

GeneMark

Version 2.5p (09.08.06)

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PROGRAM INFORMATION

Sequence : Streptomyces phage Warpy complete sequence, 132996 bp including 11458 bp terminal repeat, C
Analysis Date : 8/20/17 at 20:47:09
Pages : 64
Sequence Length : 132996 bp
GC Content : 49.56%

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

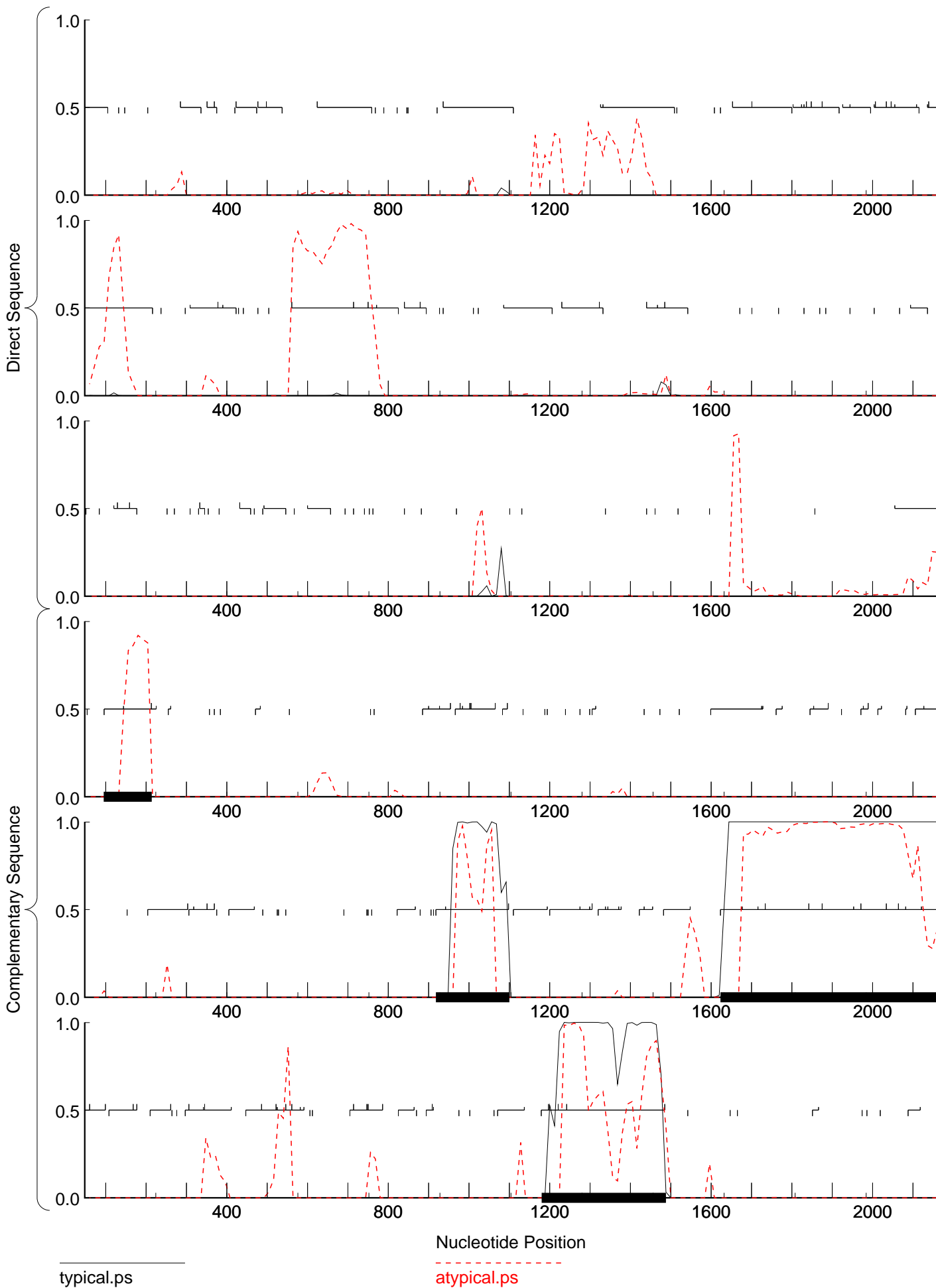
Training set derived by GeneMarkS, 4.30 October 2014
Sun Aug 20 20:47:09 2017

MATRIX INFORMATION

Matrix : -
Author : -
Order : 4

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

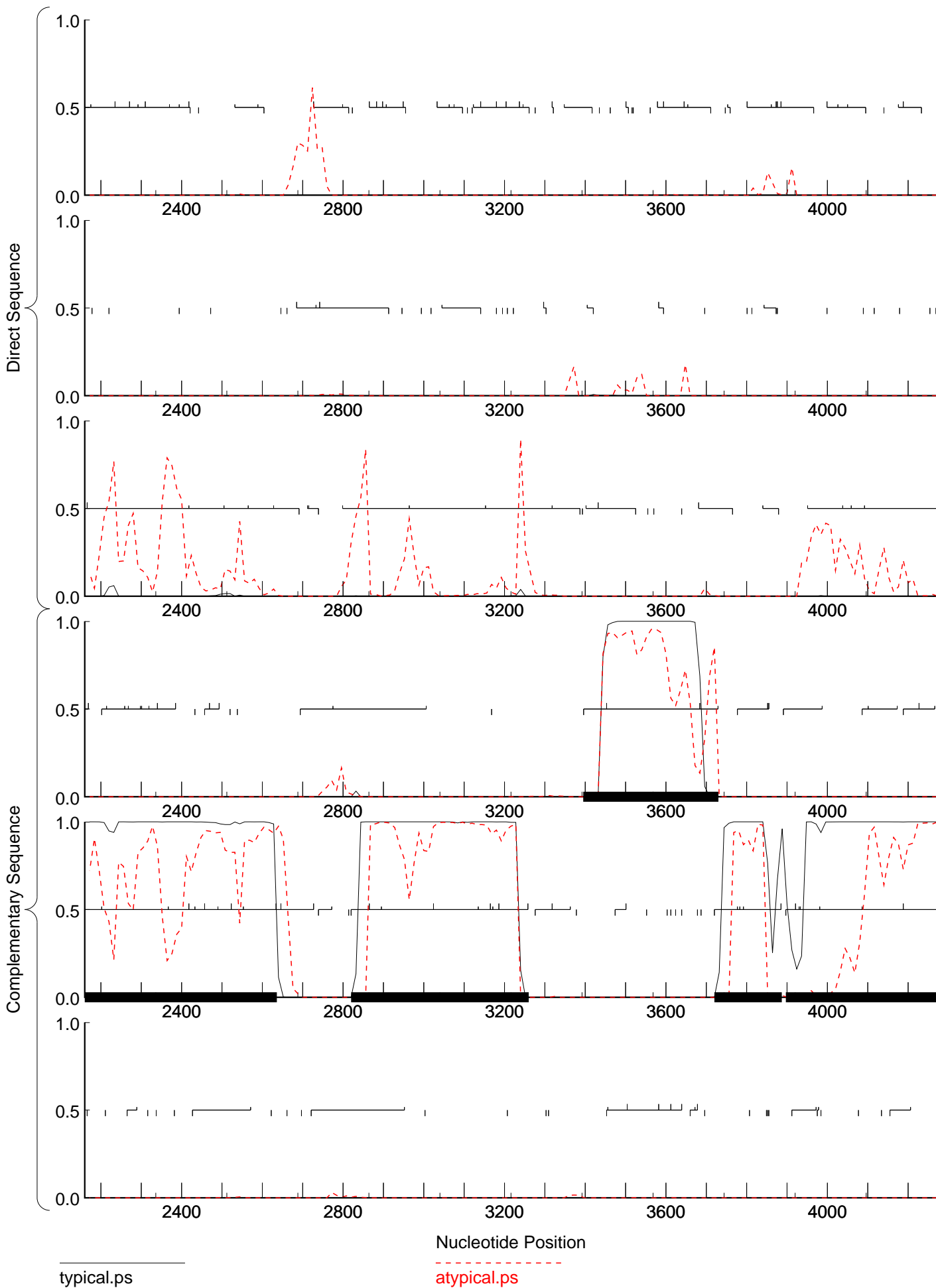
For help or information, send electronic mail to: custserv@genepro.com, or mark@amber.biology.gatech.edu



typical.ps

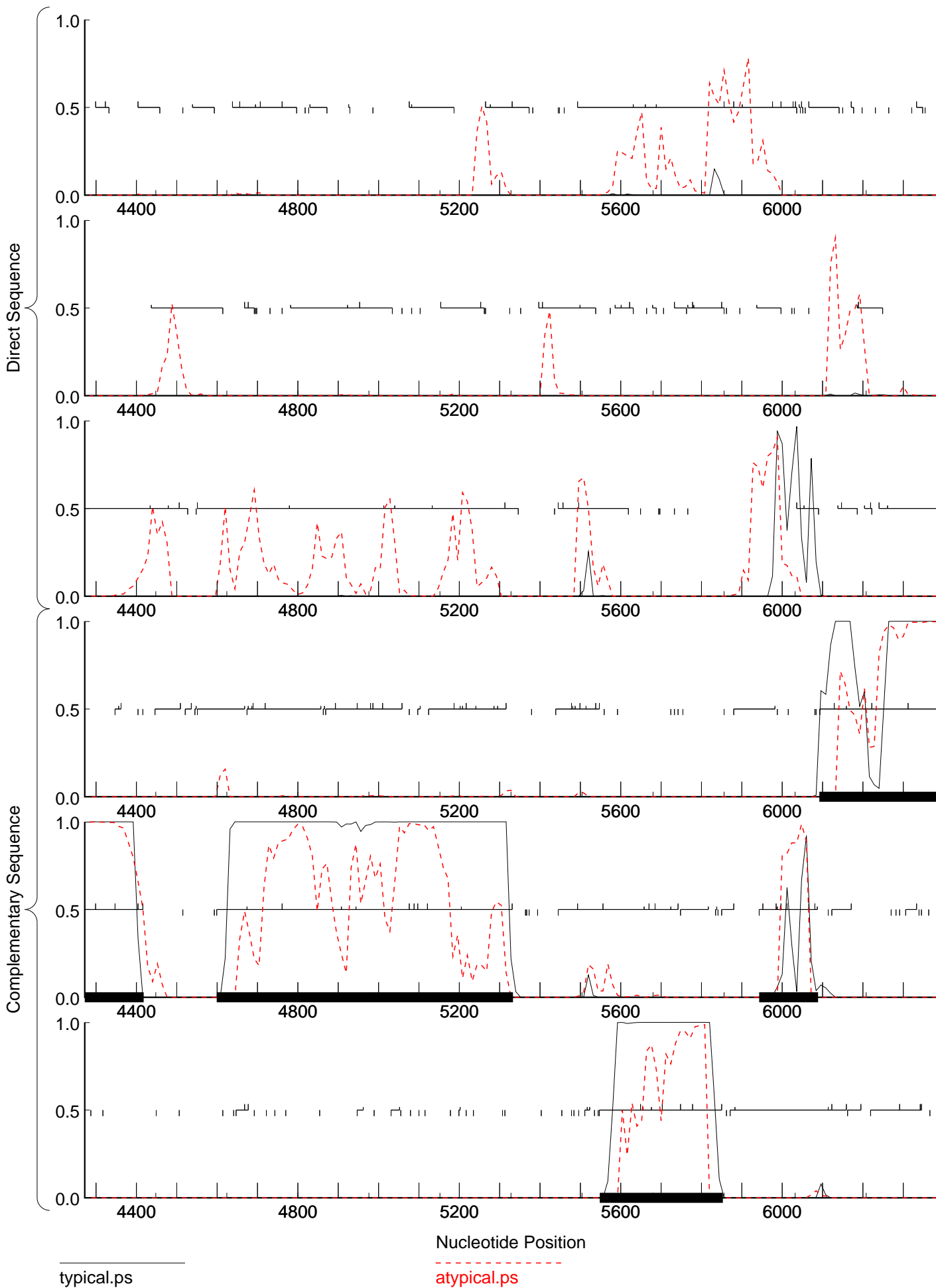
atypical.ps

hage Warty complete sequence, 132996 bp including 11458 bp terminal repeat, Cluster BE1, Order 4, Window 96, Step 12, 3/64
hage Warty complete sequence, 132996 bp including 11458 bp terminal repeat, Cluster BE1, Order 2, Window 96, Step 12, 3/64



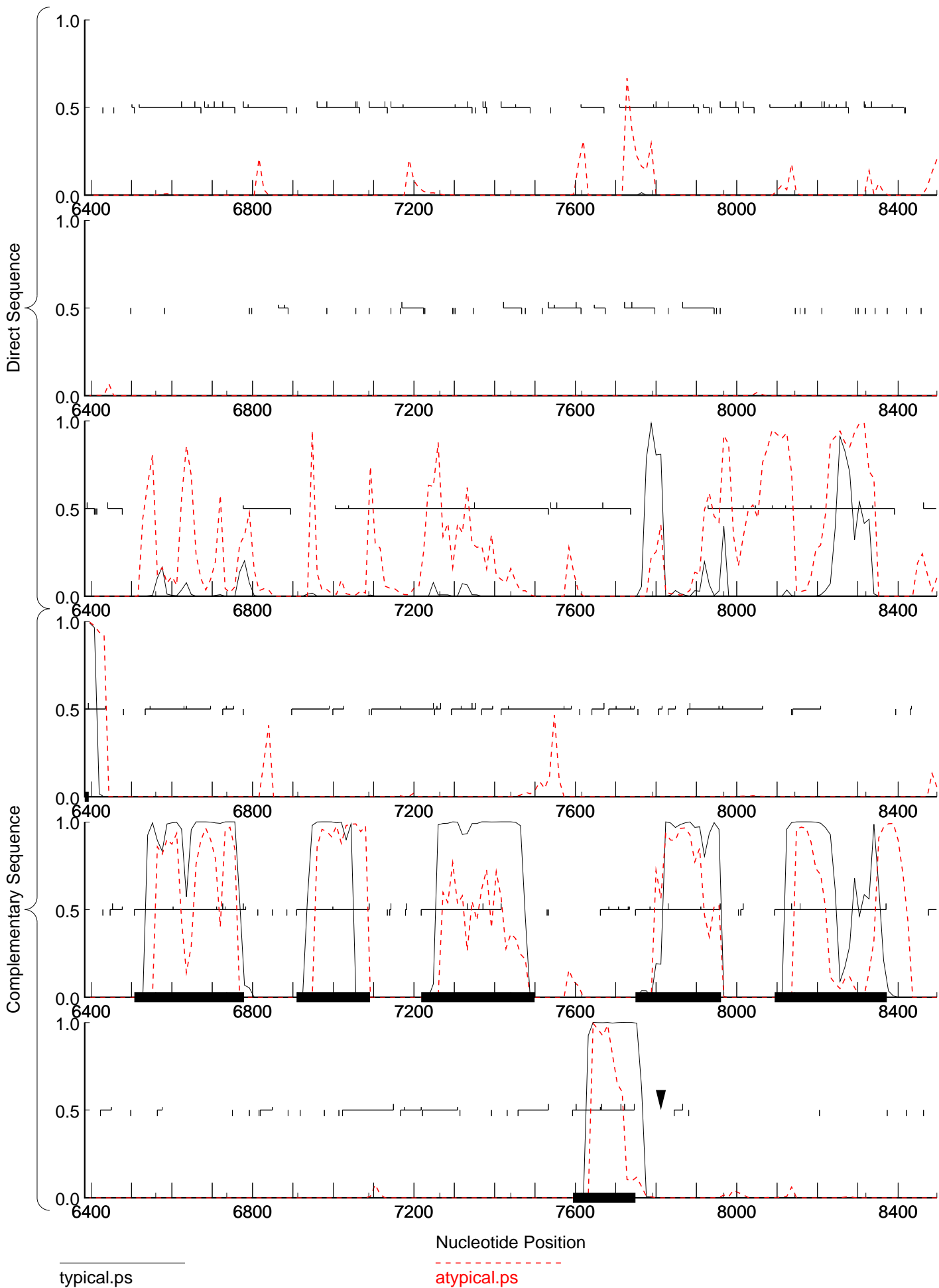
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atypical.ps



typical.ps

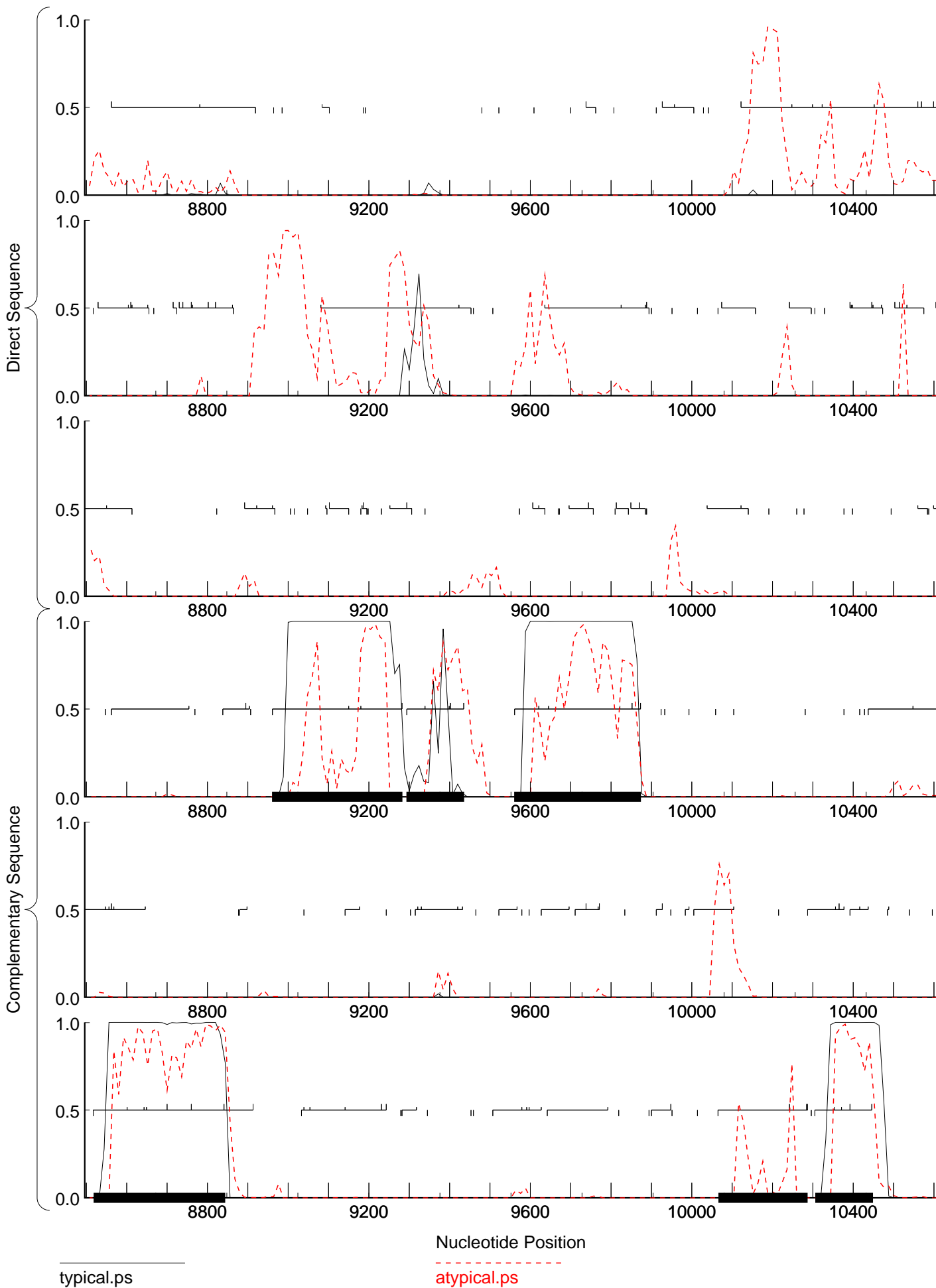
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typical.ps

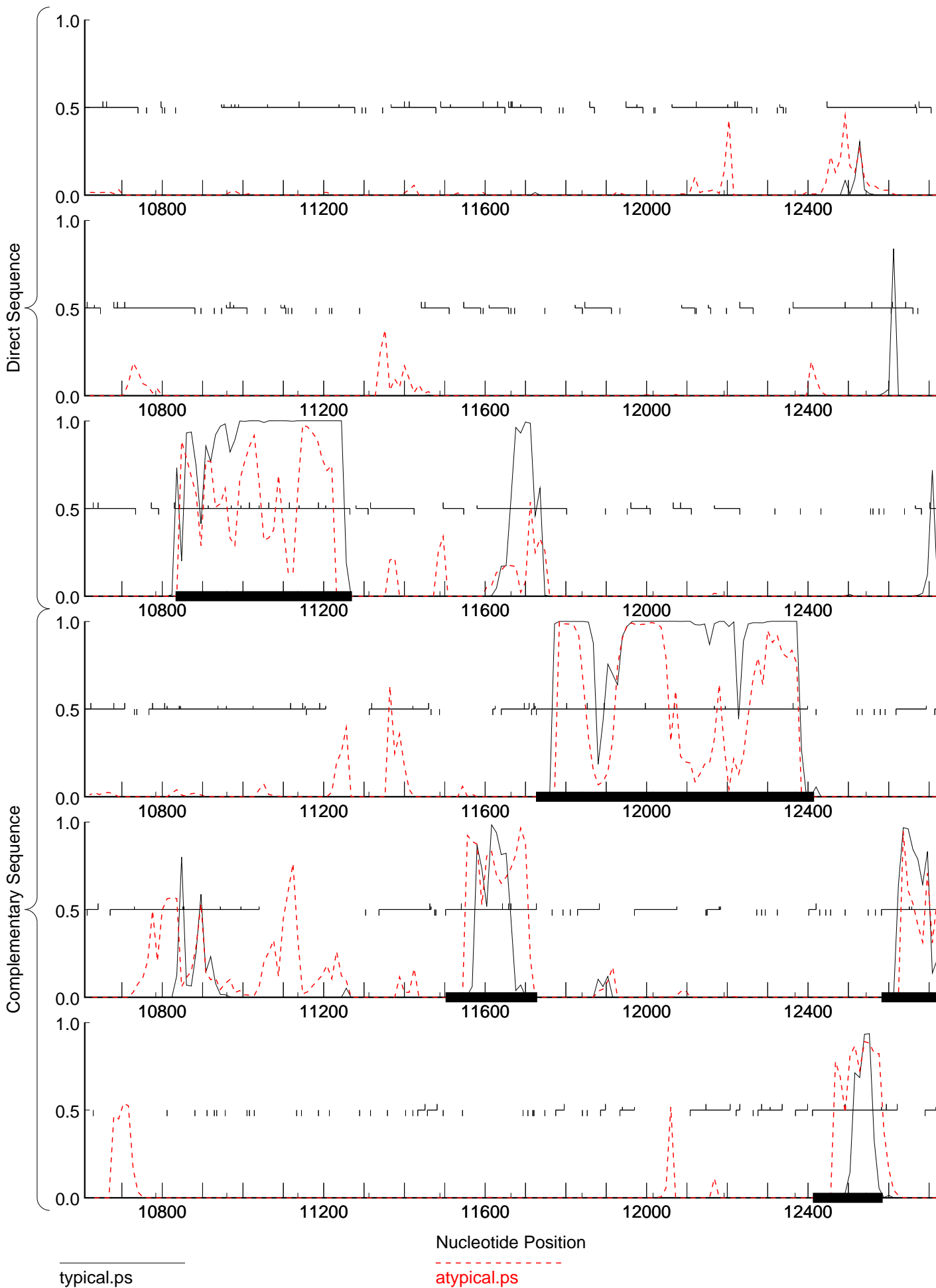
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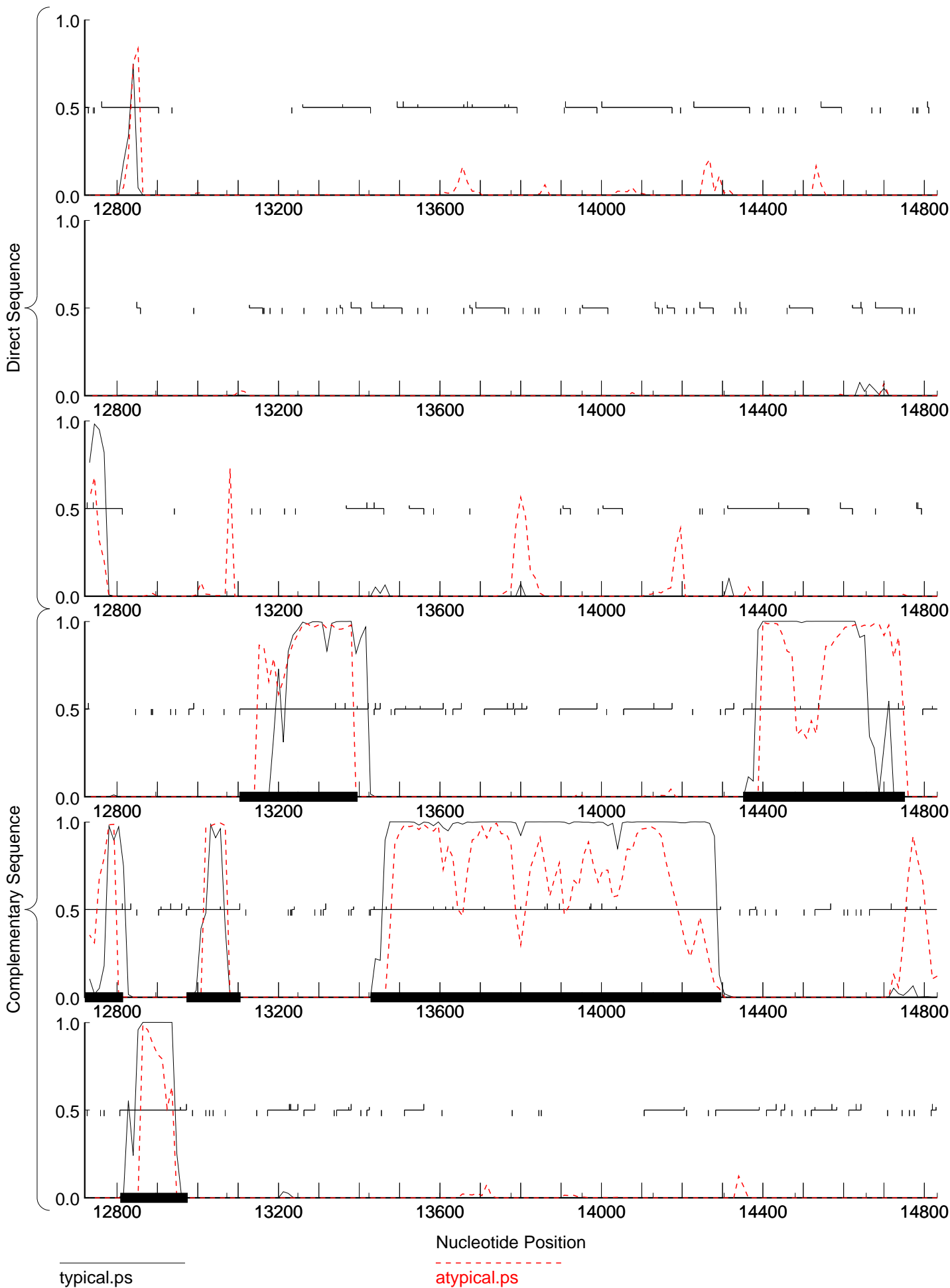
hage Warpy complete sequence, 132996 bp including 11458 bp terminal repeat, Cluster BE1, Order 4, Window 96, Step 12, 6/64
hage Warpy complete sequence, 132996 bp including 11458 bp terminal repeat, Cluster BE1, Order 2, Window 96, Step 12, 6/64

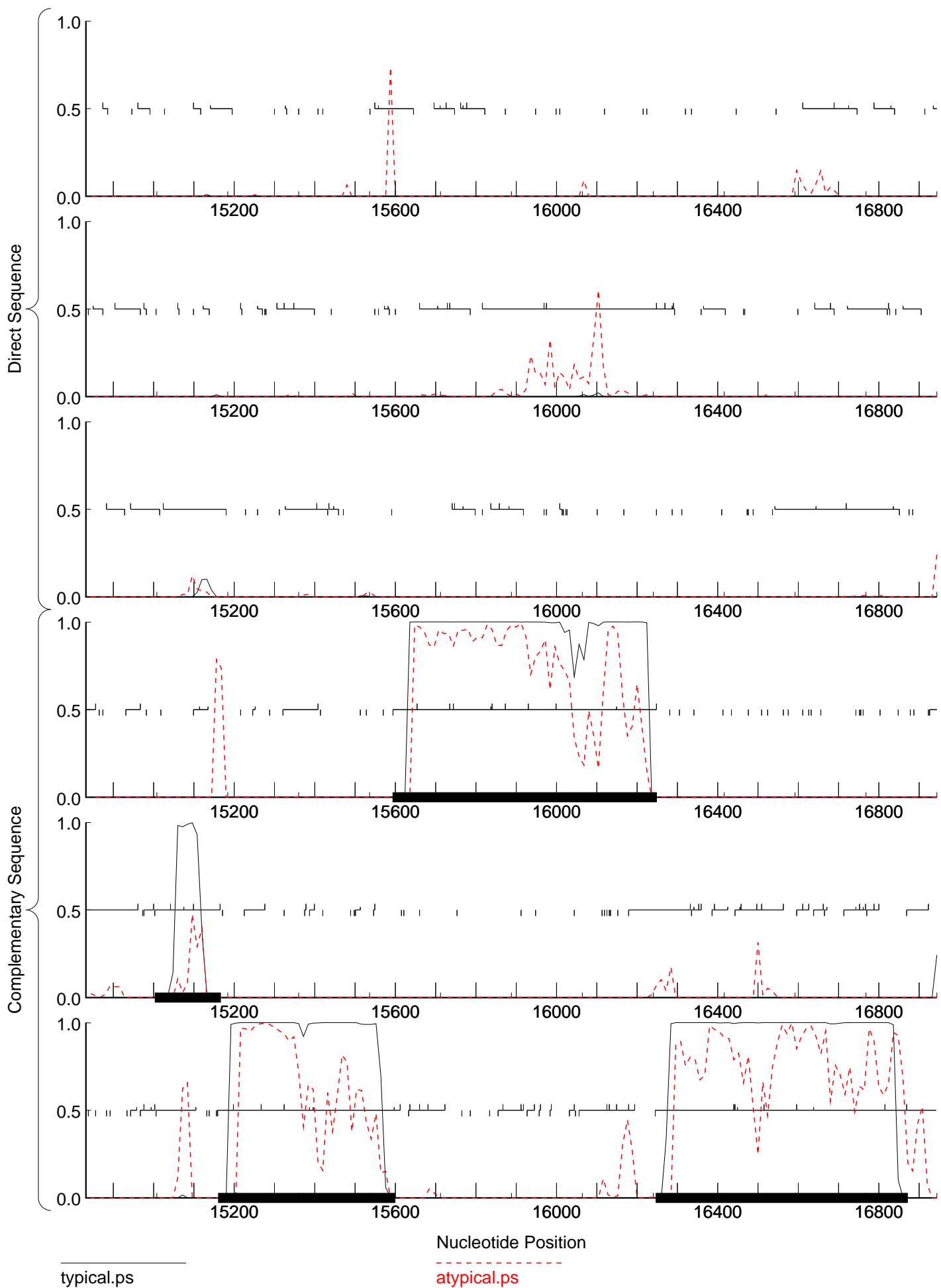


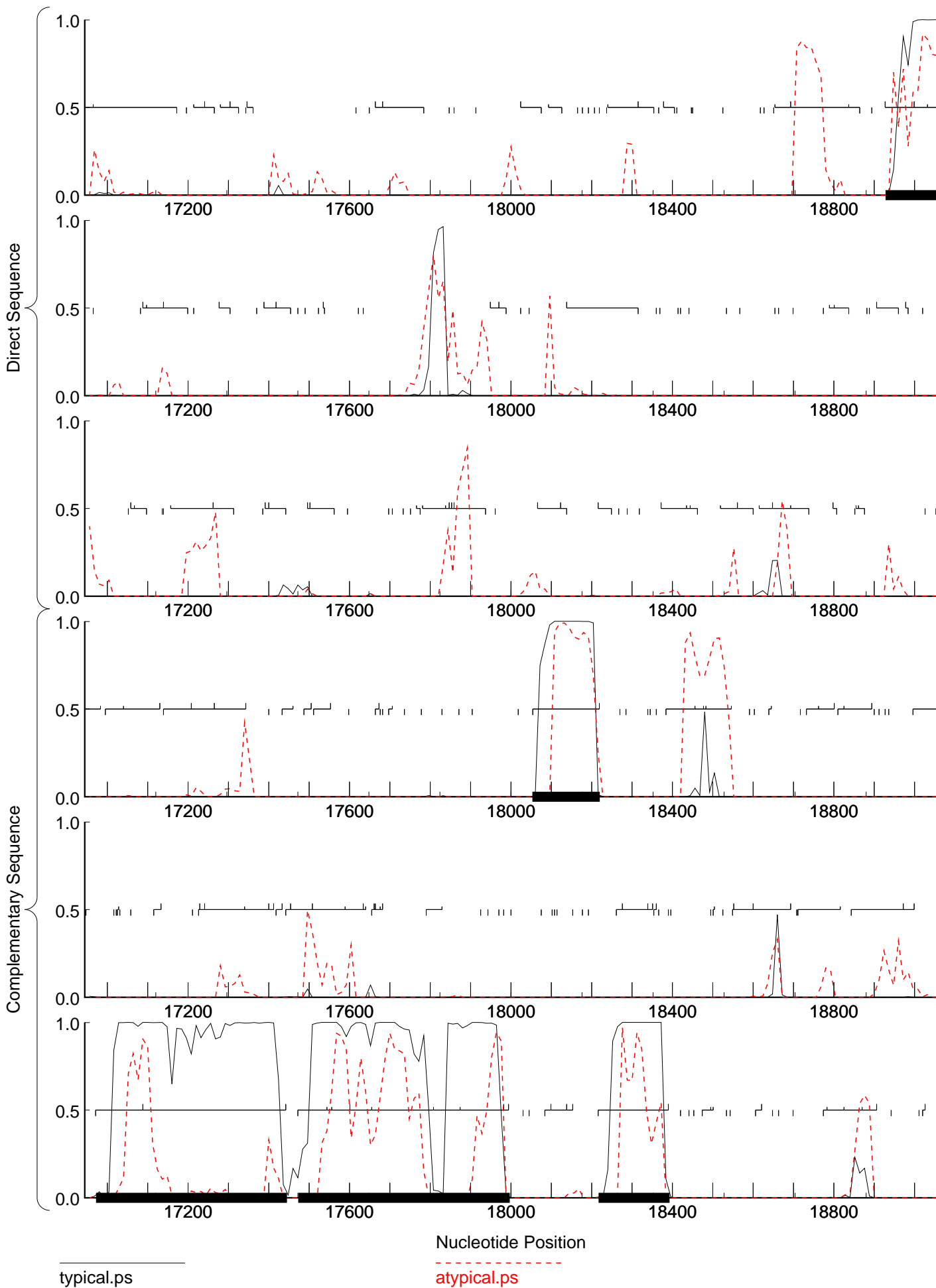
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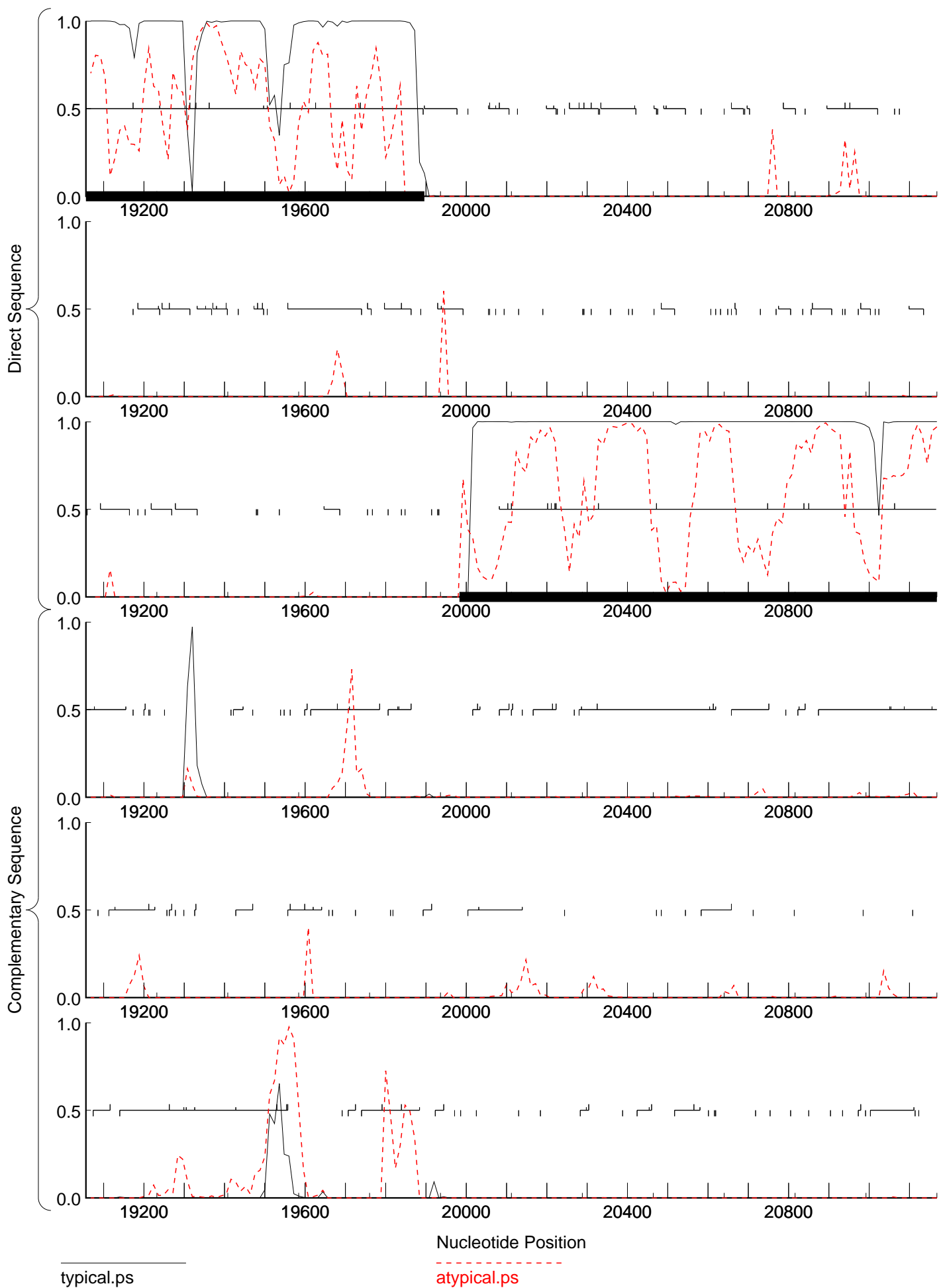
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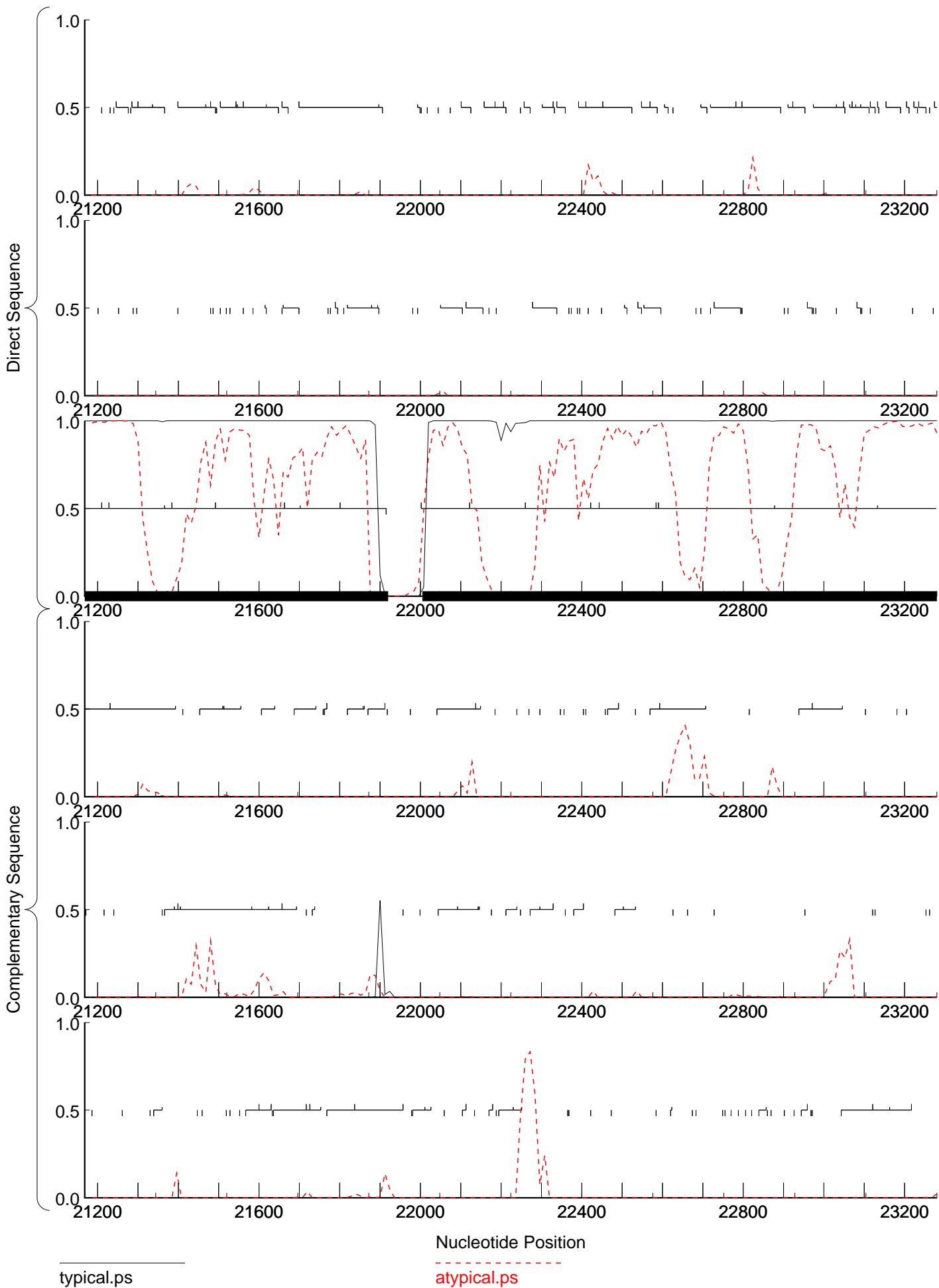


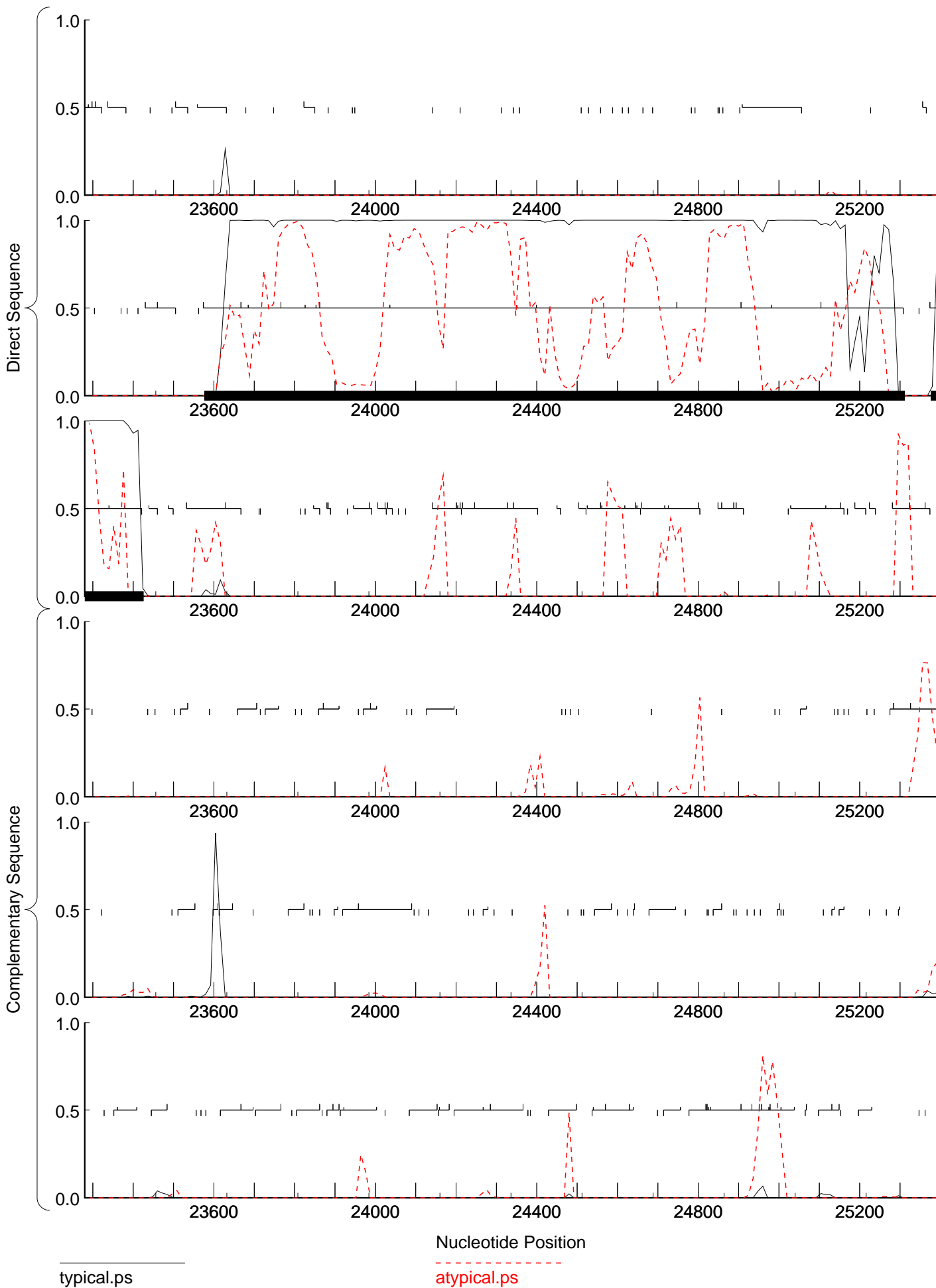


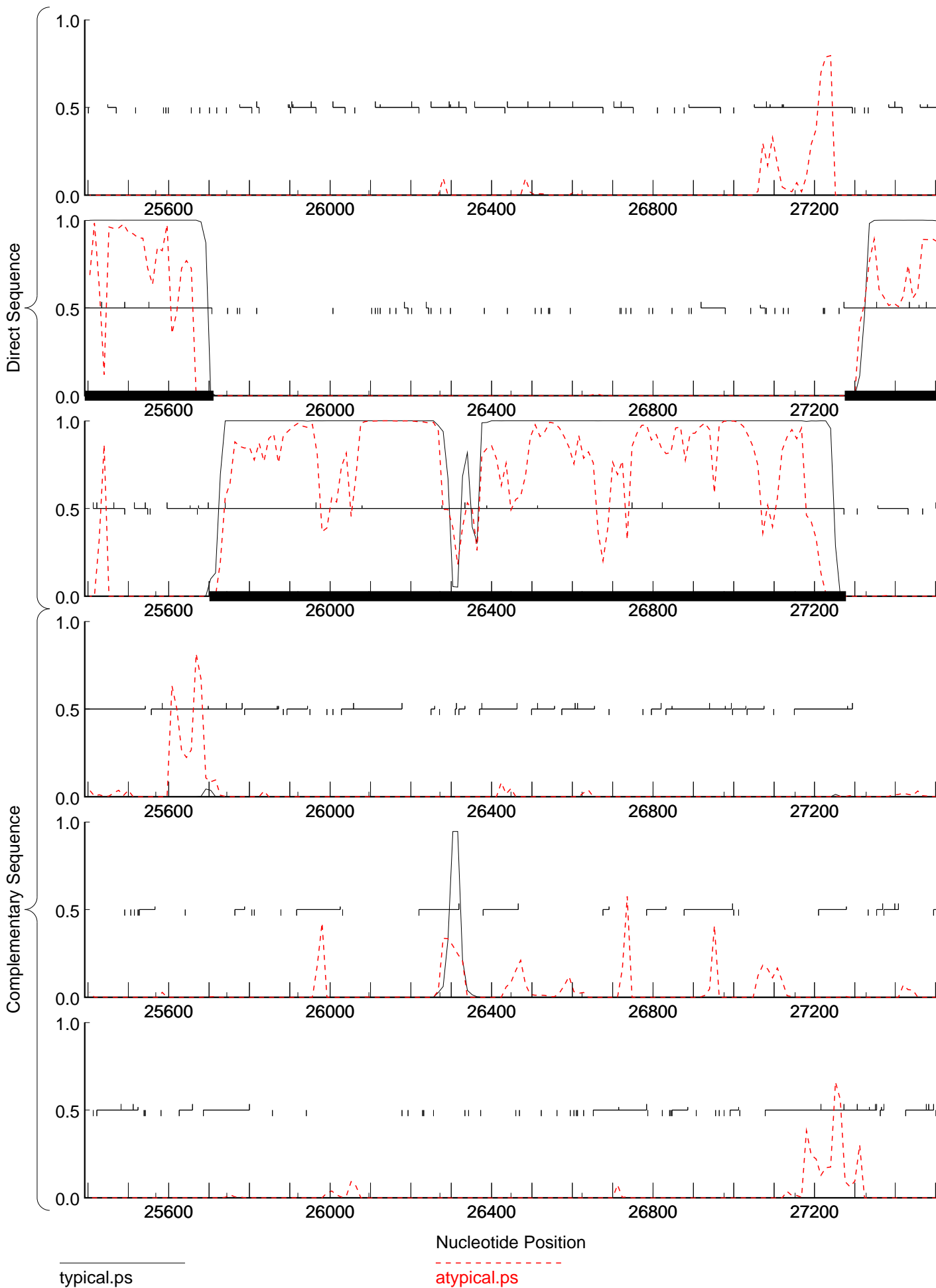


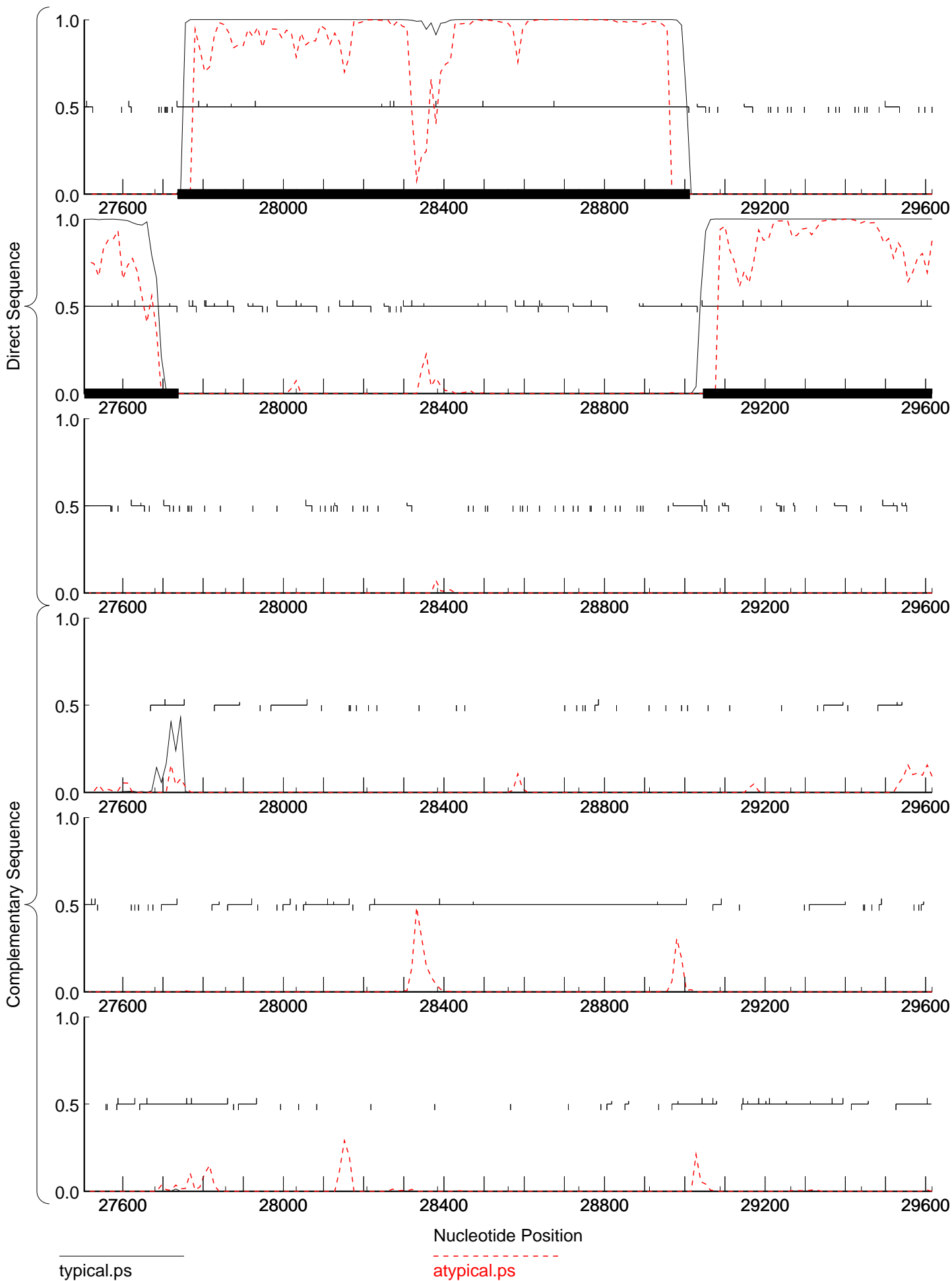


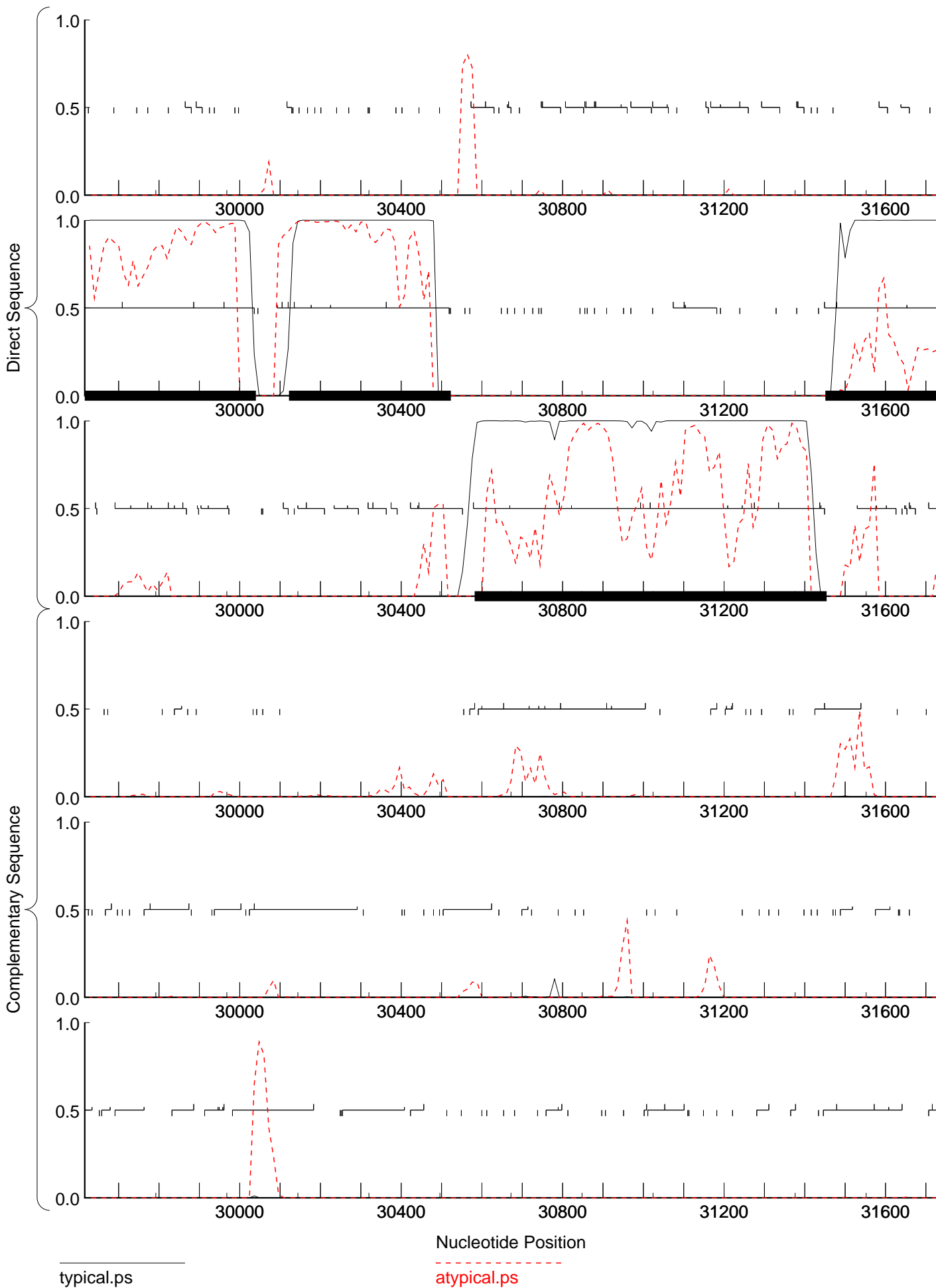


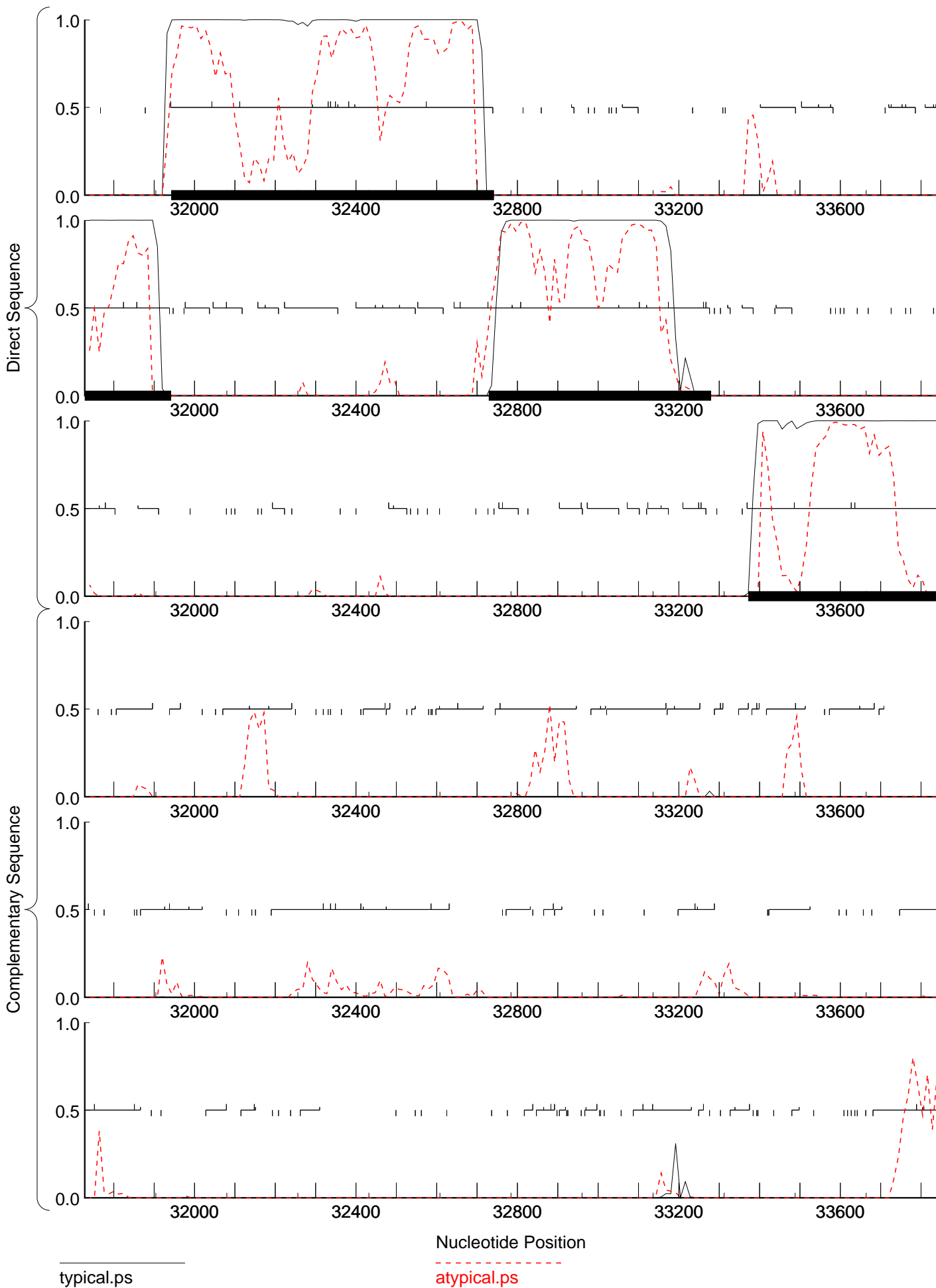


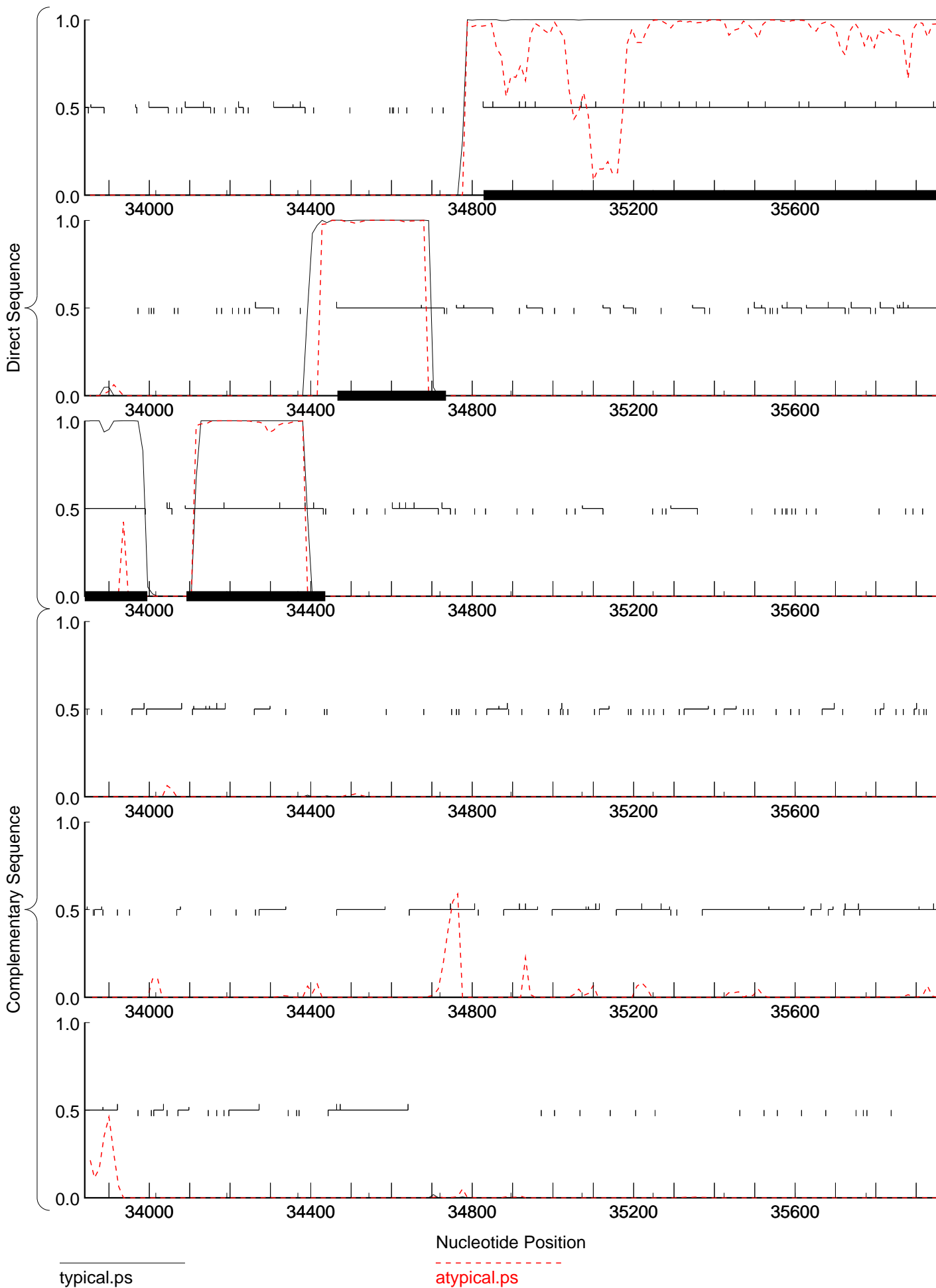


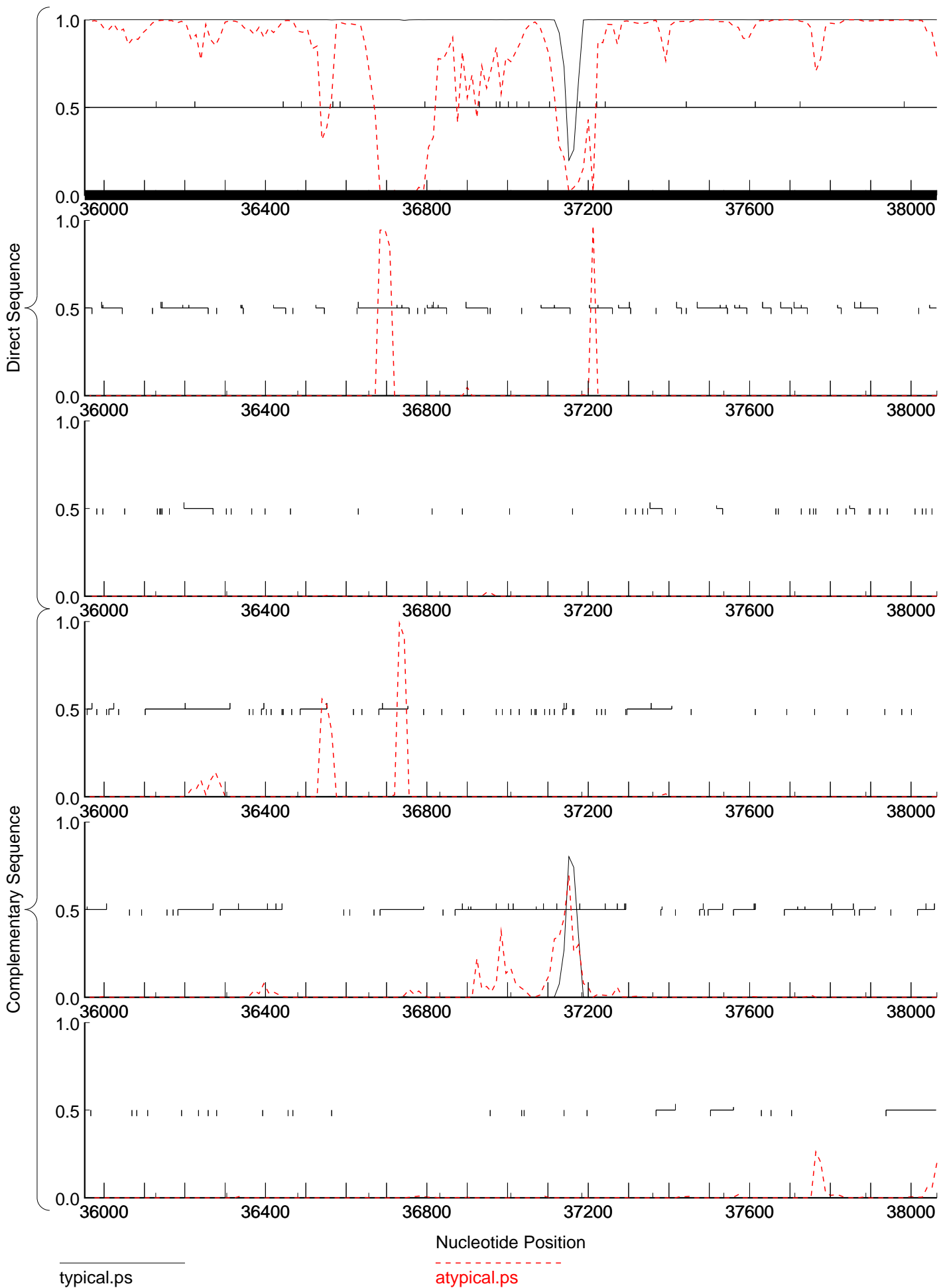






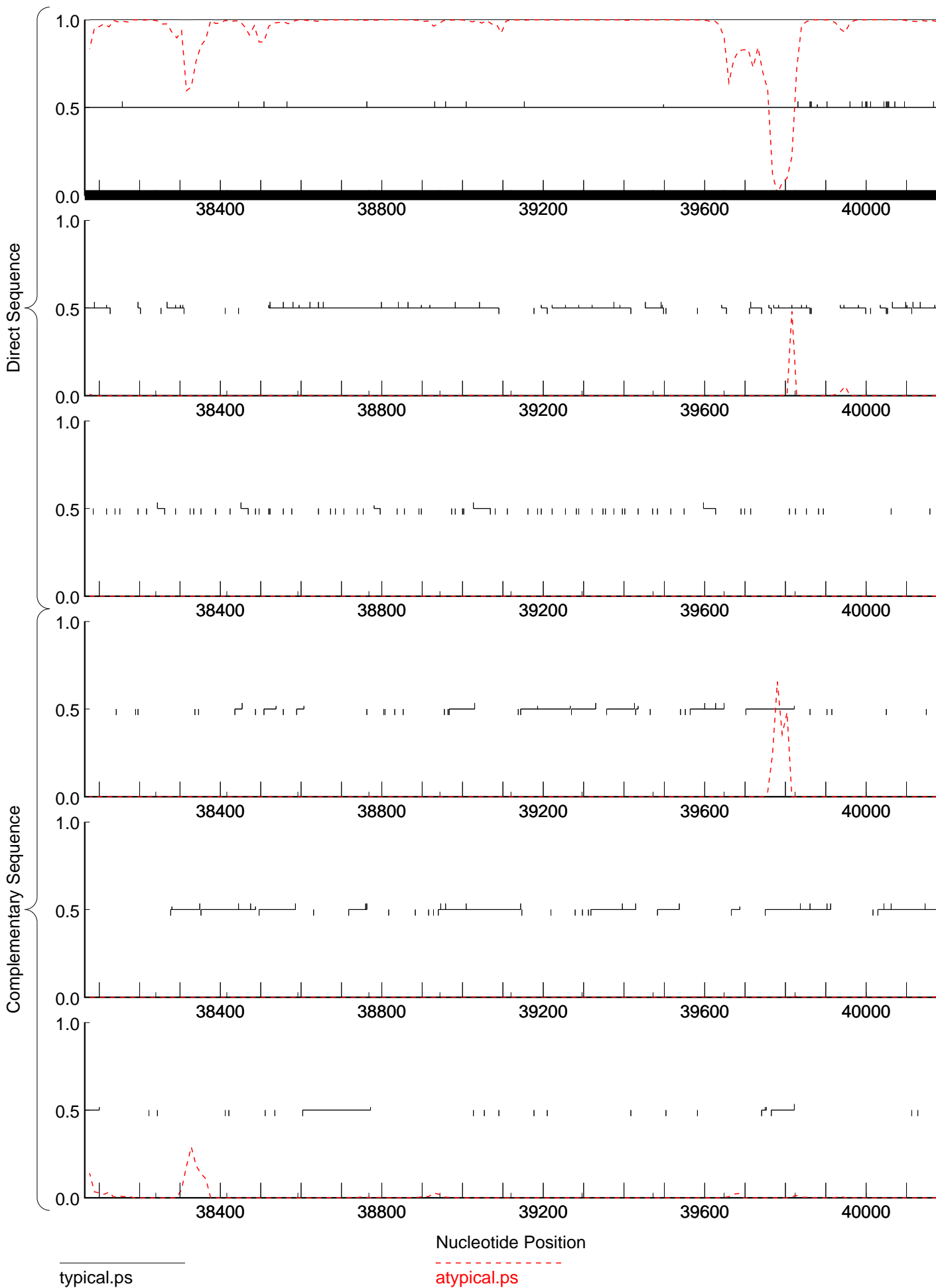


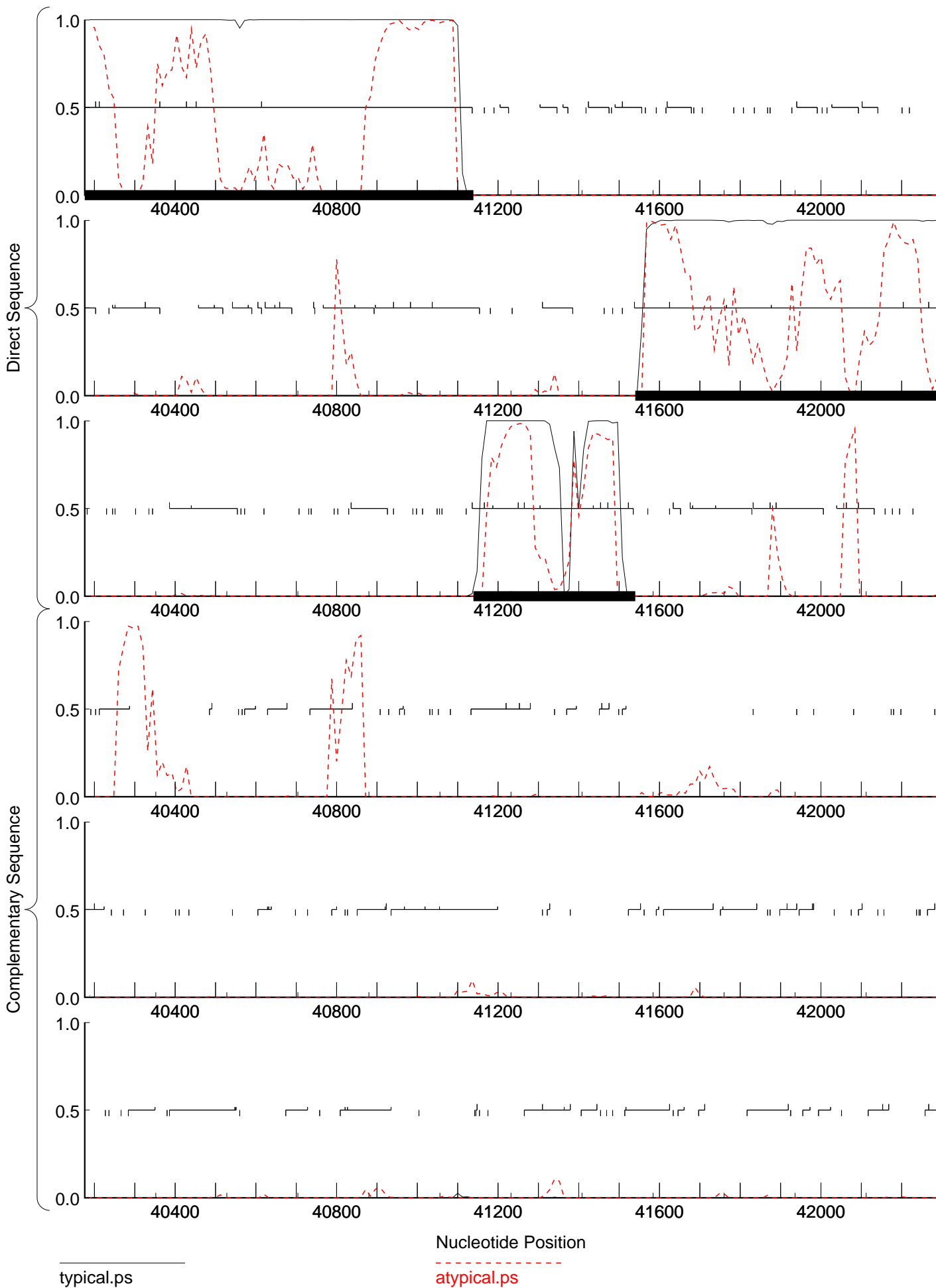


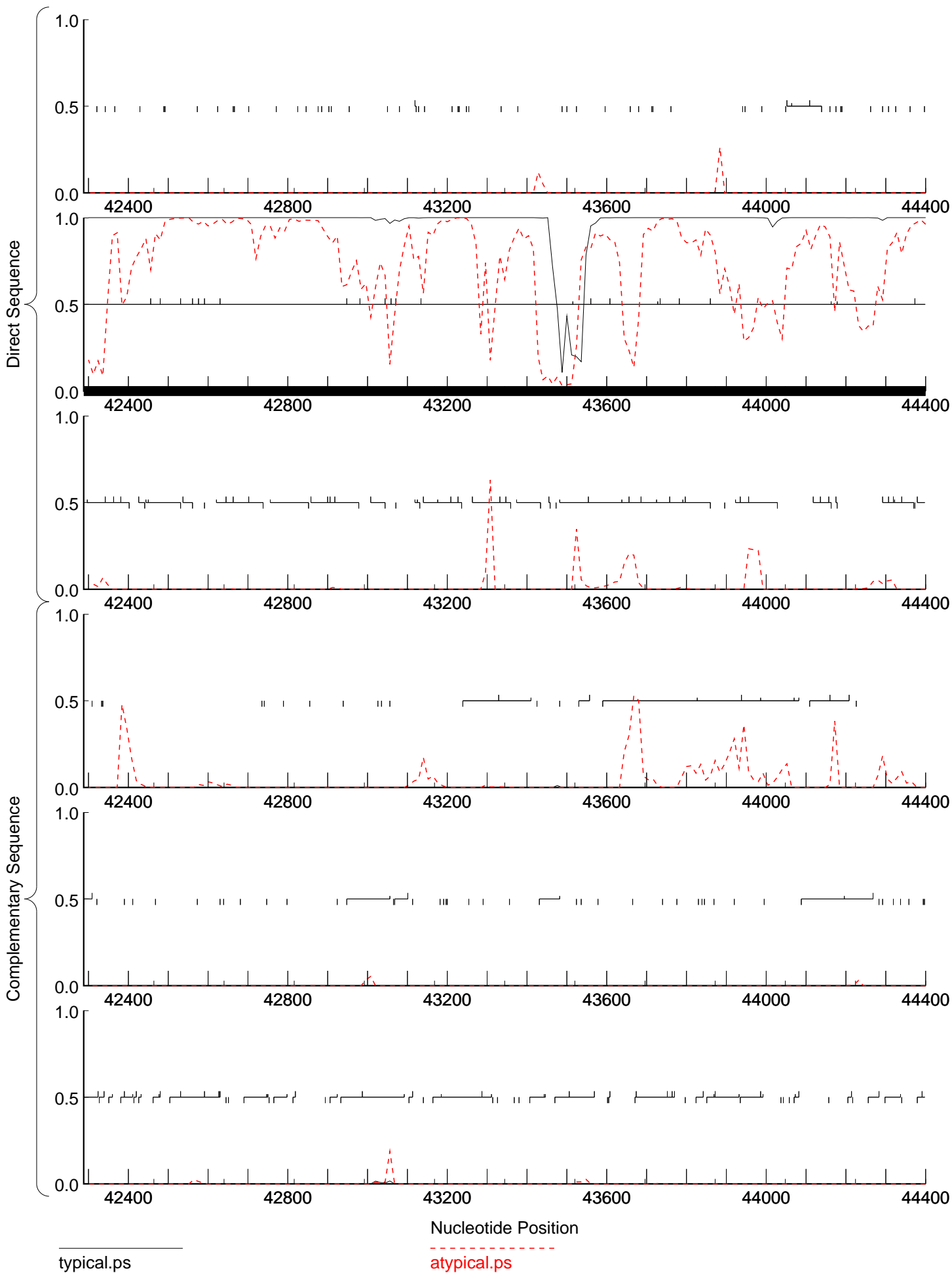


typical.ps

atypical.ps

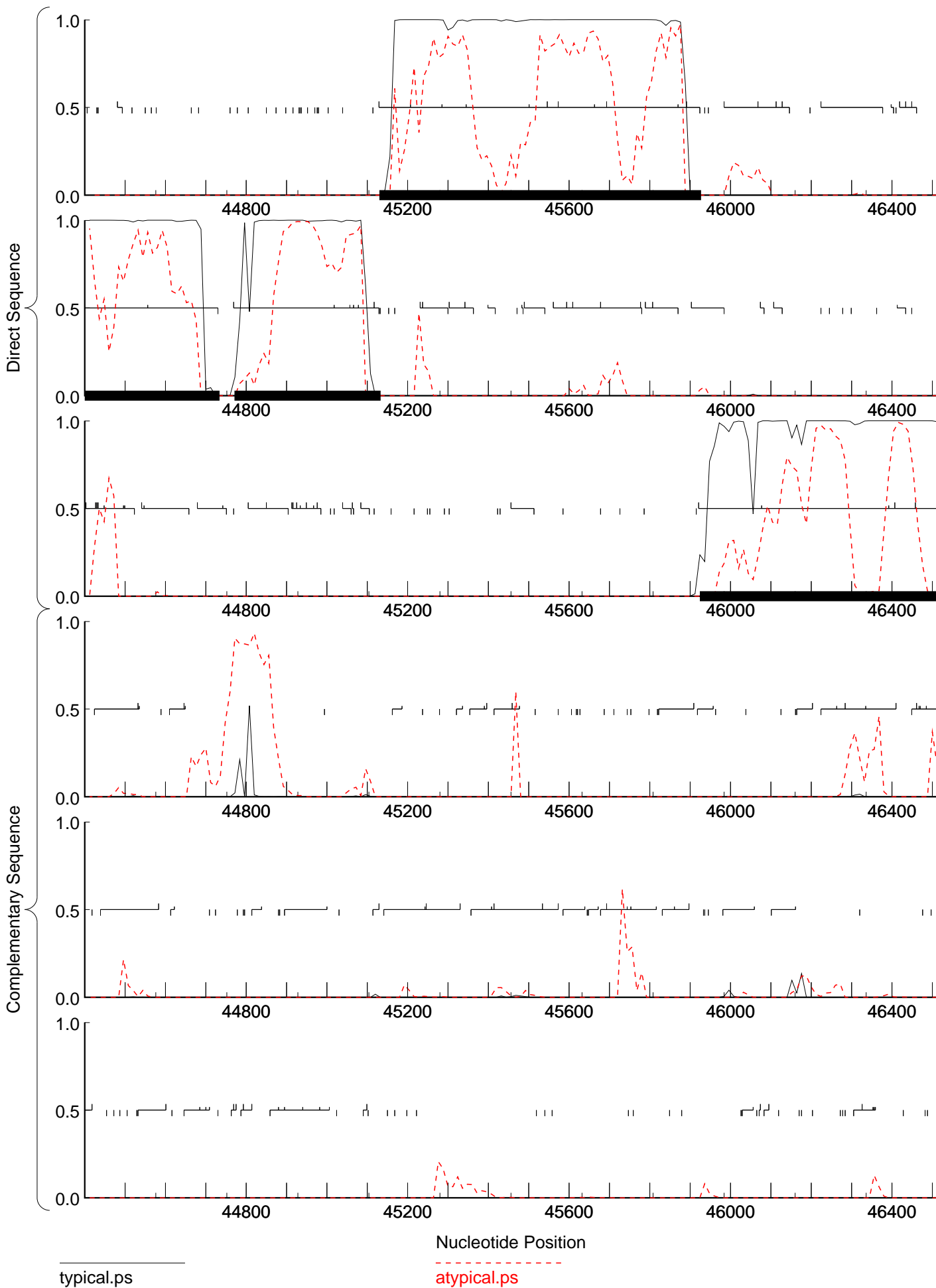






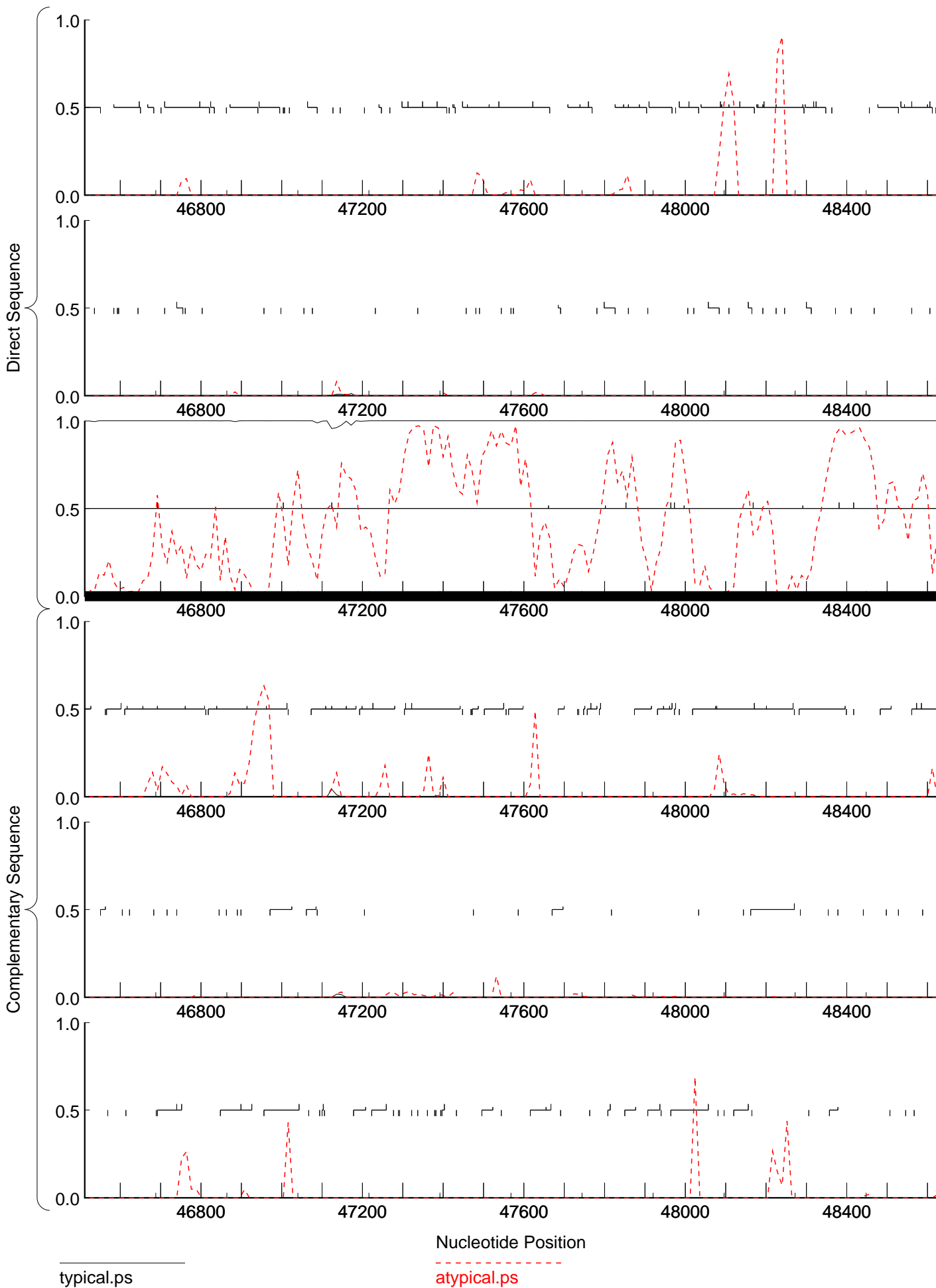
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atypical.ps



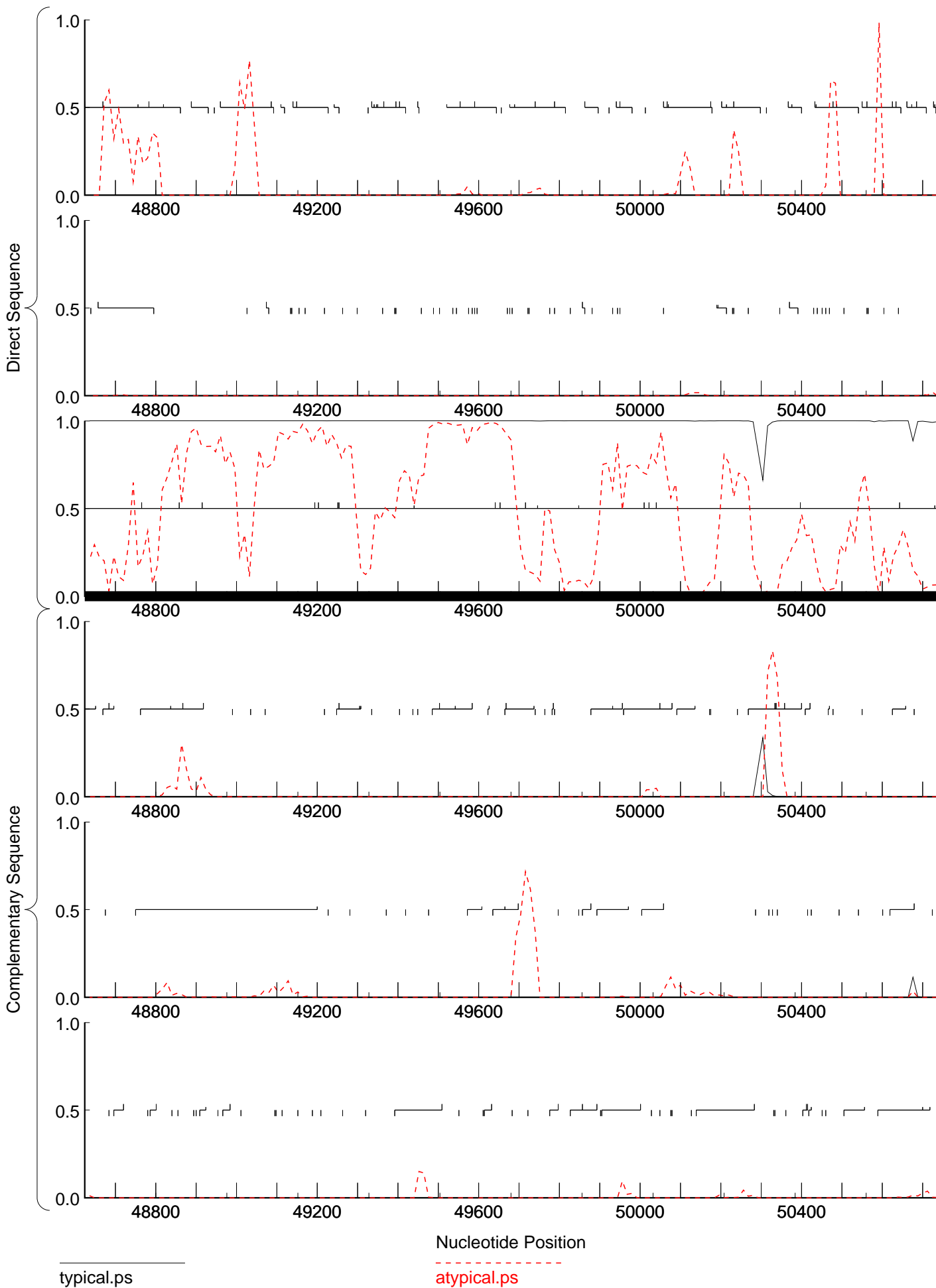
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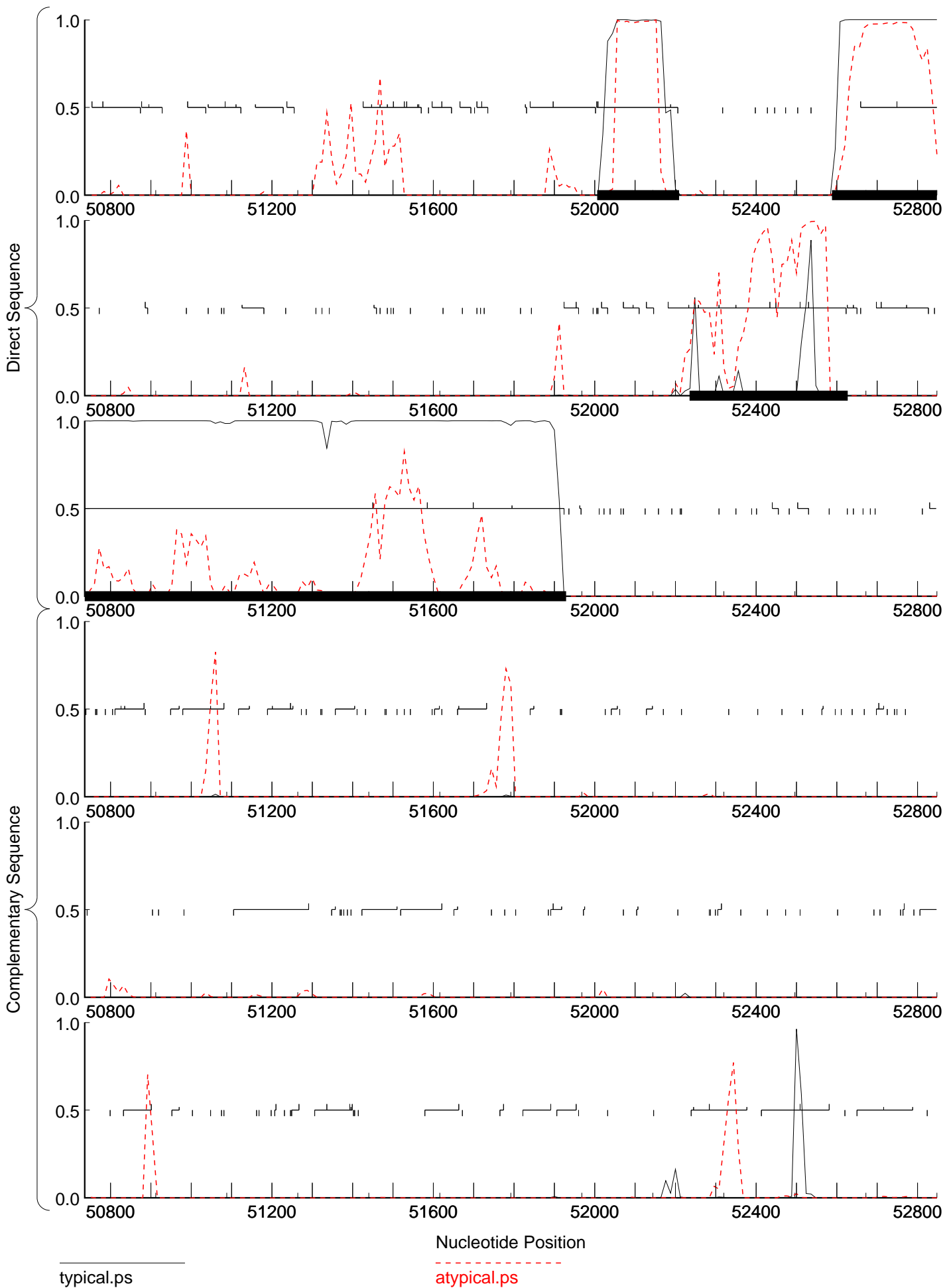
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typical.ps

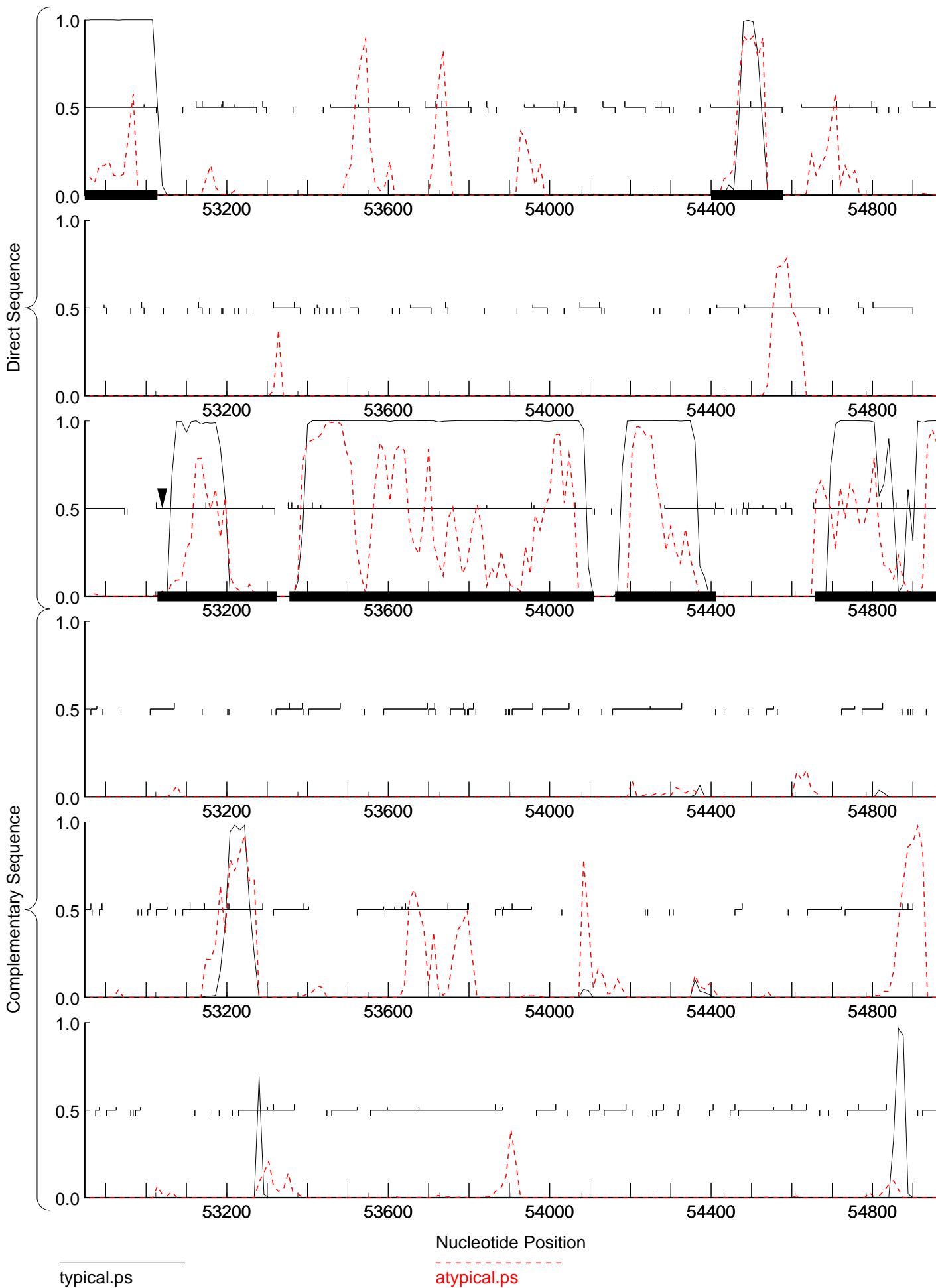
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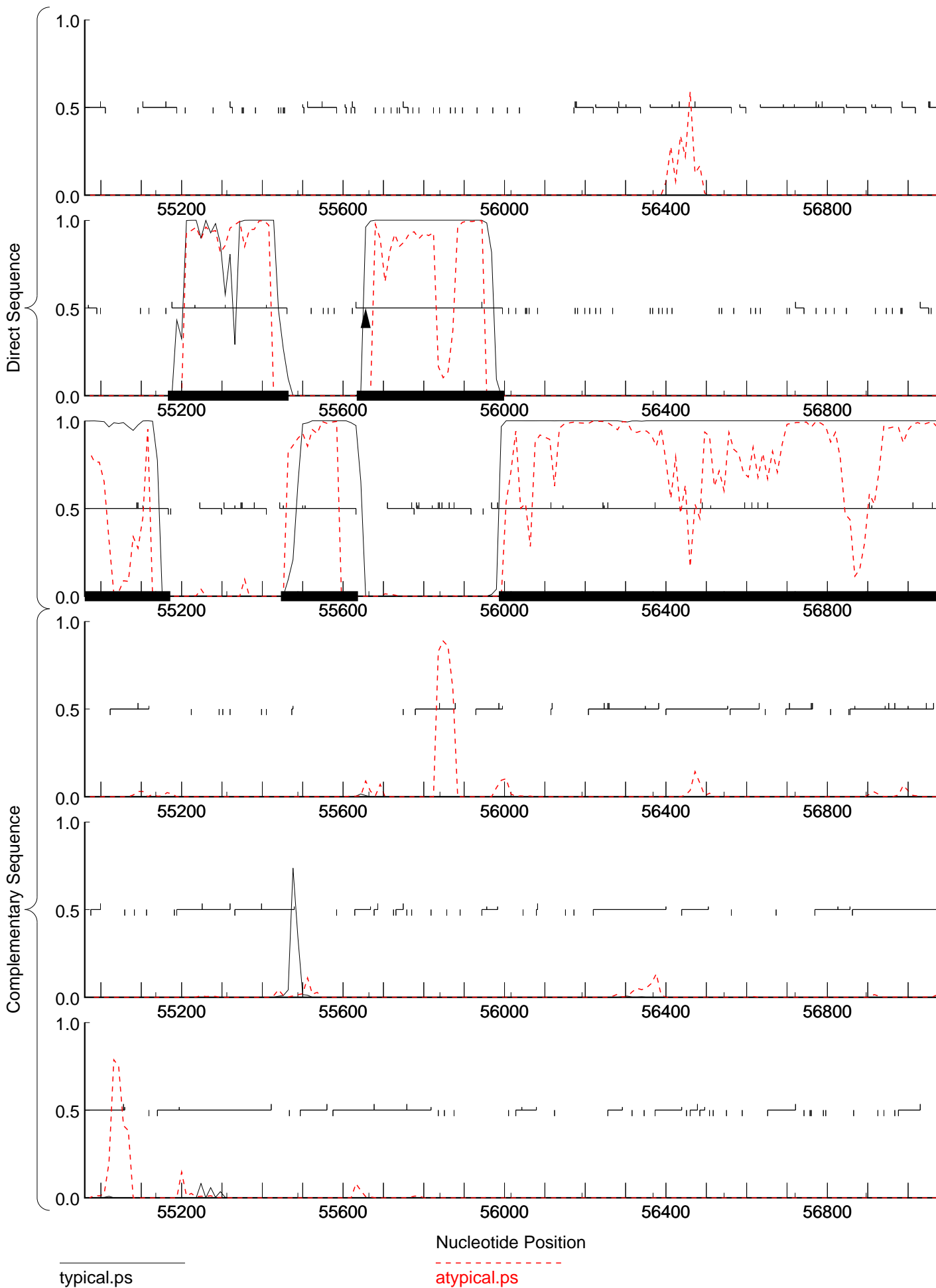
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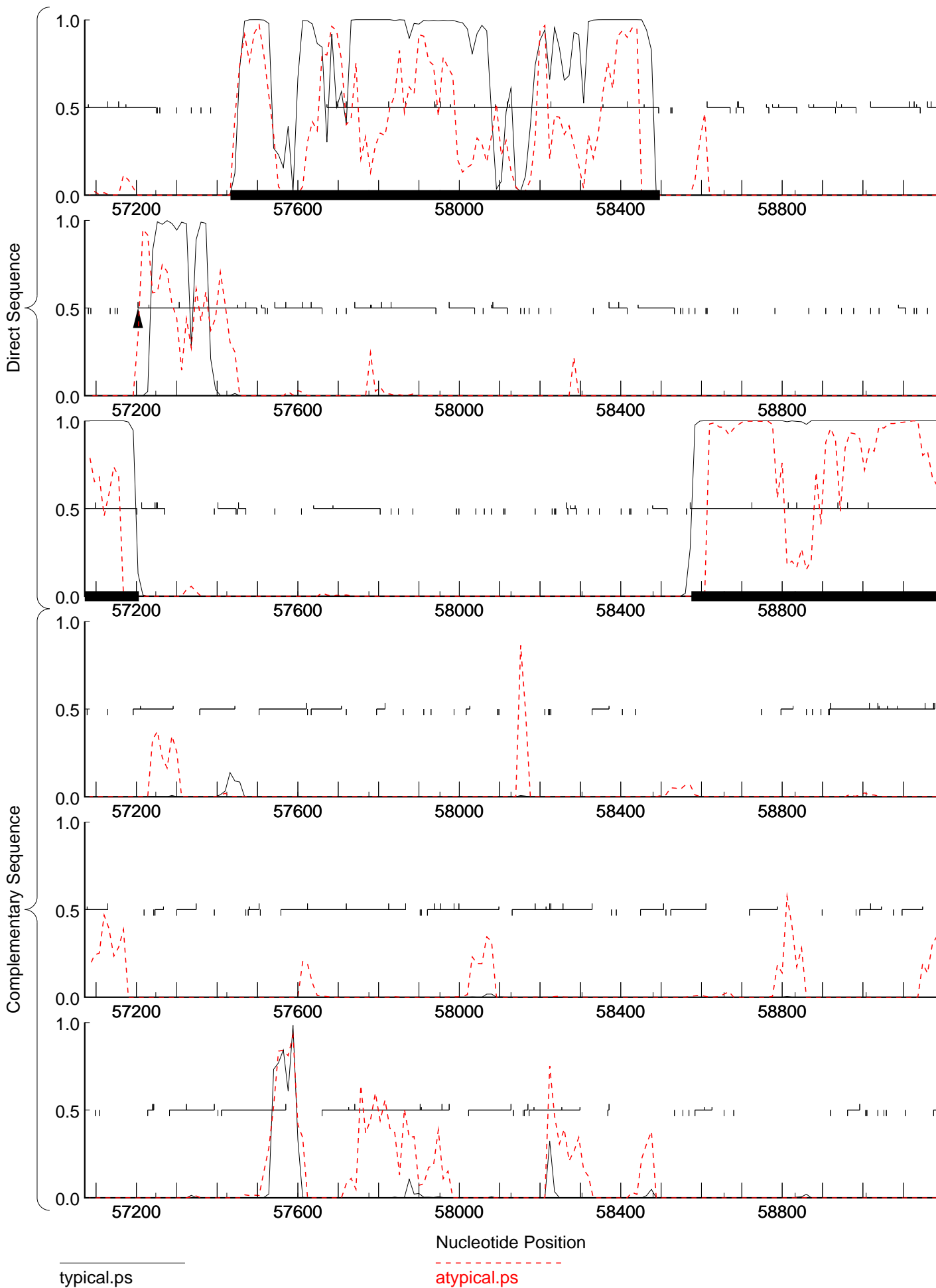
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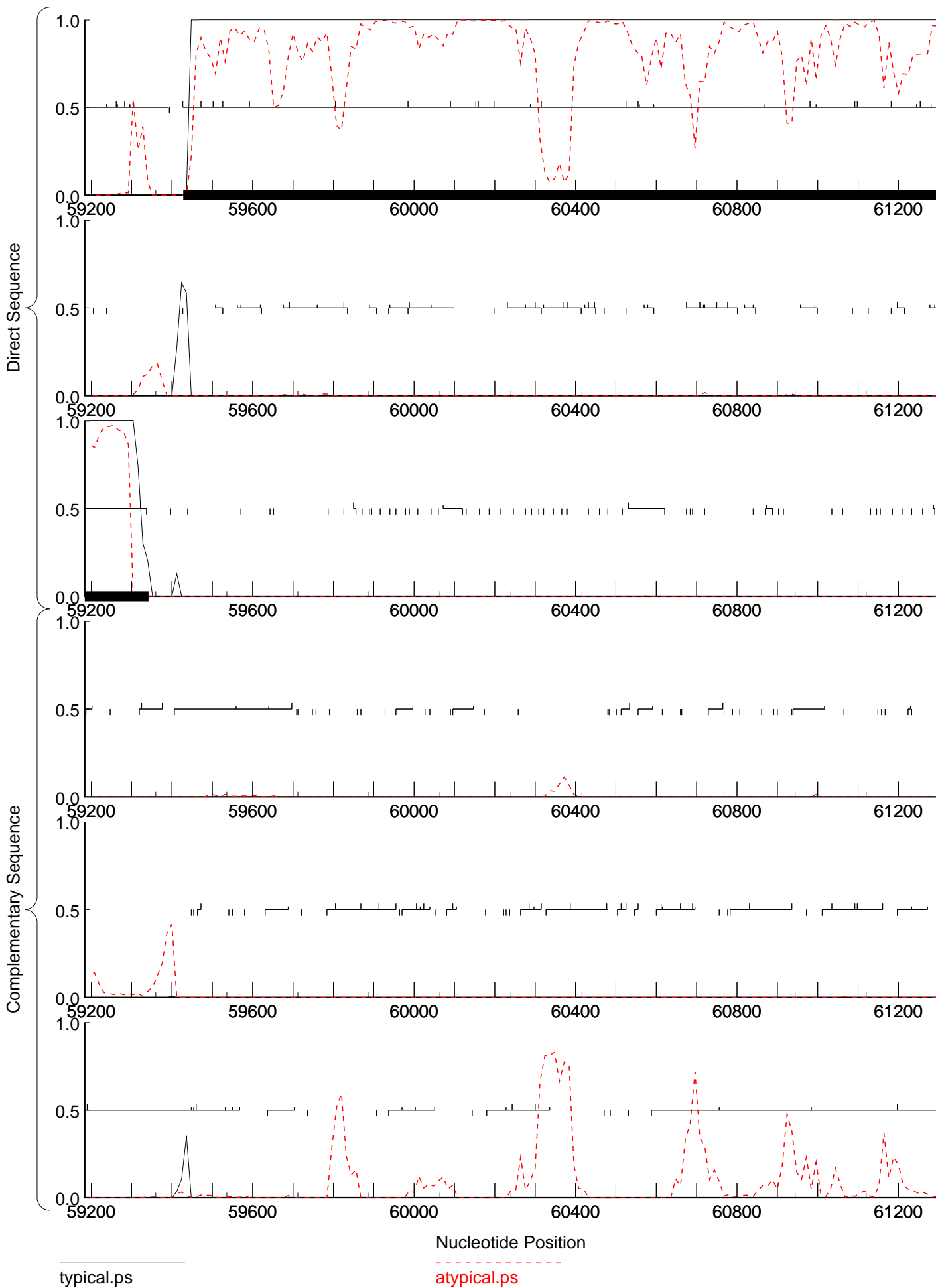
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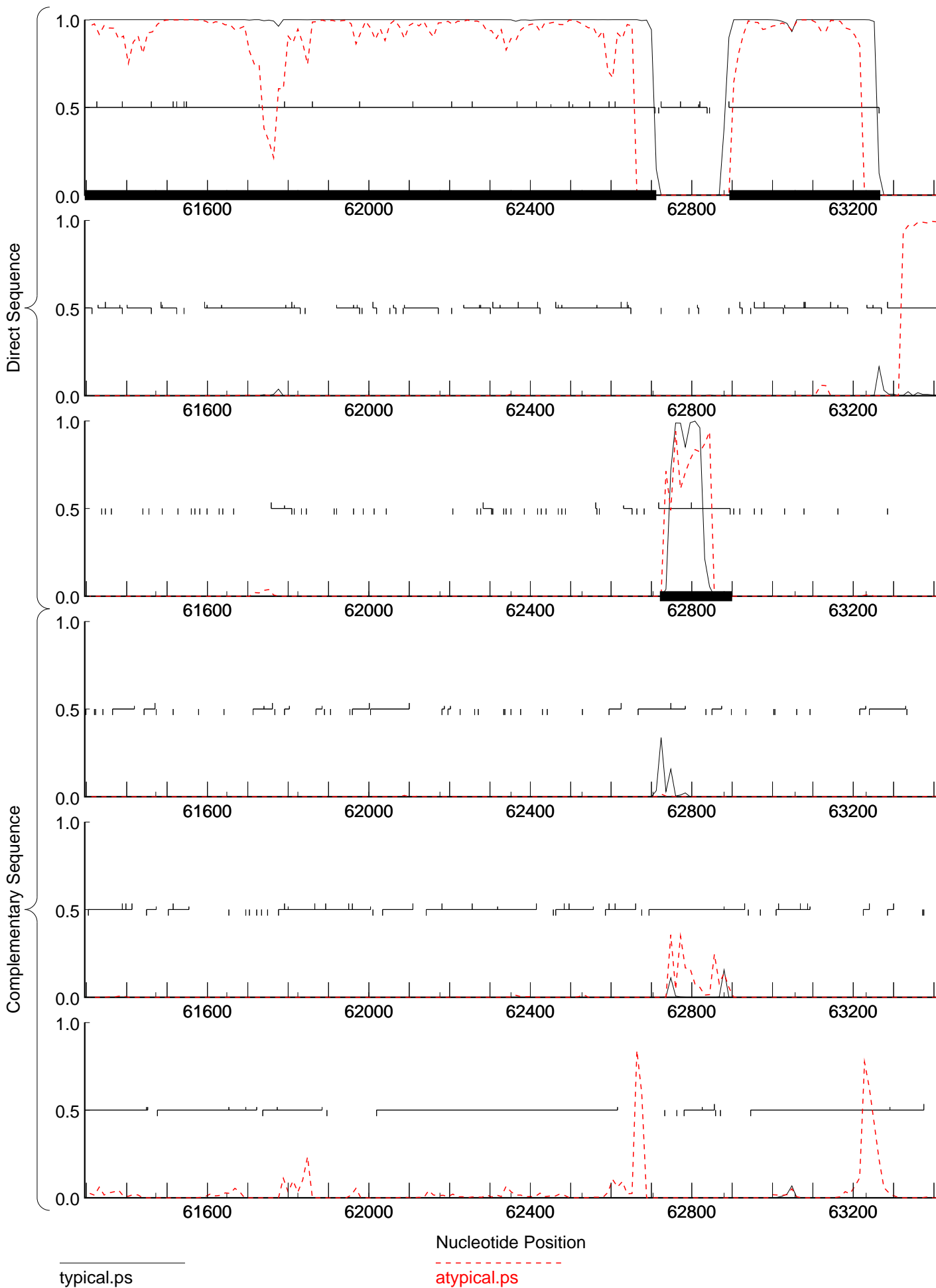




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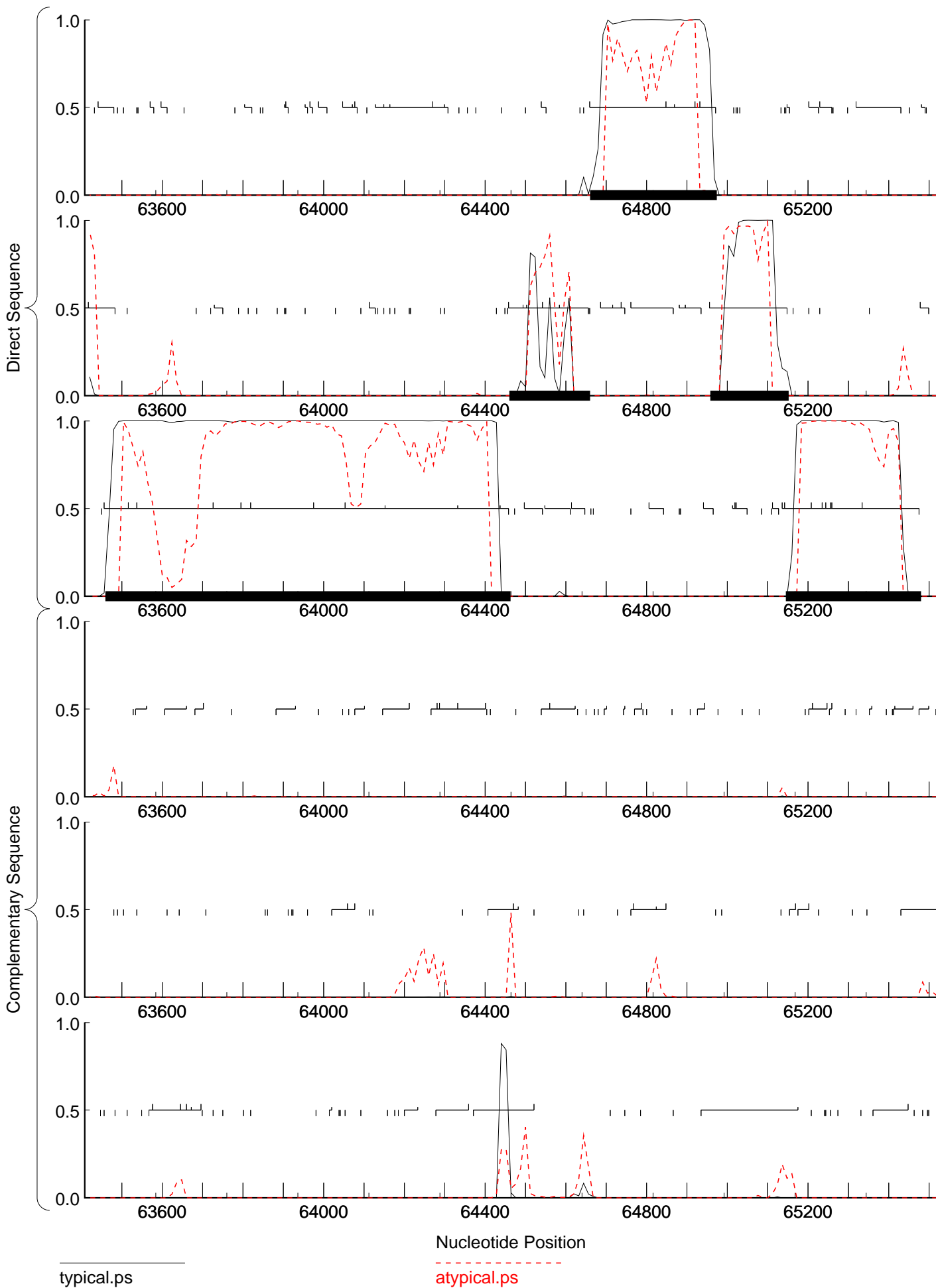
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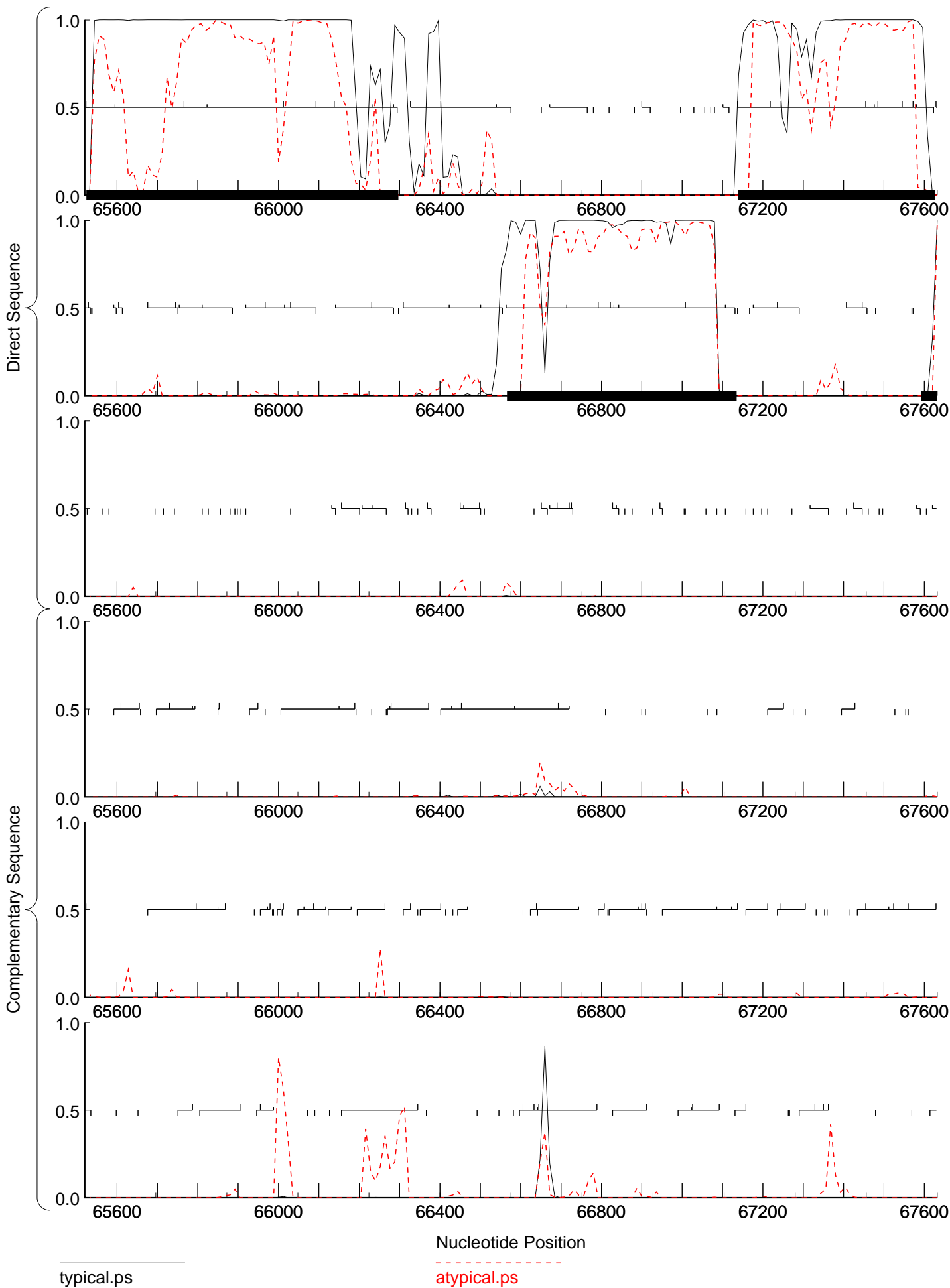
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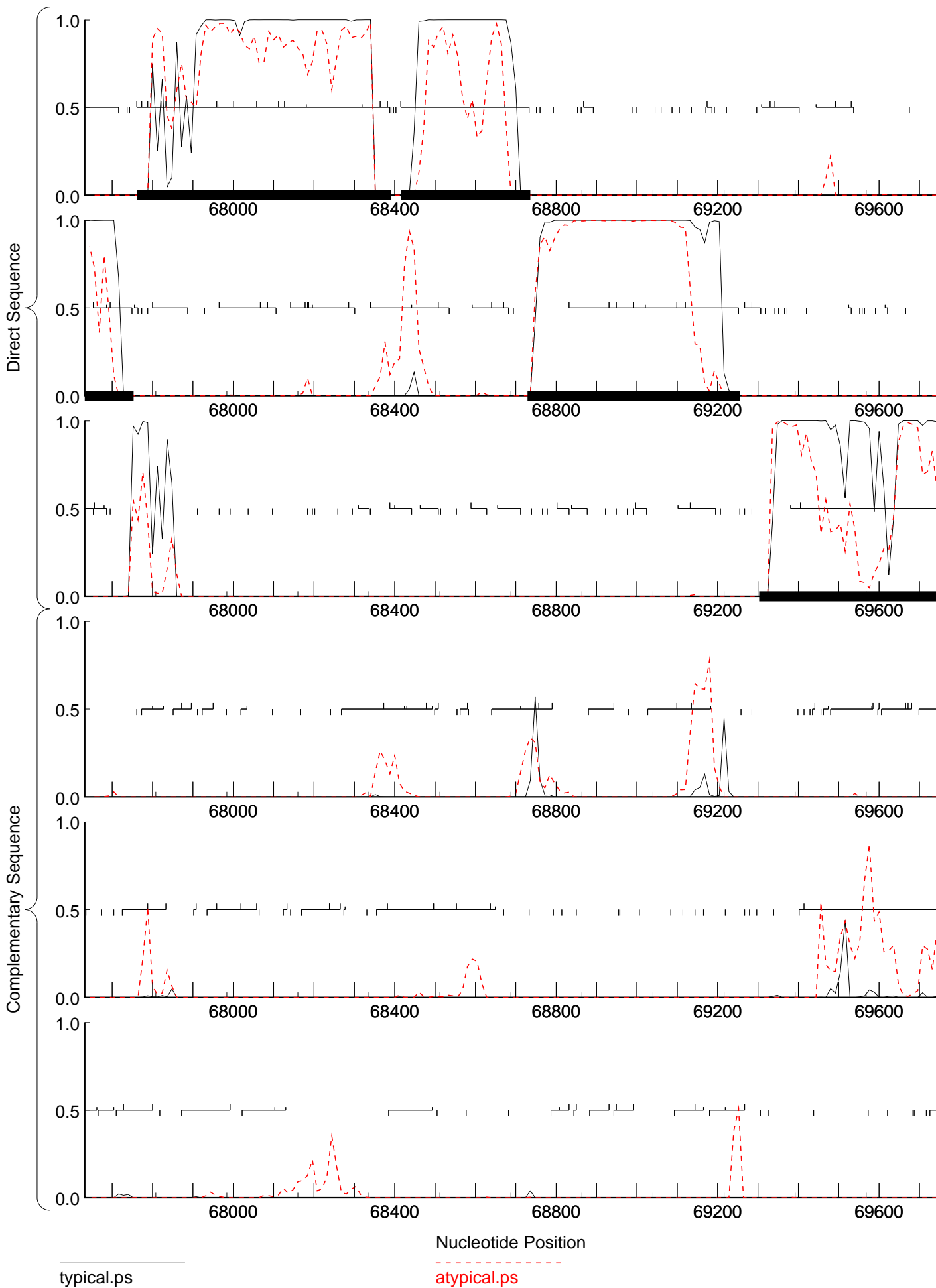
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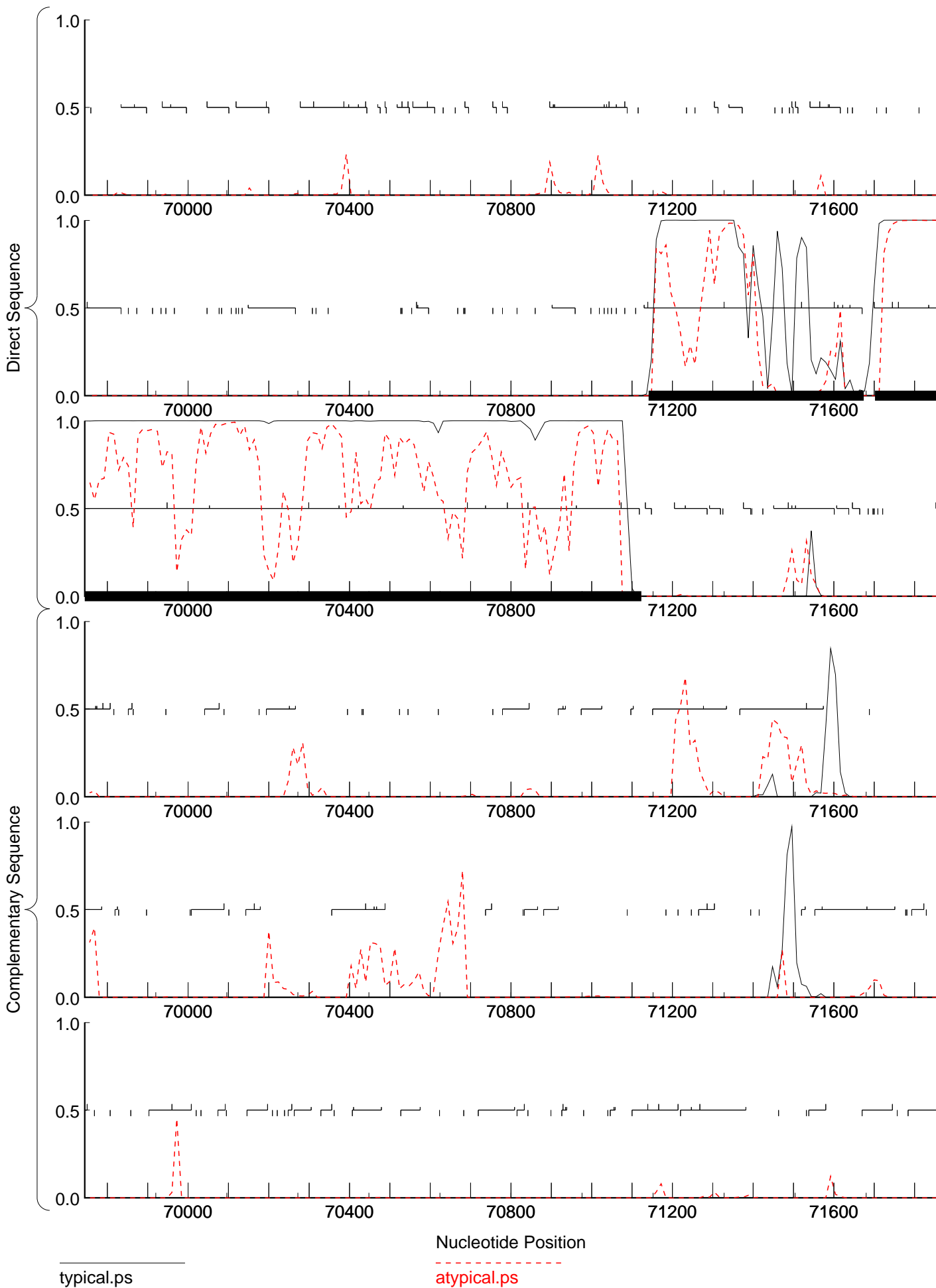
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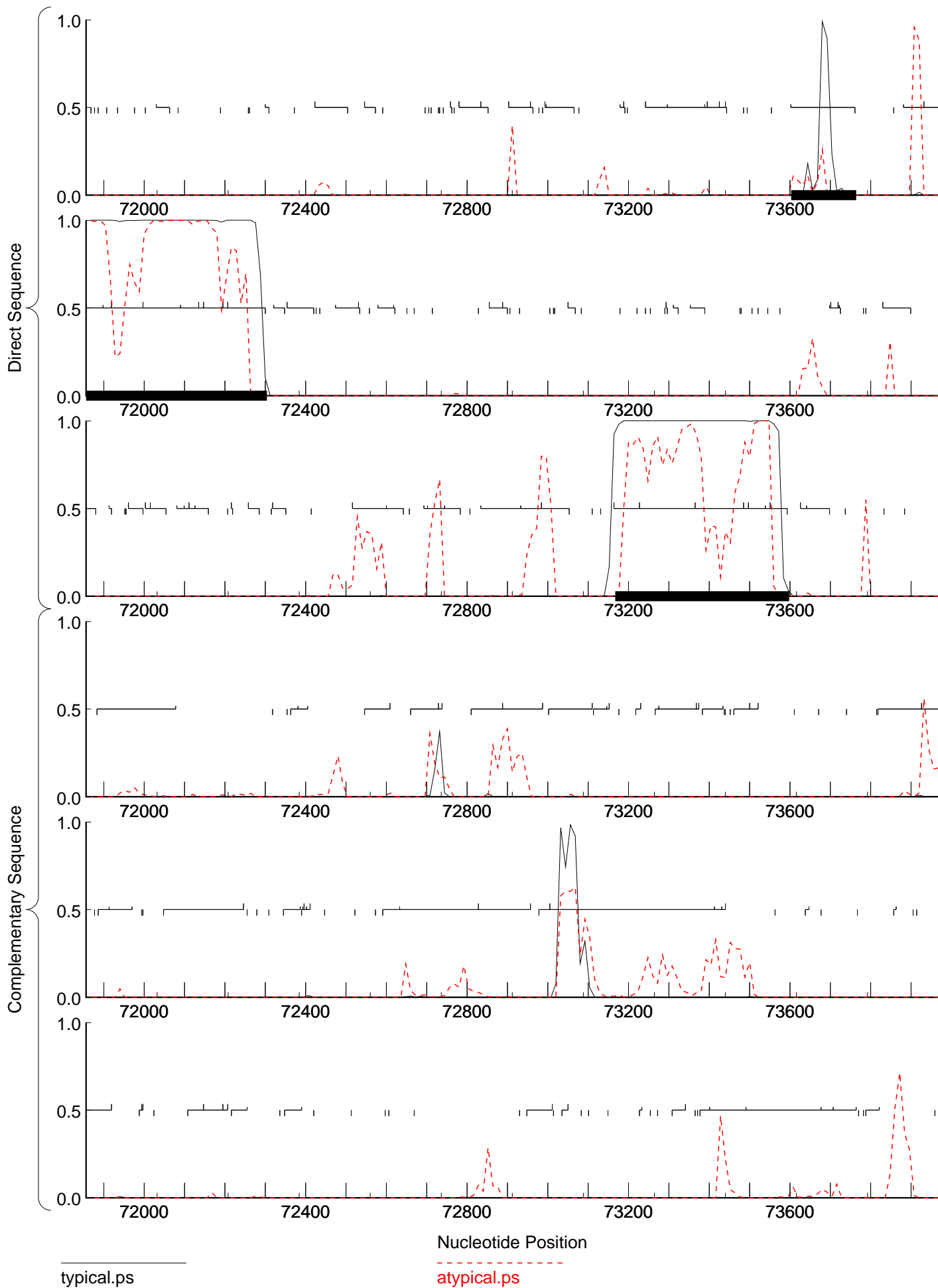
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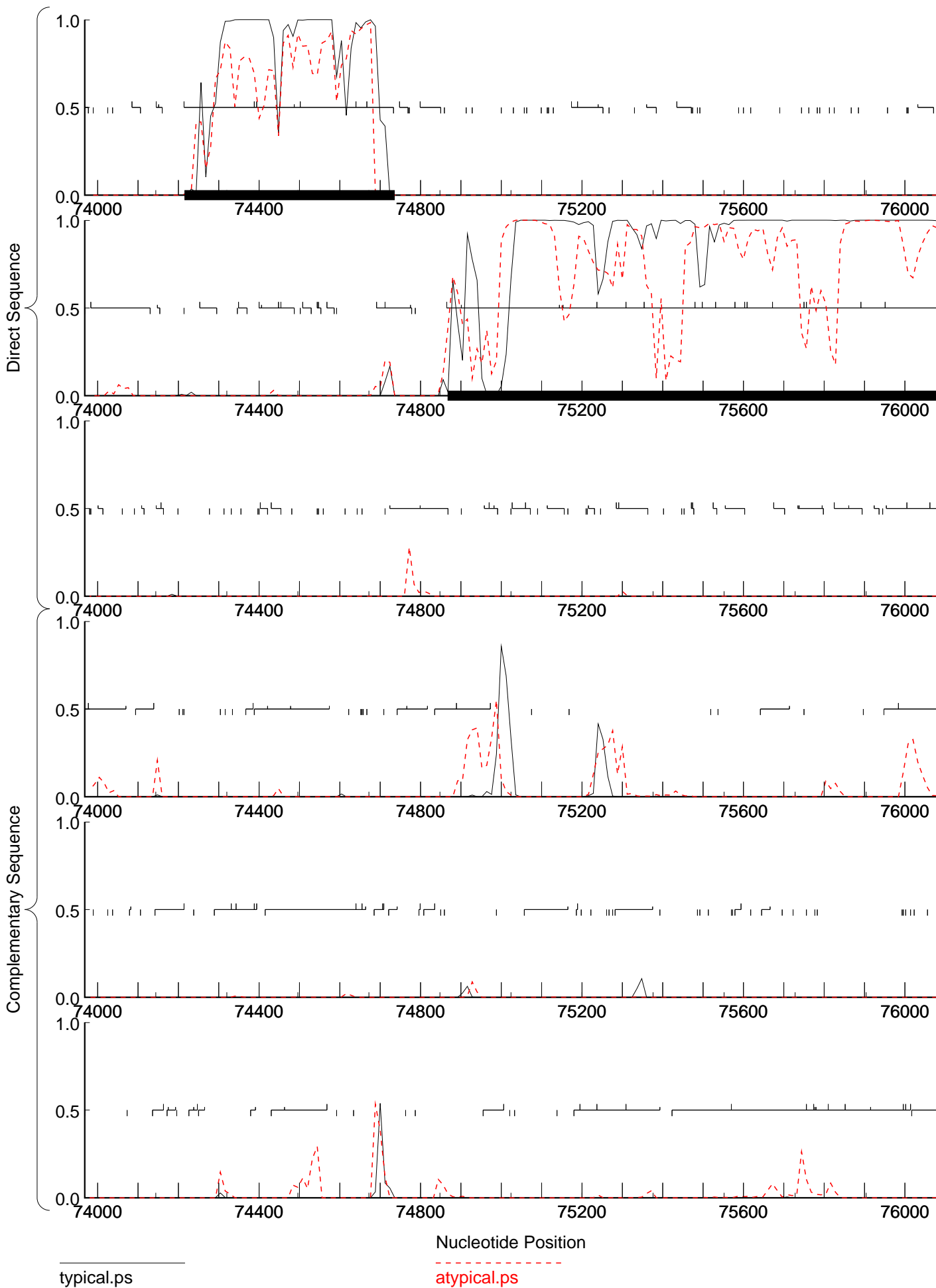


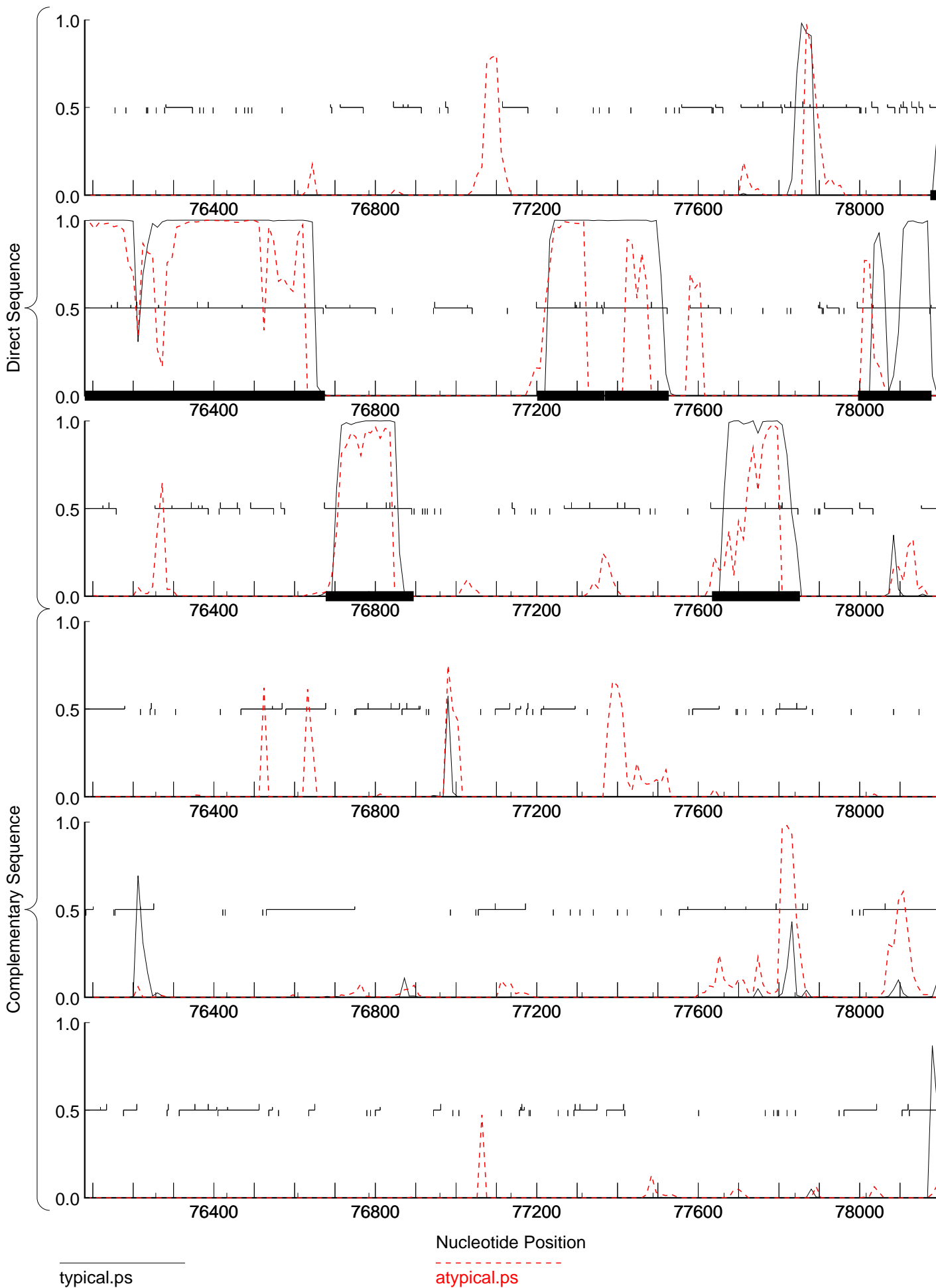
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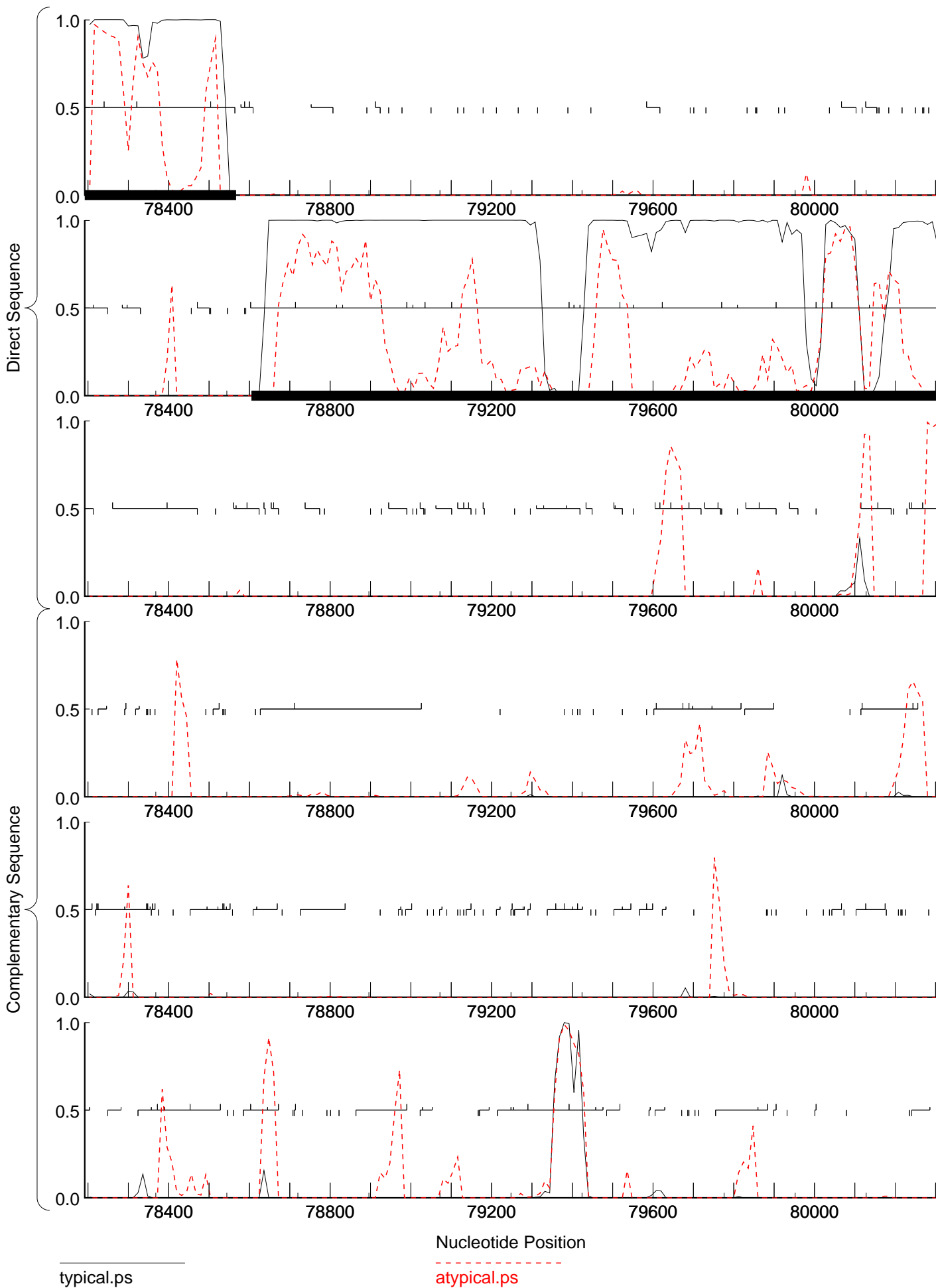
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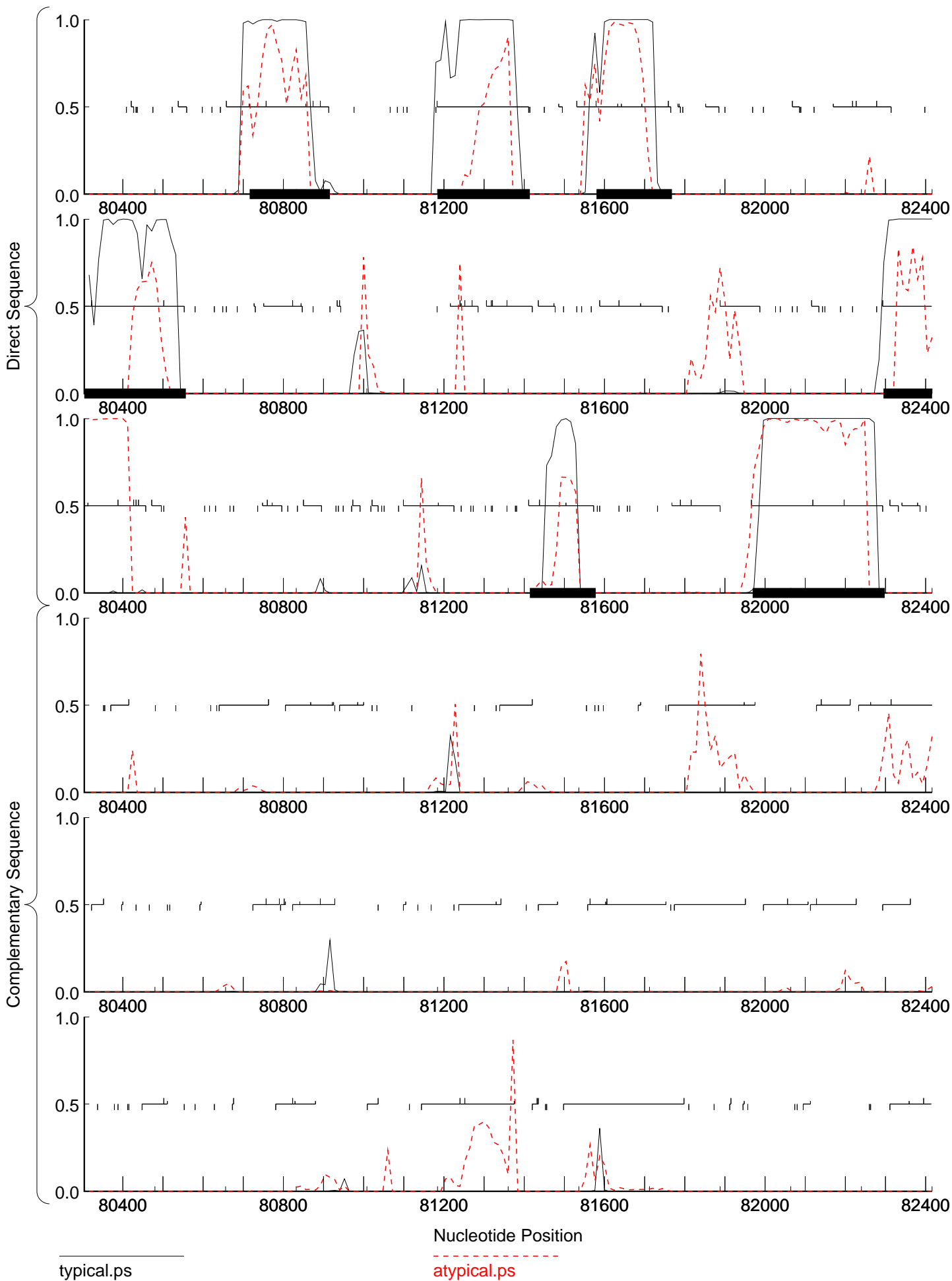






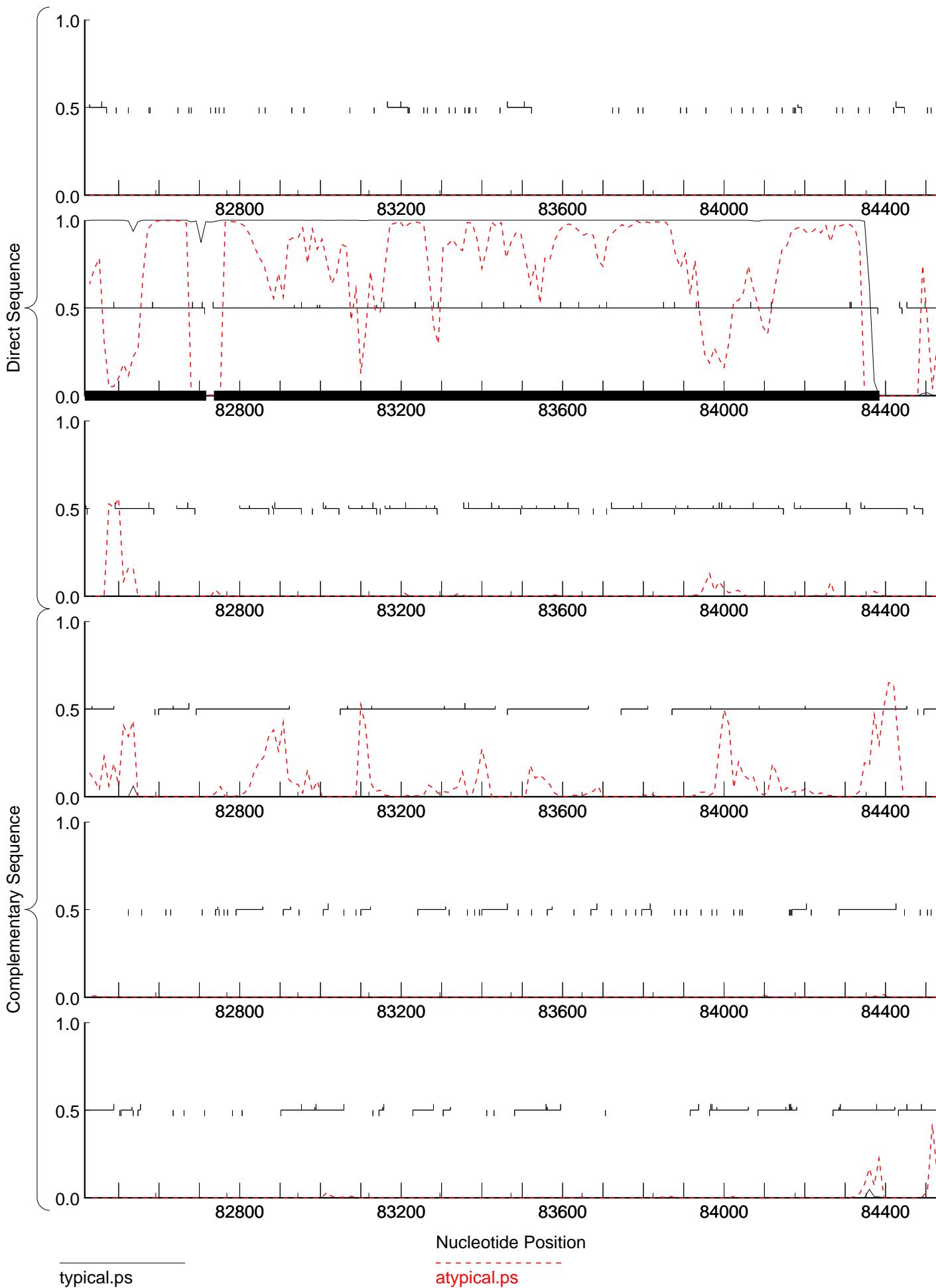
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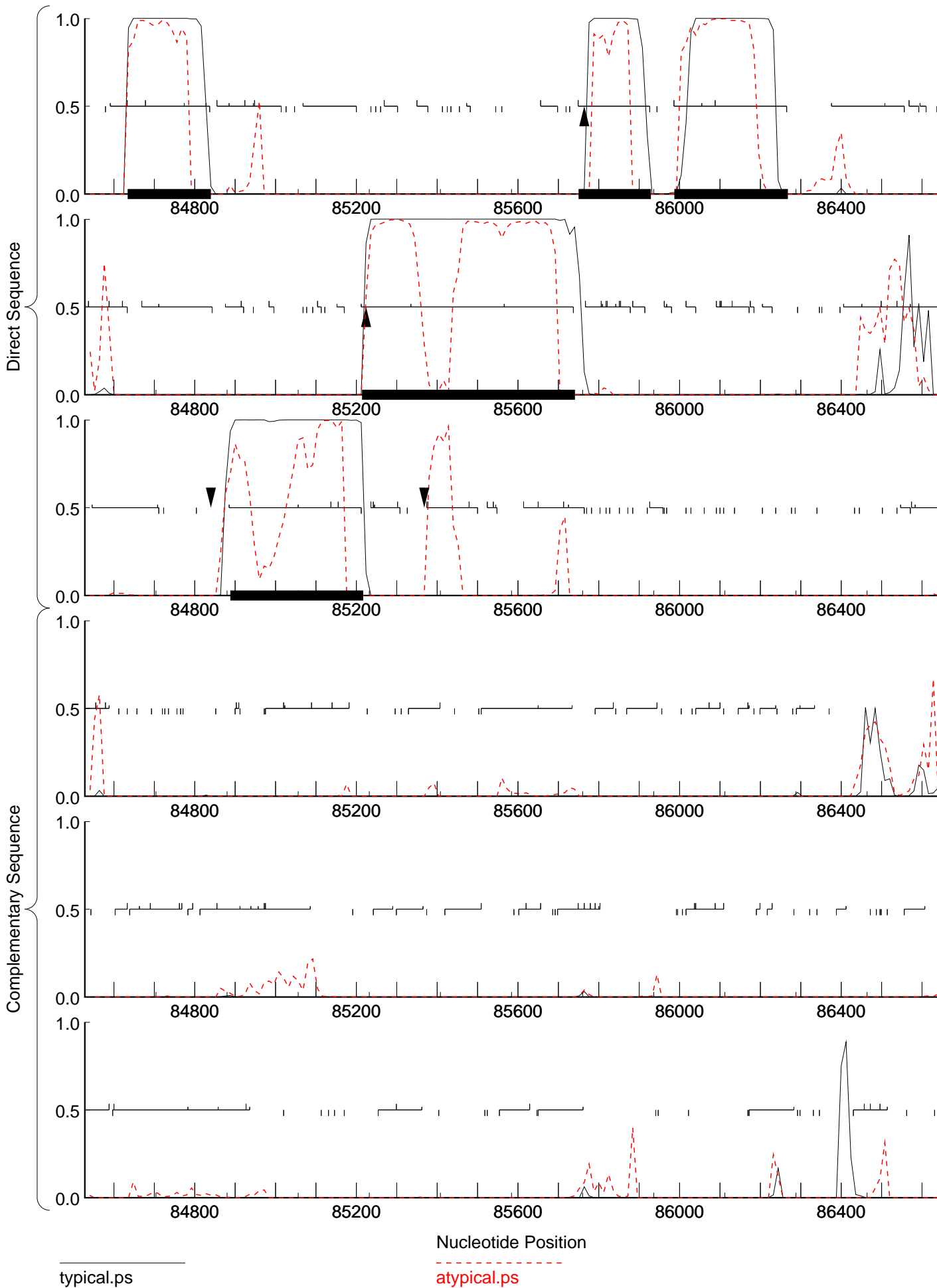
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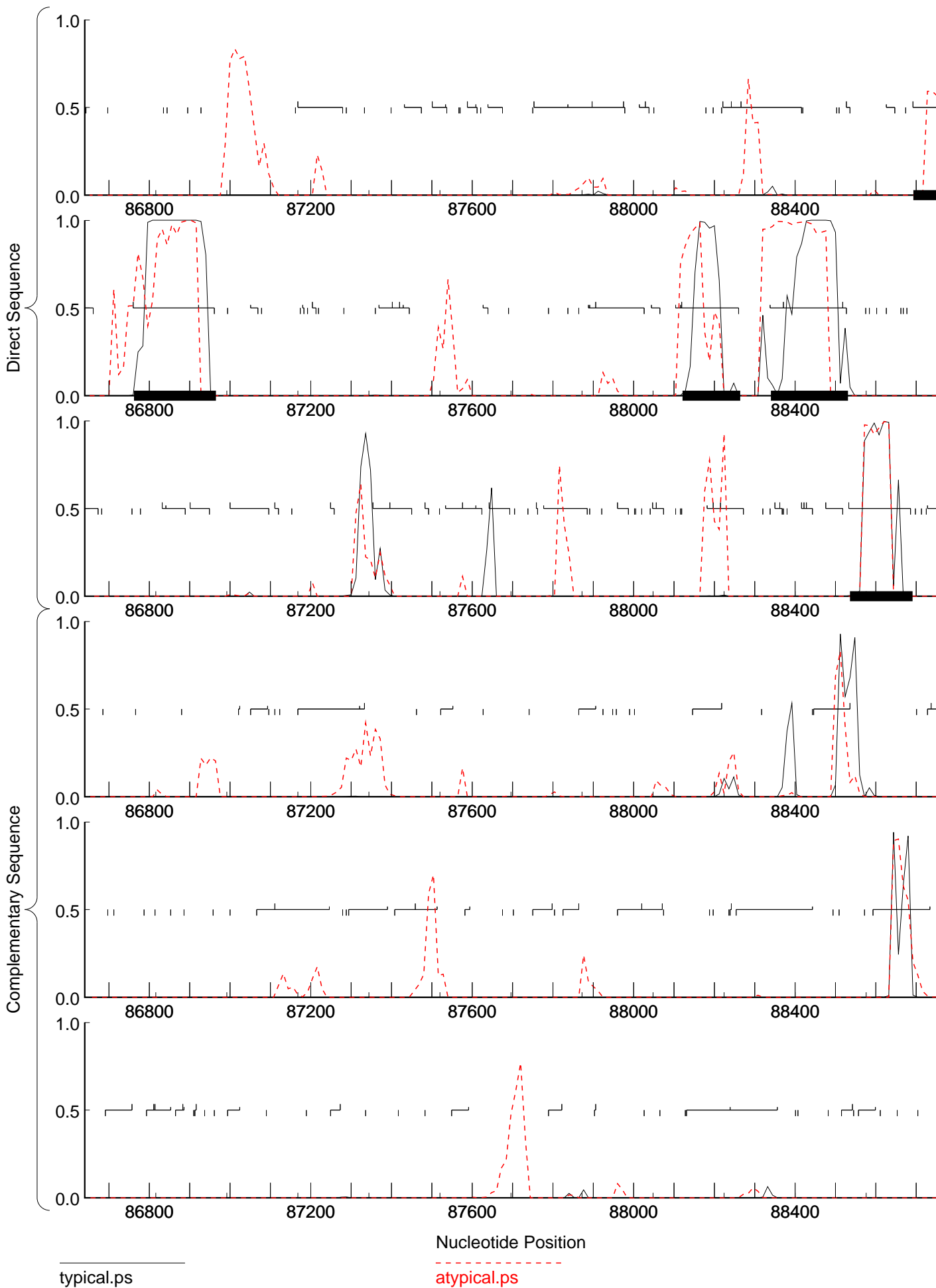


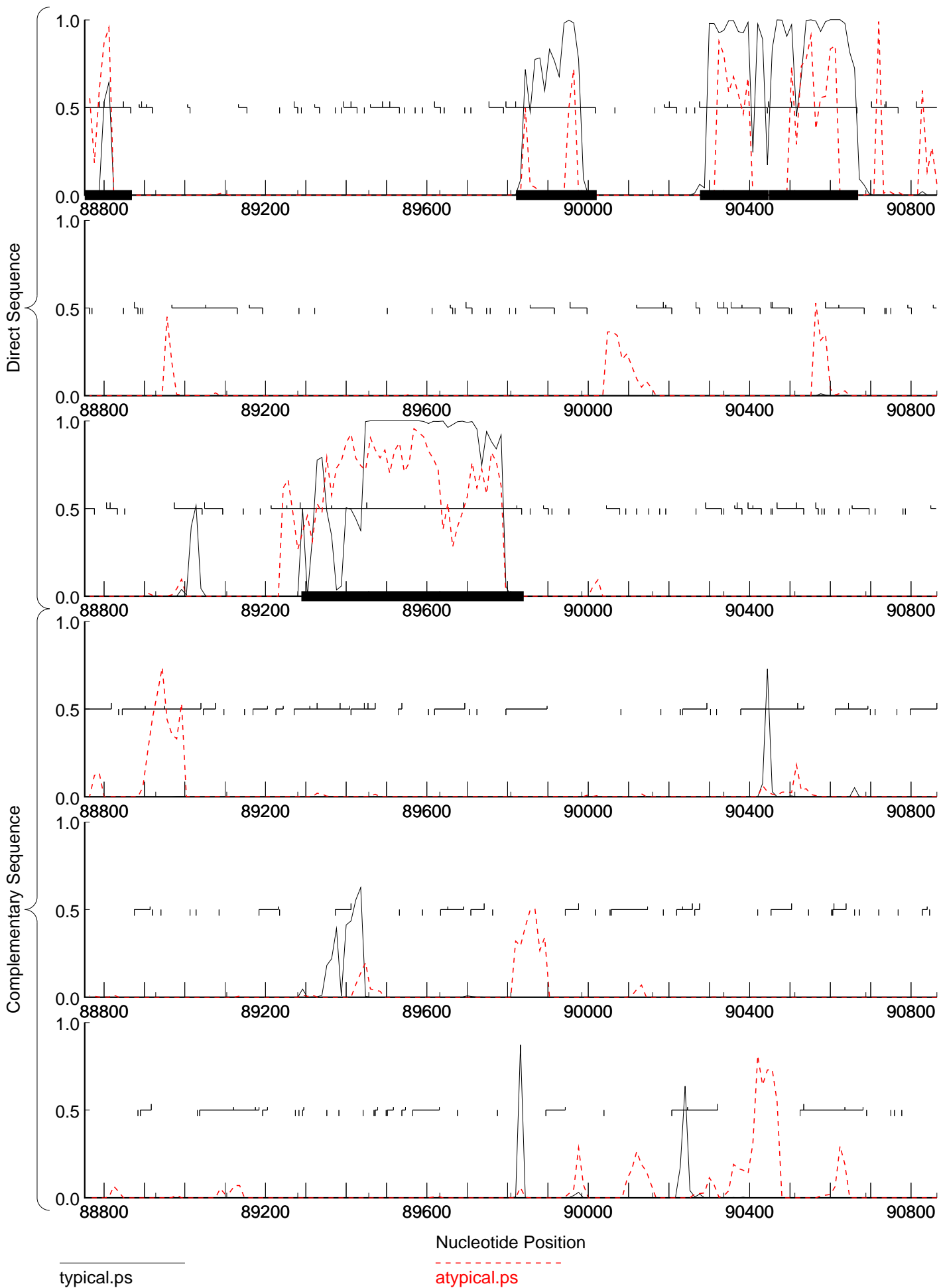
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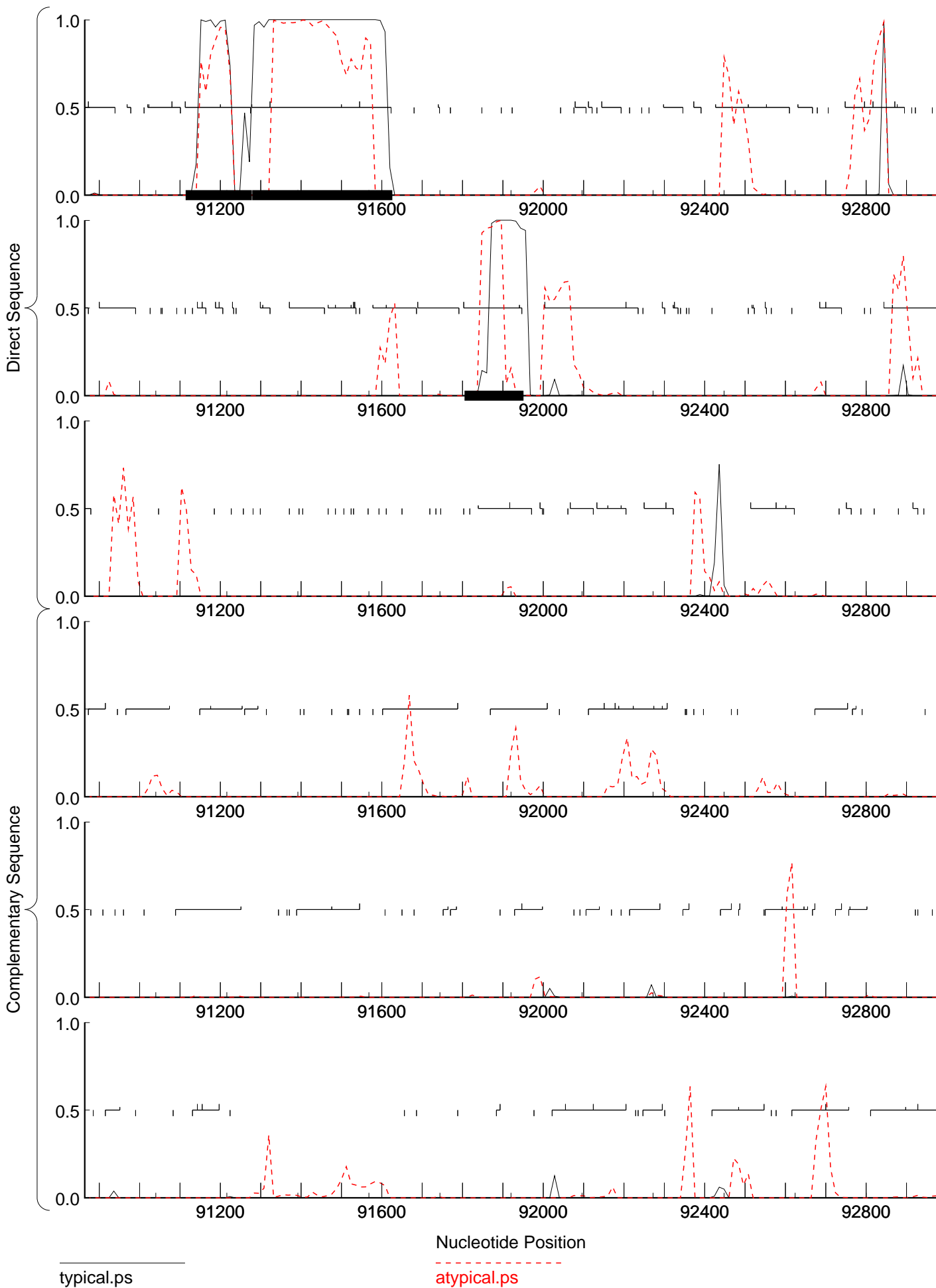
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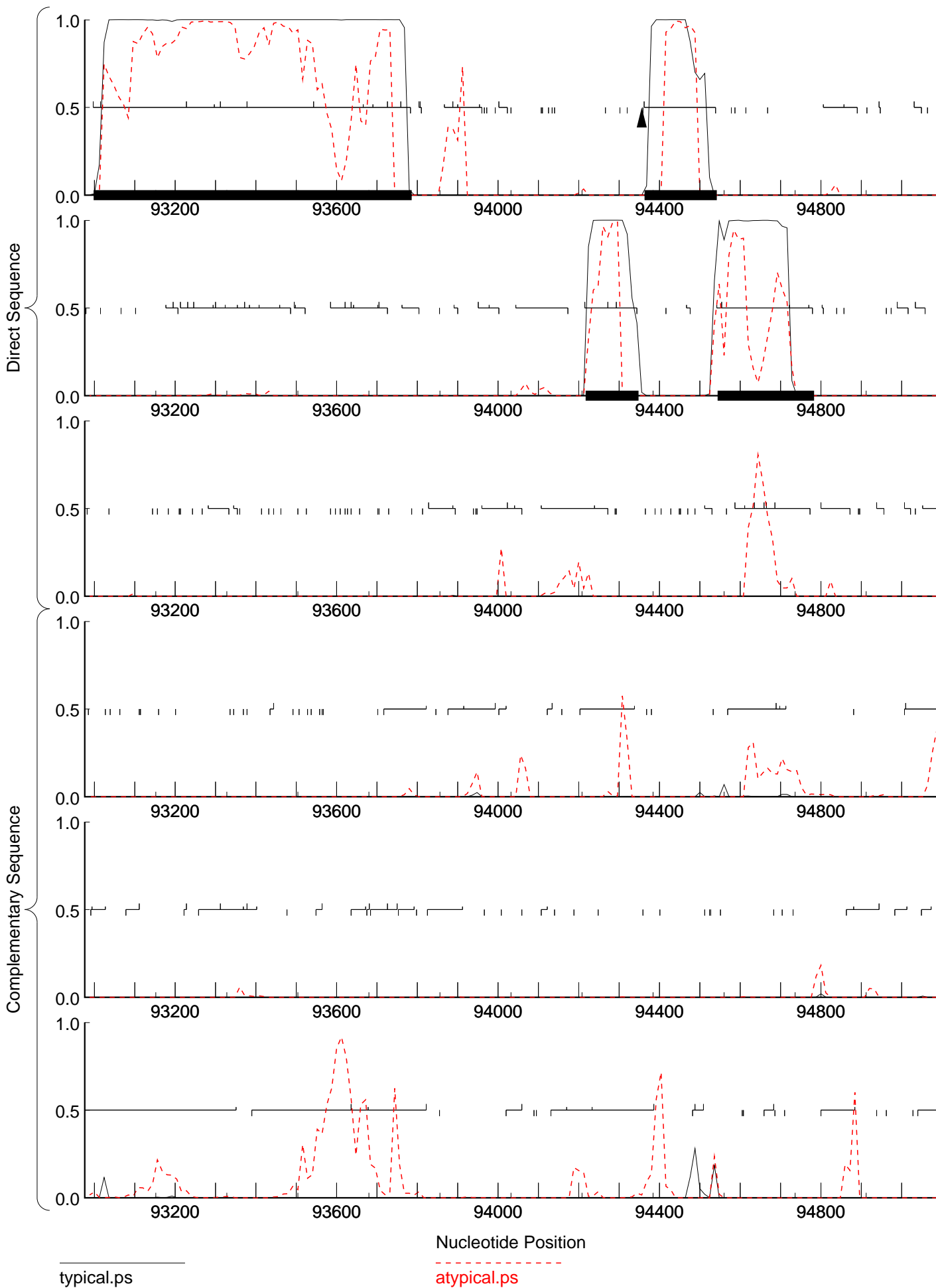


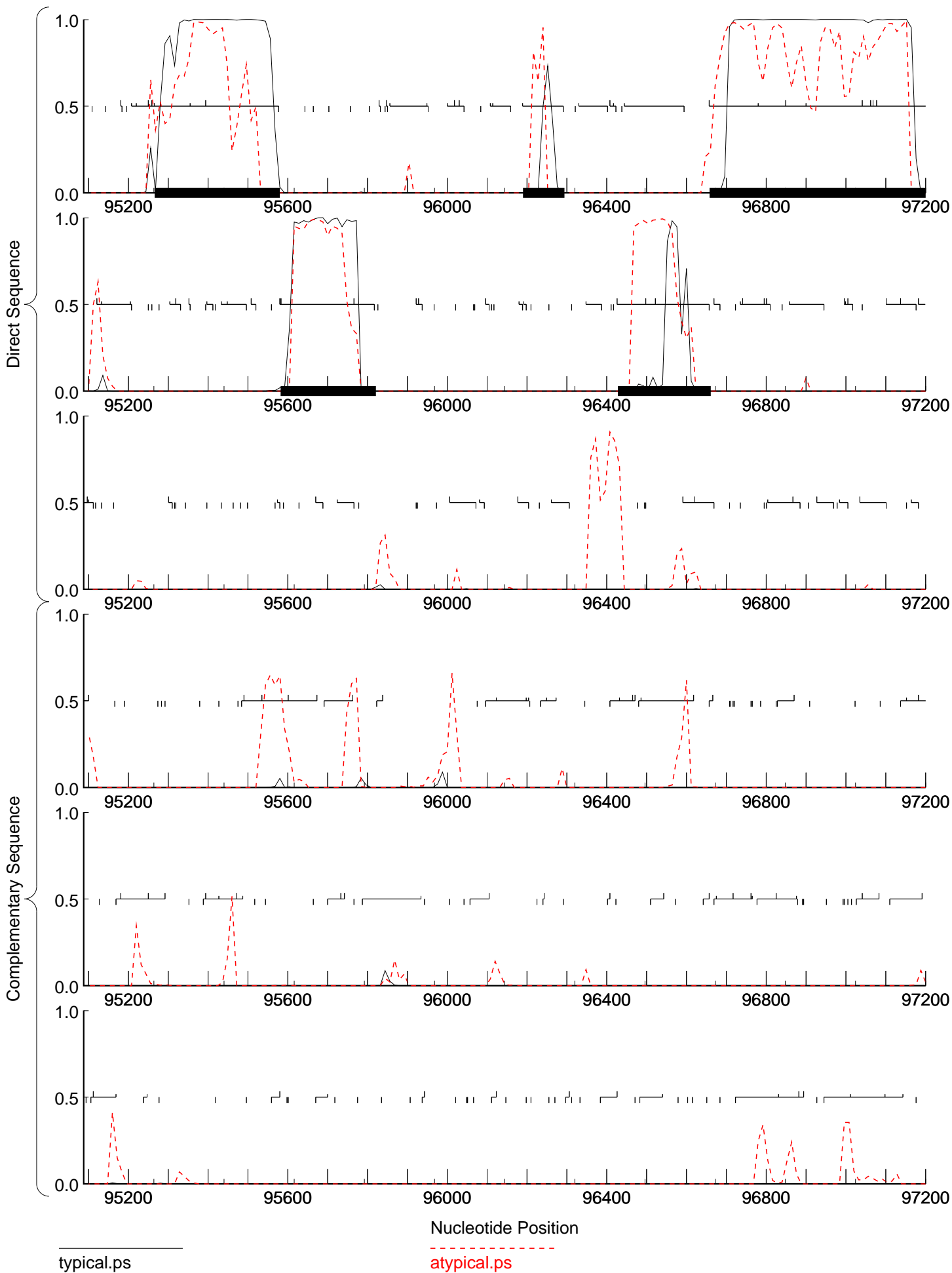


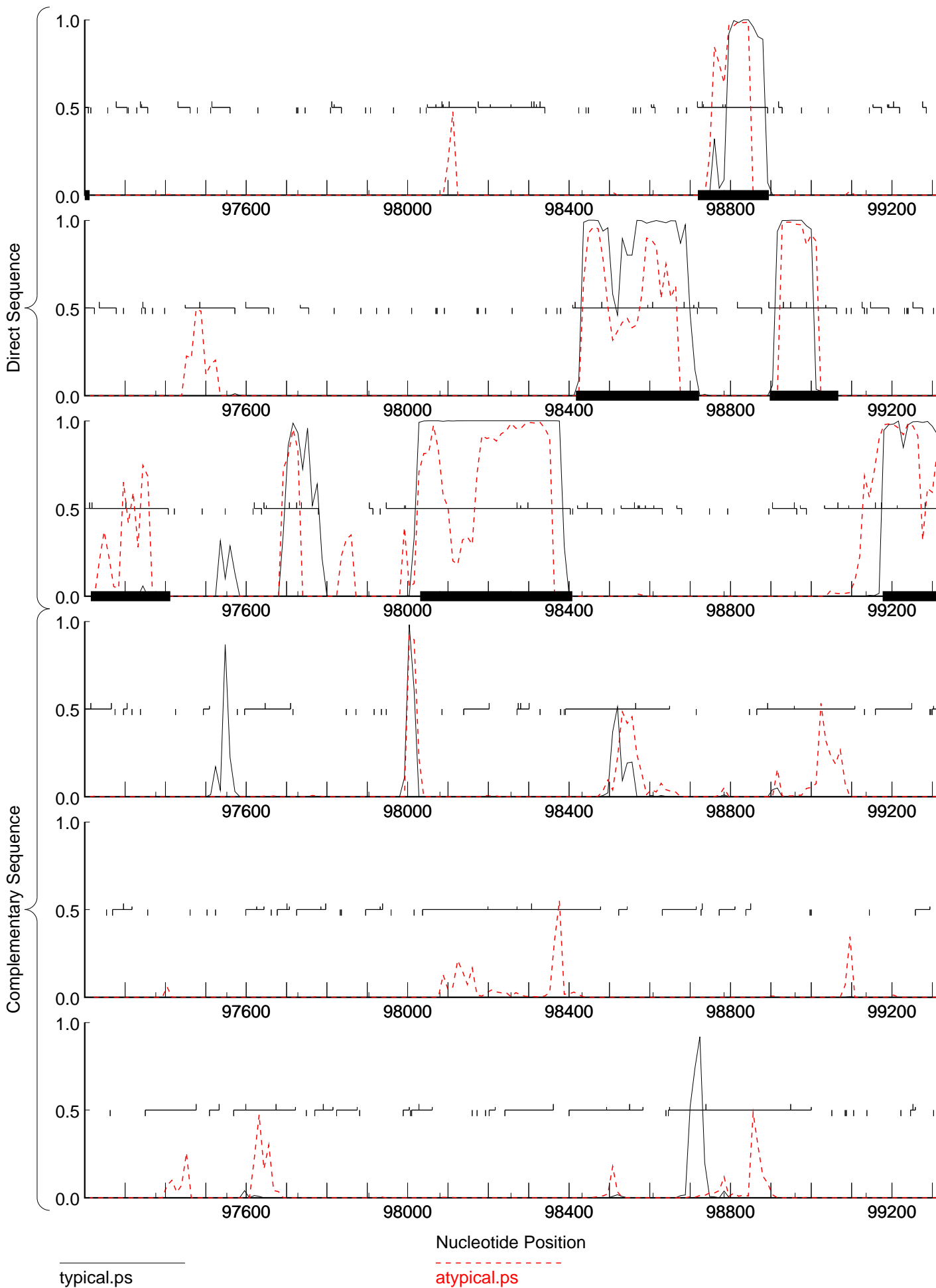






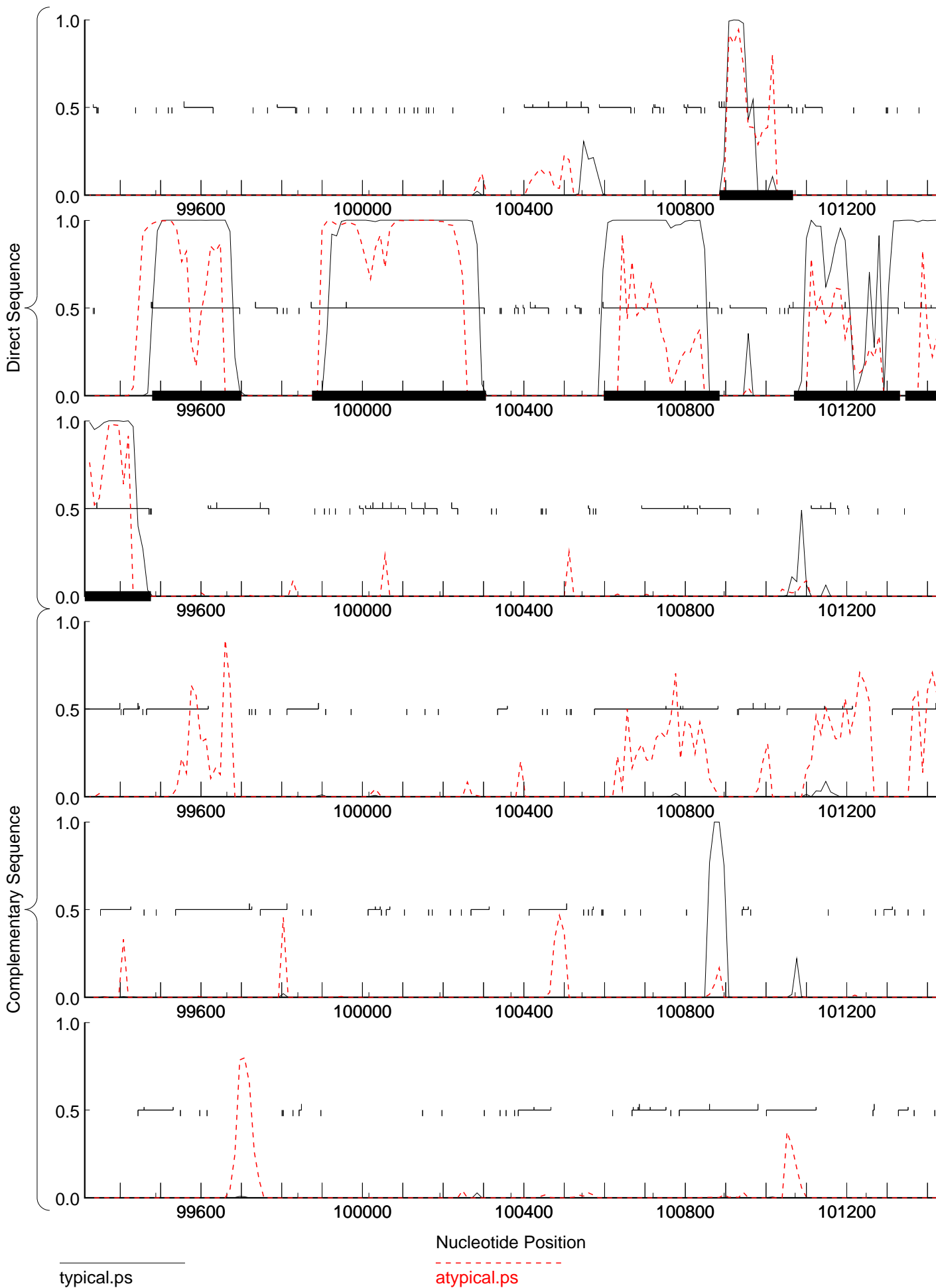


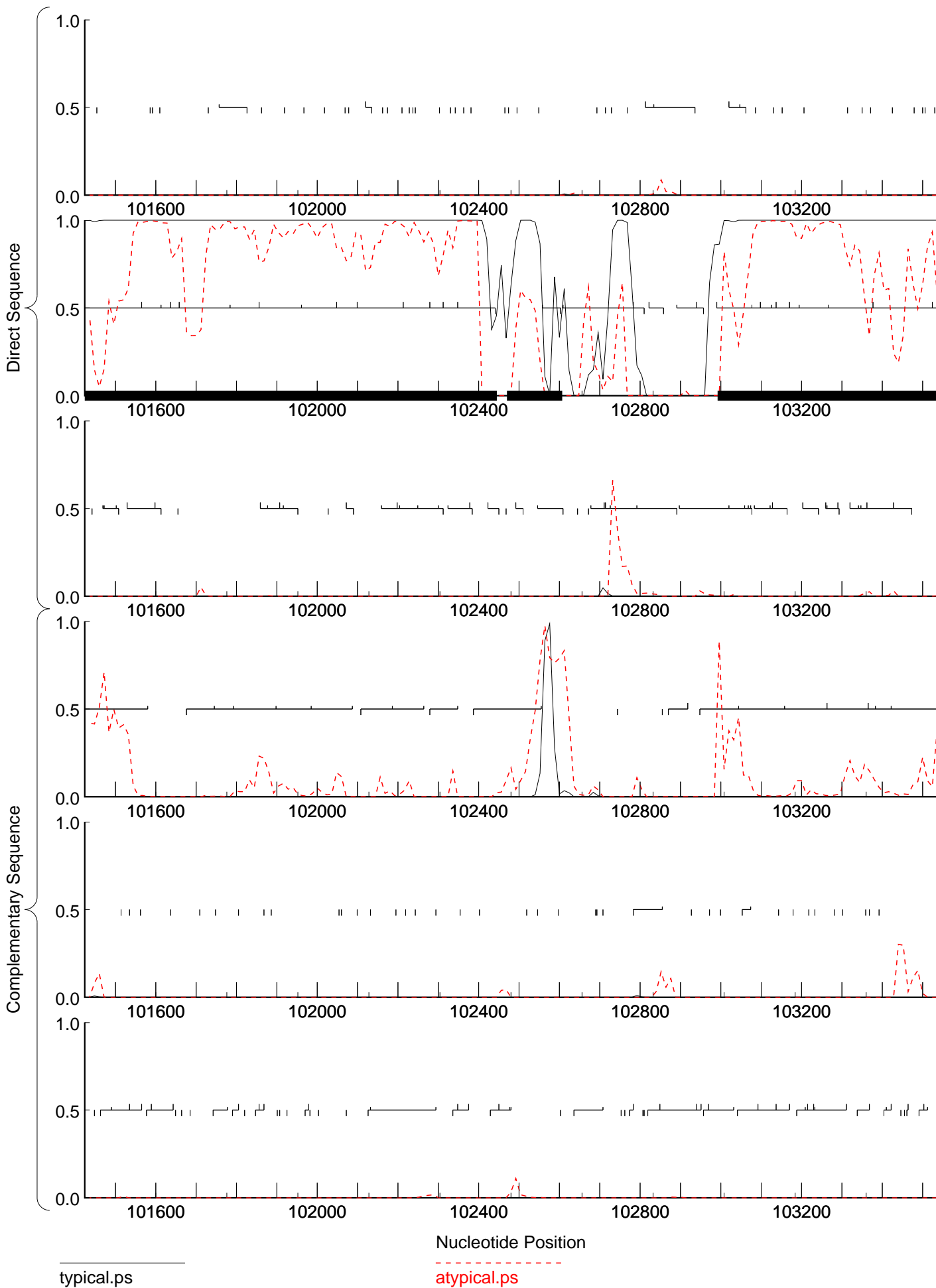


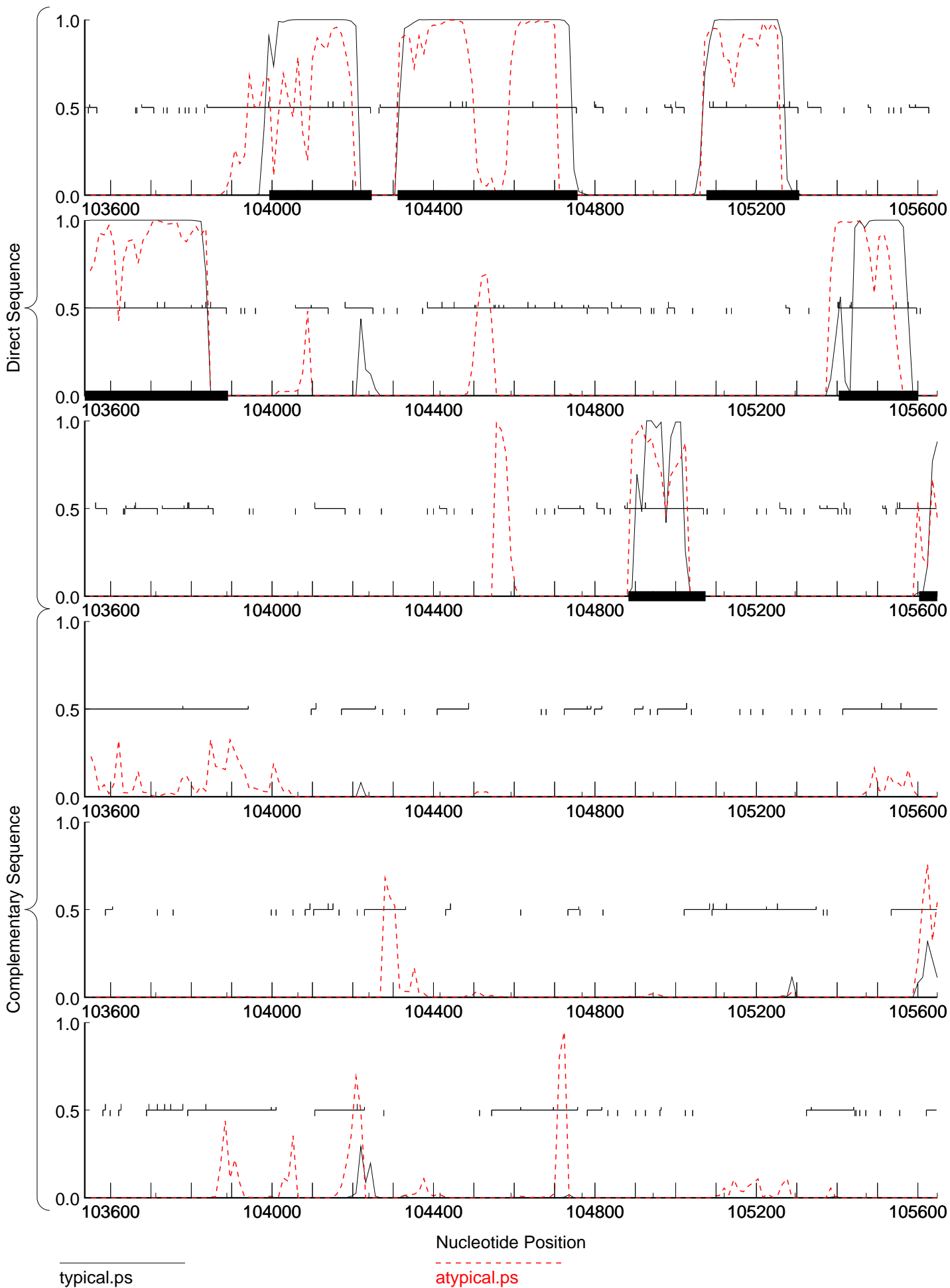


typical.ps

atypical.ps

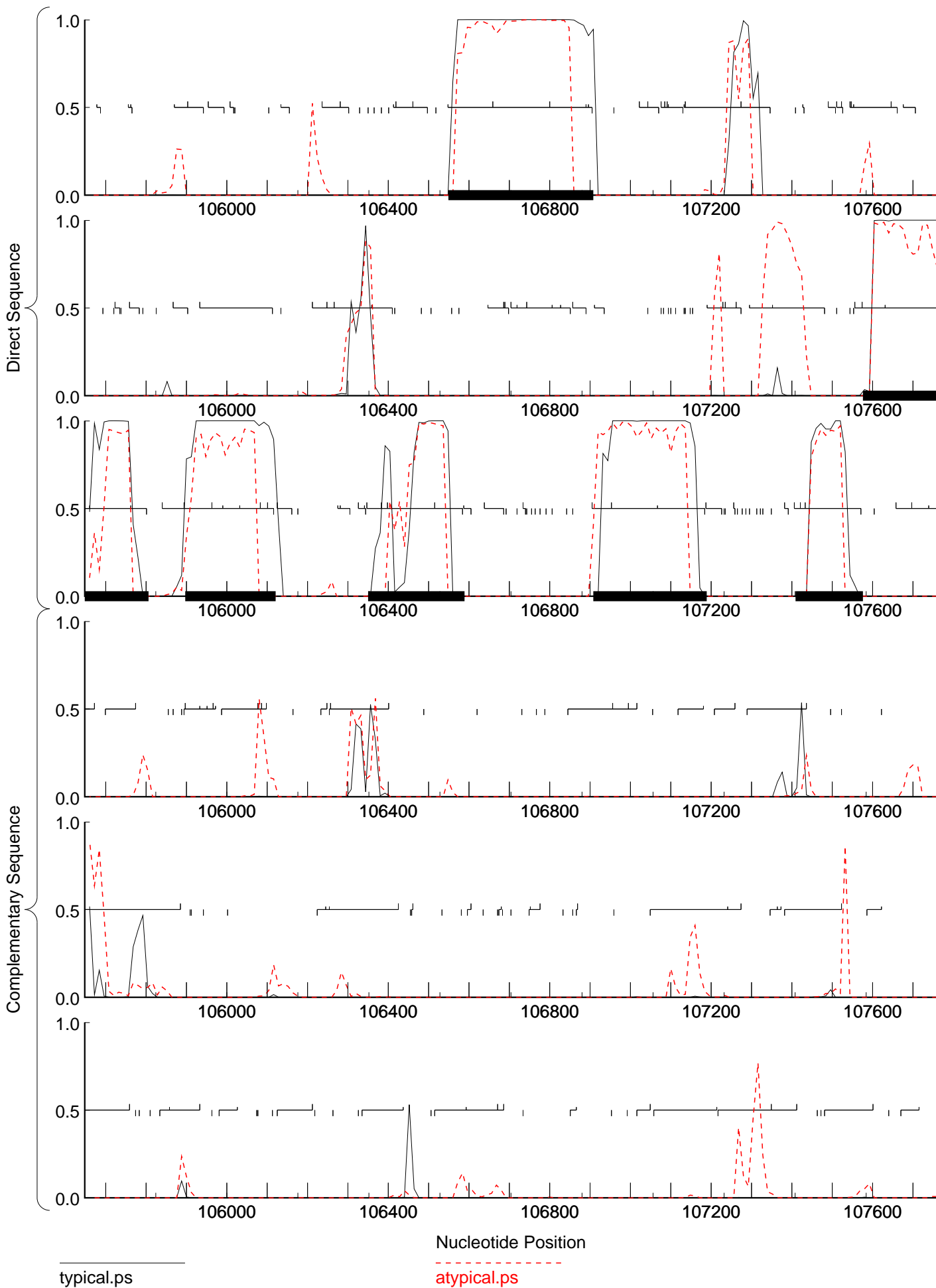






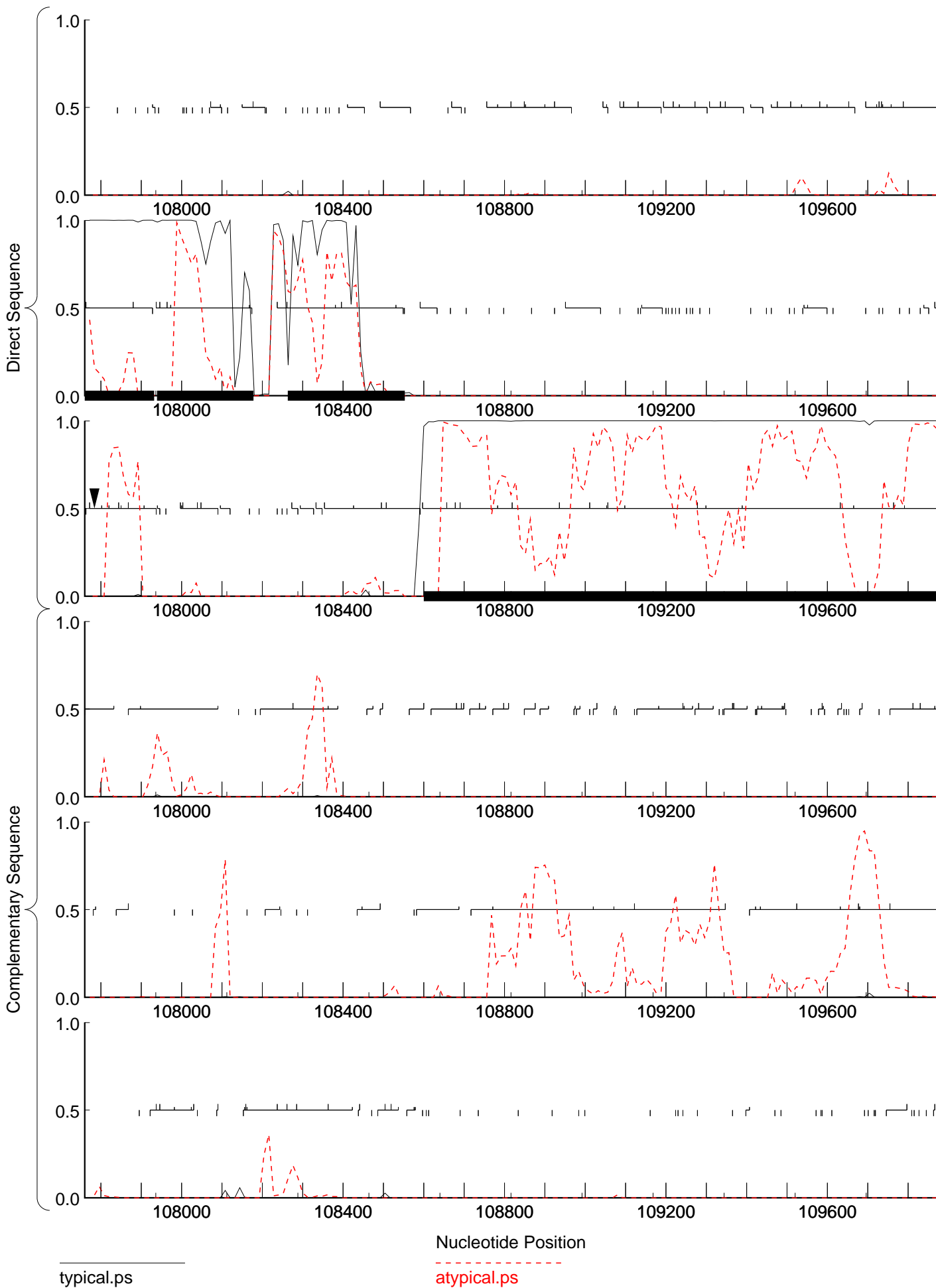
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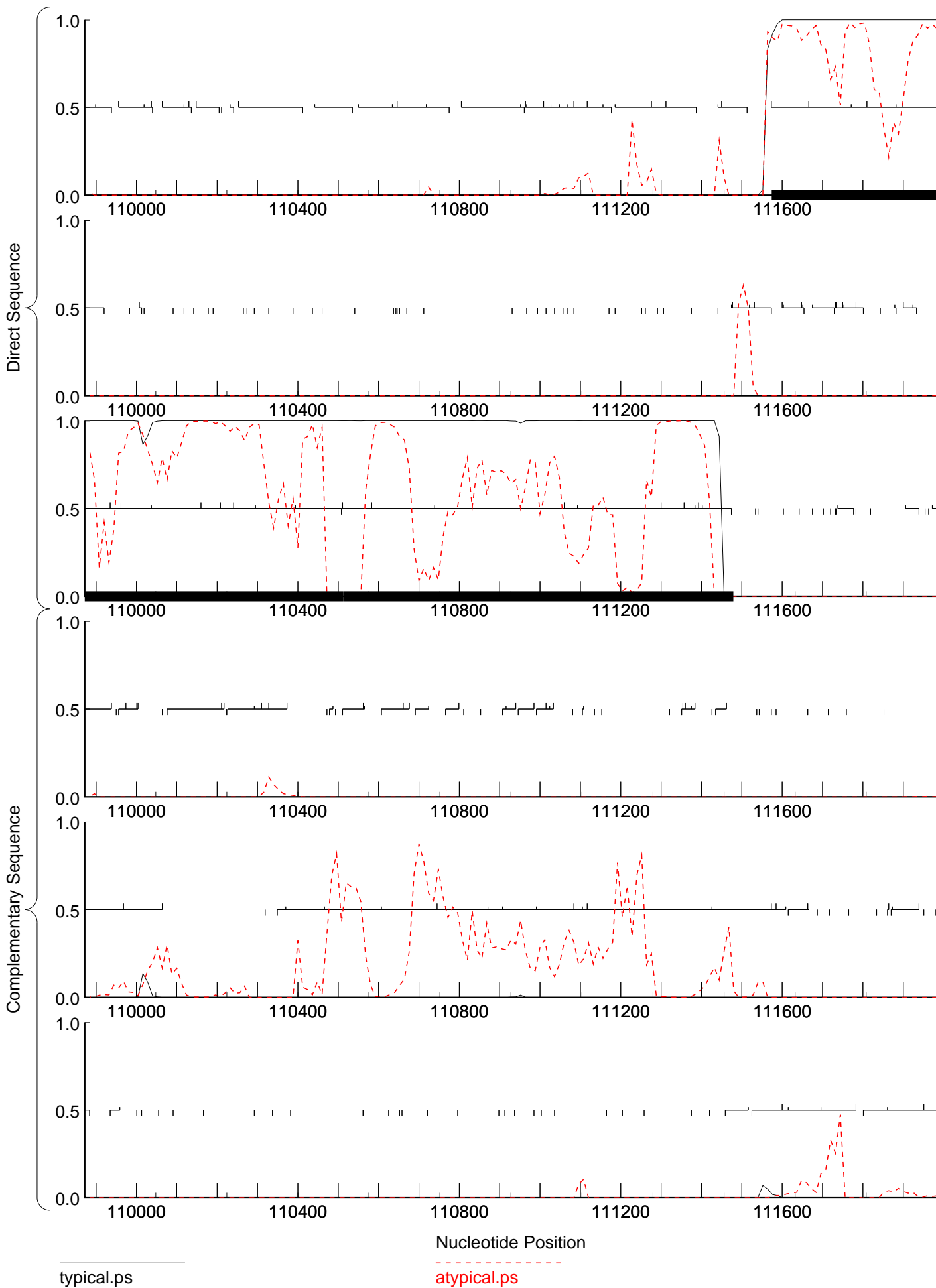
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typical.ps

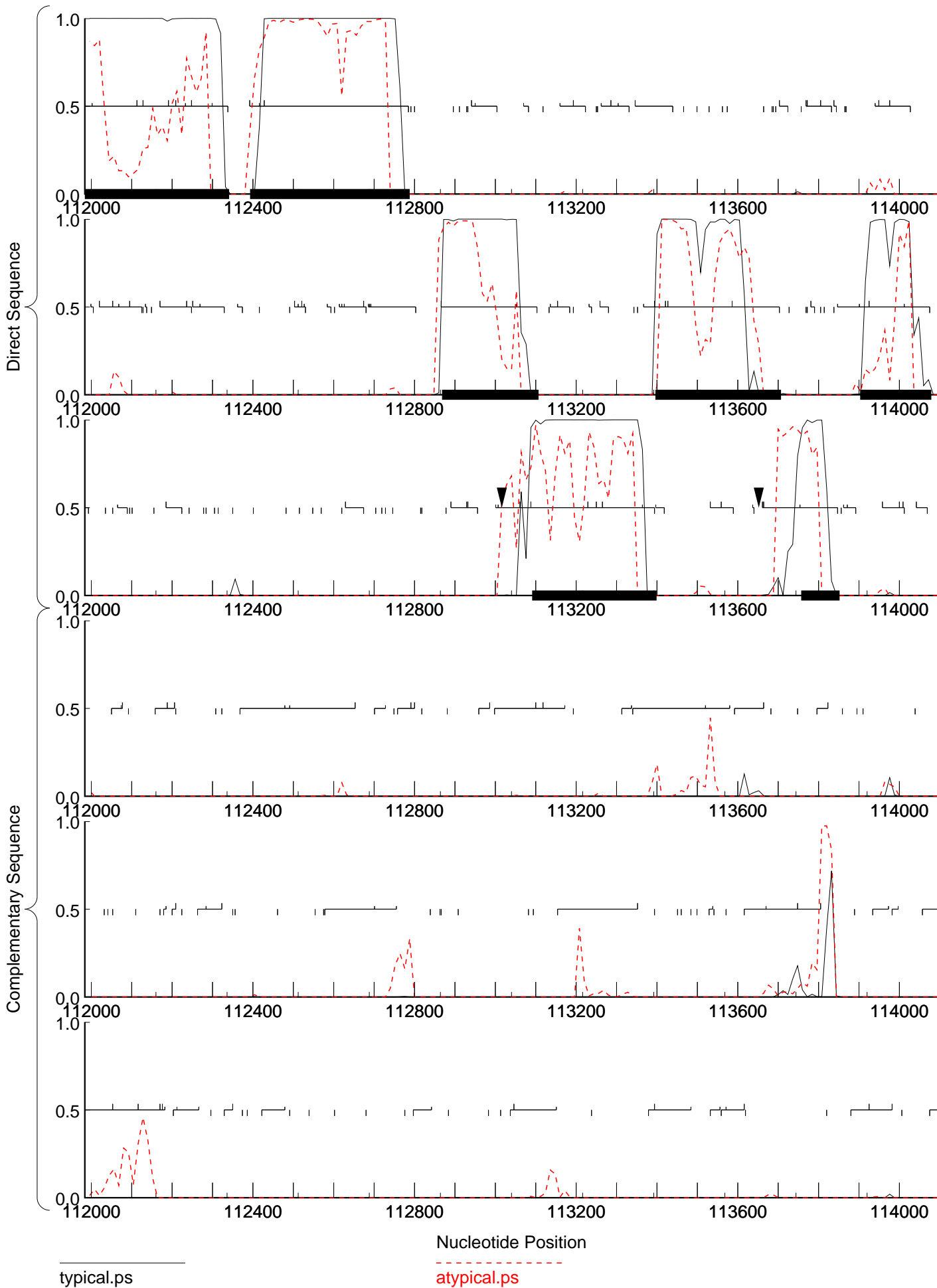
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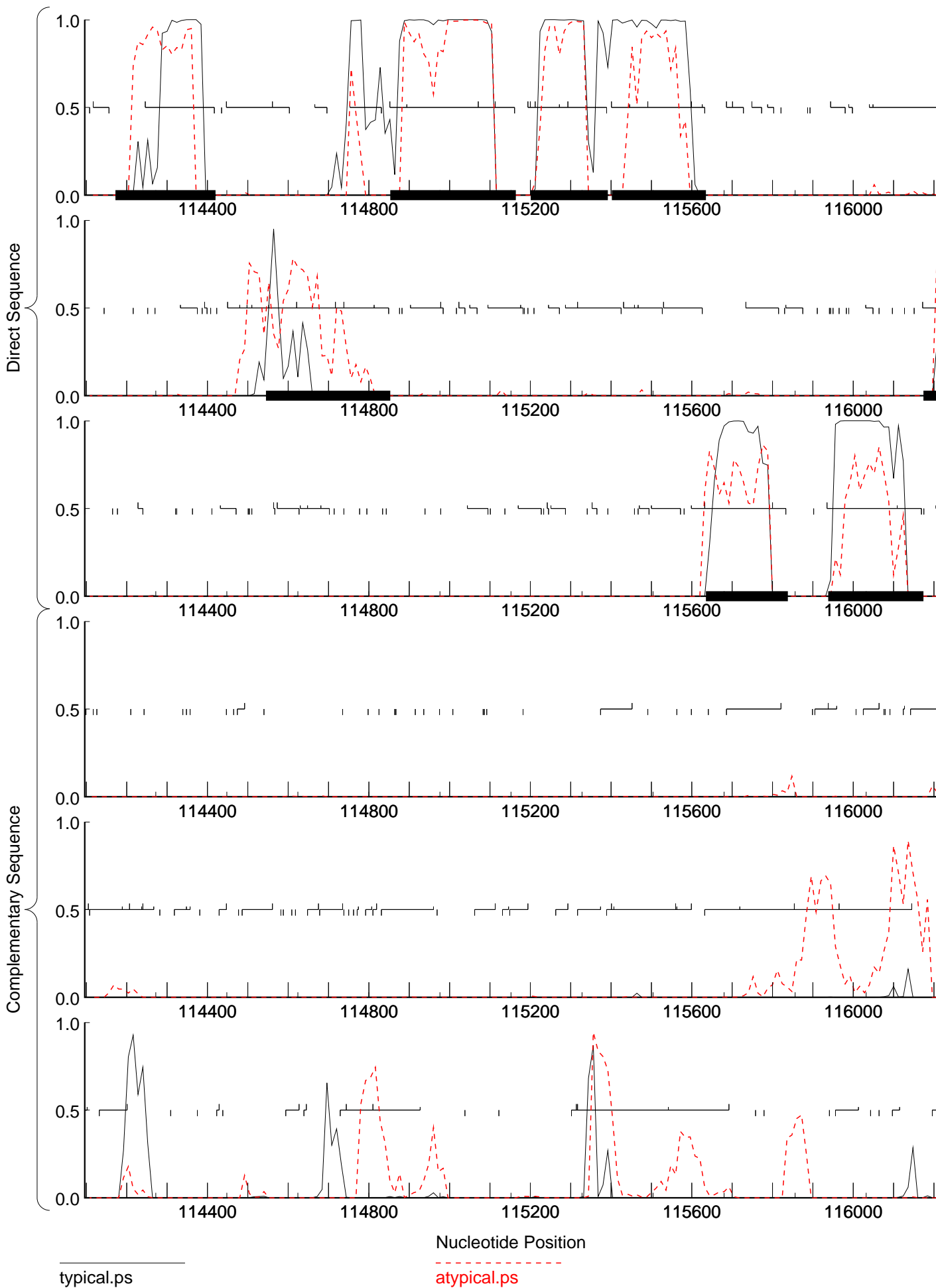




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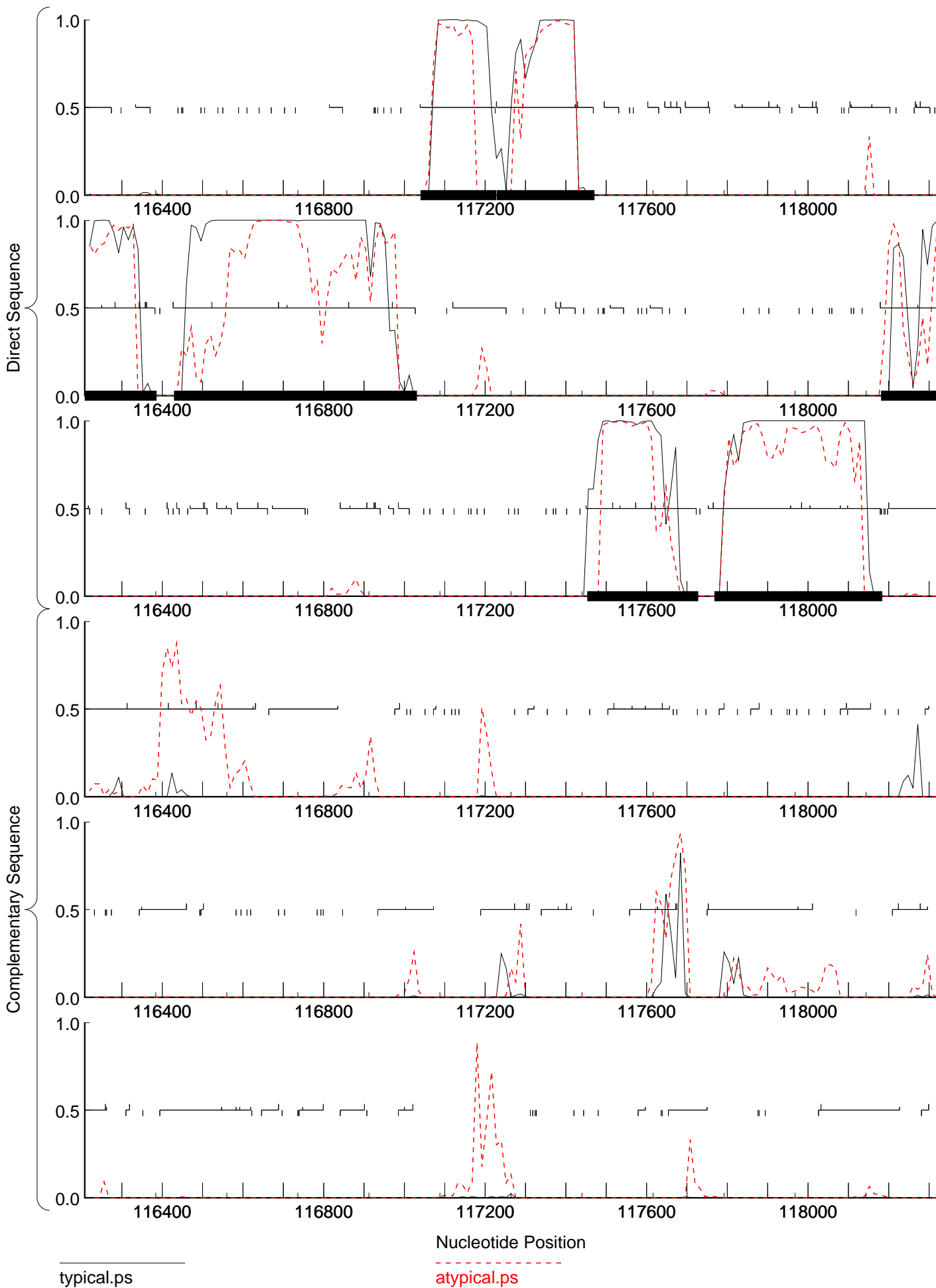
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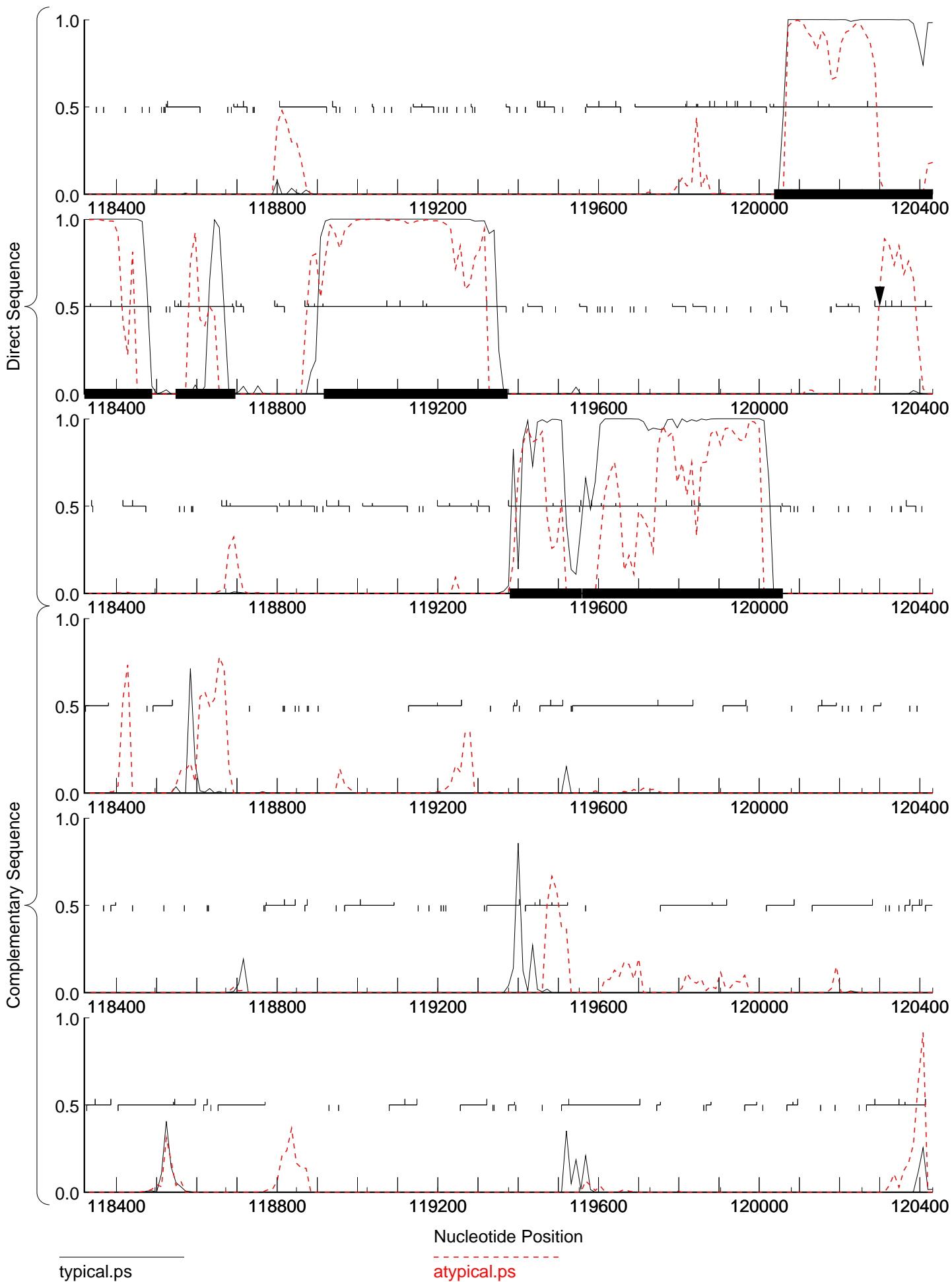
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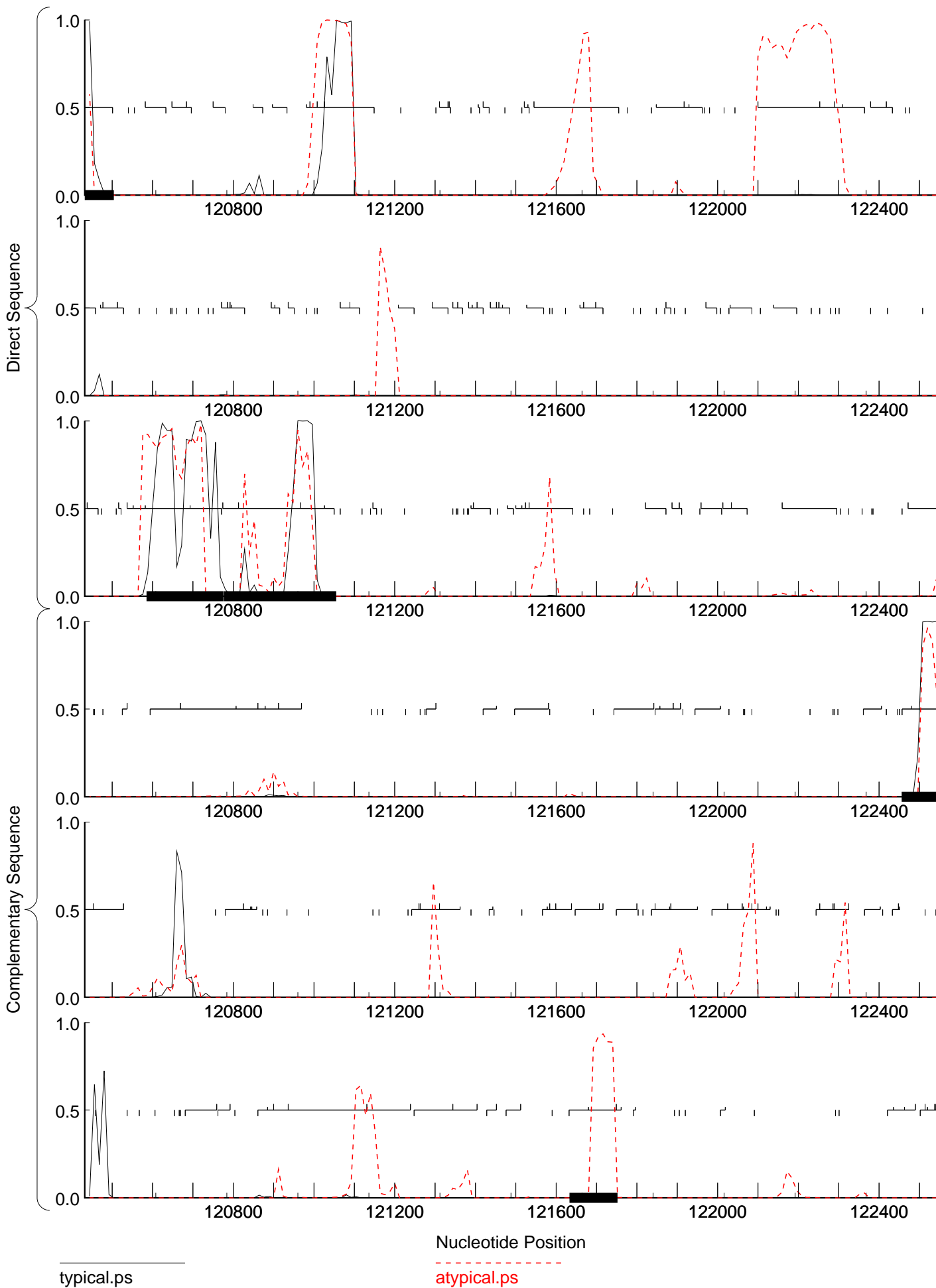
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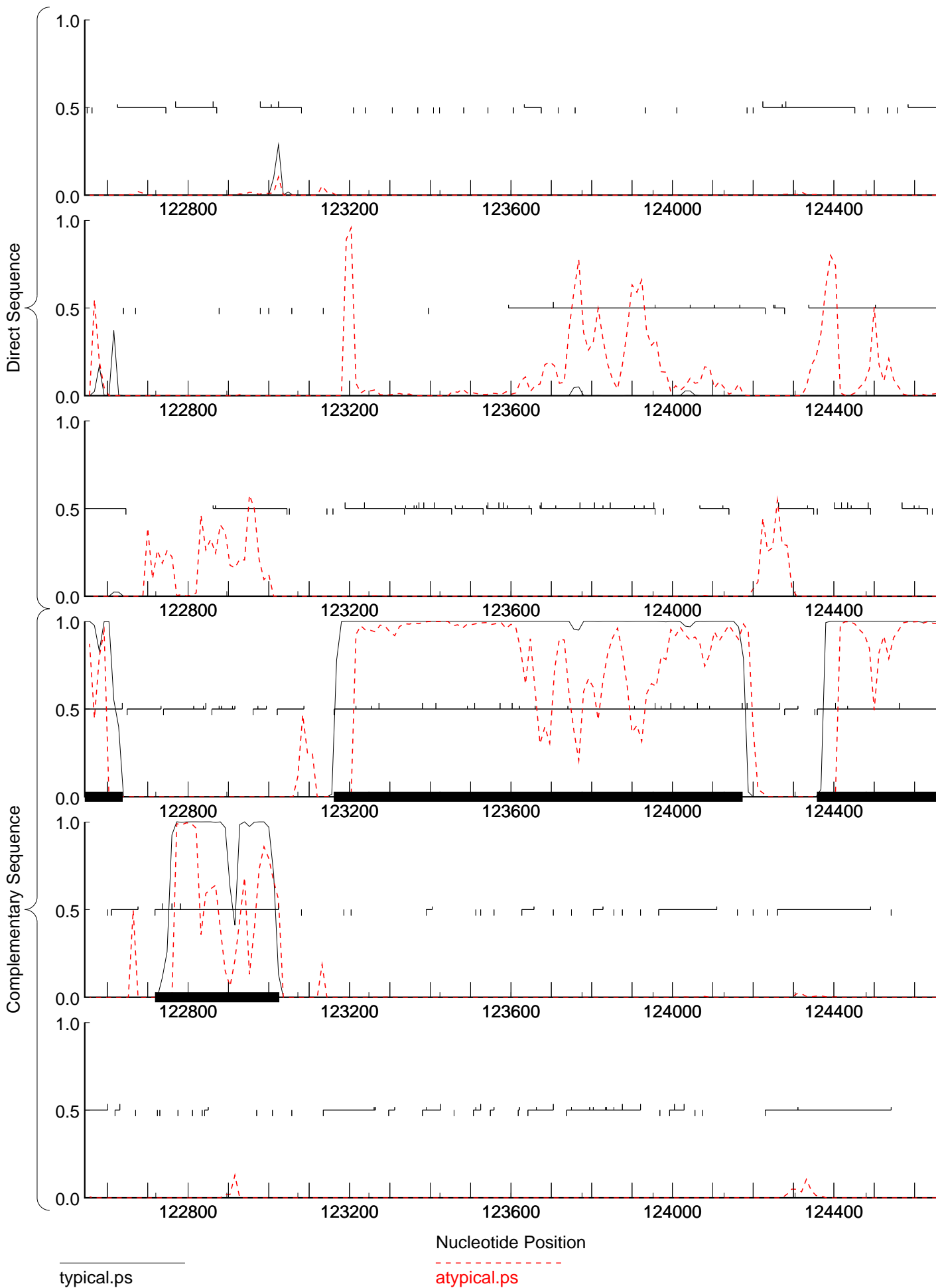


typical.ps

atypical.ps



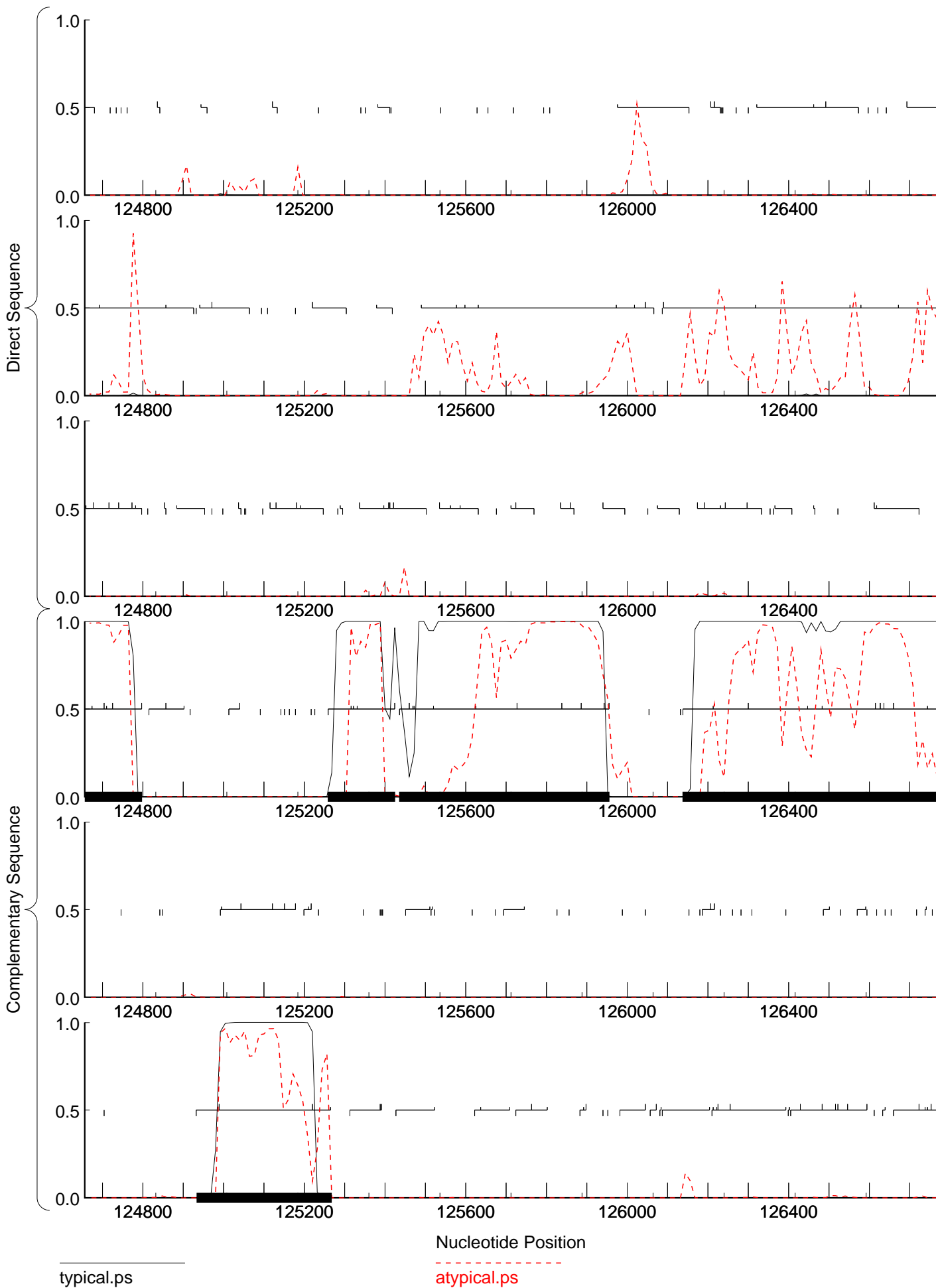


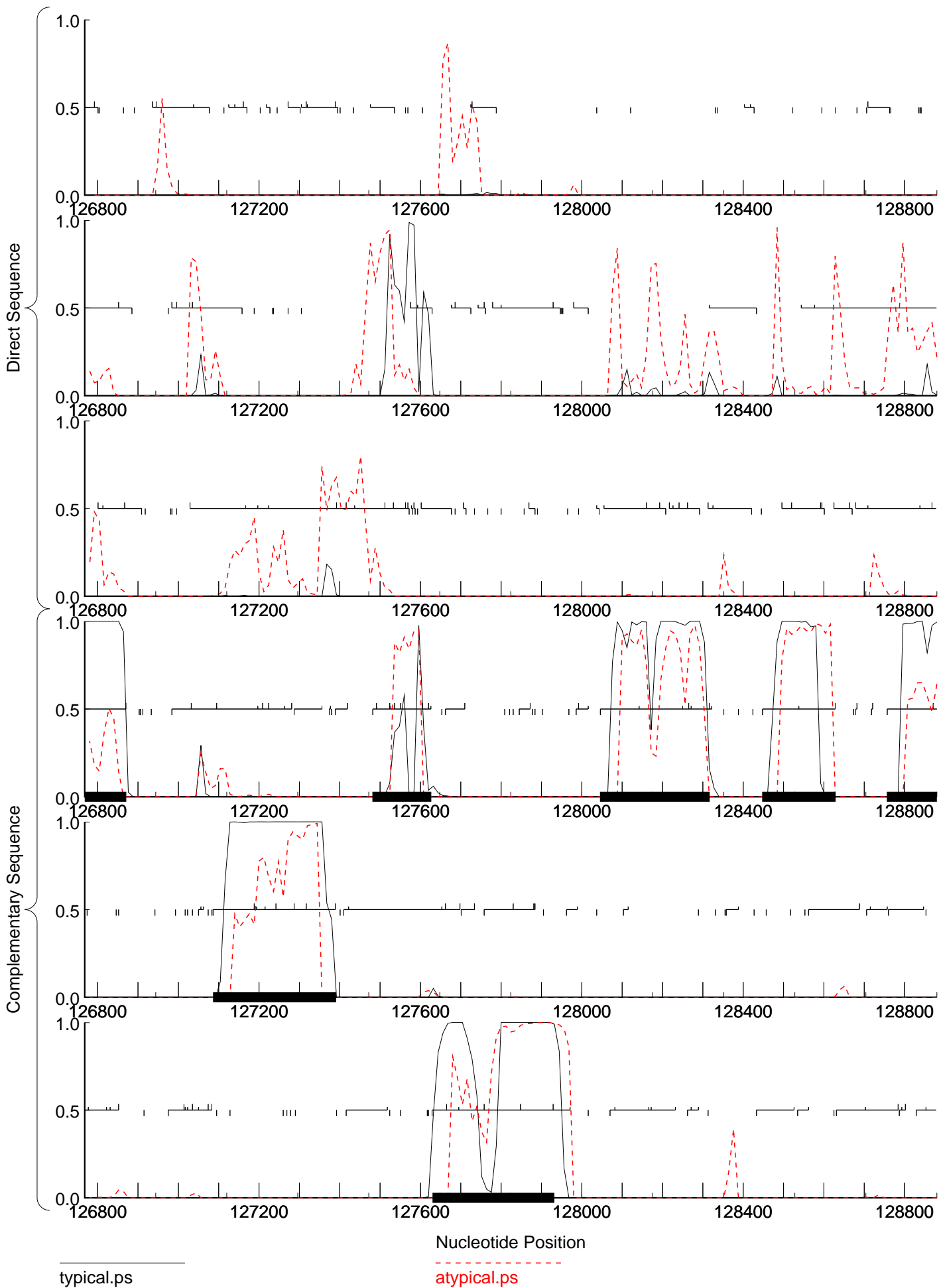


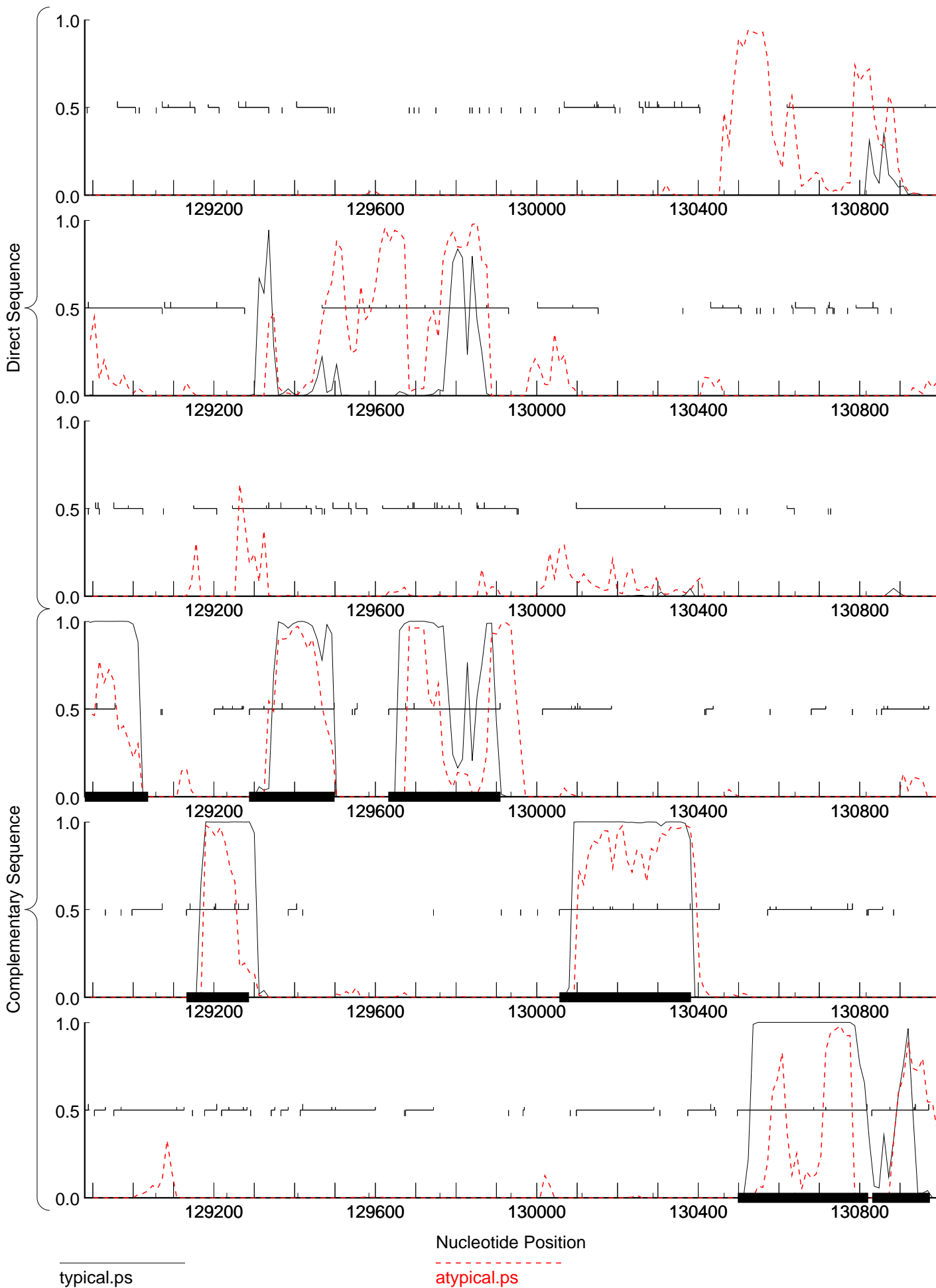
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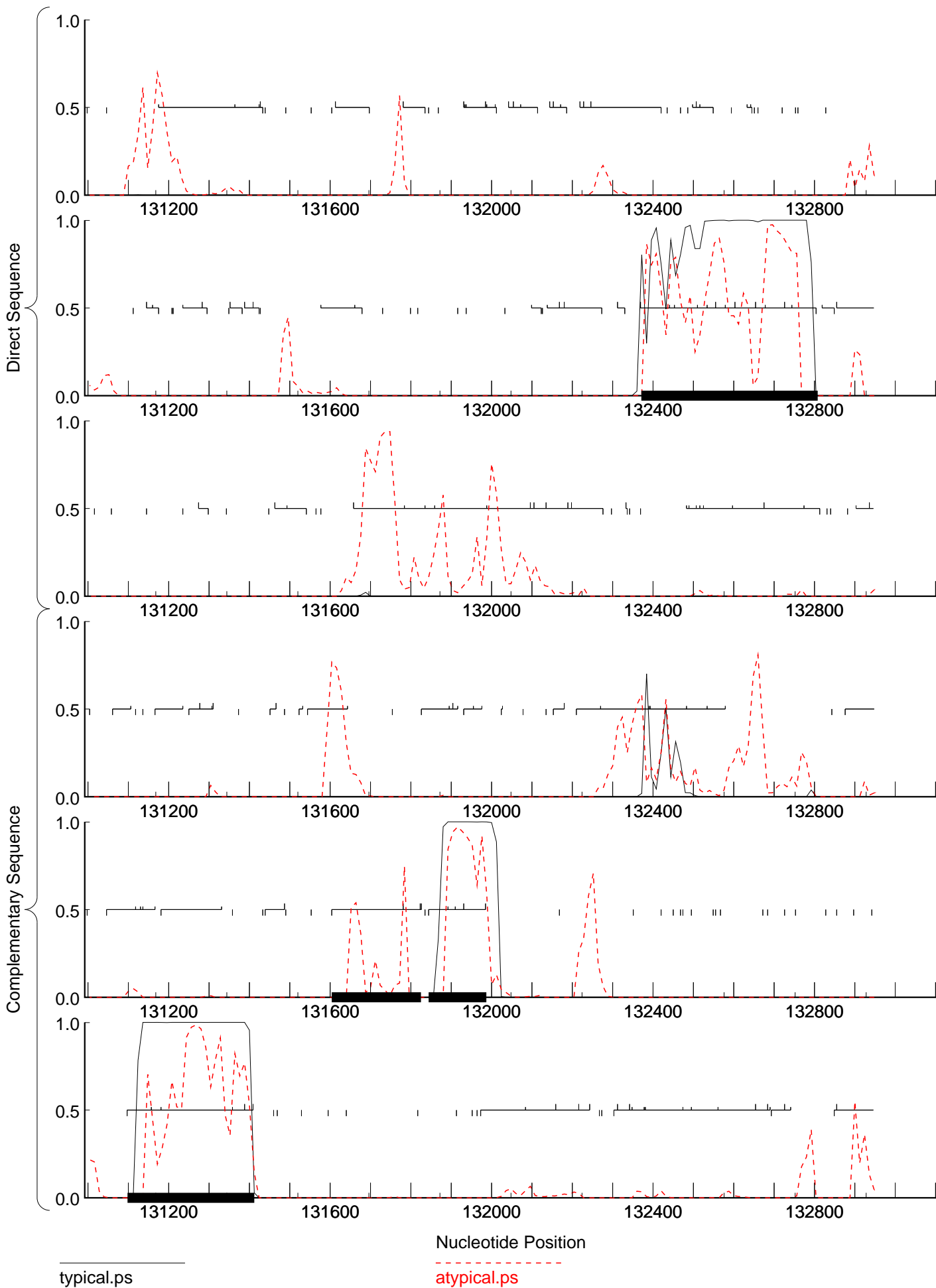
Nucleotide Position

atypical.ps









typical.ps

atypical.ps