

# GeneMark

Version 2.5p (09.08.06)

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## PROGRAM INFORMATION

Sequence : Streptomyces phage Gilson complete sequence, 128338 bp including 766 bp terminal repeat, Cl  
Analysis Date : 7/17/18 at 21:23:01  
Pages : 62  
Sequence Length : 128338 bp  
GC Content : 47.44%

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,

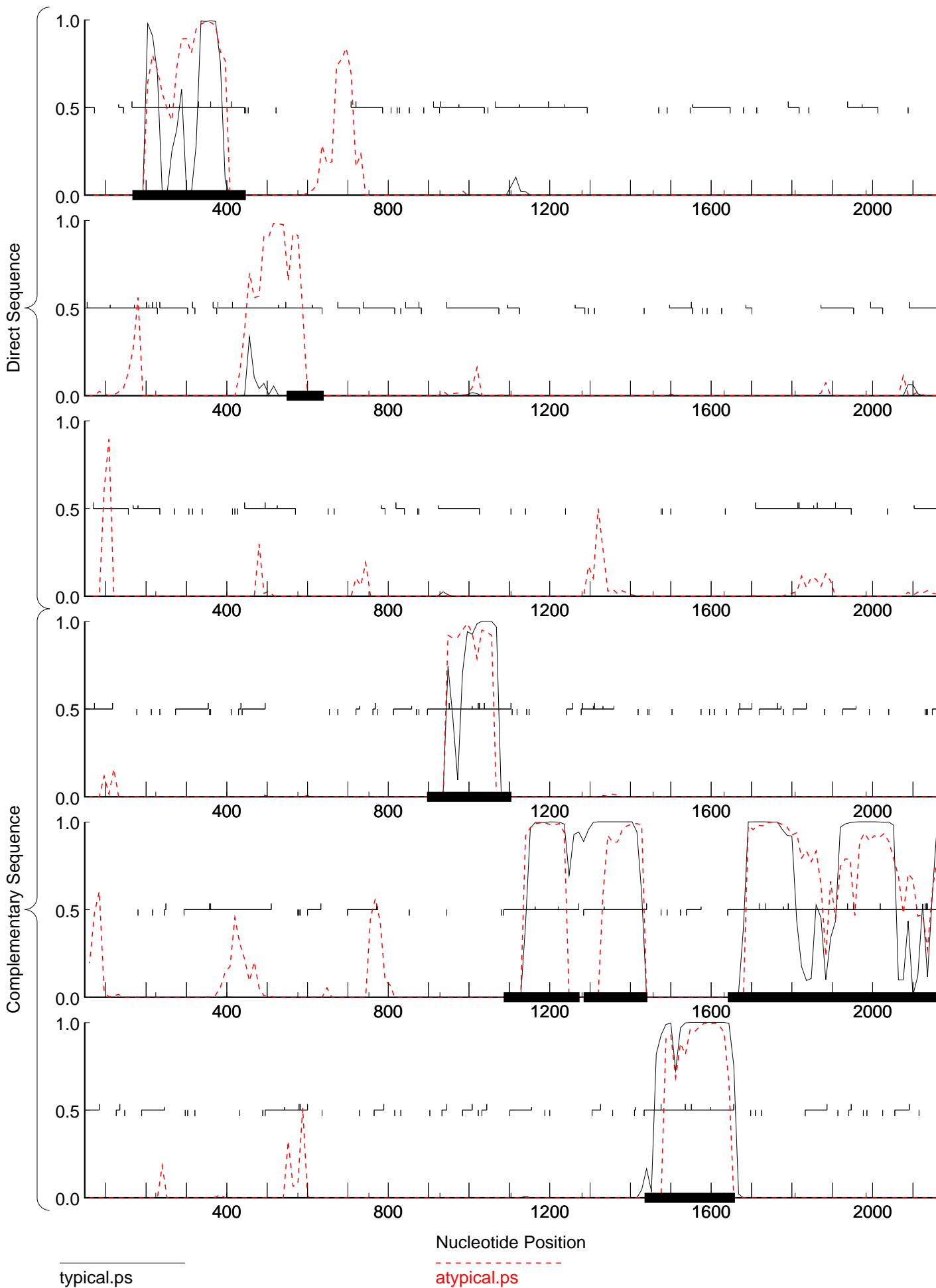
## MATRIX INFORMATION

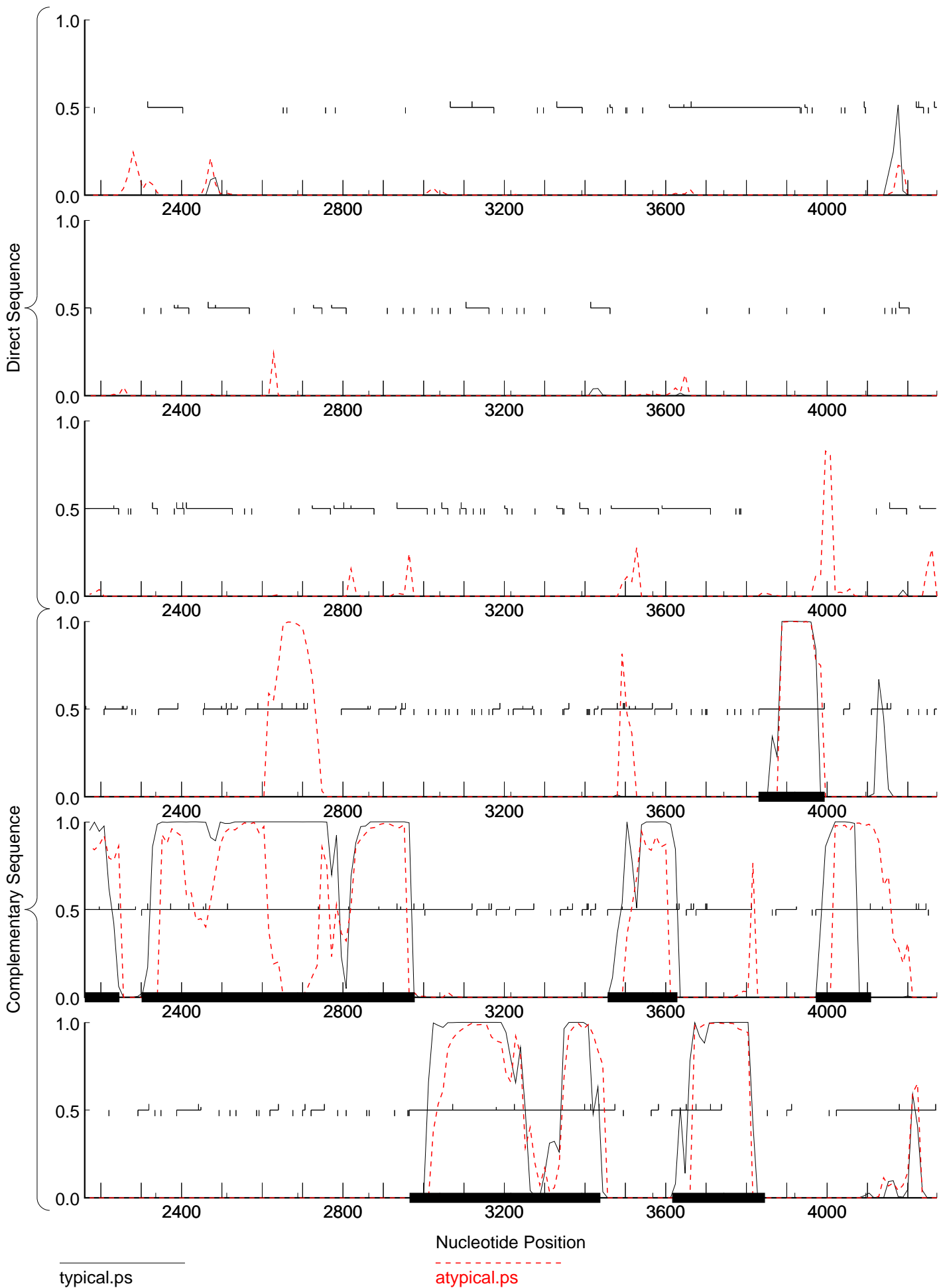
Matrix : -  
Author : -  
Order : 4

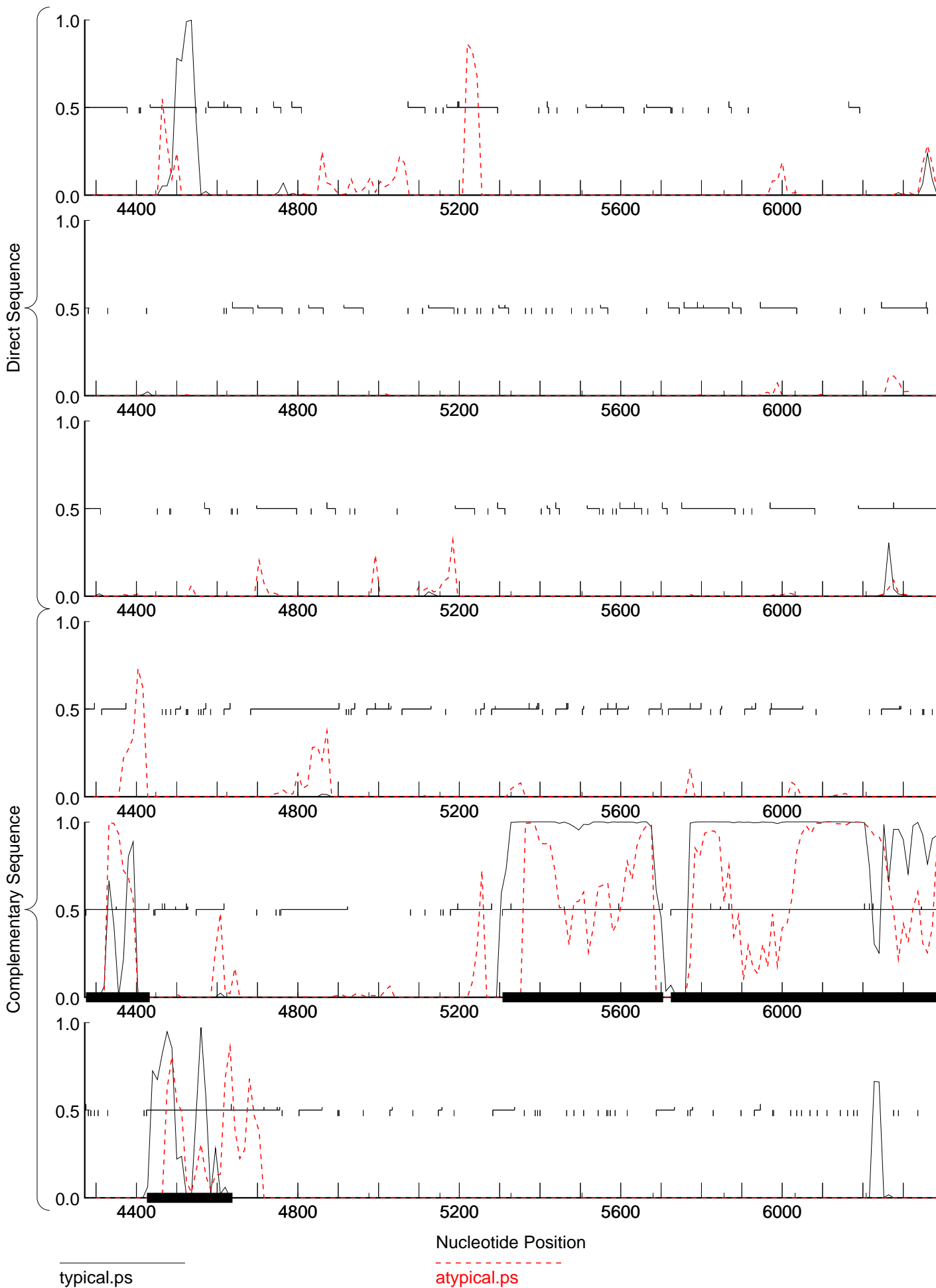
Send questions / comments to:  
Dr. M. Borodovsky  
Georgia Institute of Technology  
School of Biology  
Atlanta, GA 30332-0230

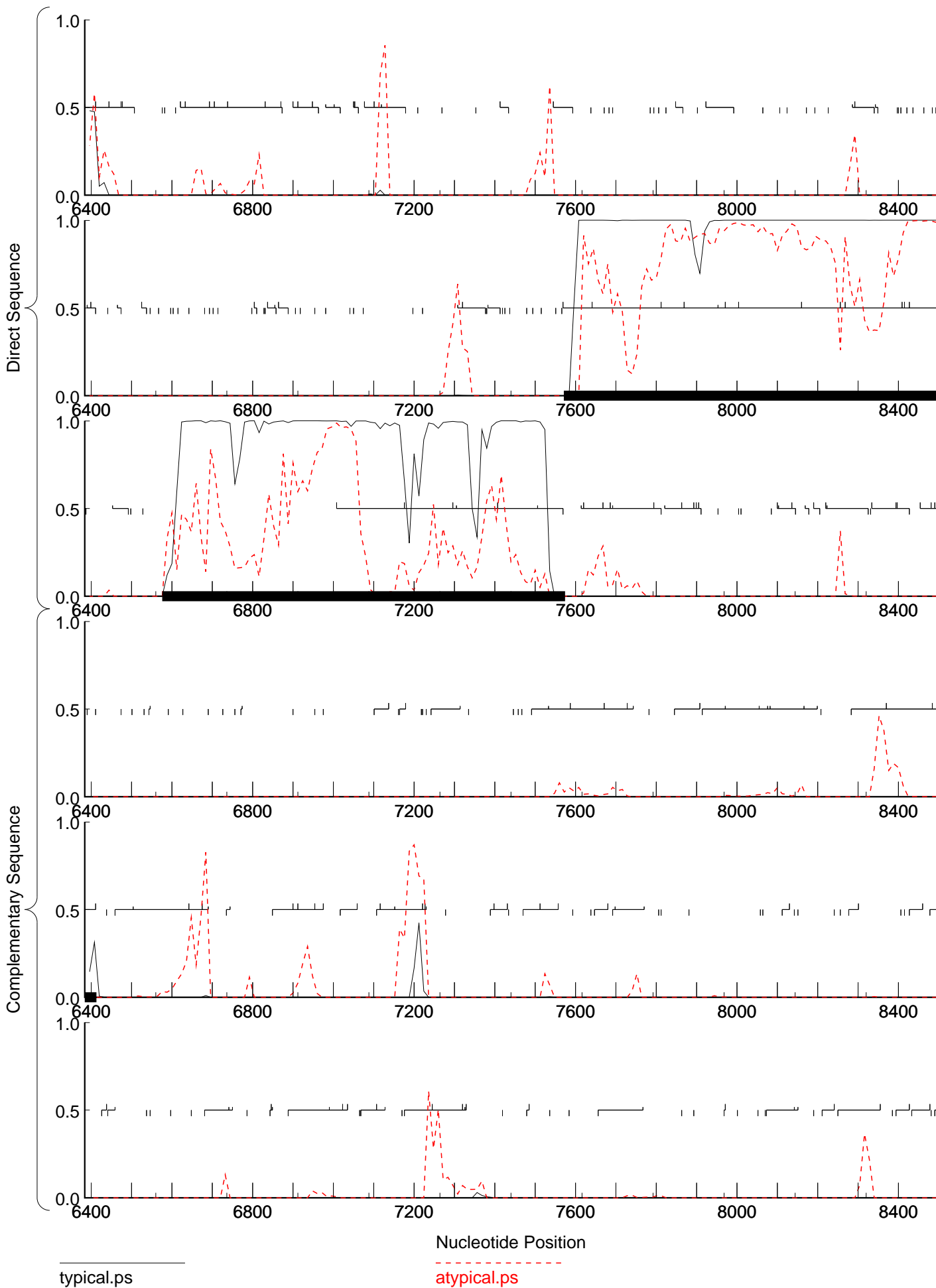
### Matrix notes & comments

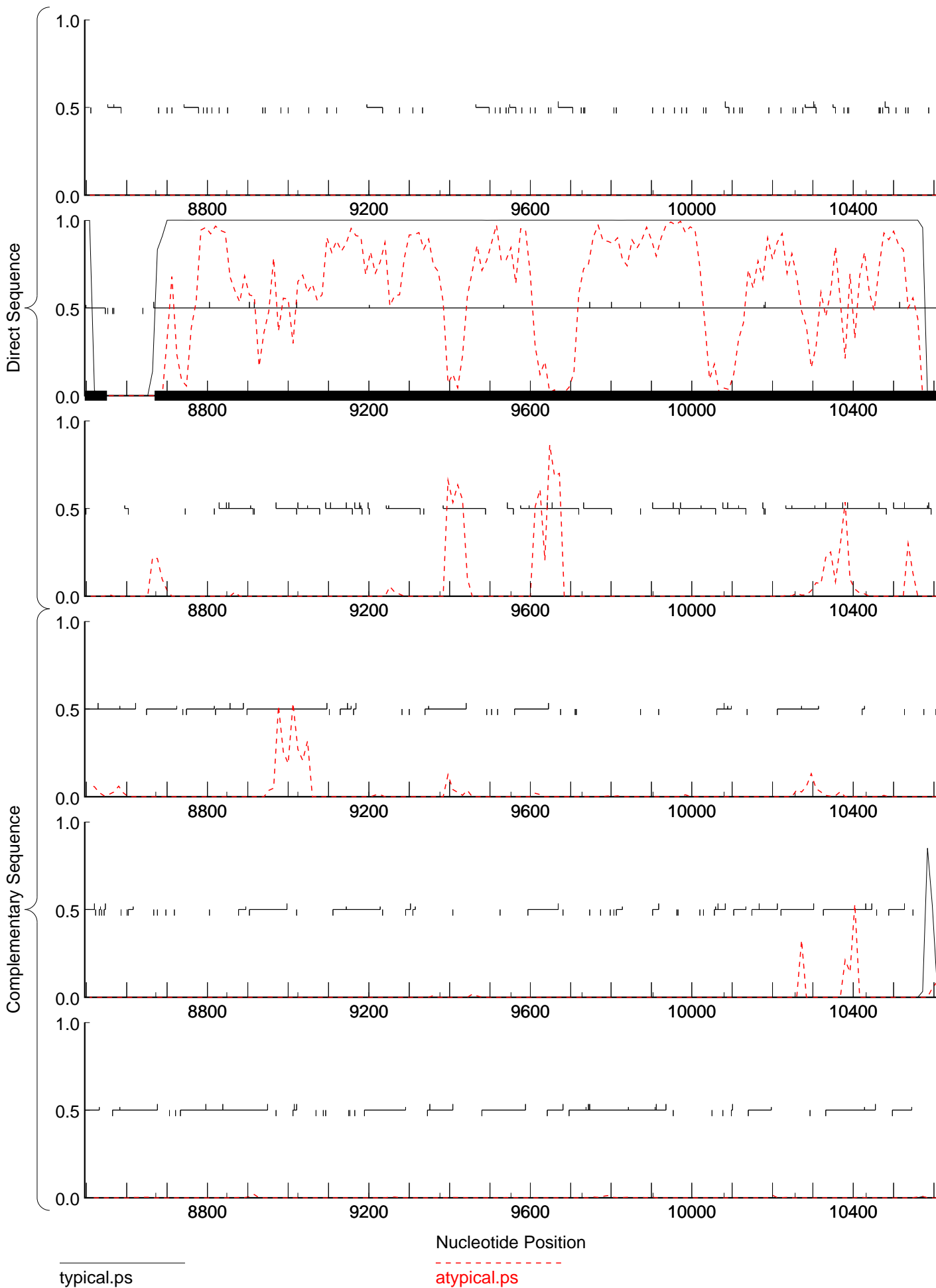
Training set derived by GeneMarkS, 4.30 October 2014  
Tue Jul 17 21:23:01 2018

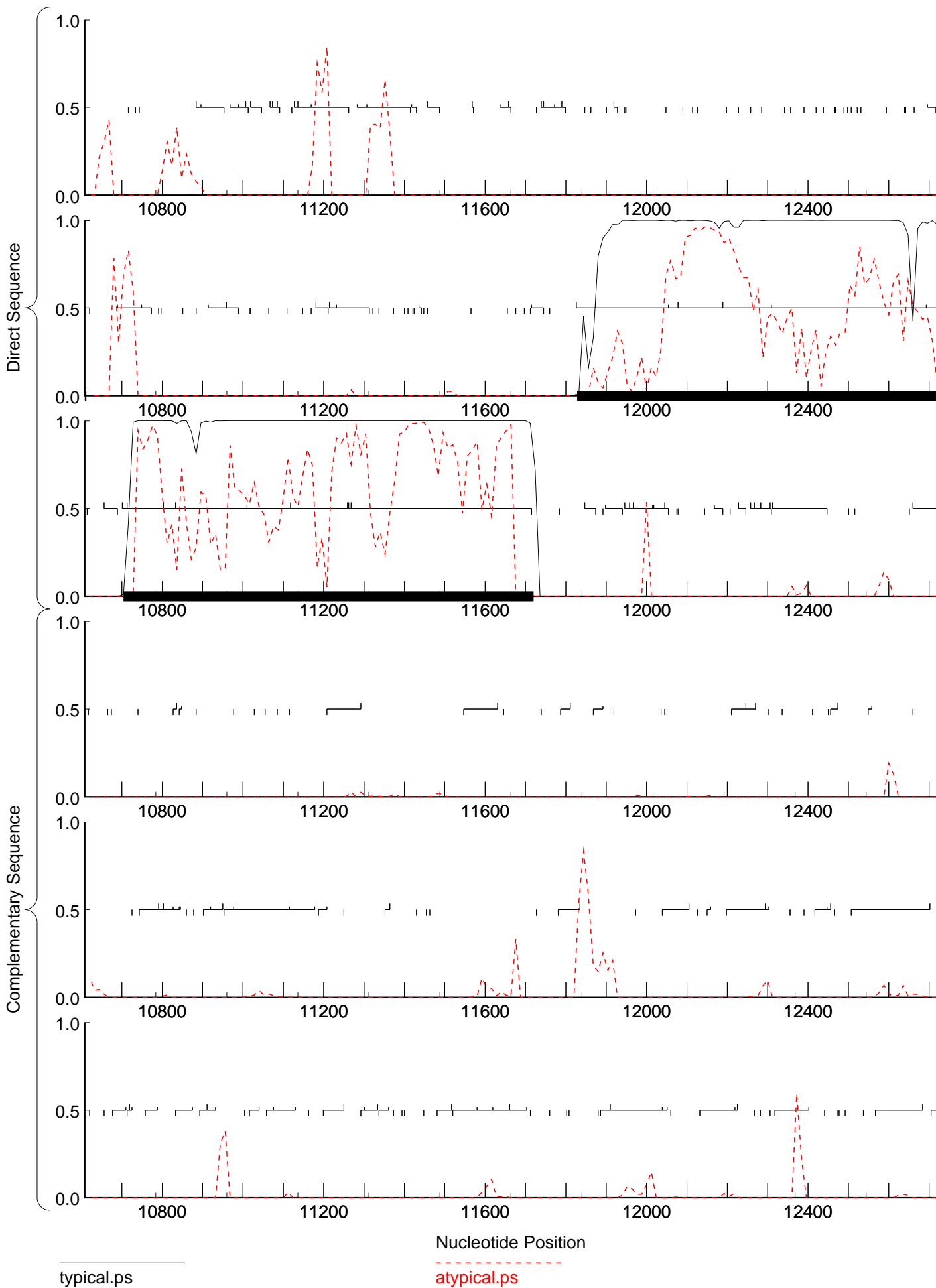






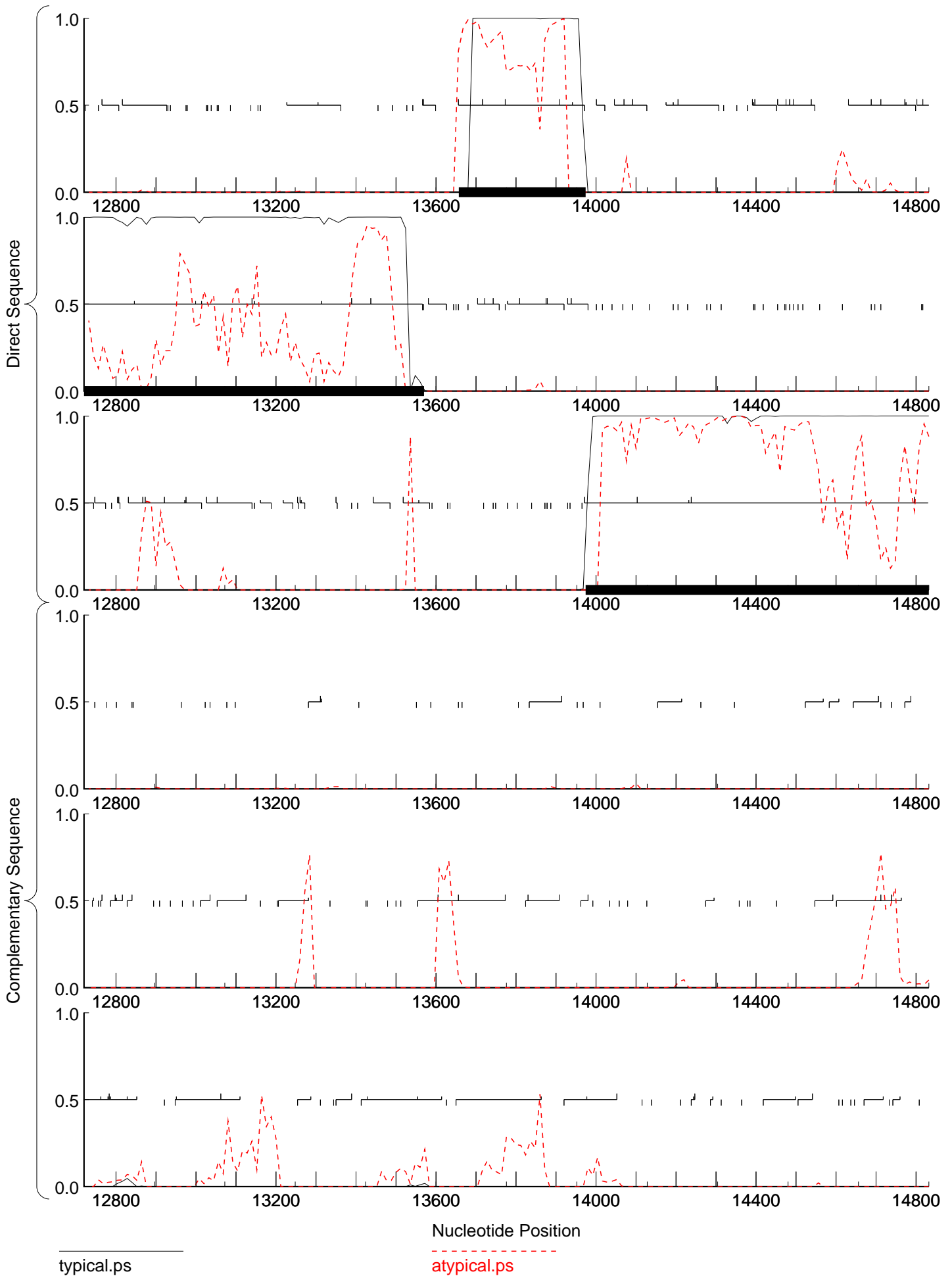




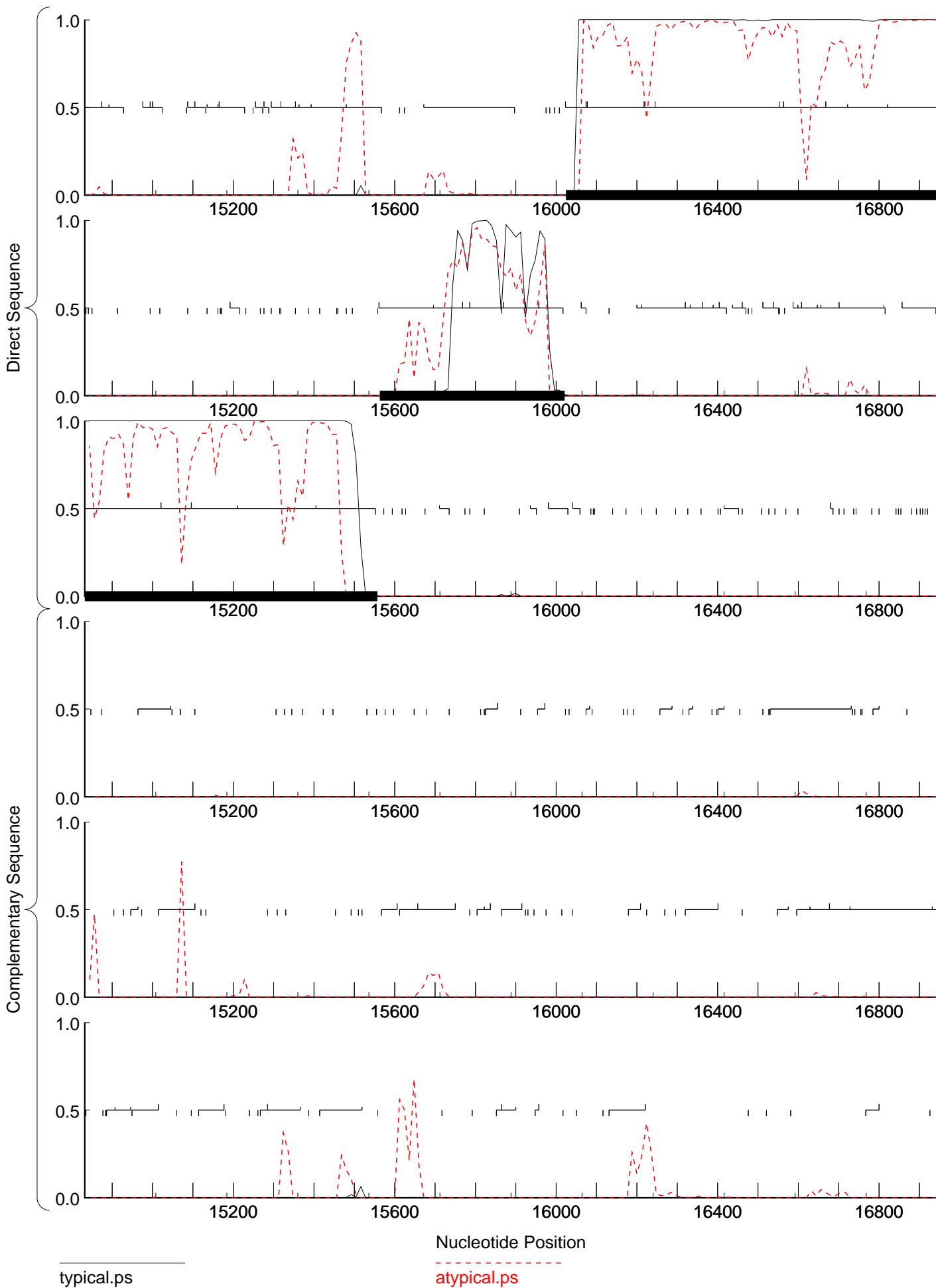


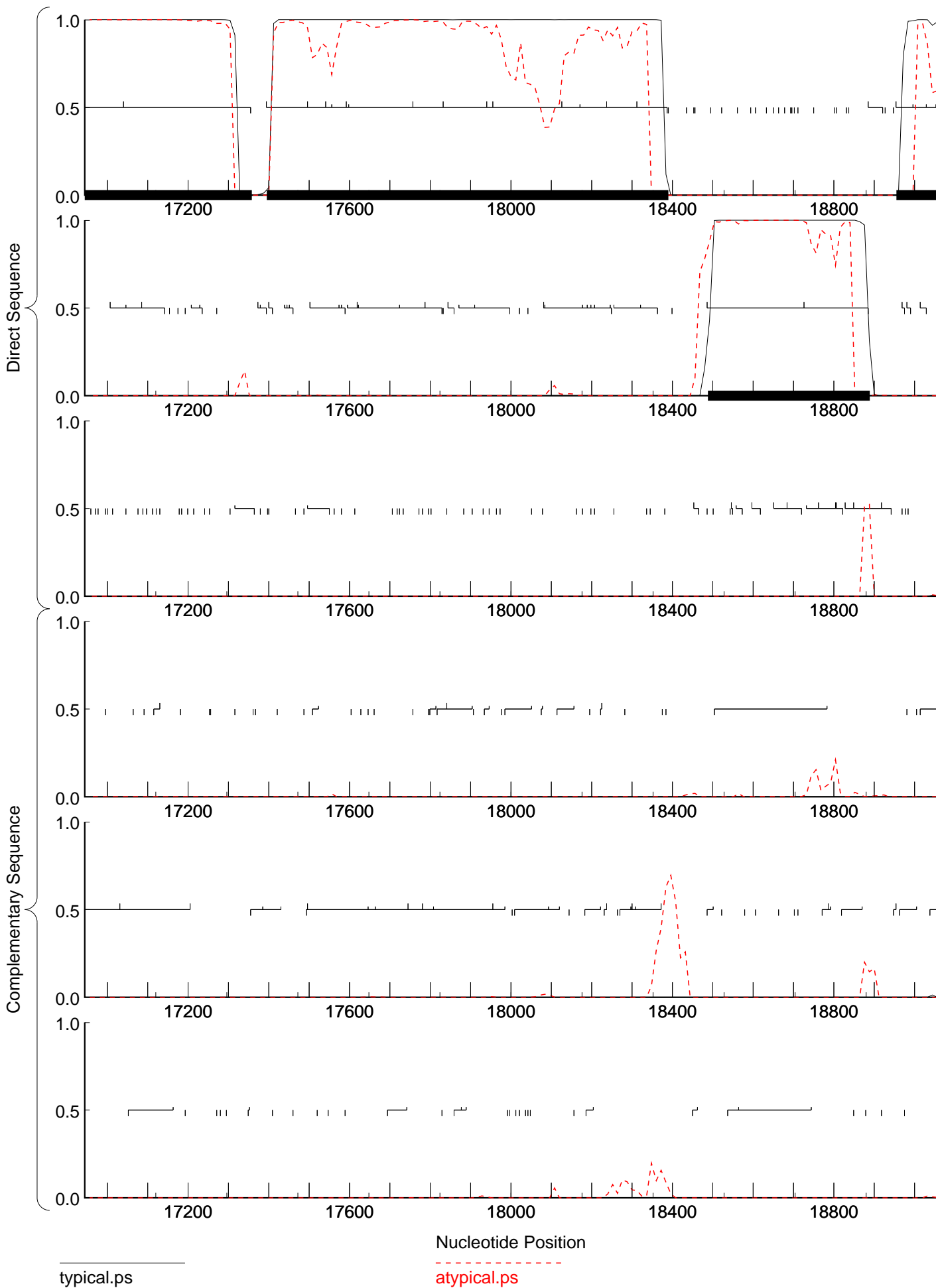
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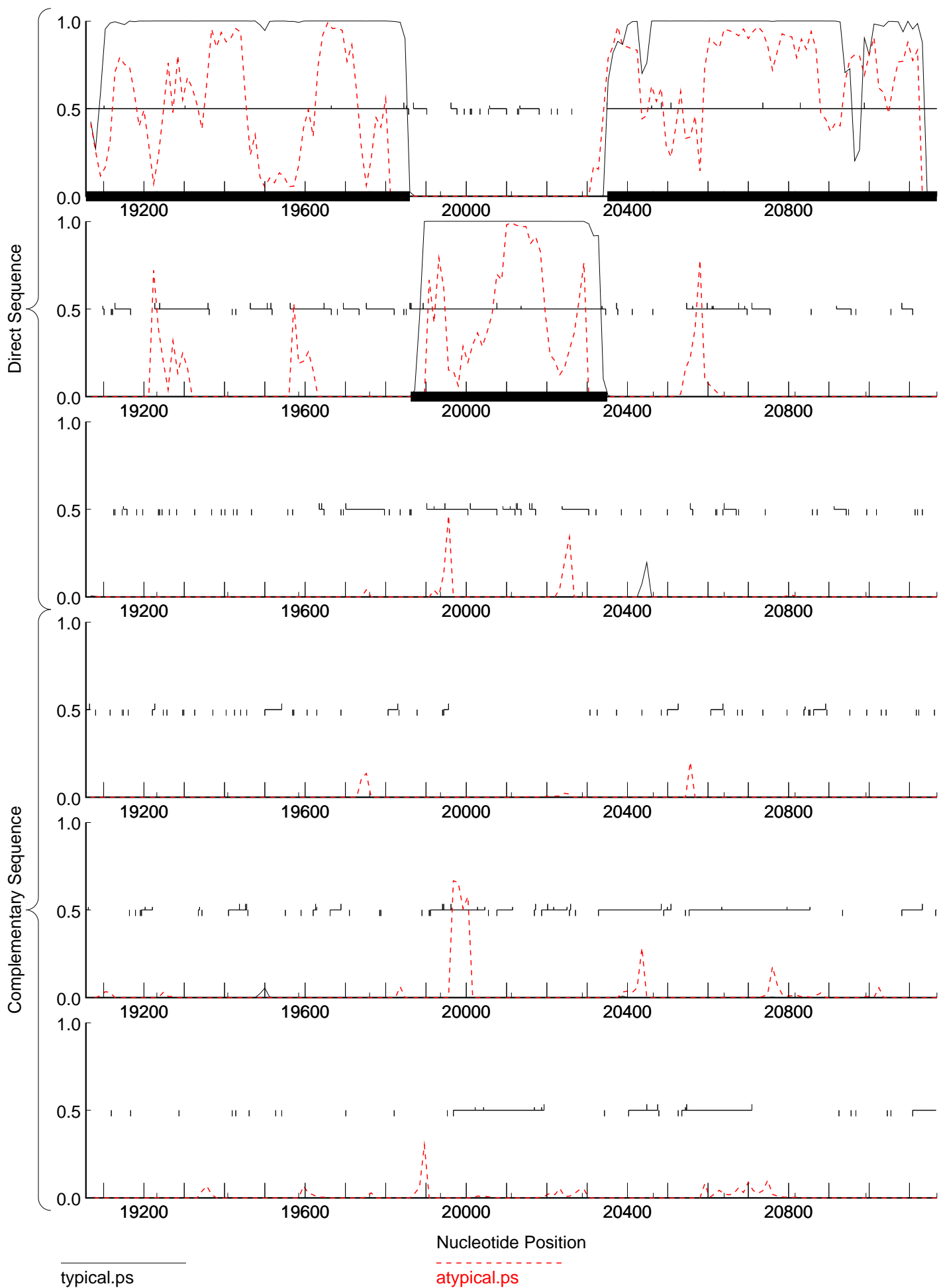
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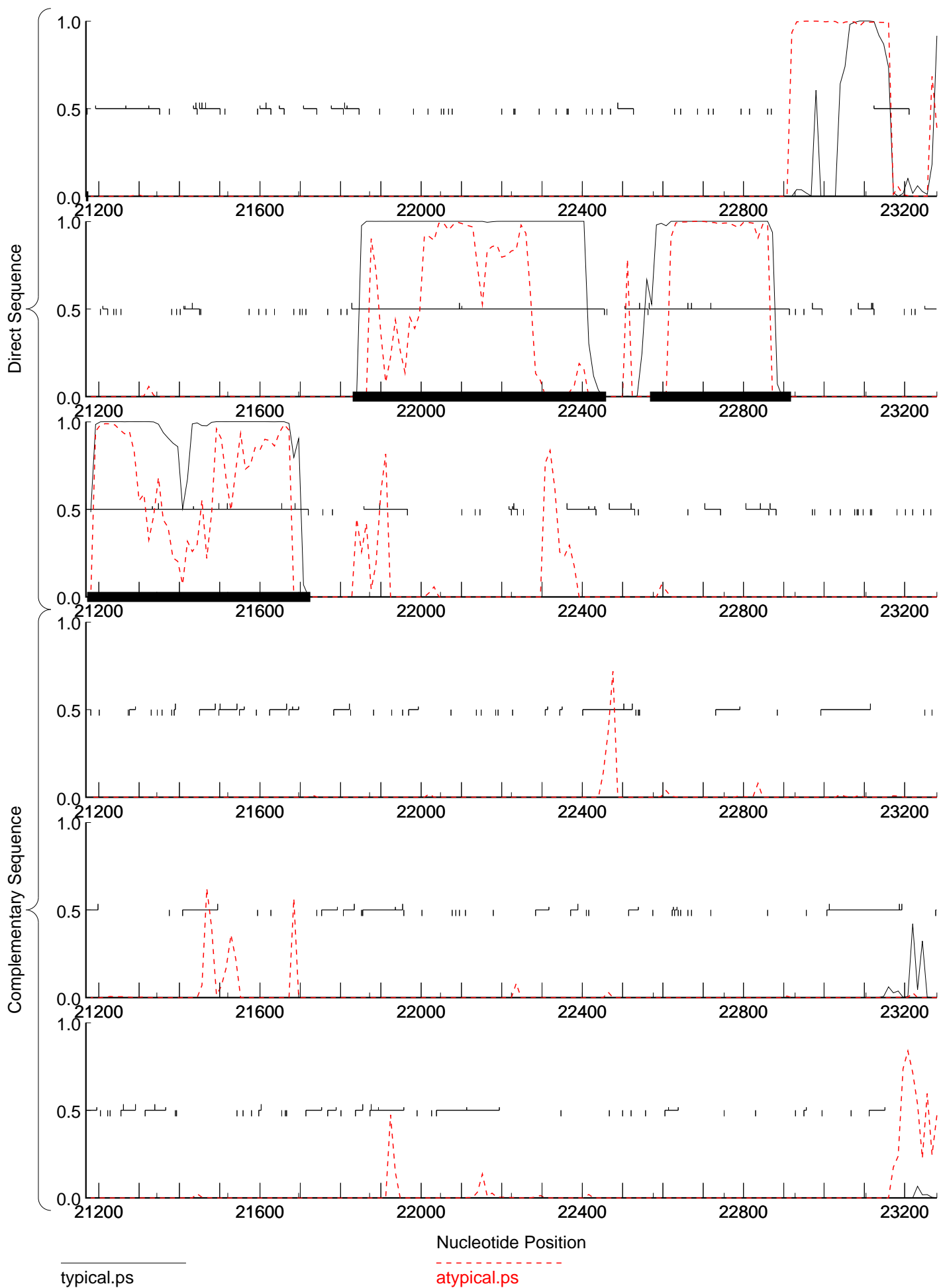






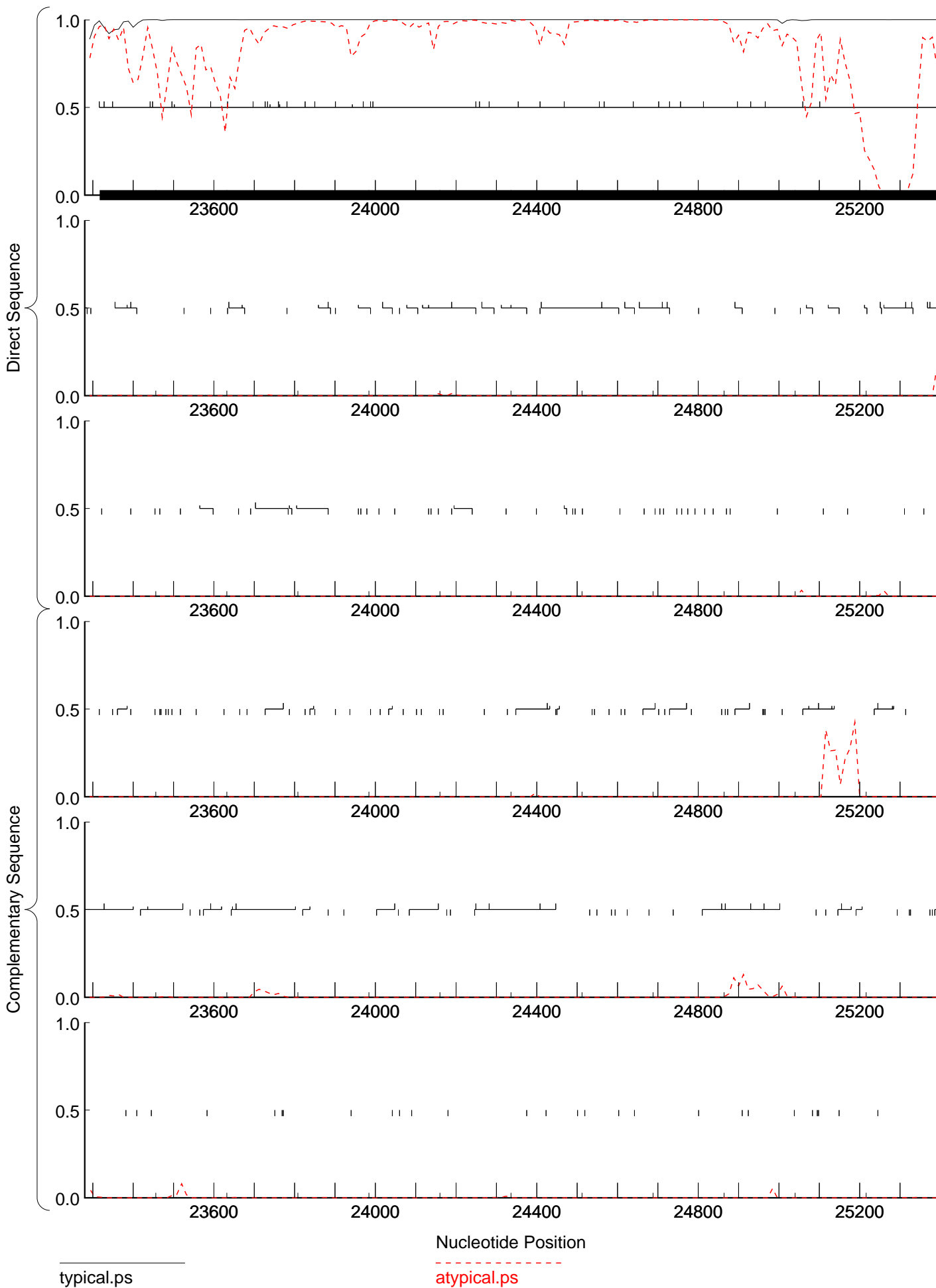
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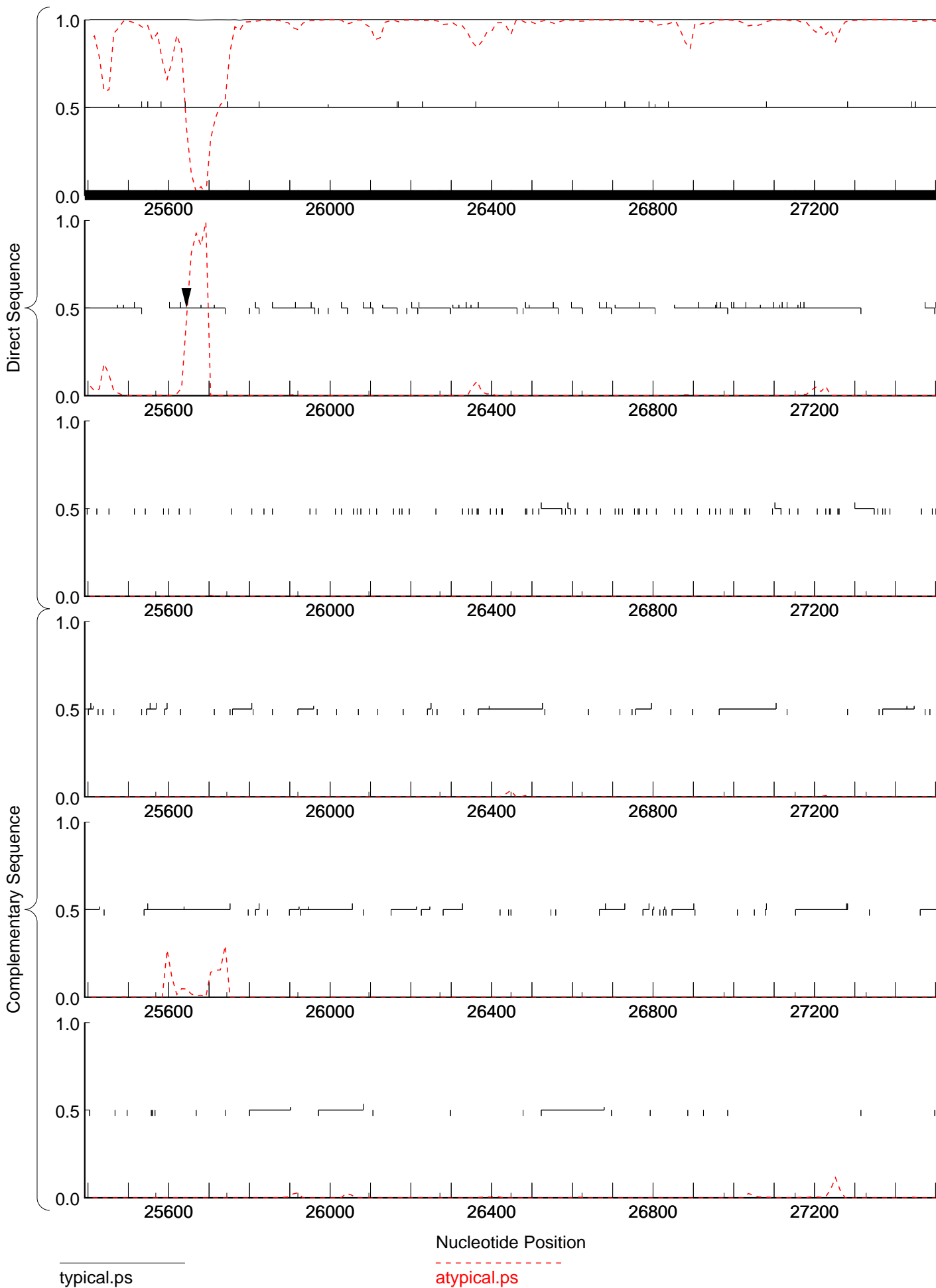
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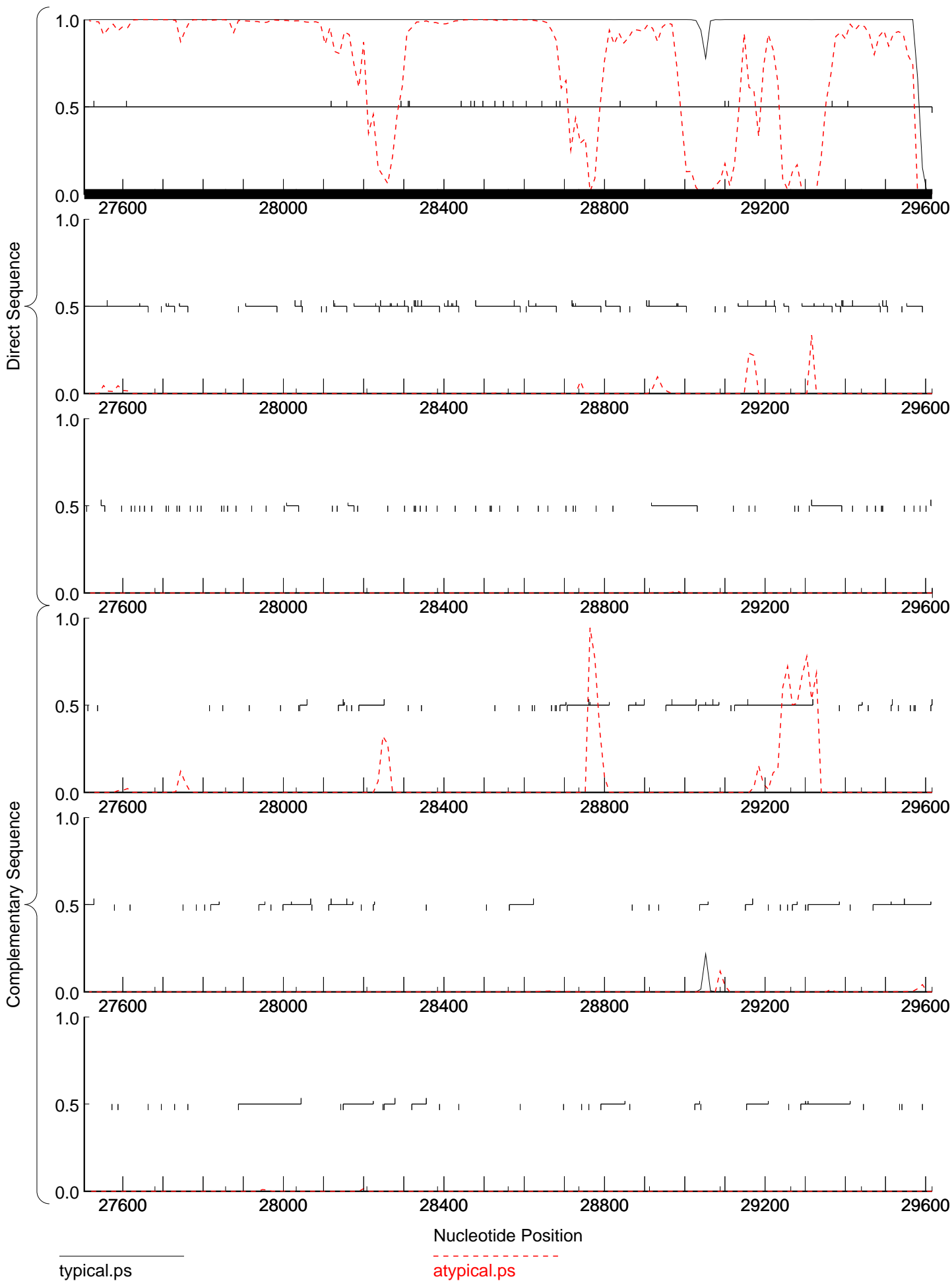


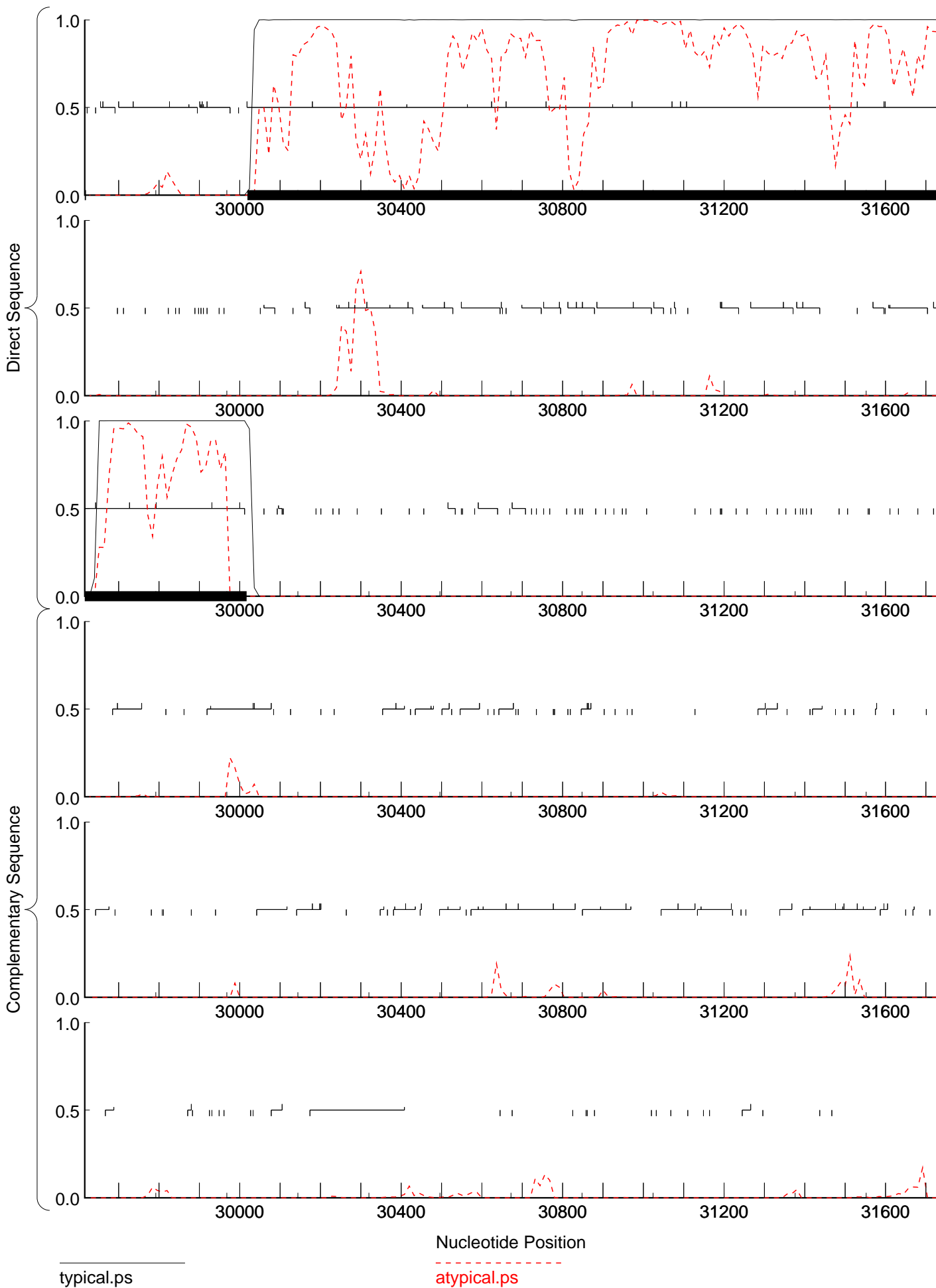
typical.ps

atypical.ps

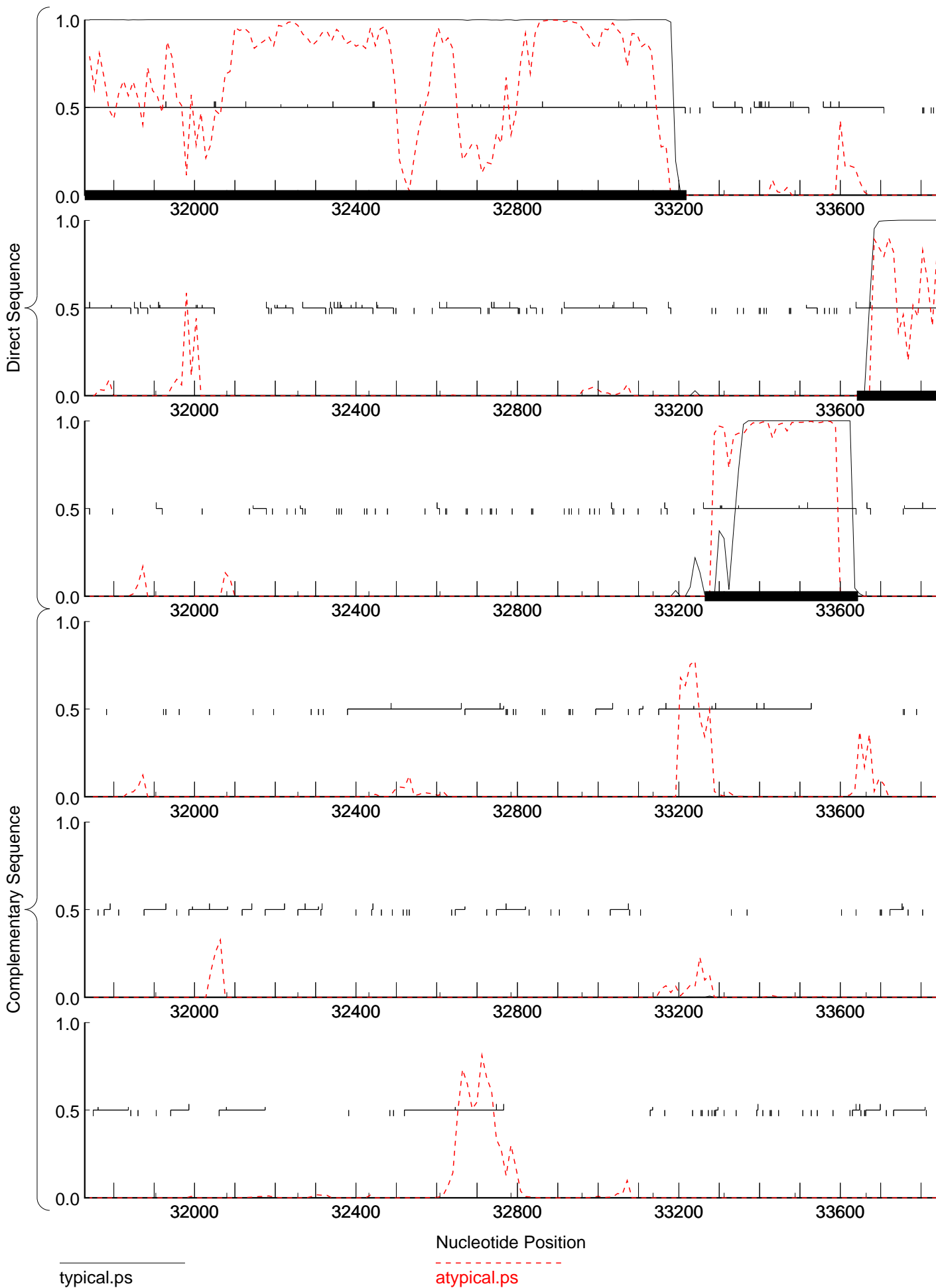


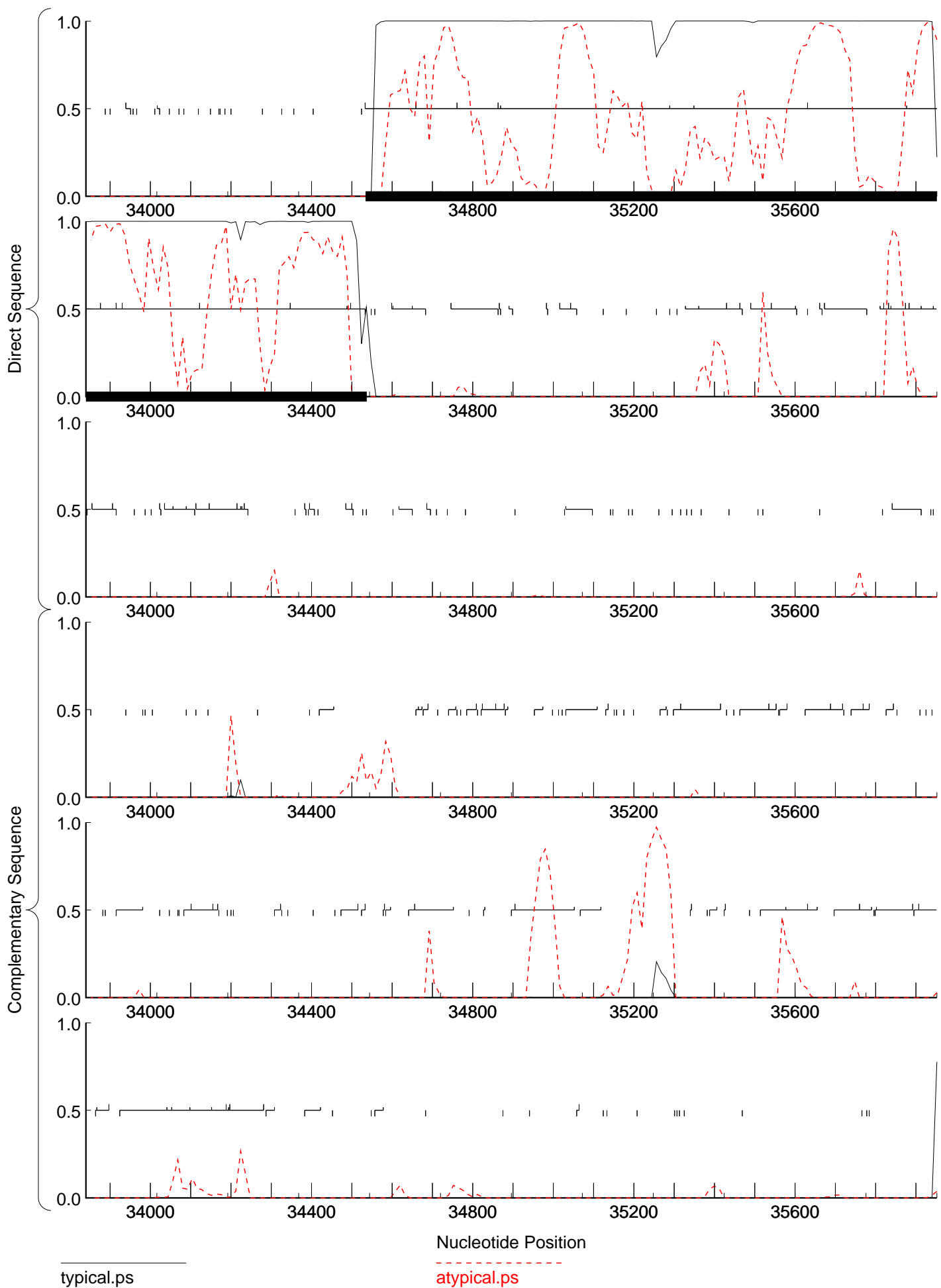


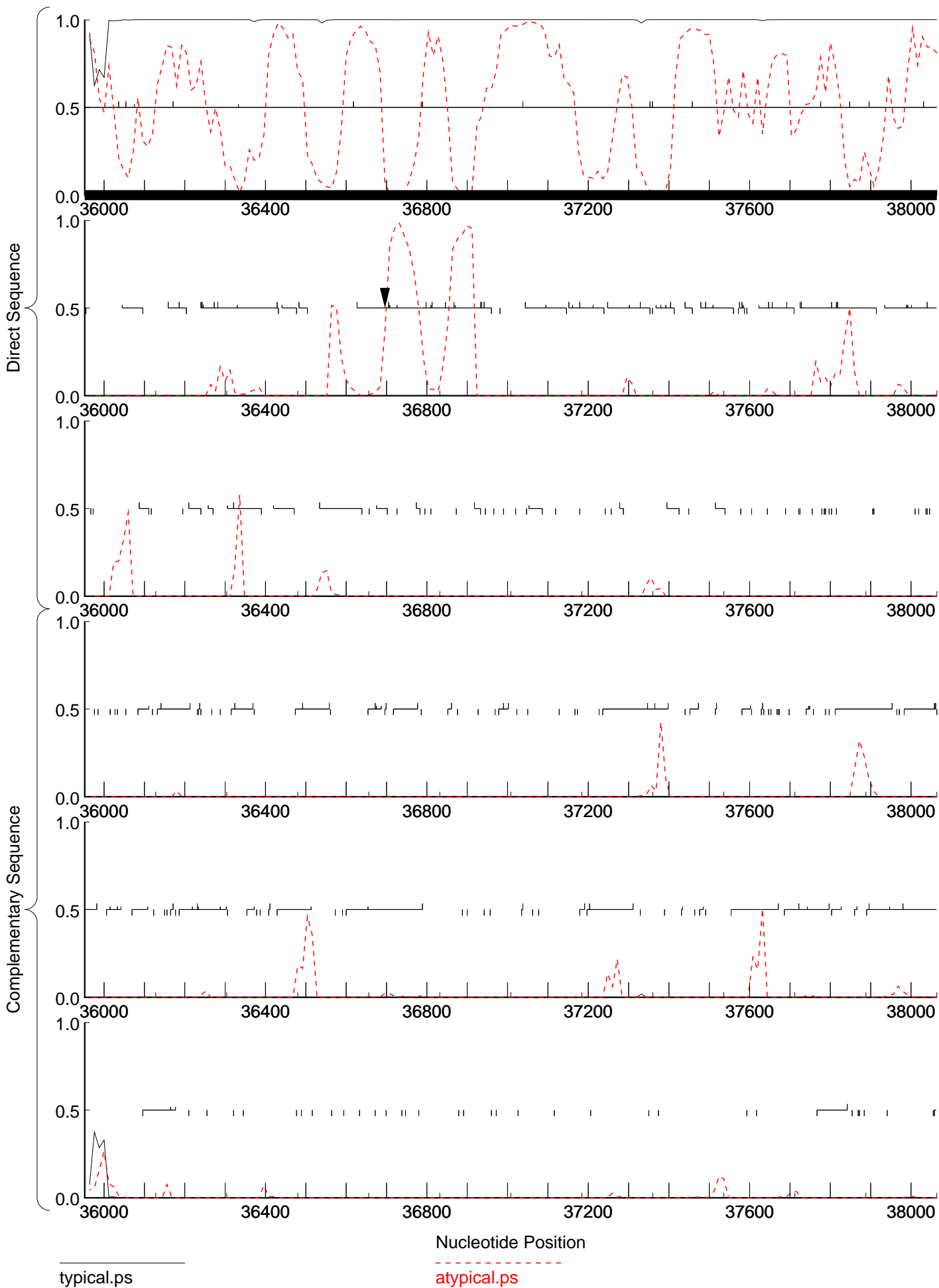






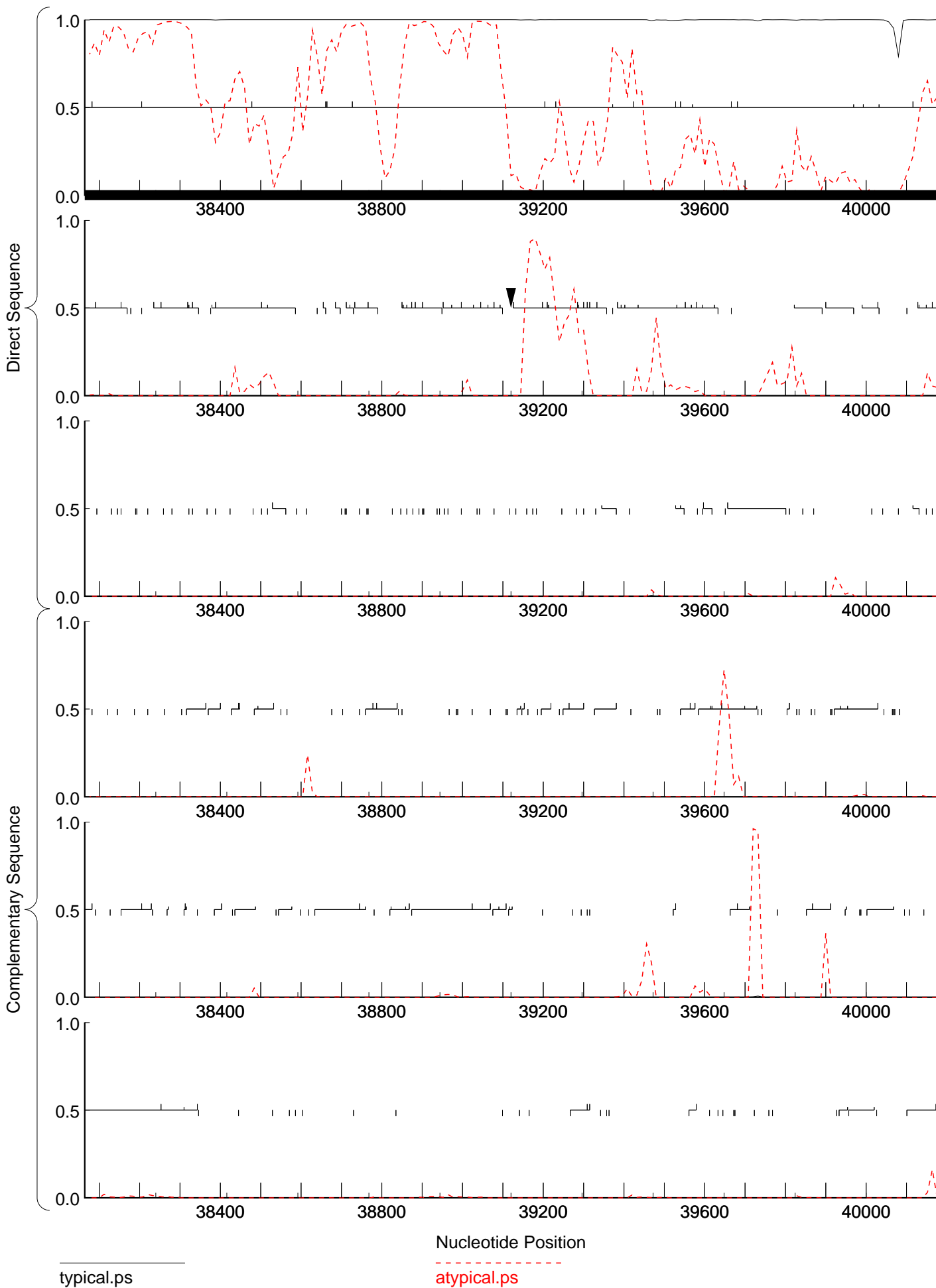






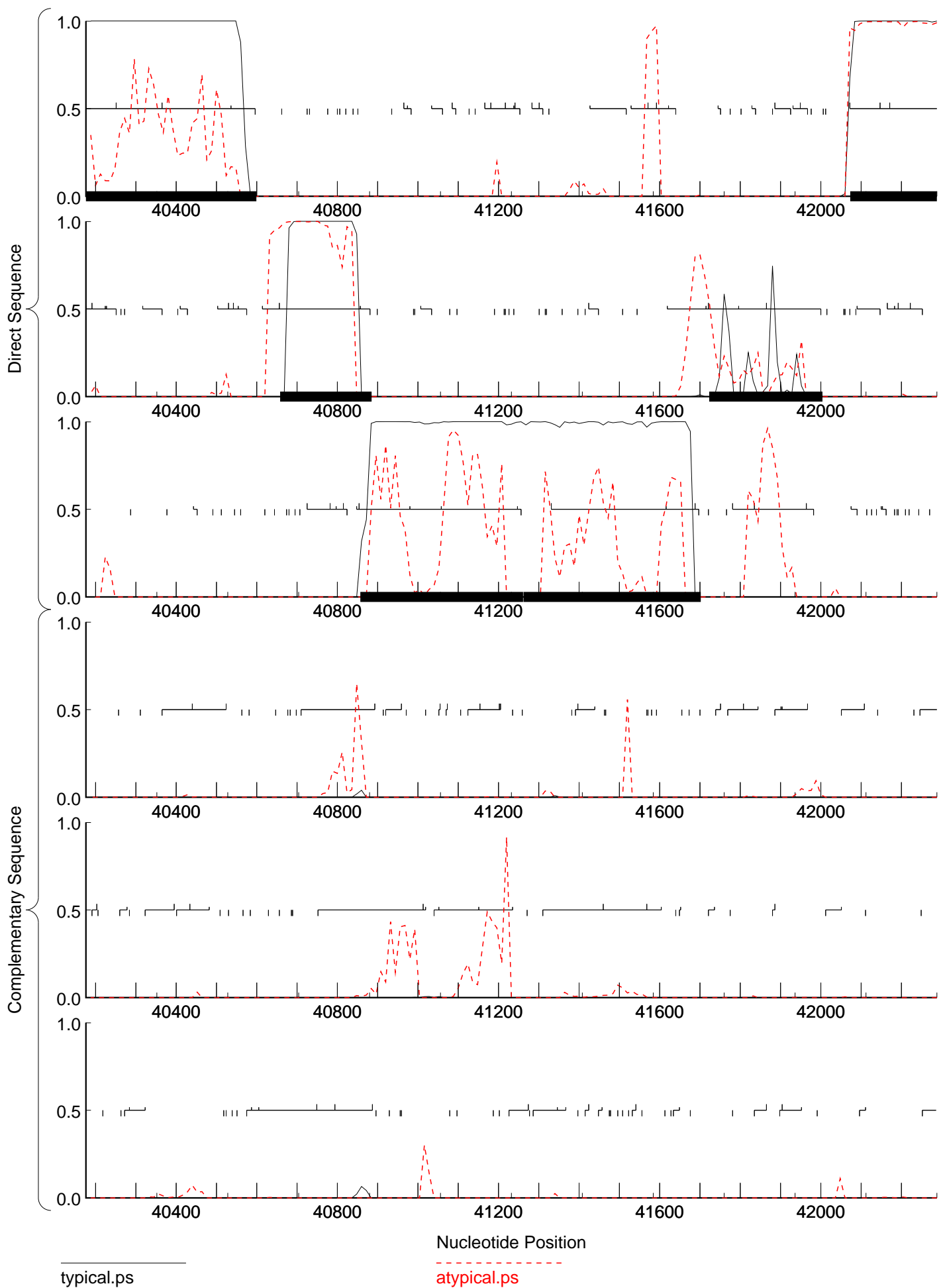
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atypical.ps



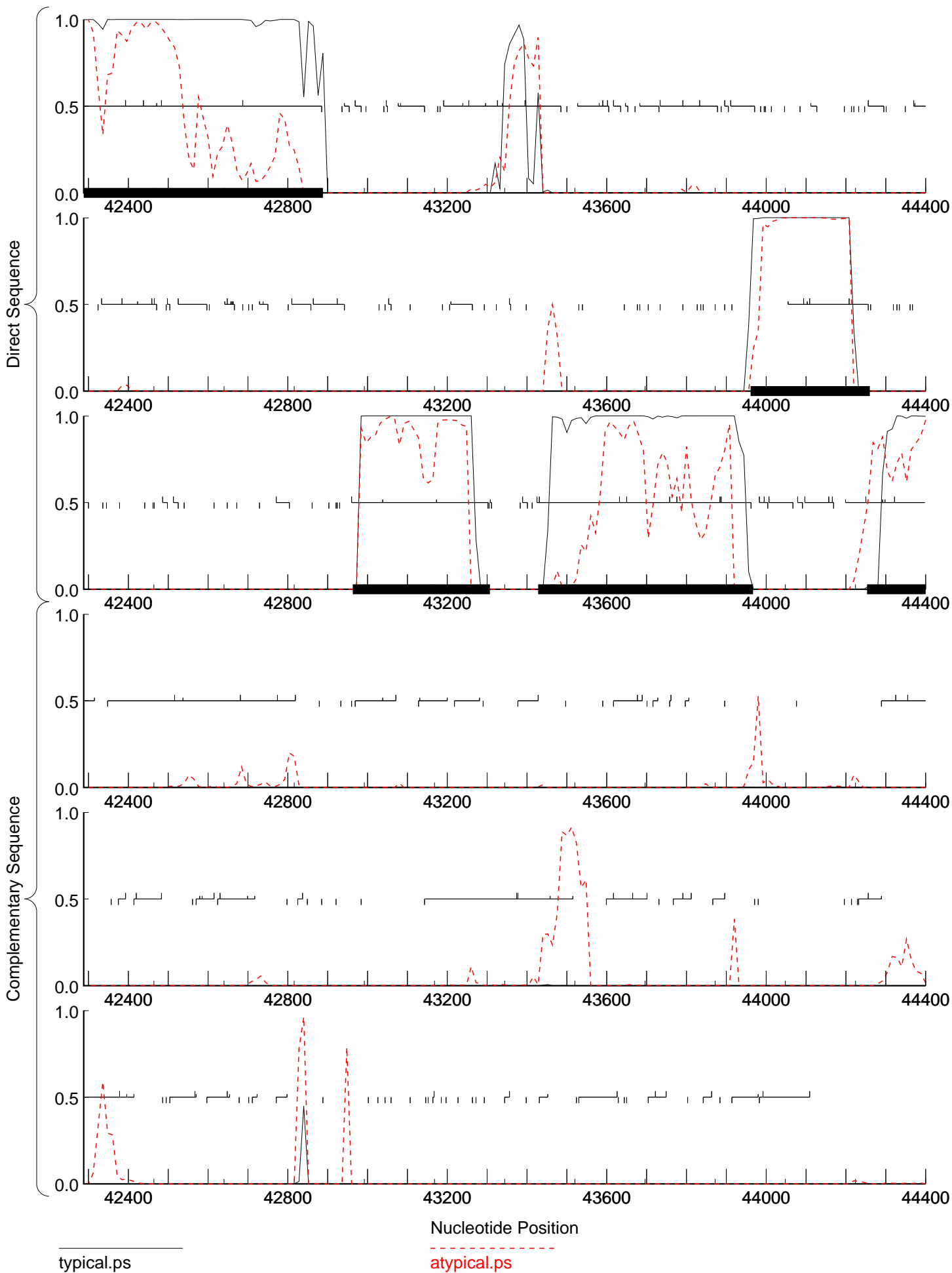
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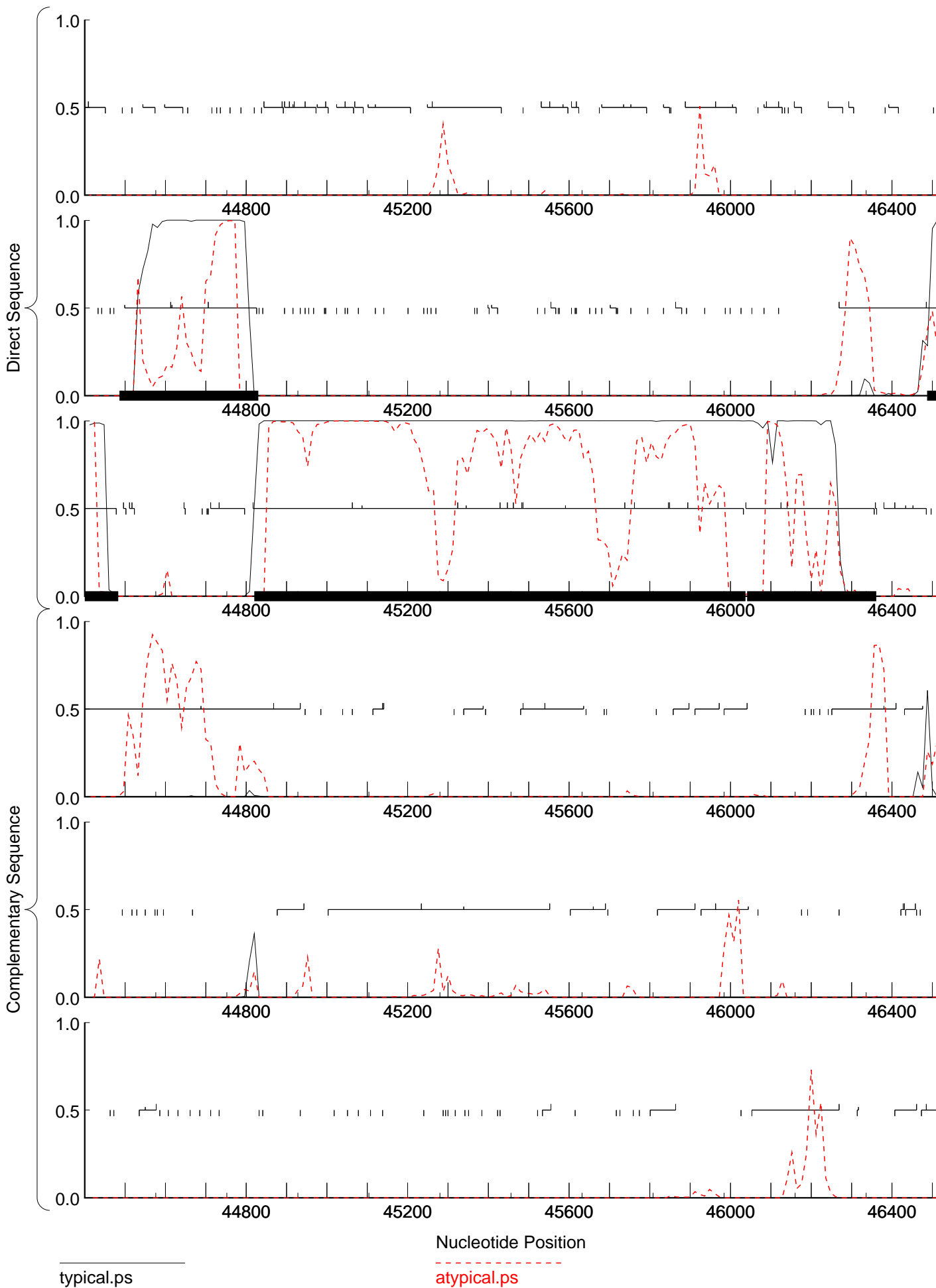
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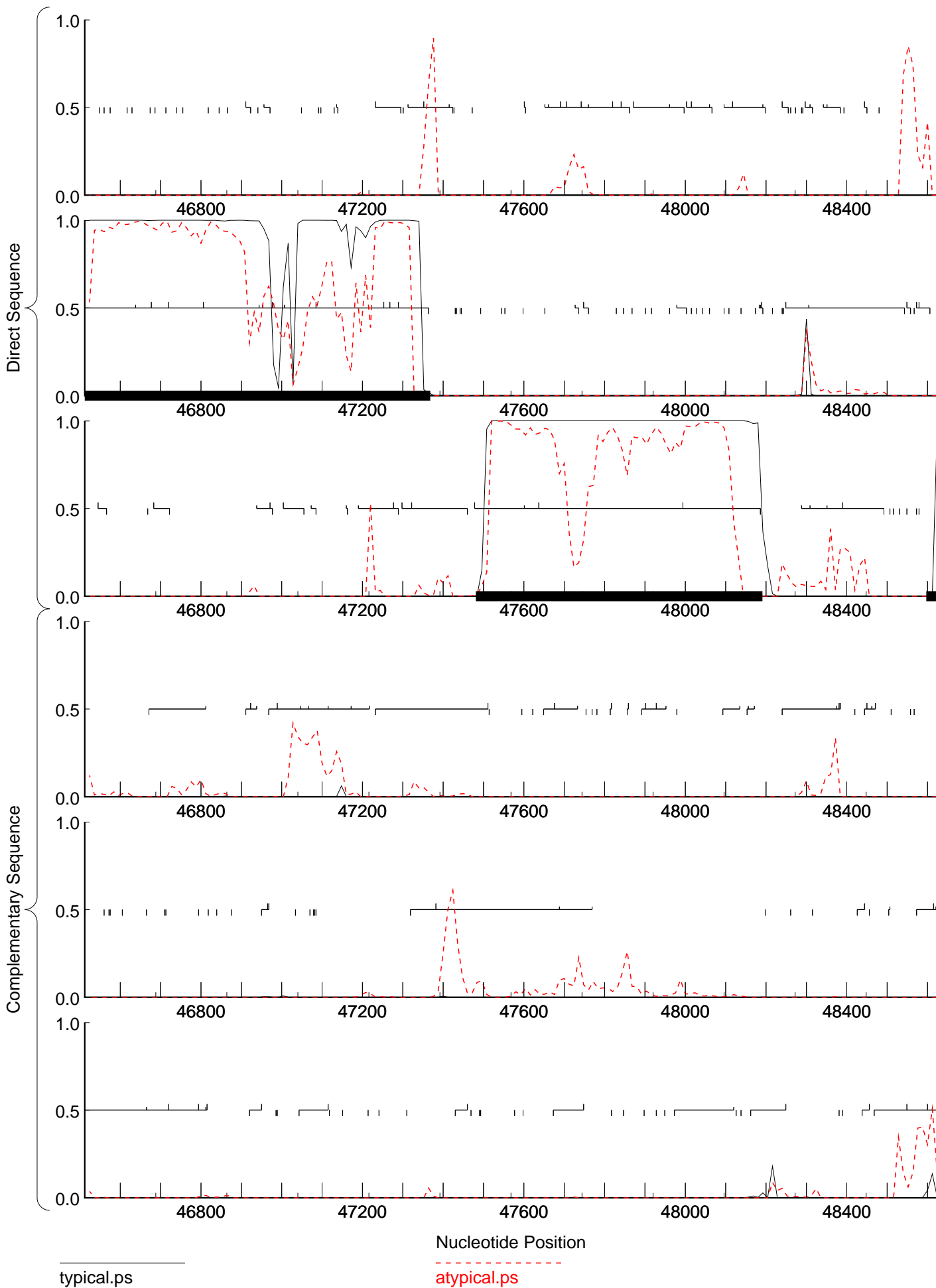


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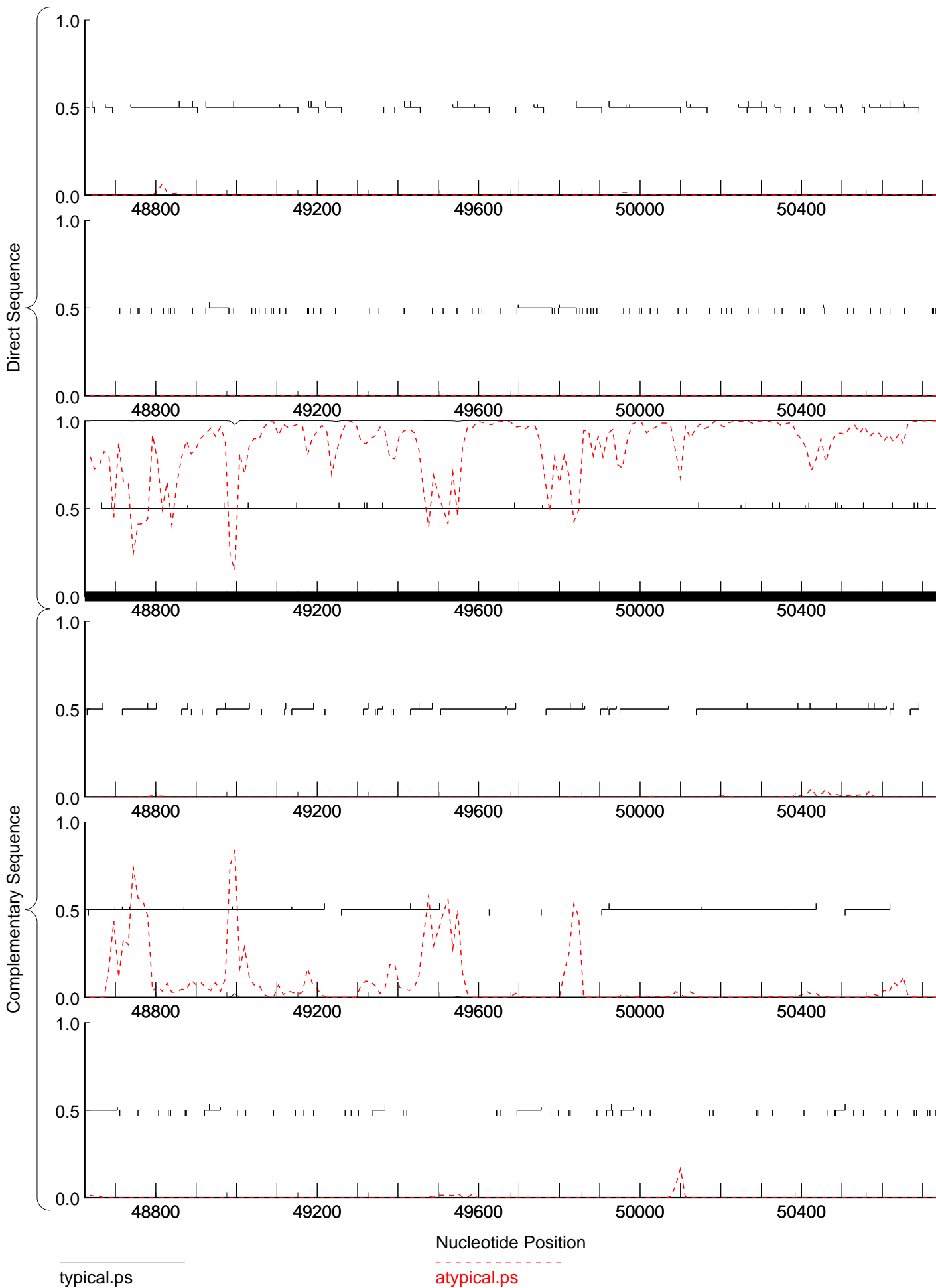
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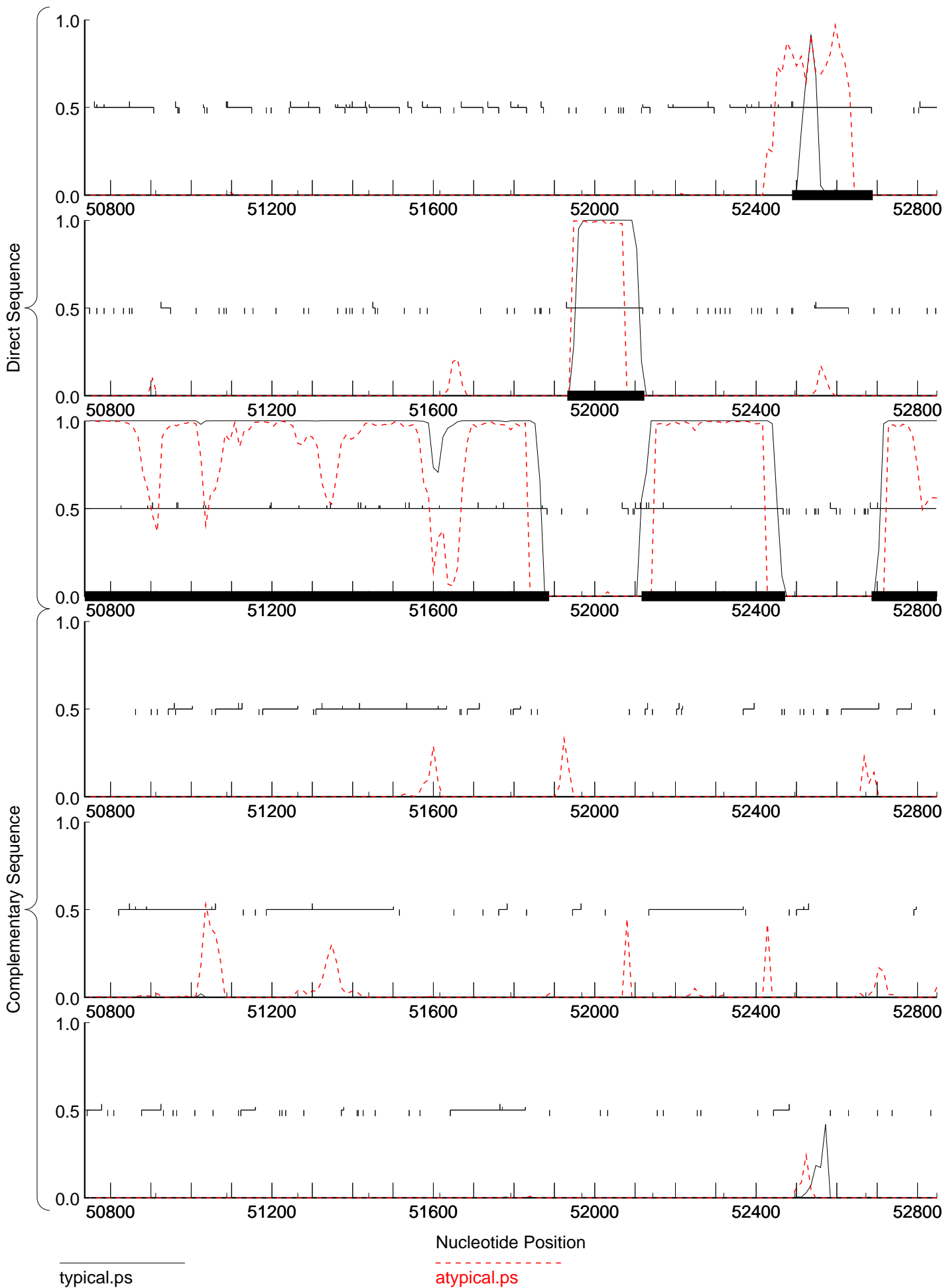


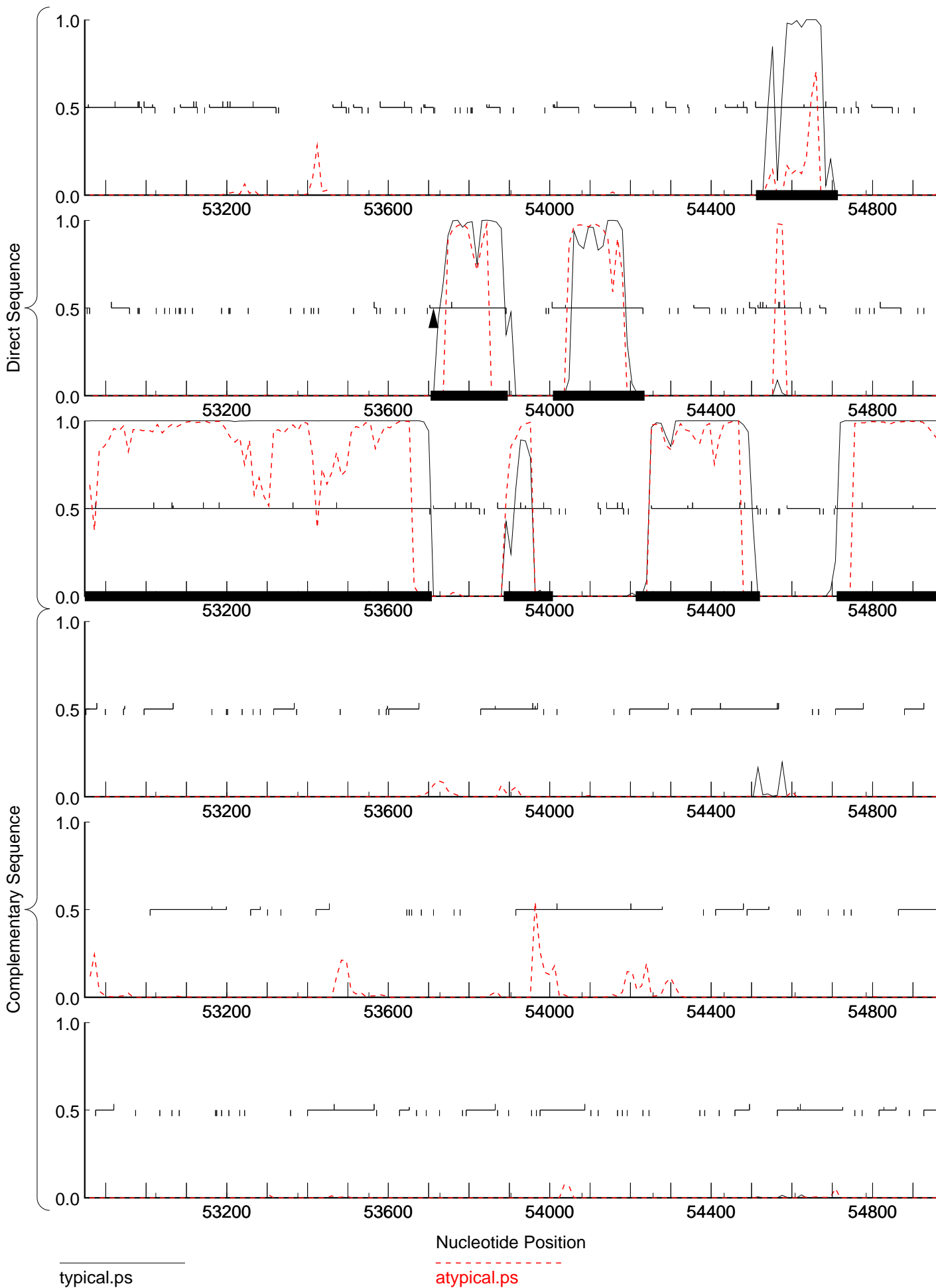


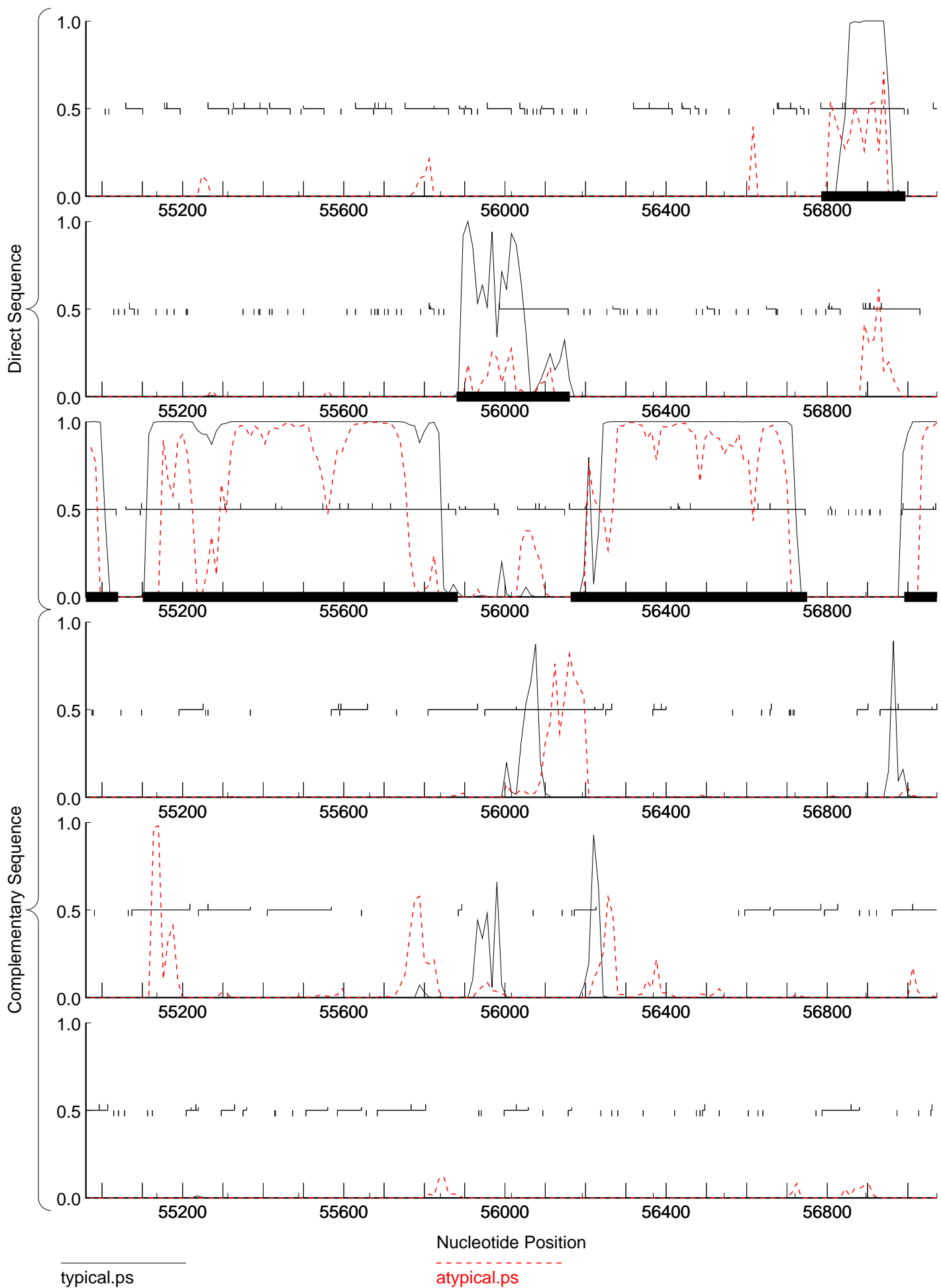


typical.ps

atypical.ps

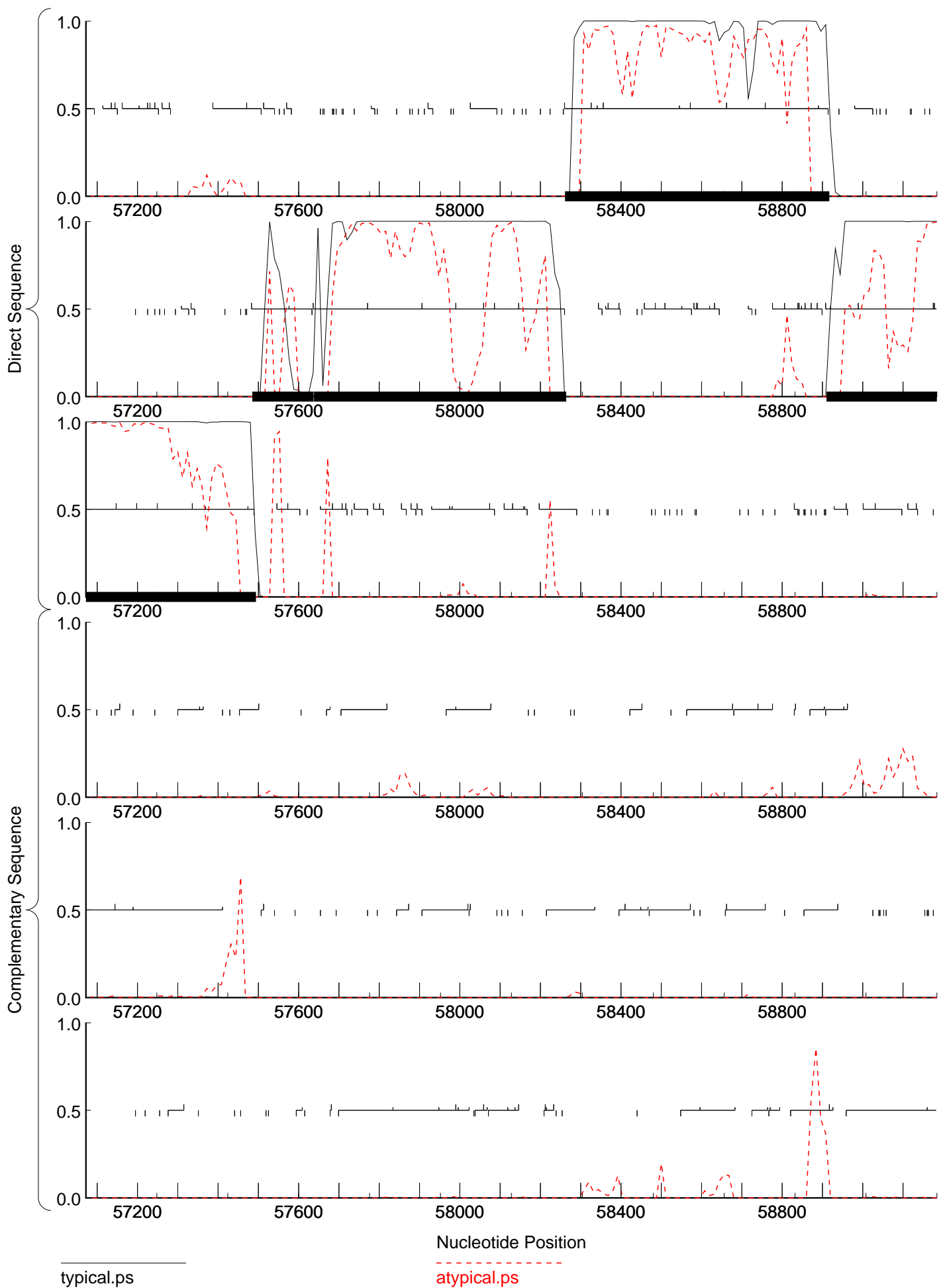






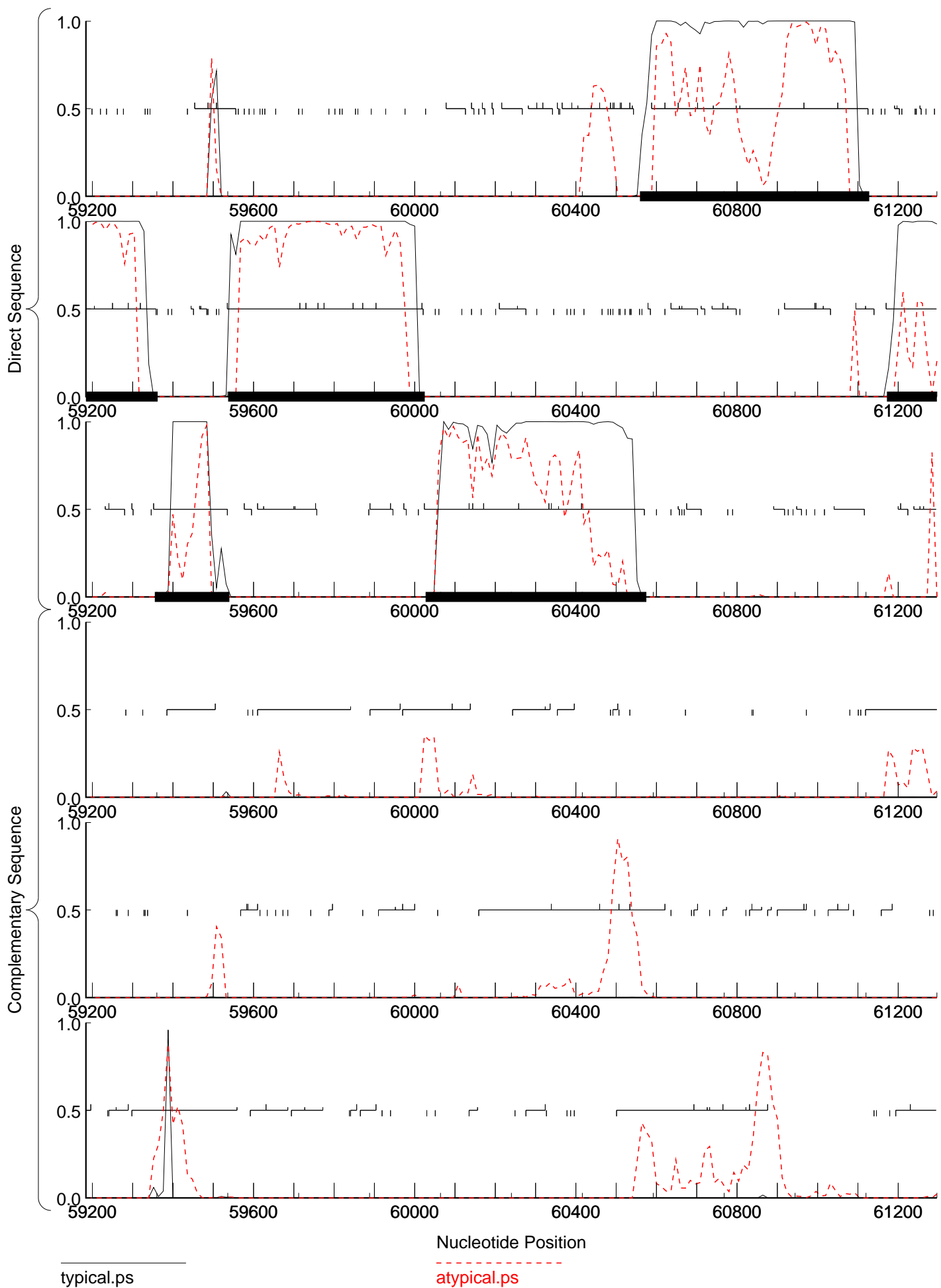
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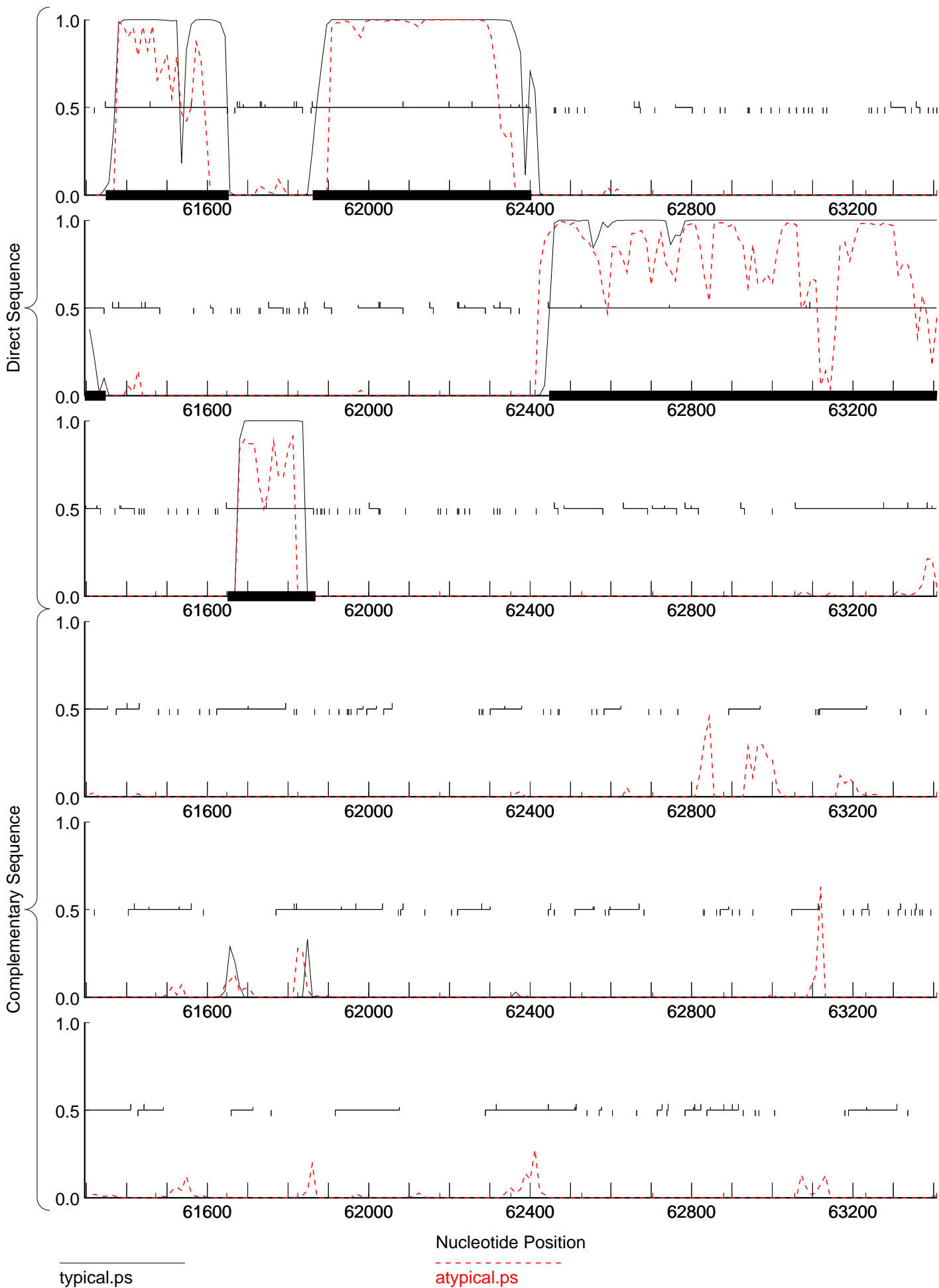
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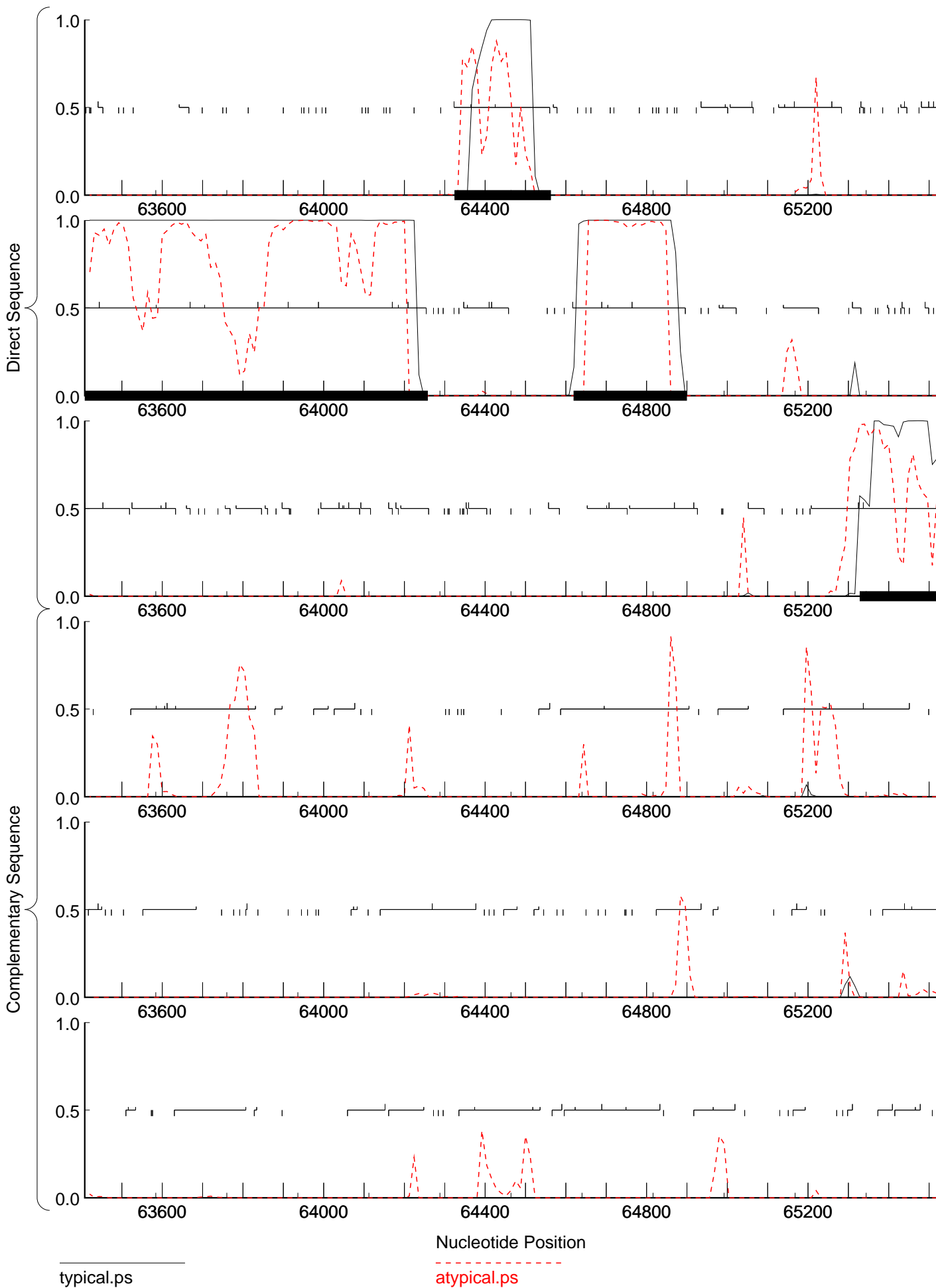


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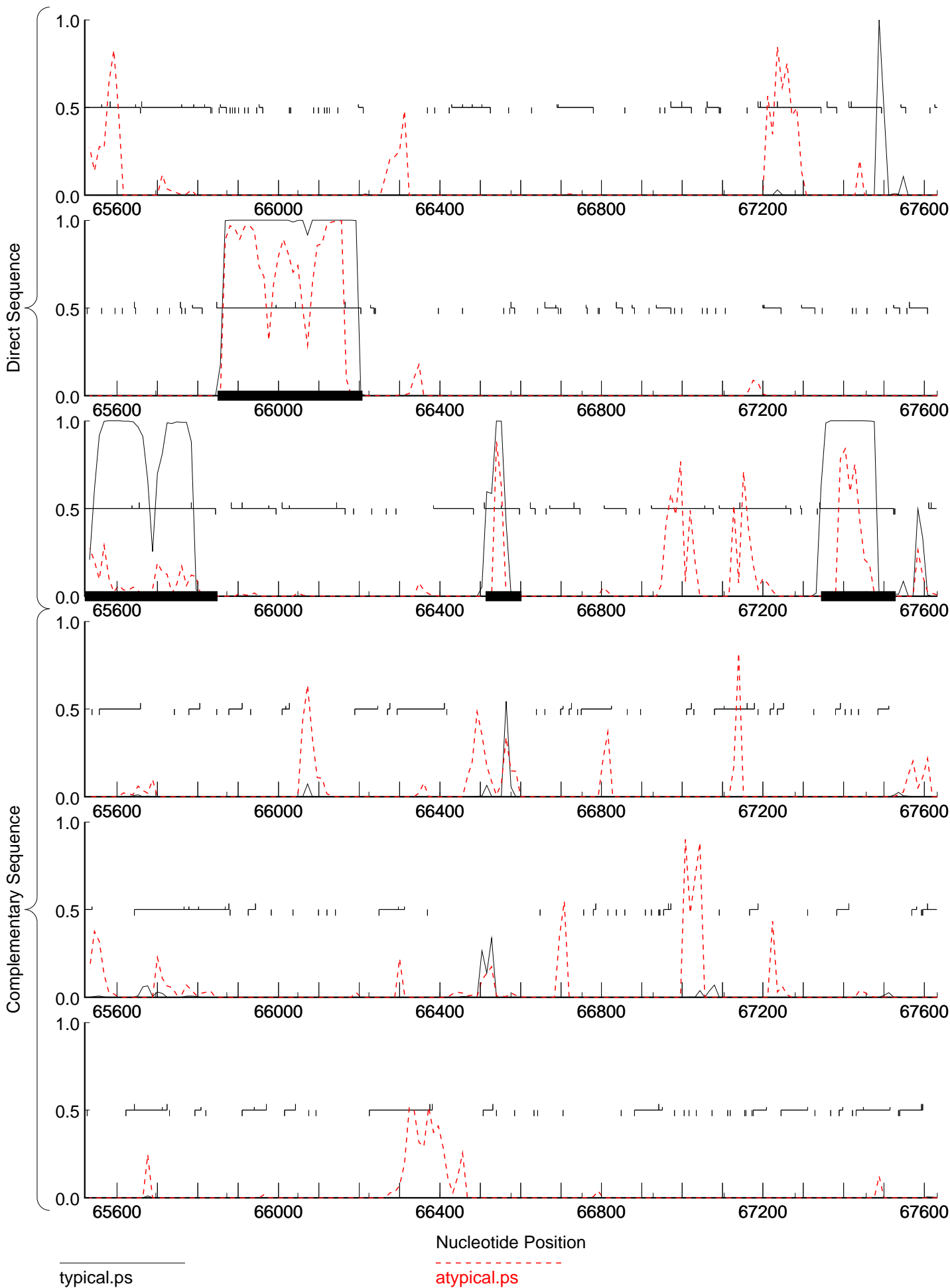
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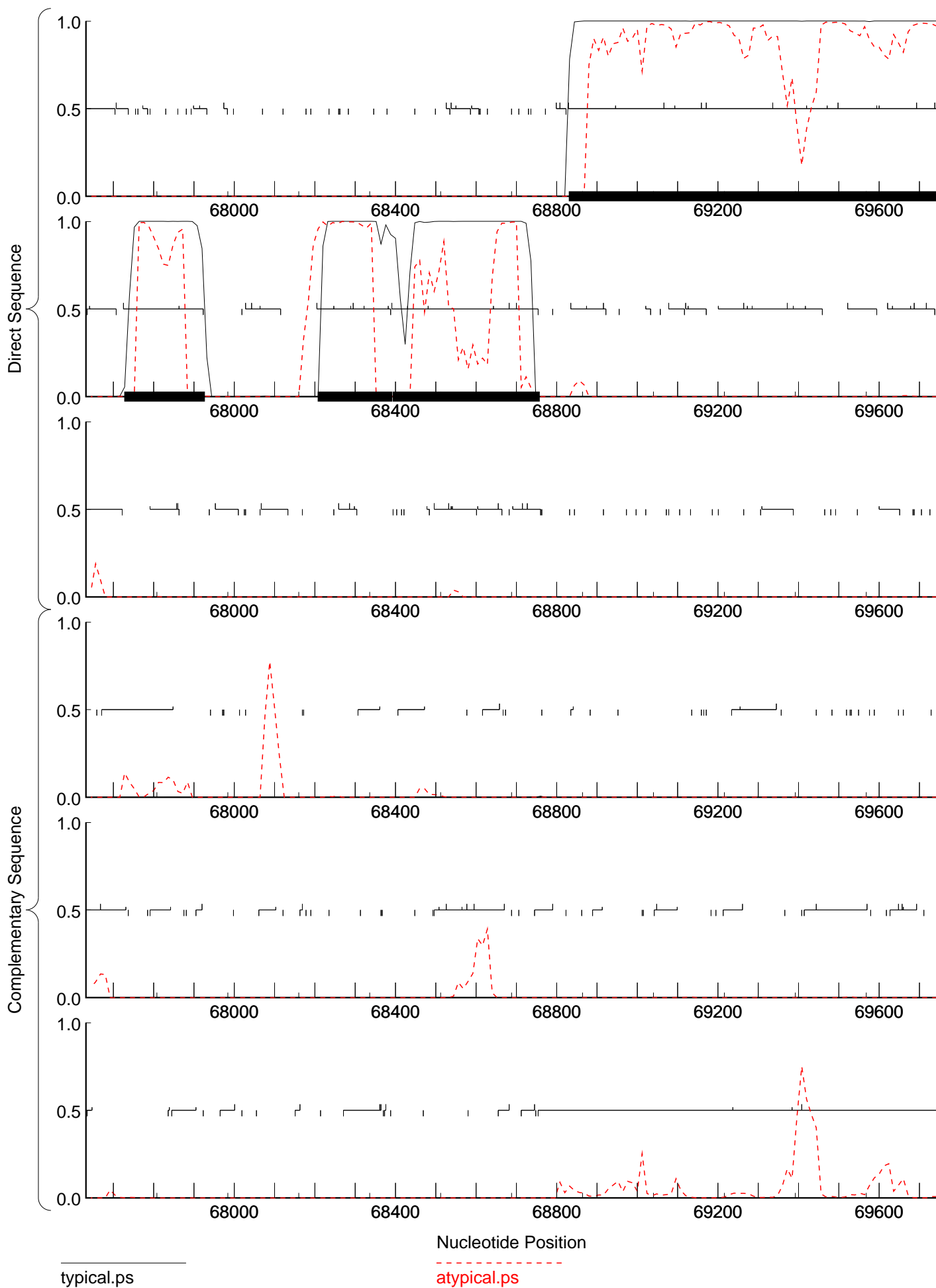


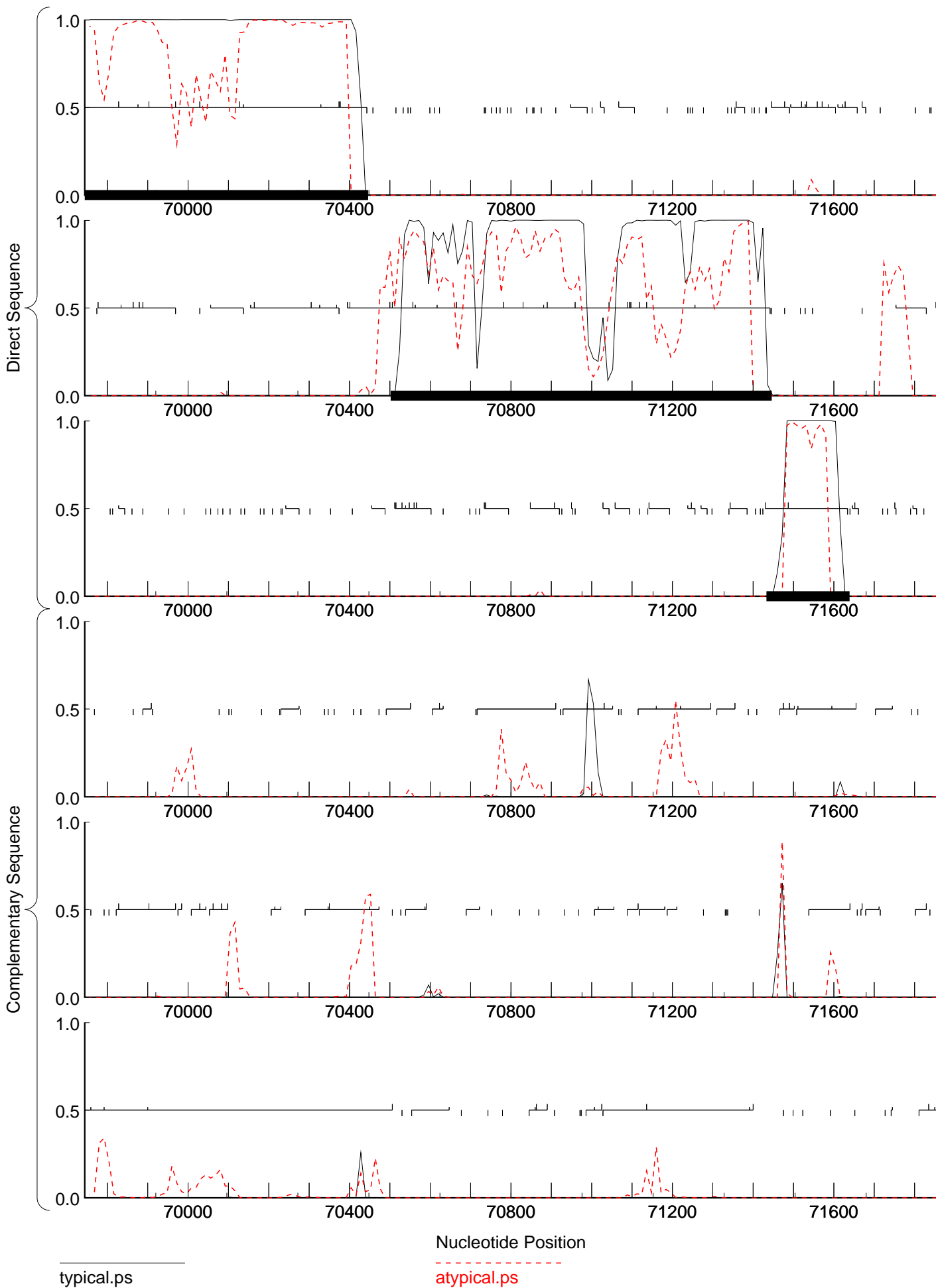


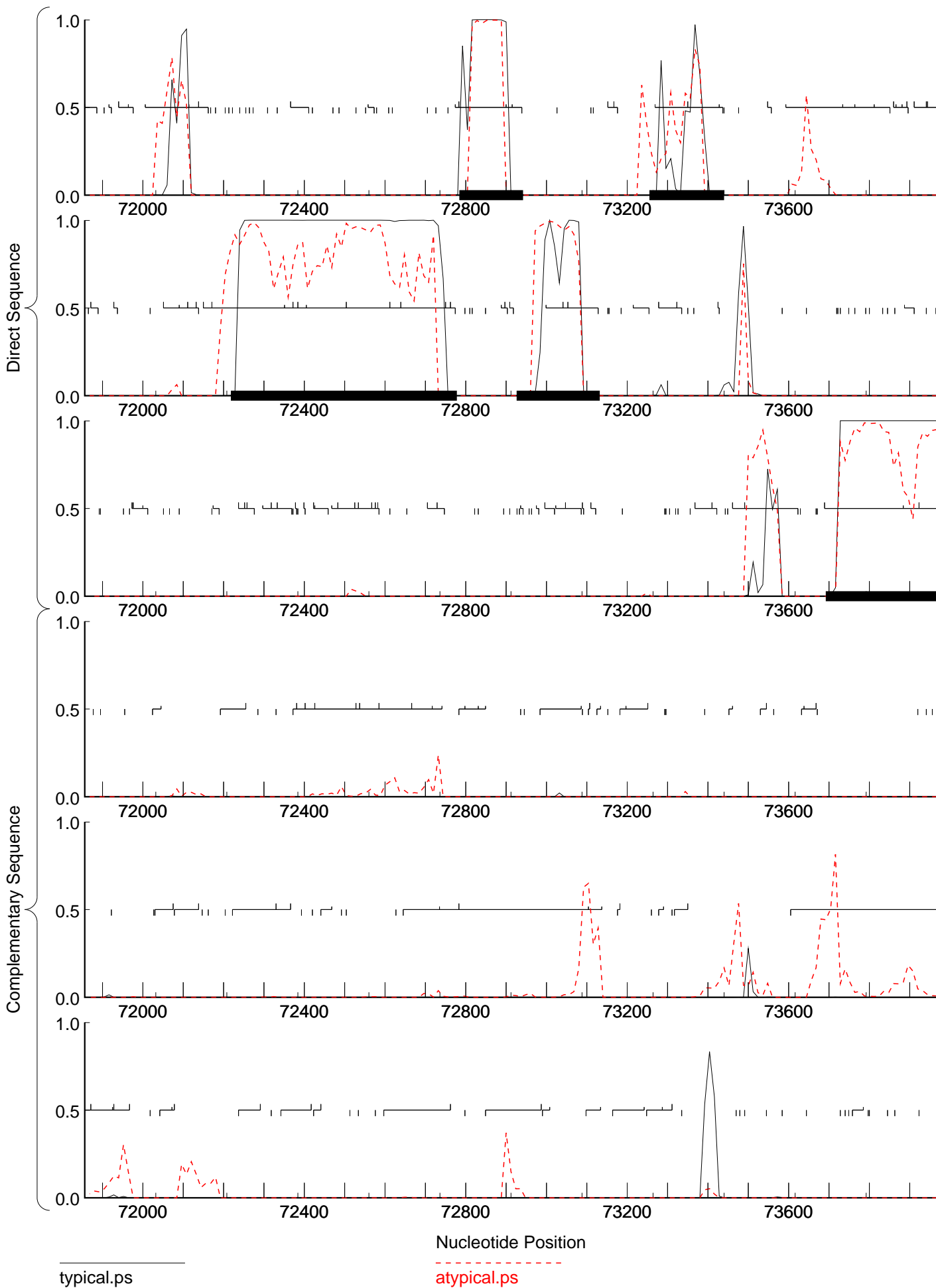


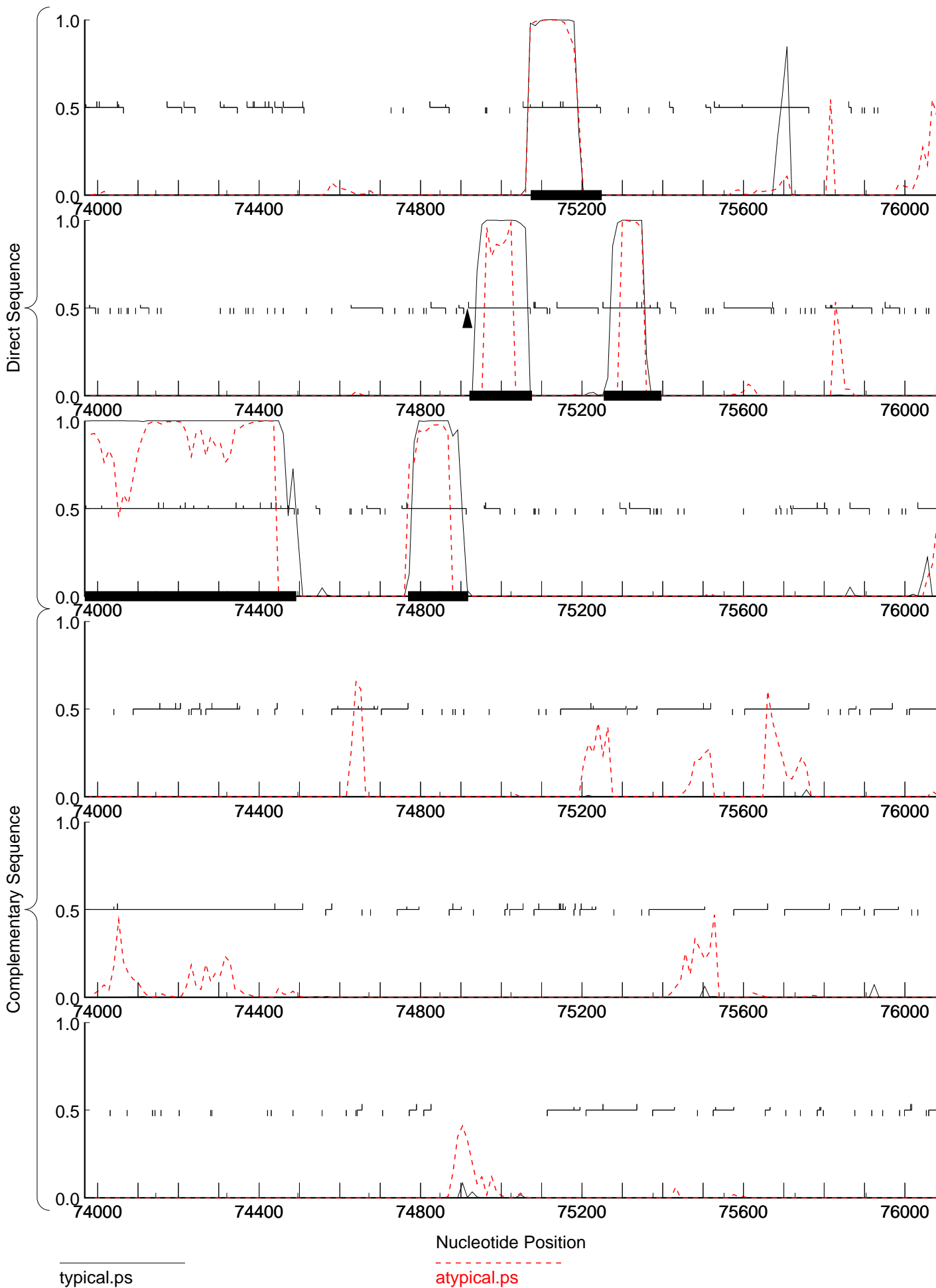
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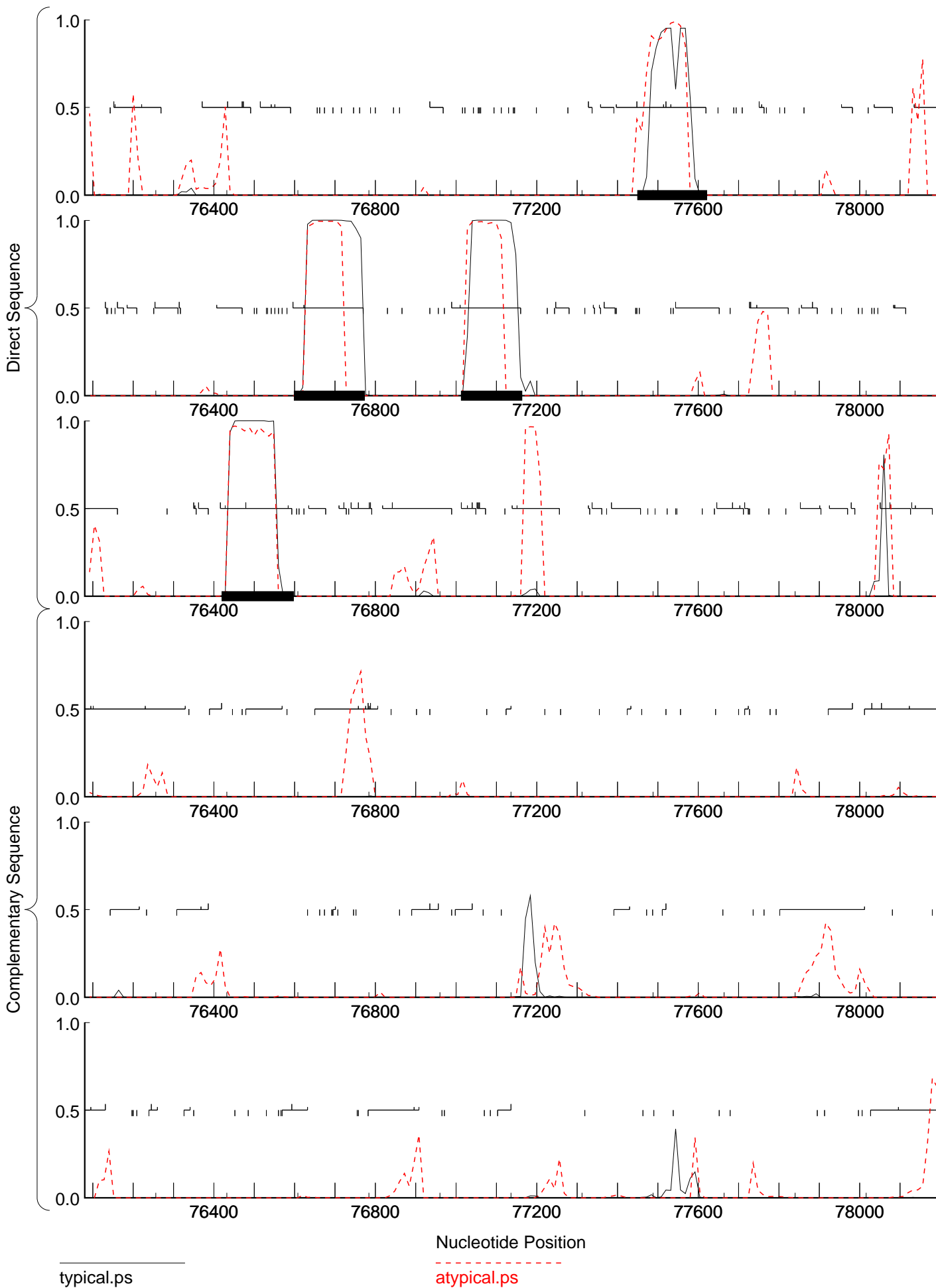
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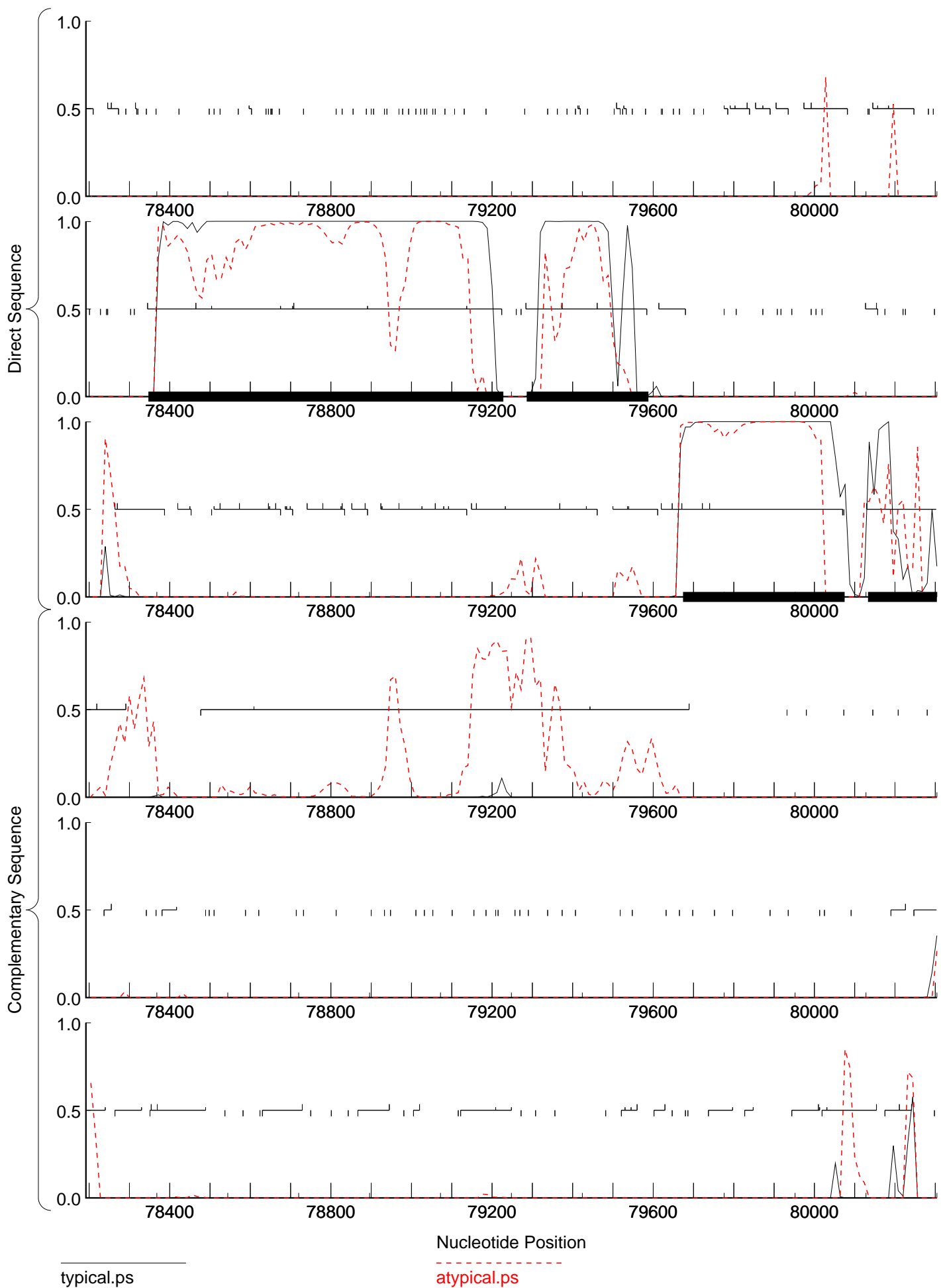




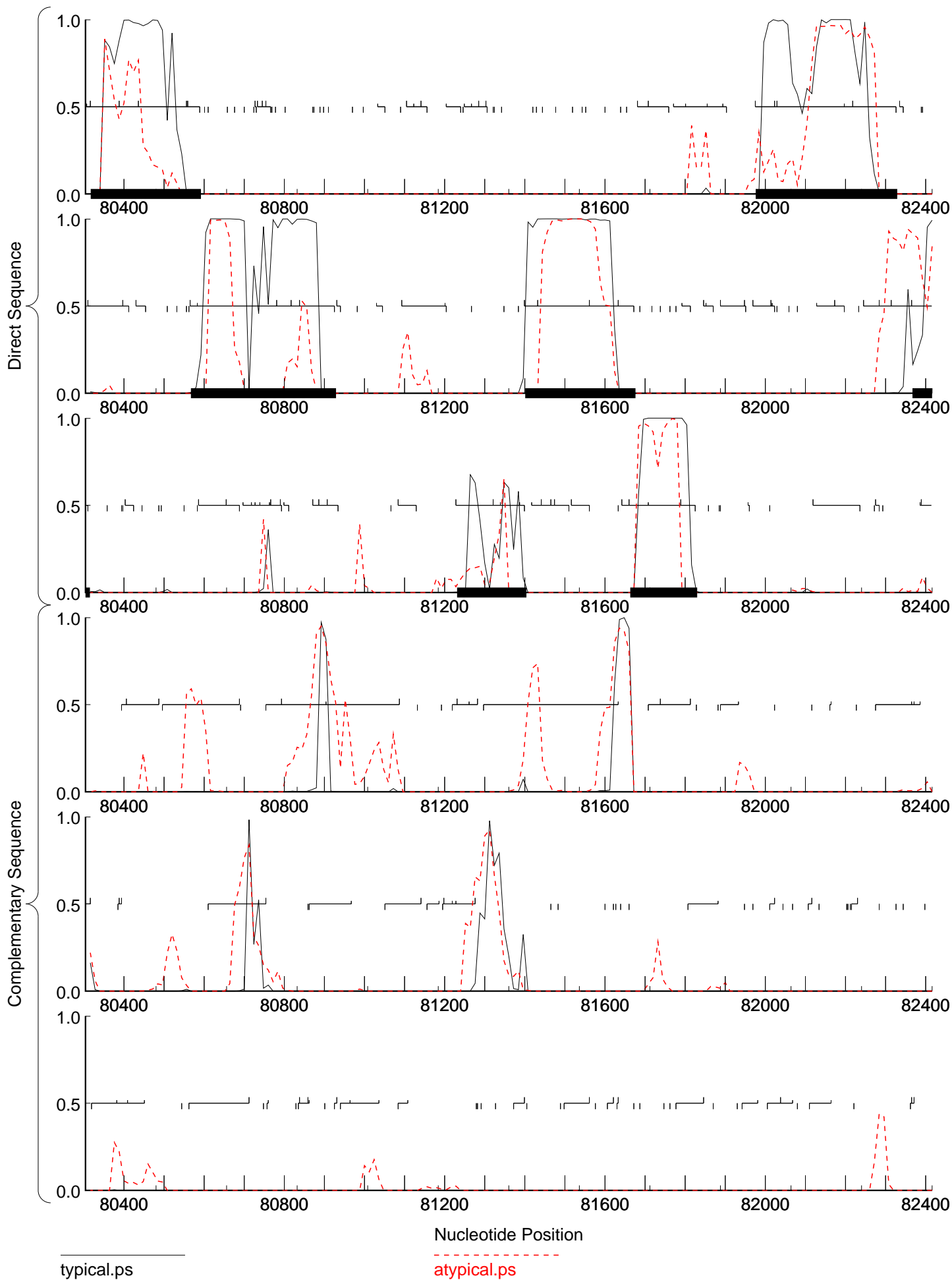








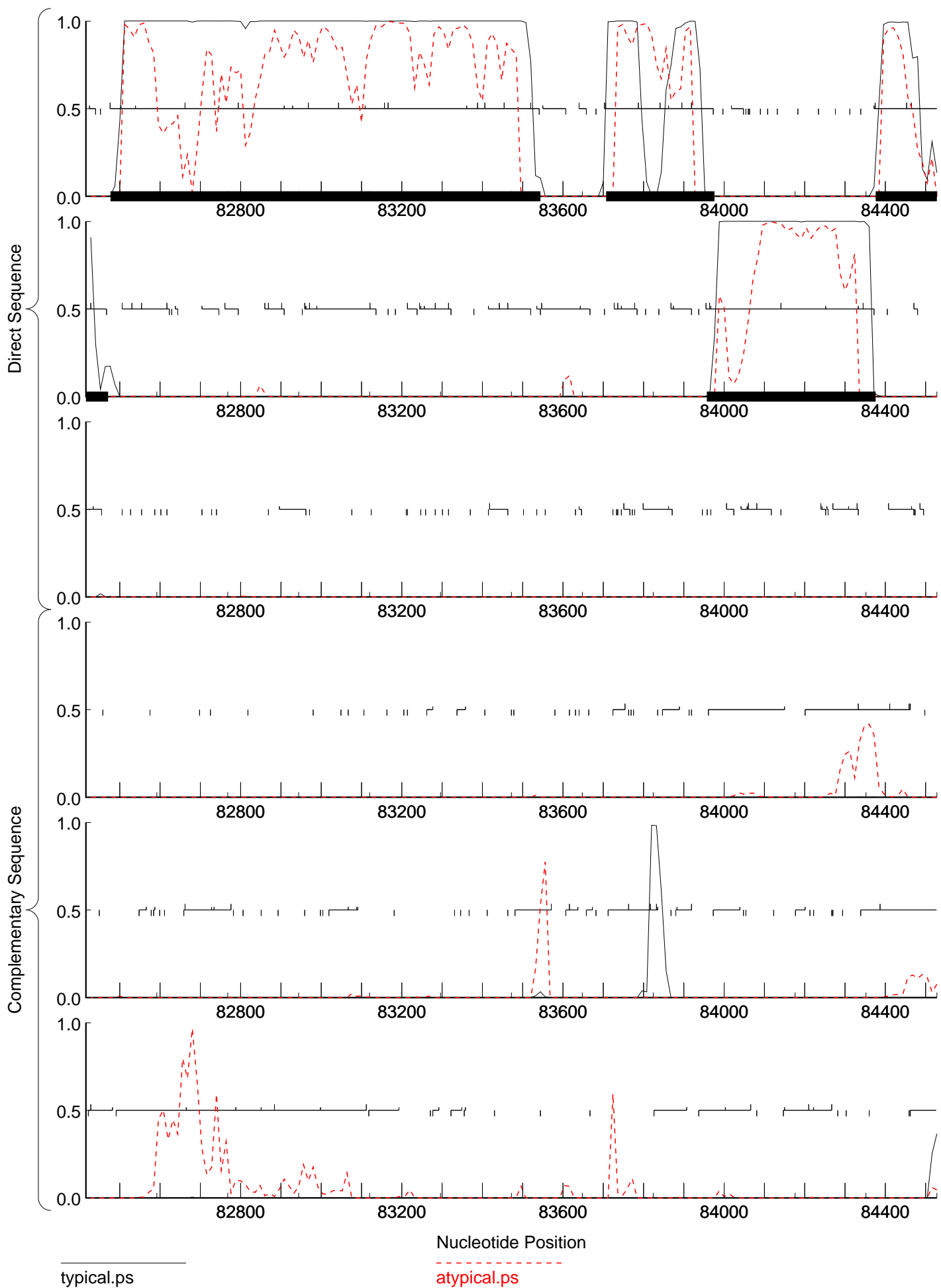
GeneMark.hmm prediction

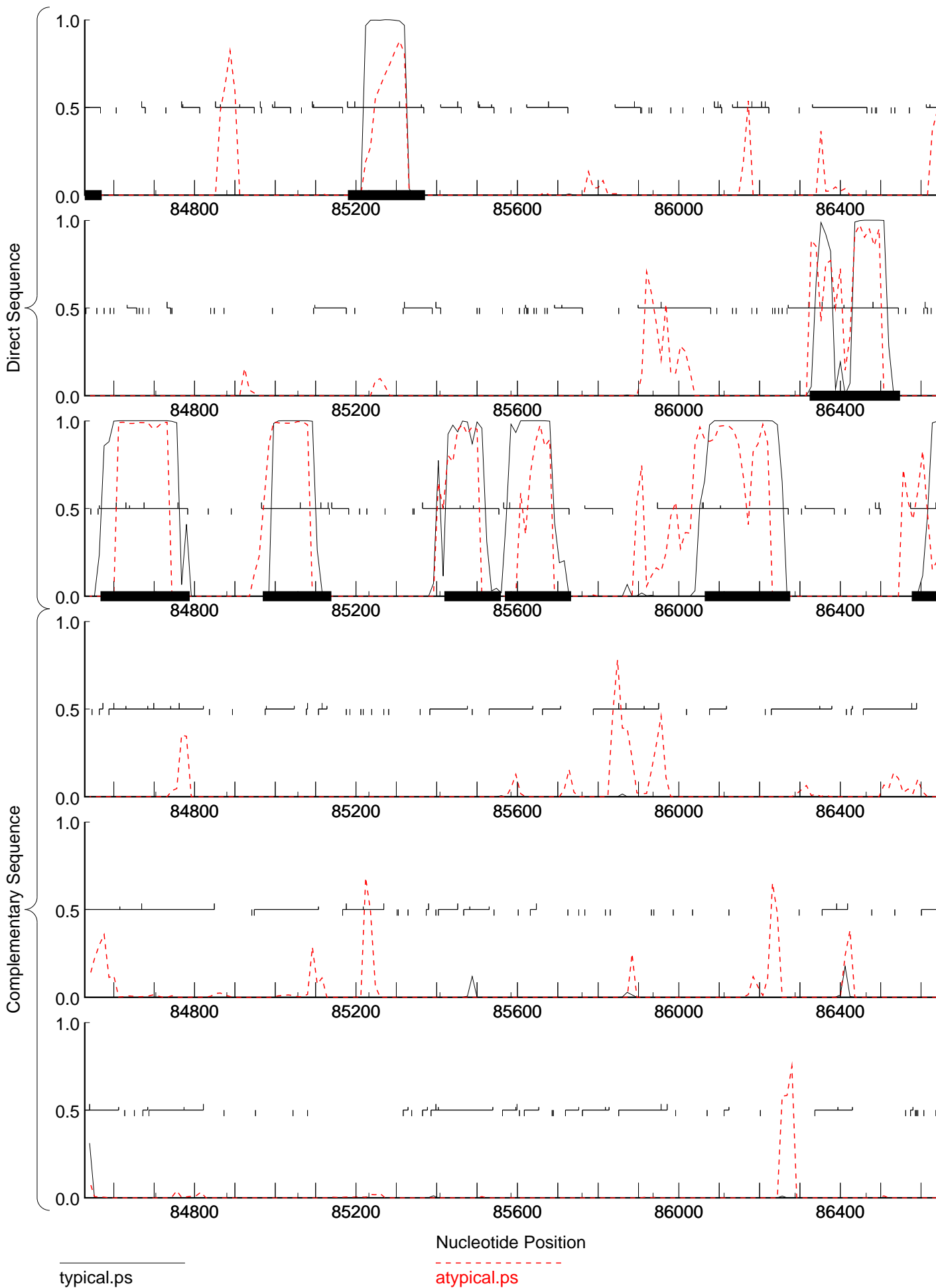


typical.ps

atypical.ps

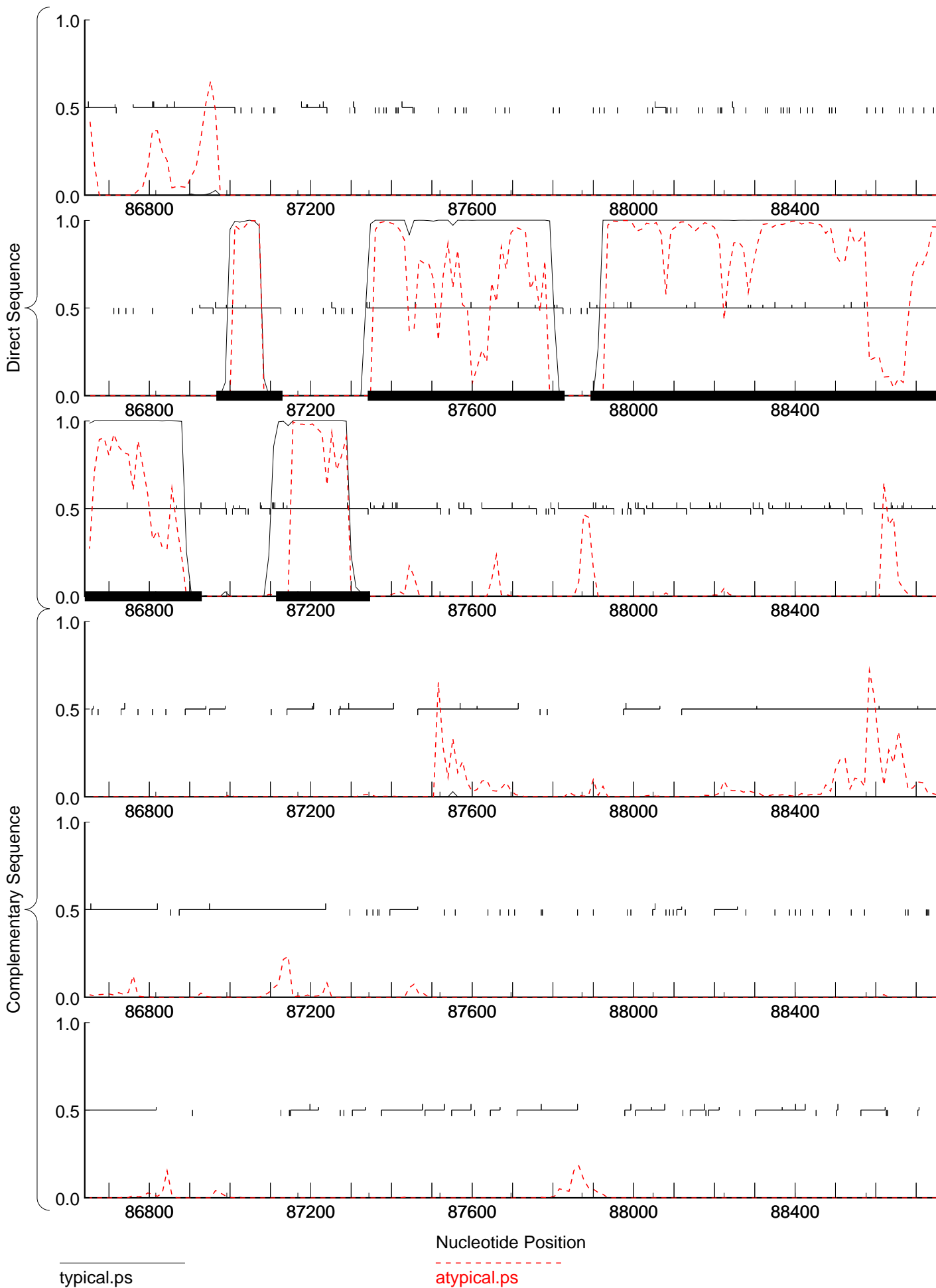


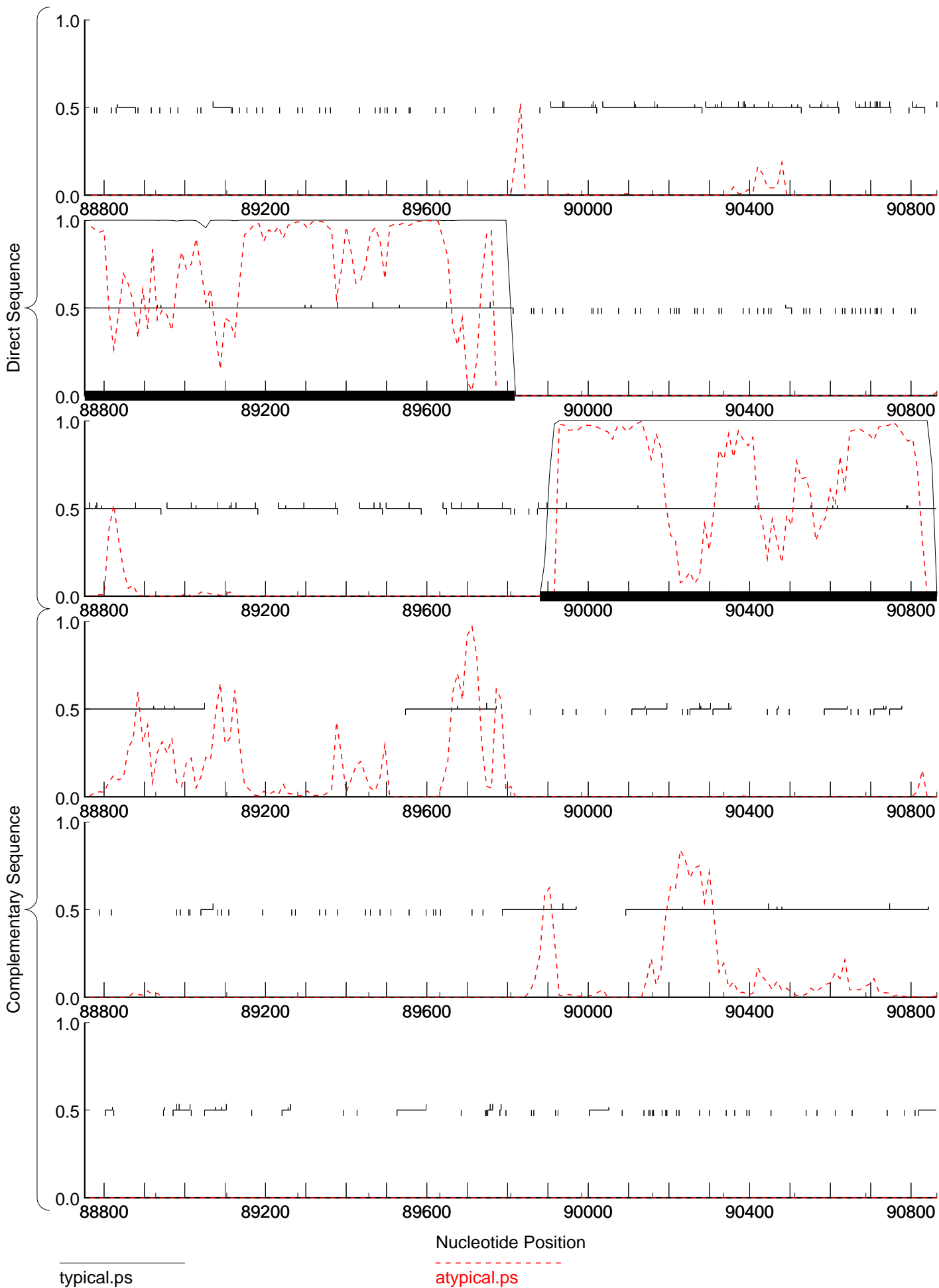


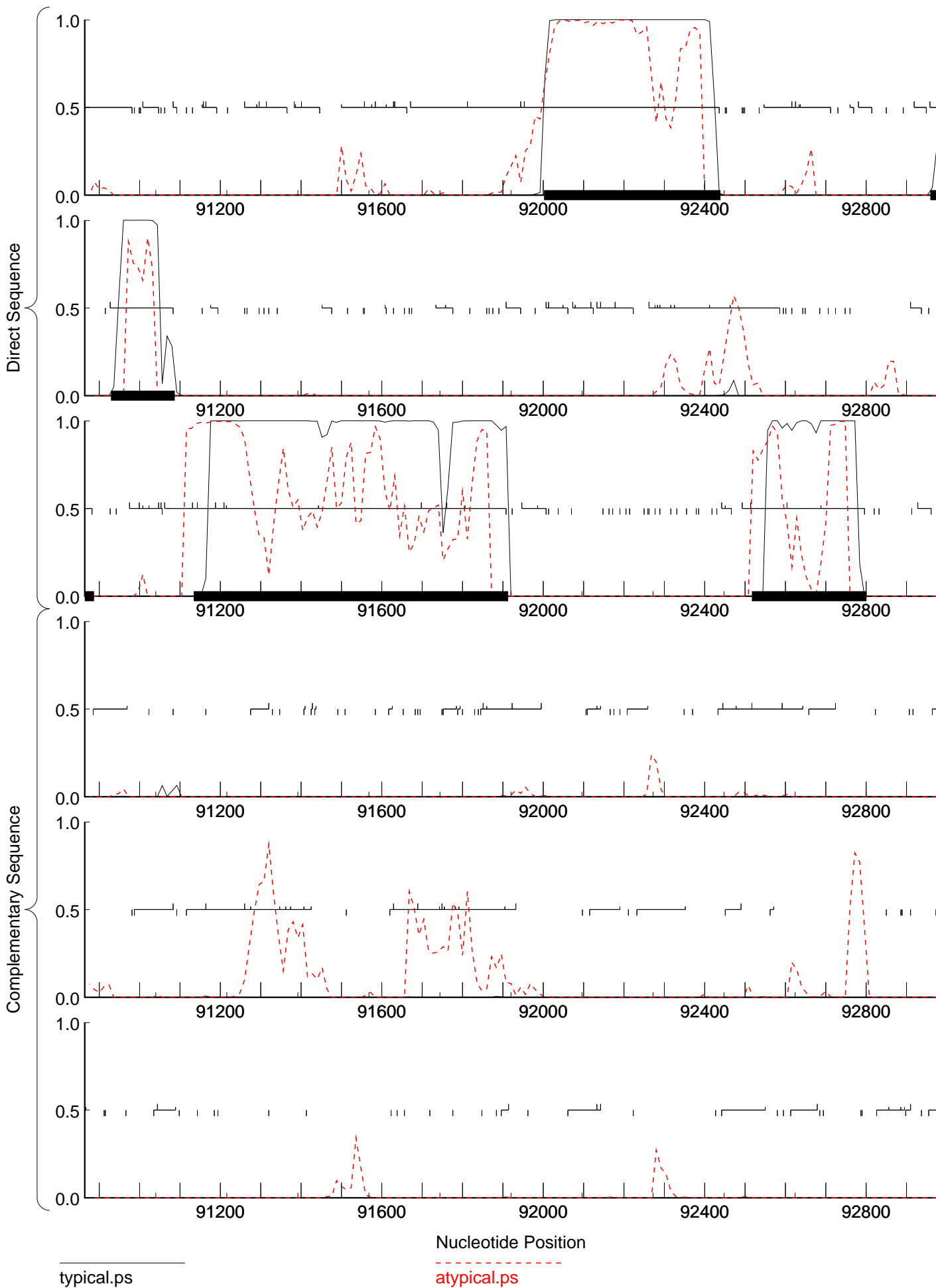


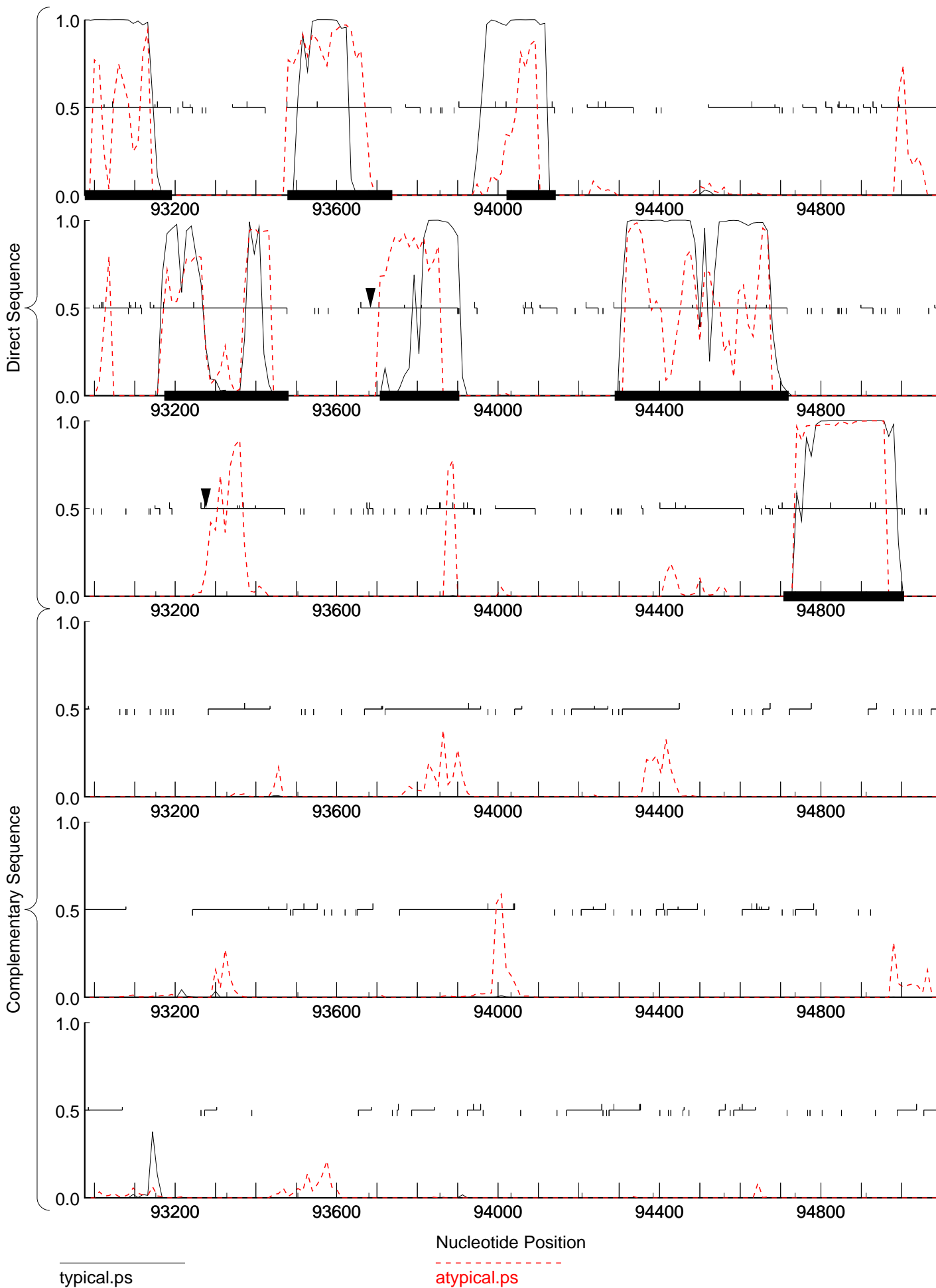
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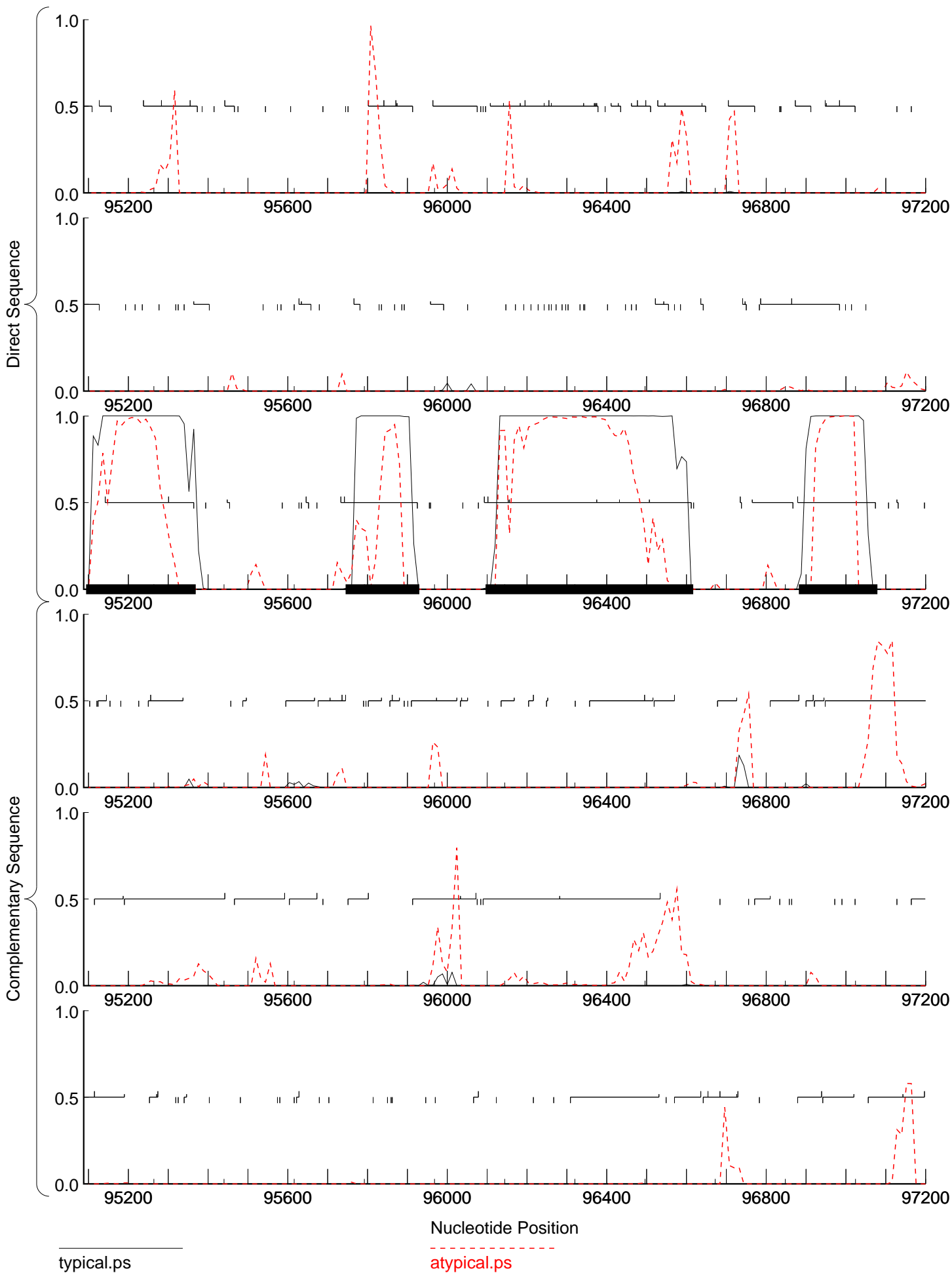
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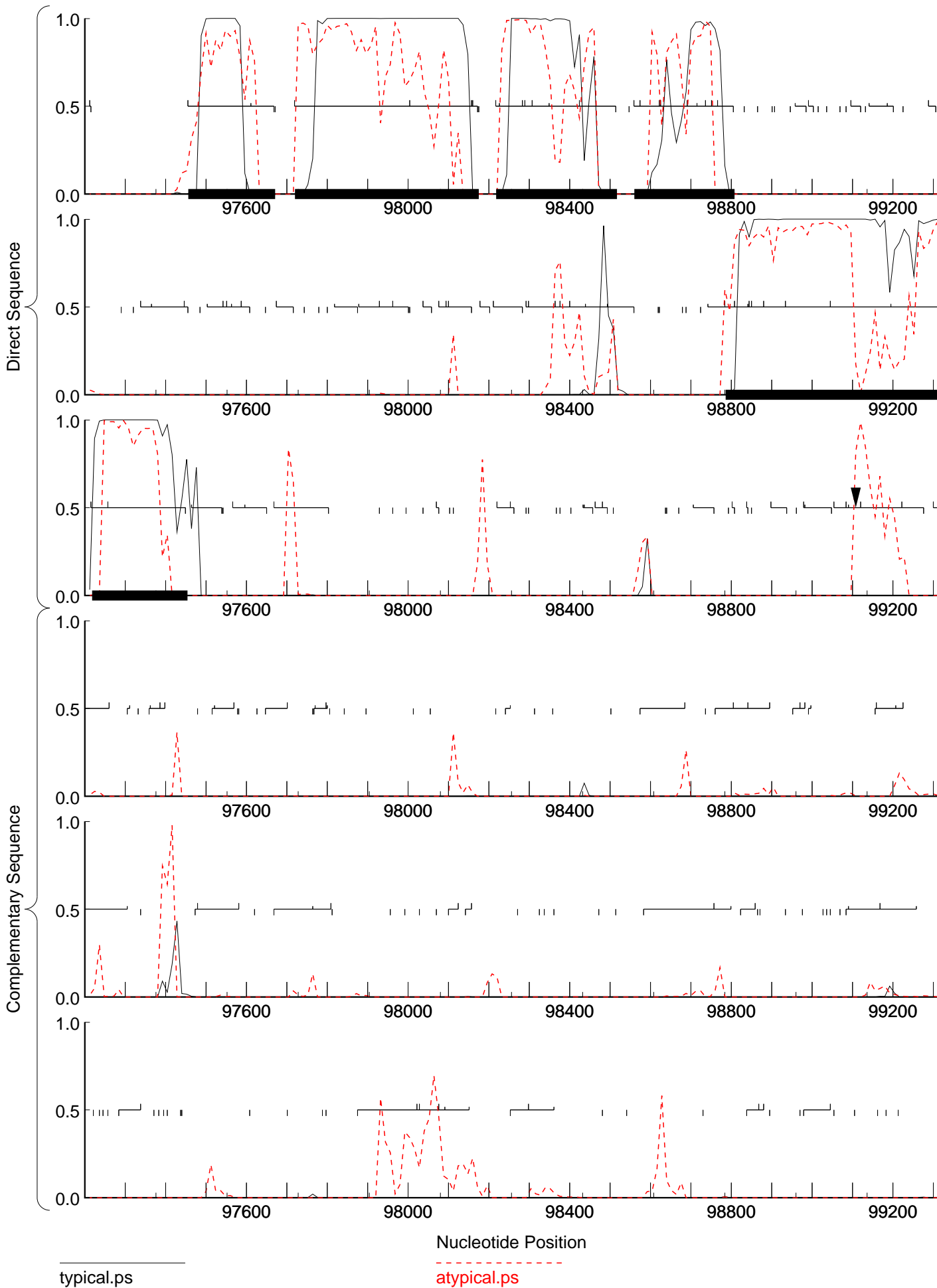




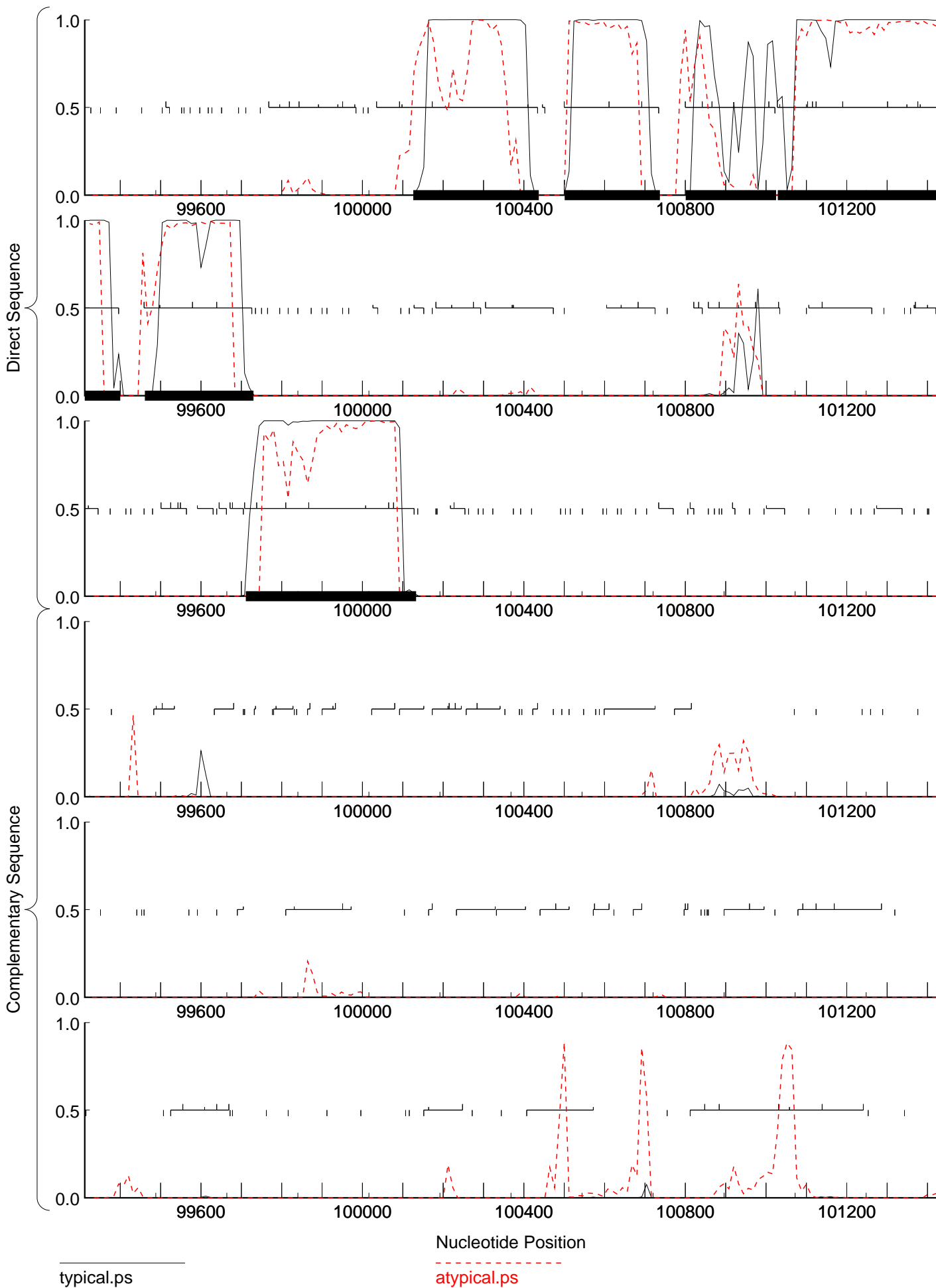


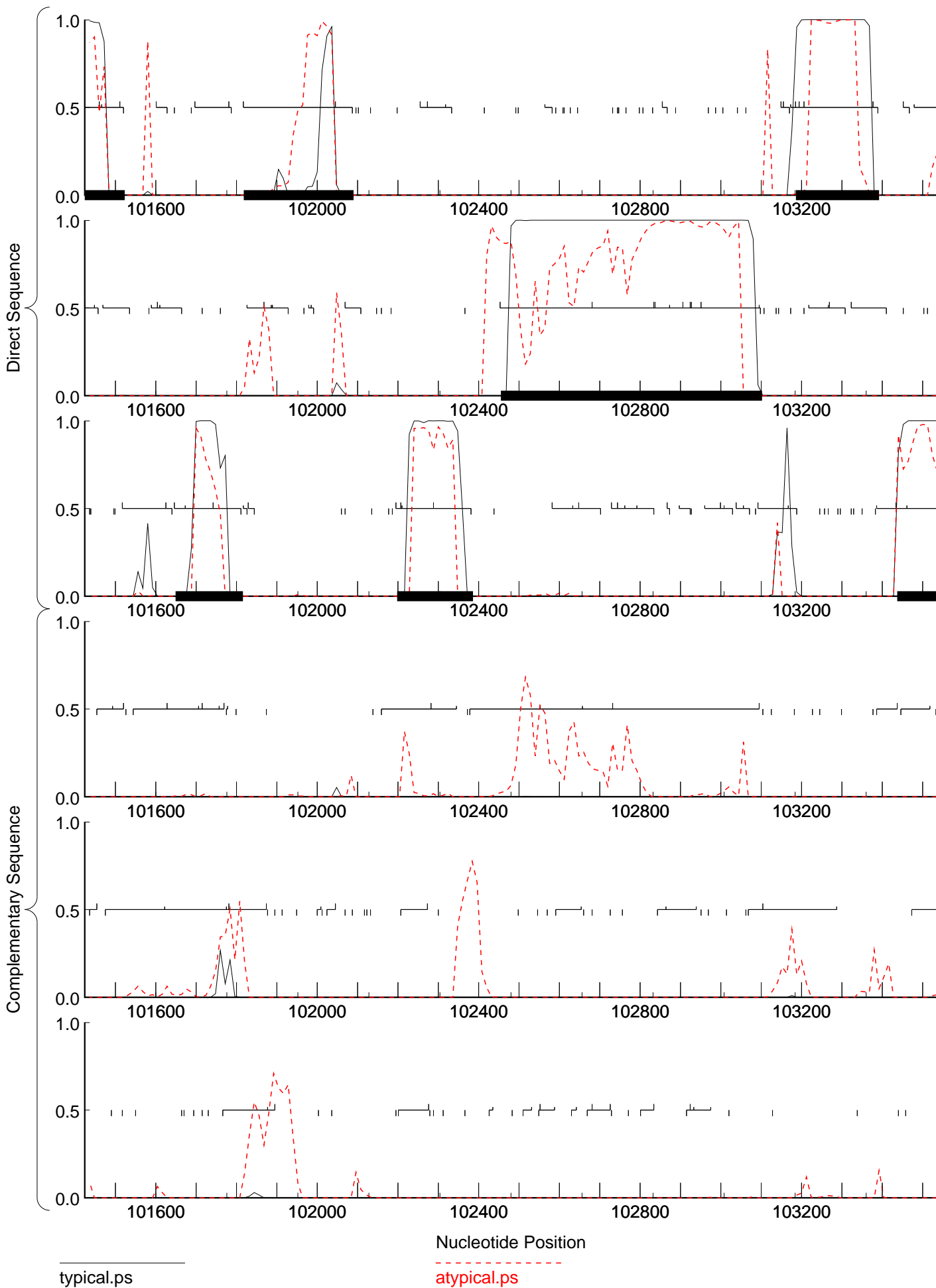


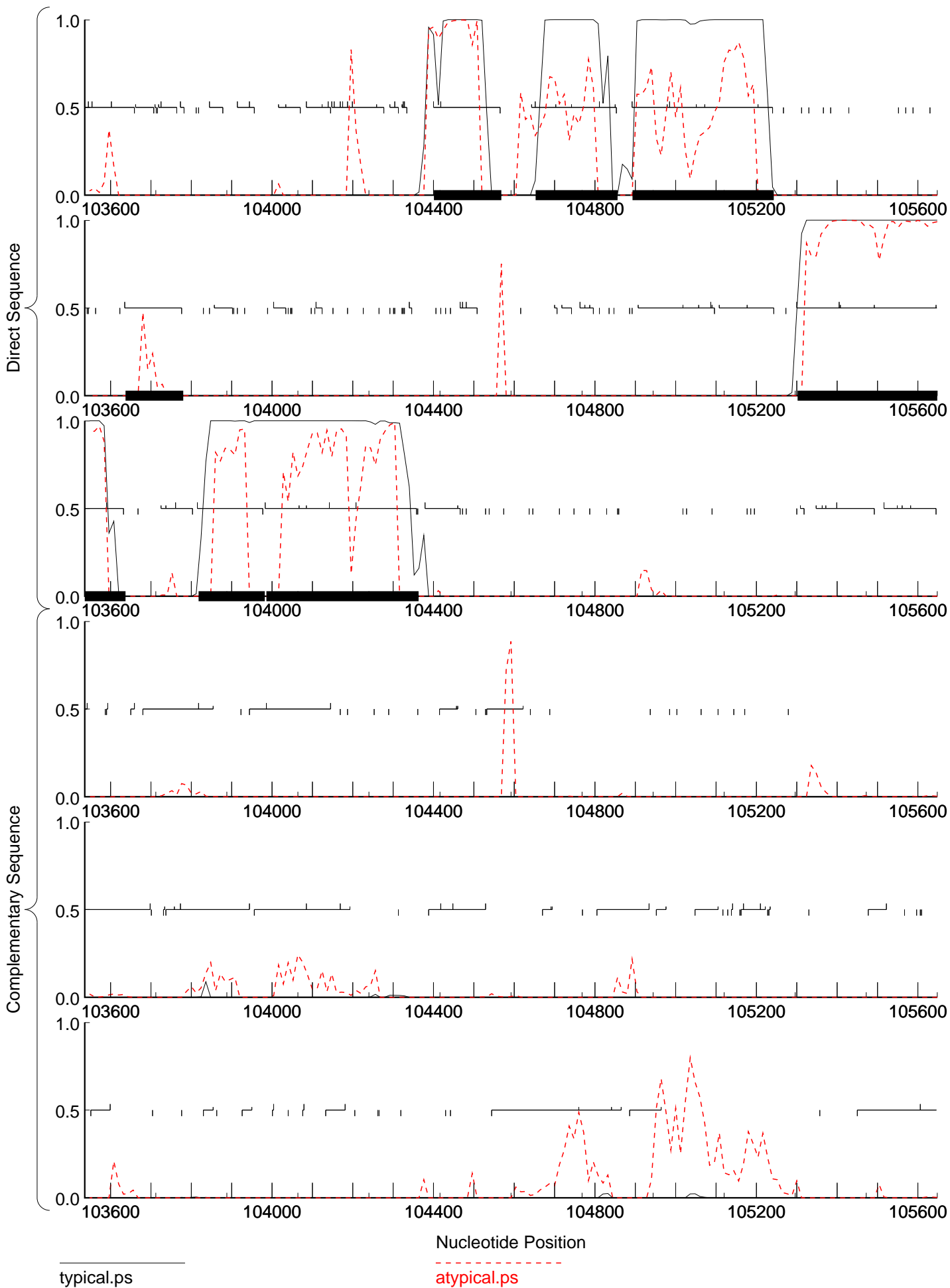


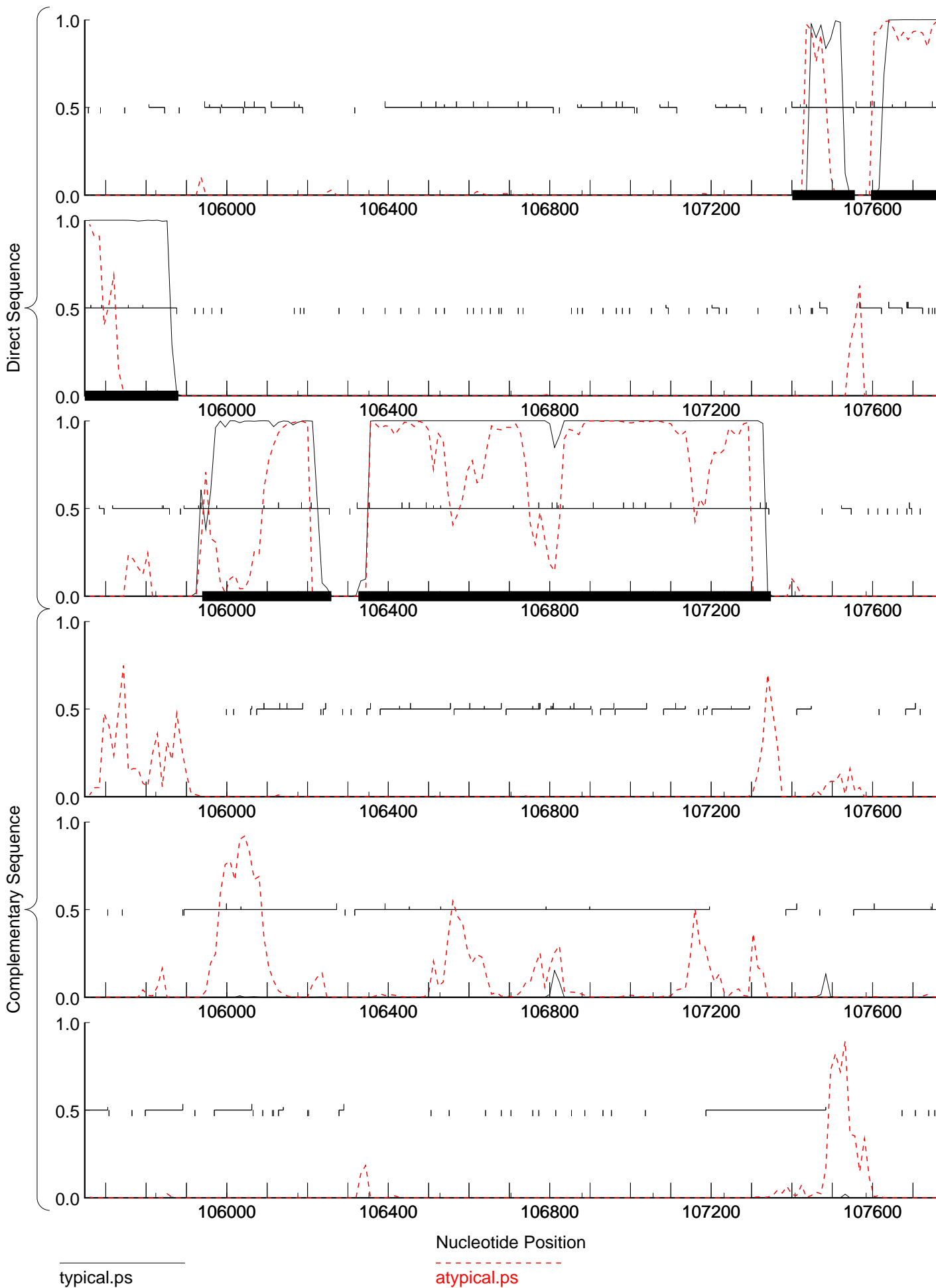






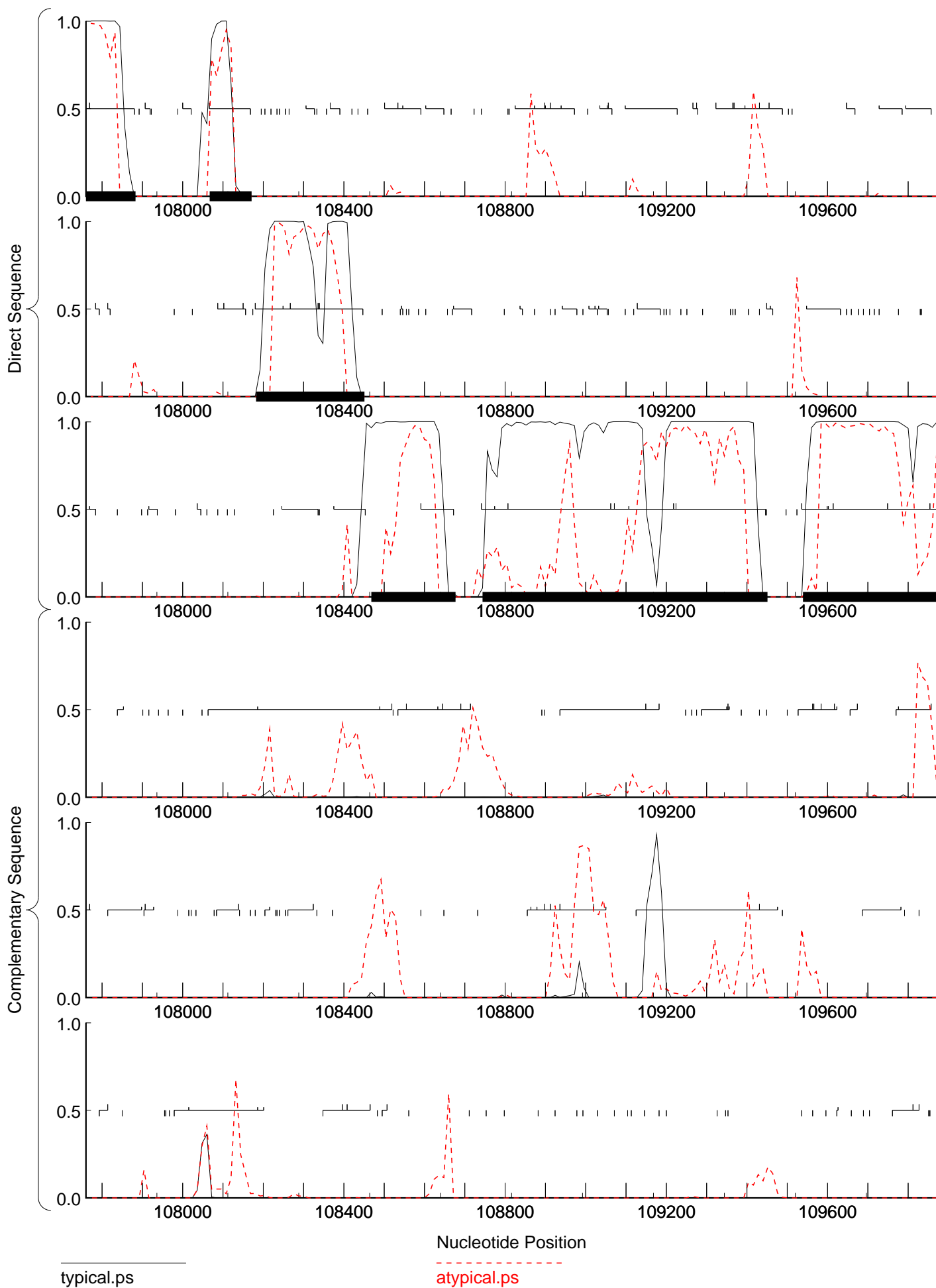


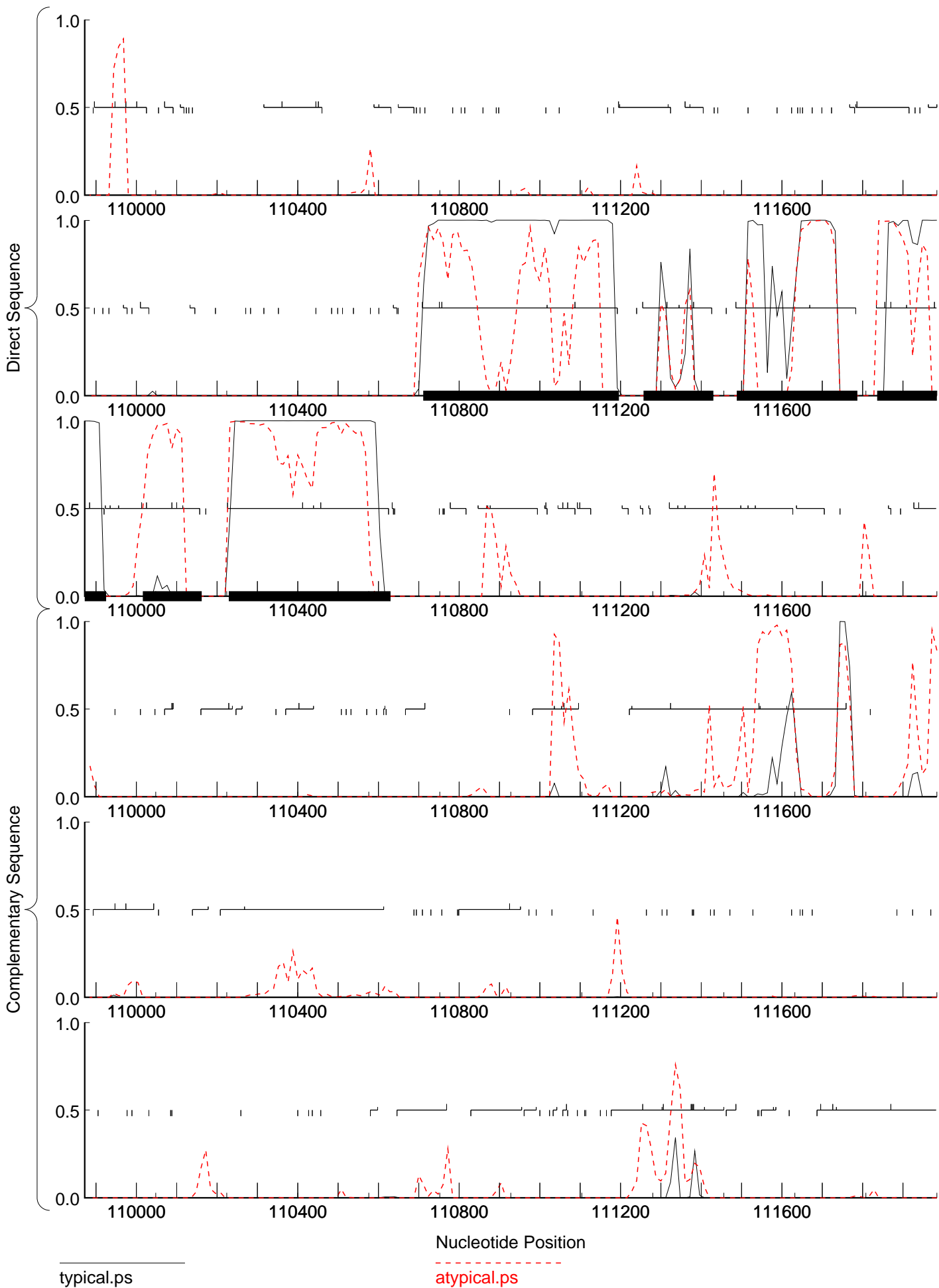


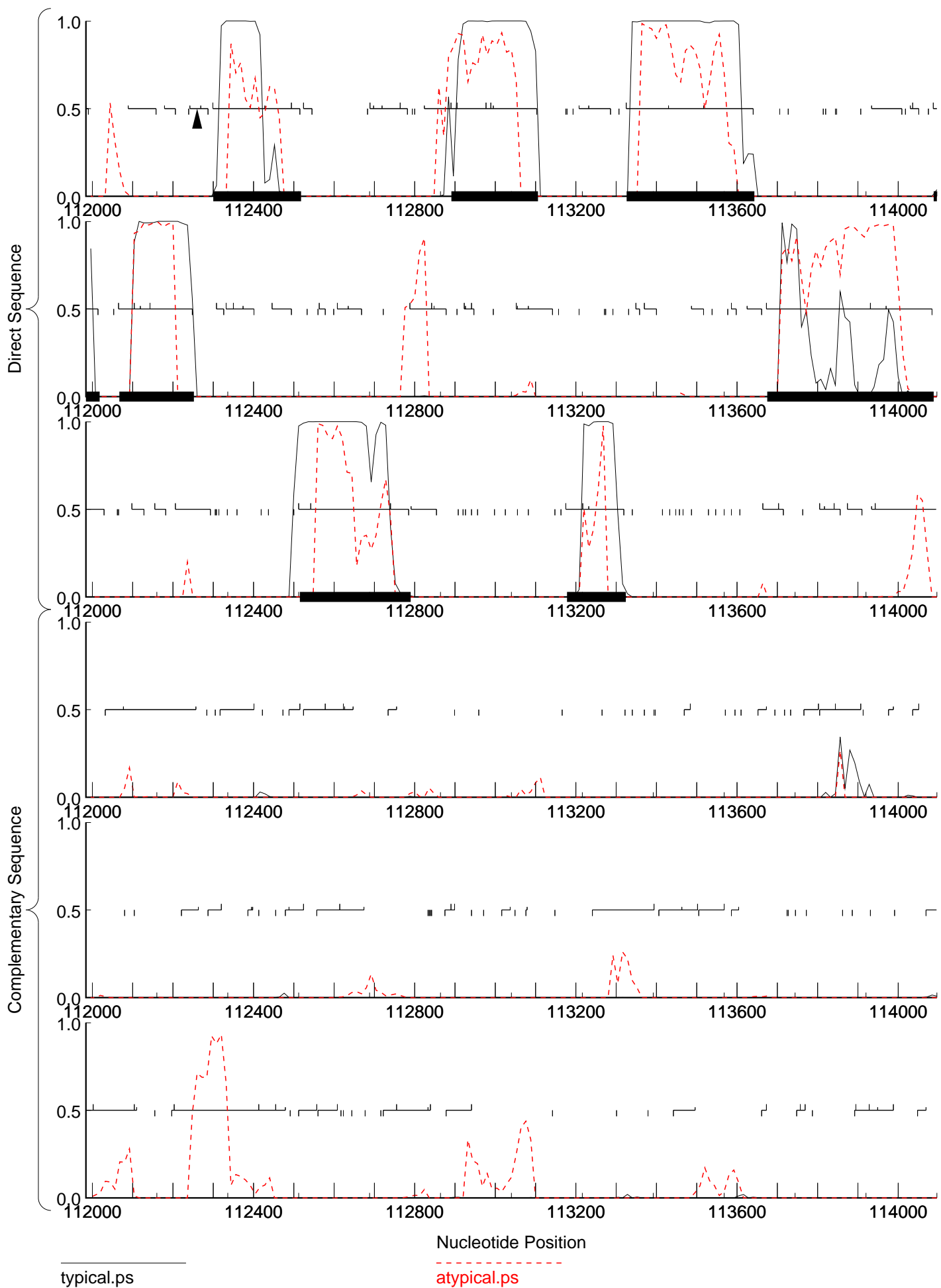


typical.ps

atypical.ps

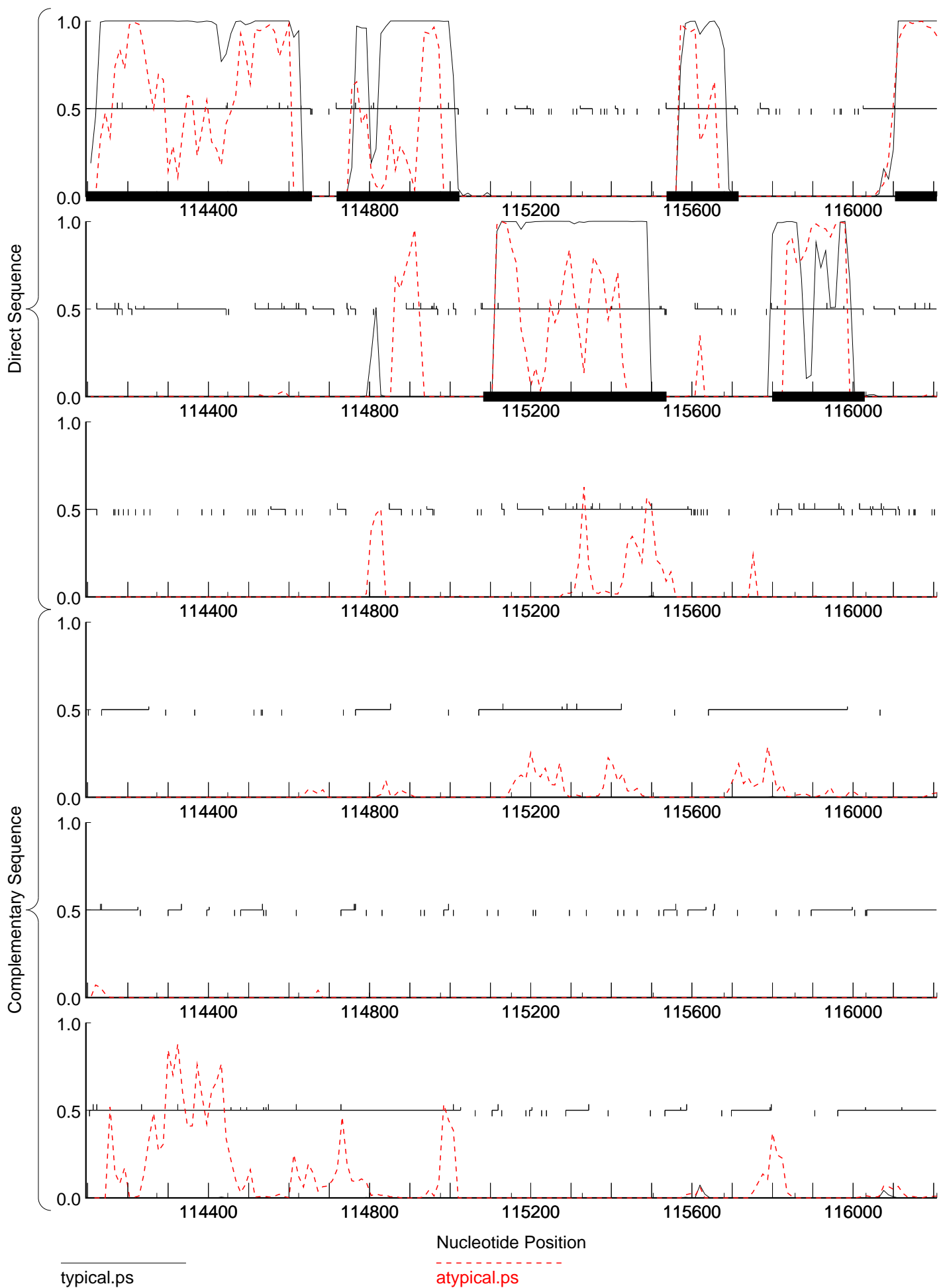




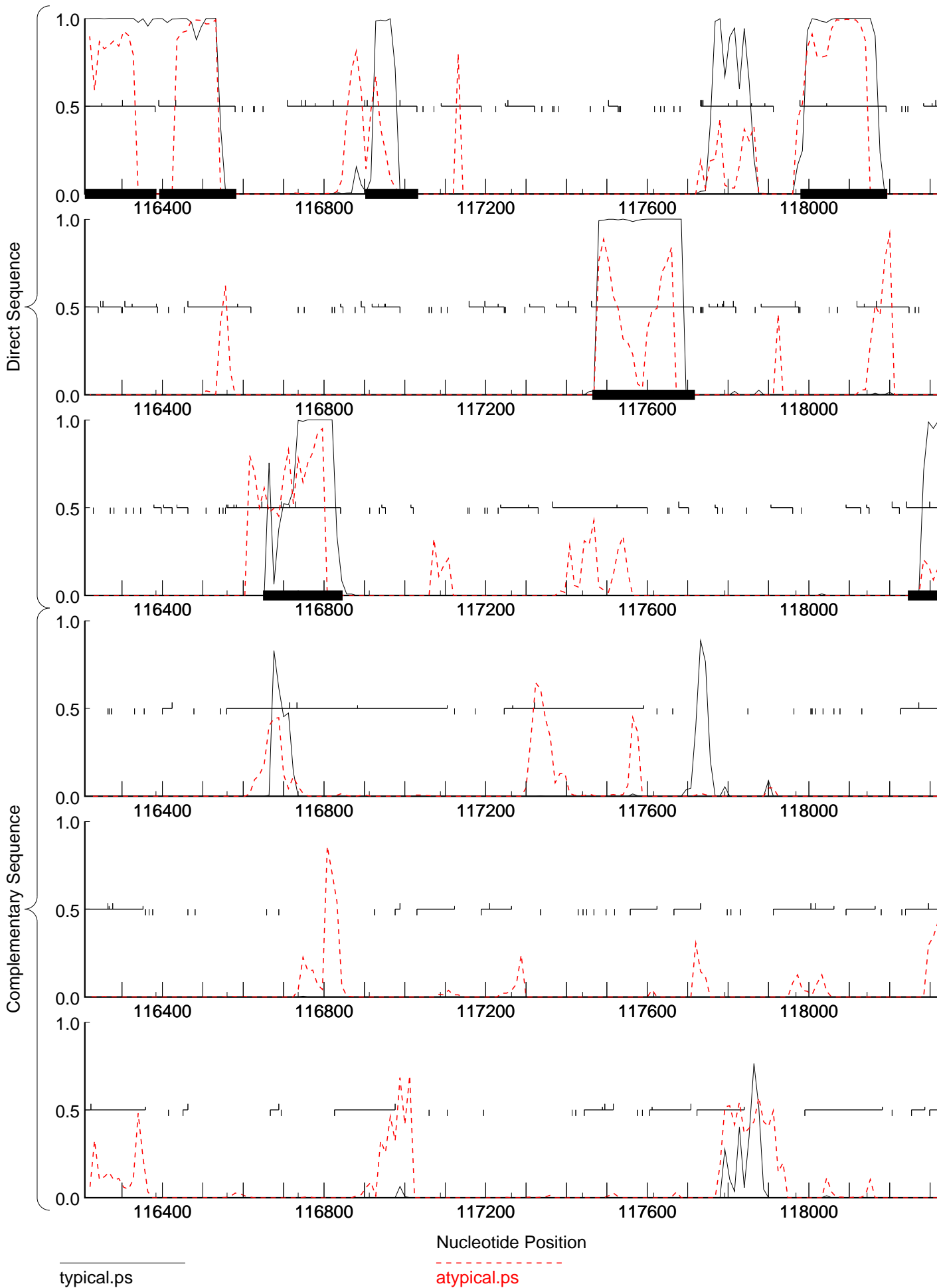


typical.ps

atypical.ps

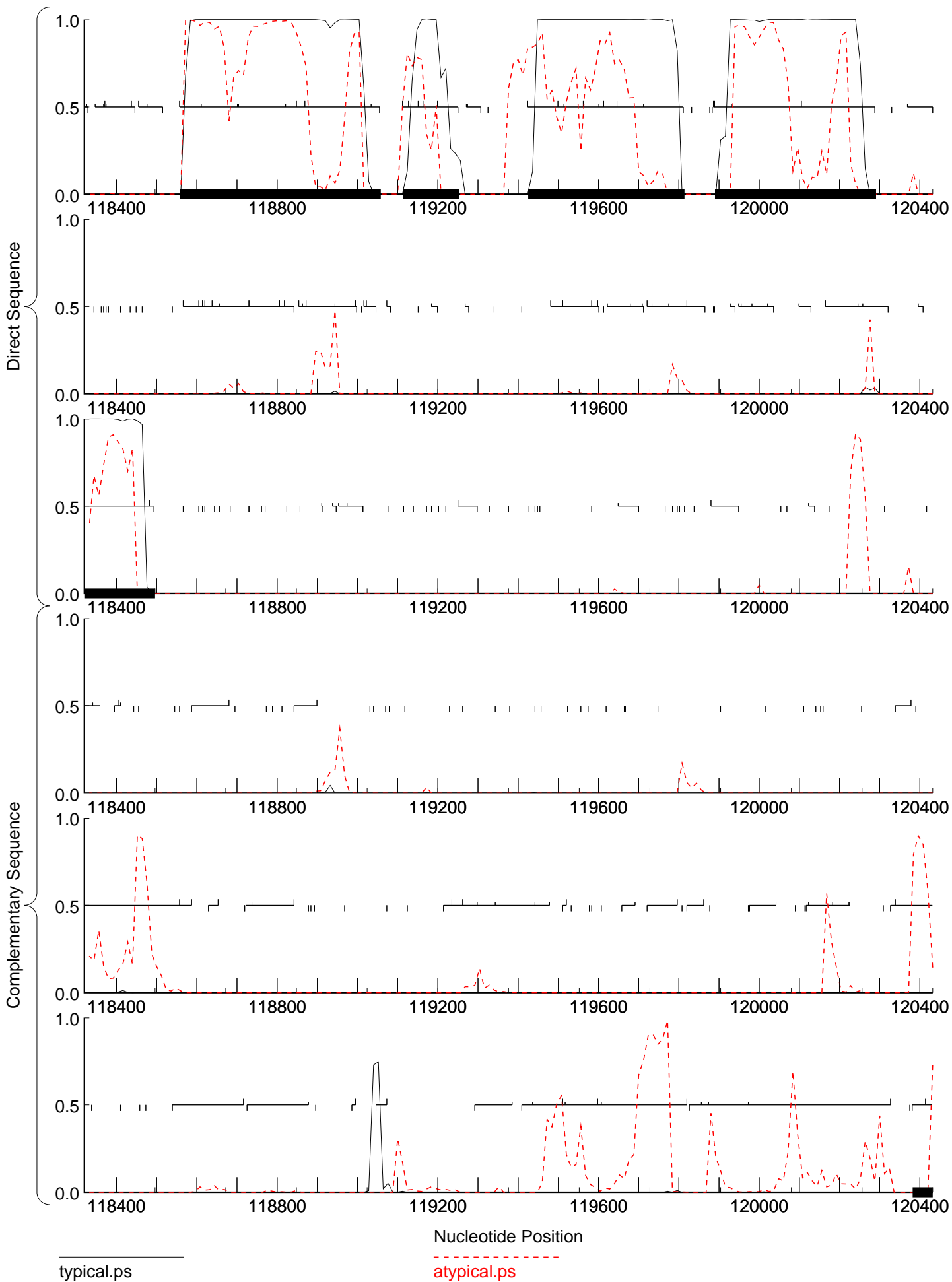


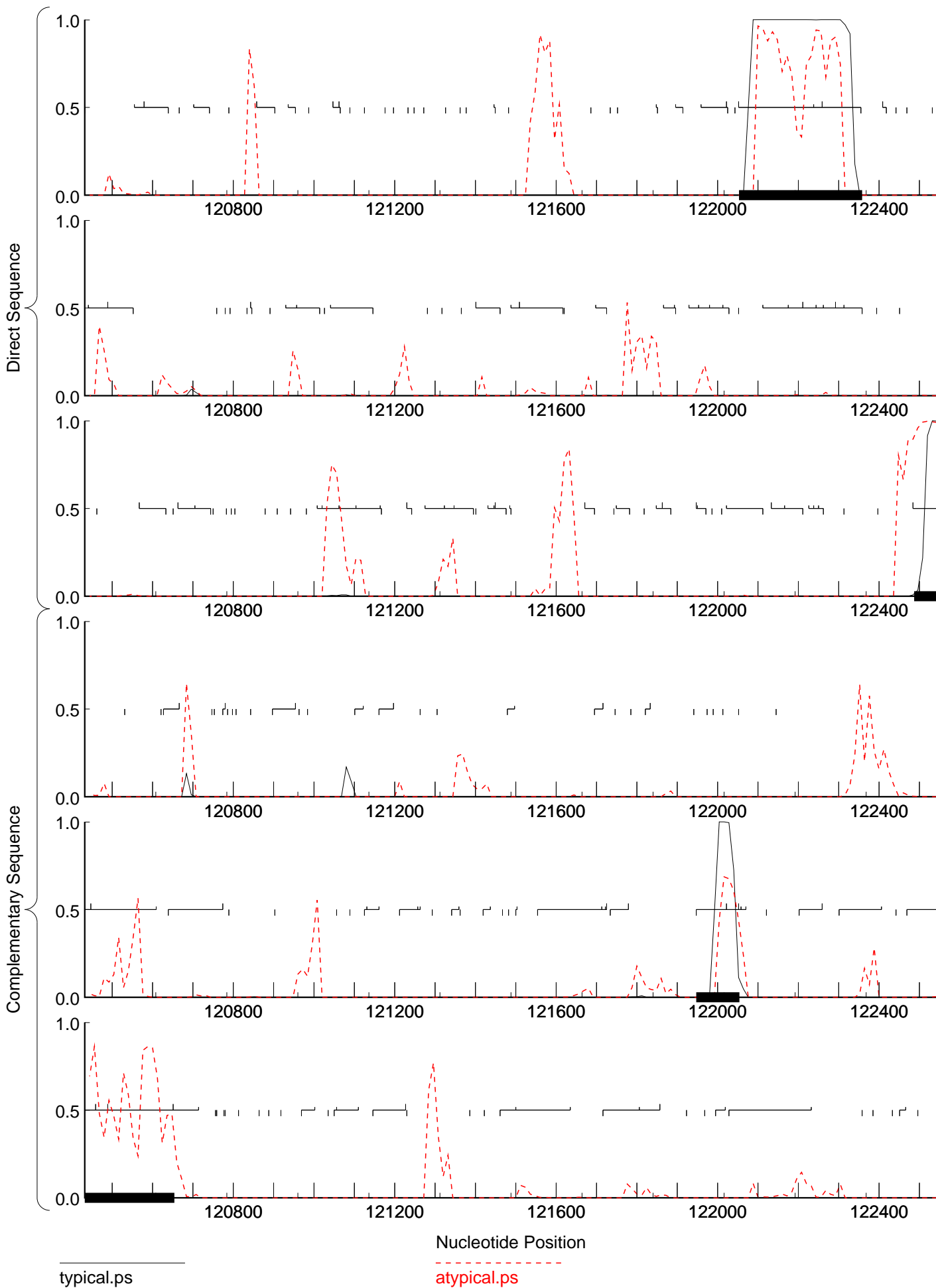


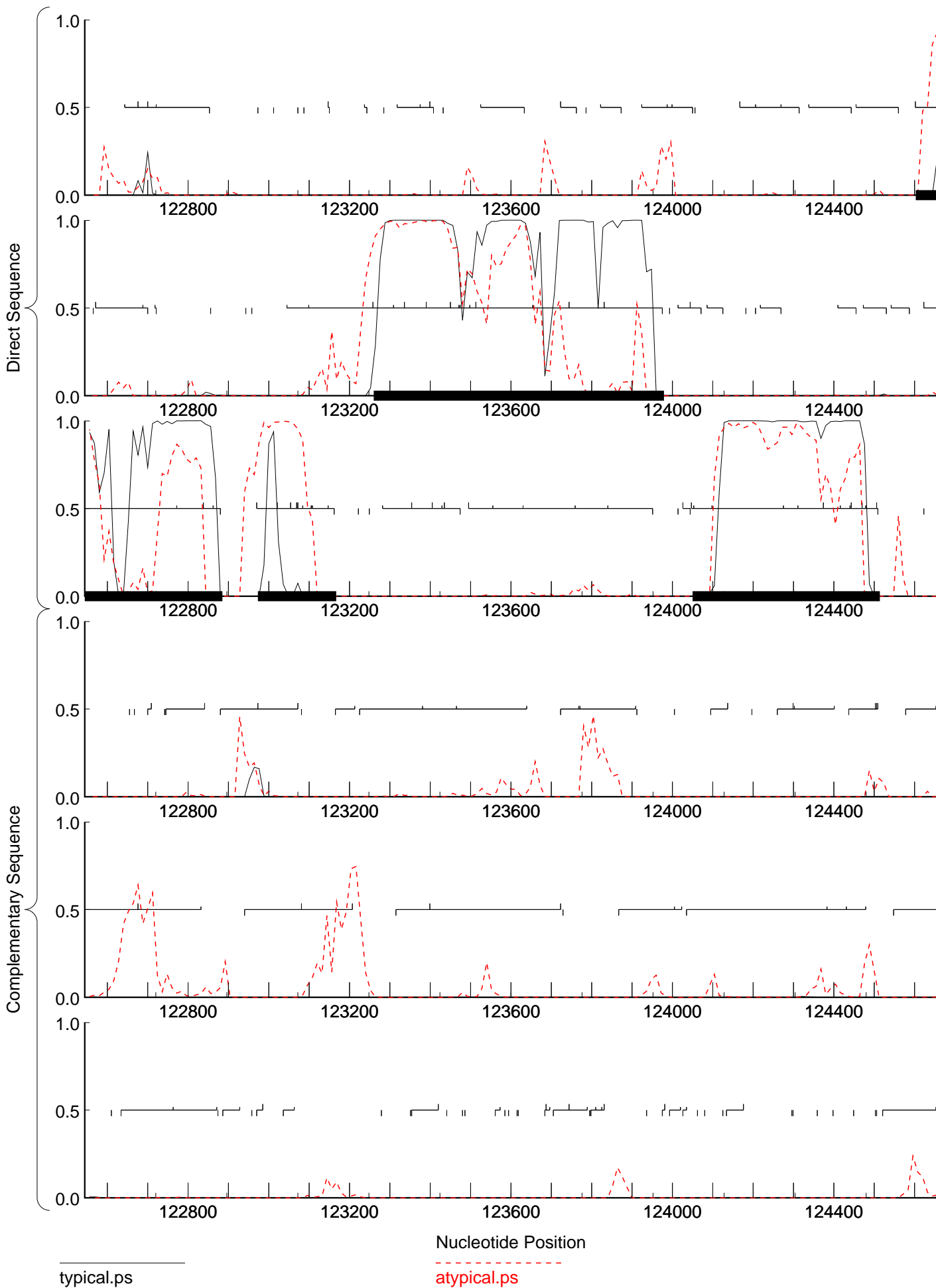


typical.ps

atypical.ps

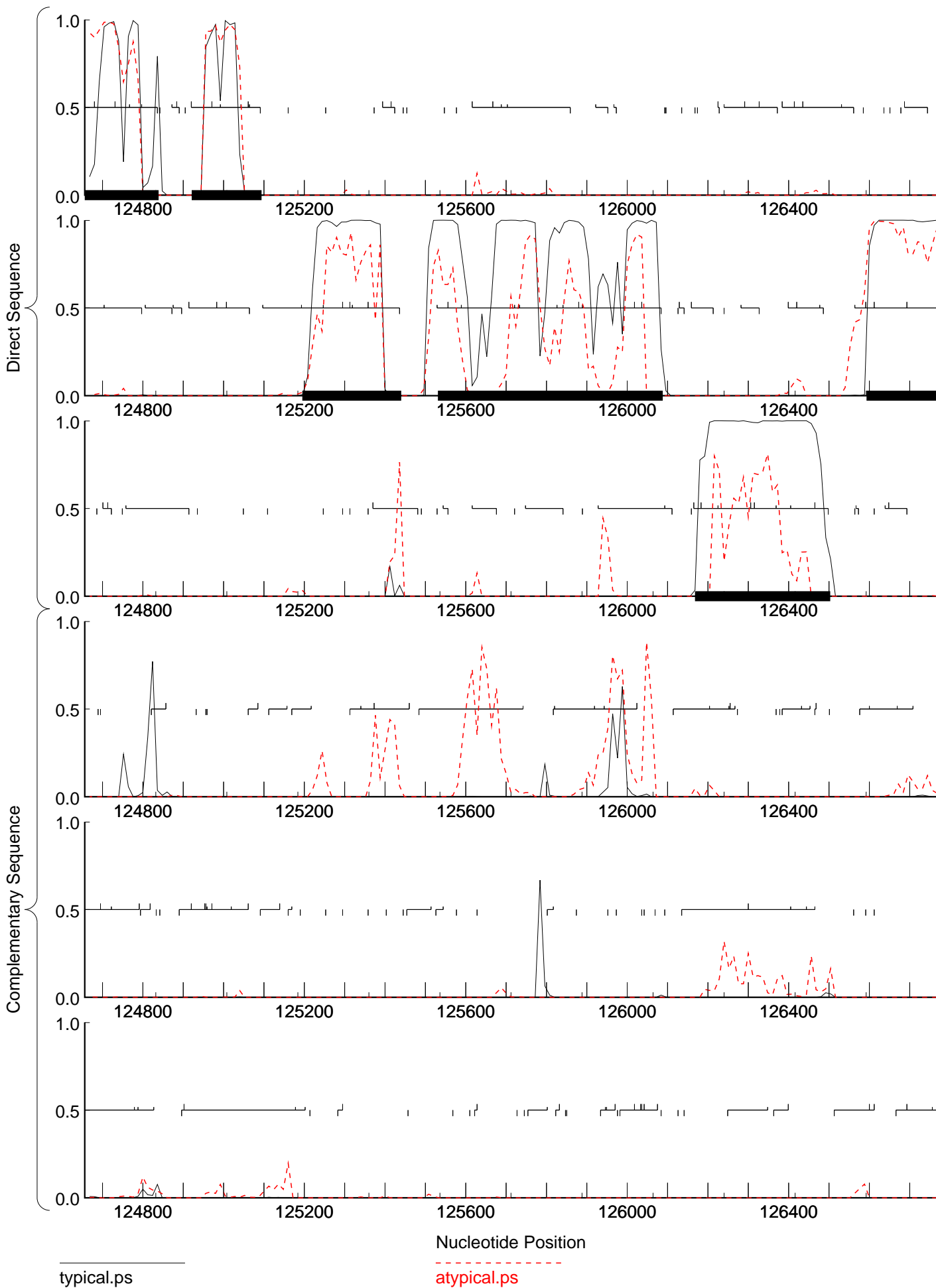






typical.ps

atypical.ps



typical.ps

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