

GeneMark

Version 2.5p (09.08.06)

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PROGRAM INFORMATION

Sequence : Mycobacterium phage Riparian complete sequence, 71199 bp, circularly permuted, Cluster R
Analysis Date : 1/18/18 at 22:36:42
Pages : 35
Sequence Length : 71199 bp
GC Content : 55.98%

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,

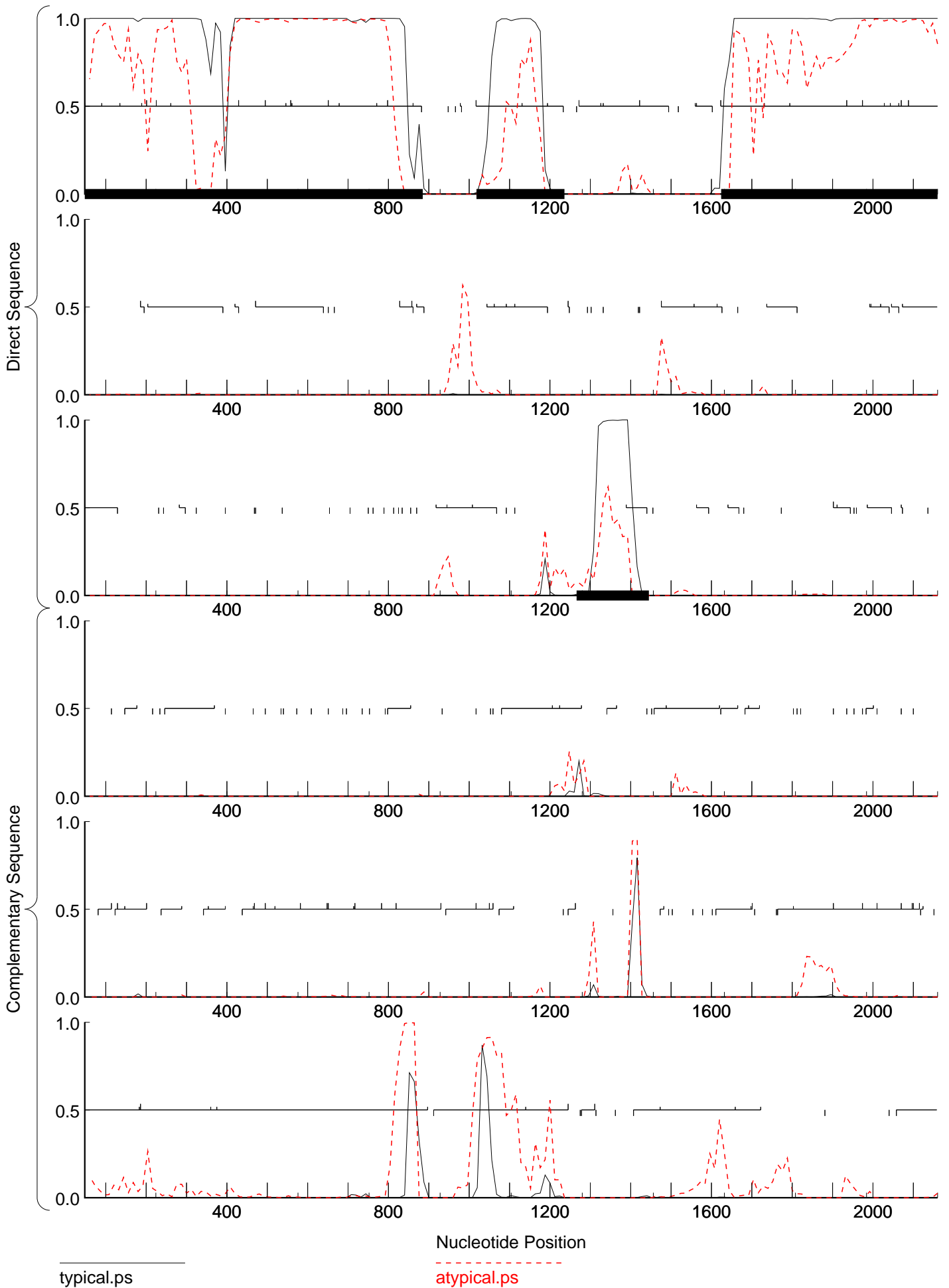
Matrix notes & comments

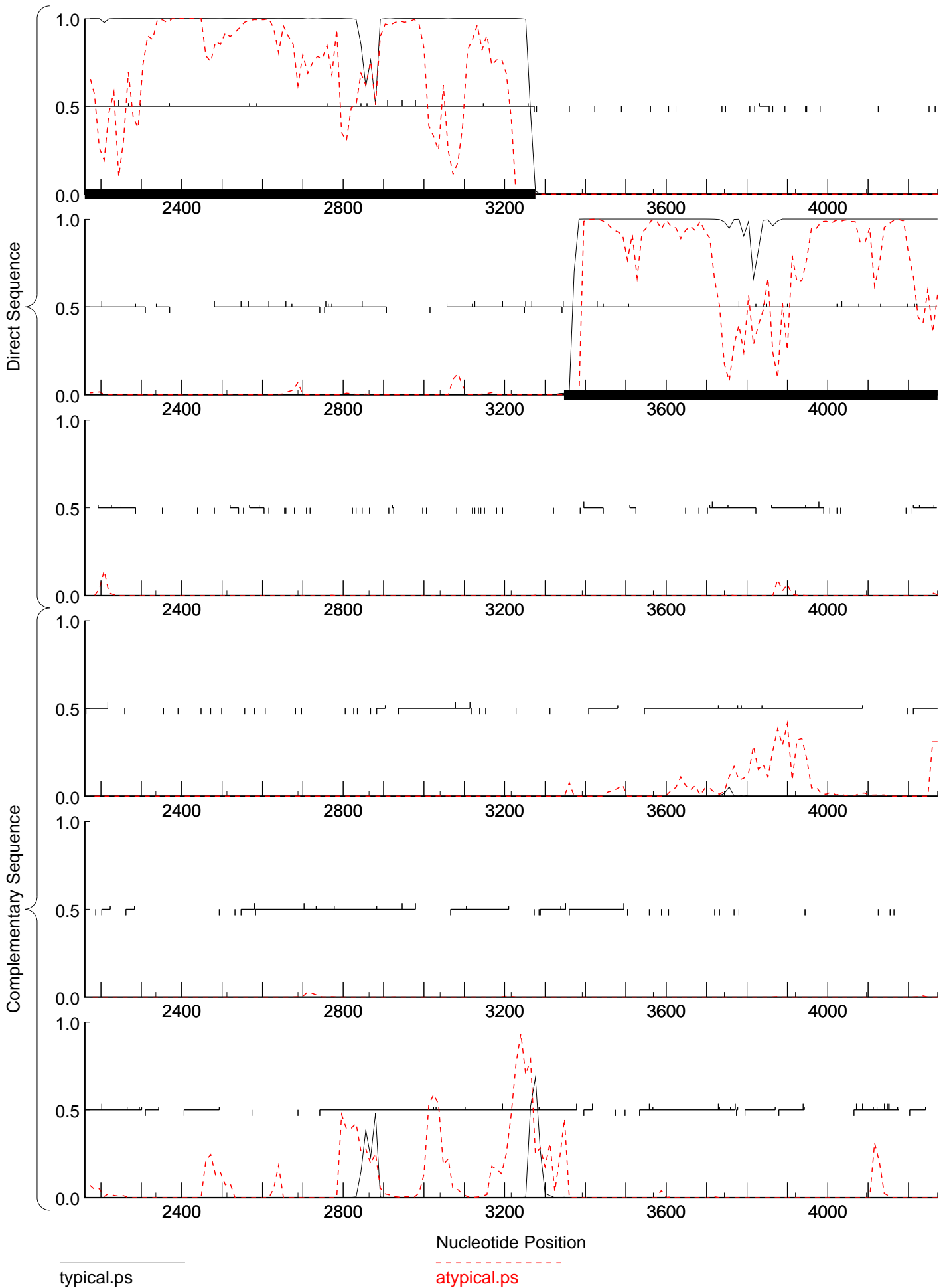
Training set derived by GeneMarkS, 4.30 October 2014
Thu Jan 18 22:36:42 2018

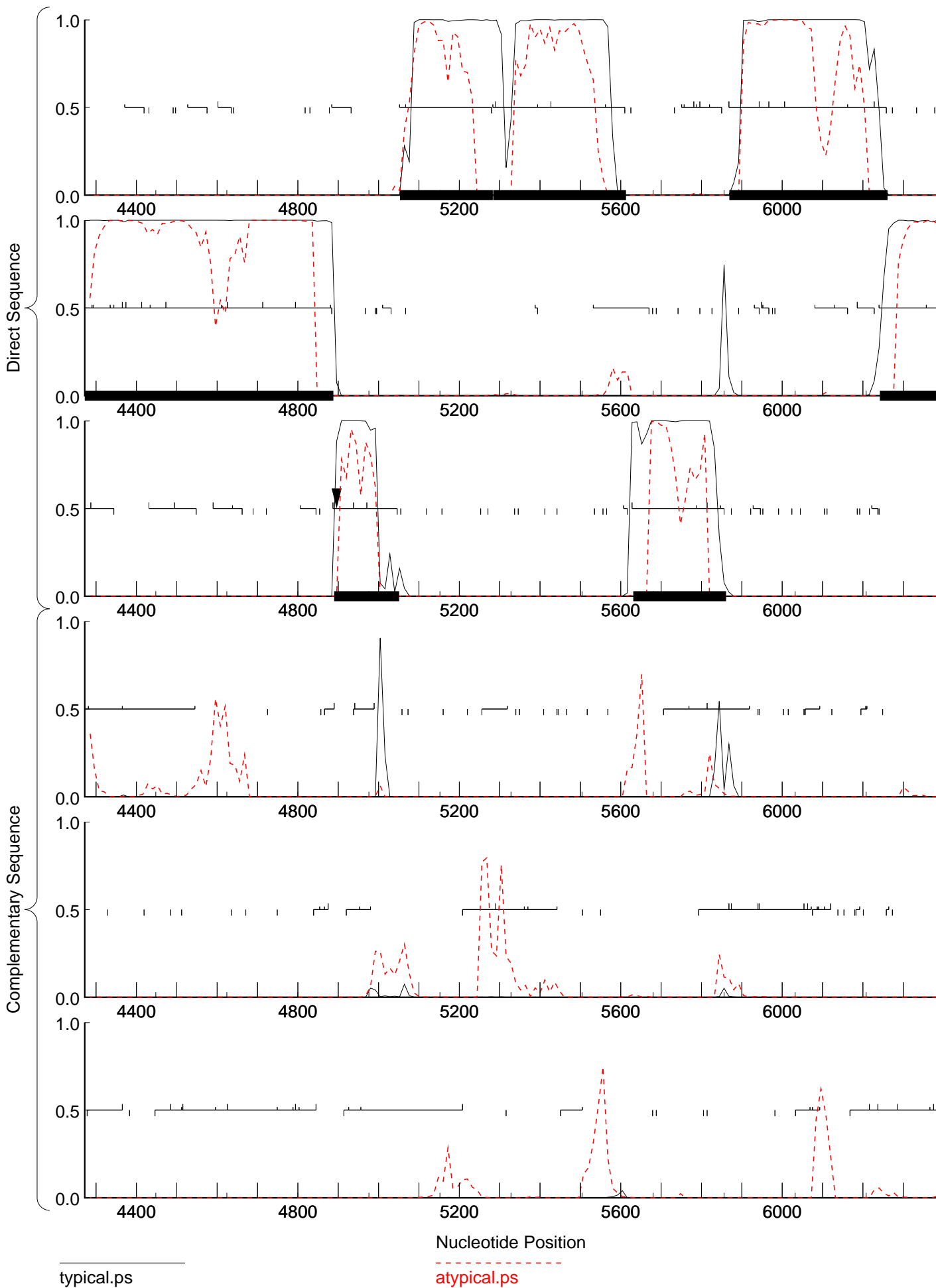
MATRIX INFORMATION

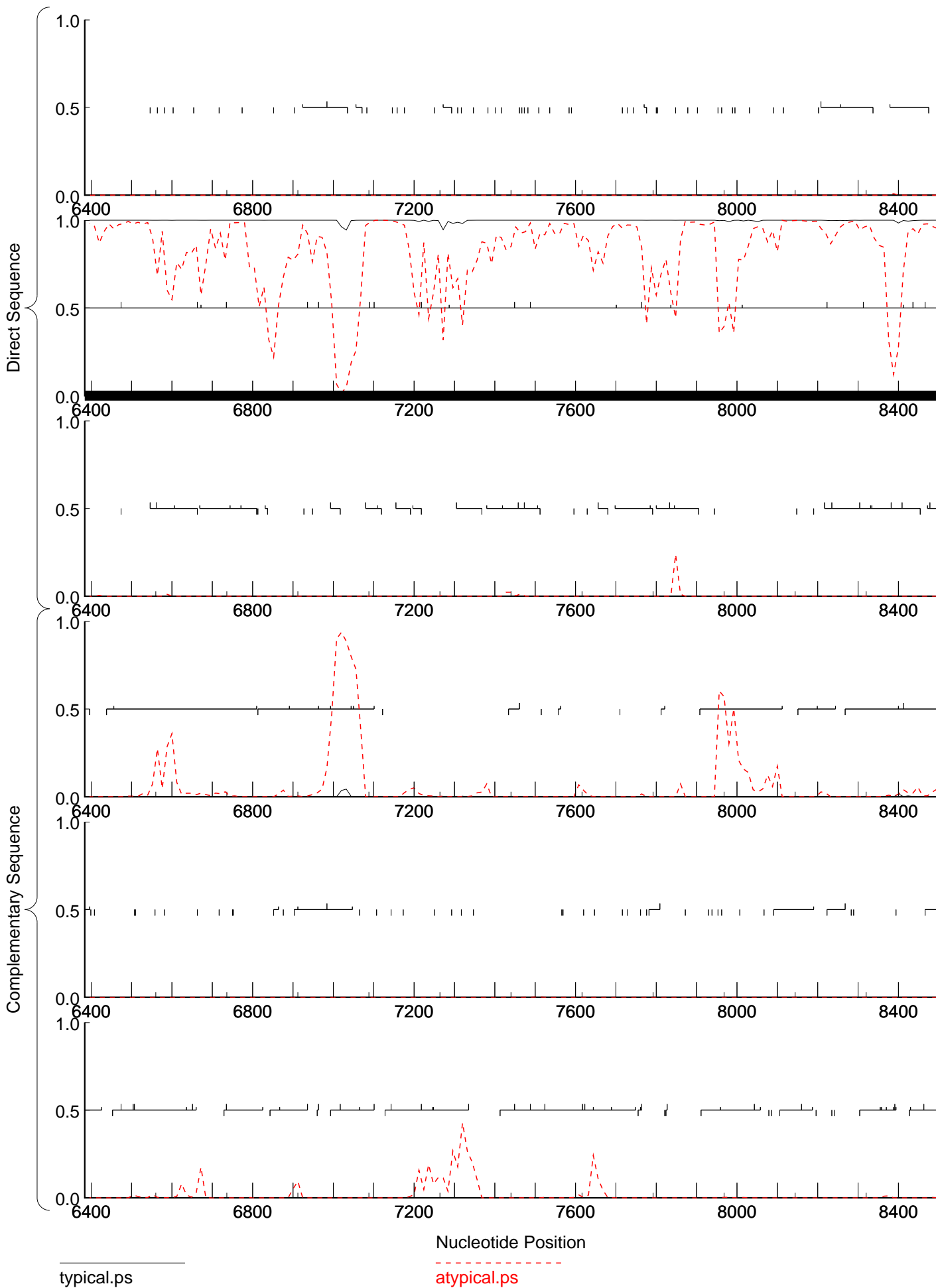
Matrix : -
Author : -
Order : 4

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



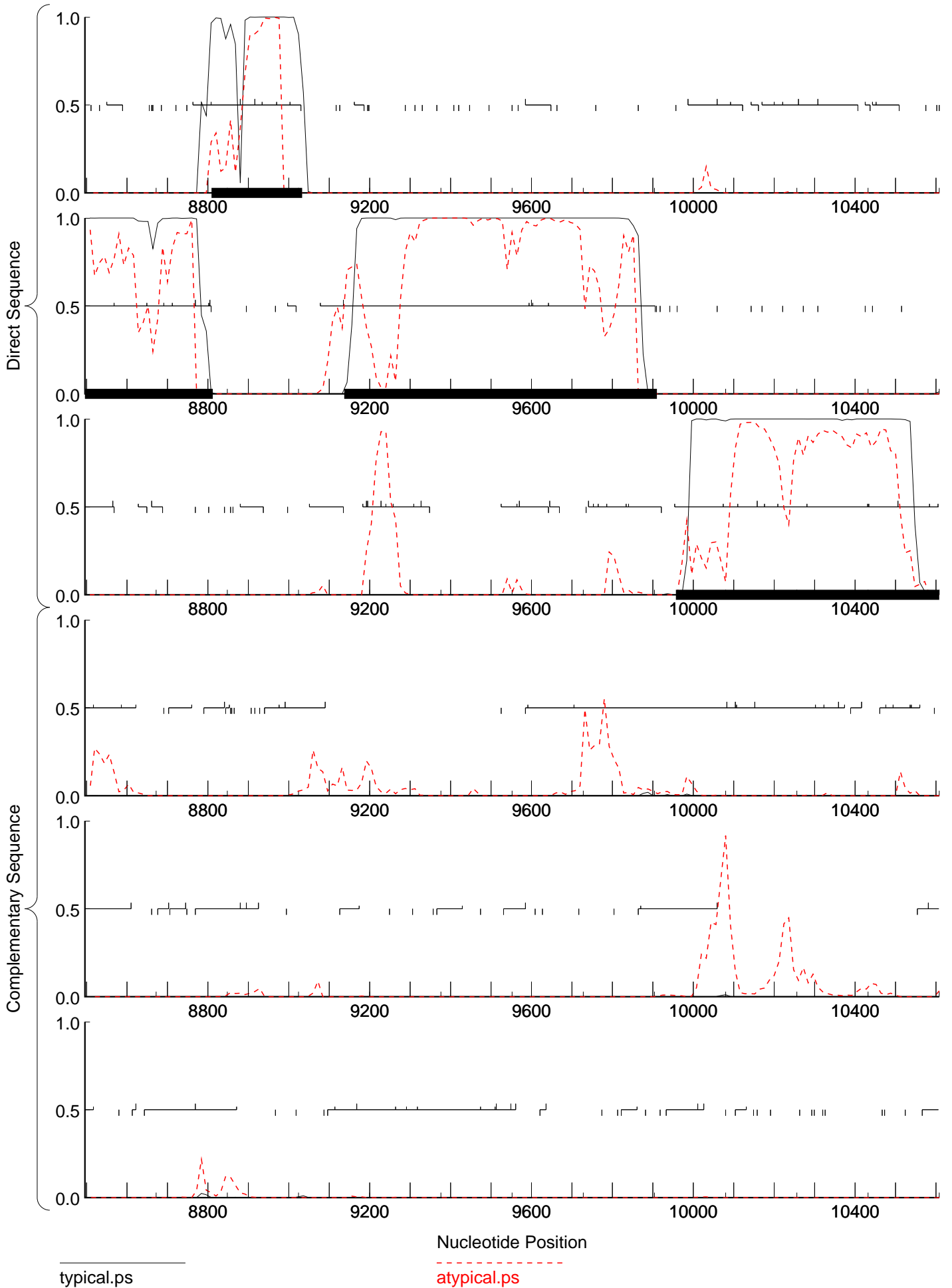


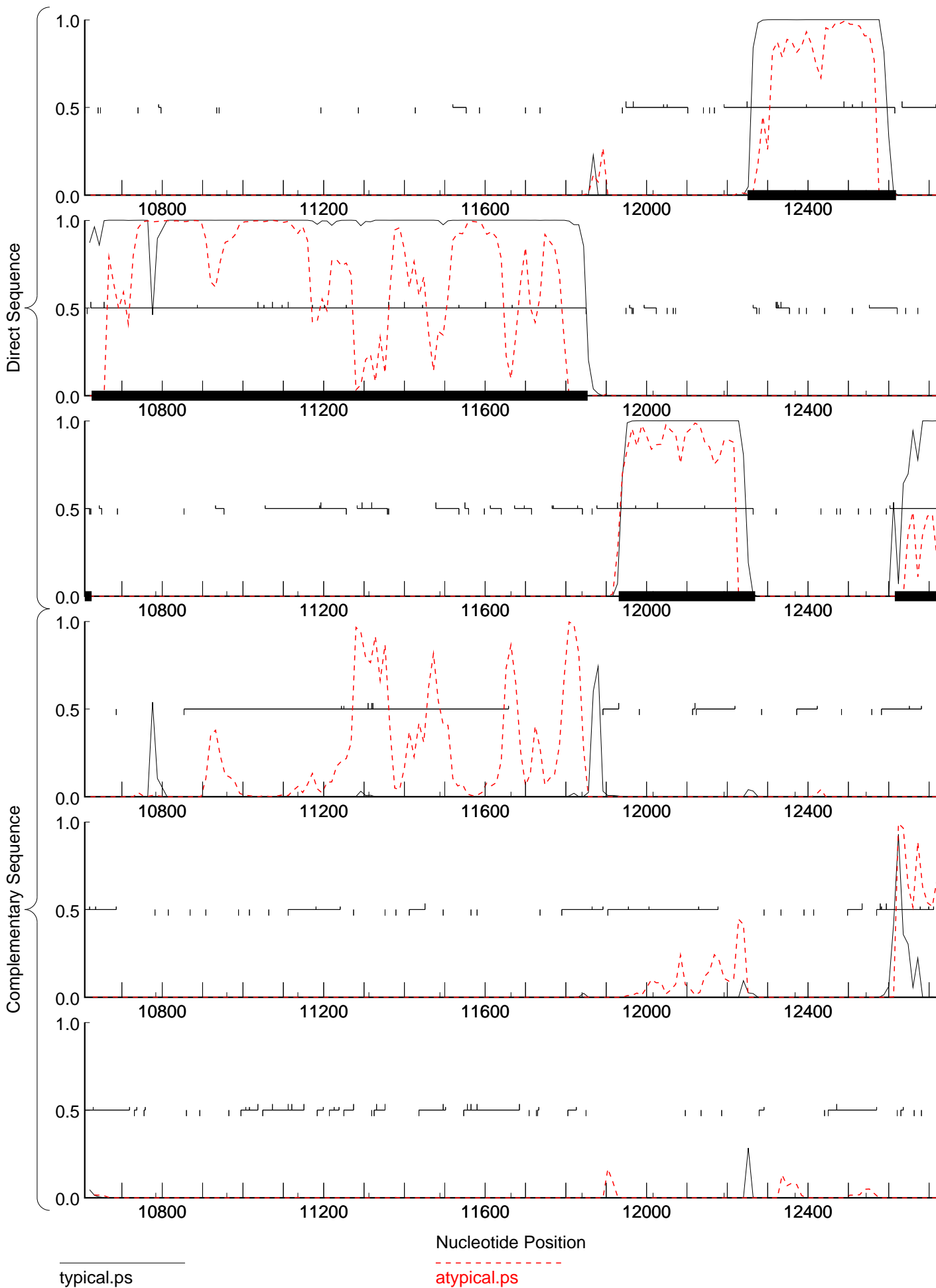




typical.ps

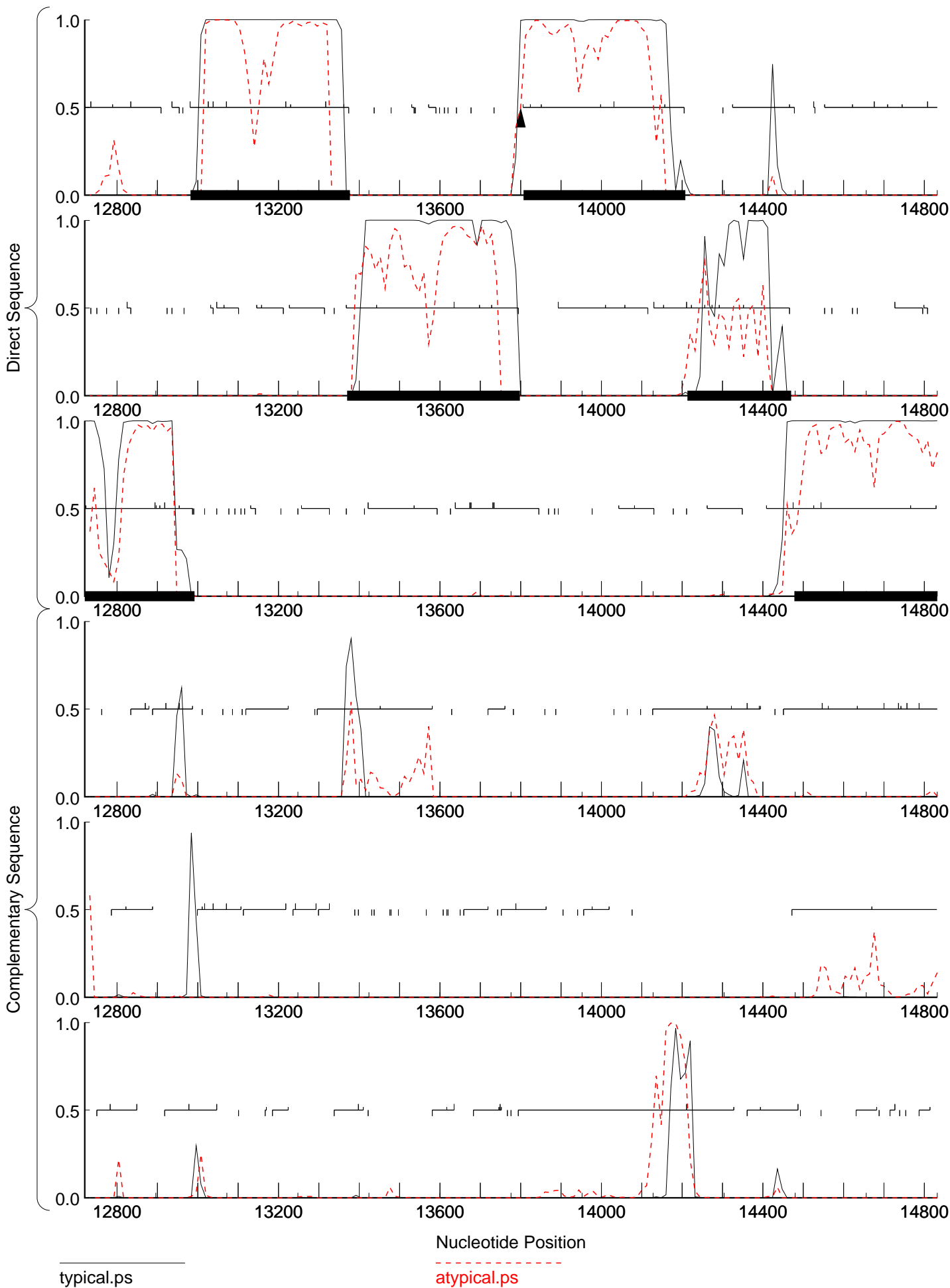
atypical.ps

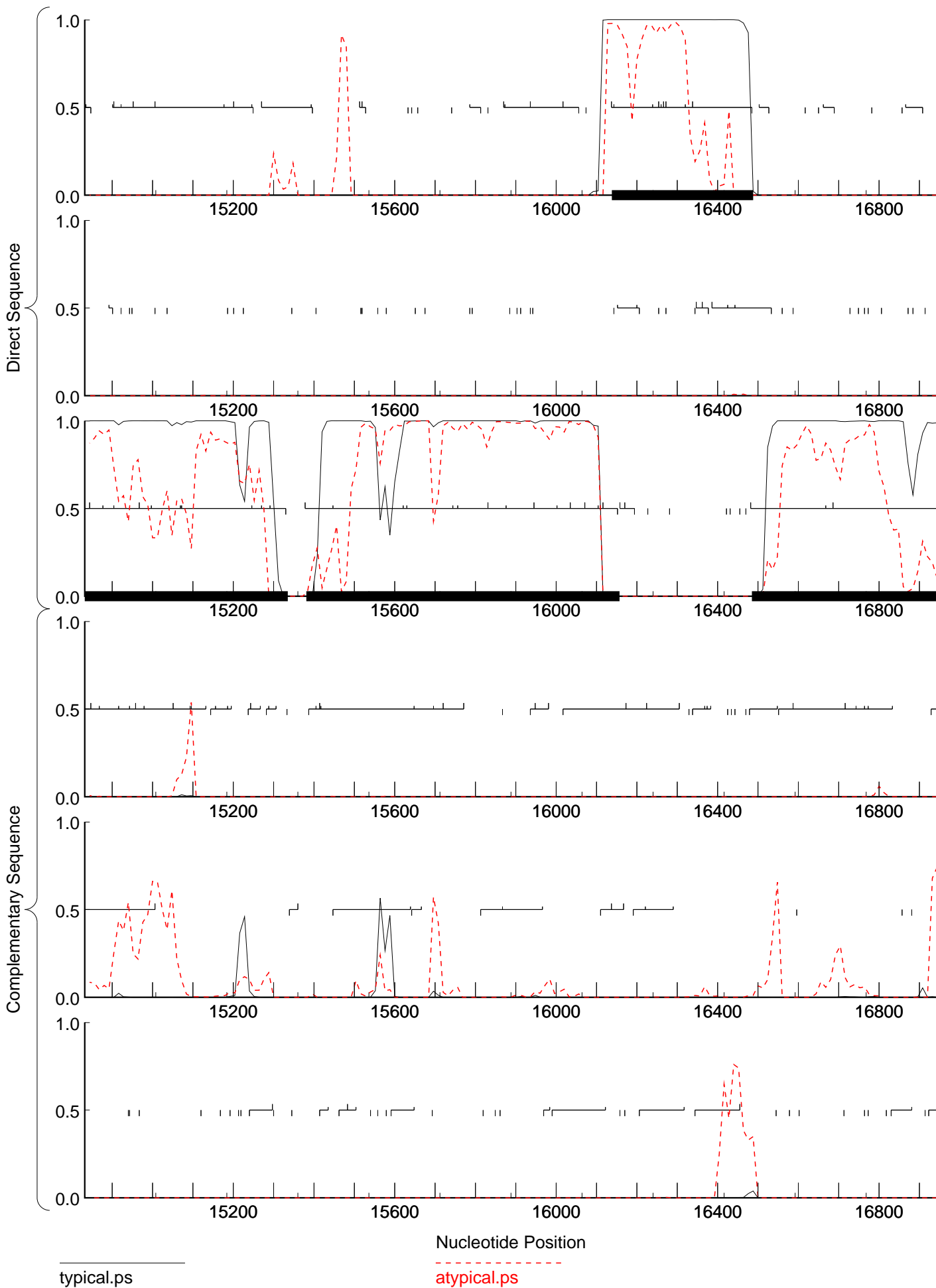


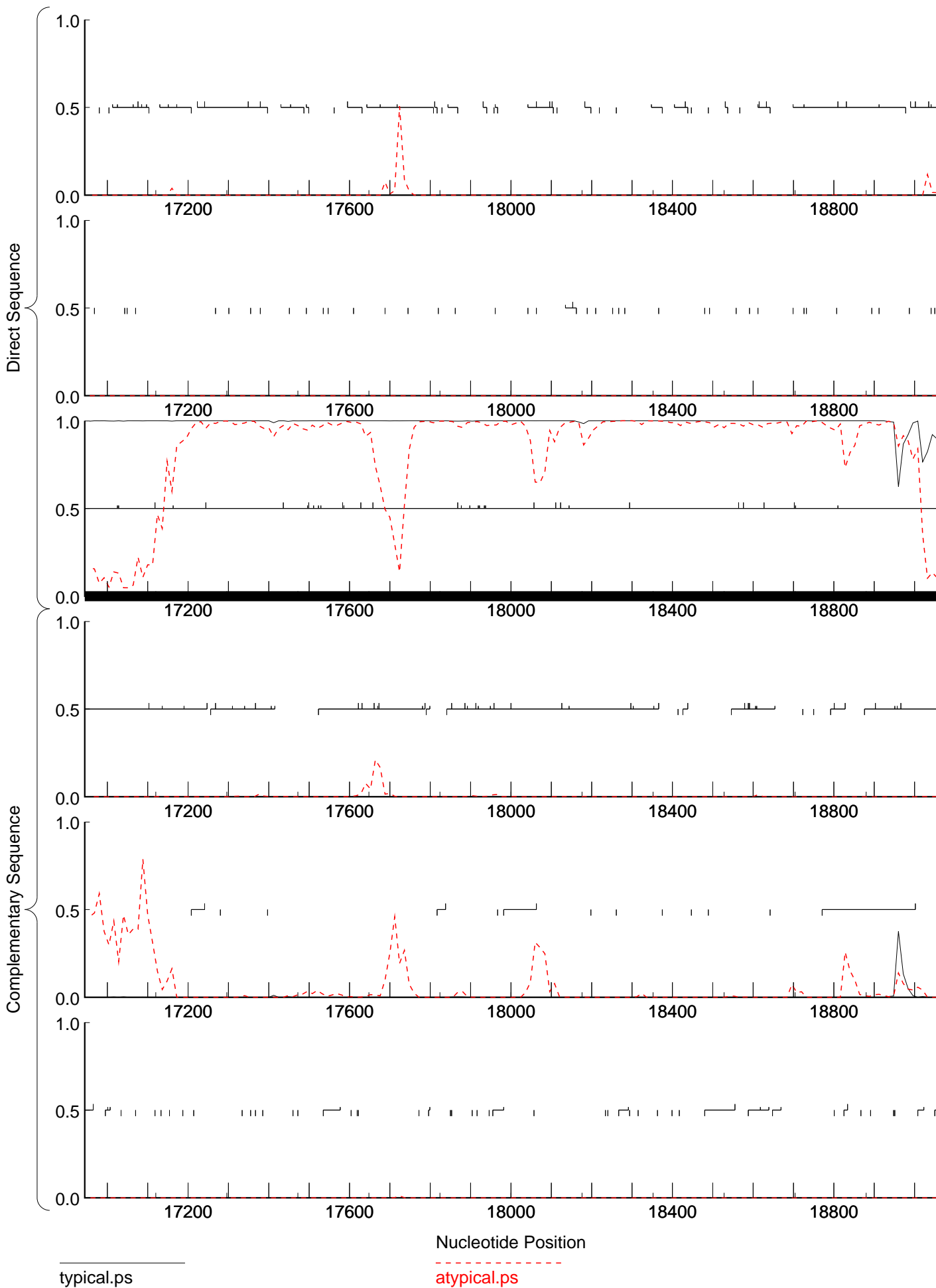


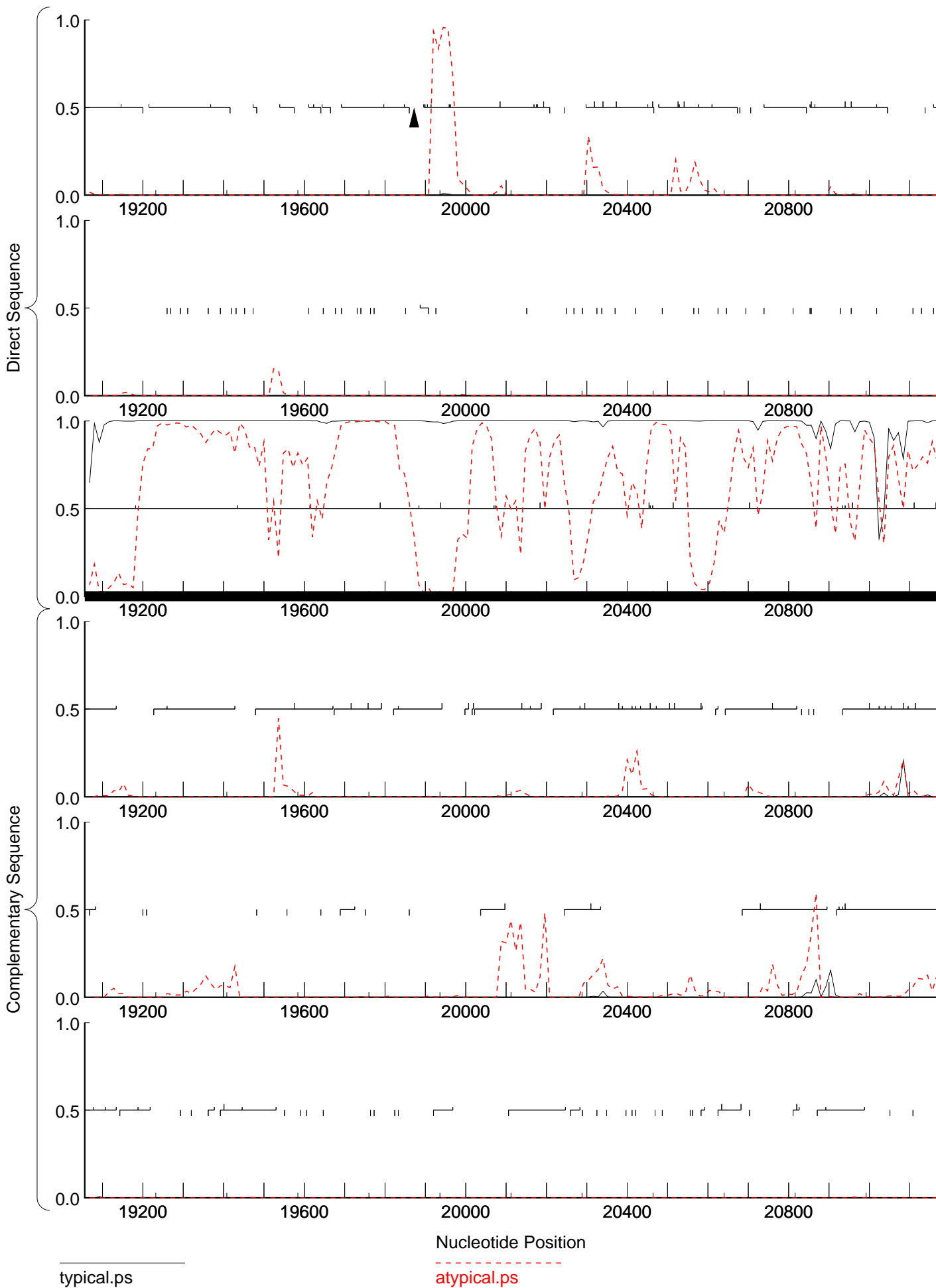
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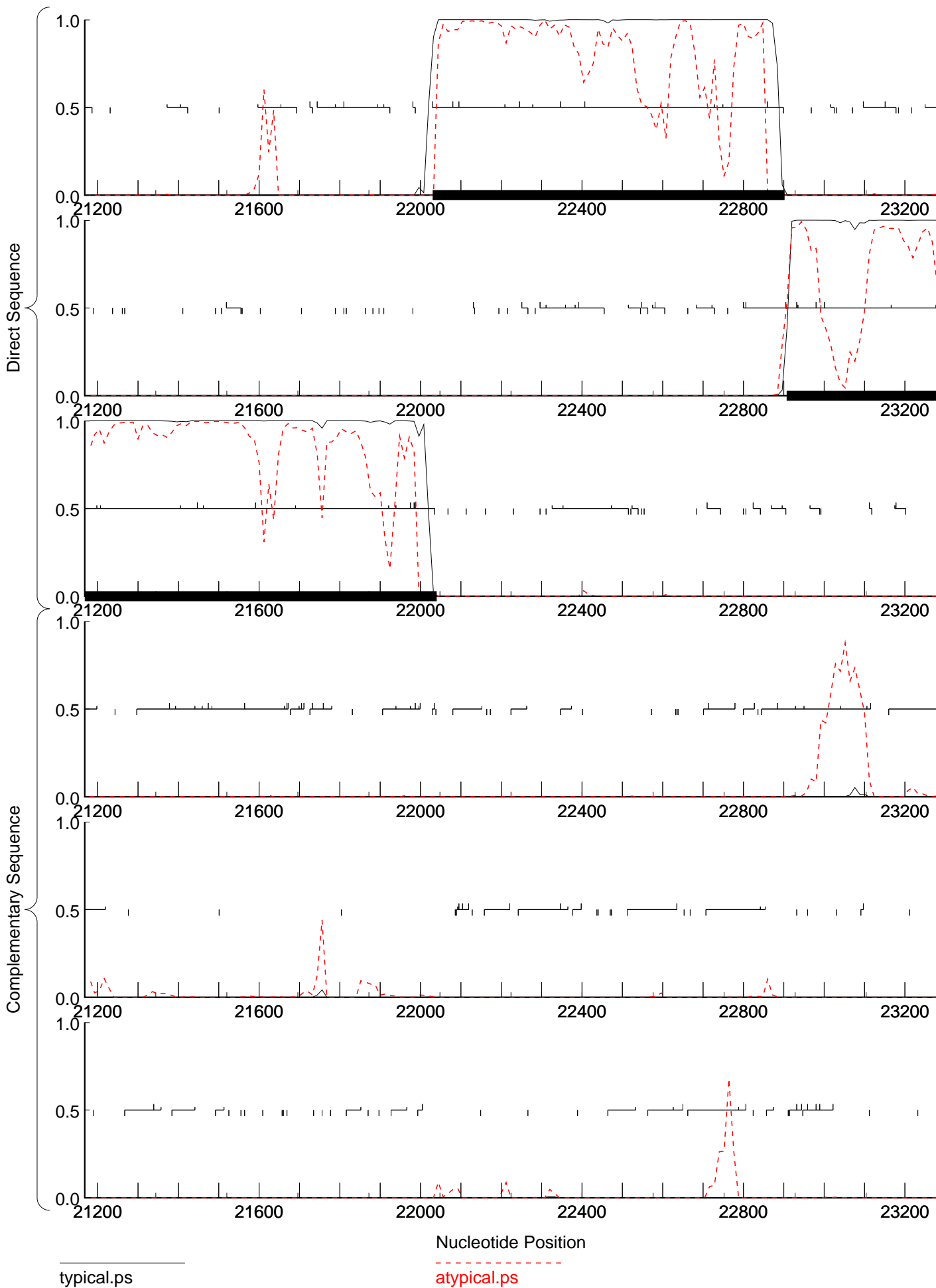
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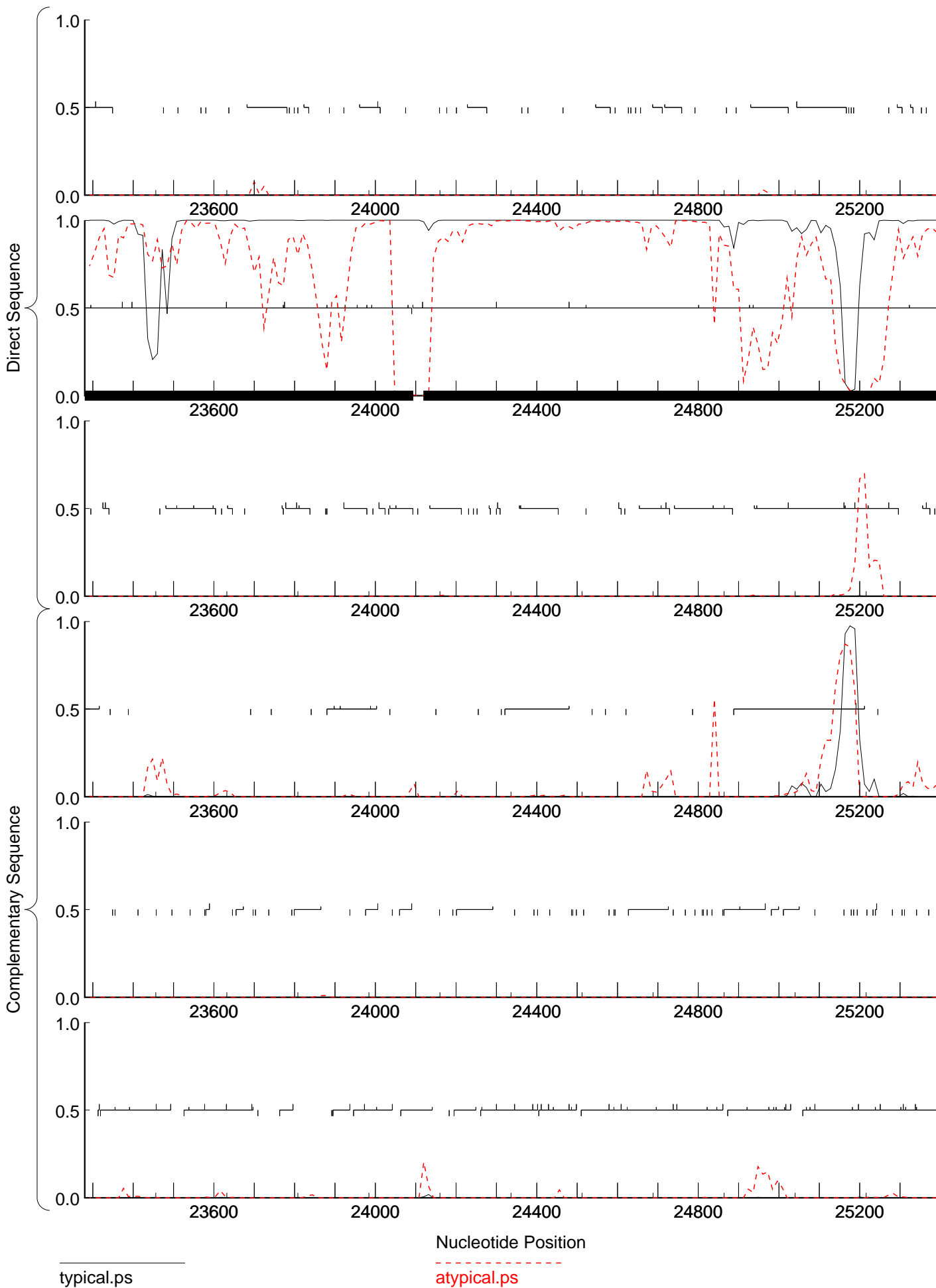


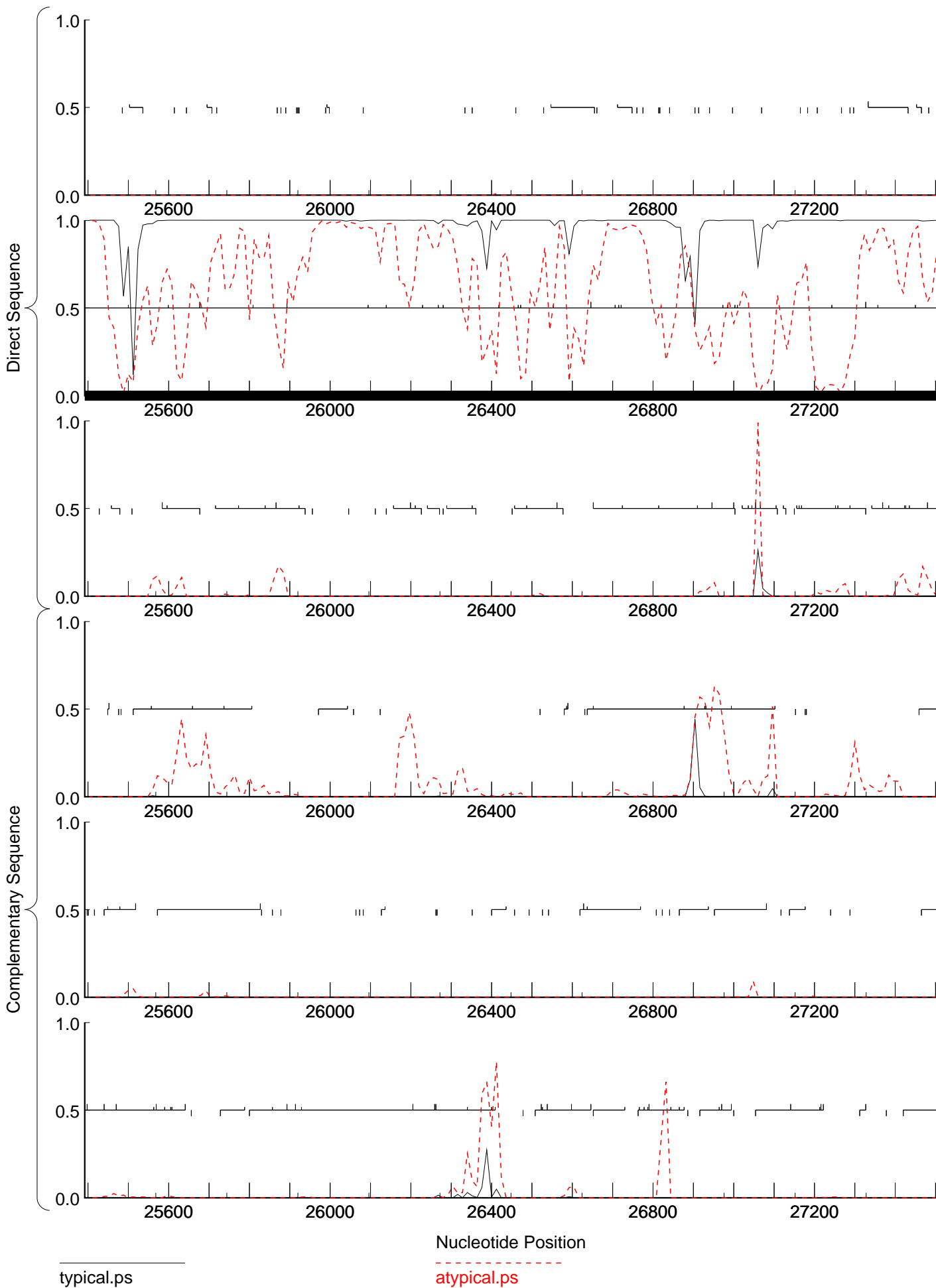






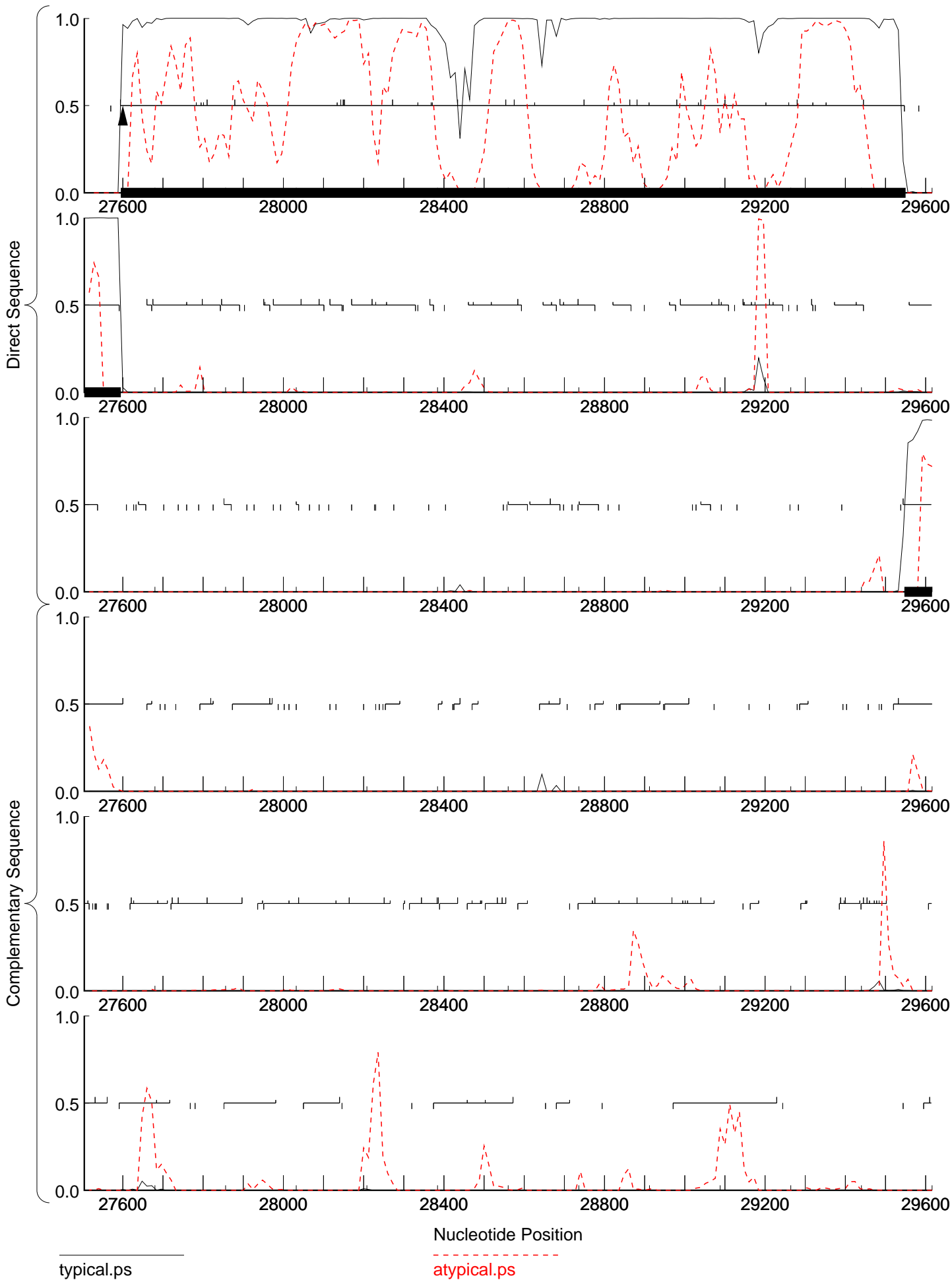


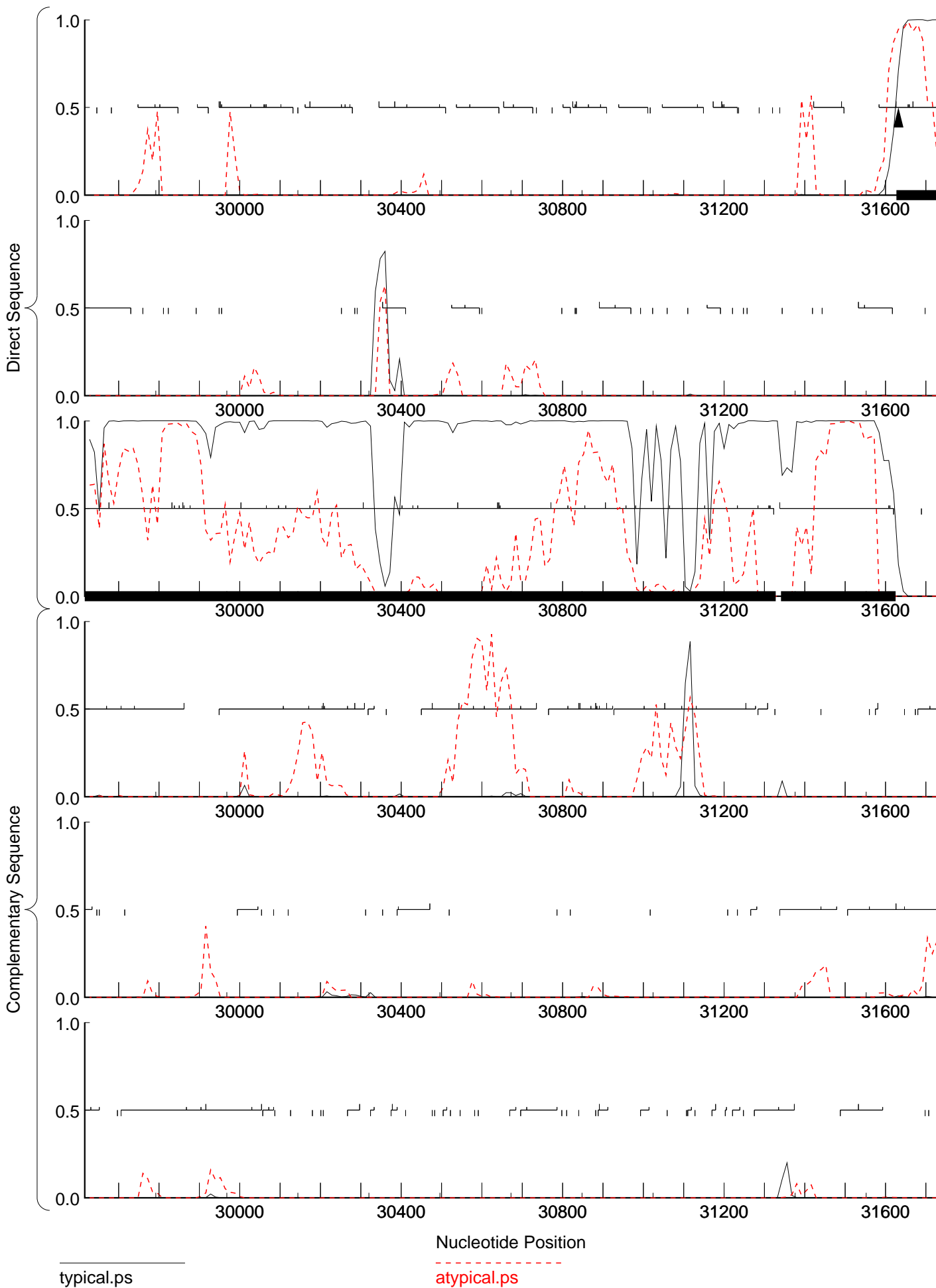




typical.ps

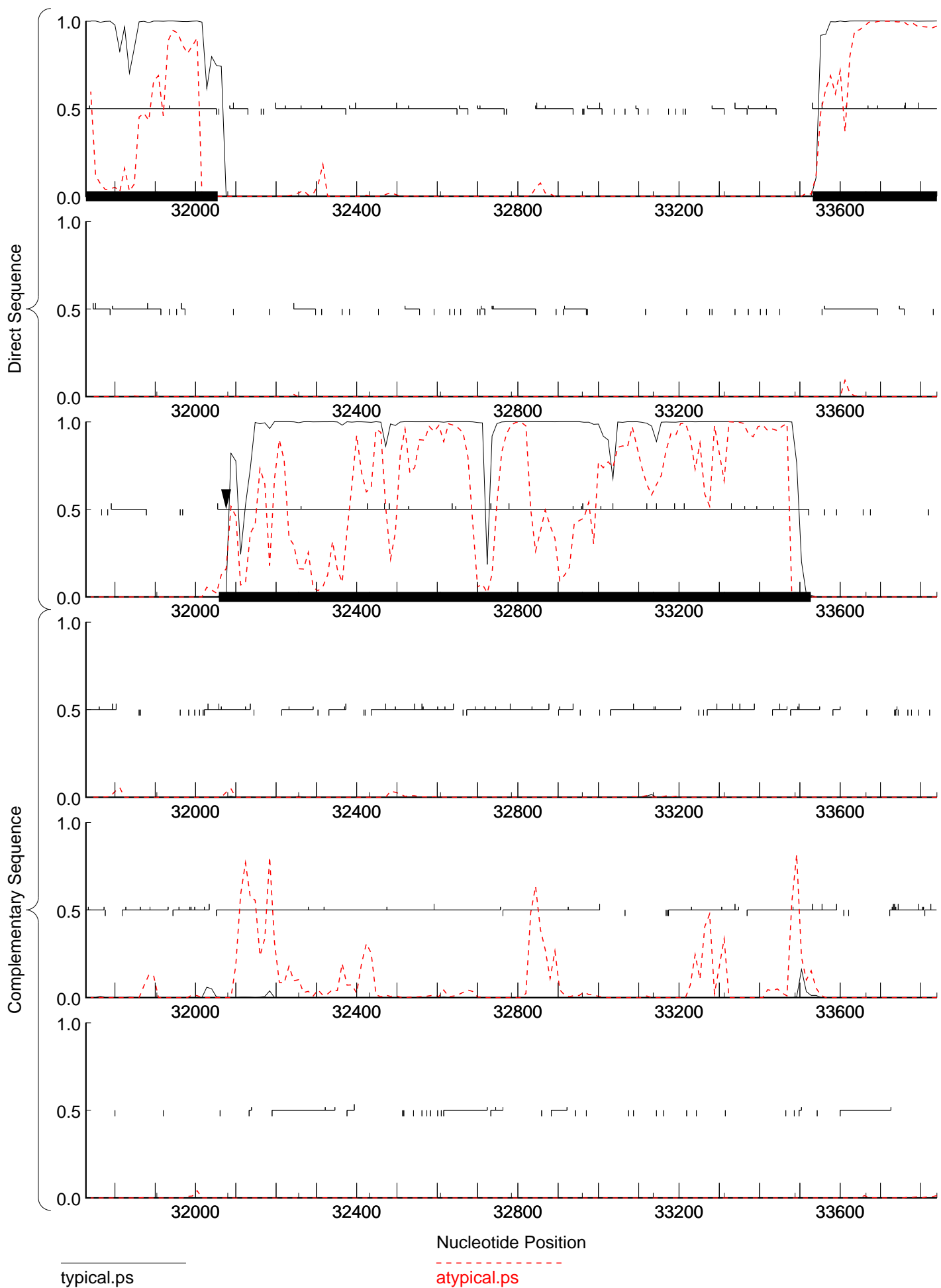
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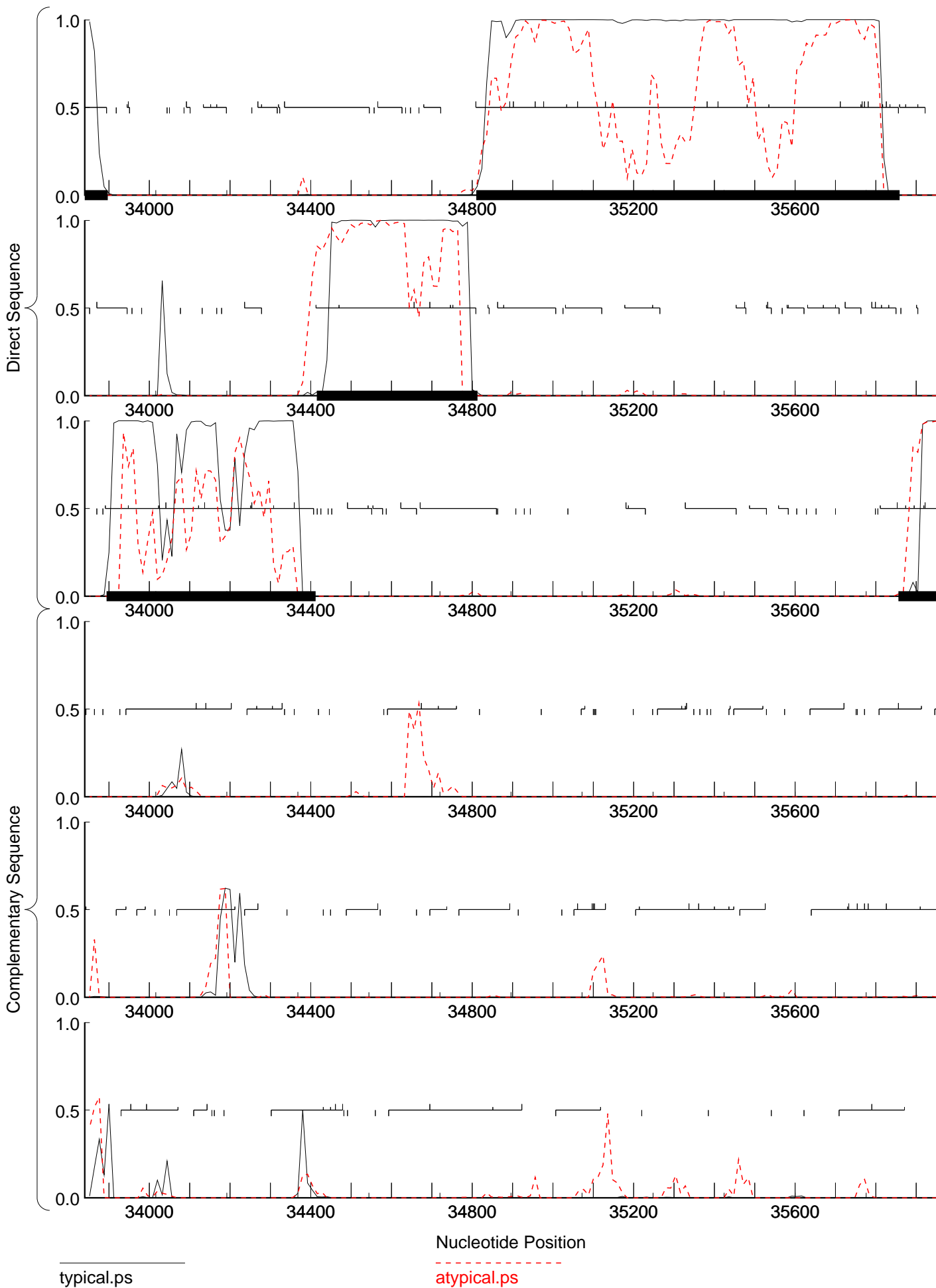


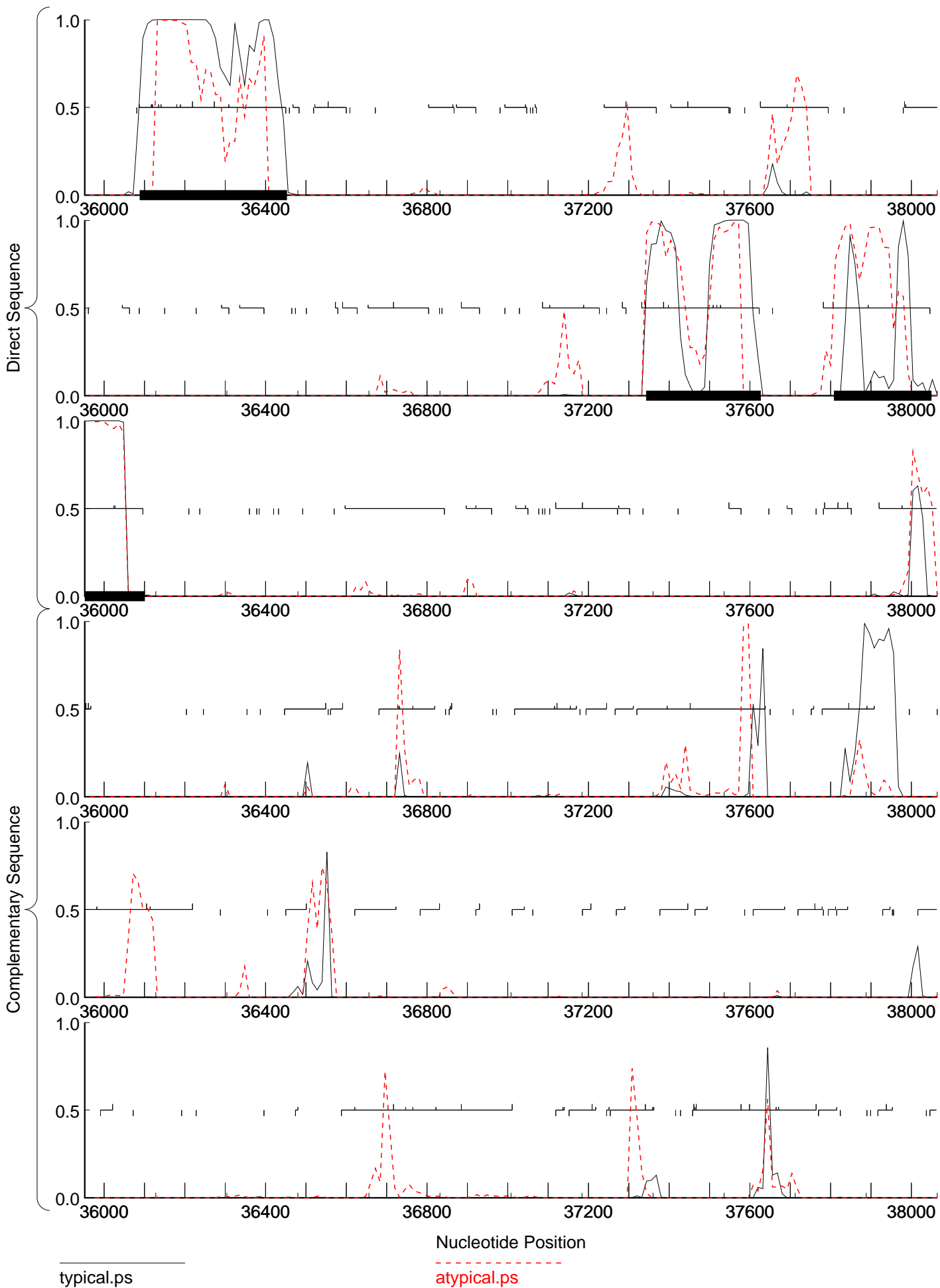


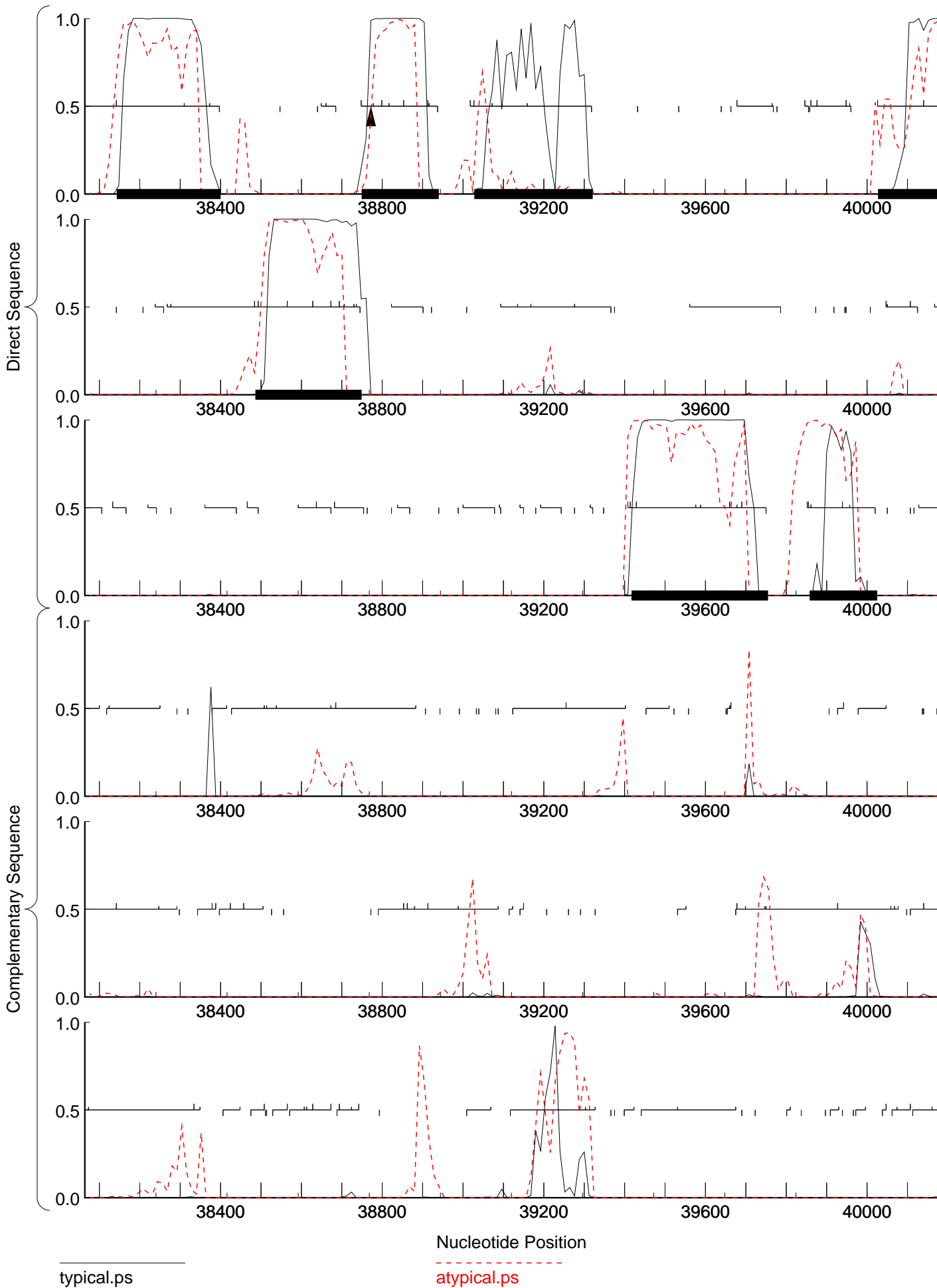
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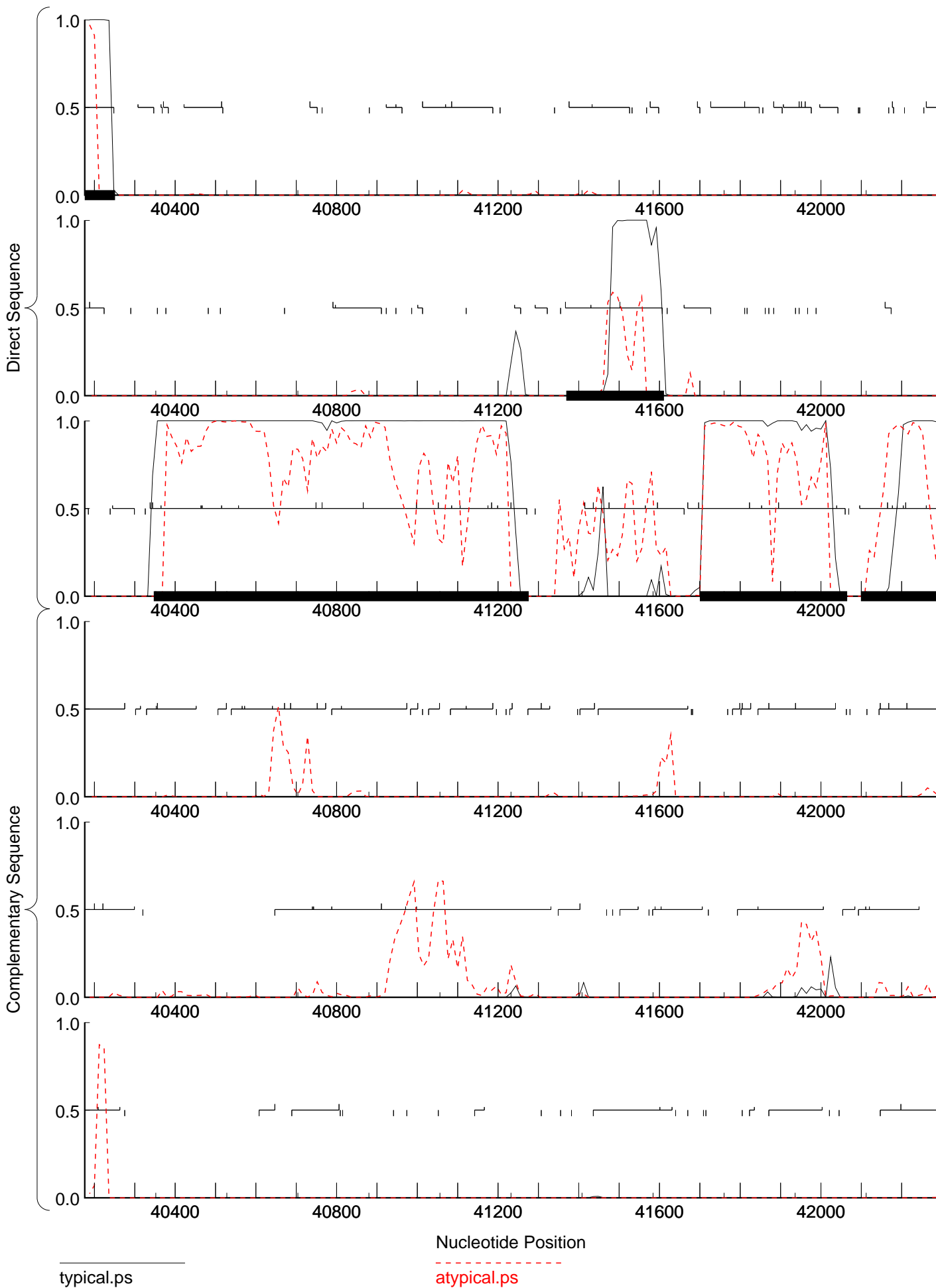
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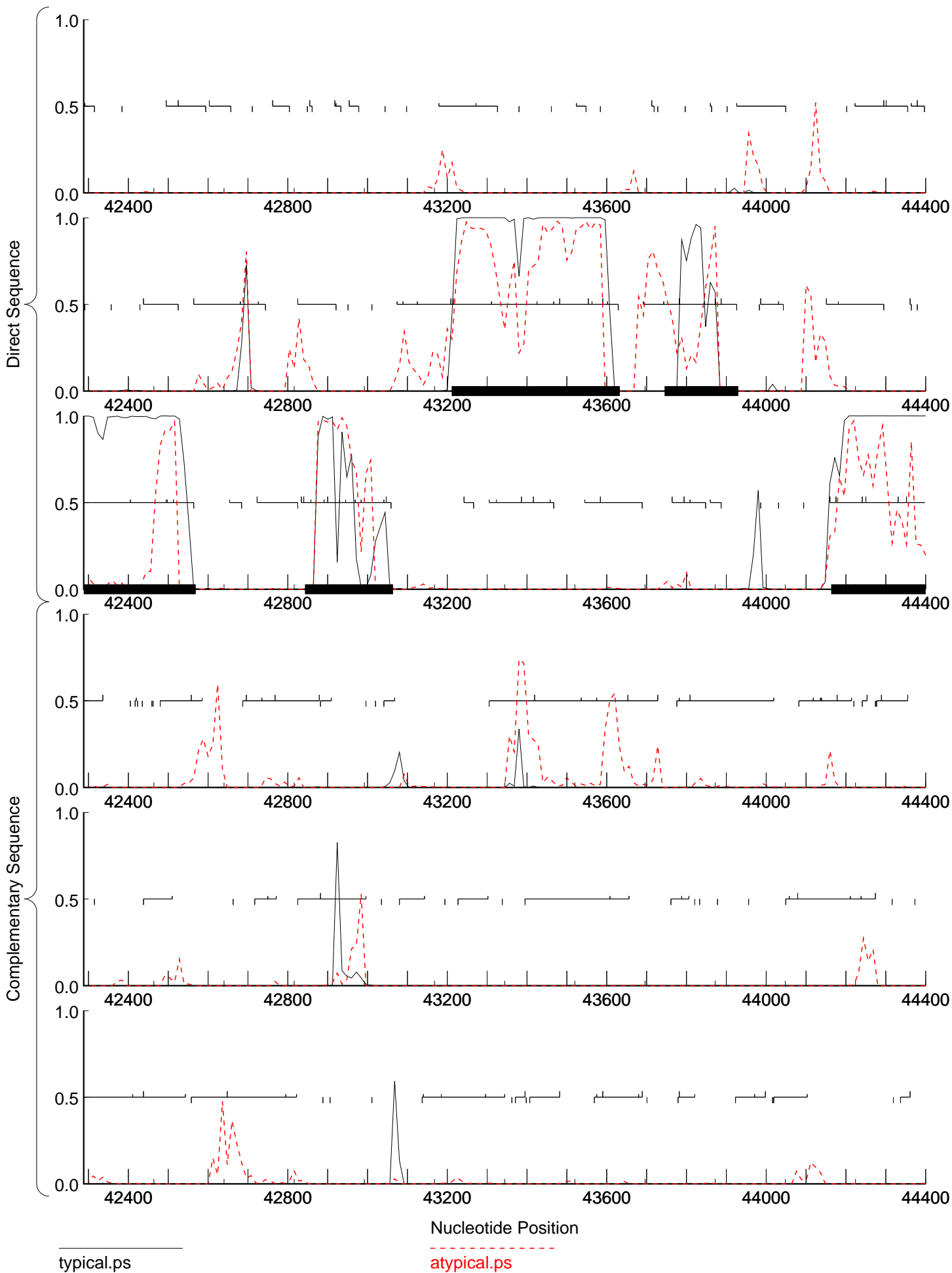


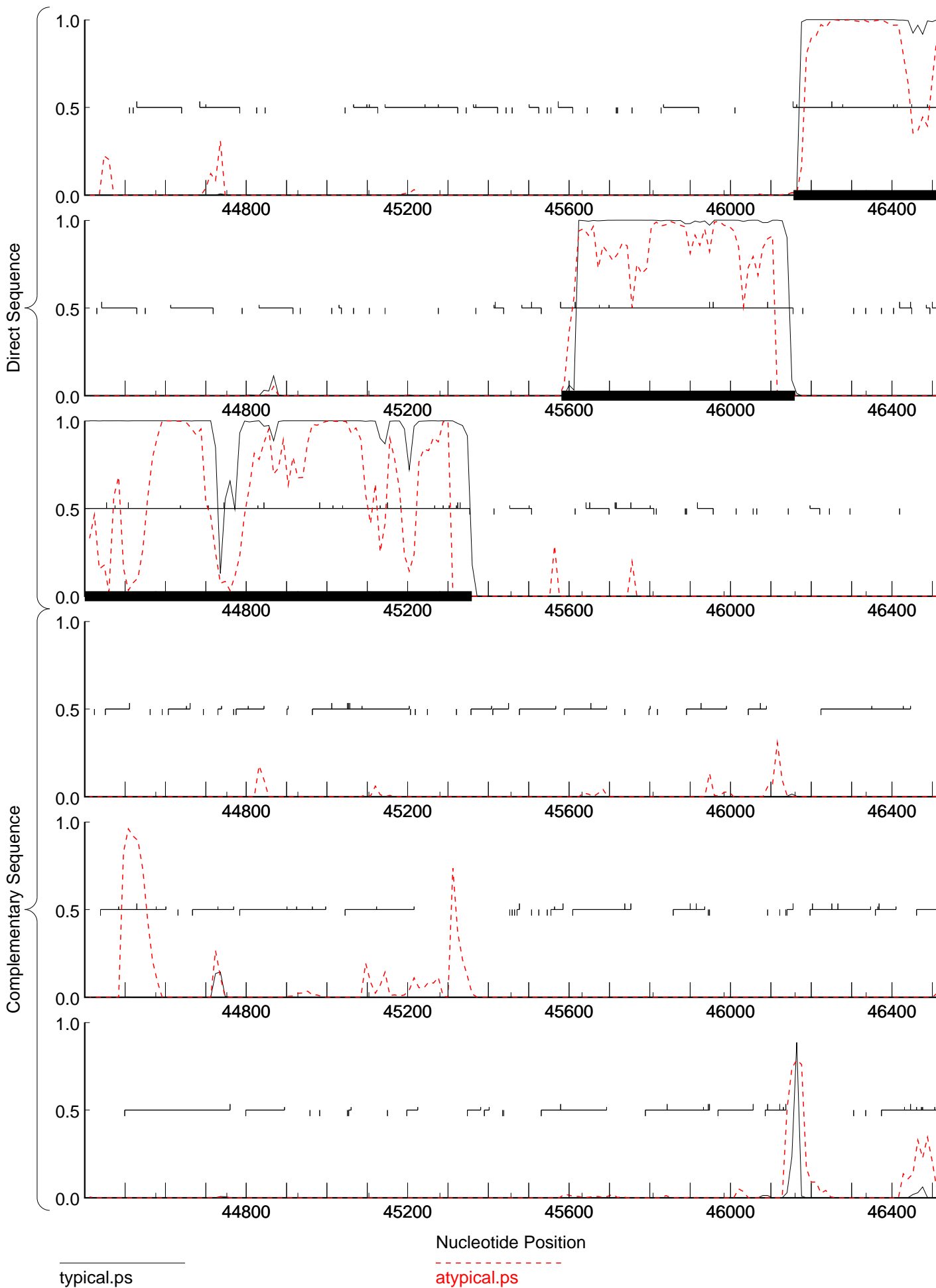






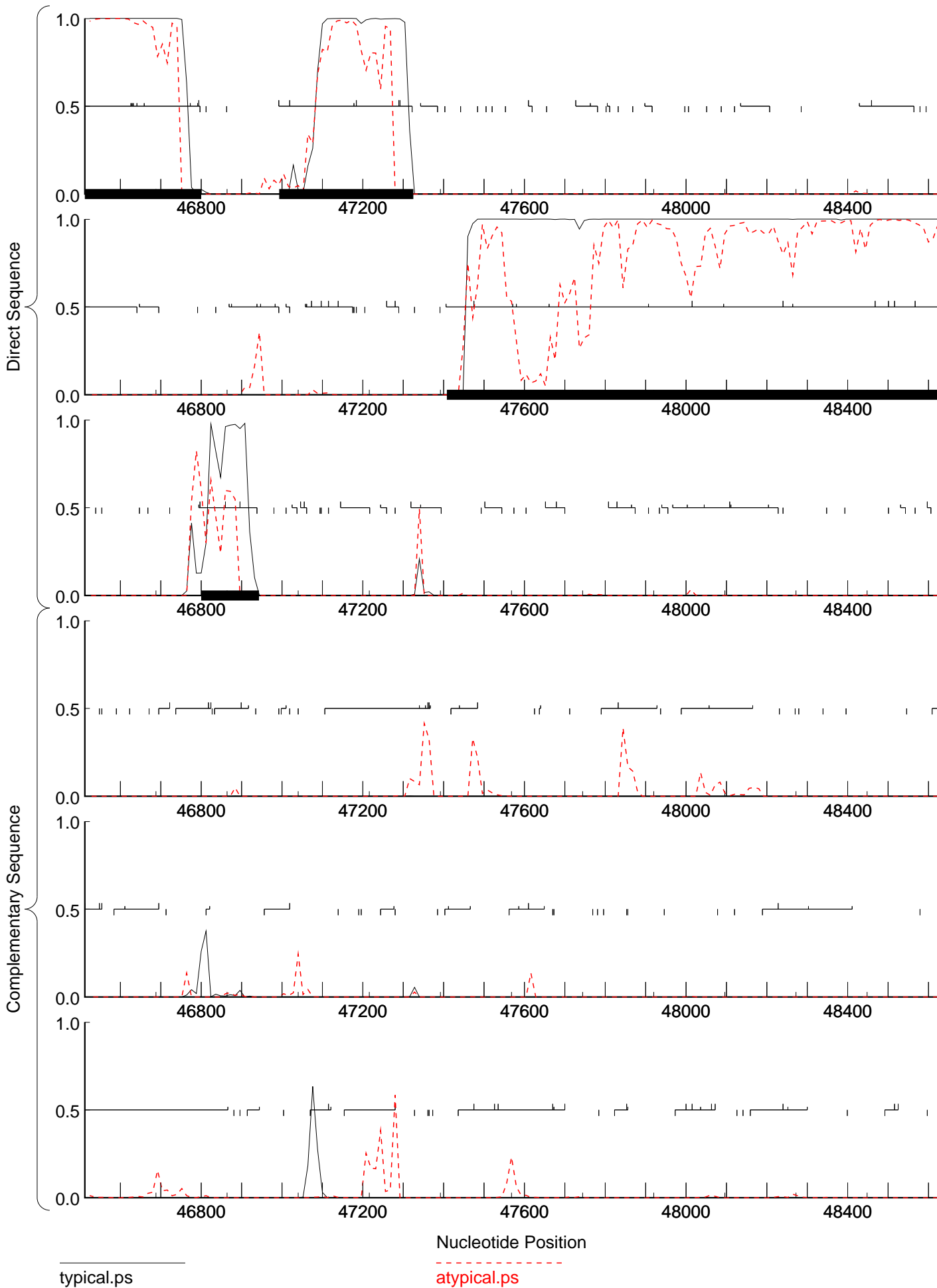


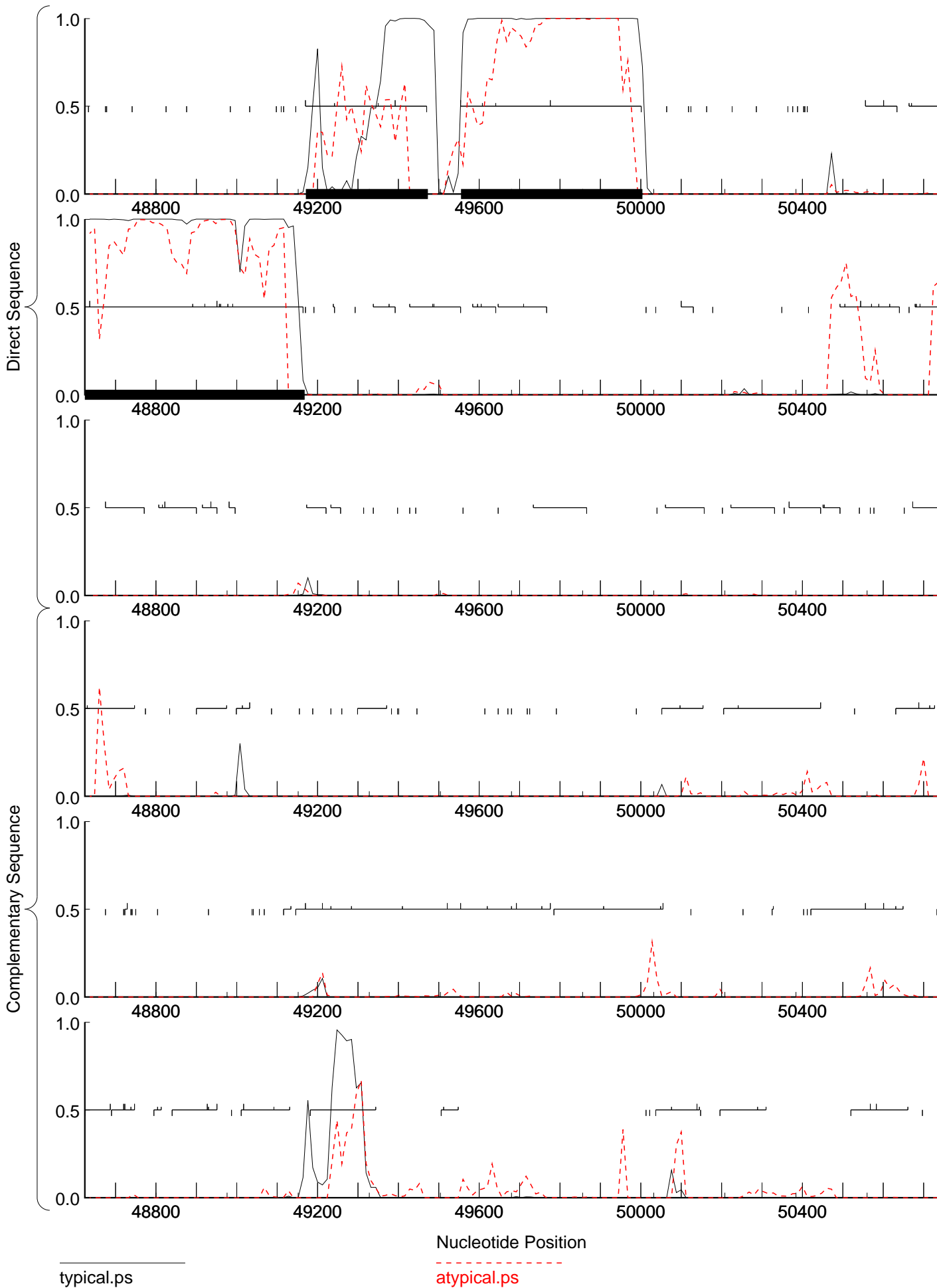


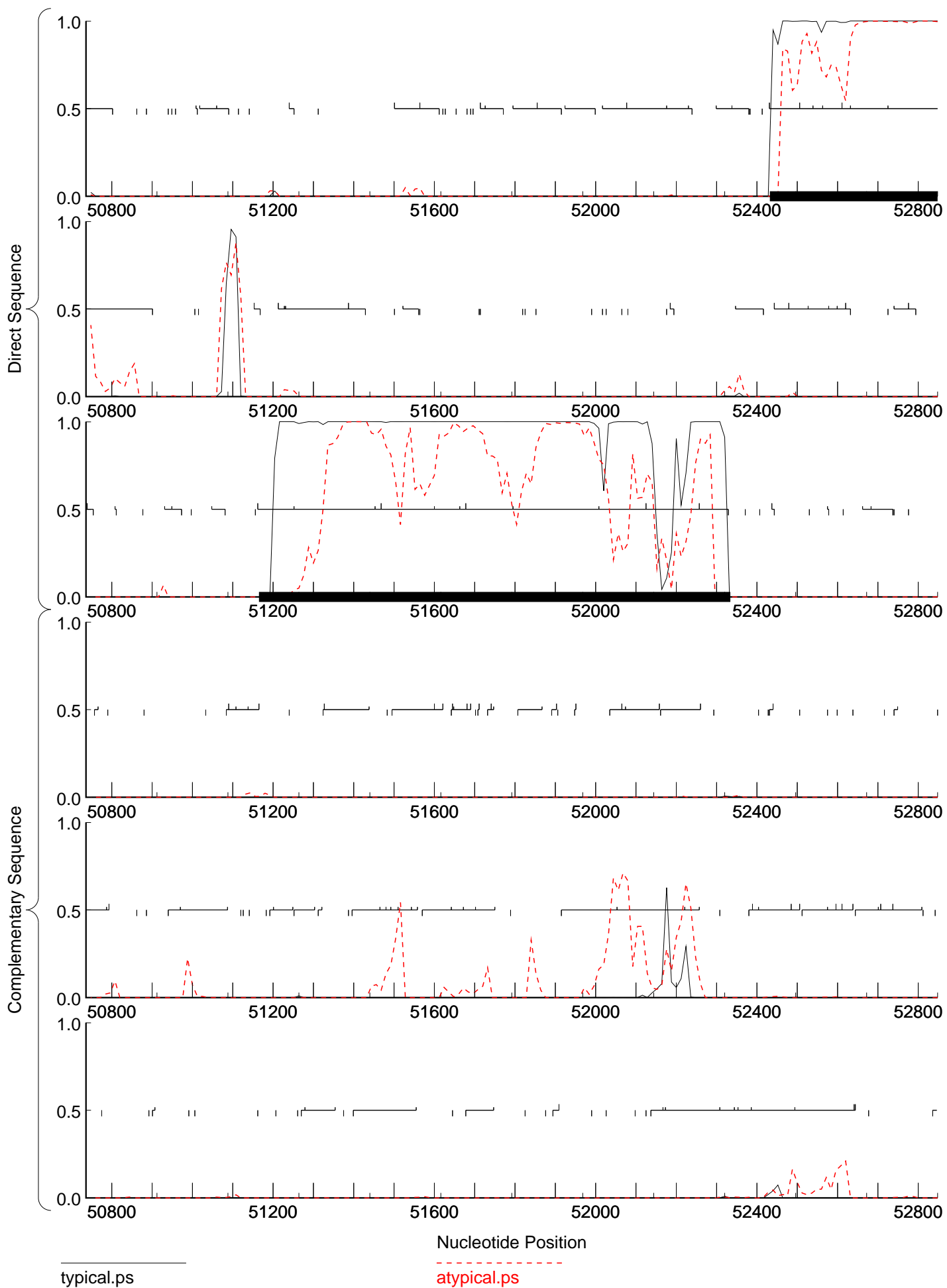


typical.ps

atypical.ps

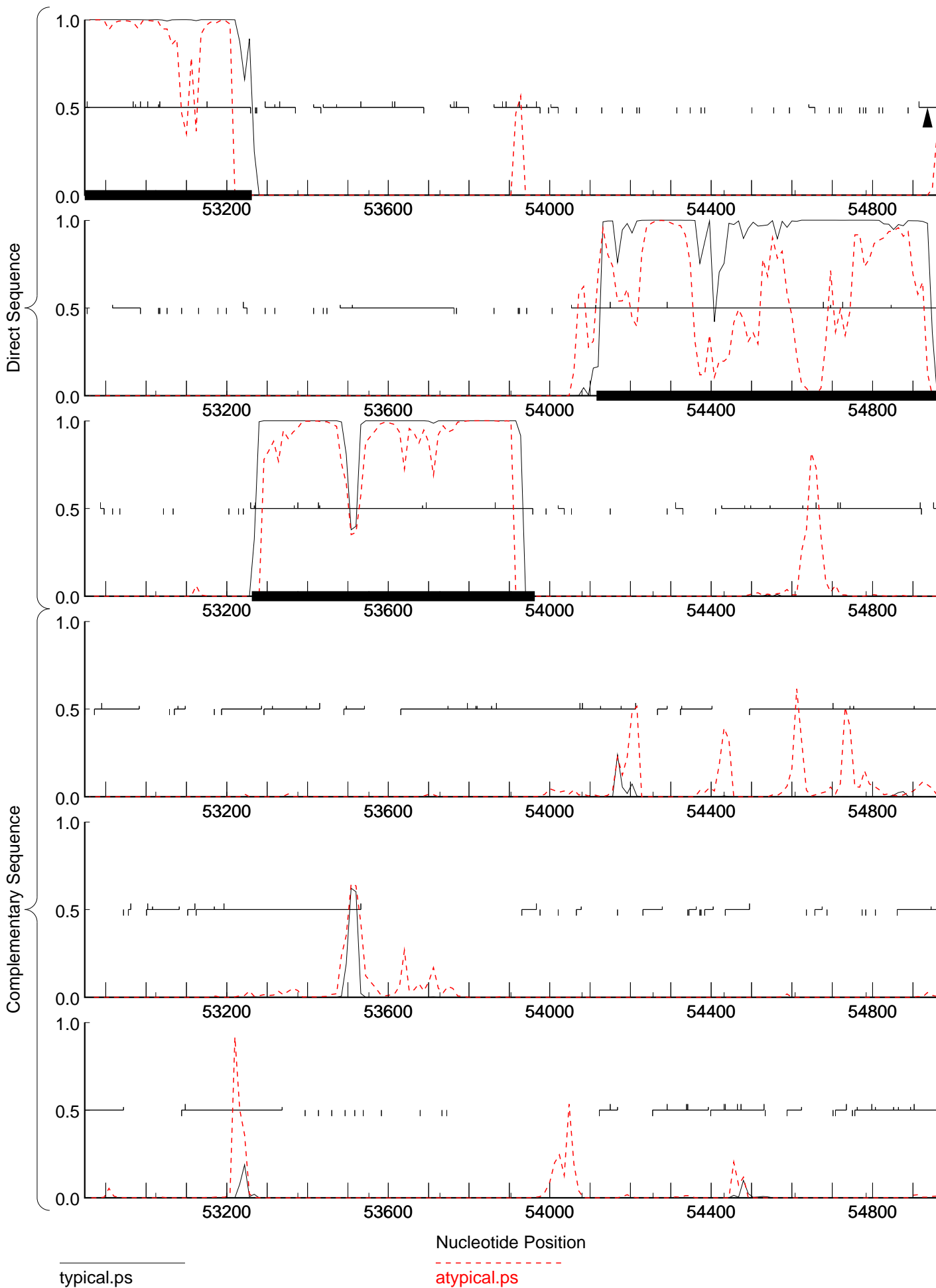






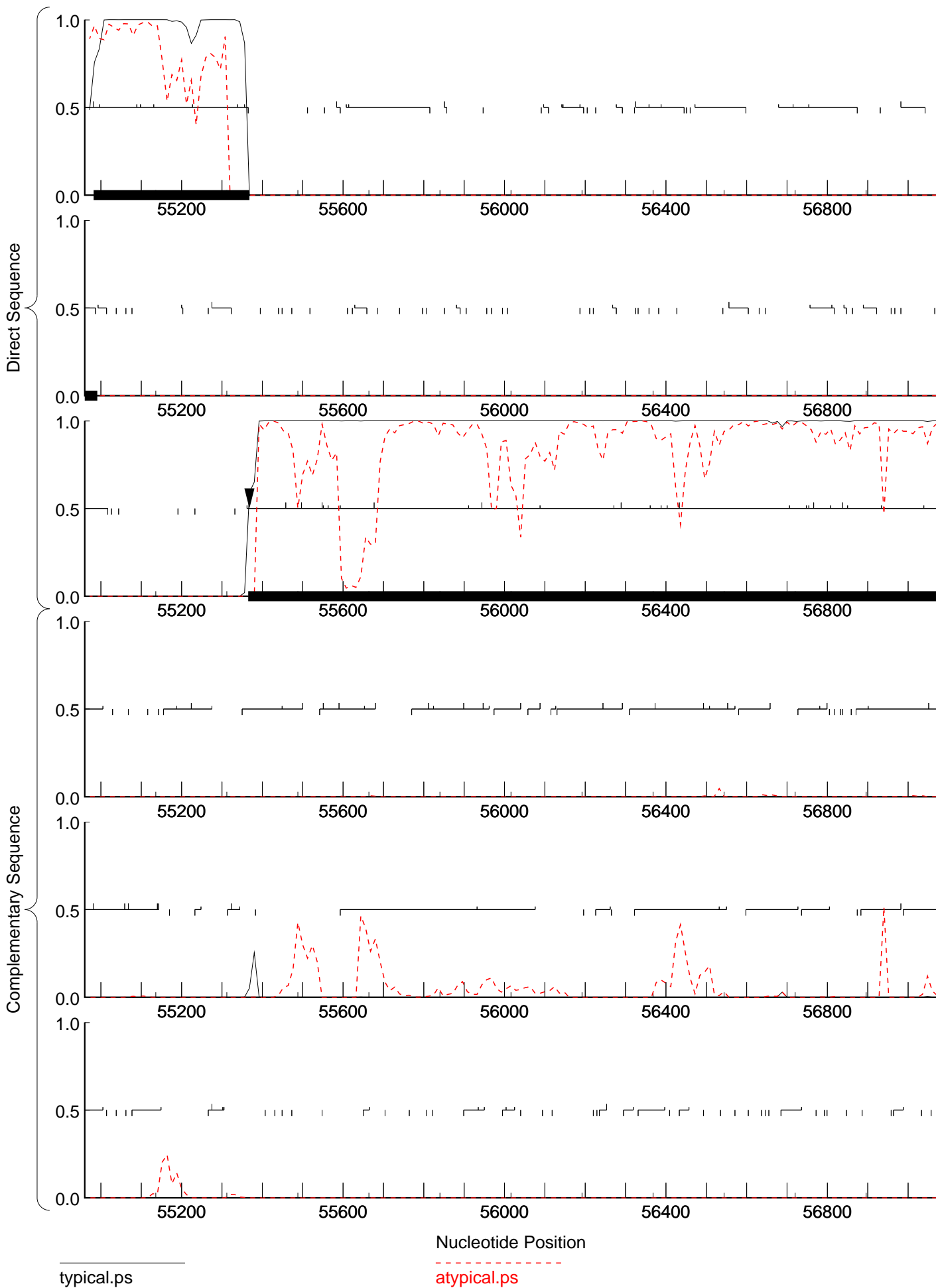
typical.ps

atypical.ps



typical.ps

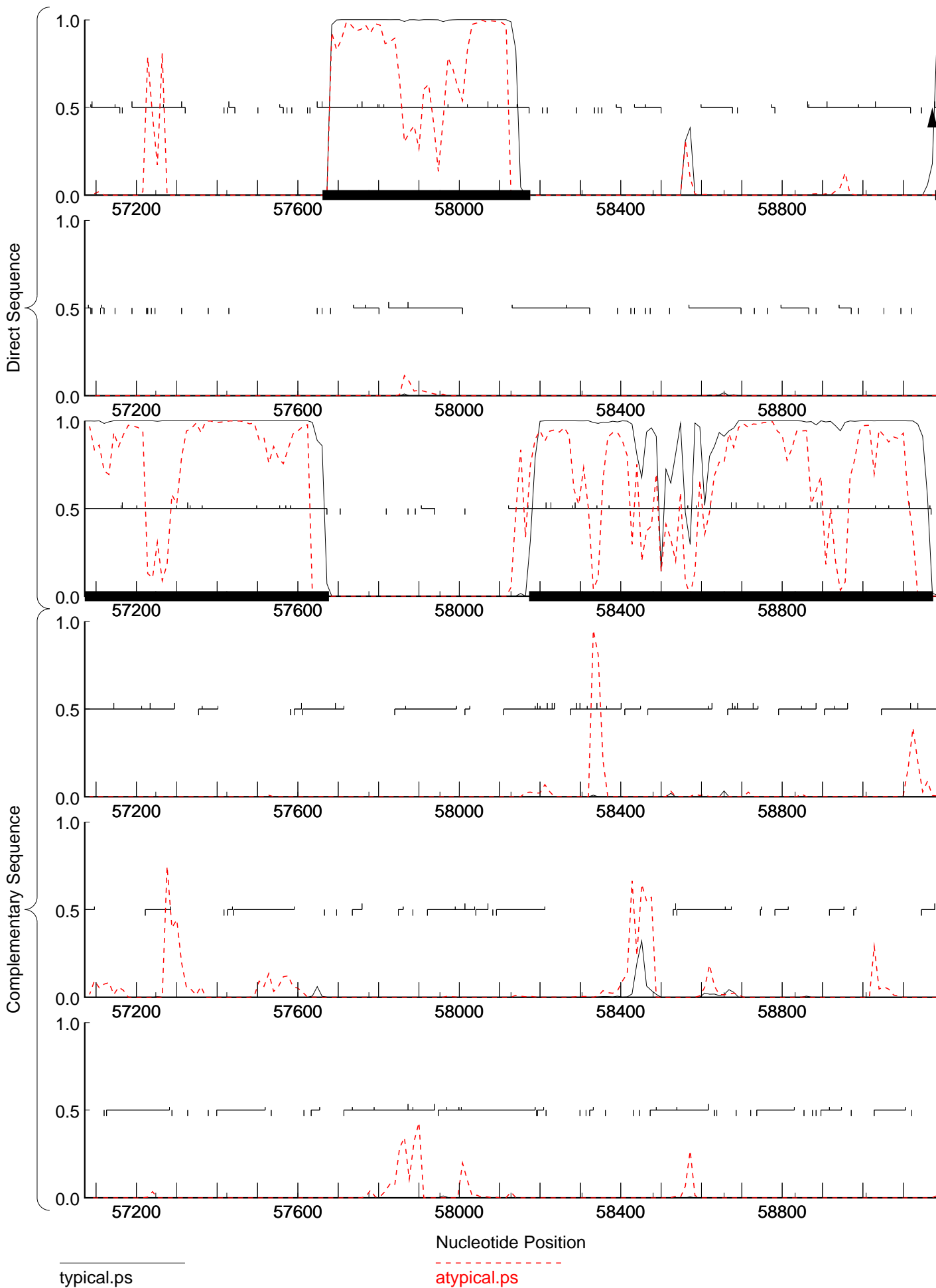
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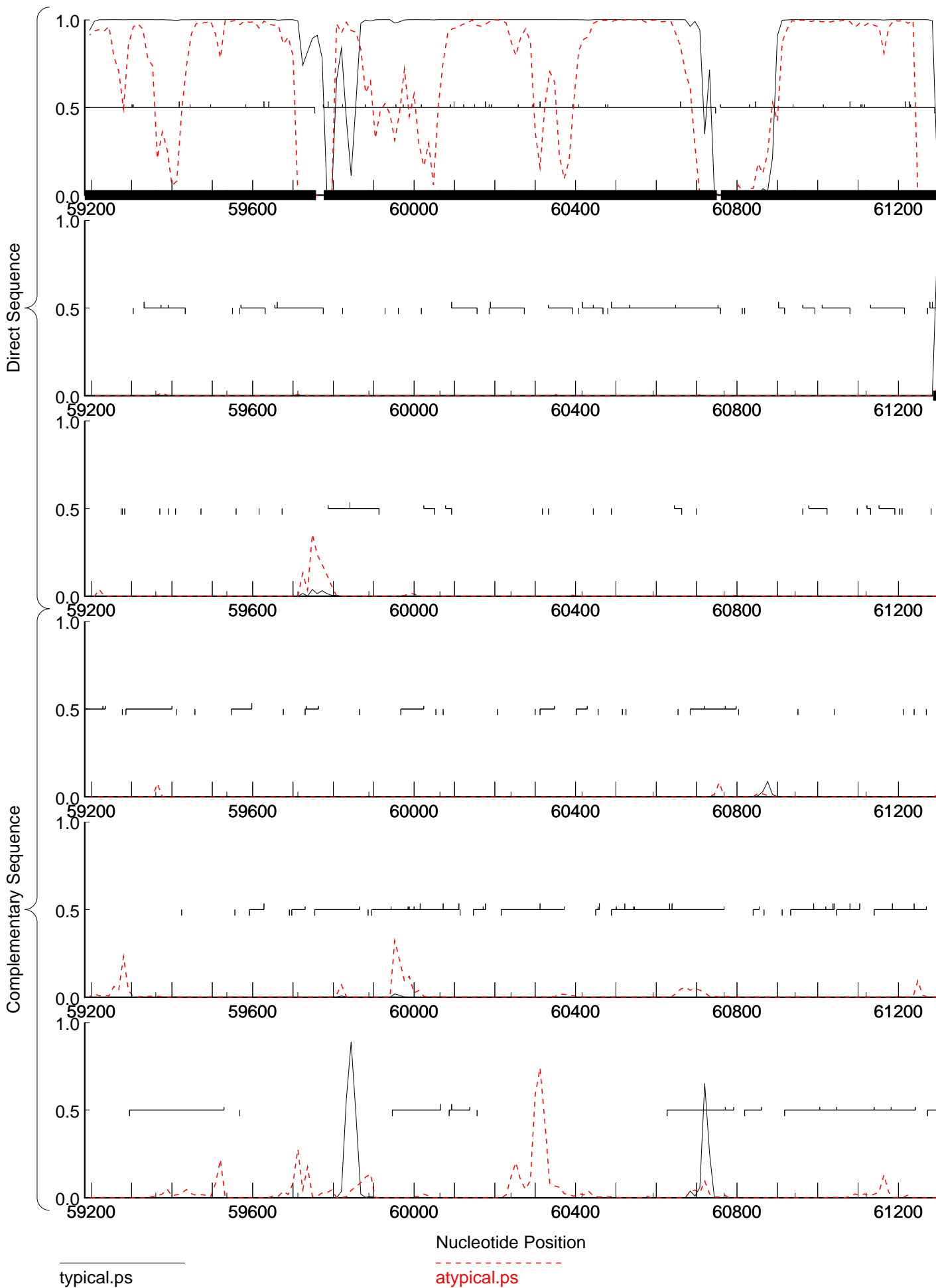


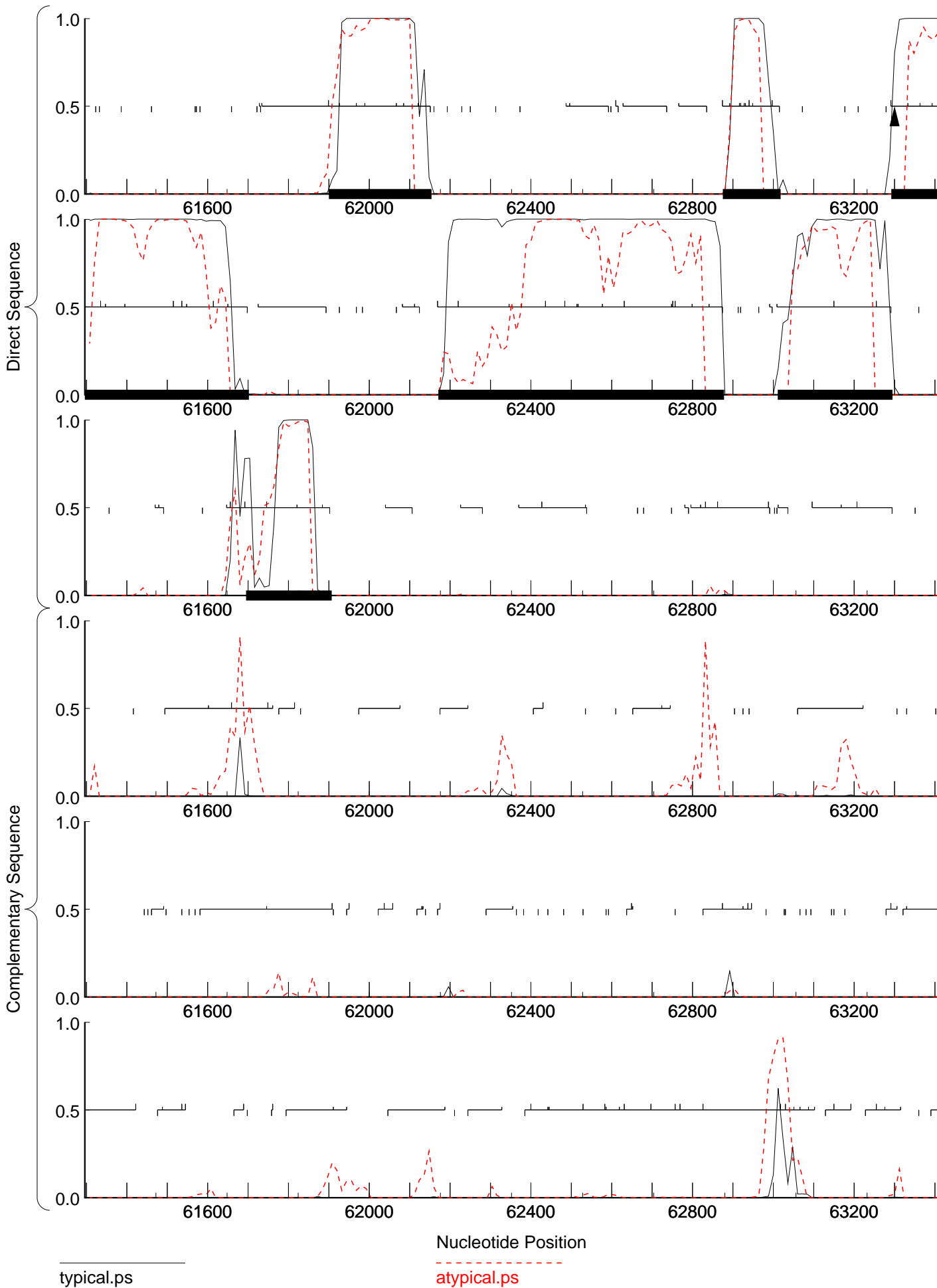
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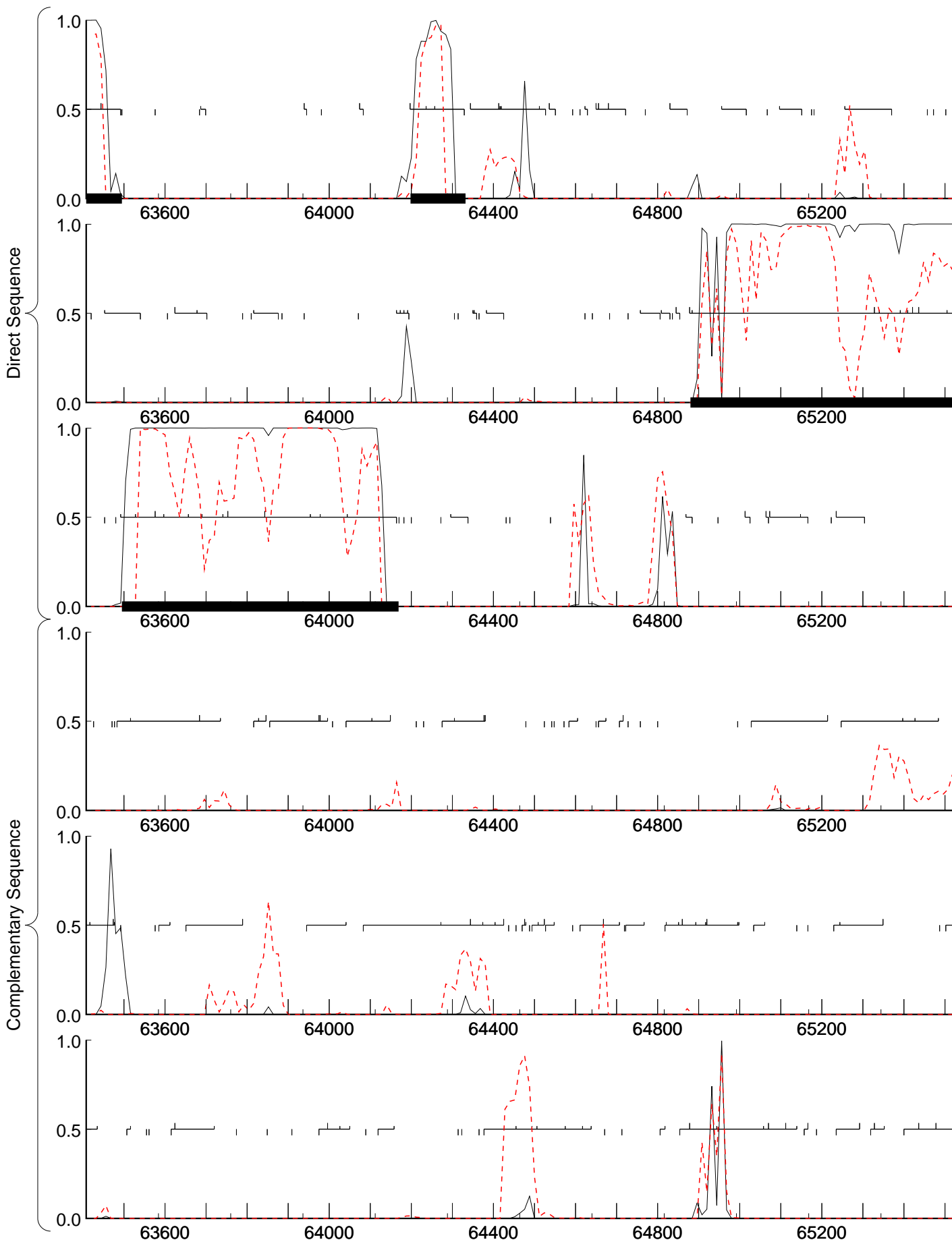
Nucleotide Position

atypical.ps





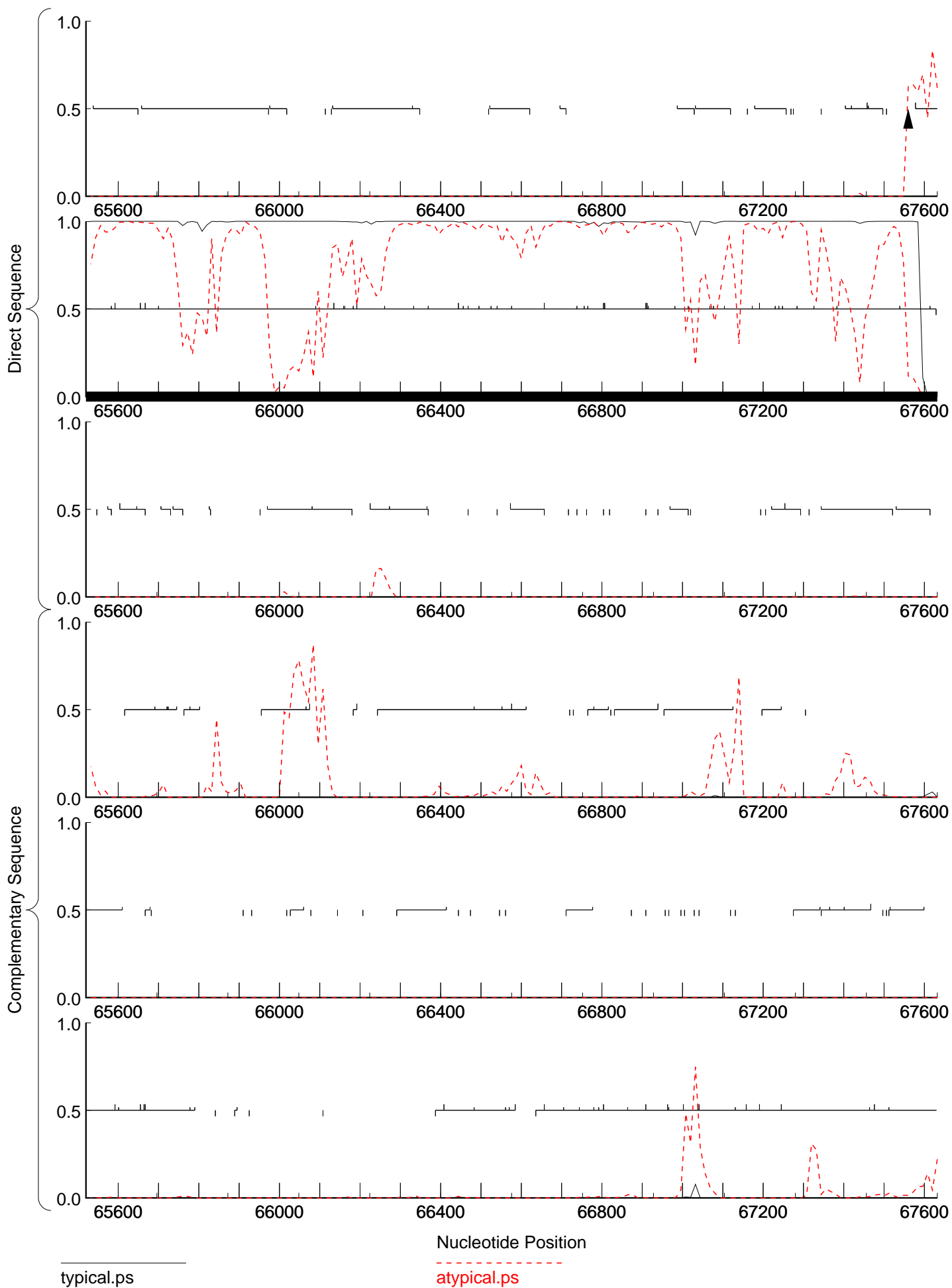


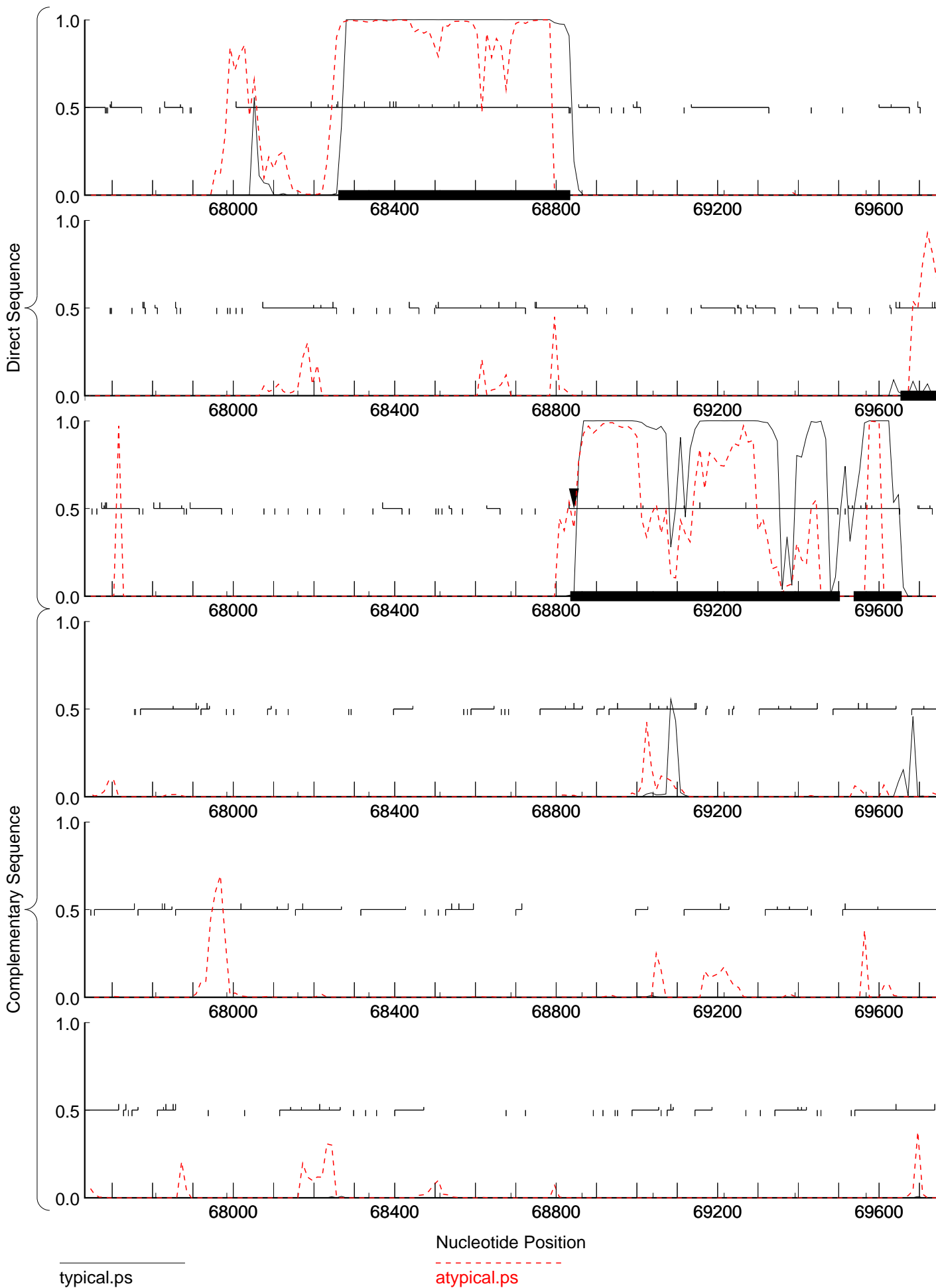


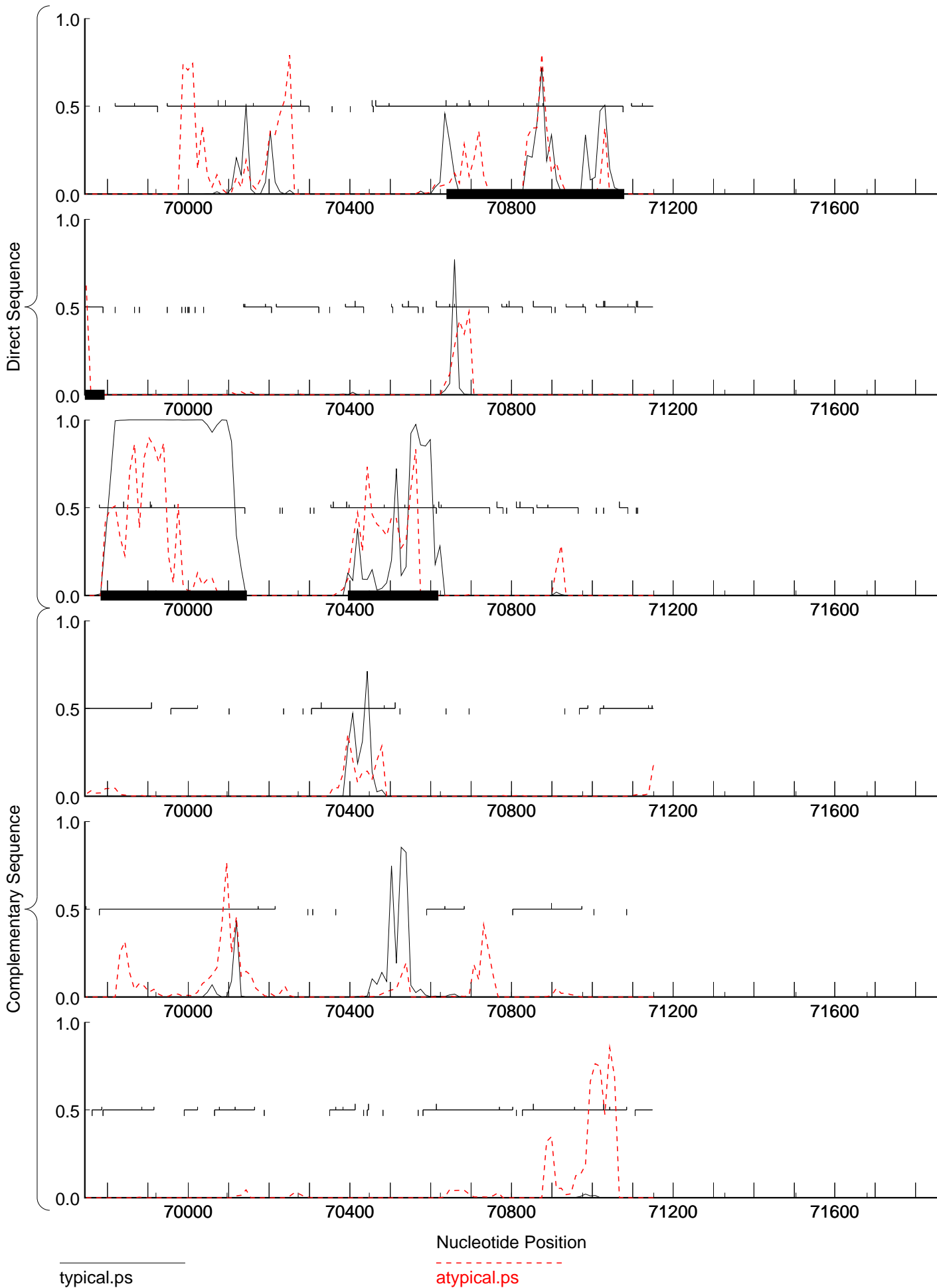
typical.ps

atypical.ps

GeneMark.hmm prediction







typical.ps

atypical.ps