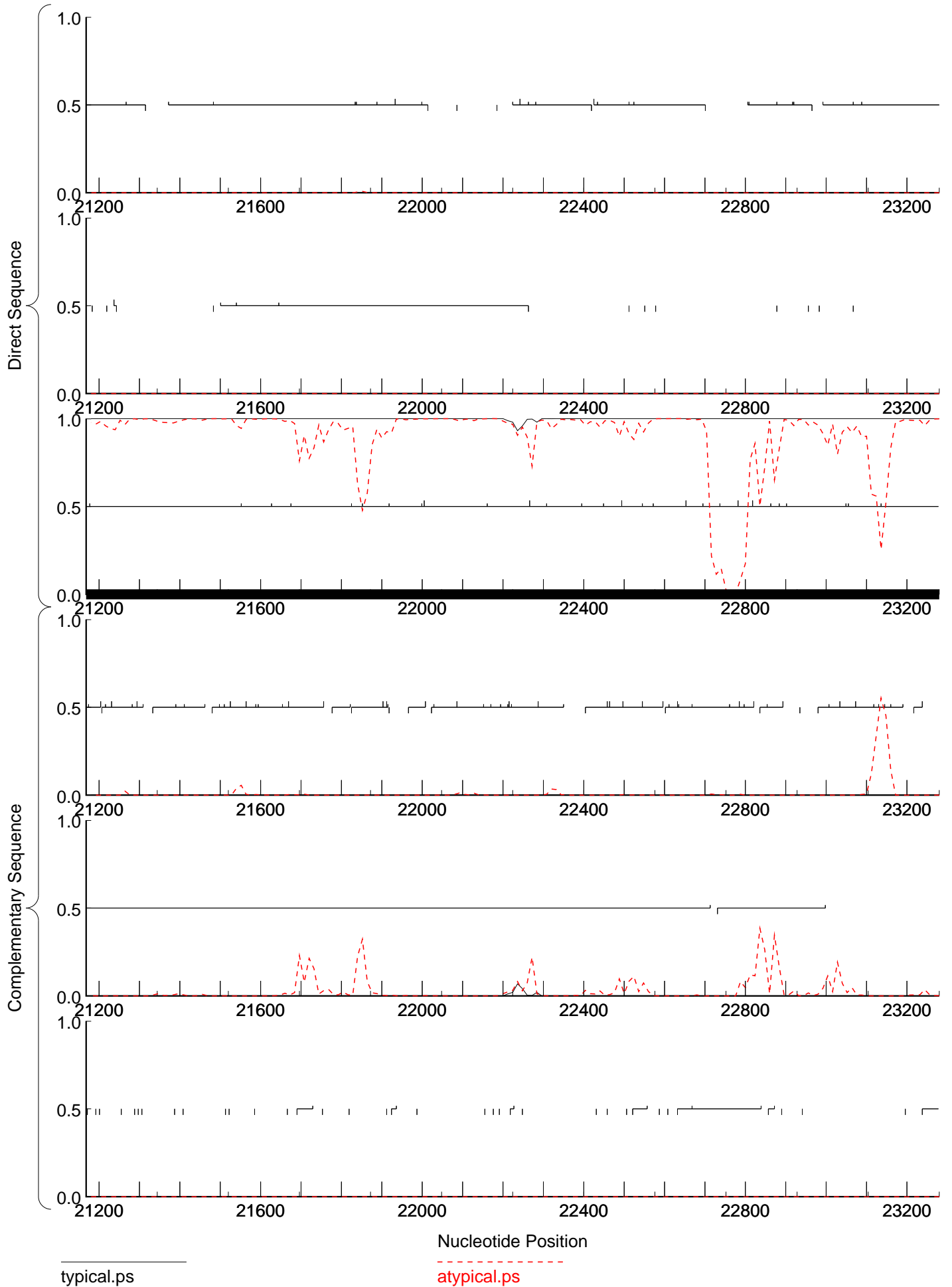
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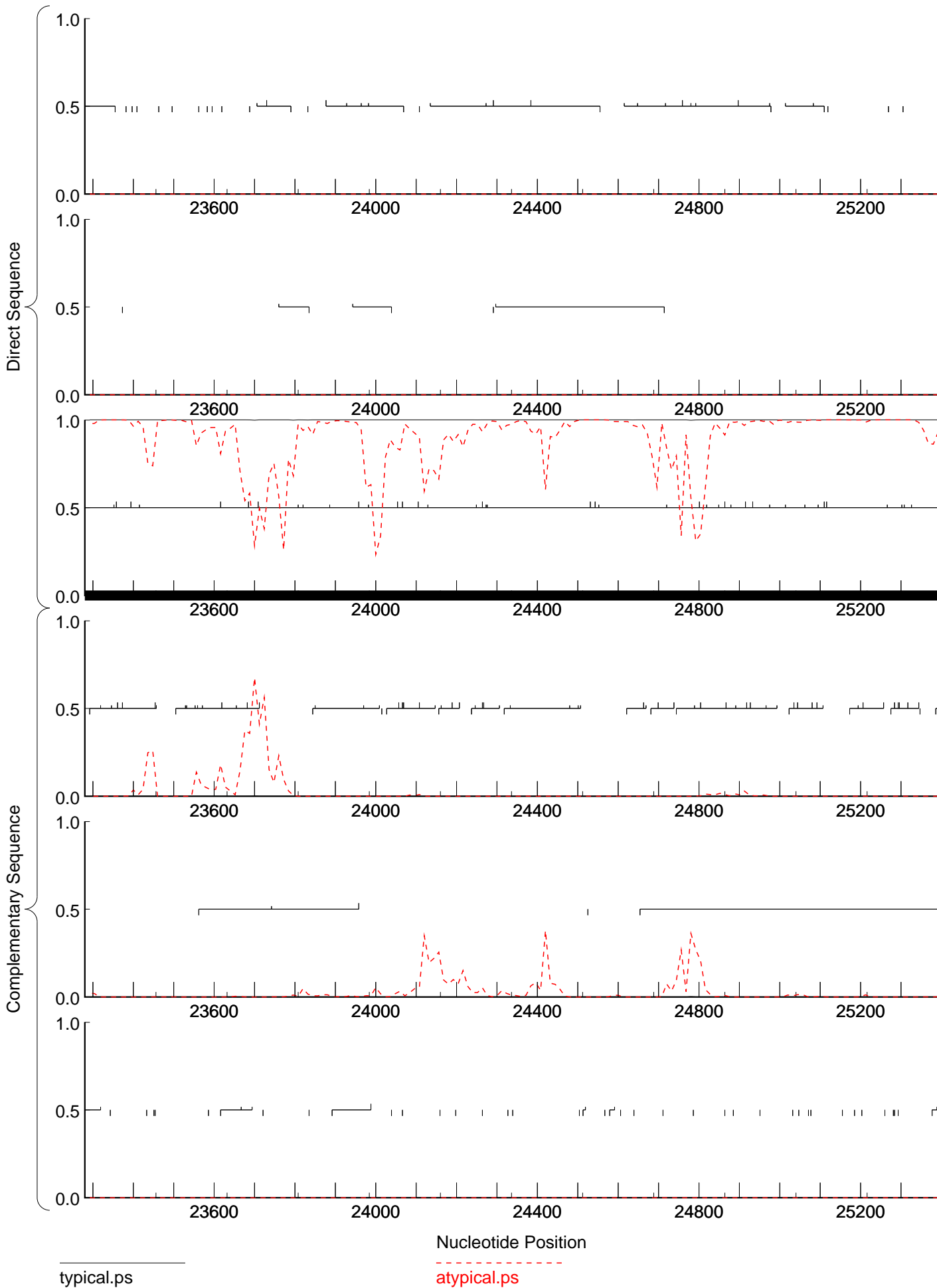


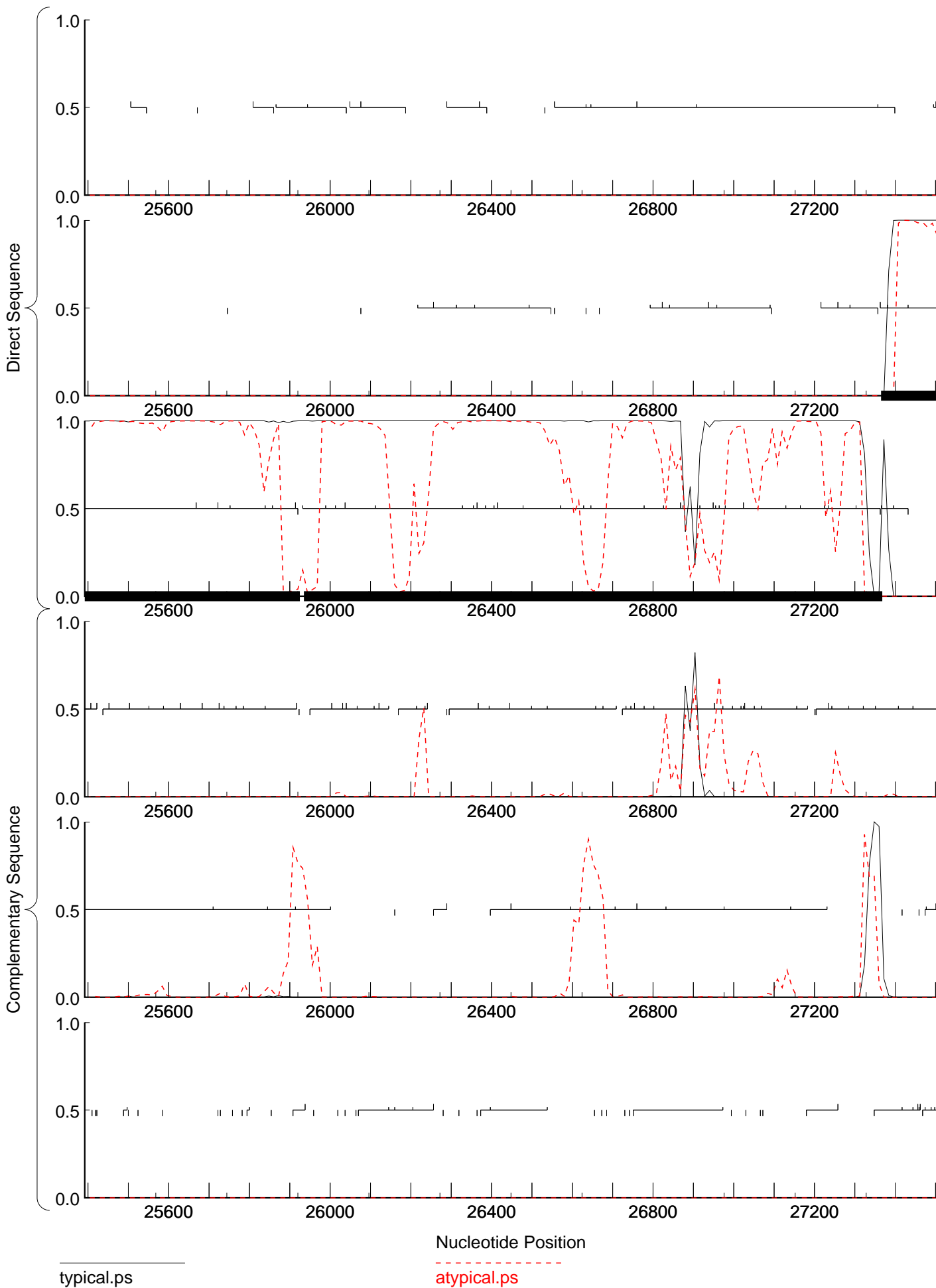
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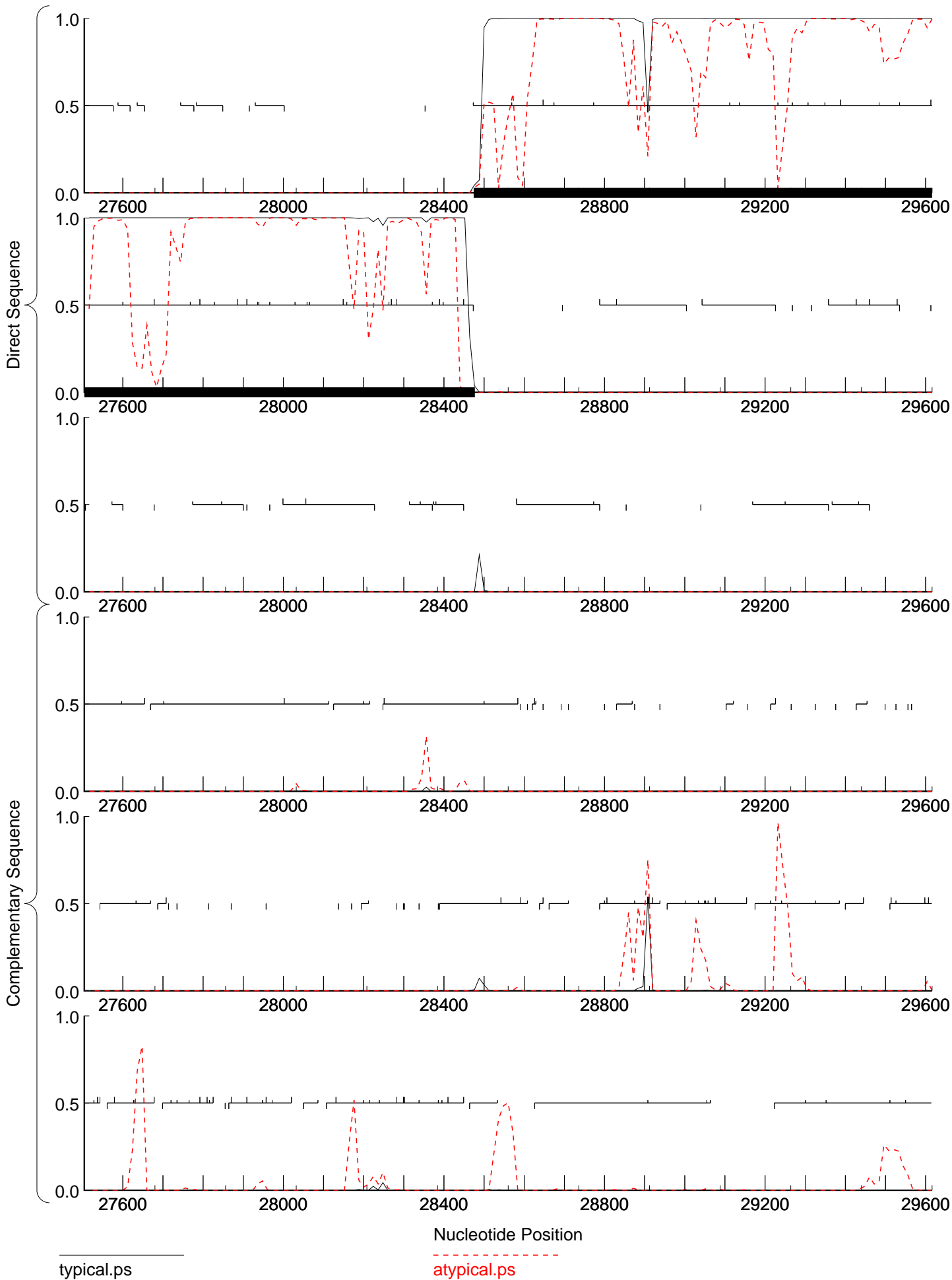
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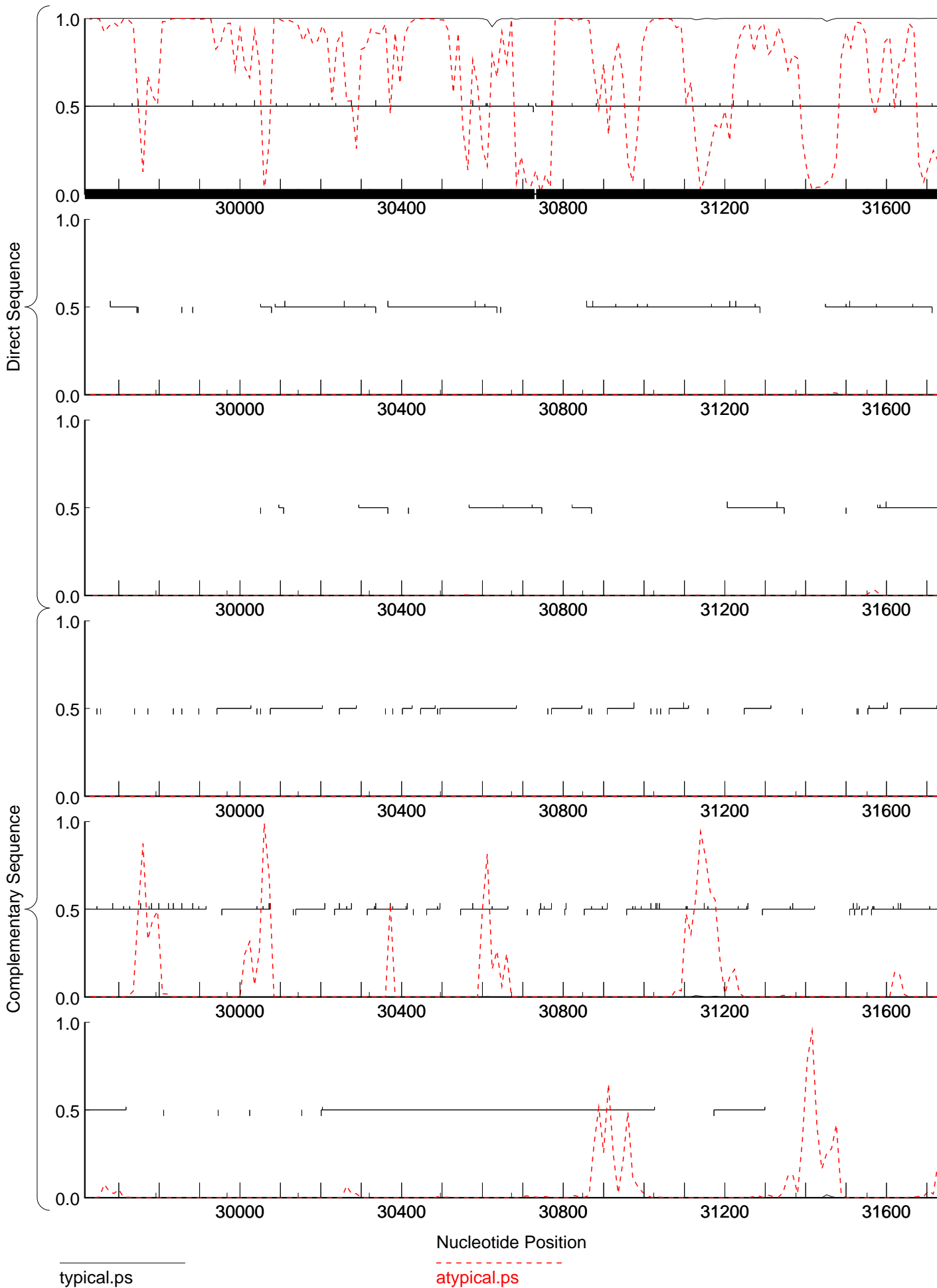




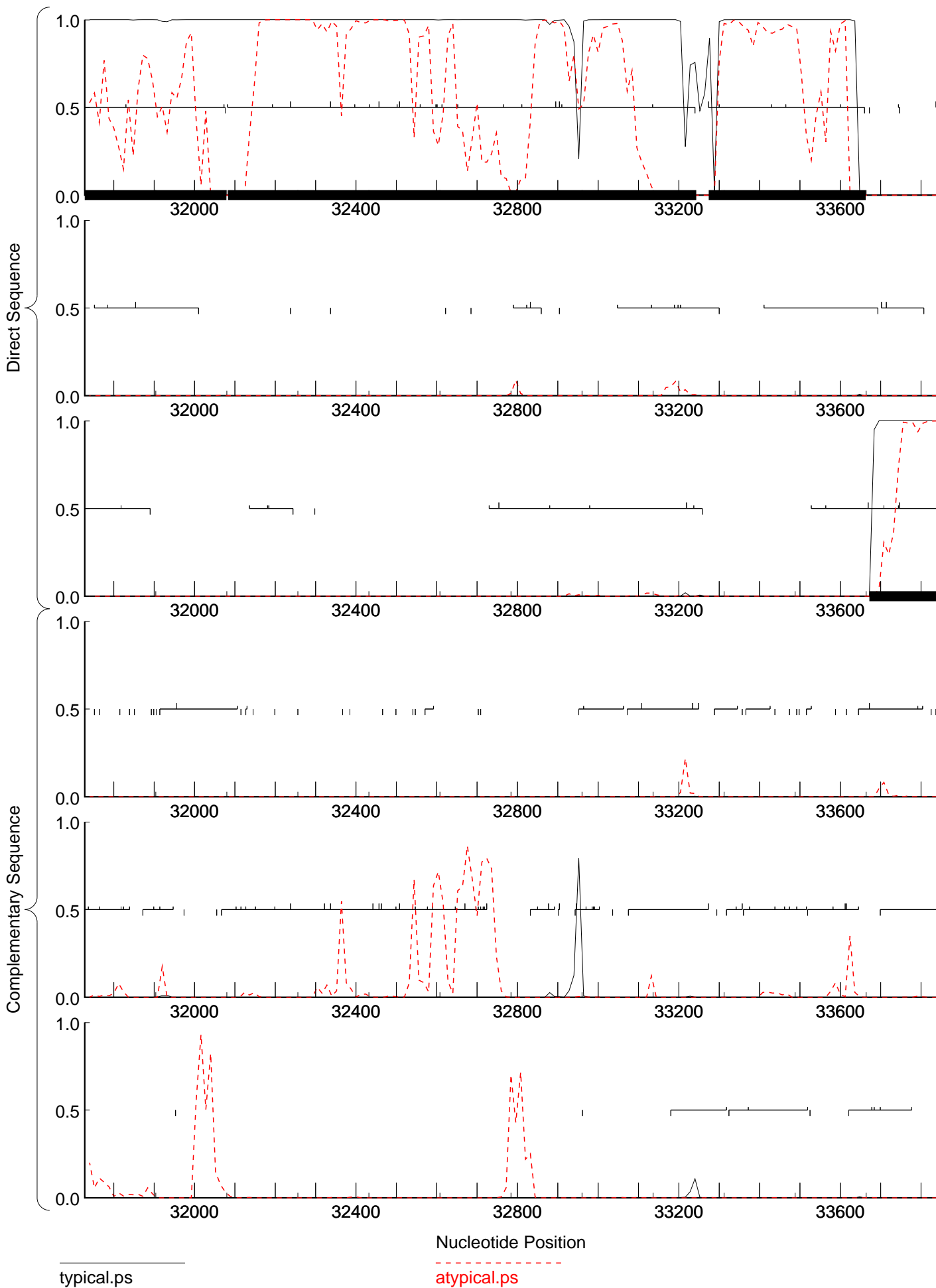


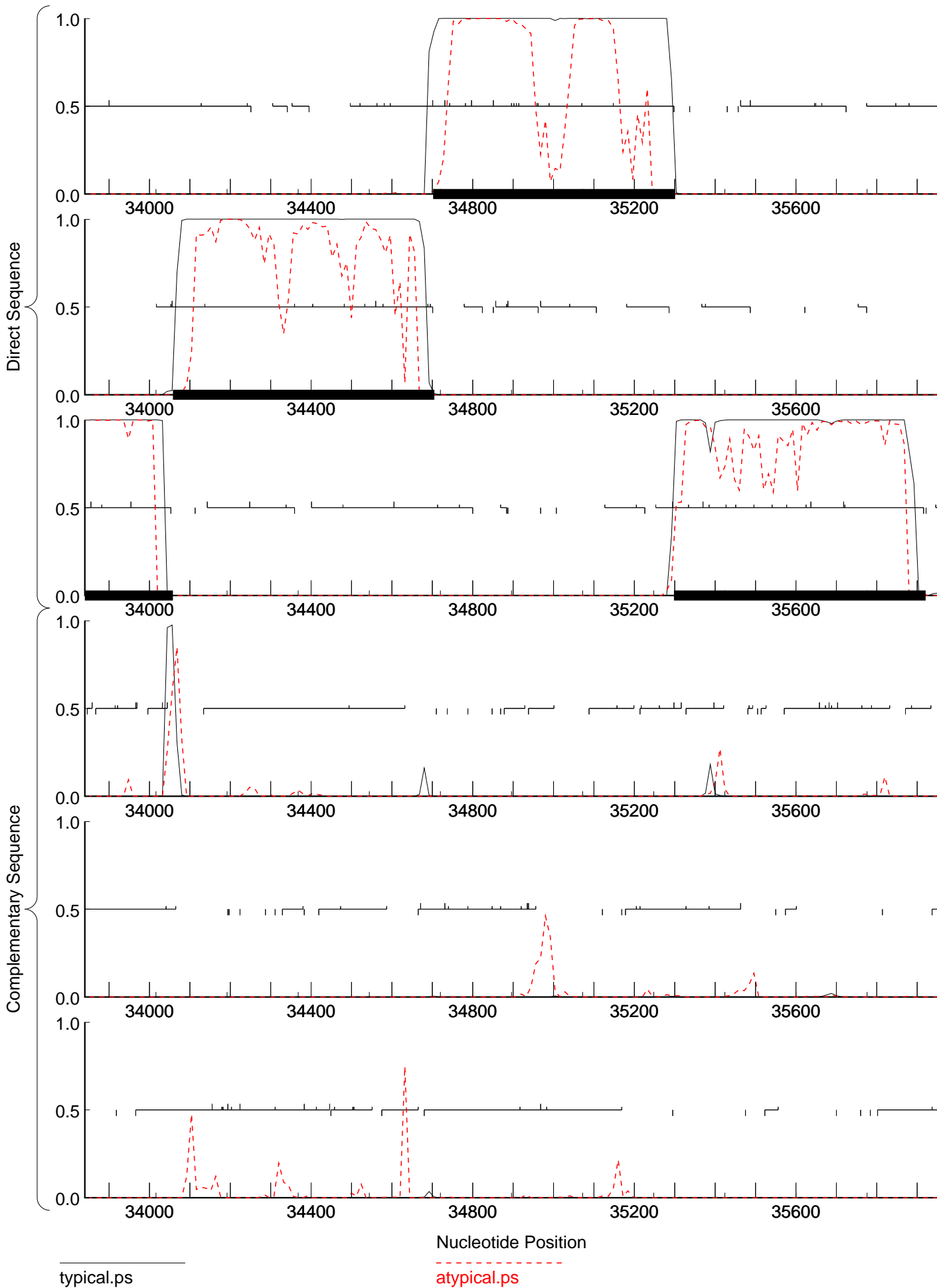


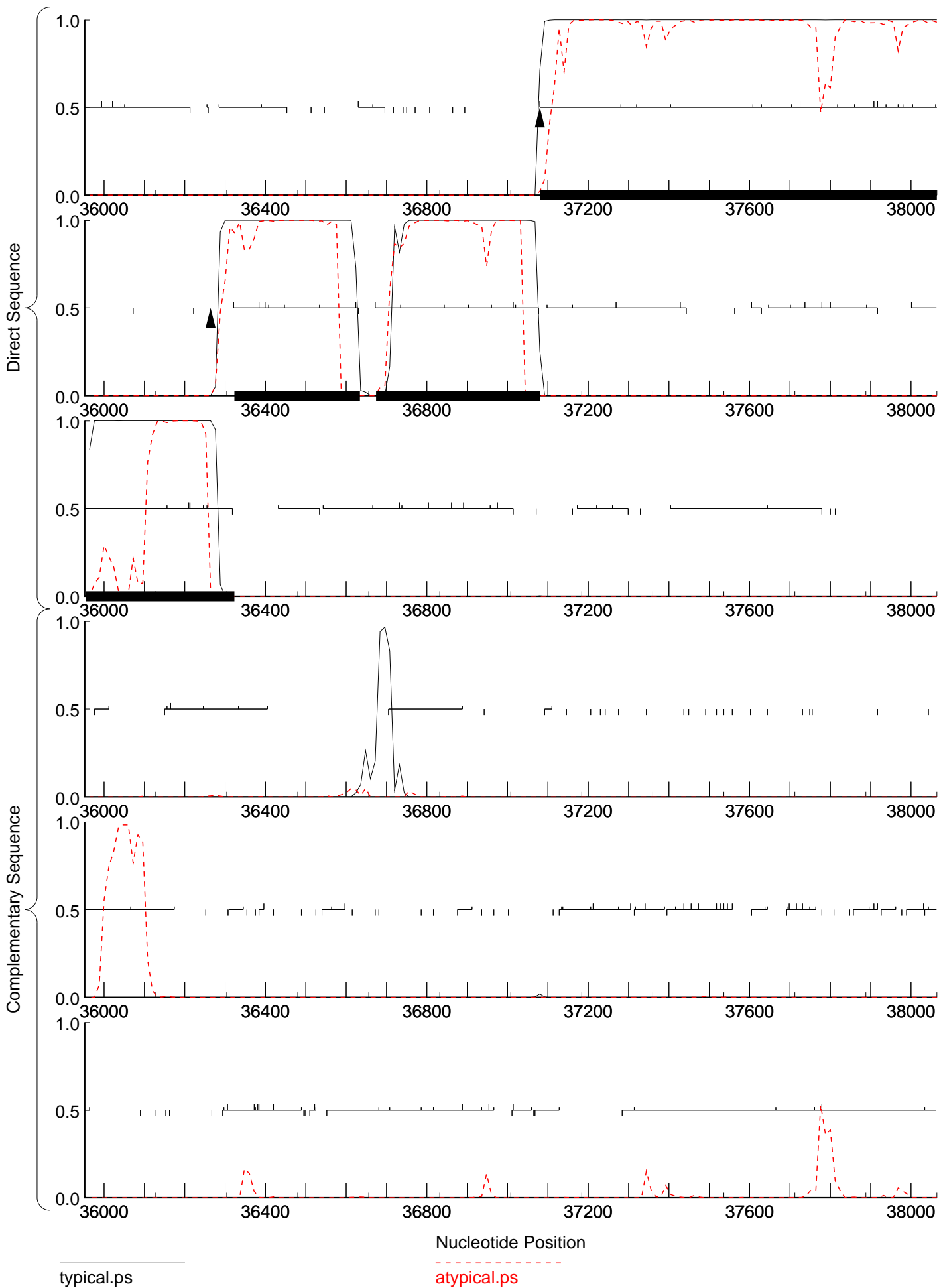


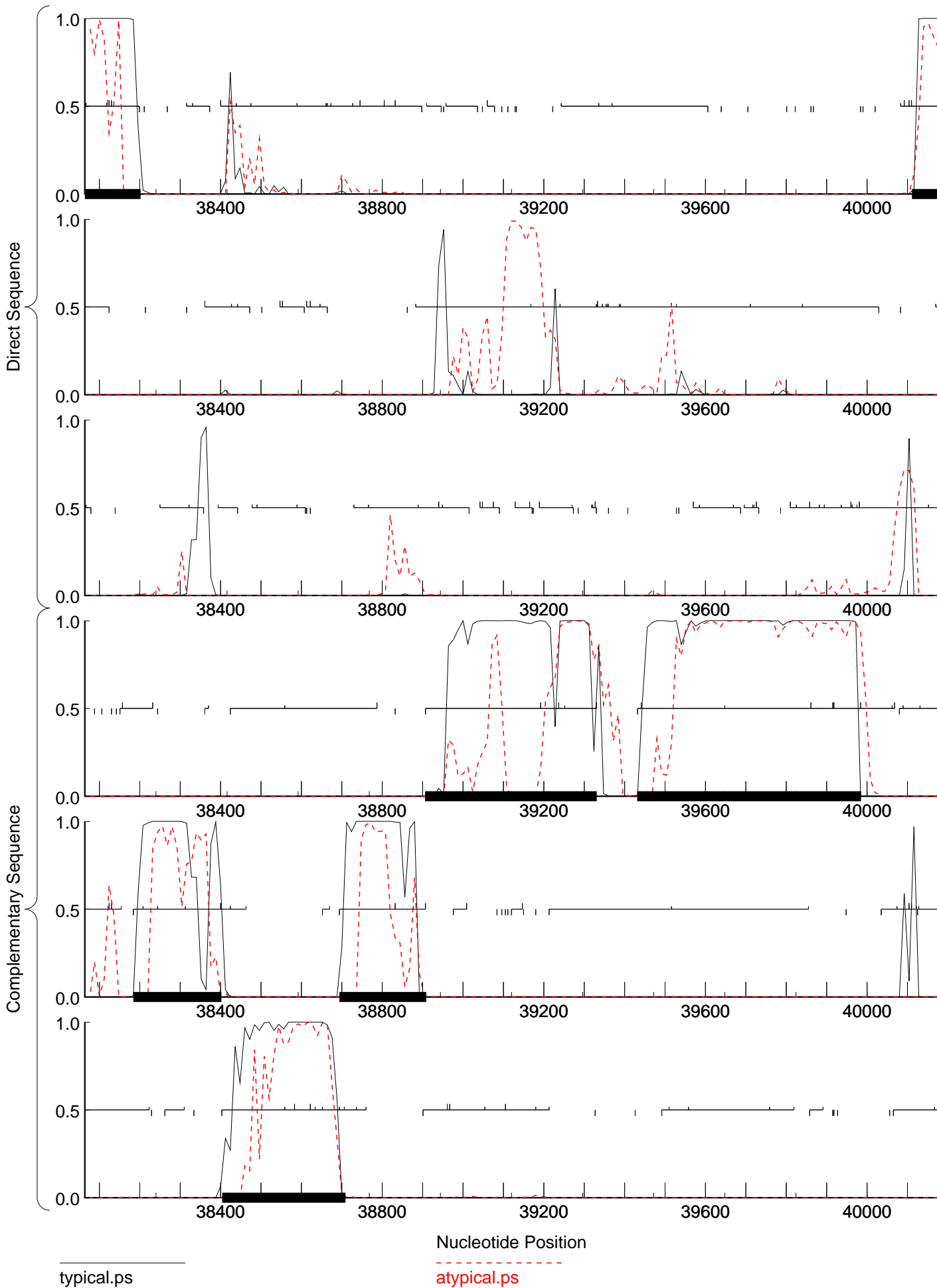








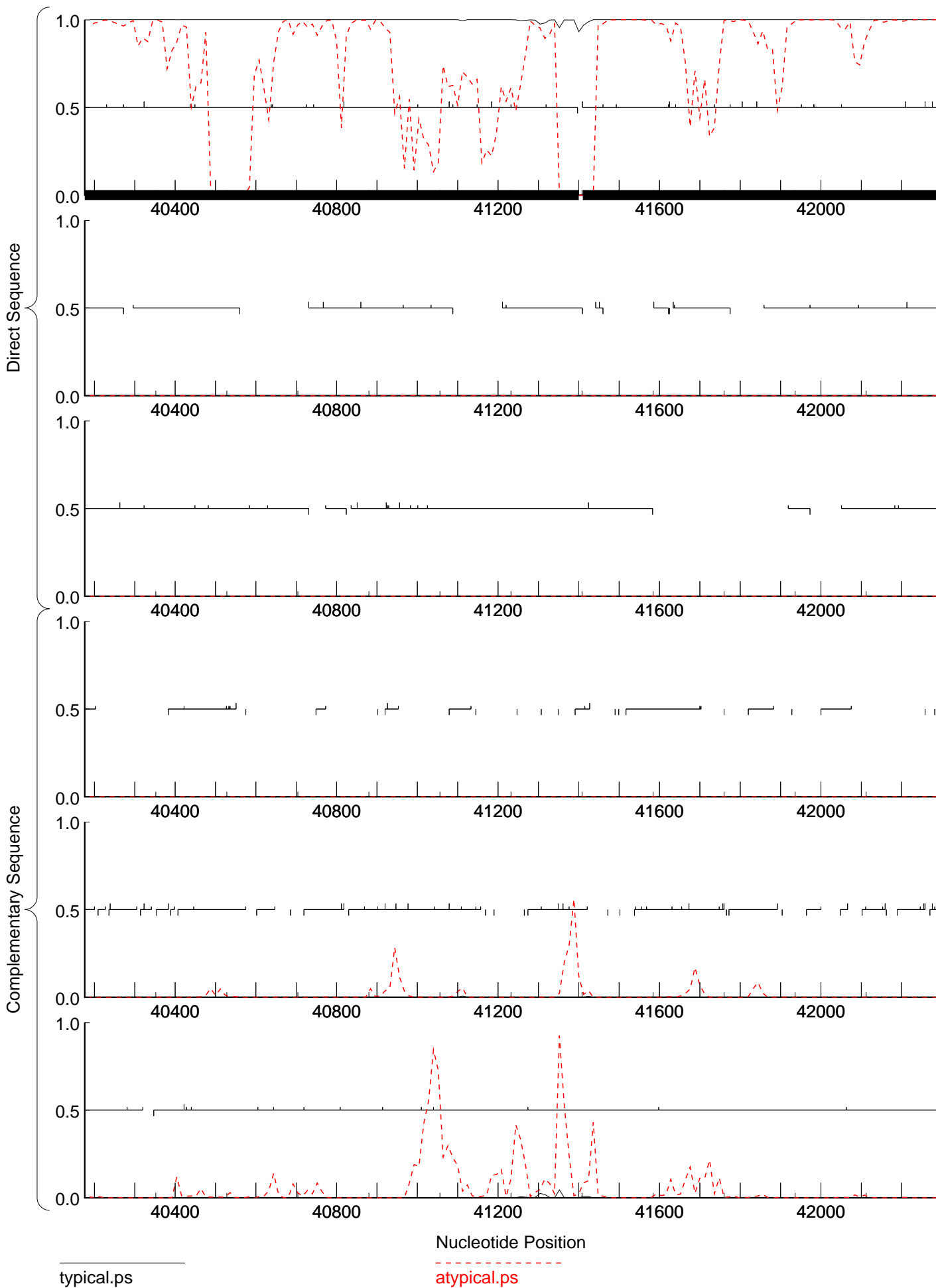


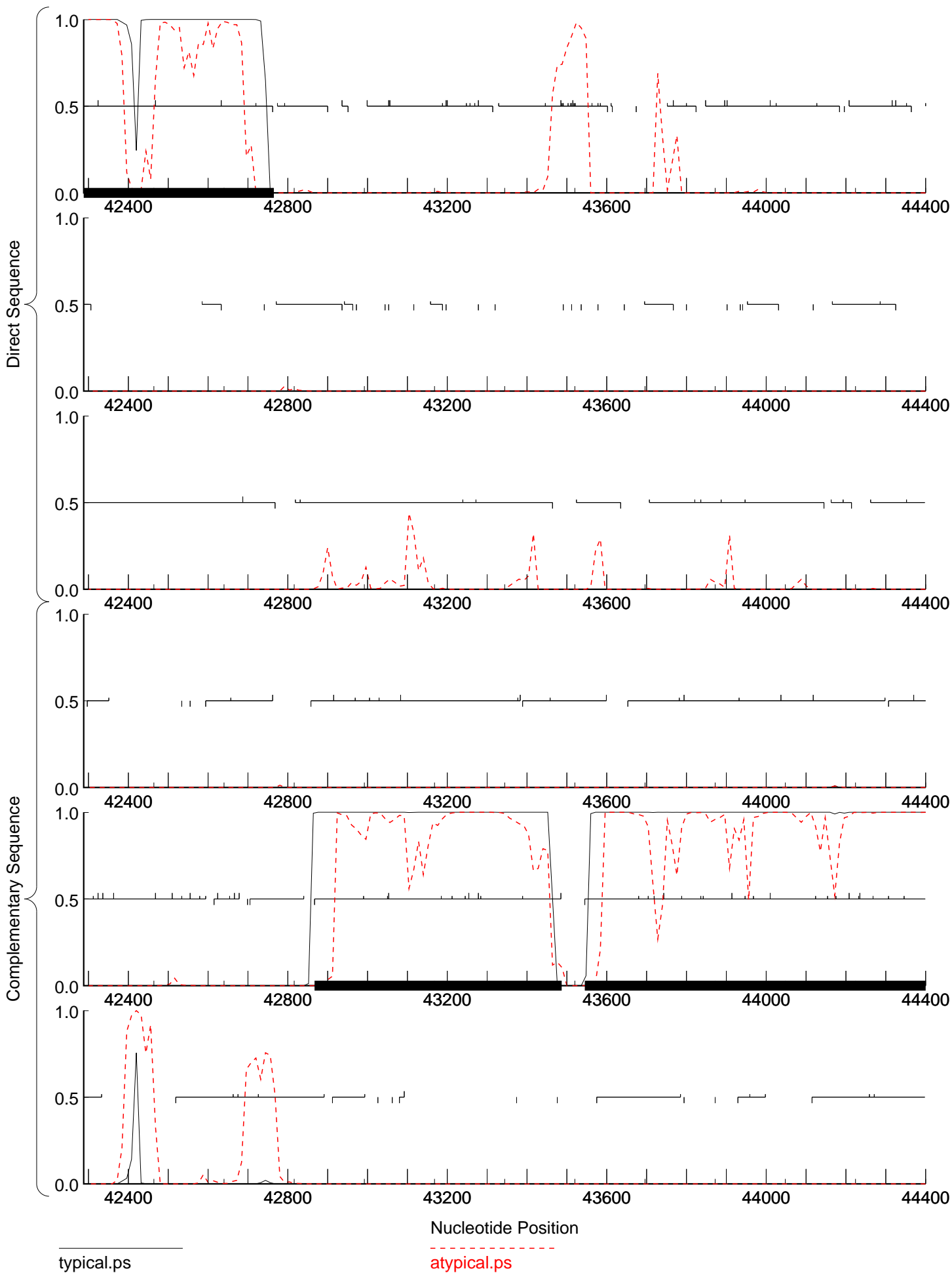


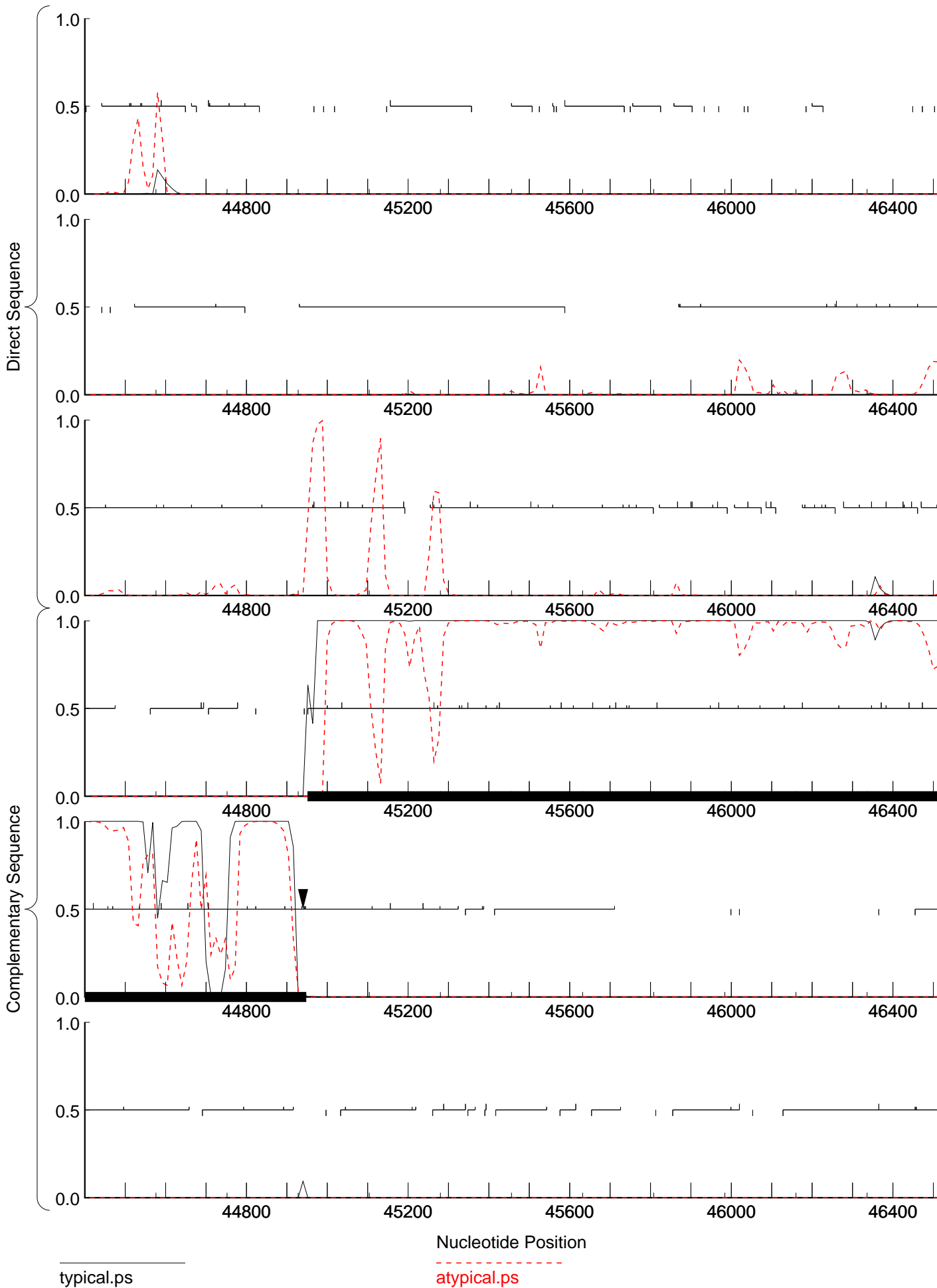
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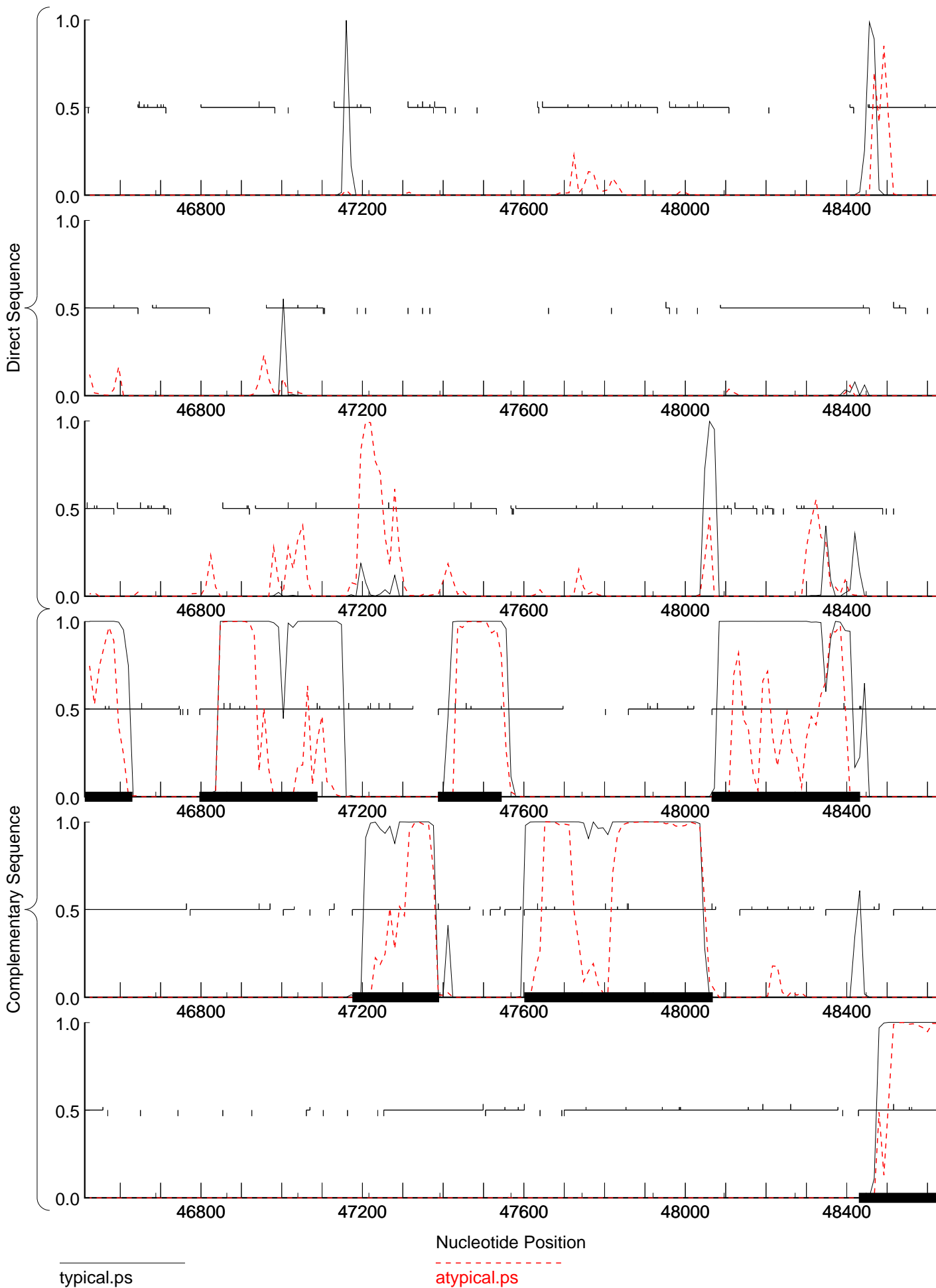
Nucleotide Position

atypical.ps

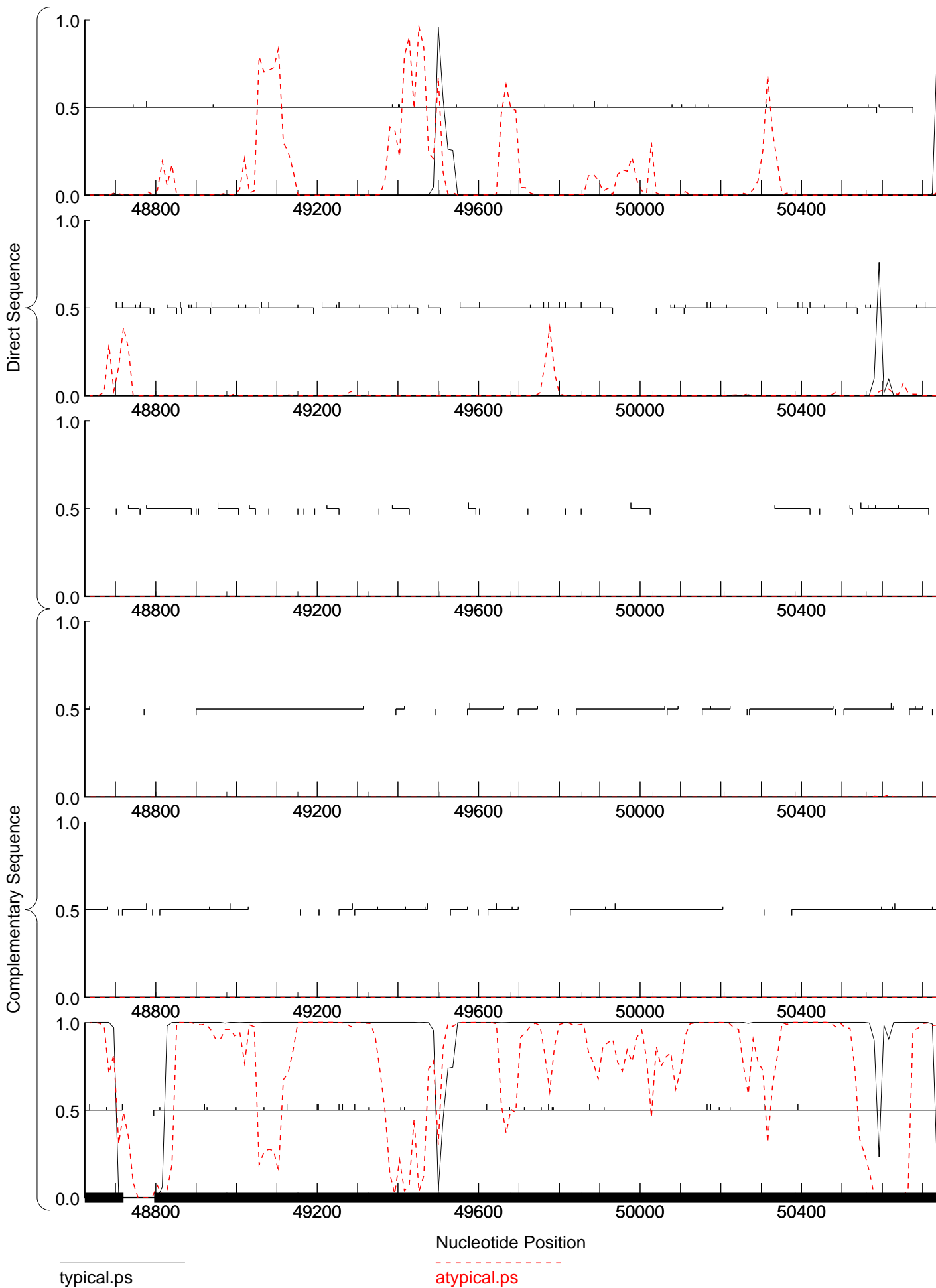






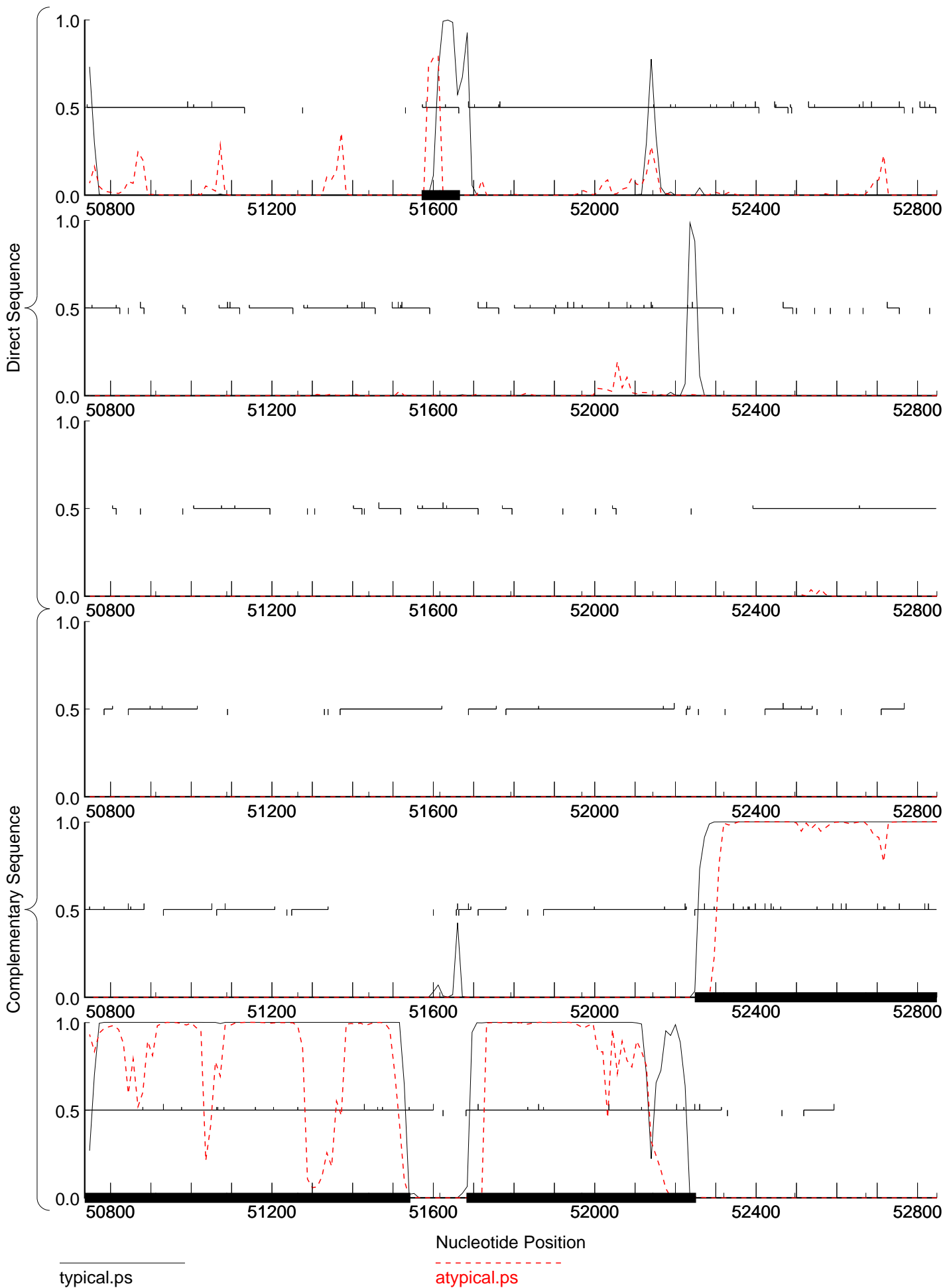


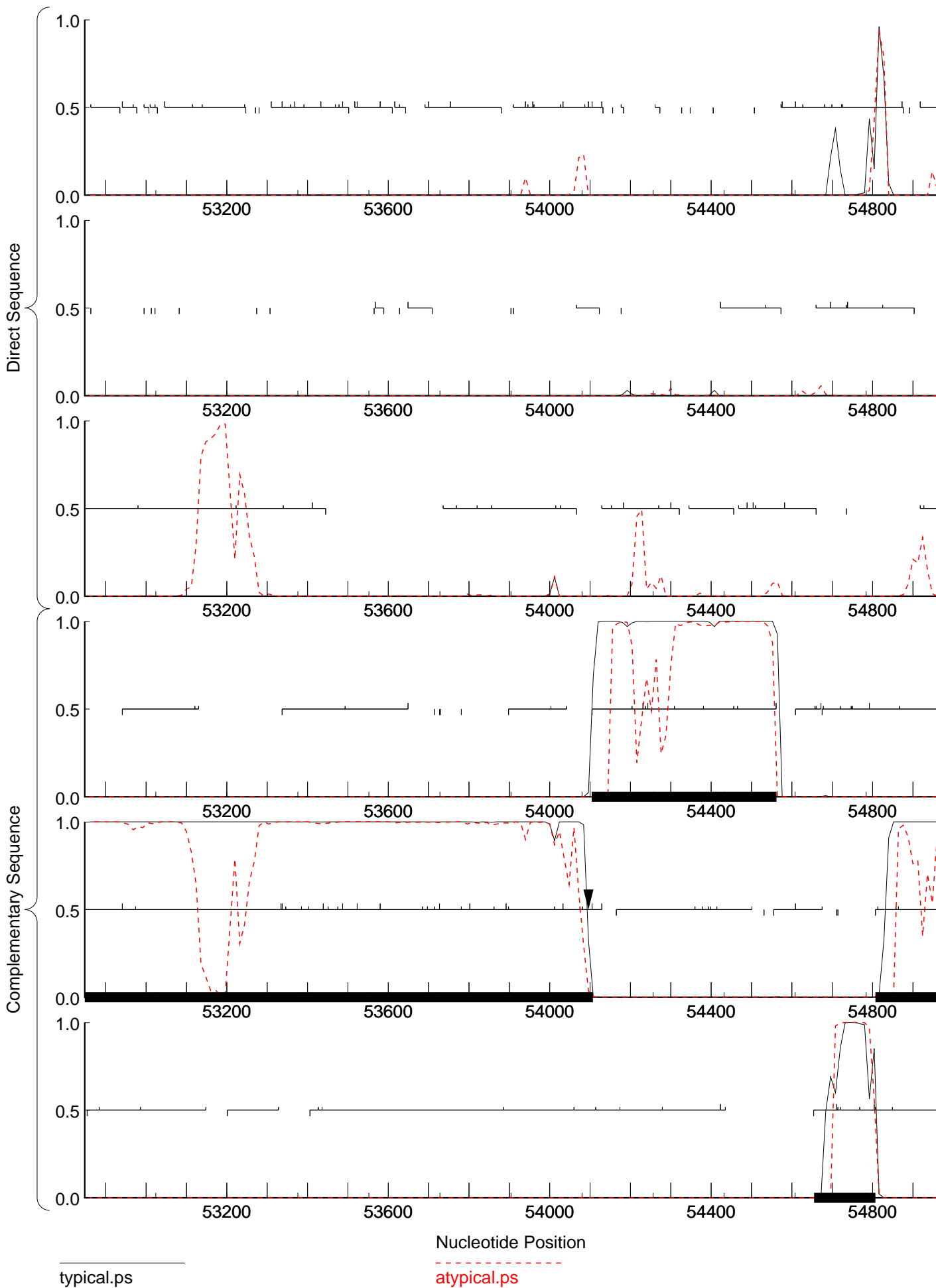




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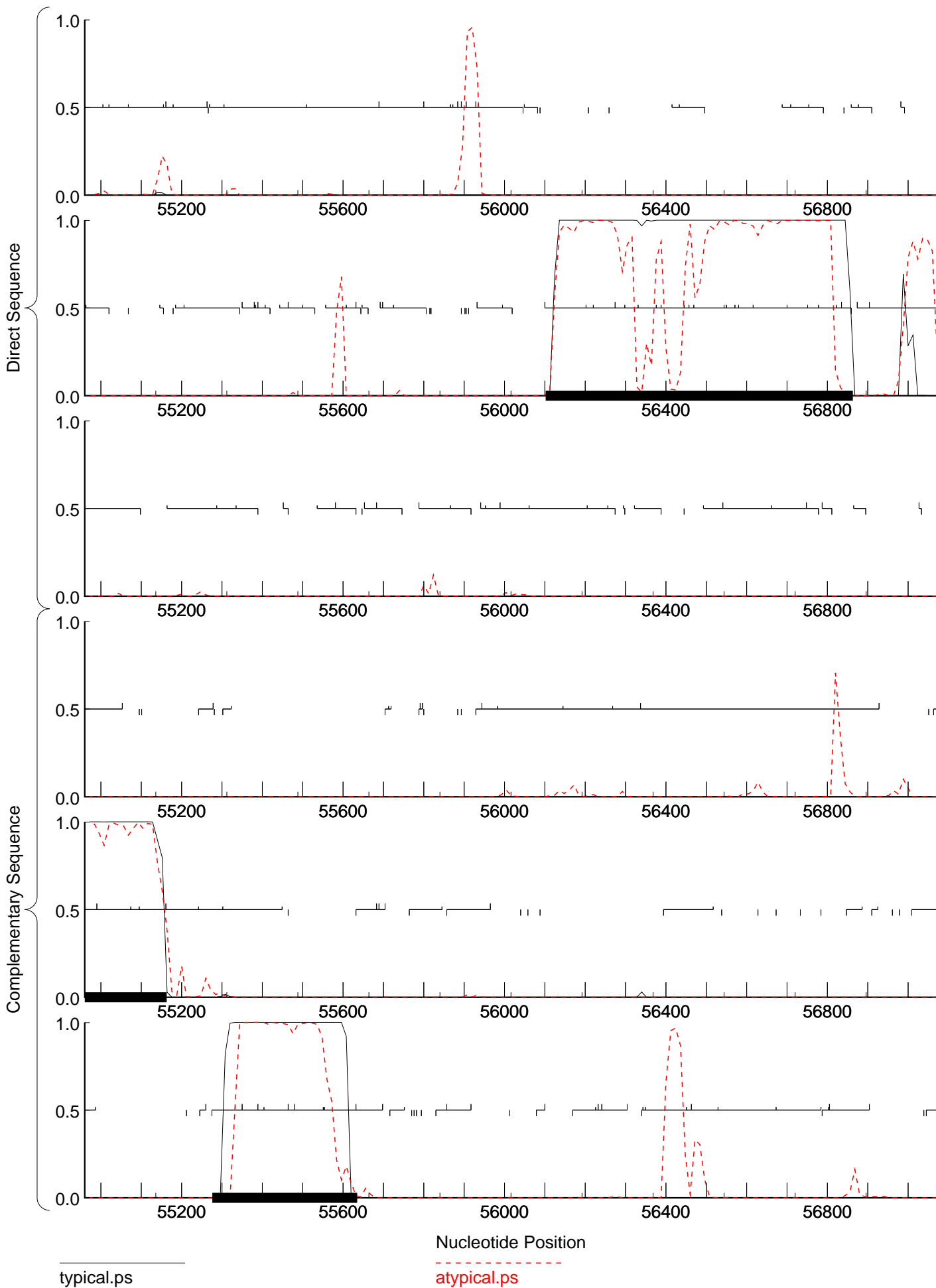
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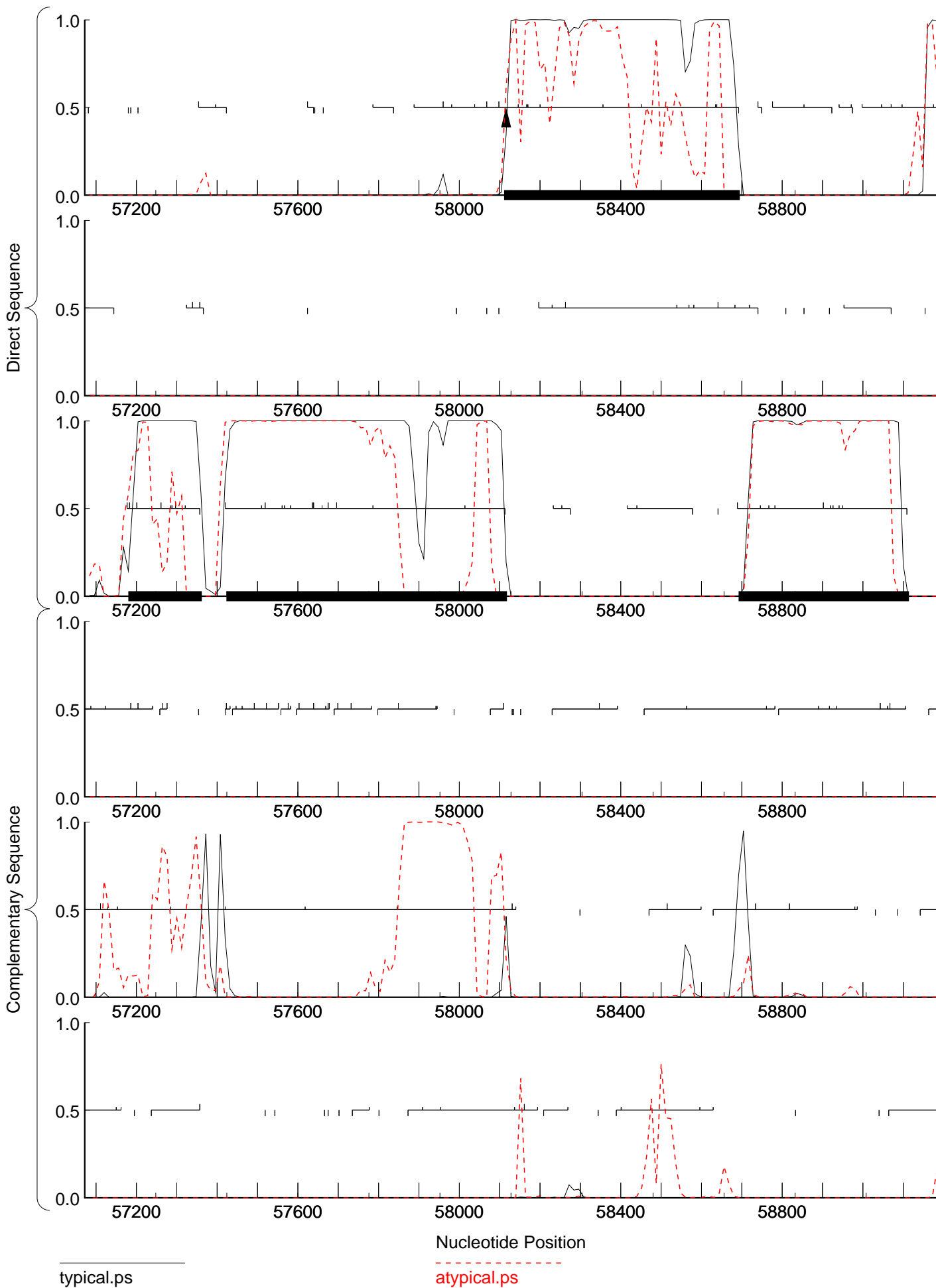




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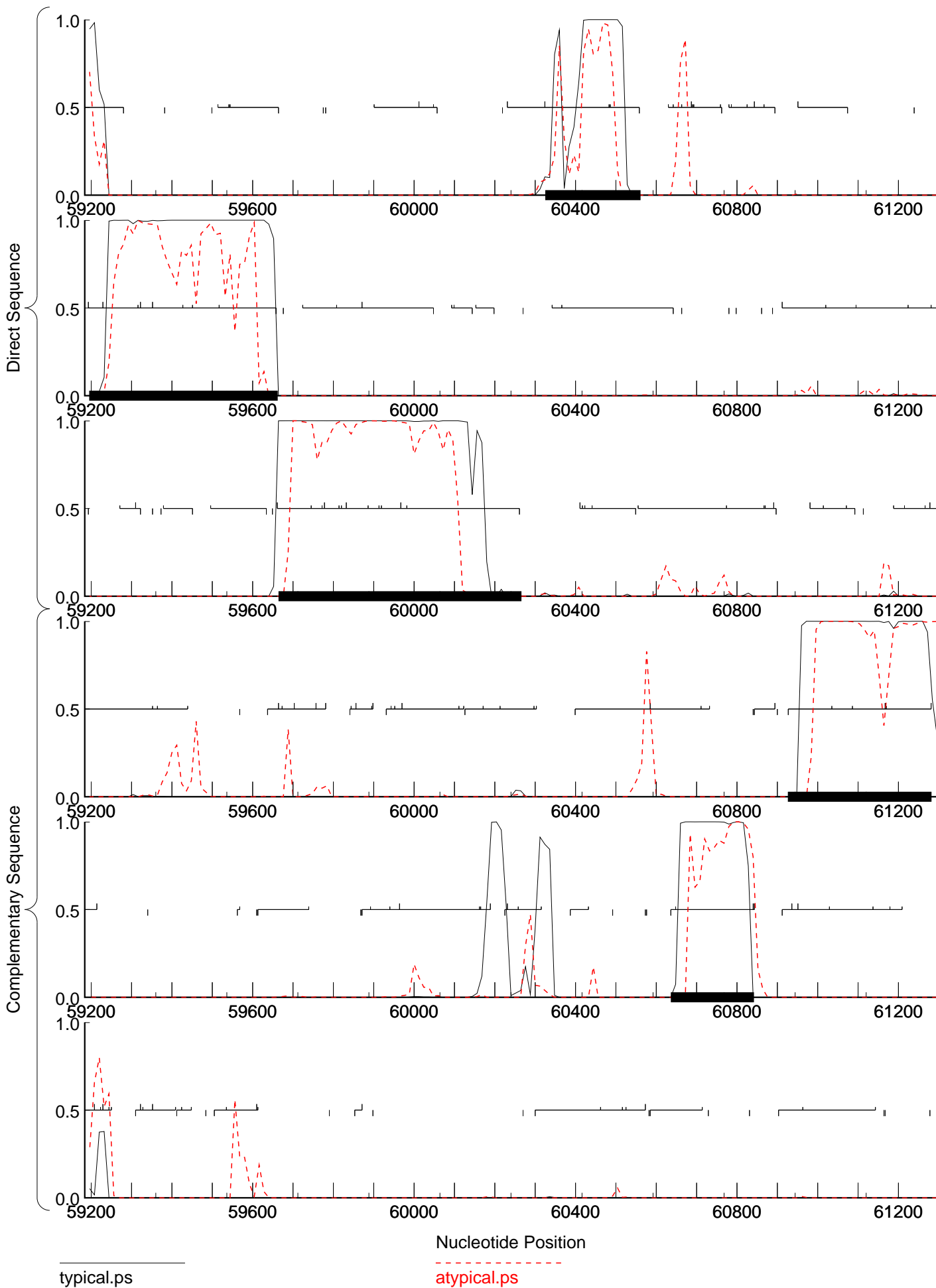
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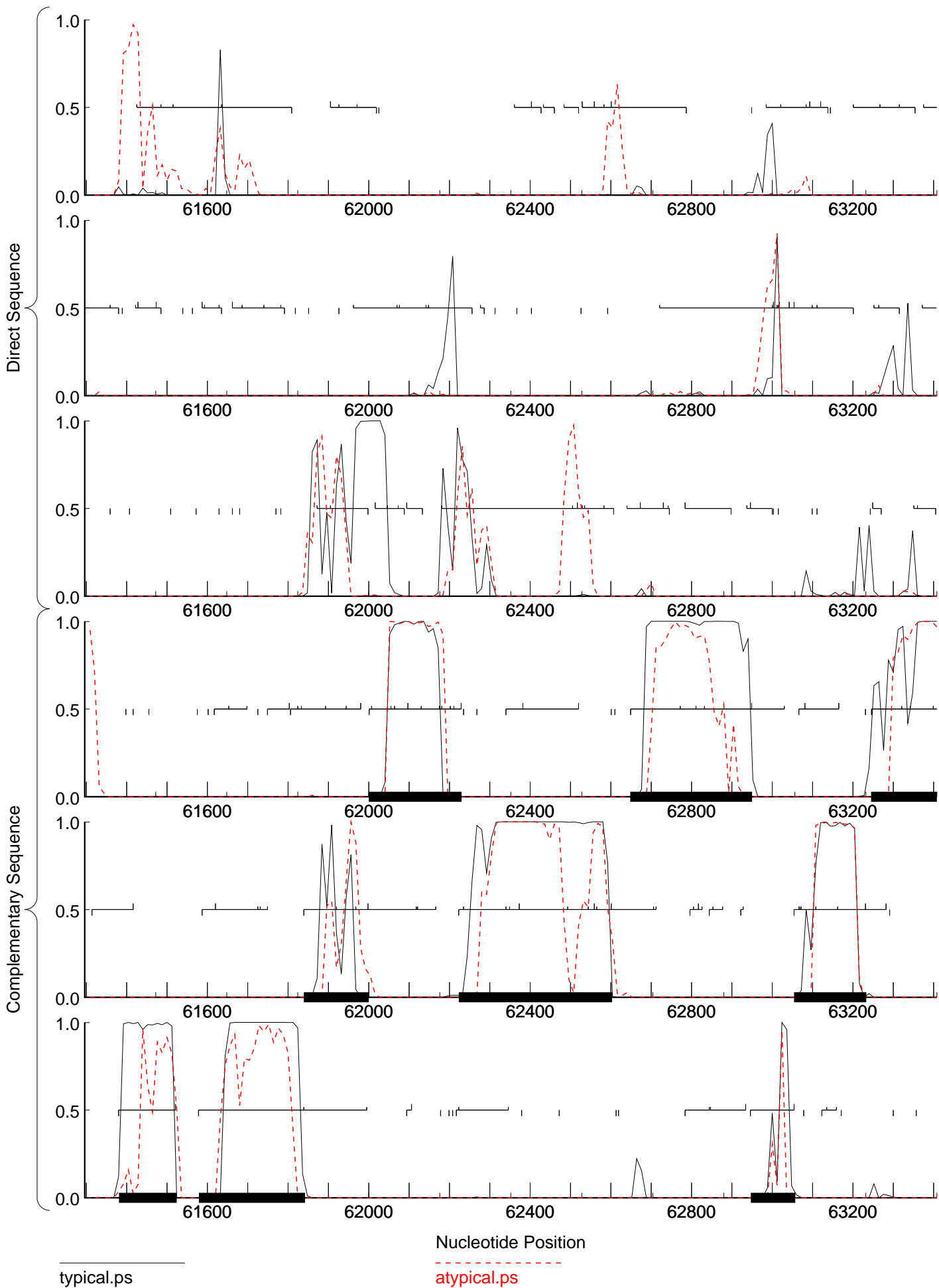




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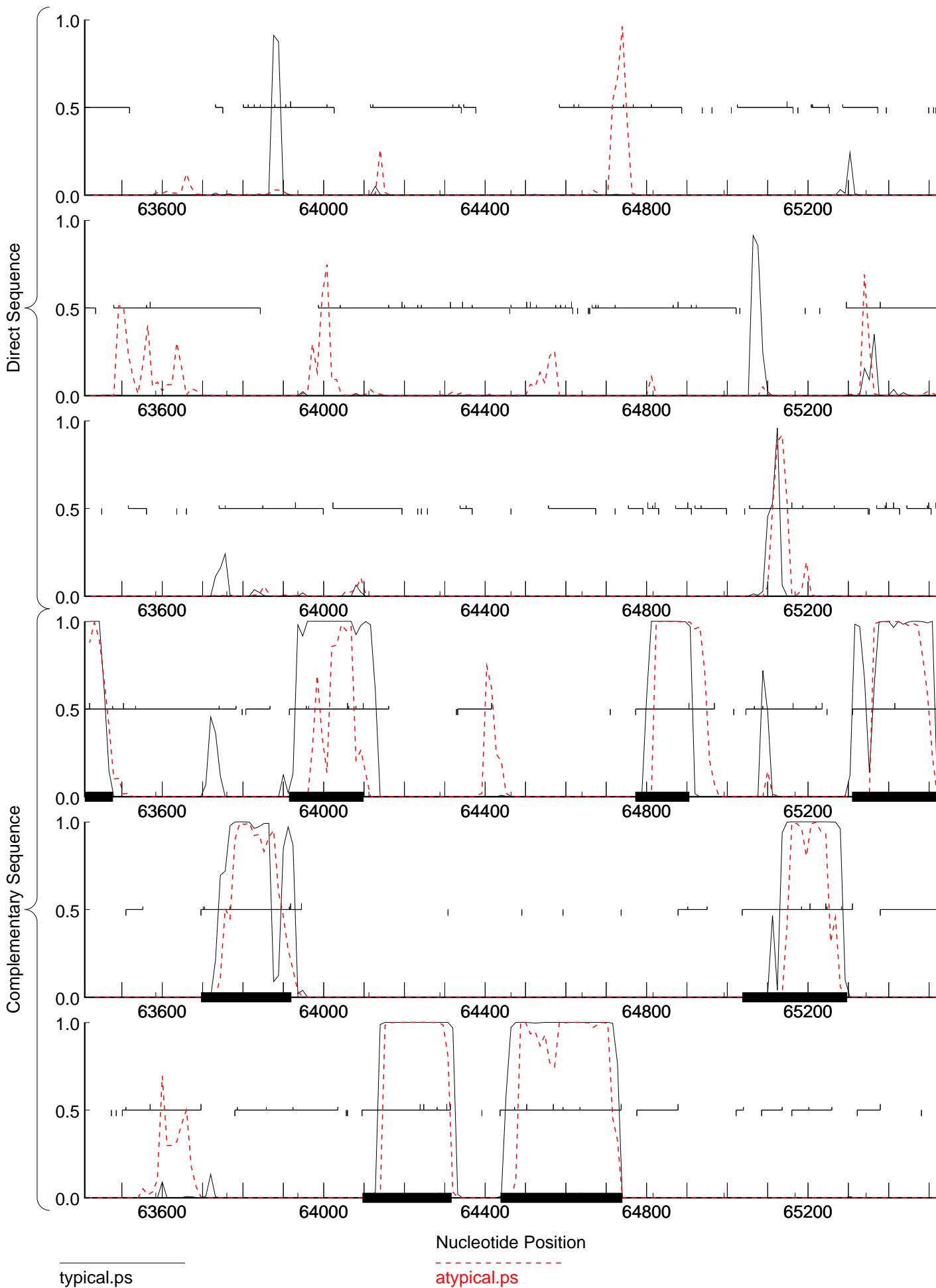
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typical.ps

atypical.ps



typical.ps

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