

GeneMark

Version 2.5p (09.08.06)

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PROGRAM INFORMATION

Sequence : Gordonia phage BENTherdunthat complete sequence, 54867 bp including 10-base 3' overhang (CT
Analysis Date : 9/21/17 at 13:42:01
Pages : 27
Sequence Length : 54867 bp
GC Content : 63.36%

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,

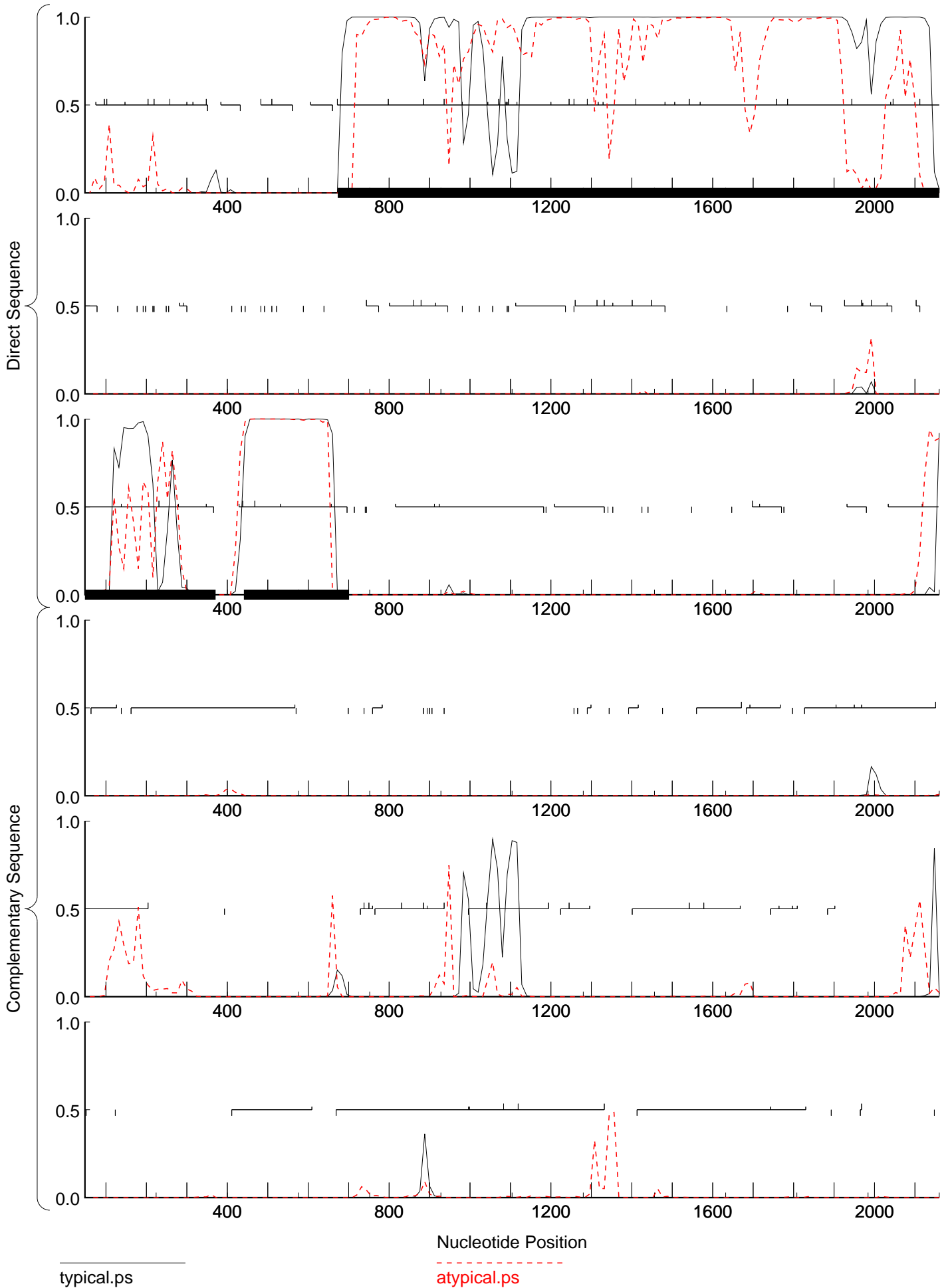
Matrix notes & comments

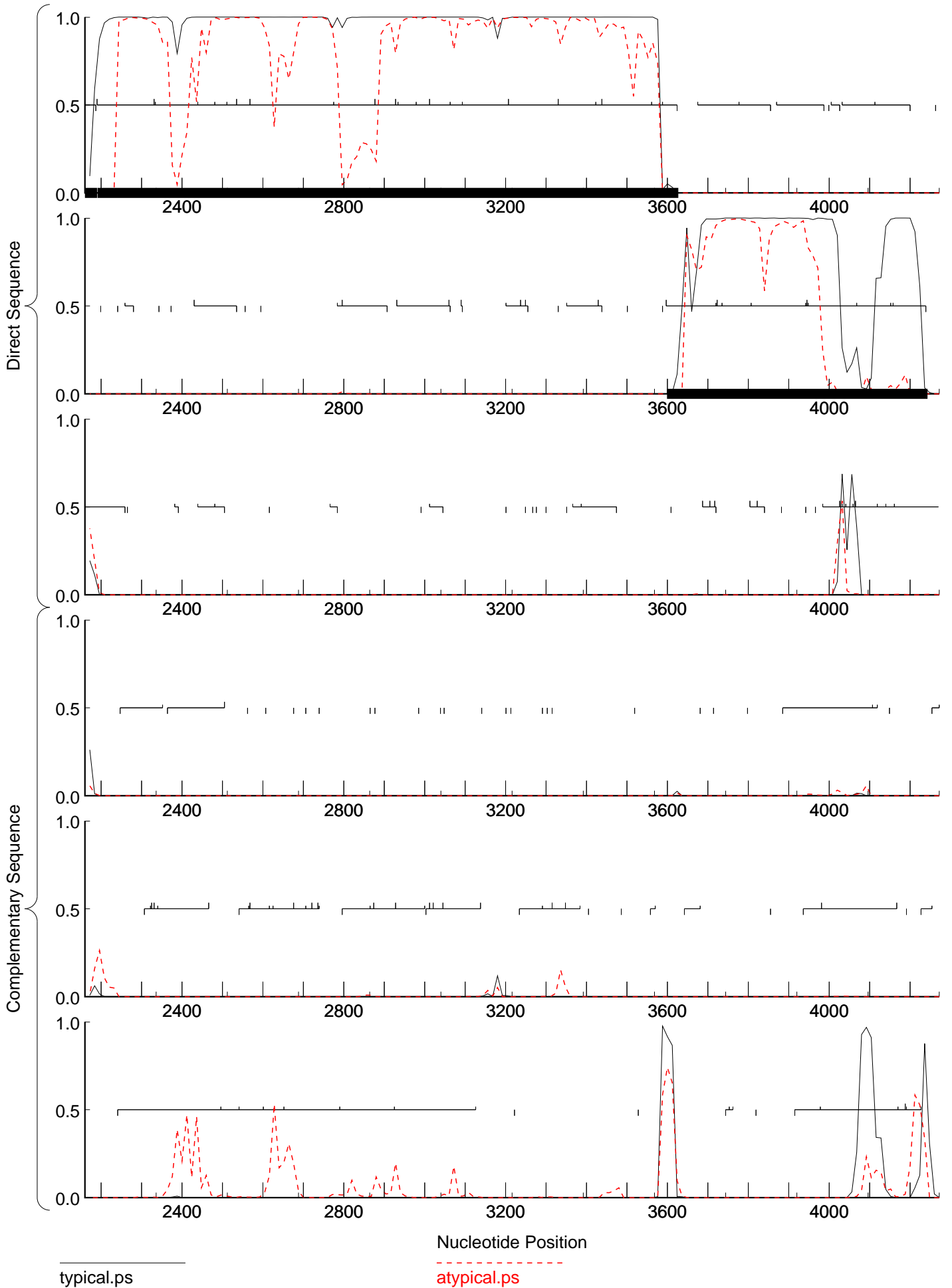
Training set derived by GeneMarkS, 4.30 October 2014
Thu Sep 21 13:42:01 2017

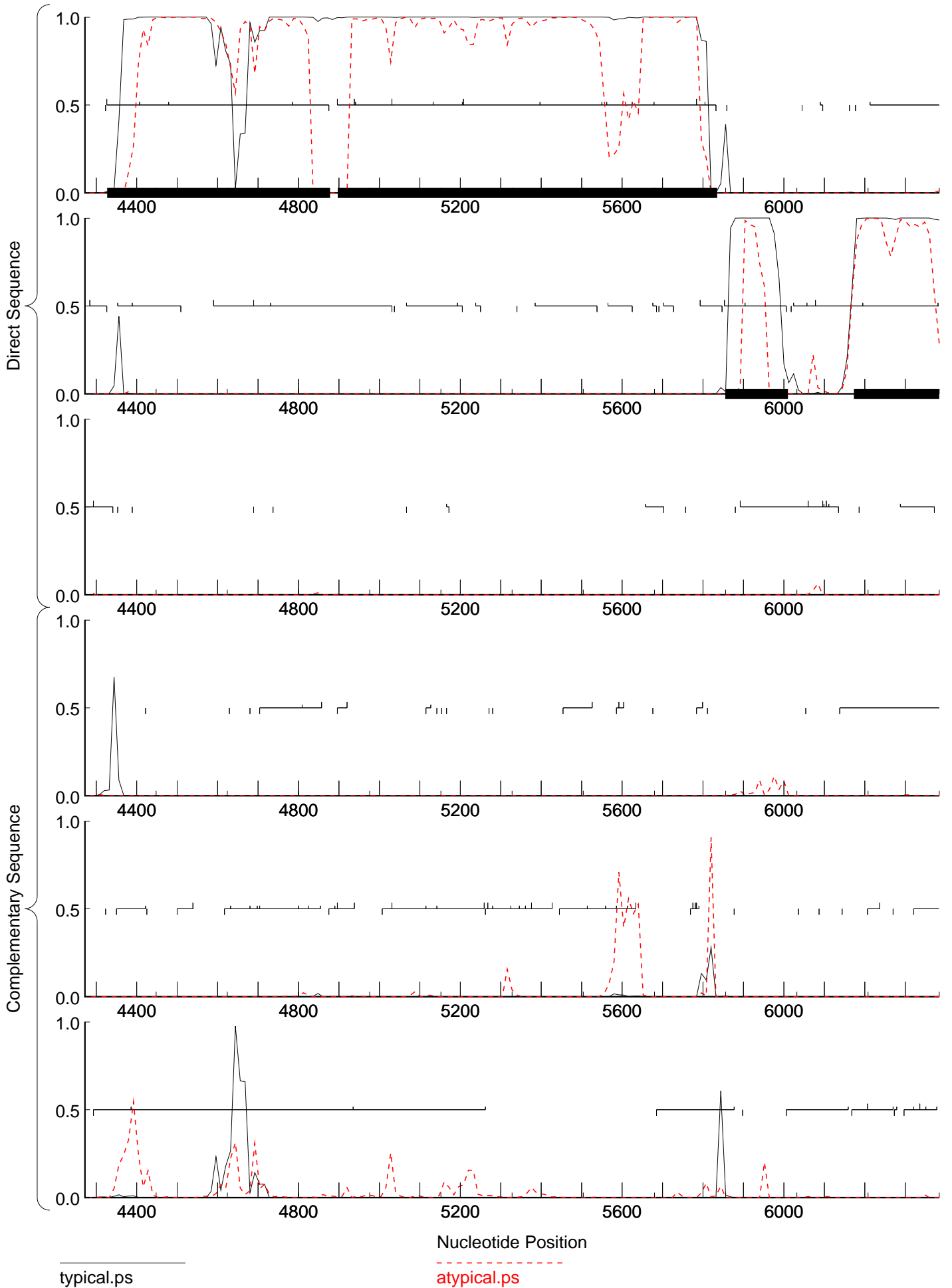
MATRIX INFORMATION

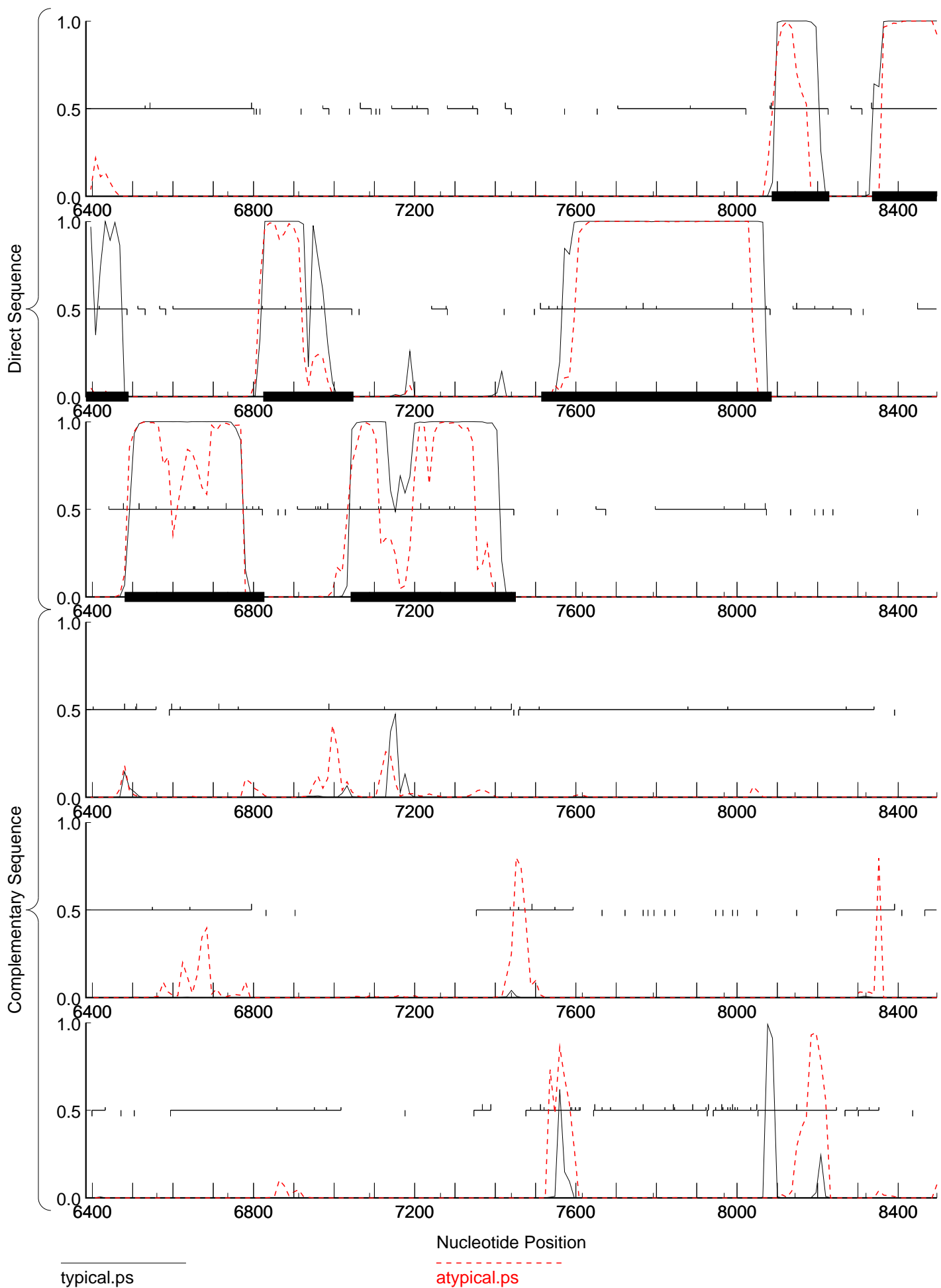
Matrix : -
Author : -
Order : 4

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



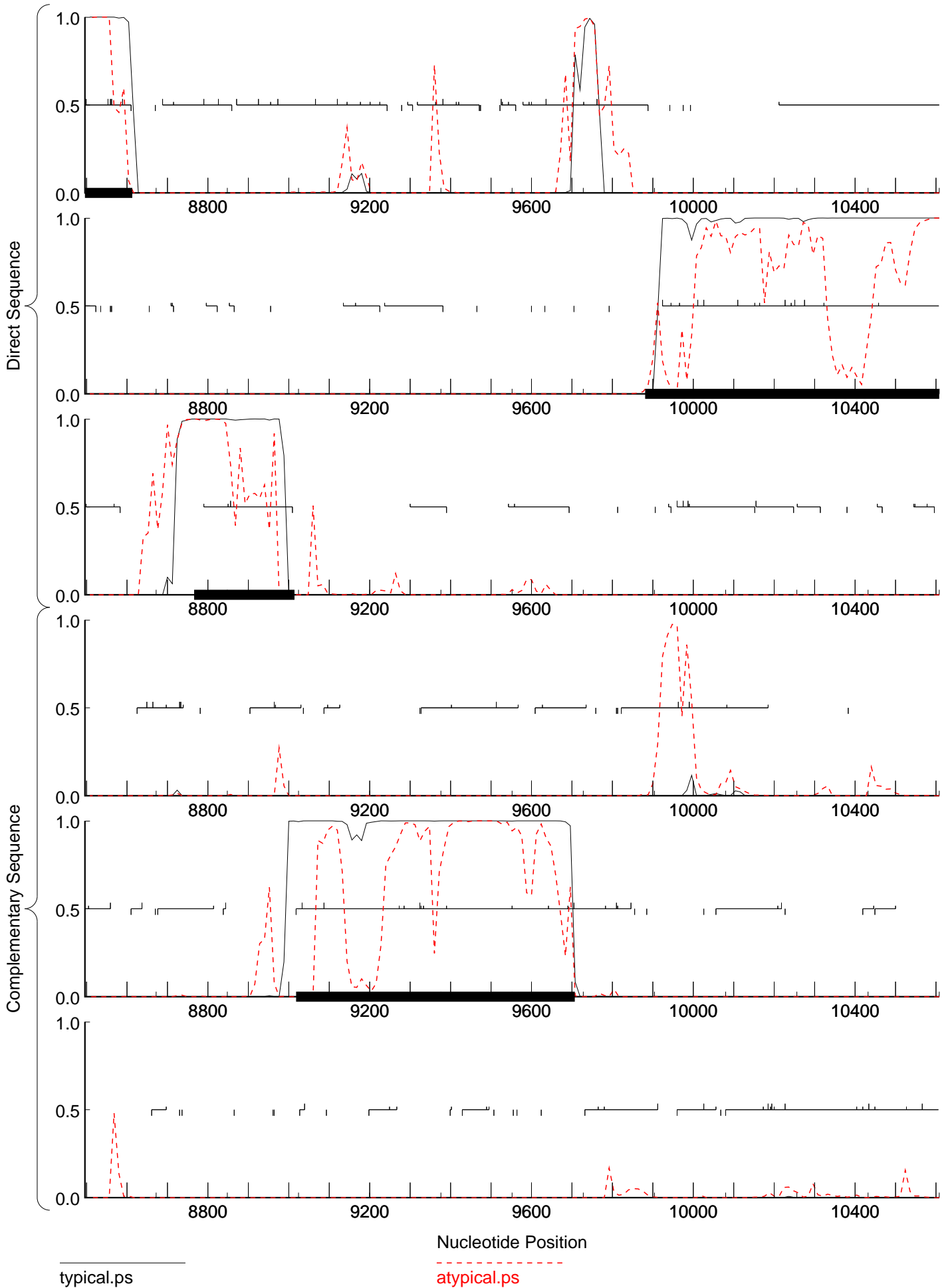


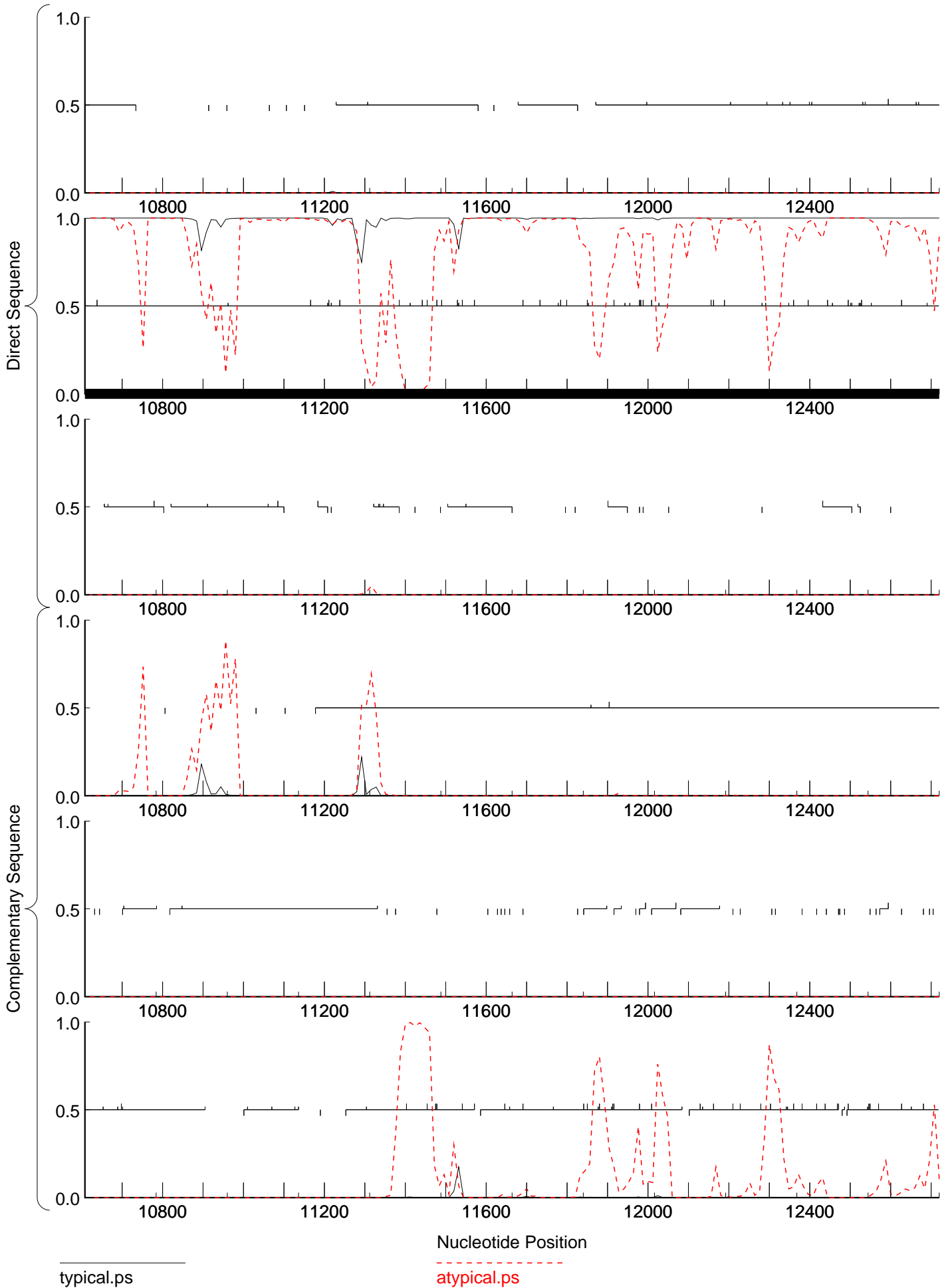


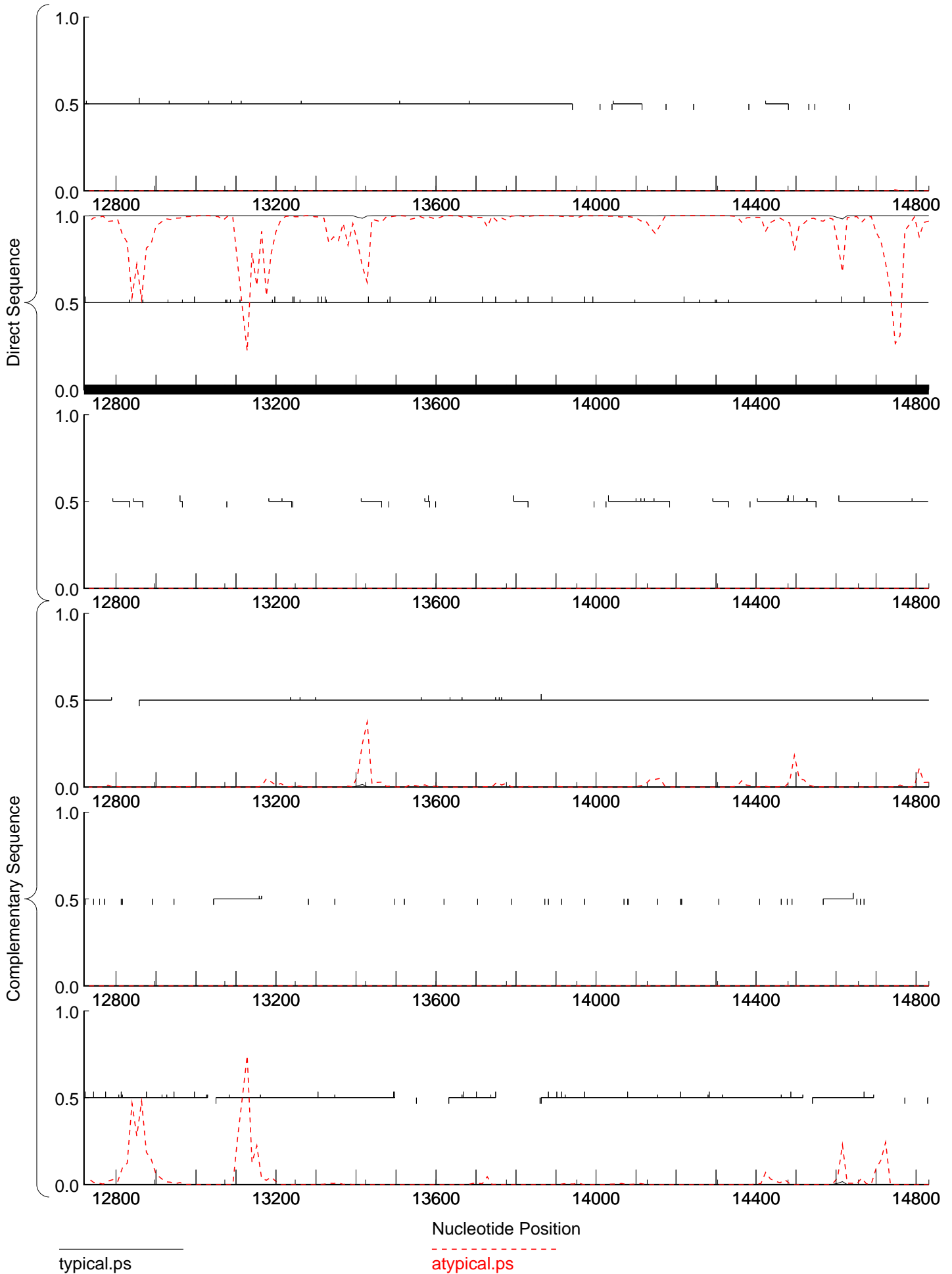


typical.ps

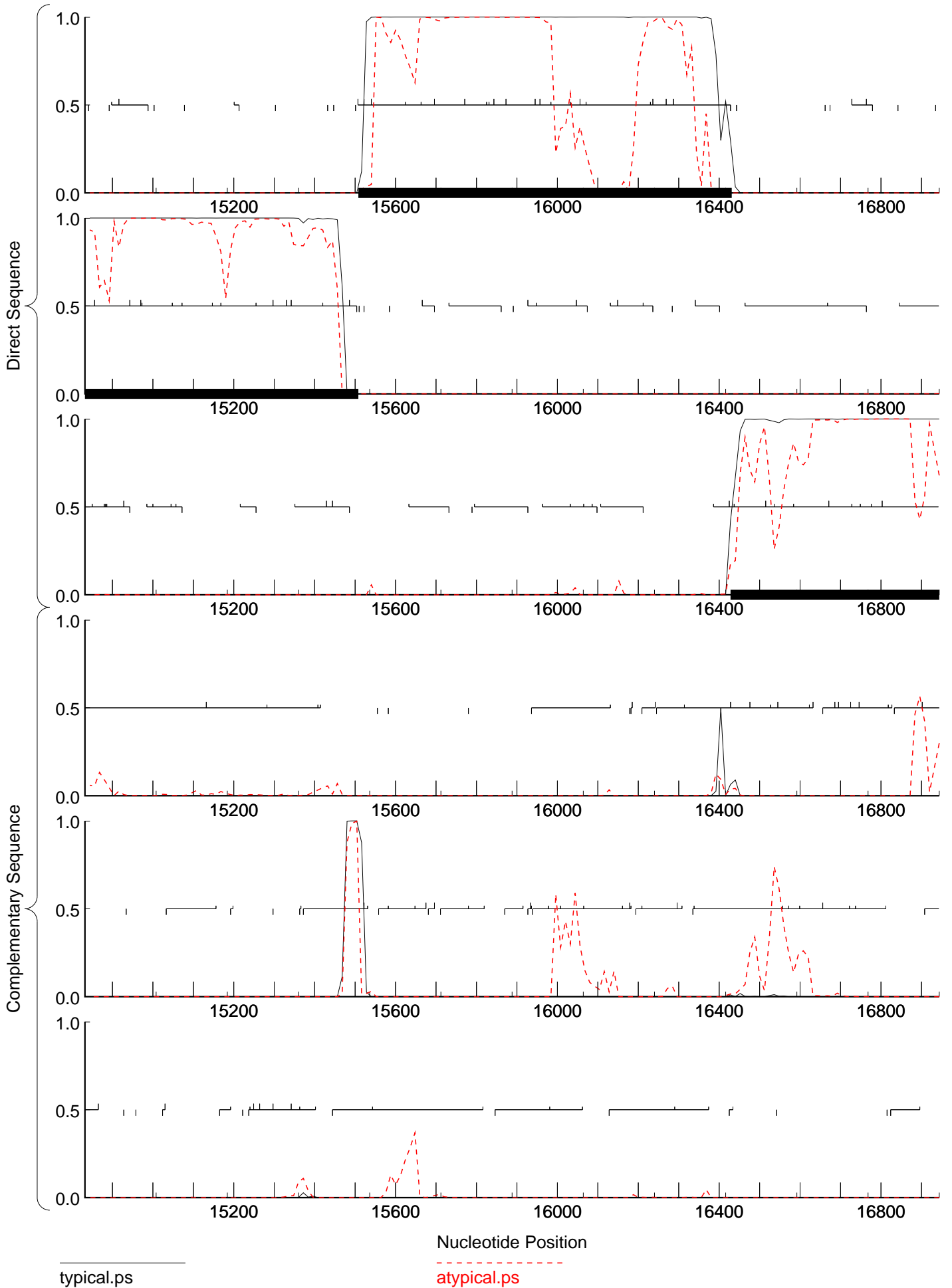
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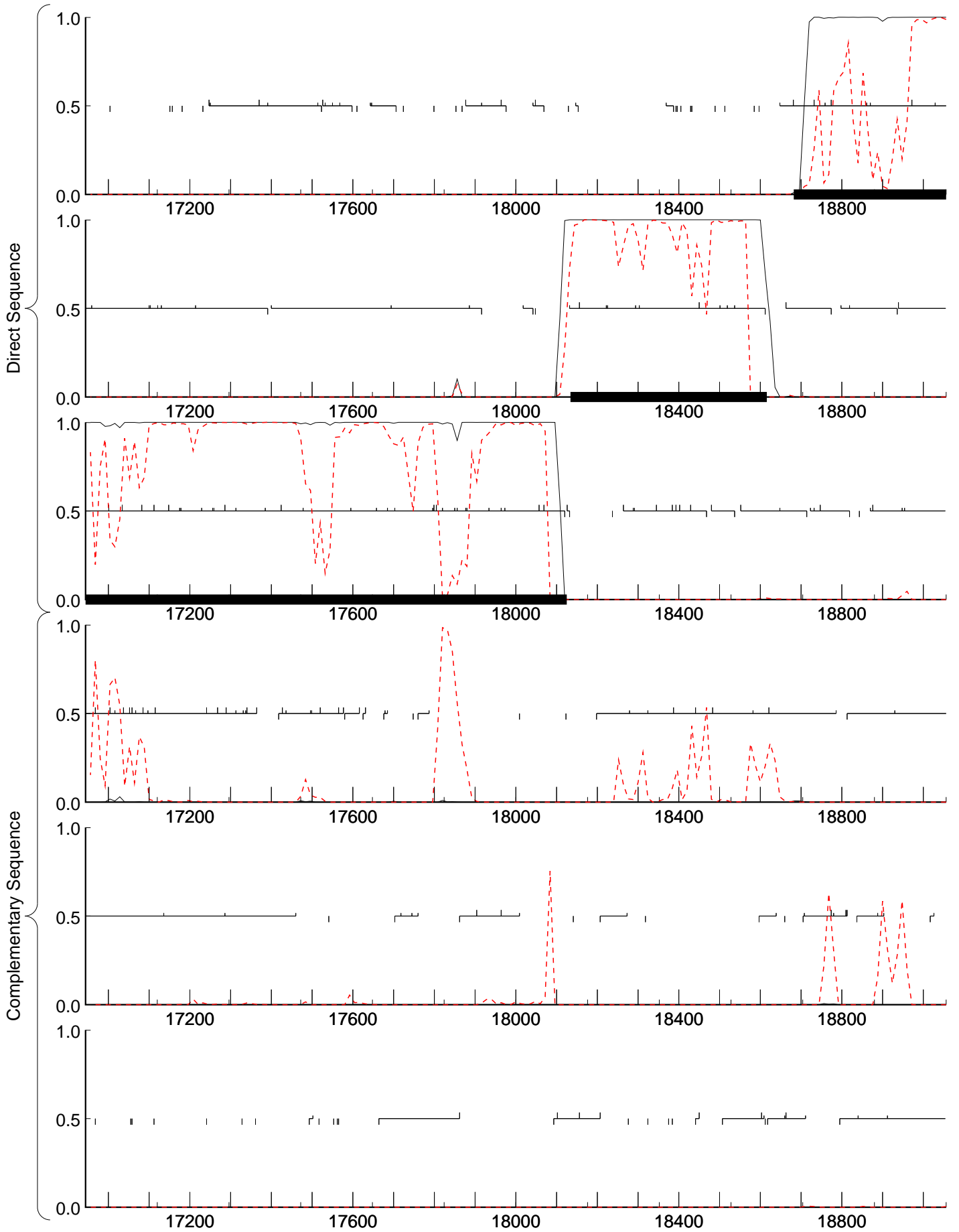






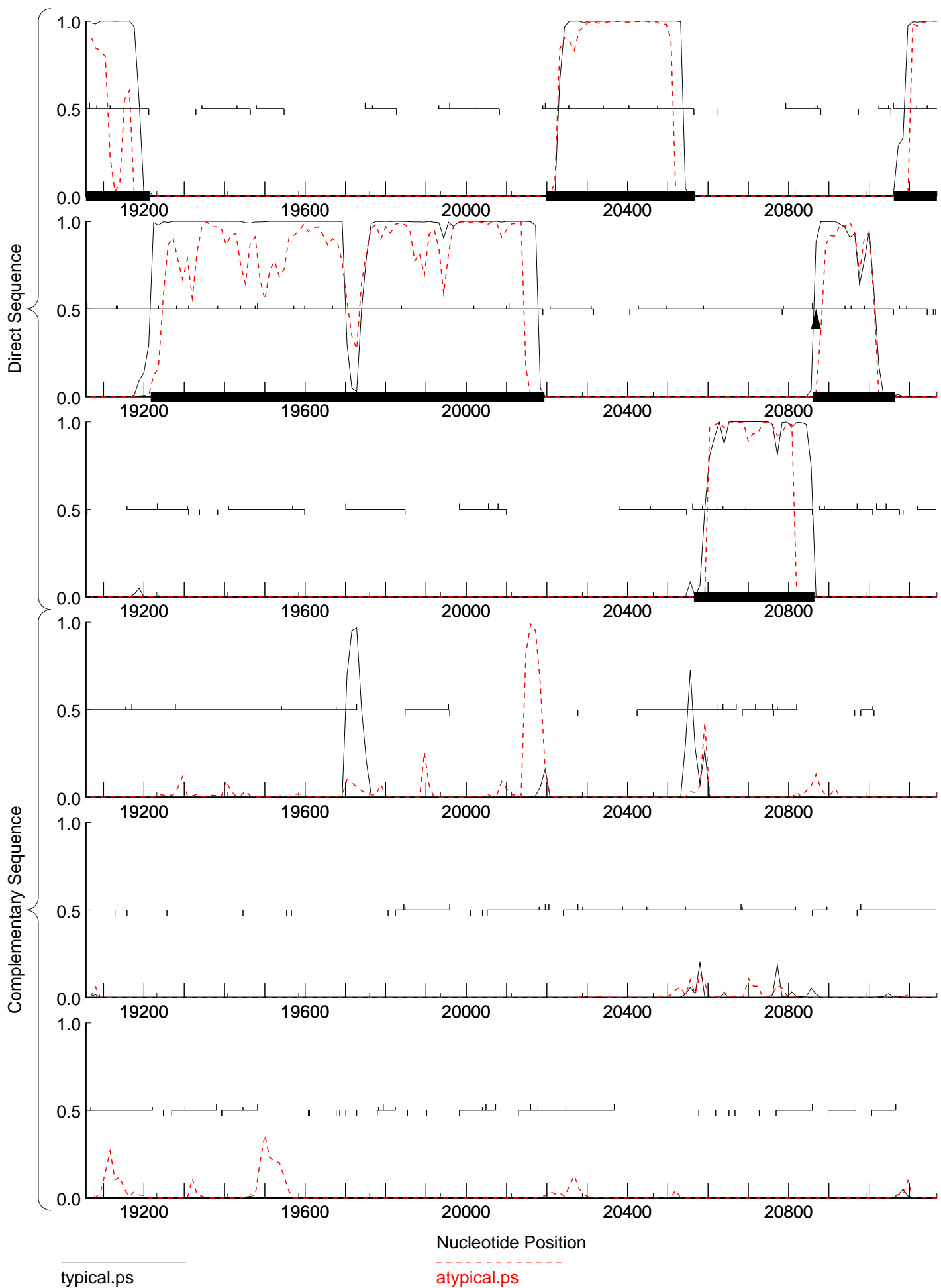
at complete sequence, 54867 bp including 10-base 3' overhang (CTCGGGGCAT), Cluster DN, Order 4, Window 96, Step 12, 9/27
at complete sequence, 54867 bp including 10-base 3' overhang (CTCGGGGCAT), Cluster DN, Order 2, Window 96, Step 12, 9/27

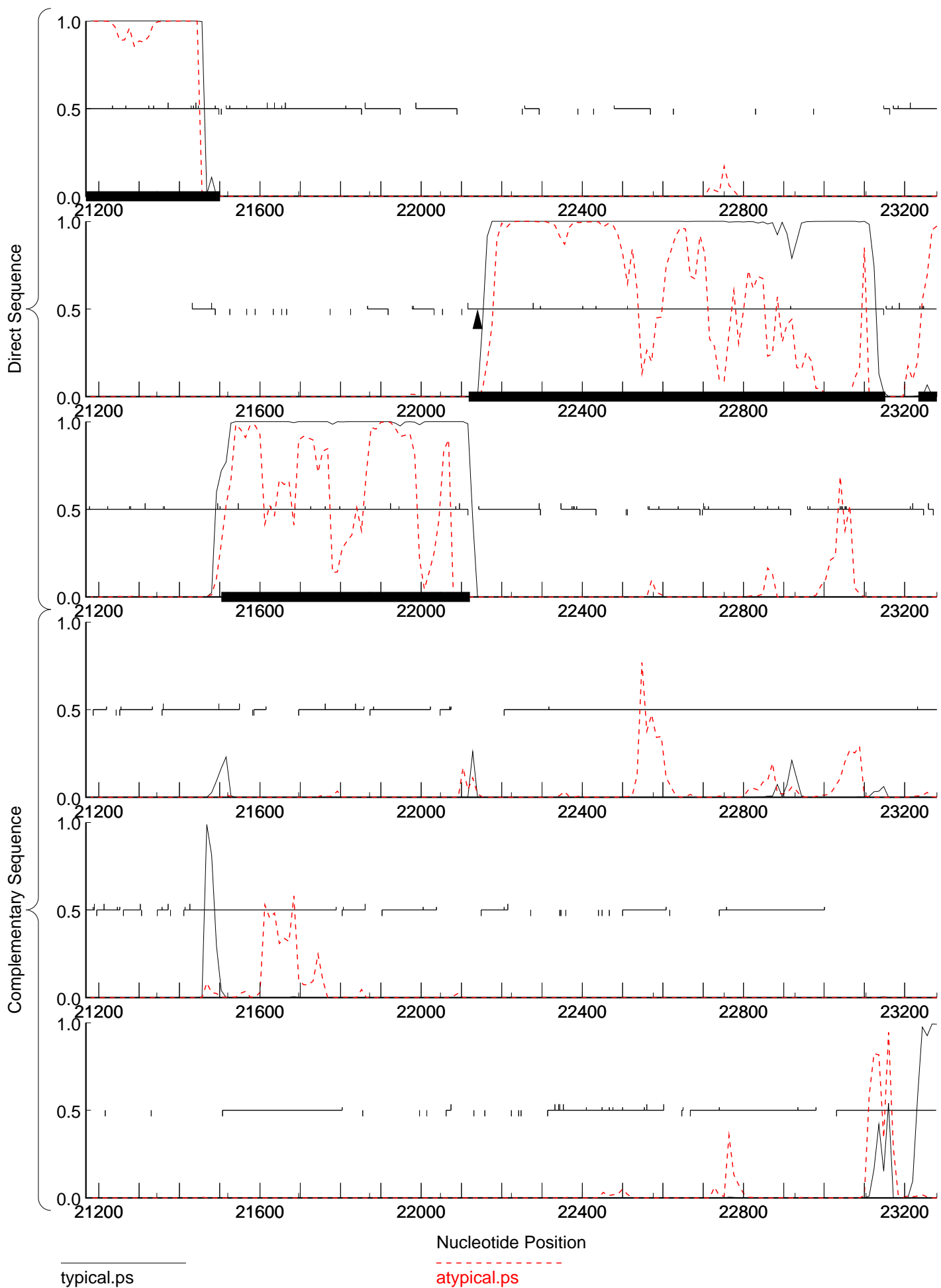


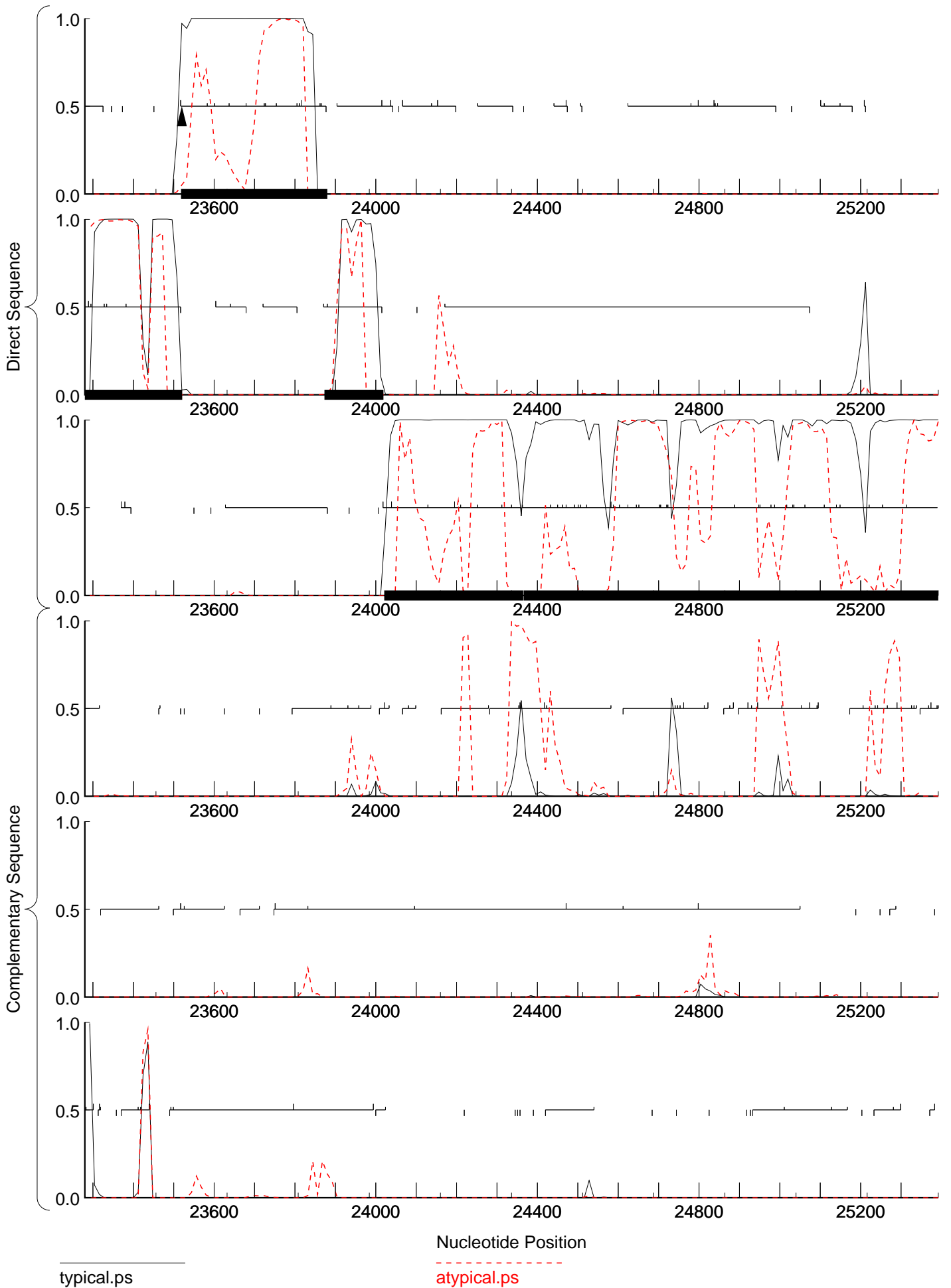


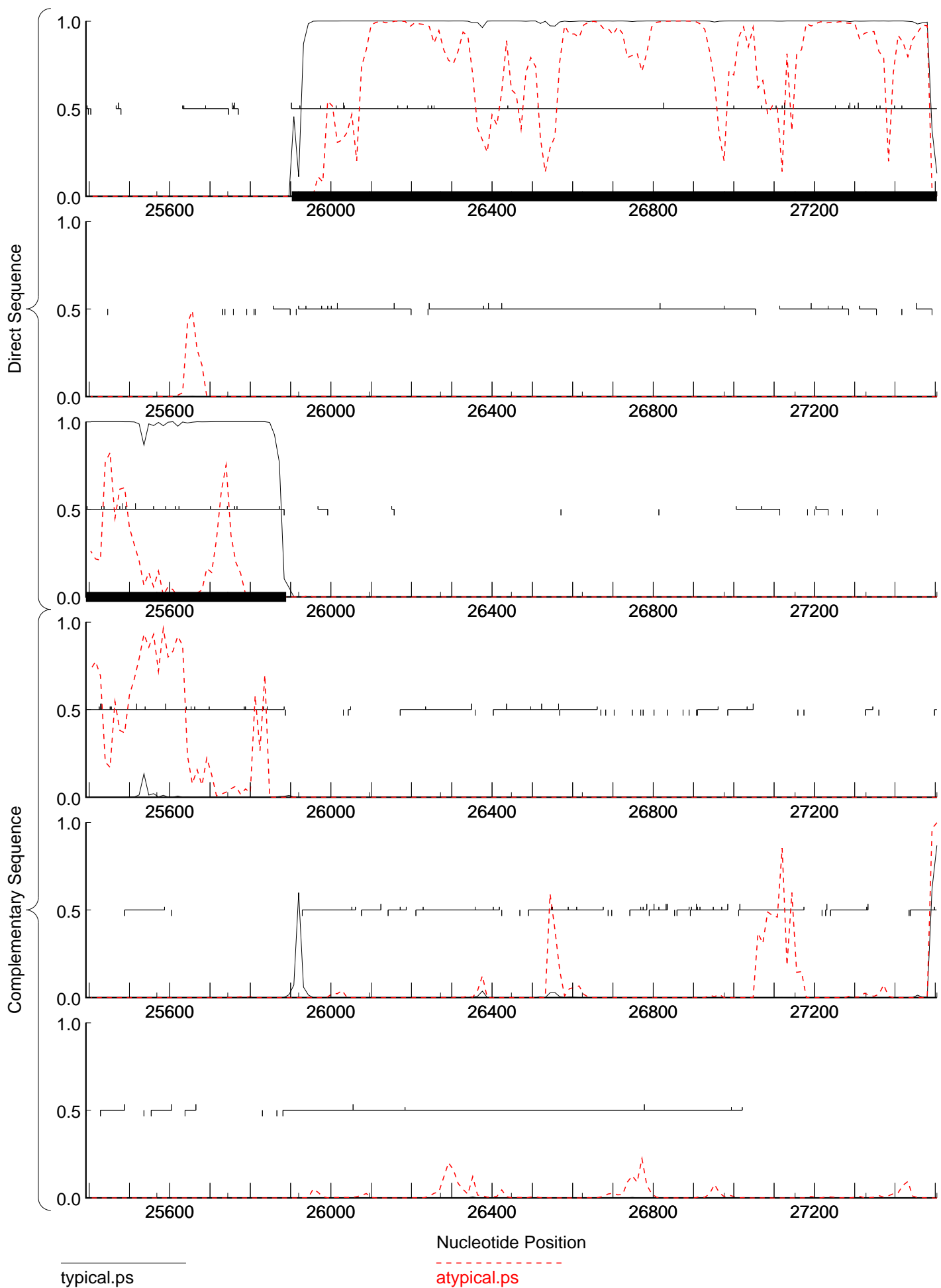
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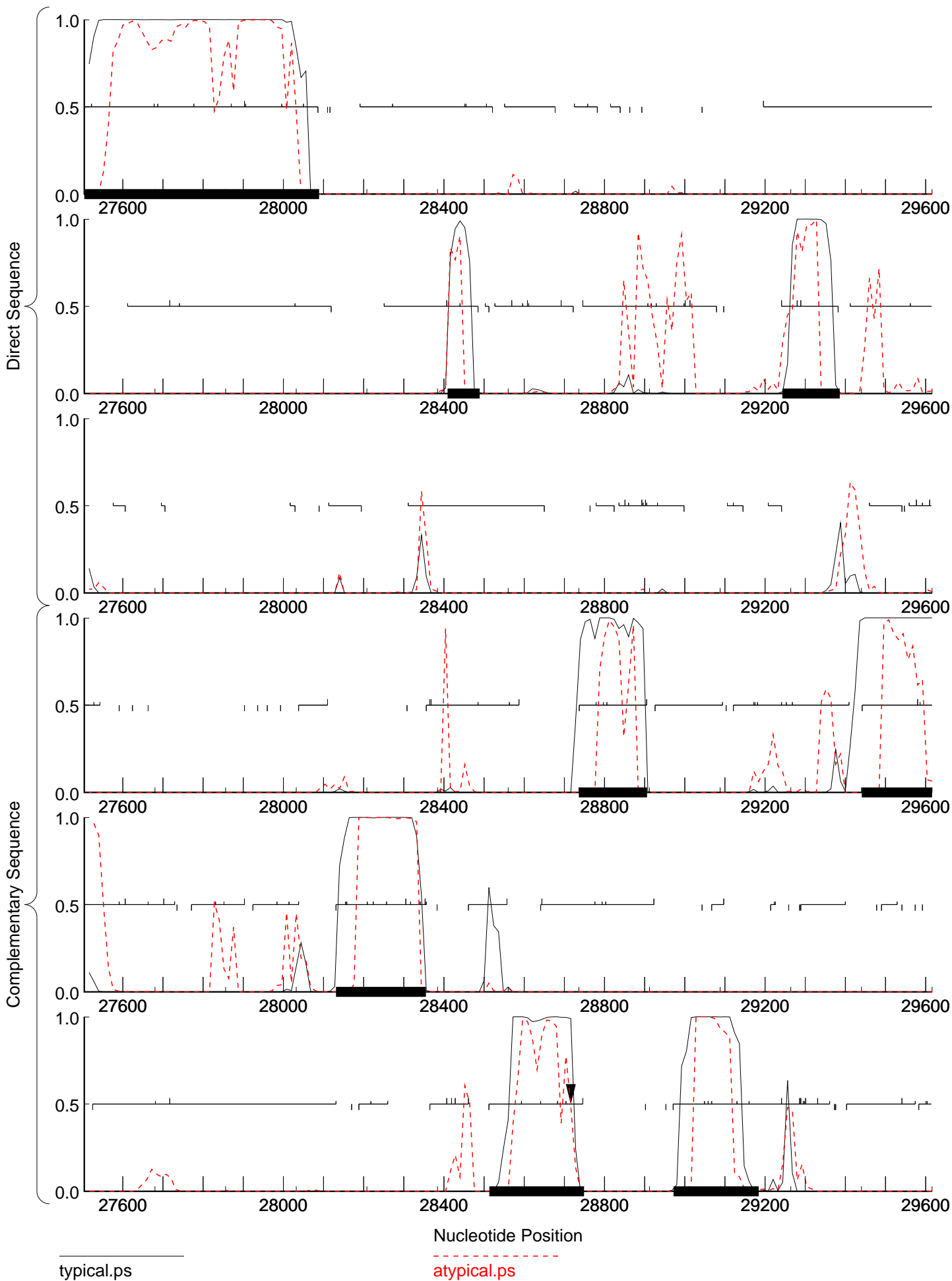
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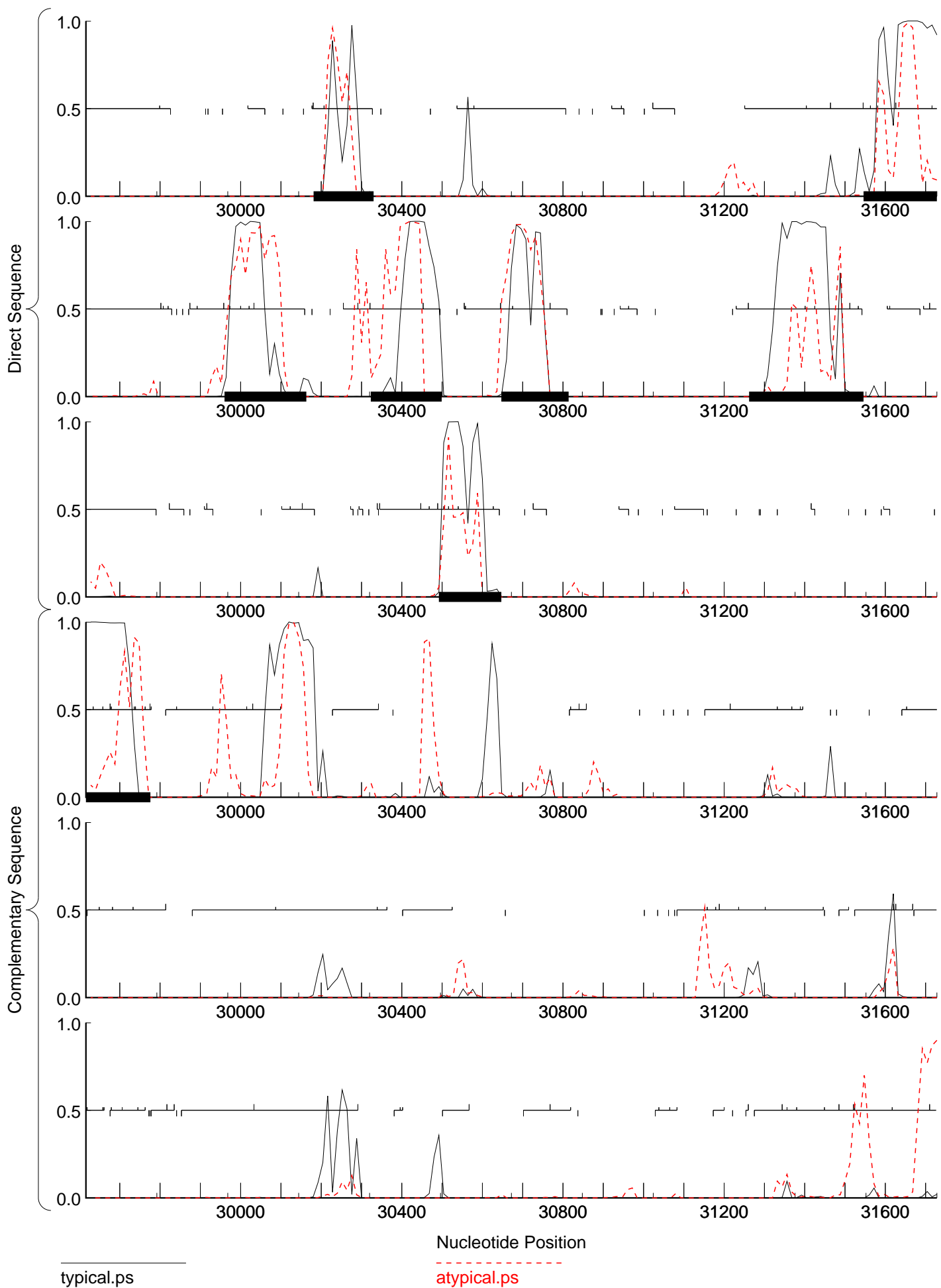


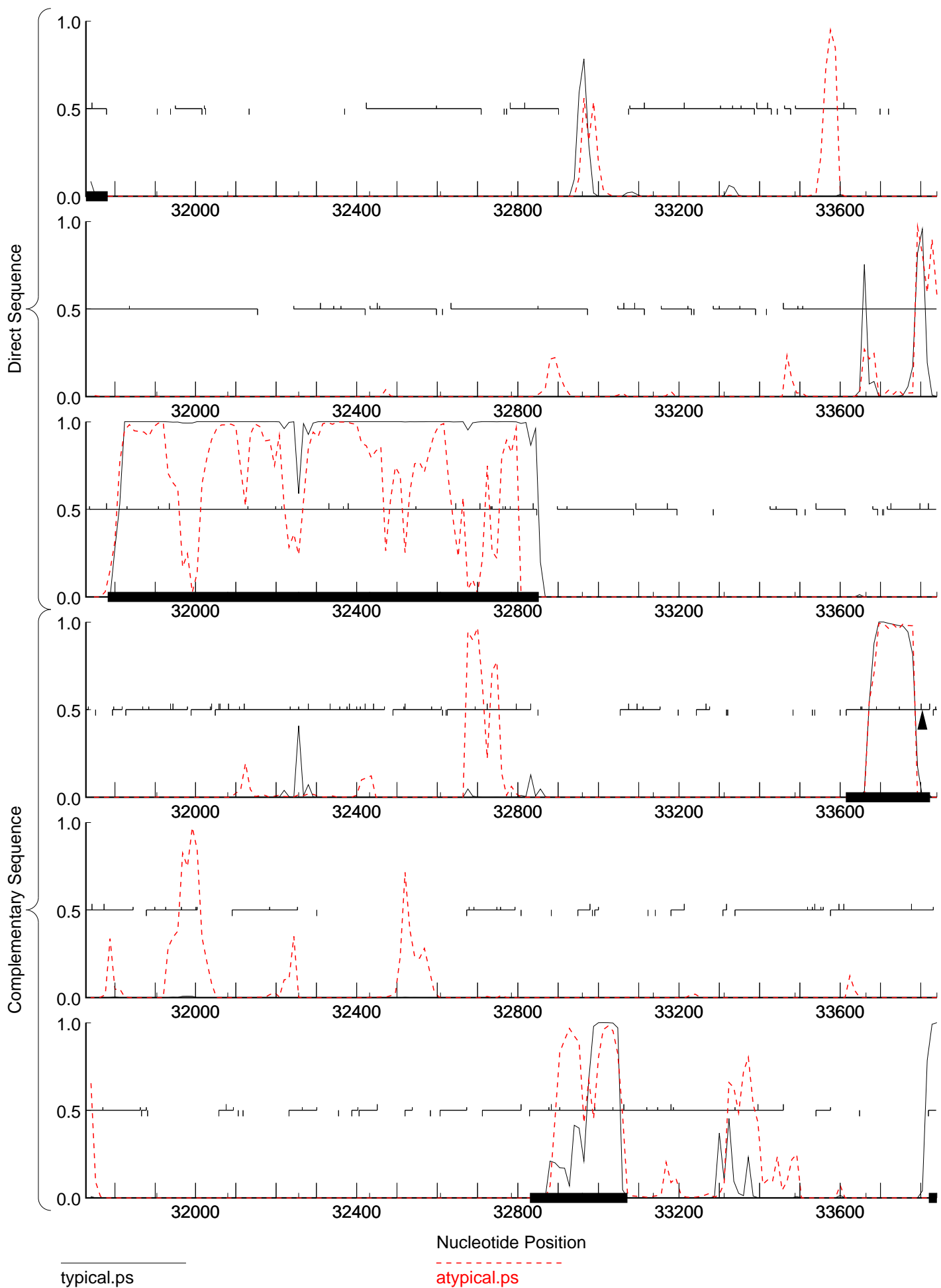






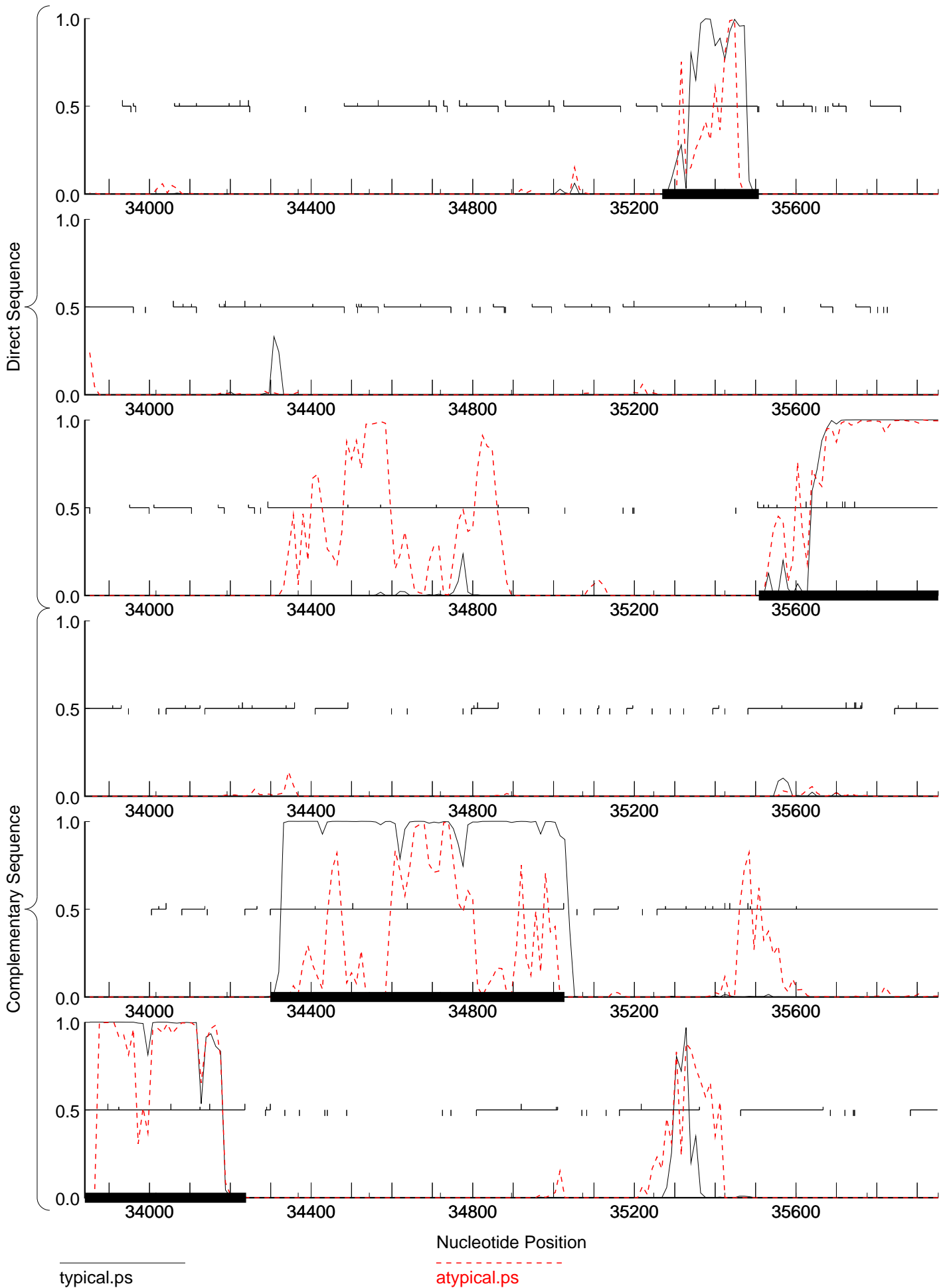


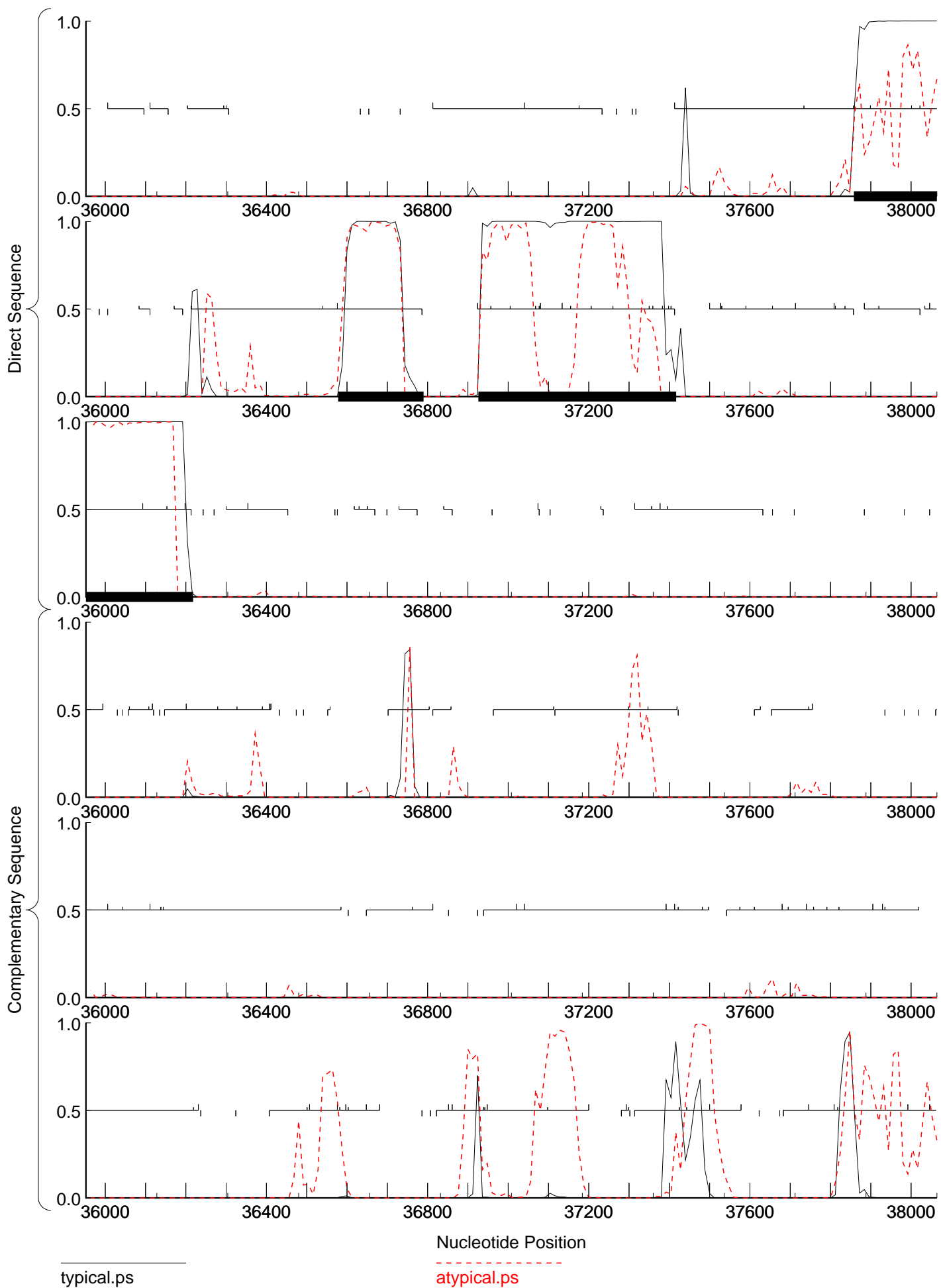




typical.ps

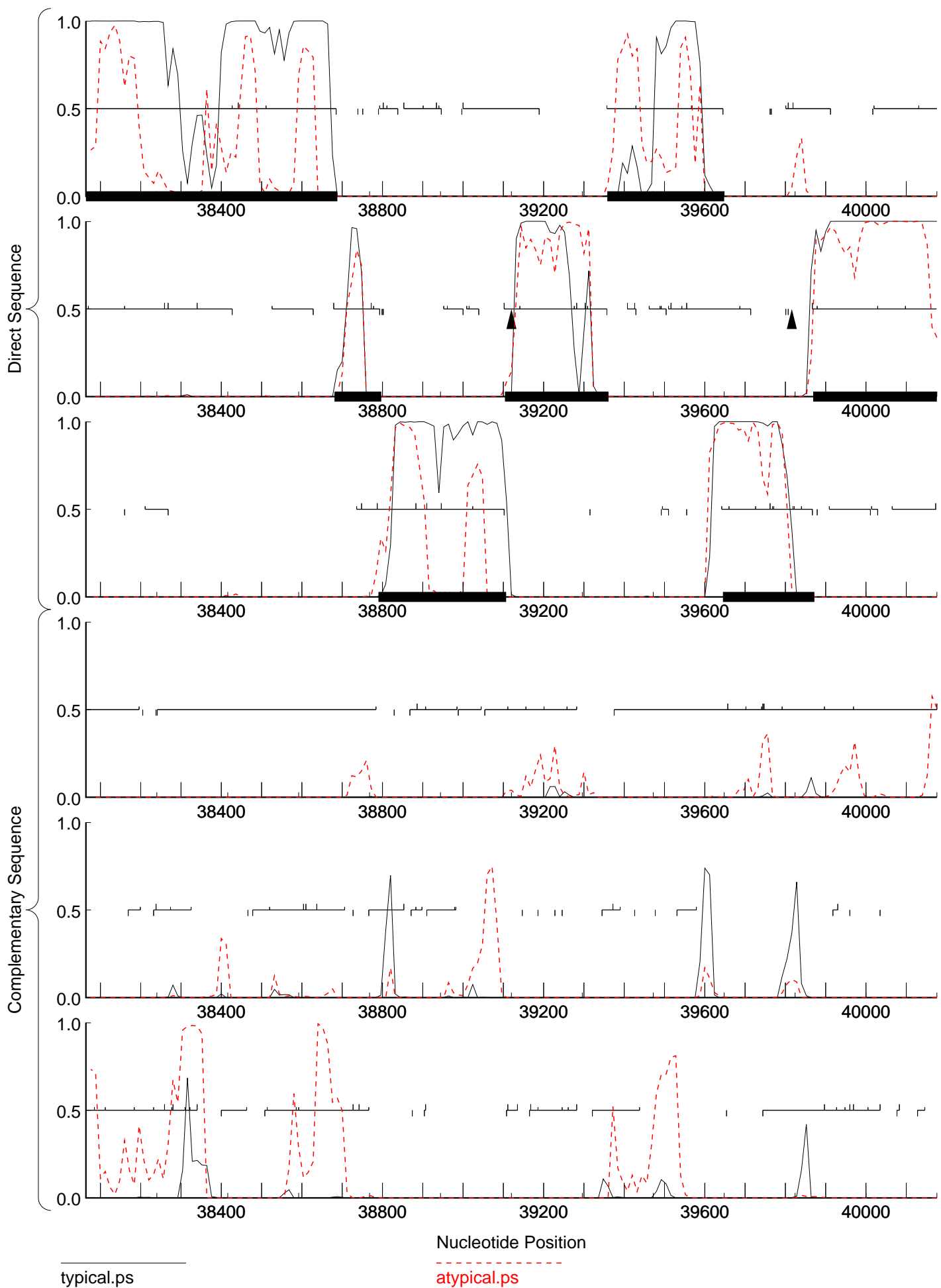
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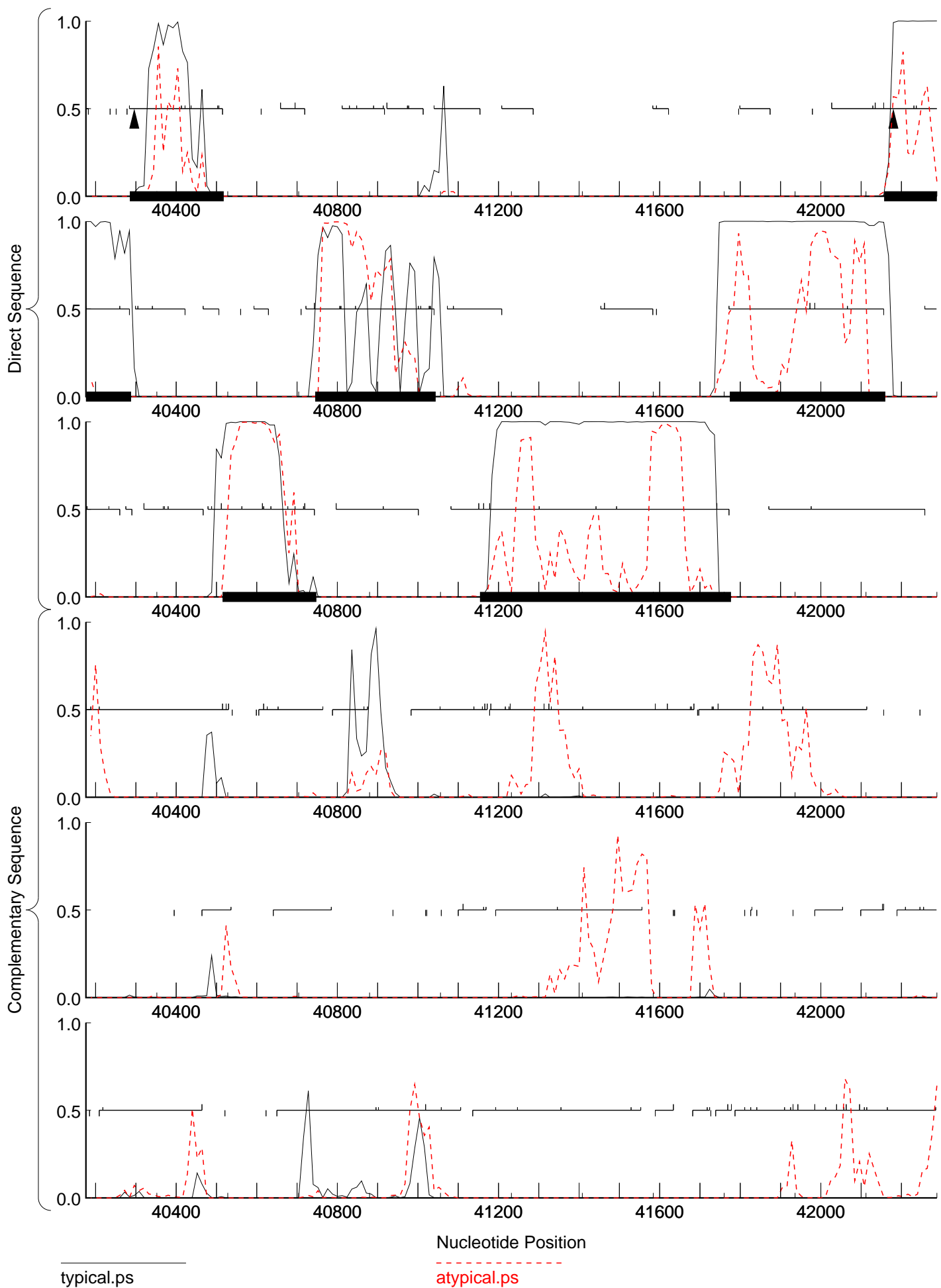




typical.ps

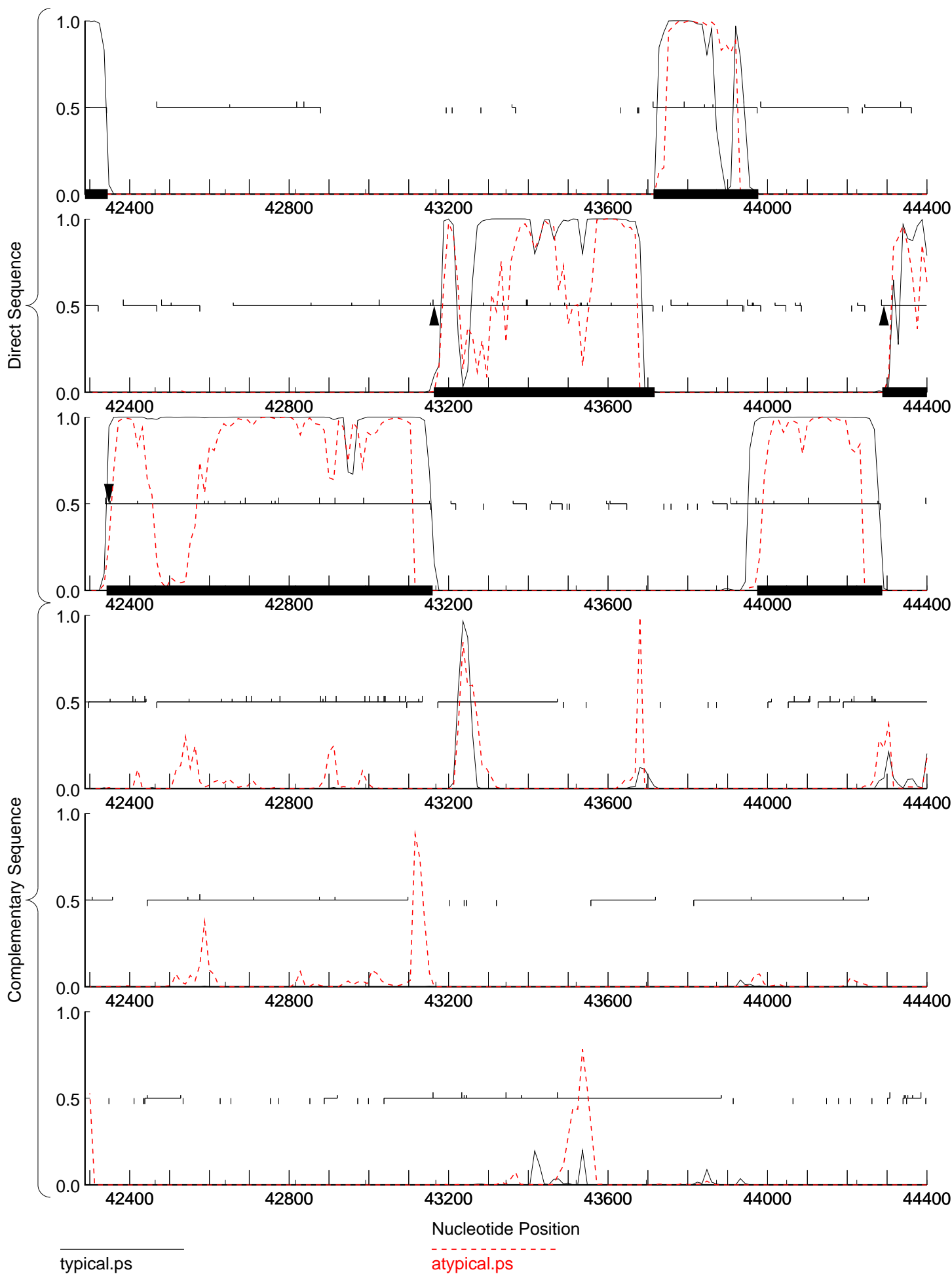
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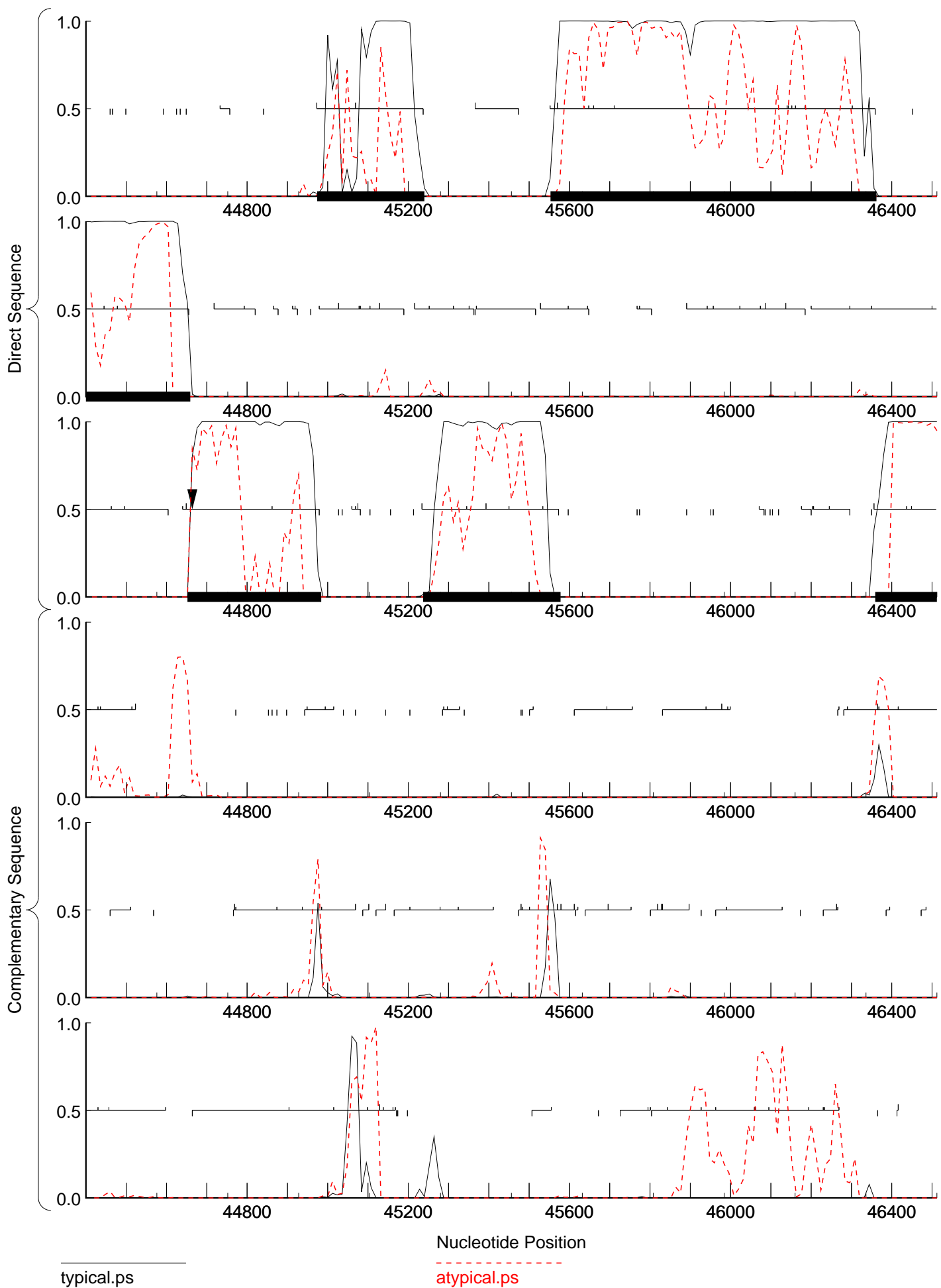


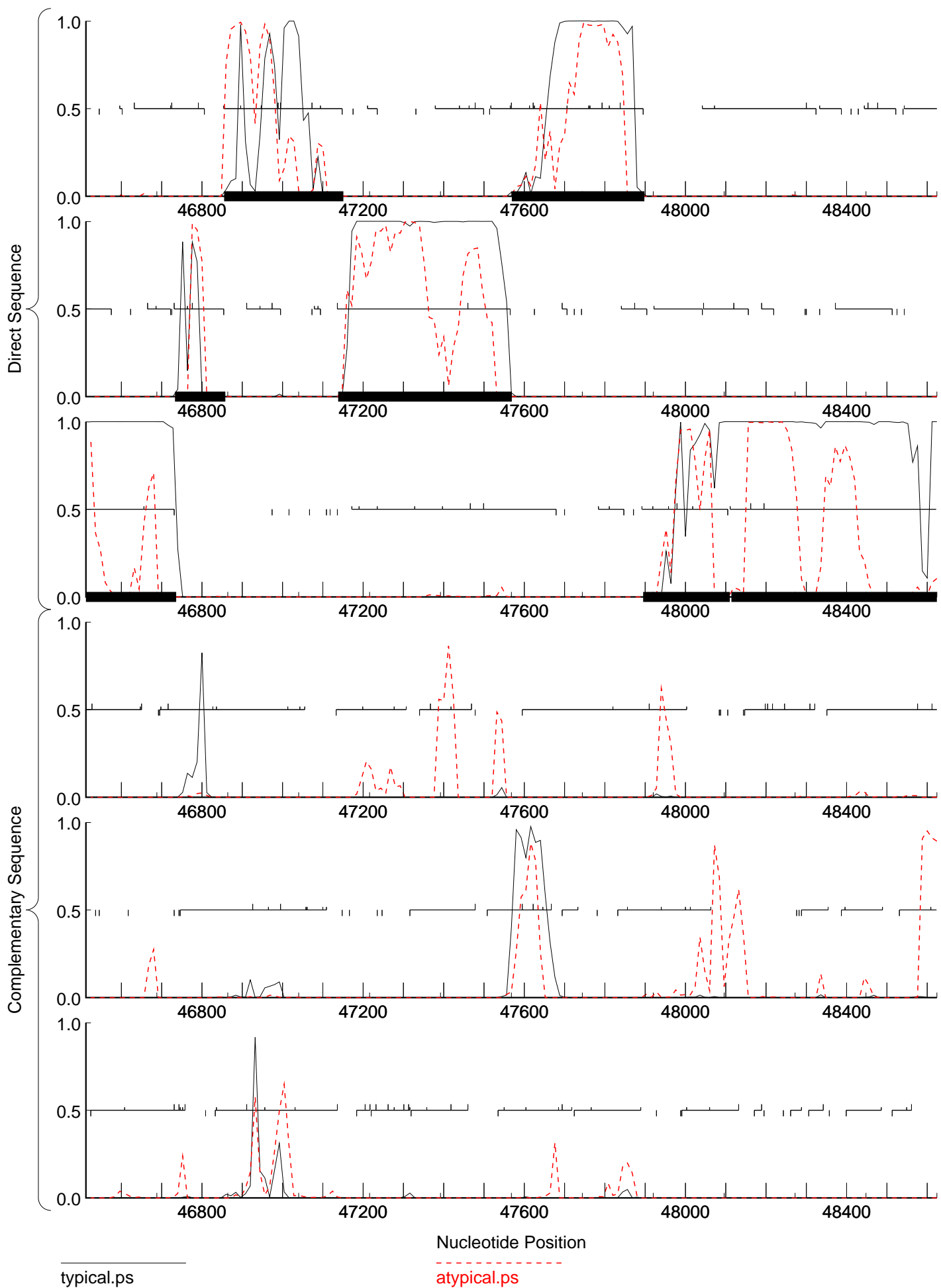


typical.ps

atypical.ps

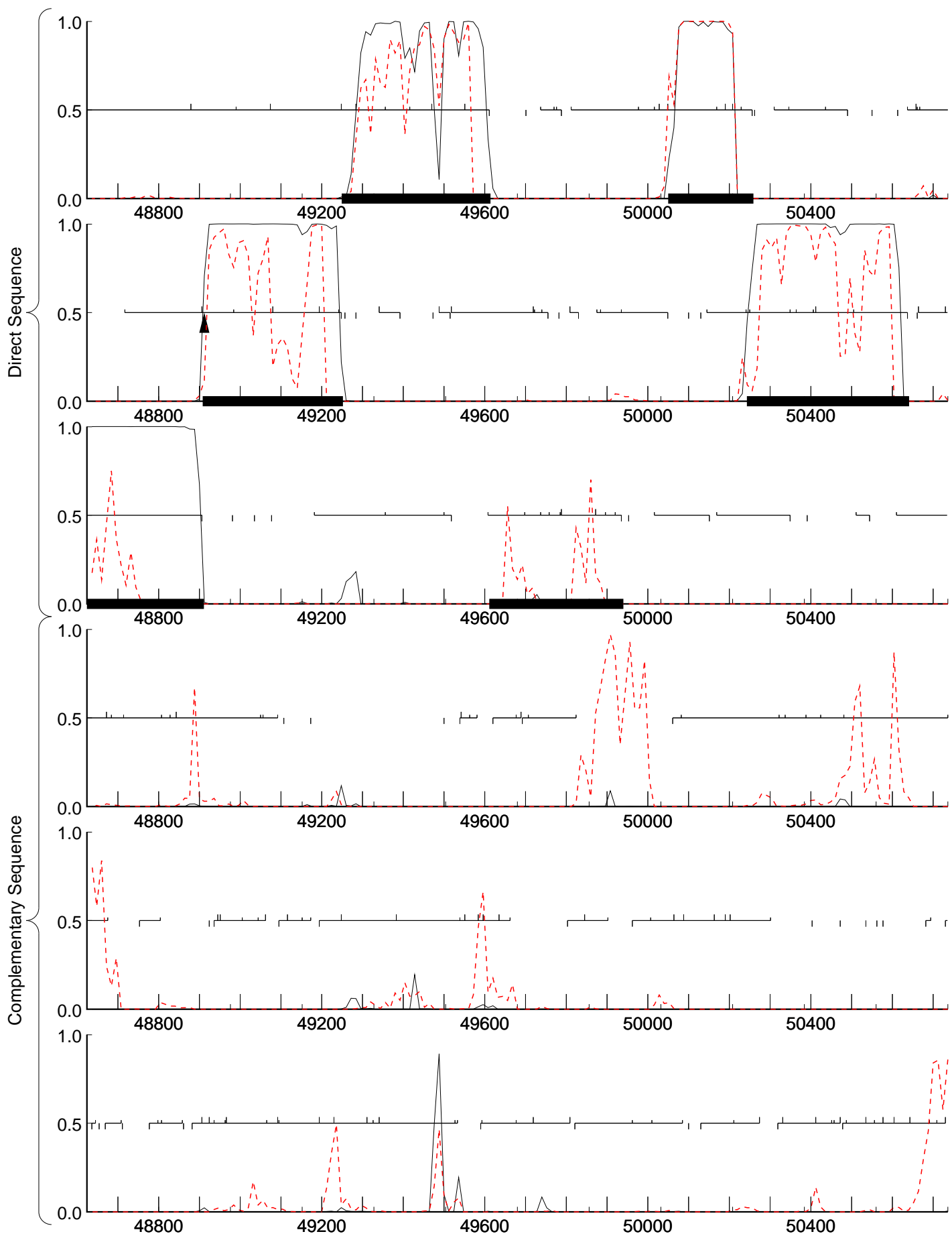






typical.ps

atypical.ps



typical.ps

atypical.ps

