

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 : 5/26/17 at 9:13:32
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,

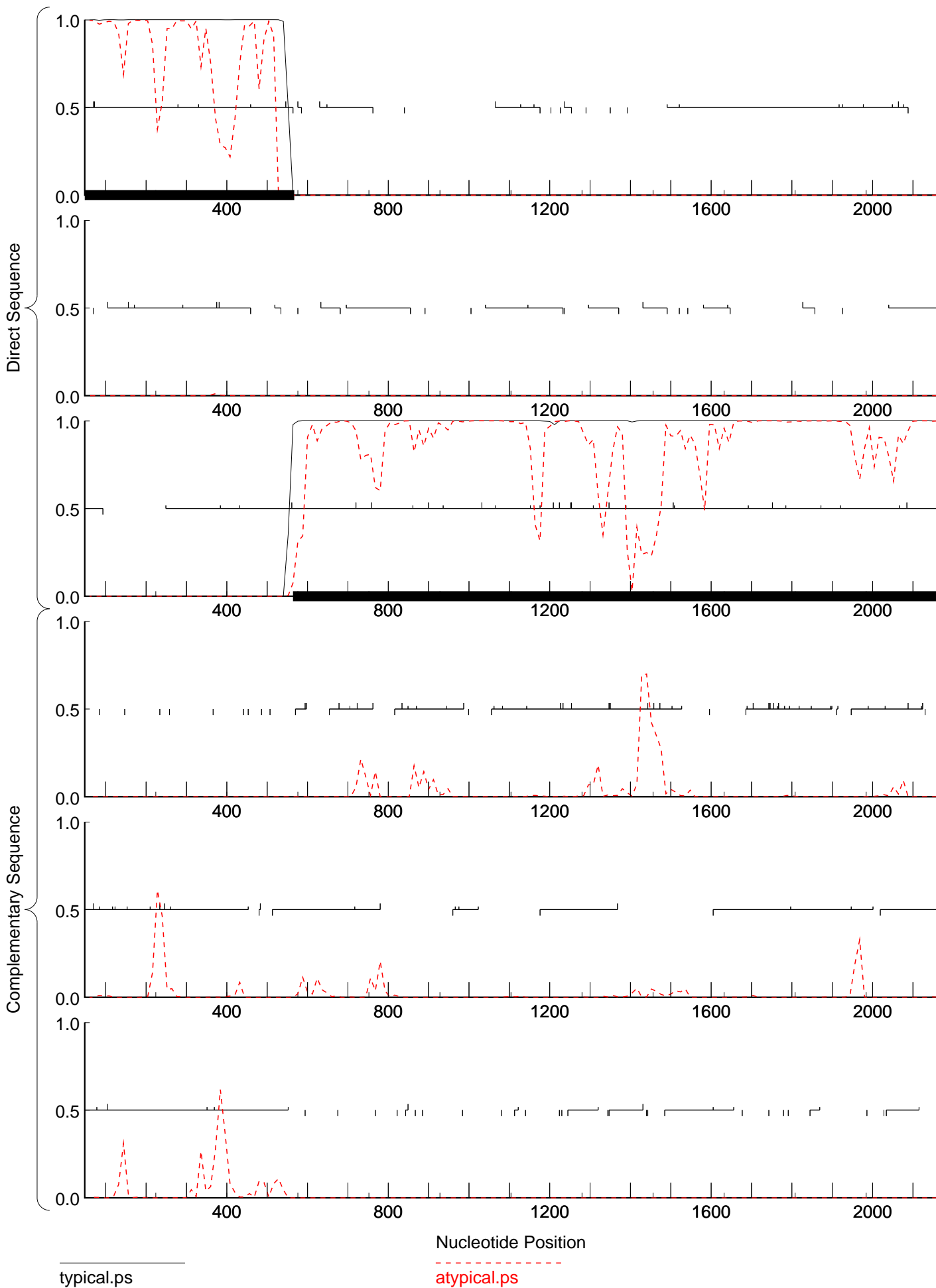
Matrix notes & comments

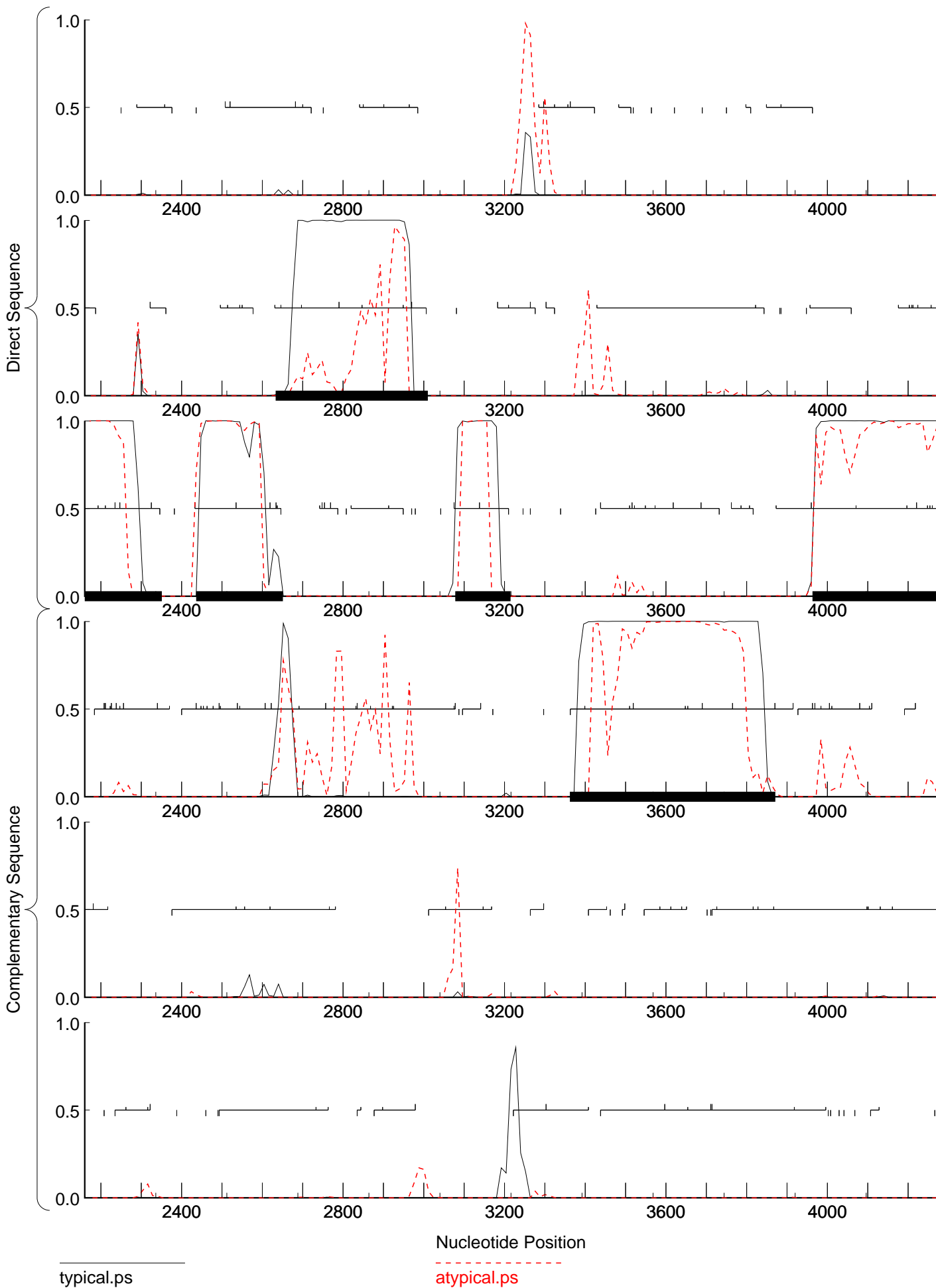
Training set derived by GeneMarkS, 4.30 October 2014
Fri May 26 09:13:31 2017

MATRIX INFORMATION

Matrix : -
Author : -
Order : 4

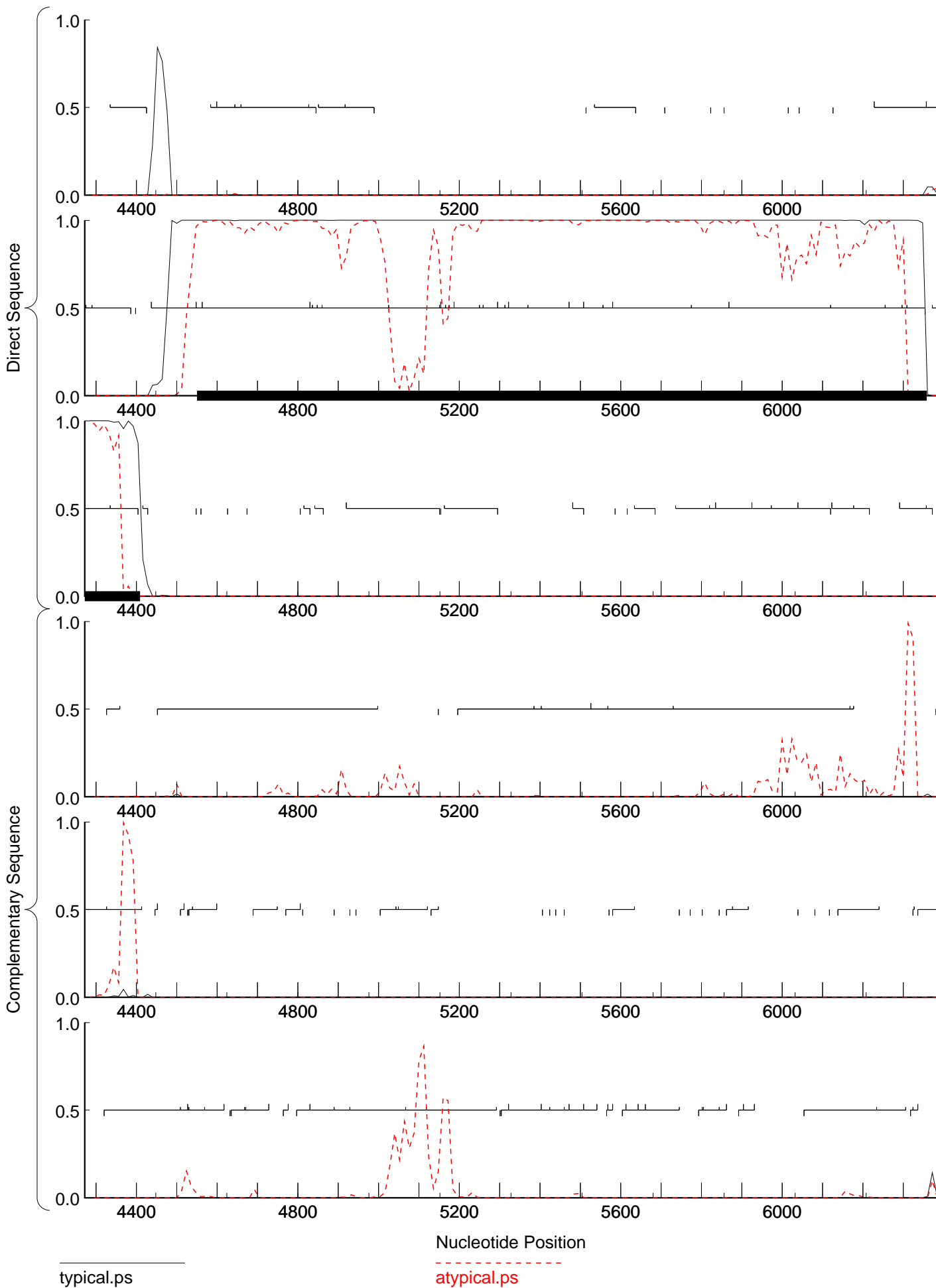
Send questions / comments to:
Dr. M. Borodovsky
Georgia Institute of Technology
School of Biology
Atlanta, GA 30332-0230

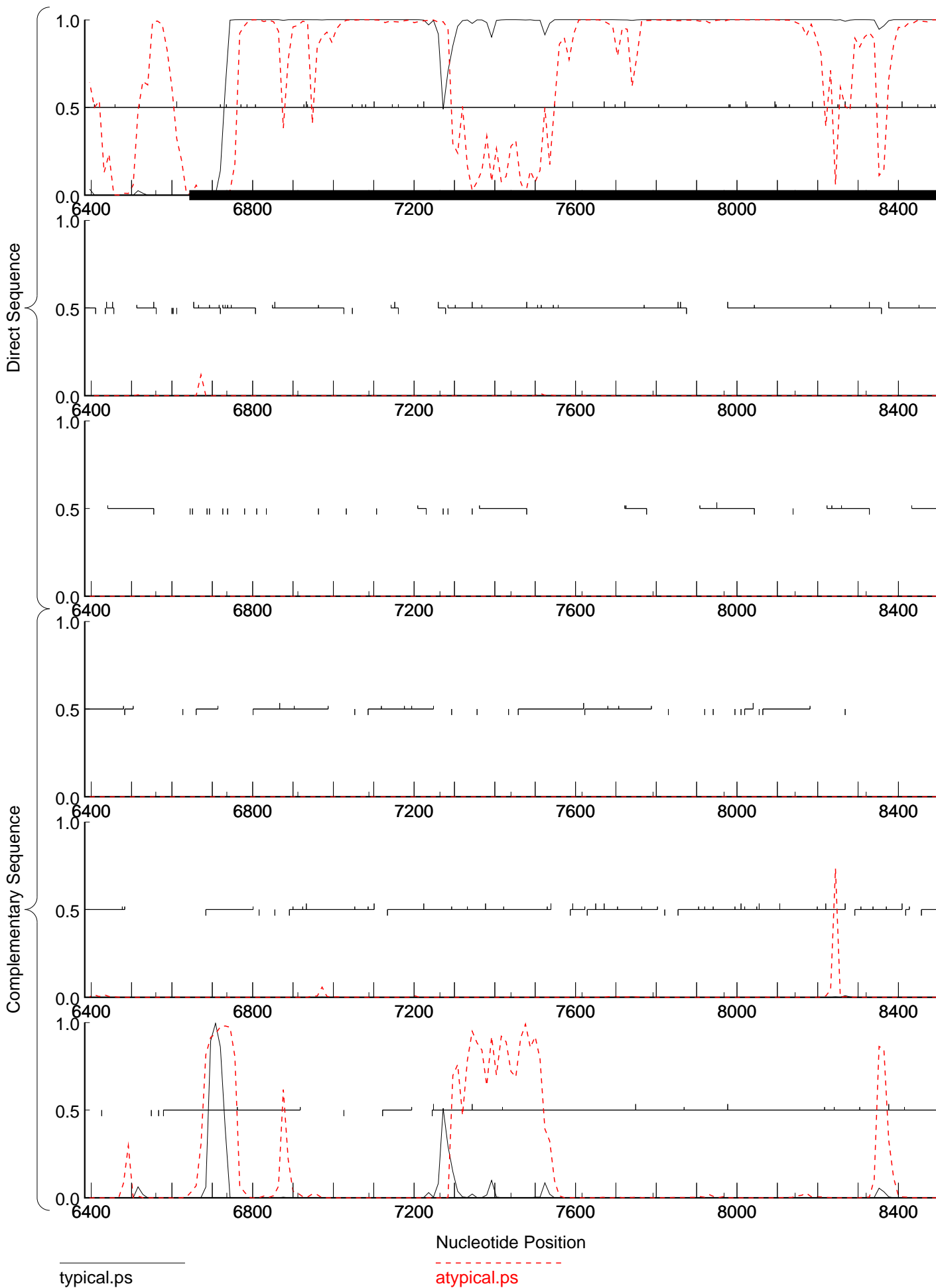




typical.ps

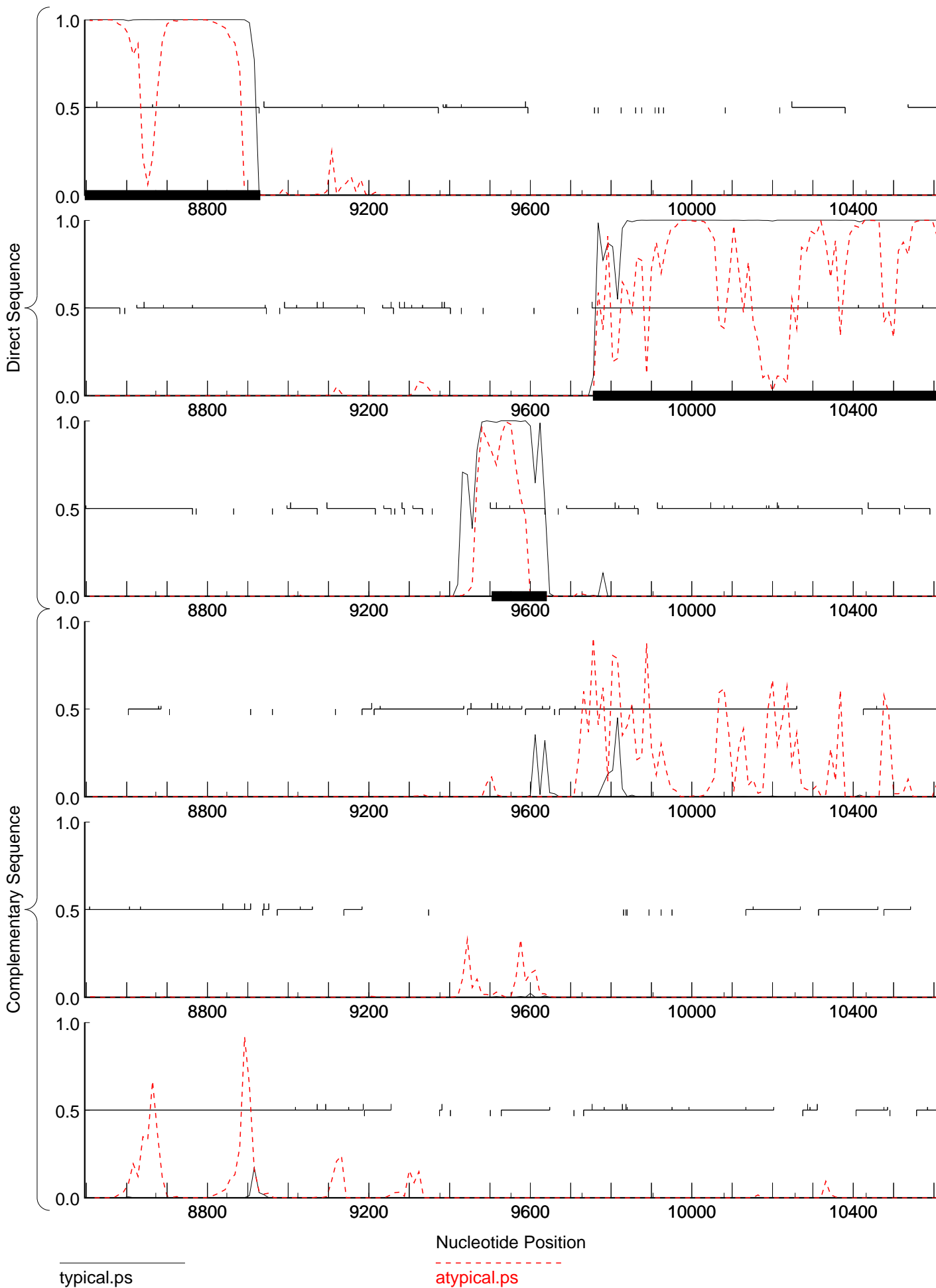
atypical.ps





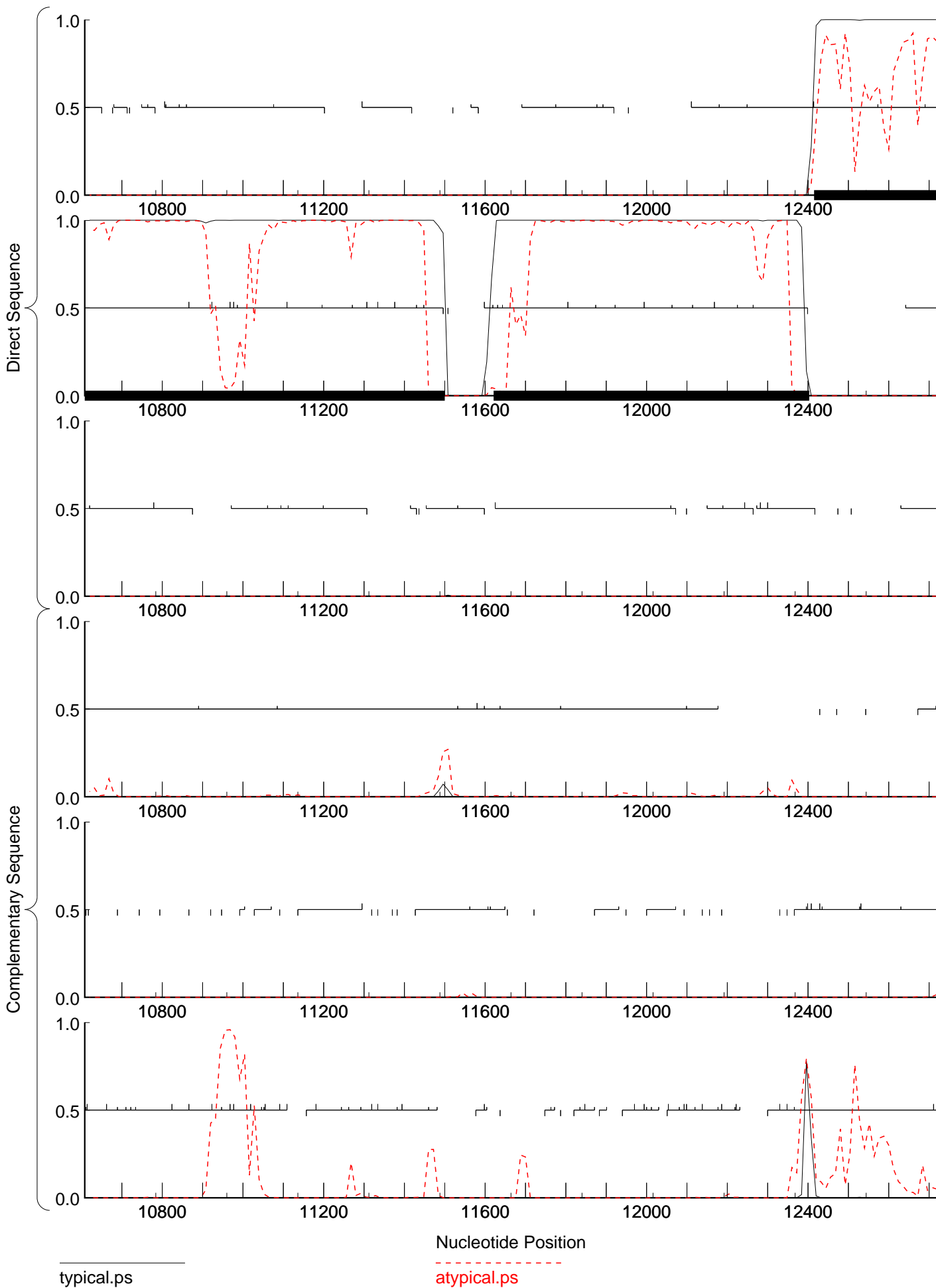
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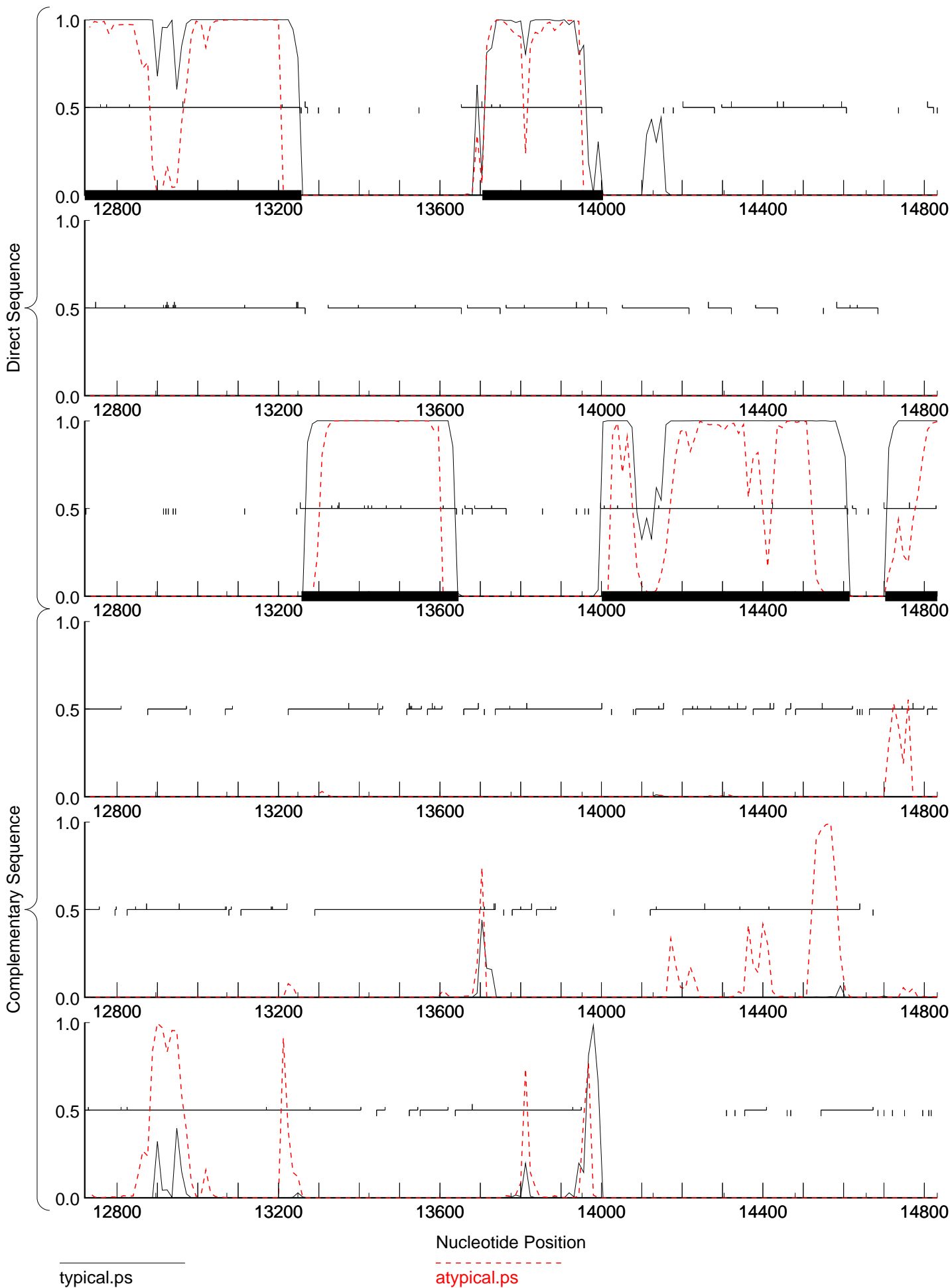
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typical.ps

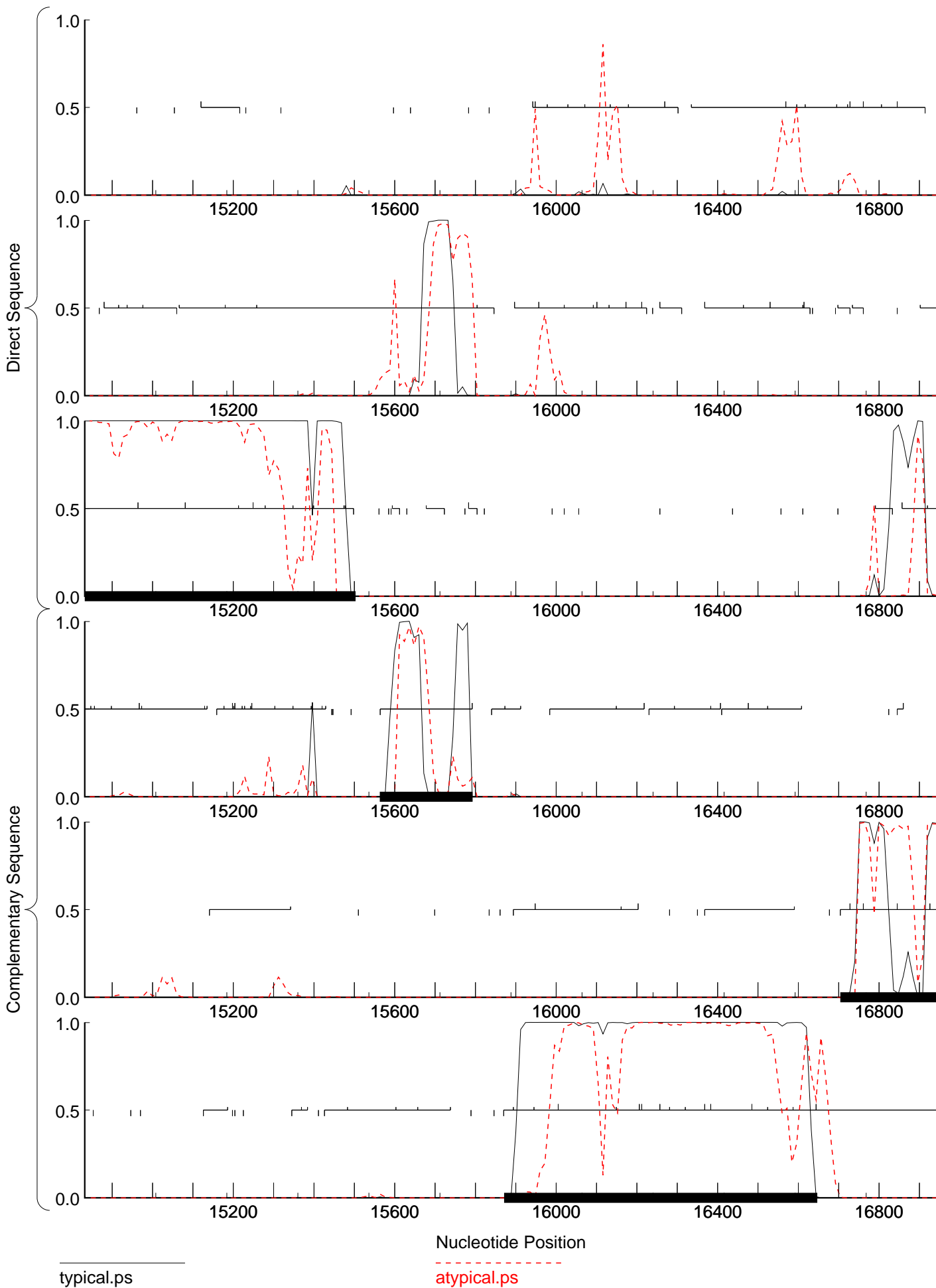
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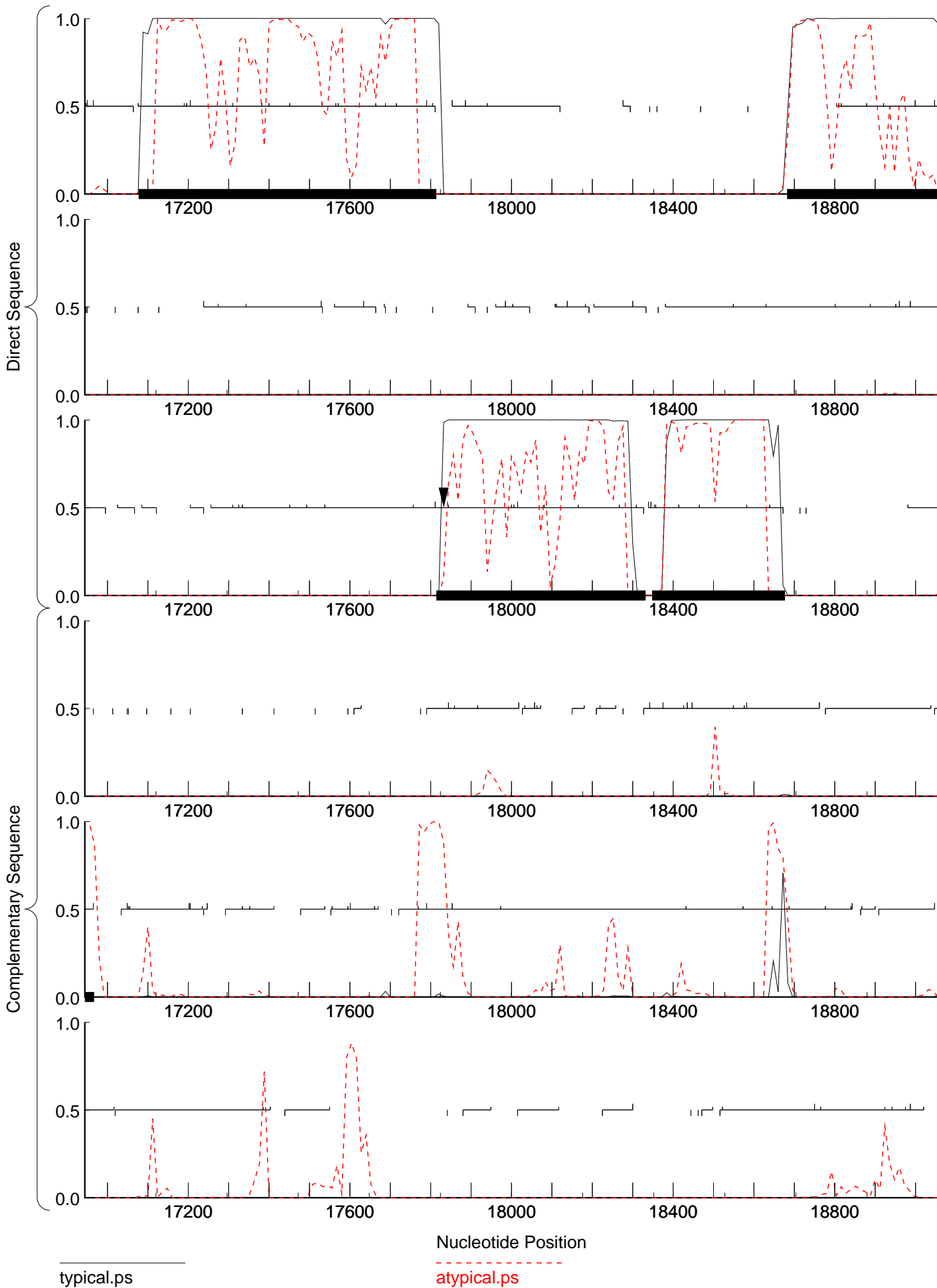


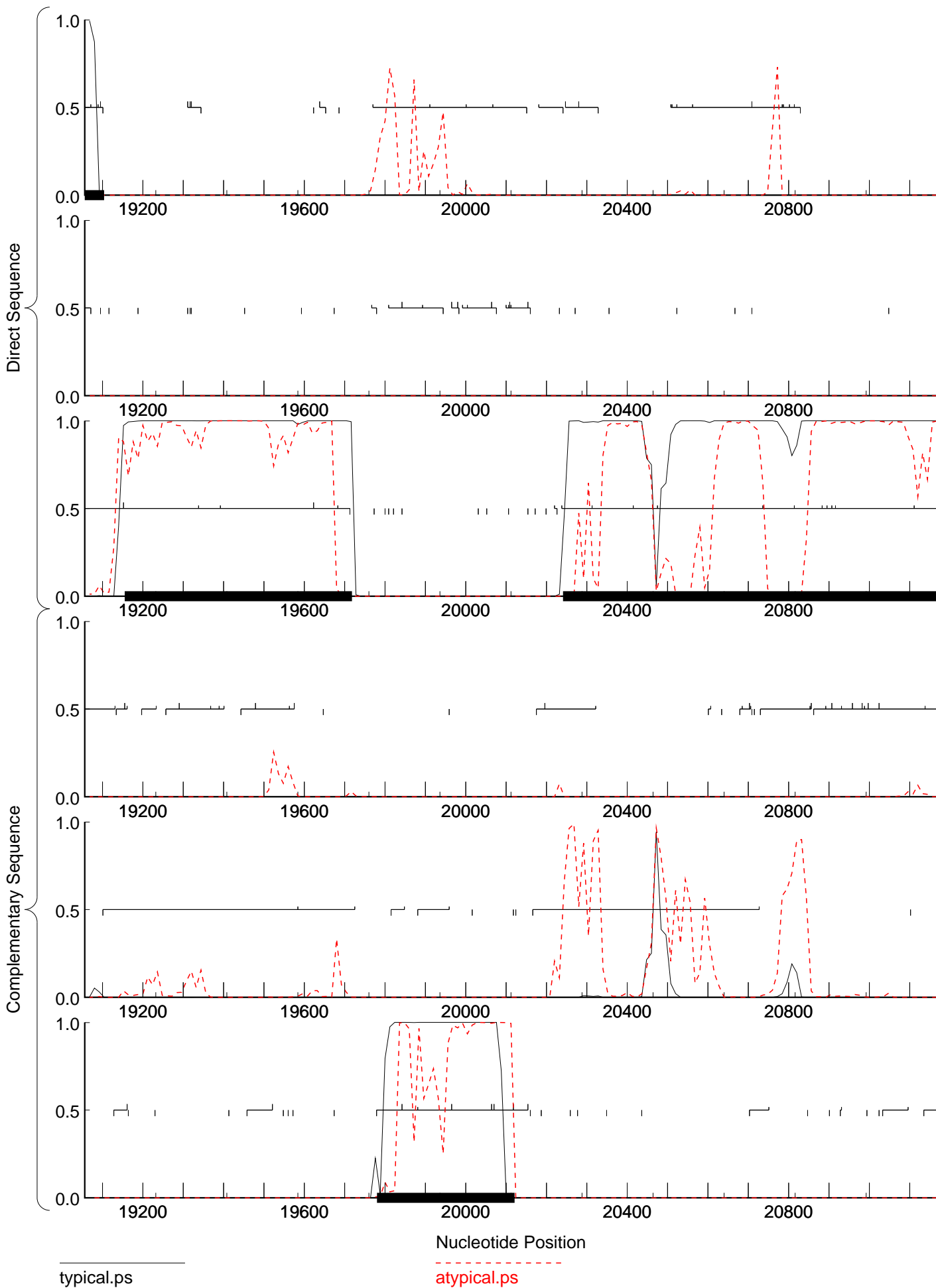


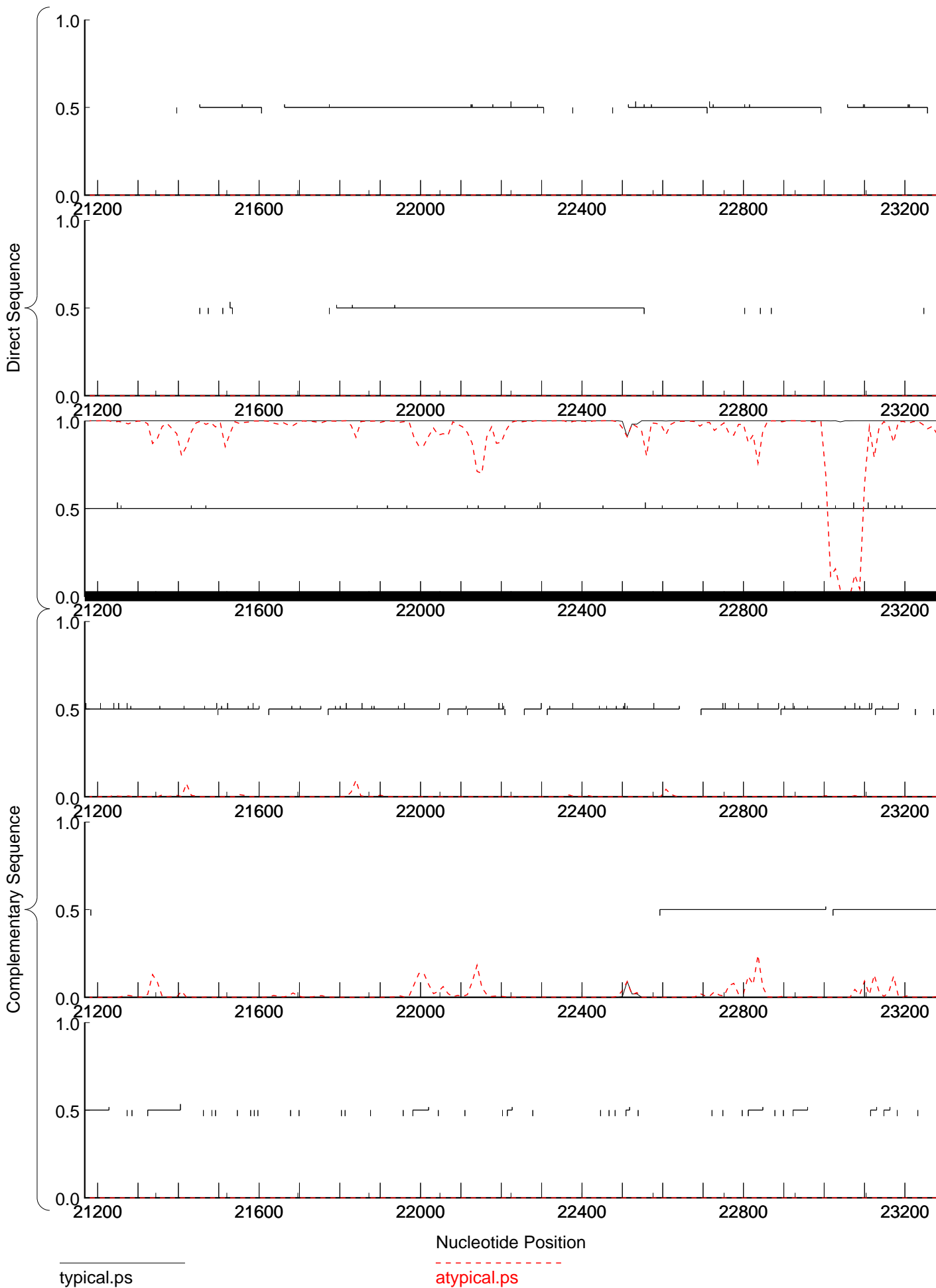
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atypical.ps



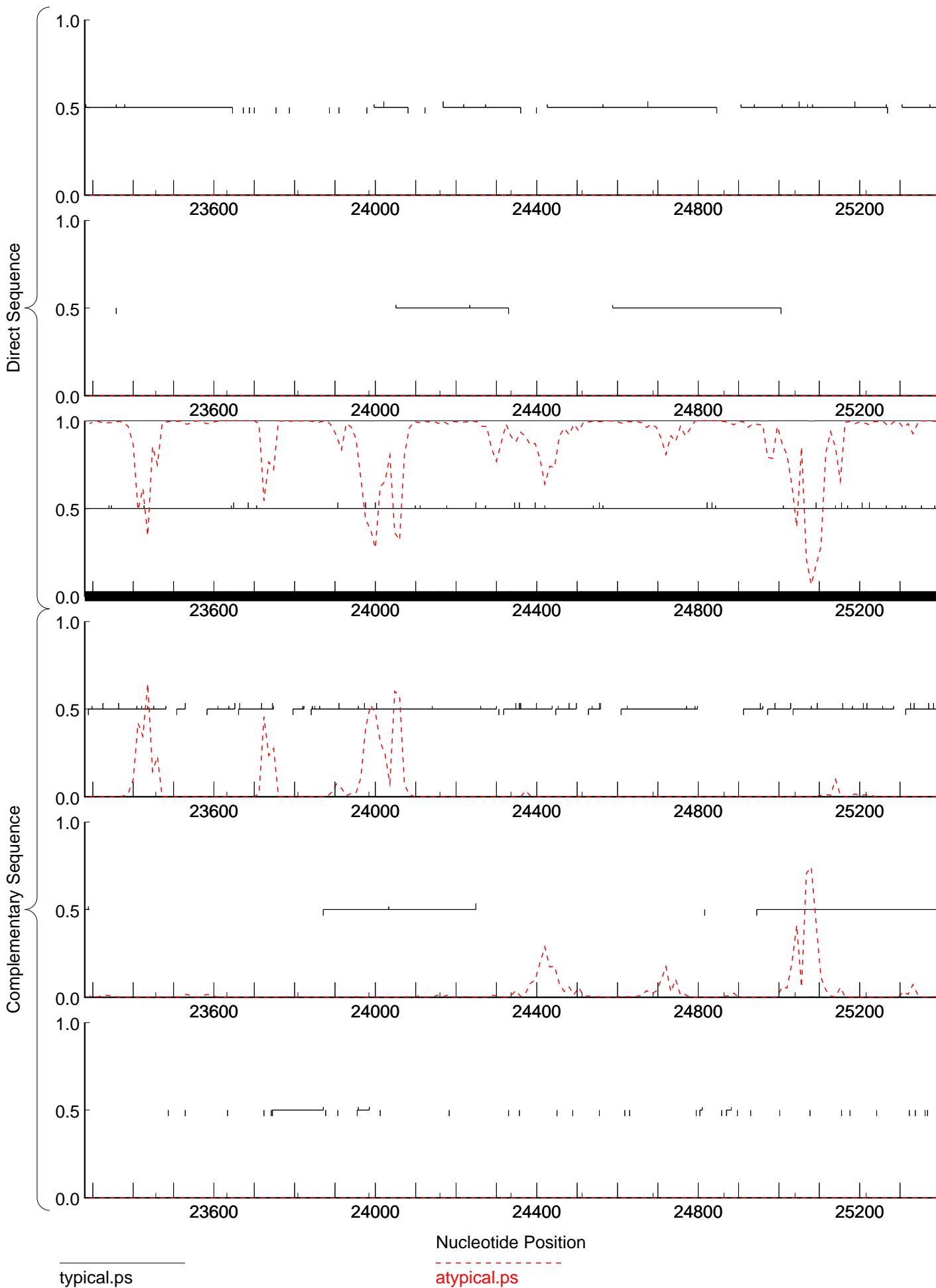






typical.ps

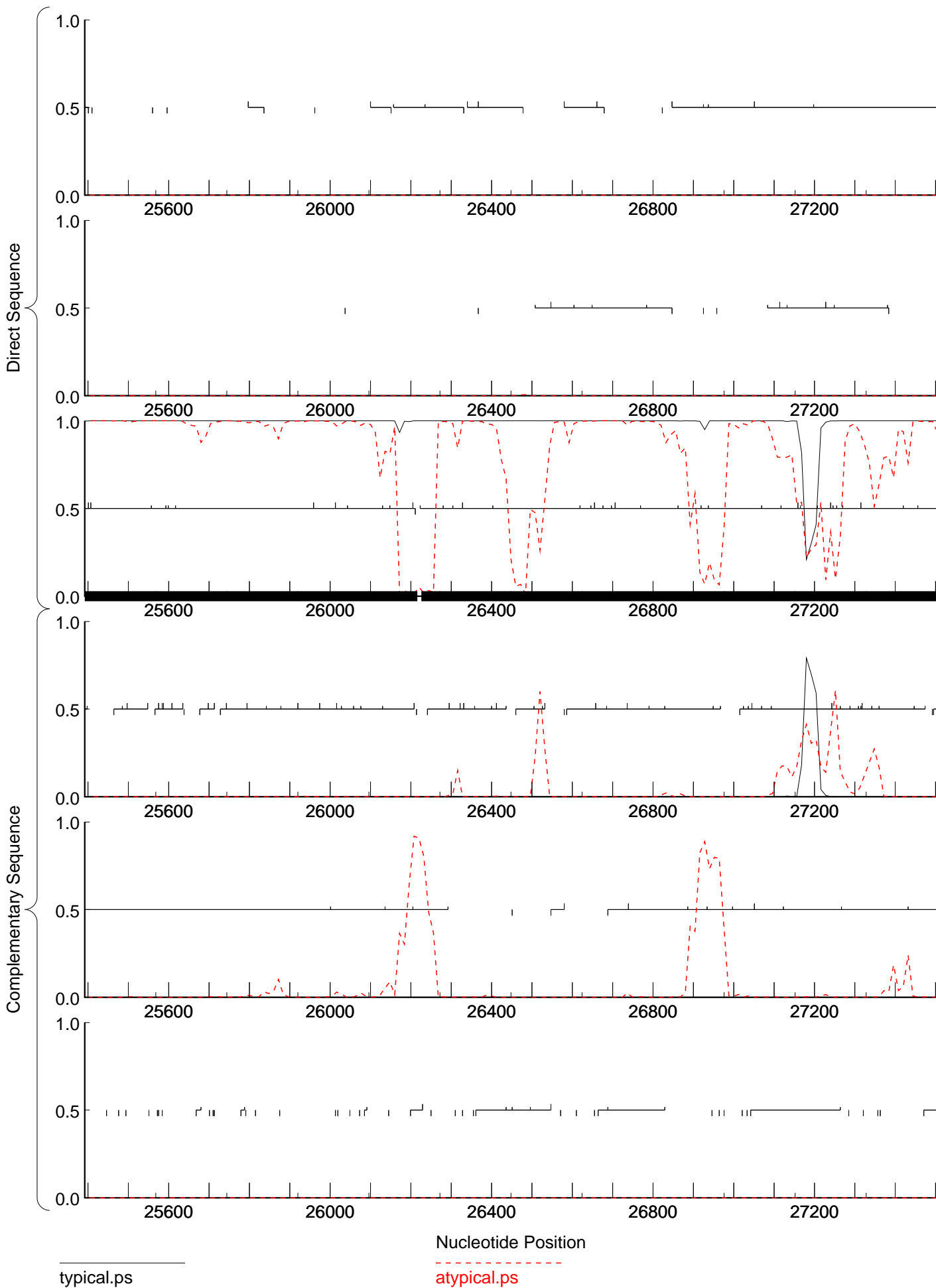
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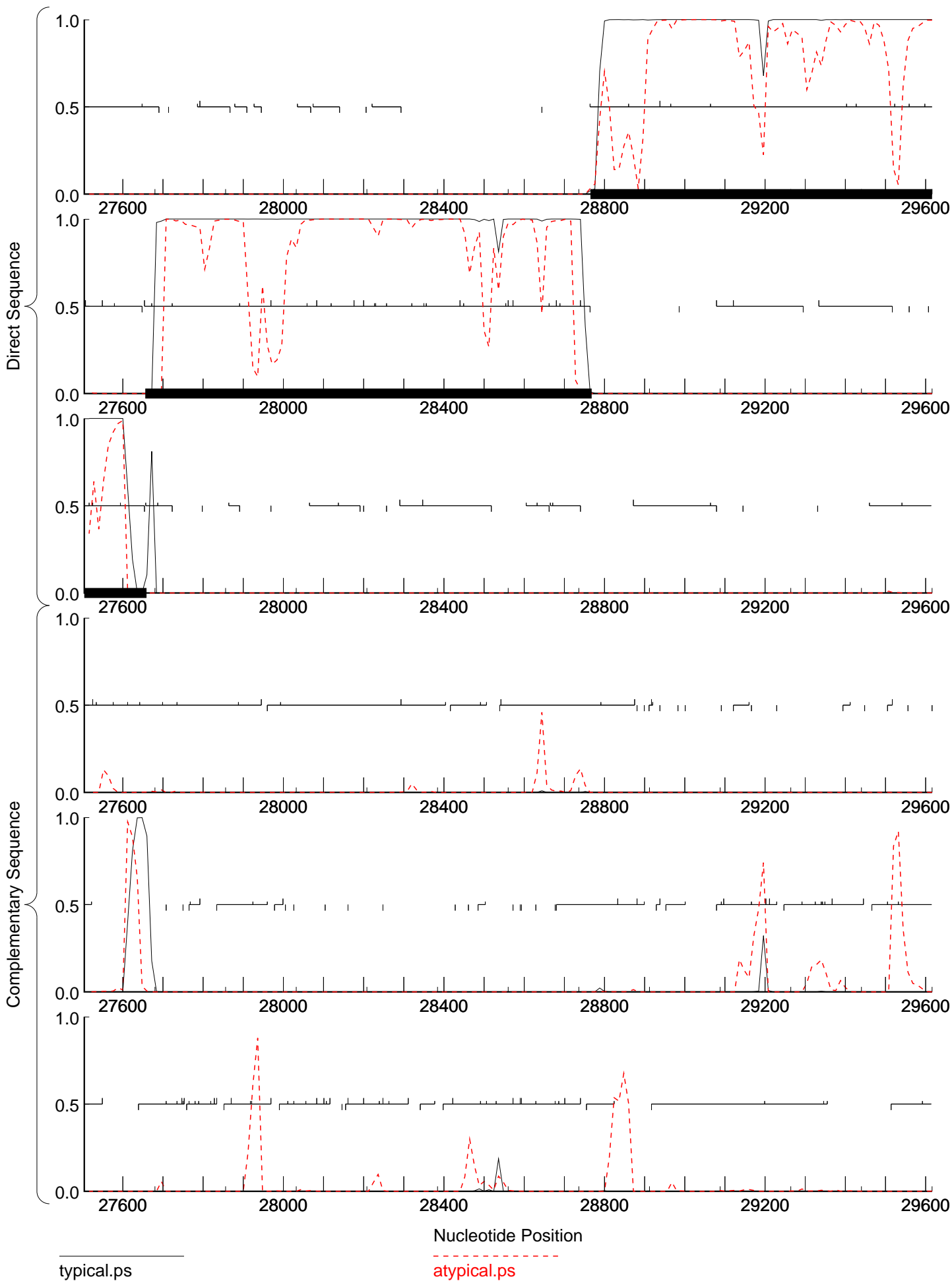


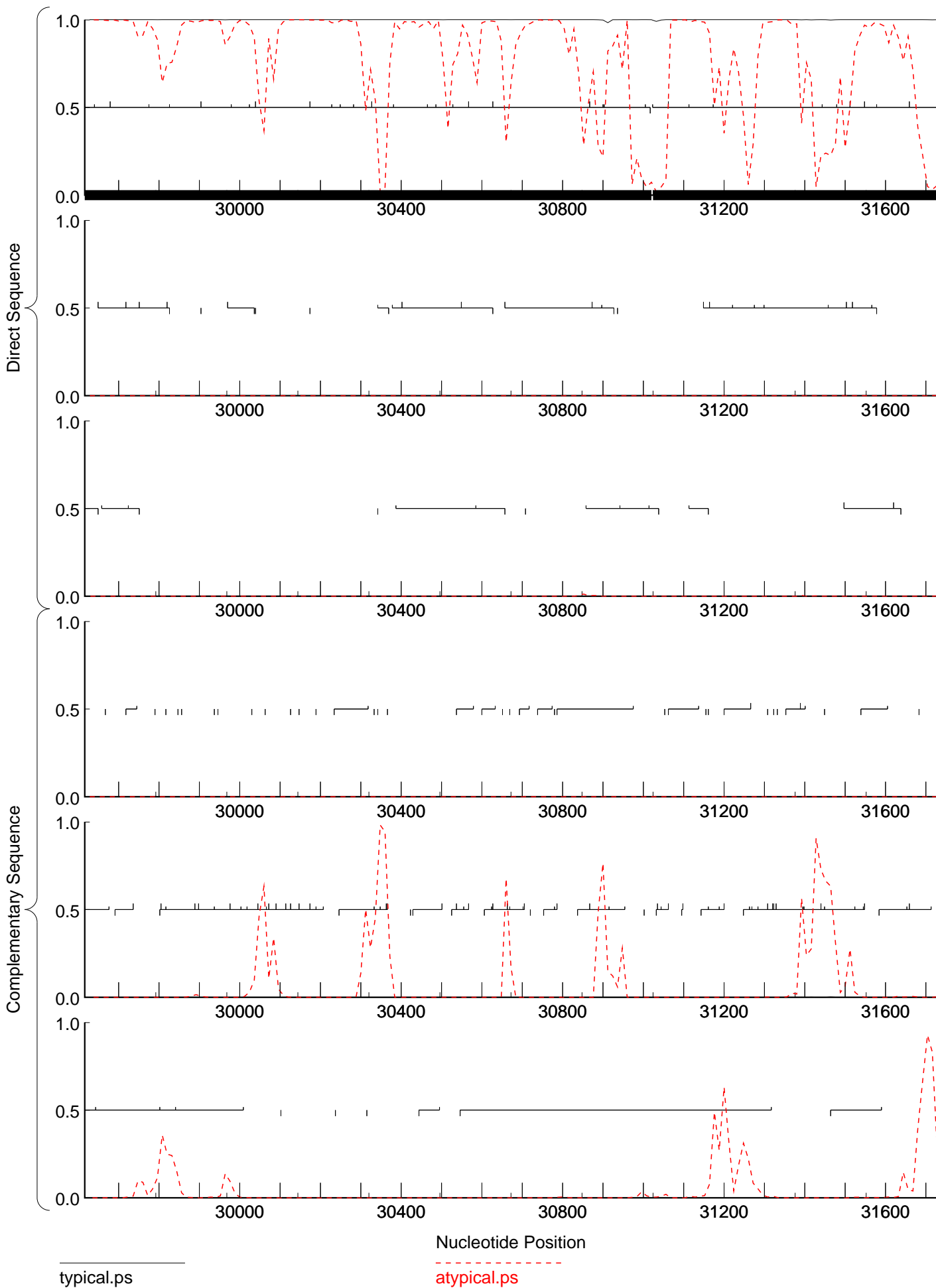
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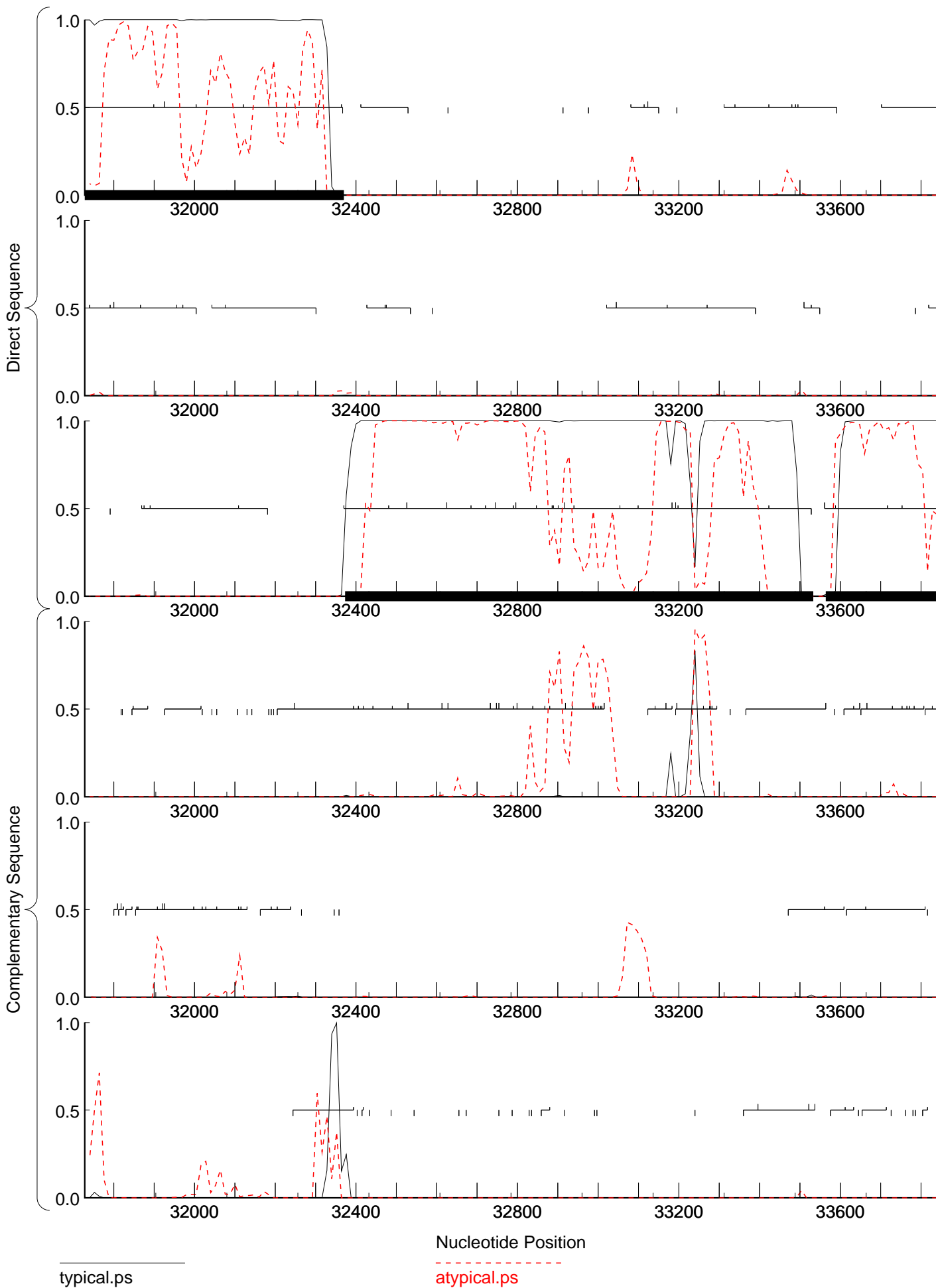
Nucleotide Position

atypical.ps



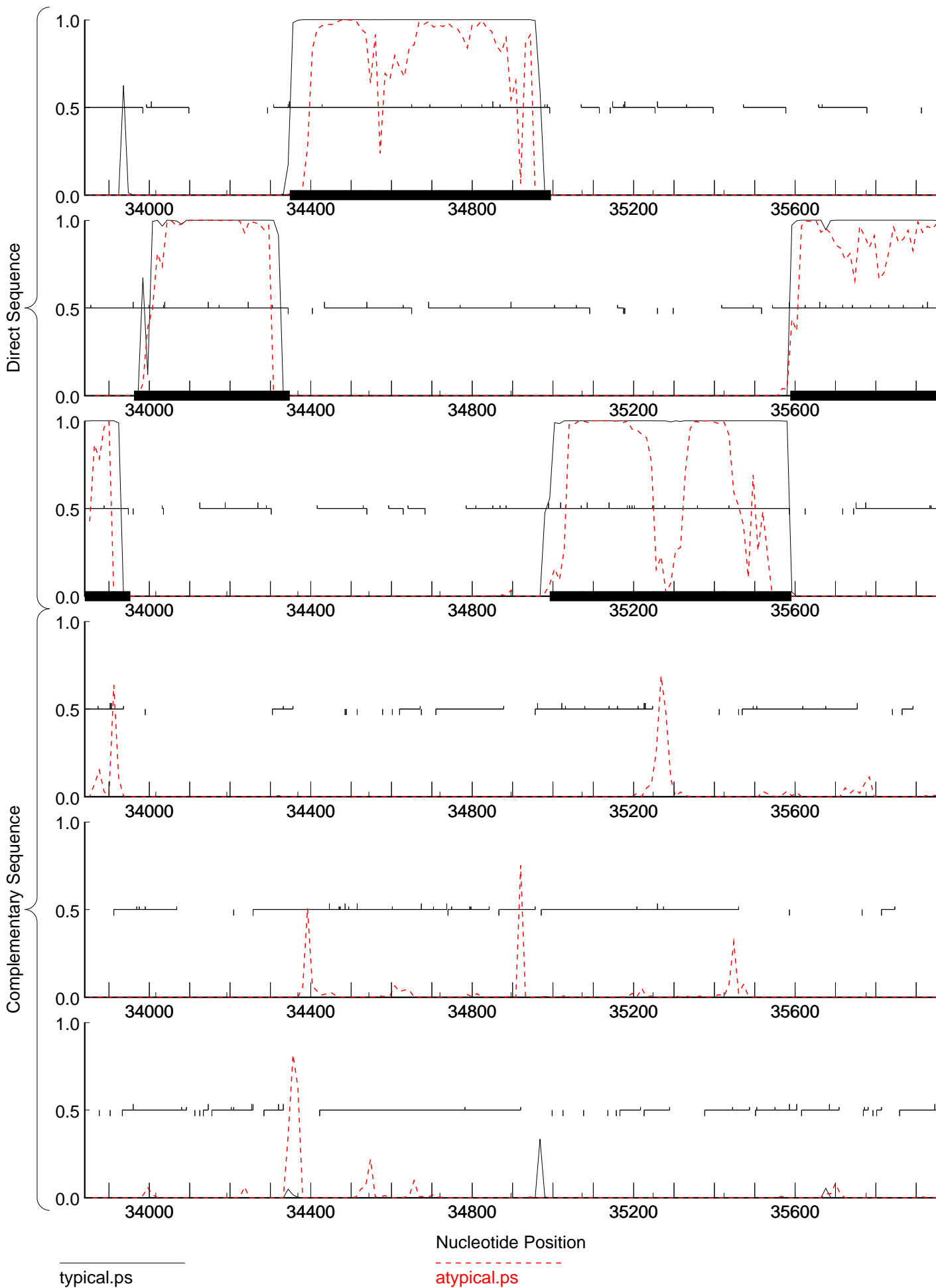


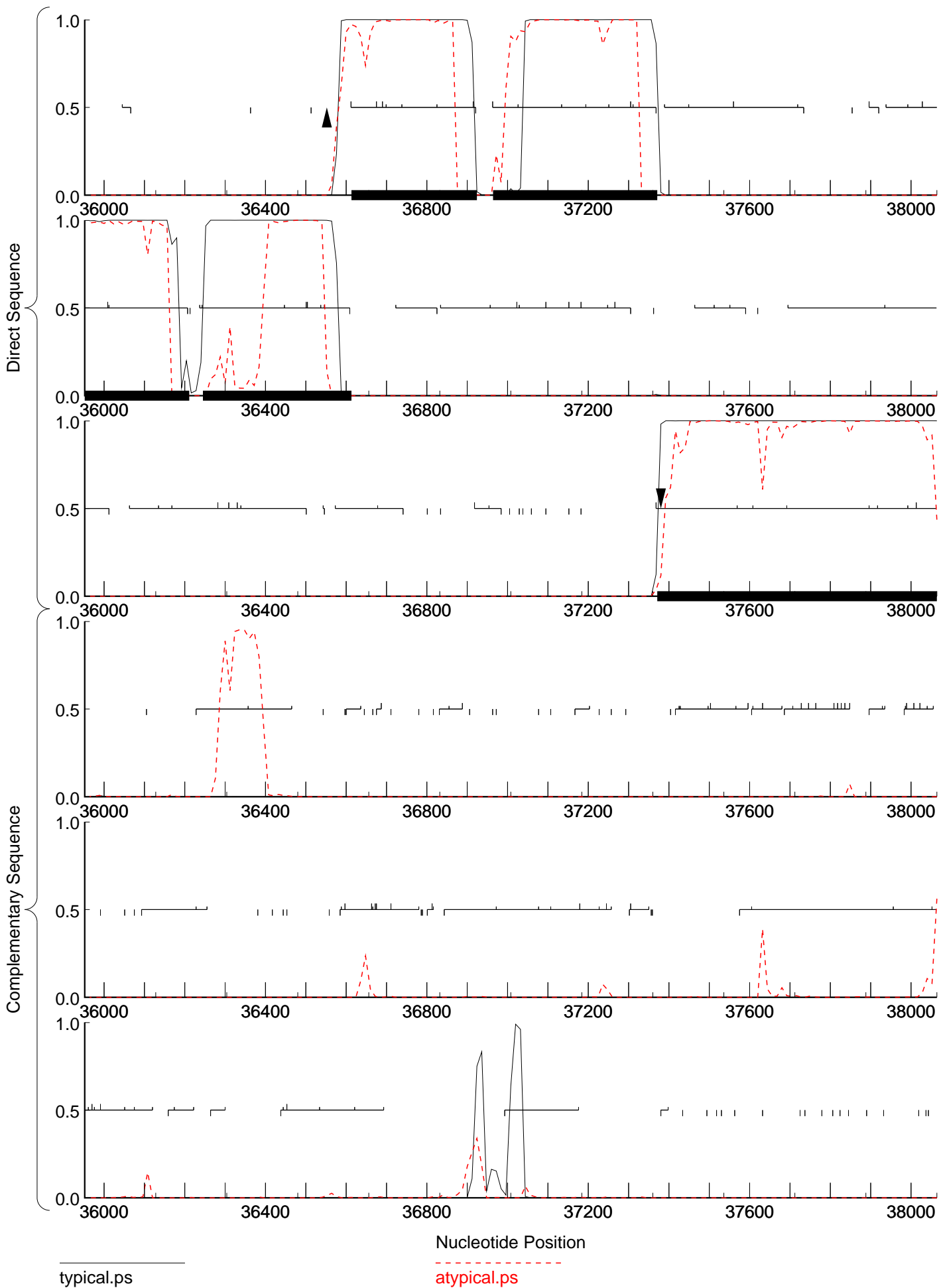


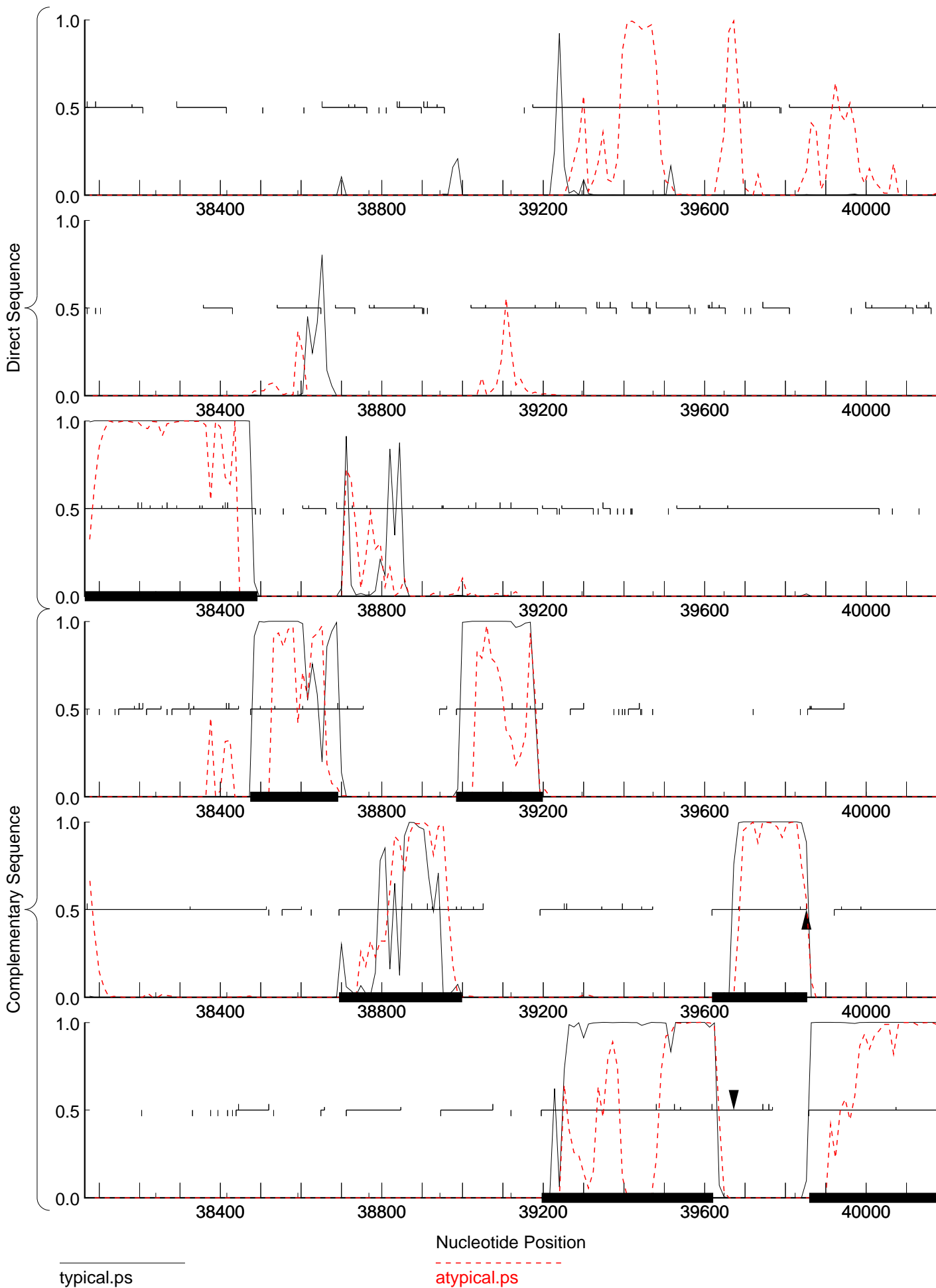


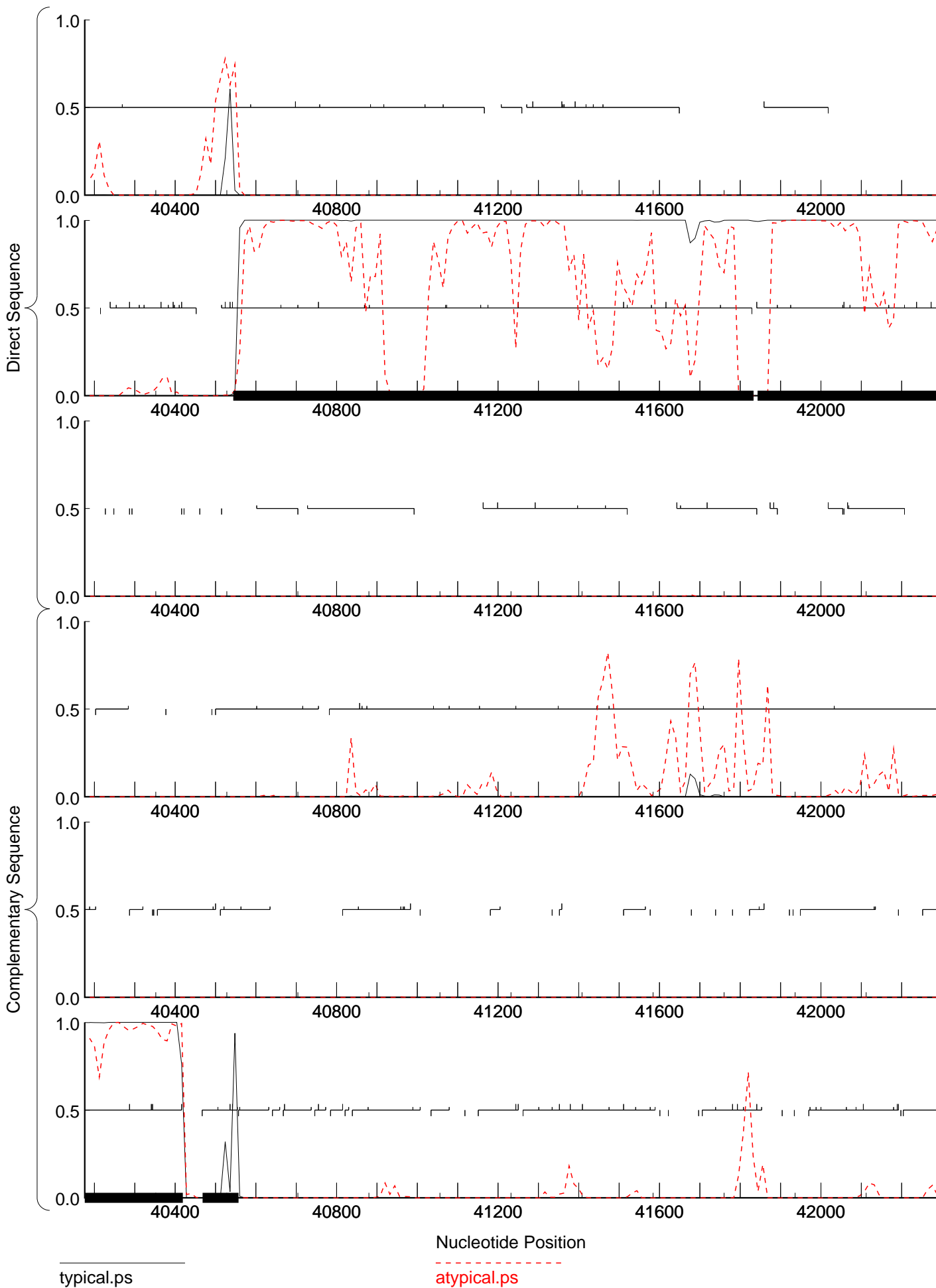
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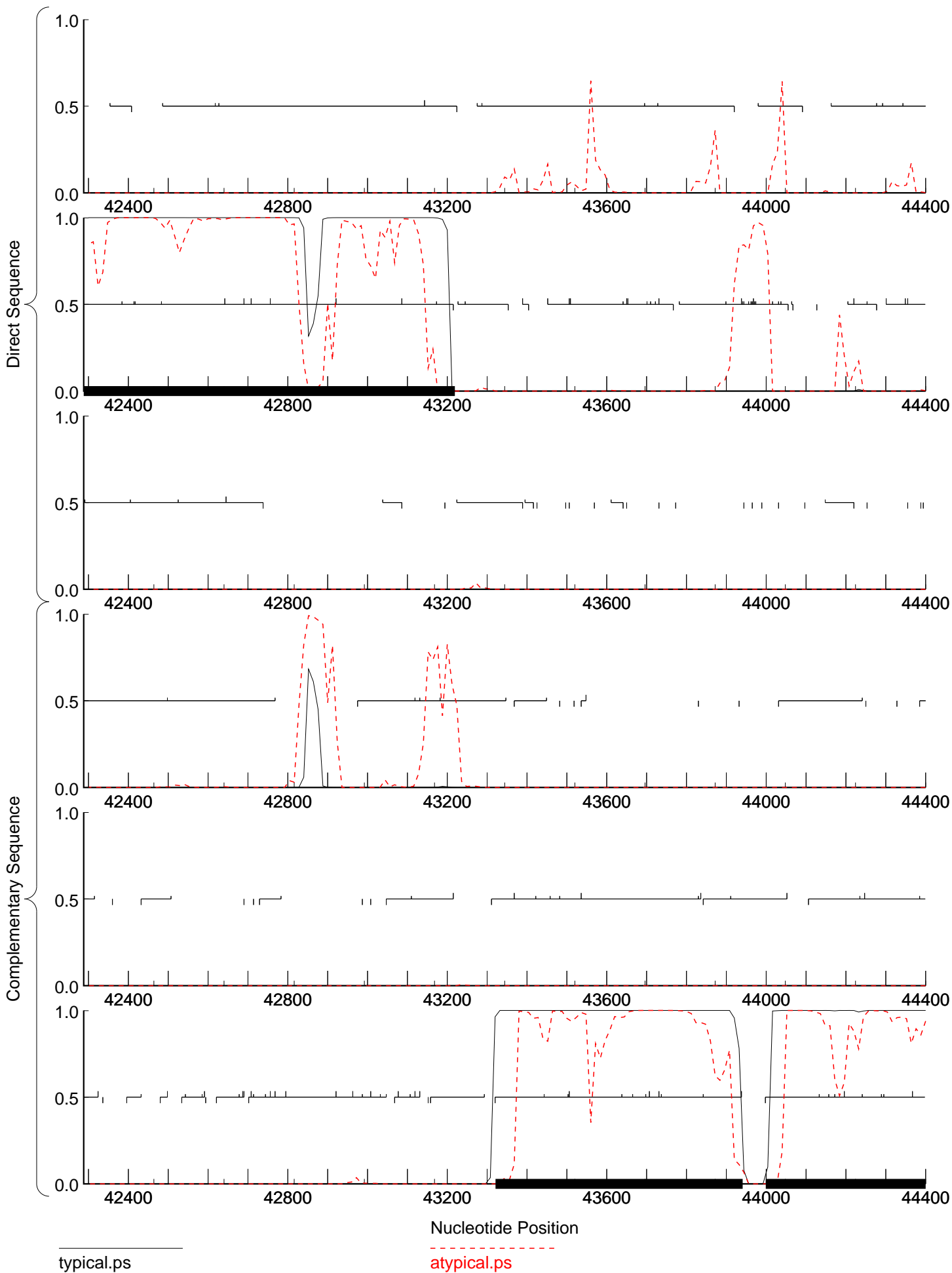
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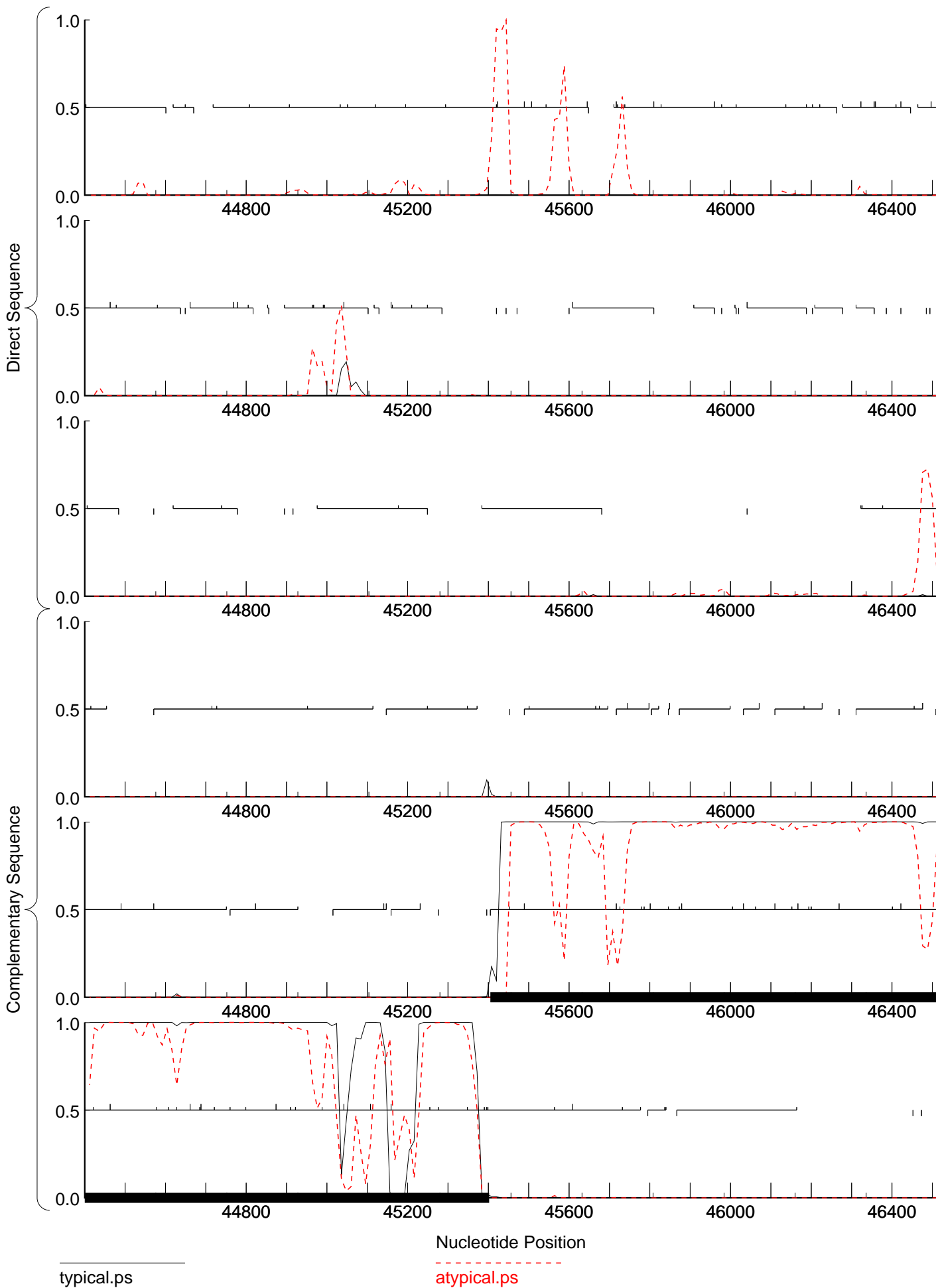


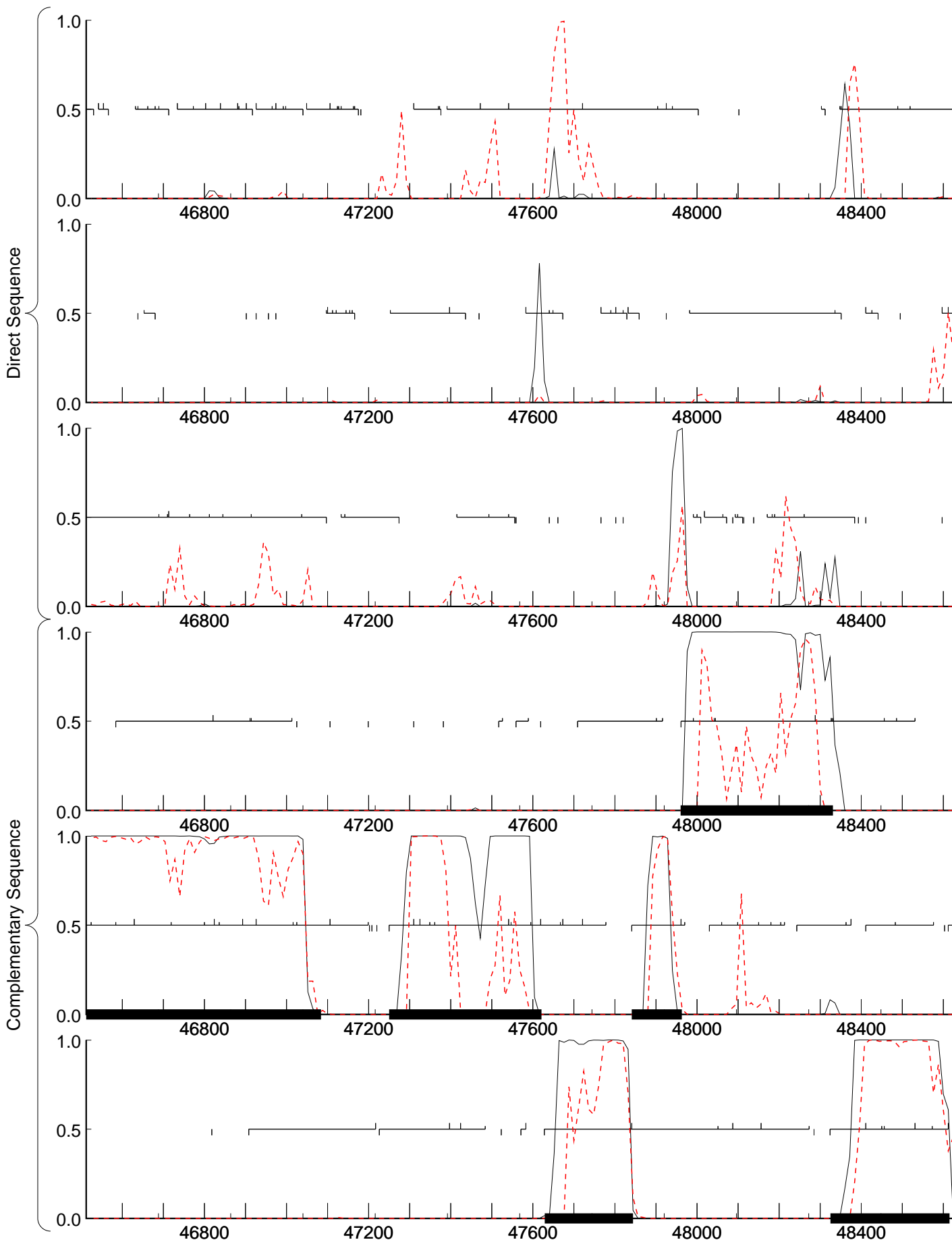






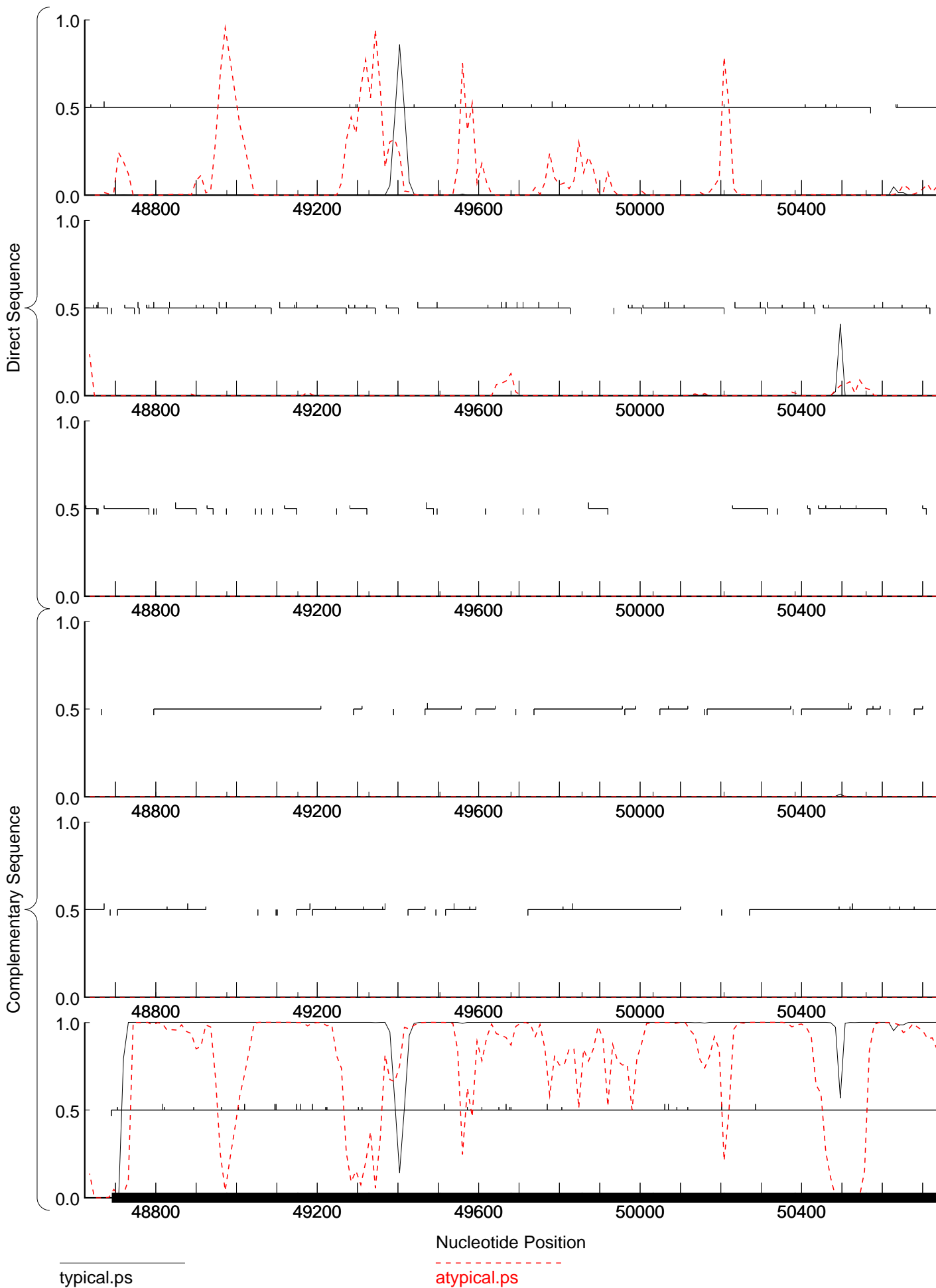


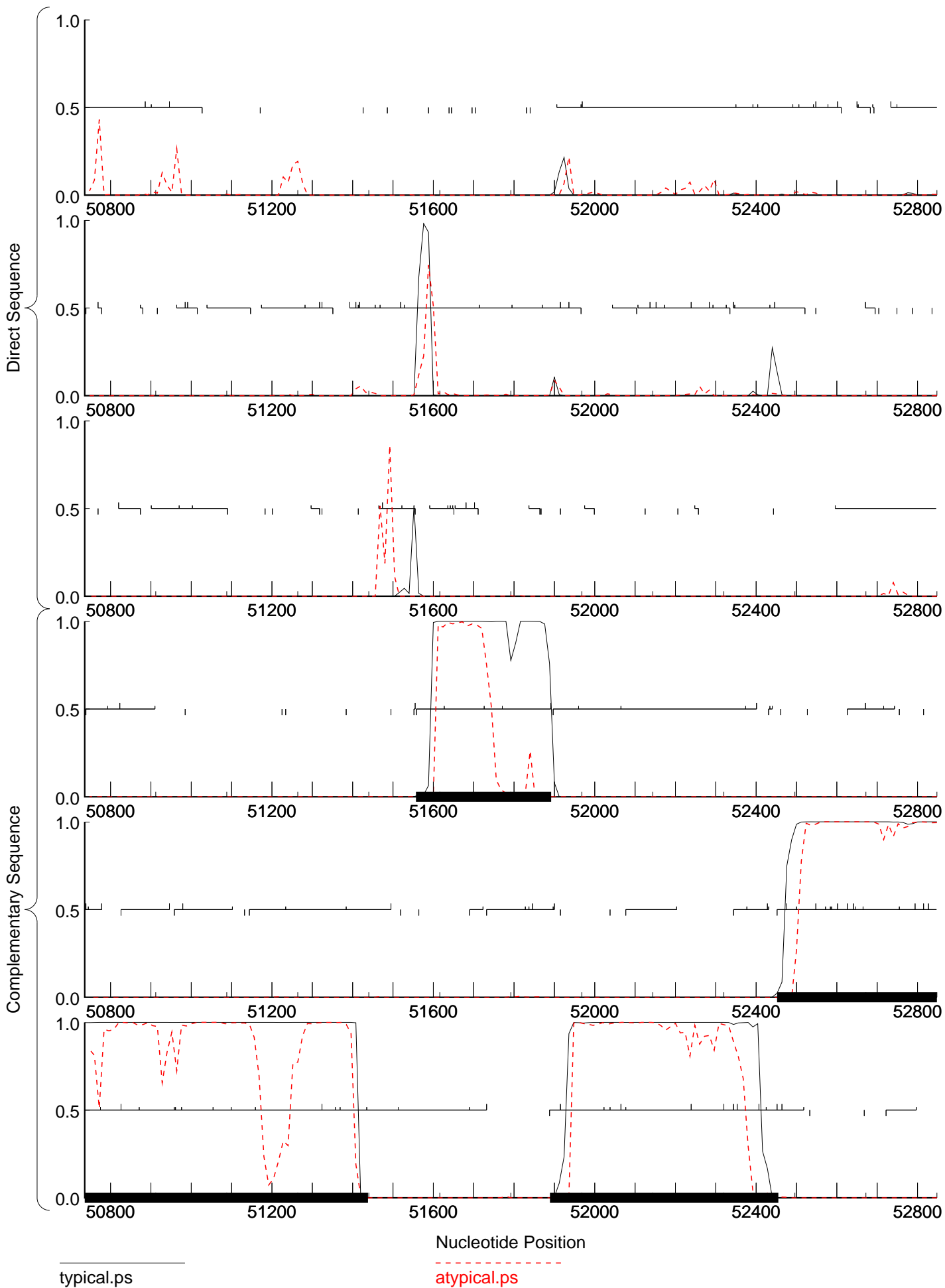


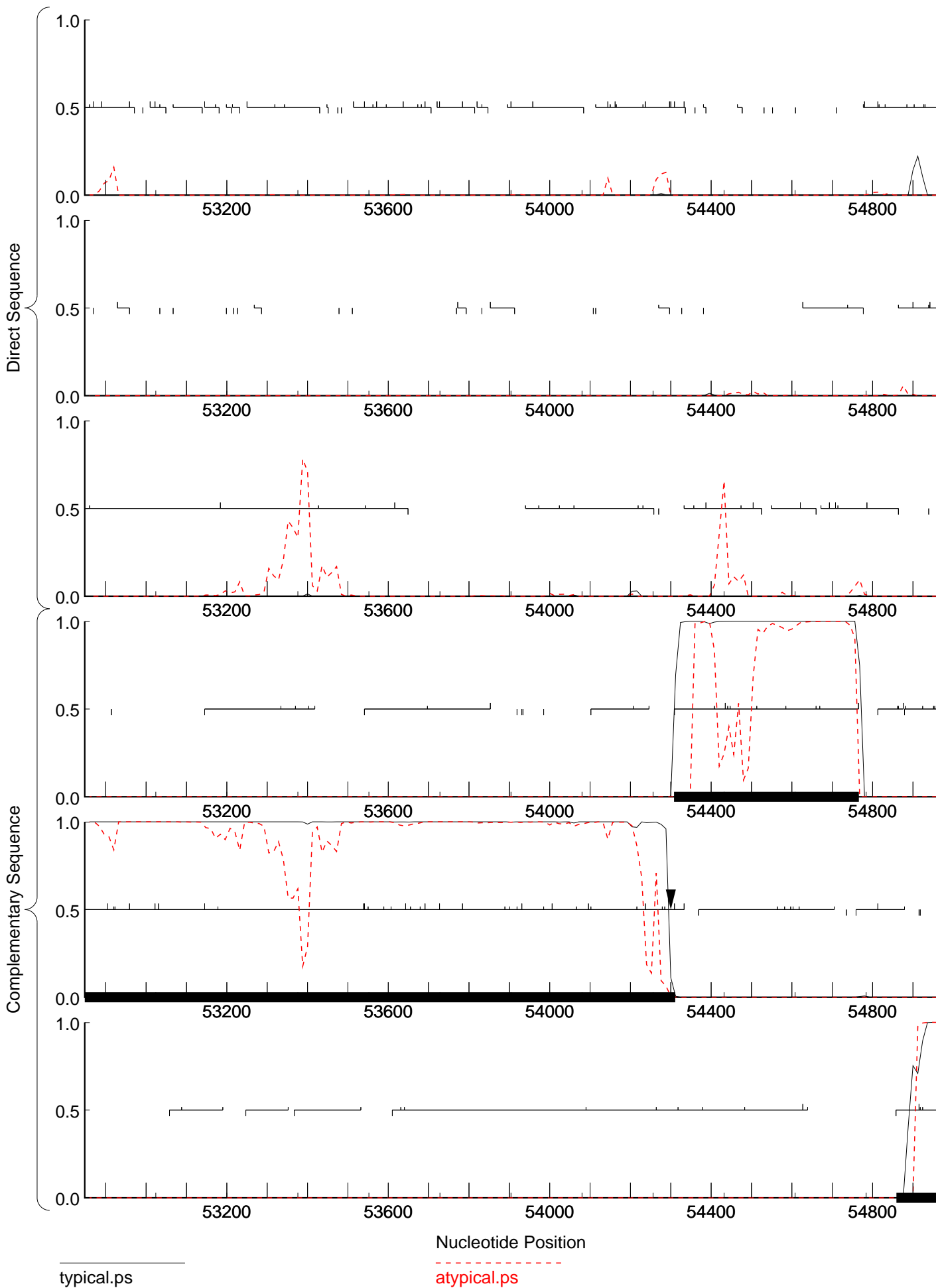


typical.ps

atypical.ps

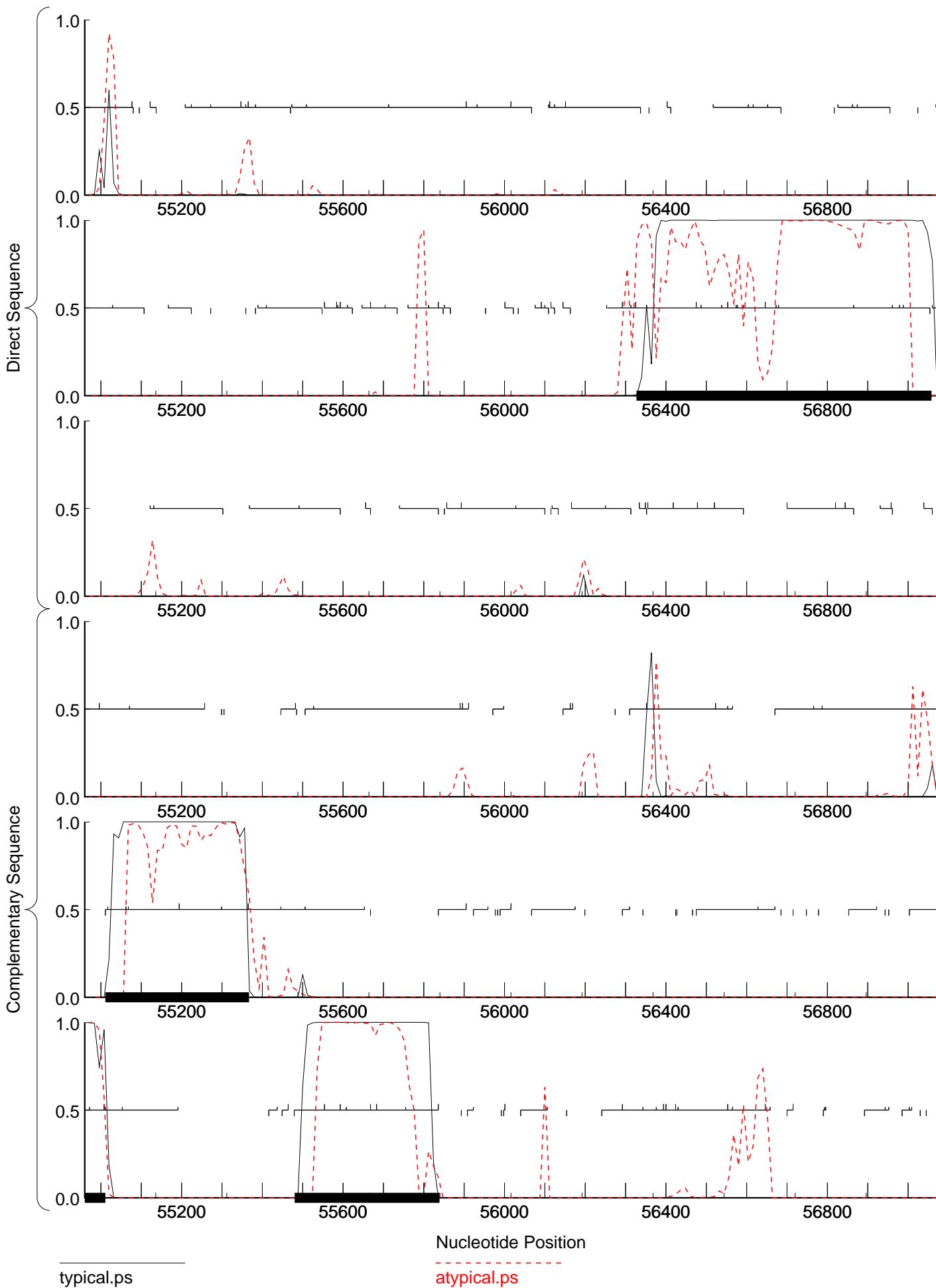


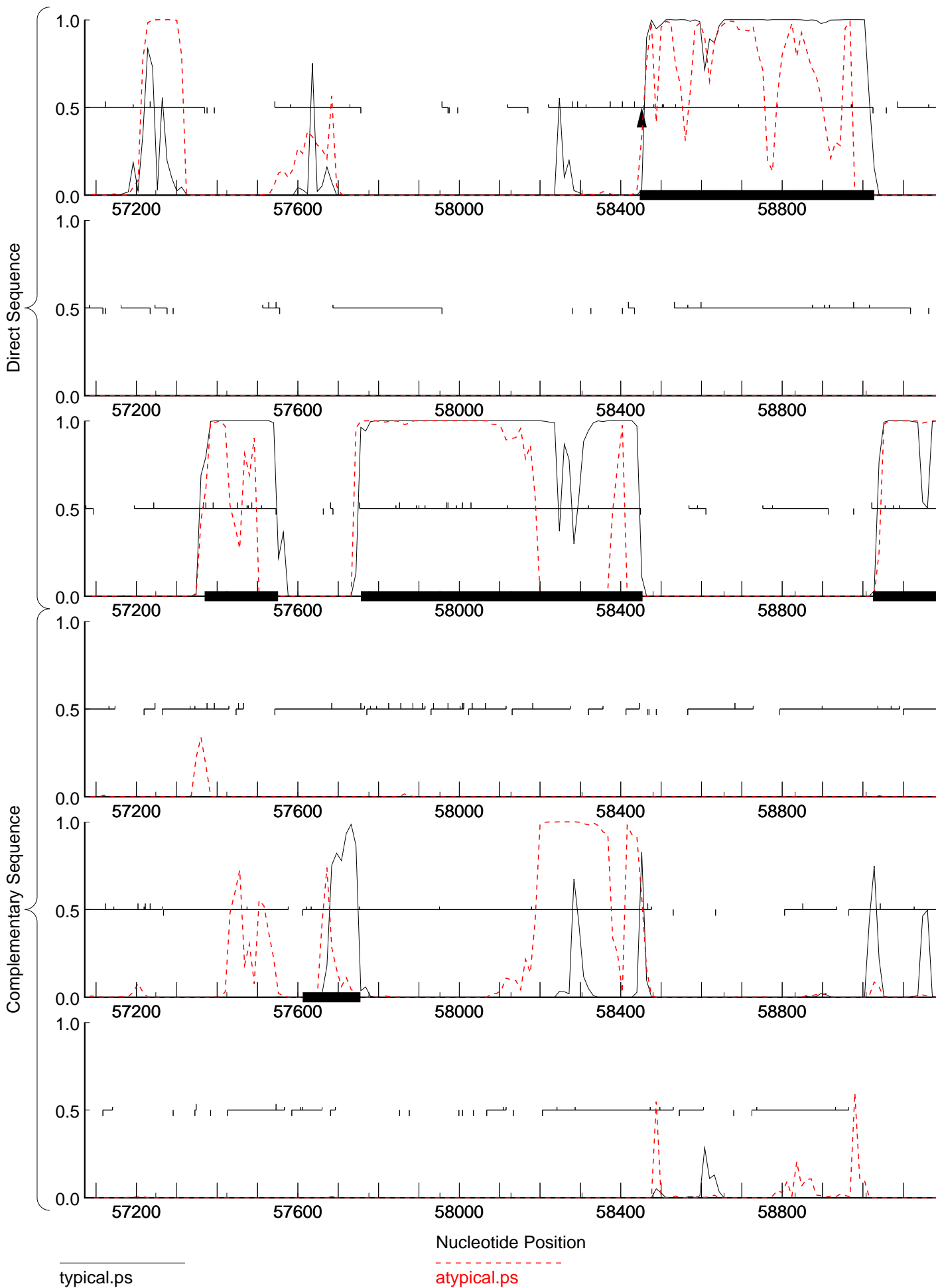


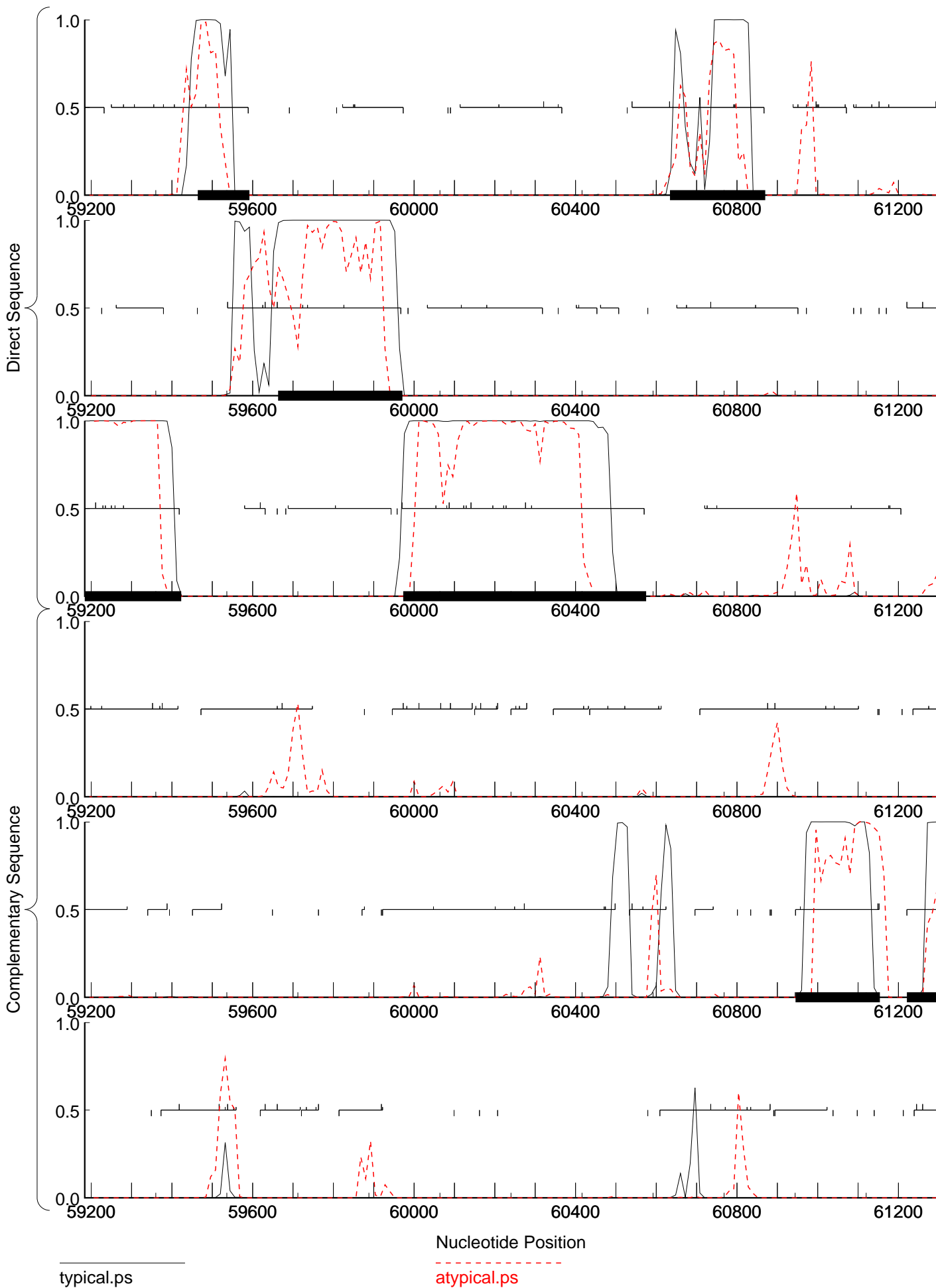


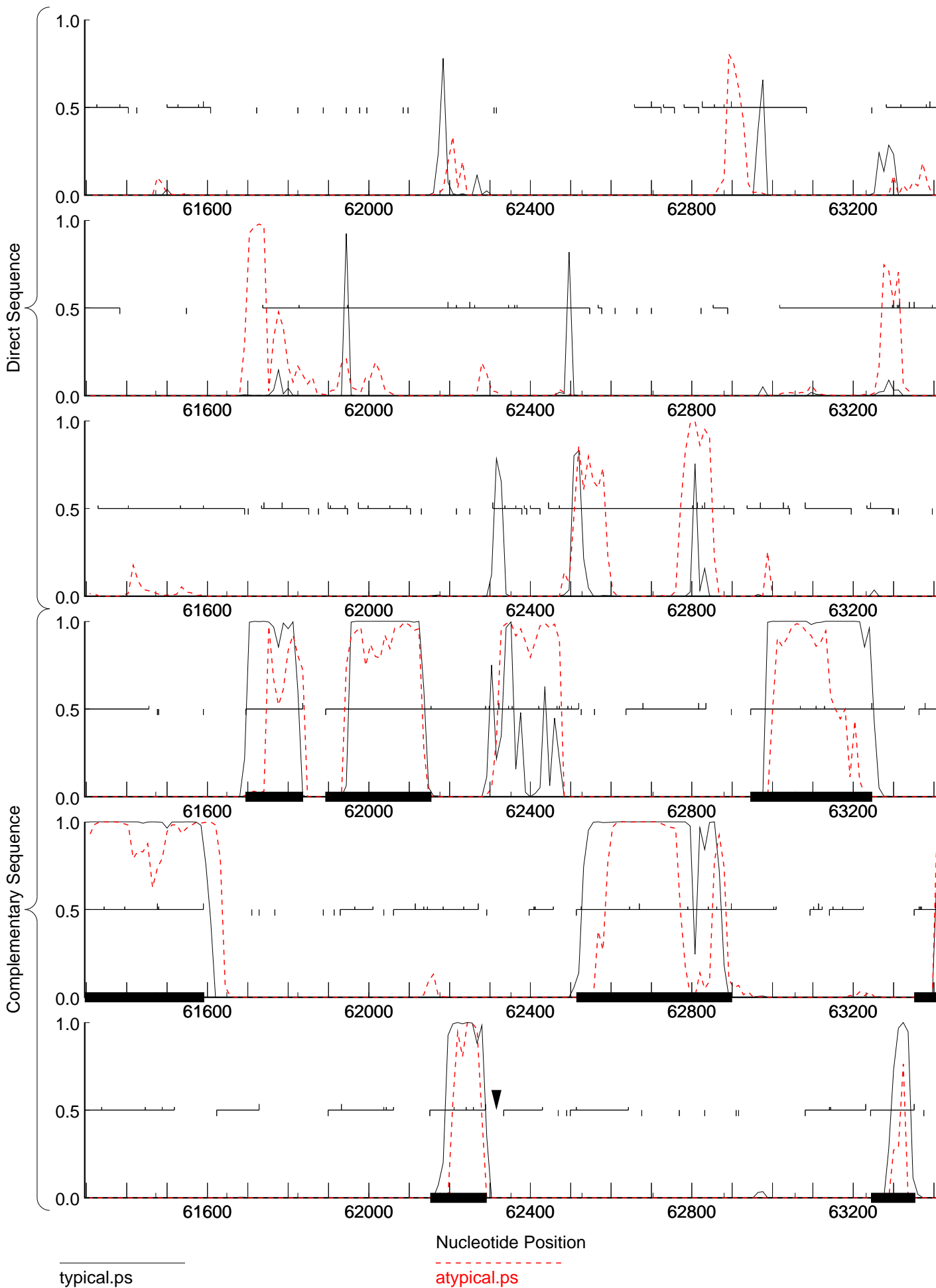
typical.ps

atypical.ps









typical.ps

atypical.ps

