

GeneMark

Version 2.5p (09.08.06)

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PROGRAM INFORMATION

Sequence : Mycobacterium phage Roots515 complete sequence, 156288 bp, circularly permuted, Cluster C1
Analysis Date : 11/19/17 at 18:55:13
Pages : 75
Sequence Length : 156288 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,

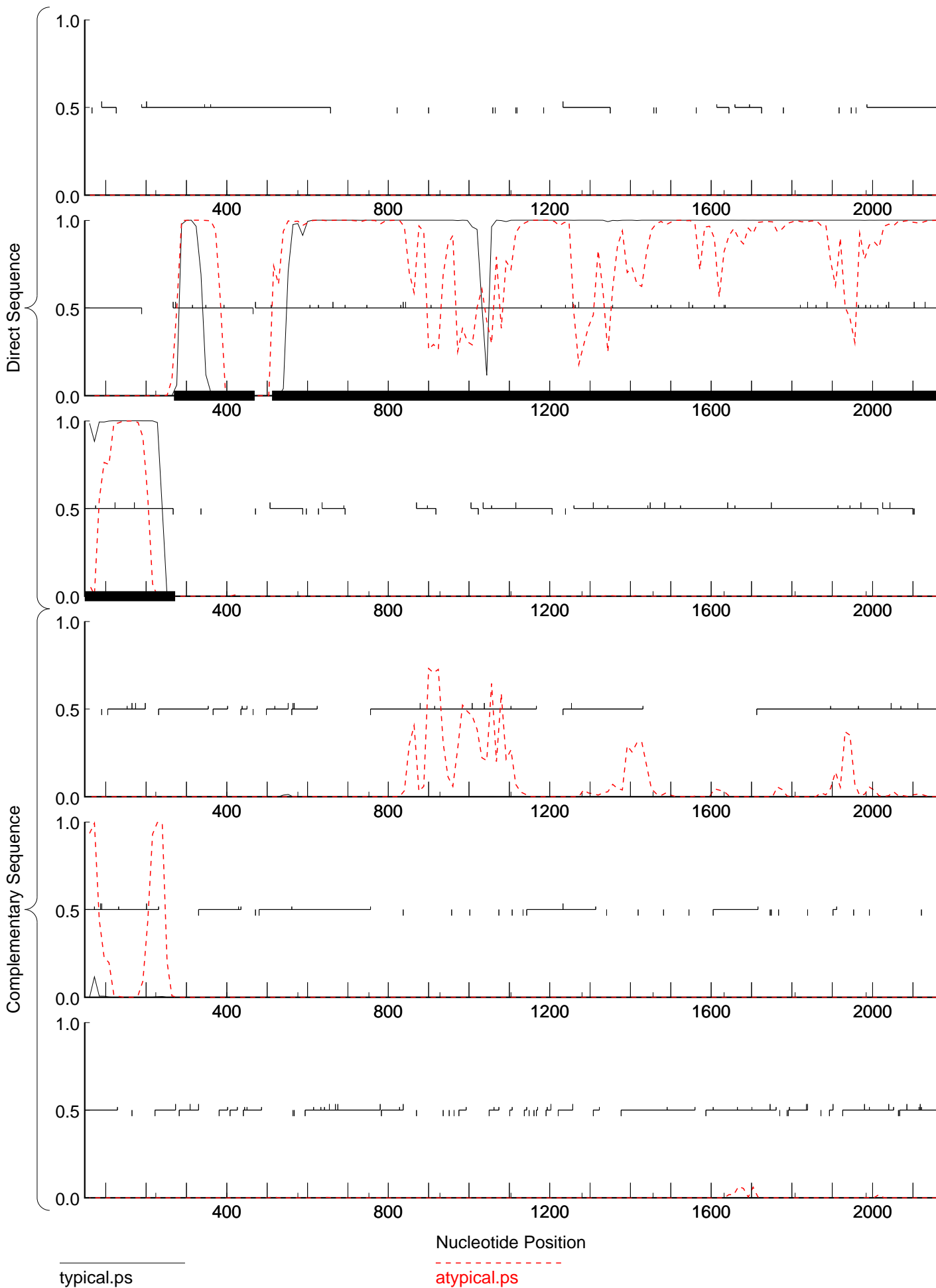
Matrix notes & comments

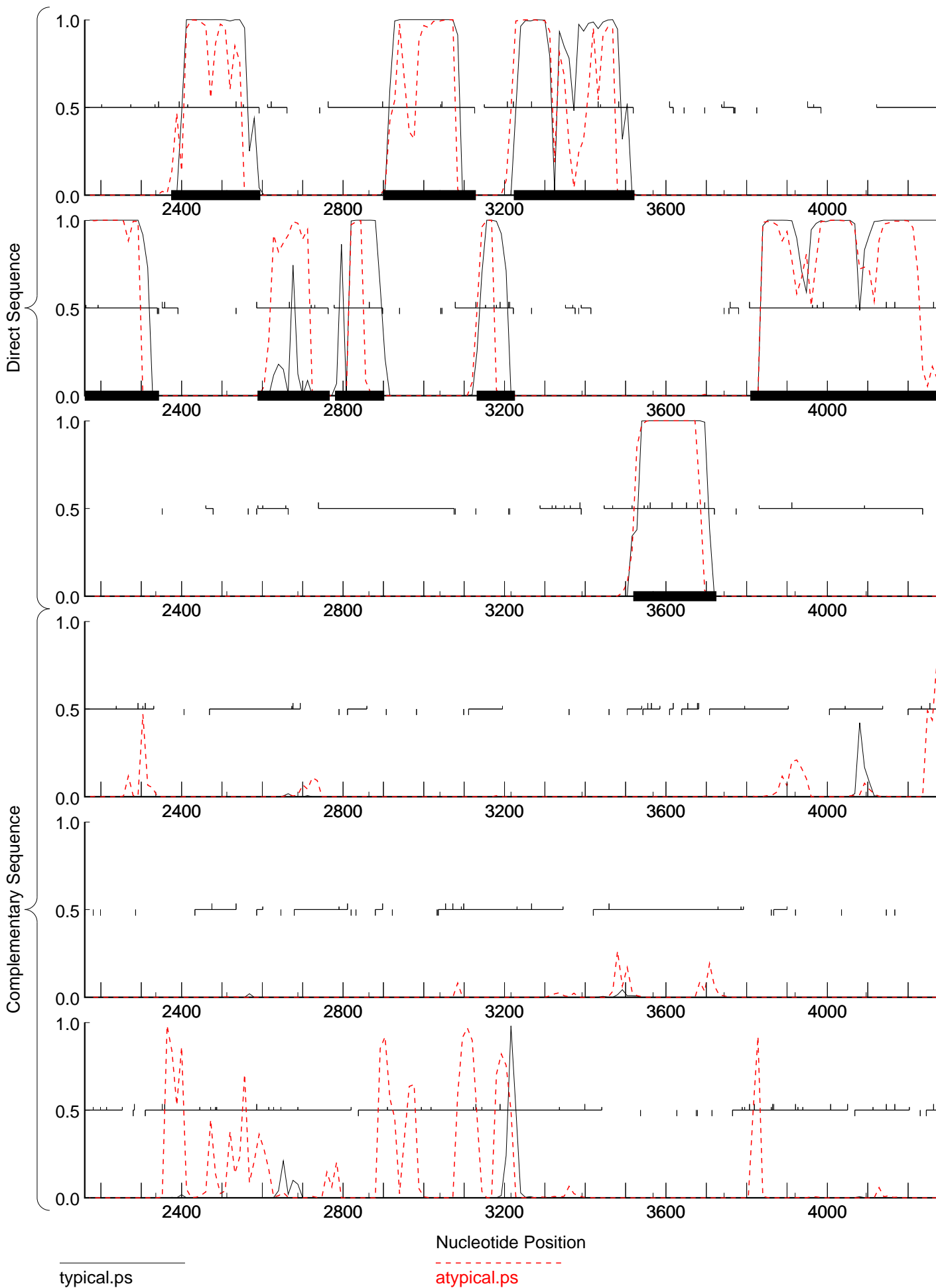
Training set derived by GeneMarkS, 4.30 October 2014
Sun Nov 19 18:55:12 2017

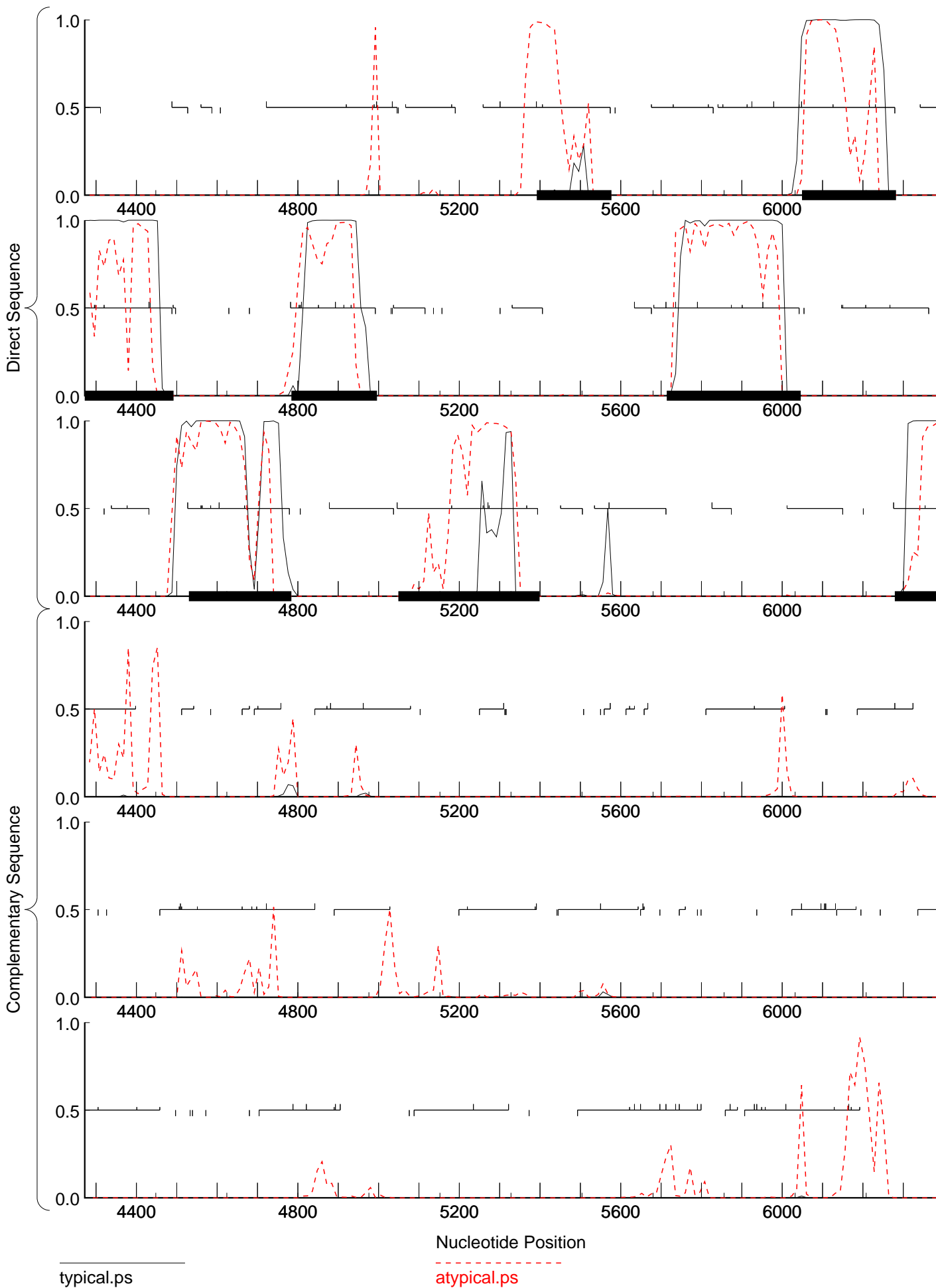
MATRIX INFORMATION

Matrix : -
Author : -
Order : 4

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

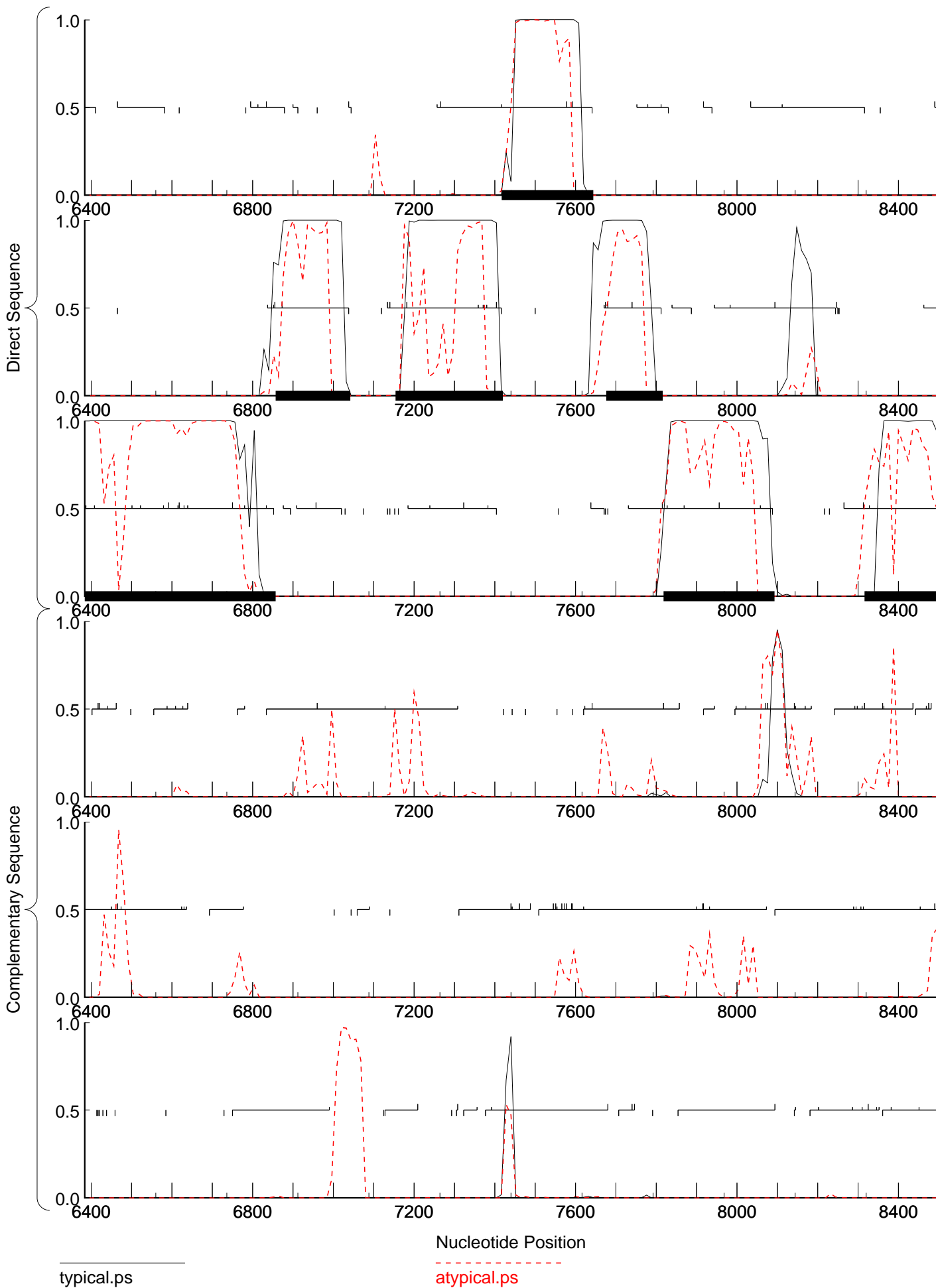


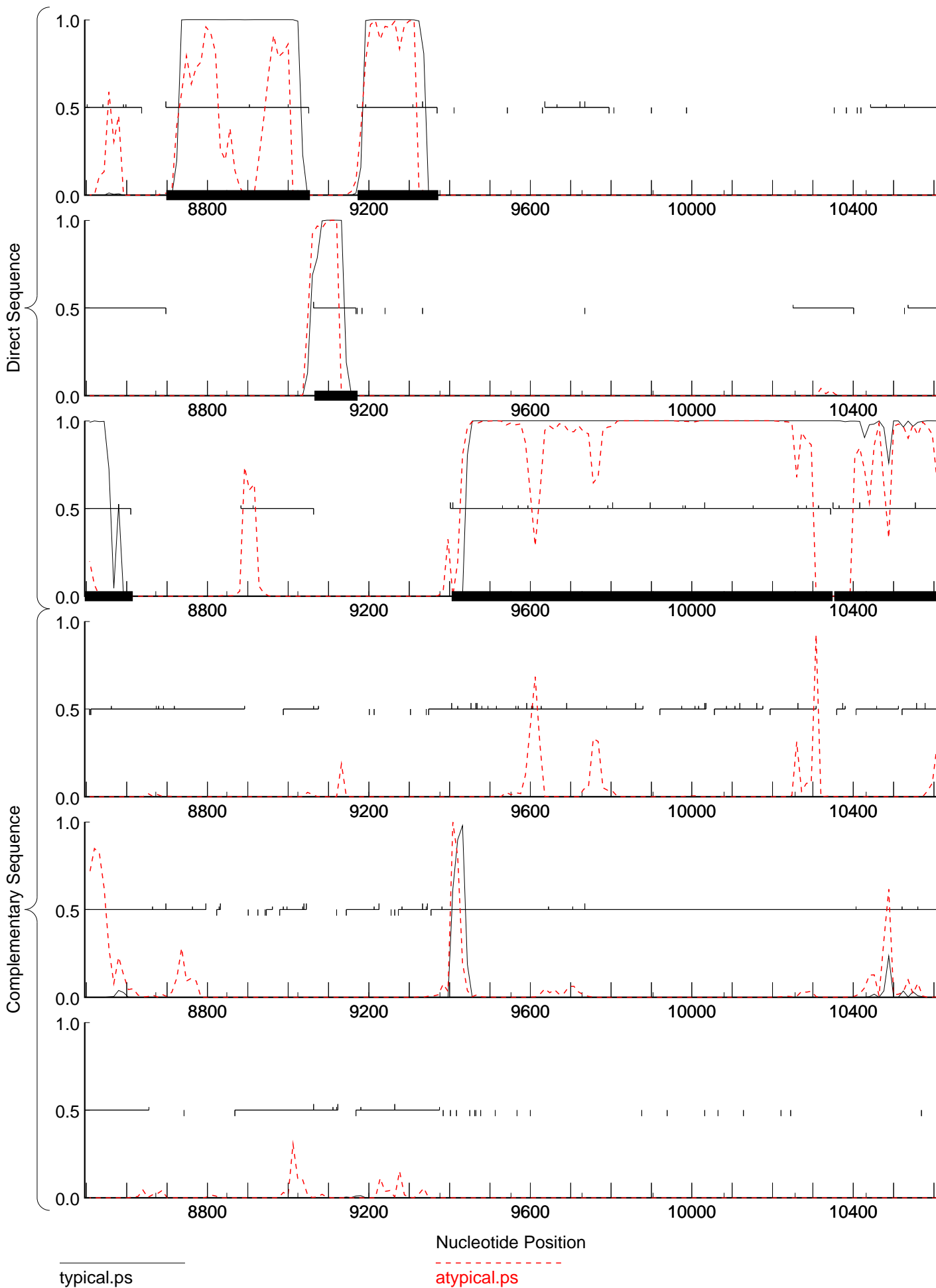


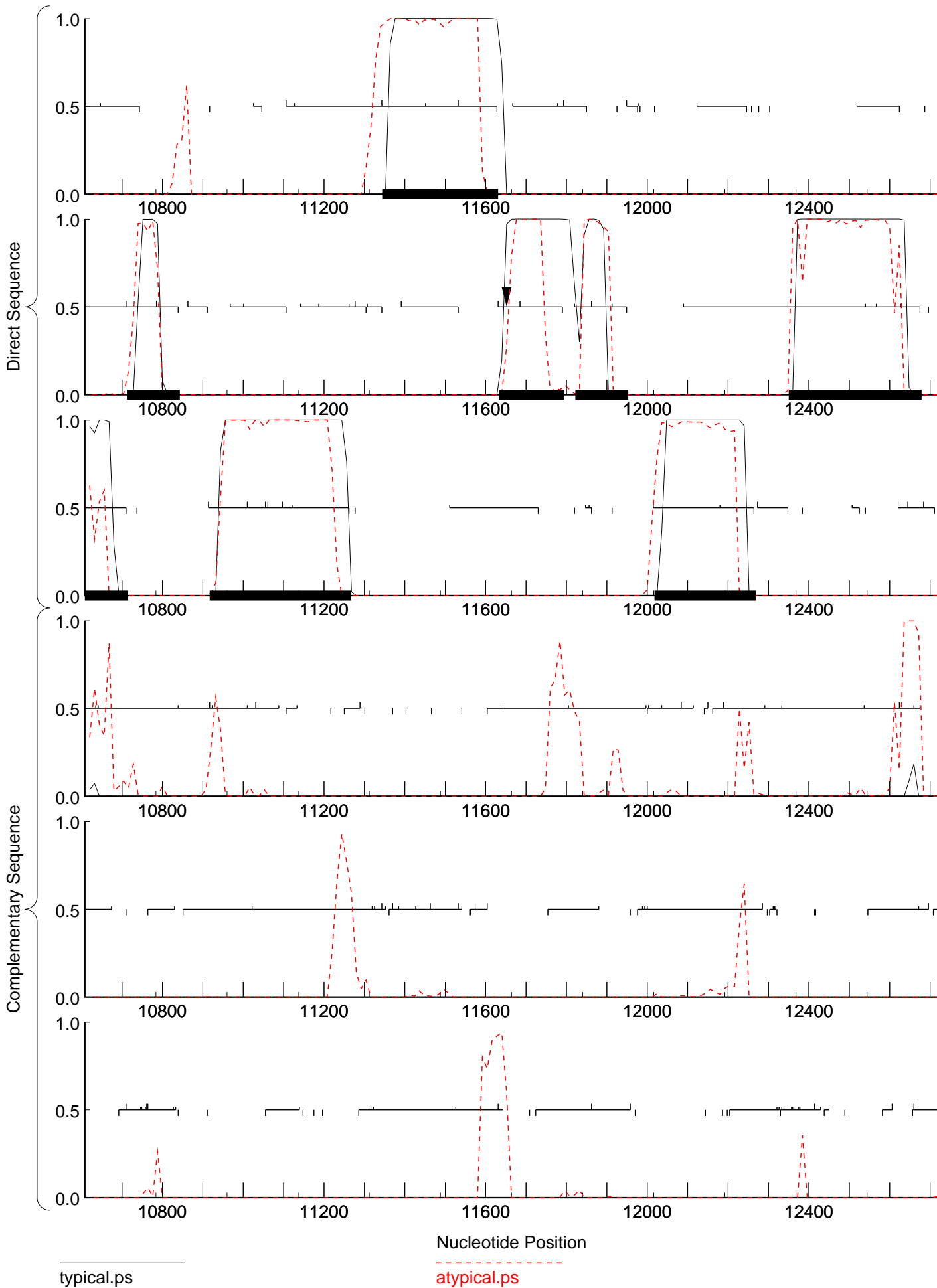


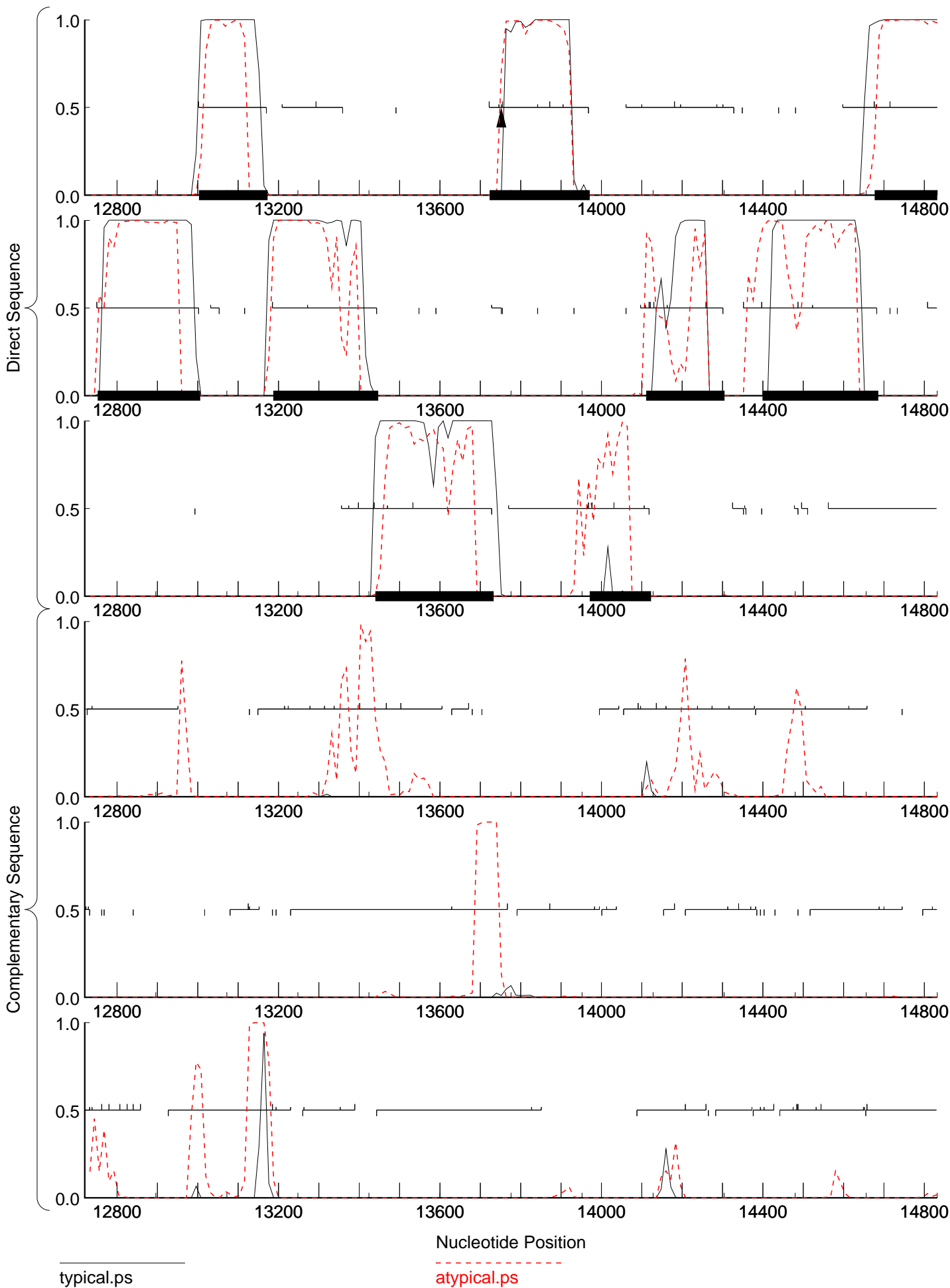
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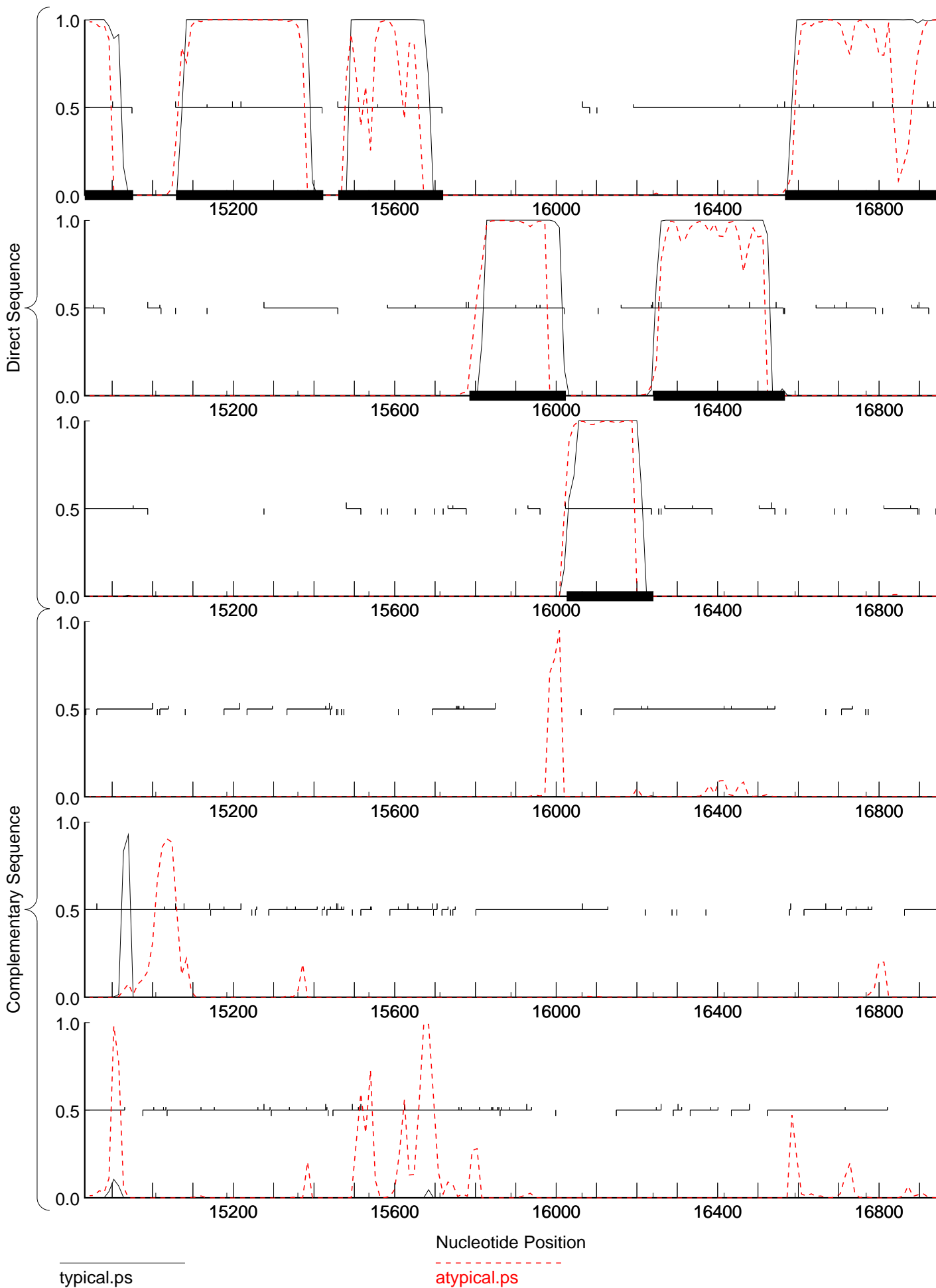
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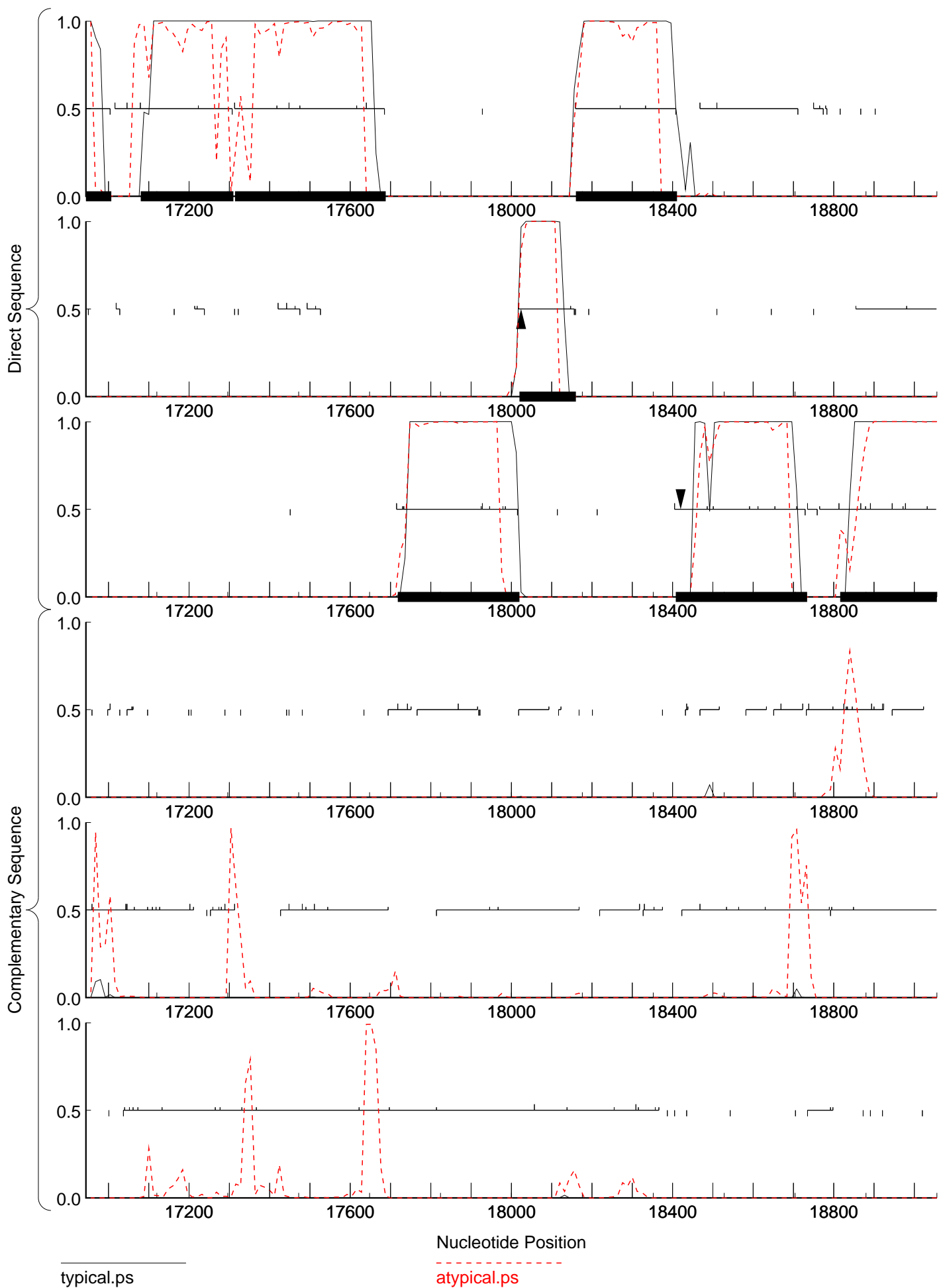


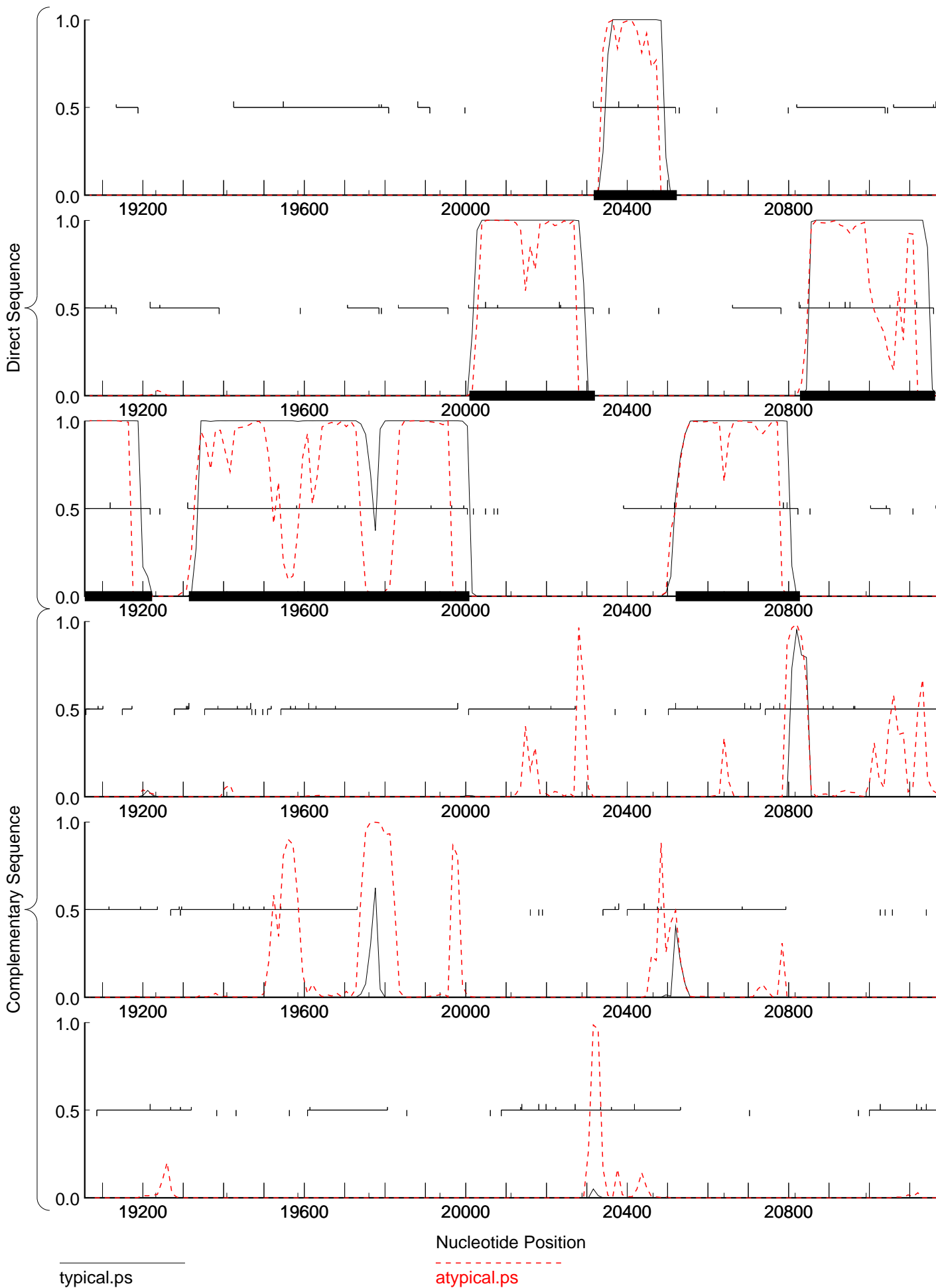


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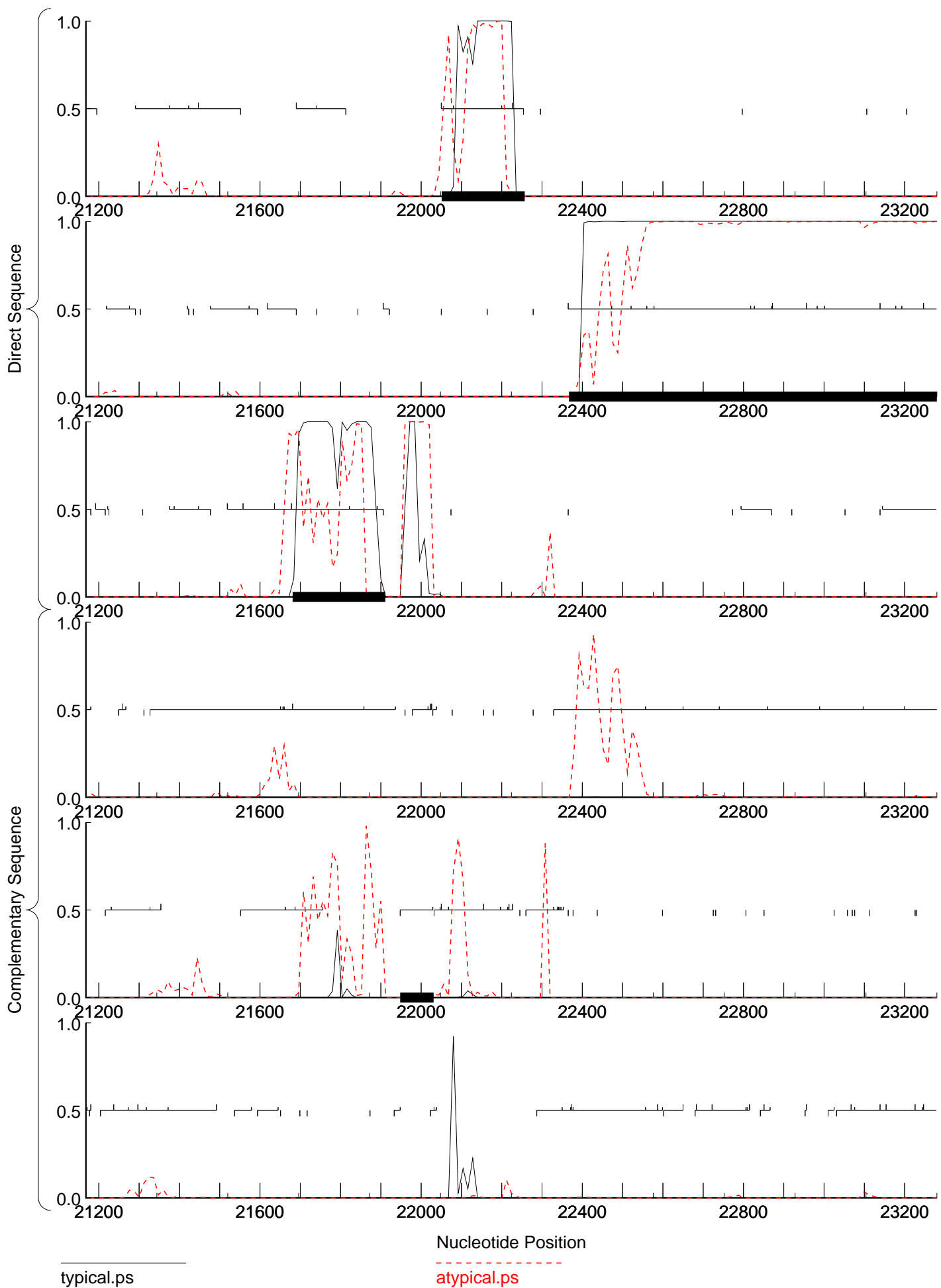
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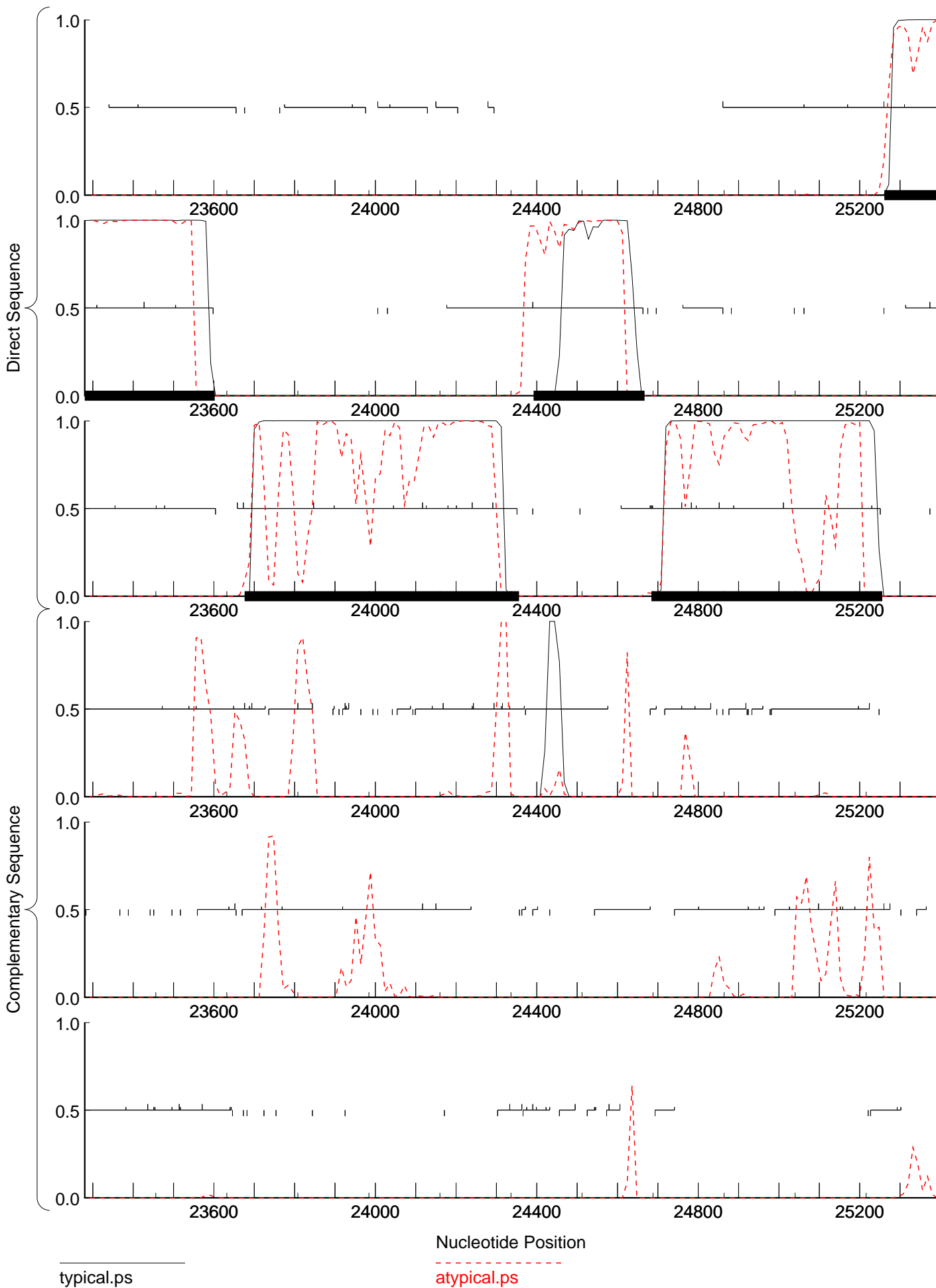
GeneMark.hmm prediction

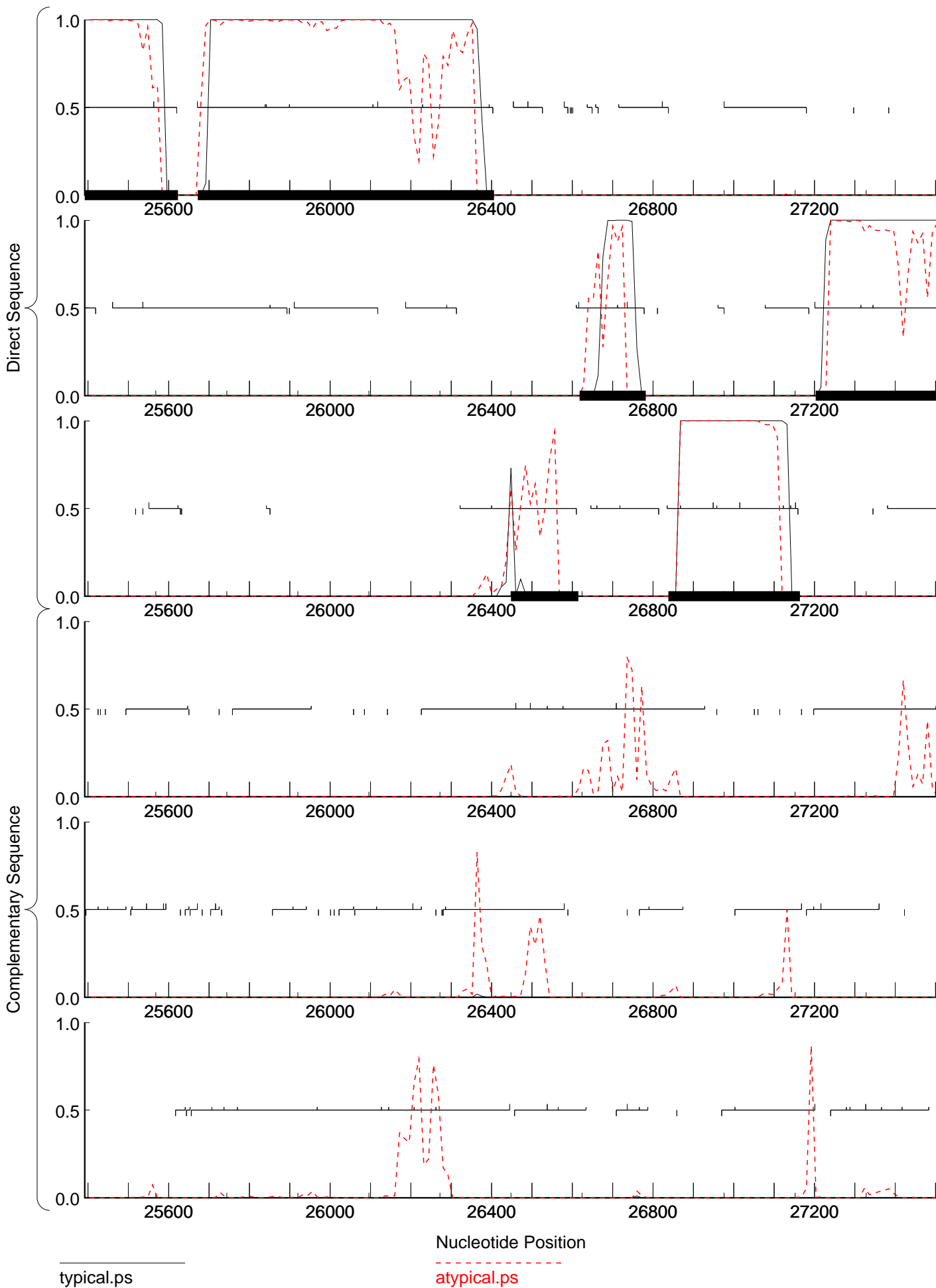




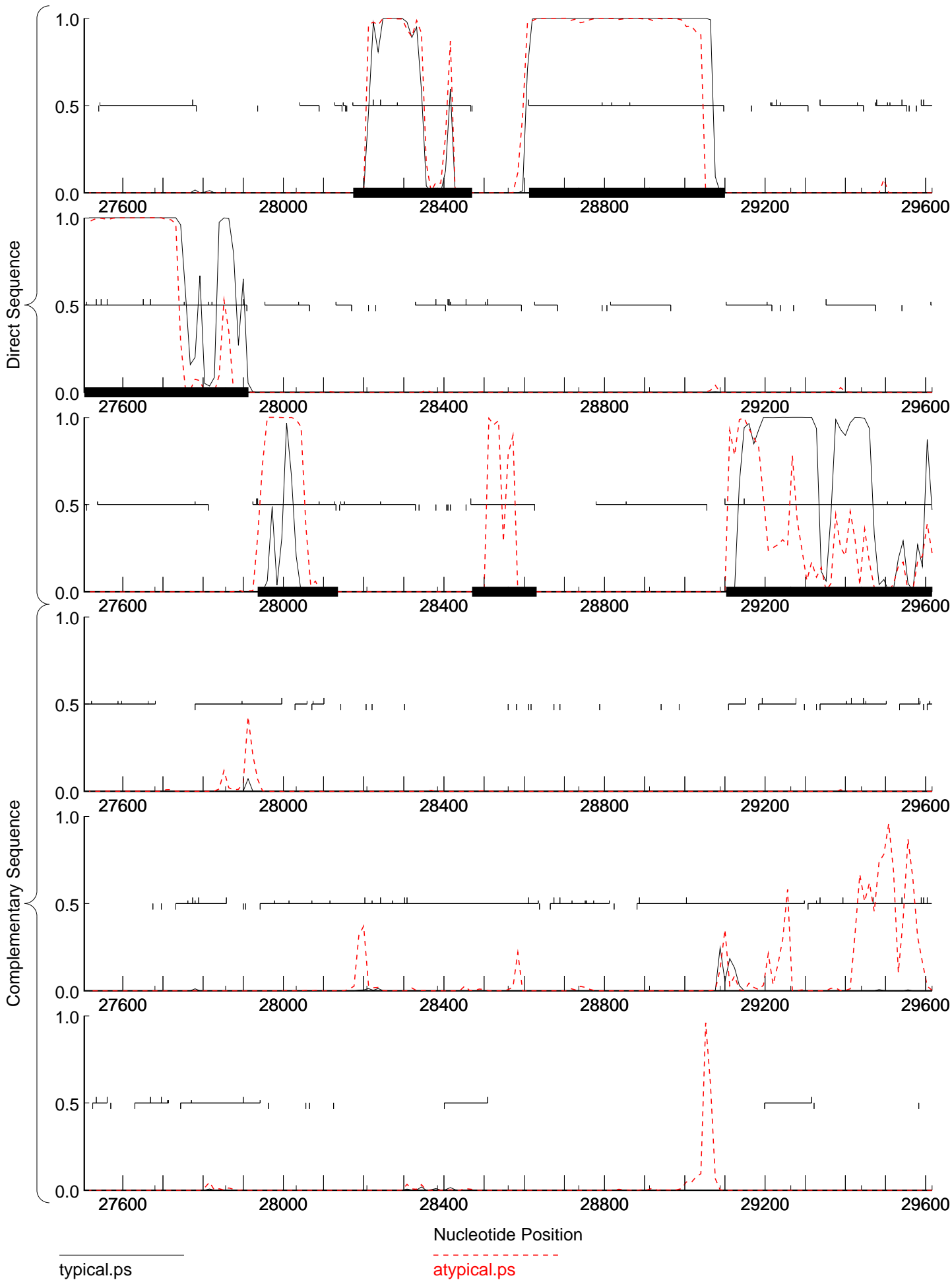
GeneMark.hmm prediction





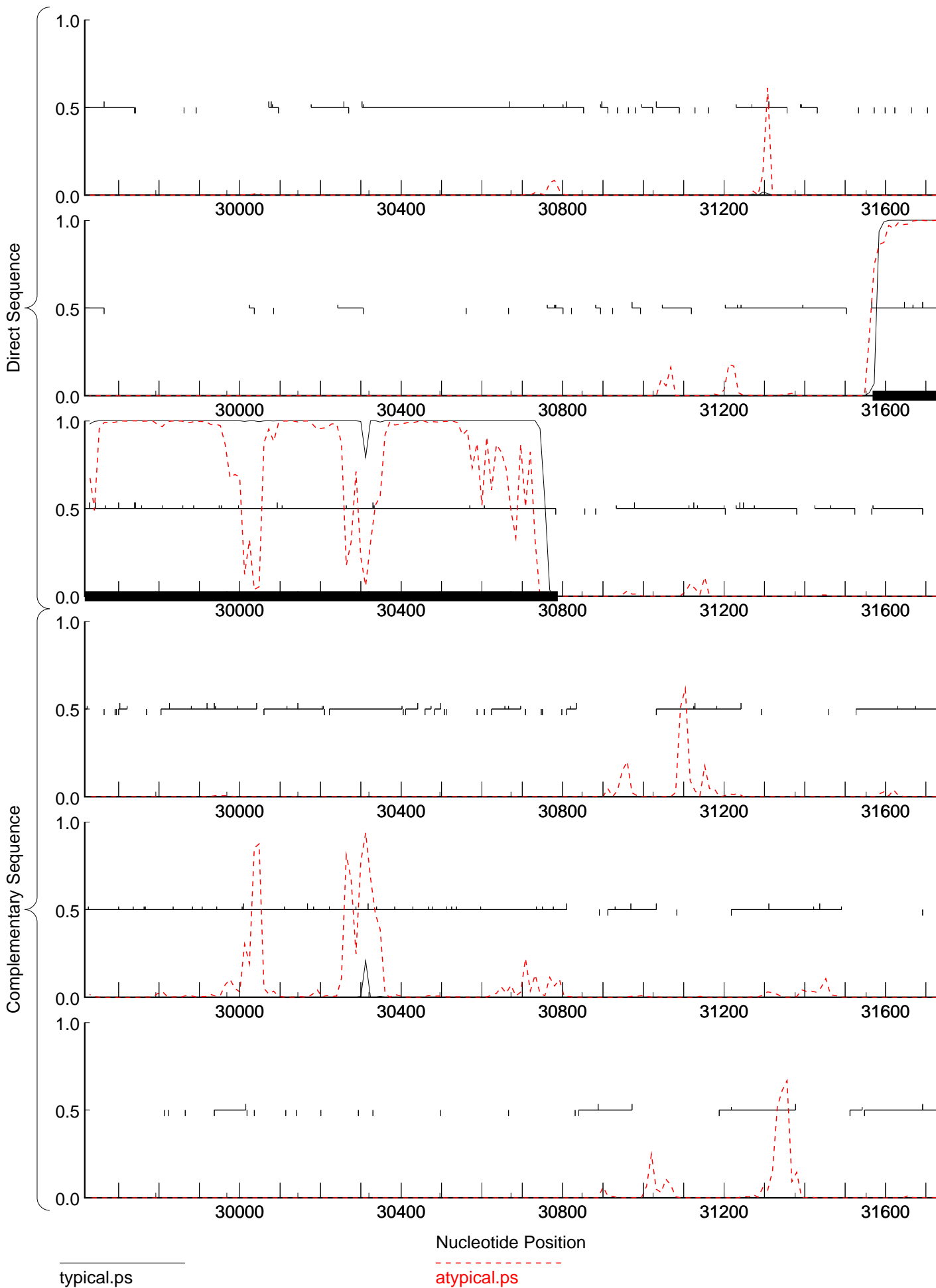


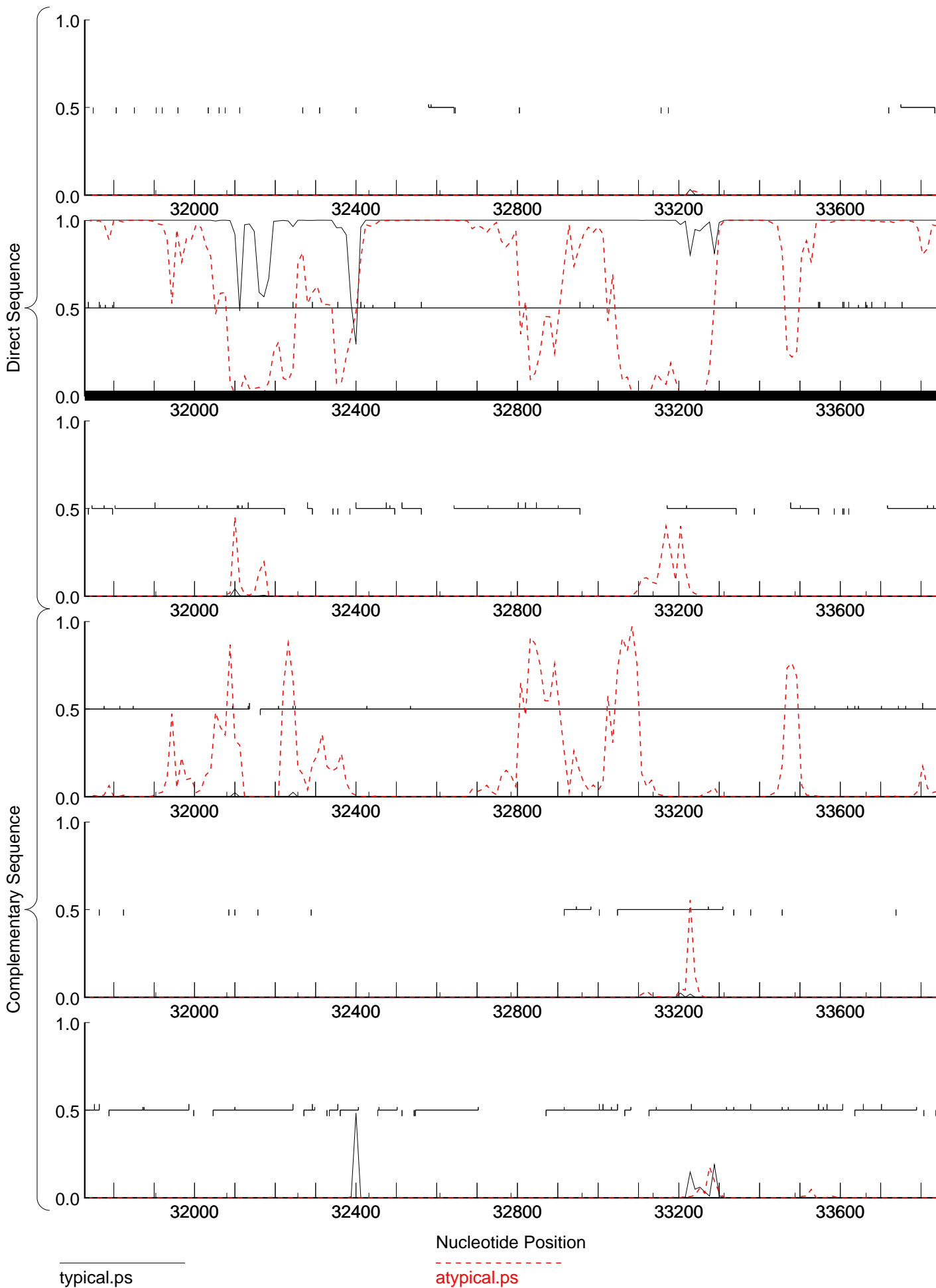
GeneMark.hmm prediction

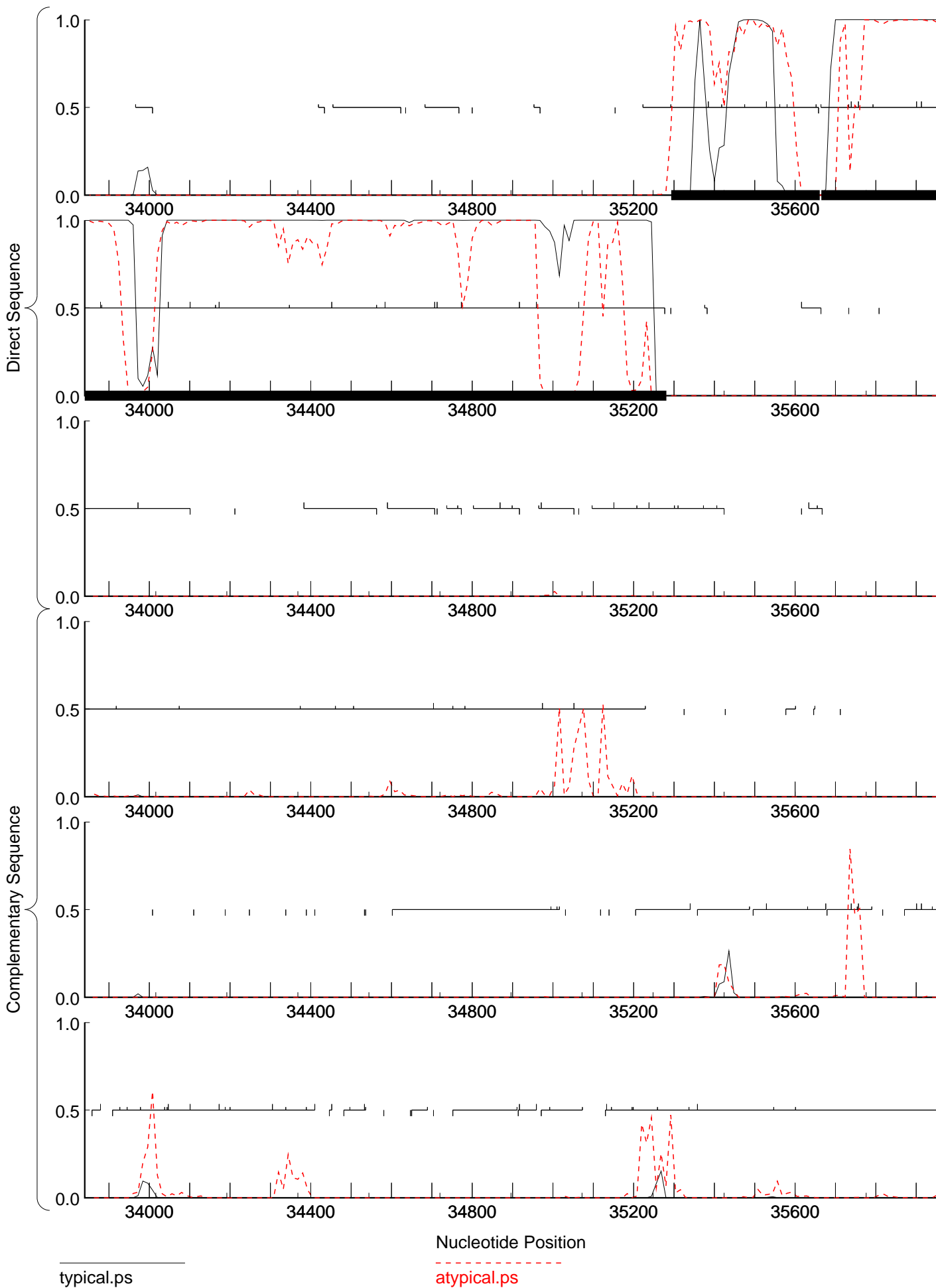


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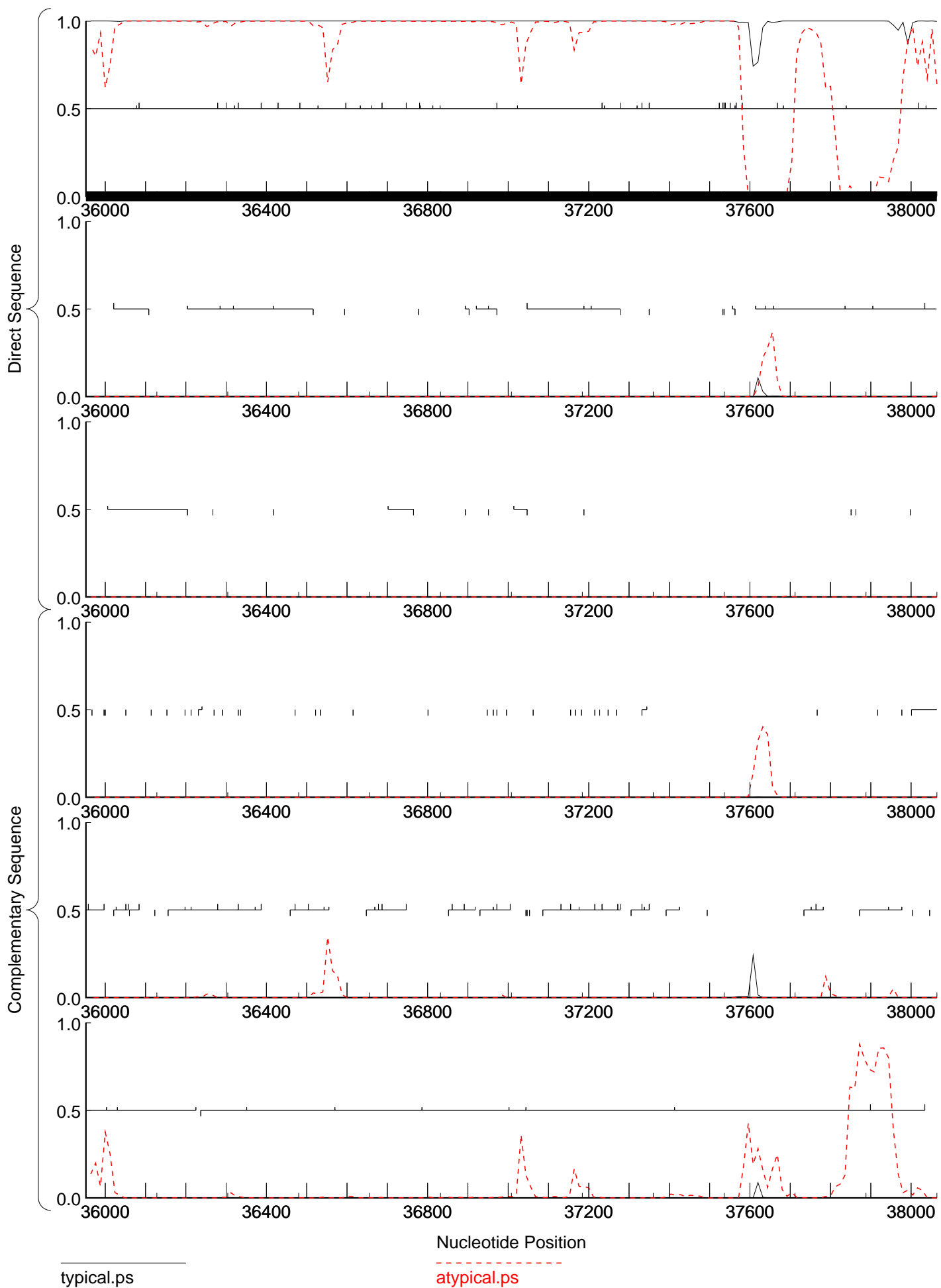
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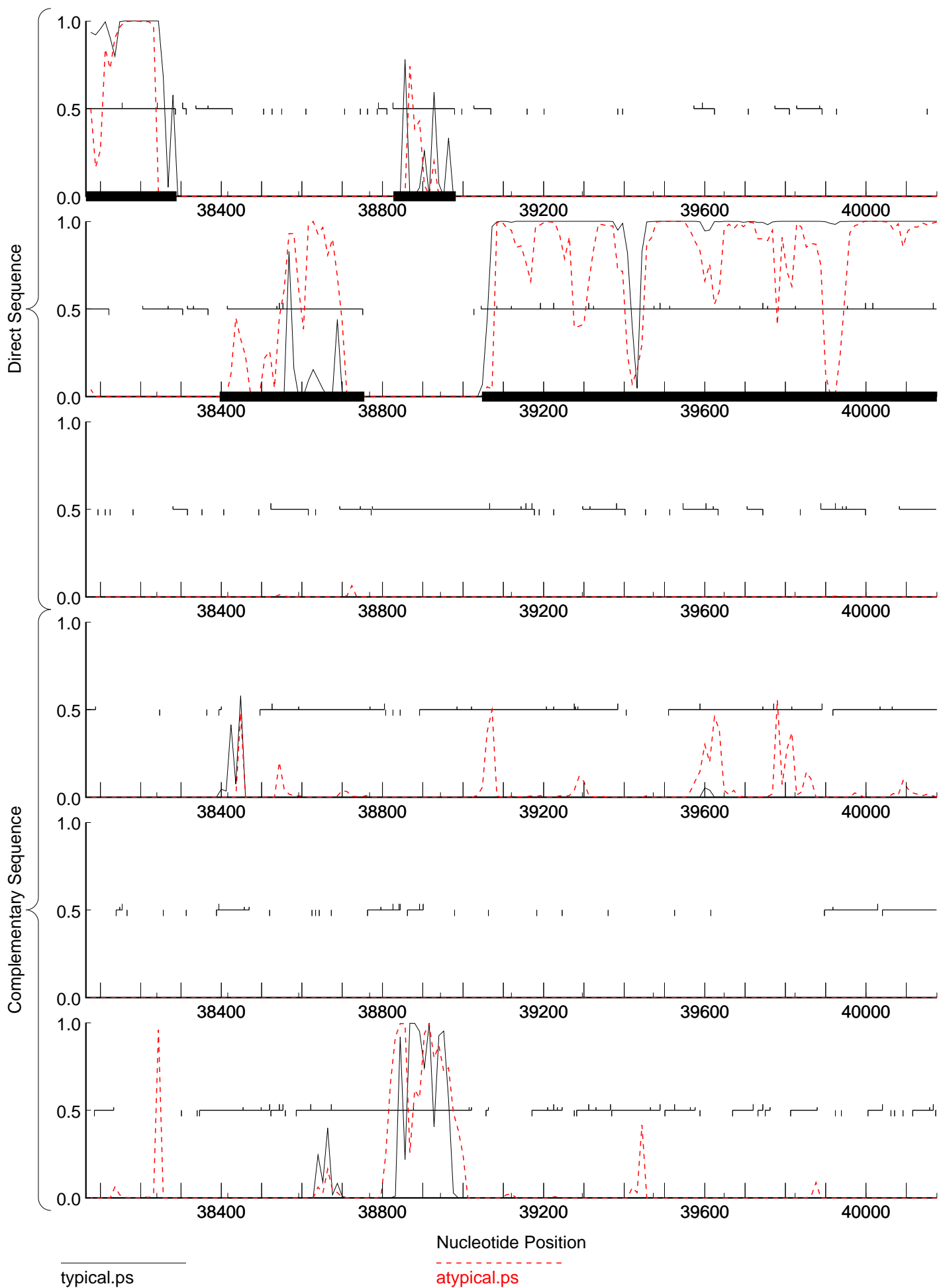




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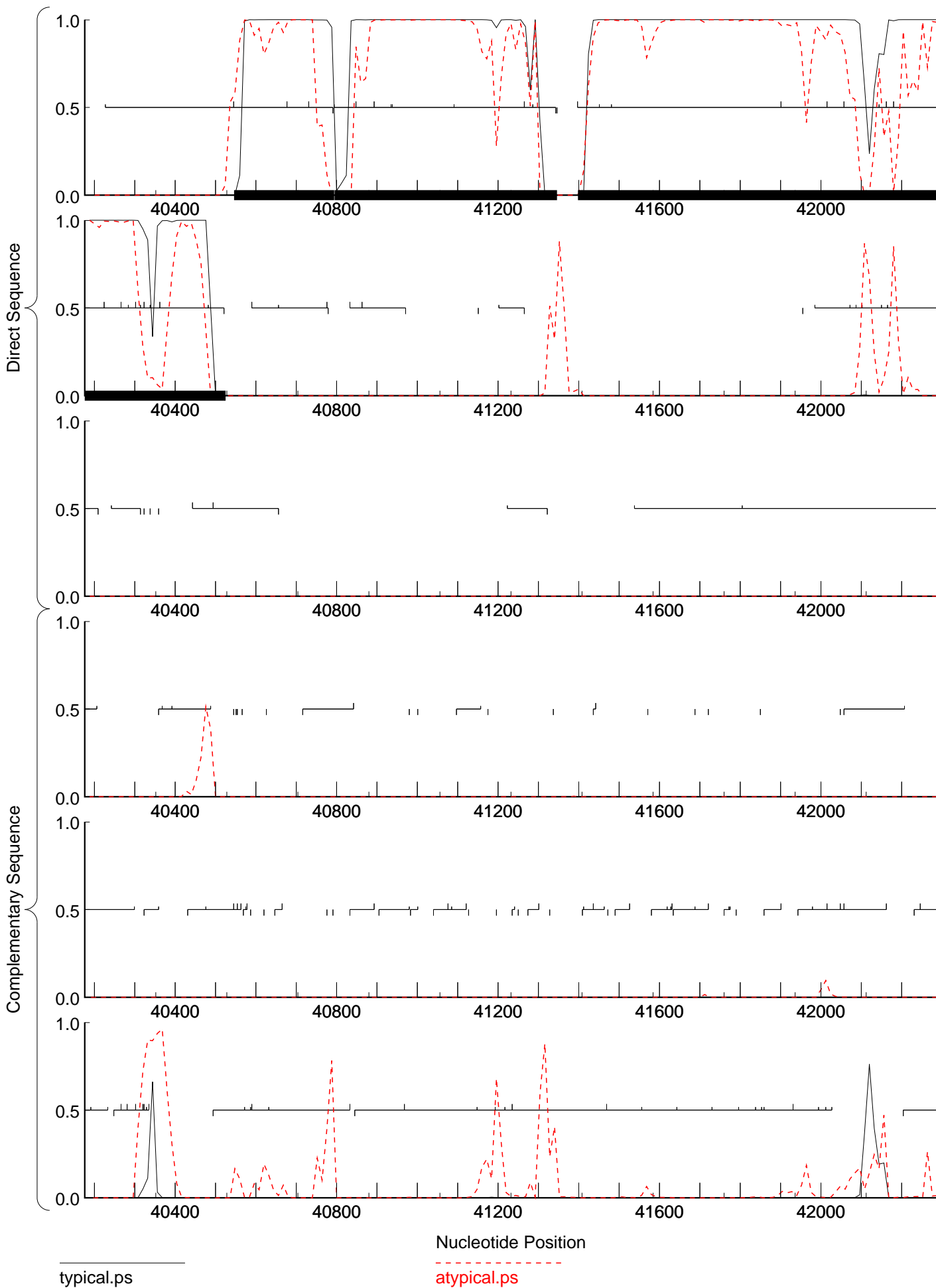


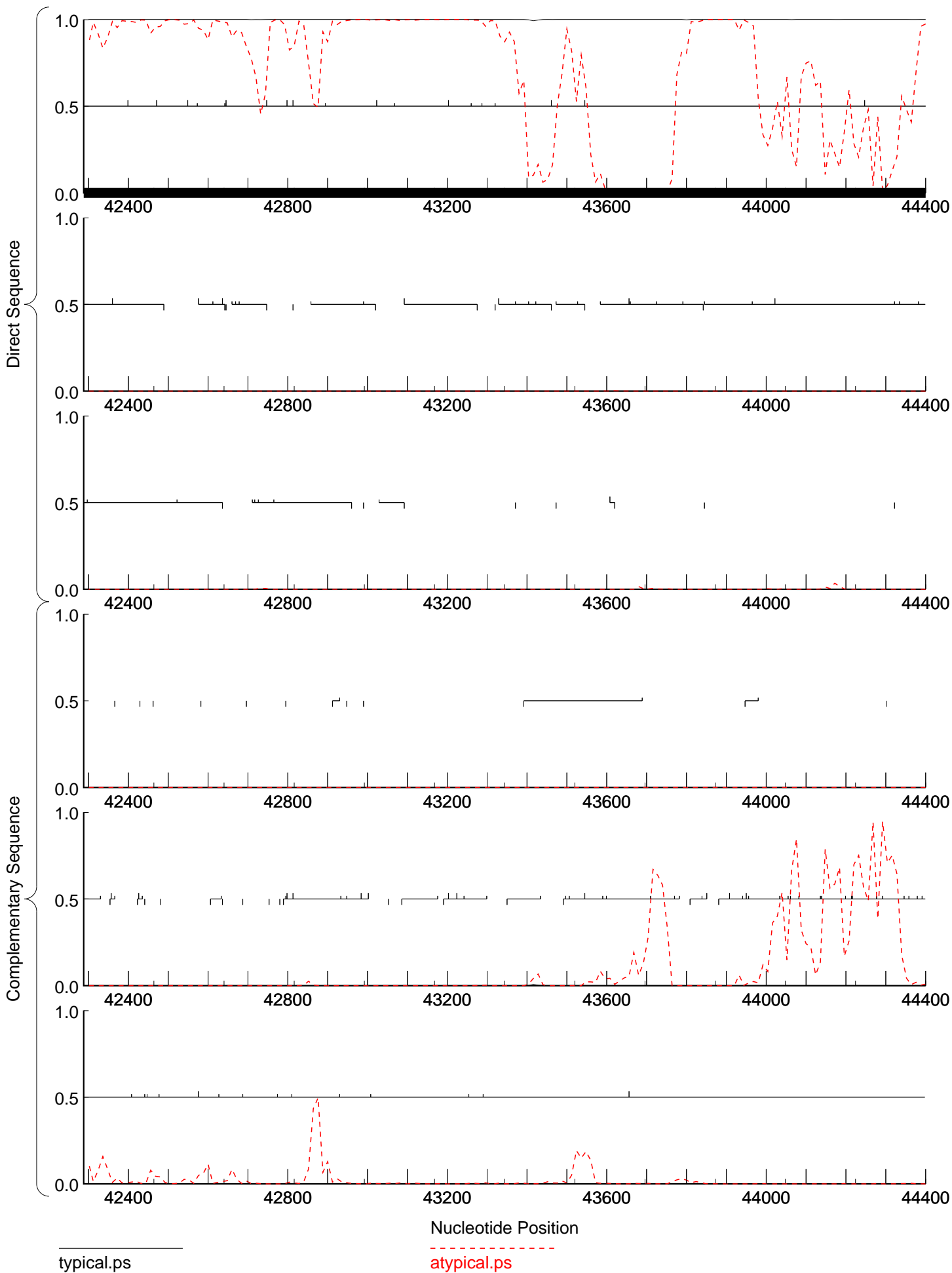
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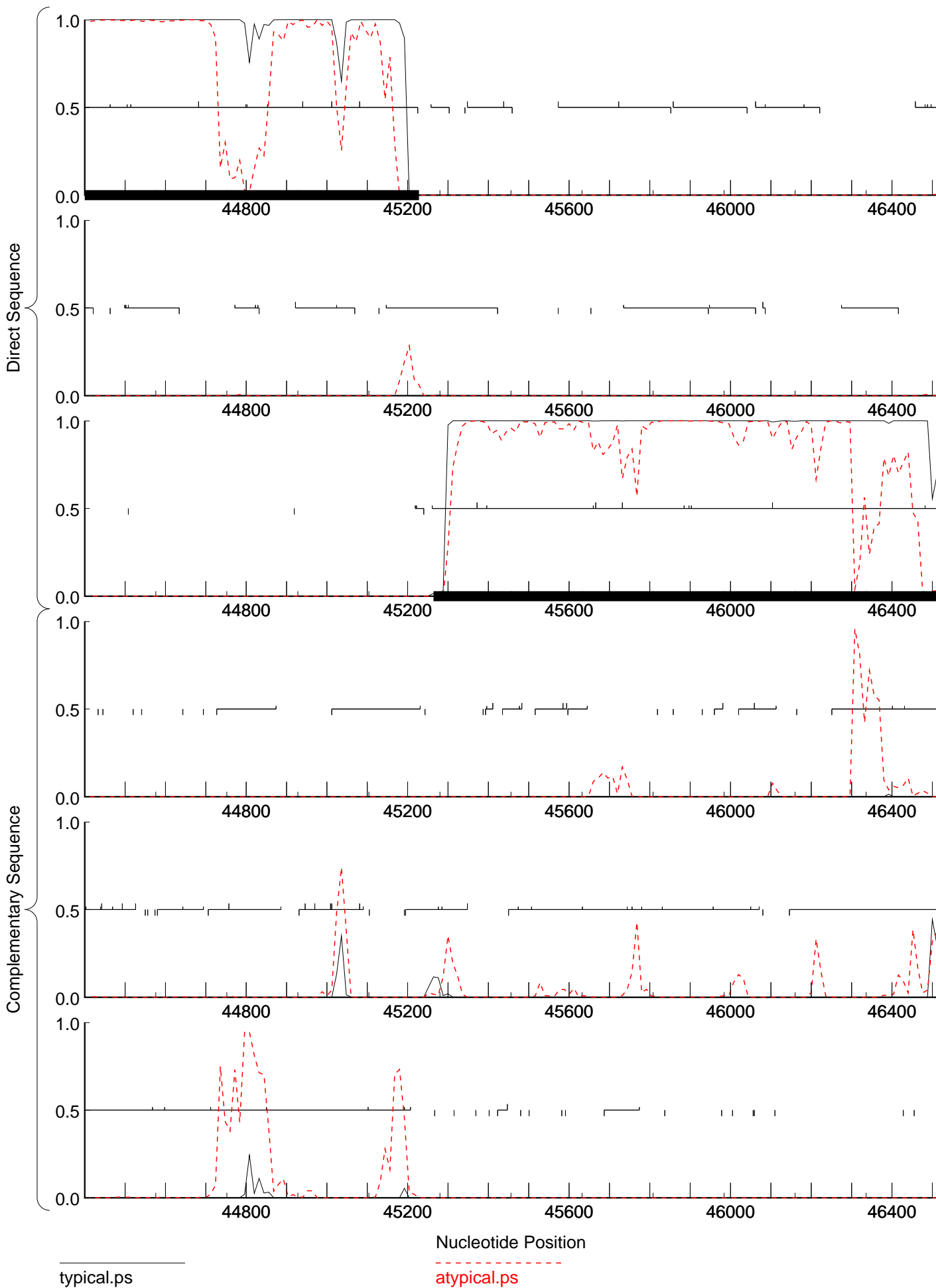


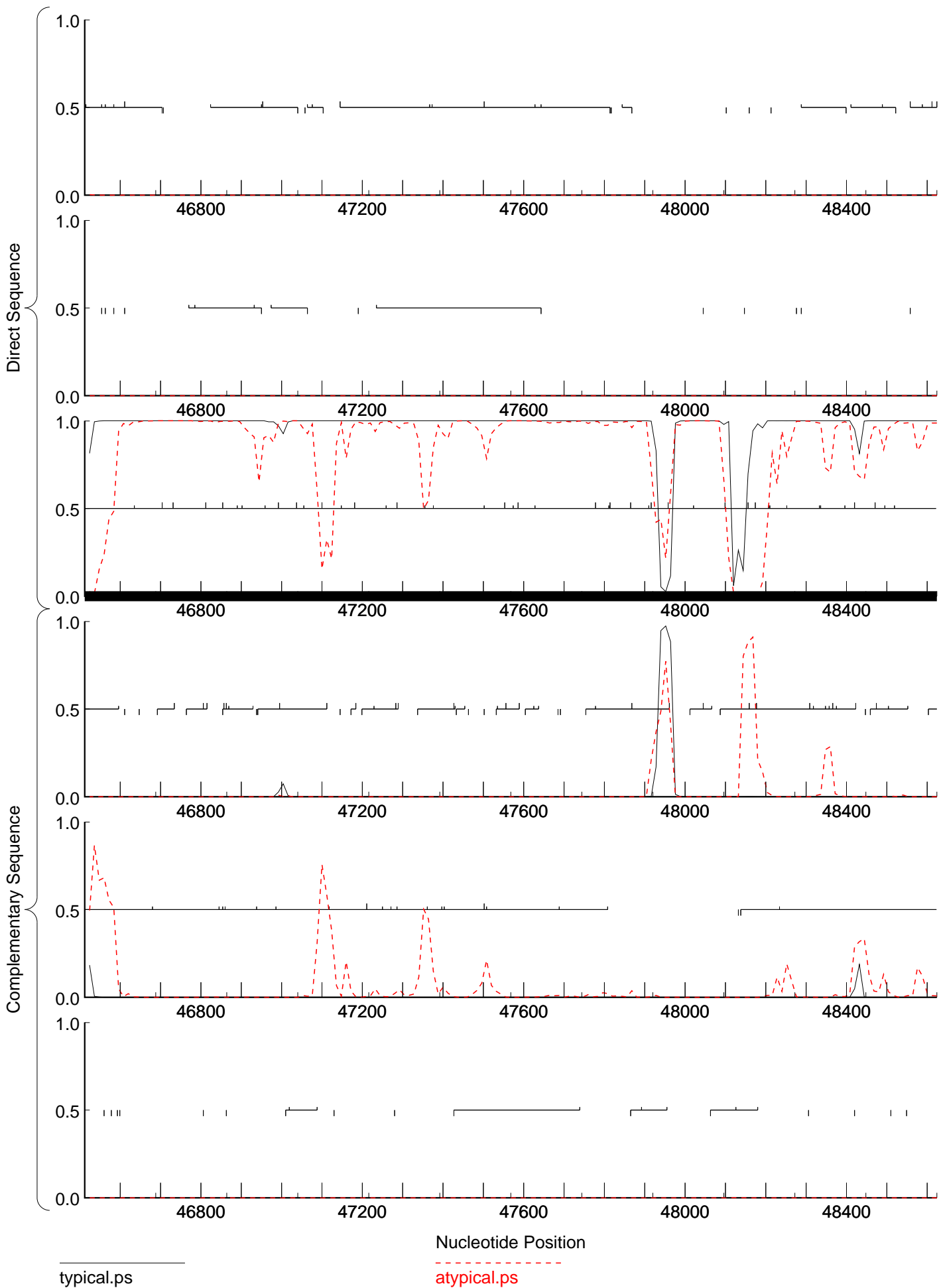
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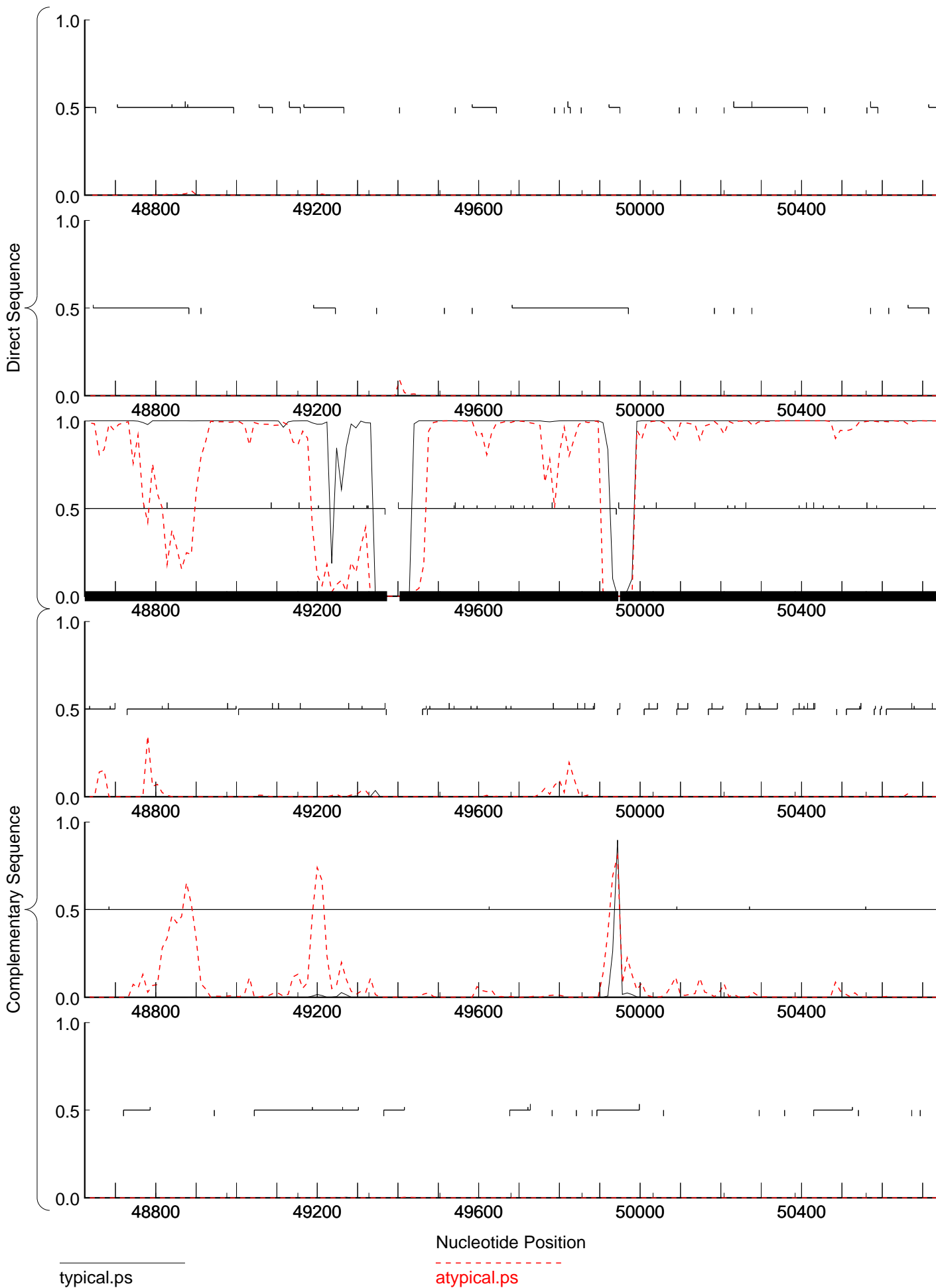


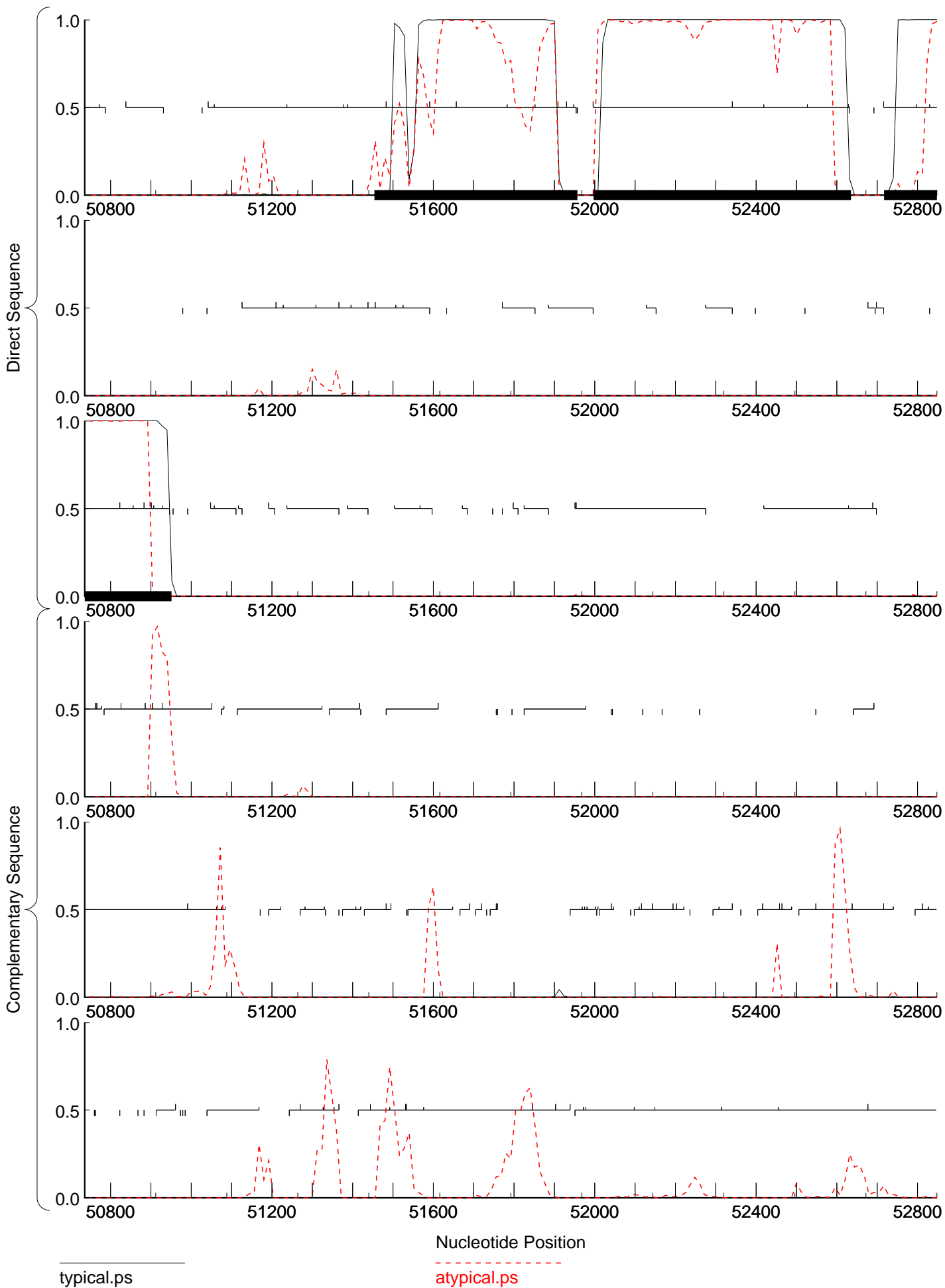




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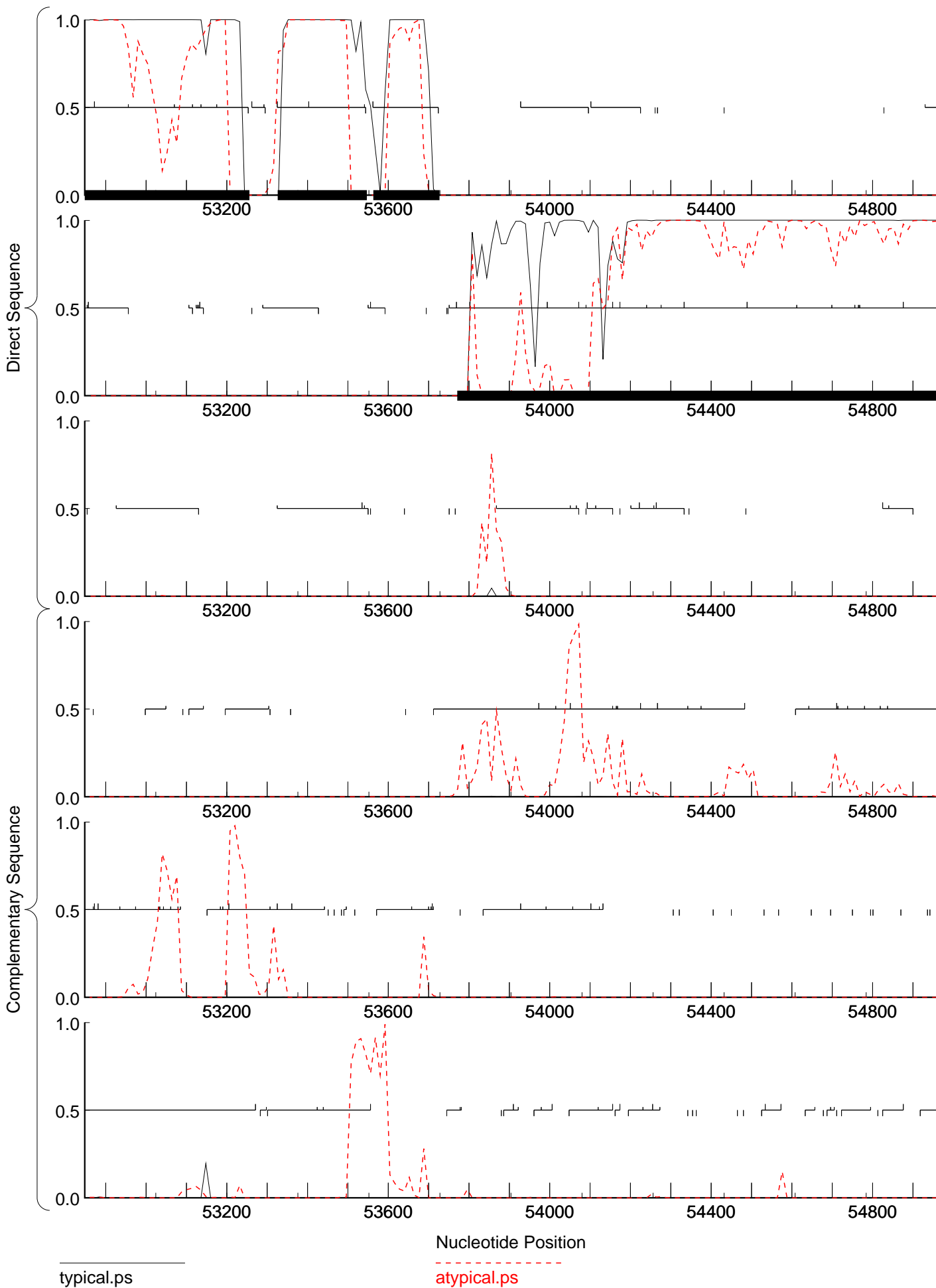
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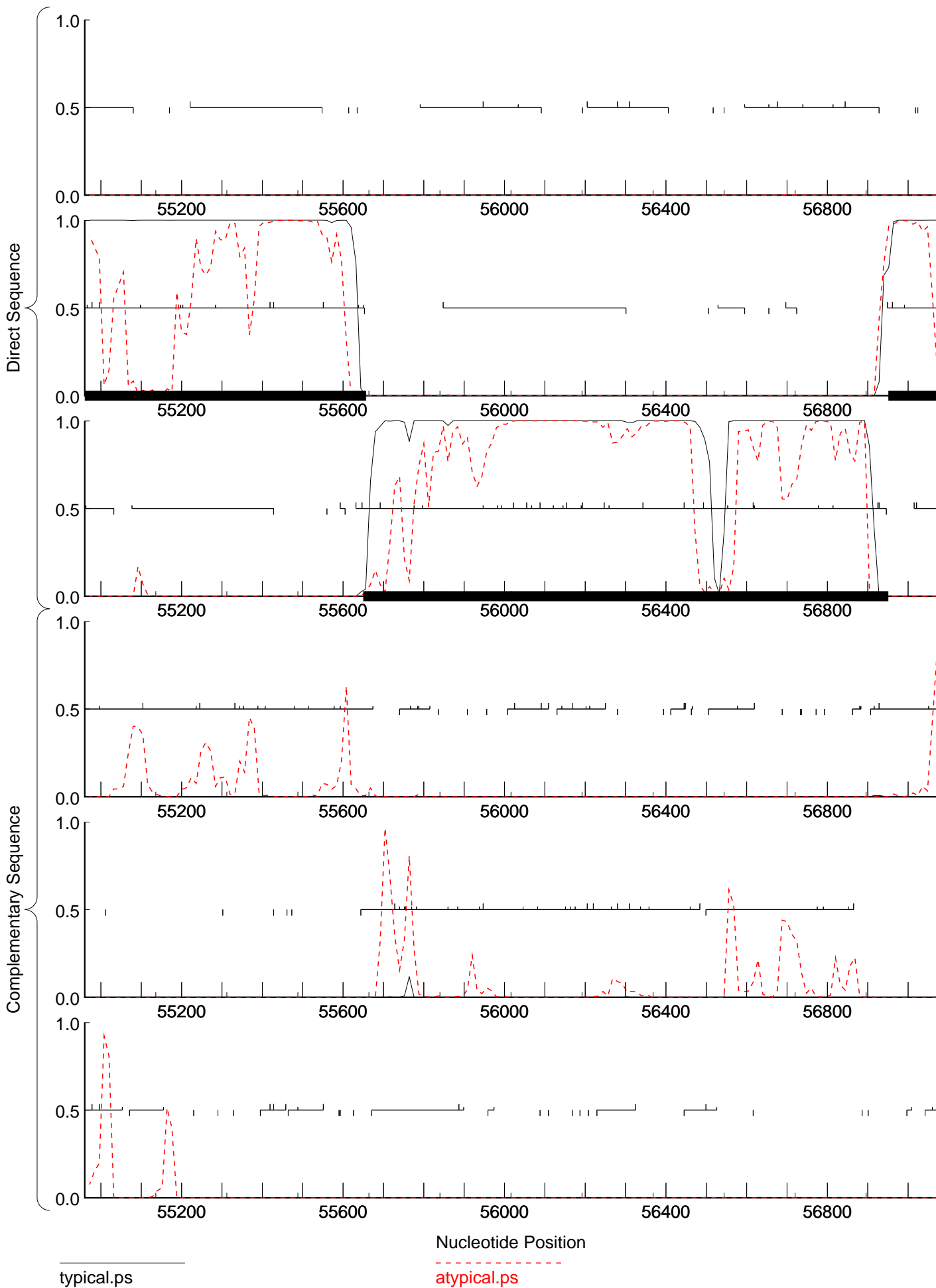
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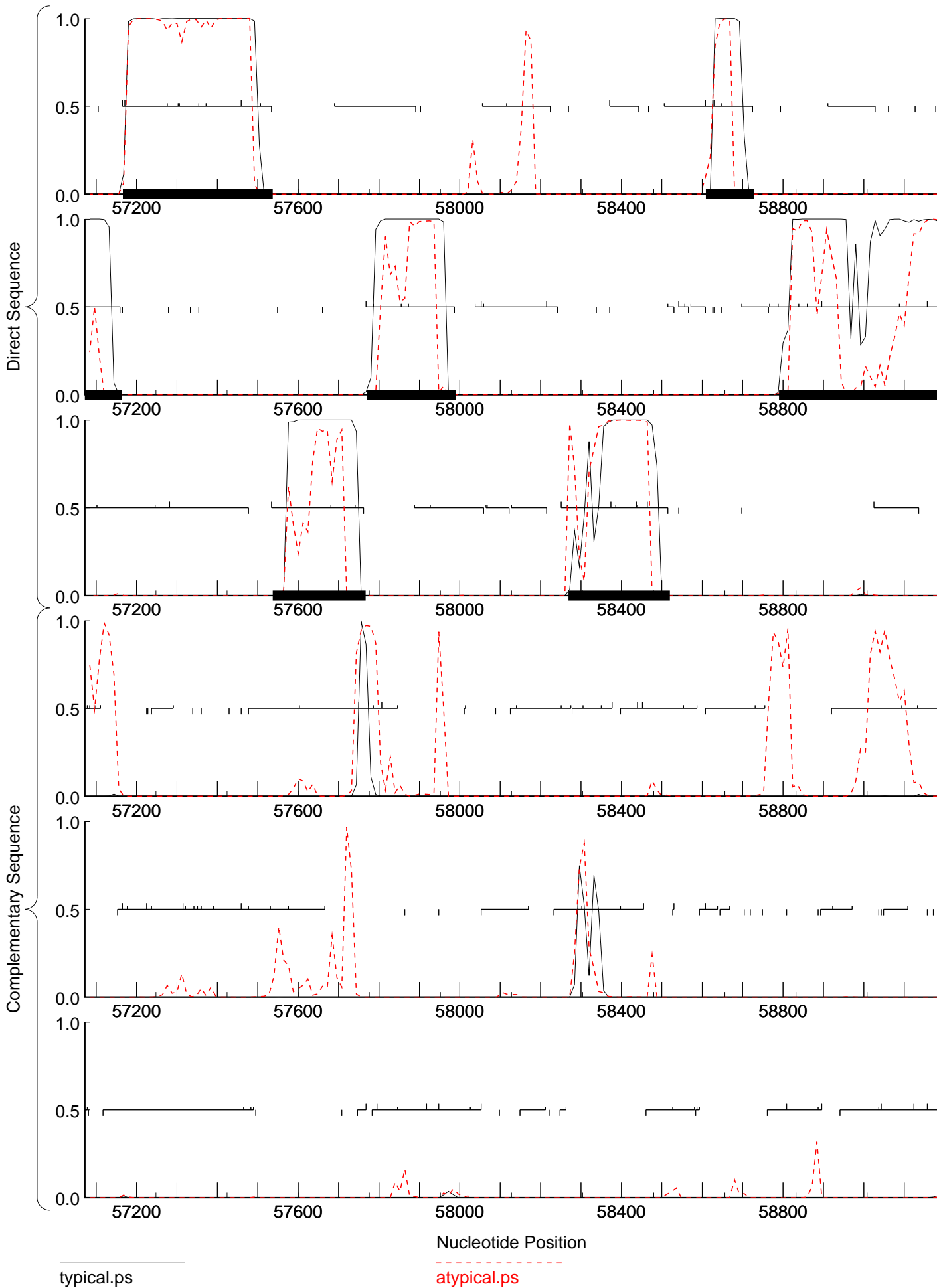
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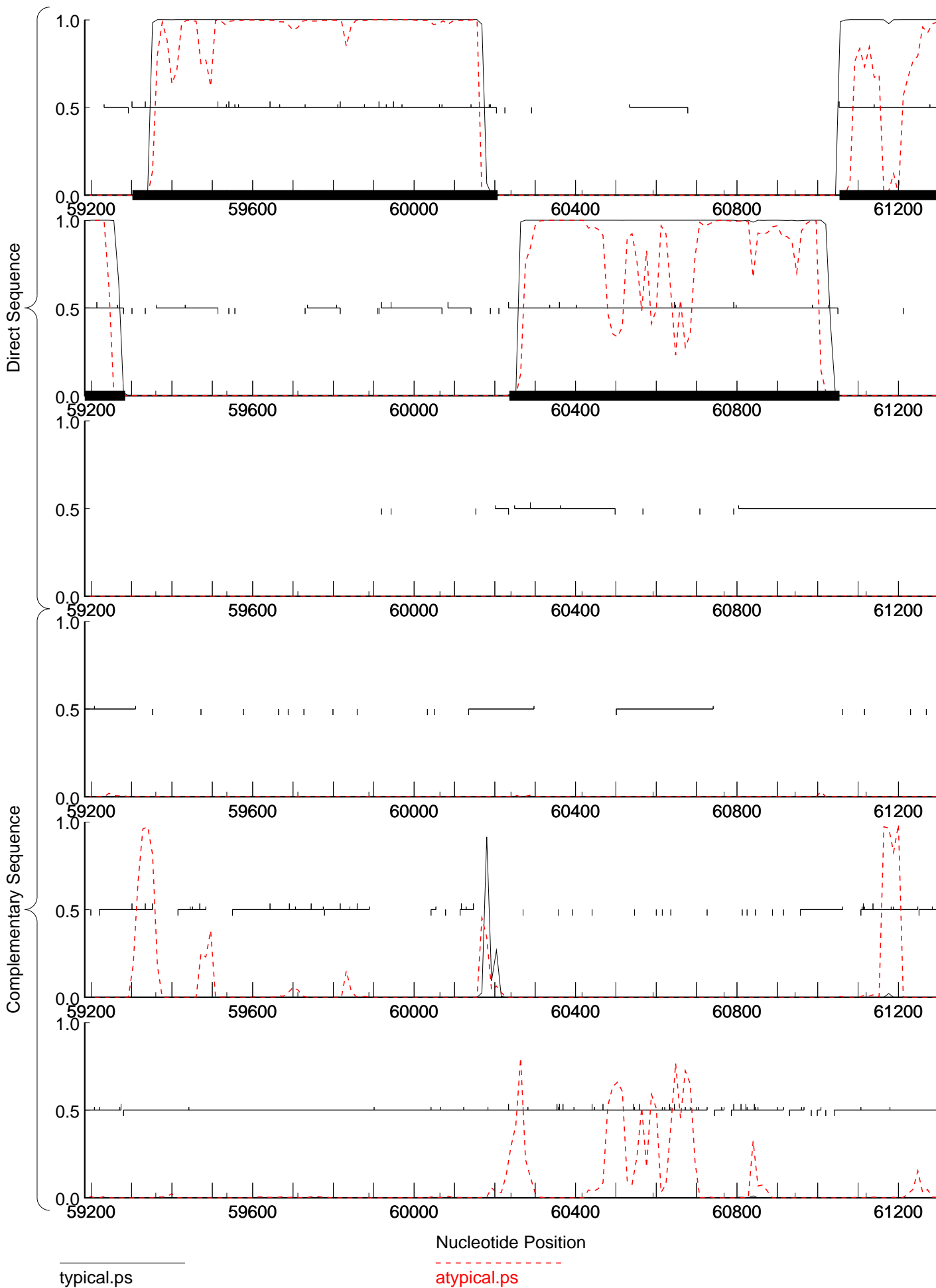


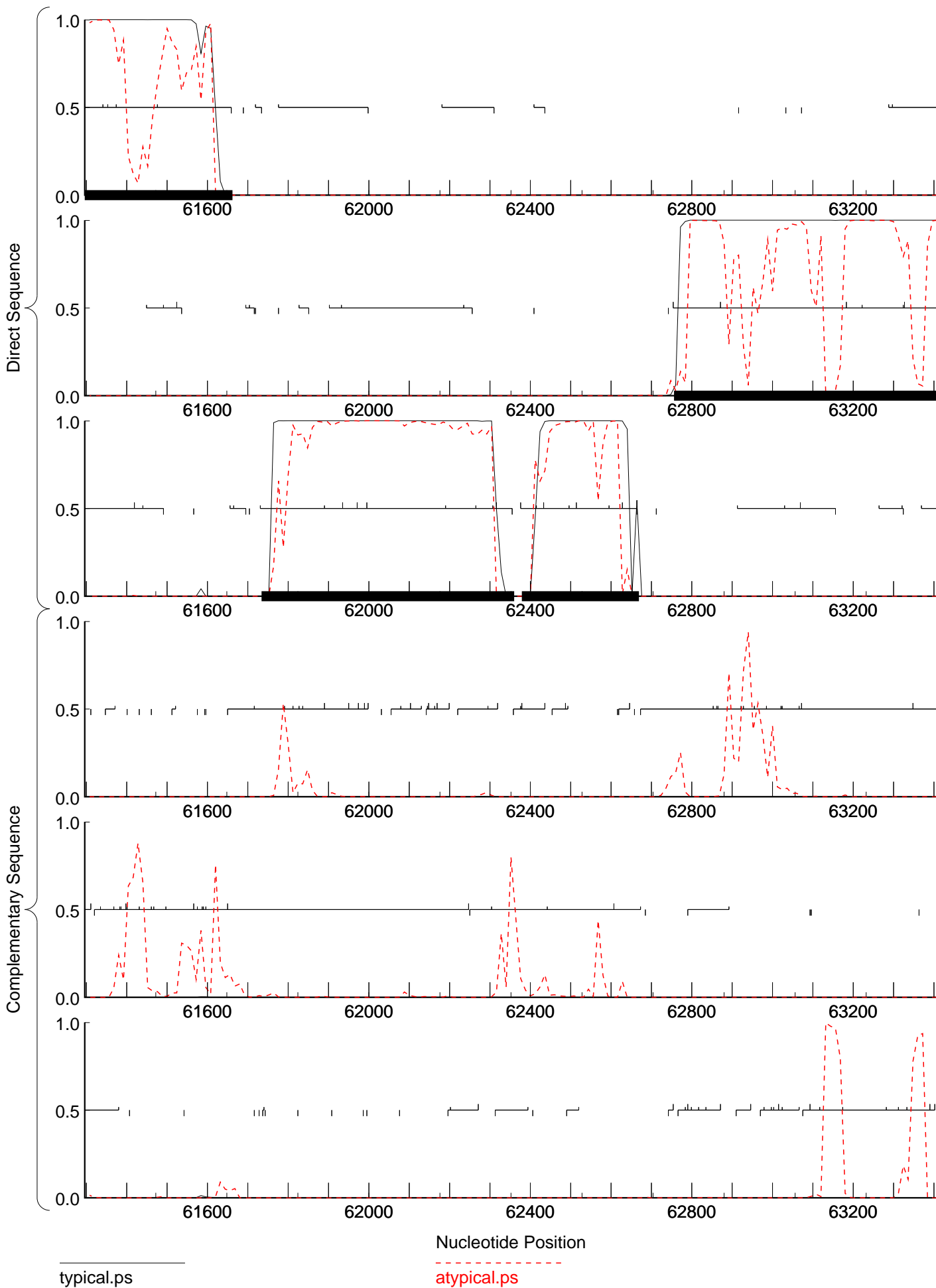
typical.ps

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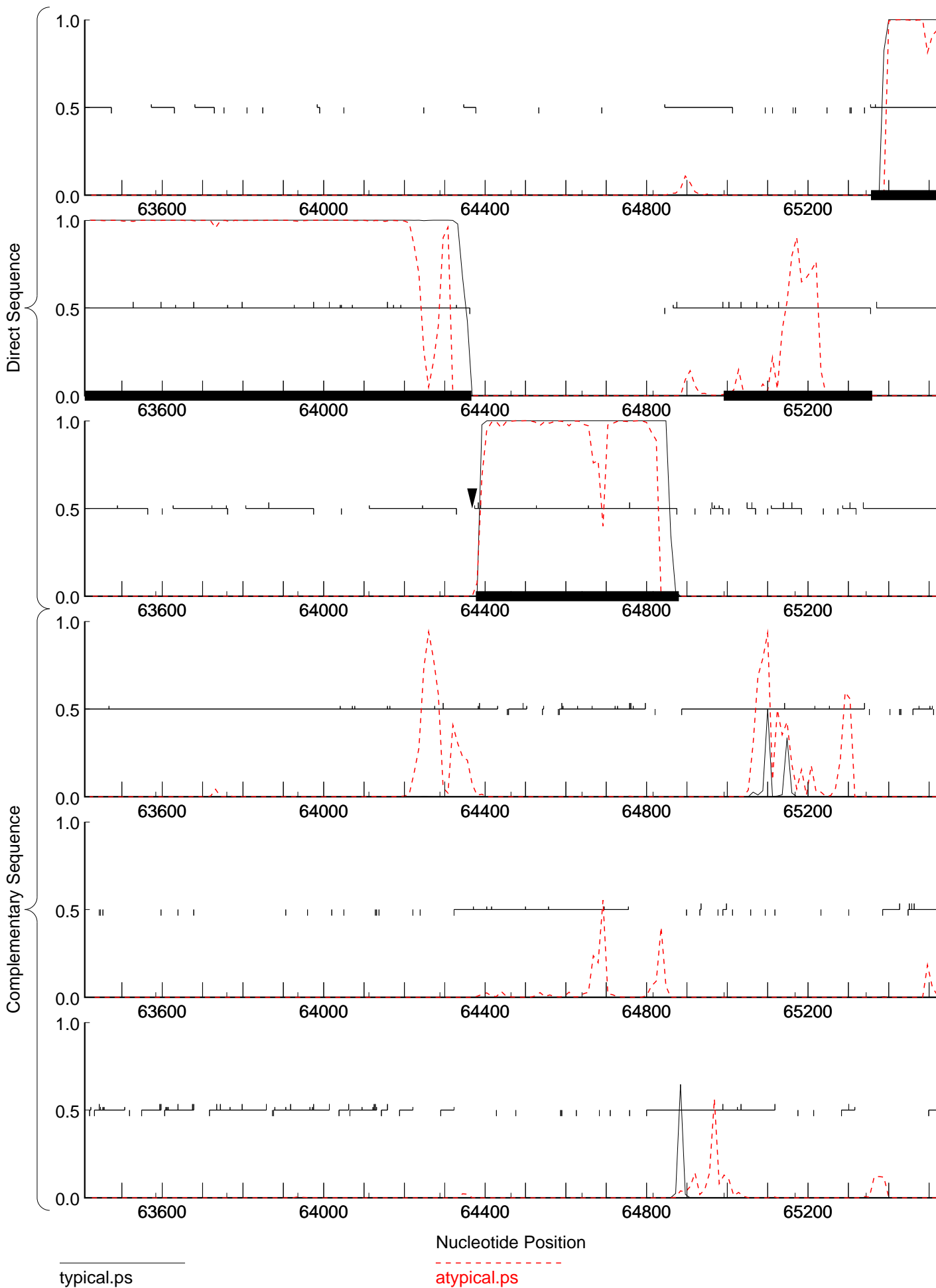


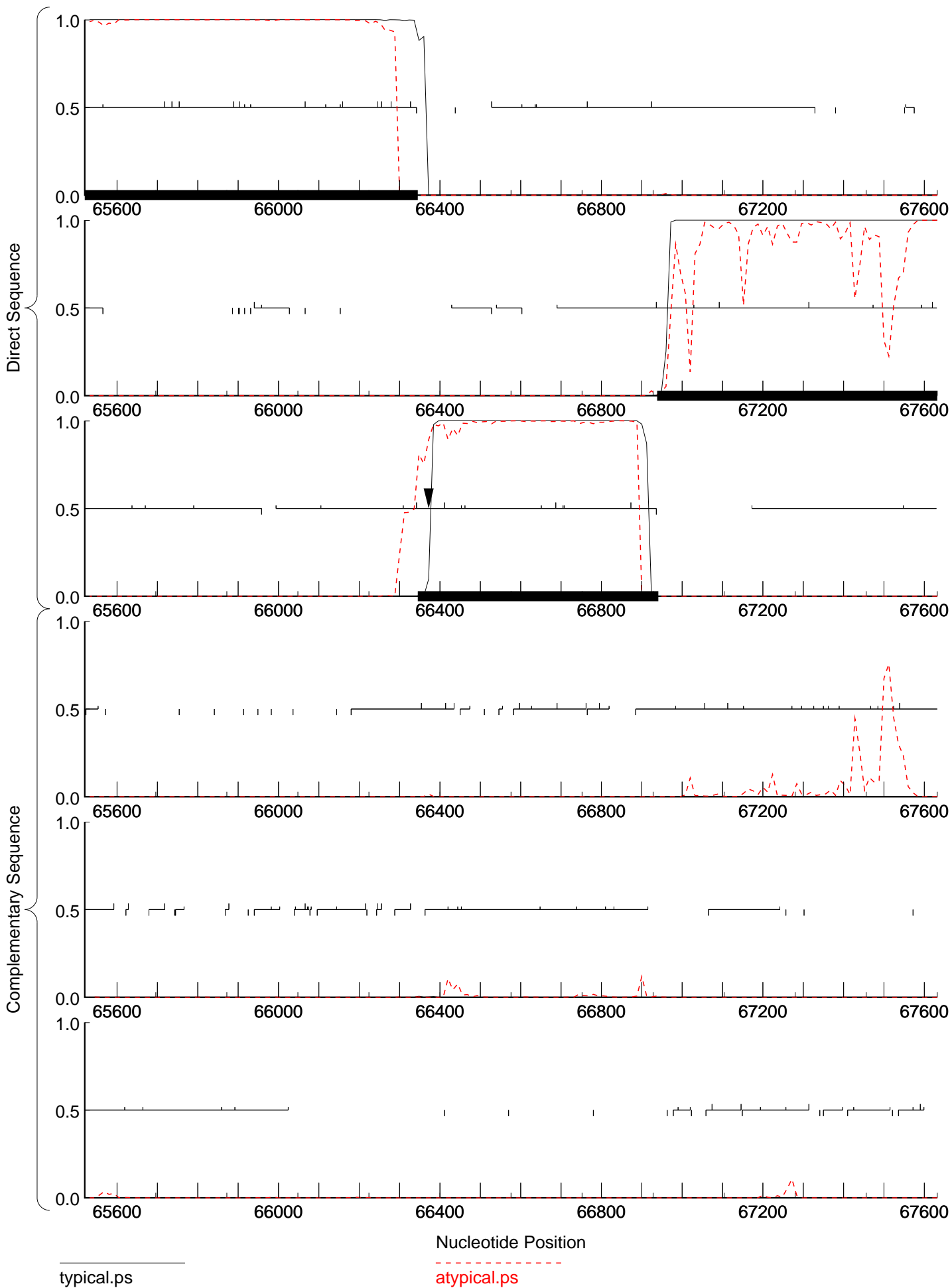




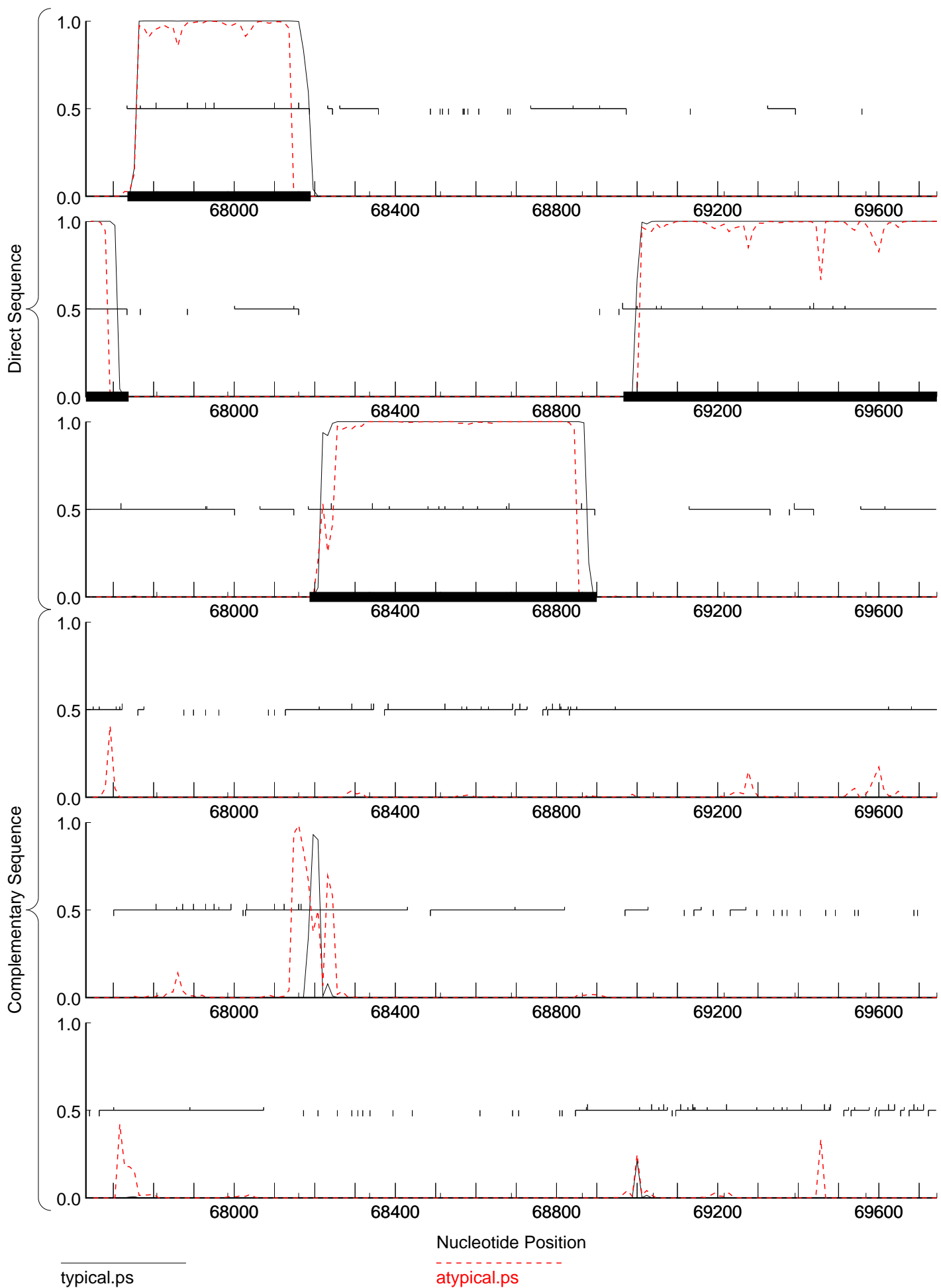
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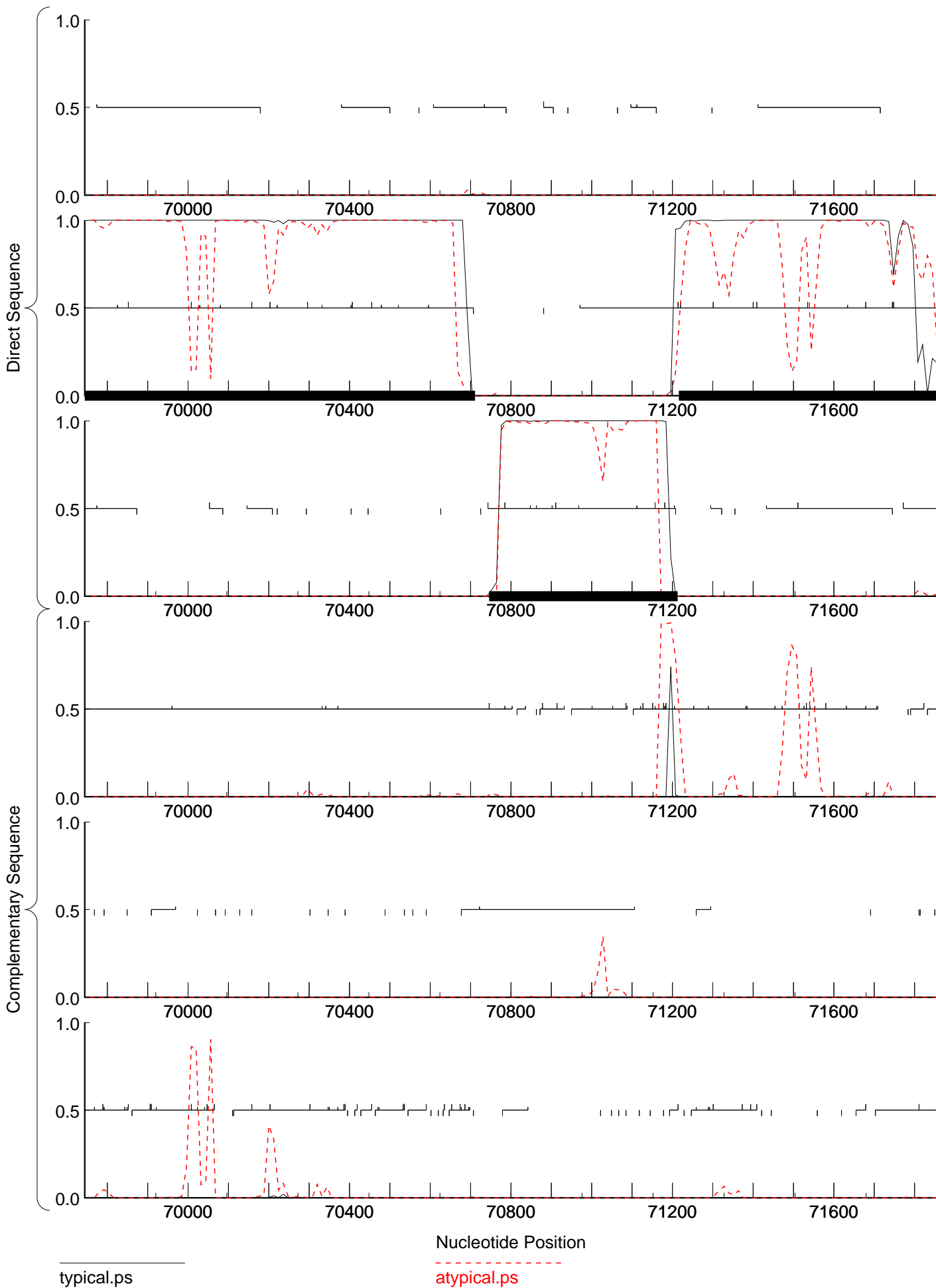
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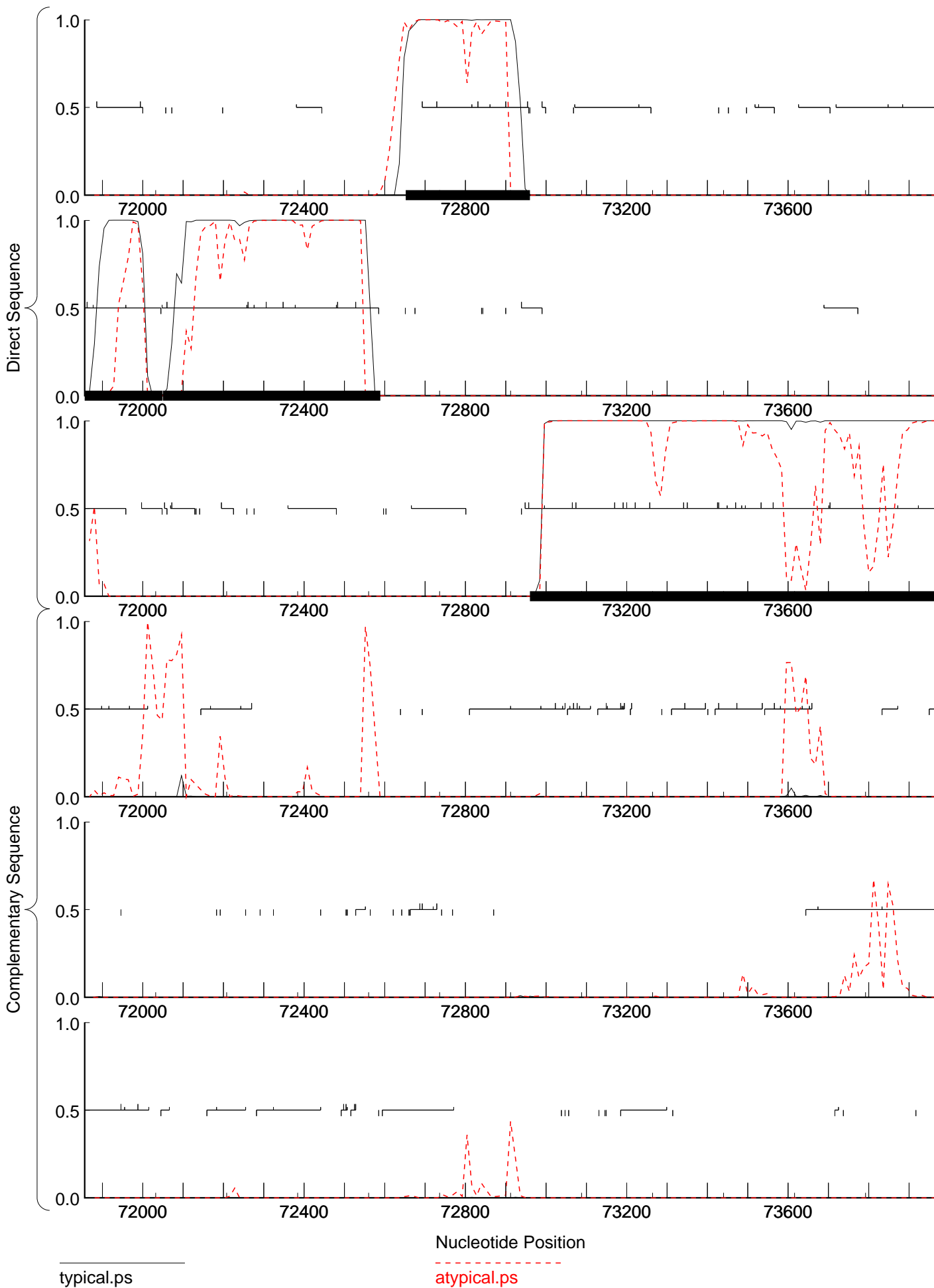
GeneMark.hmm prediction

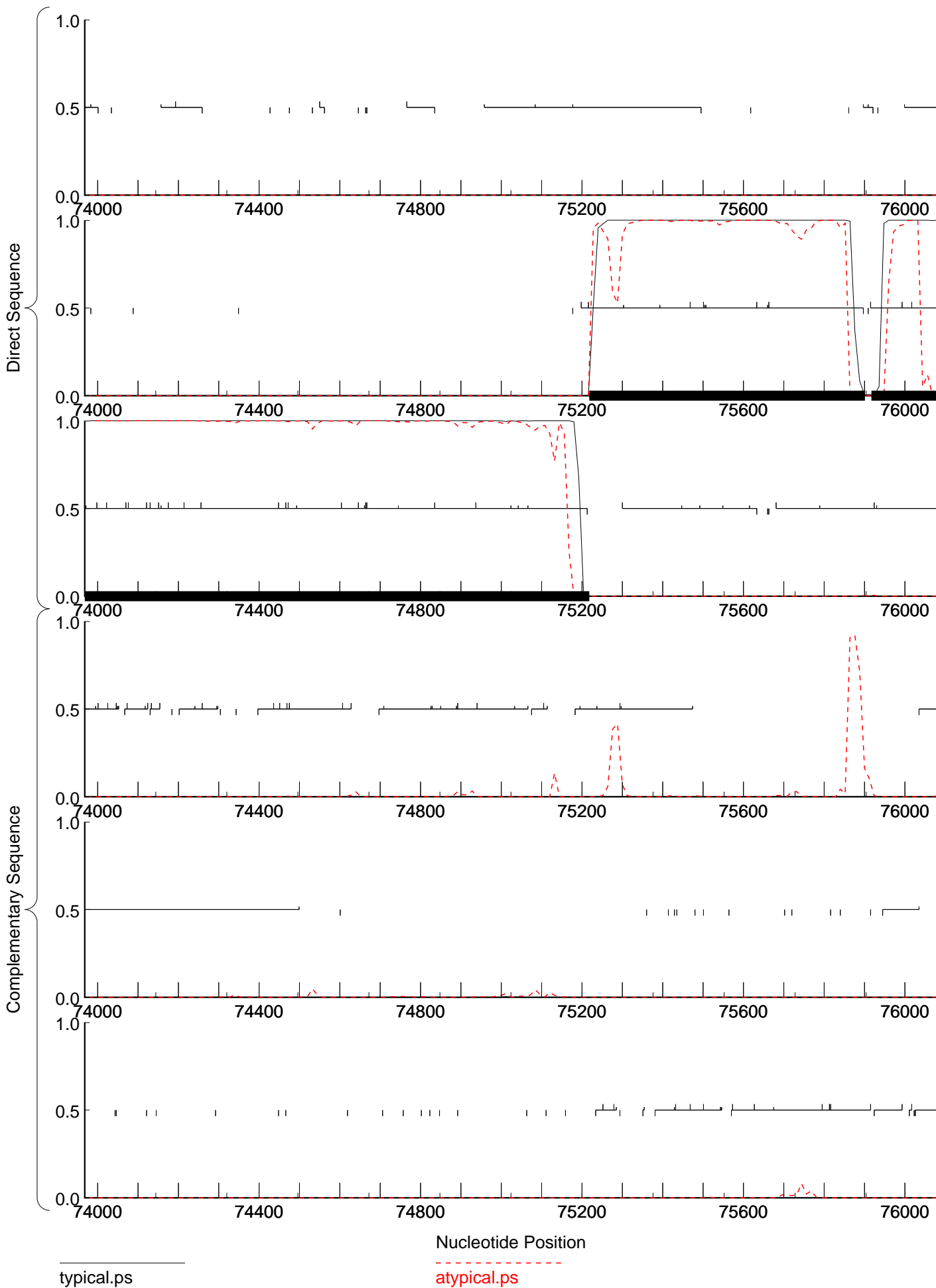


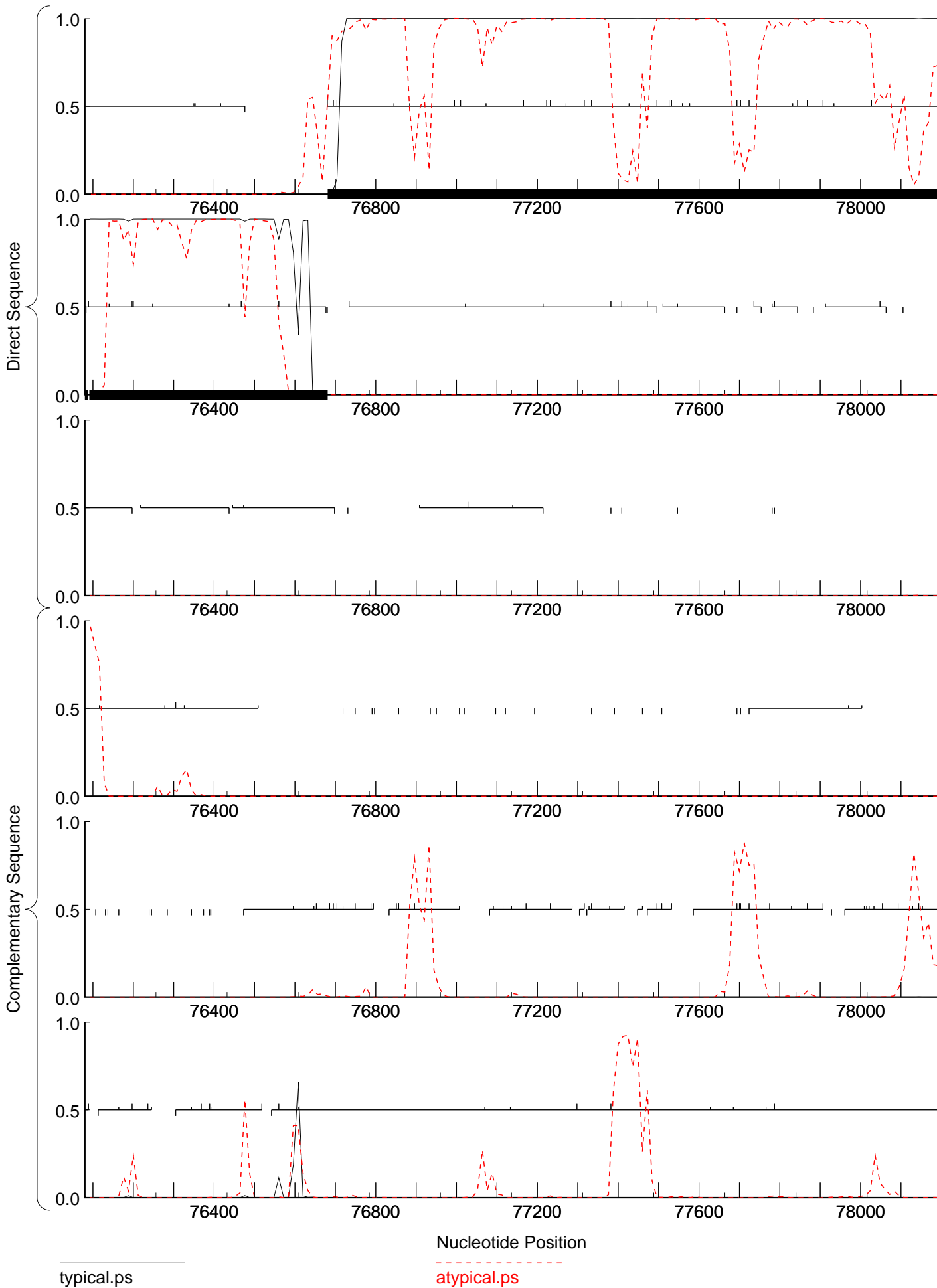


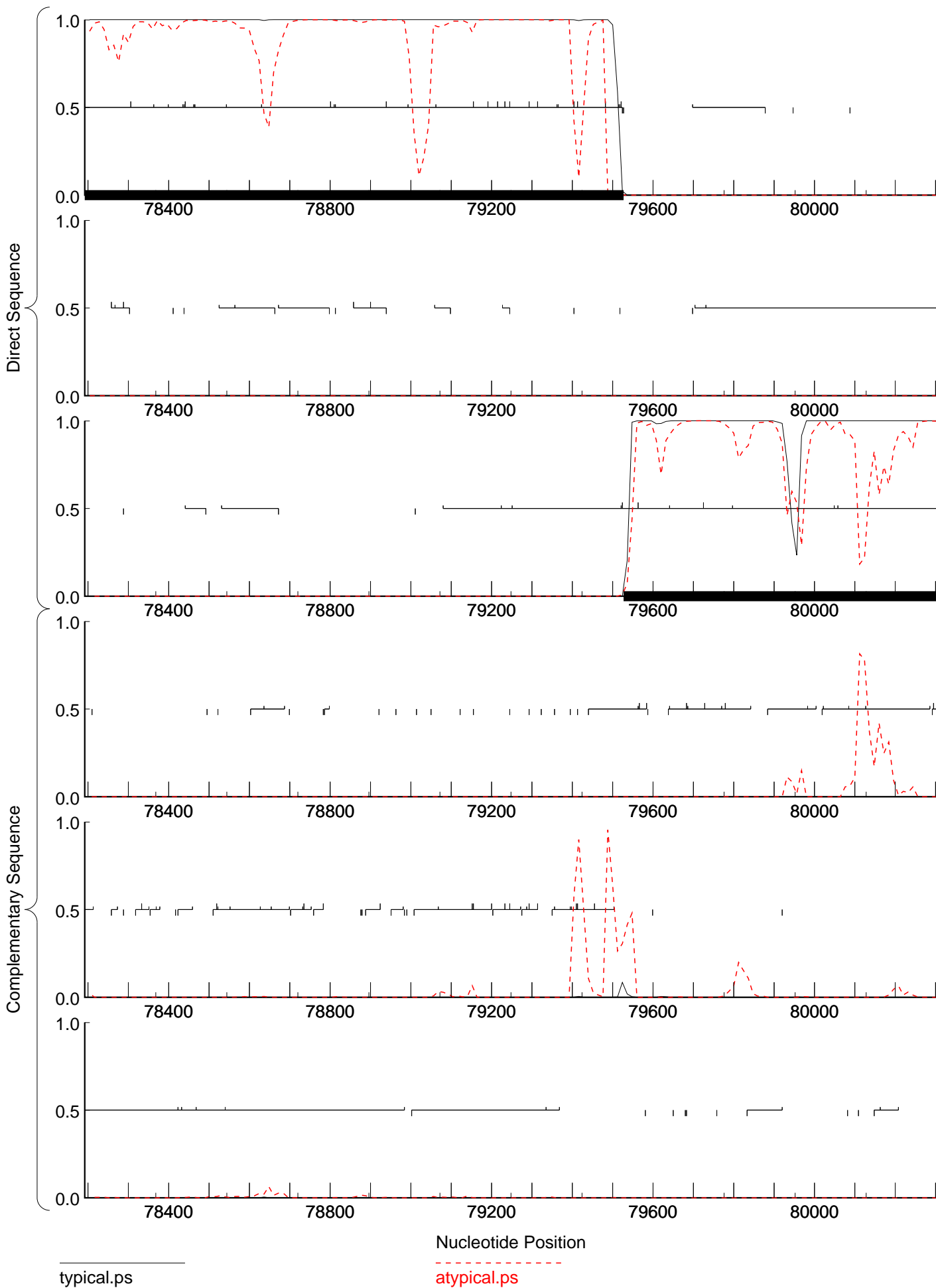
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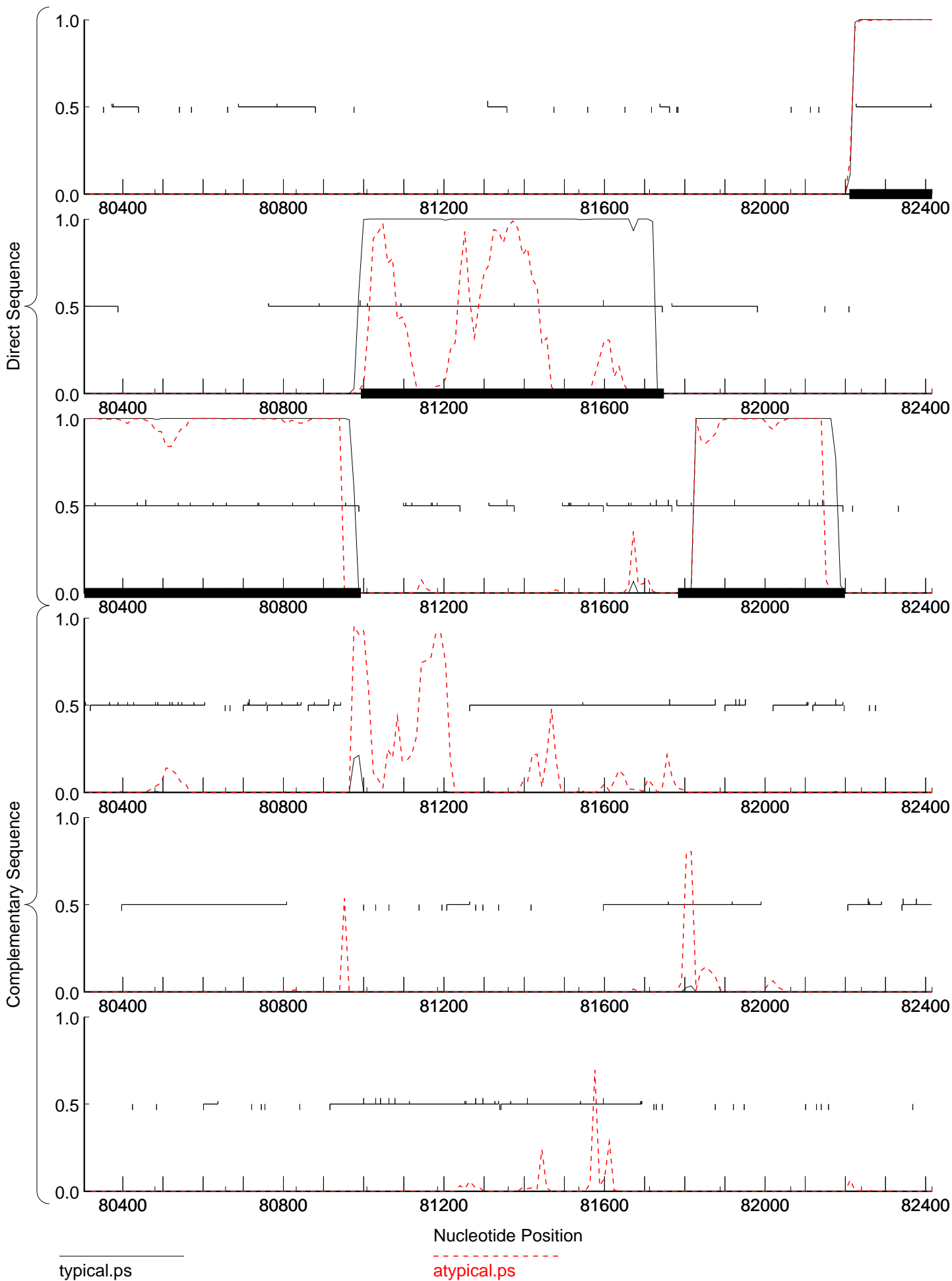


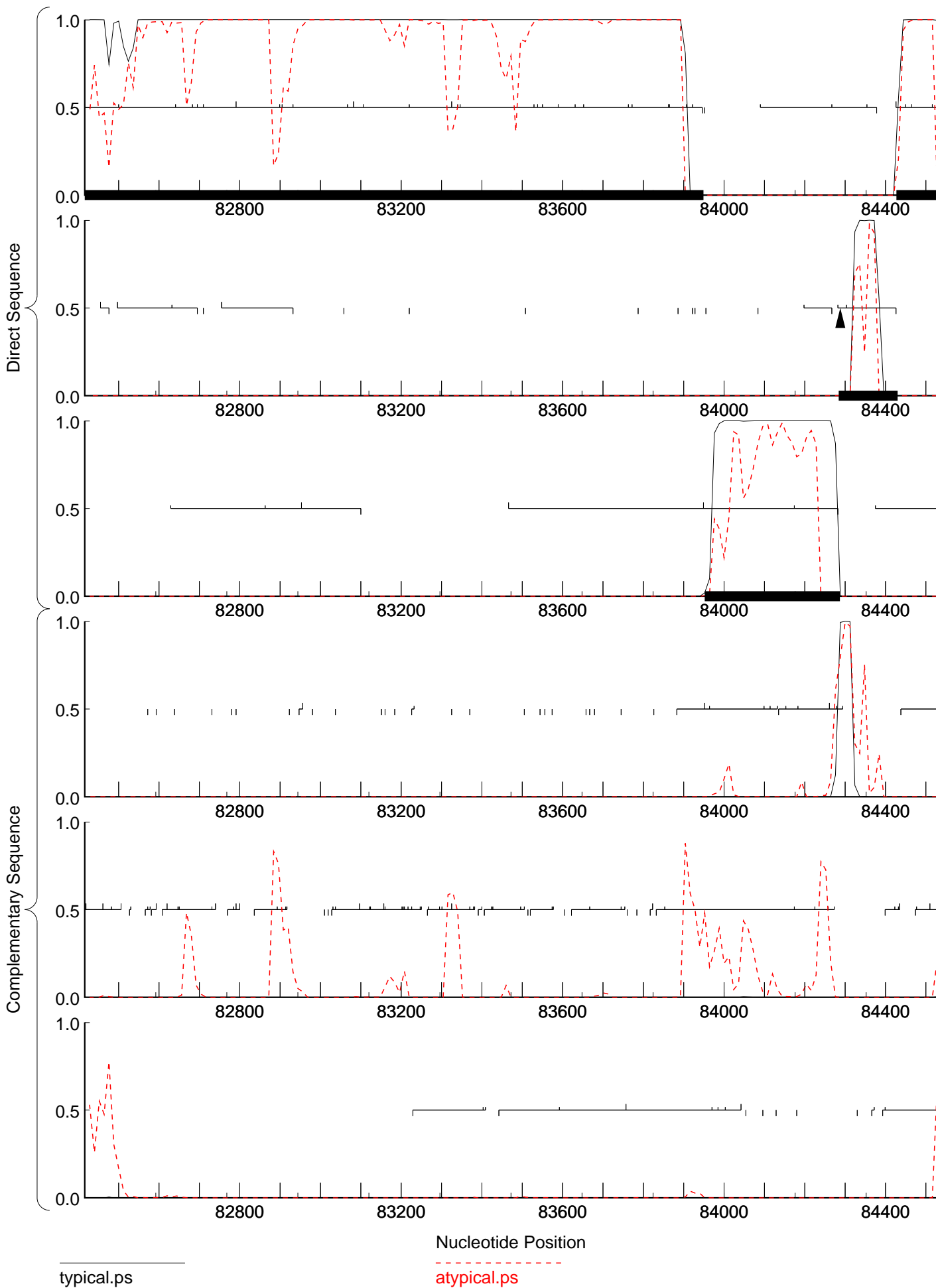




typical.ps

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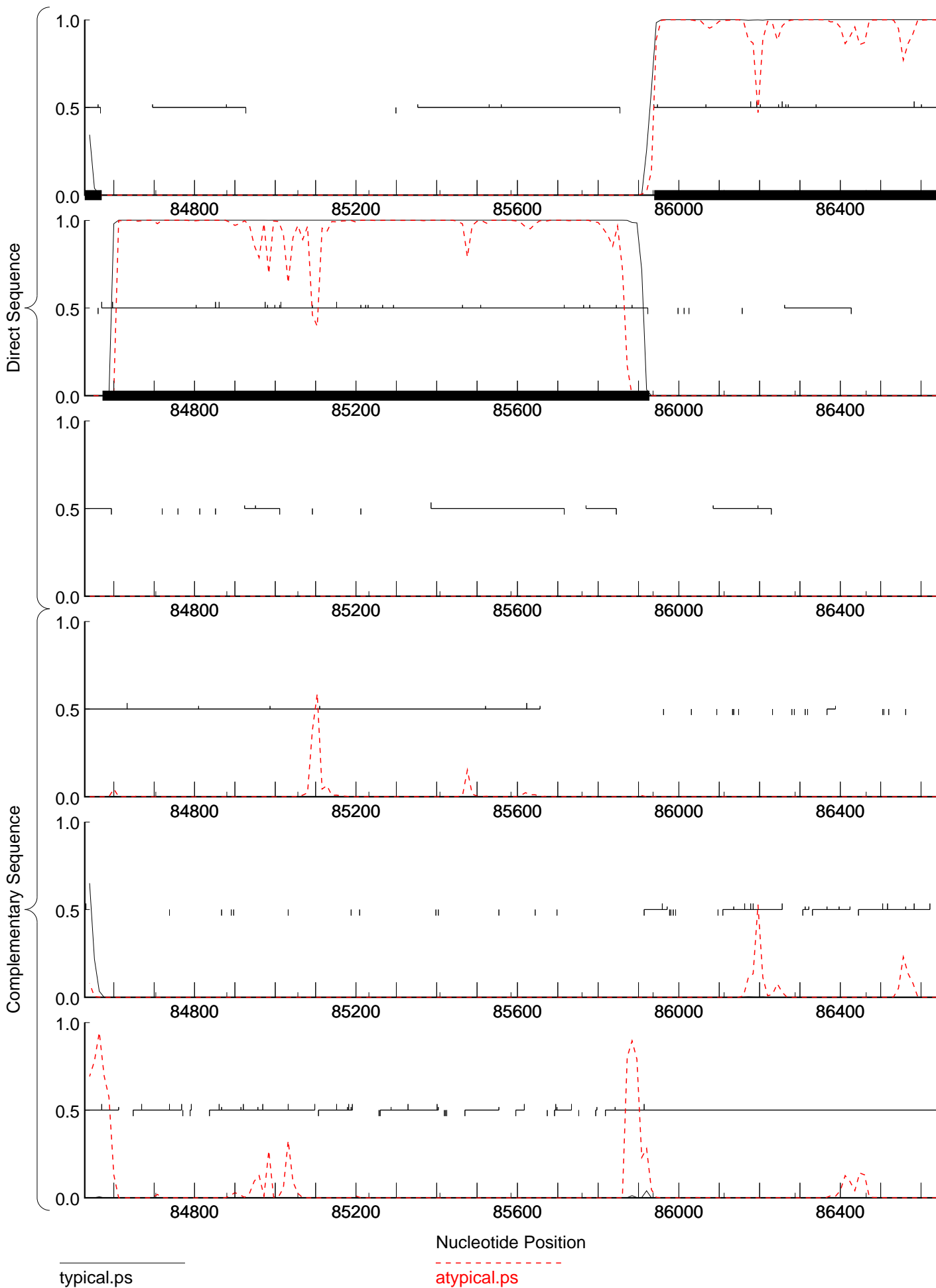


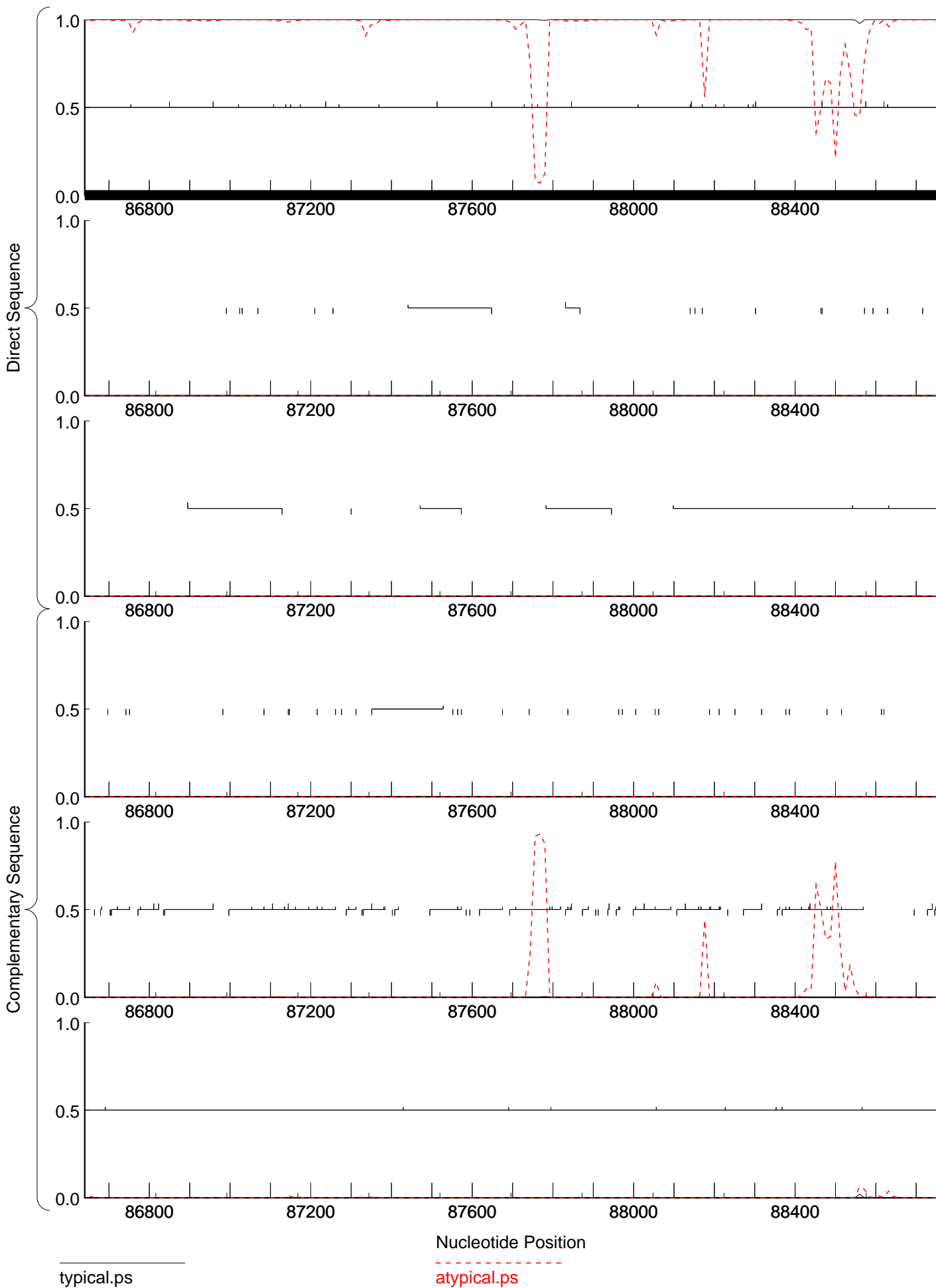


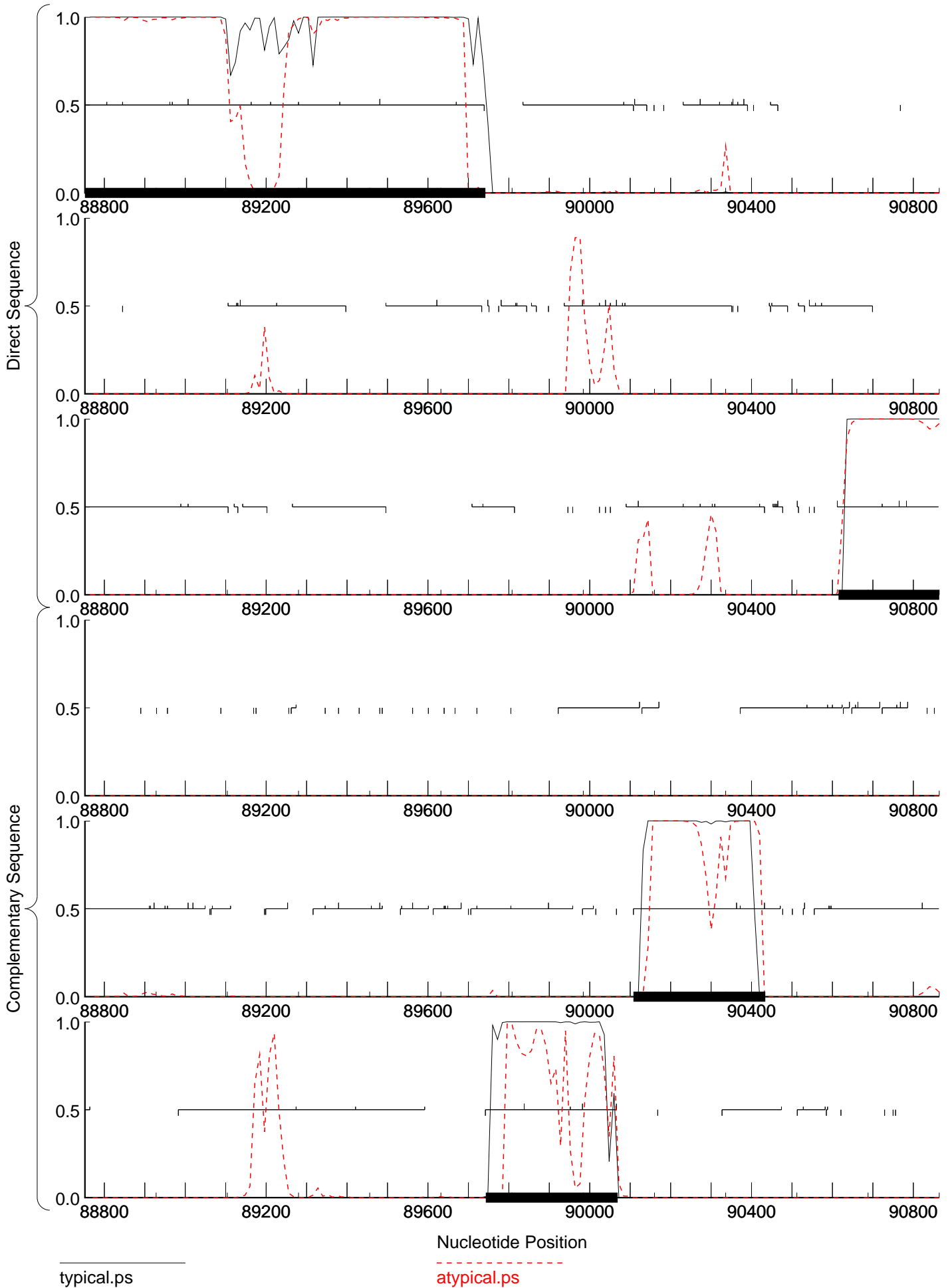
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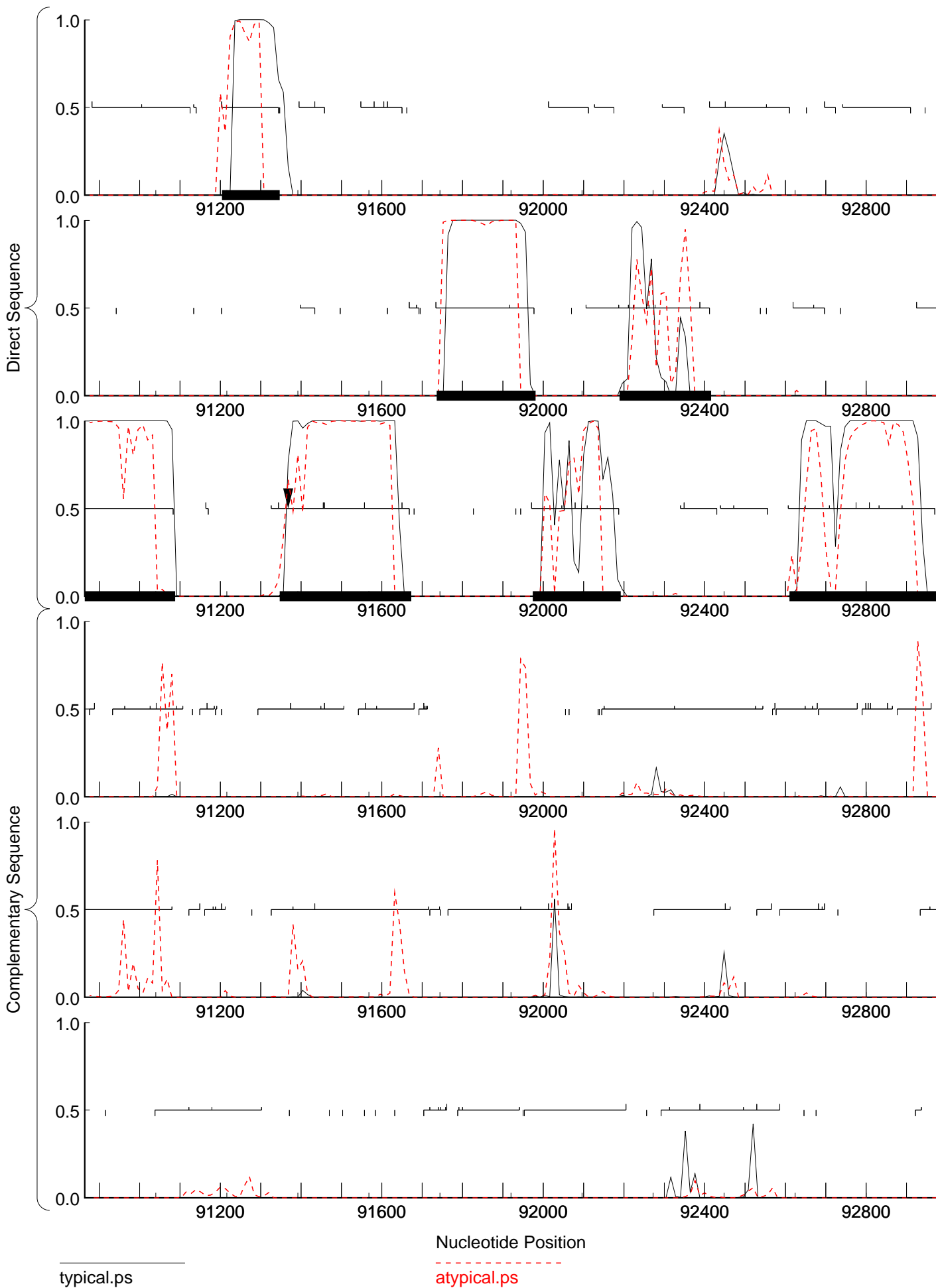
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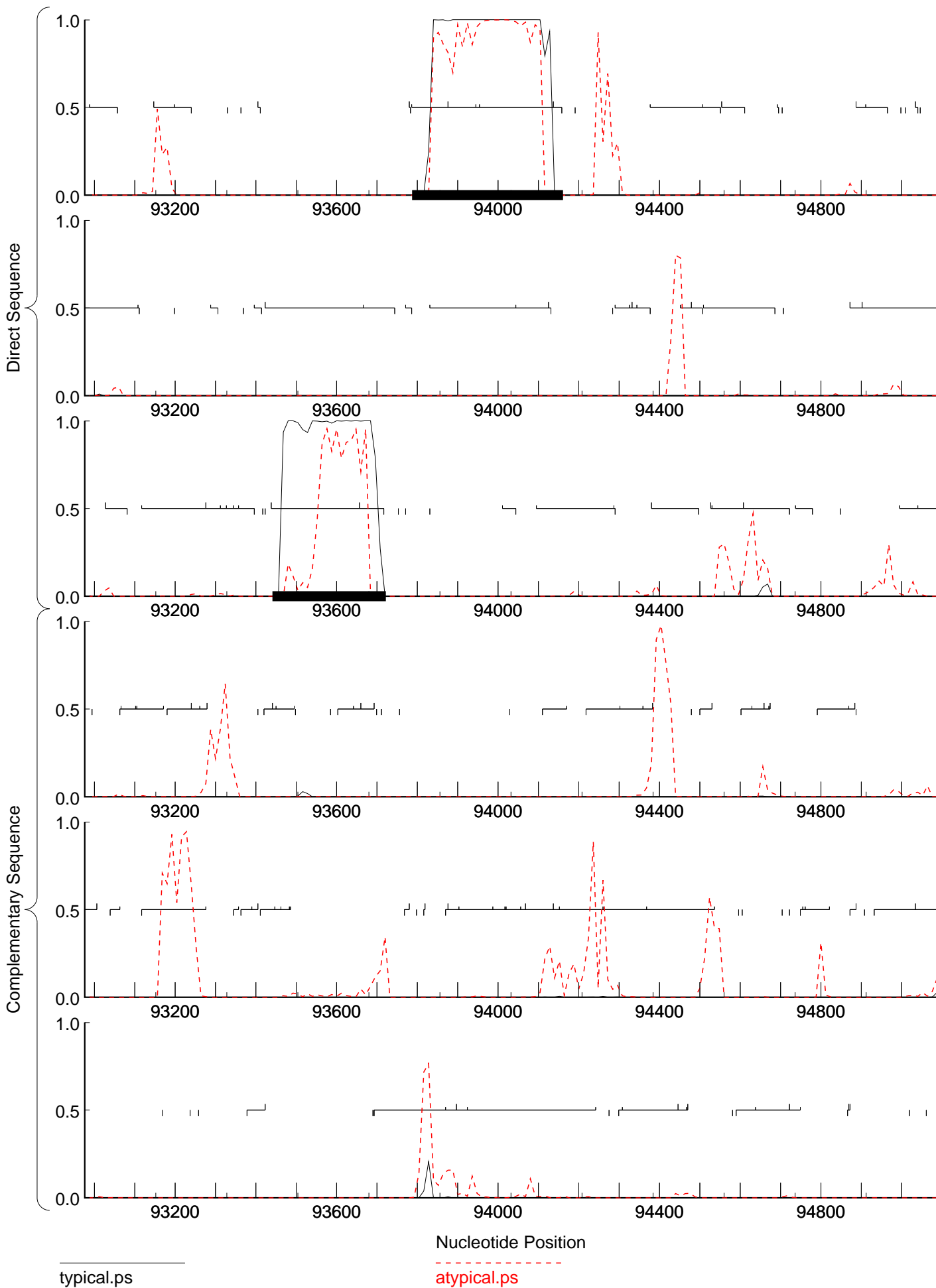
GeneMark.hmm prediction



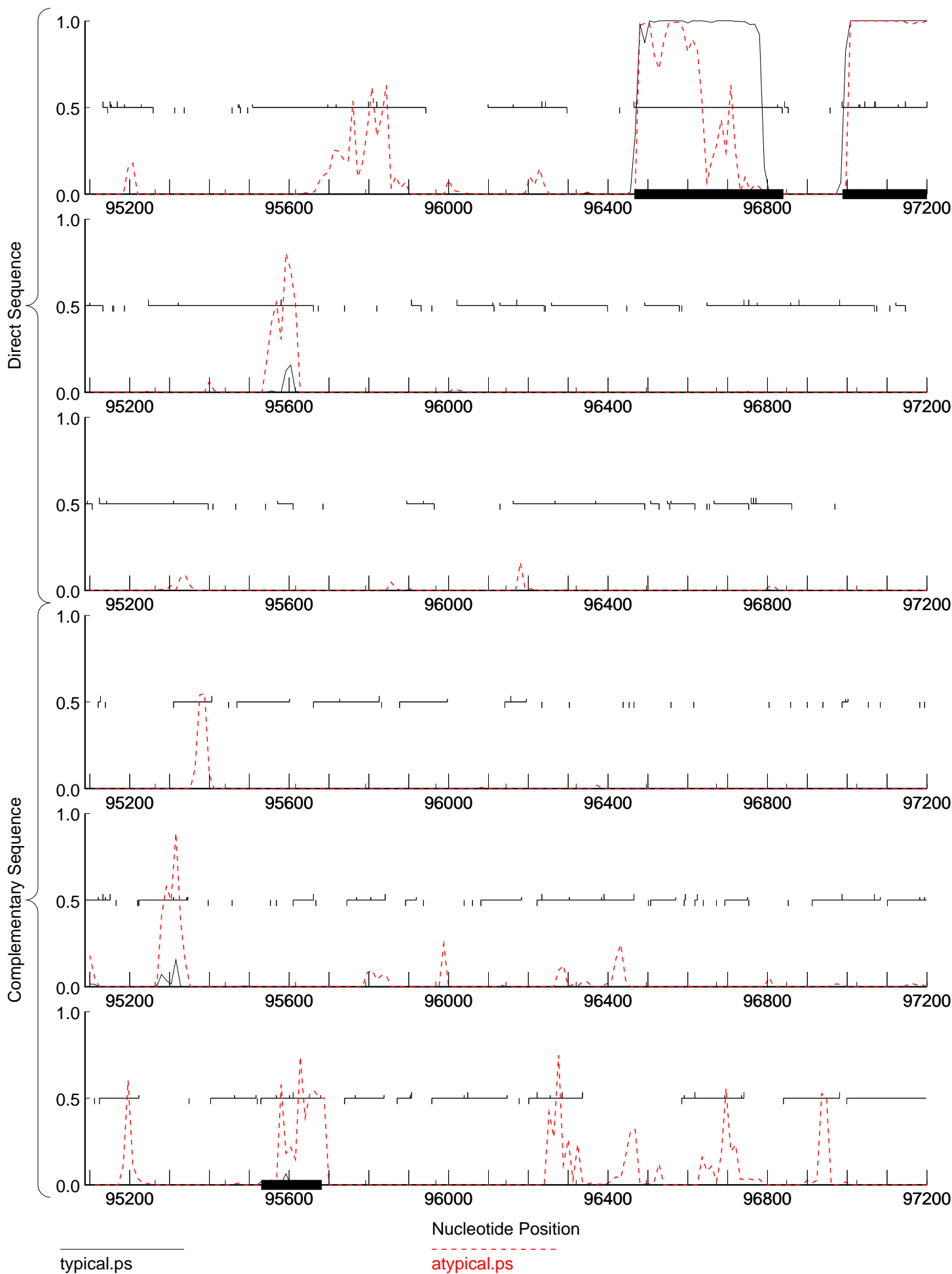






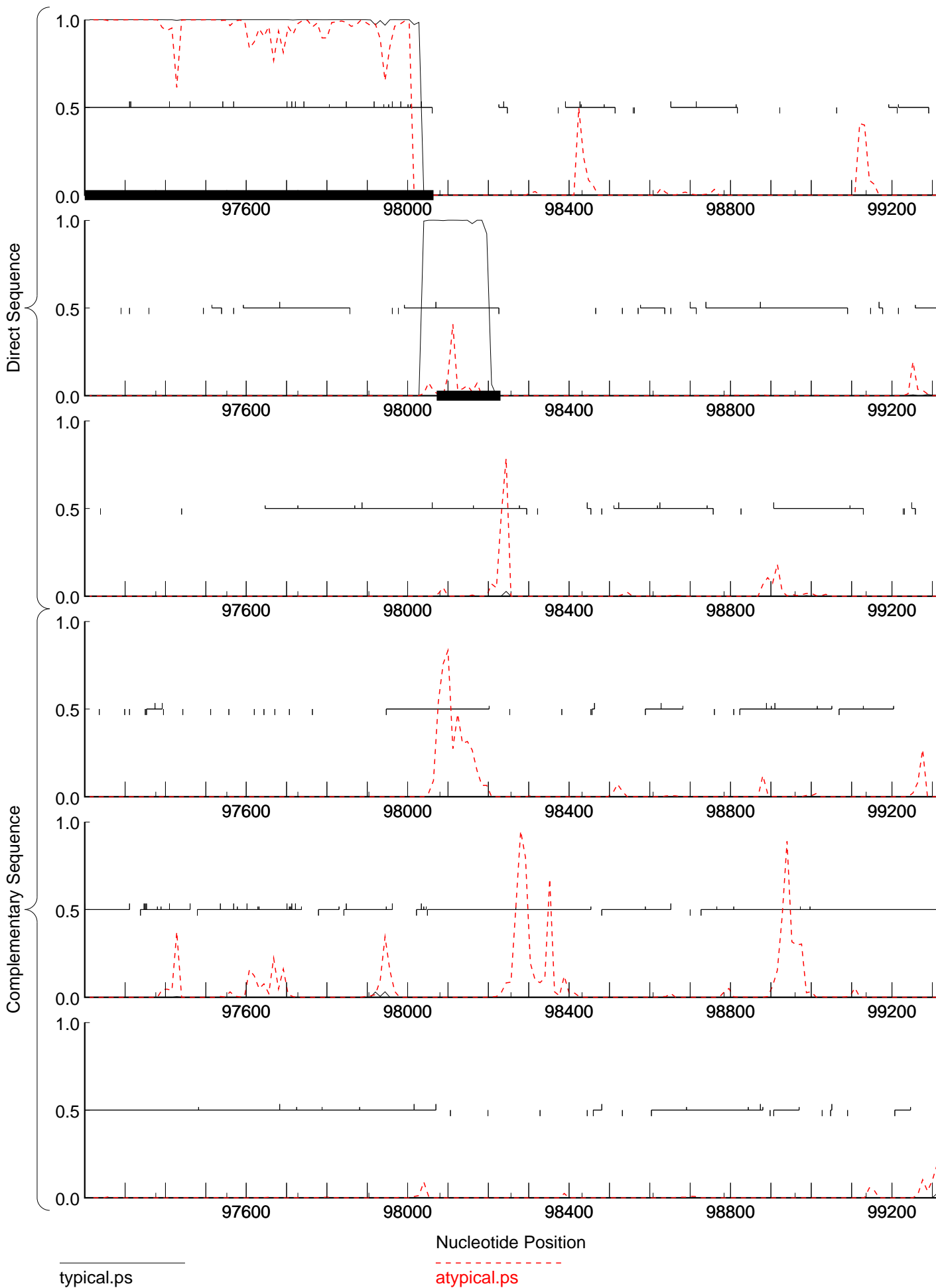


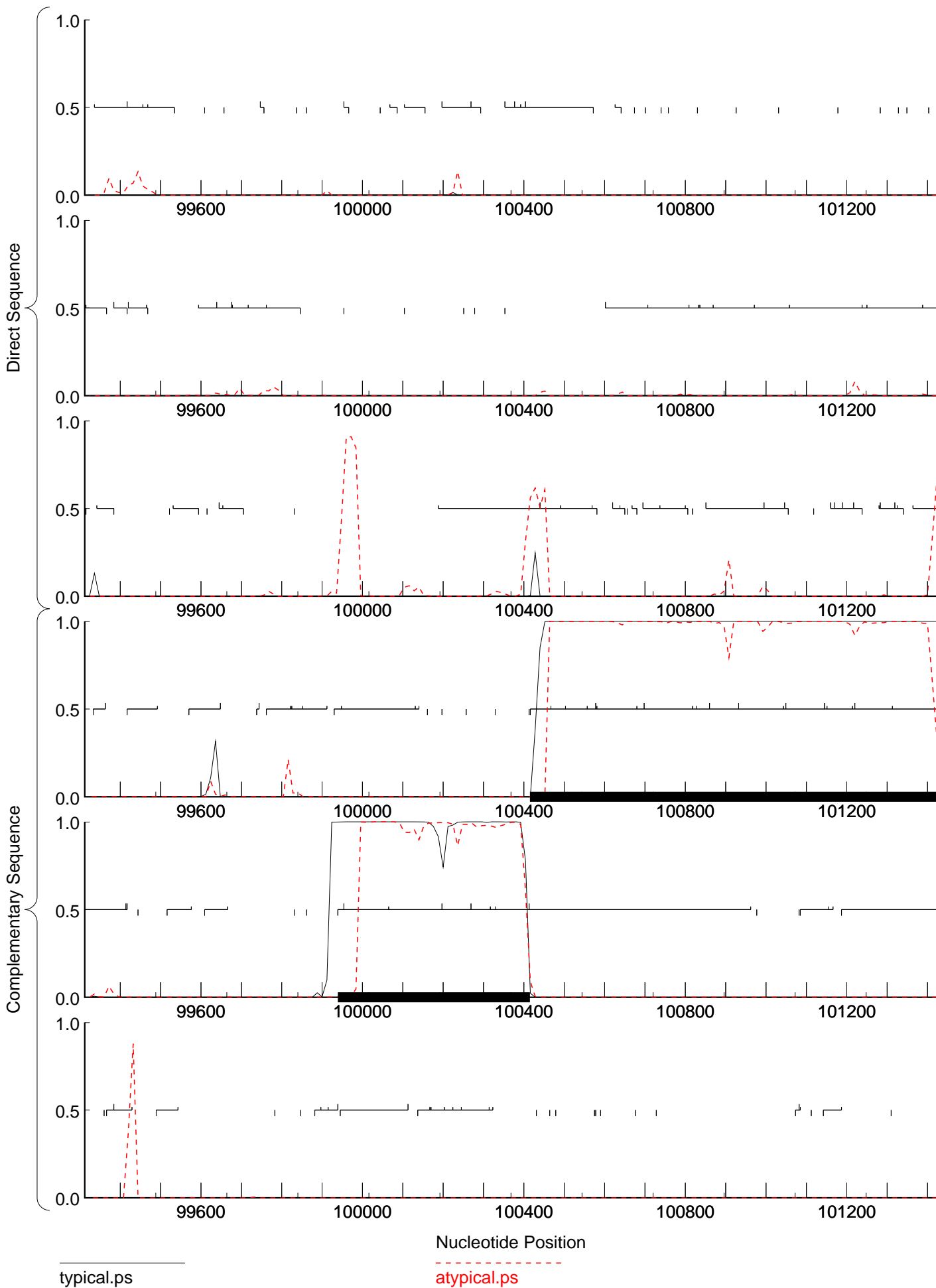
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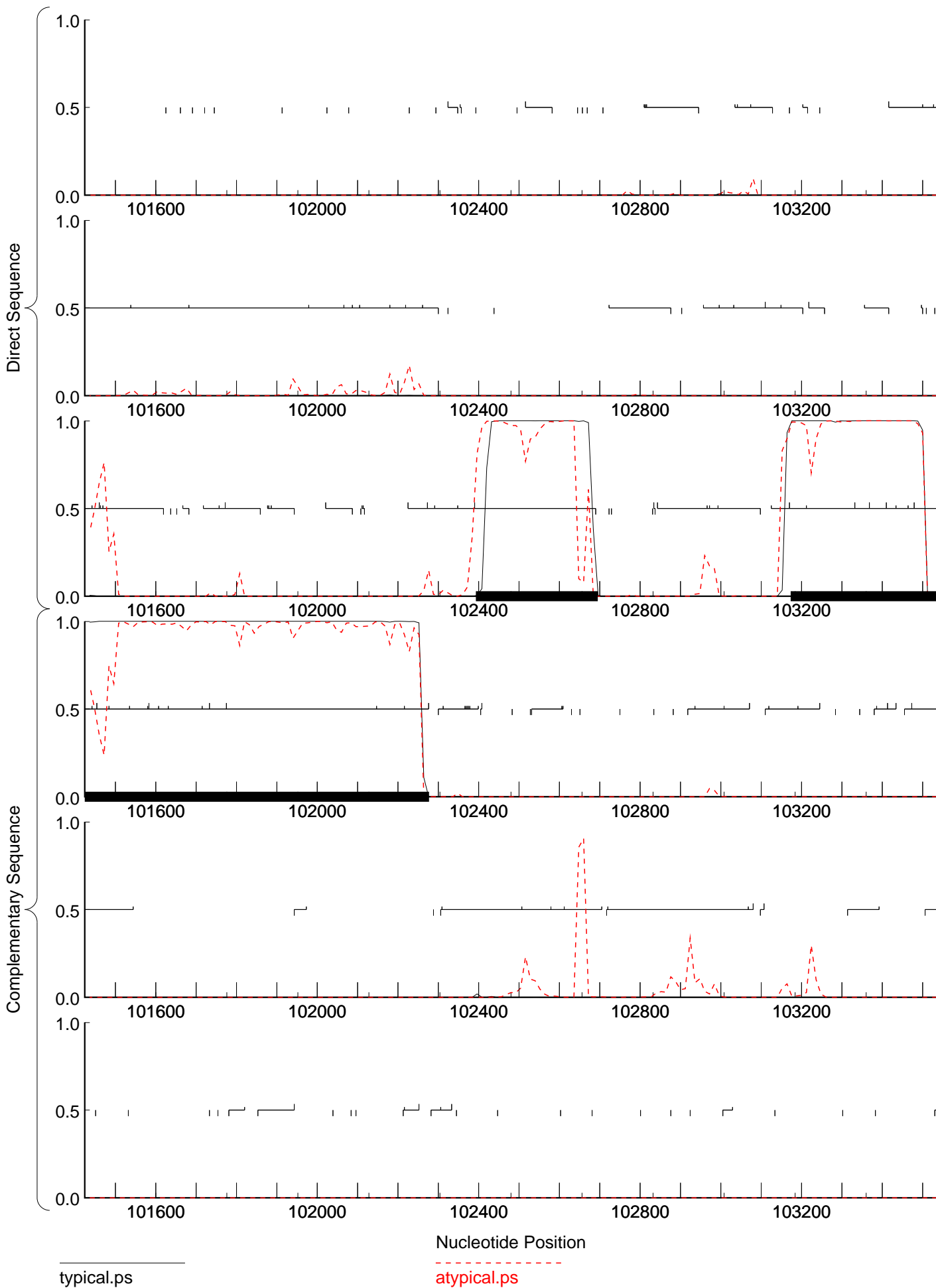


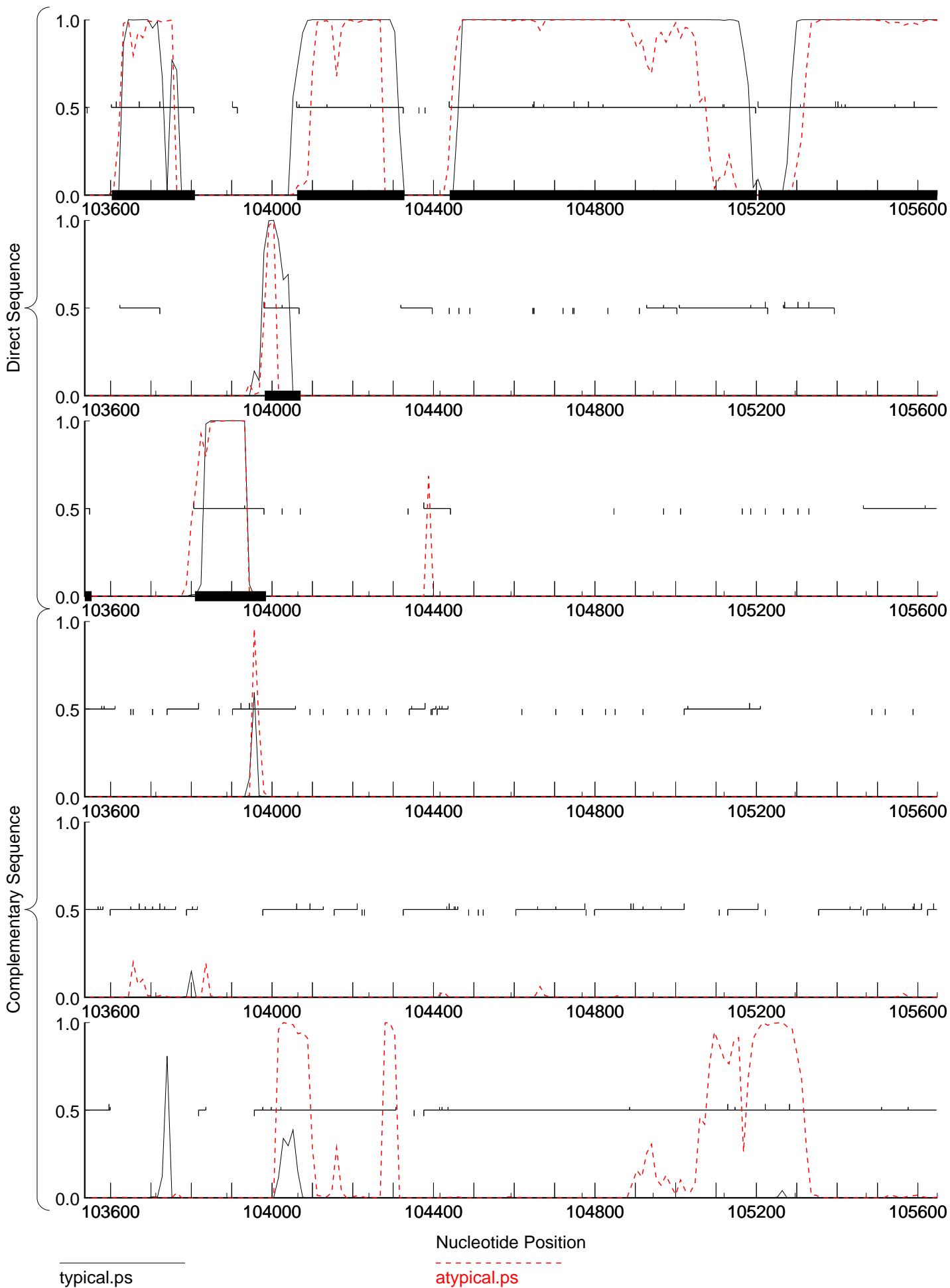
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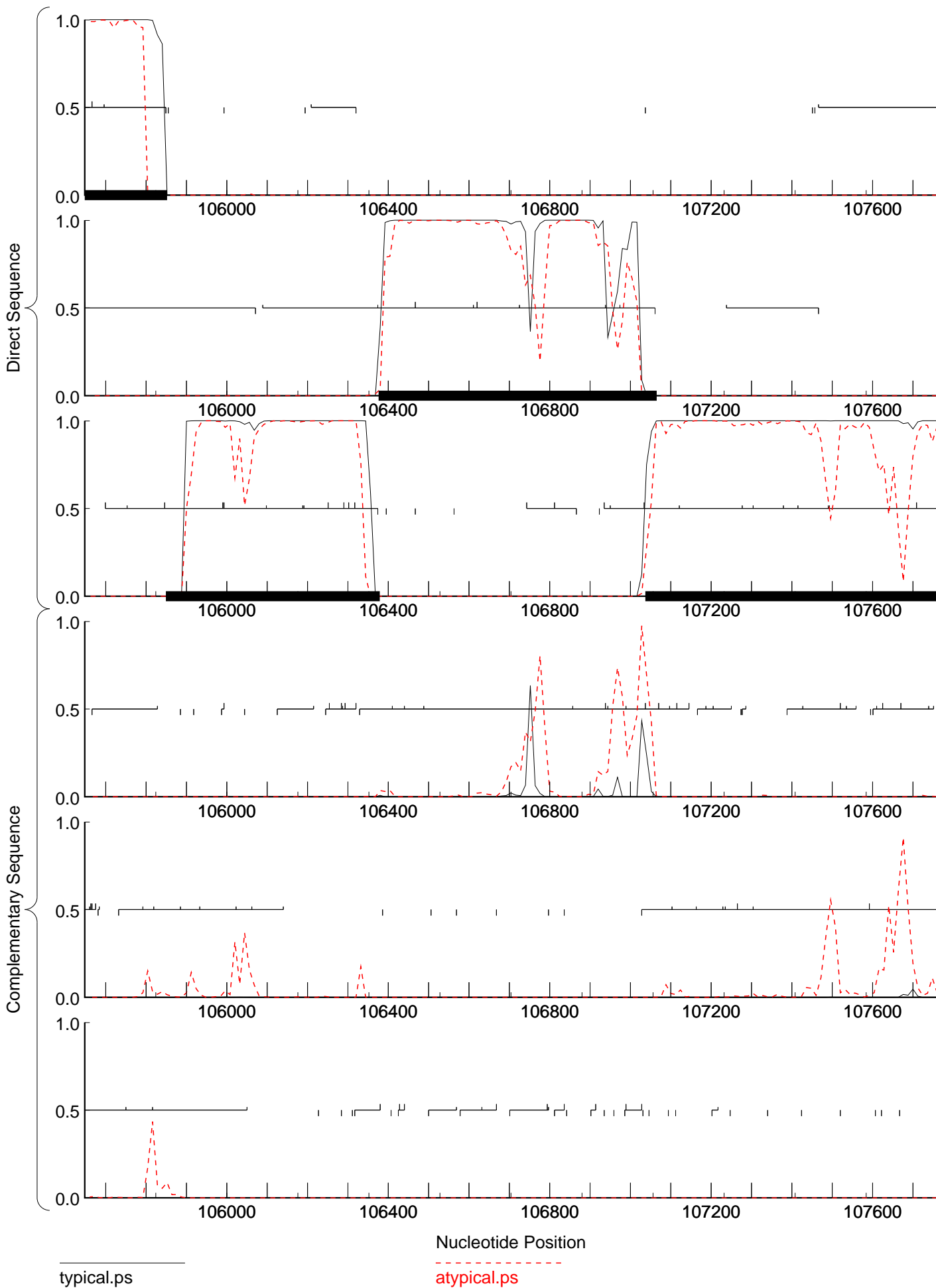
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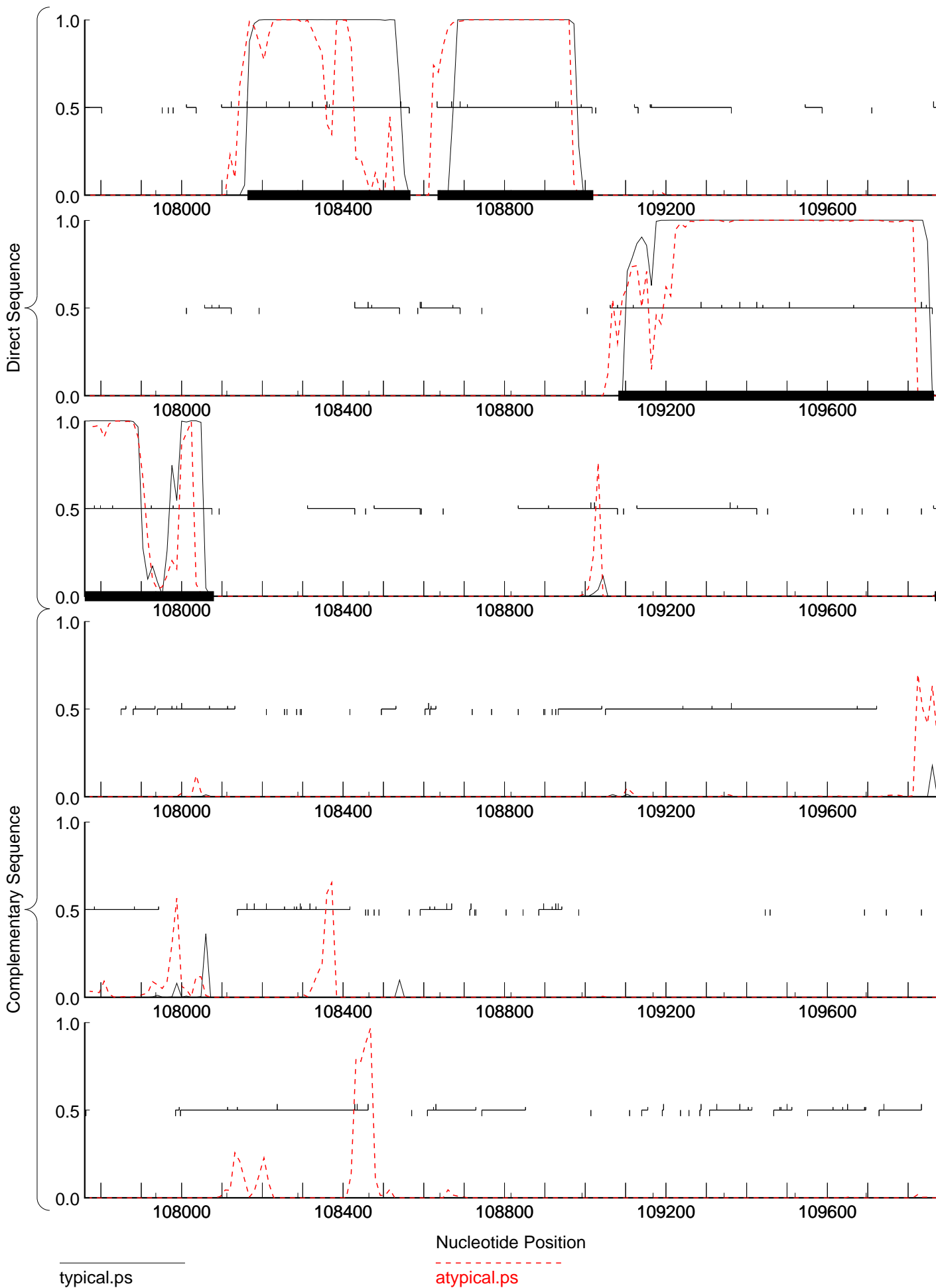


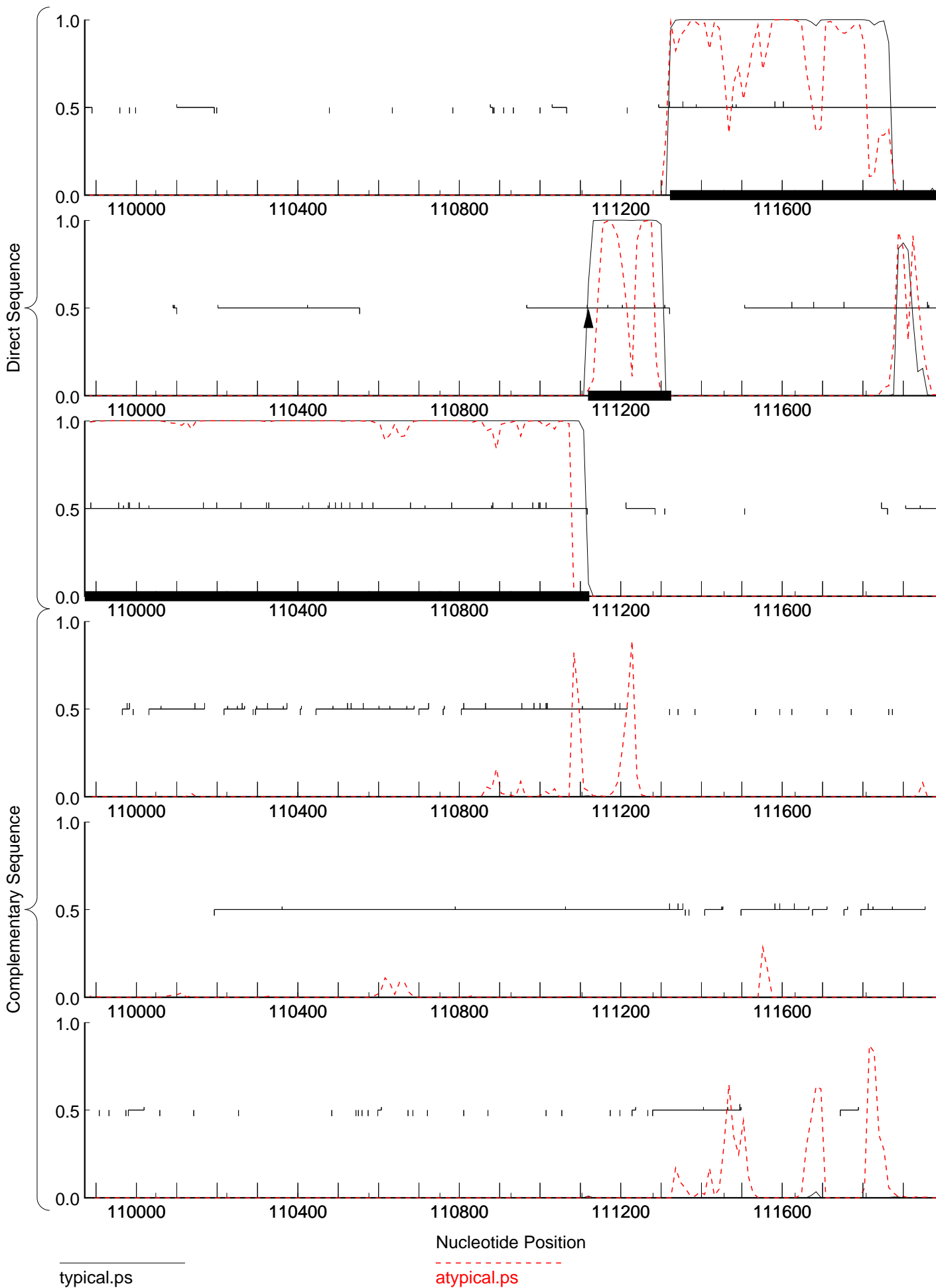




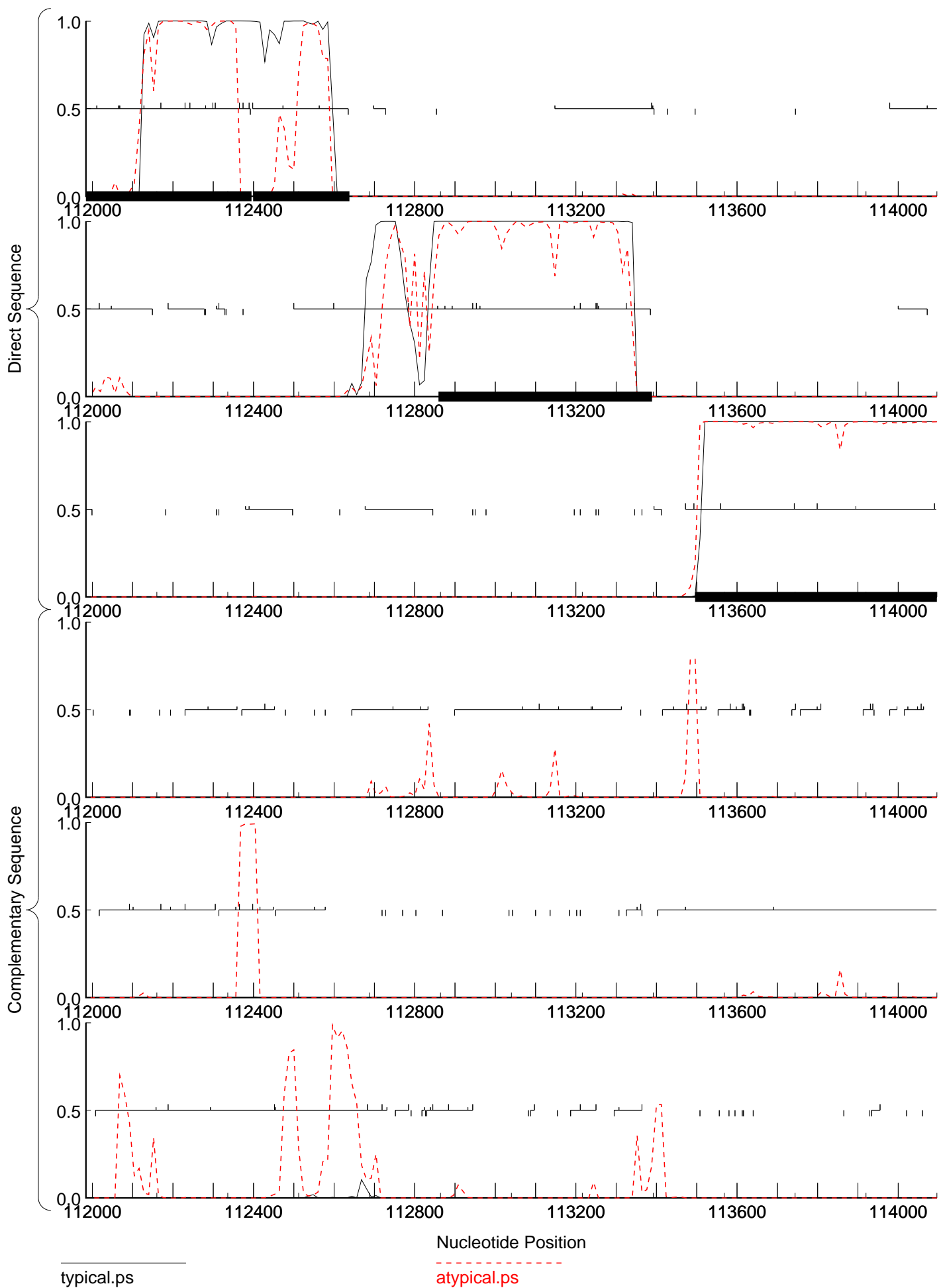






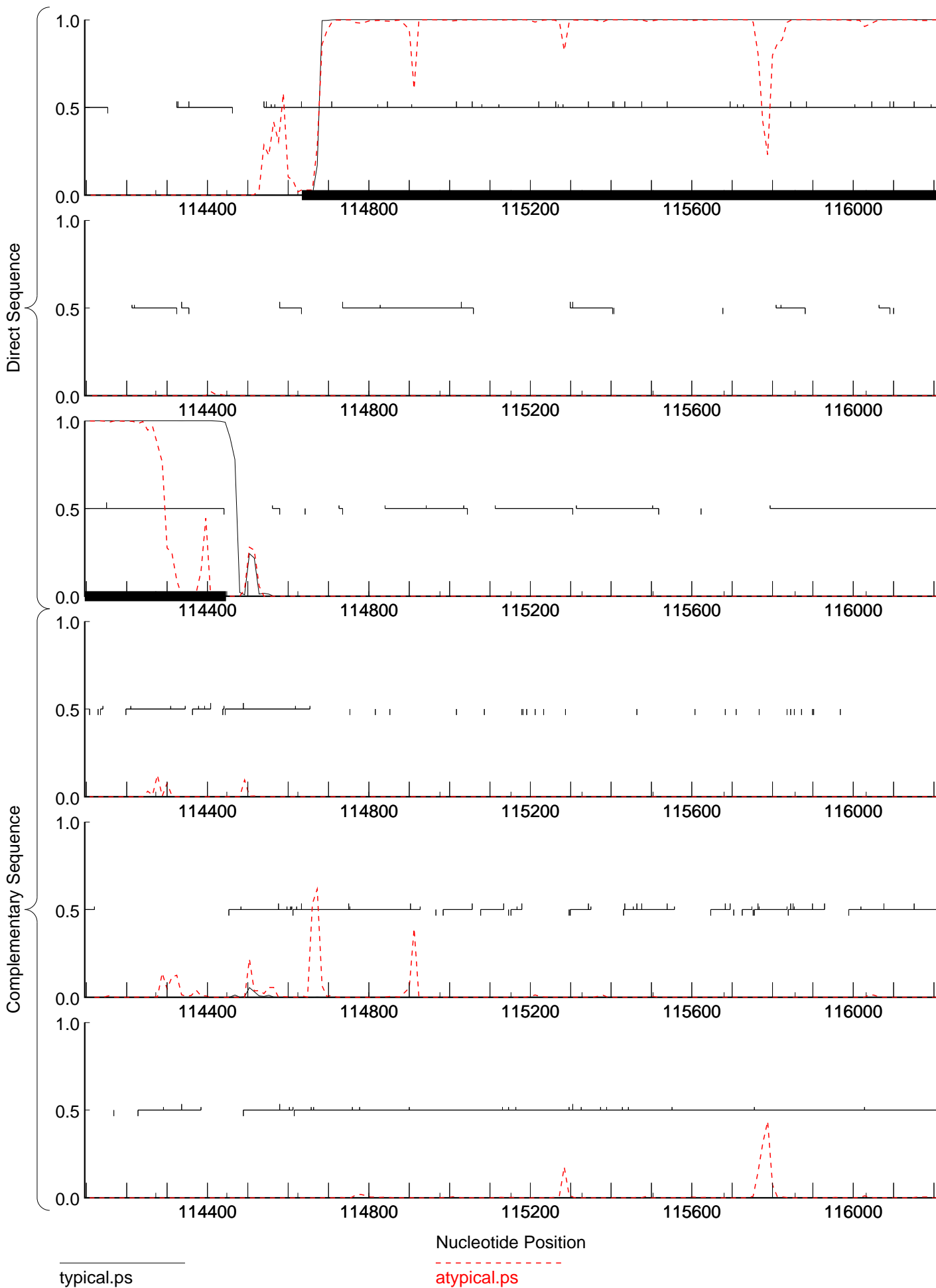


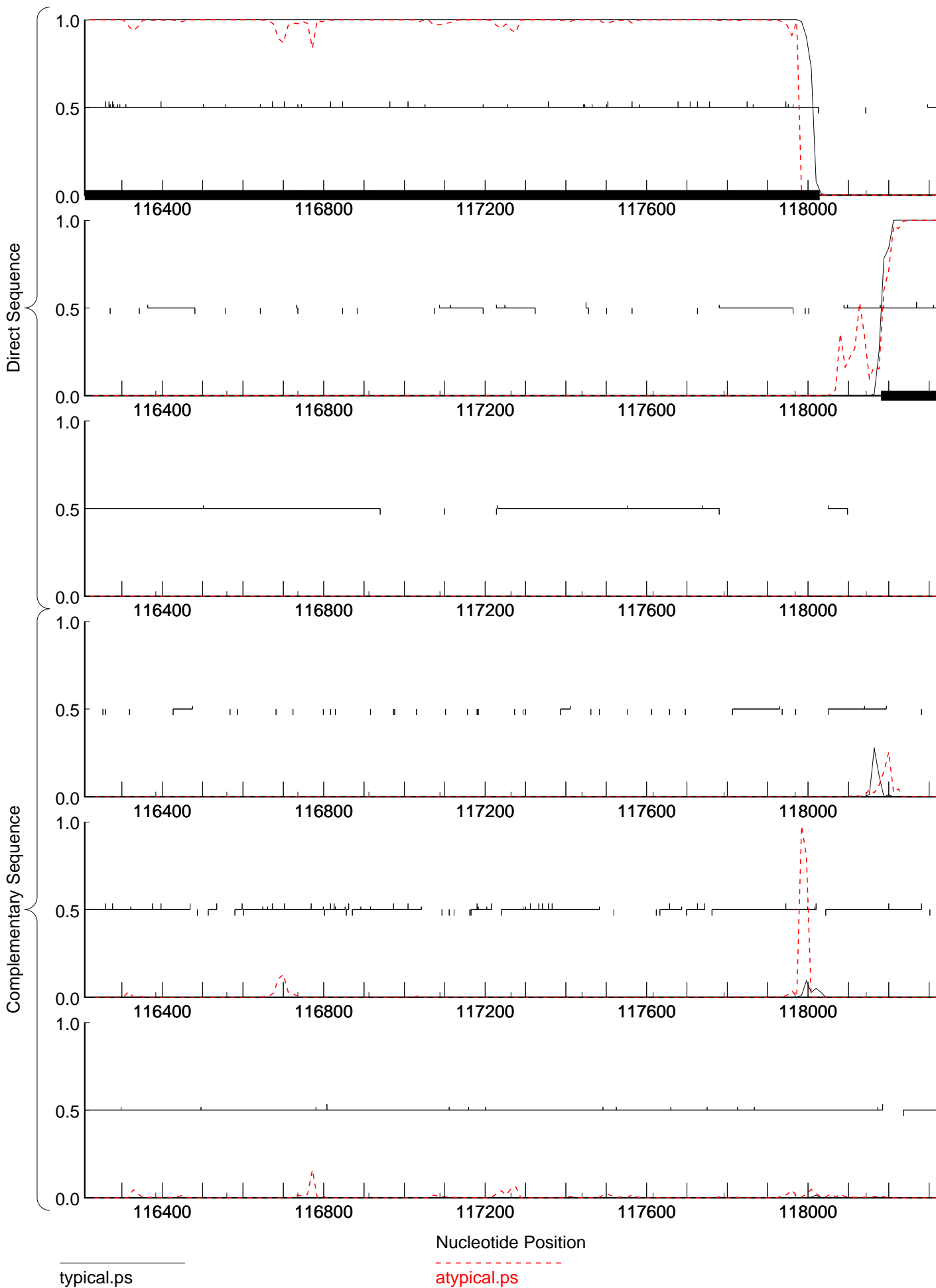
GeneMark.hmm prediction

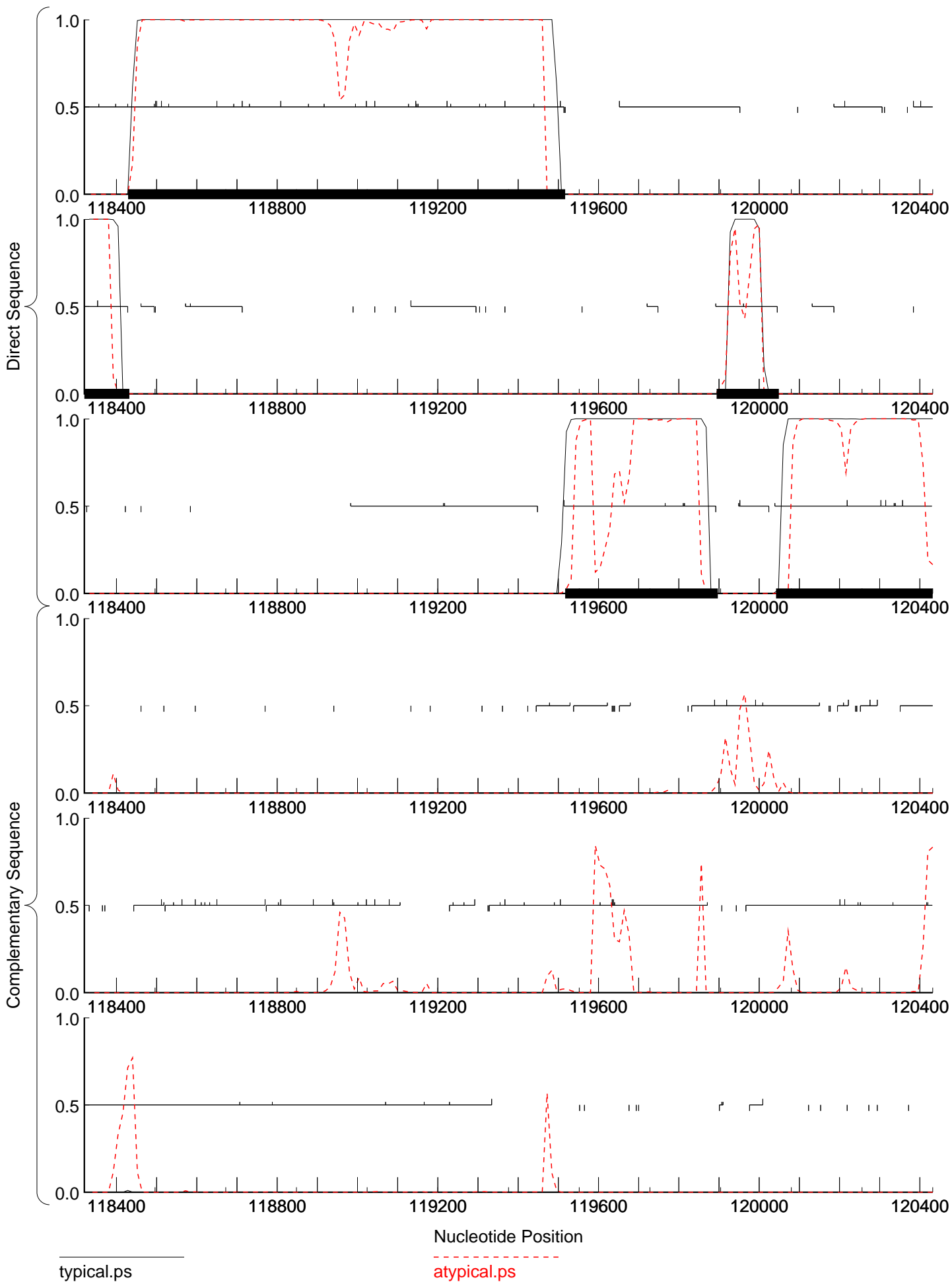


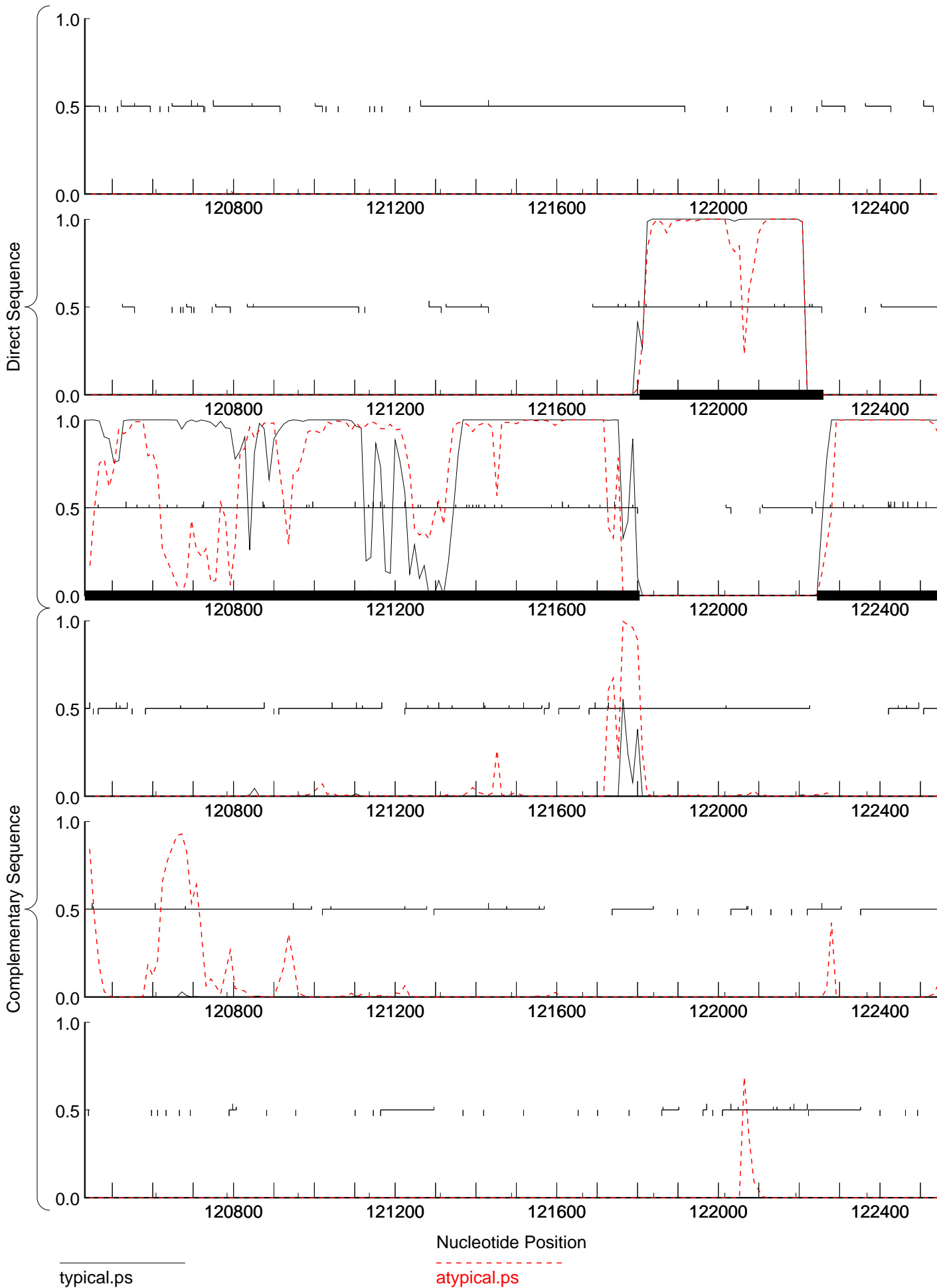
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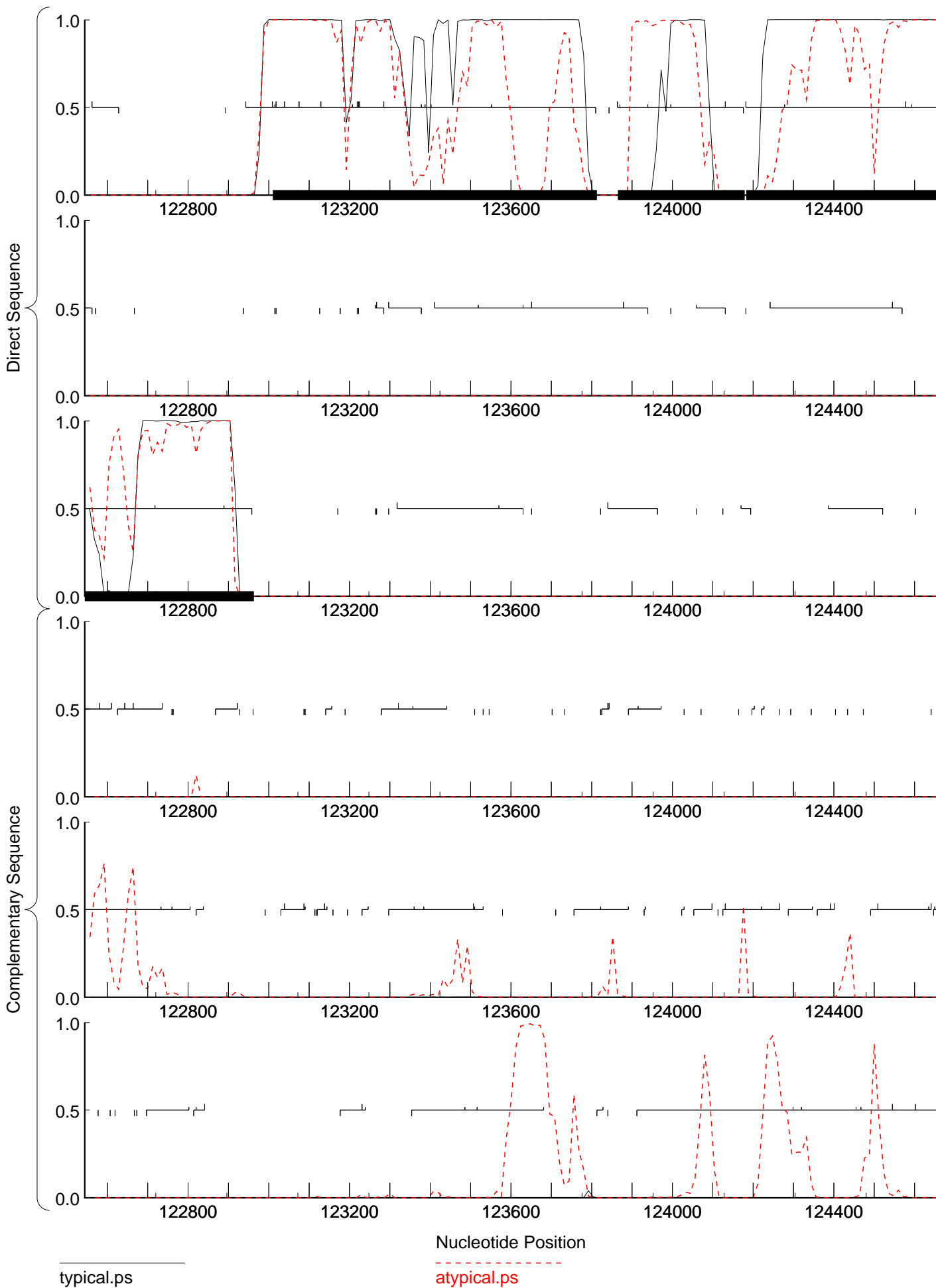
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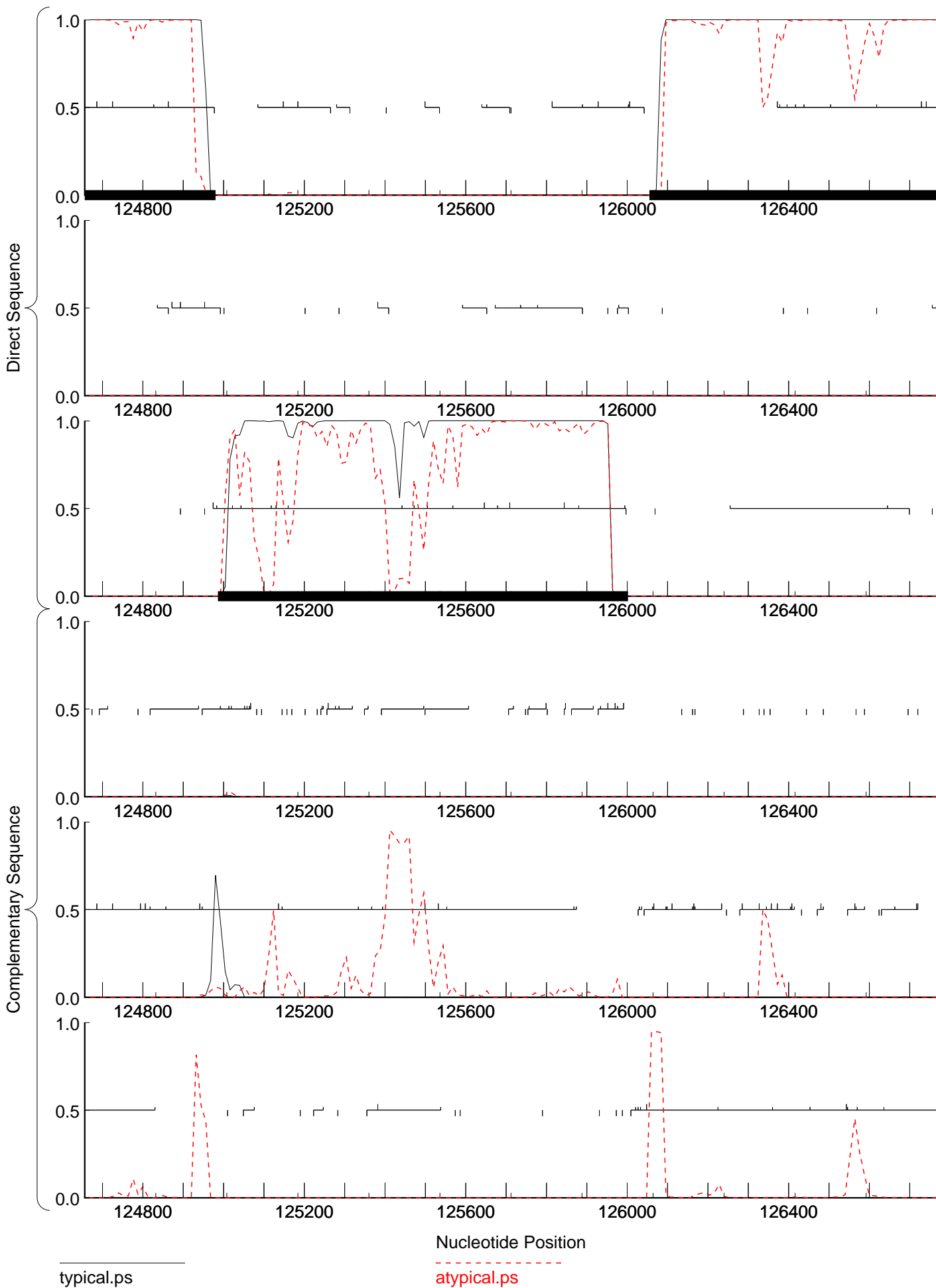






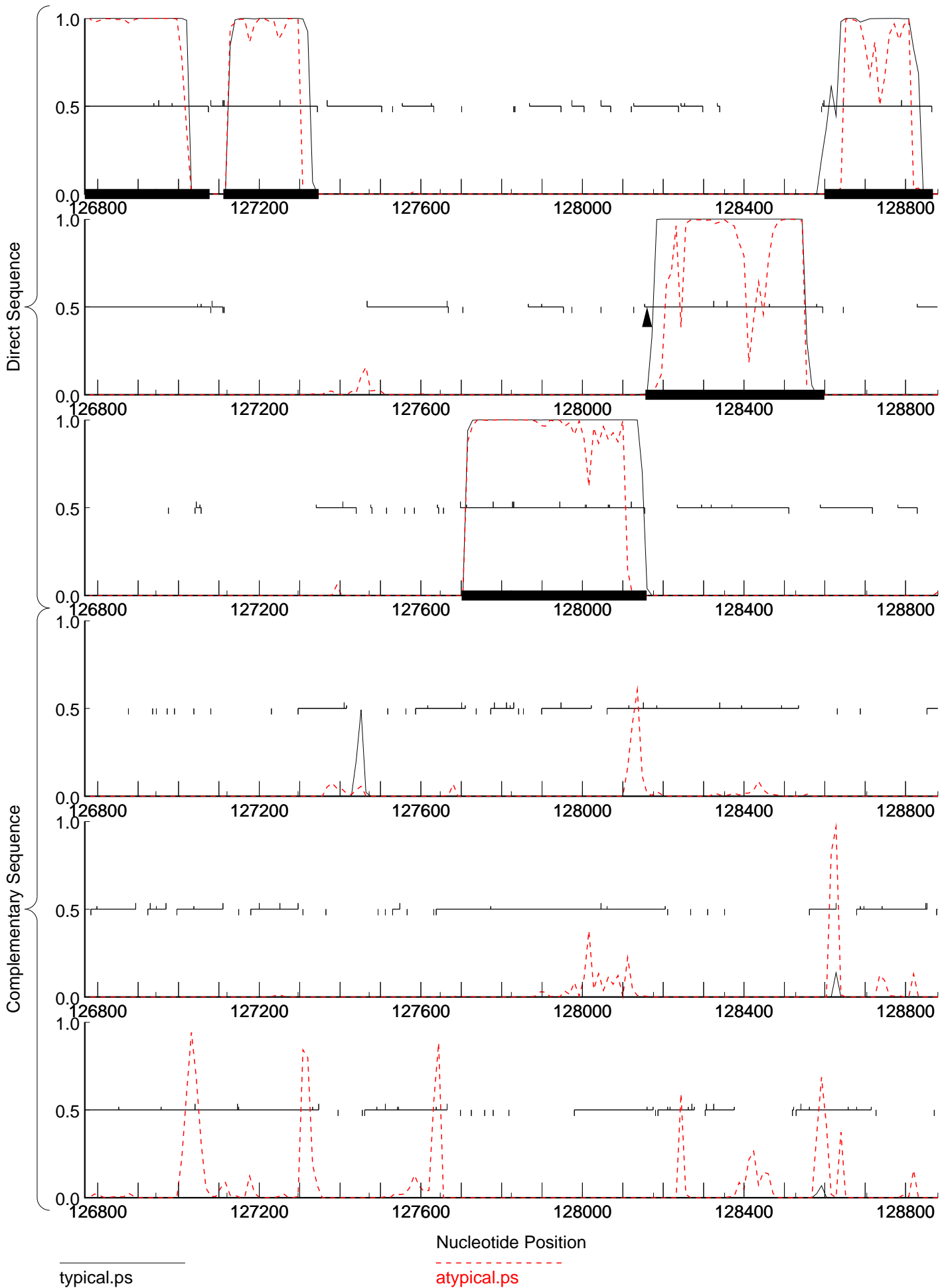


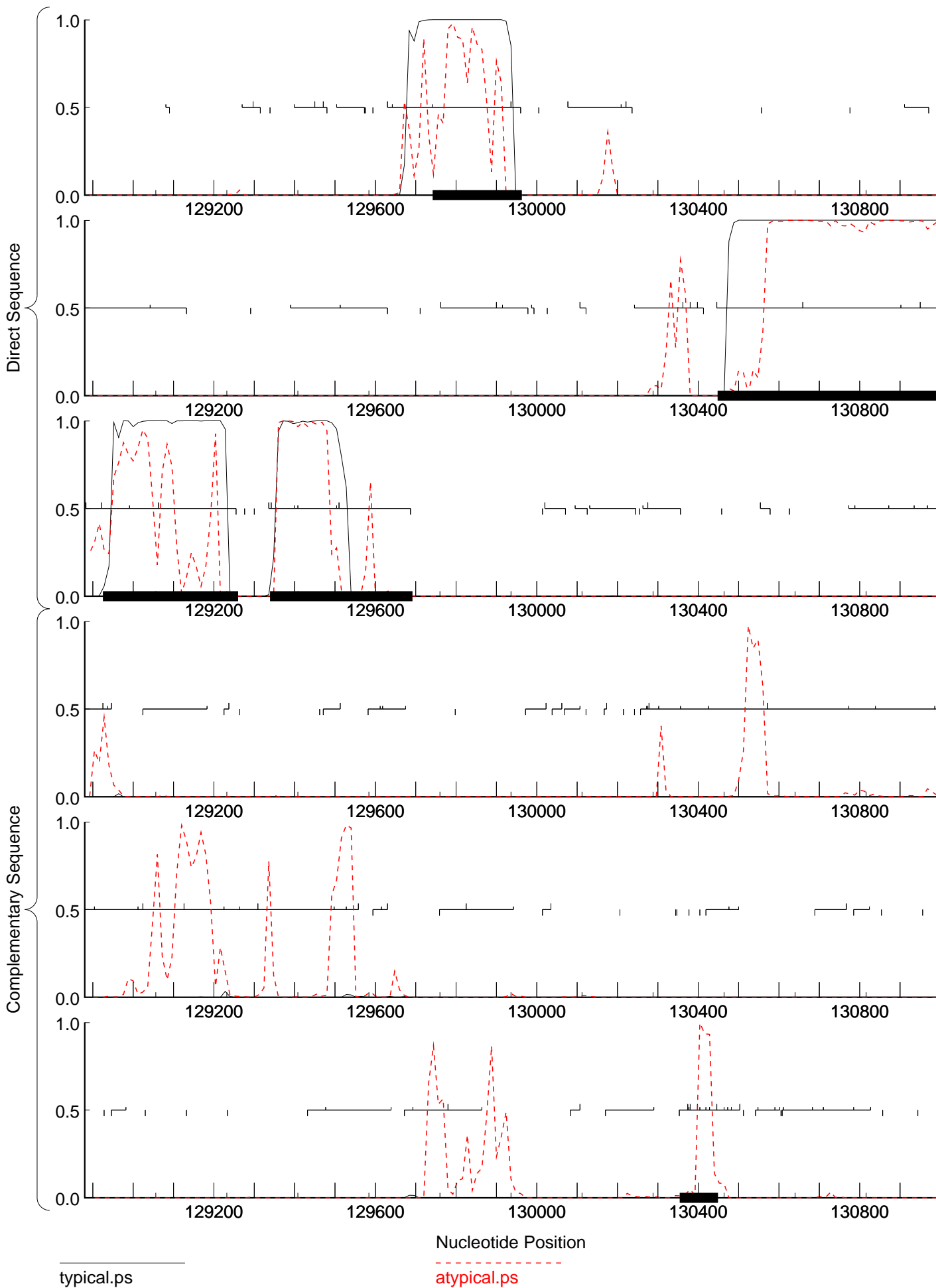


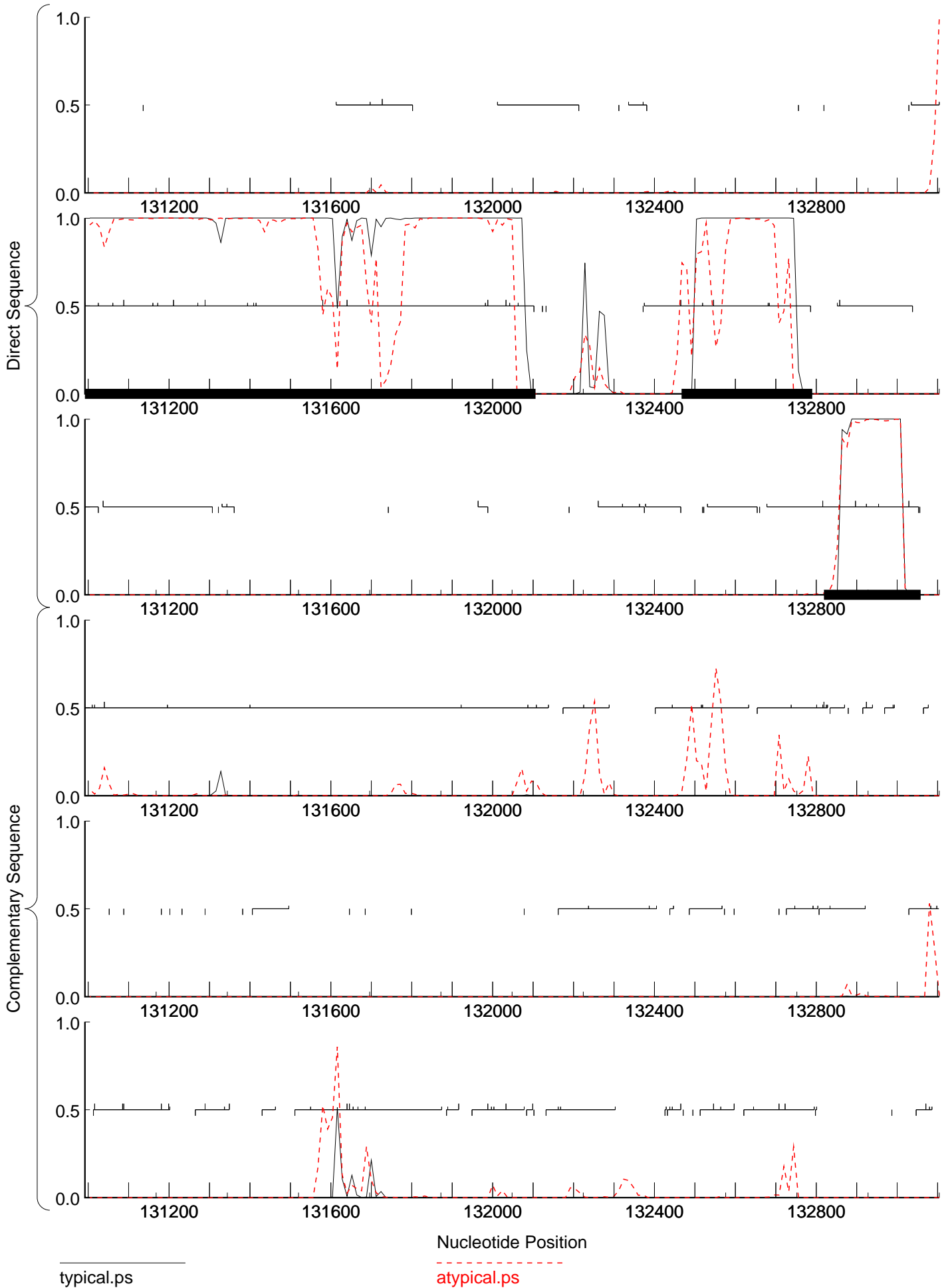


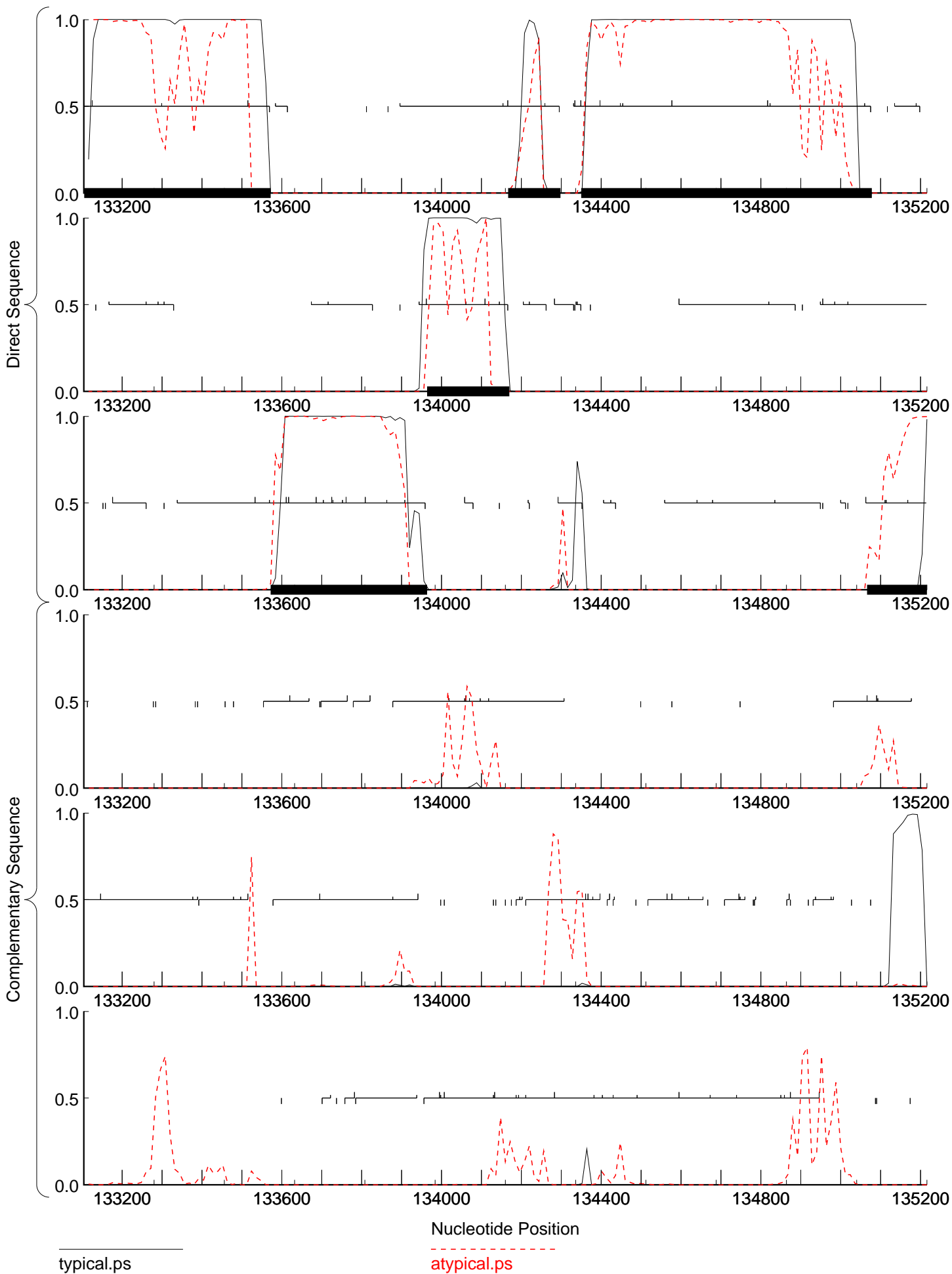
typical.ps

atypical.ps









GeneMark.hmm prediction

