

GeneMark

Version 2.5p (09.08.06)

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PROGRAM INFORMATION

Sequence : Gordonia phage Fosterous complete sequeunce, 59136 bp, circularly permuted, Cluster DE
Analysis Date : 1/18/18 at 20:28:48
Pages : 29
Sequence Length : 59136 bp
GC Content : 67.22%

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,

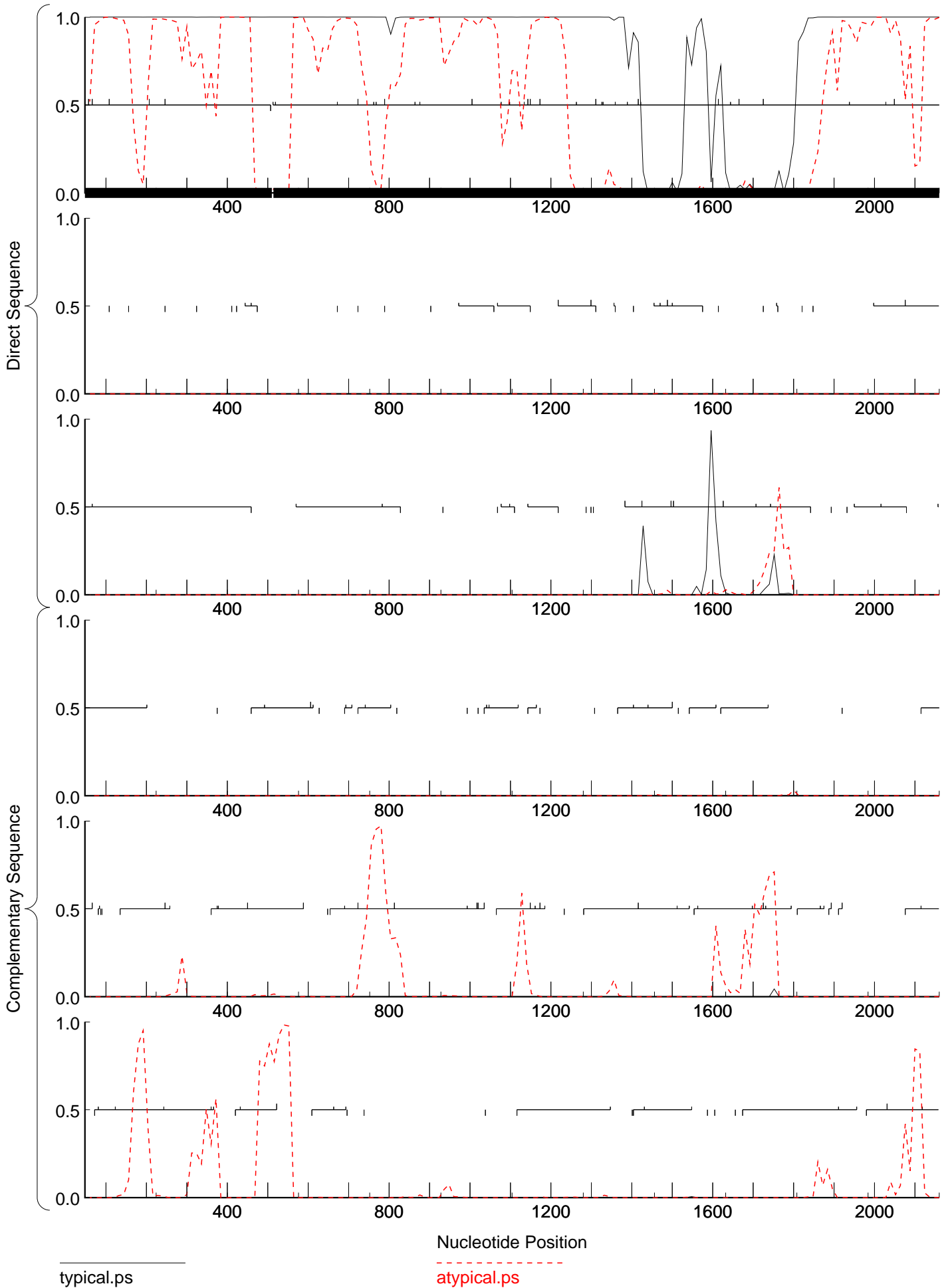
Matrix notes & comments

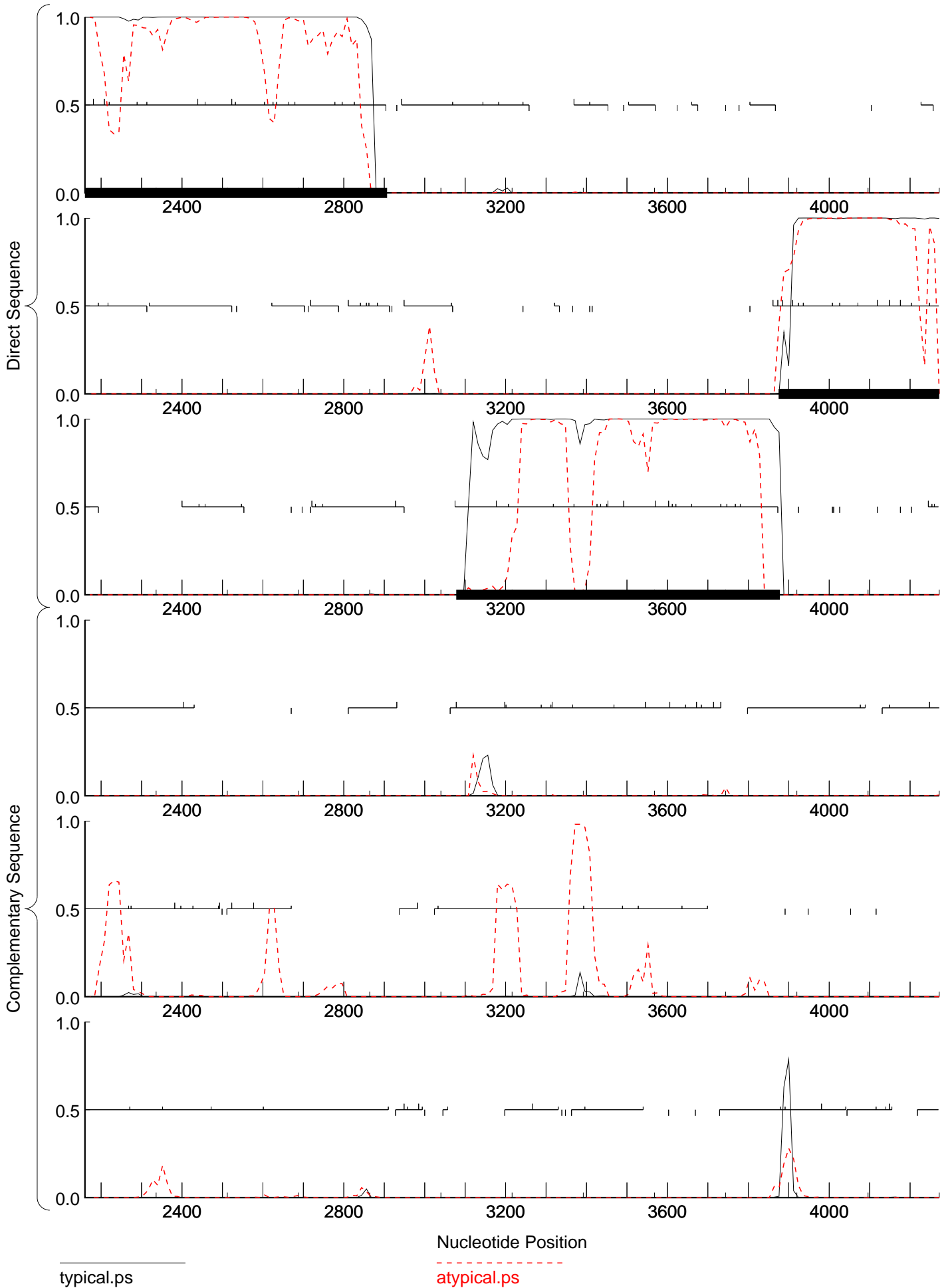
Training set derived by GeneMarkS, 4.30 October 2014
Thu Jan 18 20:28:48 2018

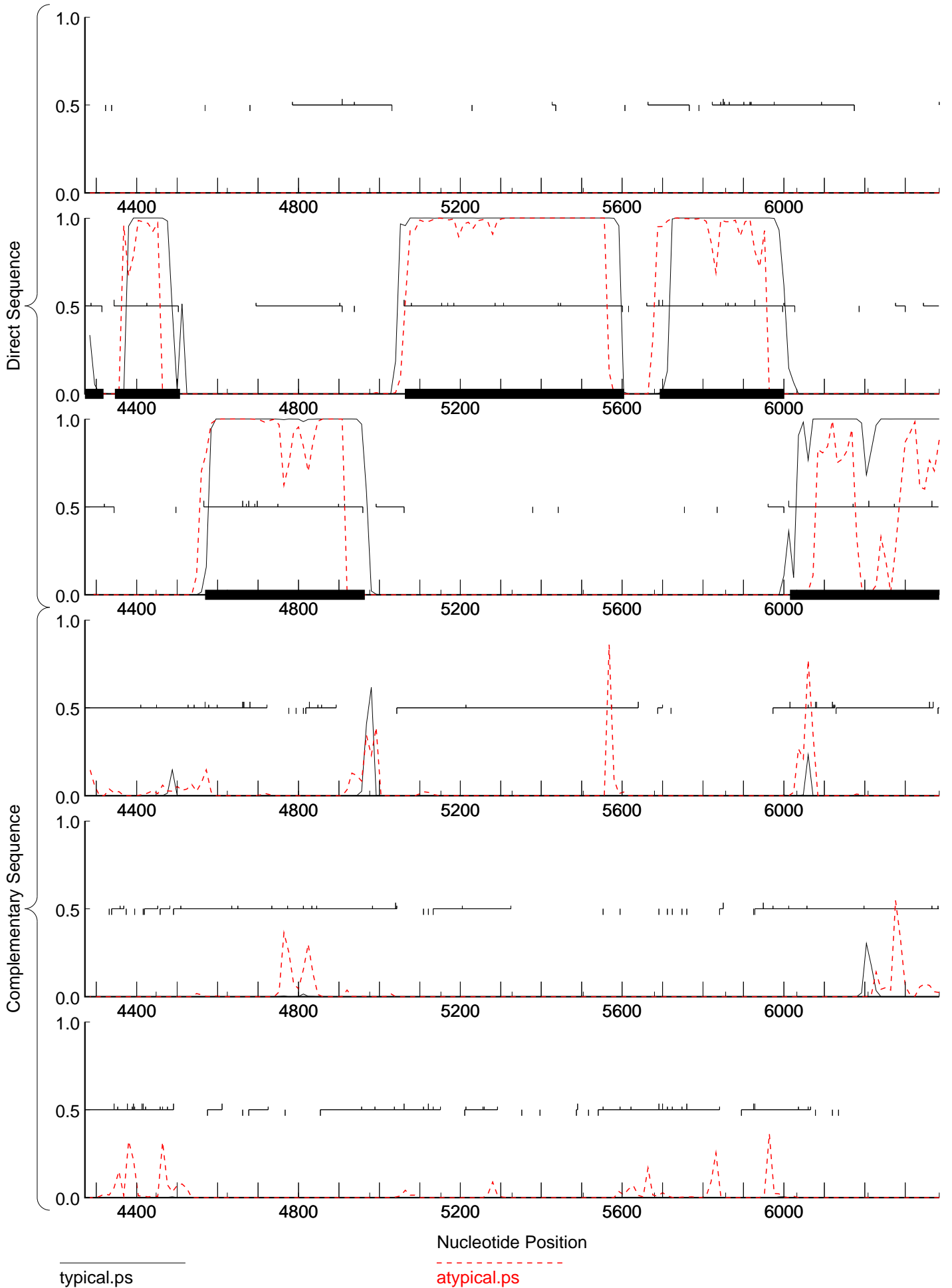
MATRIX INFORMATION

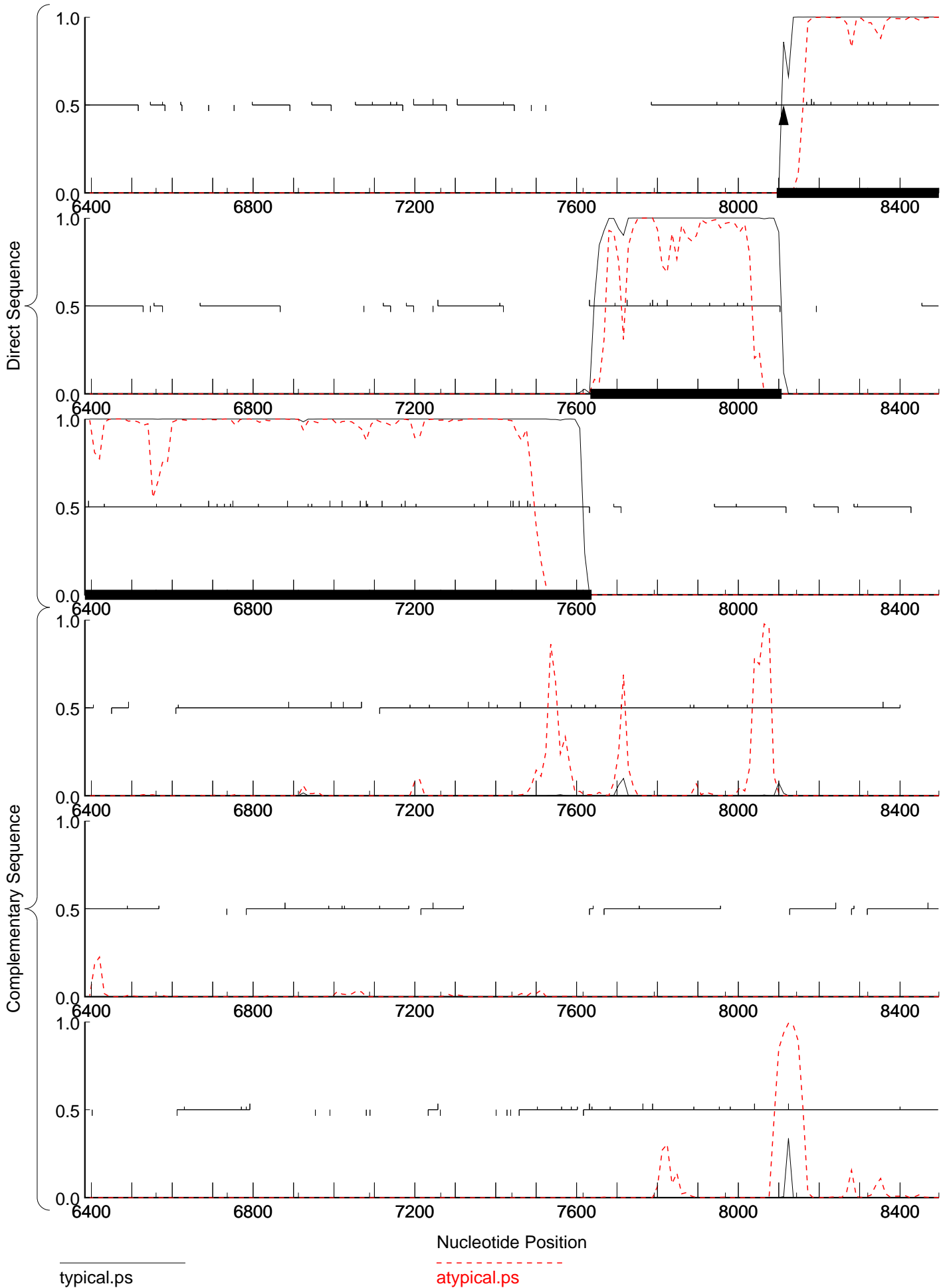
Matrix : -
Author : -
Order : 4

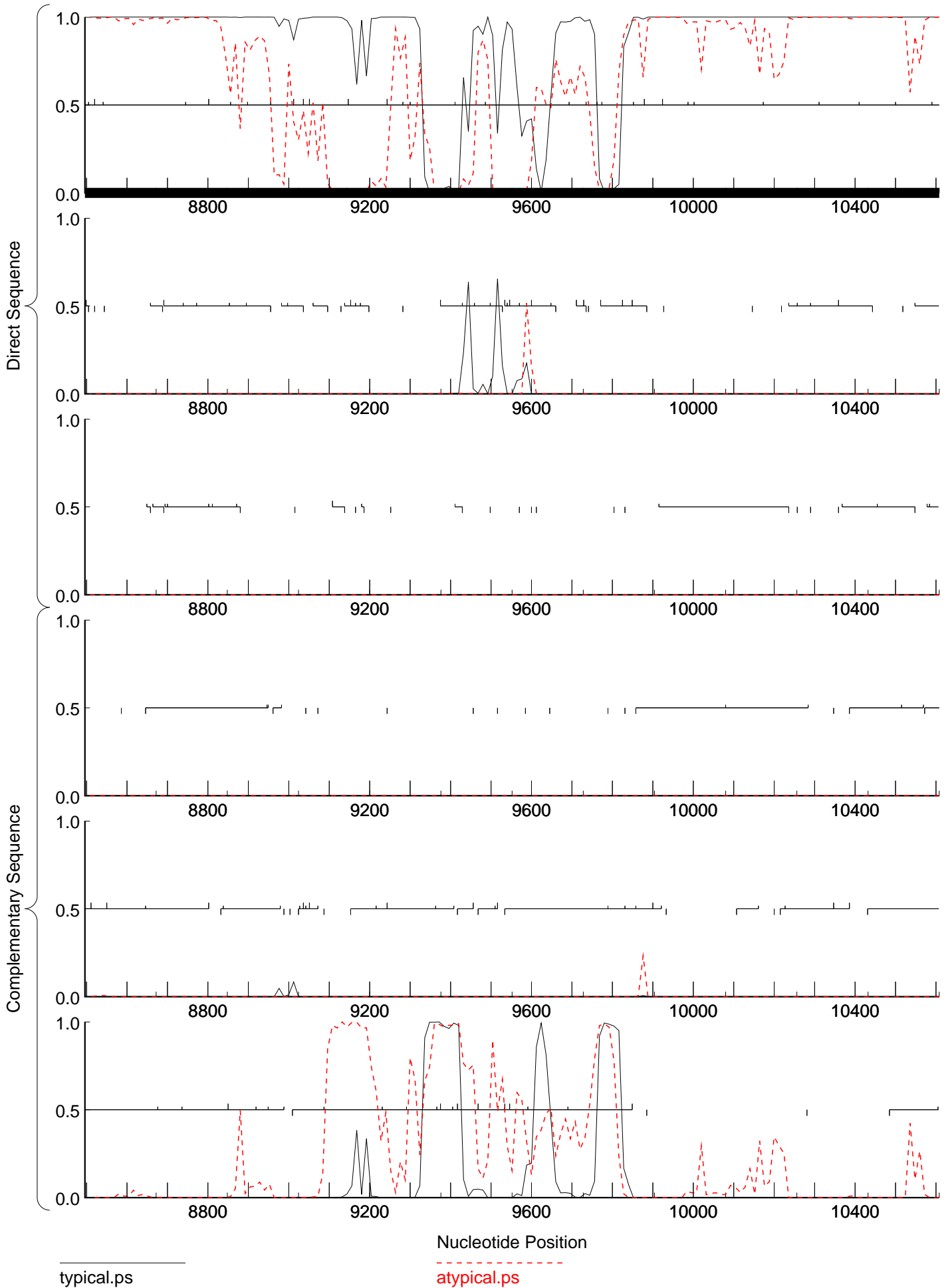
Send questions / comments to:
Dr. M. Borodovsky
Georgia Institute of Technology
School of Biology
Atlanta, GA 30332-0230

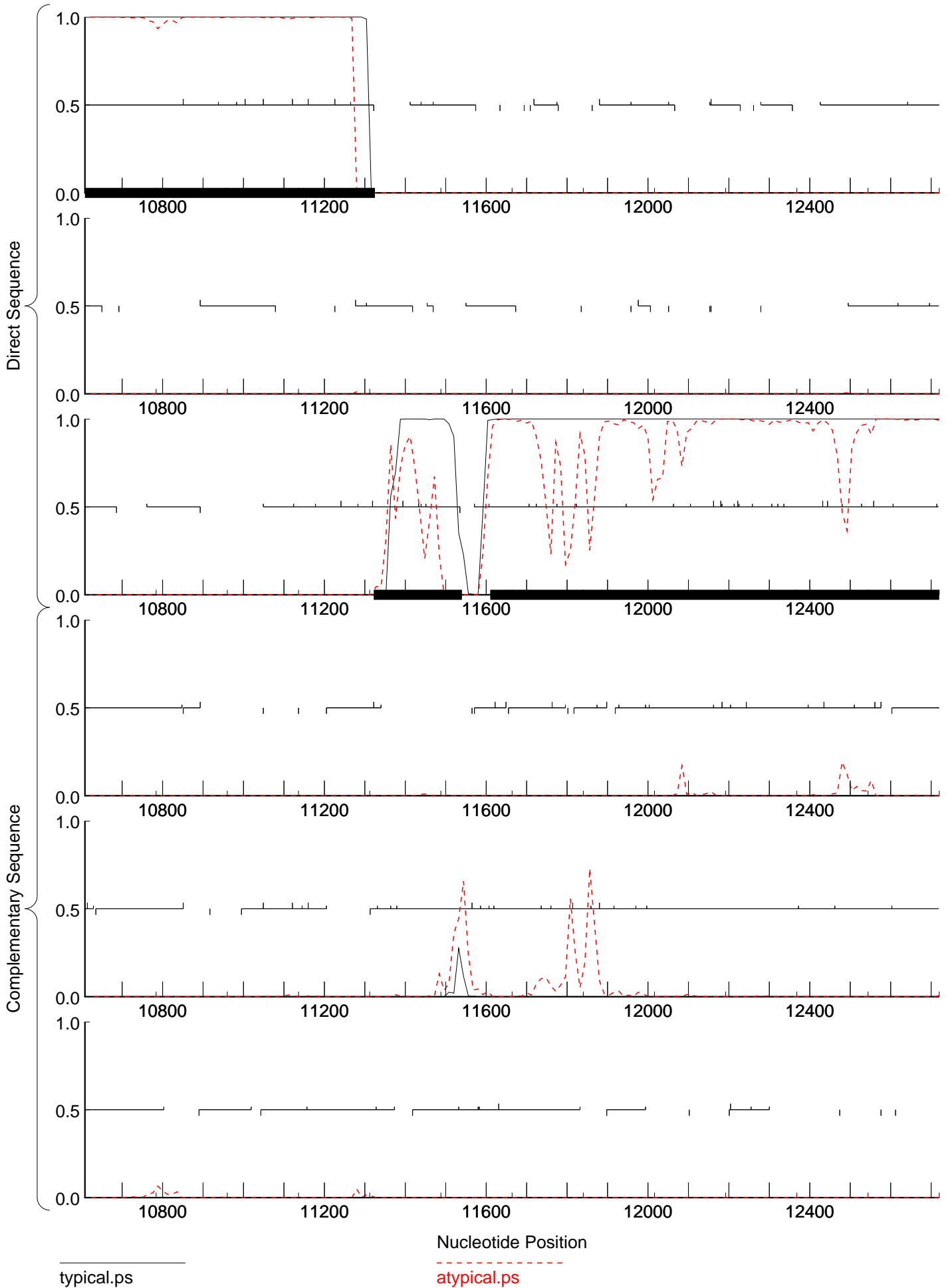


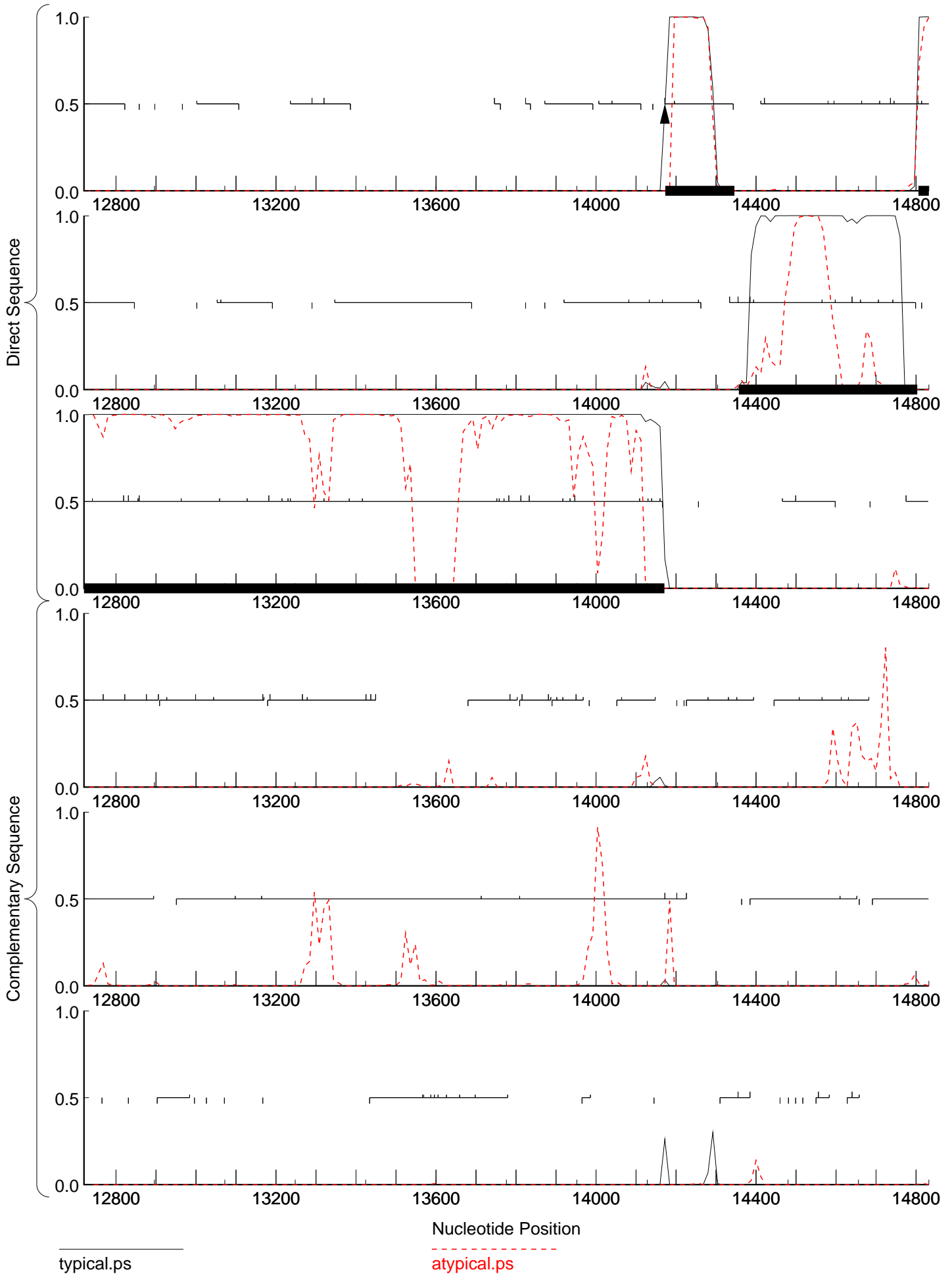


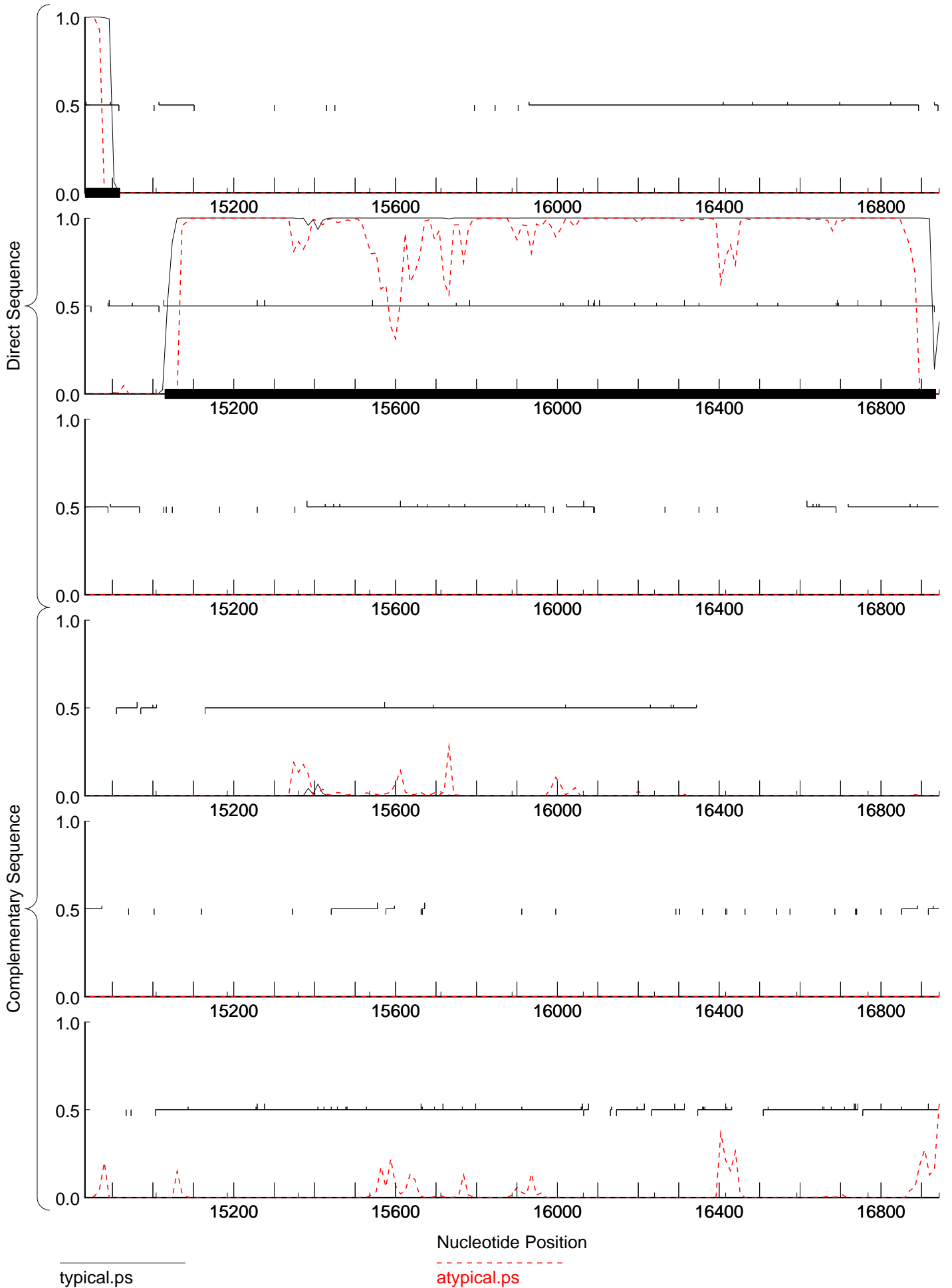


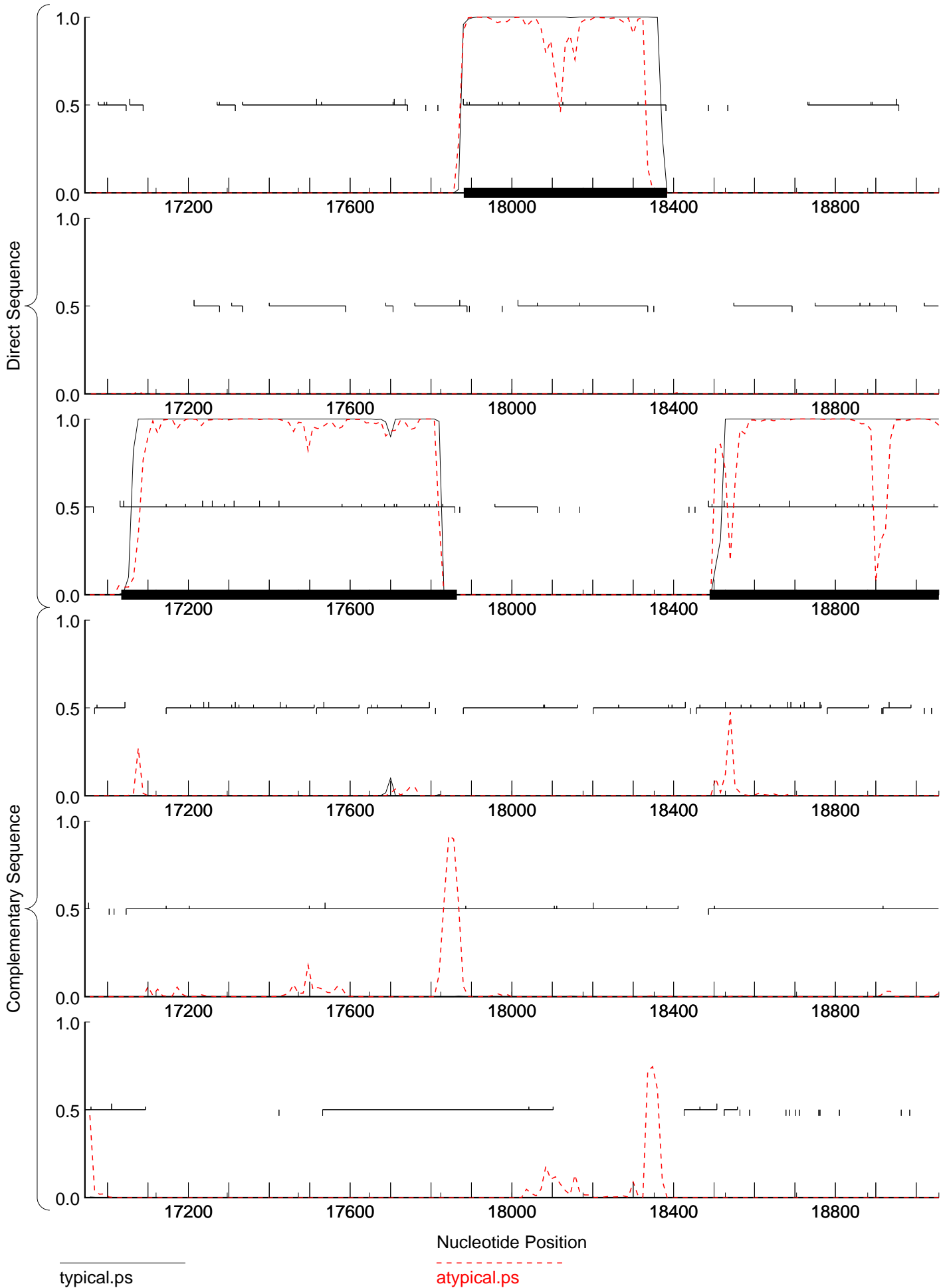


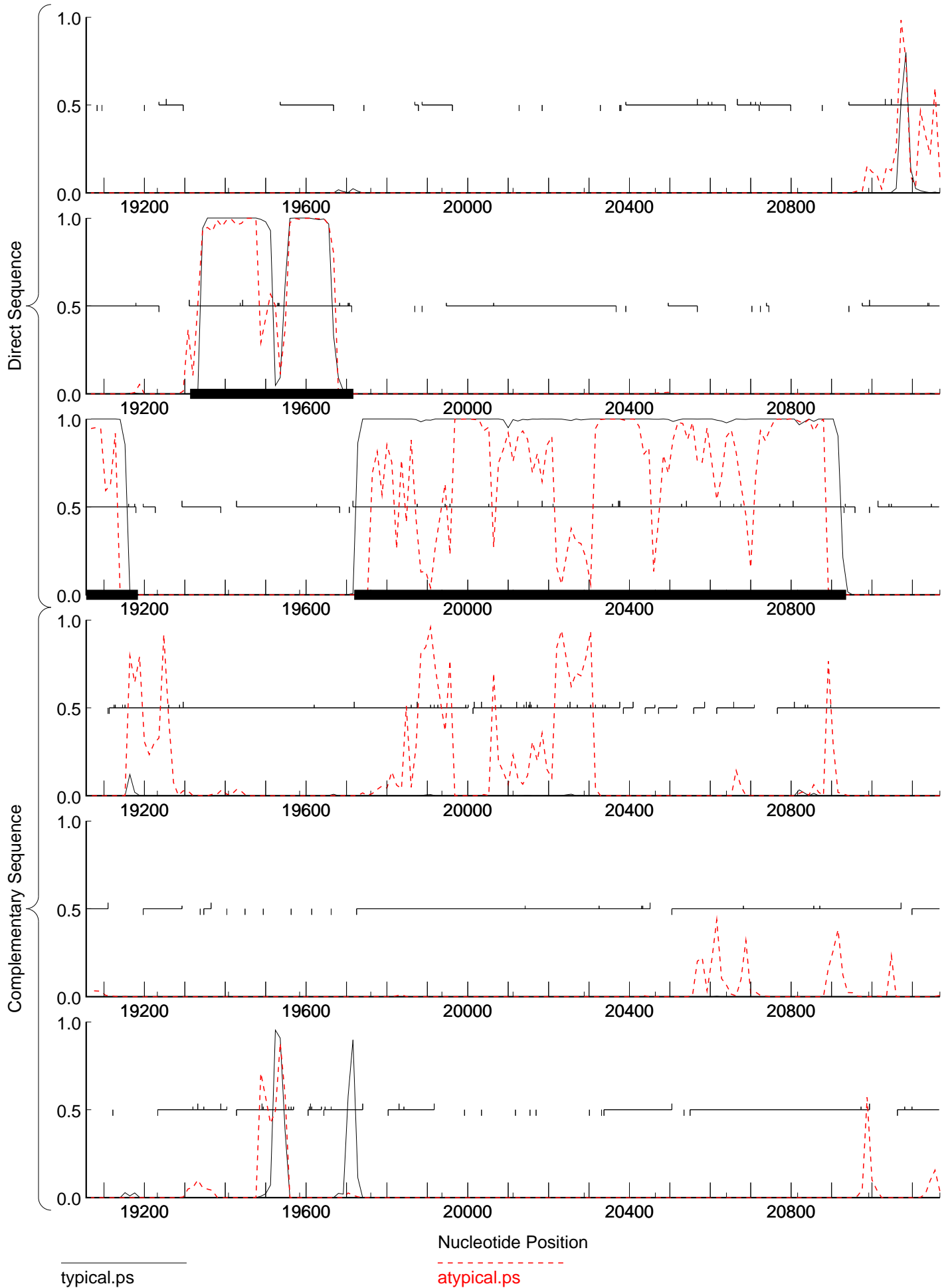


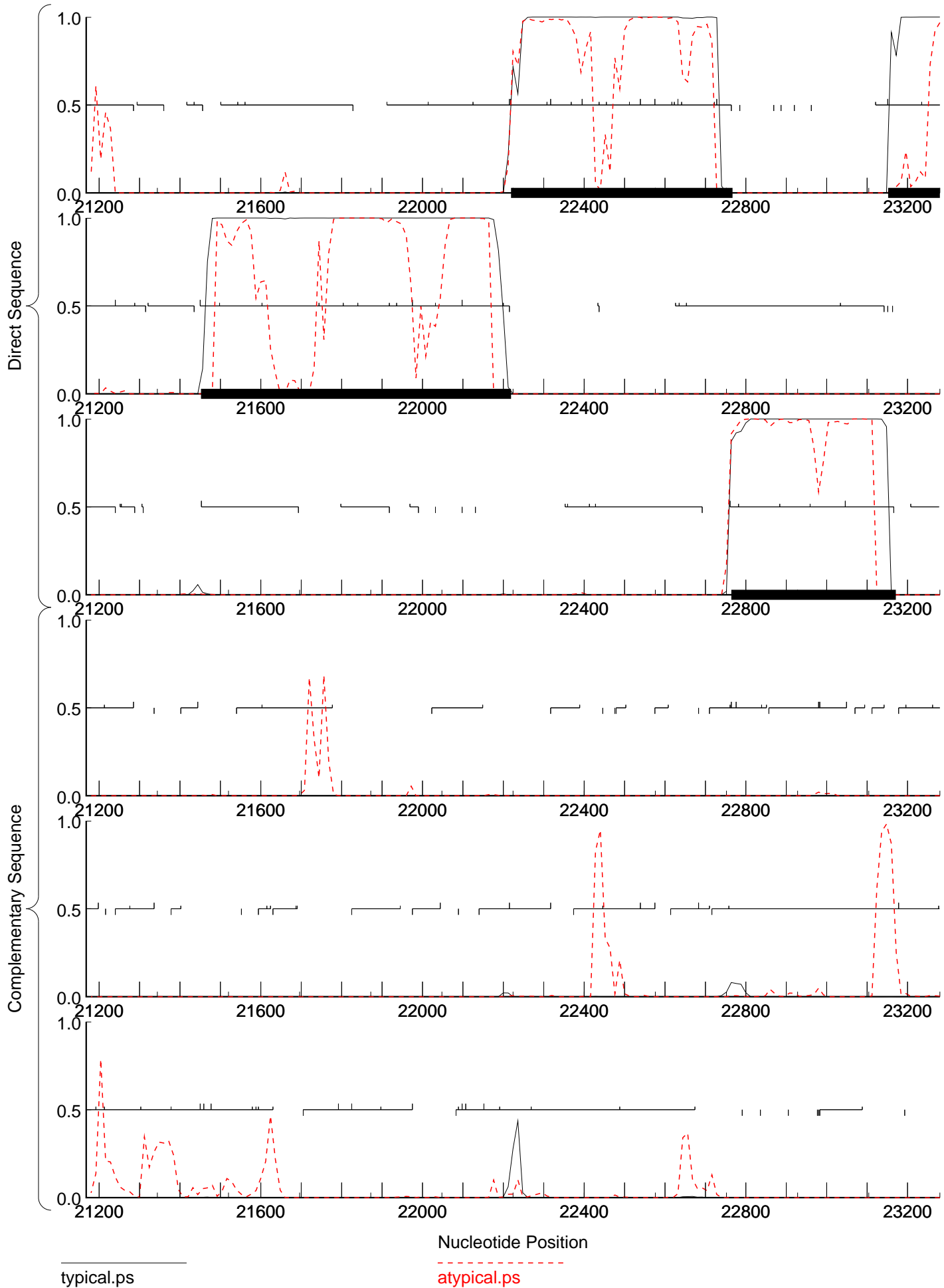


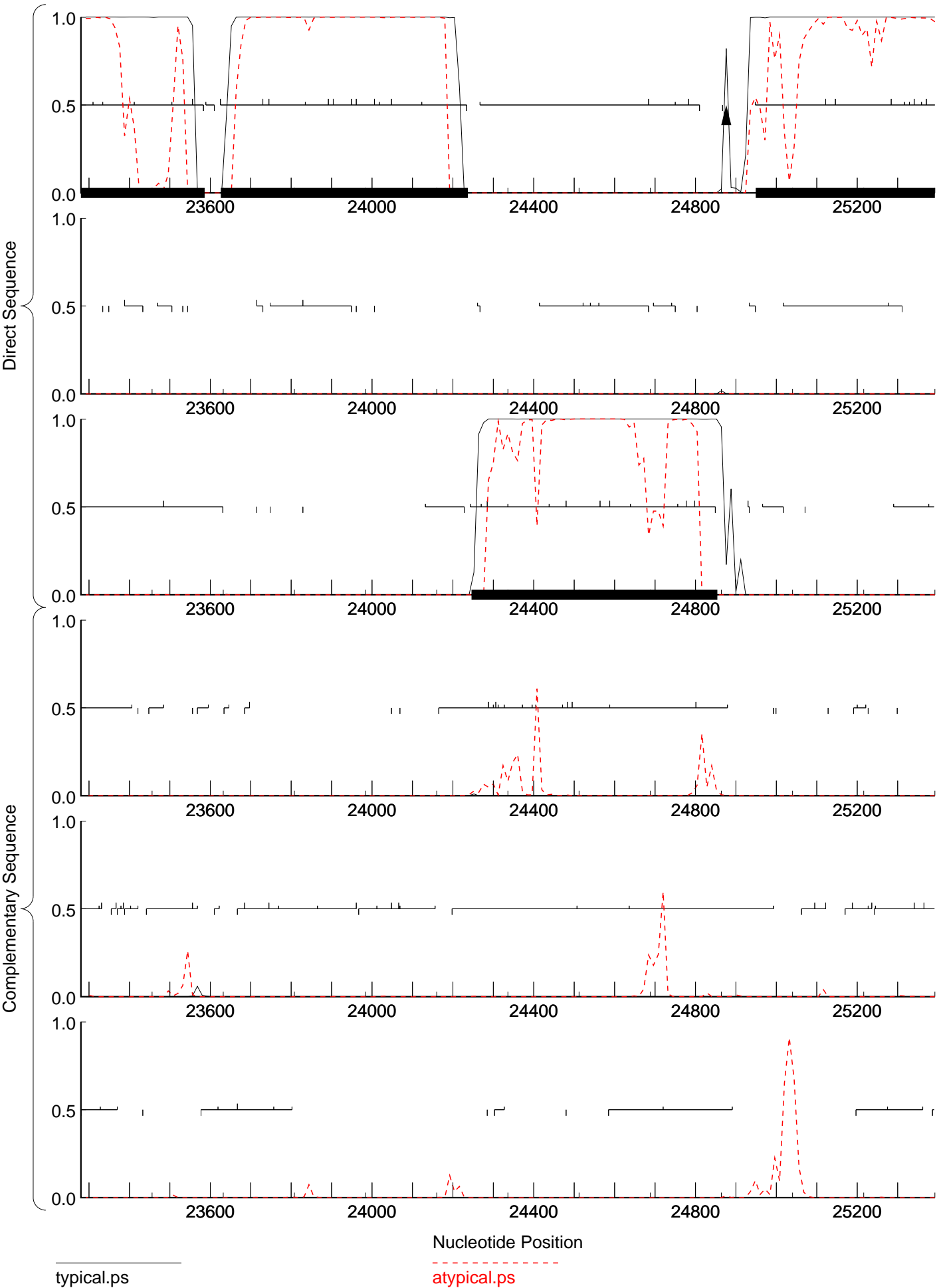


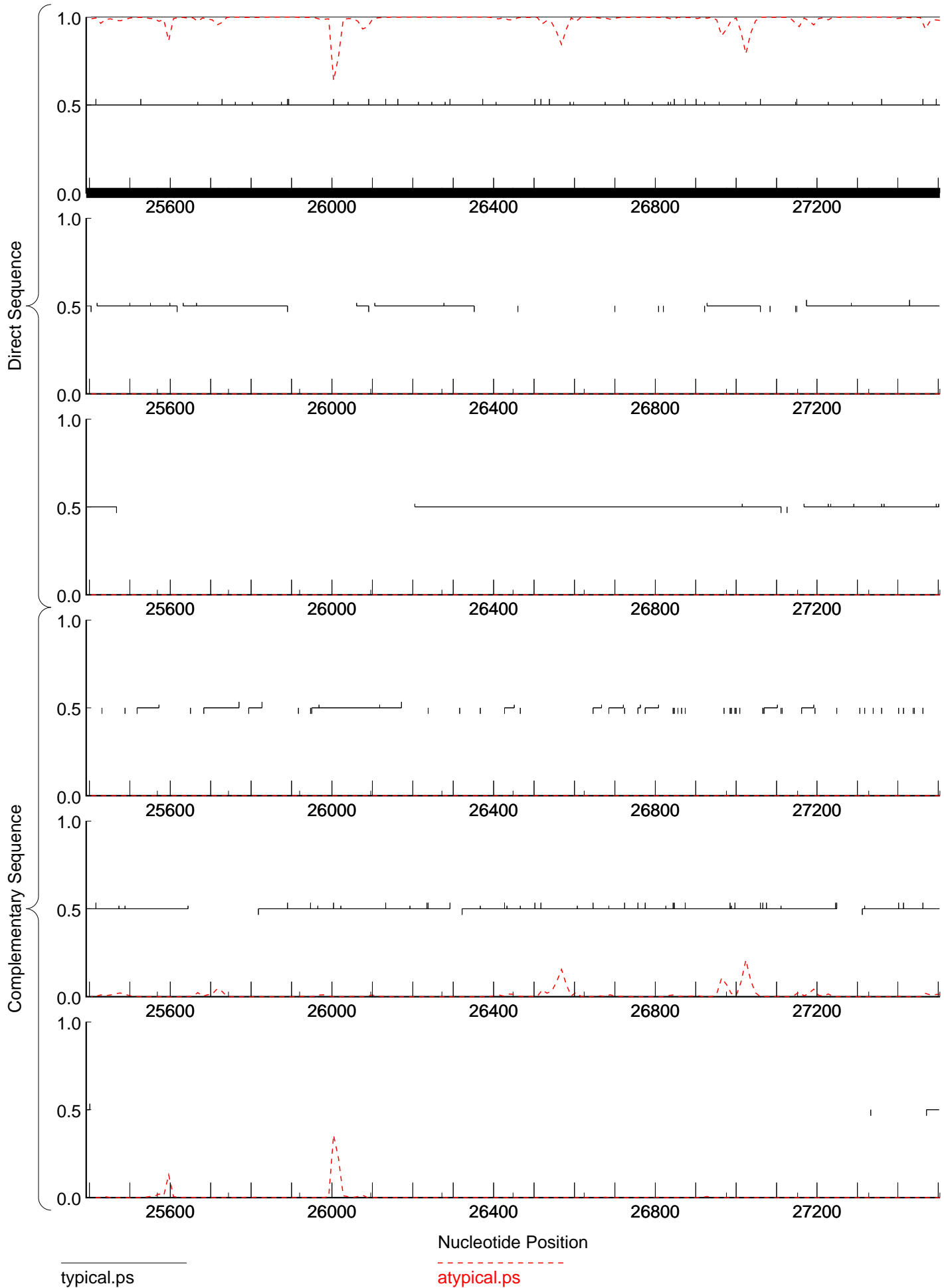


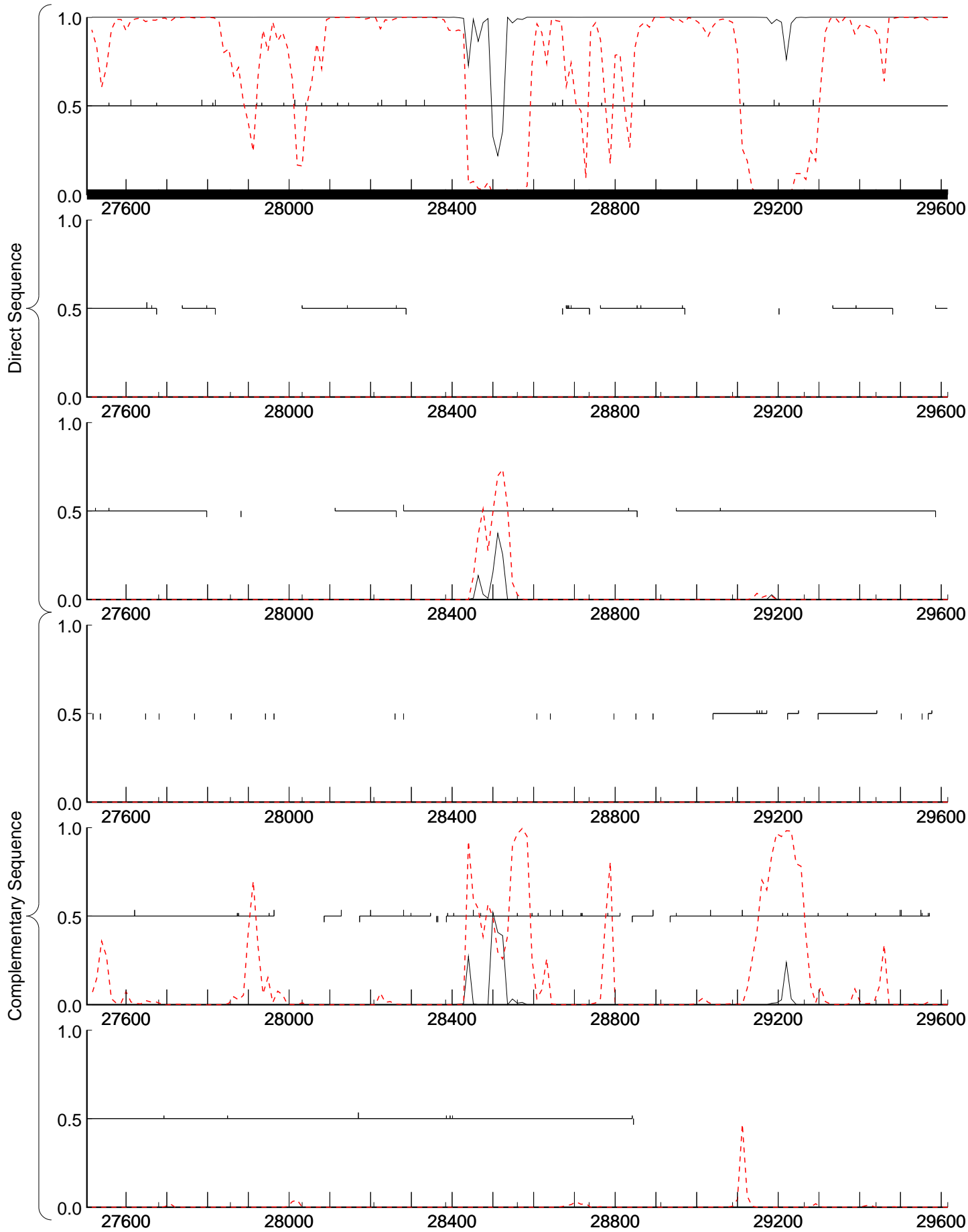




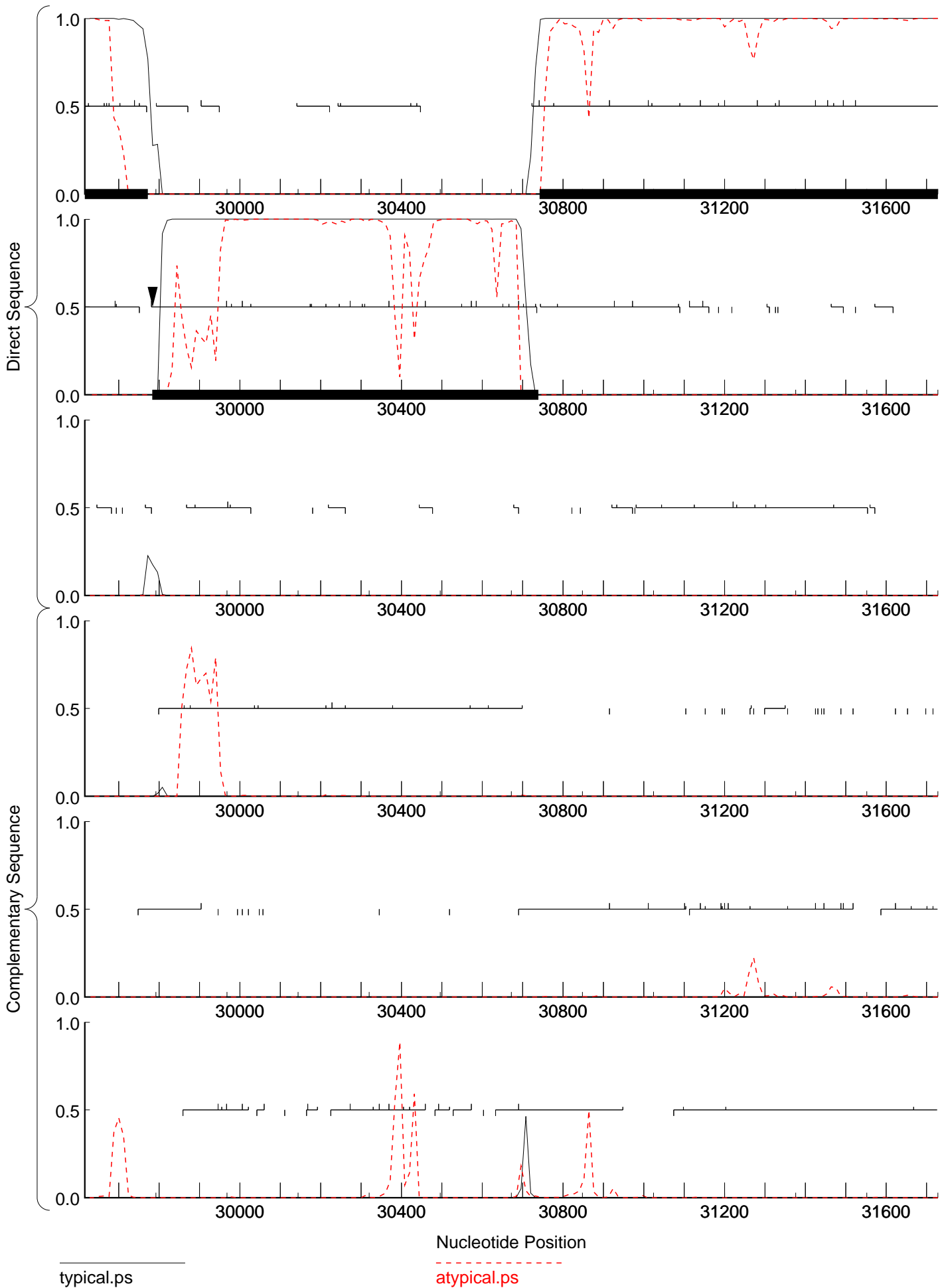






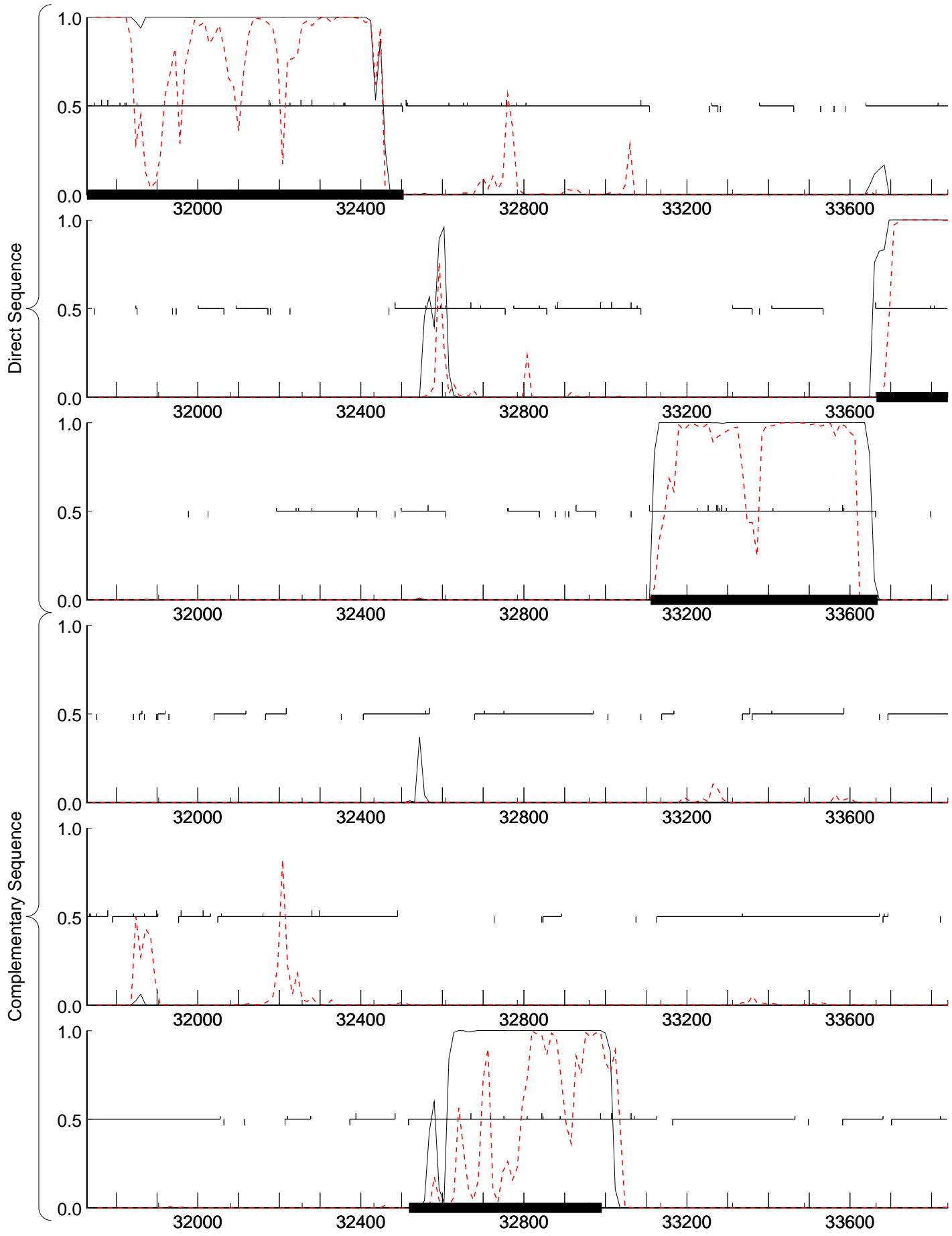


typical.ps
atypical.ps



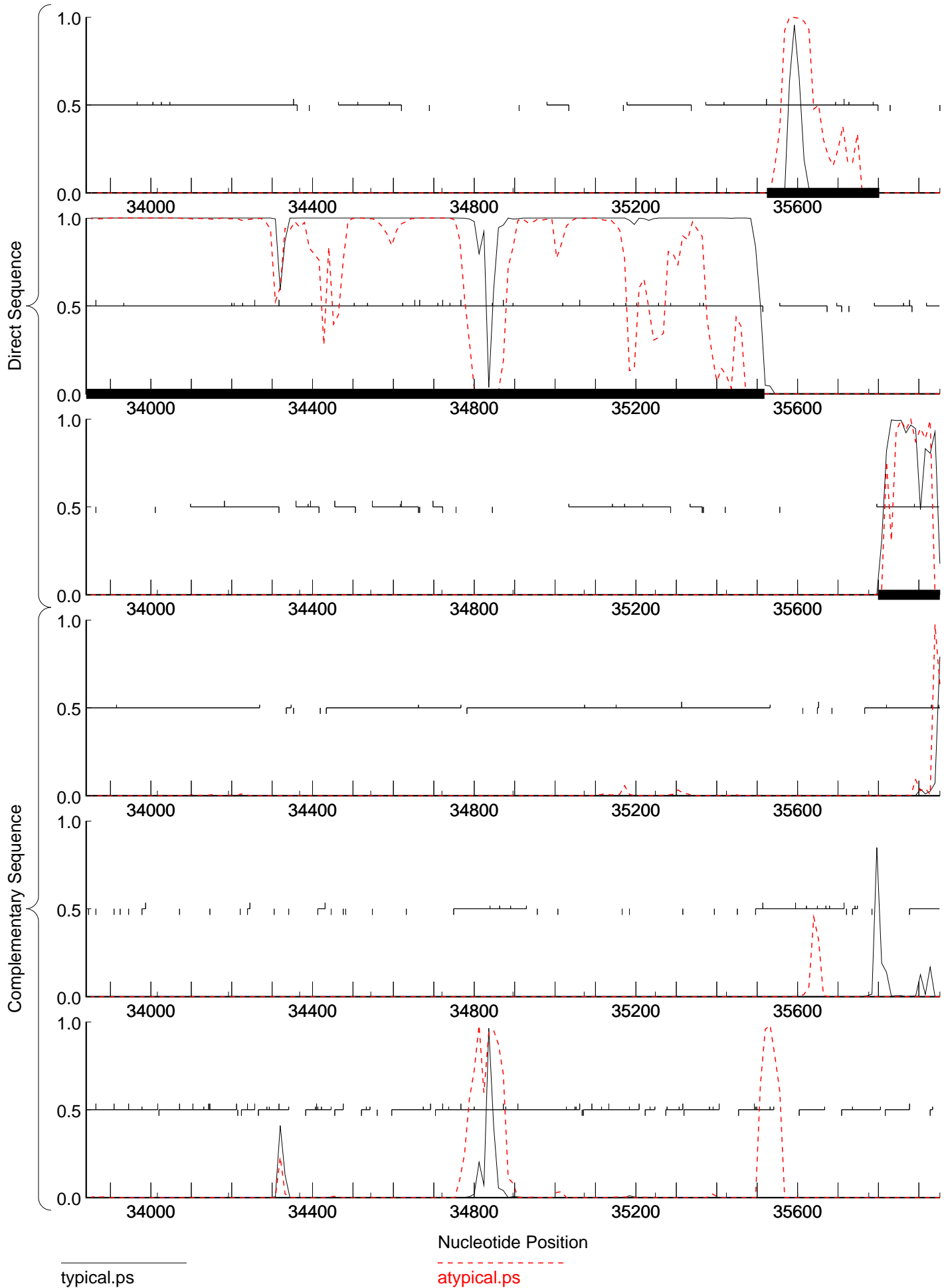
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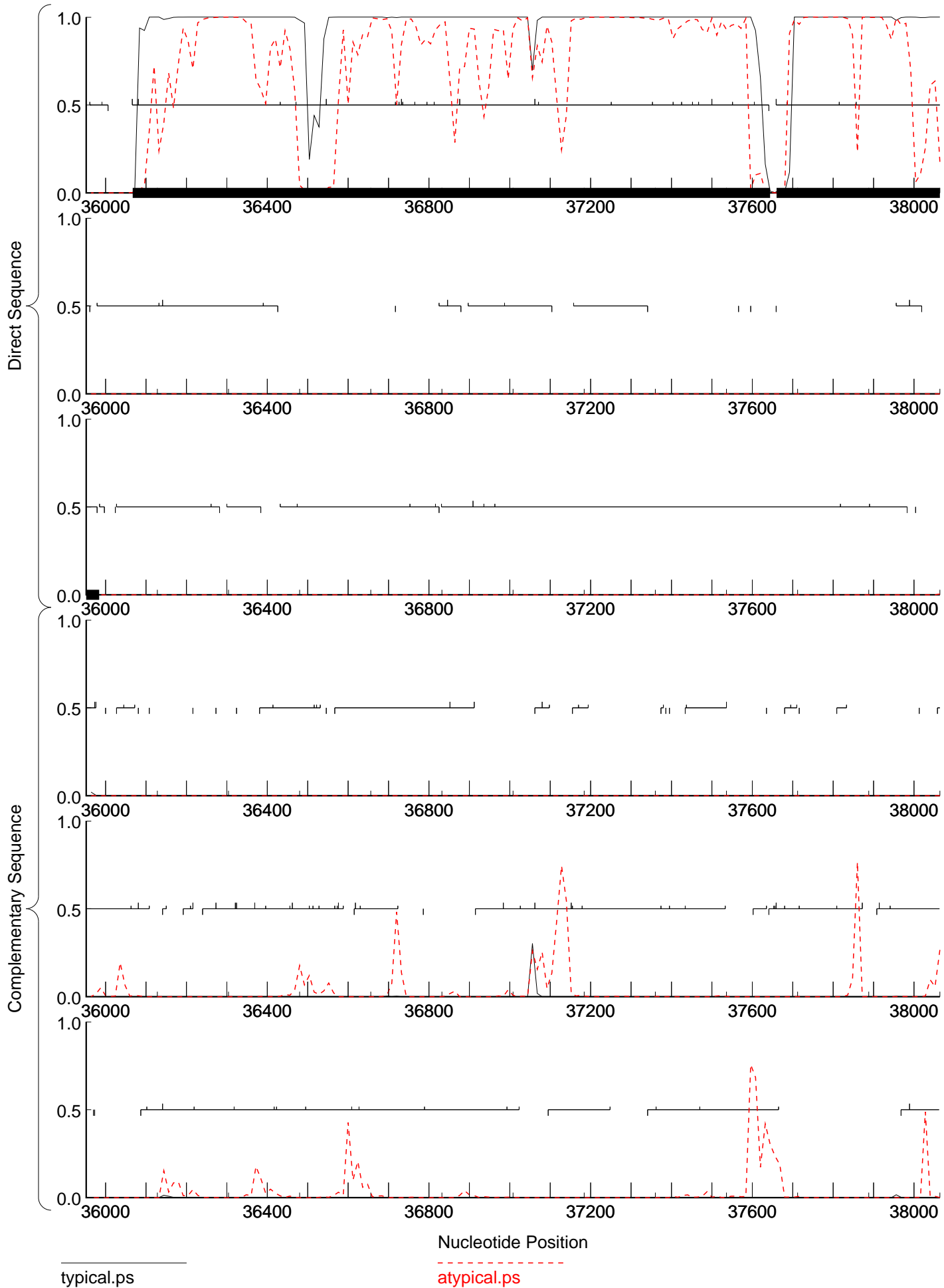
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typical.ps

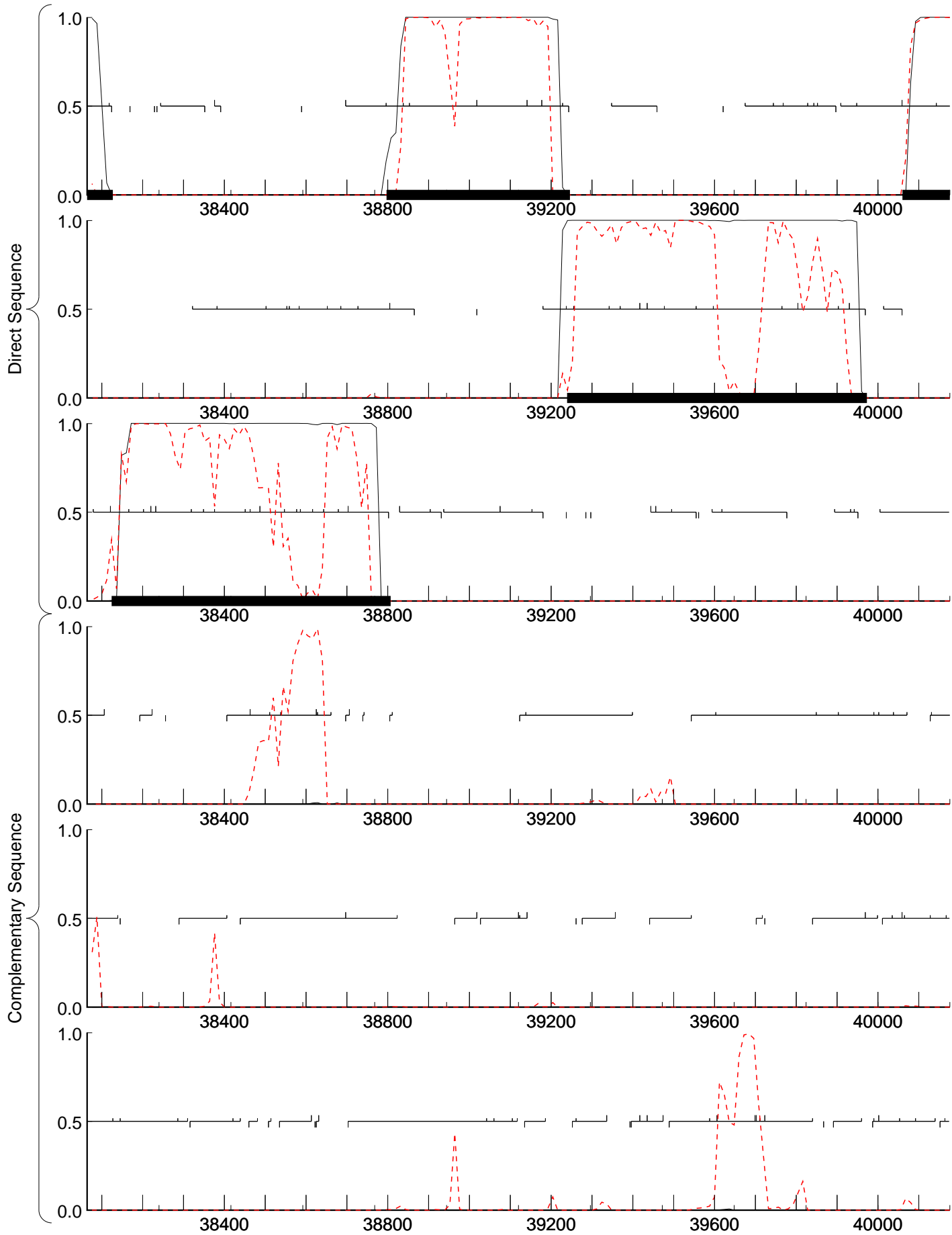
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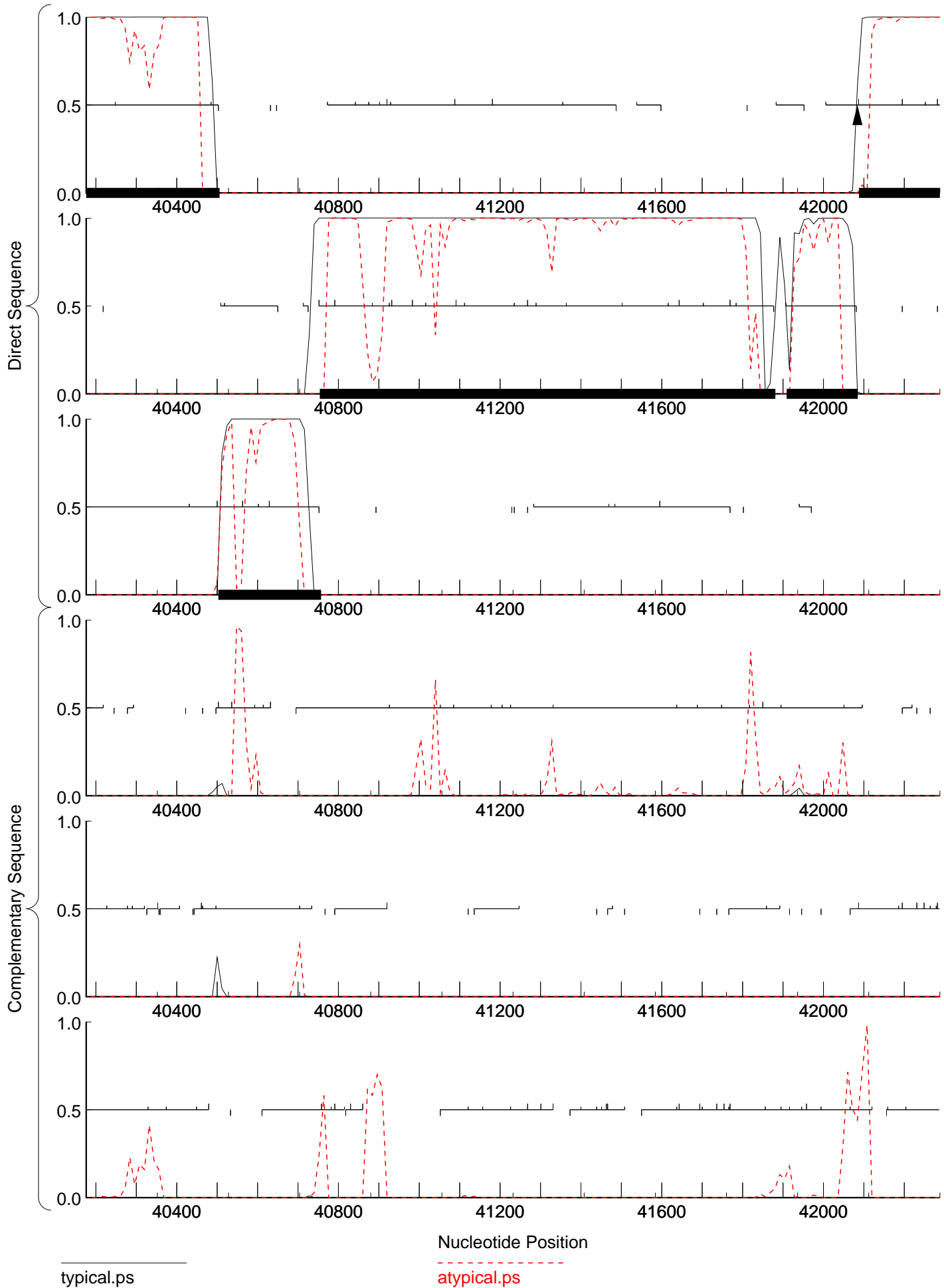


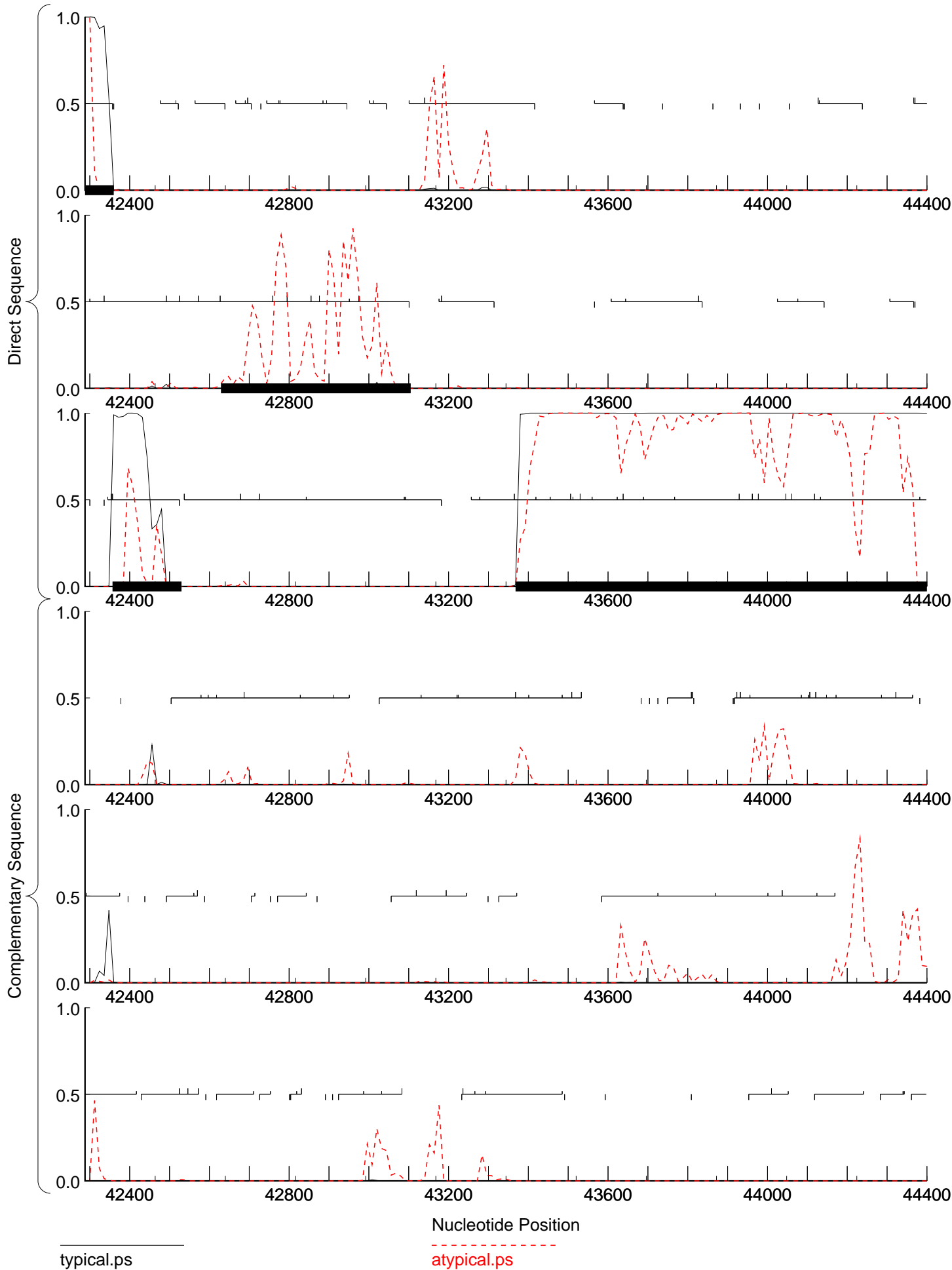


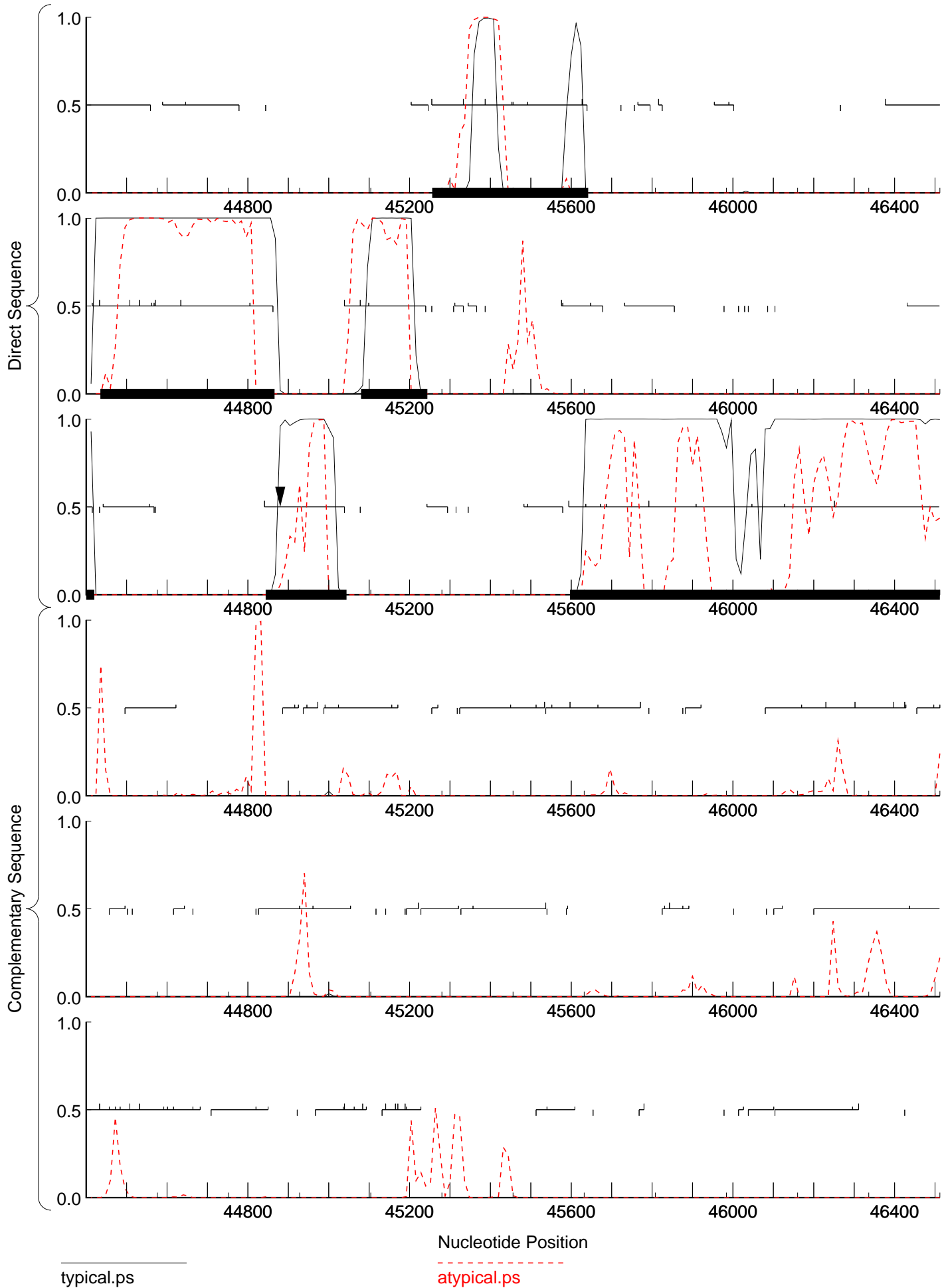
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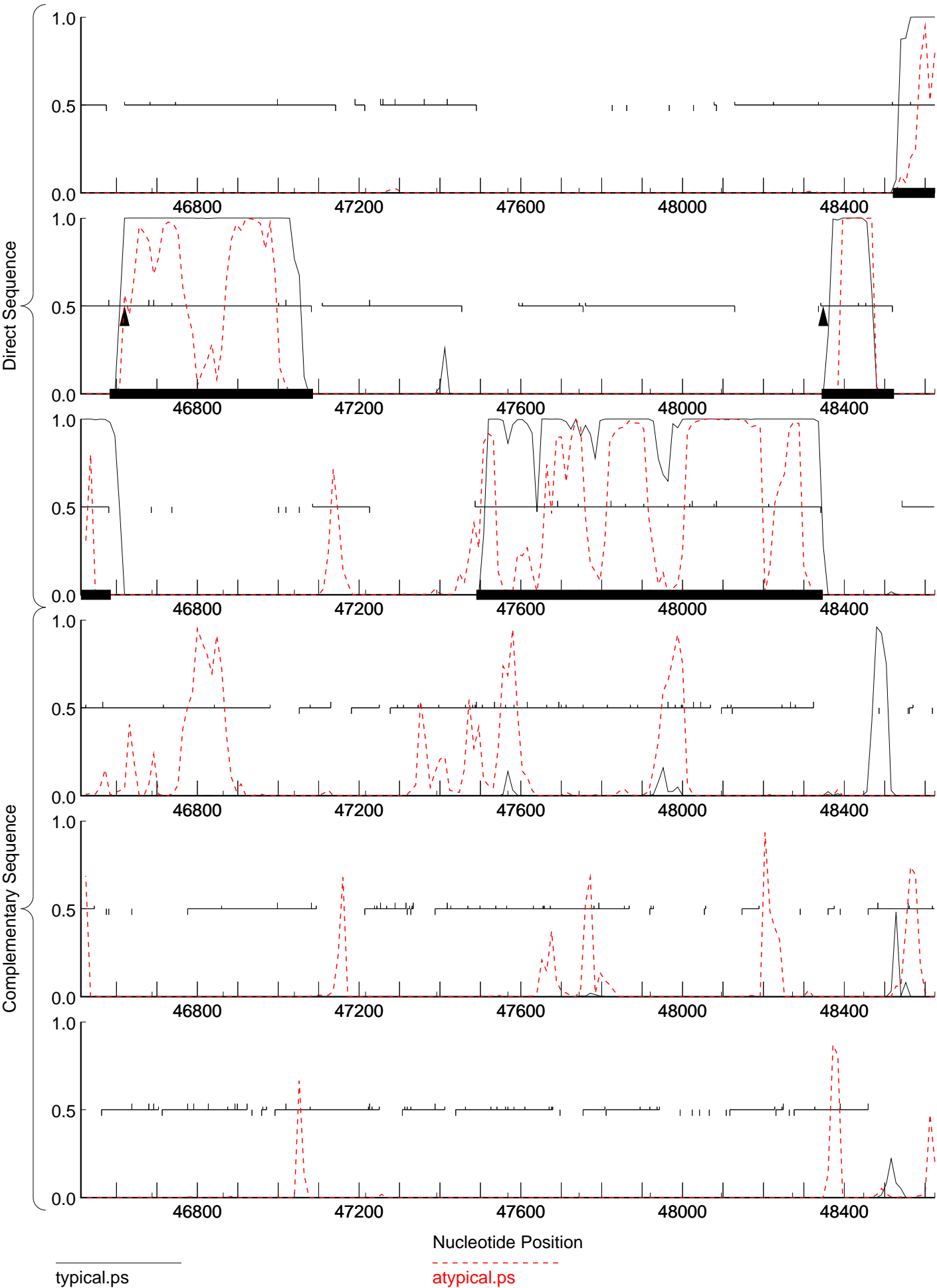
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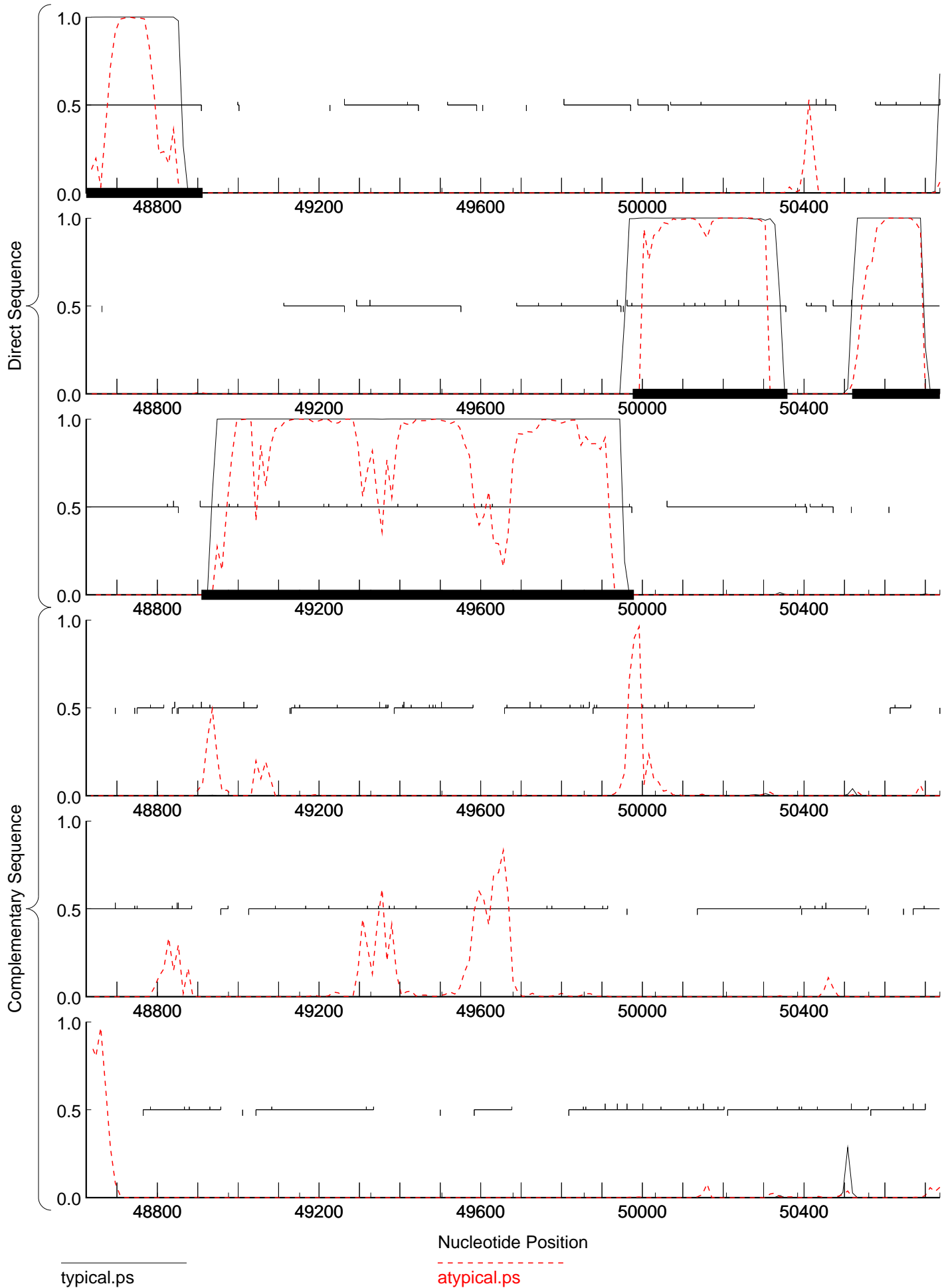


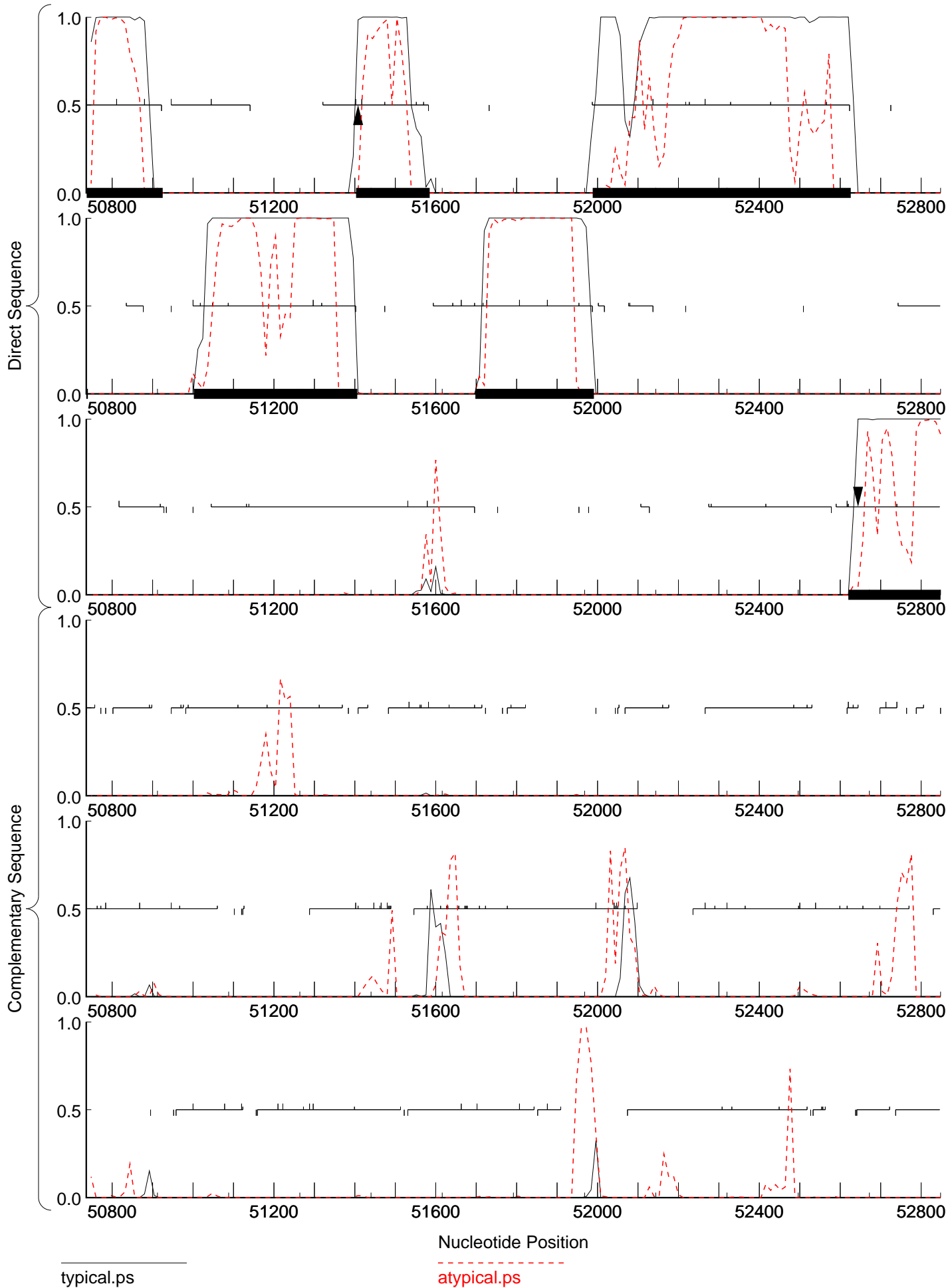


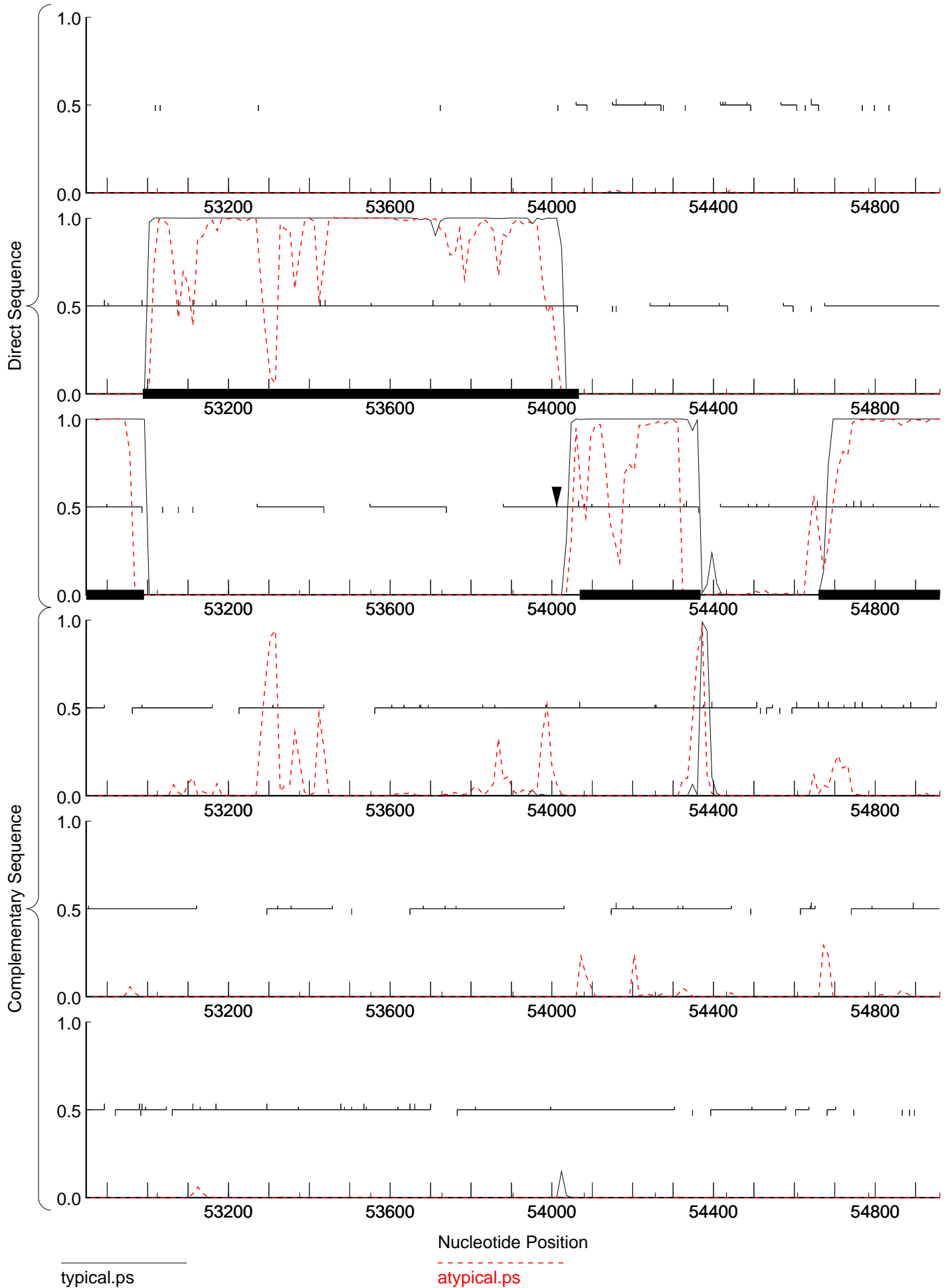


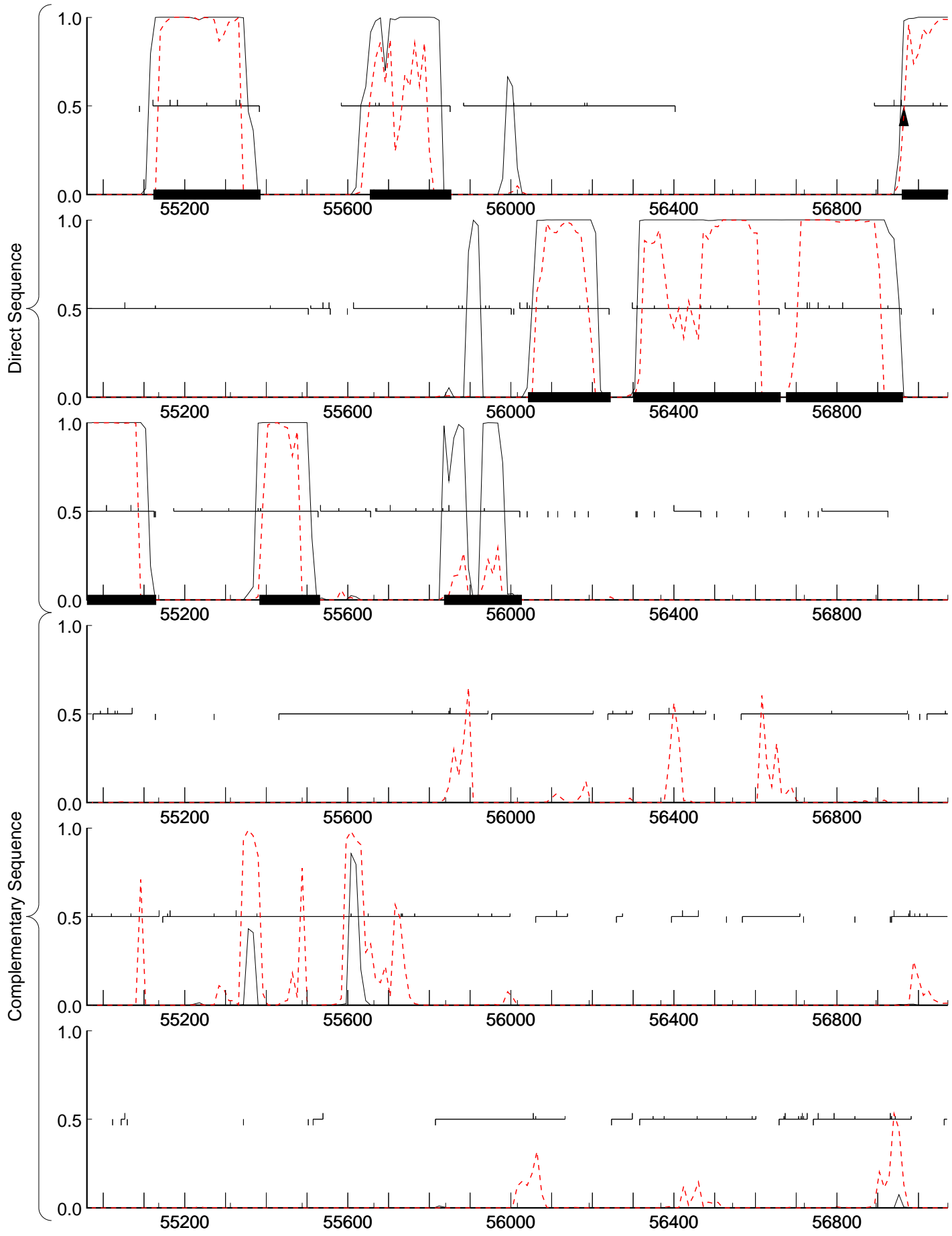








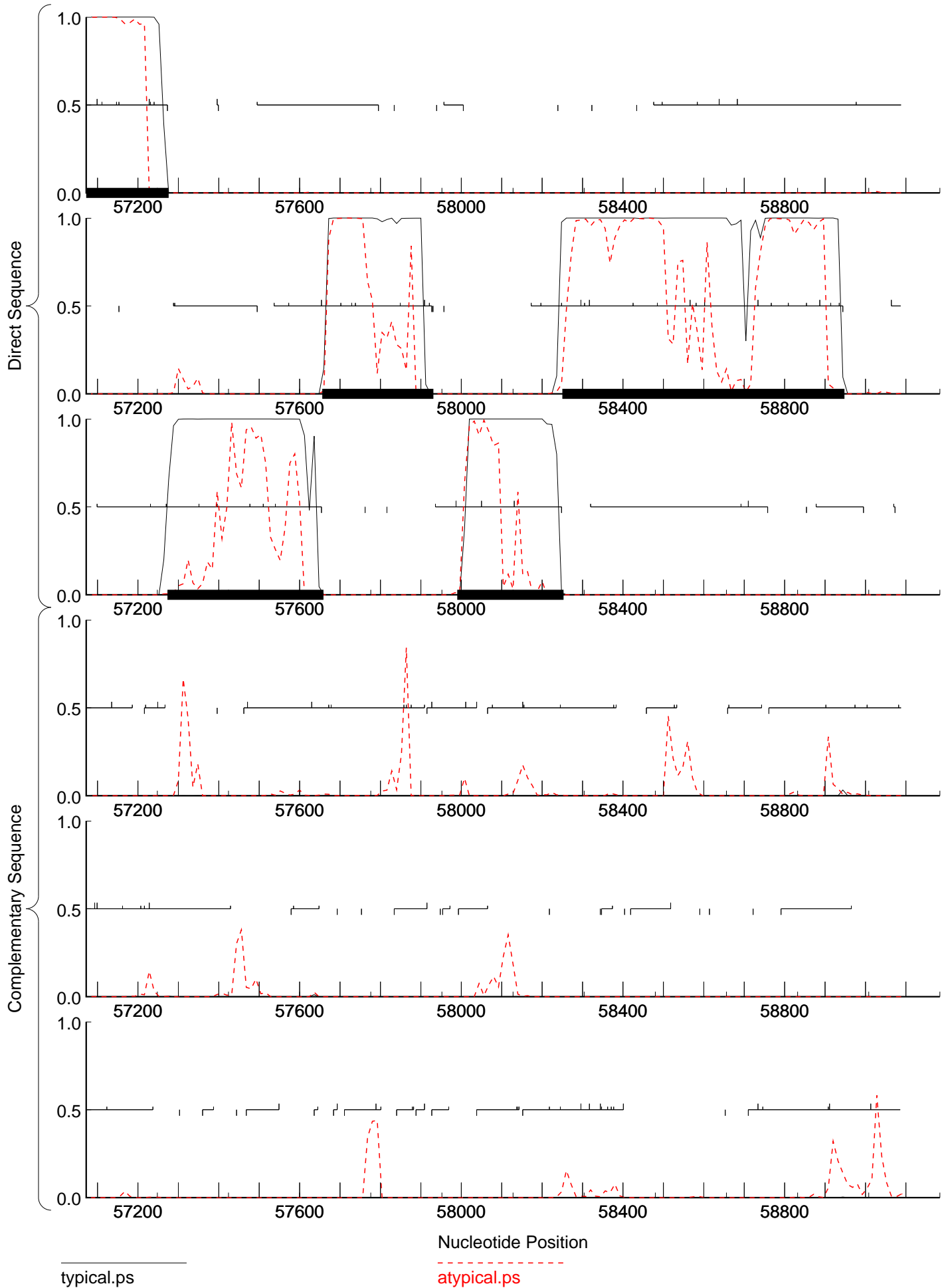




typical.ps

Nucleotide Position

atypical.ps



typical.ps

atypical.ps