

# GeneMark

Version 2.5p (09.08.06)

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## PROGRAM INFORMATION

Sequence : Mycobacterium phage Riparian complete sequence, 71199 bp, circularly permuted, Cluster R  
Analysis Date : 5/24/18 at 3:55:33  
Pages : 35  
Sequence Length : 71199 bp  
GC Content : 55.98%

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,

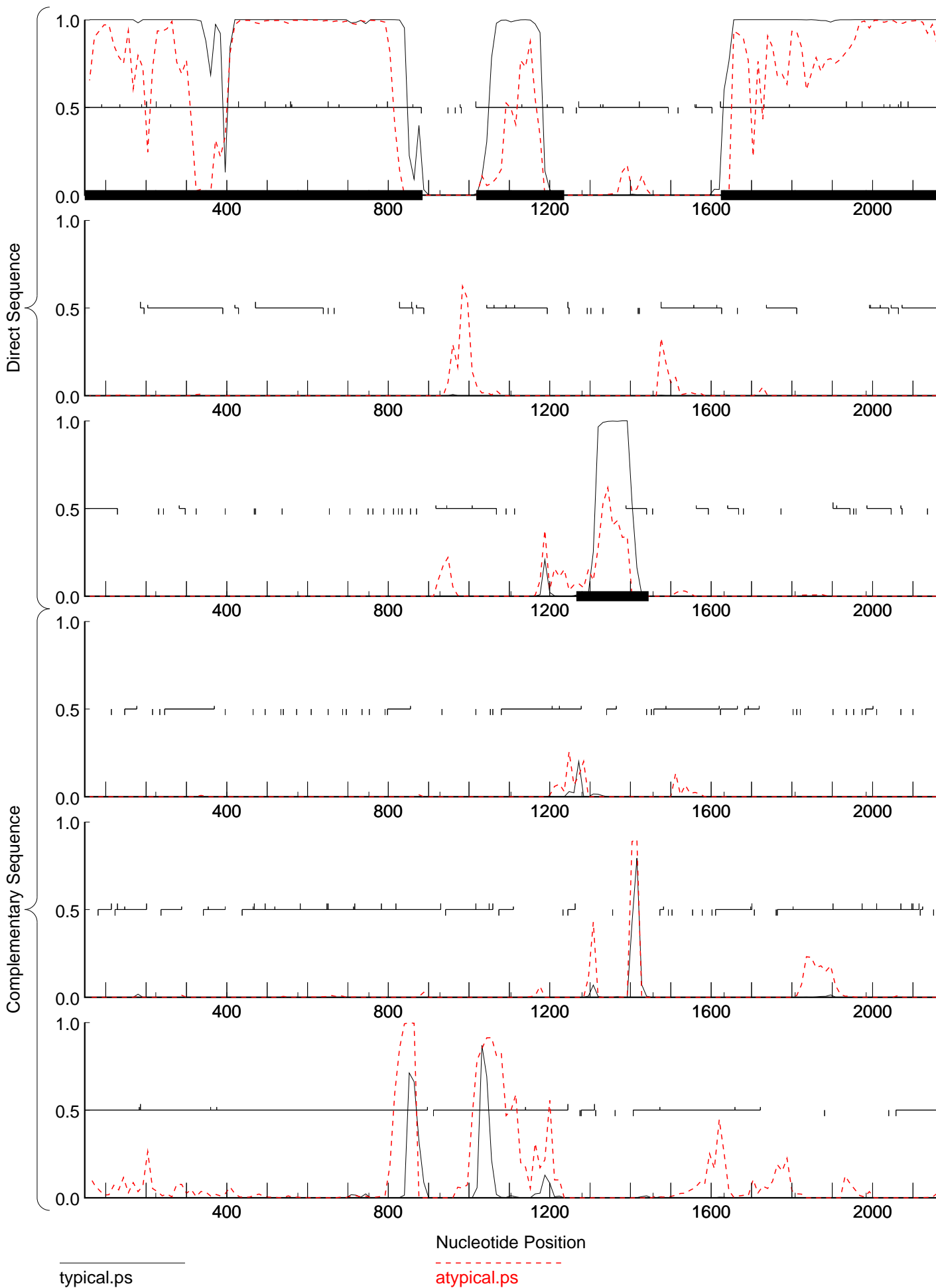
## Matrix notes & comments

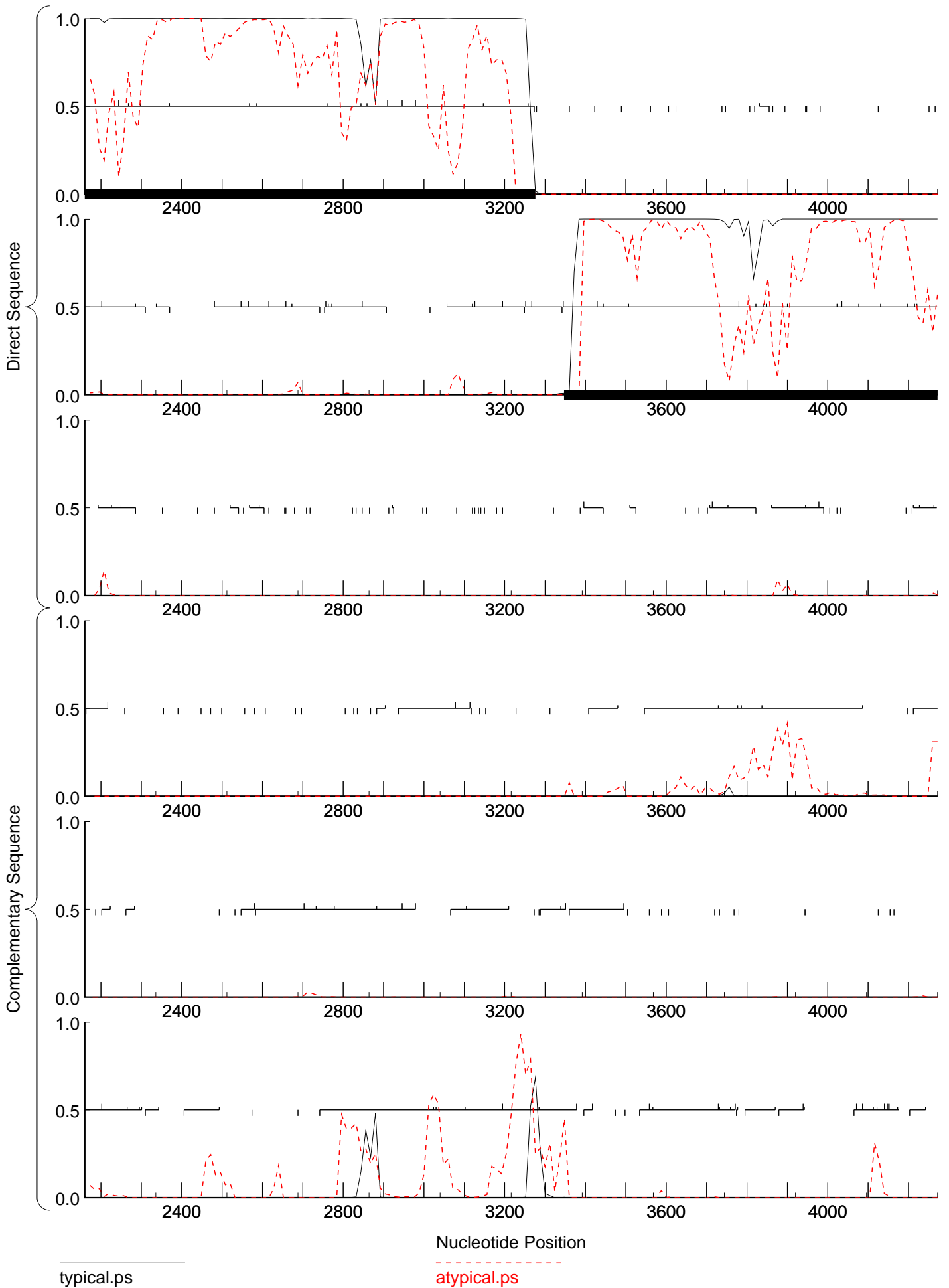
Training set derived by GeneMarkS, 4.30 October 2014  
Thu May 24 03:55:32 2018

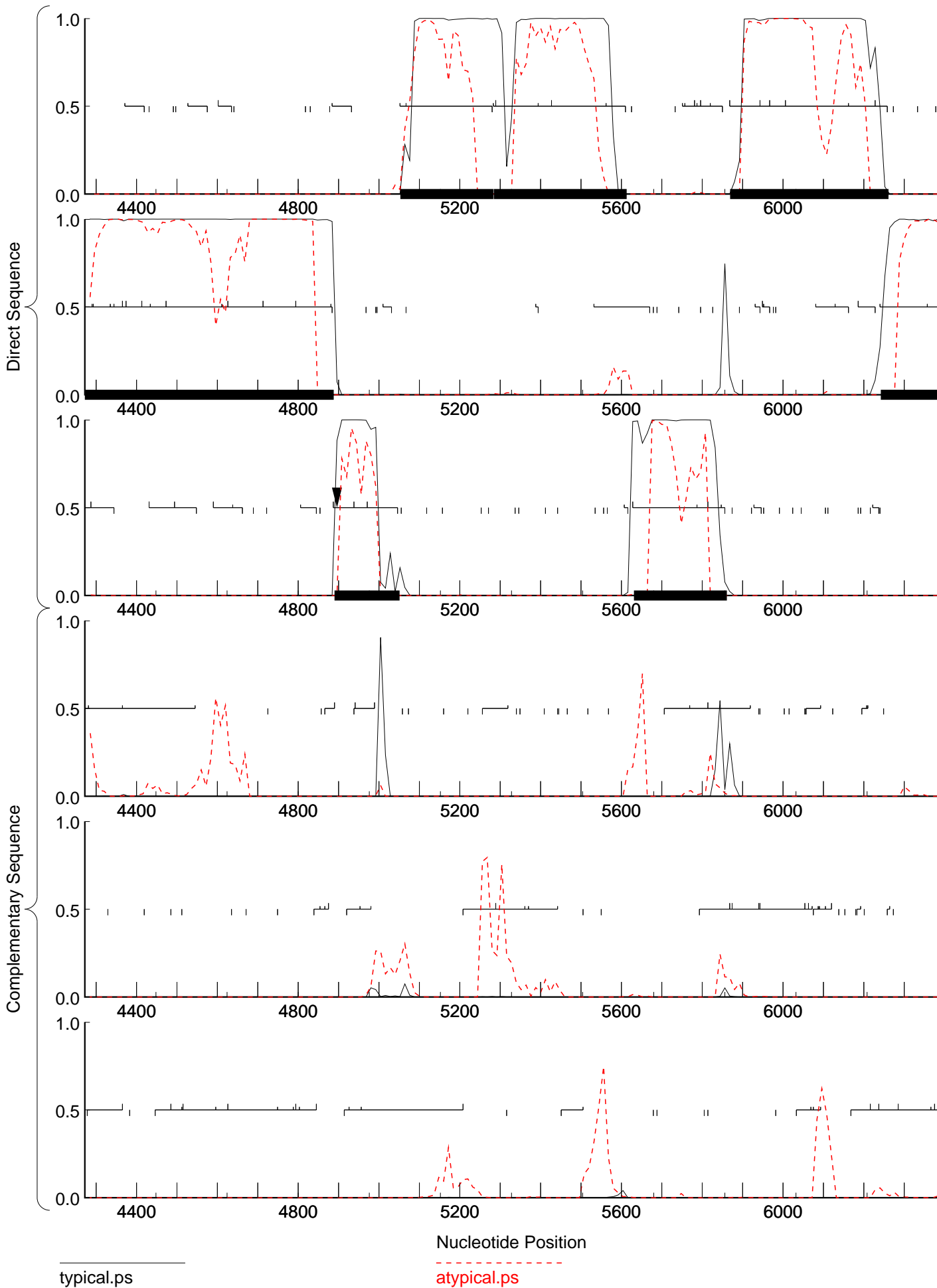
## MATRIX INFORMATION

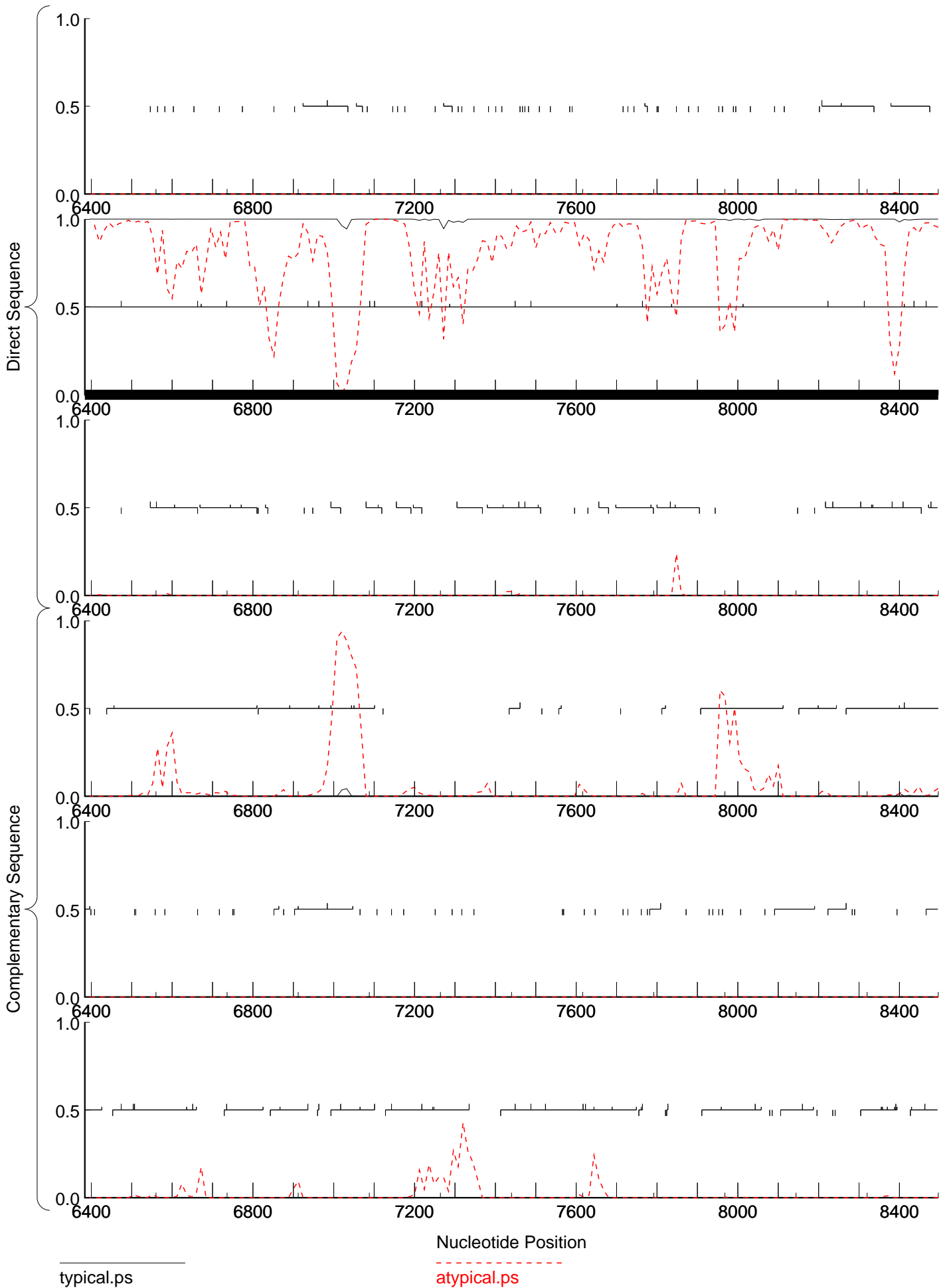
Matrix : -  
Author : -  
Order : 4

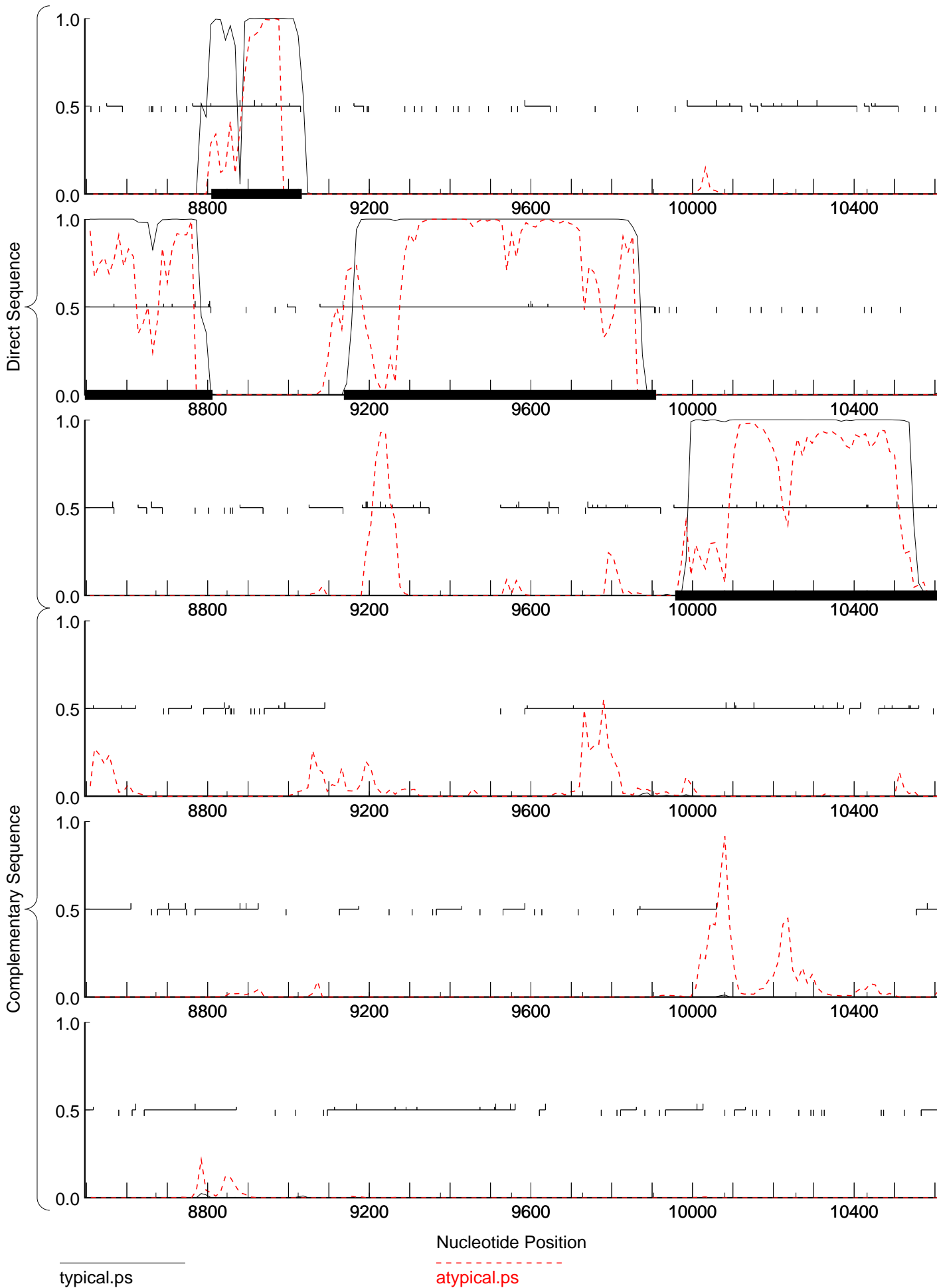
Send questions / comments to:  
Dr. M. Borodovsky  
Georgia Institute of Technology  
School of Biology  
Atlanta, GA 30332-0230

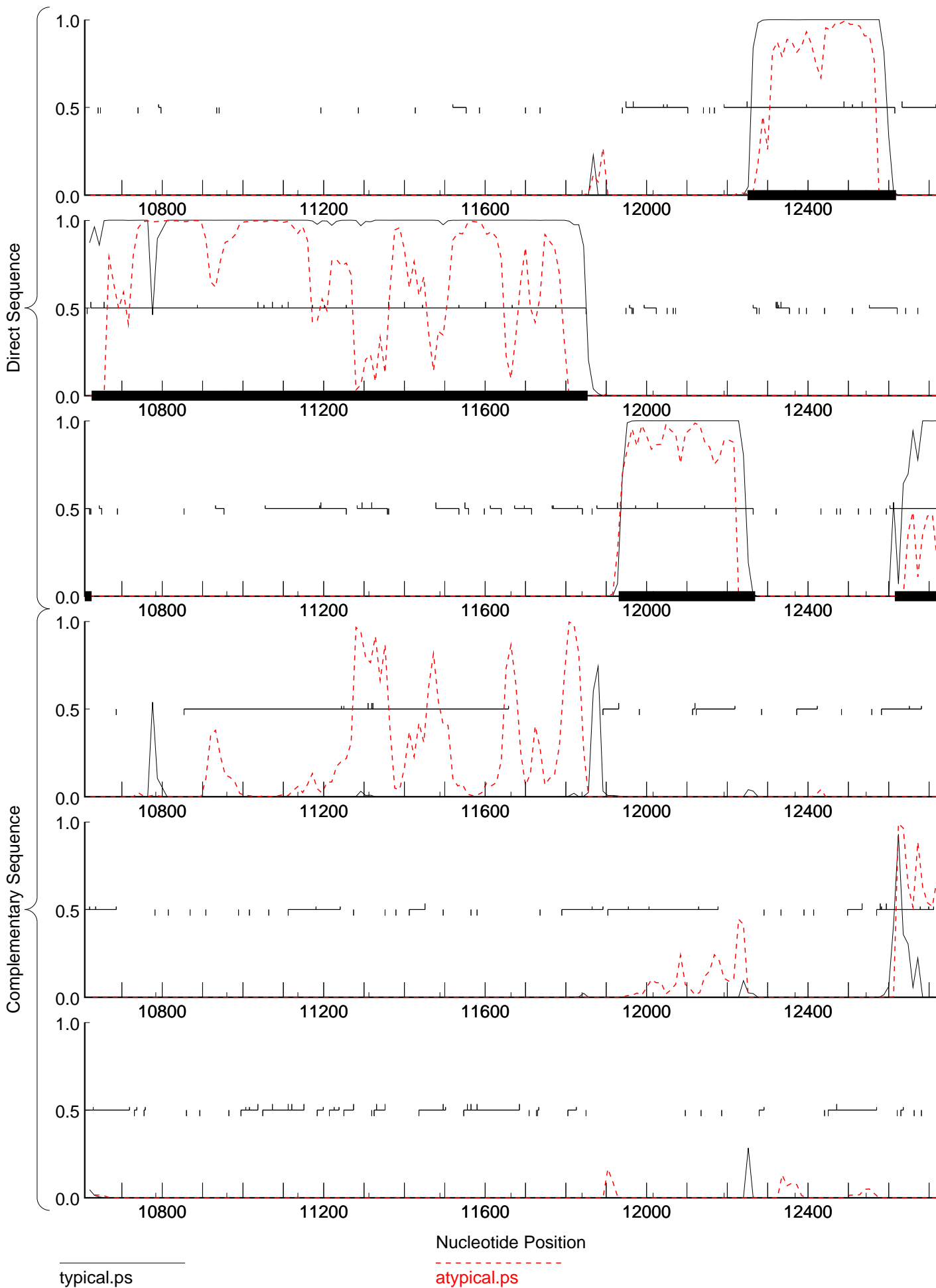


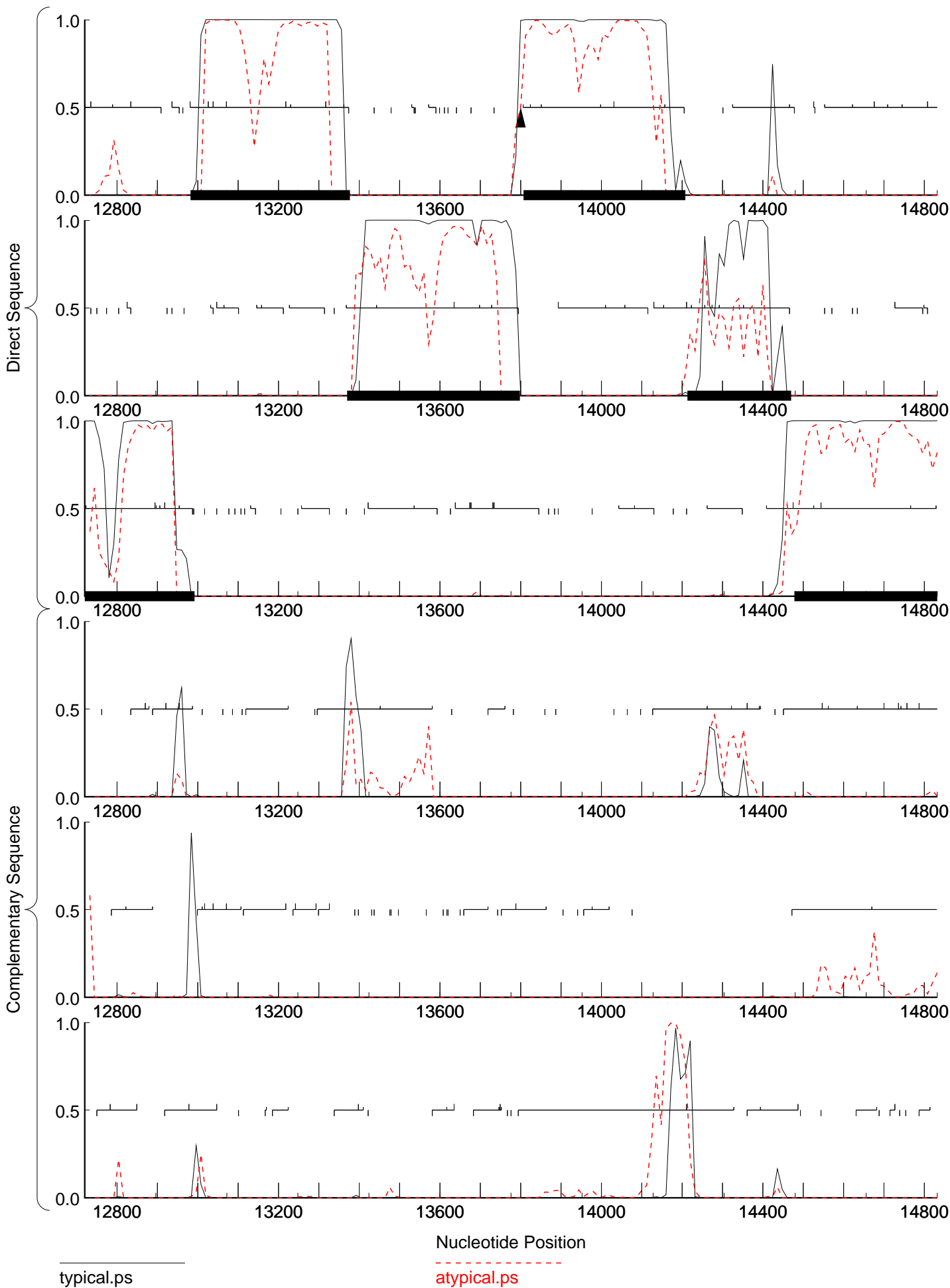








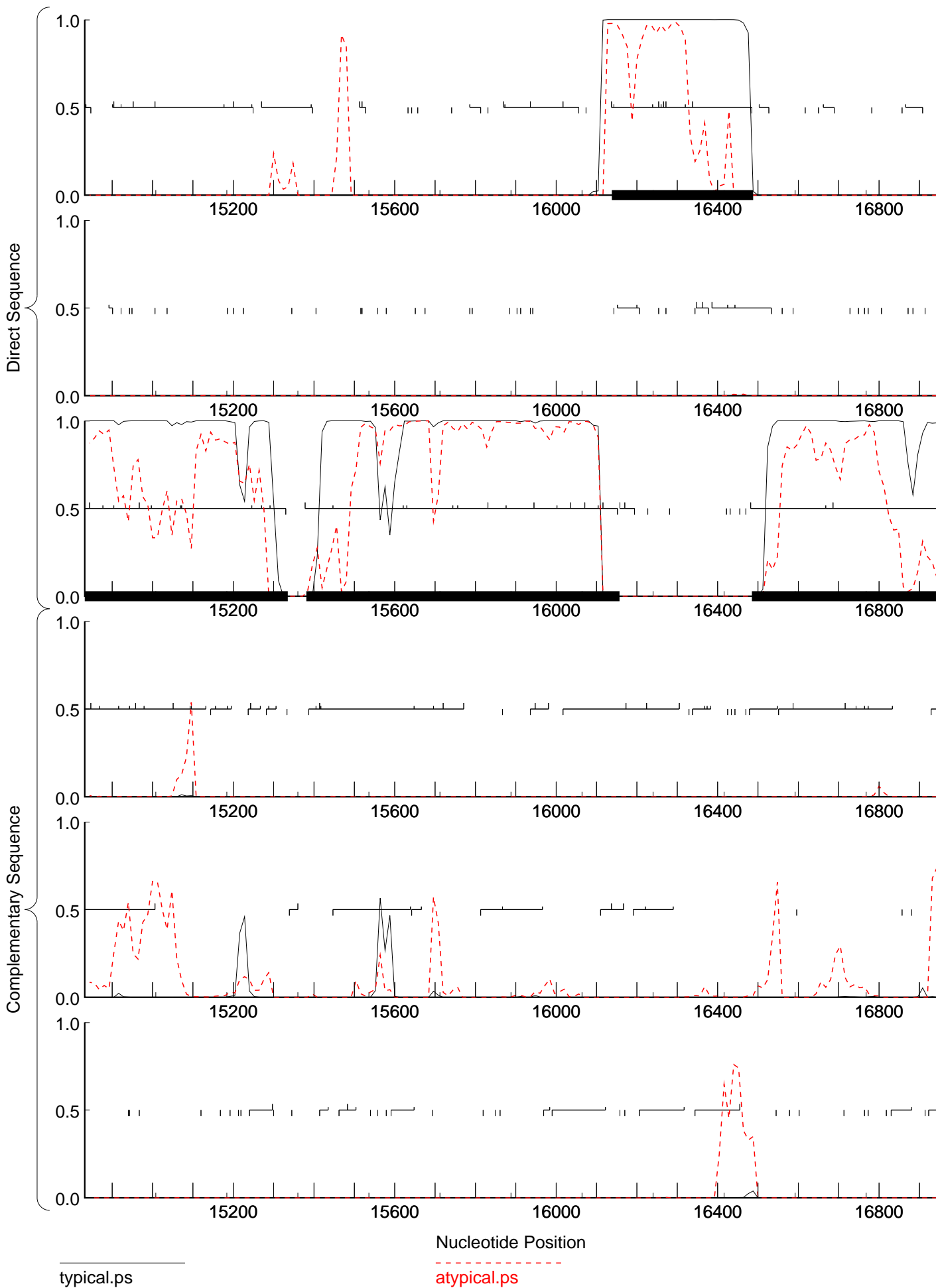




typical.ps

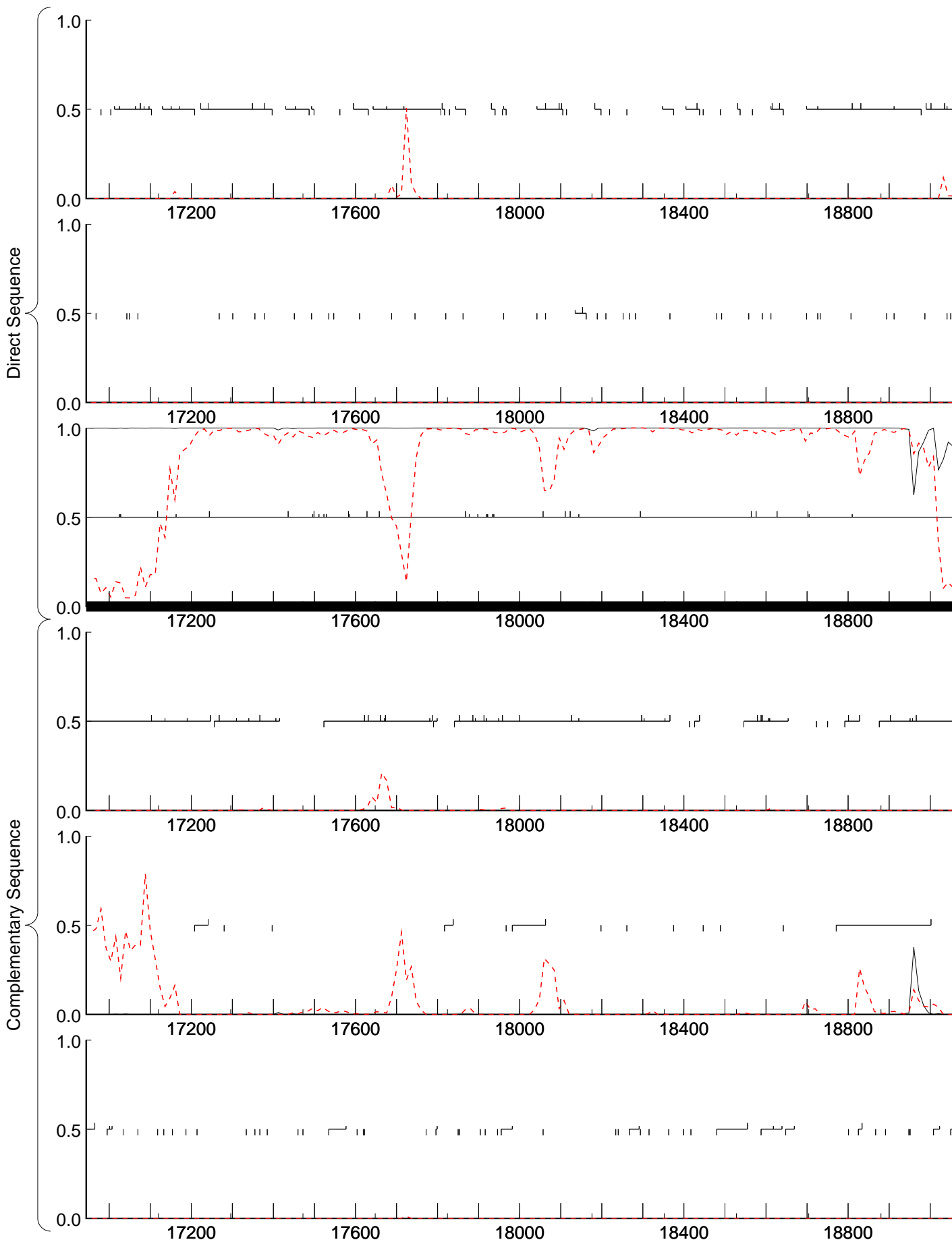
atypical.ps





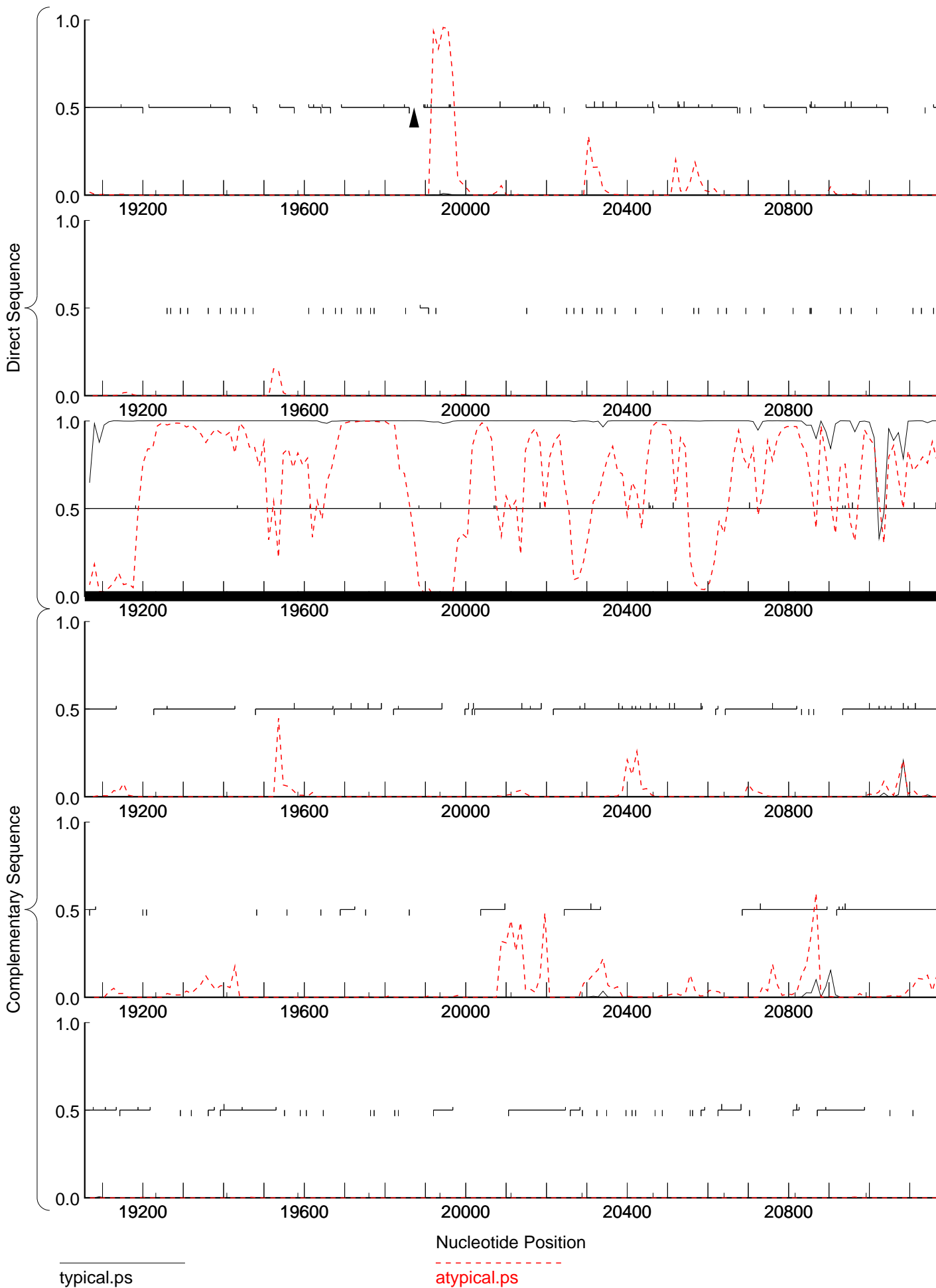
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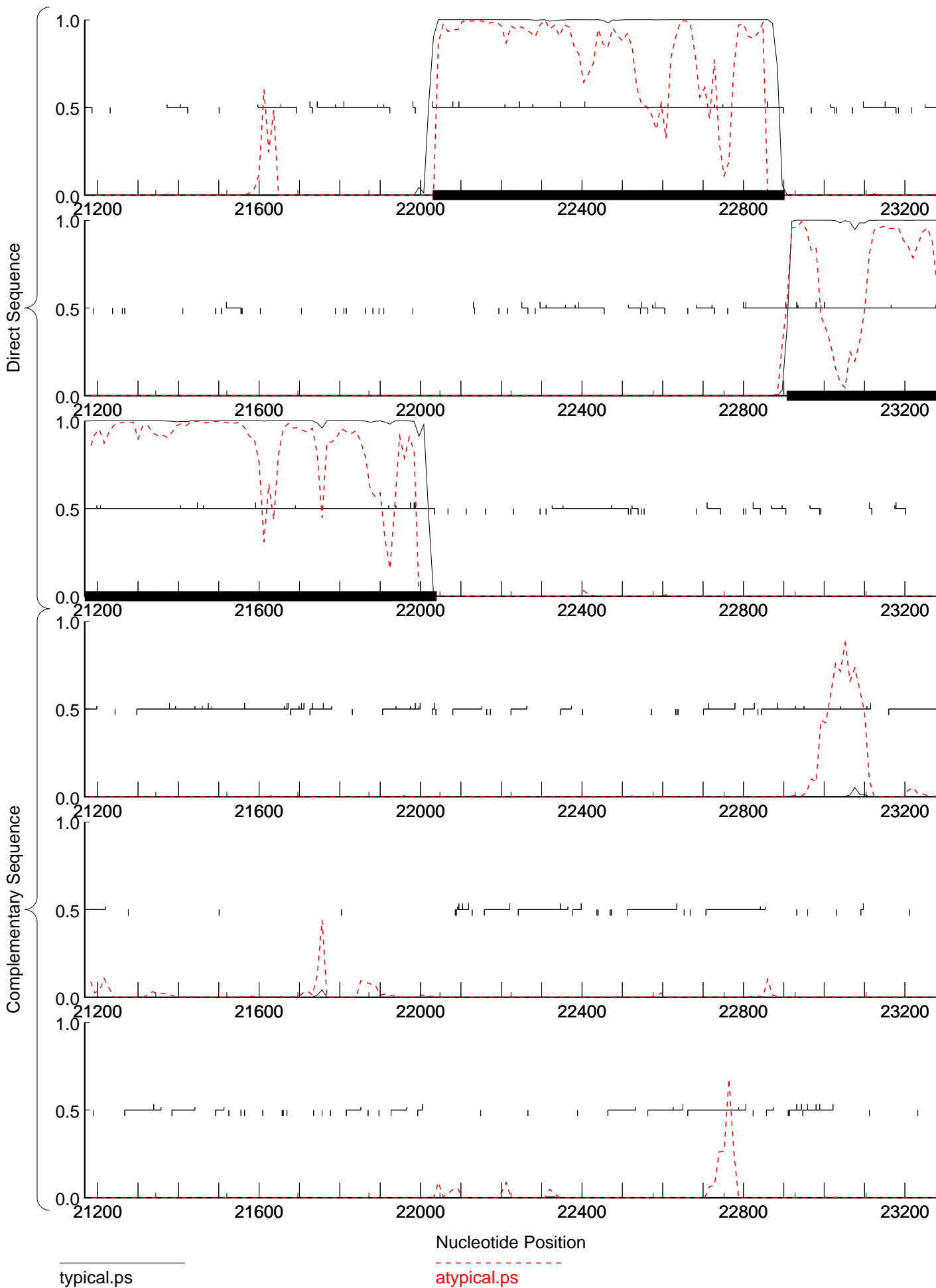
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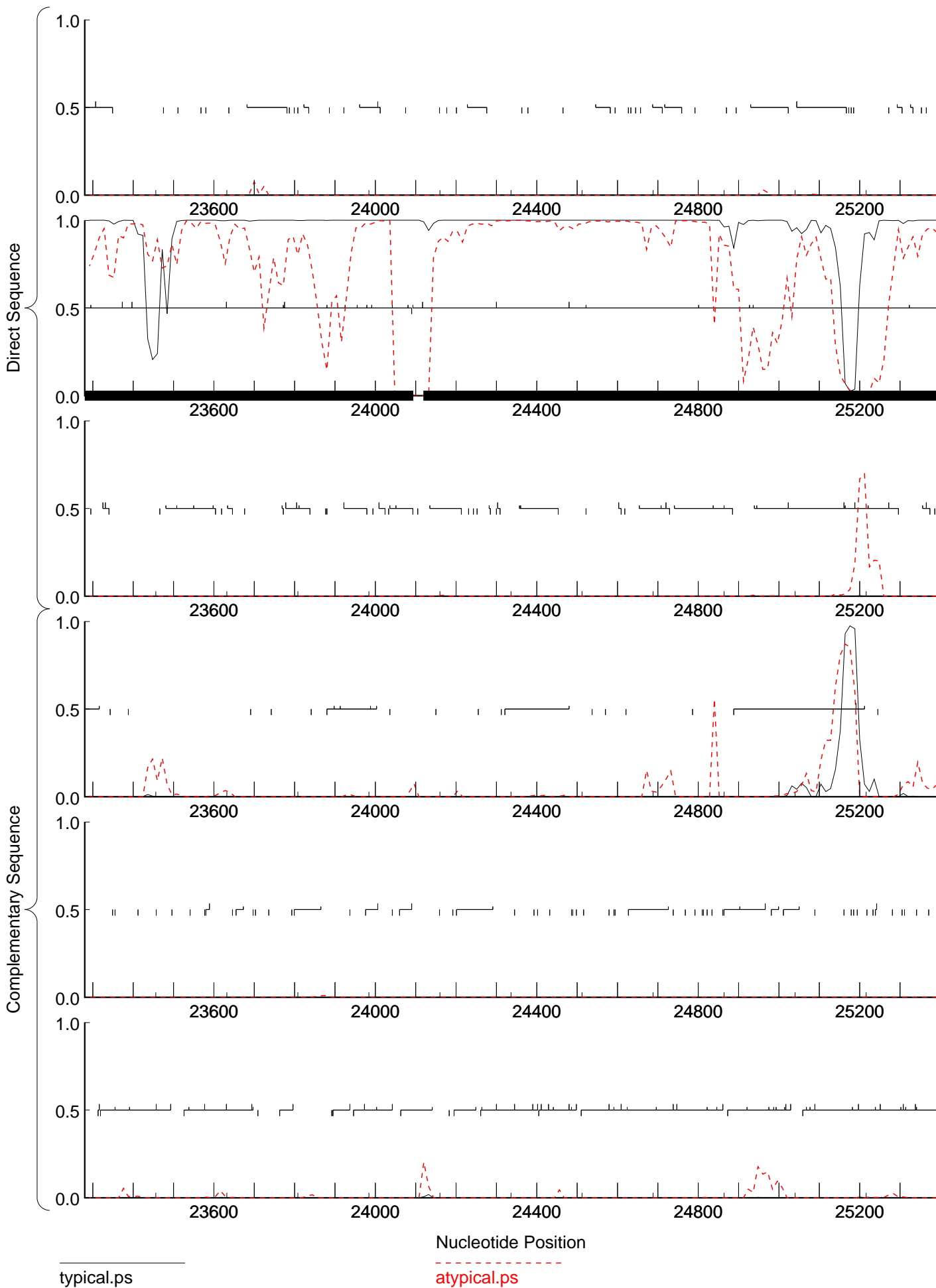


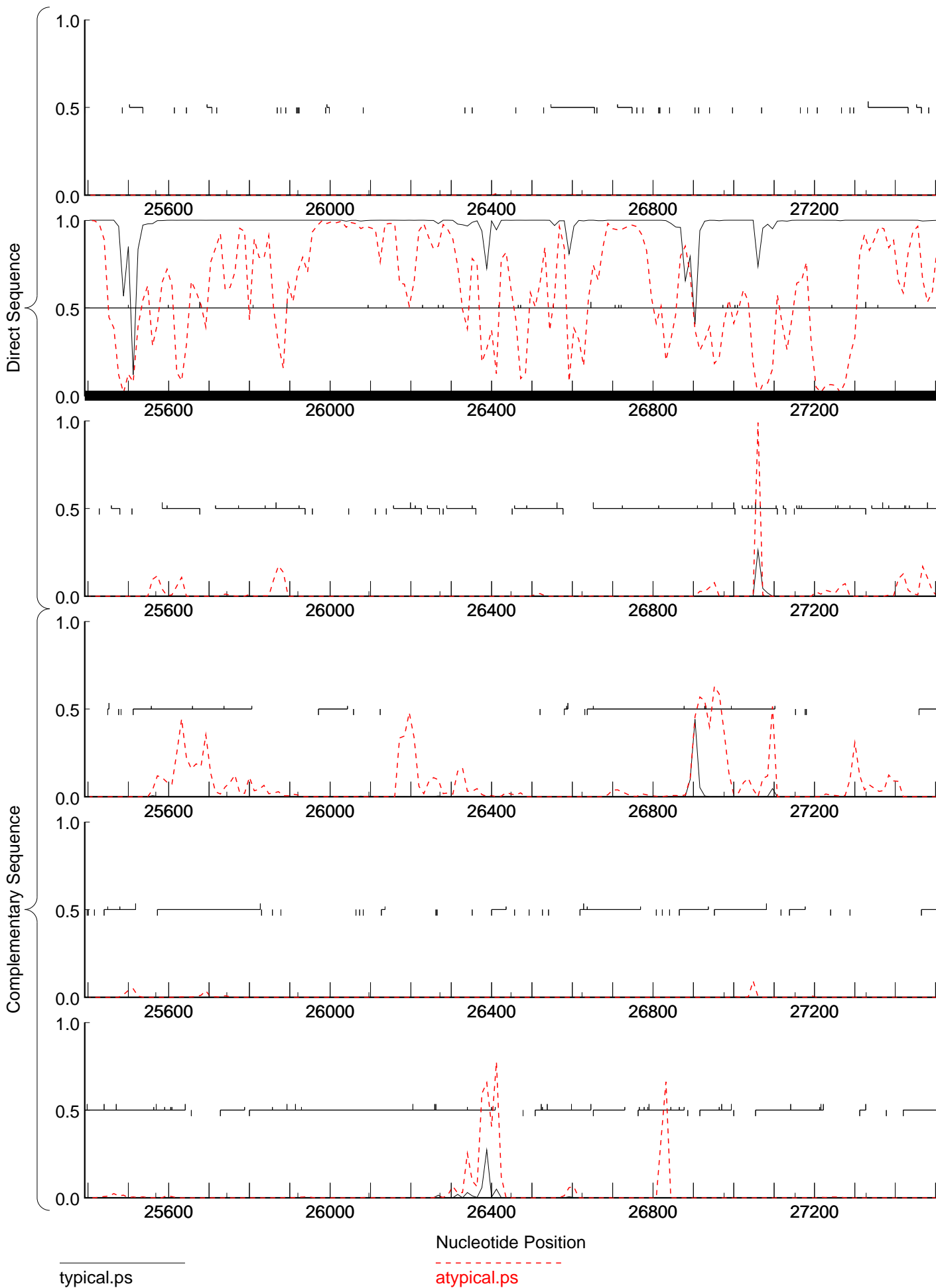
typical.ps

atypical.ps



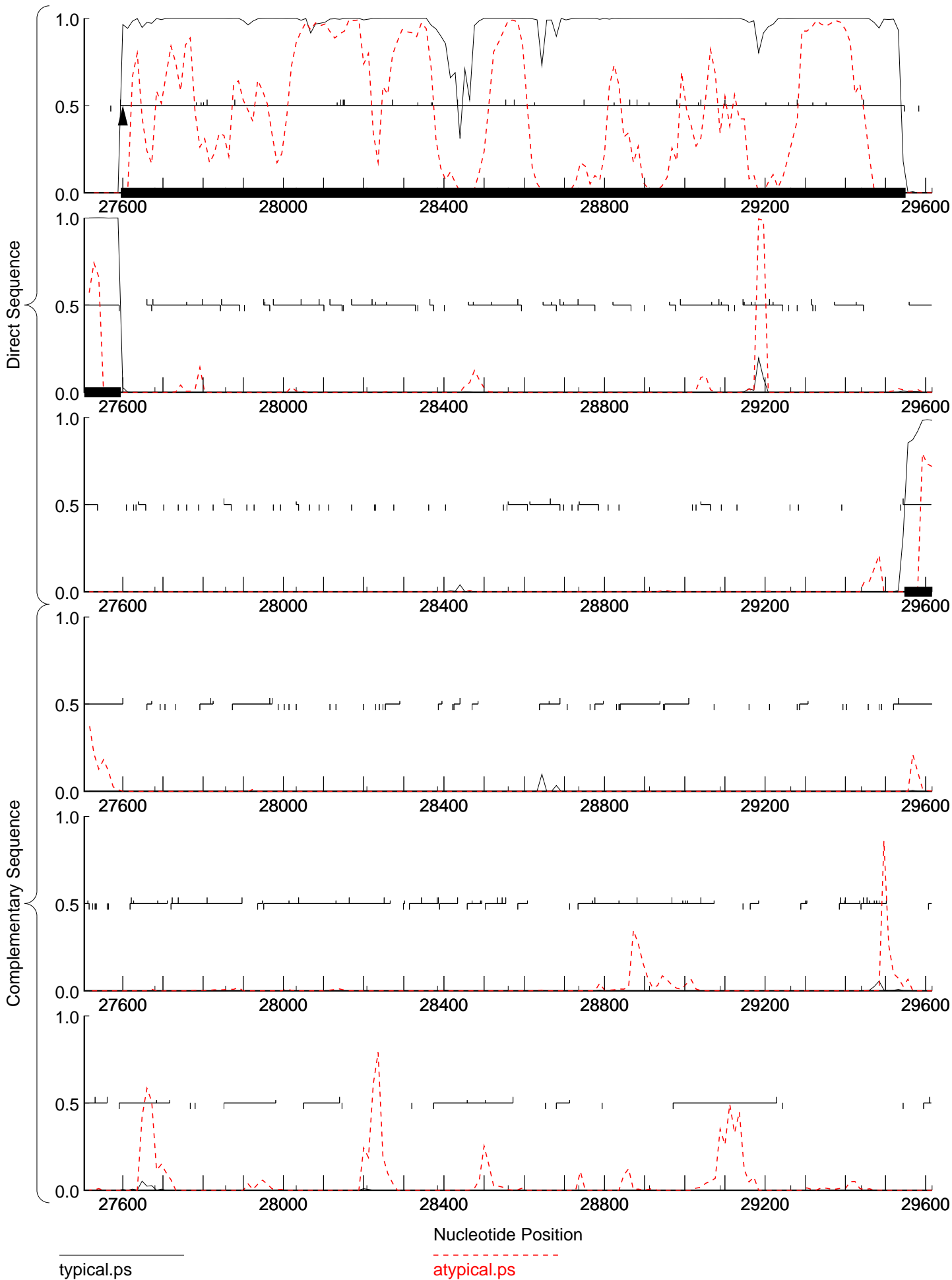






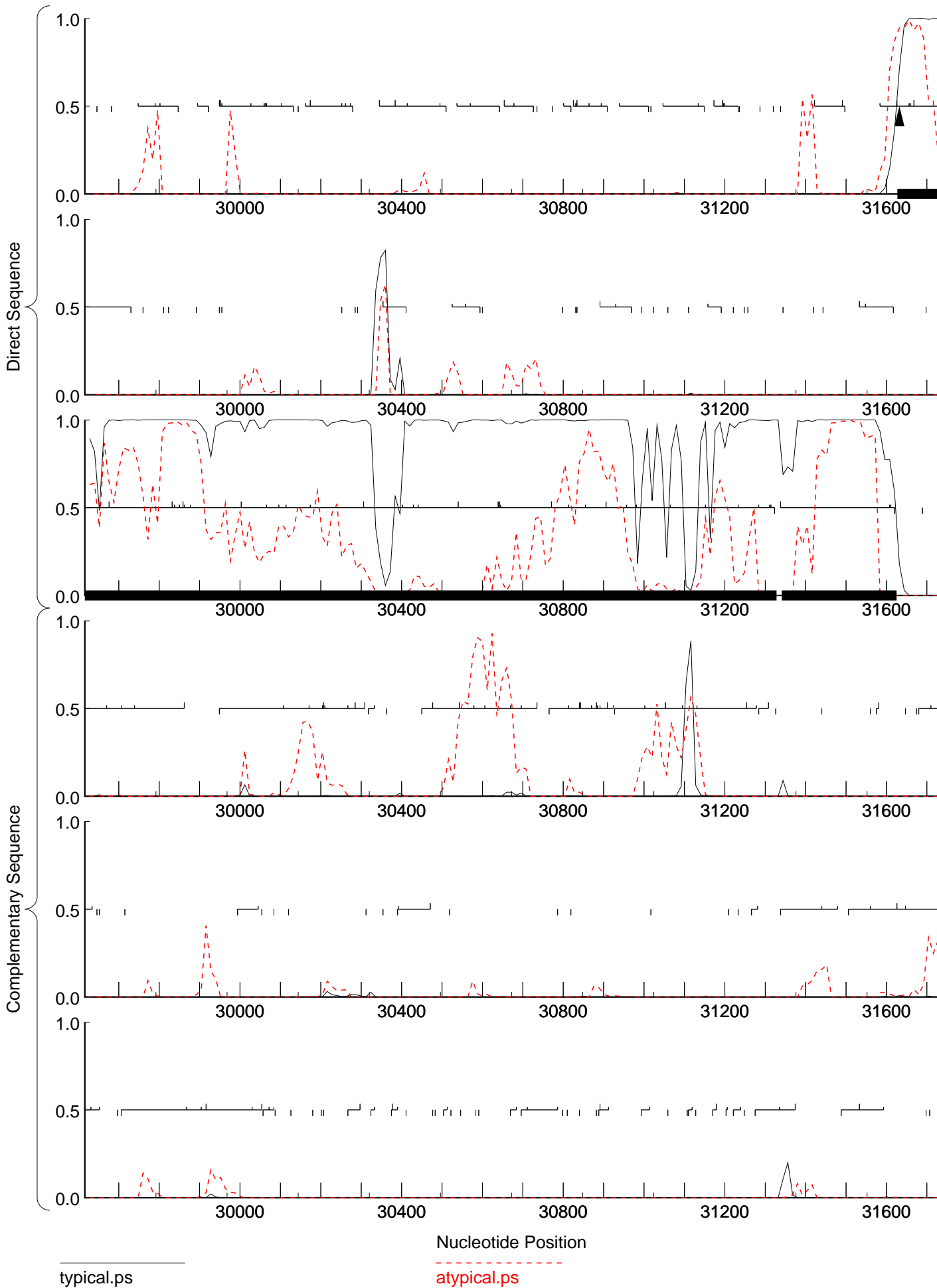
typical.ps

atypical.ps



typical.ps

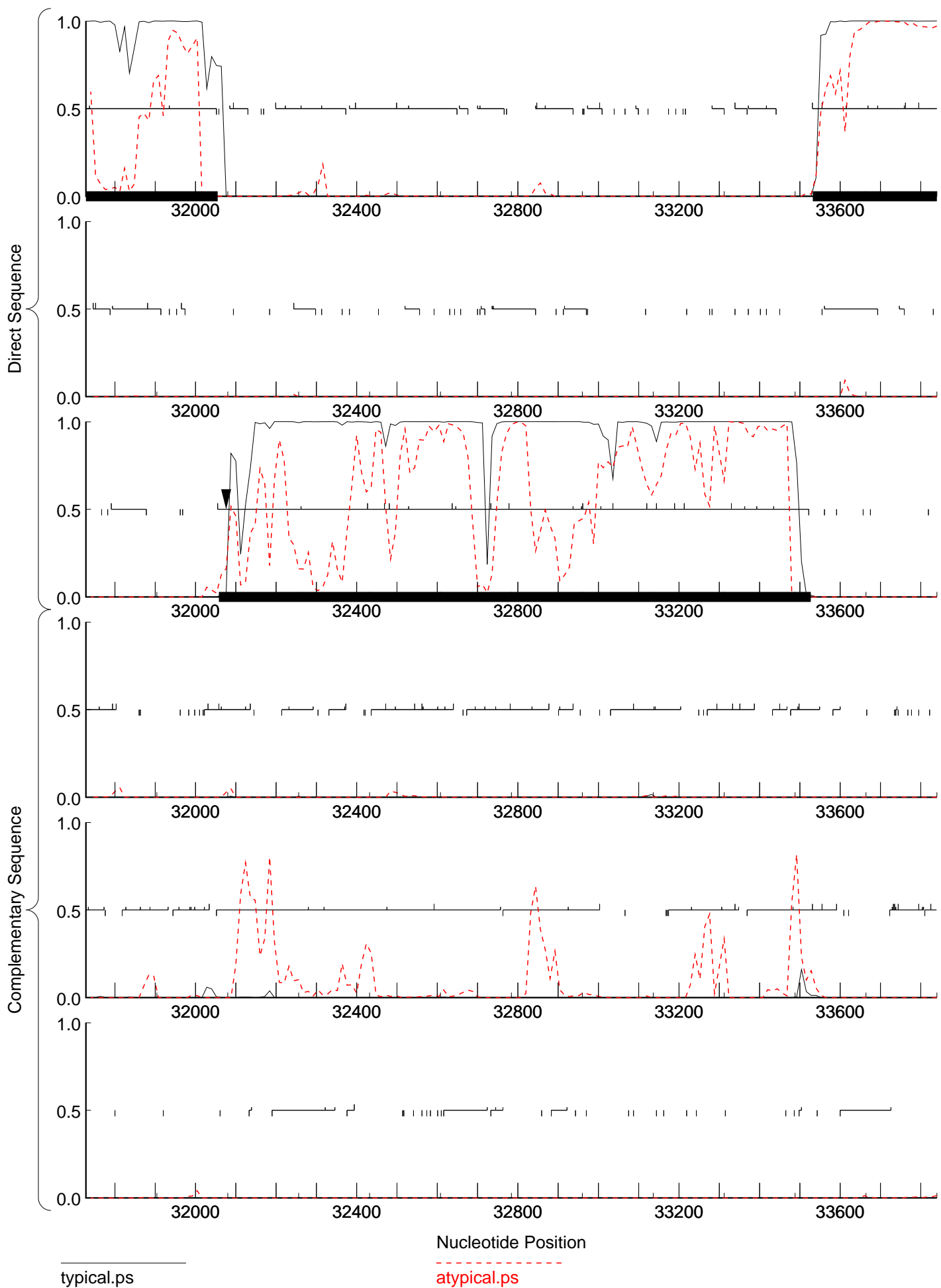
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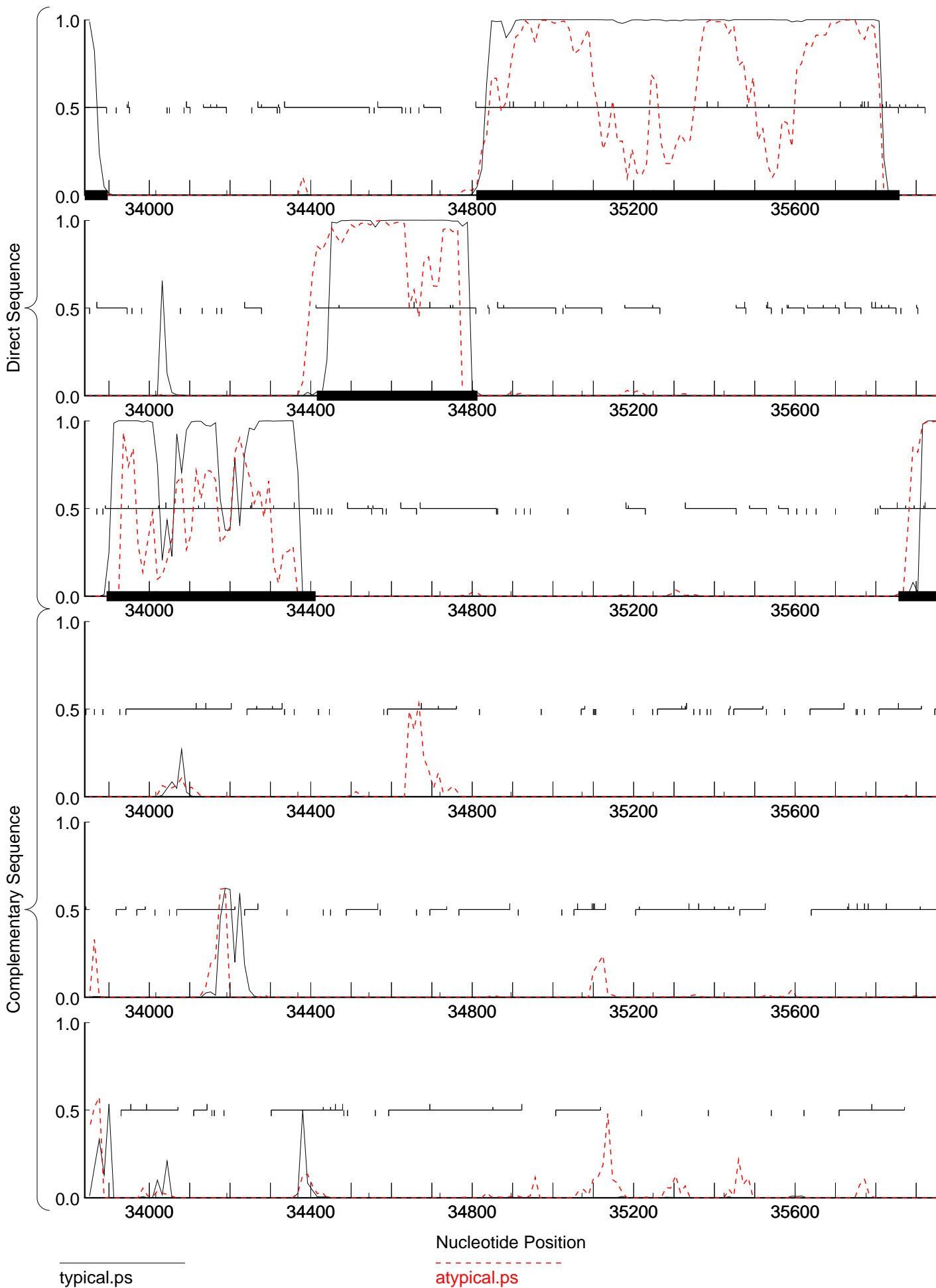


typical.ps

atypical.ps

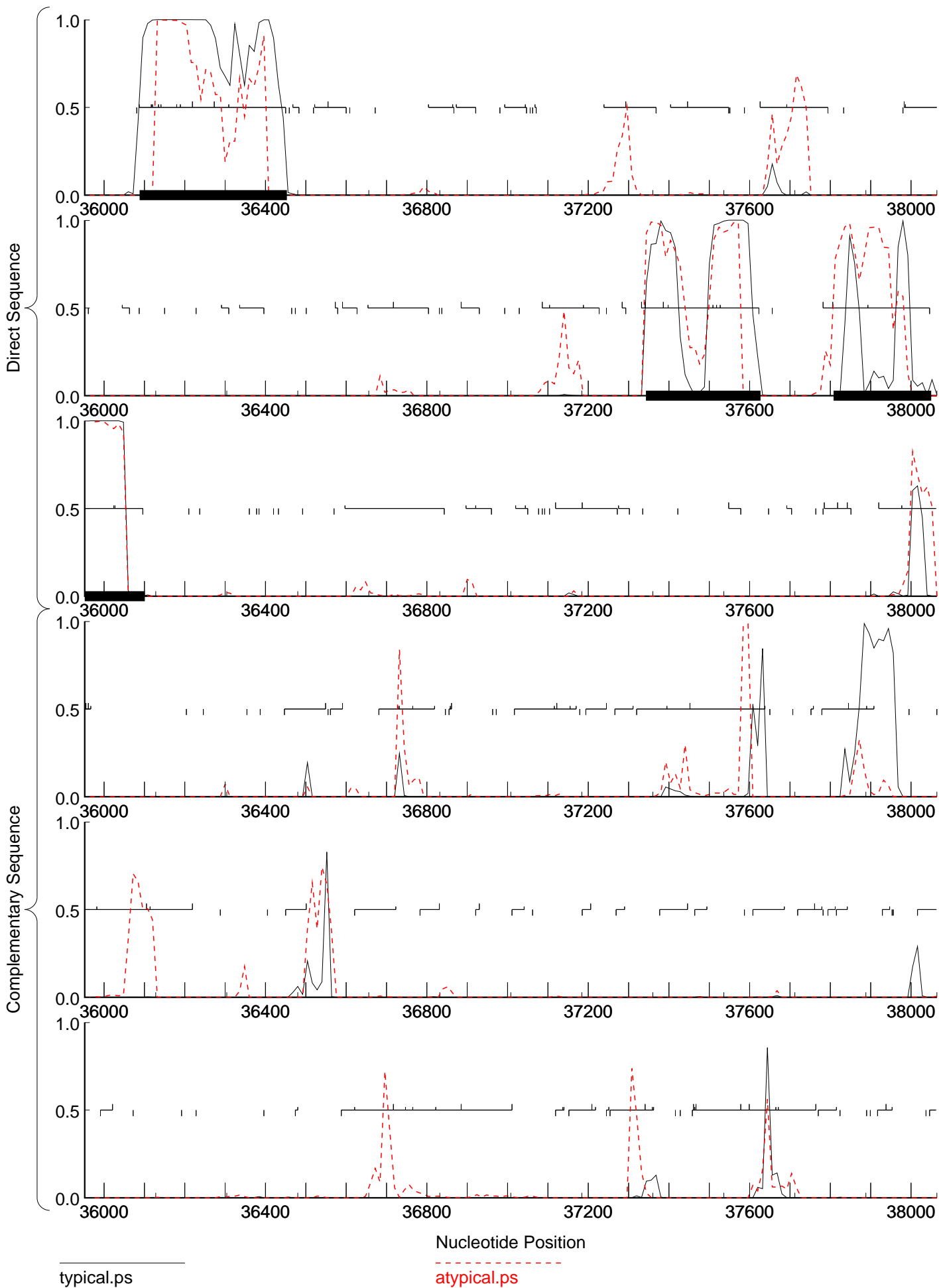






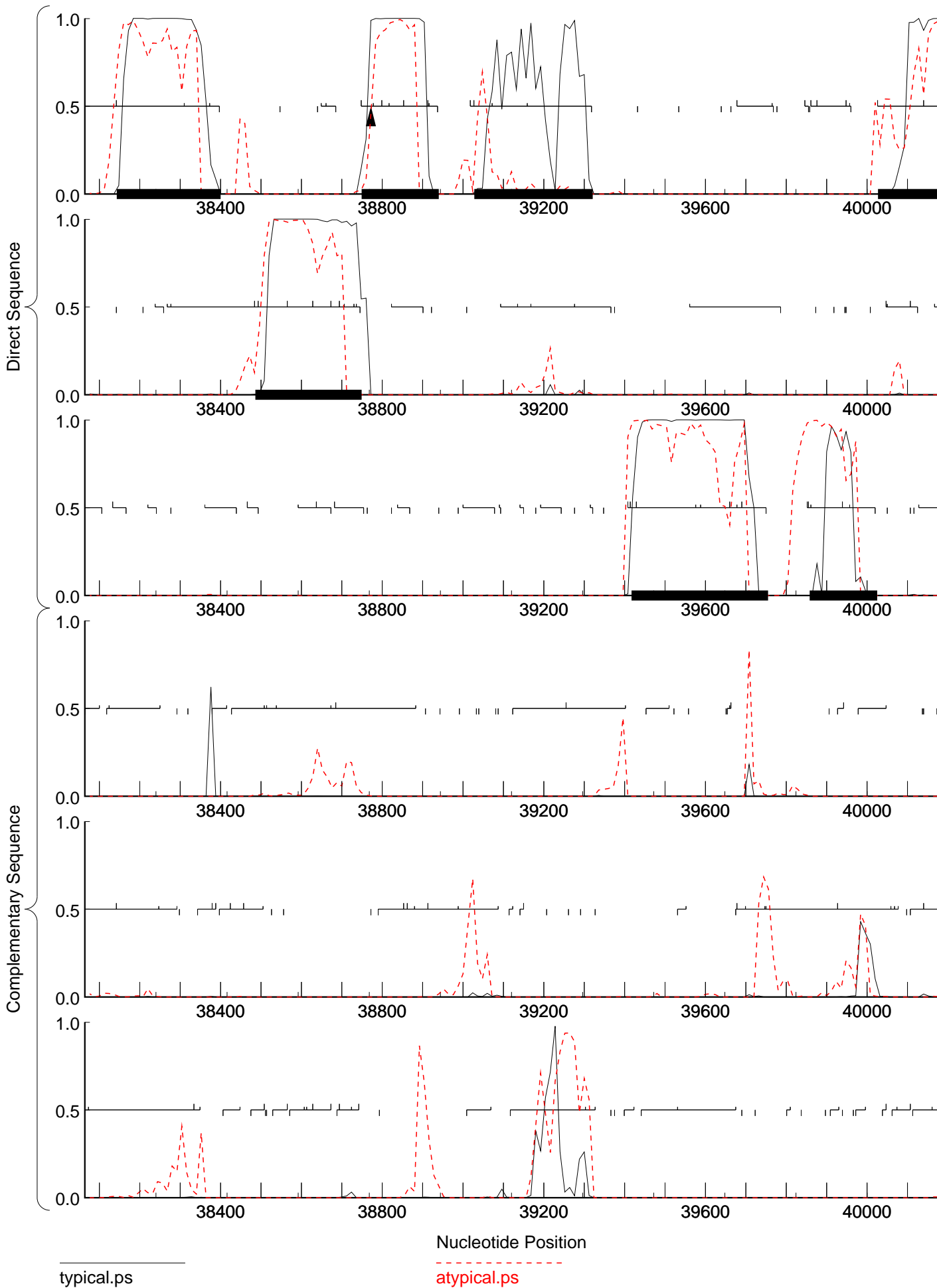
typical.ps

atypical.ps



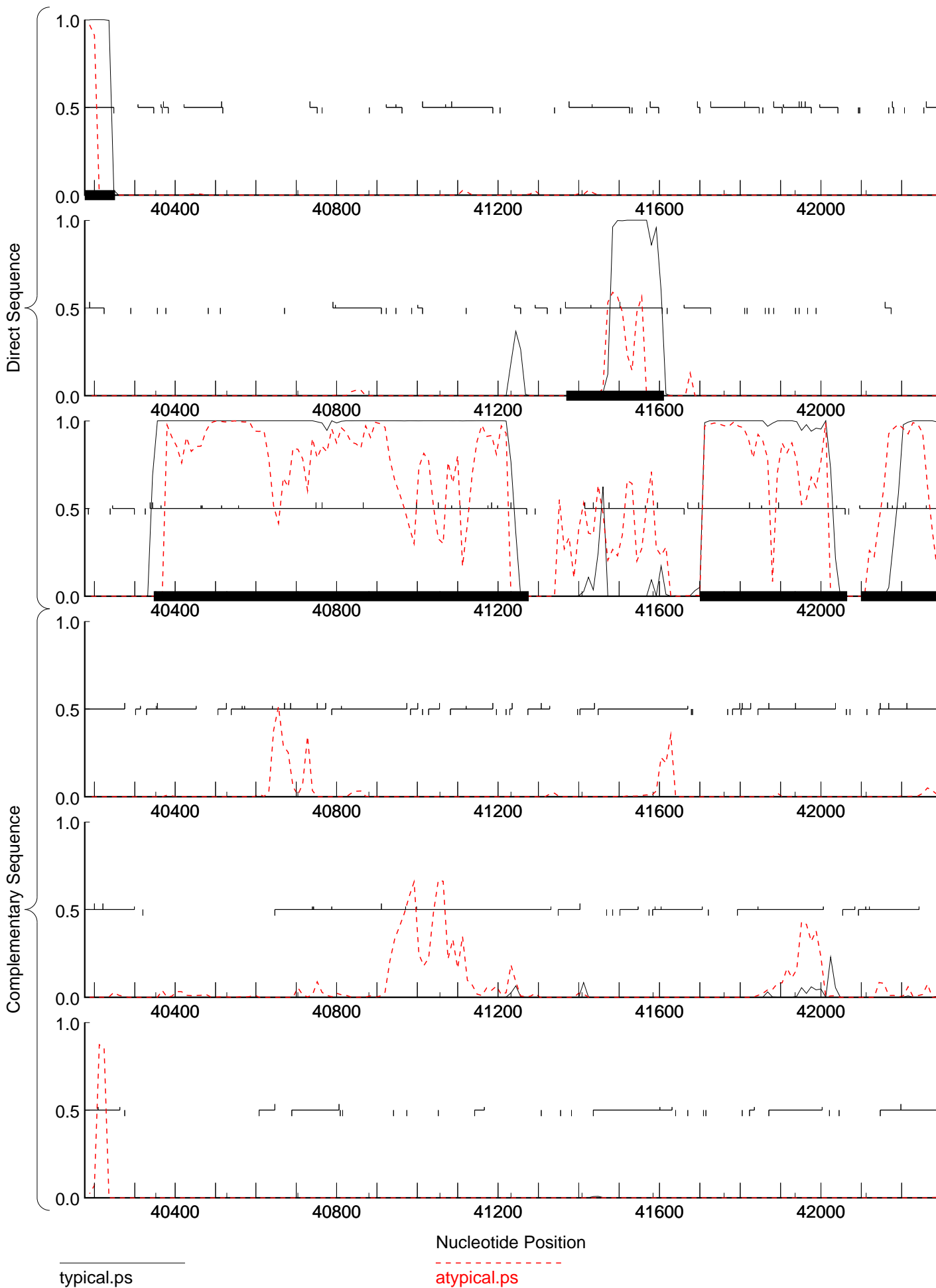
typical.ps

atypical.ps



typical.ps

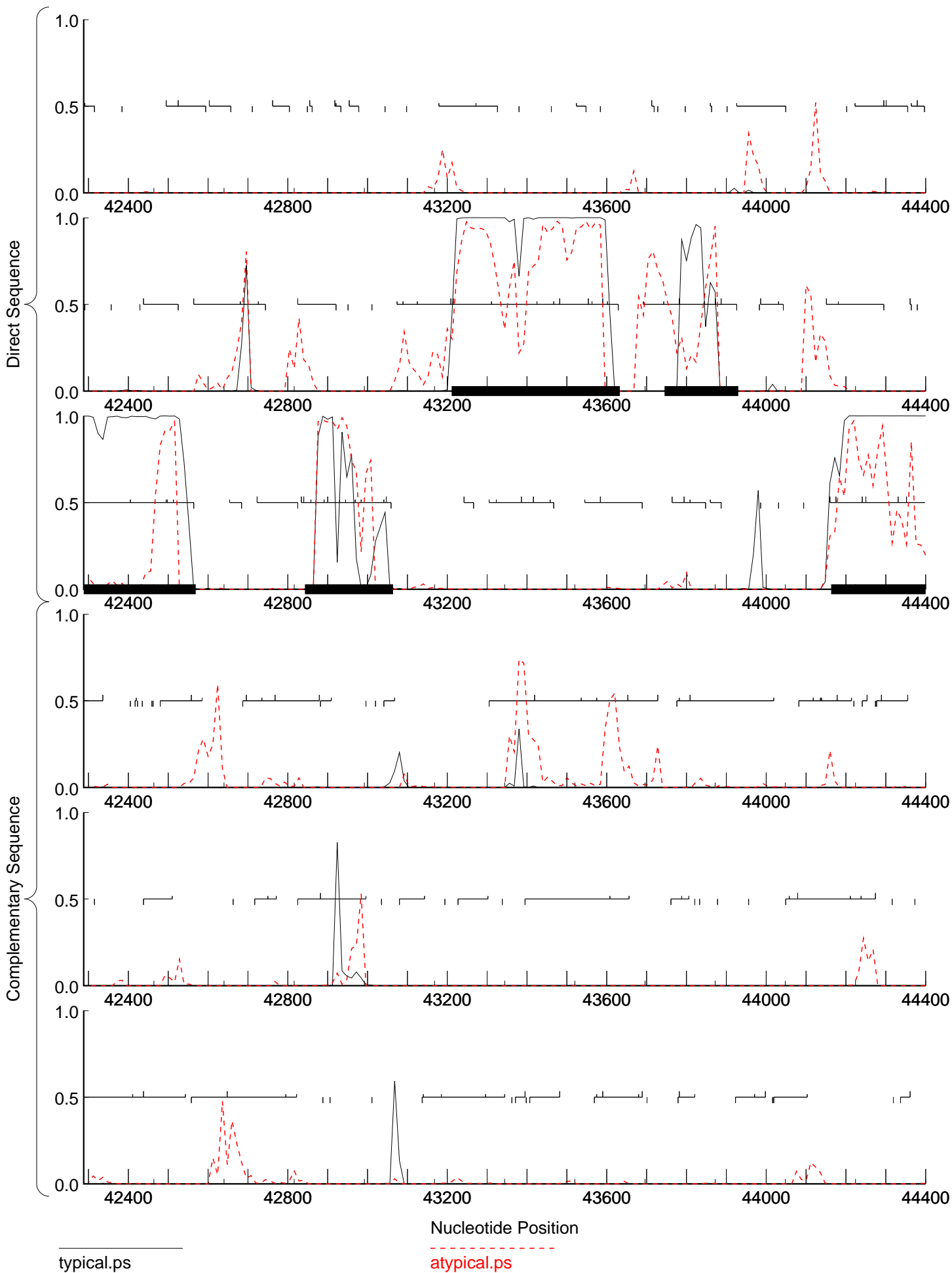
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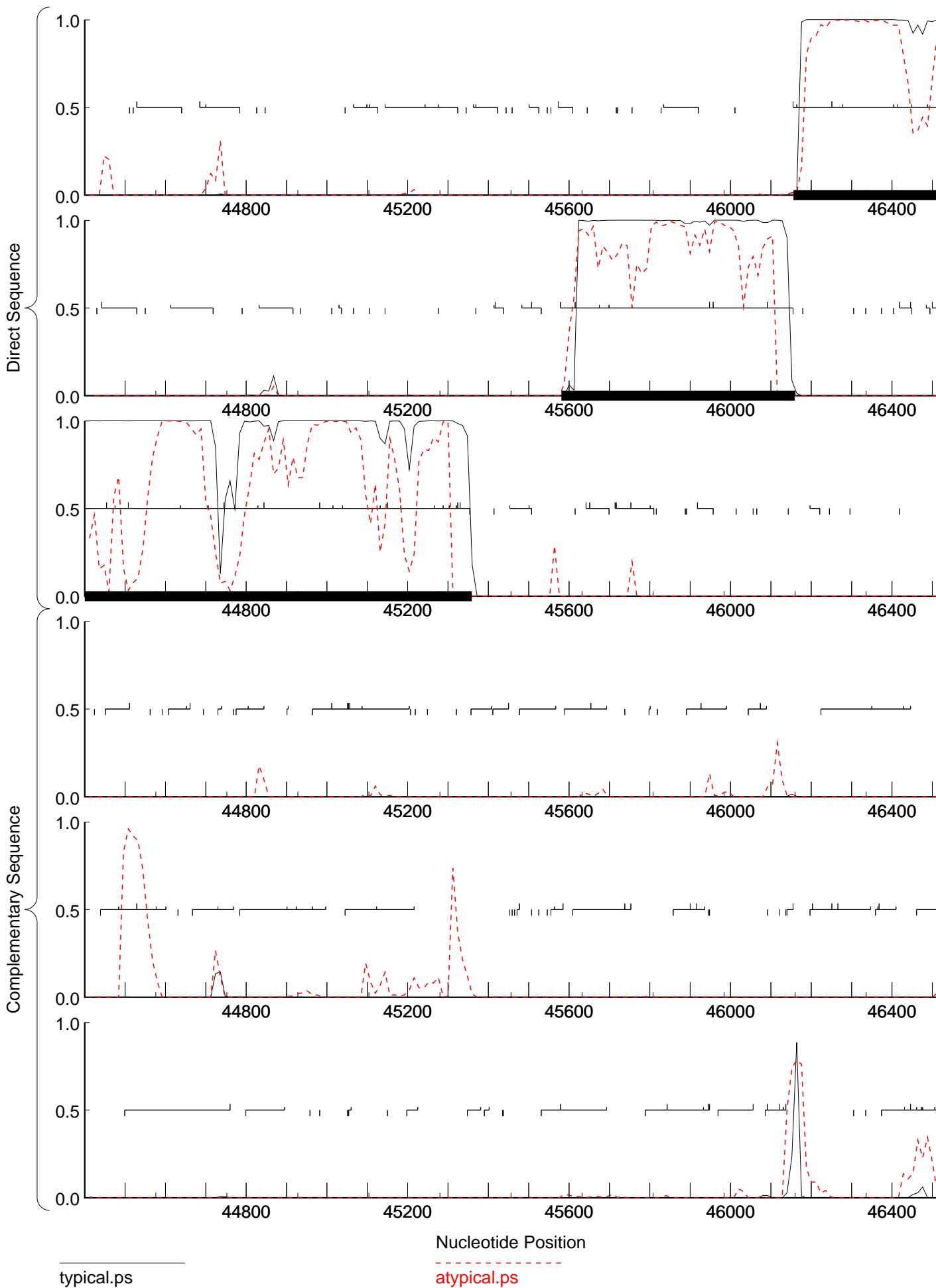


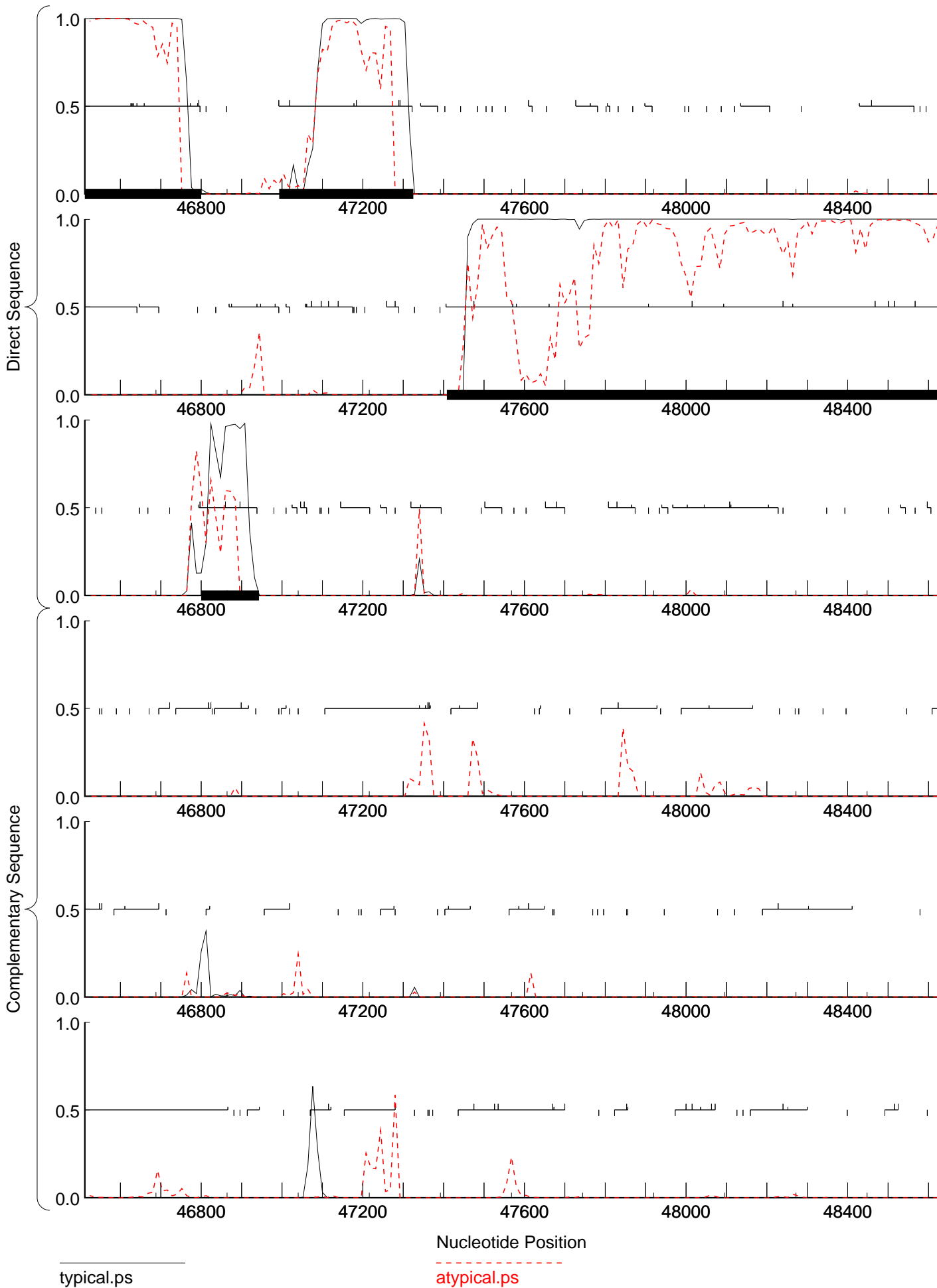
typical.ps

Nucleotide Position

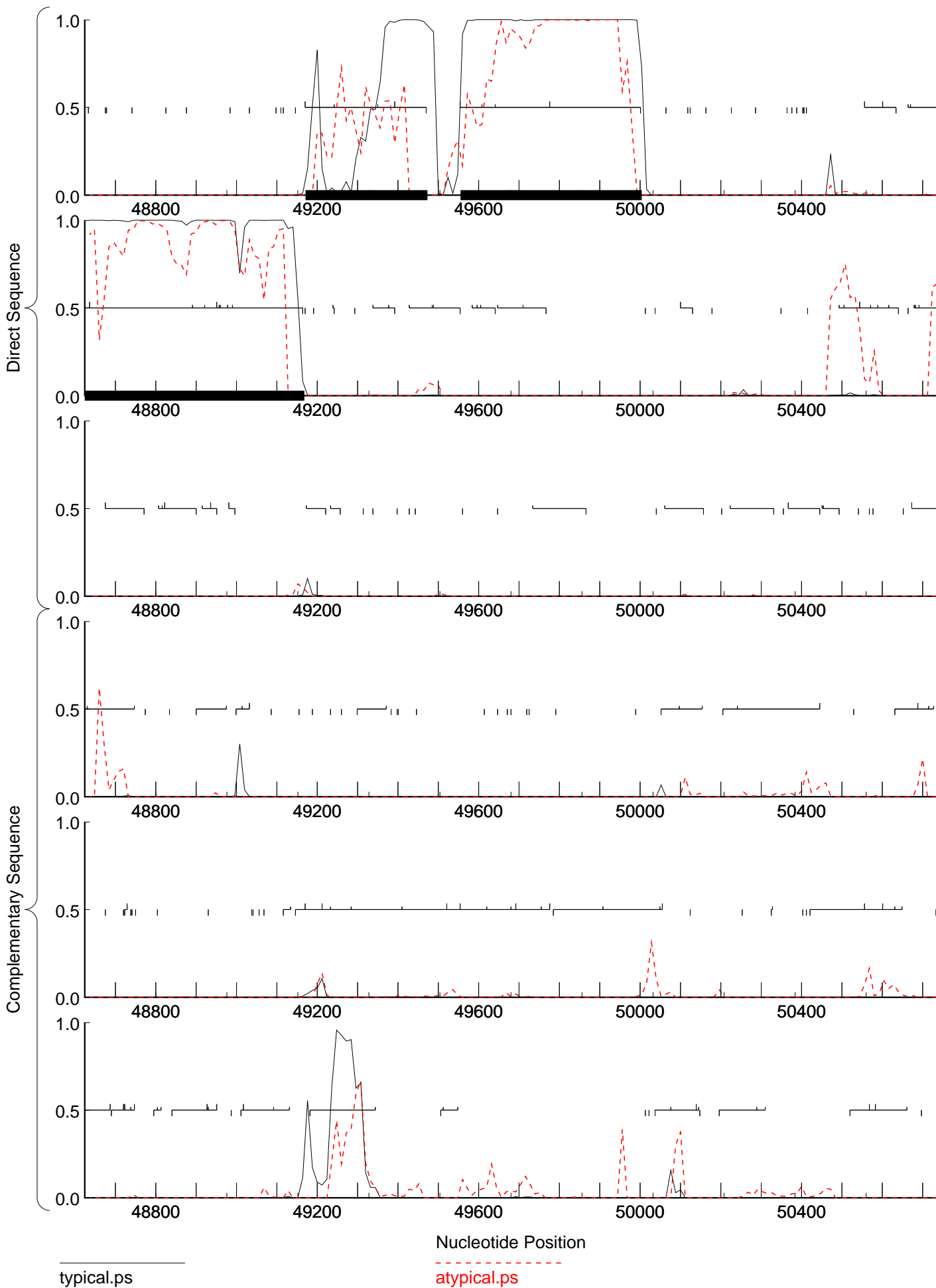
atypical.ps





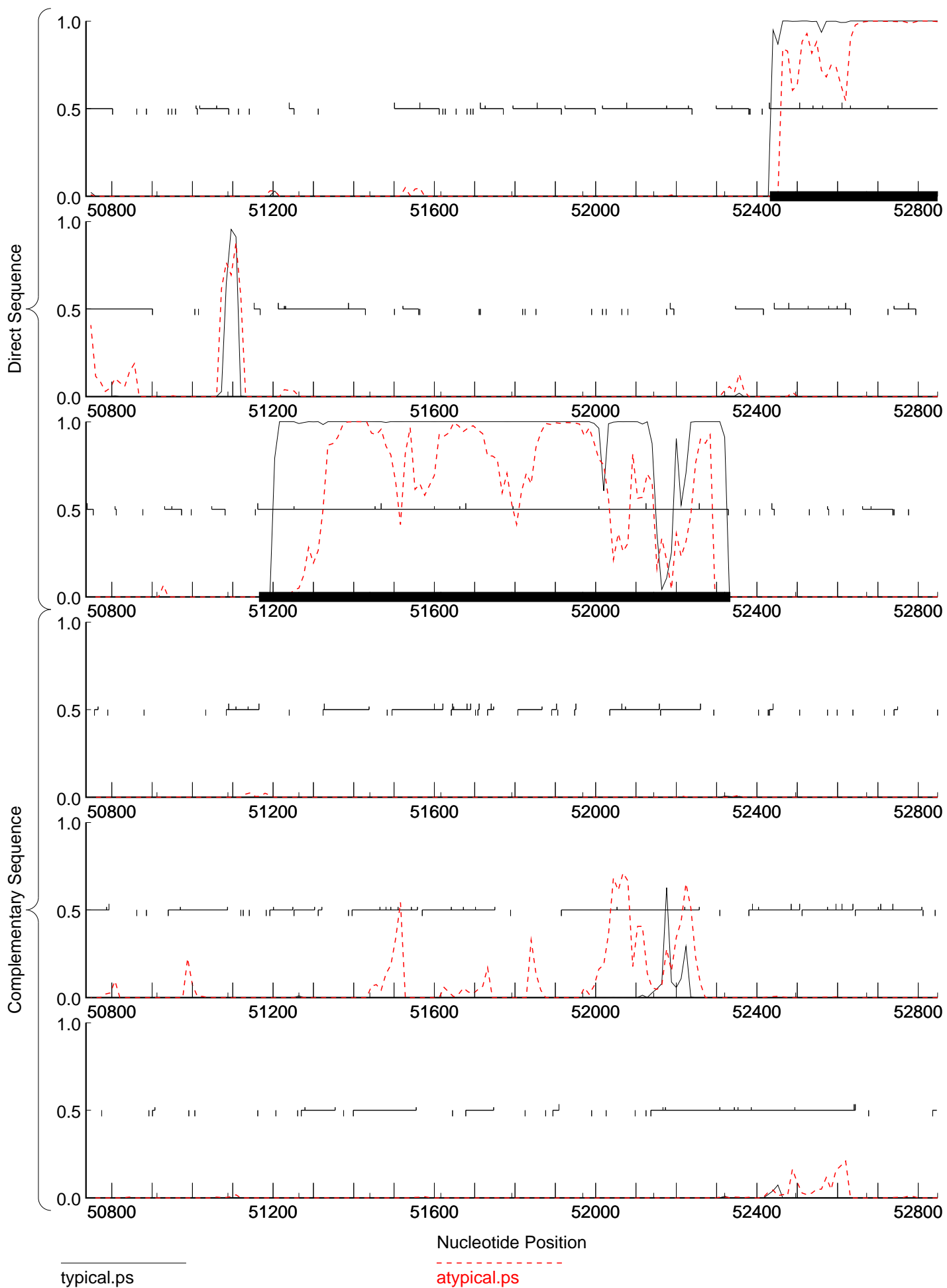


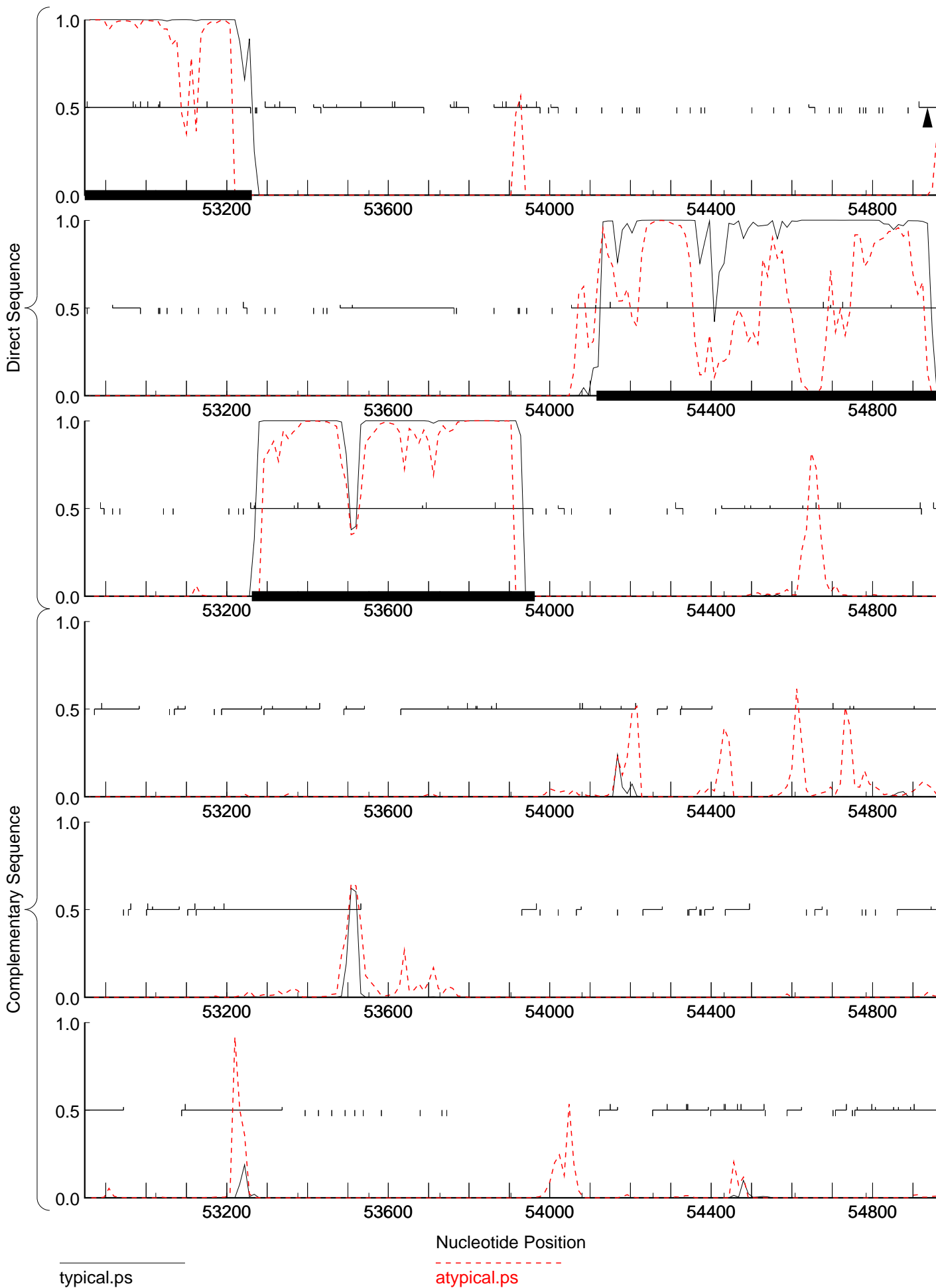


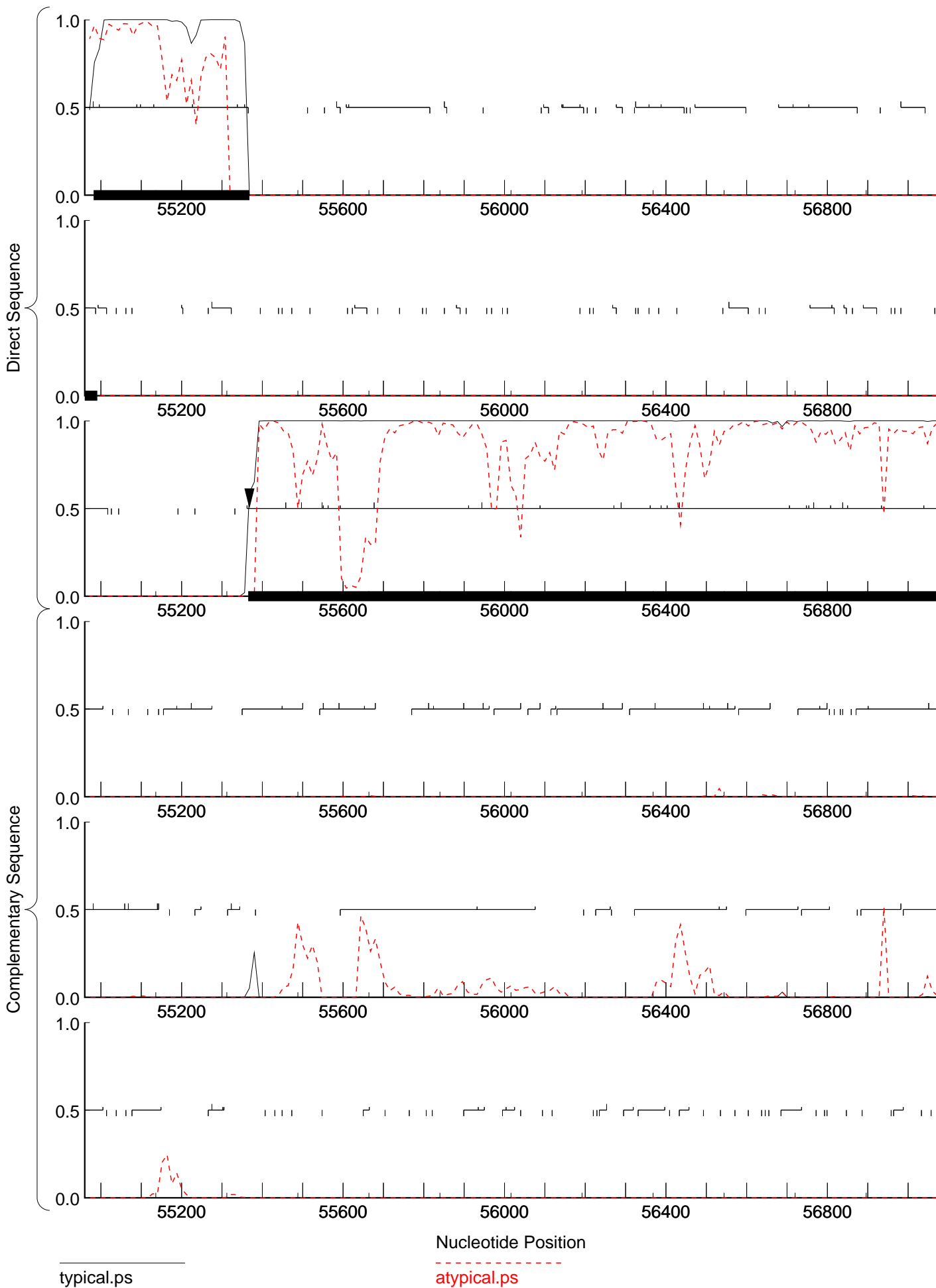


typical.ps

atypical.ps



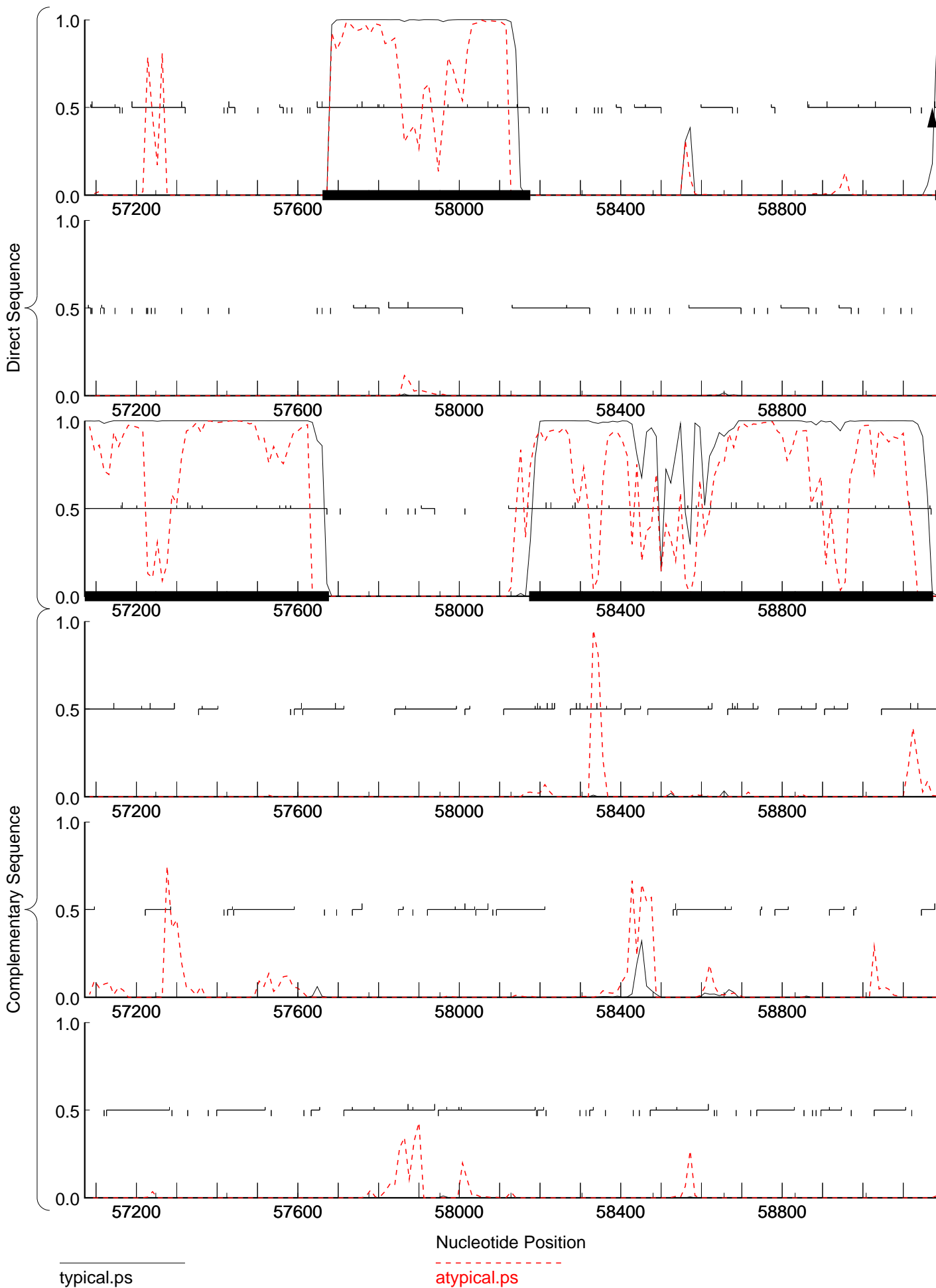




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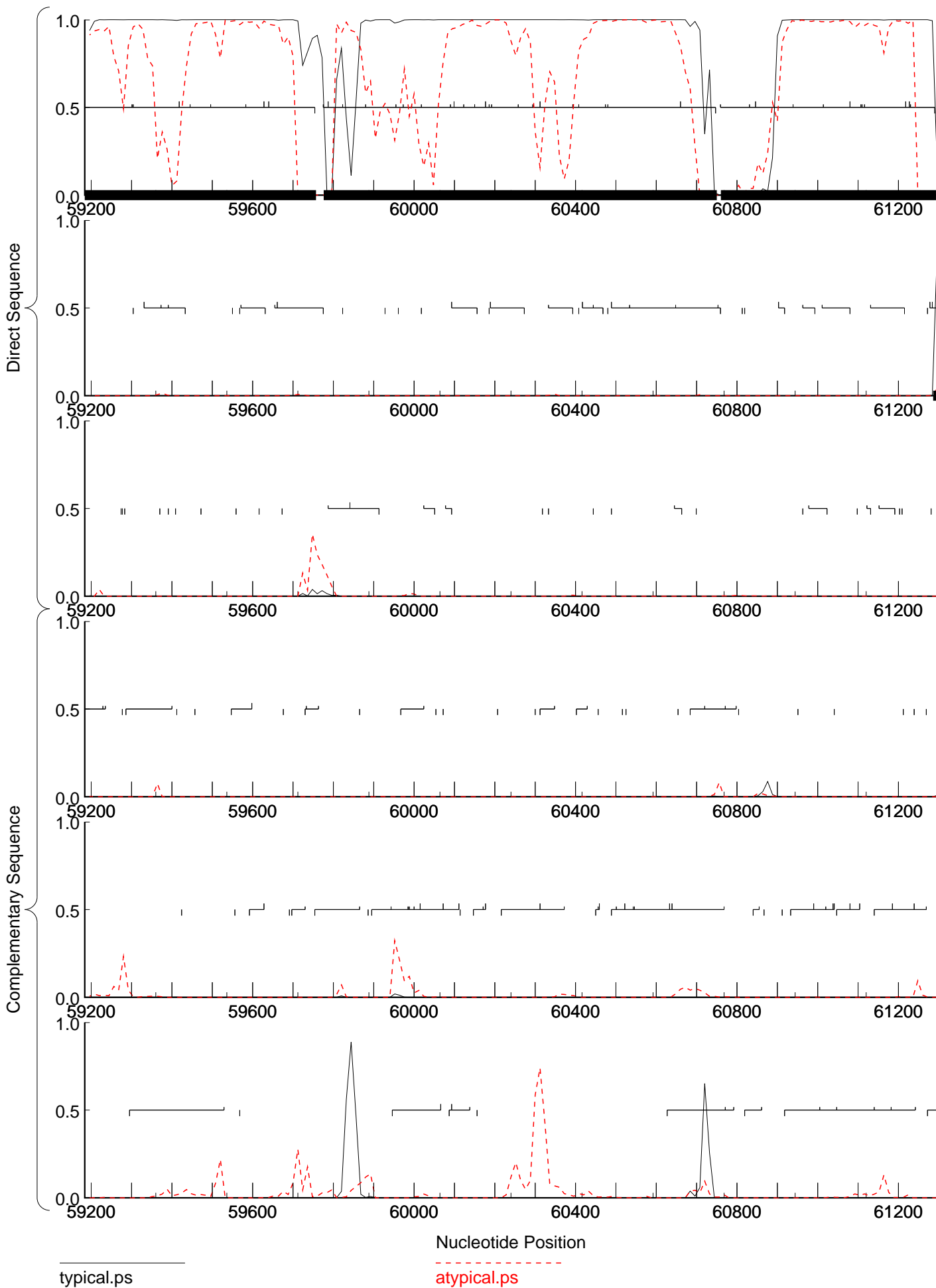
Nucleotide Position

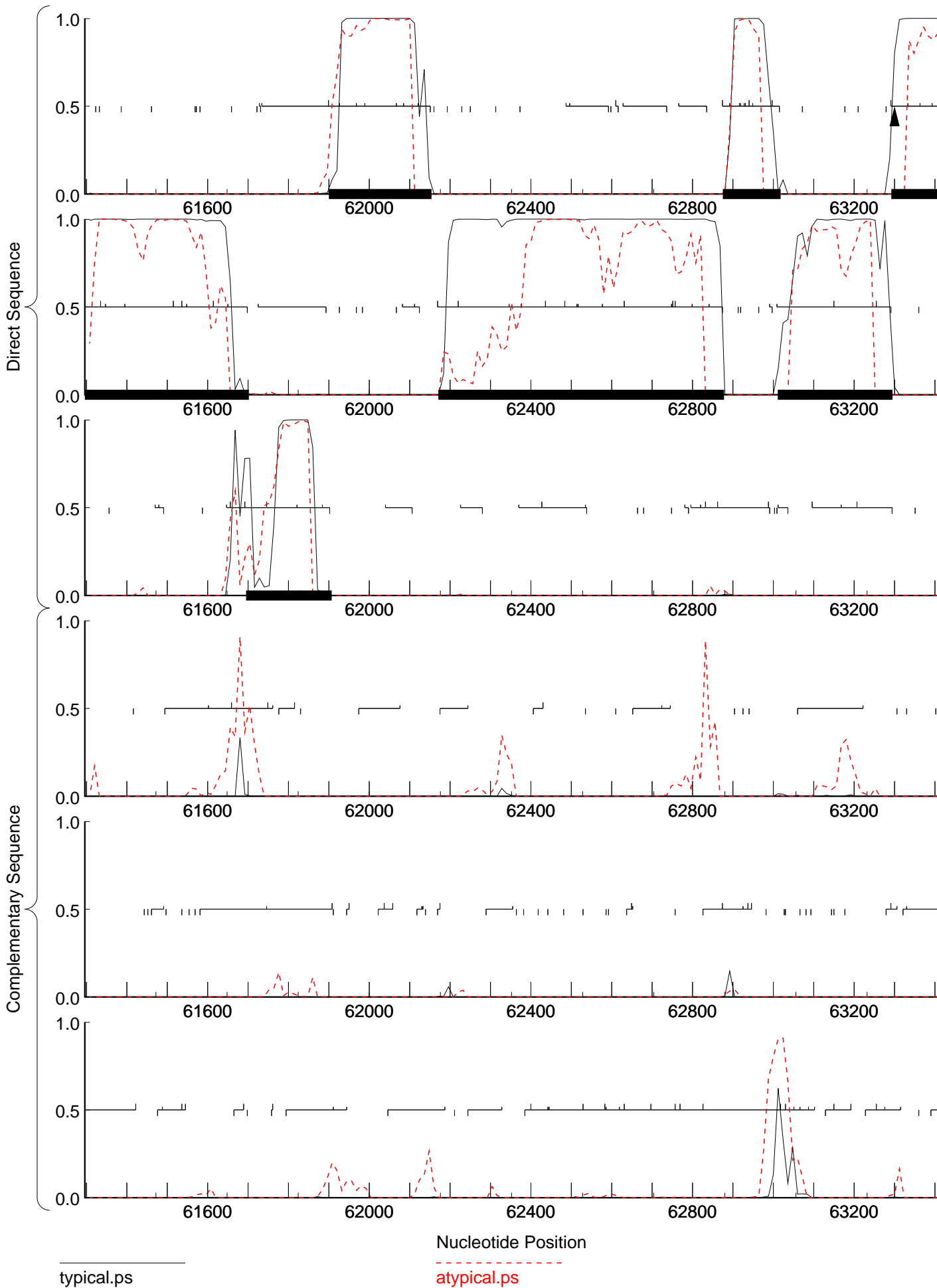
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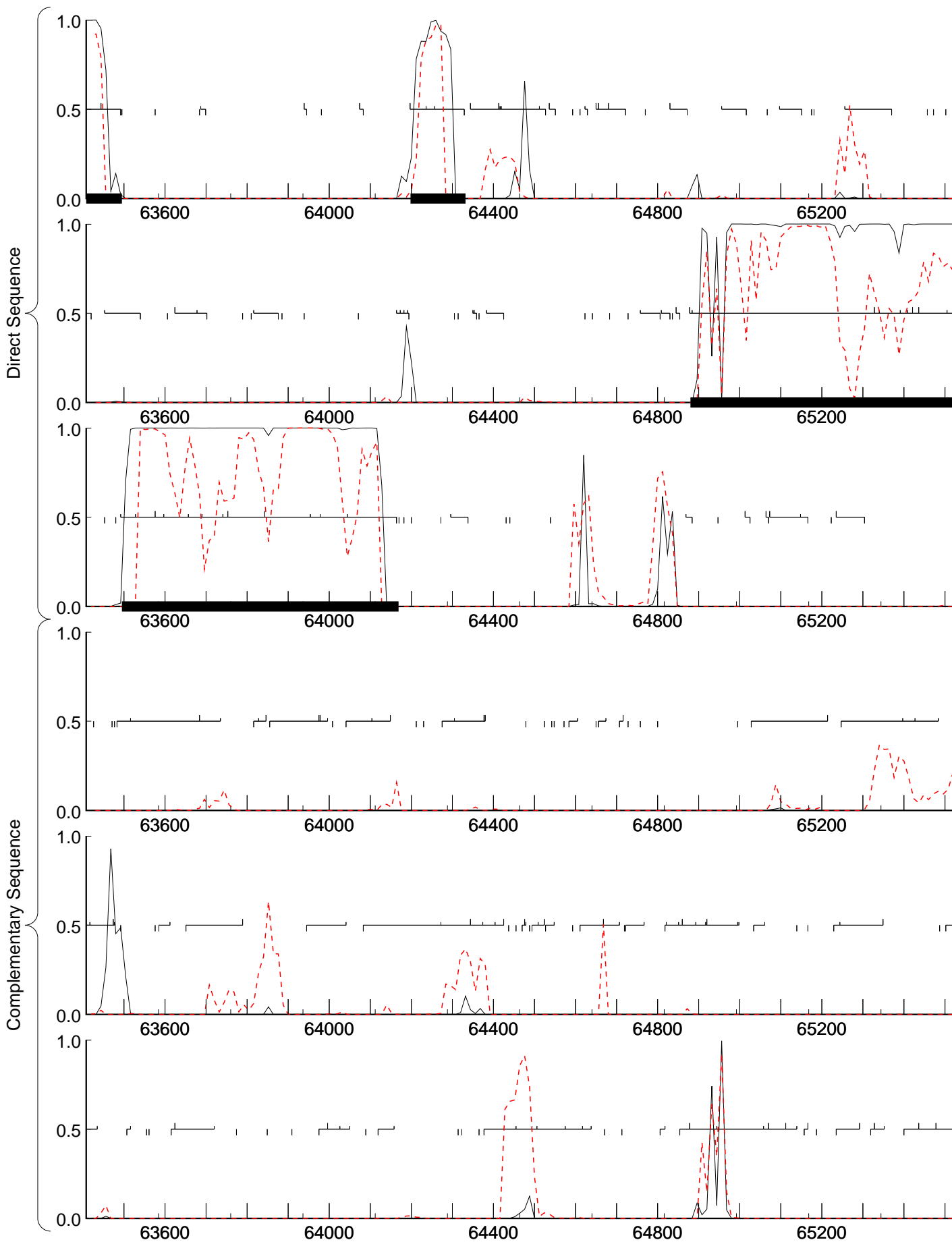


typical.ps

atypical.ps



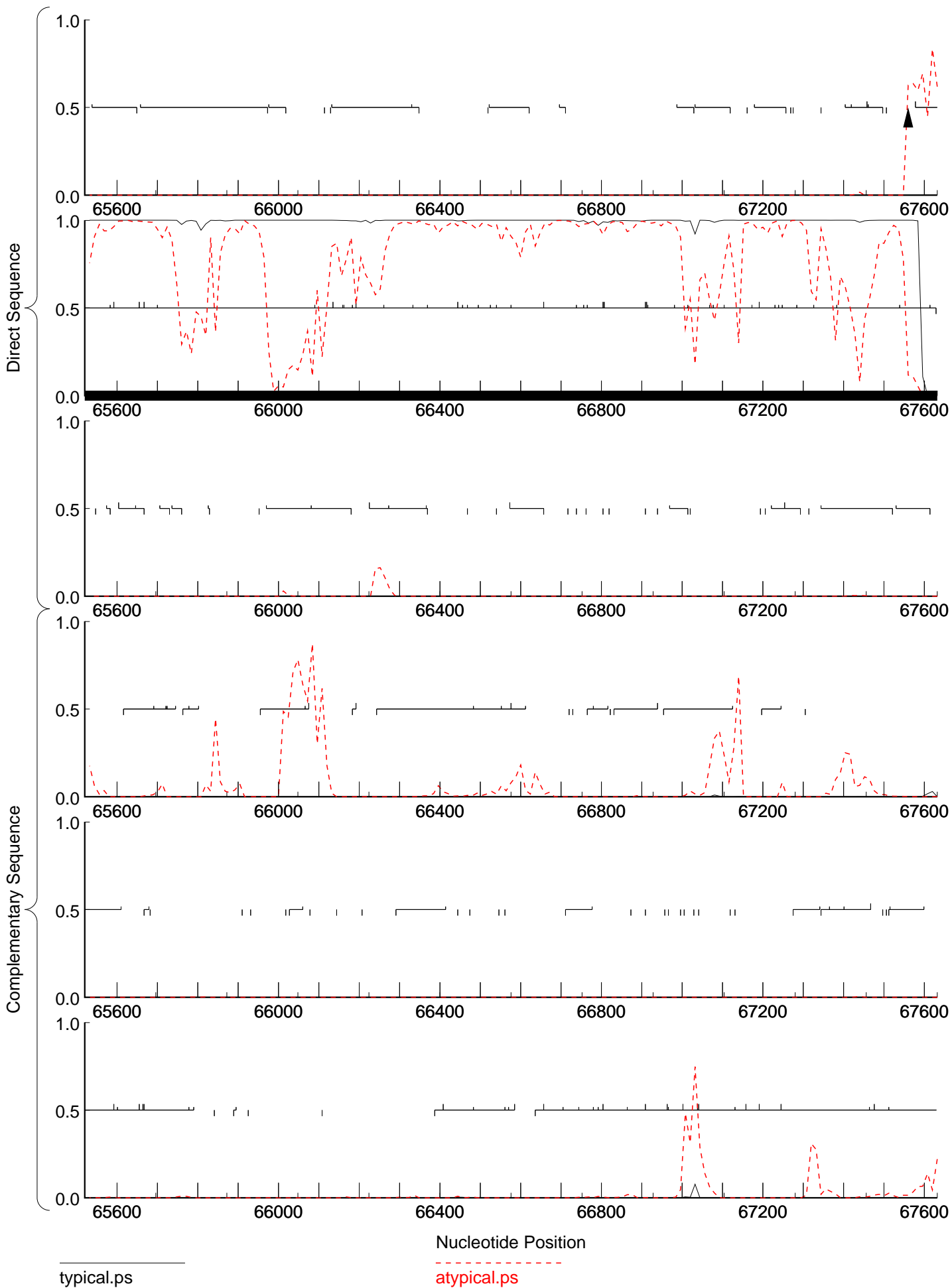


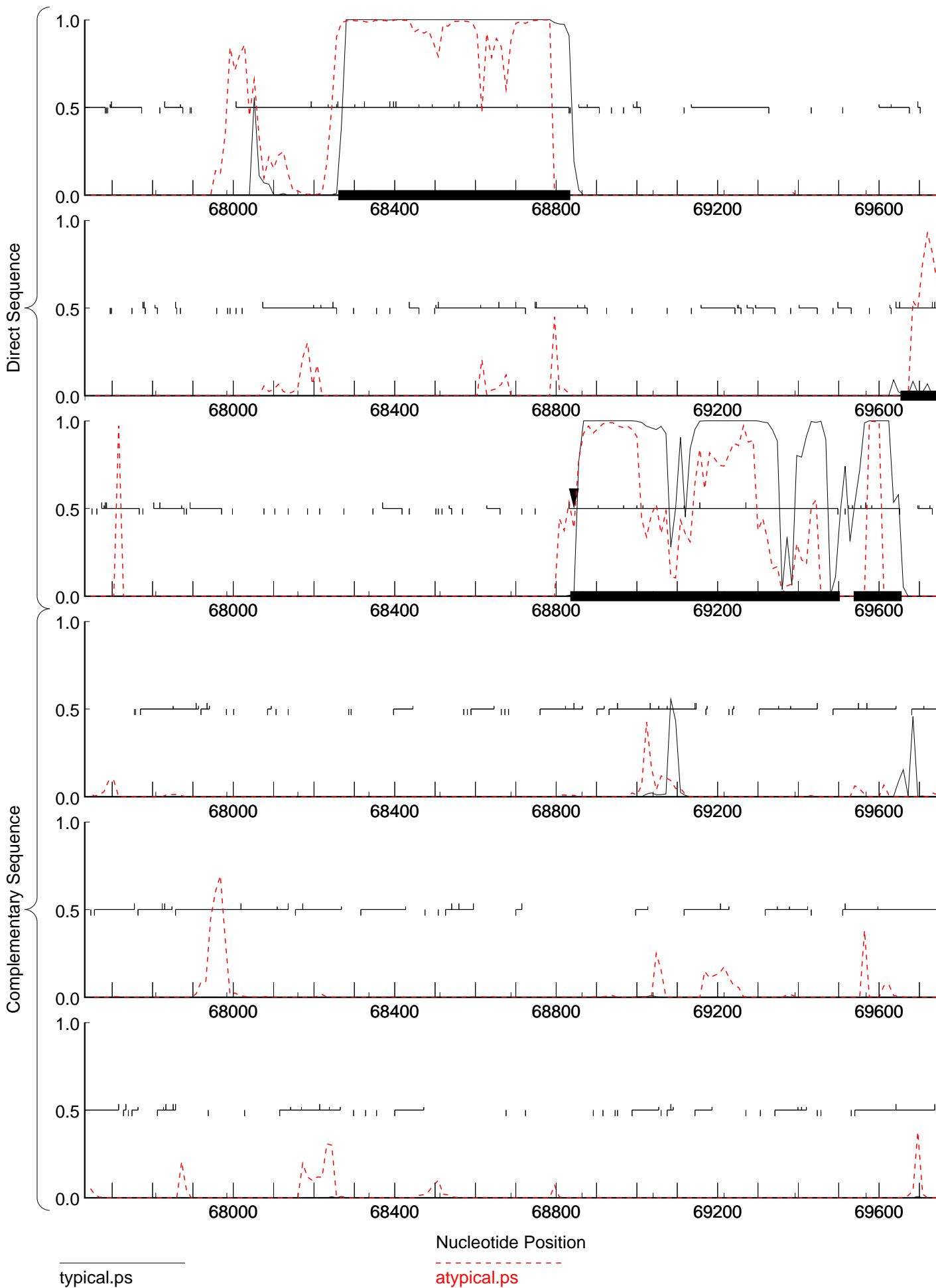


typical.ps

atypical.ps







typical.ps

atypical.ps

