

GeneMark

Version 2.5p (09.08.06)

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PROGRAM INFORMATION

Sequence : Mycobacterium phage BlackStallion complete sequence, 68714 bp, circularly permuted, Cluster
Analysis Date : 11/19/17 at 19:10:28
Pages : 34
Sequence Length : 68714 bp
GC Content : 66.50%

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,

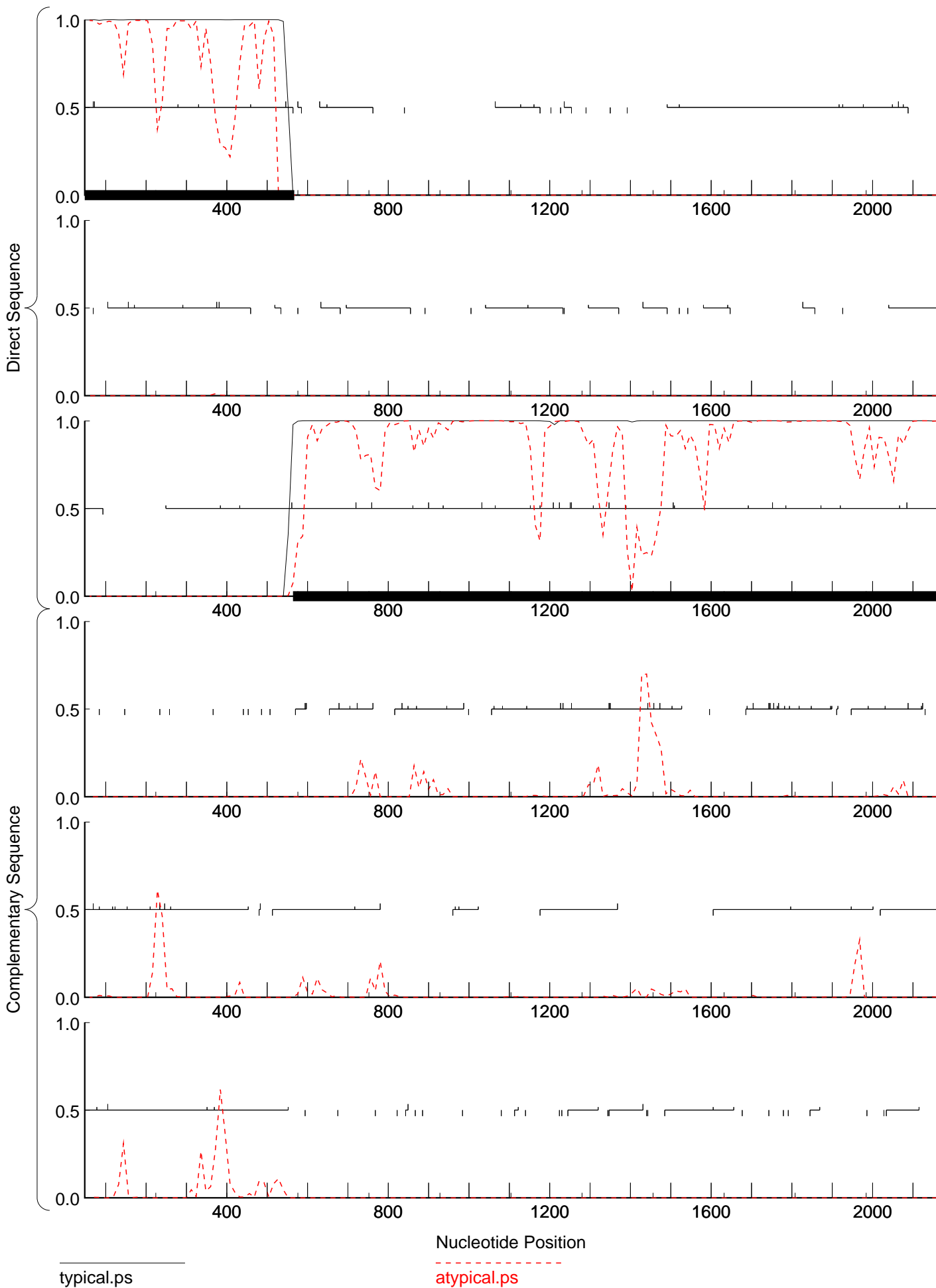
MATRIX INFORMATION

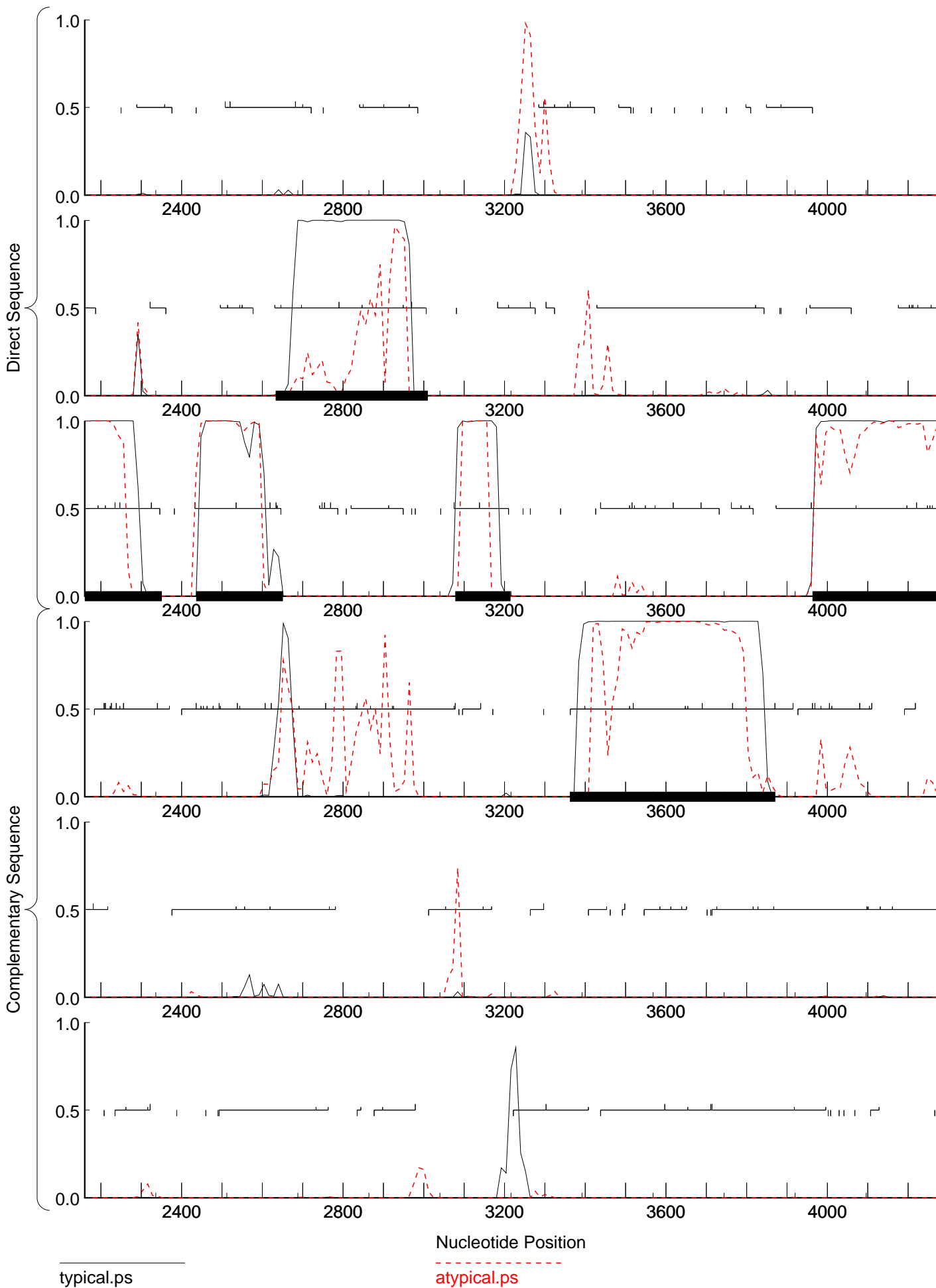
Matrix : -
Author : -
Order : 4

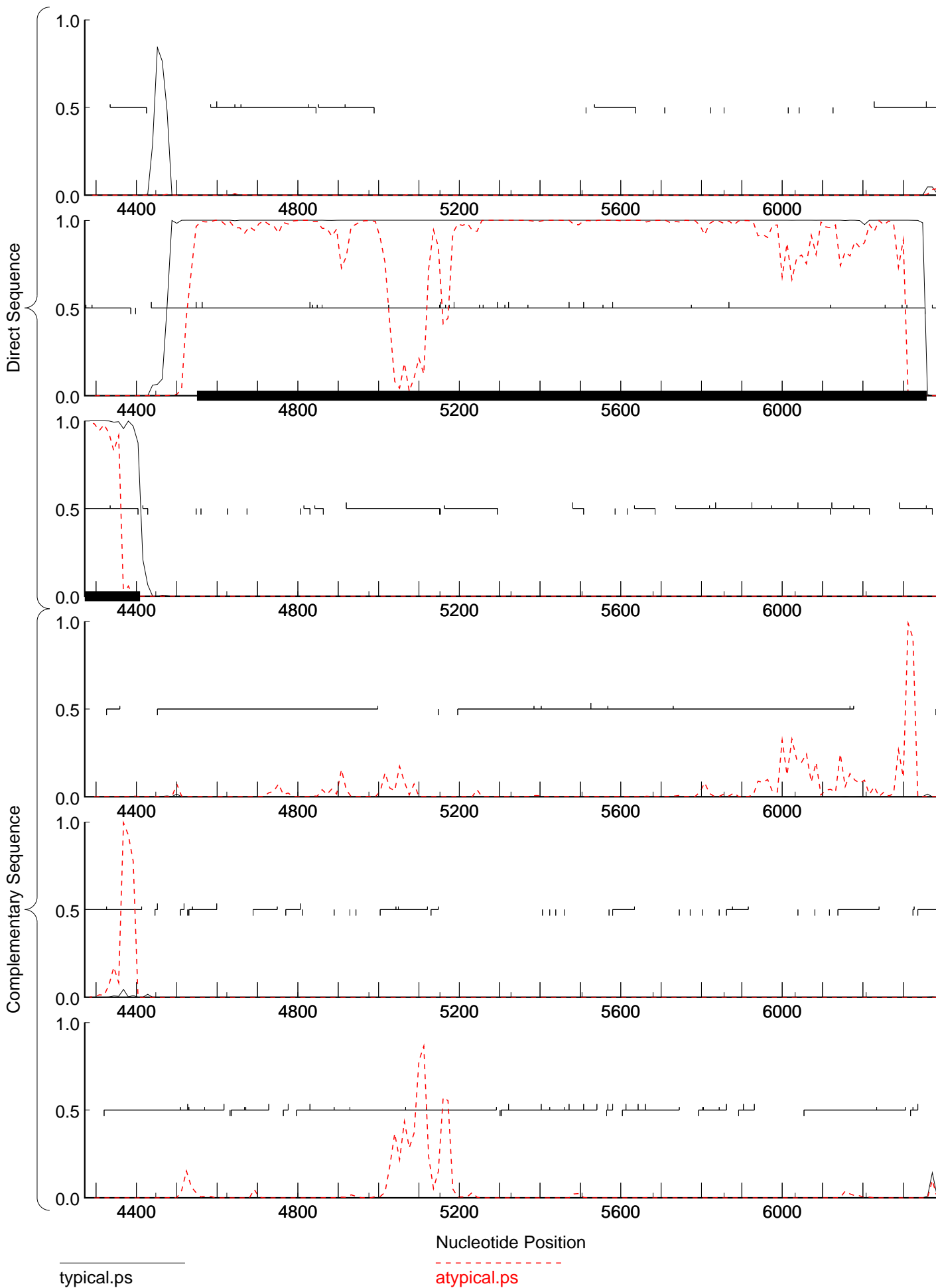
Send questions / comments to:
Dr. M. Borodovsky
Georgia Institute of Technology
School of Biology
Atlanta, GA 30332-0230

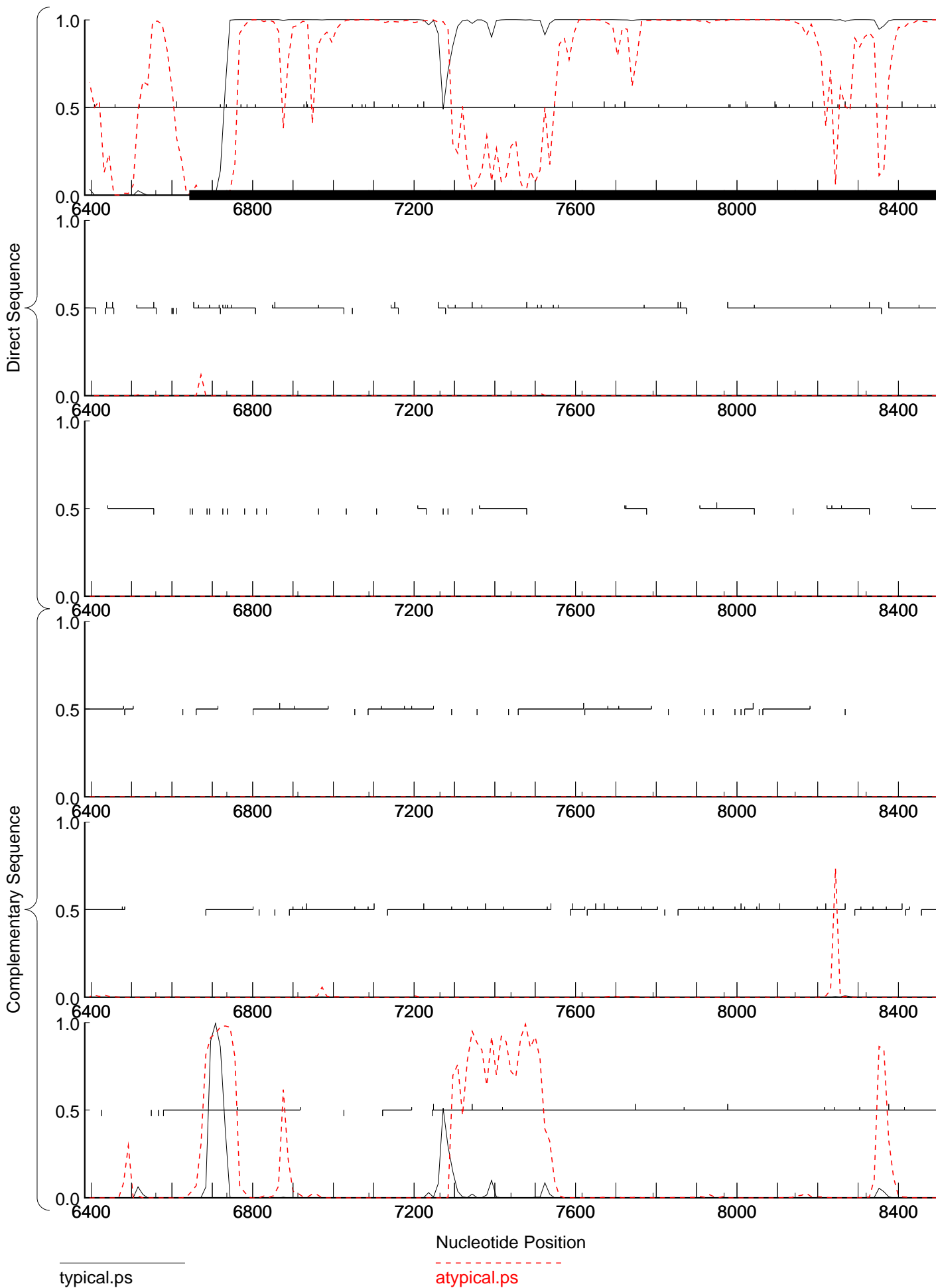
Matrix notes & comments

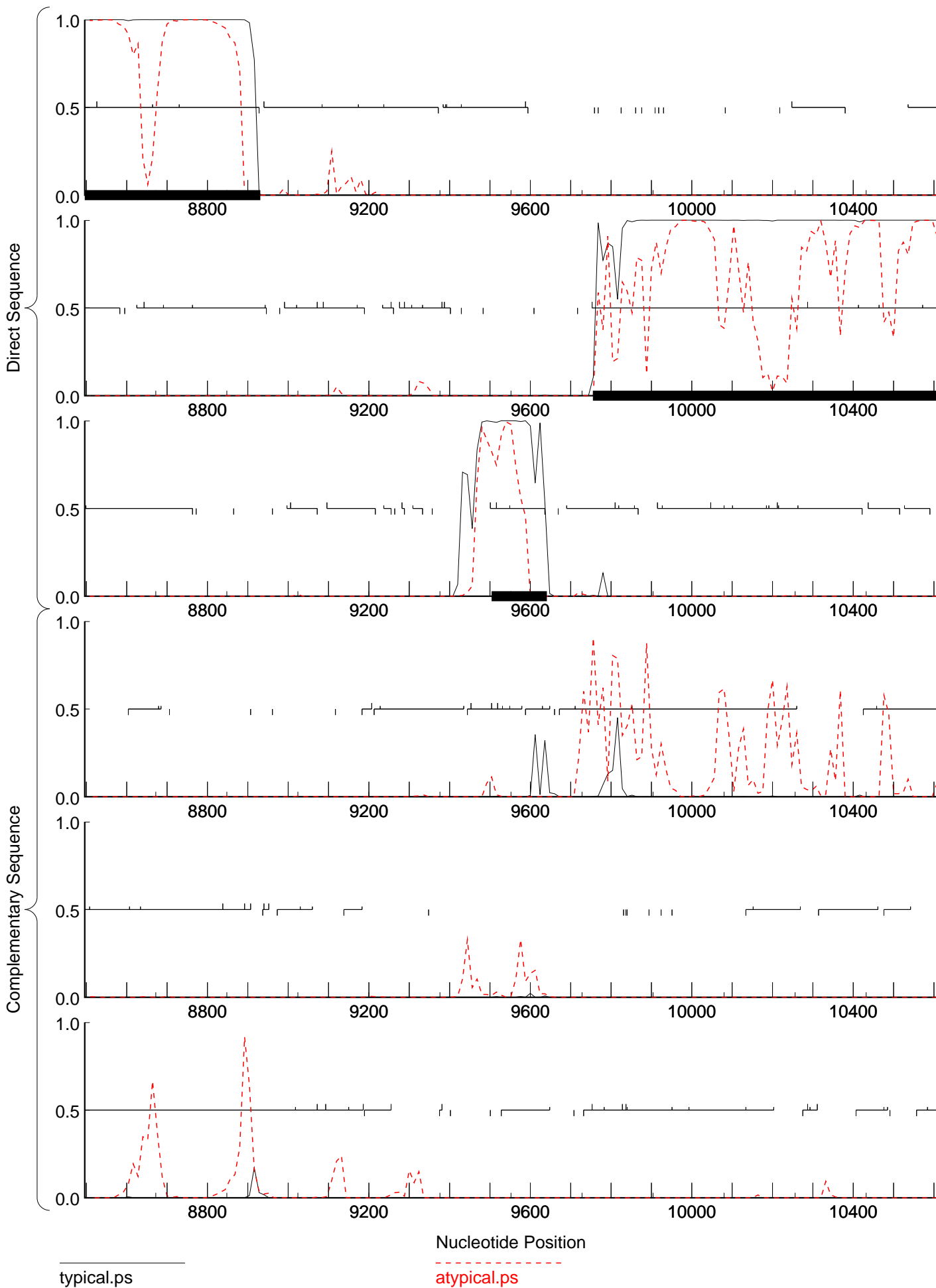
Training set derived by GeneMarkS, 4.30 October 2014
Sun Nov 19 19:10:28 2017





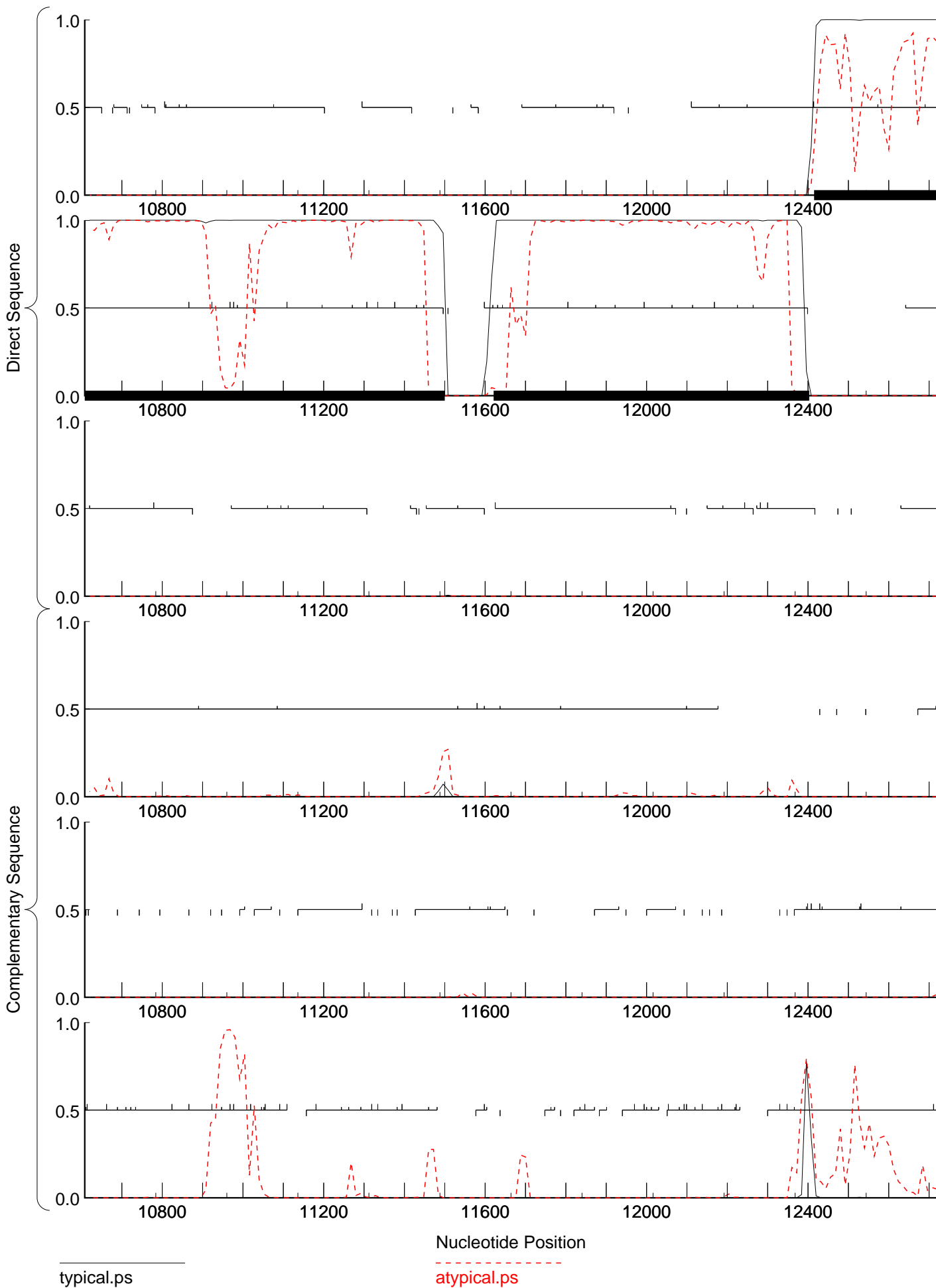


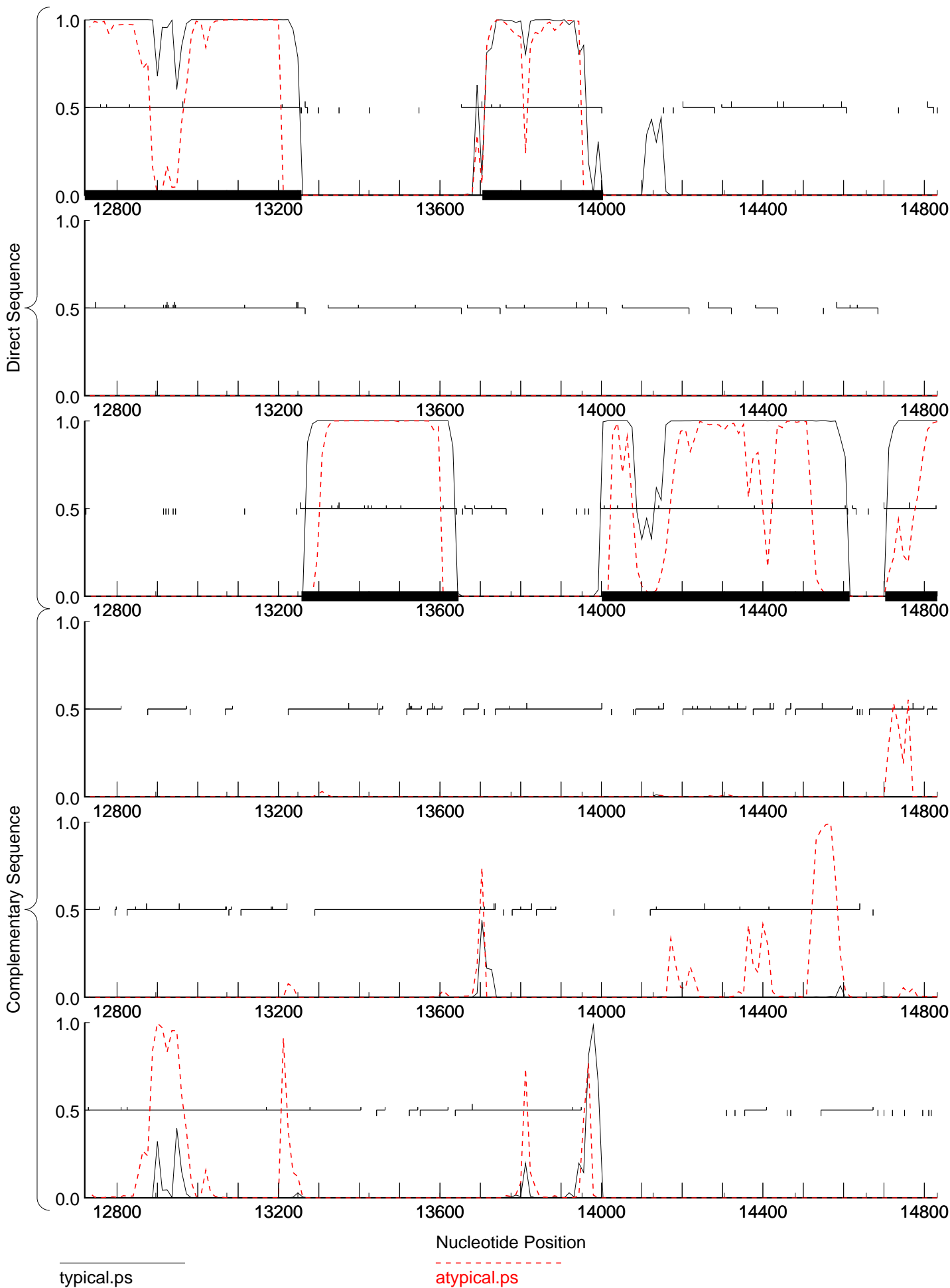


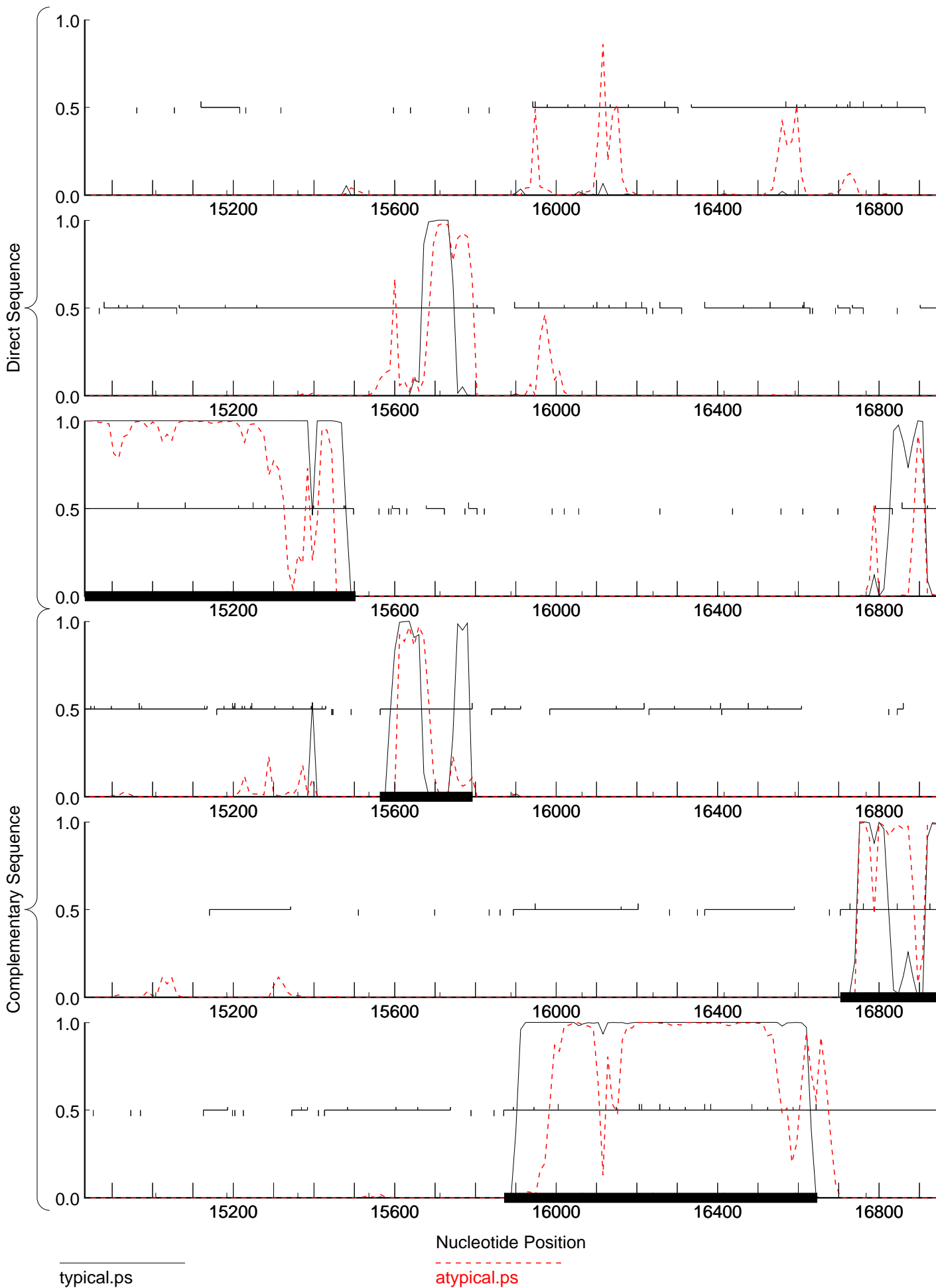


typical.ps

atypical.ps

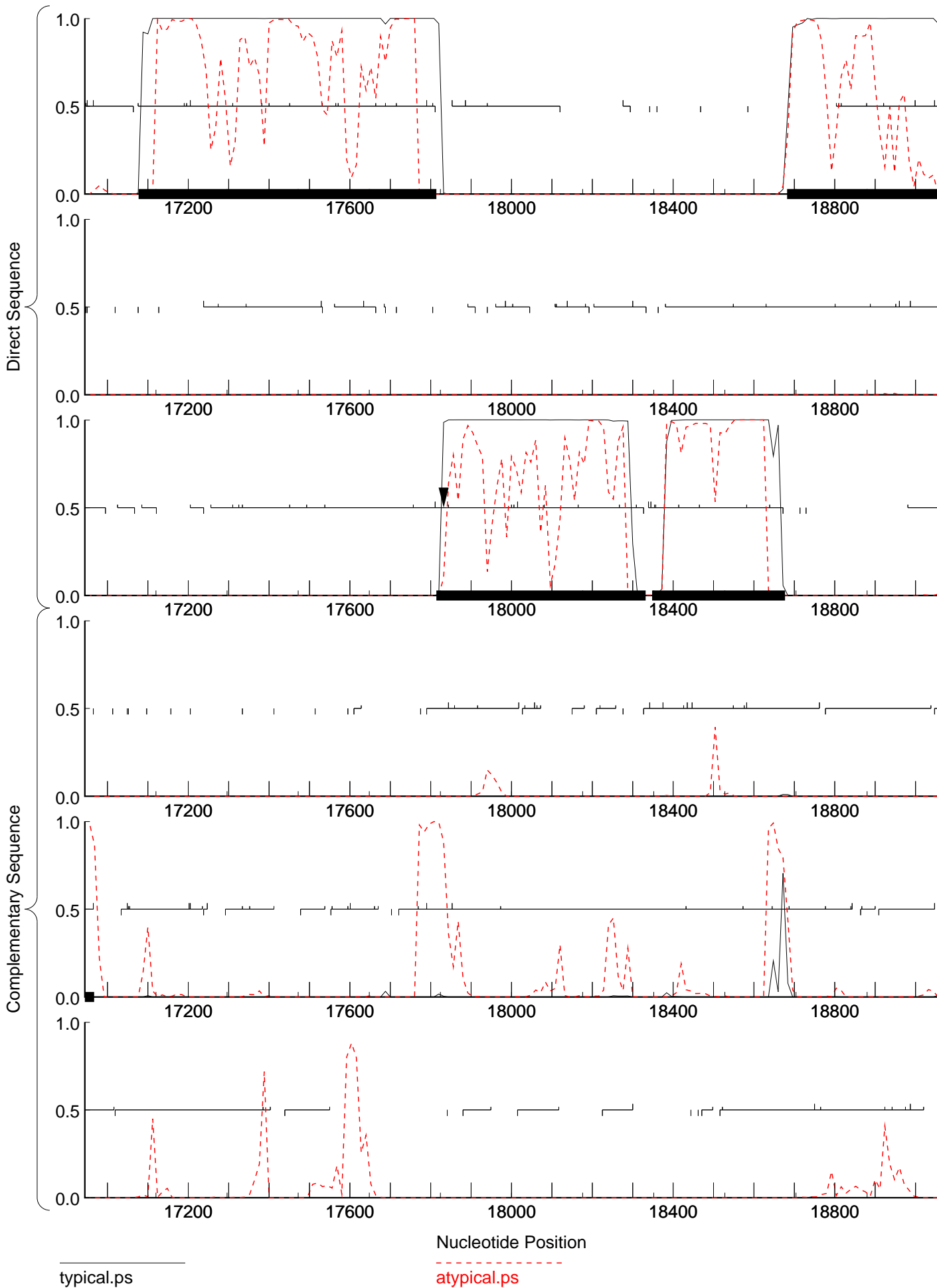


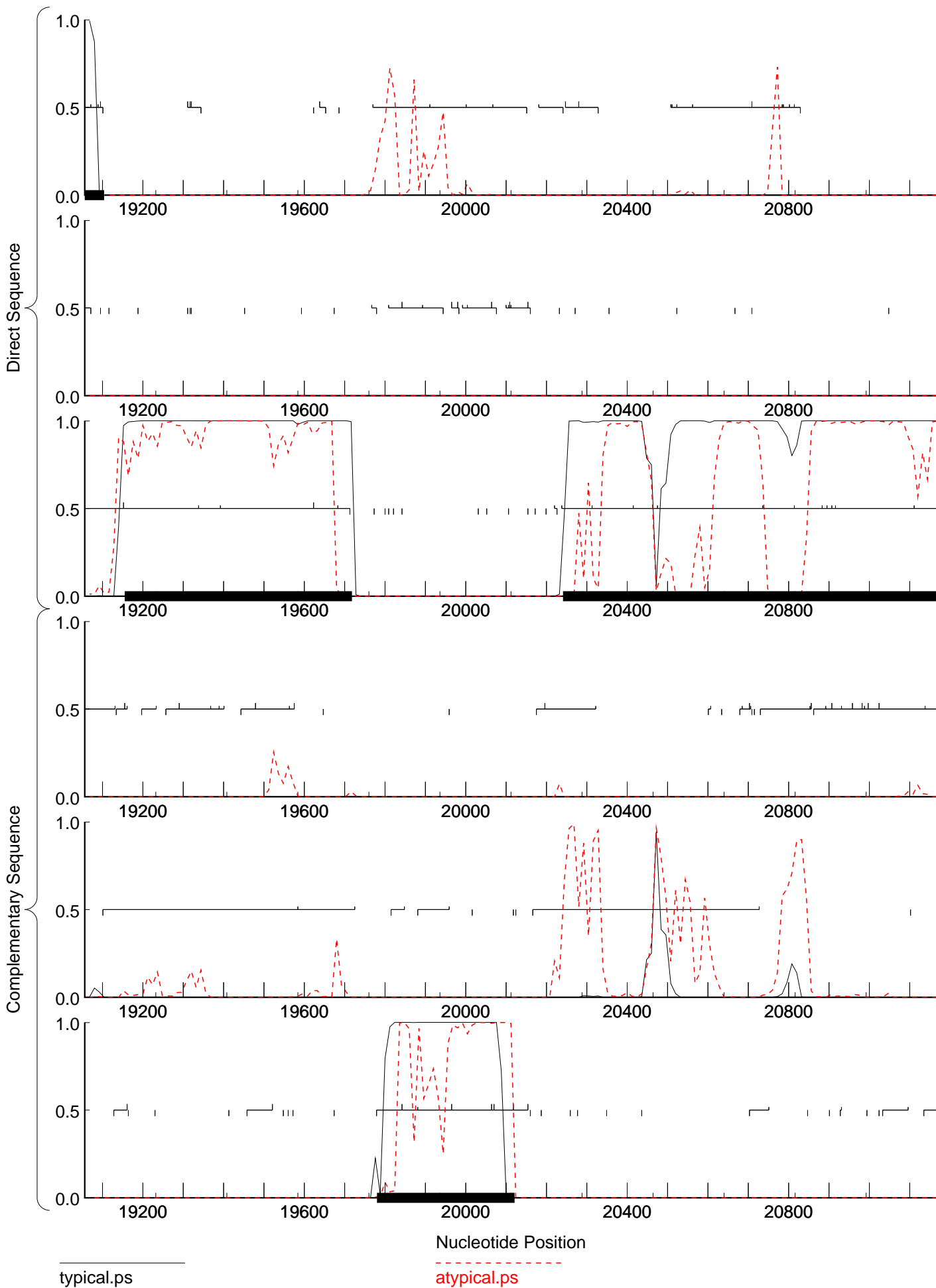


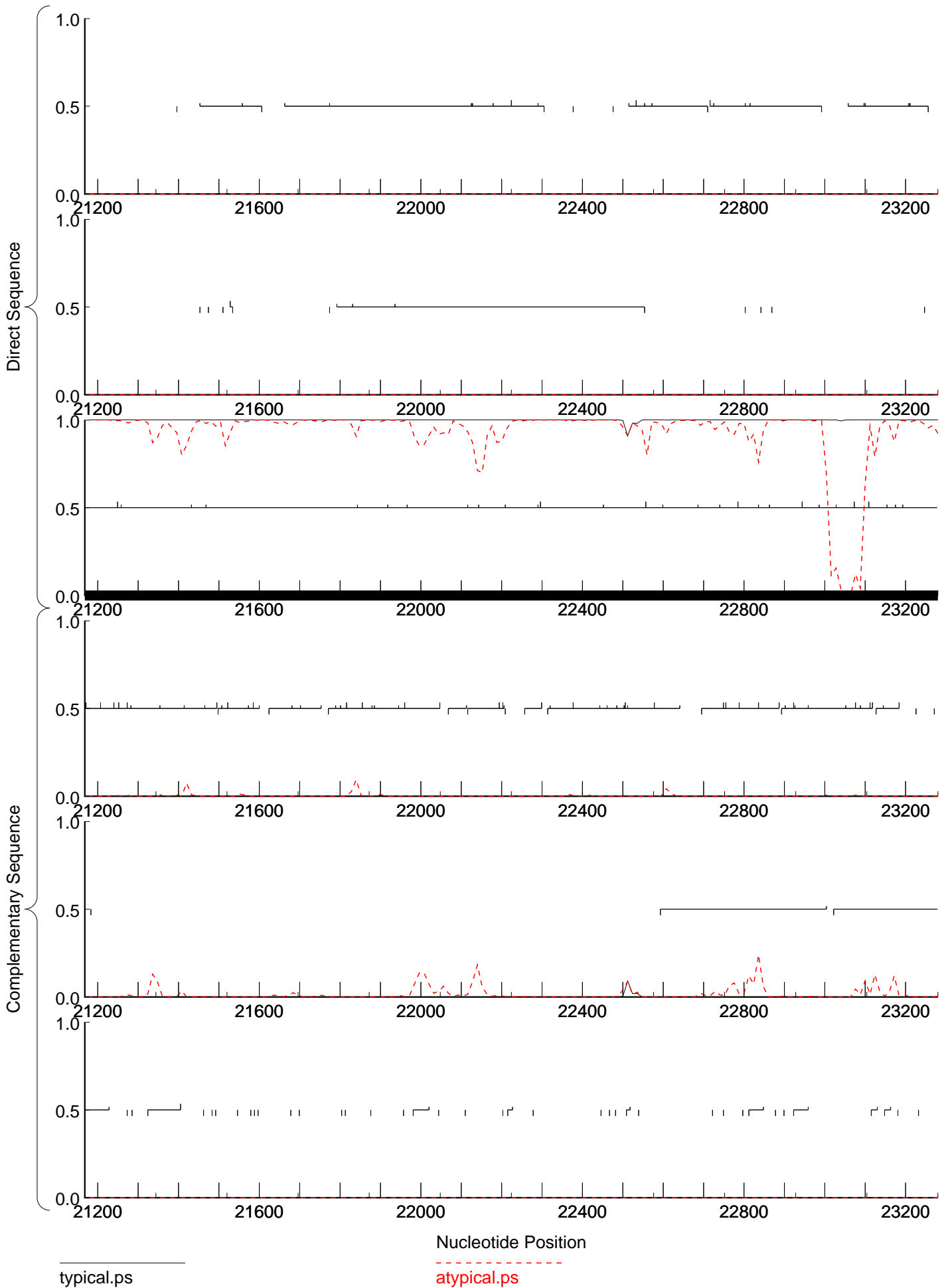


typical.ps

atypical.ps

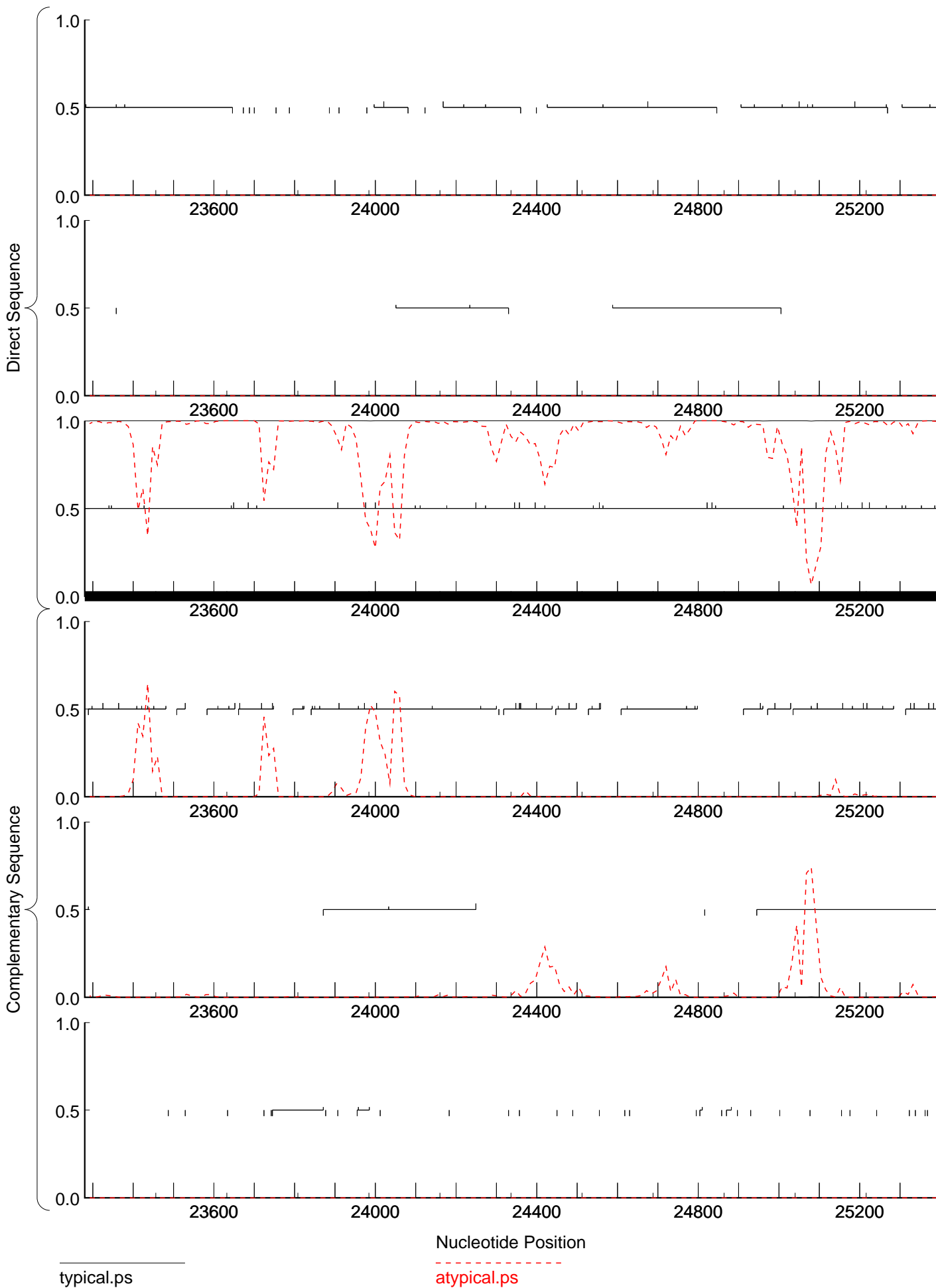


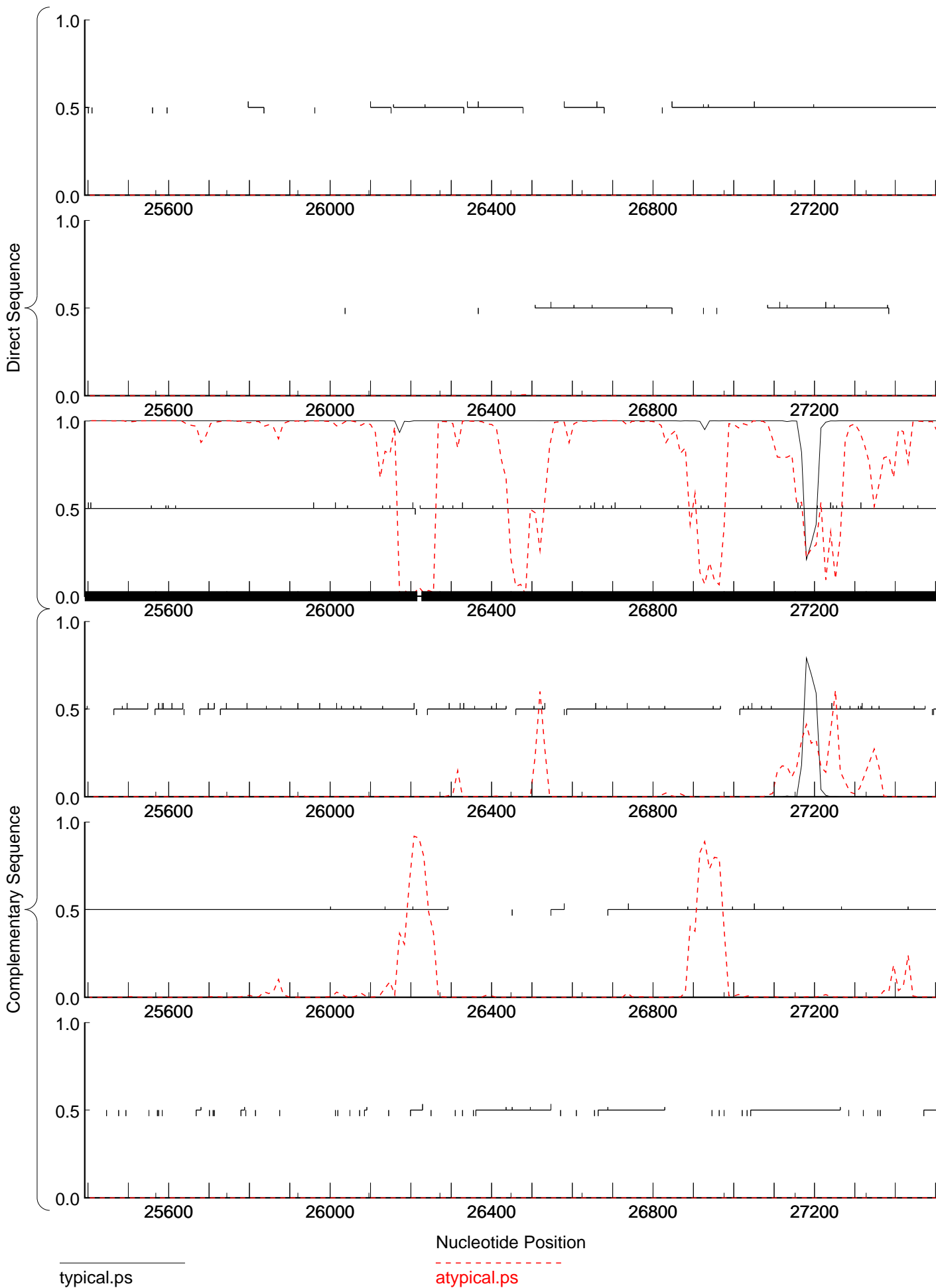


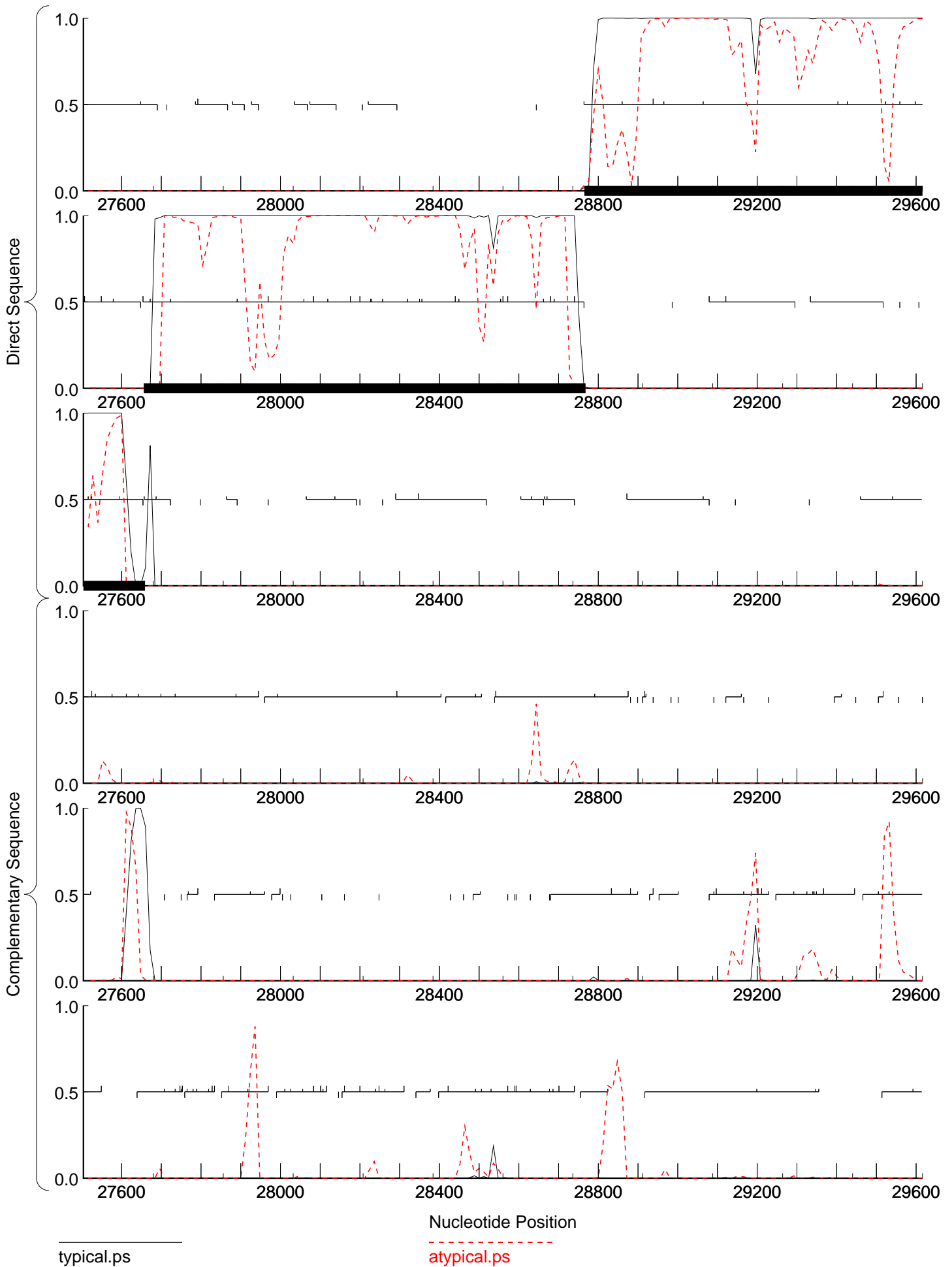


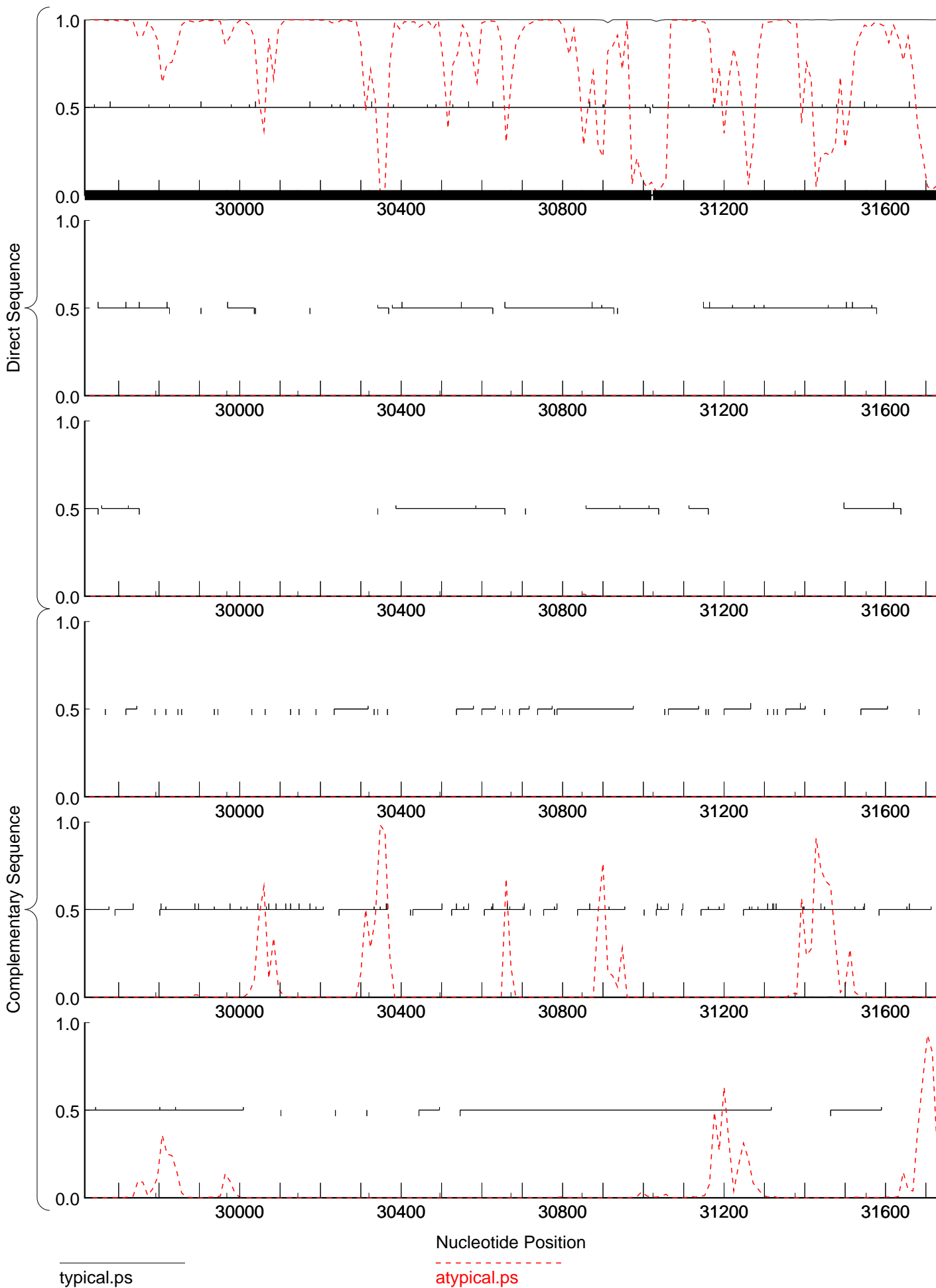
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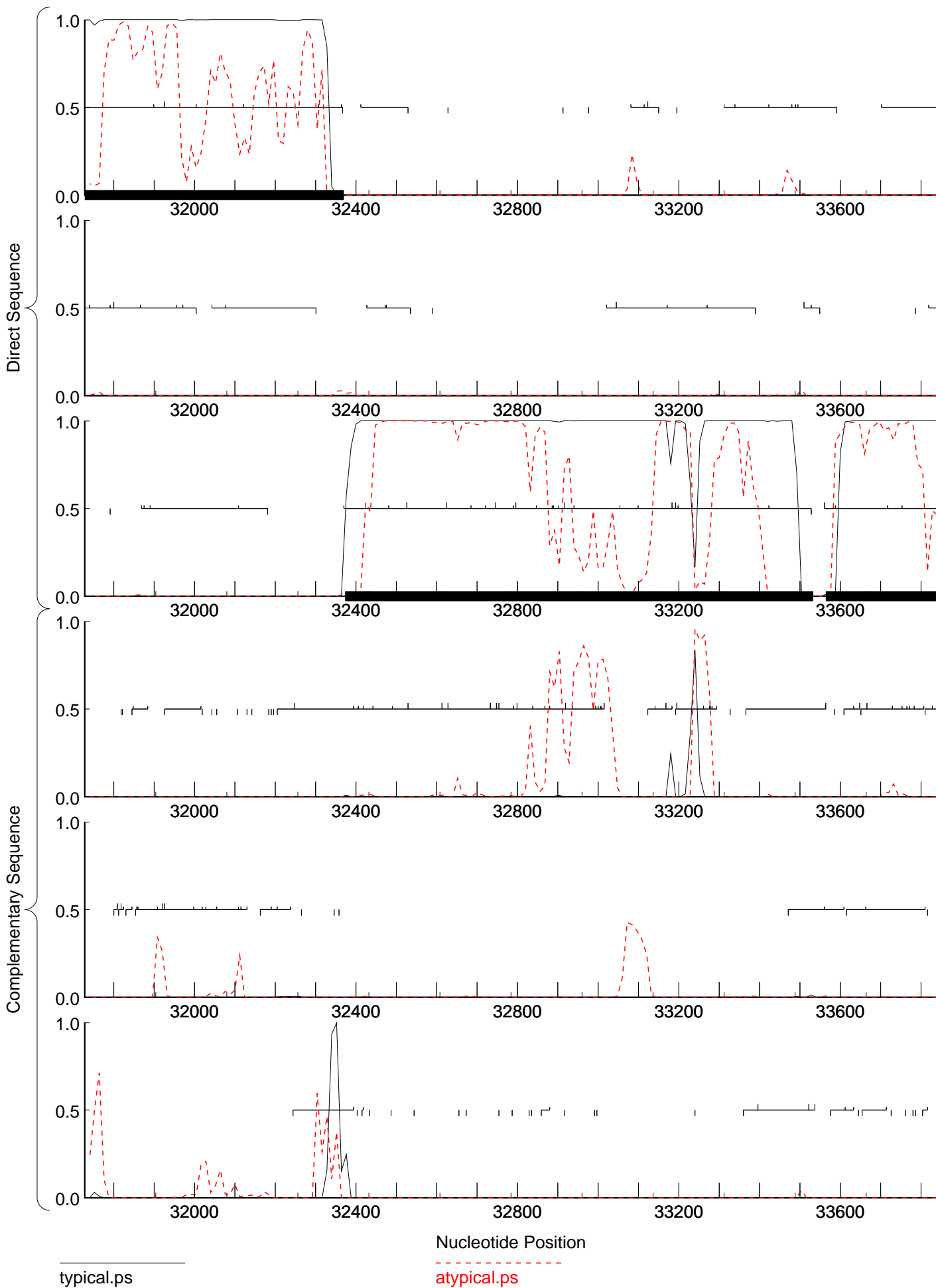
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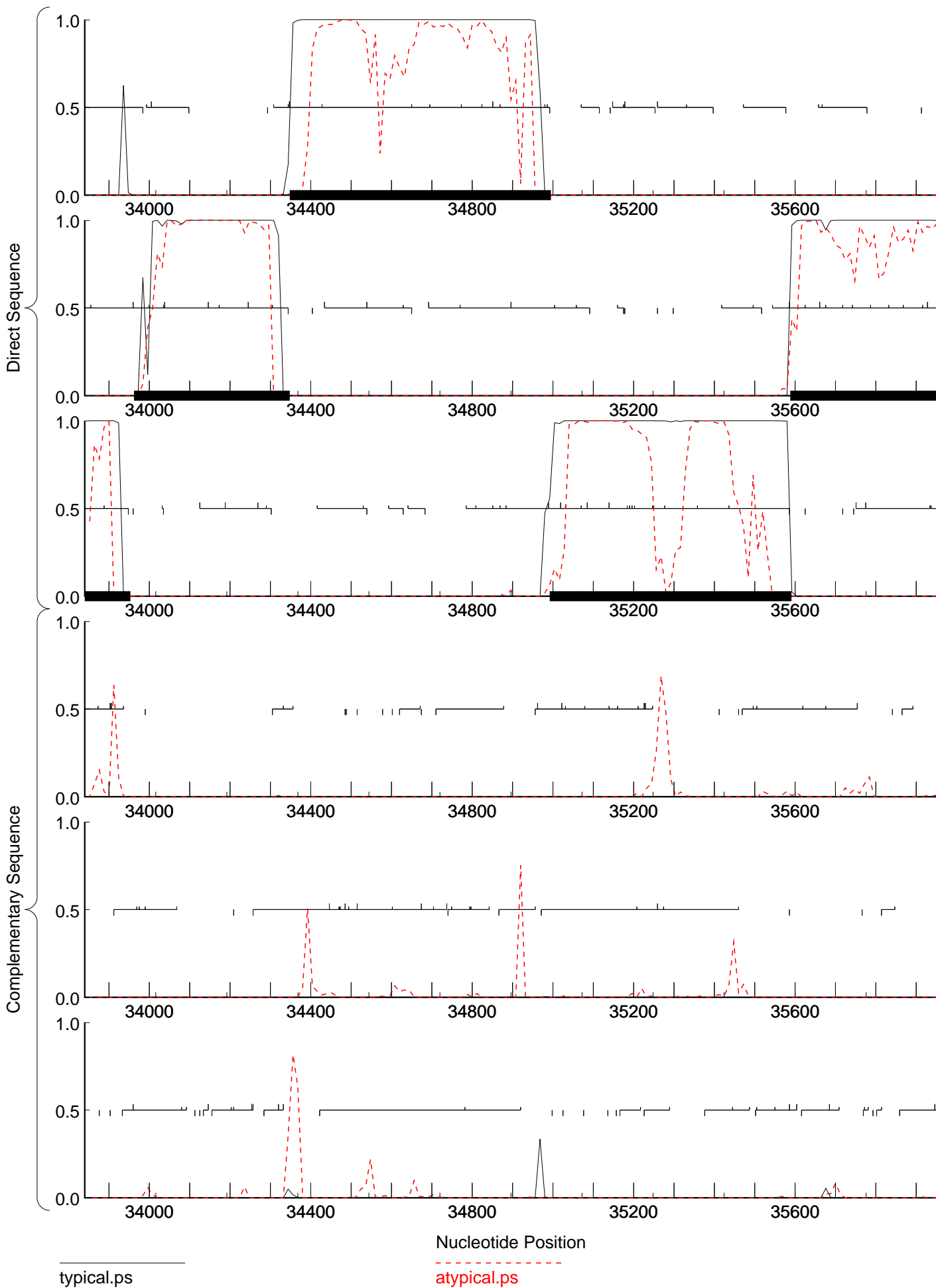






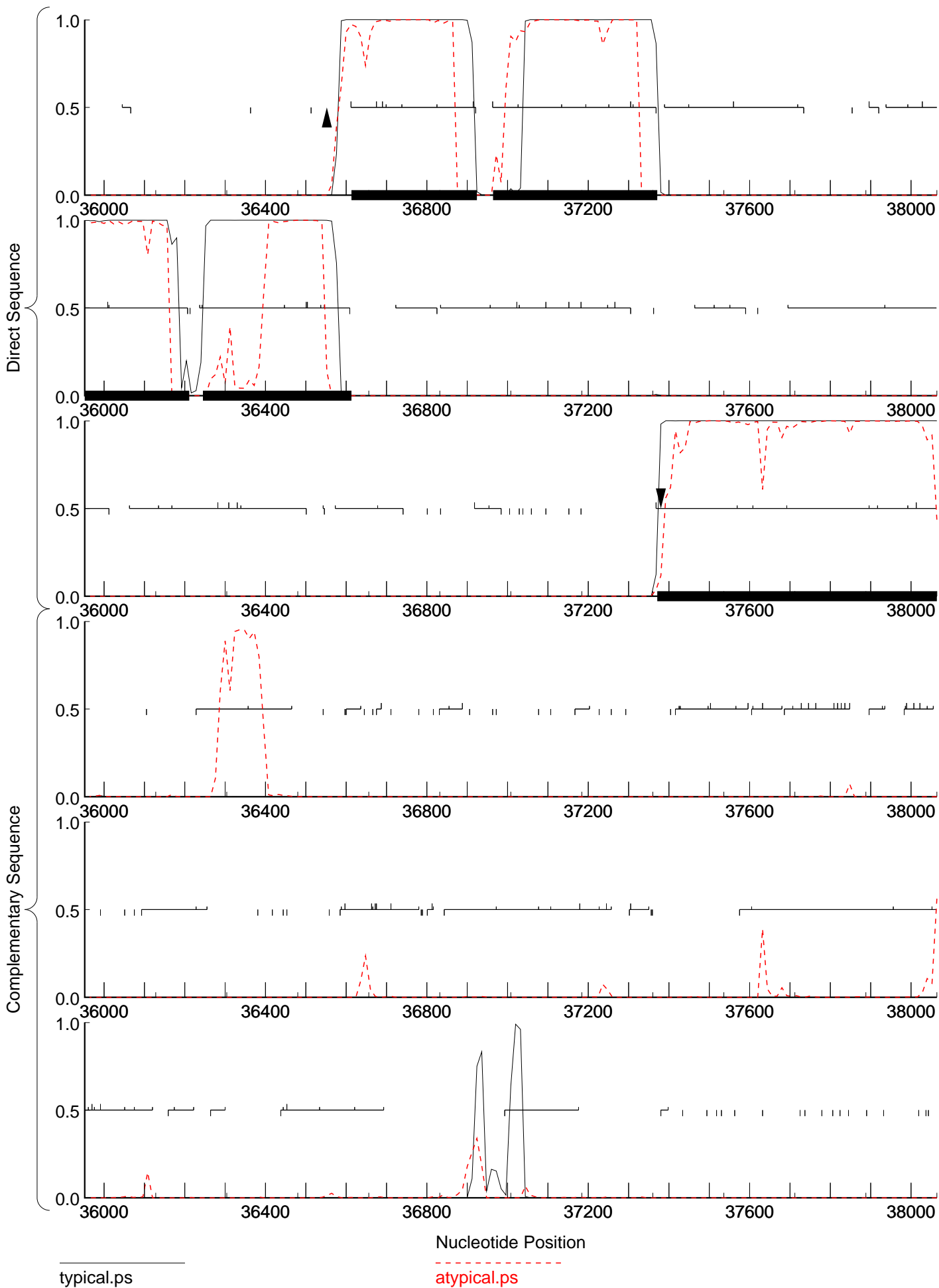
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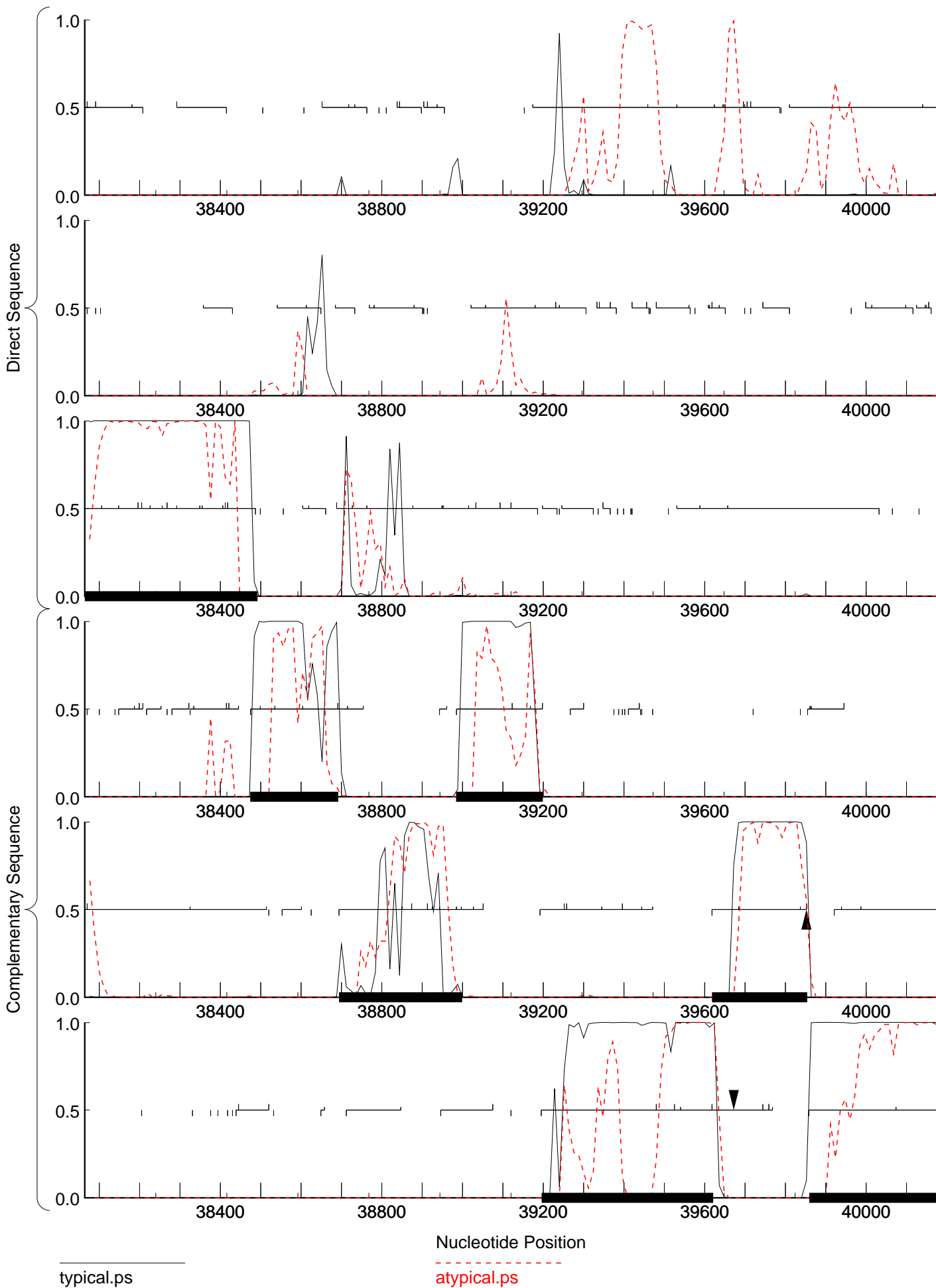
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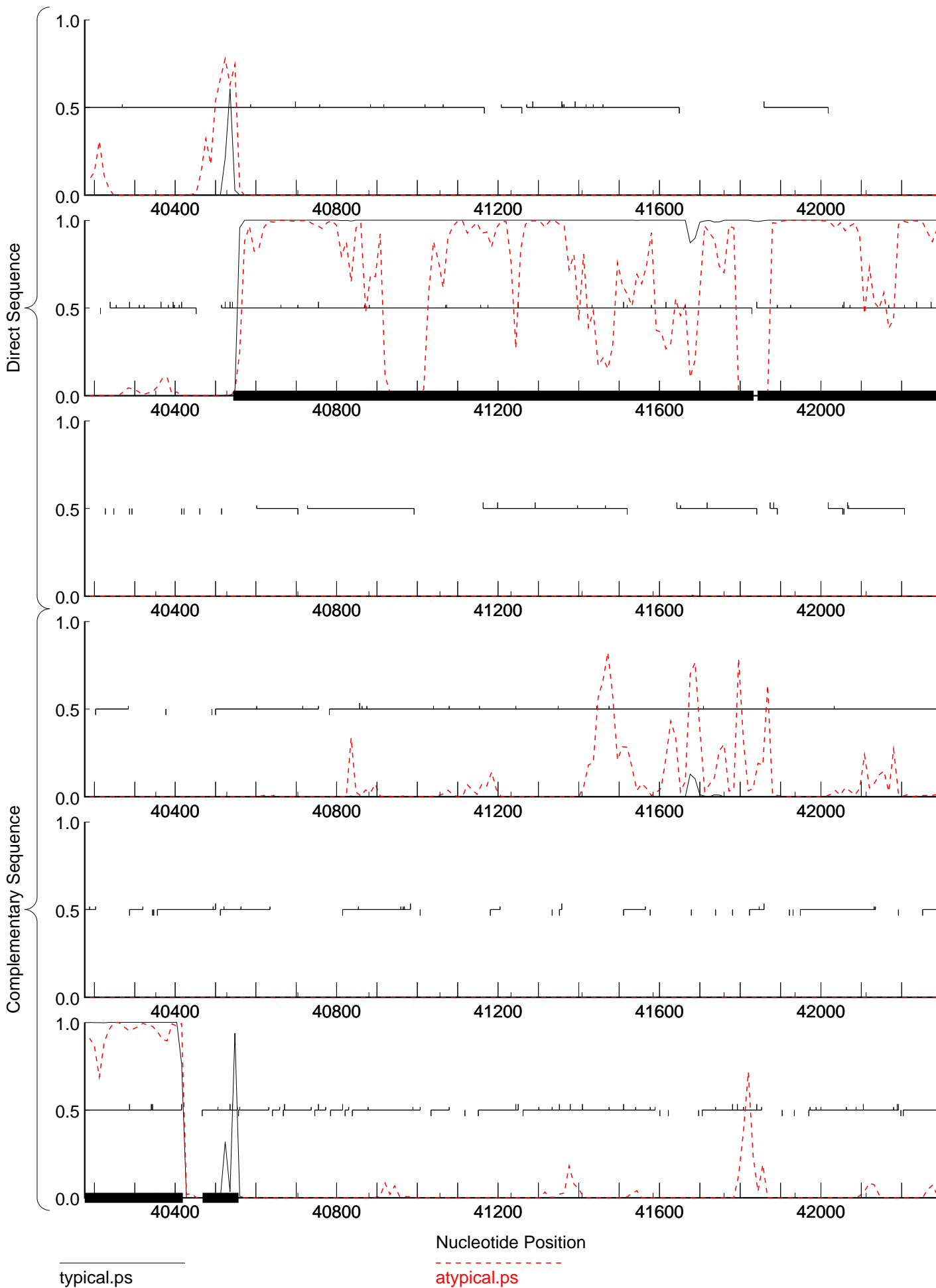


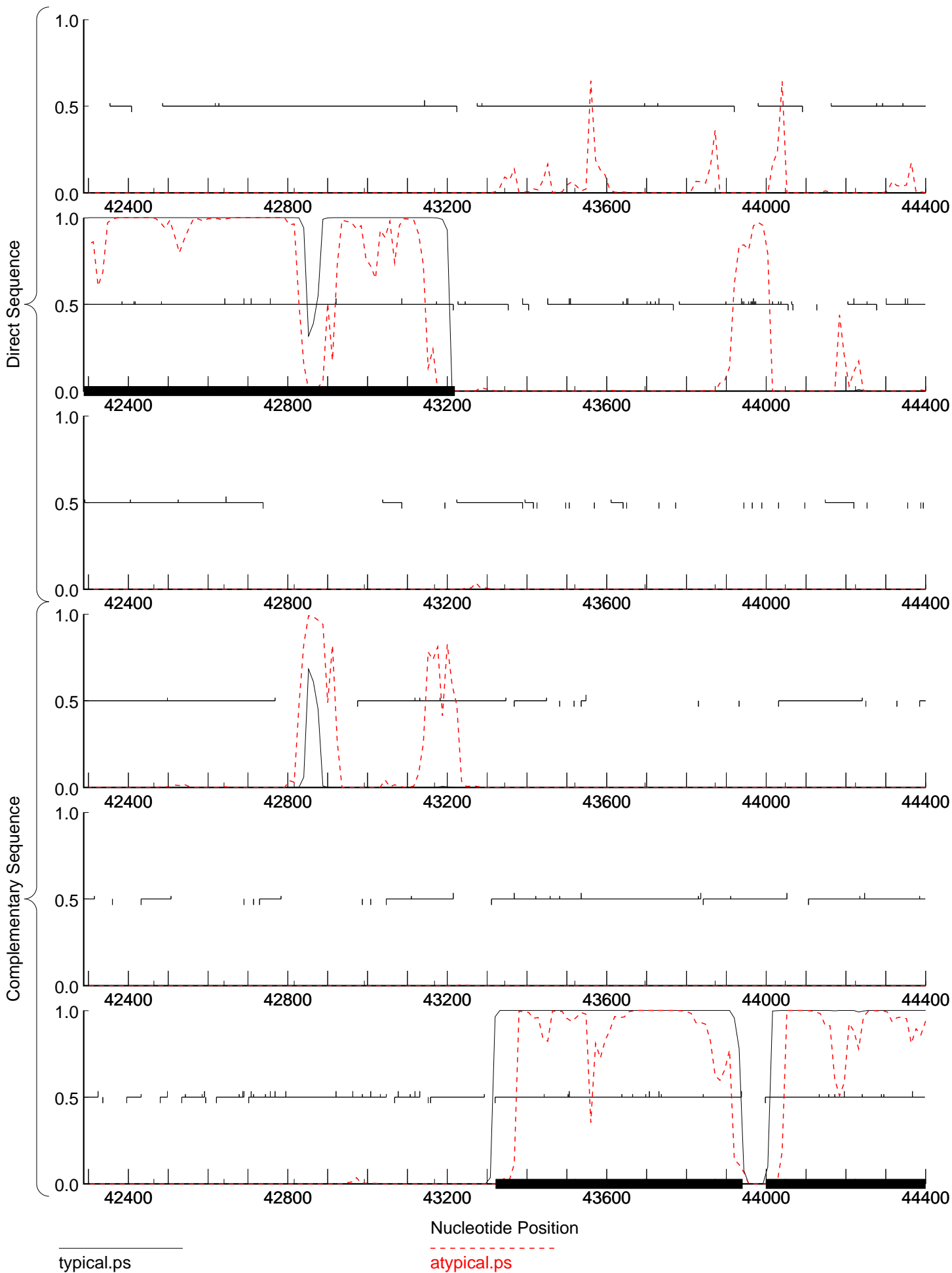
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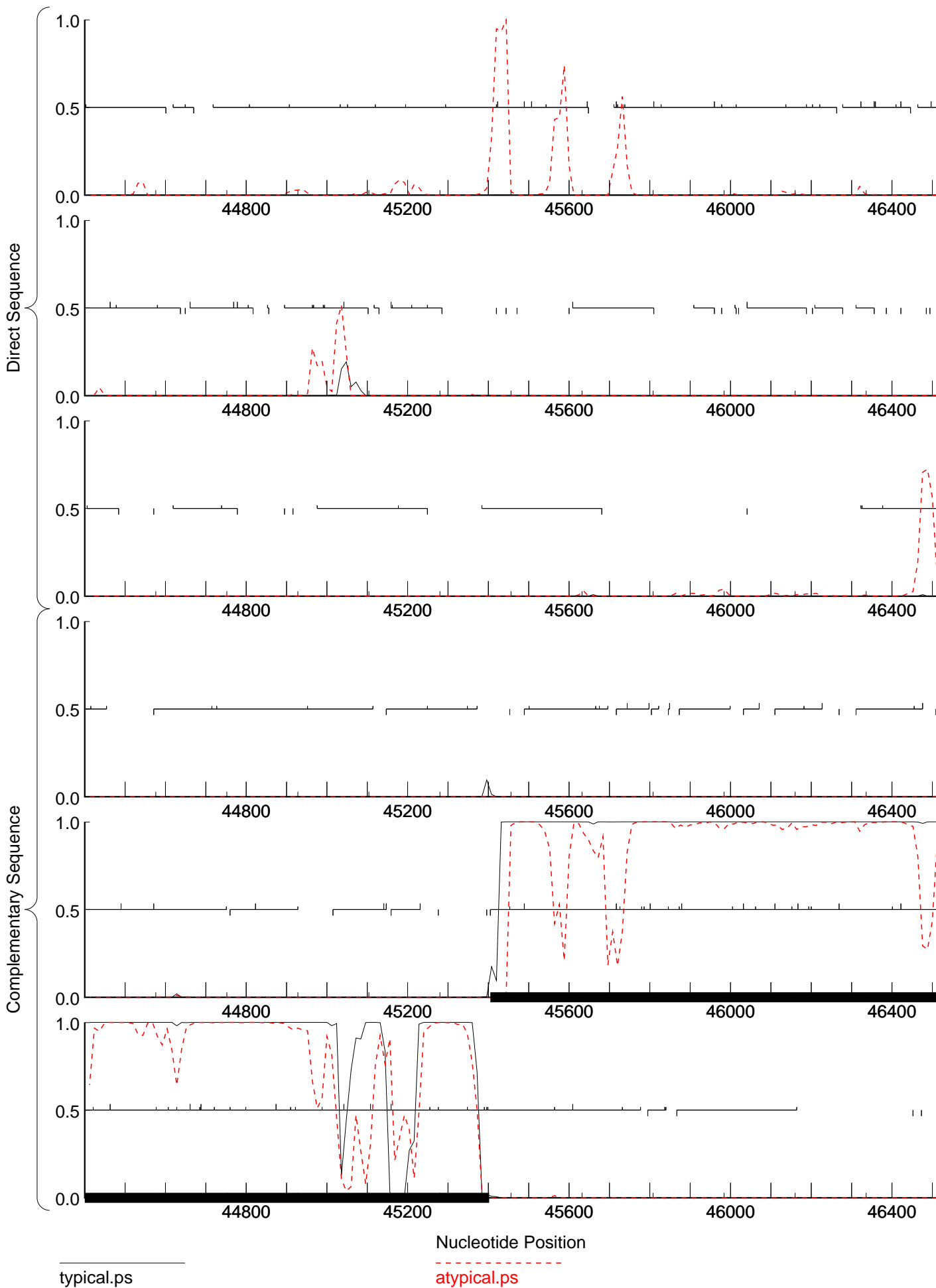
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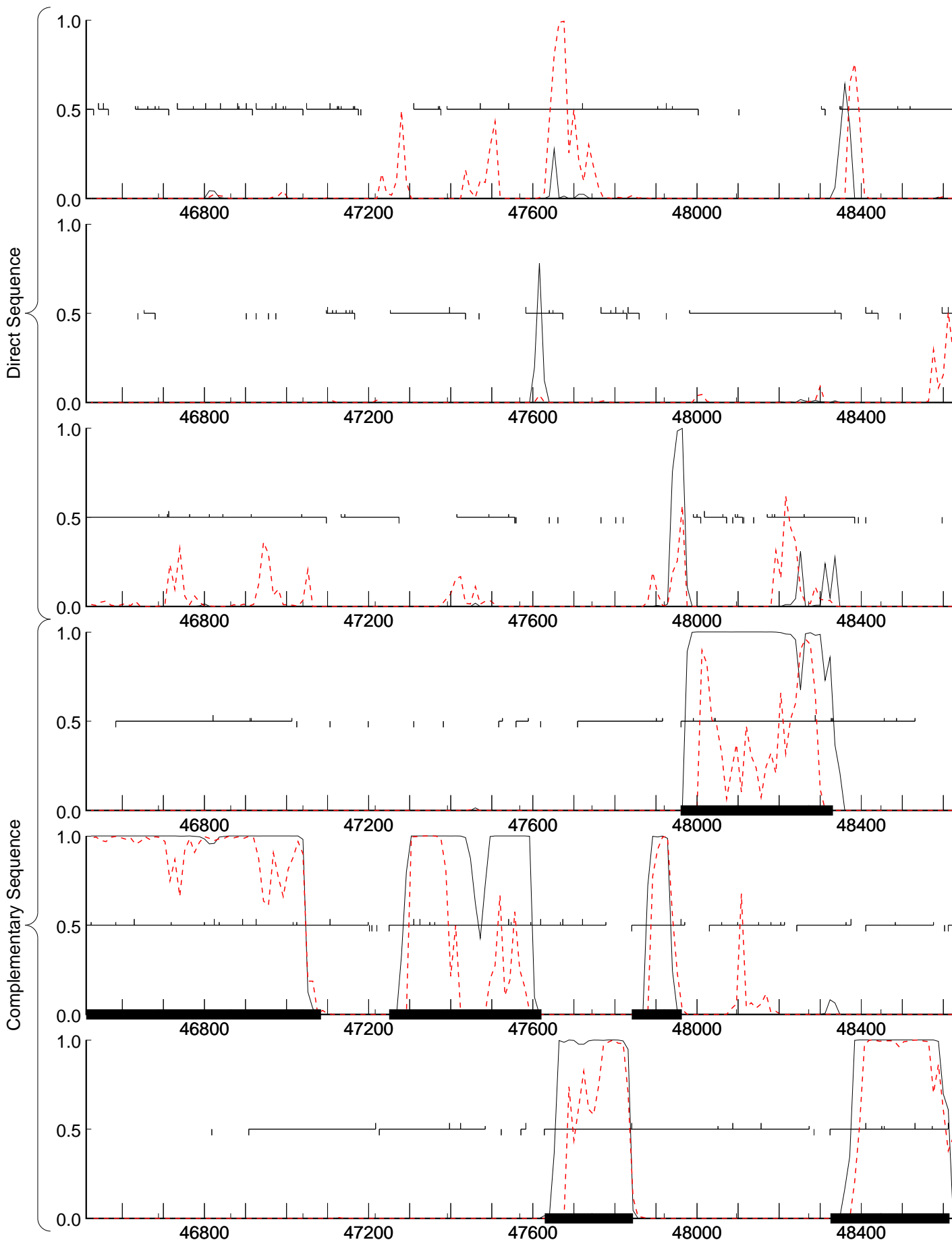


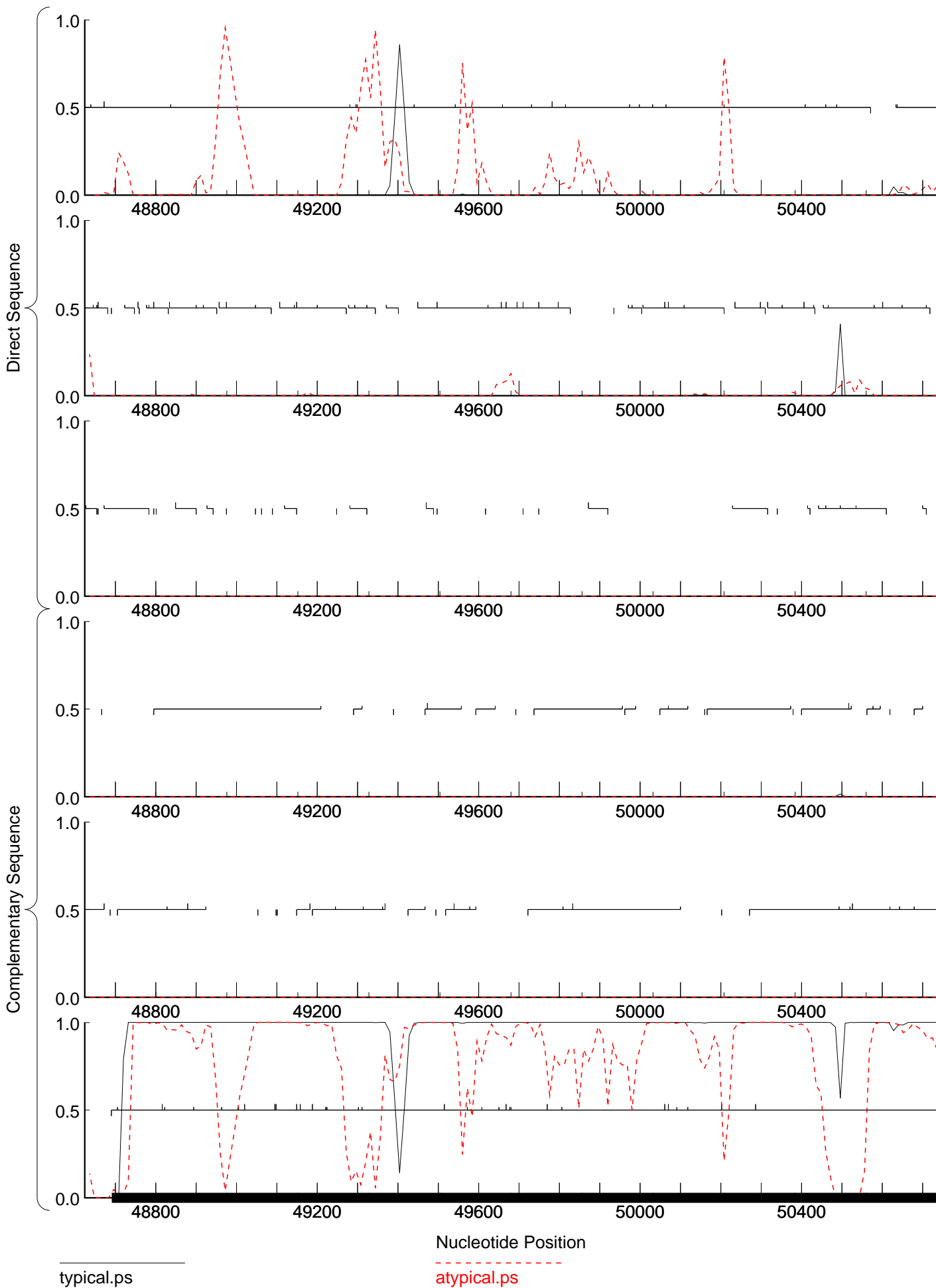


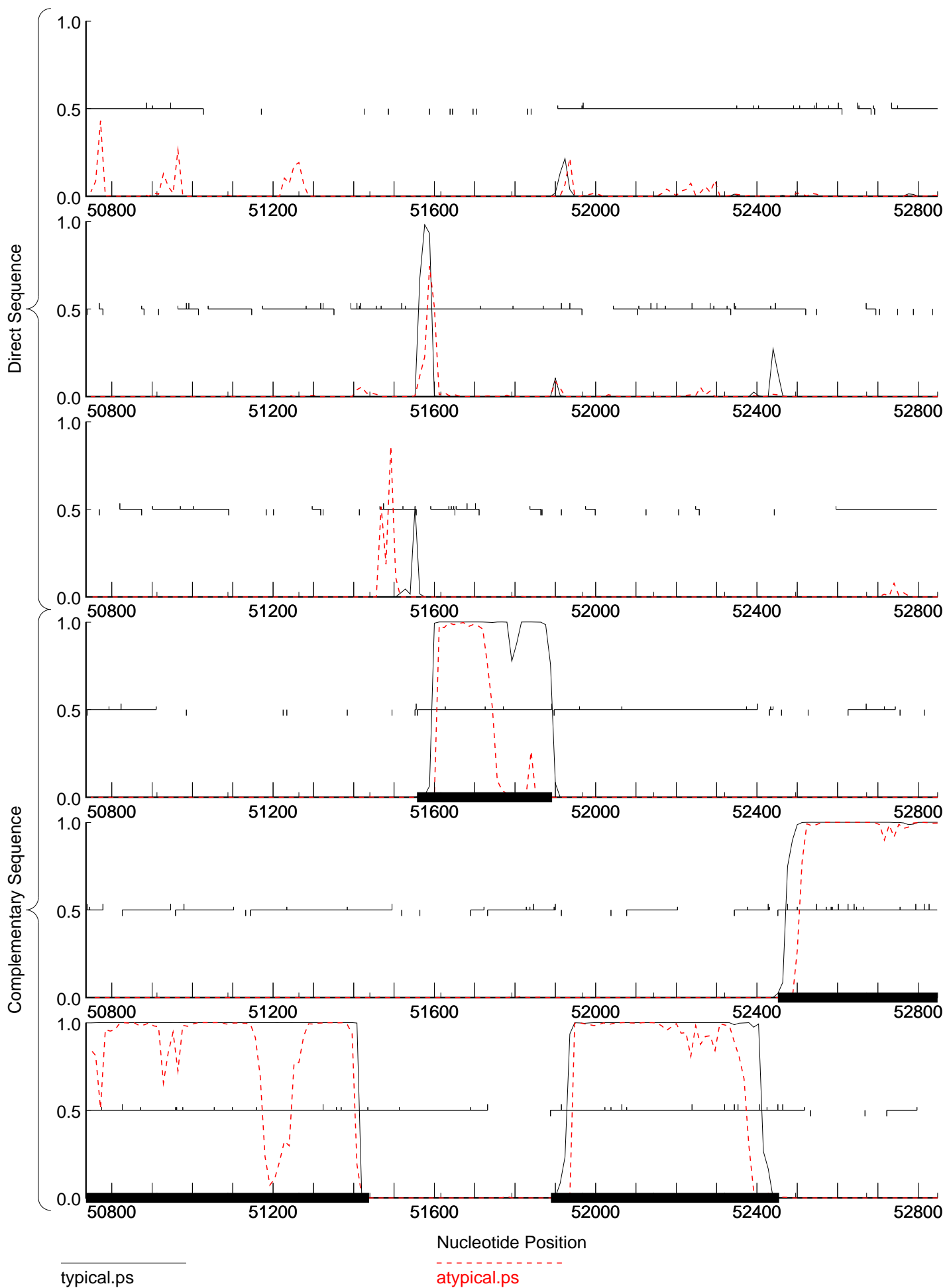


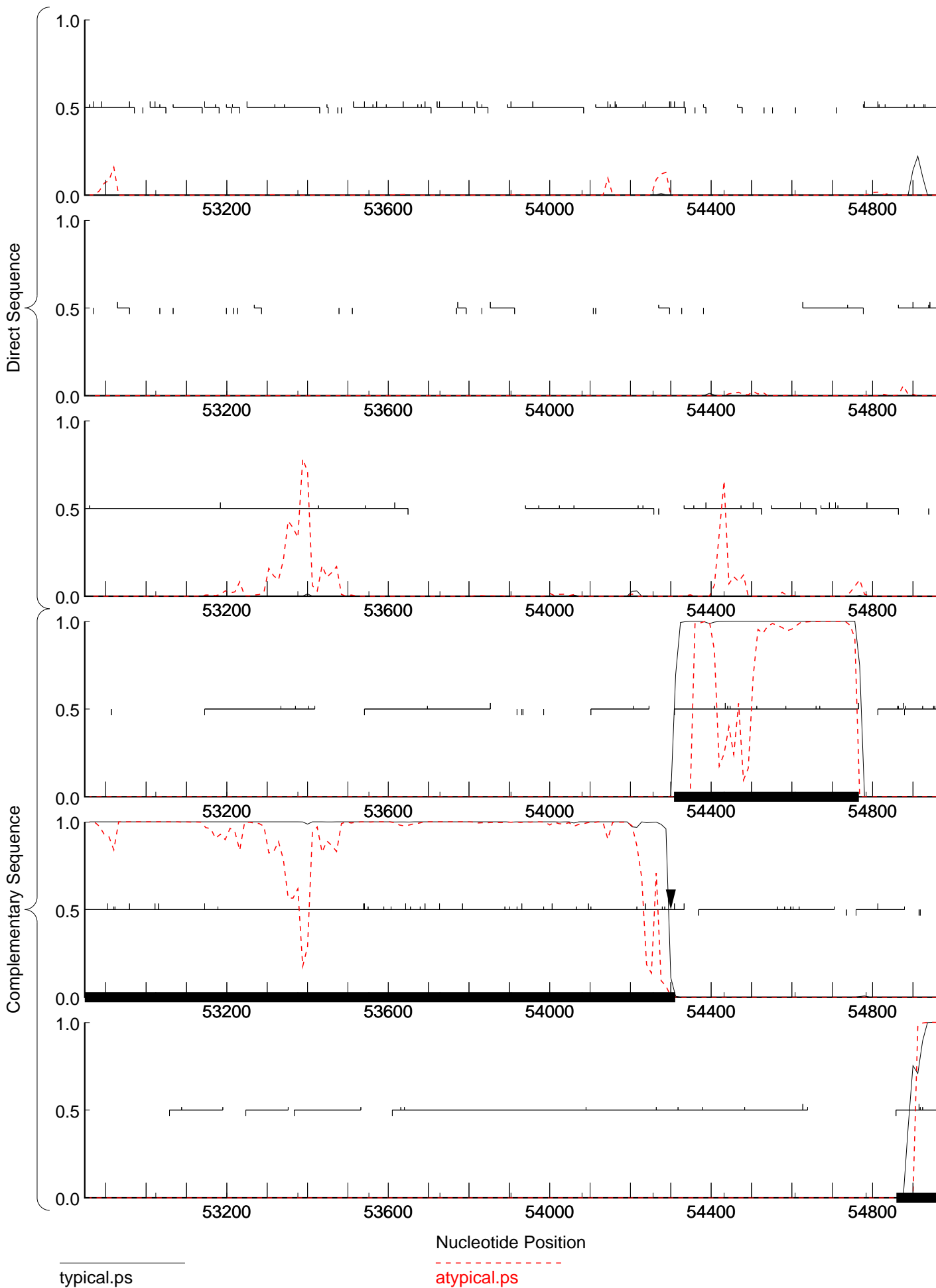








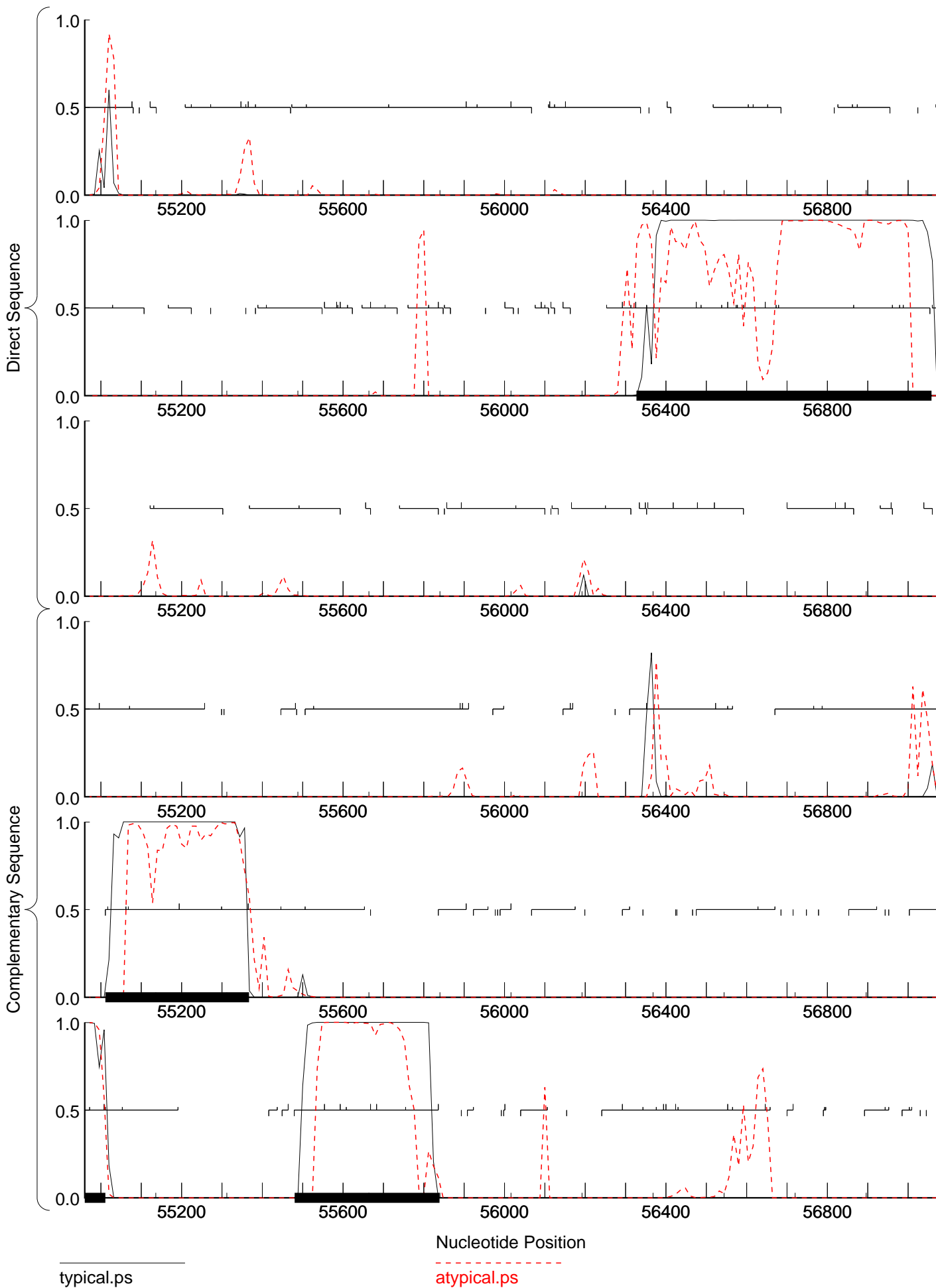


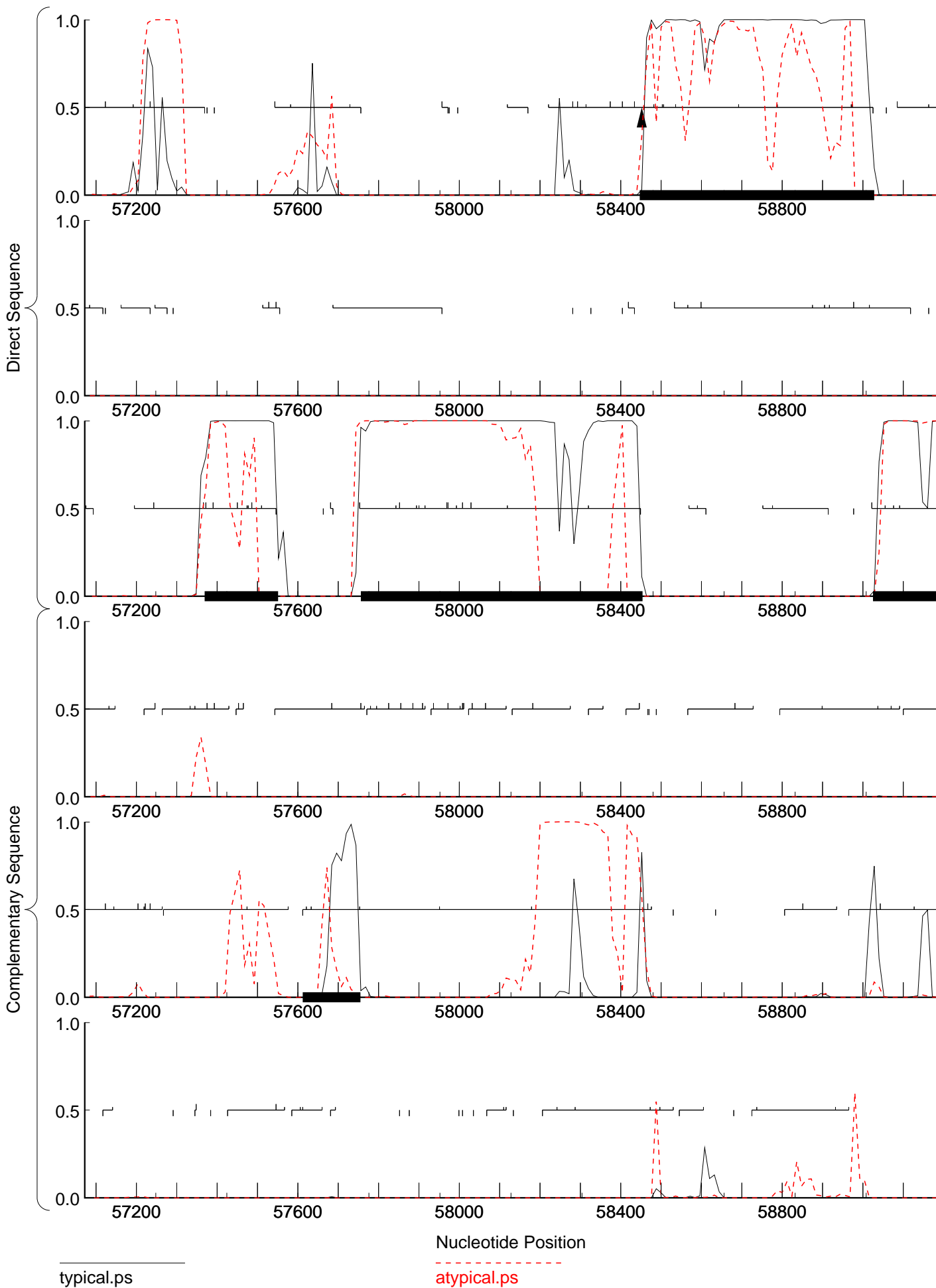


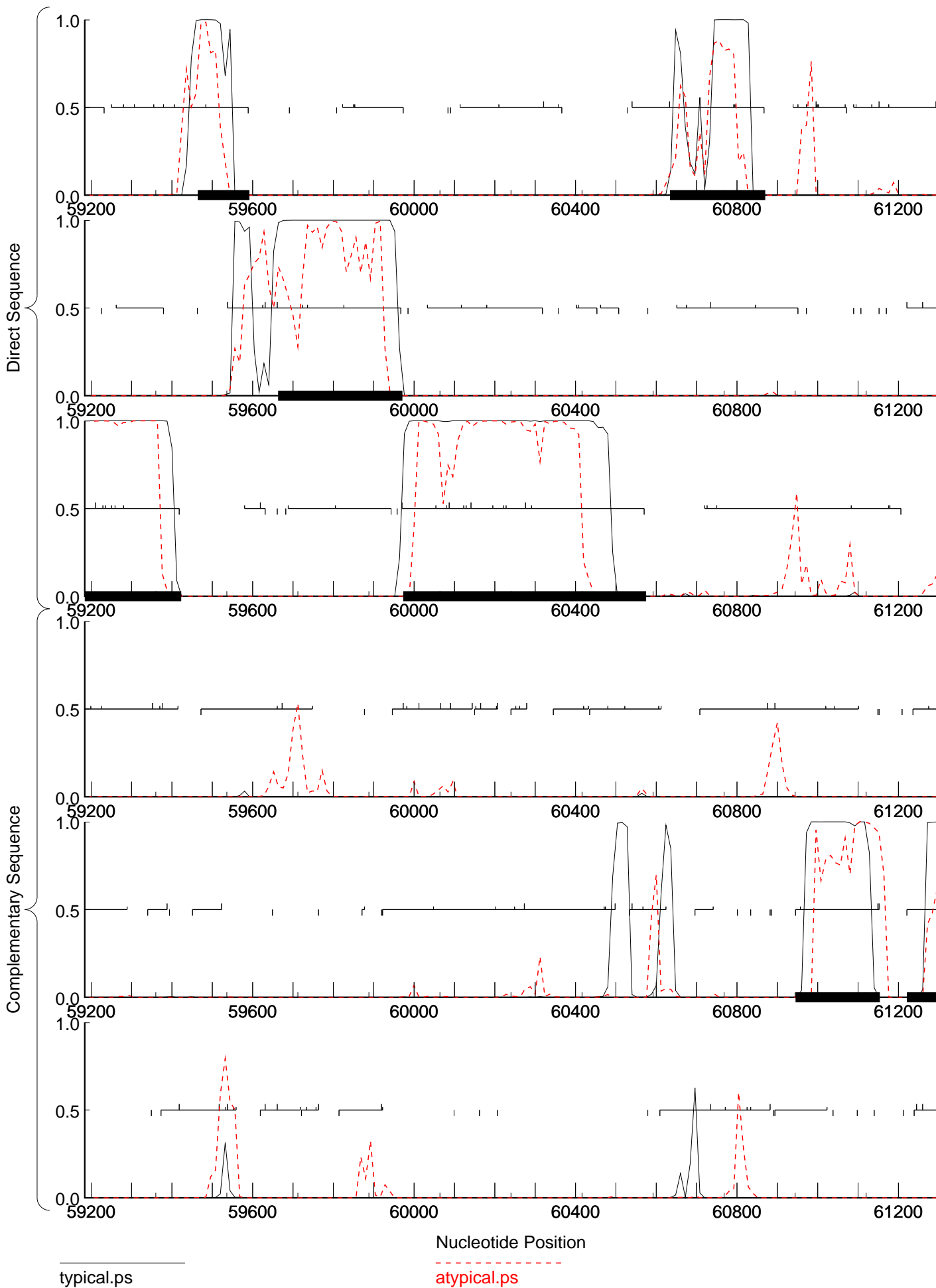
typical.ps

Nucleotide Position

atypical.ps

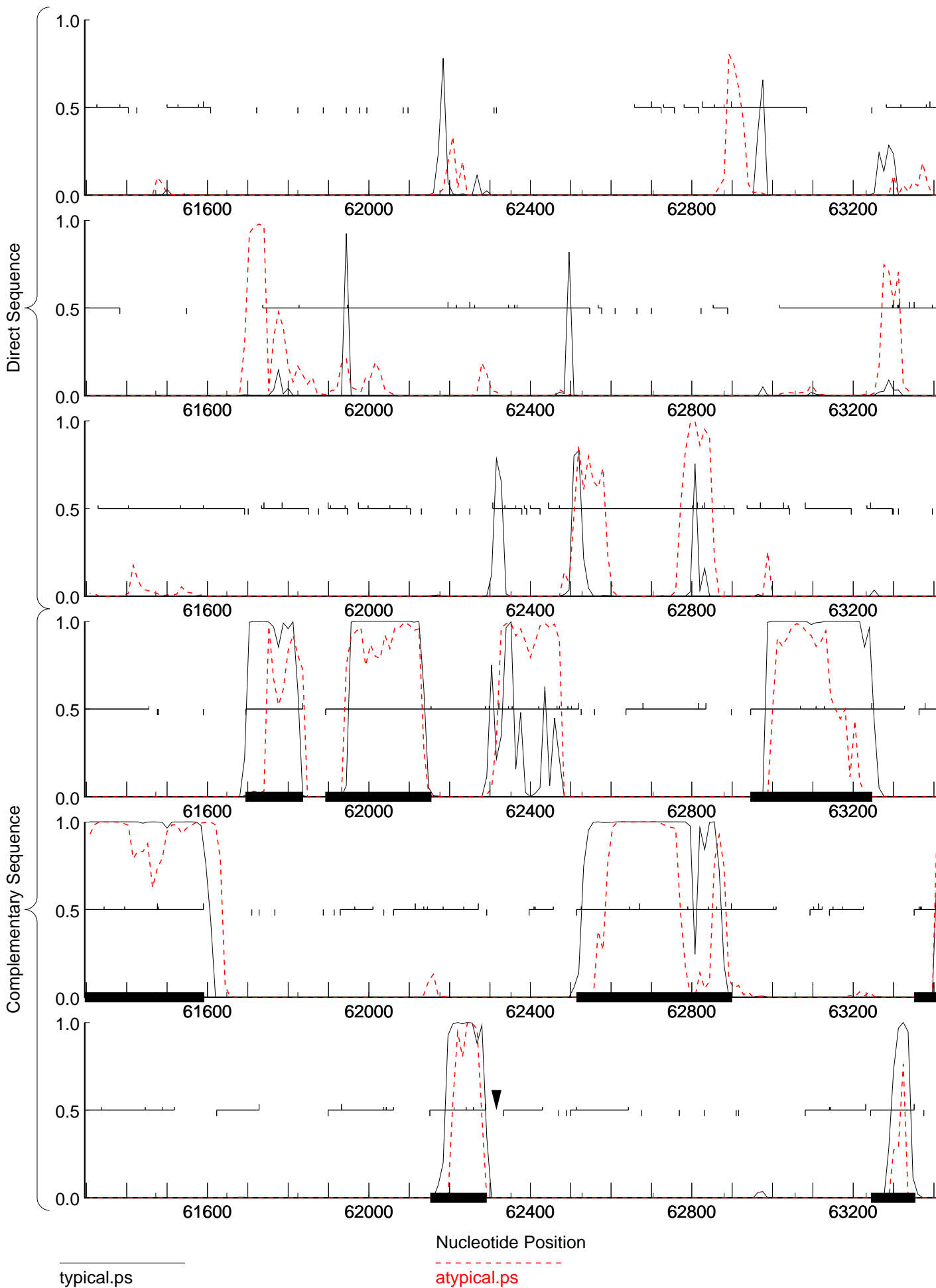






typical.ps

atypical.ps



typical.ps

atypical.ps

