

# GeneMark

Version 2.5p (09.08.06)

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## PROGRAM INFORMATION

Sequence : Mycobacterium phage Ein37 complete sequence, 53748 bp including 14 bp 3' overhang (TAAGCCGC  
Analysis Date : 5/24/17 at 13:46:06  
Pages : 27  
Sequence Length : 53748 bp  
GC Content : 67.45%

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,

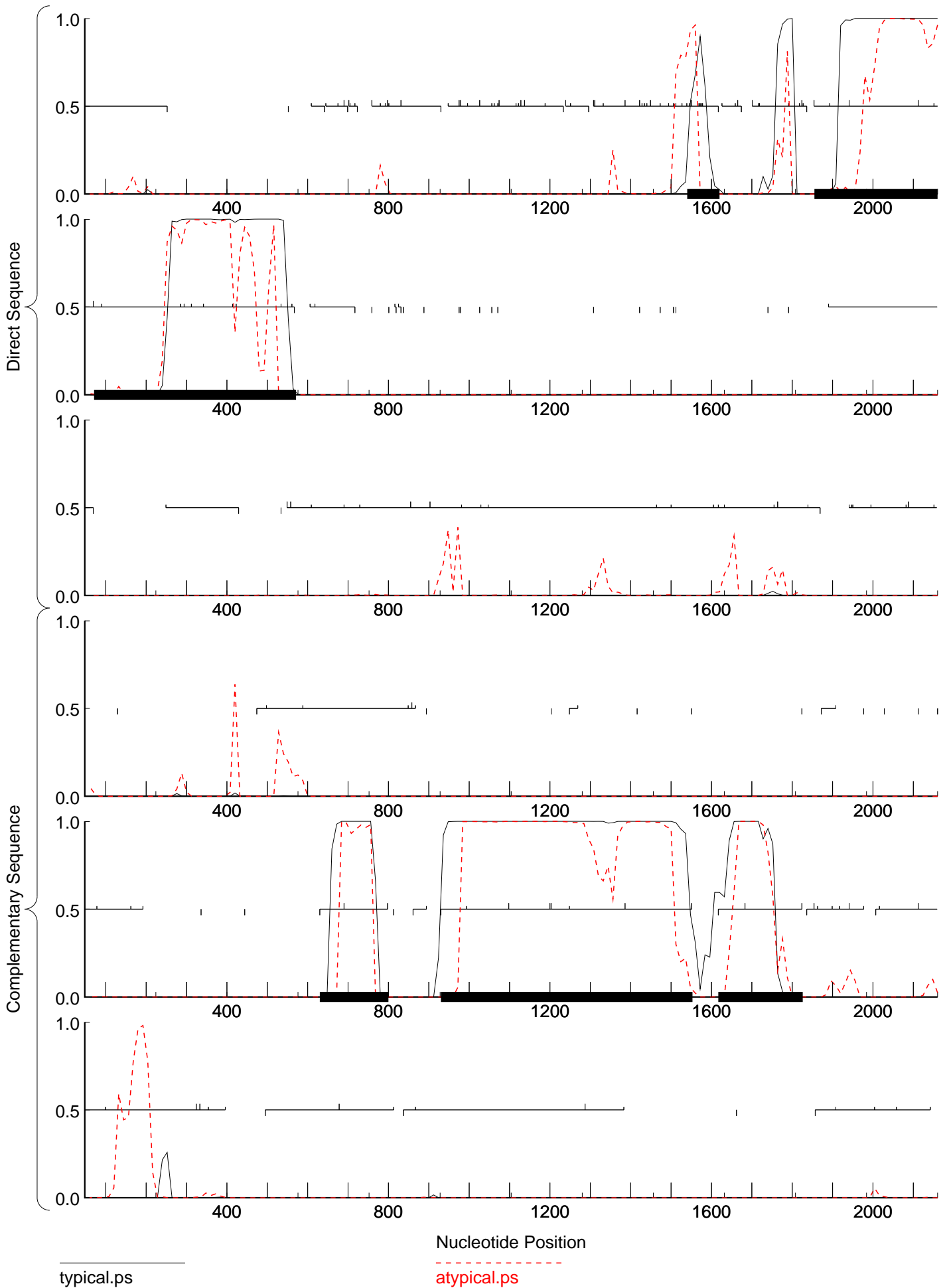
## Matrix notes & comments

Training set derived by GeneMarkS, 4.30 October 2014  
Wed May 24 13:46:06 2017

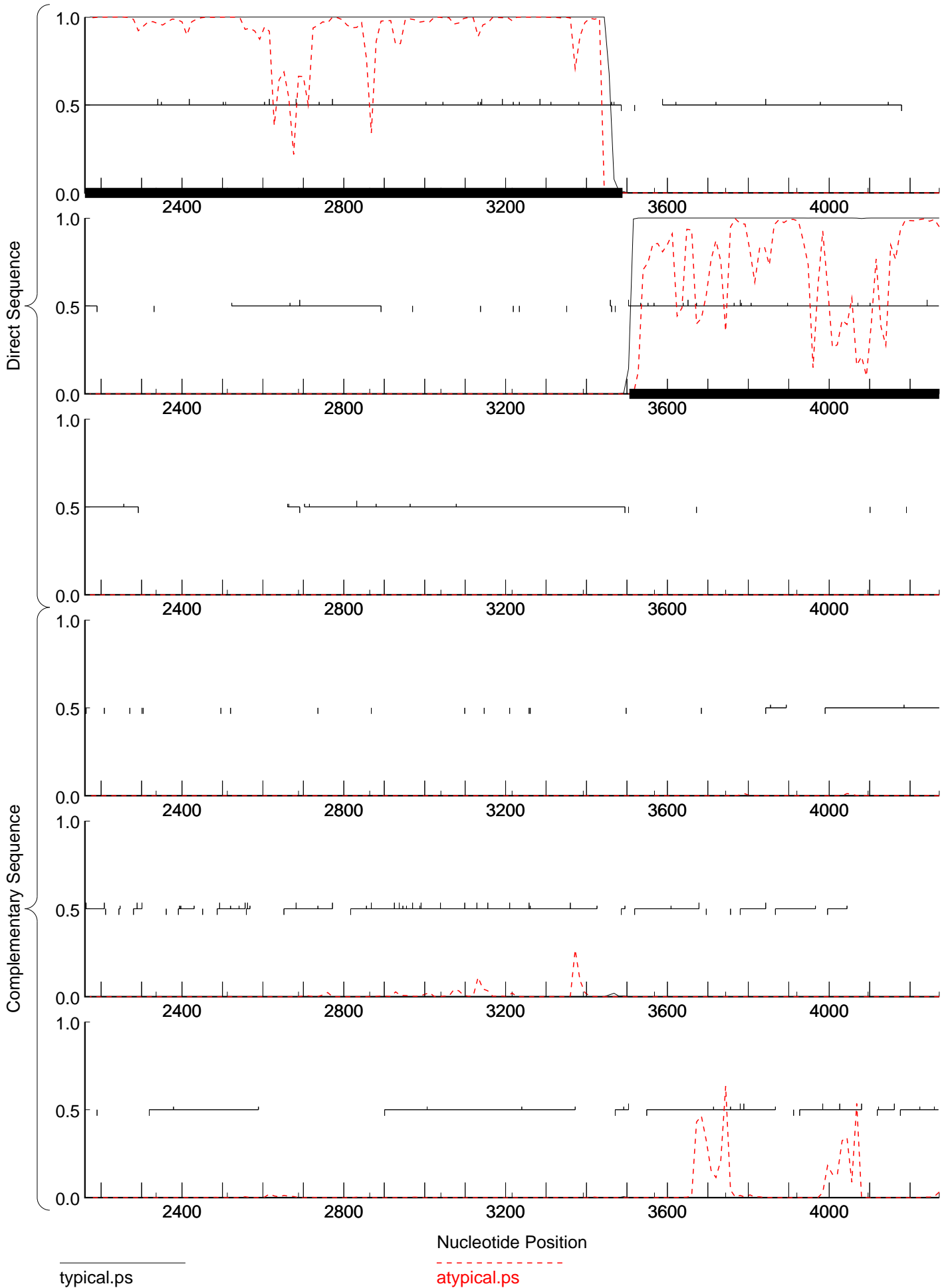
## MATRIX INFORMATION

Matrix : -  
Author : -  
Order : 4

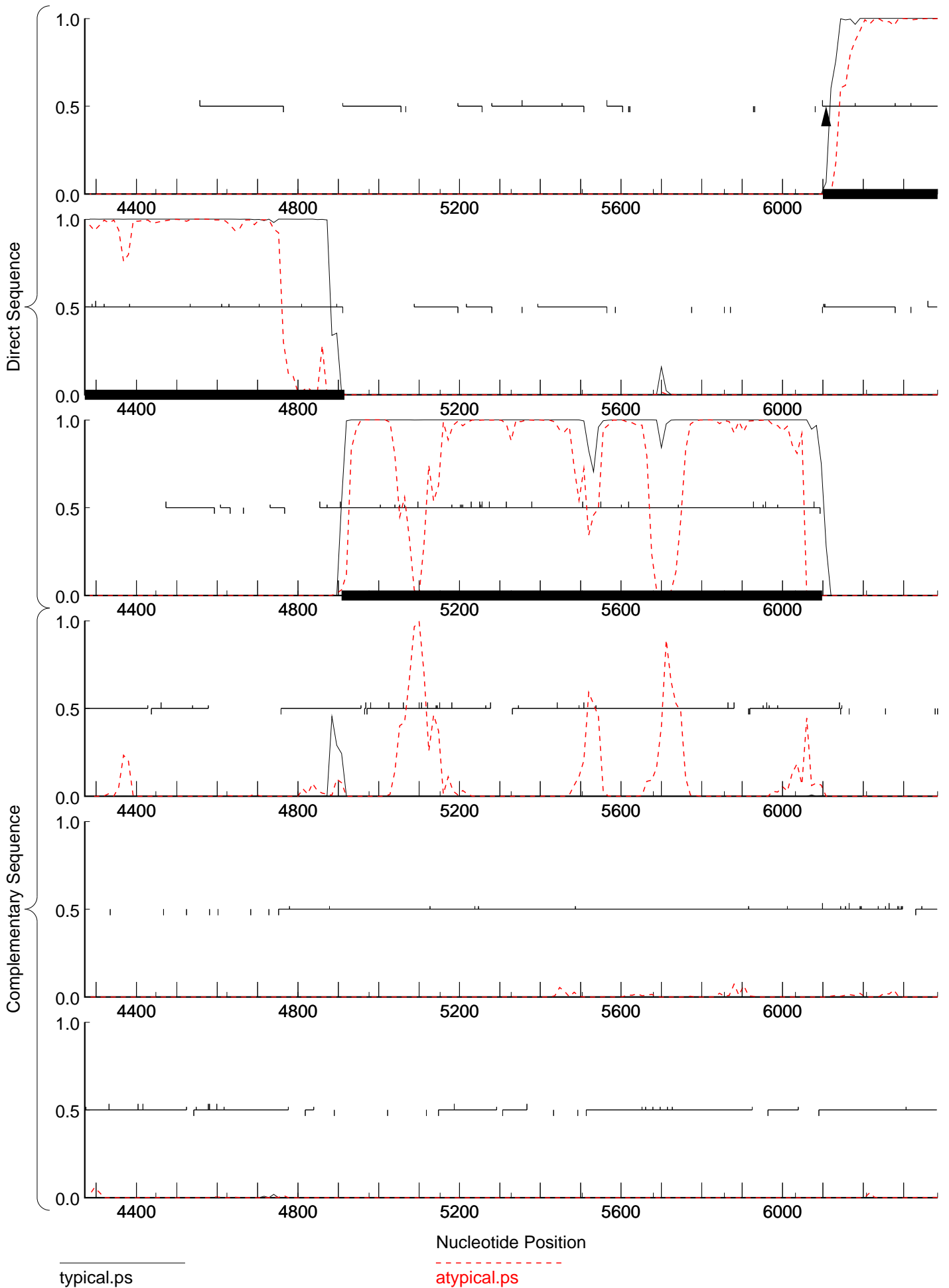
Send questions / comments to:  
Dr. M. Borodovsky  
Georgia Institute of Technology  
School of Biology  
Atlanta, GA 30332-0230



complete sequence, 53748 bp including 14 bp 3' overhang (TAAGCCGCGCGGTA), Cluster Q, Order 4, Window 96, Step 12, 3/27  
complete sequence, 53748 bp including 14 bp 3' overhang (TAAGCCGCGCGGTA), Cluster Q, Order 2, Window 96, Step 12, 3/27



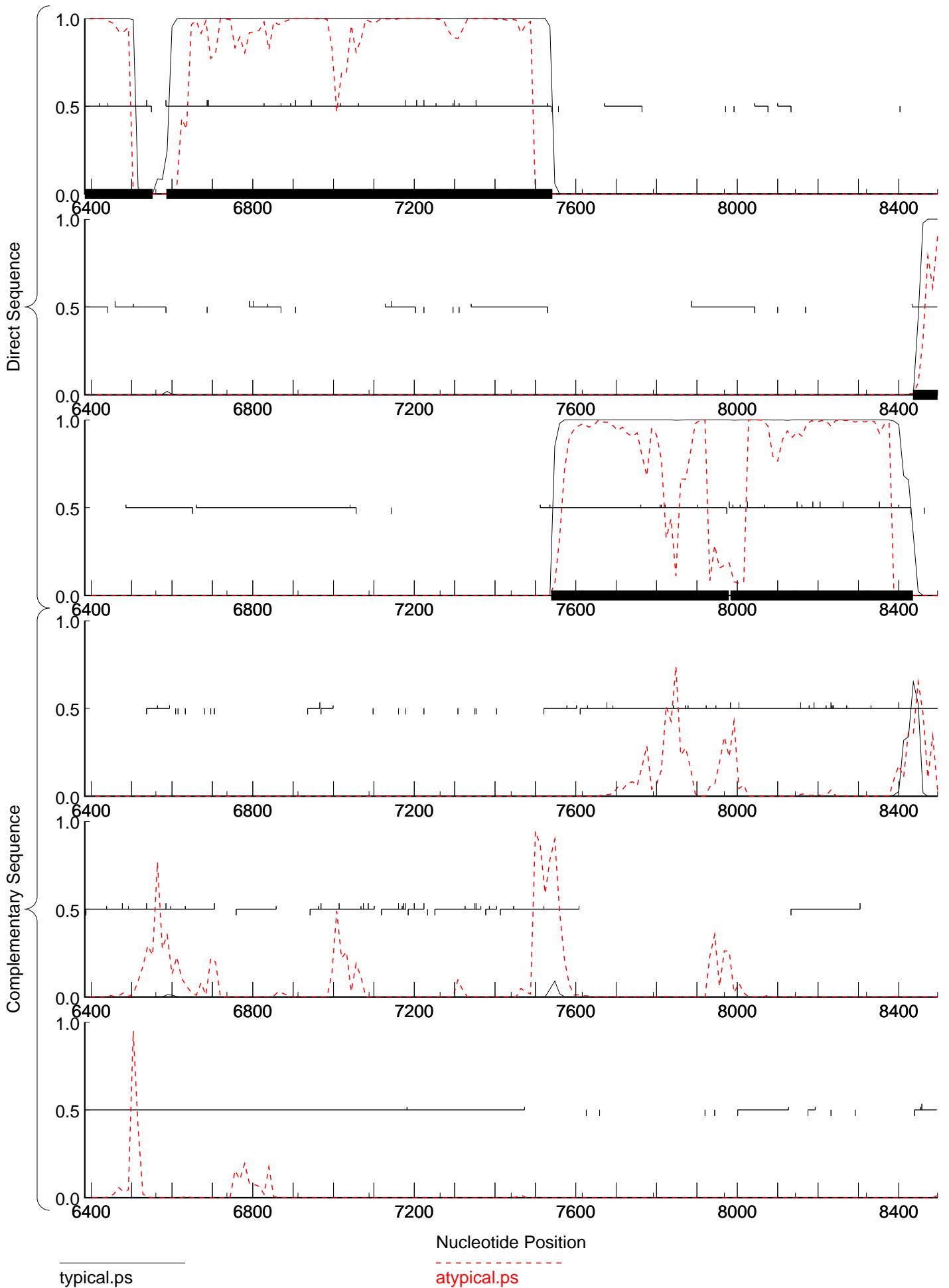
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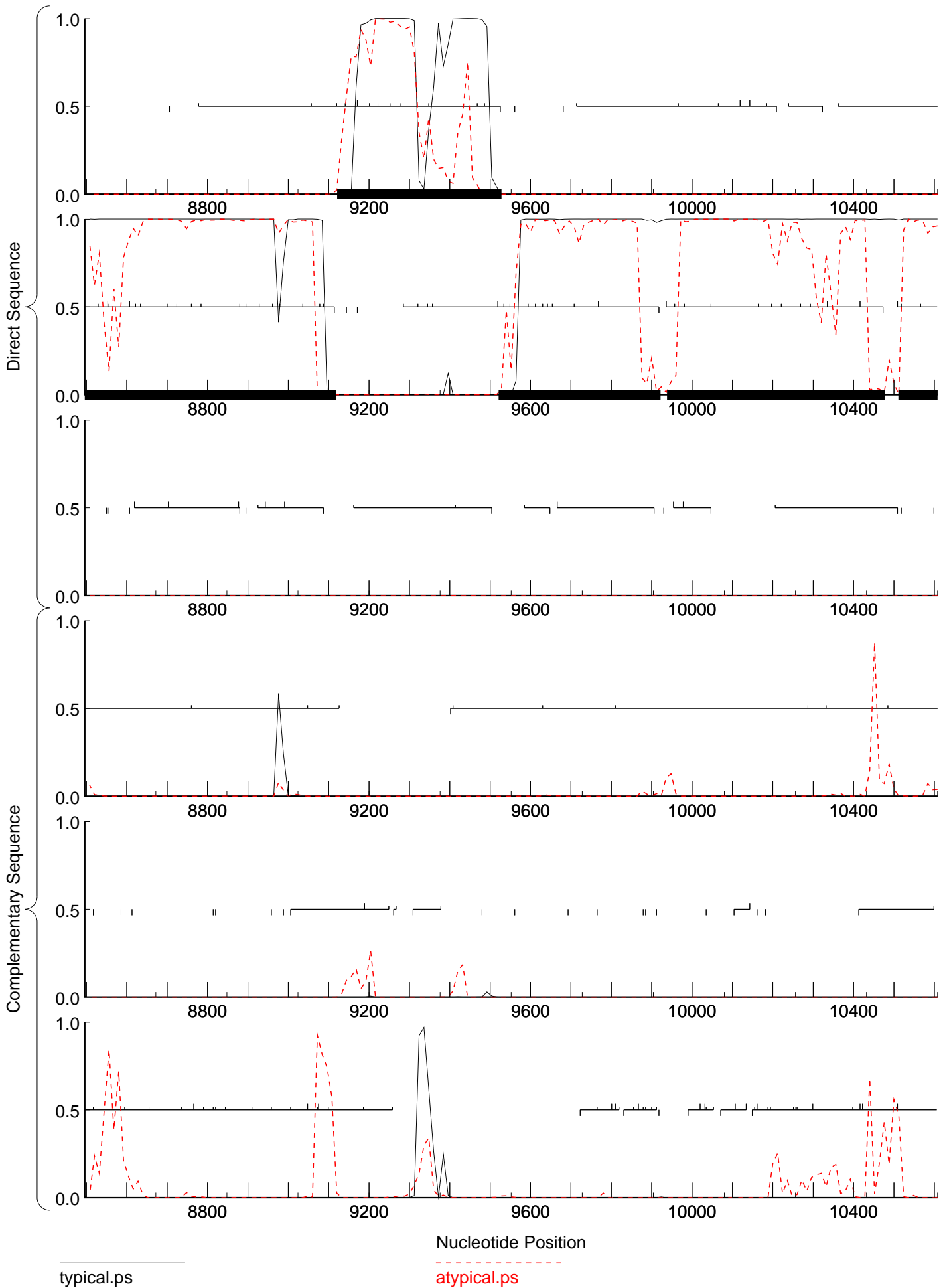


typical.ps

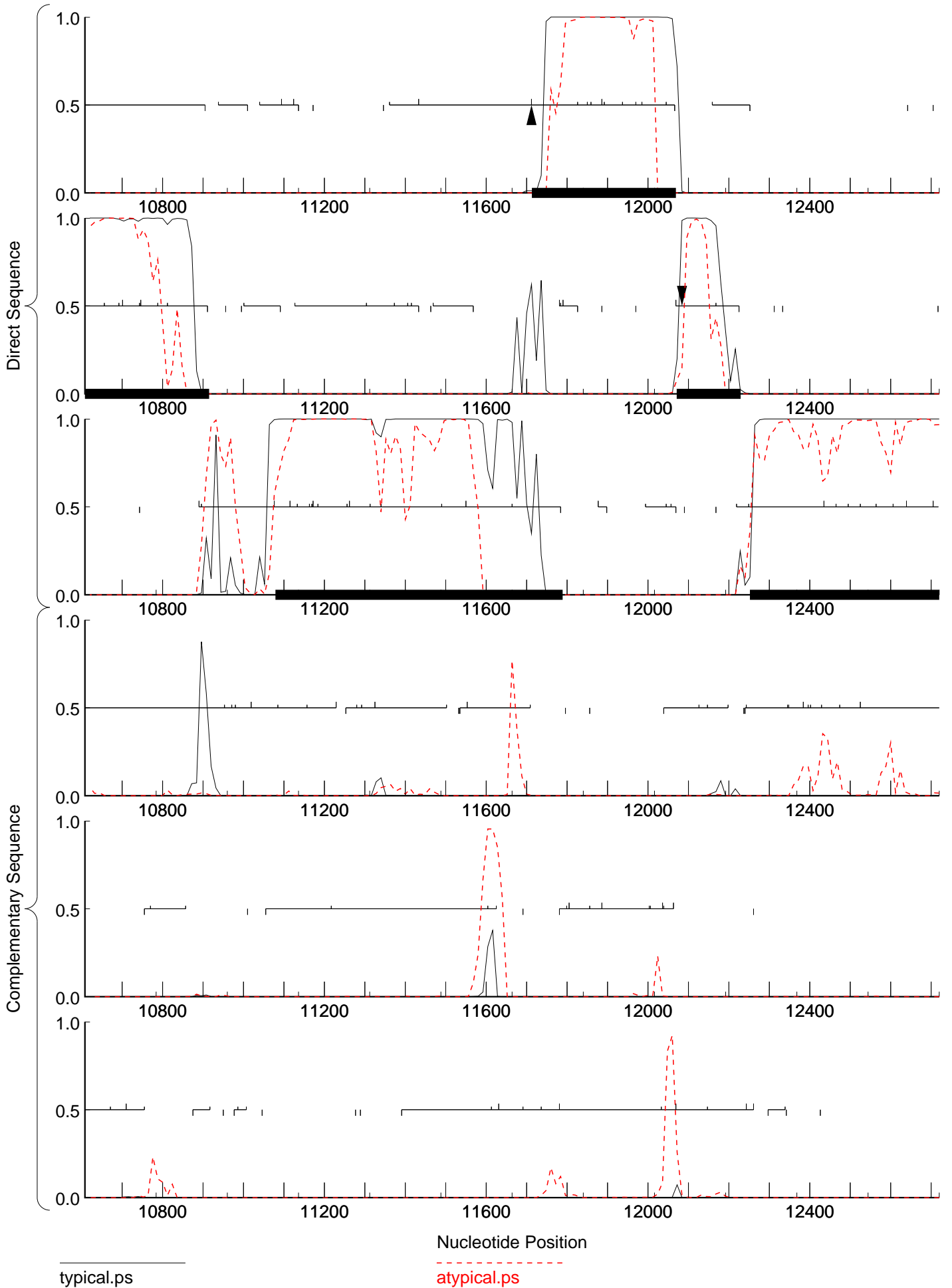
atypical.ps

complete sequence, 53748 bp including 14 bp 3' overhang (TAAGCCGCGCGGTA), Cluster Q, Order 4, Window 96, Step 12, 5/27  
complete sequence, 53748 bp including 14 bp 3' overhang (TAAGCCGCGCGGTA), Cluster Q, Order 2, Window 96, Step 12, 5/27

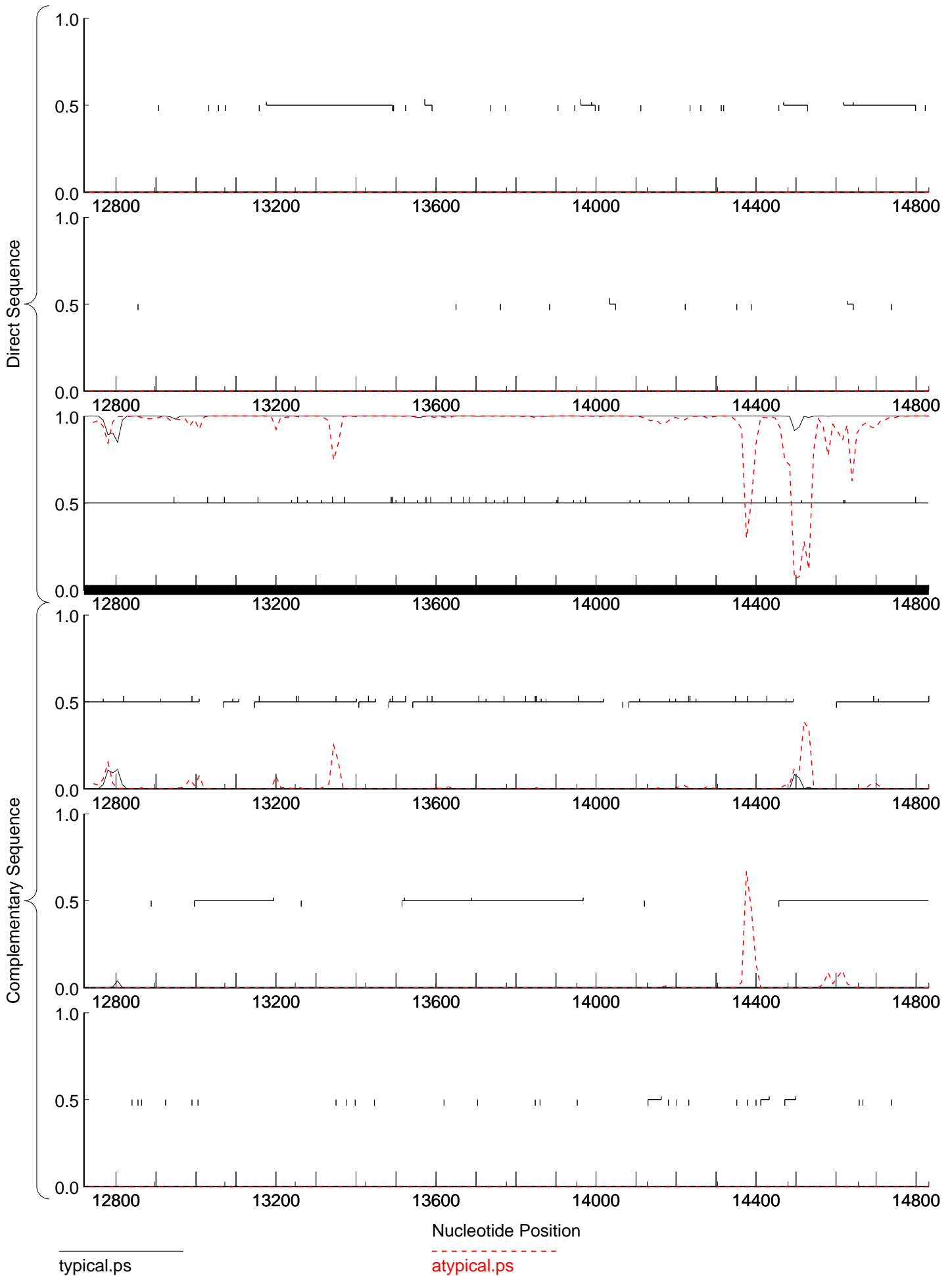




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complete sequence, 53748 bp including 14 bp 3' overhang (TAAGCCGCGCGGTA), Cluster Q, Order 2, Window 96, Step 12, 7/27

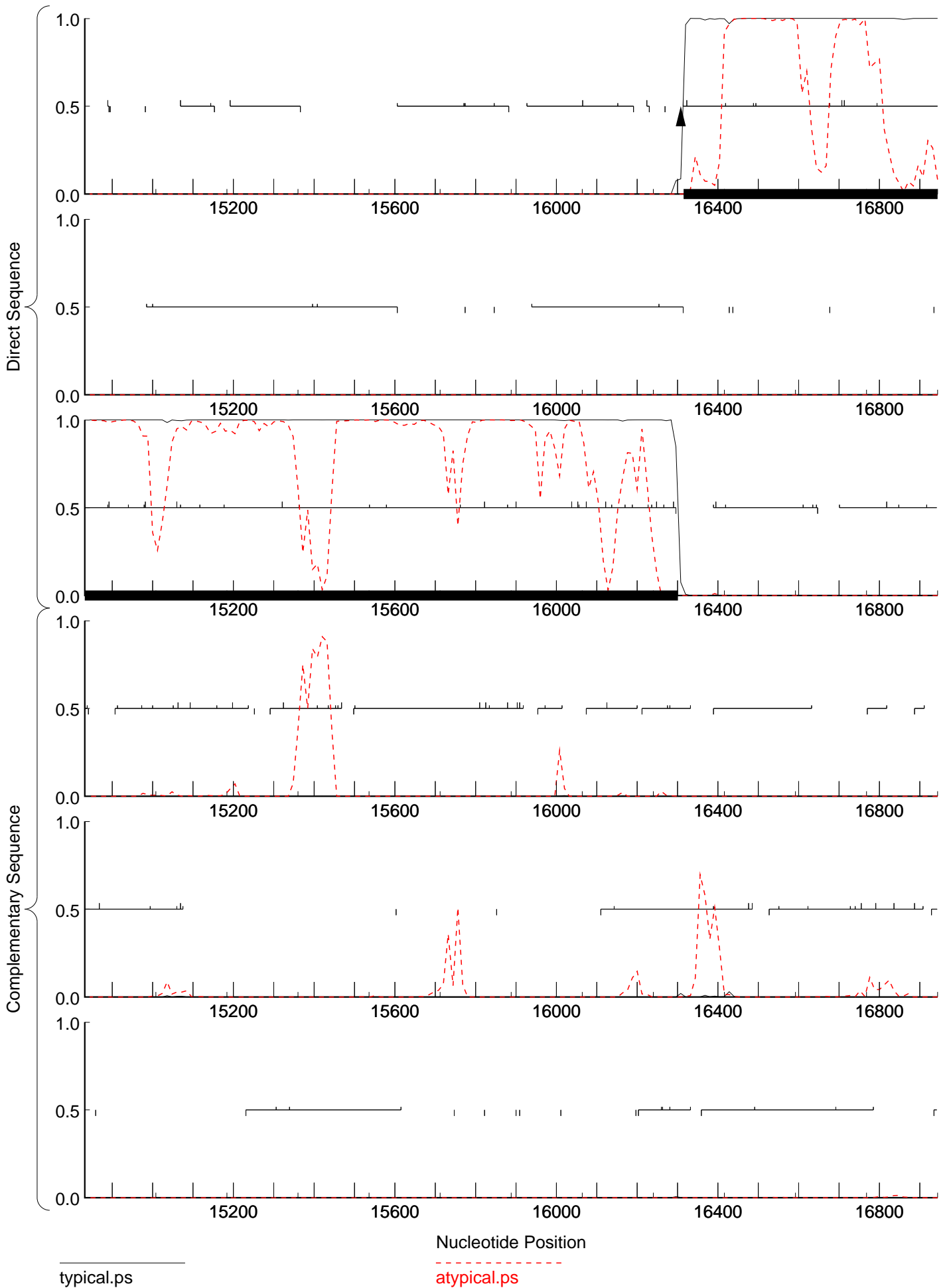


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complete sequence, 53748 bp including 14 bp 3' overhang (TAAGCCGCGCGGTA), Cluster Q, Order 2, Window 96, Step 12, 8/27



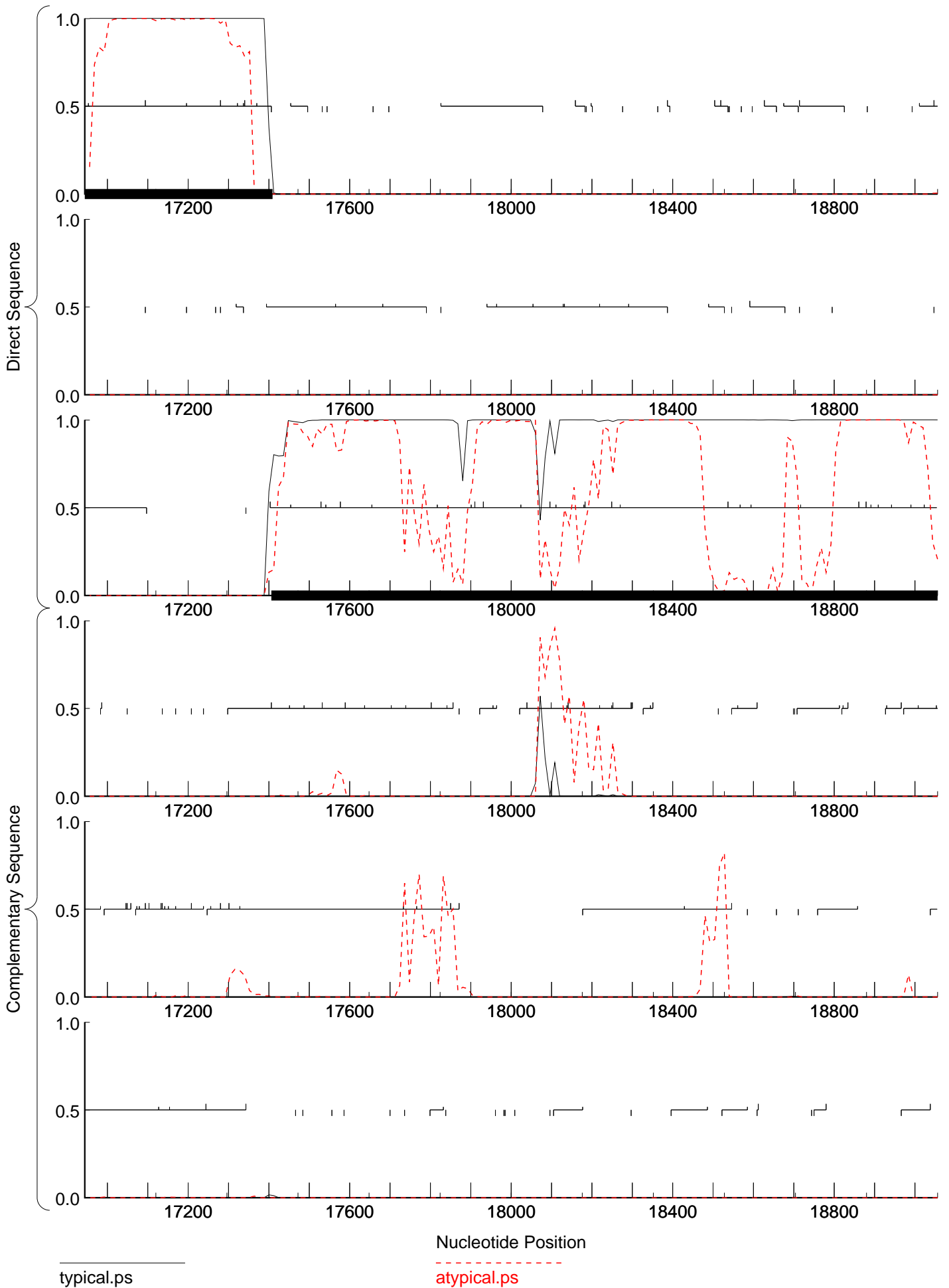


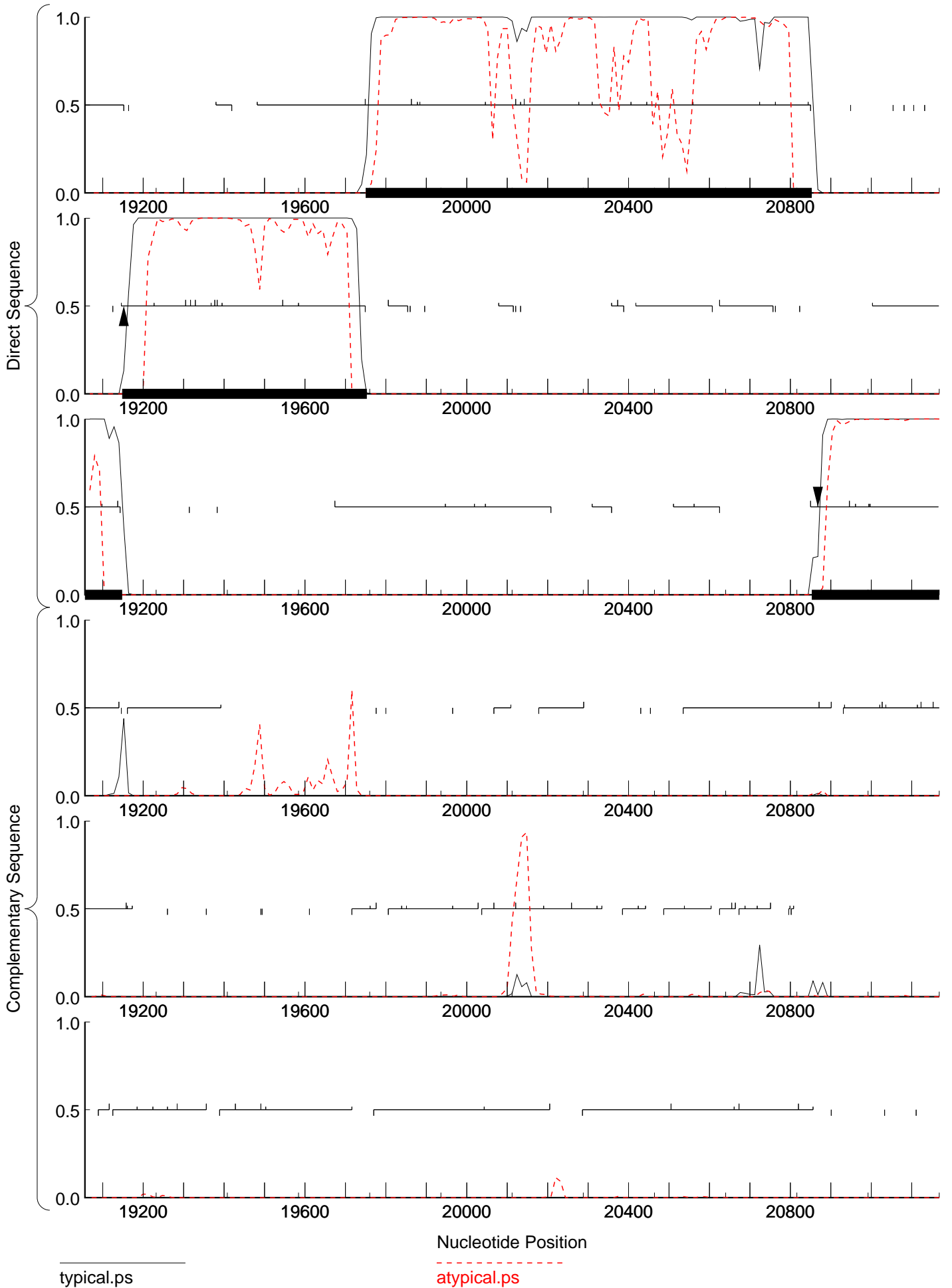
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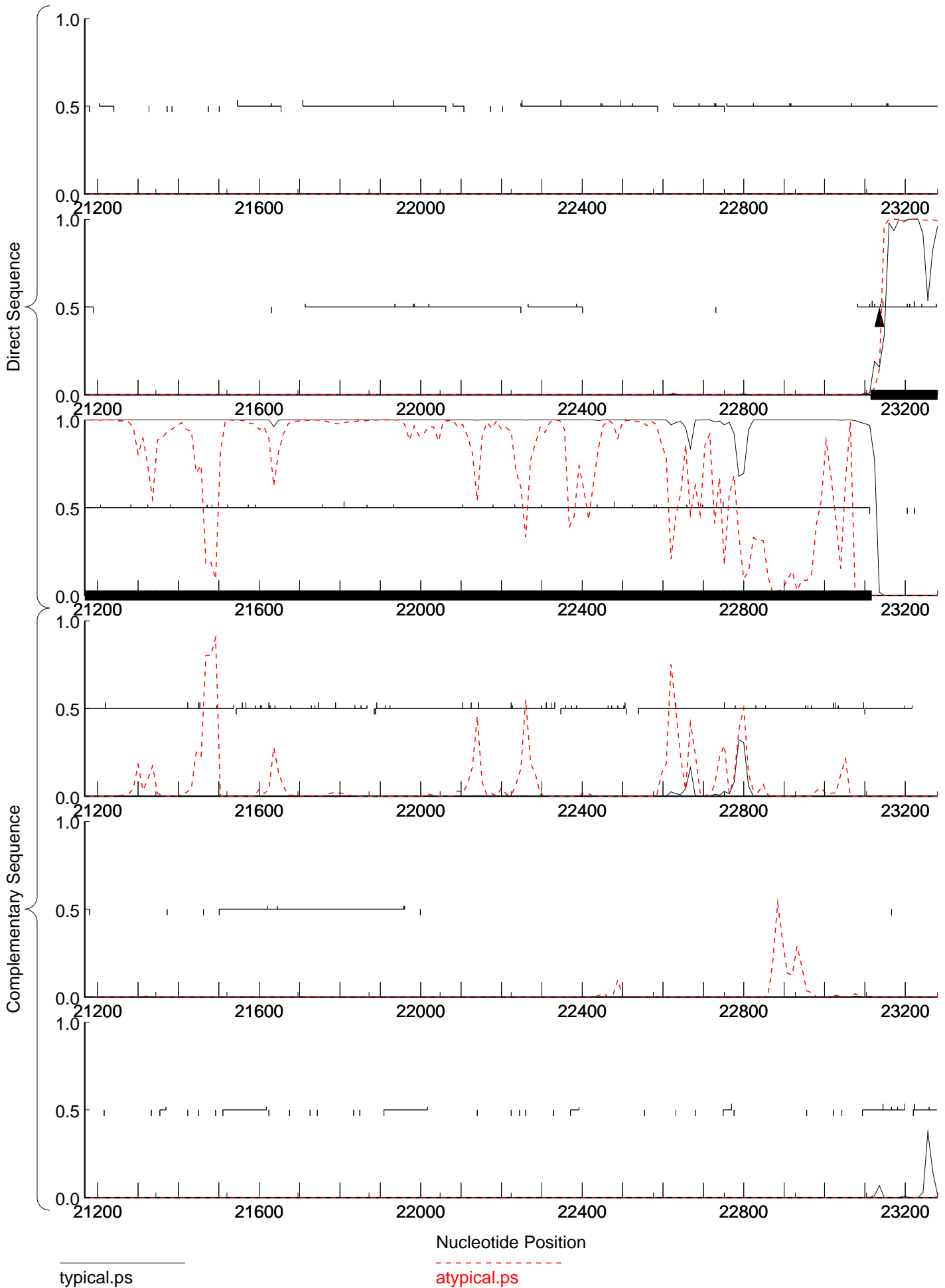


typical.ps

atypical.ps

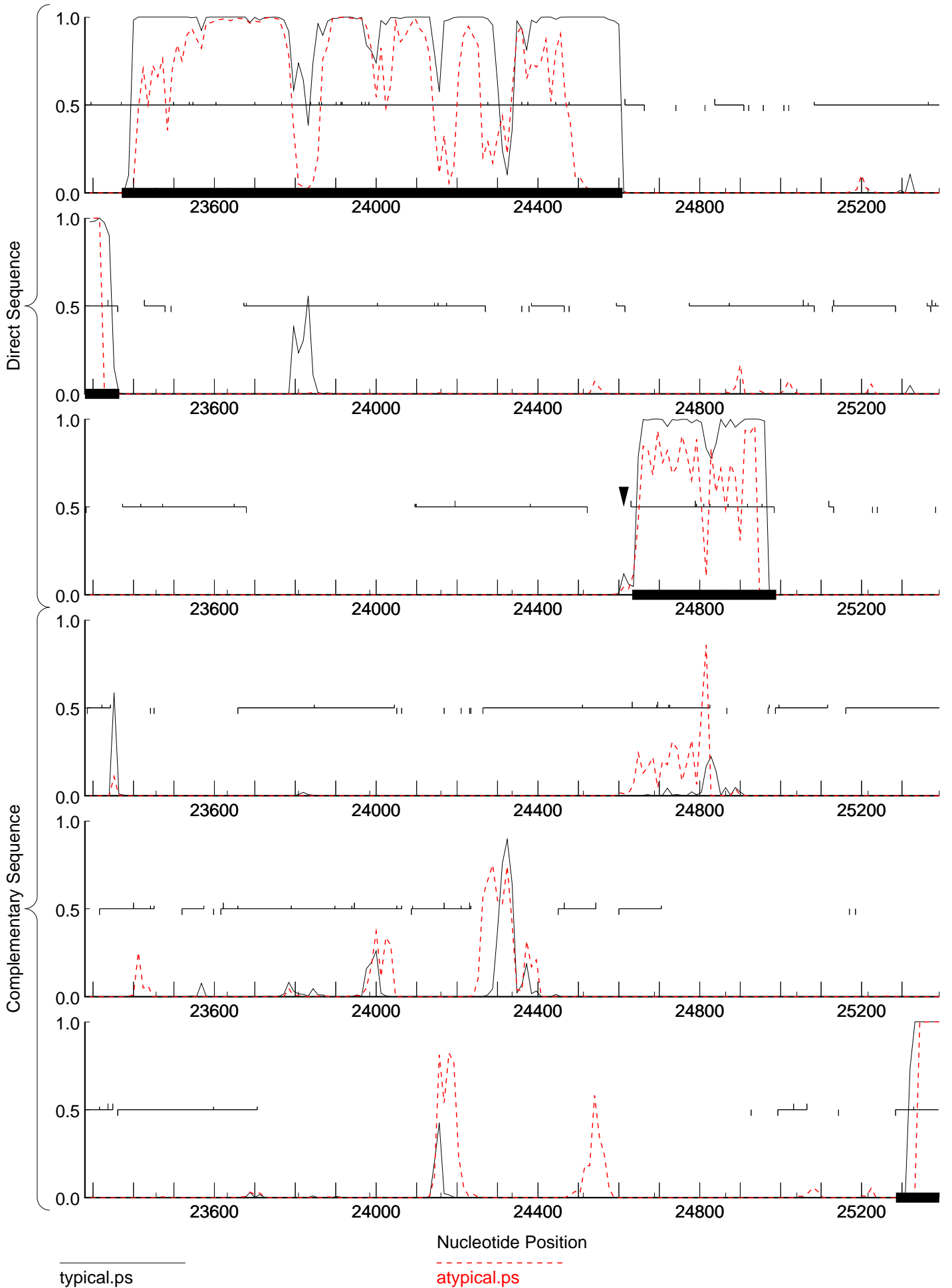






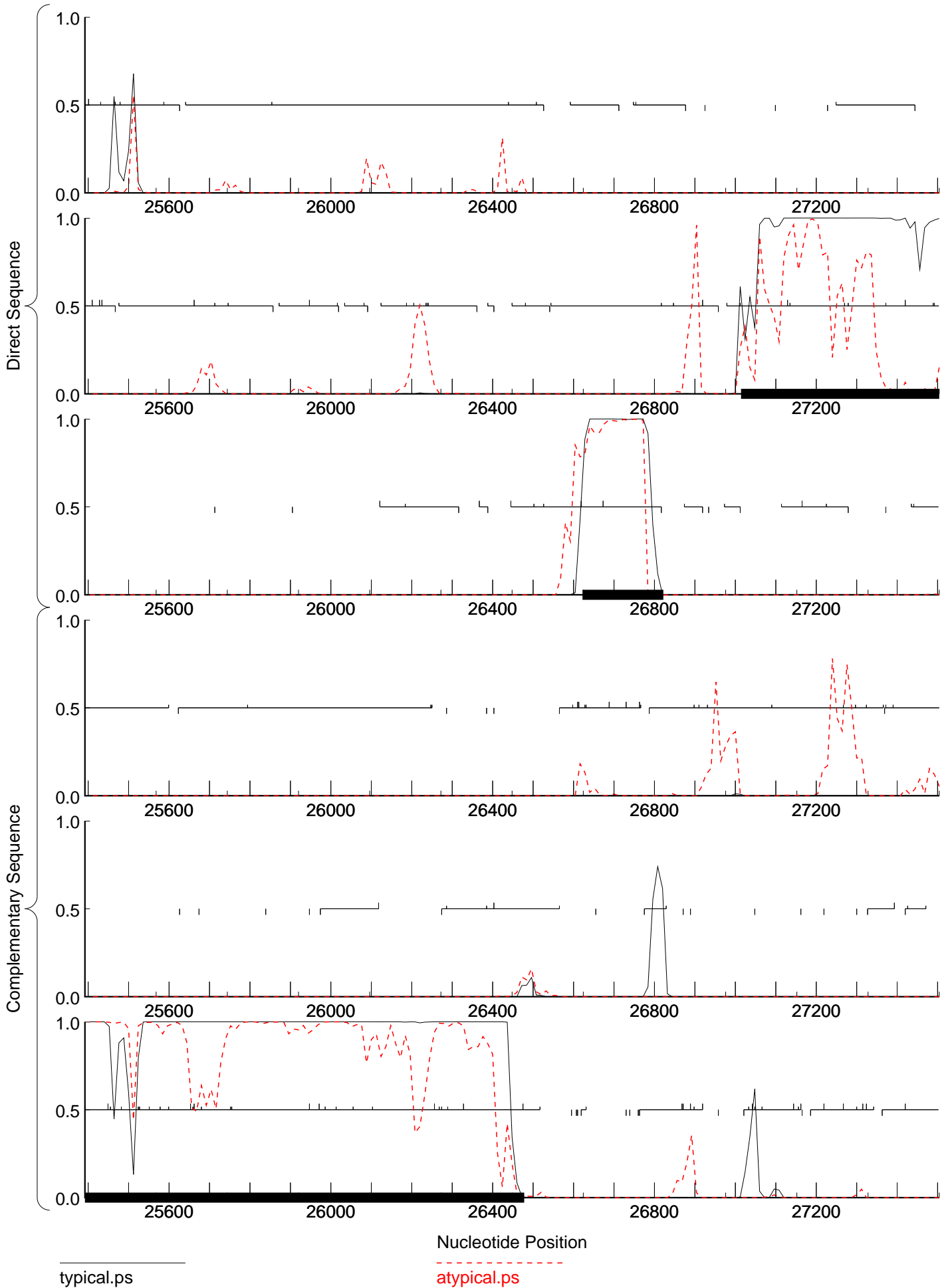
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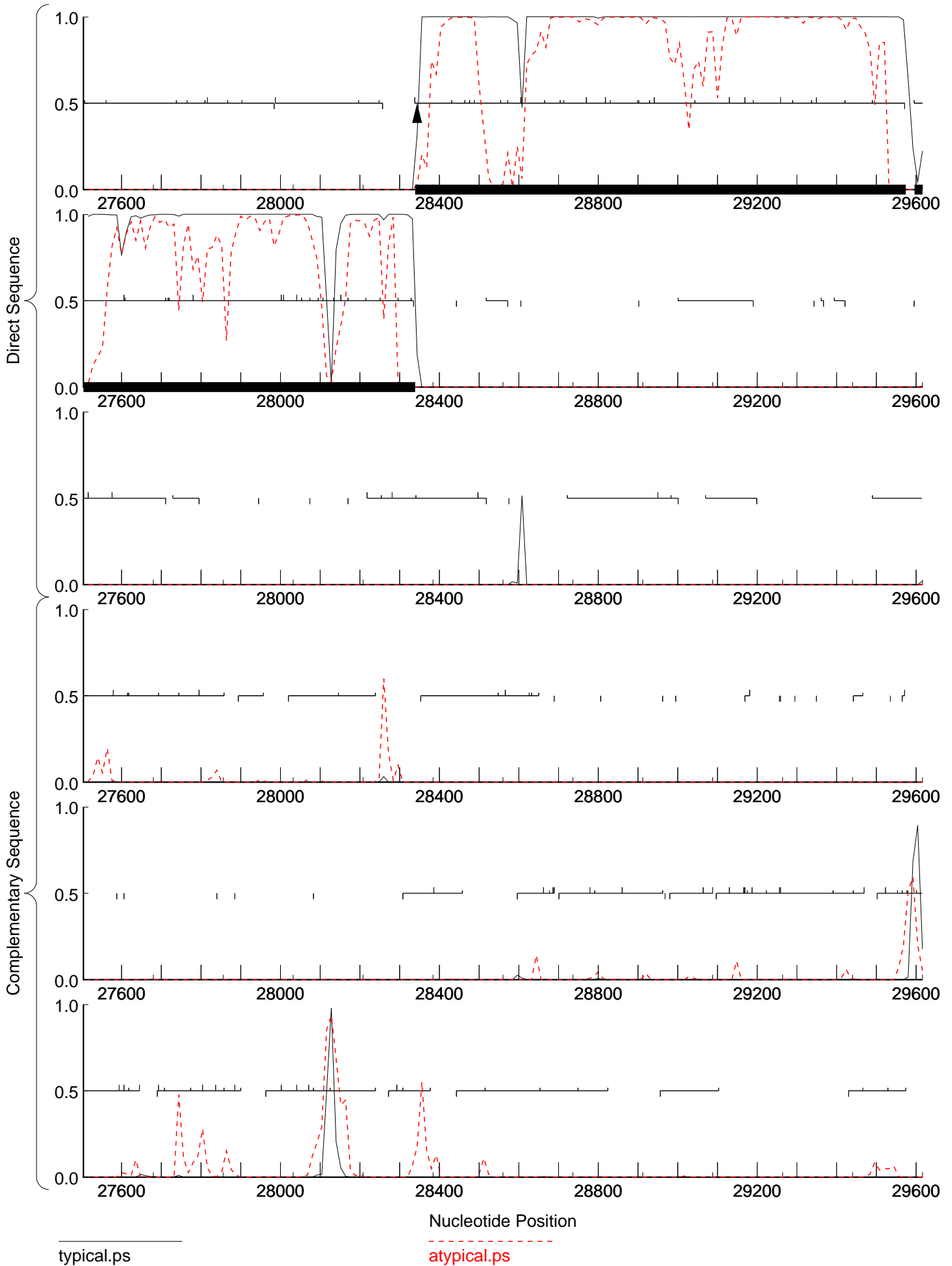
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typical.ps

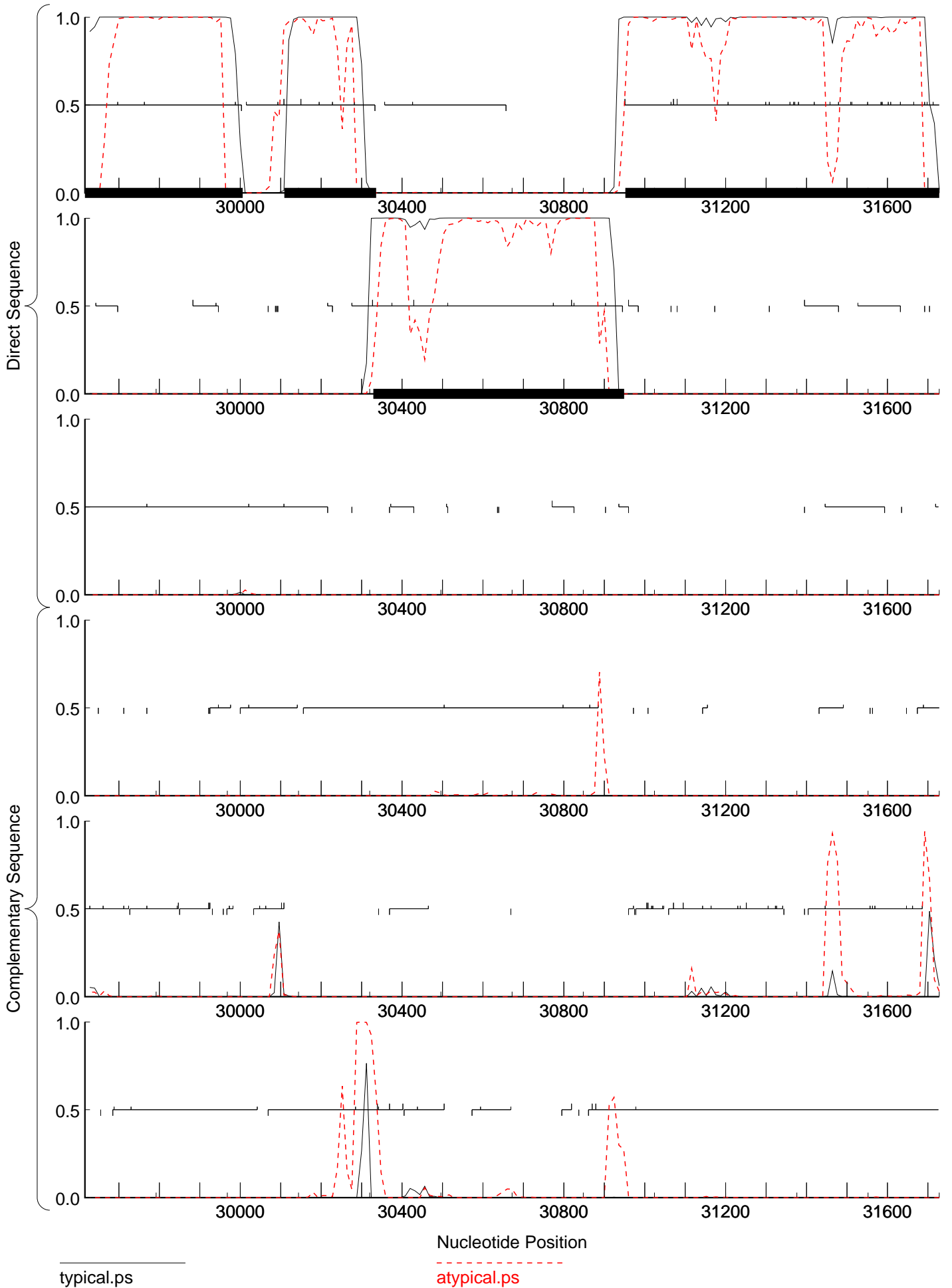
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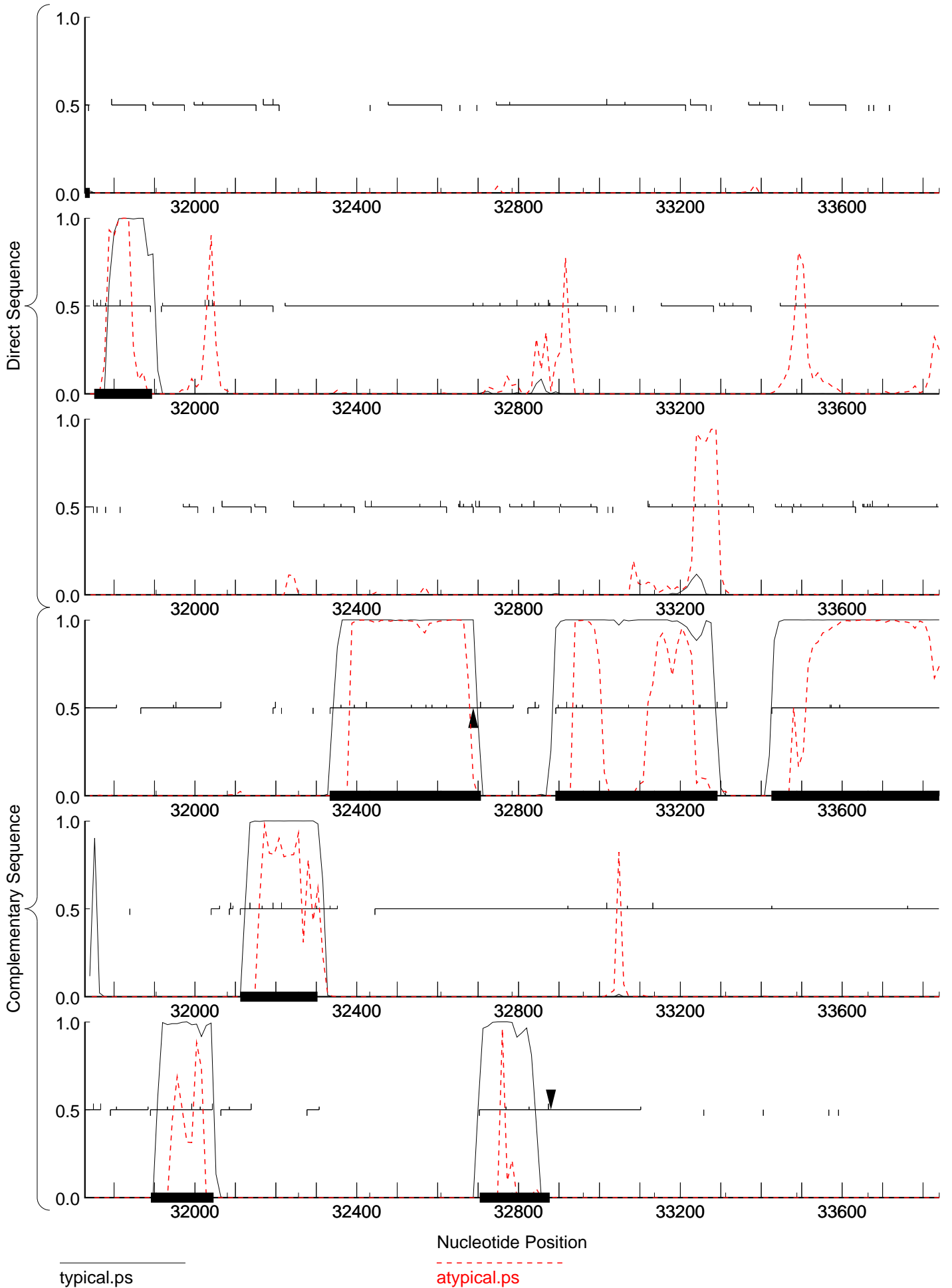


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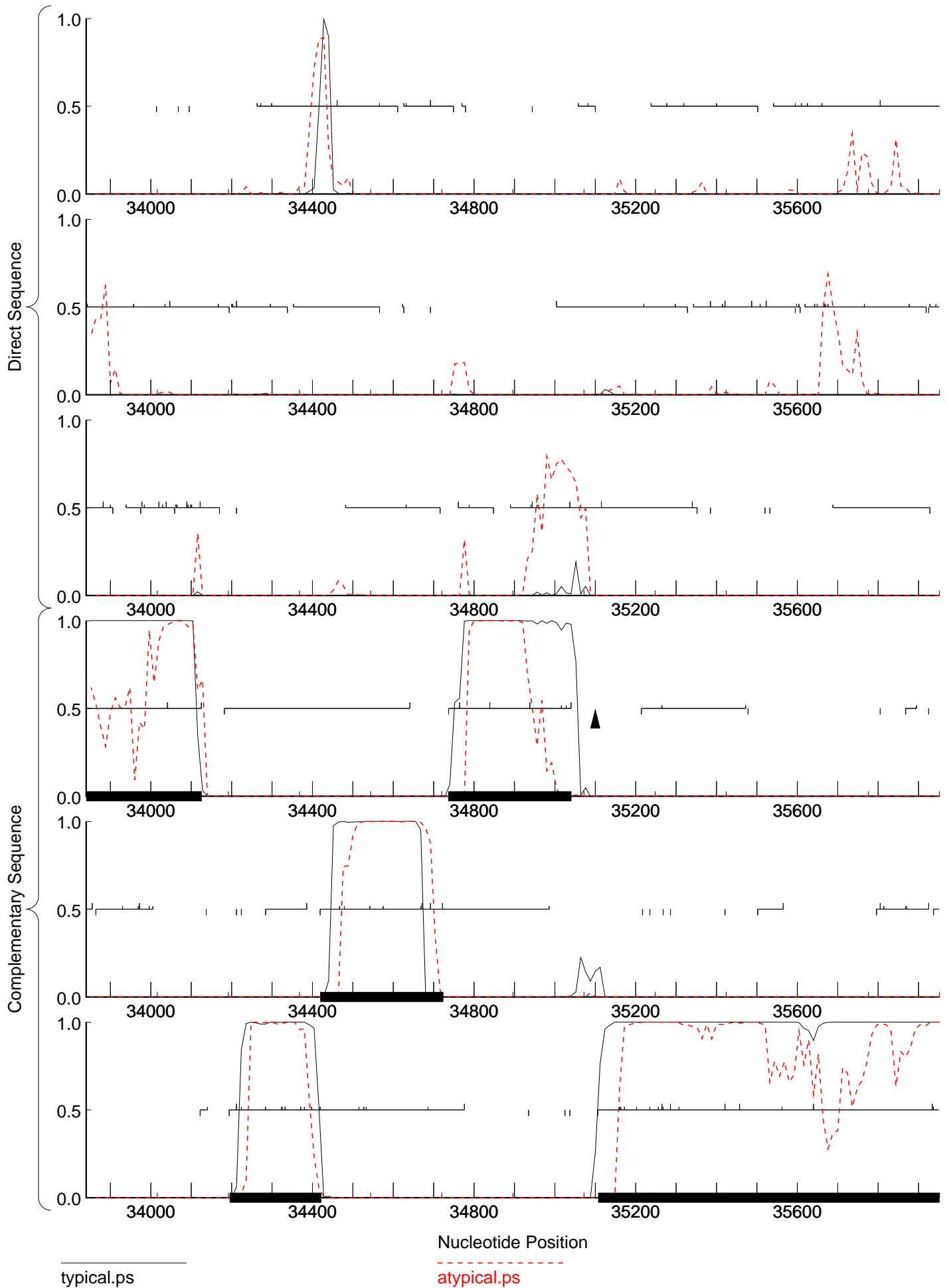
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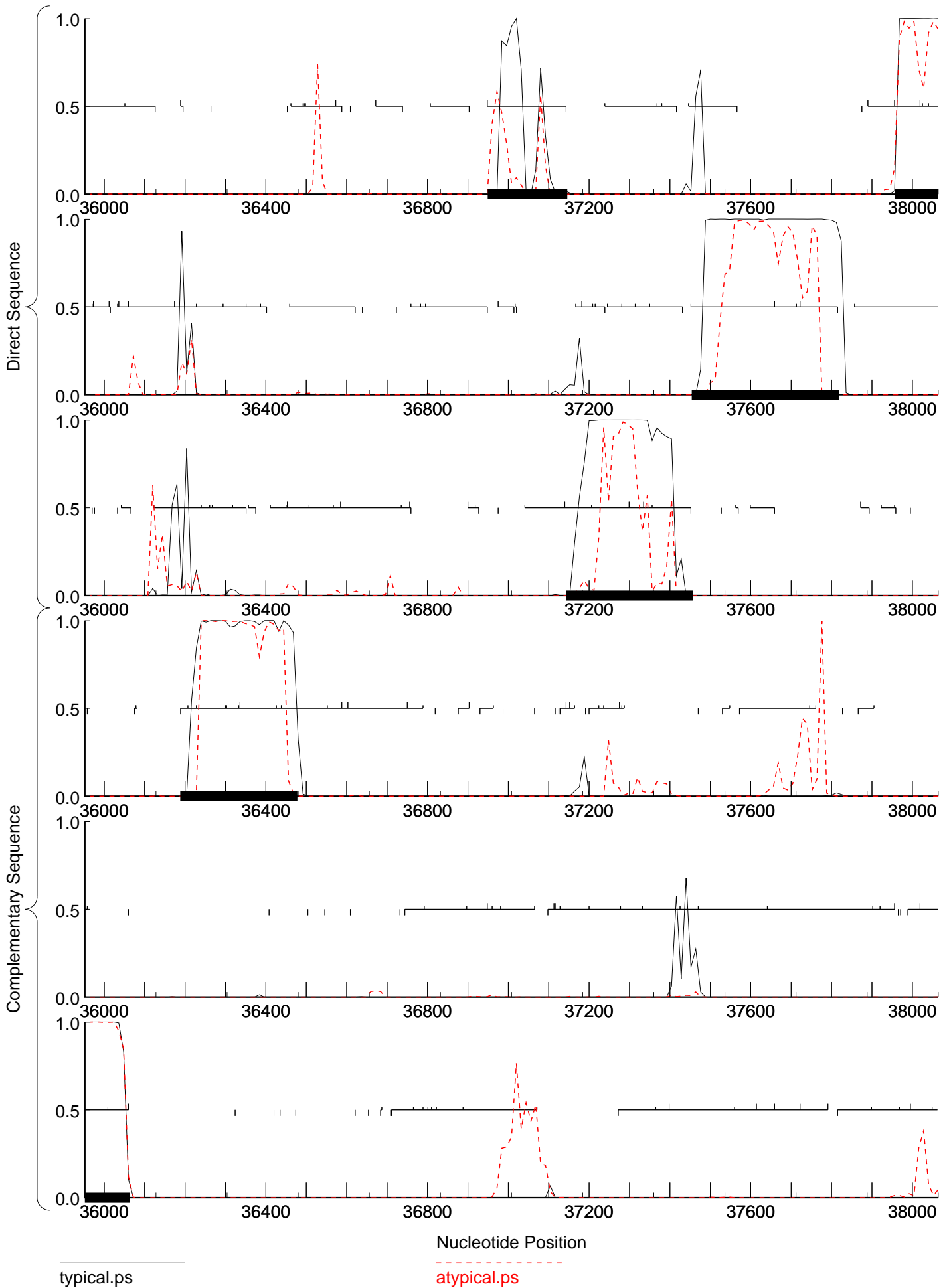


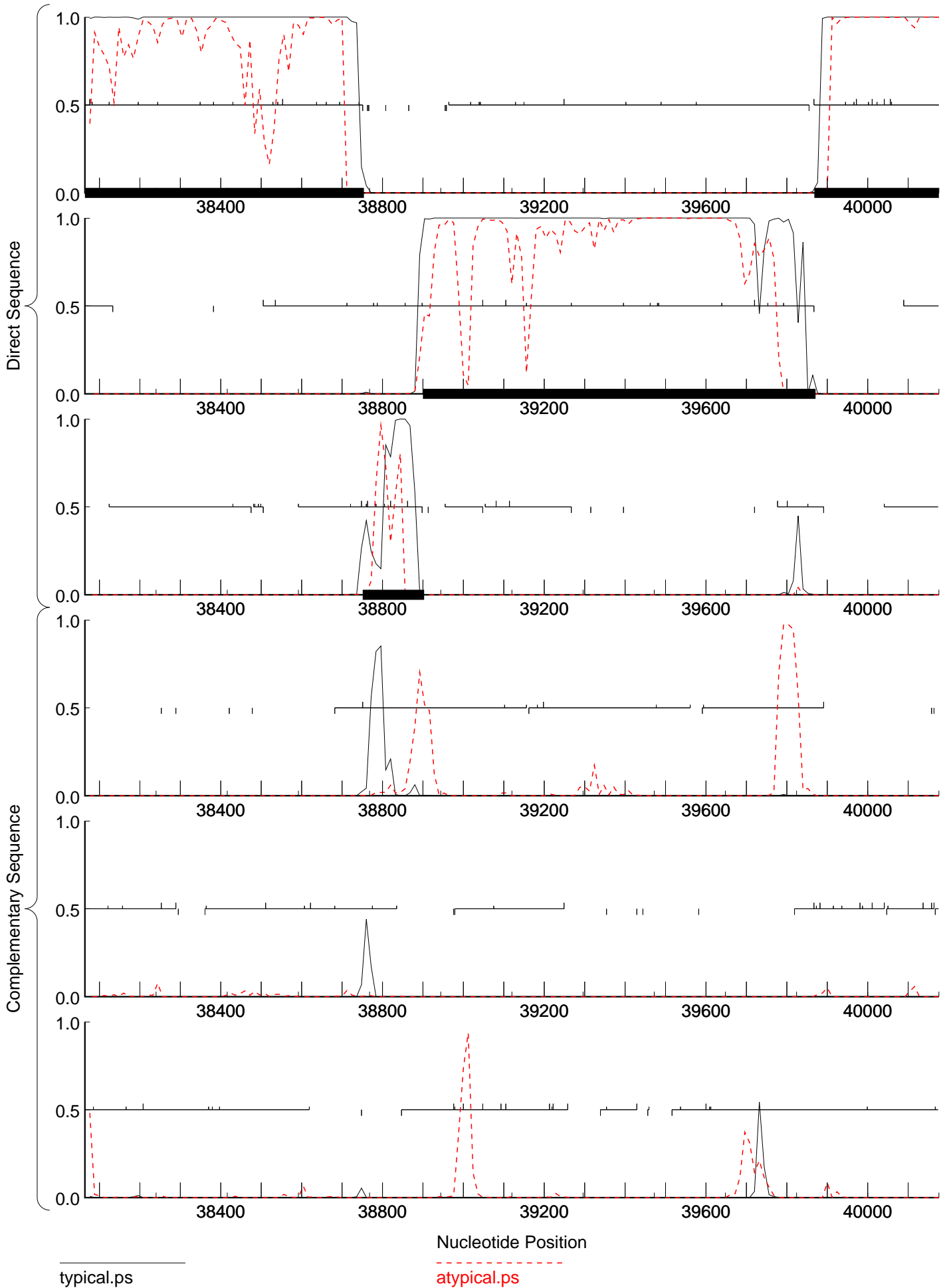
GeneMark.hmm prediction

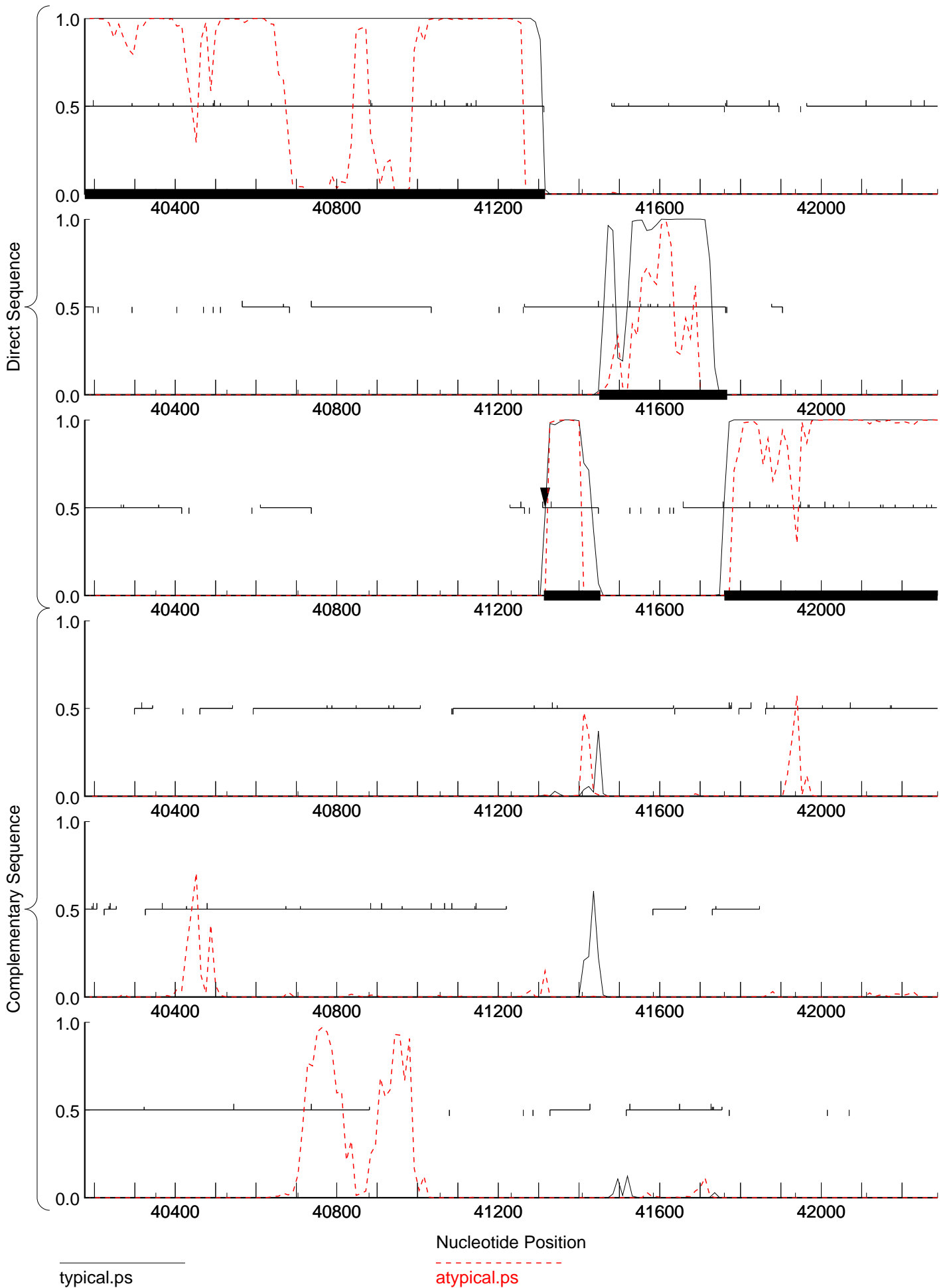


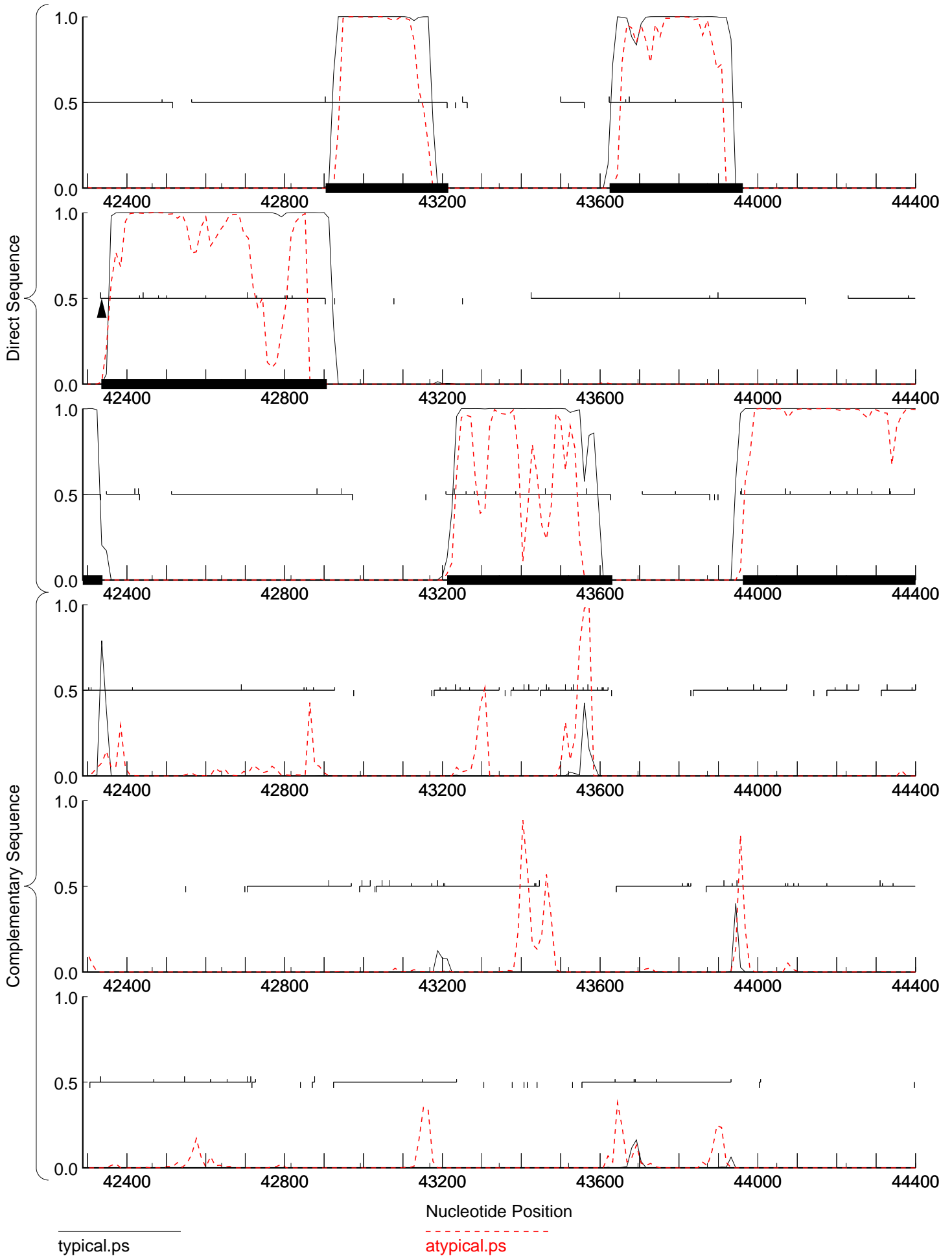
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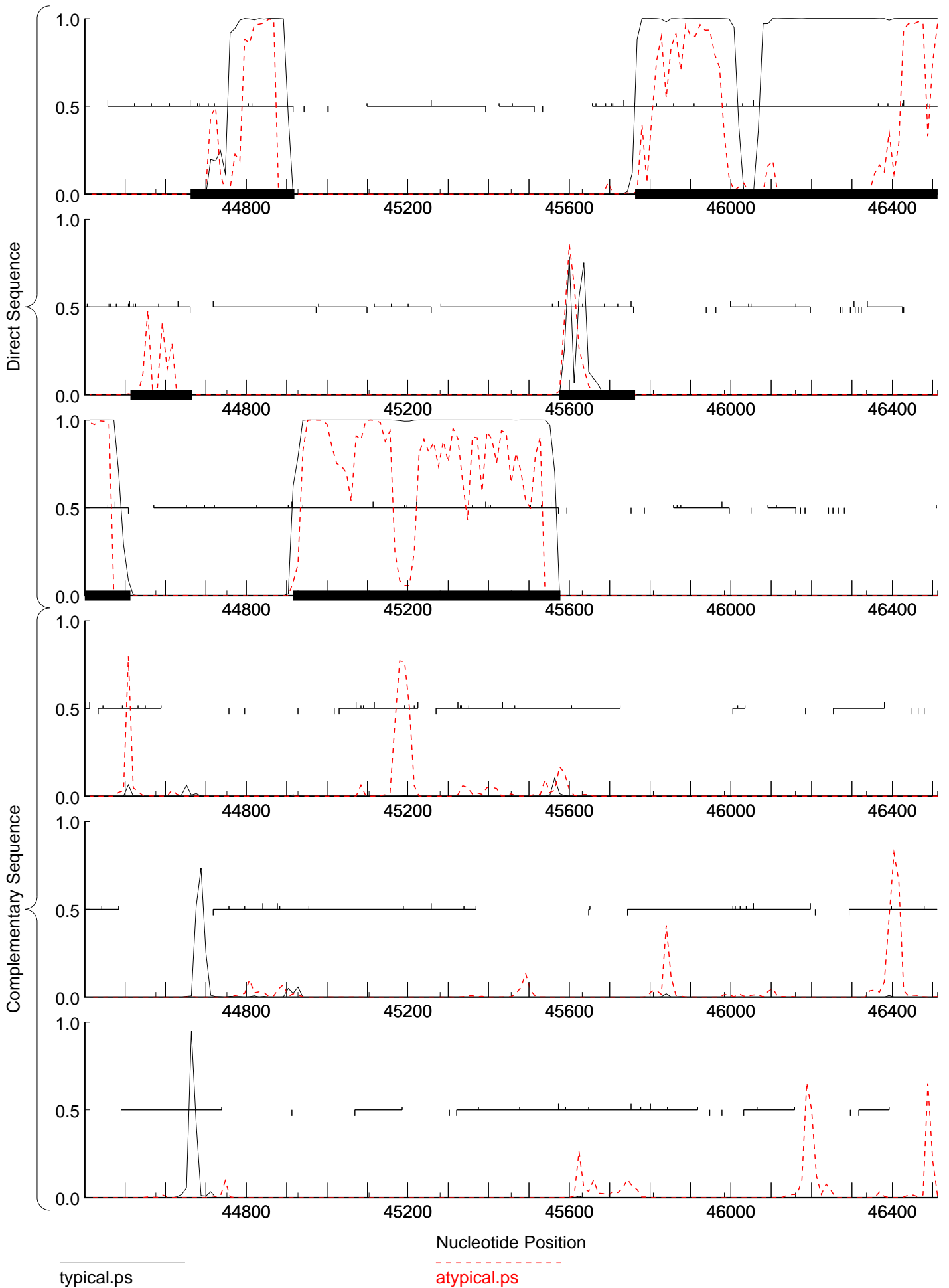
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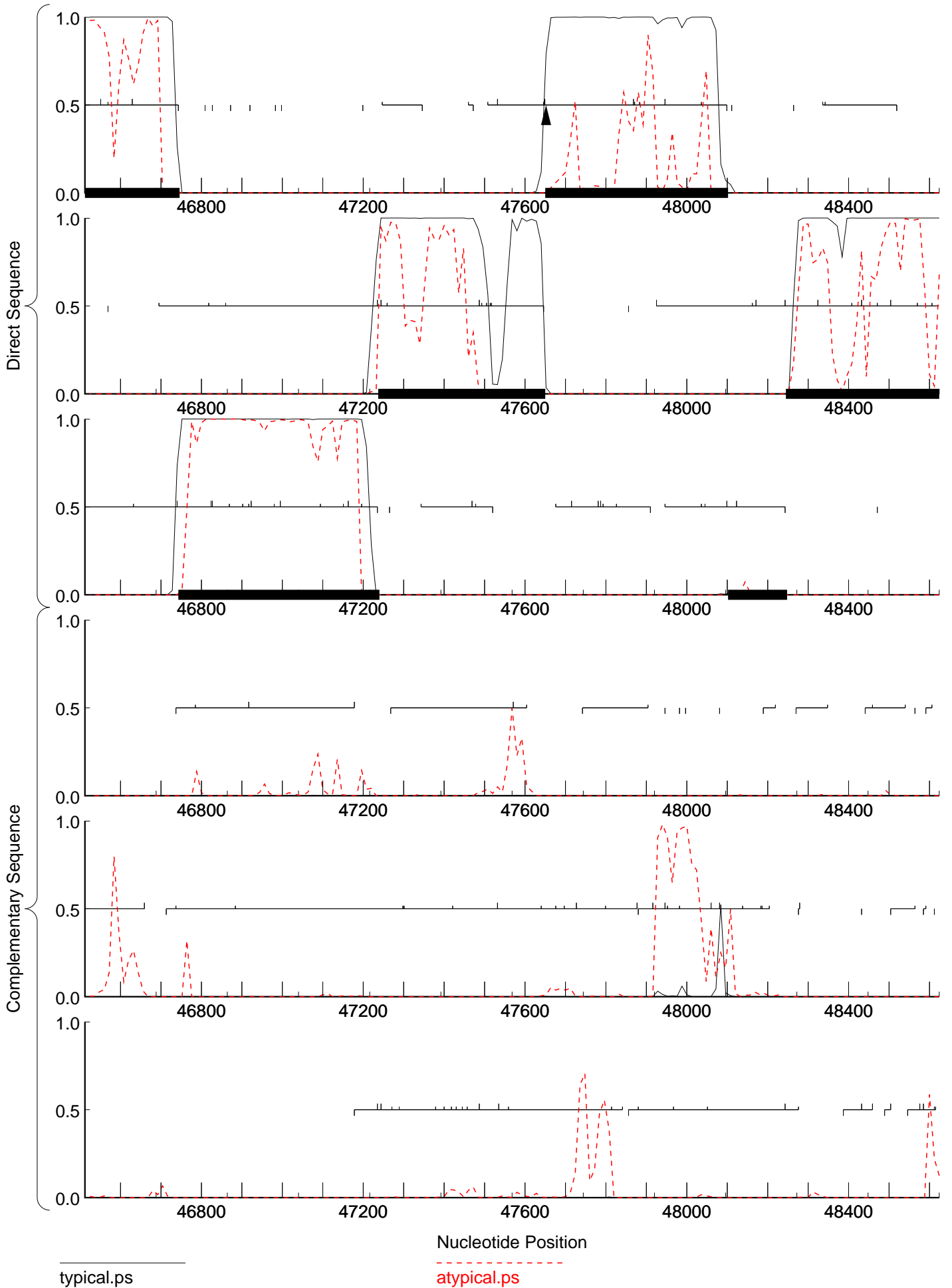






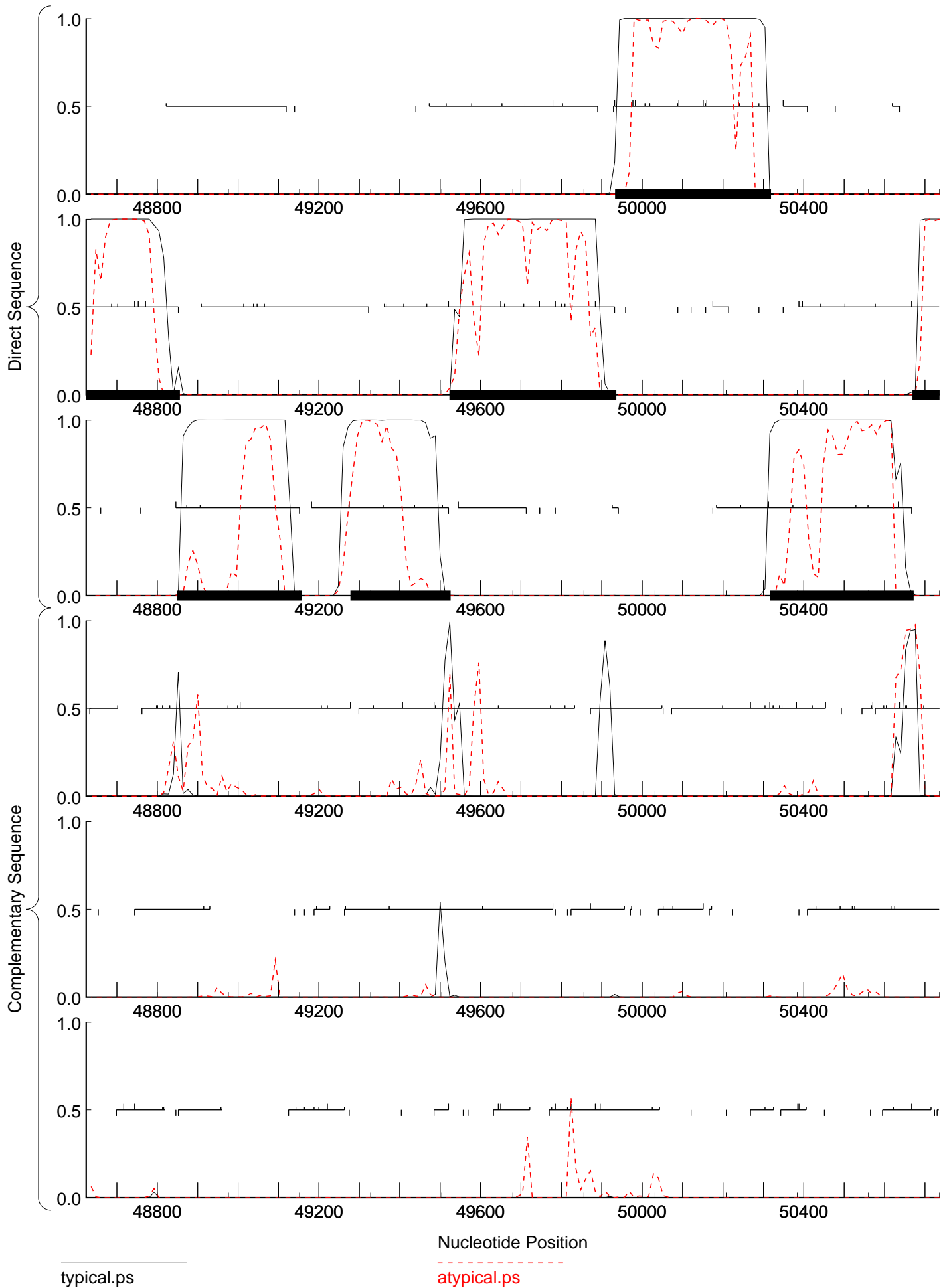








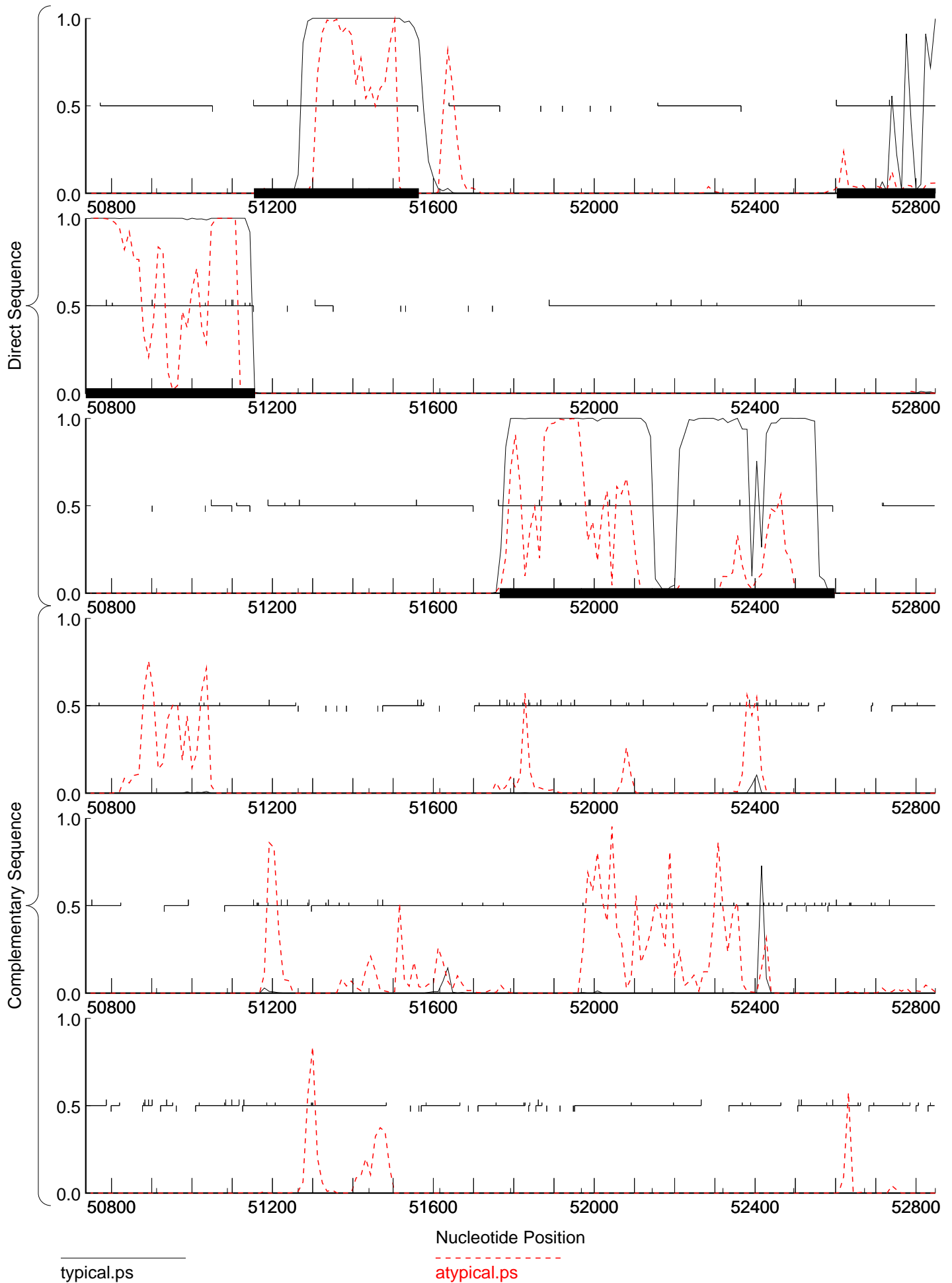
GeneMark.hmm prediction



typical.ps

atypical.ps

GeneMark.hmm prediction



GeneMark.hmm prediction

