

GeneMark

Version 2.5p (09.08.06)

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PROGRAM INFORMATION

Sequence : Mycobacterium phage BreSam8 complete sequence, 50843 bp including 10-base 3' overhang (CGGG
Analysis Date : 6/20/18 at 1:17:12
Pages : 26
Sequence Length : 50843 bp
GC Content : 64.02%

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,

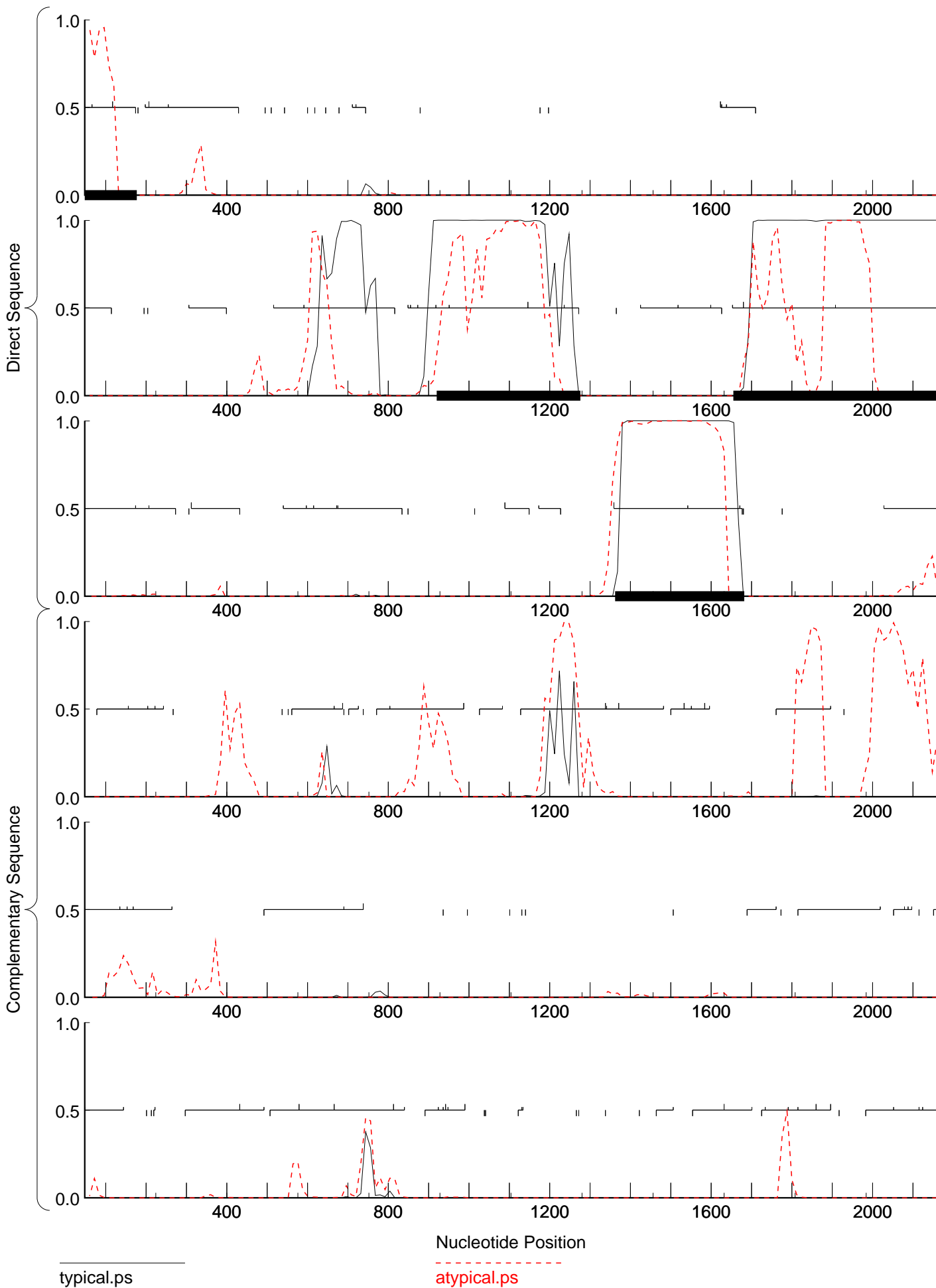
MATRIX INFORMATION

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

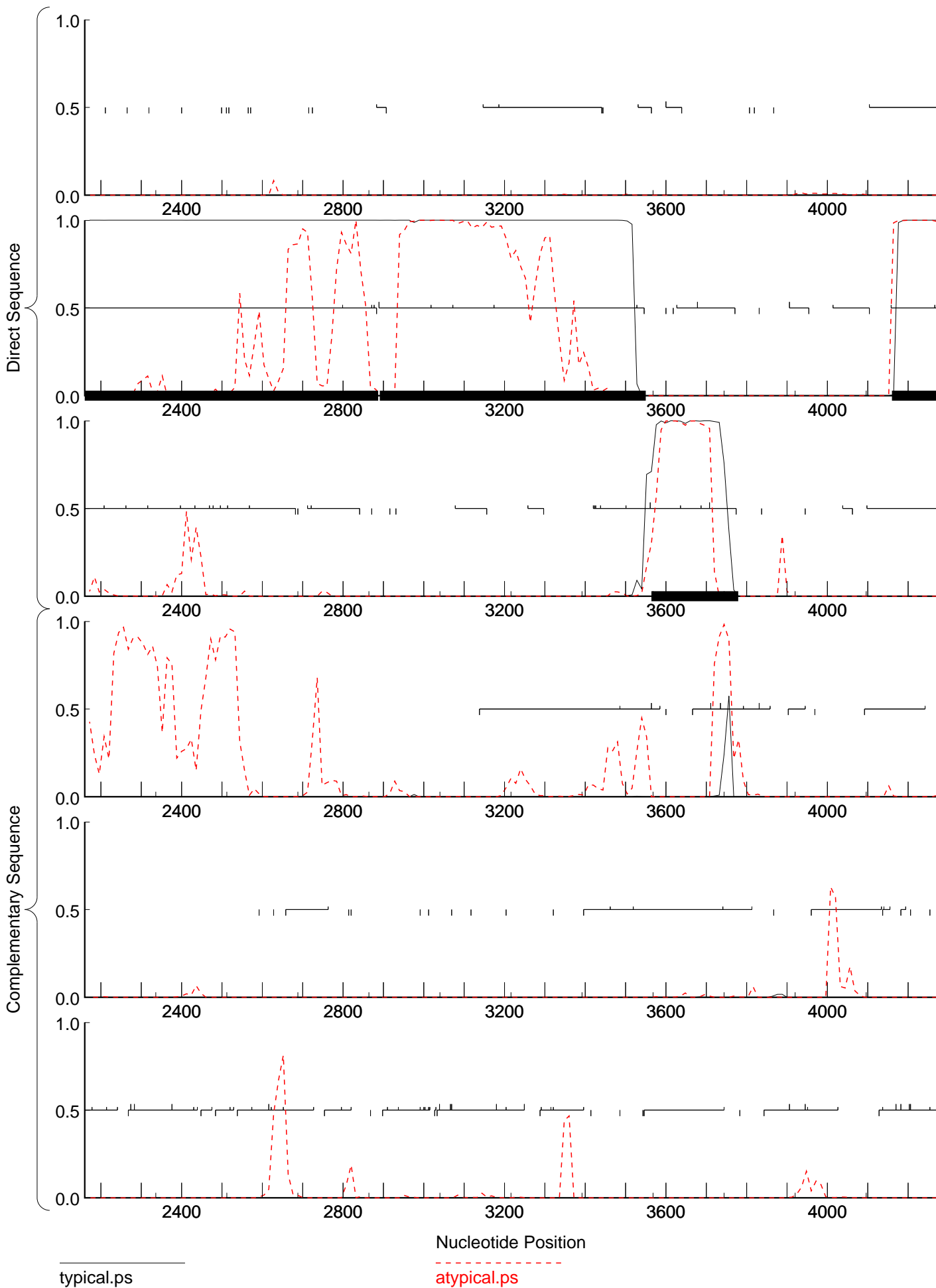
Training set derived by GeneMarkS, 4.30 October 2014
Wed Jun 20 01:17:12 2018



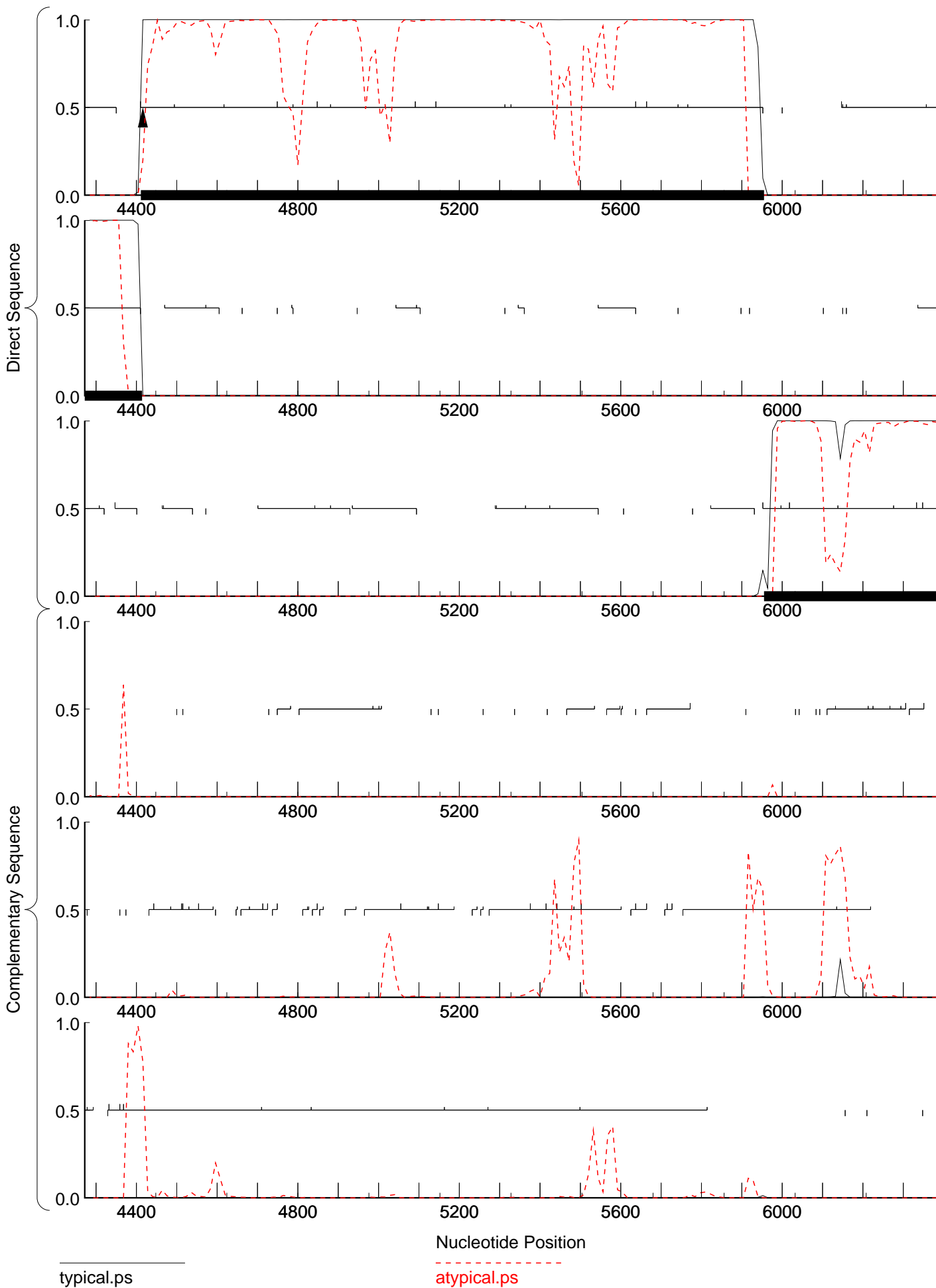
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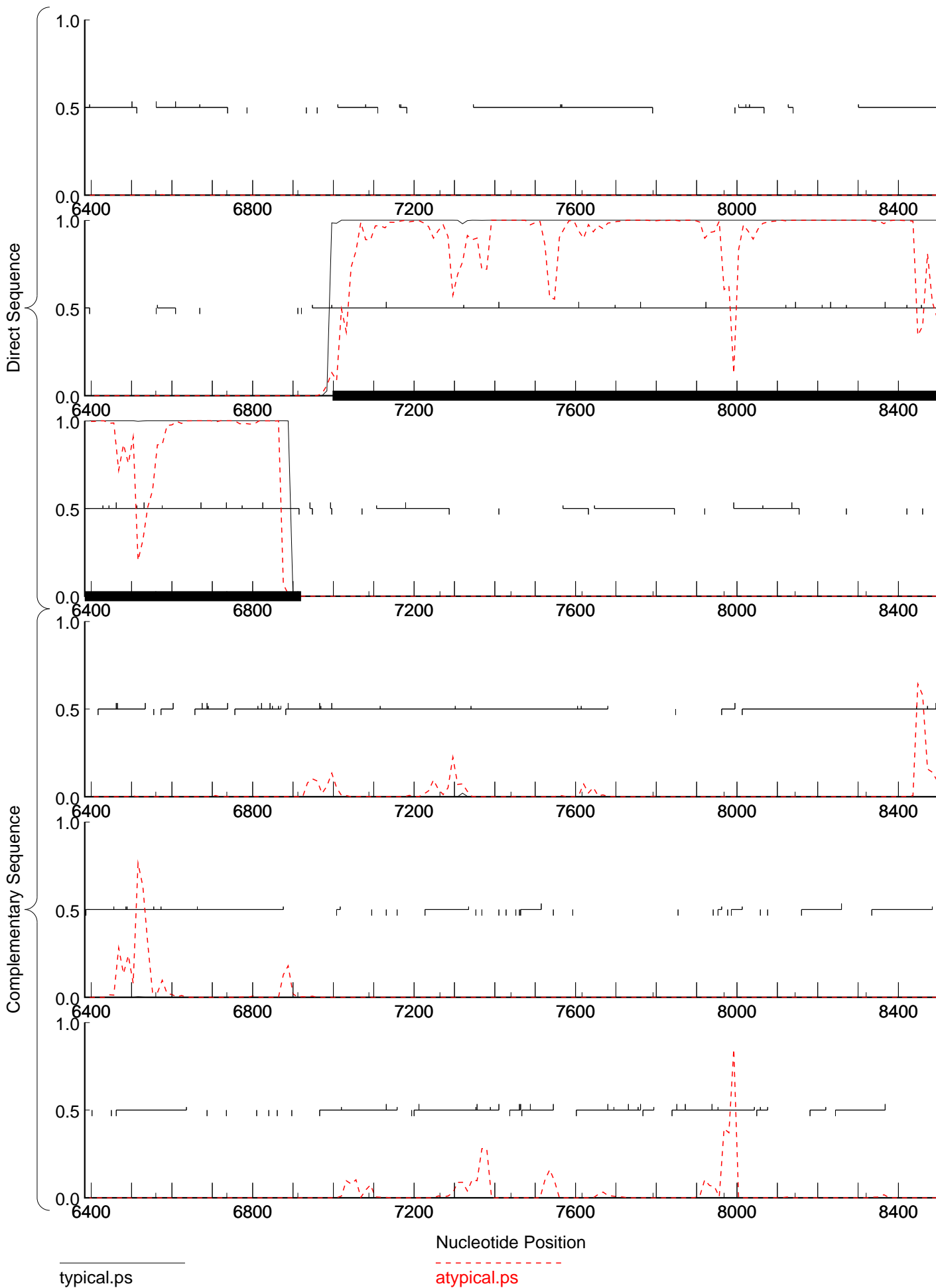
atypical.ps

8 complete sequence, 50843 bp including 10-base 3' overhang (CGGGTGGTAA), Cluster A3, Order 4, Window 96, Step 12, 3/26
8 complete sequence, 50843 bp including 10-base 3' overhang (CGGGTGGTAA), Cluster A3, Order 2, Window 96, Step 12, 3/26

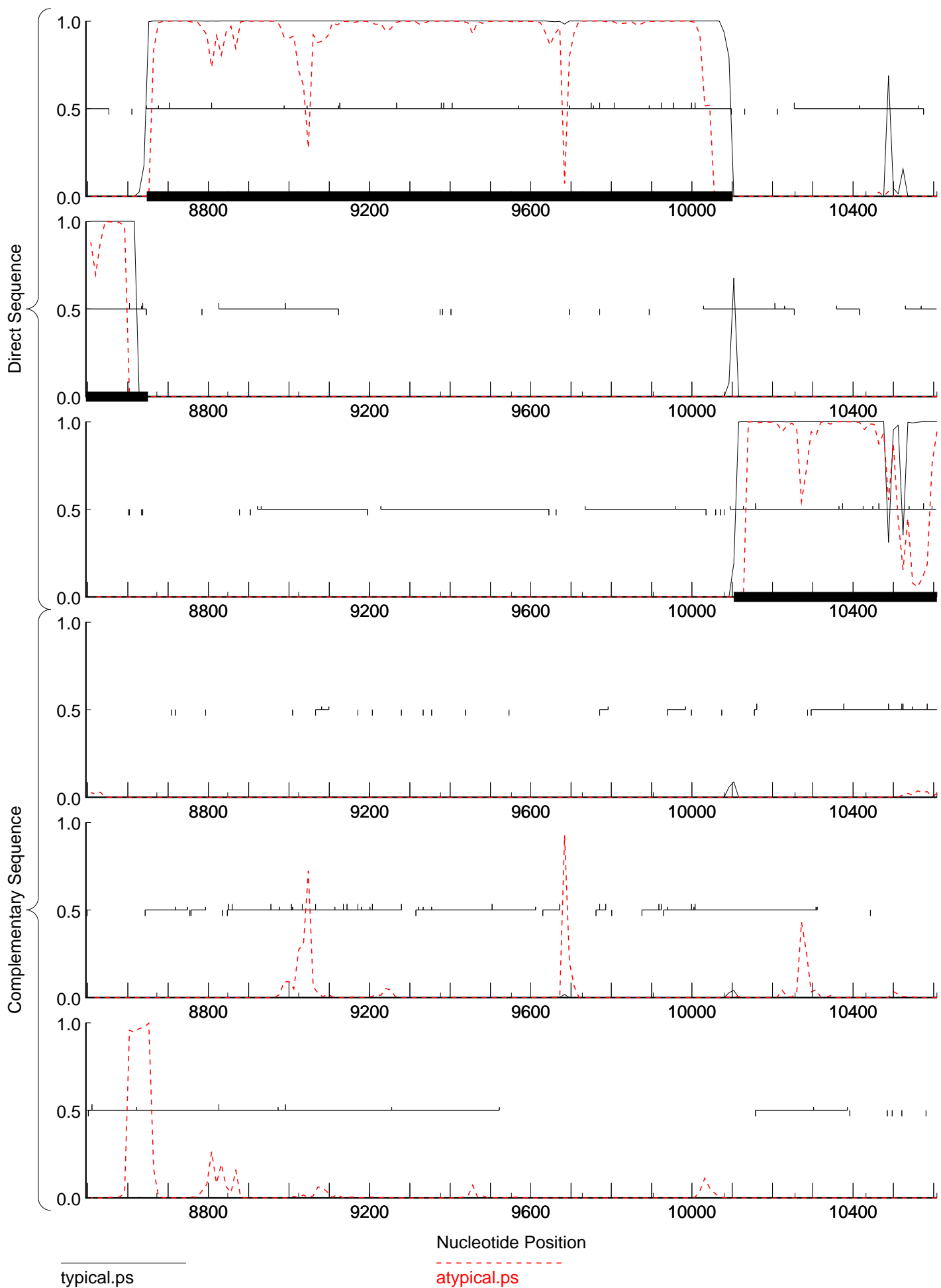


8 complete sequence, 50843 bp including 10-base 3' overhang (CGGGTGGTAA), Cluster A3, Order 4, Window 96, Step 12, 4/26
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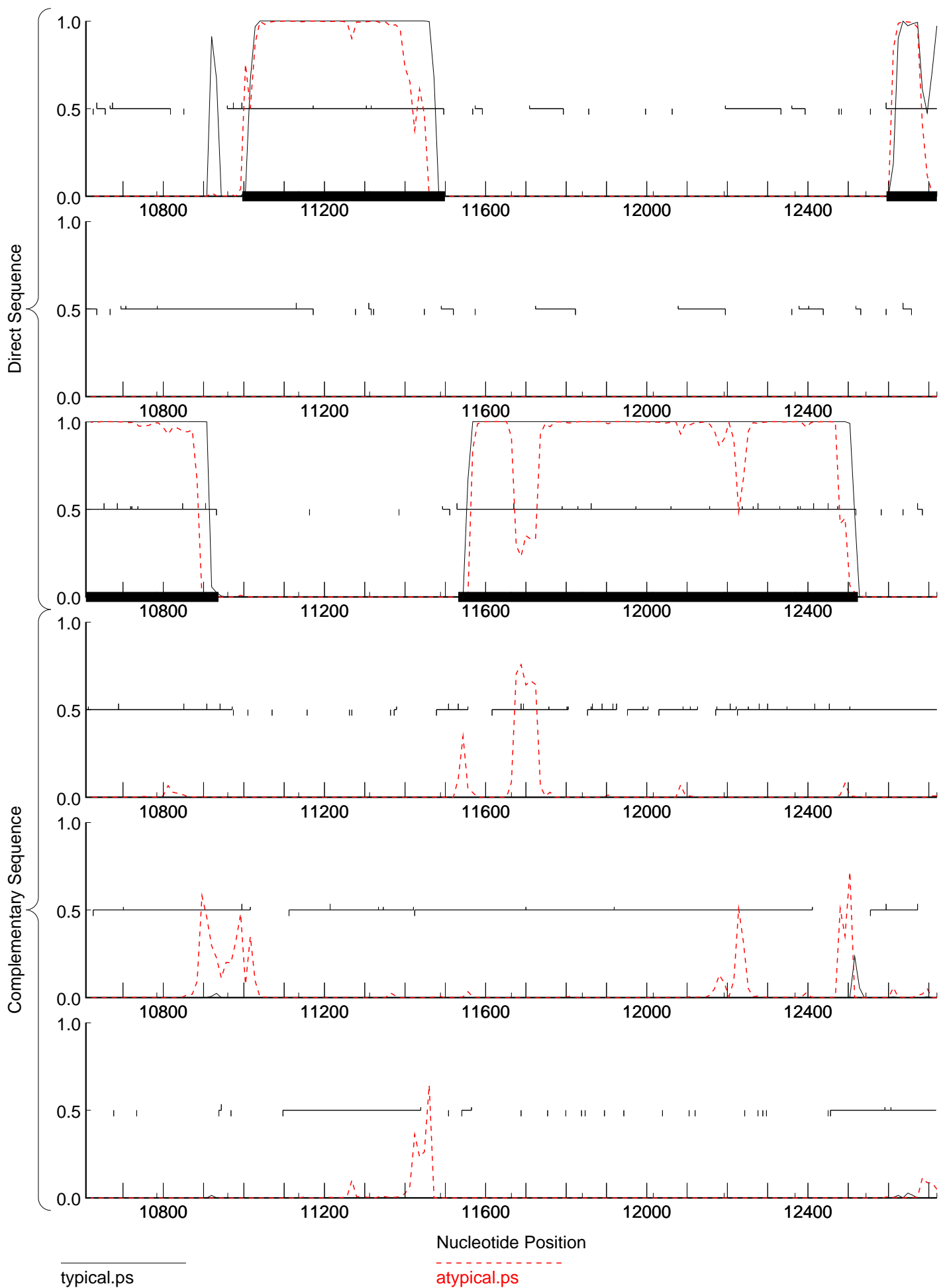




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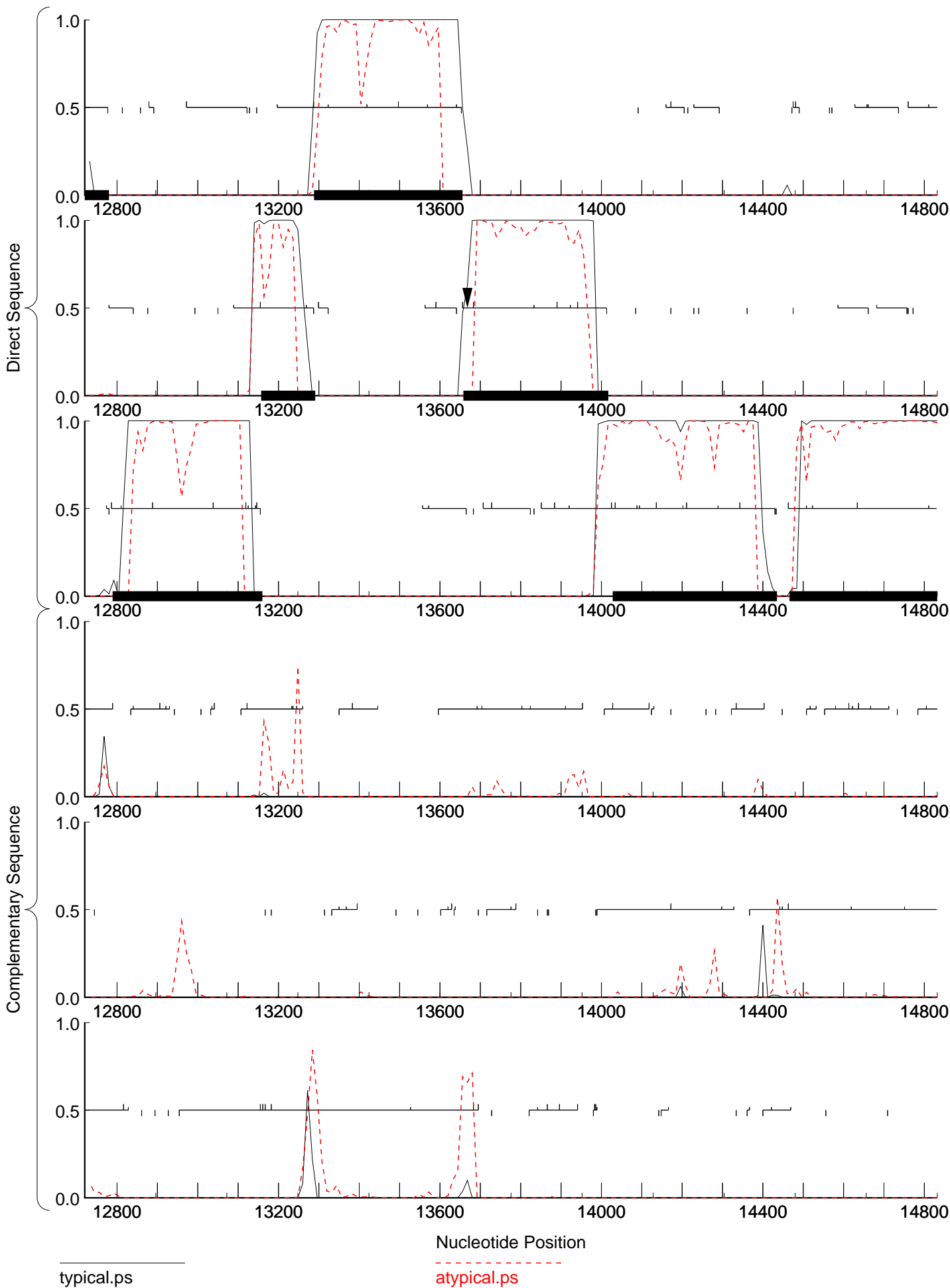


8 complete sequence, 50843 bp including 10-base 3' overhang (CGGGTGGTAA), Cluster A3, Order 4, Window 96, Step 12, 7/26
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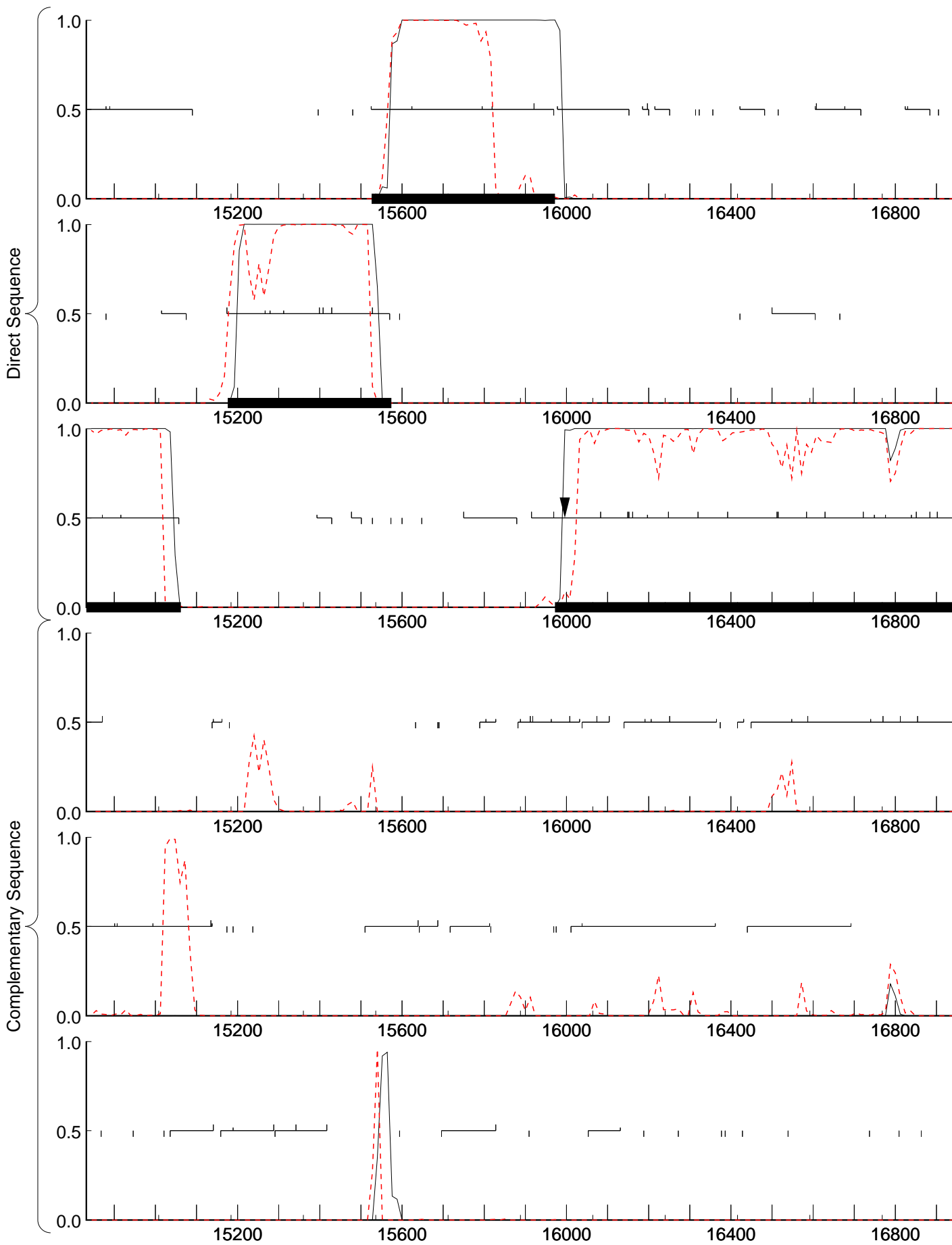


typical.ps

atypical.ps

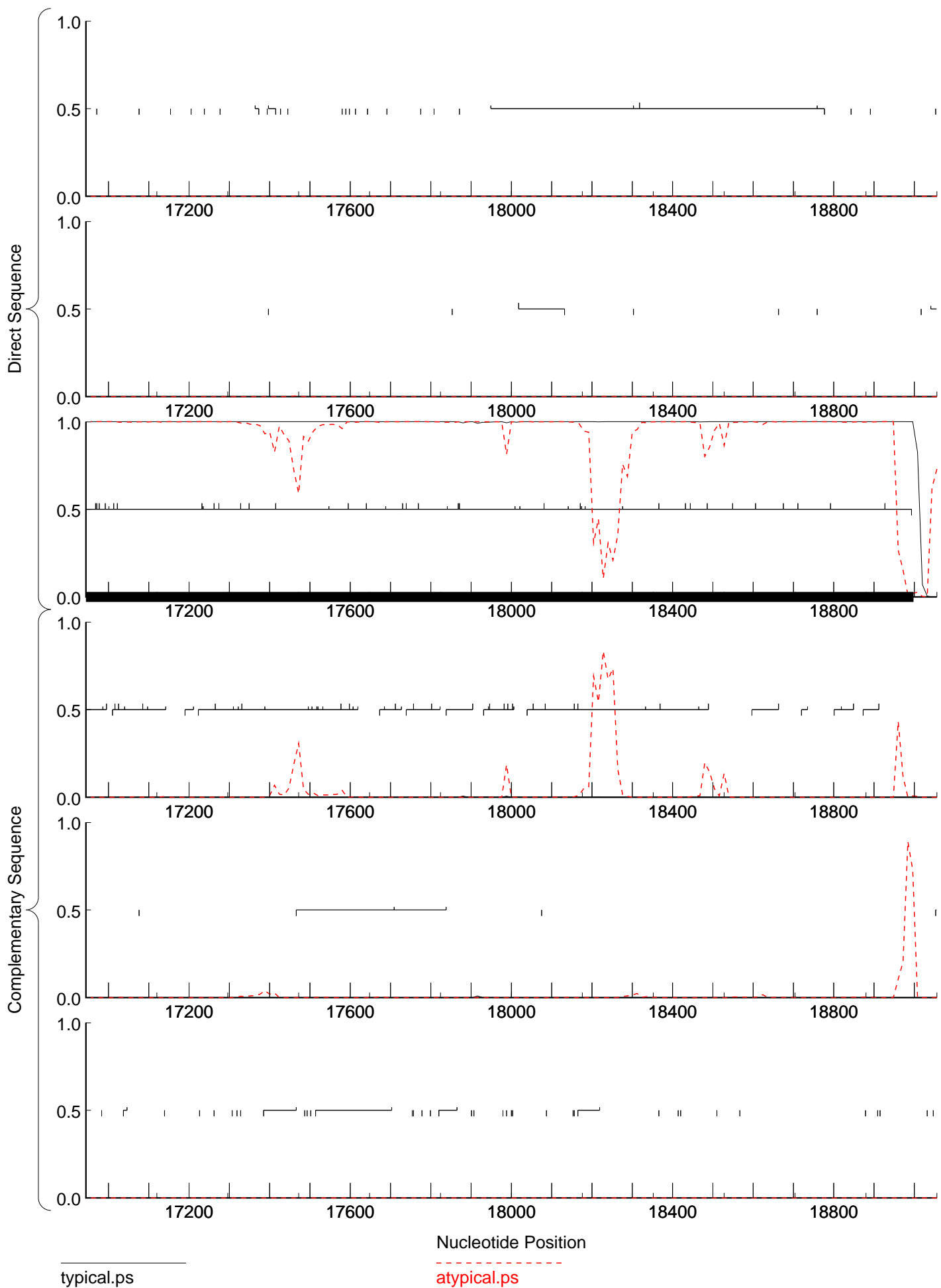


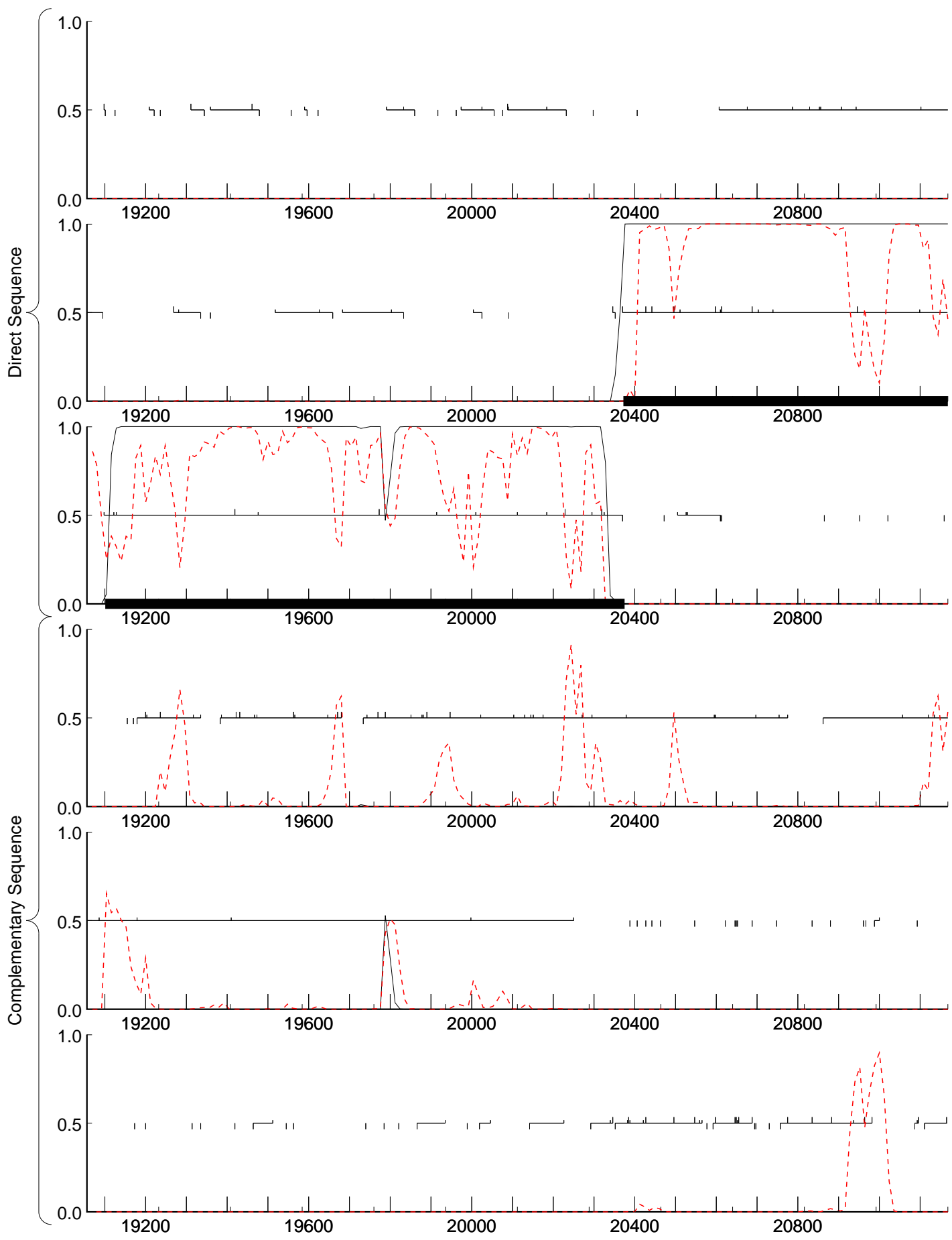
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typical.ps

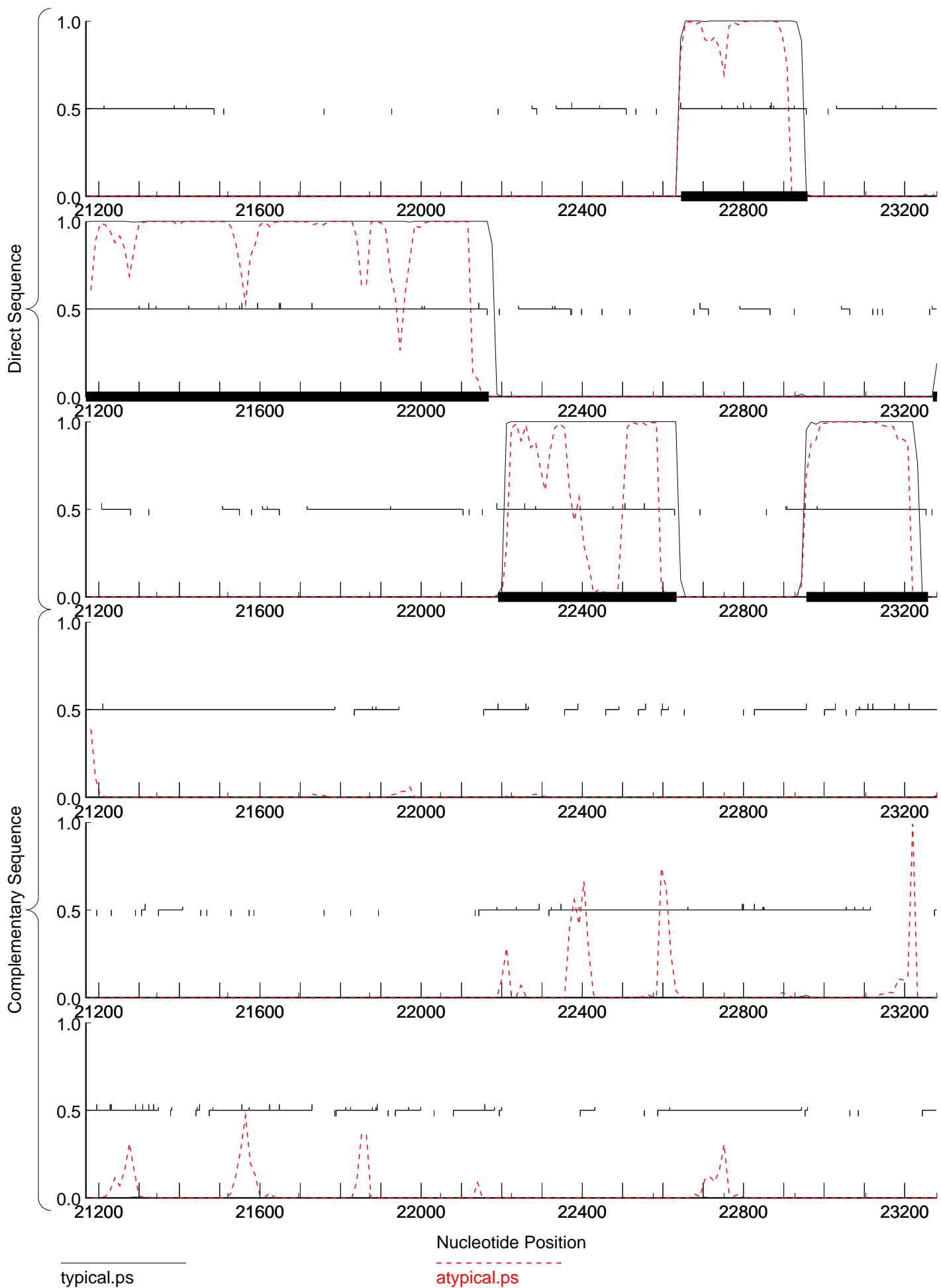
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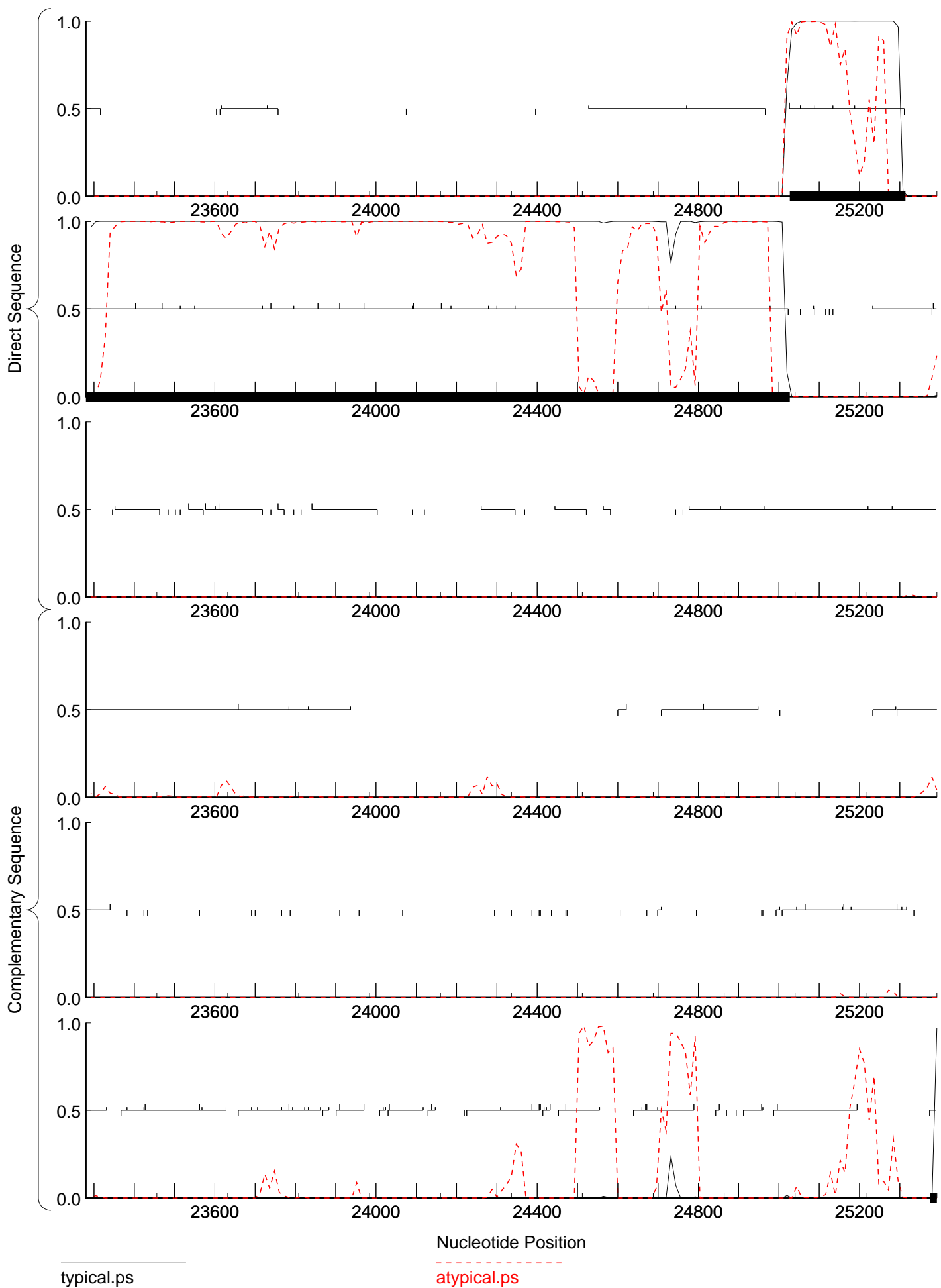
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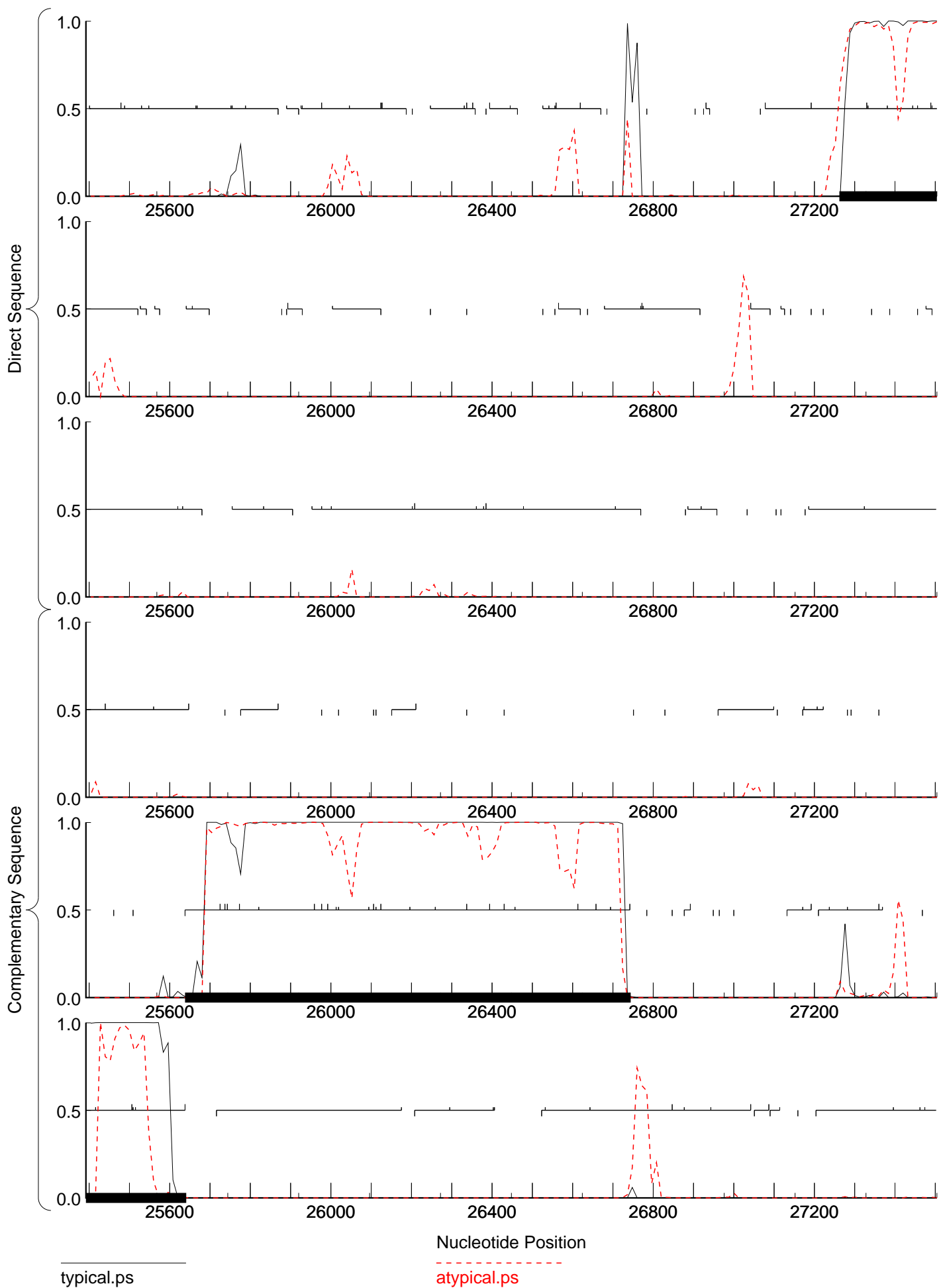
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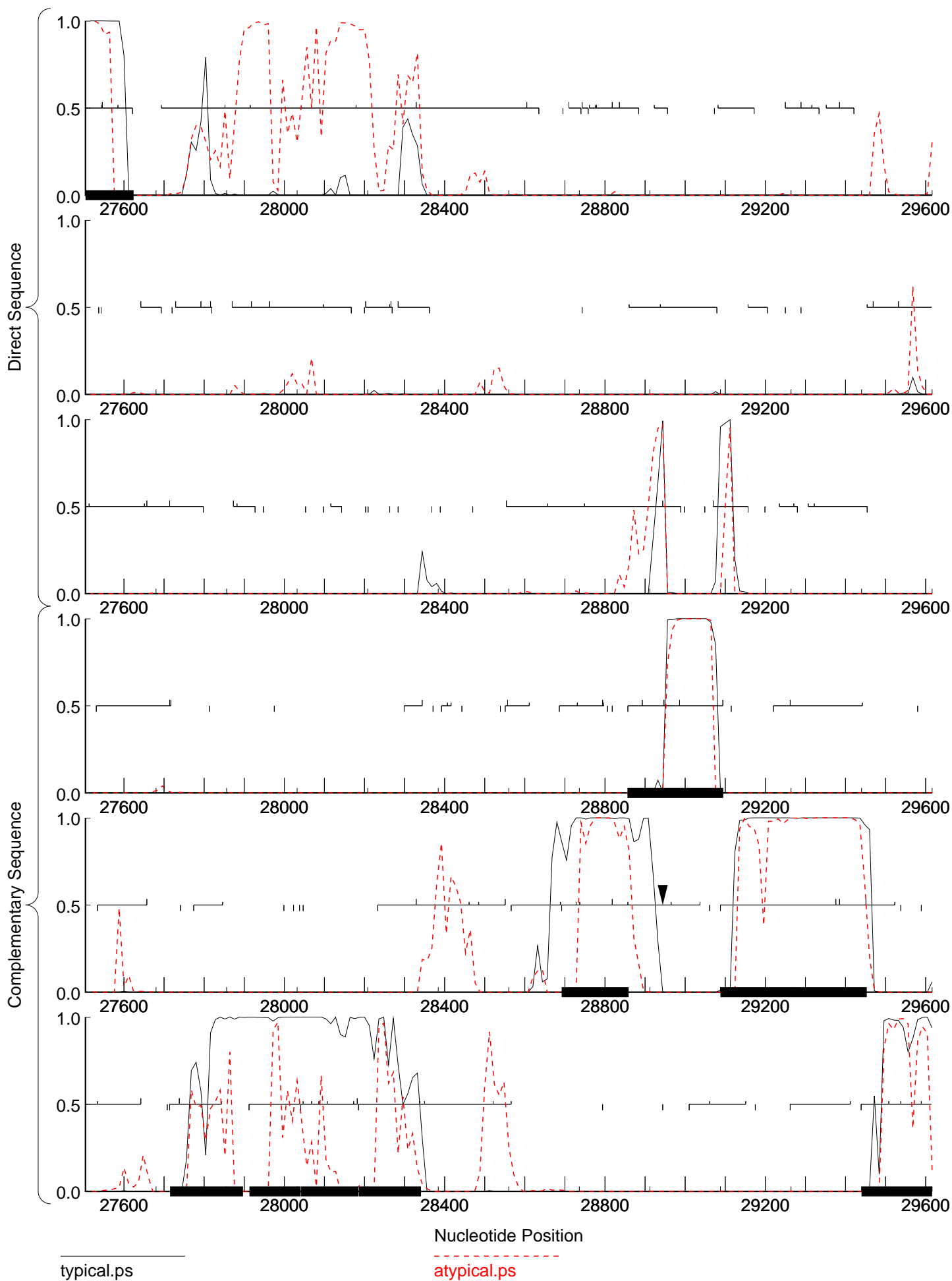


typical.ps

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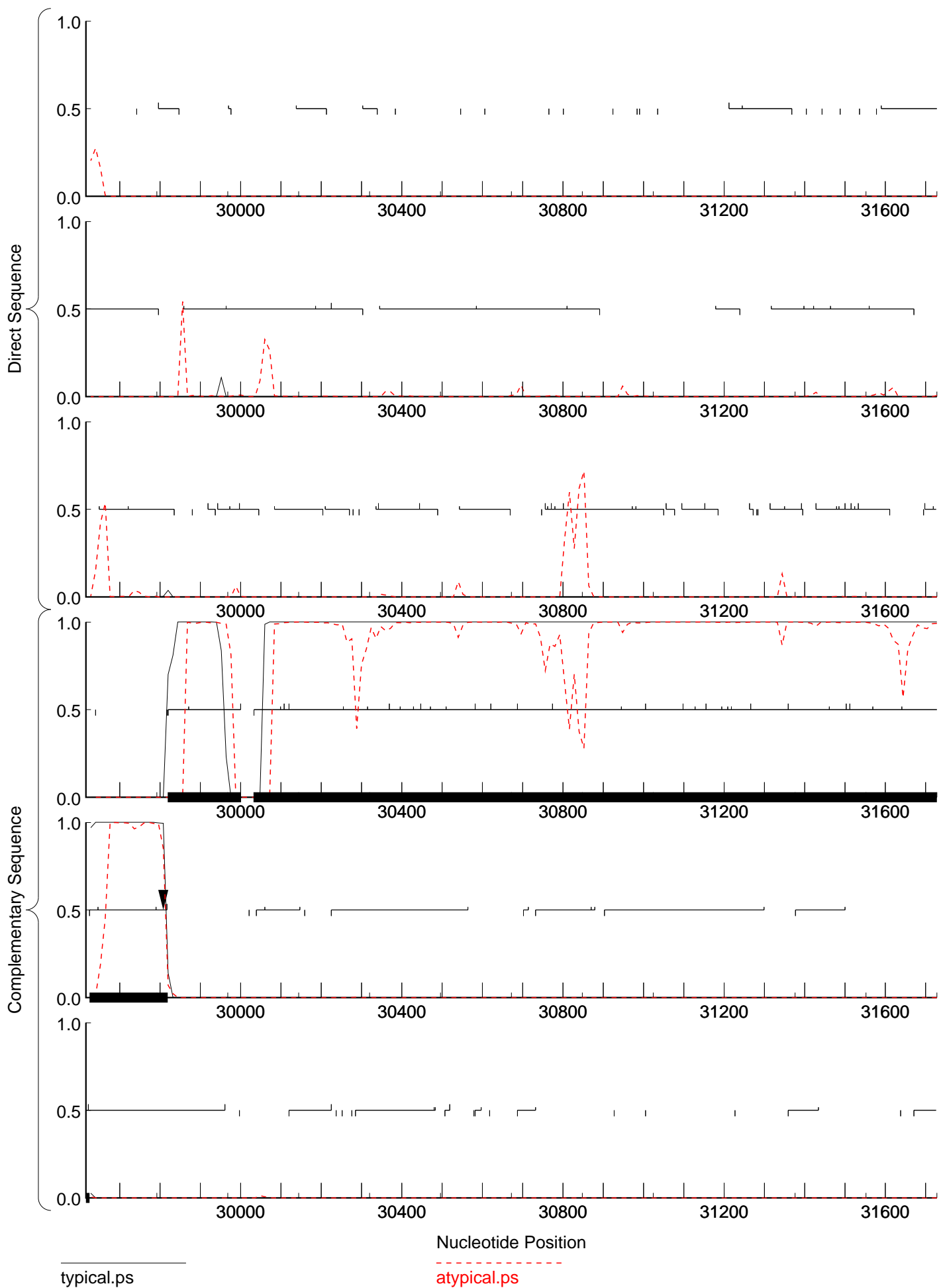


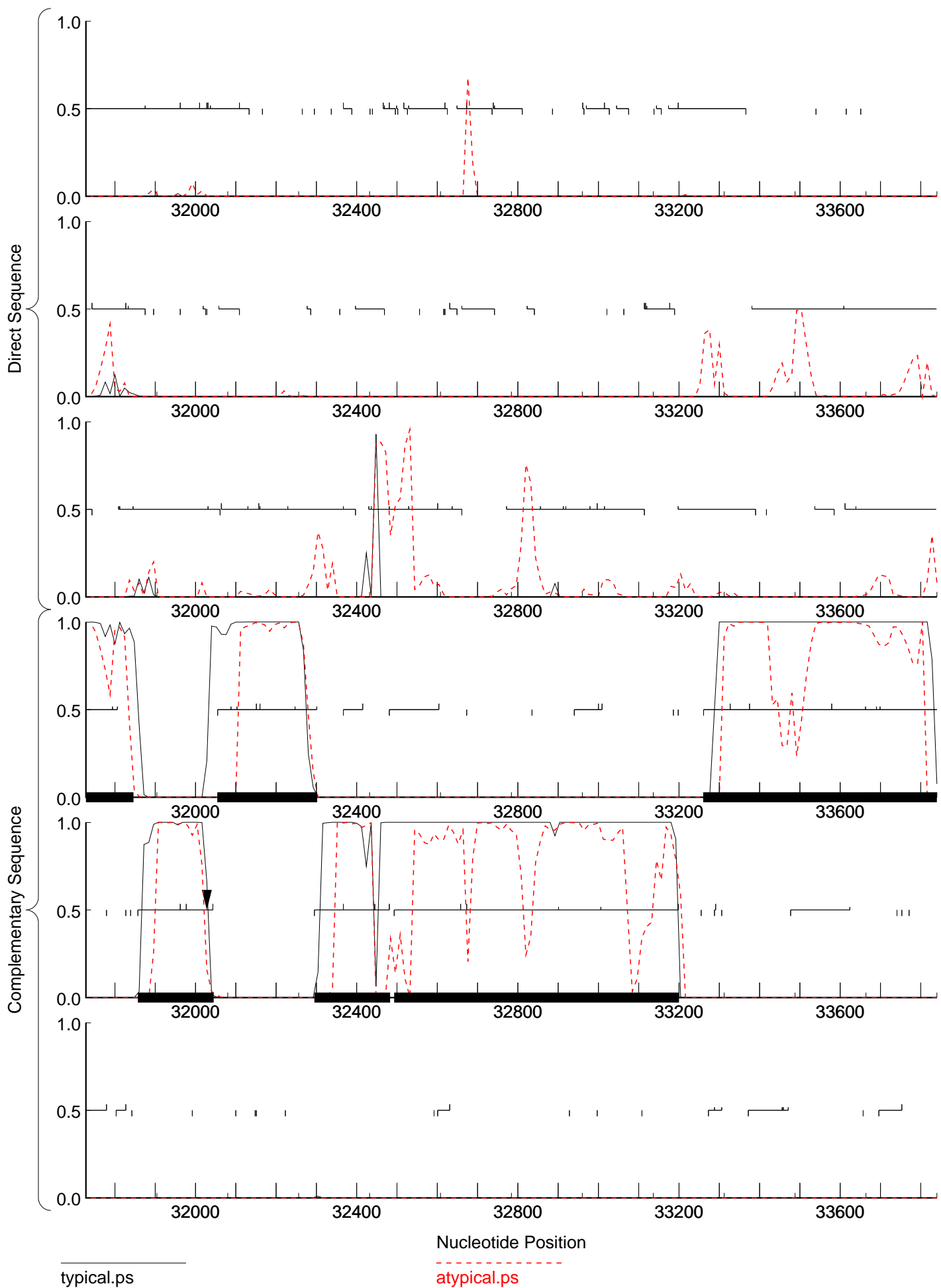




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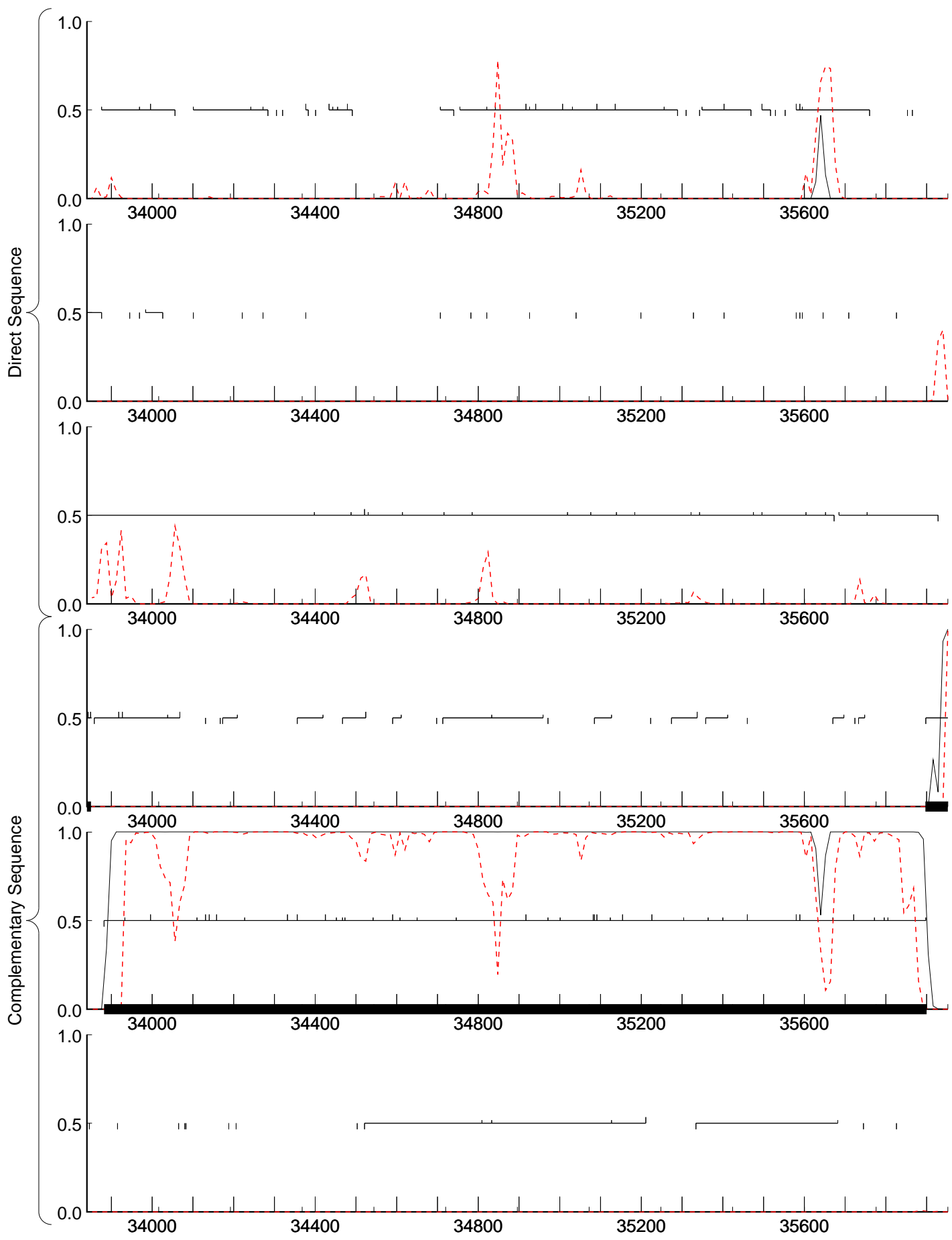
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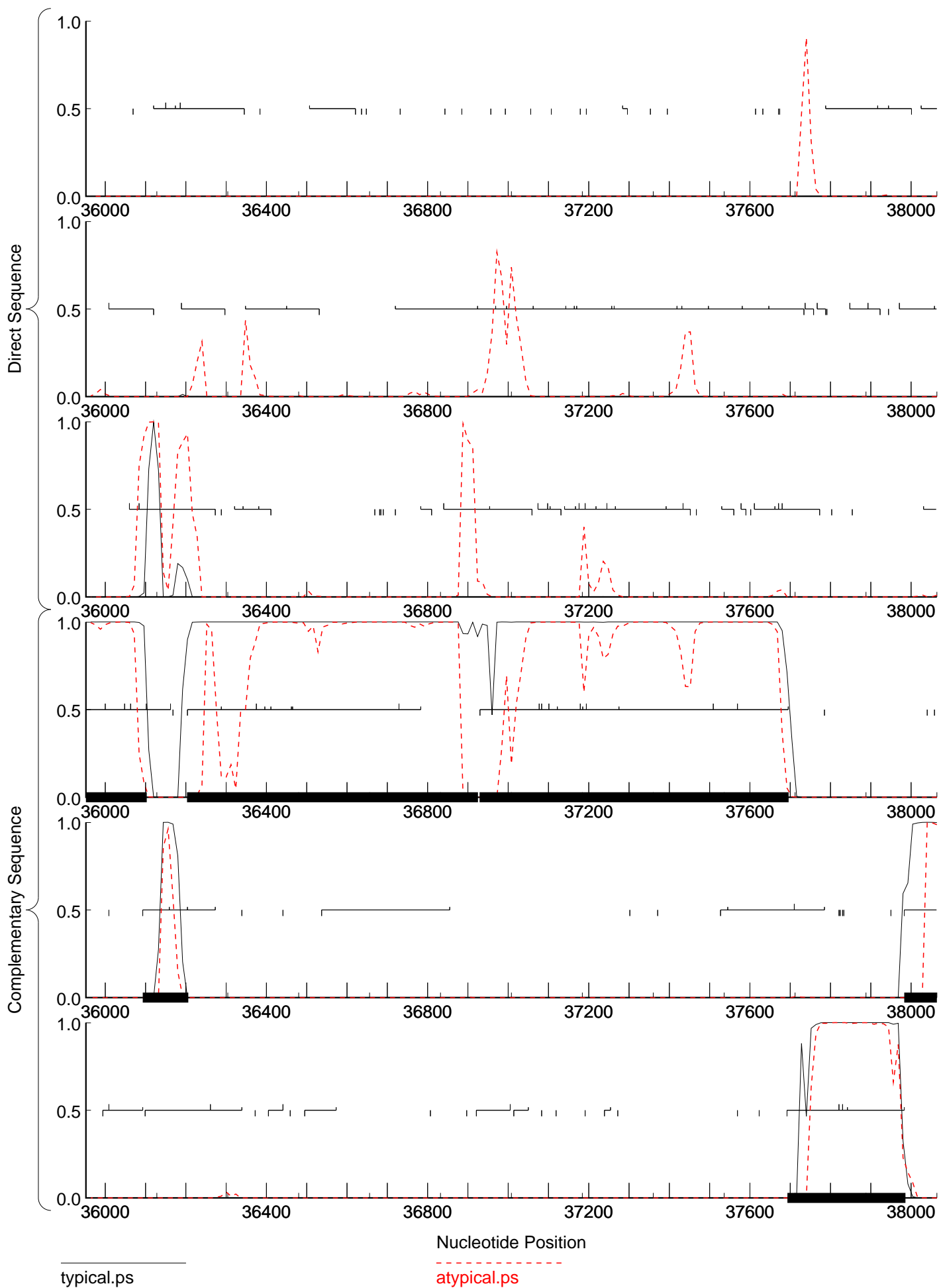
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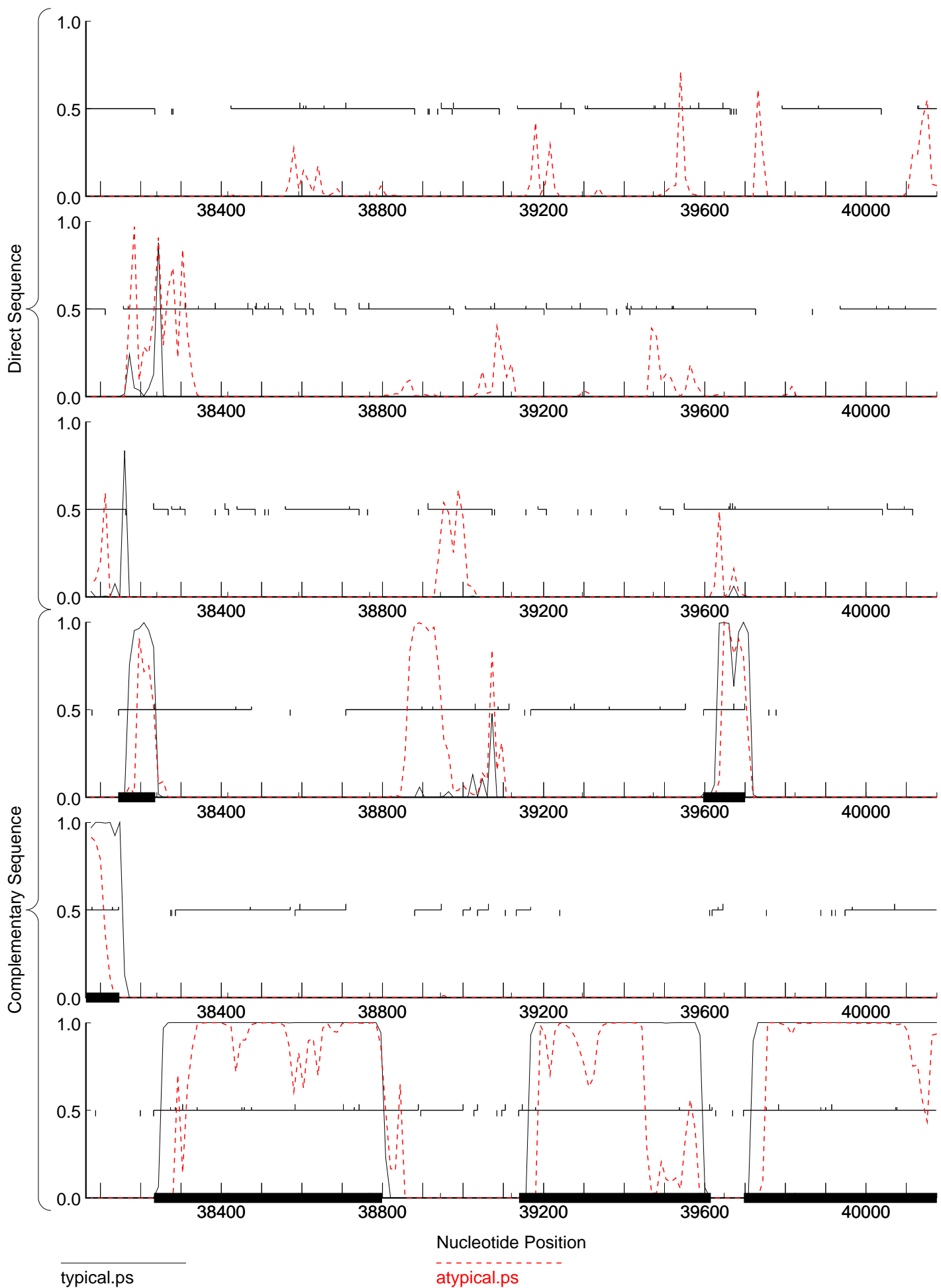
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typical.ps

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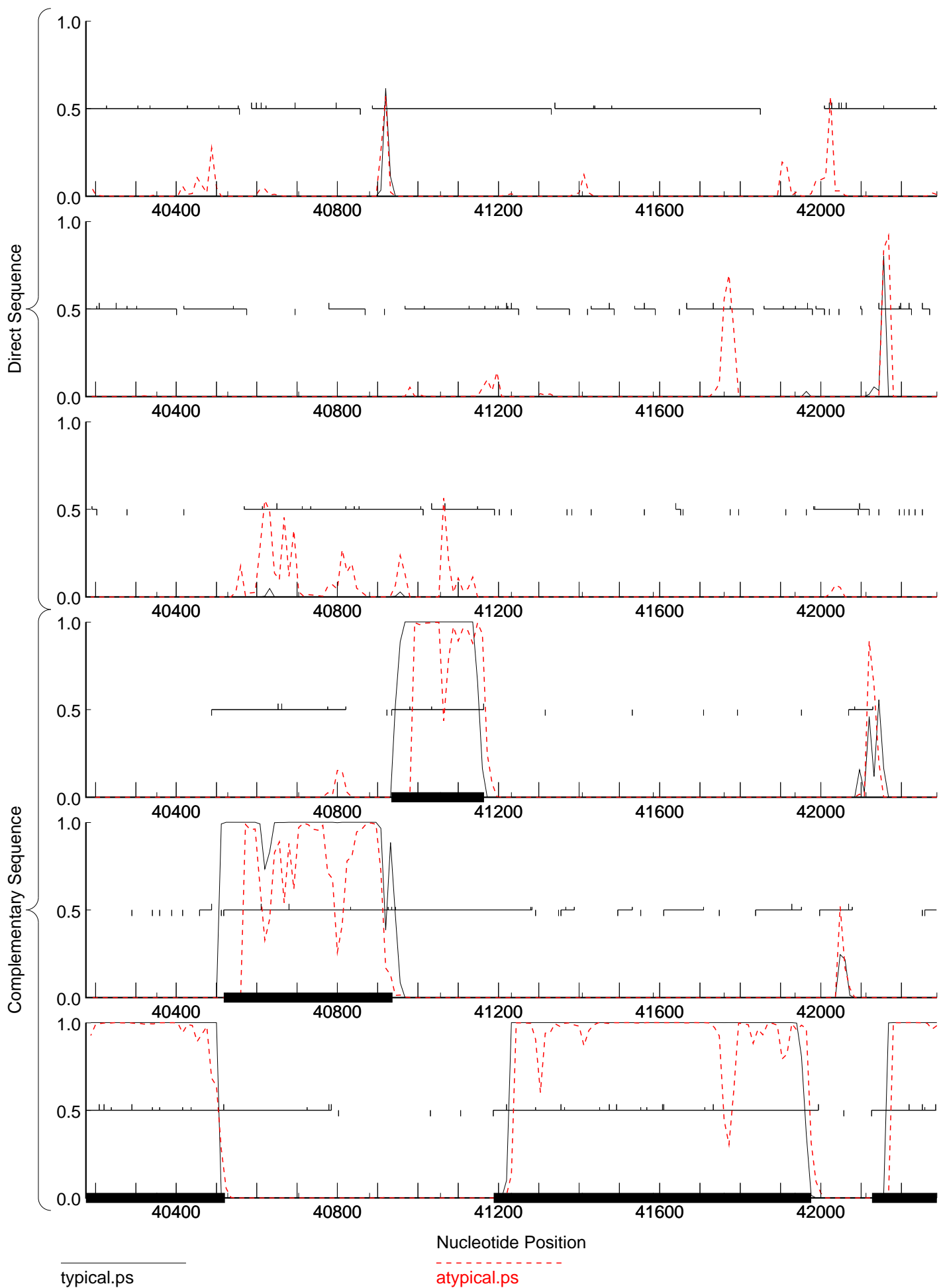


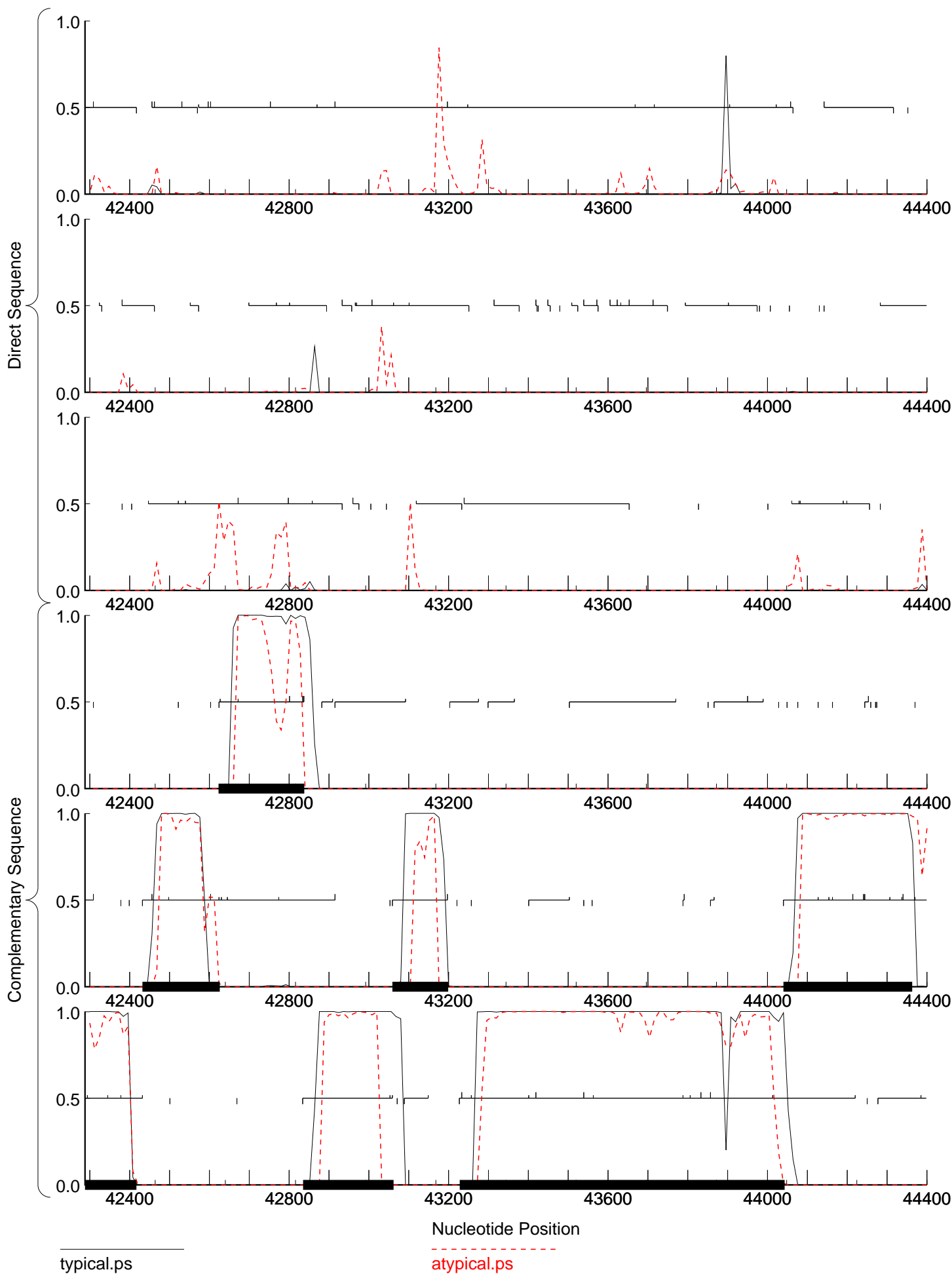


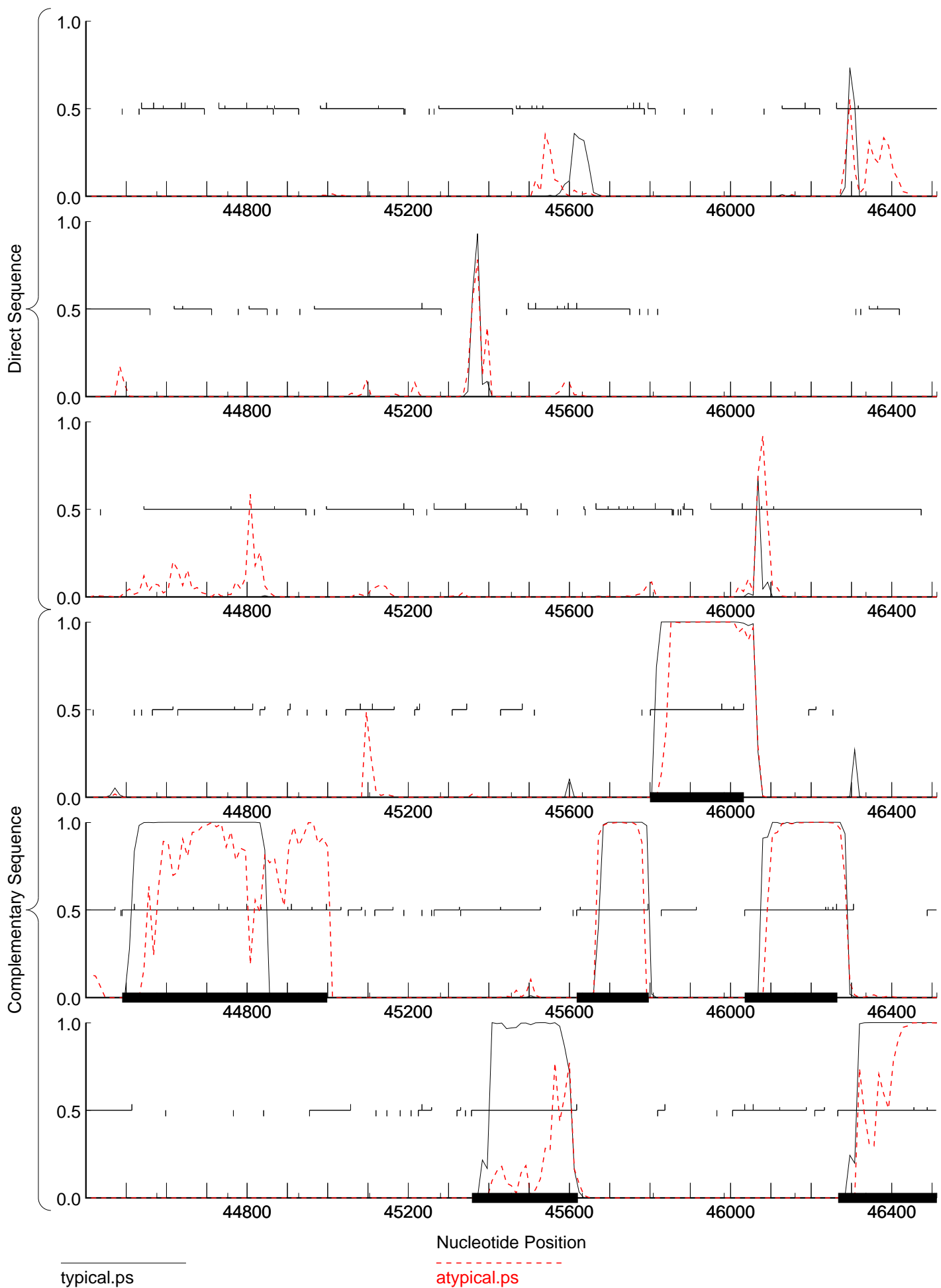
typical.ps

Nucleotide Position

atypical.ps

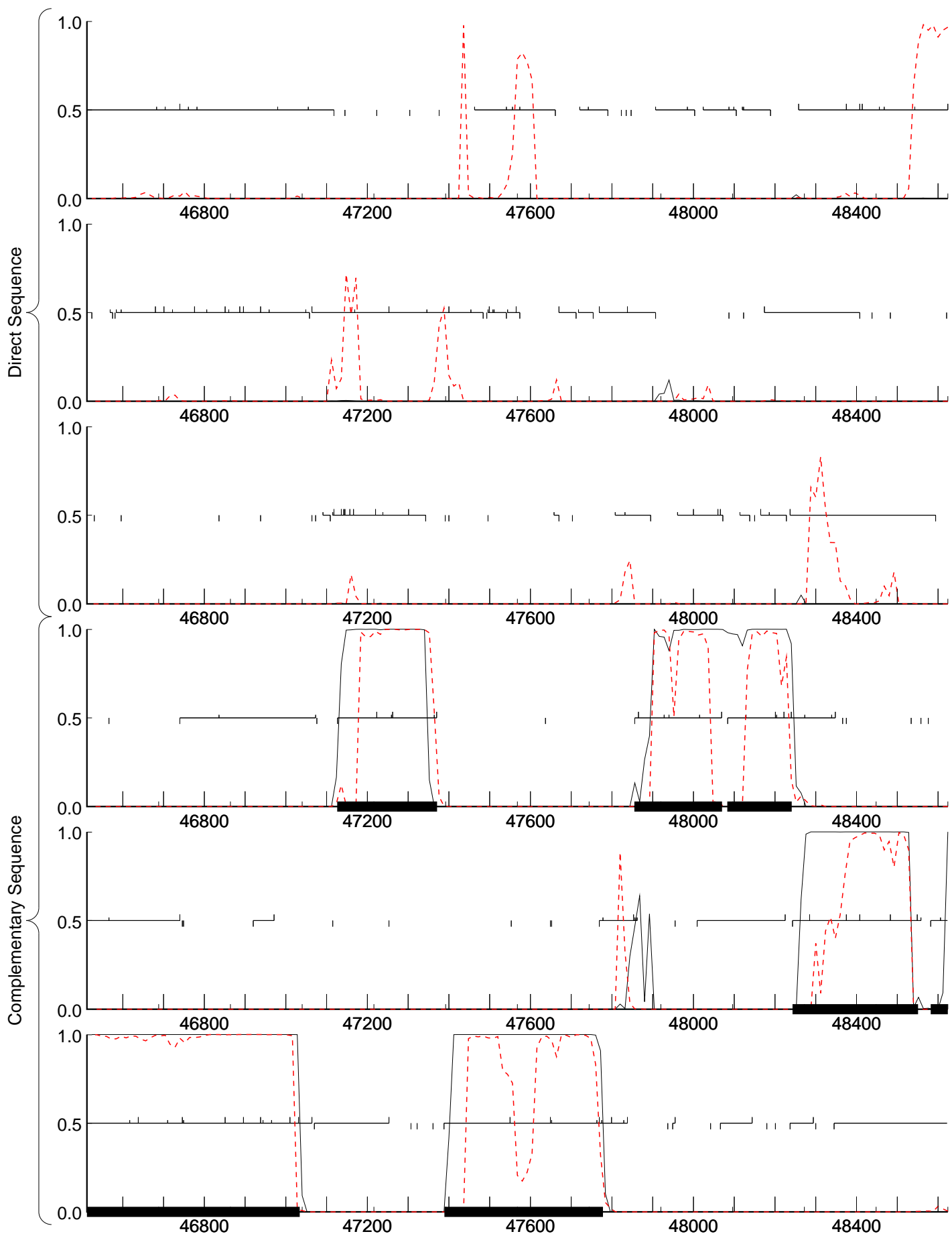






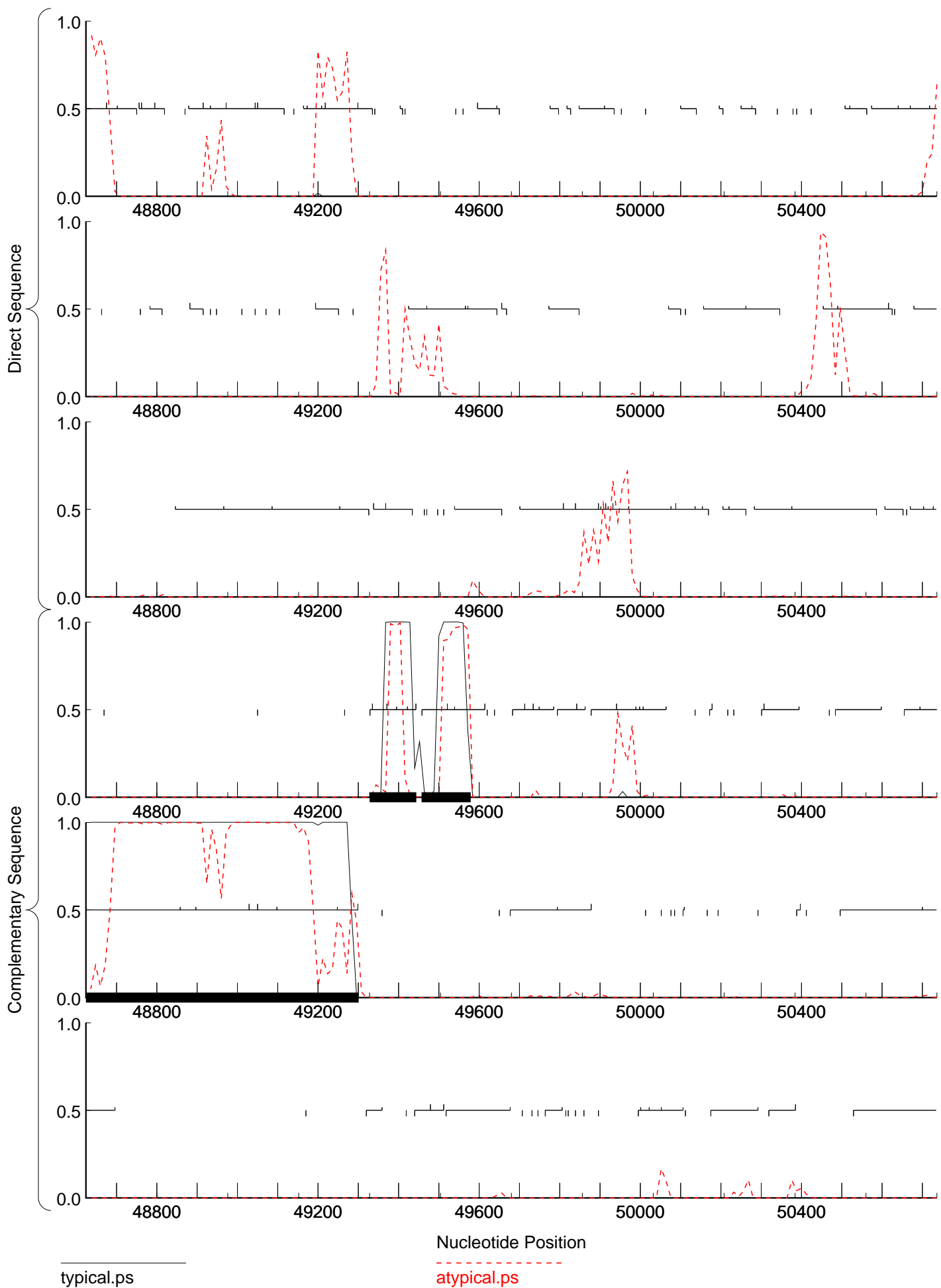
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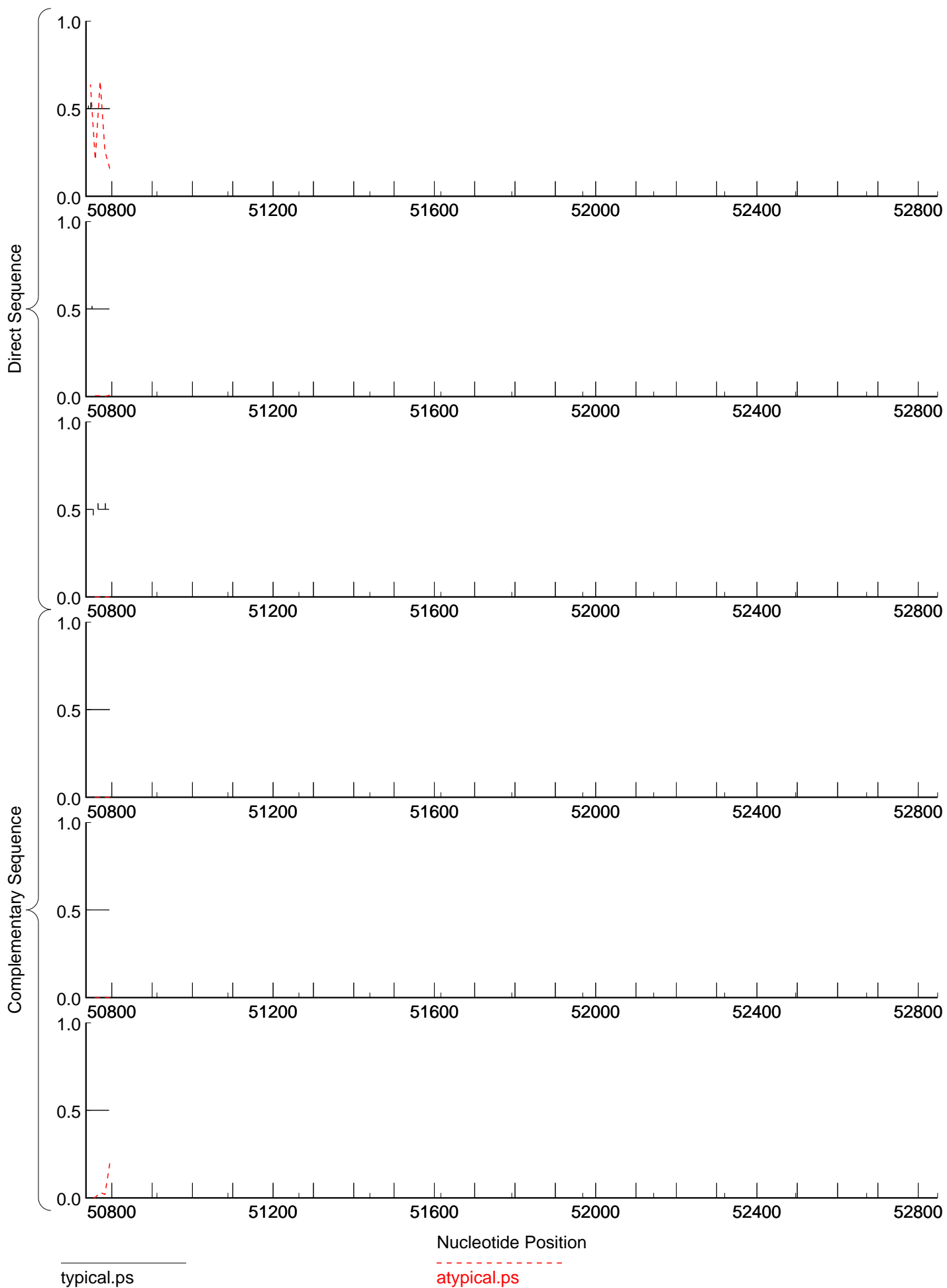
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