

GeneMark

Version 2.5p (09.08.06)

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PROGRAM INFORMATION

Sequence : Mycobacterium phage Shelob complete sequence, 156606 bp, circularly permuted, Cluster C1
Analysis Date : 5/25/18 at 20:01:56
Pages : 76
Sequence Length : 156606 bp
GC Content : 64.76%

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,

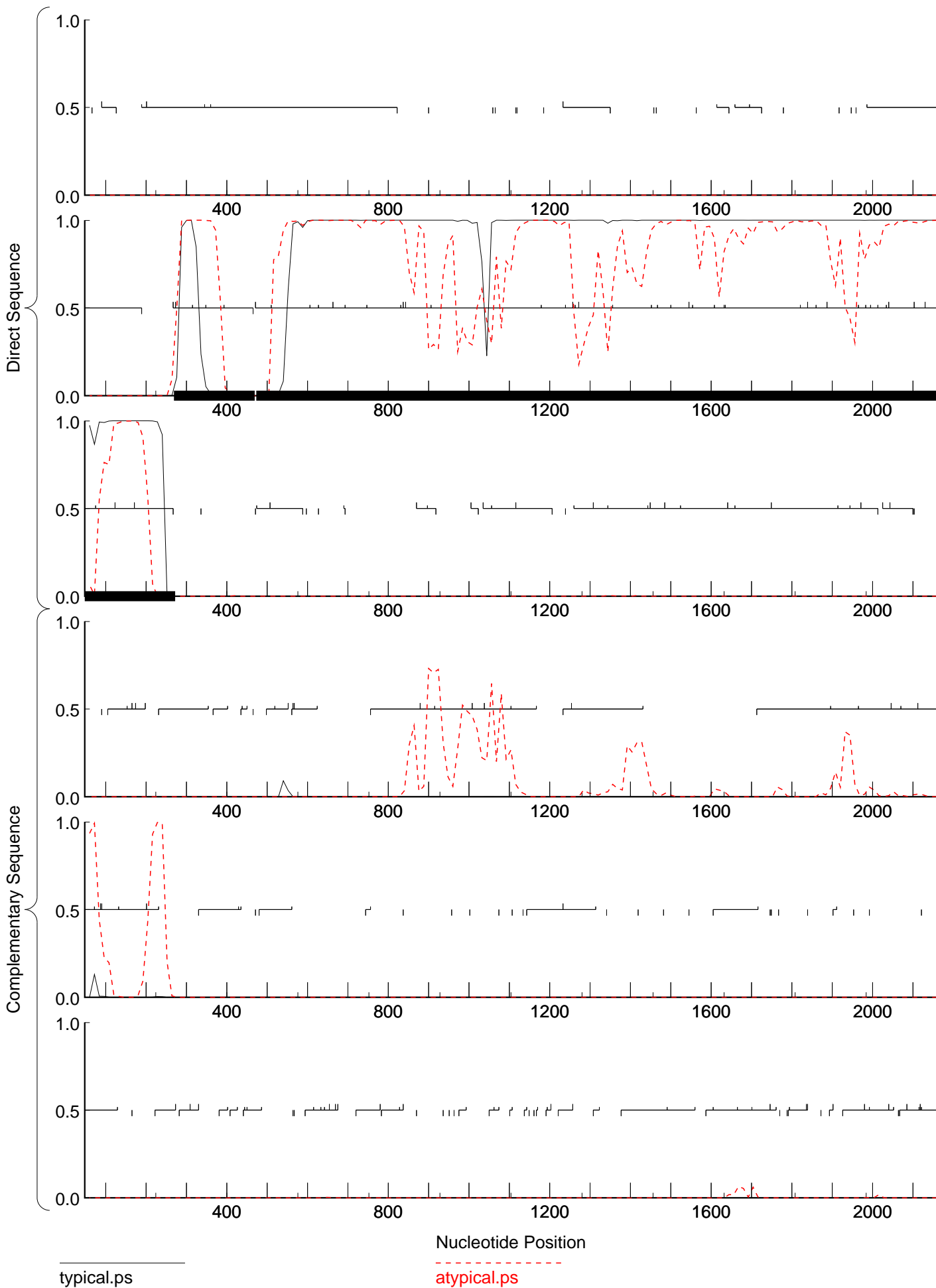
MATRIX INFORMATION

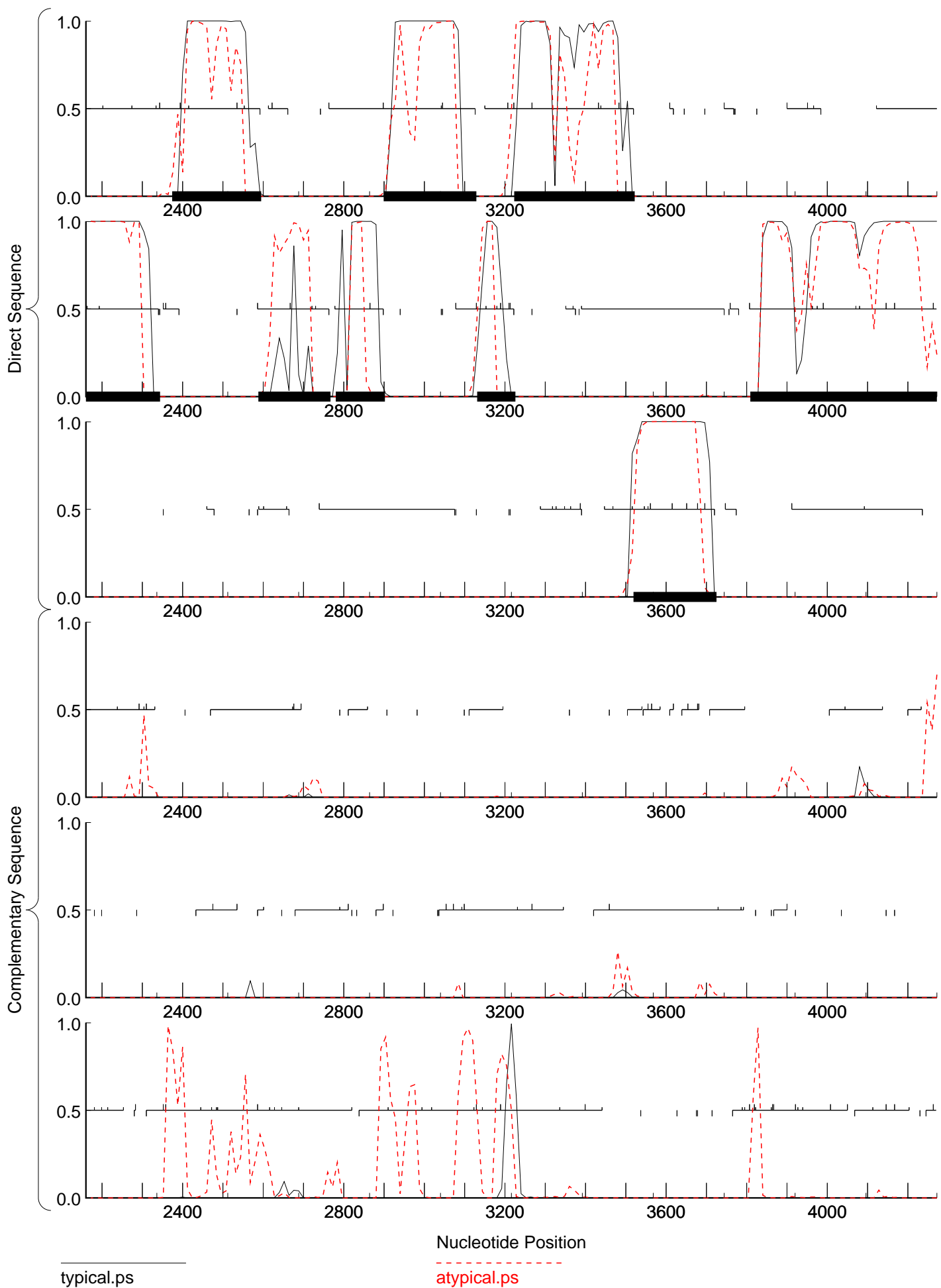
Matrix : -
Author : -
Order : 4

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

Matrix notes & comments

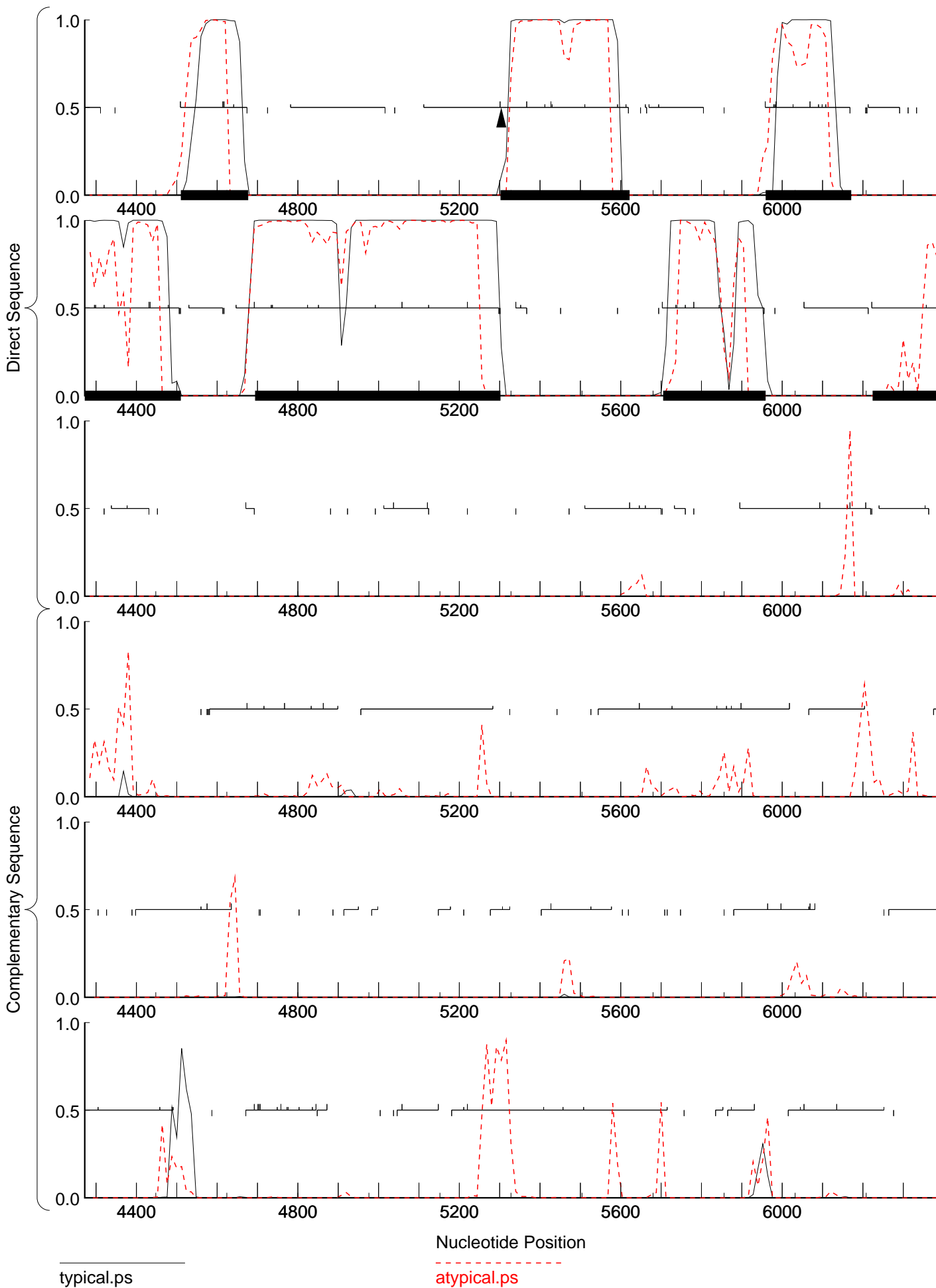
Training set derived by GeneMarkS, 4.30 October 2014
Fri May 25 20:01:56 2018

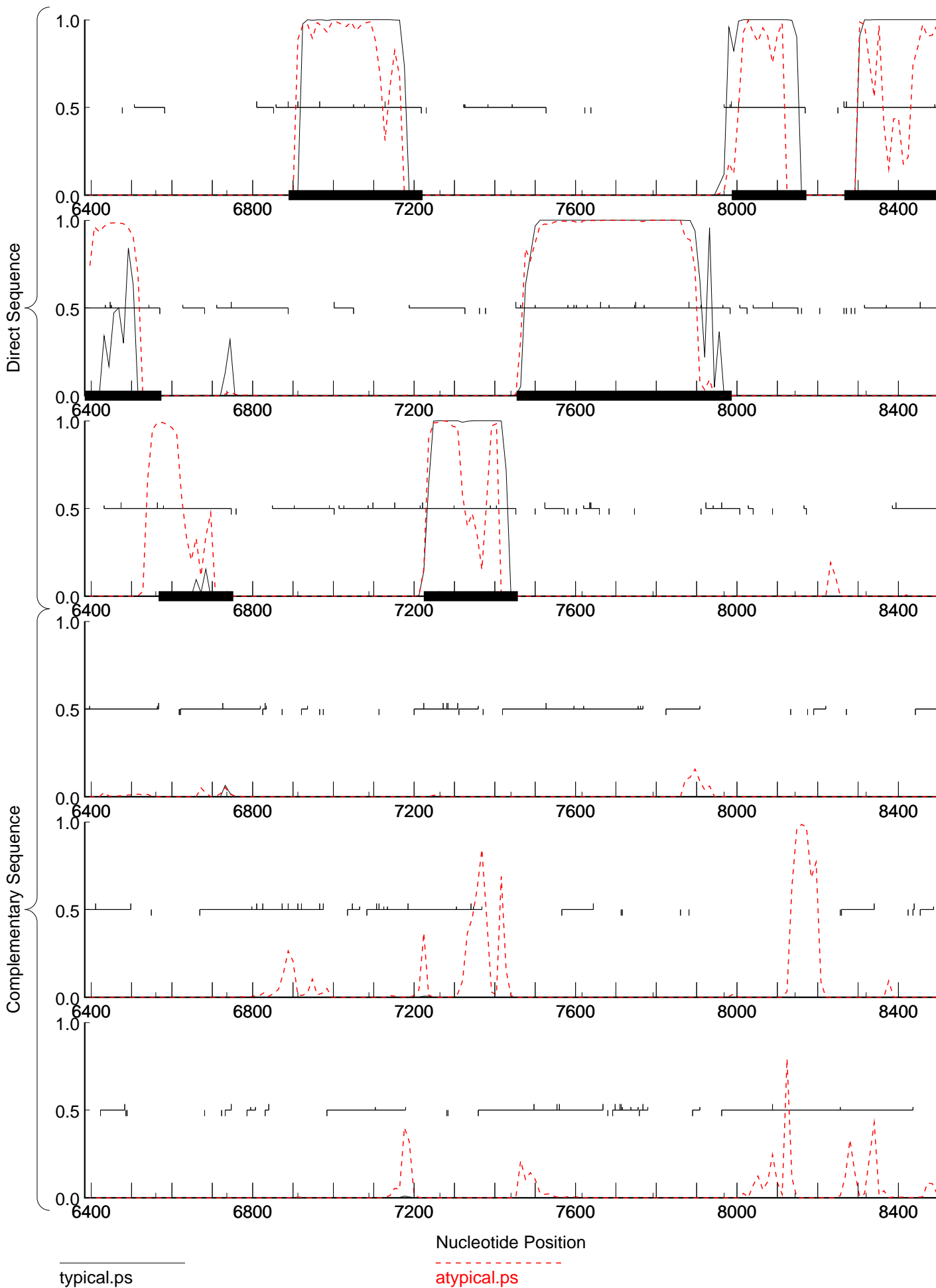


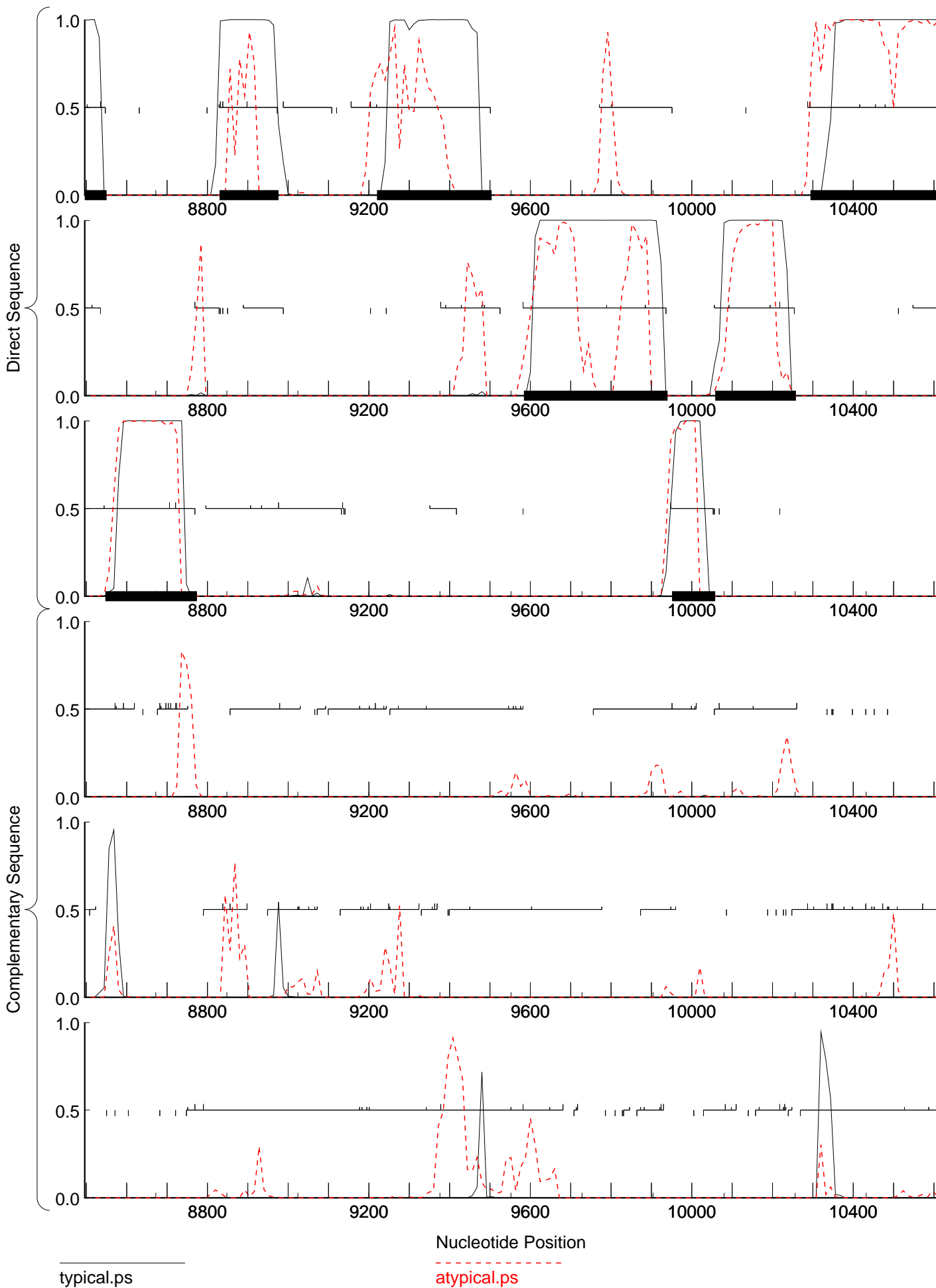


typical.ps

atypical.ps

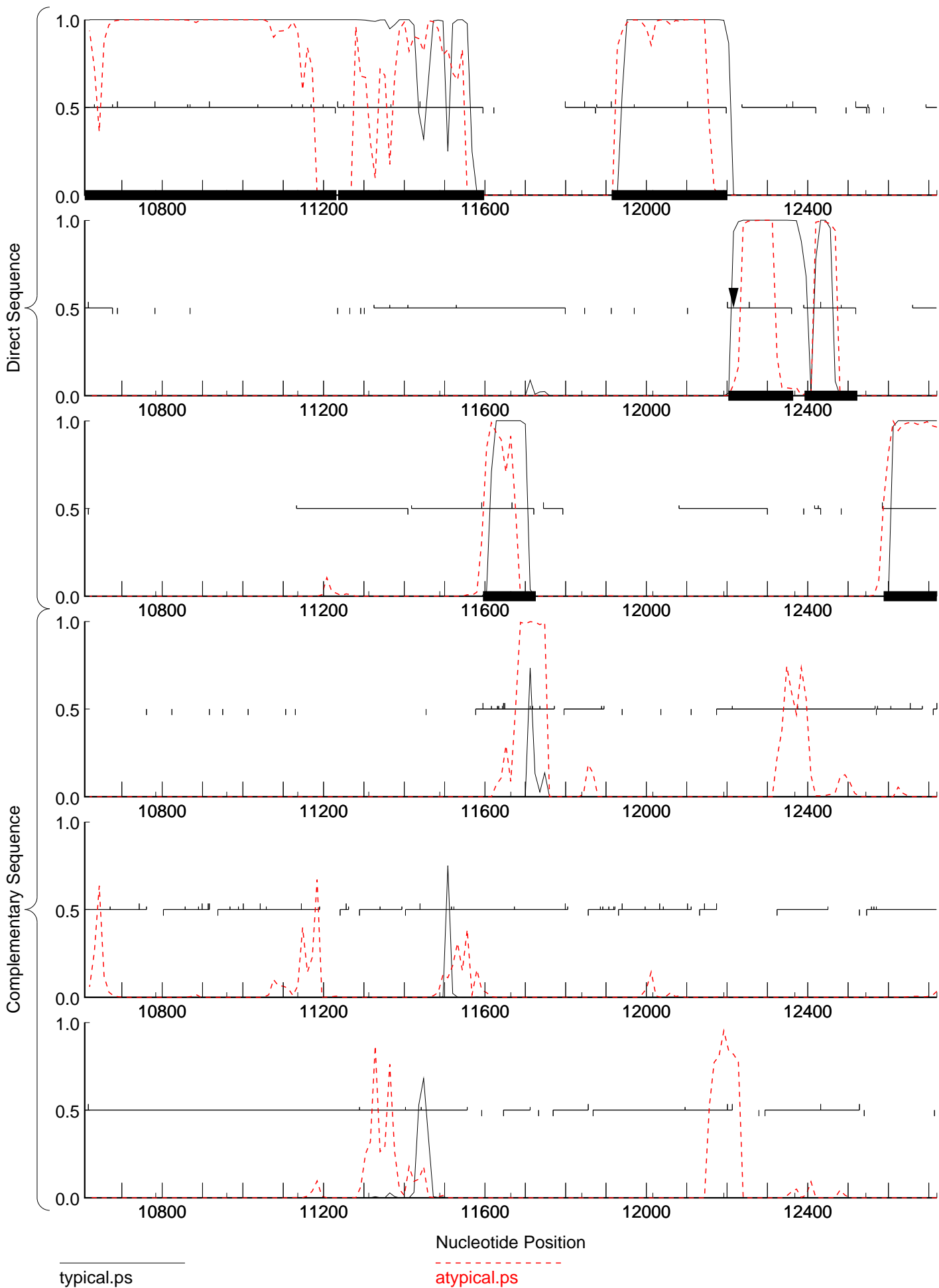






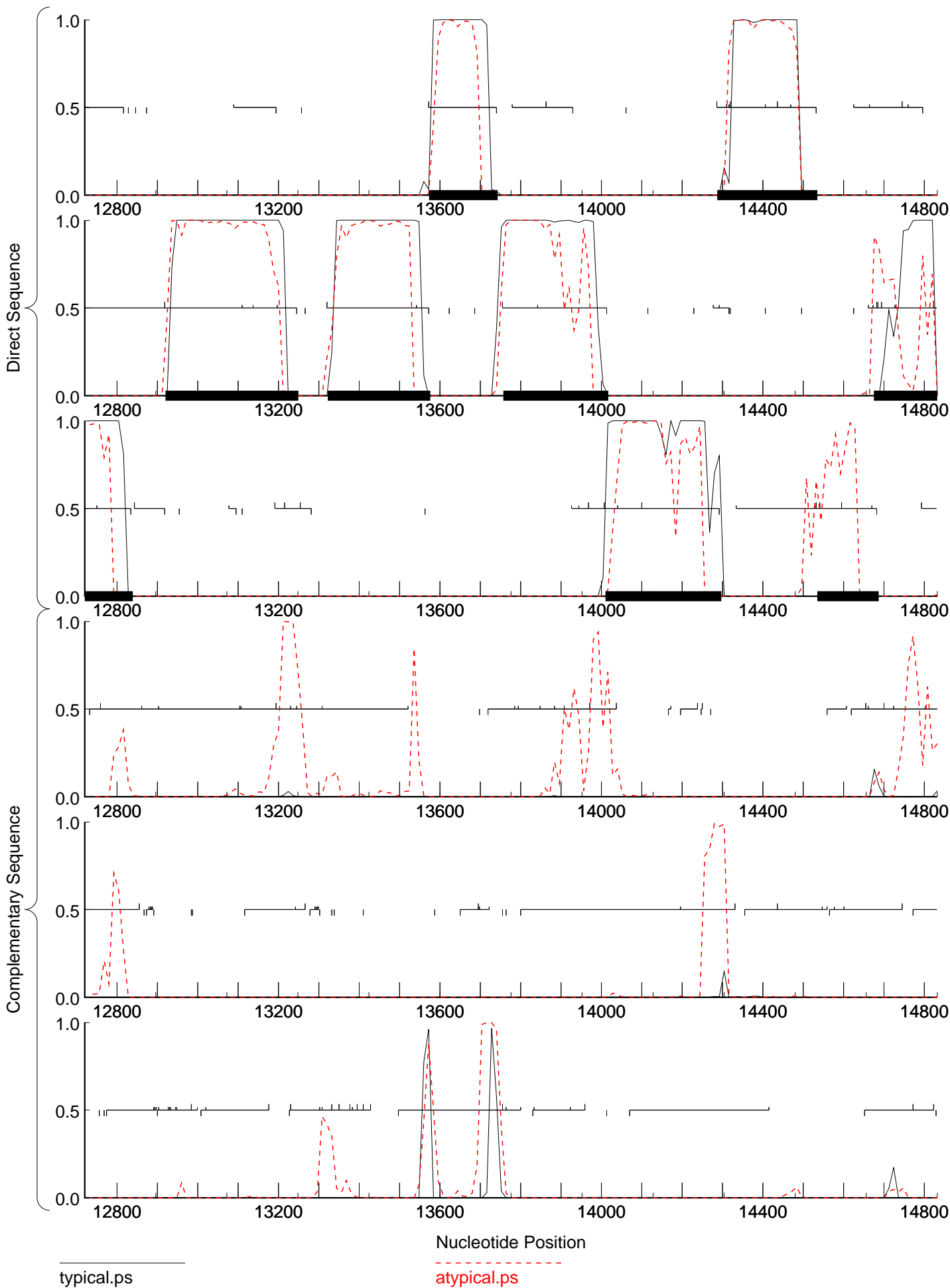
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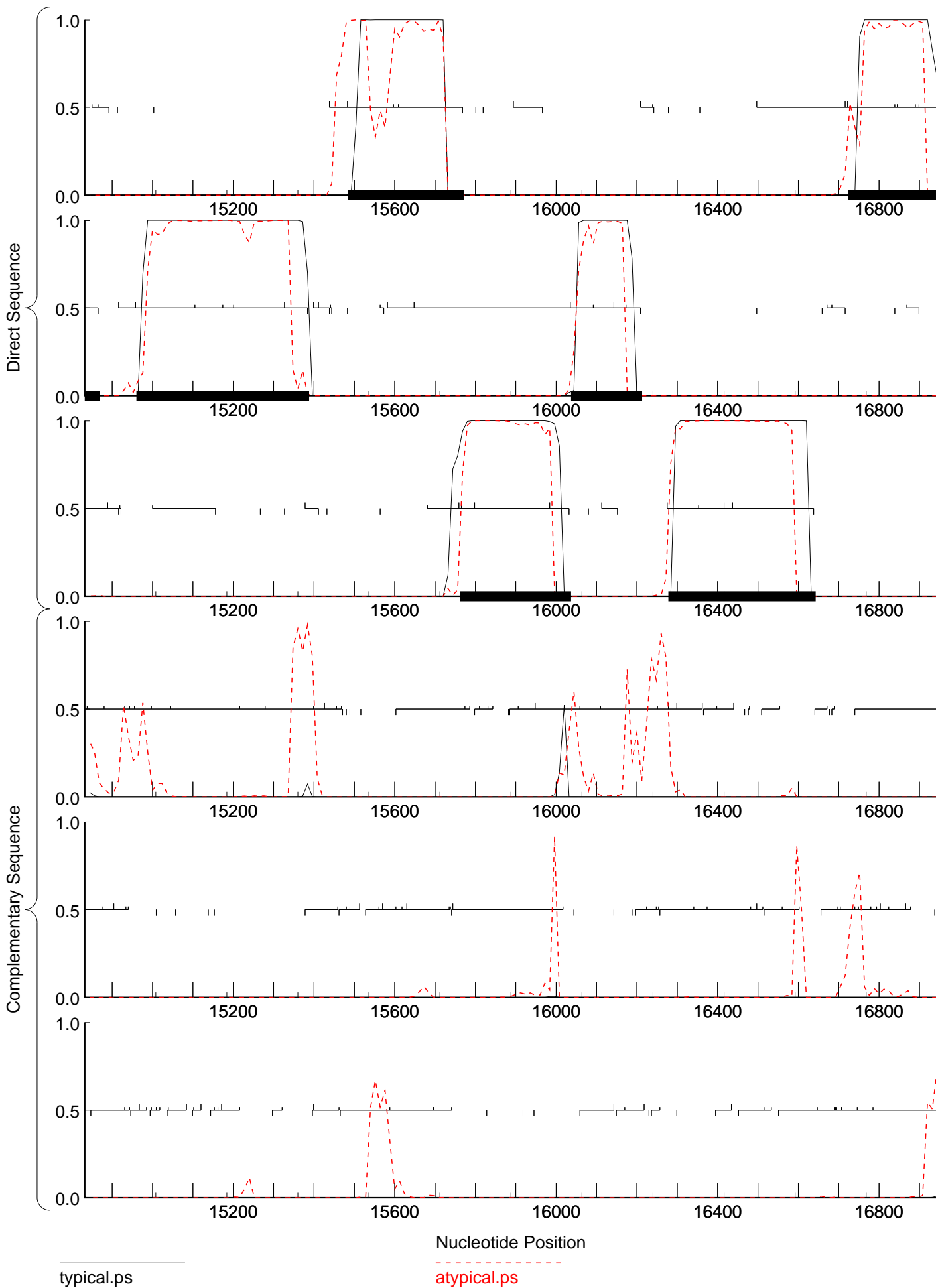
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typical.ps

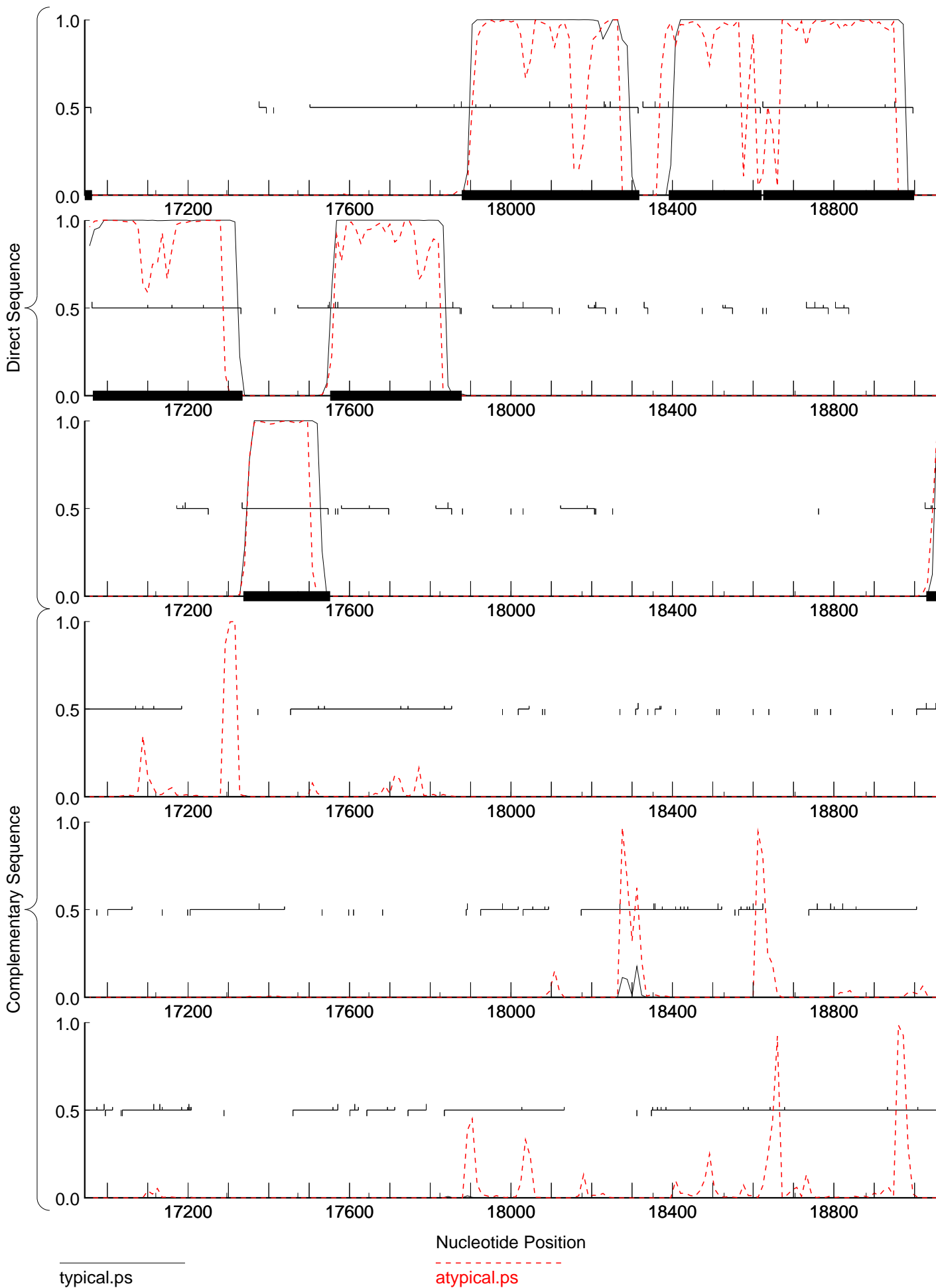
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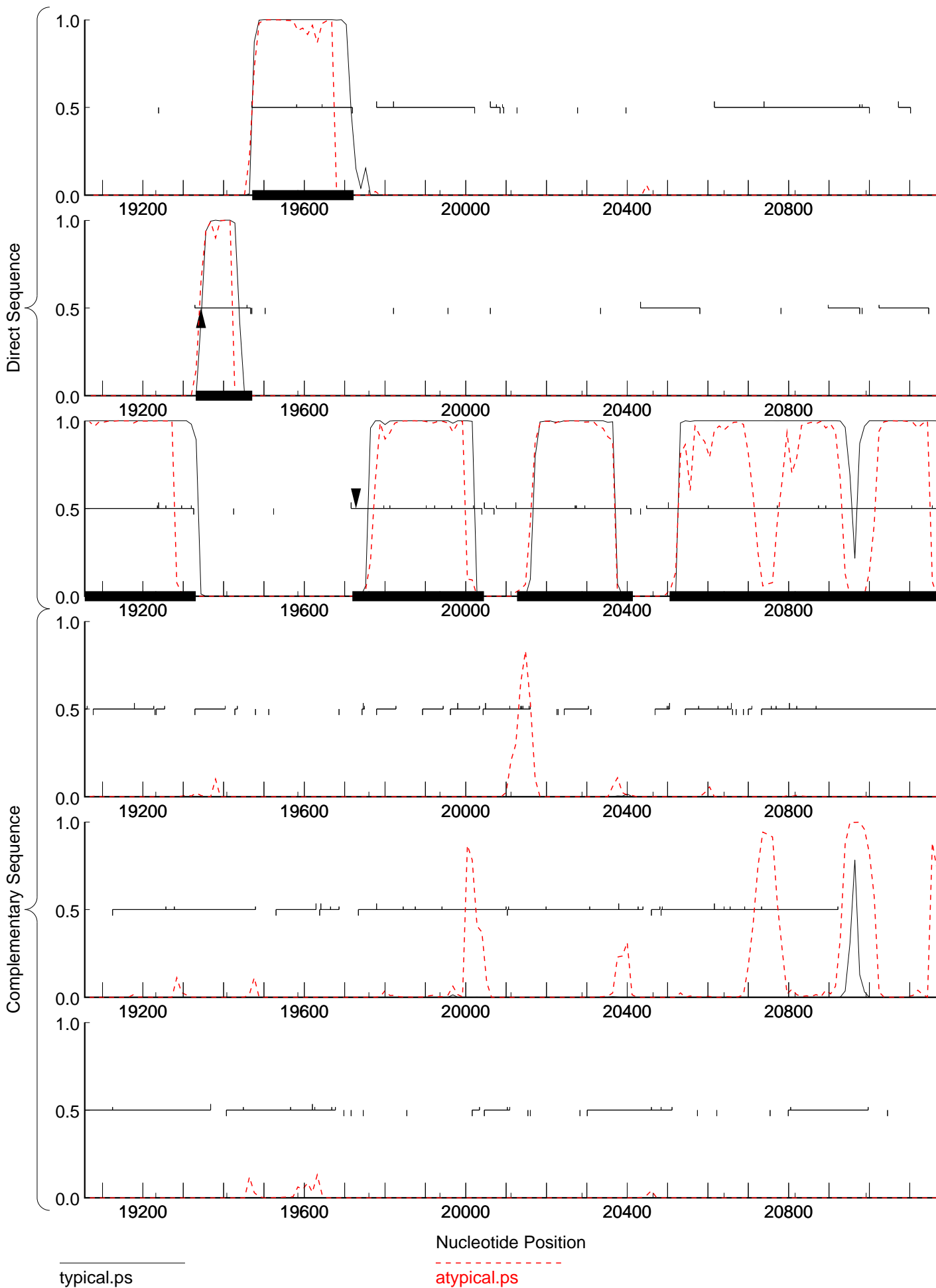




typical.ps

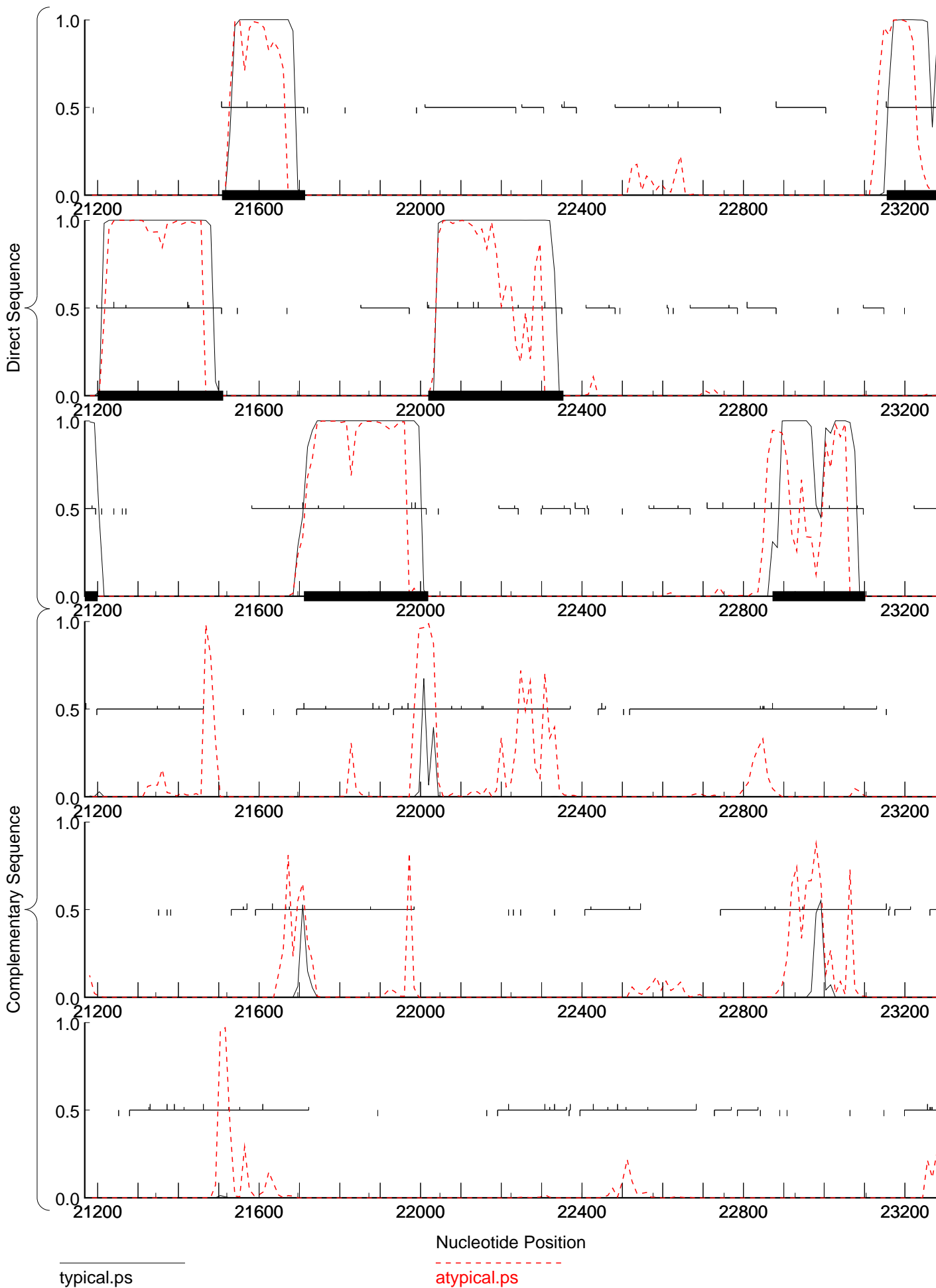
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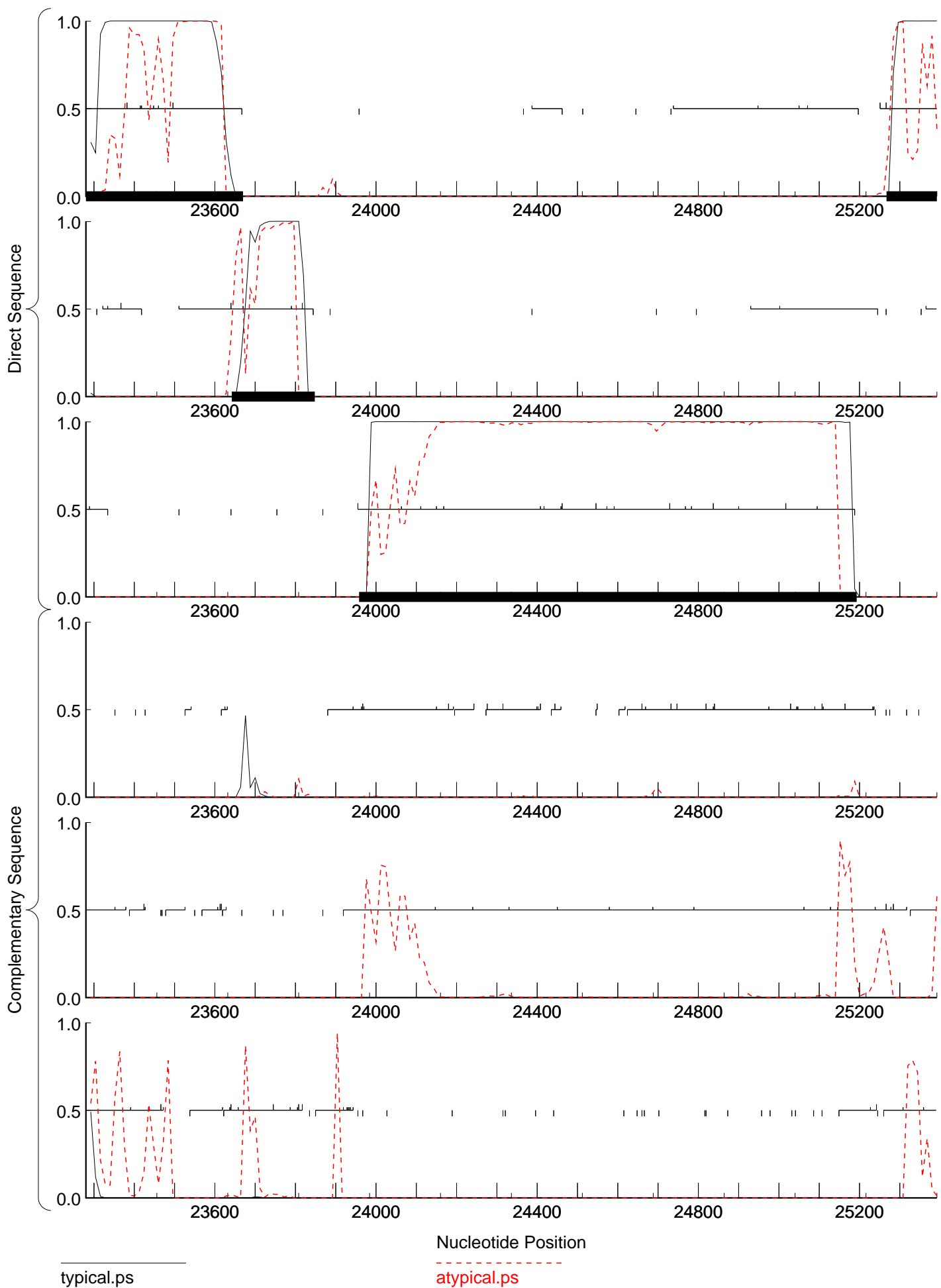
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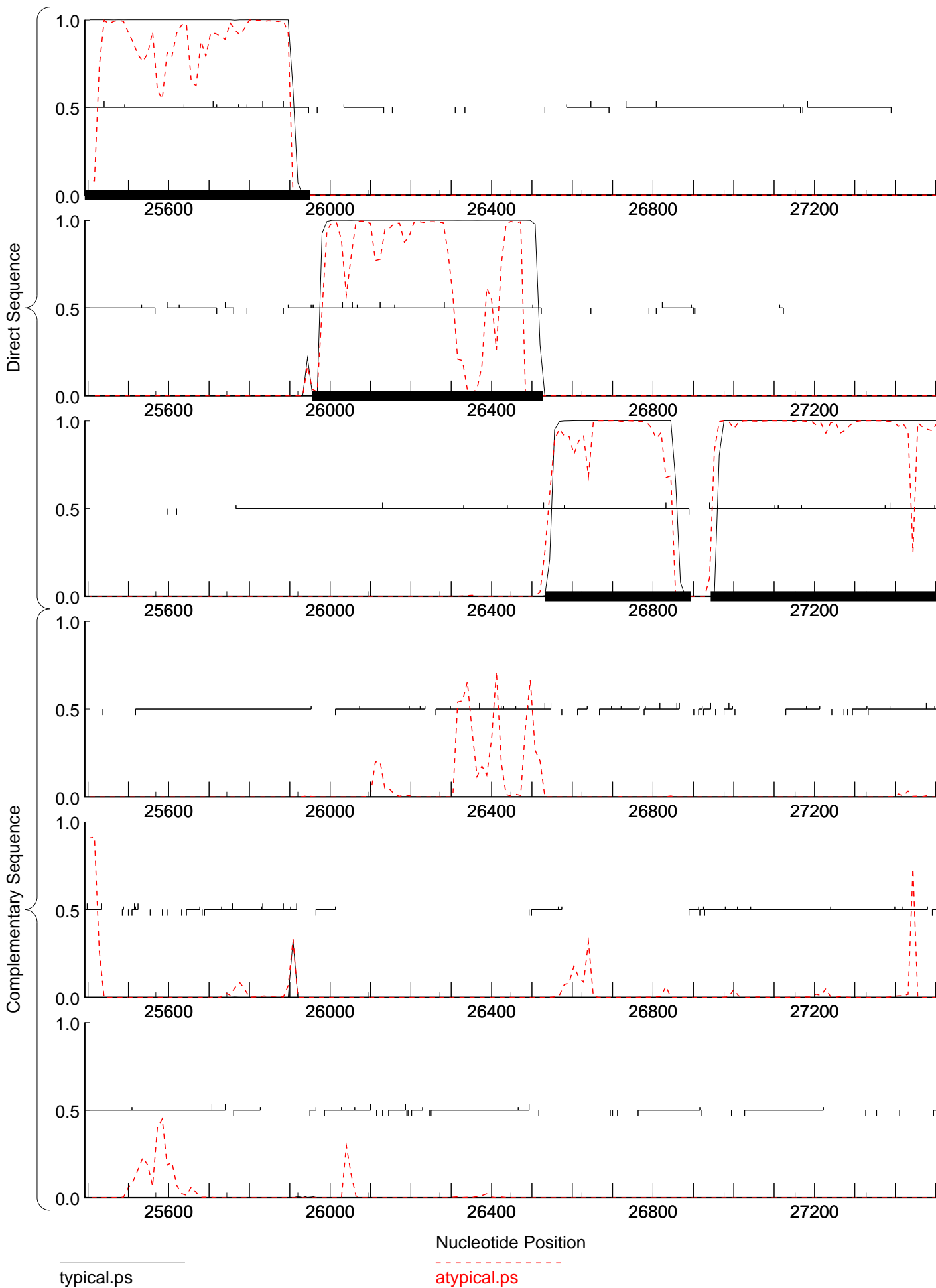
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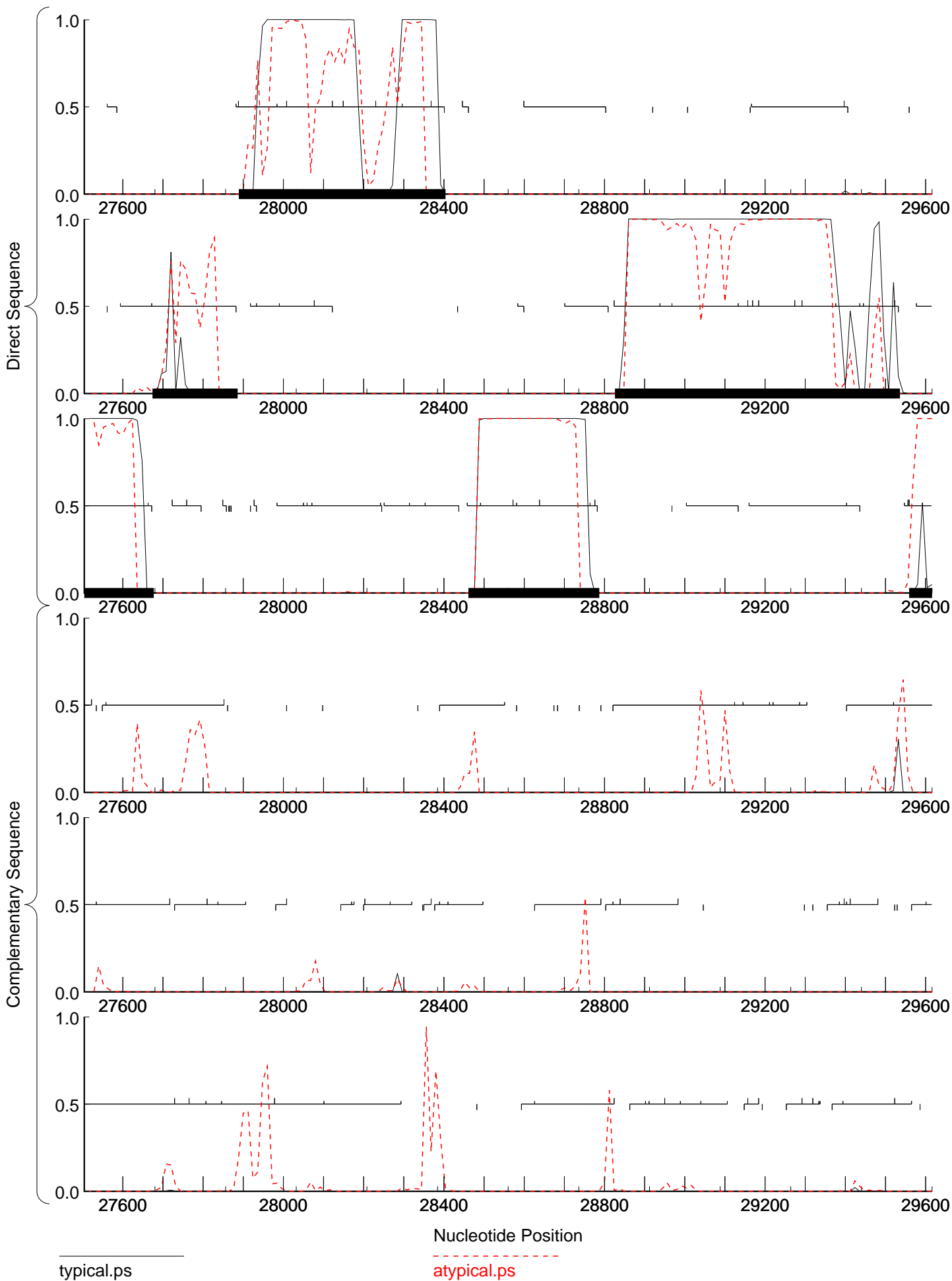


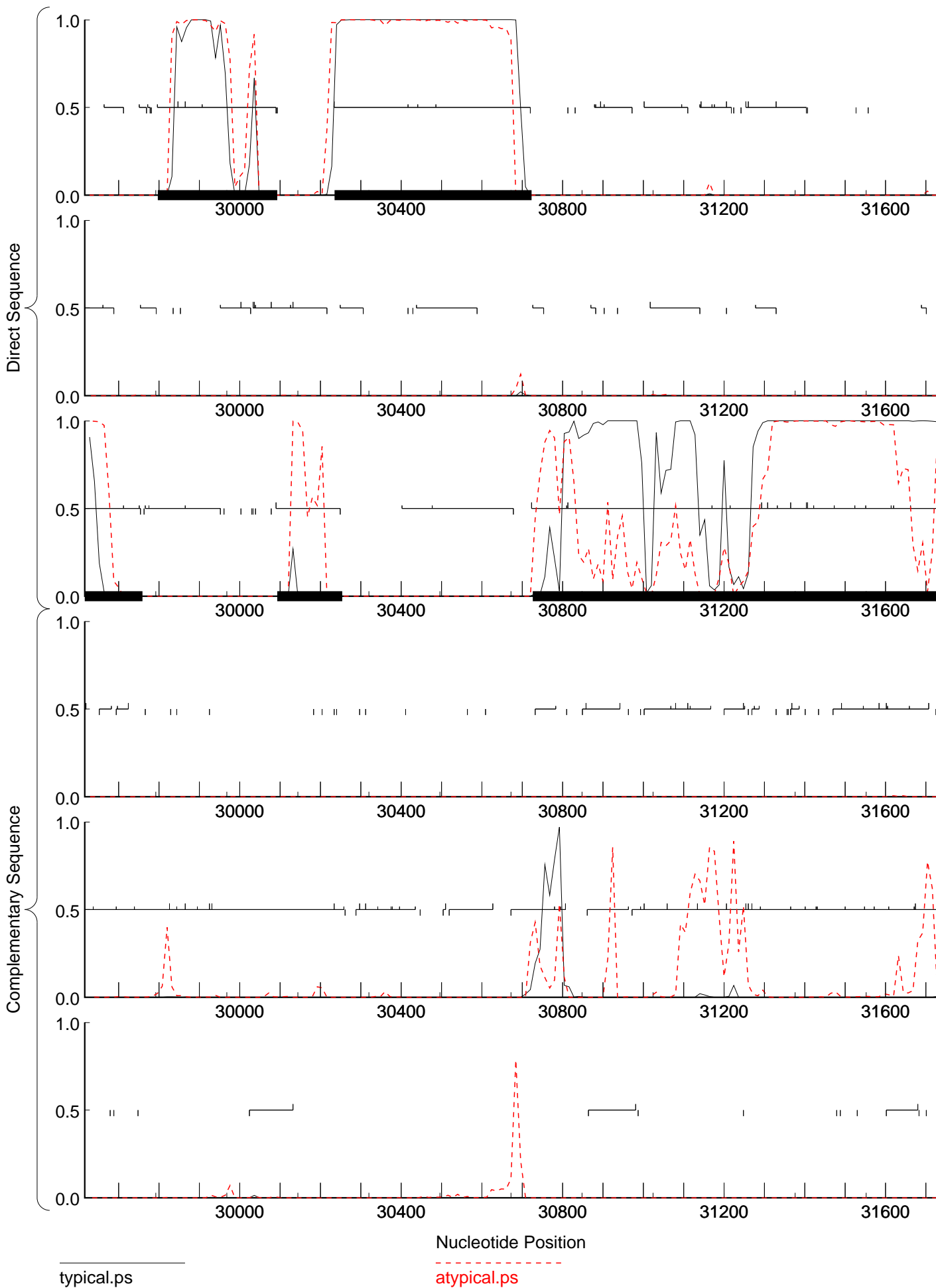
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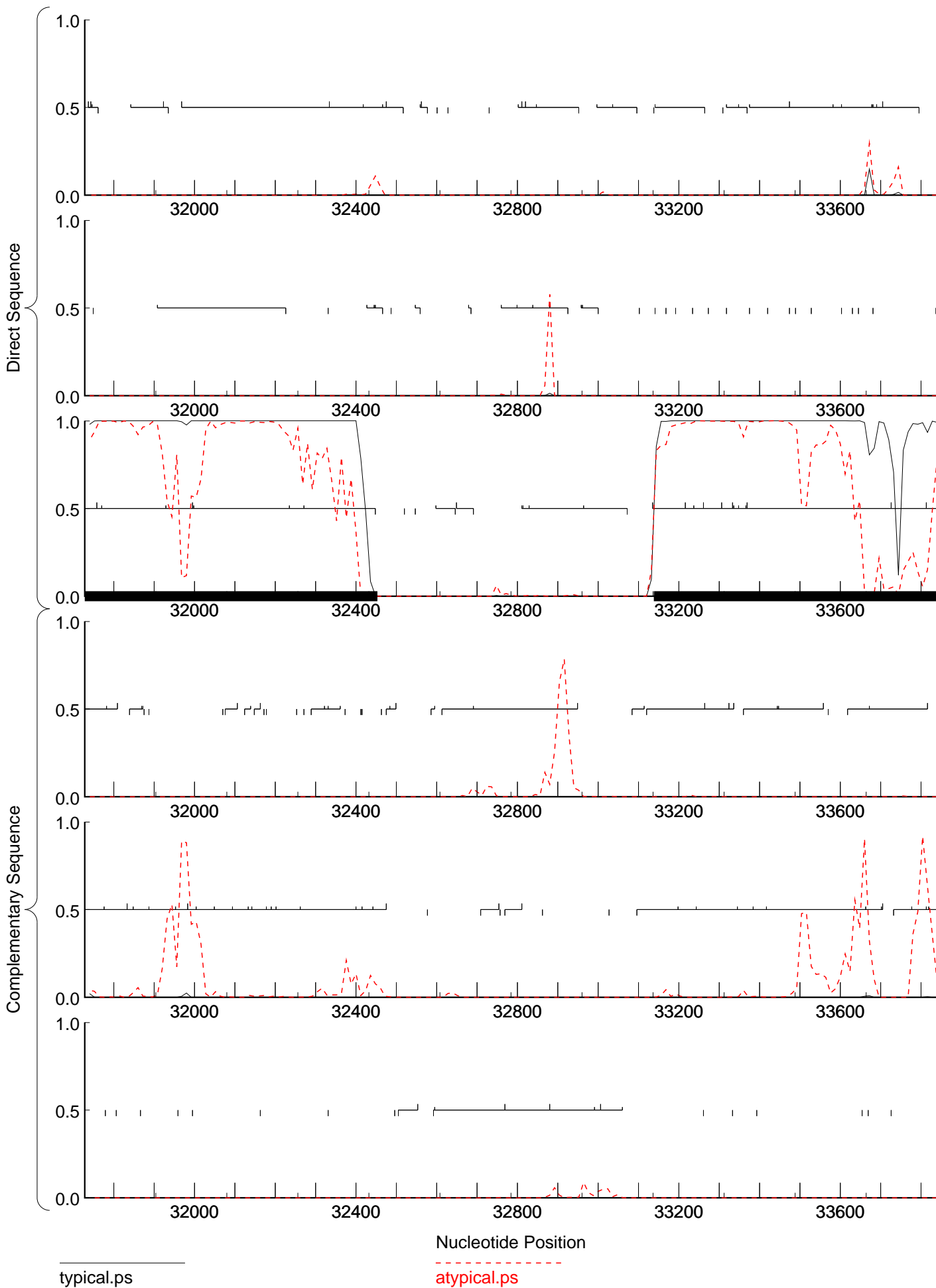
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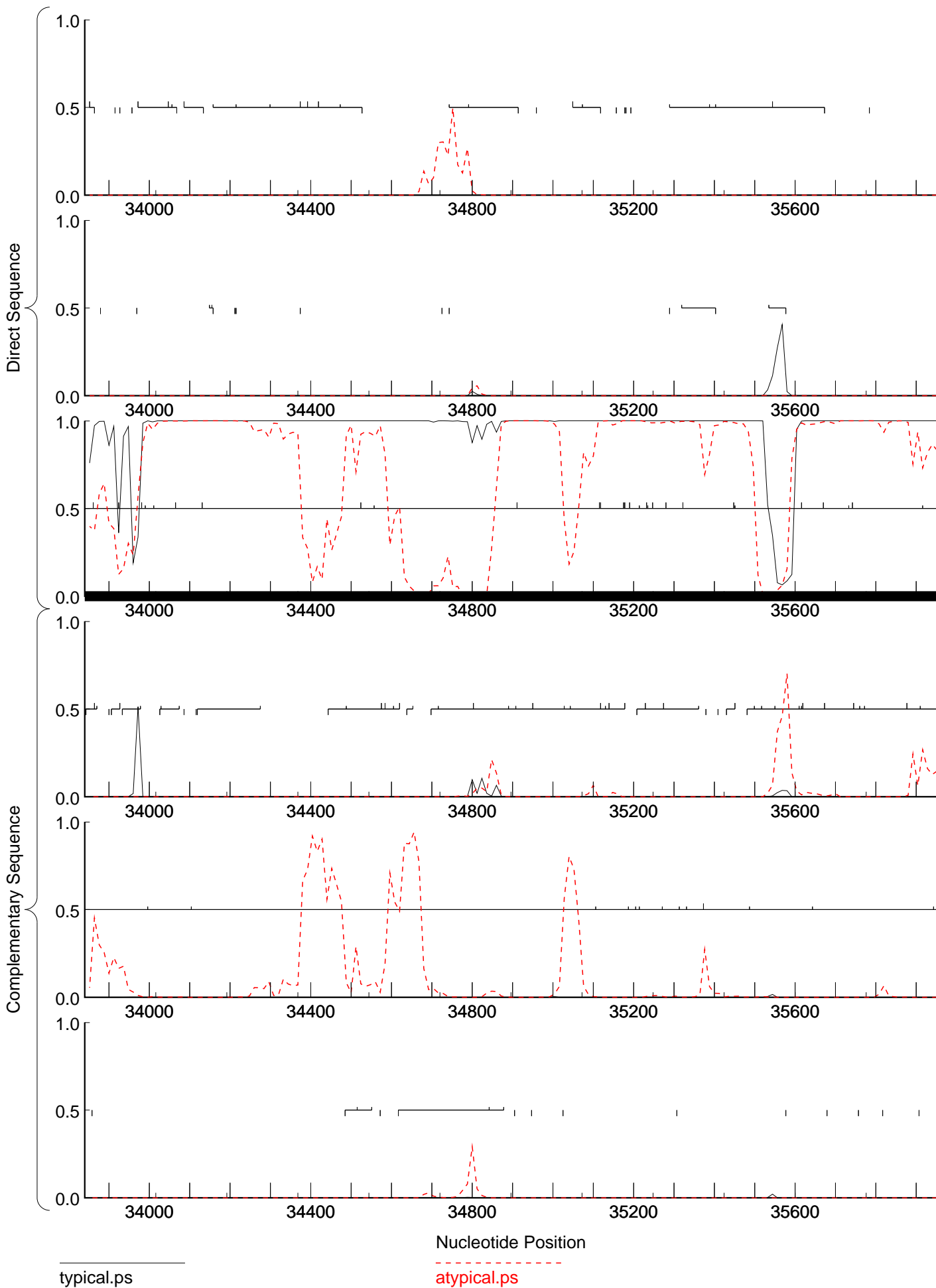


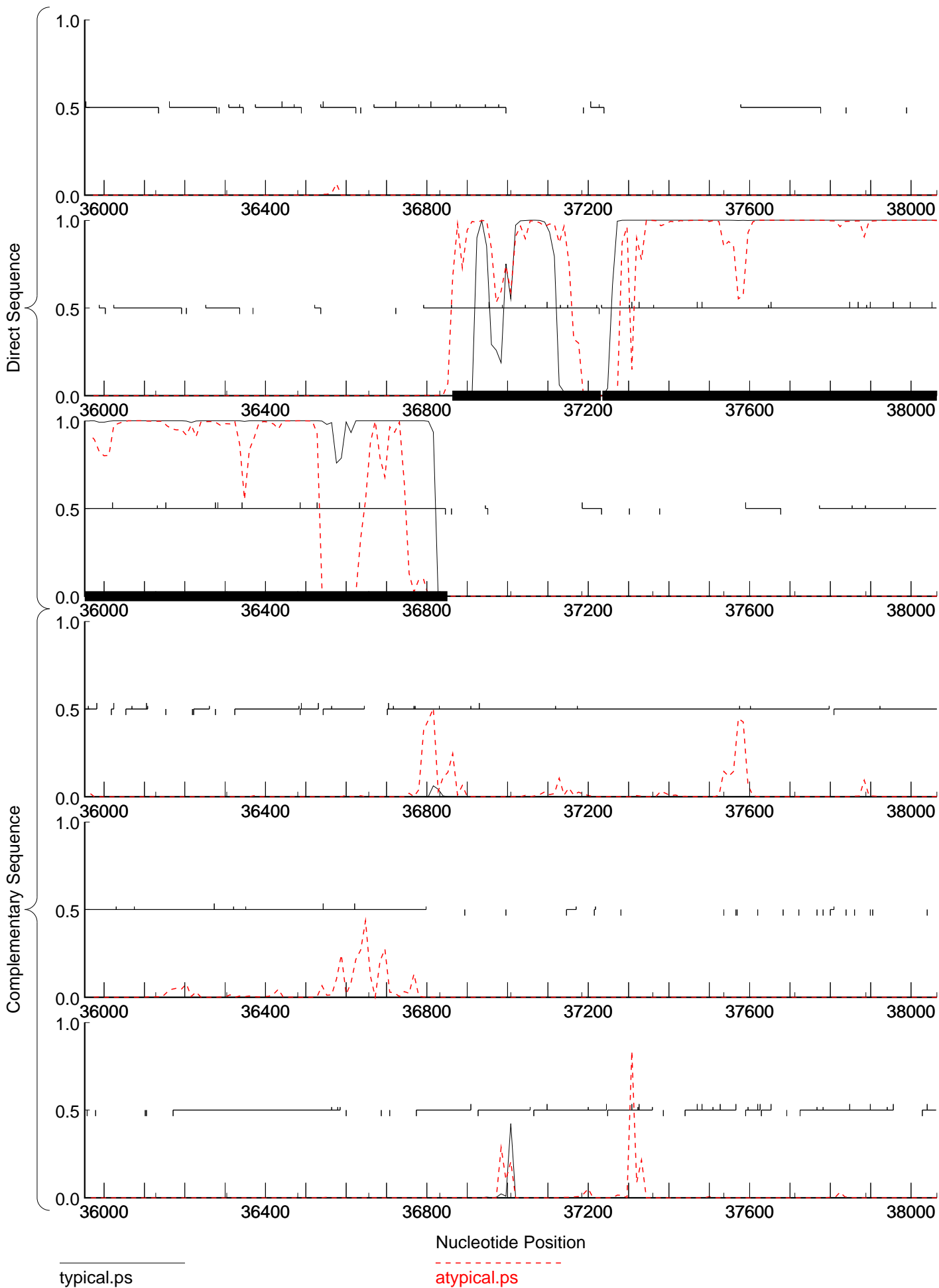


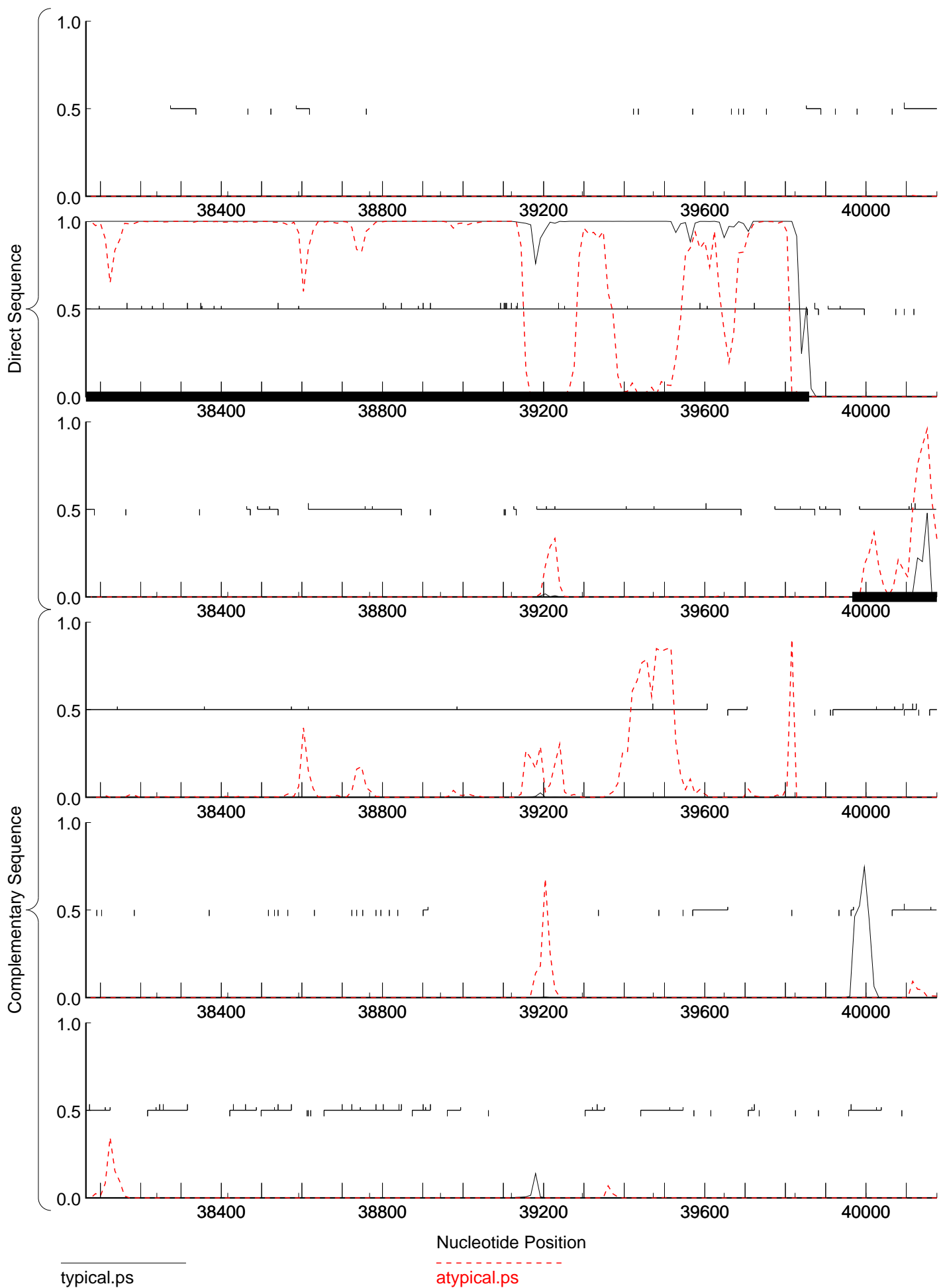


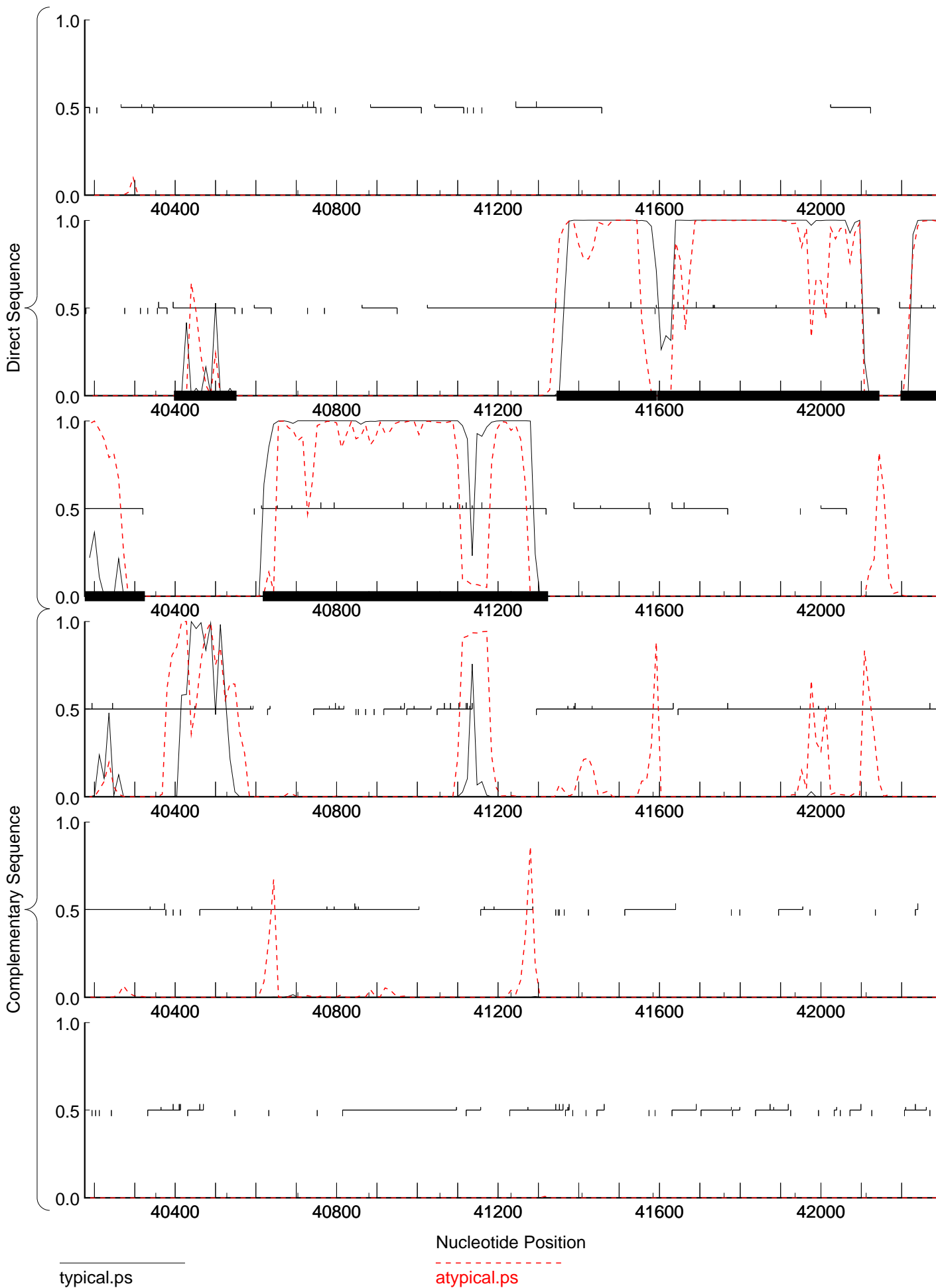


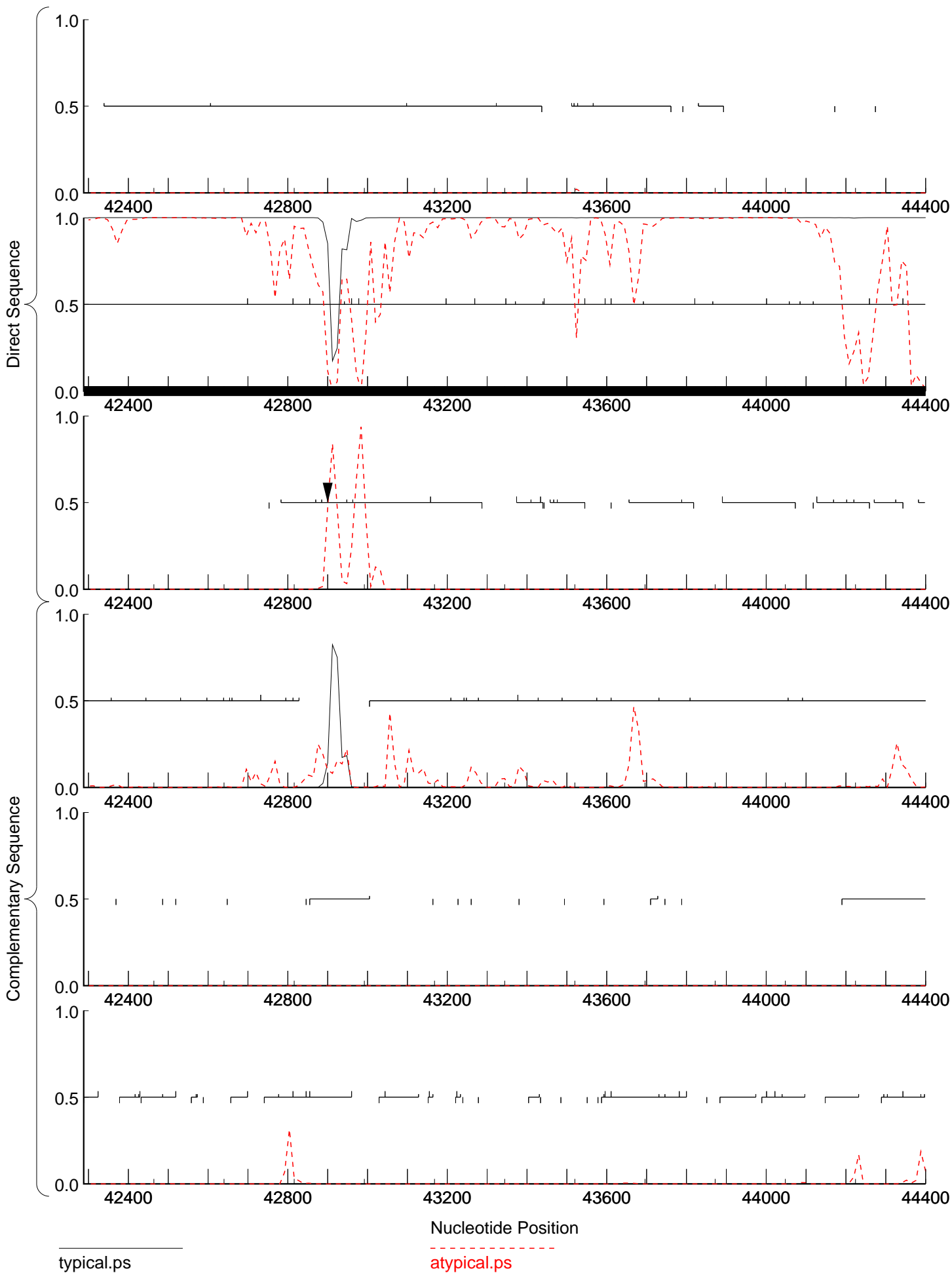






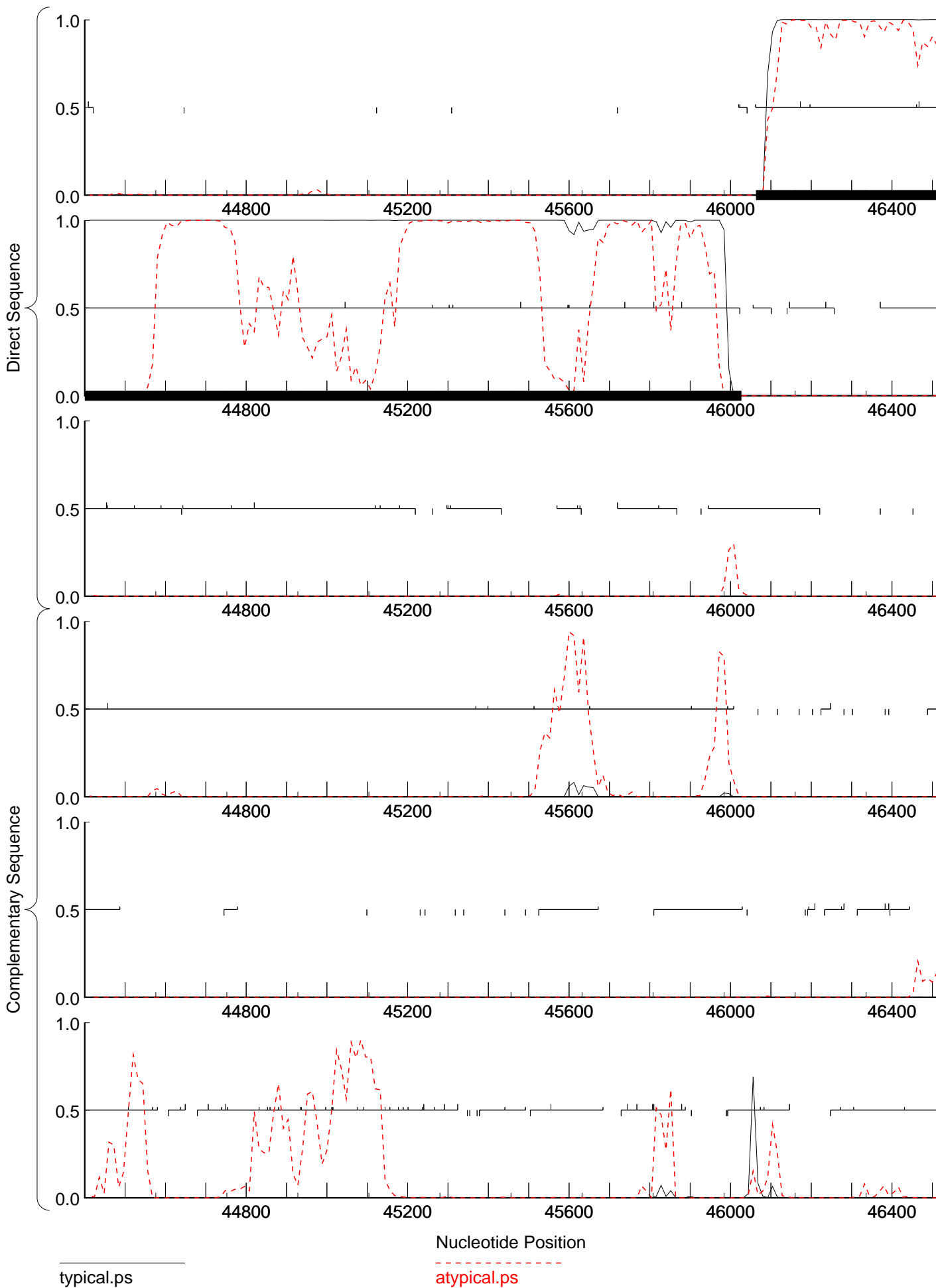


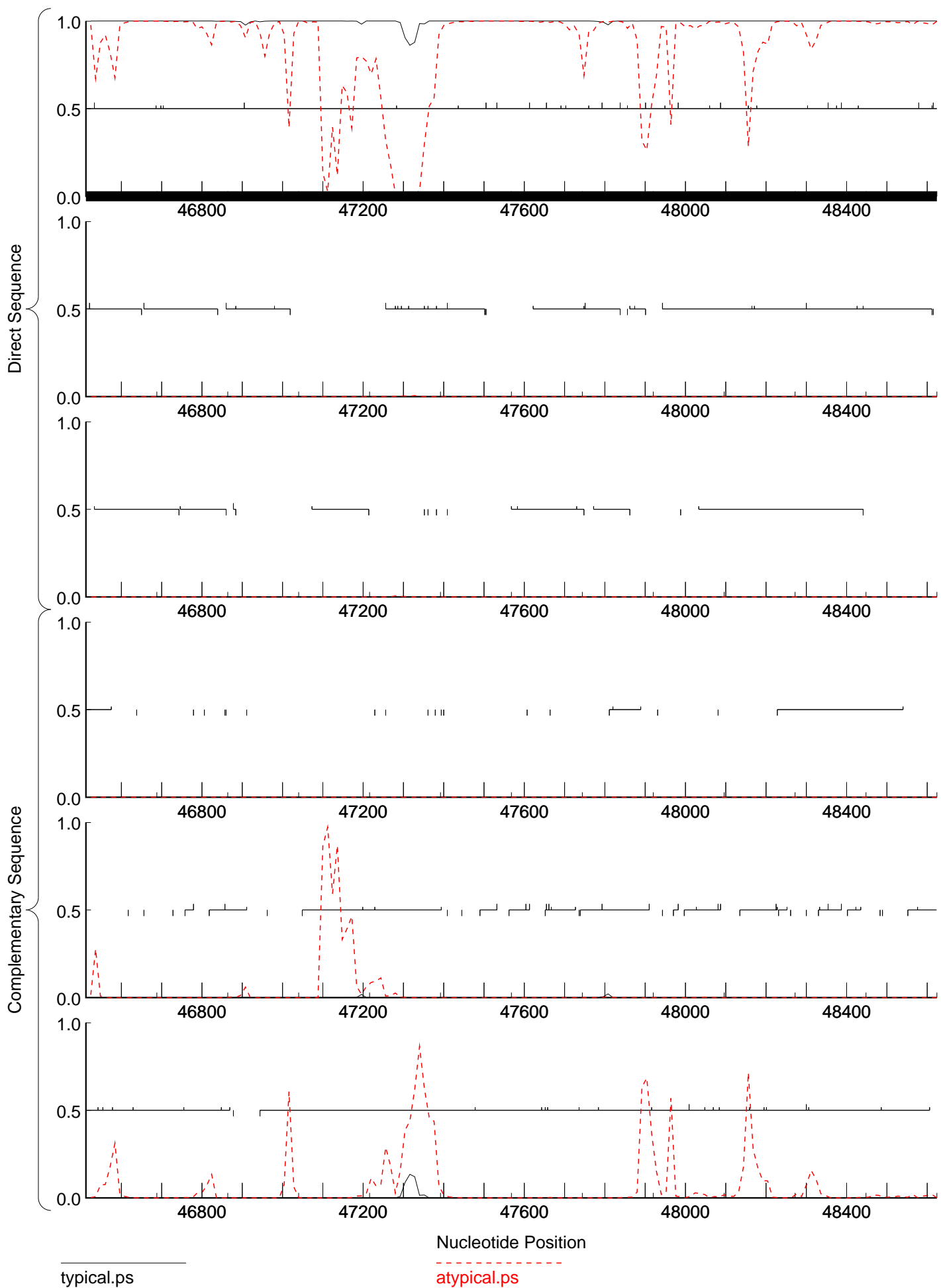


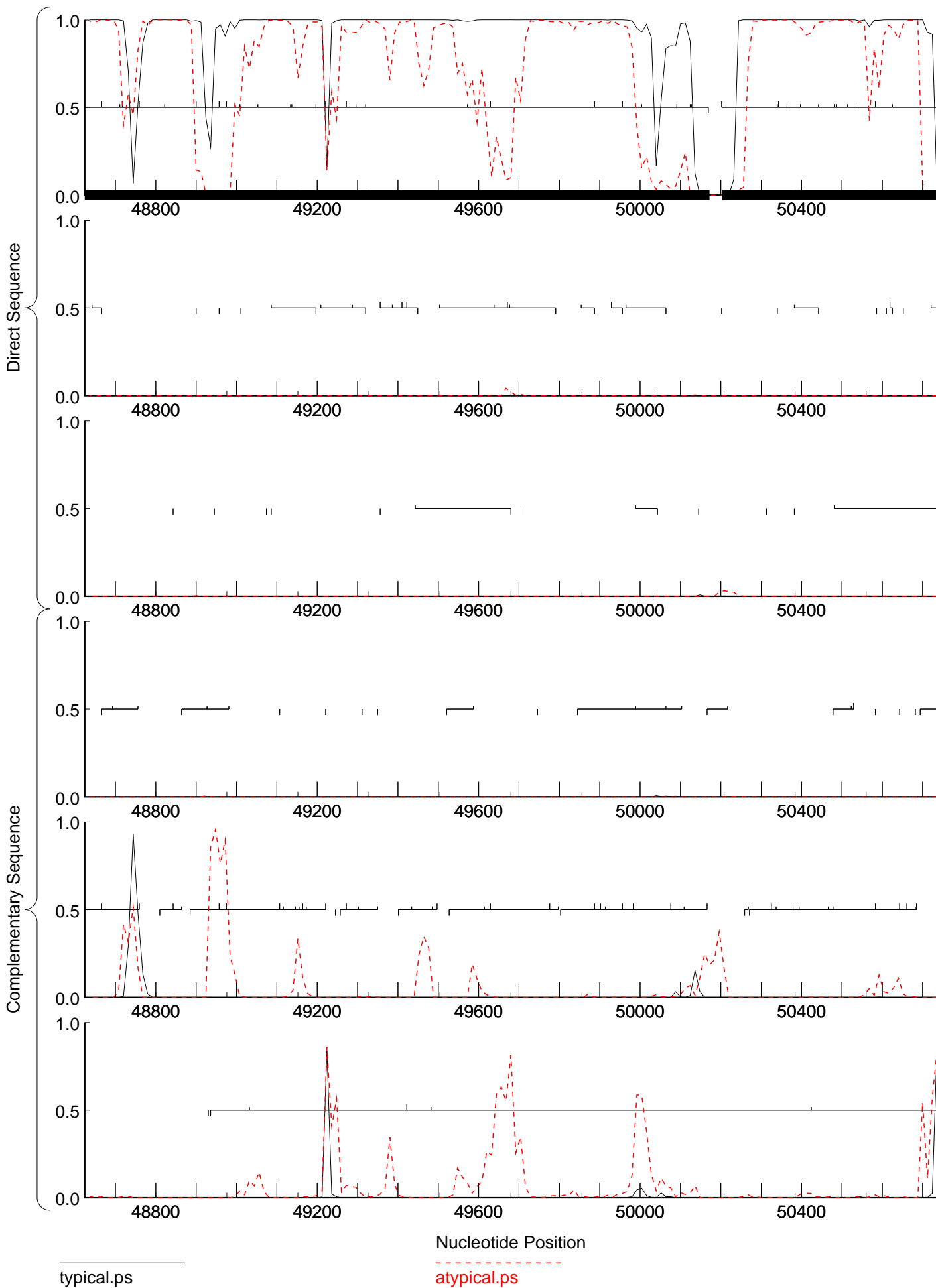


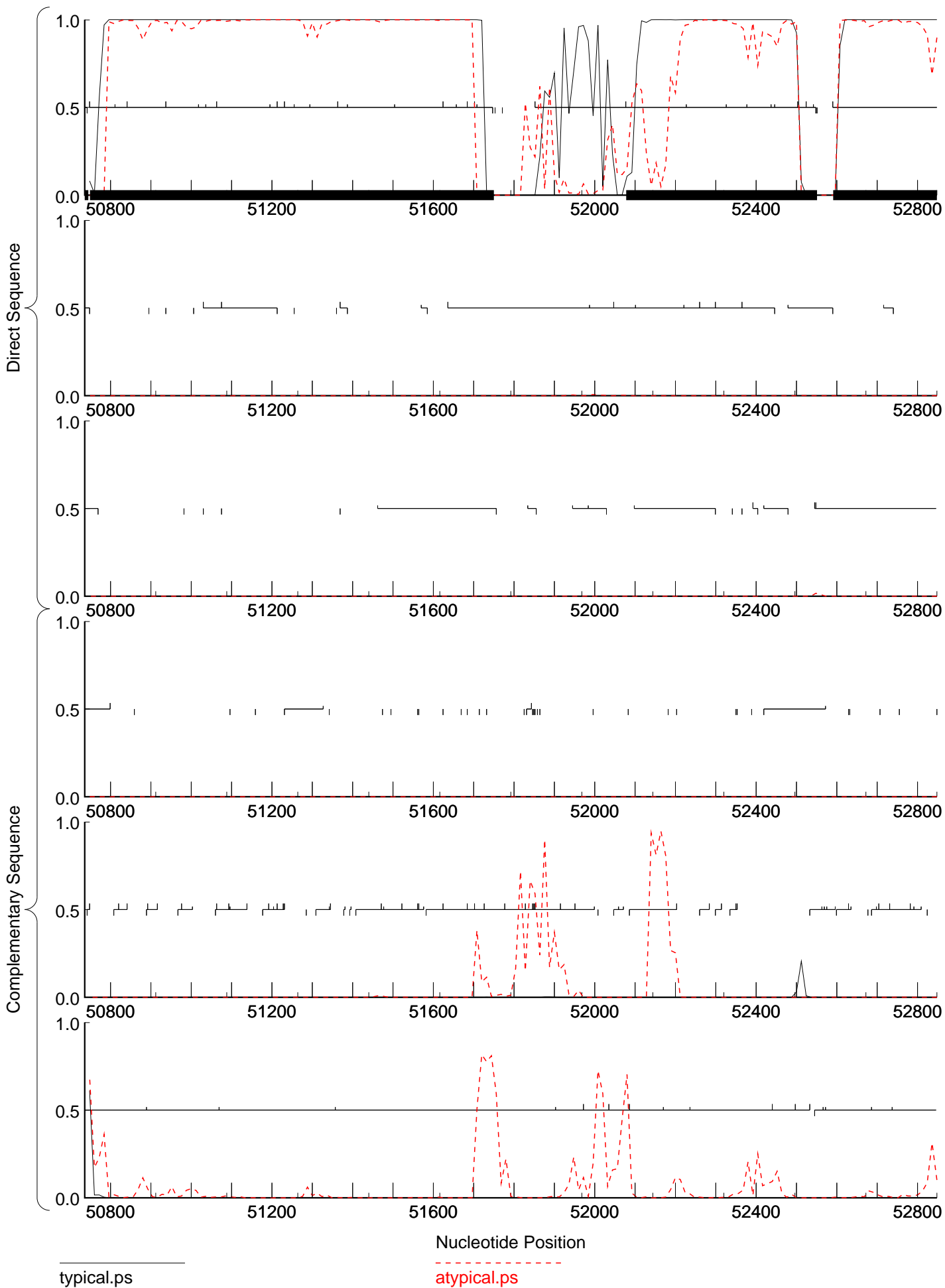
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atypical.ps



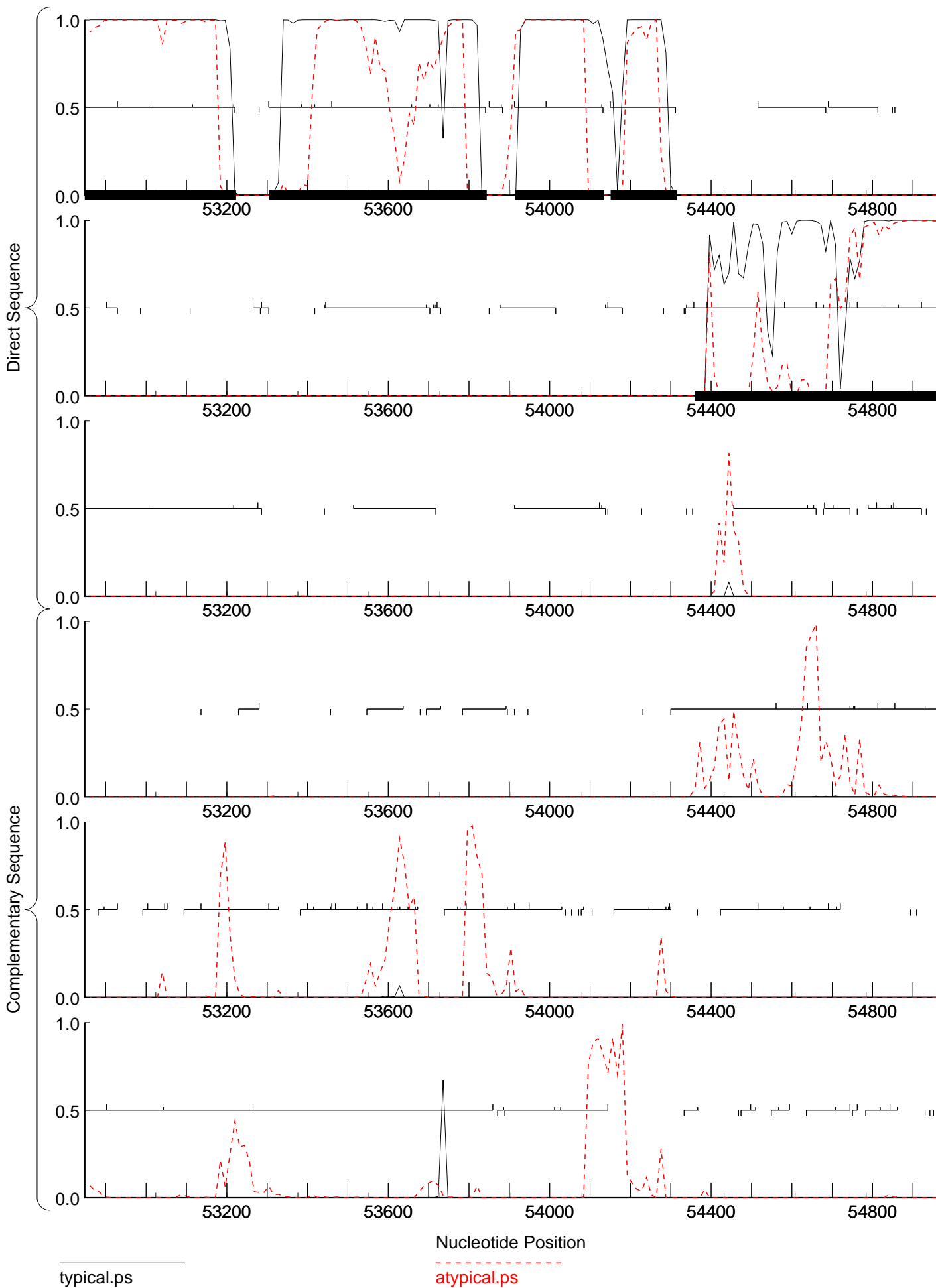






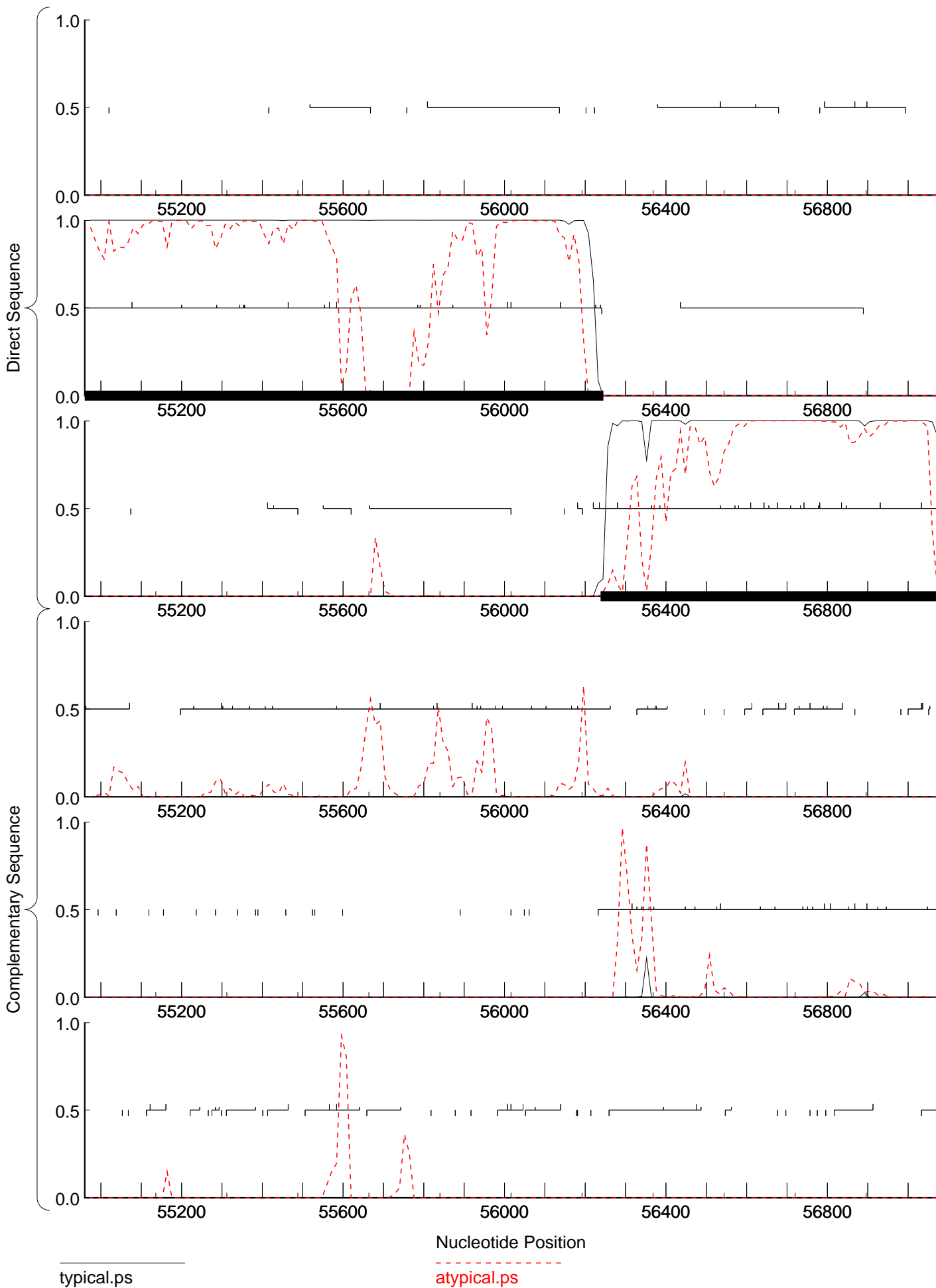
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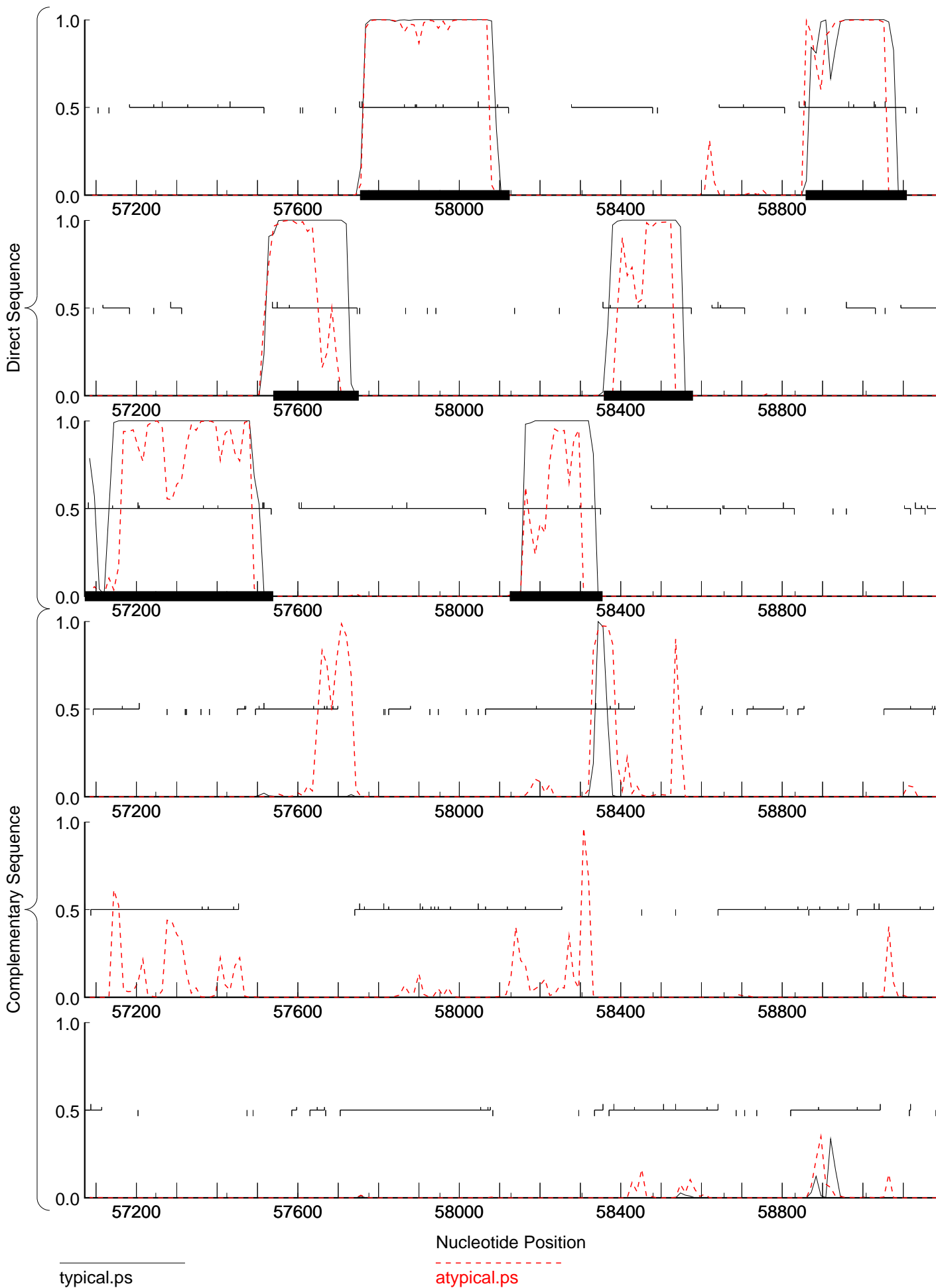
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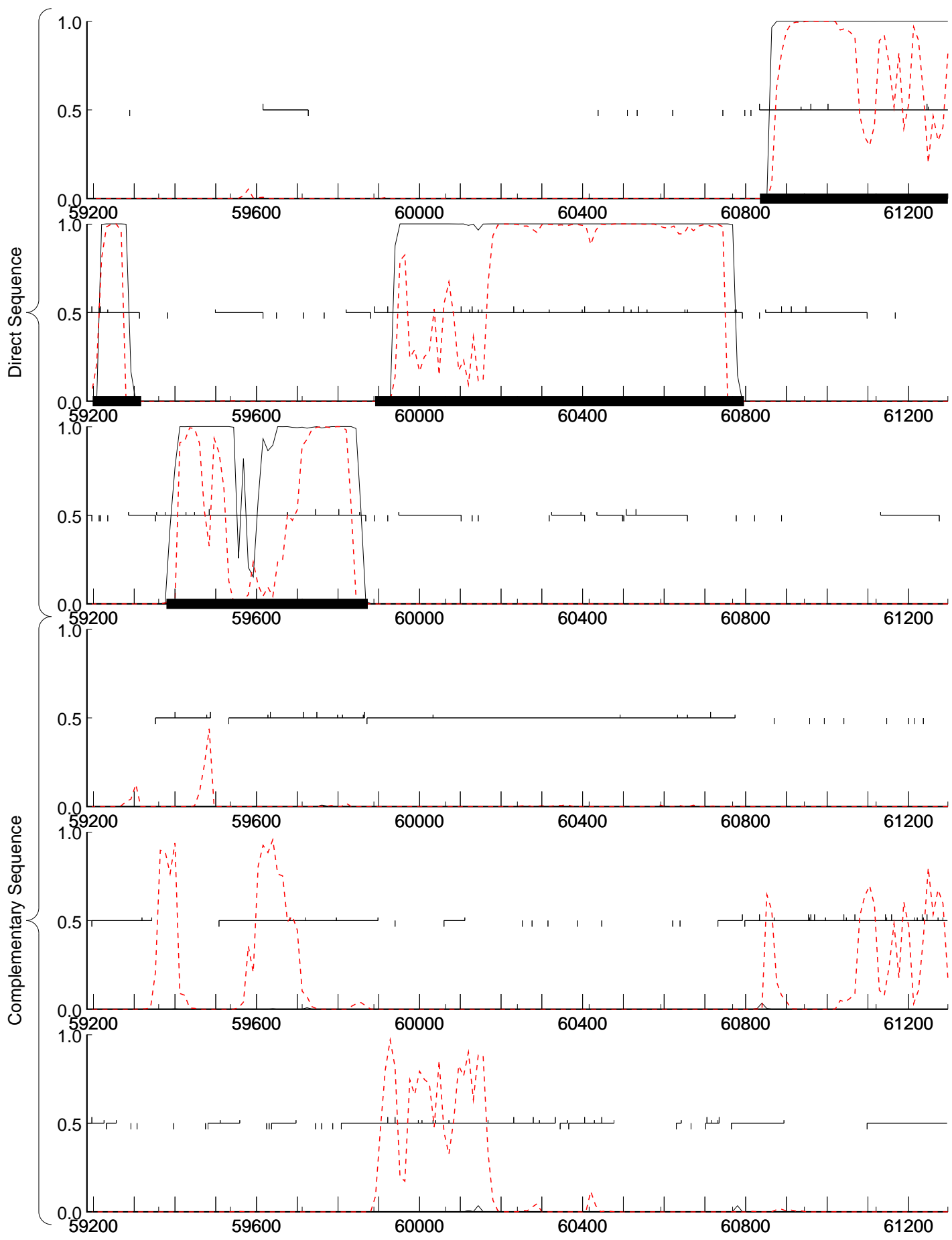
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atypical.ps



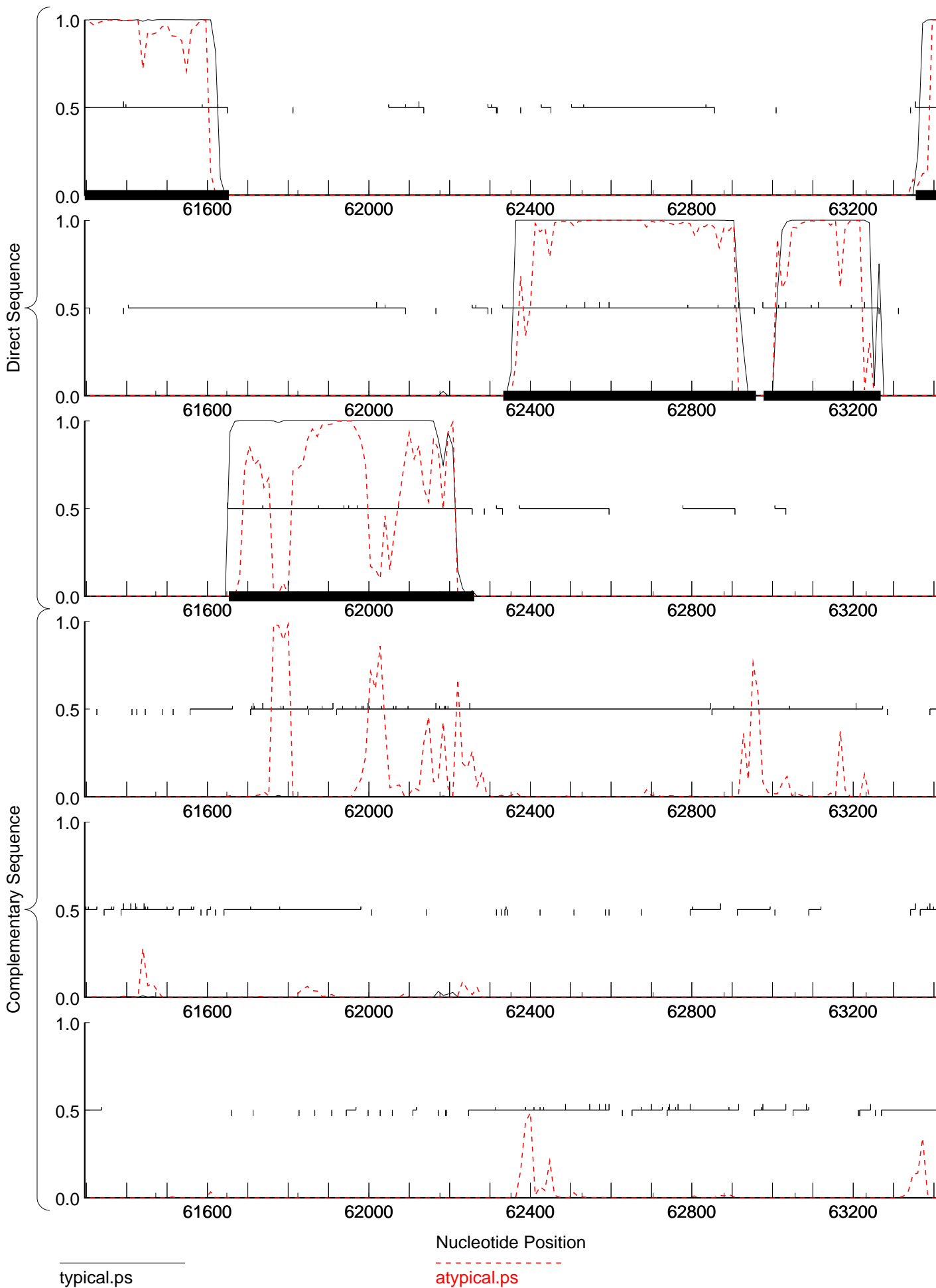


GeneMark.hmm prediction



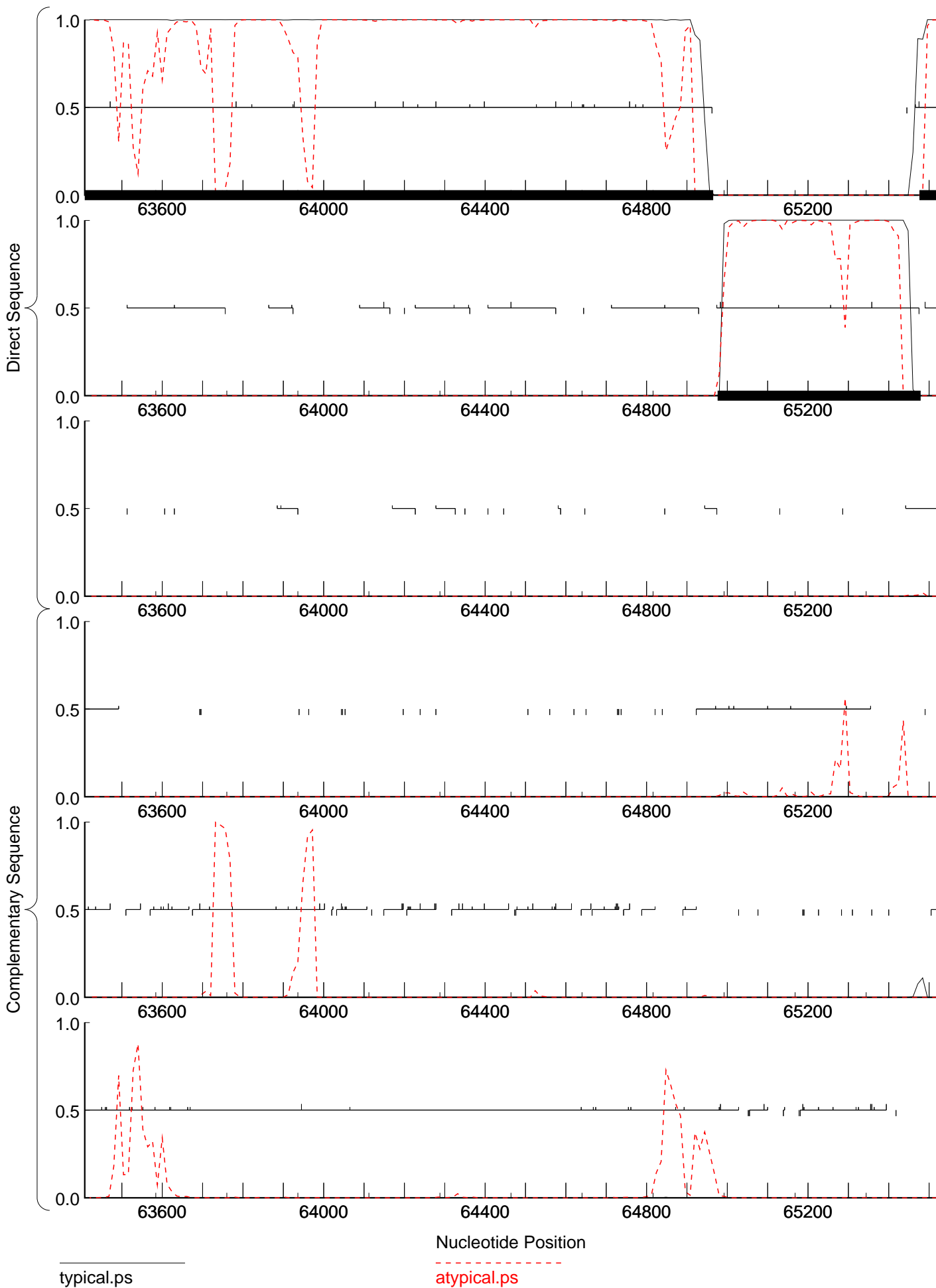
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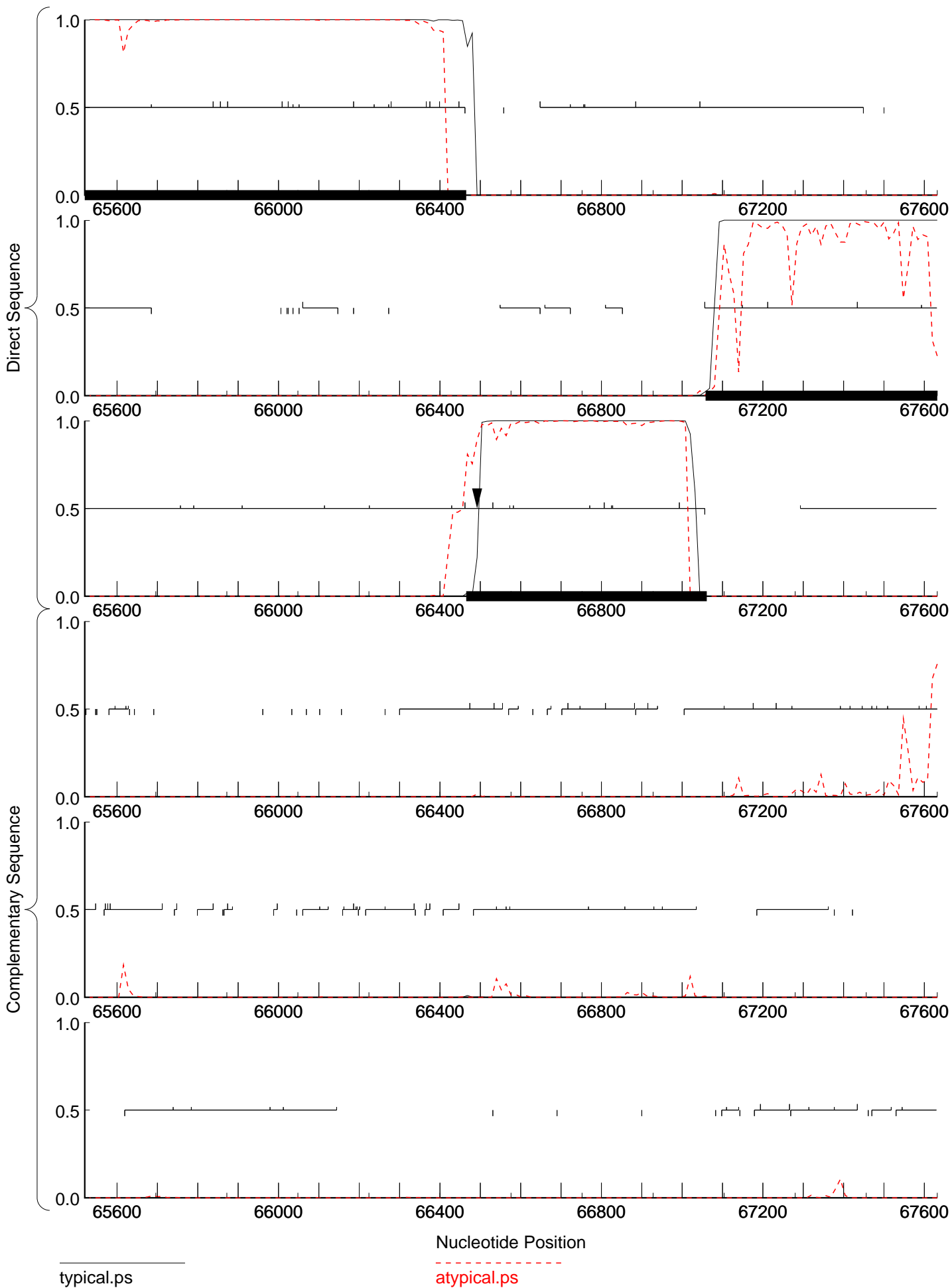
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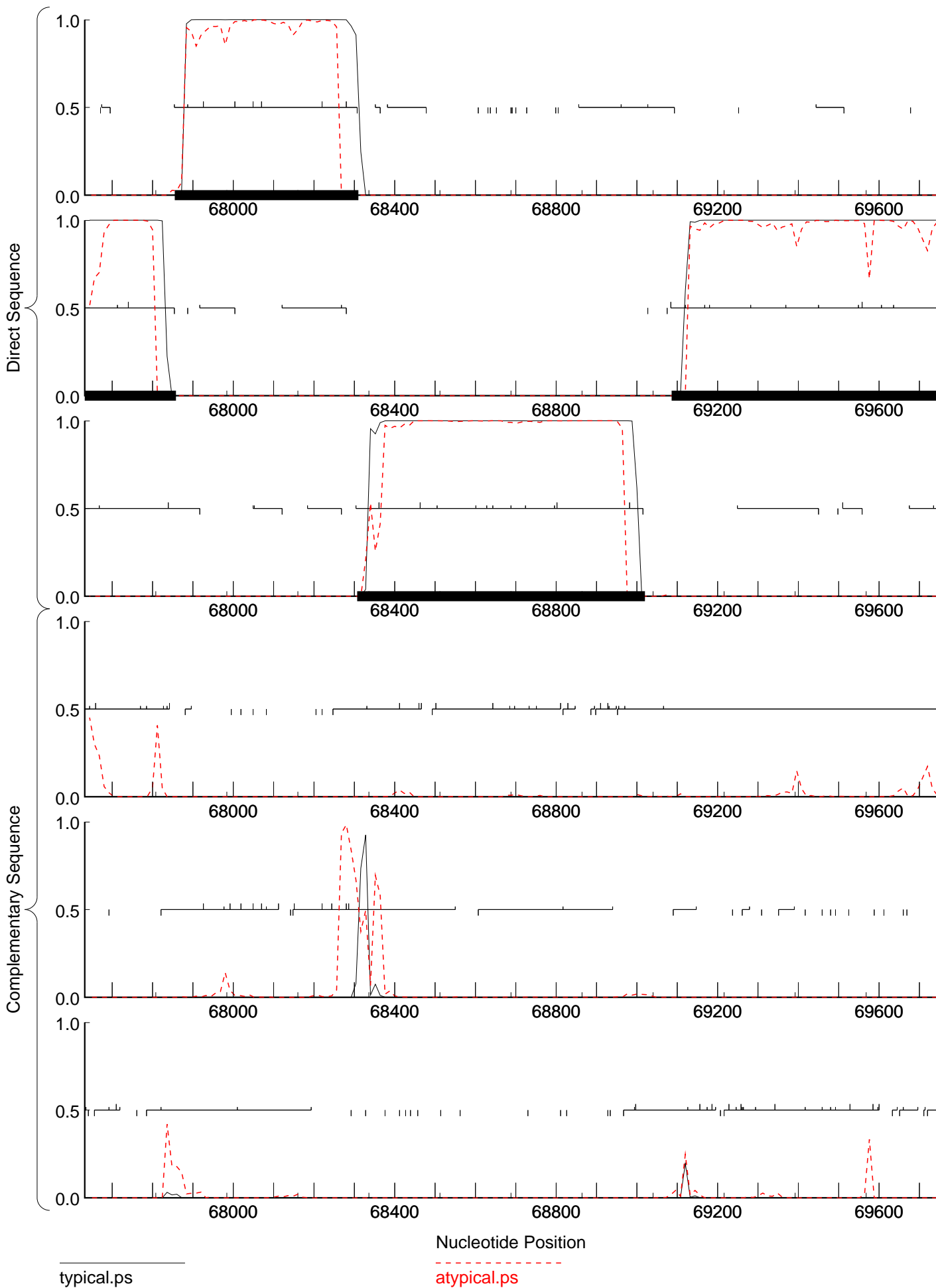


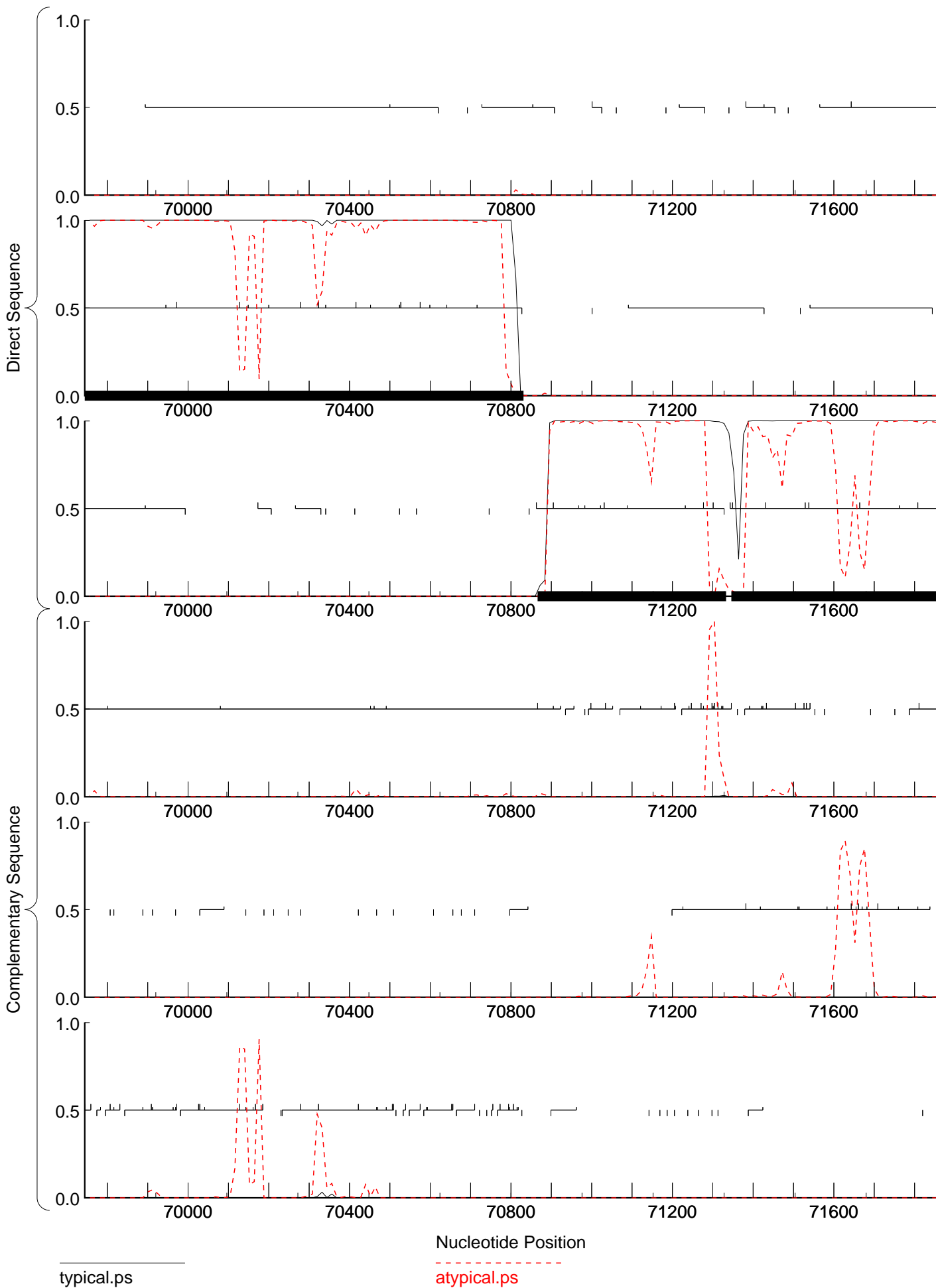
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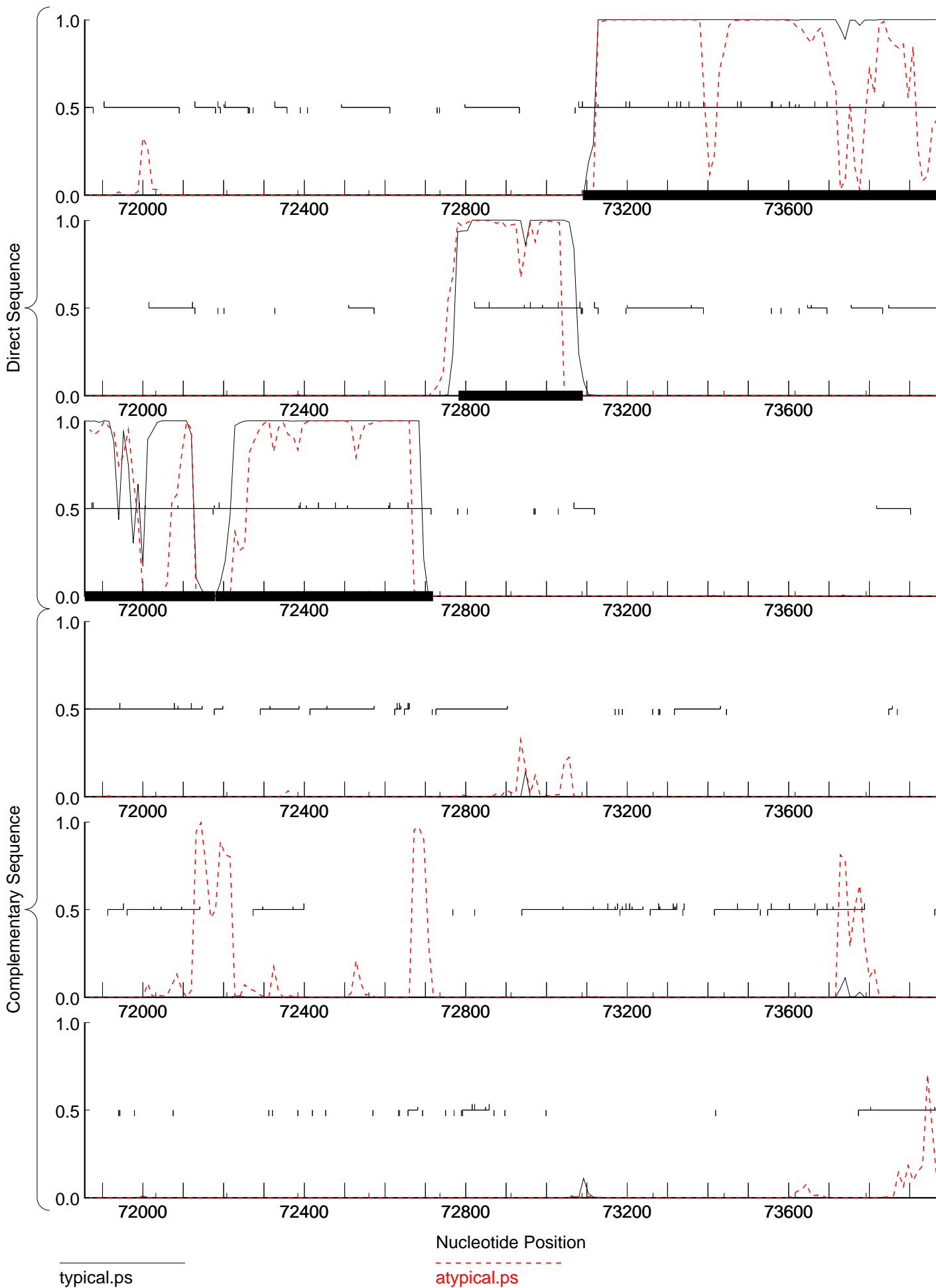
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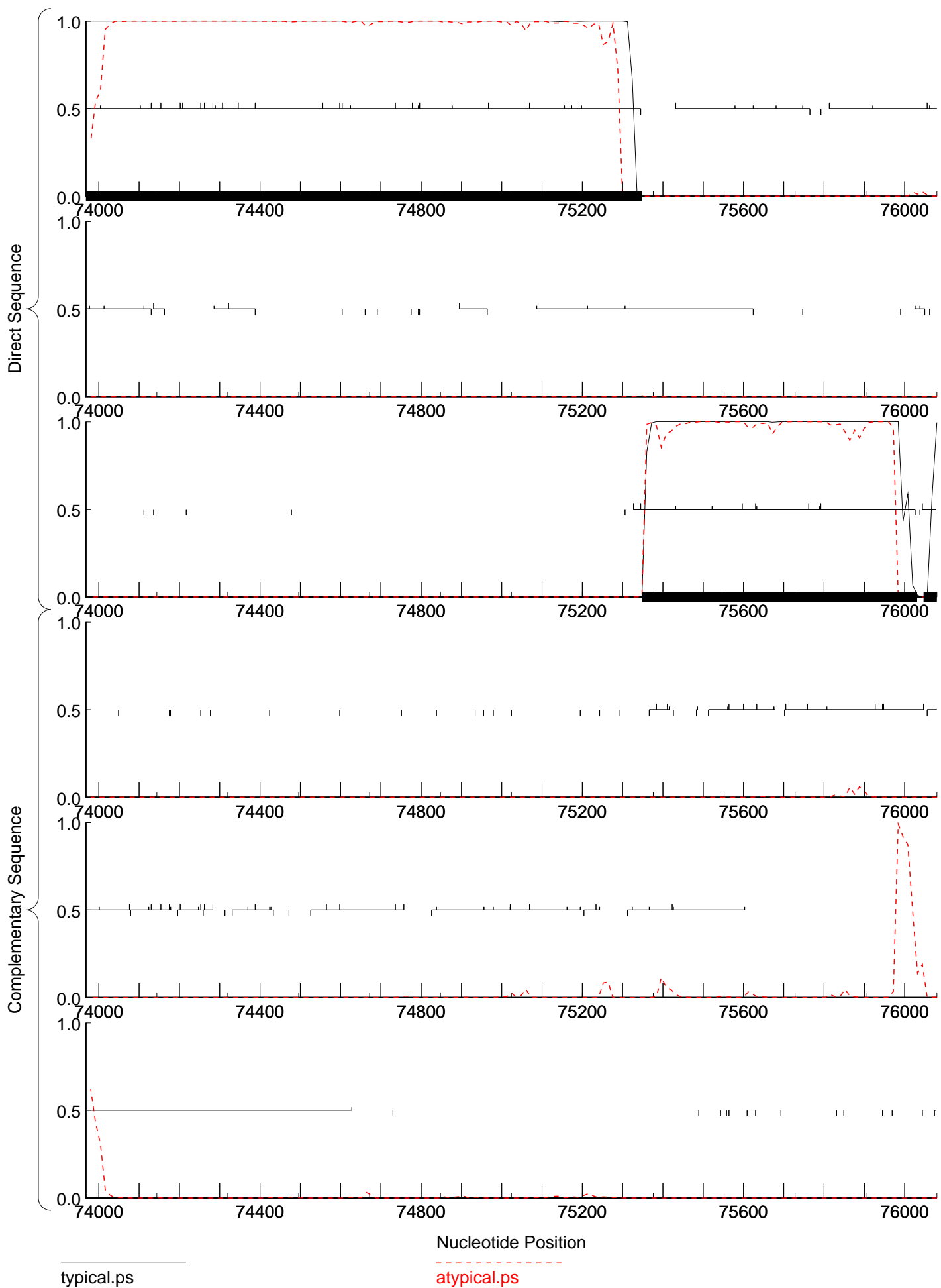


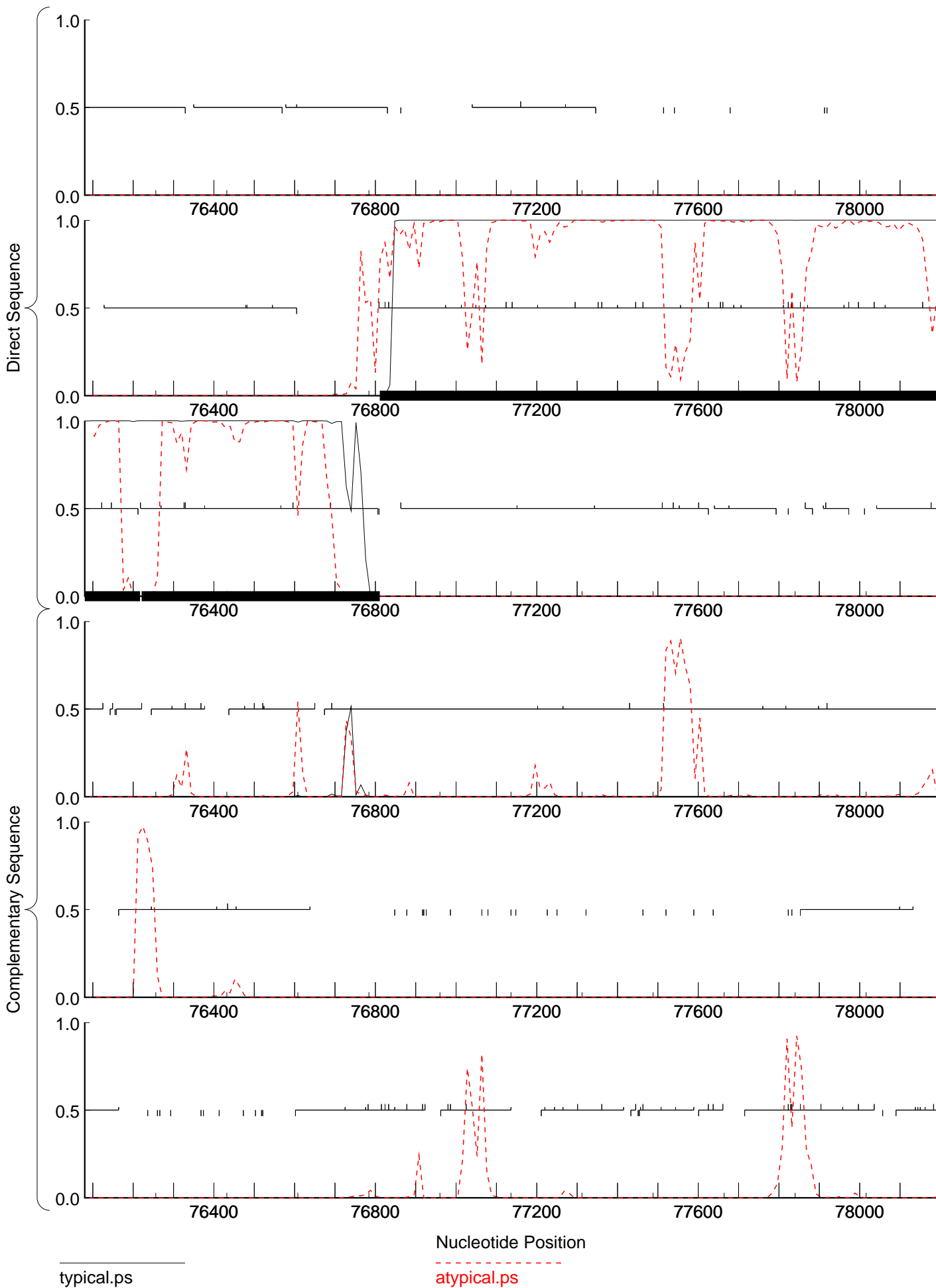


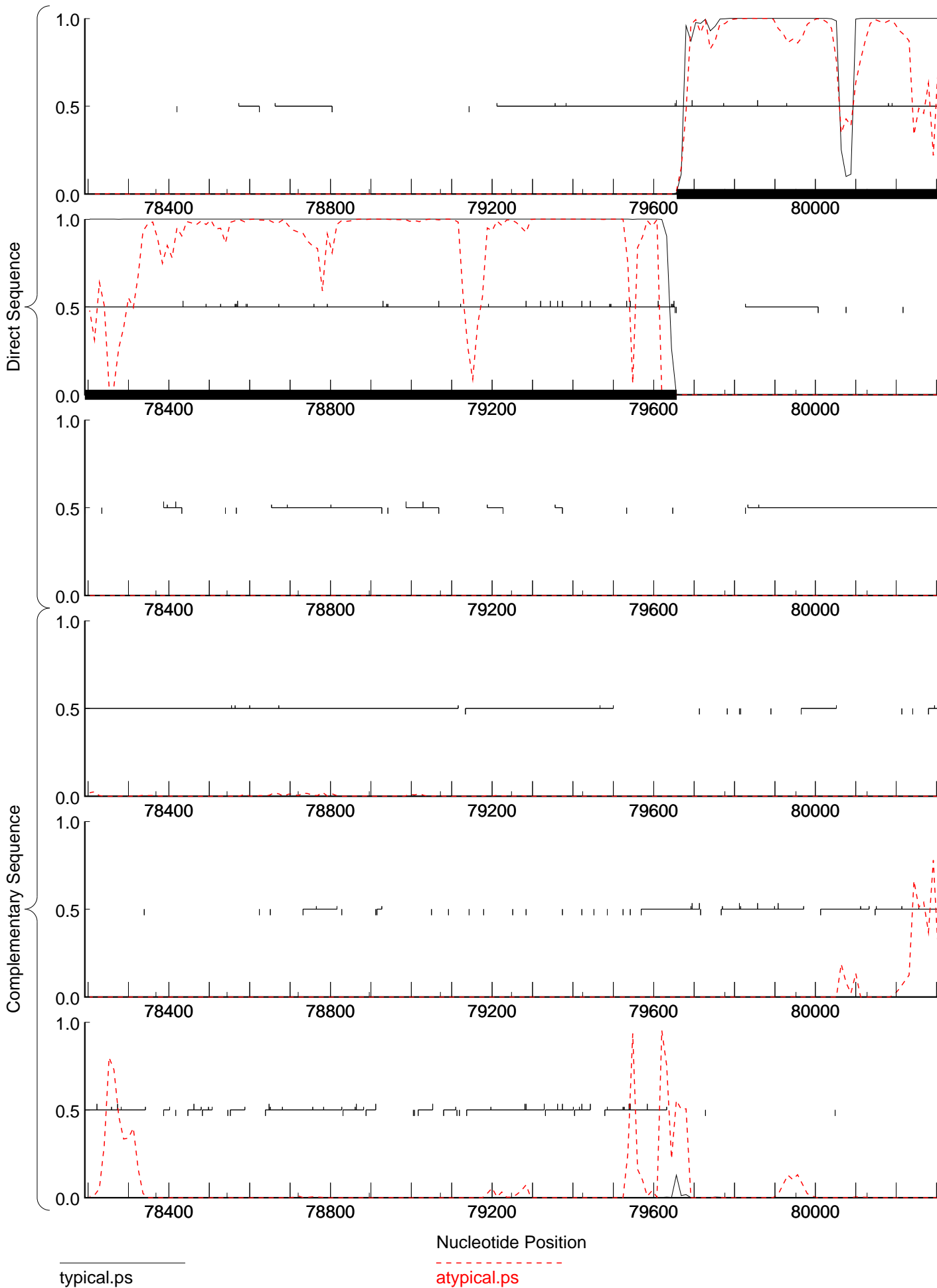


typical.ps

atypical.ps

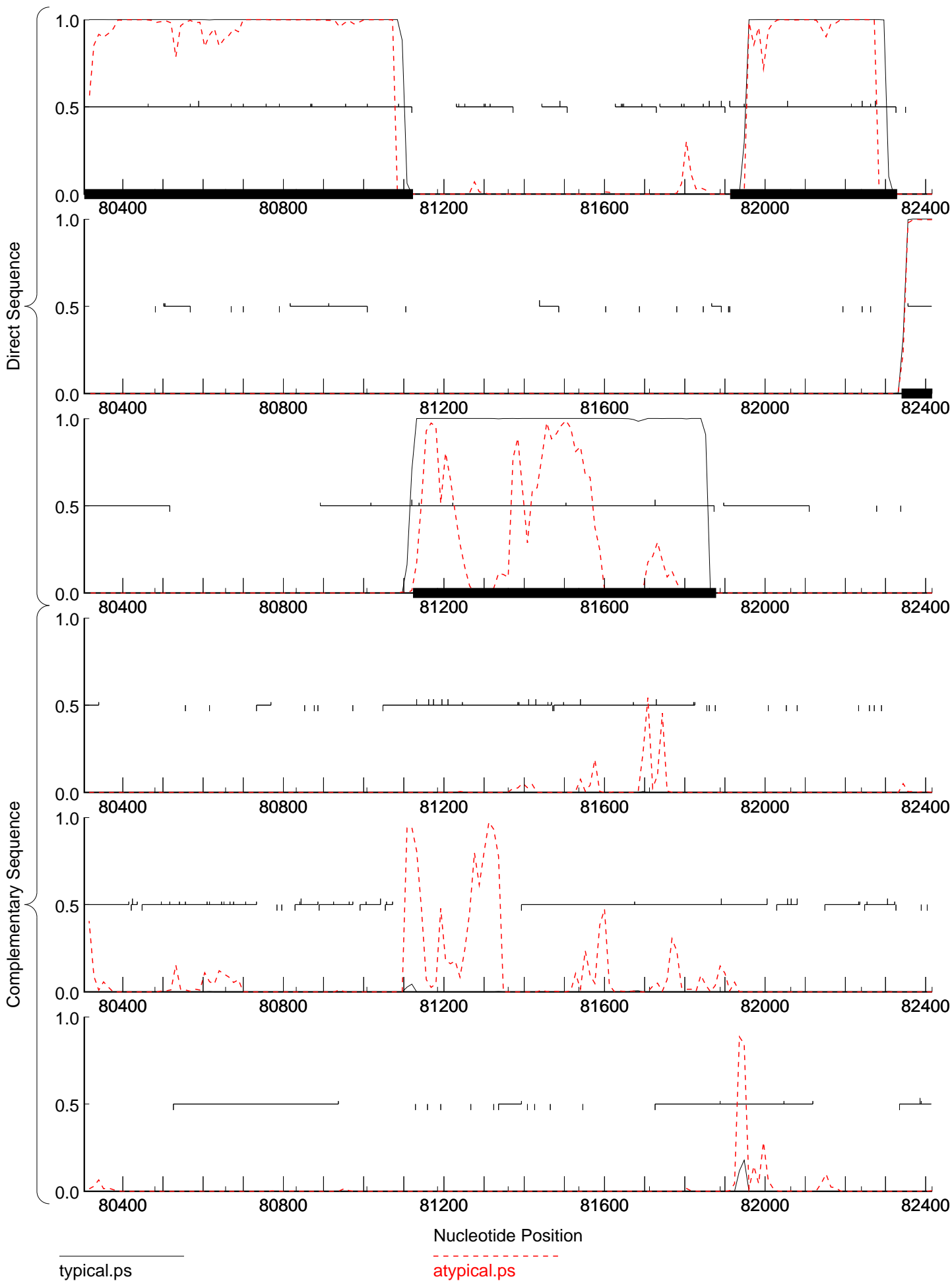






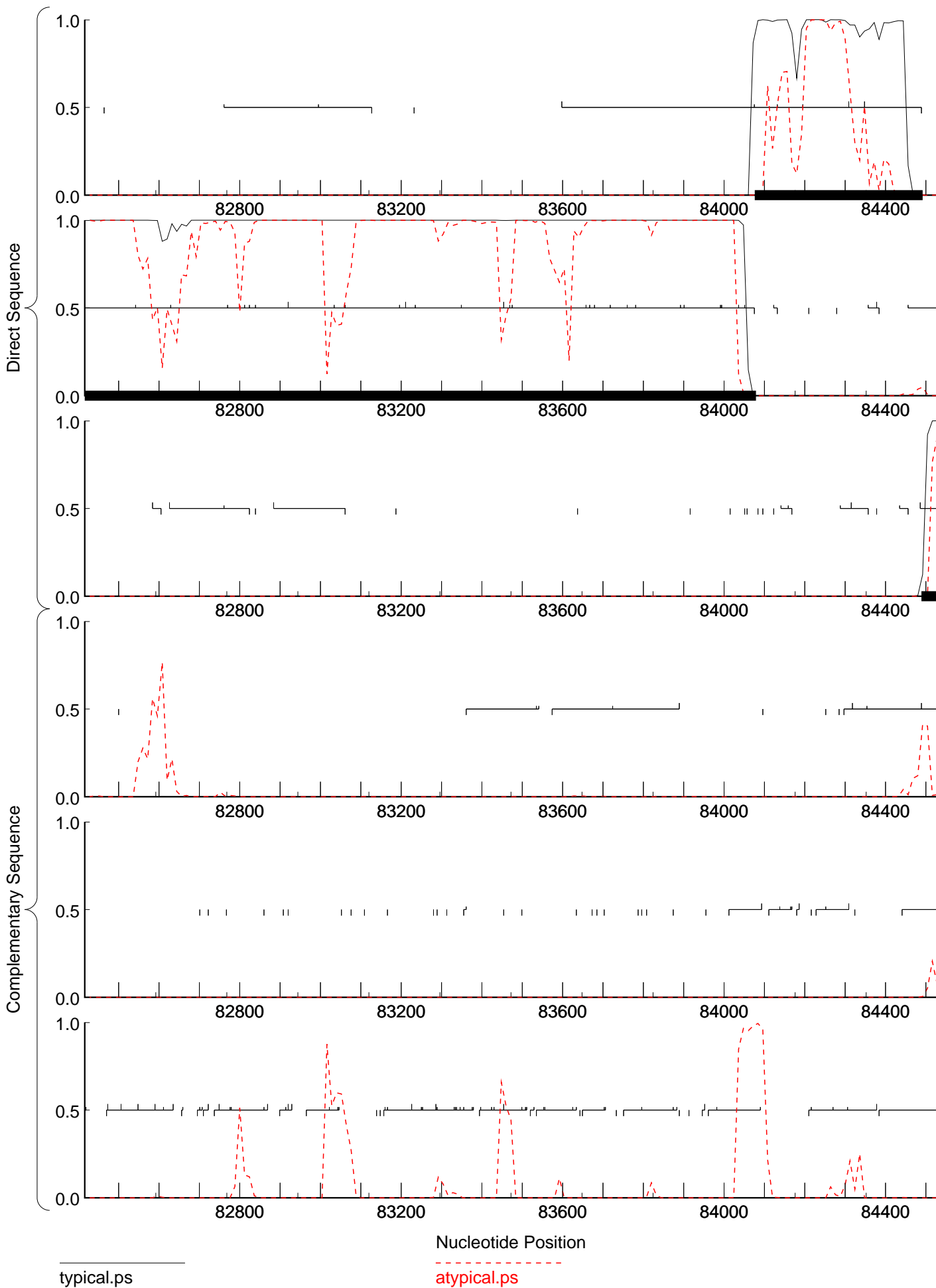
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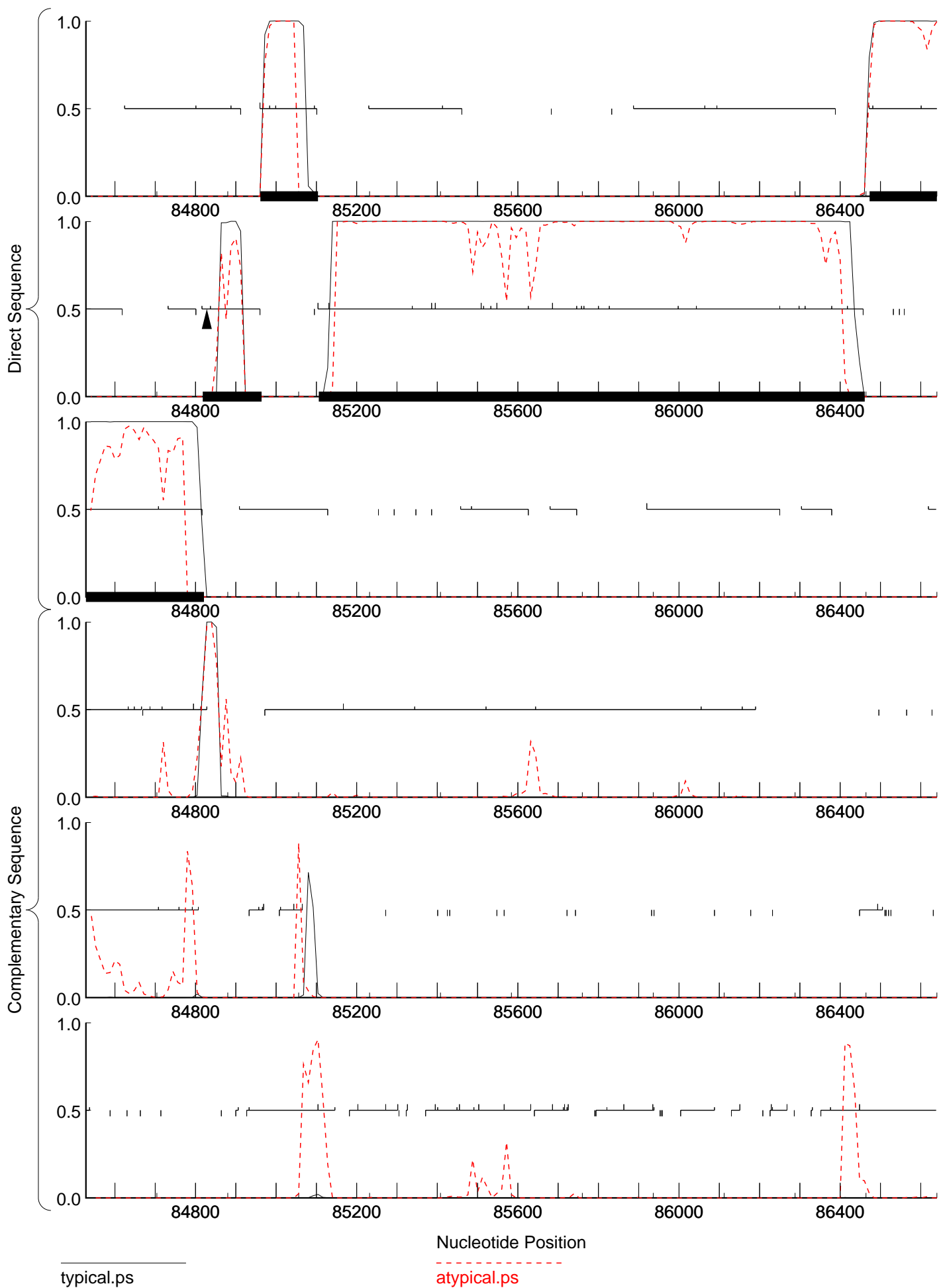
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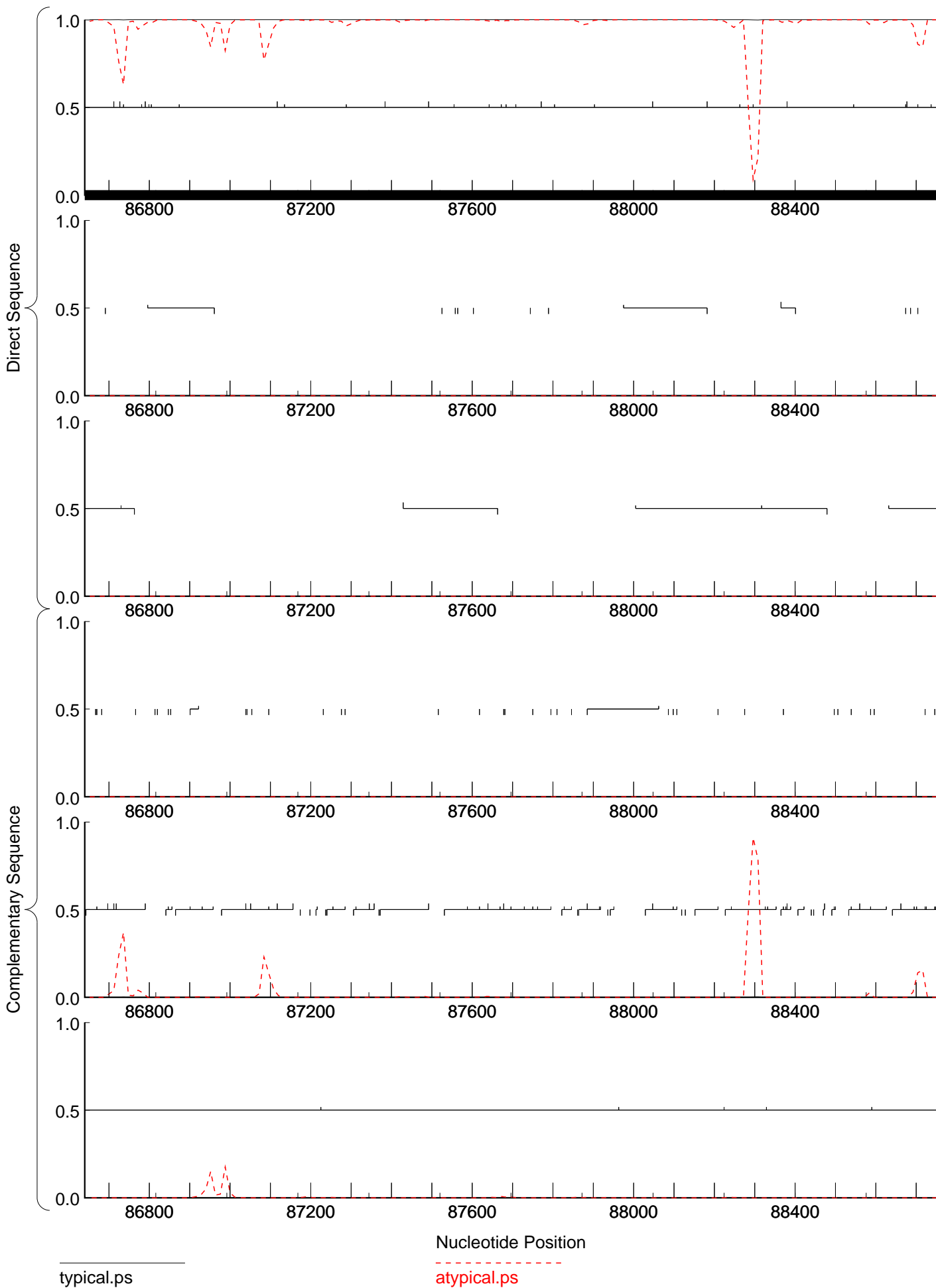


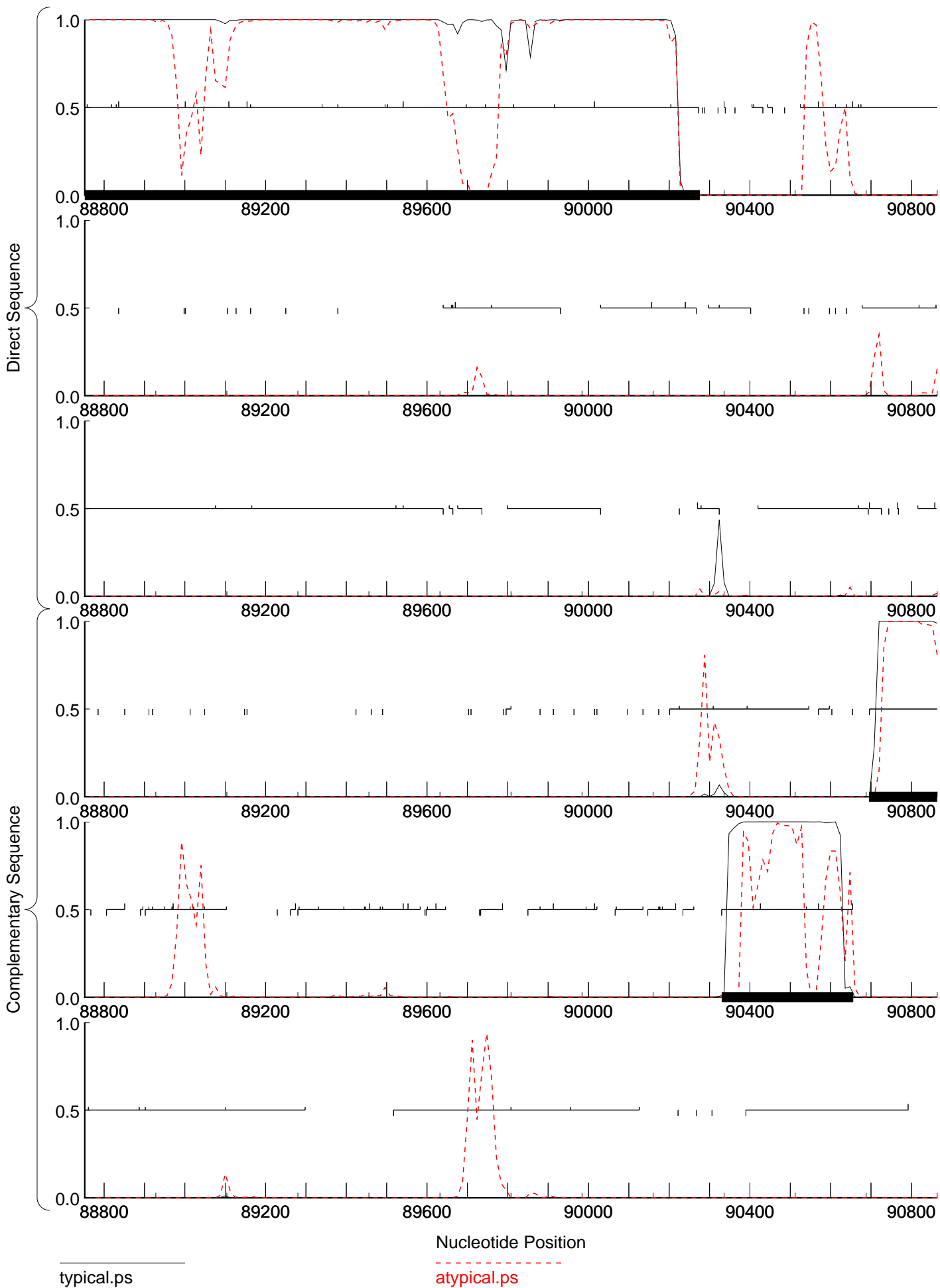
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atypical.ps



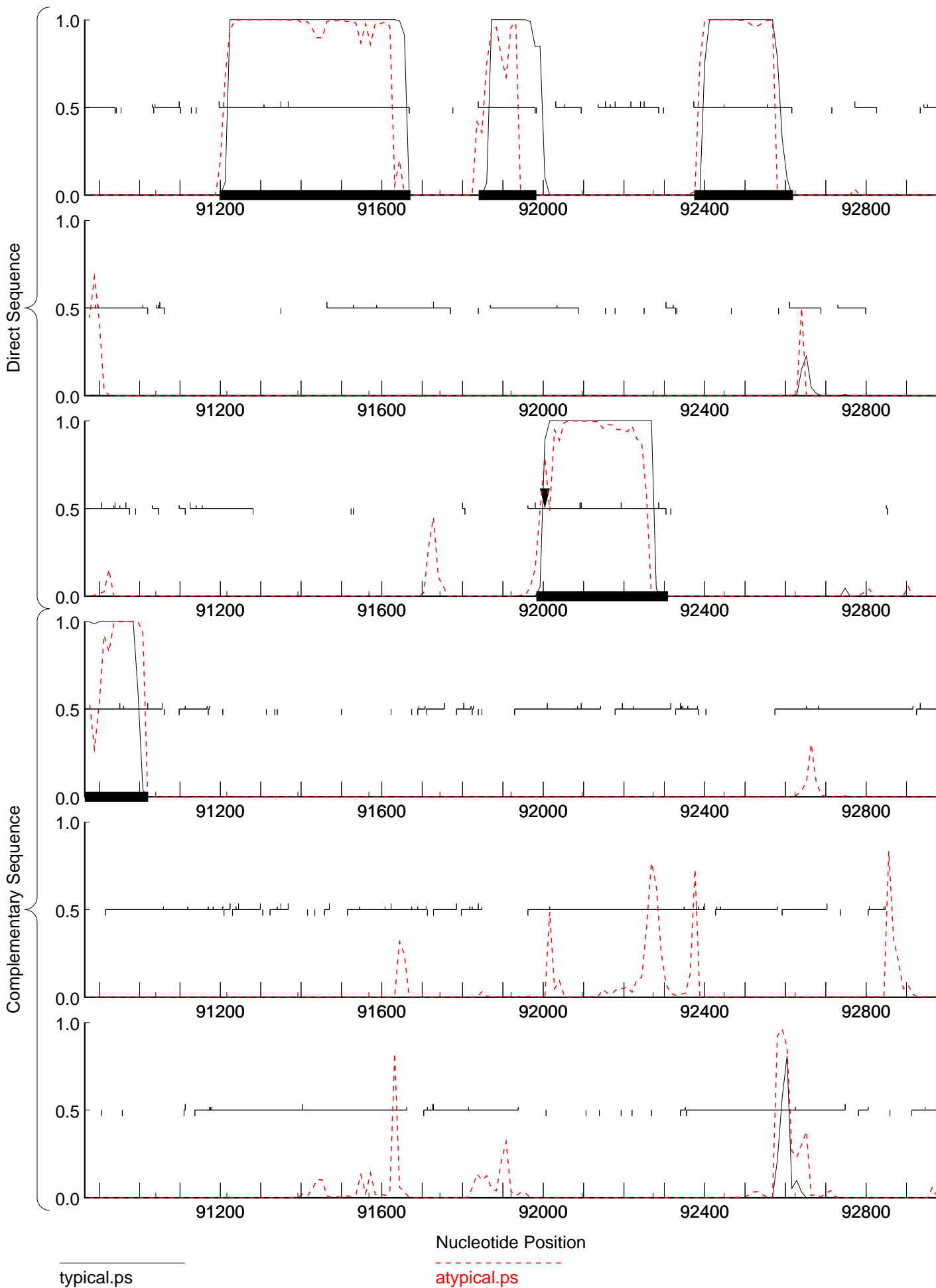


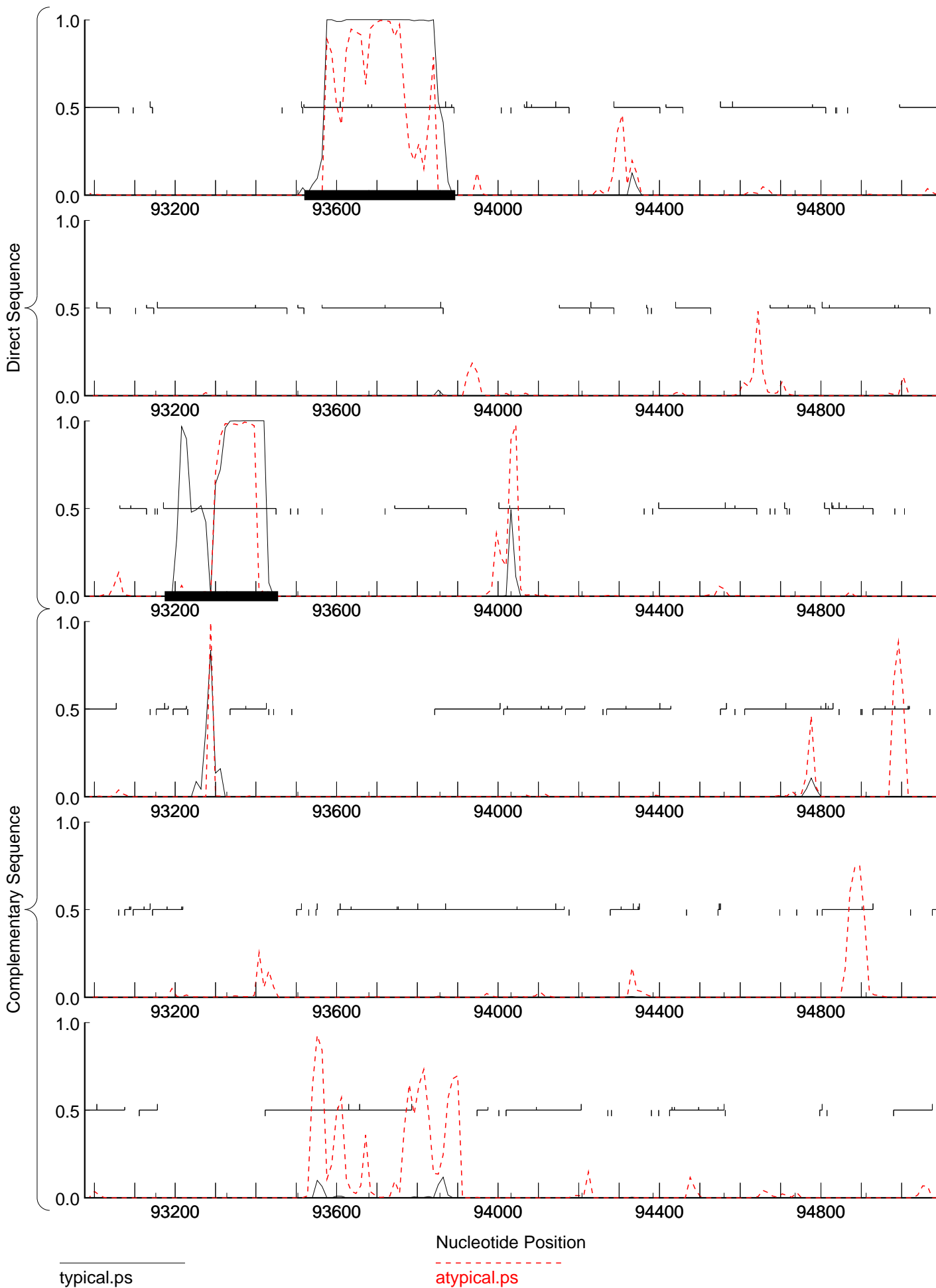




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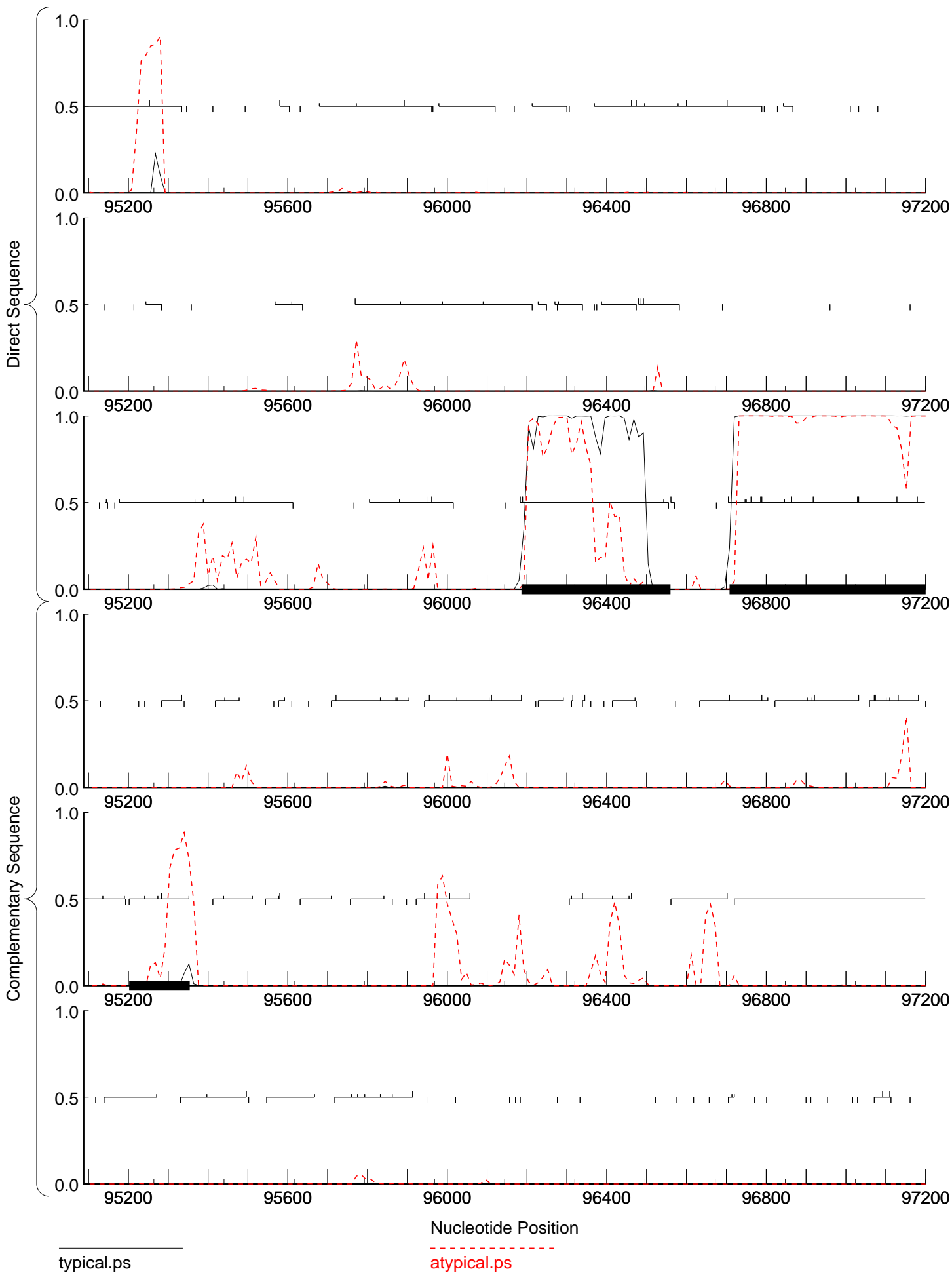
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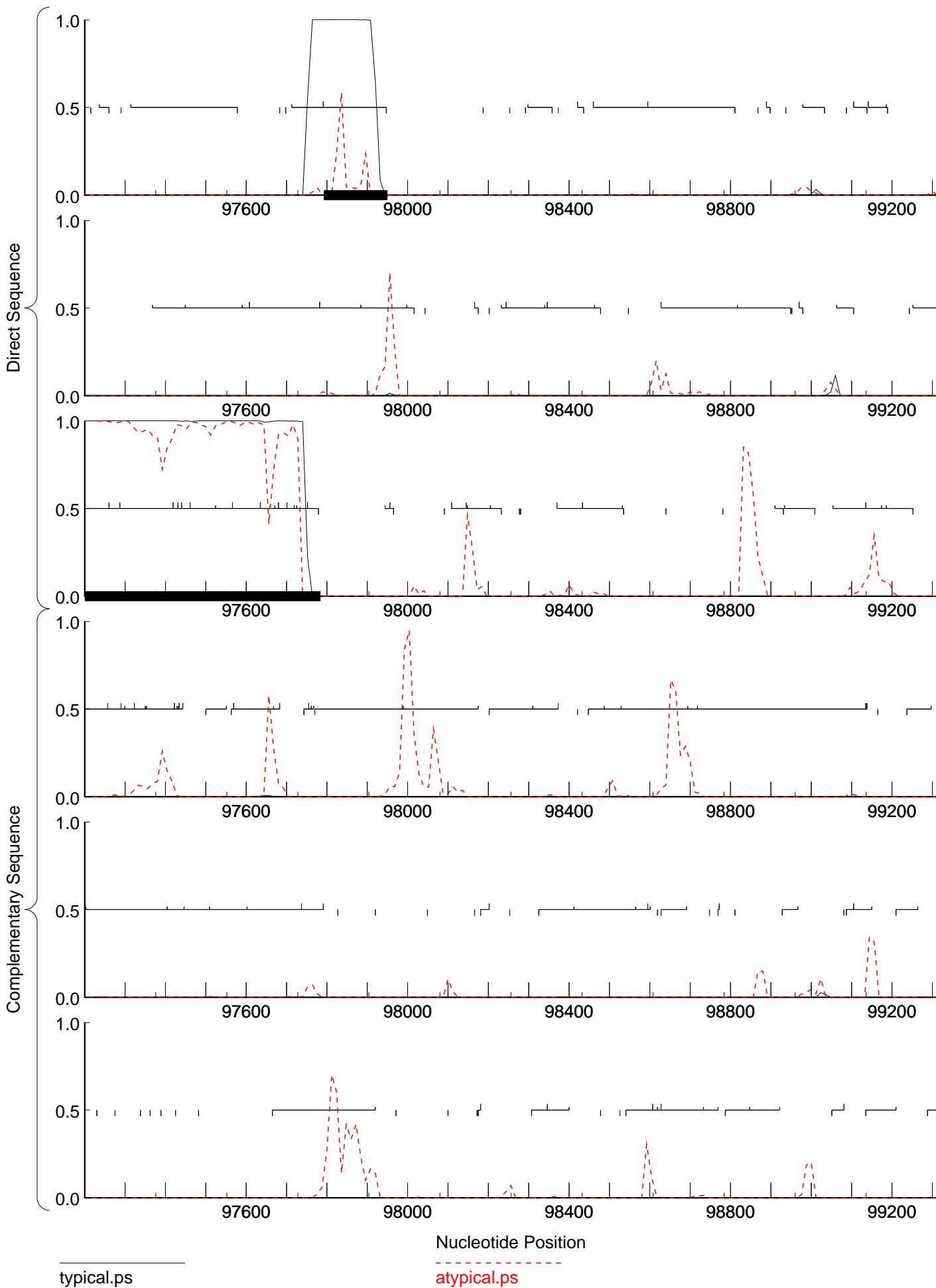


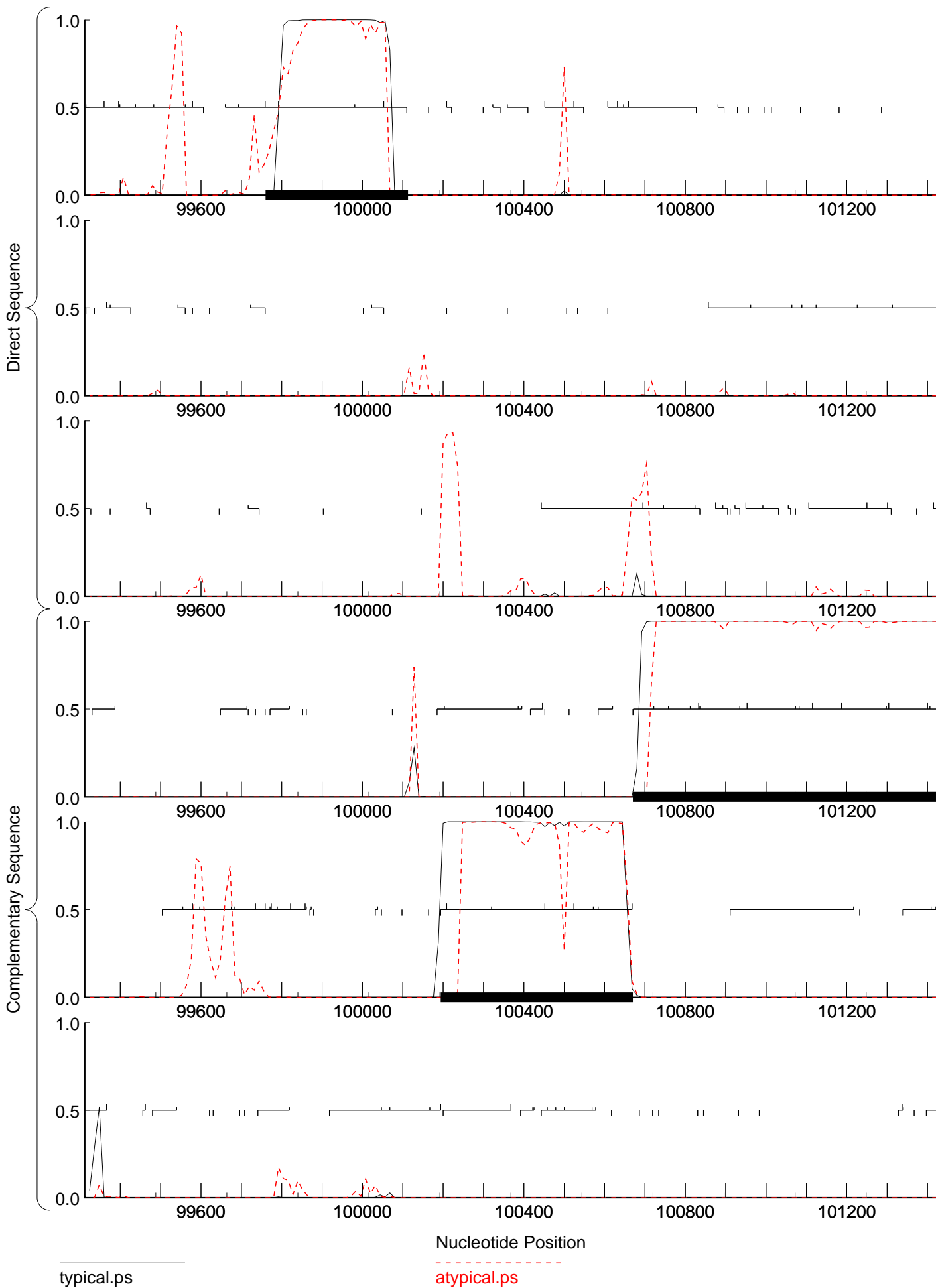


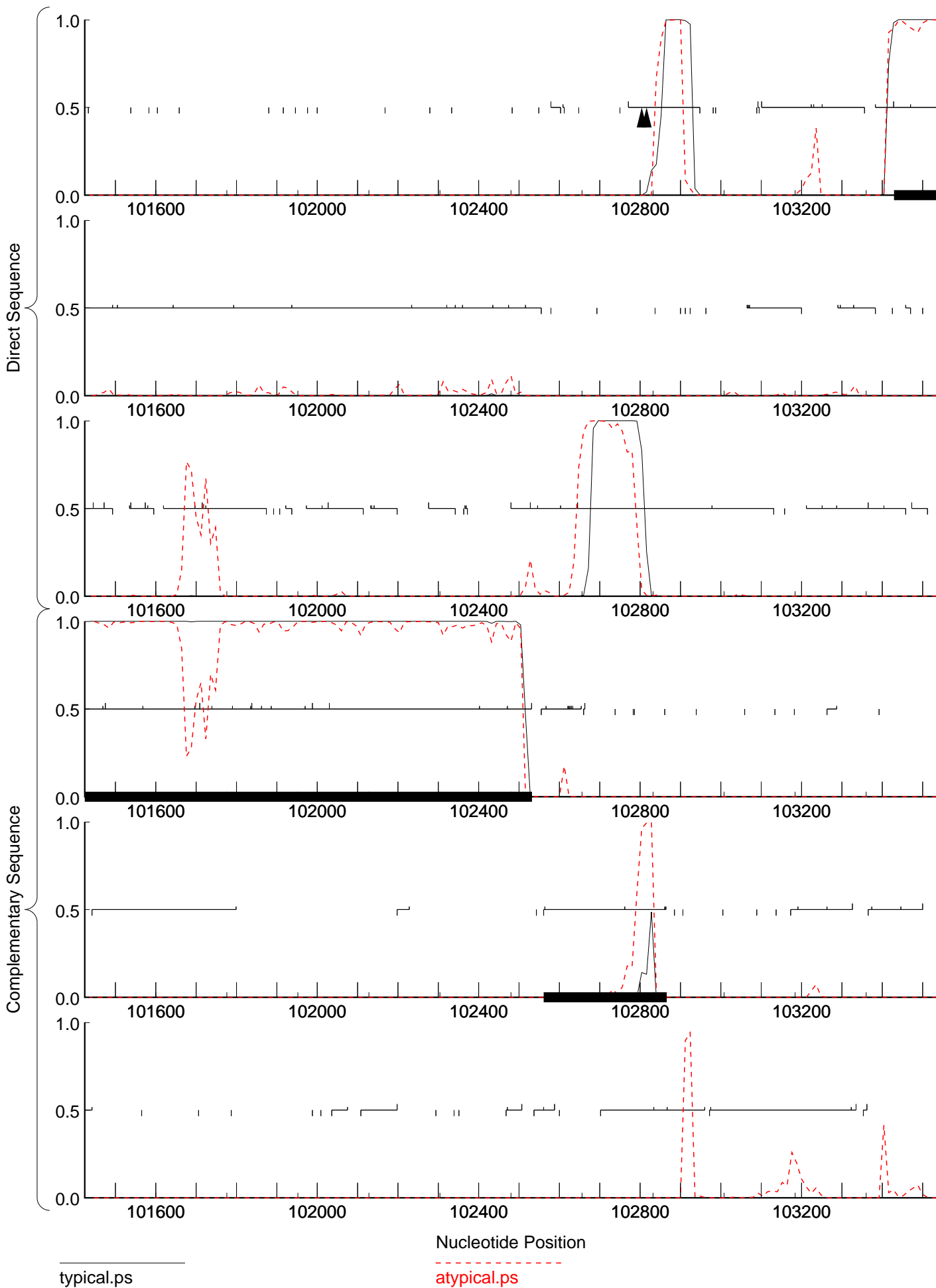
typical.ps

atypical.ps



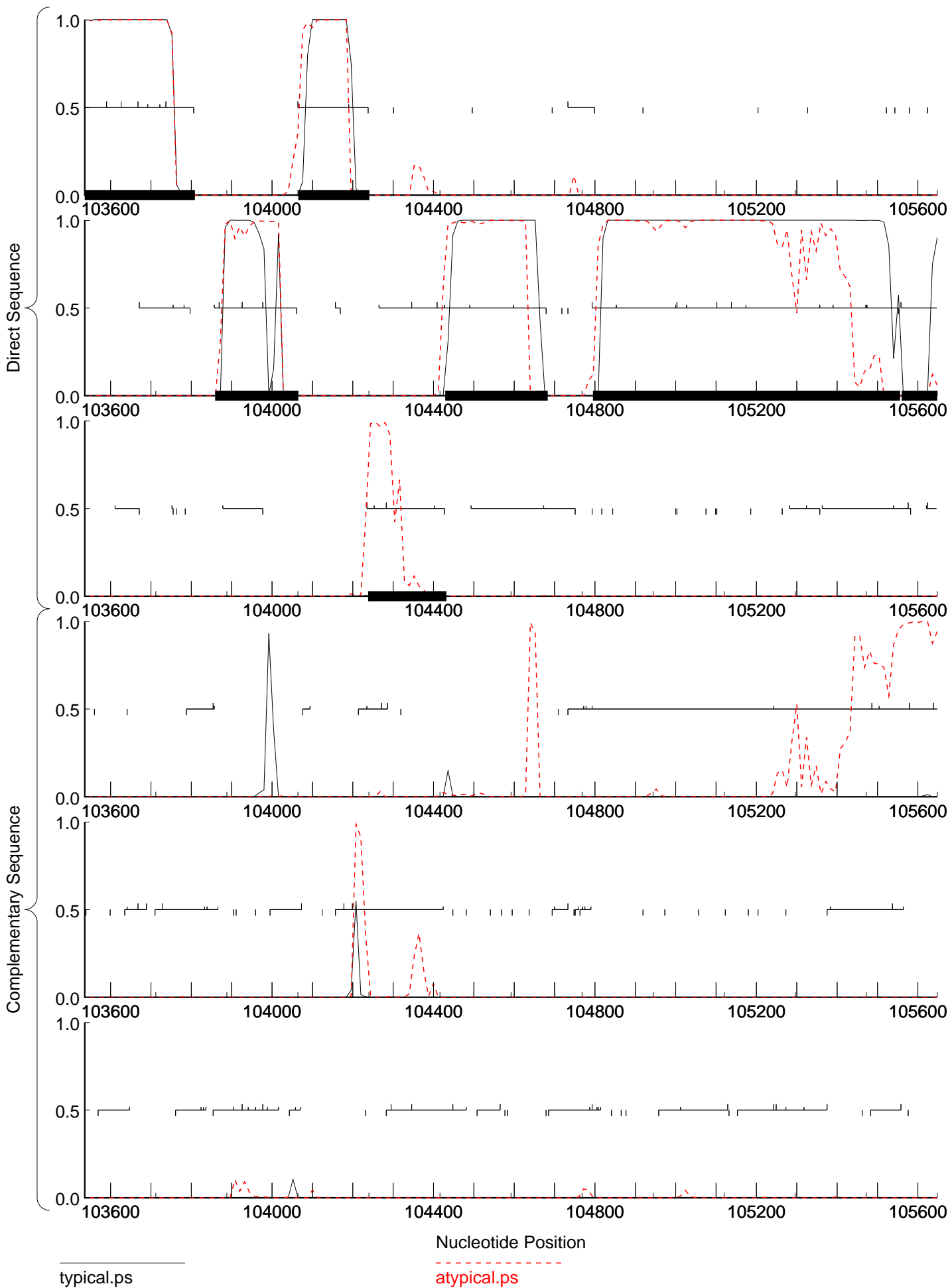


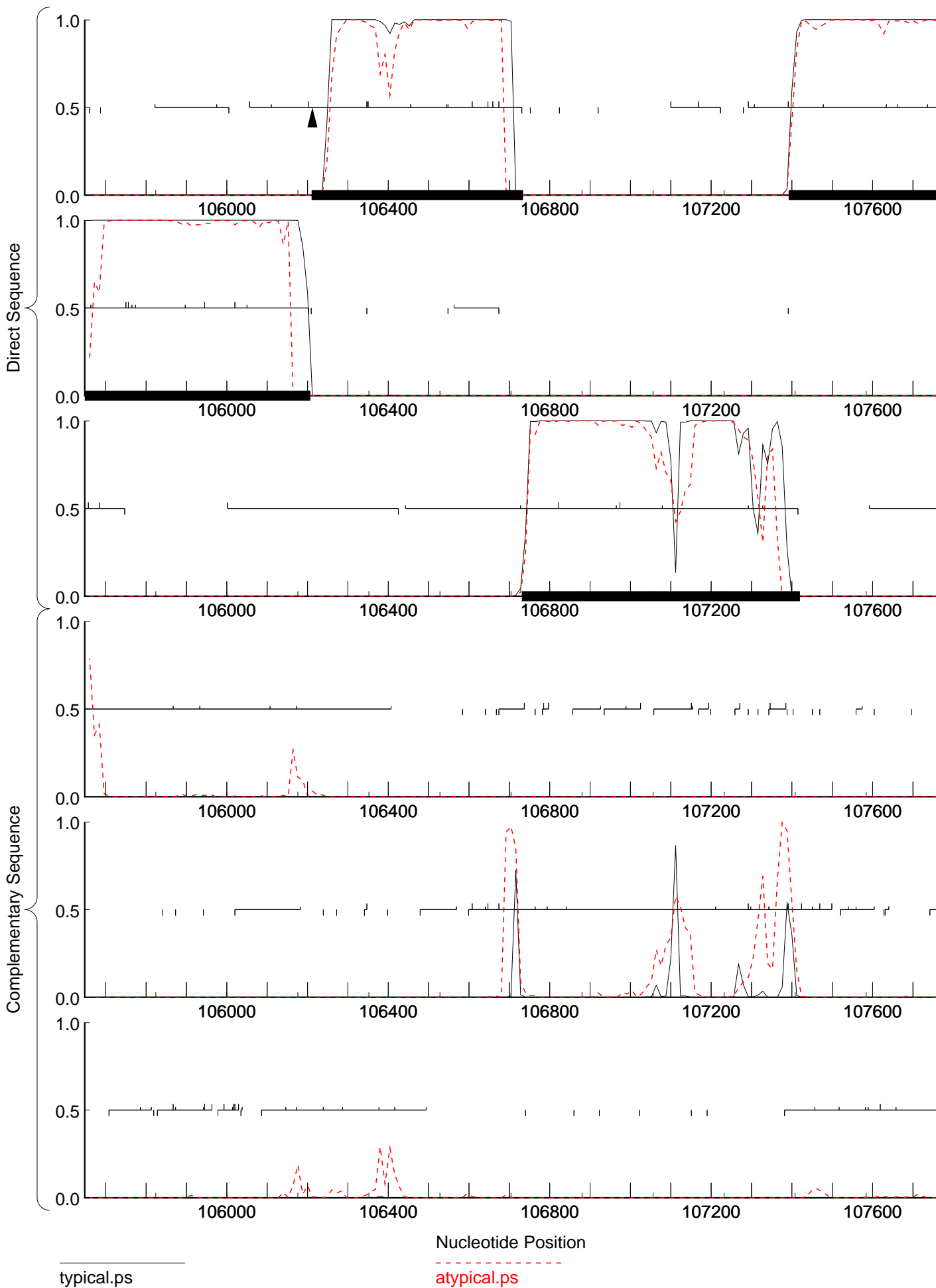


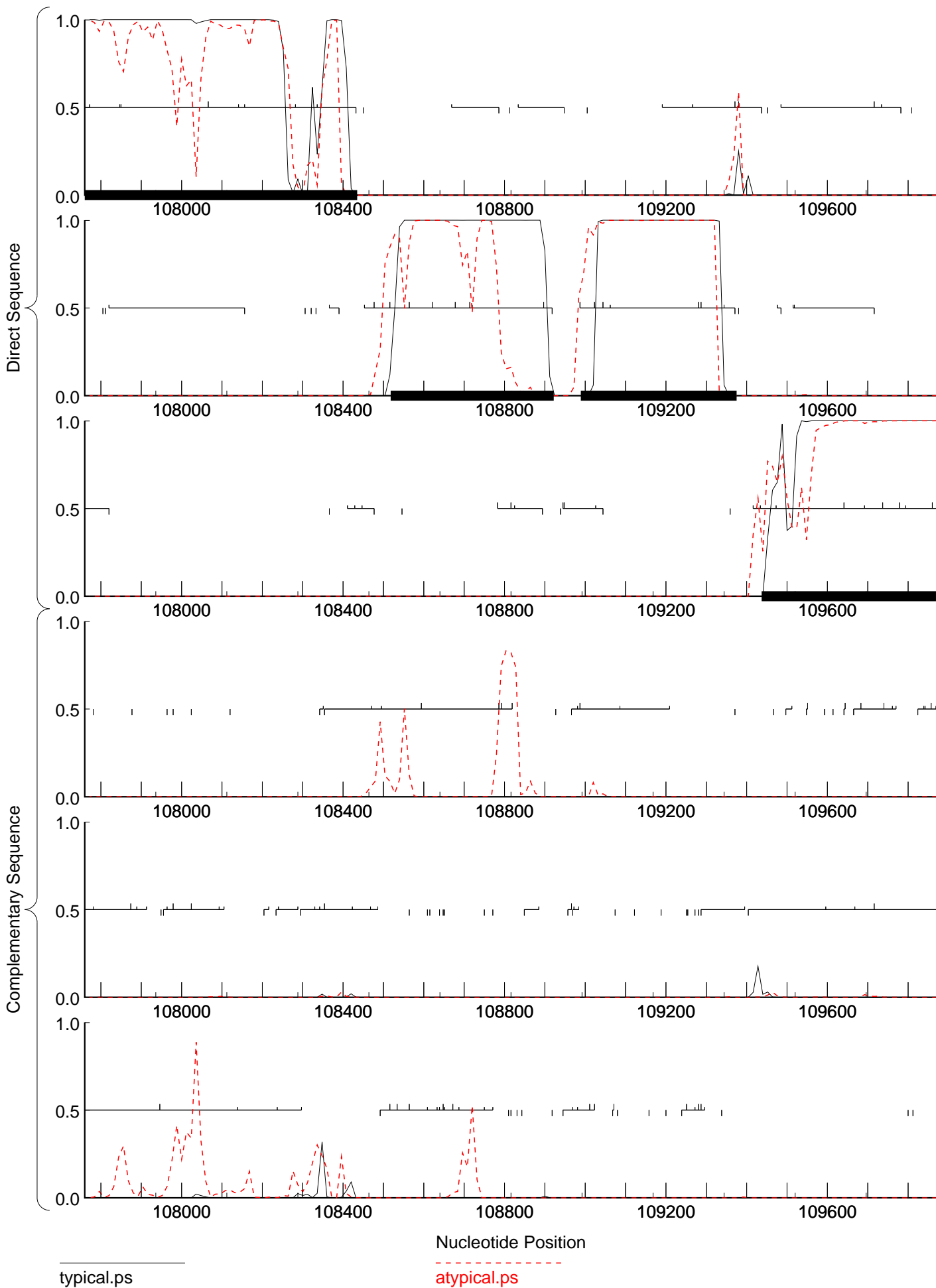


typical.ps

atypical.ps

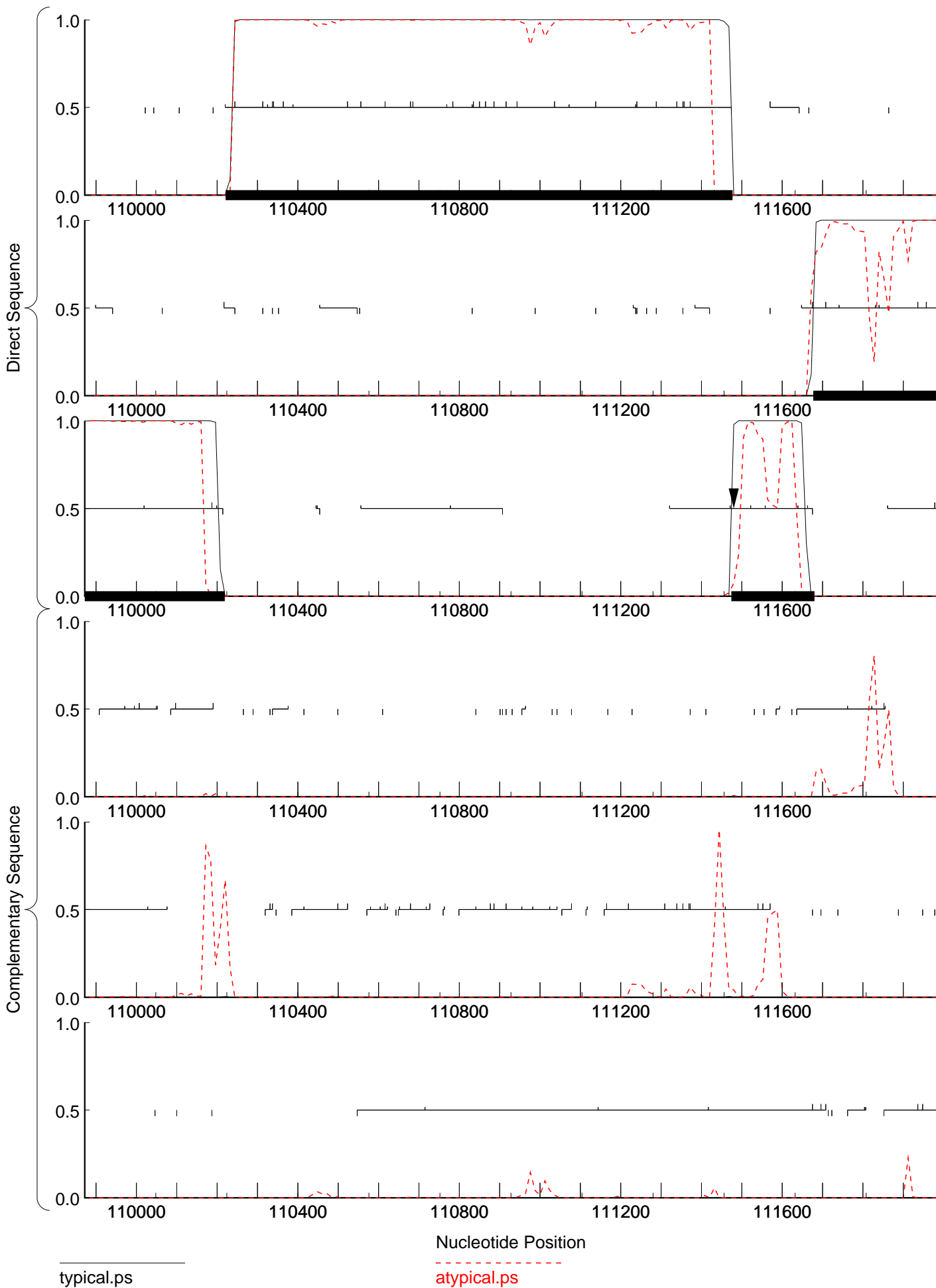






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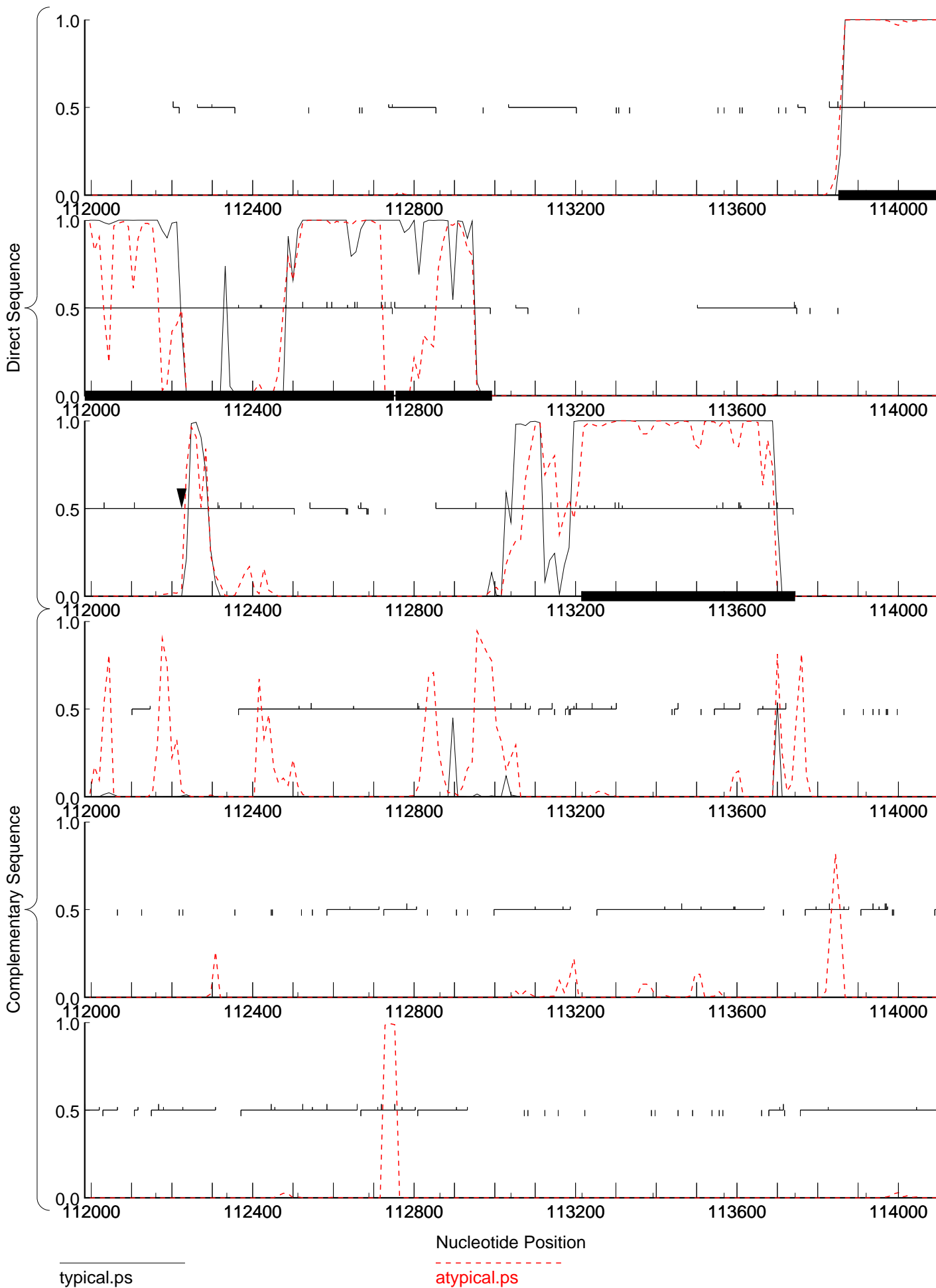
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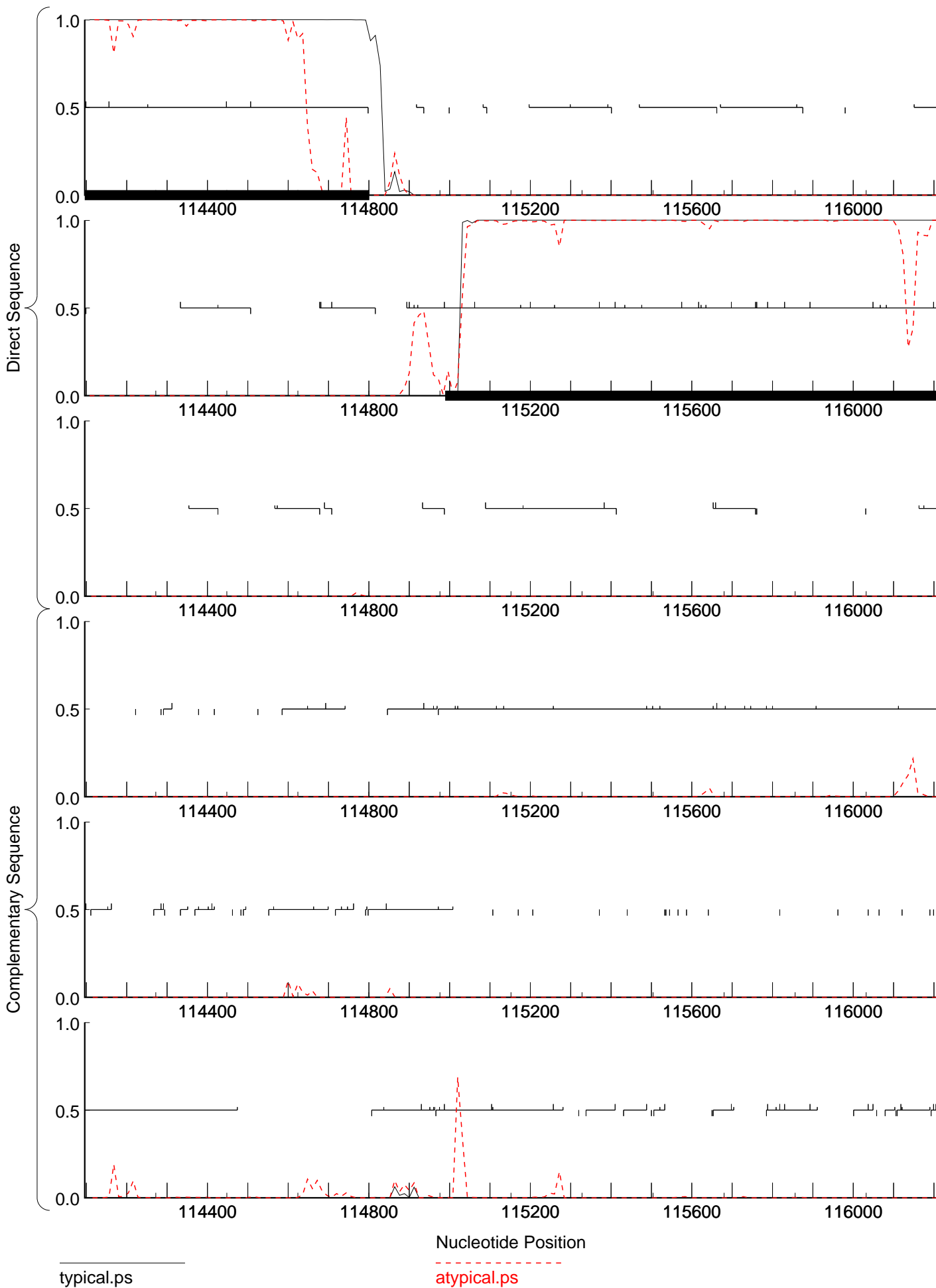


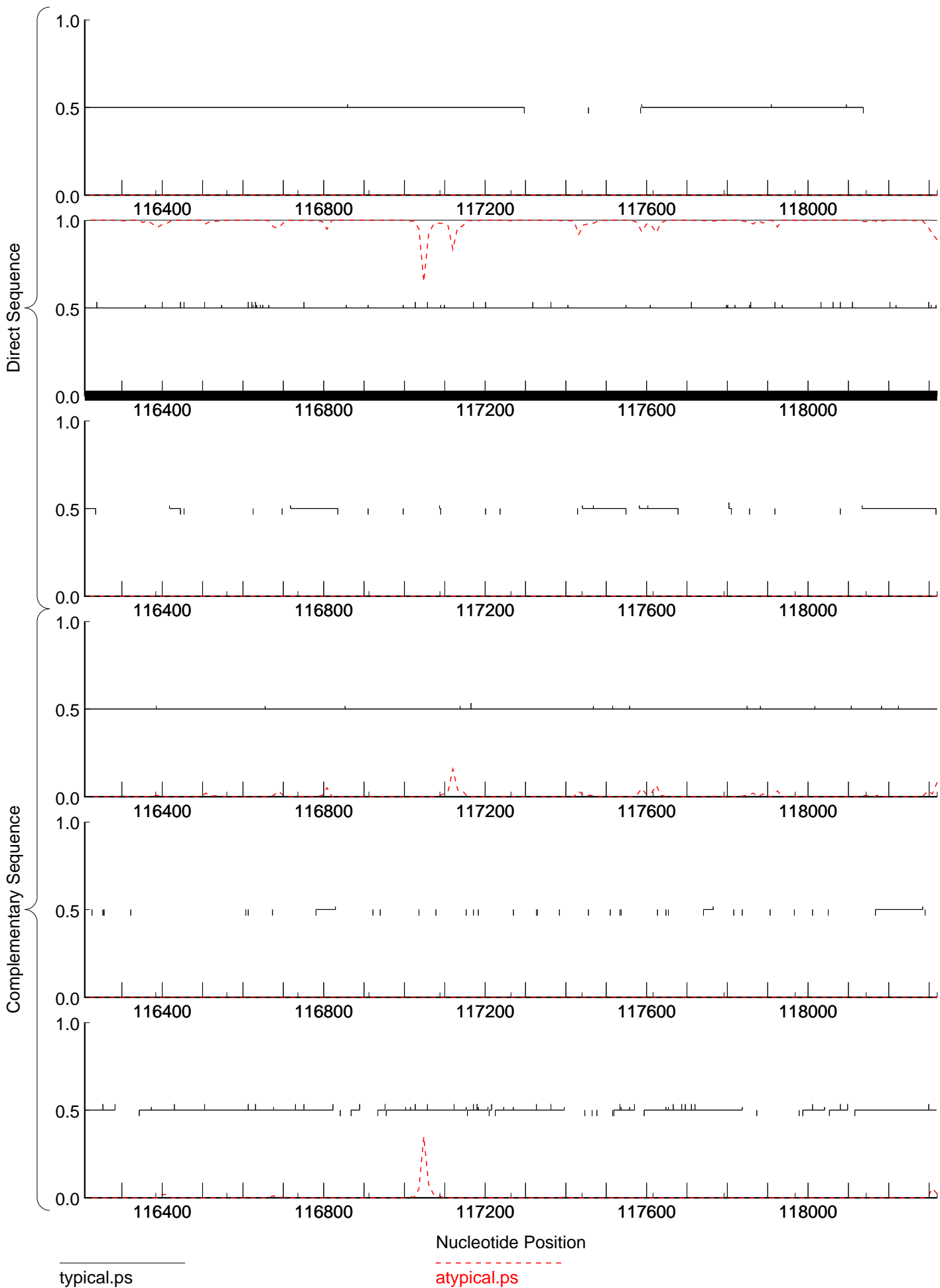
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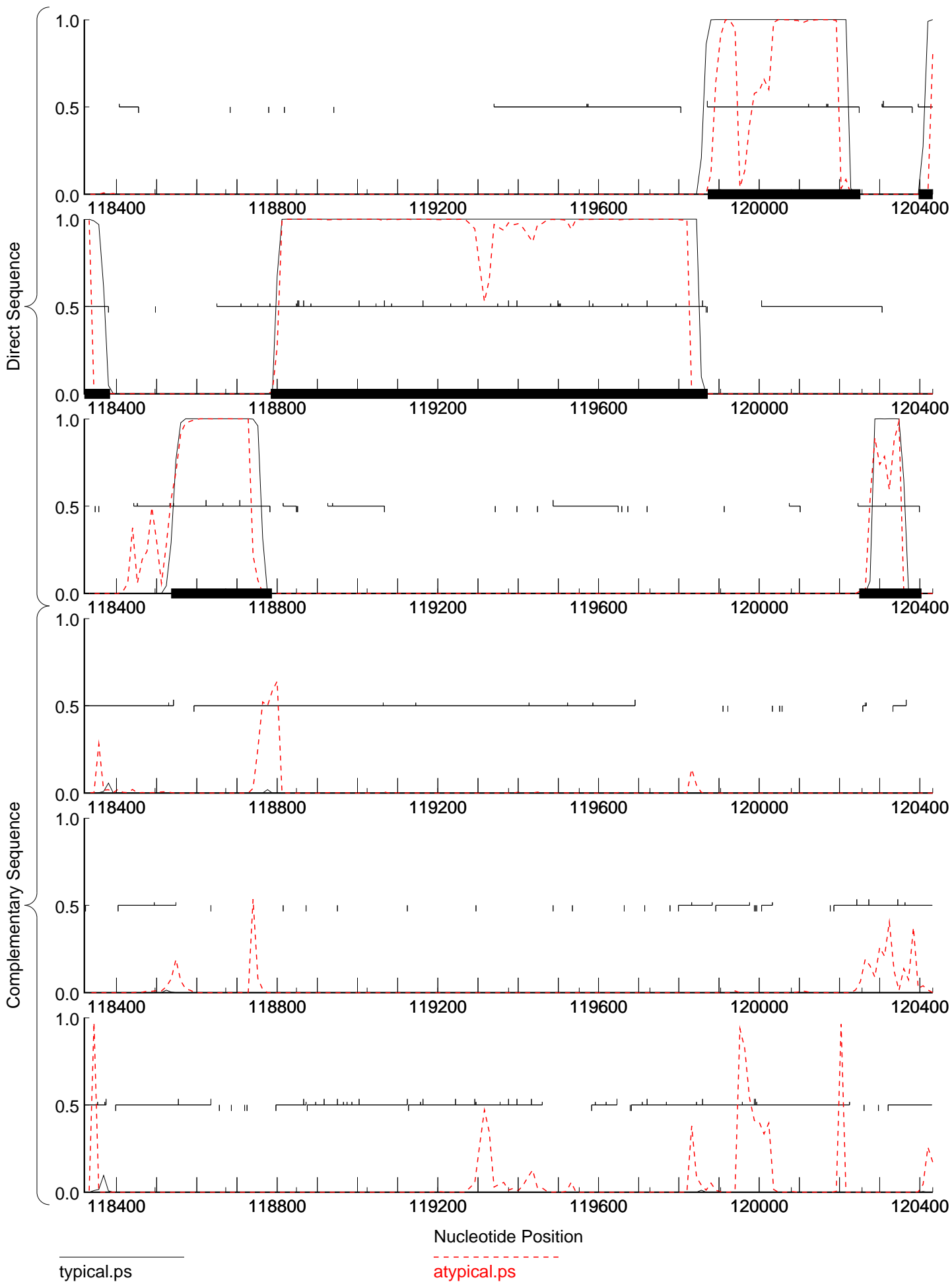
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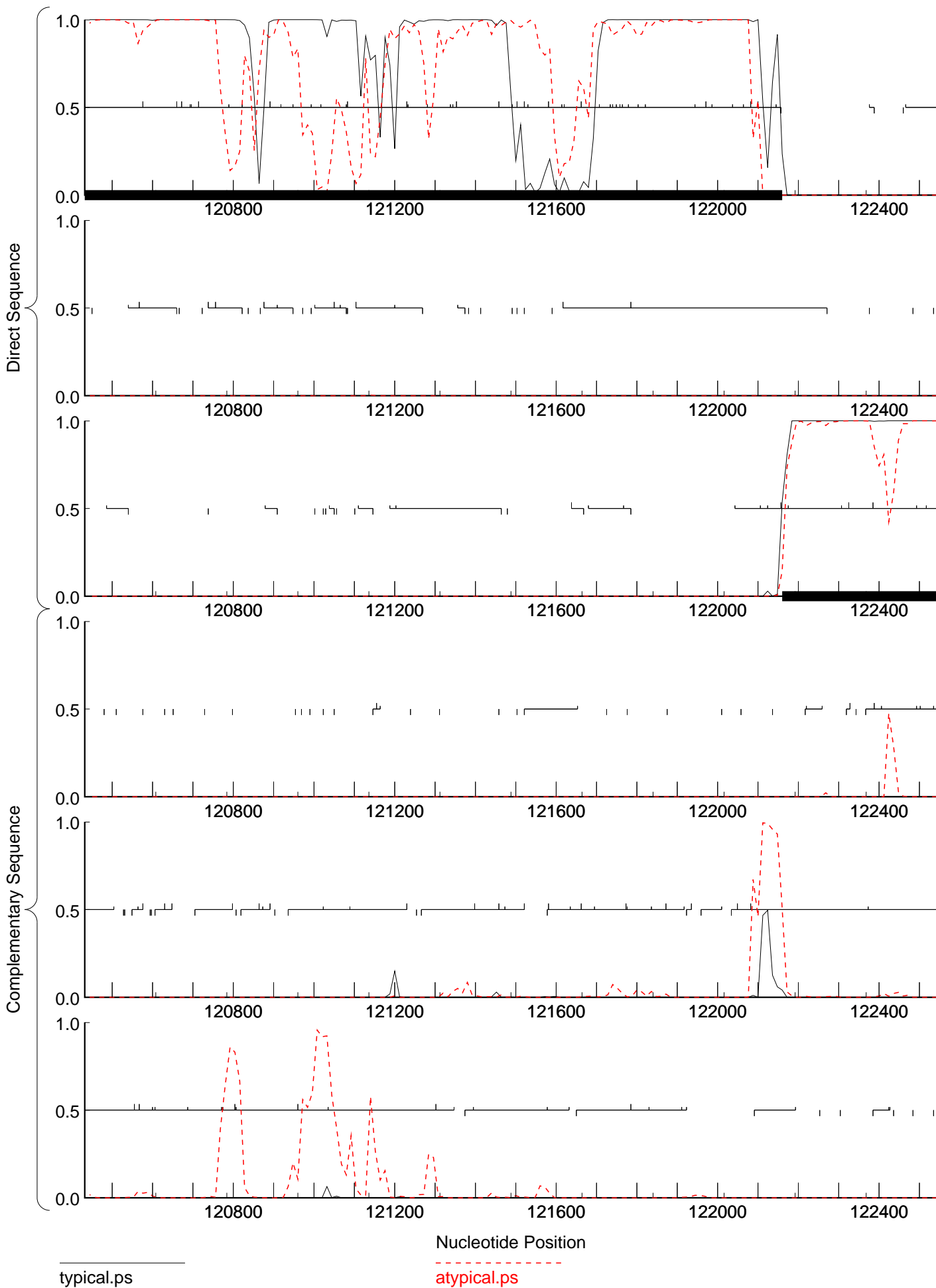
GeneMark.hmm prediction

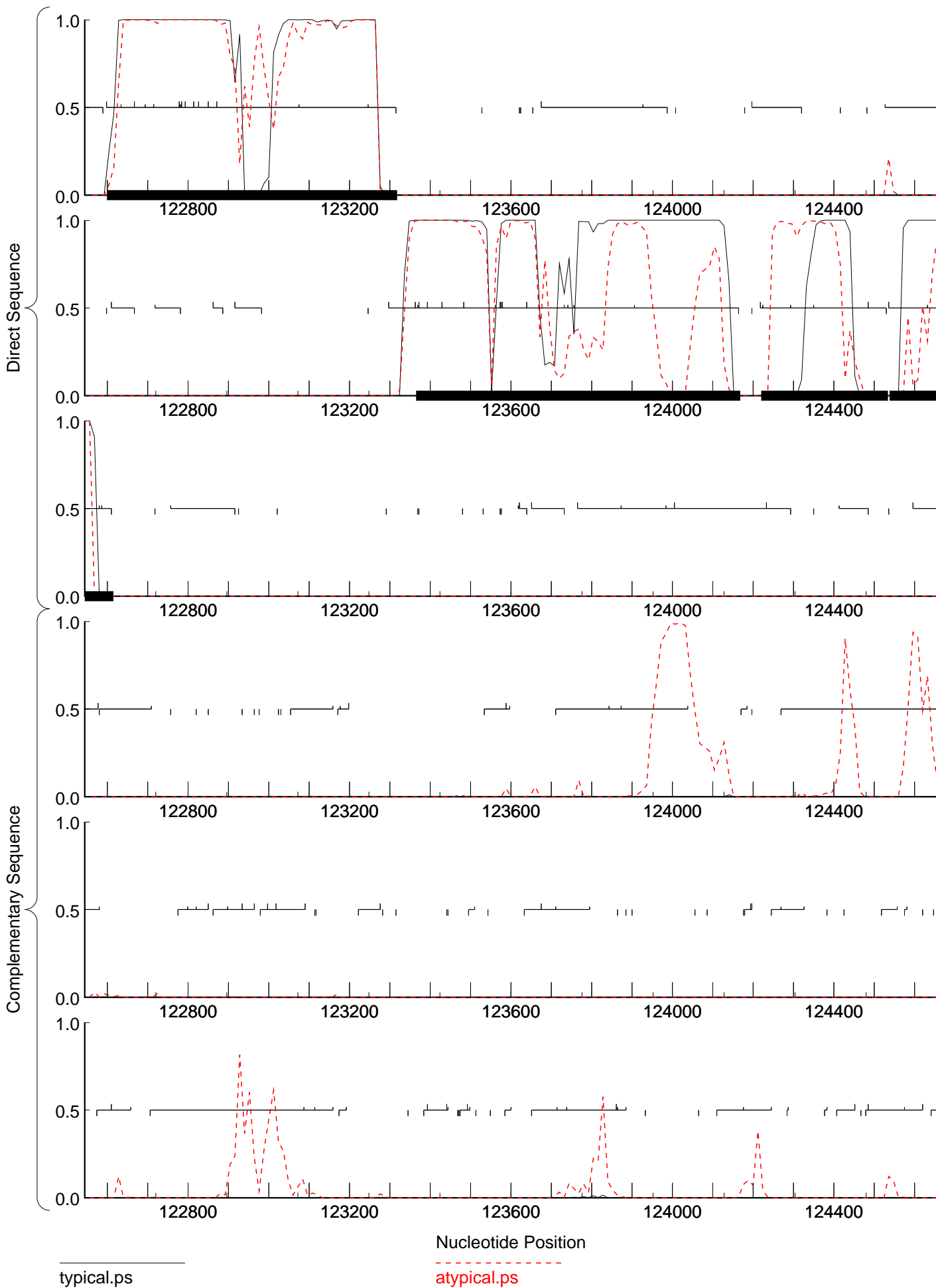


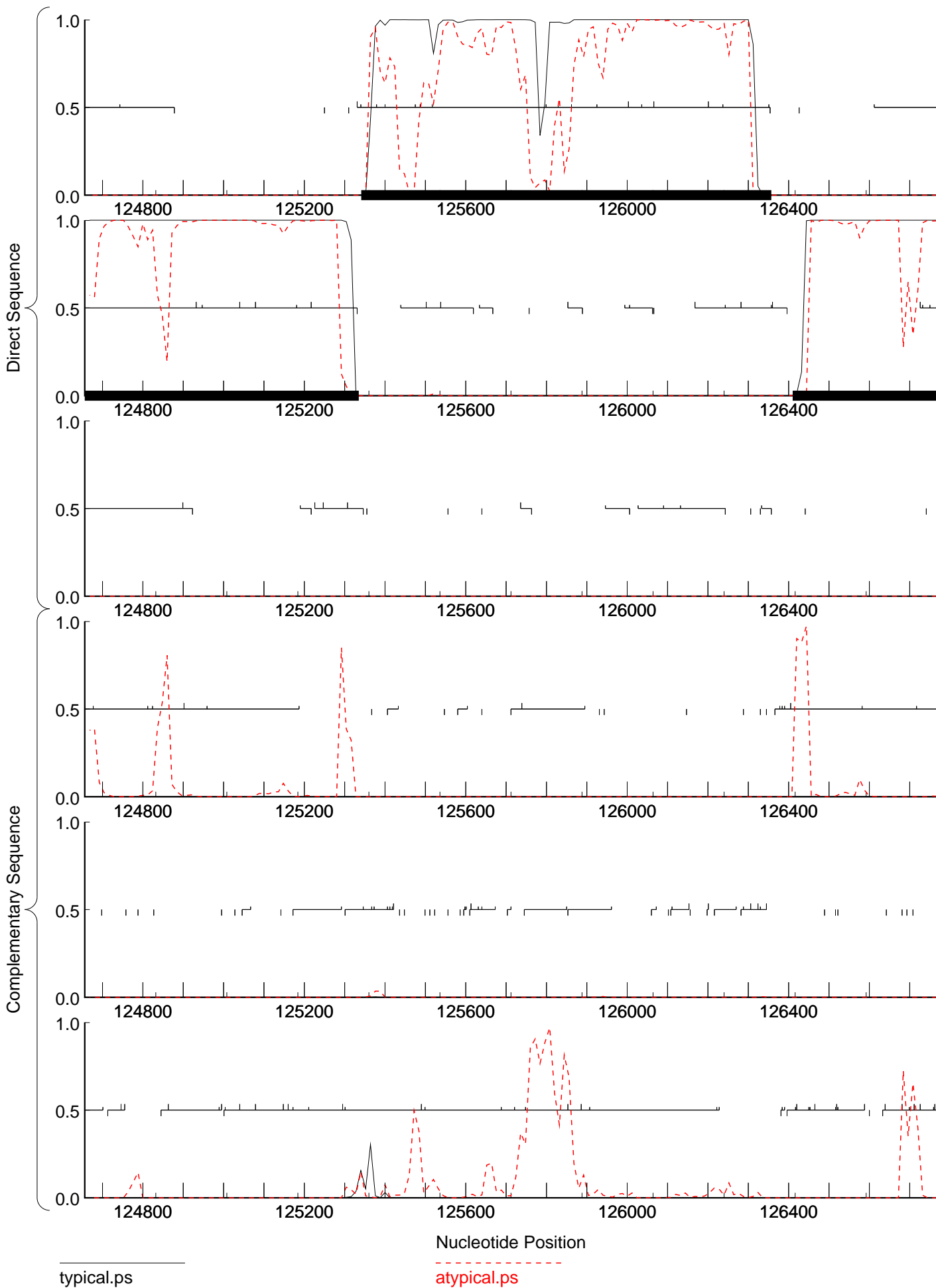


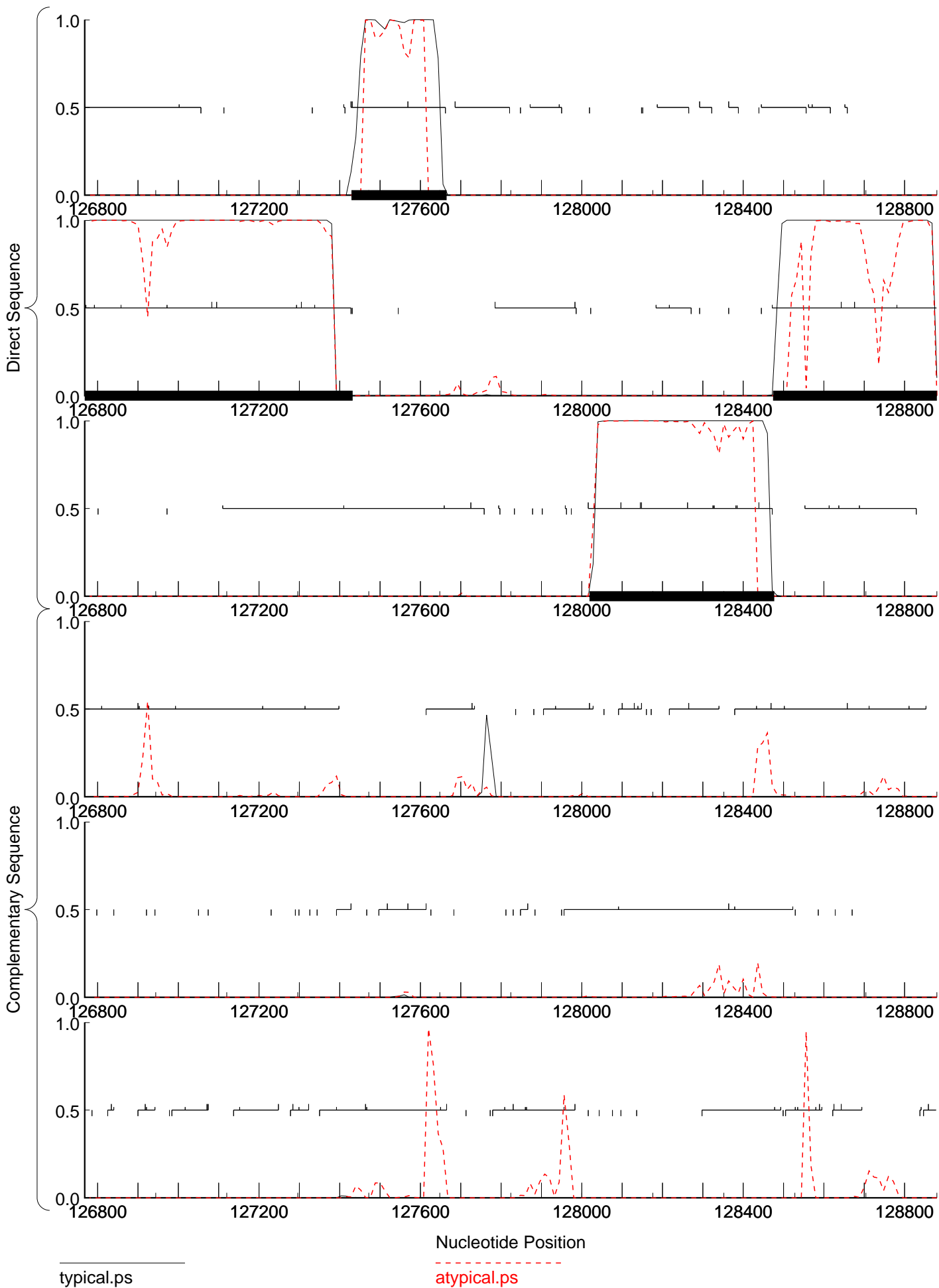


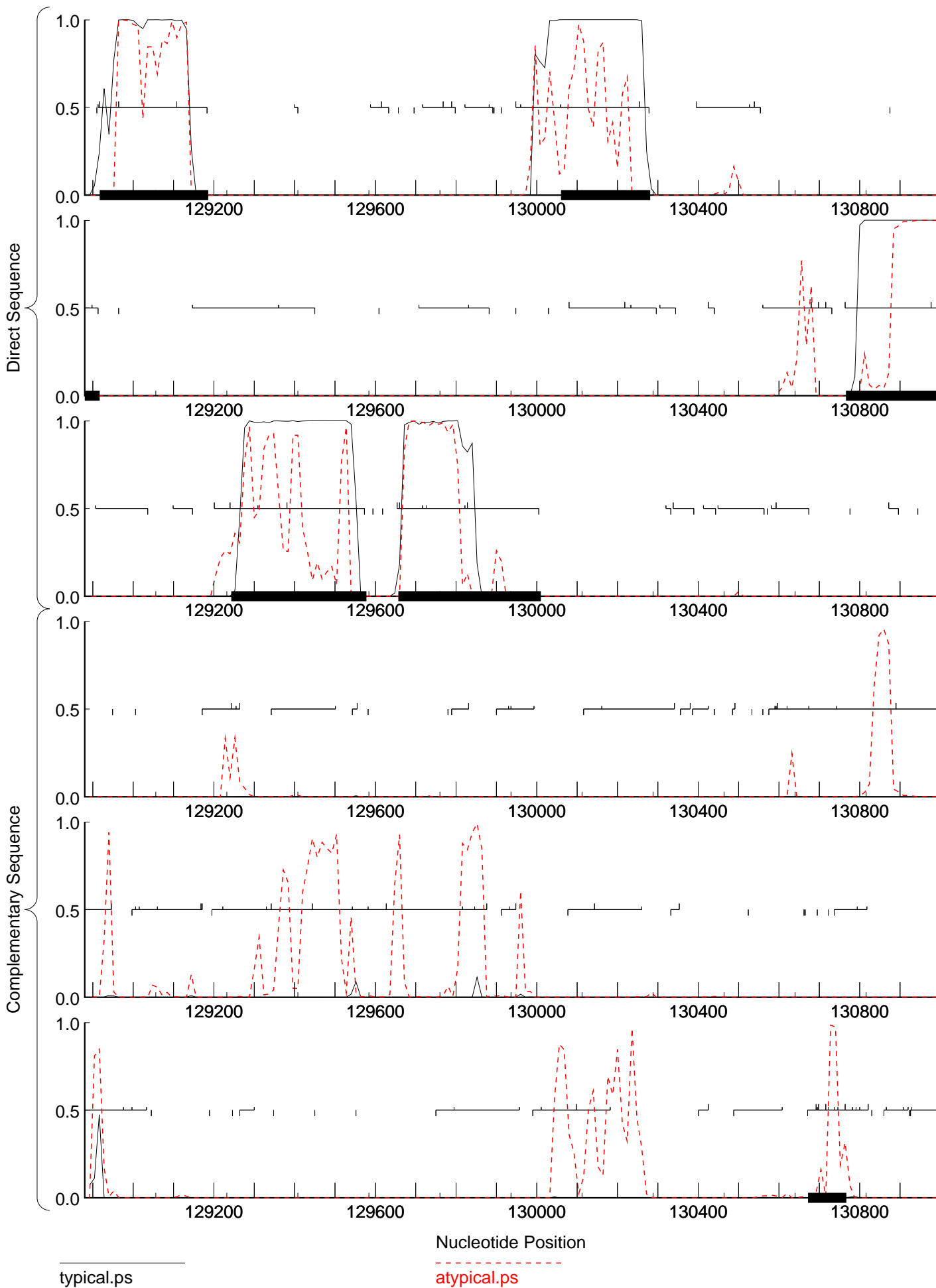






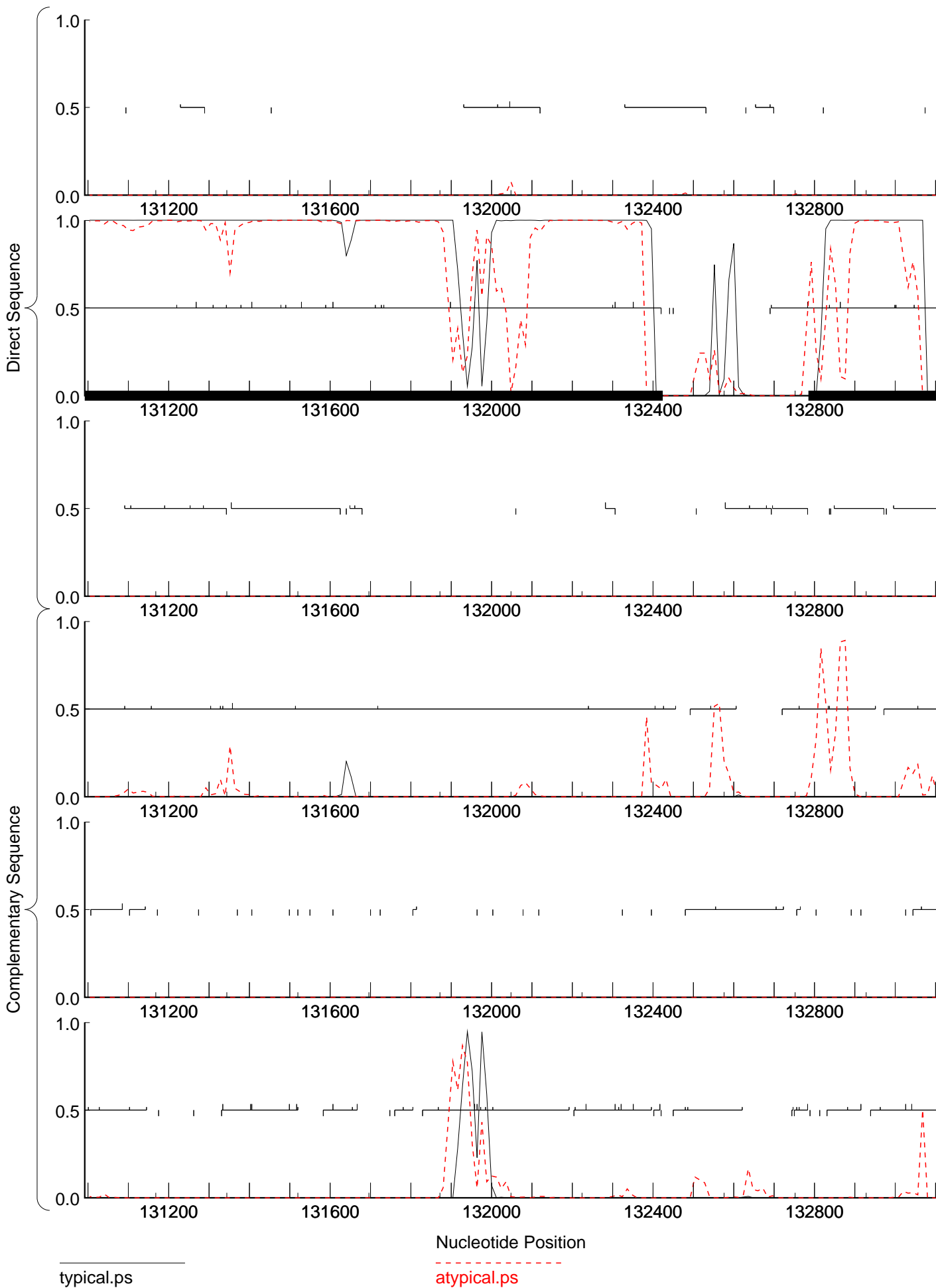




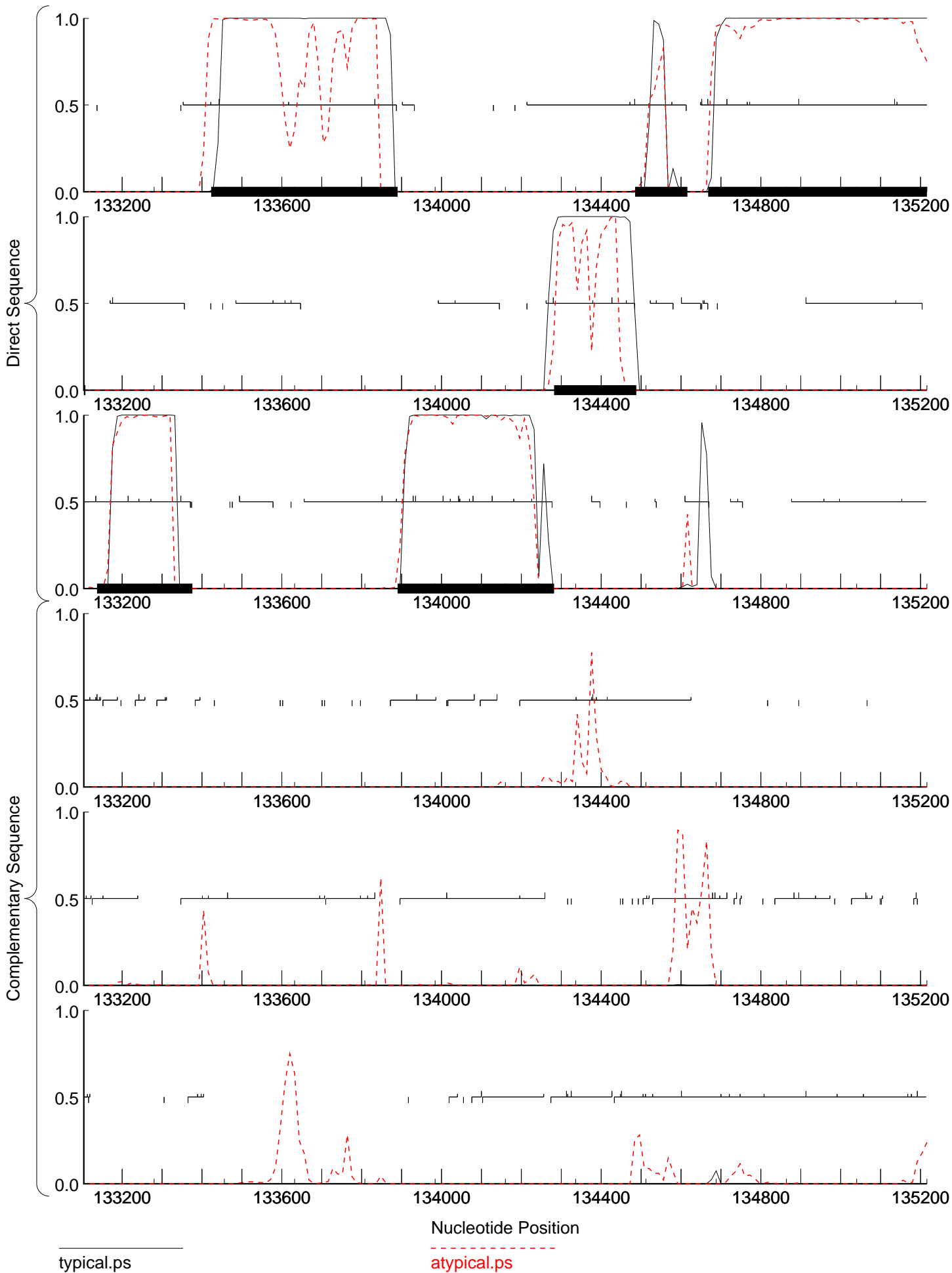


typical.ps

atypical.ps

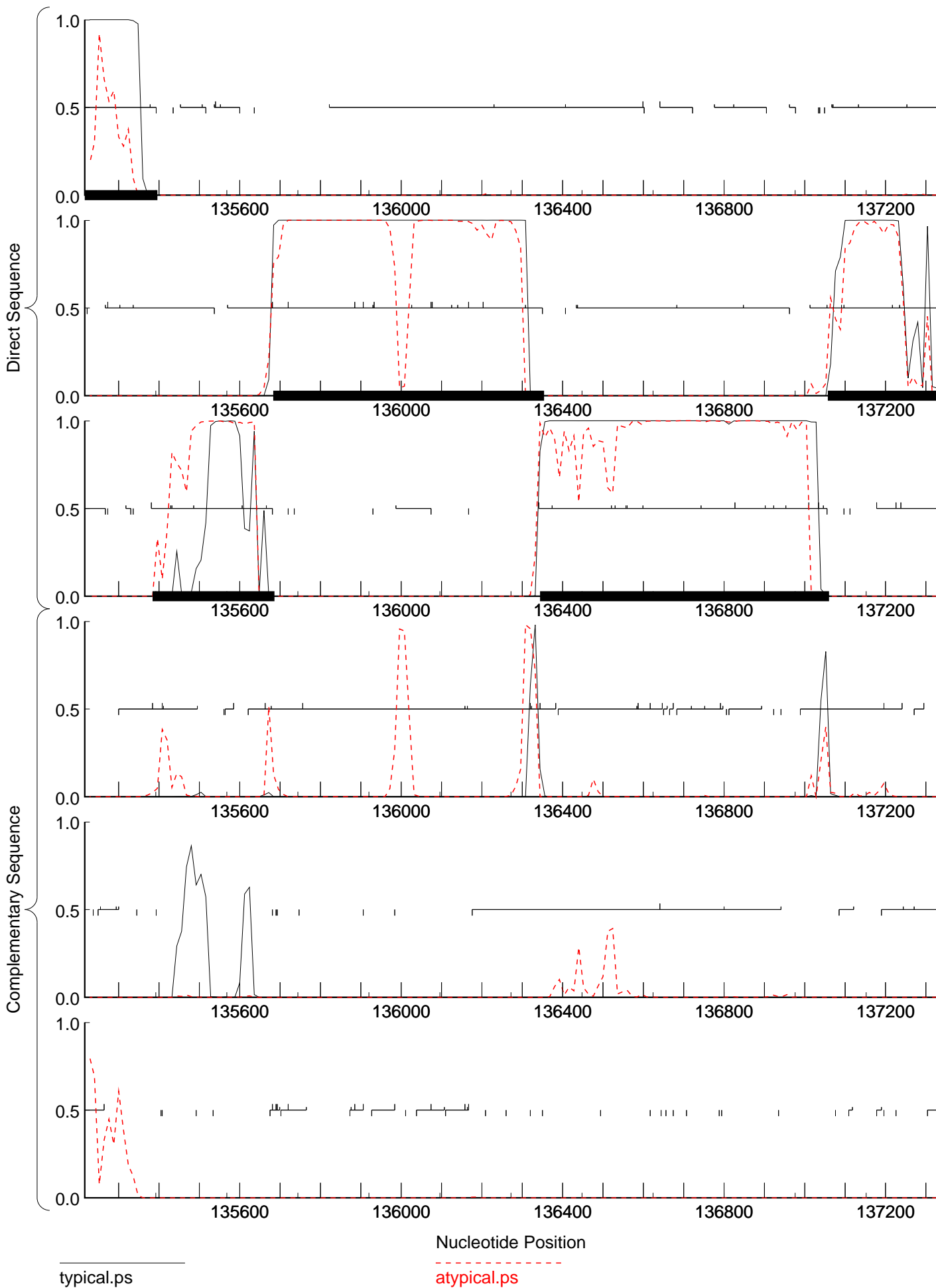


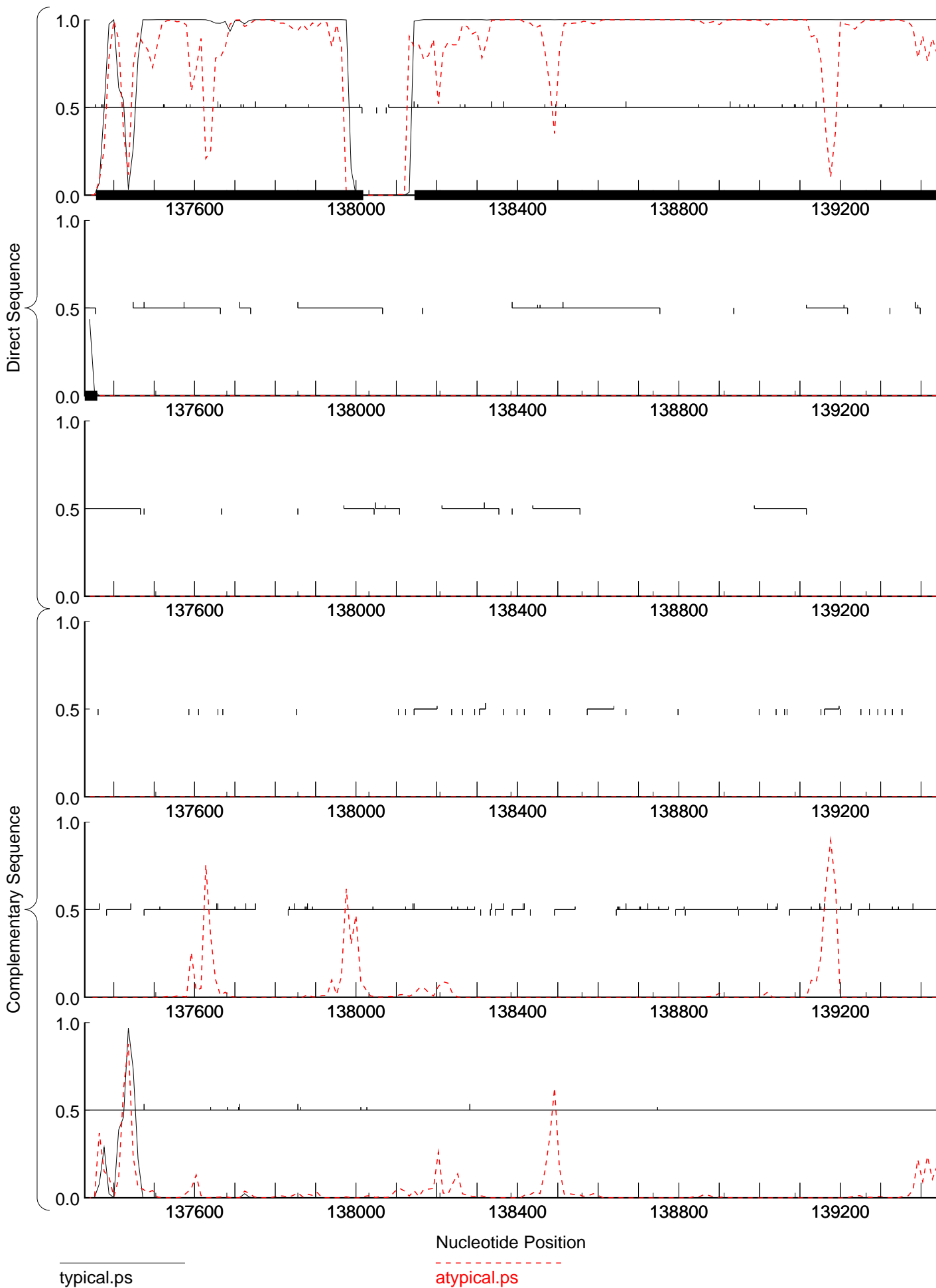
GeneMark.hmm prediction

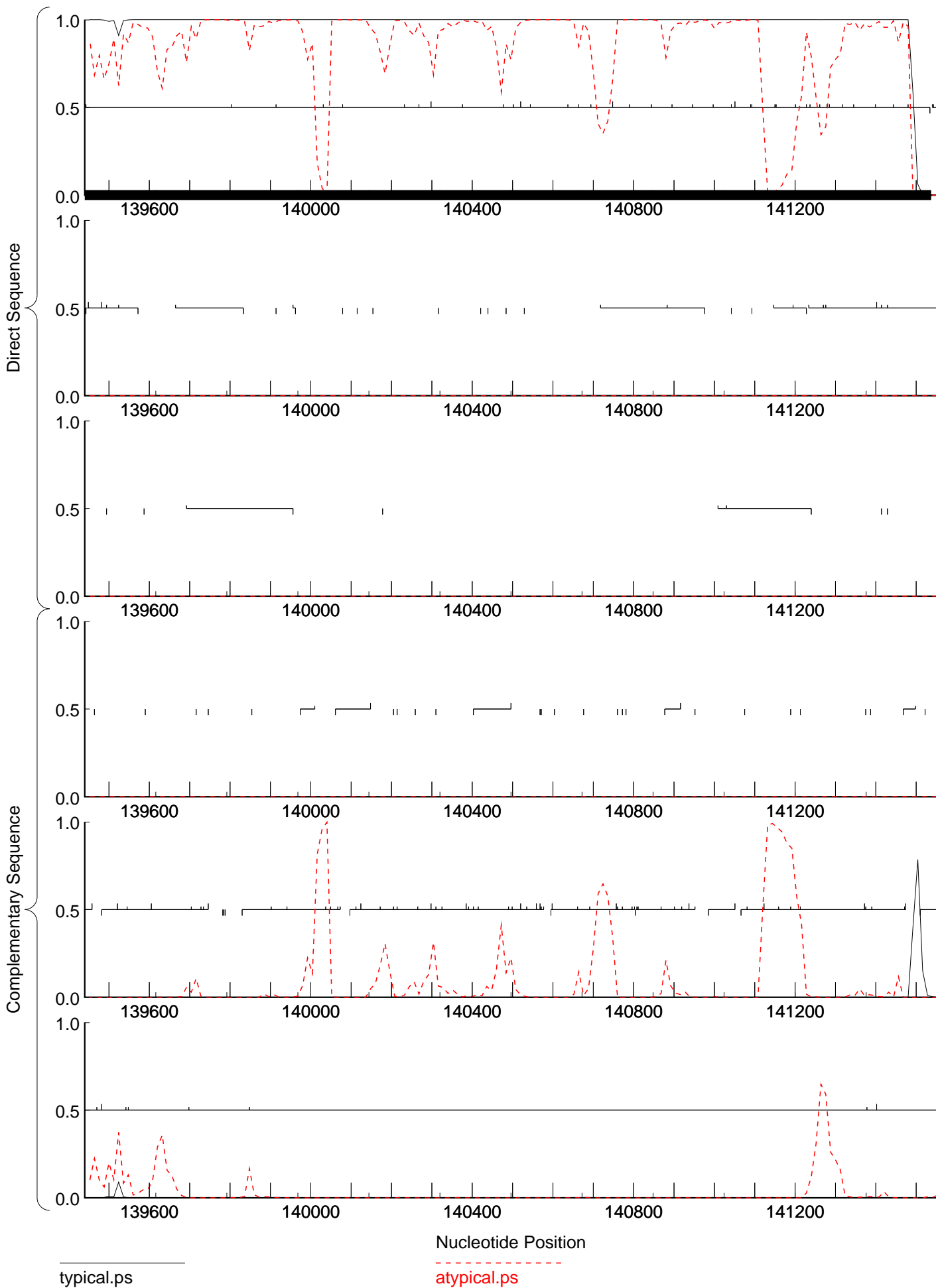


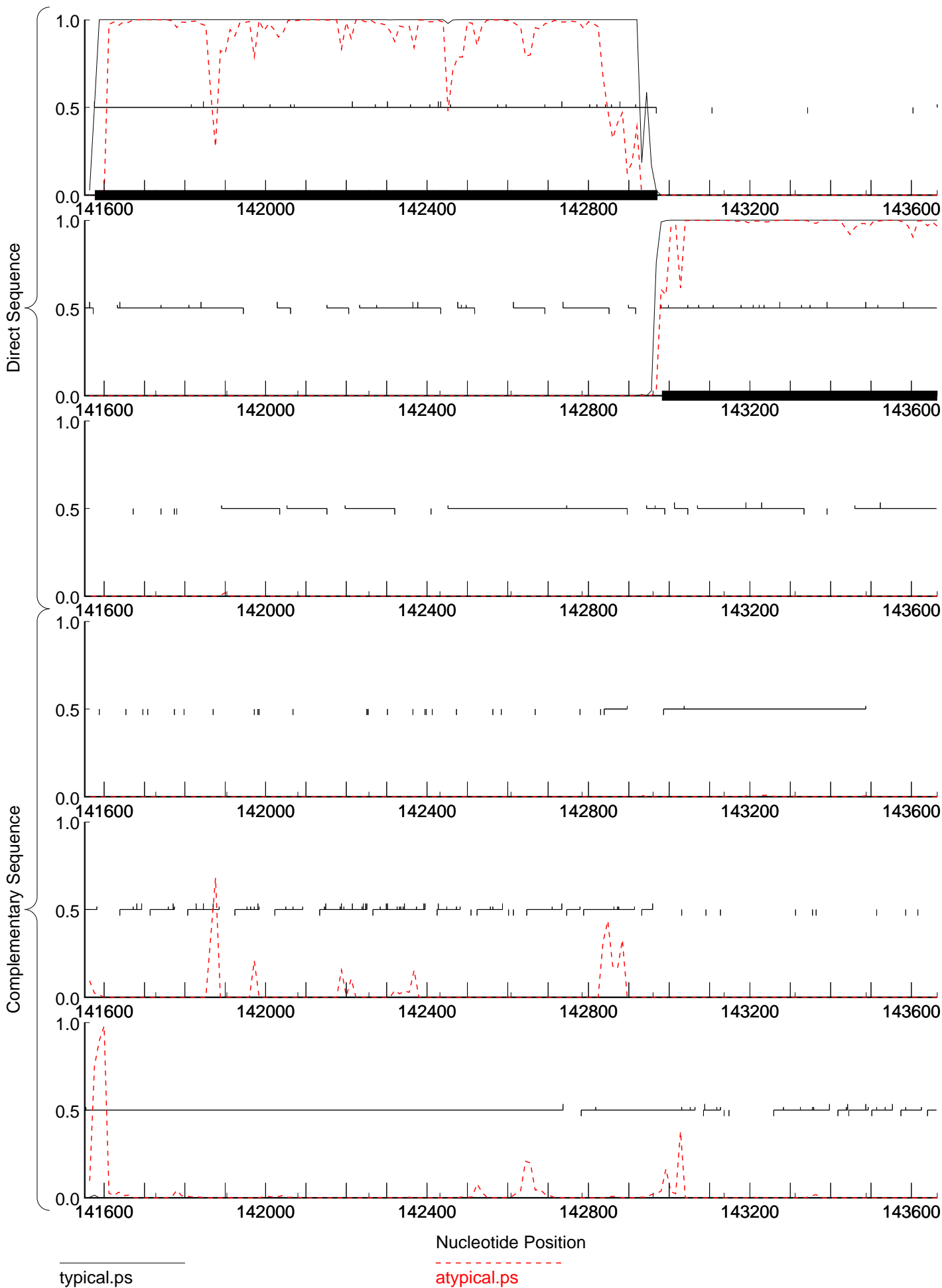
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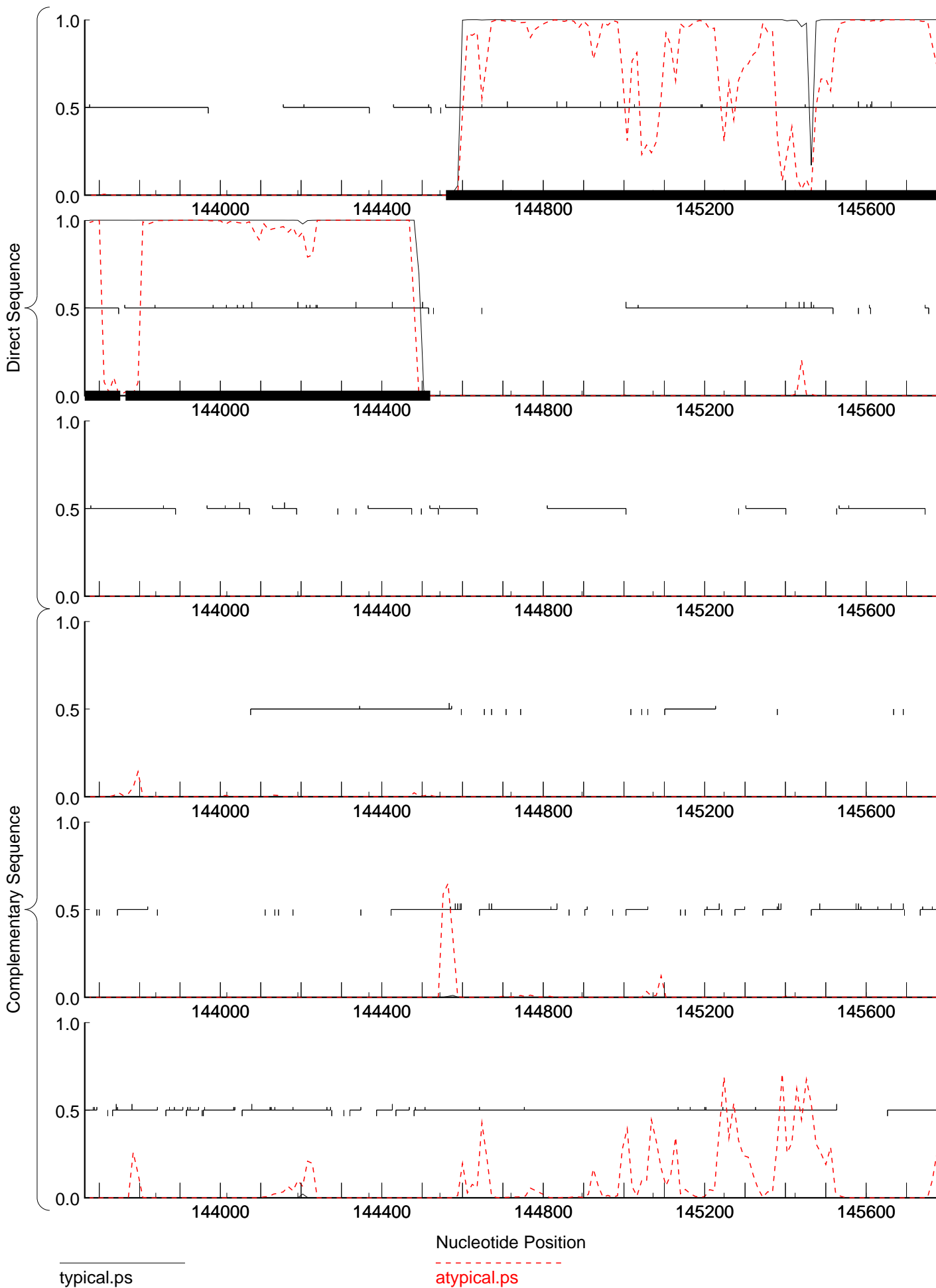
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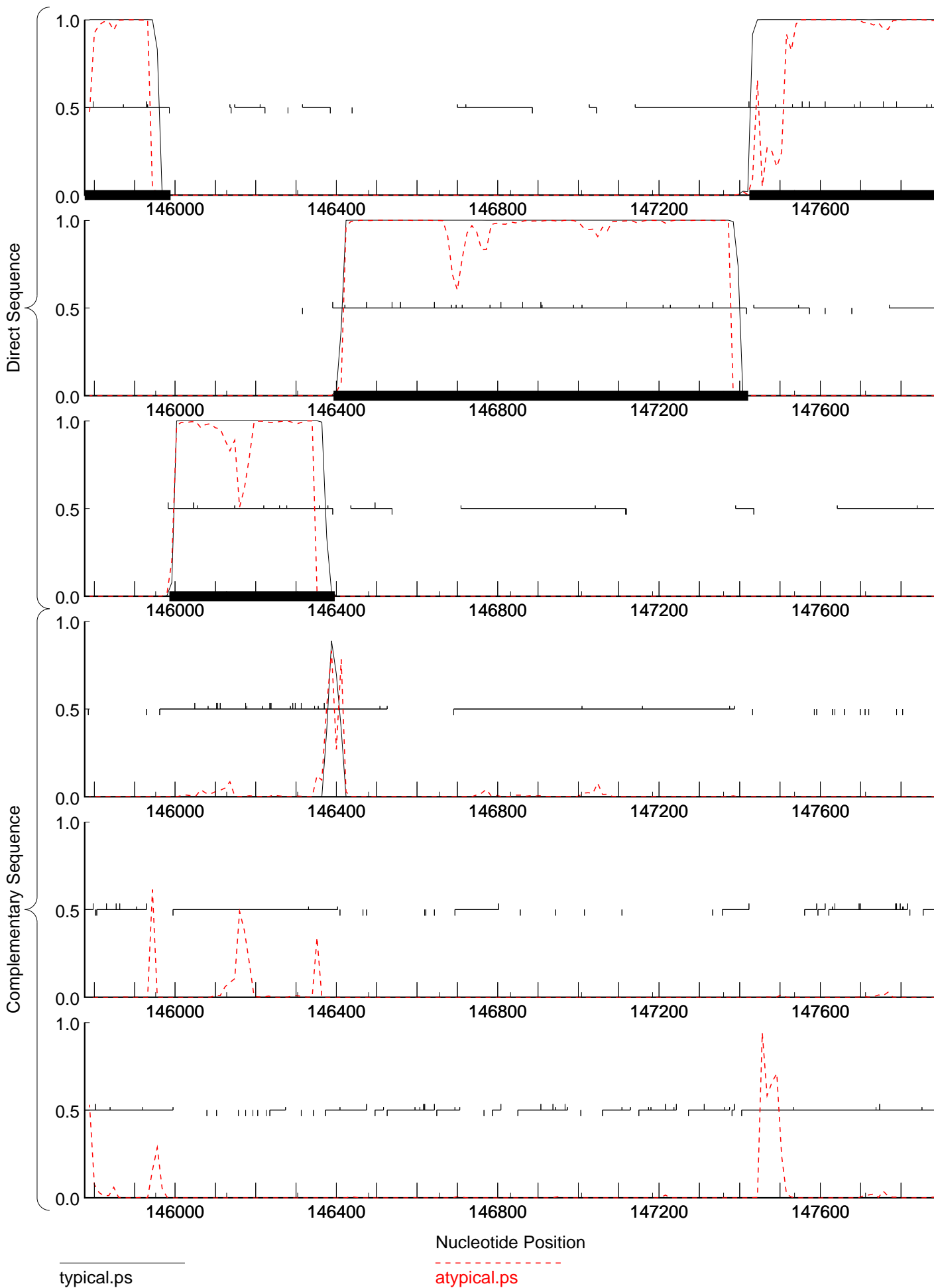


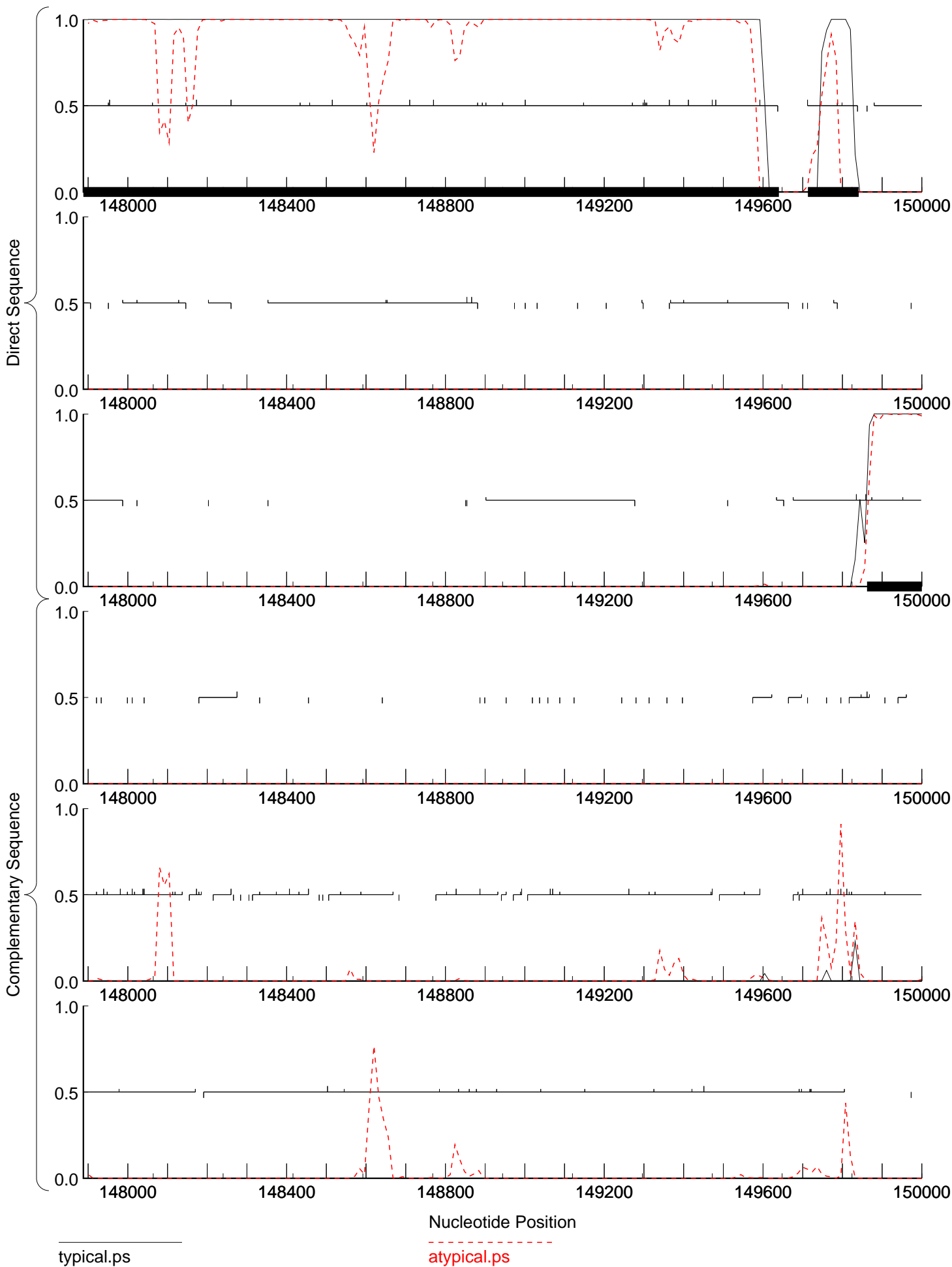


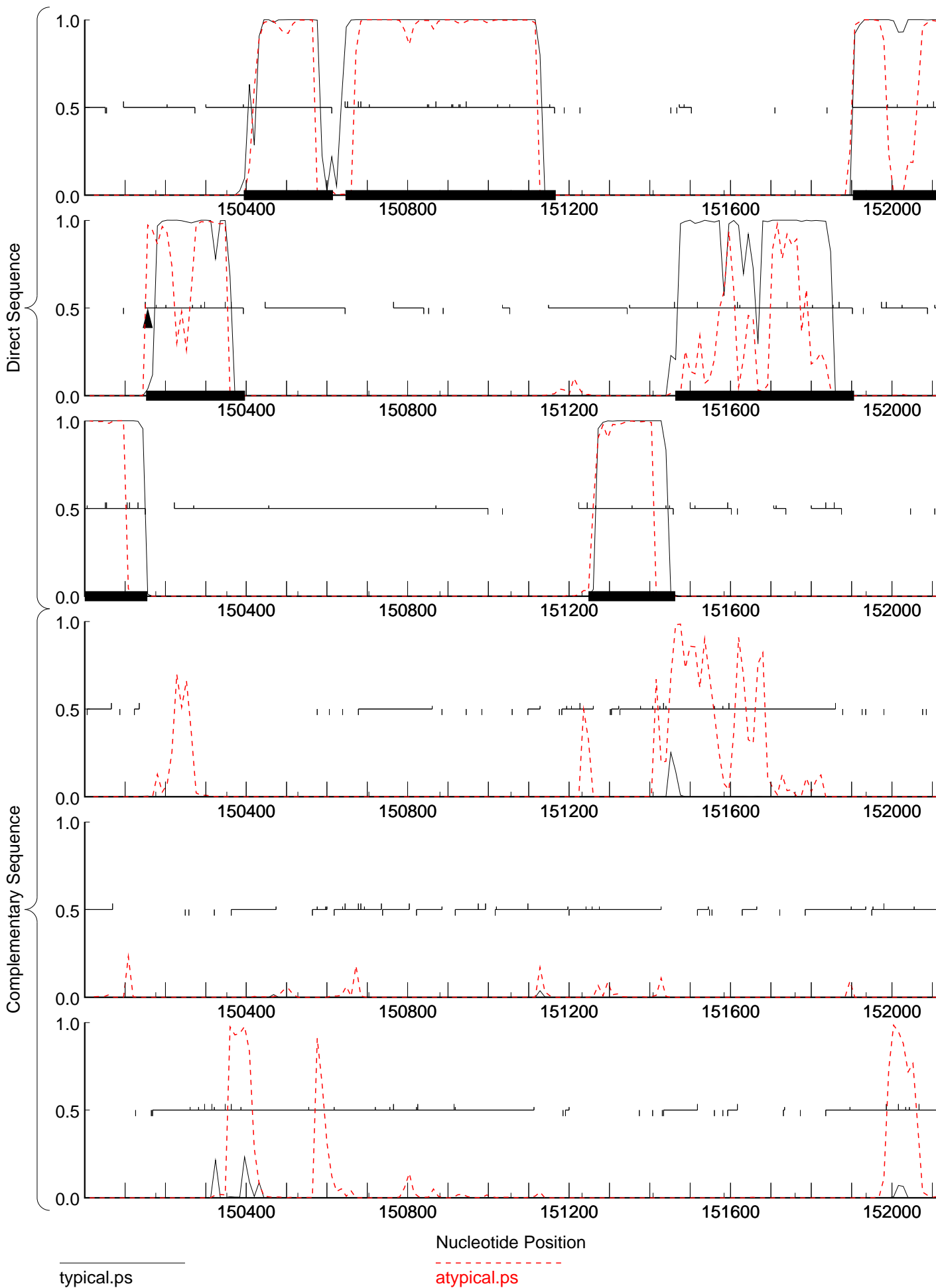






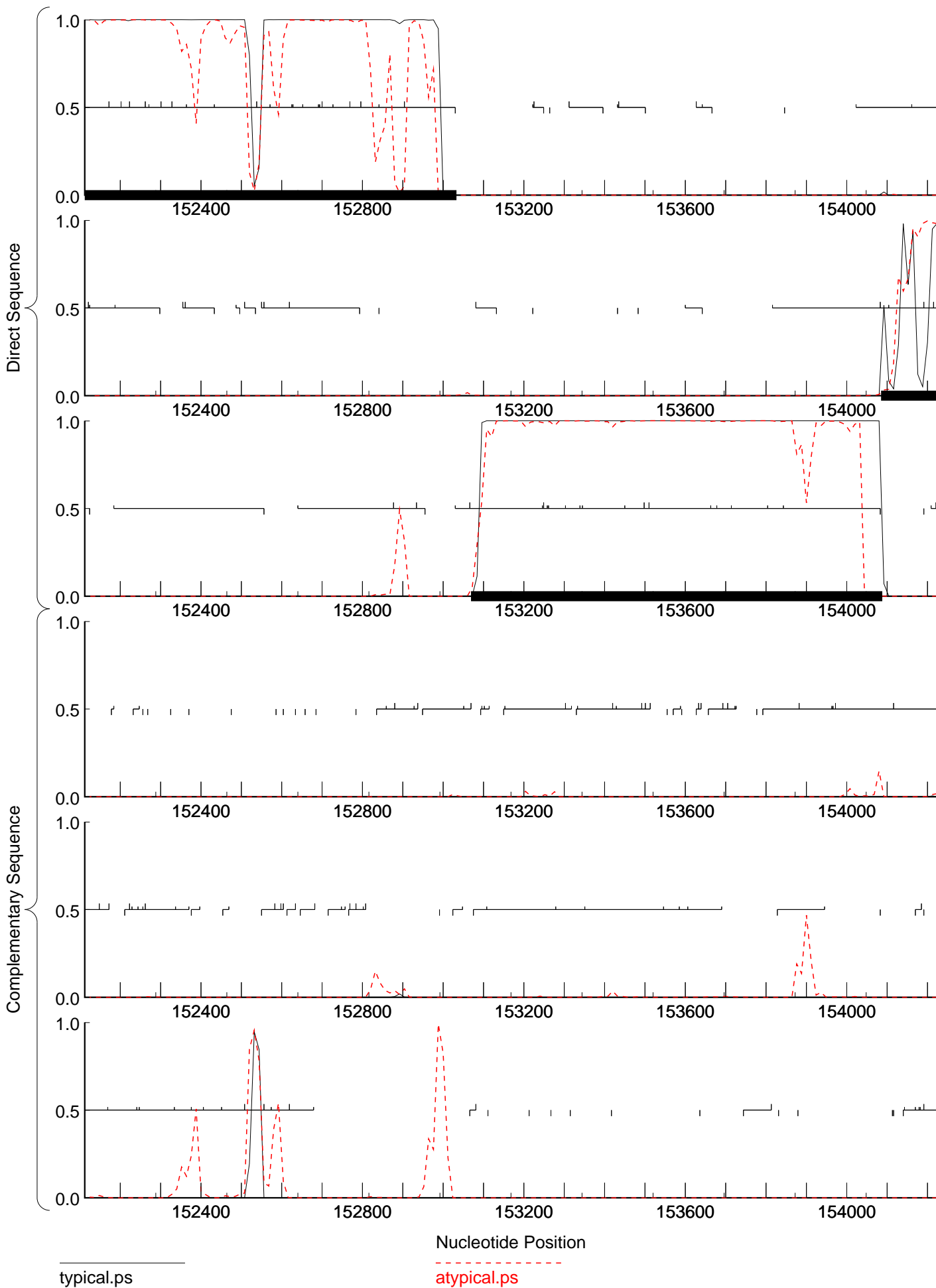


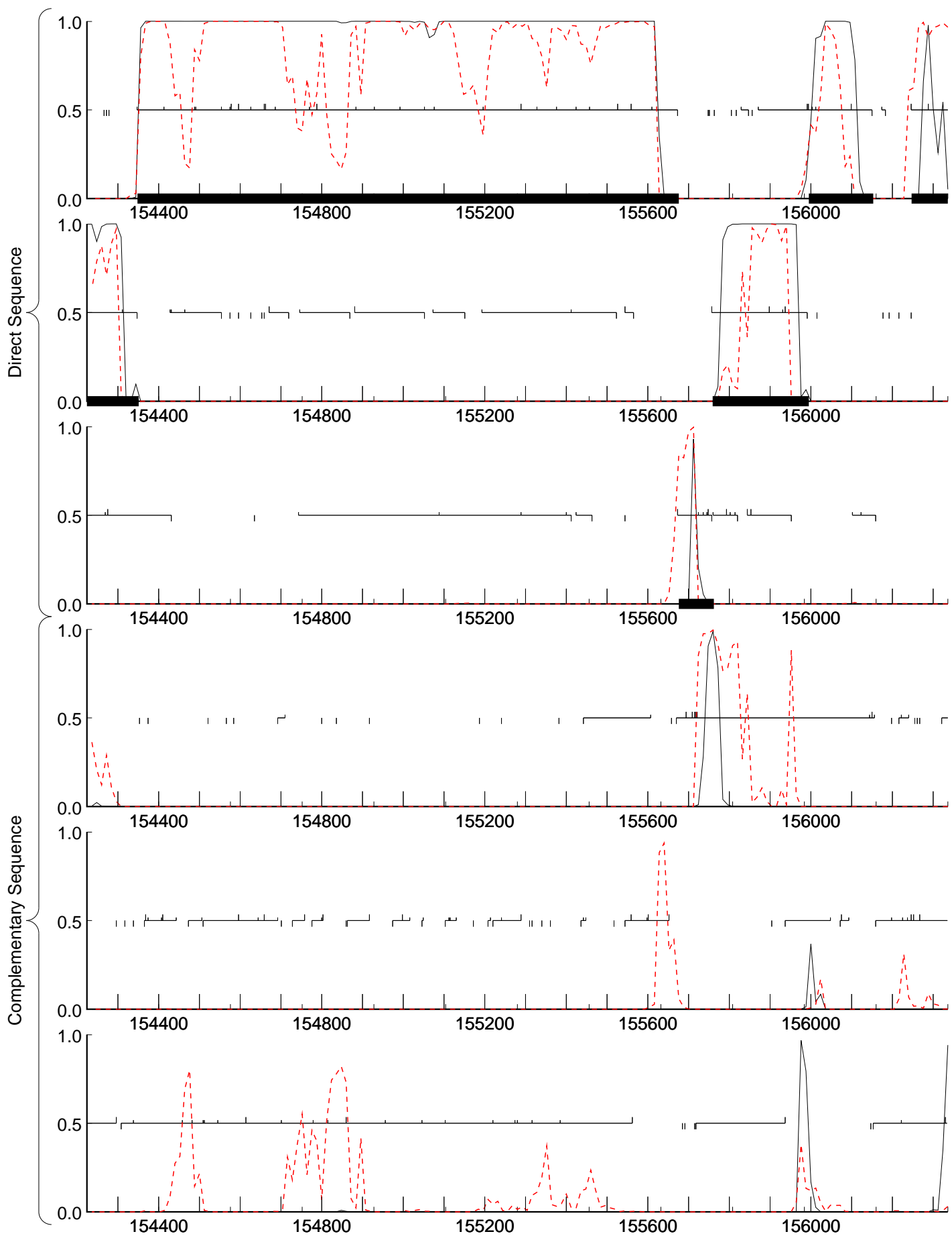




typical.ps

atypical.ps





typical.ps

atypical.ps

