

GeneMark

Version 2.5p (09.08.06)

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PROGRAM INFORMATION

Sequence : Mycobacterium phage Icee complete sequence, 74169 bp including 9-base 3' overhang (CGCTTGTC
Analysis Date : 1/18/18 at 20:20:56
Pages : 37
Sequence Length : 74169 bp
GC Content : 63.00%

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,

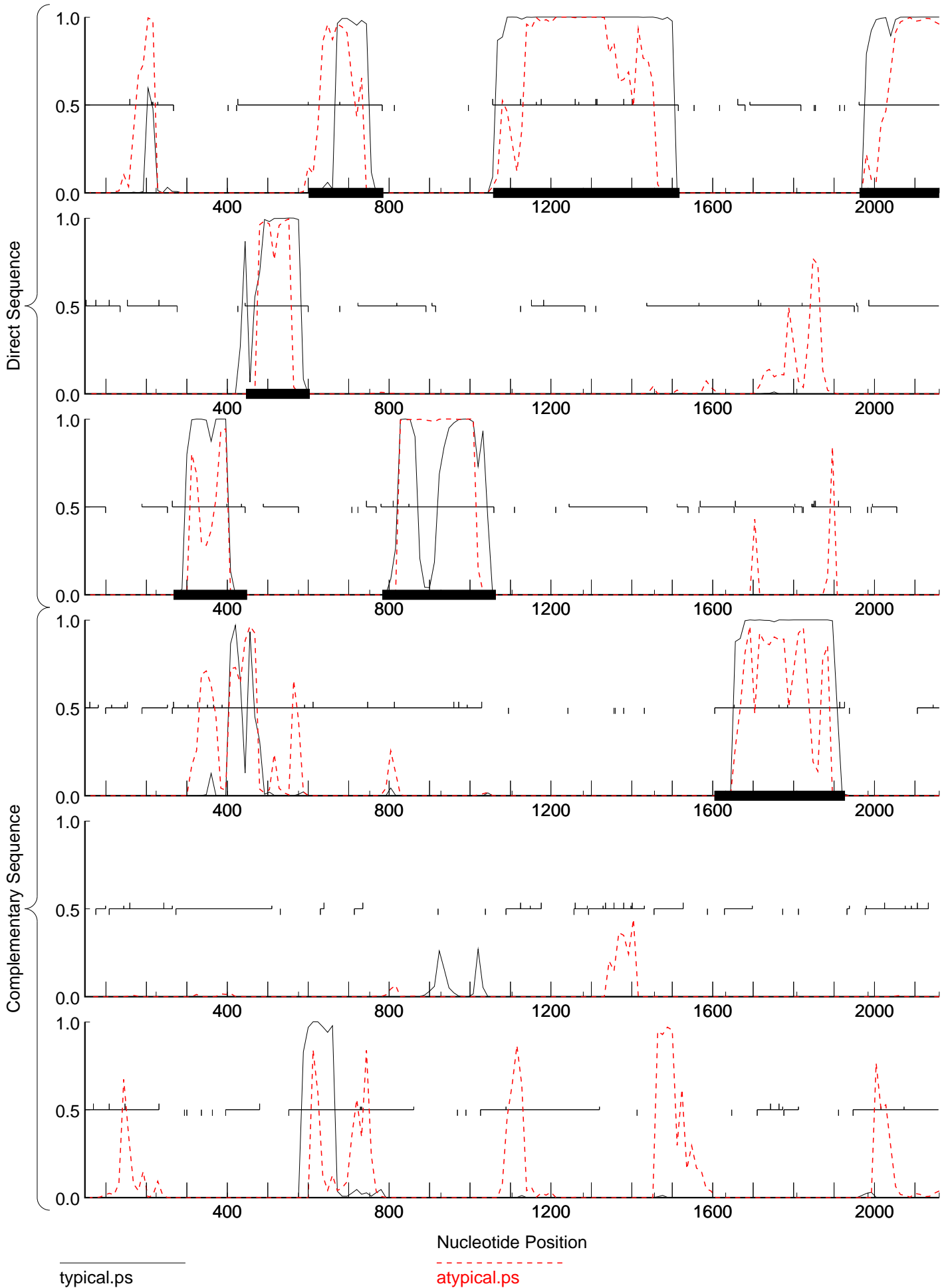
Matrix notes & comments

Training set derived by GeneMarkS, 4.30 October 2014
Thu Jan 18 20:20:56 2018

MATRIX INFORMATION

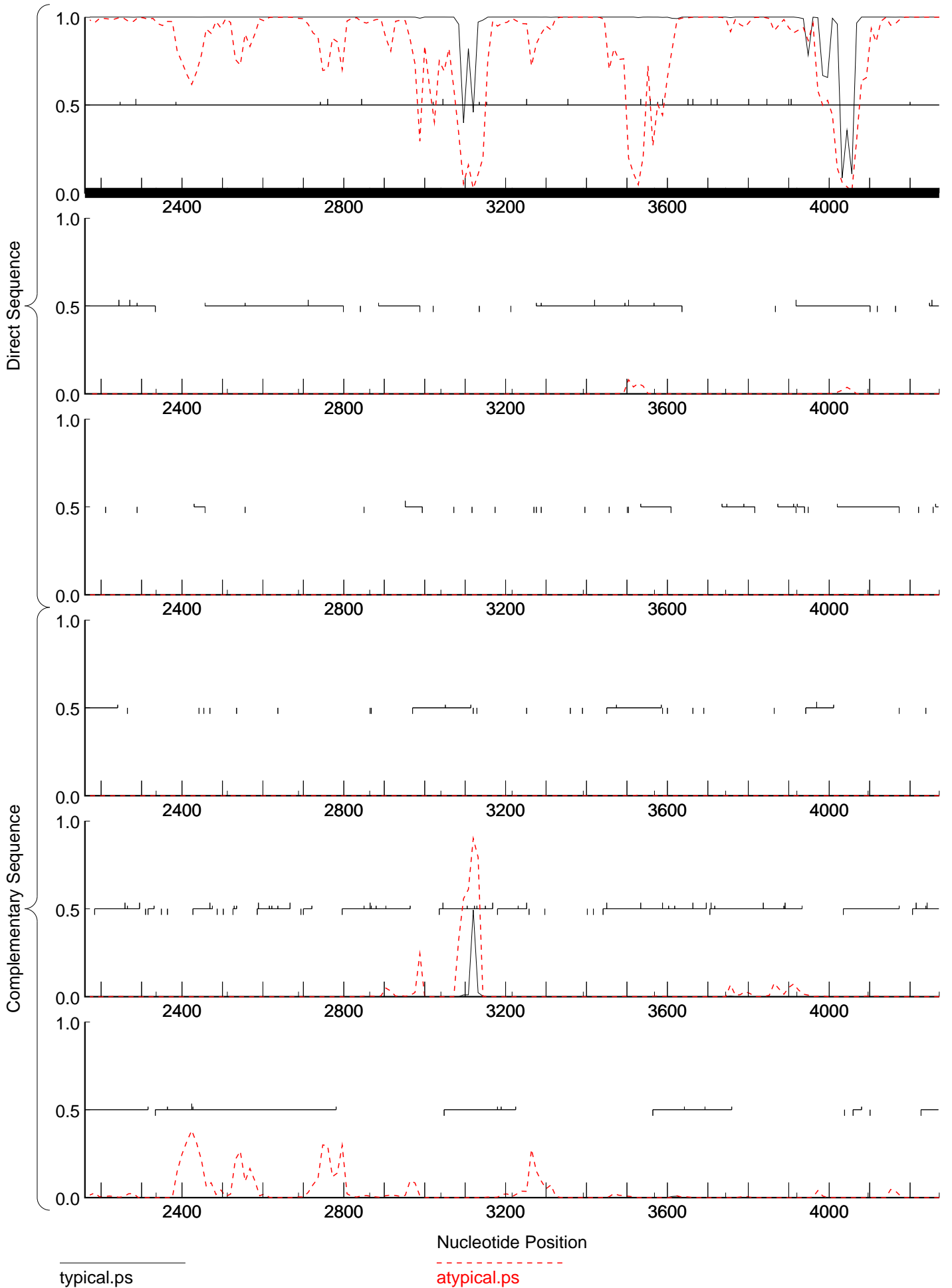
Matrix : -
Author : -
Order : 4

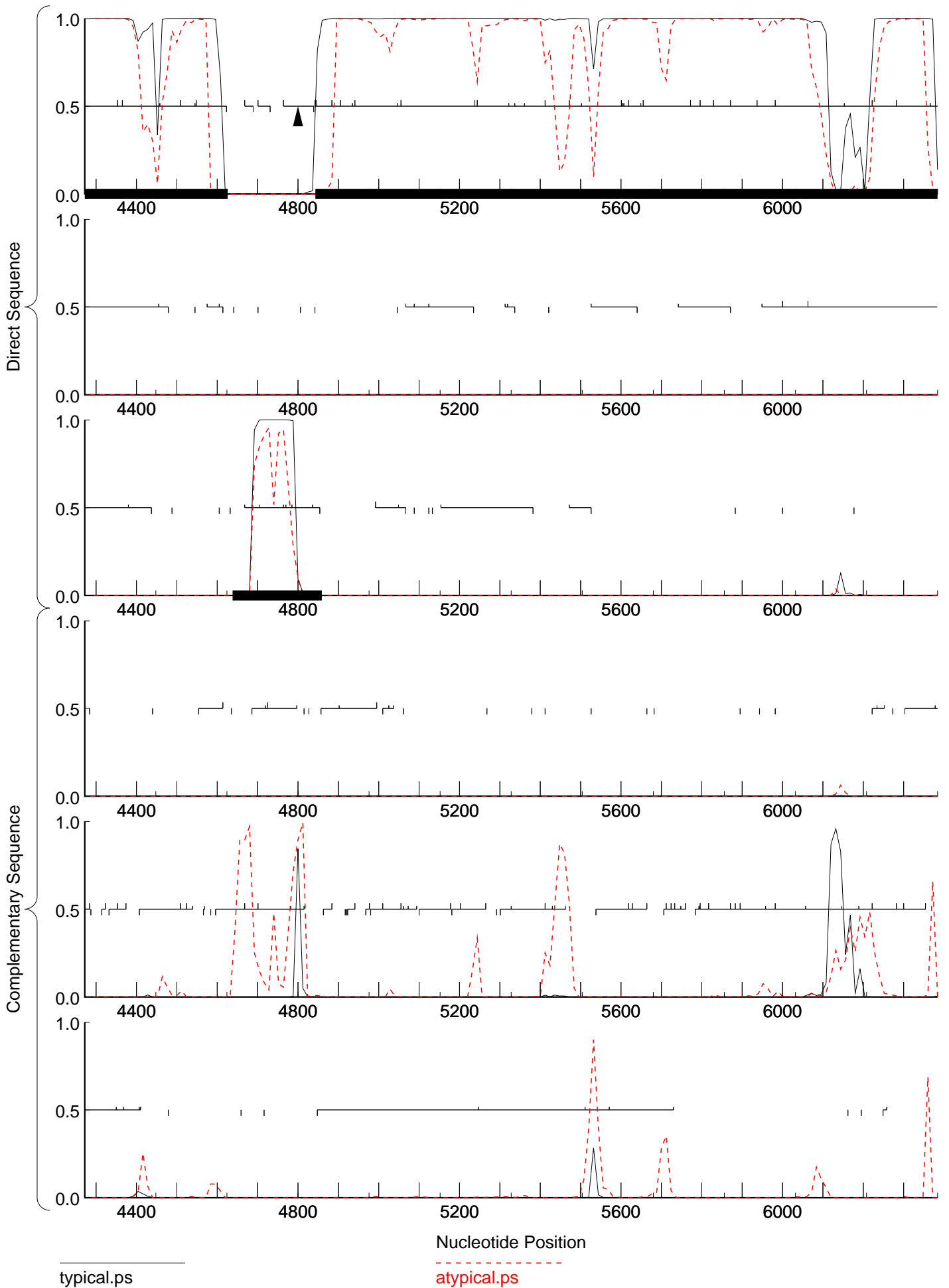
Send questions / comments to:
Dr. M. Borodovsky
Georgia Institute of Technology
School of Biology
Atlanta, GA 30332-0230

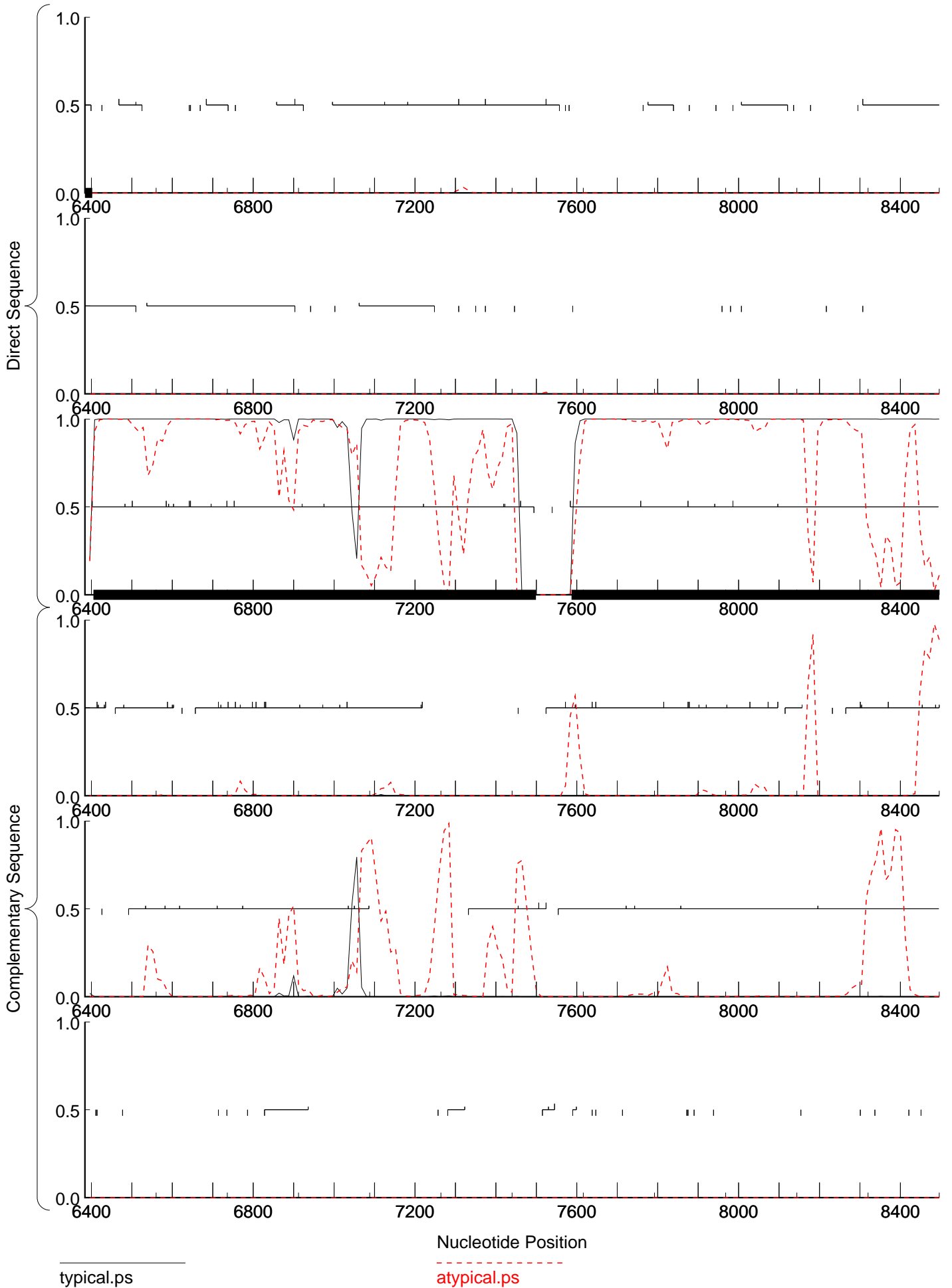


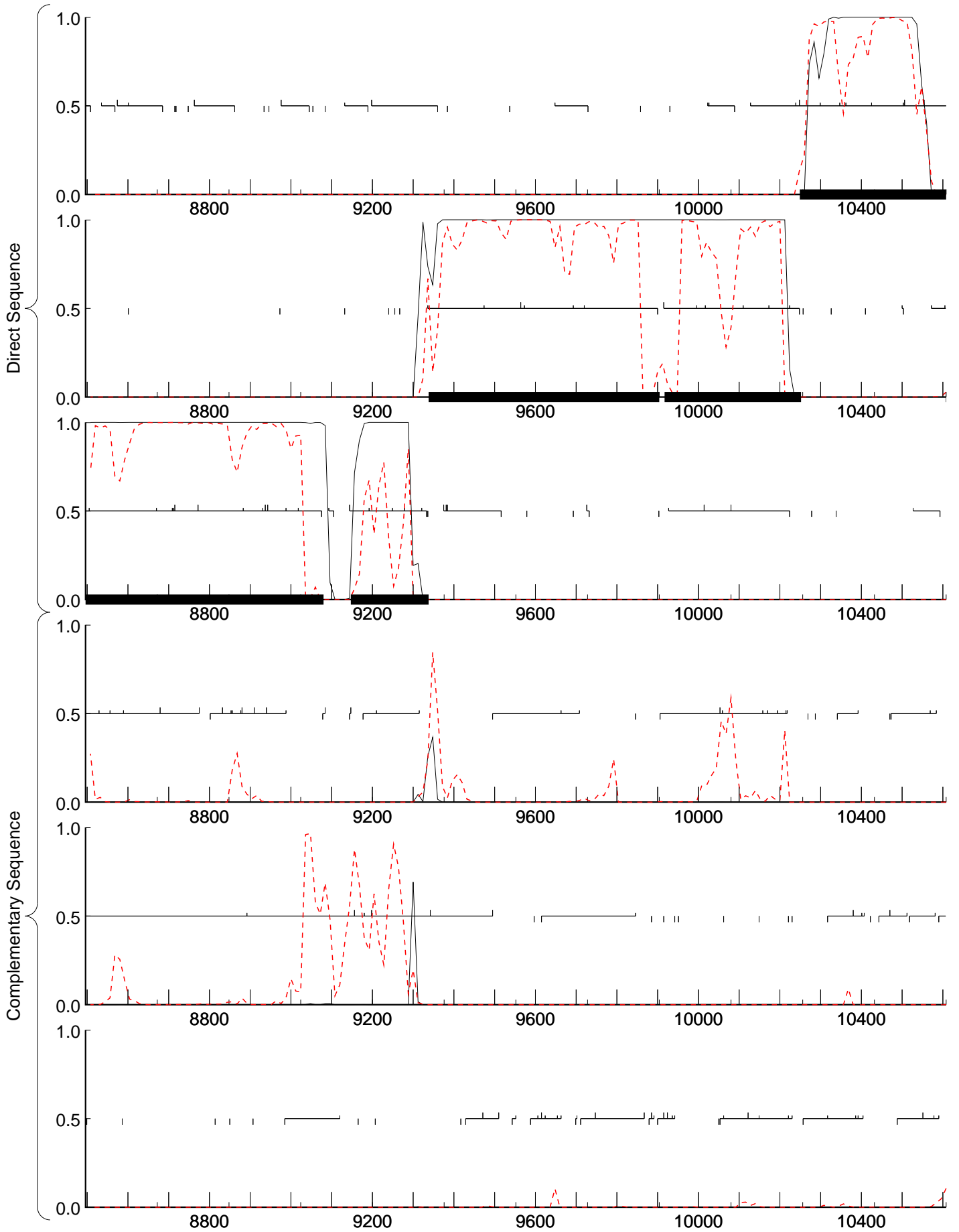
typical.ps

atypical.ps



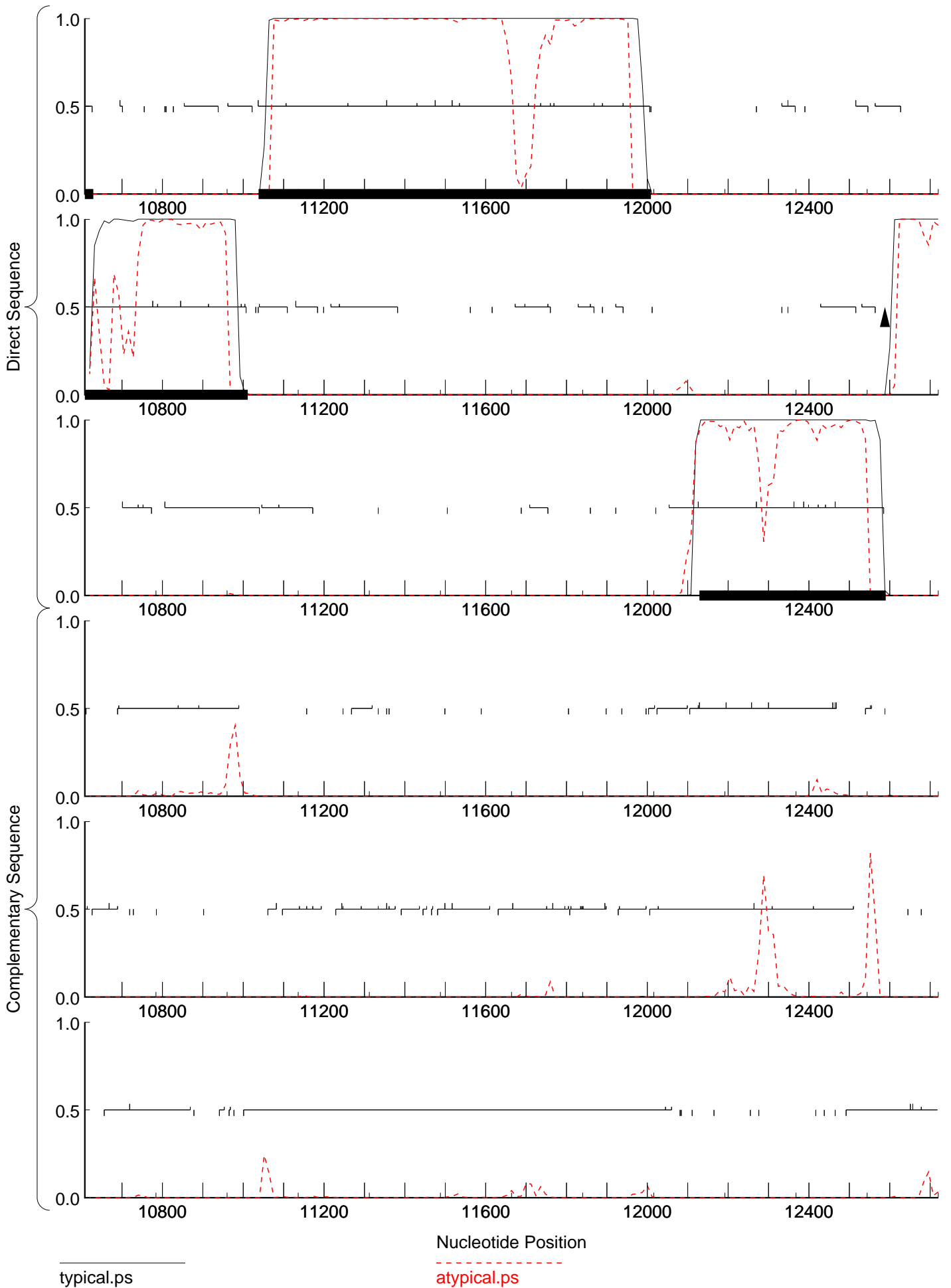


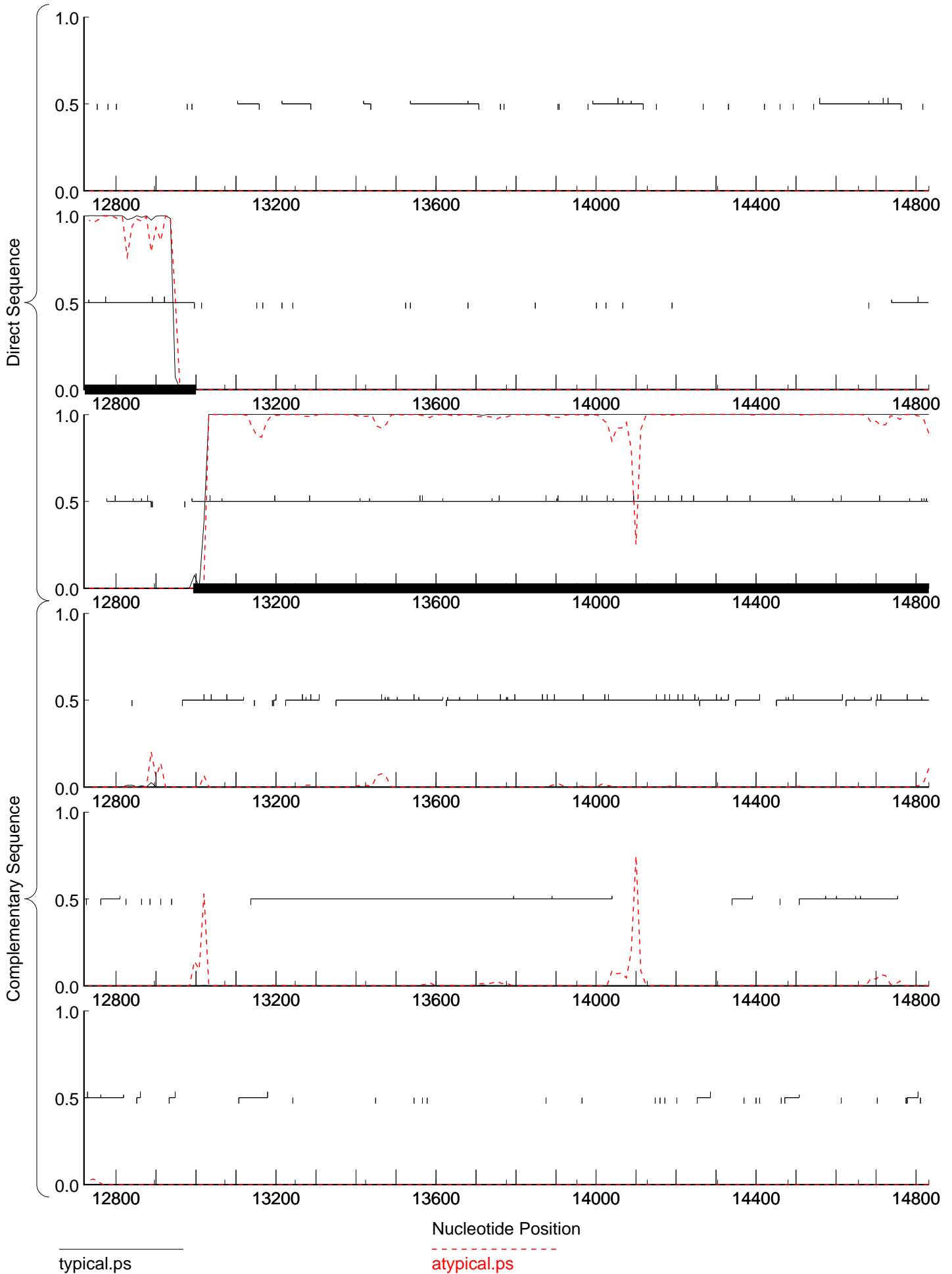




typical.ps

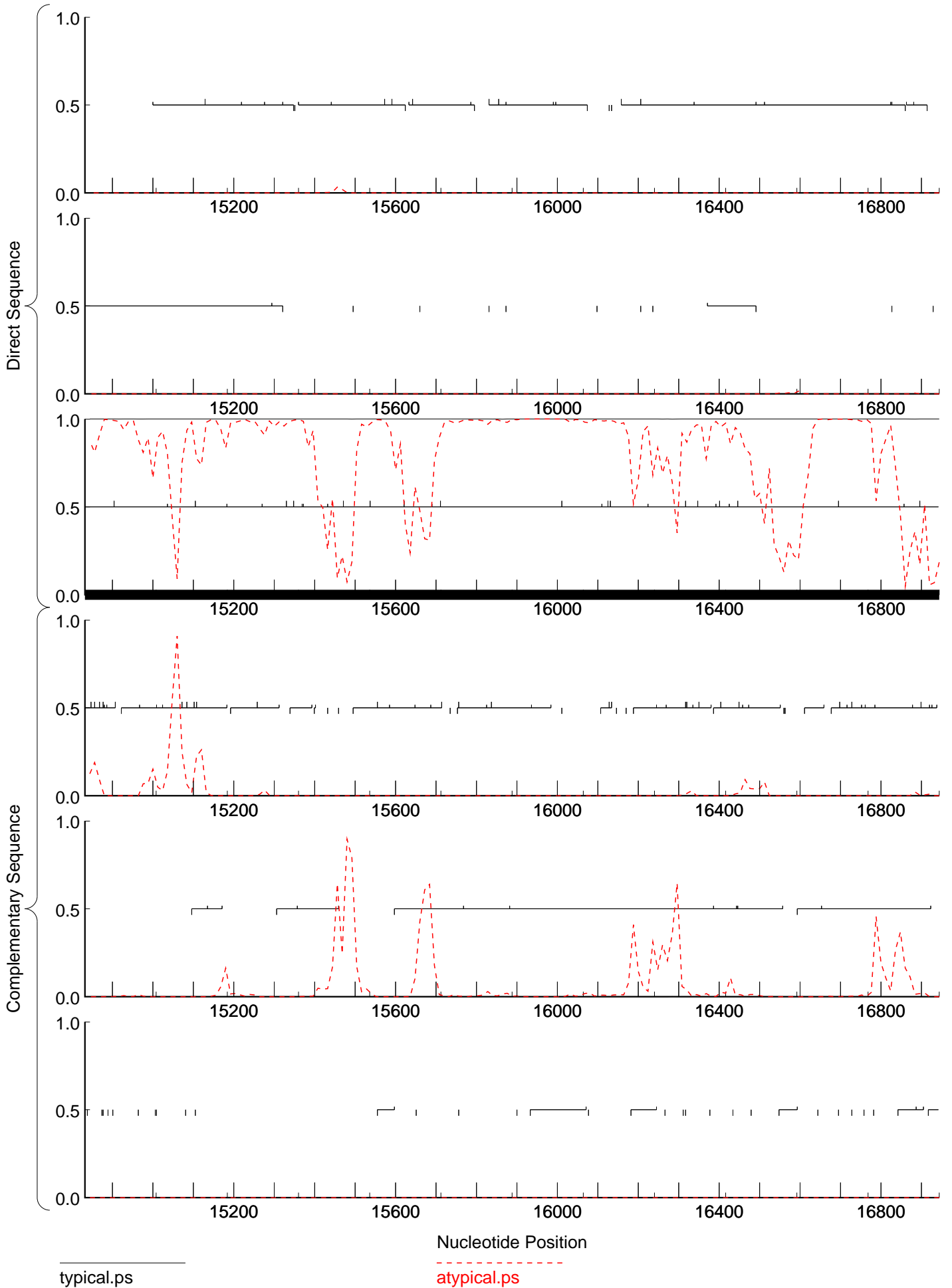
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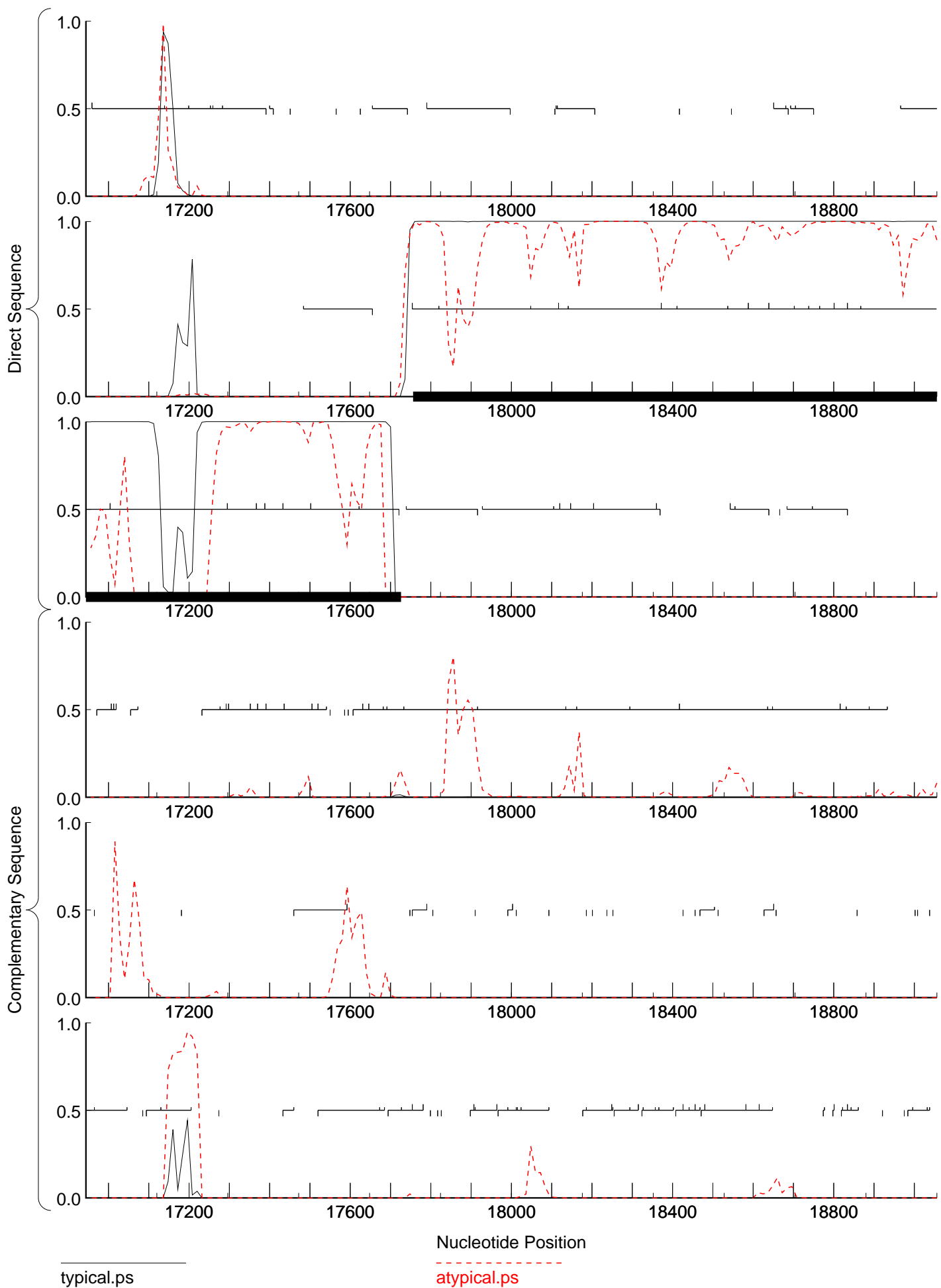


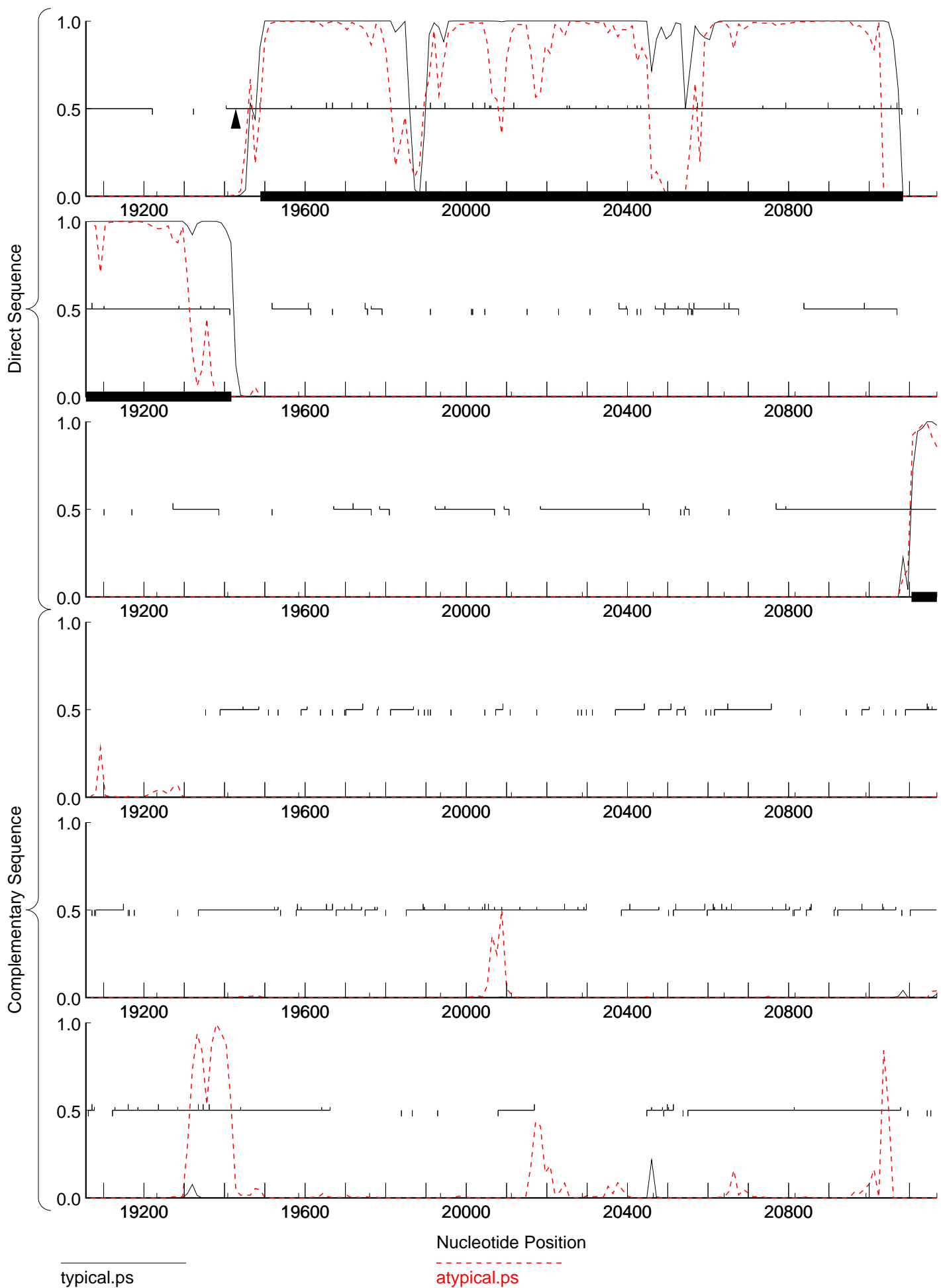


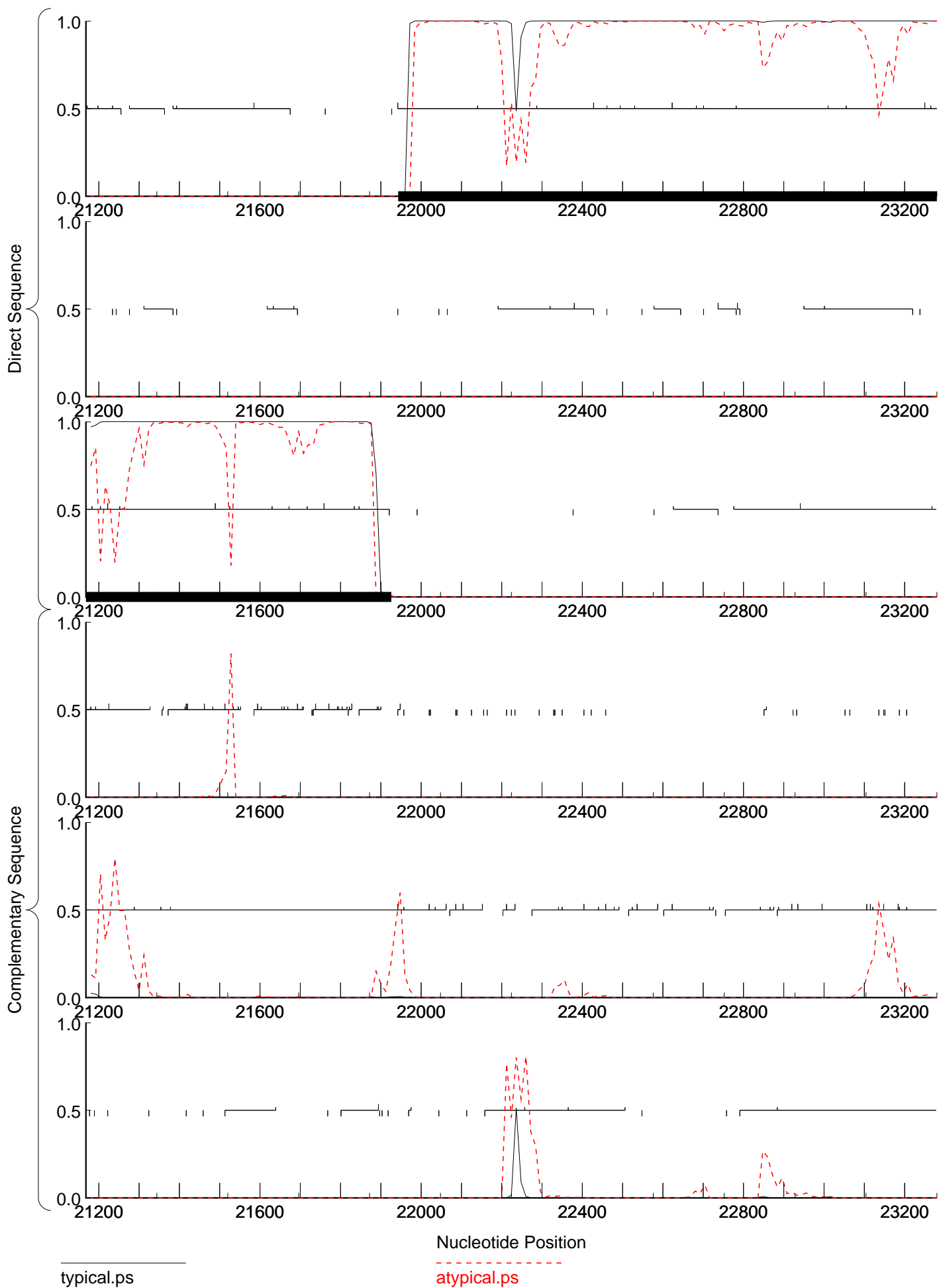
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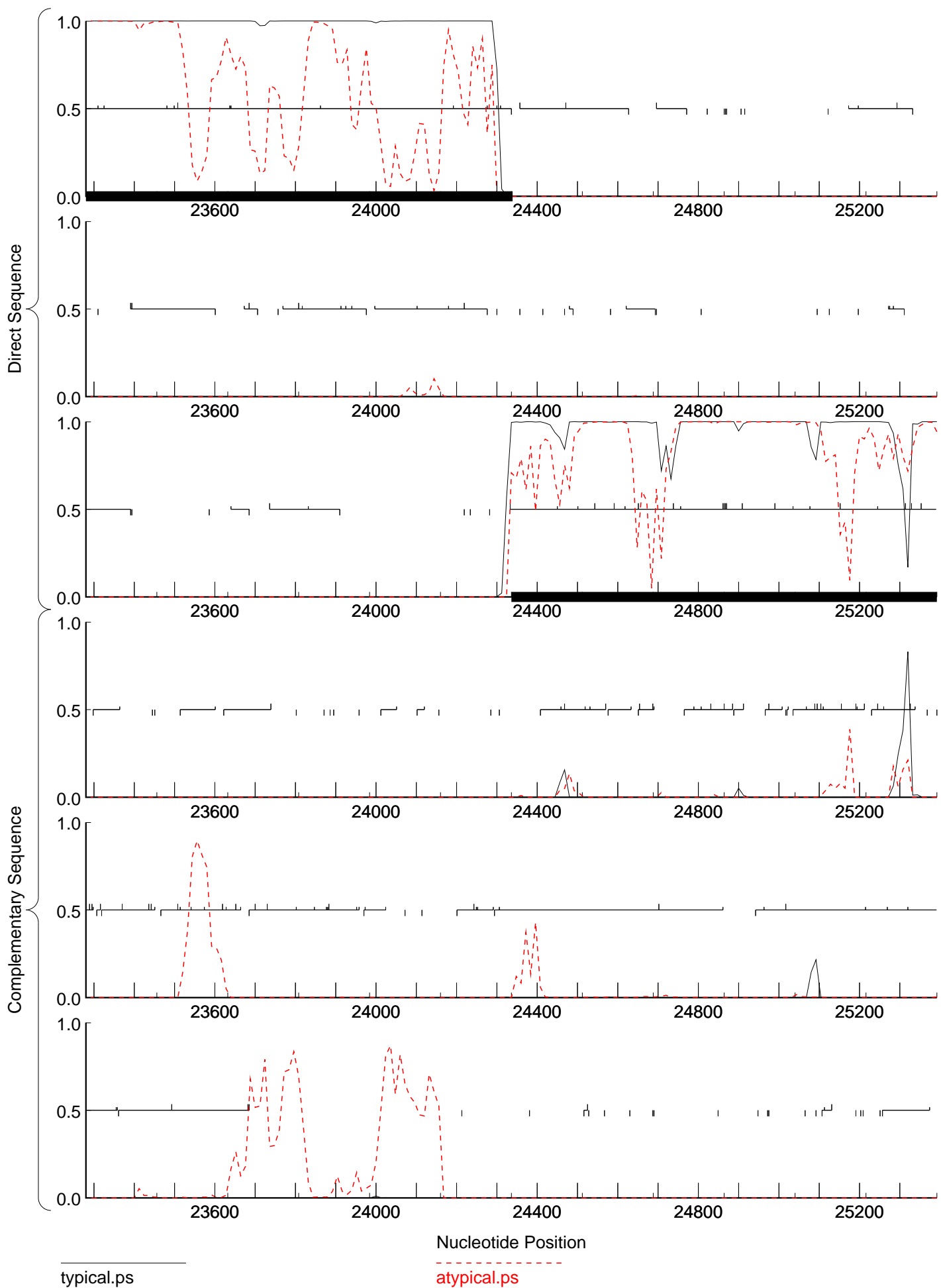
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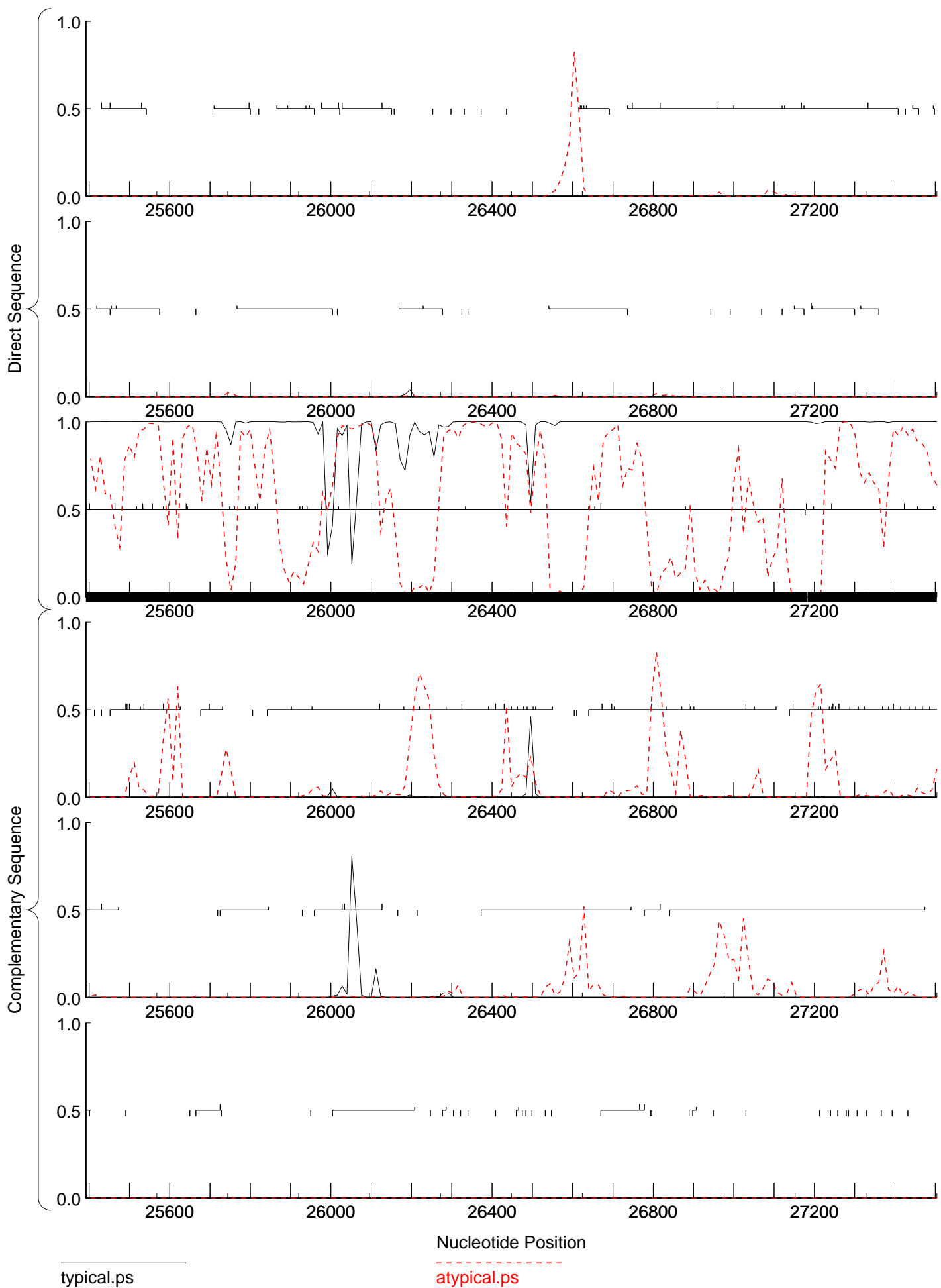


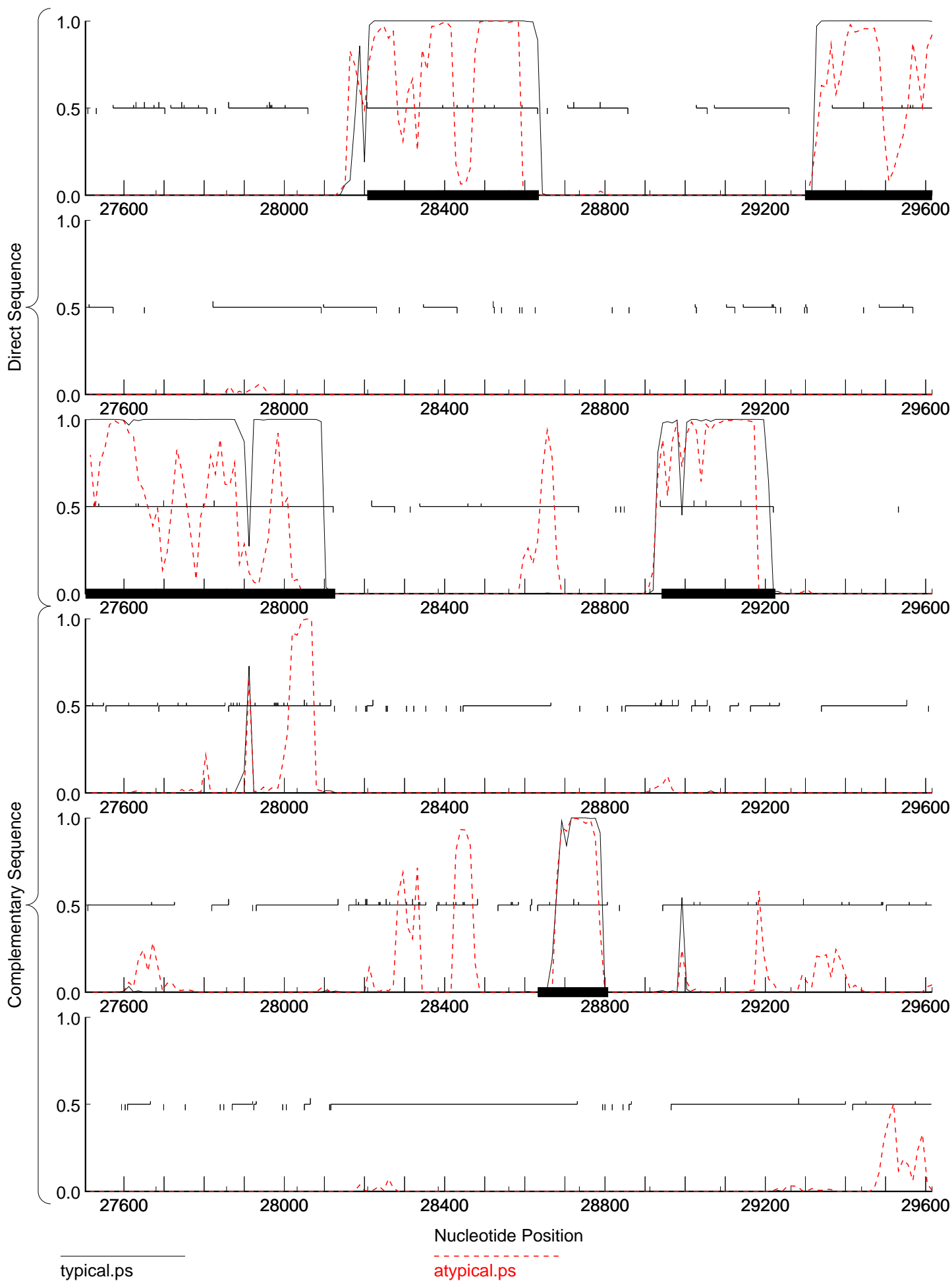






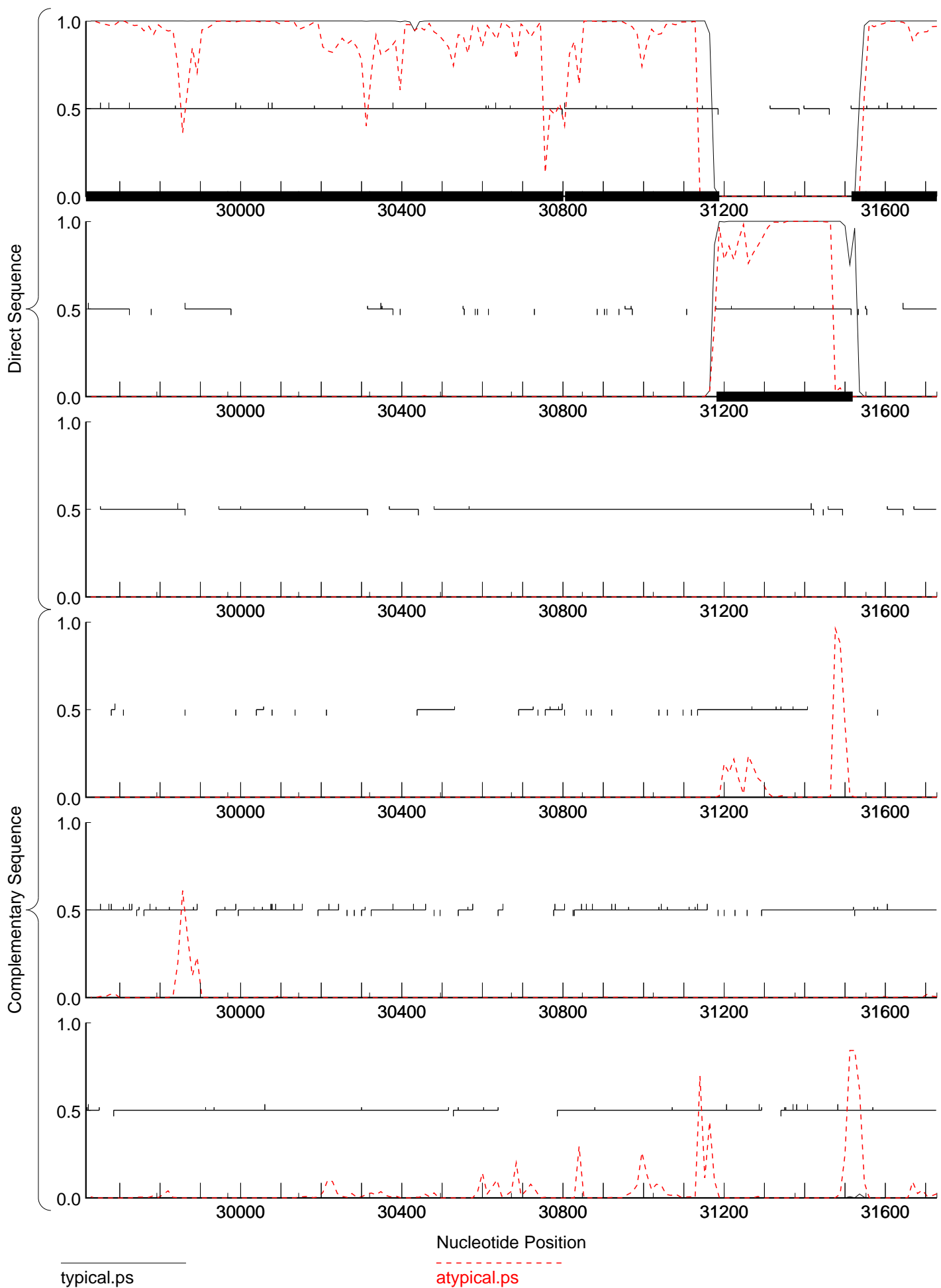


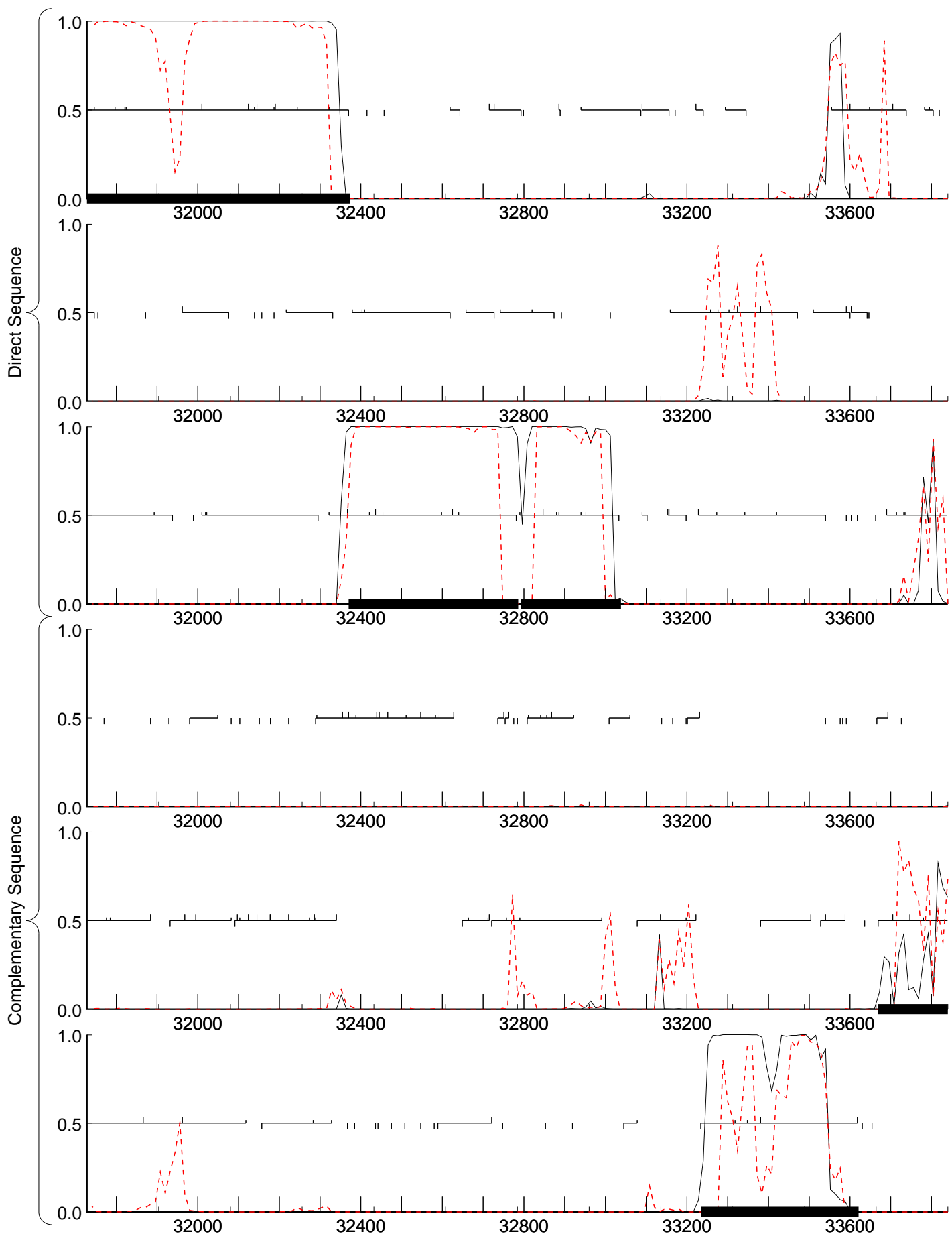




typical.ps

atypical.ps

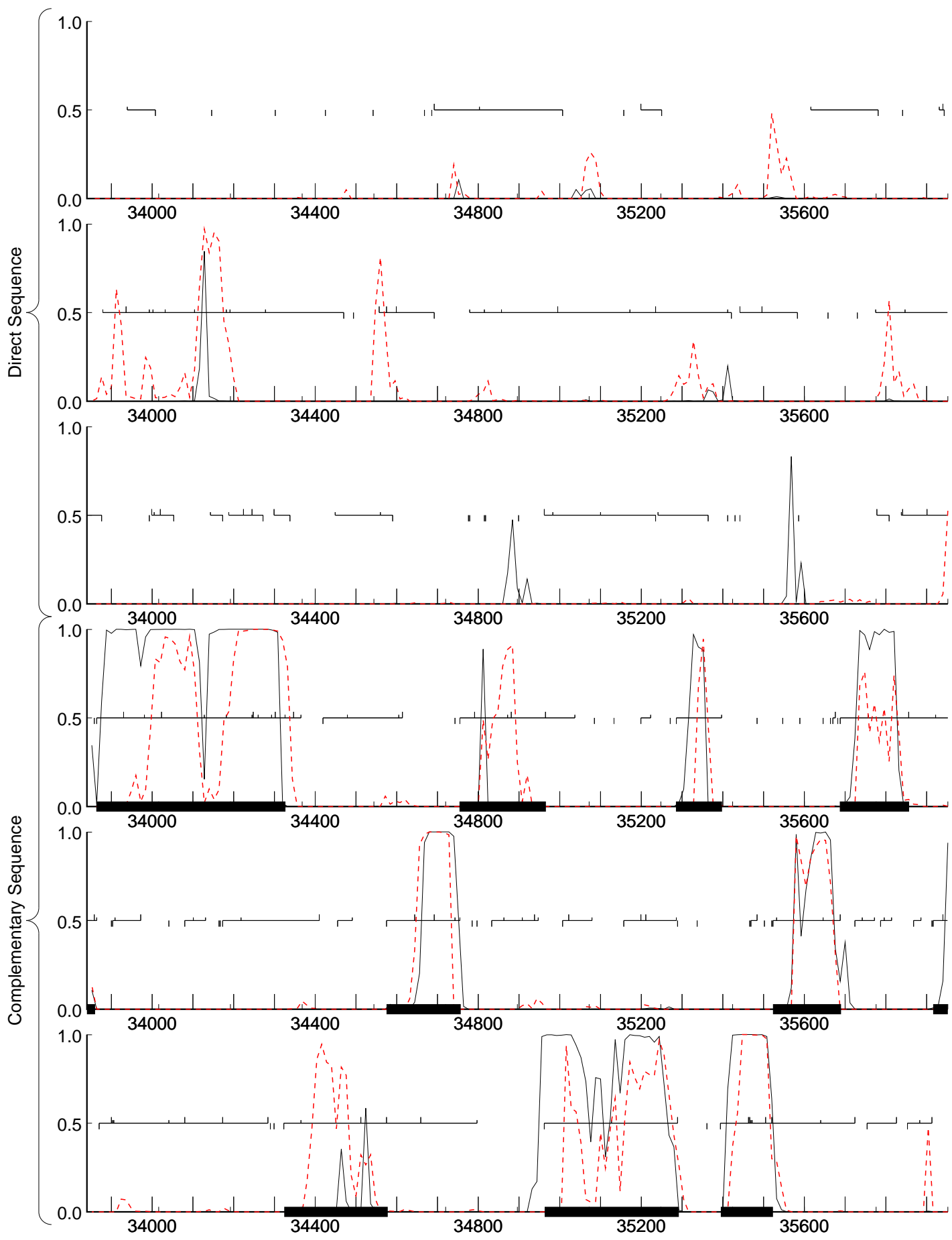




typical.ps

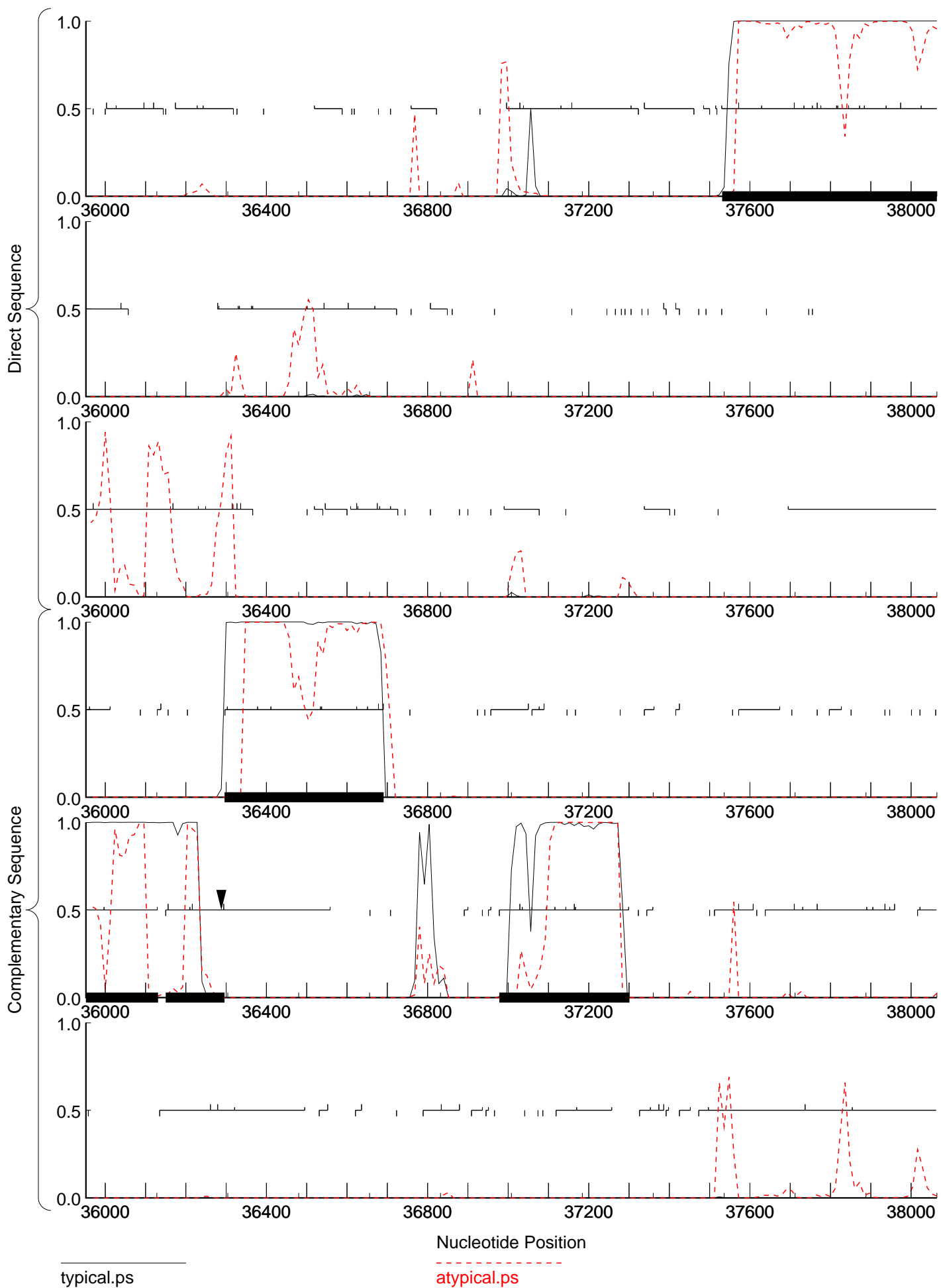
Nucleotide Position

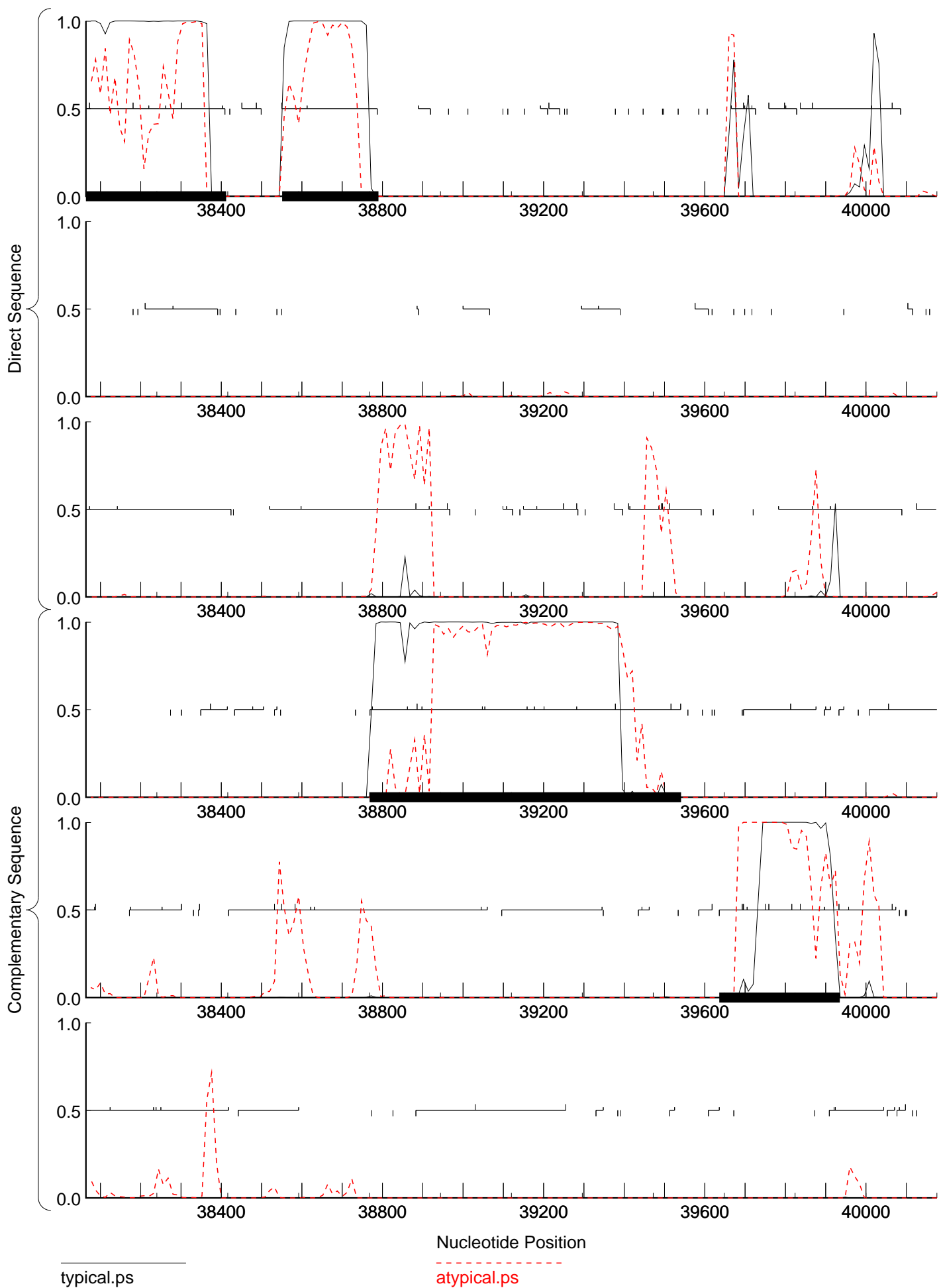
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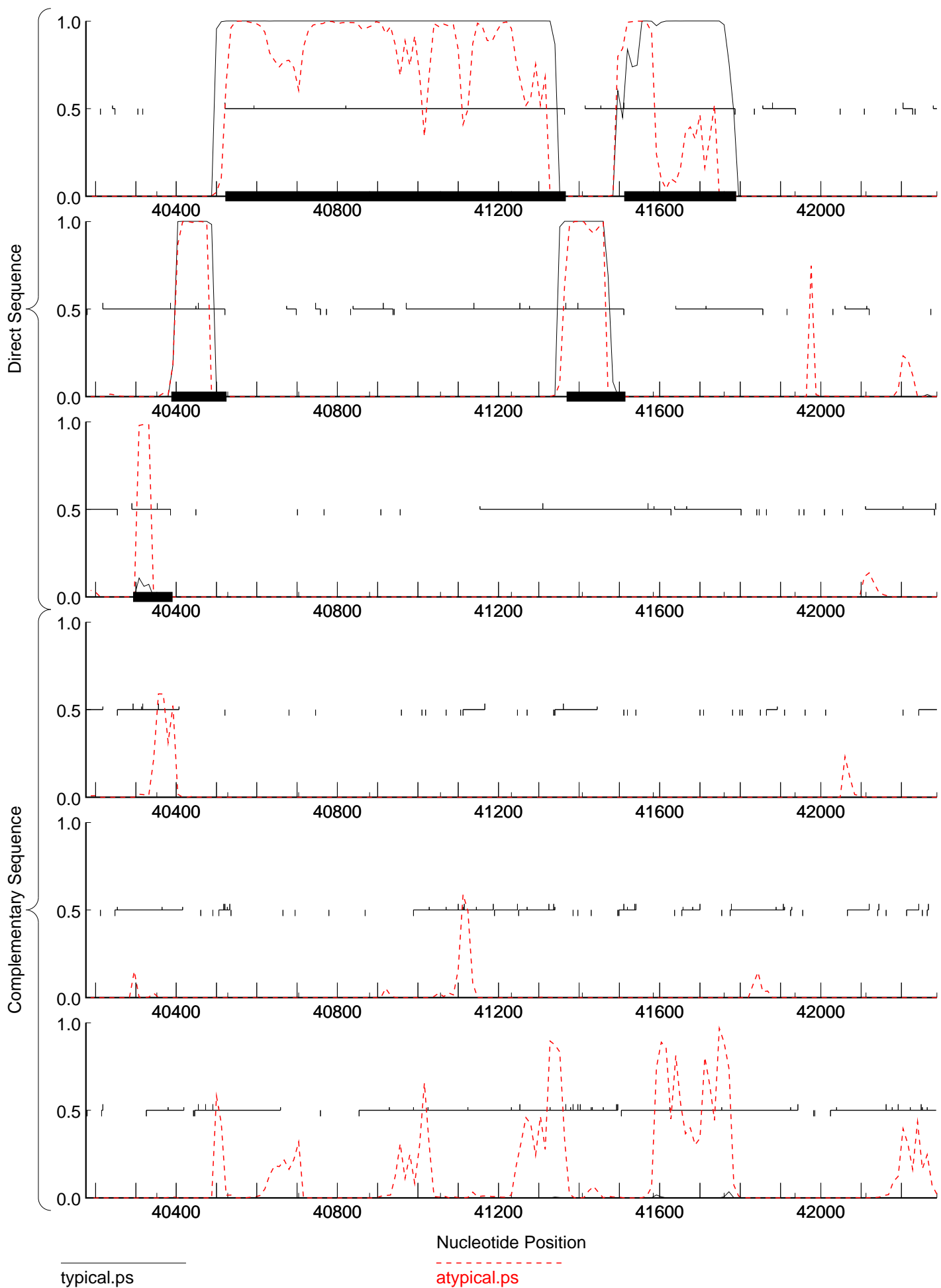


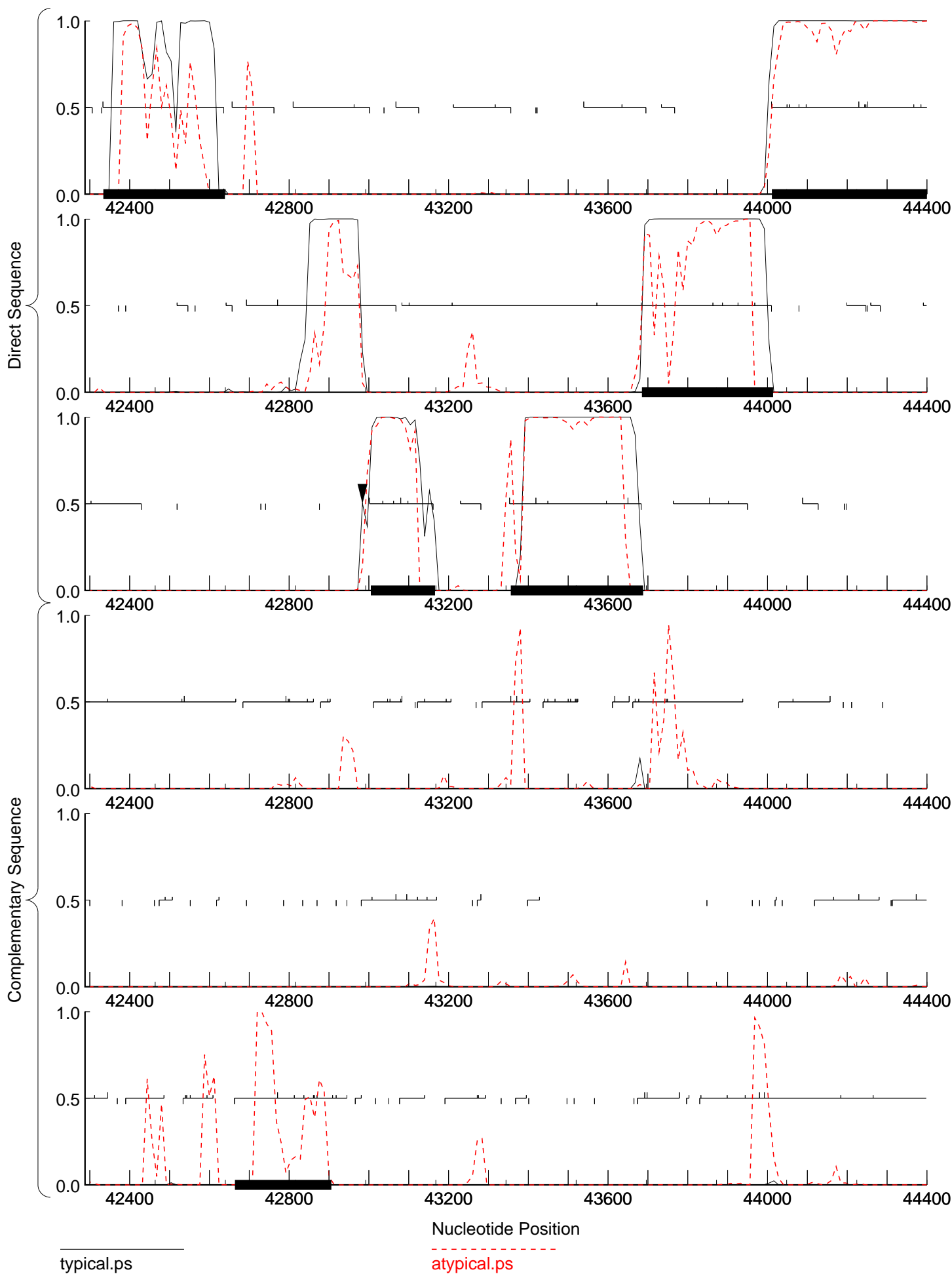
typical.ps

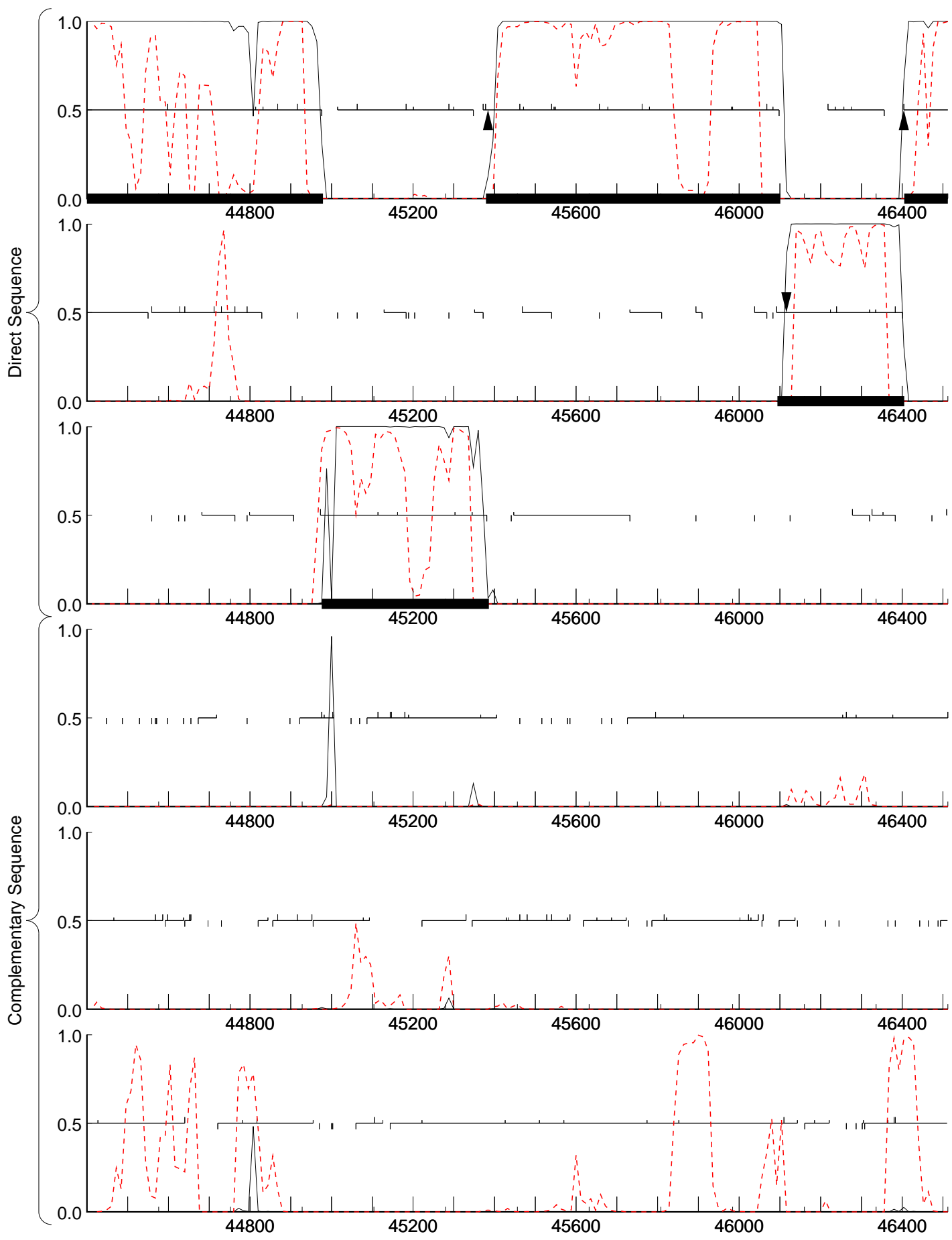
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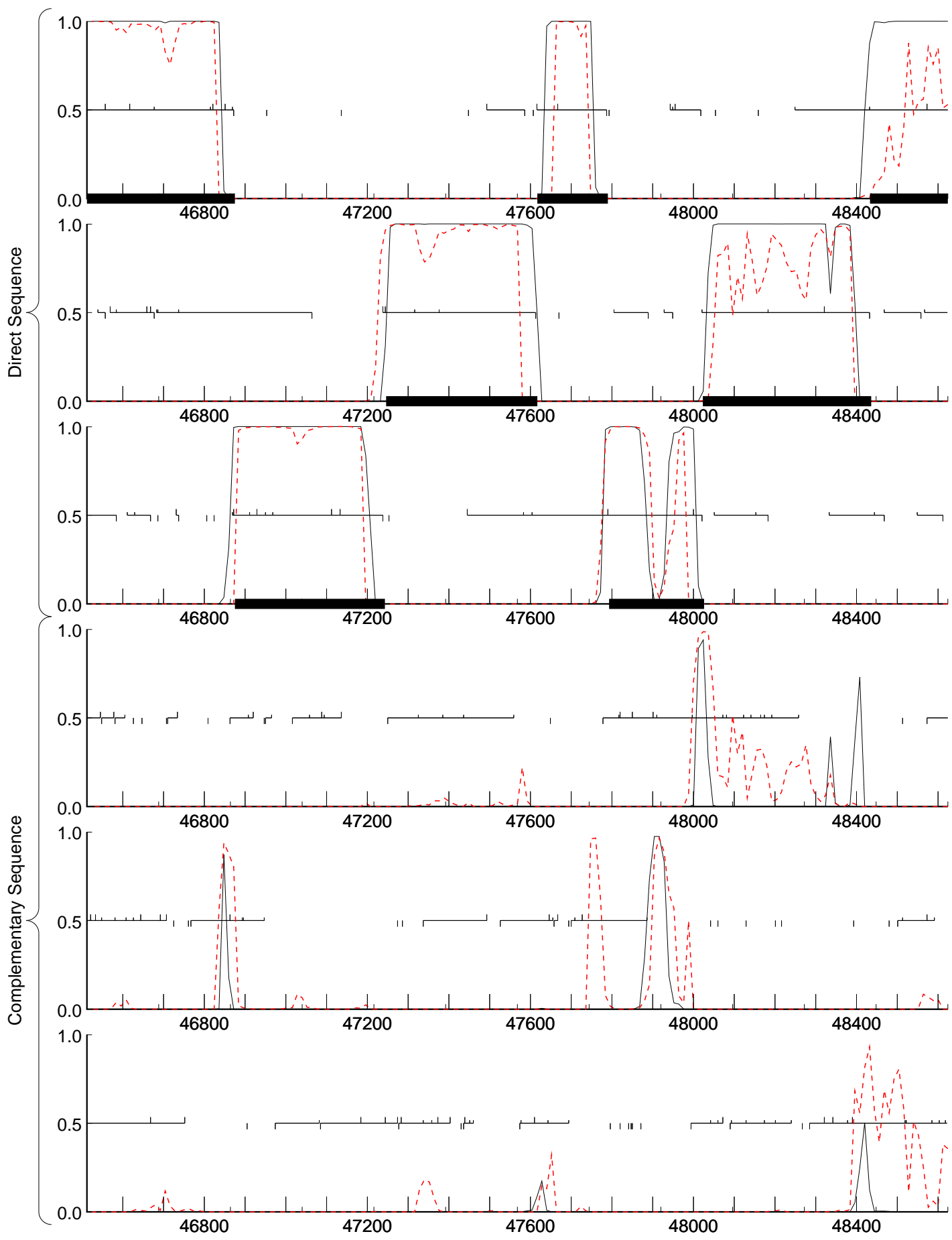






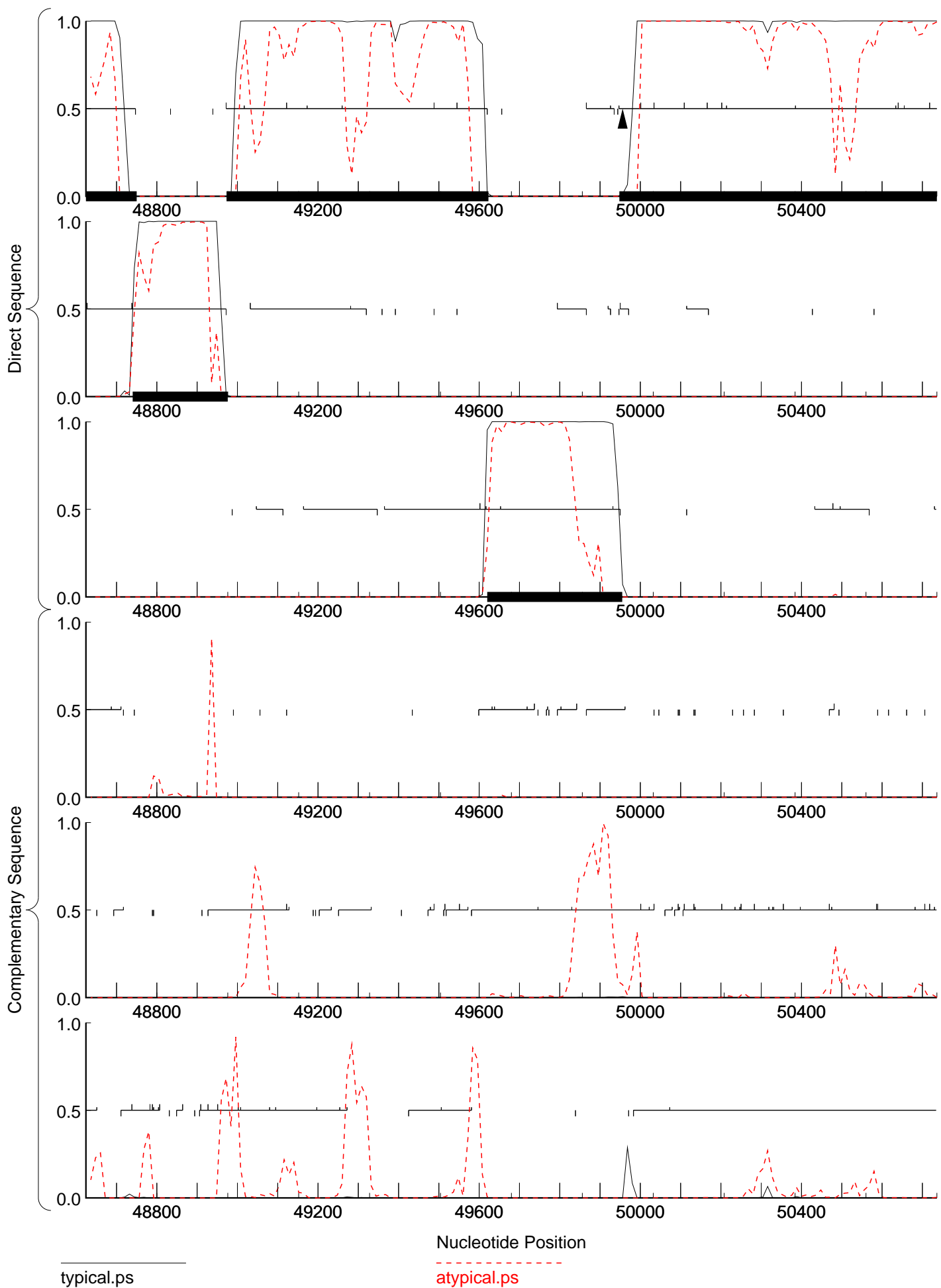
typical.ps

atypical.ps



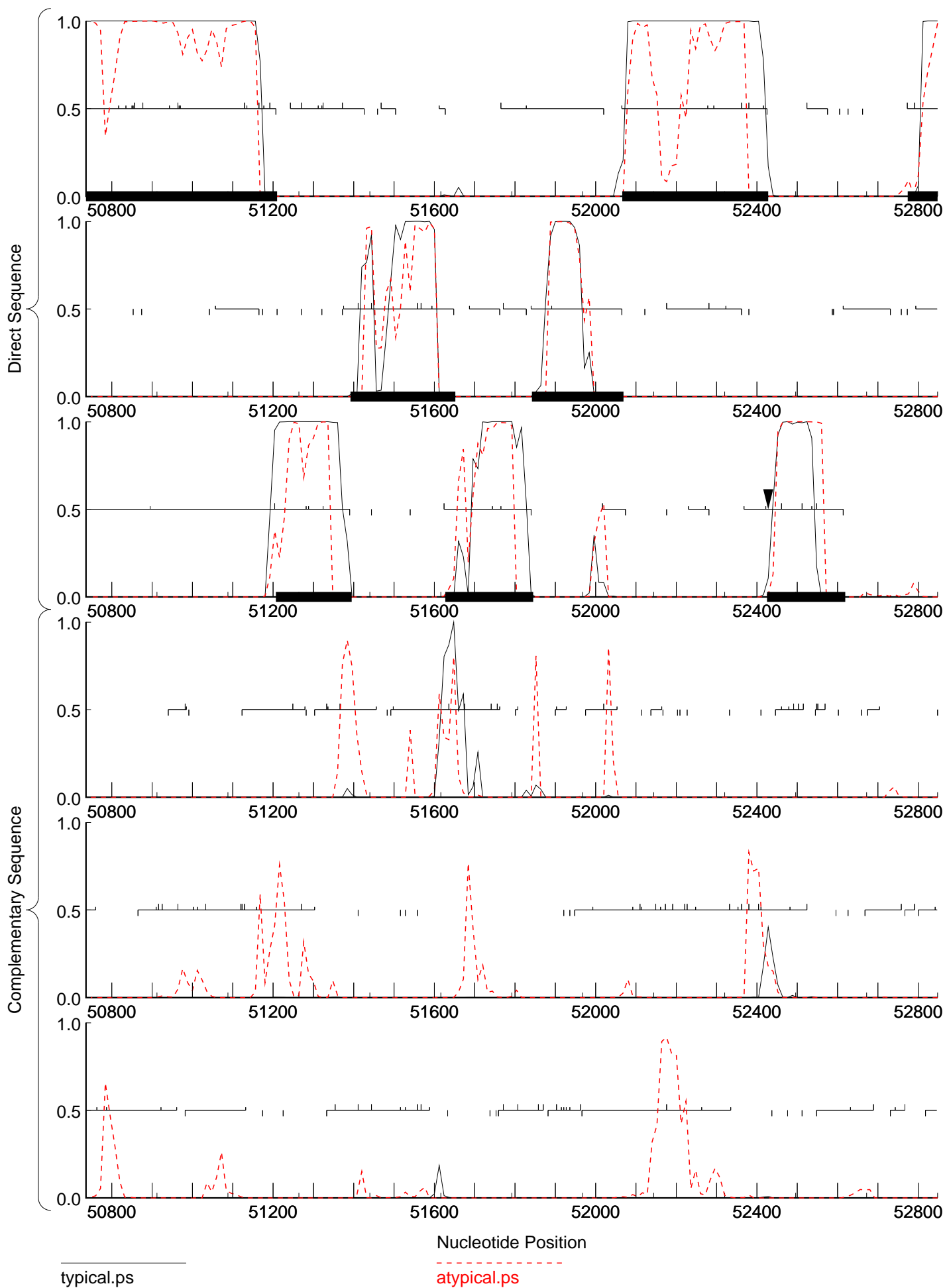
typical.ps

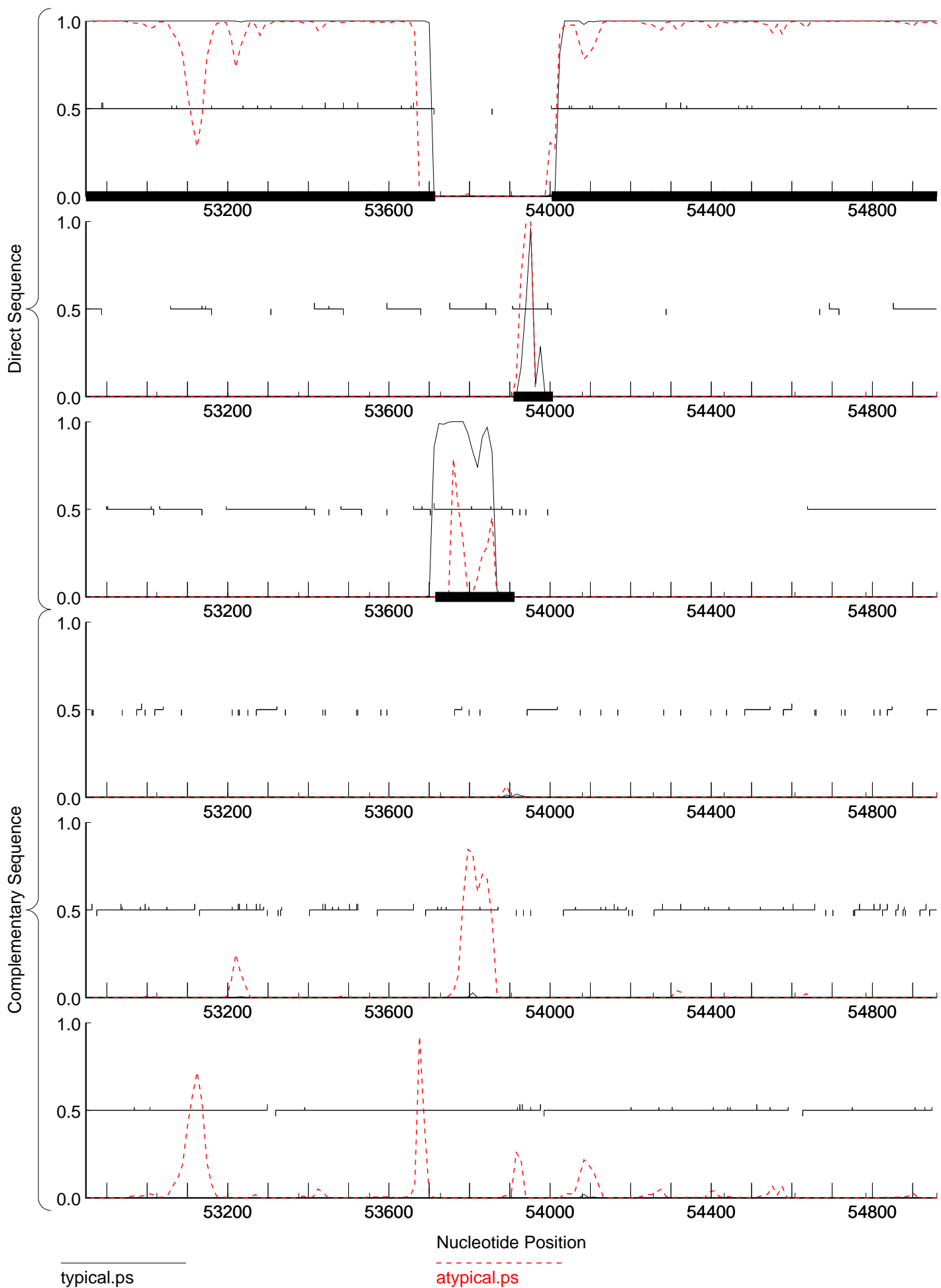
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typical.ps

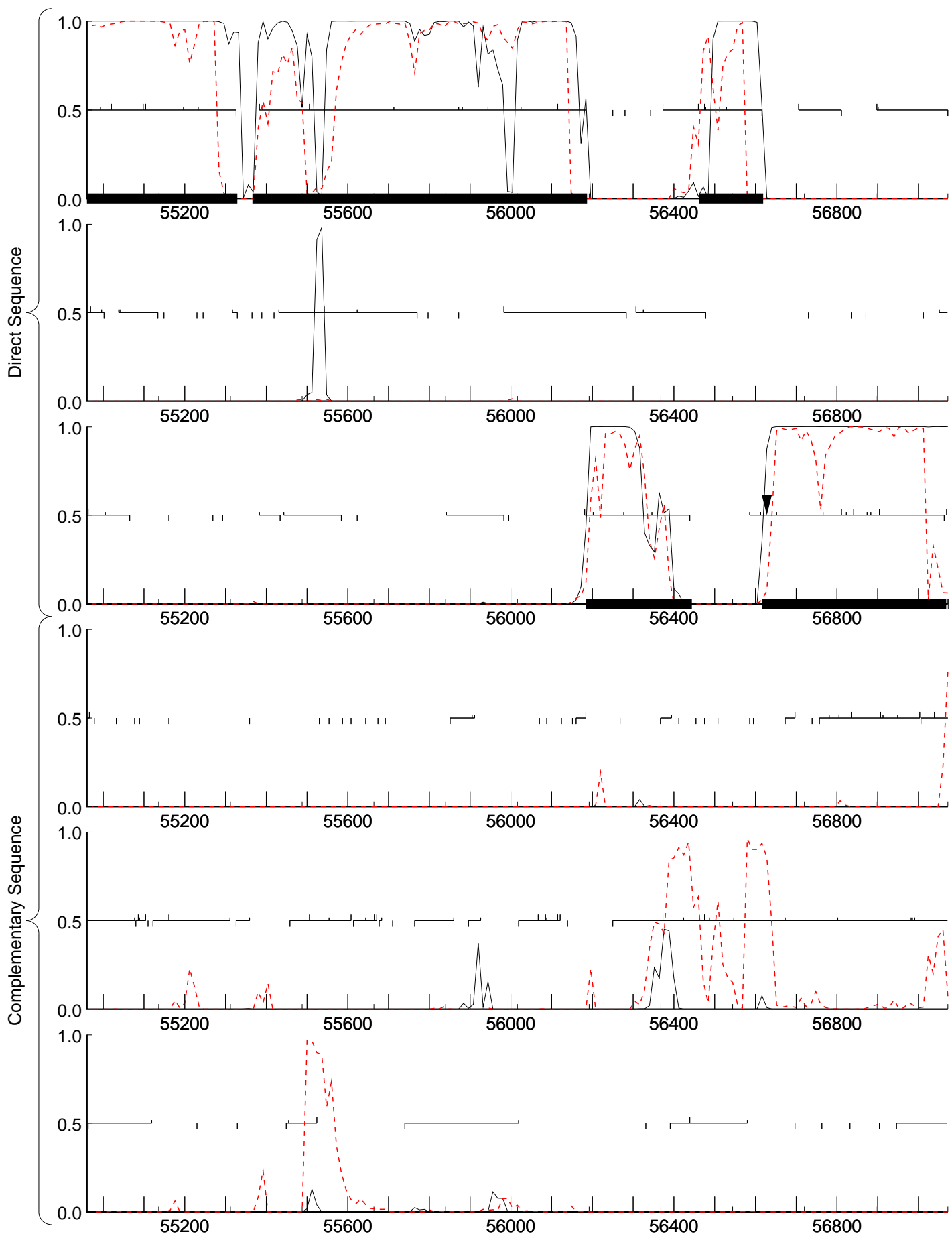
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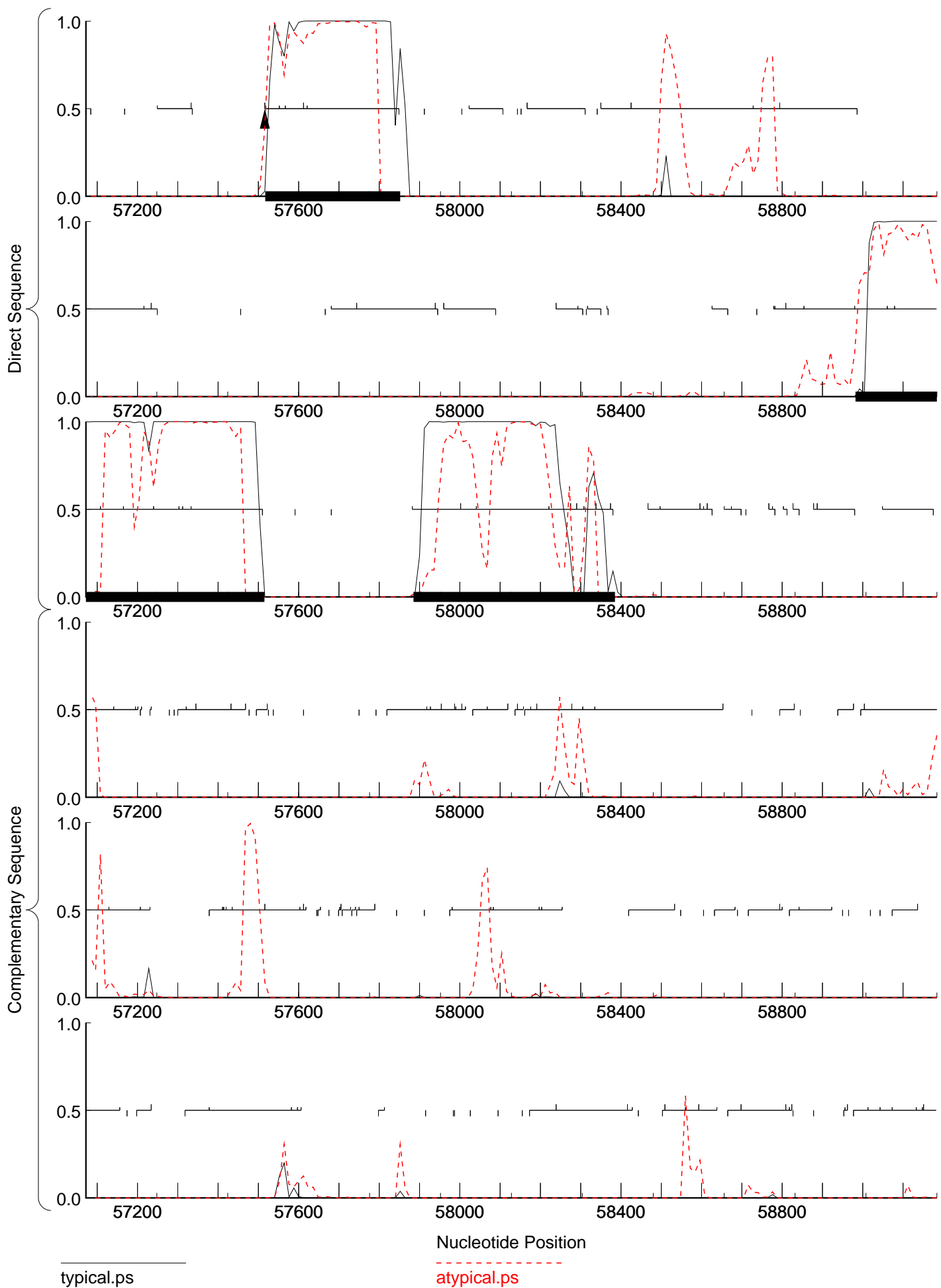
typical.ps

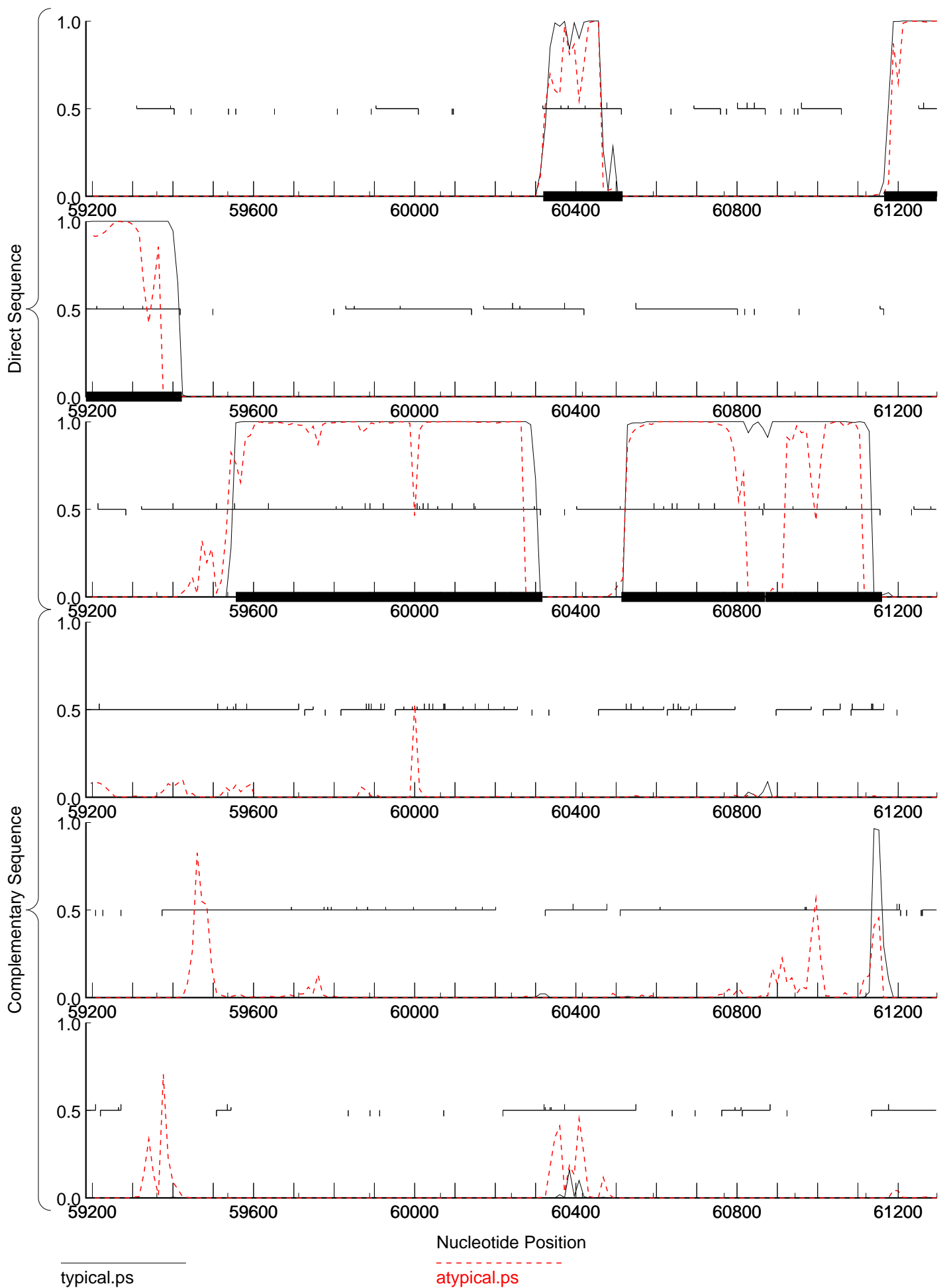
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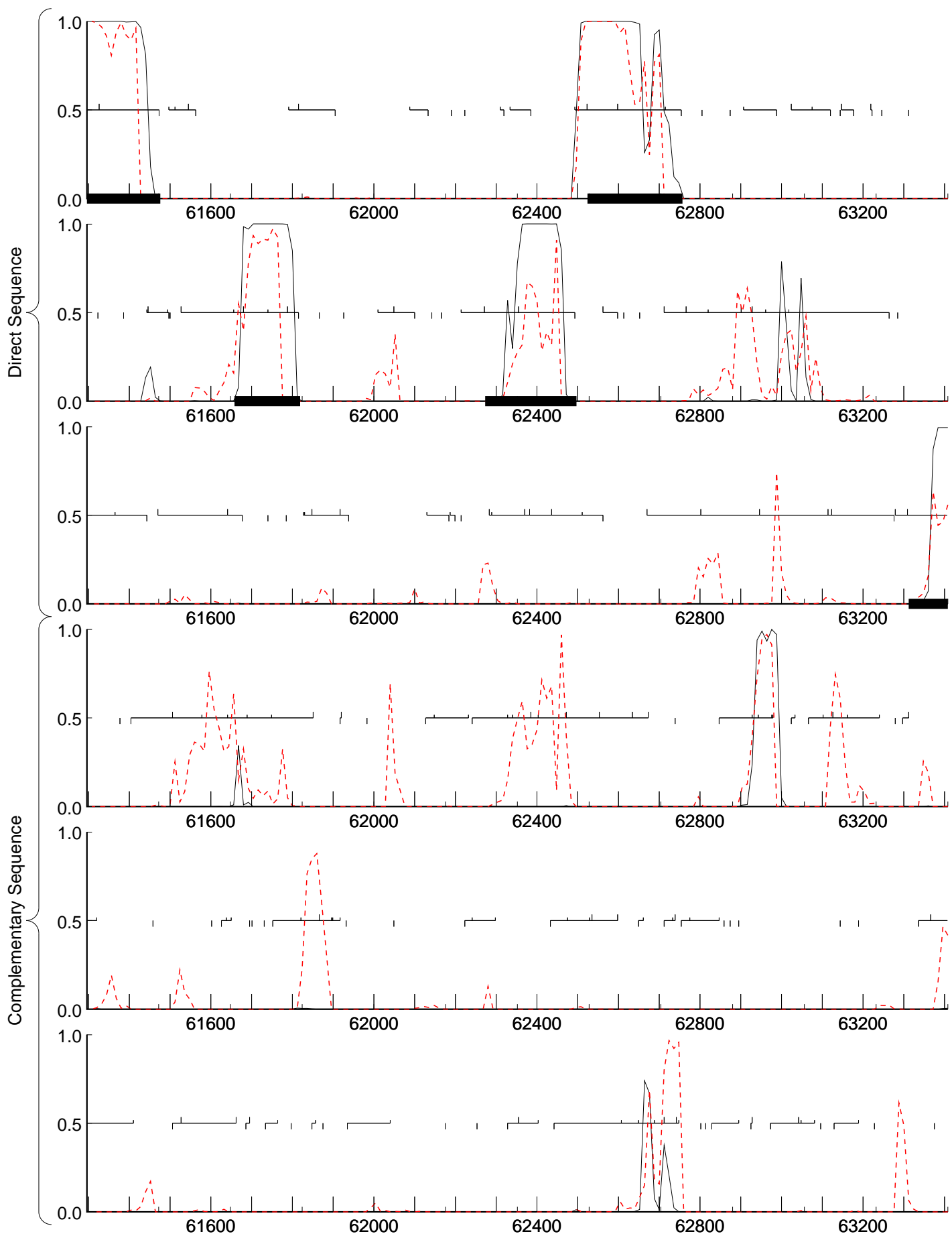


typical.ps

atypical.ps

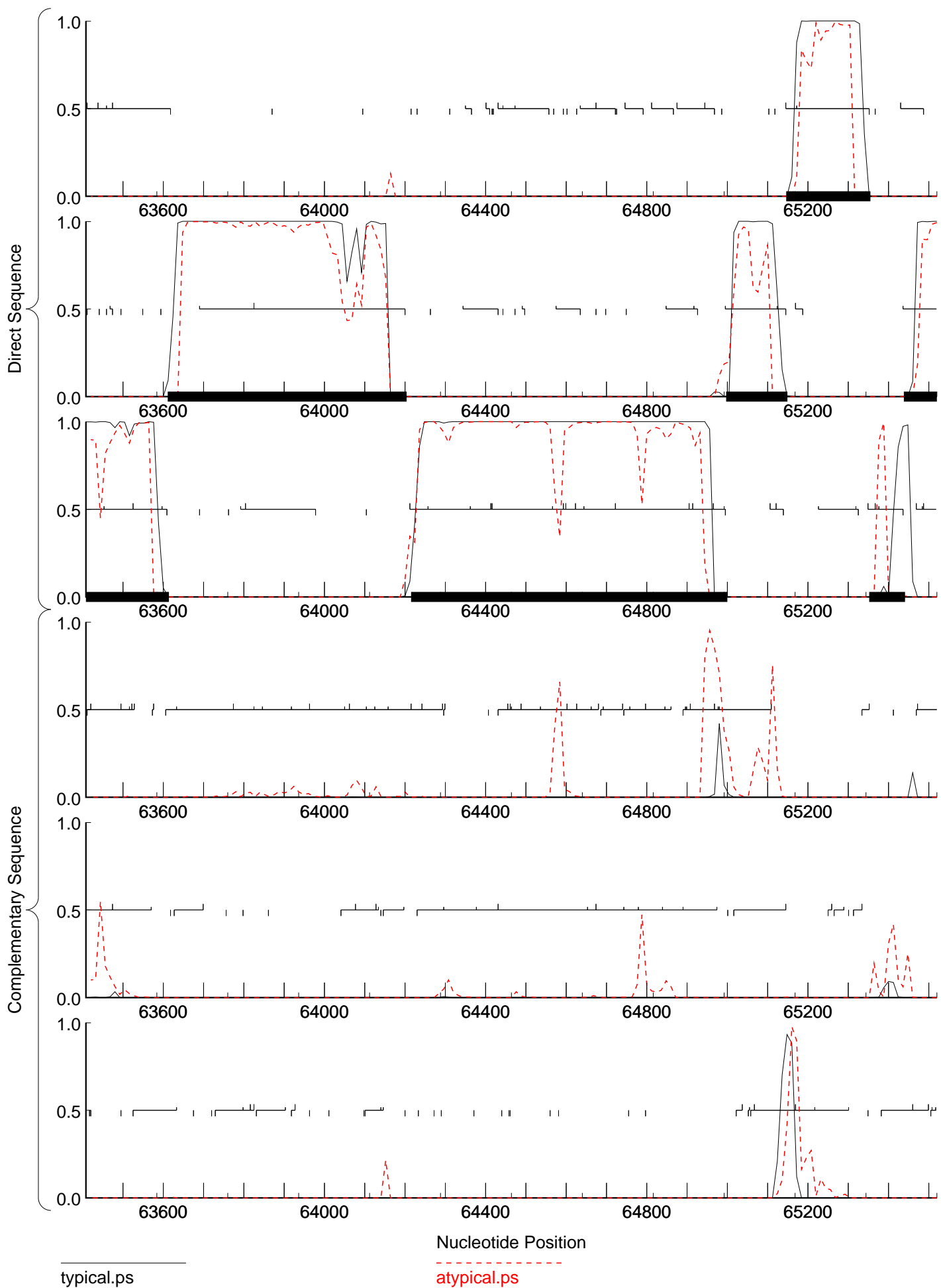






typical.ps

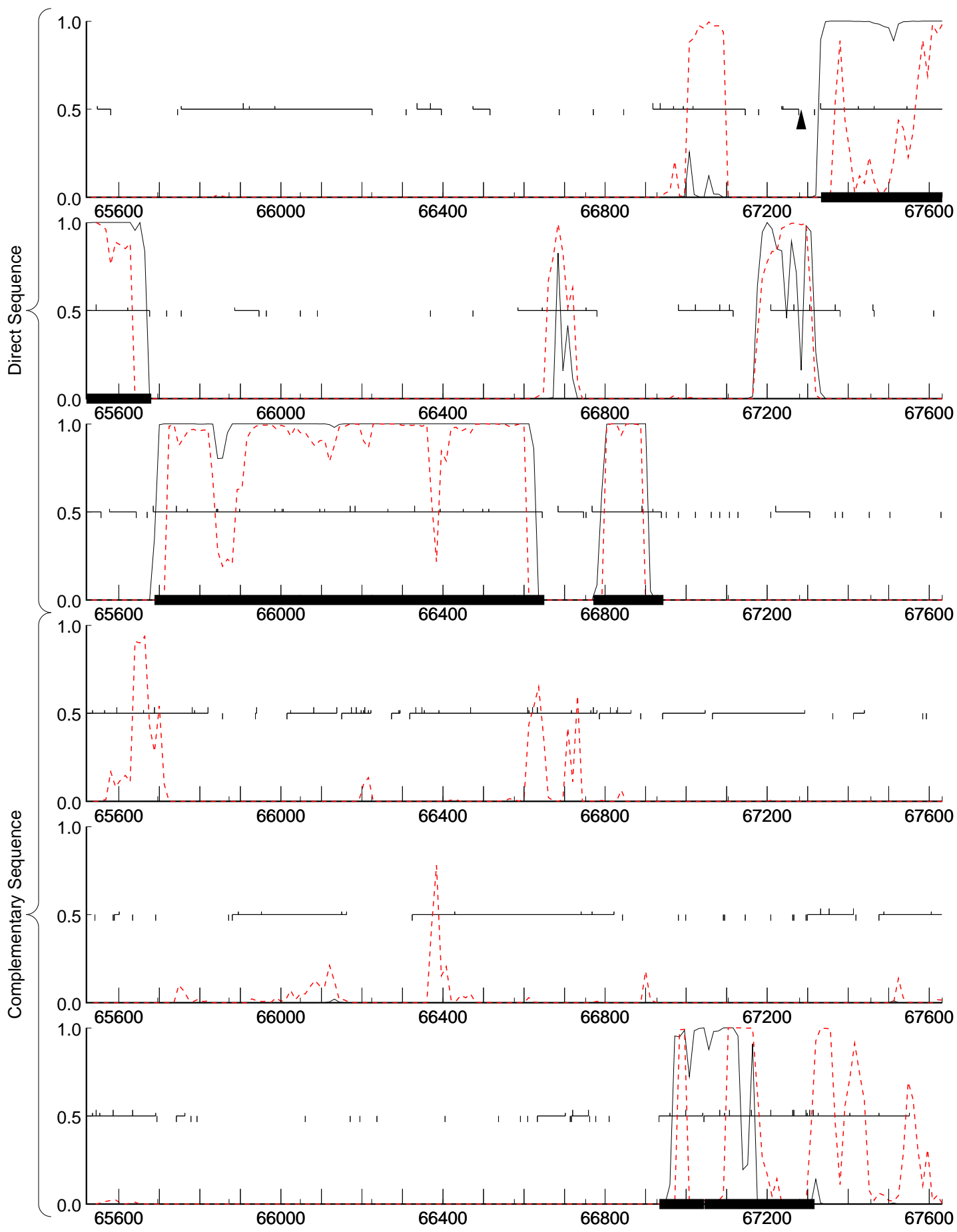
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typical.ps

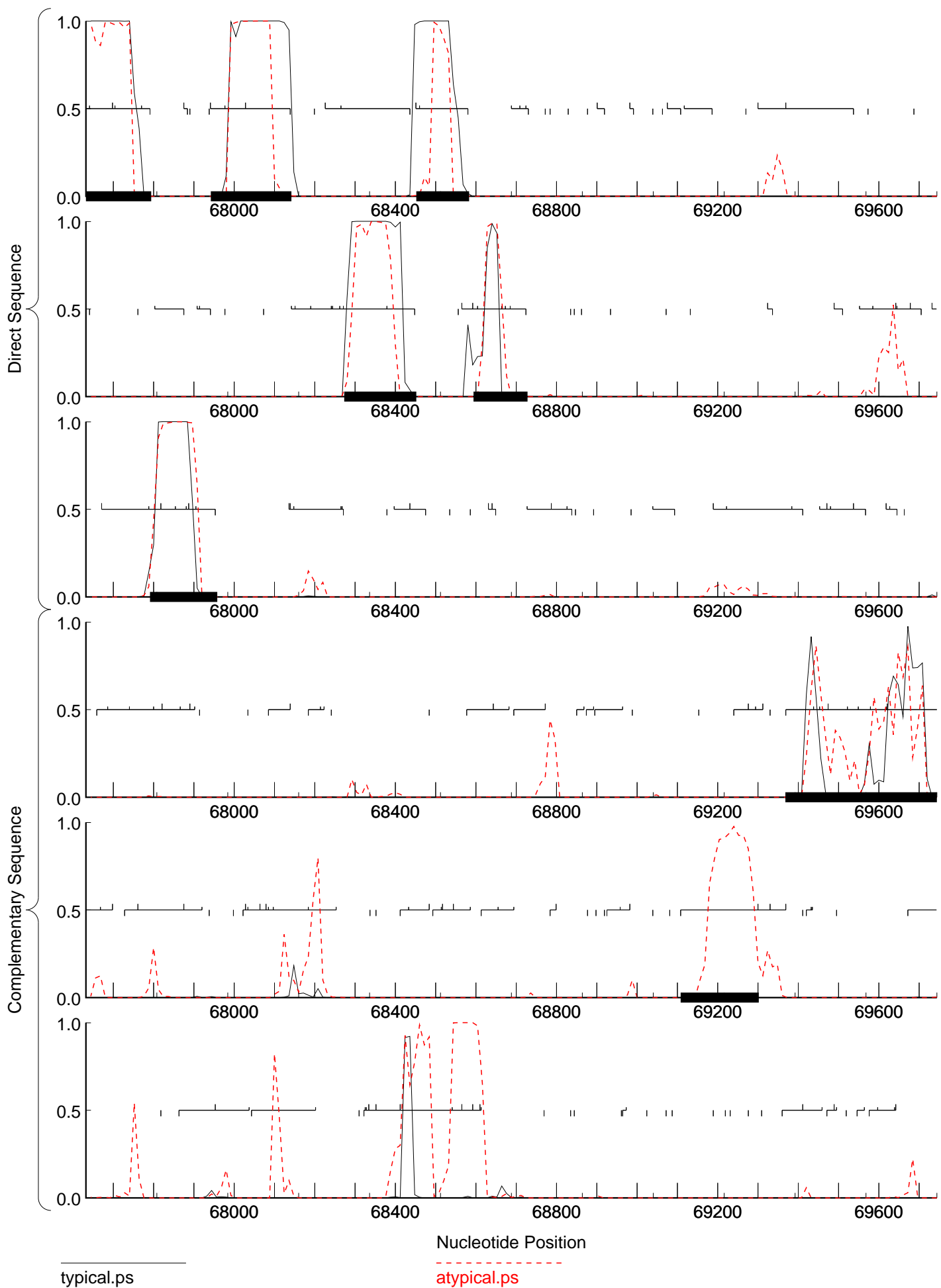
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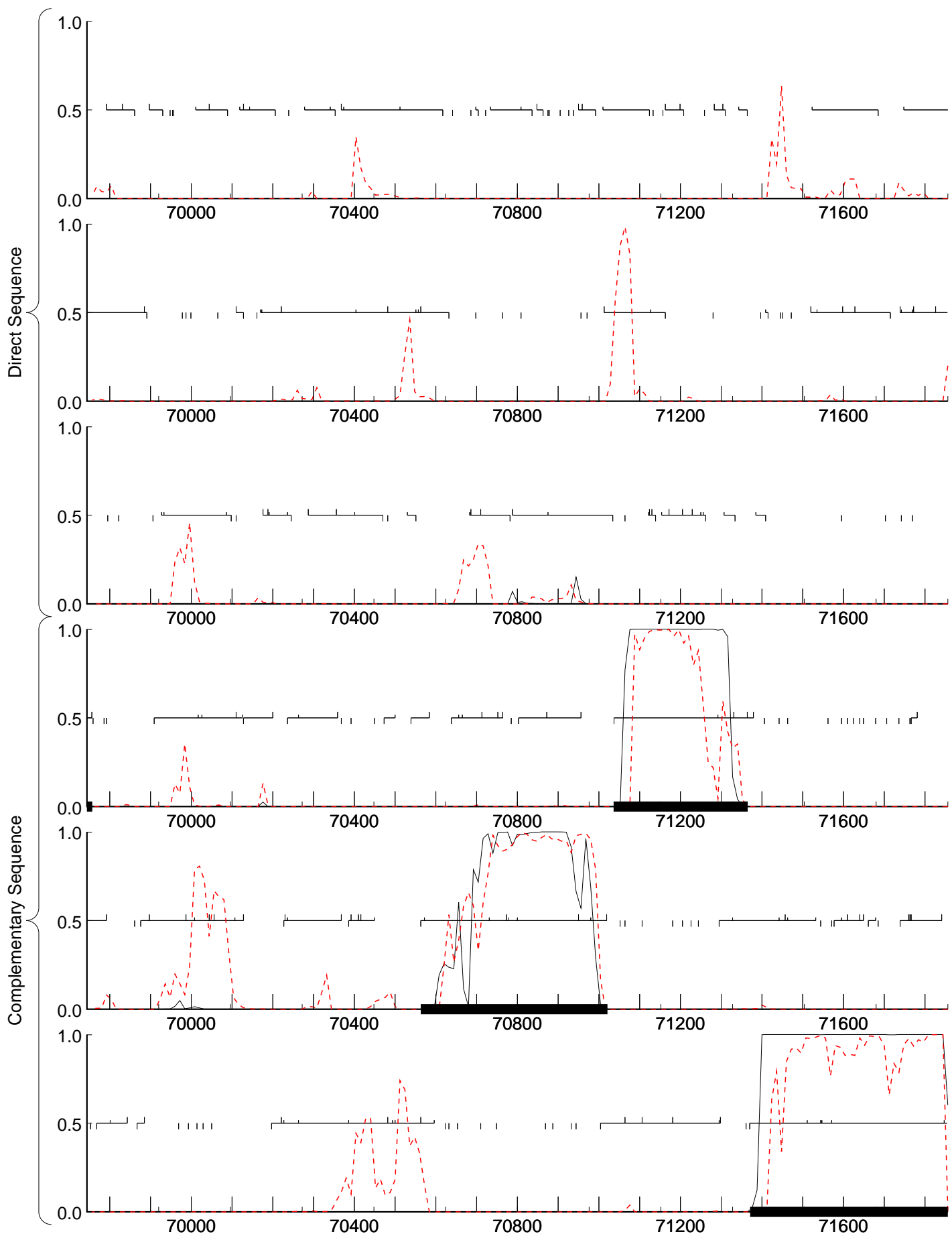
GeneMark.hmm prediction



typical.ps

atypical.ps

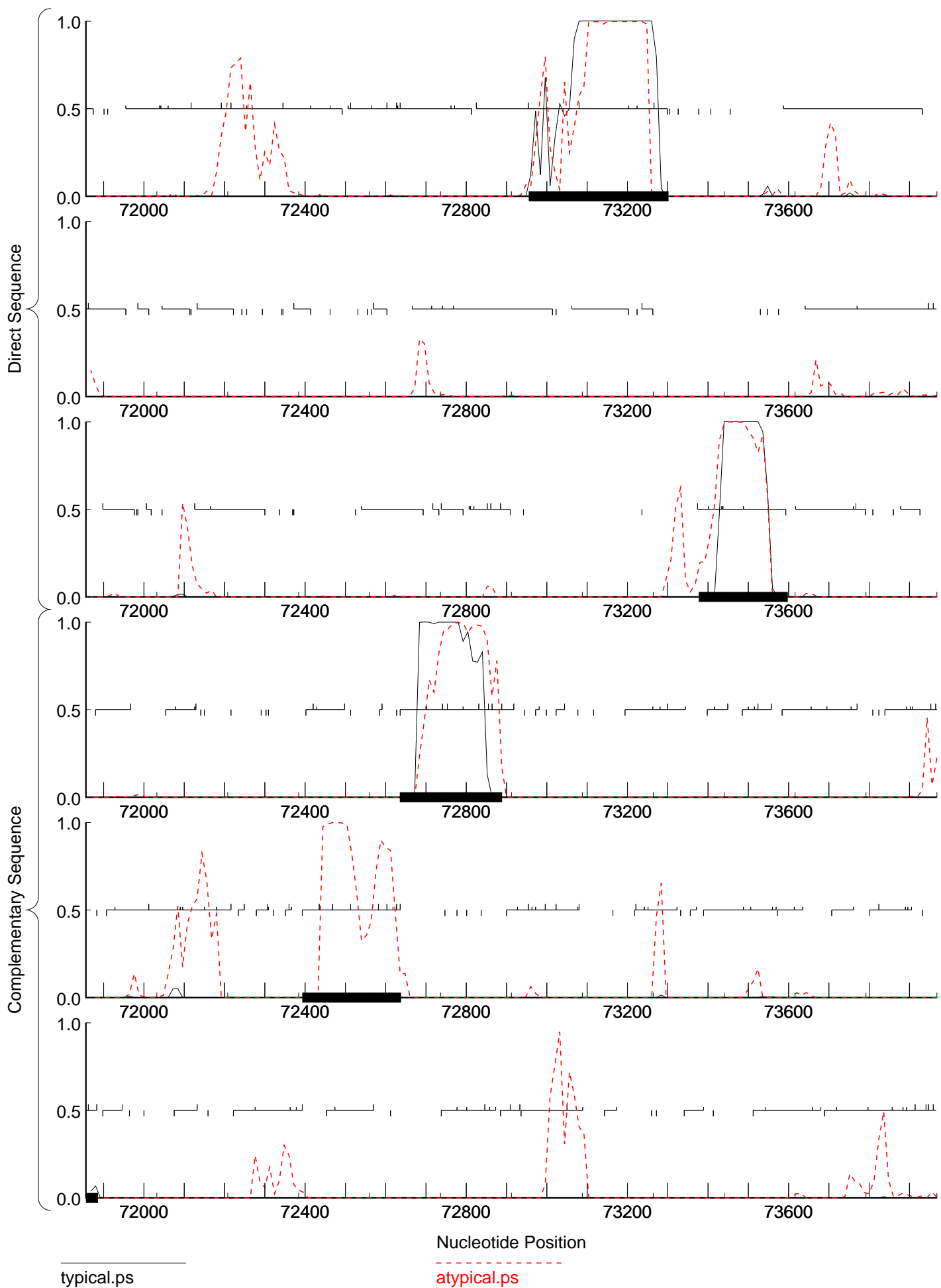




typical.ps

Nucleotide Position

atypical.ps



typical.ps

atypical.ps

Icee complete sequence, 74169 bp including 9-base 3' overhang (CGCTTGTC), Cluster E, Order 4, Window 96, Step 12, 37/37
GeneMark.hmm prediction
Icee complete sequence, 74169 bp including 9-base 3' overhang (CGCTTGTC), Cluster E, Order 2, Window 96, Step 12, 37/37

