

GeneMark

Version 2.5p (09.08.06)

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PROGRAM INFORMATION

Sequence : Mycobacterium phage Rahel complete sequence, 155955 bp, circularly permuted, Cluster C1
Analysis Date : 6/21/18 at 7:56:14
Pages : 75
Sequence Length : 155955 bp
GC Content : 64.70%

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,

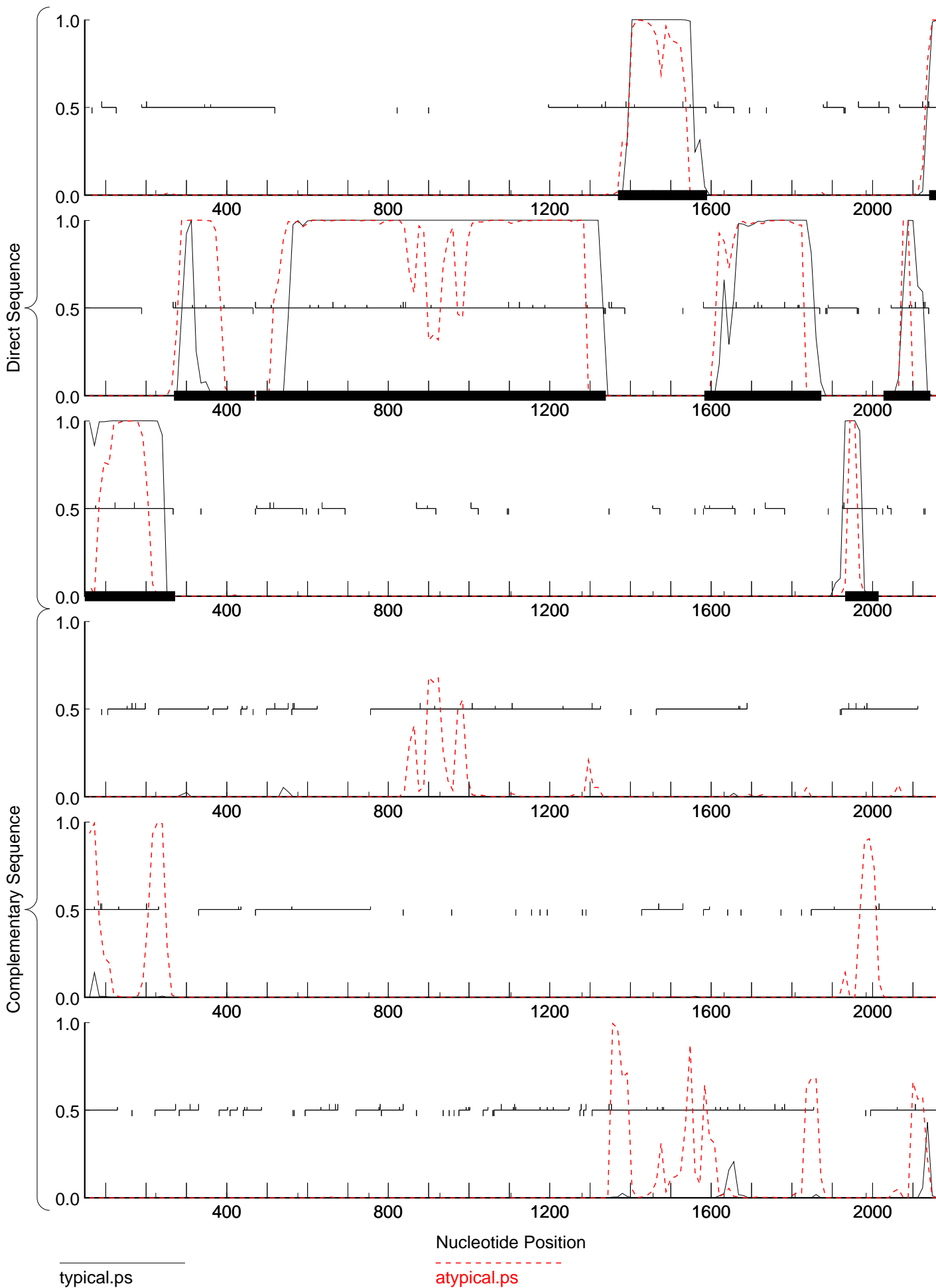
Matrix notes & comments

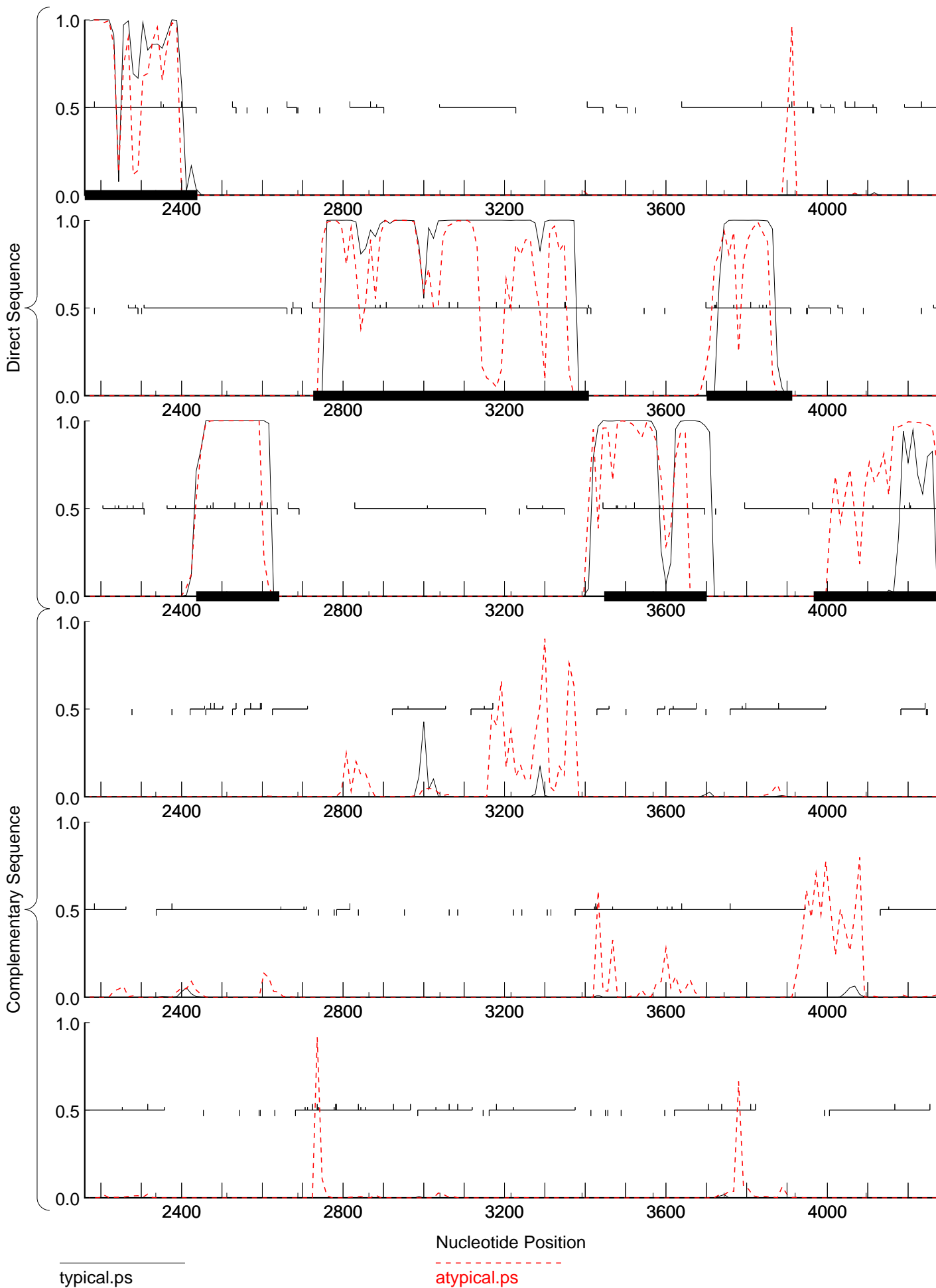
Training set derived by GeneMarkS, 4.30 October 2014
Thu Jun 21 07:56:14 2018

MATRIX INFORMATION

Matrix : -
Author : -
Order : 4

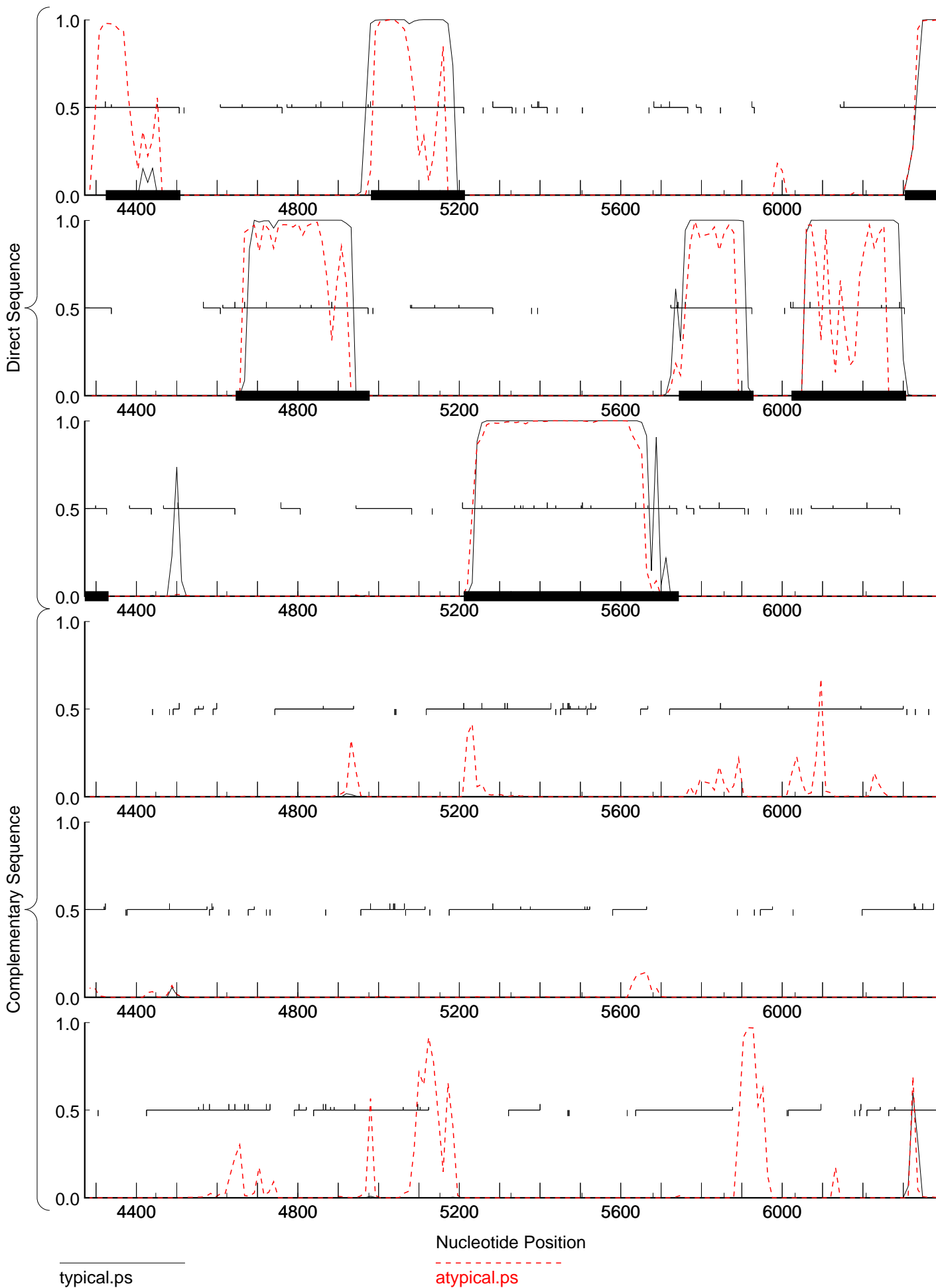
Send questions / comments to:
Dr. M. Borodovsky
Georgia Institute of Technology
School of Biology
Atlanta, GA 30332-0230

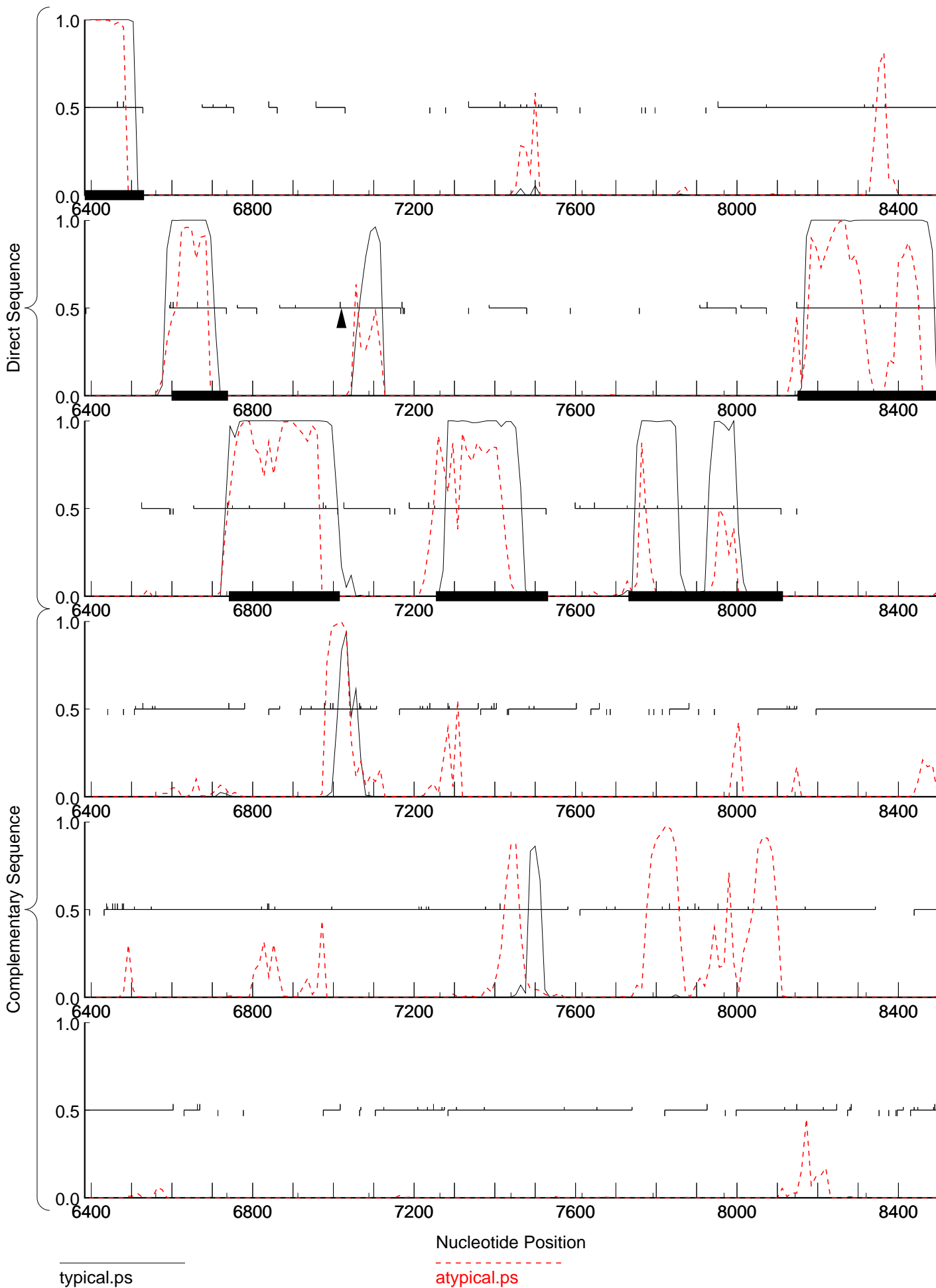




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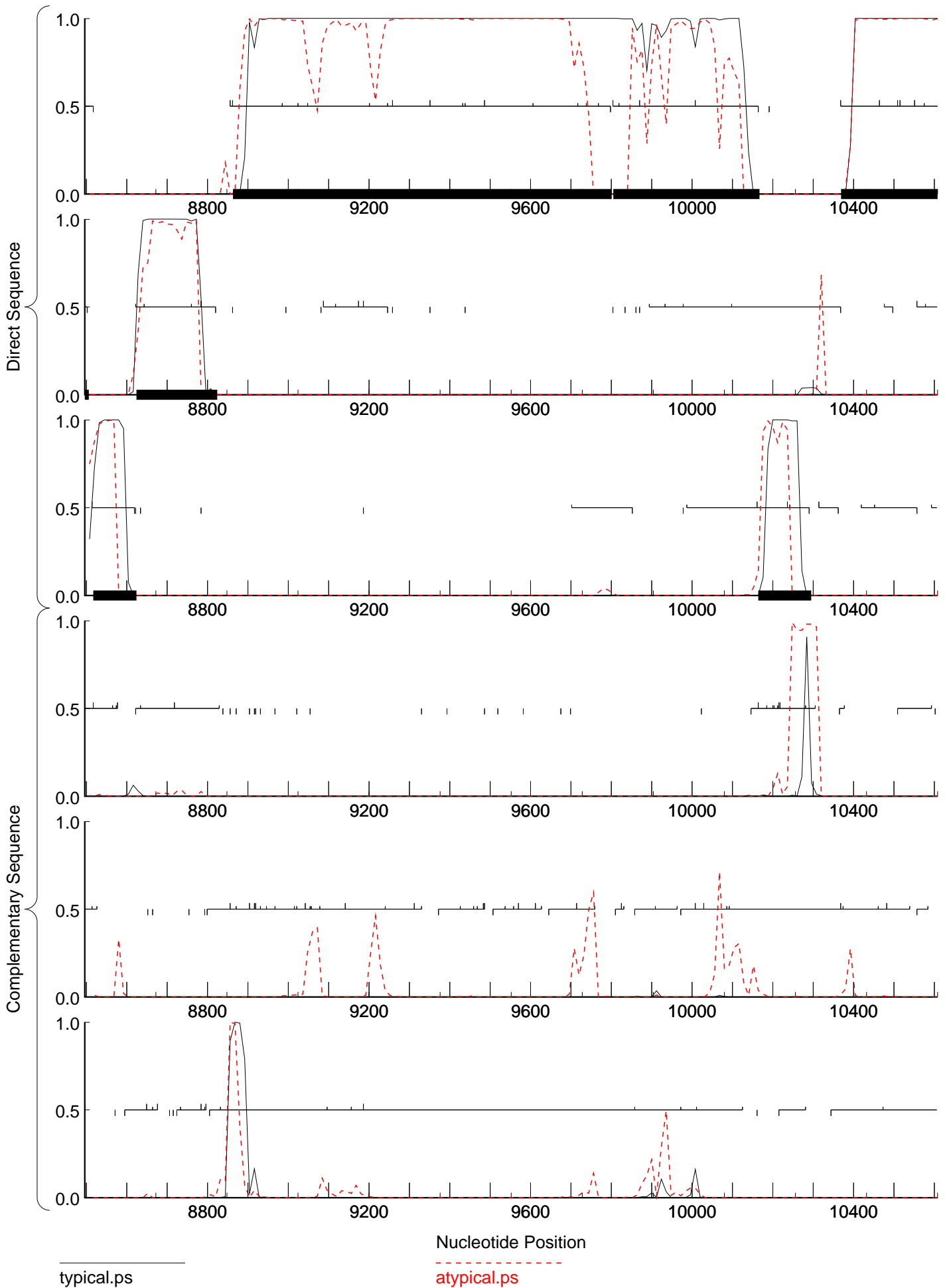
atypical.ps

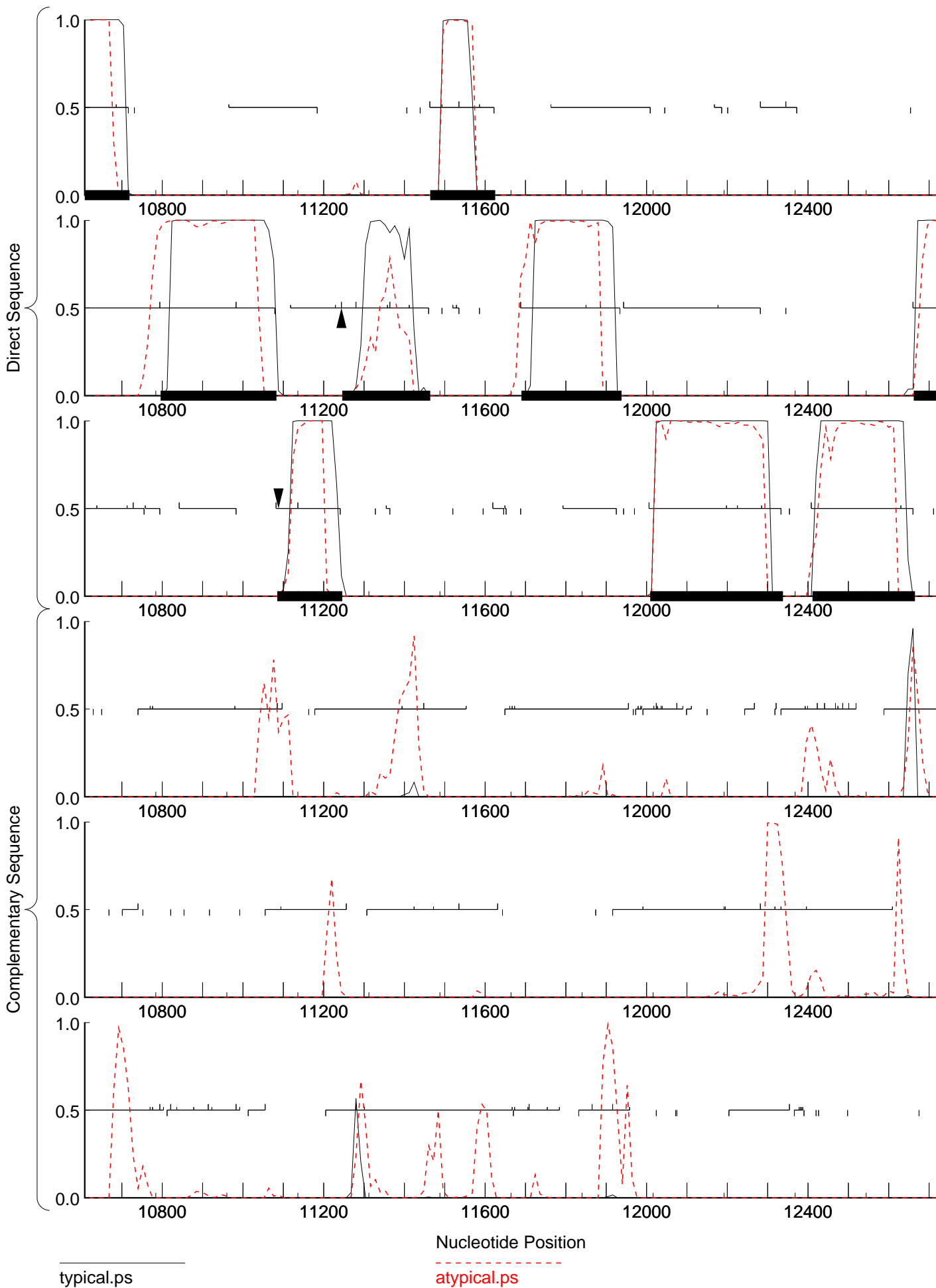


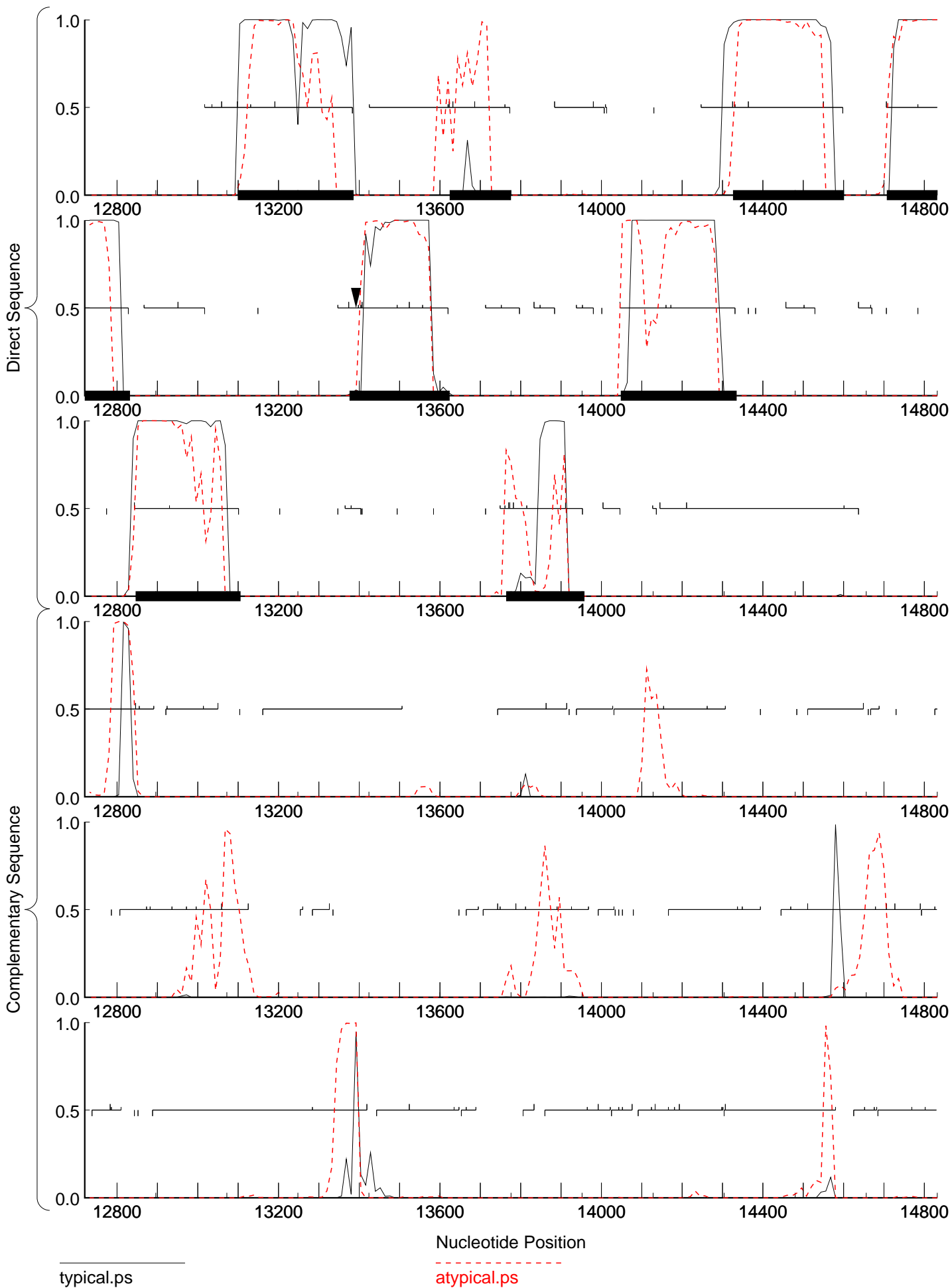


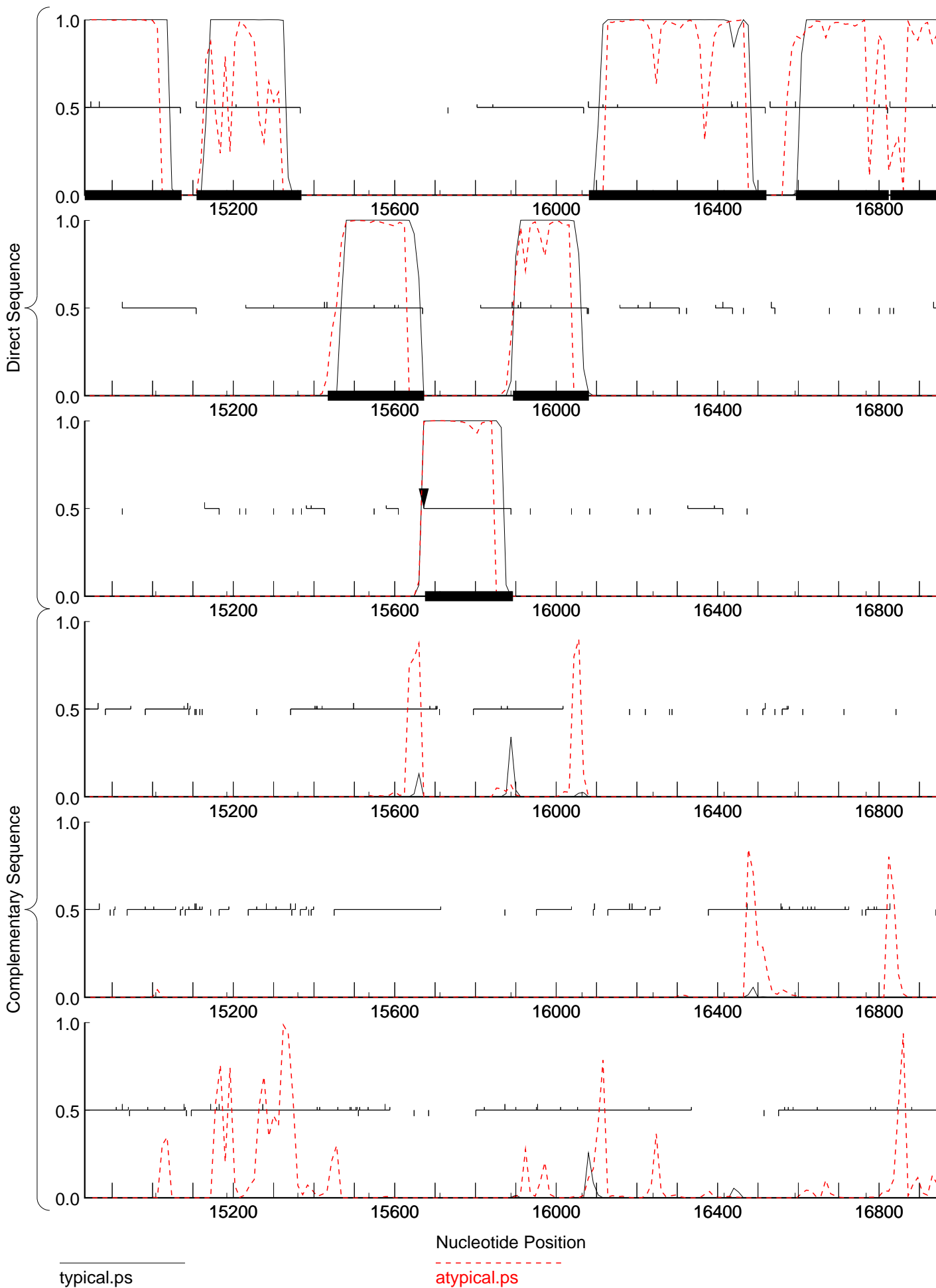
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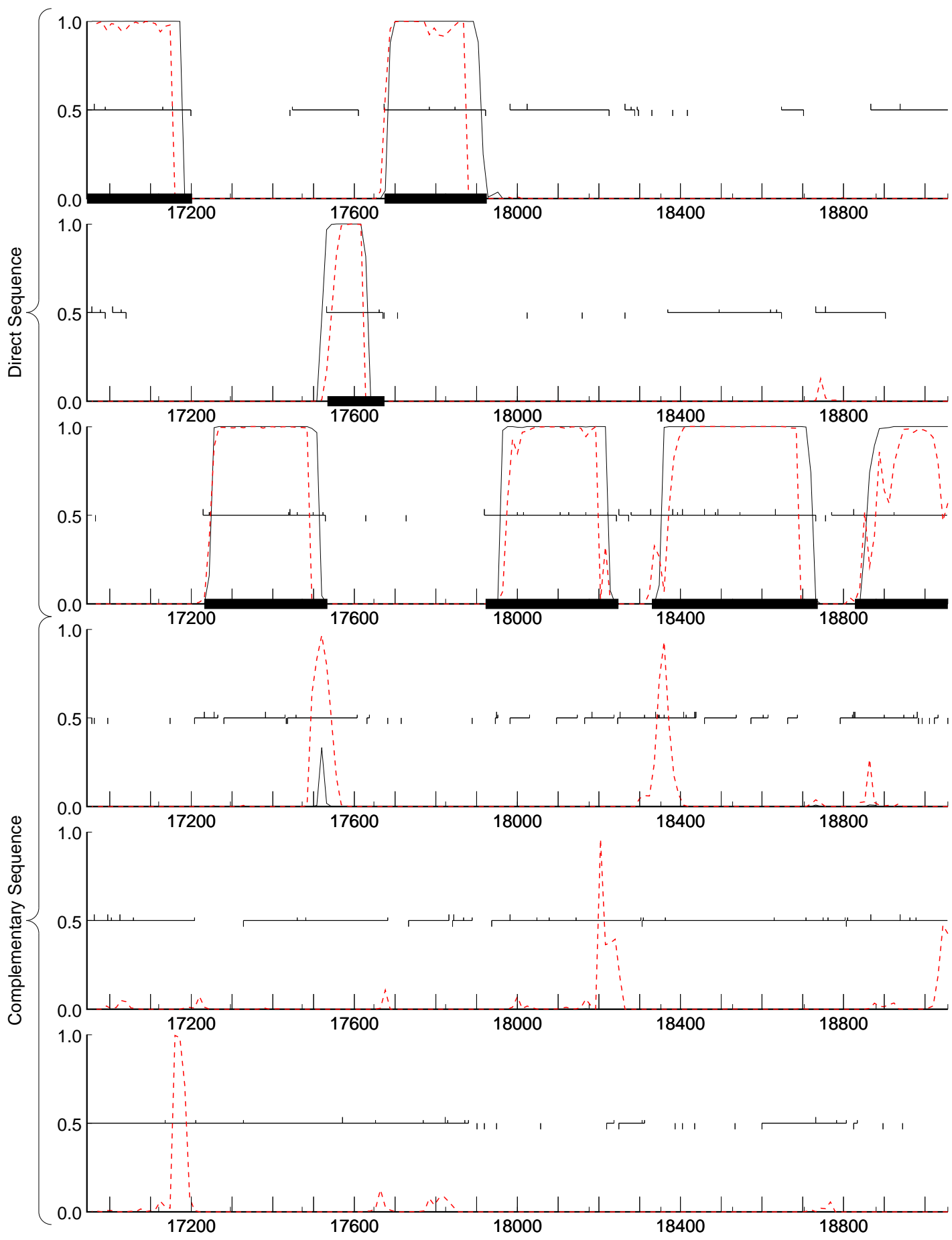
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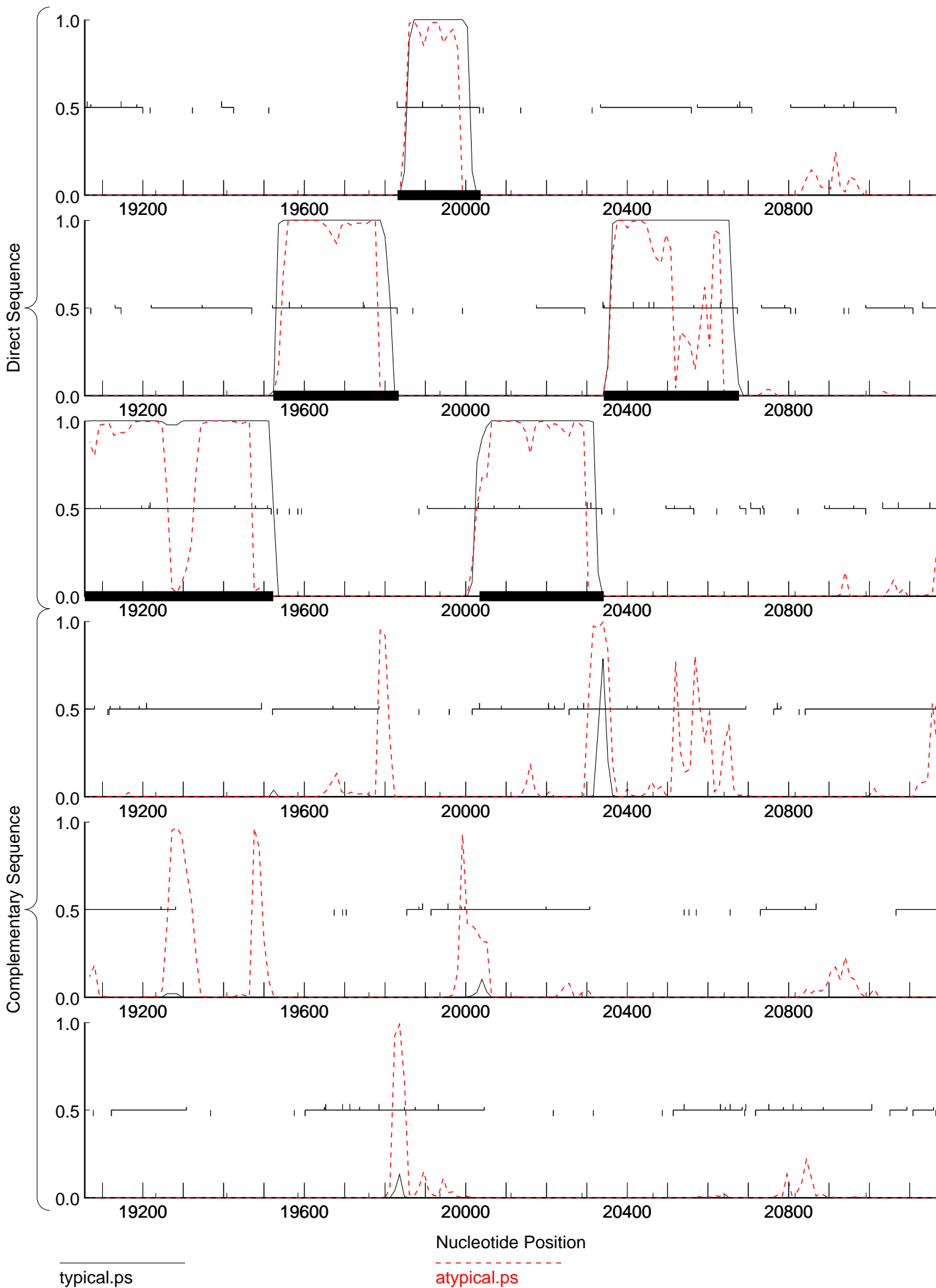


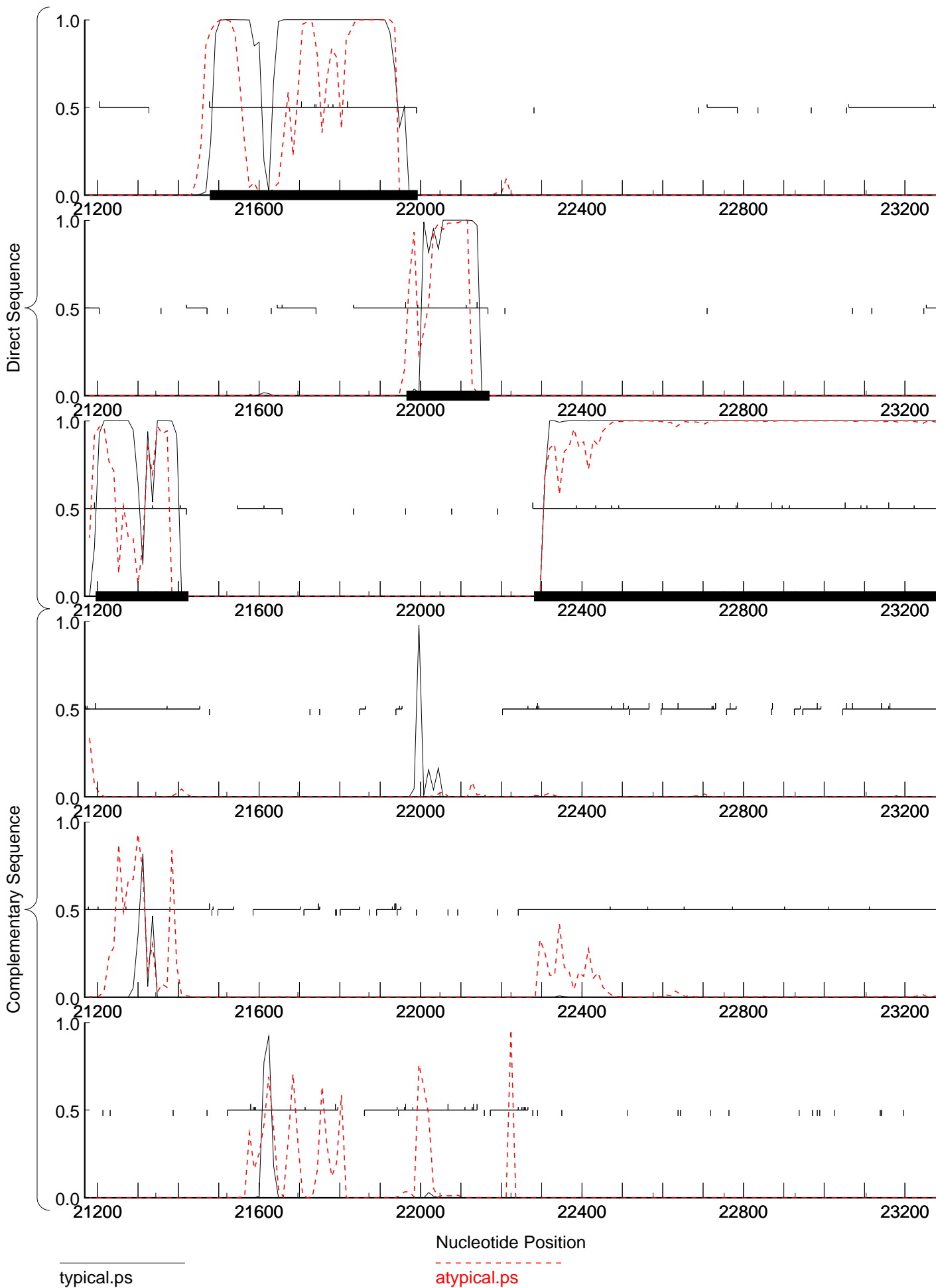




typical.ps

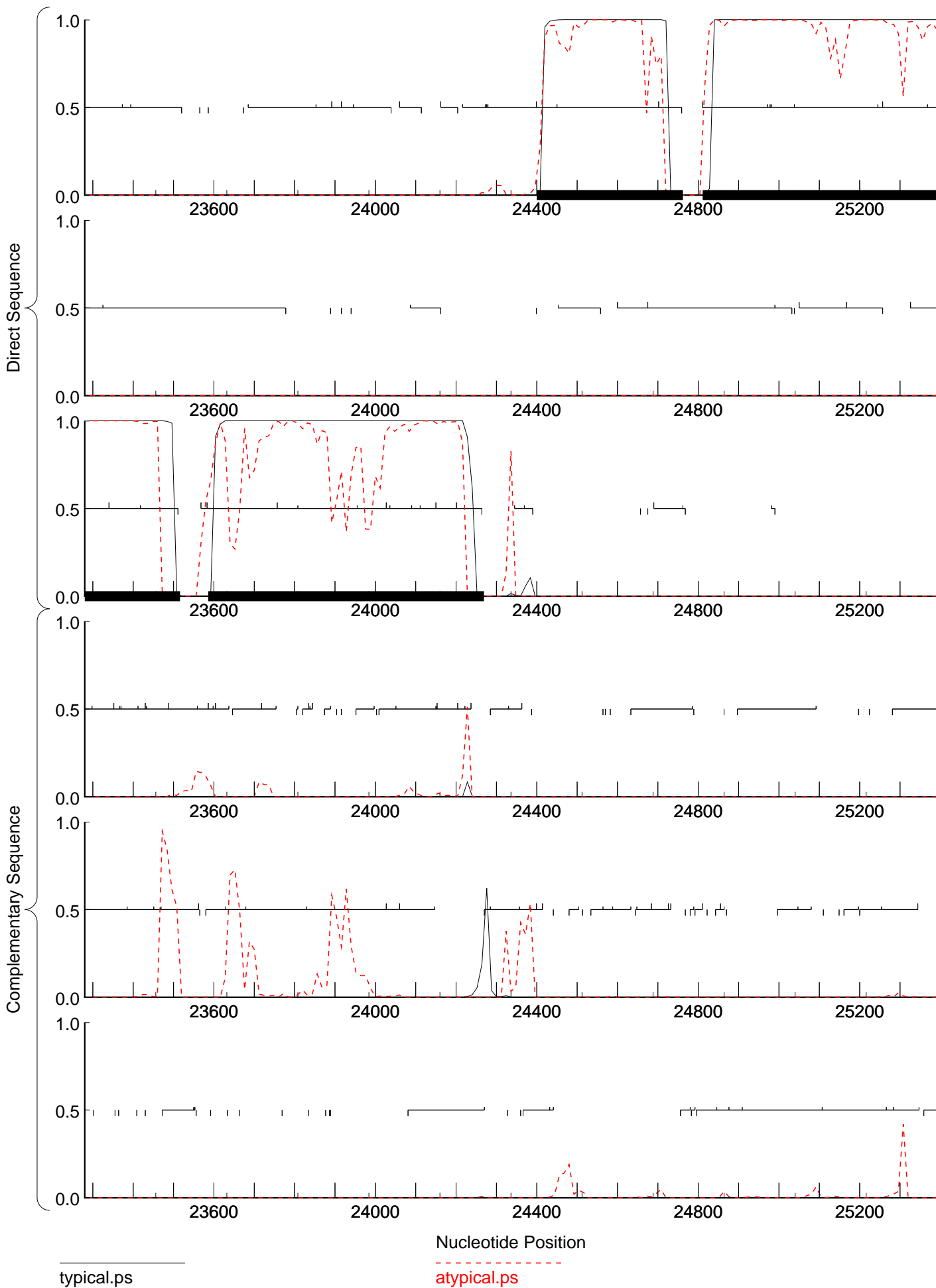
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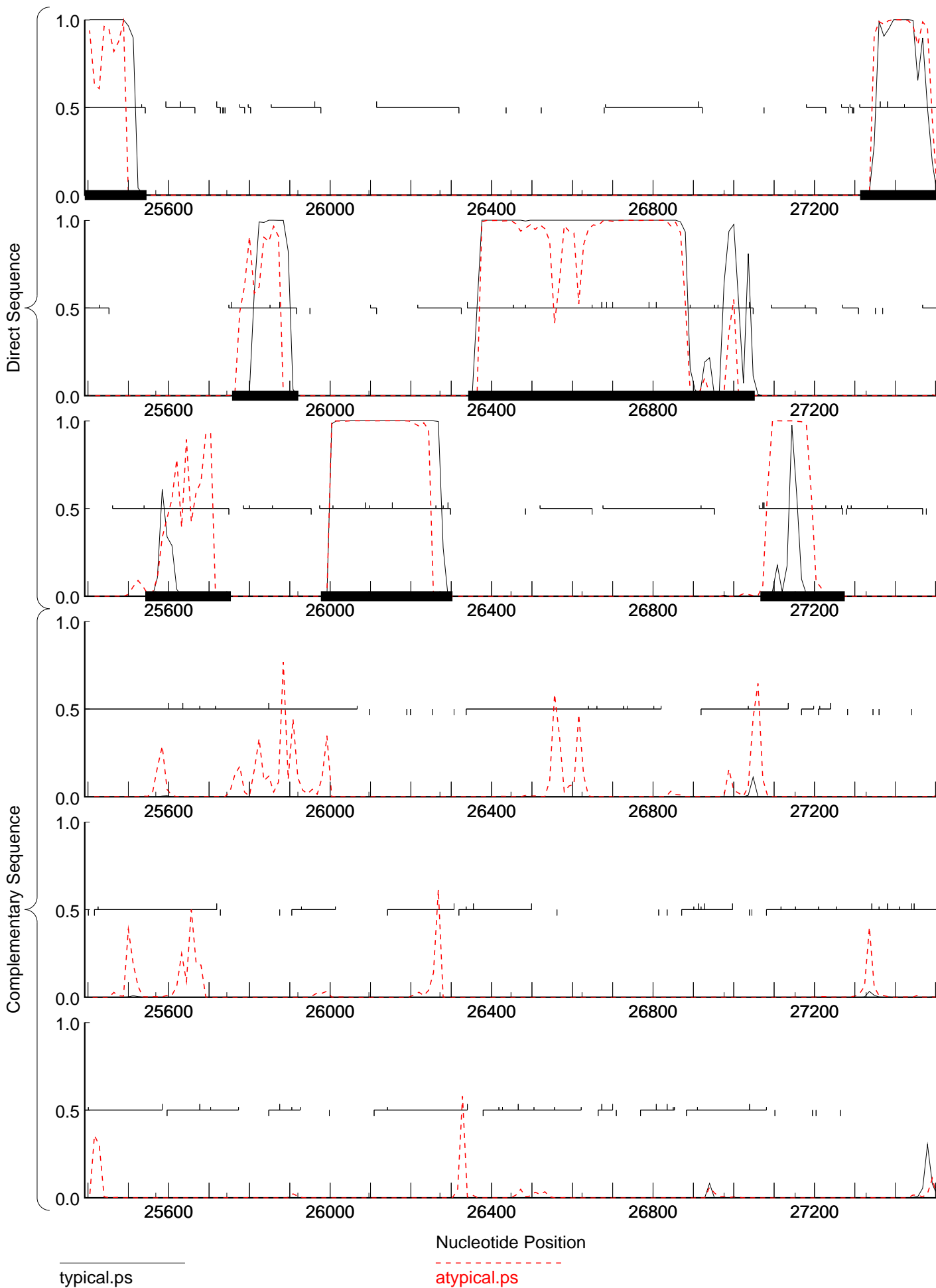


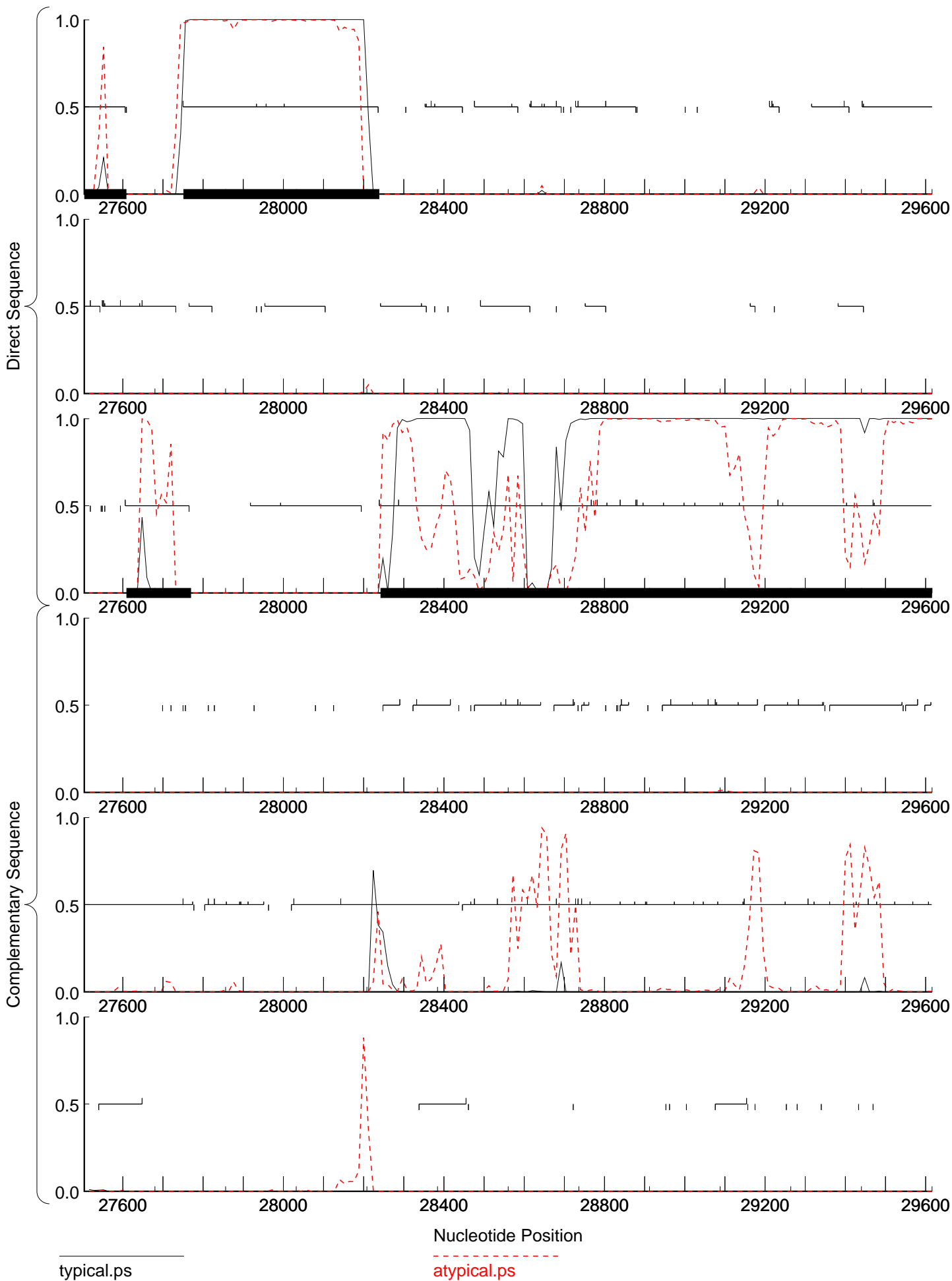


typical.ps

atypical.ps

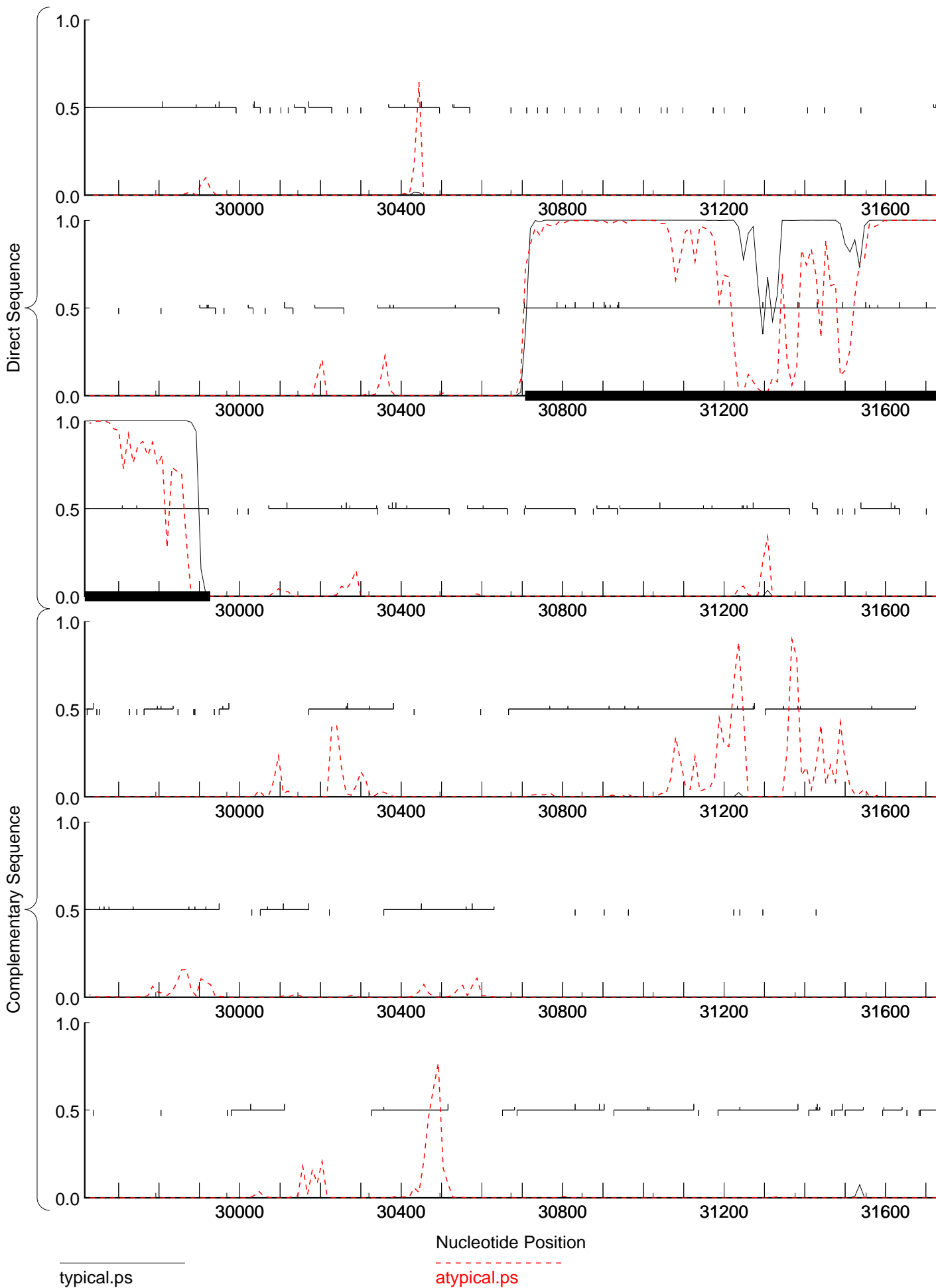


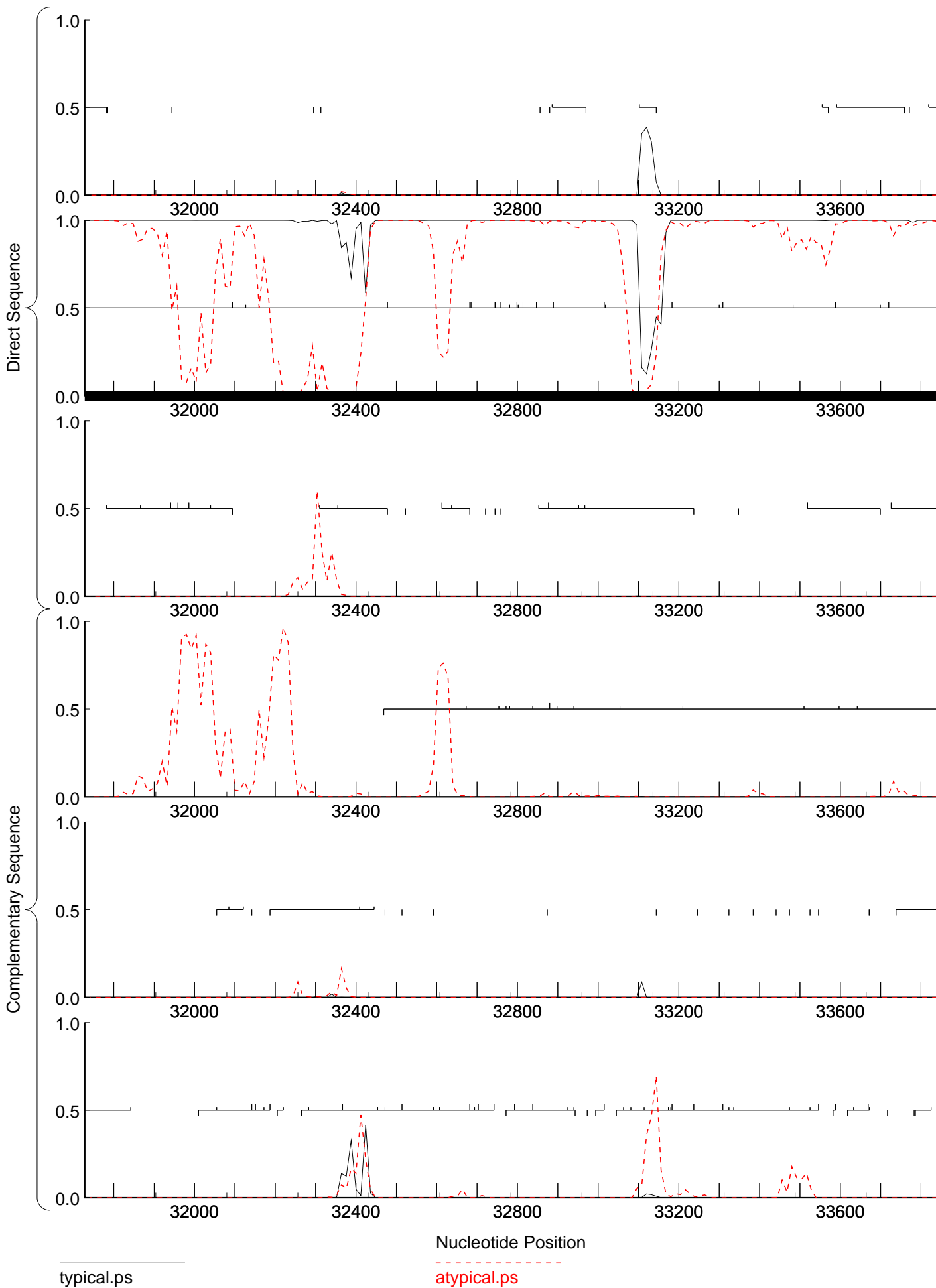


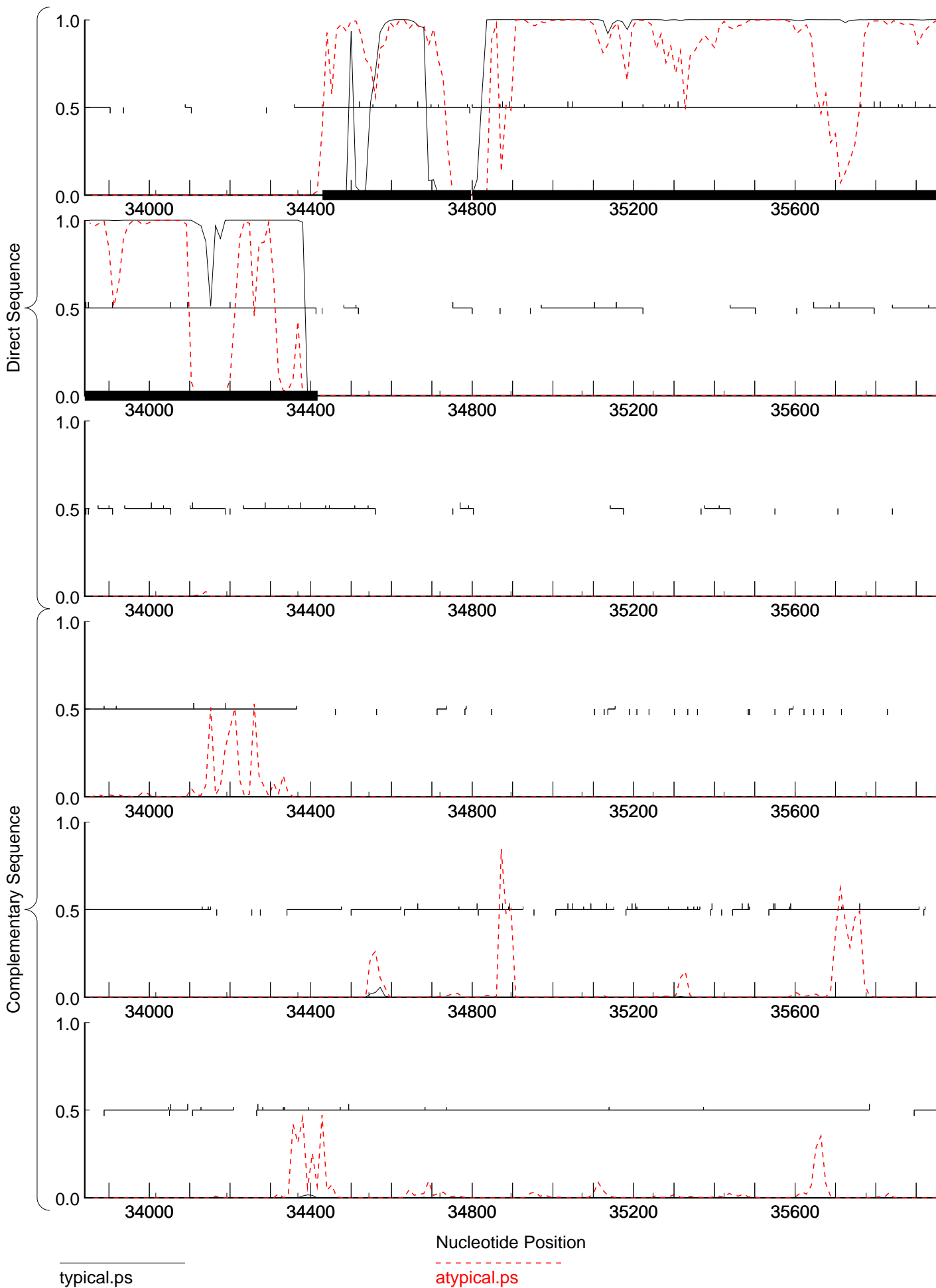


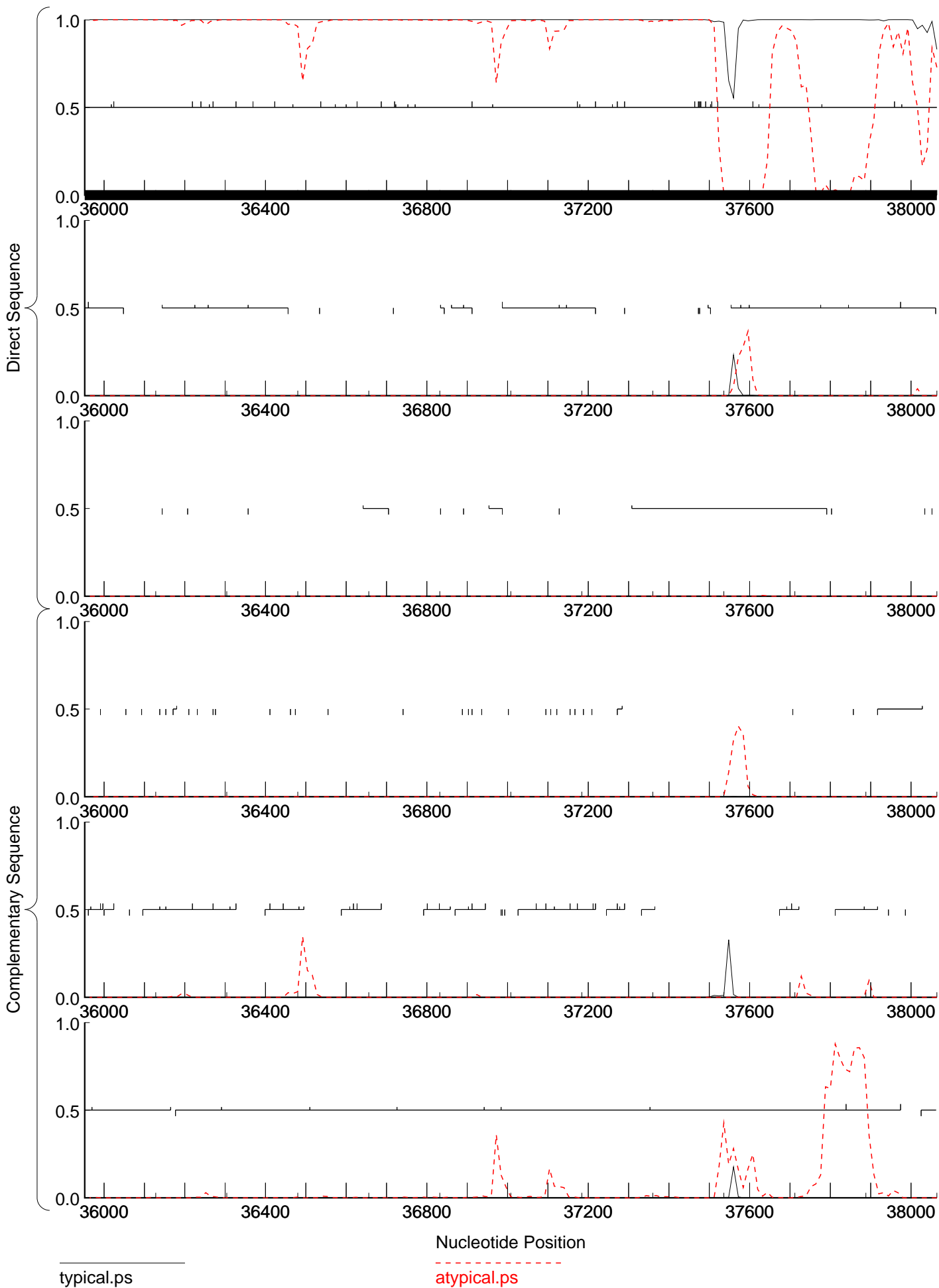
typical.ps

atypical.ps

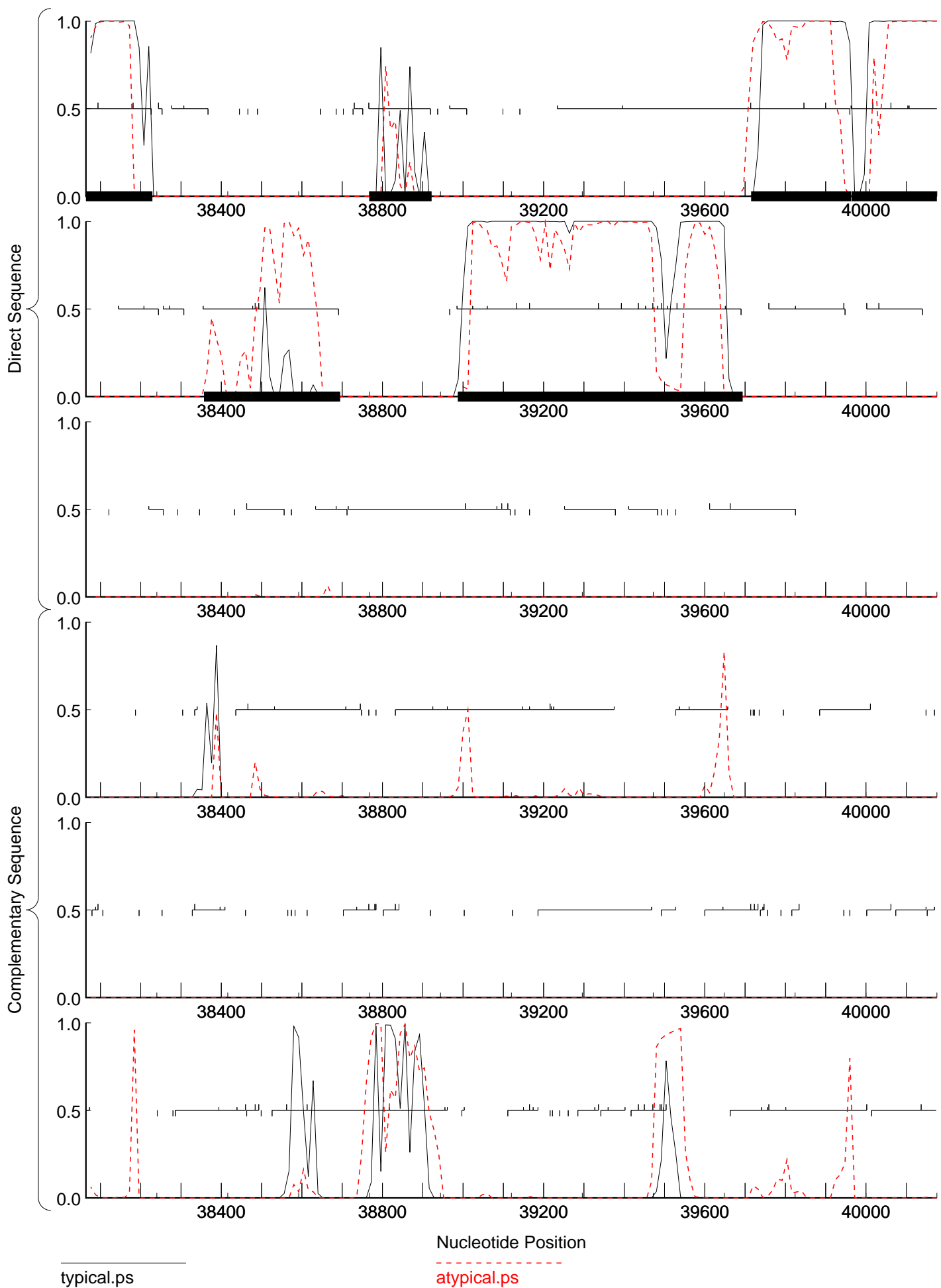


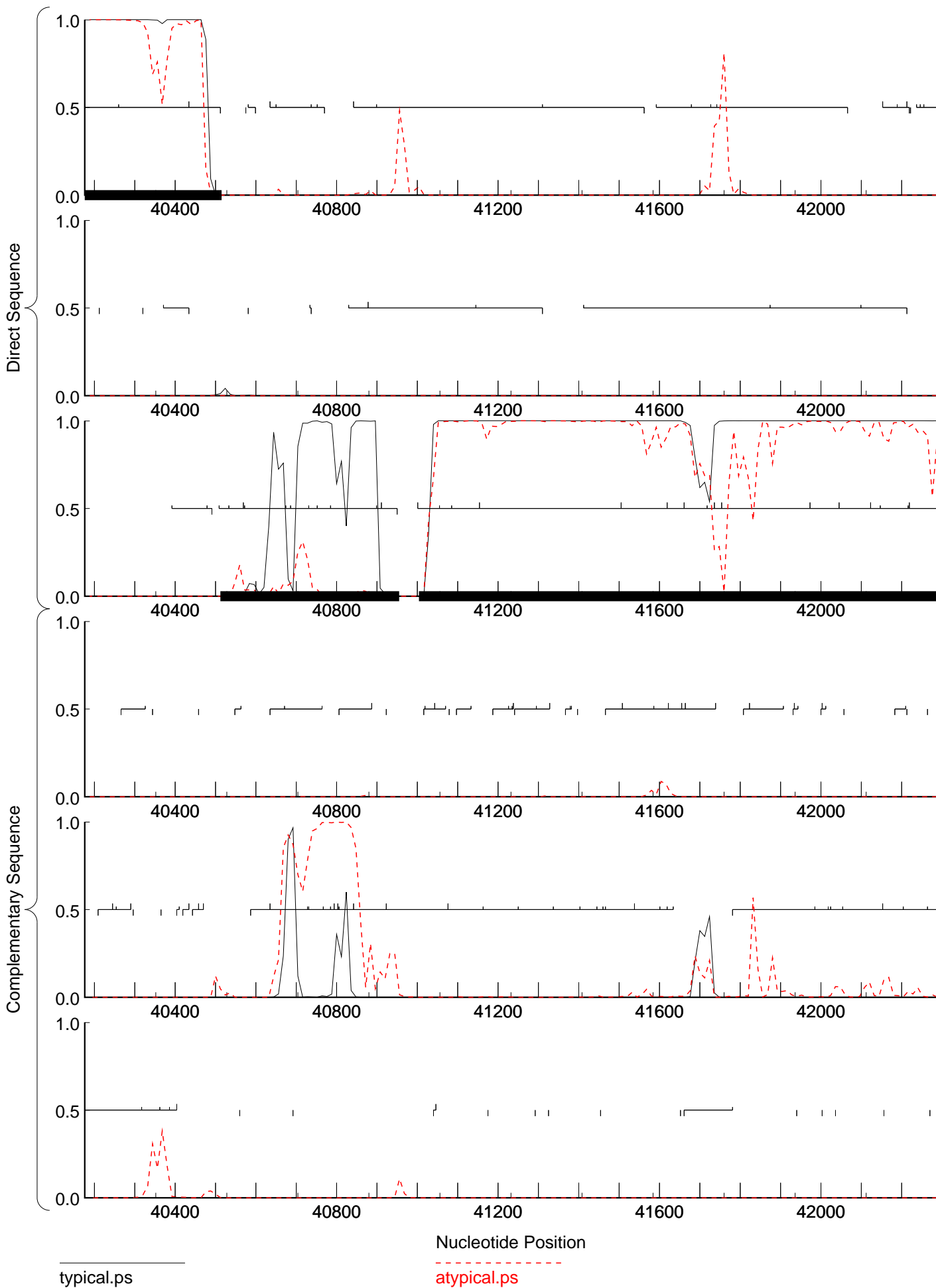


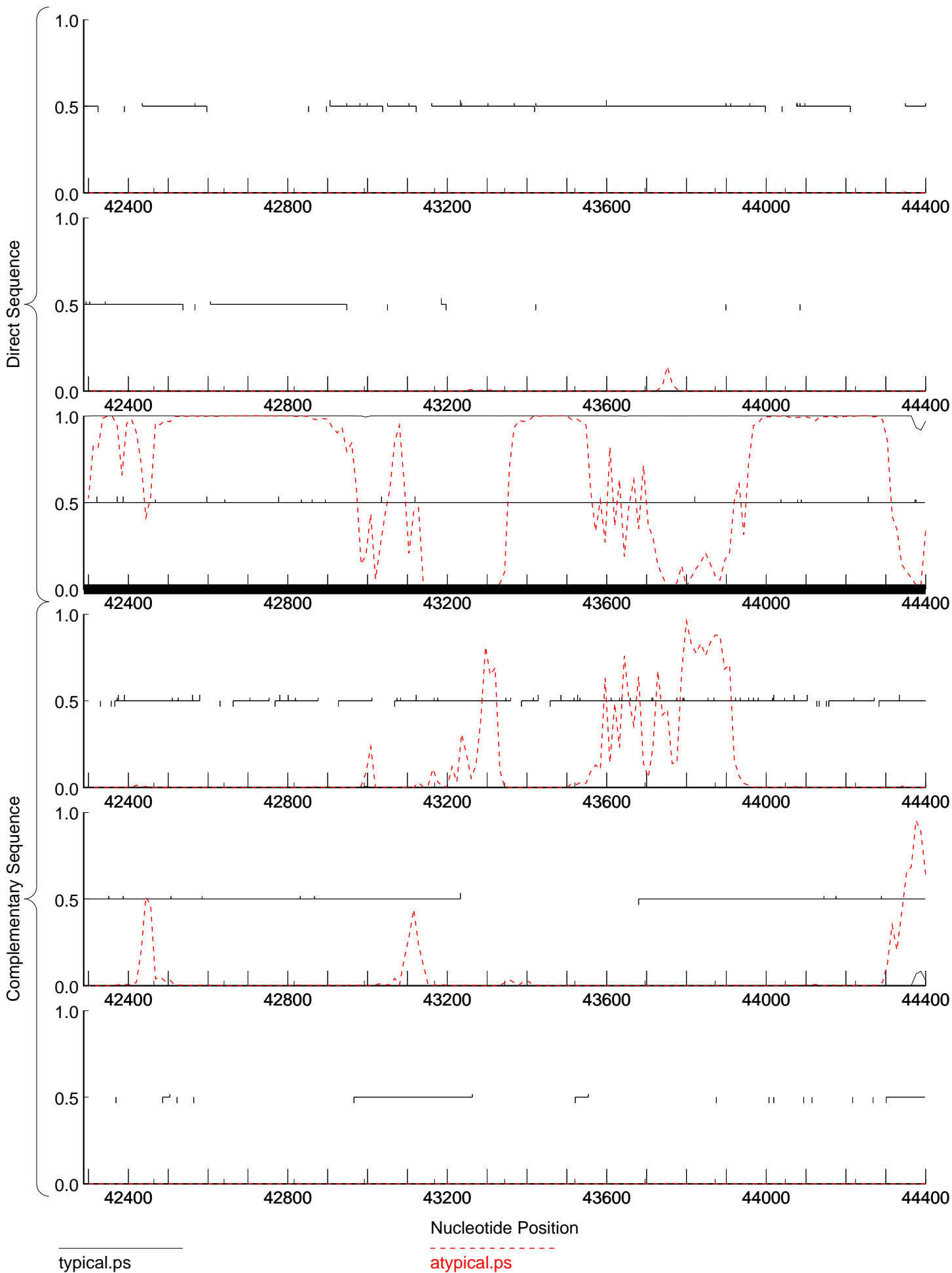


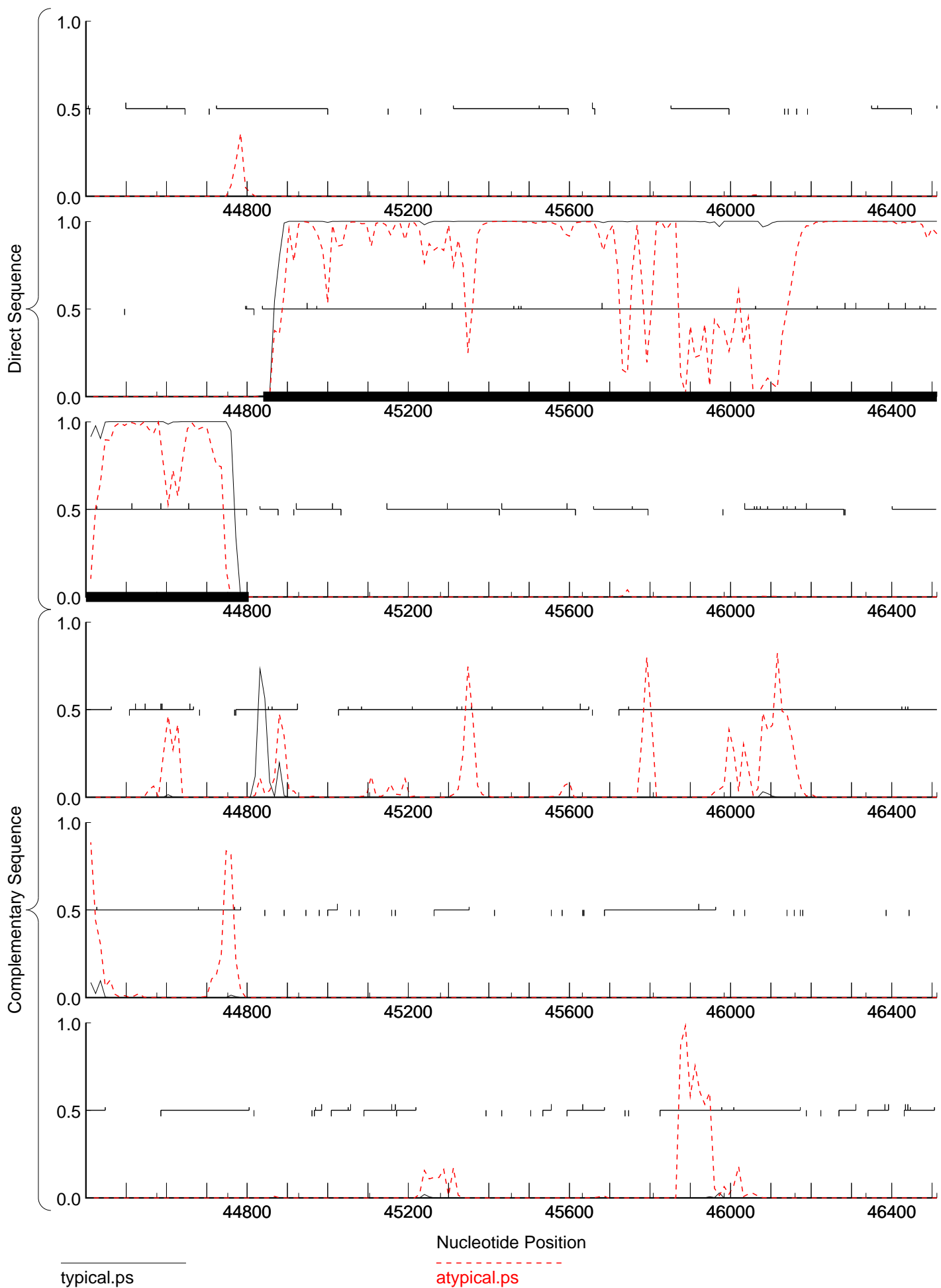


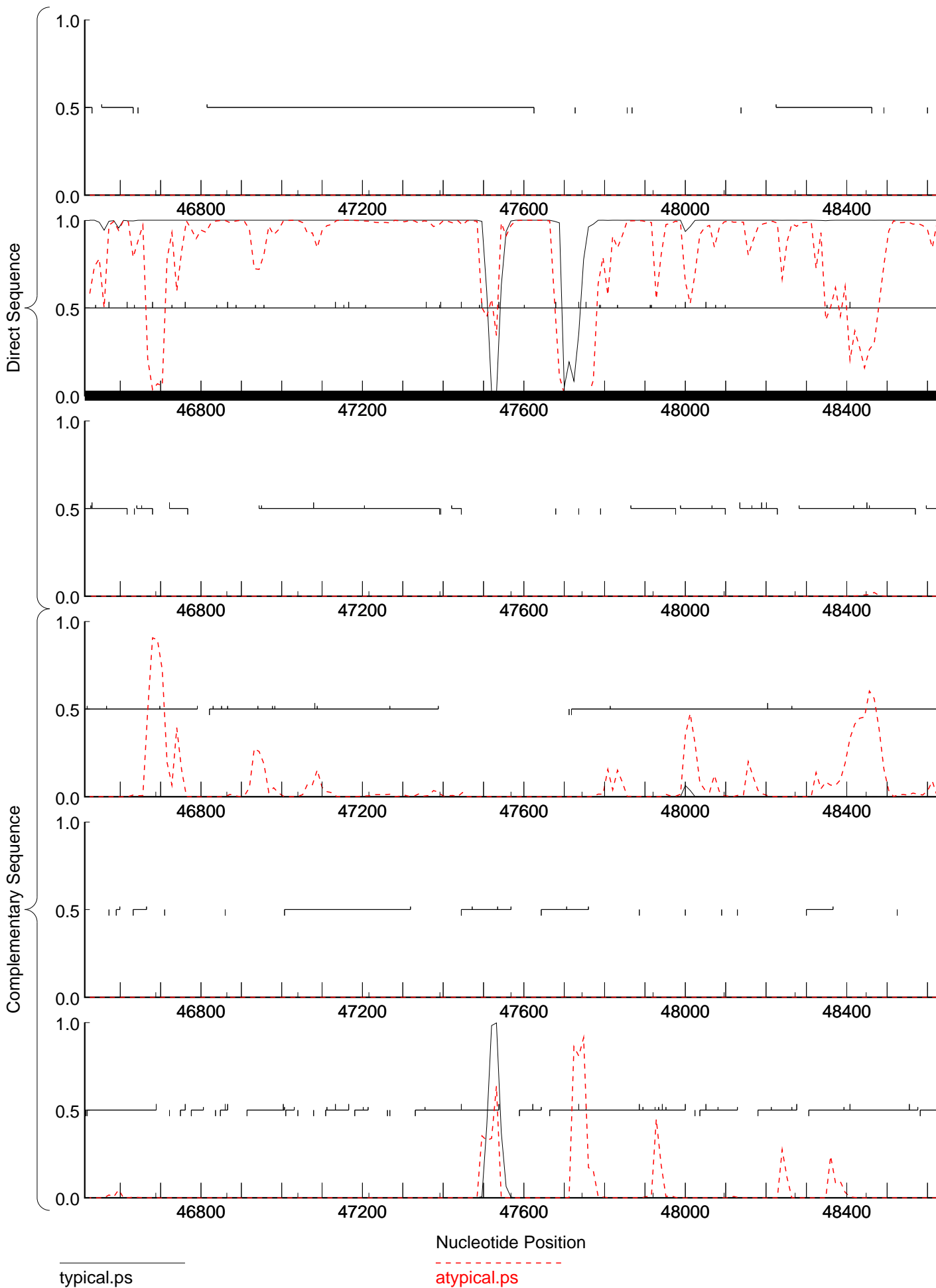
GeneMark.hmm prediction





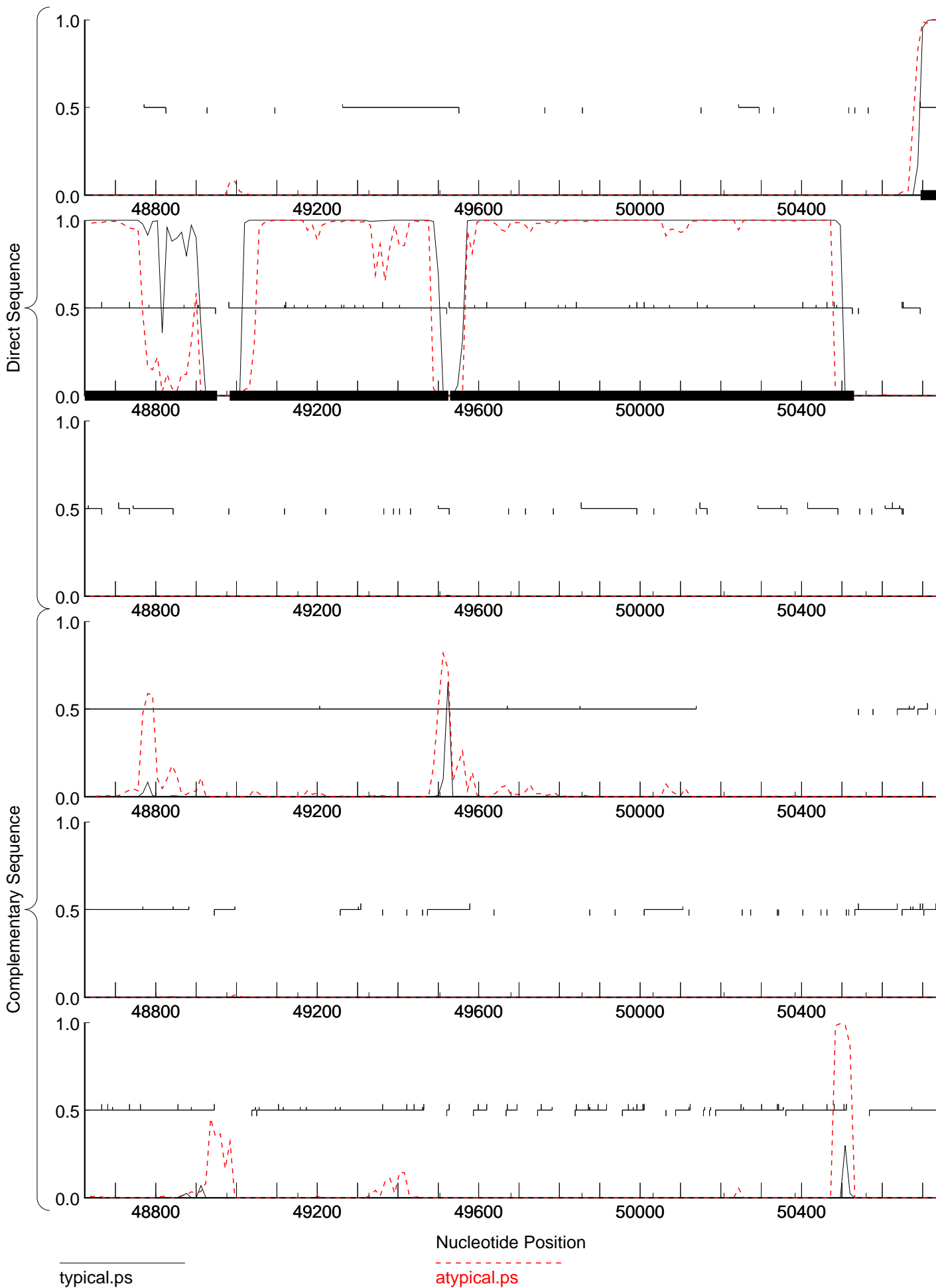


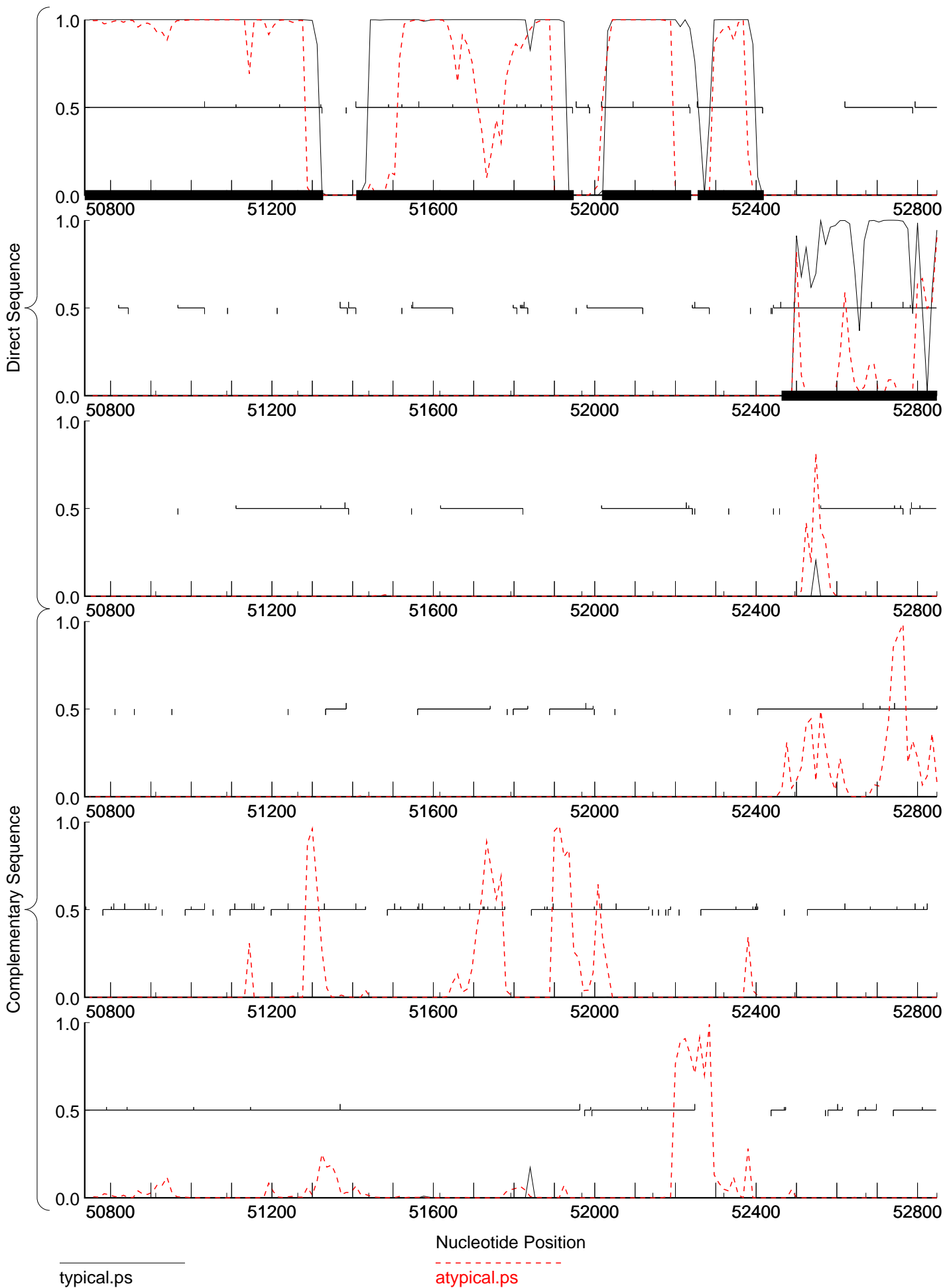


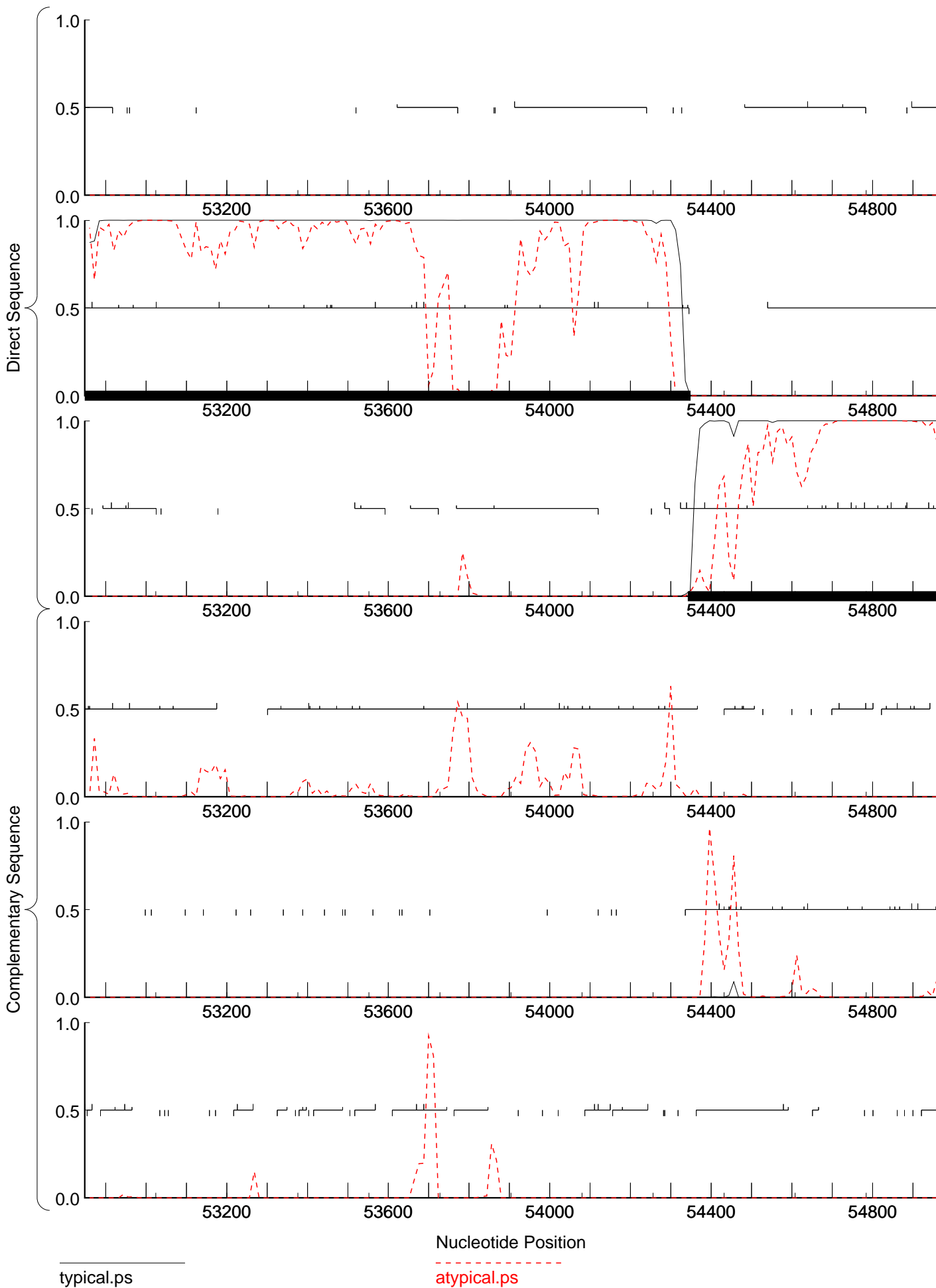


typical.ps

atypical.ps

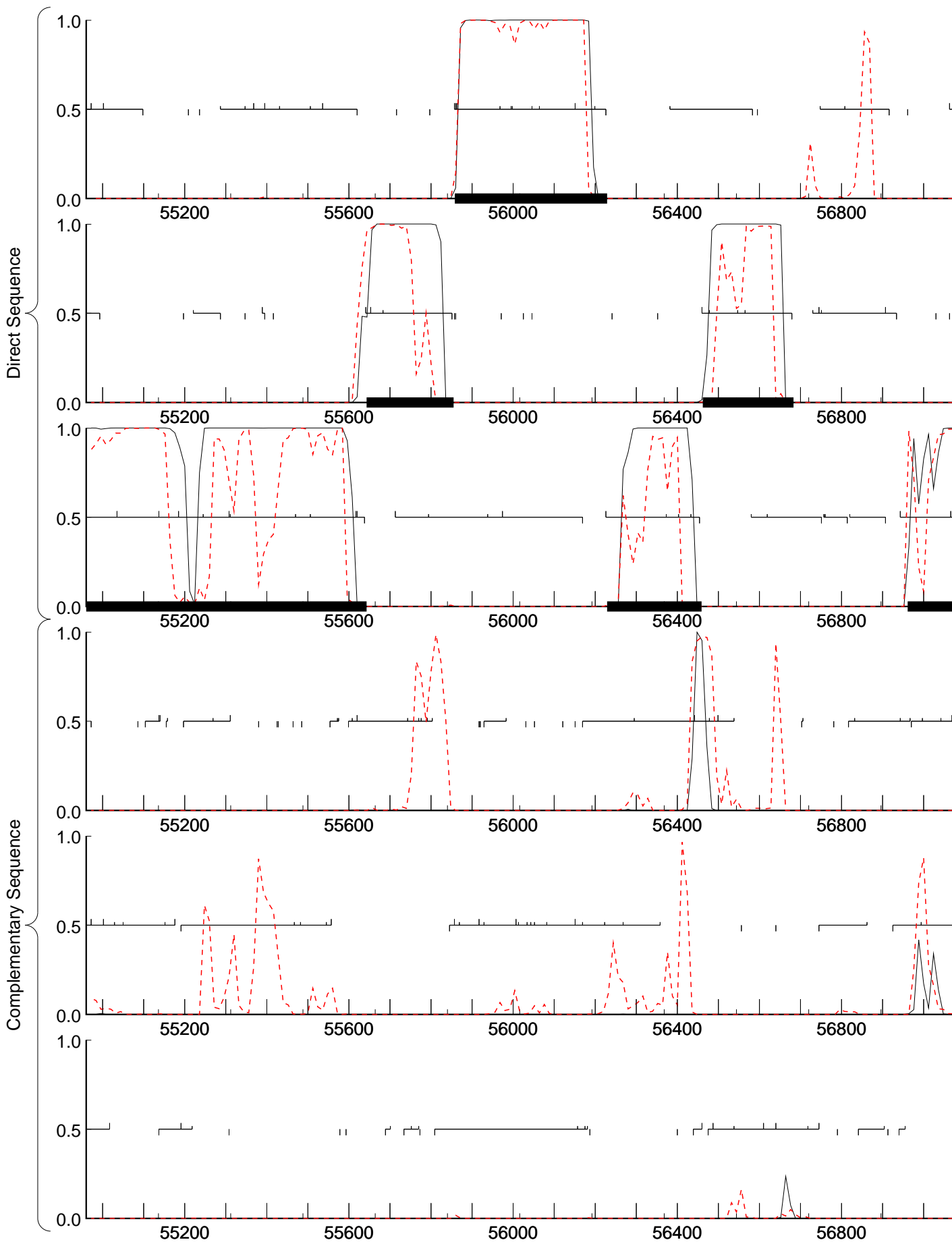






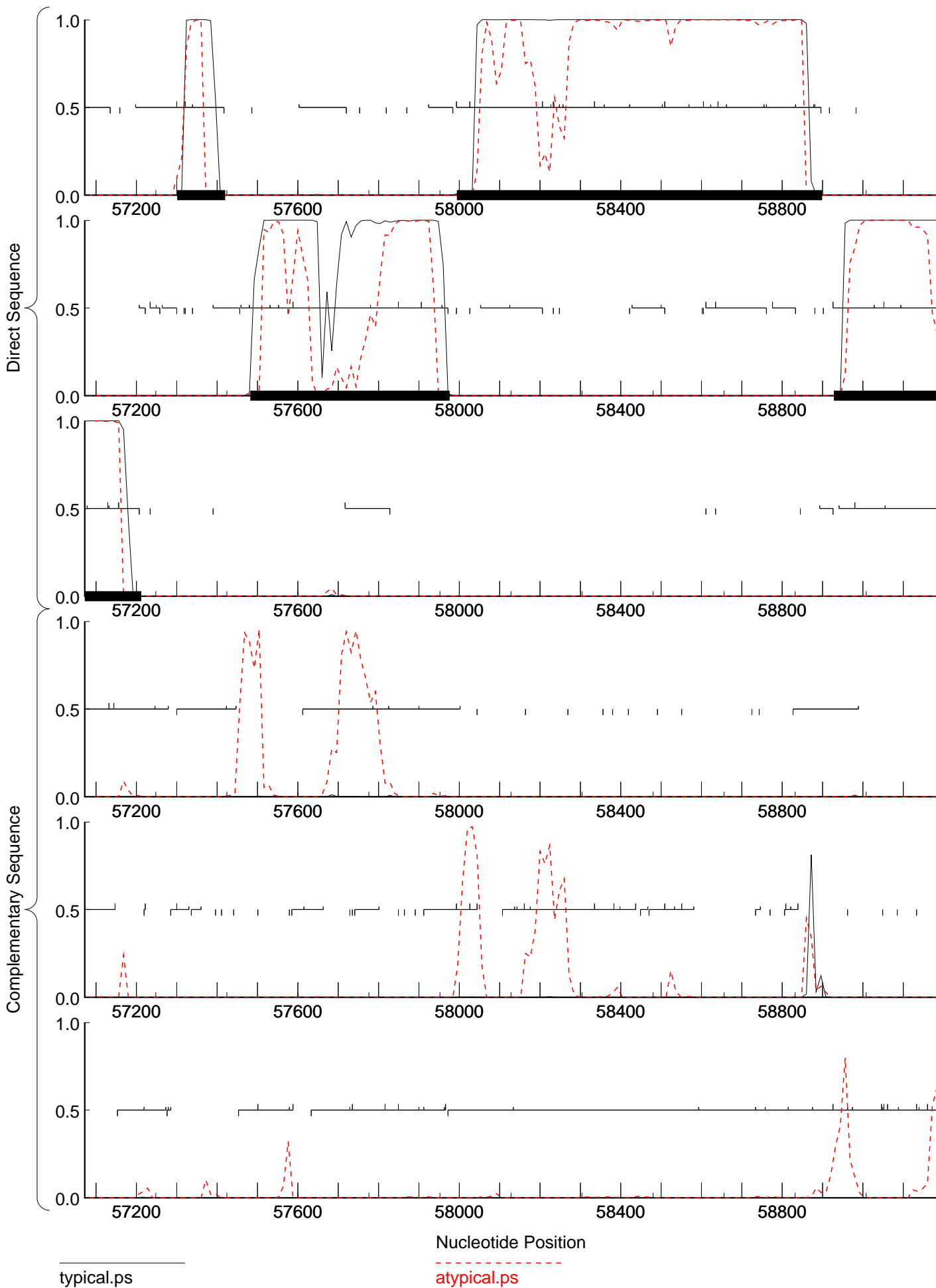
typical.ps

atypical.ps



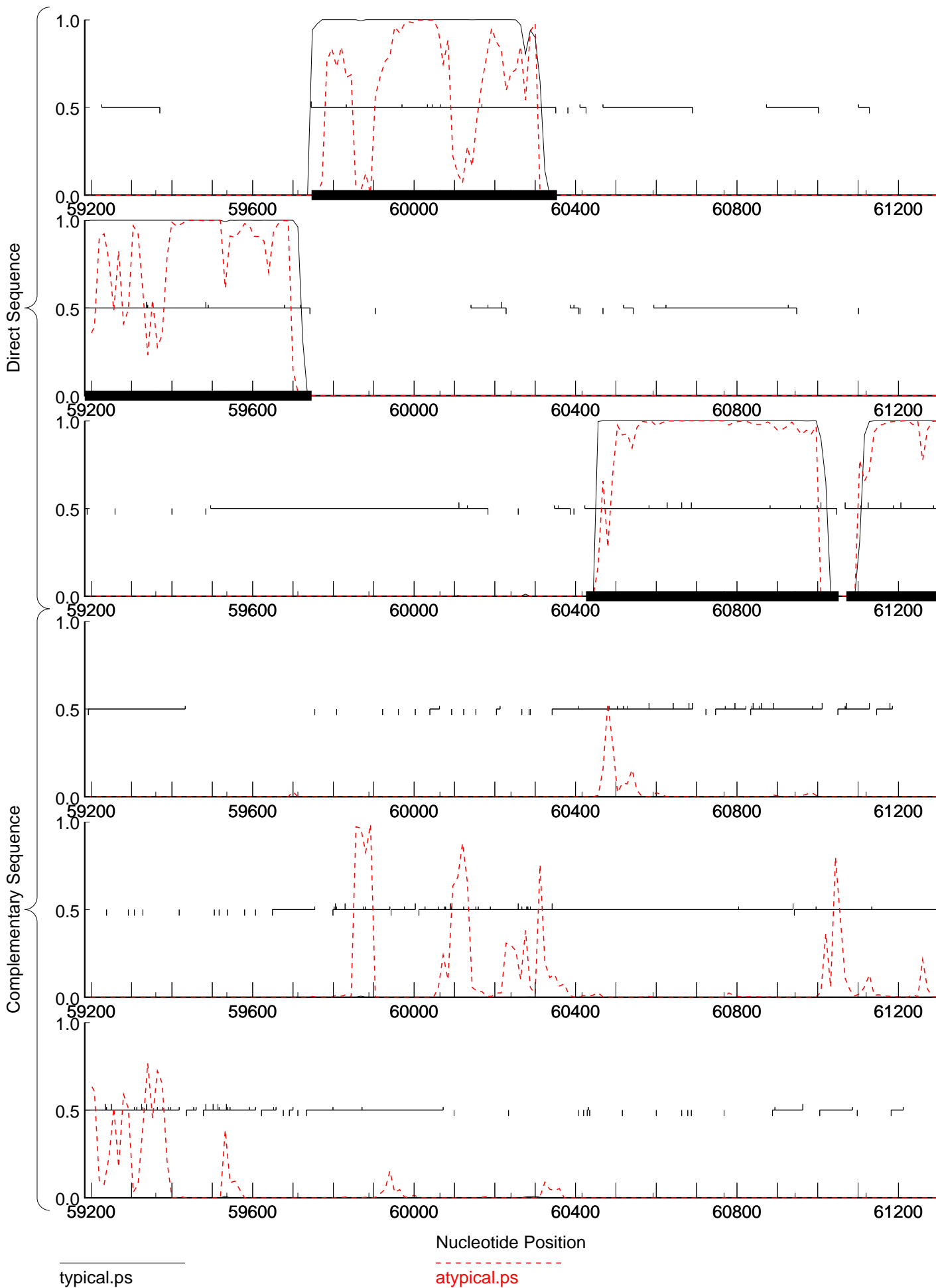
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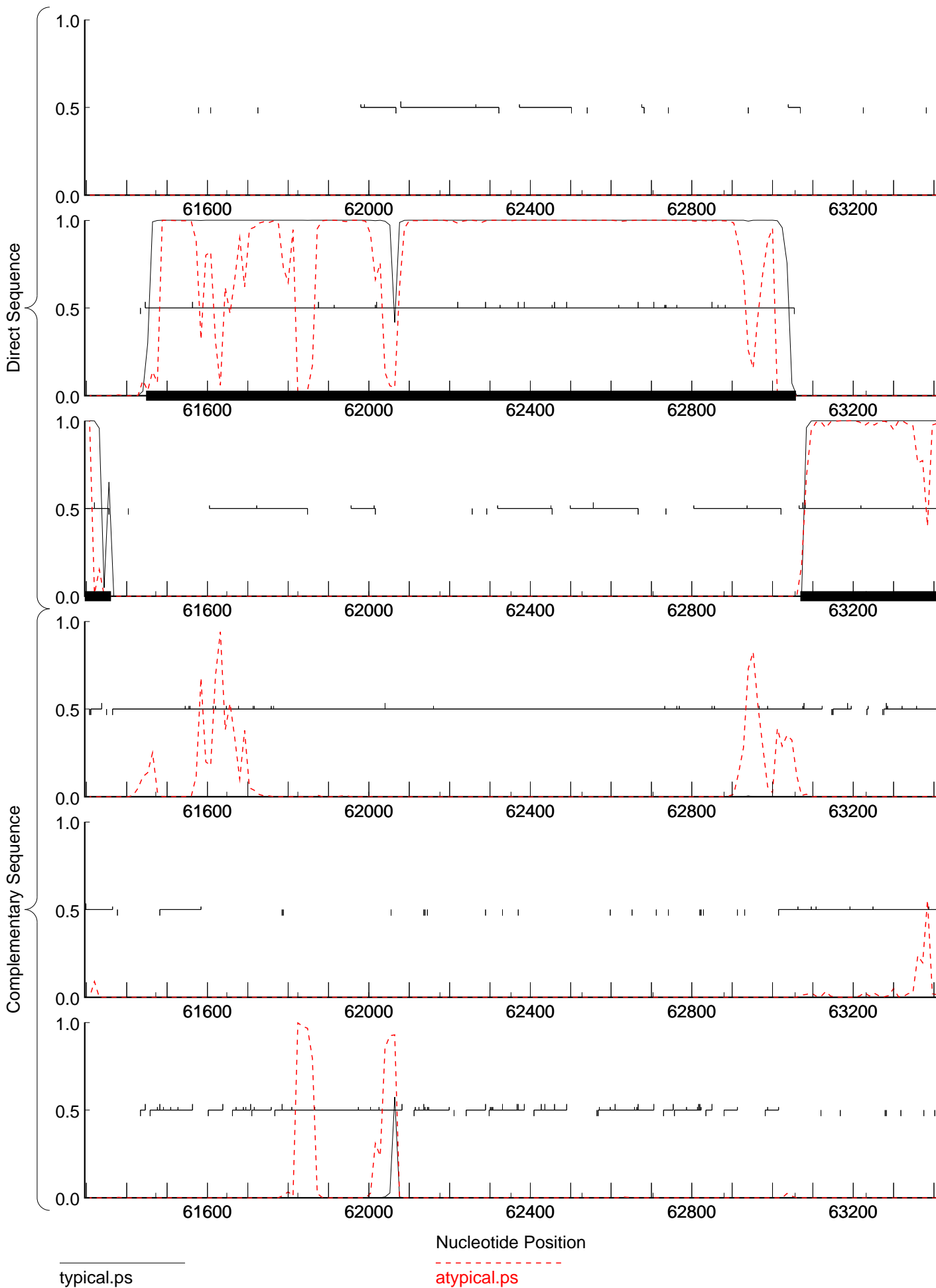
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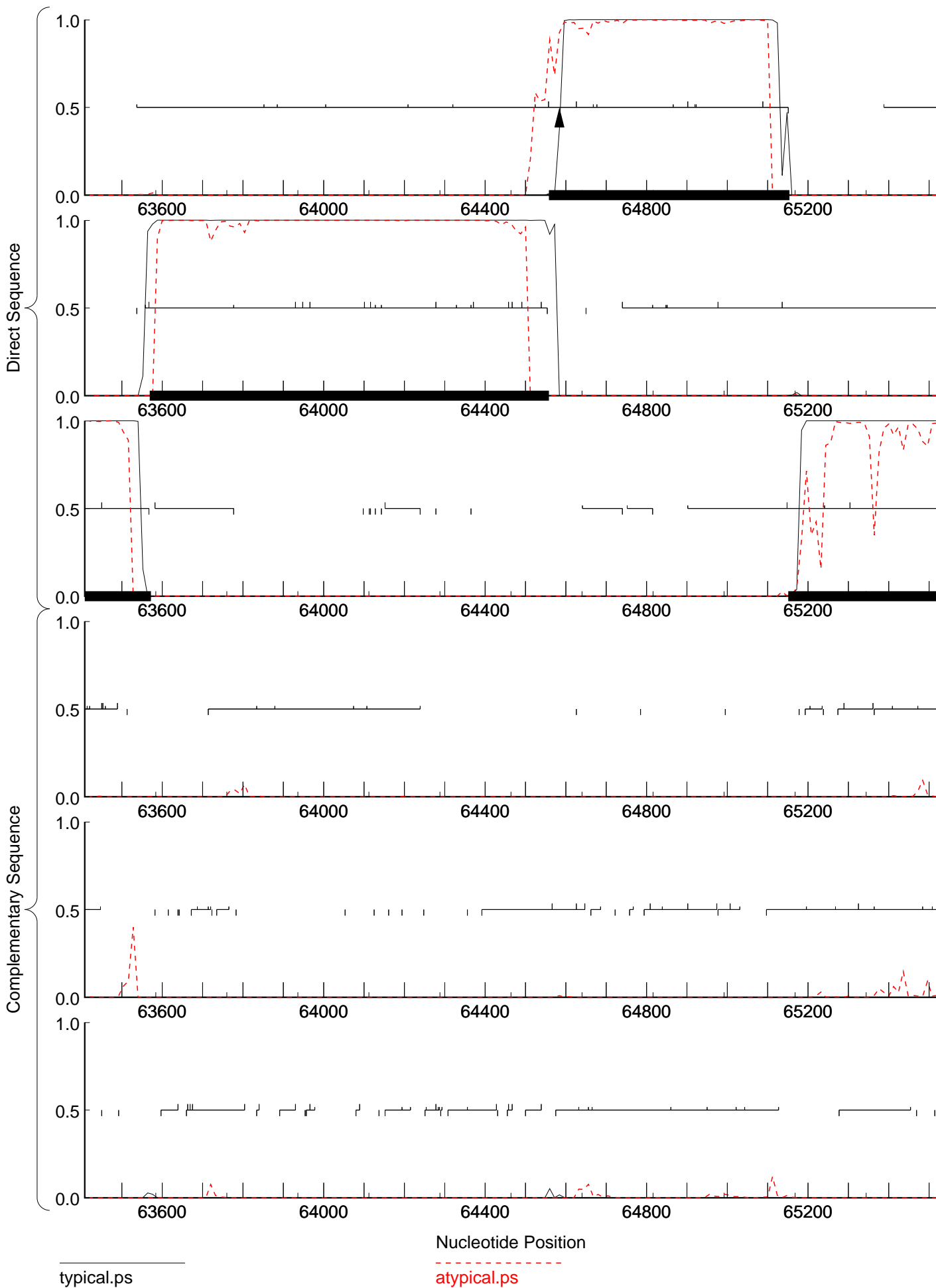


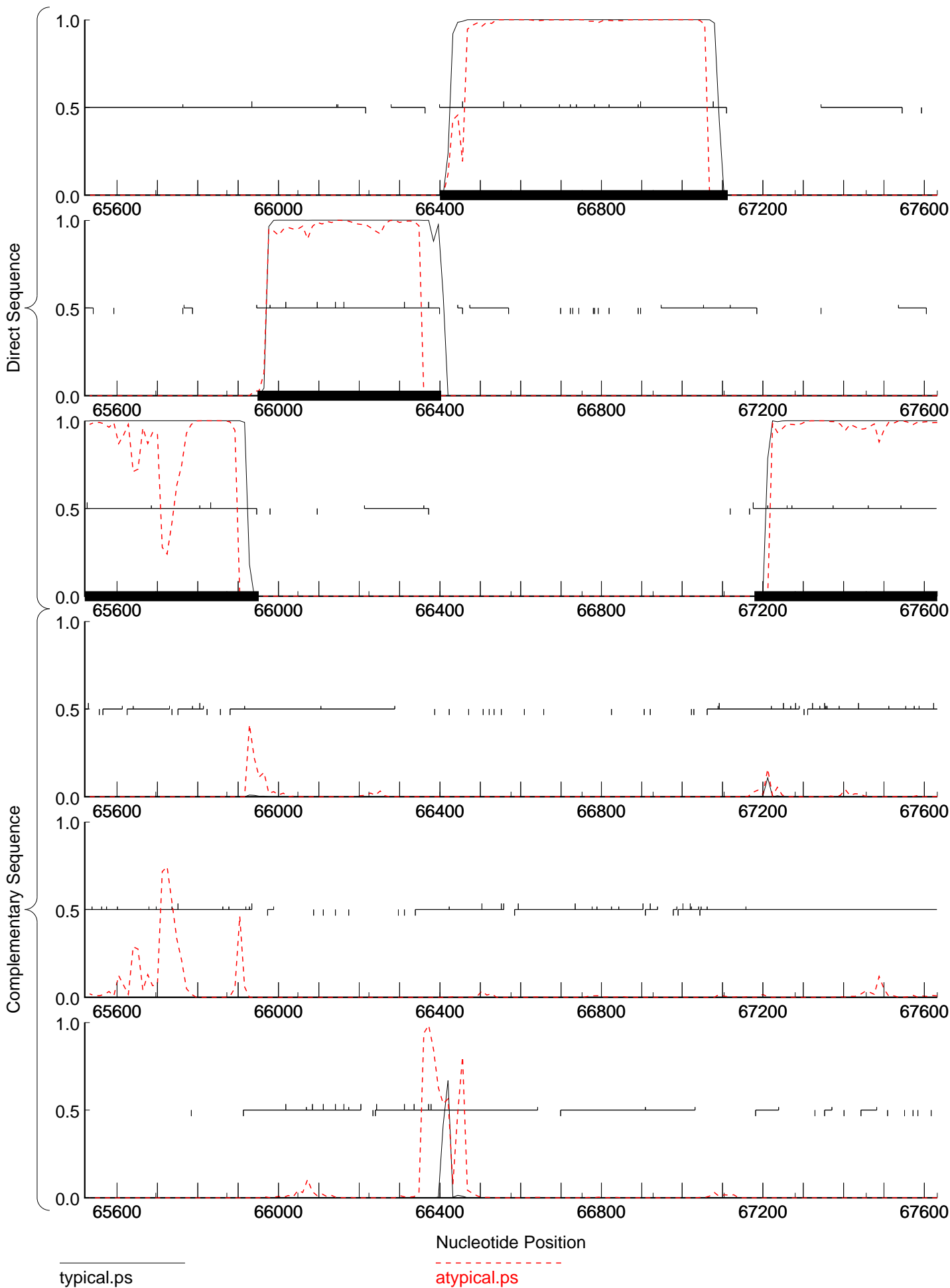
typical.ps

atypical.ps



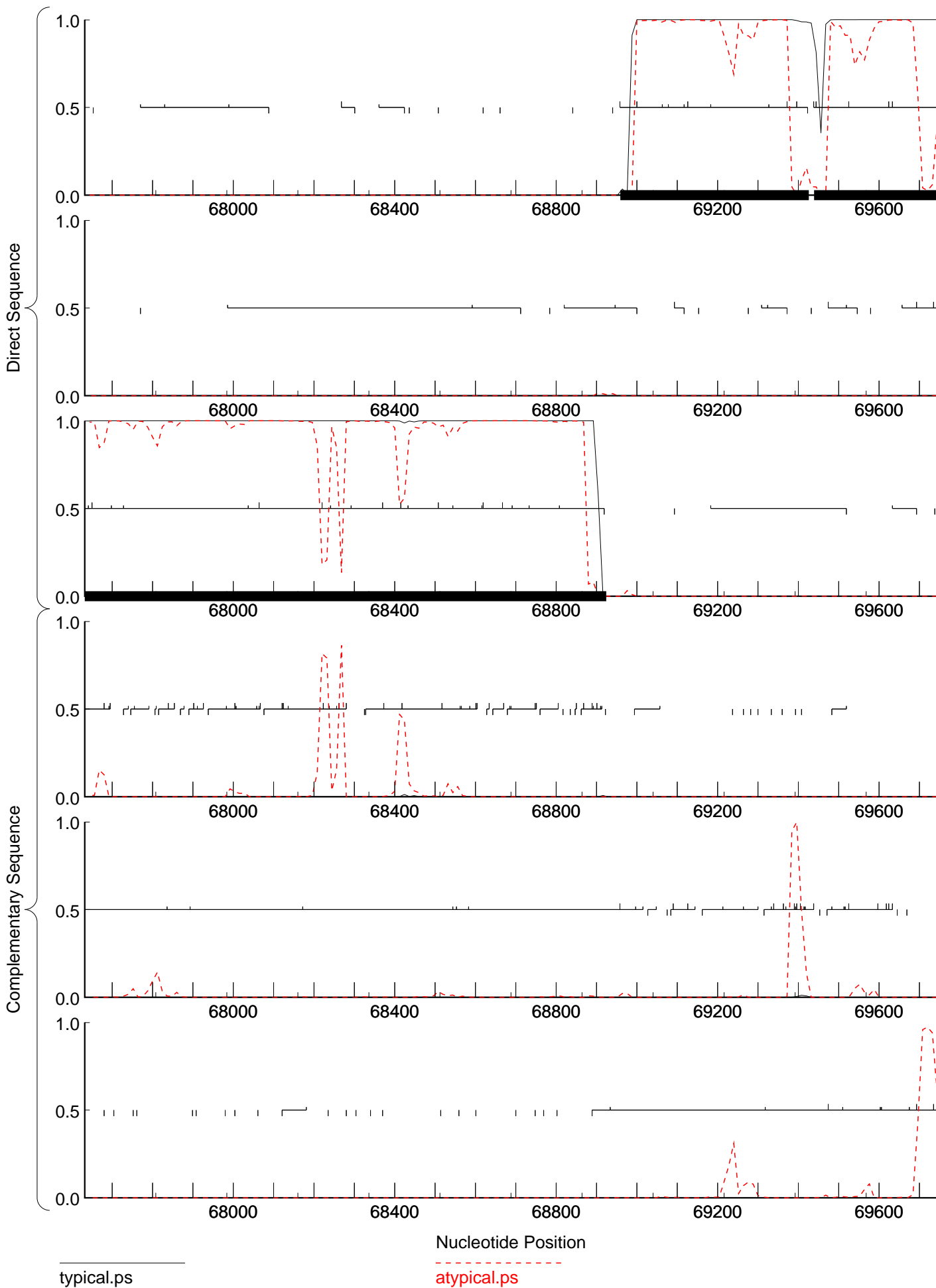


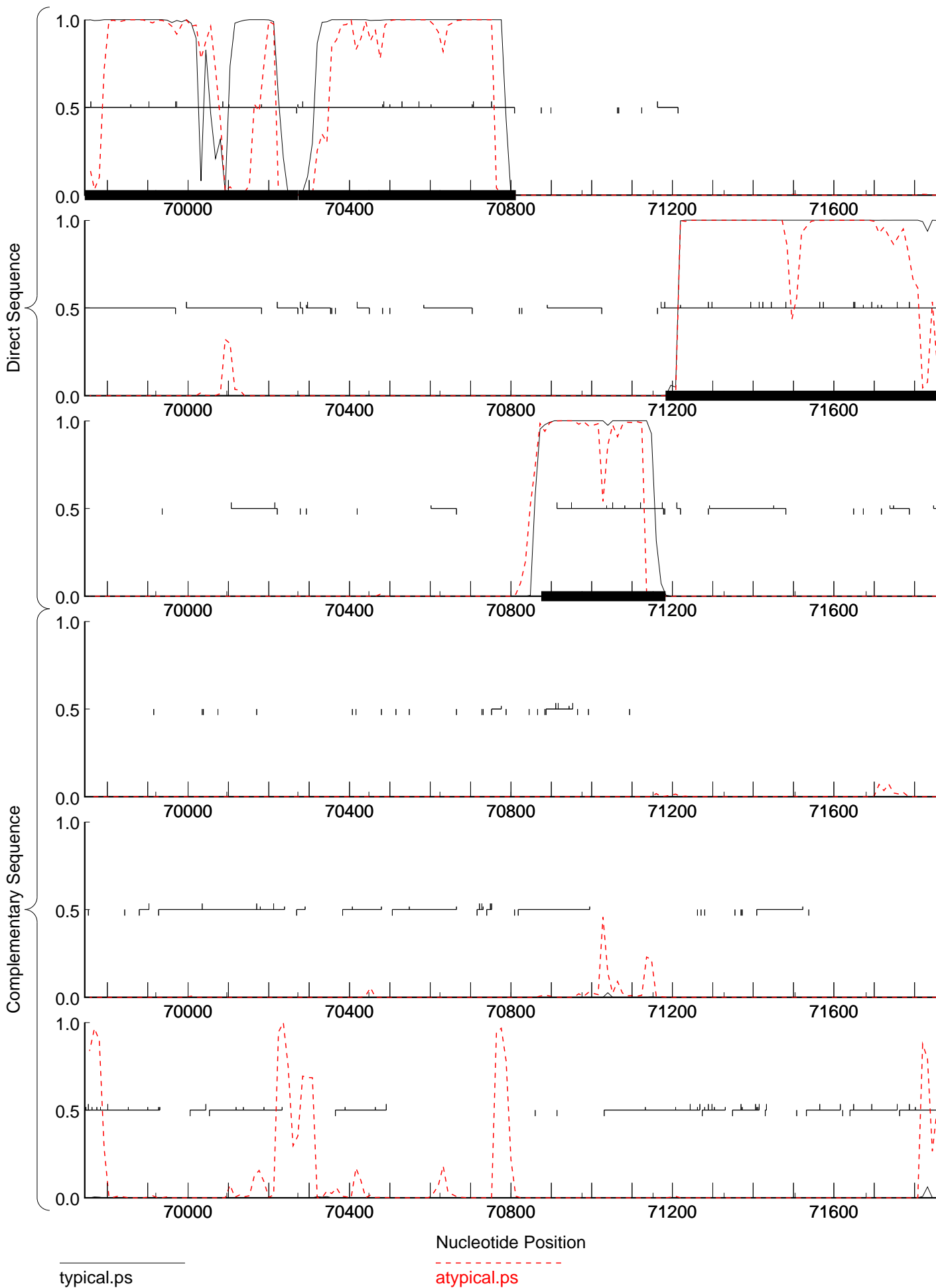


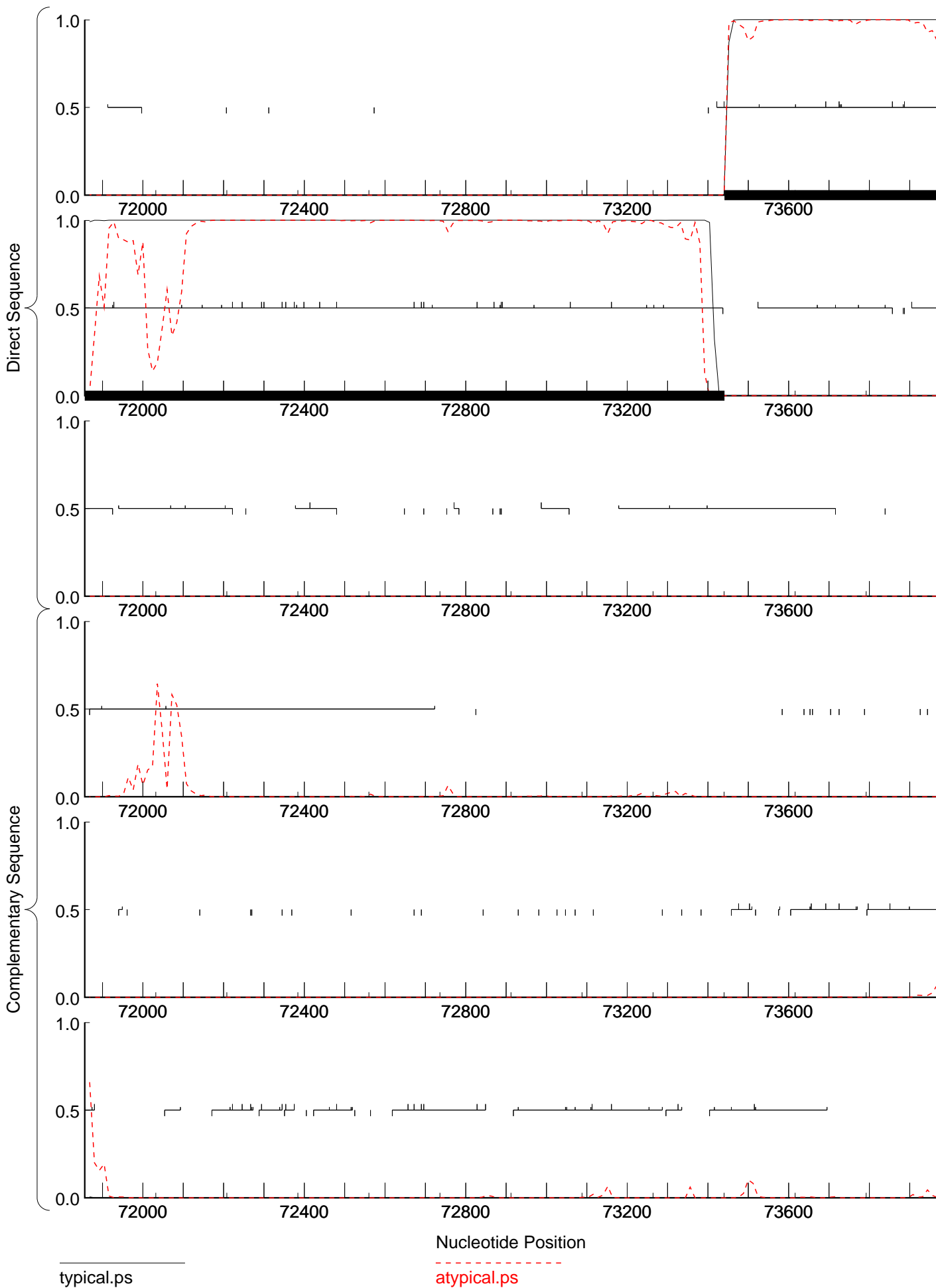


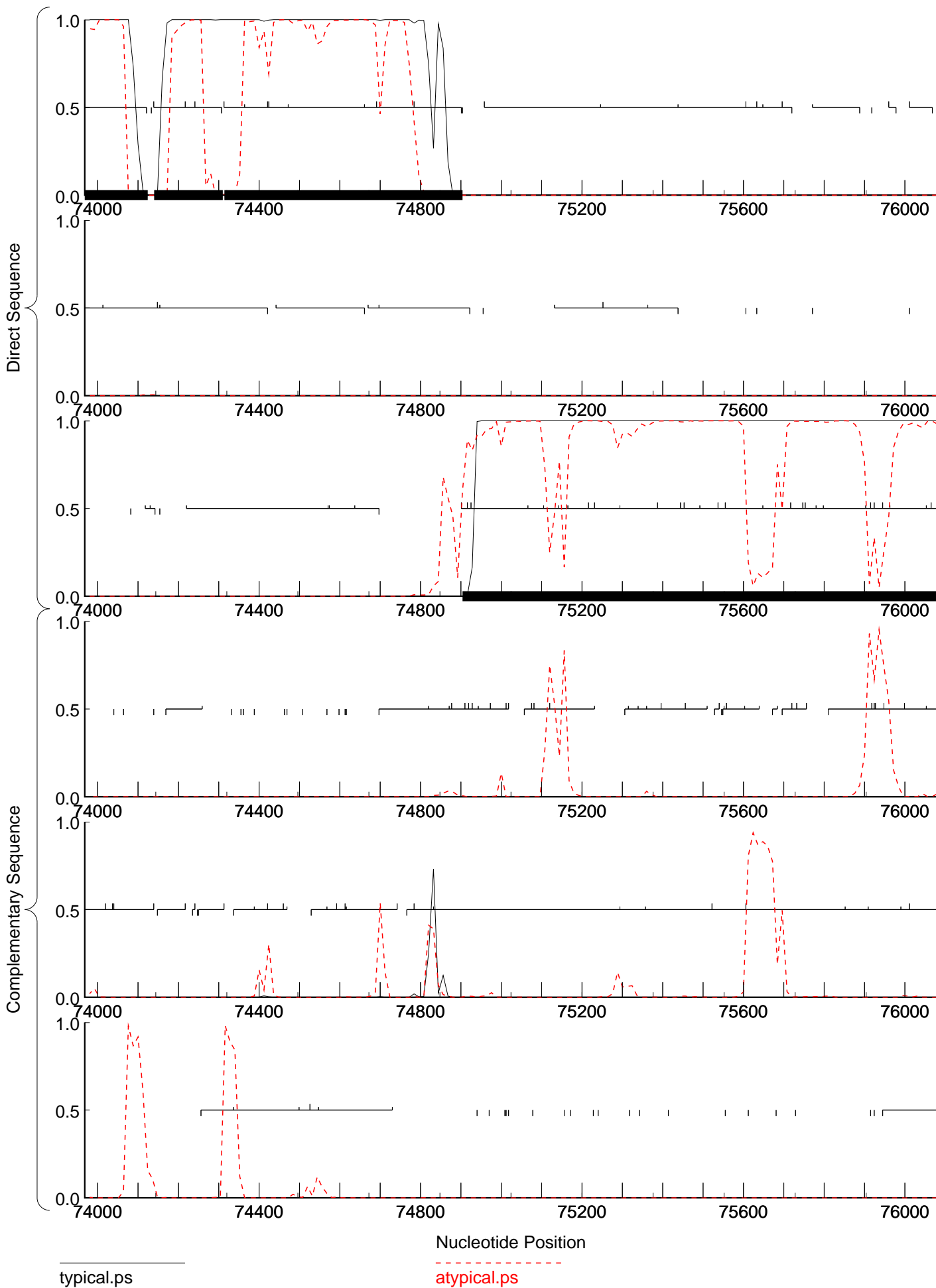
typical.ps

atypical.ps



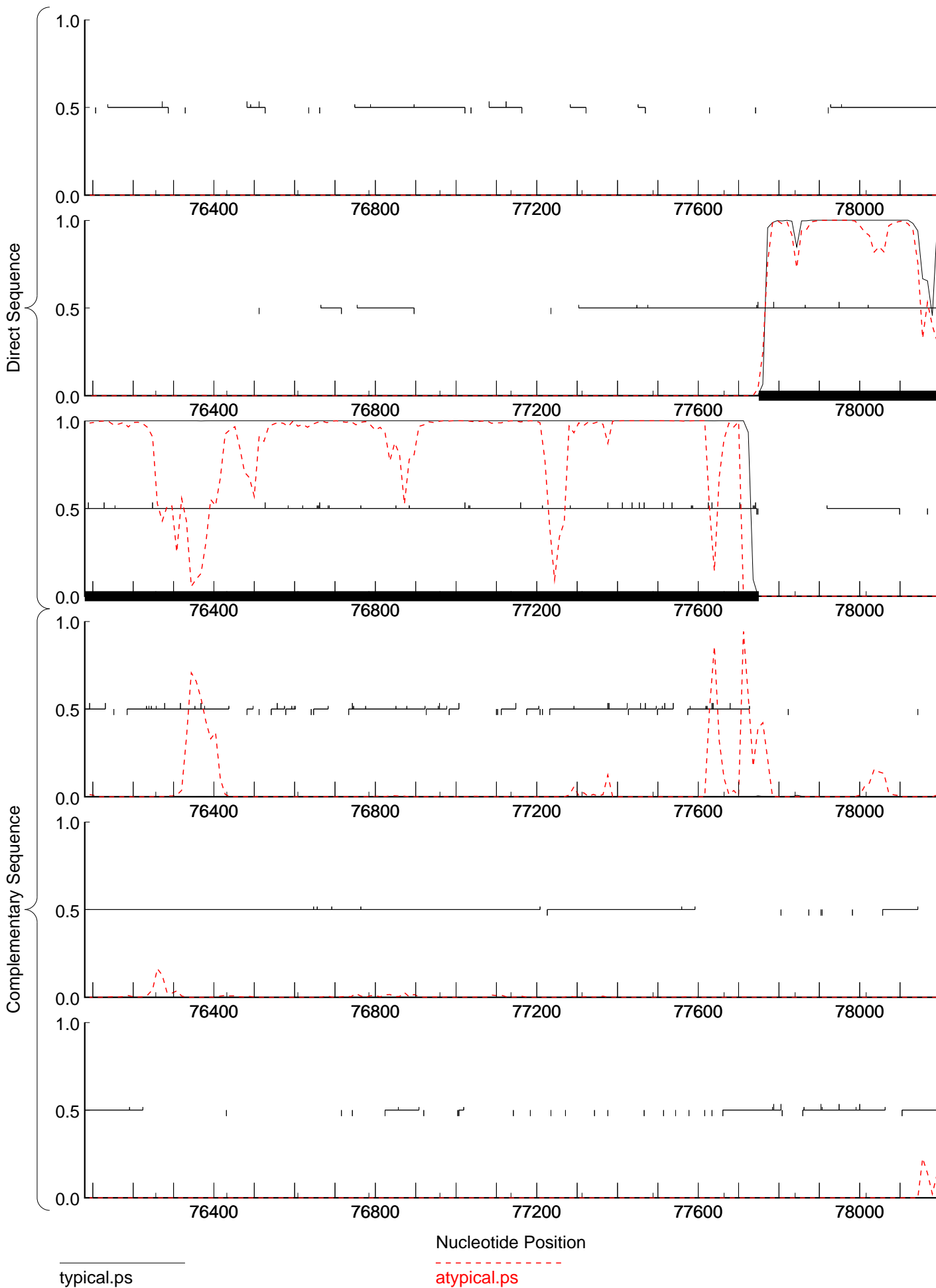






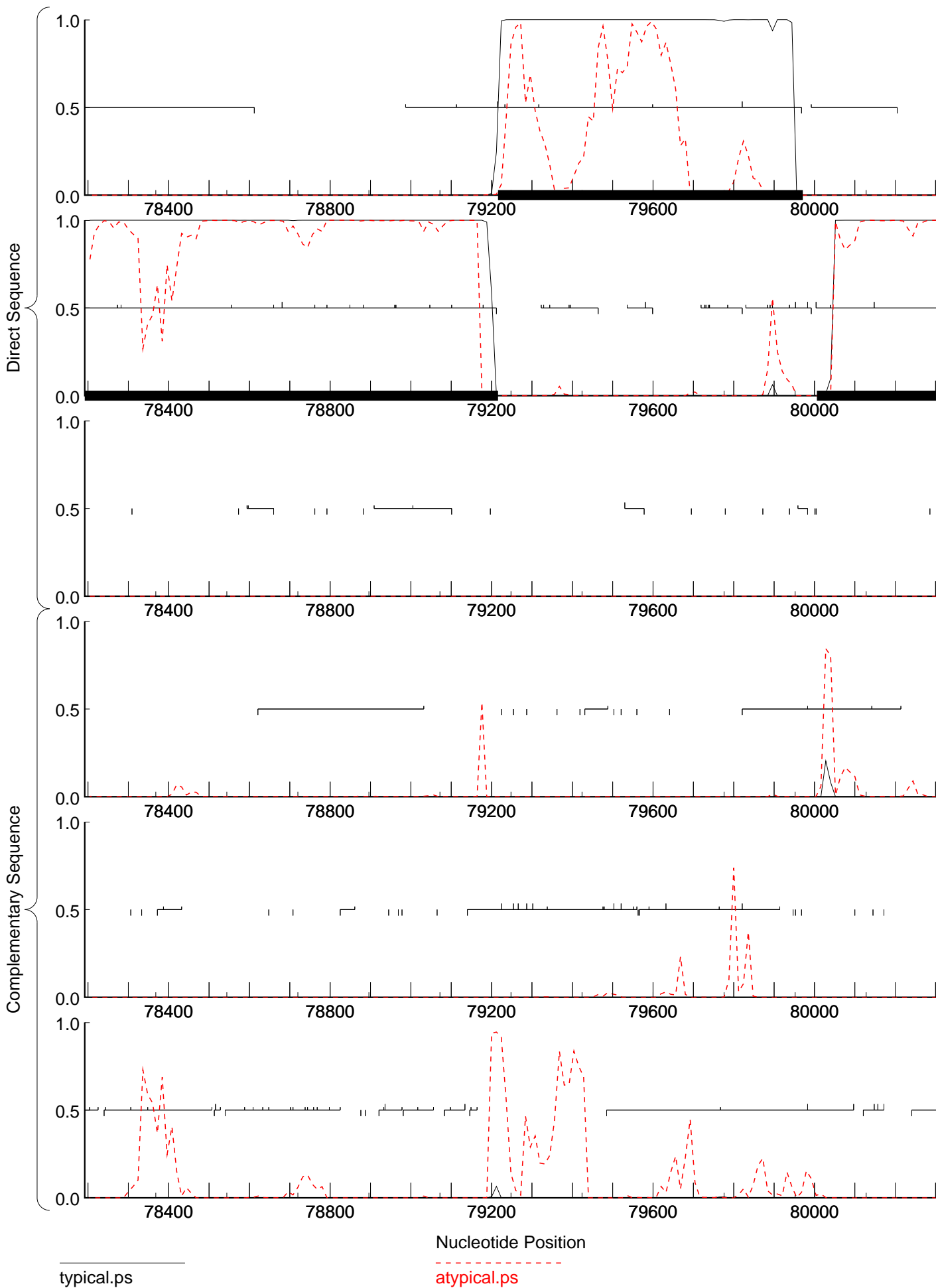
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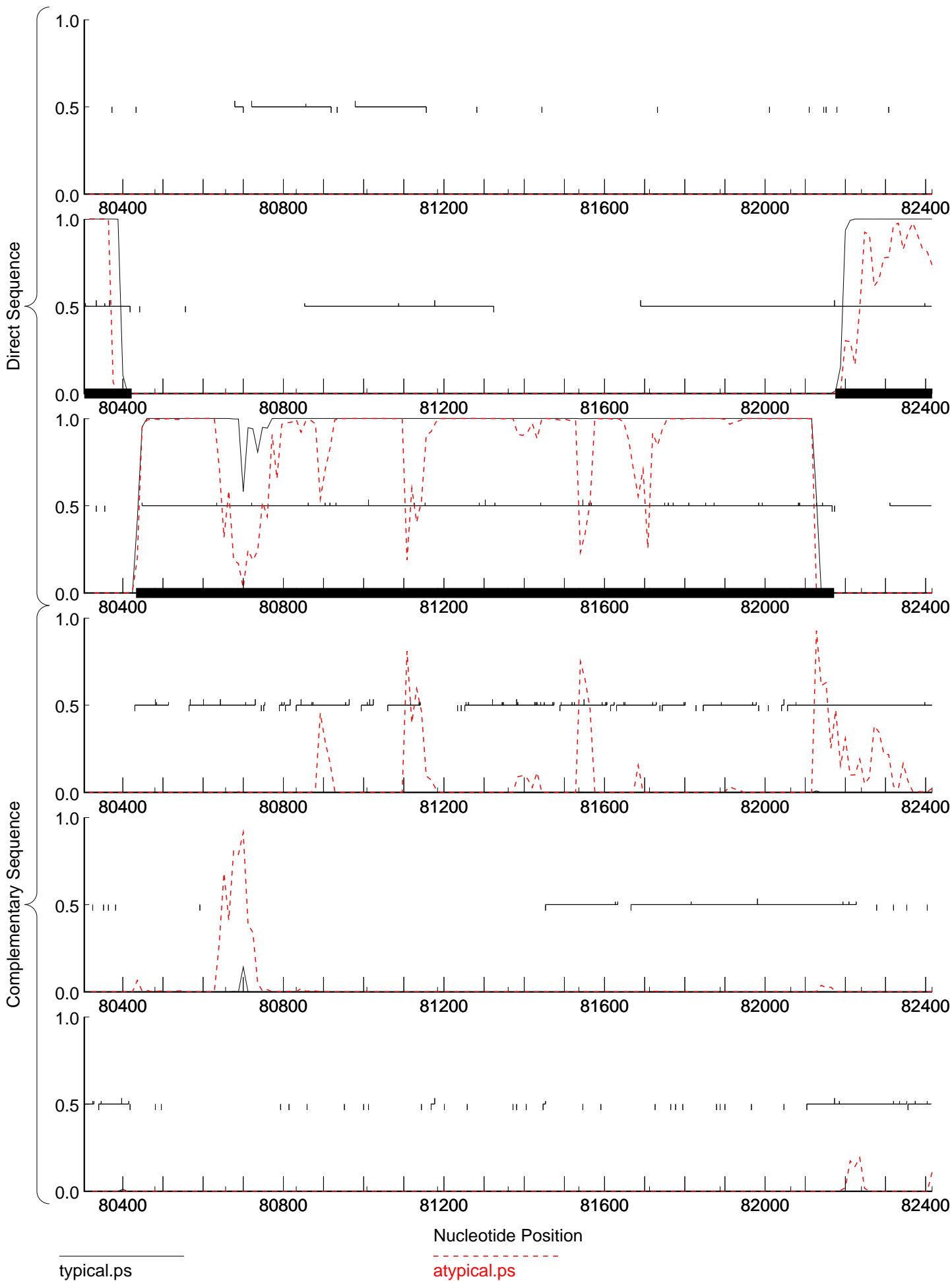
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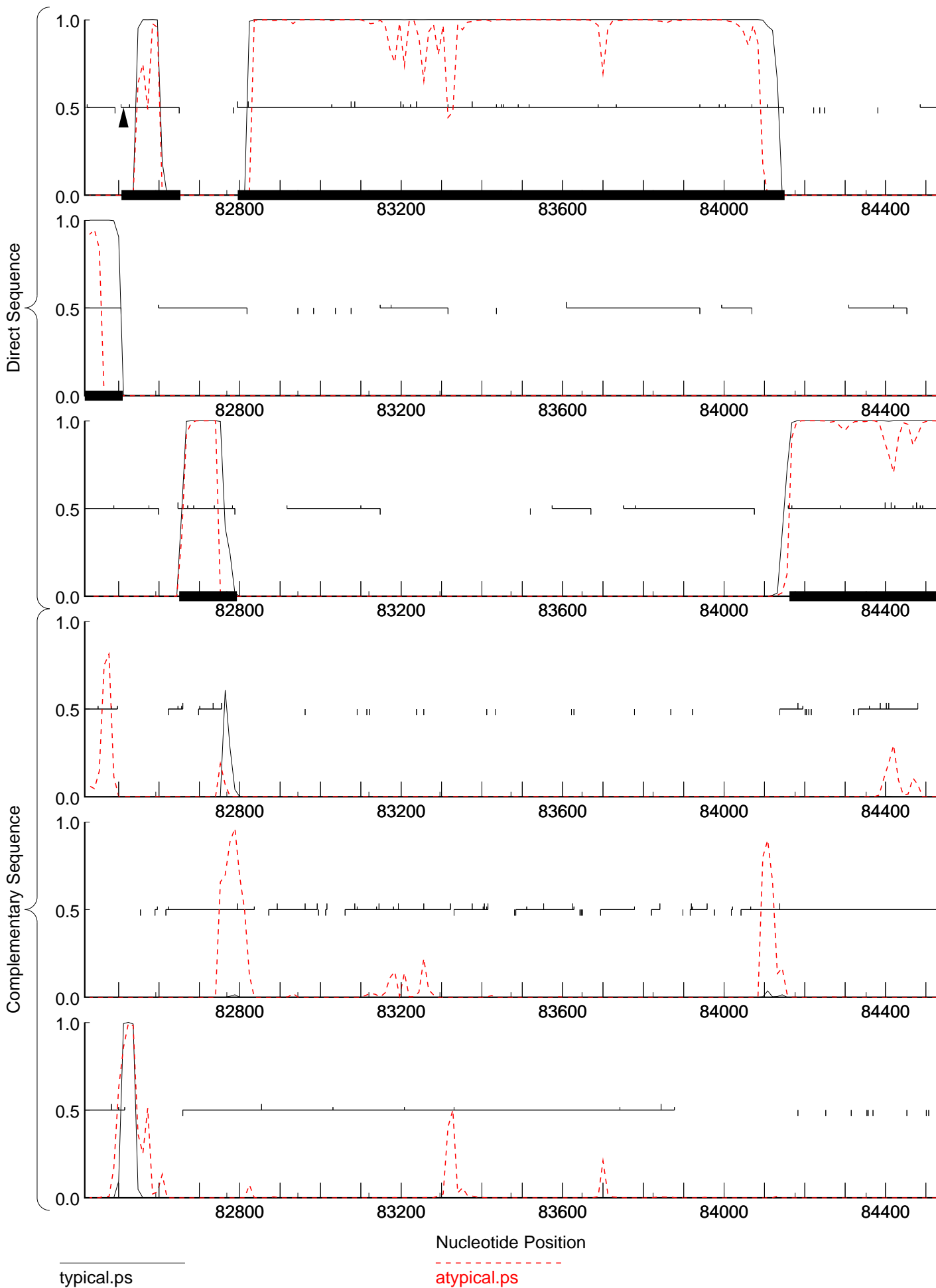


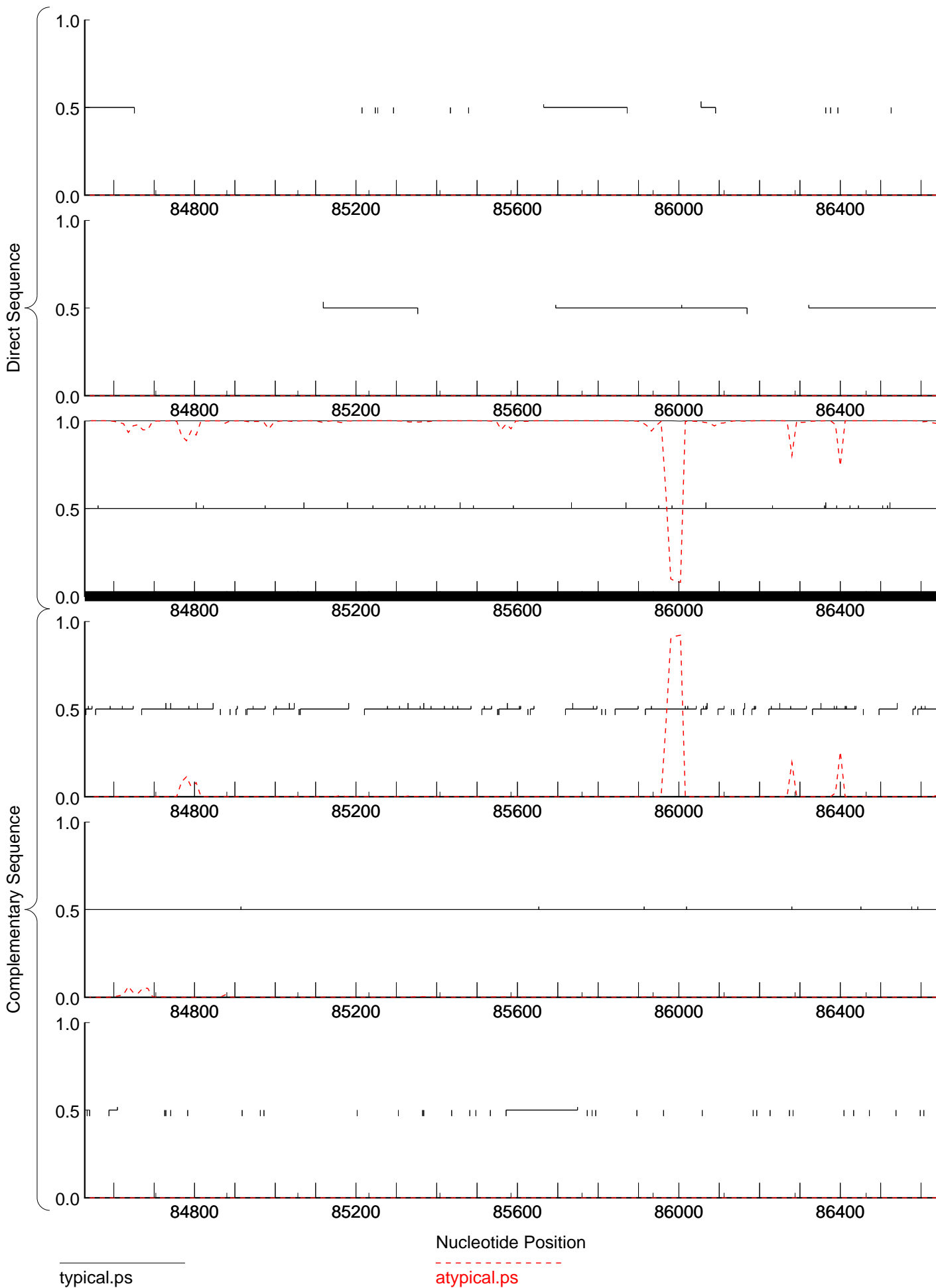
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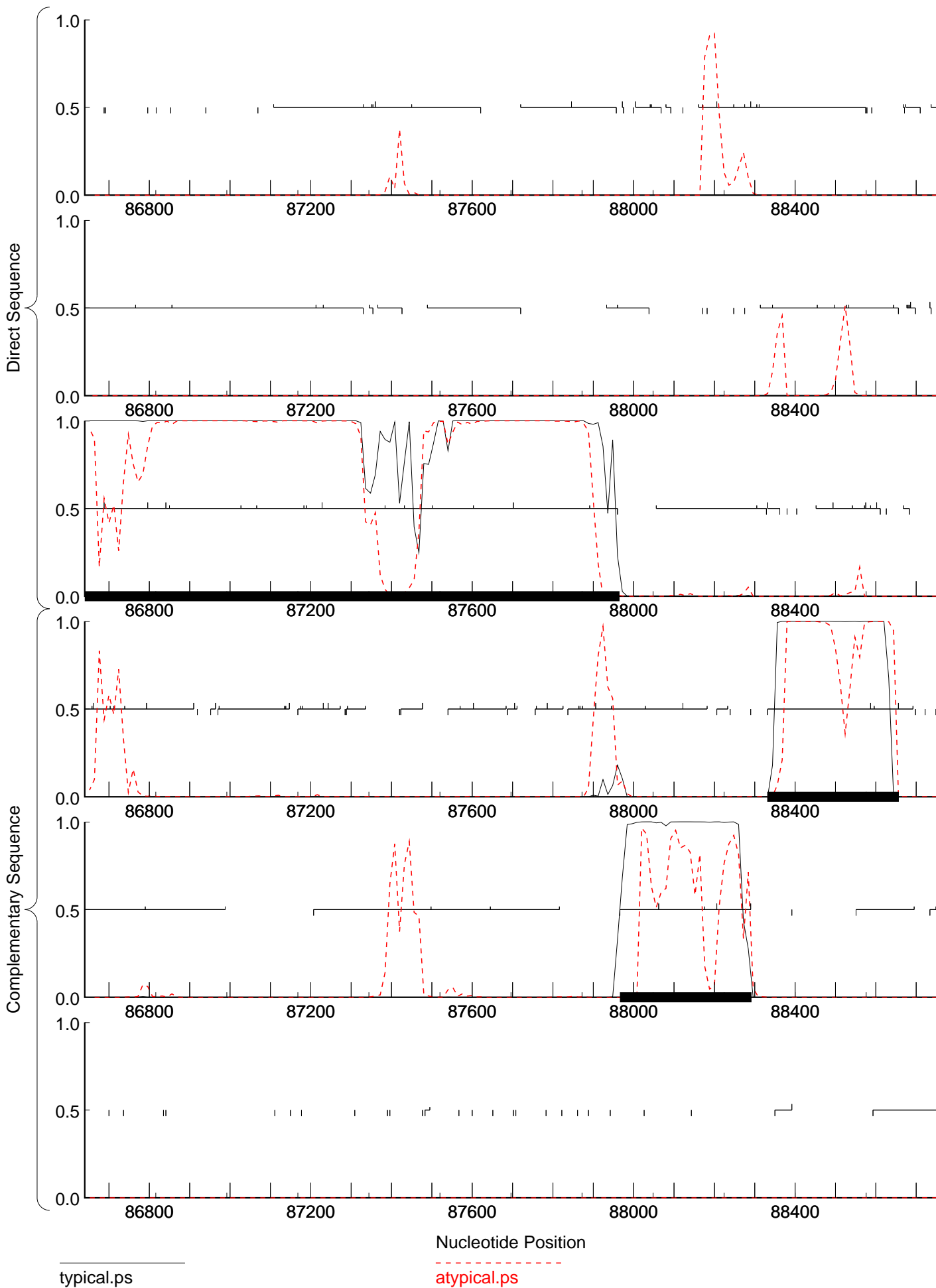
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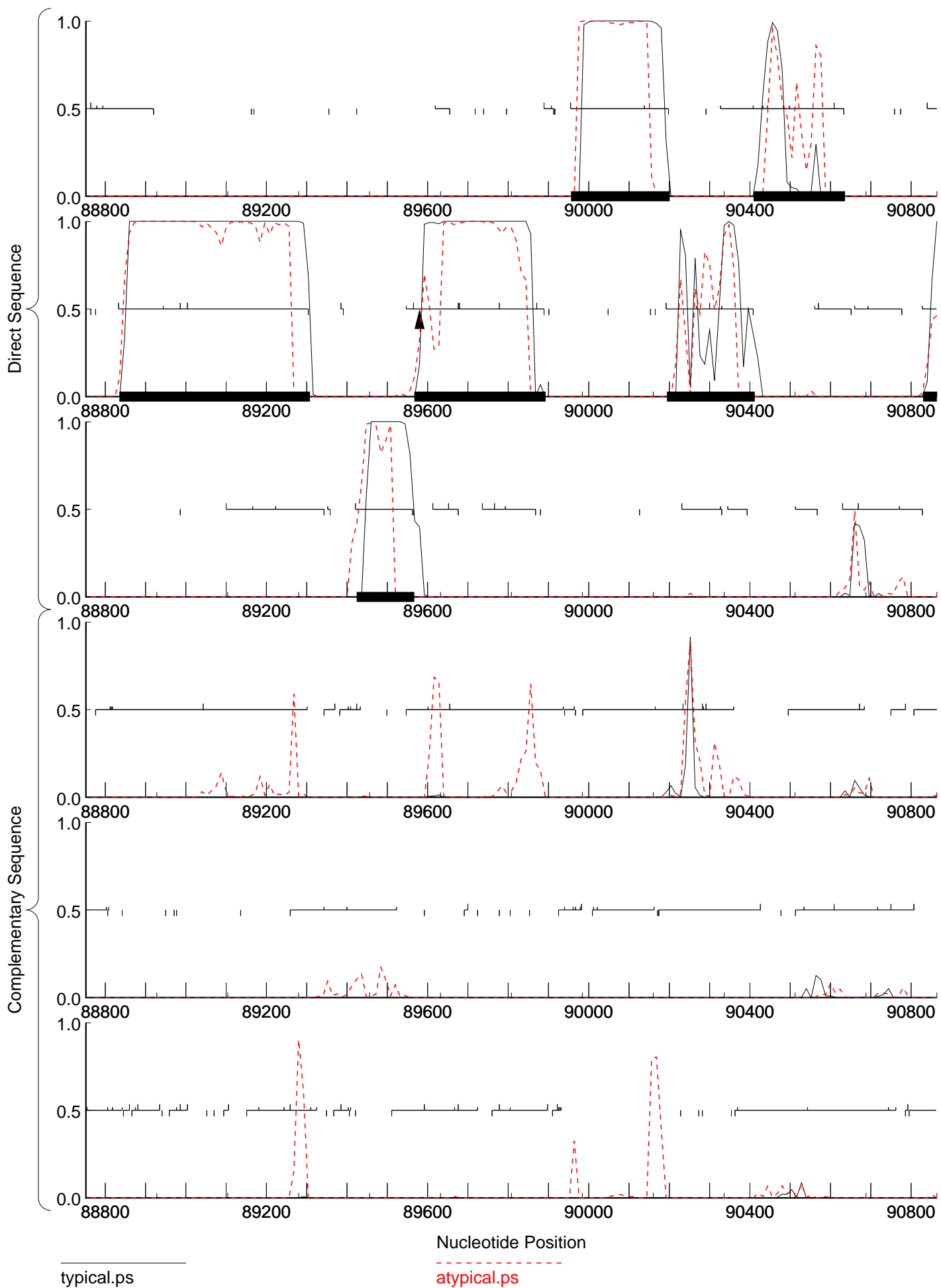






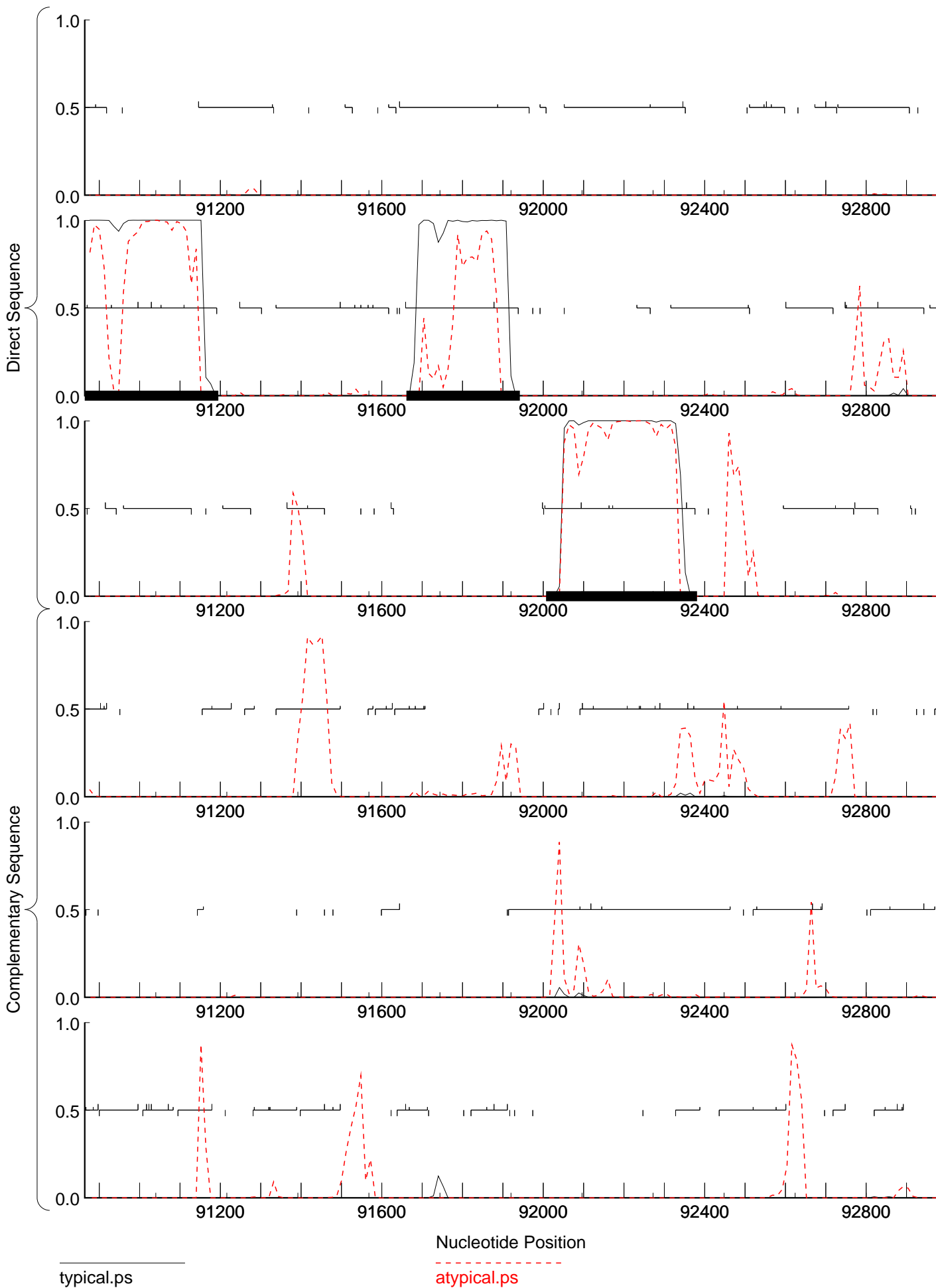


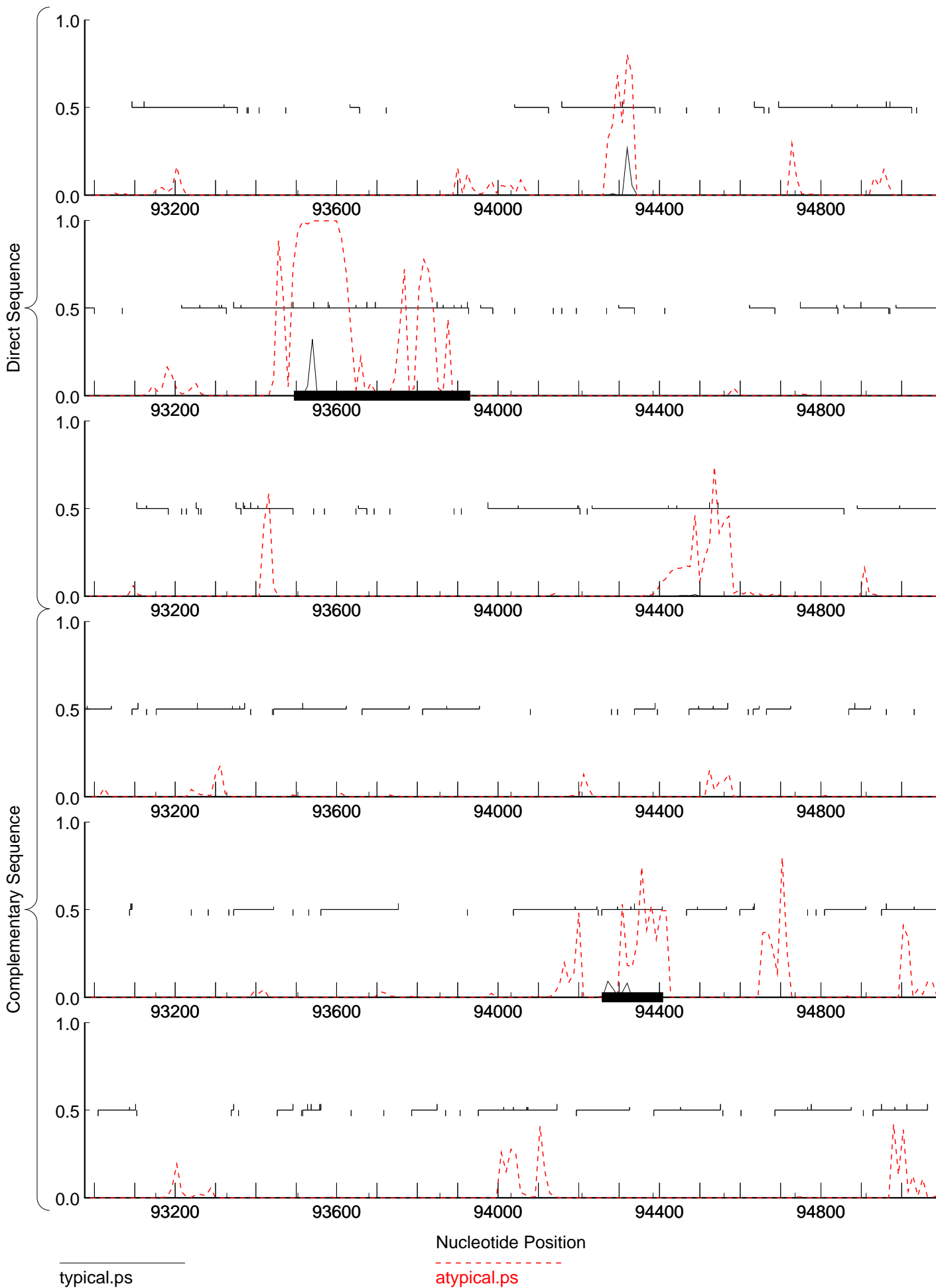
GeneMark.hmm prediction



typical.ps

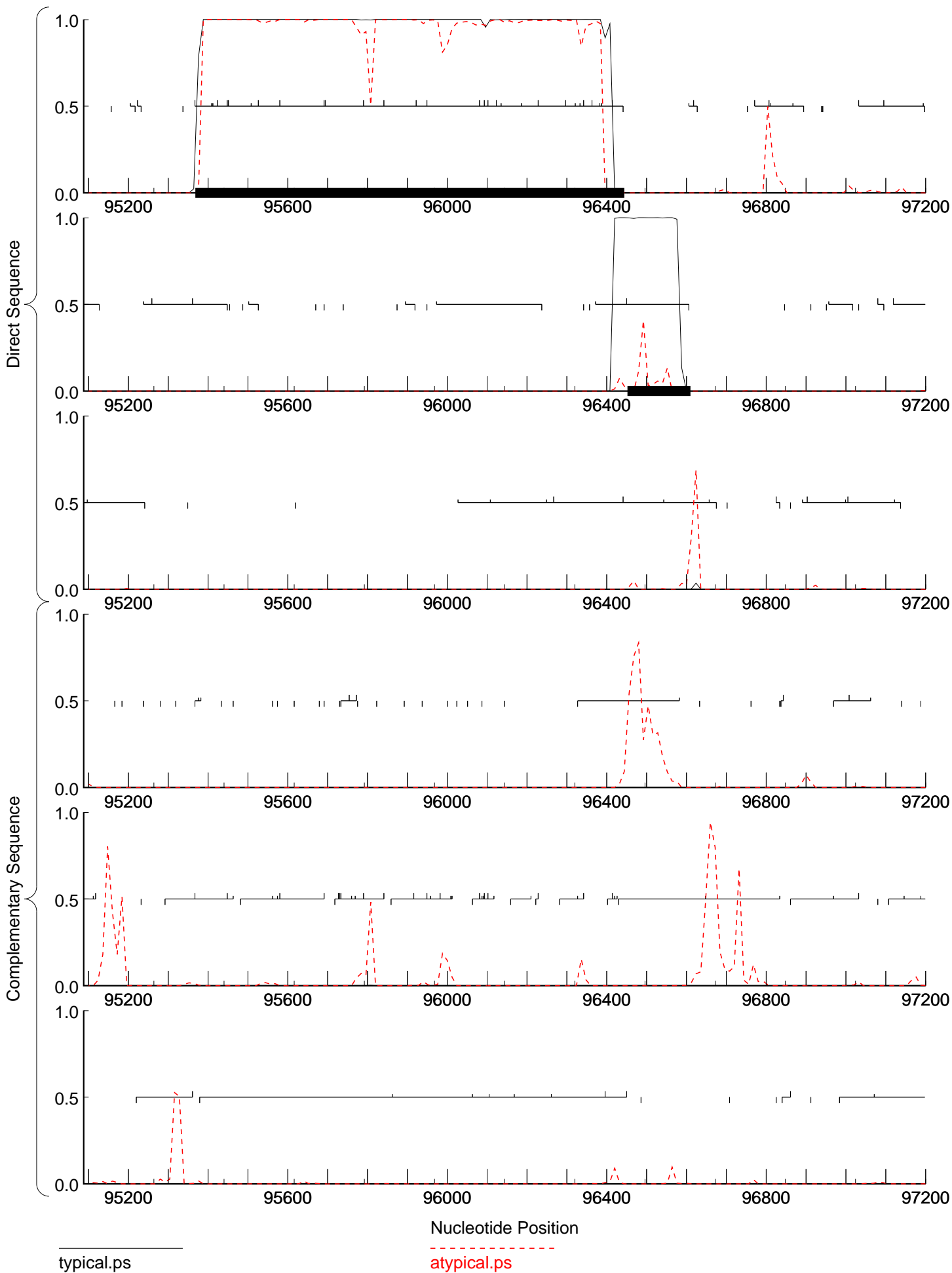
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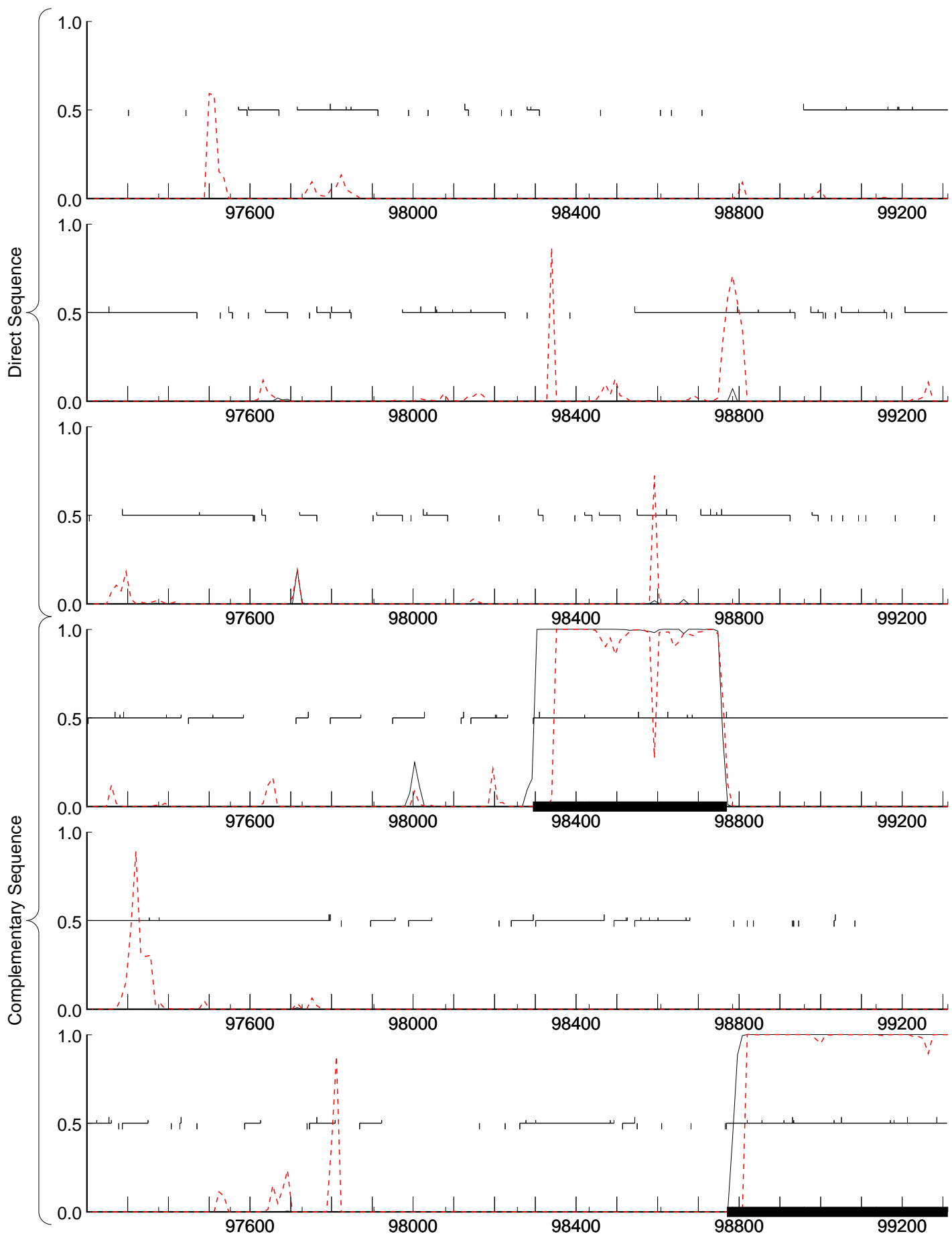


typical.ps

atypical.ps

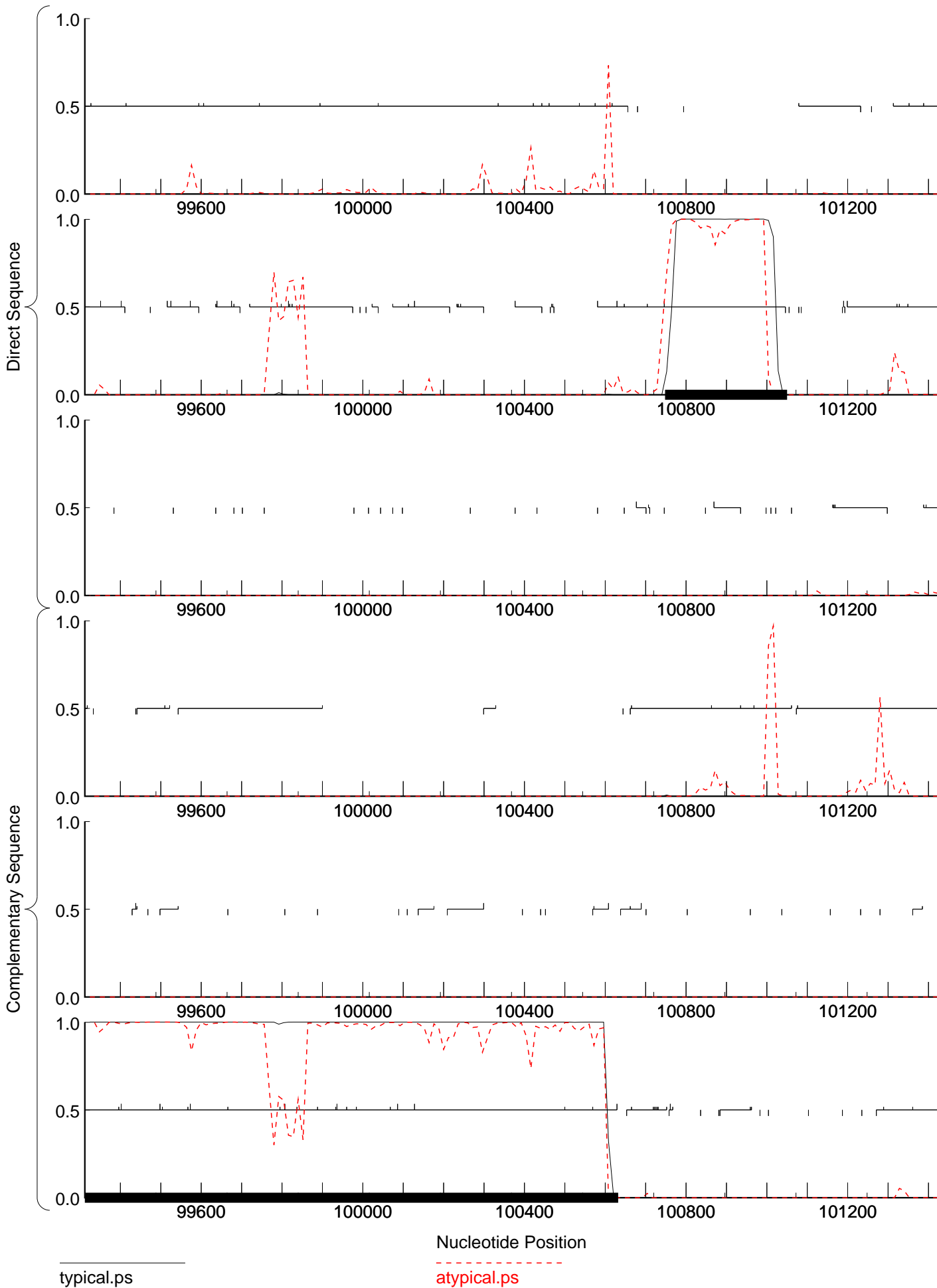


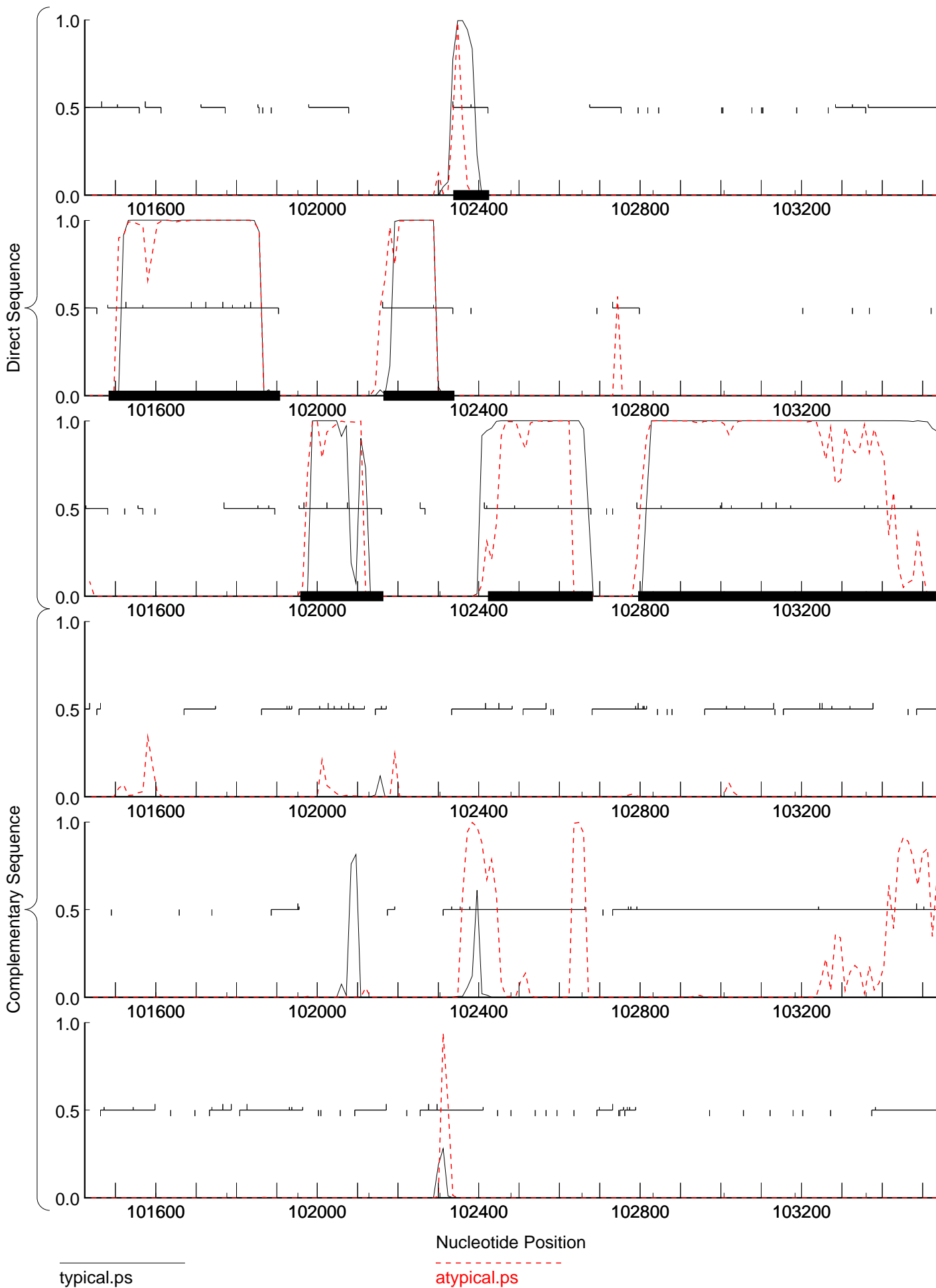
GeneMark.hmm prediction

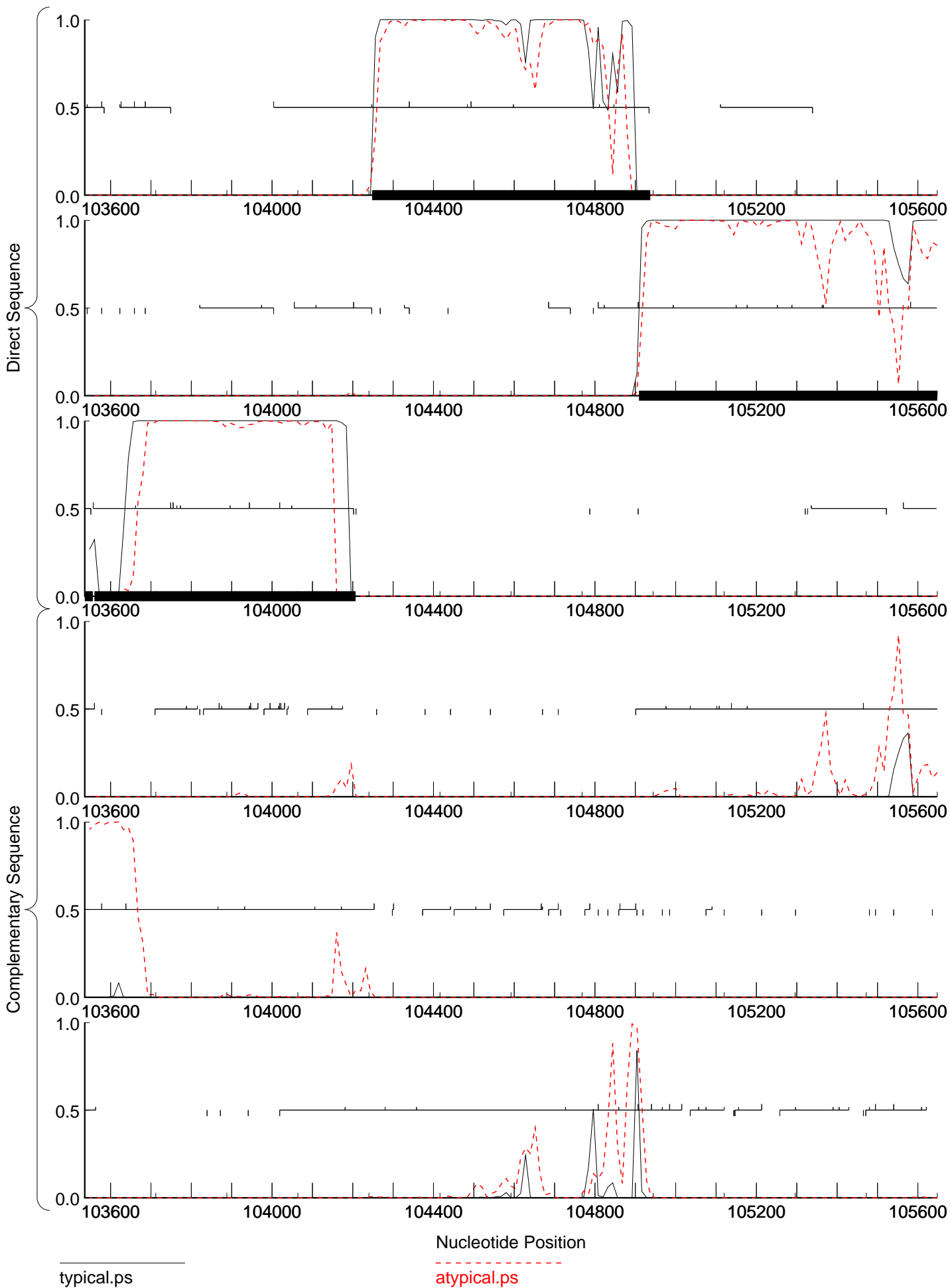


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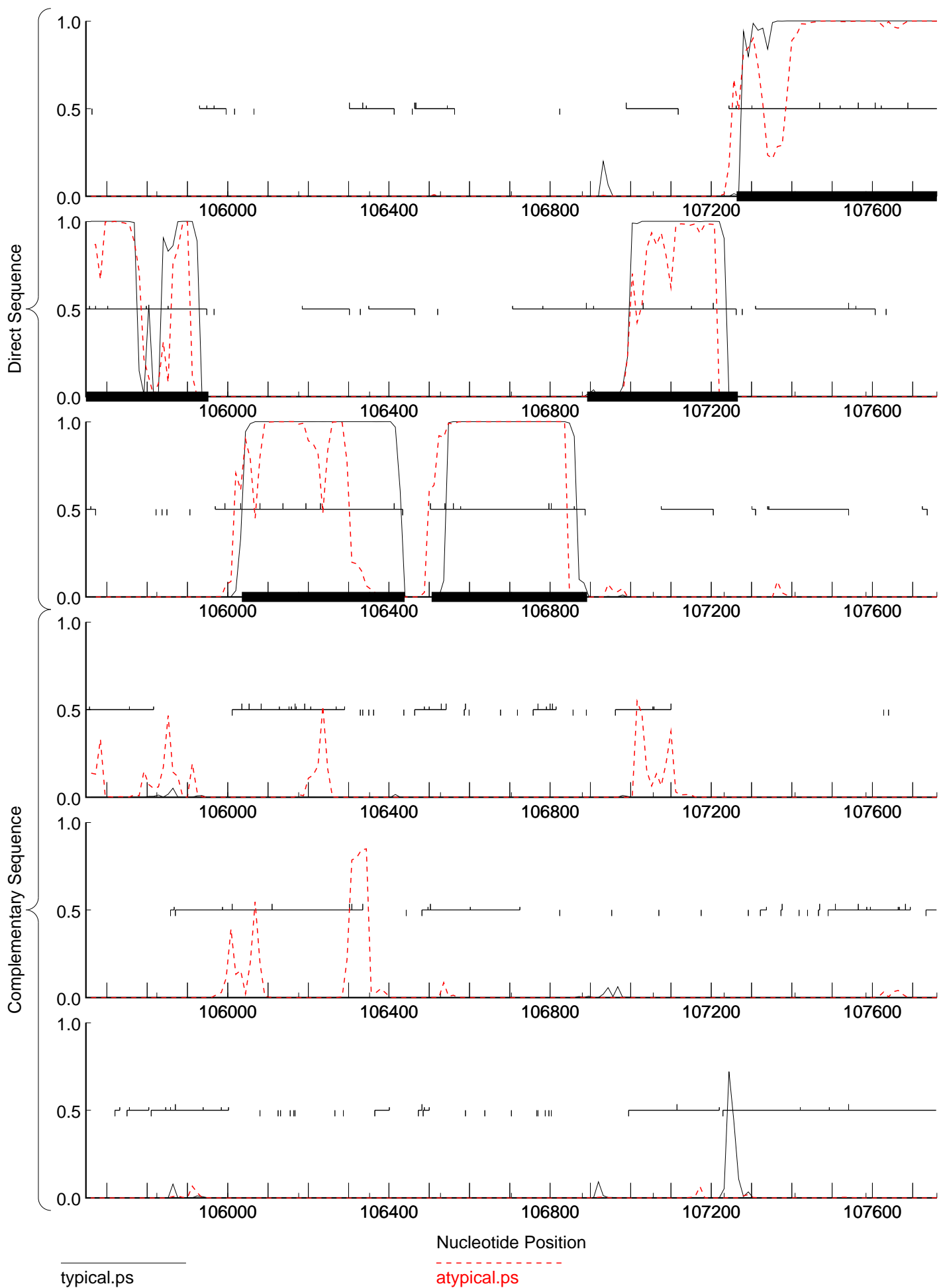
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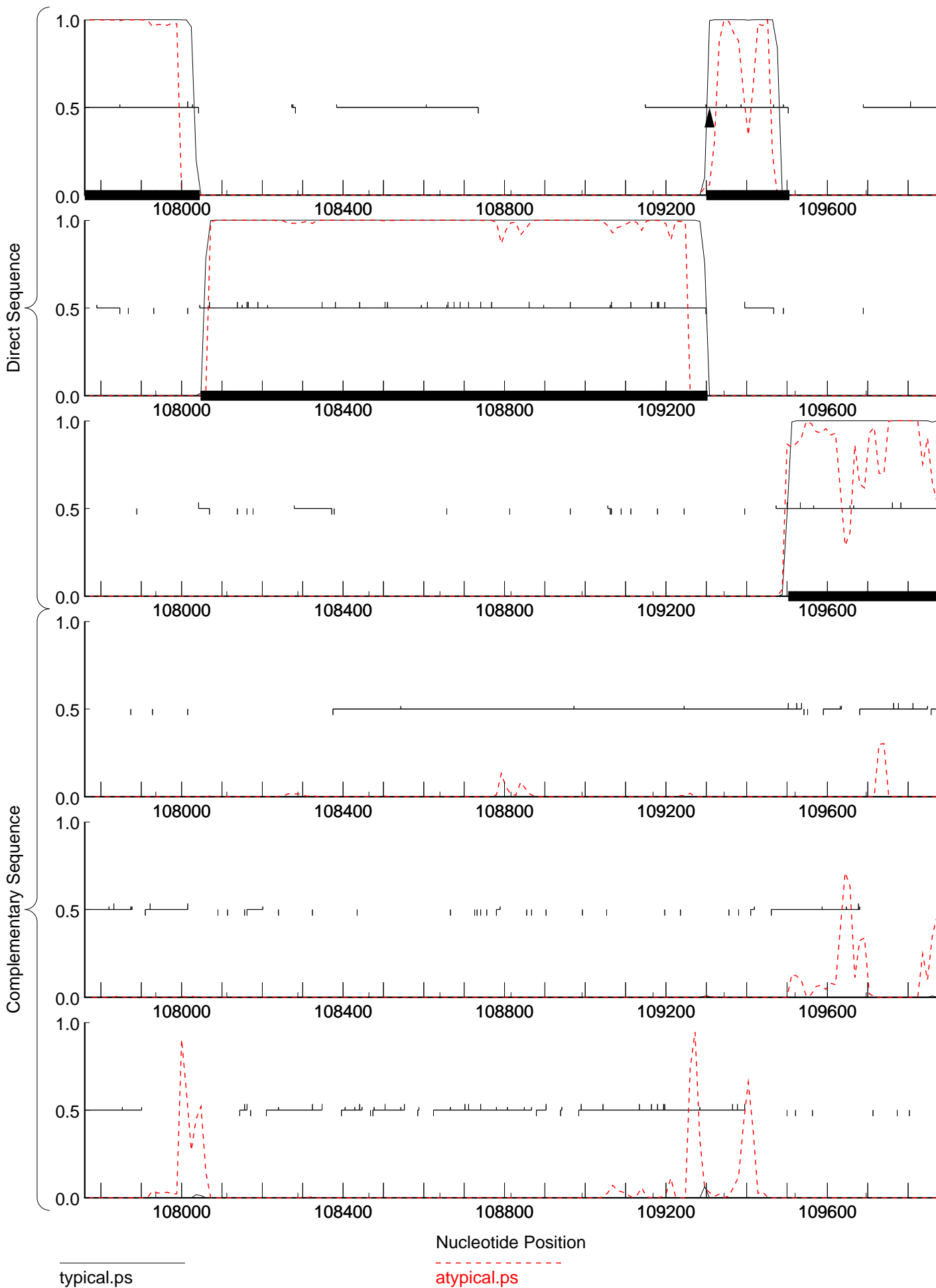


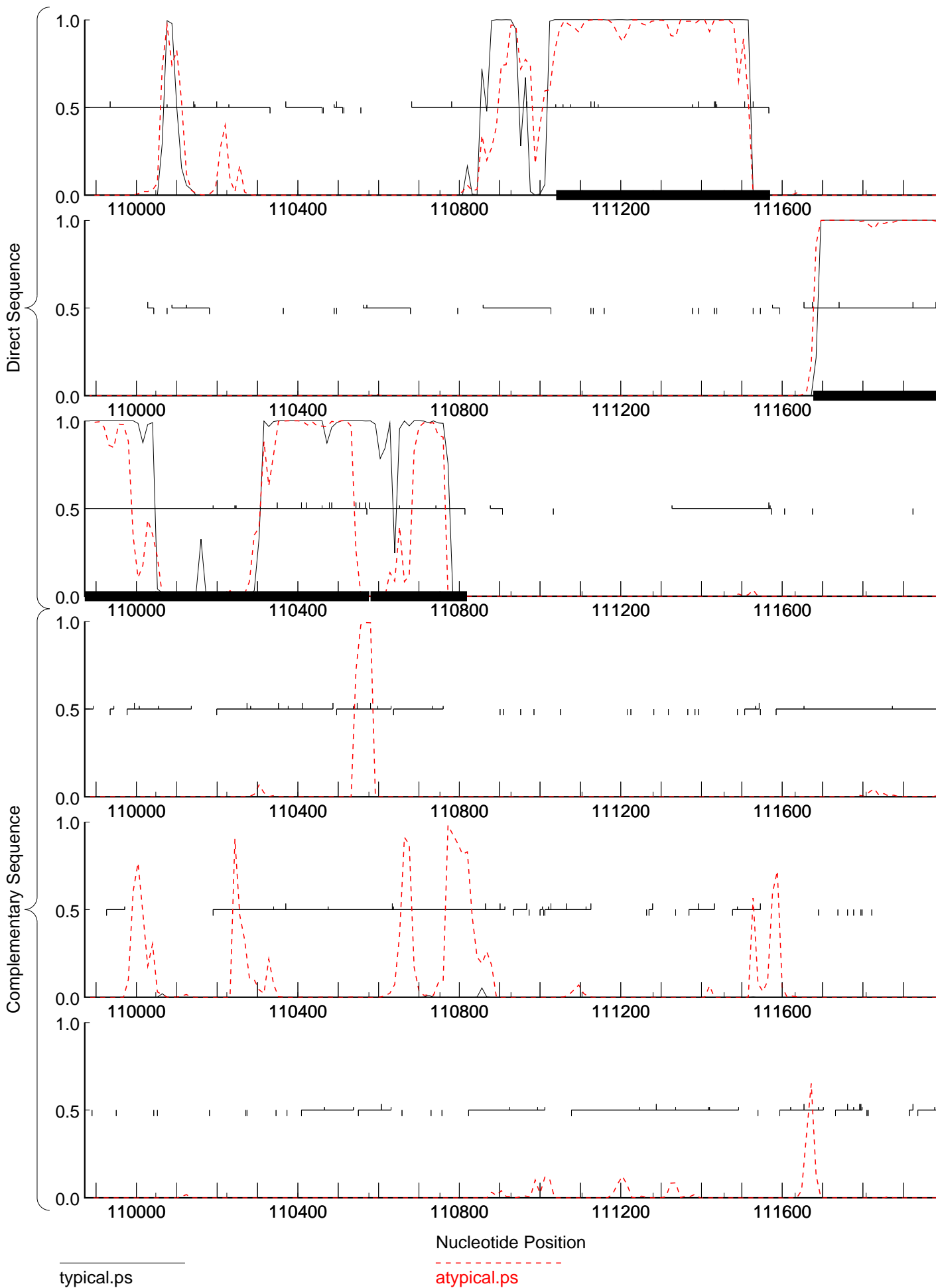




GeneMark.hmm prediction

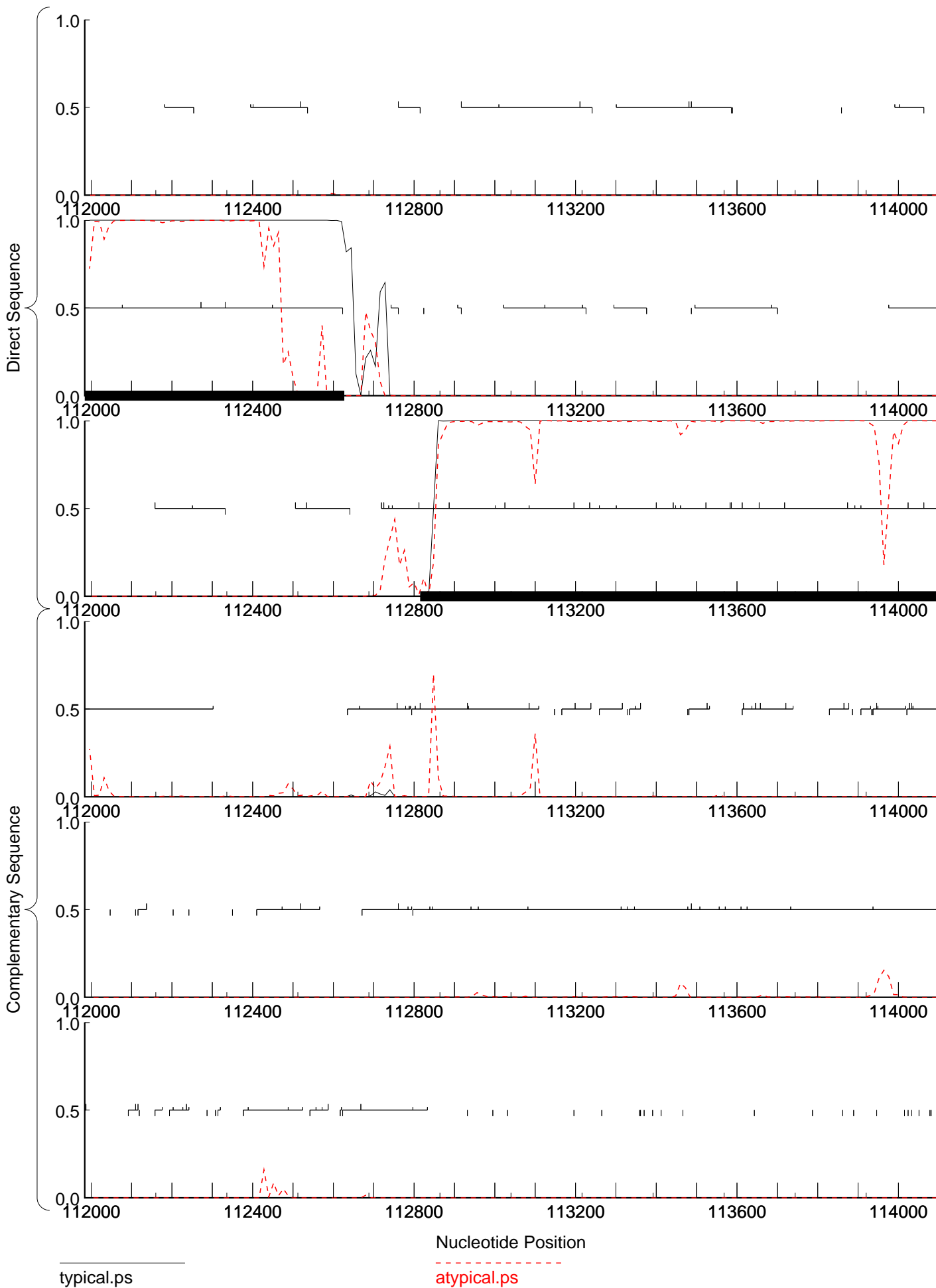


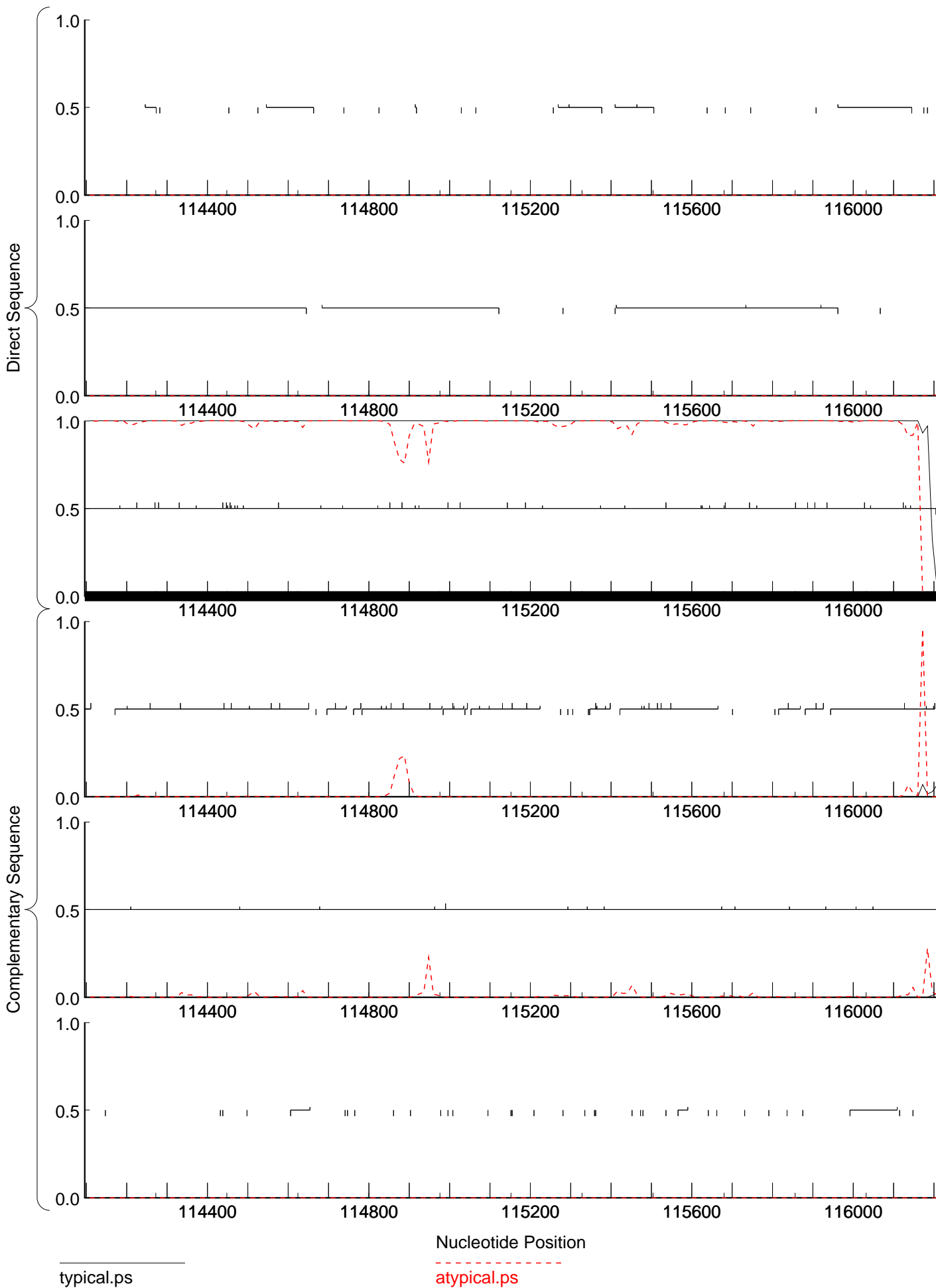


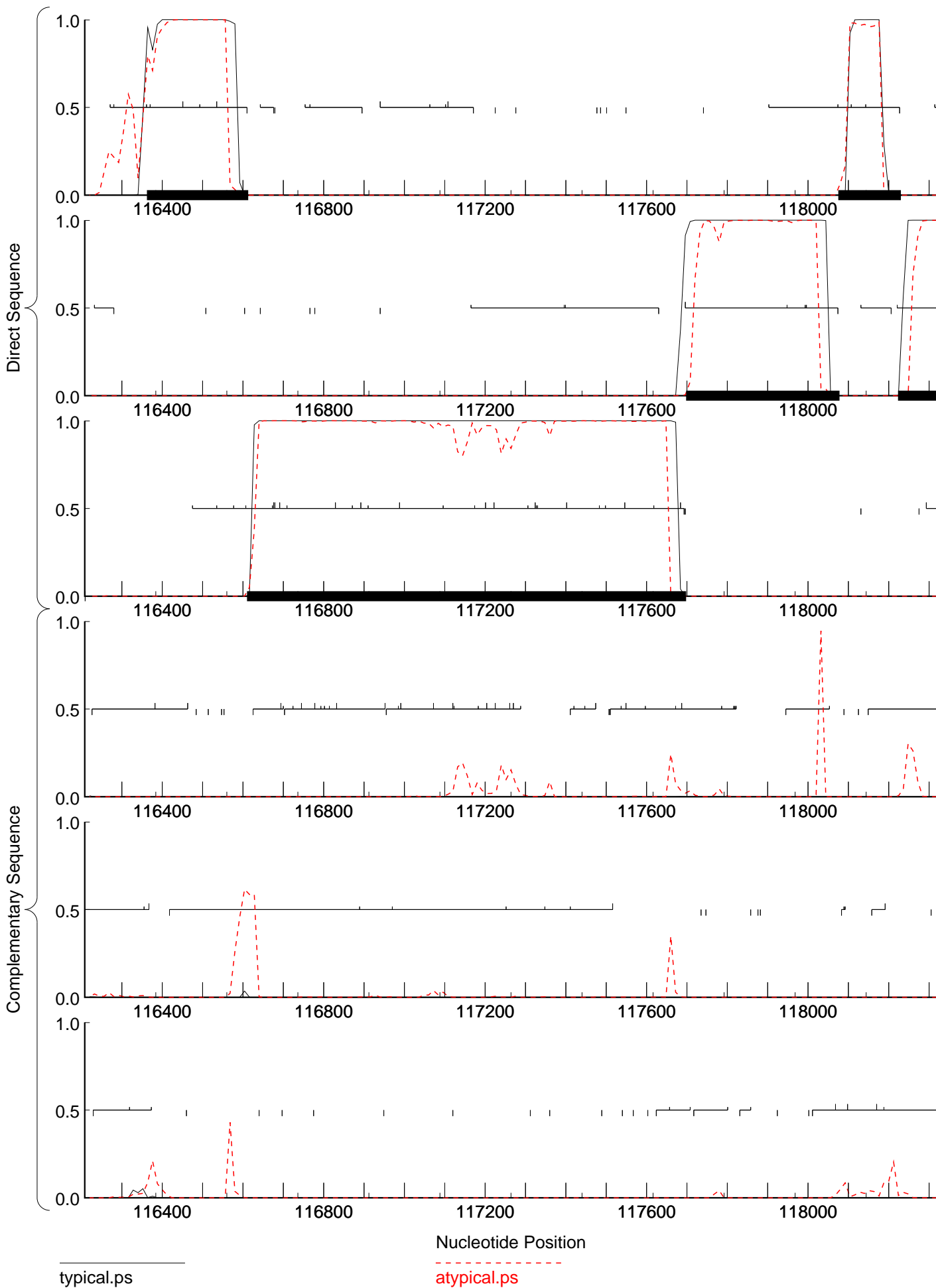


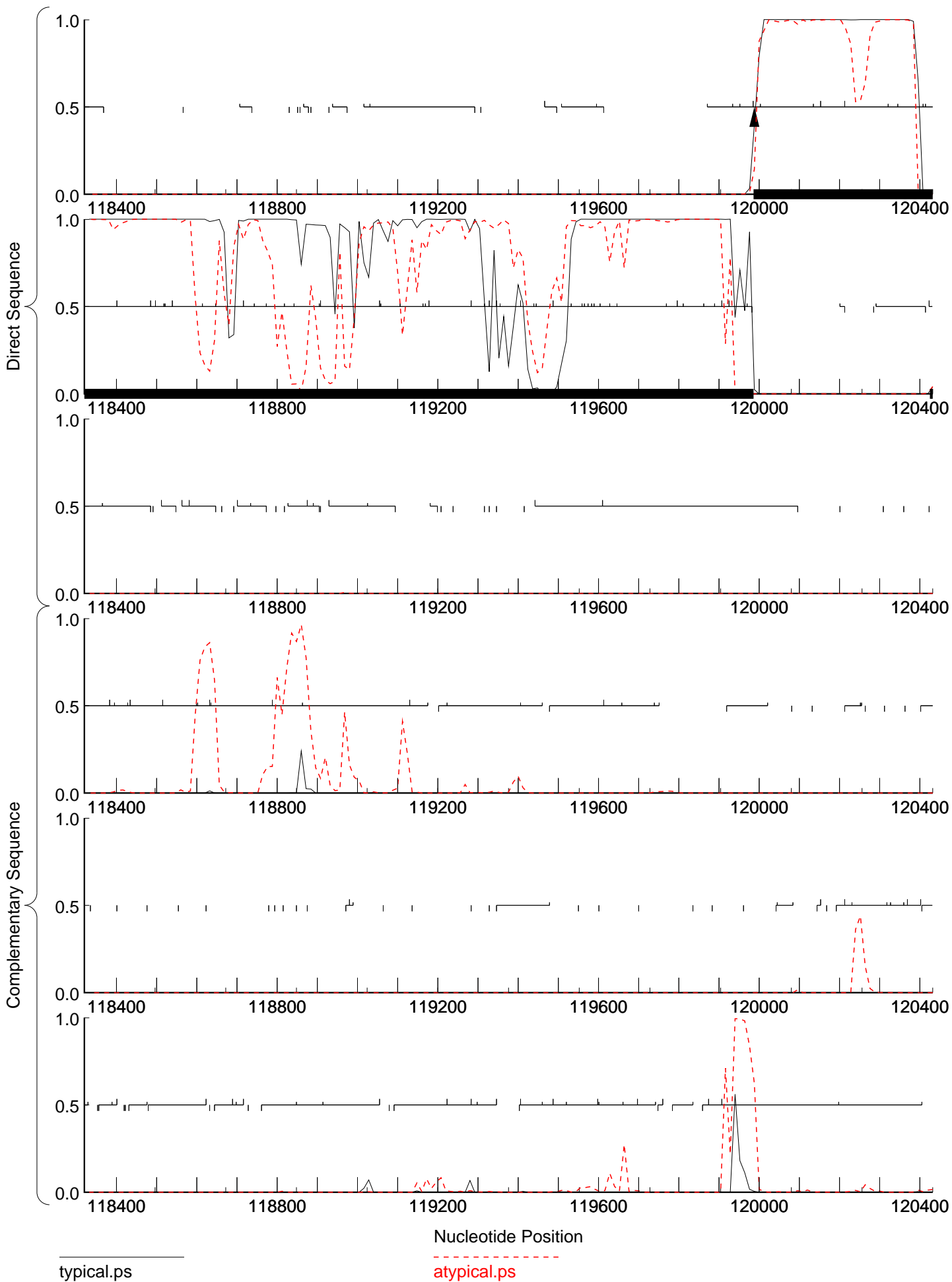
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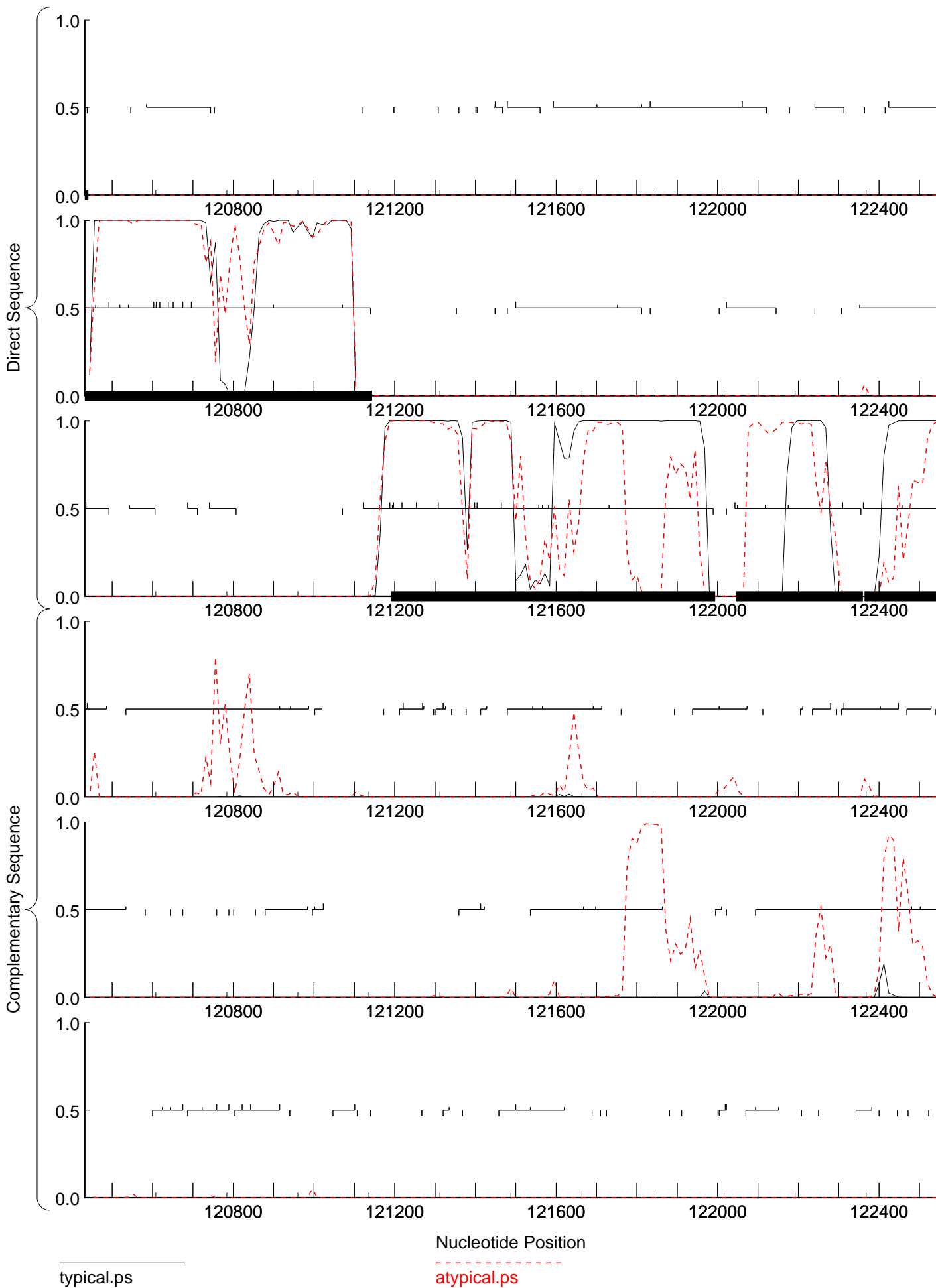
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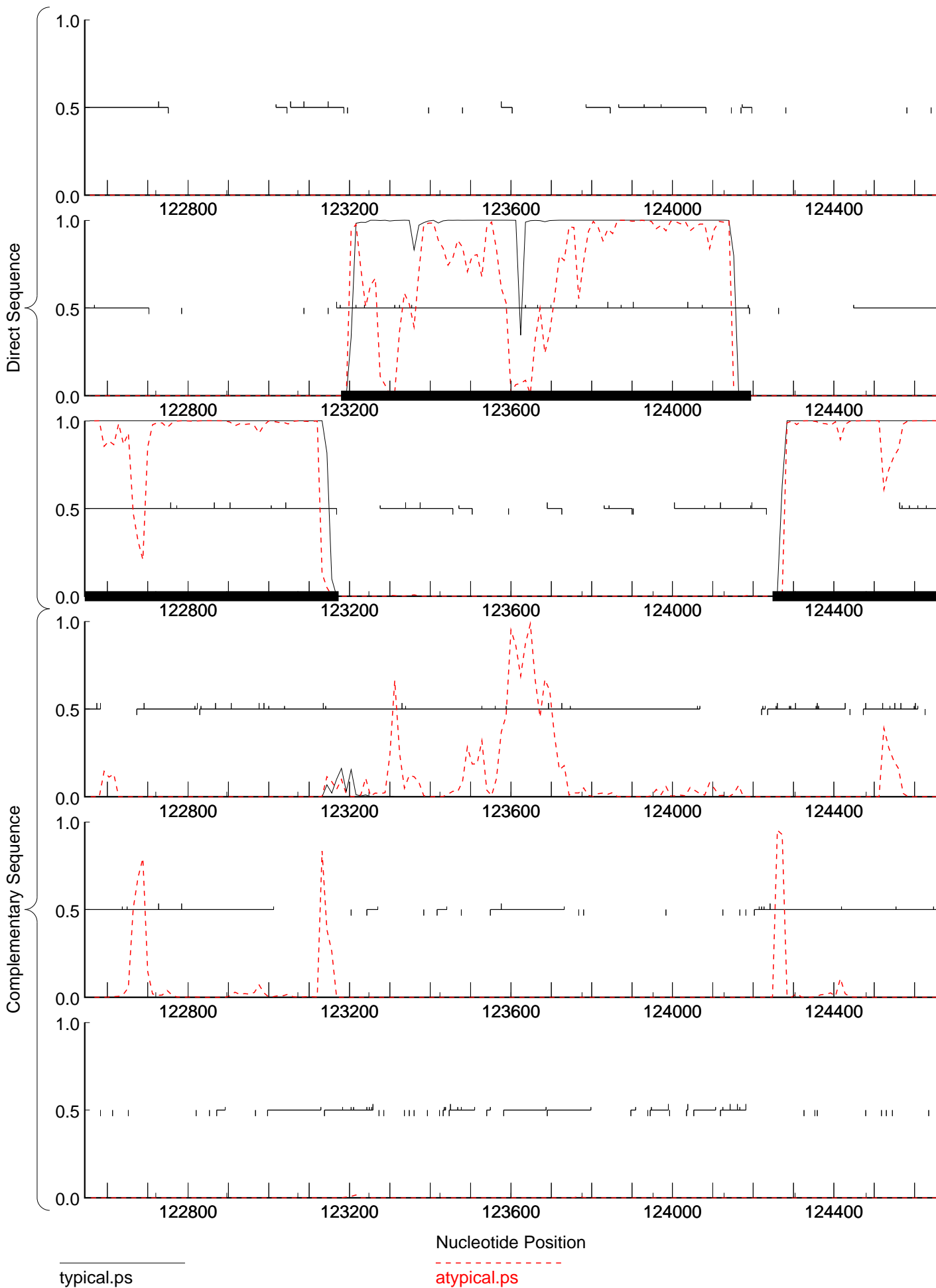








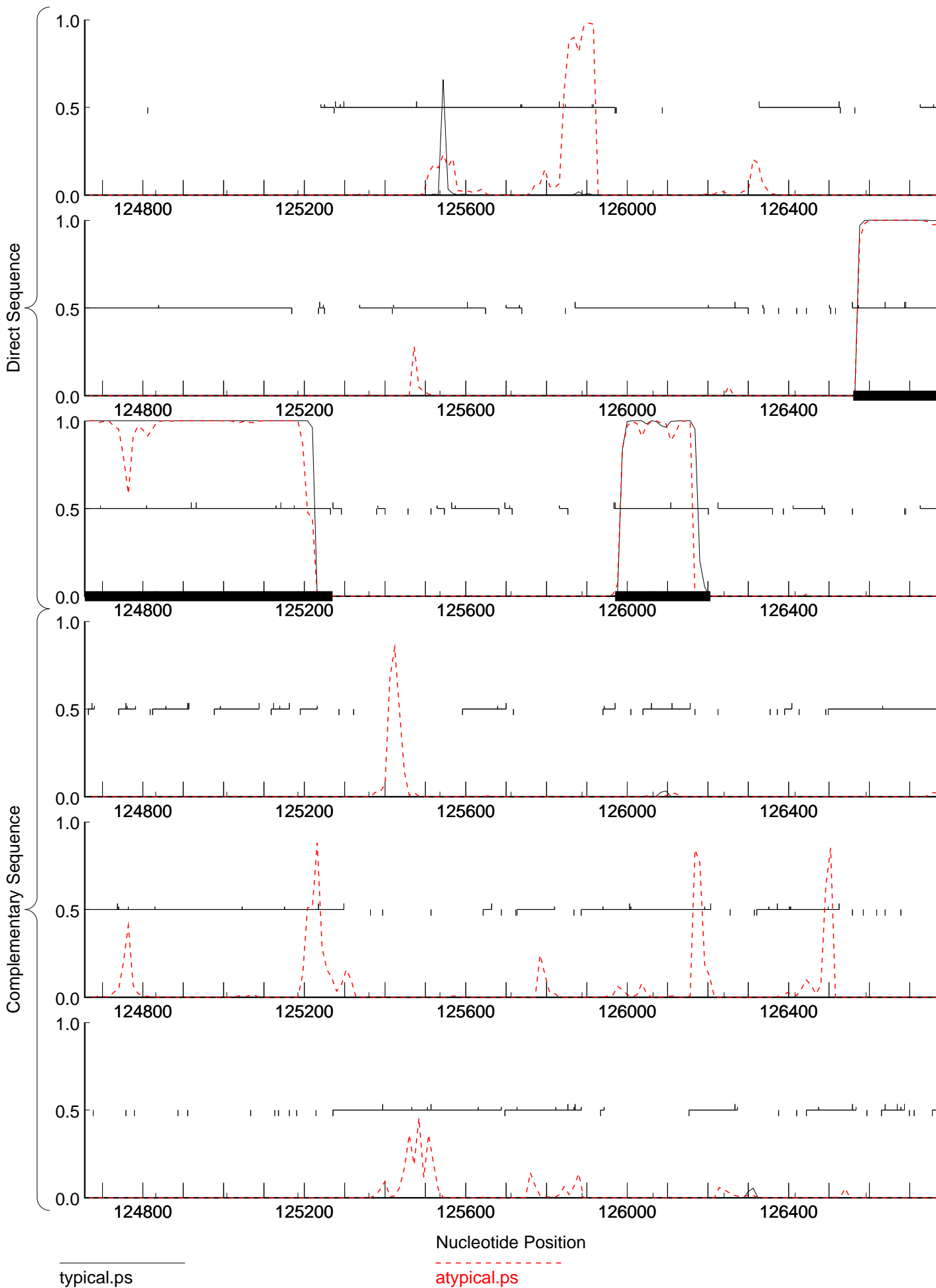




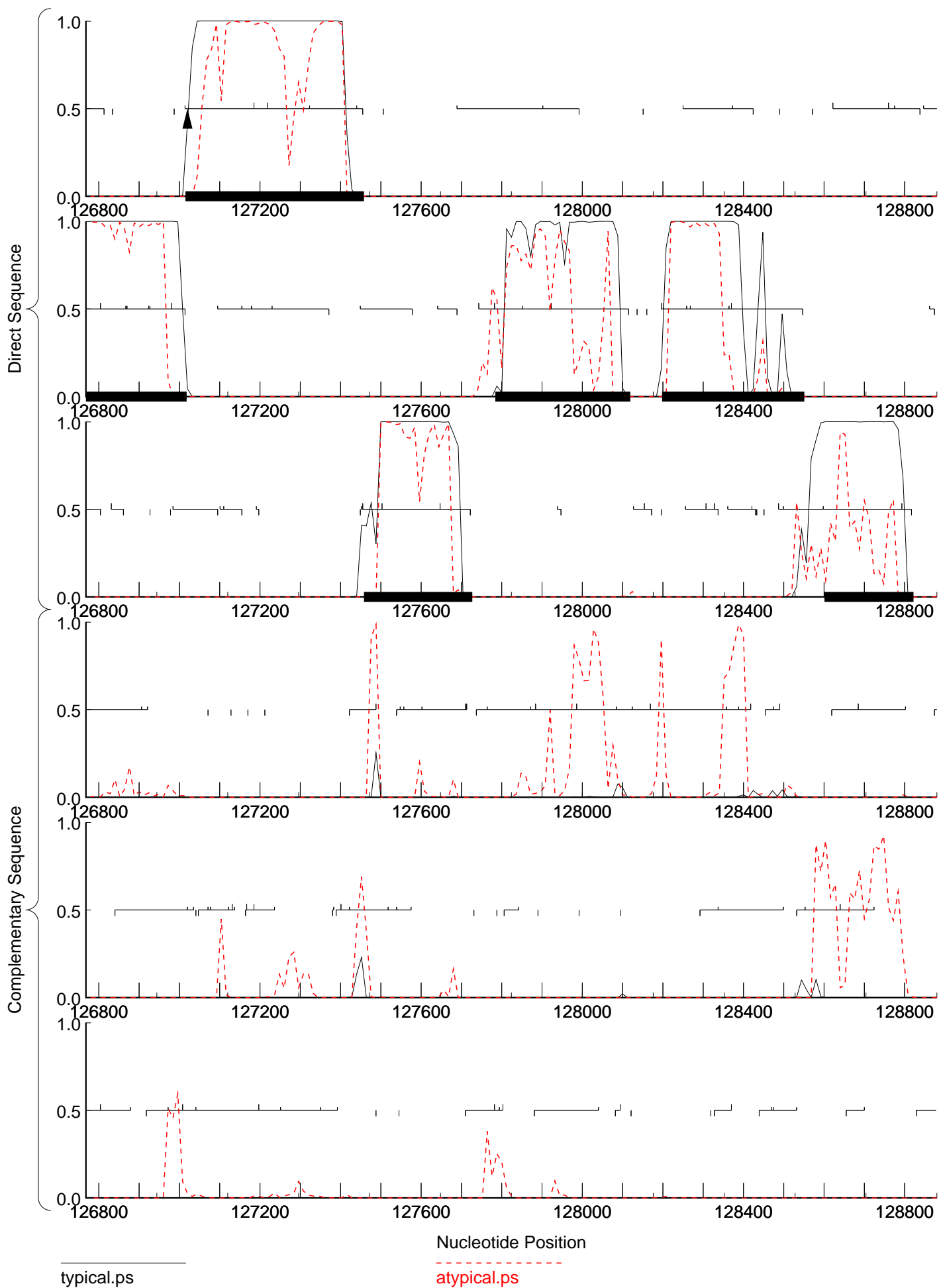
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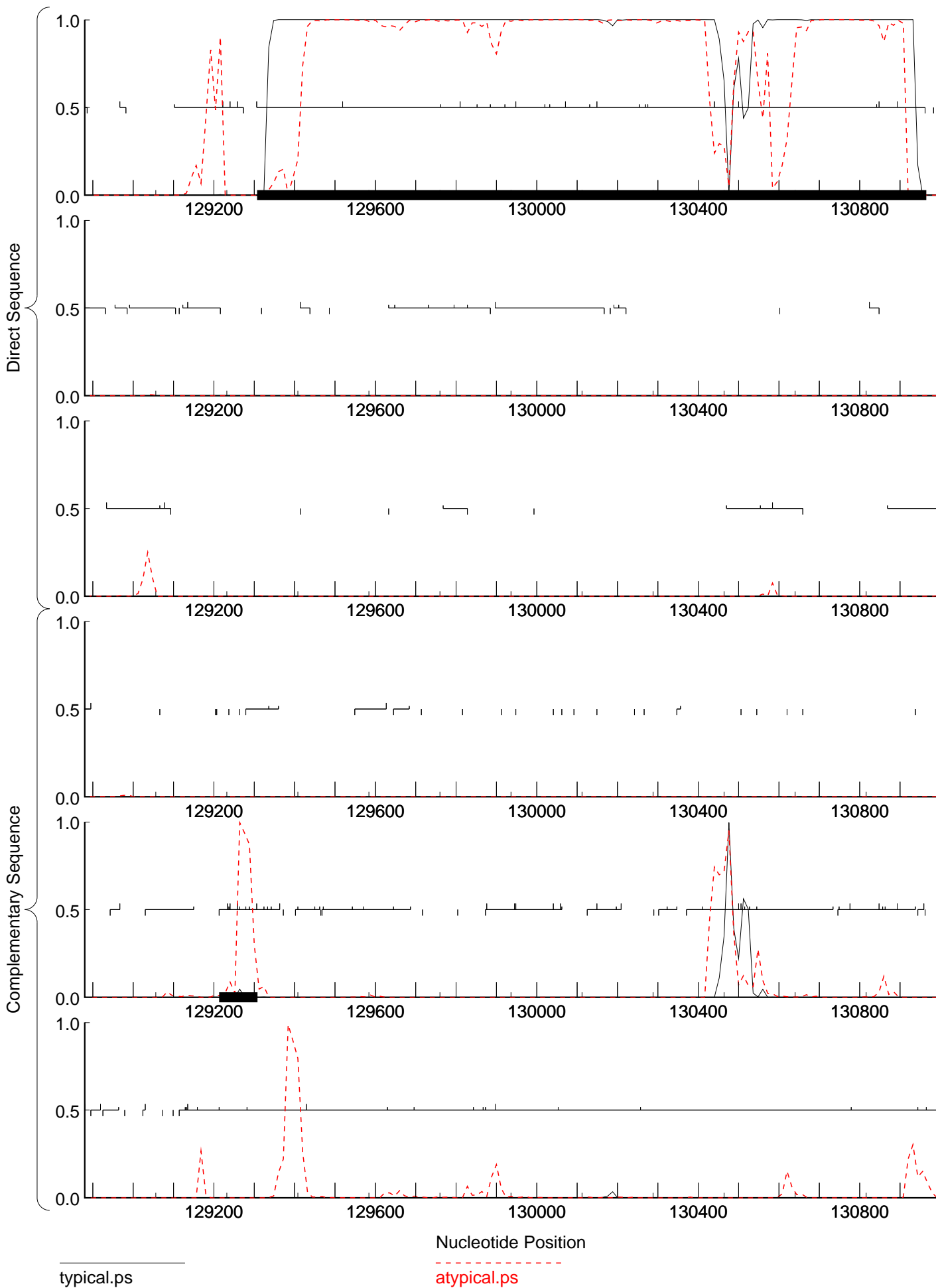
Nucleotide Position

atypical.ps

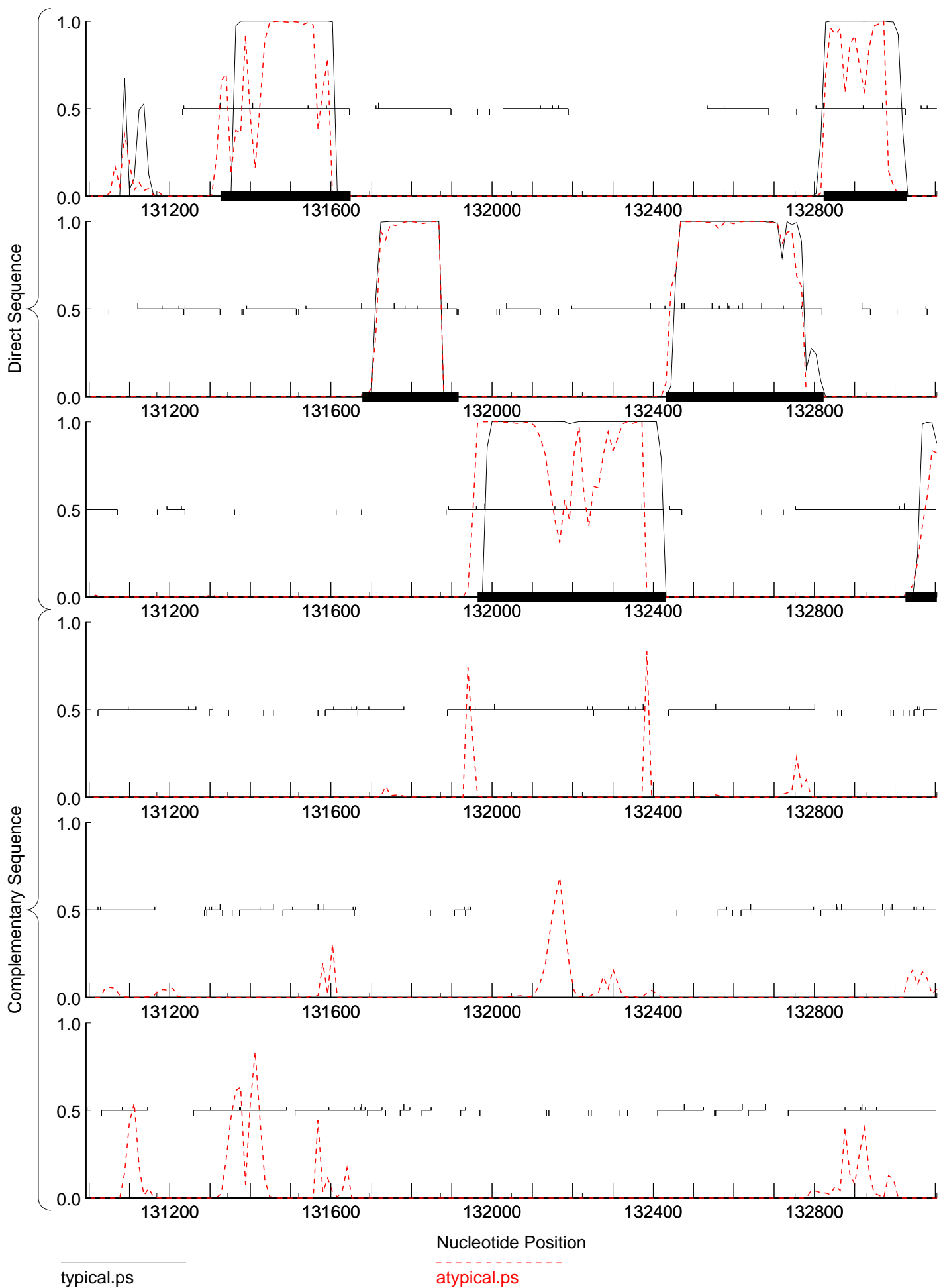


GeneMark.hmm prediction



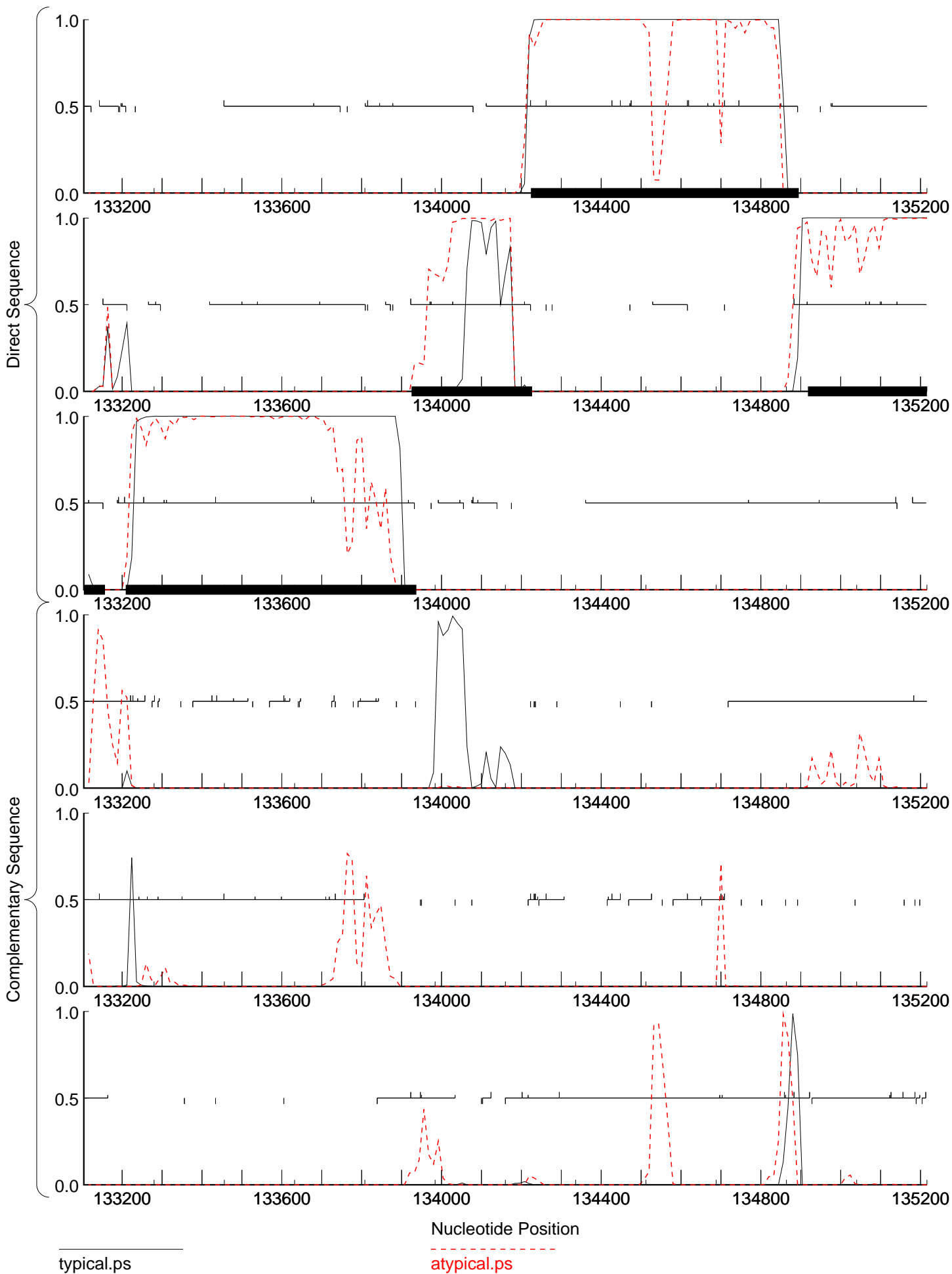


GeneMark.hmm prediction



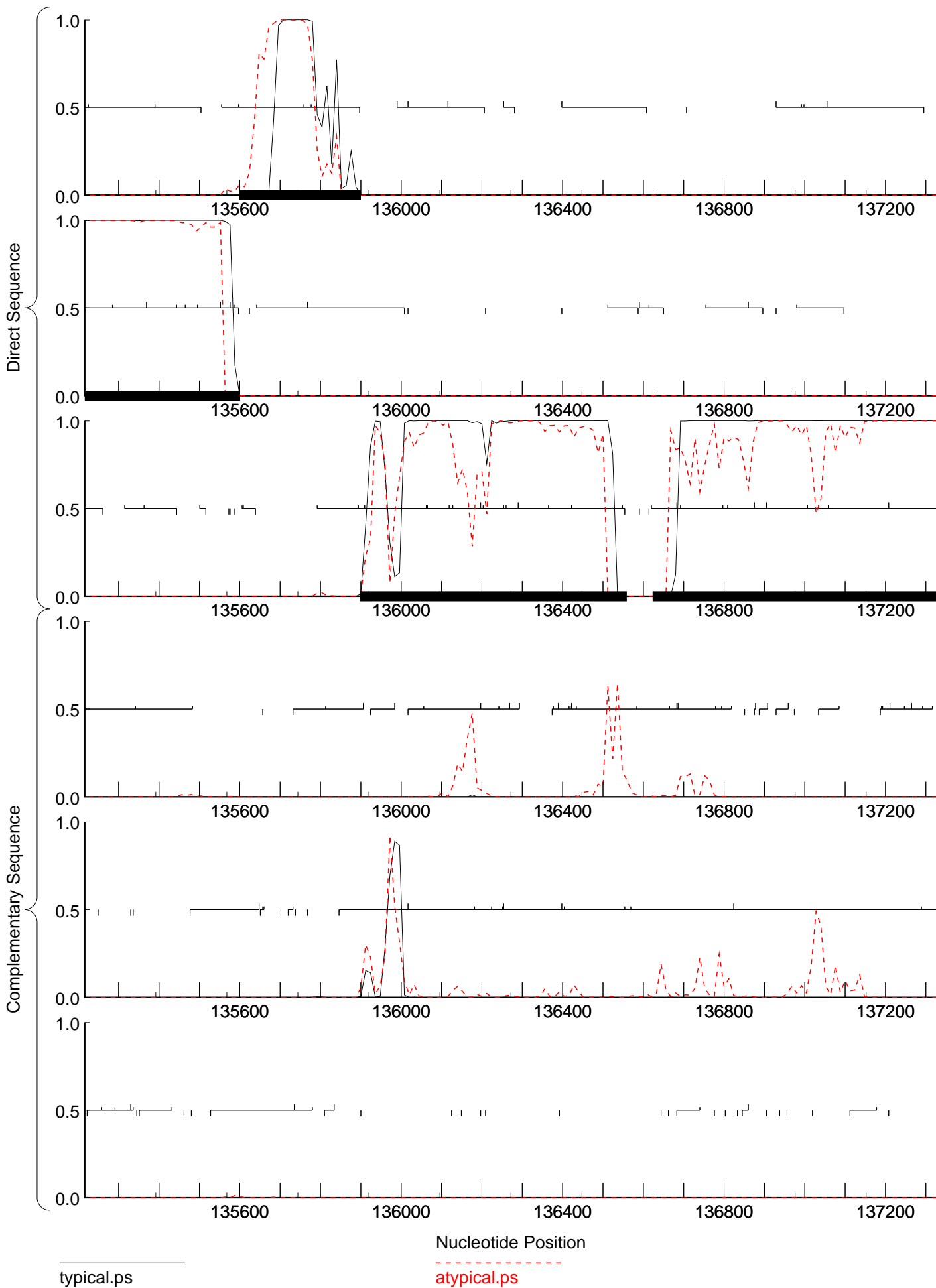
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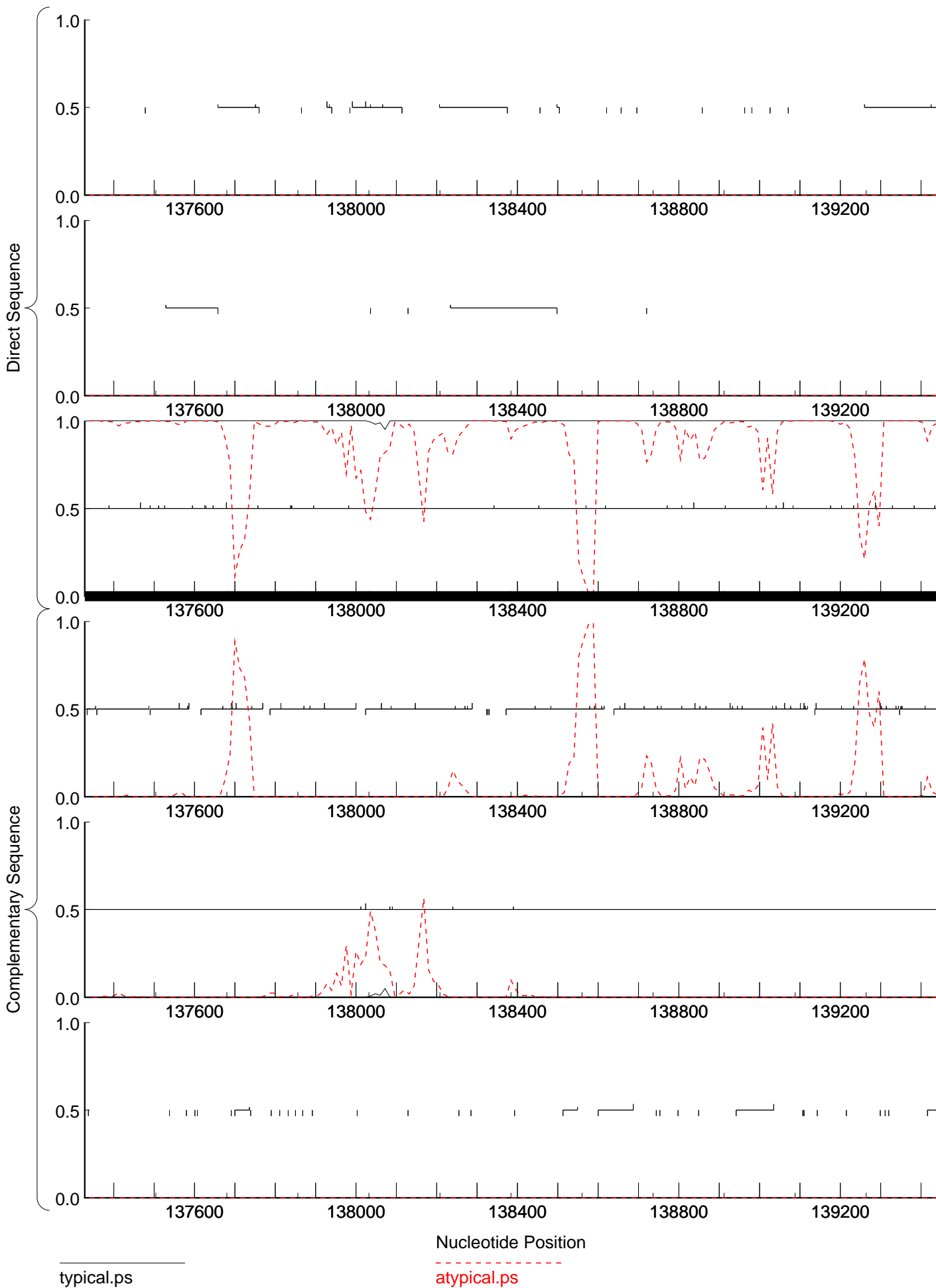
atypical.ps



typical.ps

atypical.ps





typical.ps

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