

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 : 3/17/18 at 20:26:01
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,

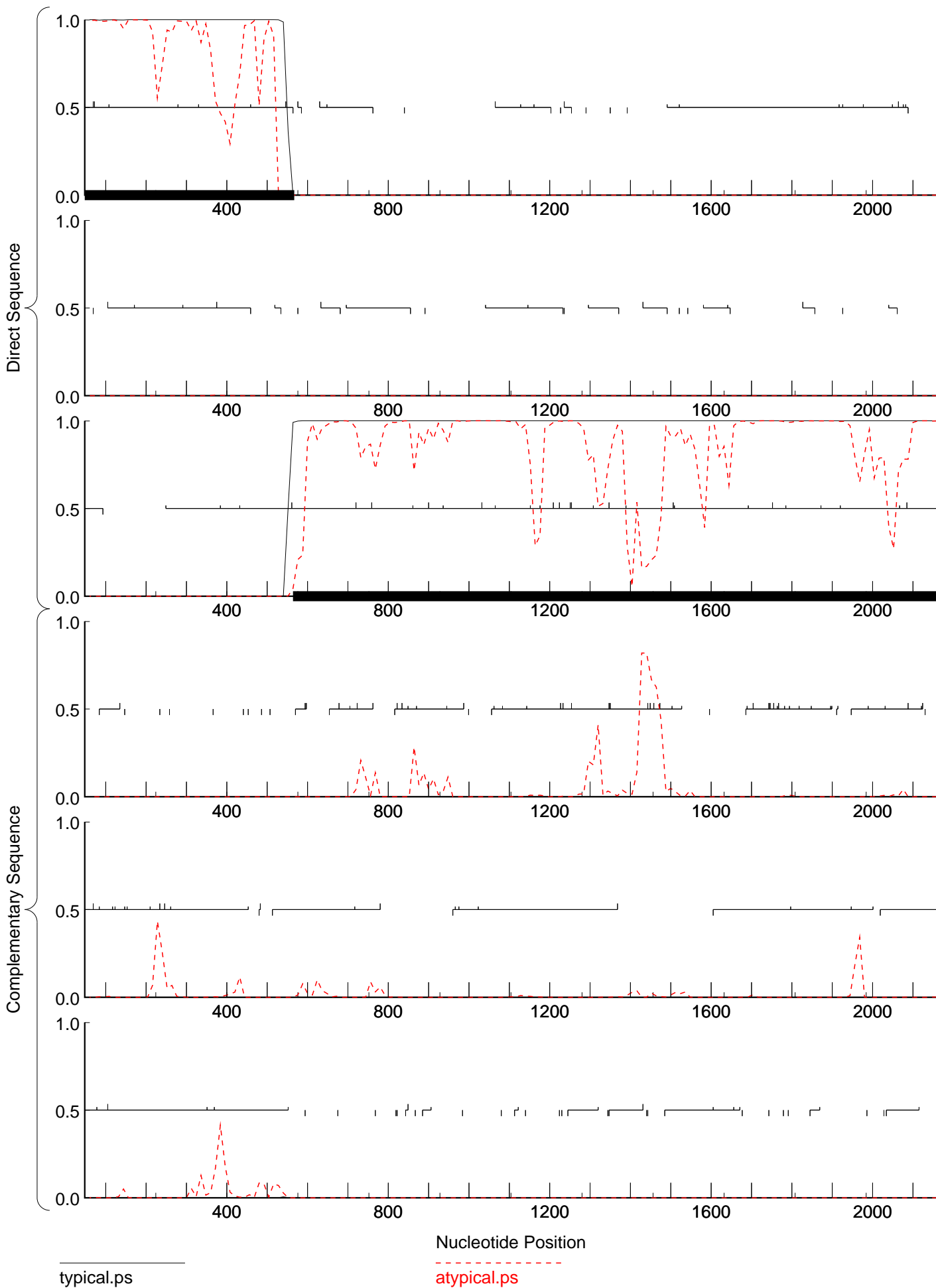
MATRIX INFORMATION

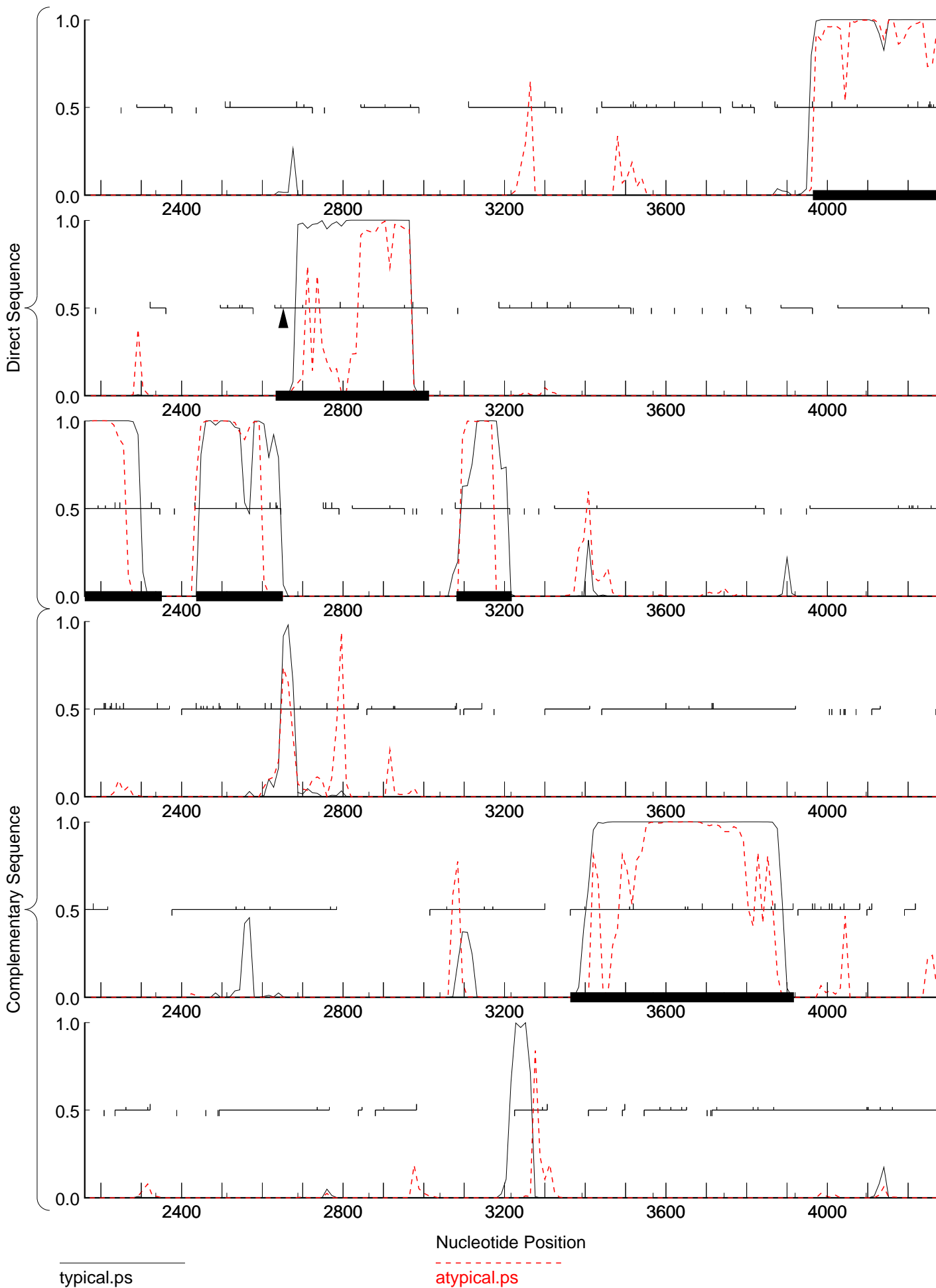
Matrix : -
Author : -
Order : 4

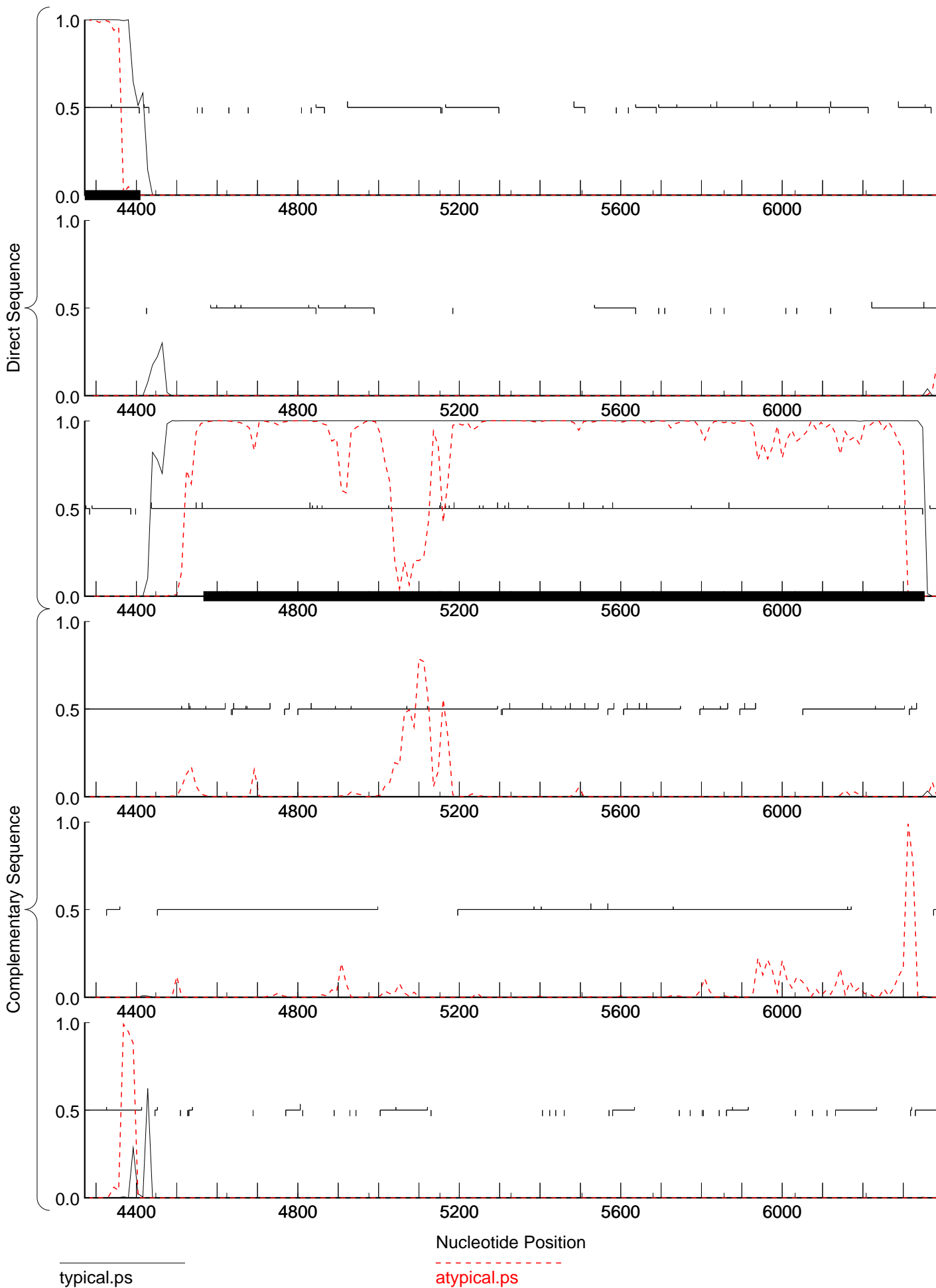
Send questions / comments to:
Dr. M. Borodovsky
Georgia Institute of Technology
School of Biology
Atlanta, GA 30332-0230

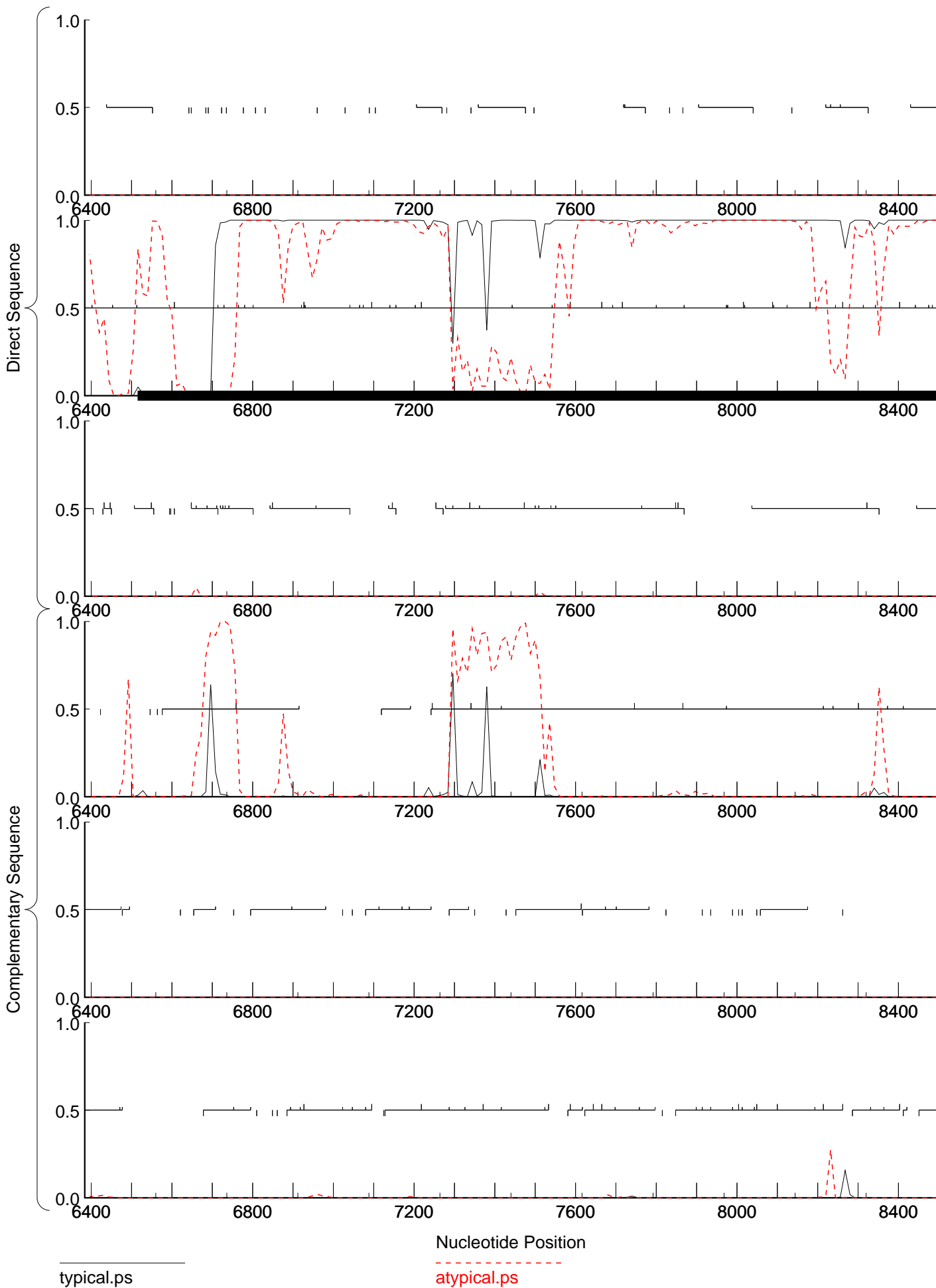
Matrix notes & comments

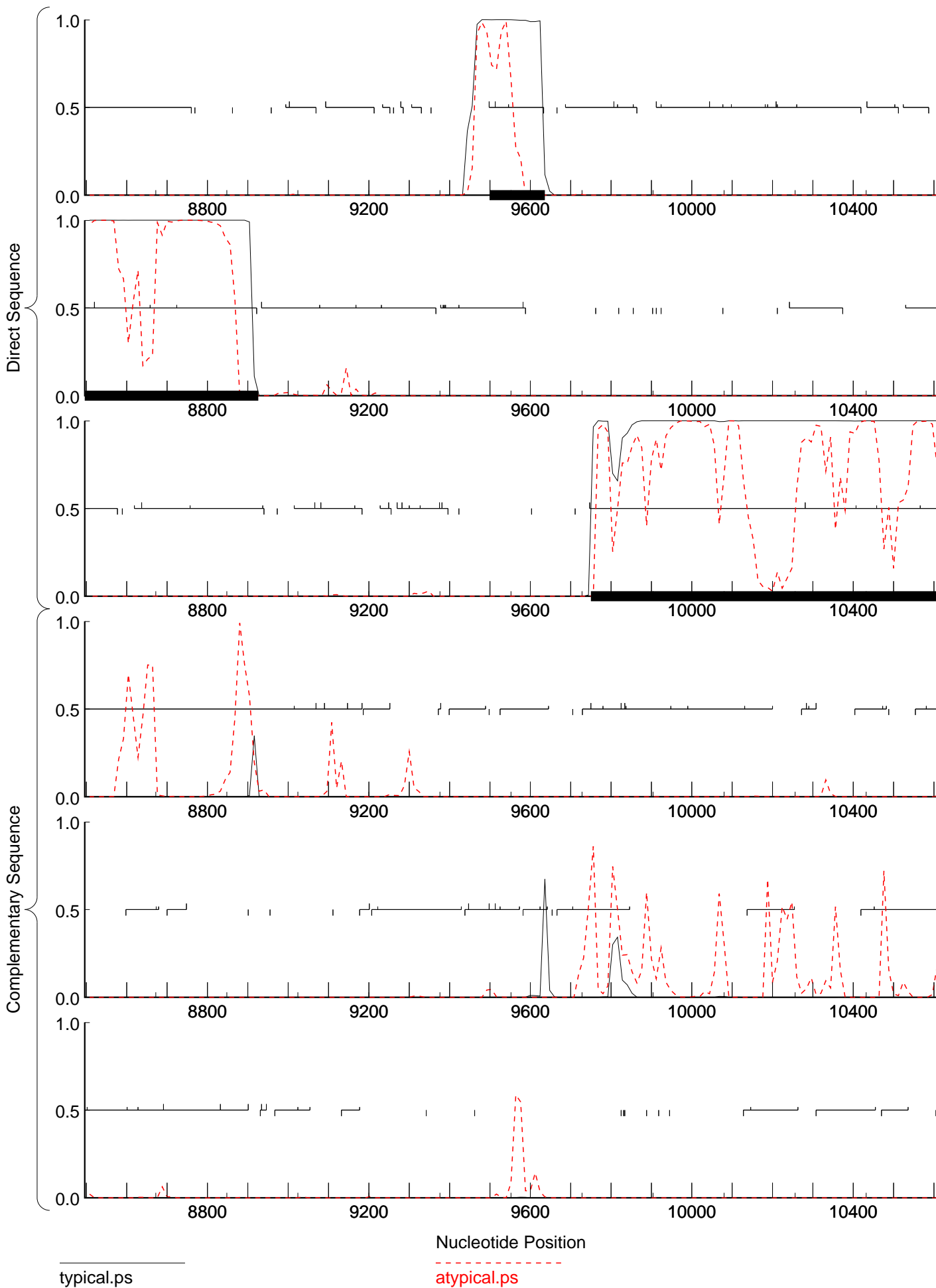
Training set derived by GeneMarkS, 4.30 October 2014
Sat Mar 17 20:26:01 2018

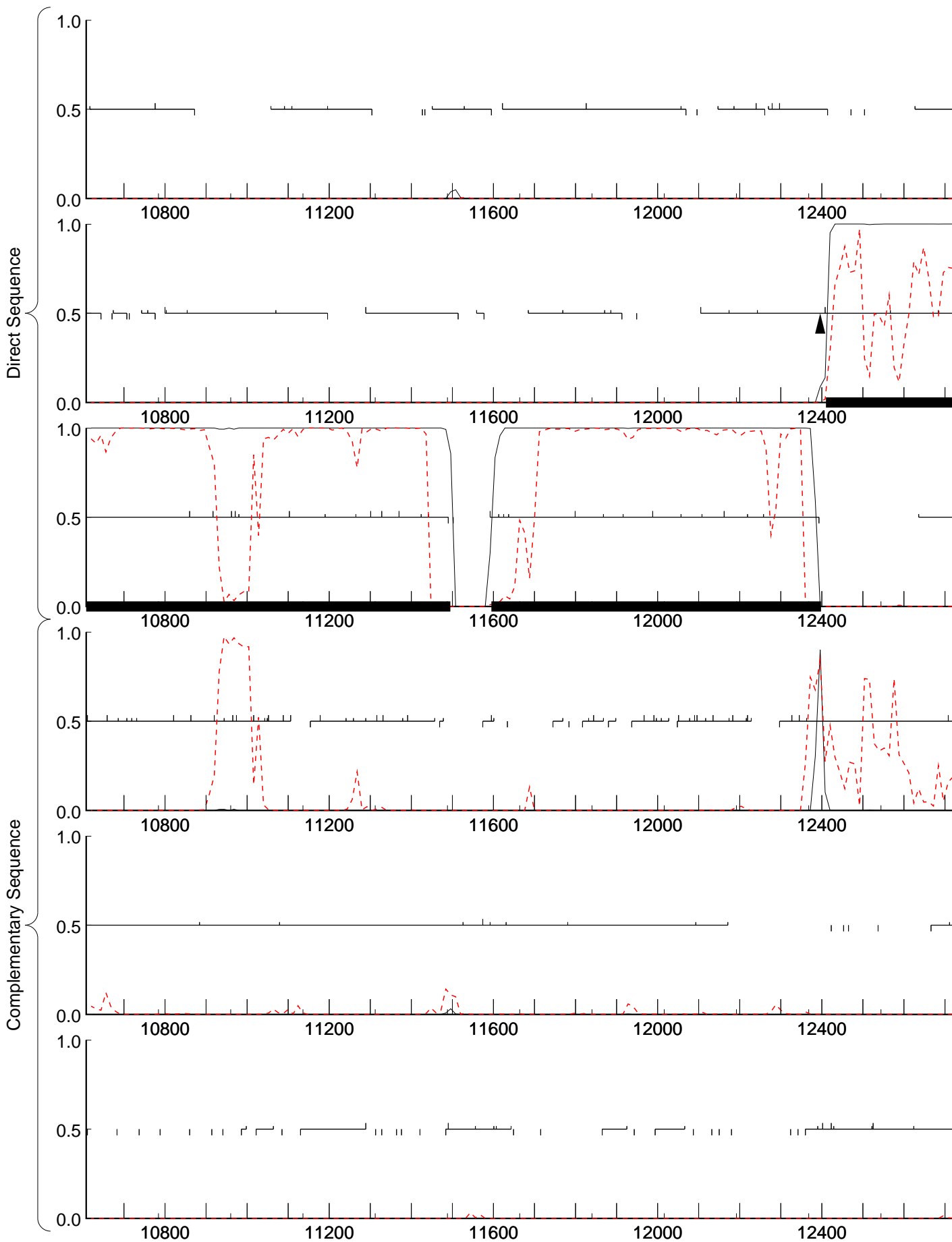






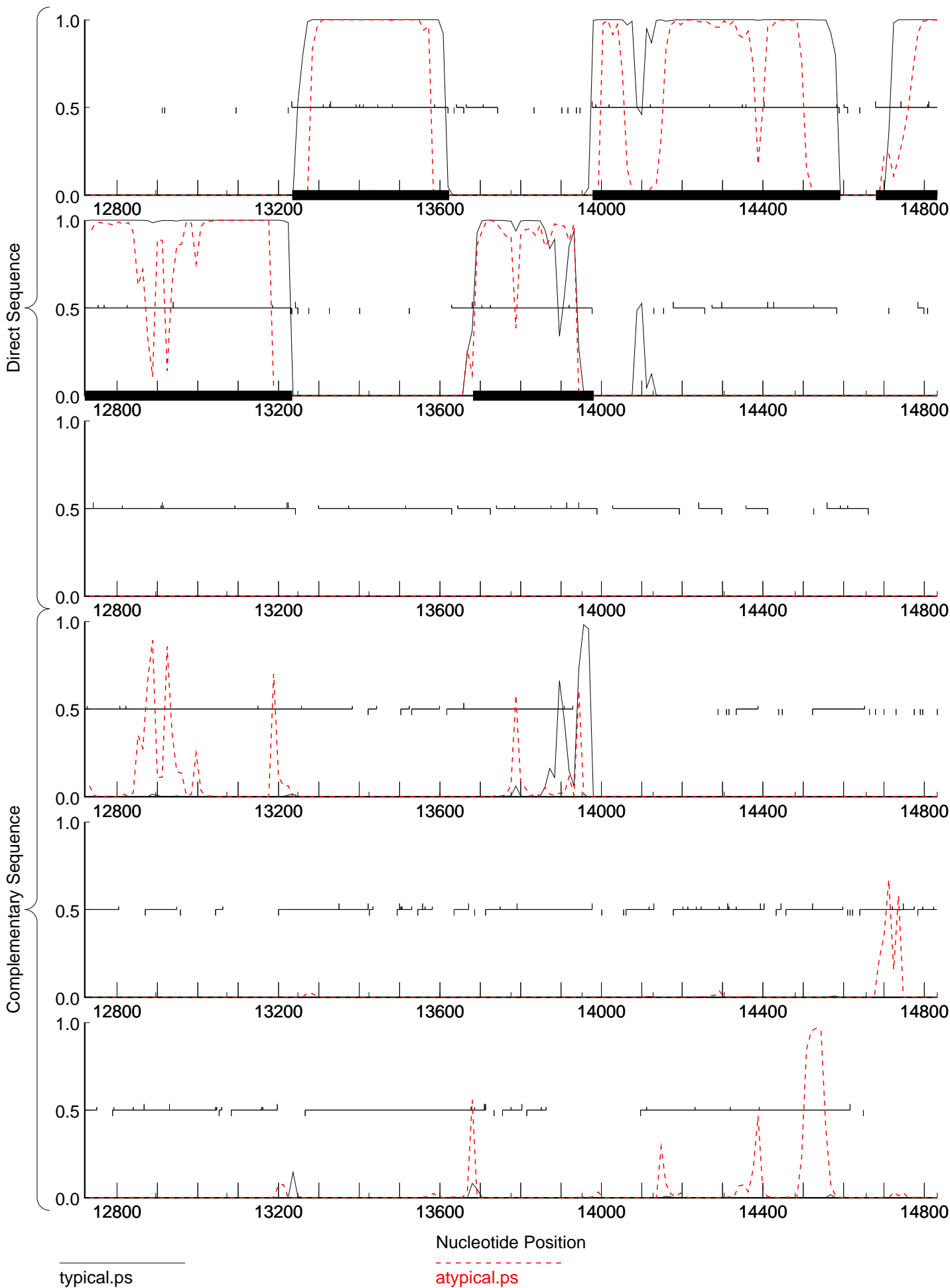


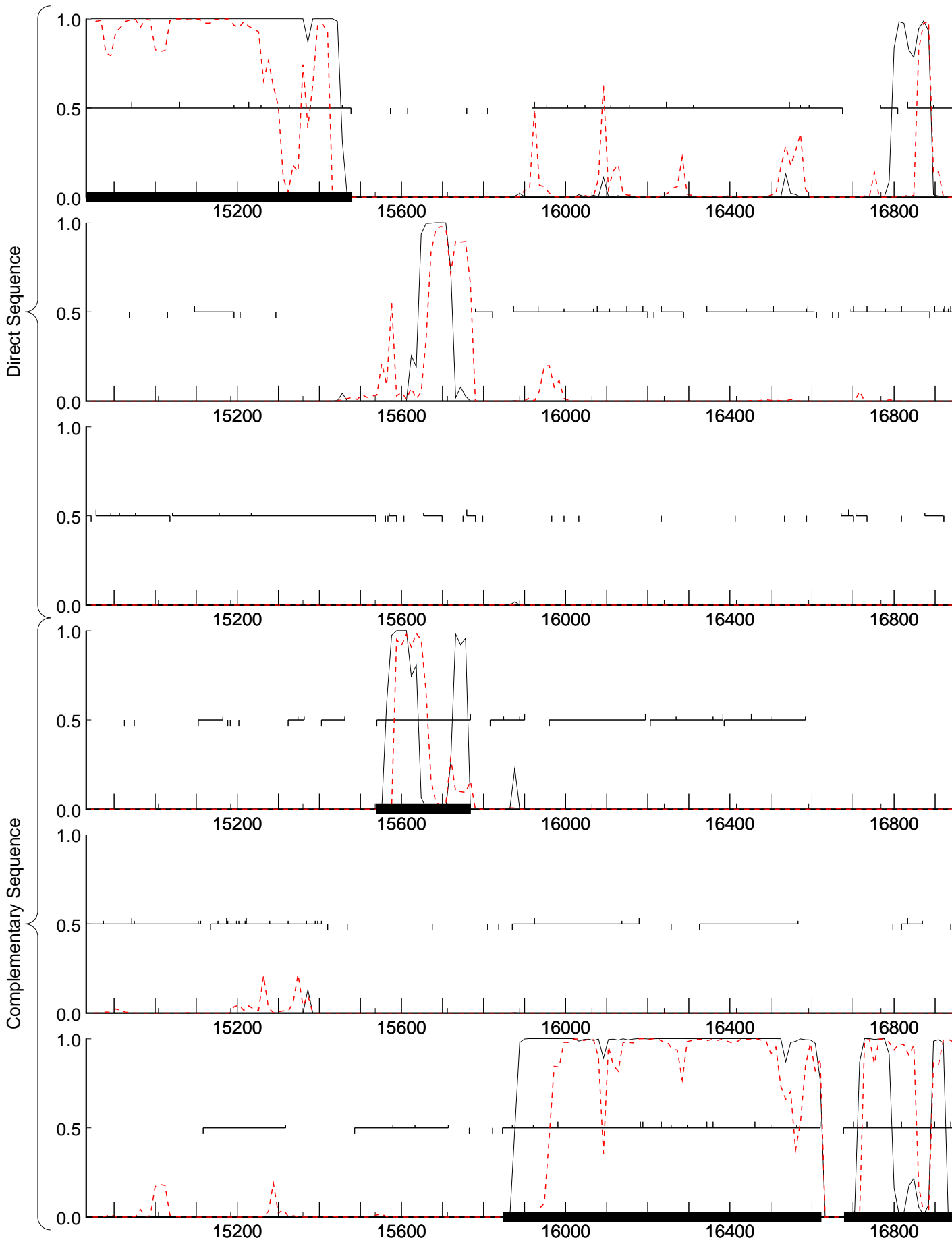




typical.ps

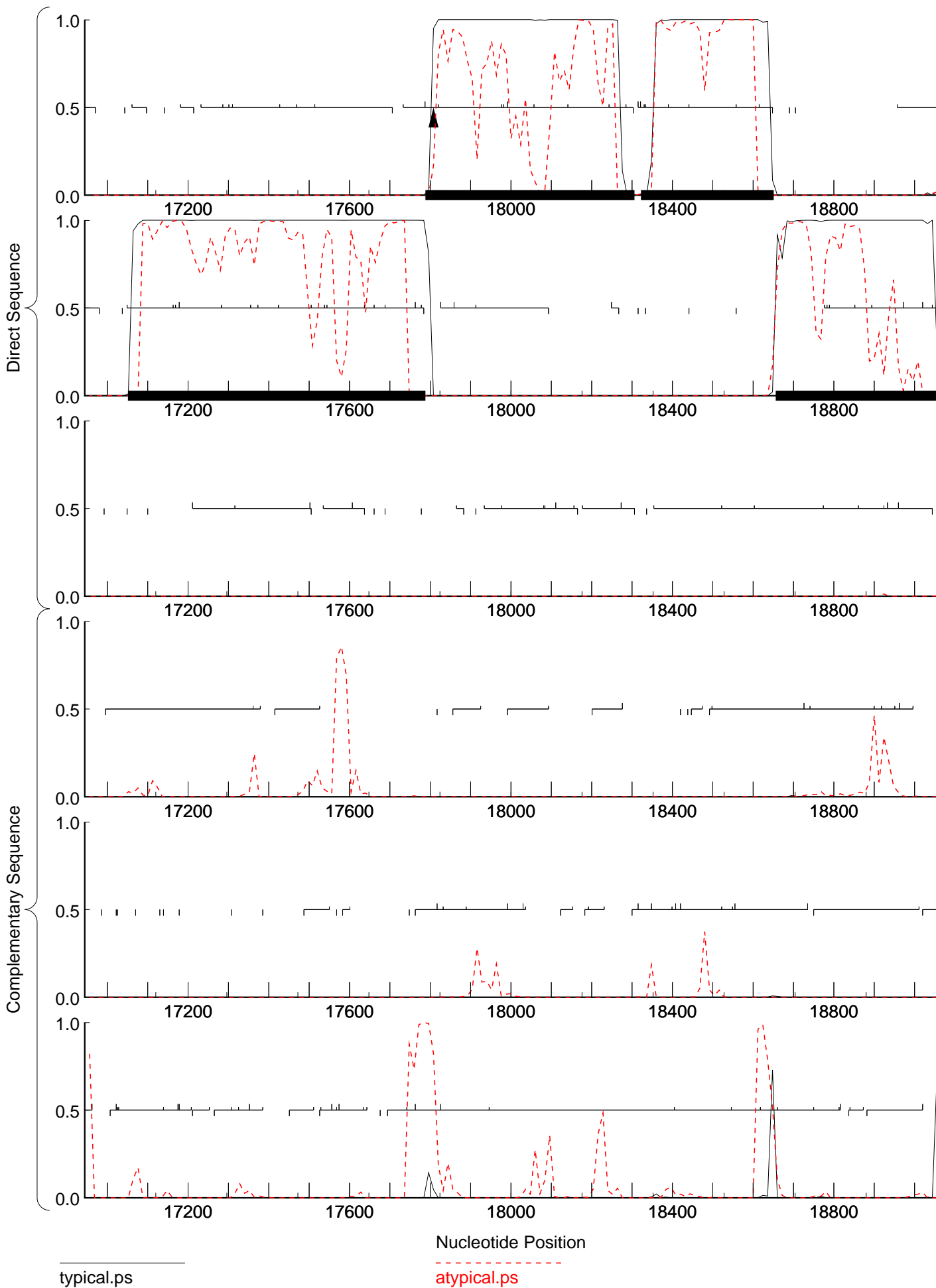
atypical.ps

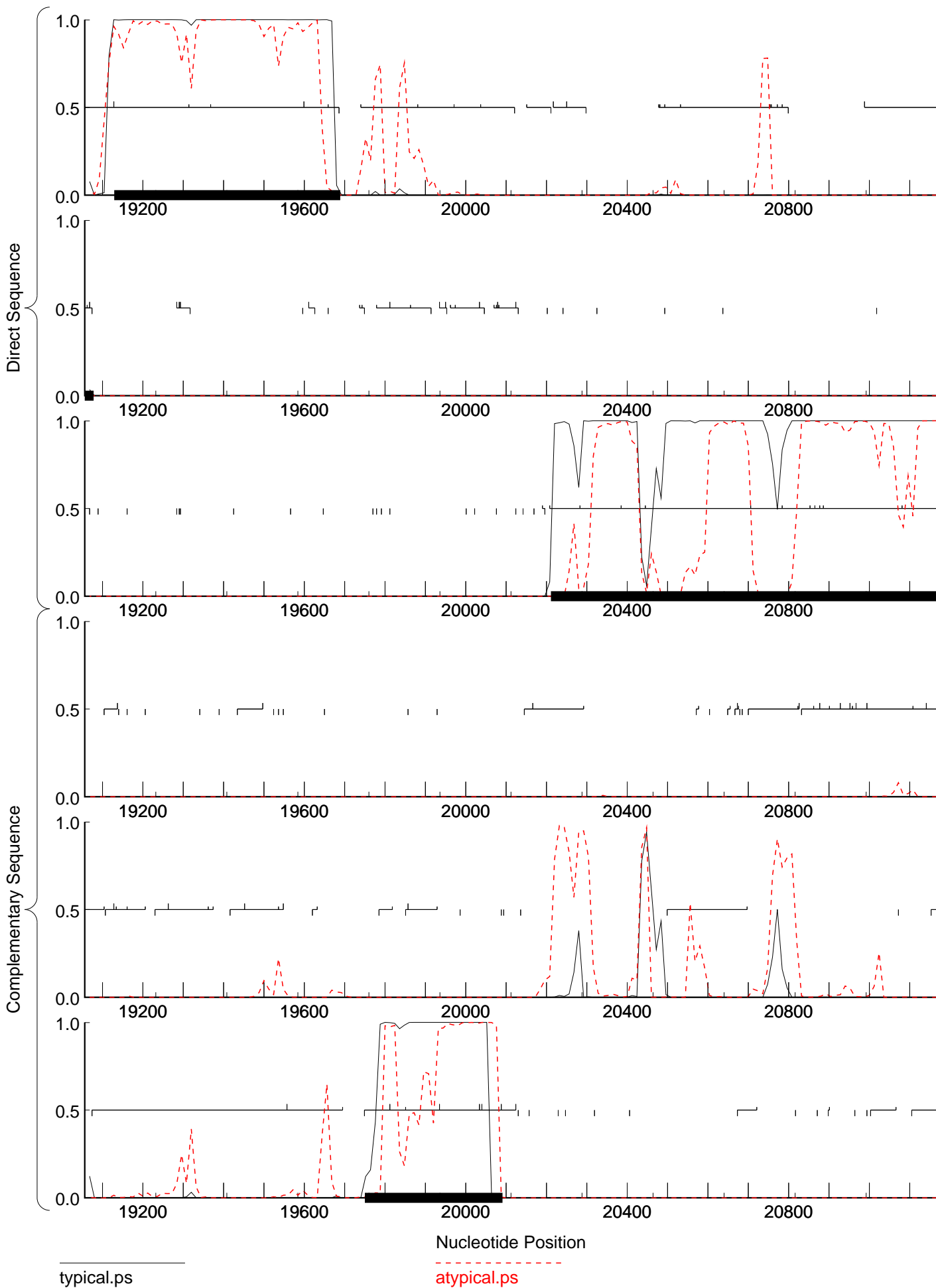




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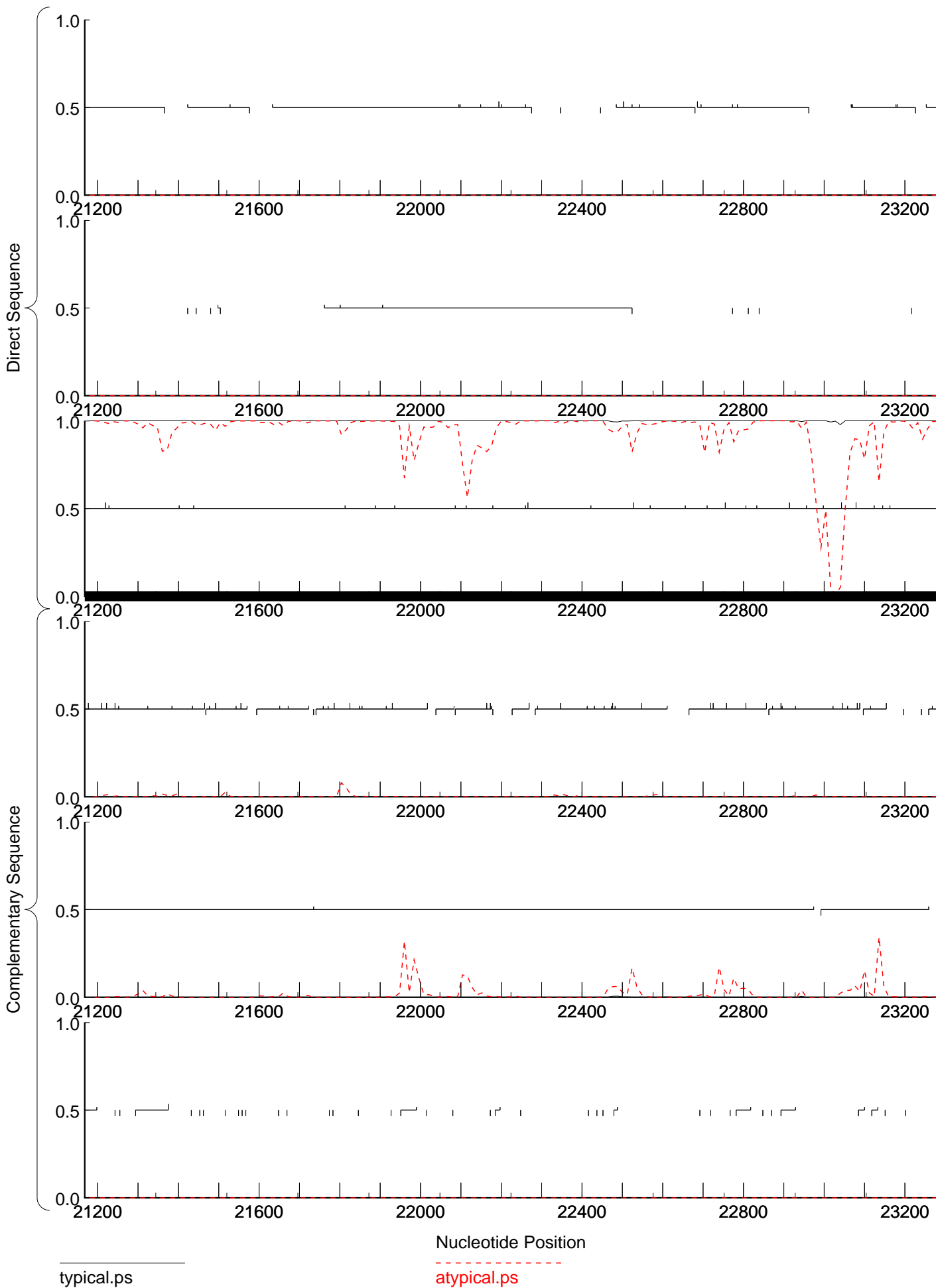
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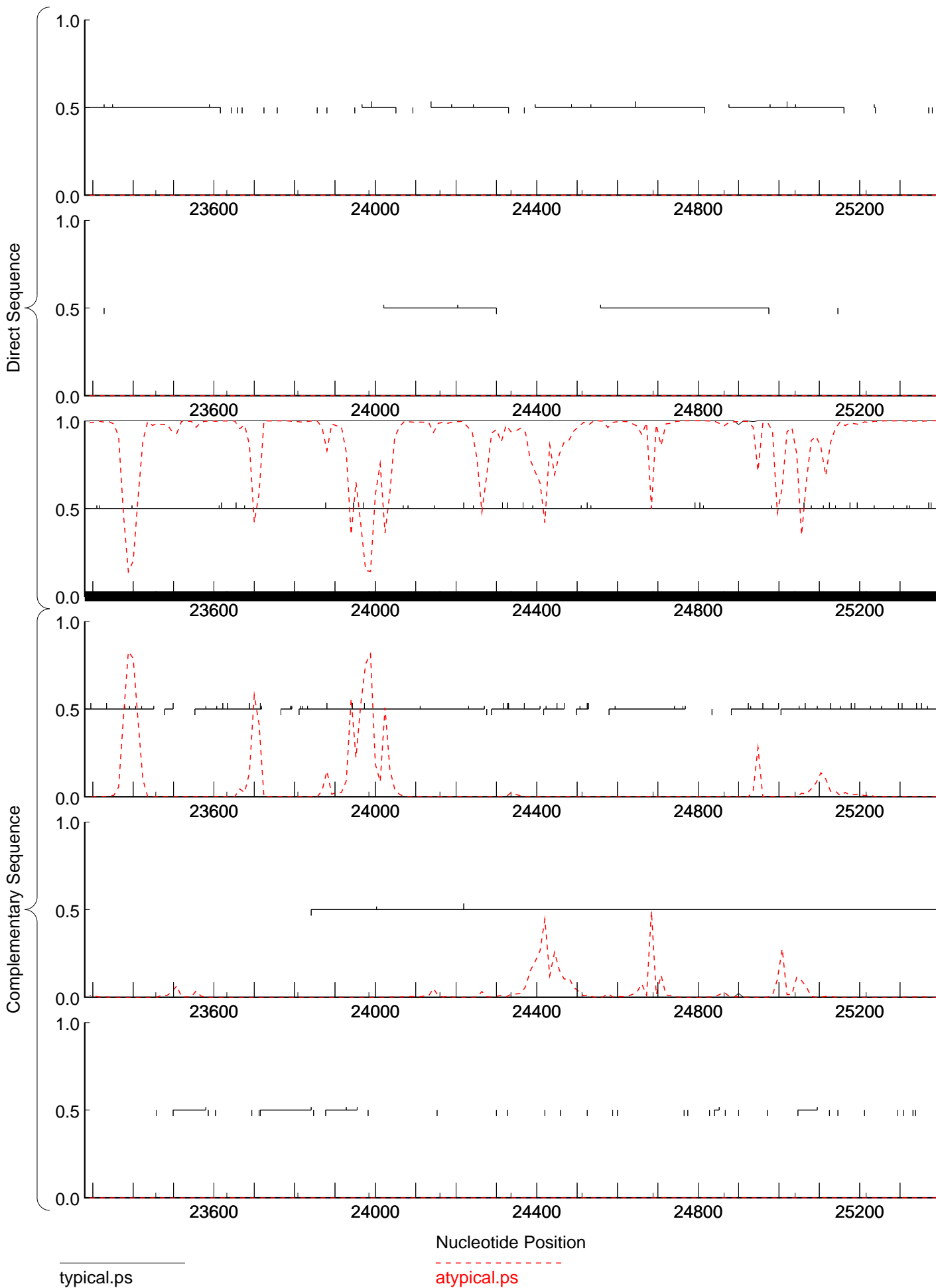
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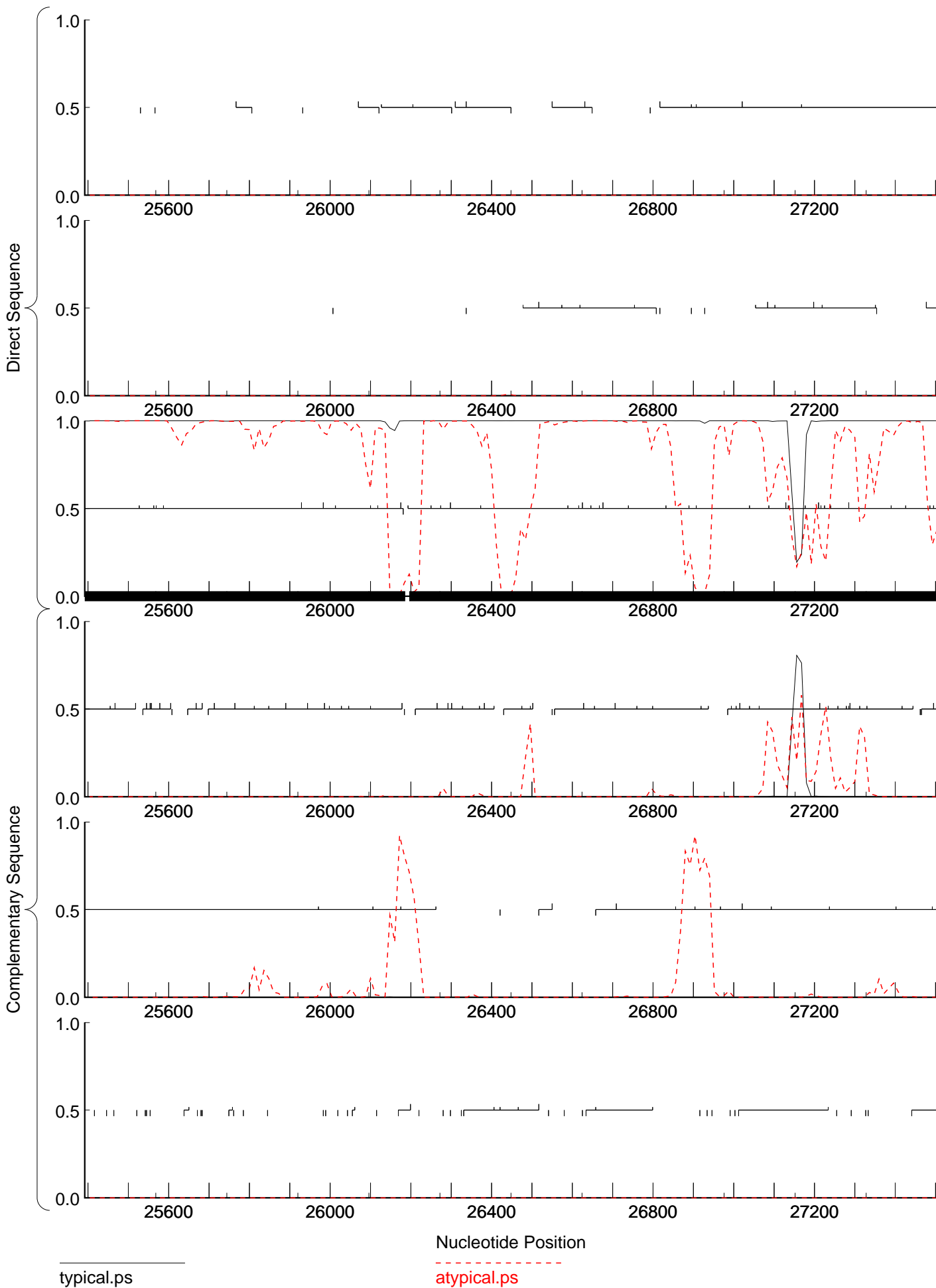
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typical.ps

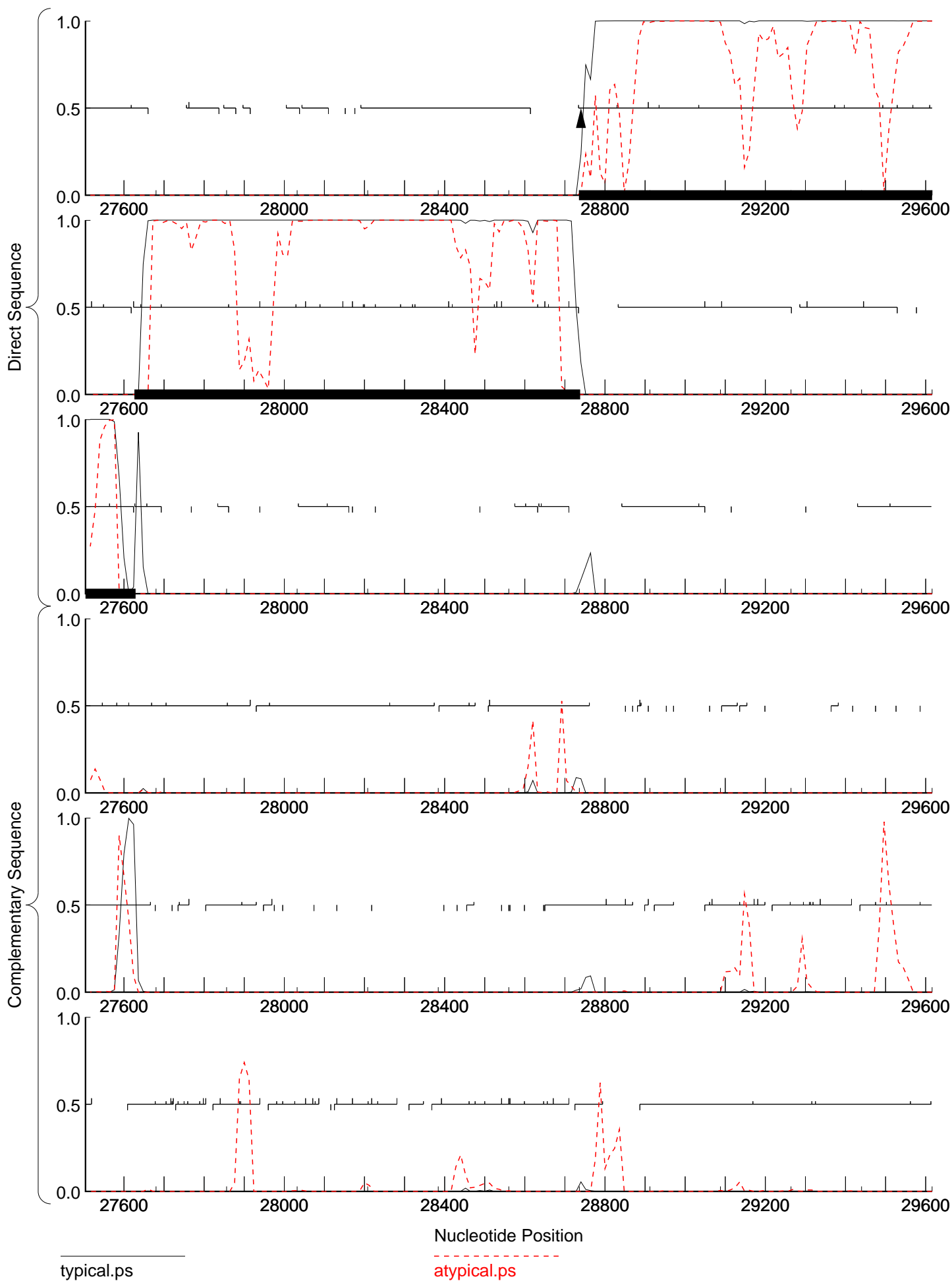
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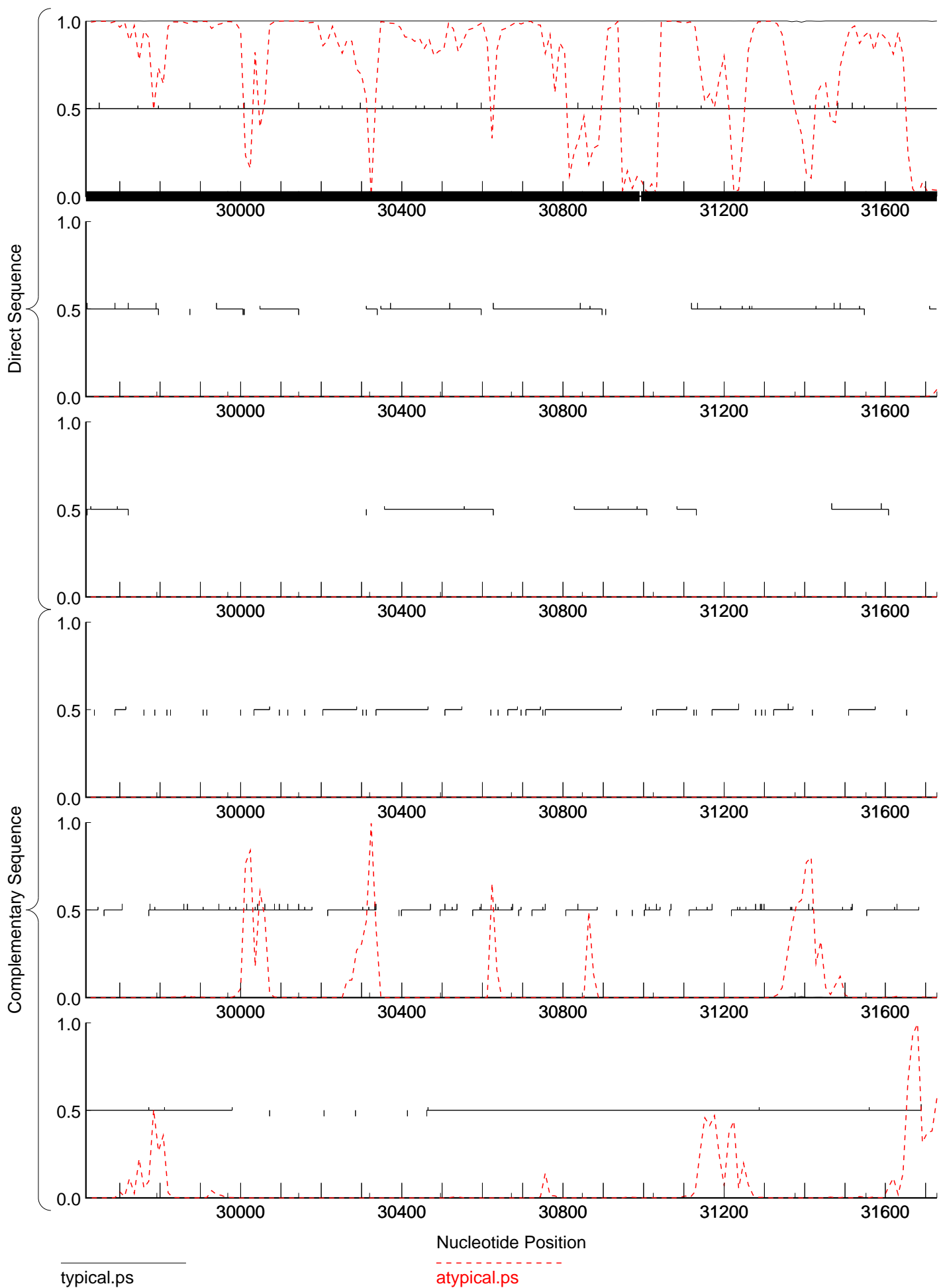


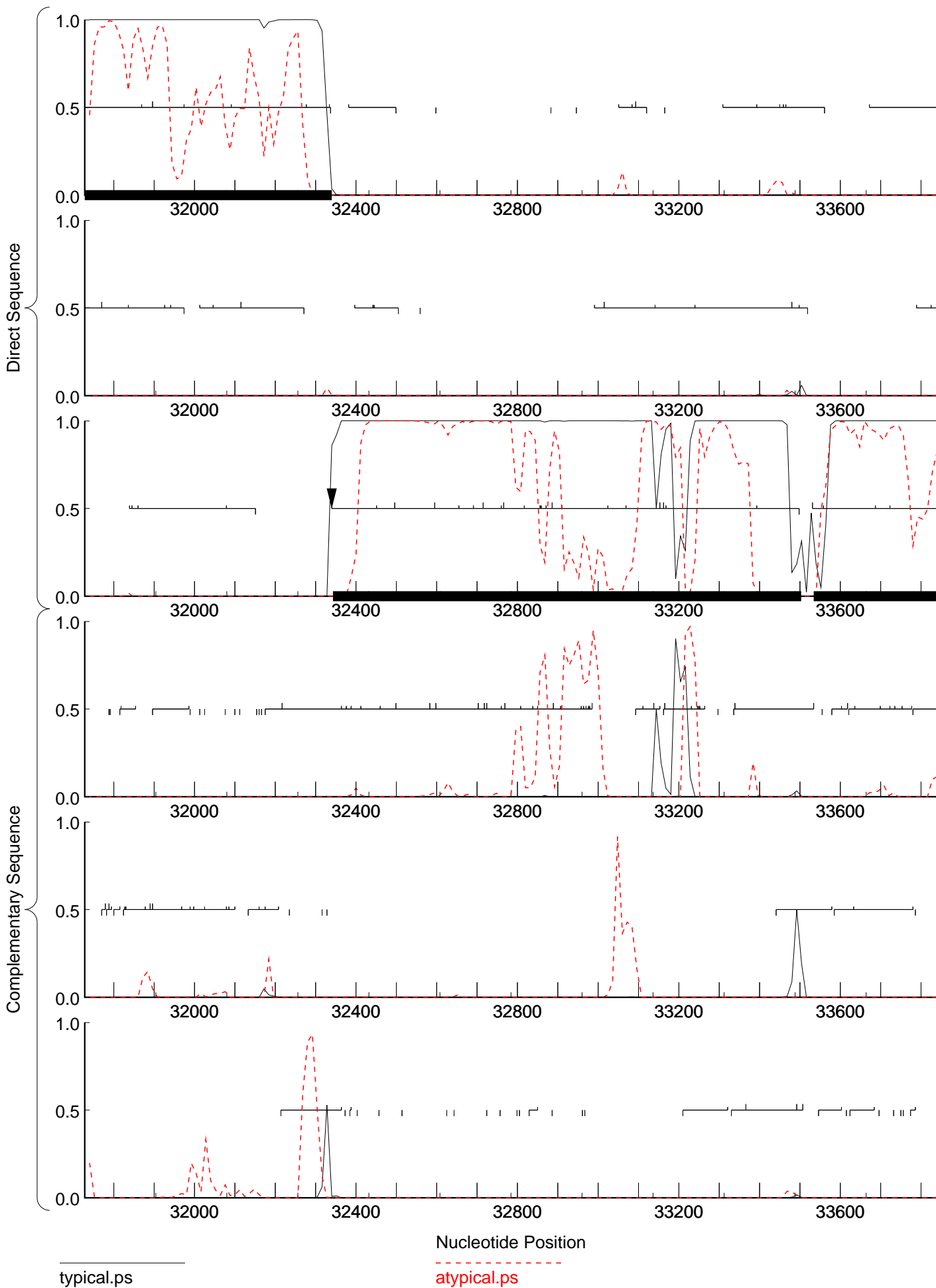


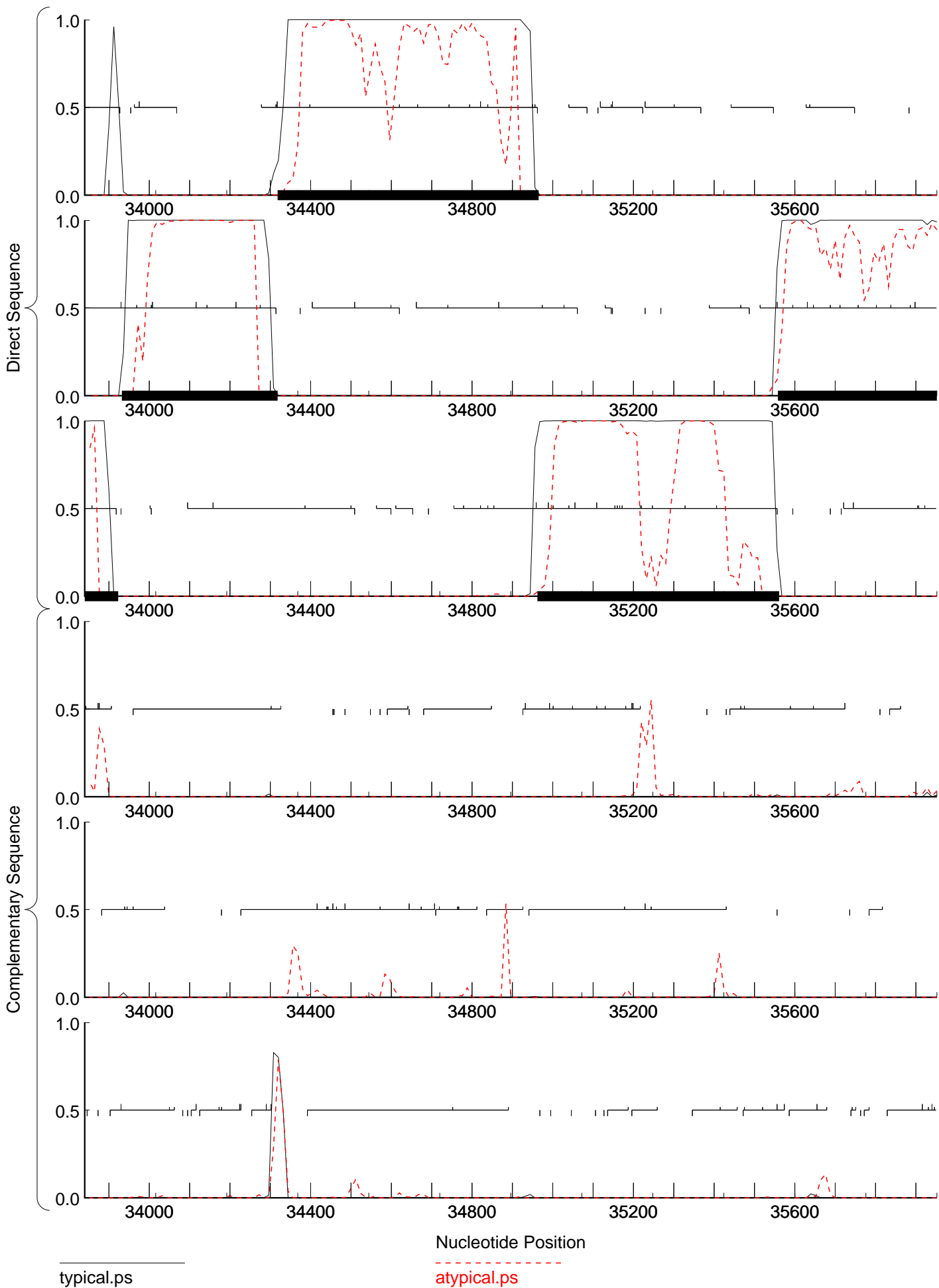
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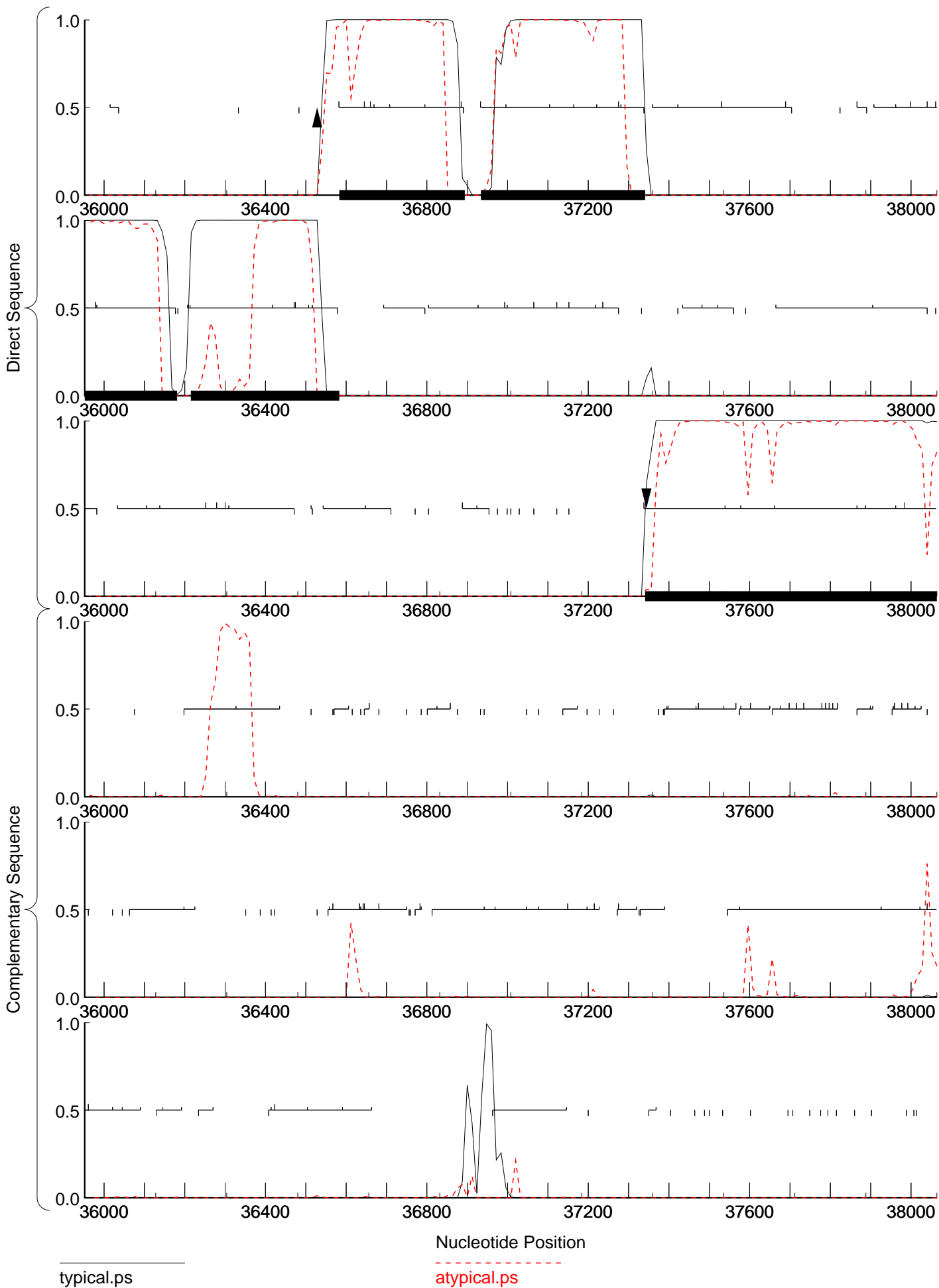
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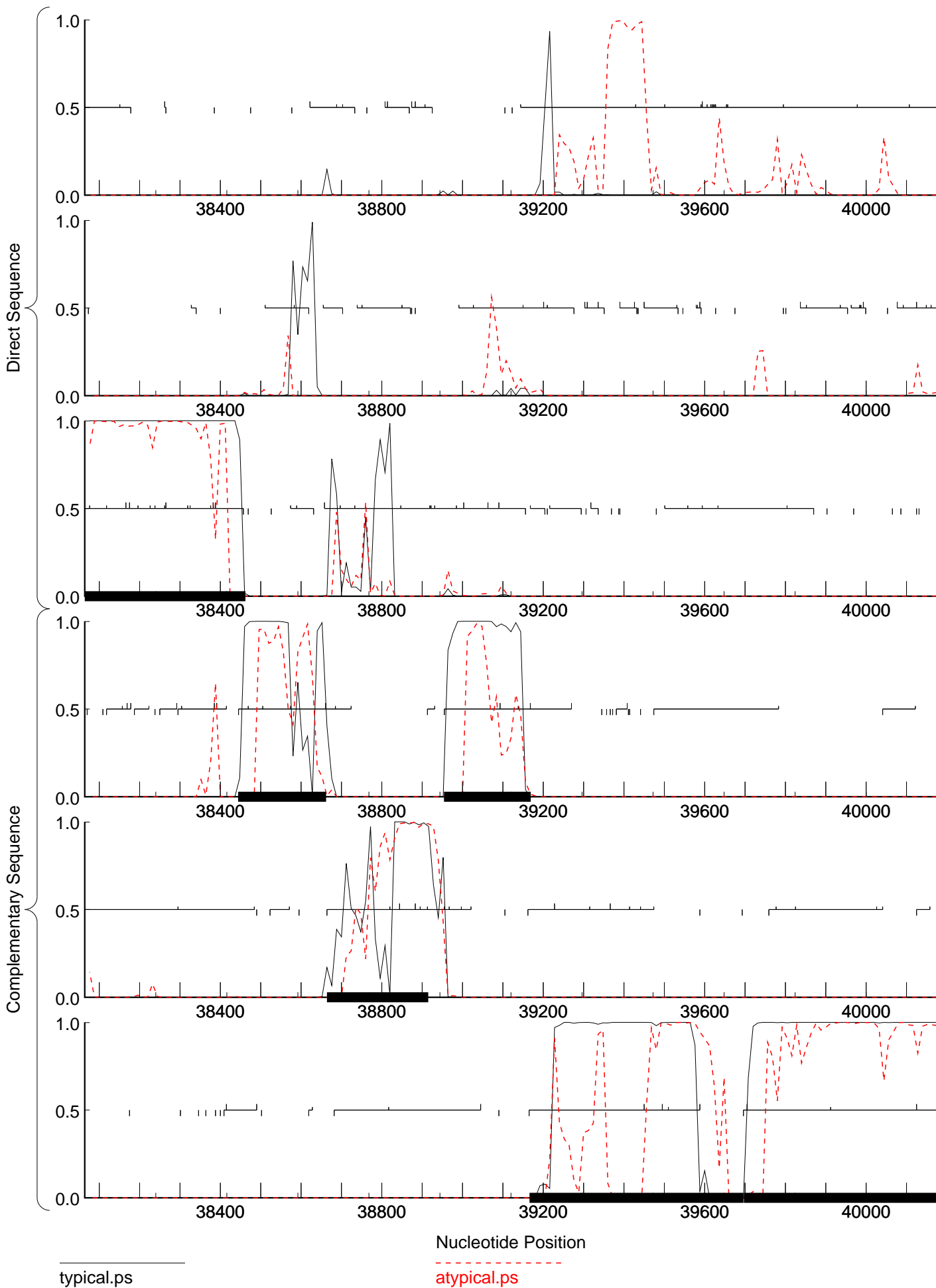








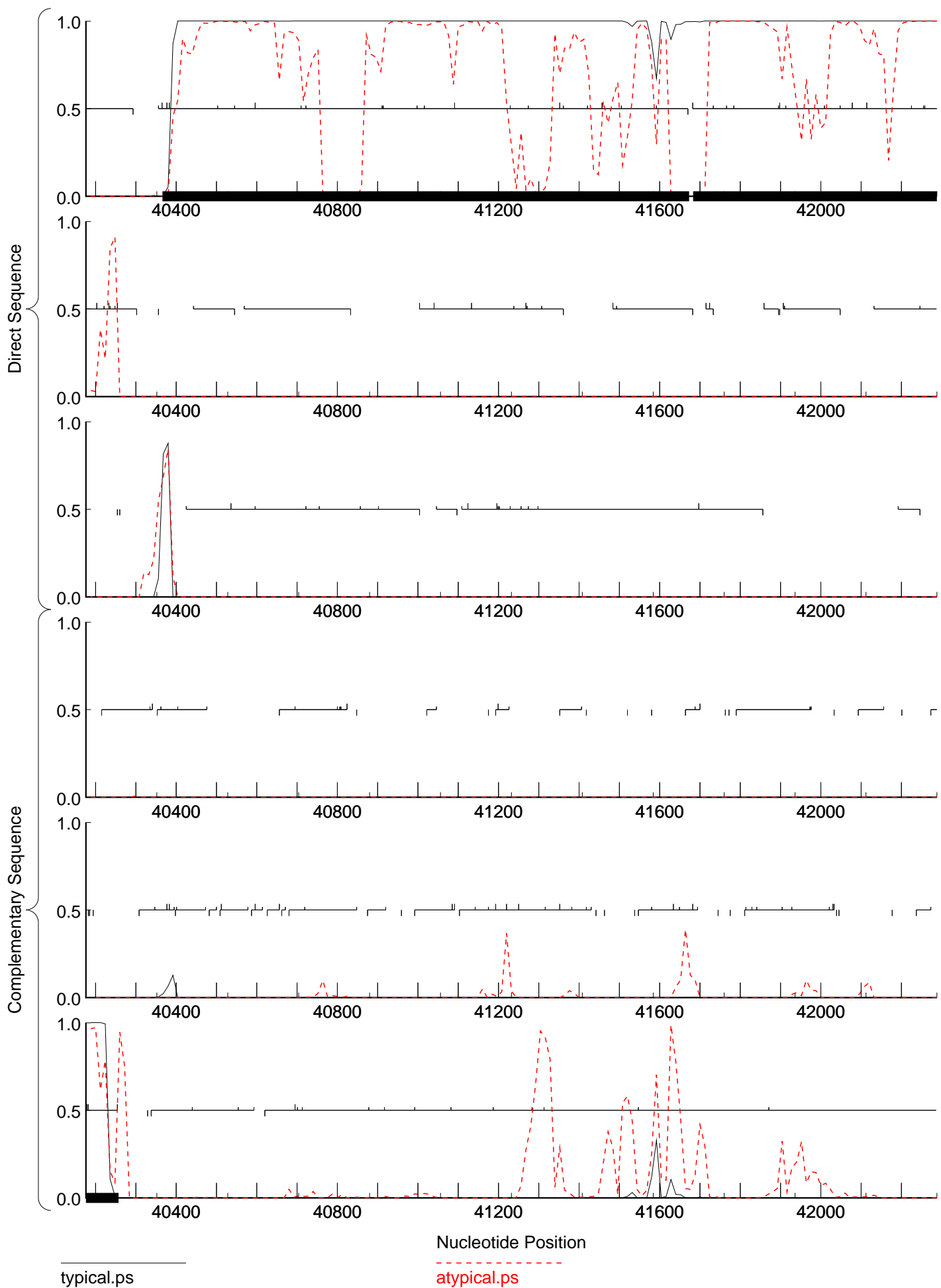


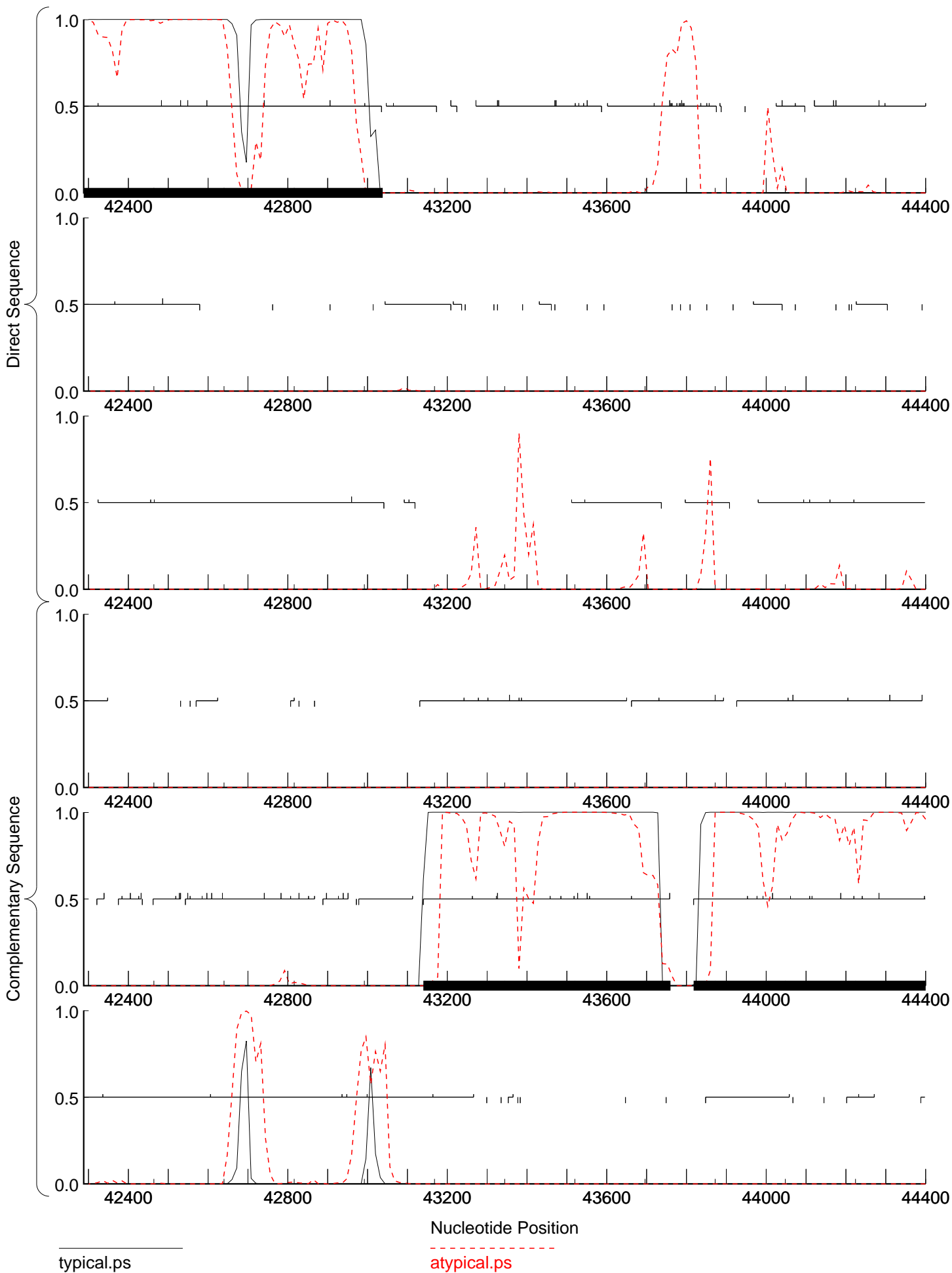


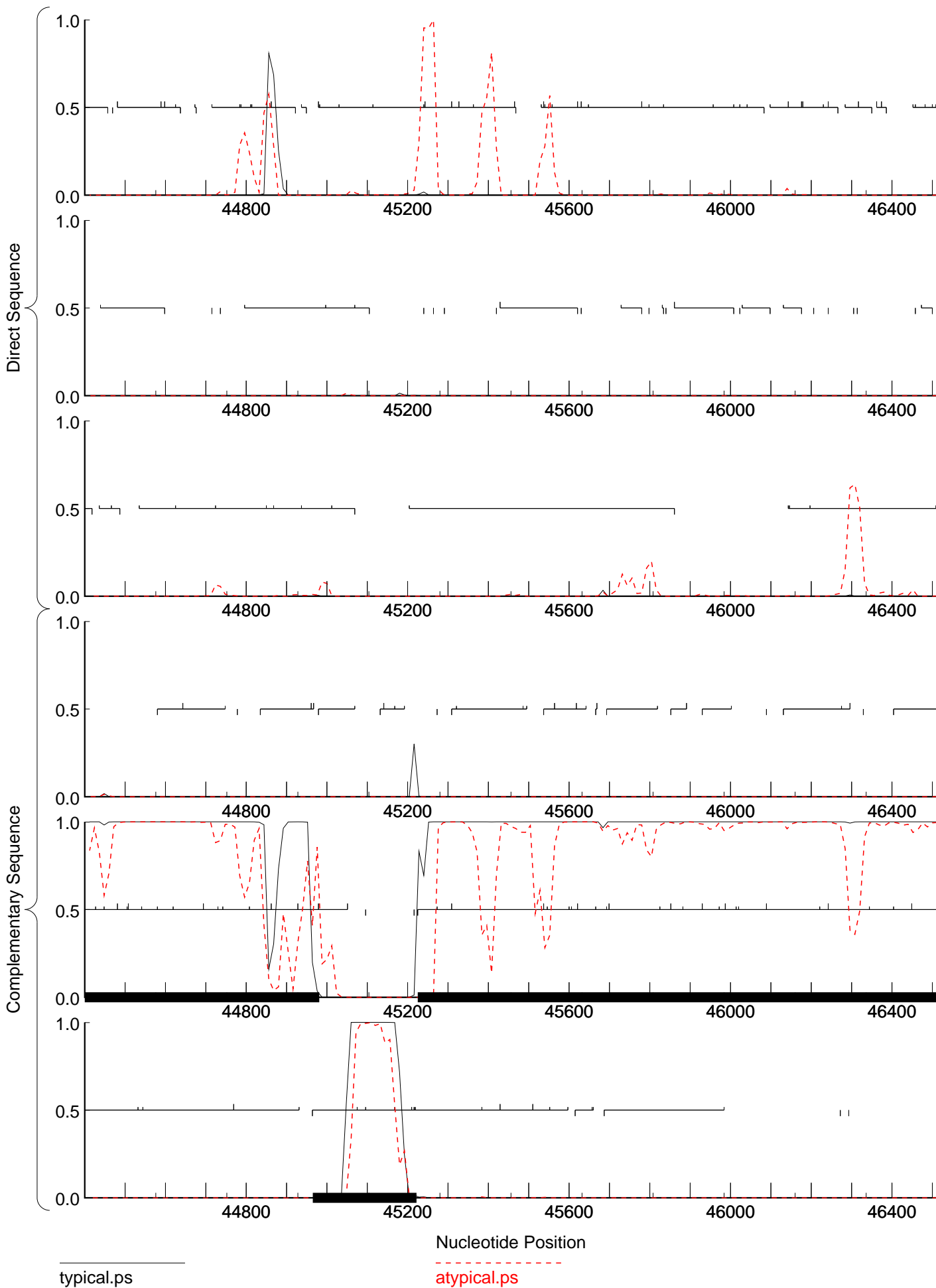
typical.ps

Nucleotide Position

atypical.ps

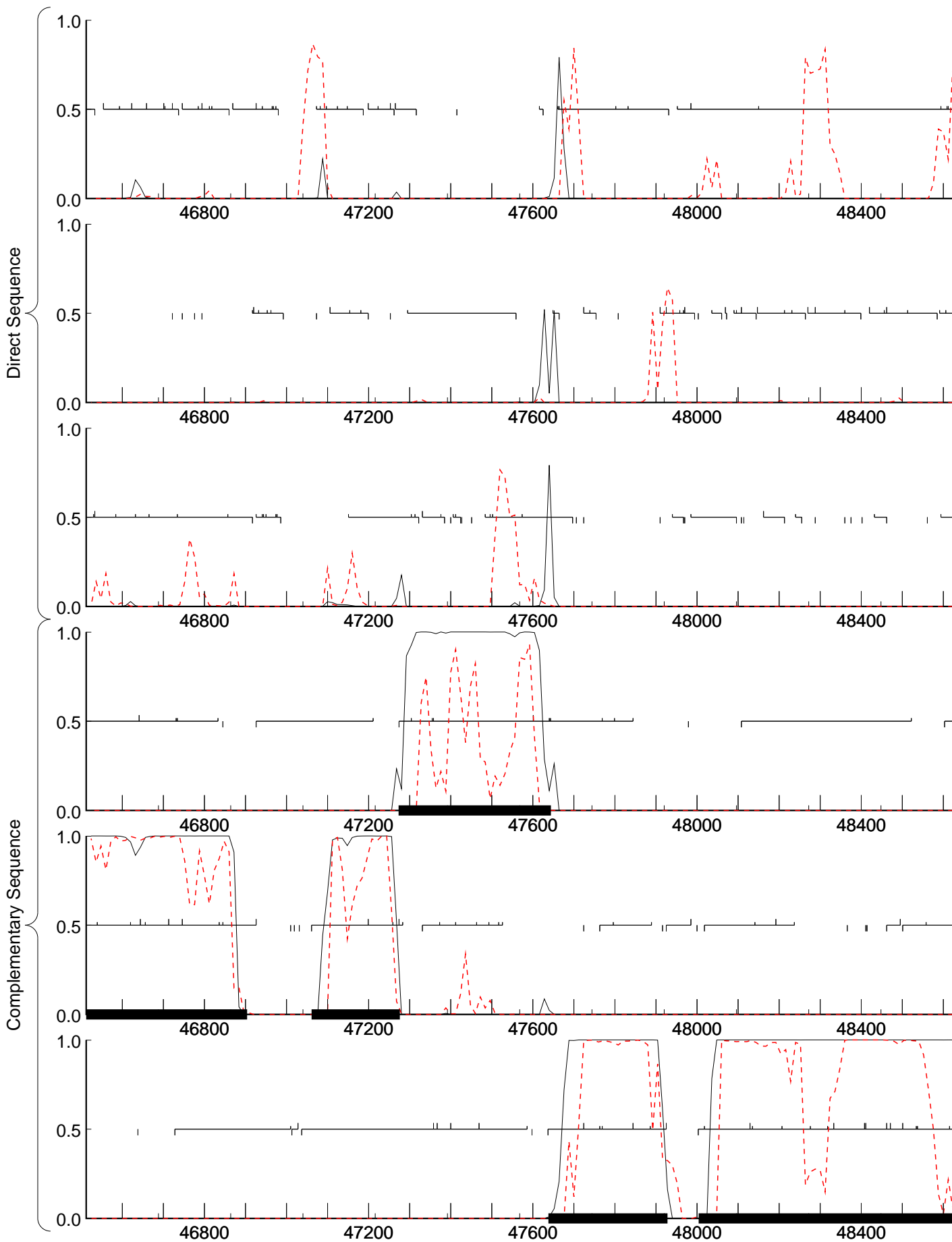






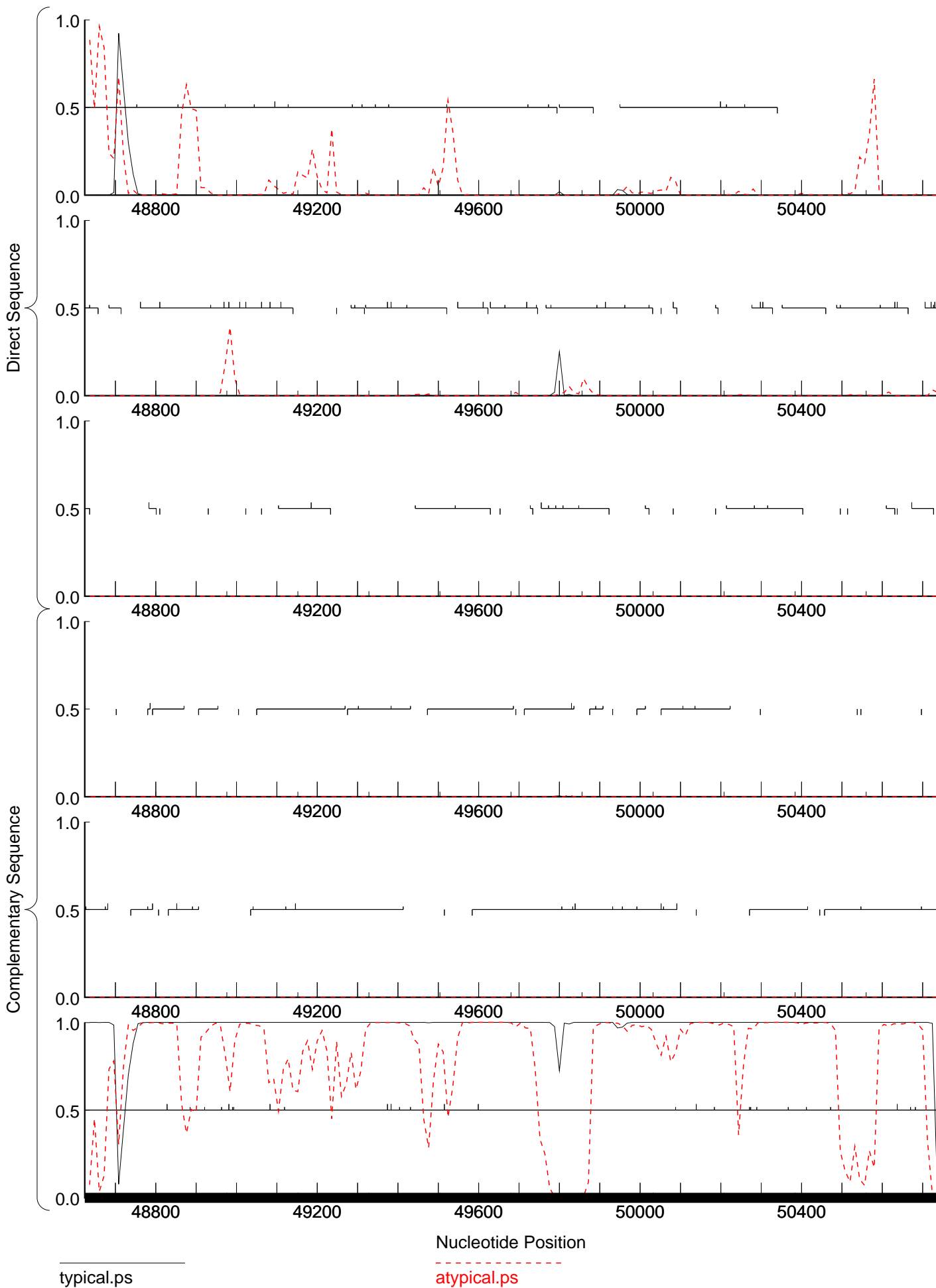
typical.ps

atypical.ps



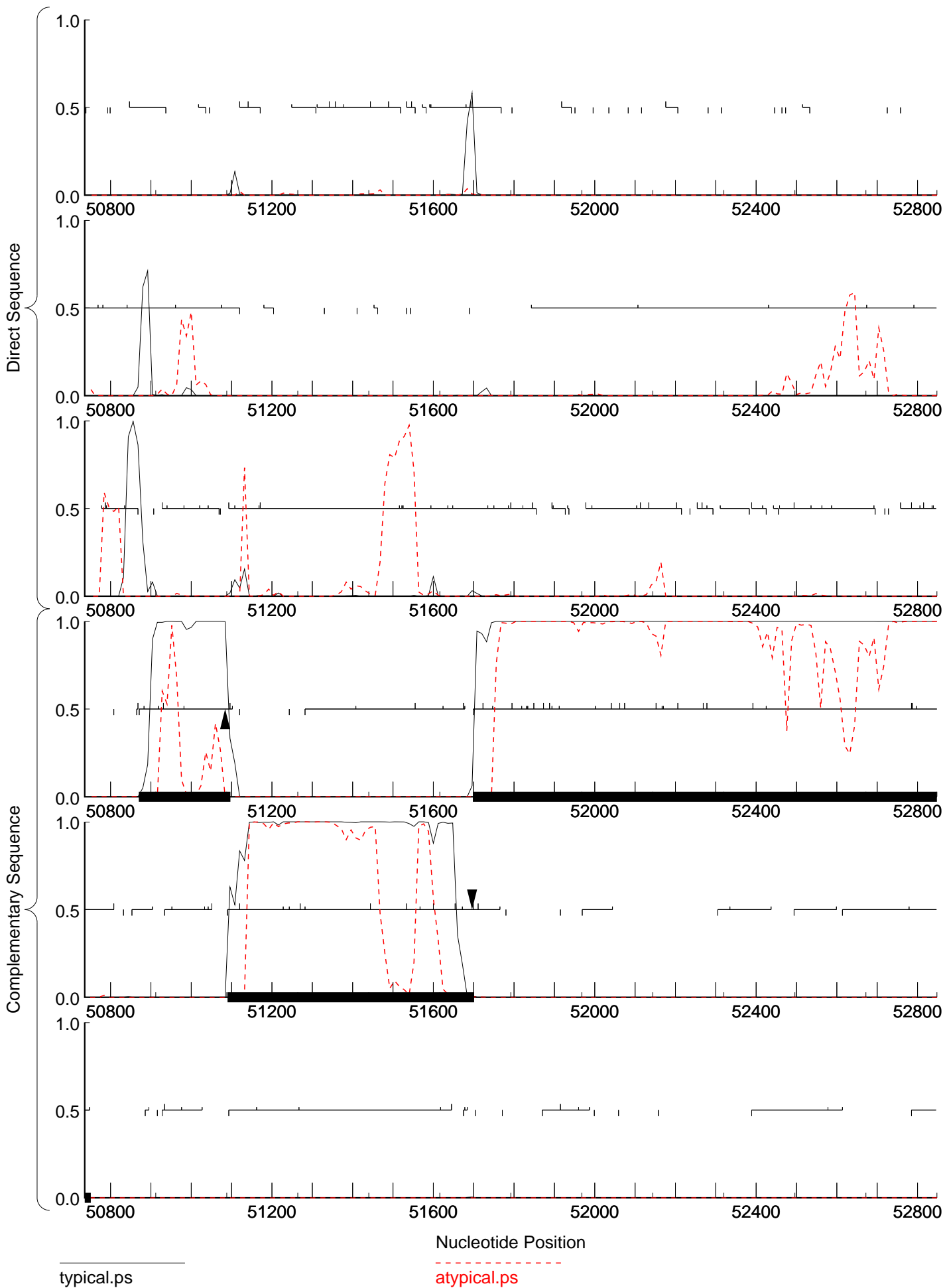
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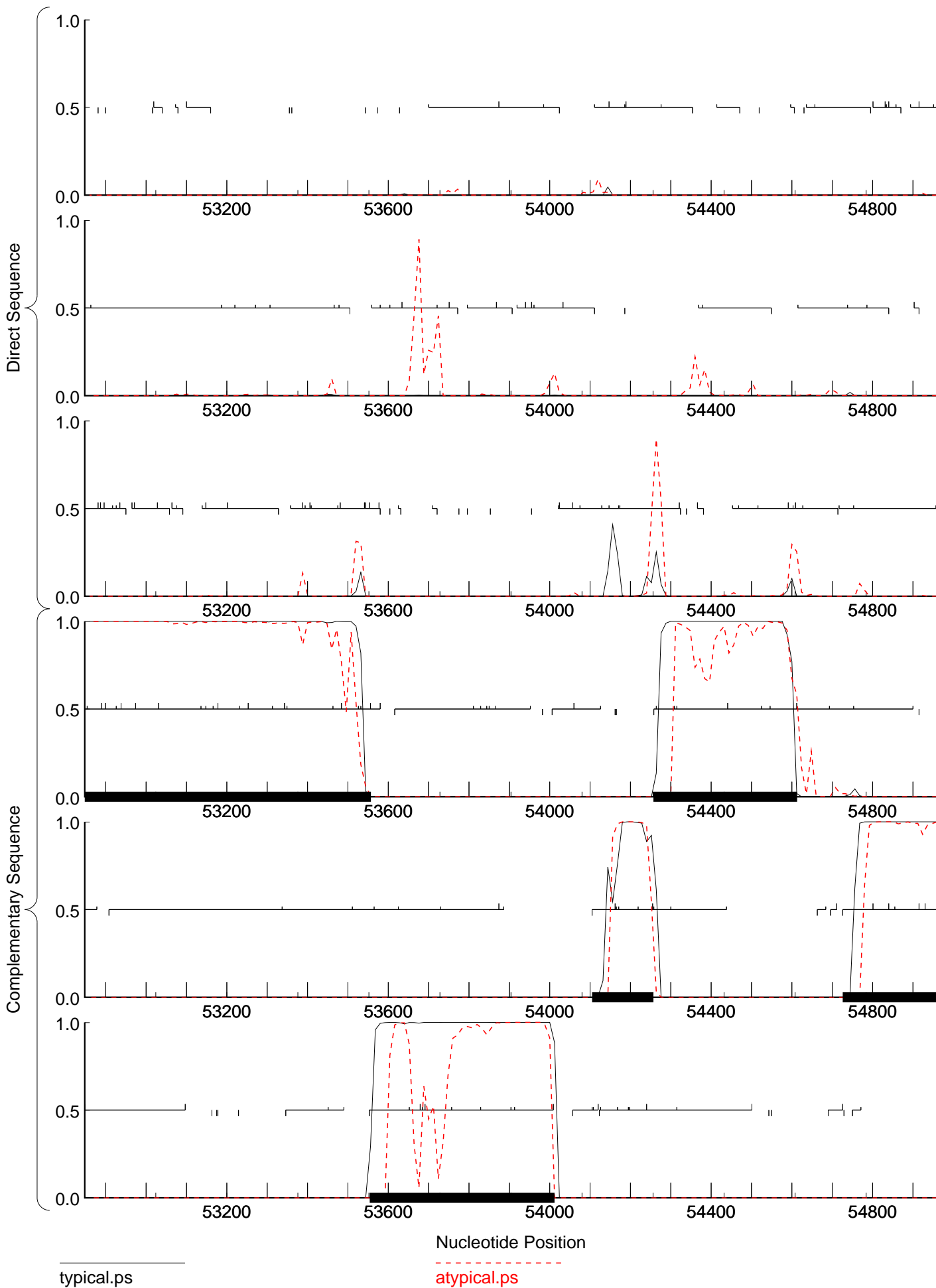
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typical.ps

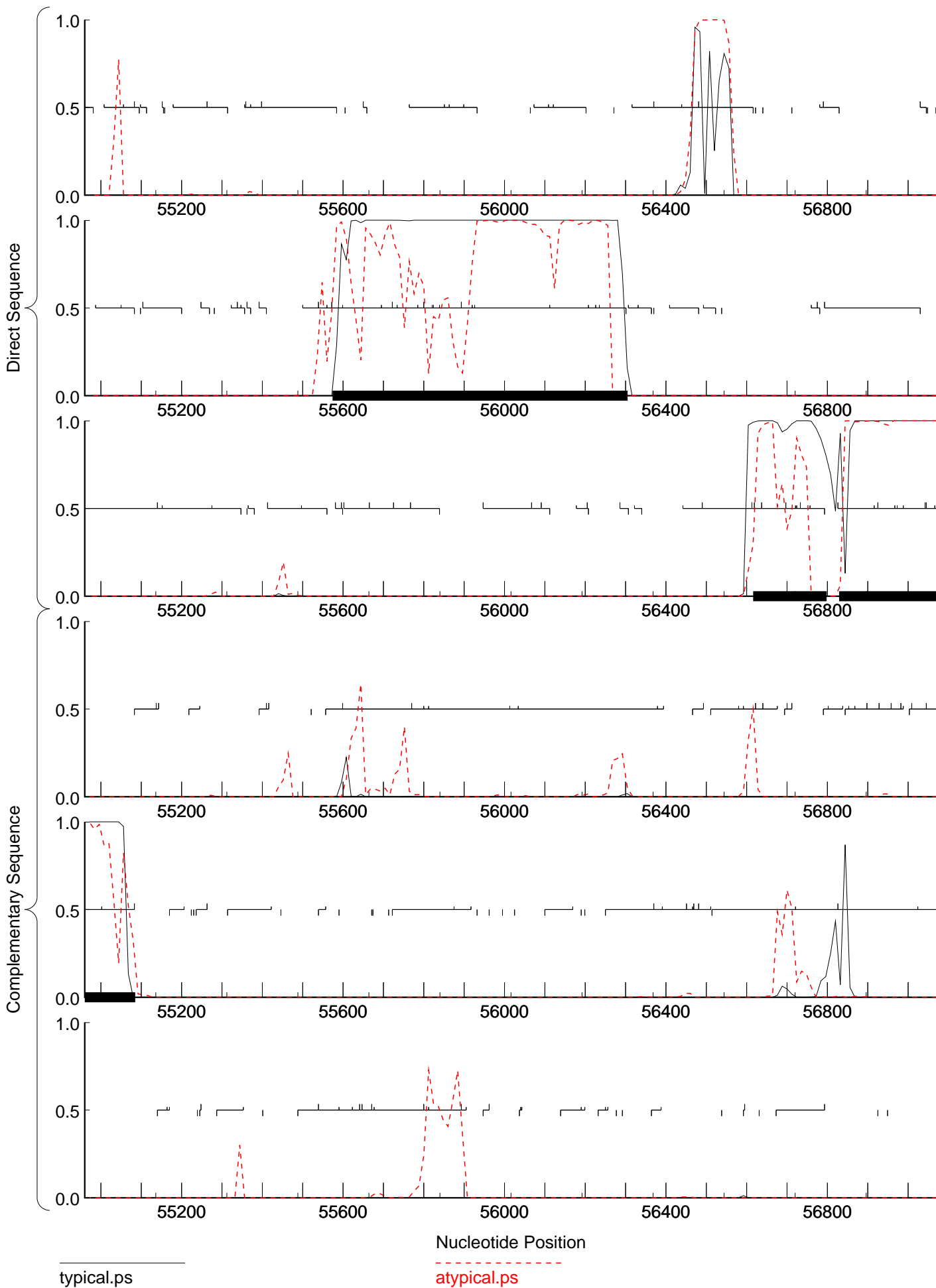
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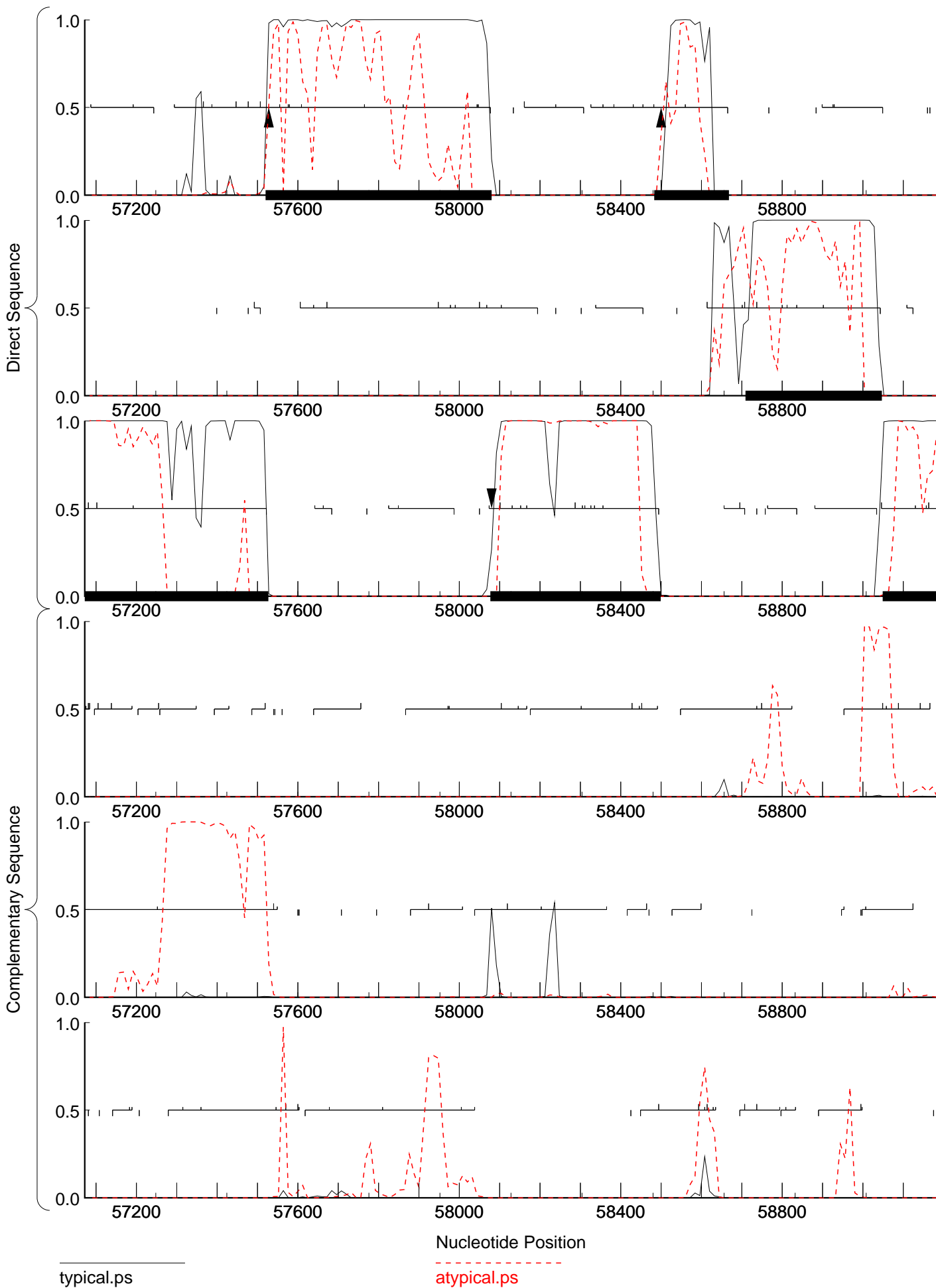




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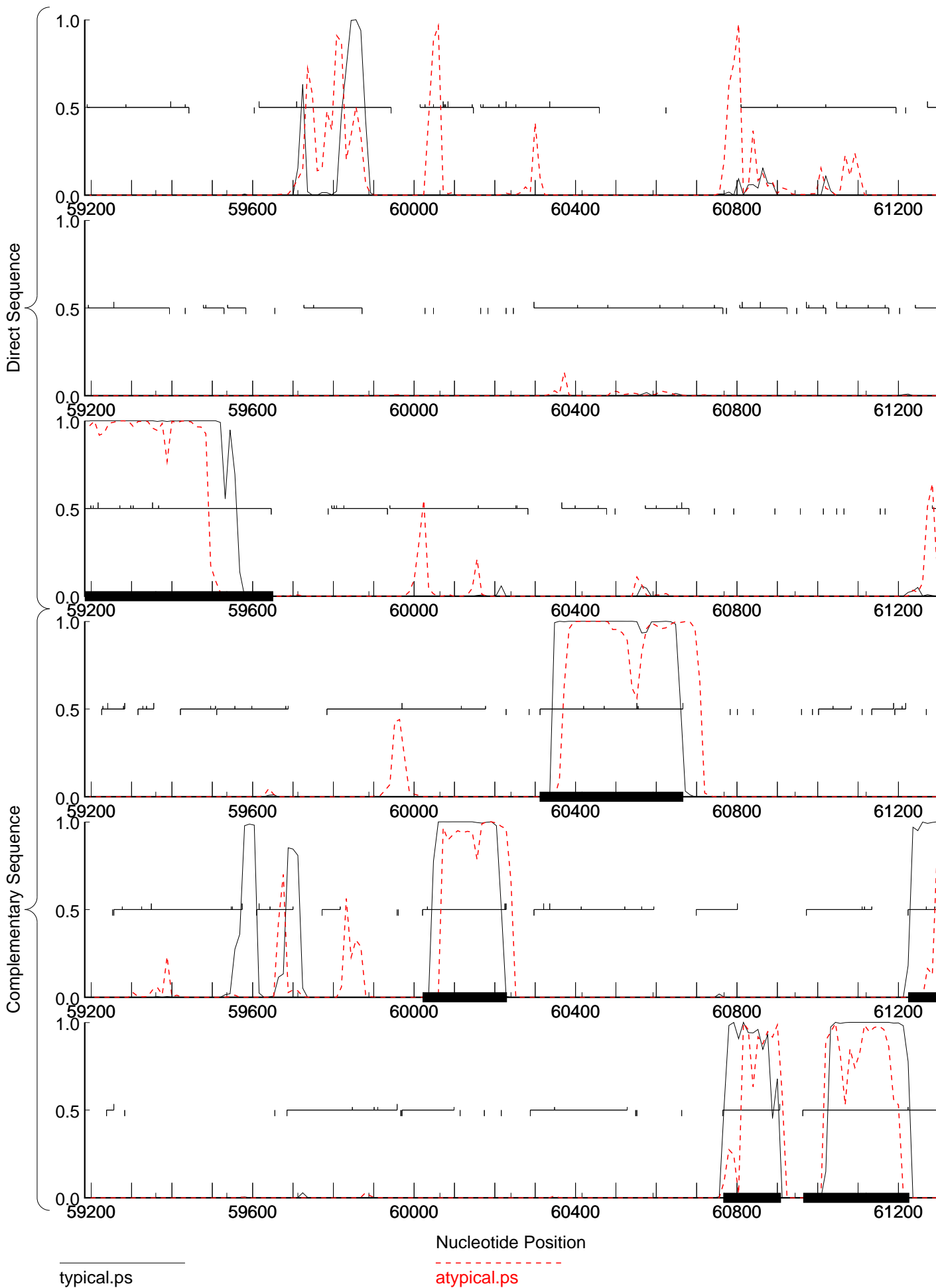
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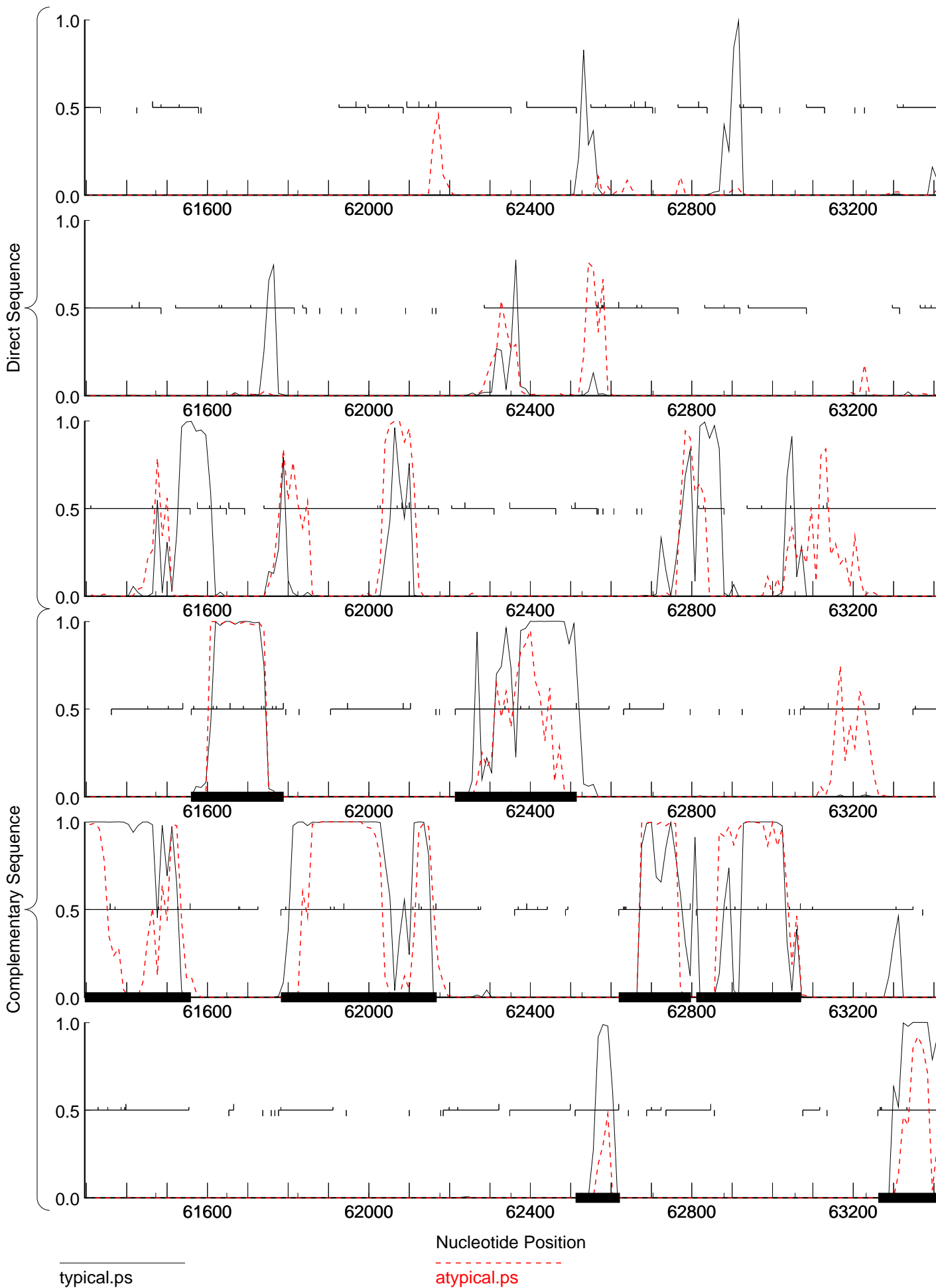
typical.ps

atypical.ps



typical.ps

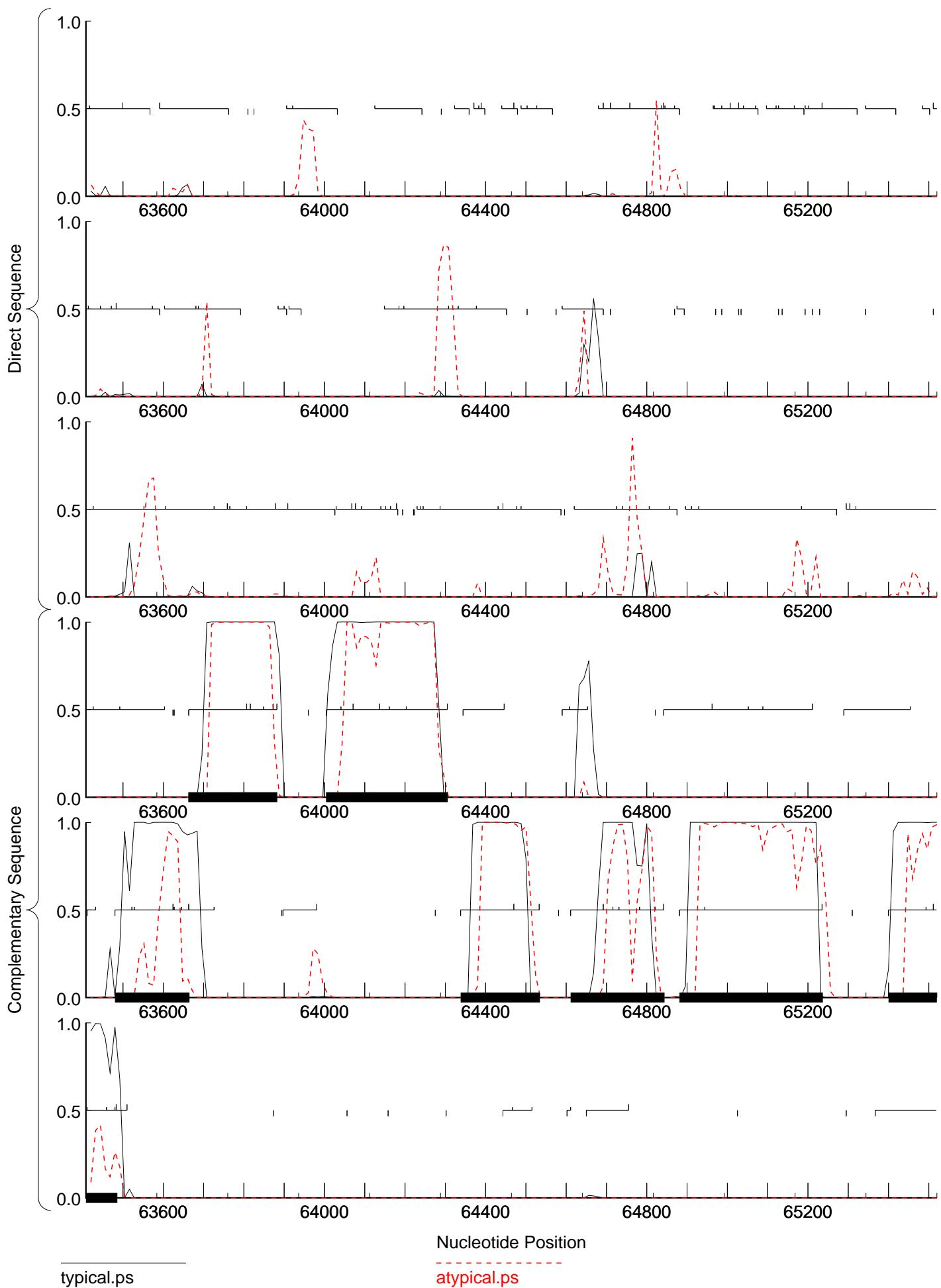
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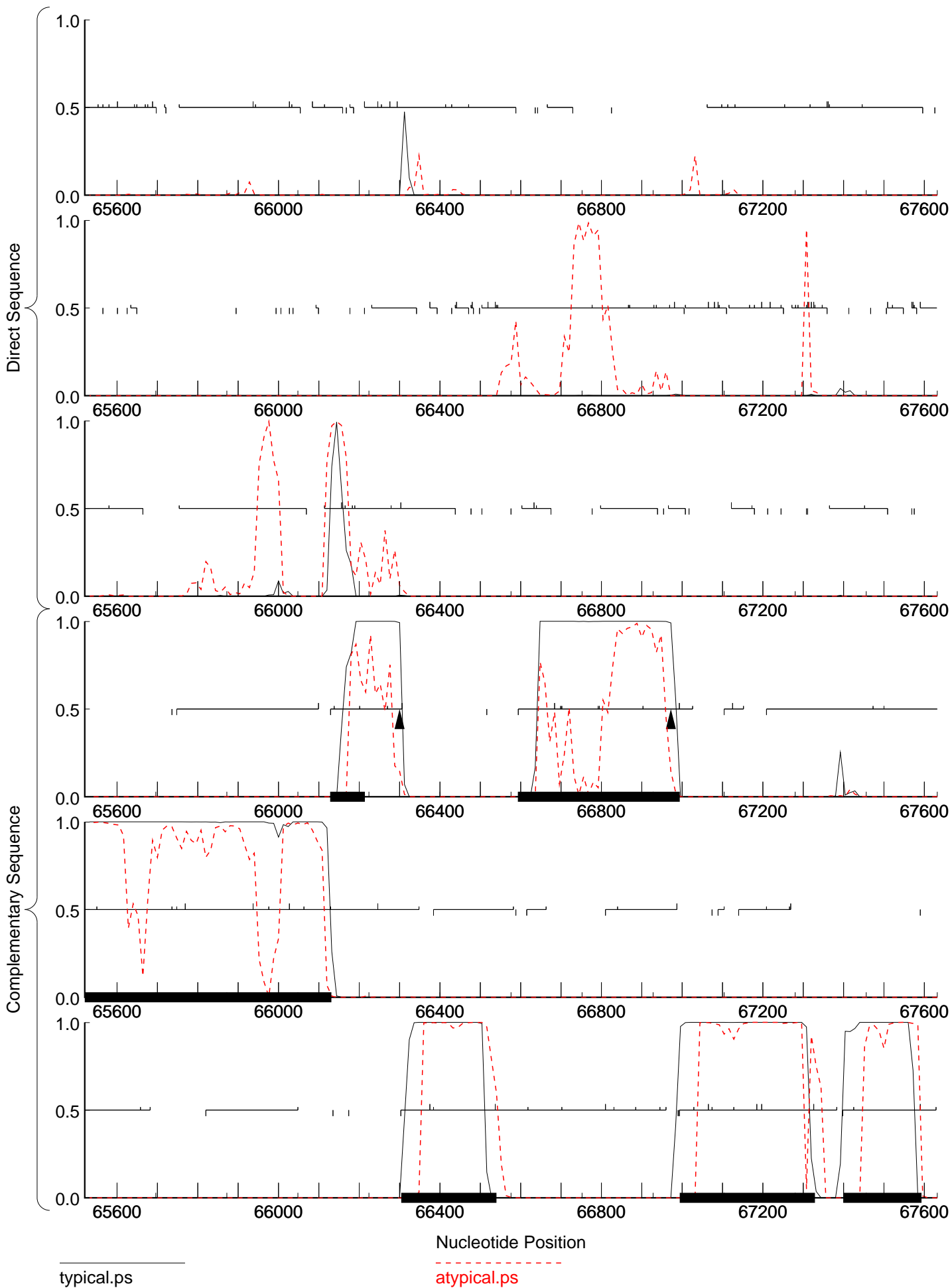


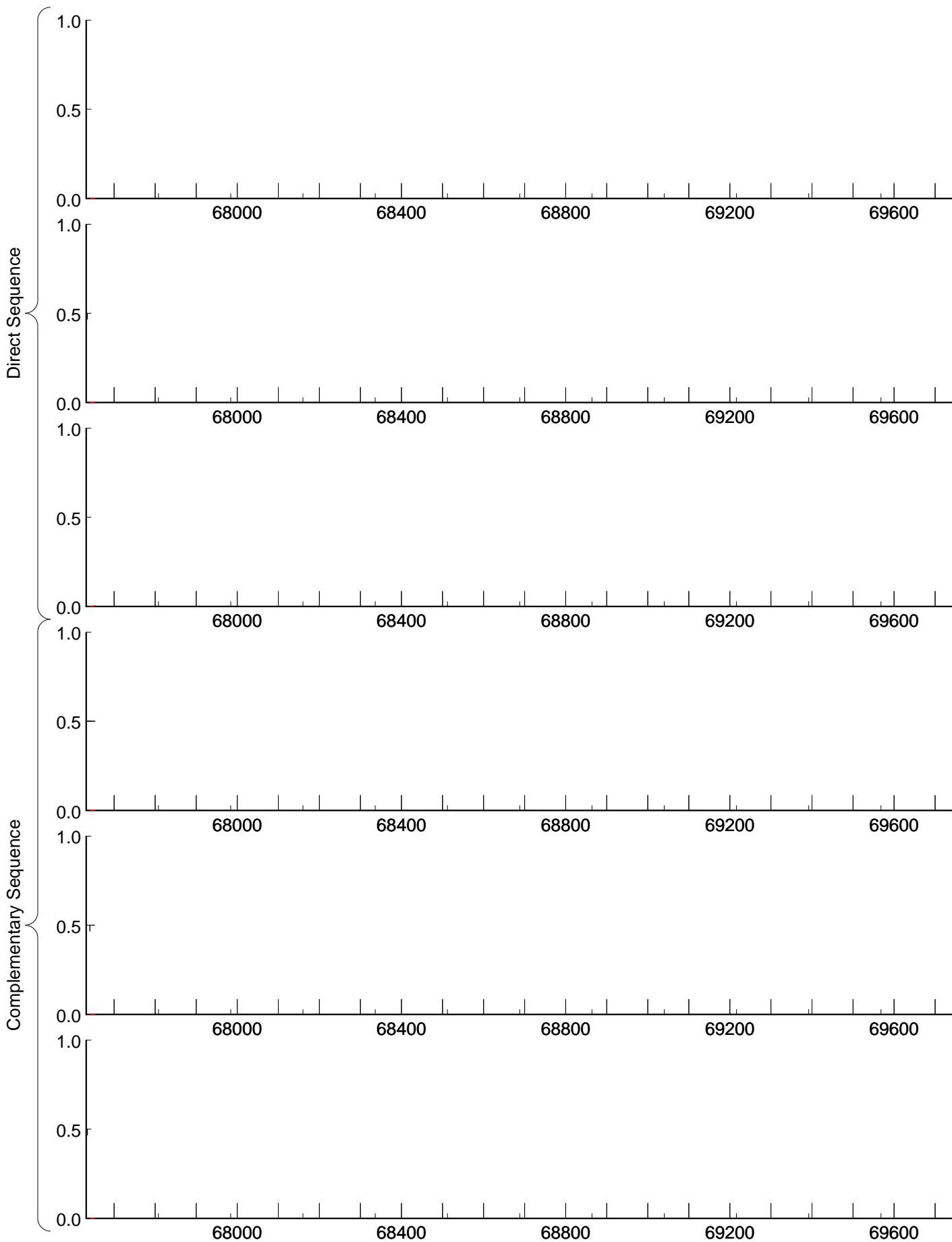
typical.ps

Nucleotide Position

atypical.ps







typical.ps

Nucleotide Position

atypical.ps