

GeneMark

Version 2.5p (09.08.06)

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PROGRAM INFORMATION

Sequence : Mycobacterium phage SDcharge11 complete sequence, 67702 bp, circularly permuted, Cluster B1
Analysis Date : 7/16/18 at 12:26:05
Pages : 34
Sequence Length : 67702 bp
GC Content : 66.52%

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,

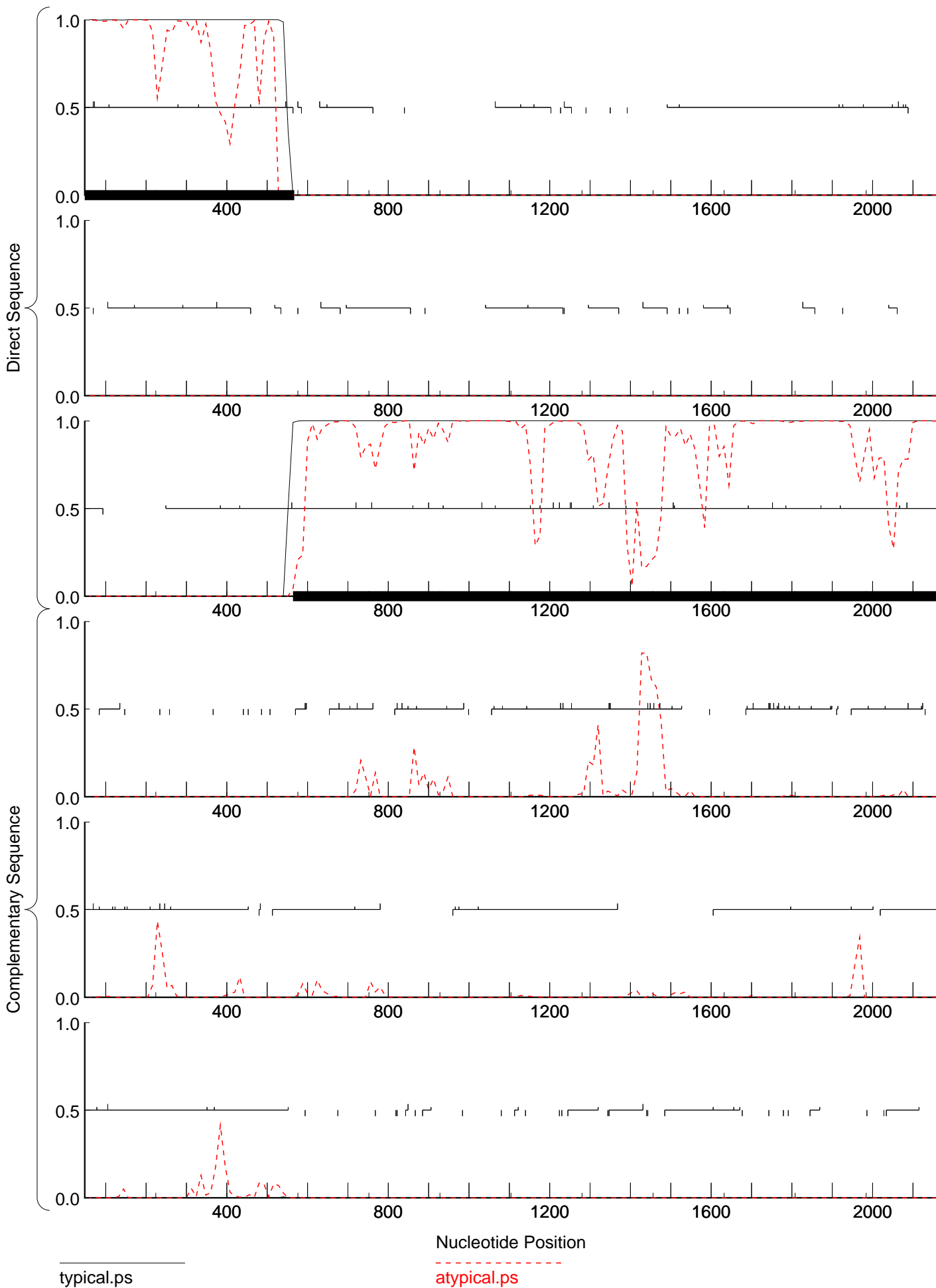
MATRIX INFORMATION

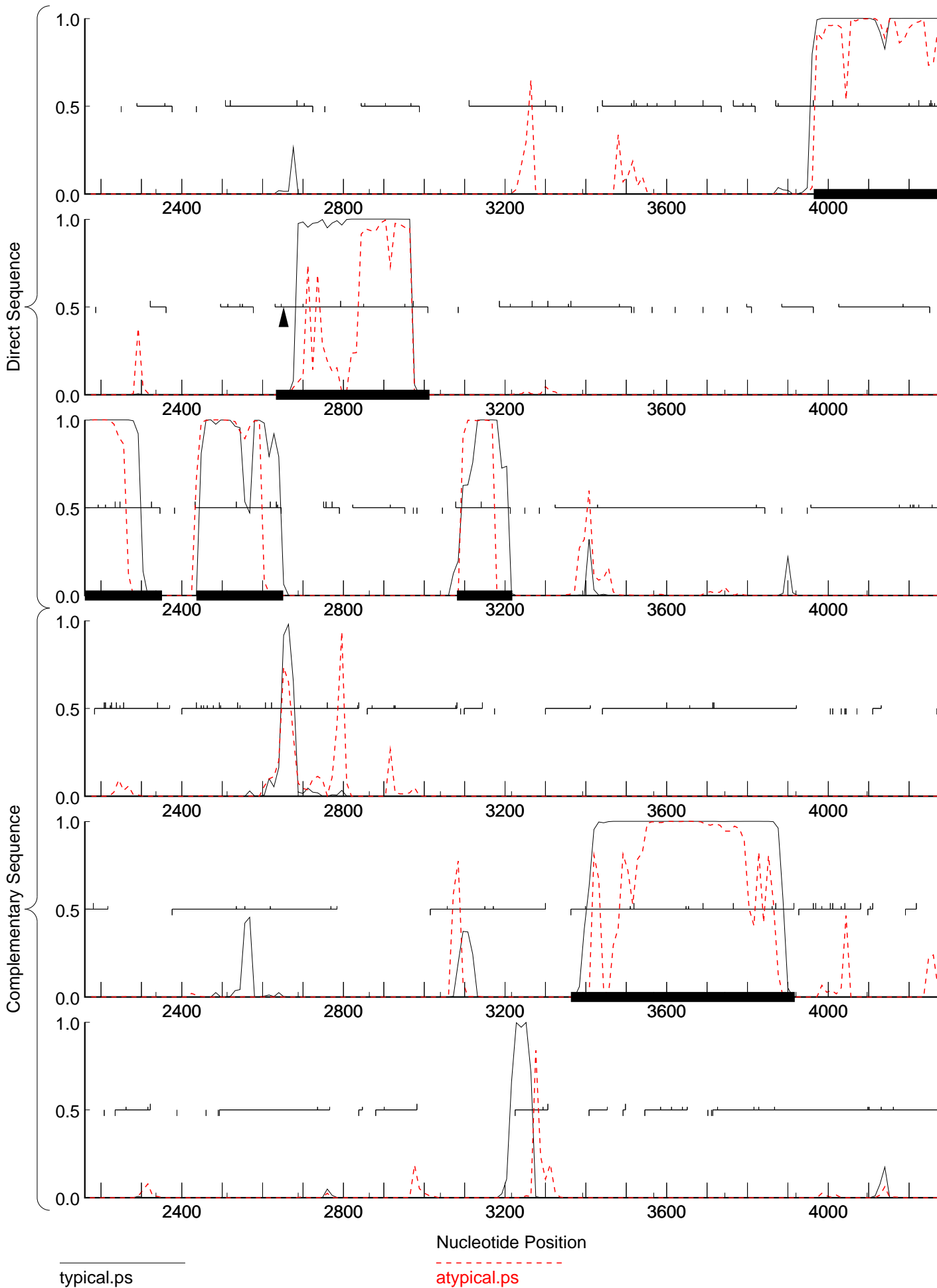
Matrix : -
Author : -
Order : 4

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

Matrix notes & comments

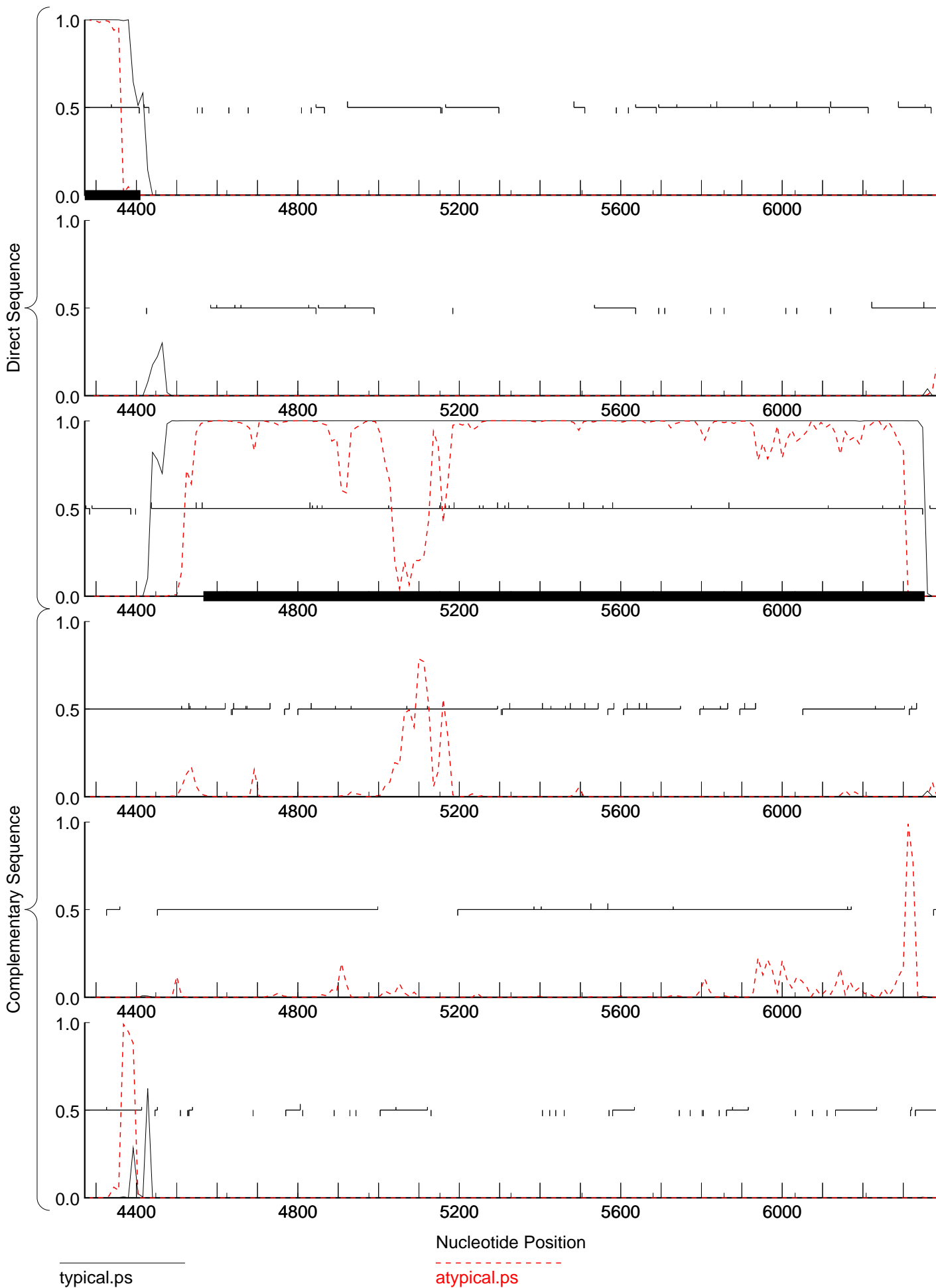
Training set derived by GeneMarkS, 4.30 October 2014
Mon Jul 16 12:26:04 2018

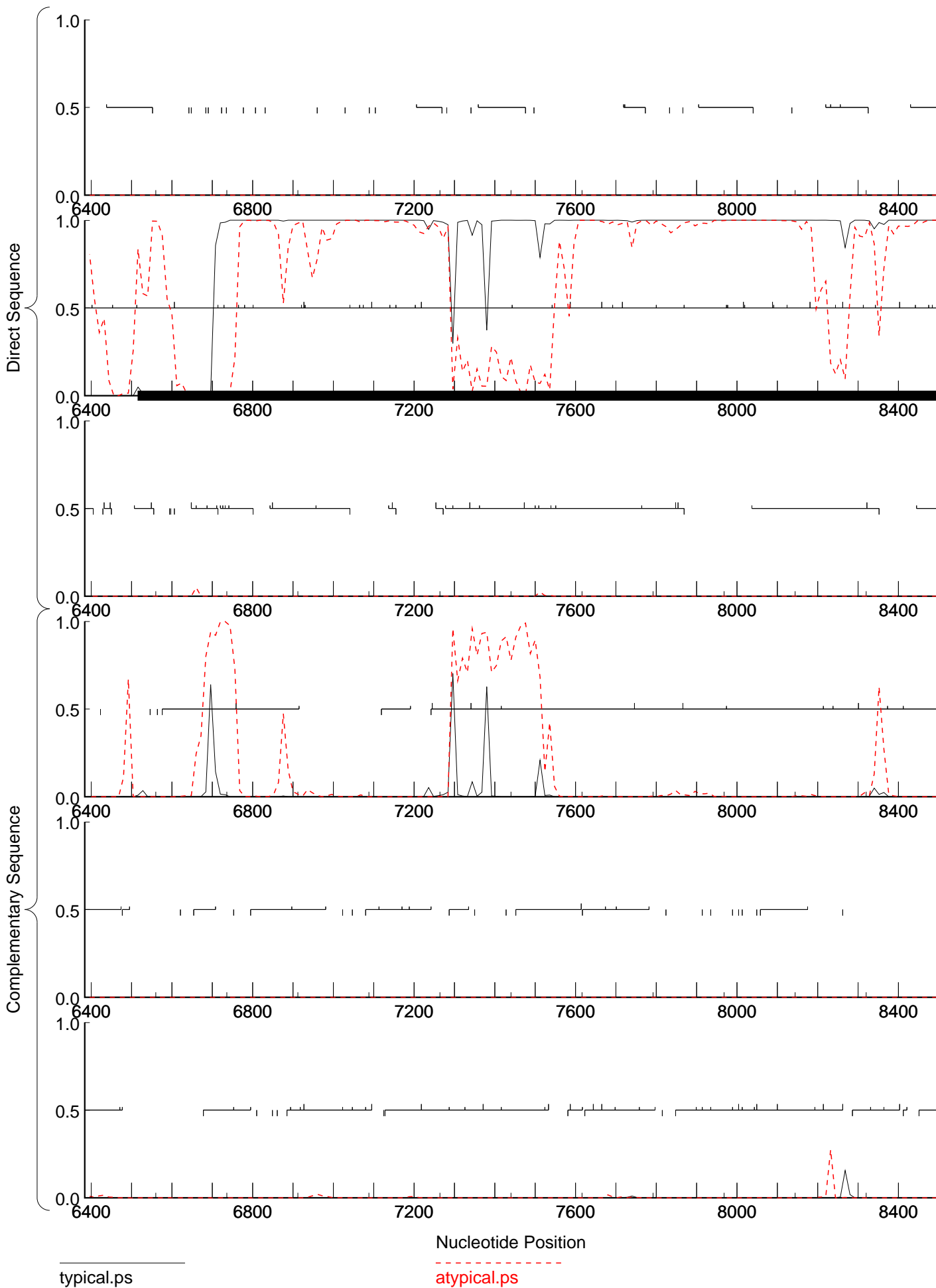




typical.ps

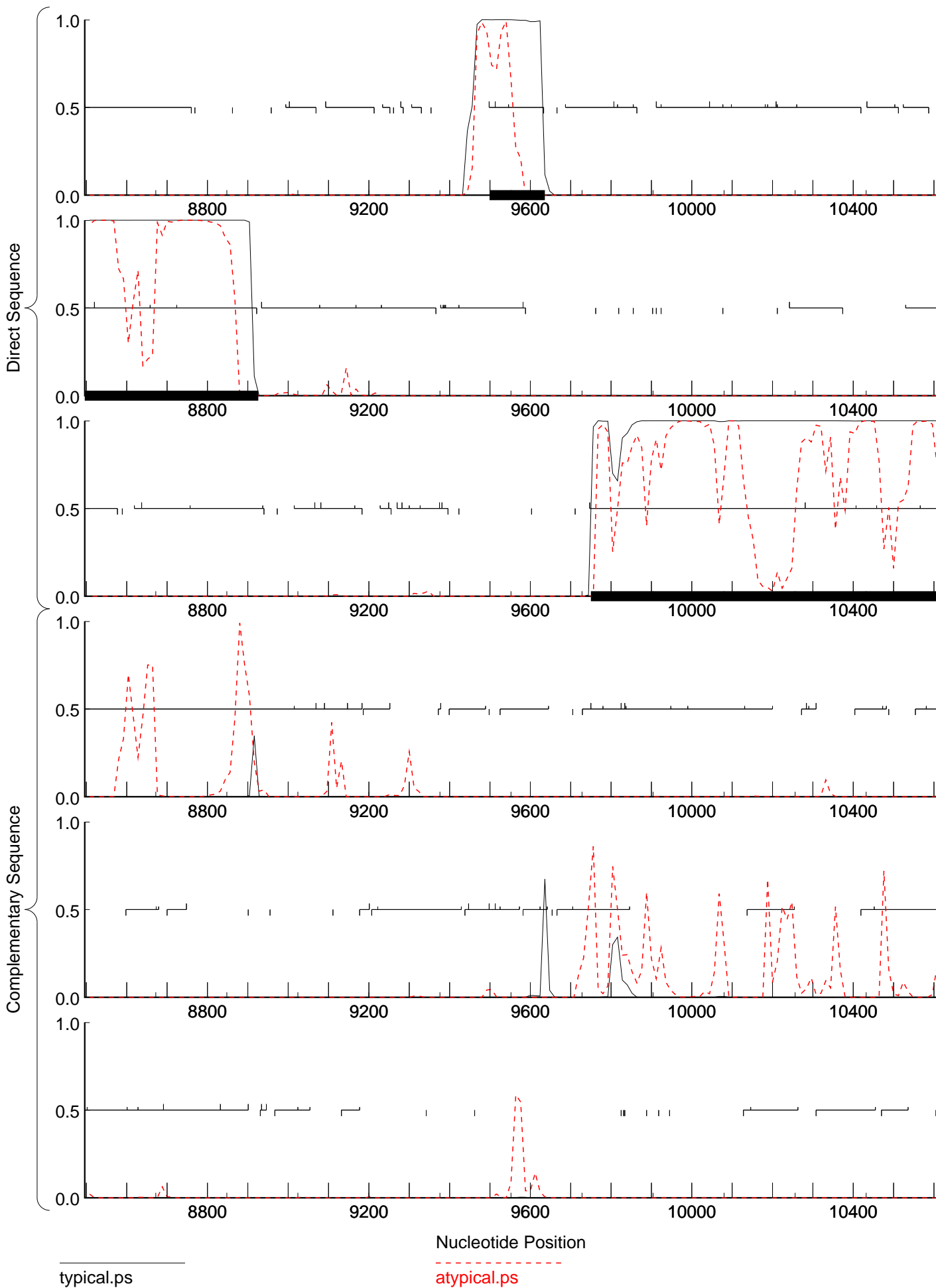
atypical.ps

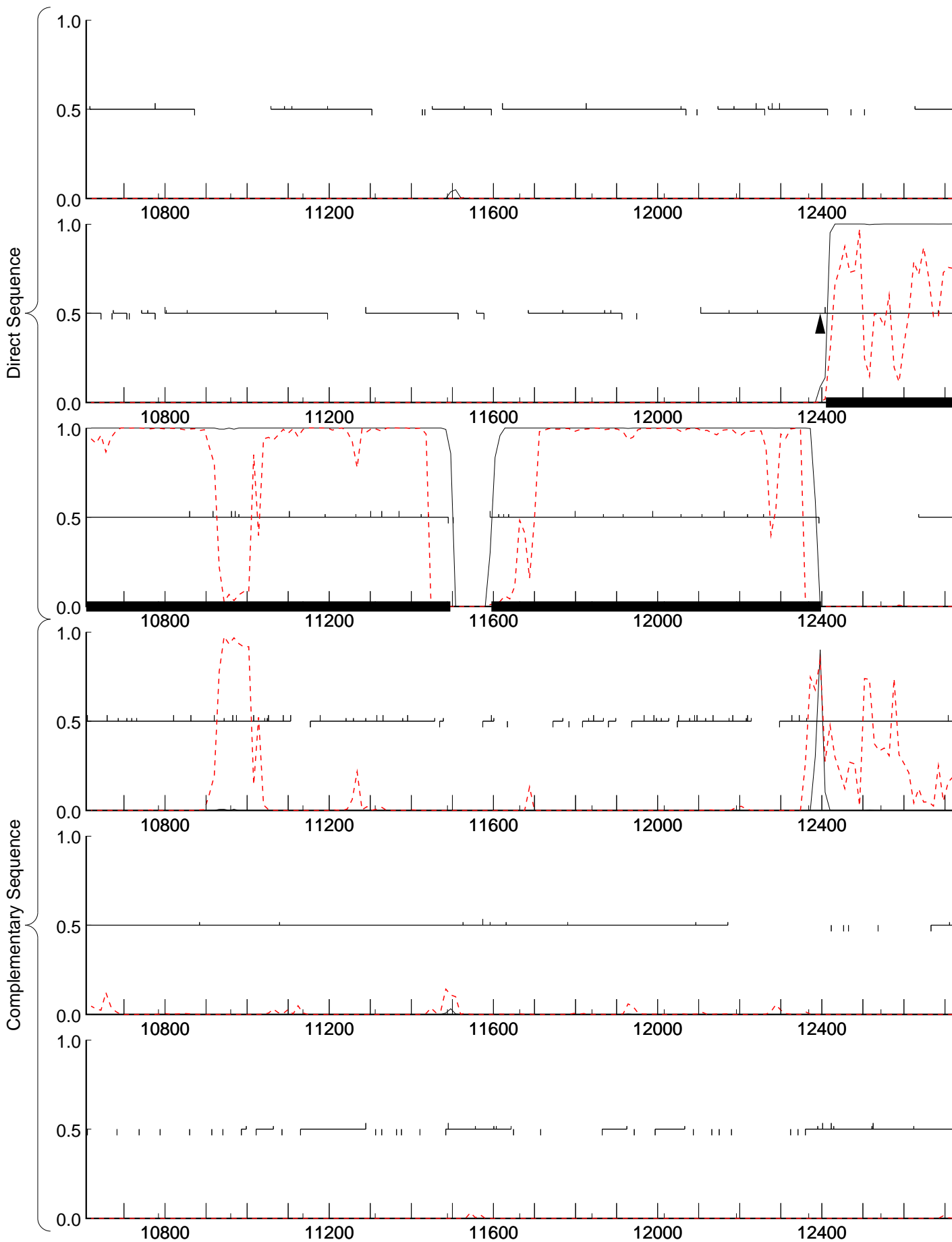




typical.ps

atypical.ps

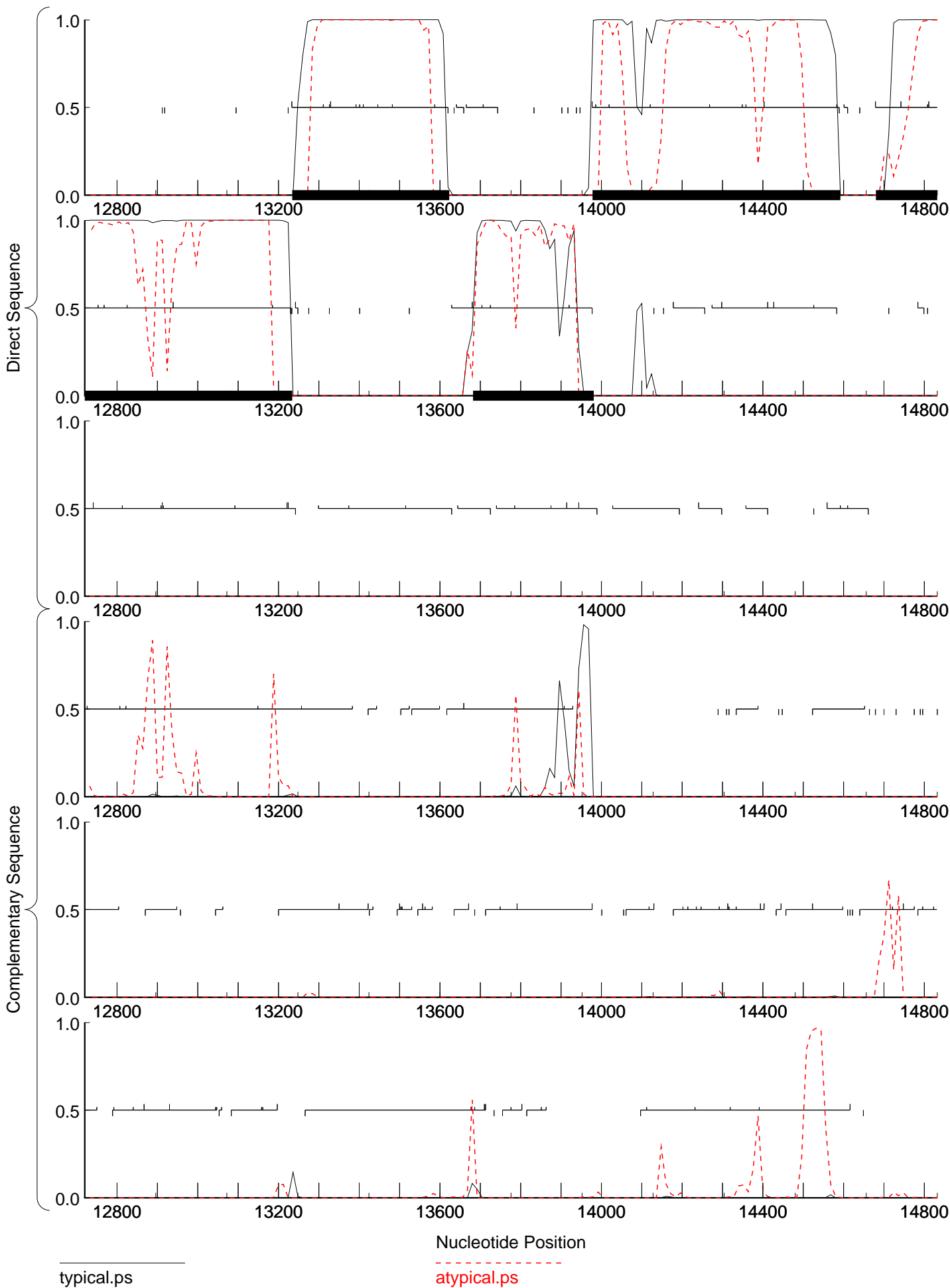


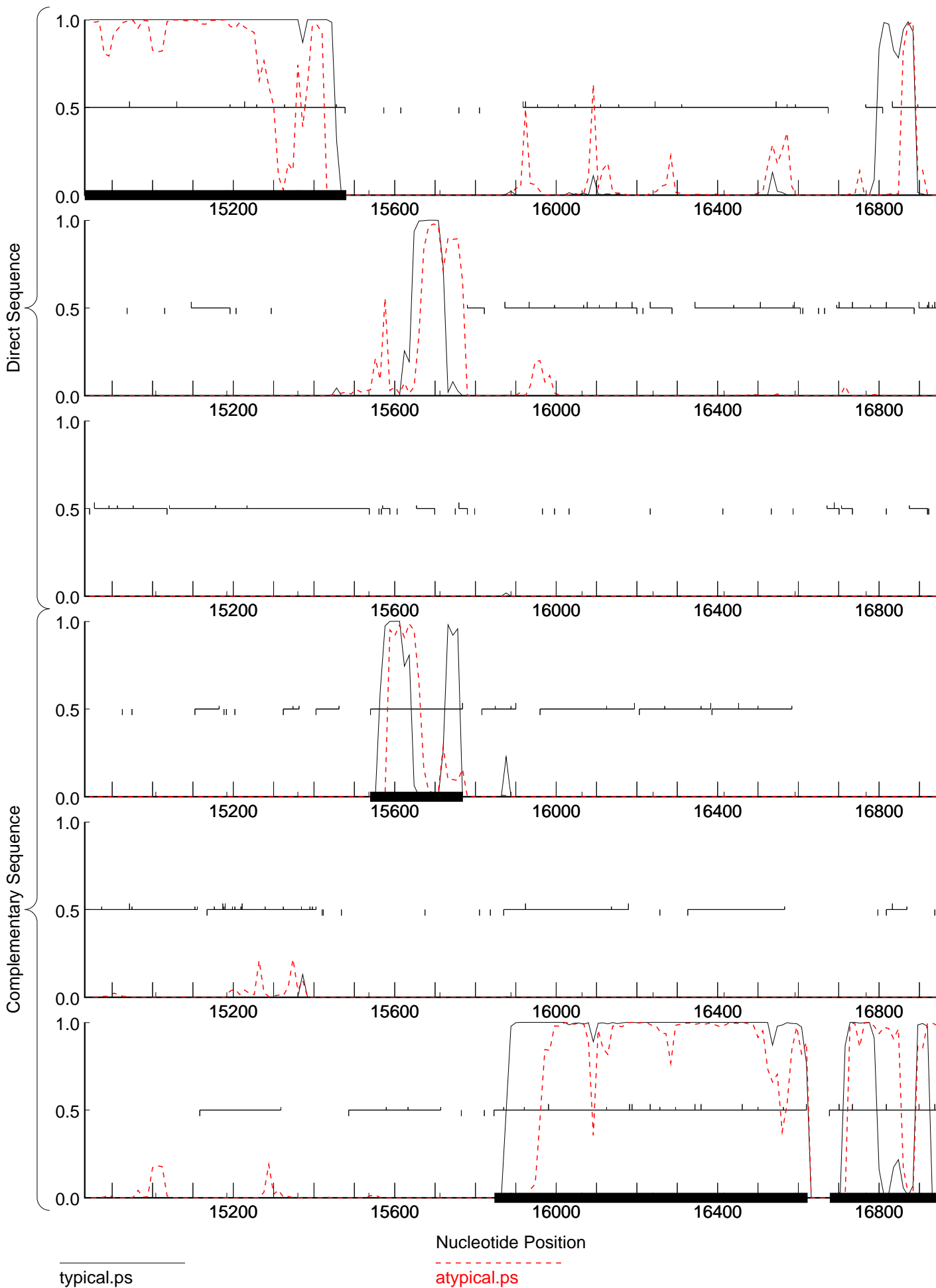


typical.ps

Nucleotide Position

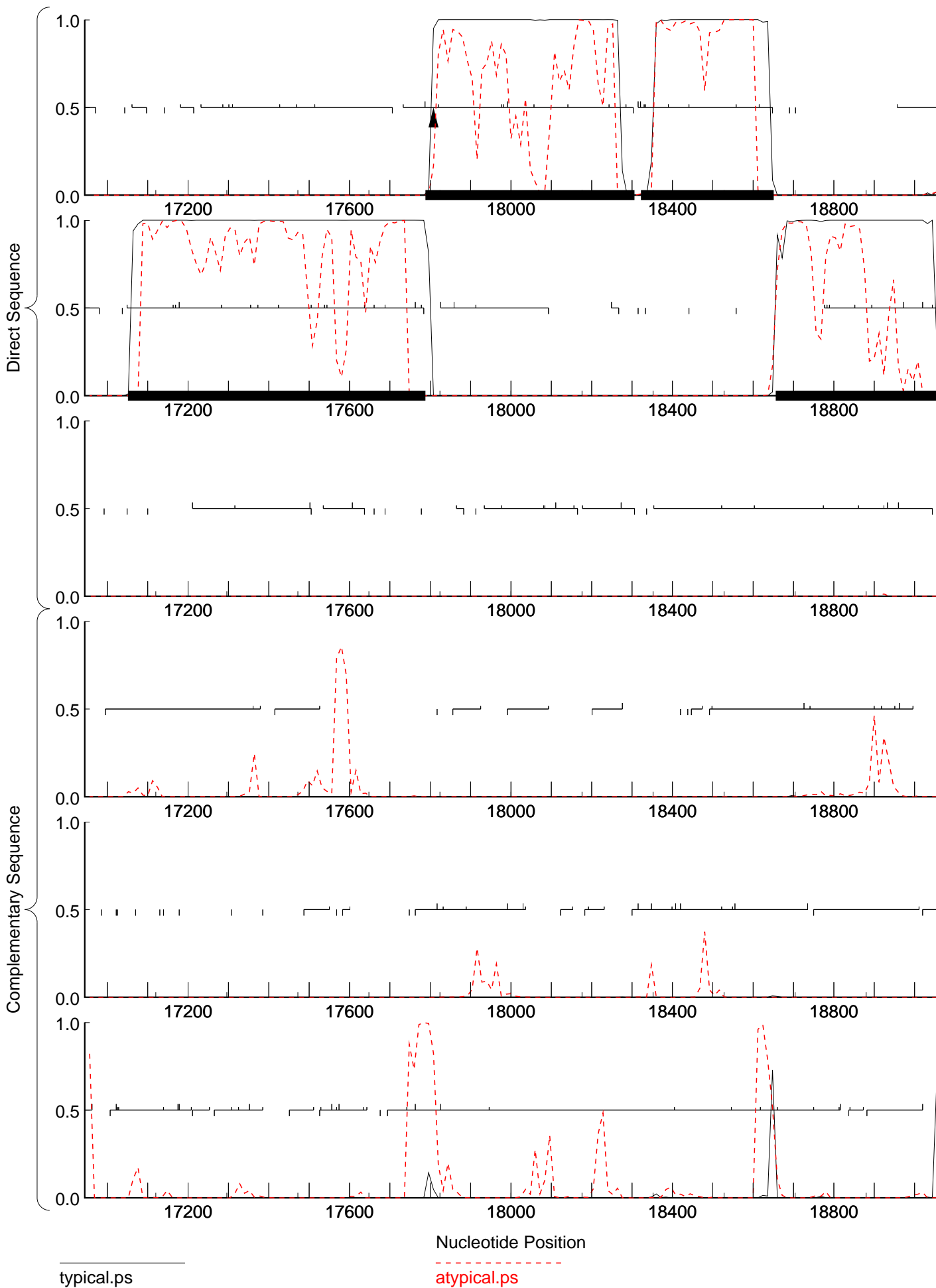
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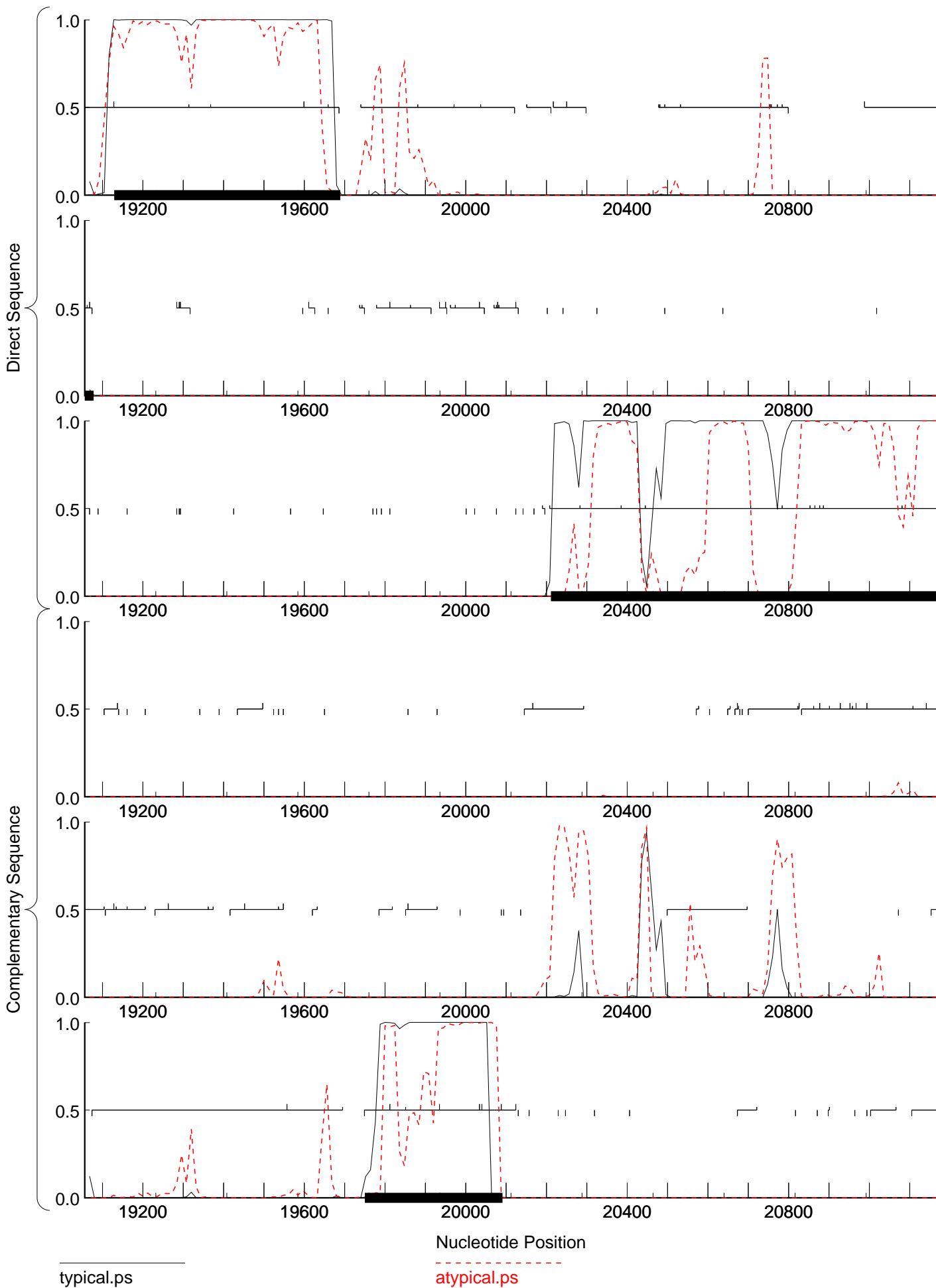




typical.ps

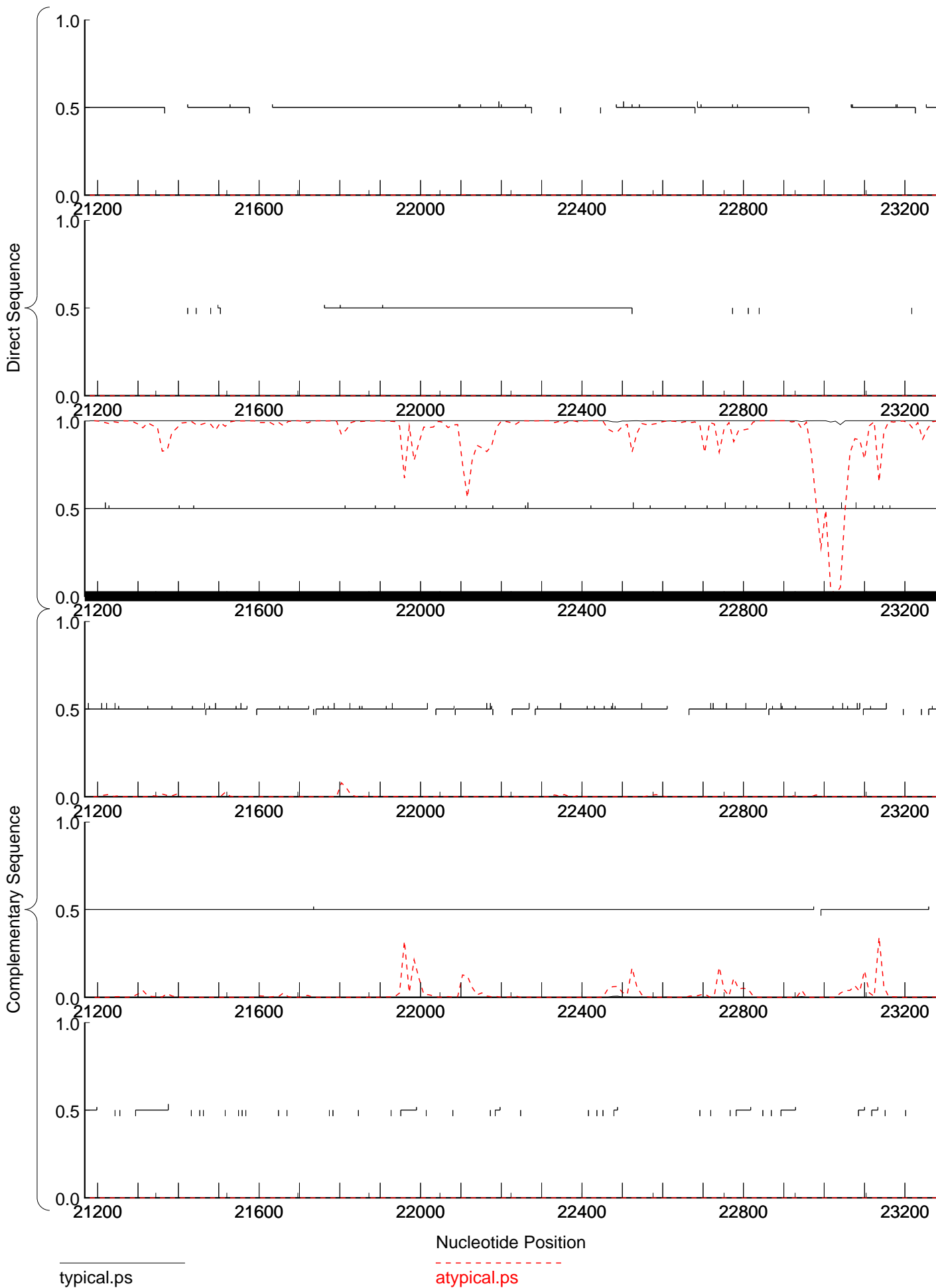
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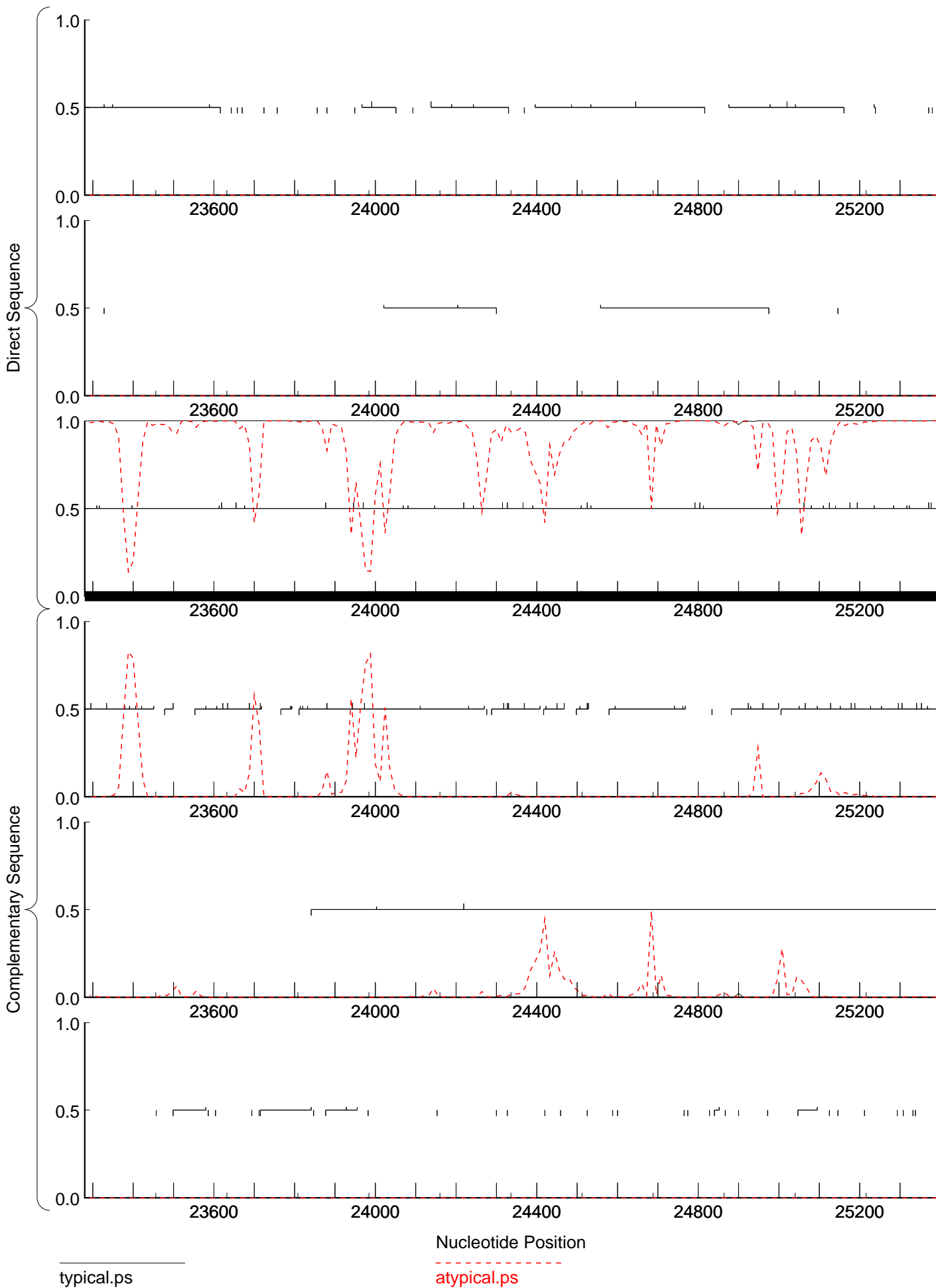


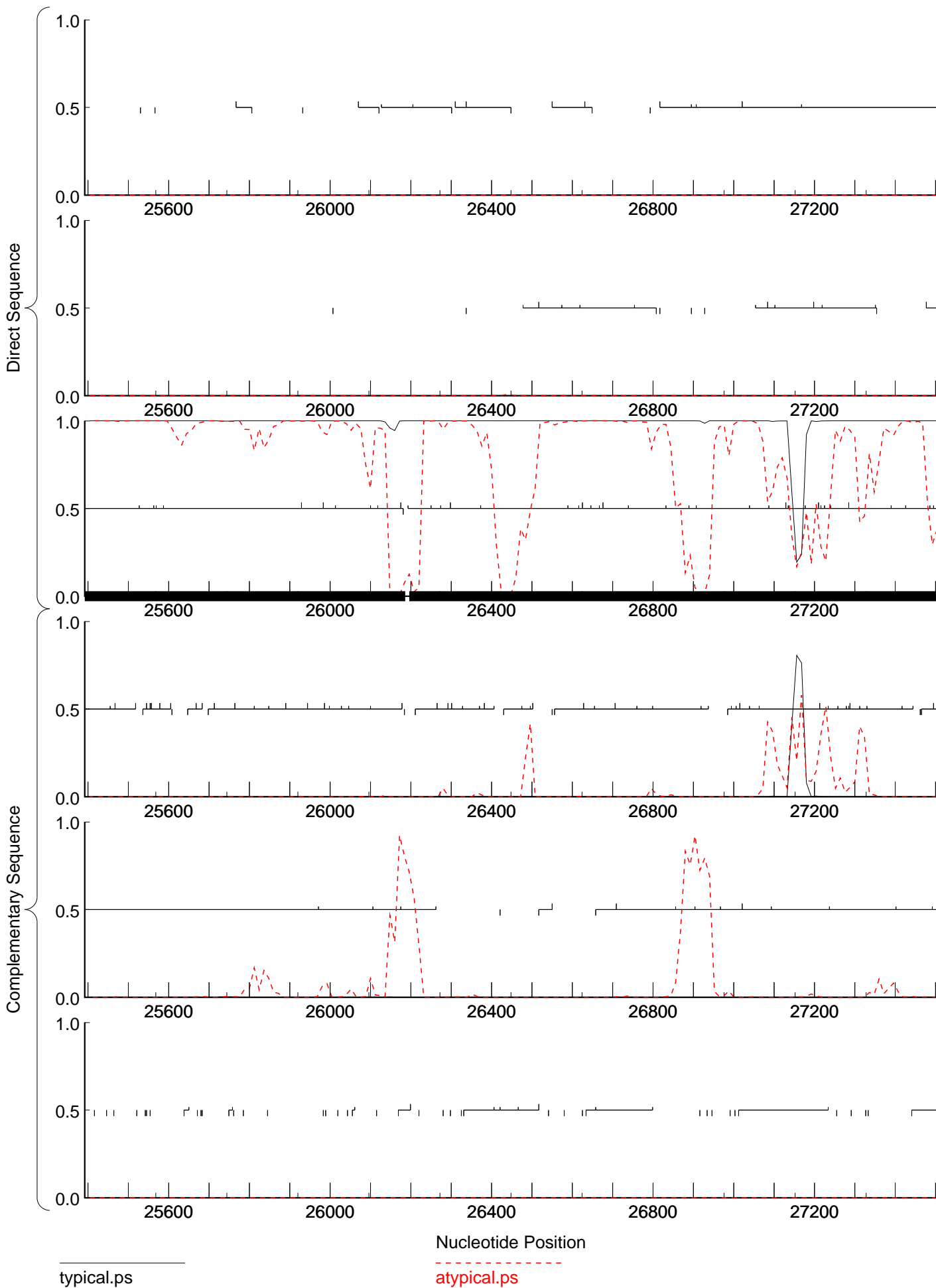


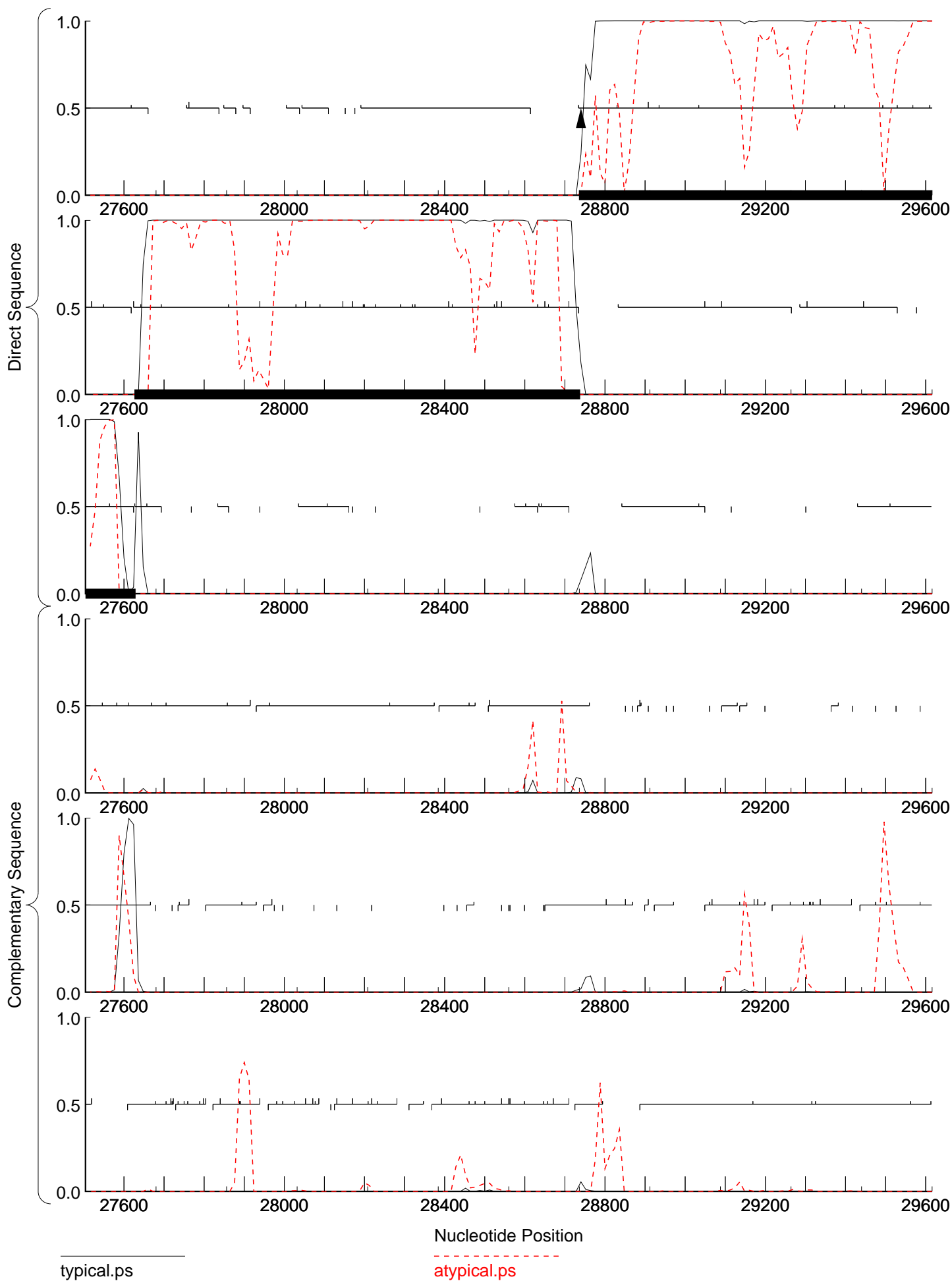
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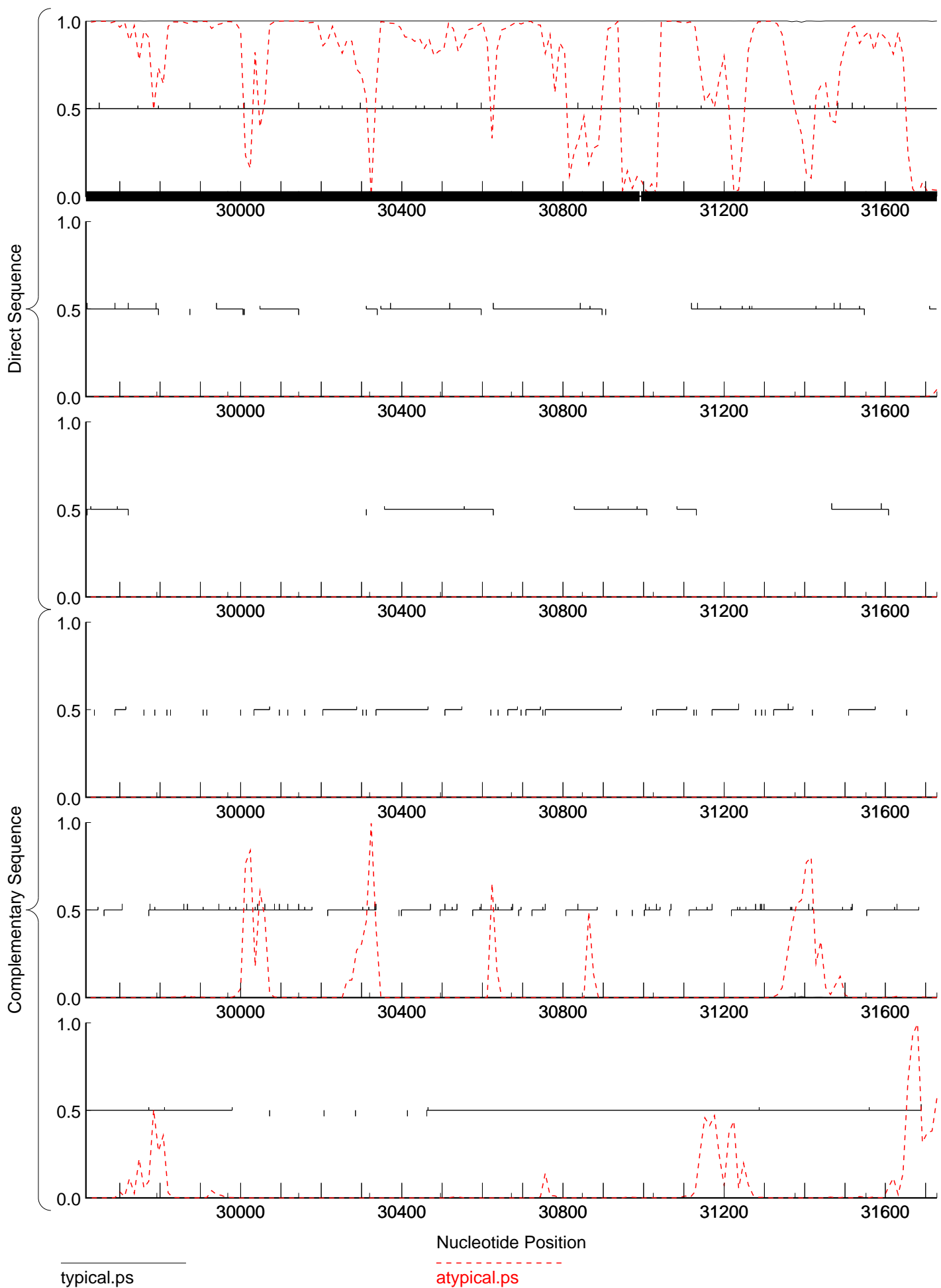
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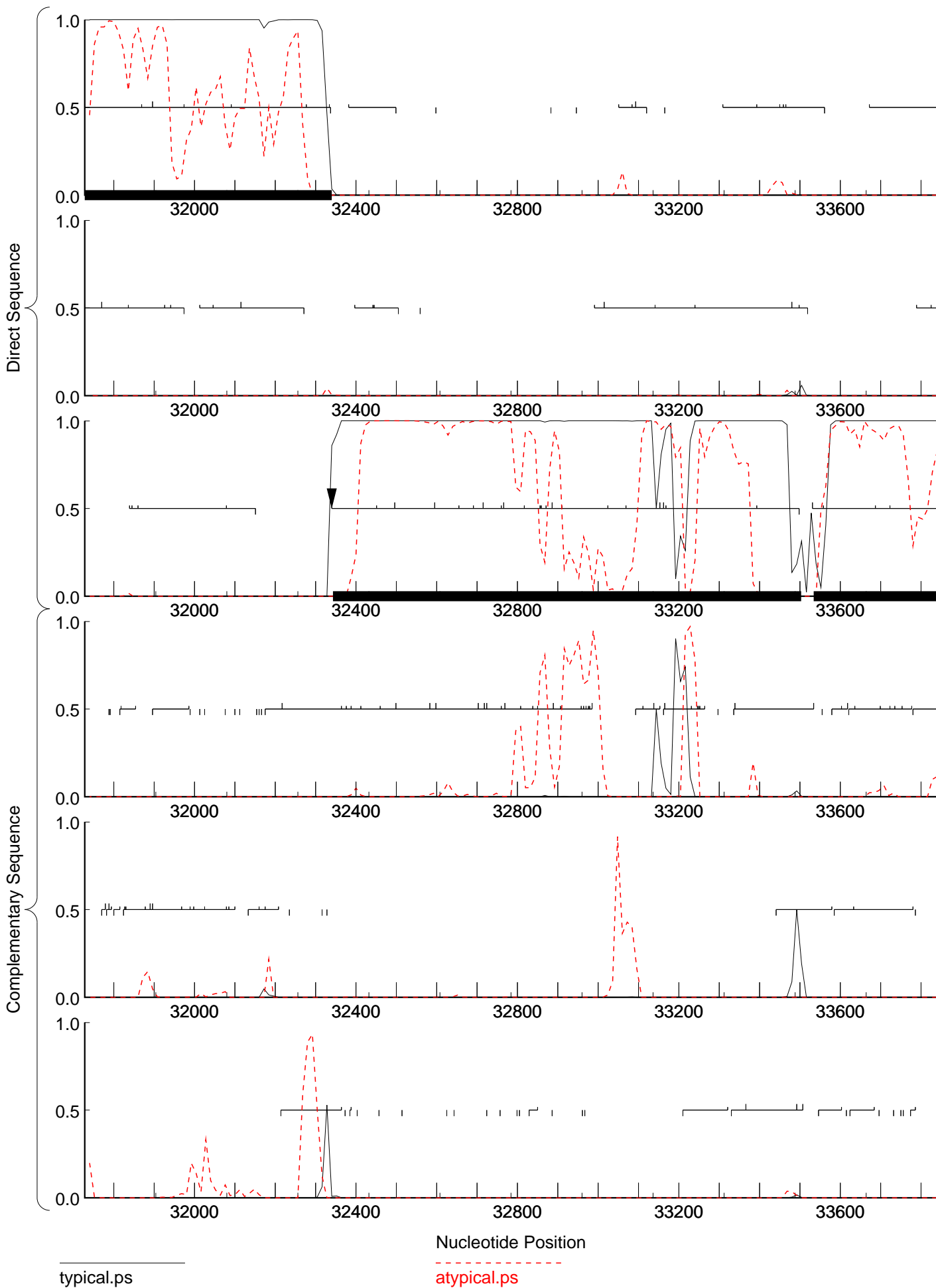


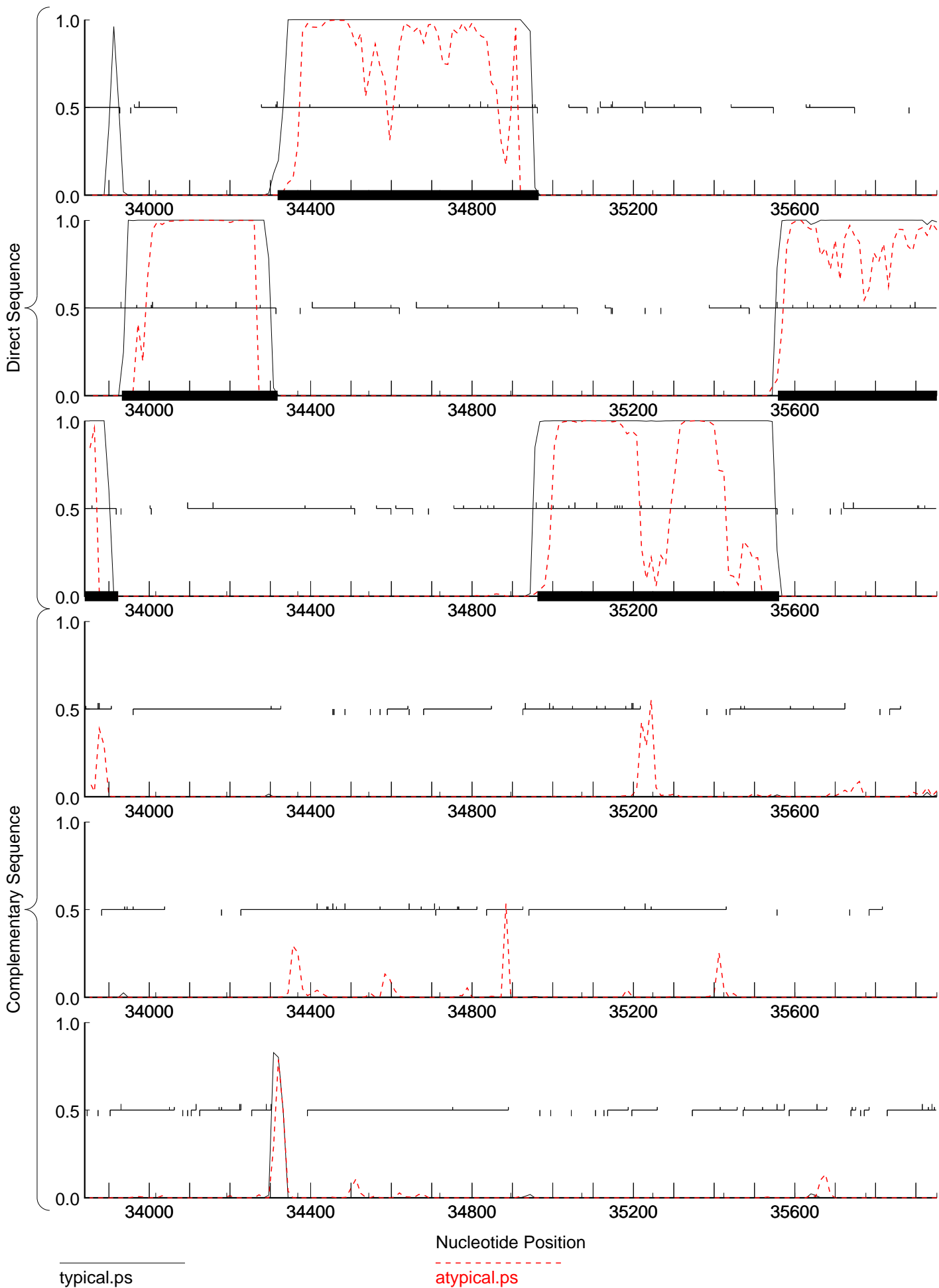


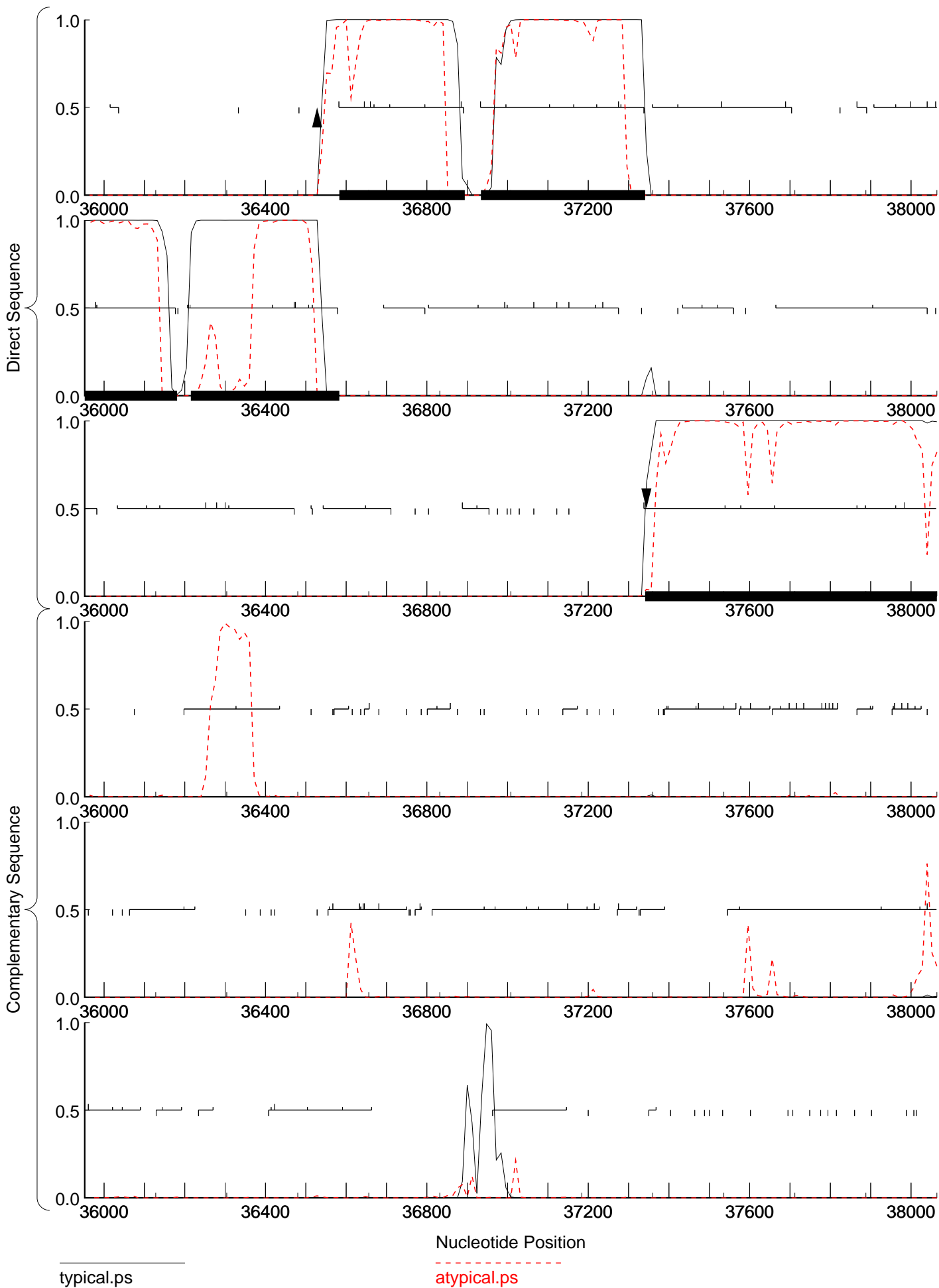


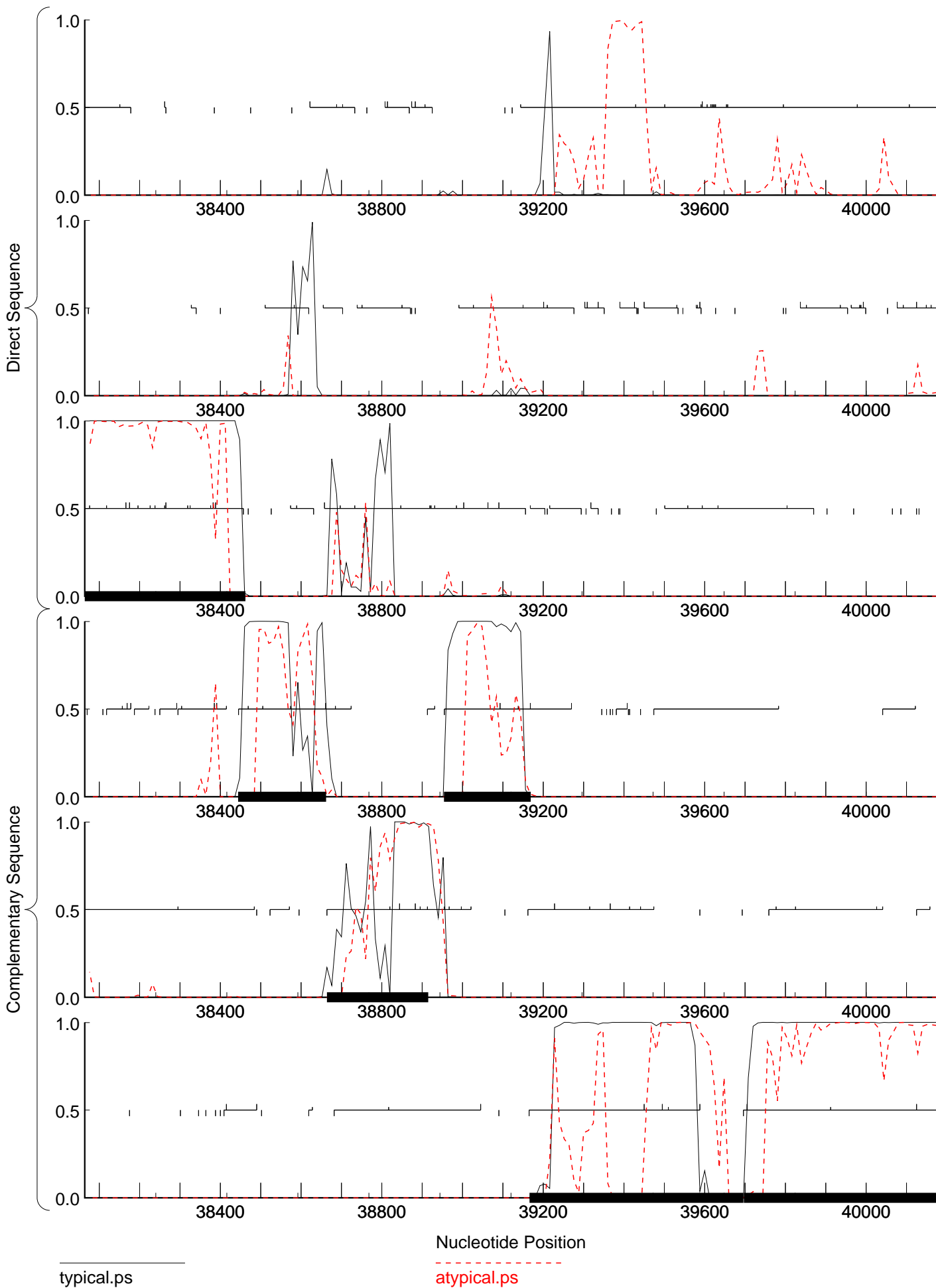






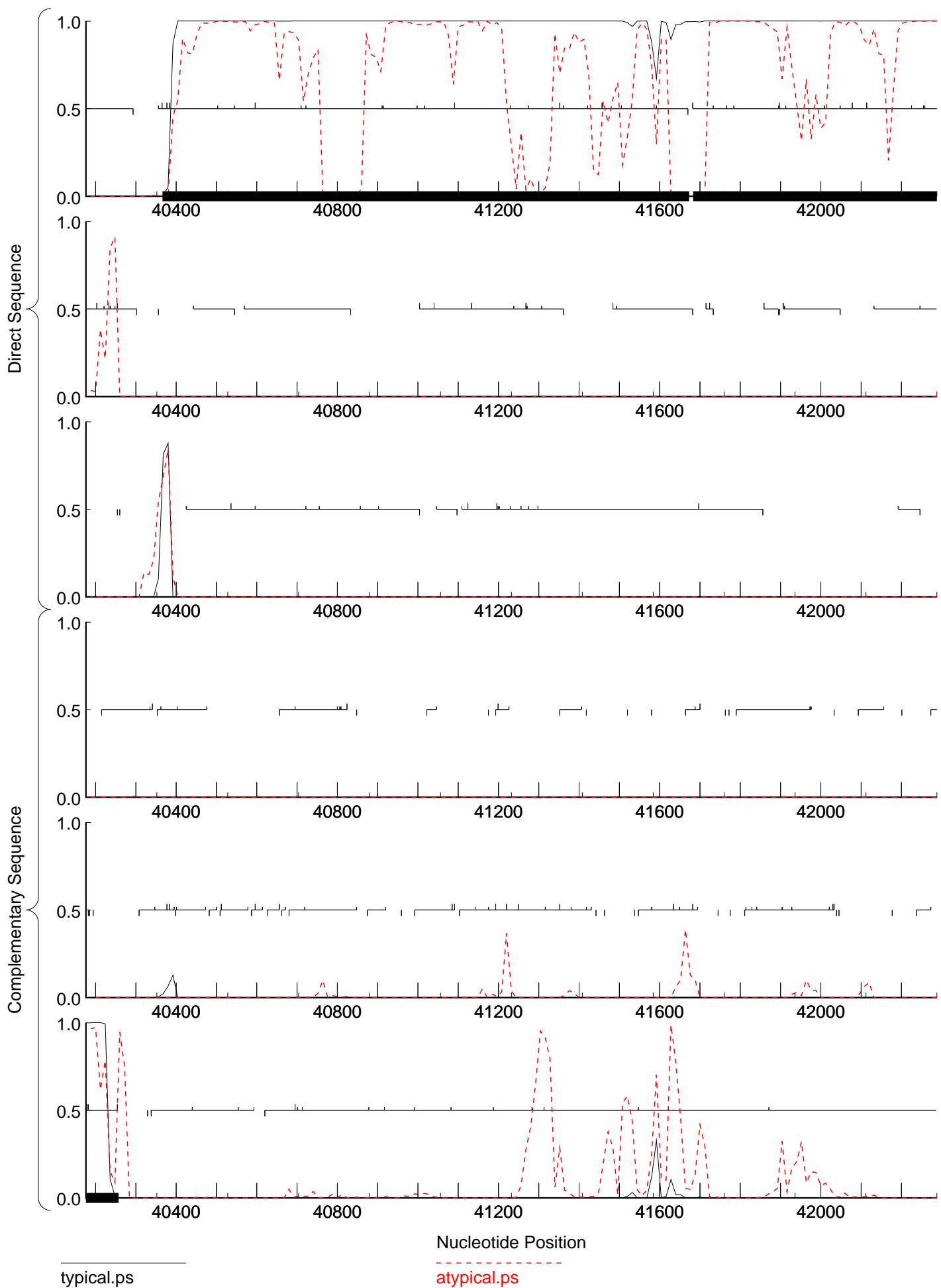


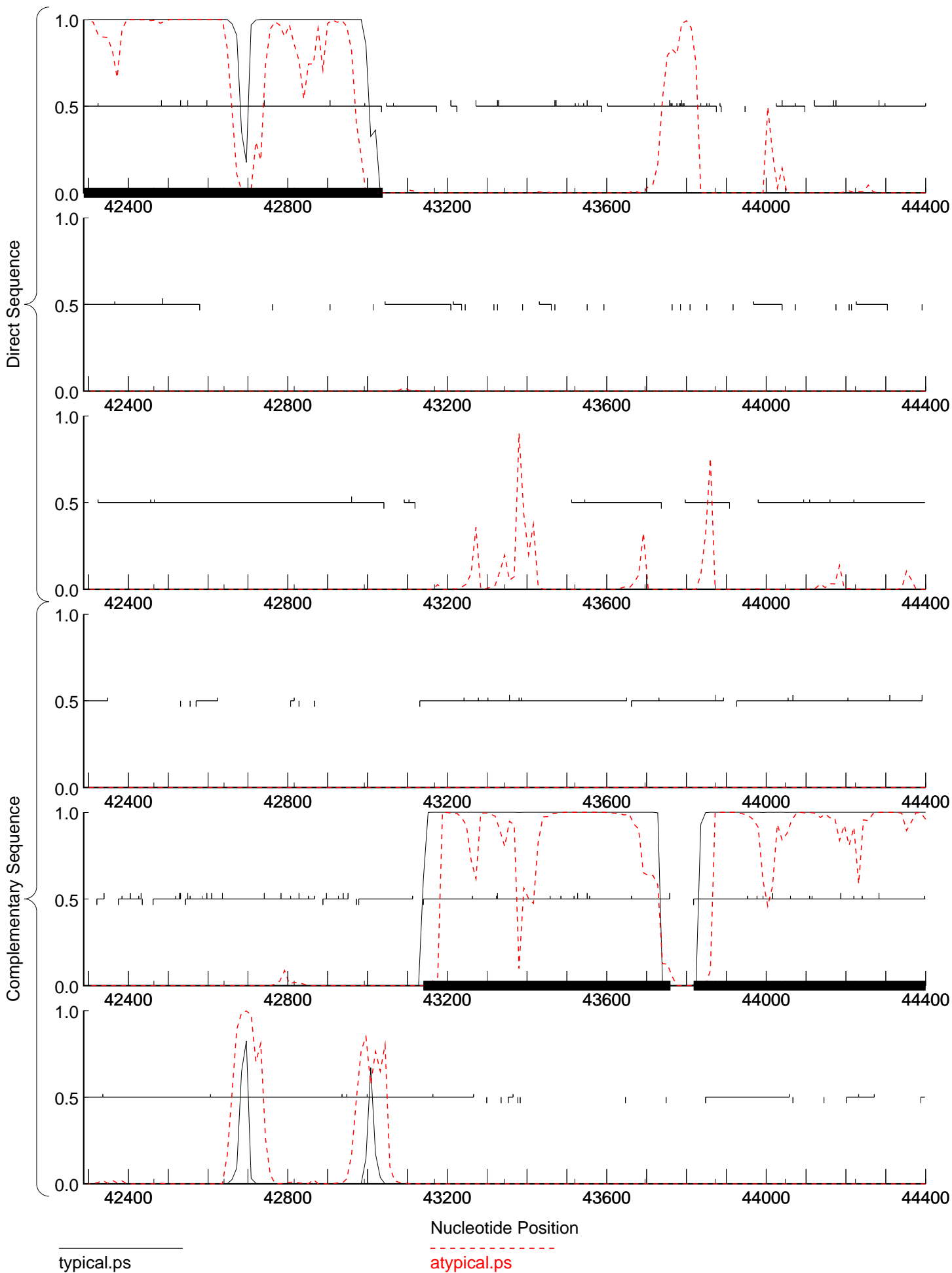


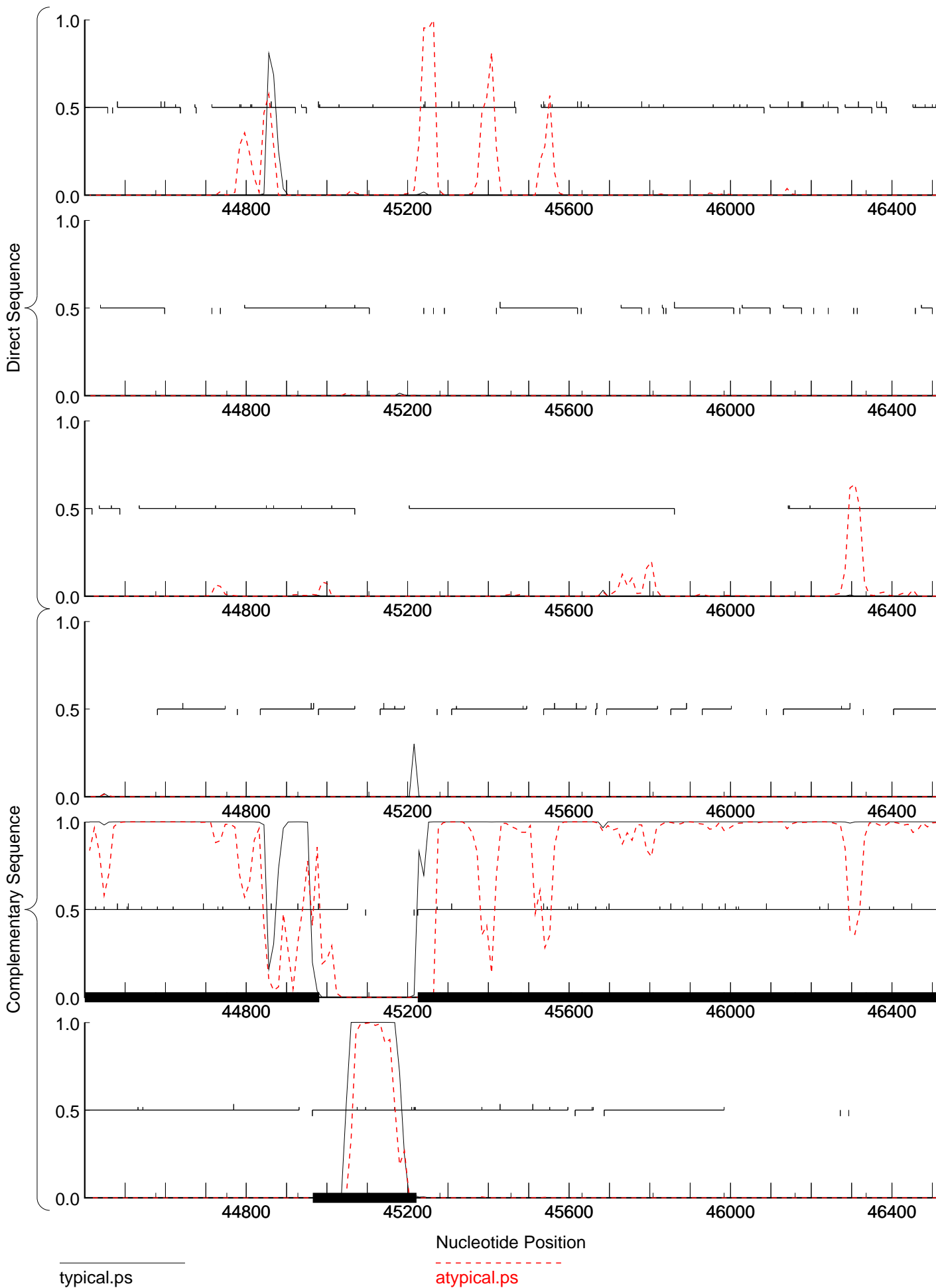


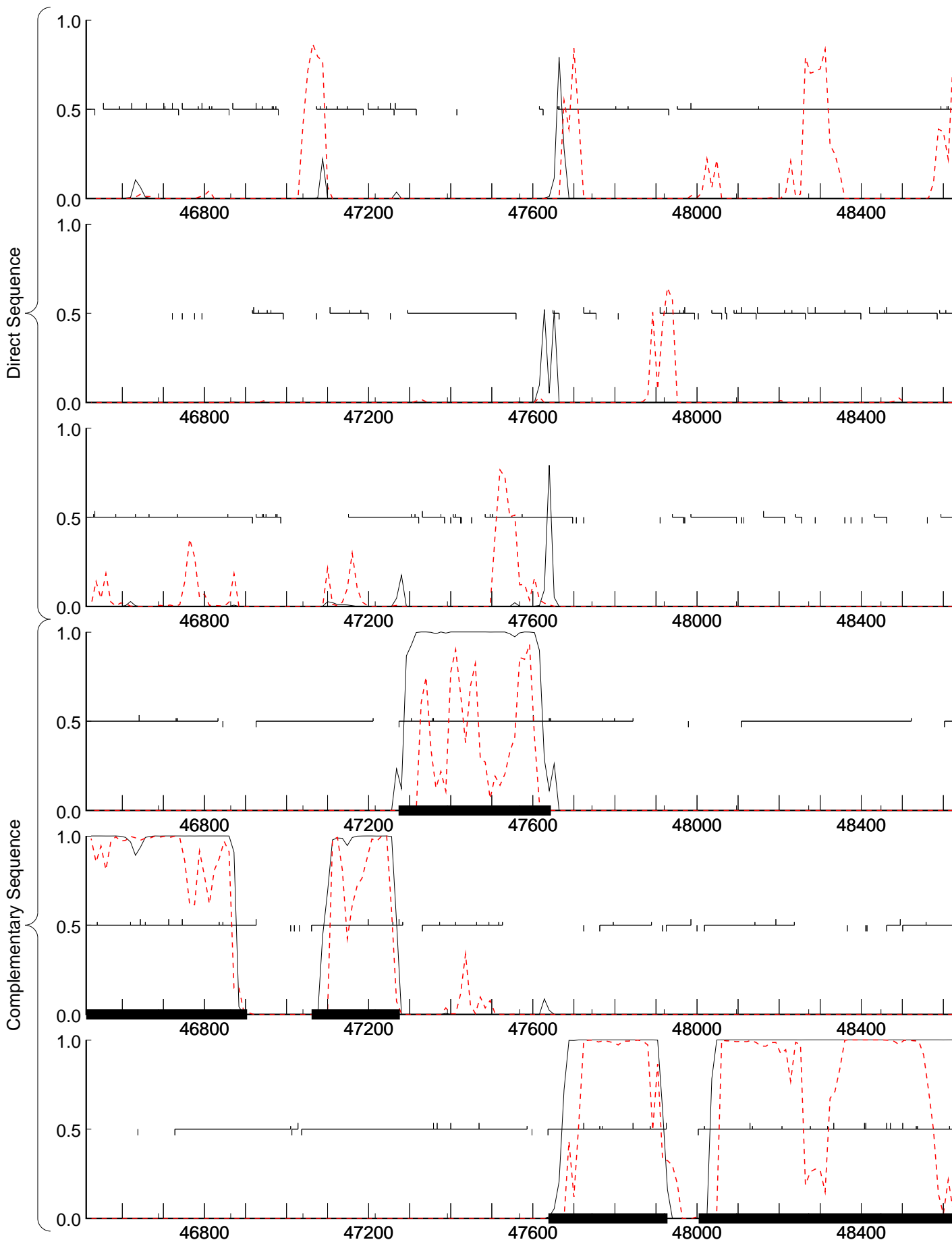
typical.ps

atypical.ps



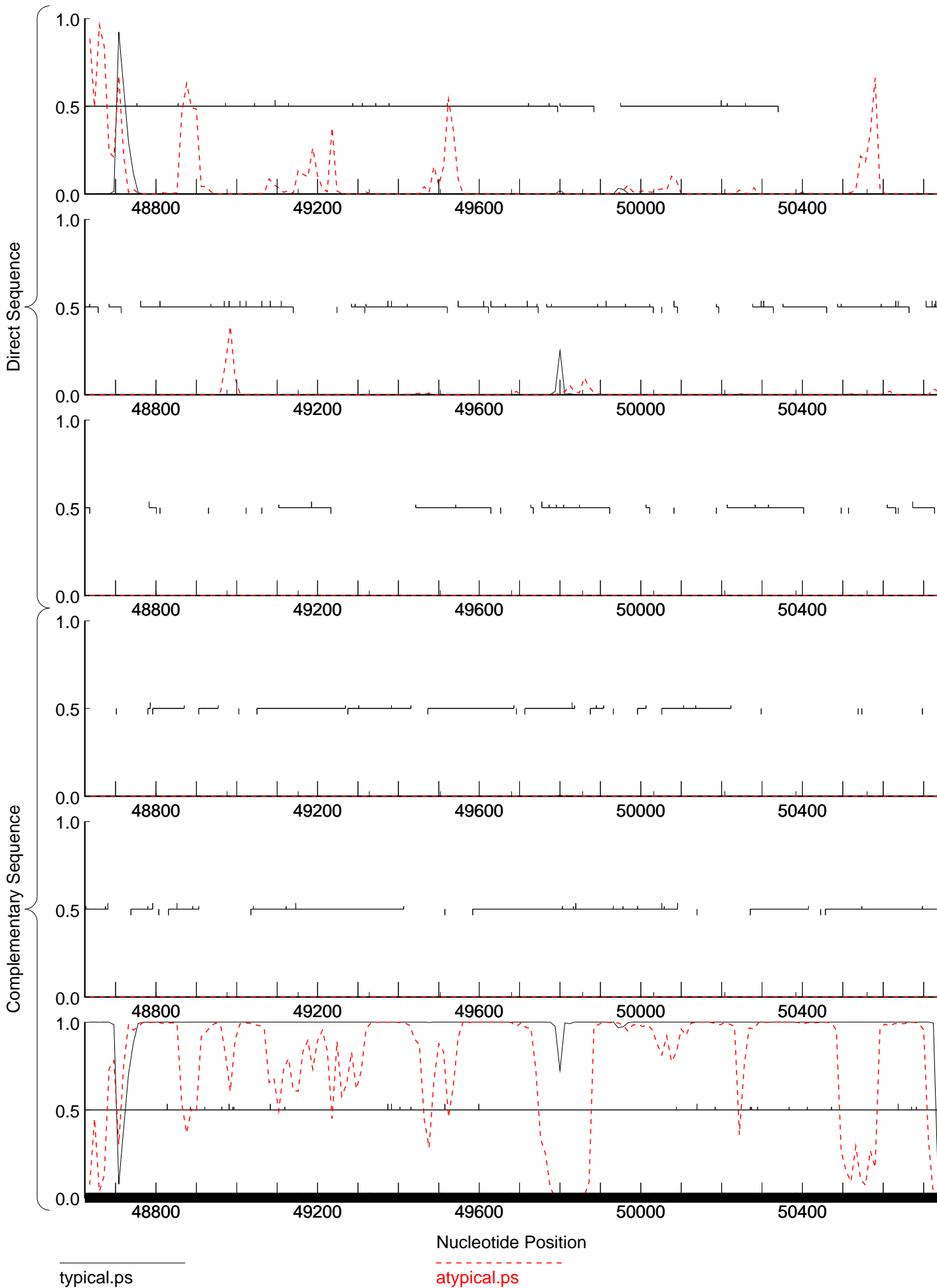






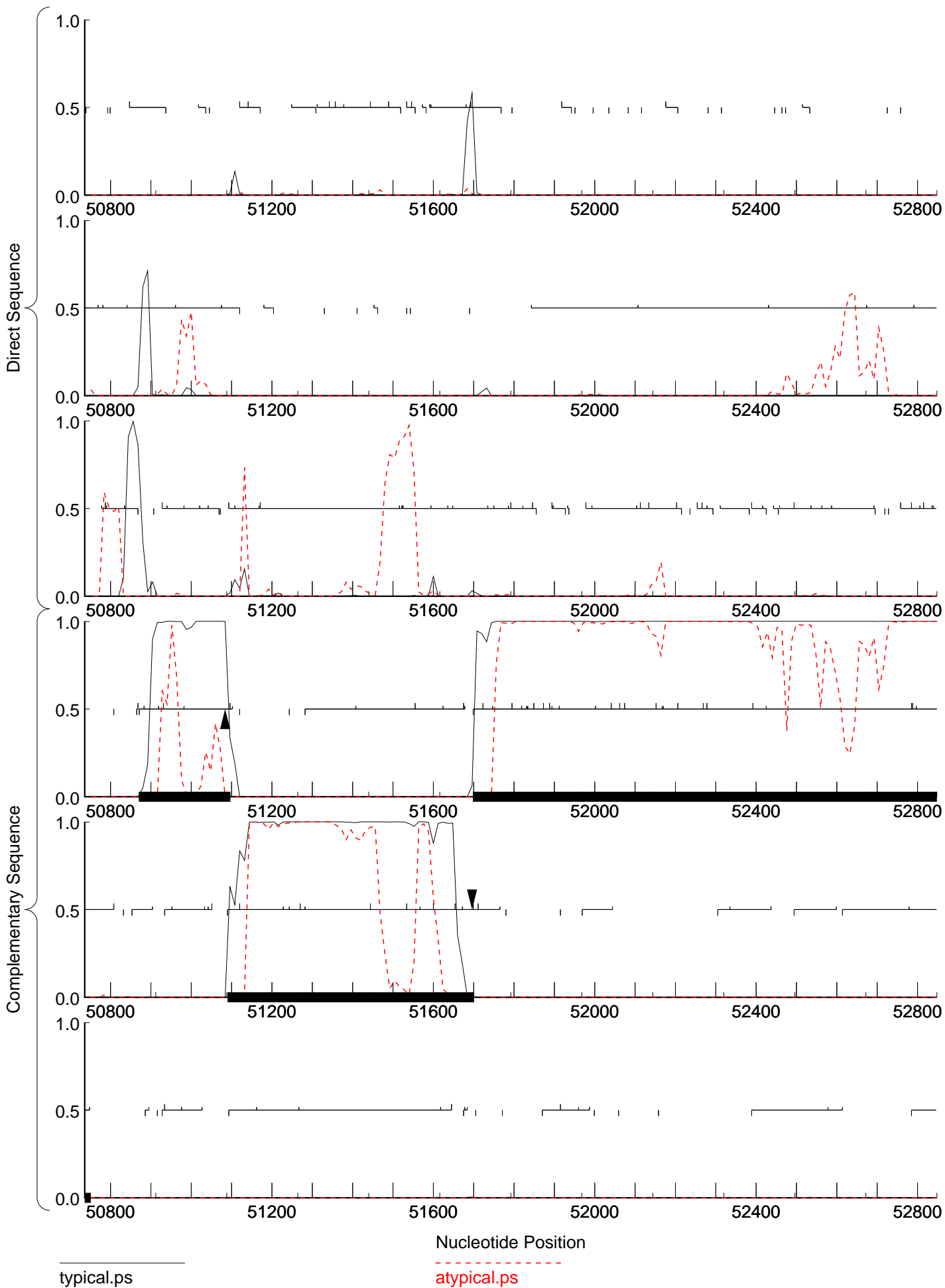
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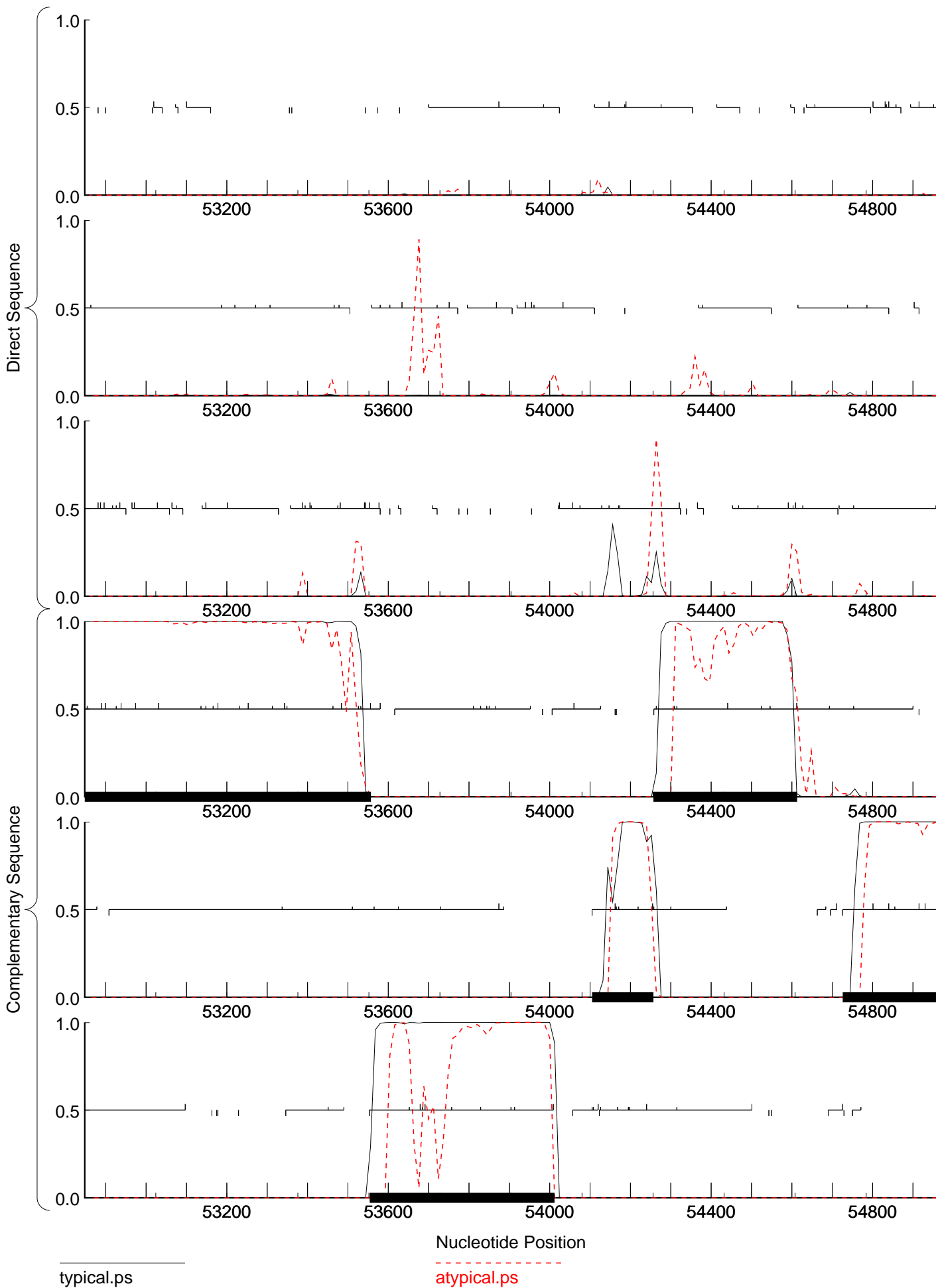
atypical.ps



typical.ps

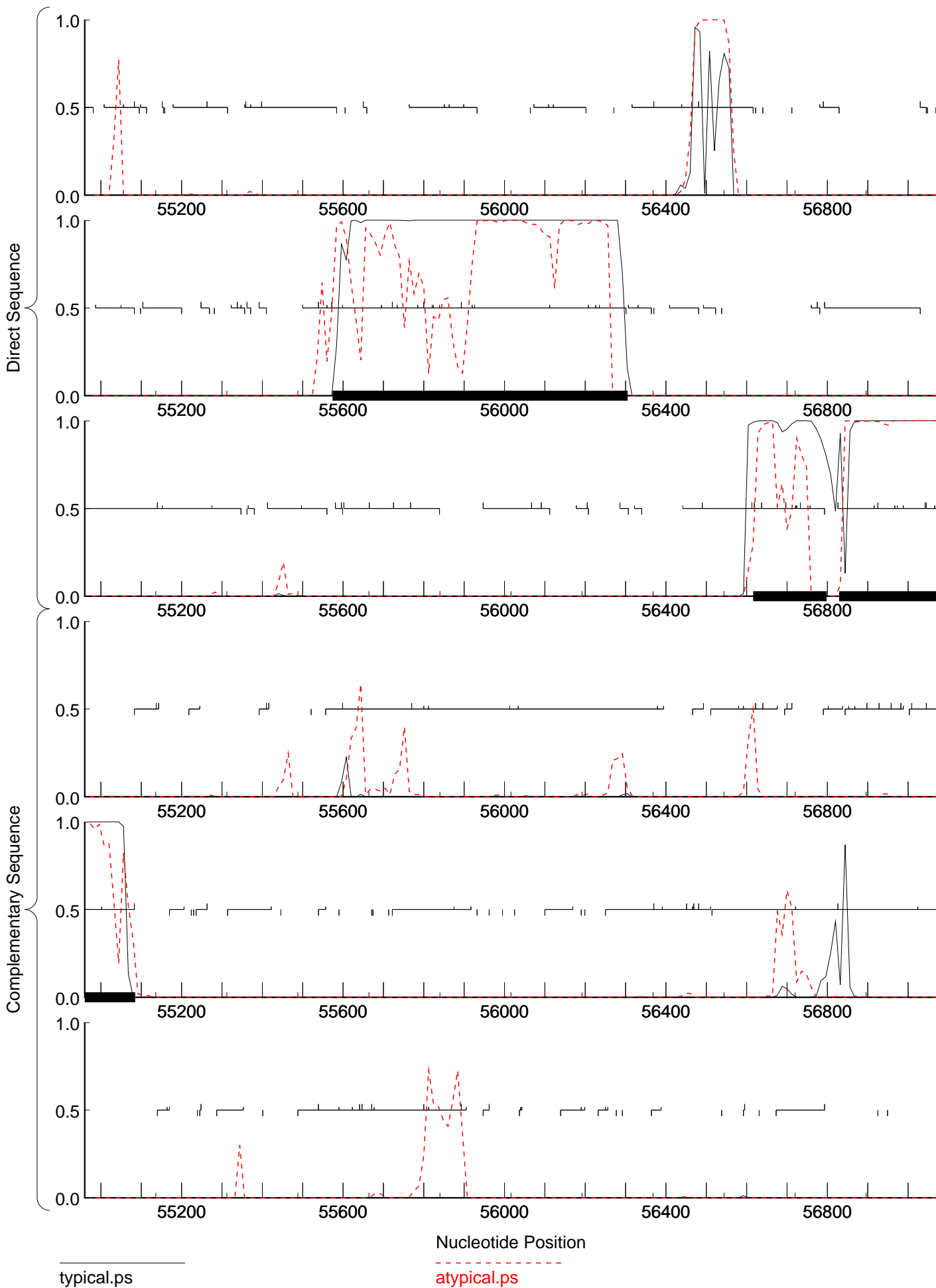
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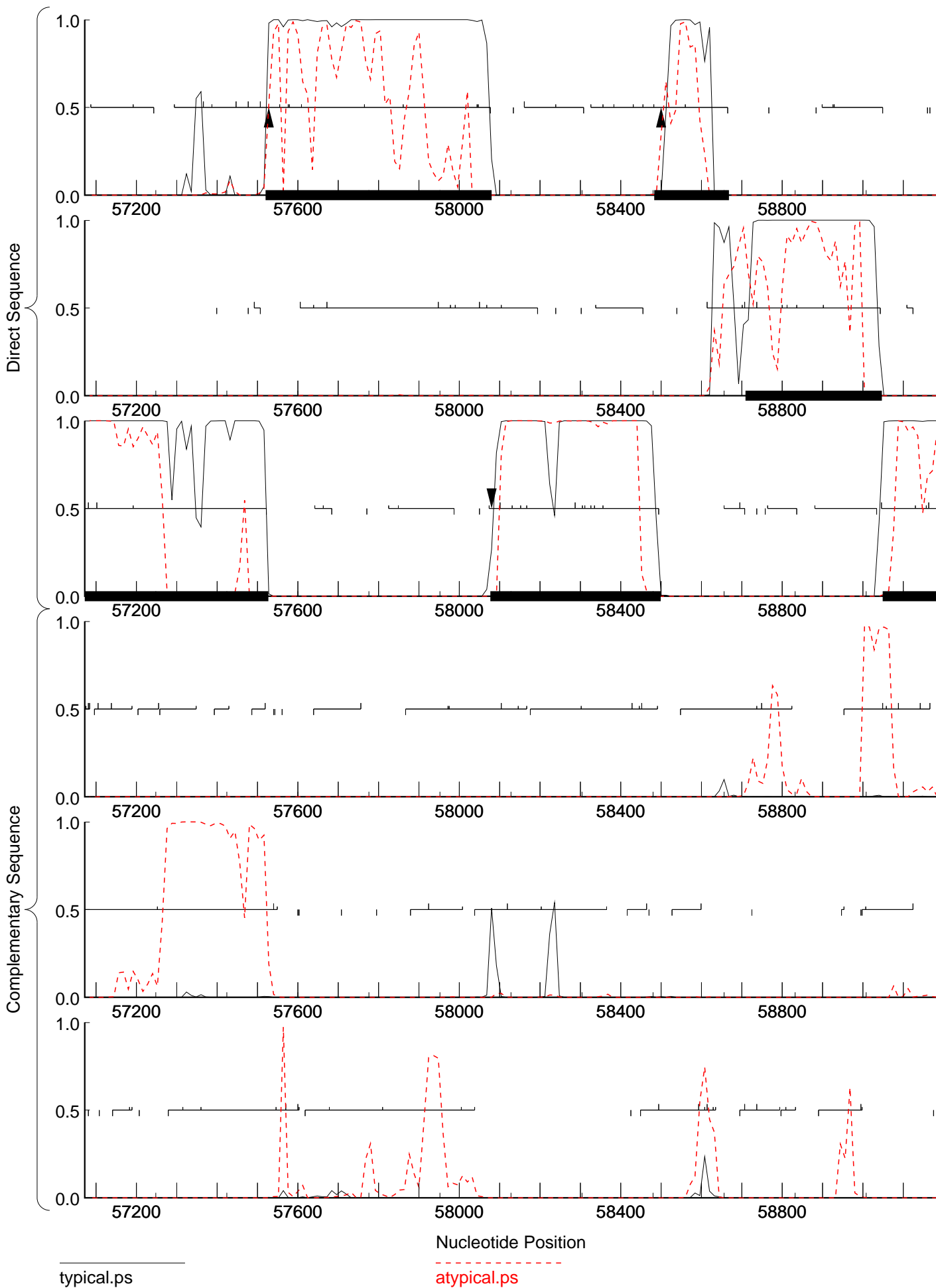


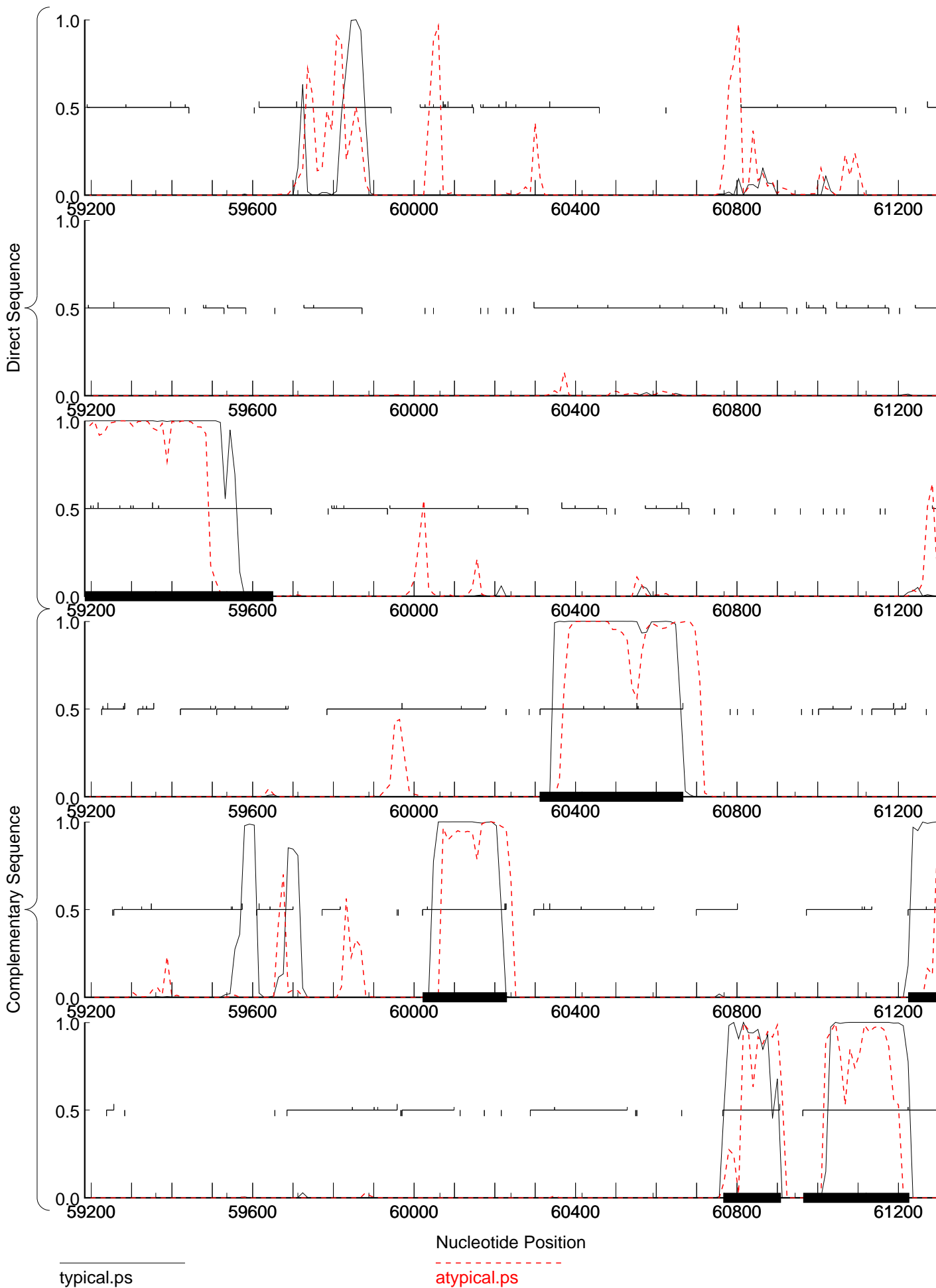


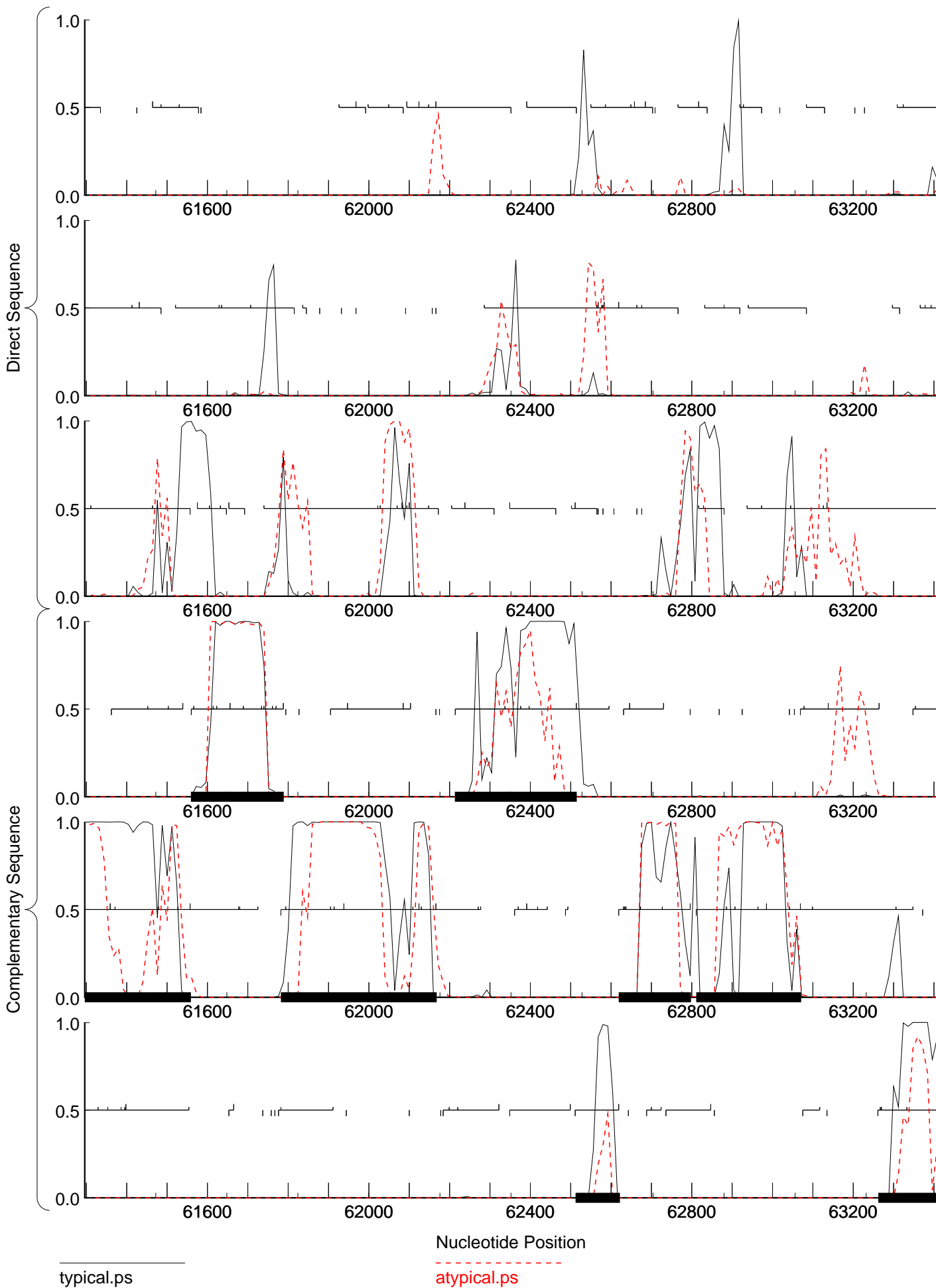
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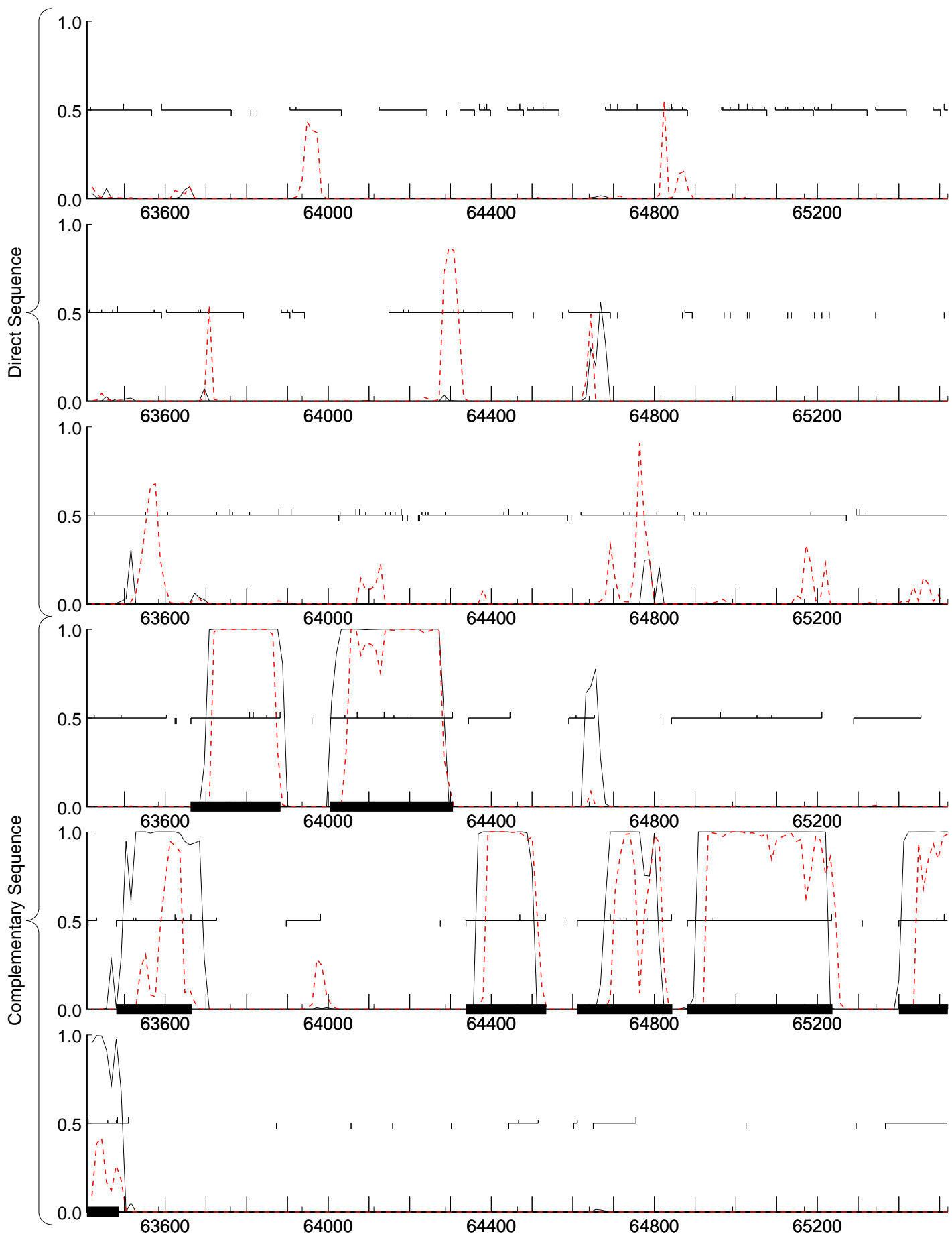
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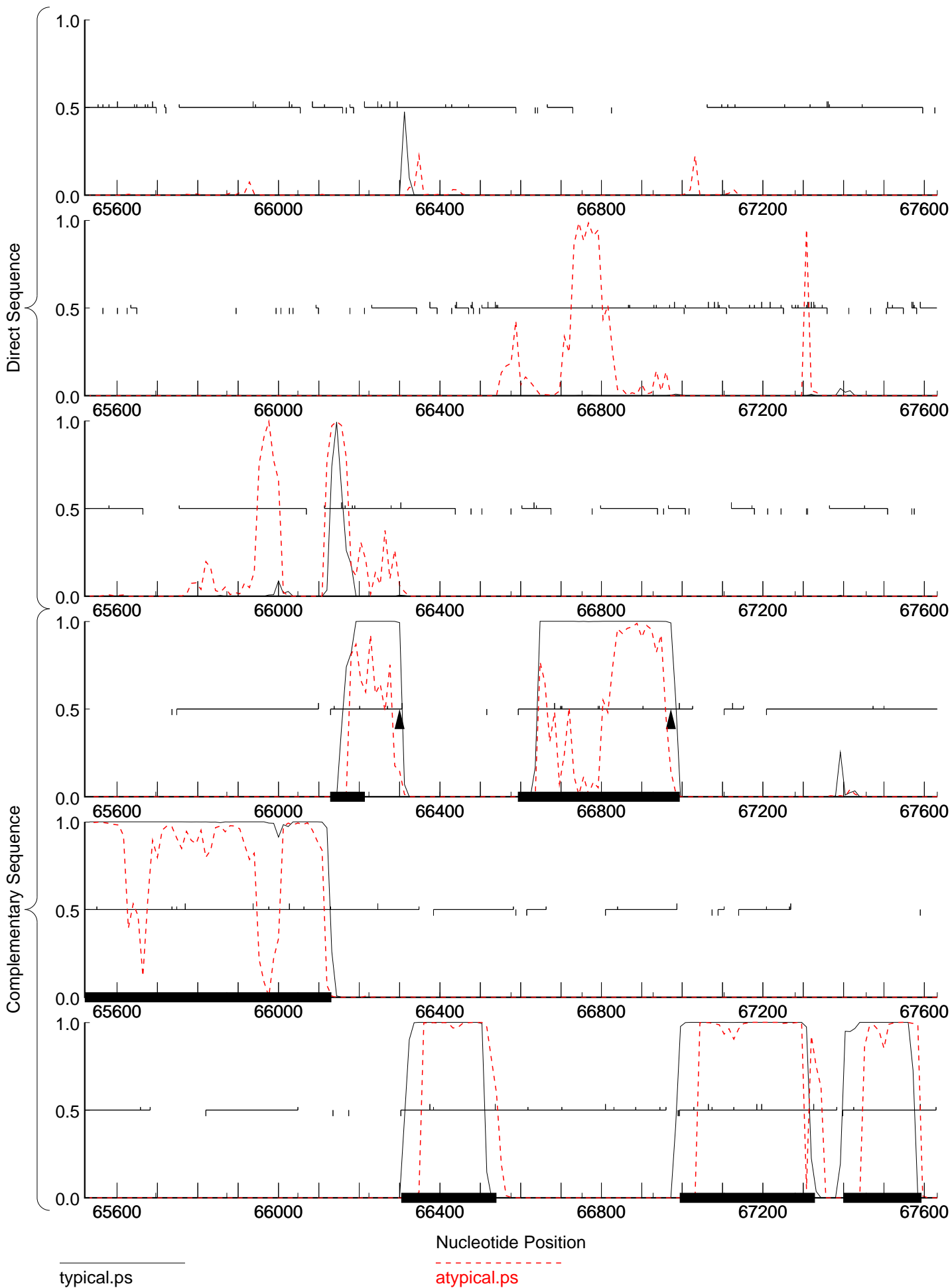


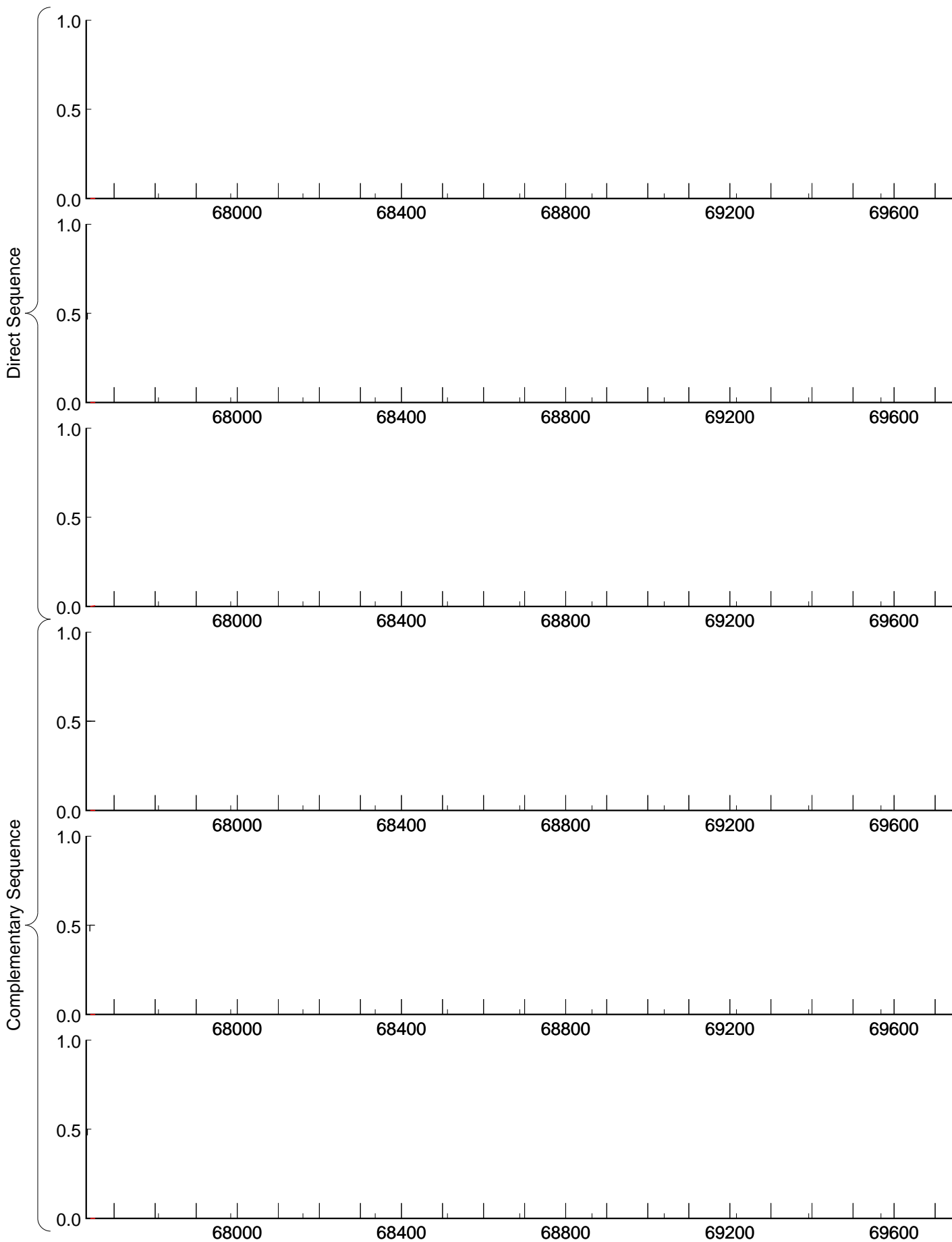


typical.ps

atypical.ps

Nucleotide Position





typical.ps

Nucleotide Position

atypical.ps