

GeneMark

Version 2.5p (09.08.06)

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PROGRAM INFORMATION

Sequence : Mycobacterium phage DoctorDiddles complete sequence, 75070 bp including 9-base 3' overhang
Analysis Date : 8/20/18 at 8:29:28
Pages : 37
Sequence Length : 75070 bp
GC Content : 62.81%

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,

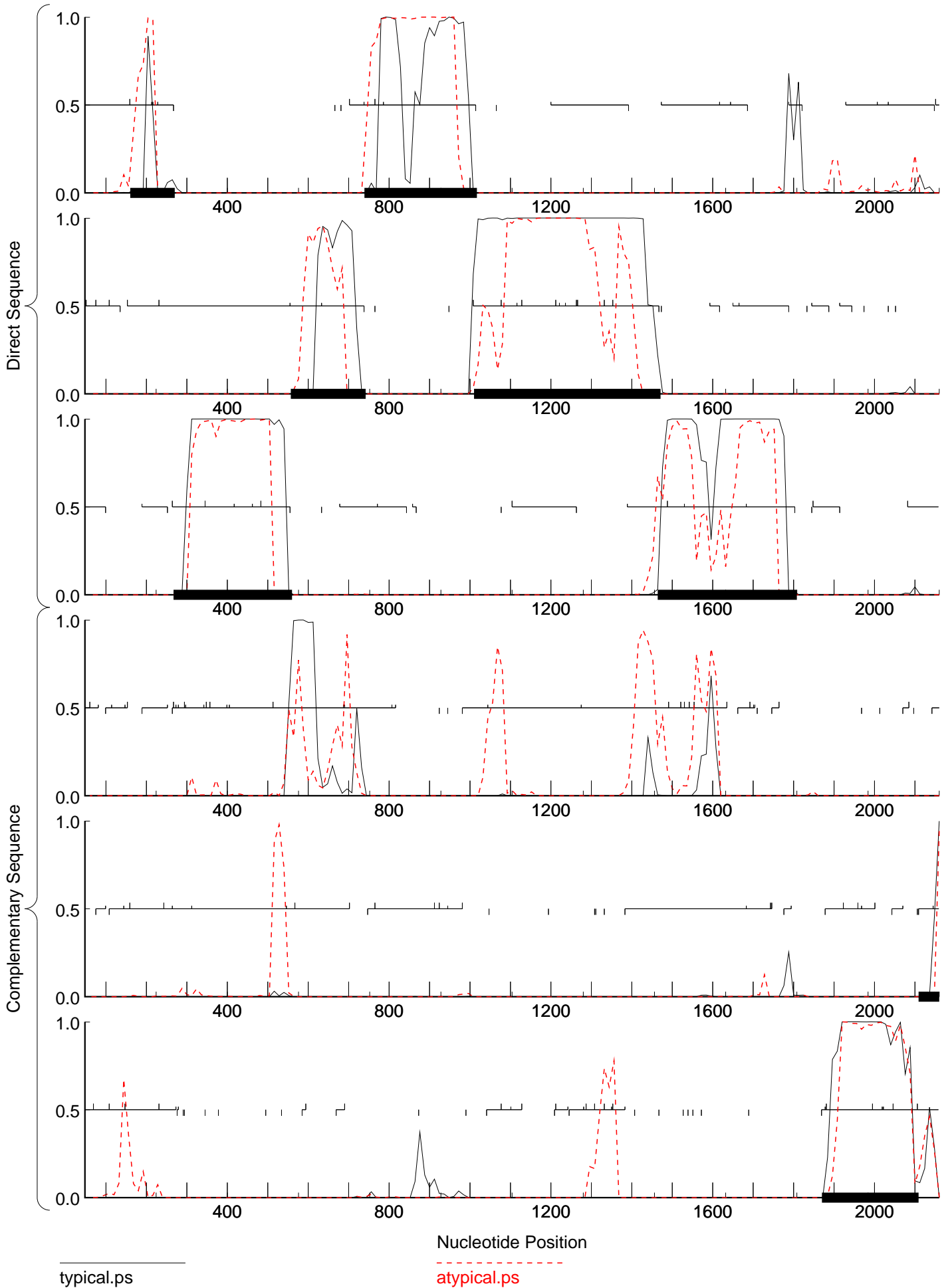
MATRIX INFORMATION

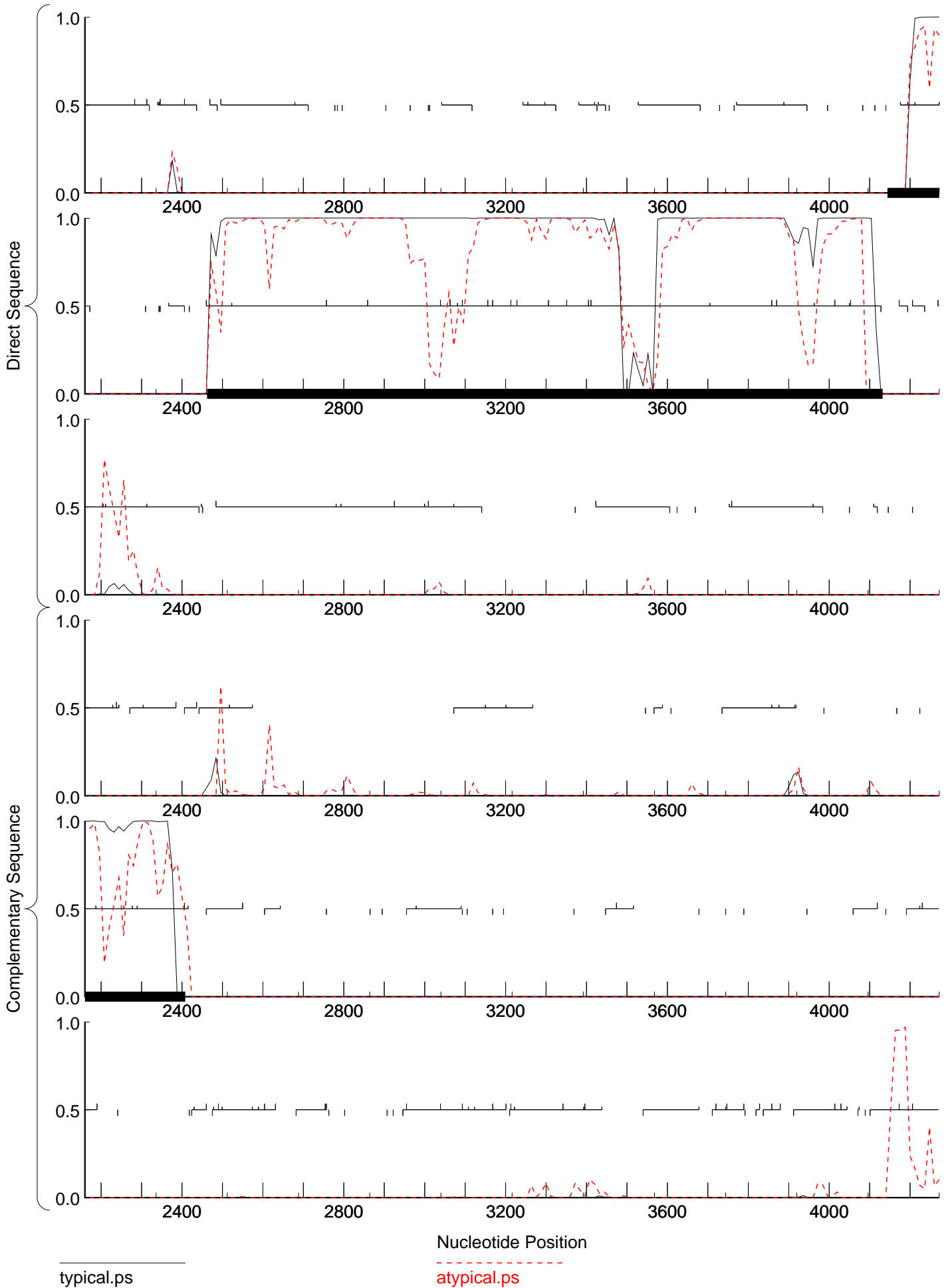
Matrix : -
Author : -
Order : 4

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

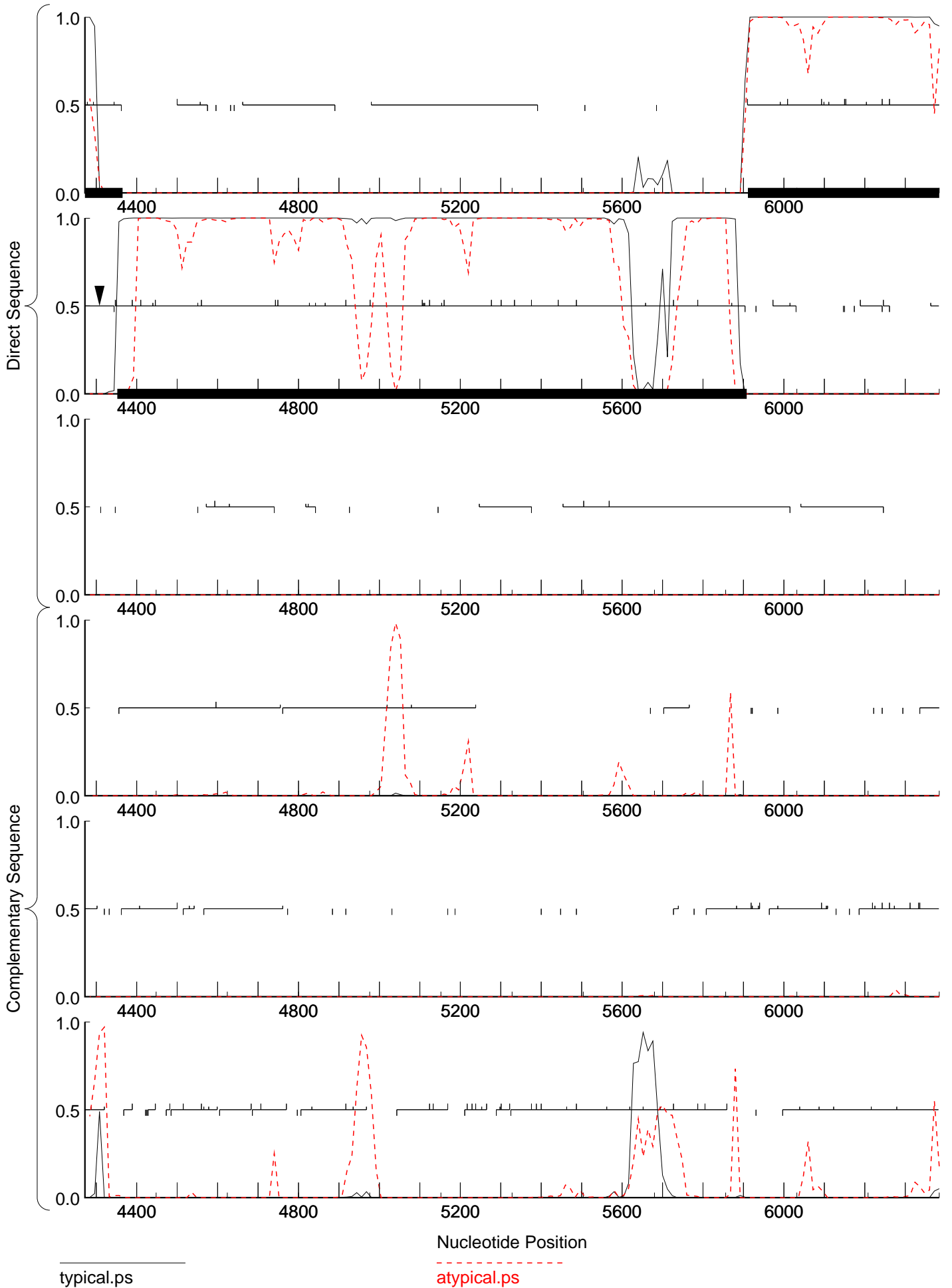
Matrix notes & comments

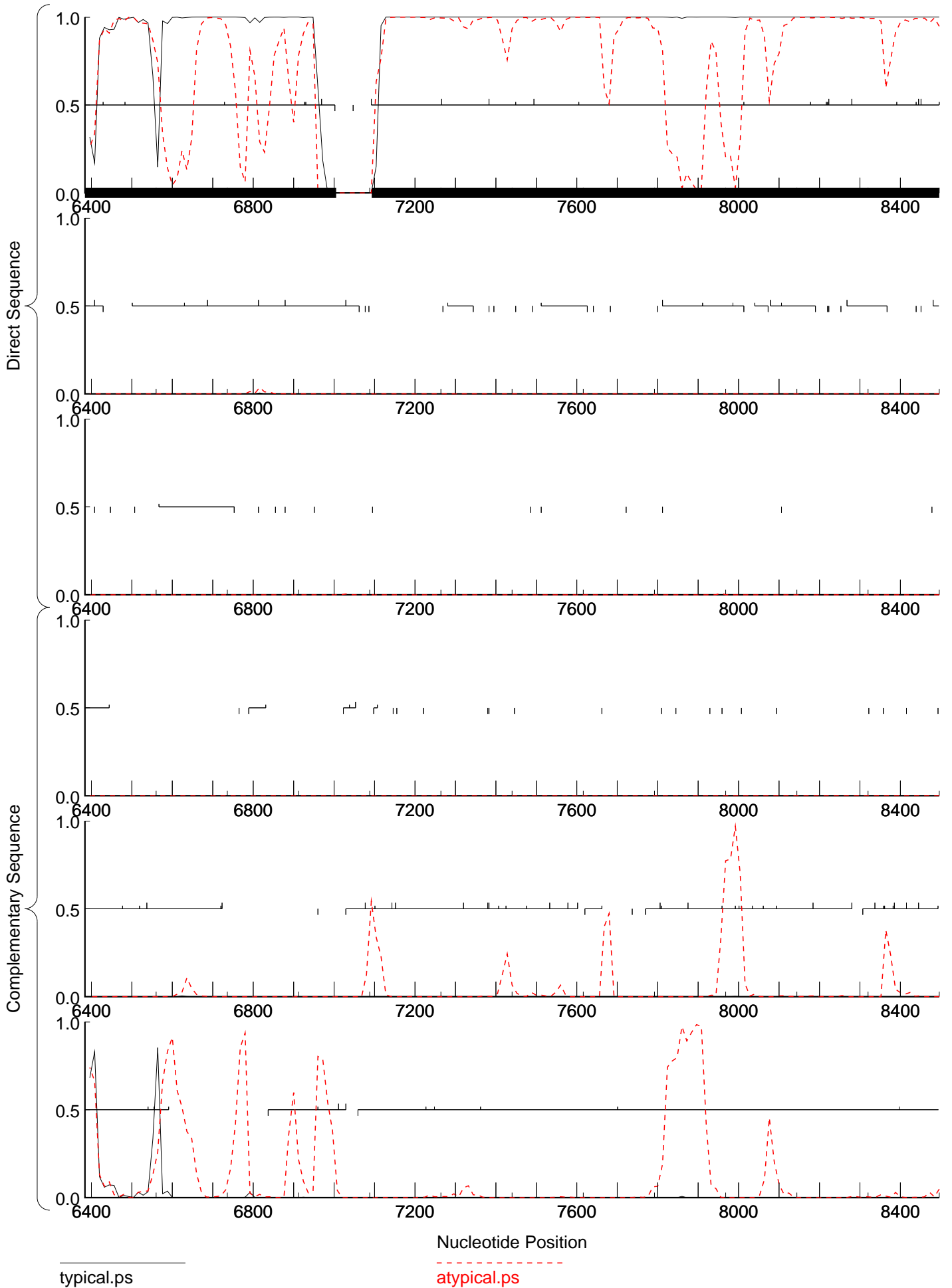
Training set derived by GeneMarkS, 4.30 October 2014
Mon Aug 20 08:29:28 2018

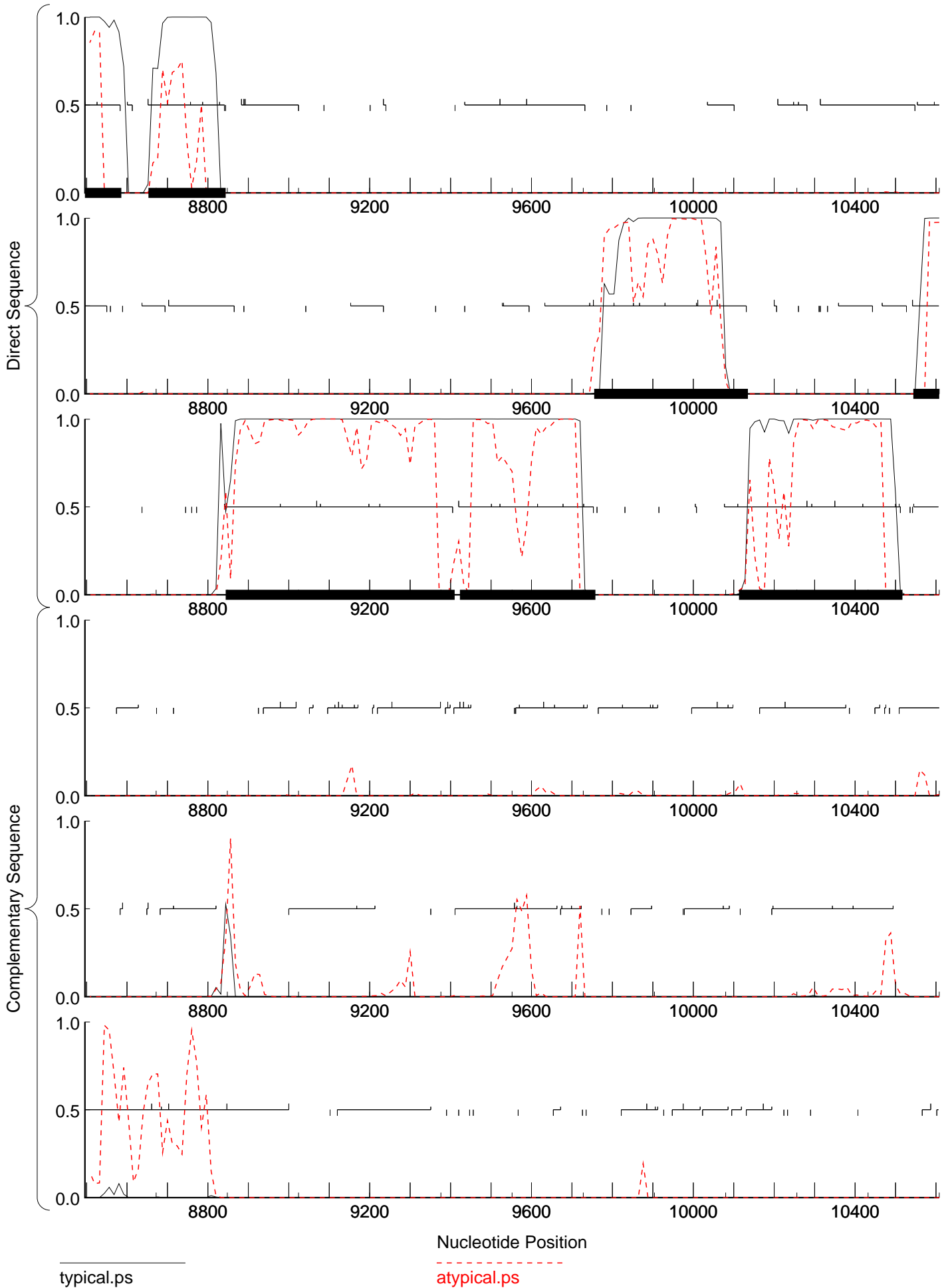




...iddles complete sequence, 75070 bp including 9-base 3' overhang (CGCTTGTC), Cluster E, Order 4, Window 96, Step 12, 4/37
...iddles complete sequence, 75070 bp including 9-base 3' overhang (CGCTTGTC), Cluster E, Order 2, Window 96, Step 12, 4/37

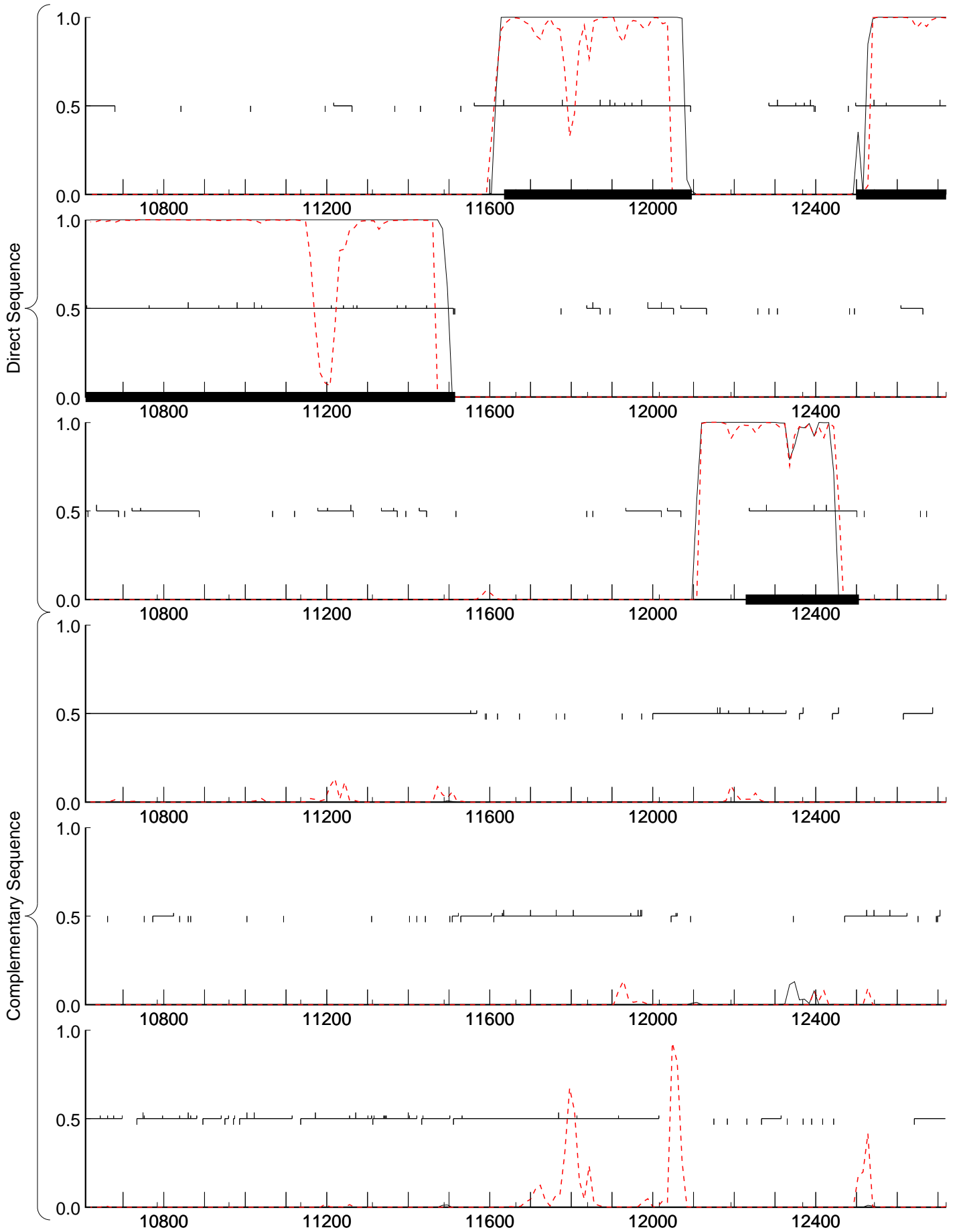






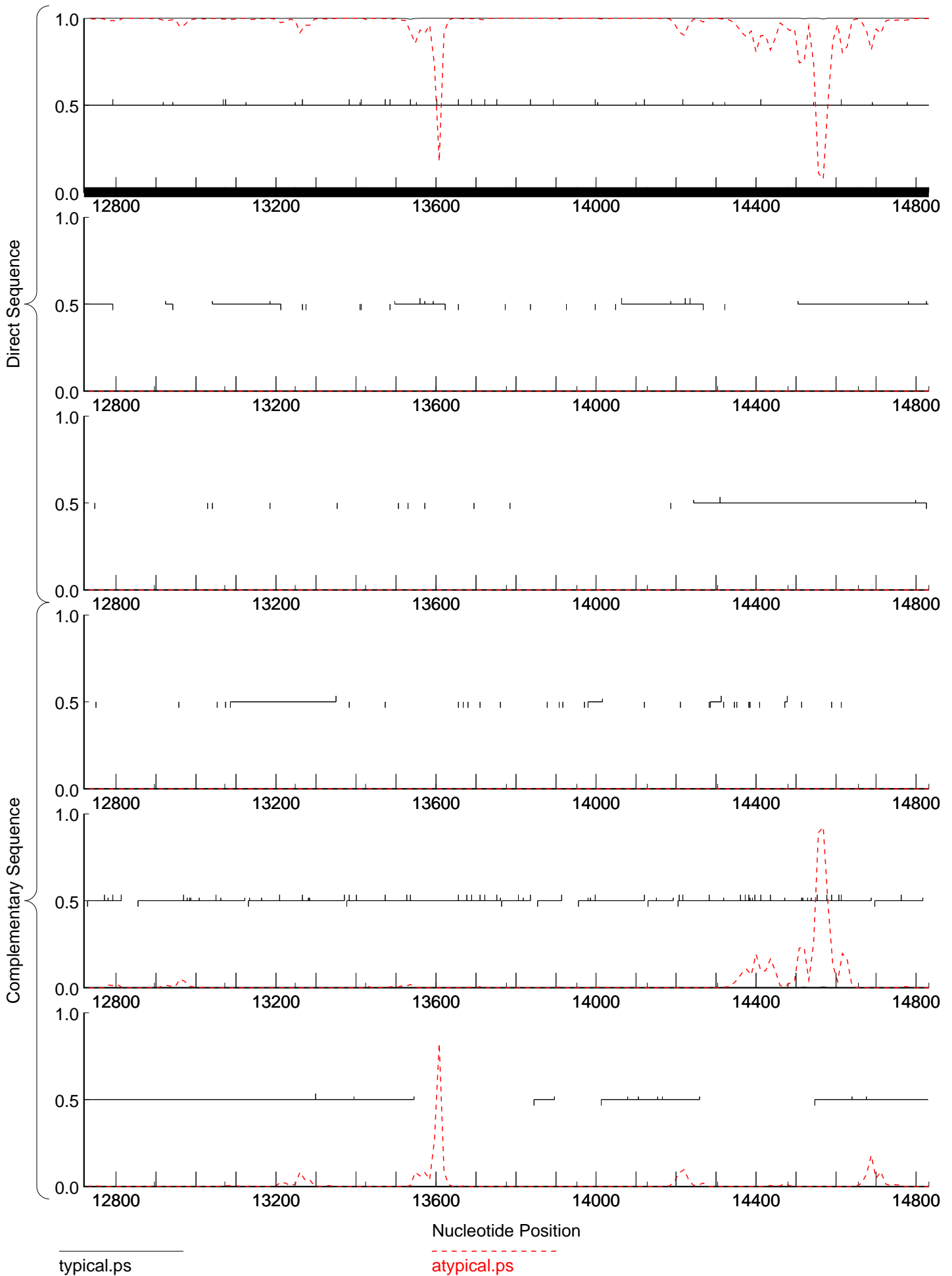
typical.ps

atypical.ps



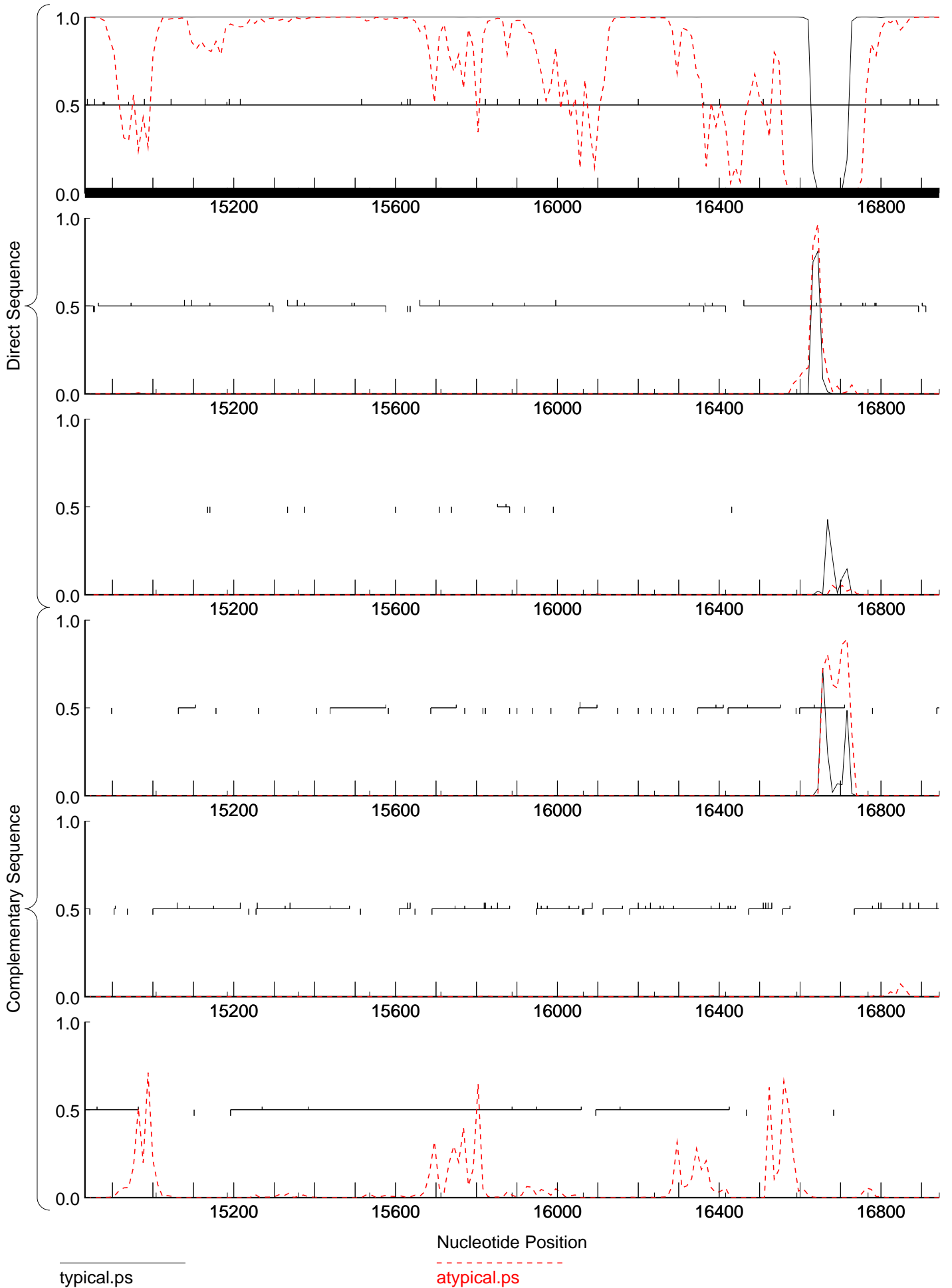
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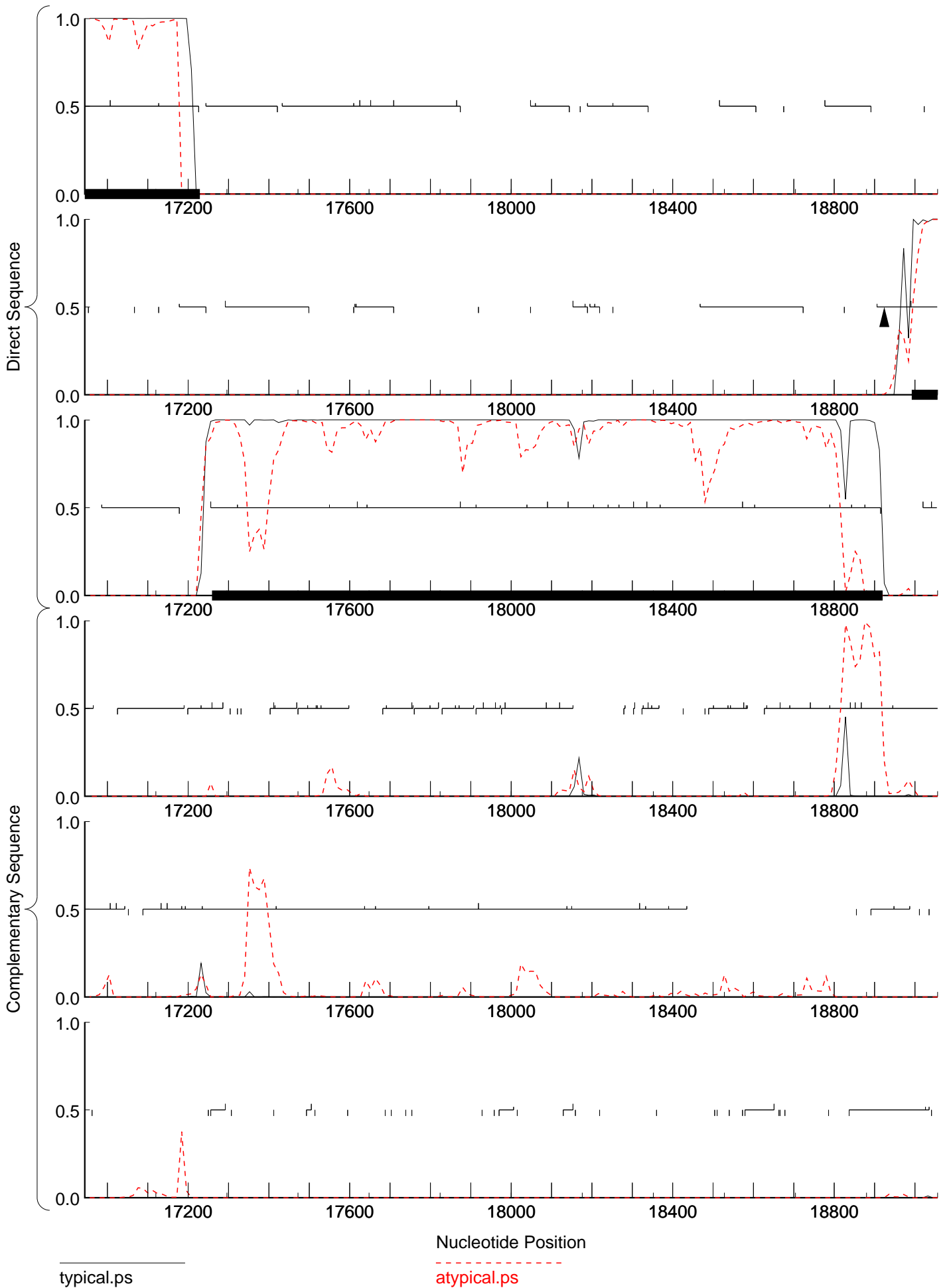
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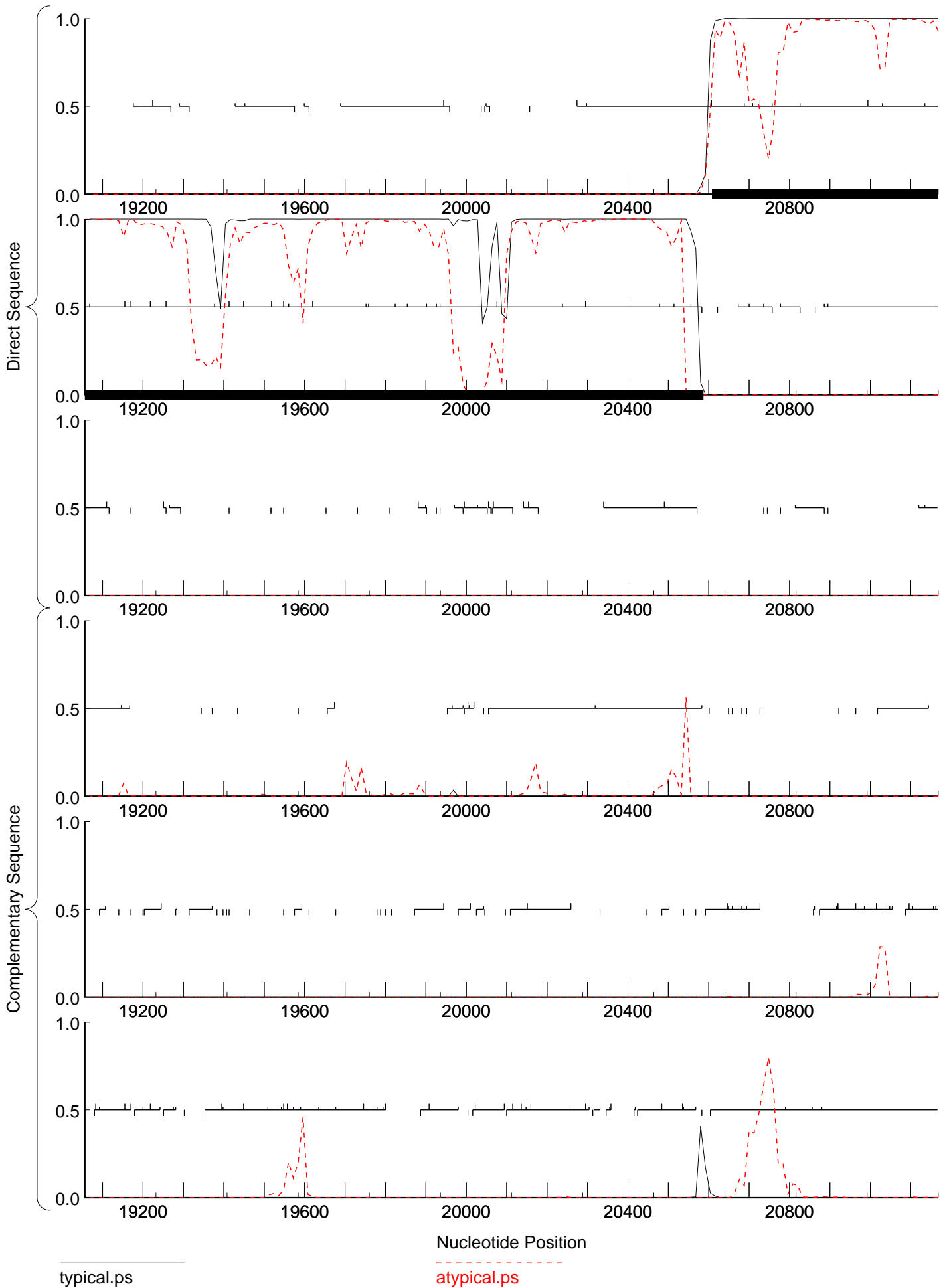


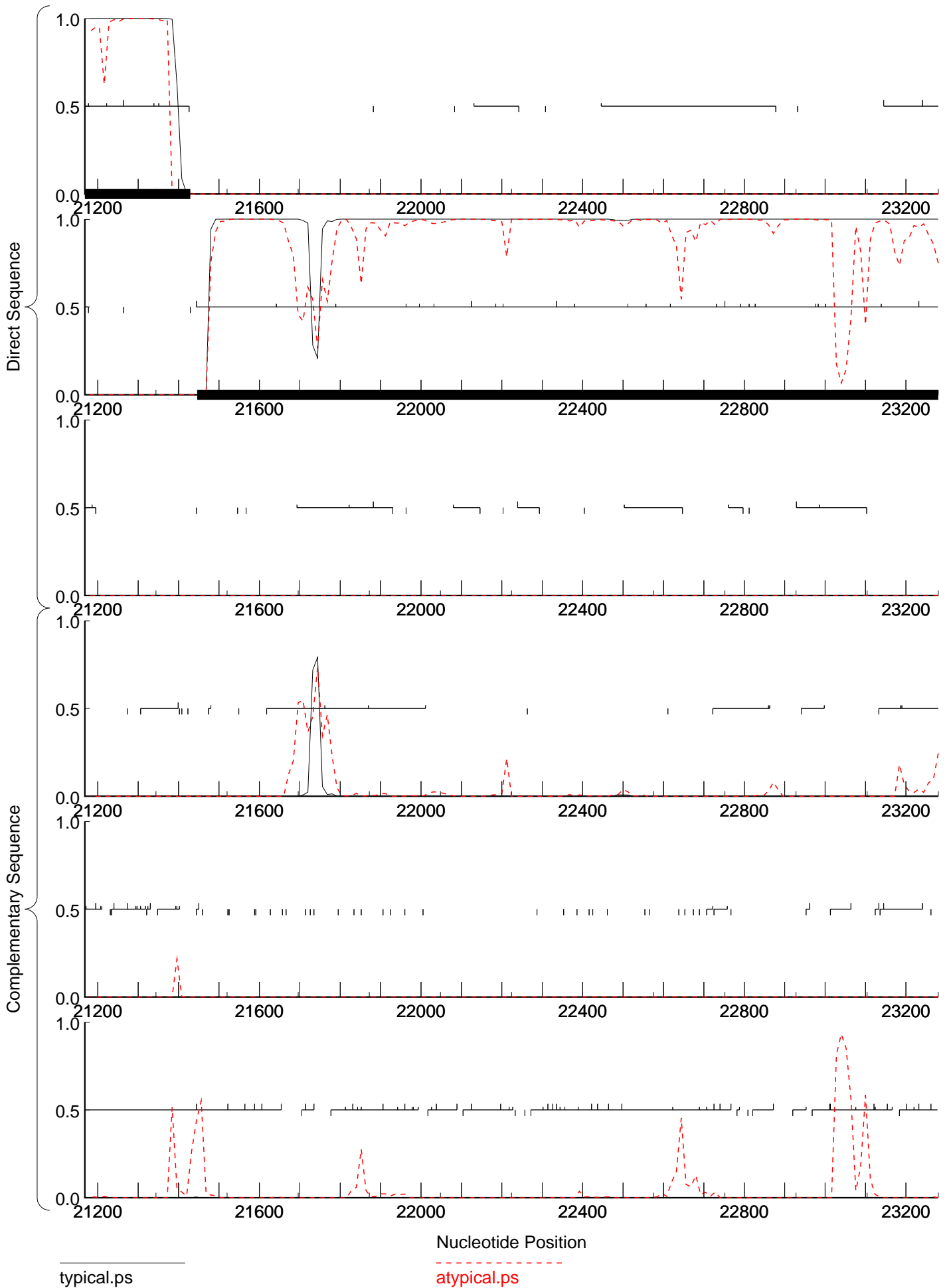
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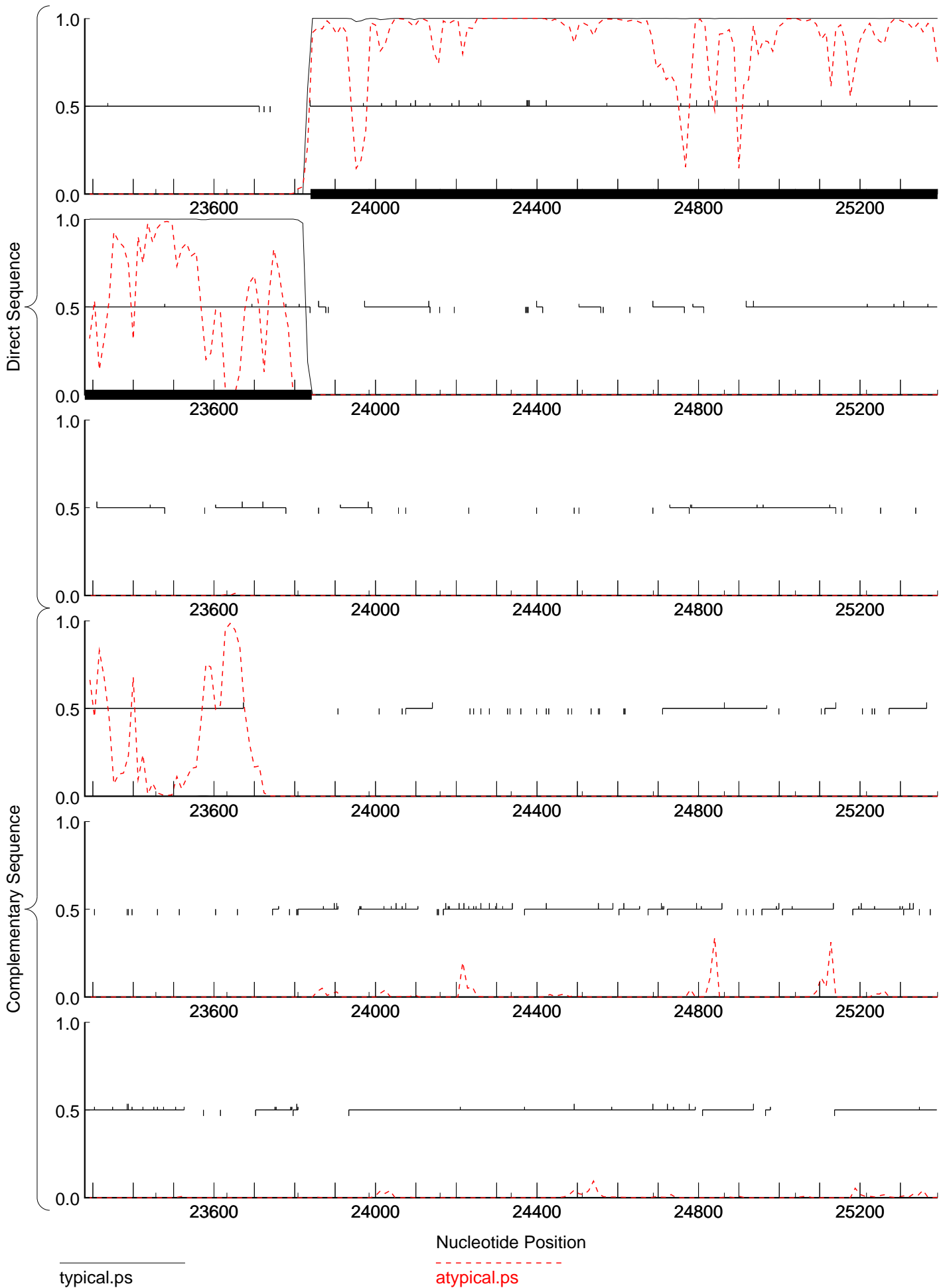
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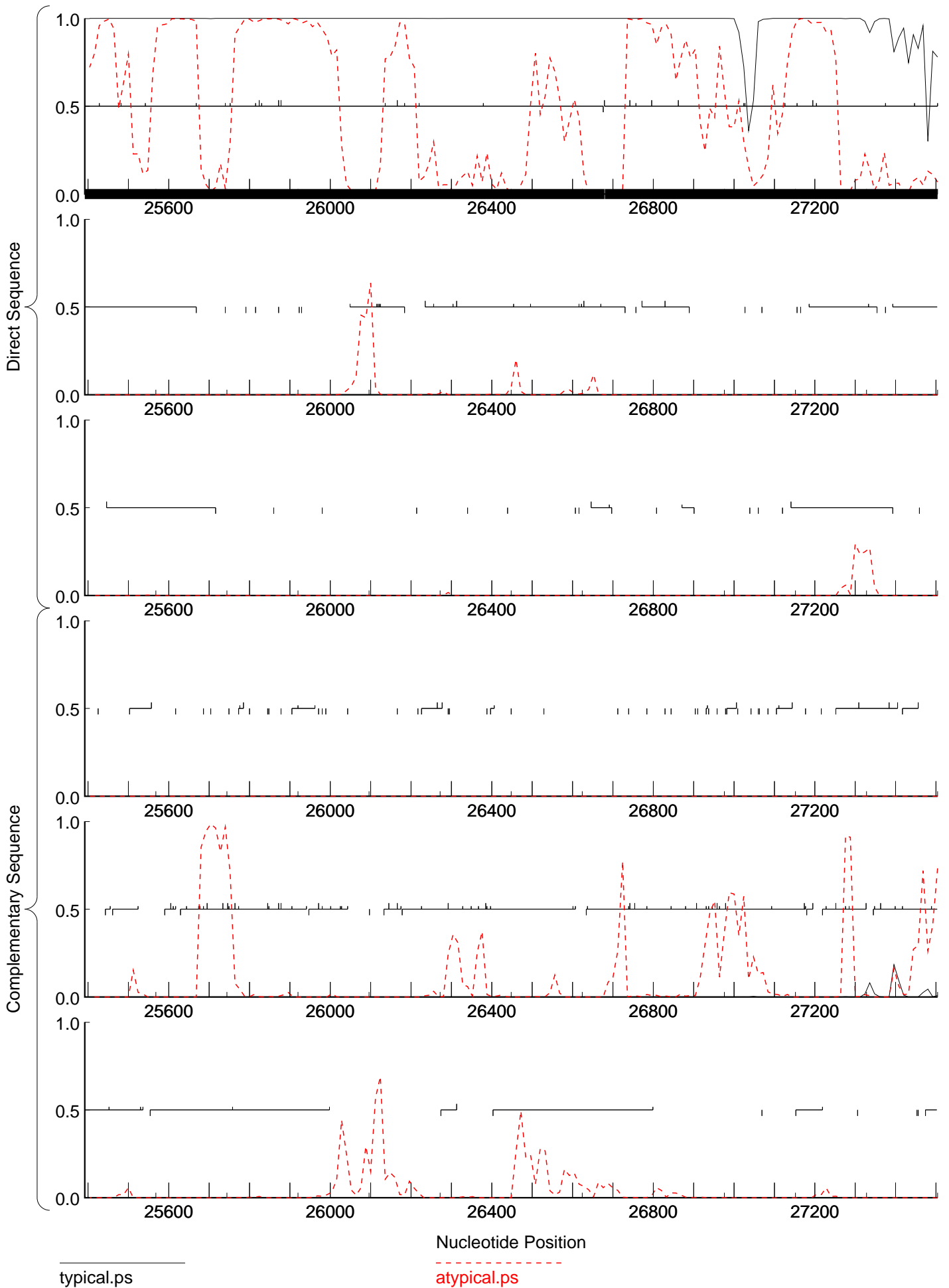






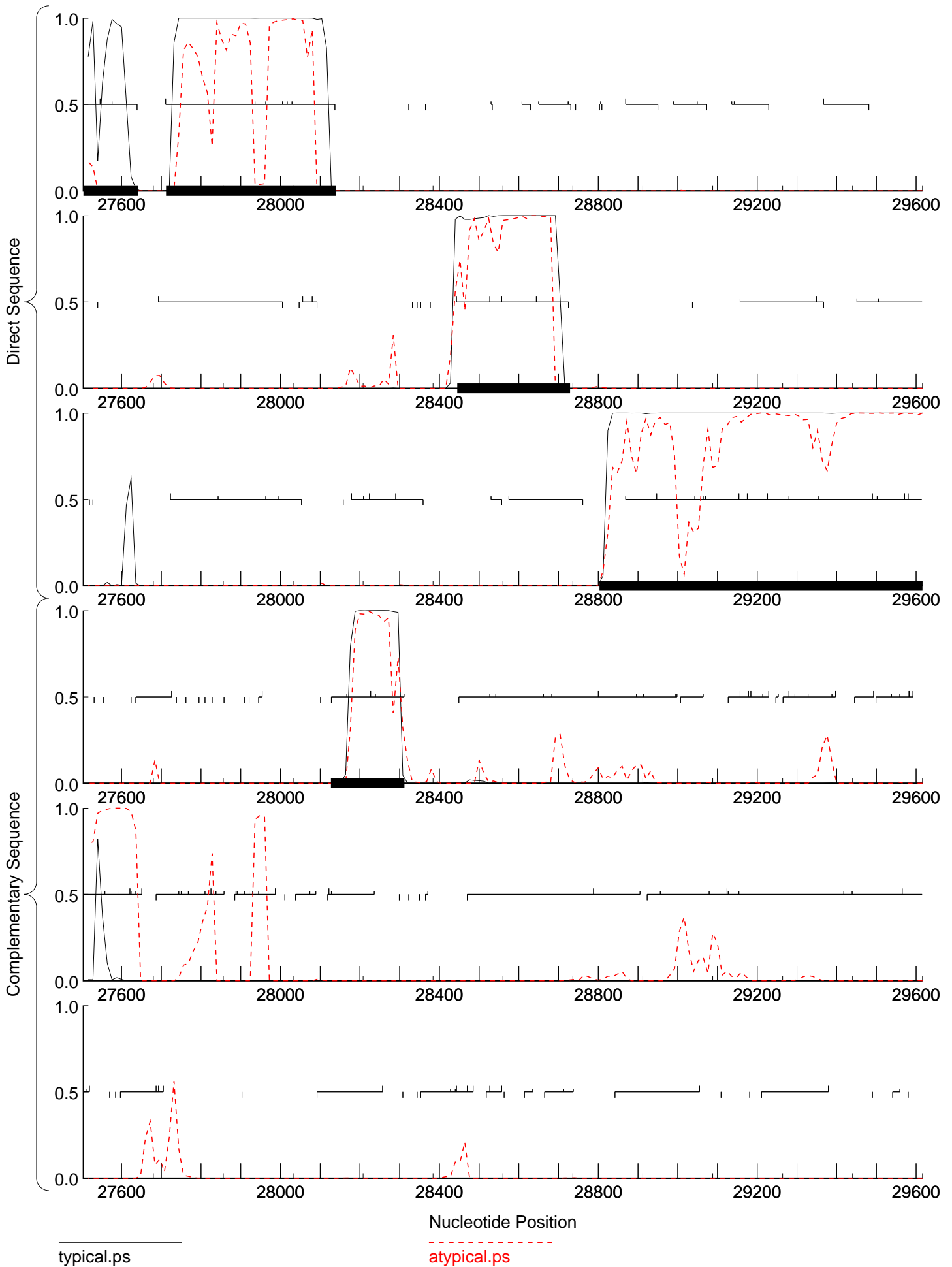


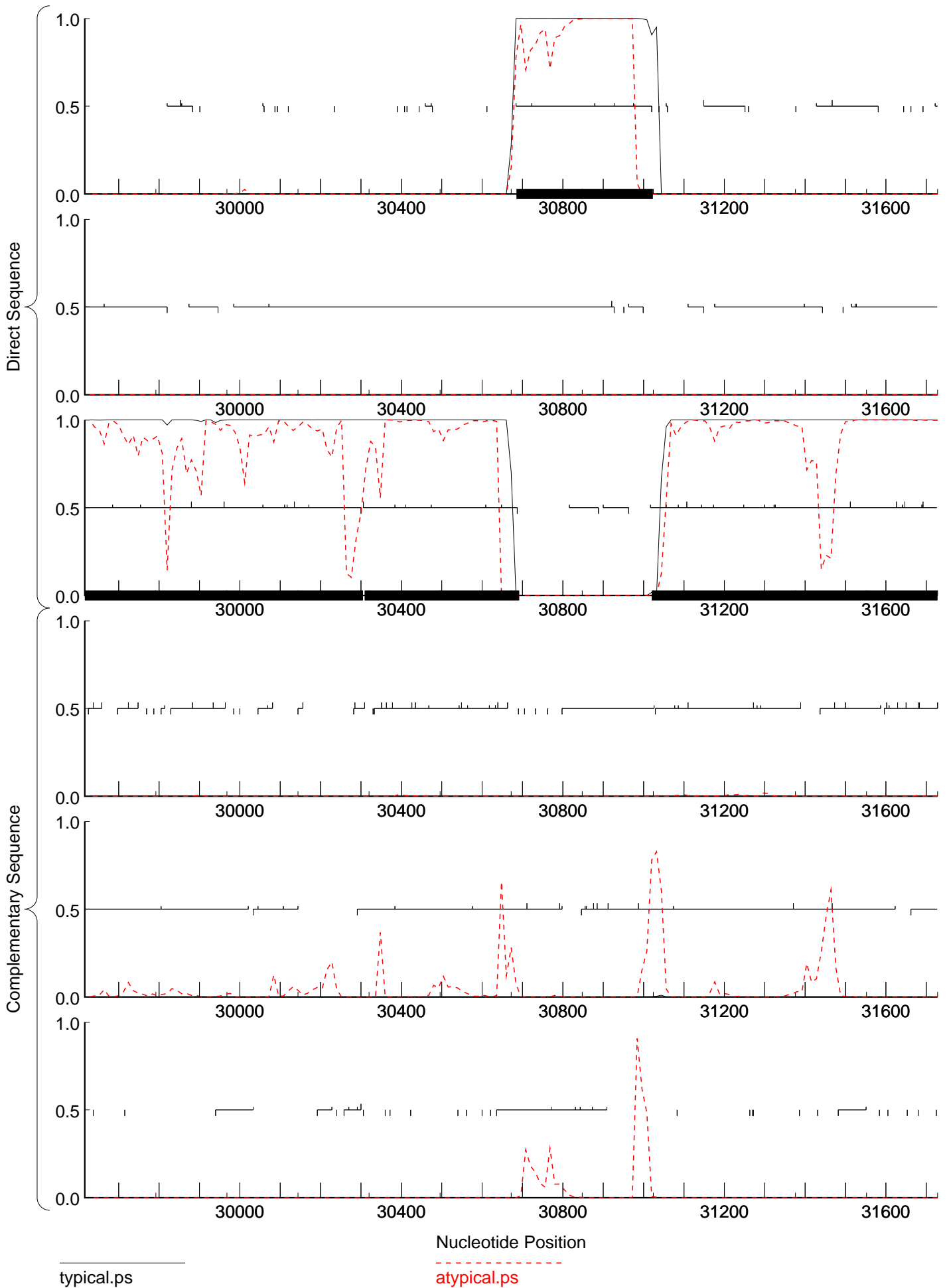


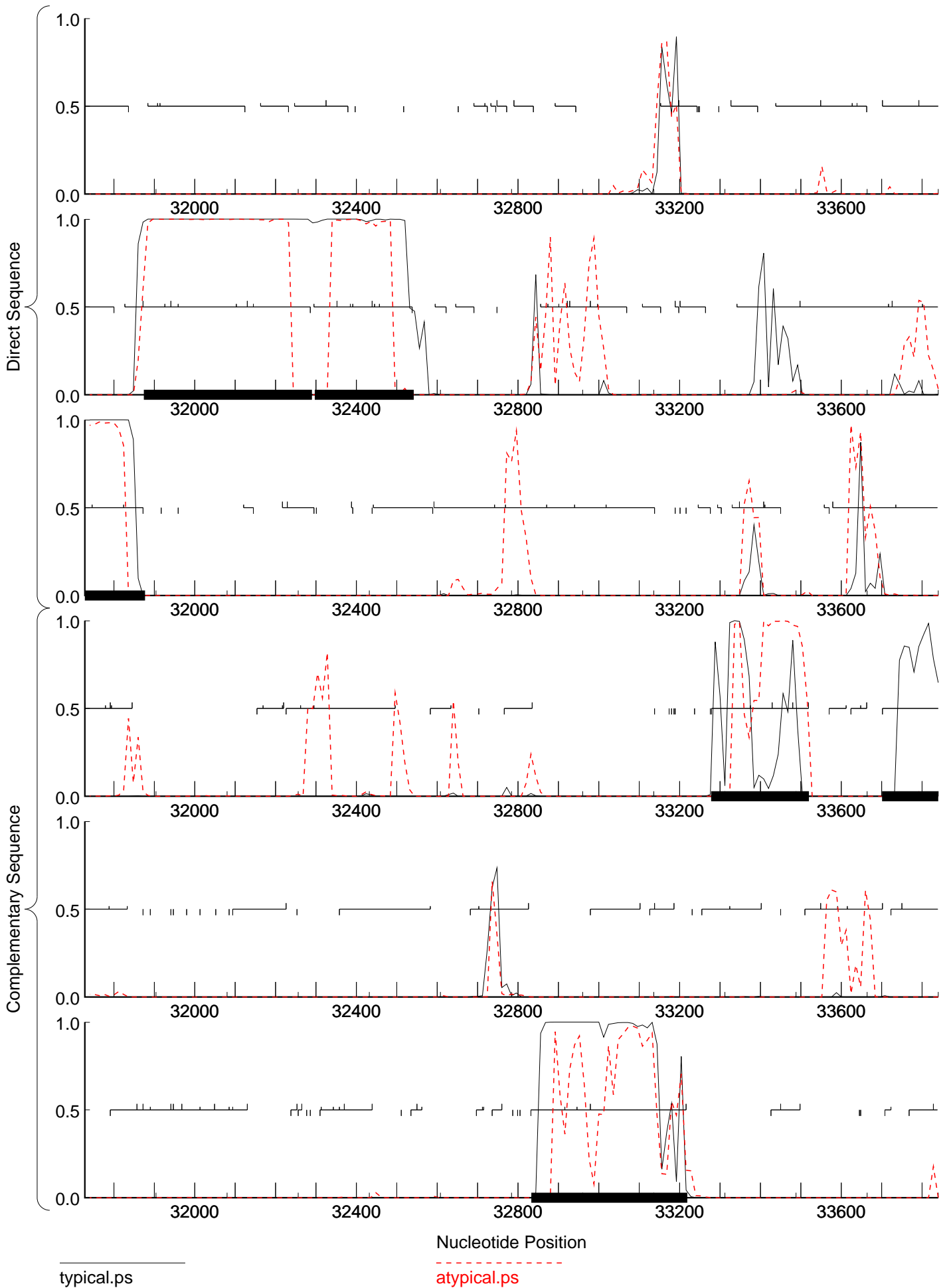


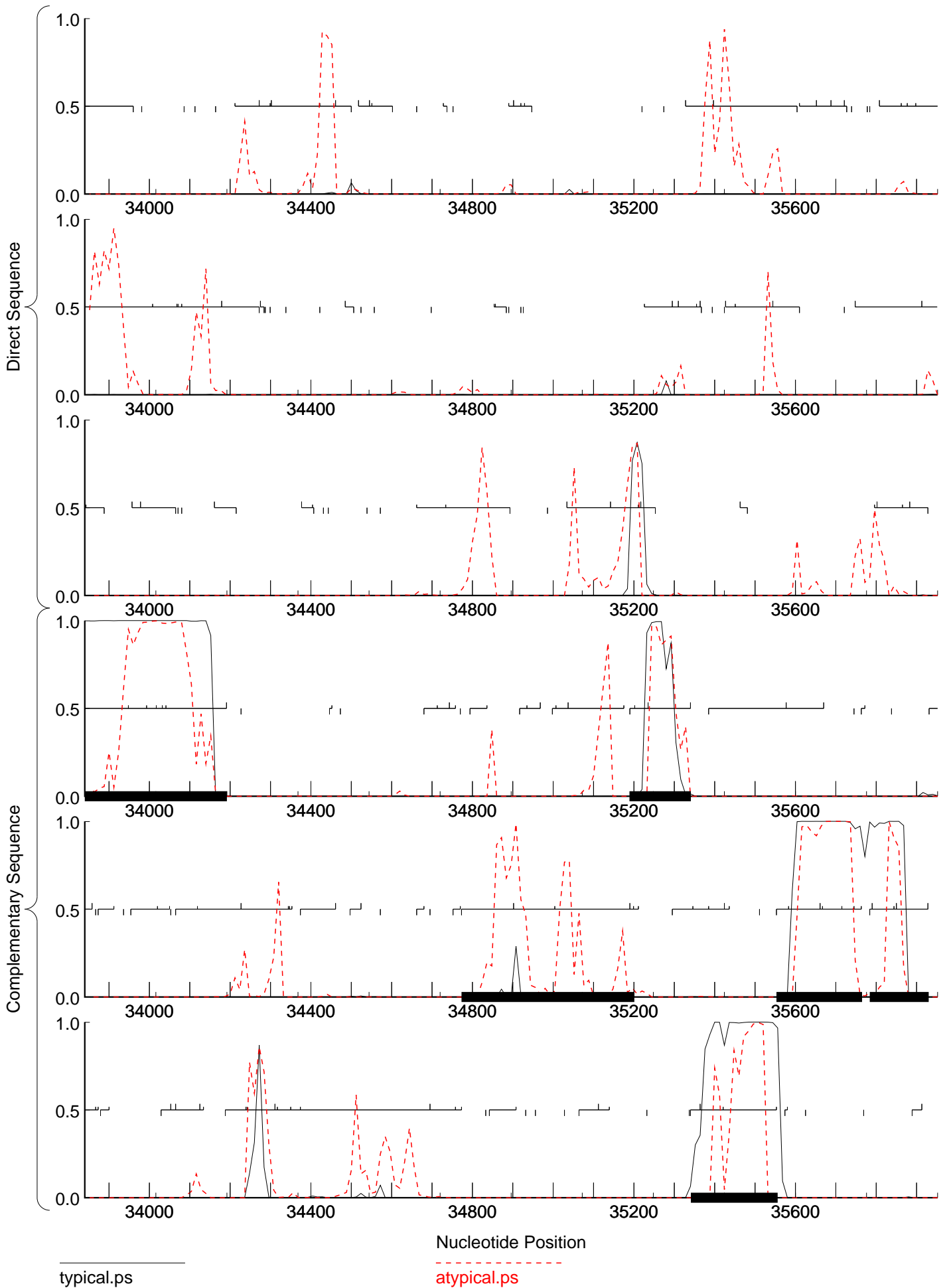
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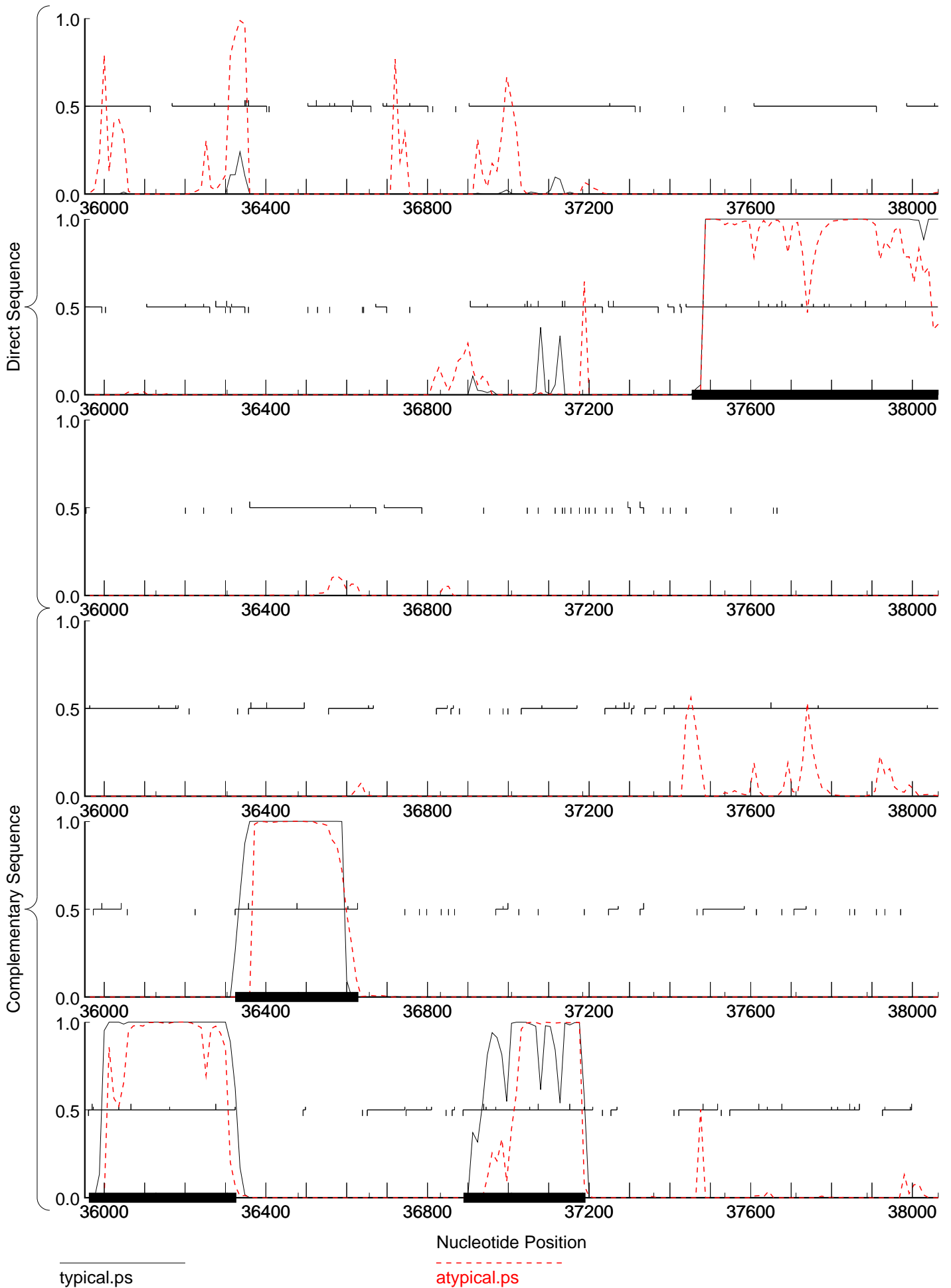
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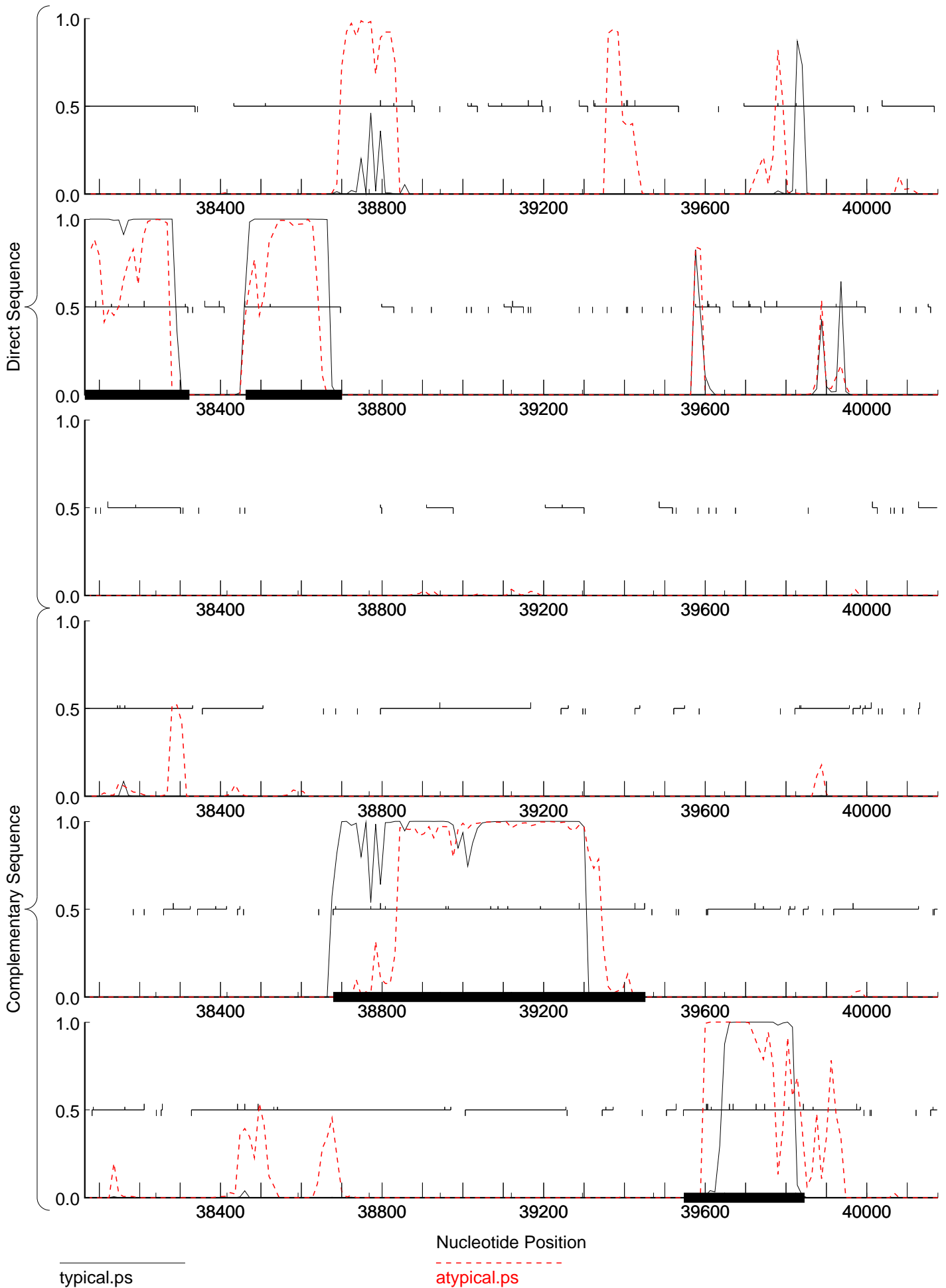


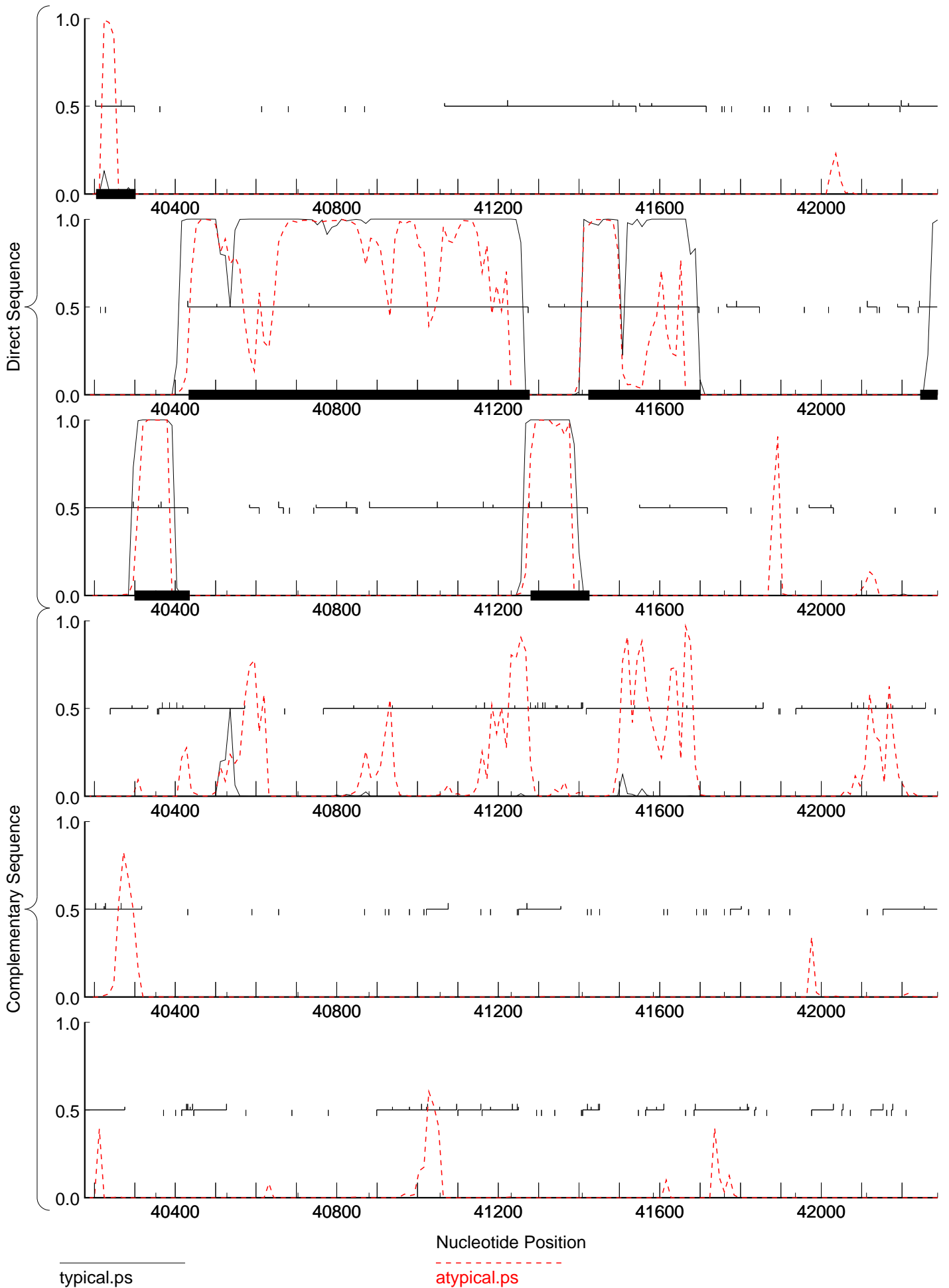


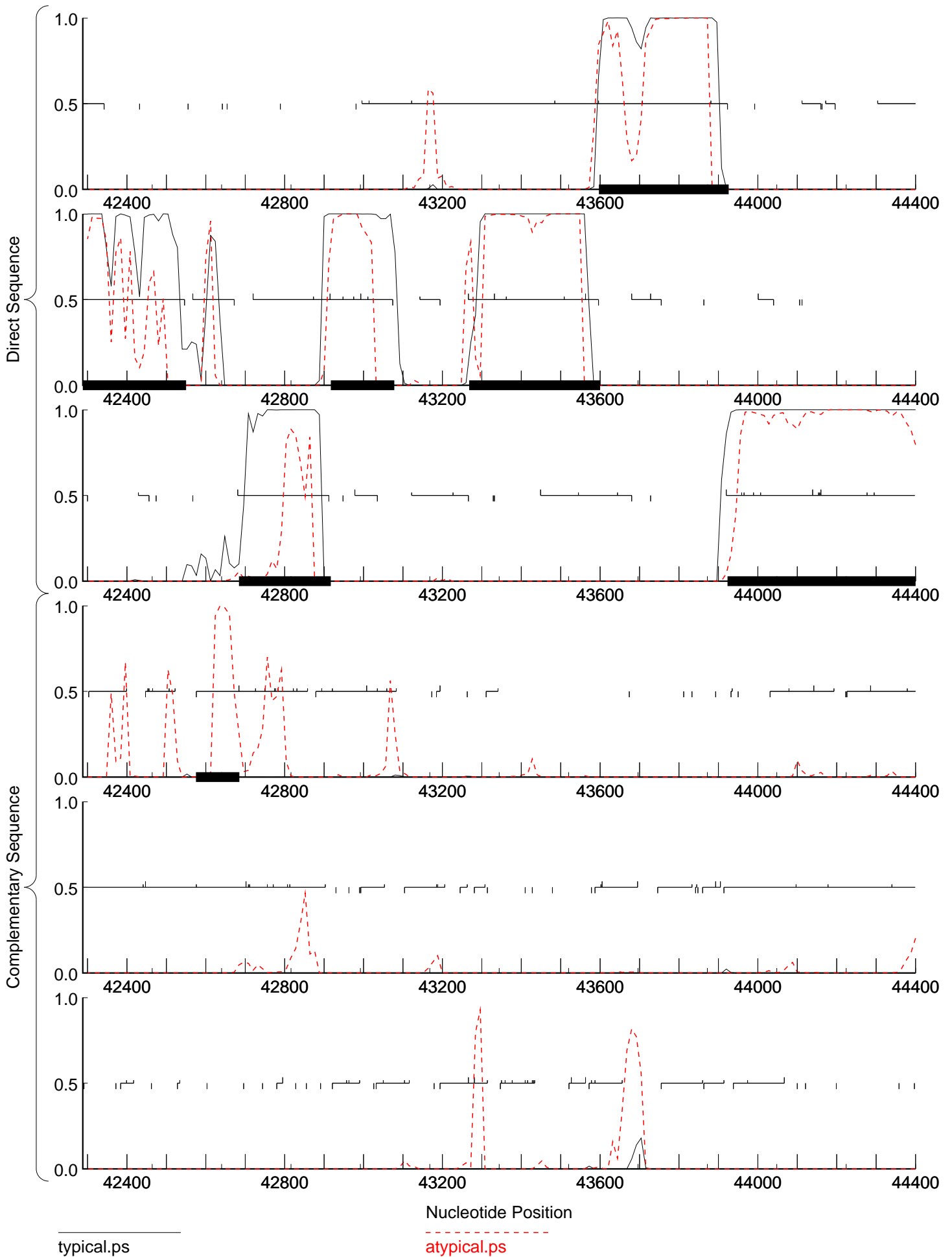






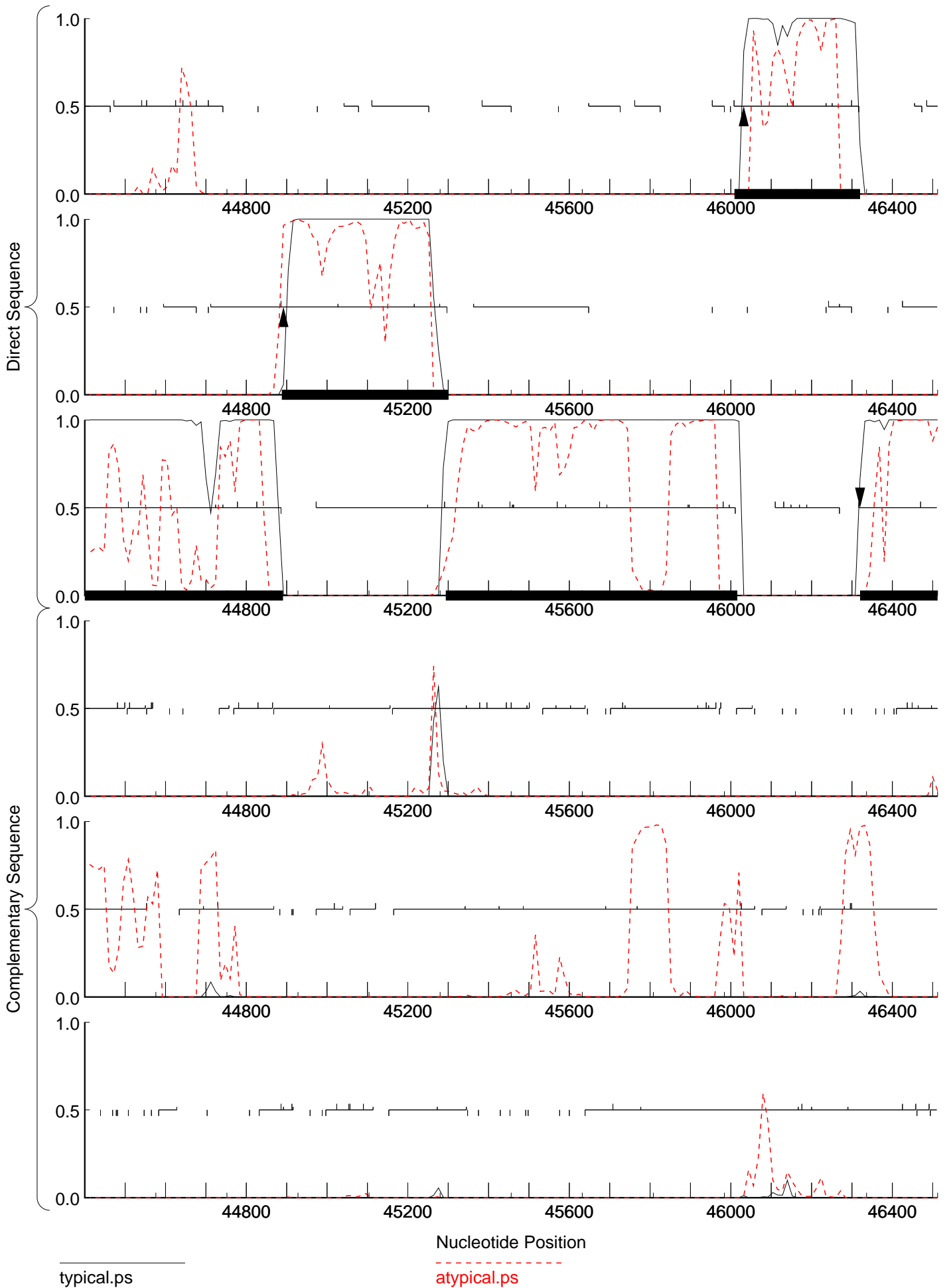


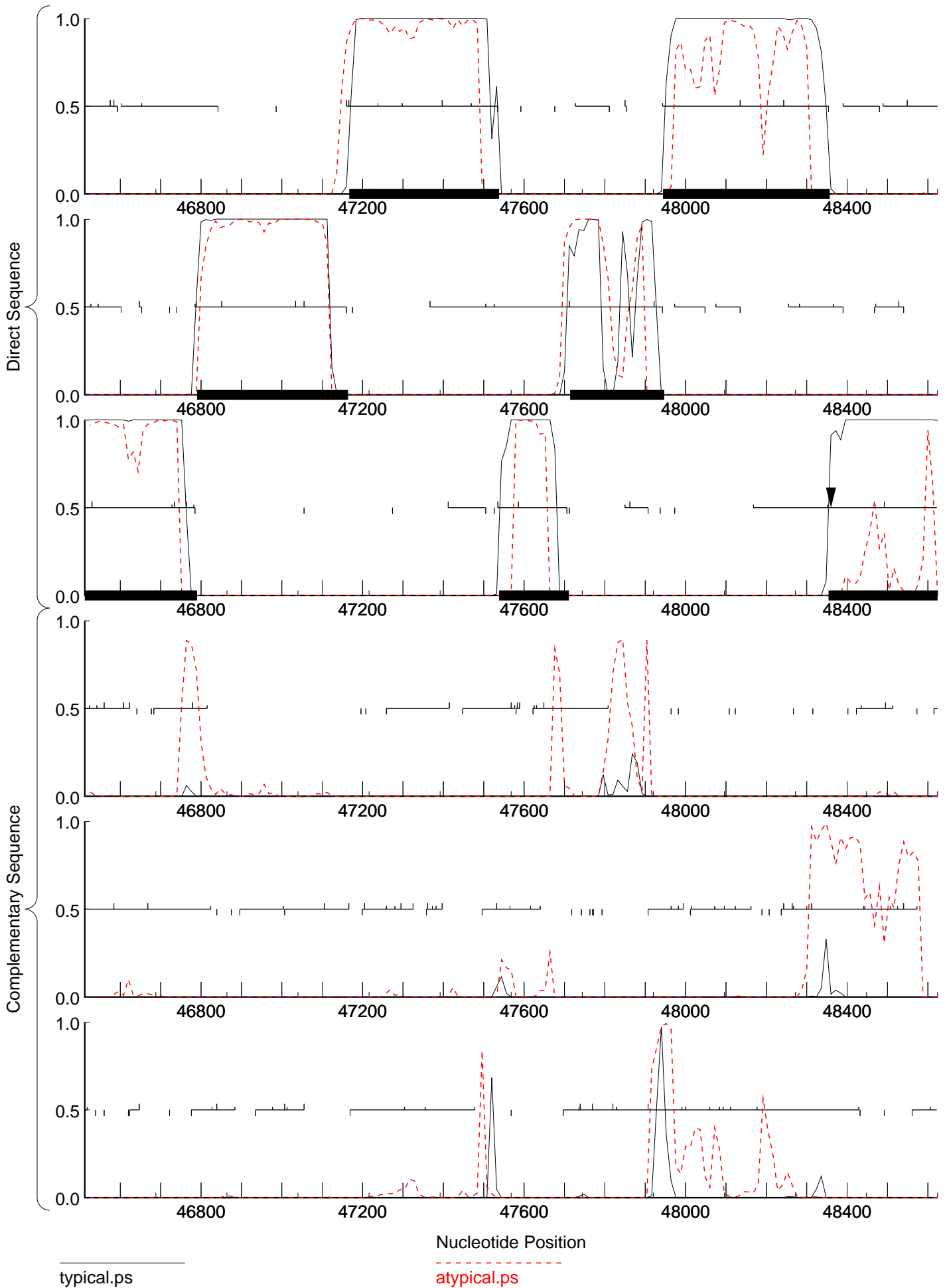


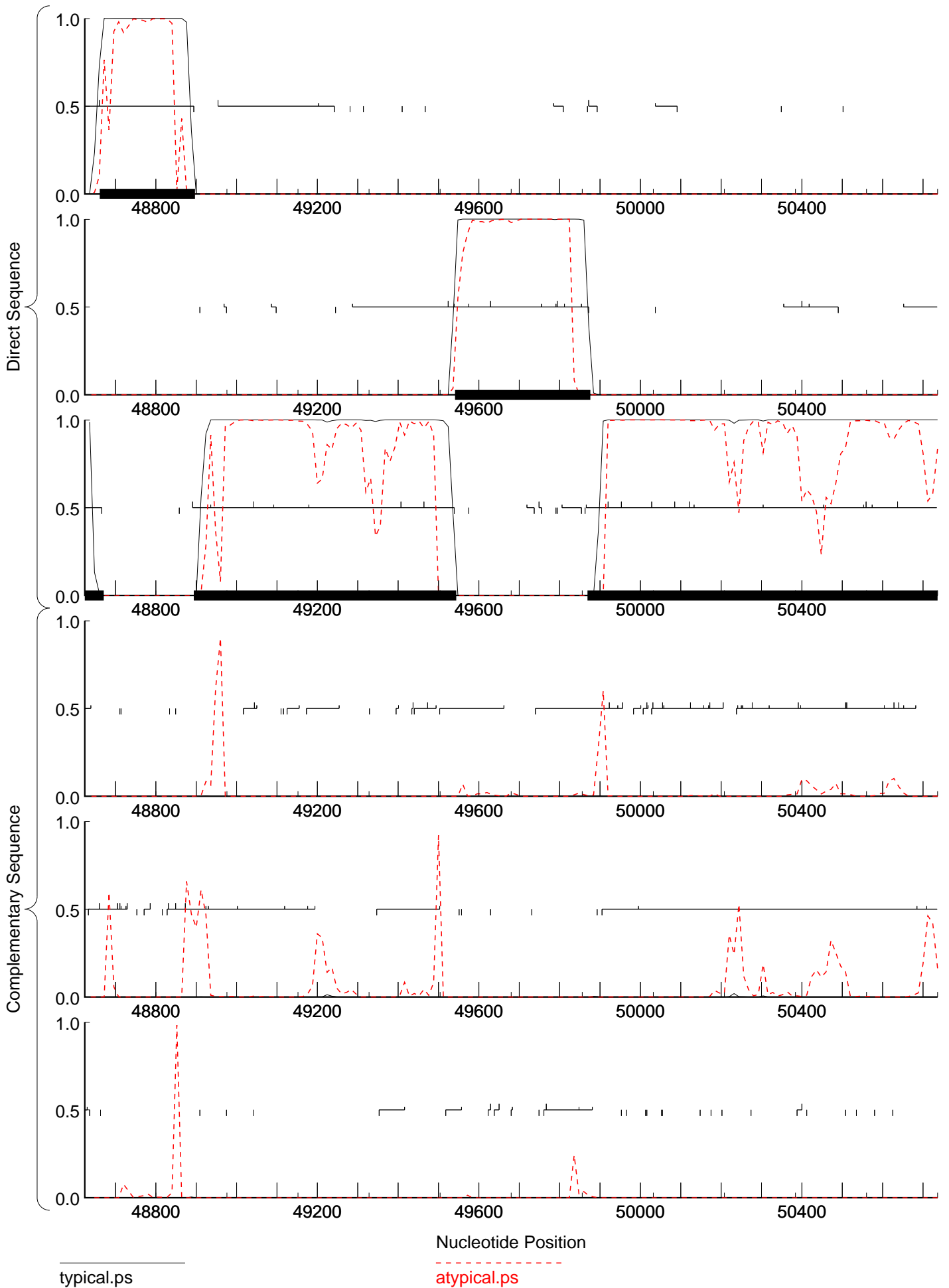


typical.ps

atypical.ps

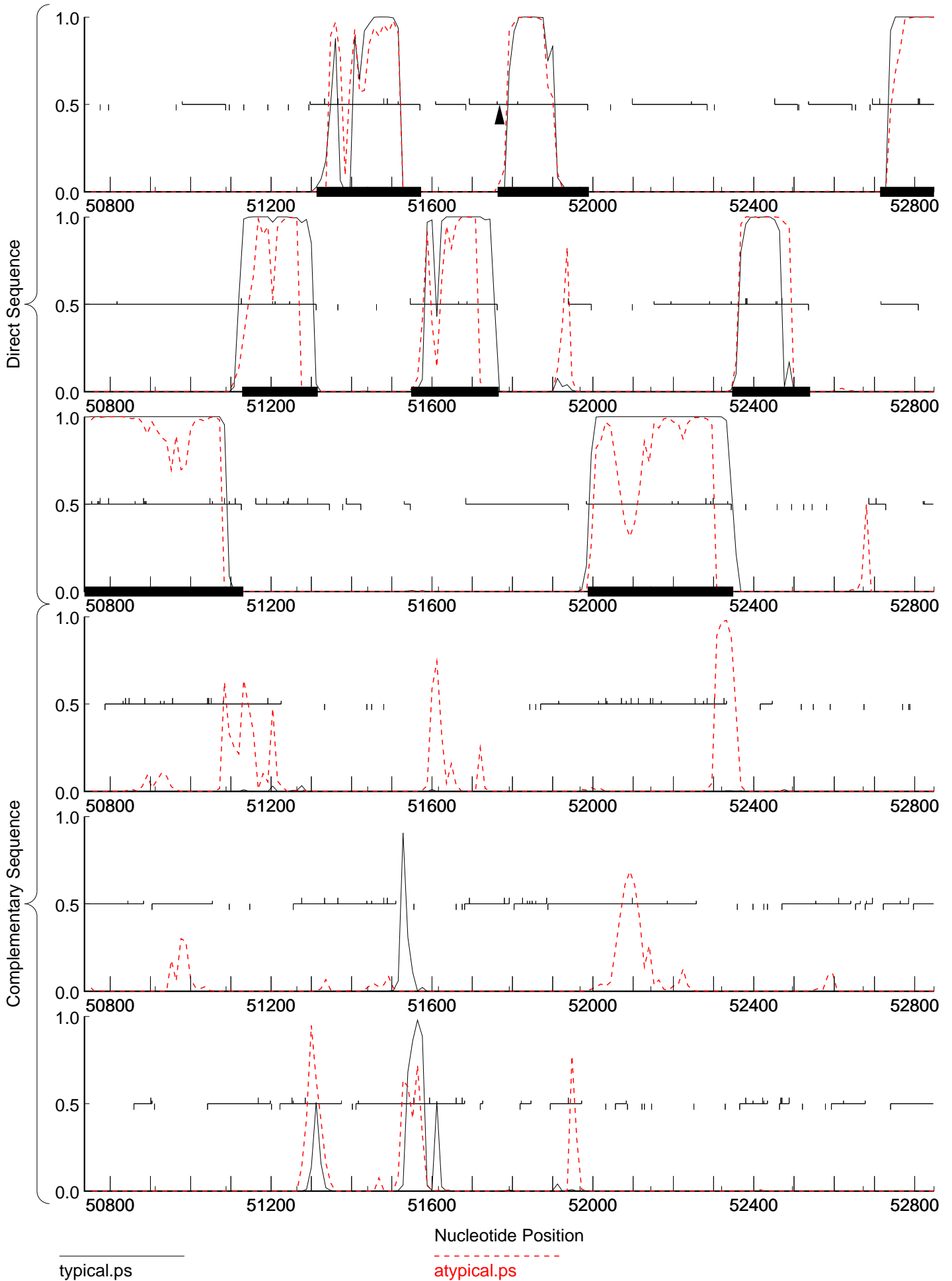


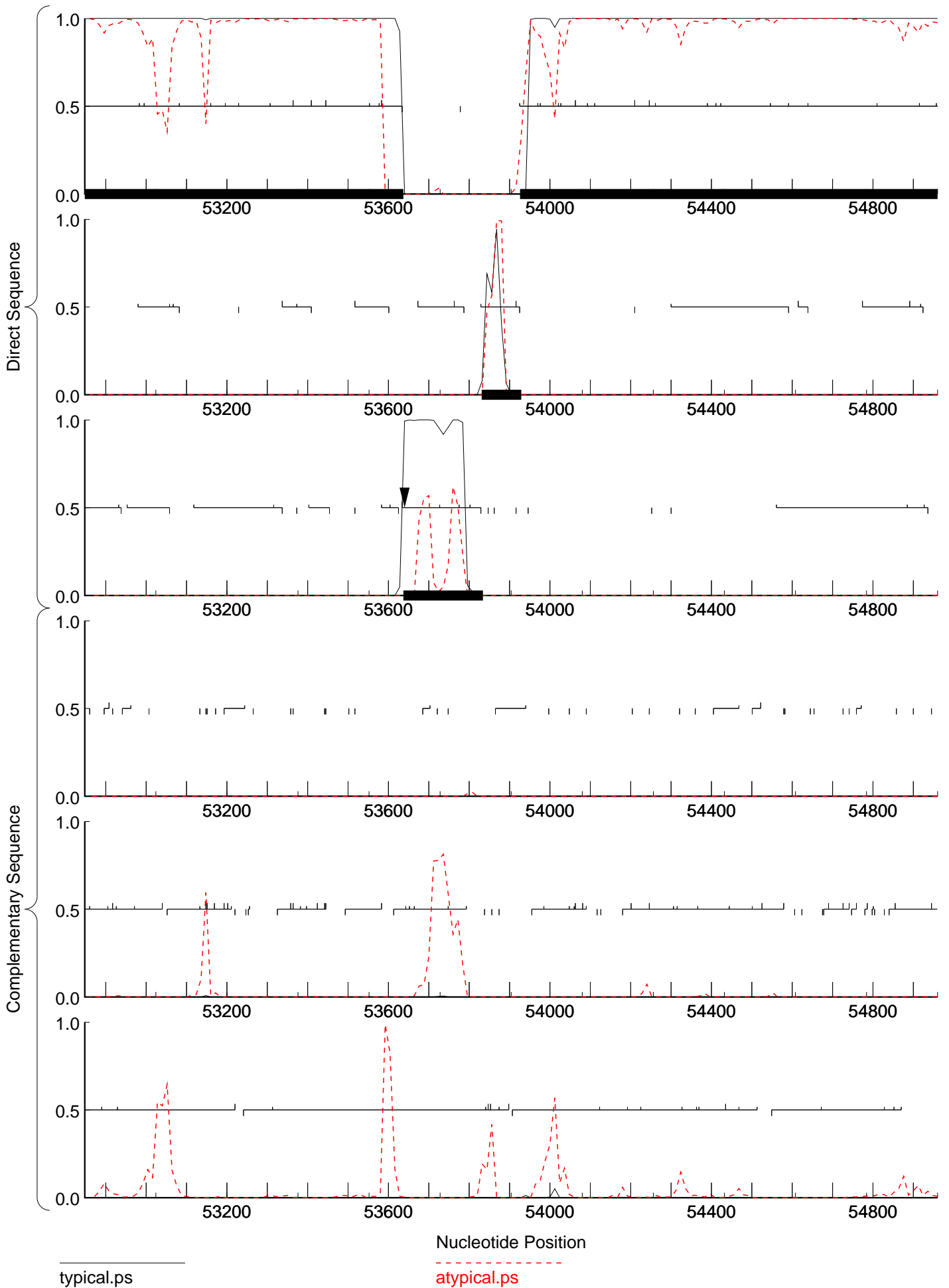


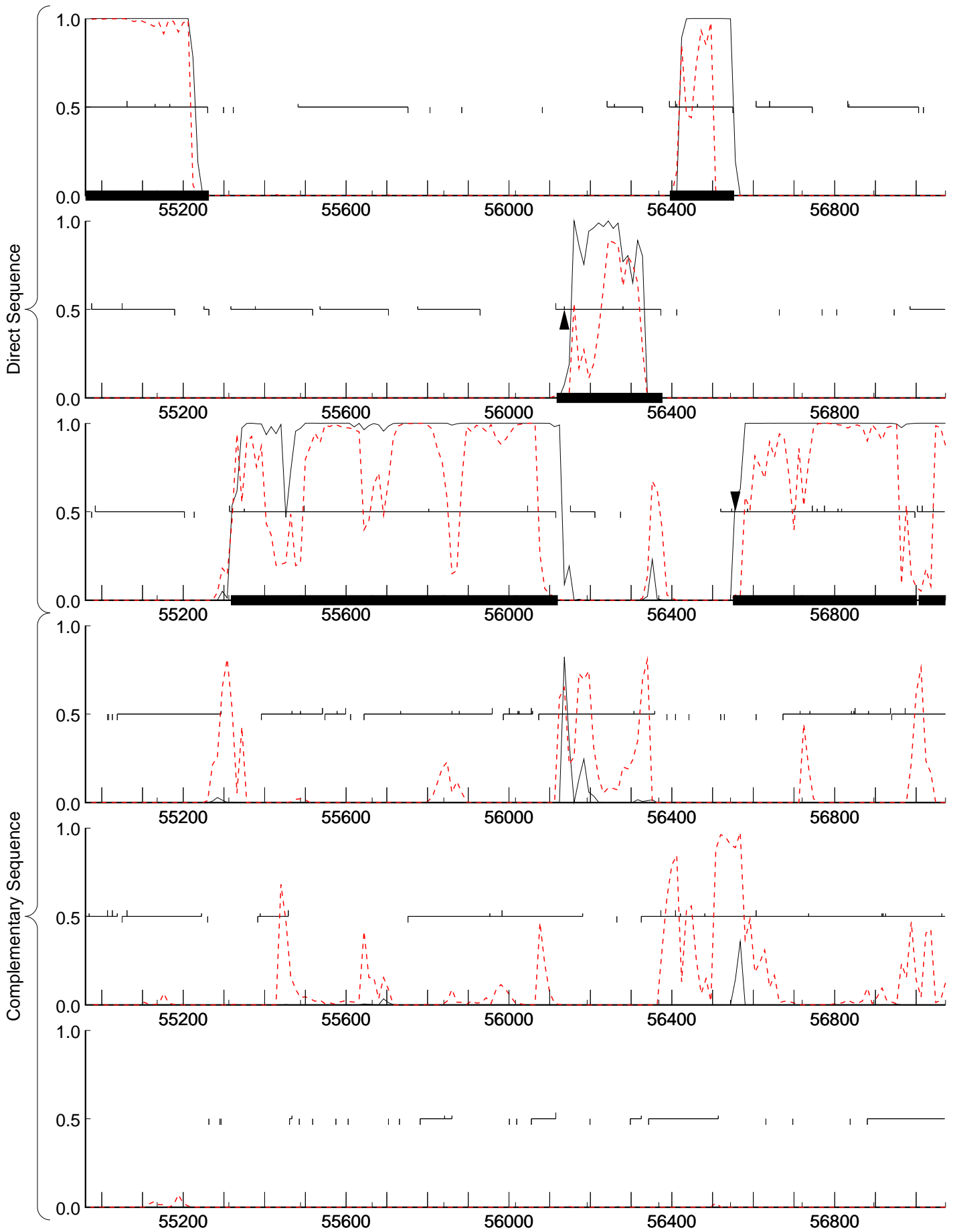


typical.ps

atypical.ps

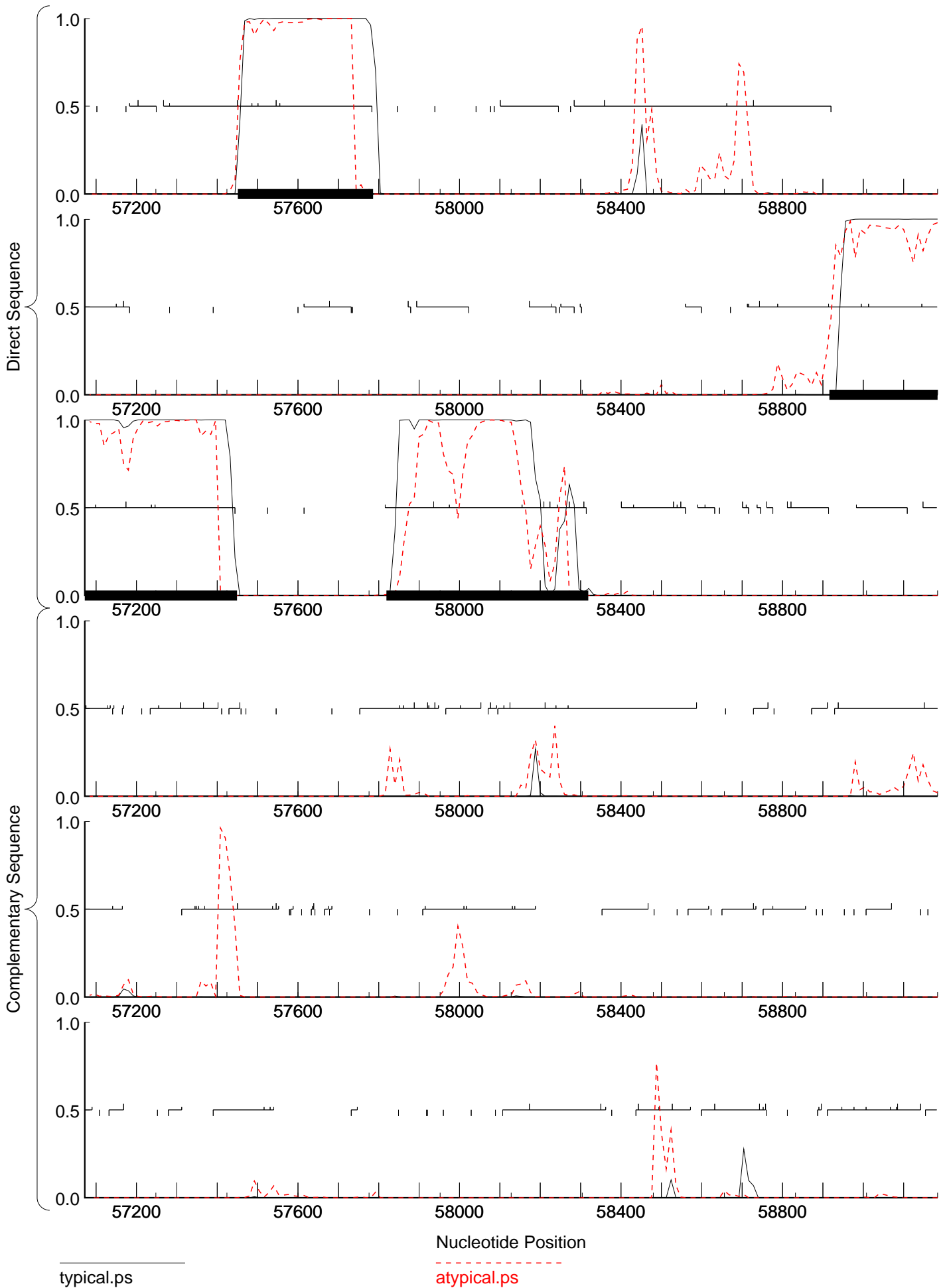


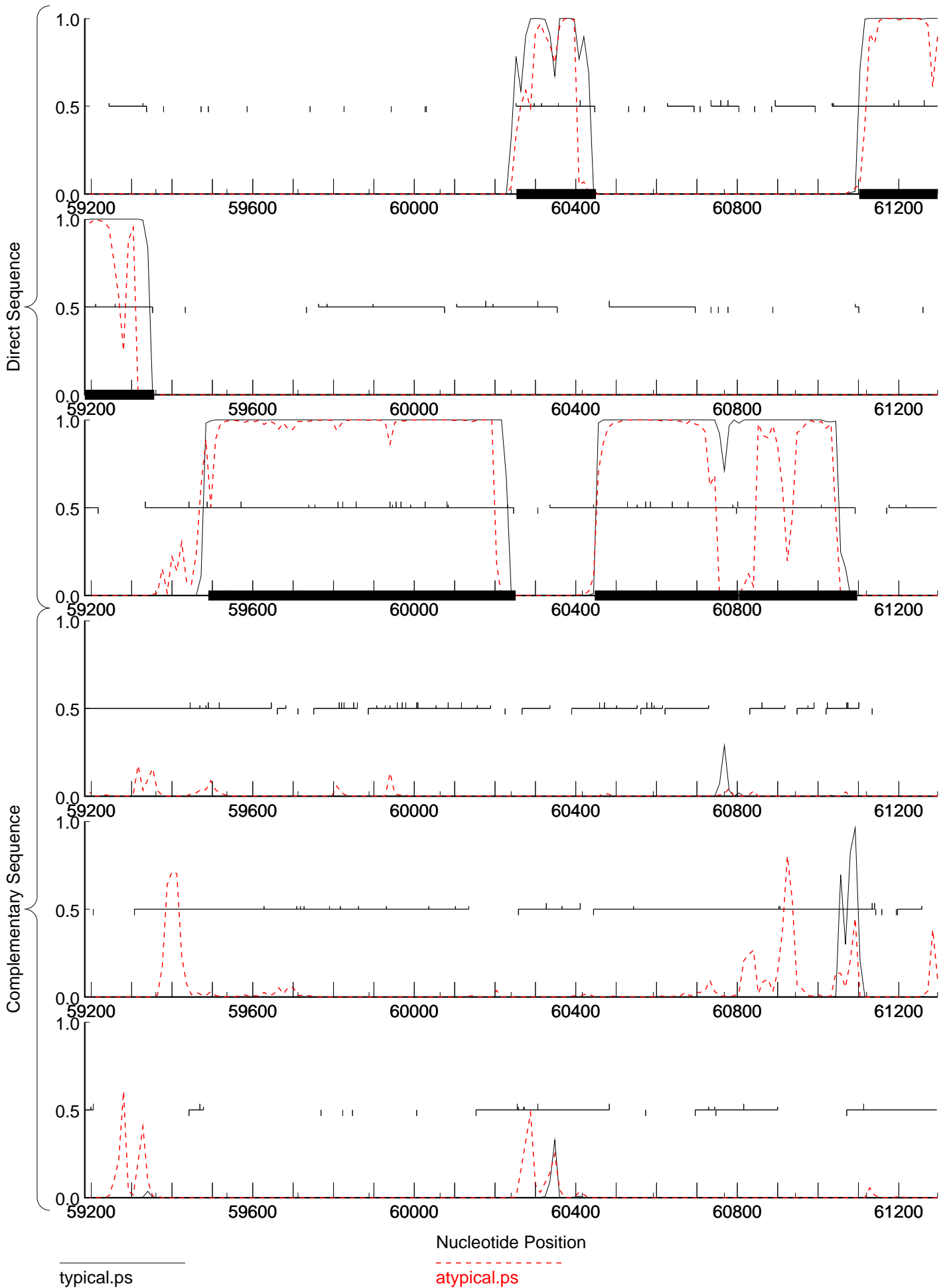


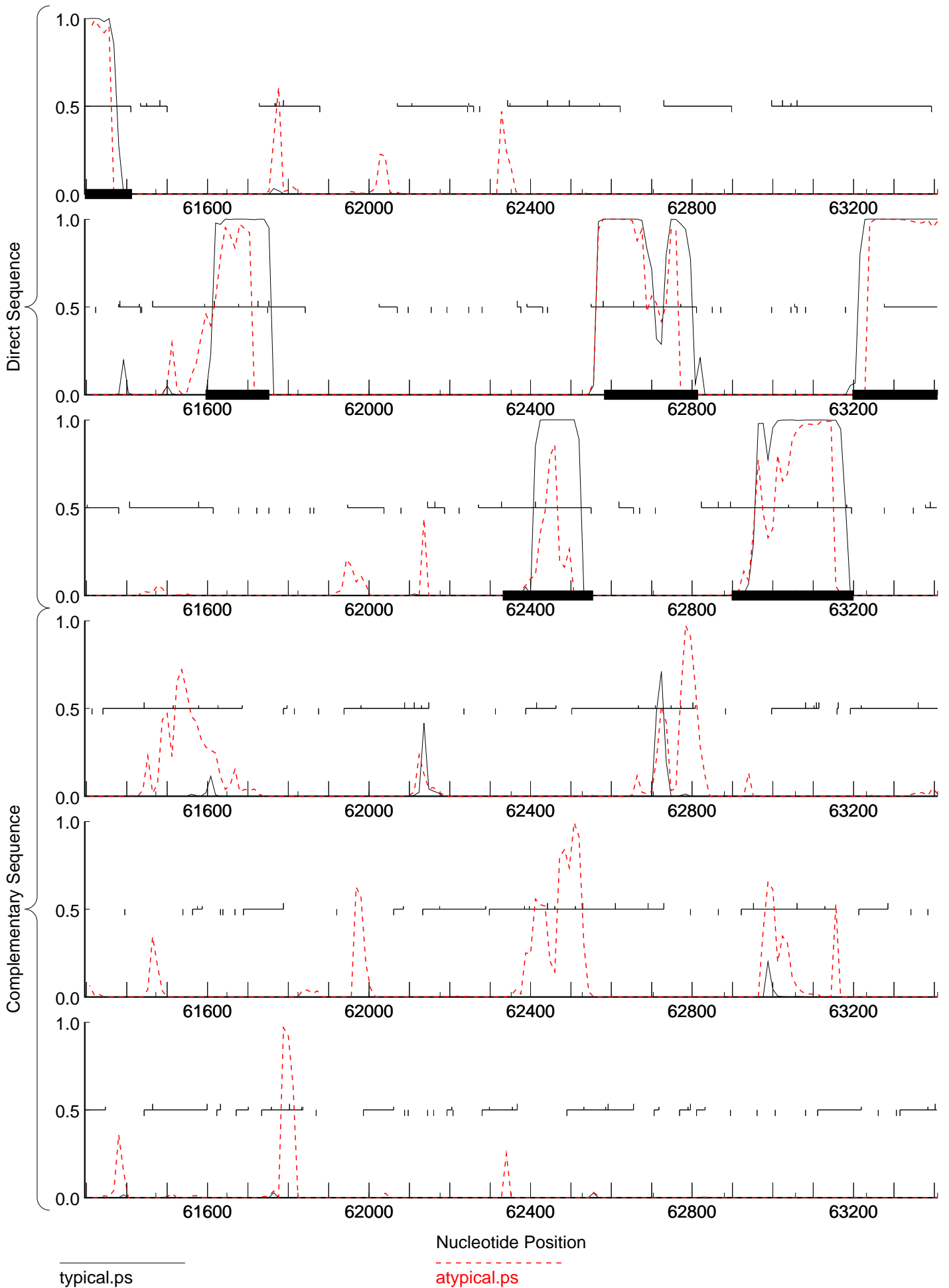


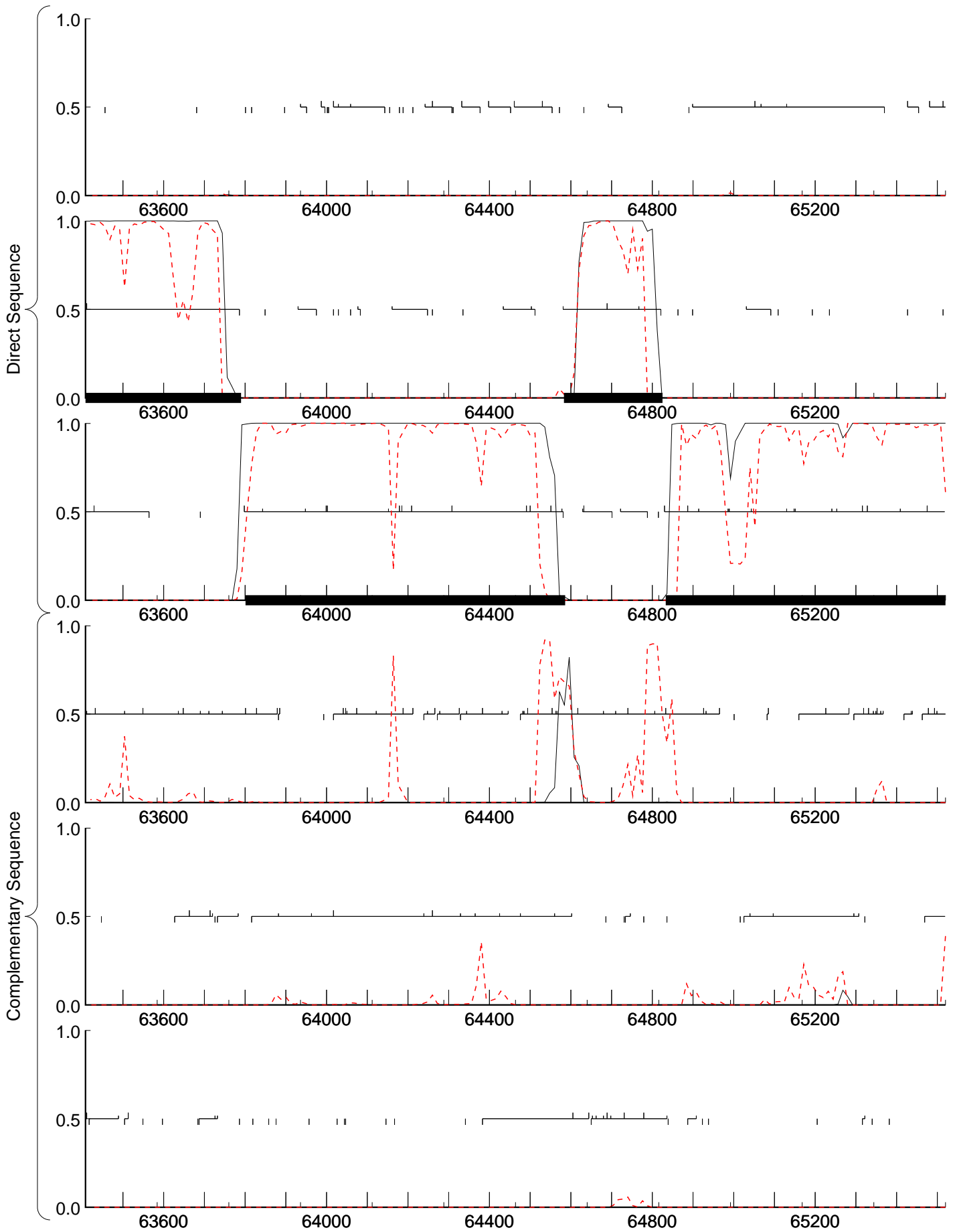
typical.ps

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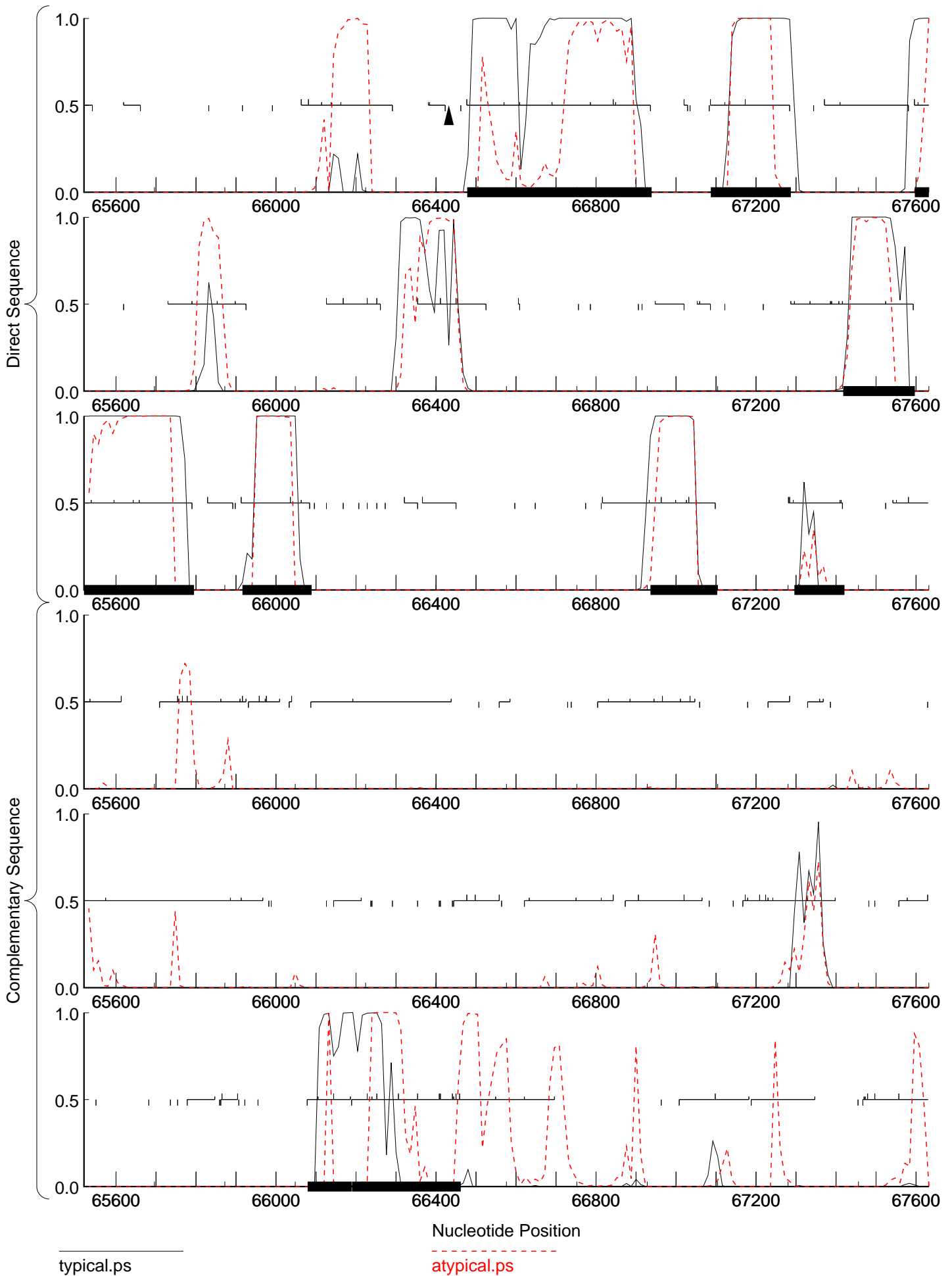




typical.ps

Nucleotide Position

atypical.ps



typical.ps

atypical.ps

