

# GeneMark

Version 2.5p (09.08.06)

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## PROGRAM INFORMATION

Sequence : Mycobacterium phage Zulu complete sequence, 52499 bp including 10-base 3' overhang (CGGTCGG  
Analysis Date : 8/18/17 at 2:57:22  
Pages : 26  
Sequence Length : 52499 bp  
GC Content : 61.42%

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,

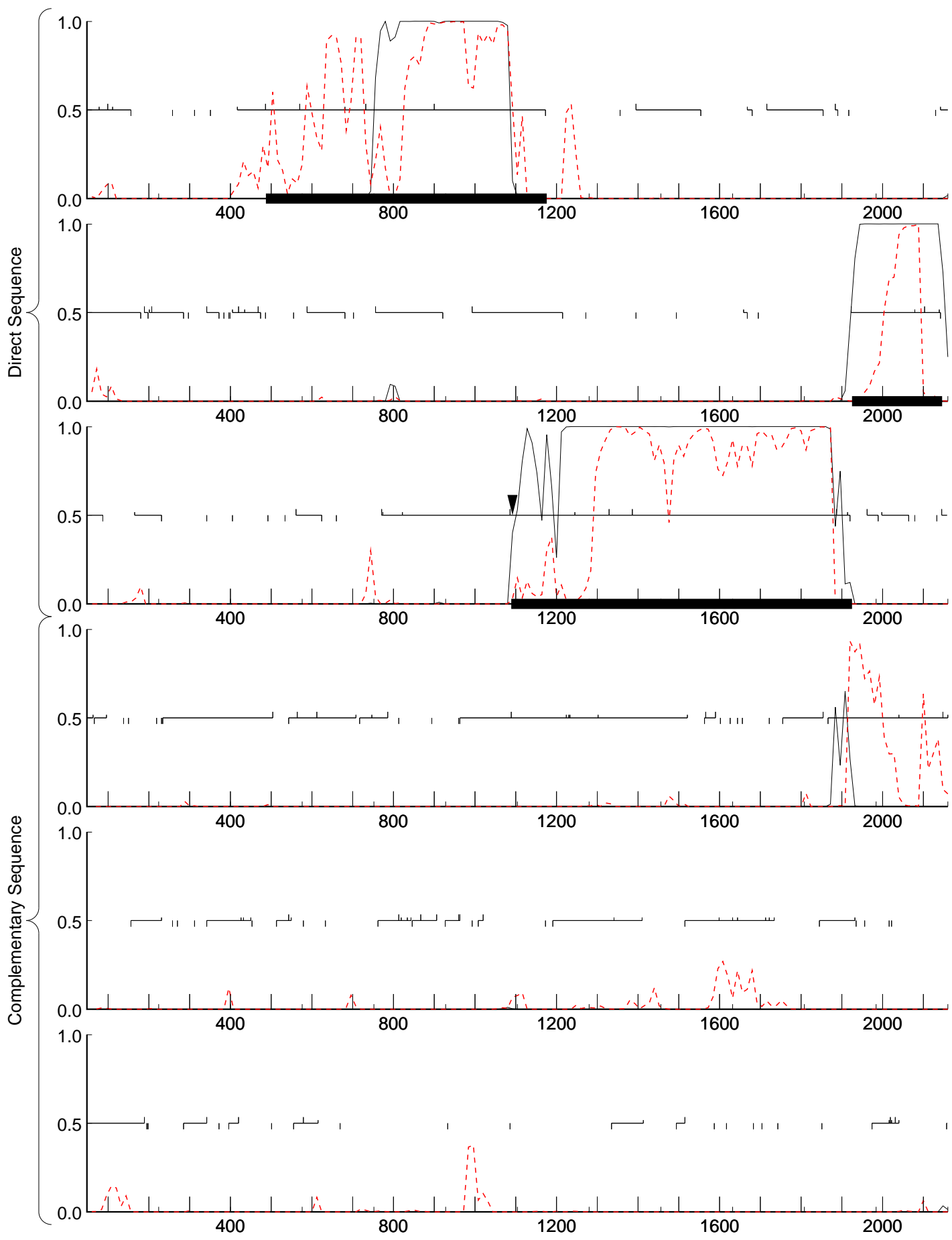
## MATRIX INFORMATION

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

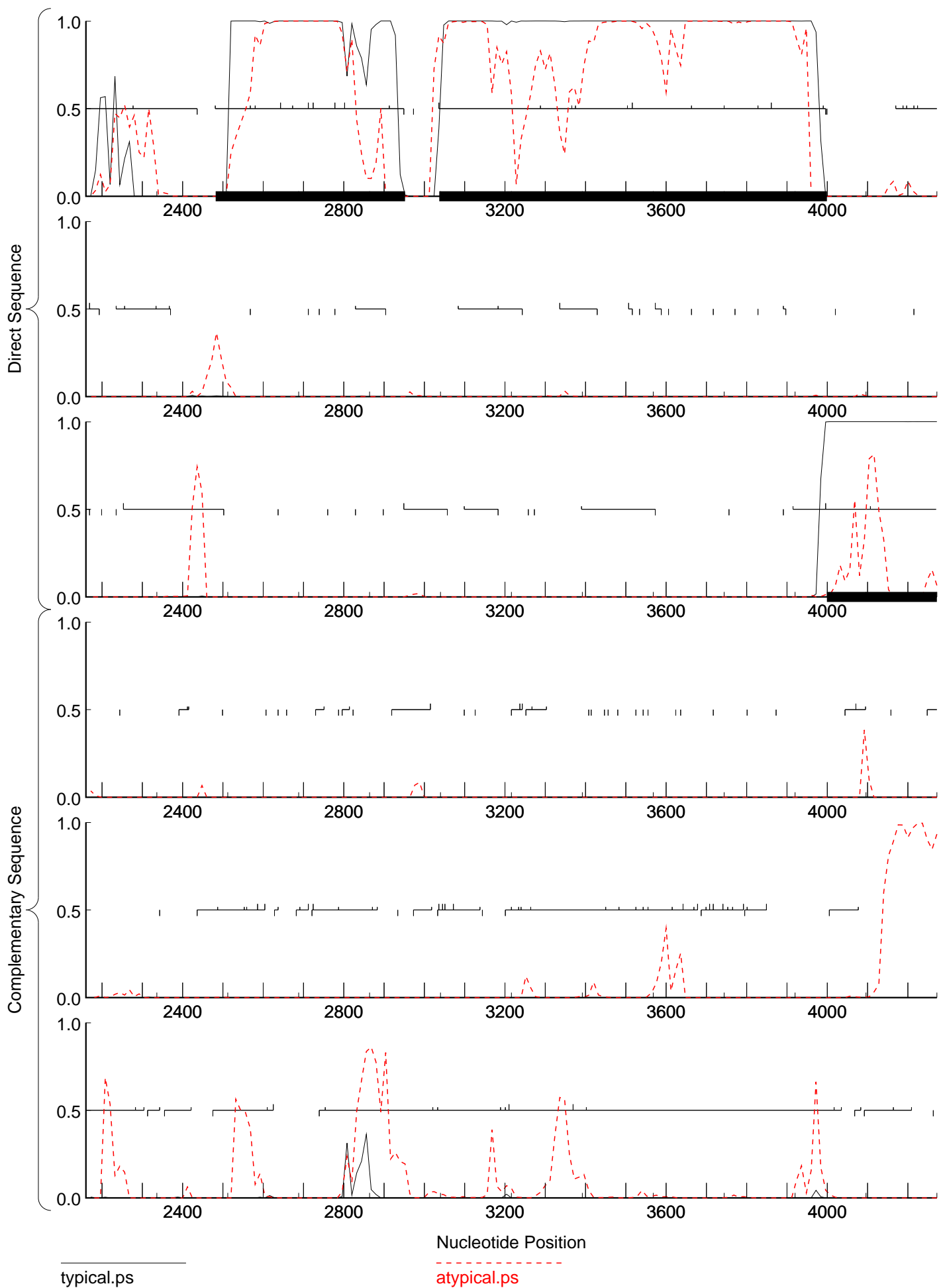
Training set derived by GeneMarkS, 4.30 October 2014  
Fri Aug 18 02:57:22 2017



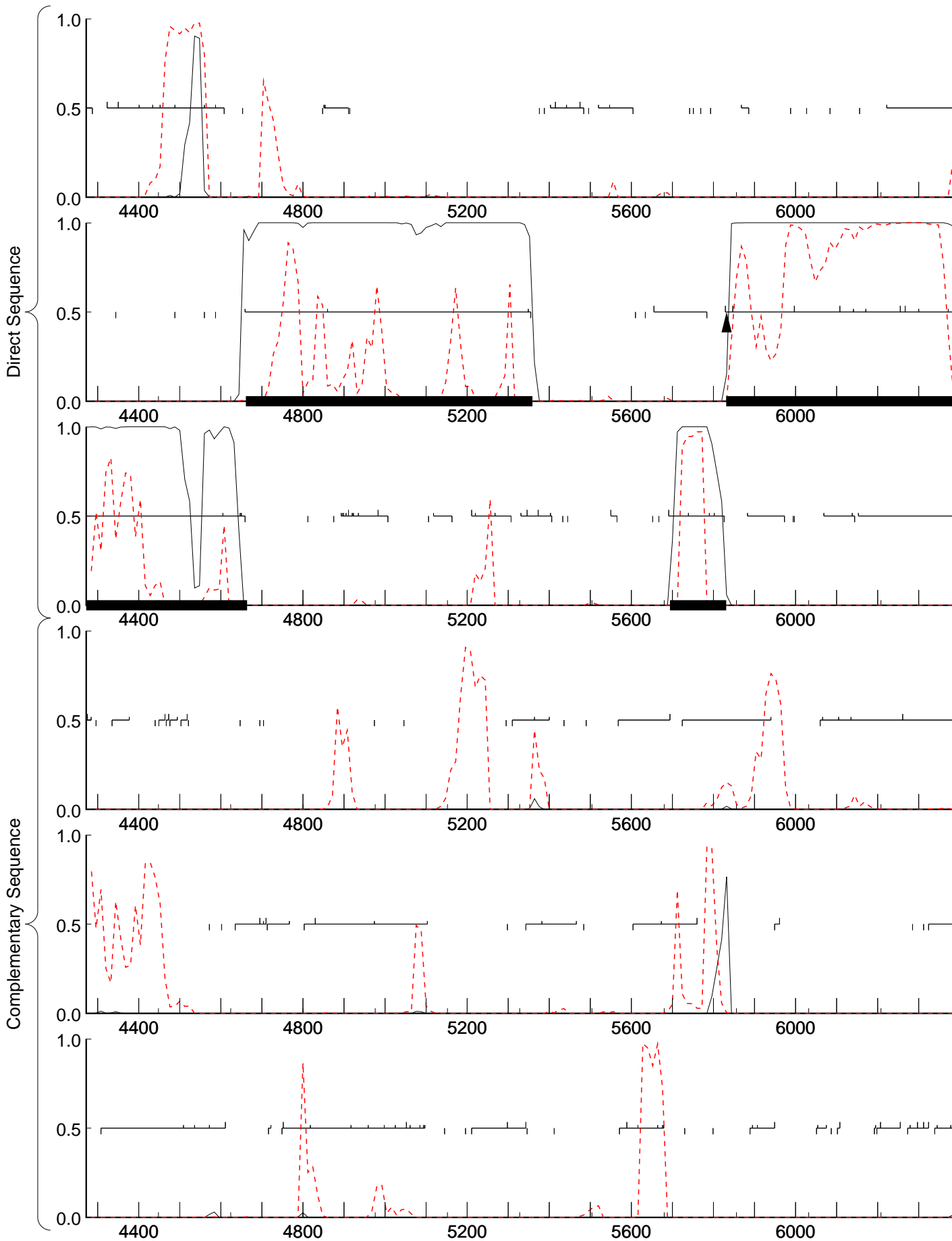
typical.ps

atypical.ps

u complete sequence, 52499 bp including 10-base 3' overhang (CGGTCGGTAA), Cluster A6, Order 4, Window 96, Step 12, 3/26  
u complete sequence, 52499 bp including 10-base 3' overhang (CGGTCGGTAA), Cluster A6, Order 2, Window 96, Step 12, 3/26

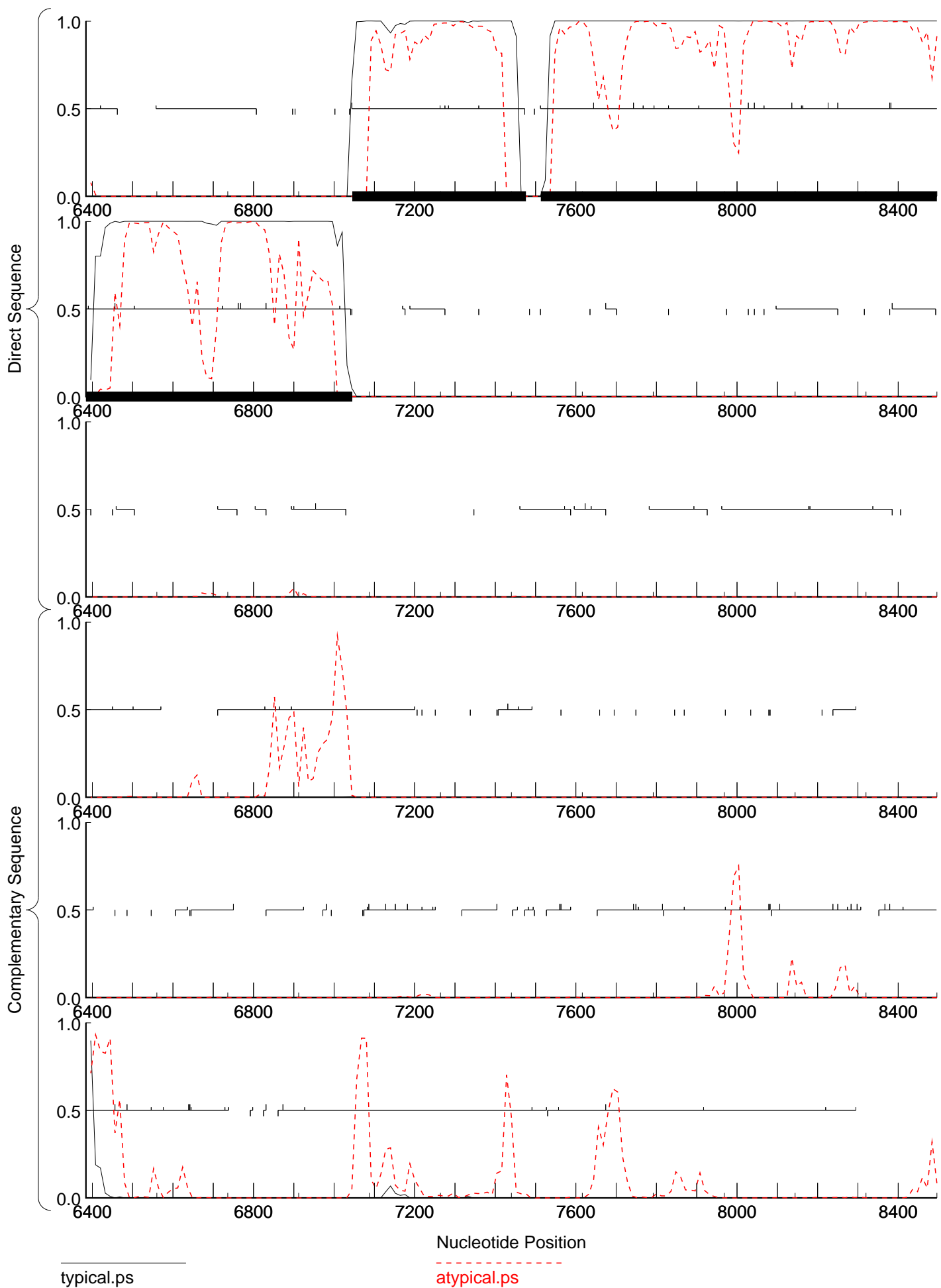


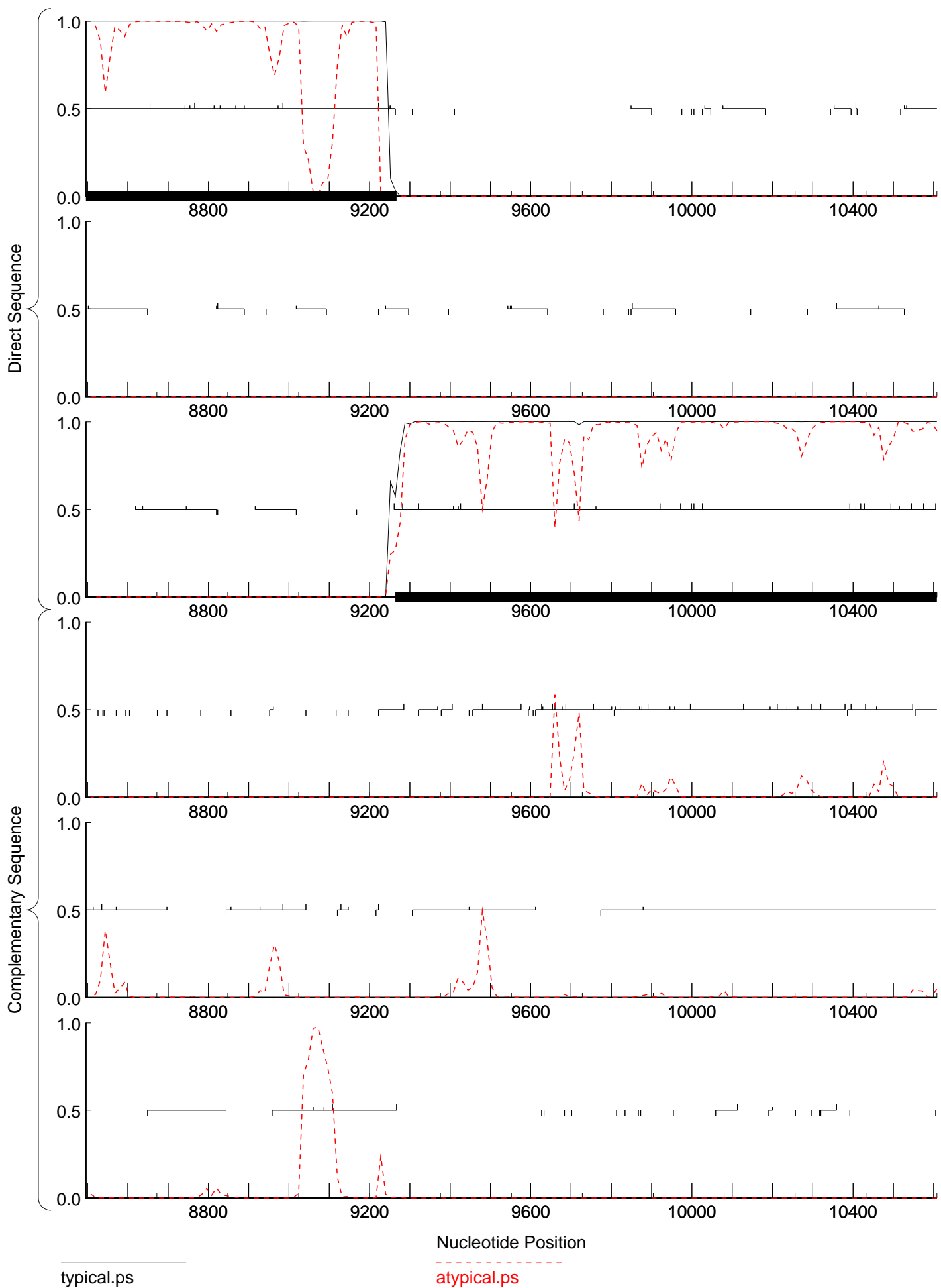
GeneMark.hmm prediction

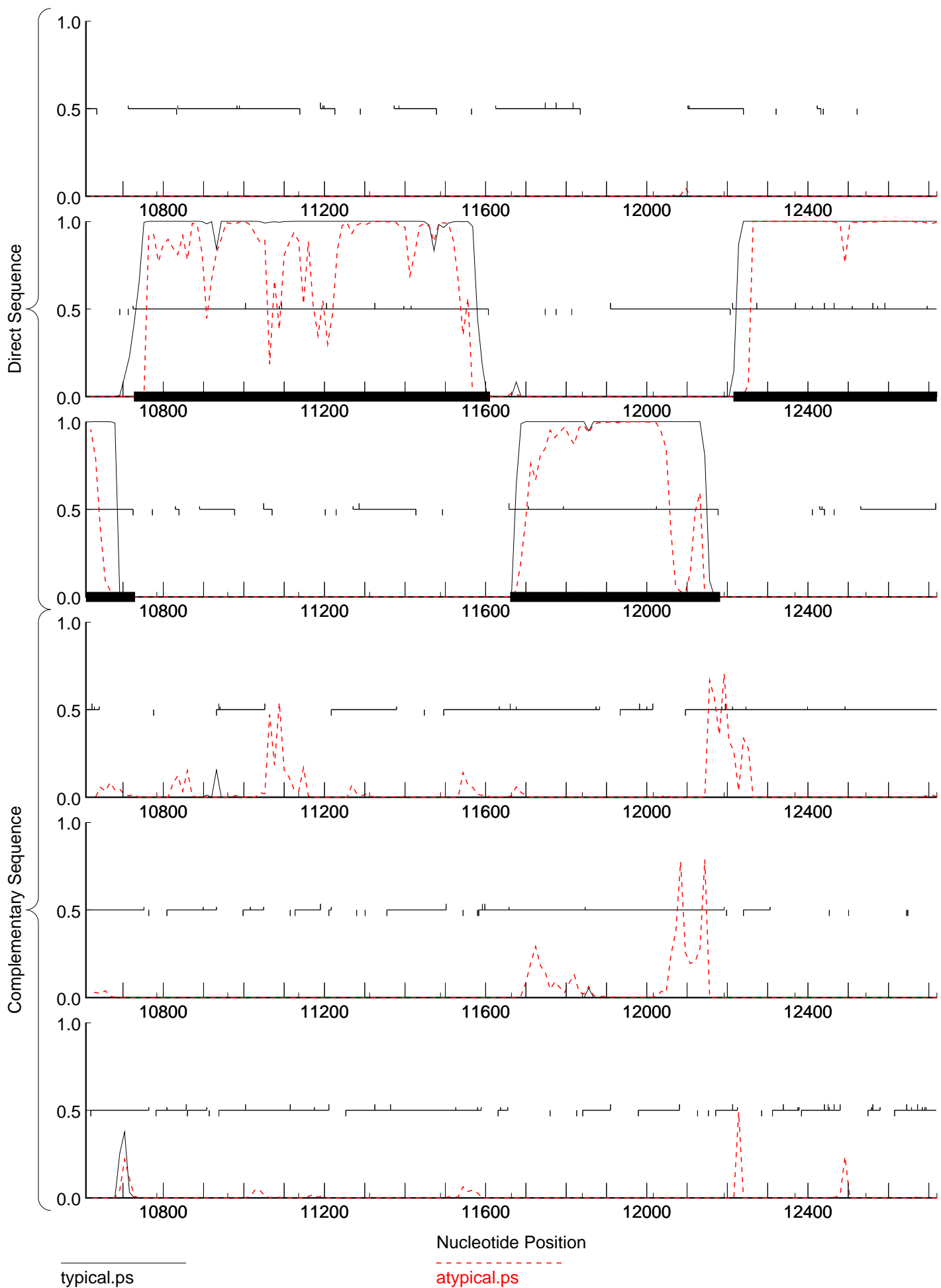


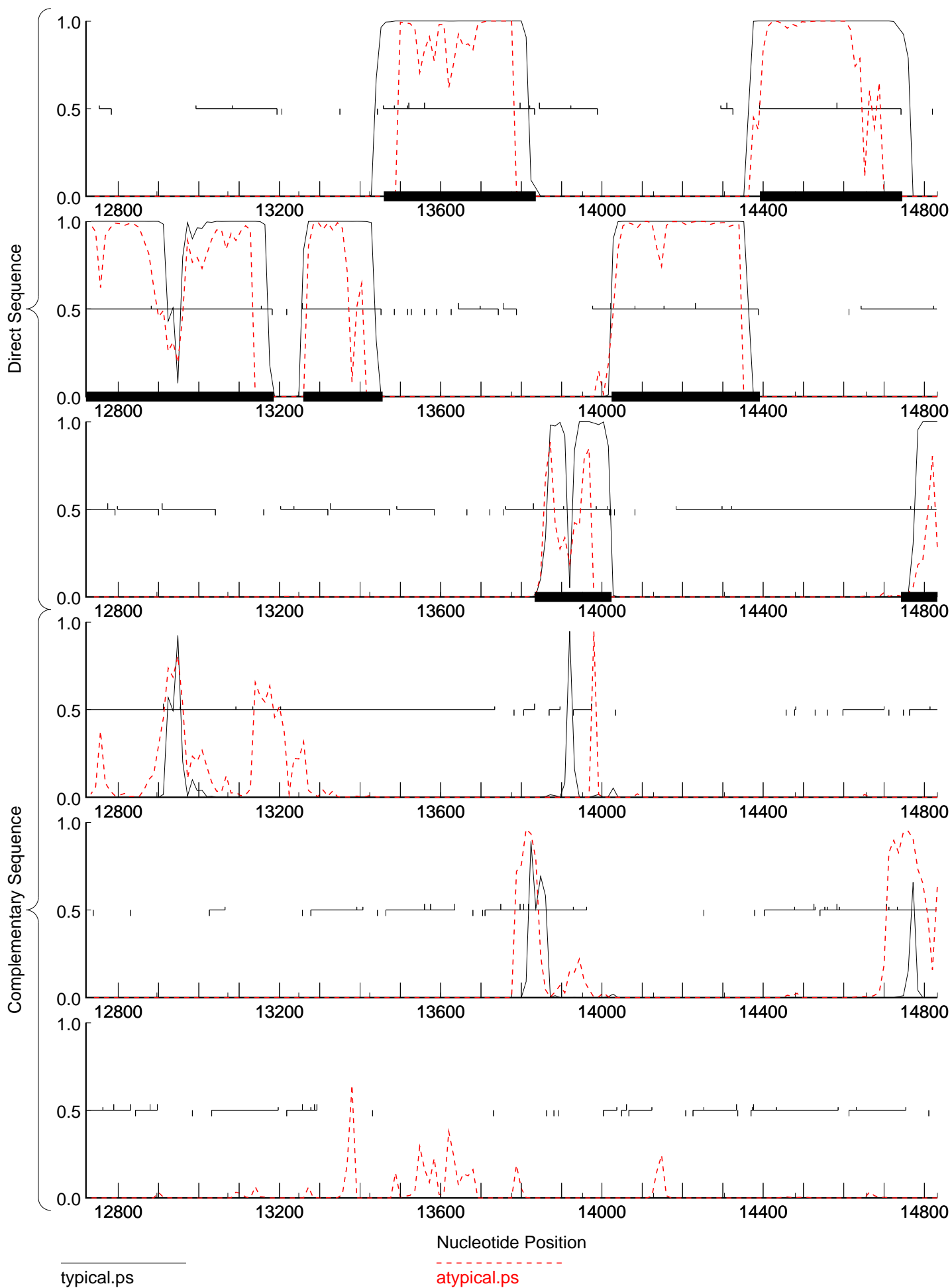
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atypical.ps

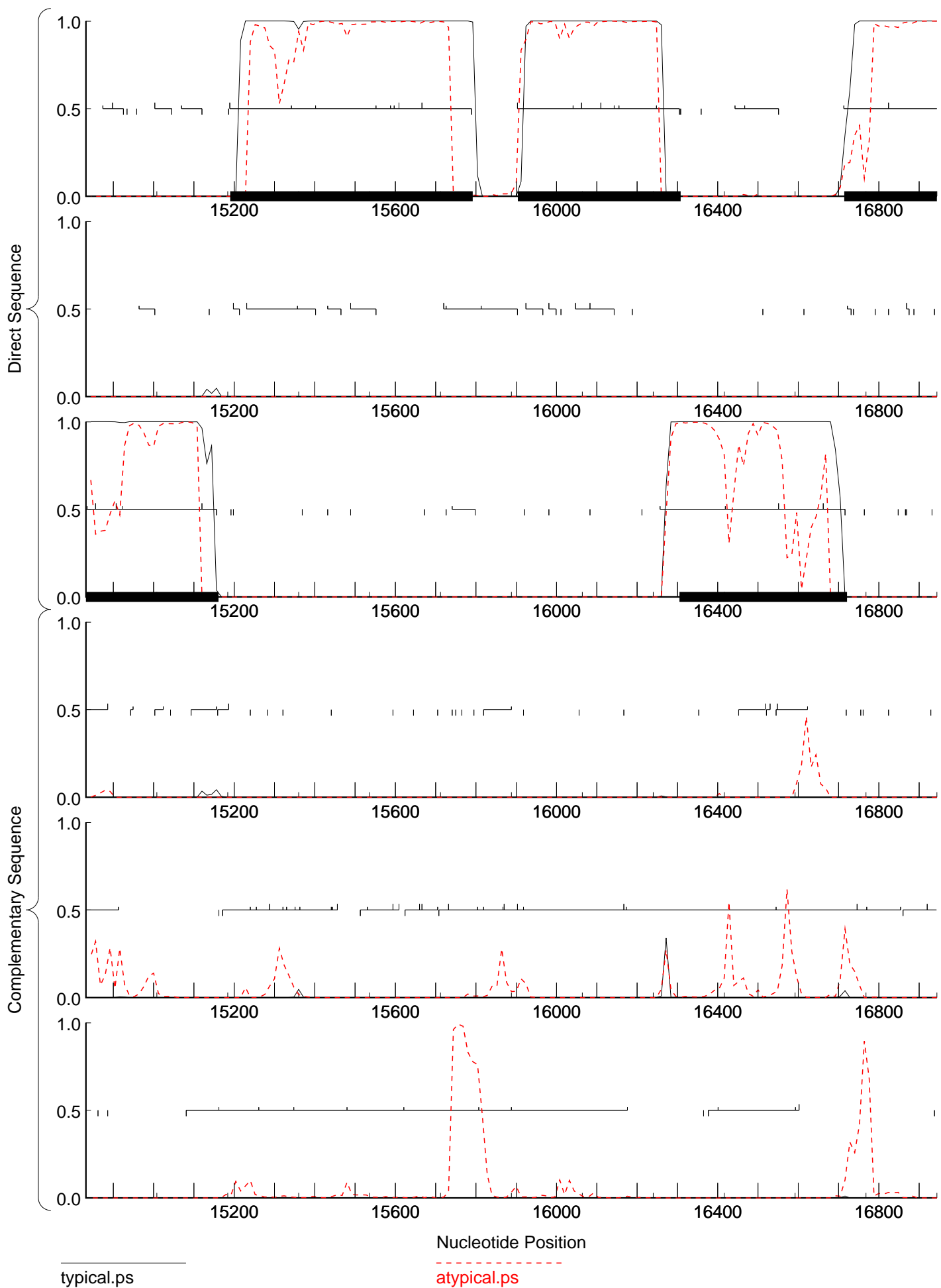






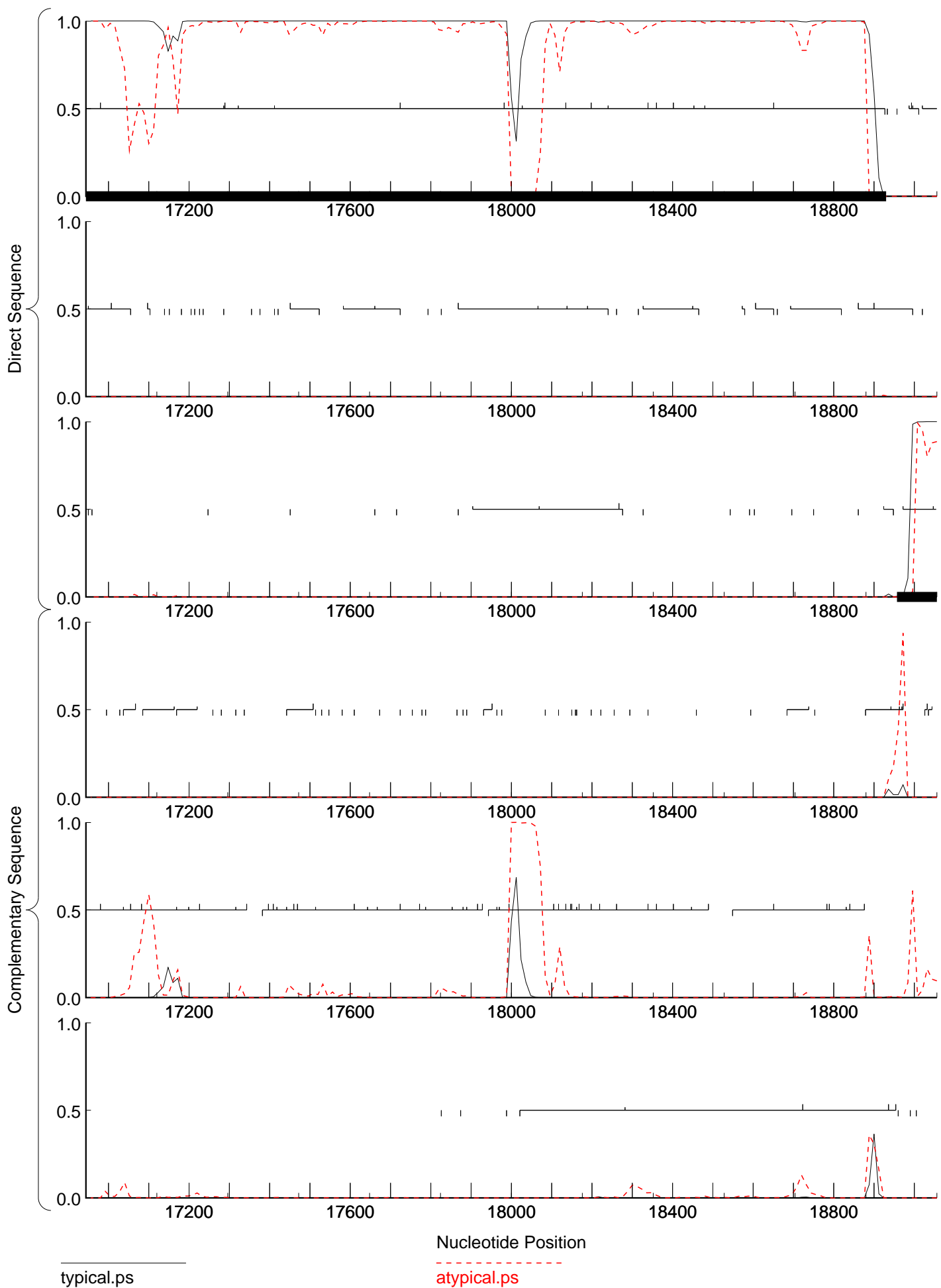


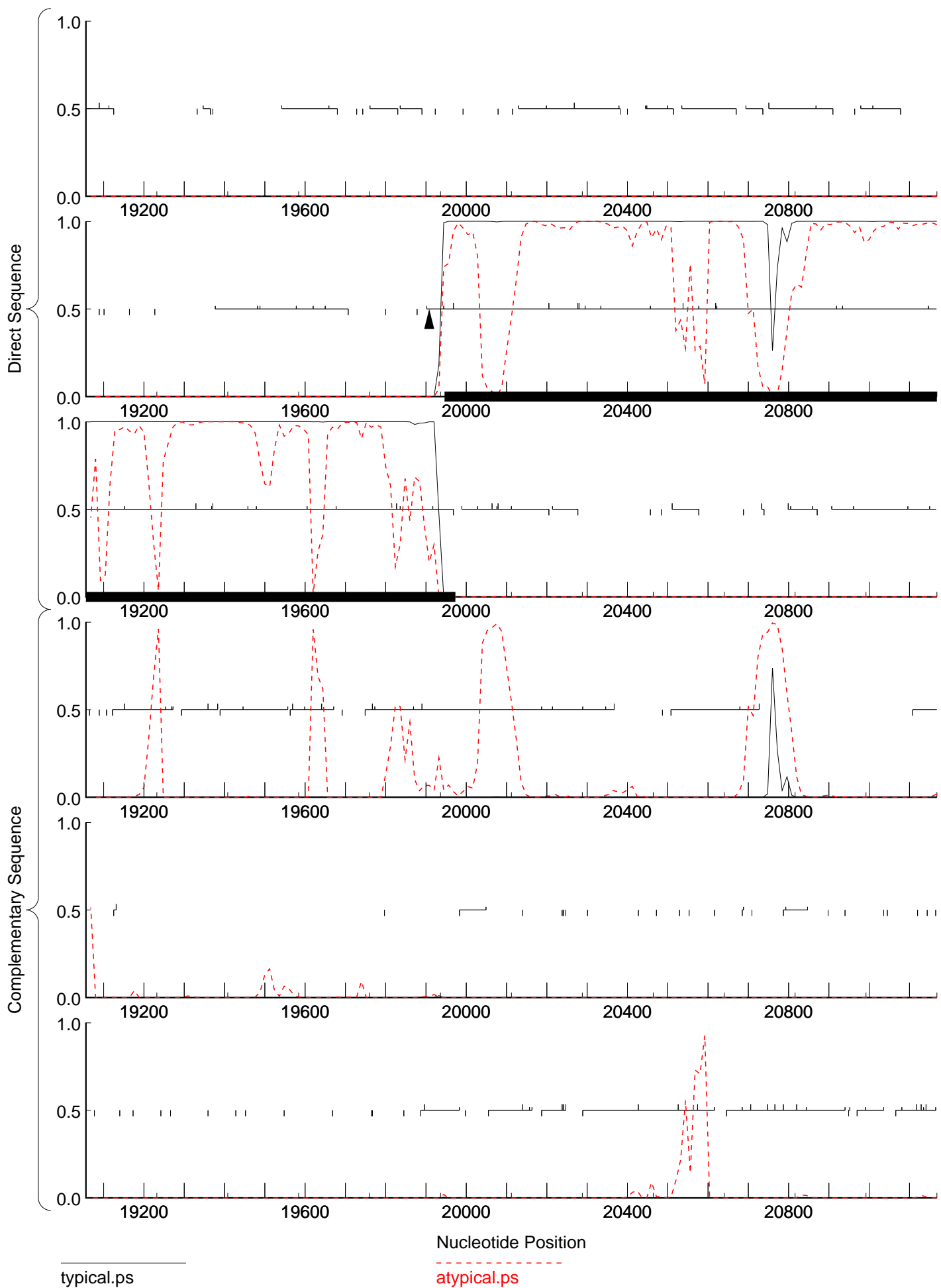


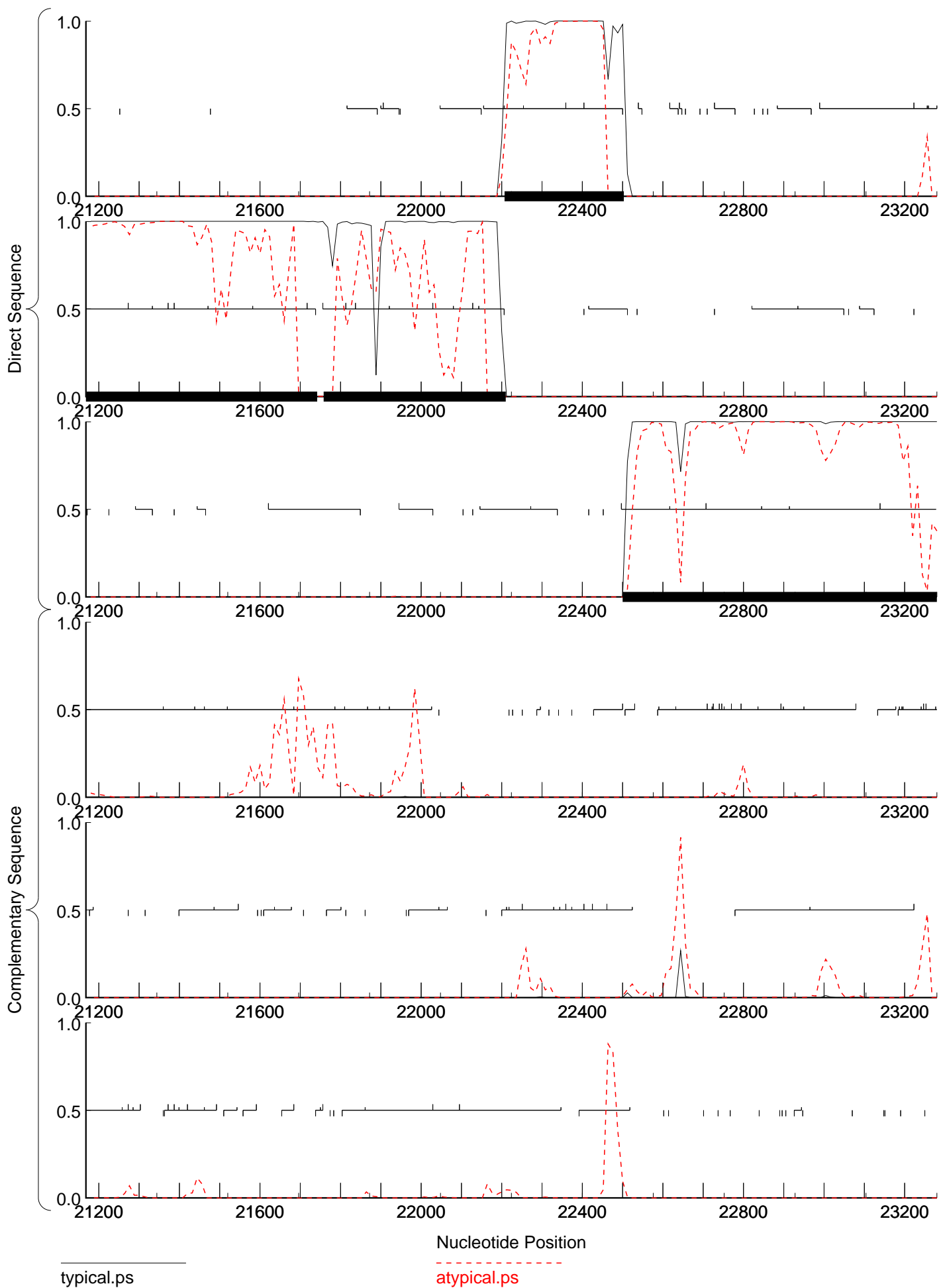


typical.ps

atypical.ps

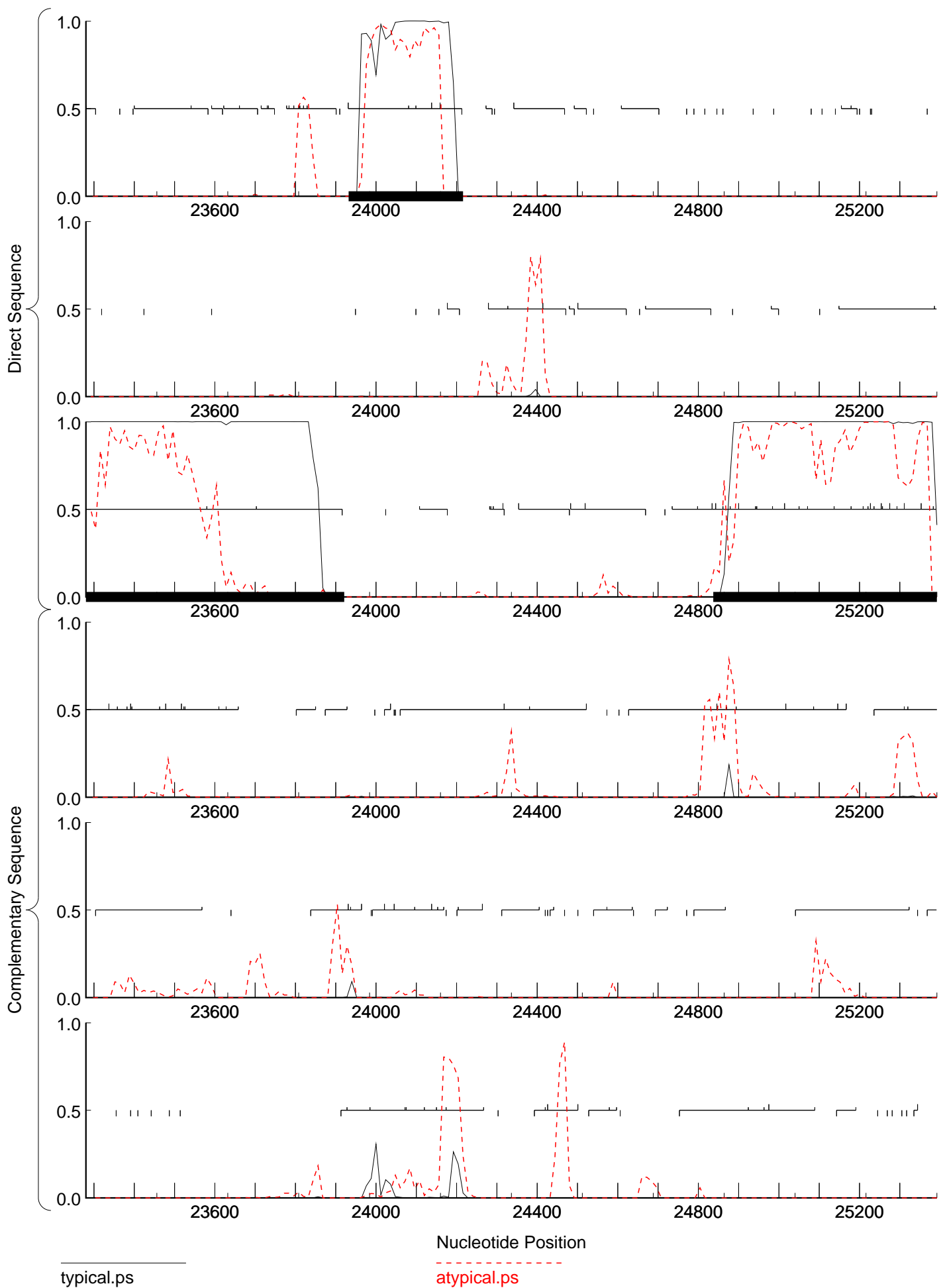






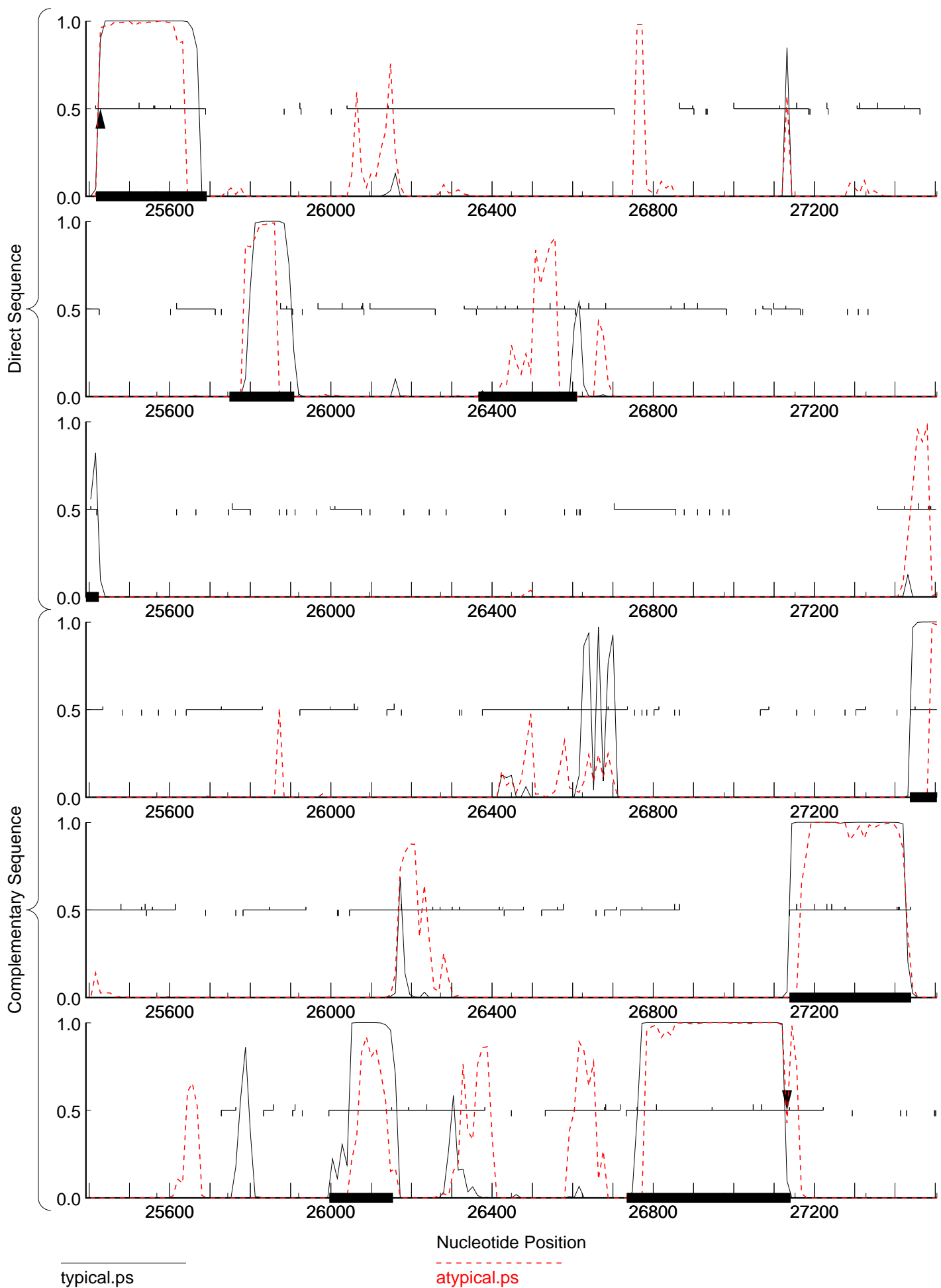
typical.ps

atypical.ps



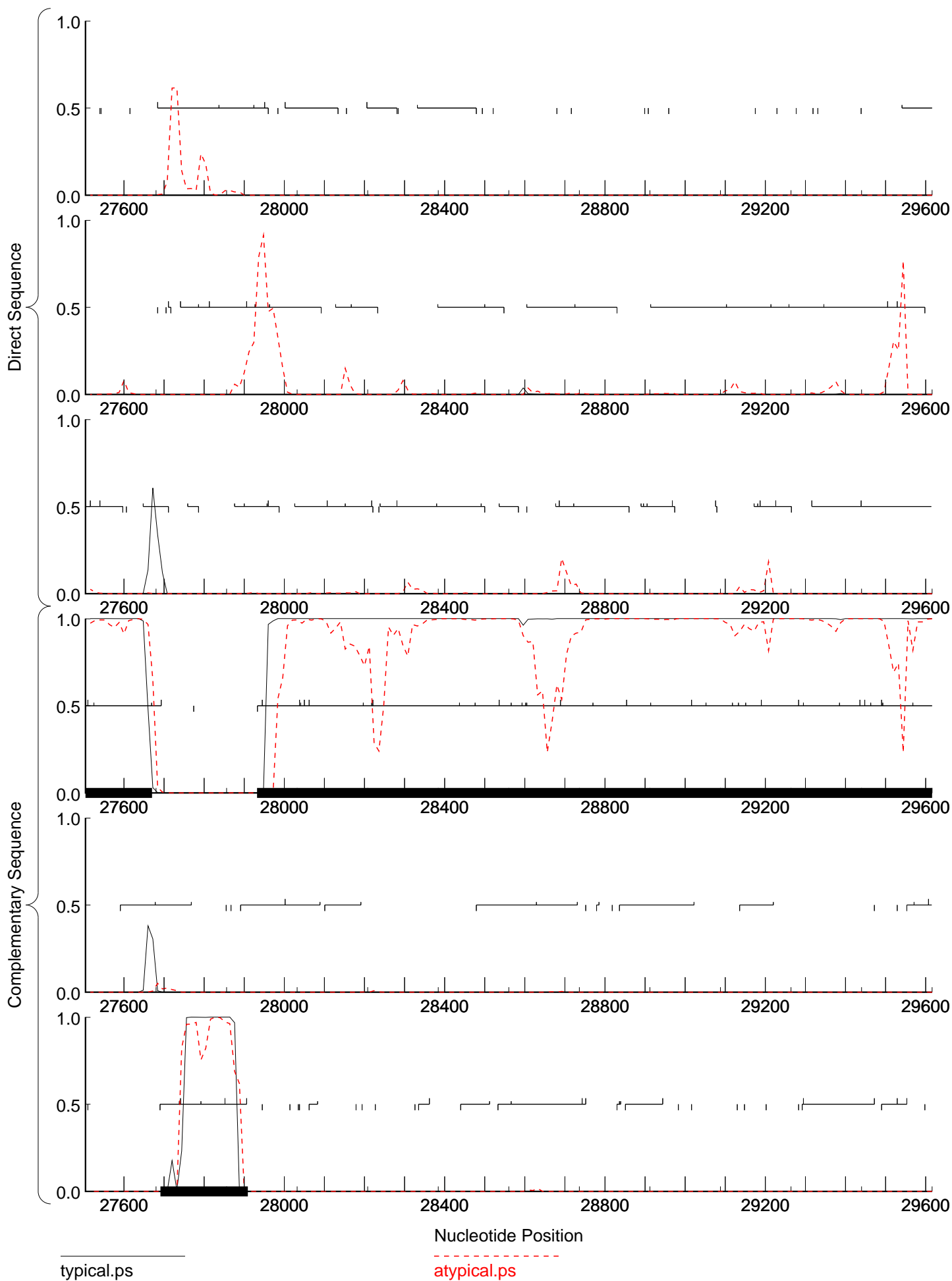
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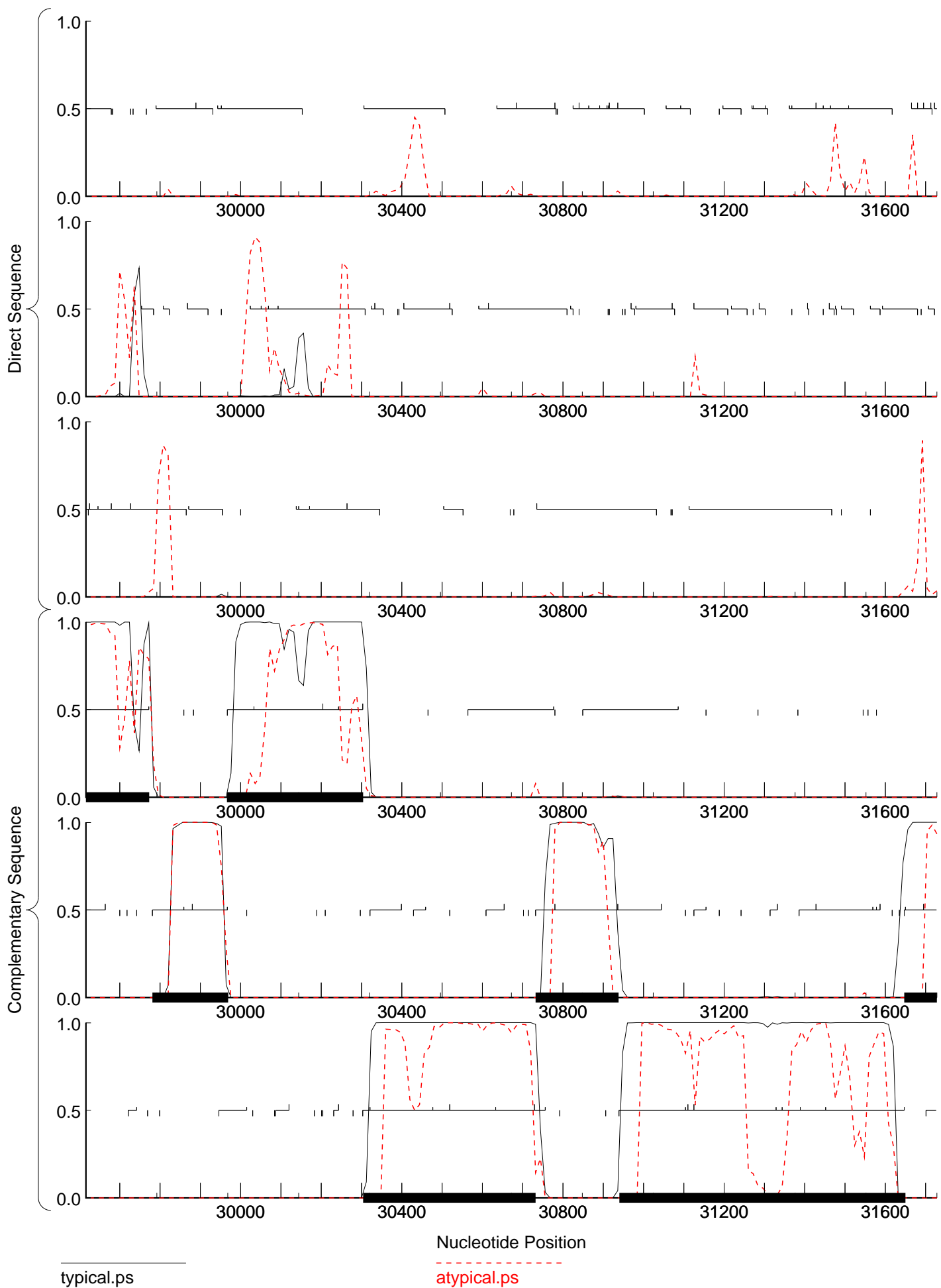
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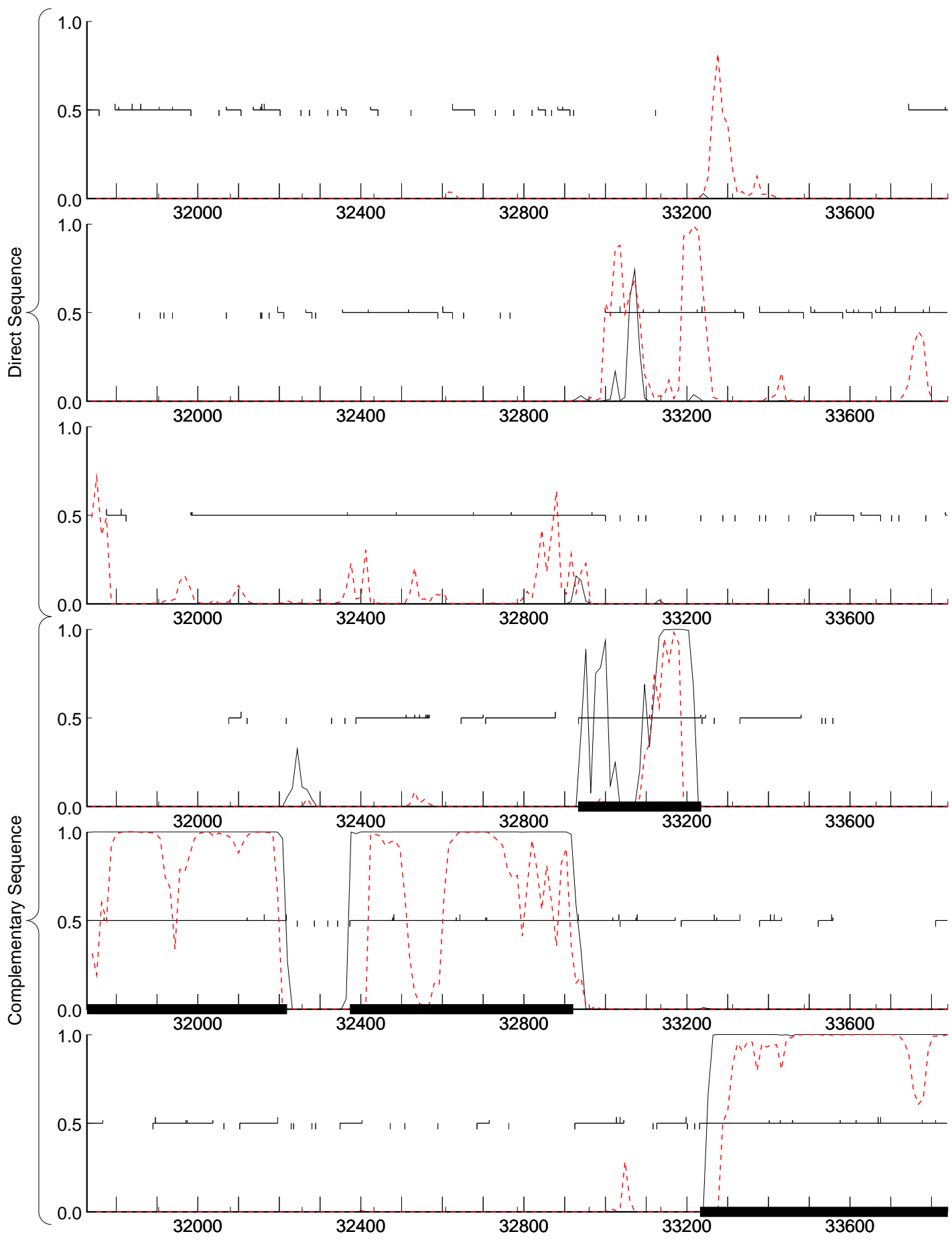
typical.ps

atypical.ps



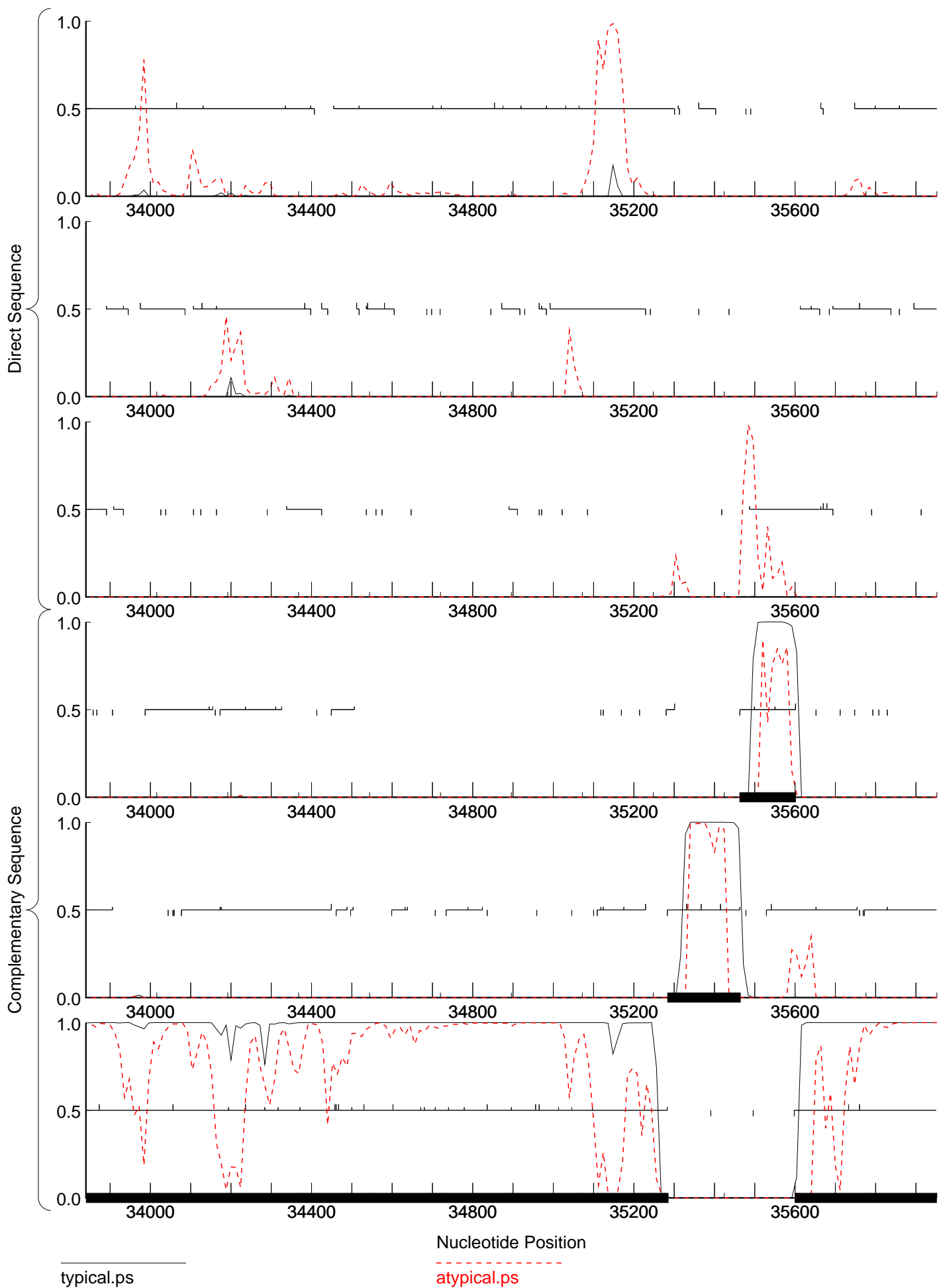


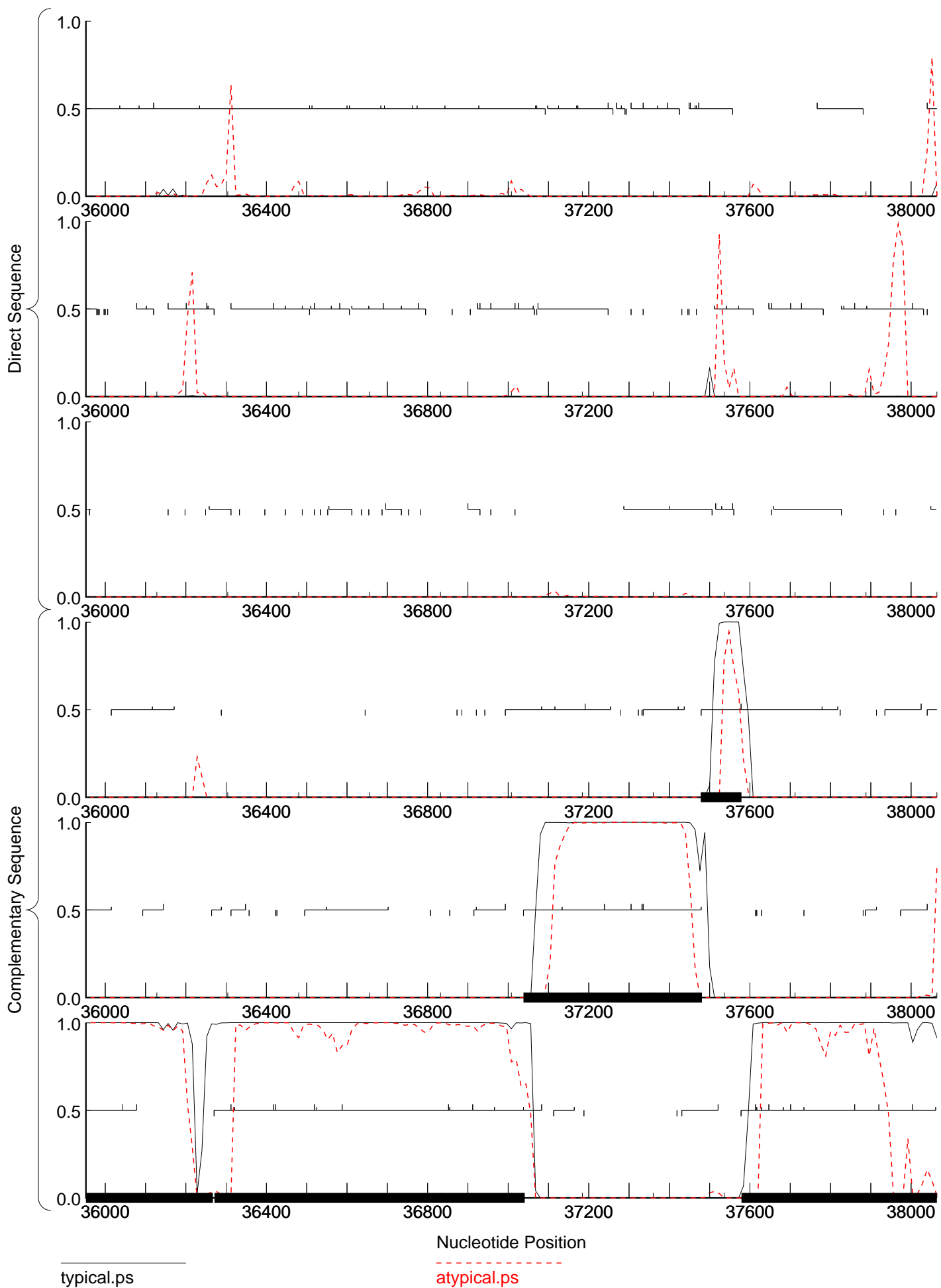


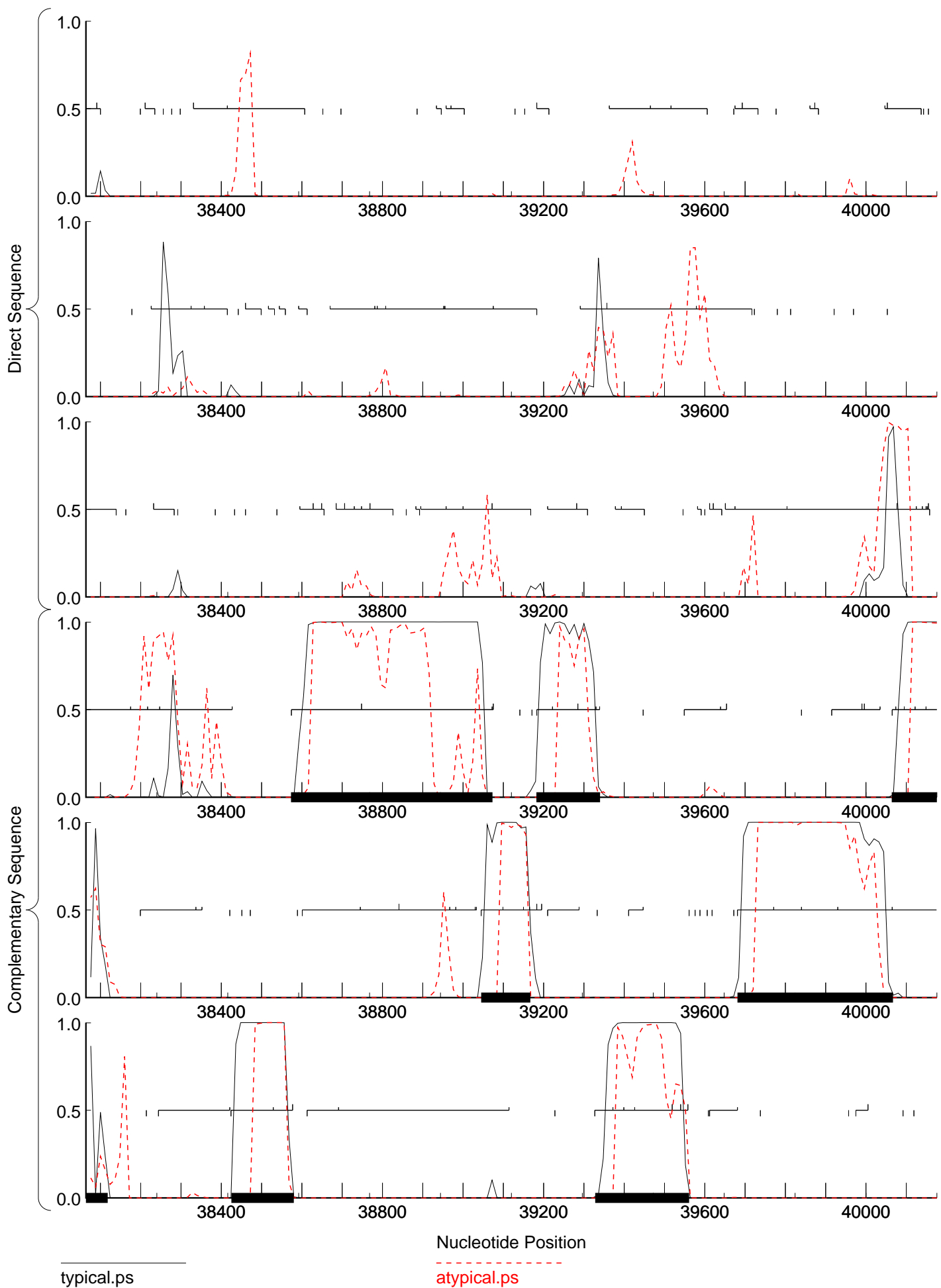


typical.ps

atypical.ps

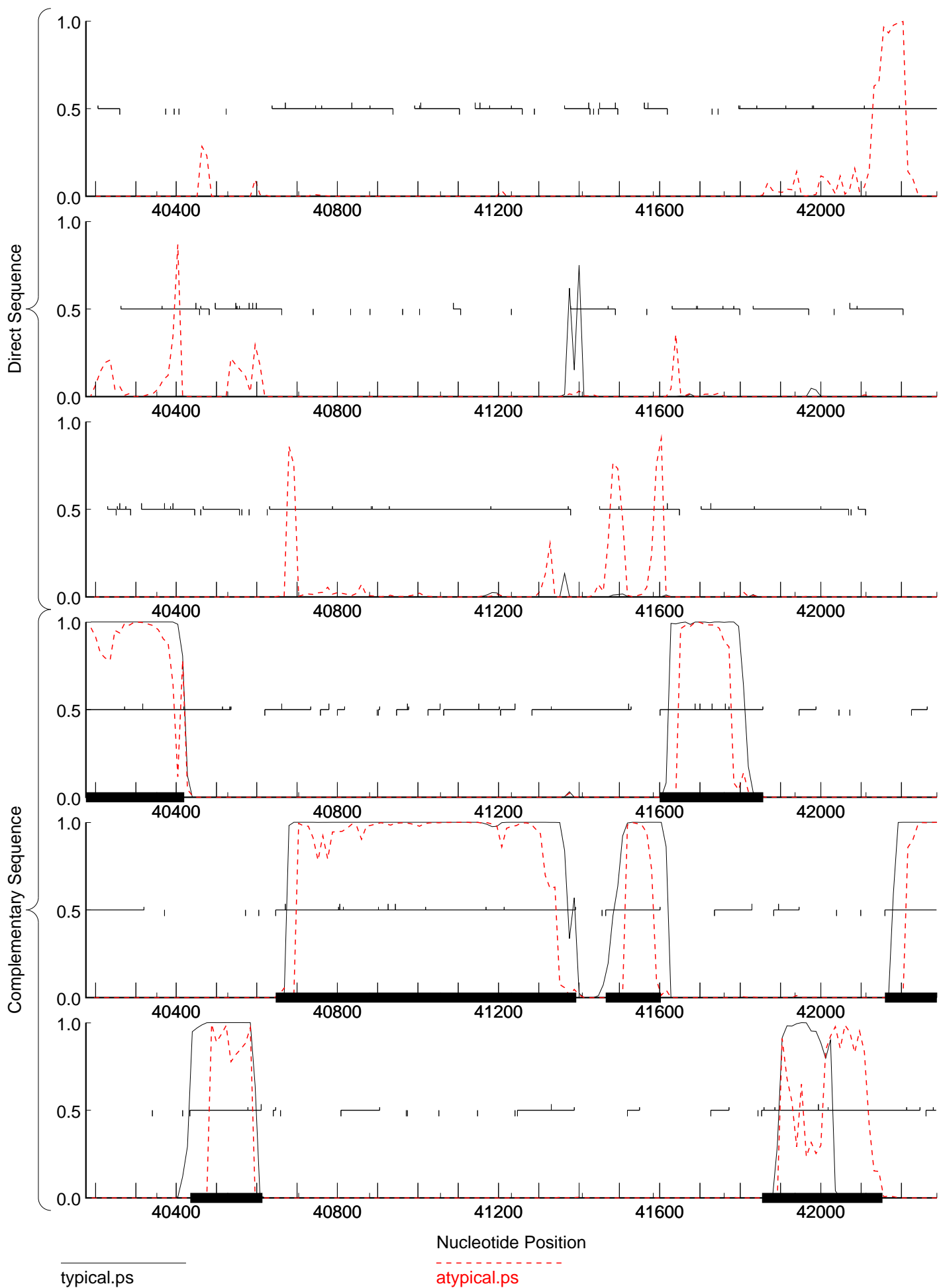


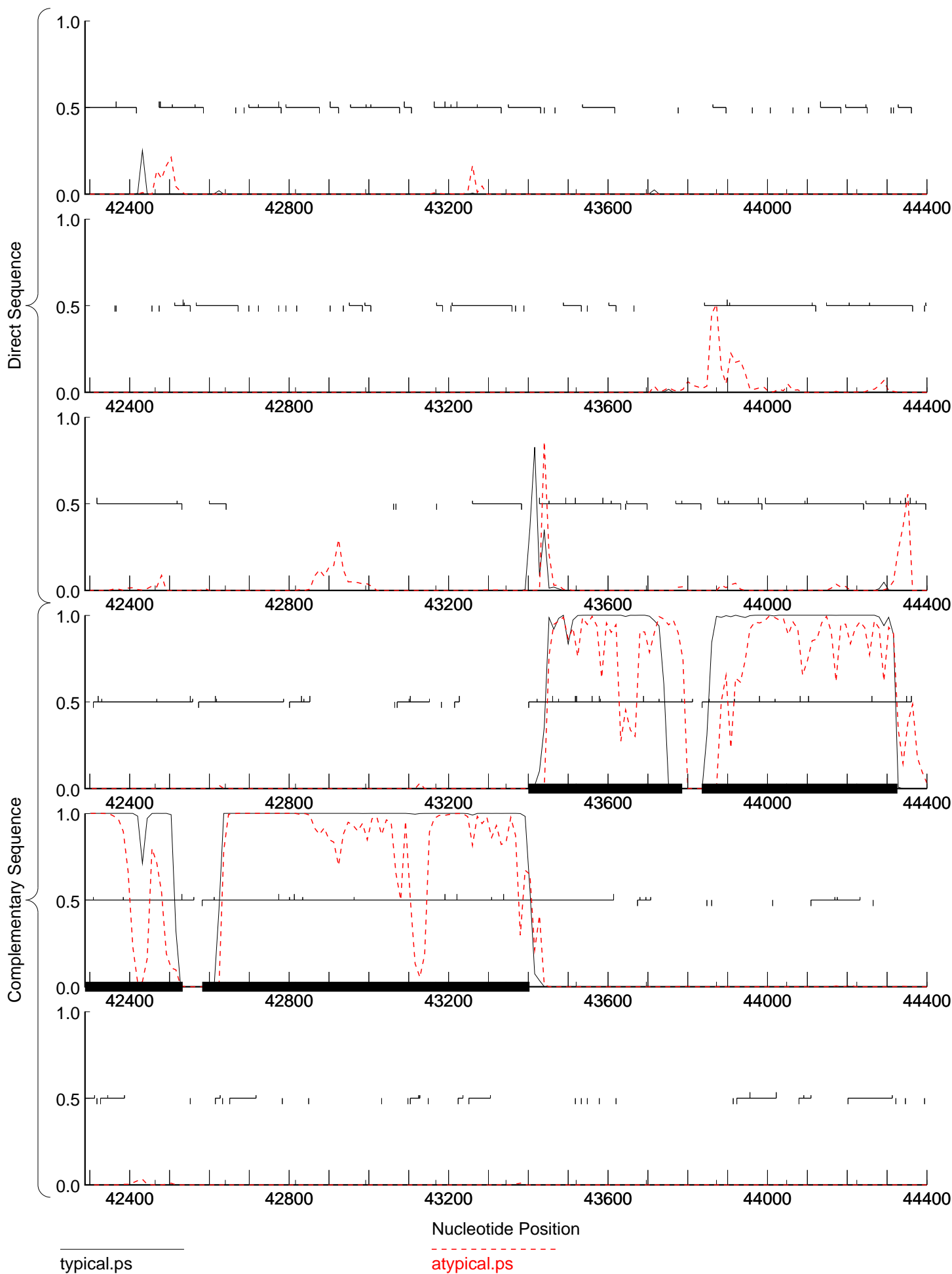


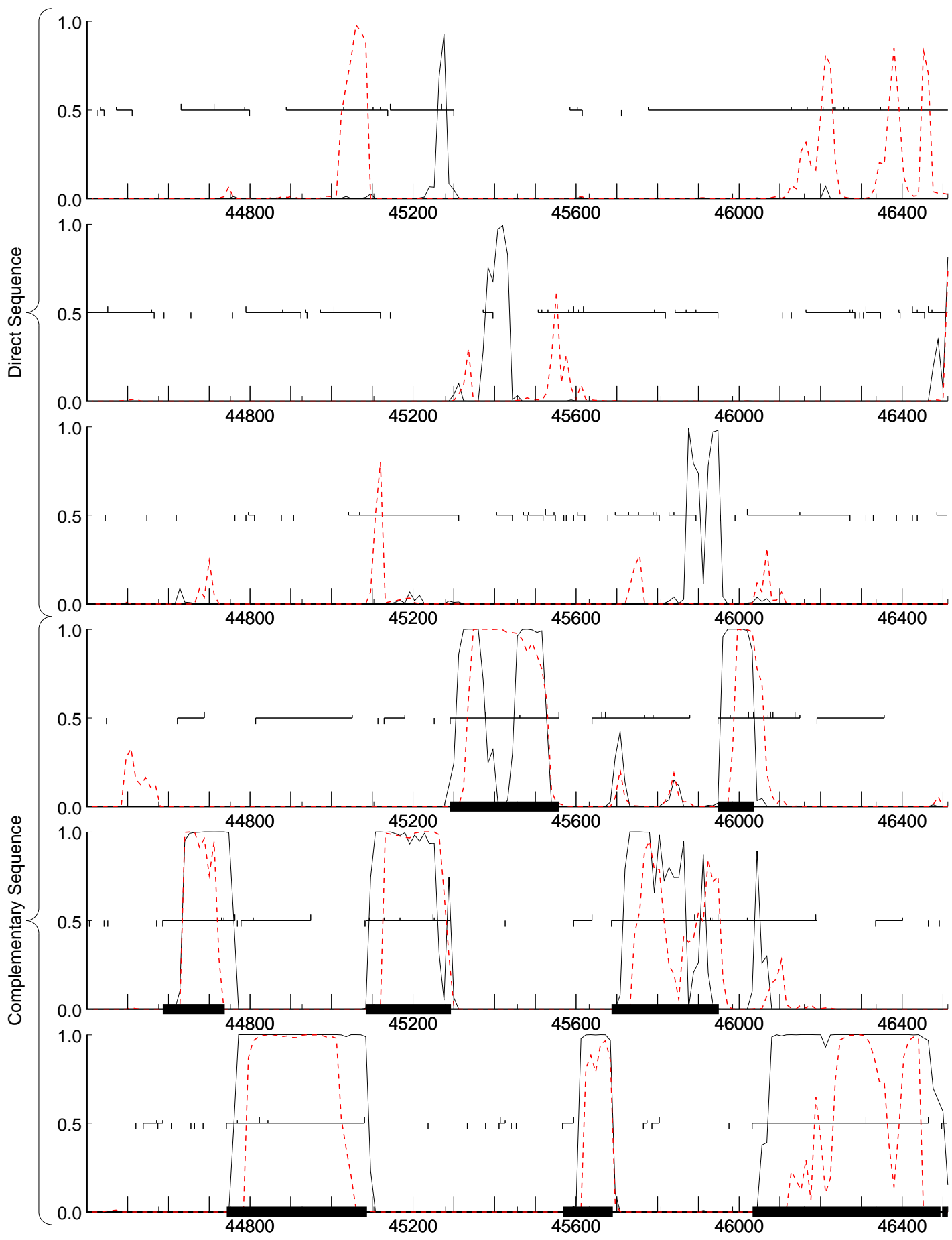


typical.ps

atypical.ps

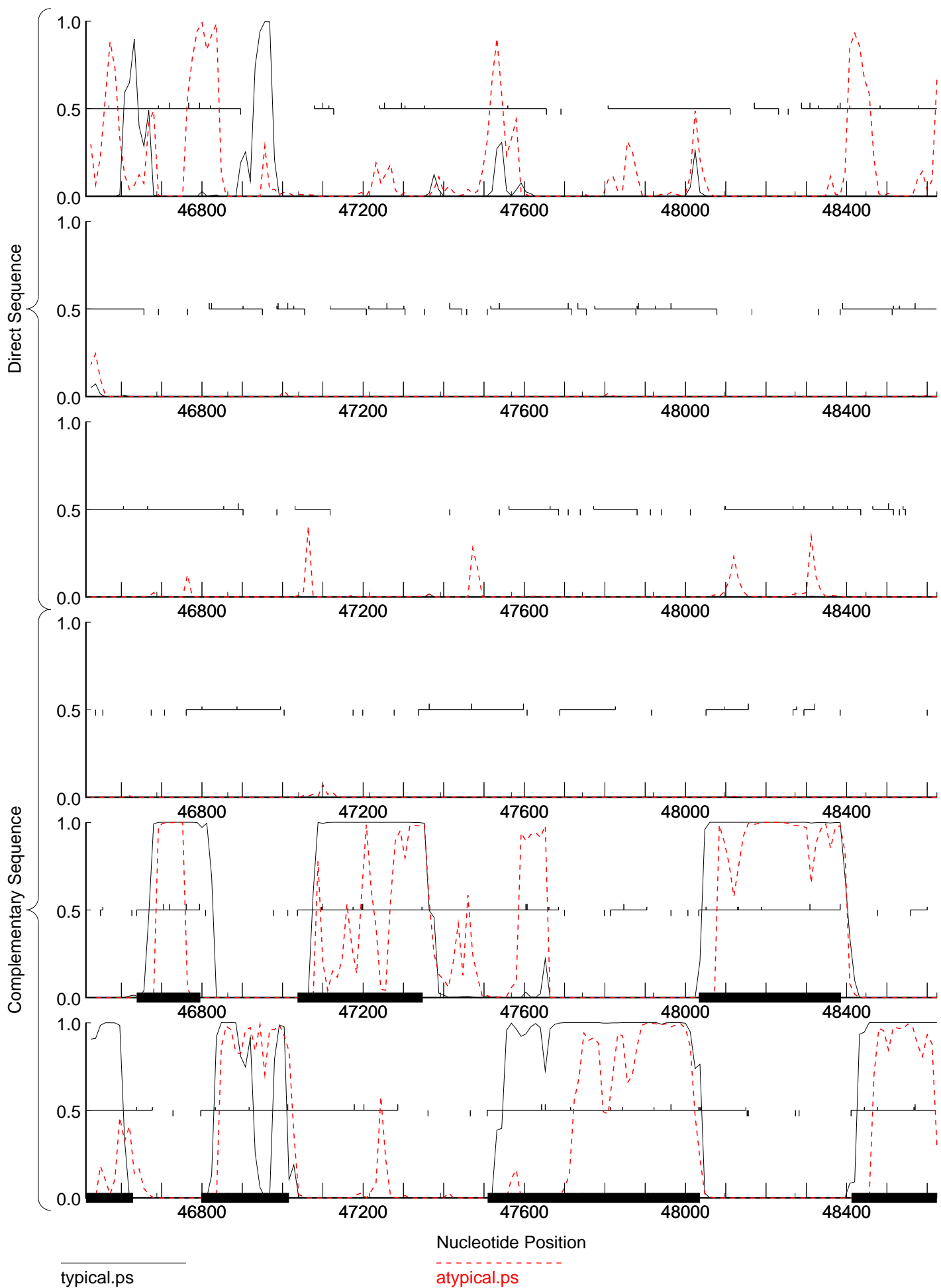






typical.ps

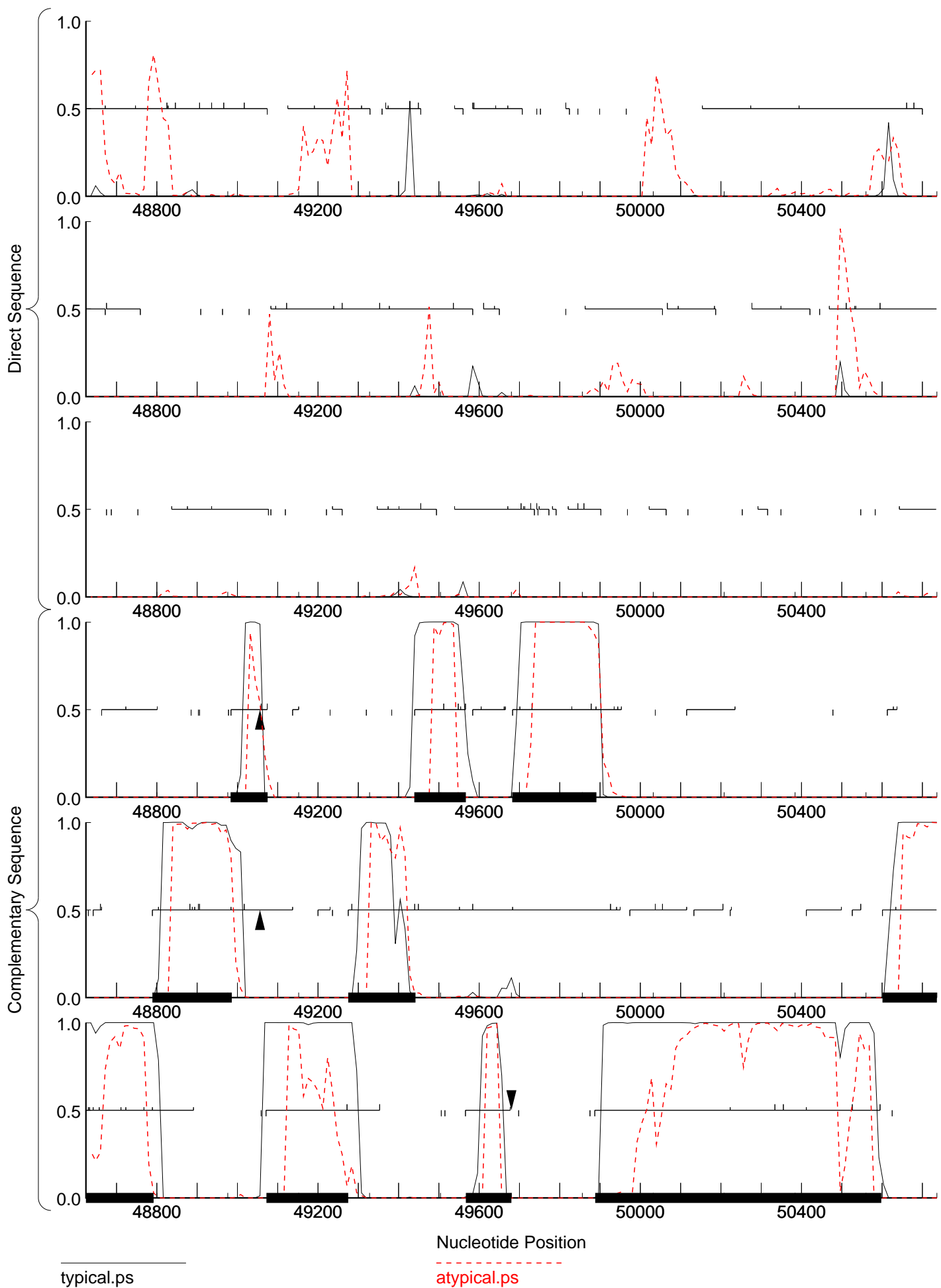
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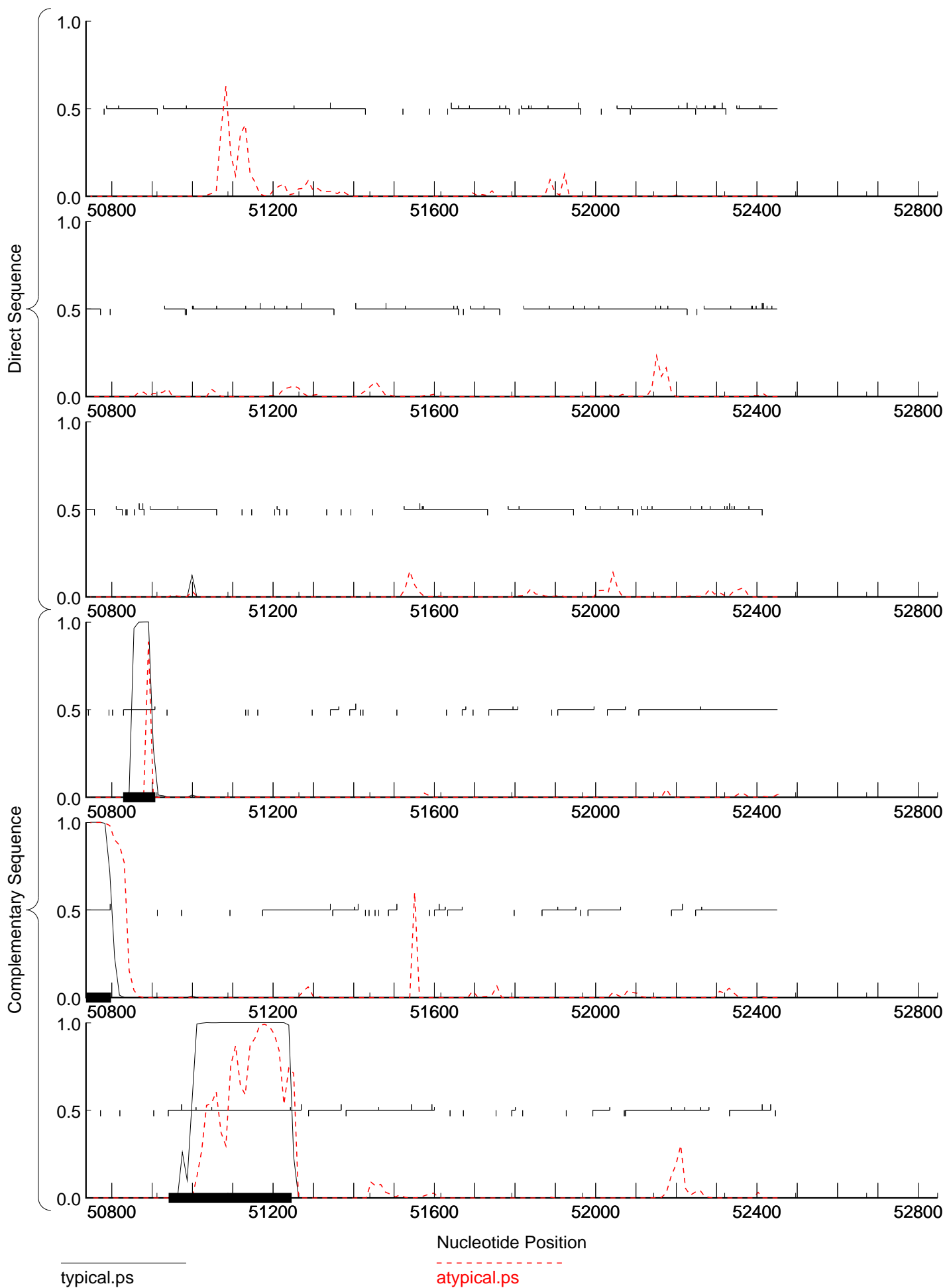


typical.ps

atypical.ps







typical.ps

atypical.ps