

# GeneMark

Version 2.5p (09.08.06)

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## PROGRAM INFORMATION

Sequence : Gordonia phage Fairfaxidum complete sequence, 50187 bp including 10-base 3' overhang (TCGCC  
Analysis Date : 1/18/18 at 20:27:00  
Pages : 25  
Sequence Length : 50187 bp  
GC Content : 66.58%

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,

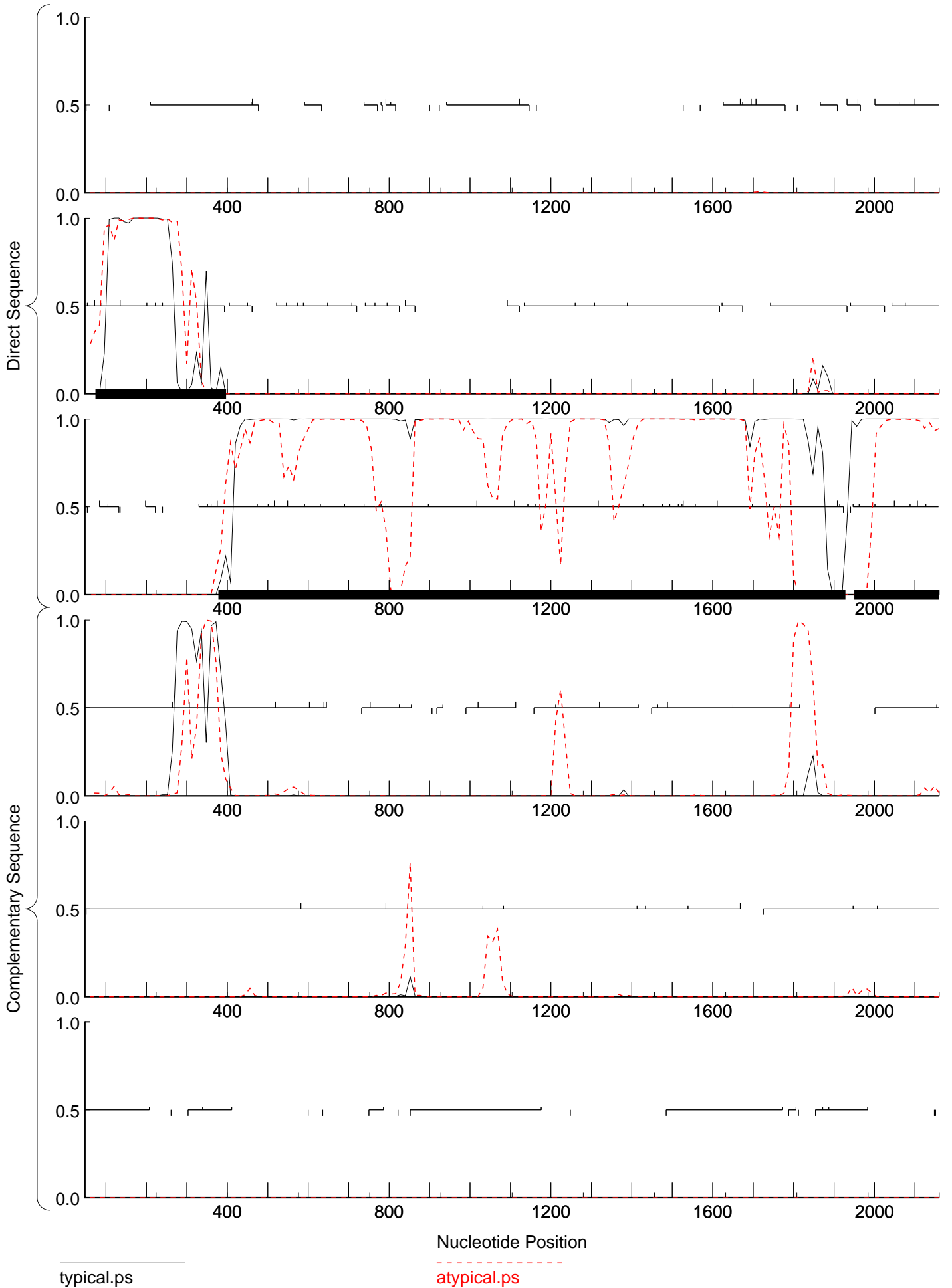
## Matrix notes & comments

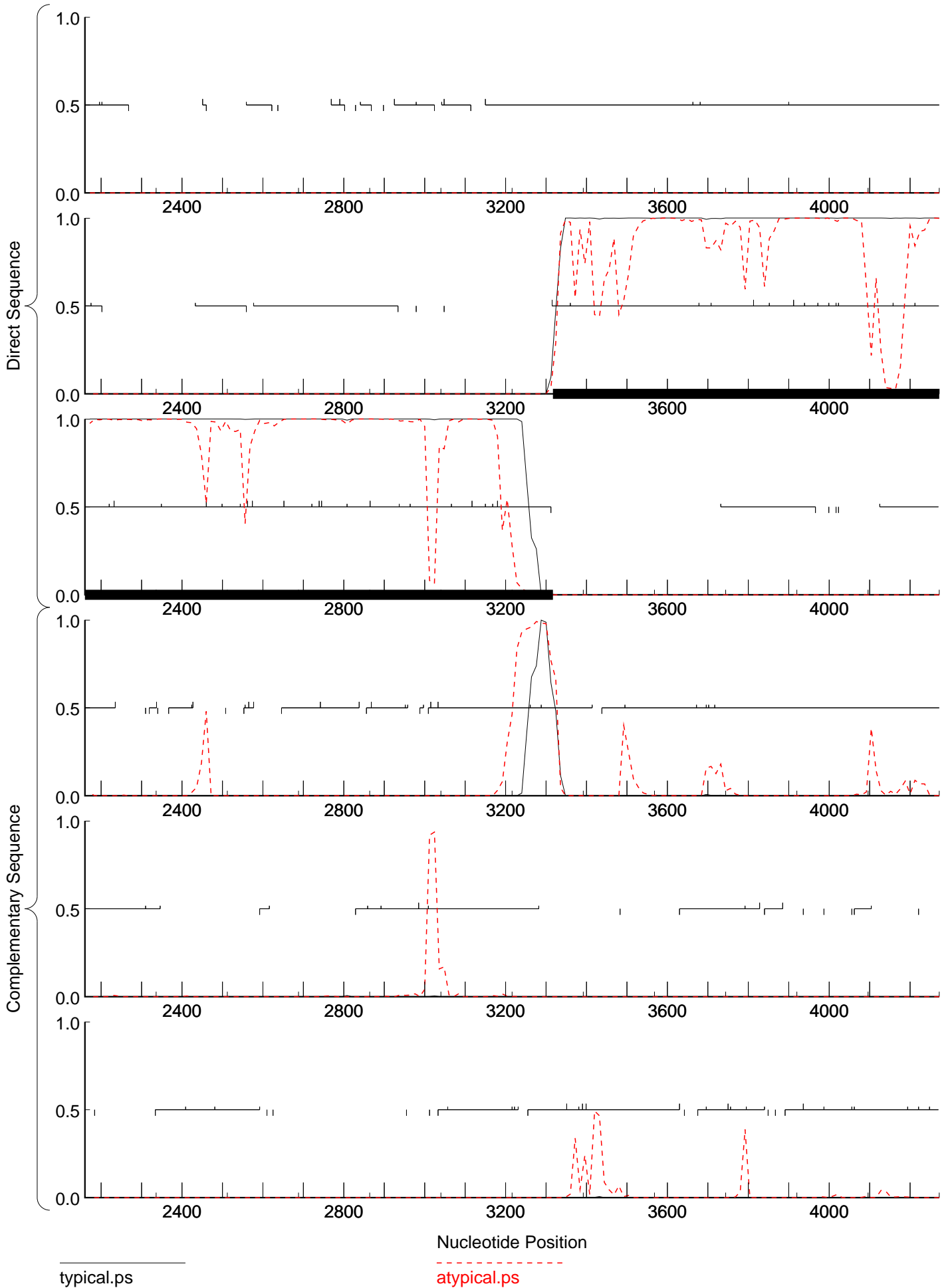
Training set derived by GeneMarkS, 4.30 October 2014  
Thu Jan 18 20:27:00 2018

## MATRIX INFORMATION

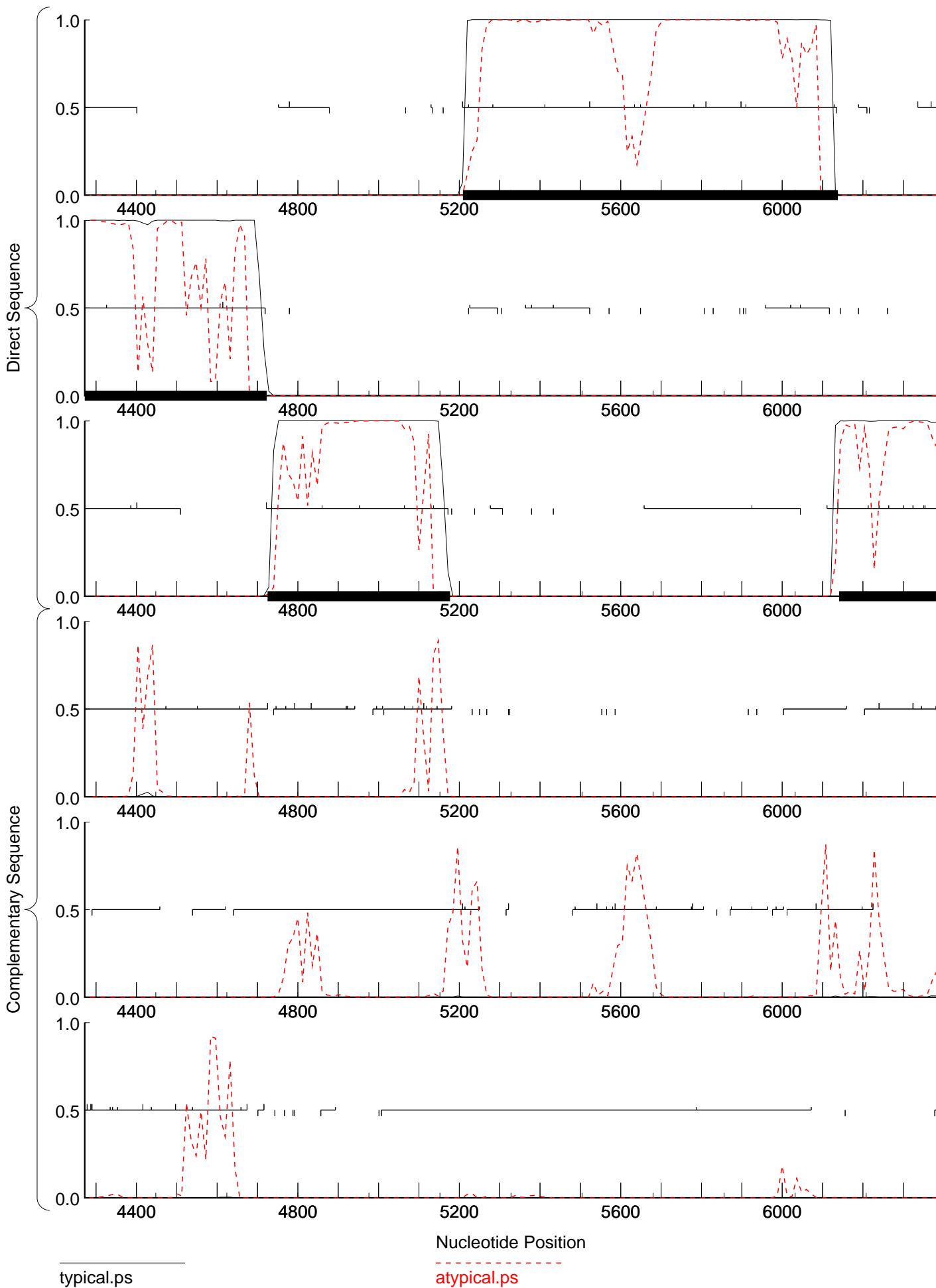
Matrix : -  
Author : -  
Order : 4

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





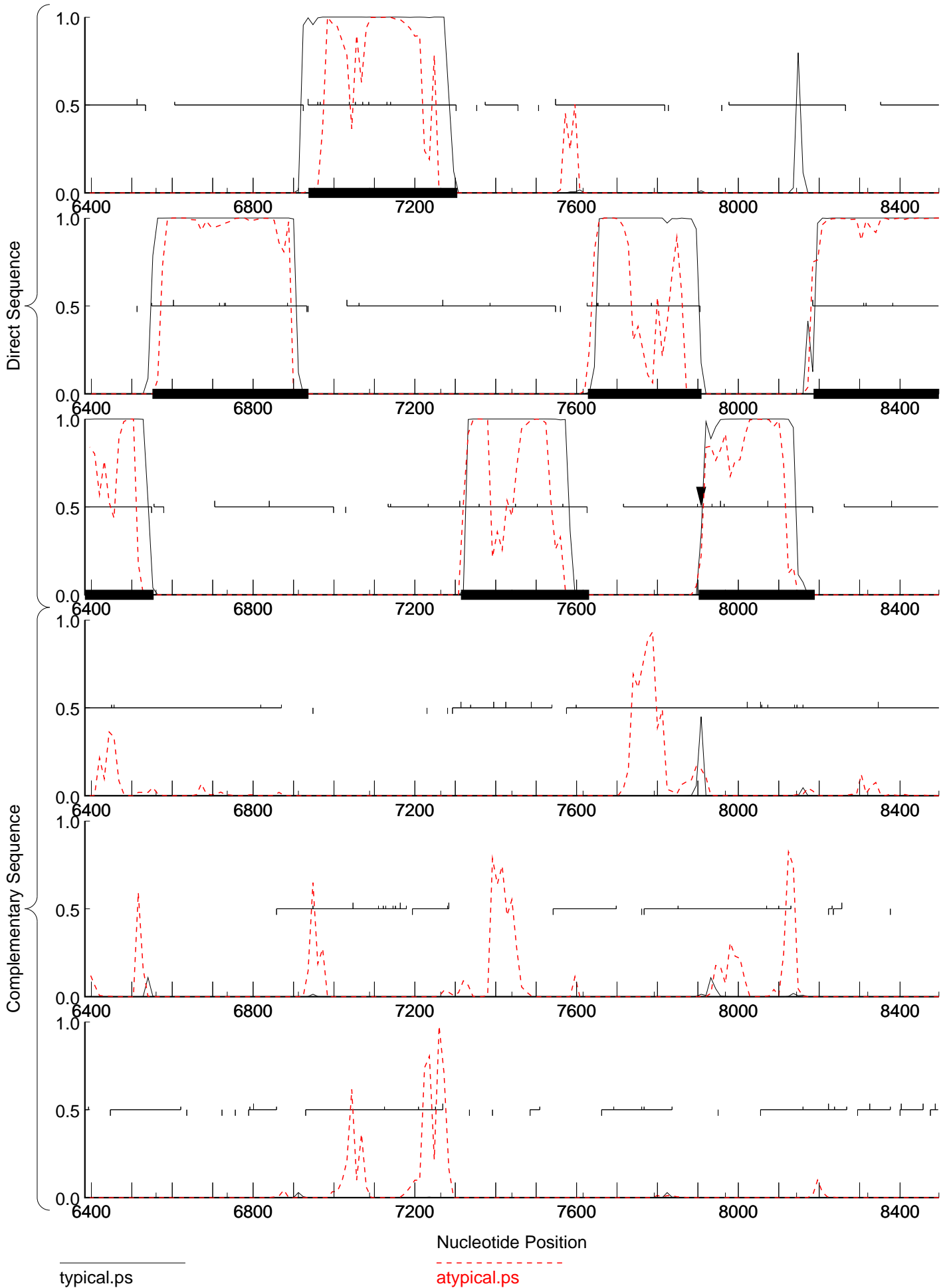
GeneMark.hmm prediction

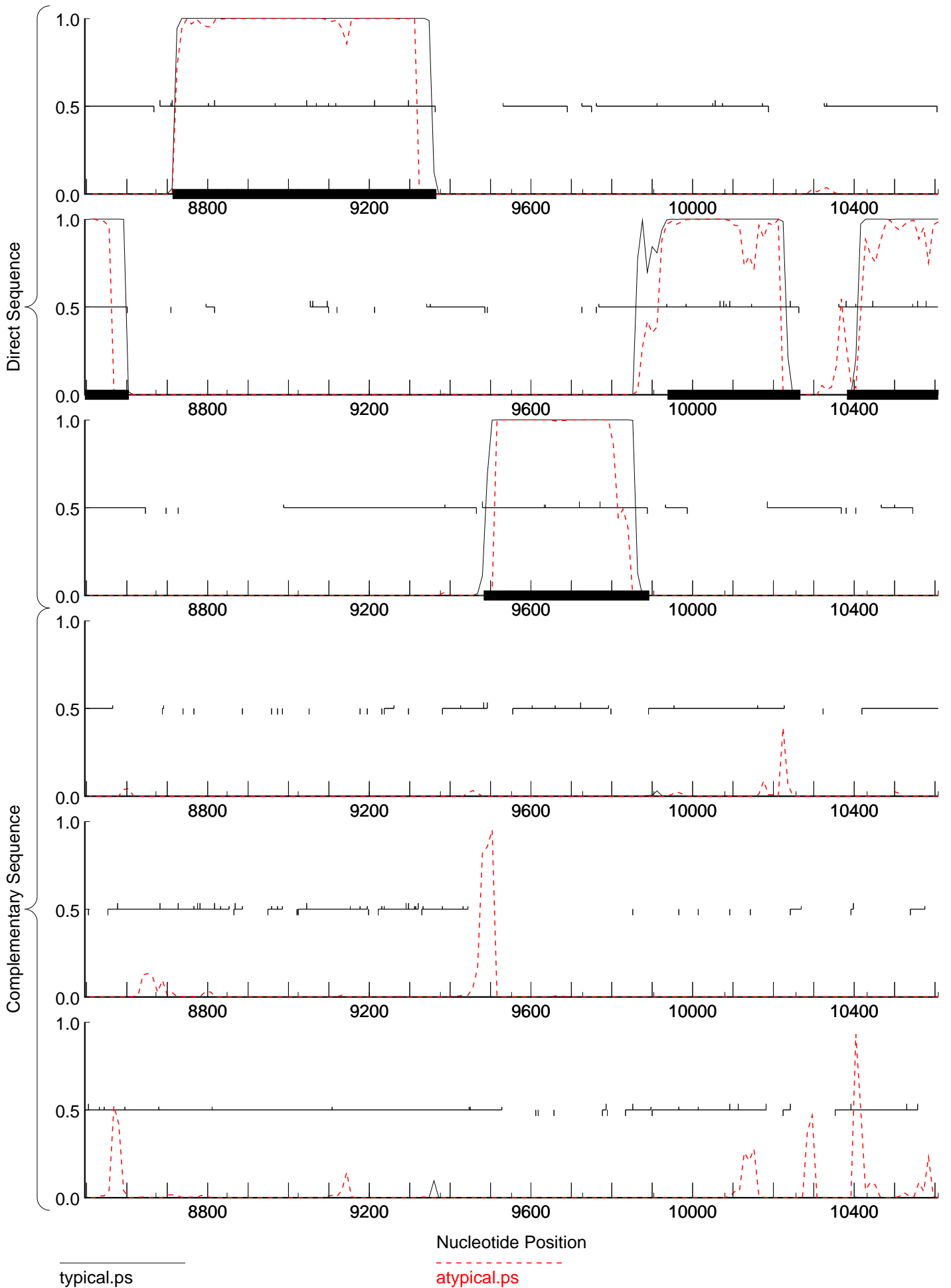


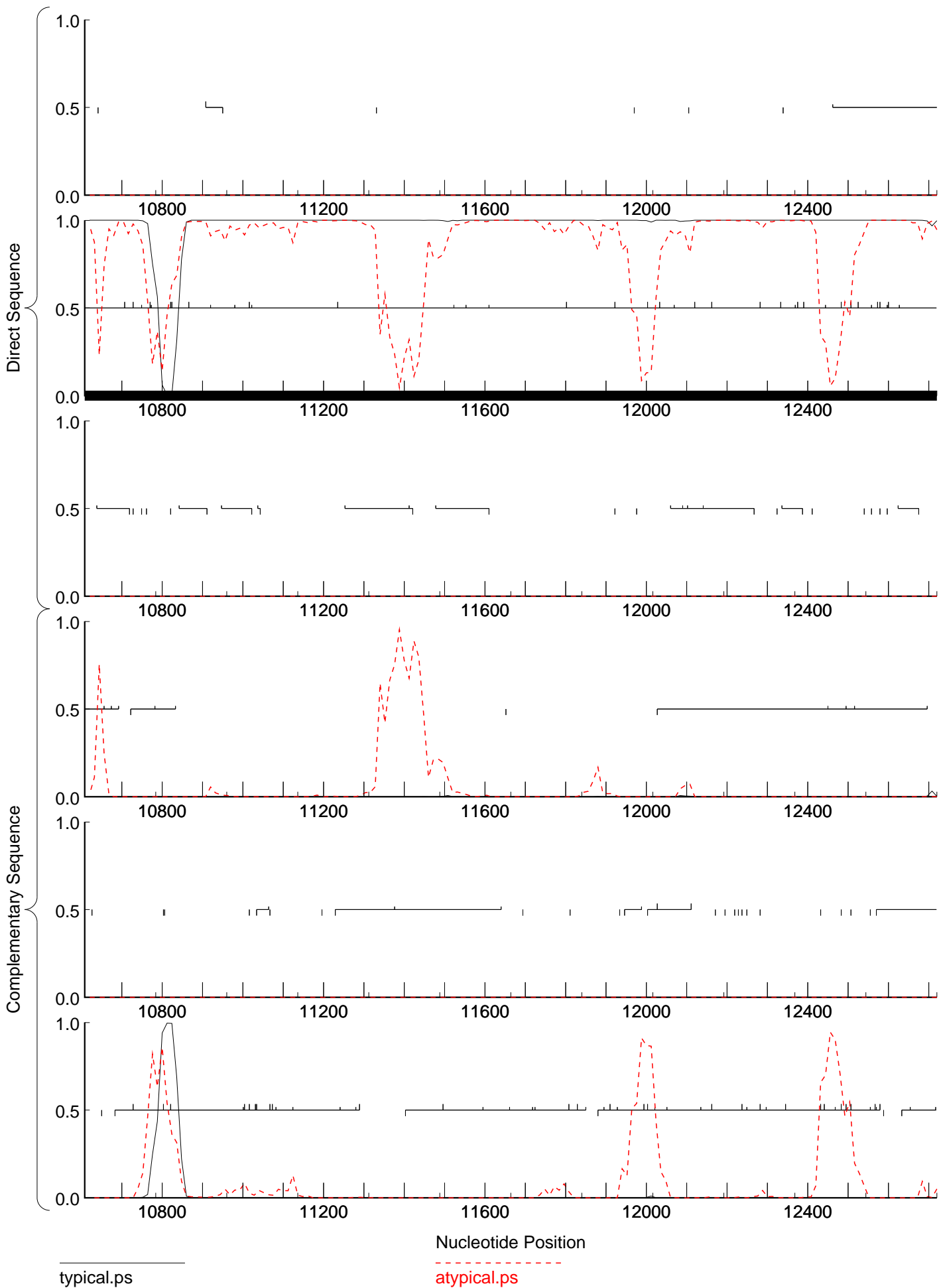
typical.ps

atypical.ps

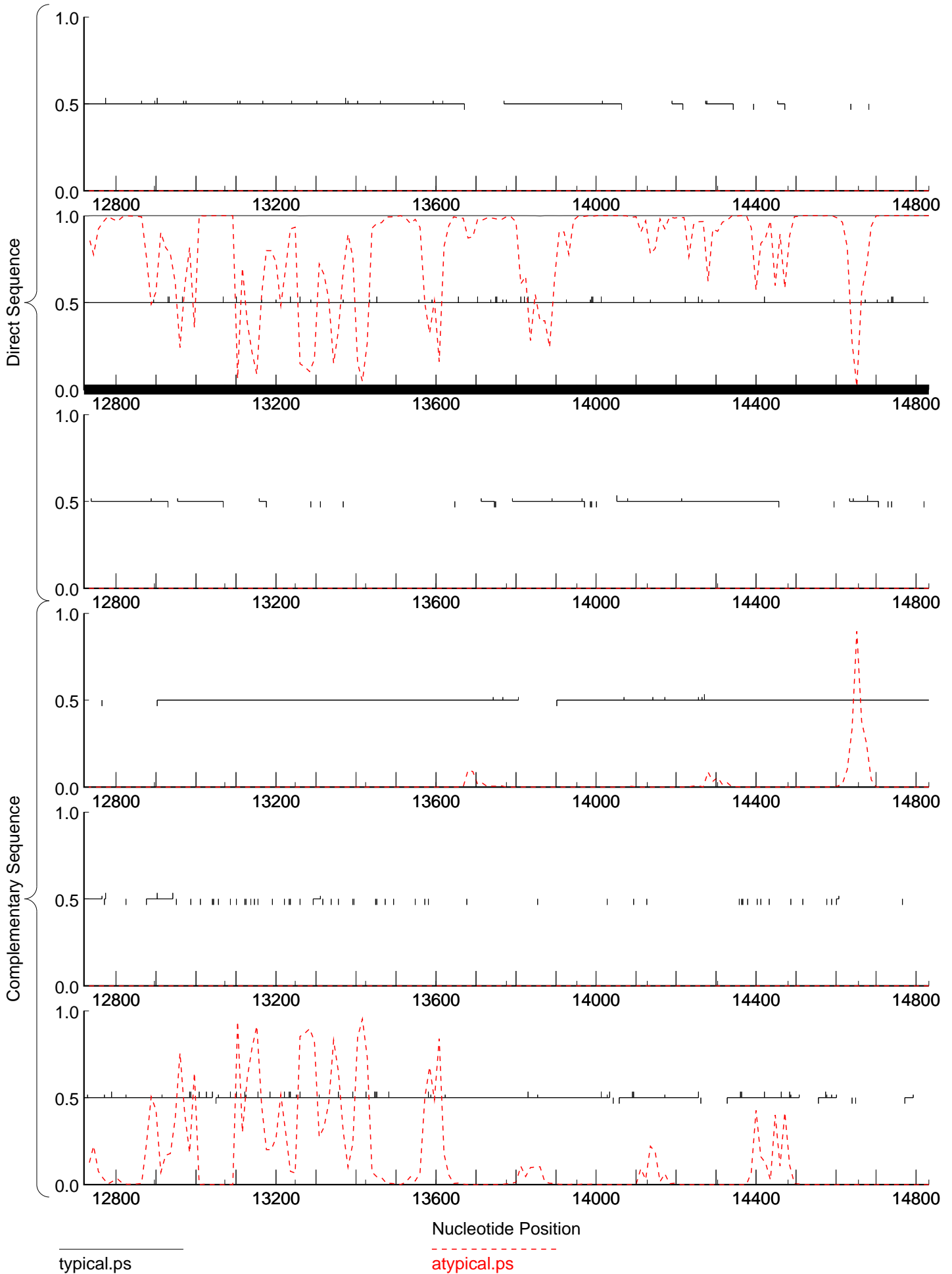
GeneMark.hmm prediction



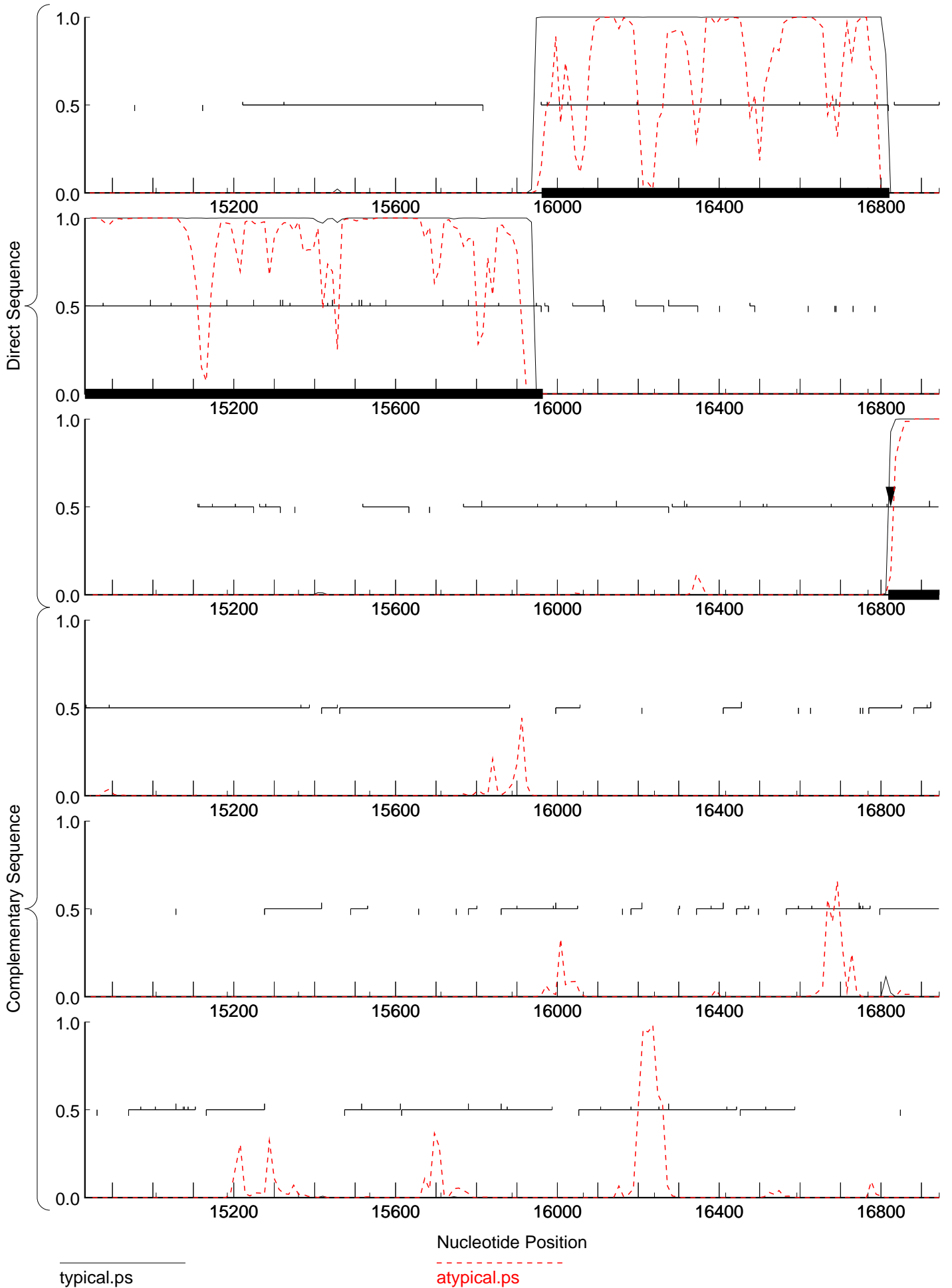


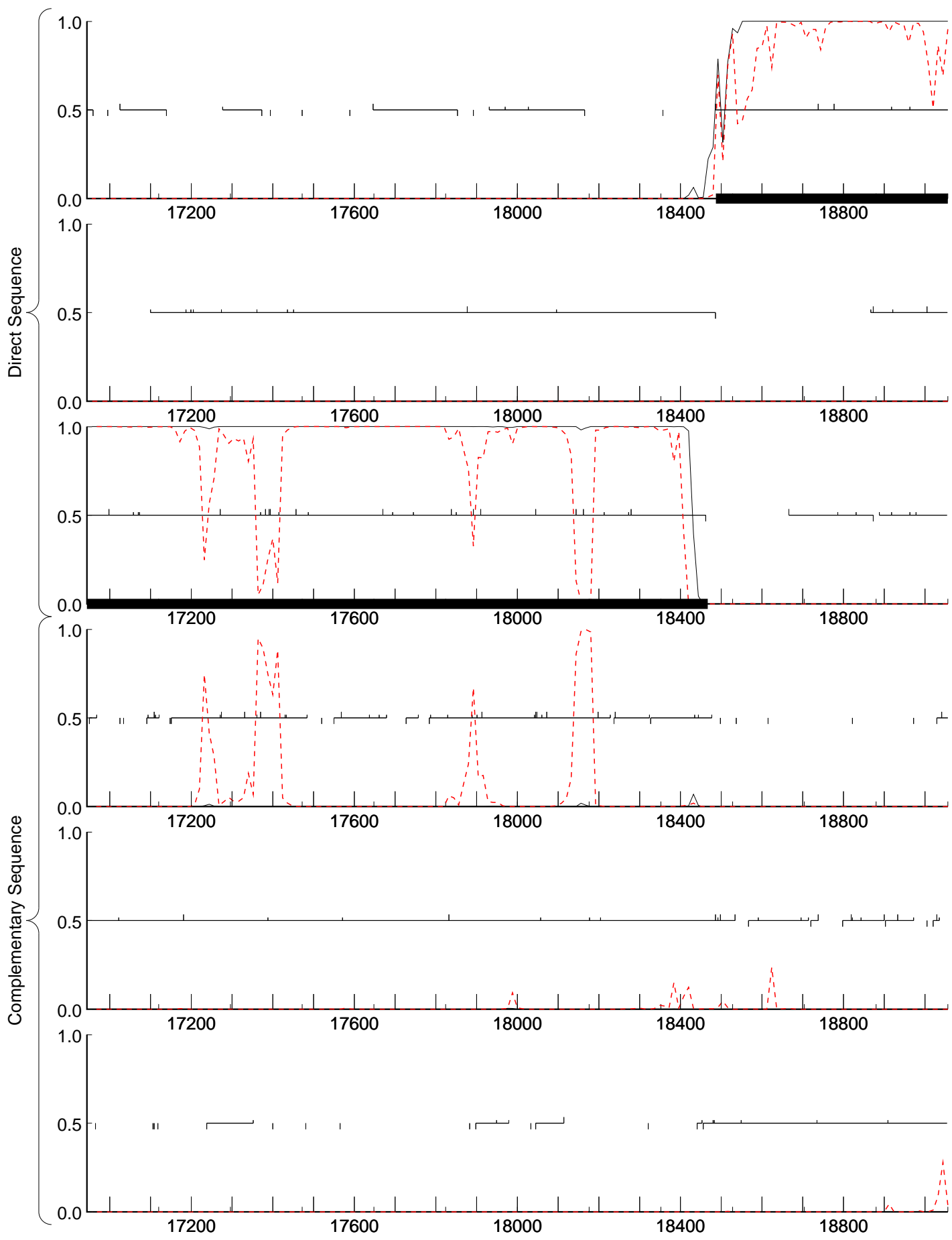


GeneMark.hmm prediction



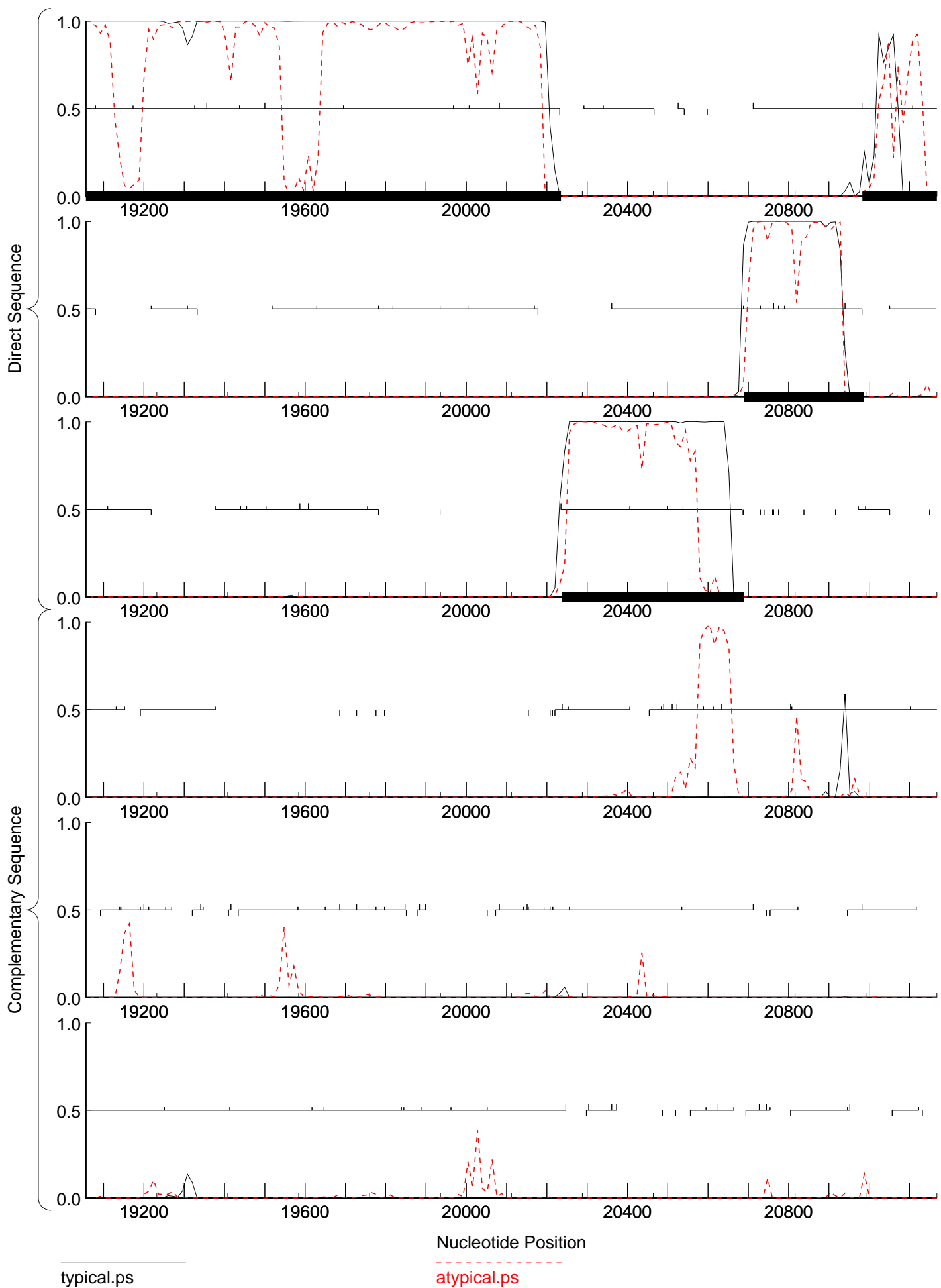


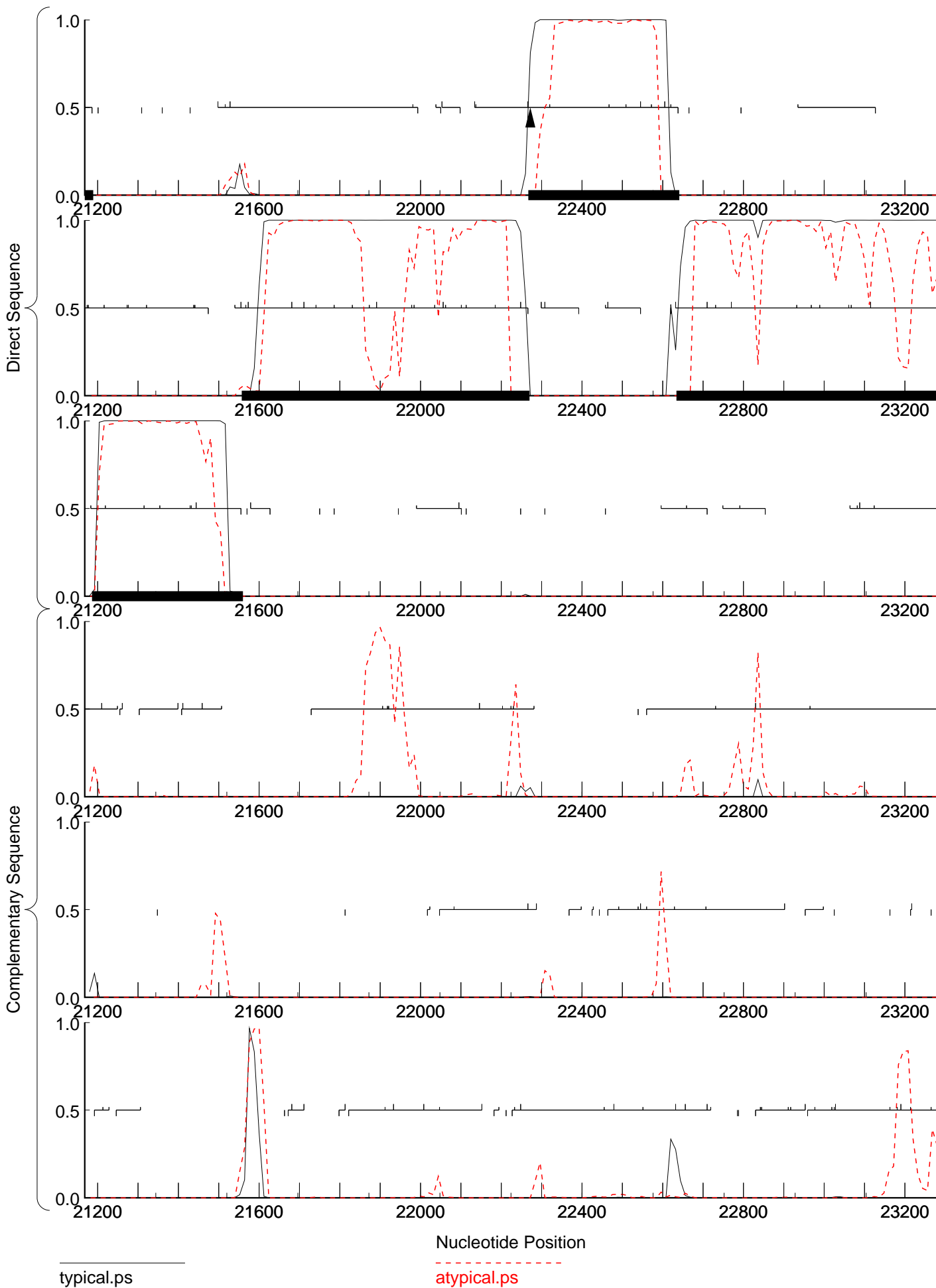


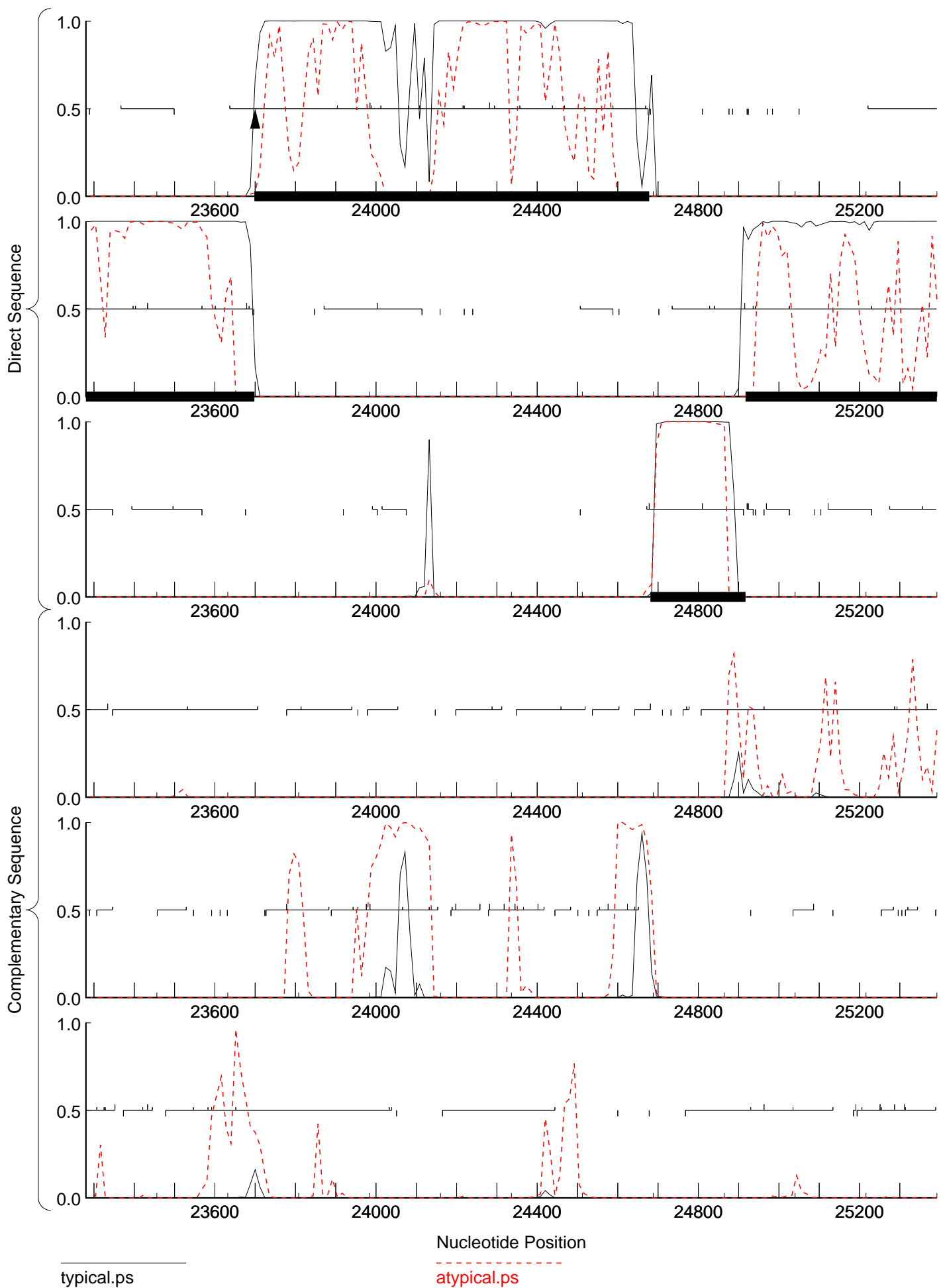


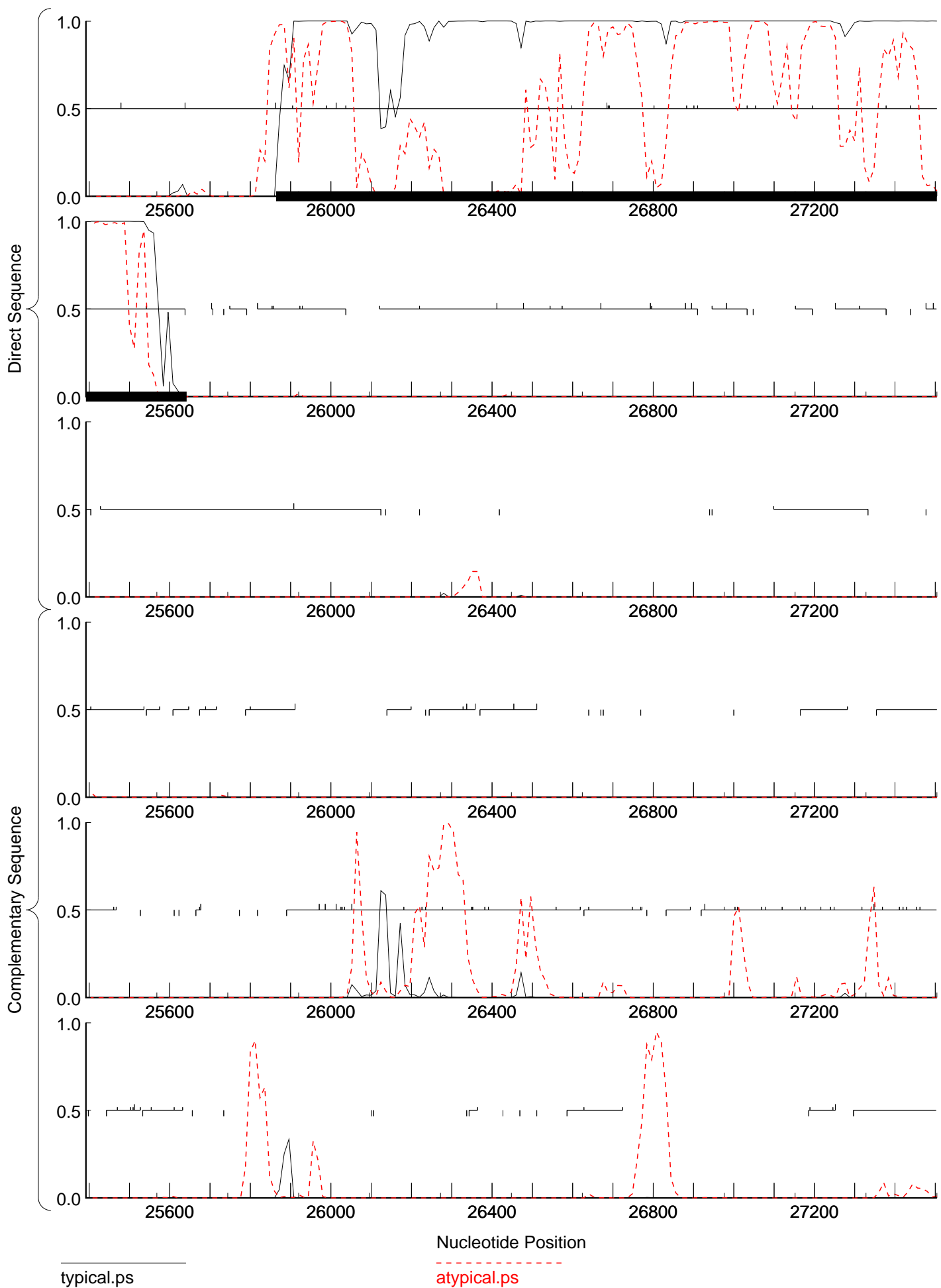
typical.ps

atypical.ps

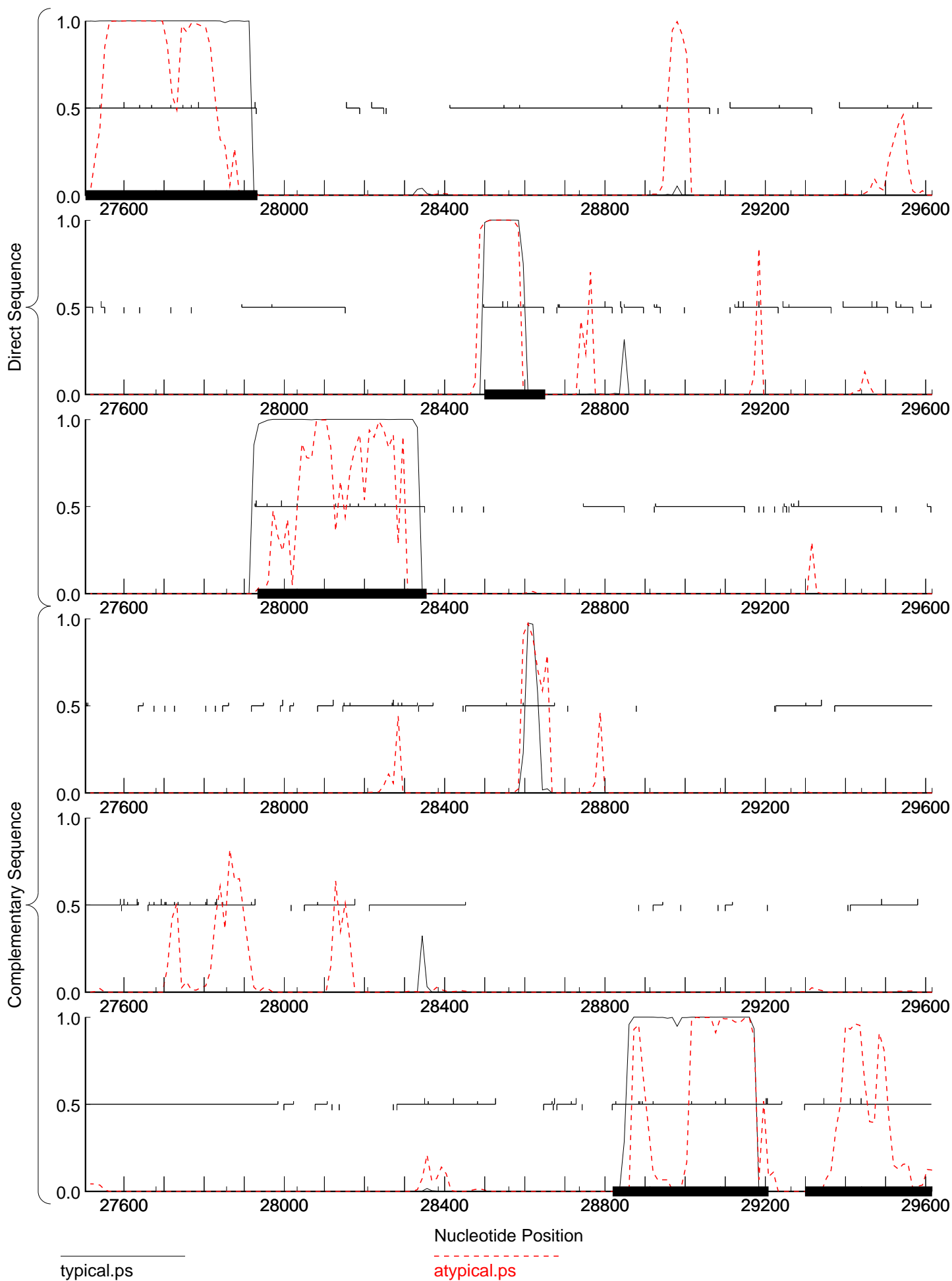


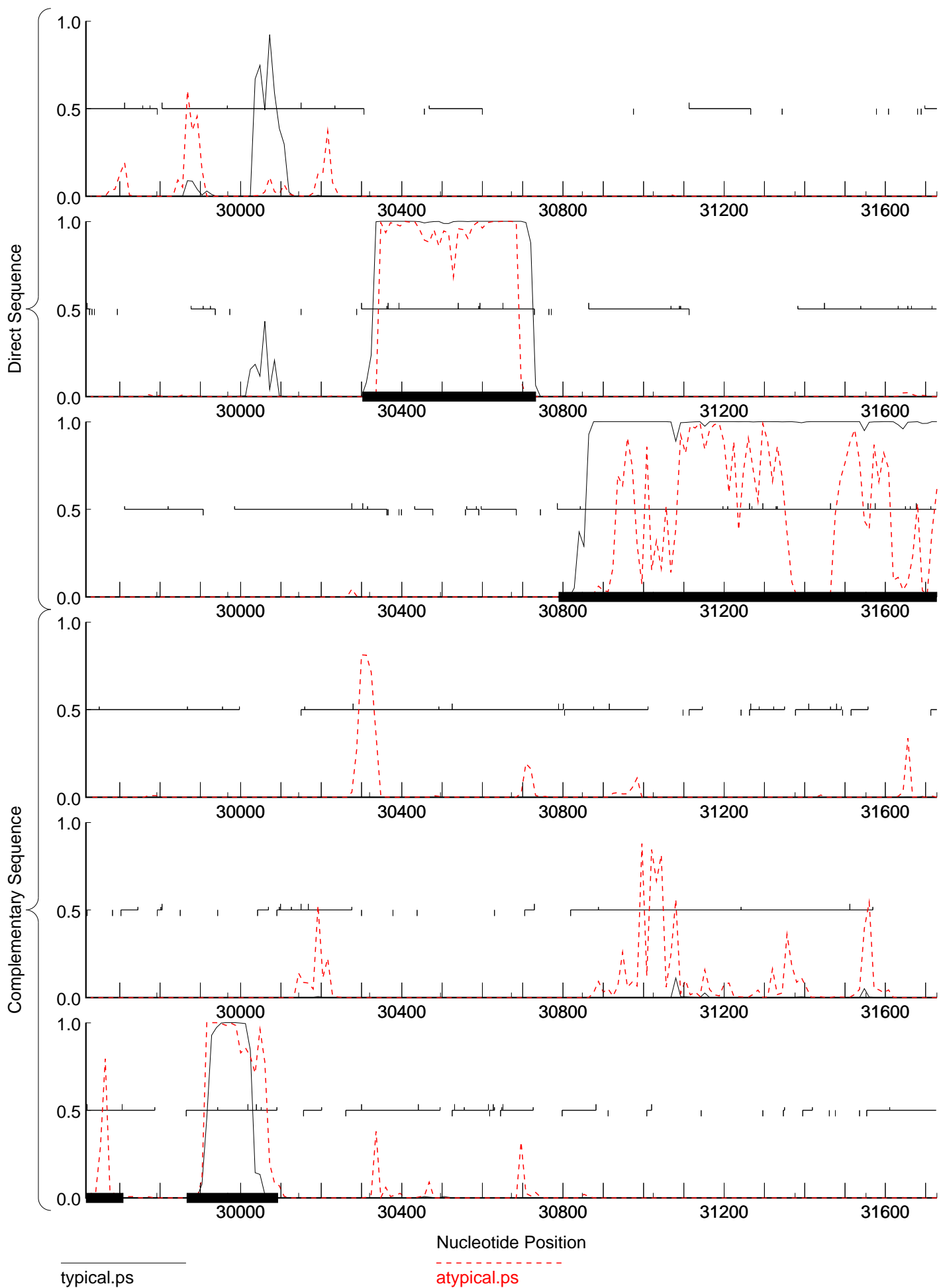




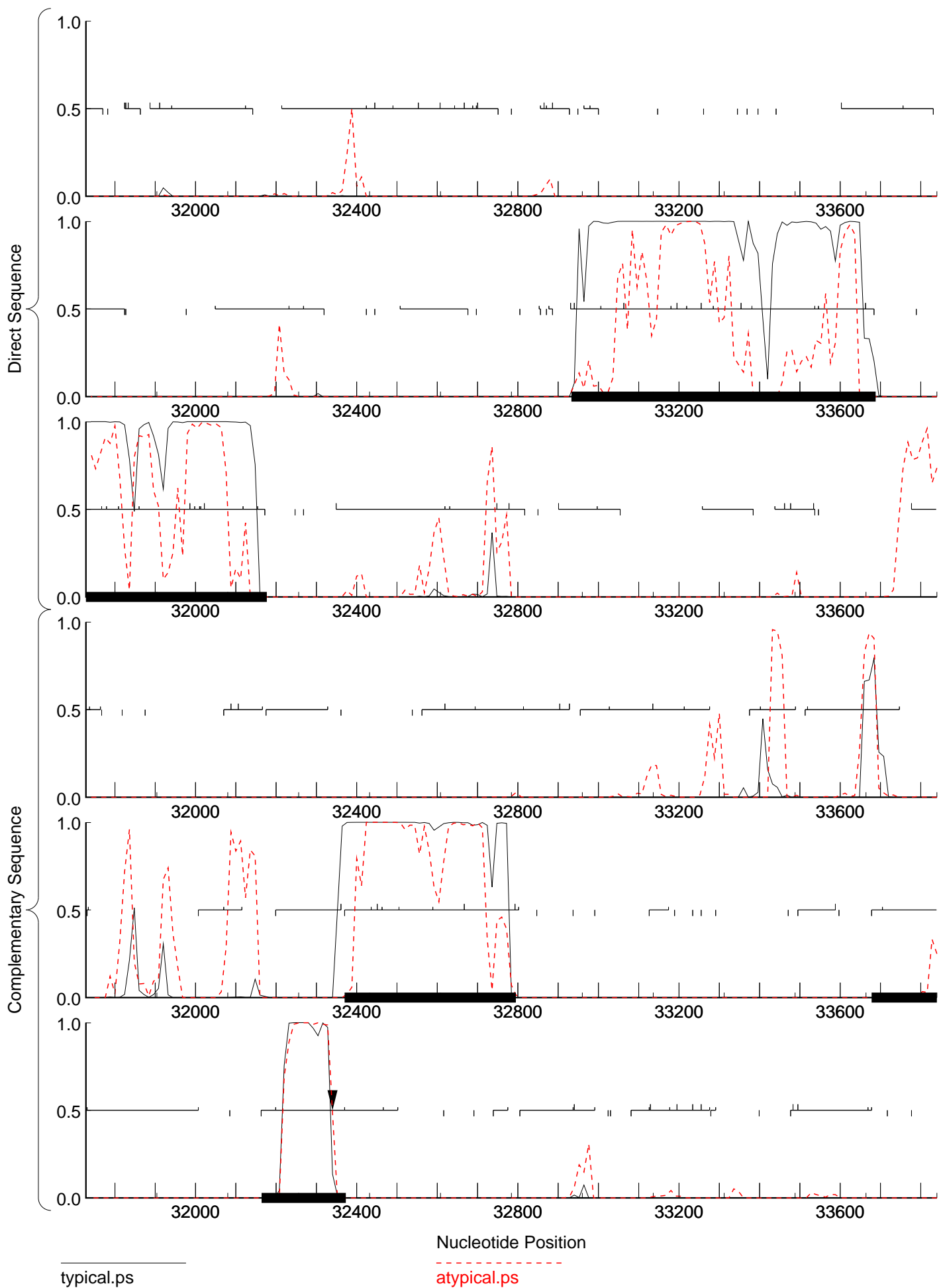


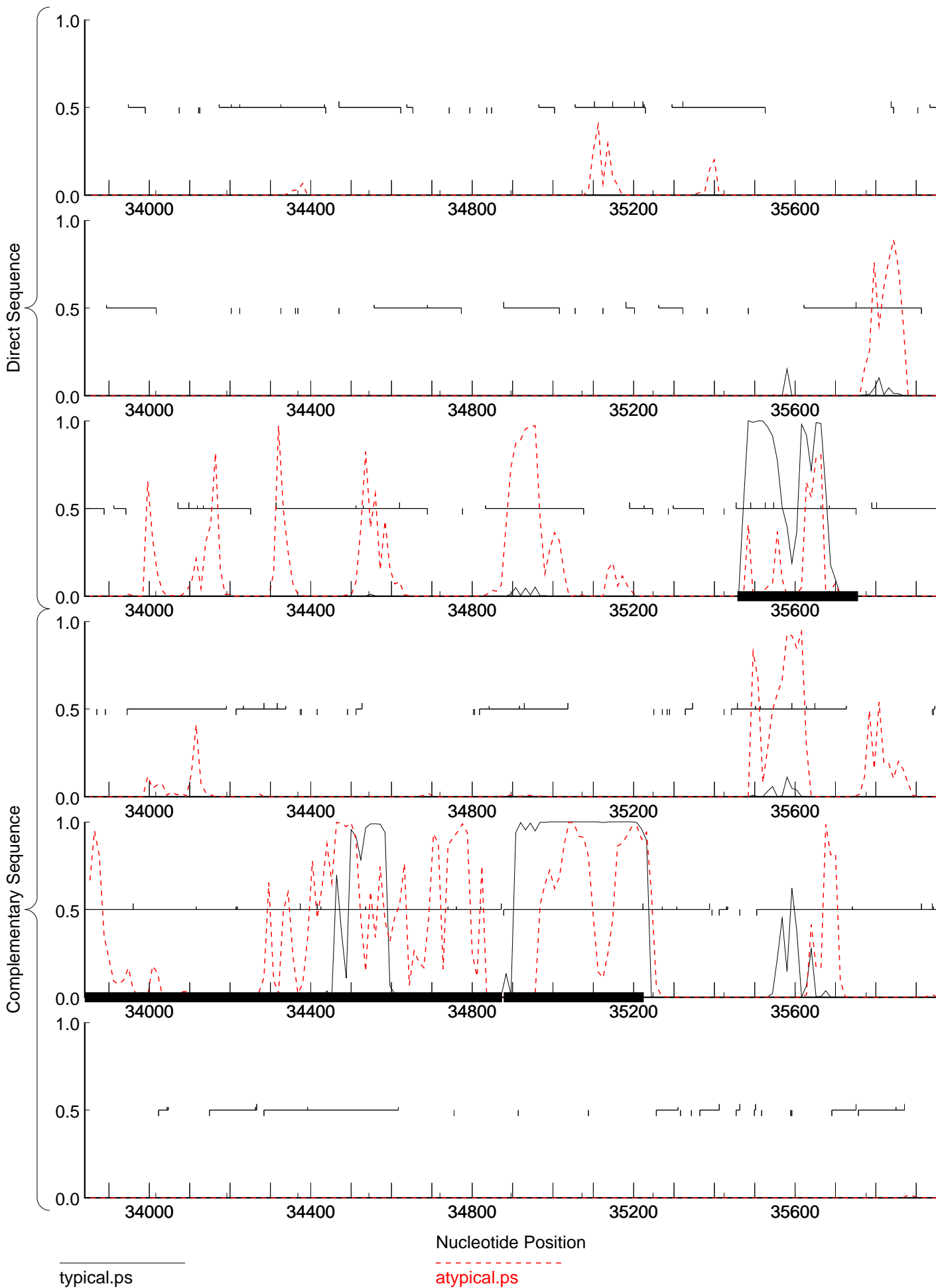
complete sequence, 50187 bp including 10-base 3' overhang (TCGCCGGTGA), Cluster CV, Order 4, Window 96, Step 12, 15/25  
complete sequence, 50187 bp including 10-base 3' overhang (TCGCCGGTGA), Cluster CV, Order 2, Window 96, Step 12, 15/25





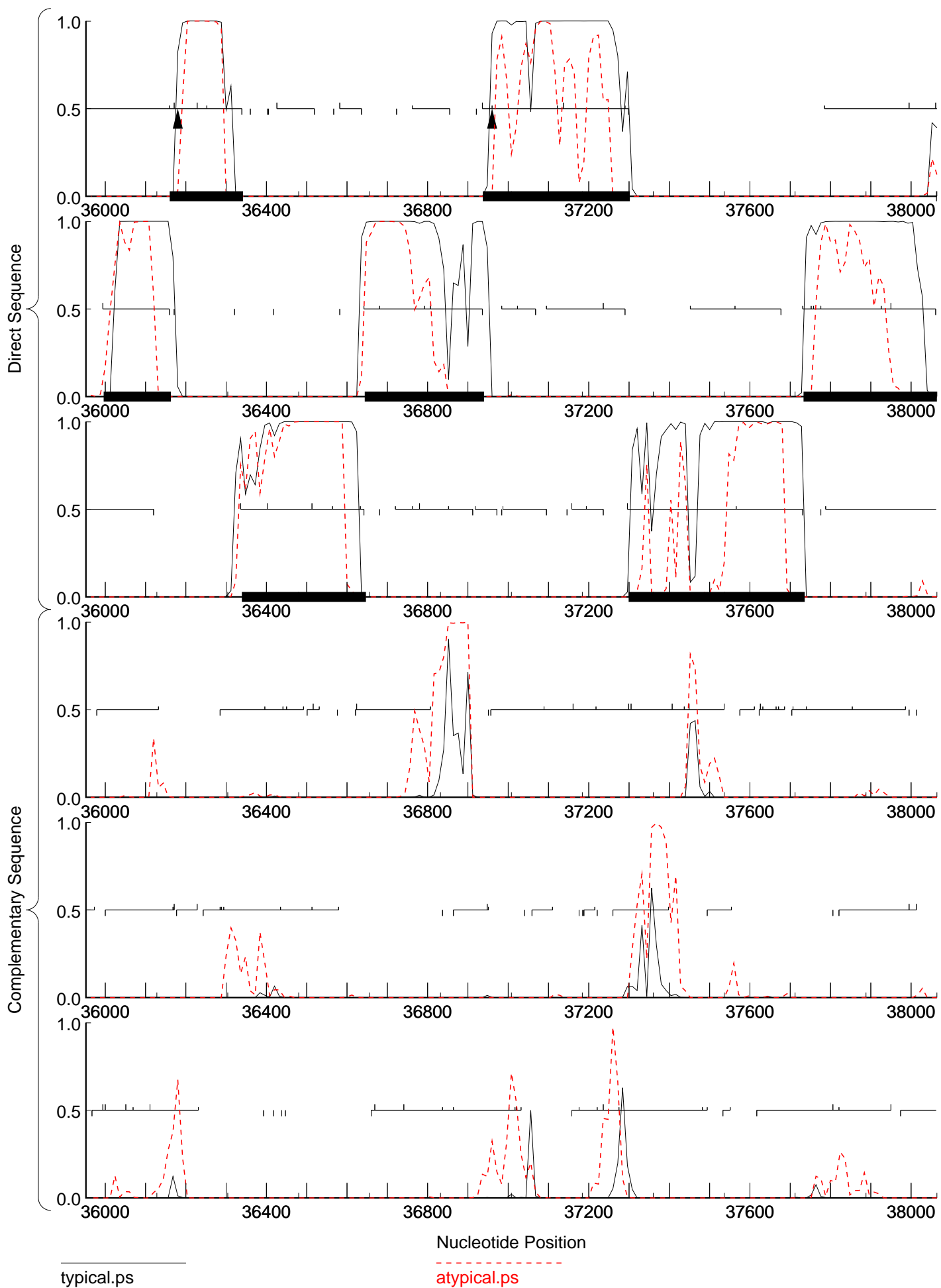






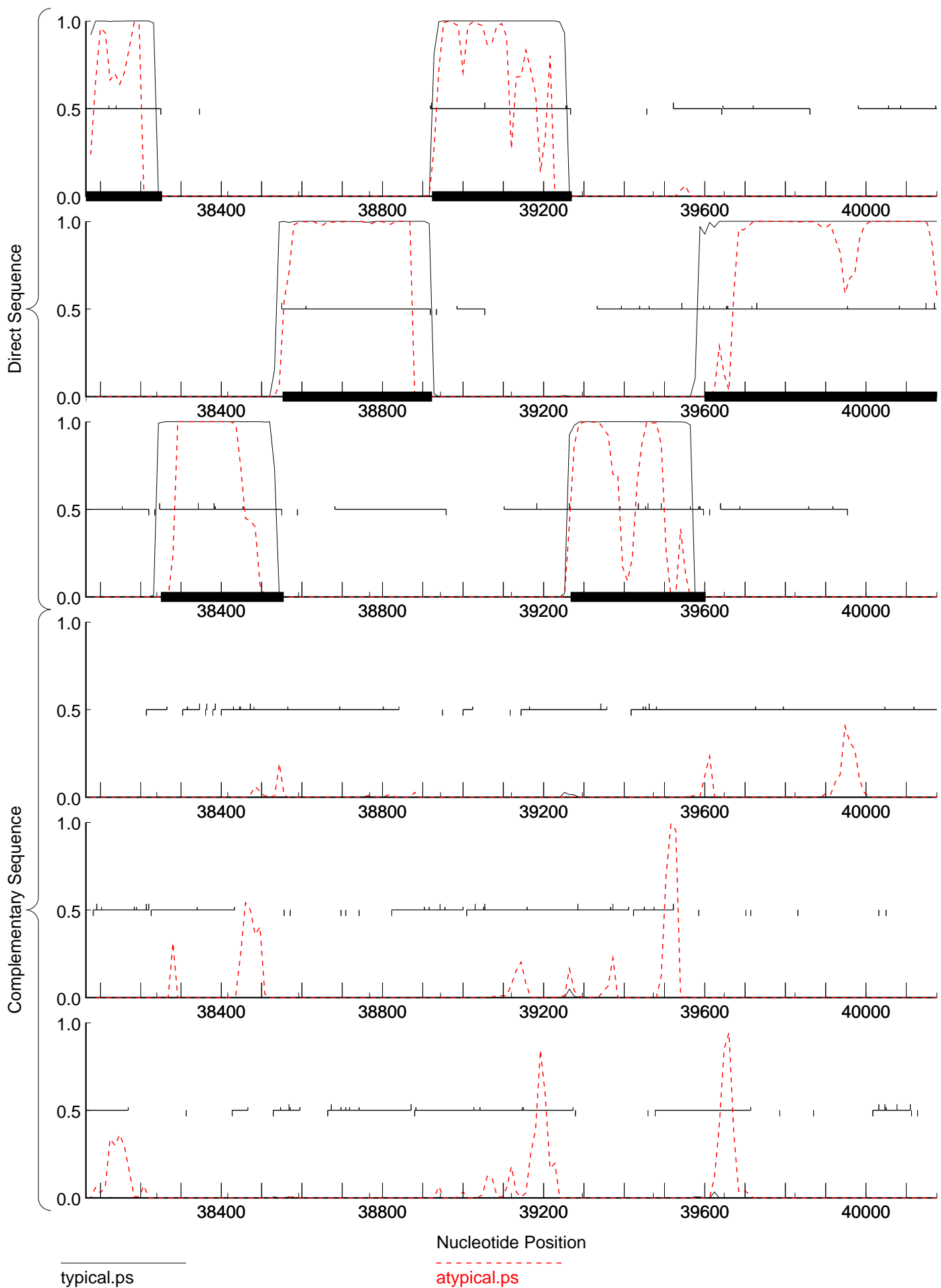
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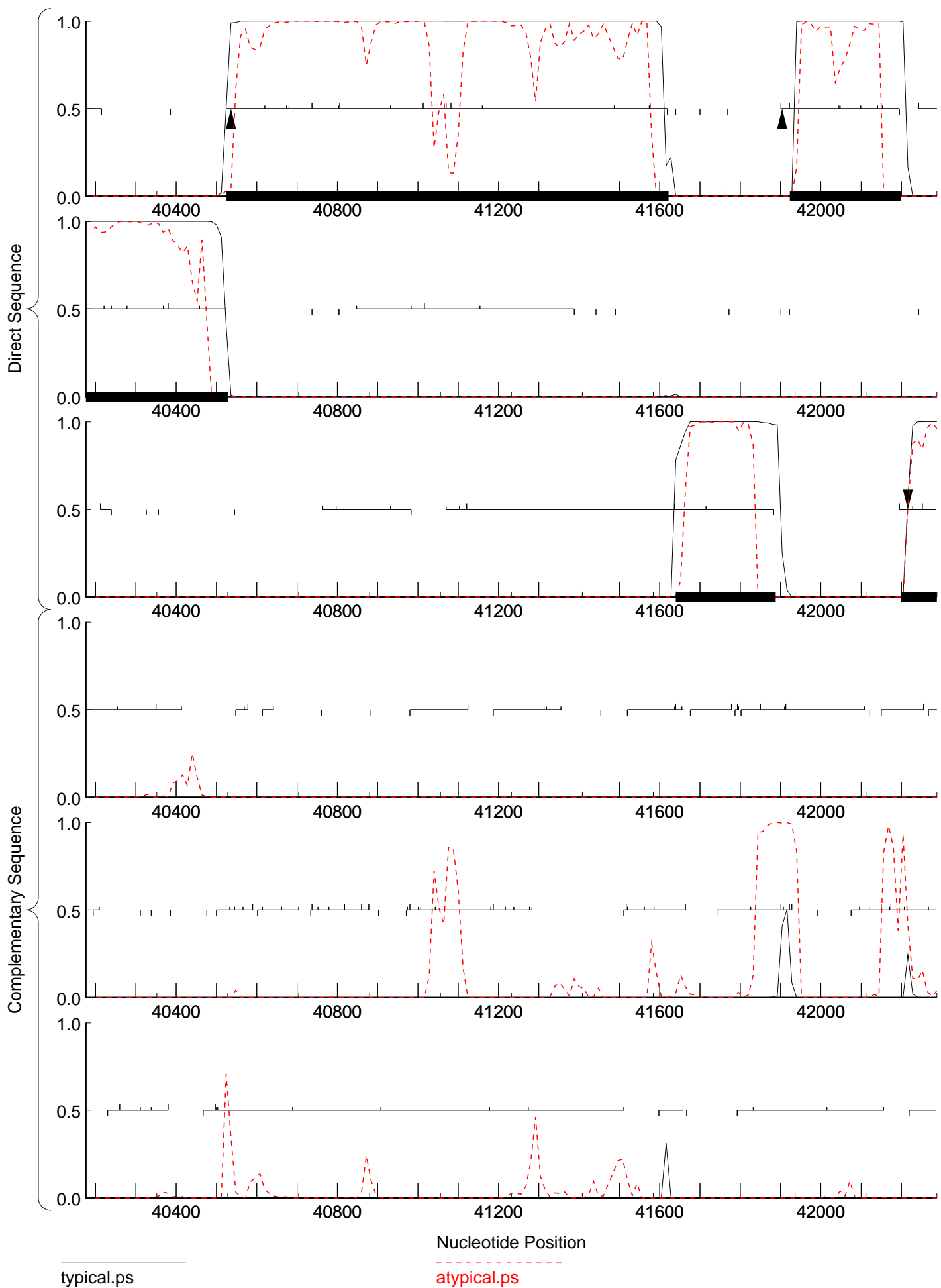
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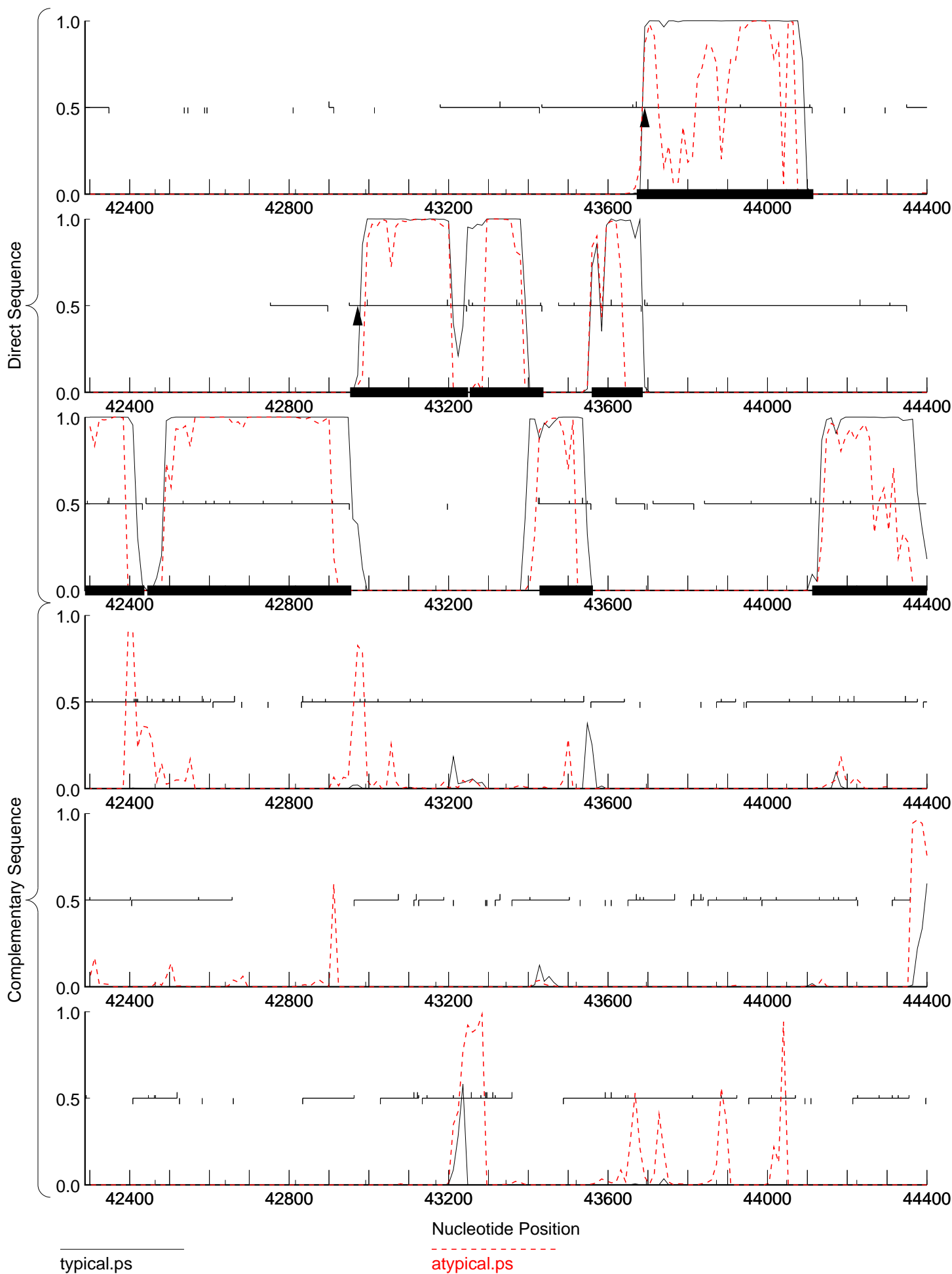


typical.ps

atypical.ps

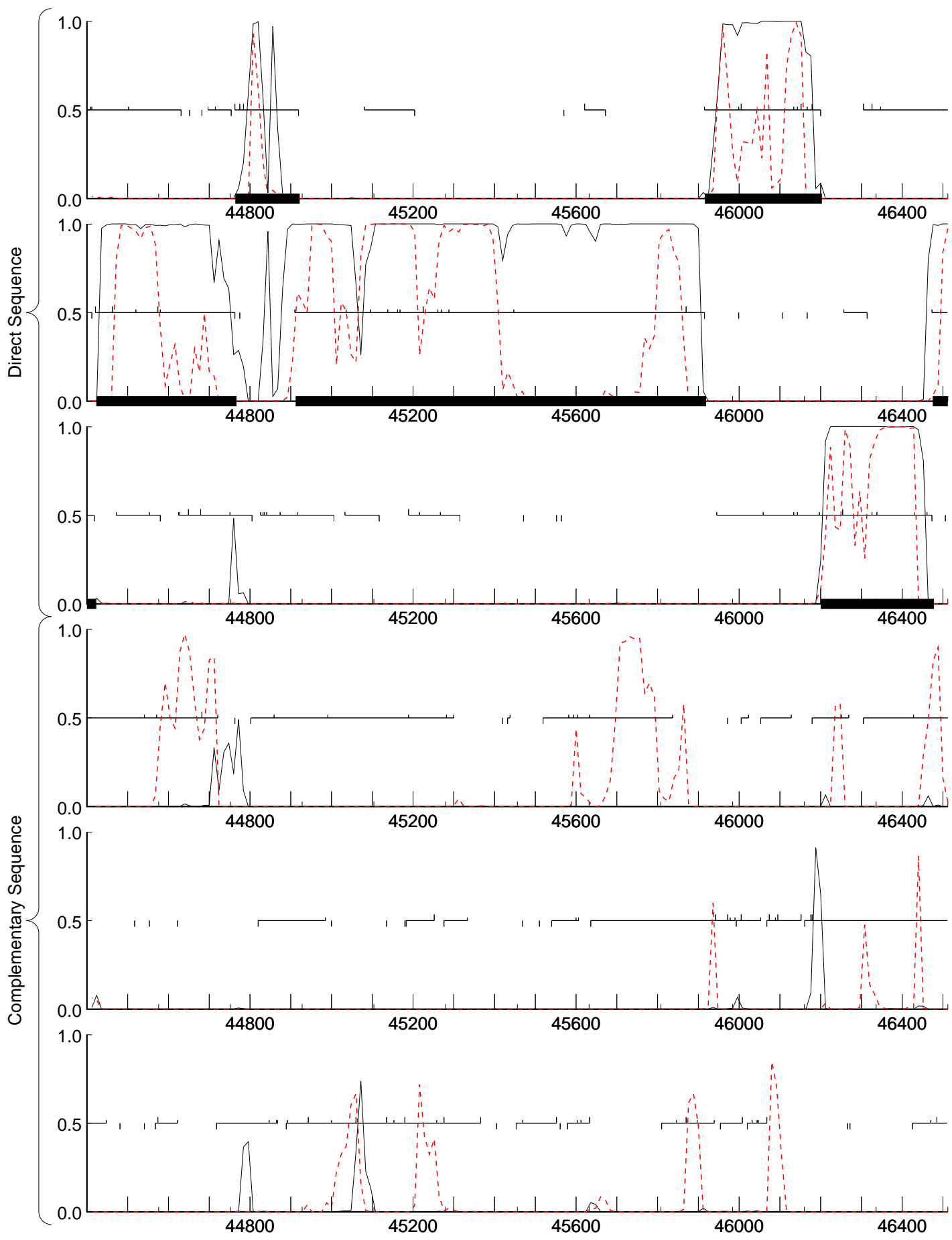






typical.ps

atypical.ps



typical.ps

atypical.ps

