

GeneMark

Version 2.5p (09.08.06)

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PROGRAM INFORMATION

Sequence : Mycobacterium phage ZygoTaiga complete sequence, 157204 bp, circularly permuted, Cluster C1
Analysis Date : 10/19/17 at 17:55:09
Pages : 76
Sequence Length : 157204 bp
GC Content : 64.69%

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

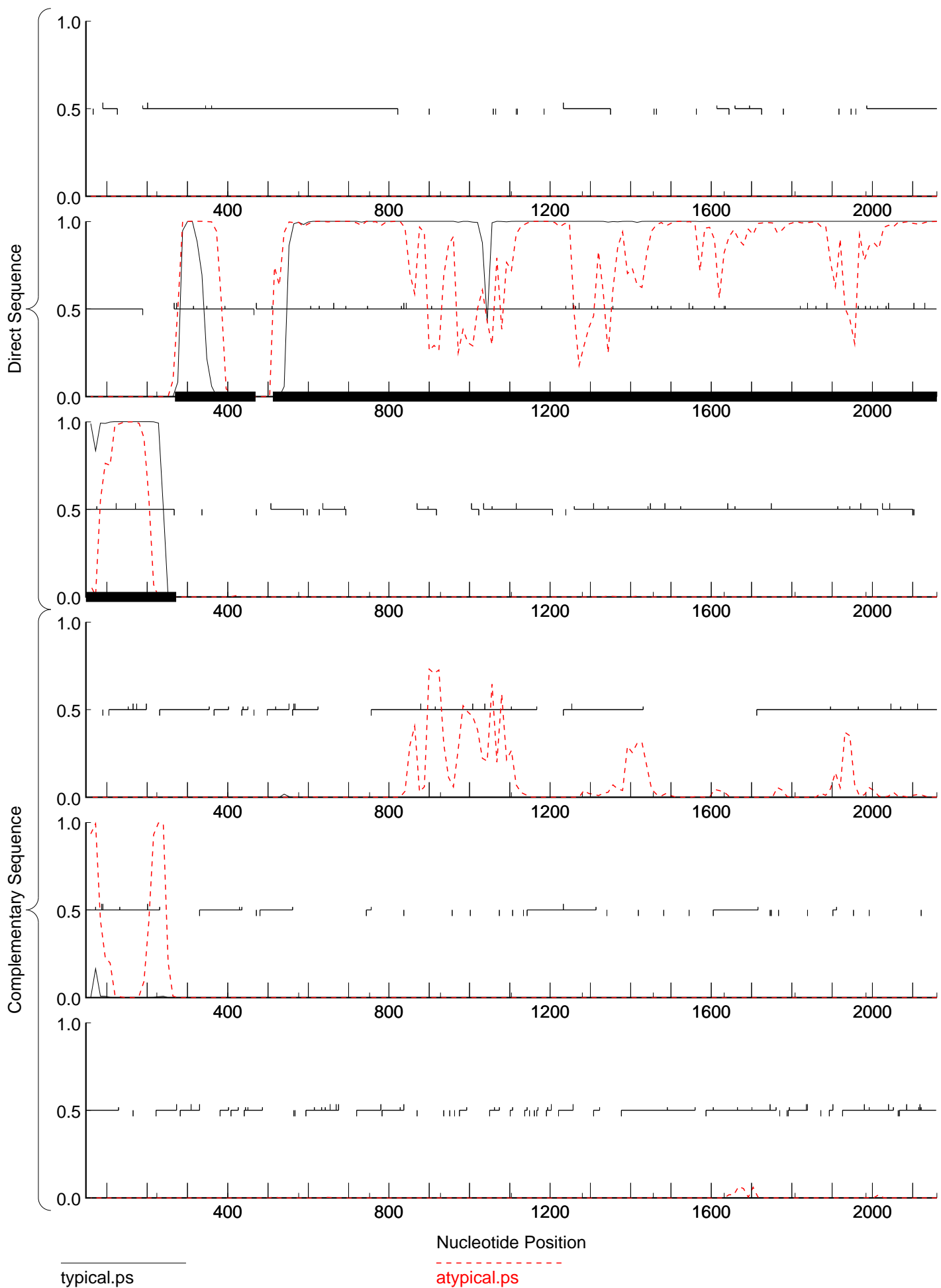
Training set derived by GeneMarkS, 4.30 October 2014
Thu Oct 19 17:55:09 2017

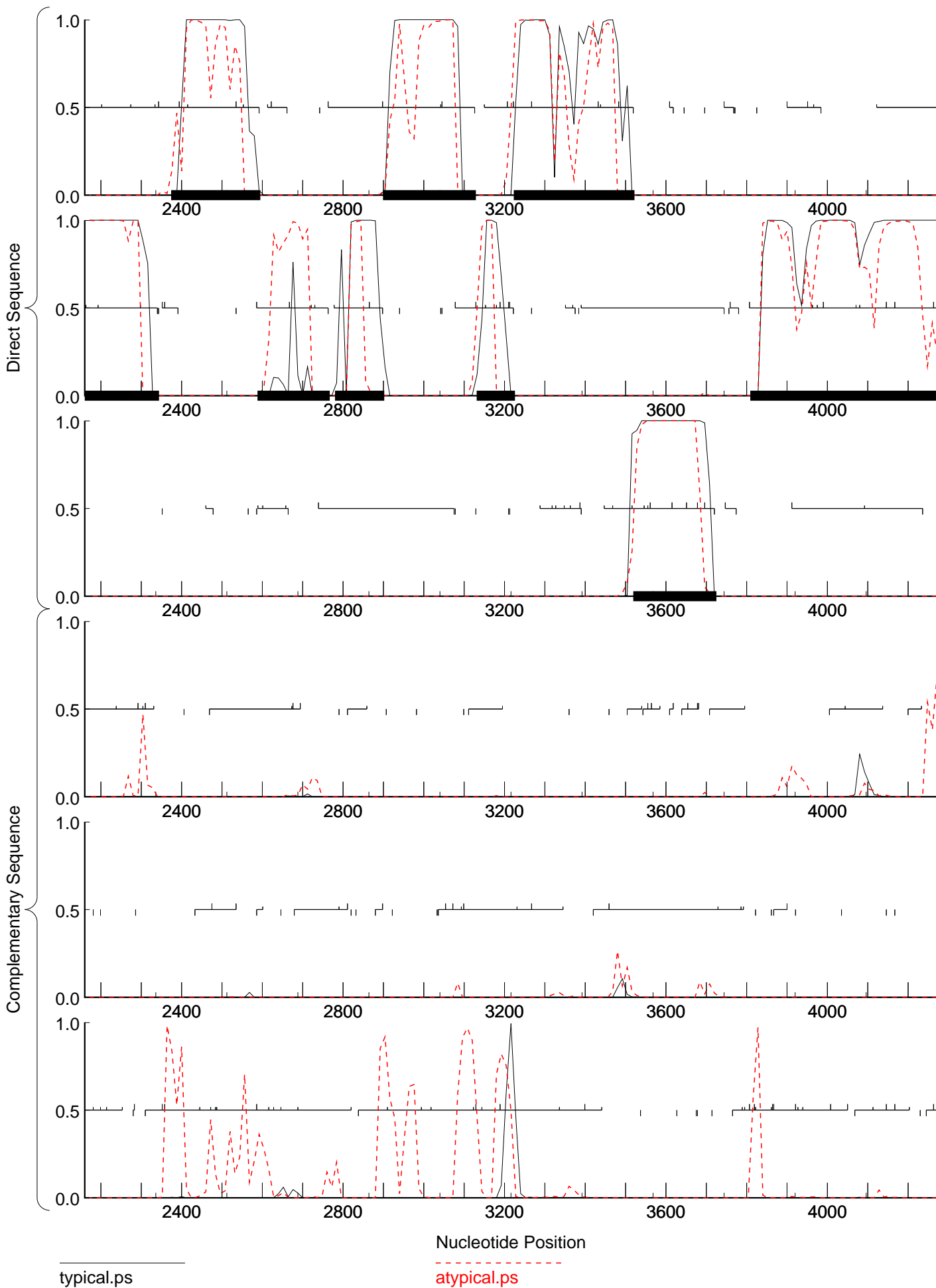
MATRIX INFORMATION

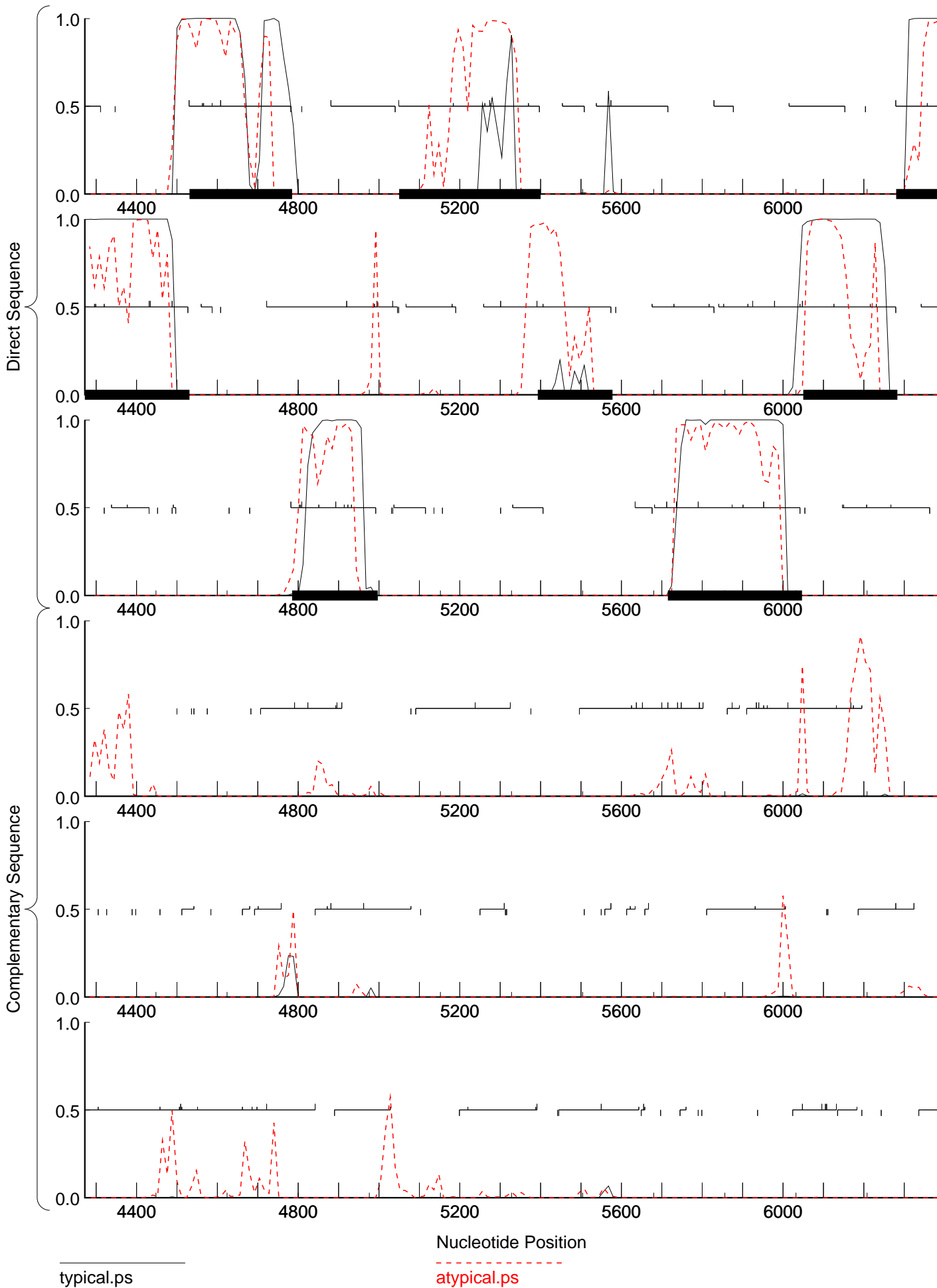
Matrix : -
Author : -
Order : 4

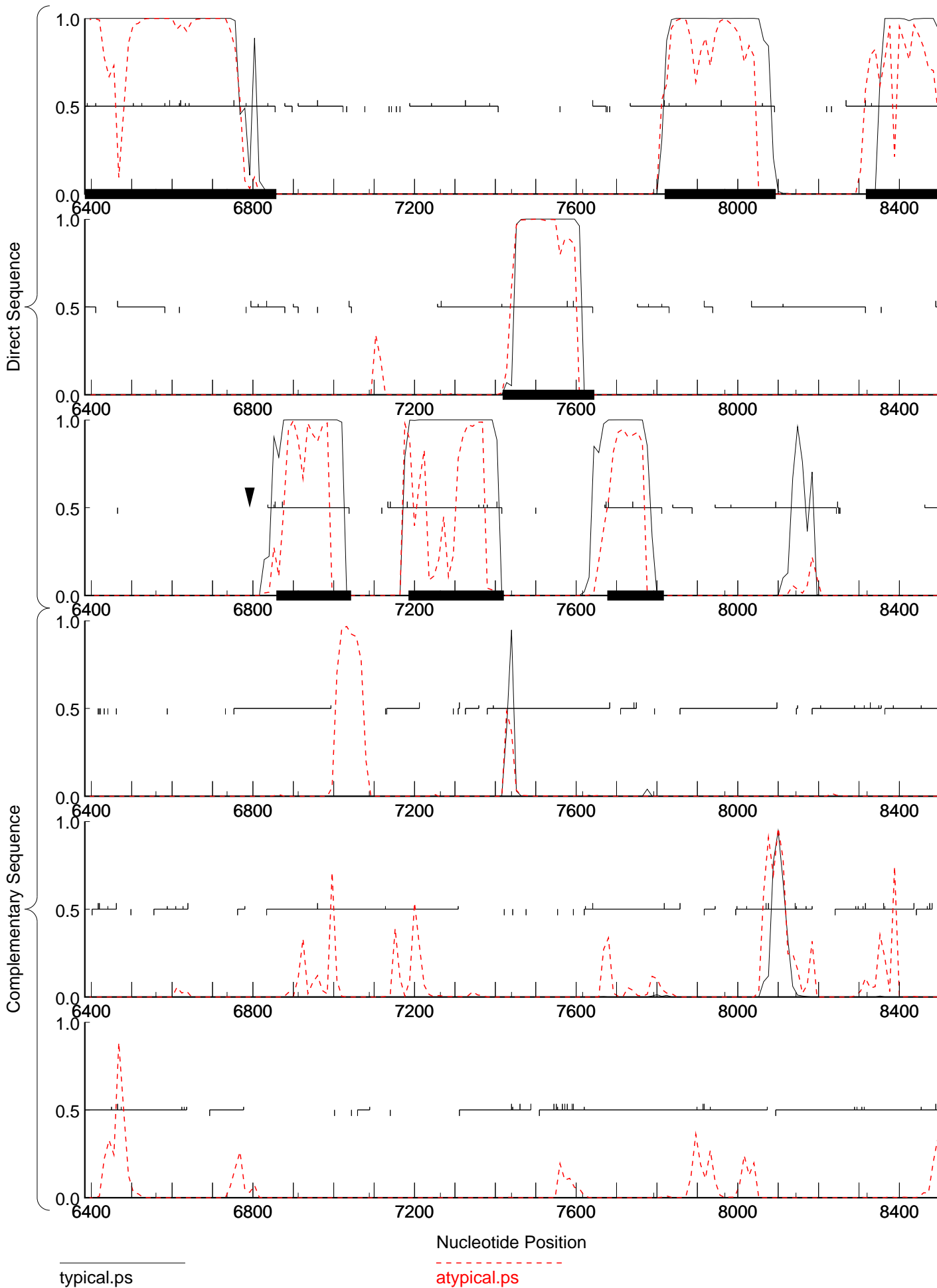
Send questions / comments to:
Dr. M. Borodovsky
Georgia Institute of Technology
School of Biology
Atlanta, GA 30332-0230

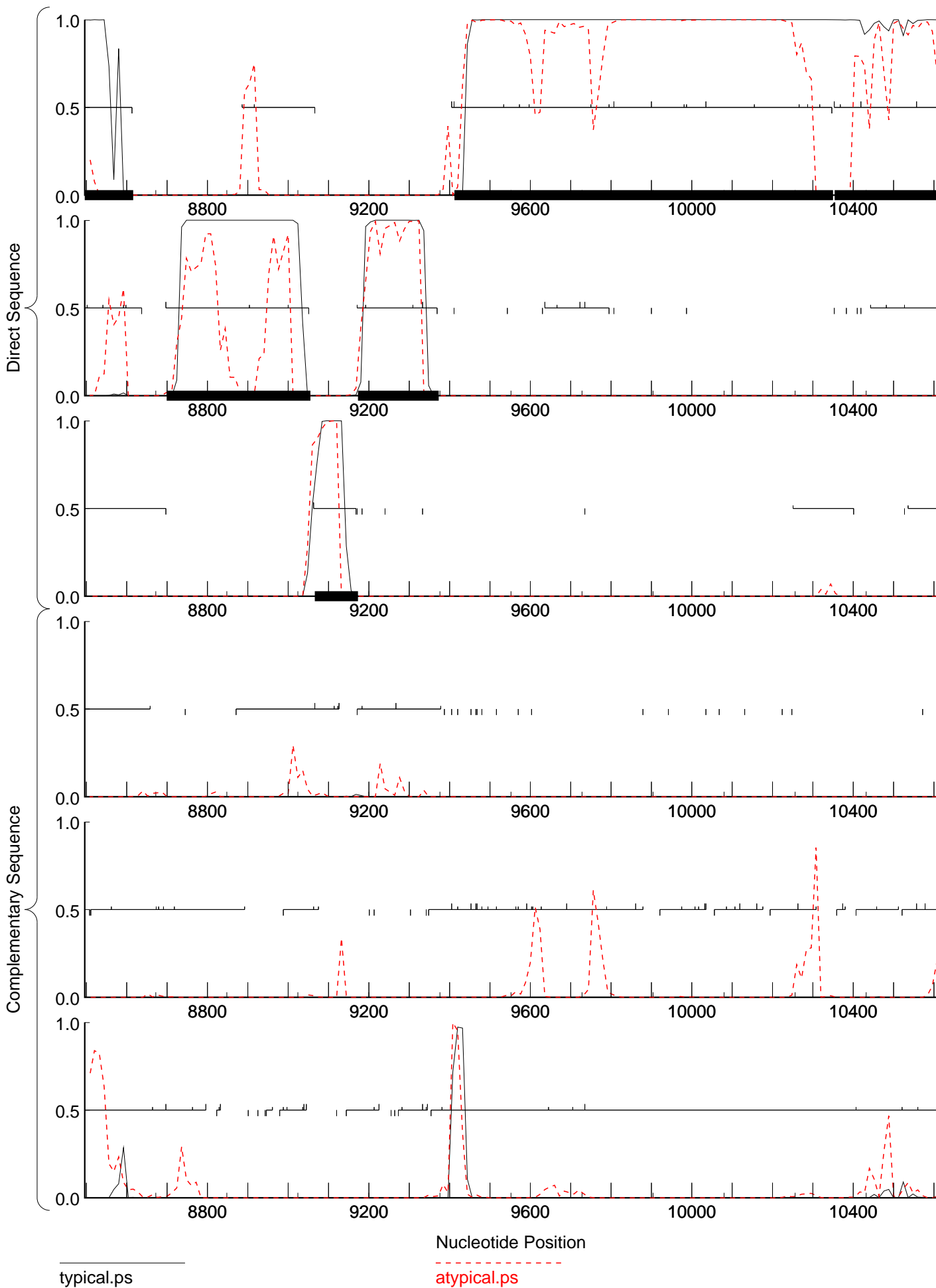
GeneMark.hmm prediction

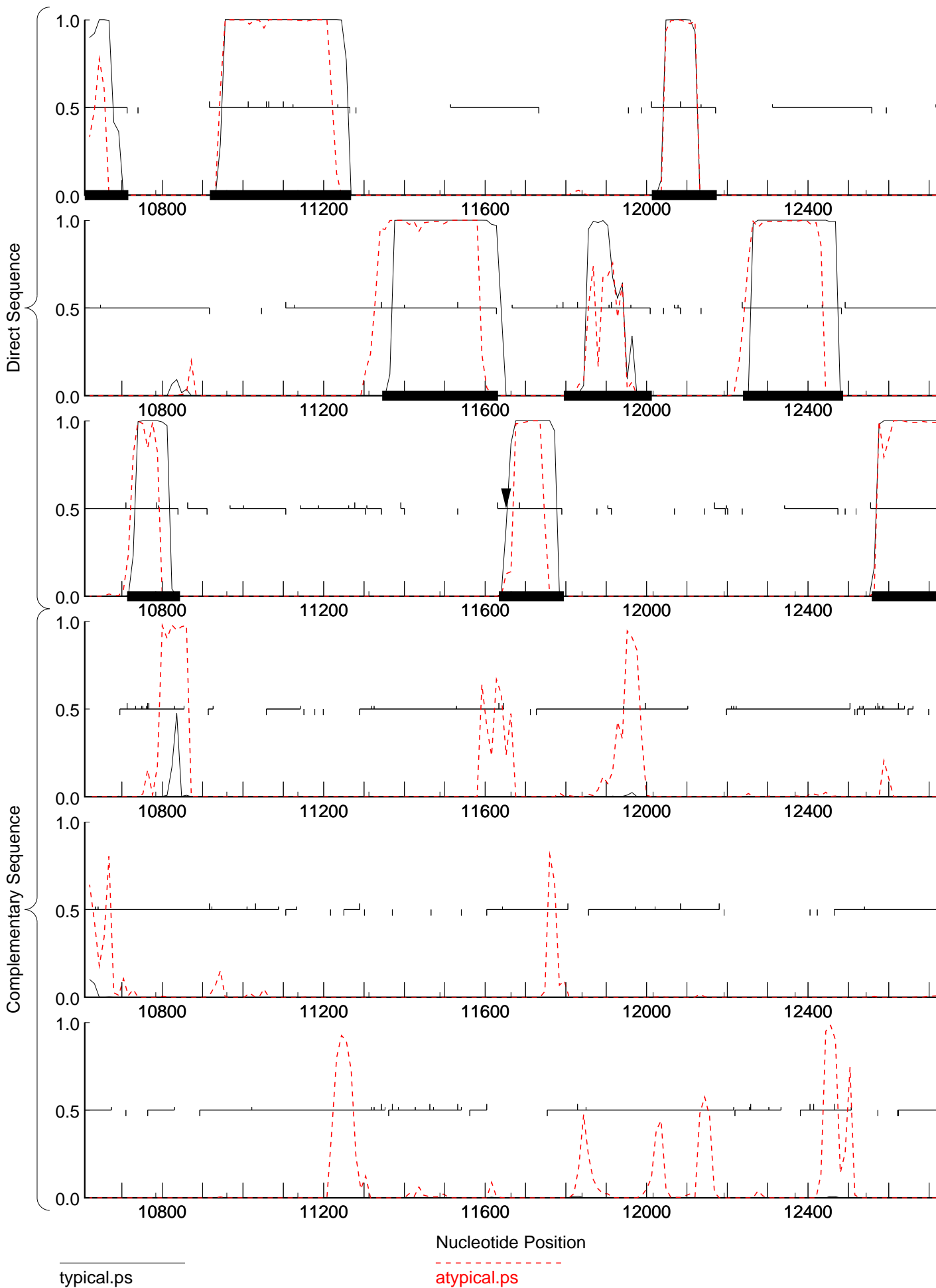


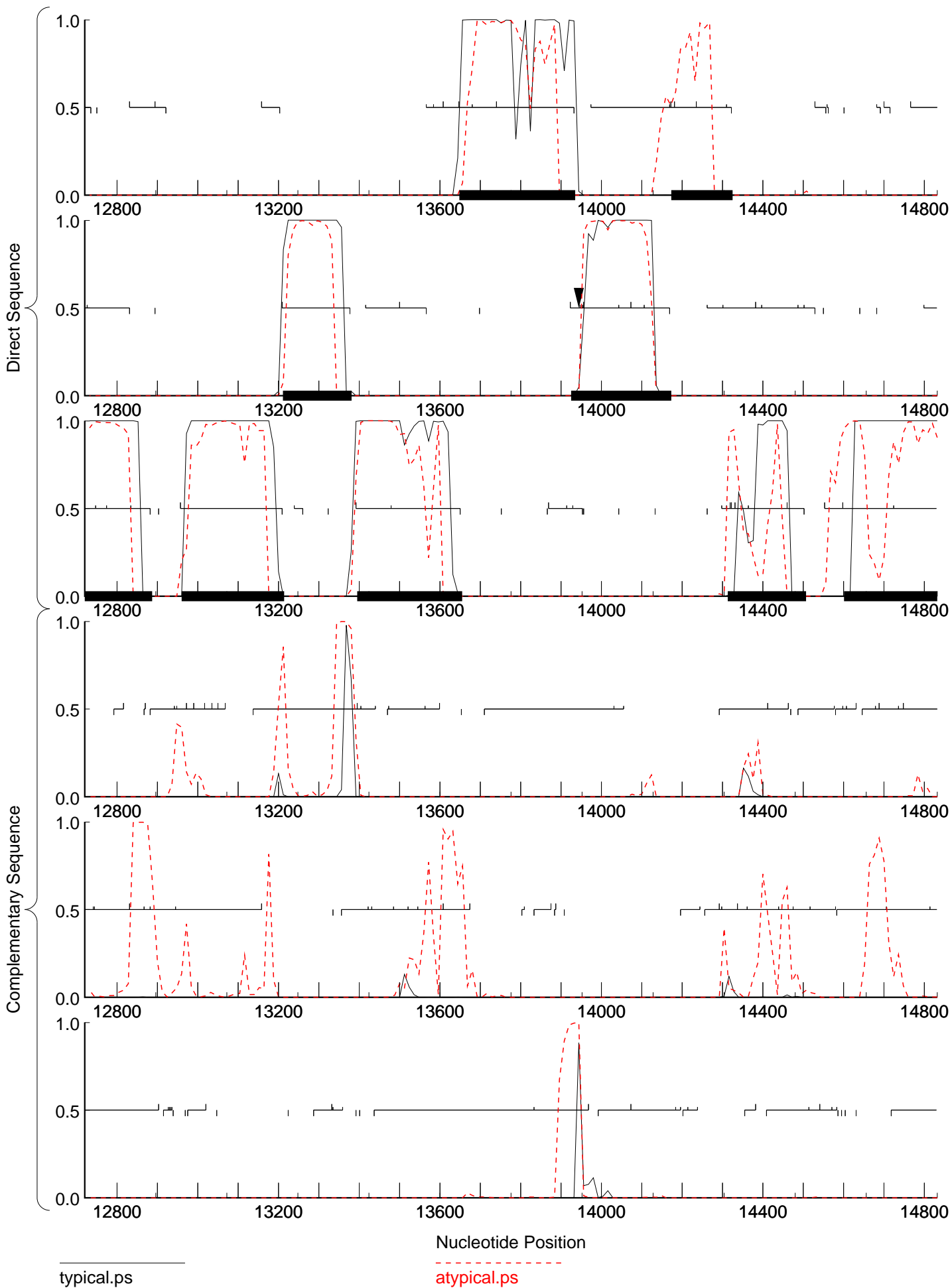


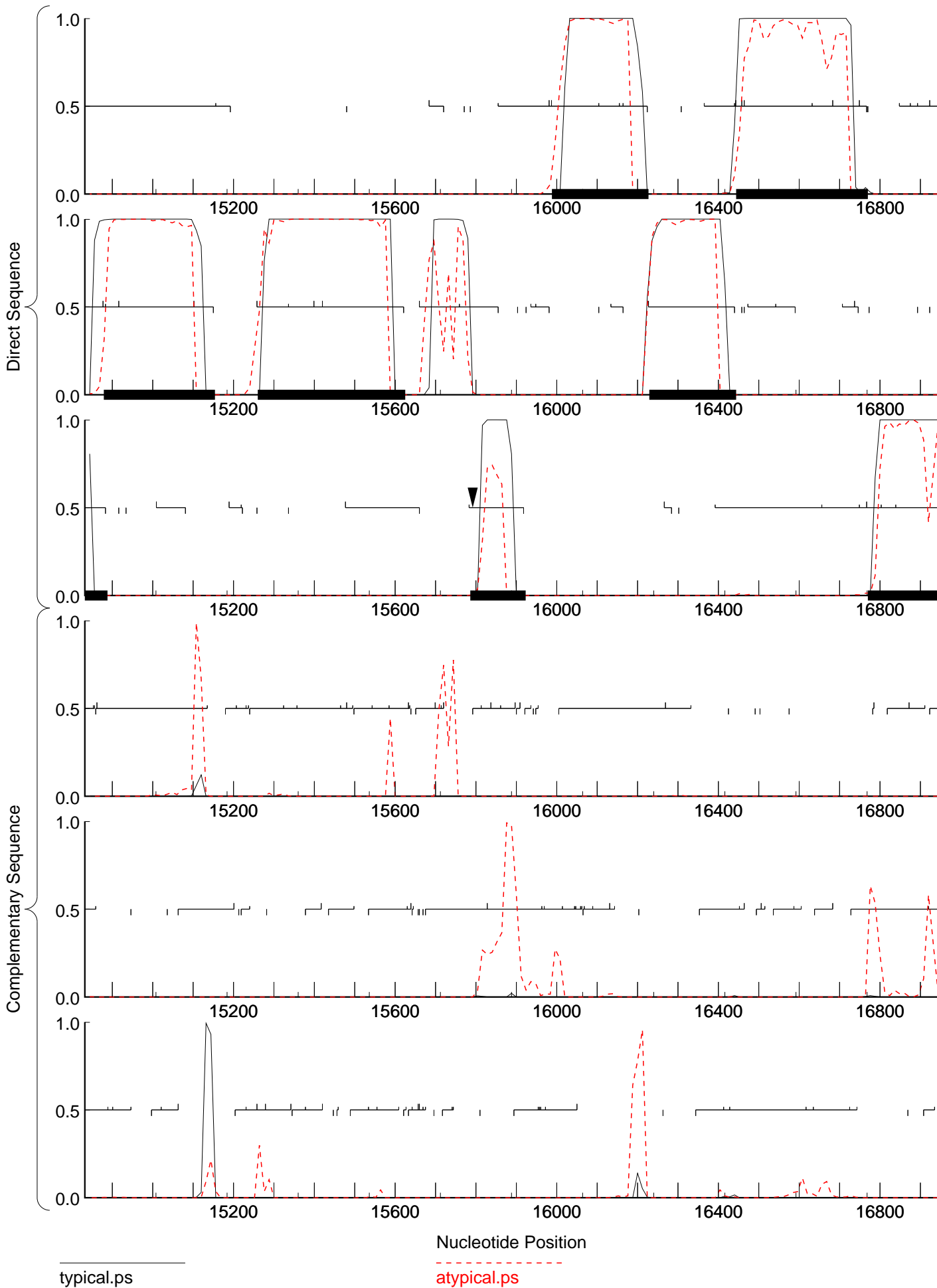


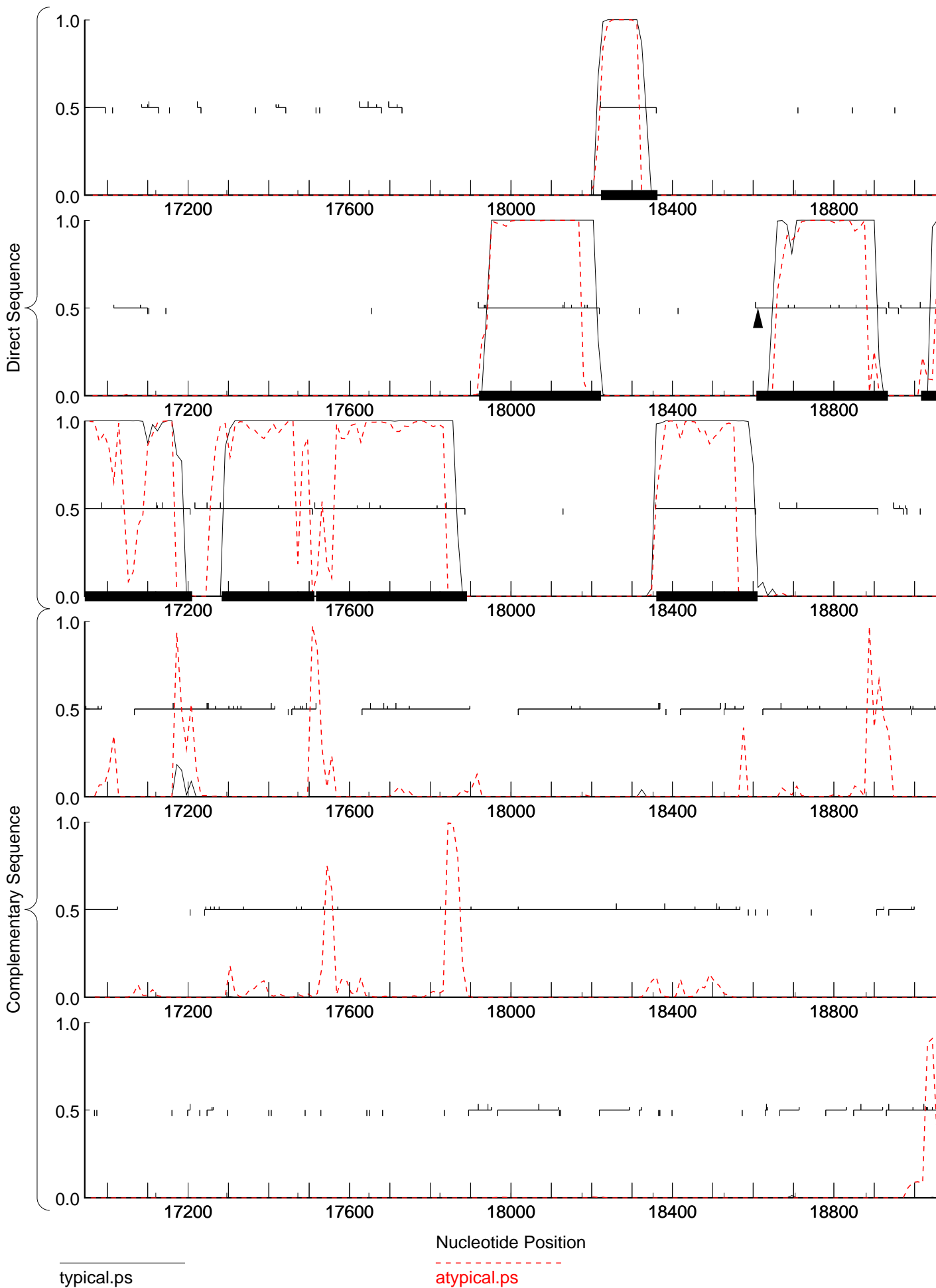






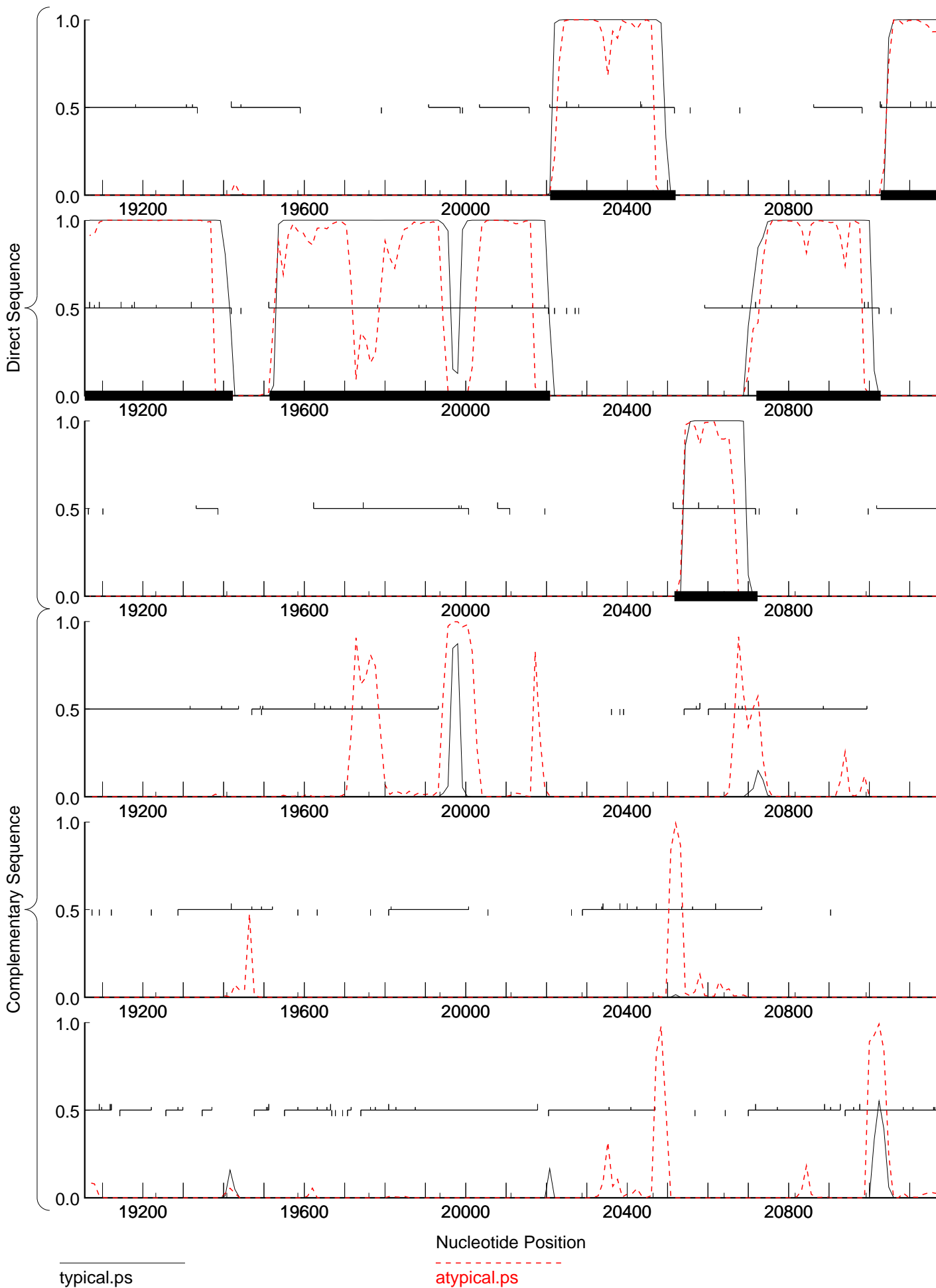






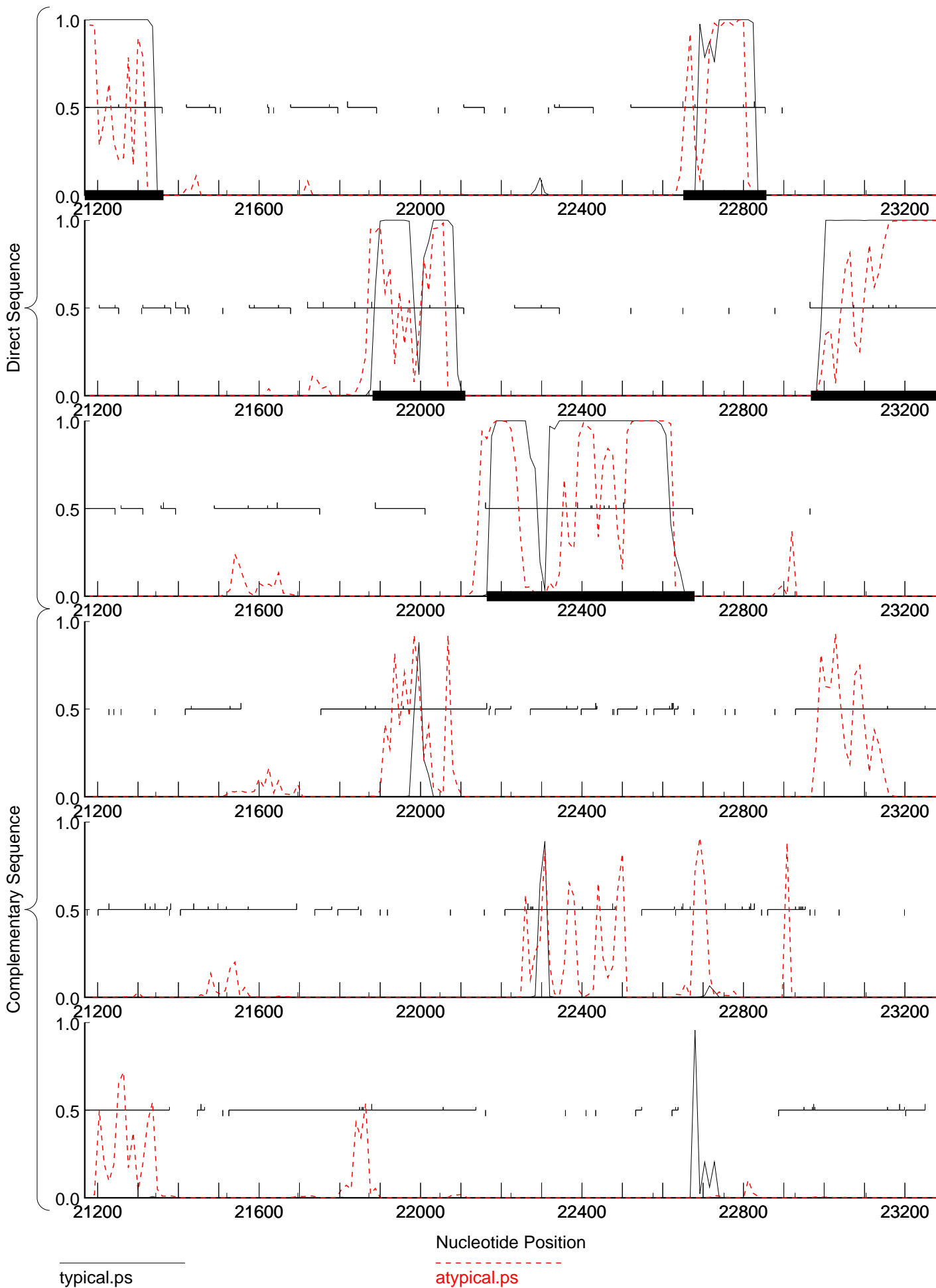
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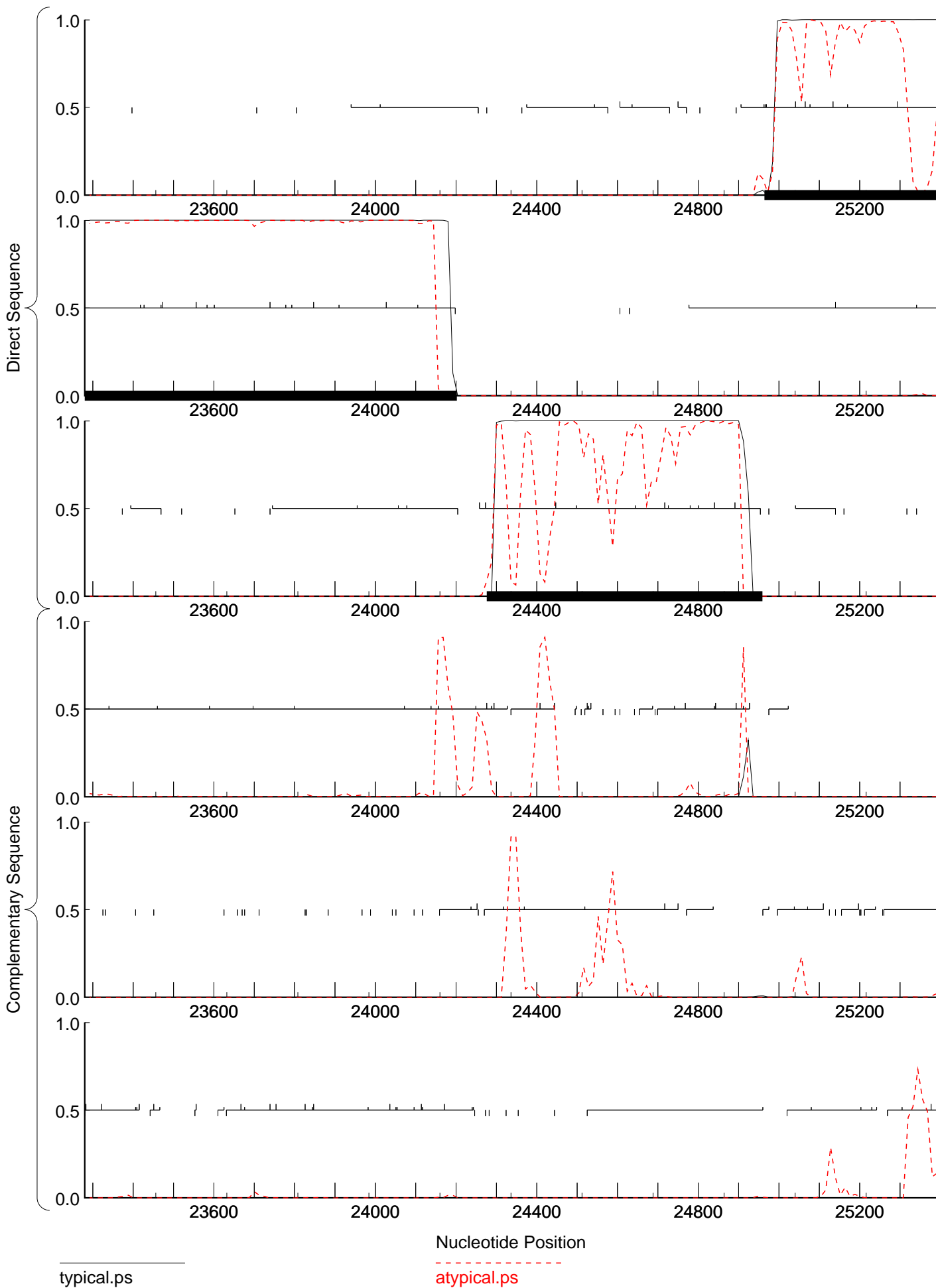
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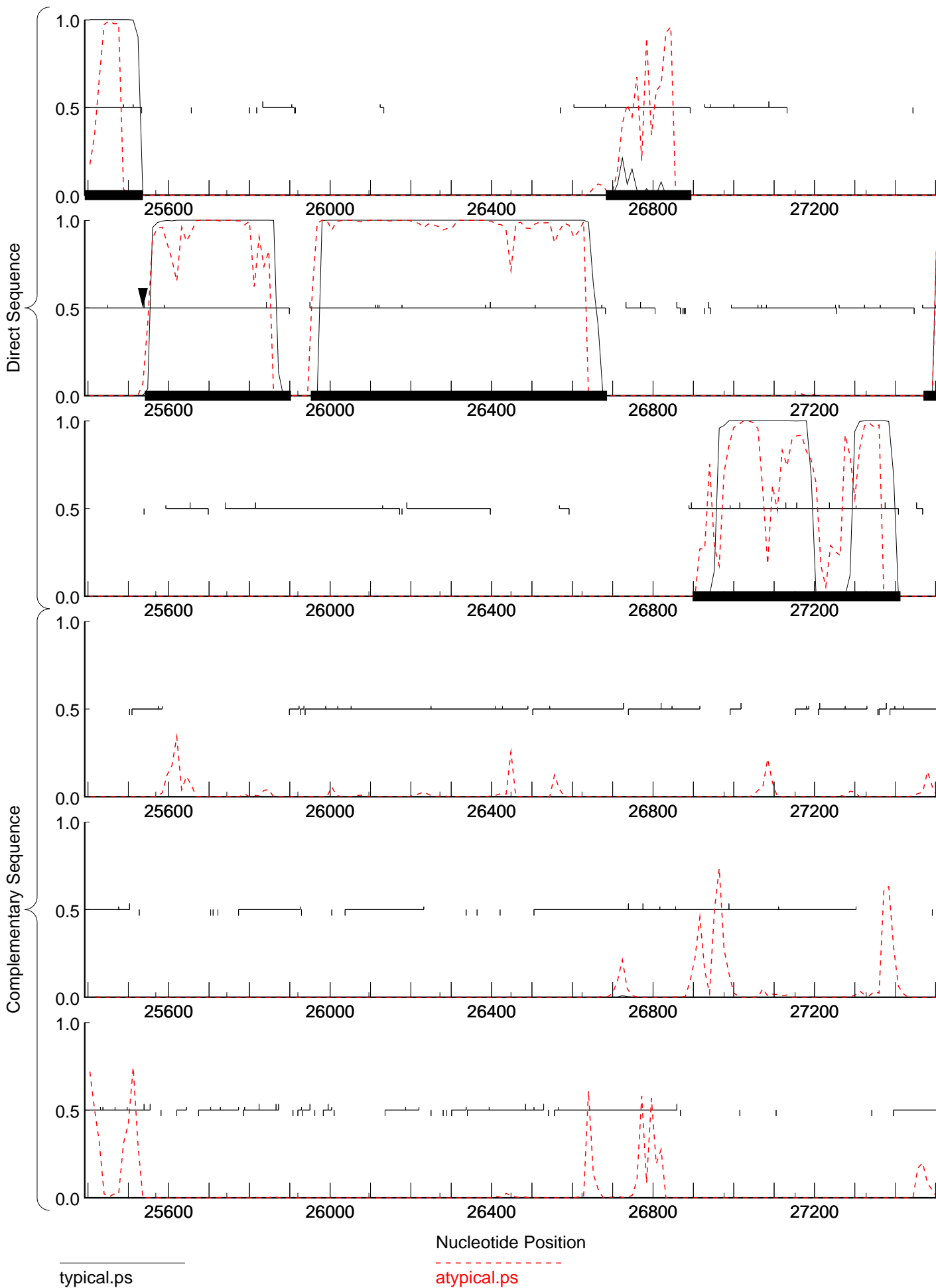


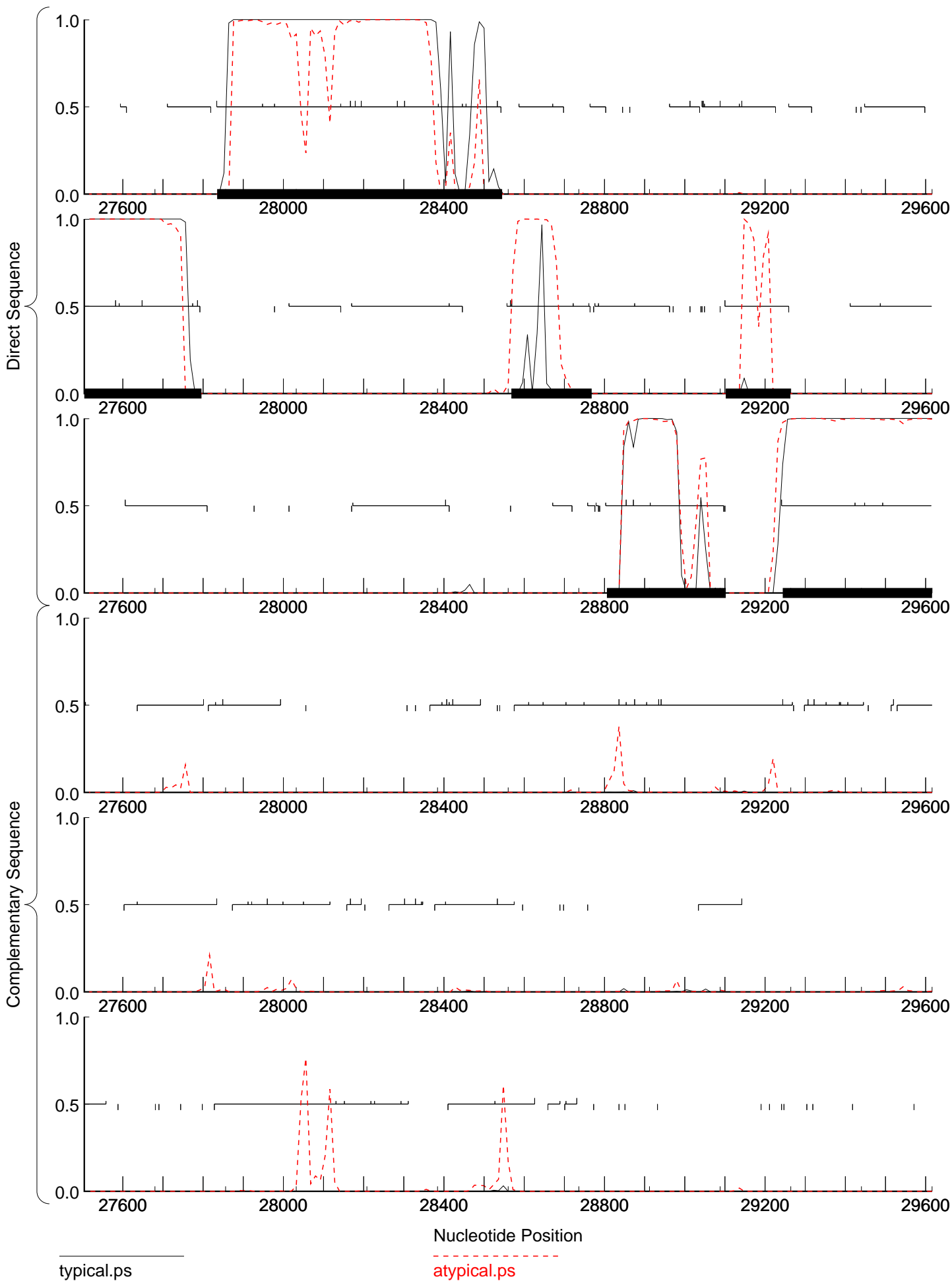
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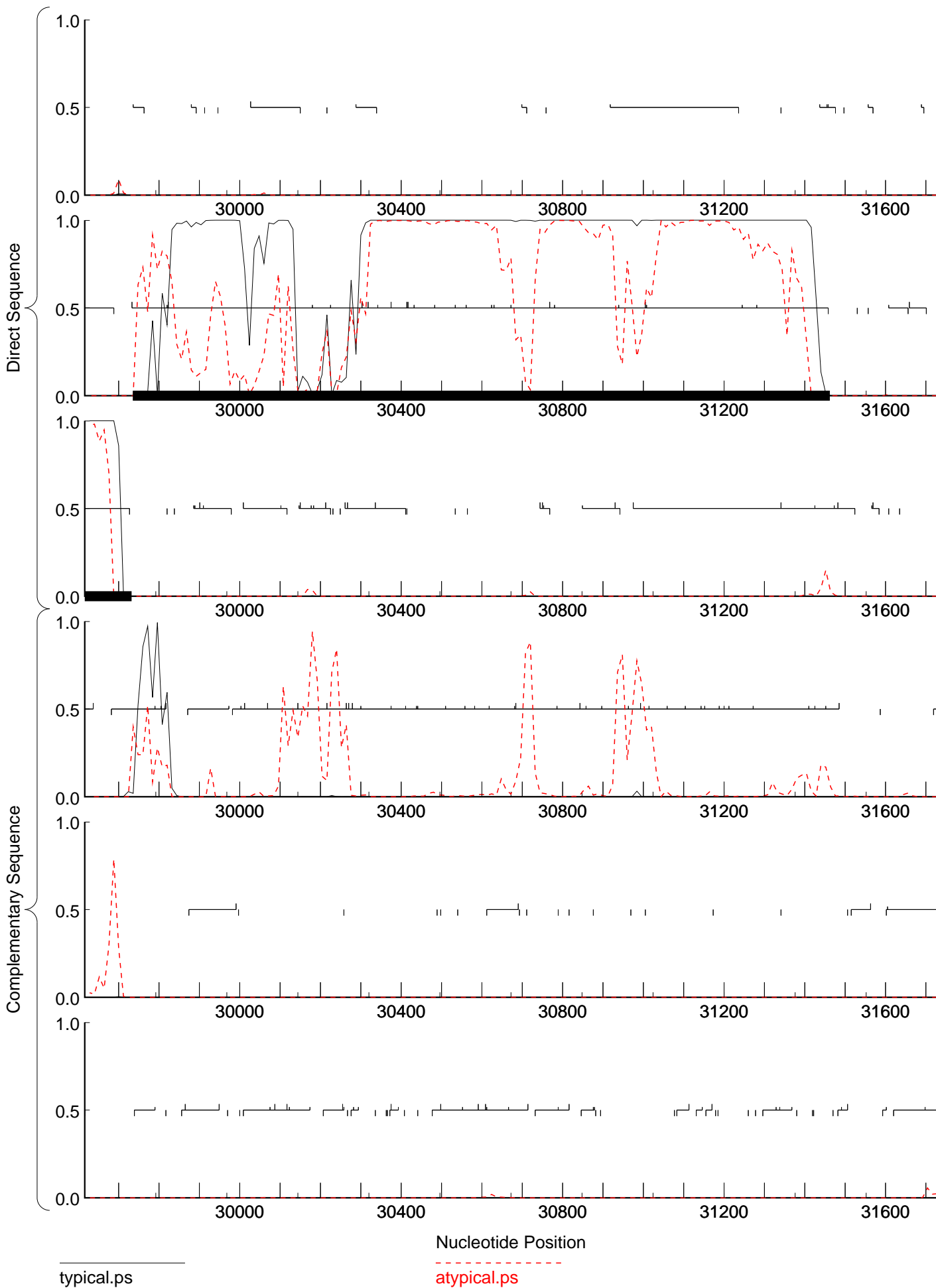
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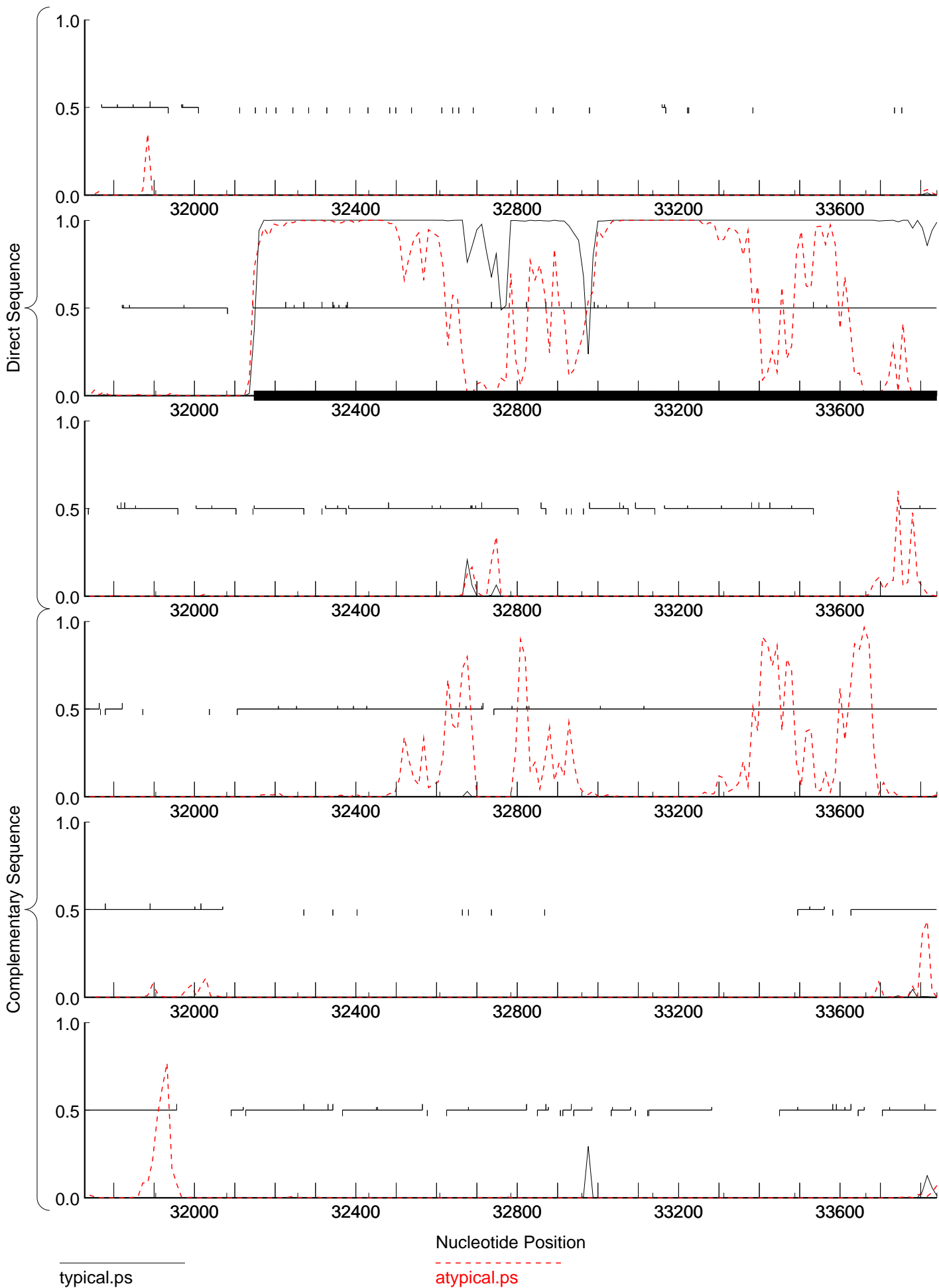


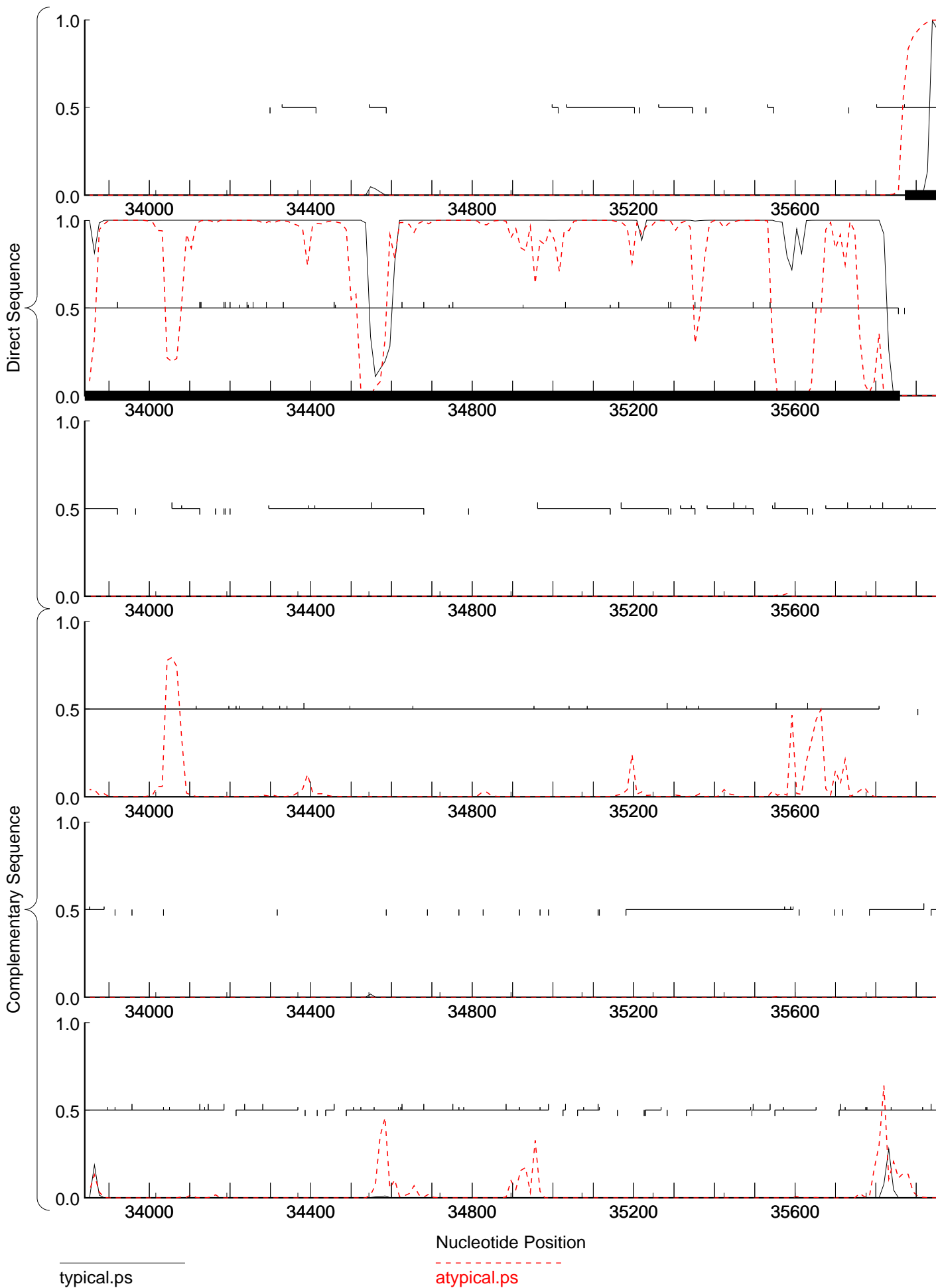


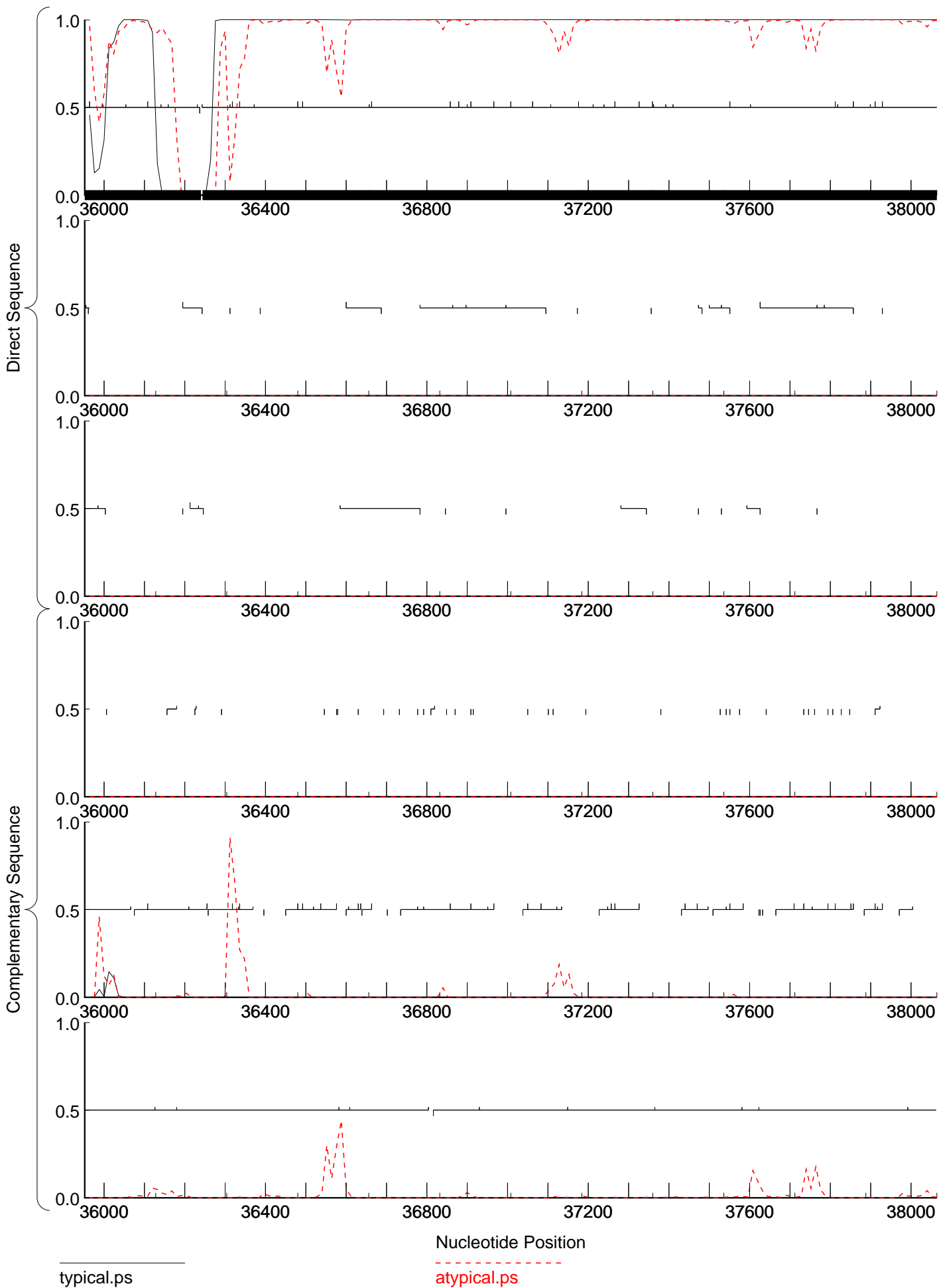


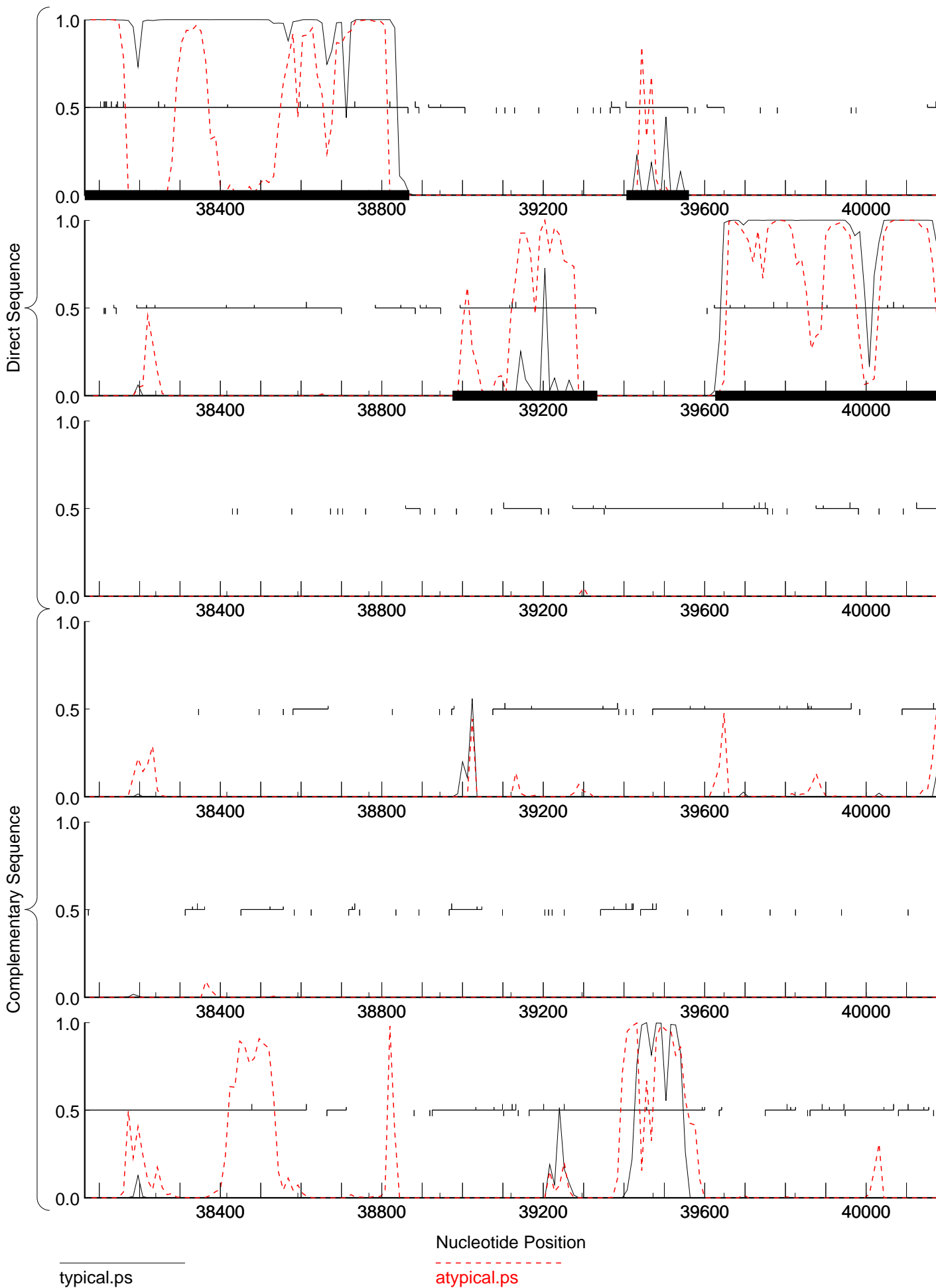






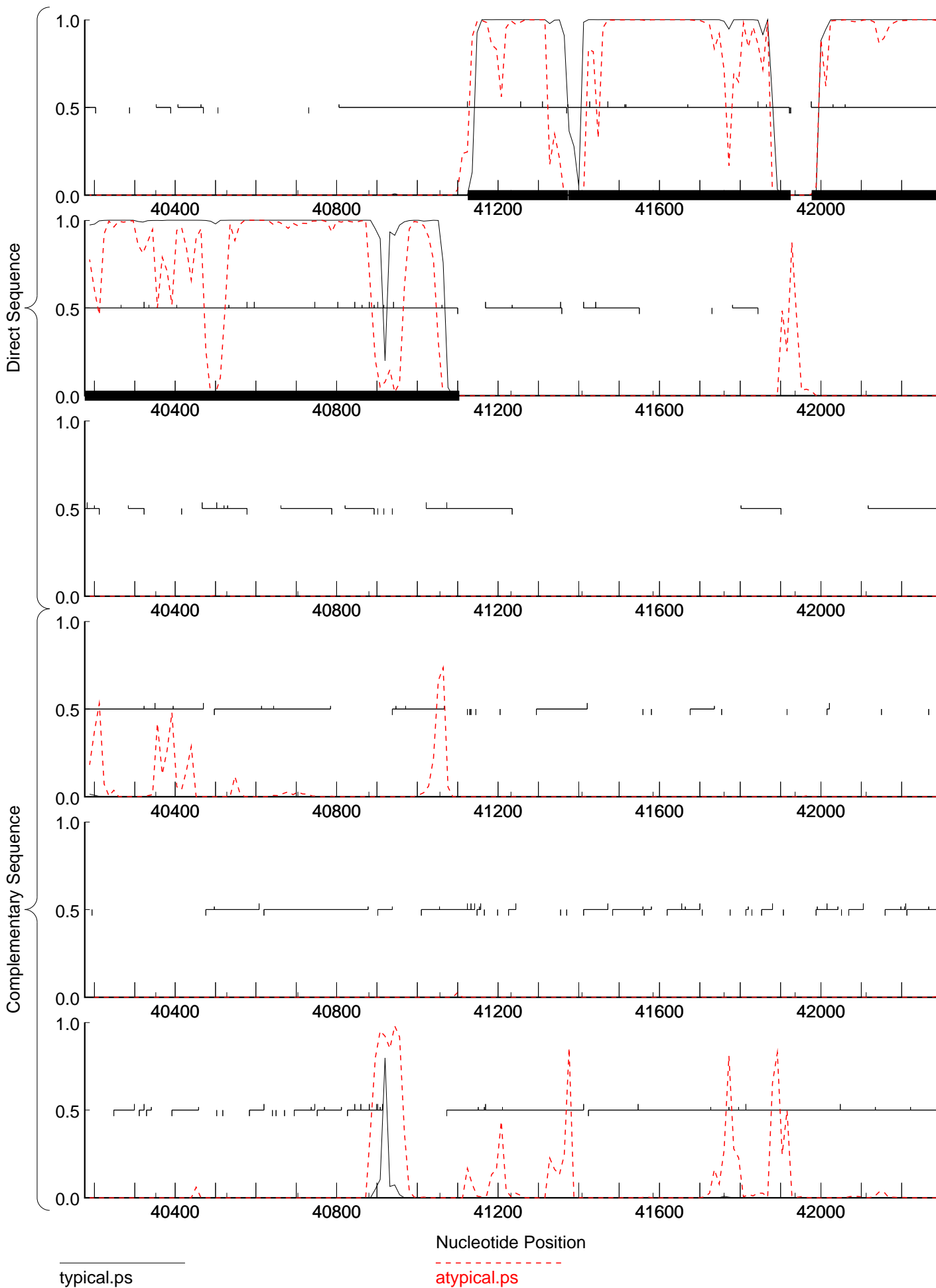


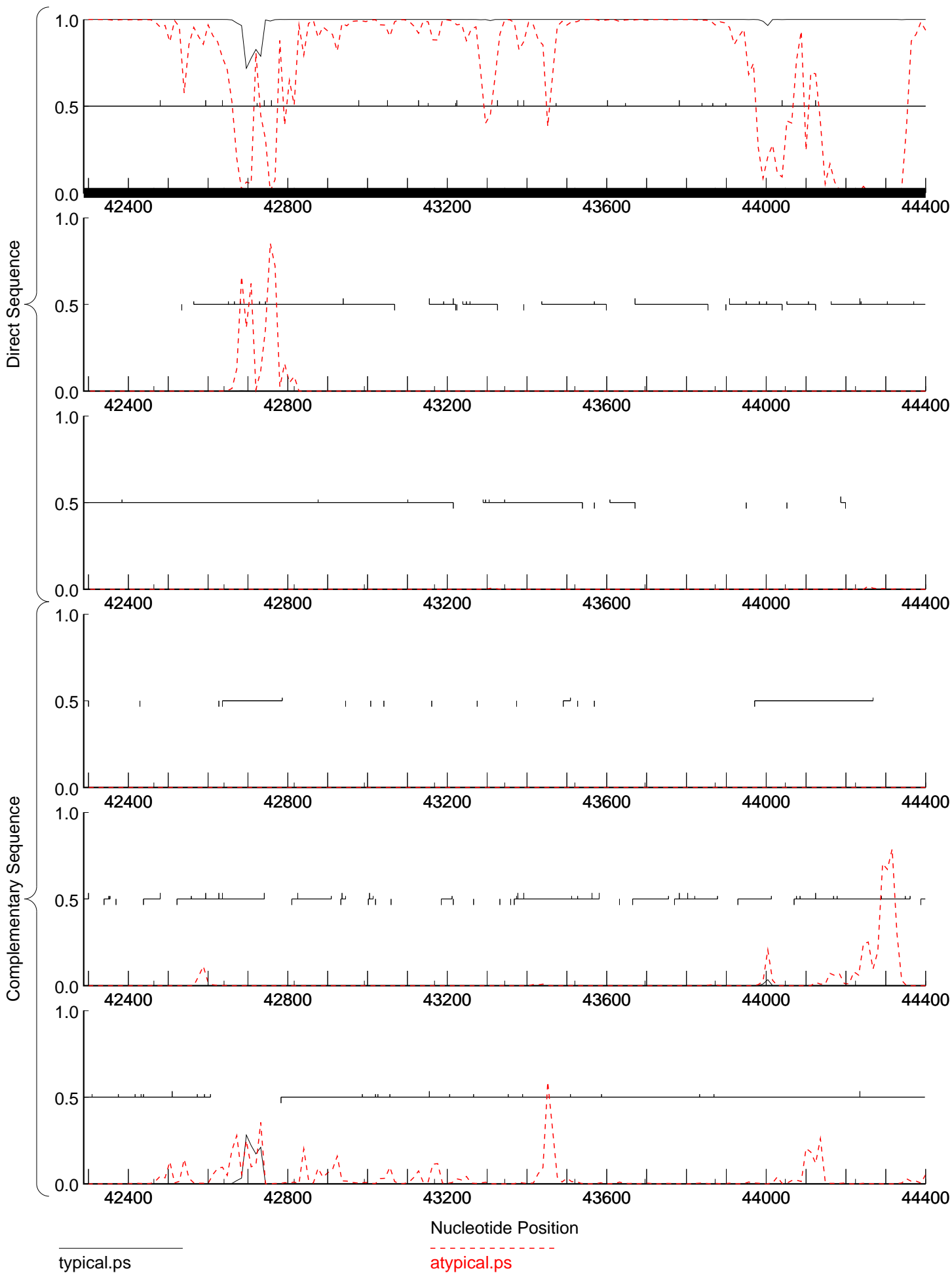


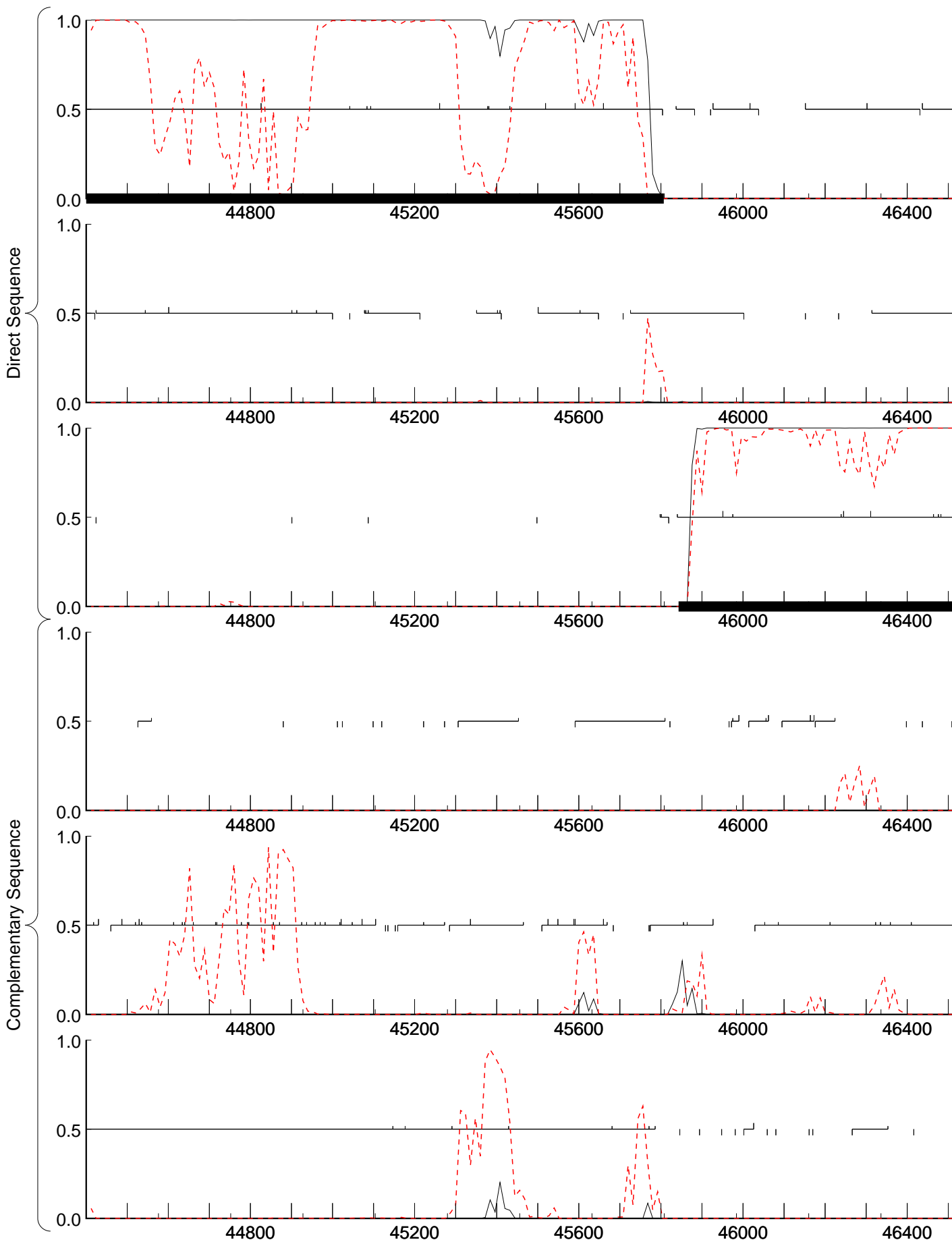


typical.ps

atypical.ps

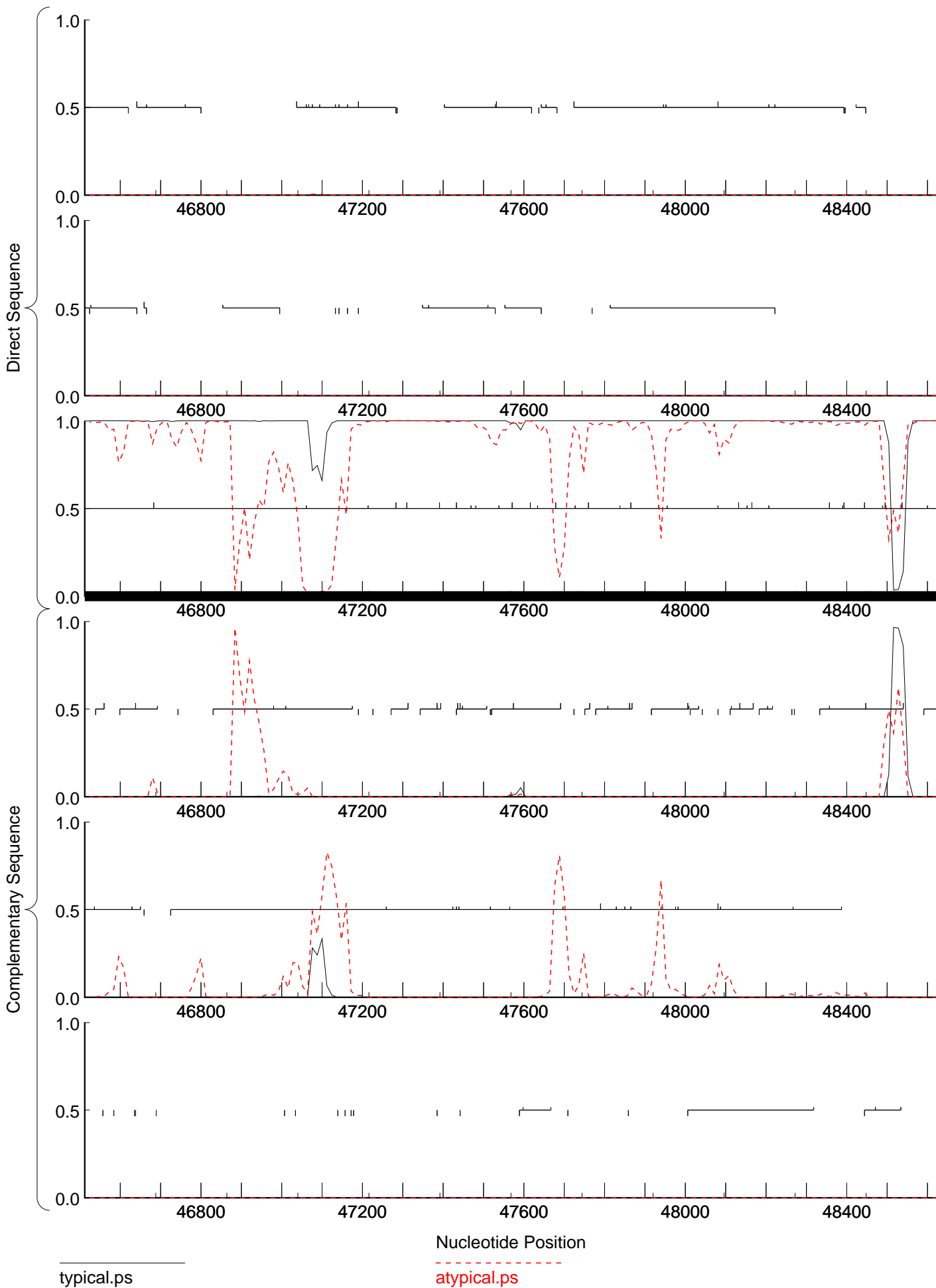






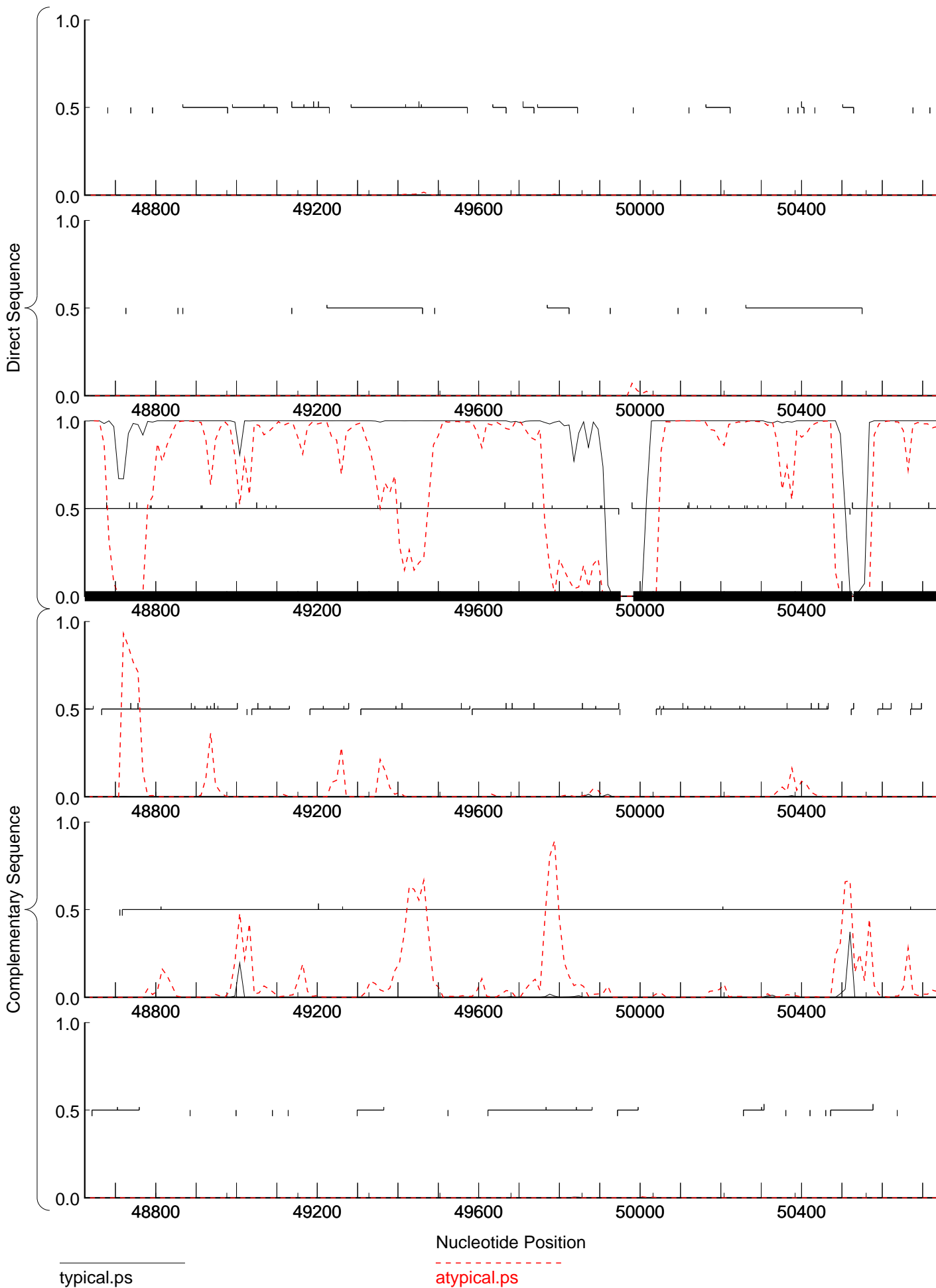
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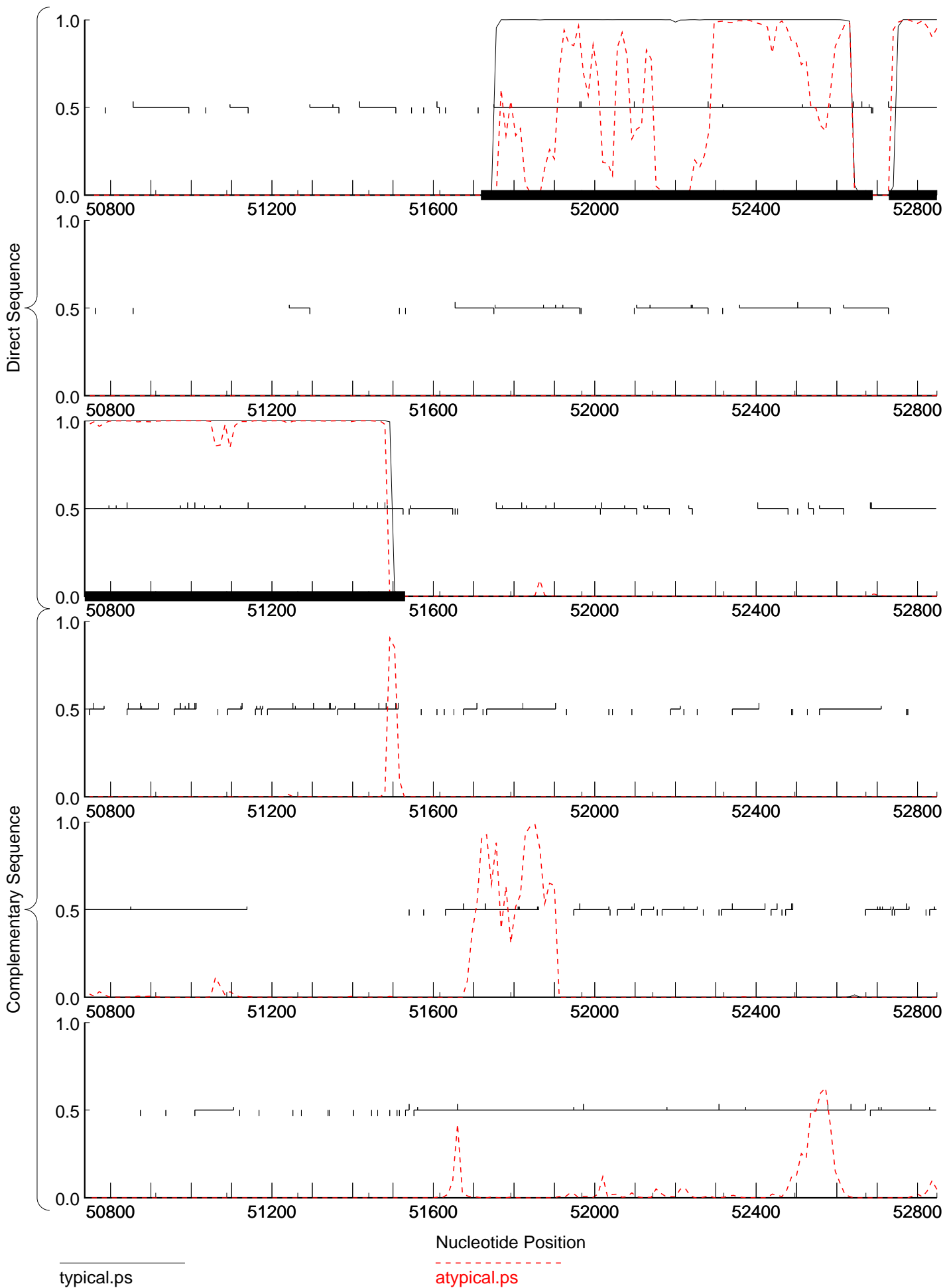
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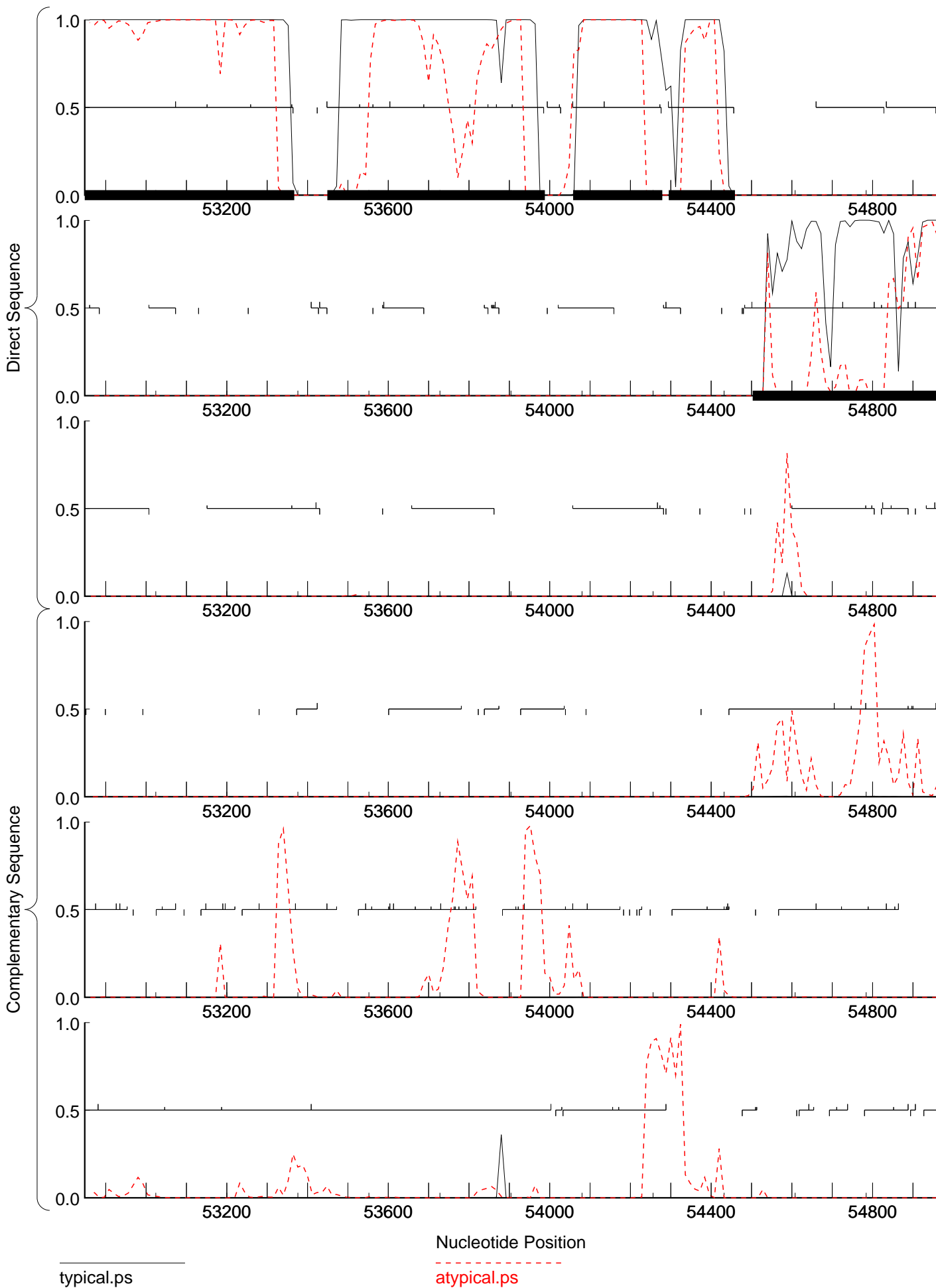
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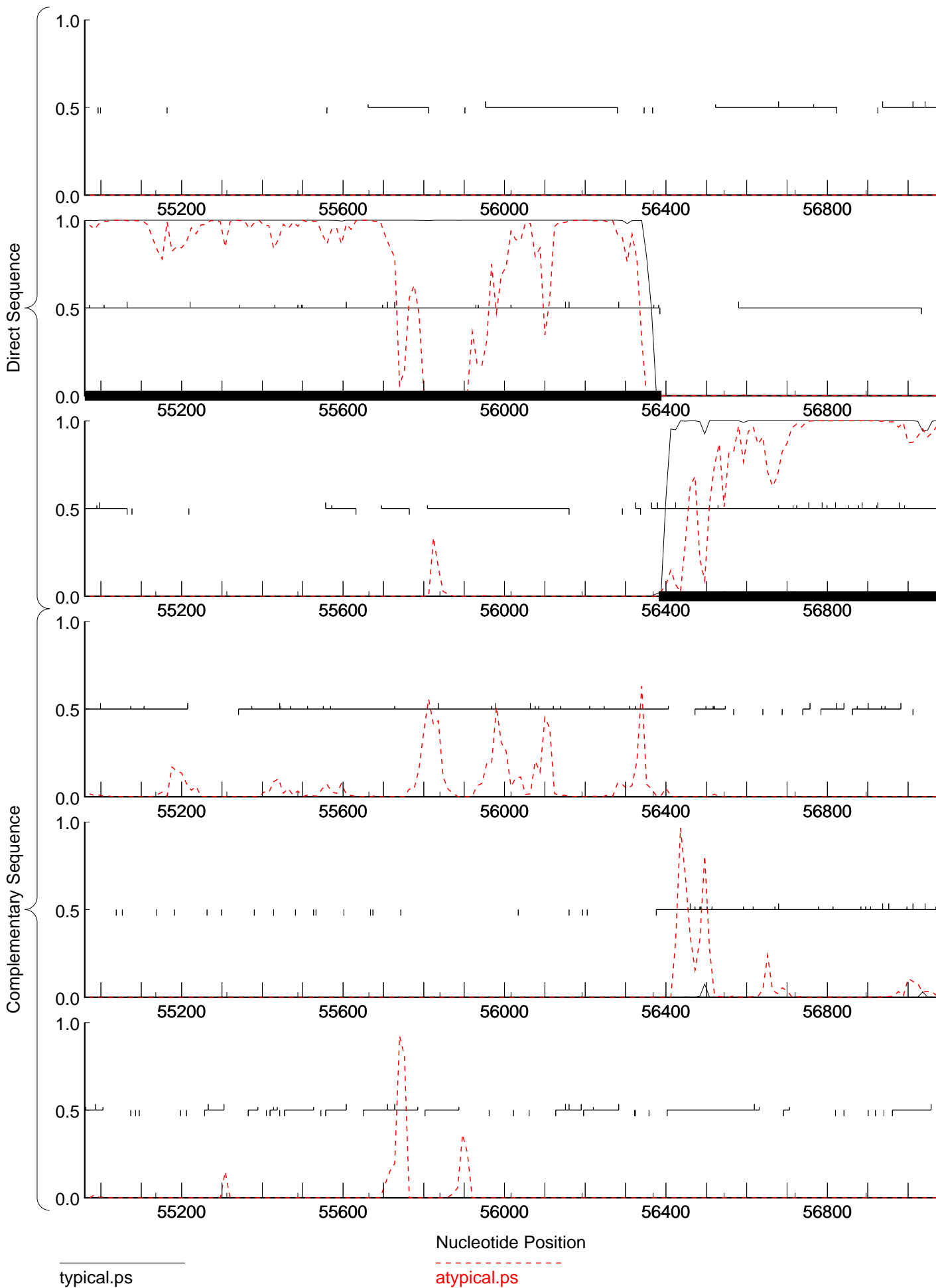


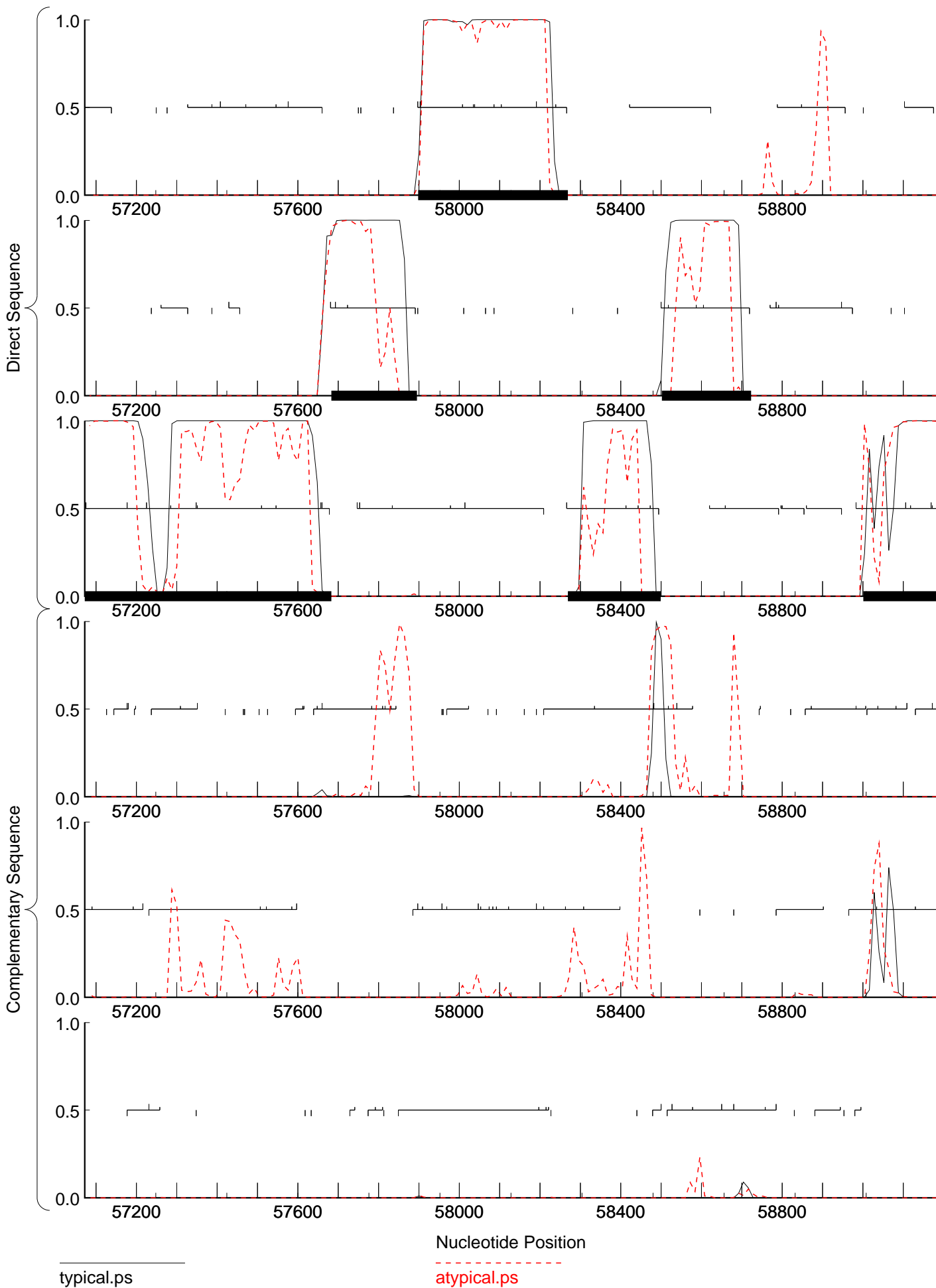
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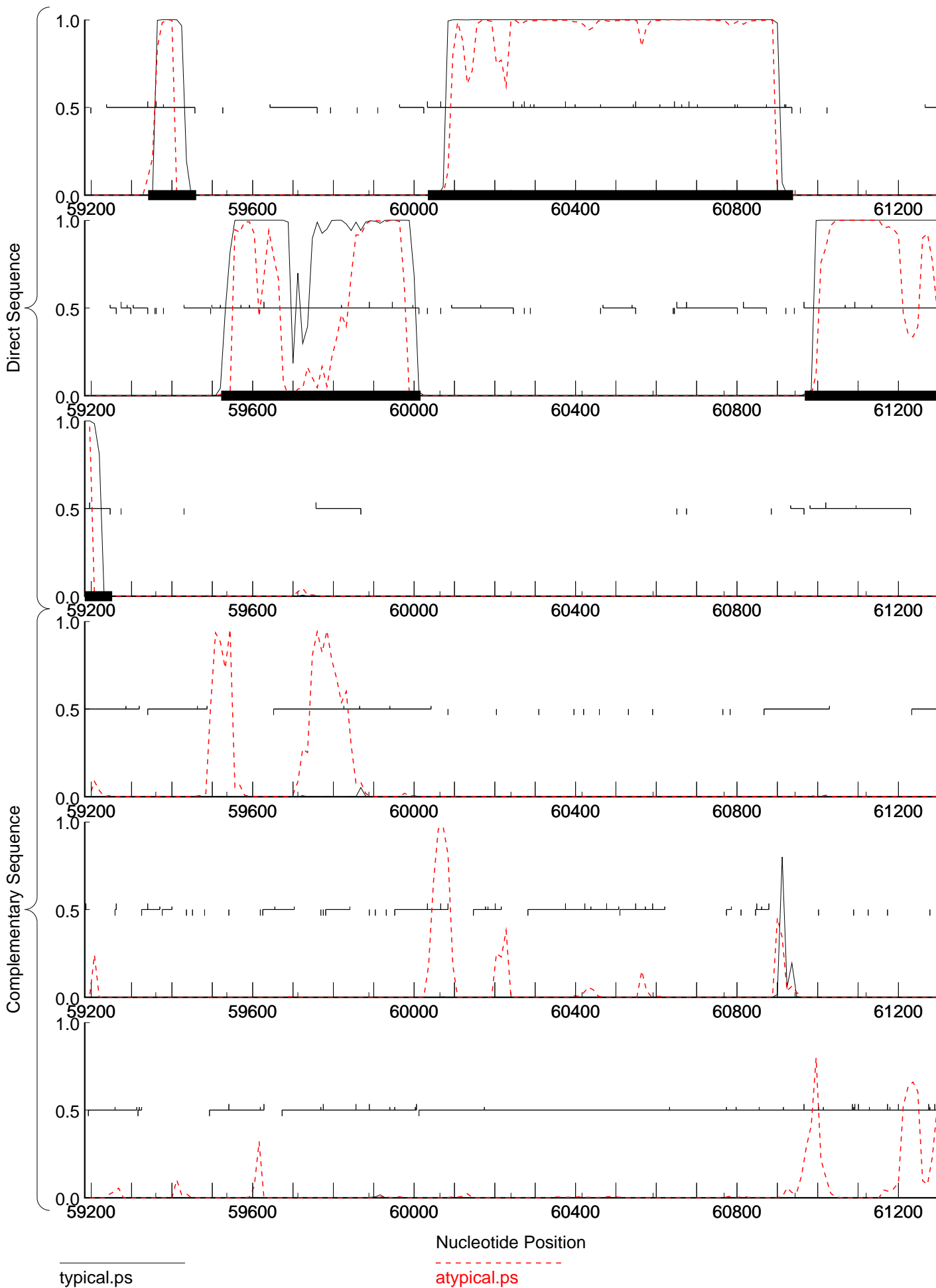
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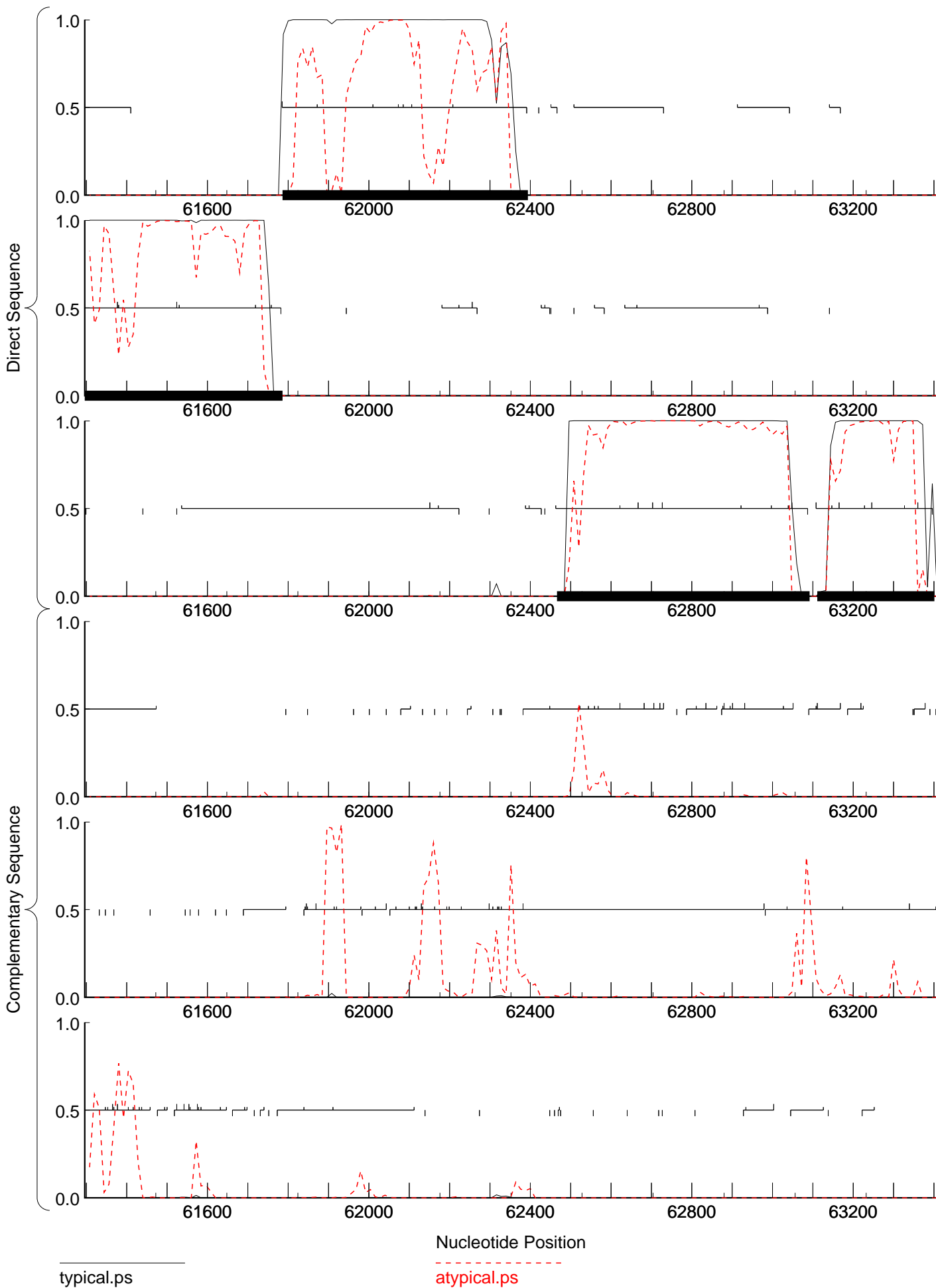


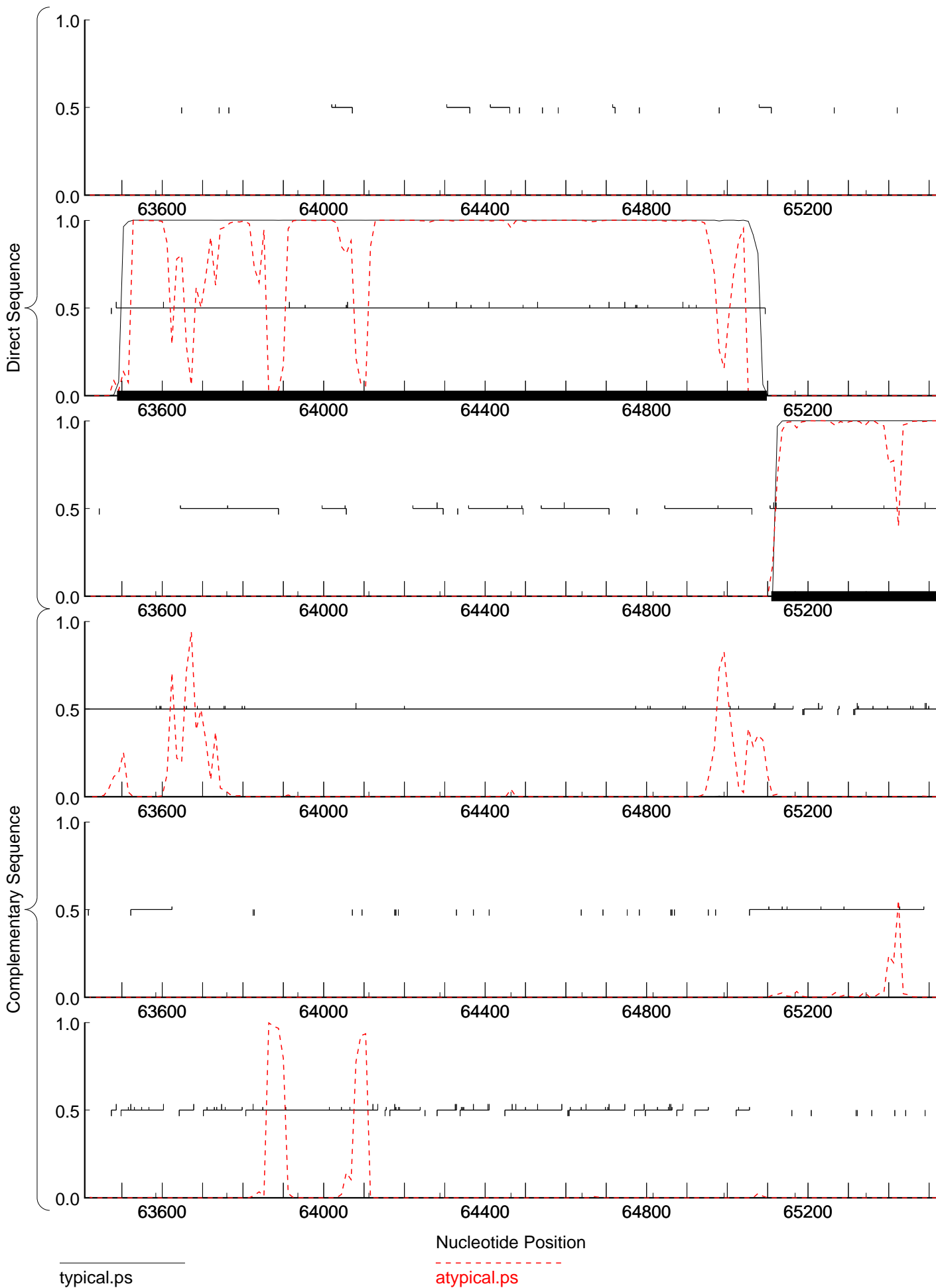


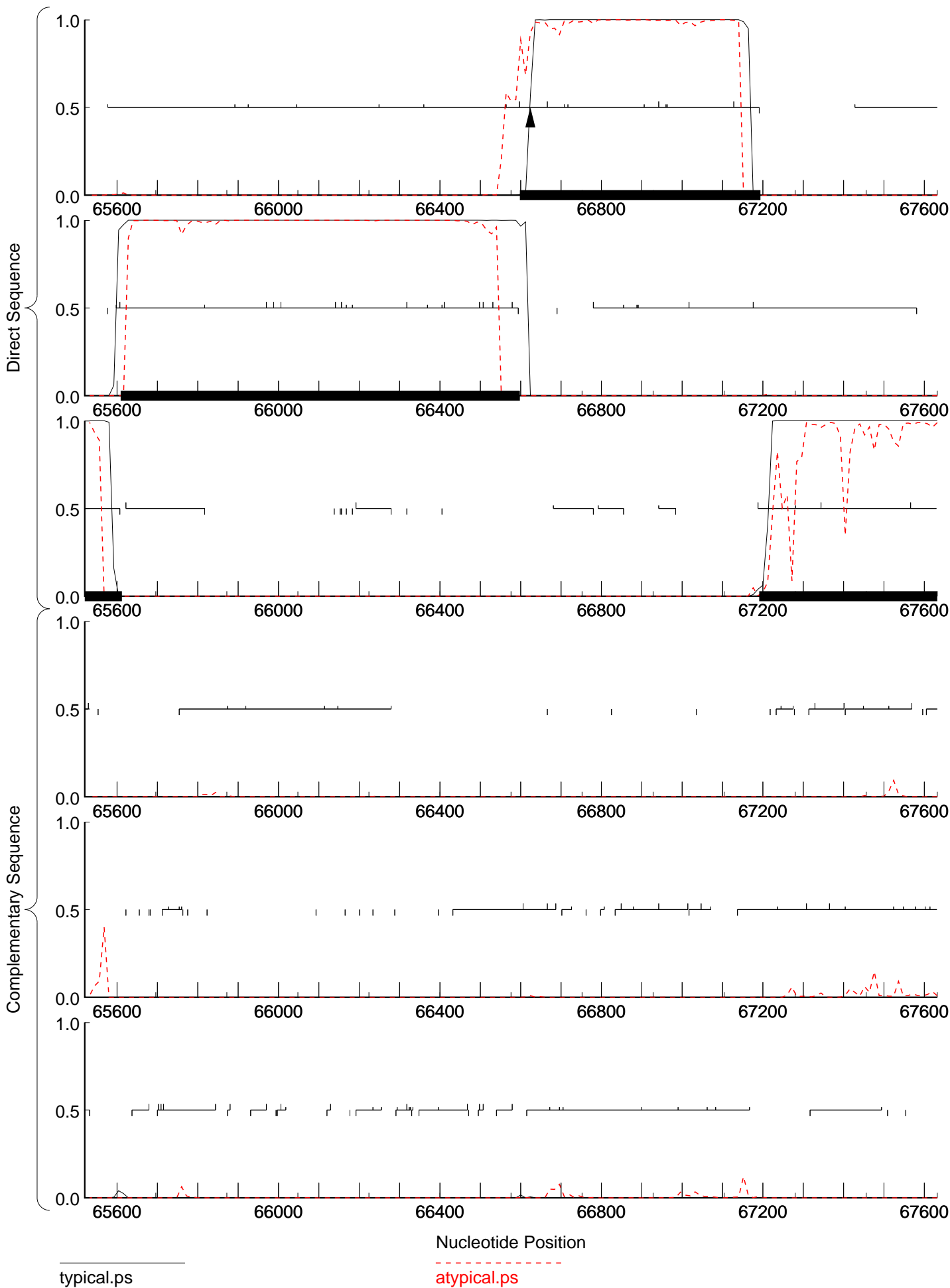


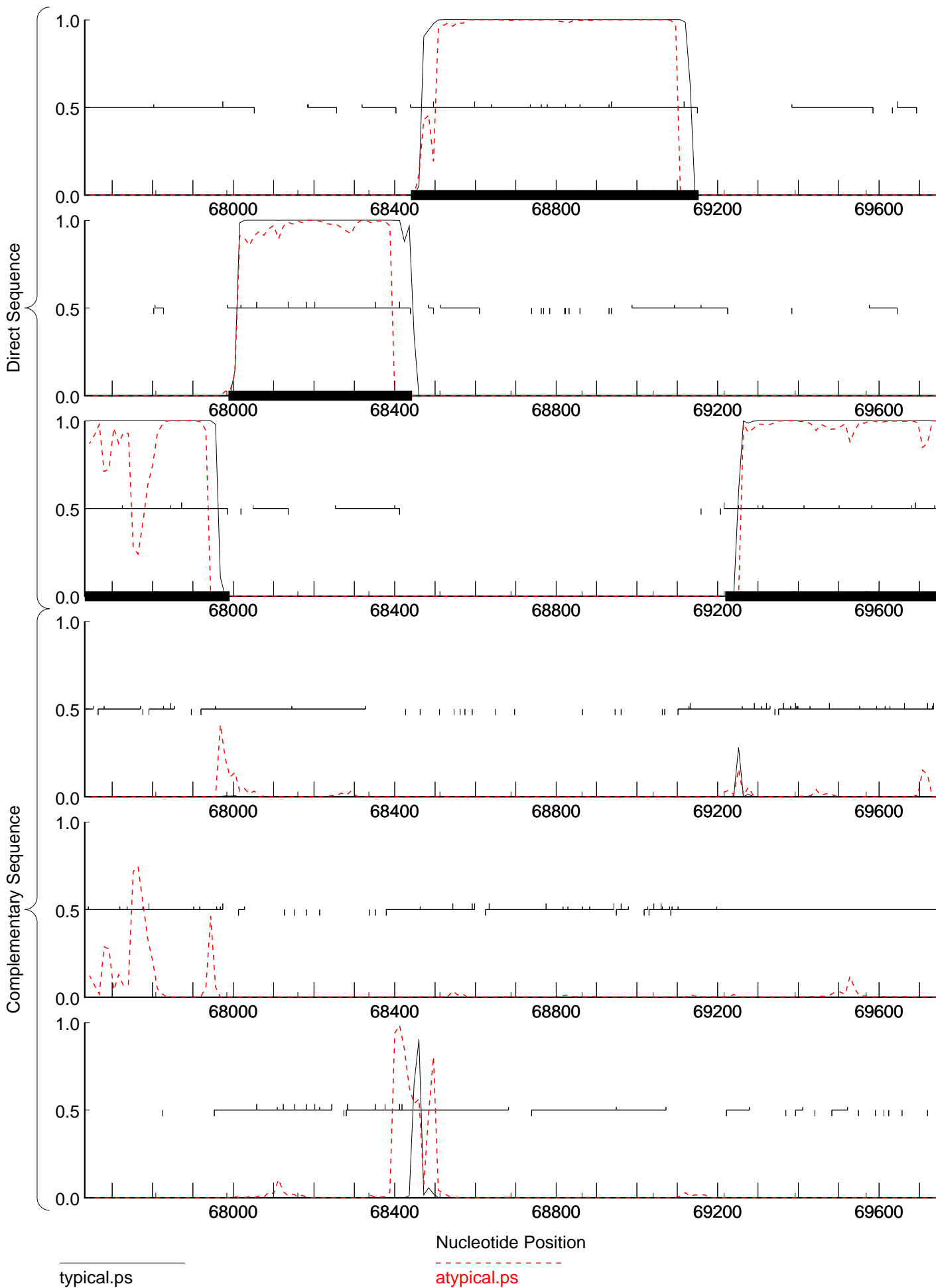


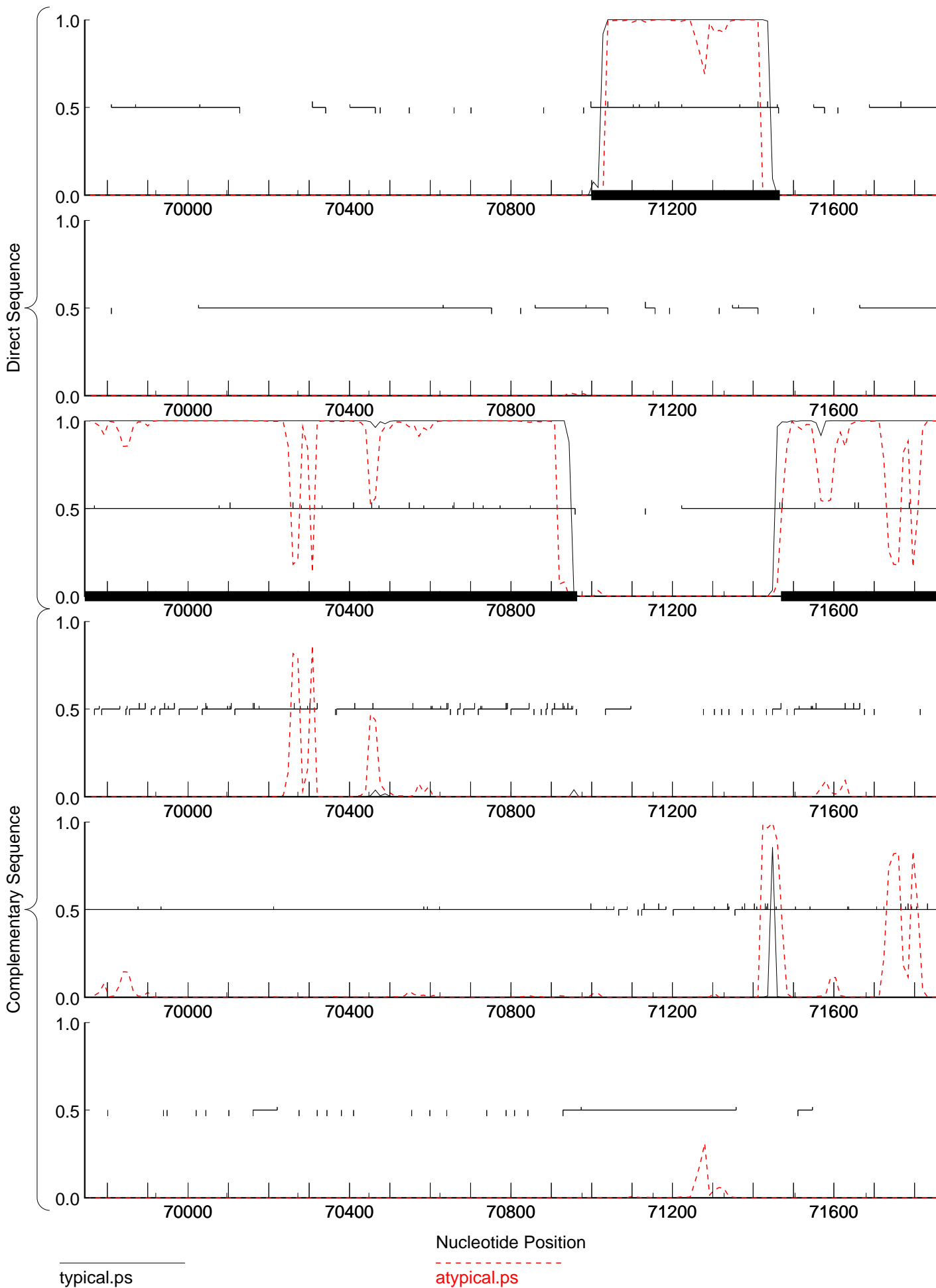


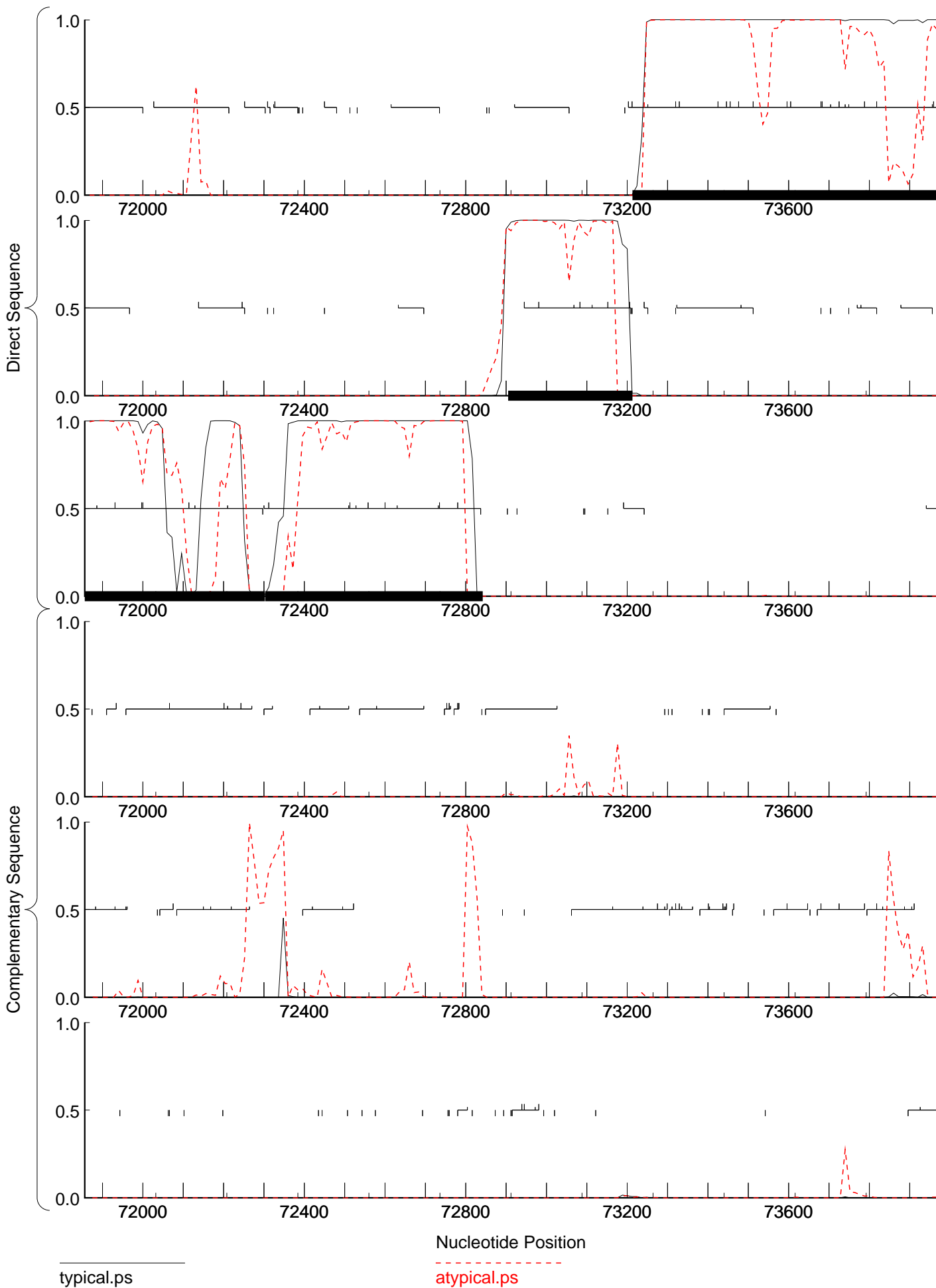


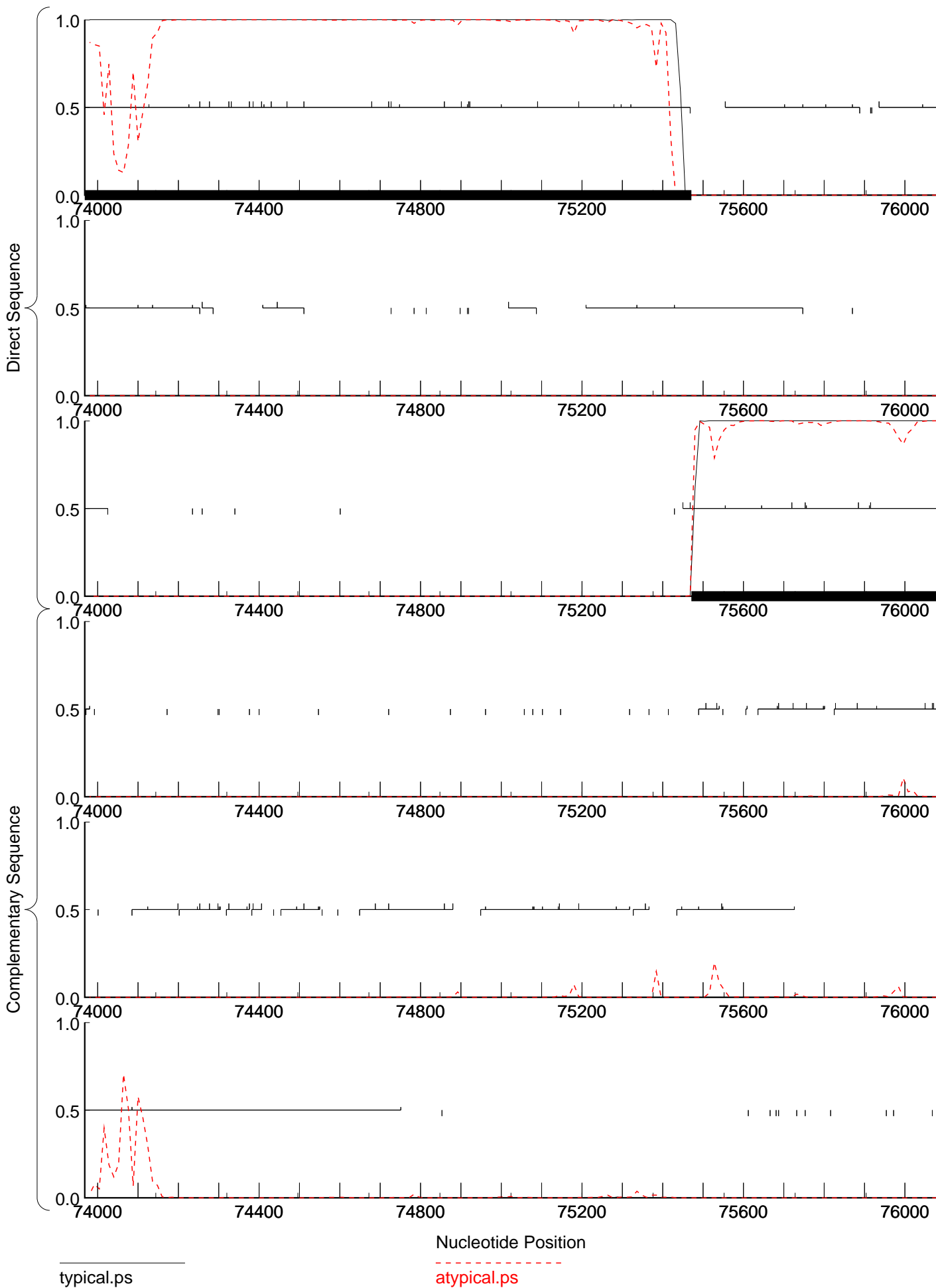


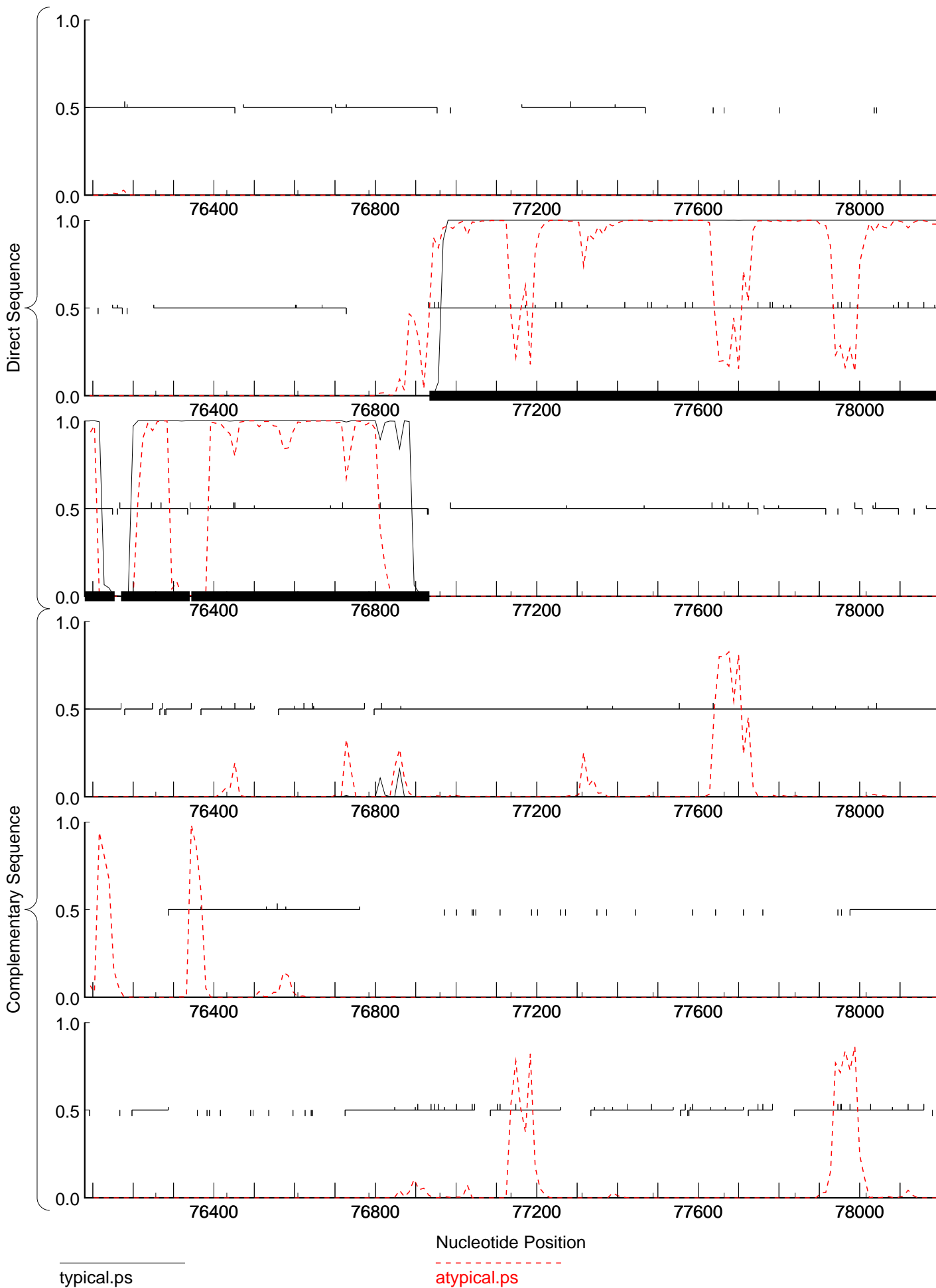


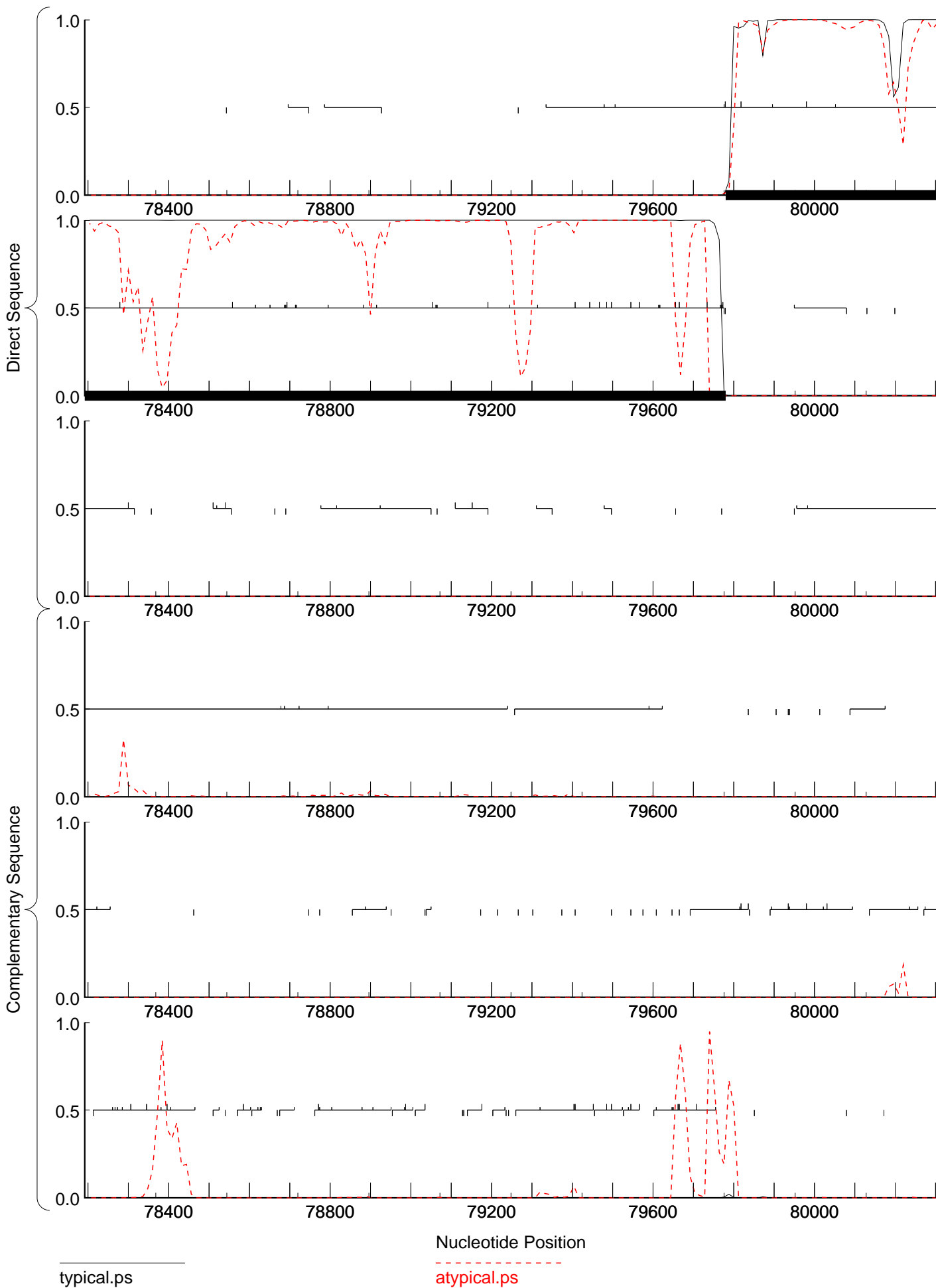


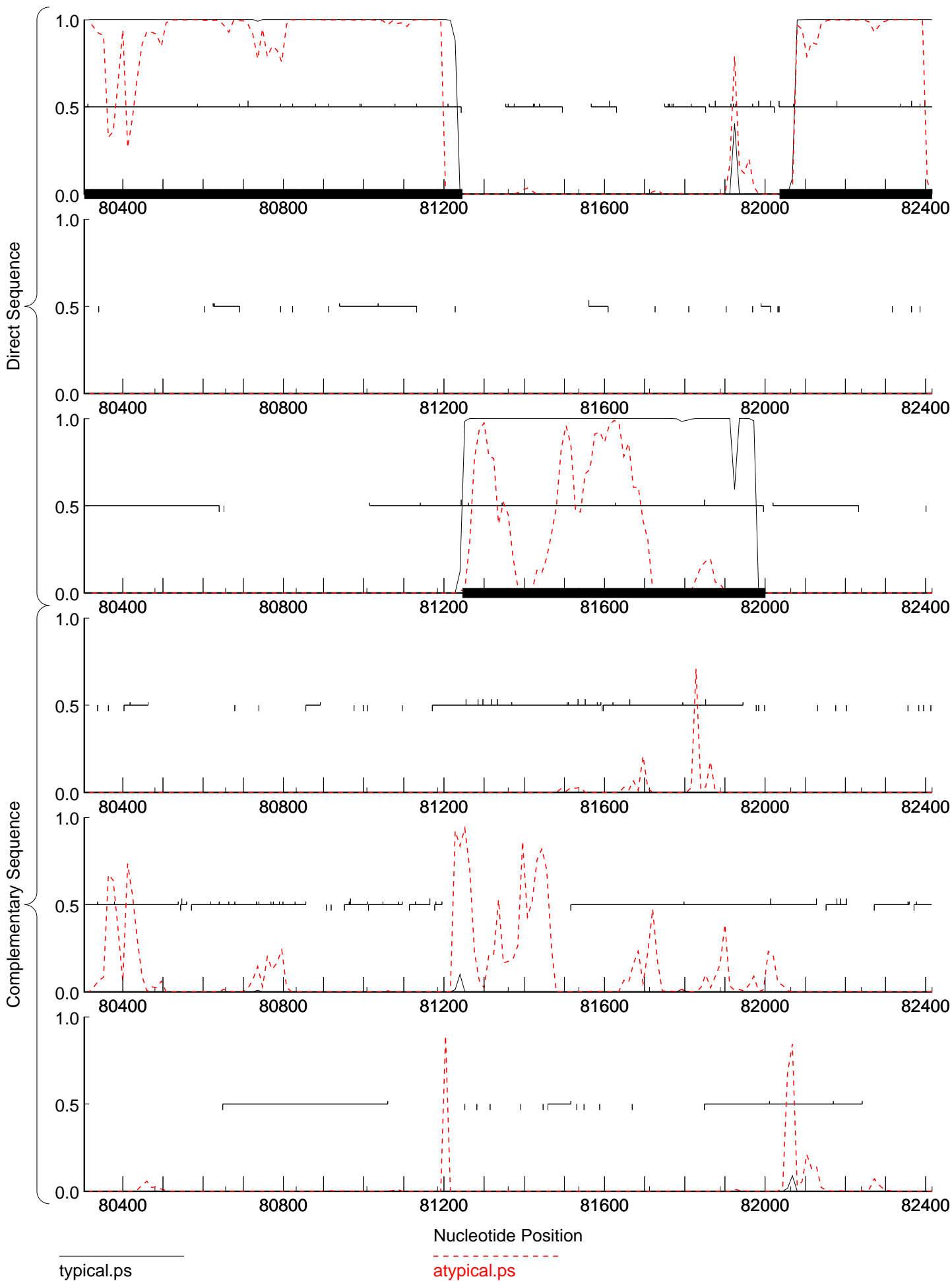






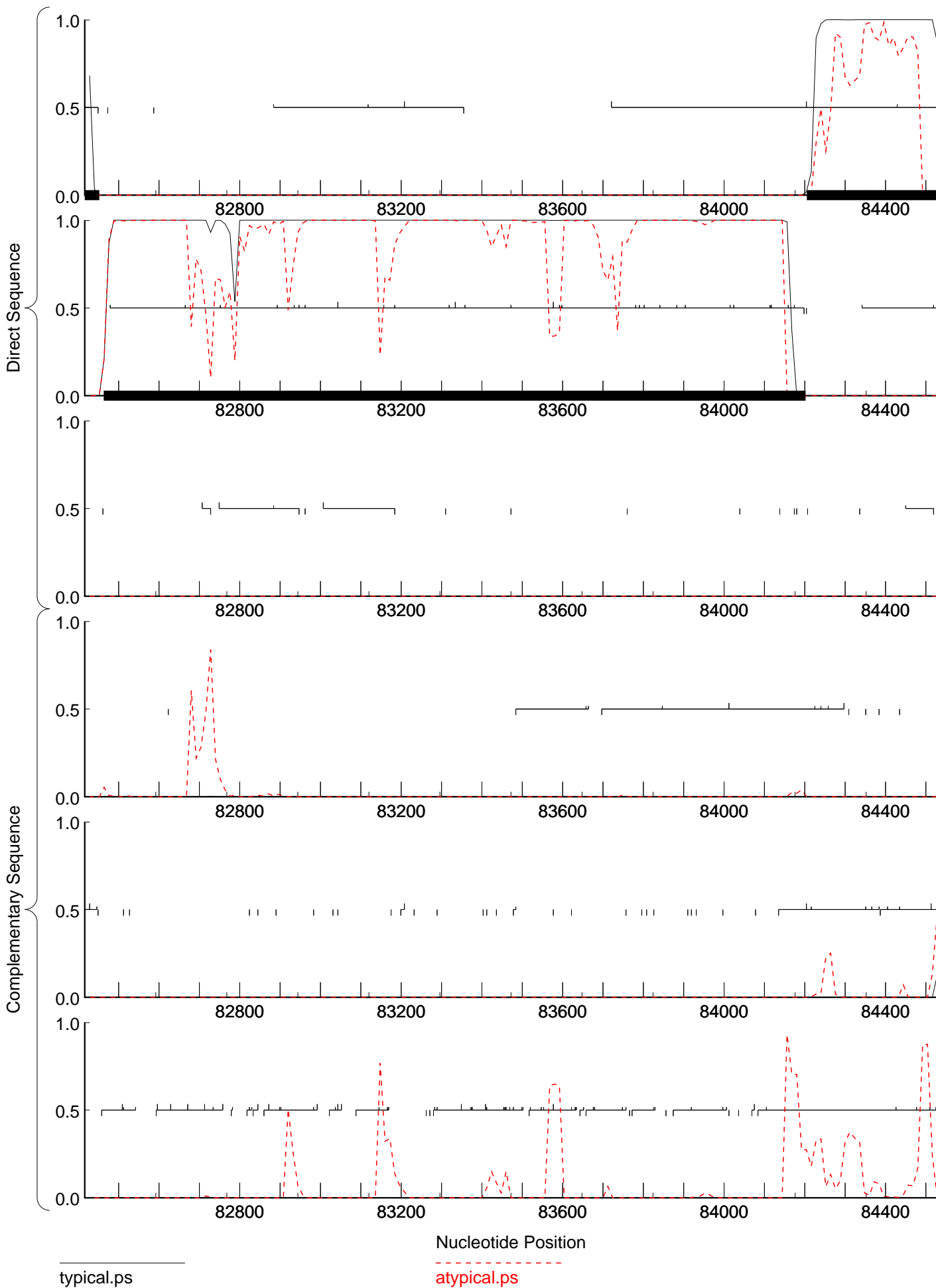


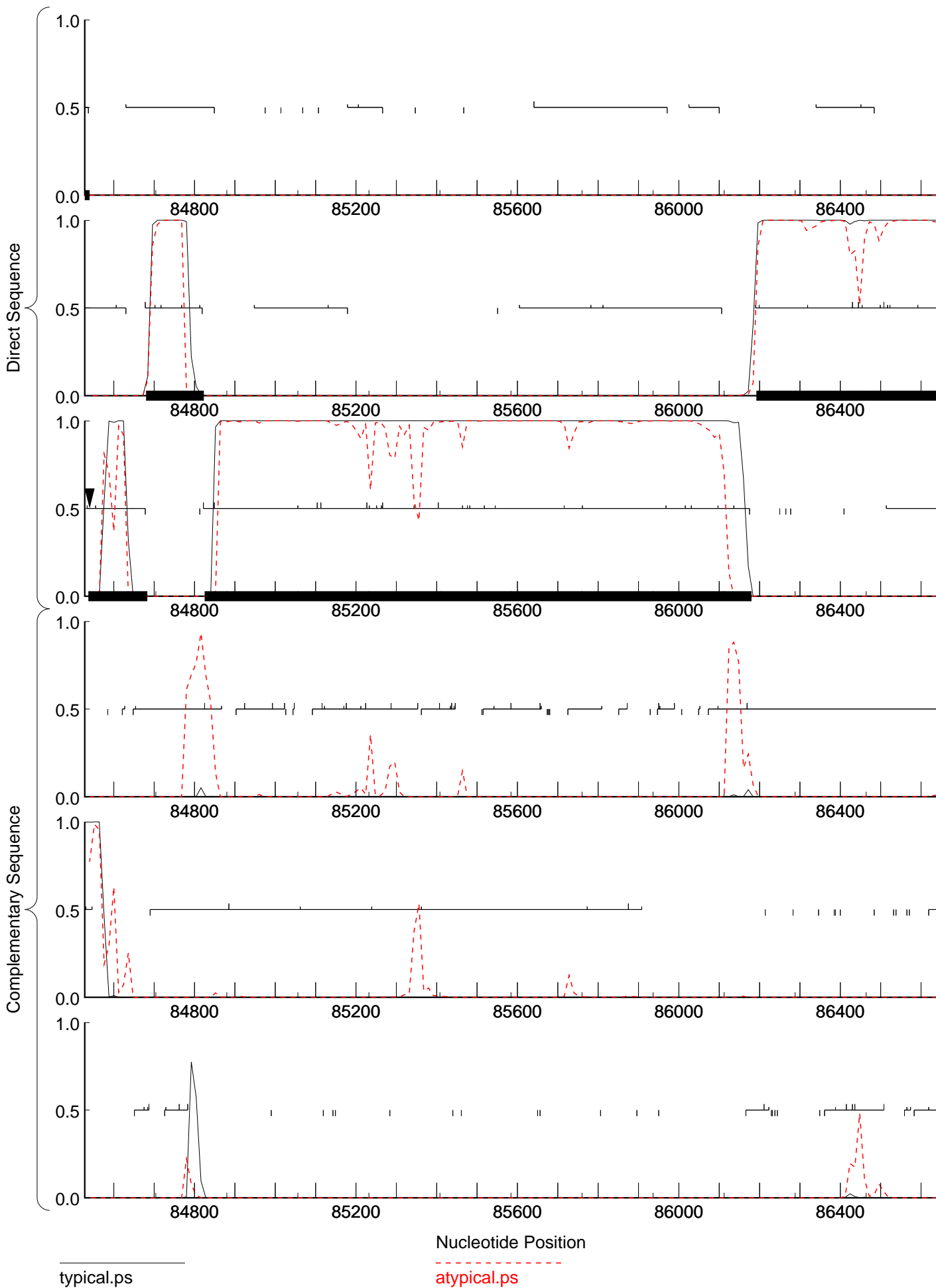


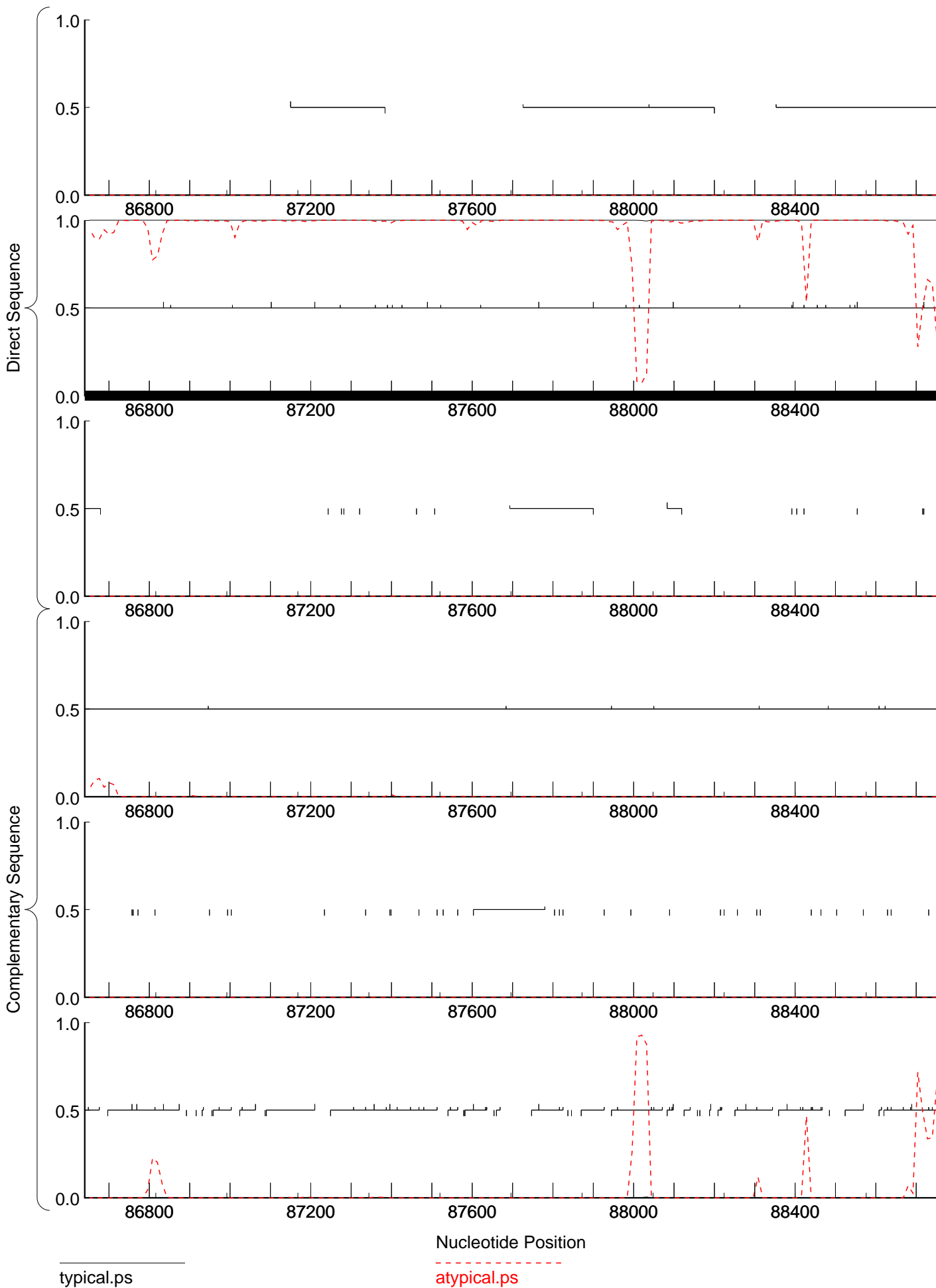


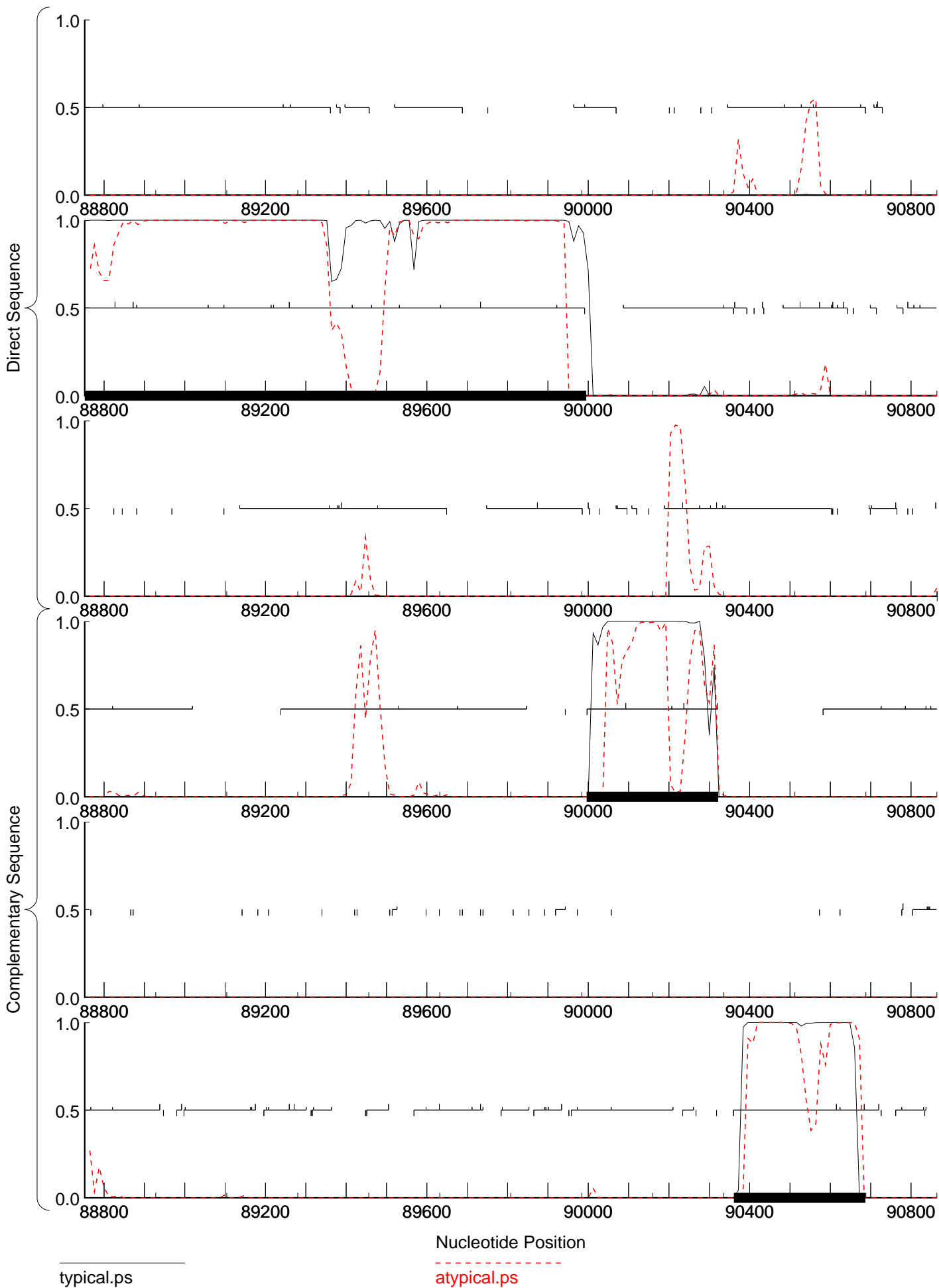
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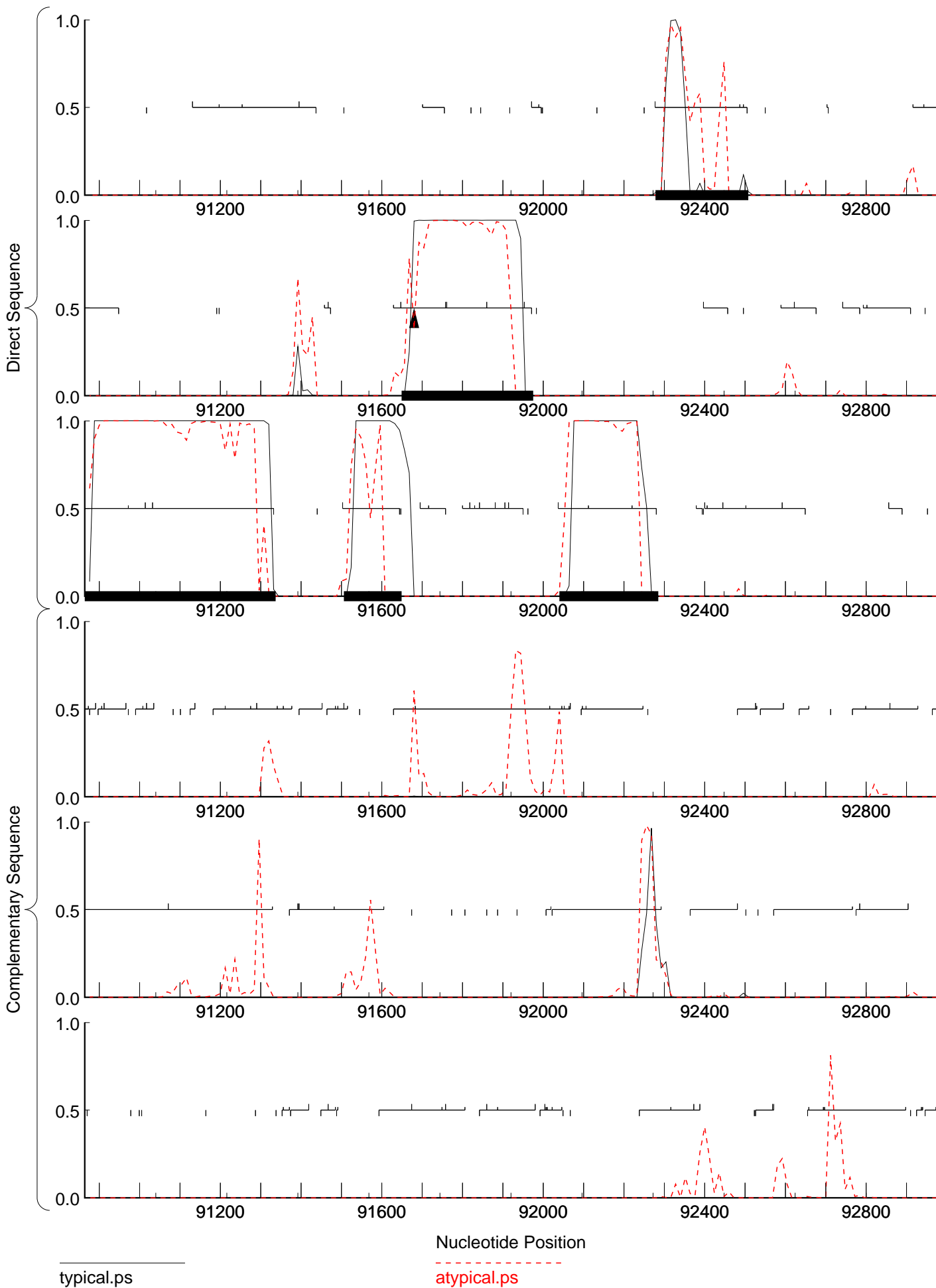
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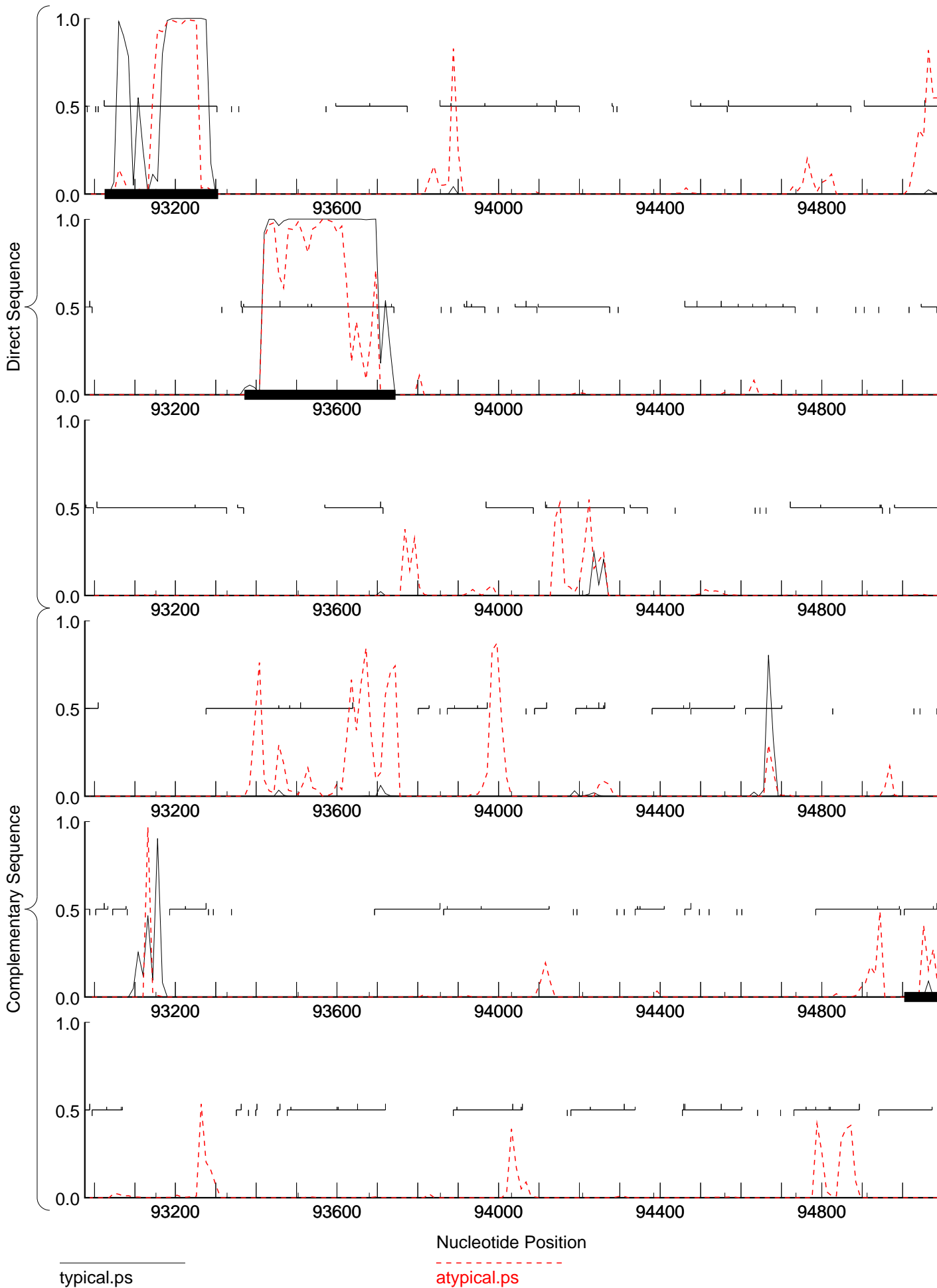


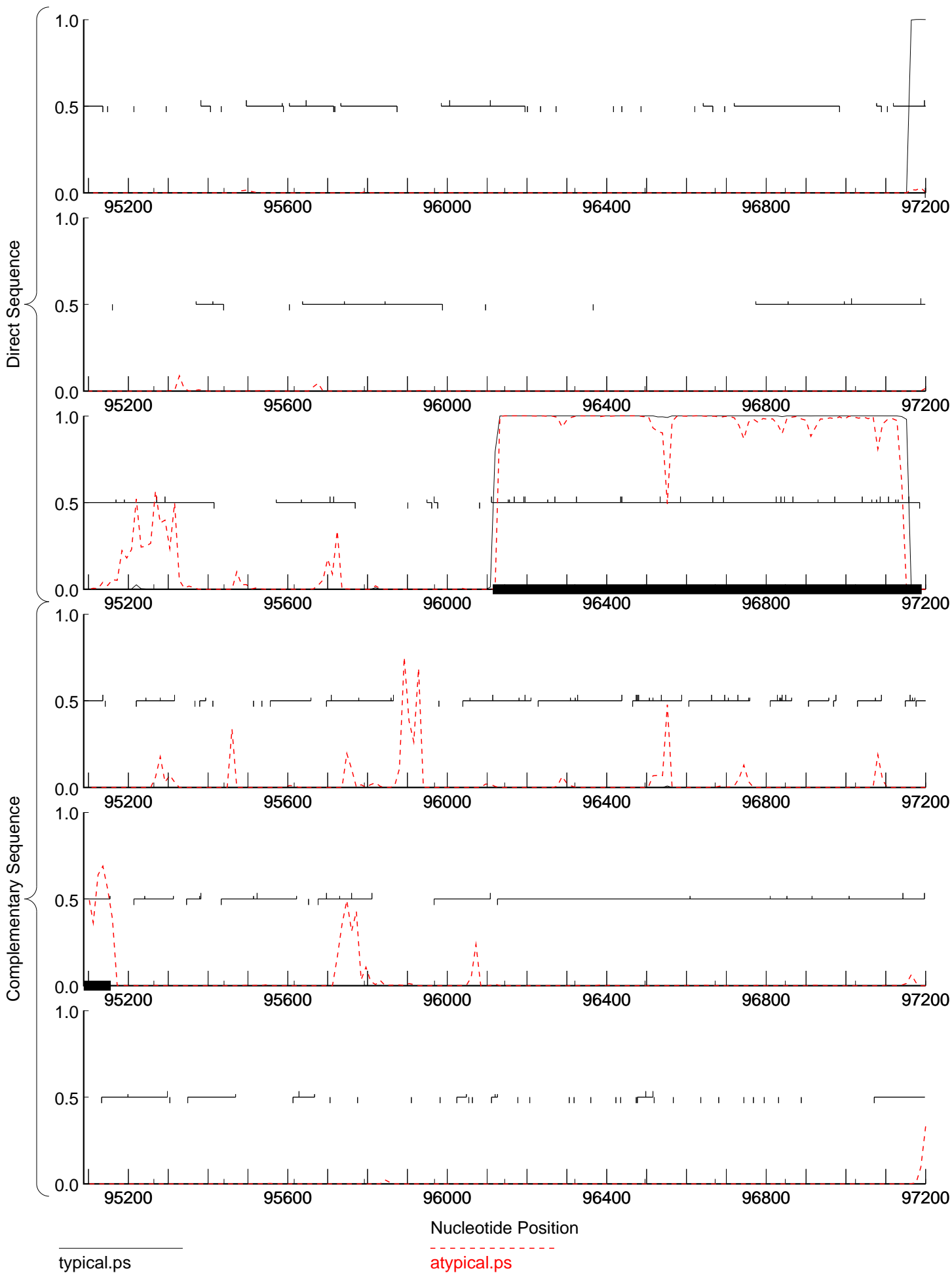


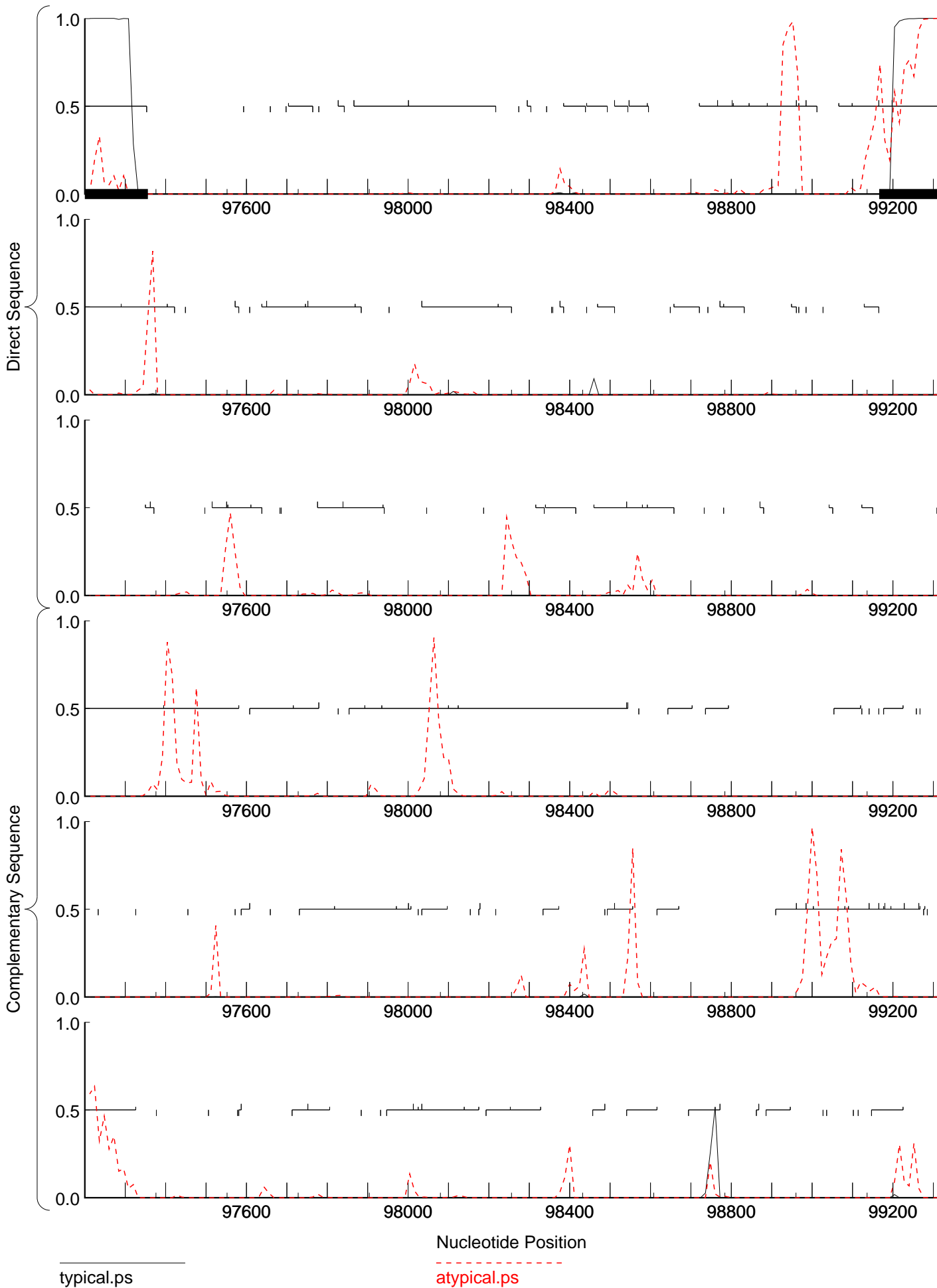


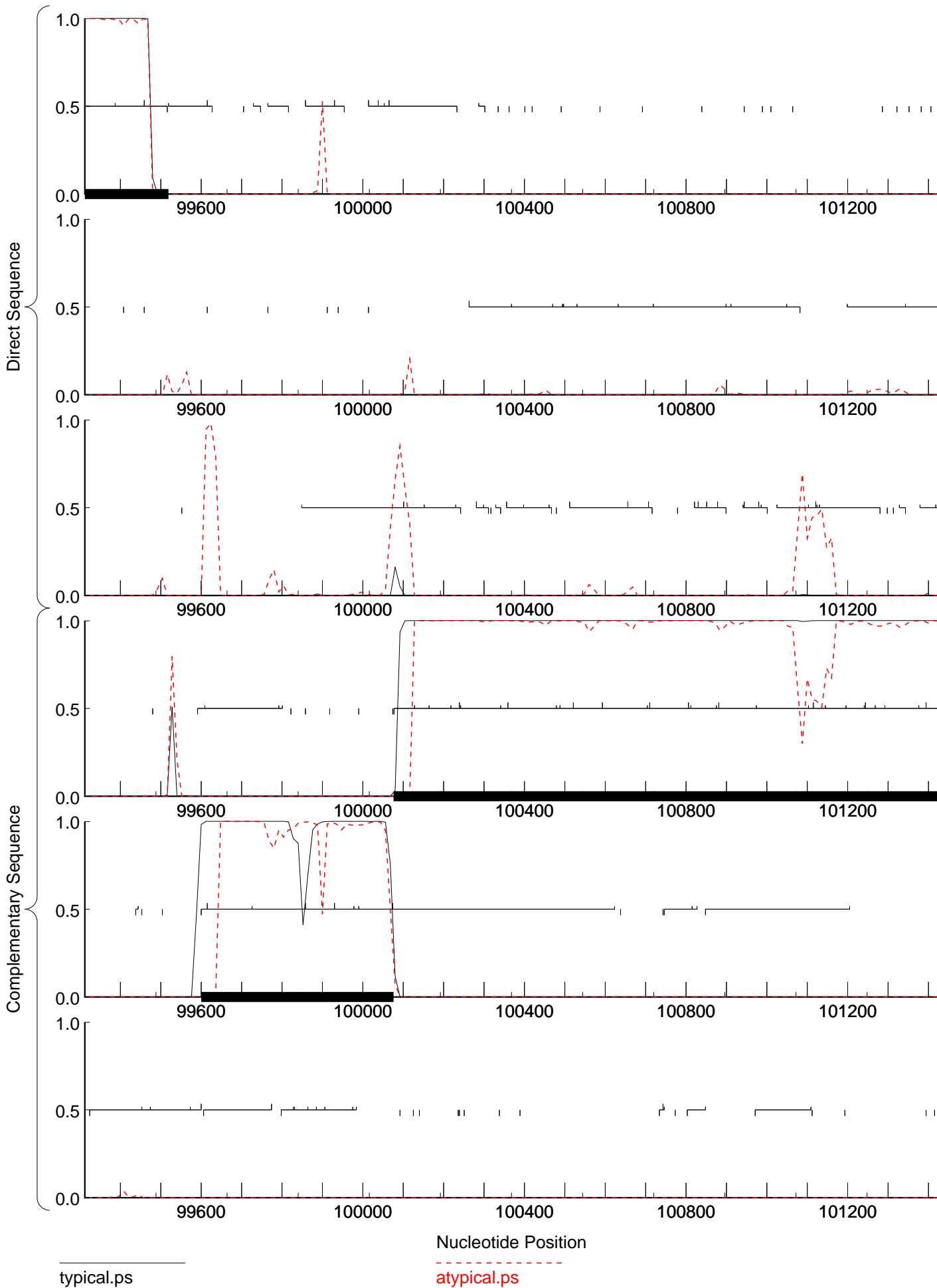
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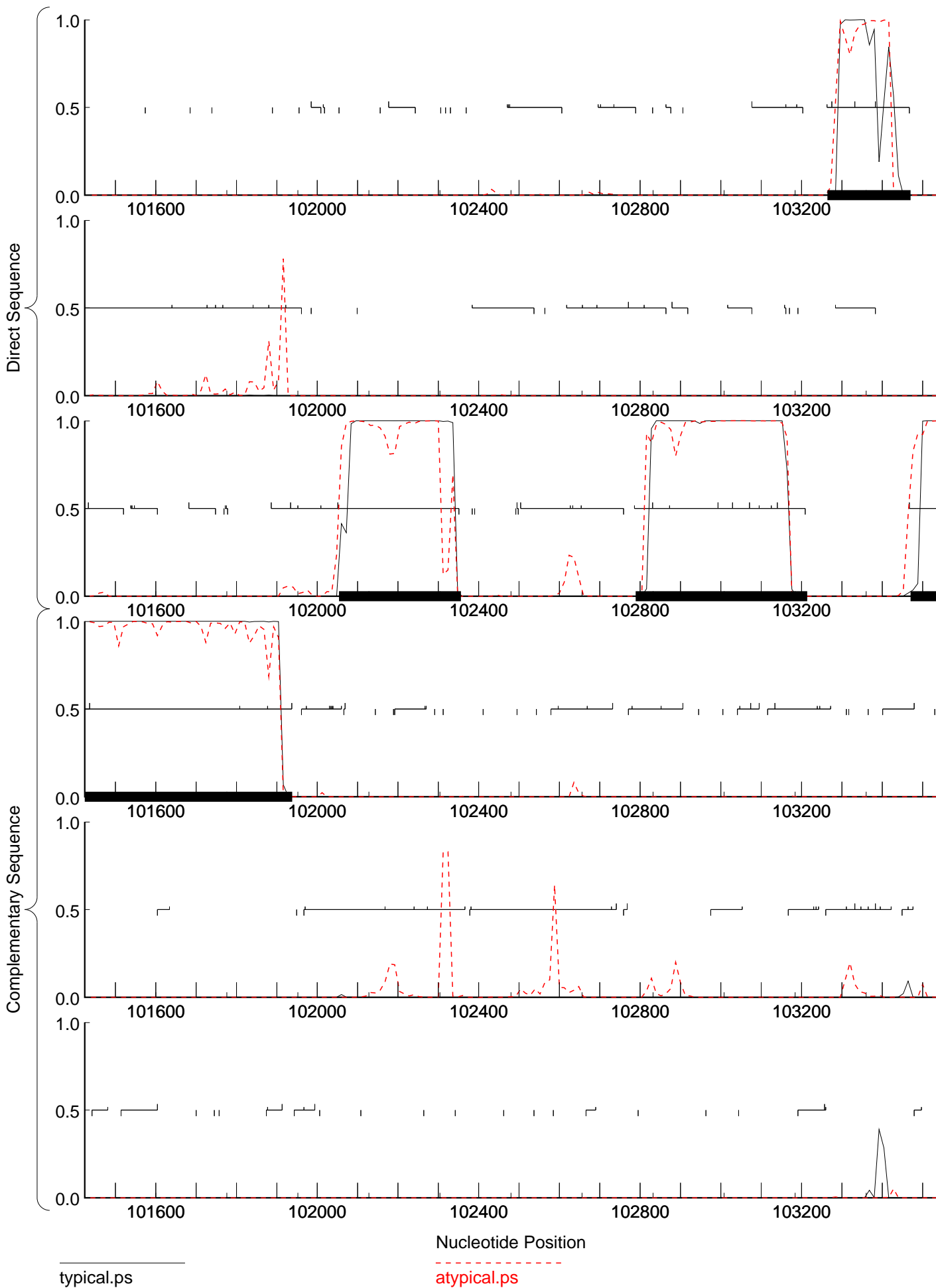
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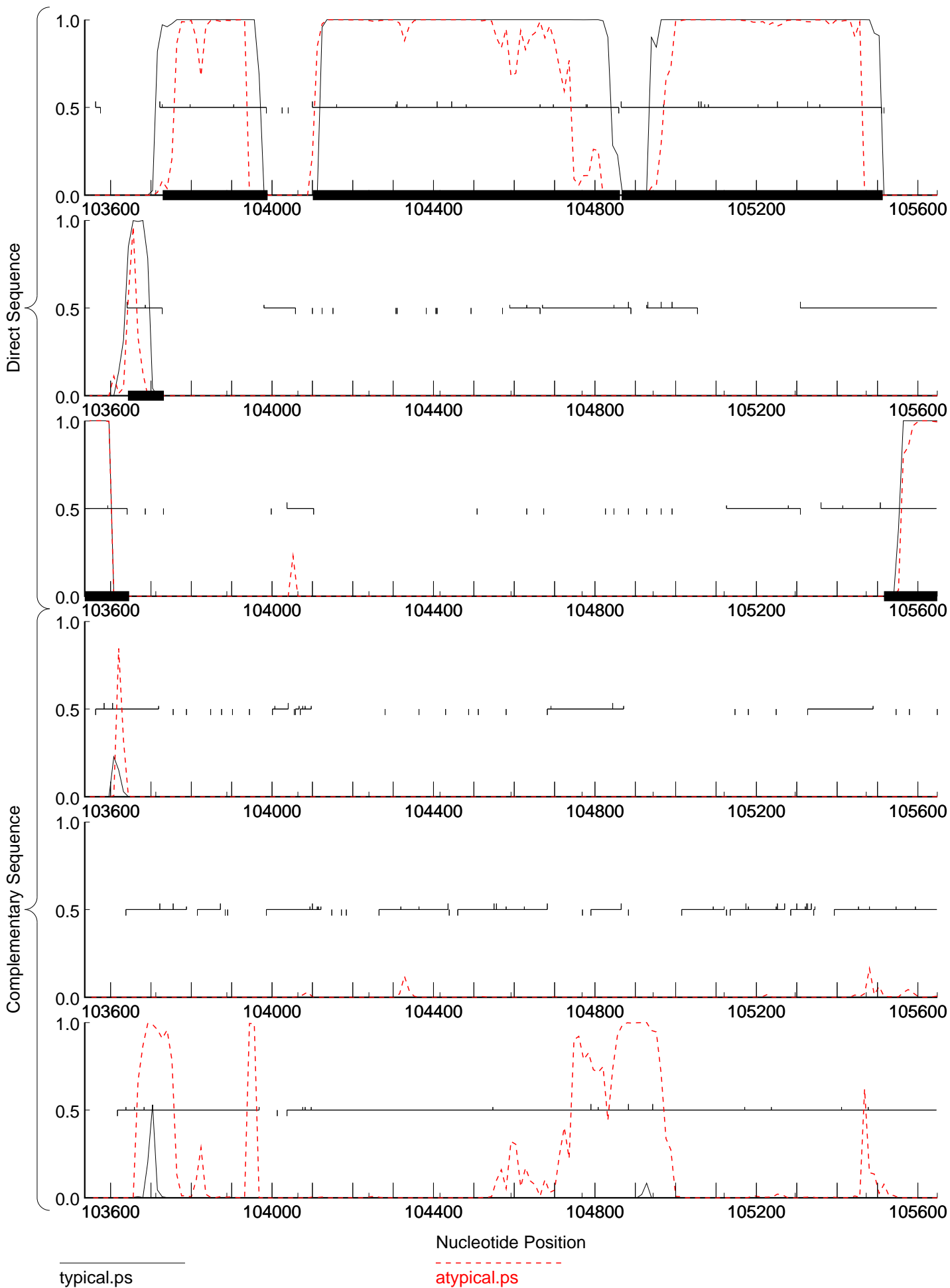


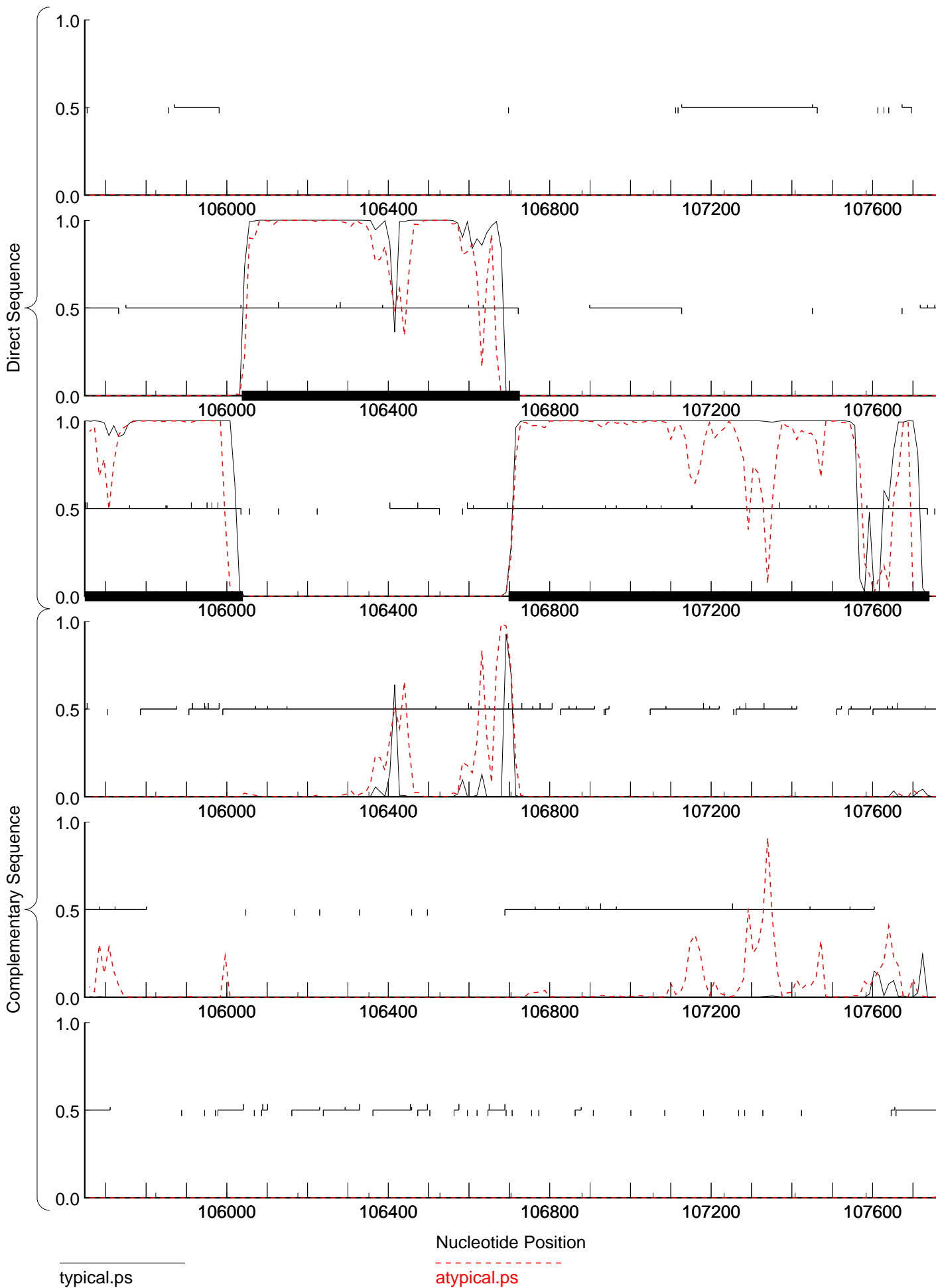


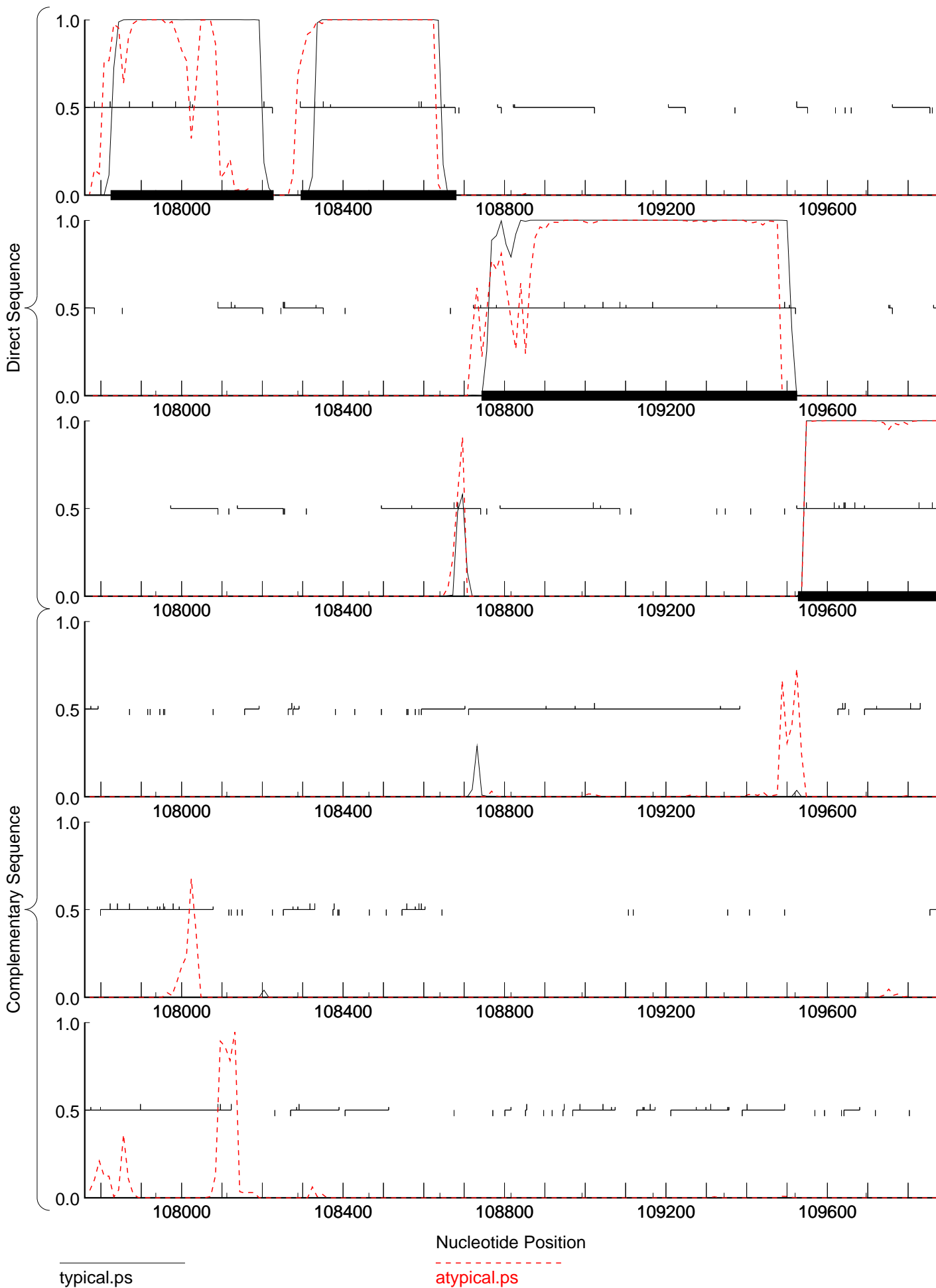


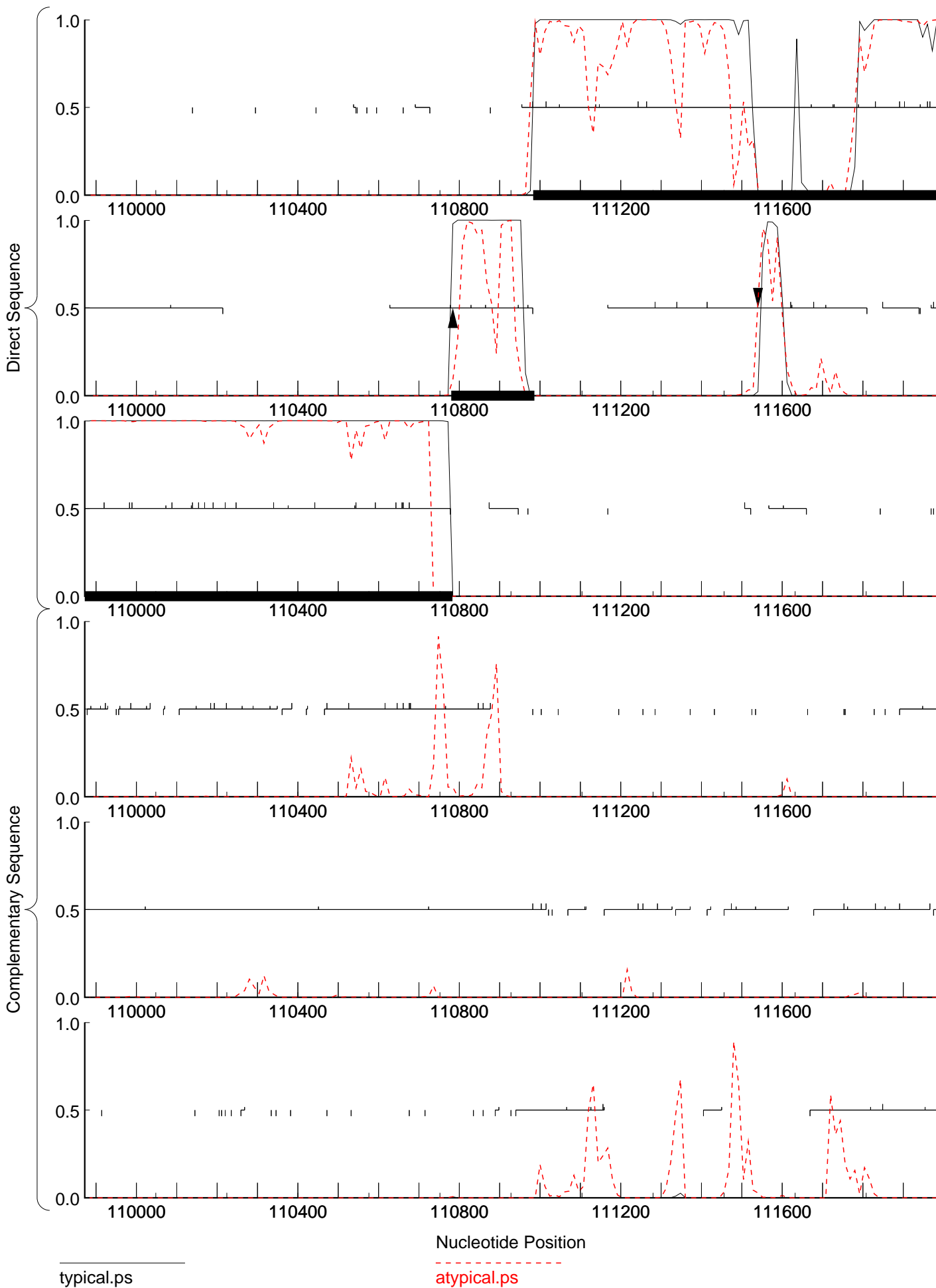


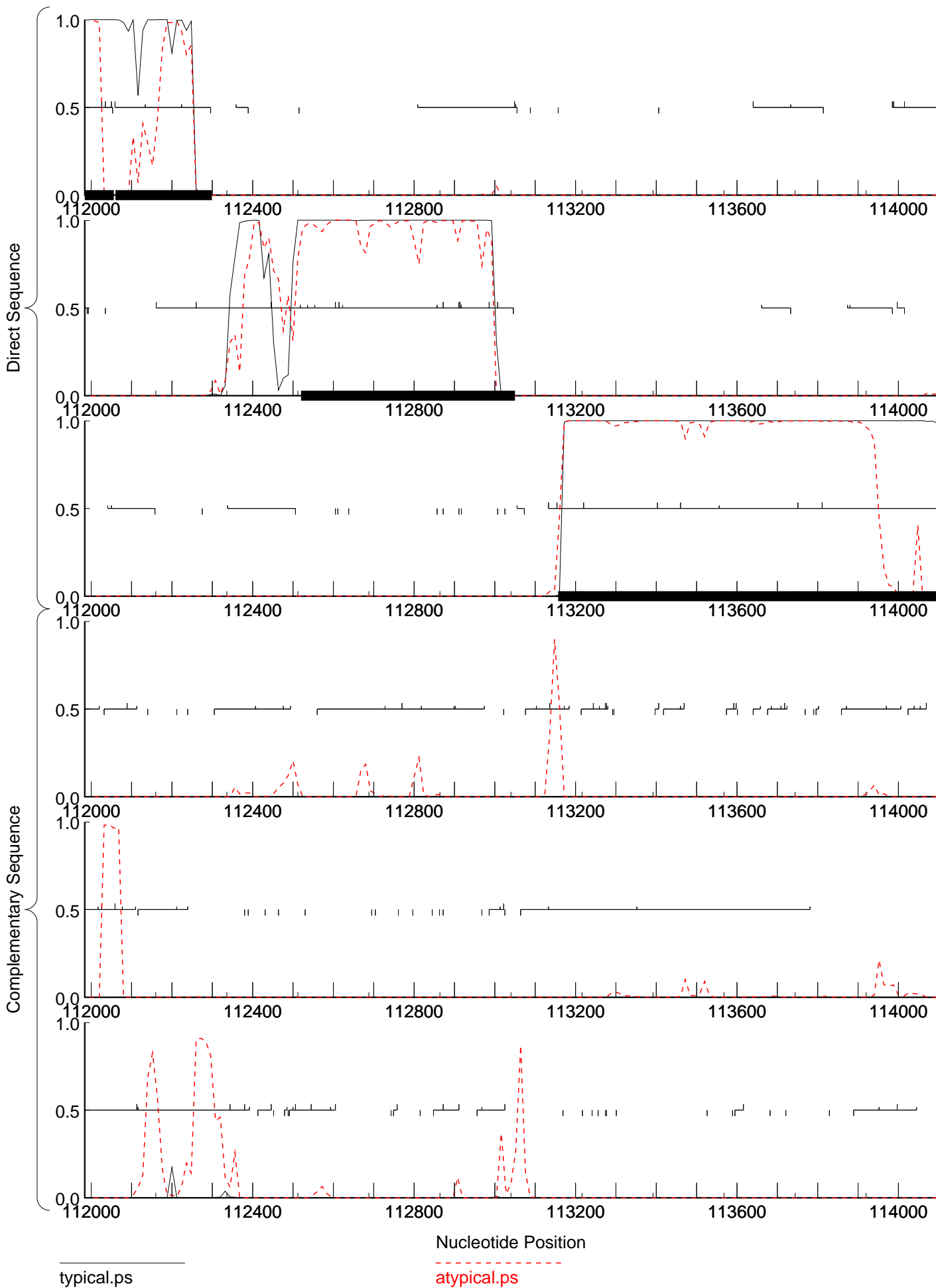


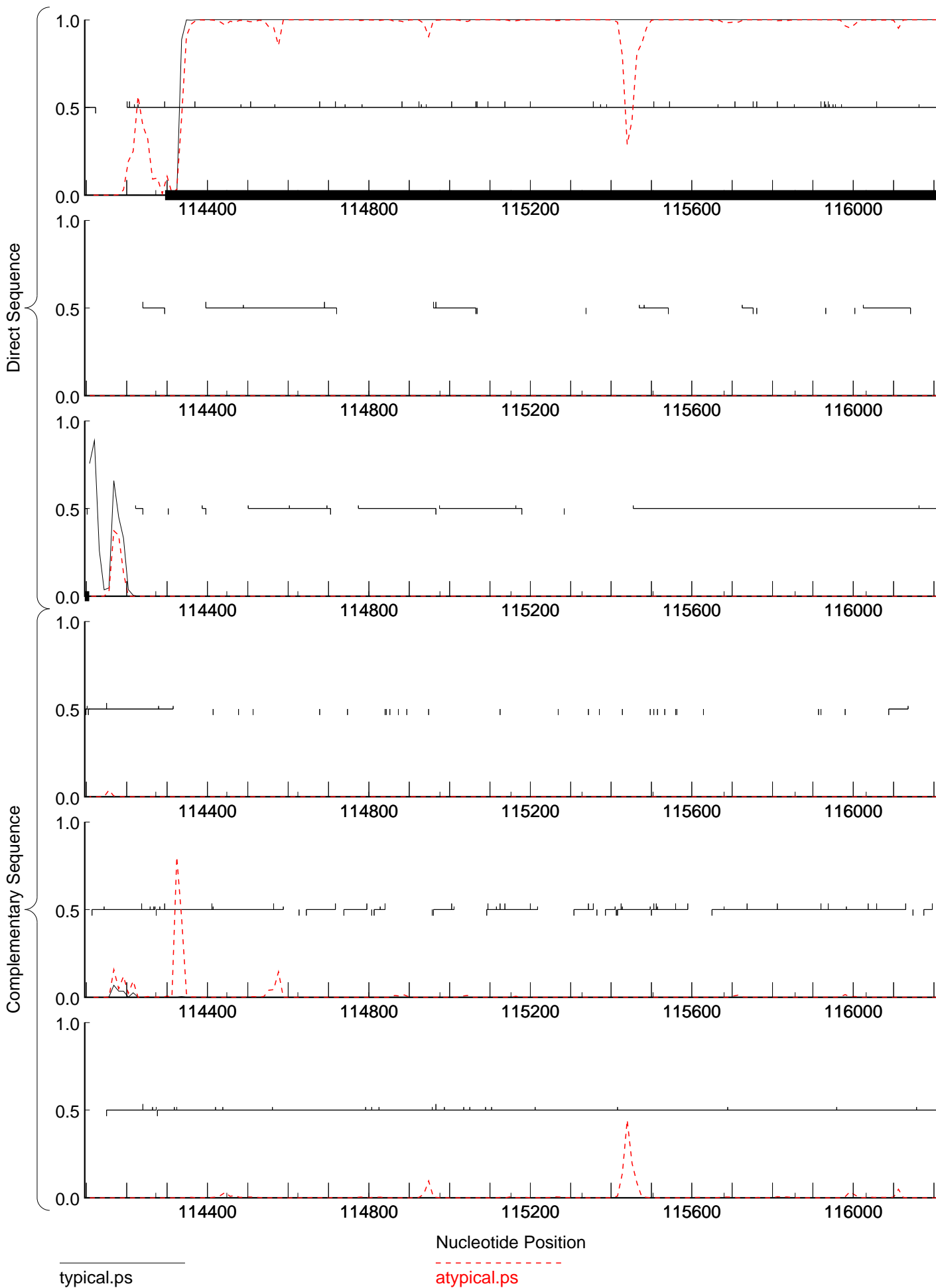


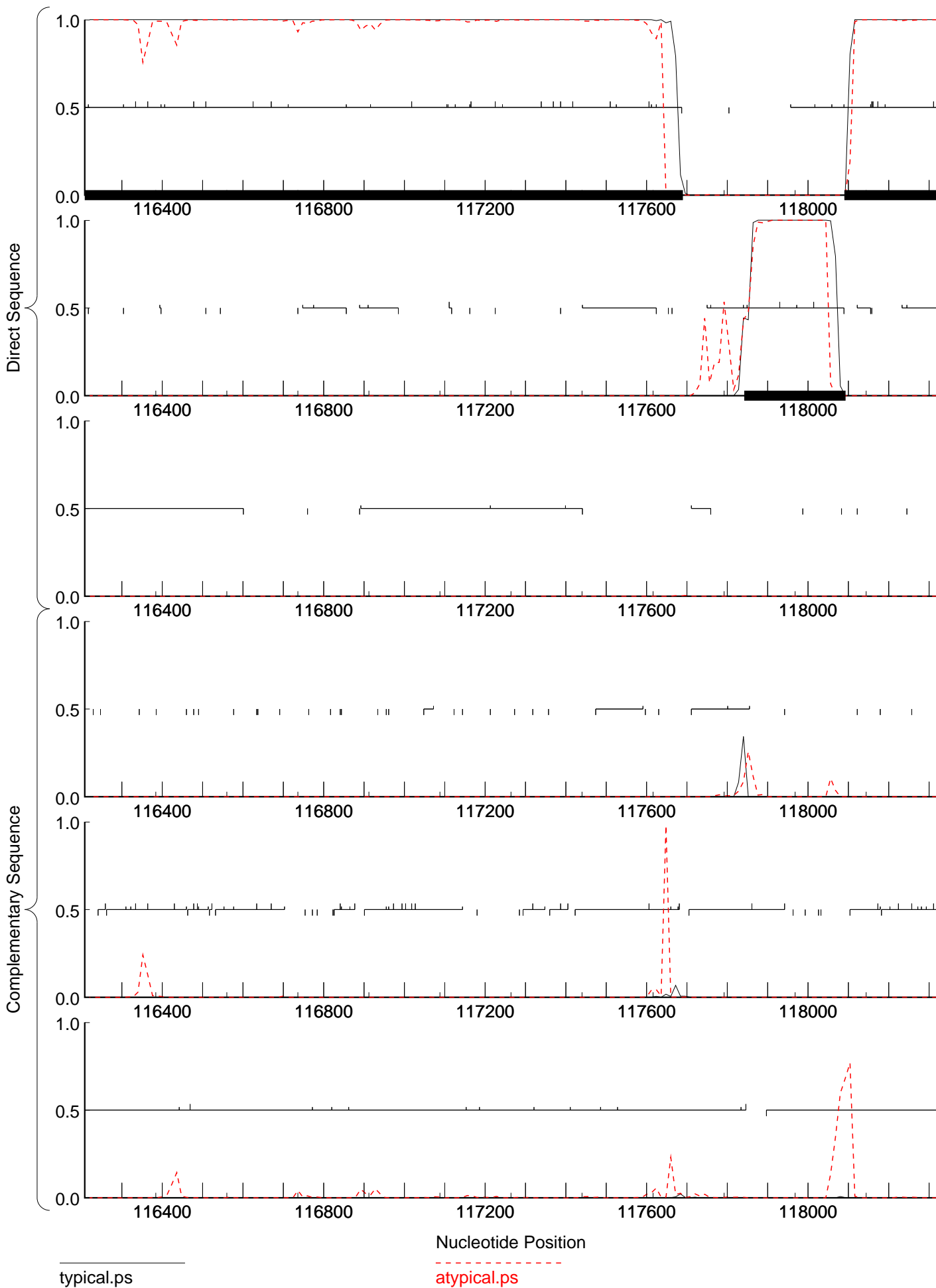


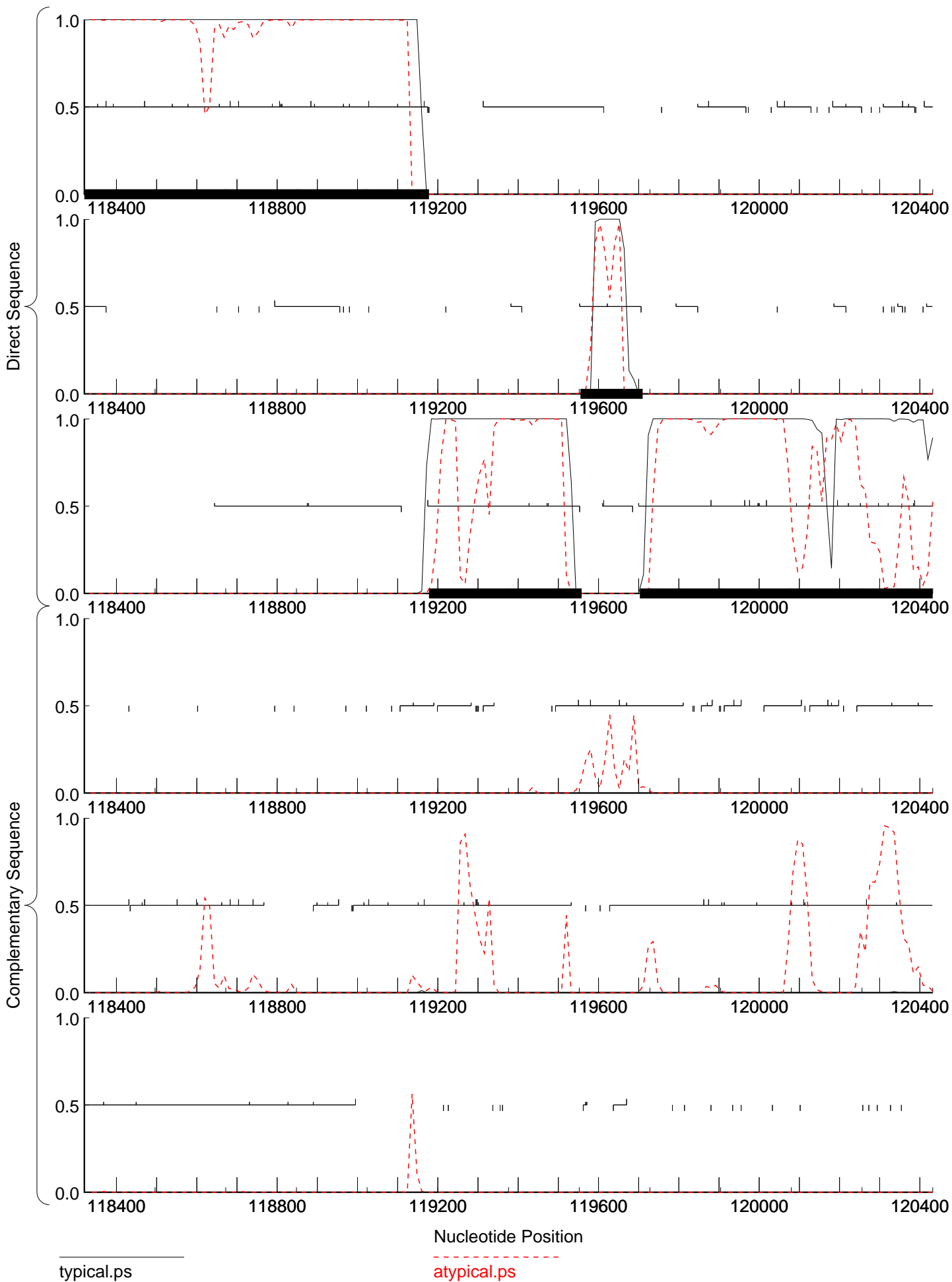


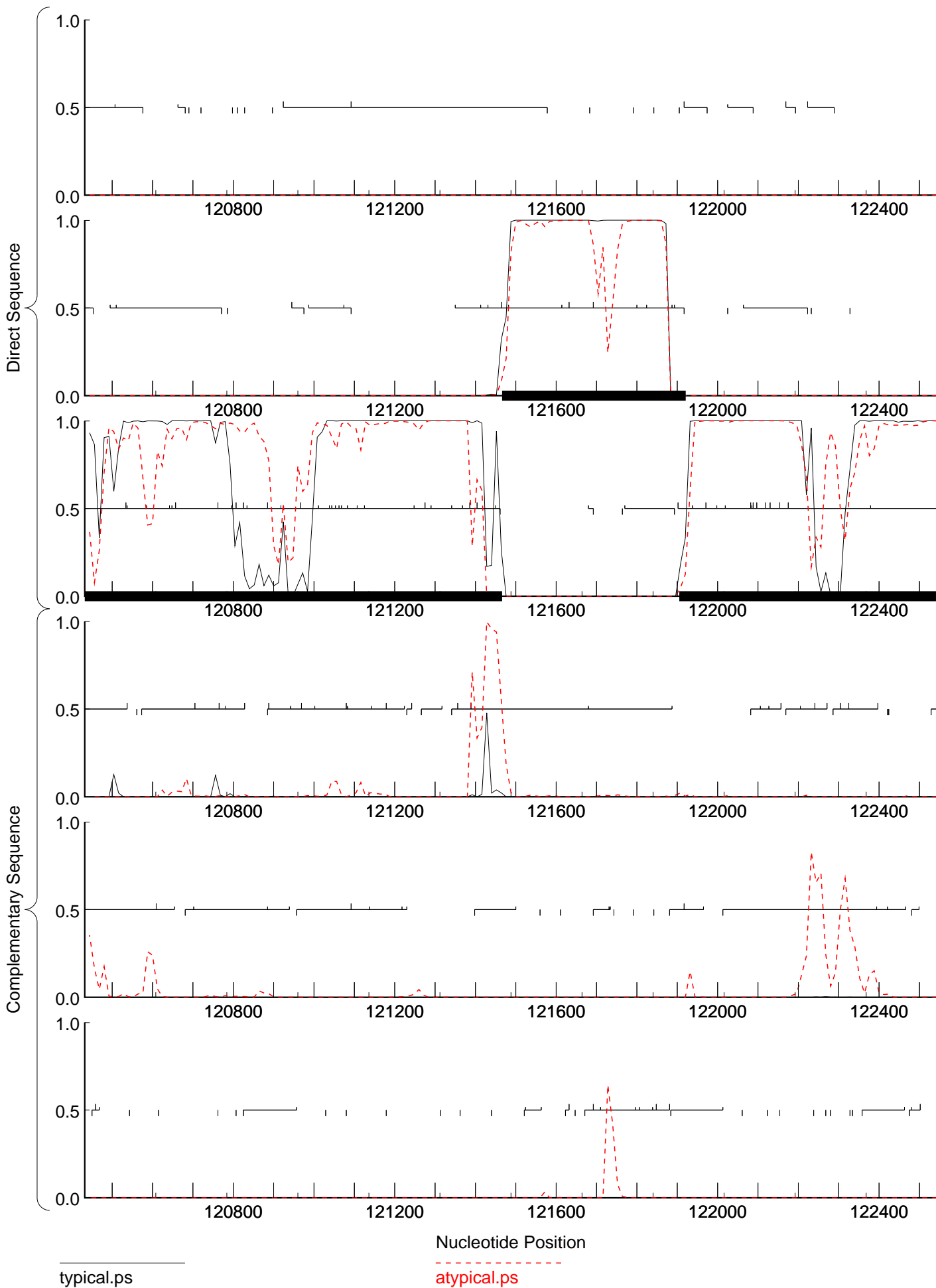


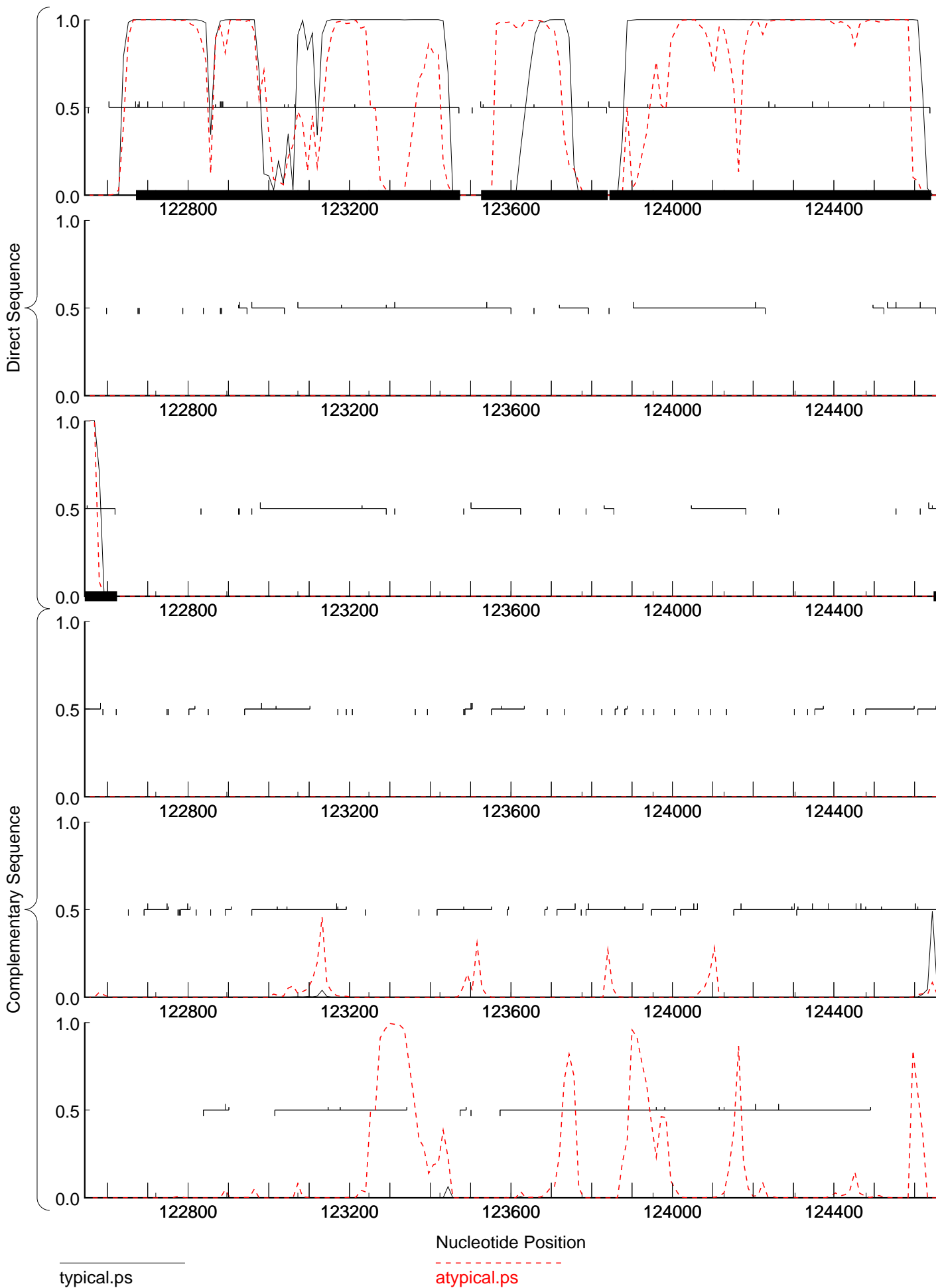






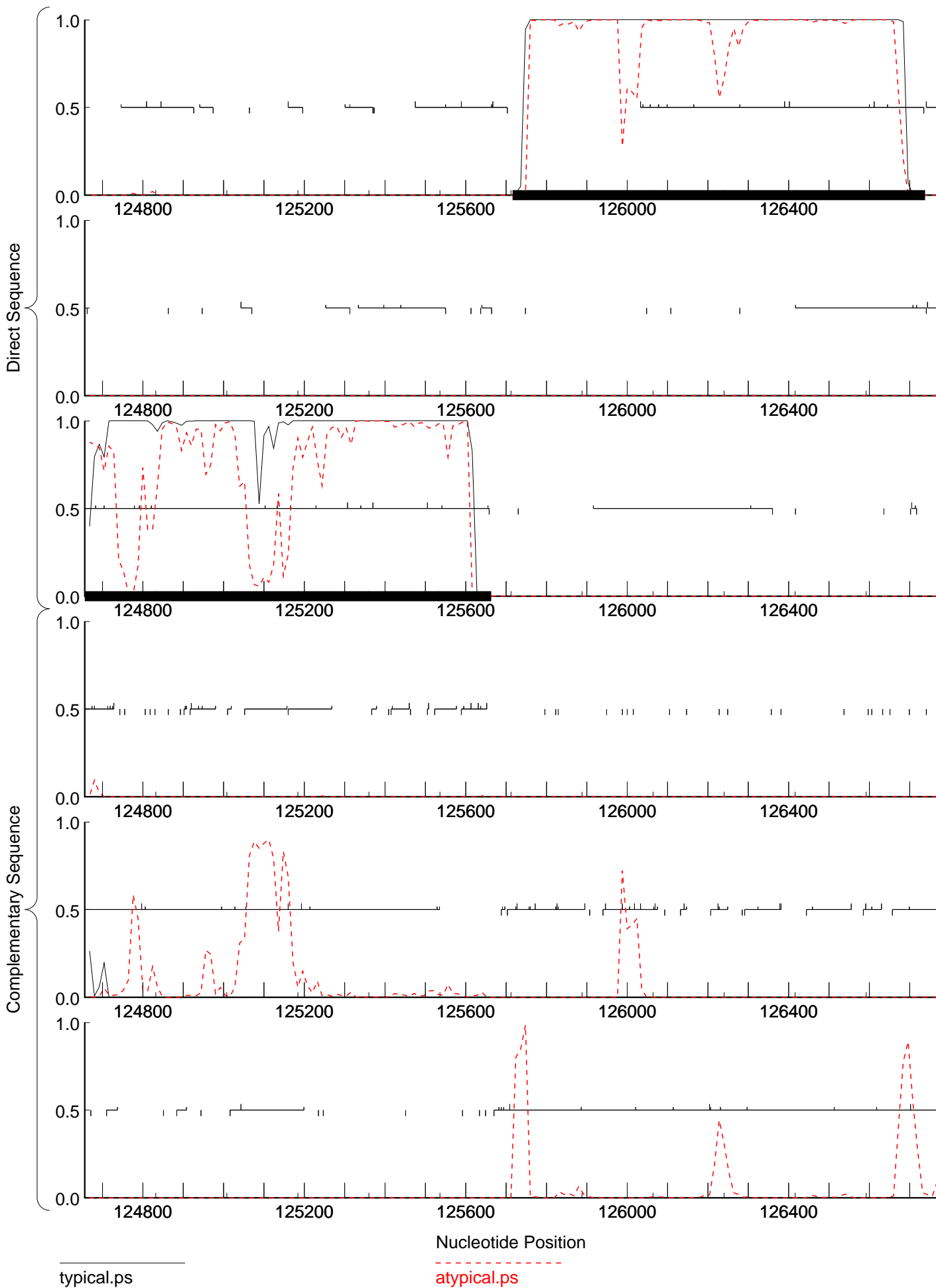


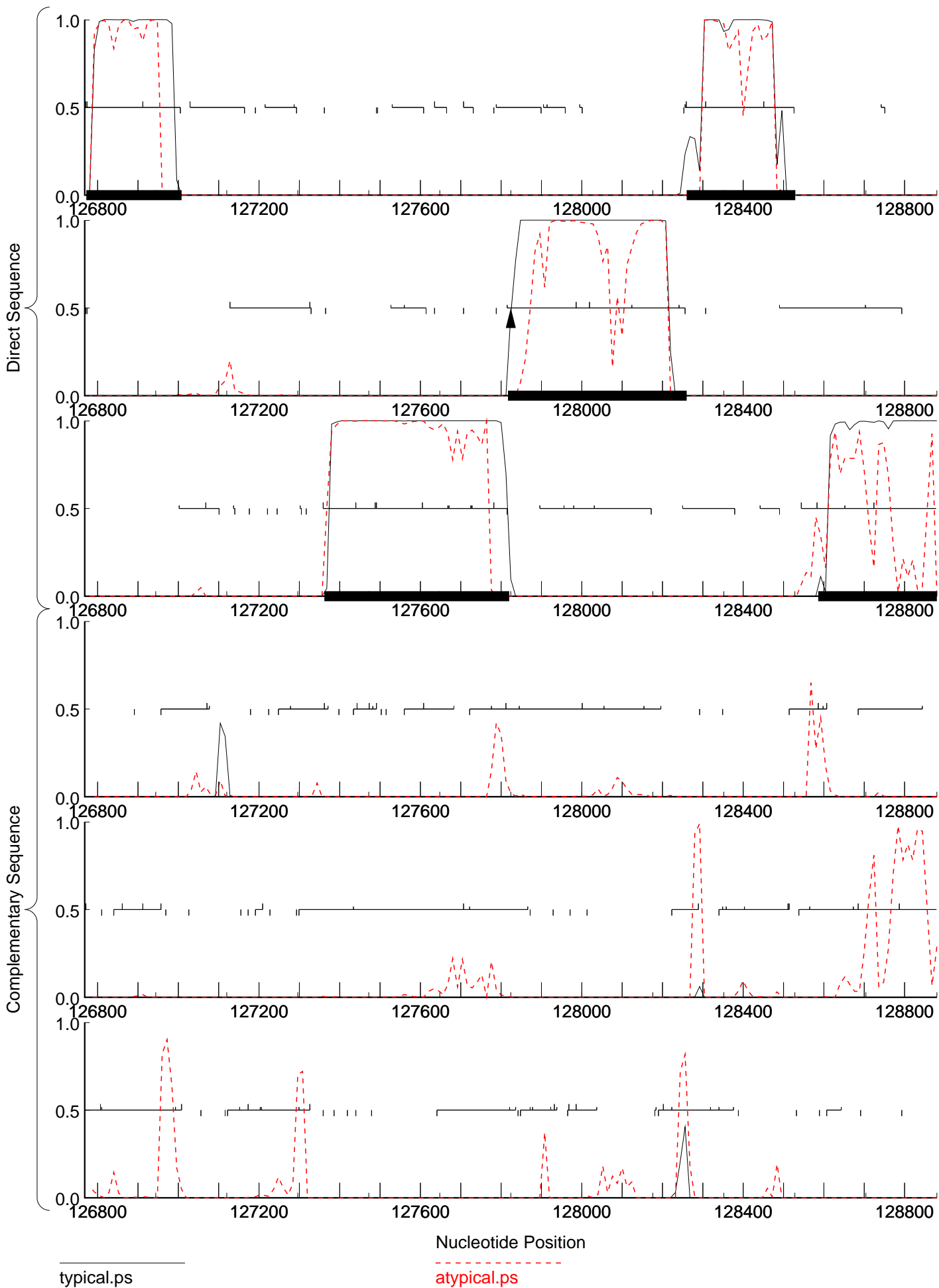


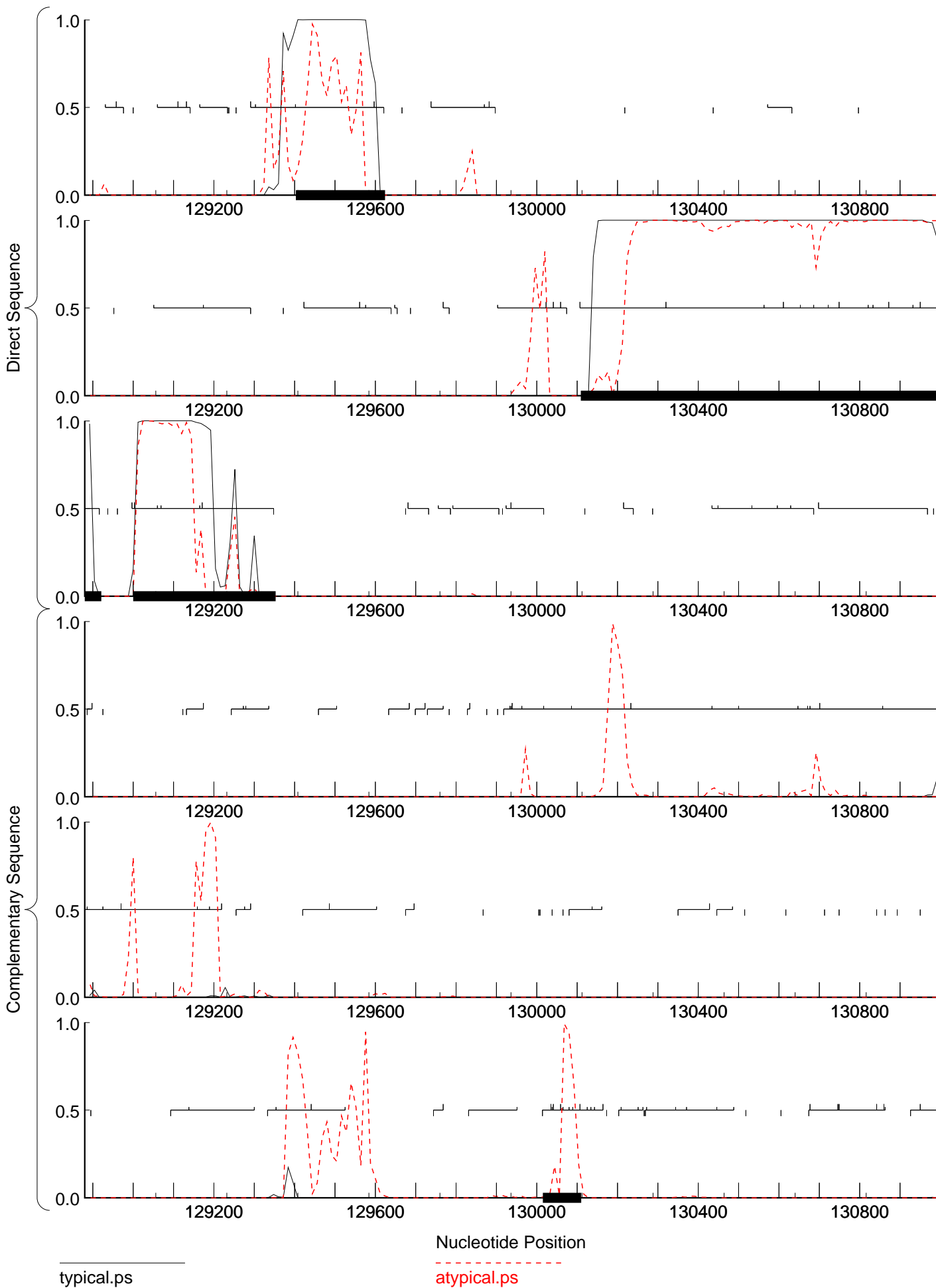


typical.ps

atypical.ps

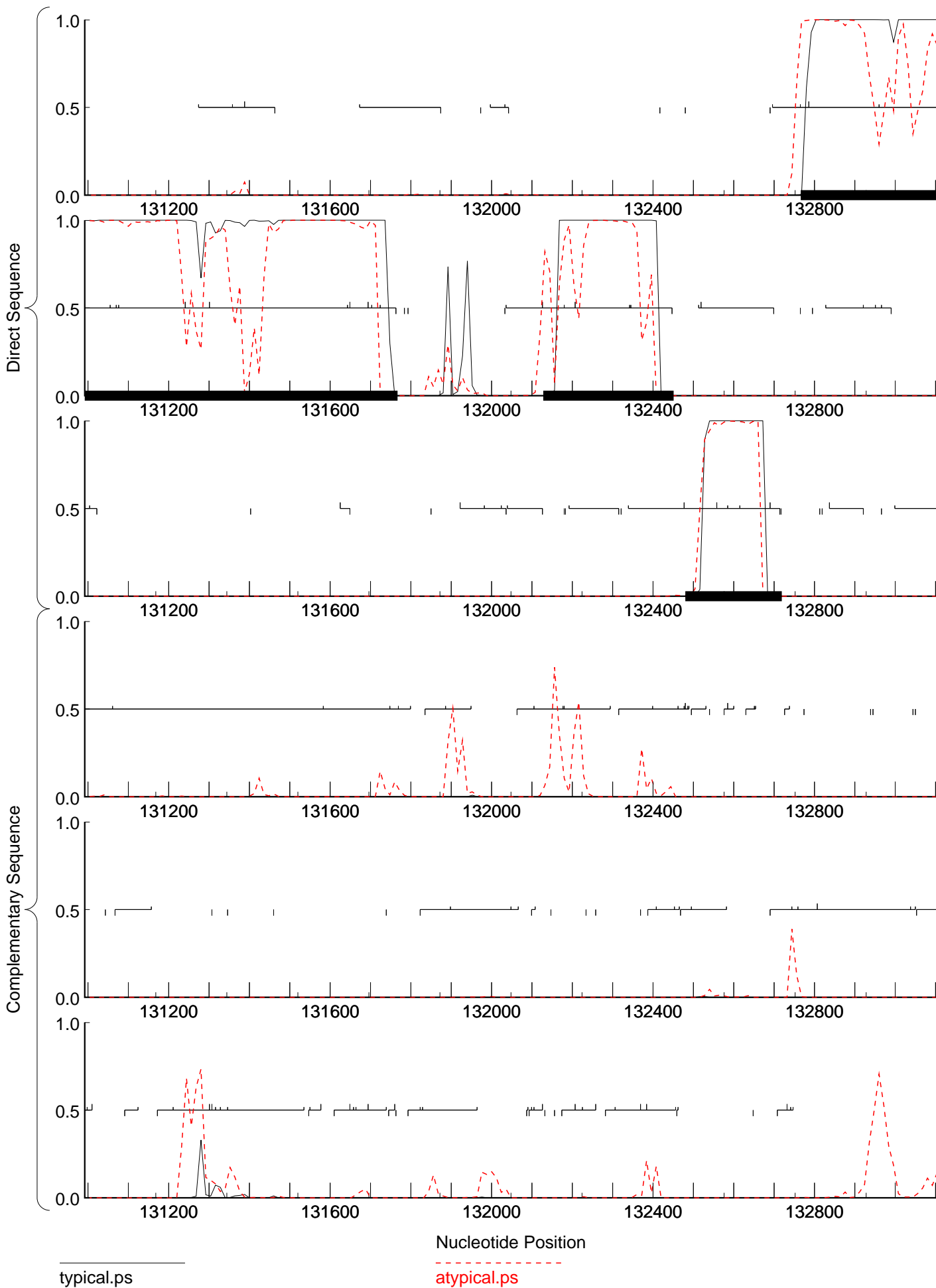






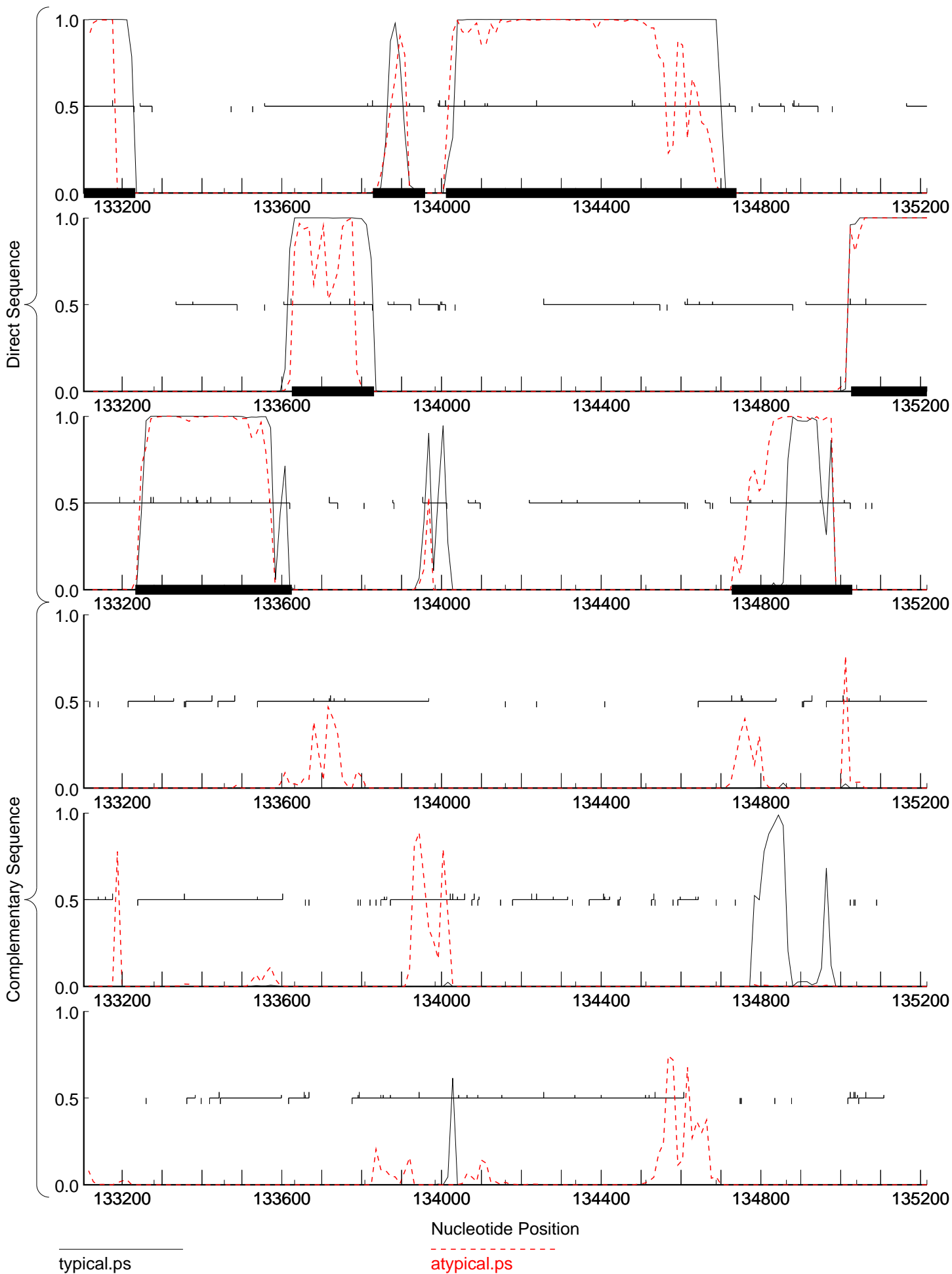
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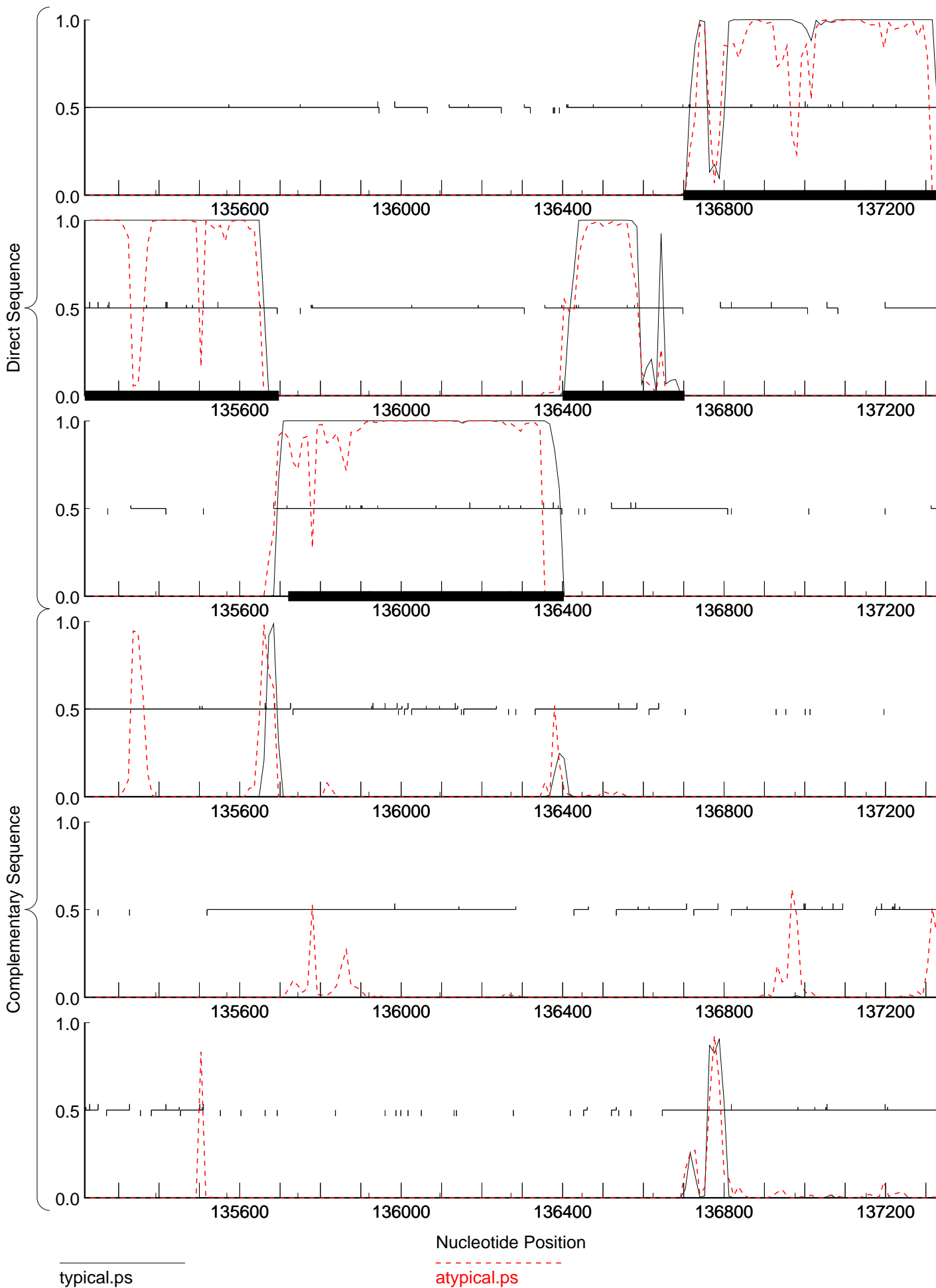
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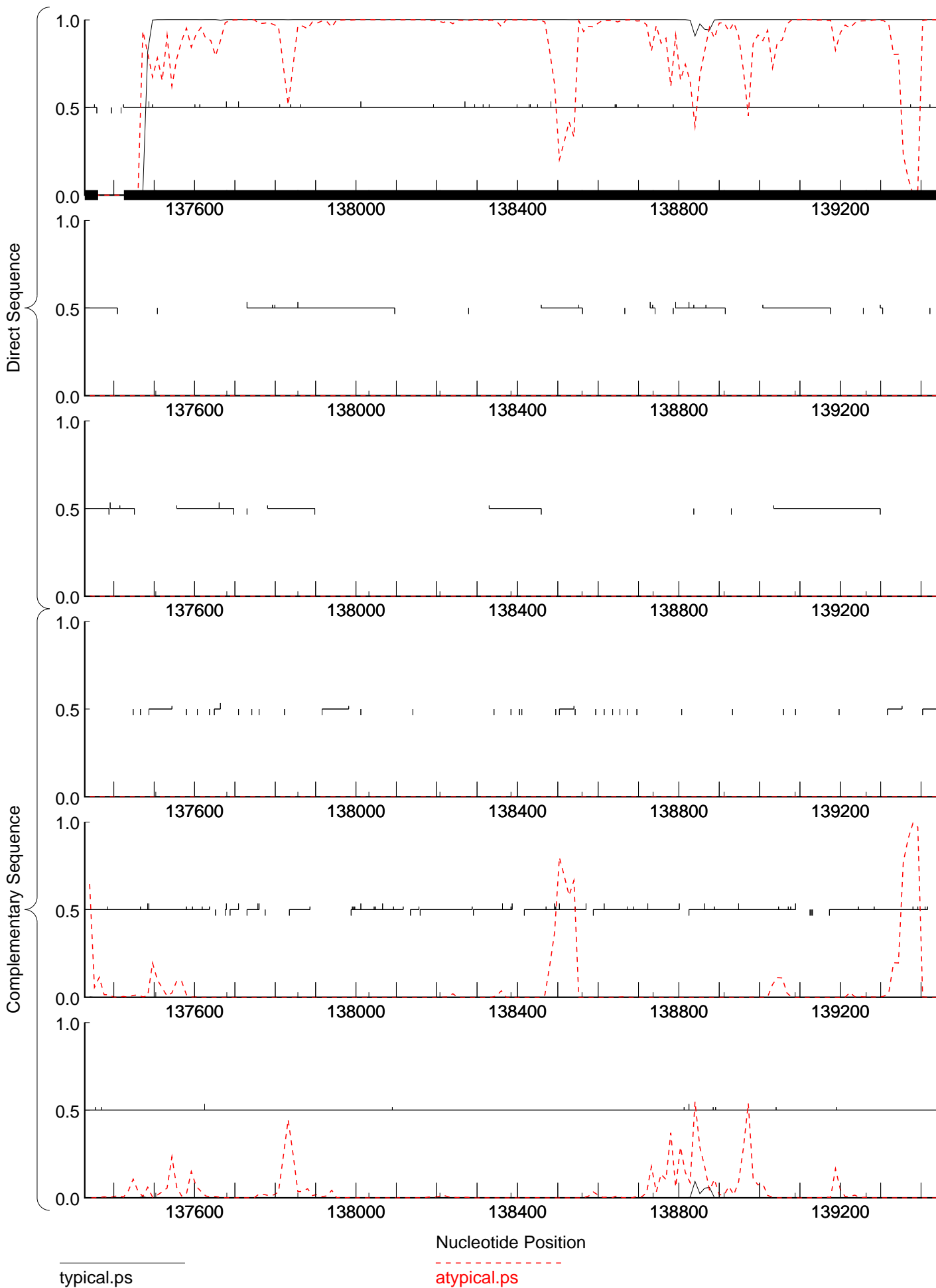


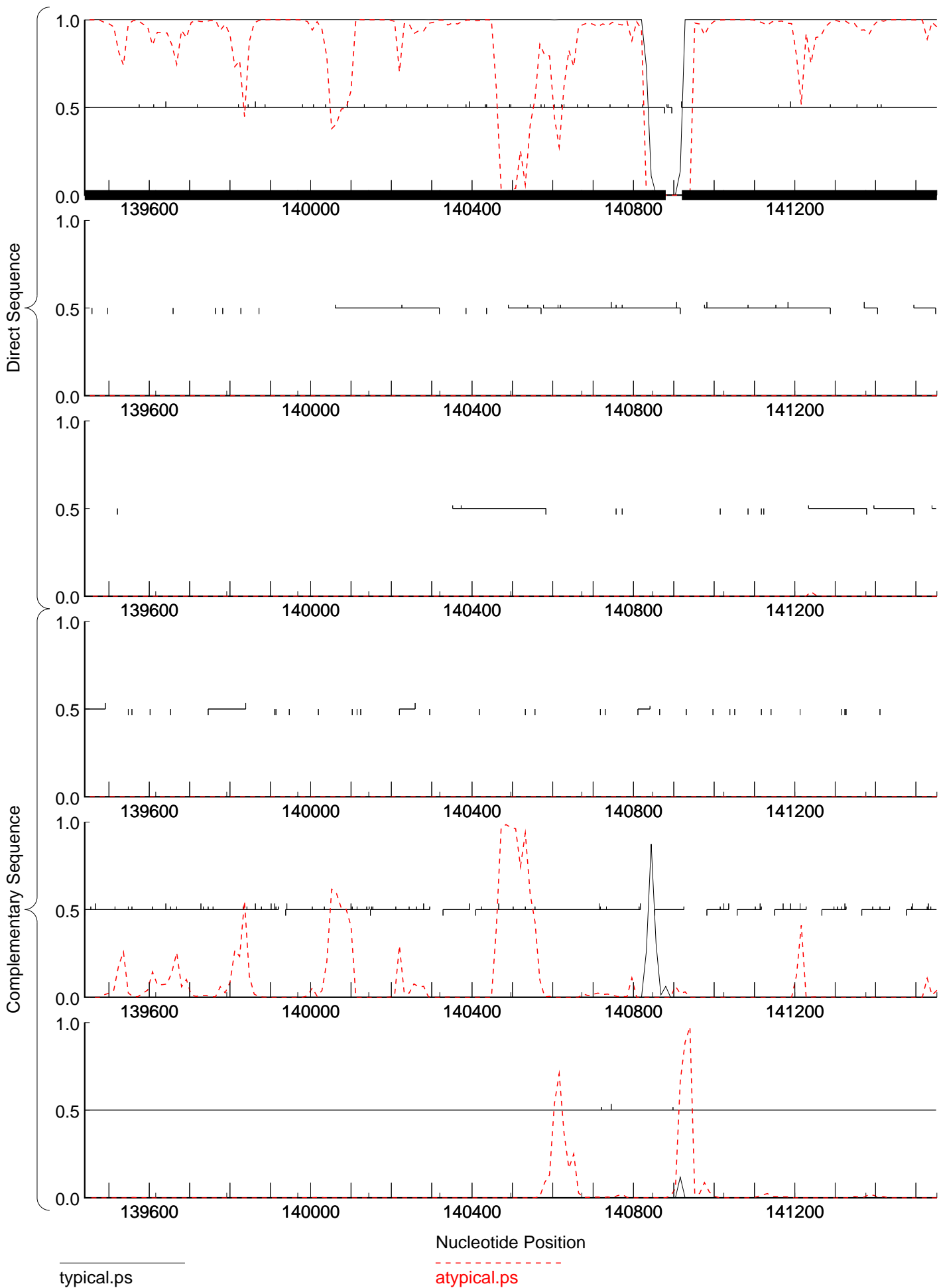
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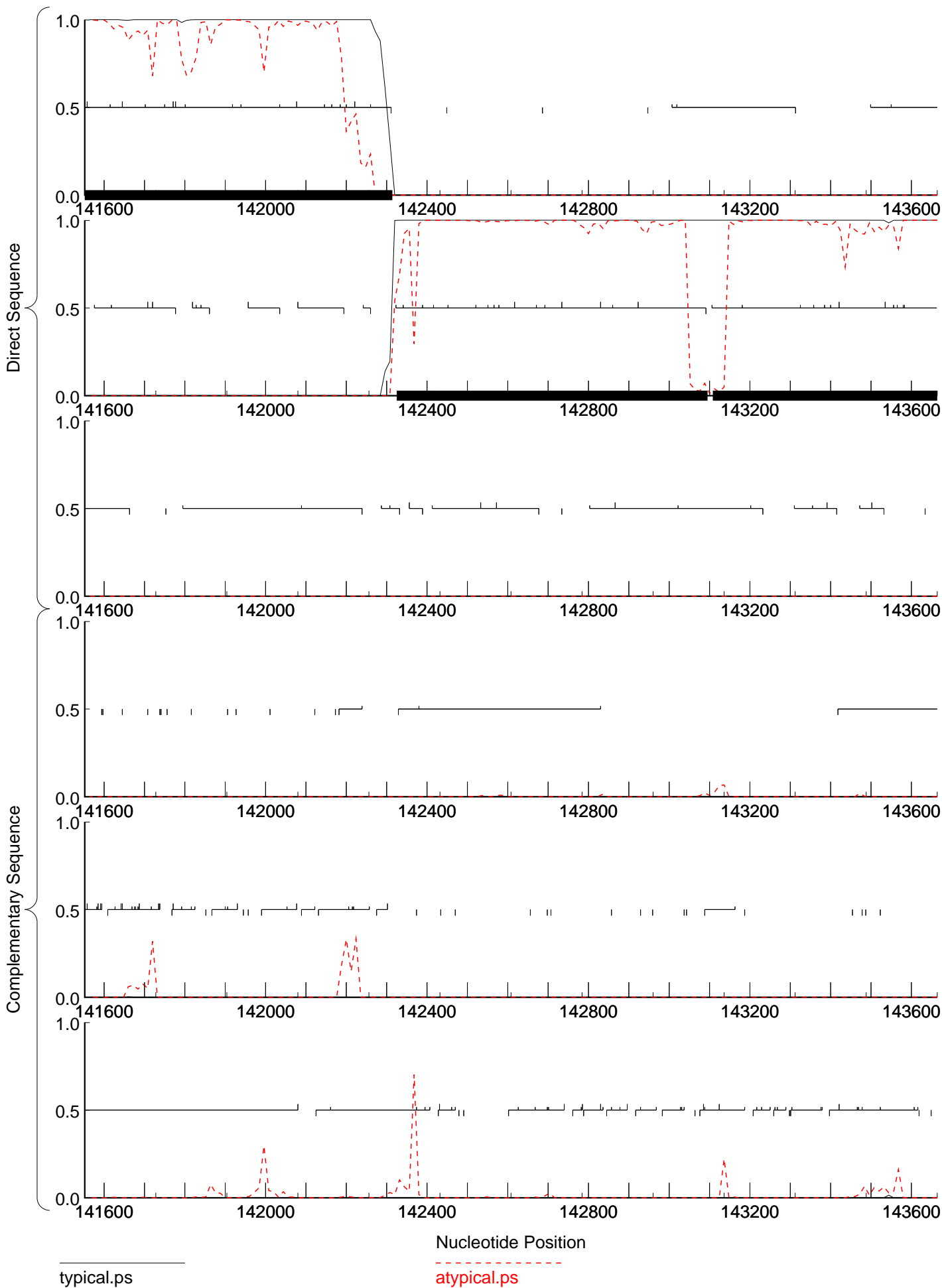
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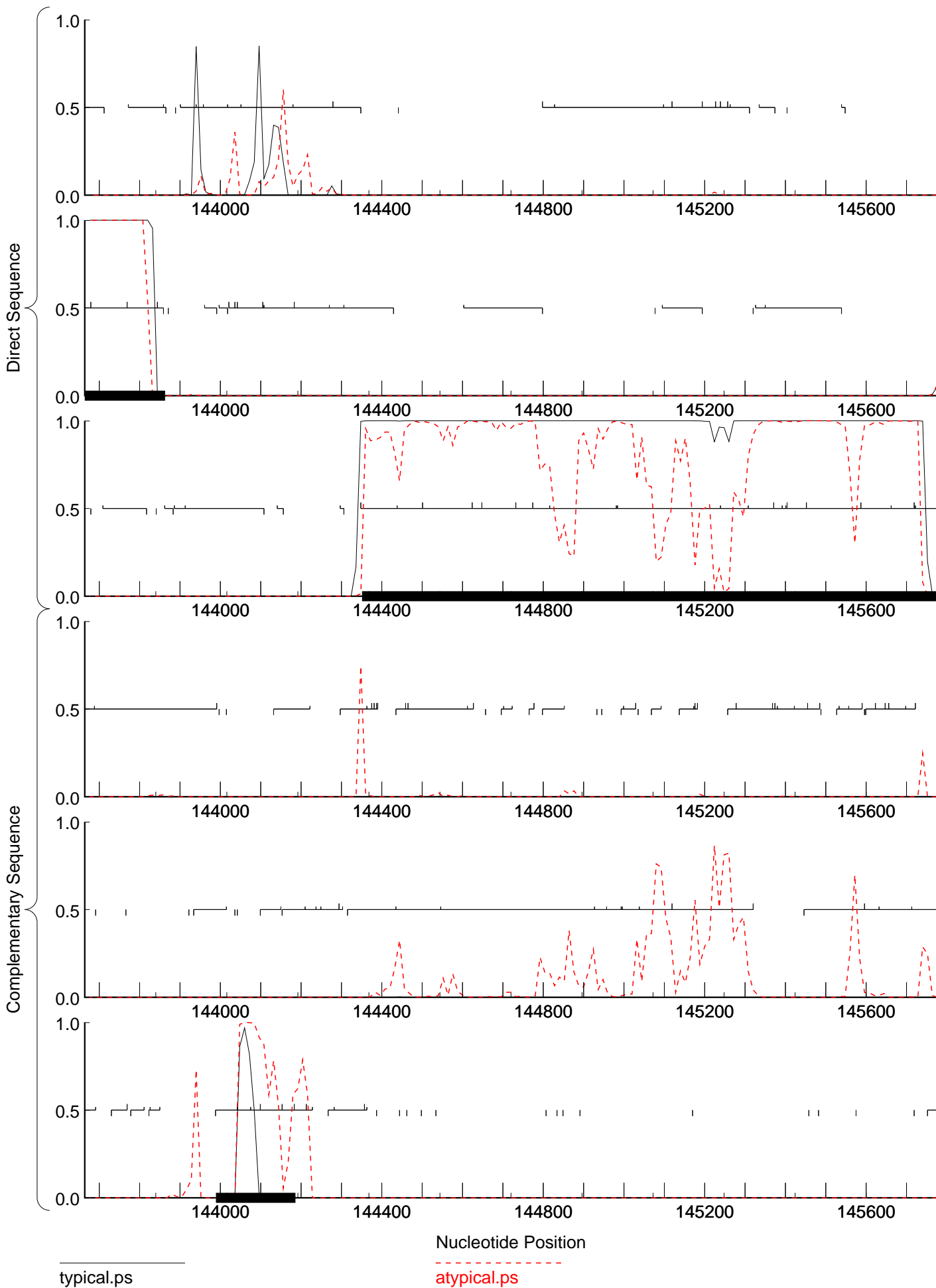






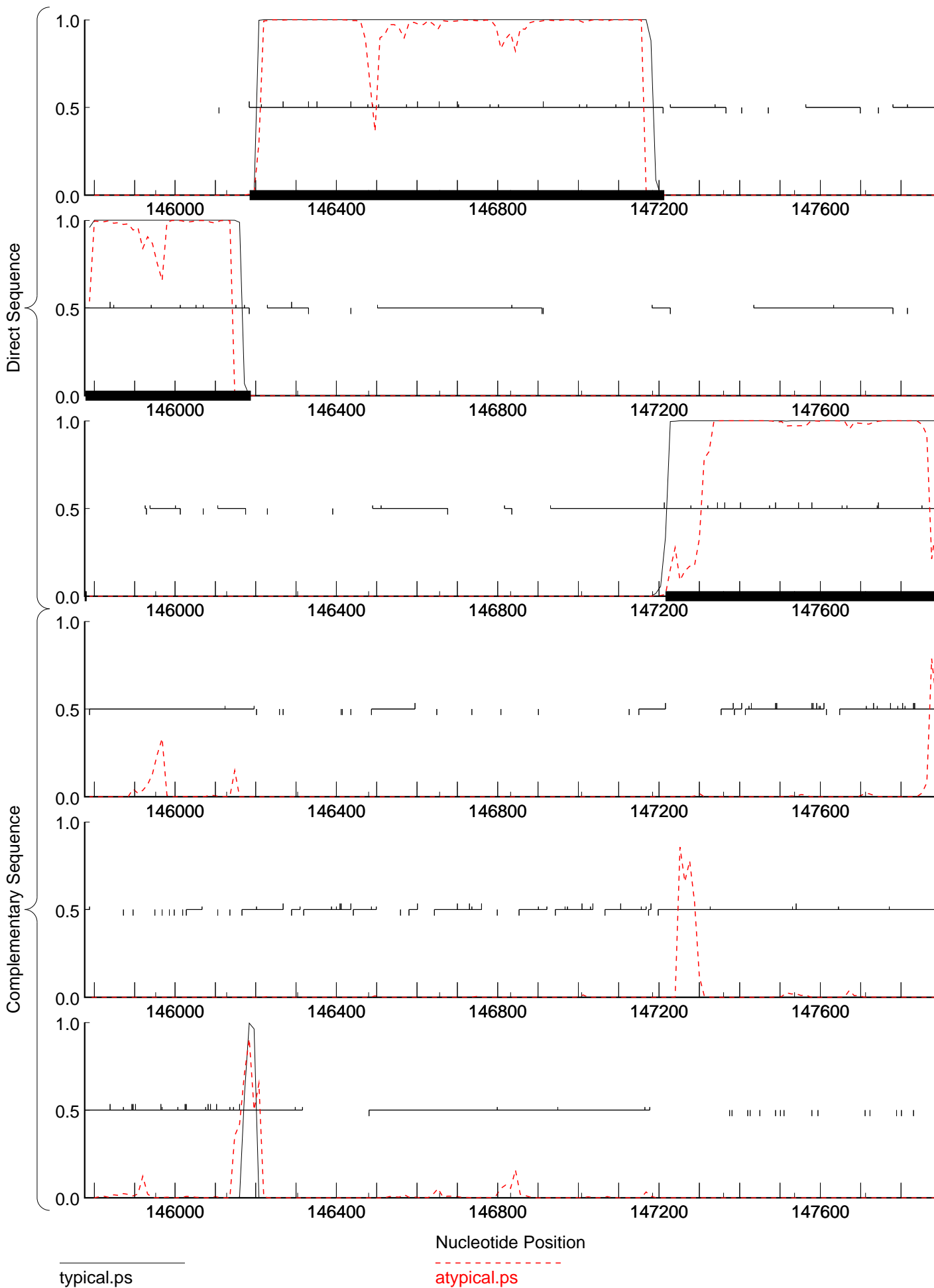






typical.ps

atypical.ps



typical.ps

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