

# GeneMark

Version 2.5p (09.08.06)

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## PROGRAM INFORMATION

Sequence : Mycobacterium phage MaryV complete sequence, 76413 bp including 11-base 3' overhang (ACCACT  
Analysis Date : 4/20/18 at 12:20:51  
Pages : 38  
Sequence Length : 76413 bp  
GC Content : 56.88%

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,

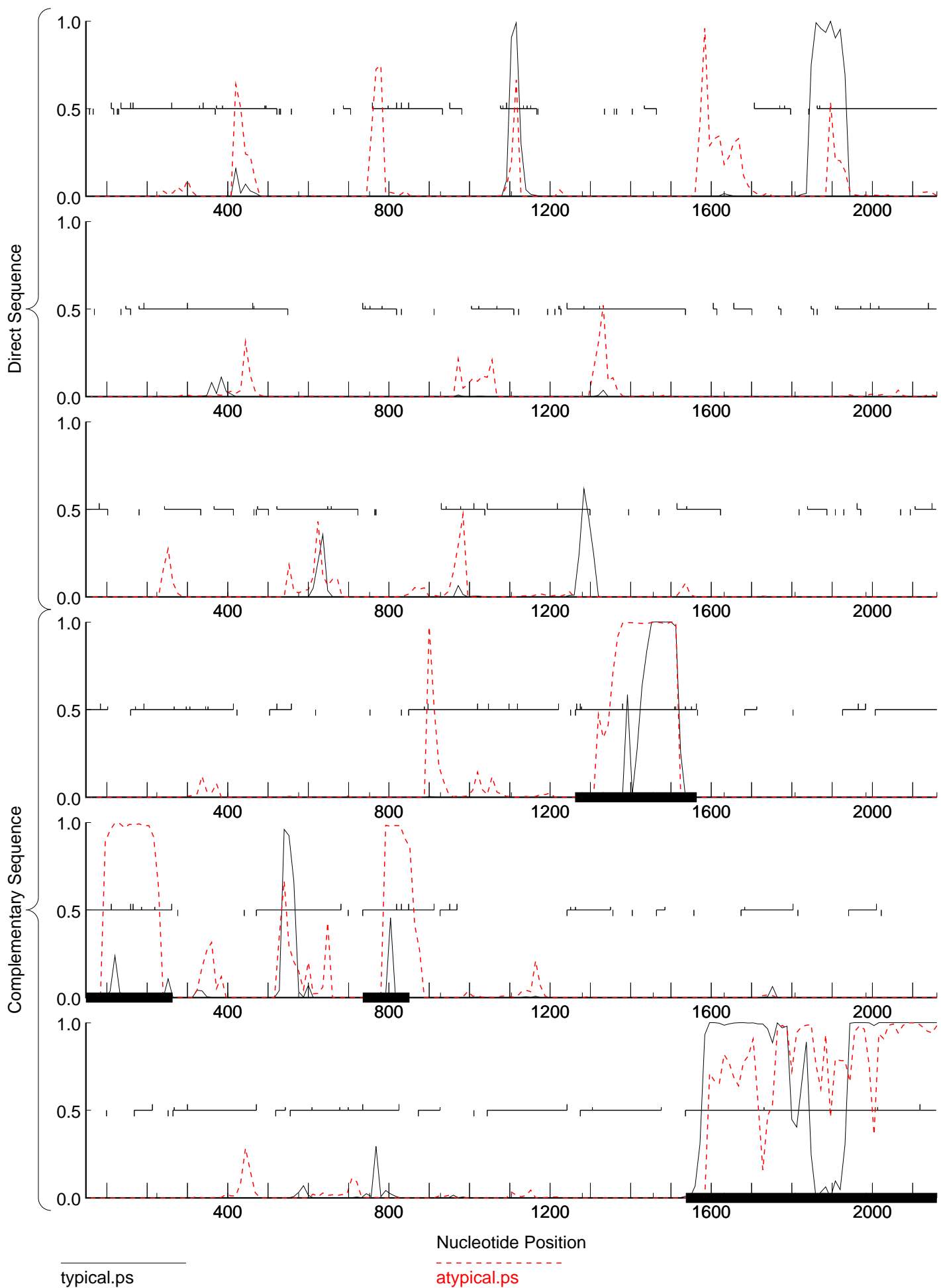
## Matrix notes & comments

Training set derived by GeneMarkS, 4.30 October 2014  
Fri Apr 20 12:20:51 2018

## MATRIX INFORMATION

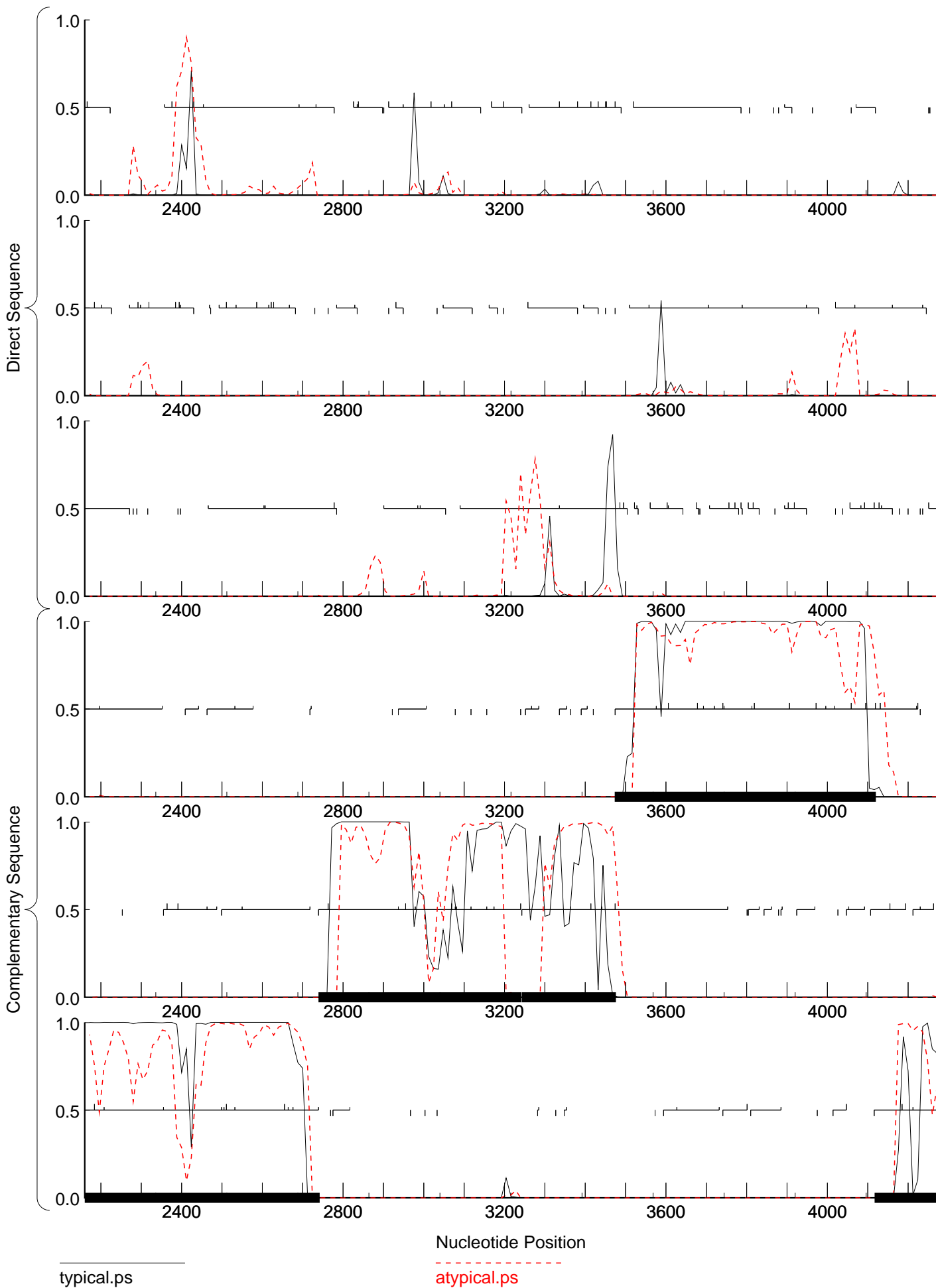
Matrix : -  
Author : -  
Order : 4

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



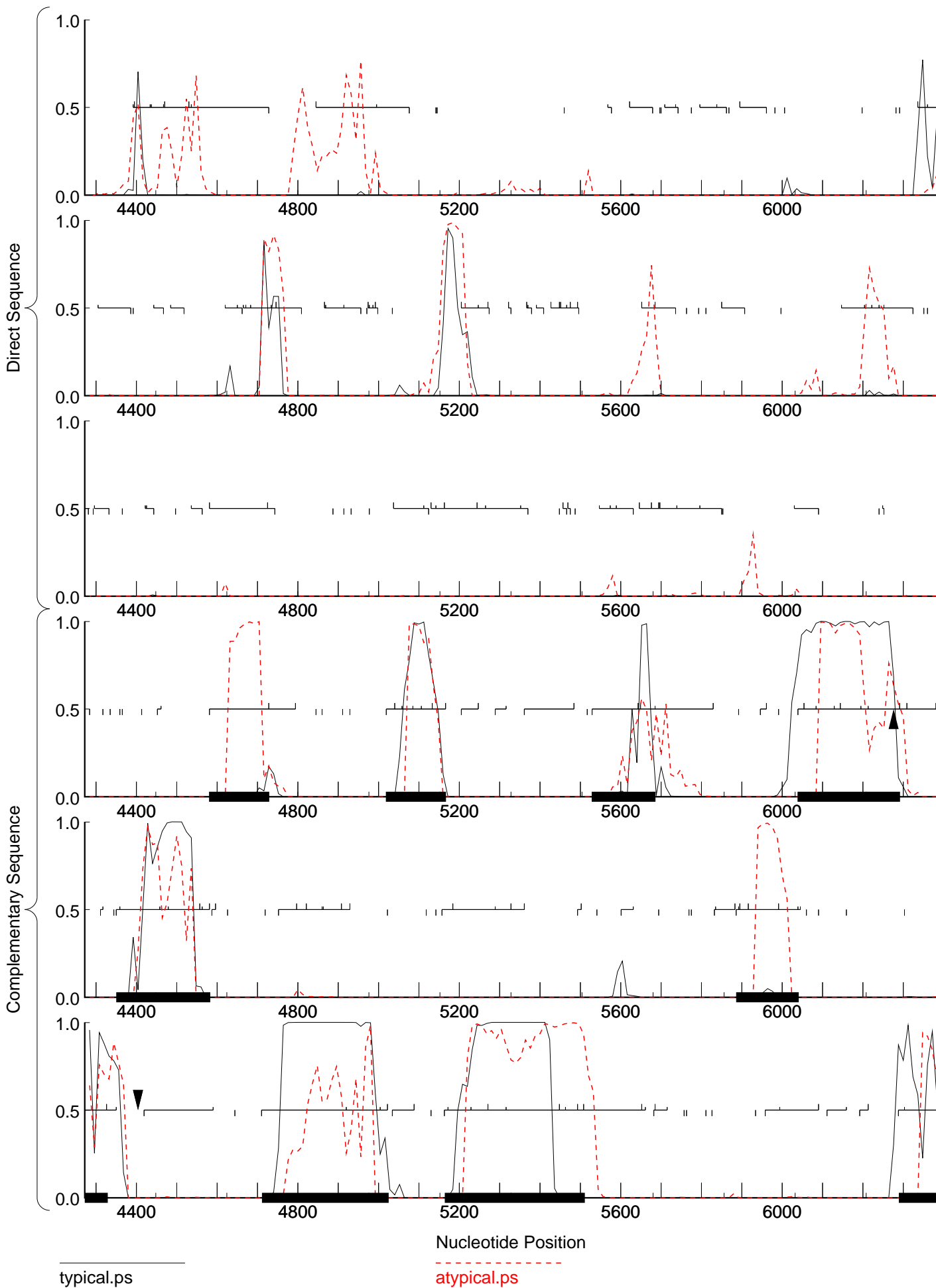
typical.ps

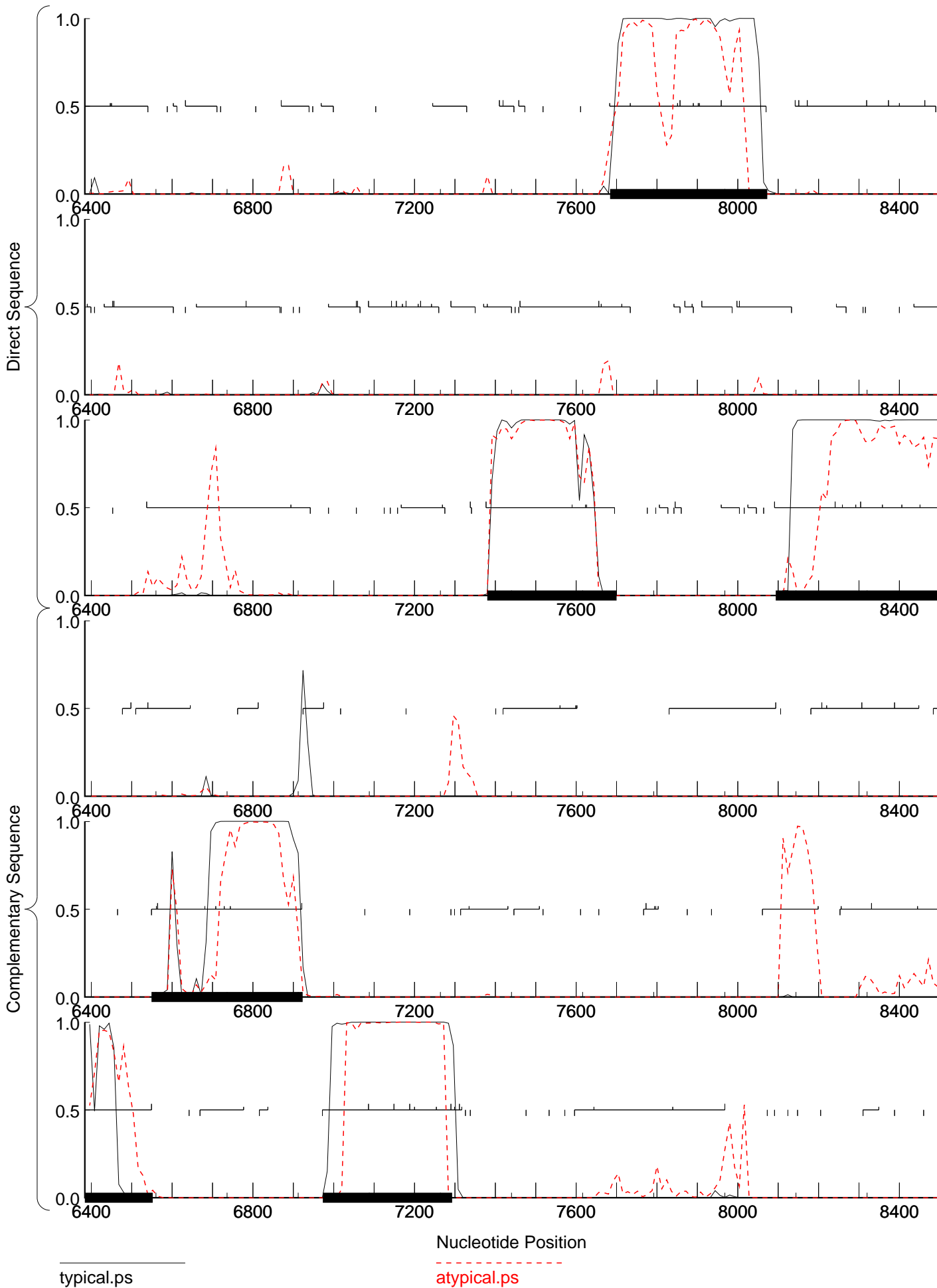
atypical.ps



typical.ps

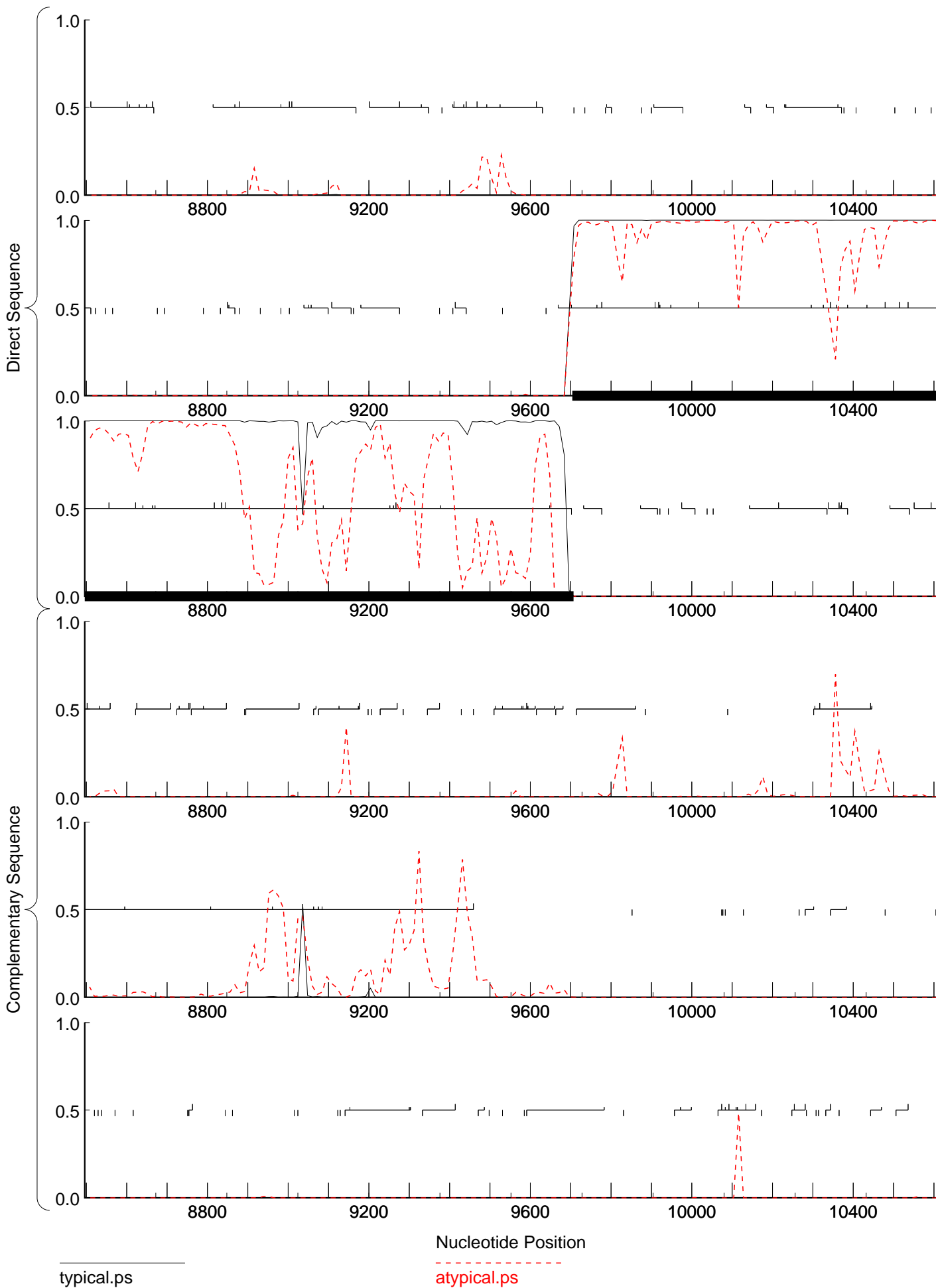
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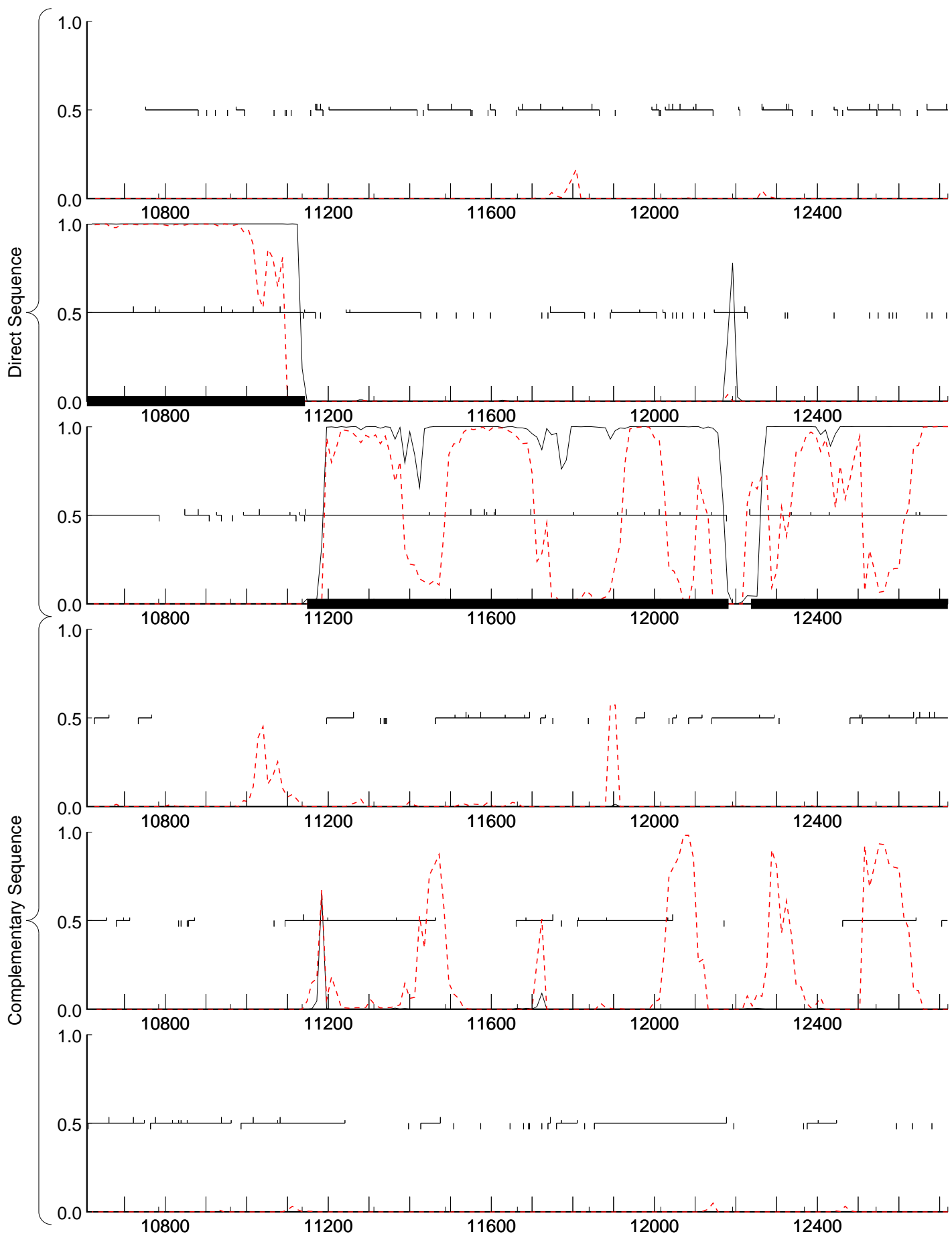




typical.ps

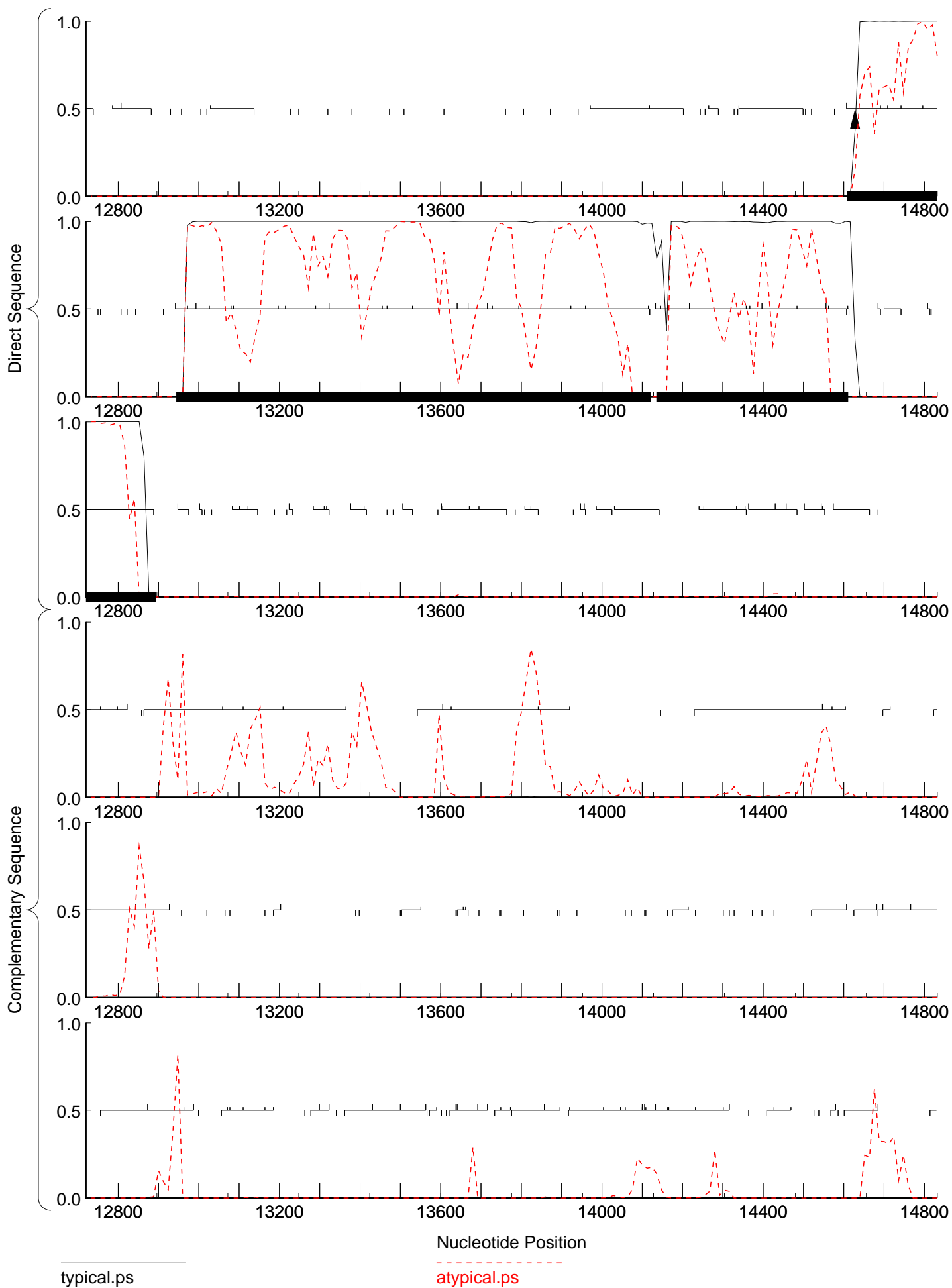
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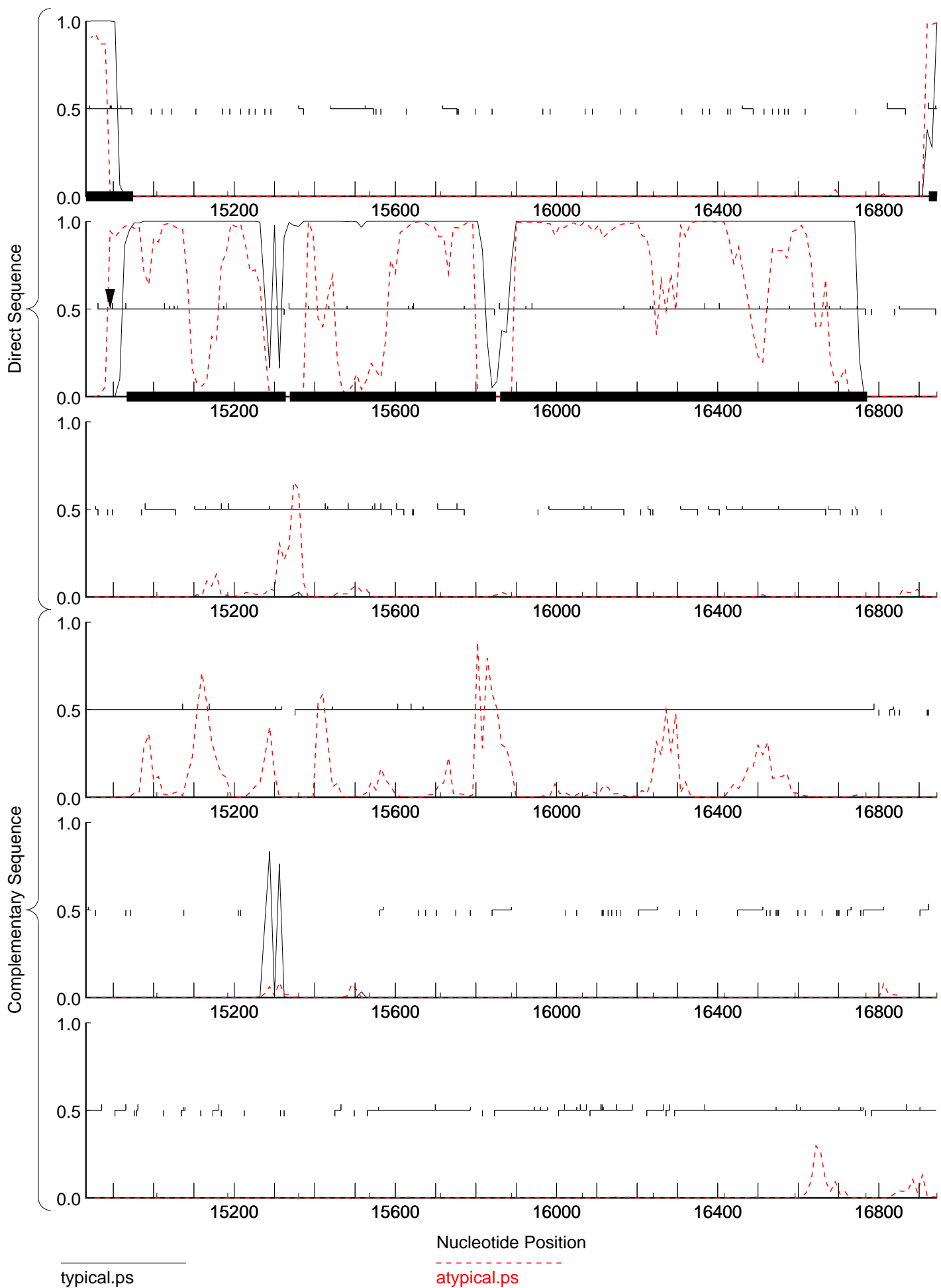


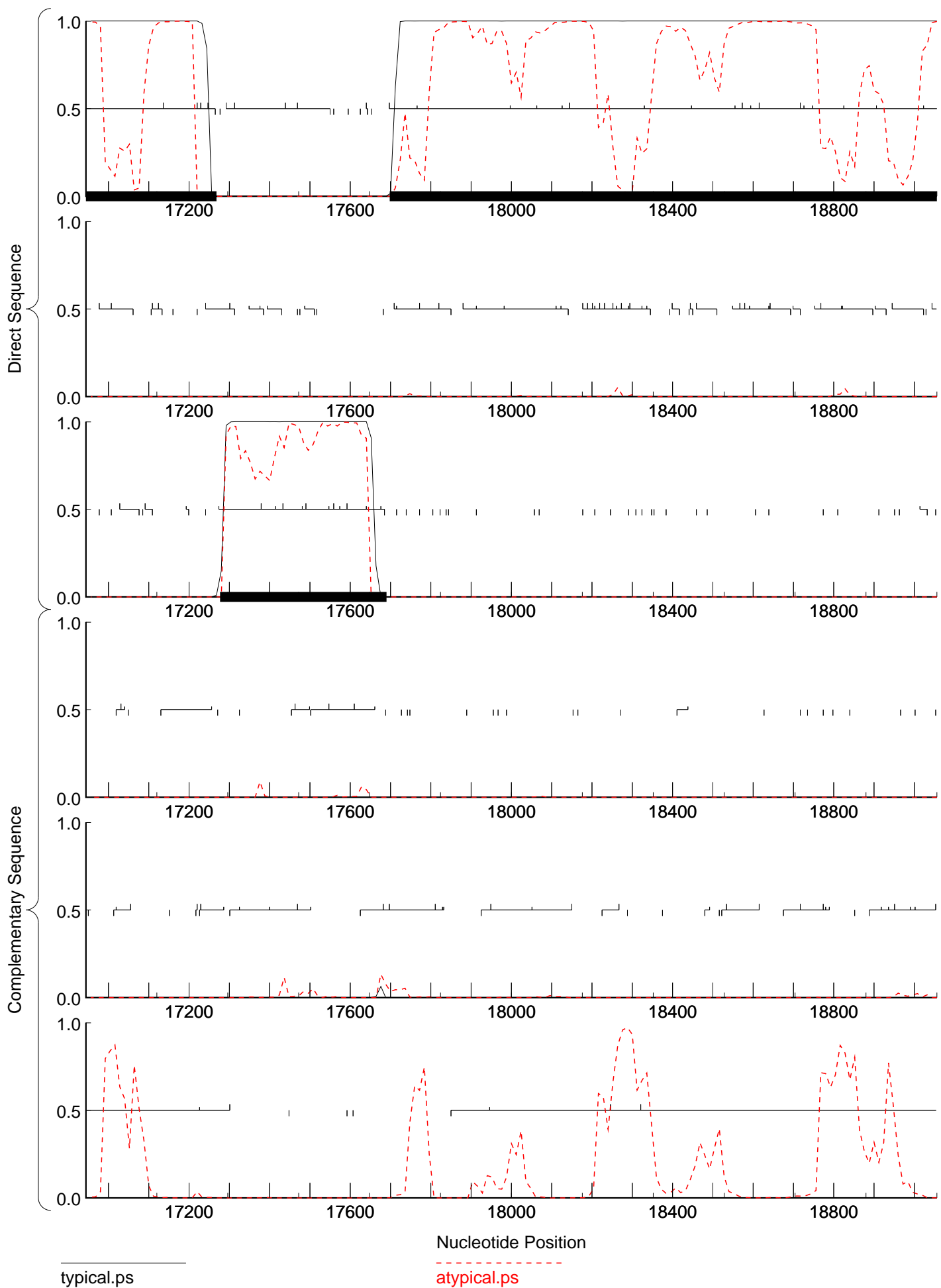
typical.ps

atypical.ps



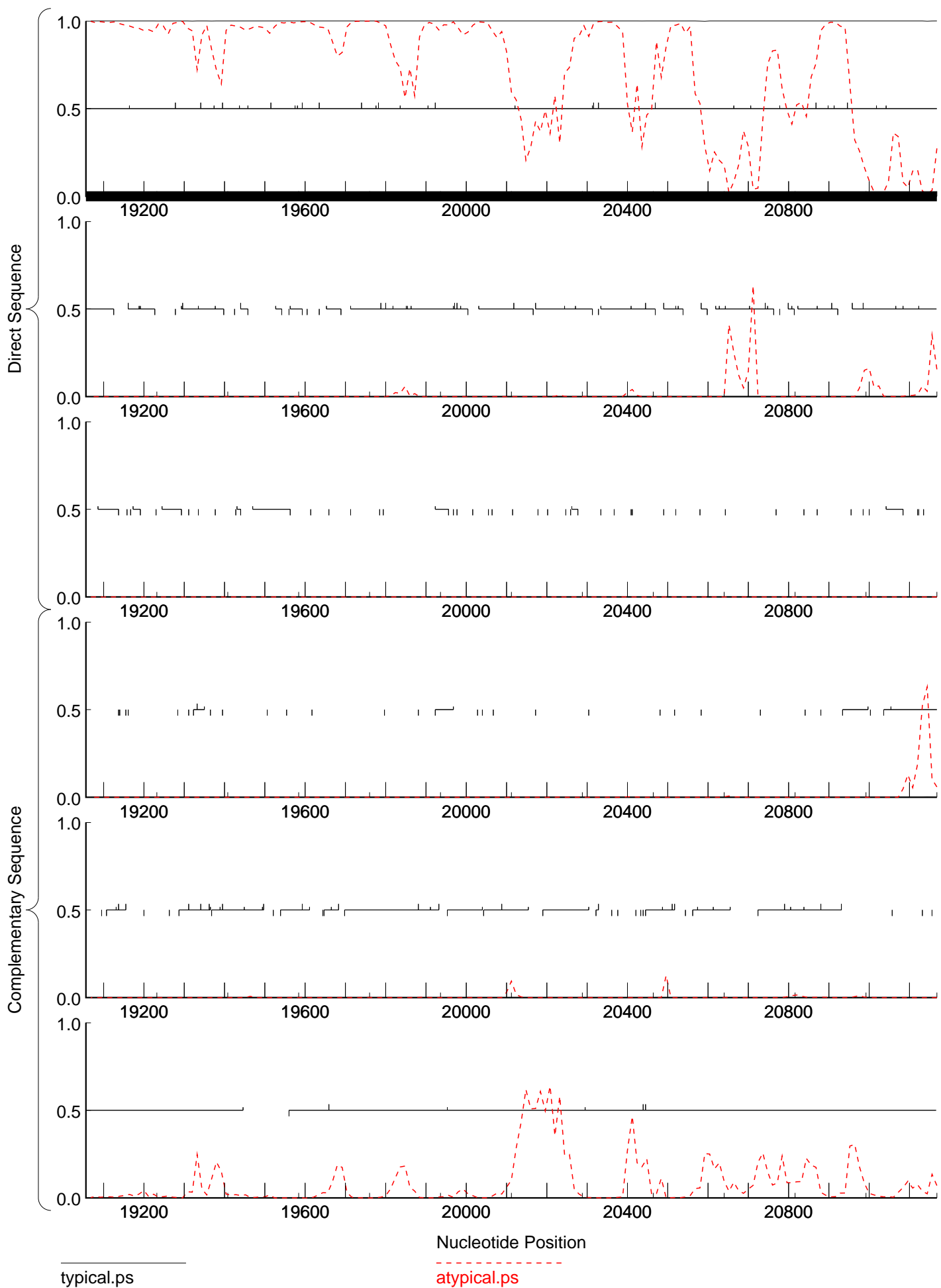






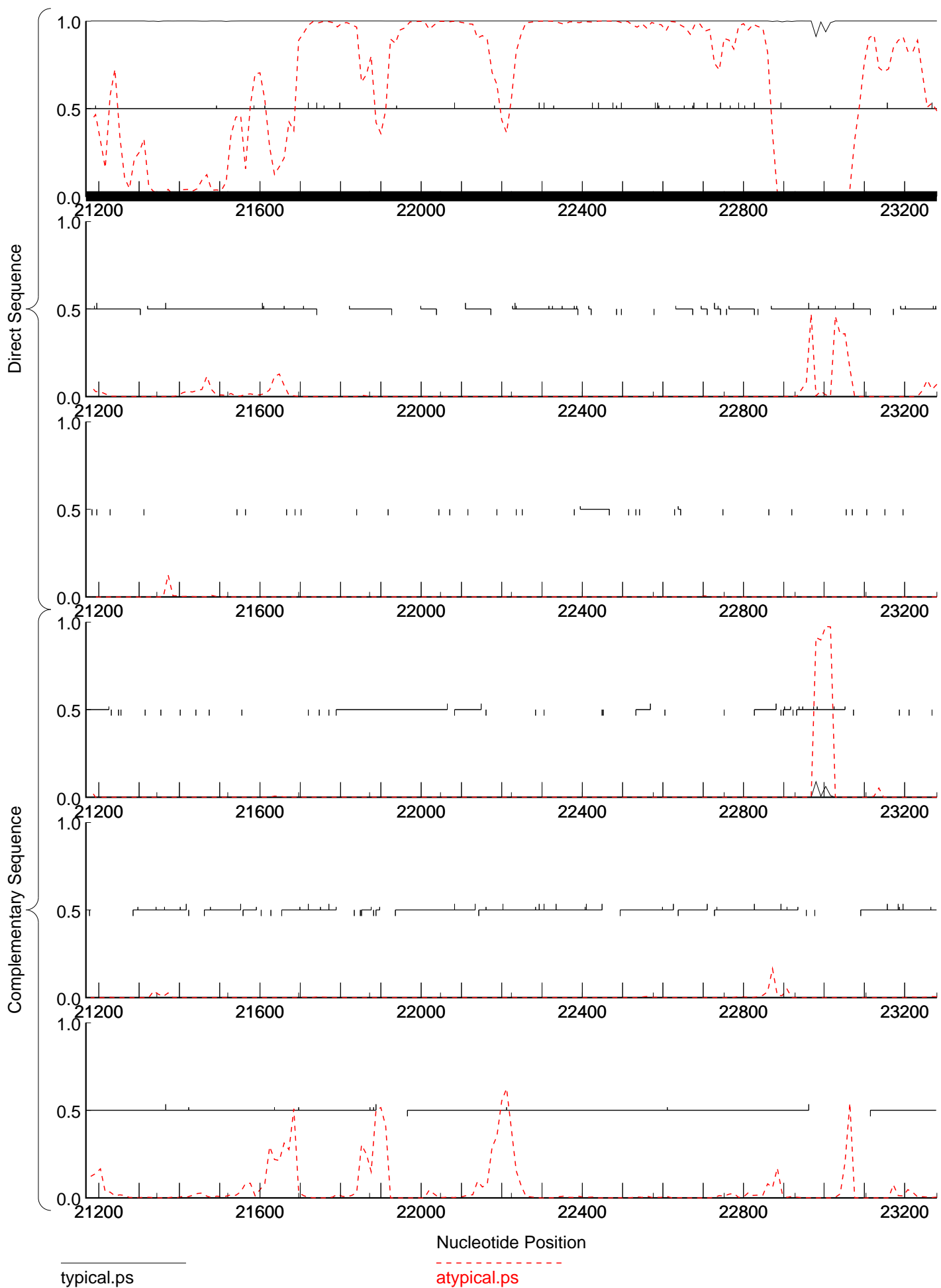
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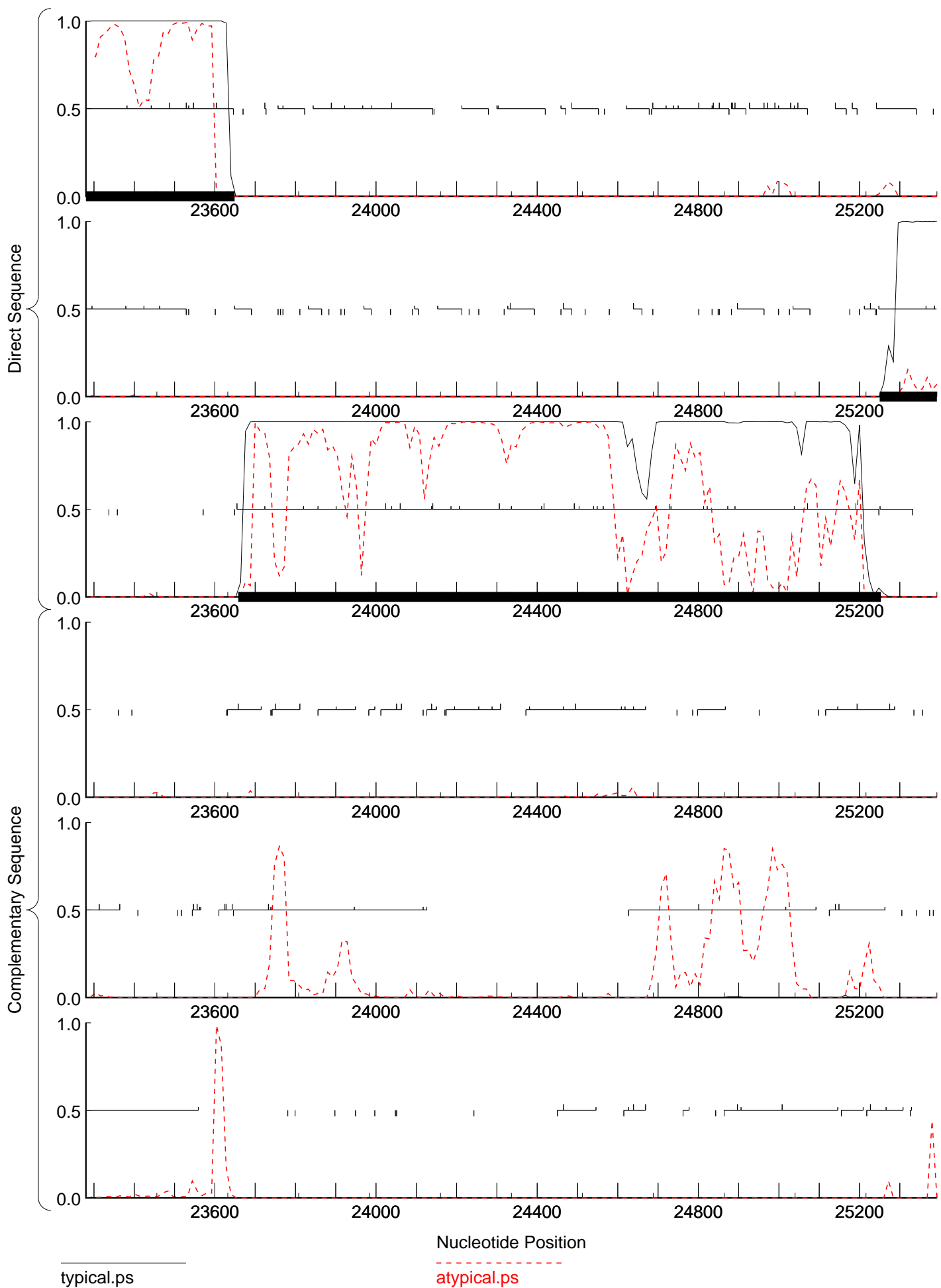
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typical.ps

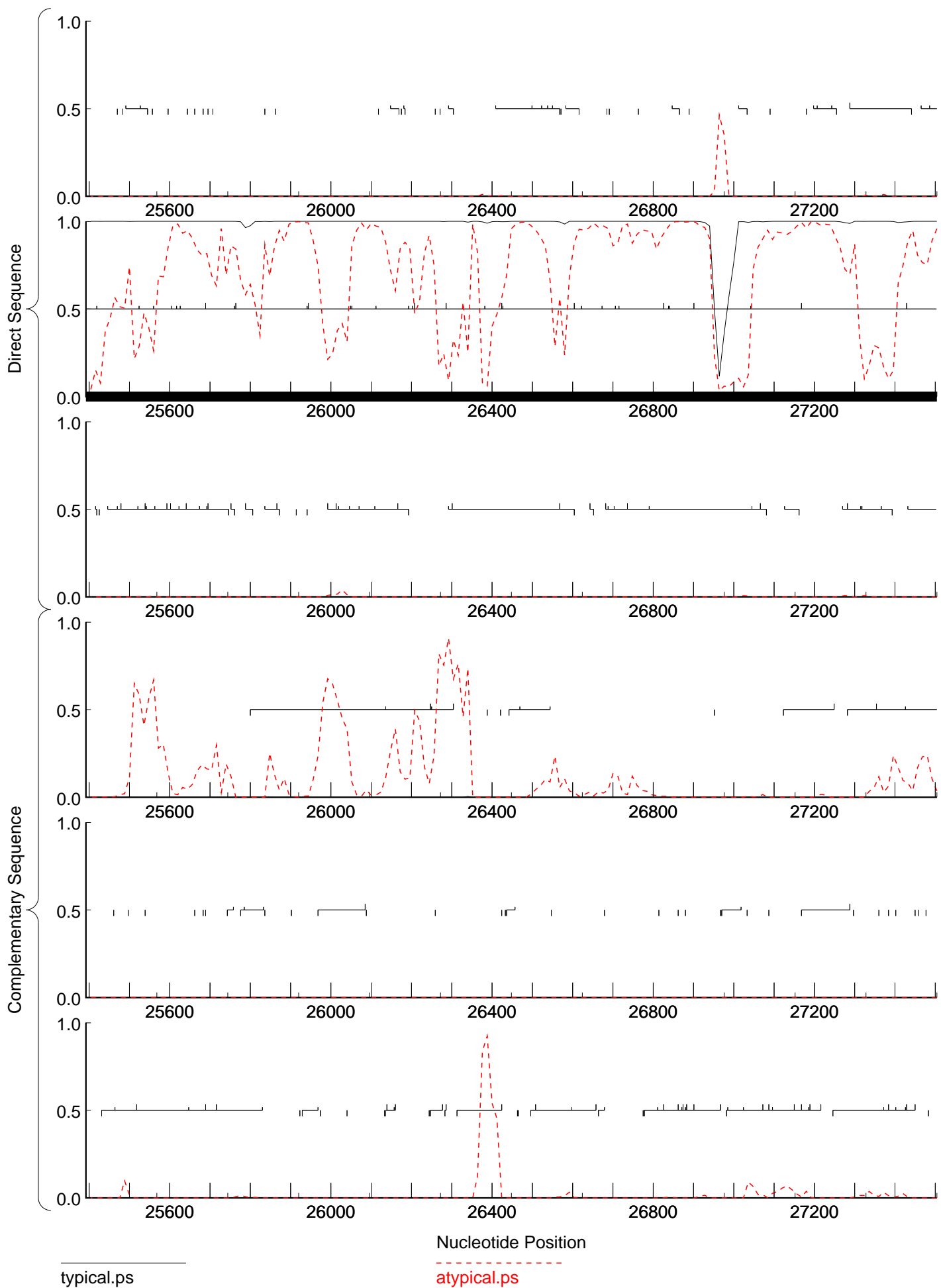
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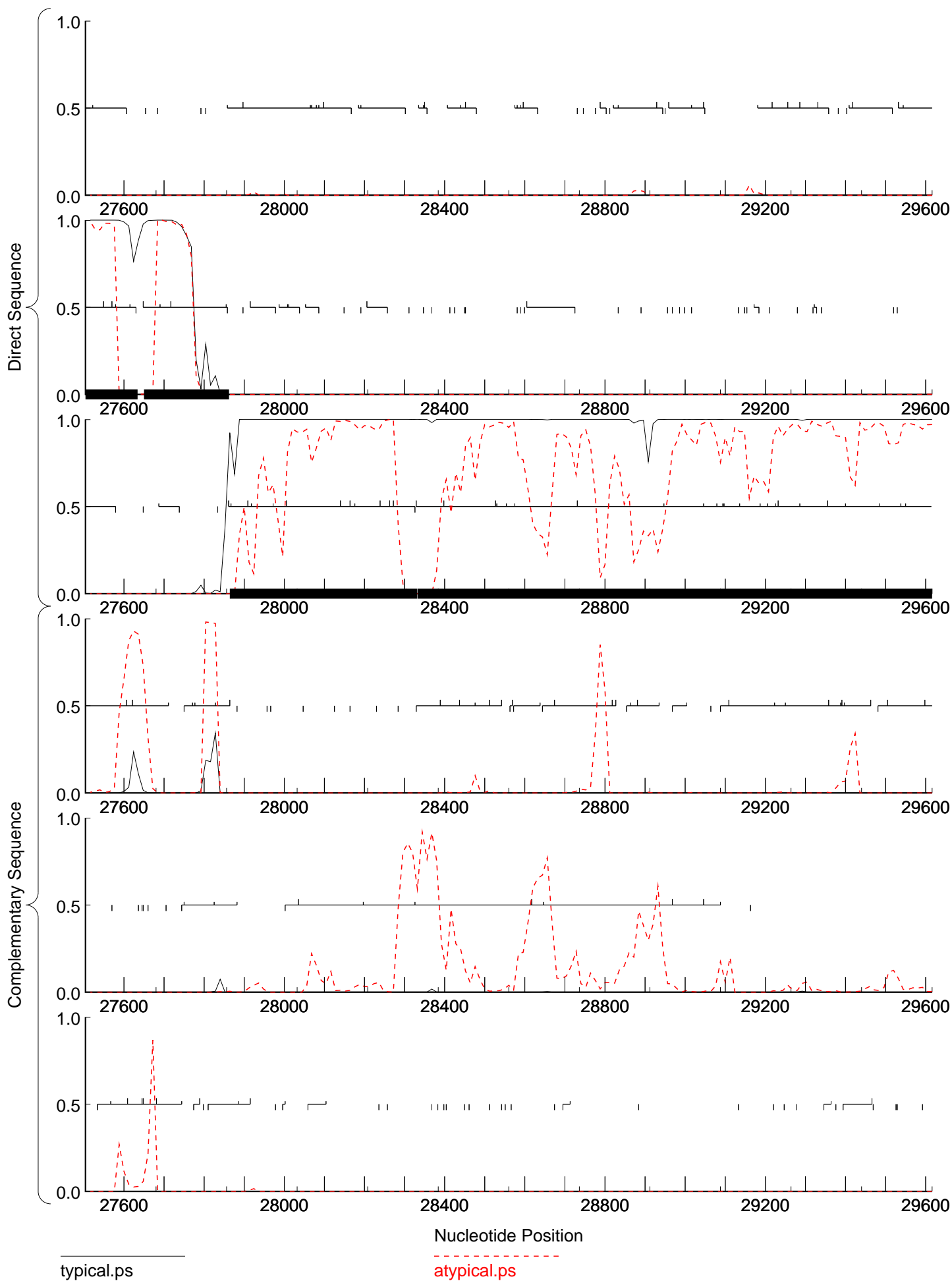
typical.ps

atypical.ps



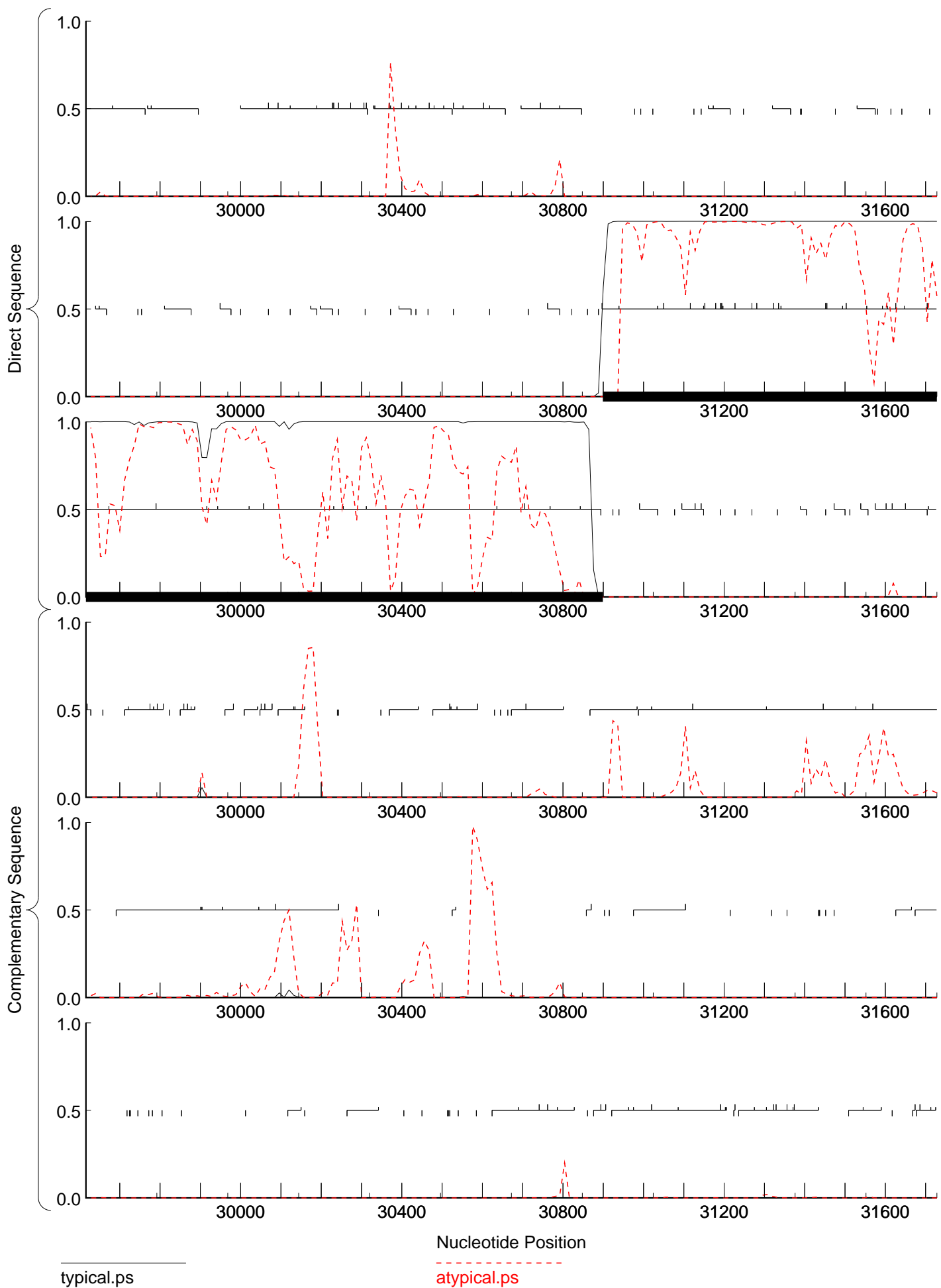
typical.ps

atypical.ps

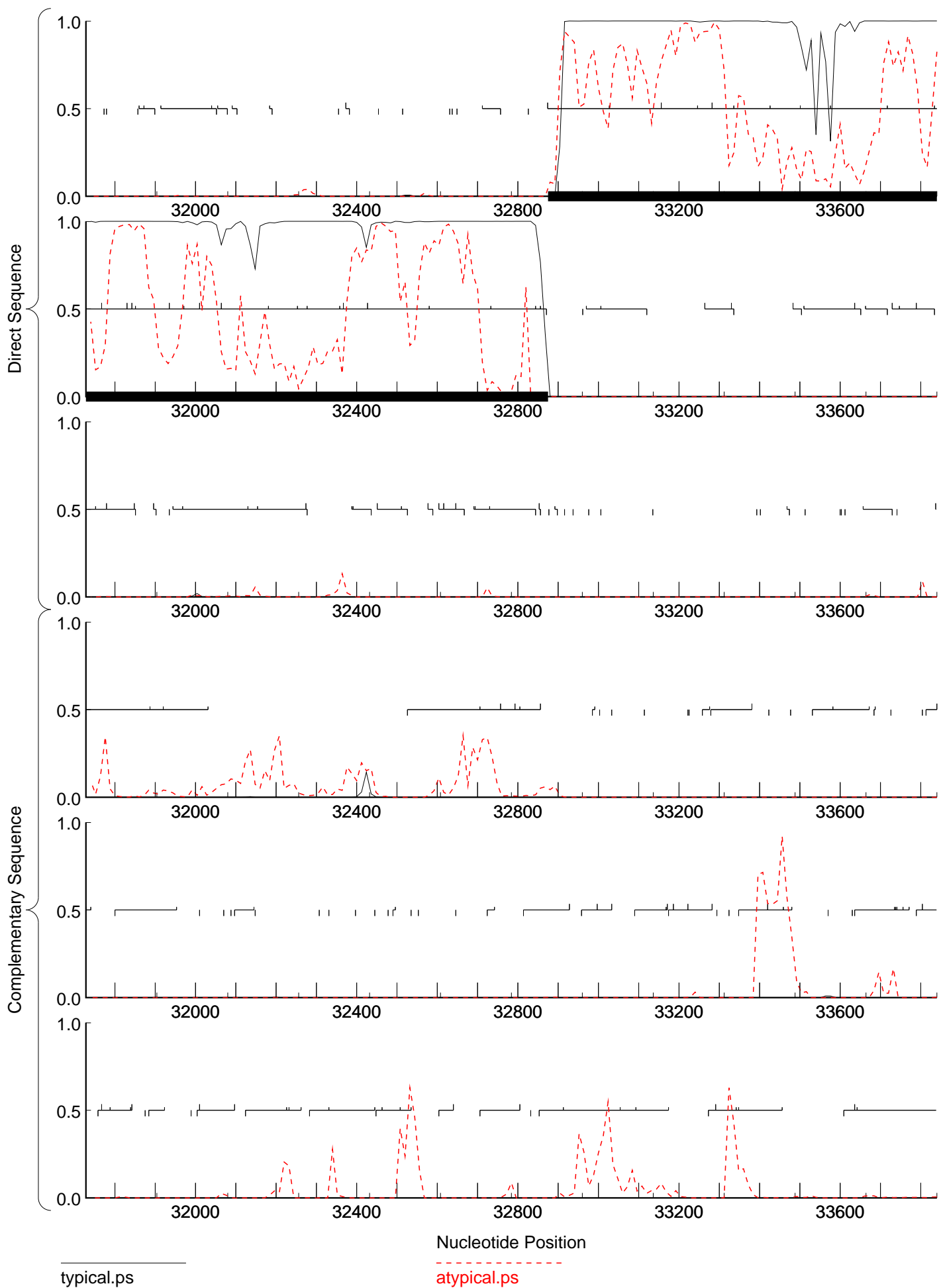


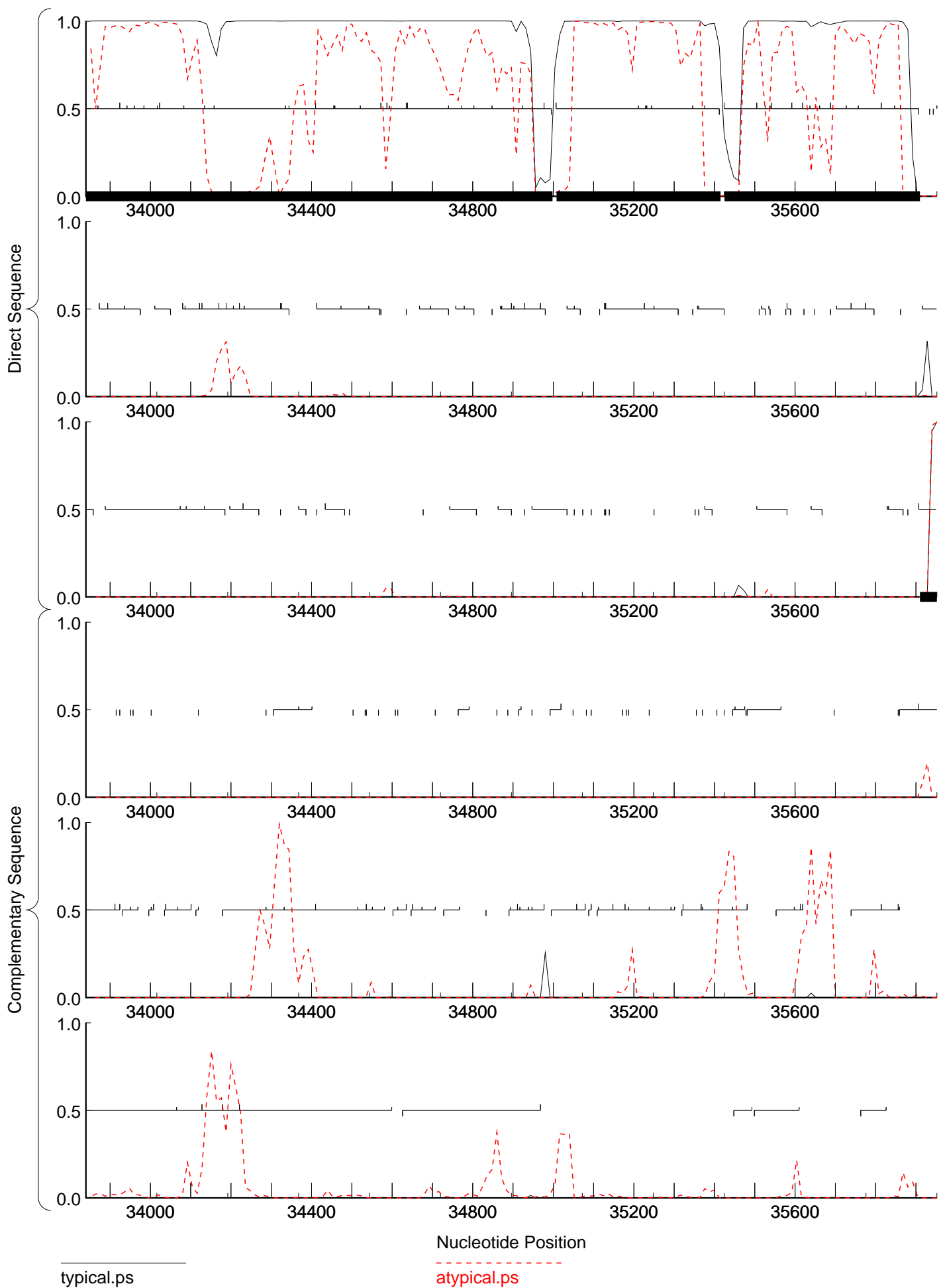
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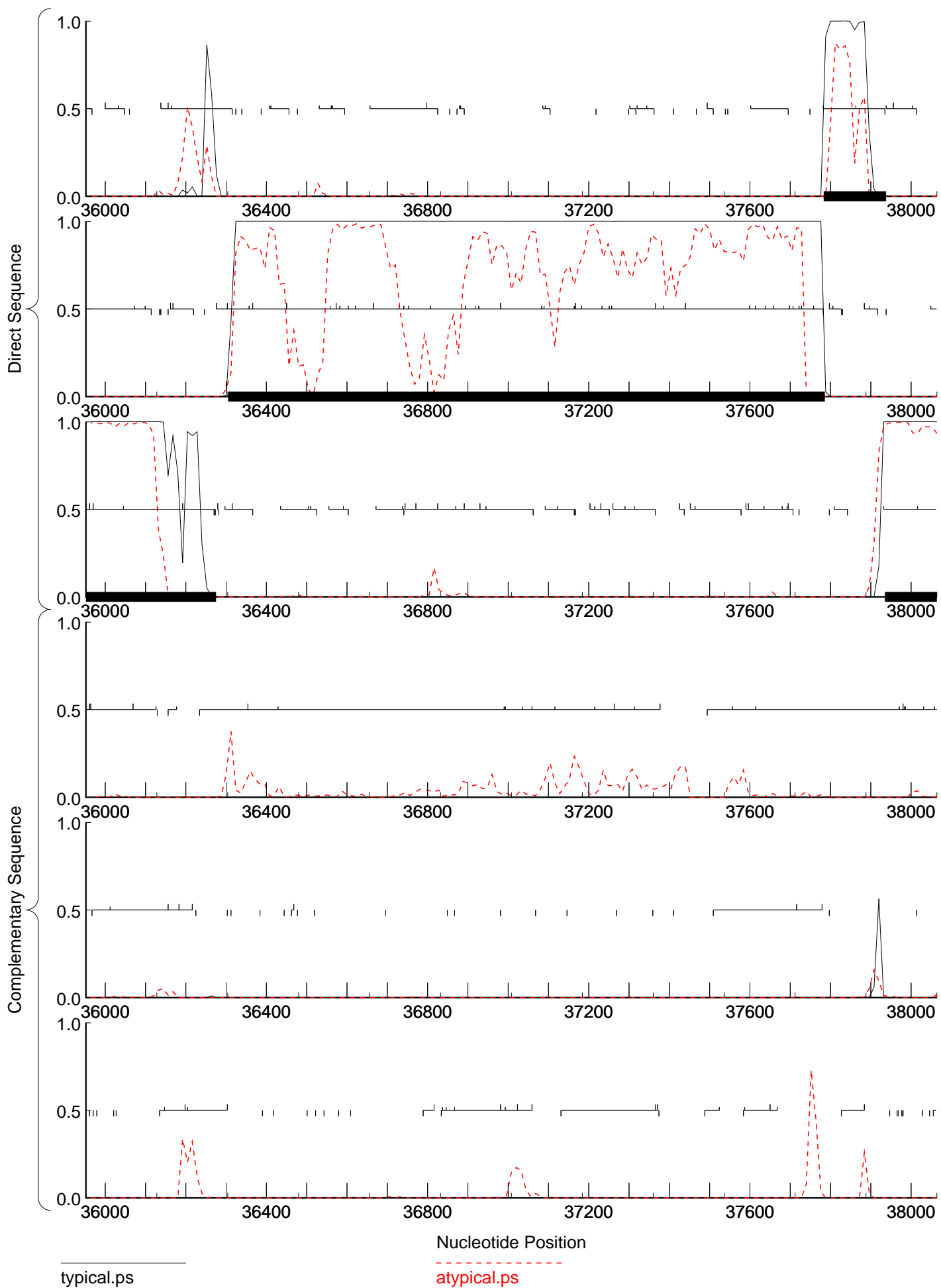
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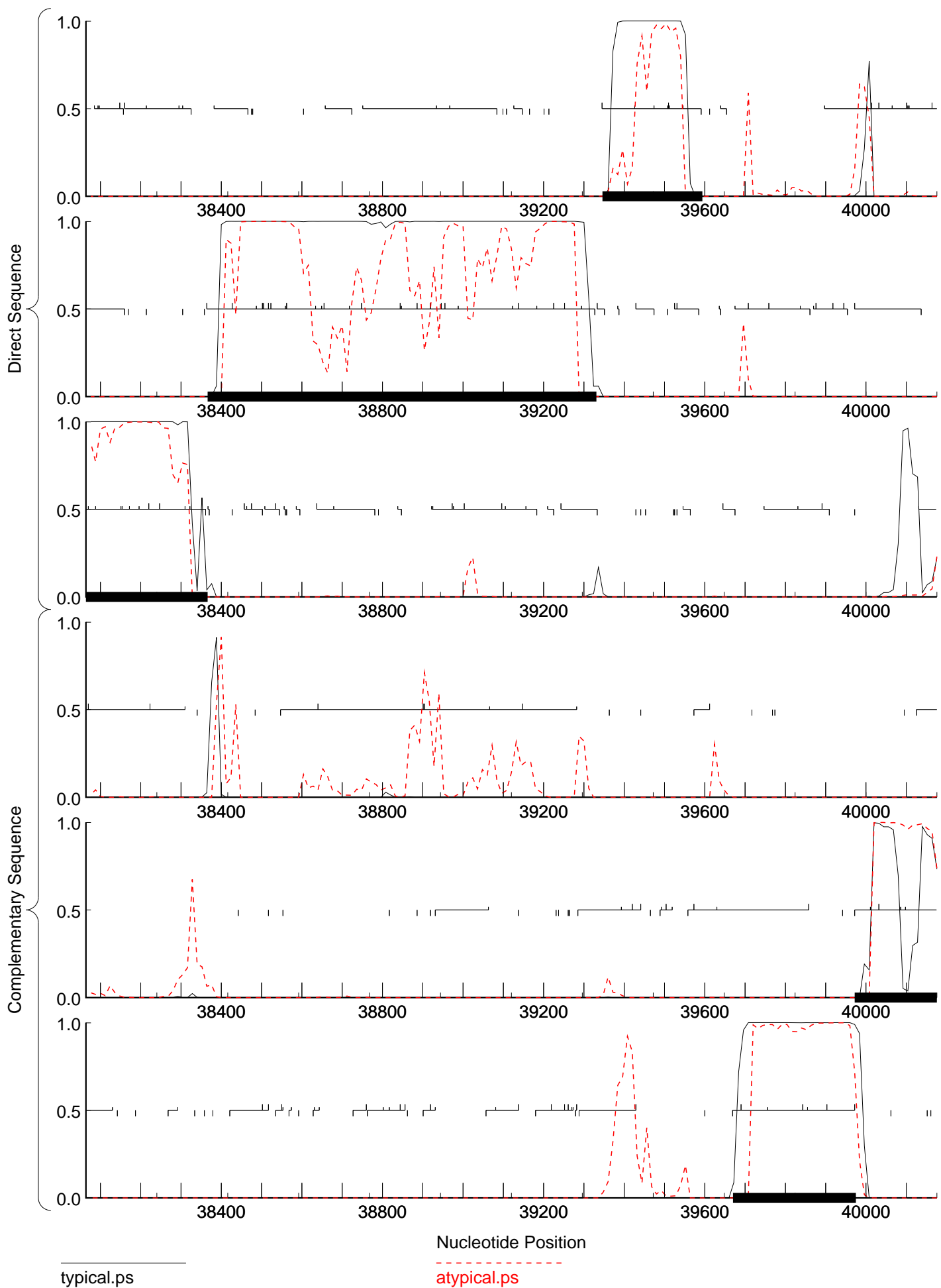


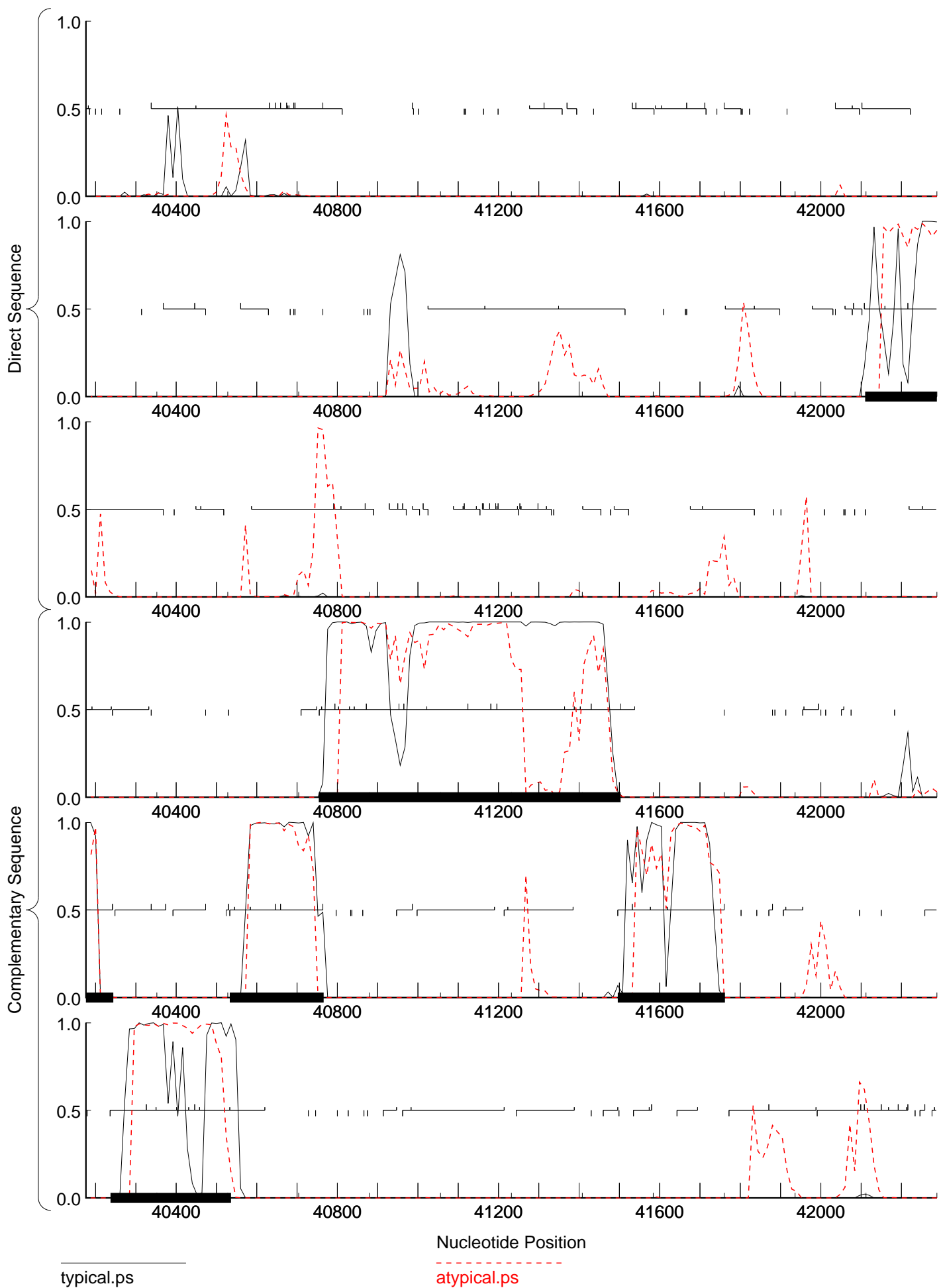




typical.ps

atypical.ps

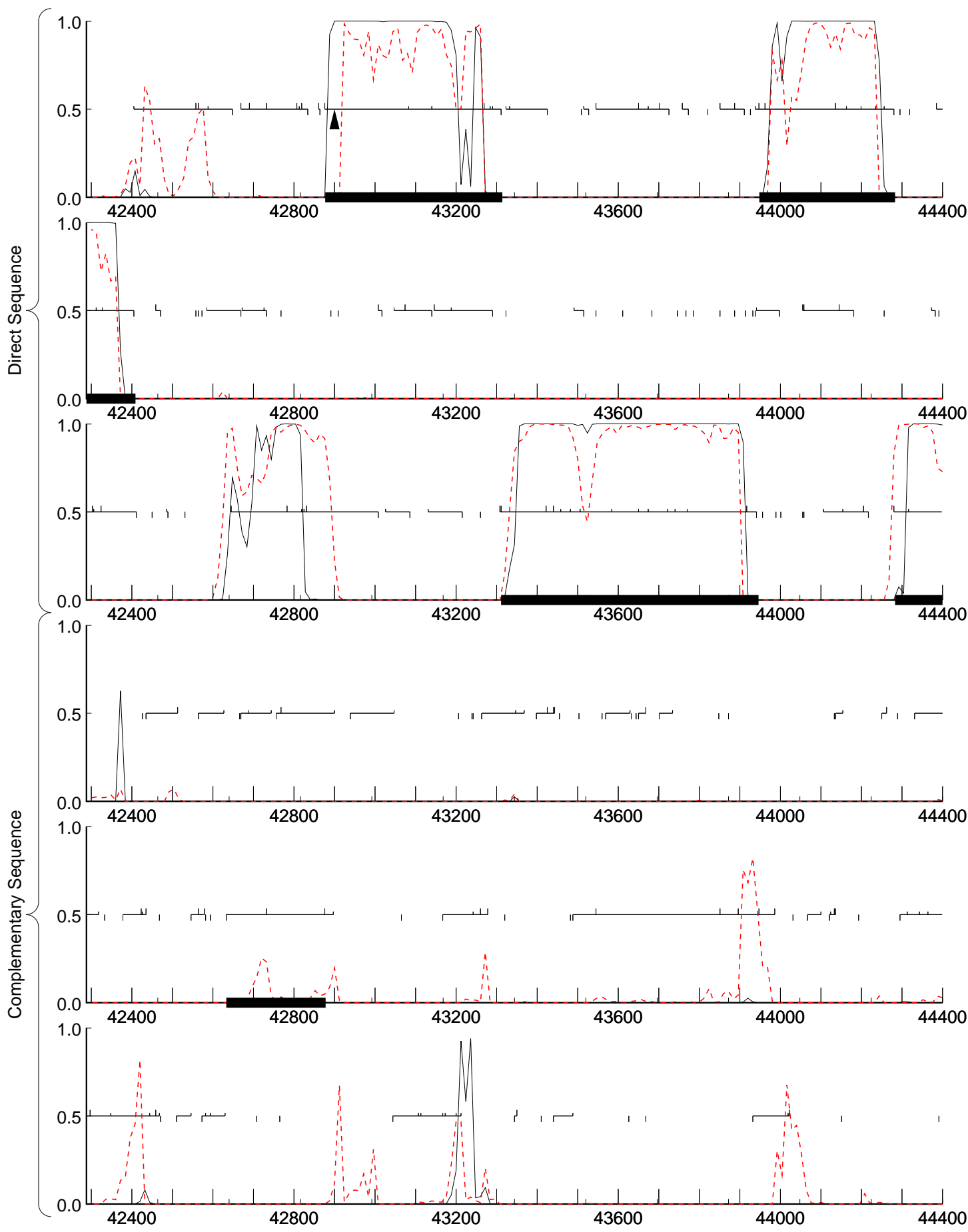




typical.ps

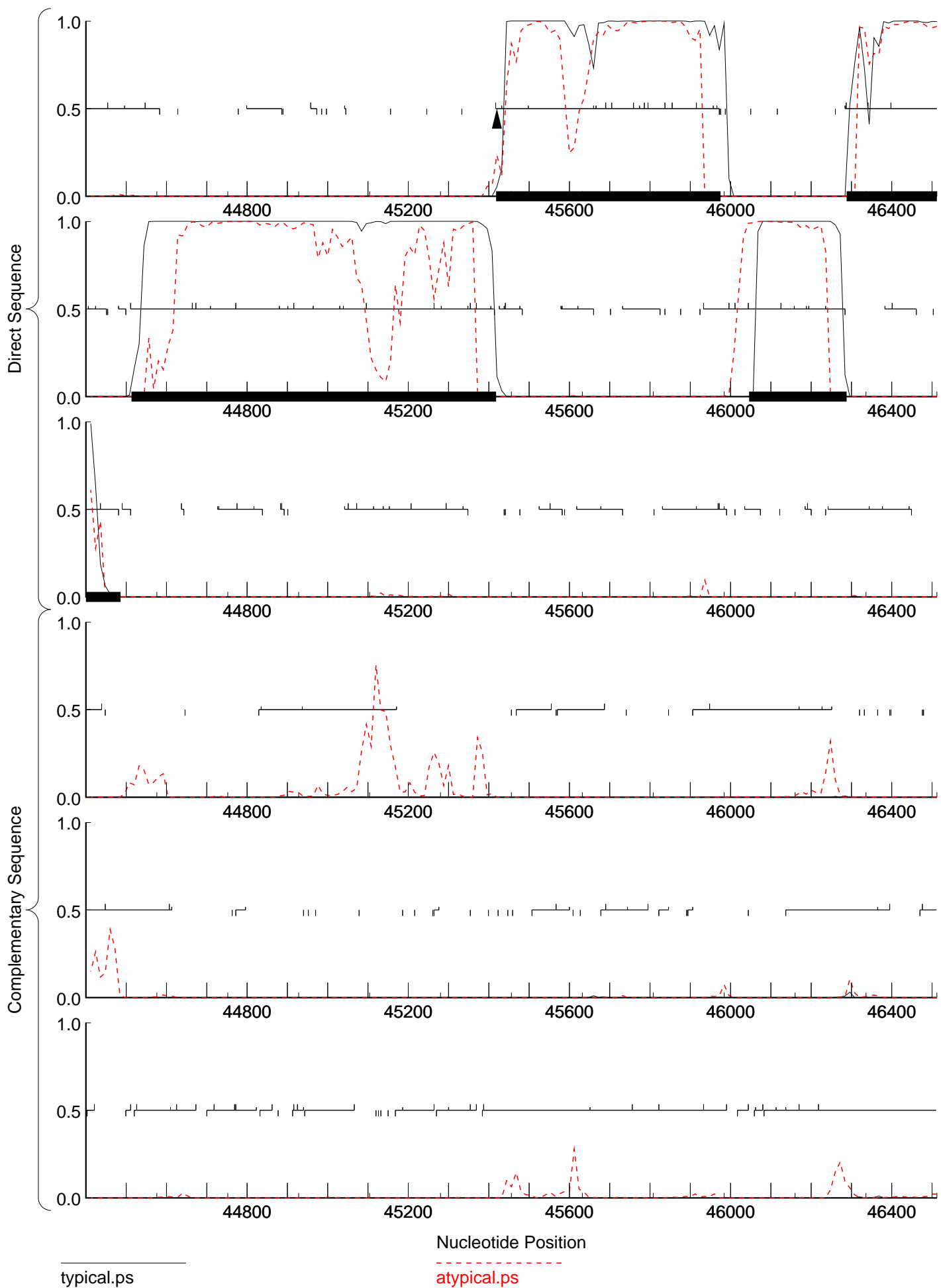
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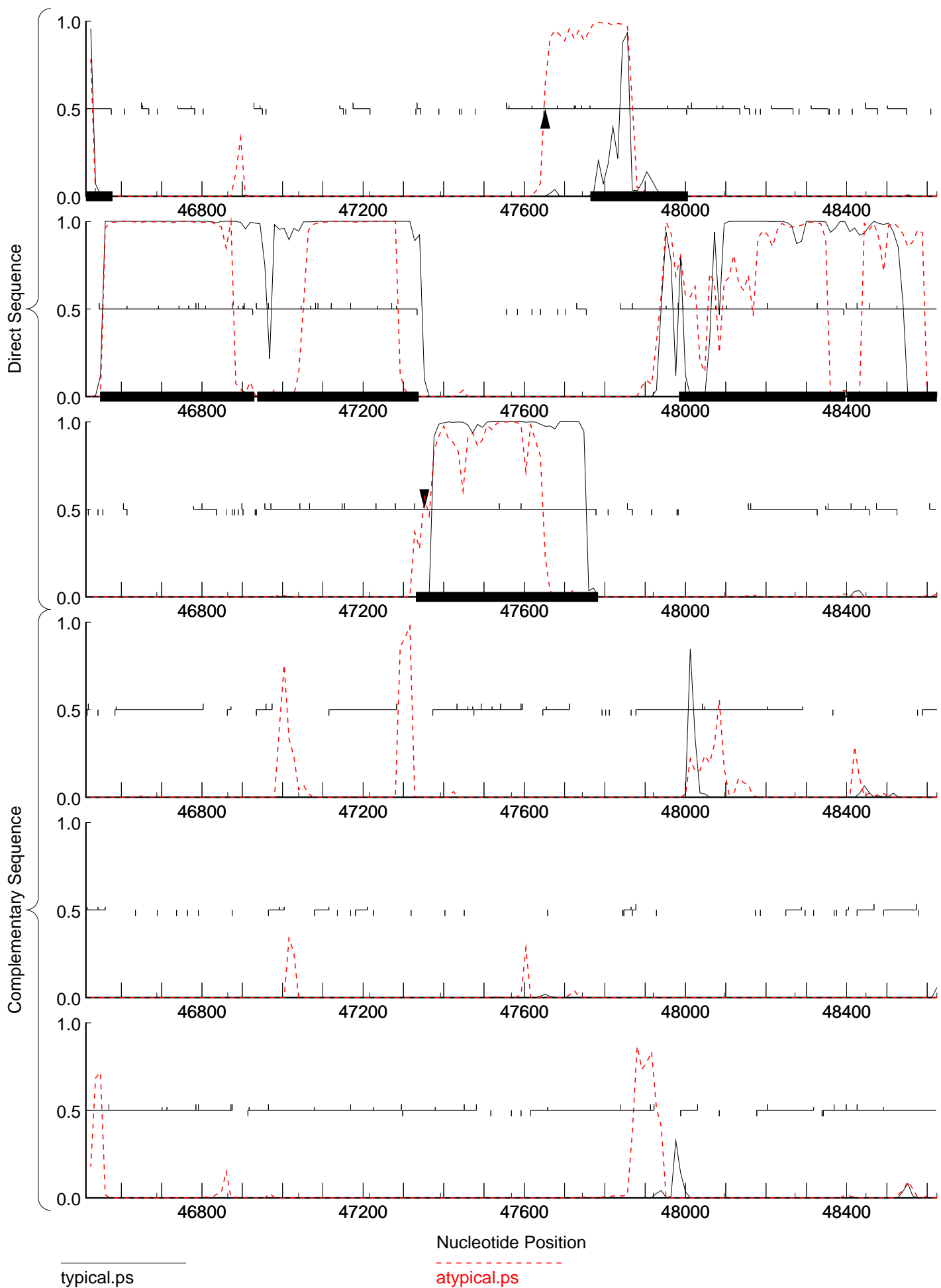
GeneMark.hmm prediction



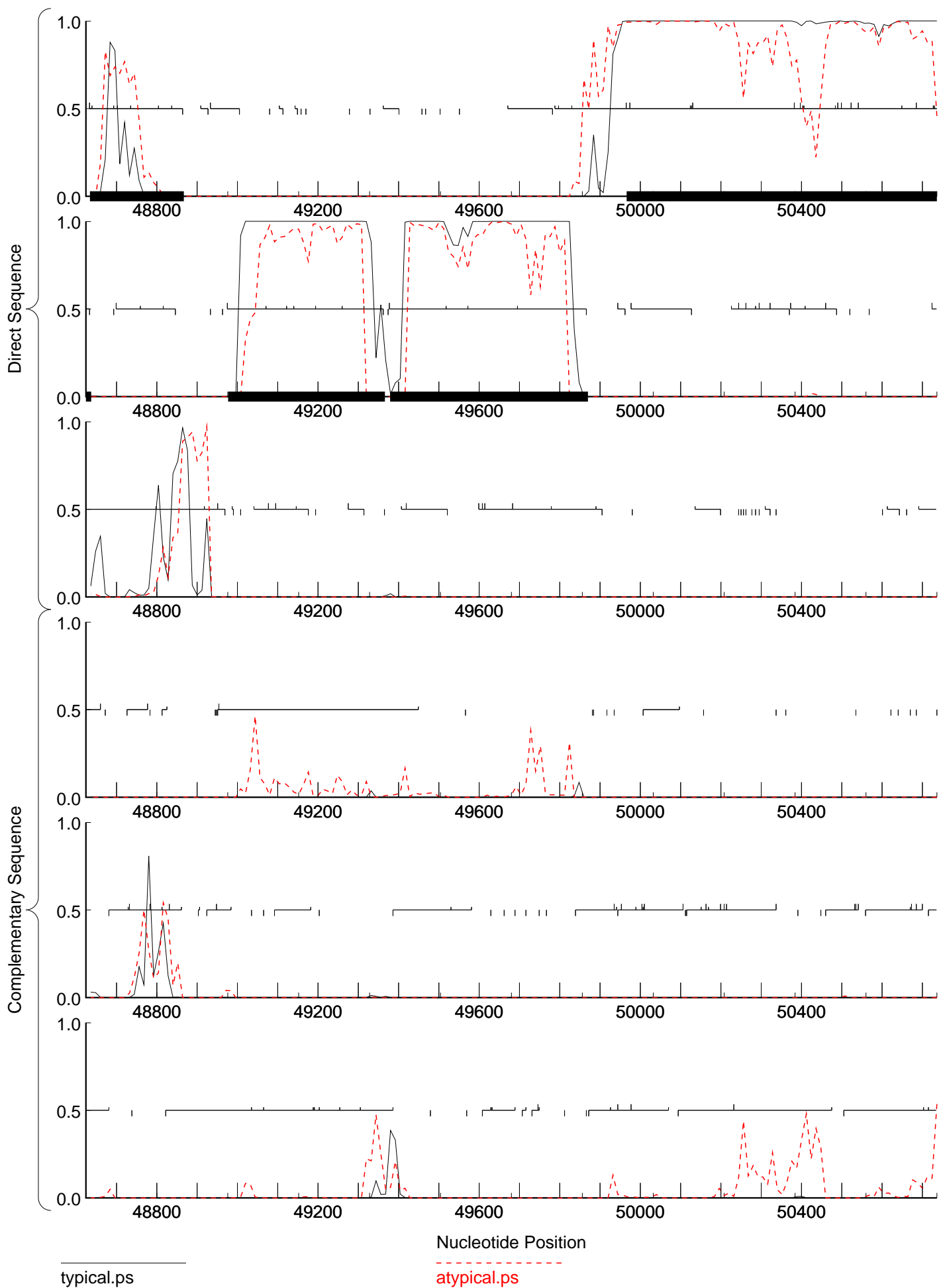
typical.ps

atypical.ps



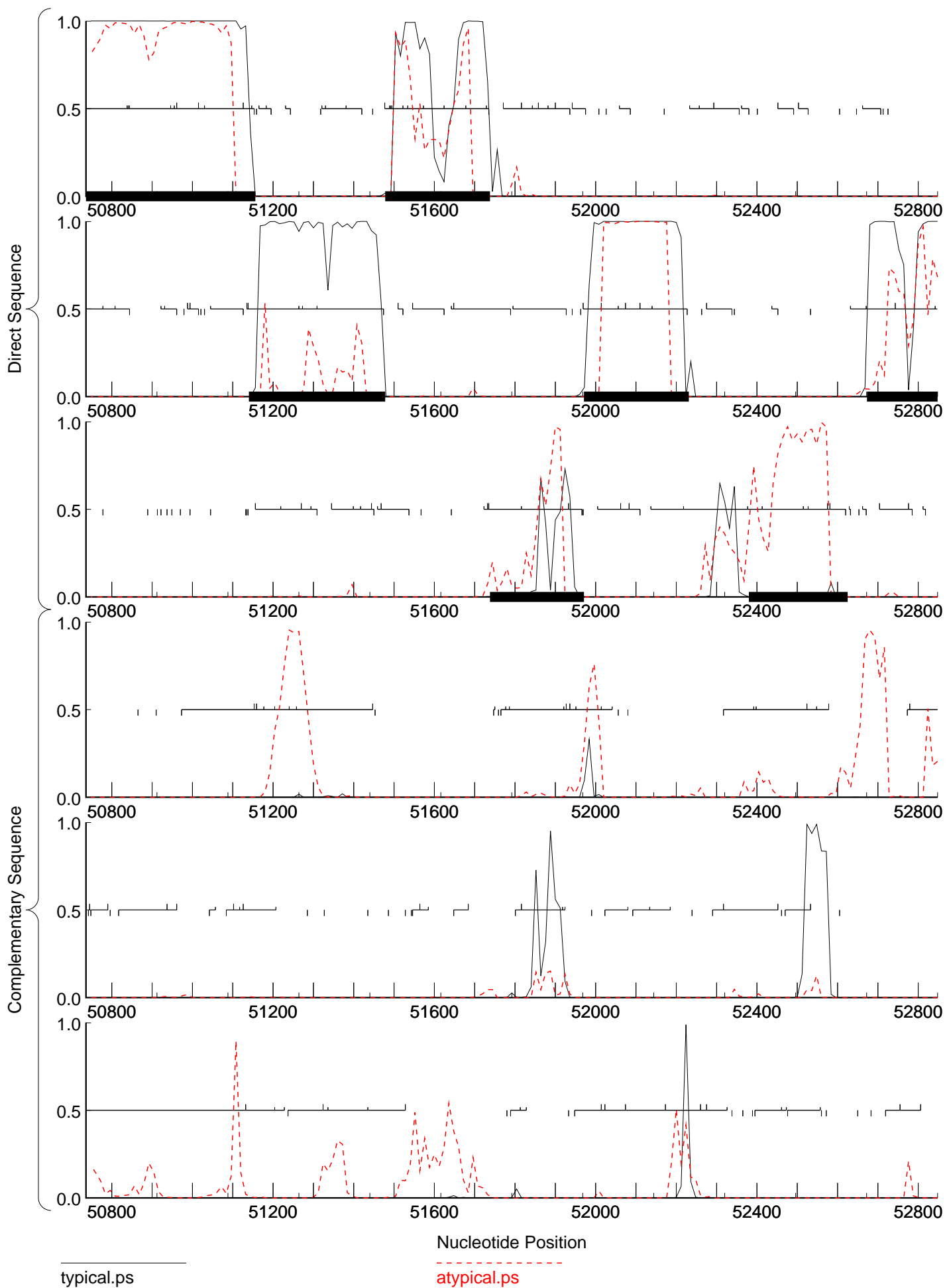




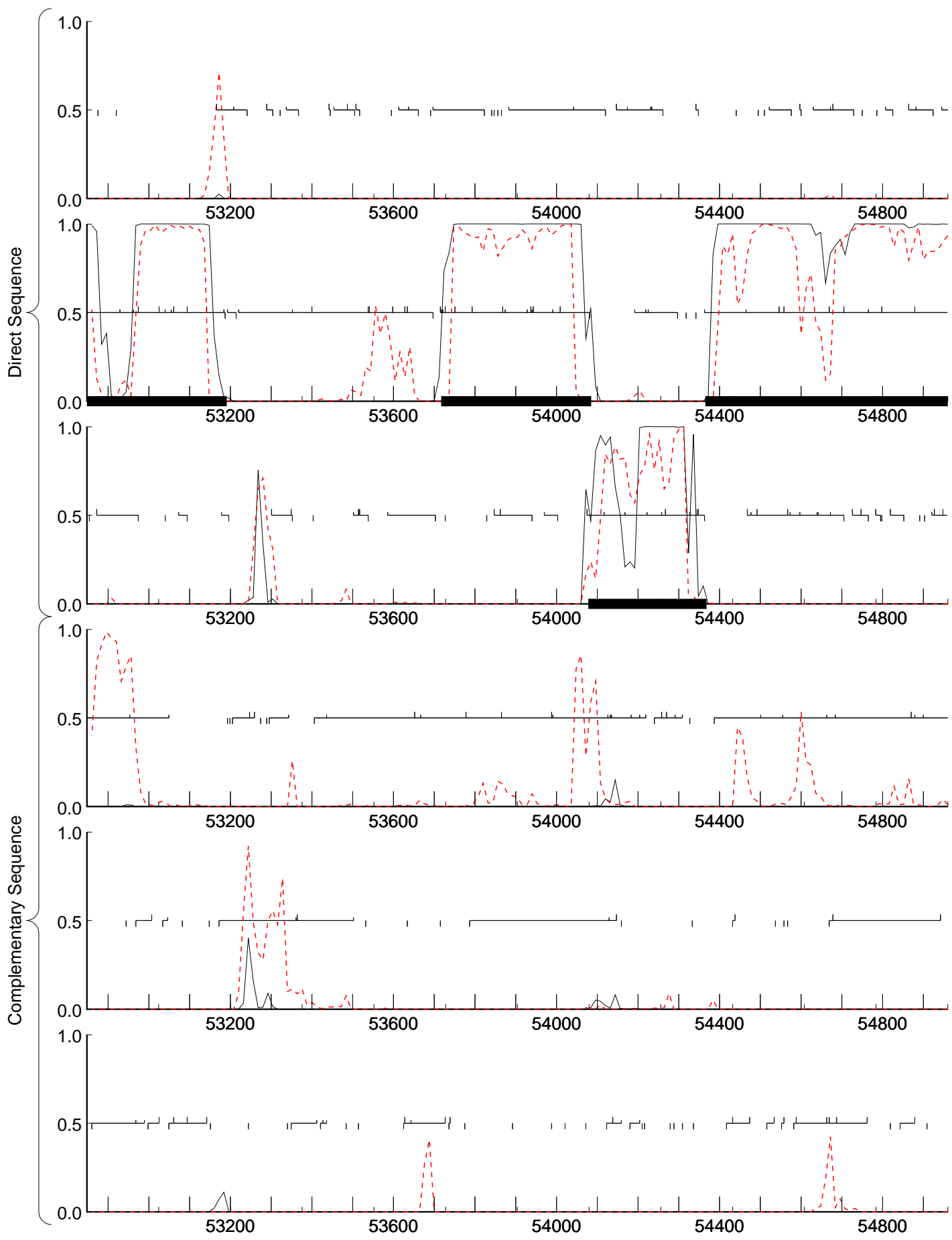


typical.ps

atypical.ps

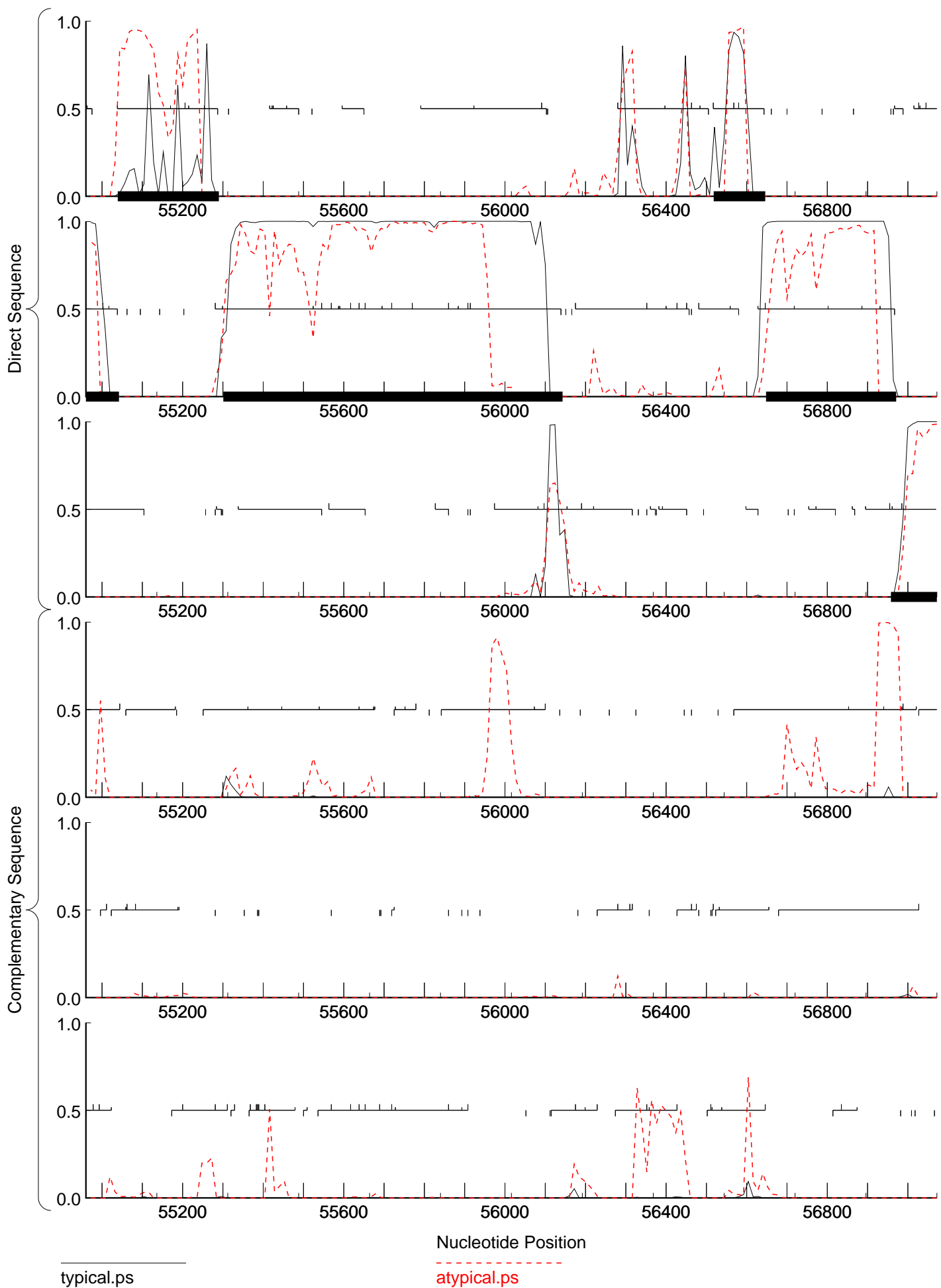


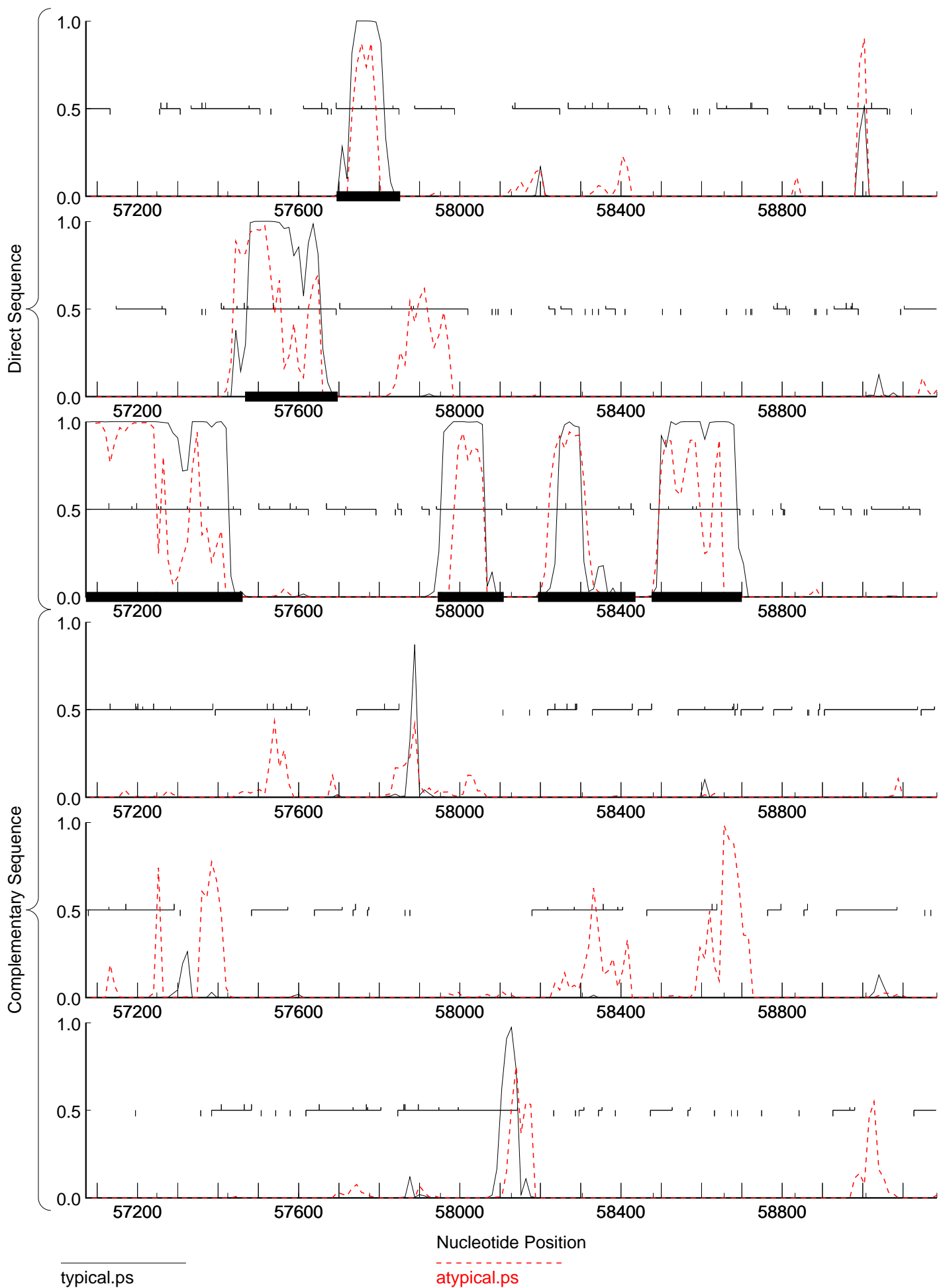
GeneMark.hmm prediction

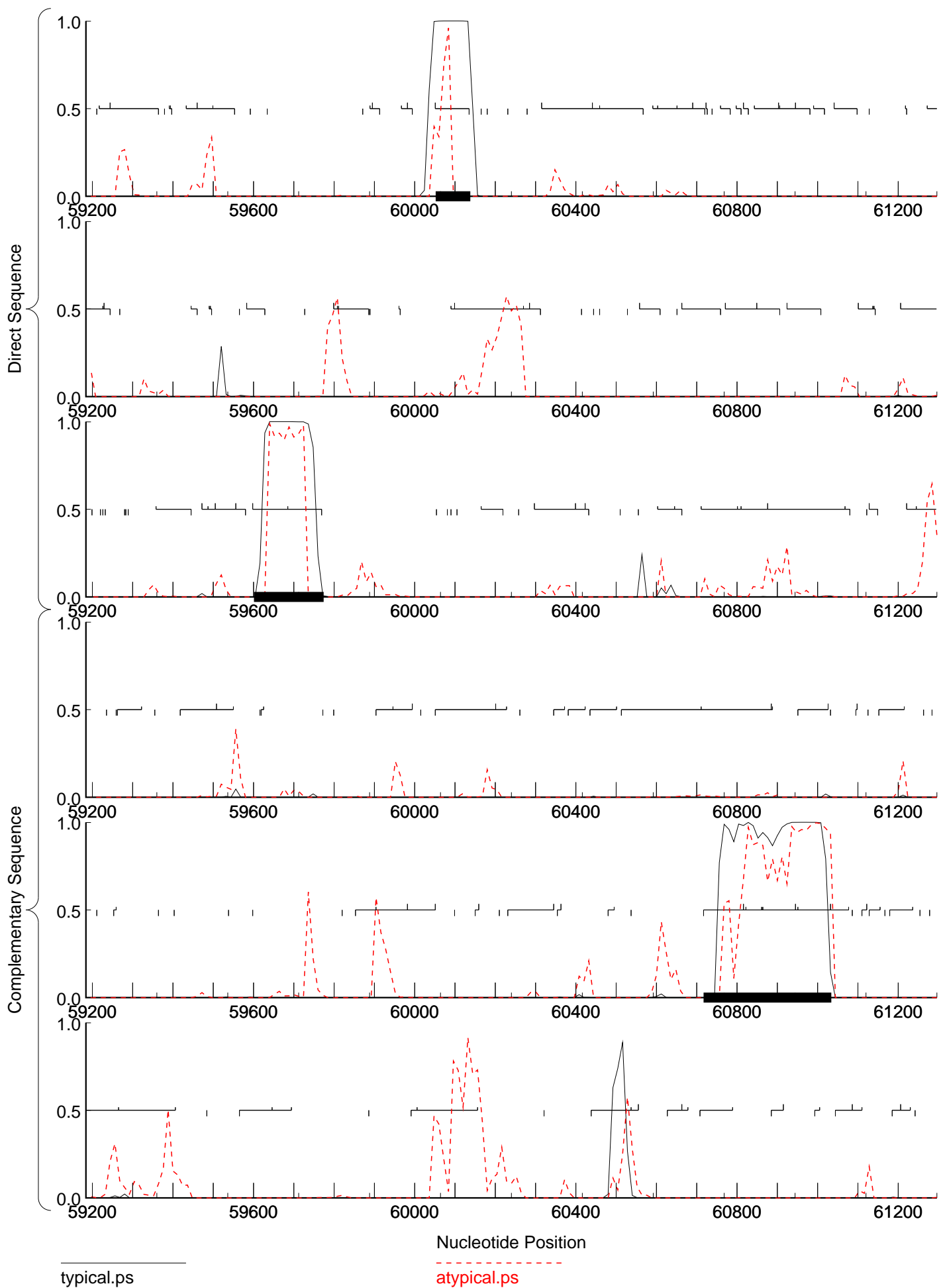


typical.ps

atypical.ps



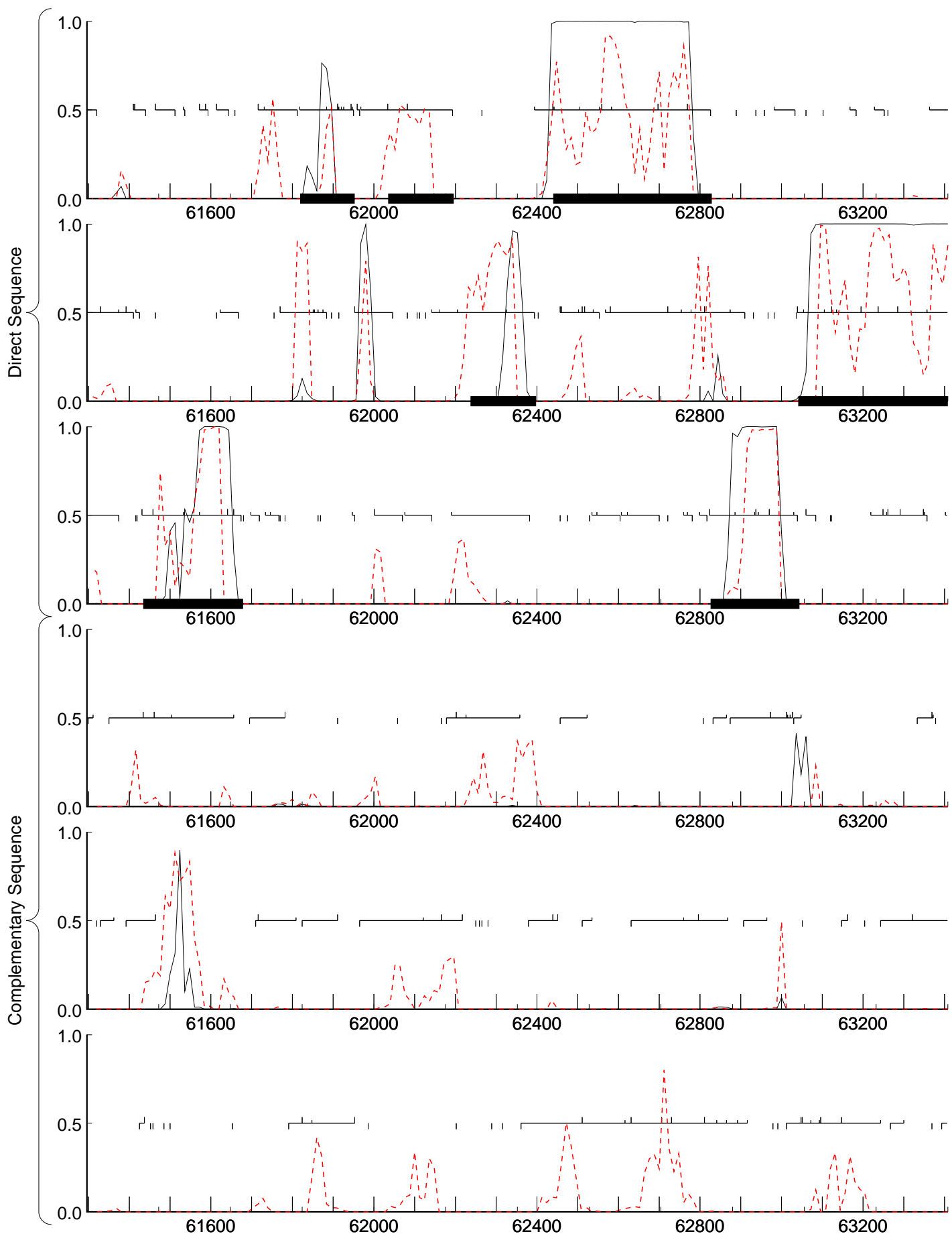




typical.ps

atypical.ps

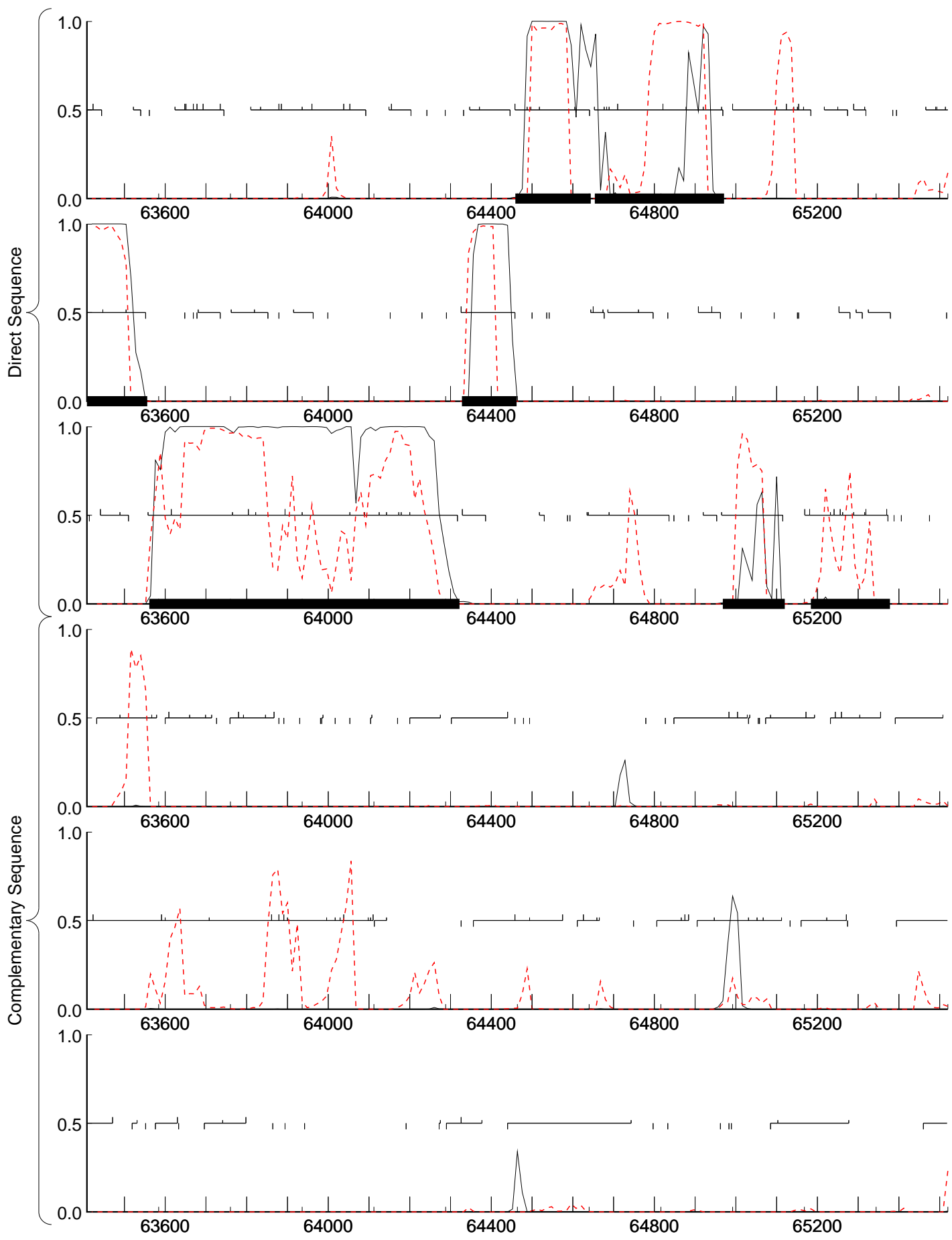
GeneMark.hmm prediction



typical.ps

atypical.ps

GeneMark.hmm prediction

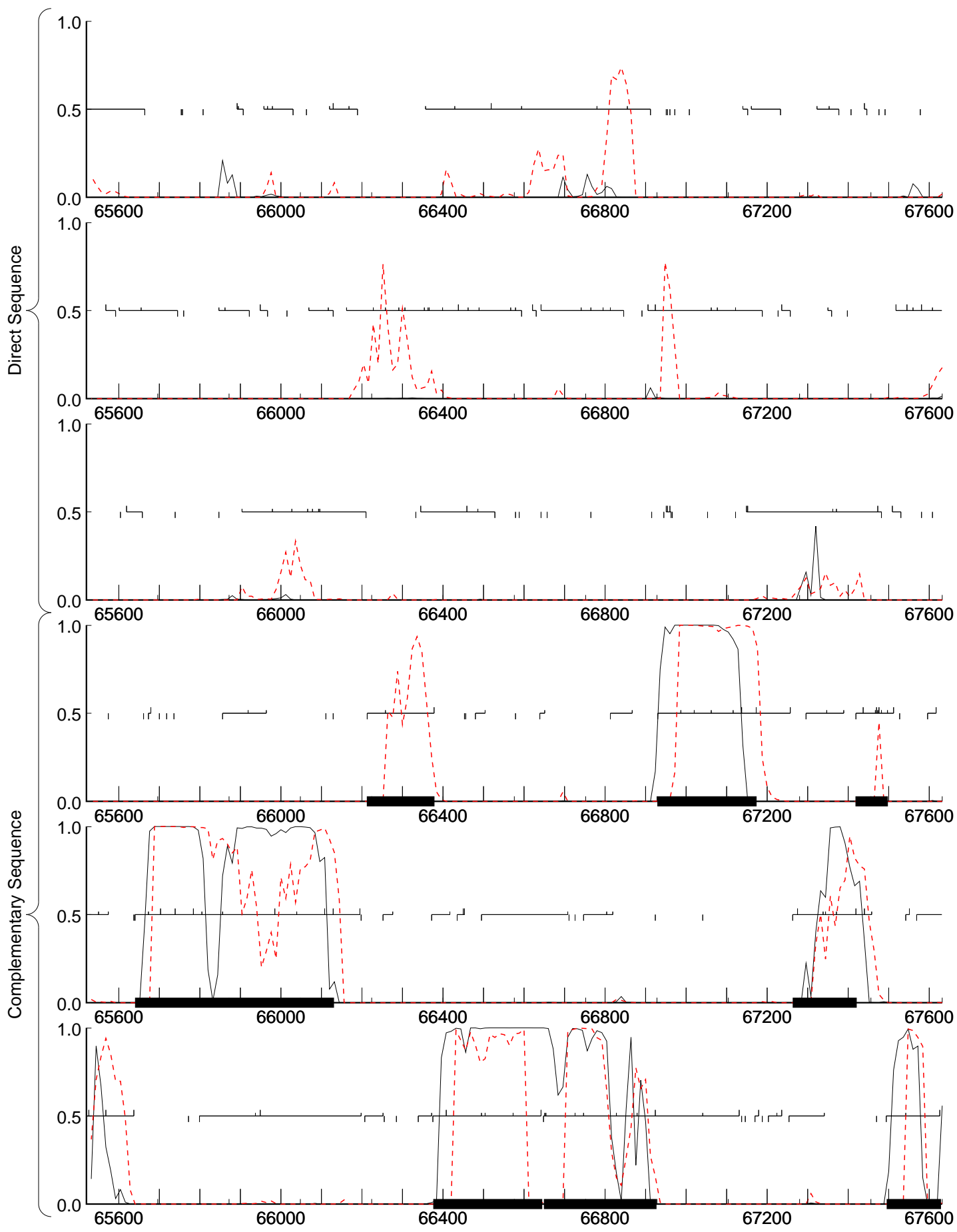


typical.ps

atypical.ps

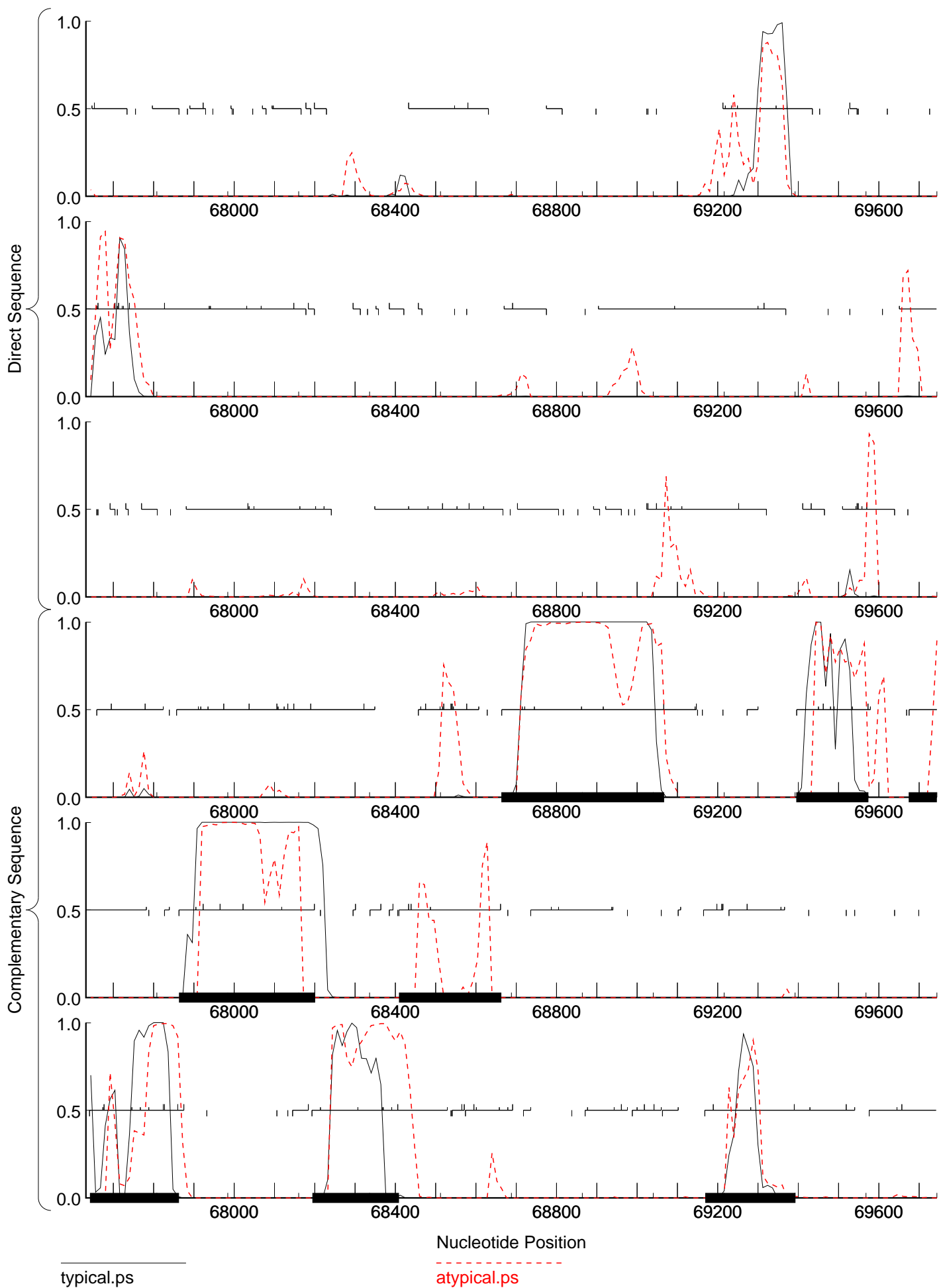


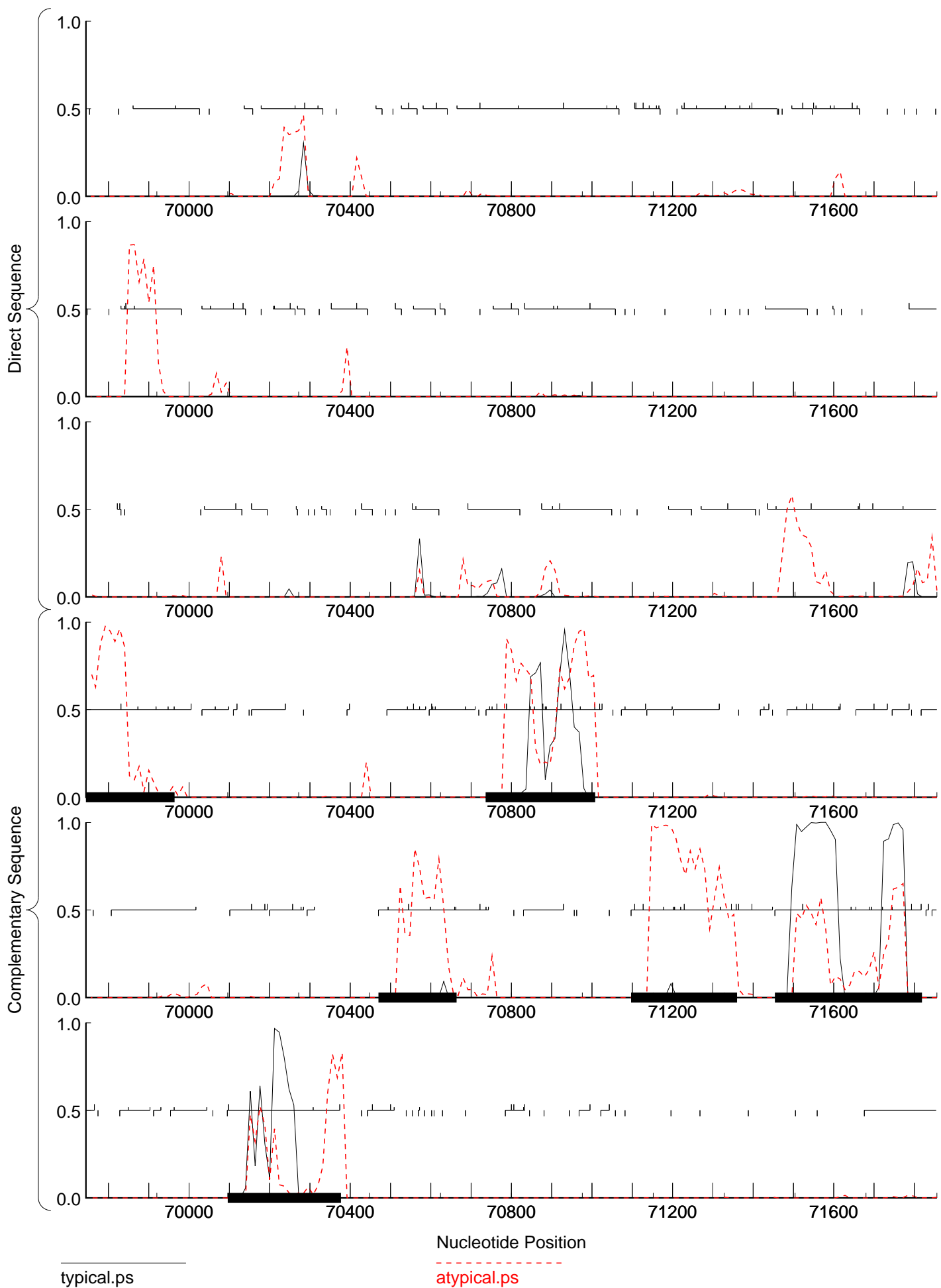
GeneMark.hmm prediction



typical.ps

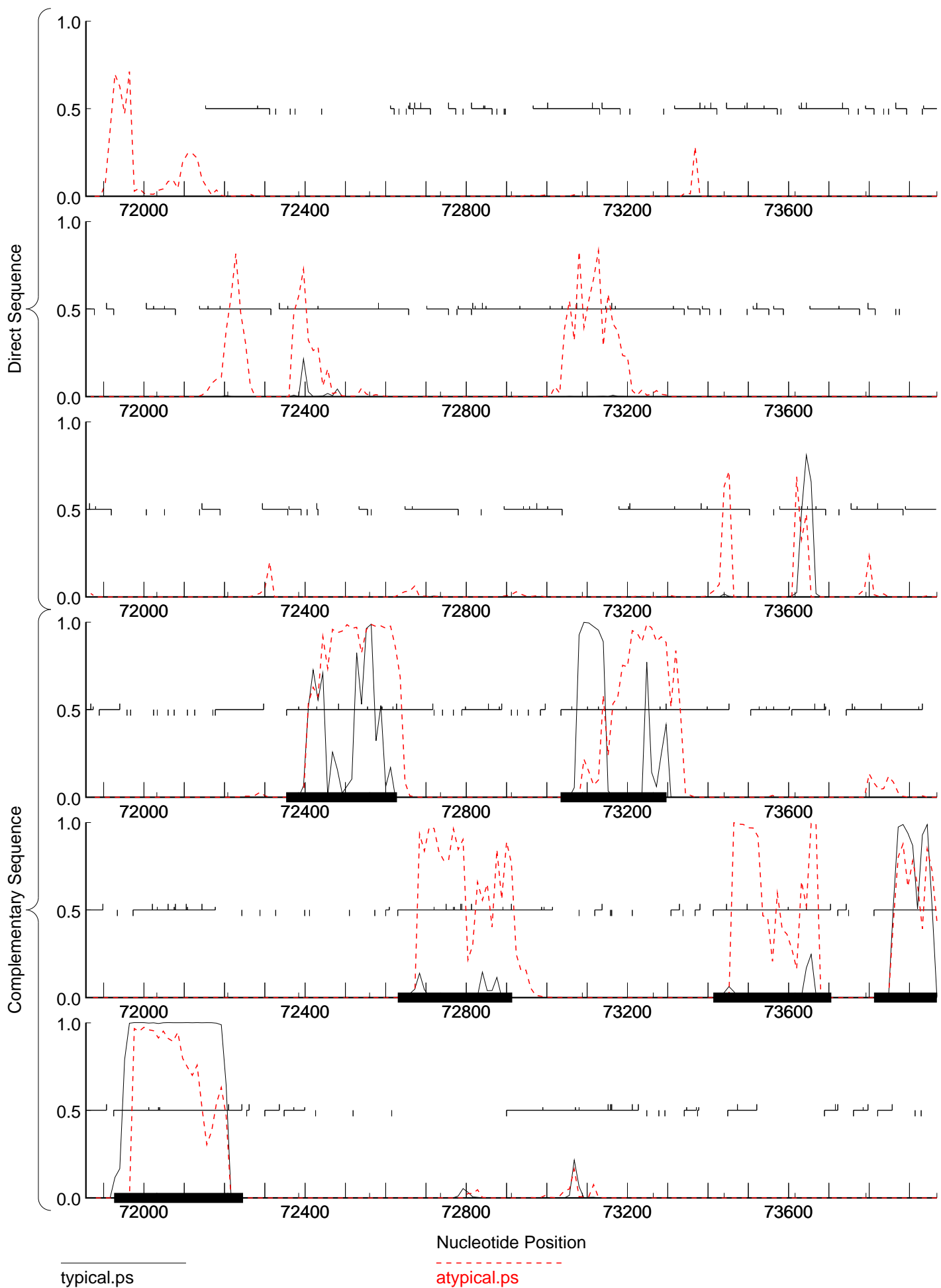
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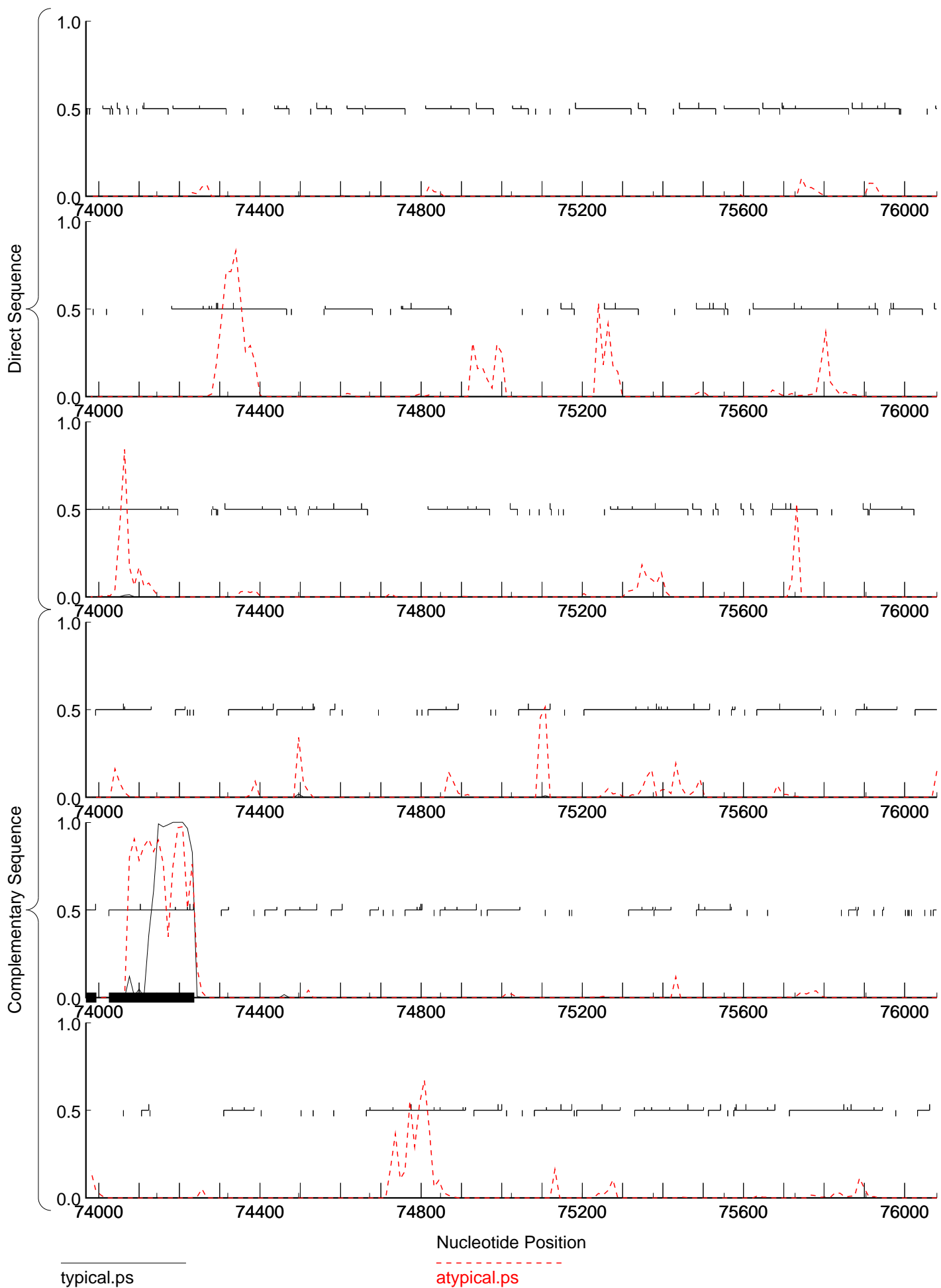




typical.ps

atypical.ps





typical.ps

atypical.ps

