

GeneMark

Version 2.5p (09.08.06)

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PROGRAM INFORMATION

Sequence : Gordonia phage Yvonnestic complete sequence, 98136 bp including 10-base 3' overhang (CGCG)
Analysis Date : 6/22/18 at 14:34:55
Pages : 48
Sequence Length : 98136 bp
GC Content : 59.75%

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,

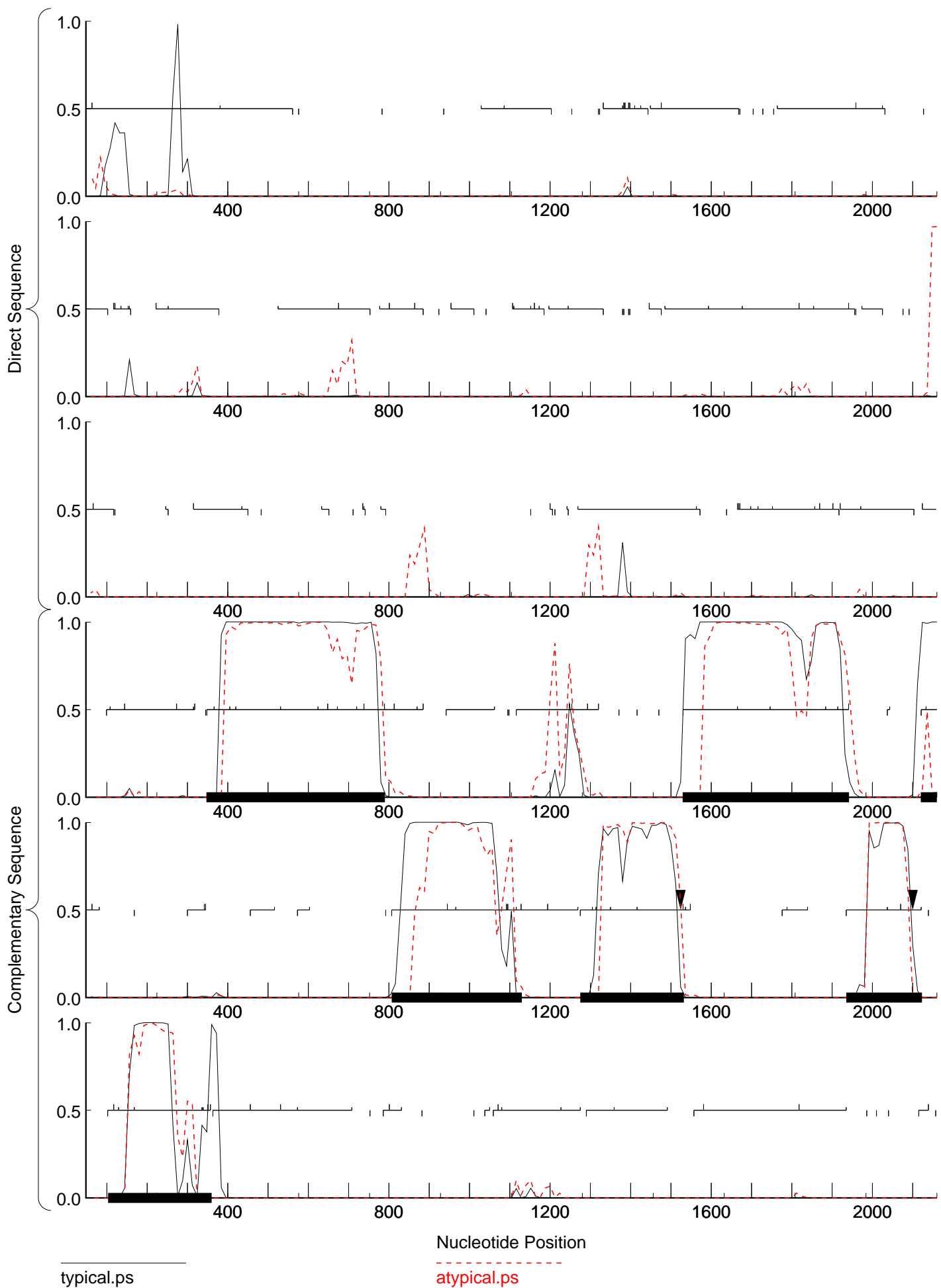
MATRIX INFORMATION

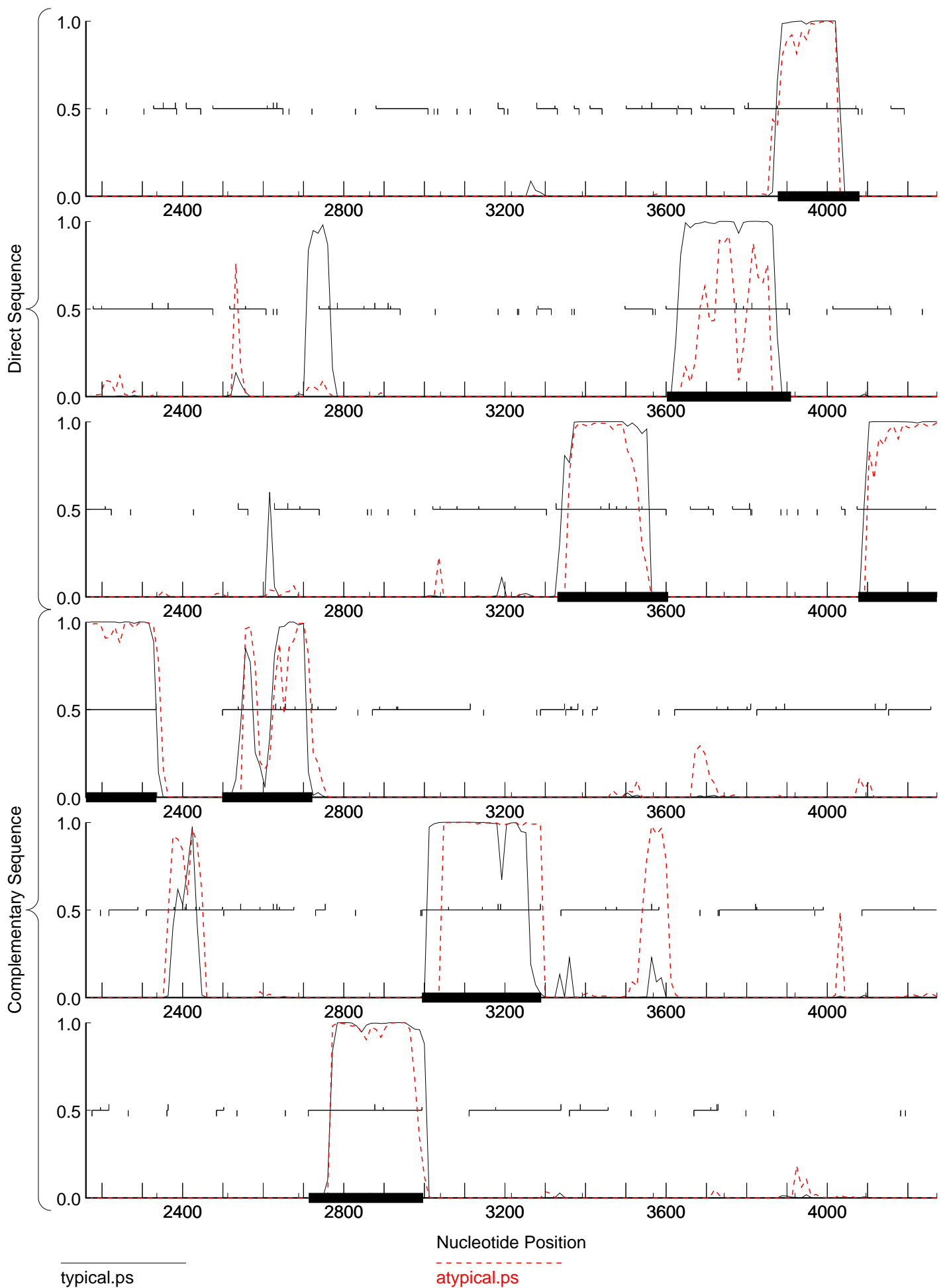
Matrix : -
Author : -
Order : 4

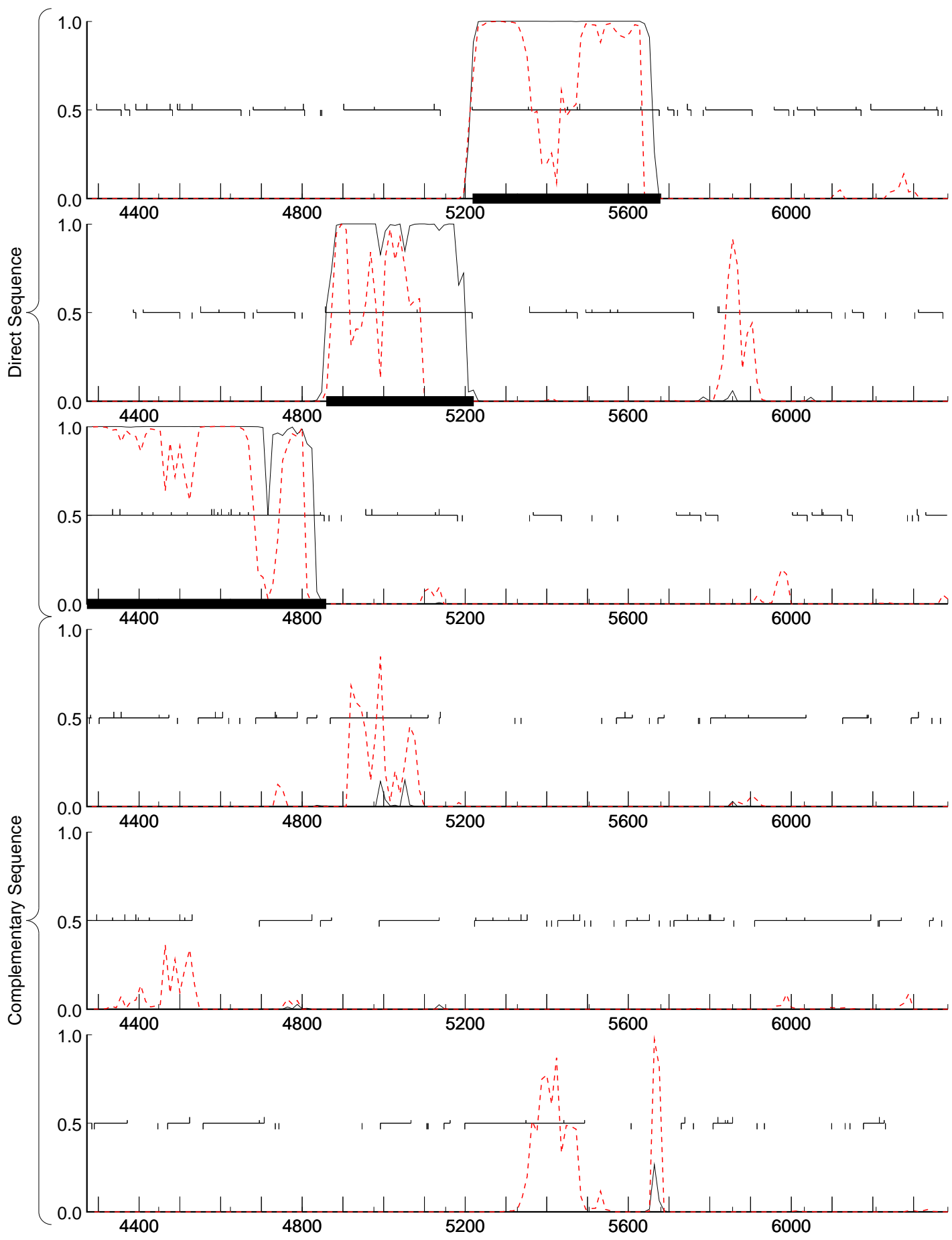
Send questions / comments to:
Dr. M. Borodovsky
Georgia Institute of Technology
School of Biology
Atlanta, GA 30332-0230

Matrix notes & comments

Training set derived by GeneMarkS, 4.30 October 2014
Fri Jun 22 14:34:55 2018

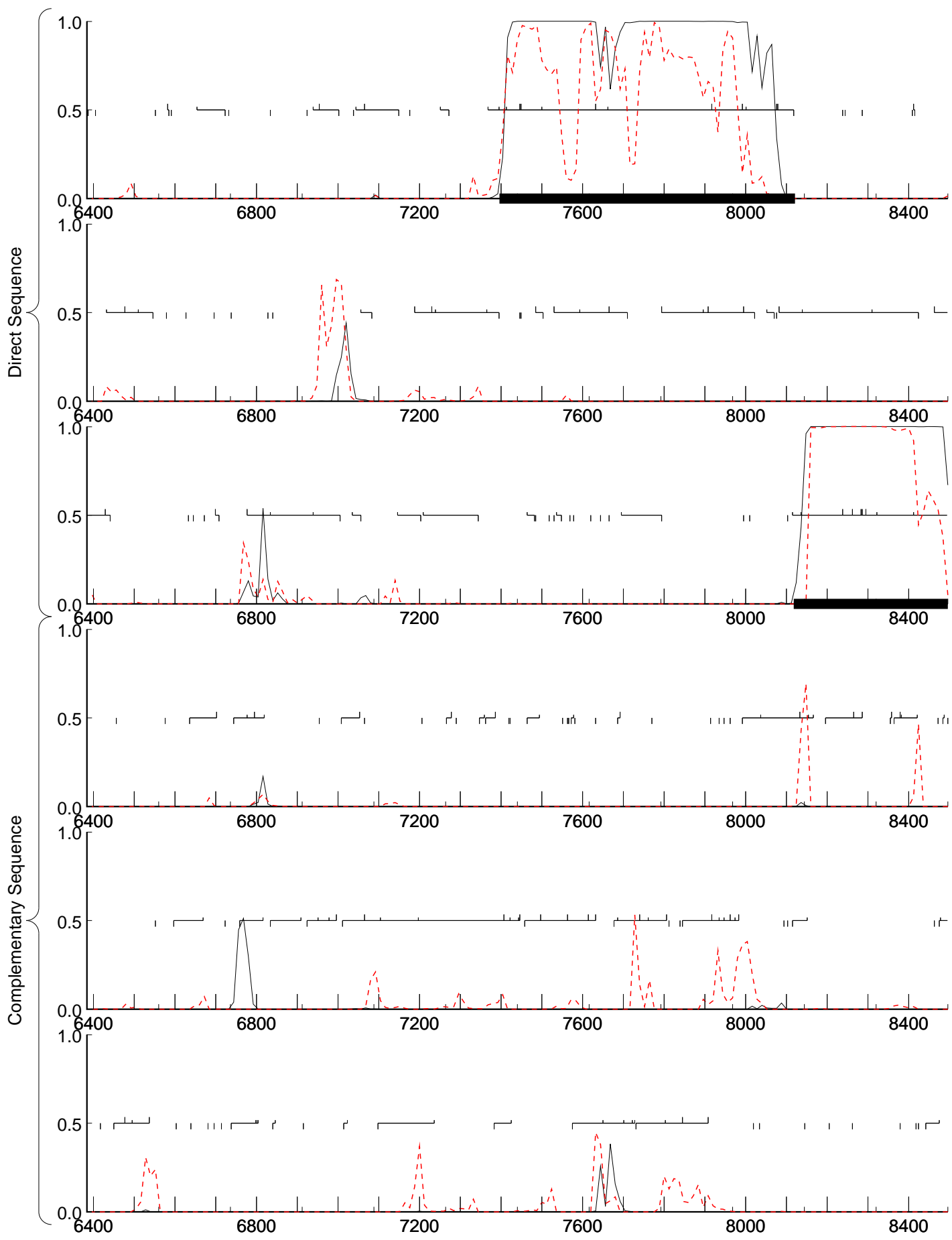






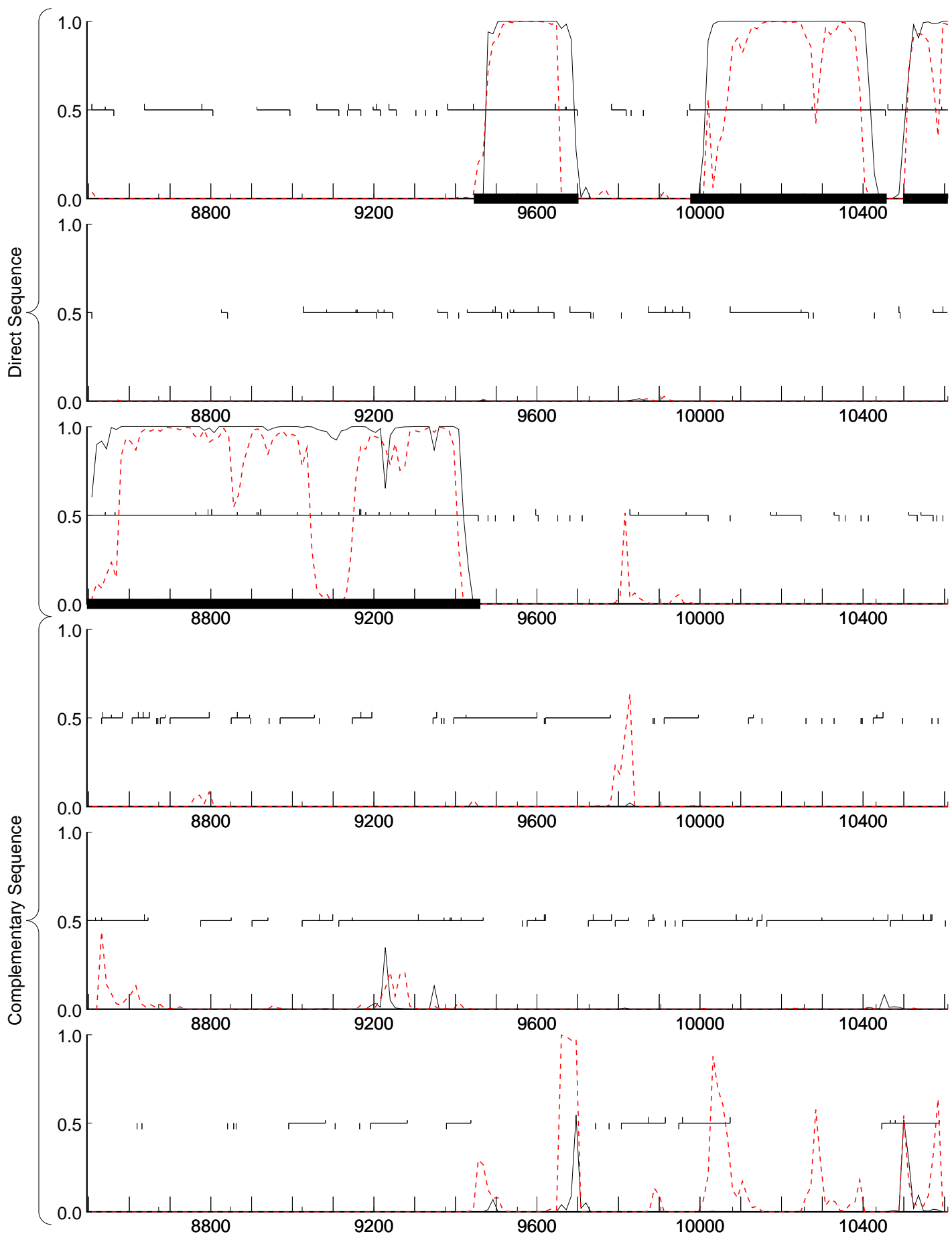
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atypical.ps



typical.ps

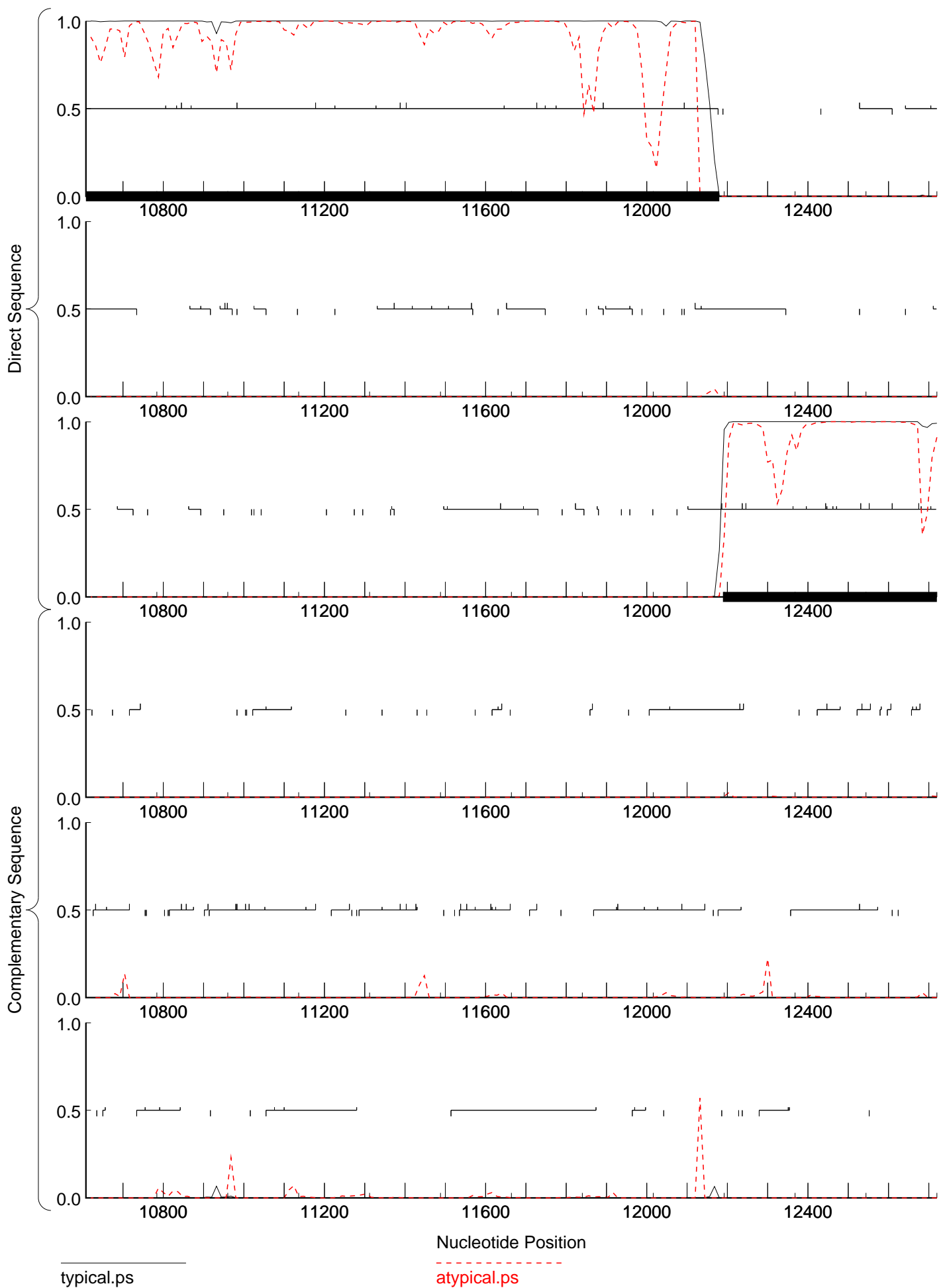
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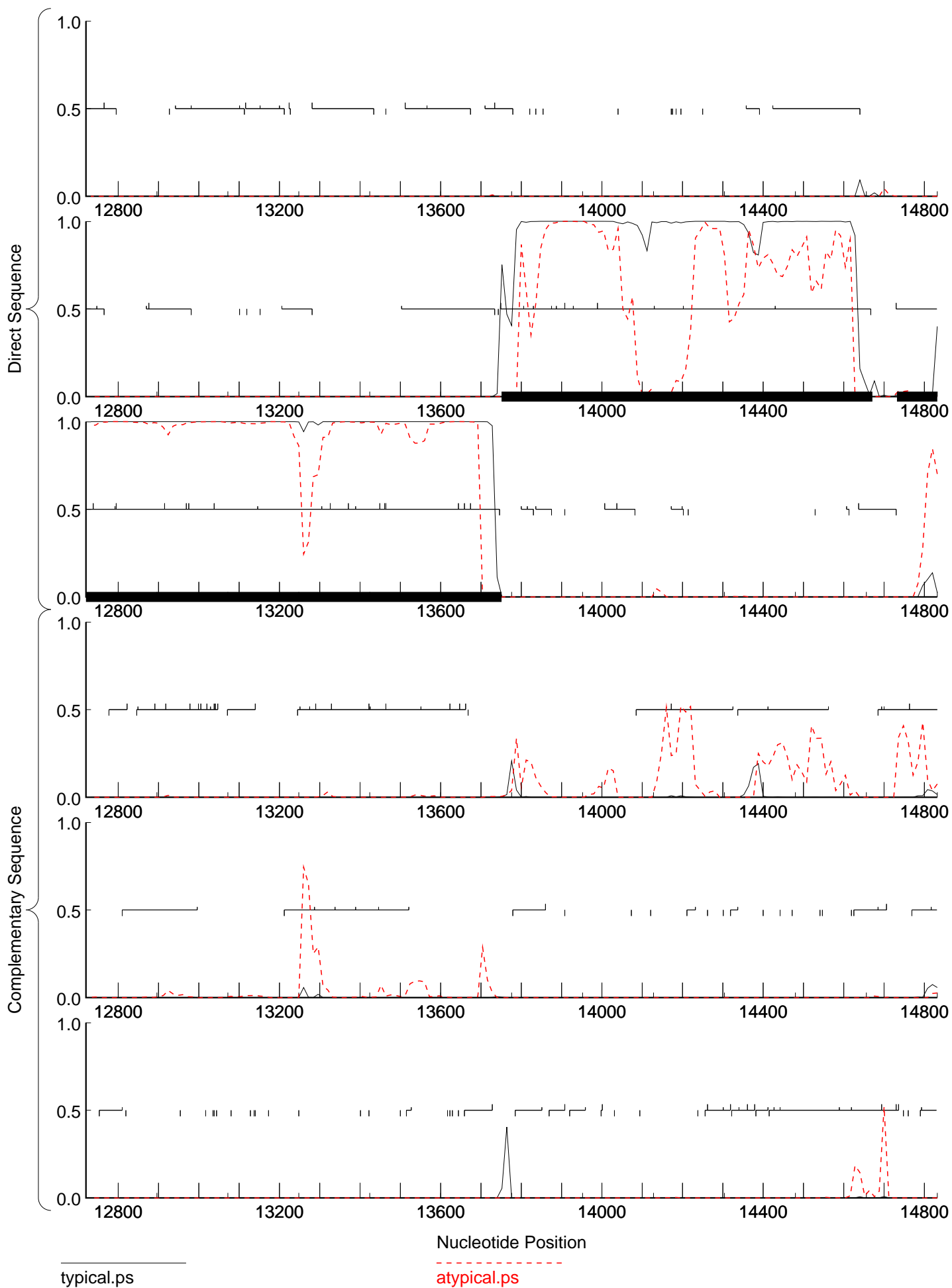


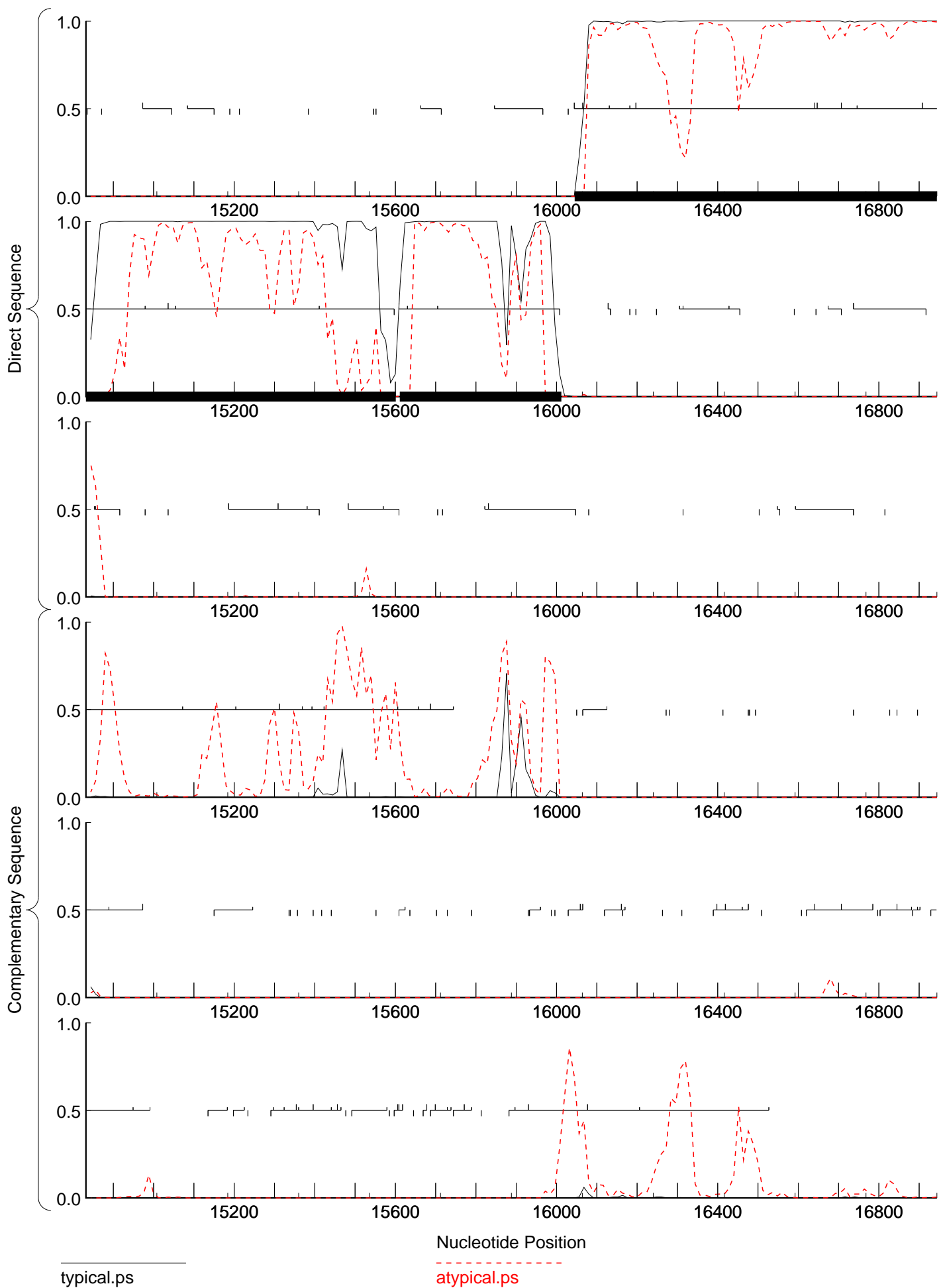
typical.ps

atypical.ps

Yvonnetastic complete sequence, 98136 bp including 10-base 3' overhang (CGCGAAGCTC), Order 4, Window 96, Step 12, 7/48
Yvonnetastic complete sequence, 98136 bp including 10-base 3' overhang (CGCGAAGCTC), Order 2, Window 96, Step 12, 7/48

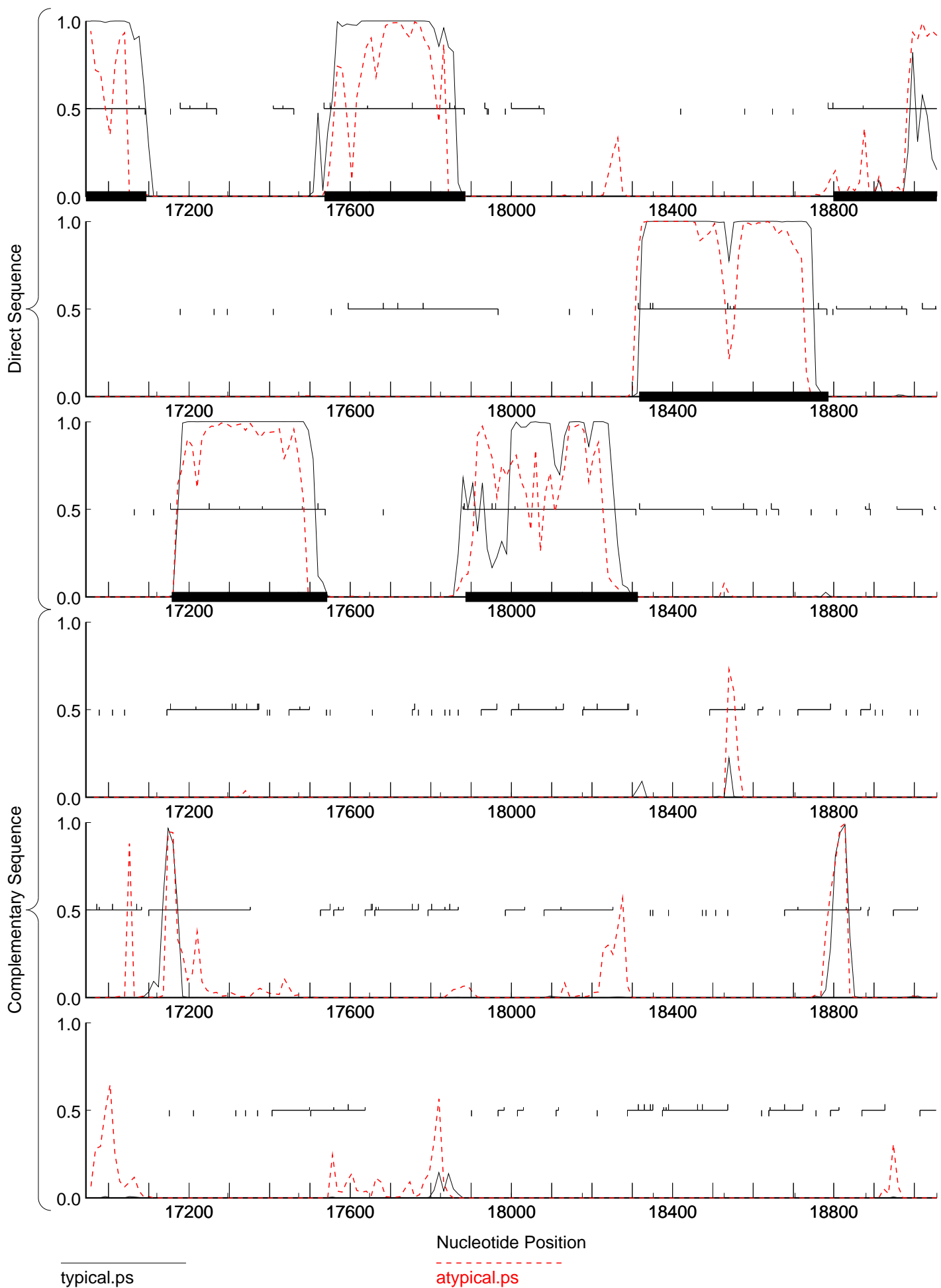




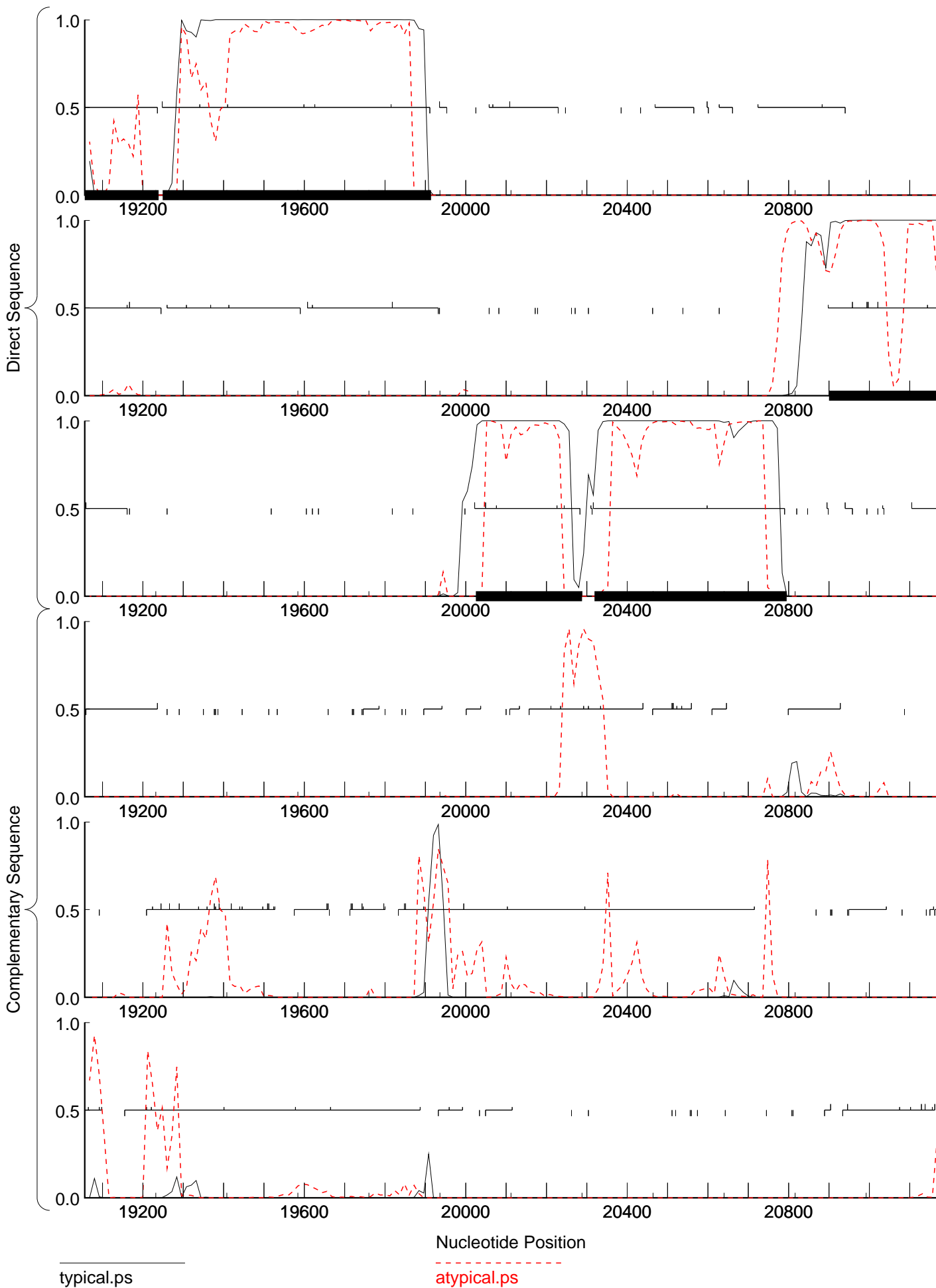


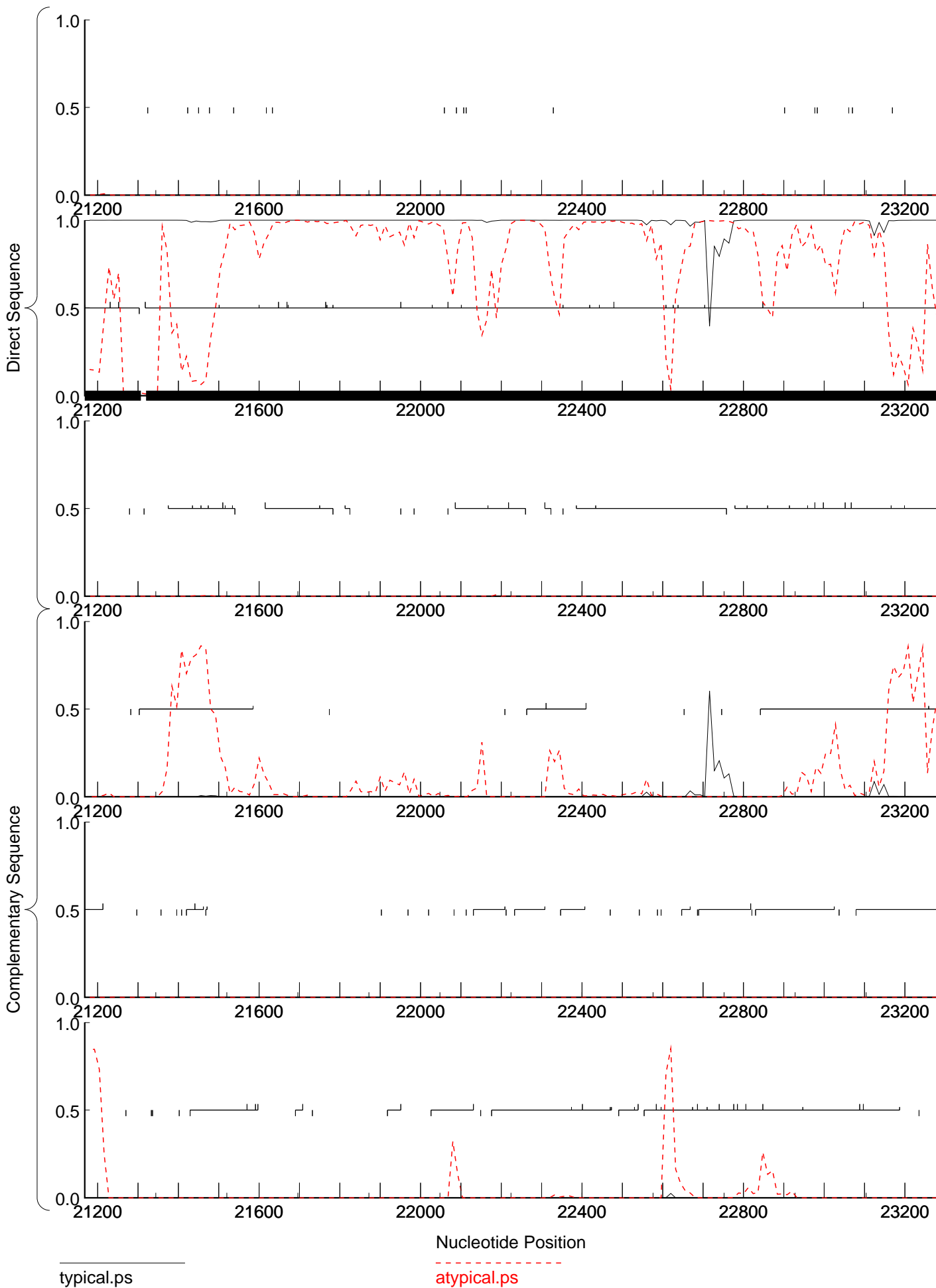
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vonnetastic complete sequence, 98136 bp including 10-base 3' overhang (CGCGAAGCTC), Order 4, Window 96, Step 12, 11/48
GeneMark.hmm prediction
vonnetastic complete sequence, 98136 bp including 10-base 3' overhang (CGCGAAGCTC), Order 2, Window 96, Step 12, 11/48

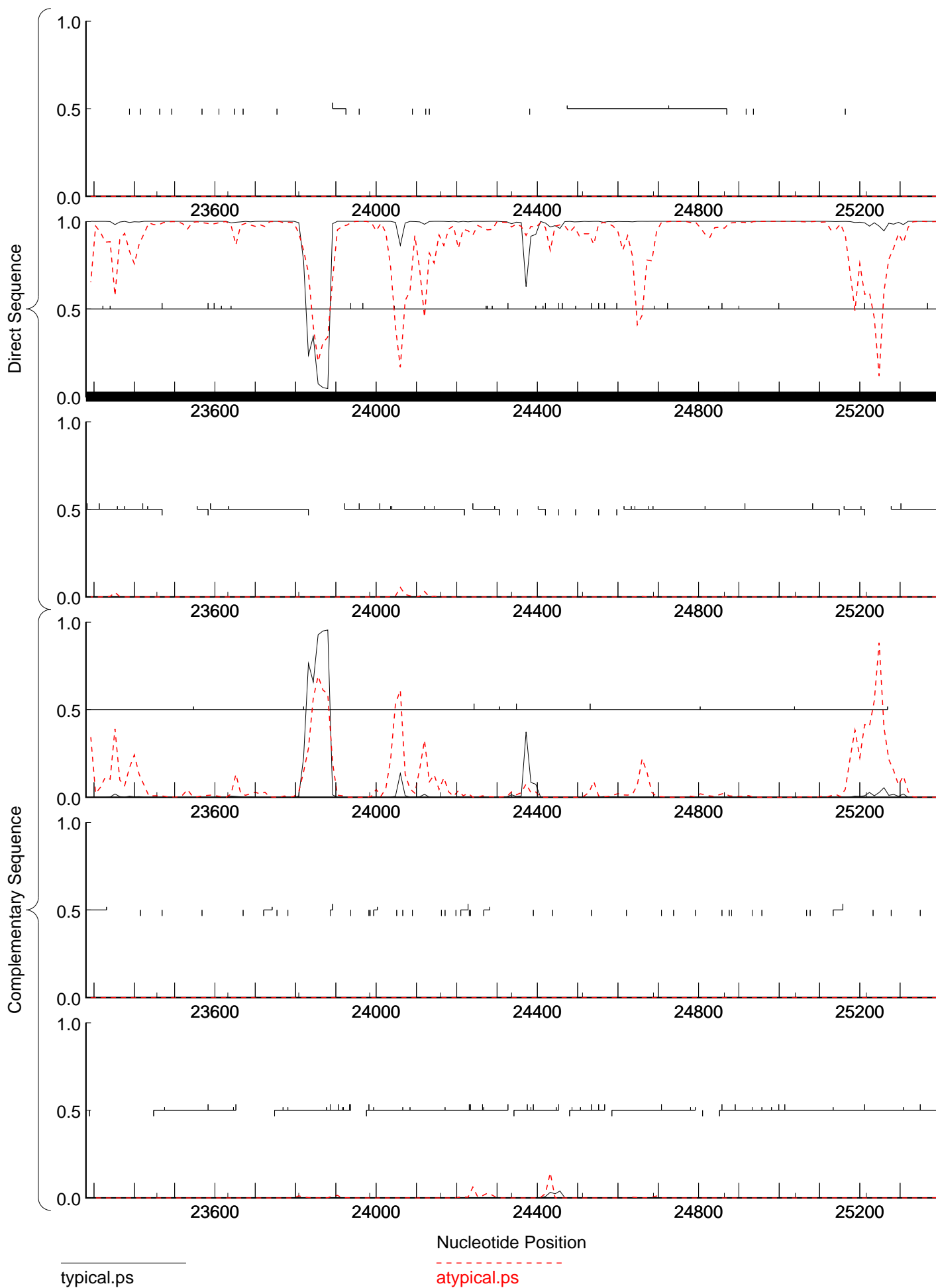




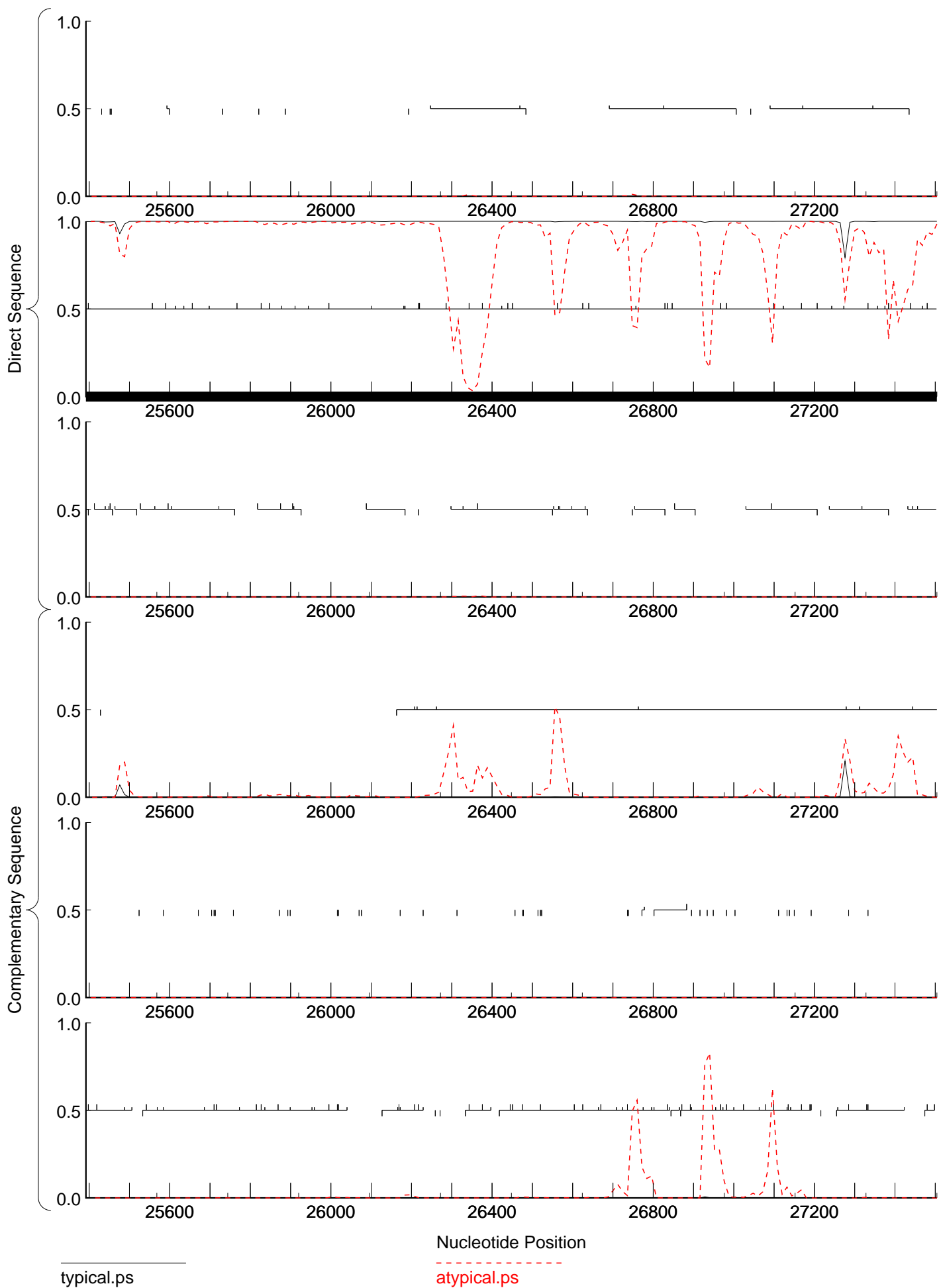
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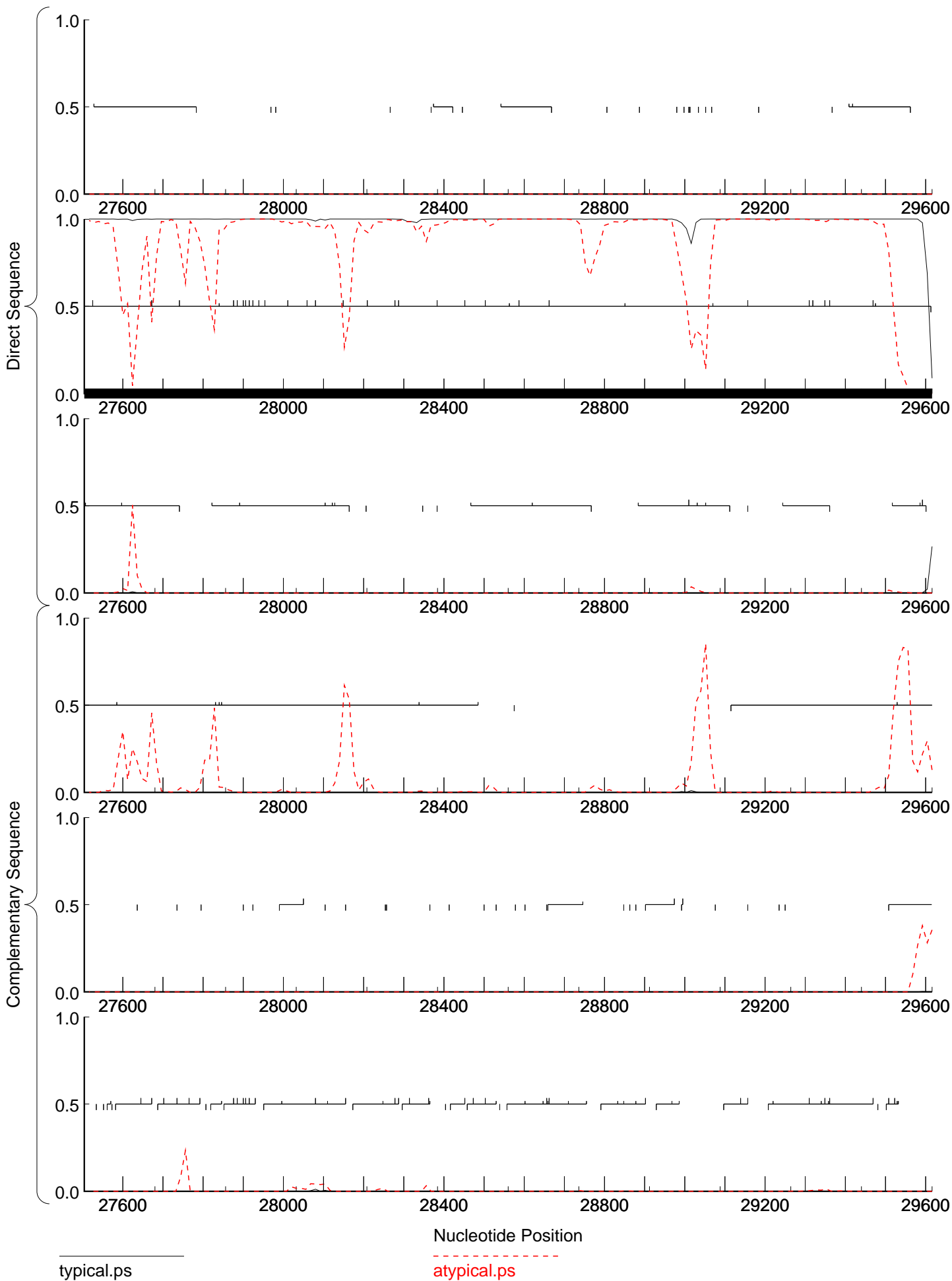
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GeneMark.hmm prediction
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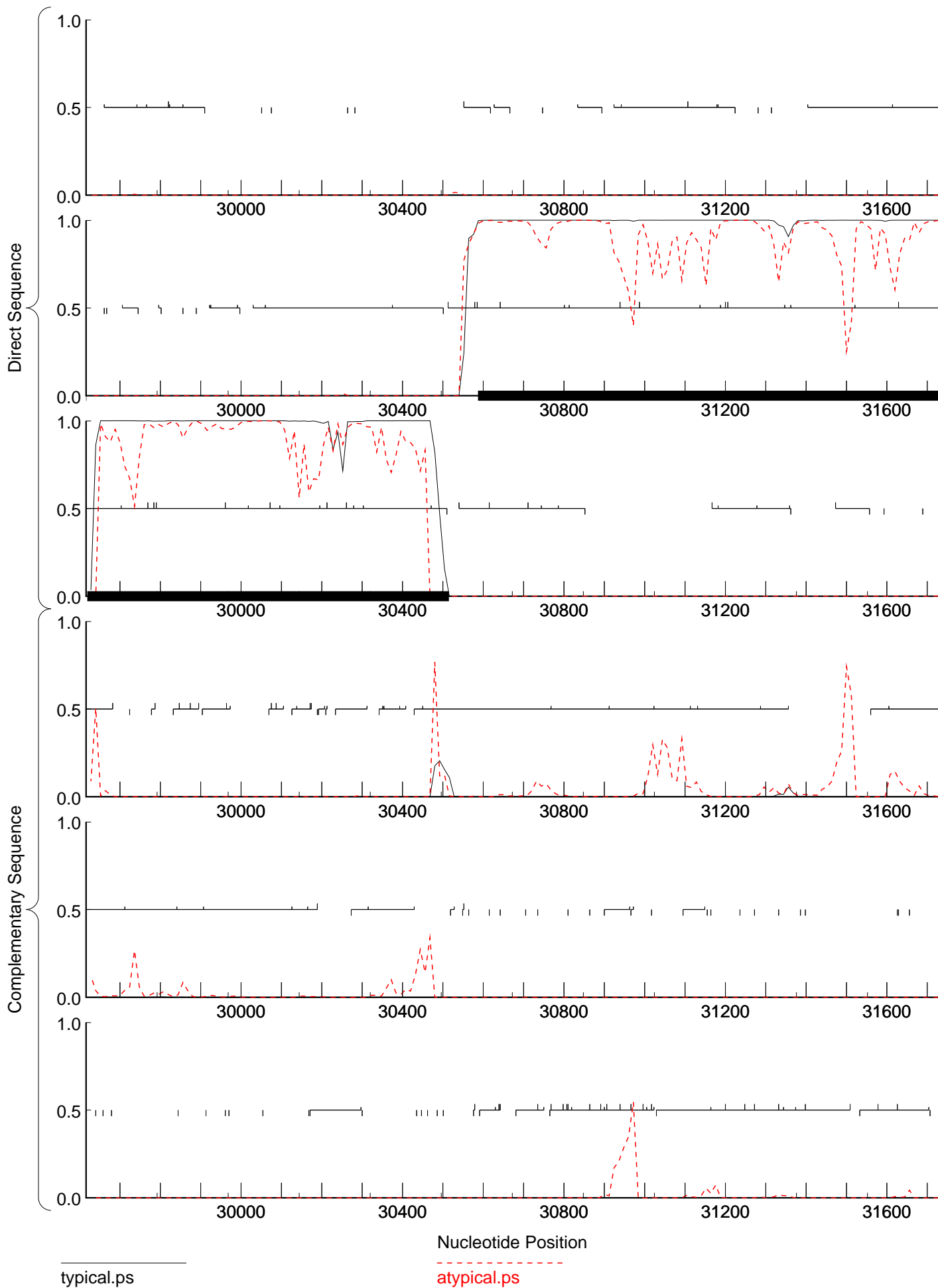
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GeneMark.hmm prediction
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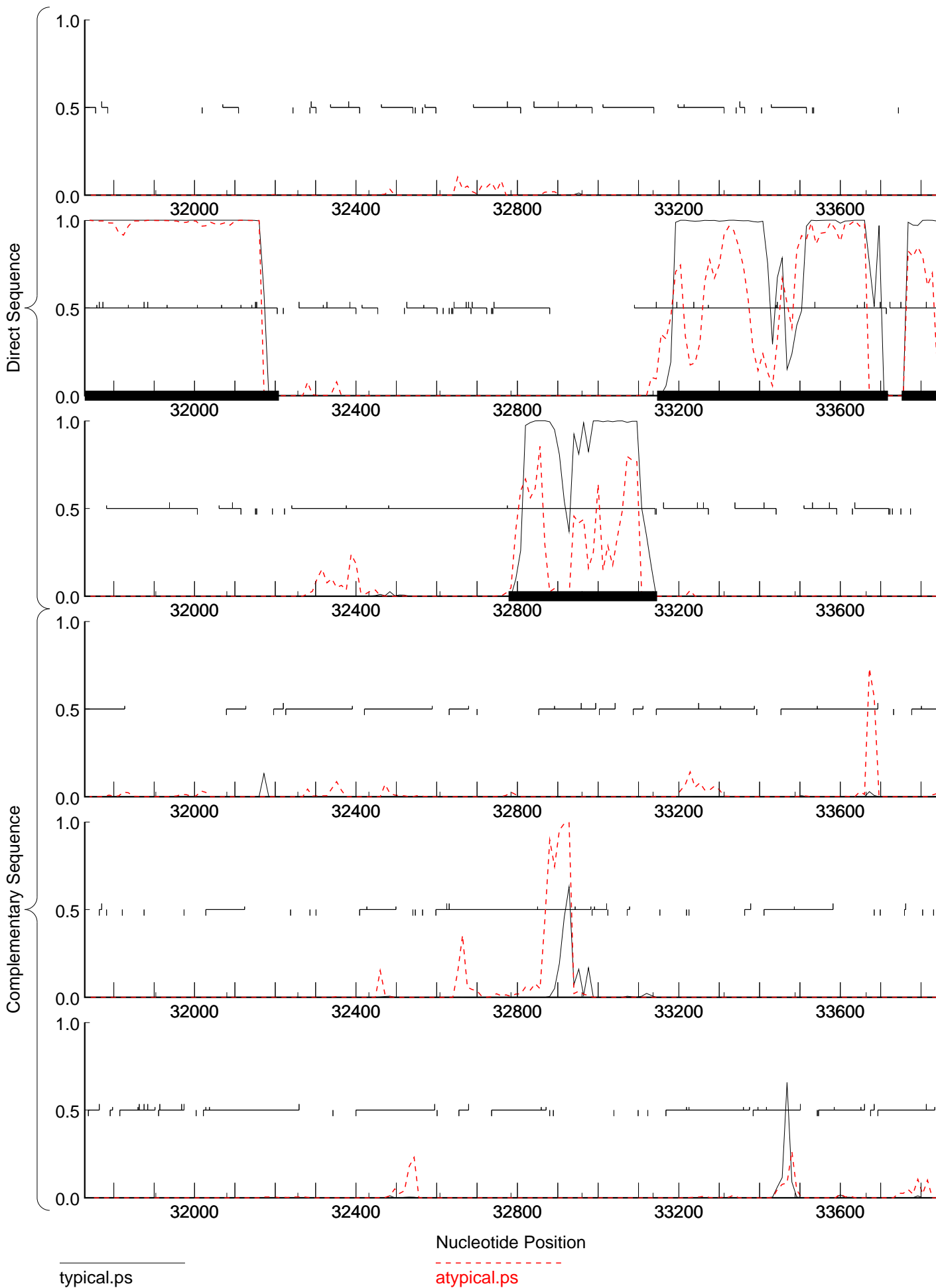


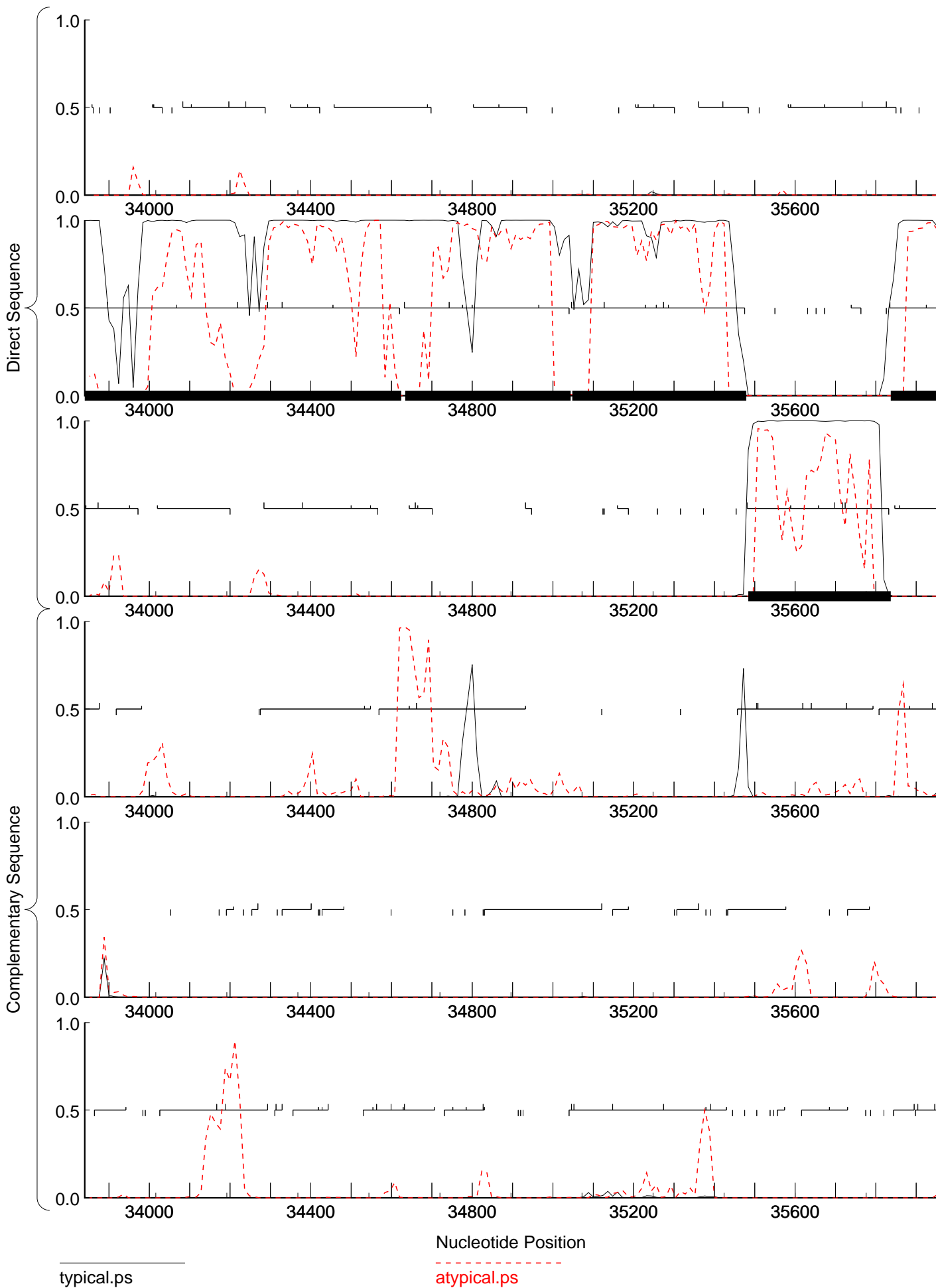
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GeneMark.hmm prediction
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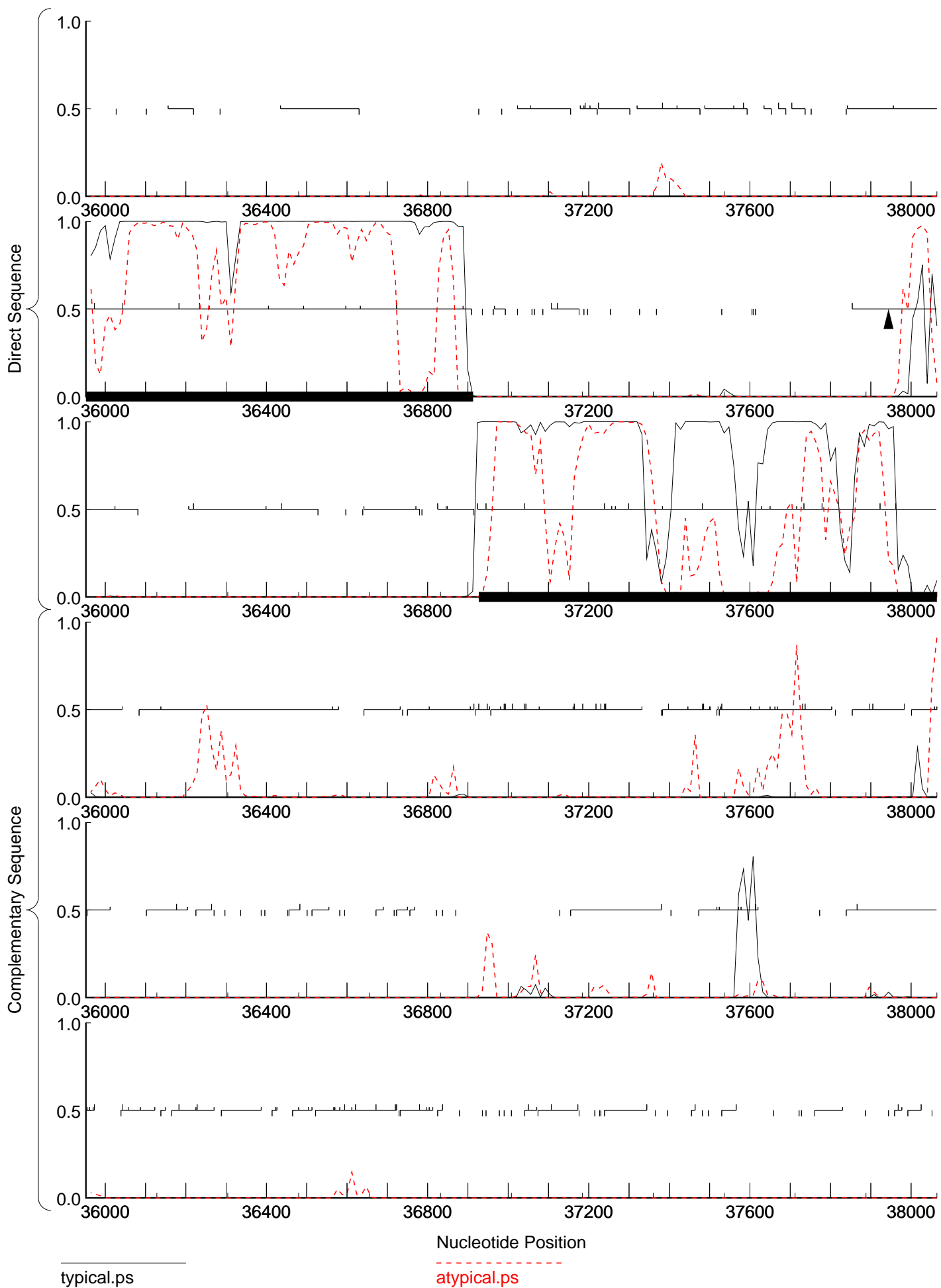


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GeneMark.hmm prediction
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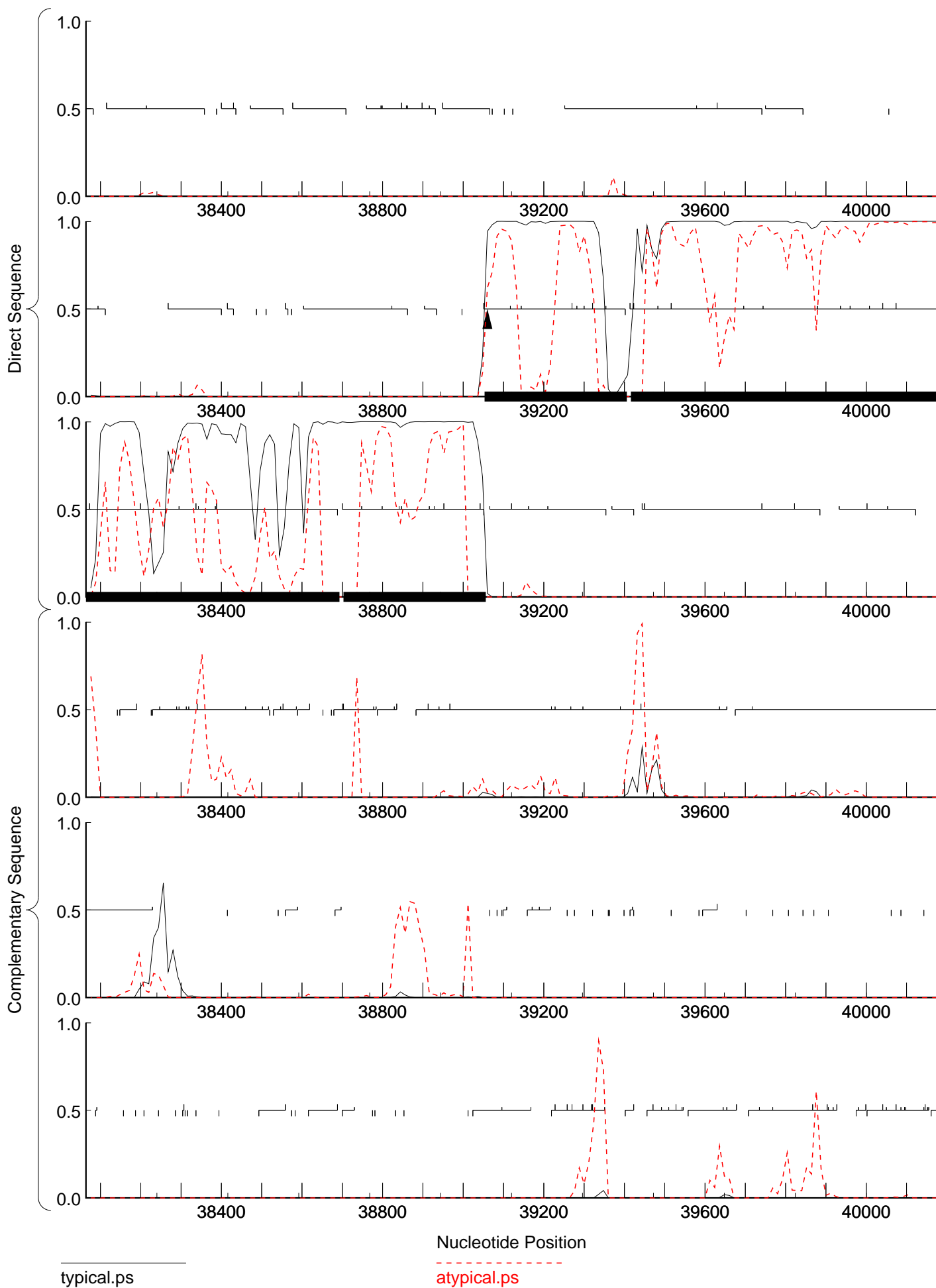


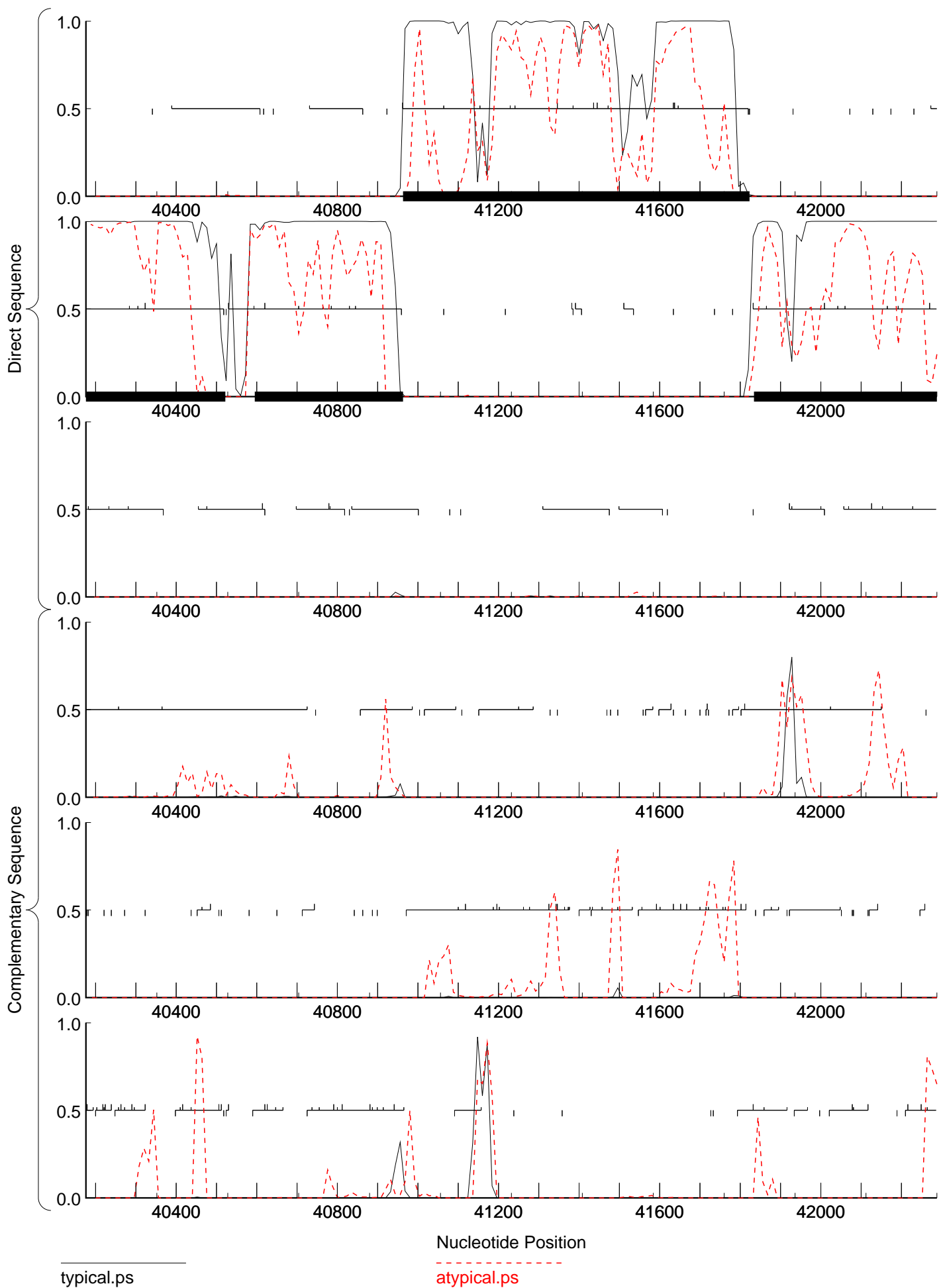


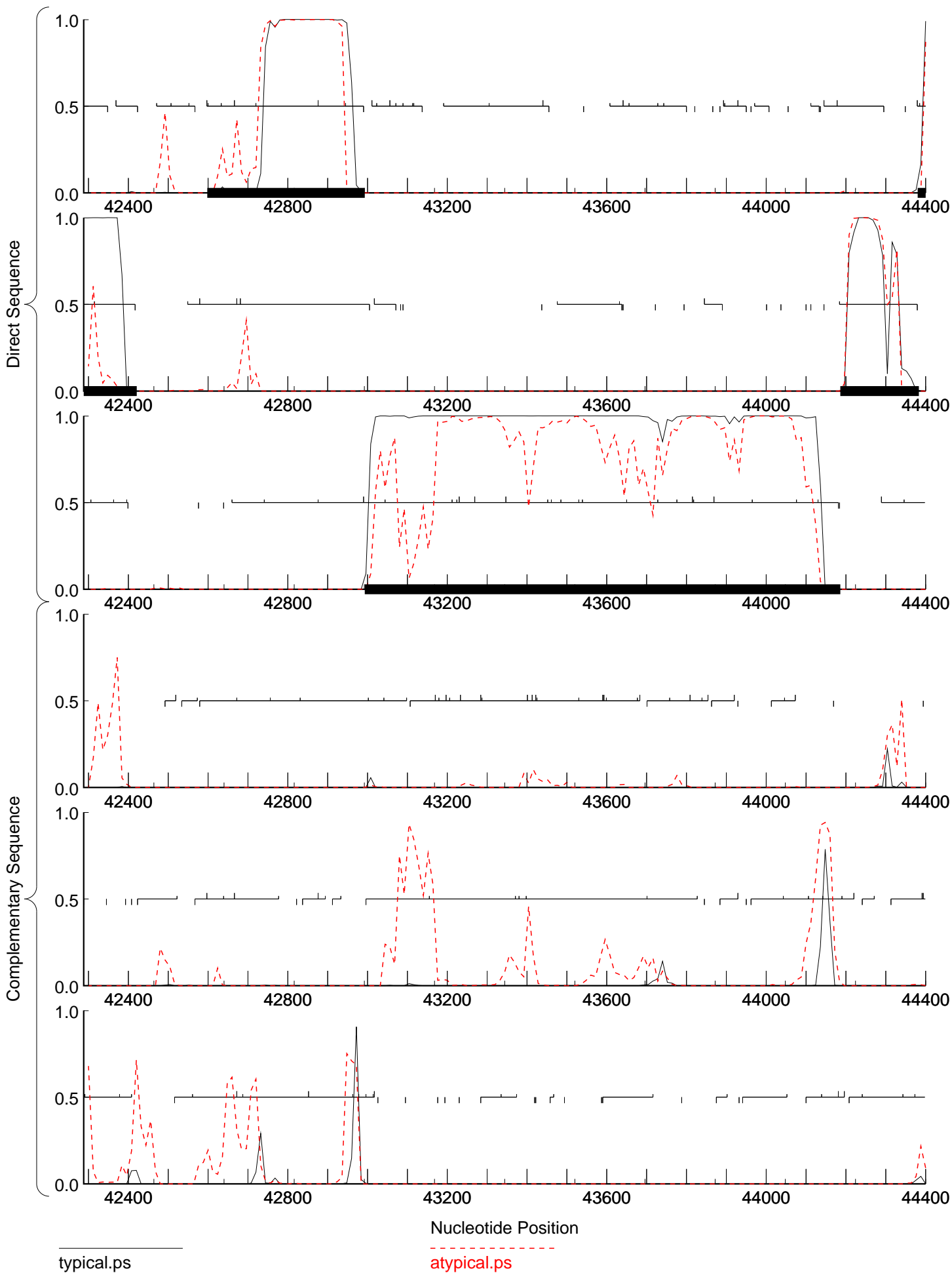


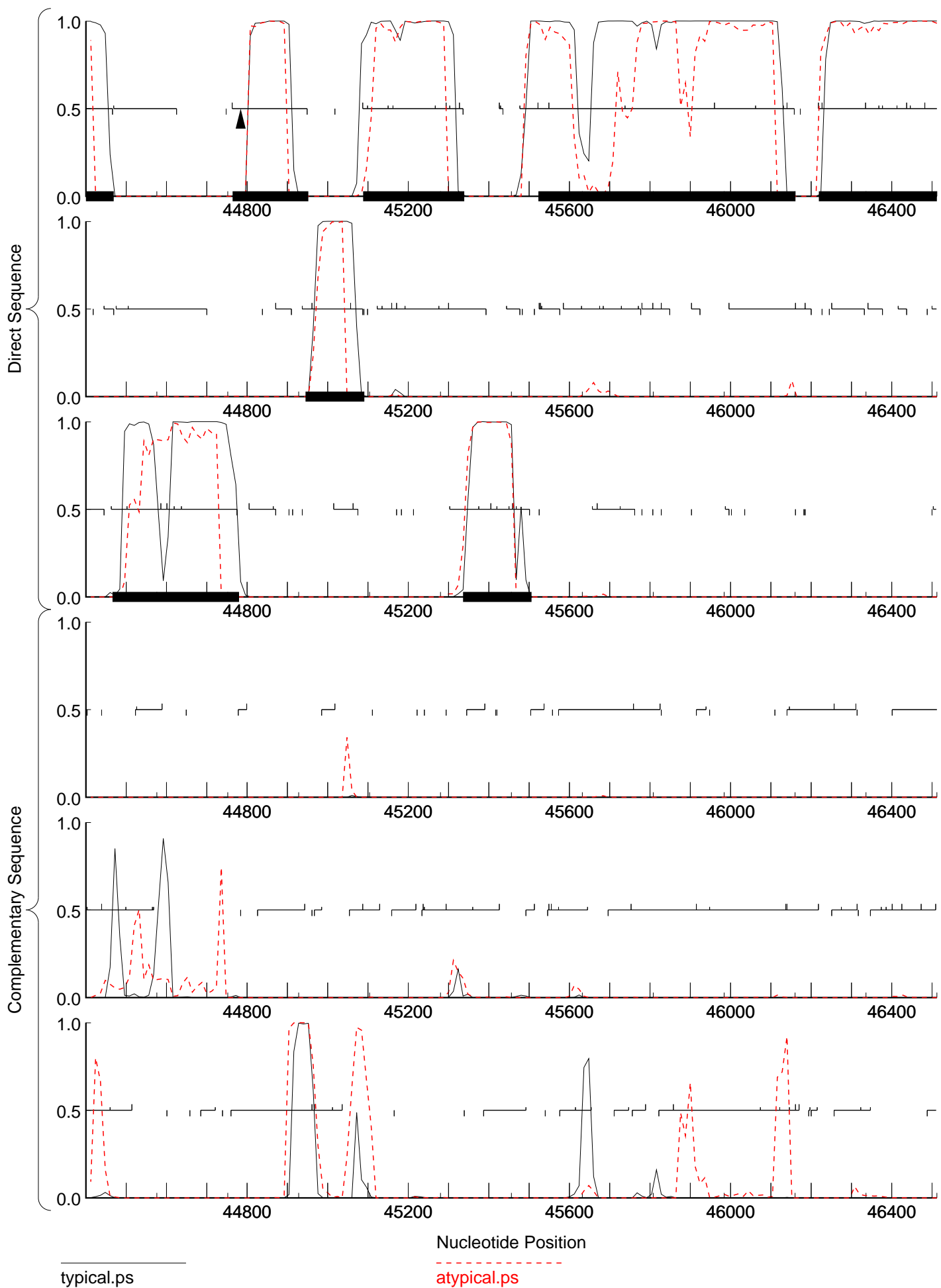
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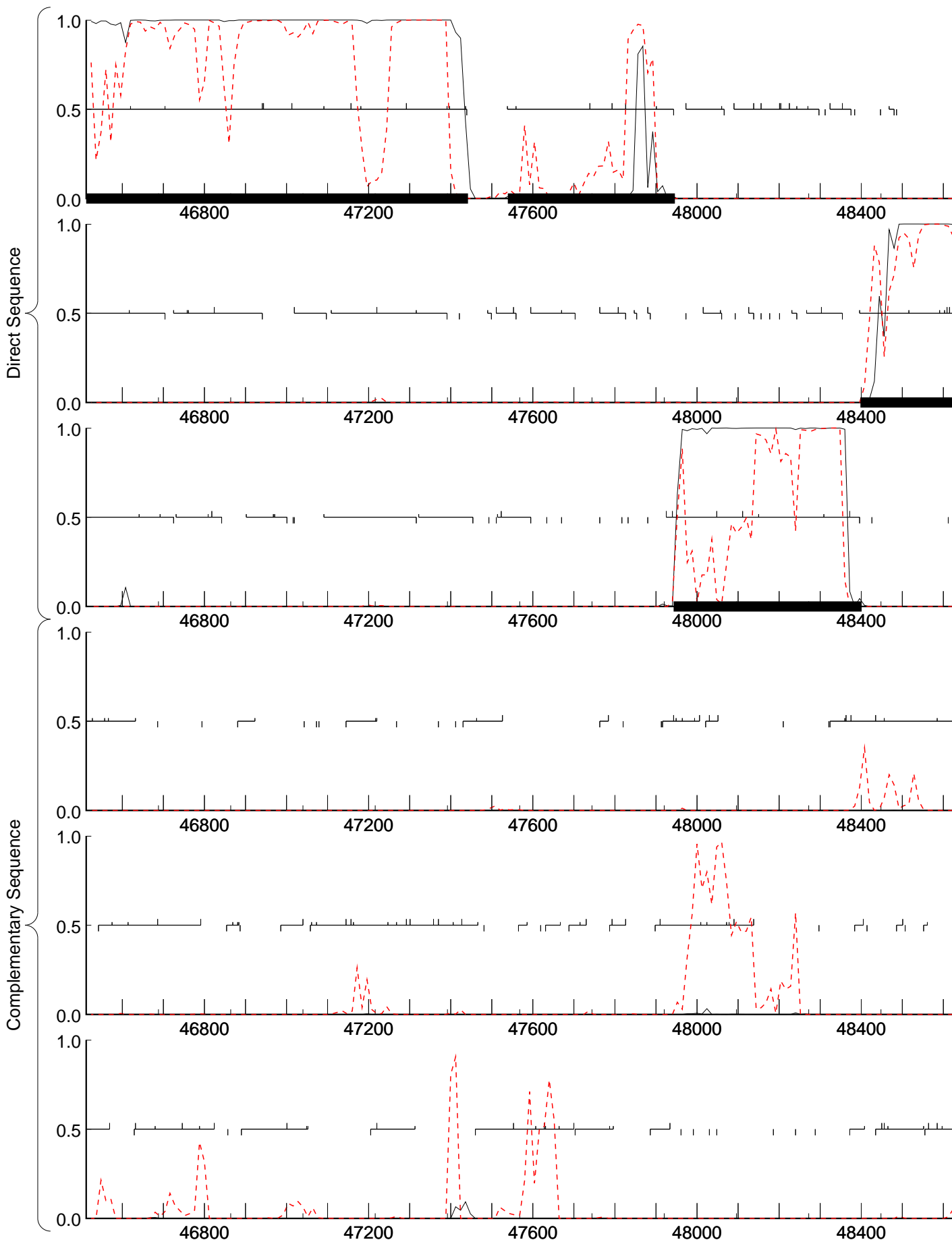
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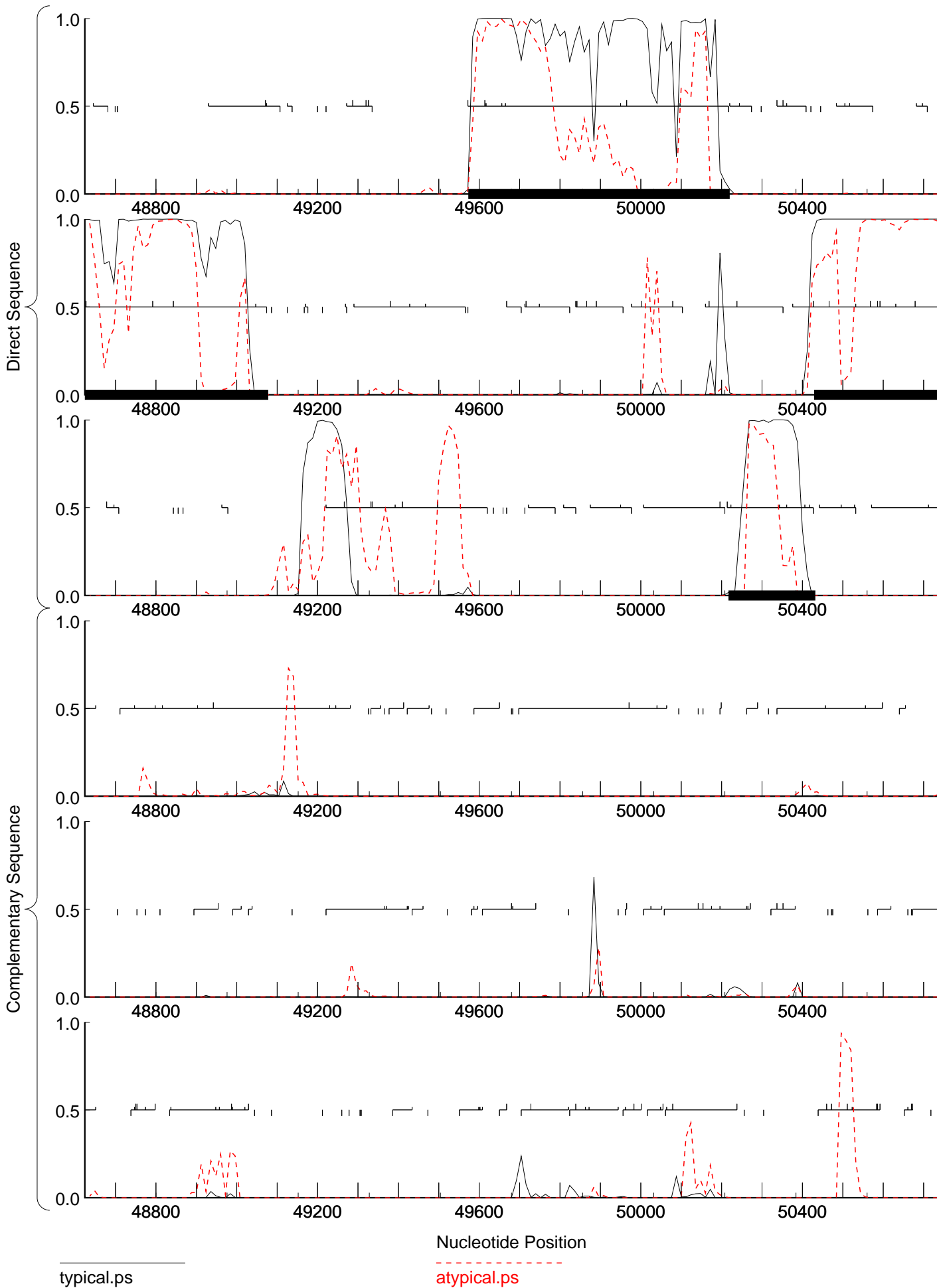






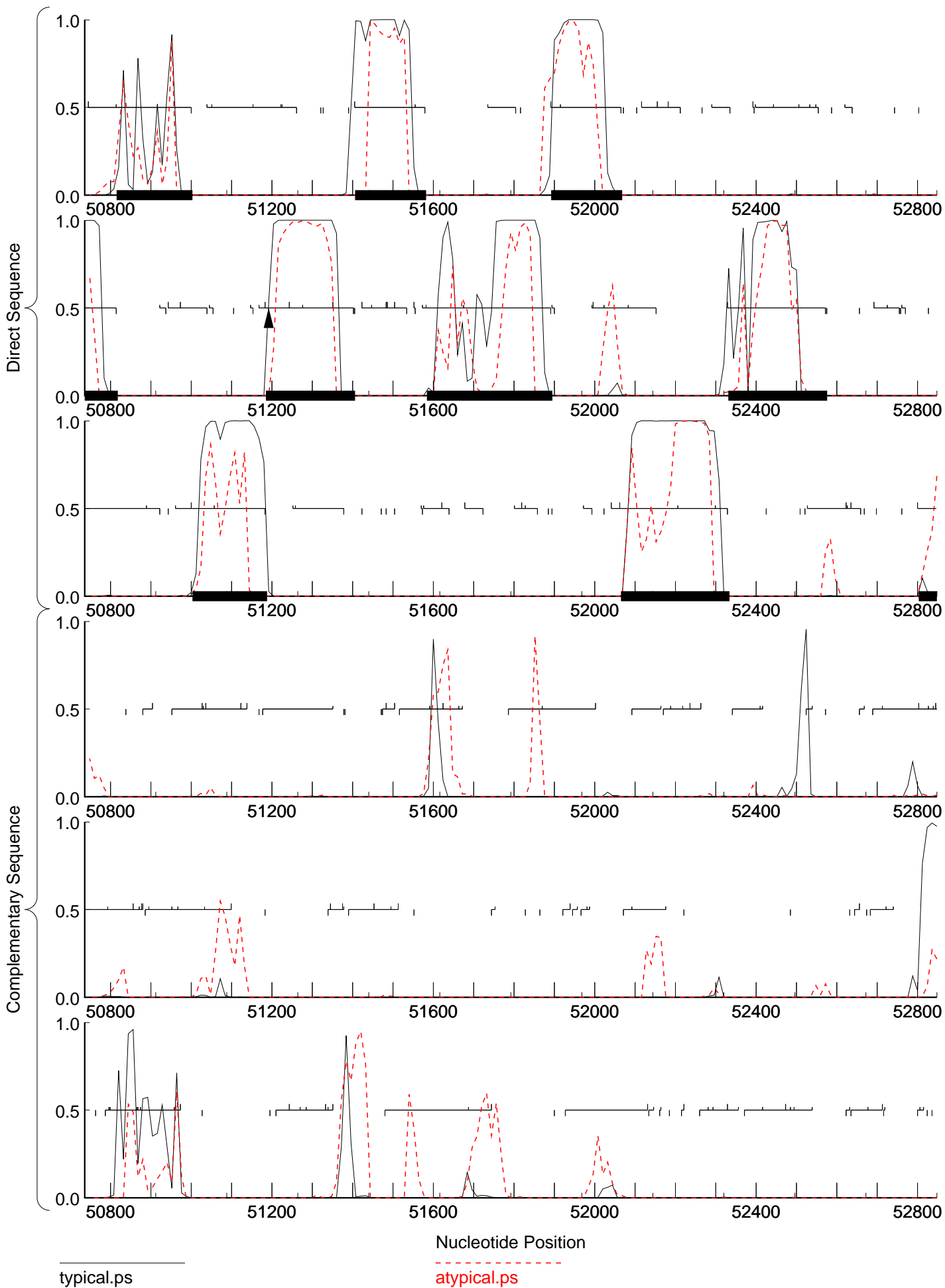
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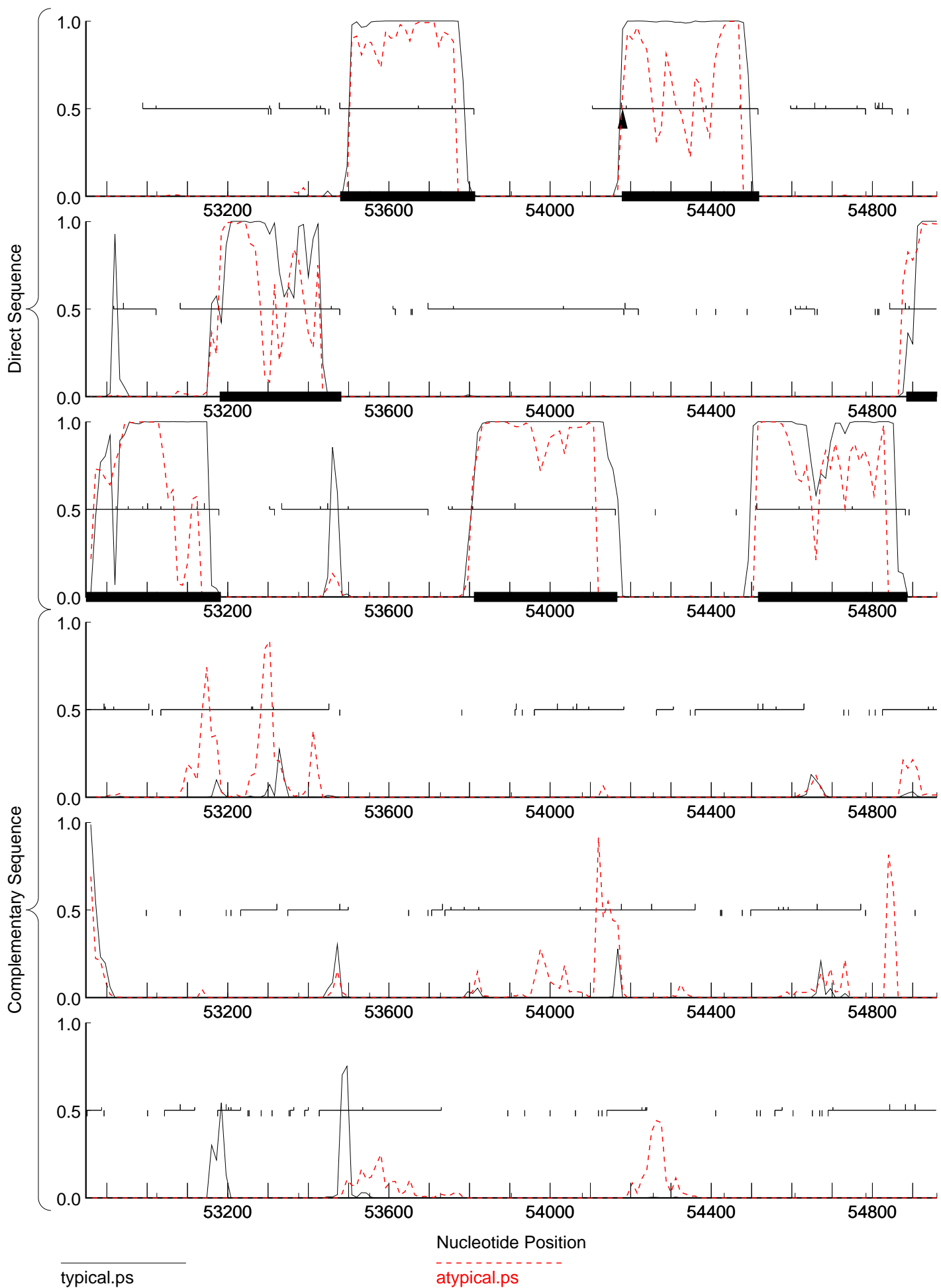
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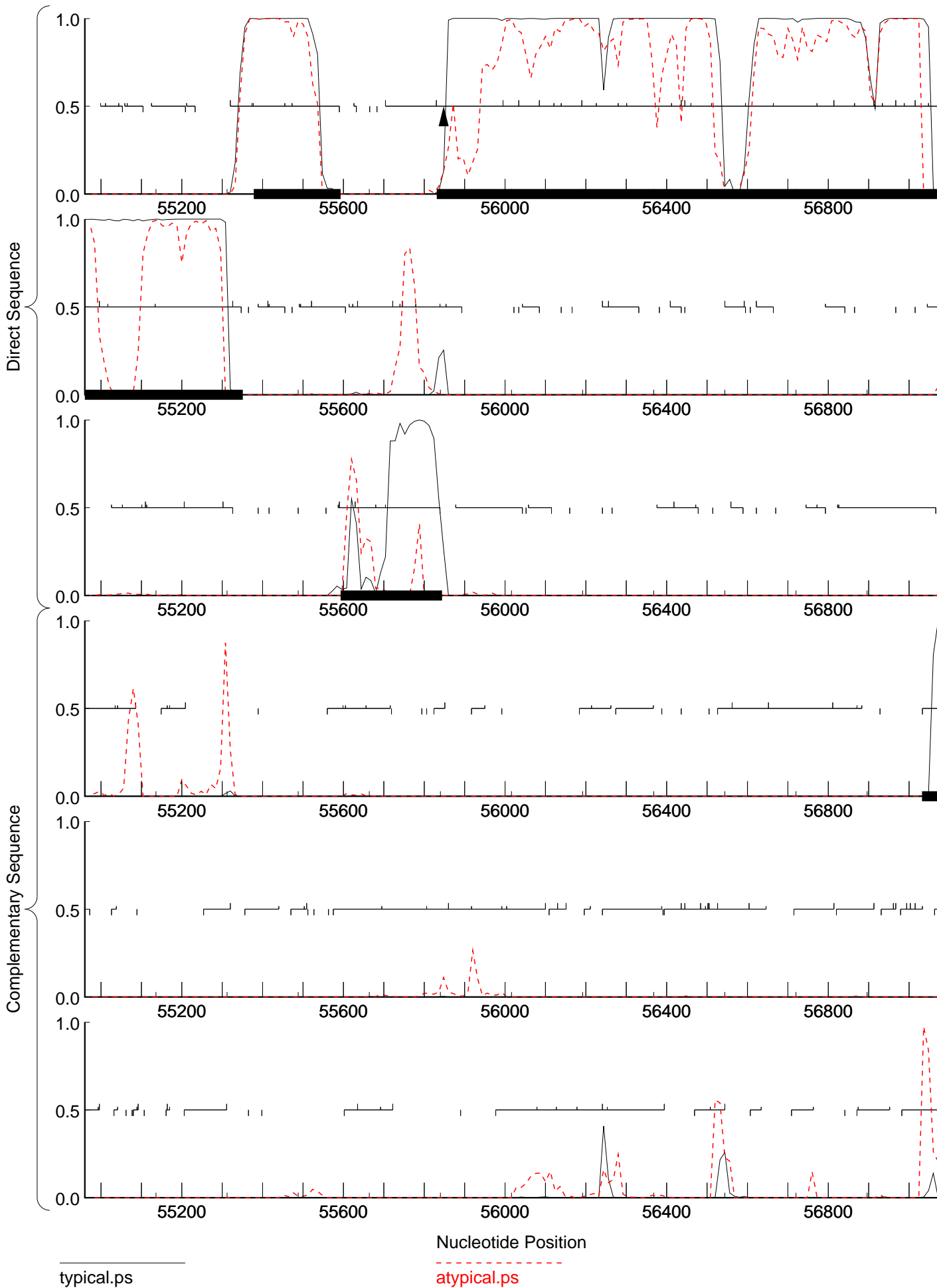
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typical.ps

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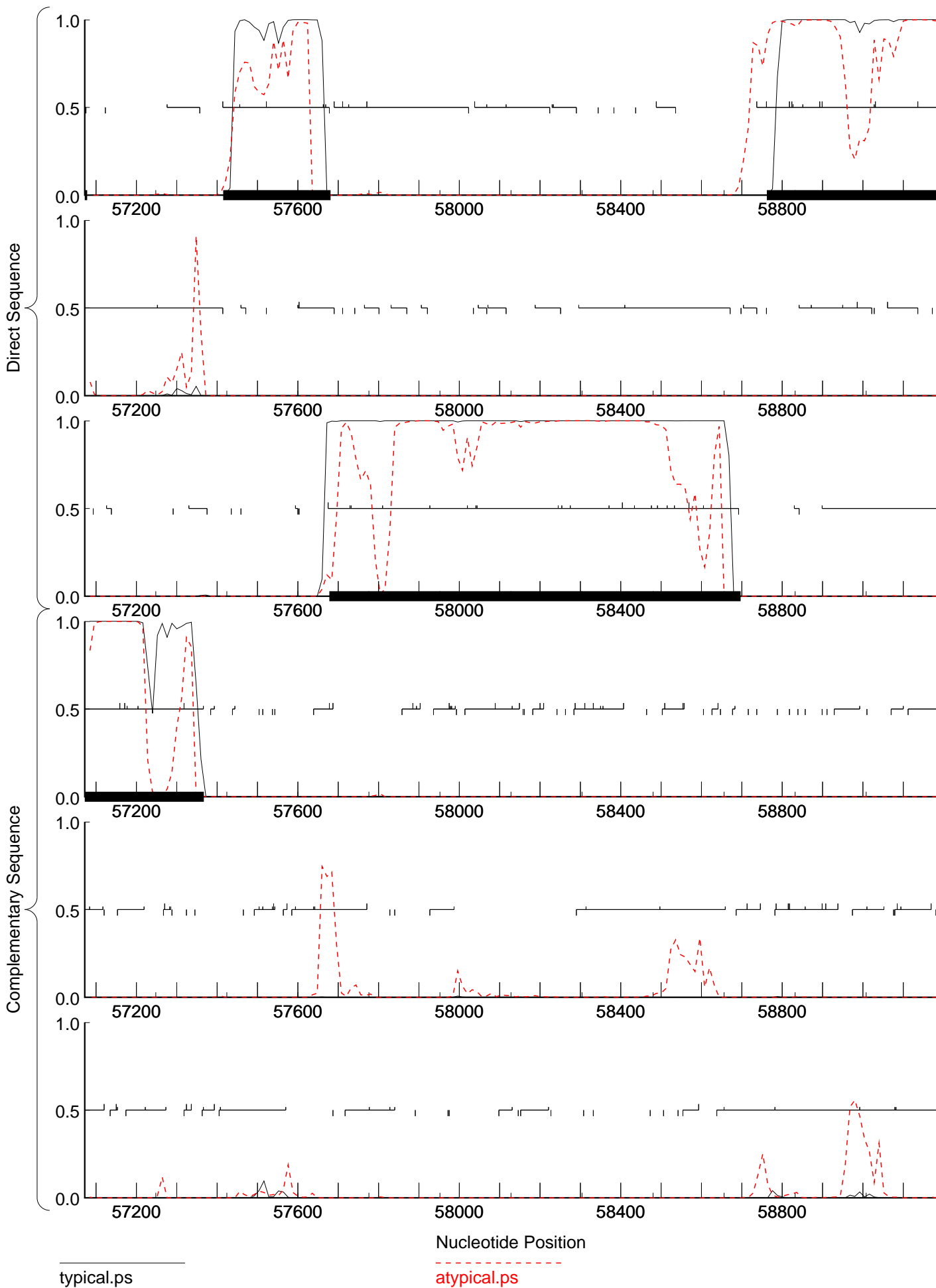


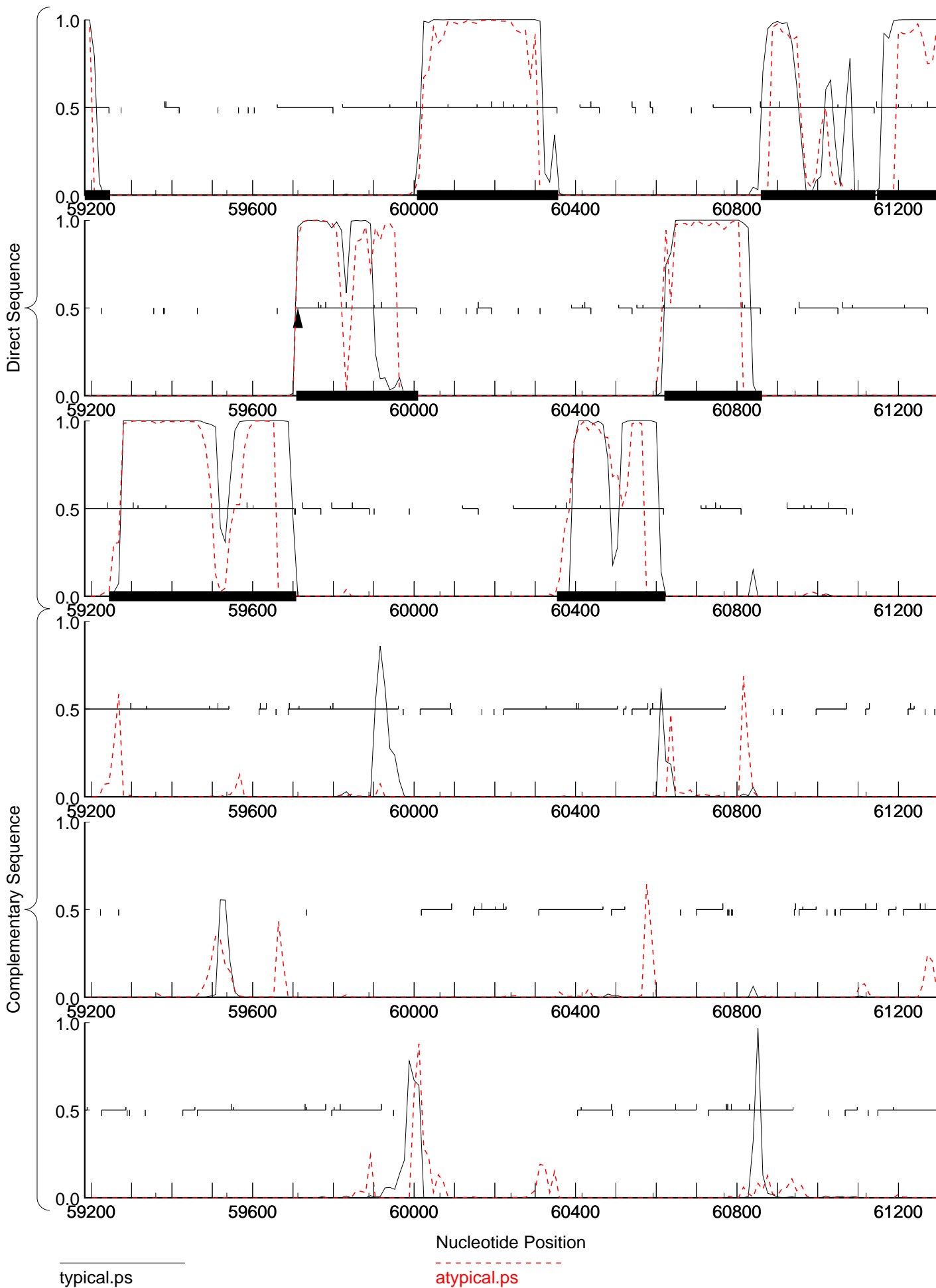


typical.ps

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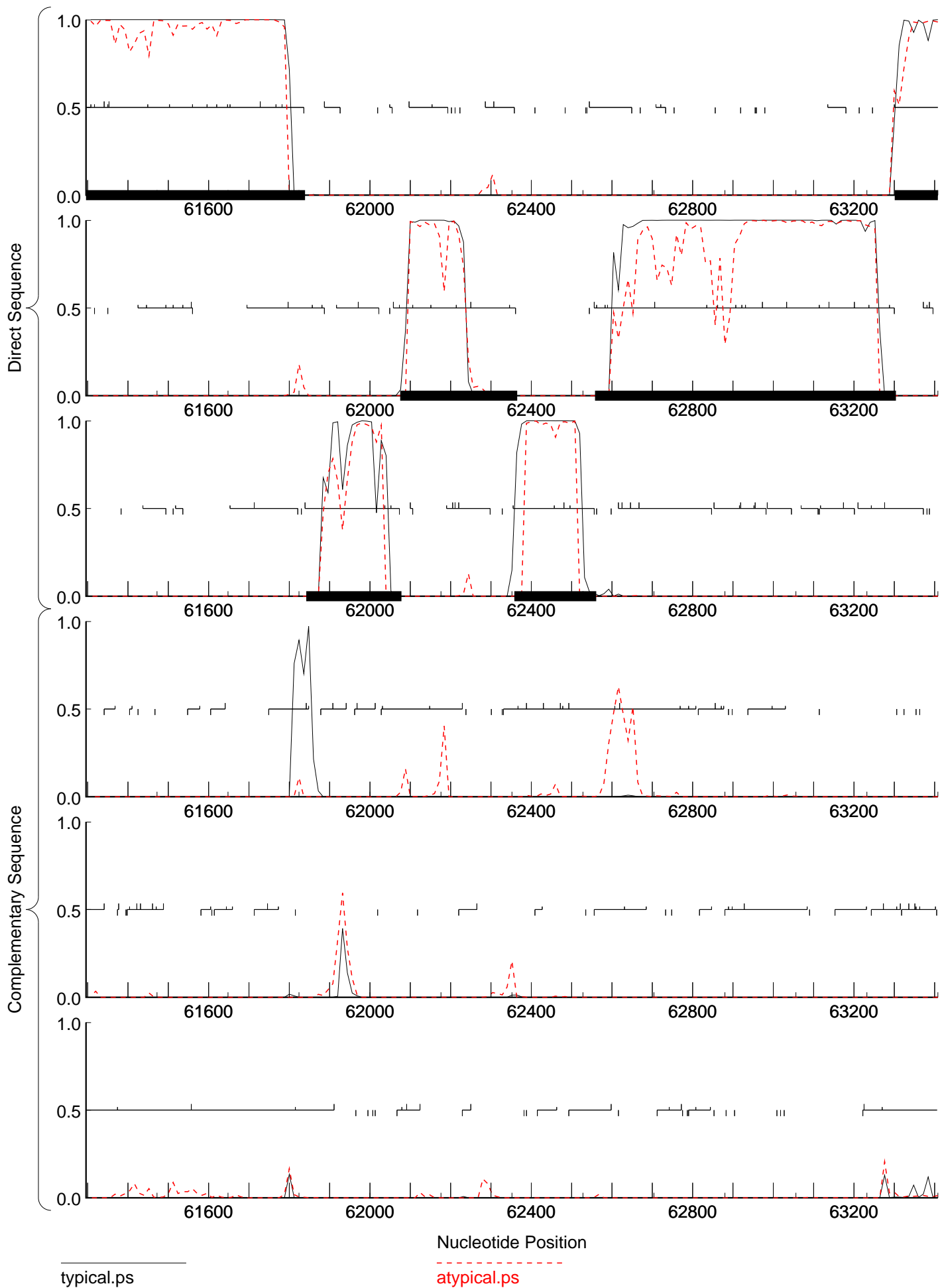
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GeneMark.hmm prediction
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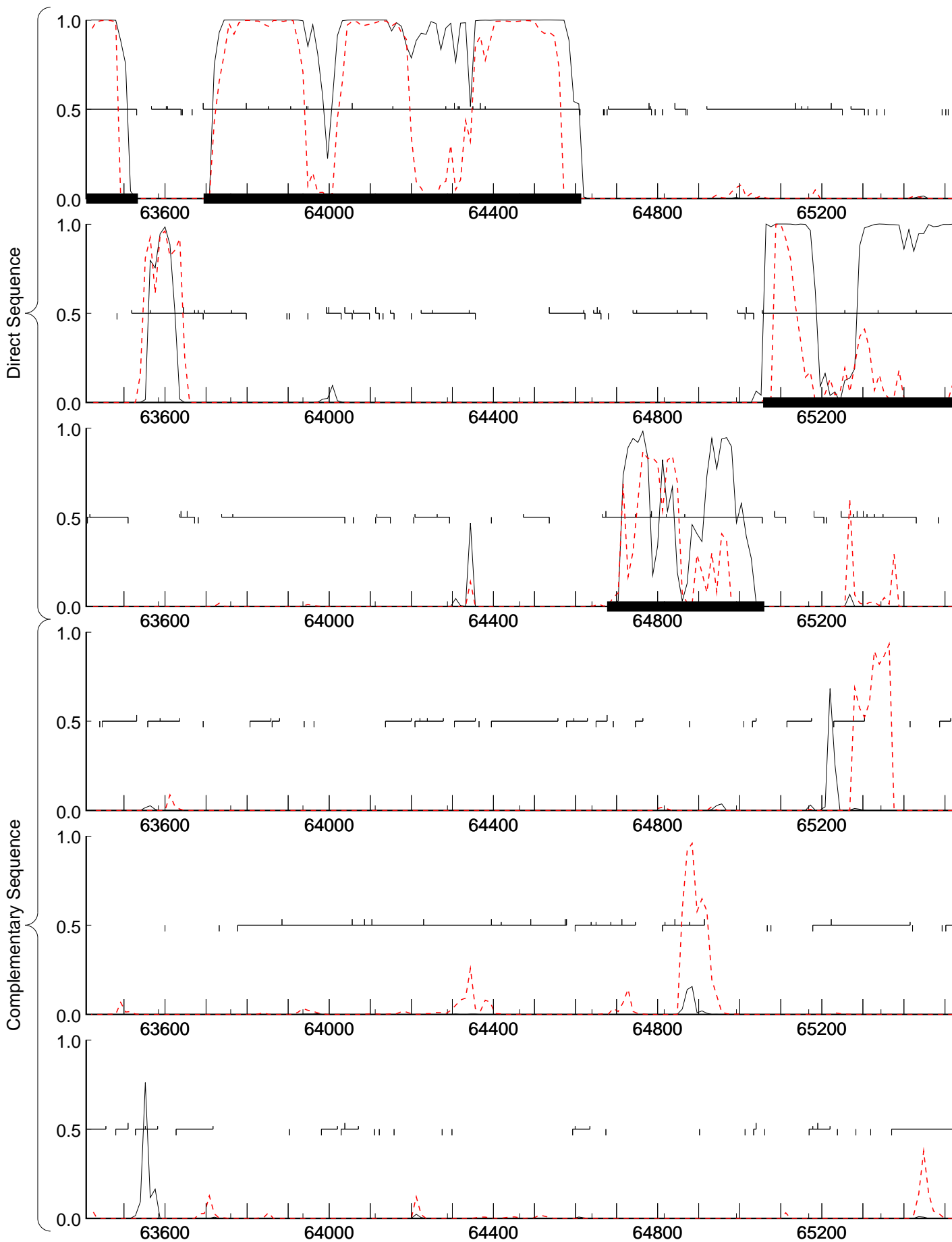




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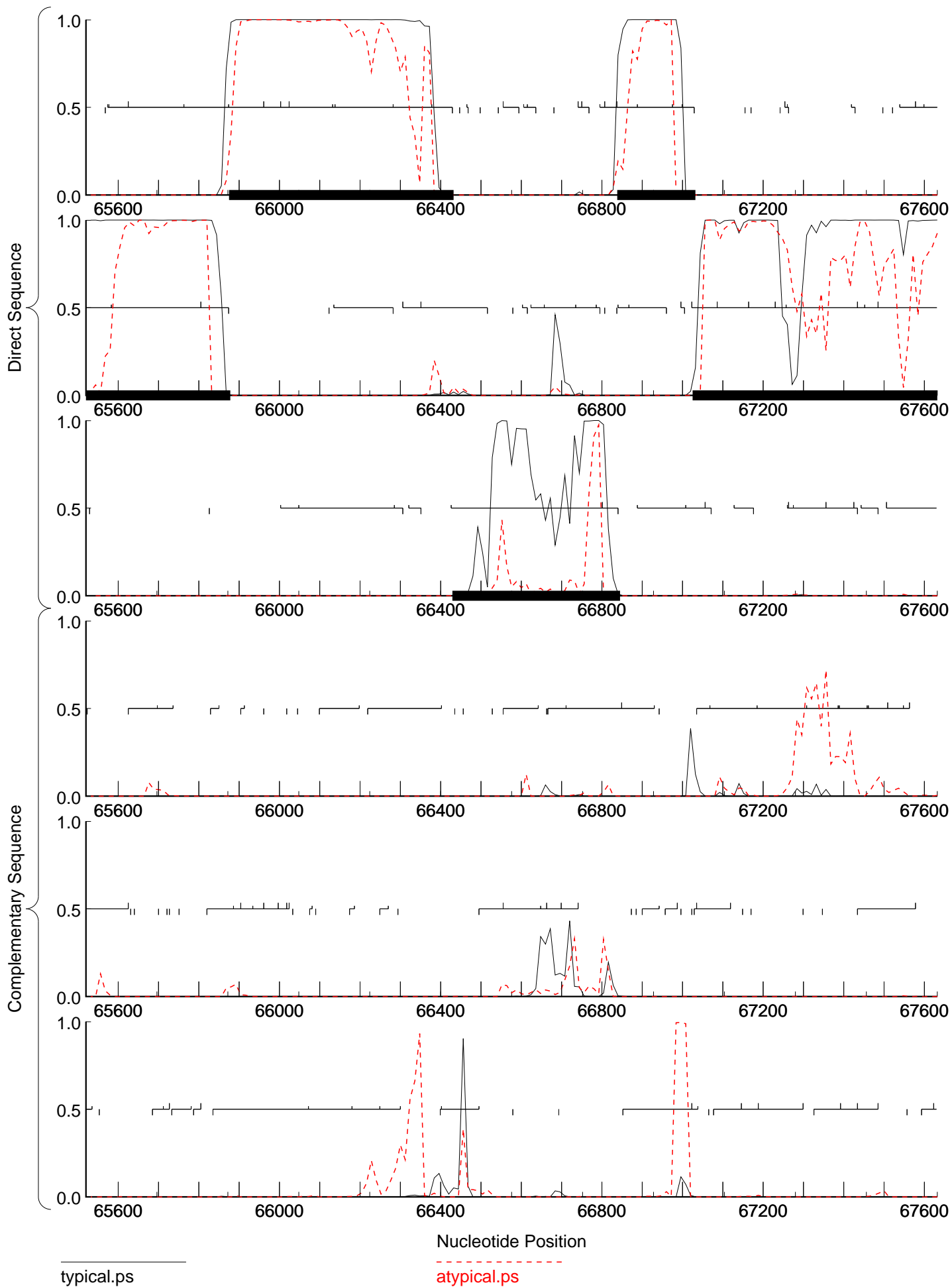
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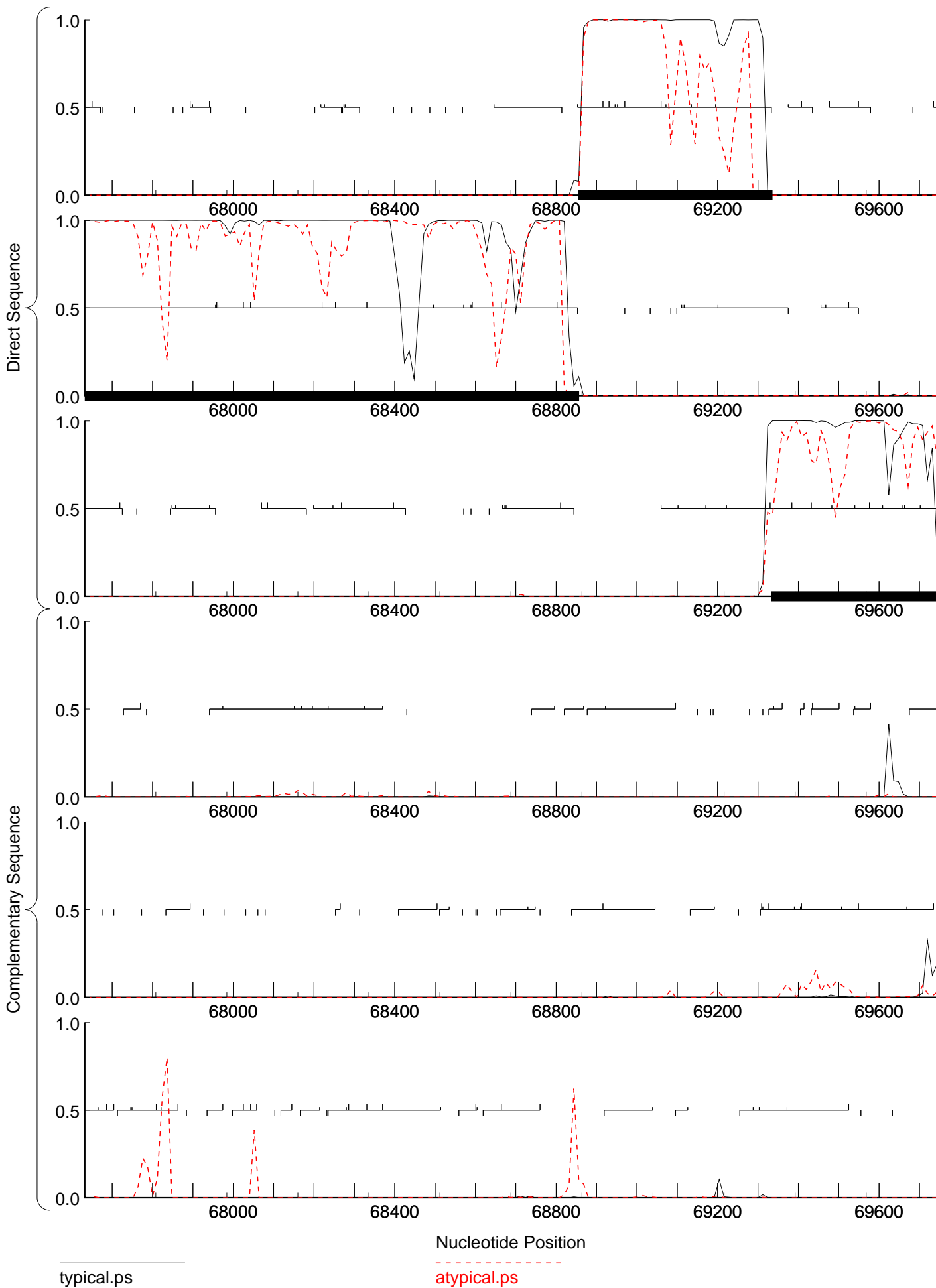
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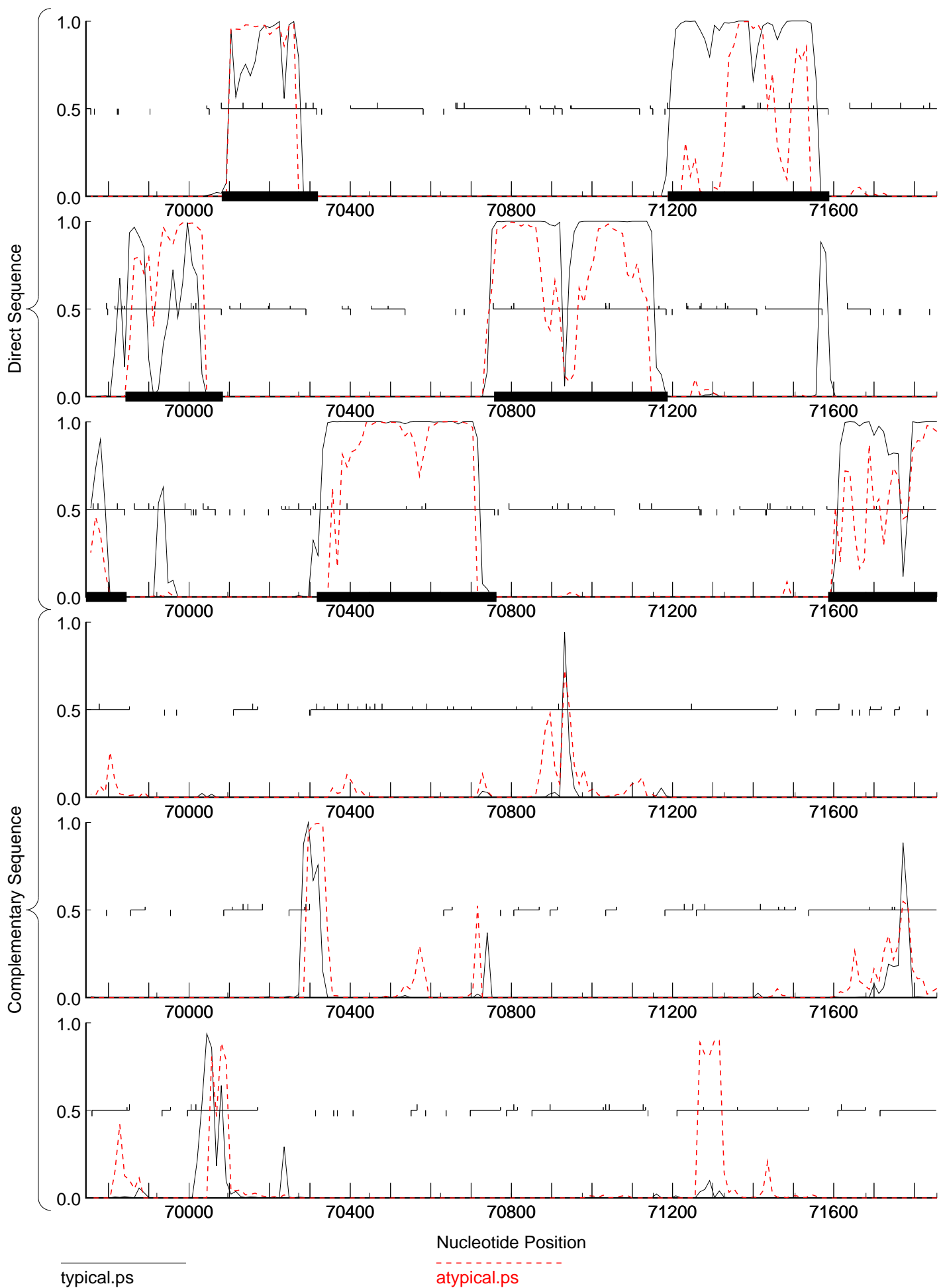
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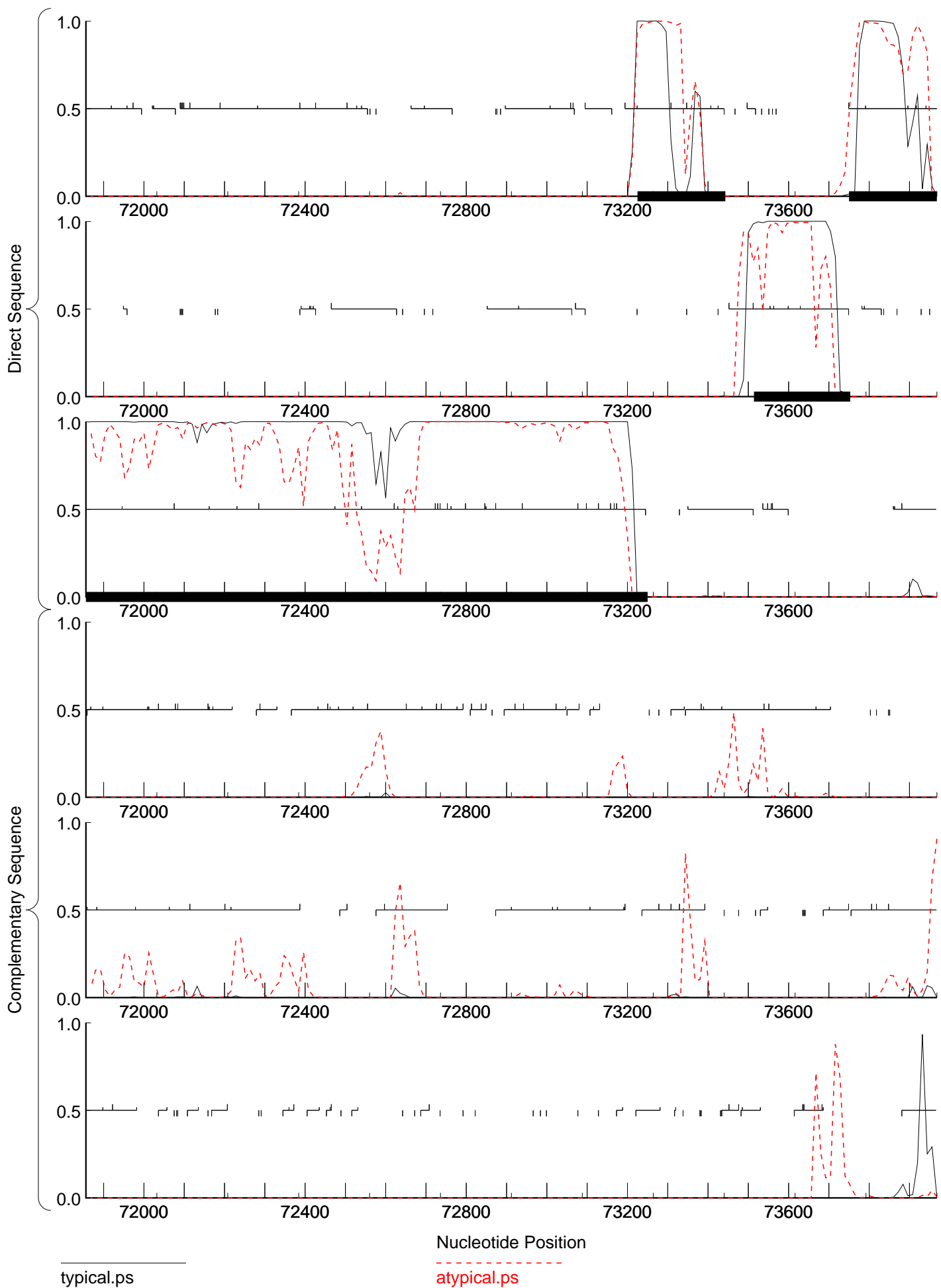
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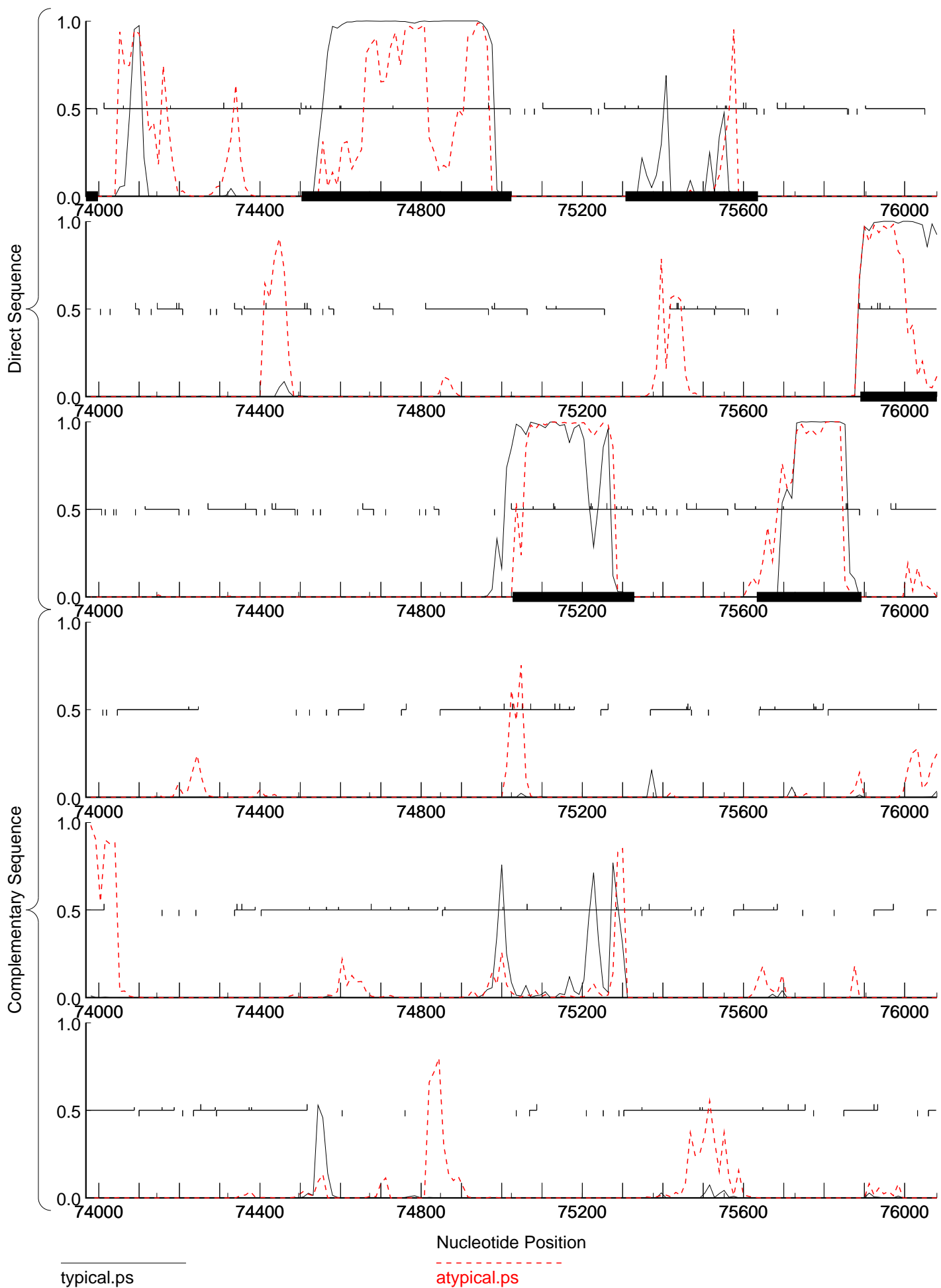




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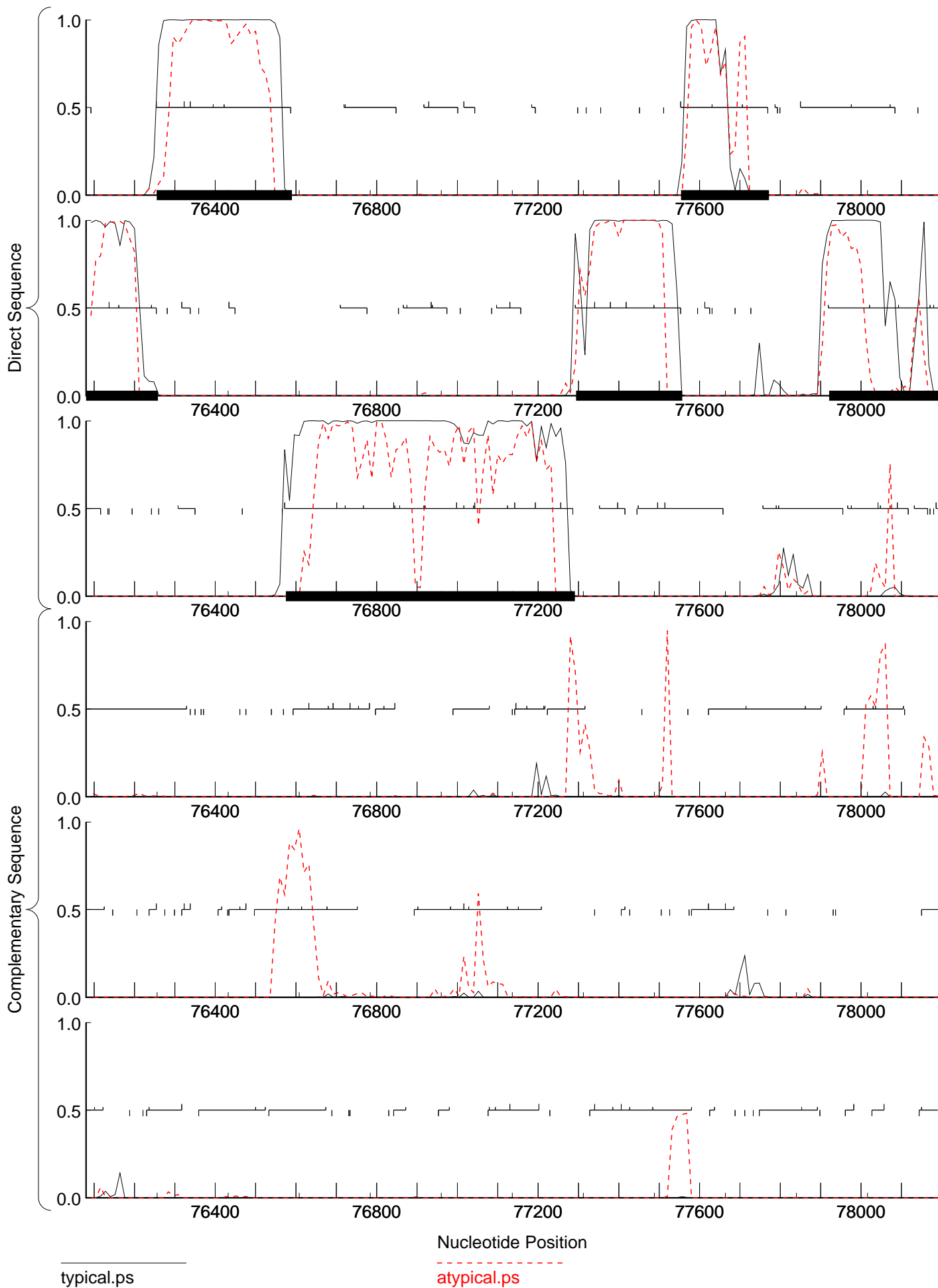
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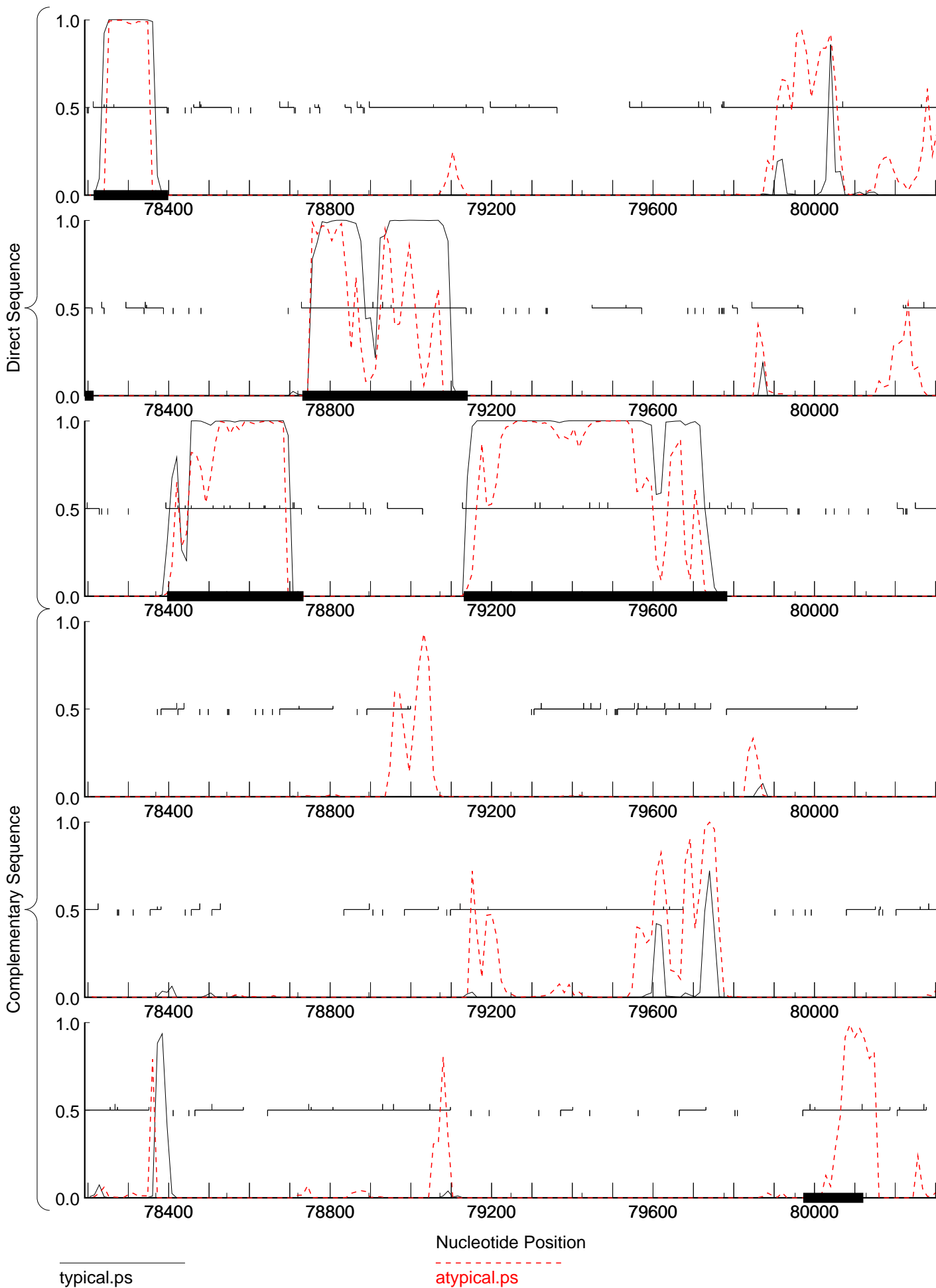




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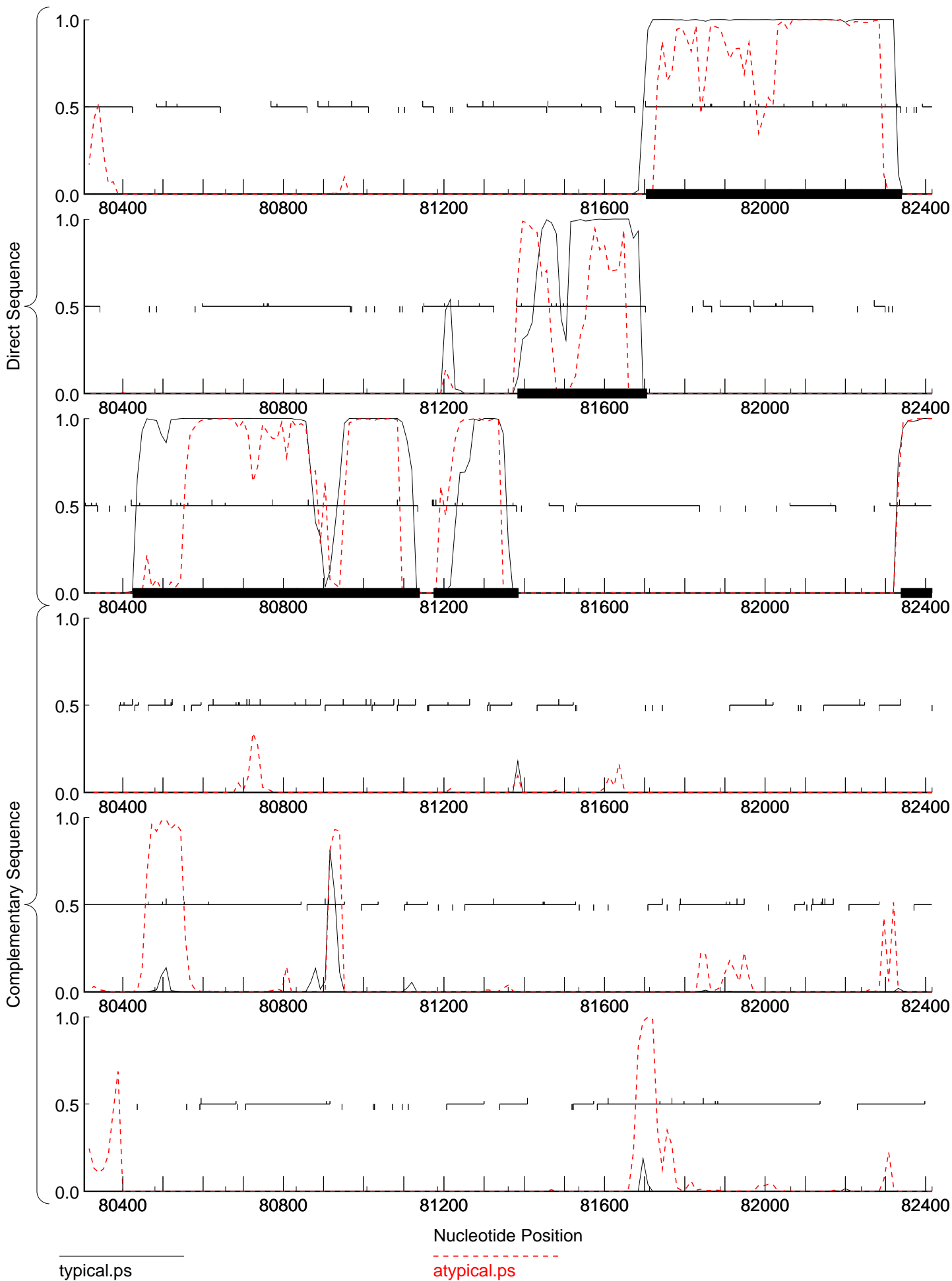
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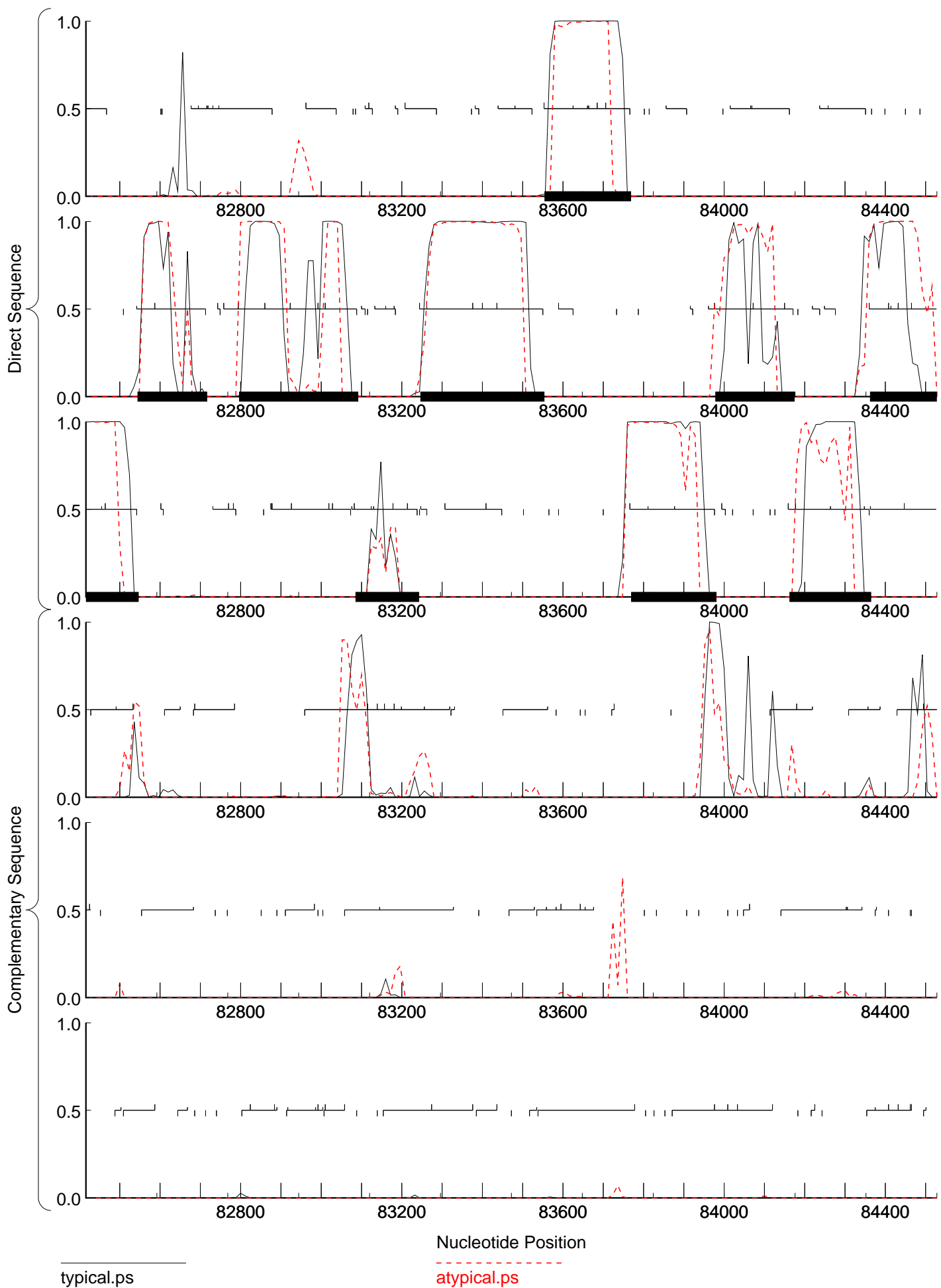


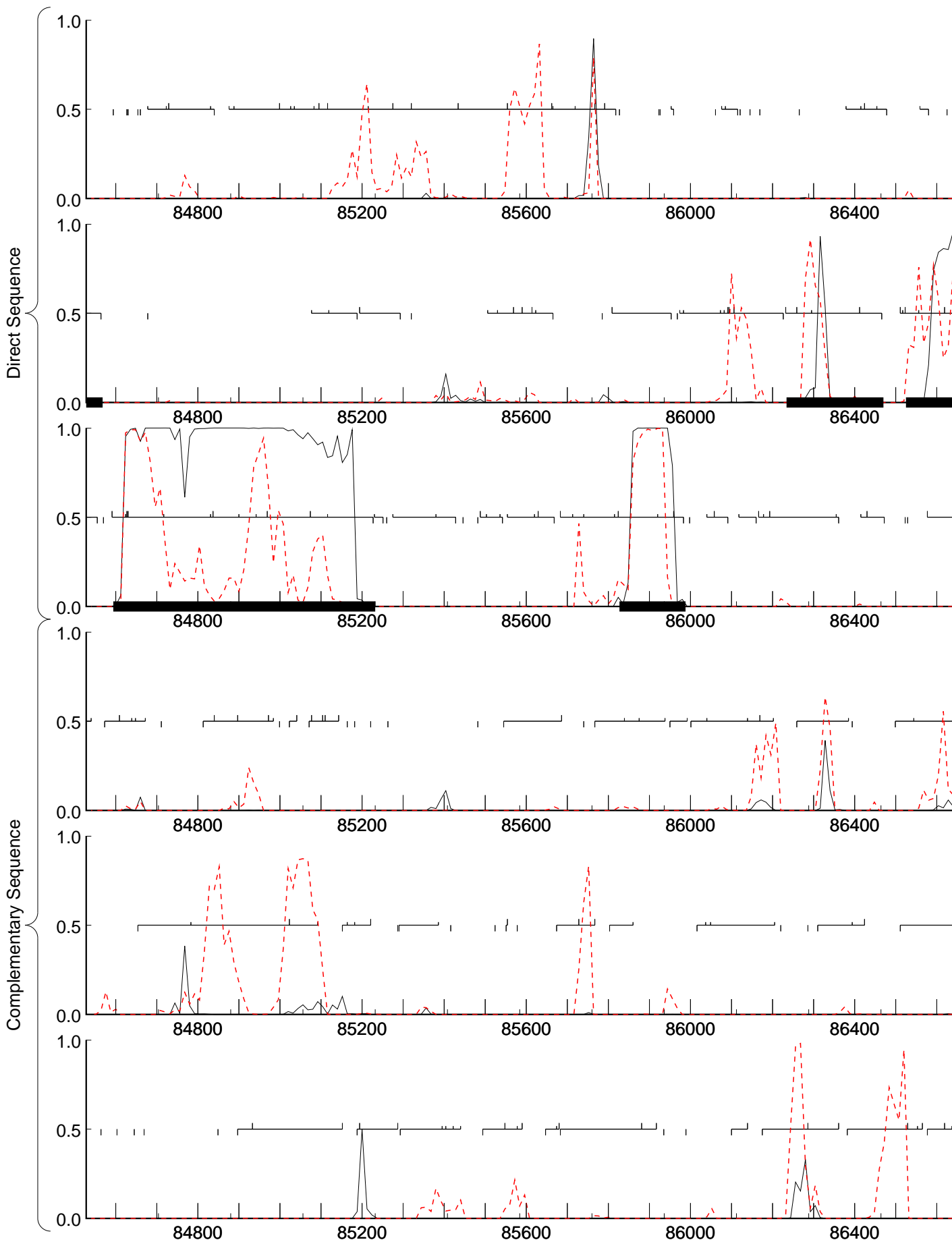


typical.ps

atypical.ps



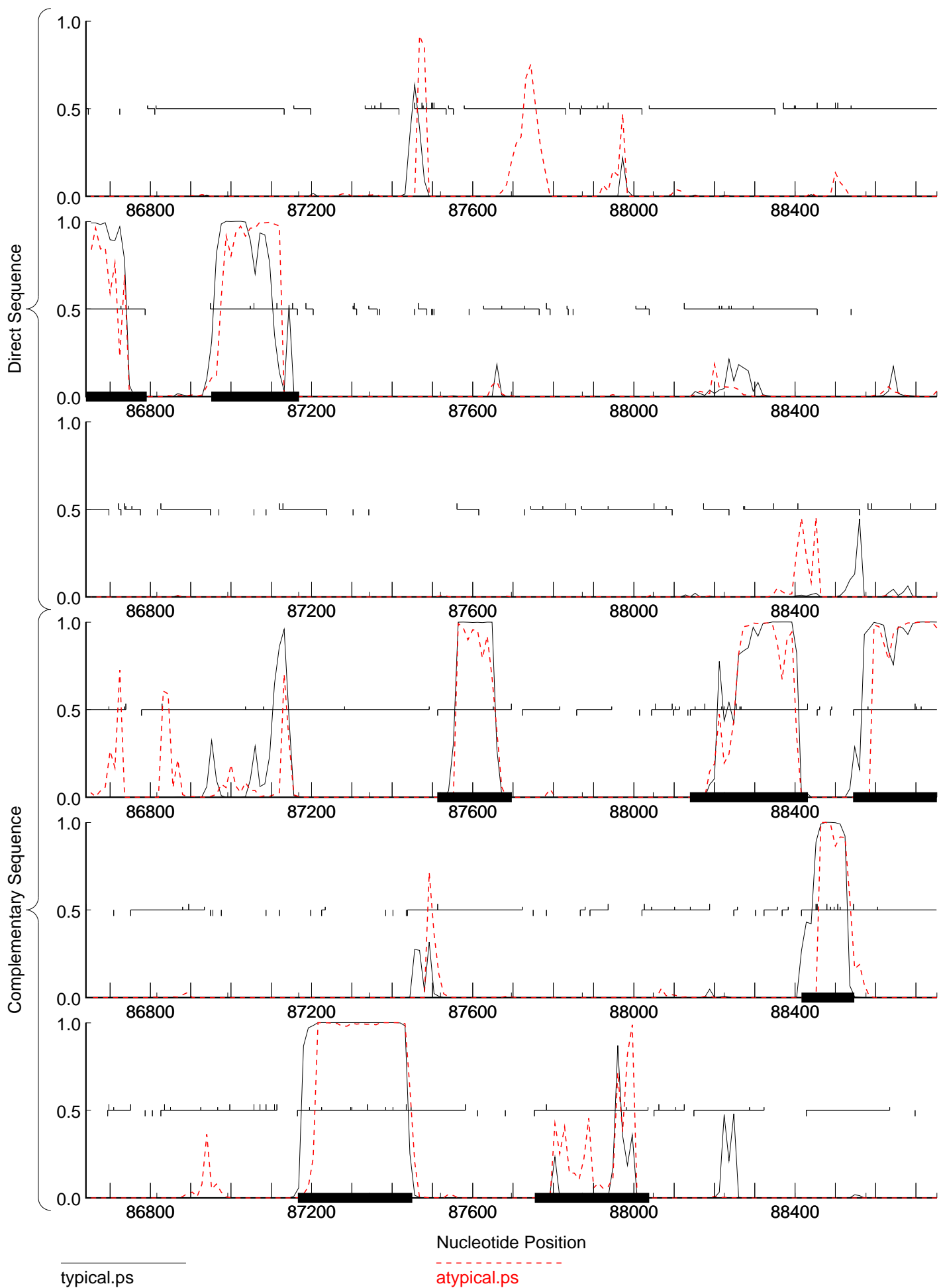




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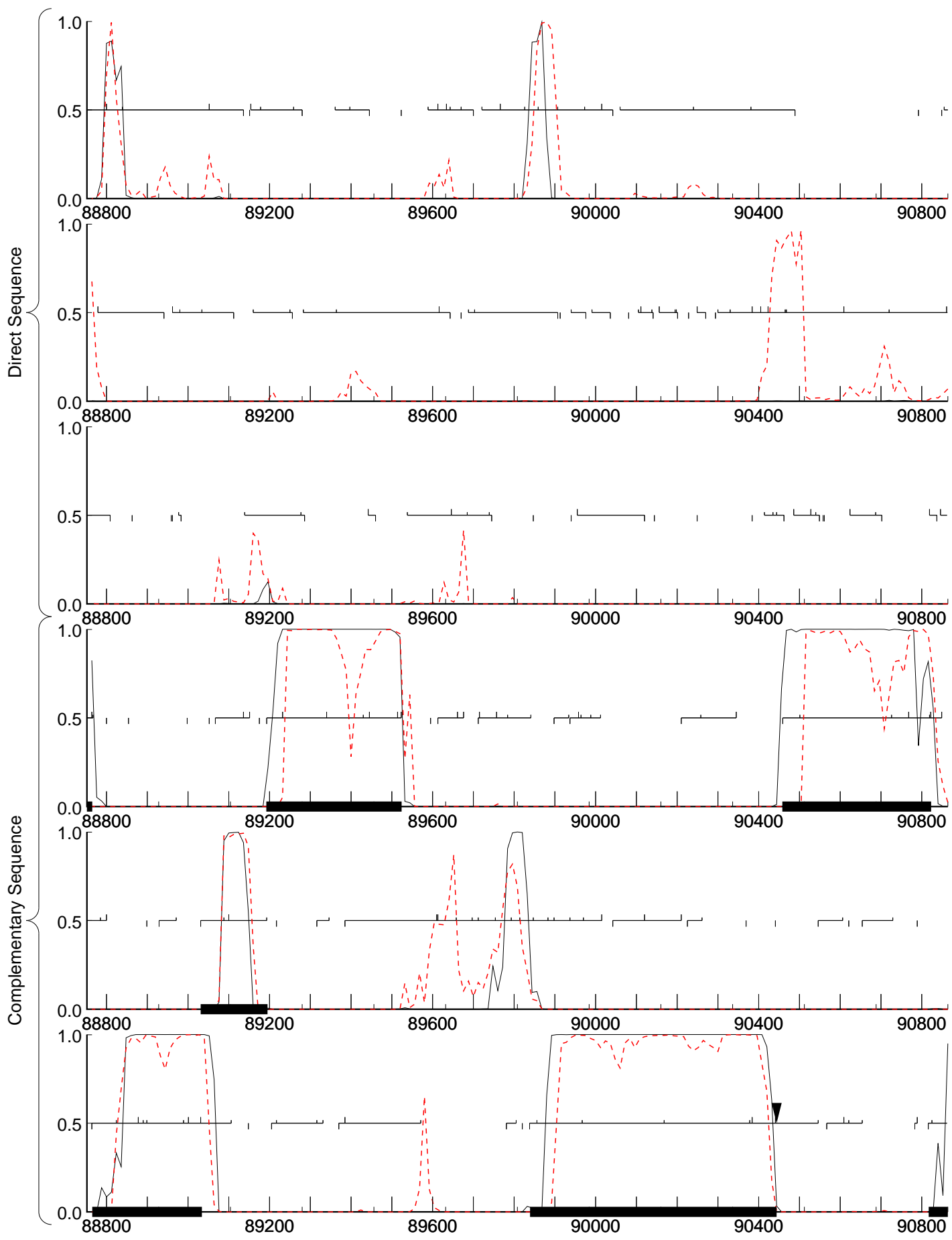
Nucleotide Position

atypical.ps



typical.ps

atypical.ps



typical.ps

atypical.ps

