

# GeneMark

Version 2.5p (09.08.06)

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## PROGRAM INFORMATION

Sequence : Mycobacterium phage Bartimeaus complete sequence, 51374 bp including 10-base 3' overhang (C  
Analysis Date : 1/22/18 at 9:33:53  
Pages : 26  
Sequence Length : 51374 bp  
GC Content : 63.87%

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,

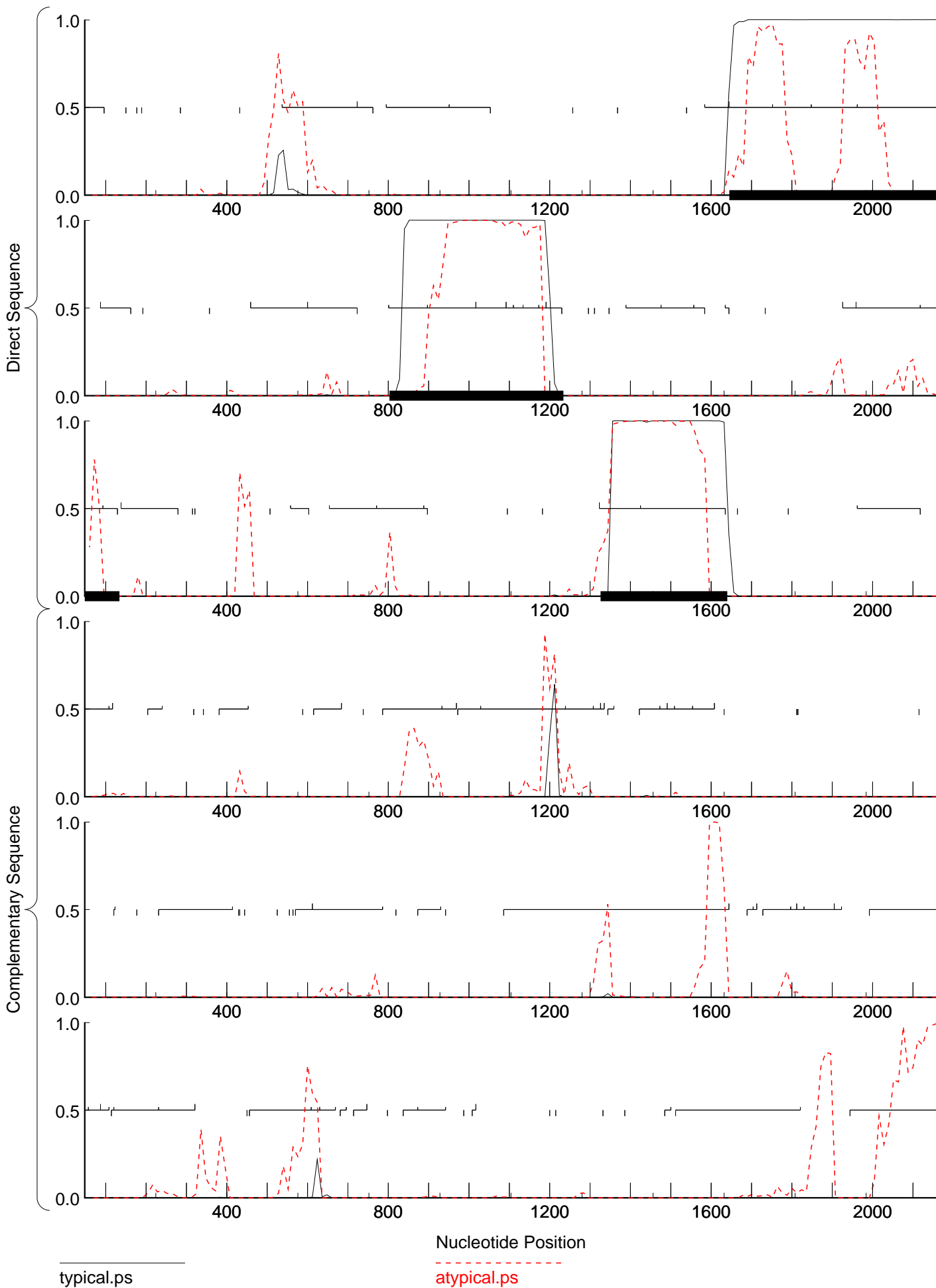
## Matrix notes & comments

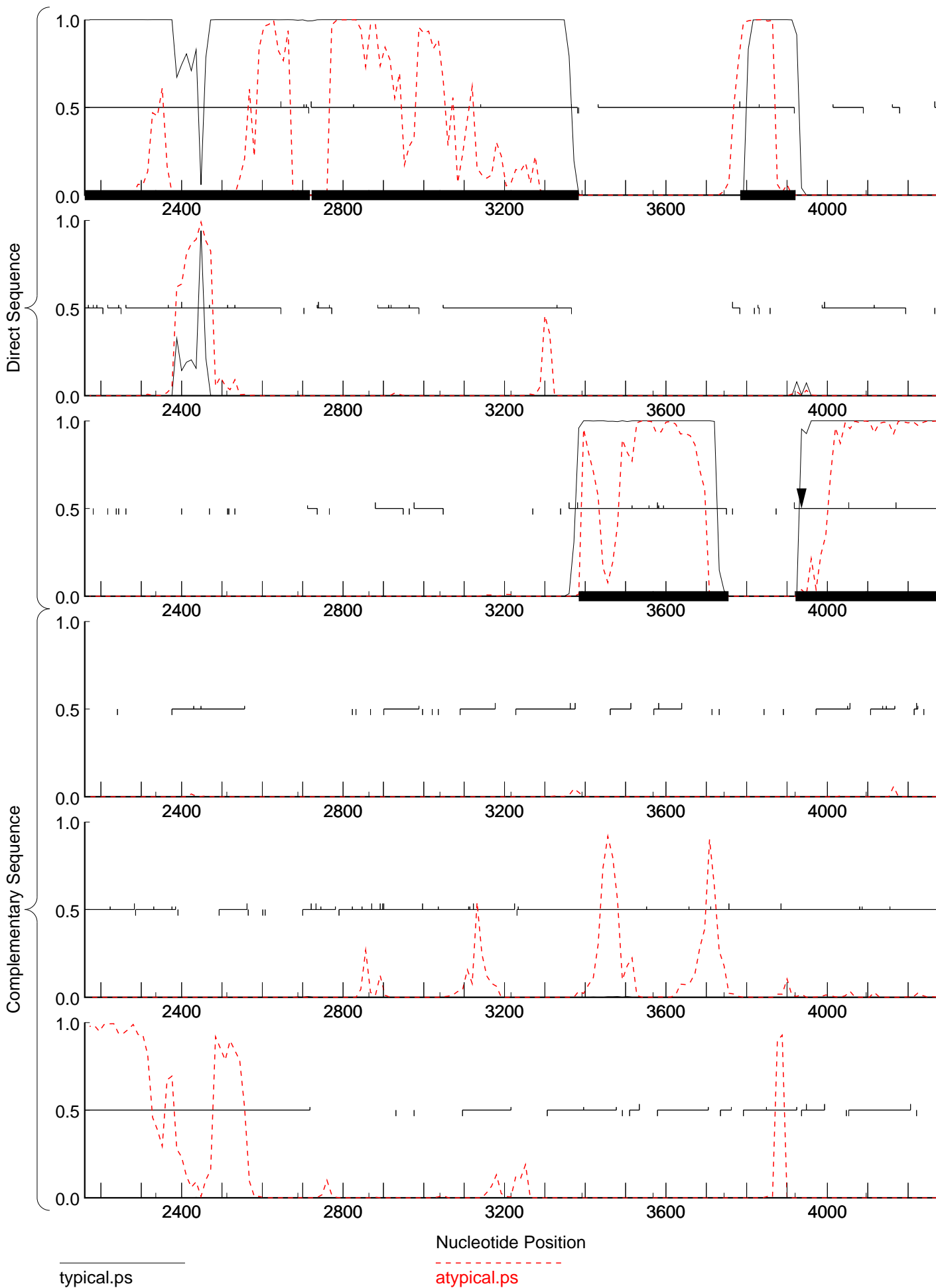
Training set derived by GeneMarkS, 4.30 October 2014  
Mon Jan 22 09:33:53 2018

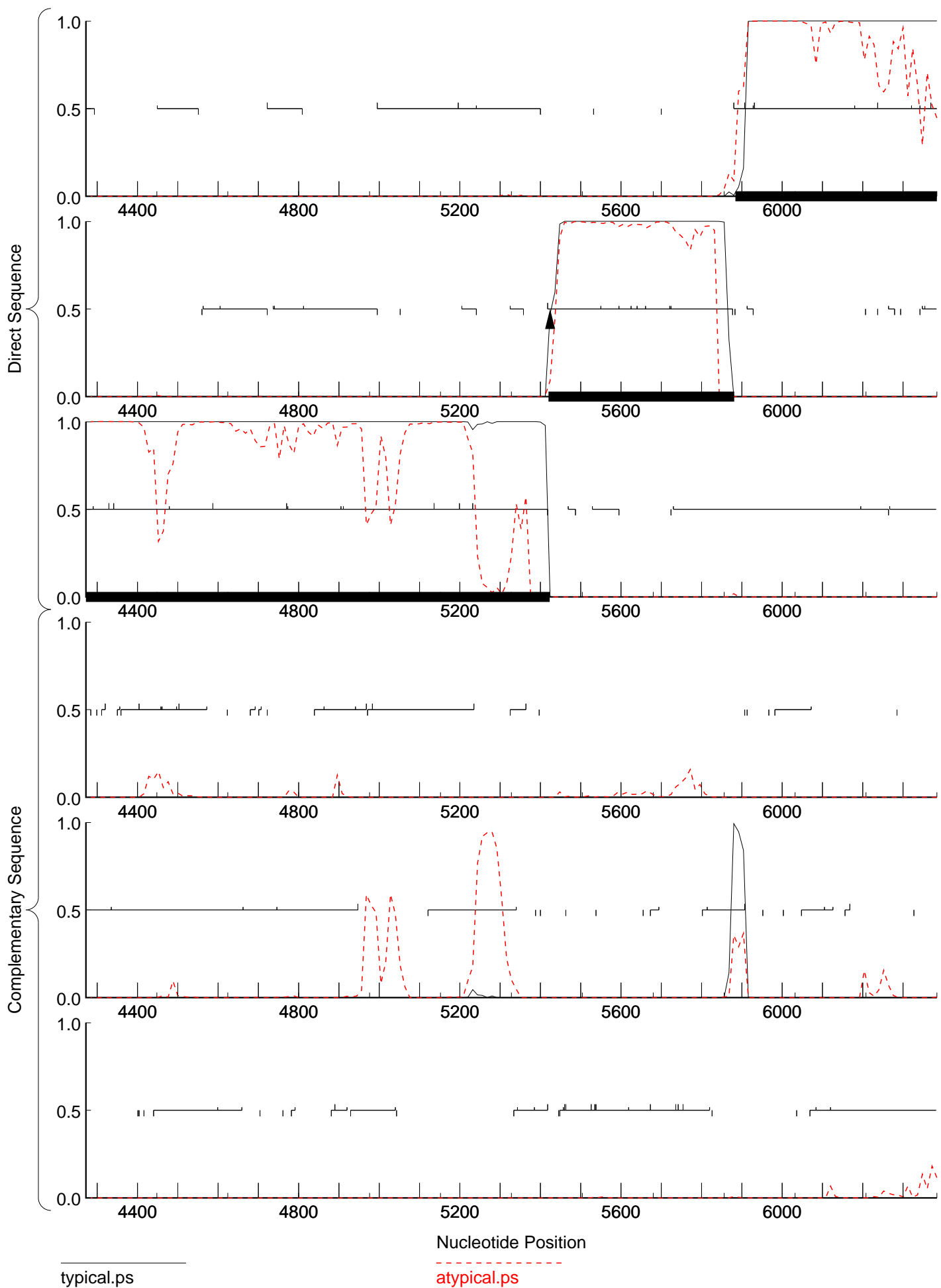
## MATRIX INFORMATION

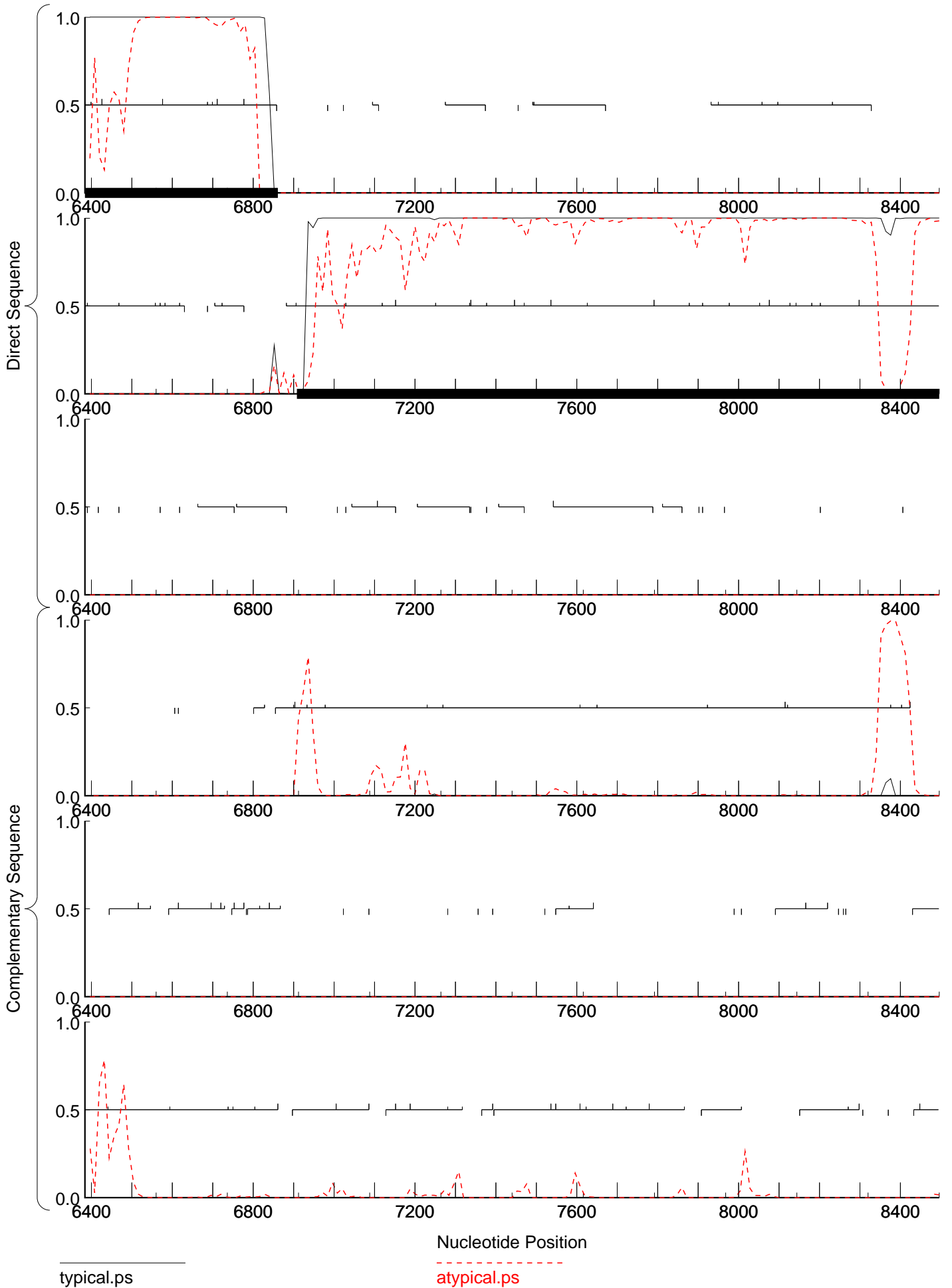
Matrix : -  
Author : -  
Order : 4

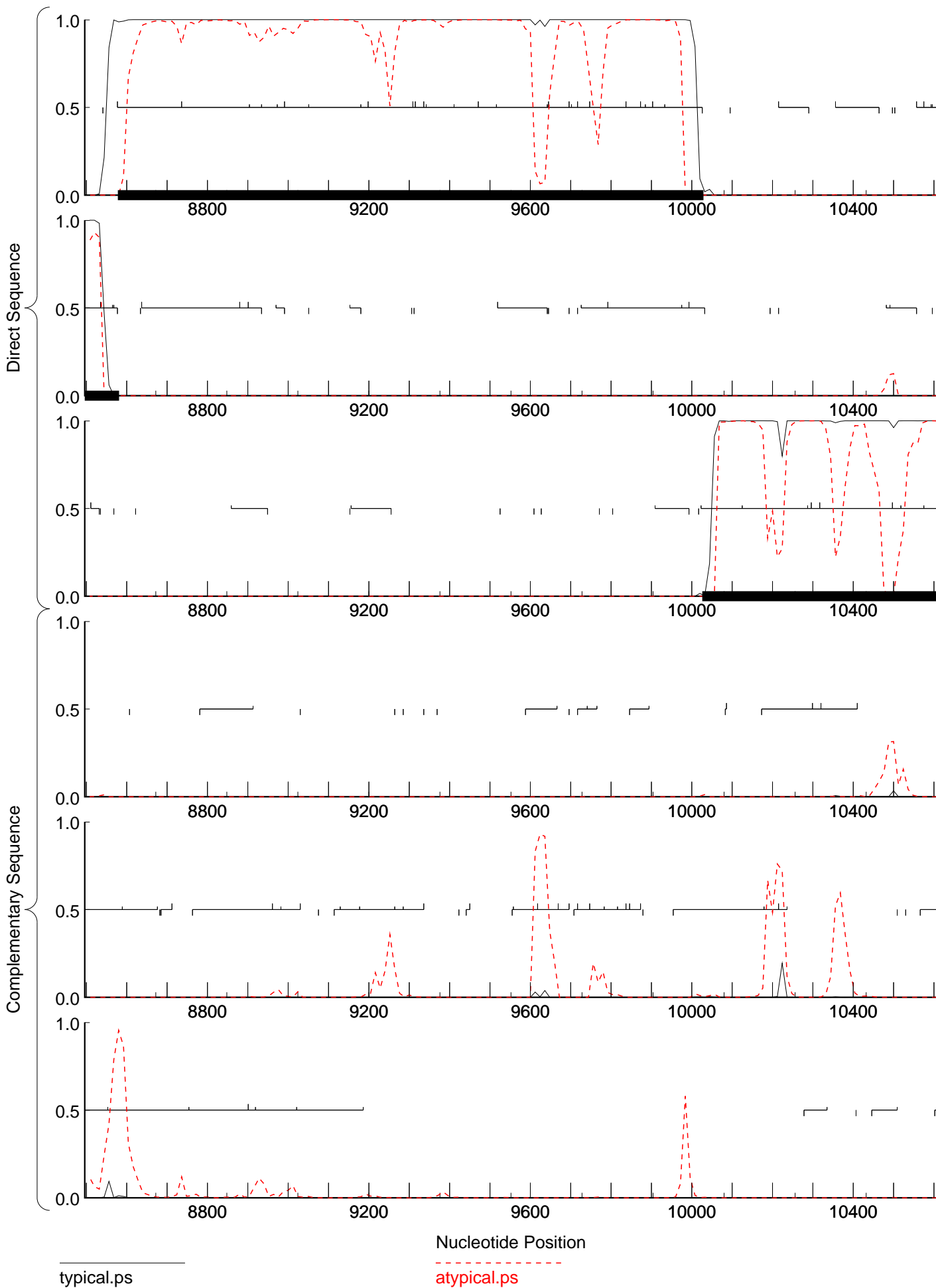
Send questions / comments to:  
Dr. M. Borodovsky  
Georgia Institute of Technology  
School of Biology  
Atlanta, GA 30332-0230



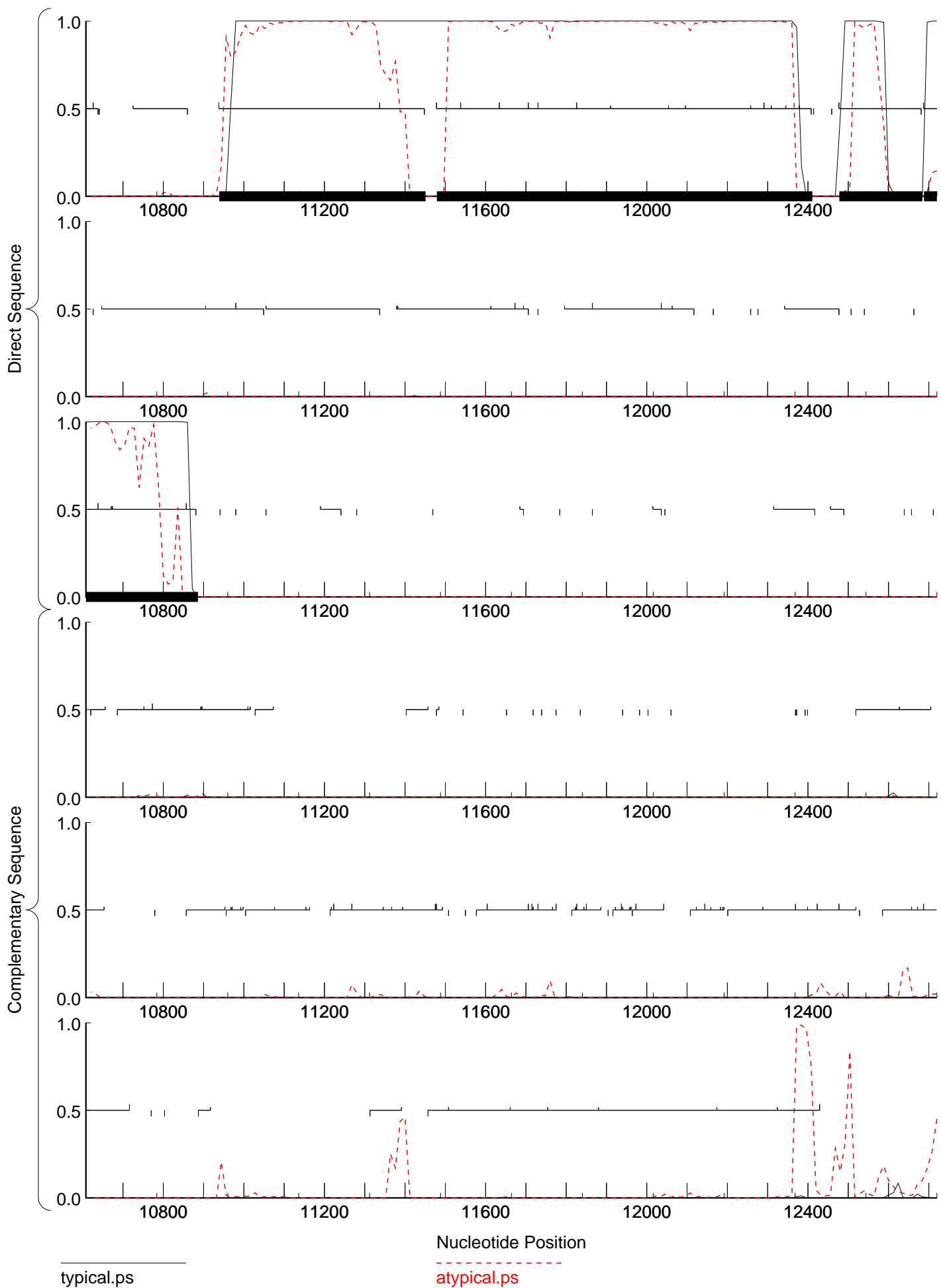




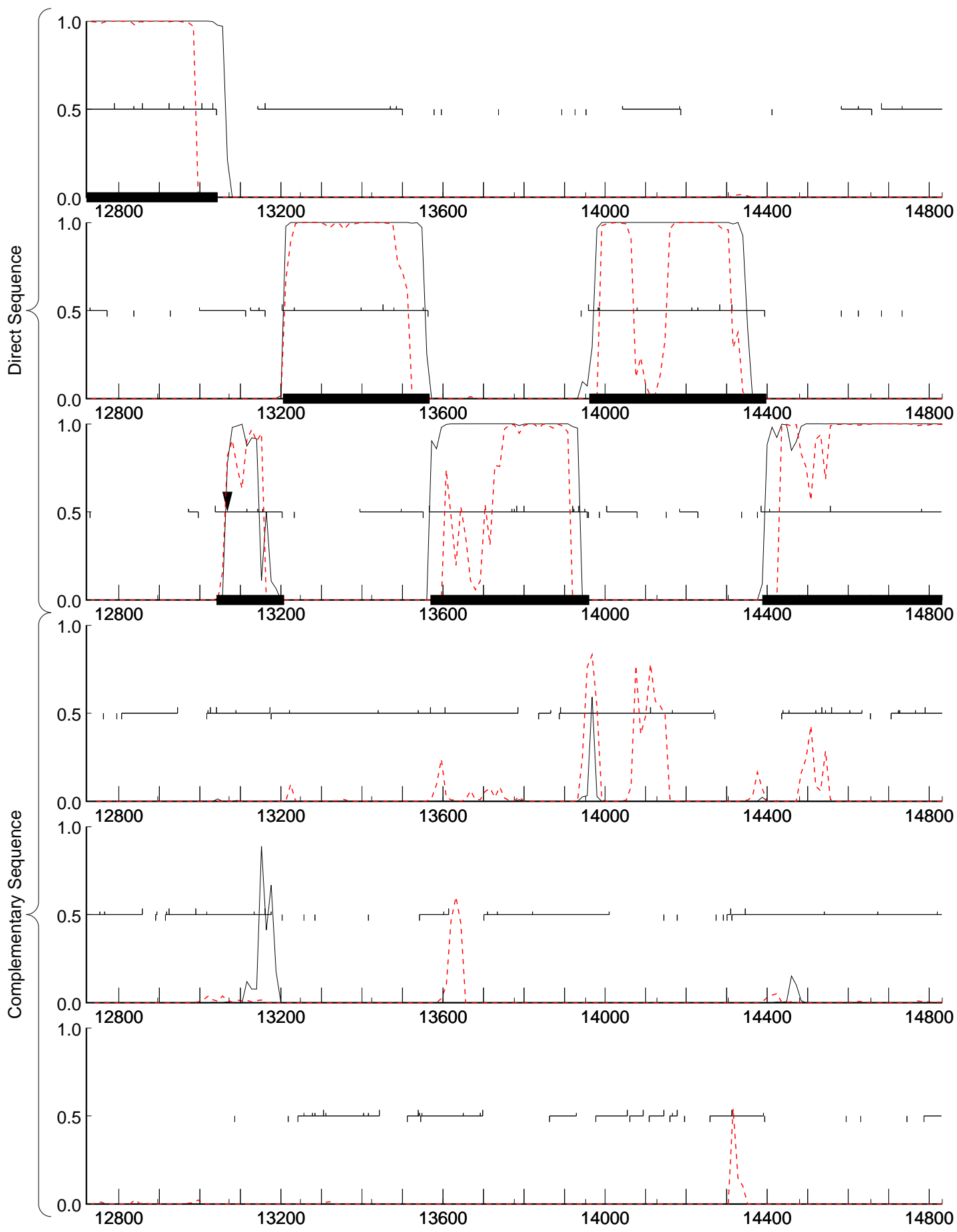




s complete sequence, 51374 bp including 10-base 3' overhang (CGGCCGGTAA), Cluster A4, Order 4, Window 96, Step 12, 7/26  
s complete sequence, 51374 bp including 10-base 3' overhang (CGGCCGGTAA), Cluster A4, Order 2, Window 96, Step 12, 7/26



GeneMark.hmm prediction

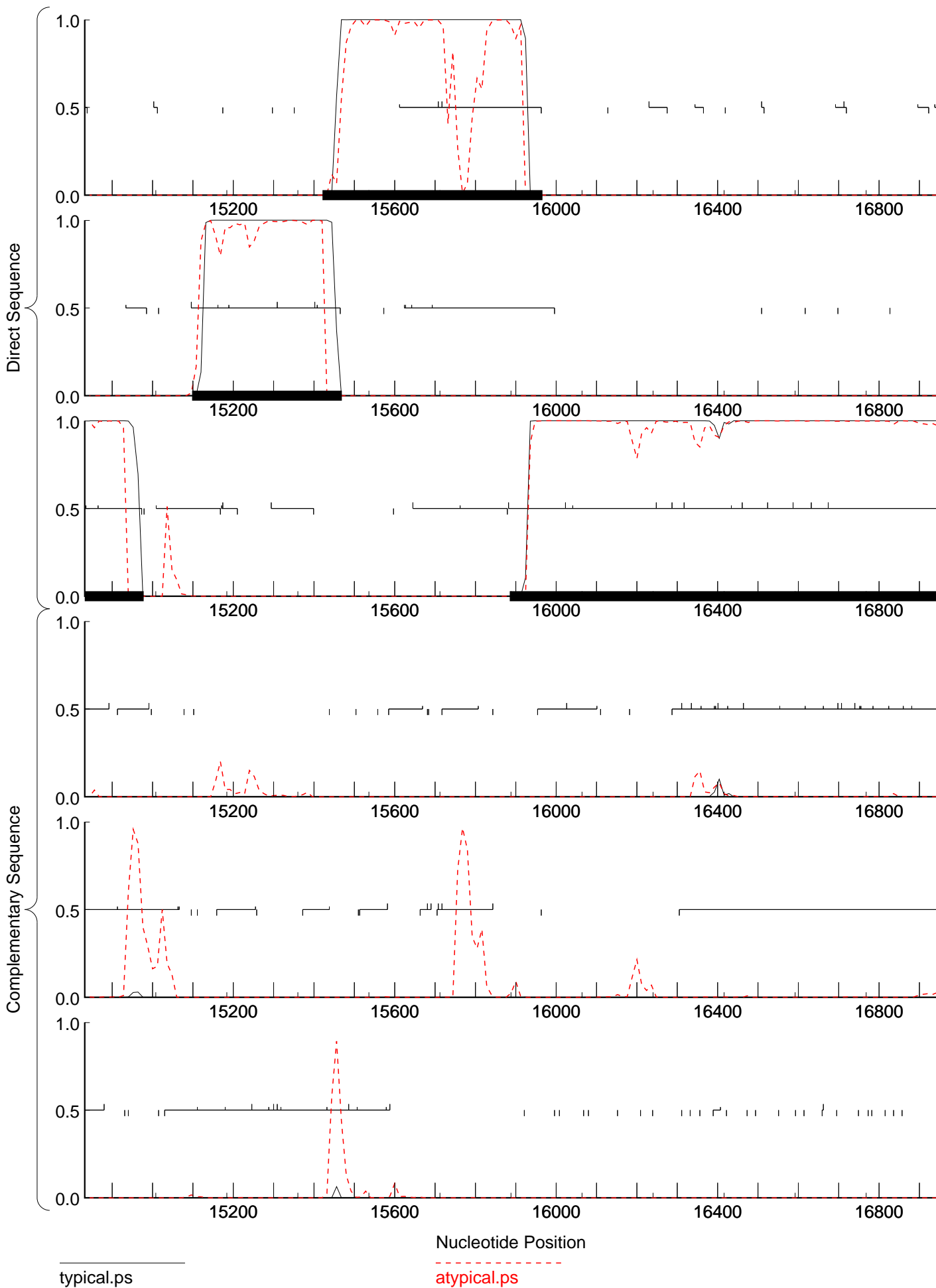


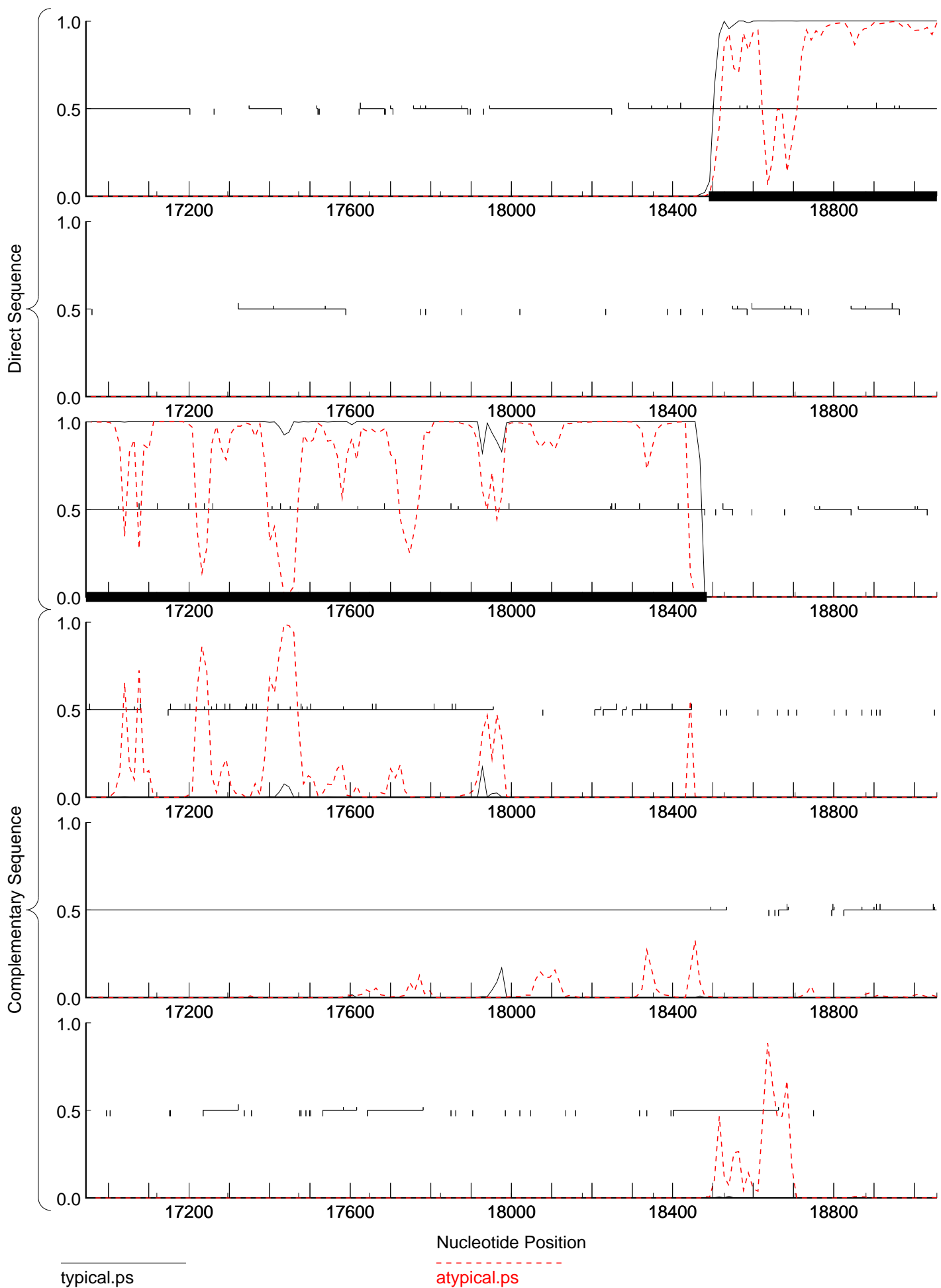
typical.ps

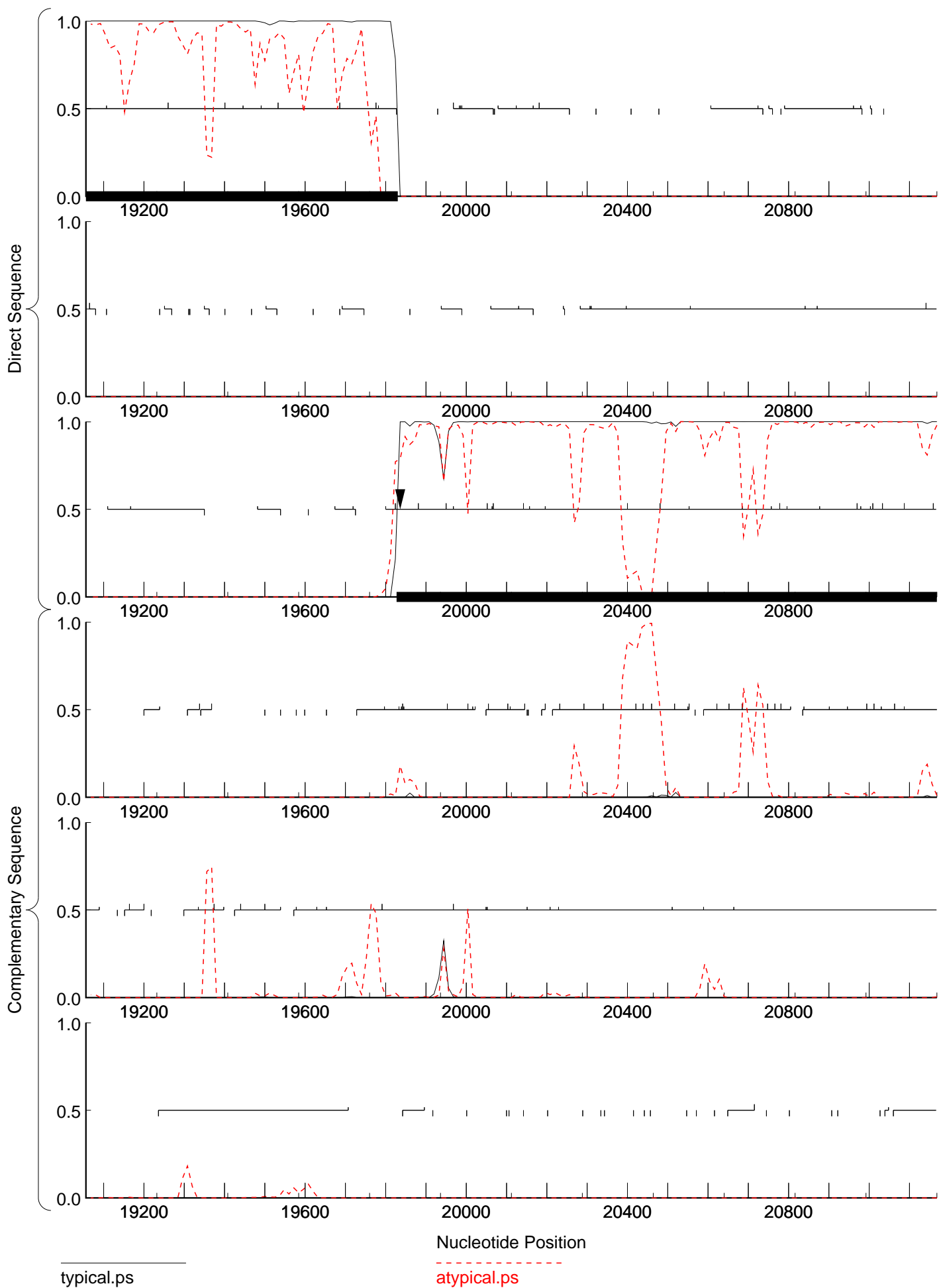
atypical.ps

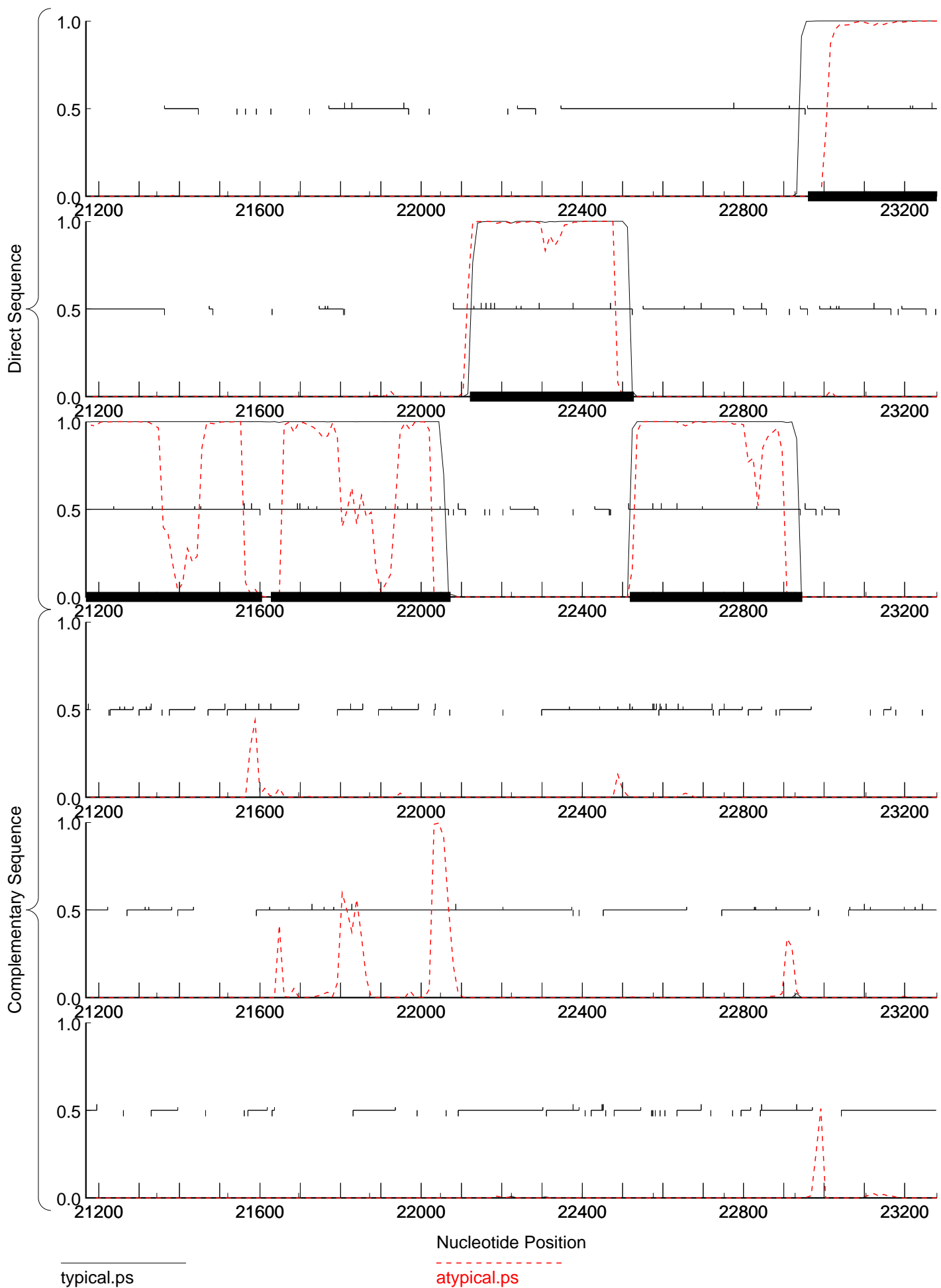
Nucleotide Position

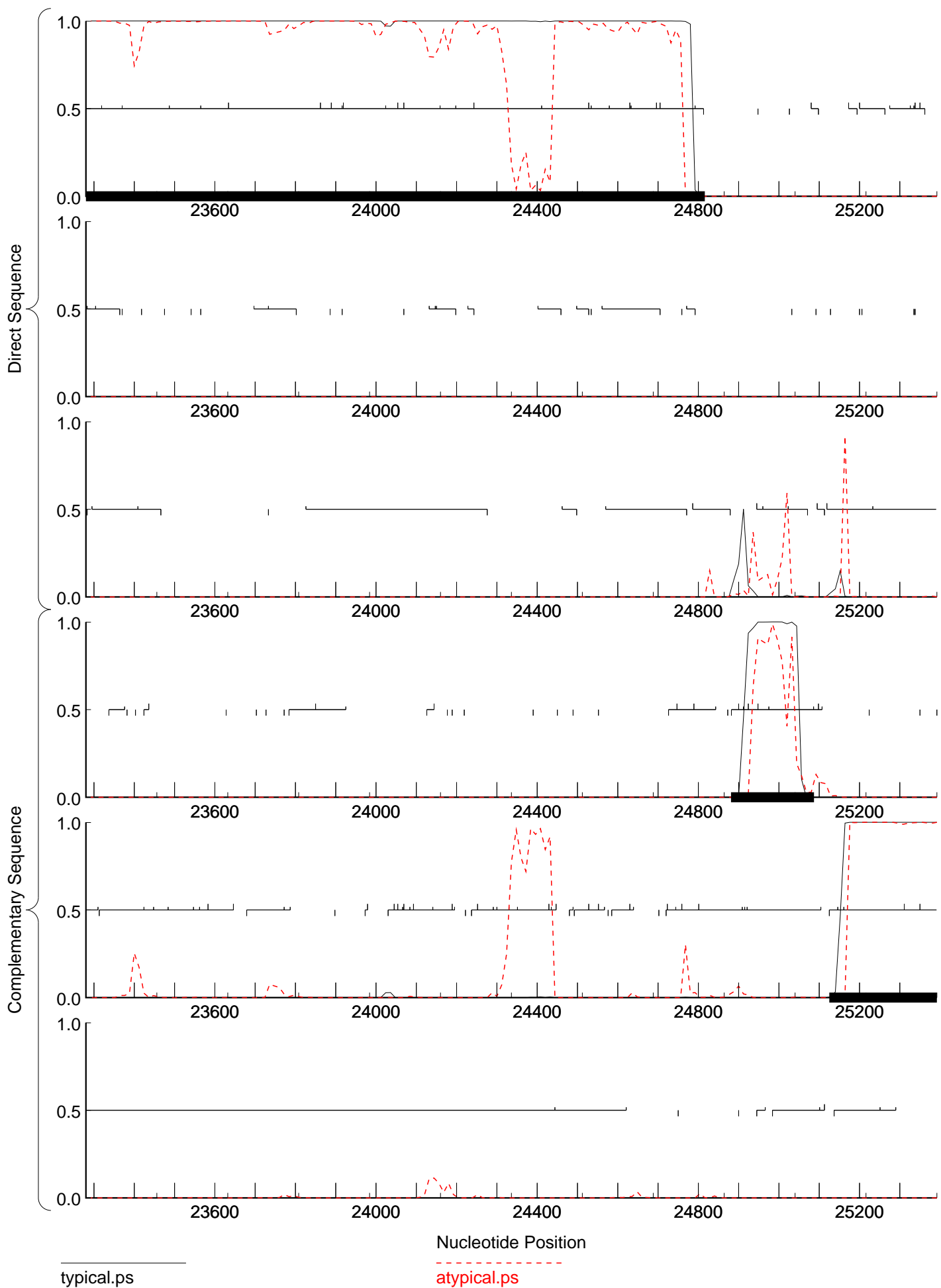


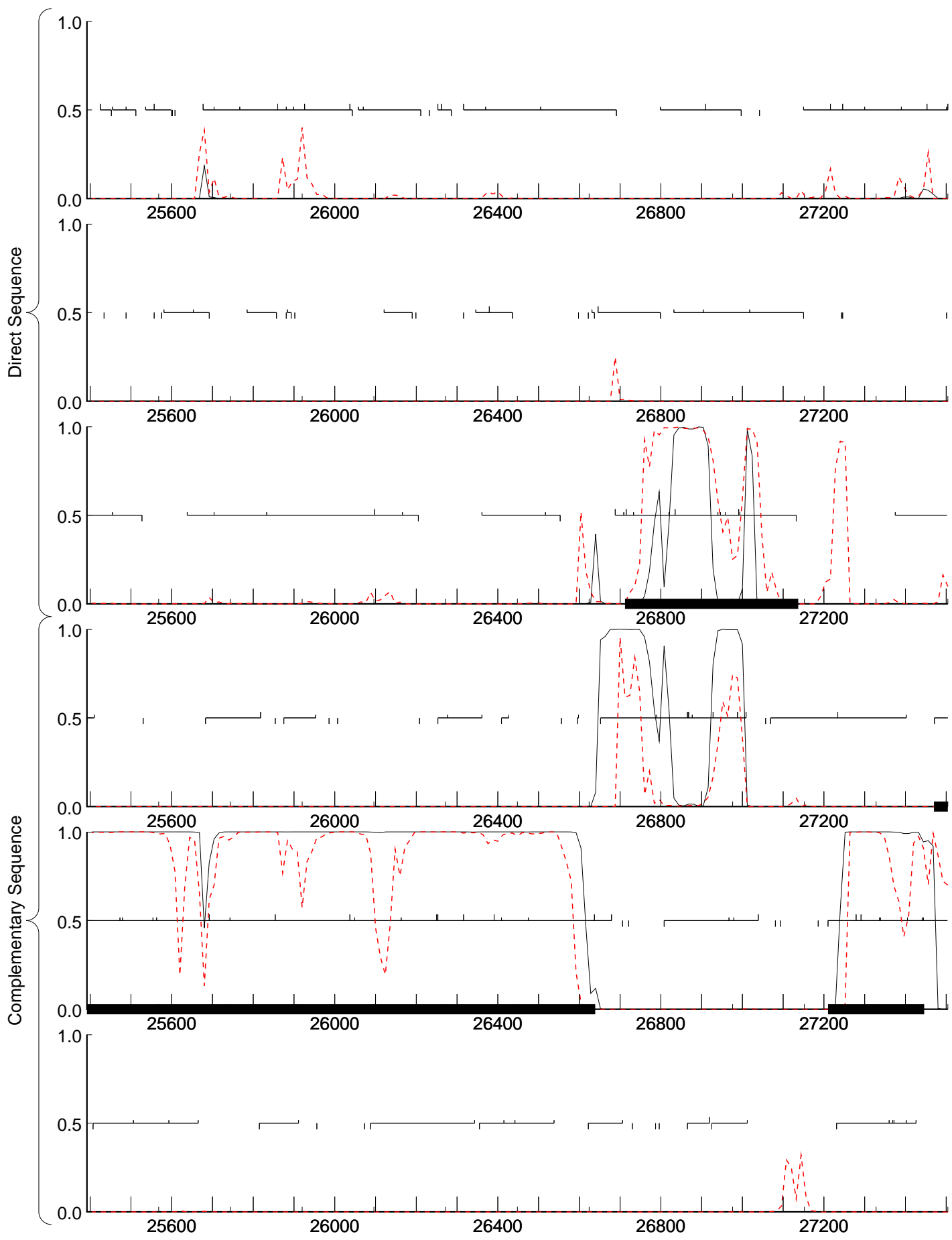






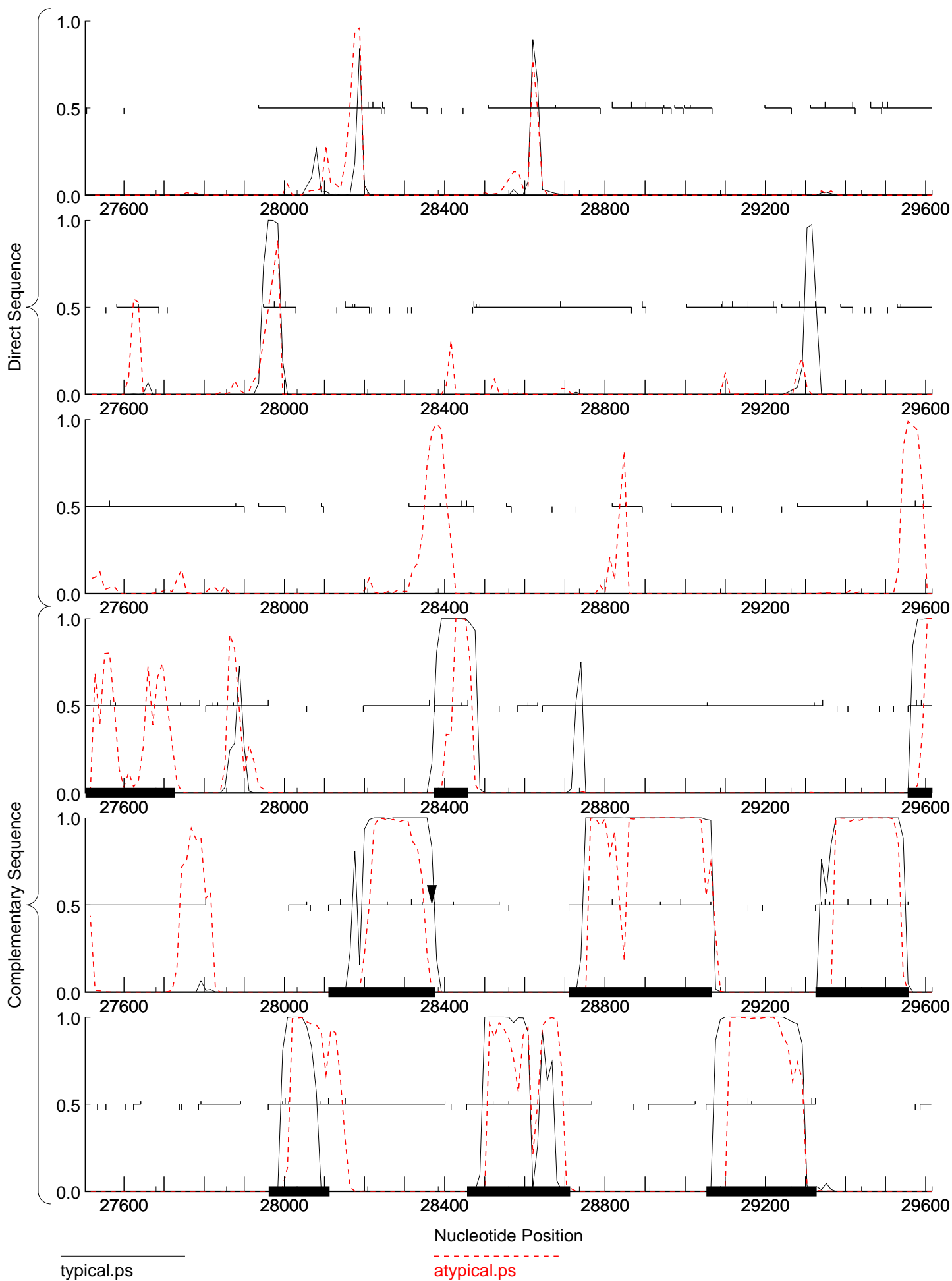






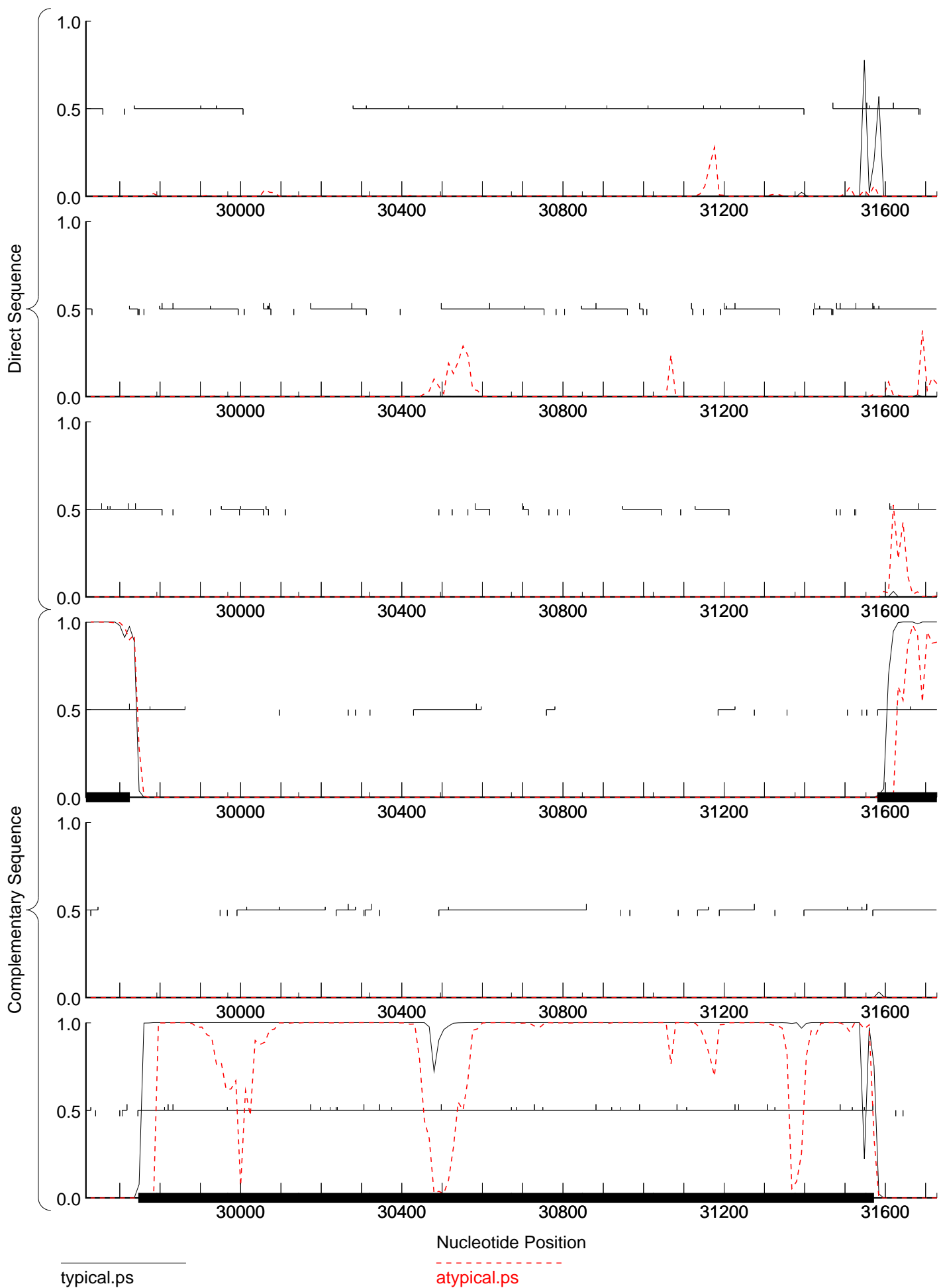
typical.ps

atypical.ps



typical.ps

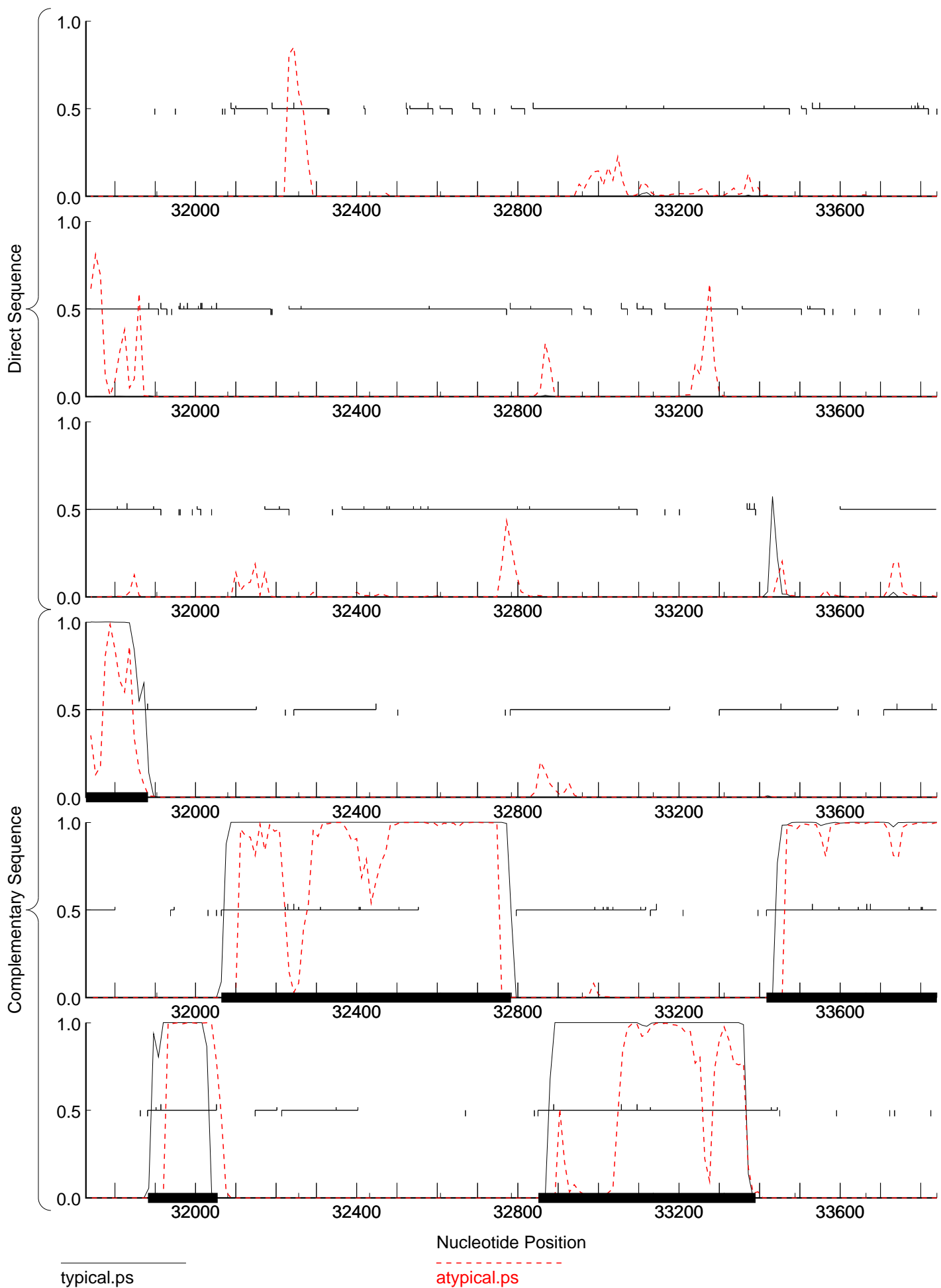
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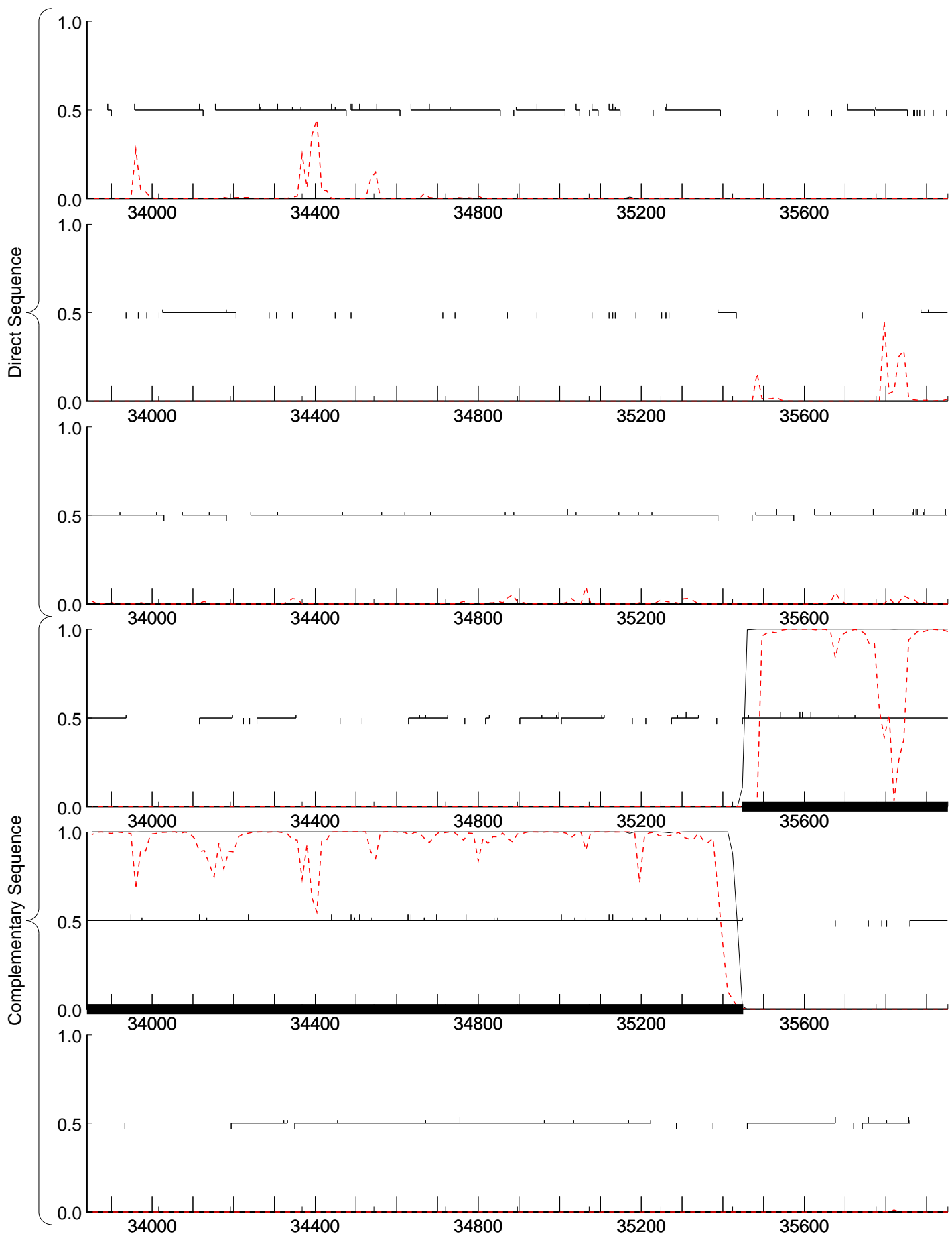
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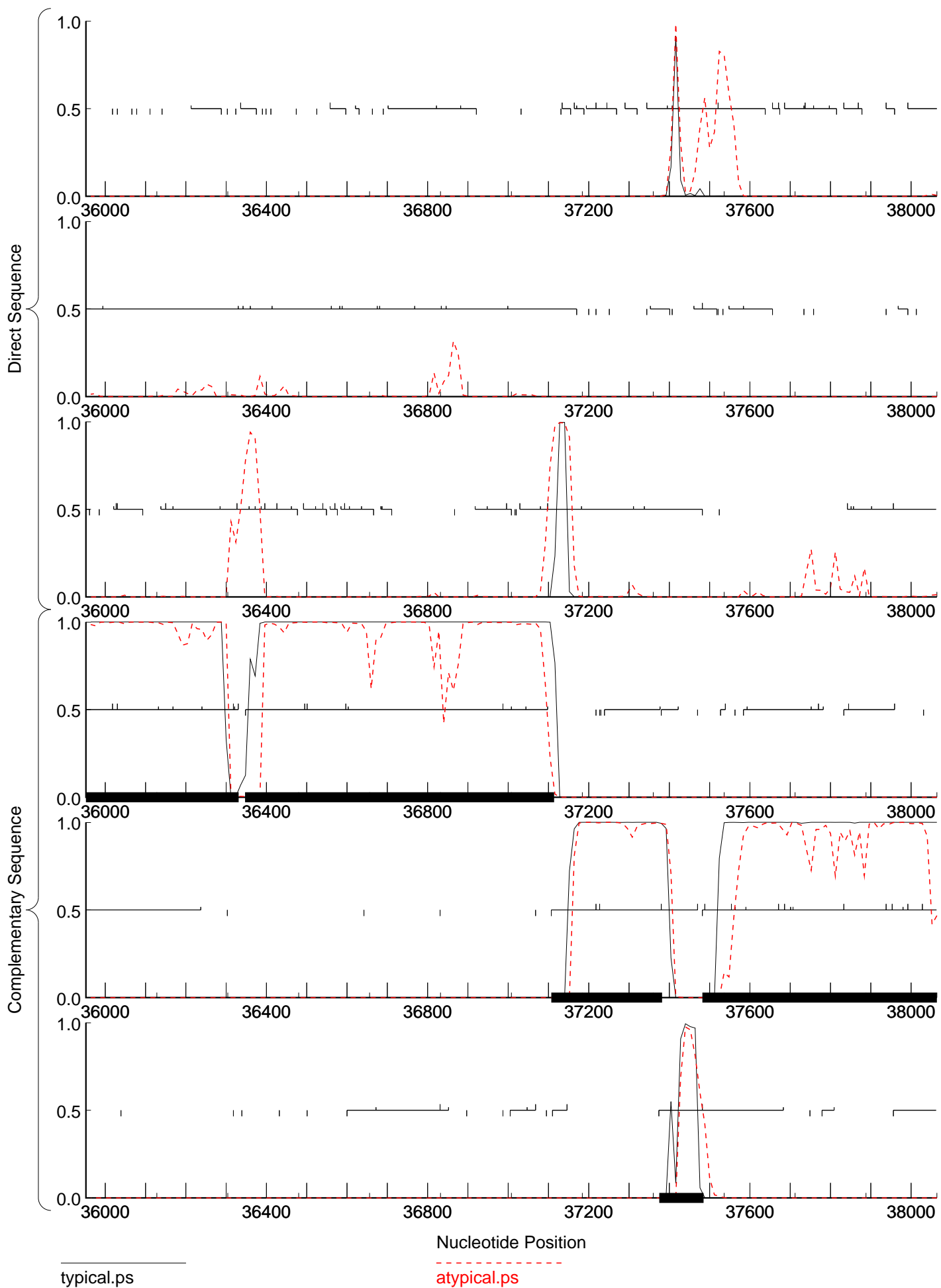


GeneMark.hmm prediction



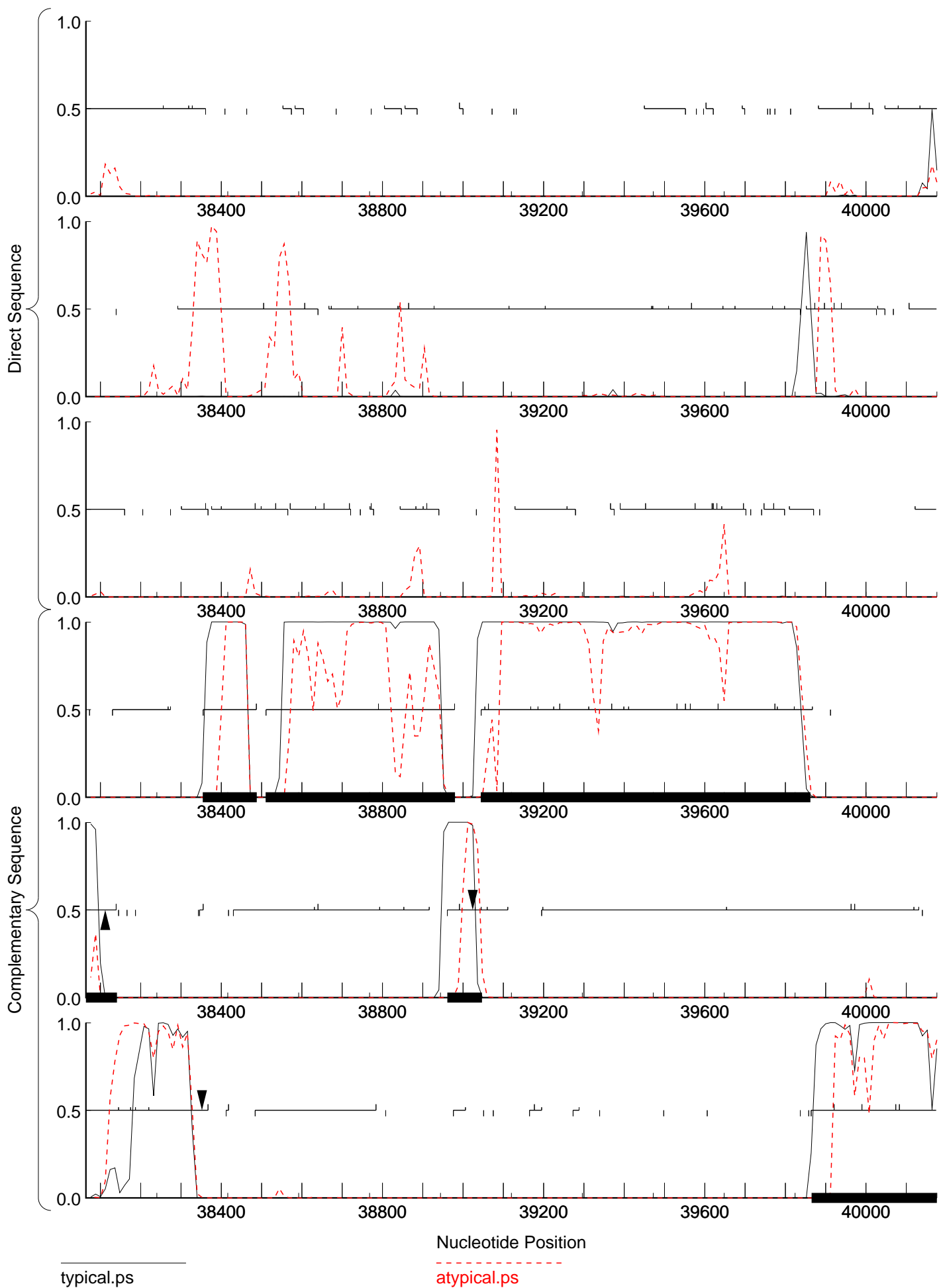
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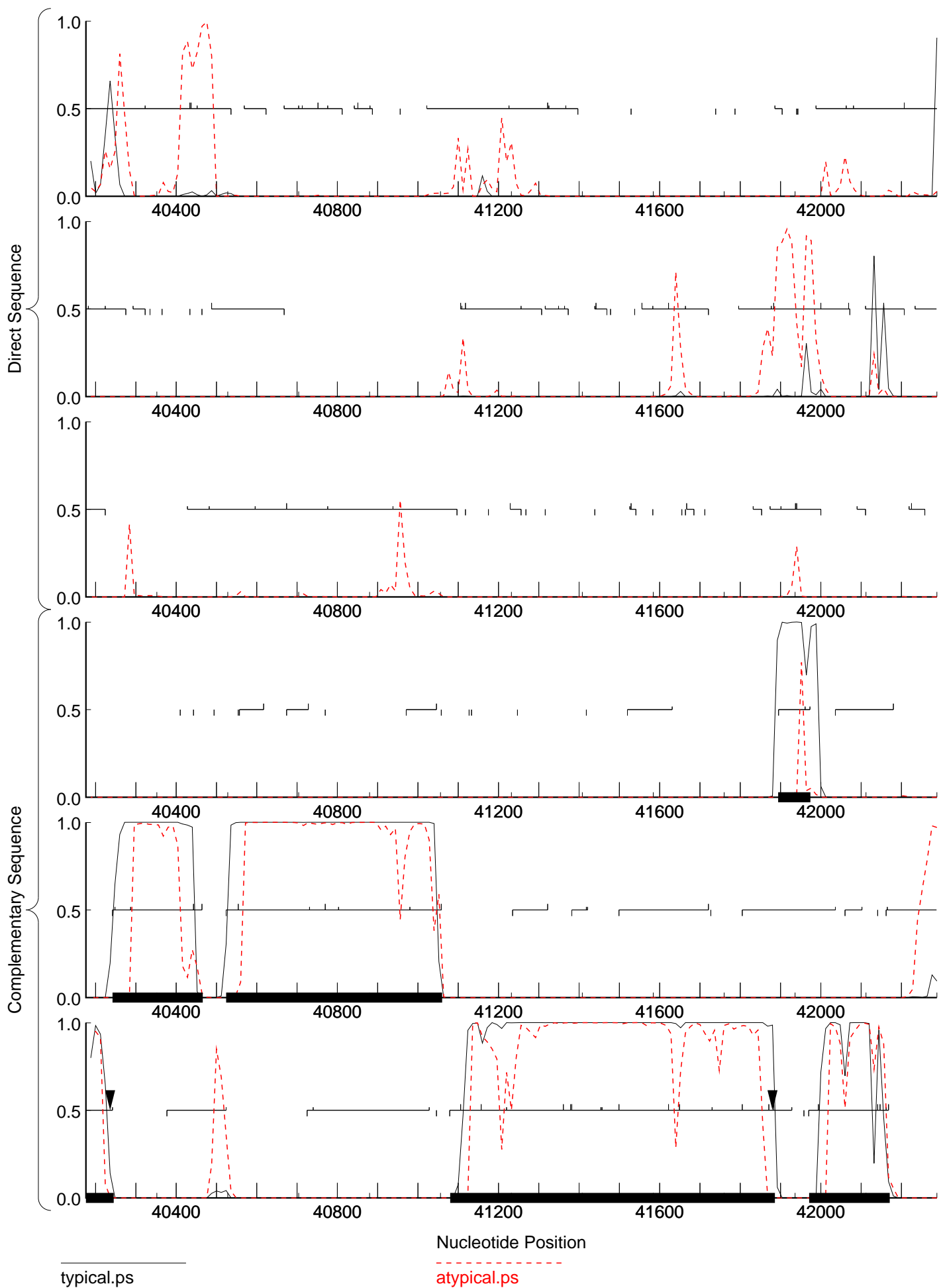
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typical.ps

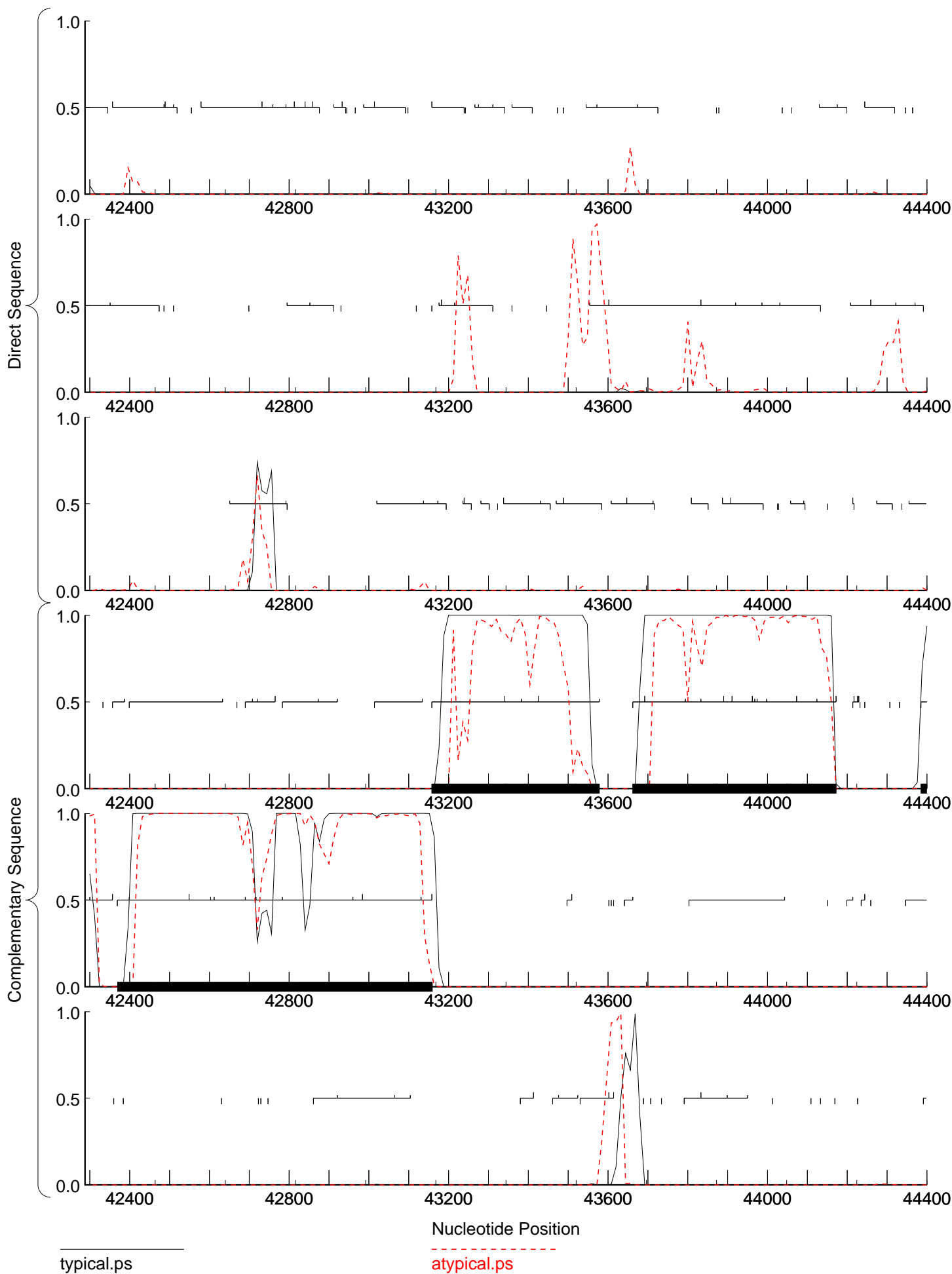
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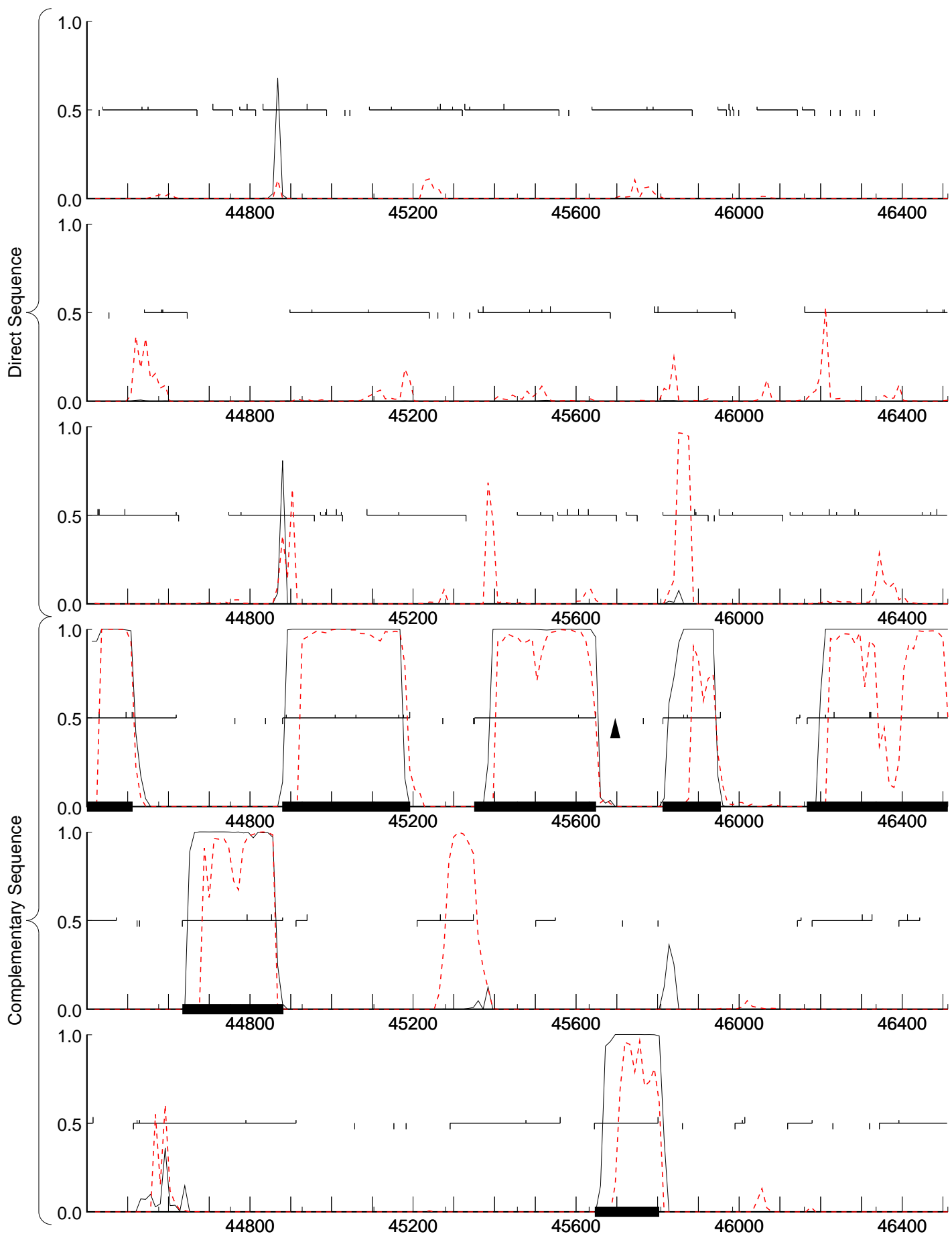




typical.ps

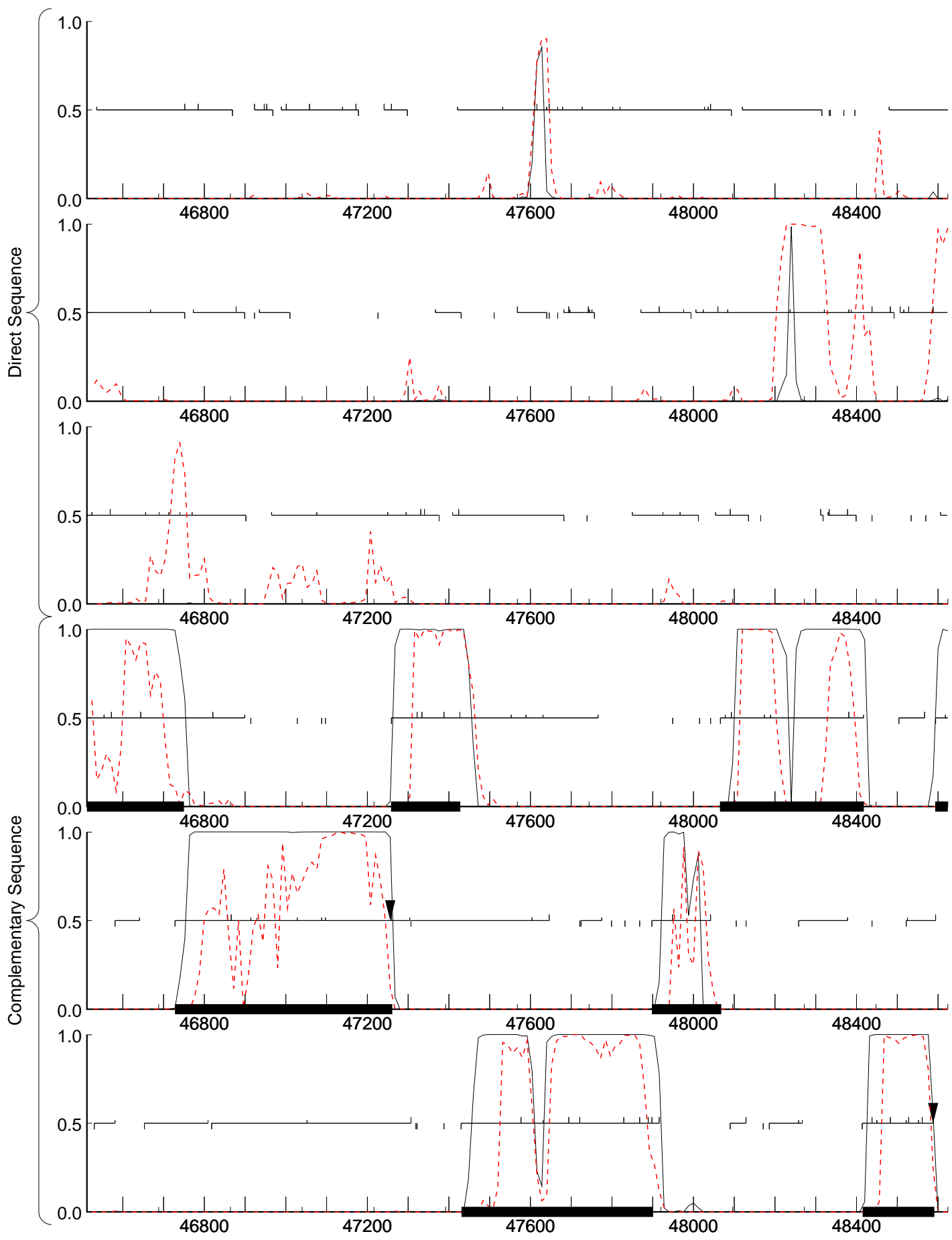
atypical.ps





typical.ps

atypical.ps



typical.ps

atypical.ps



