

# GeneMark

Version 2.5p (09.08.06)

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## PROGRAM INFORMATION

Sequence : Mycobacterium phage Lilbit complete sequence, 65106 bp including 11-base 3' overhang (GCGCG)  
Analysis Date : 3/17/18 at 16:22:24  
Pages : 32  
Sequence Length : 65106 bp  
GC Content : 63.37%

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,

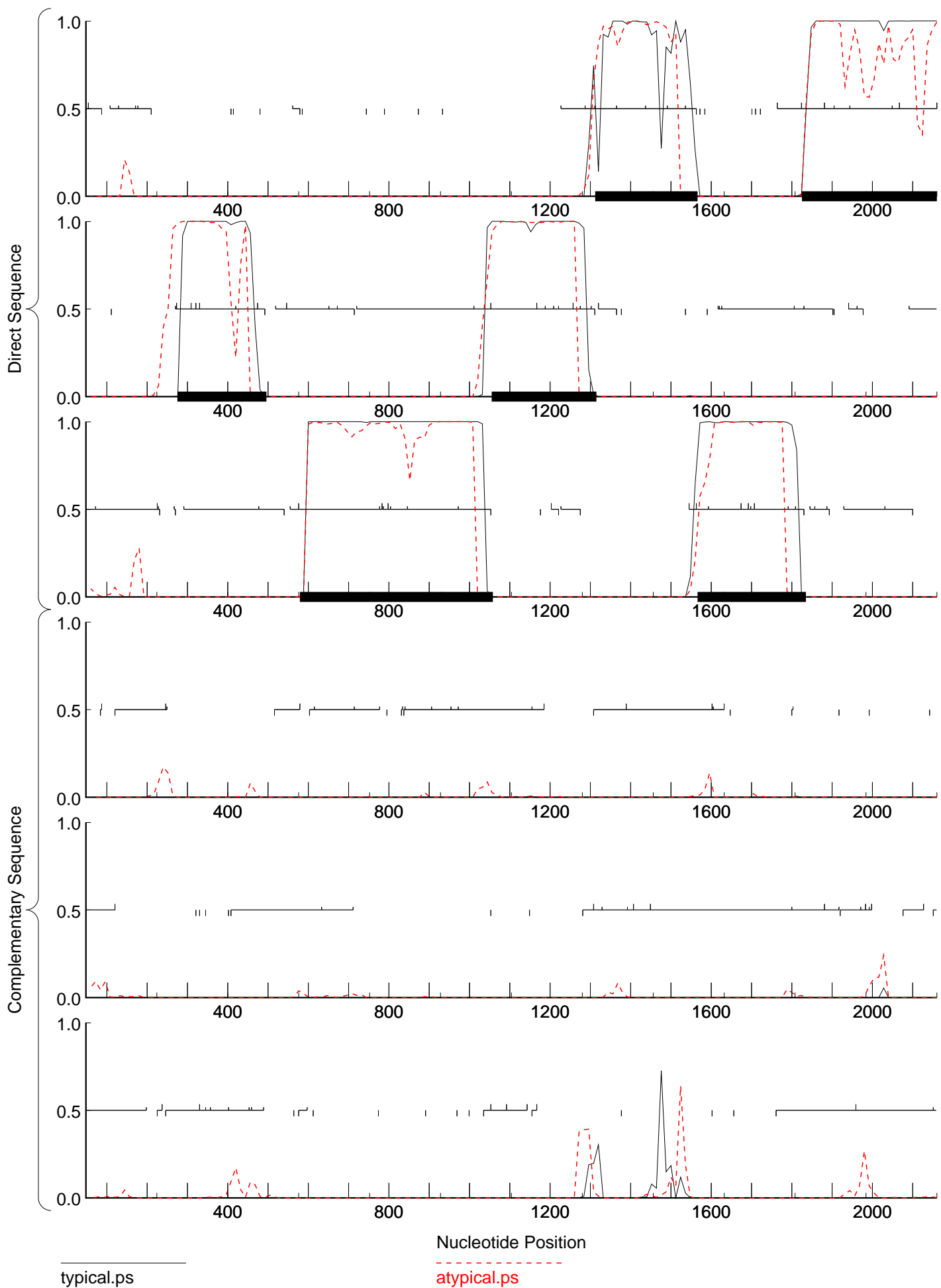
## Matrix notes & comments

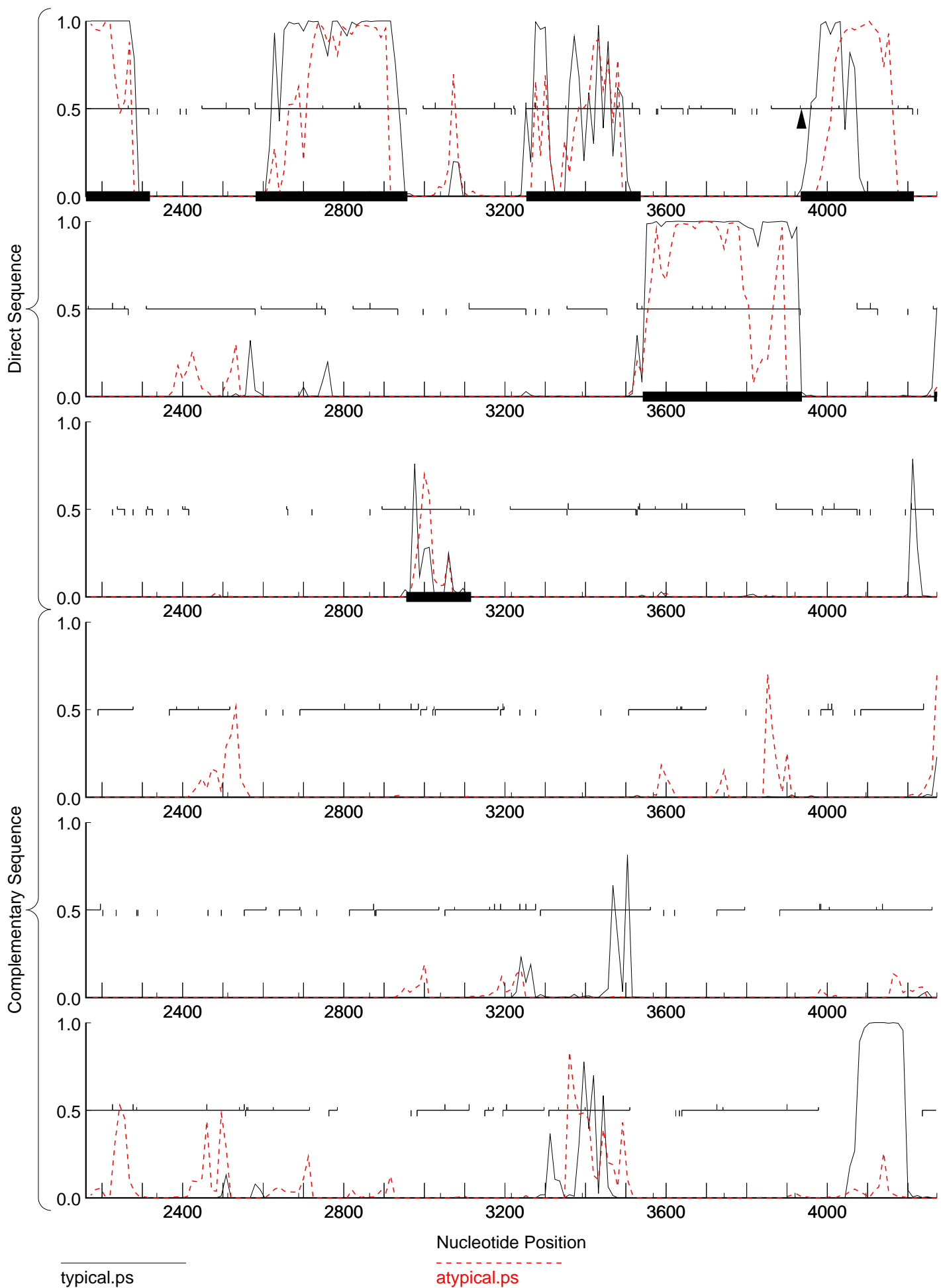
Training set derived by GeneMarkS, 4.30 October 2014  
Sat Mar 17 16:22:24 2018

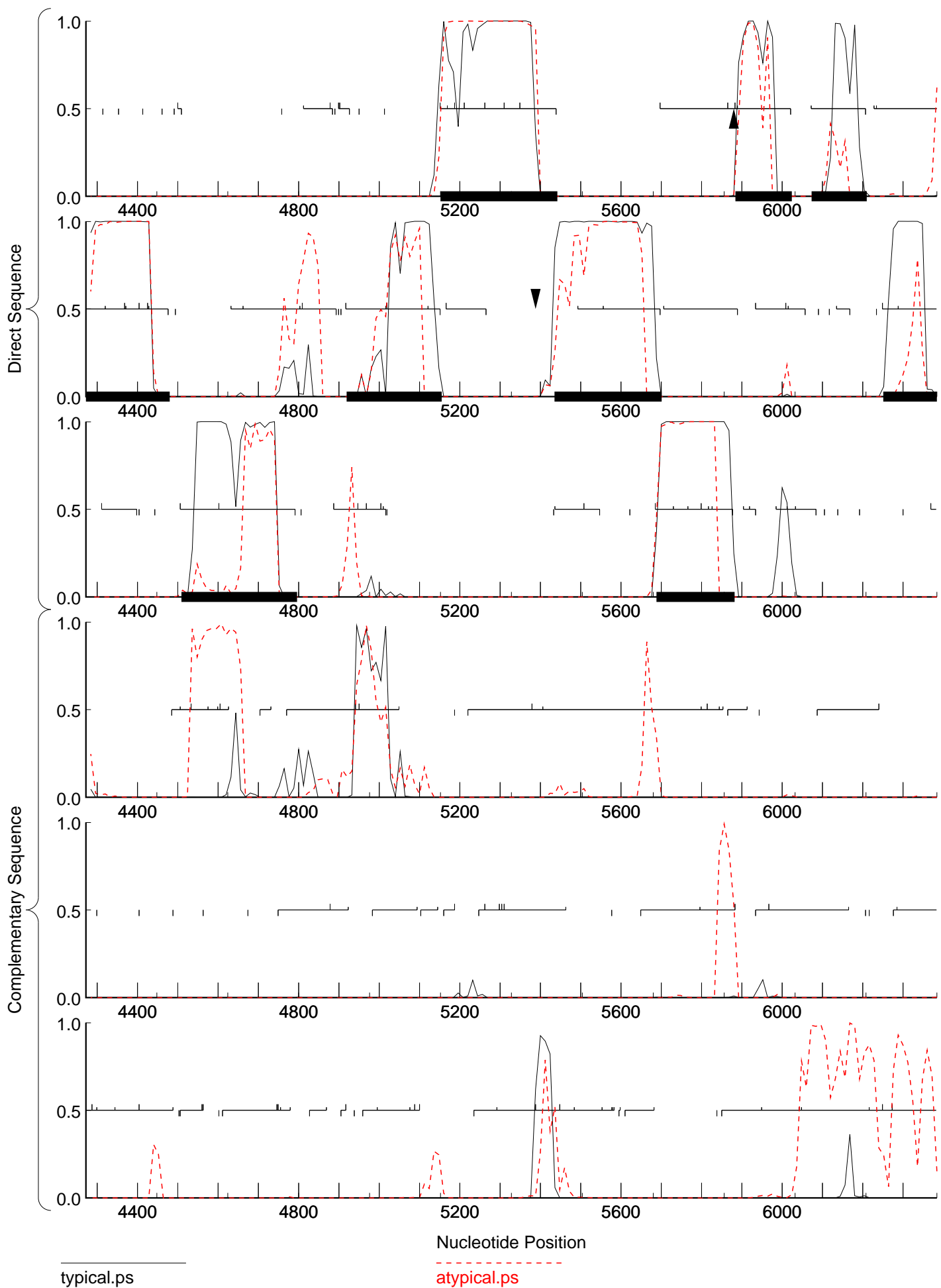
## MATRIX INFORMATION

Matrix : -  
Author : -  
Order : 4

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

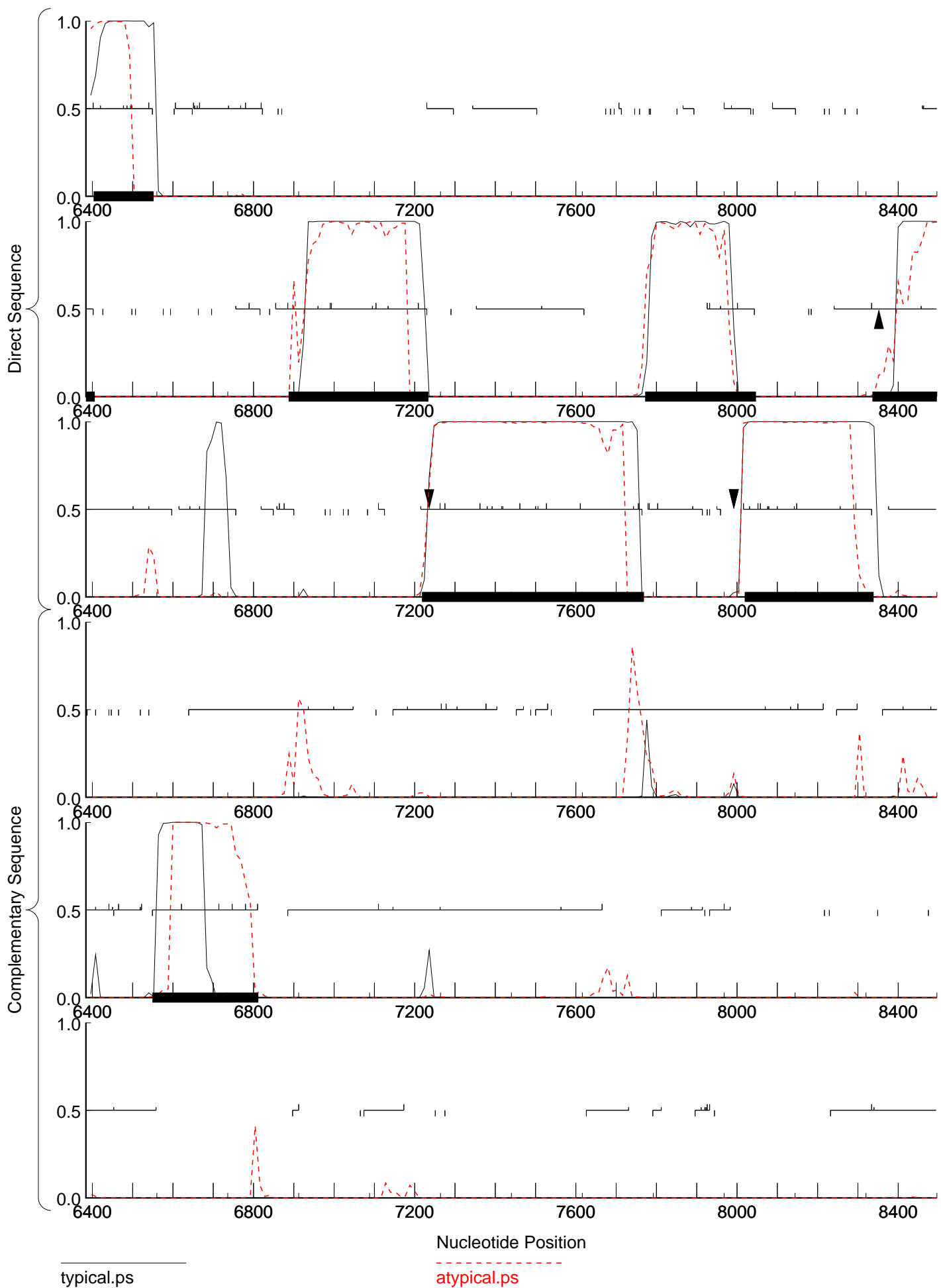


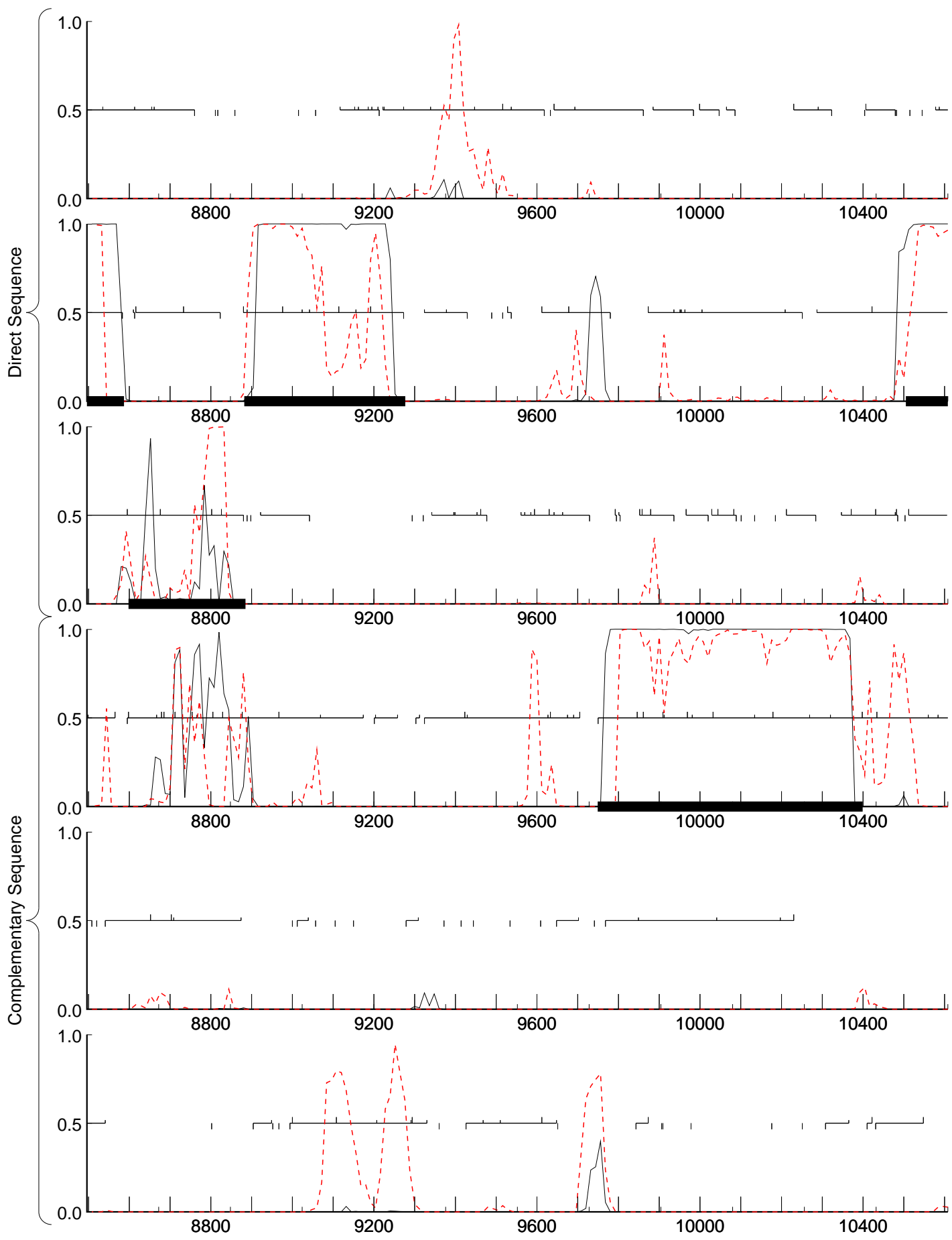




typical.ps

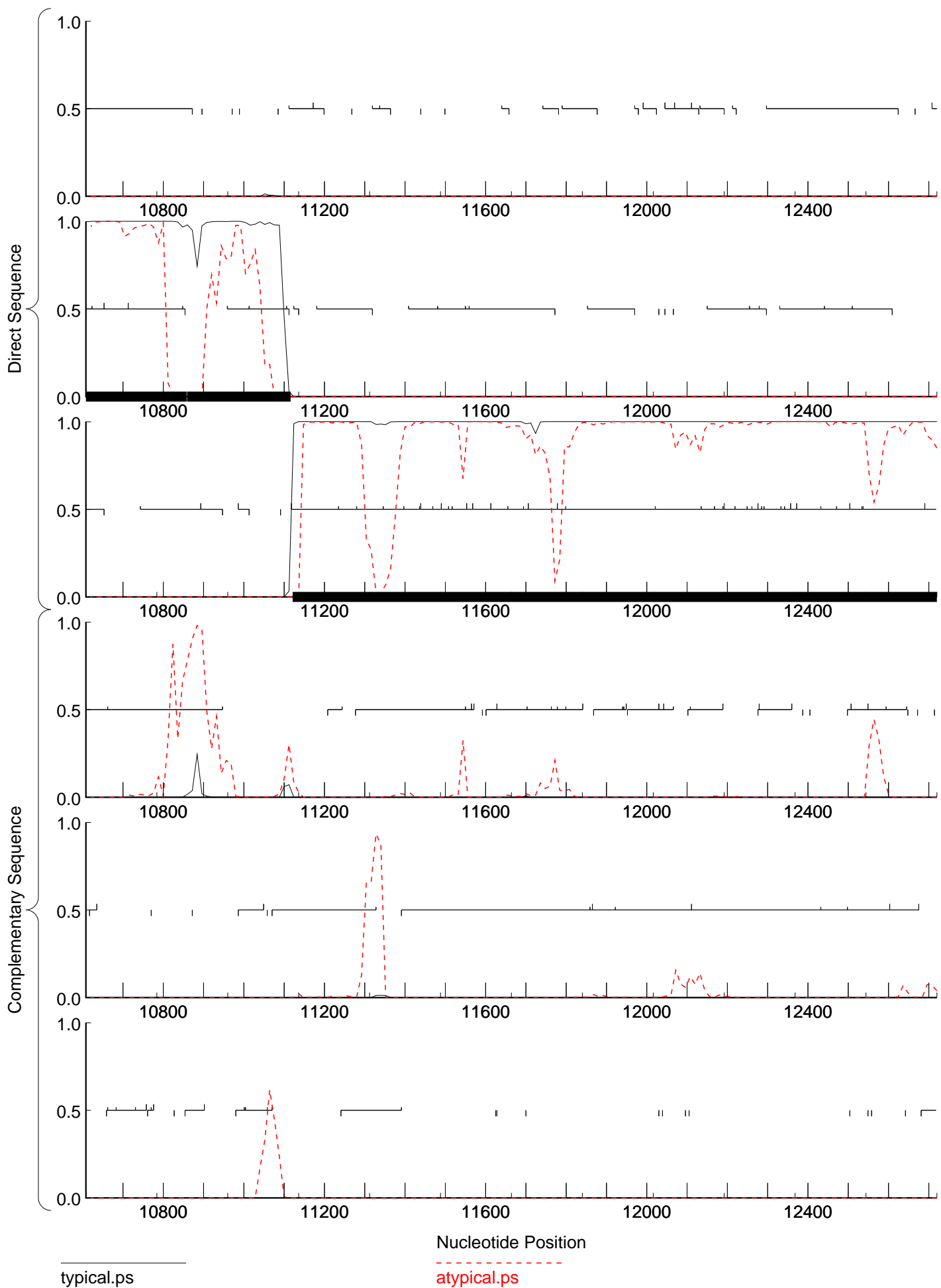
atypical.ps





typical.ps

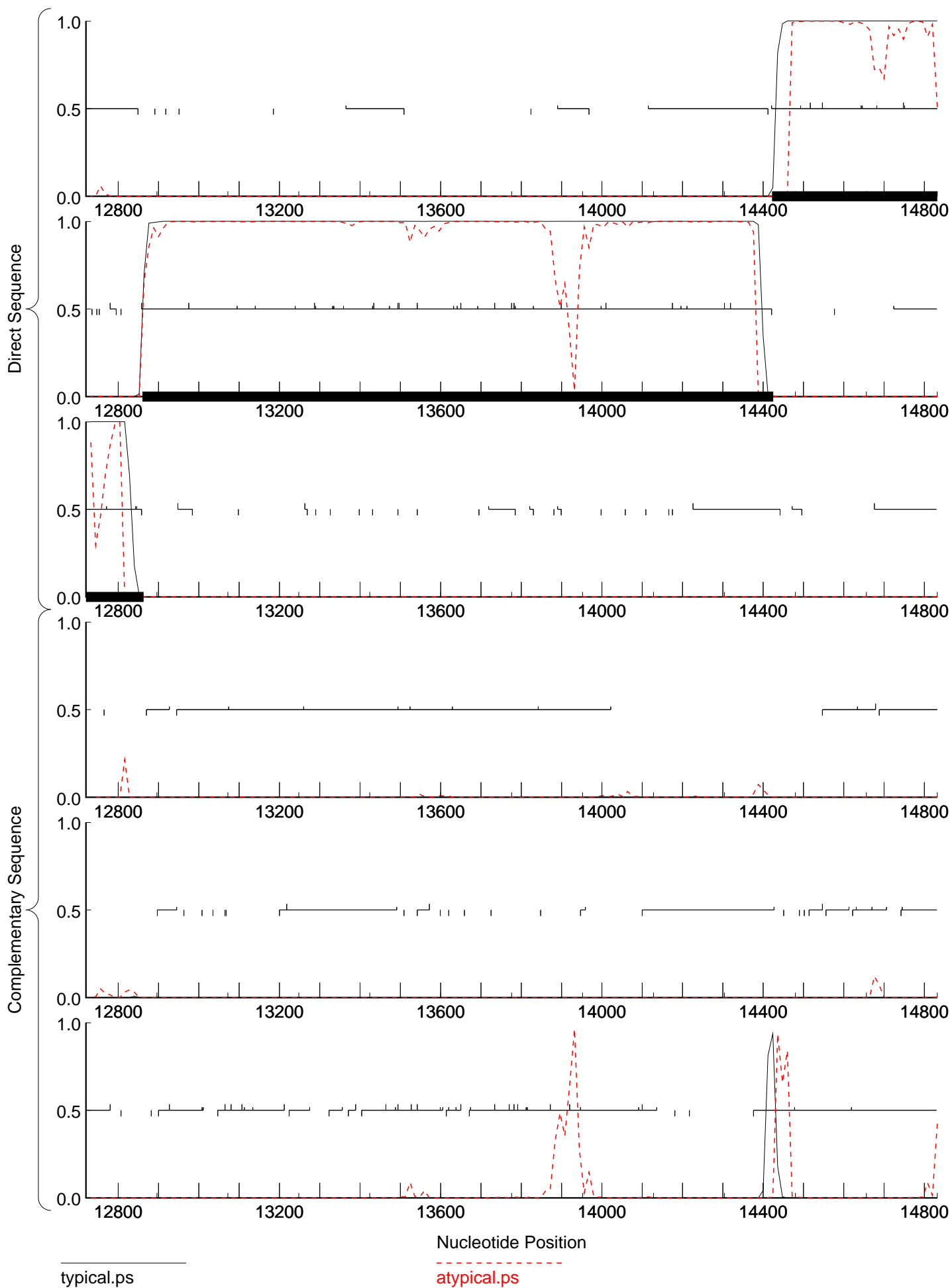
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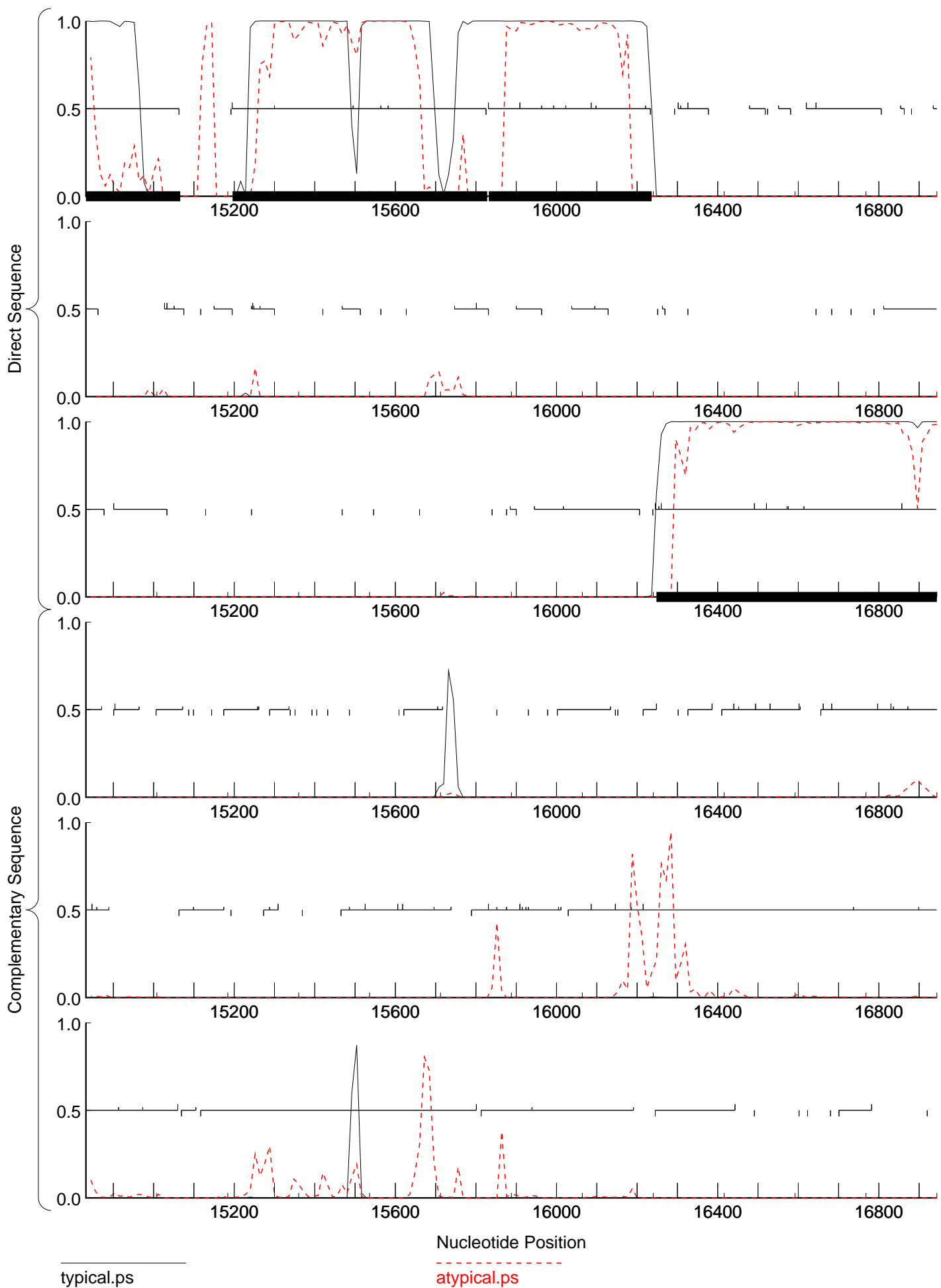
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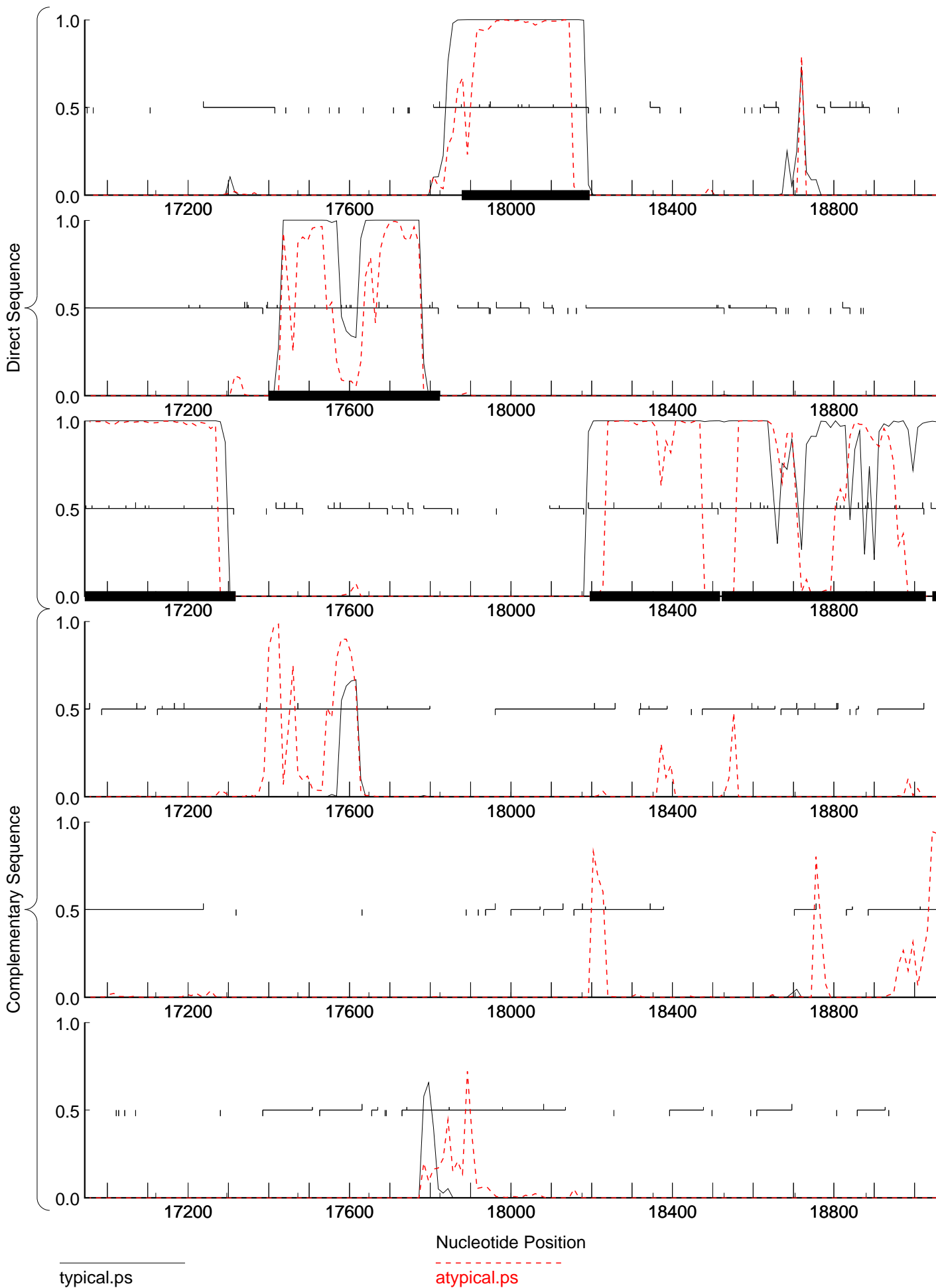
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complete sequence, 65106 bp including 11-base 3' overhang (GCGCGCAGCGC), Cluster S, Order 4, Window 96, Step 12, 8/32  
complete sequence, 65106 bp including 11-base 3' overhang (GCGCGCAGCGC), Cluster S, Order 2, Window 96, Step 12, 8/32



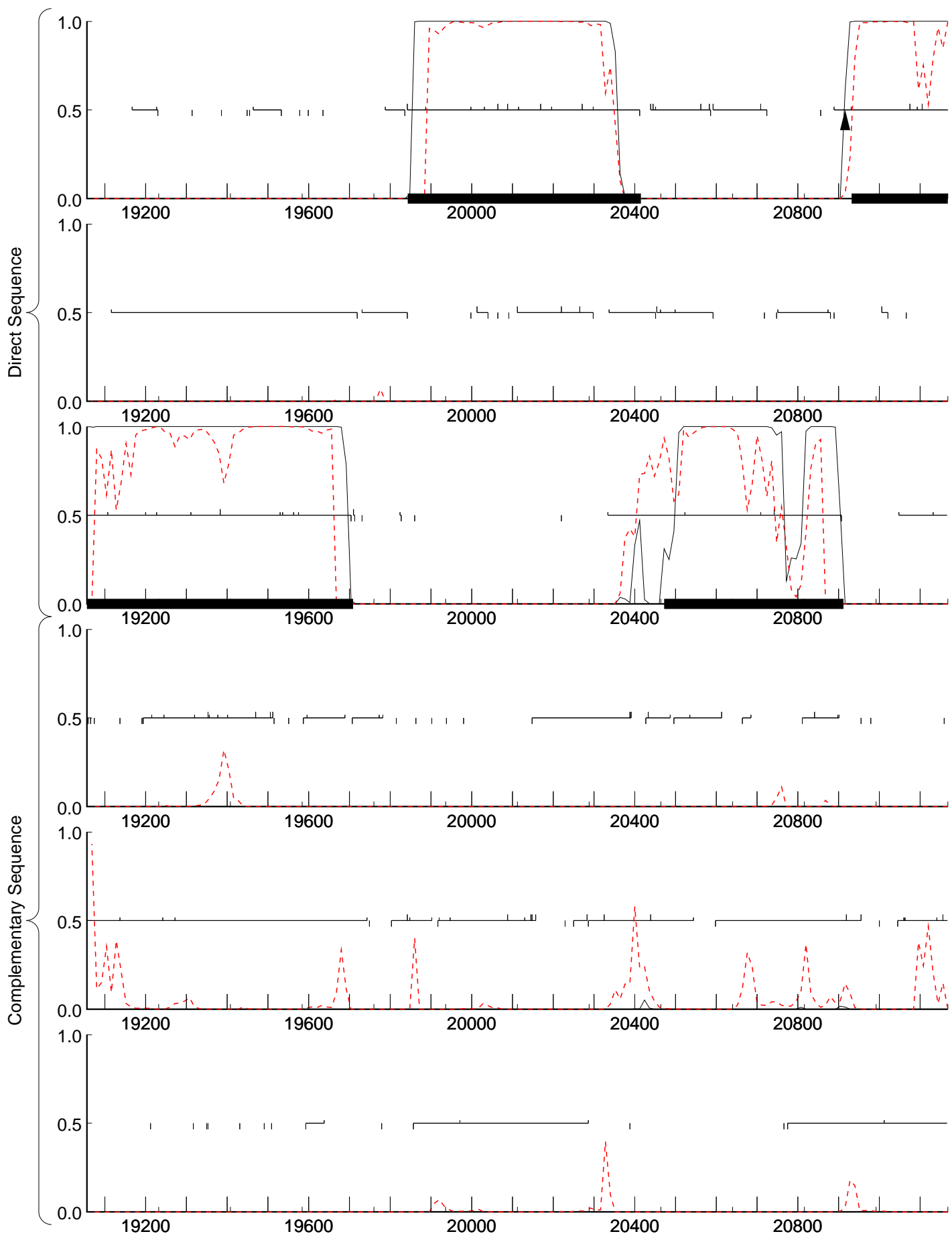






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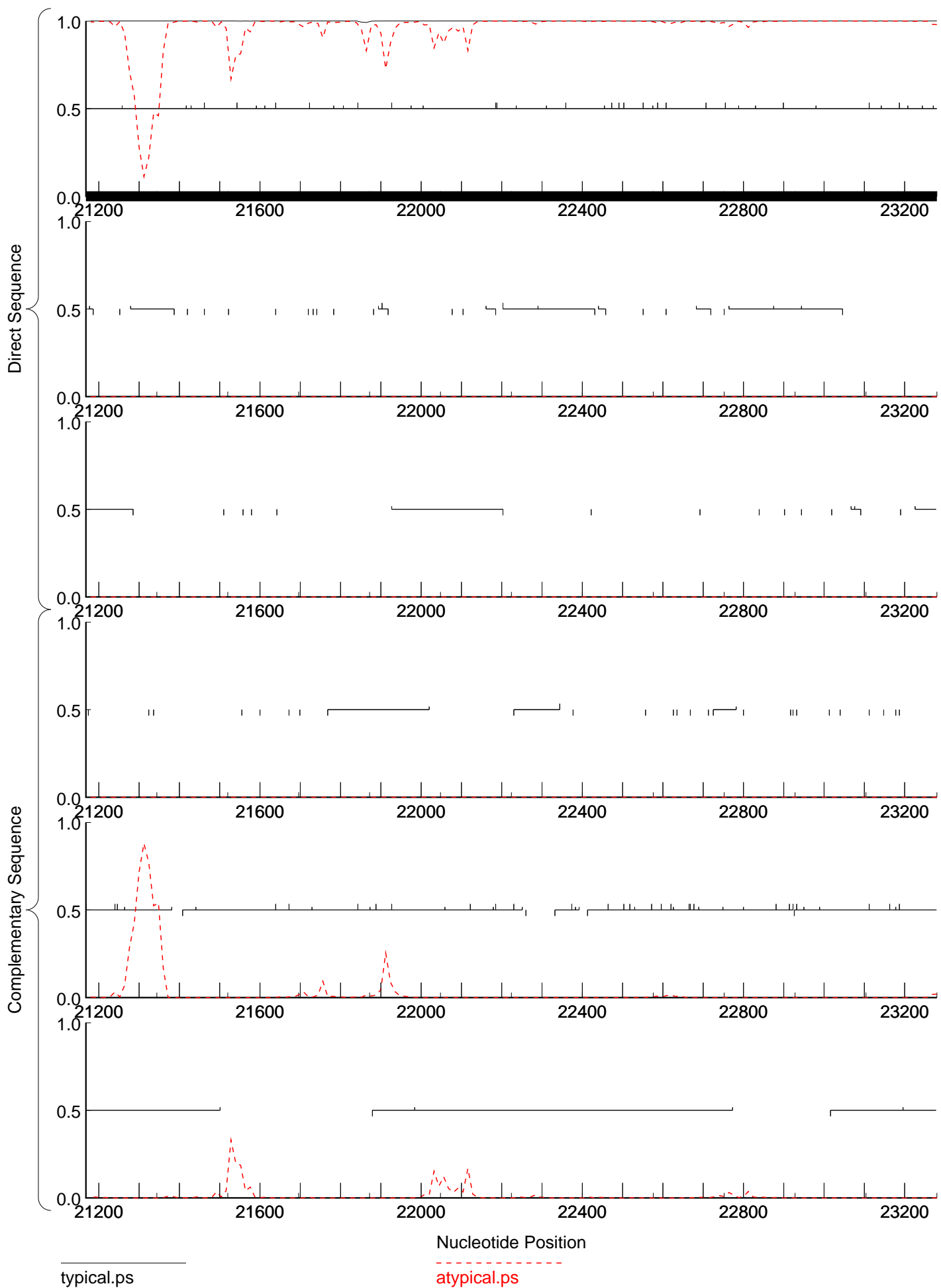
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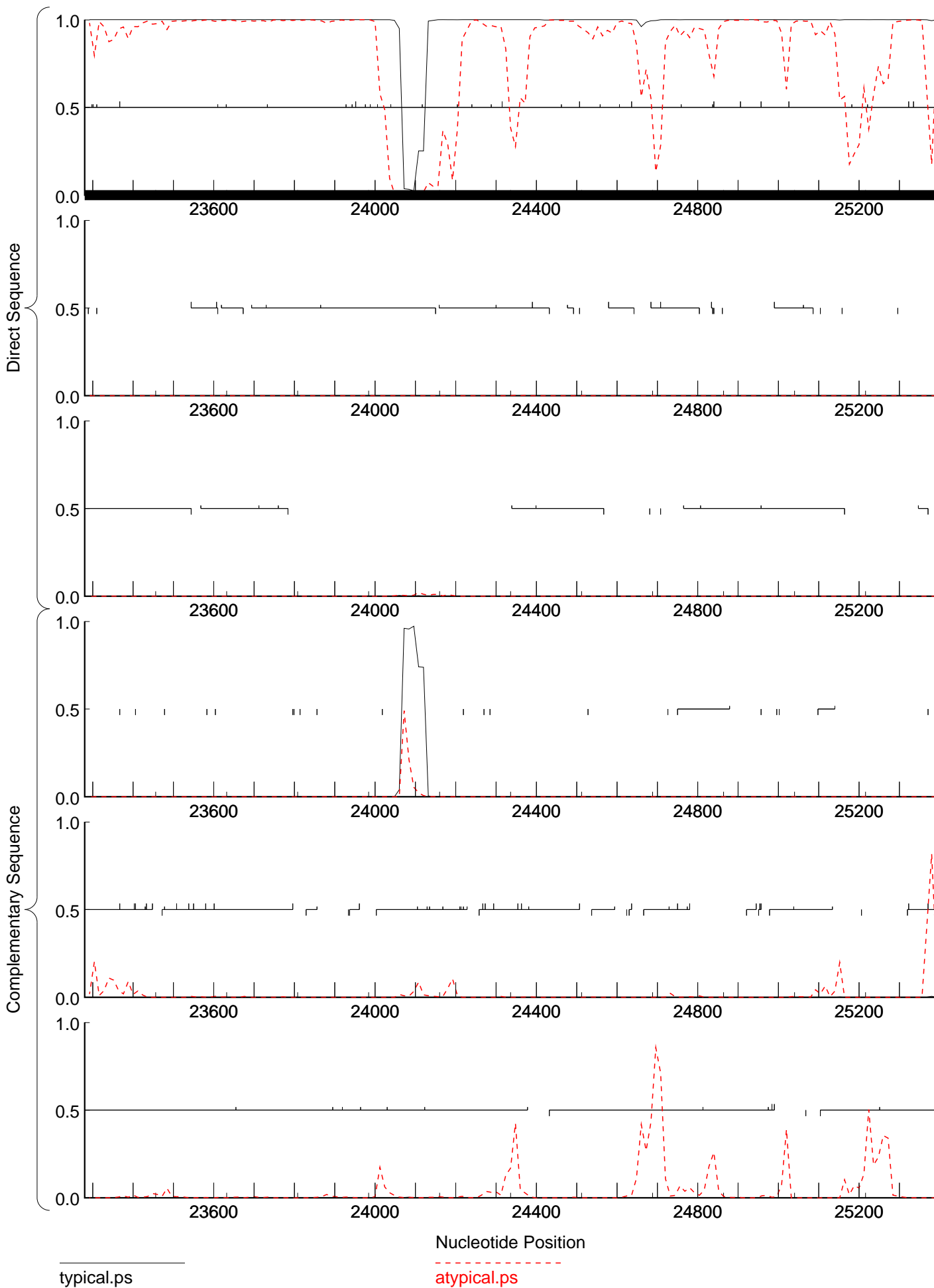
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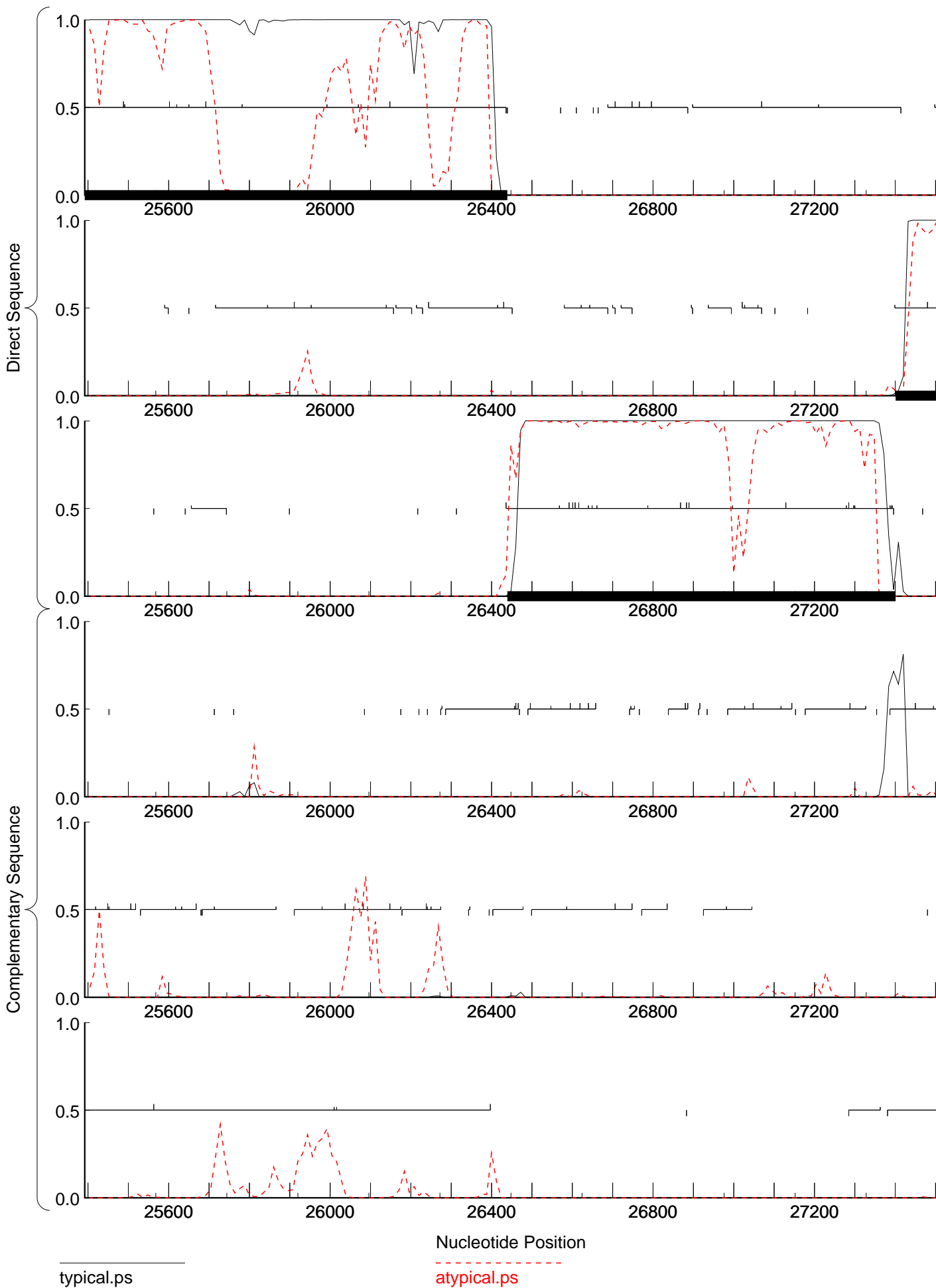
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complete sequence, 65106 bp including 11-base 3' overhang (GCGCGCAGCGC), Cluster S, Order 4, Window 96, Step 12, 12/32  
complete sequence, 65106 bp including 11-base 3' overhang (GCGCGCAGCGC), Cluster S, Order 2, Window 96, Step 12, 12/32



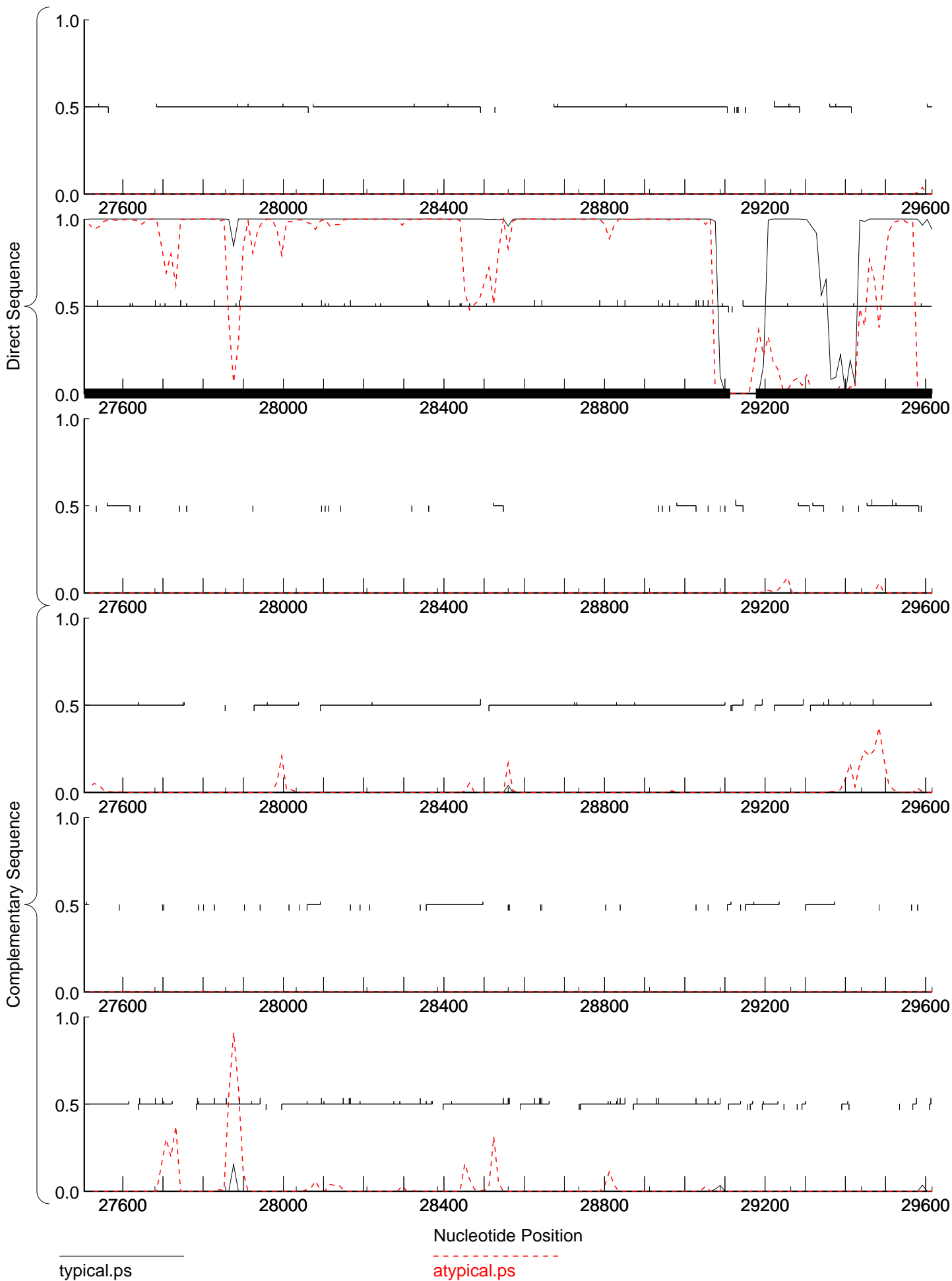
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complete sequence, 65106 bp including 11-base 3' overhang (GCGCGCAGCGC), Cluster S, Order 2, Window 96, Step 12, 13/32





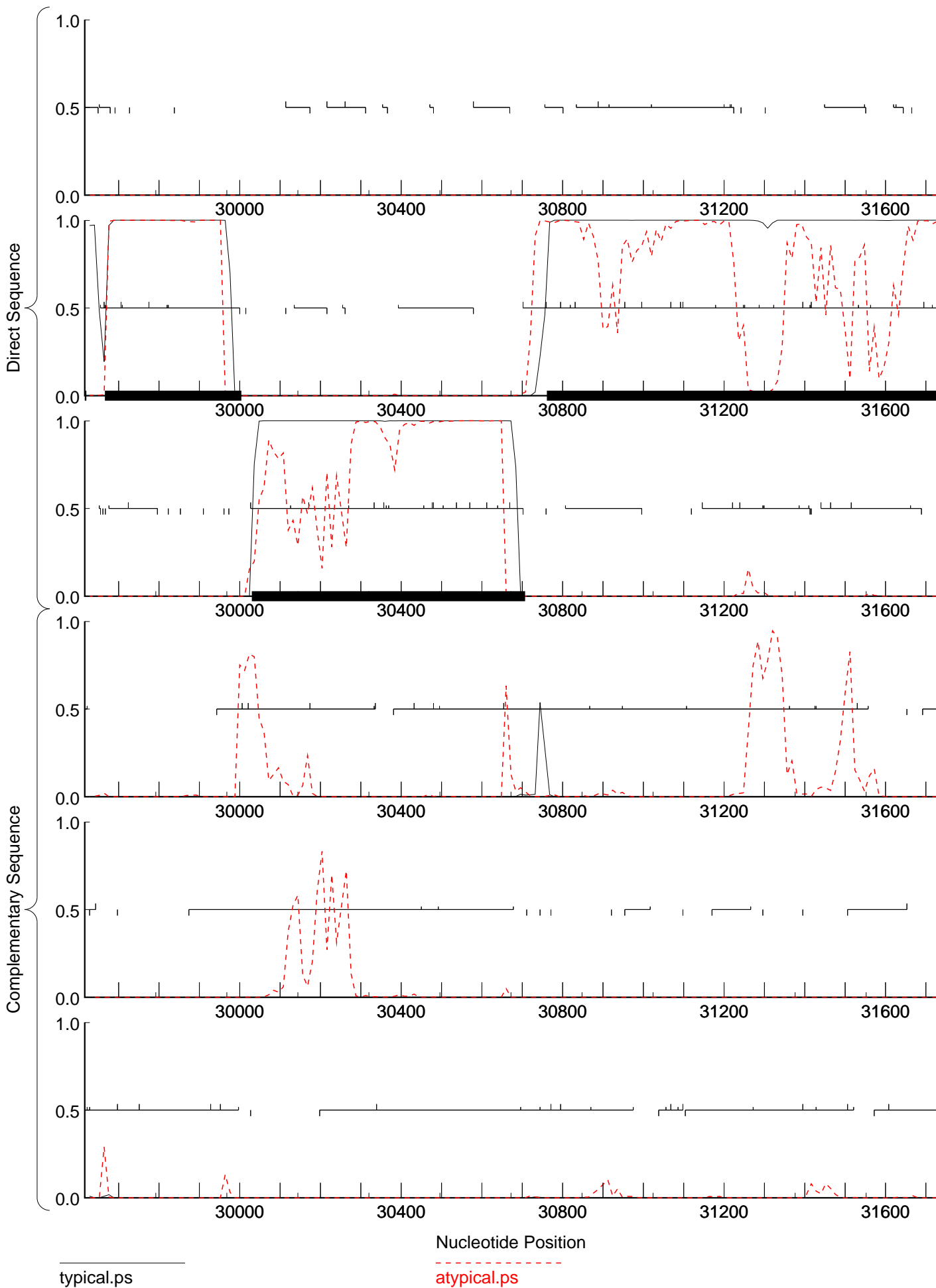
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atypical.ps

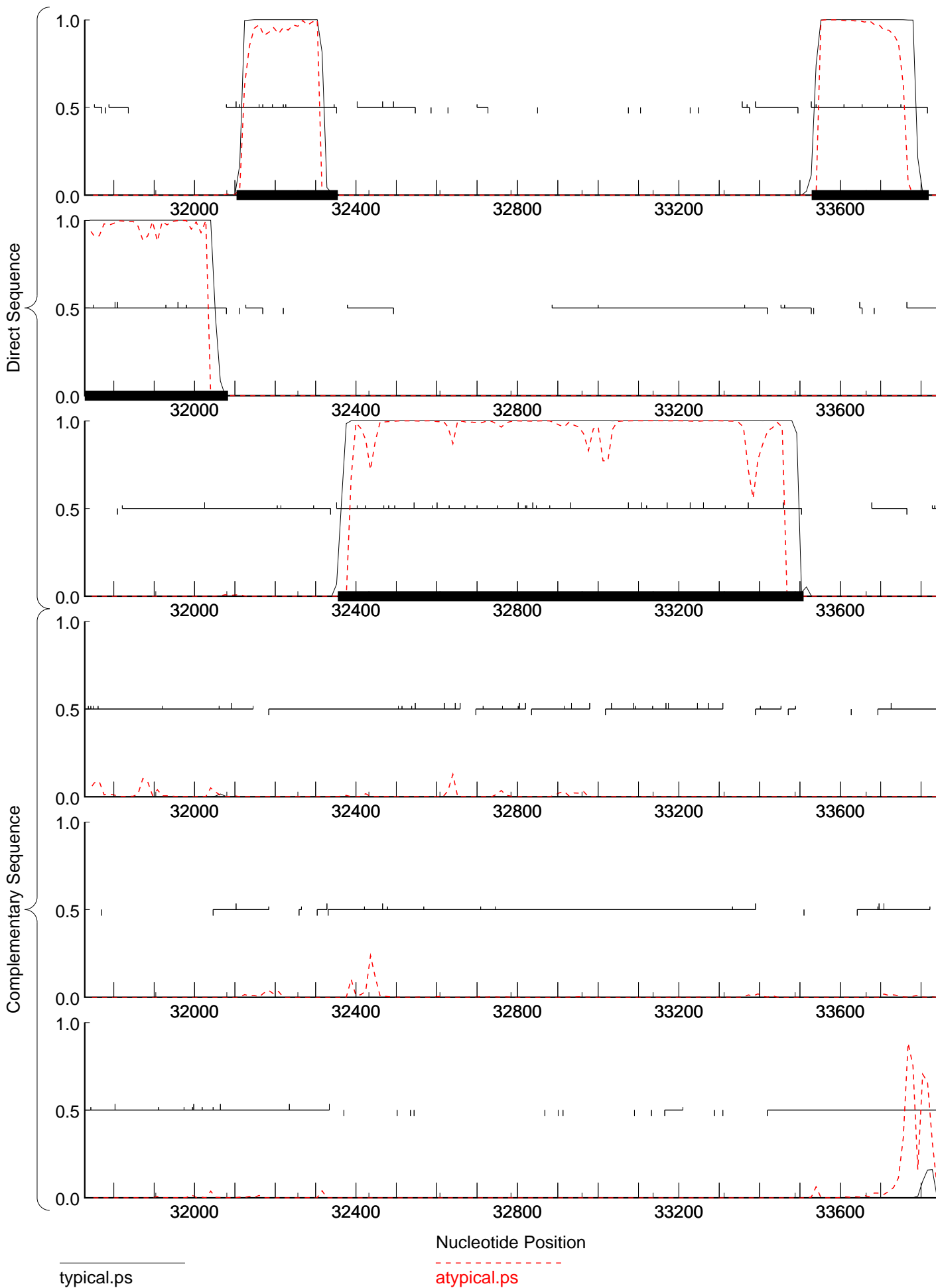


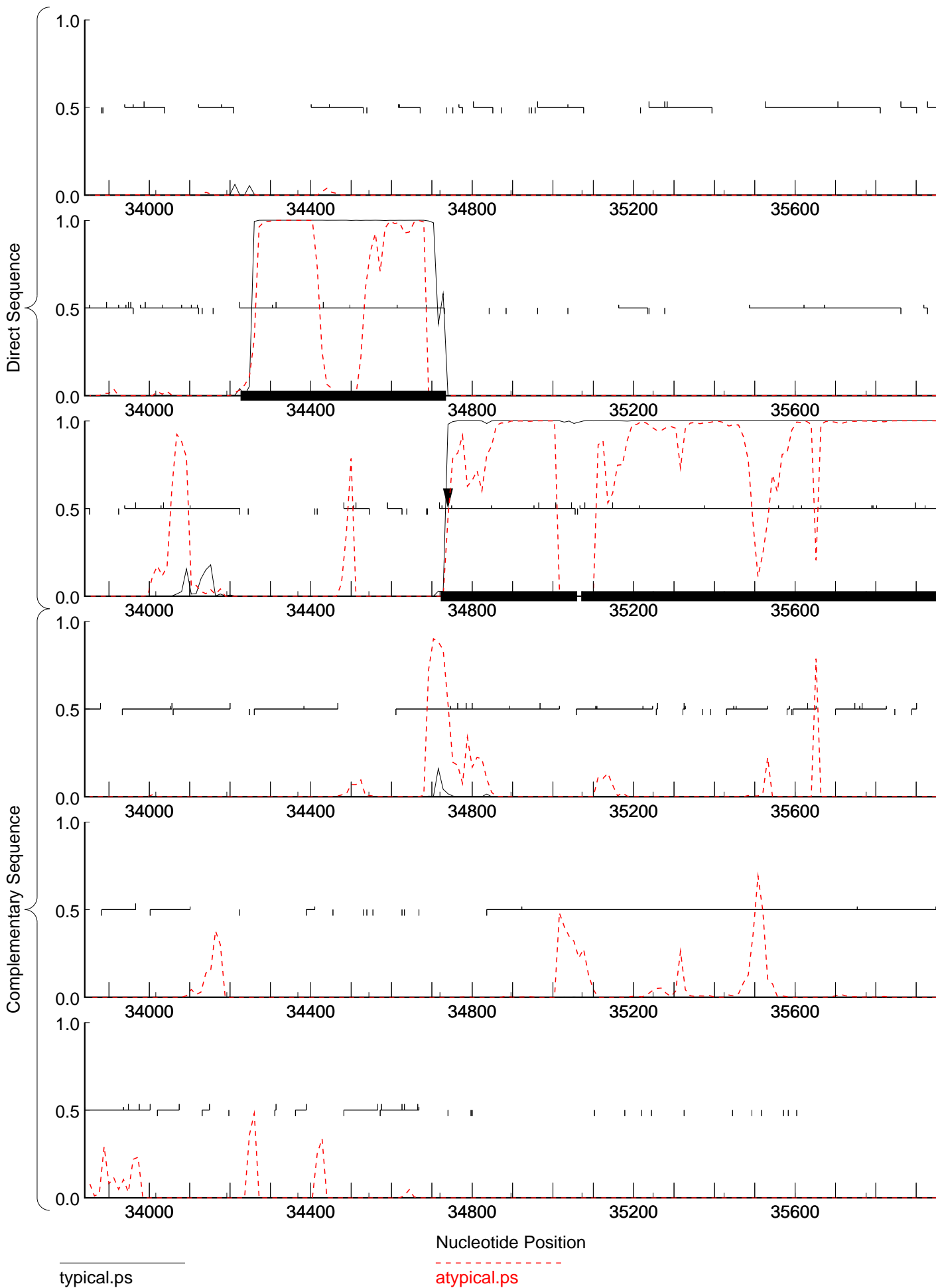
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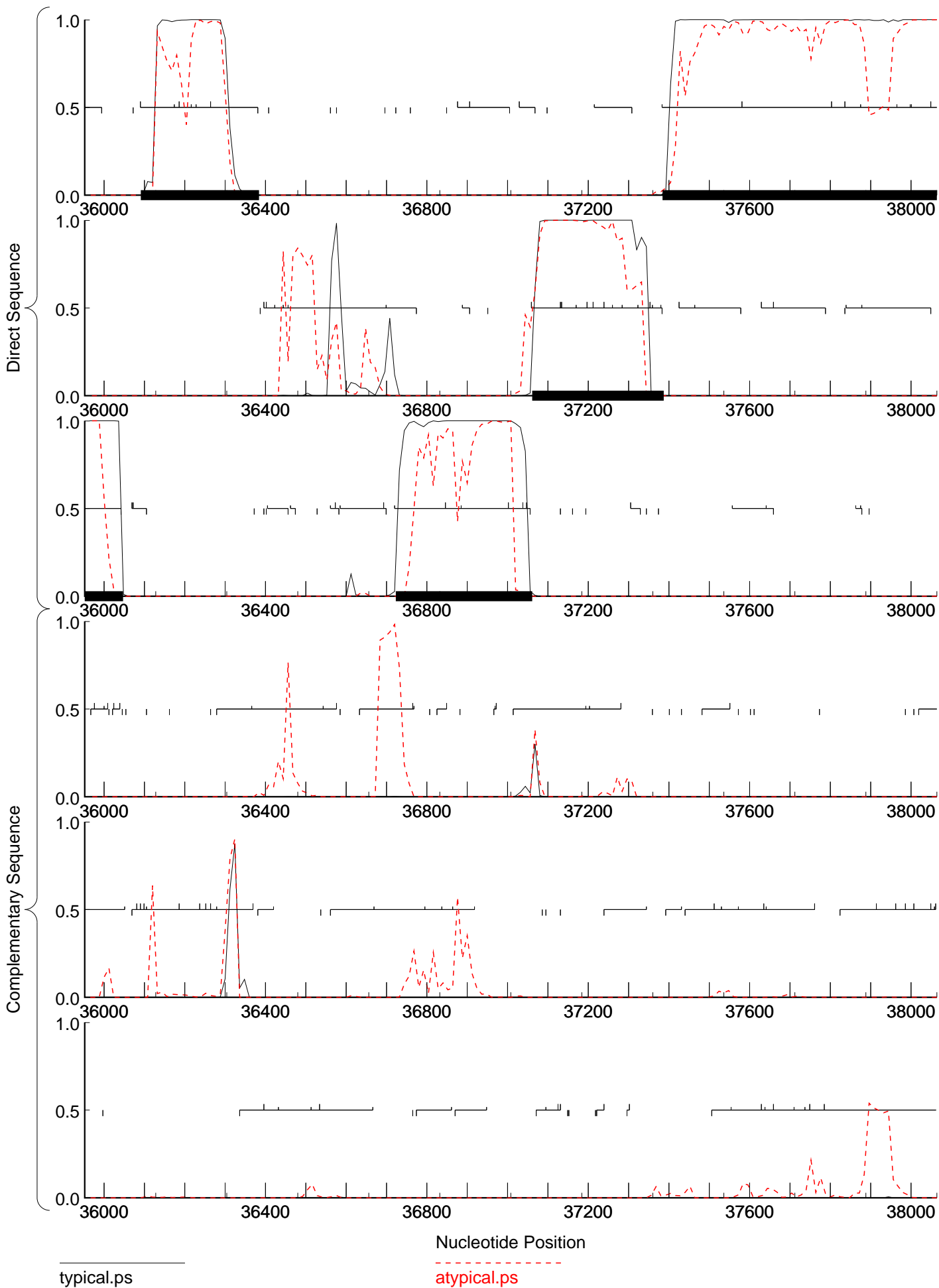






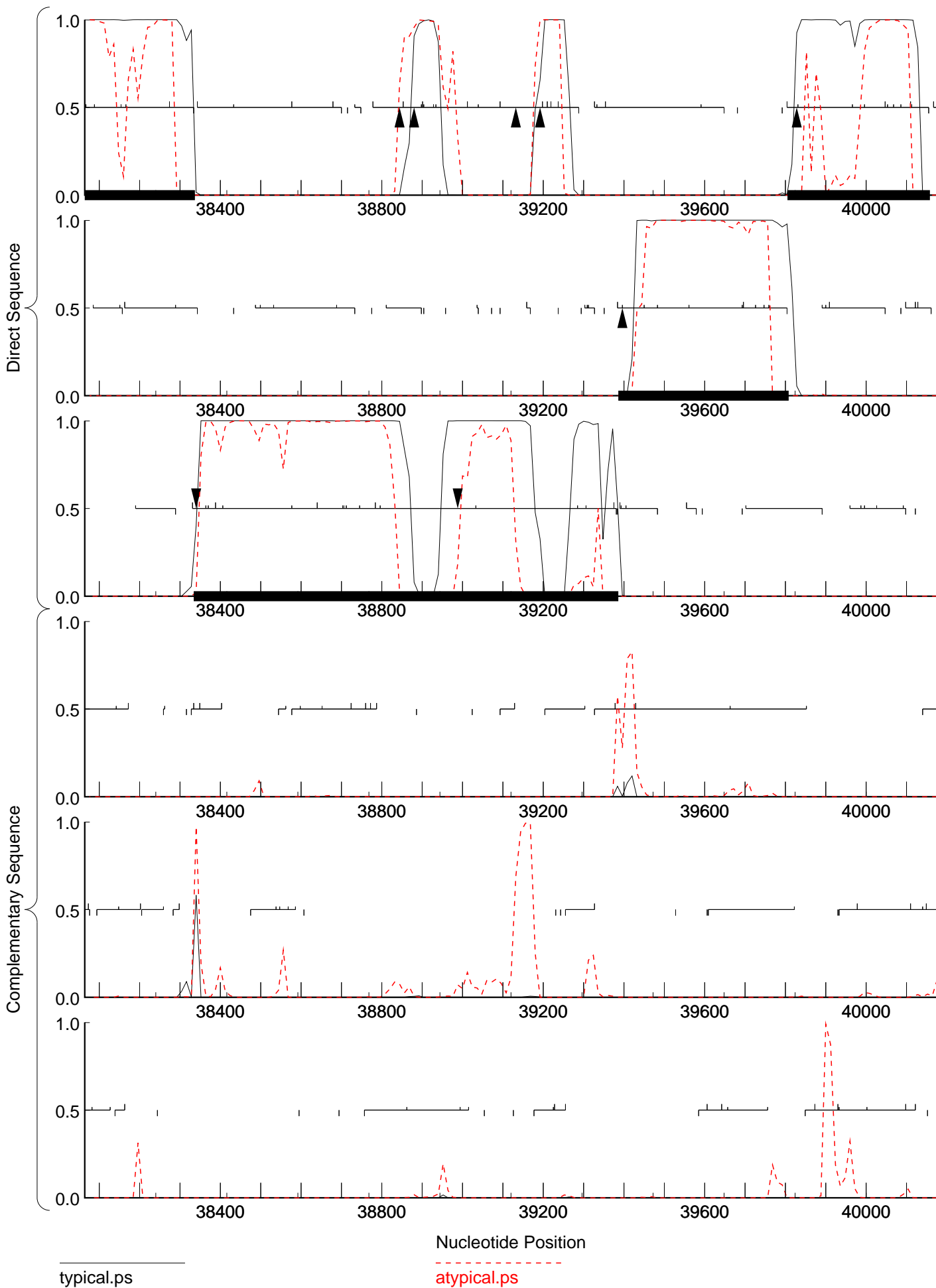
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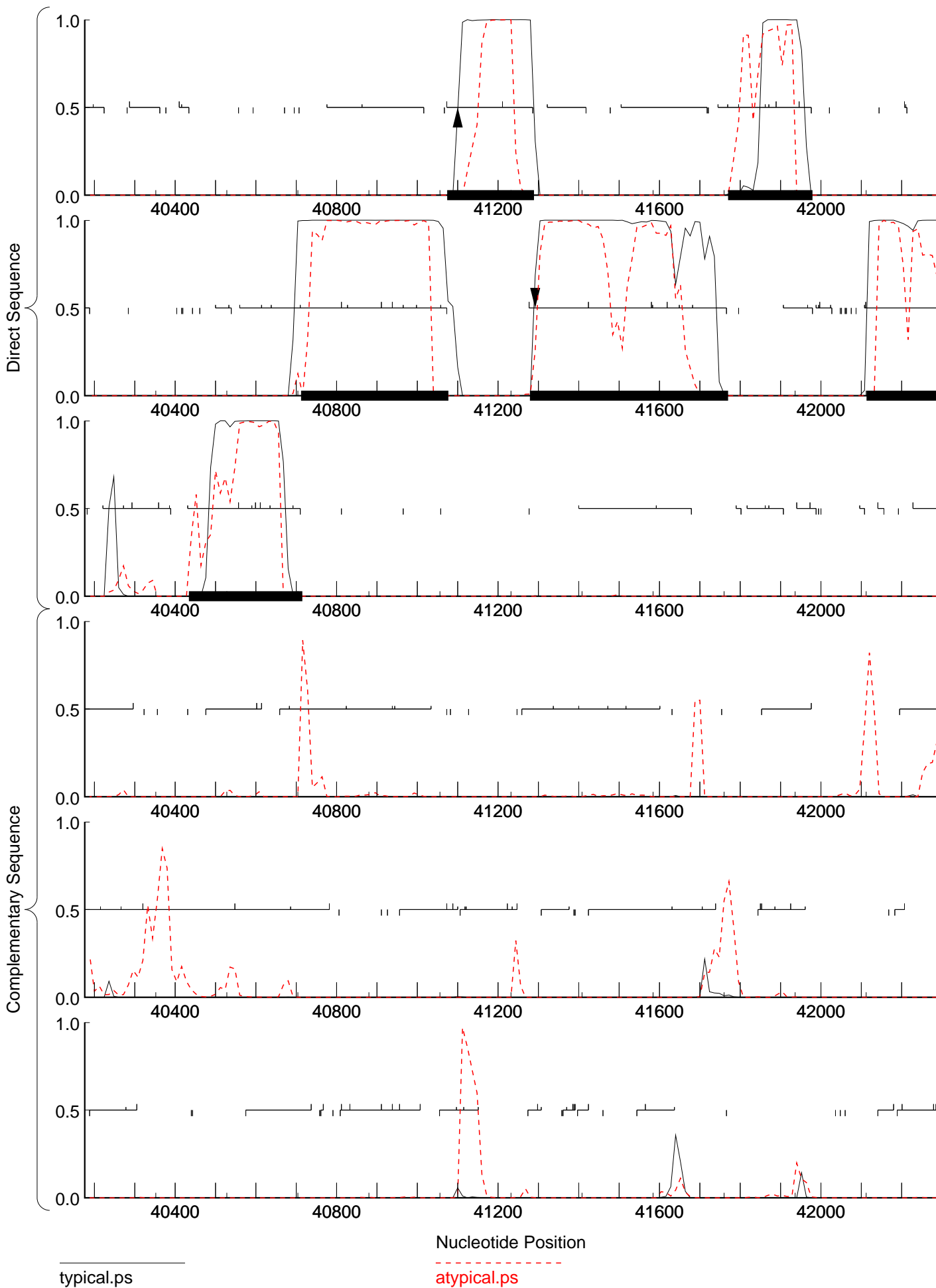
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typical.ps

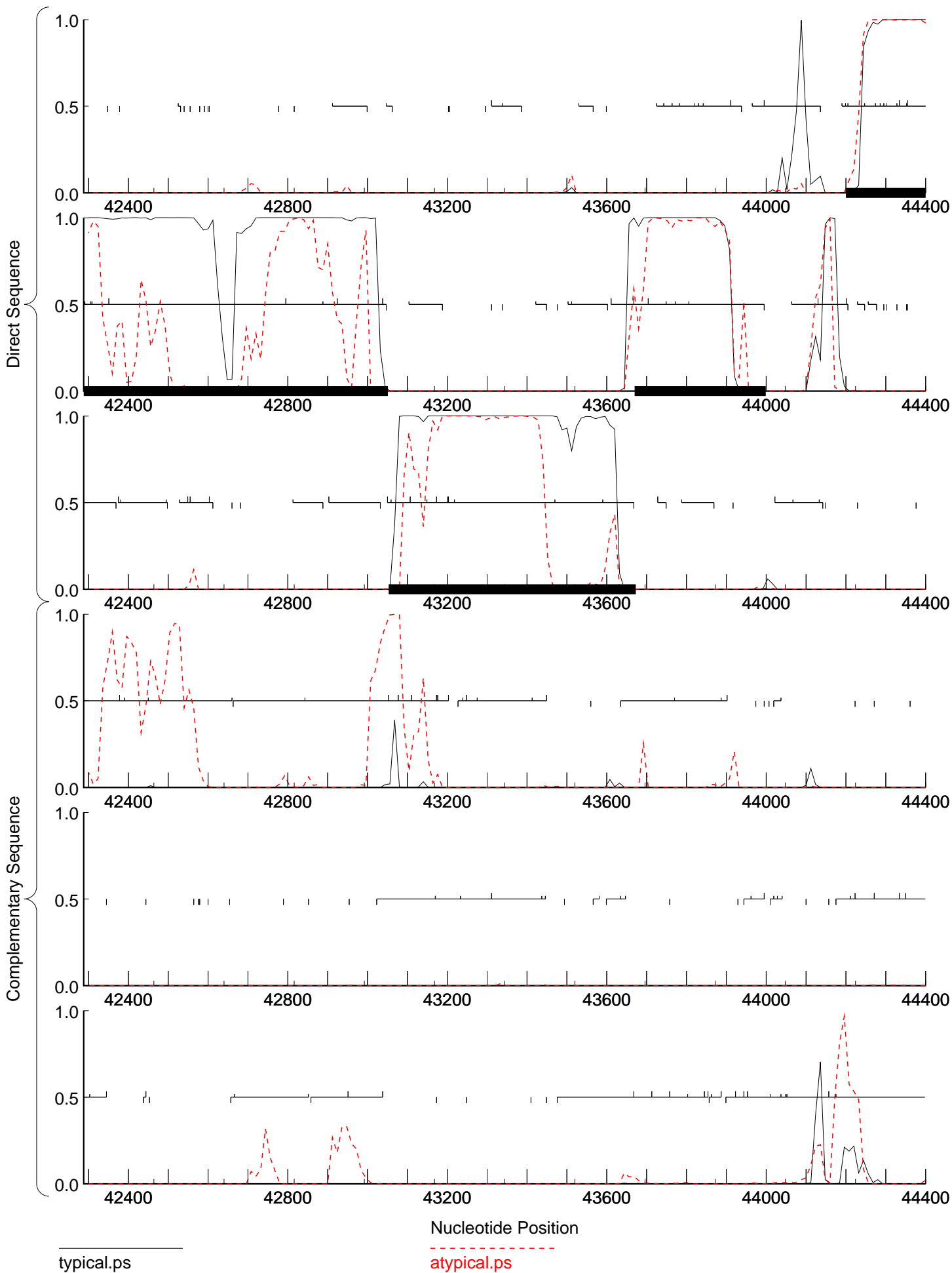
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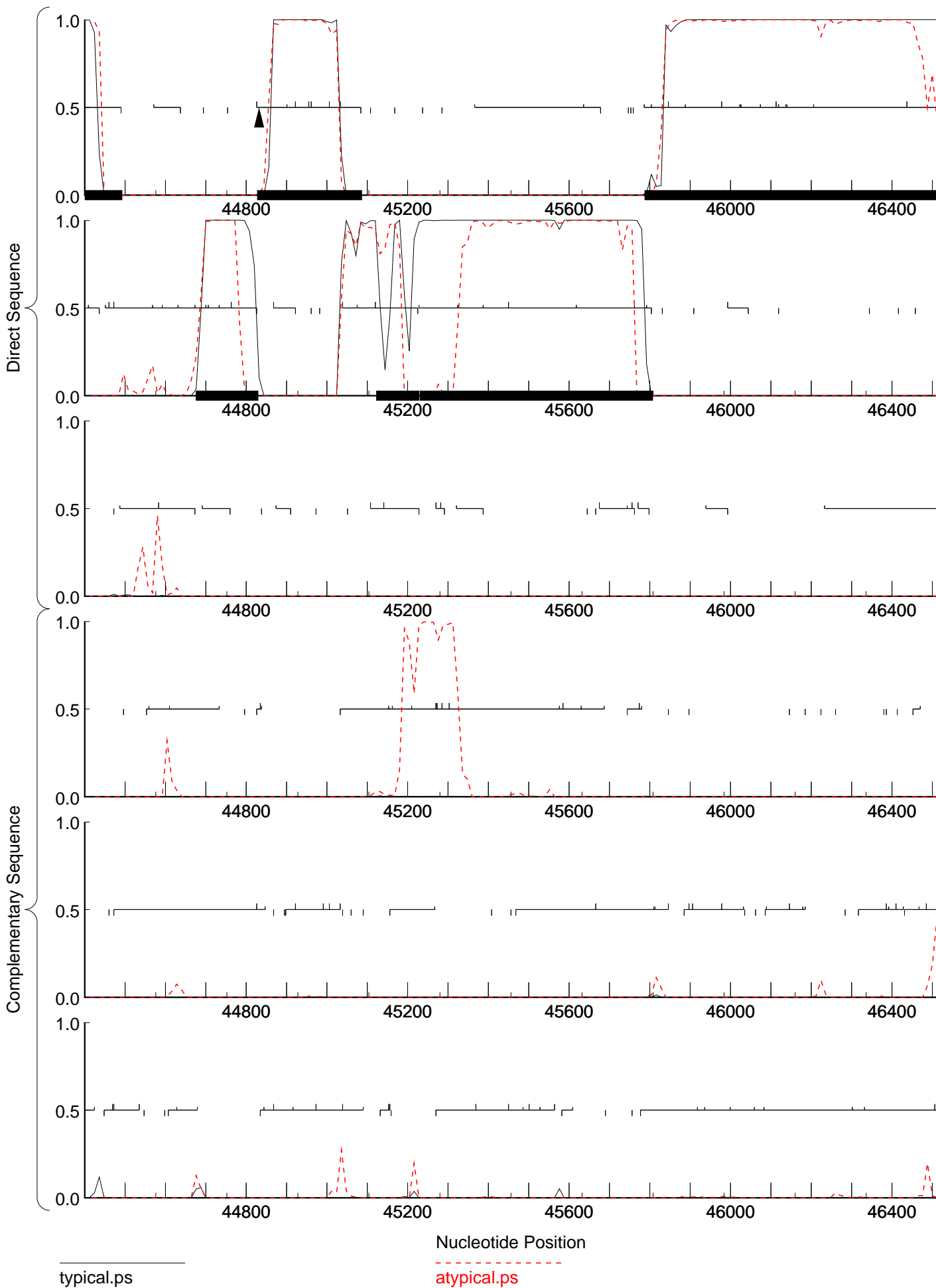
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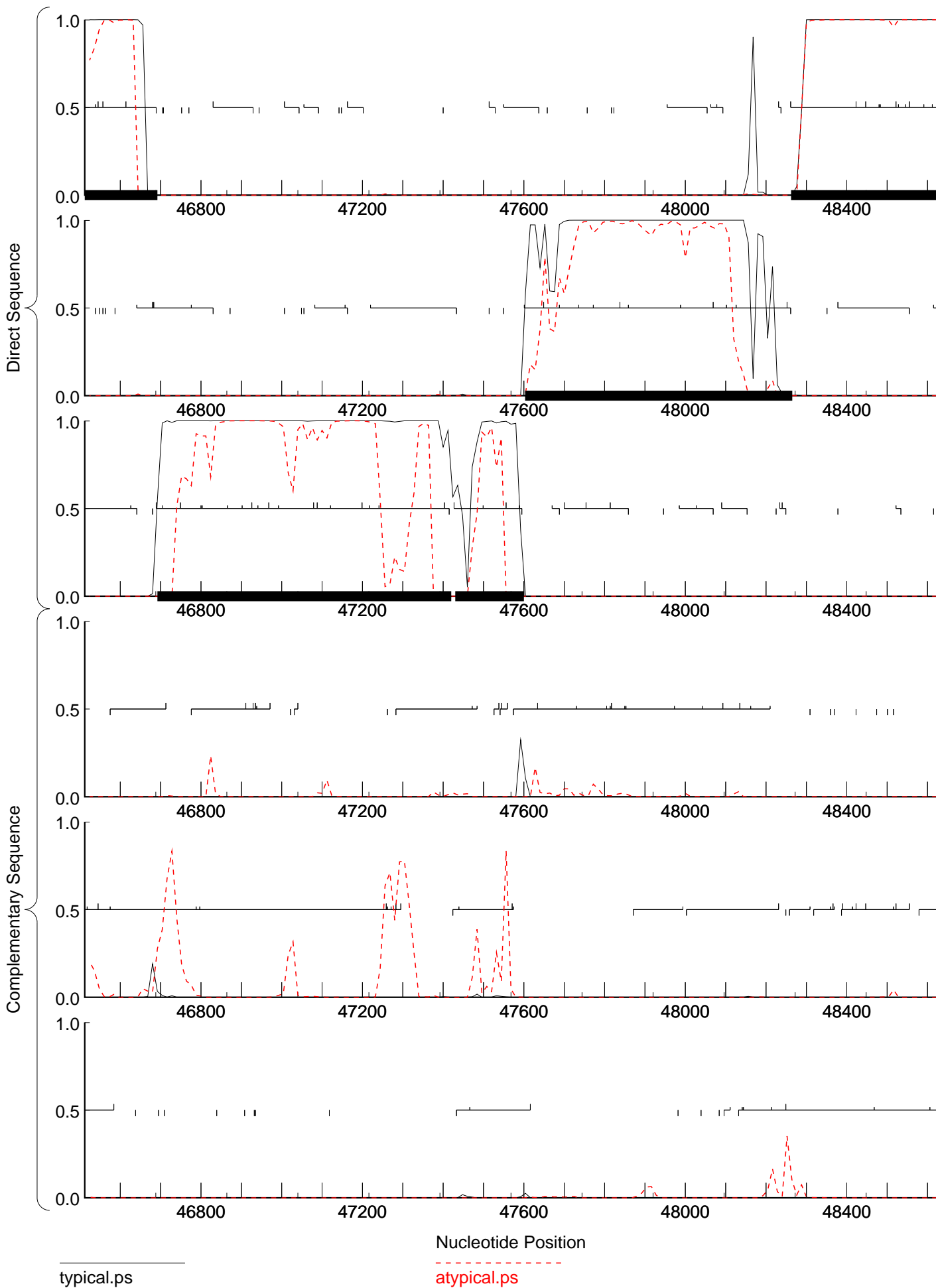
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typical.ps

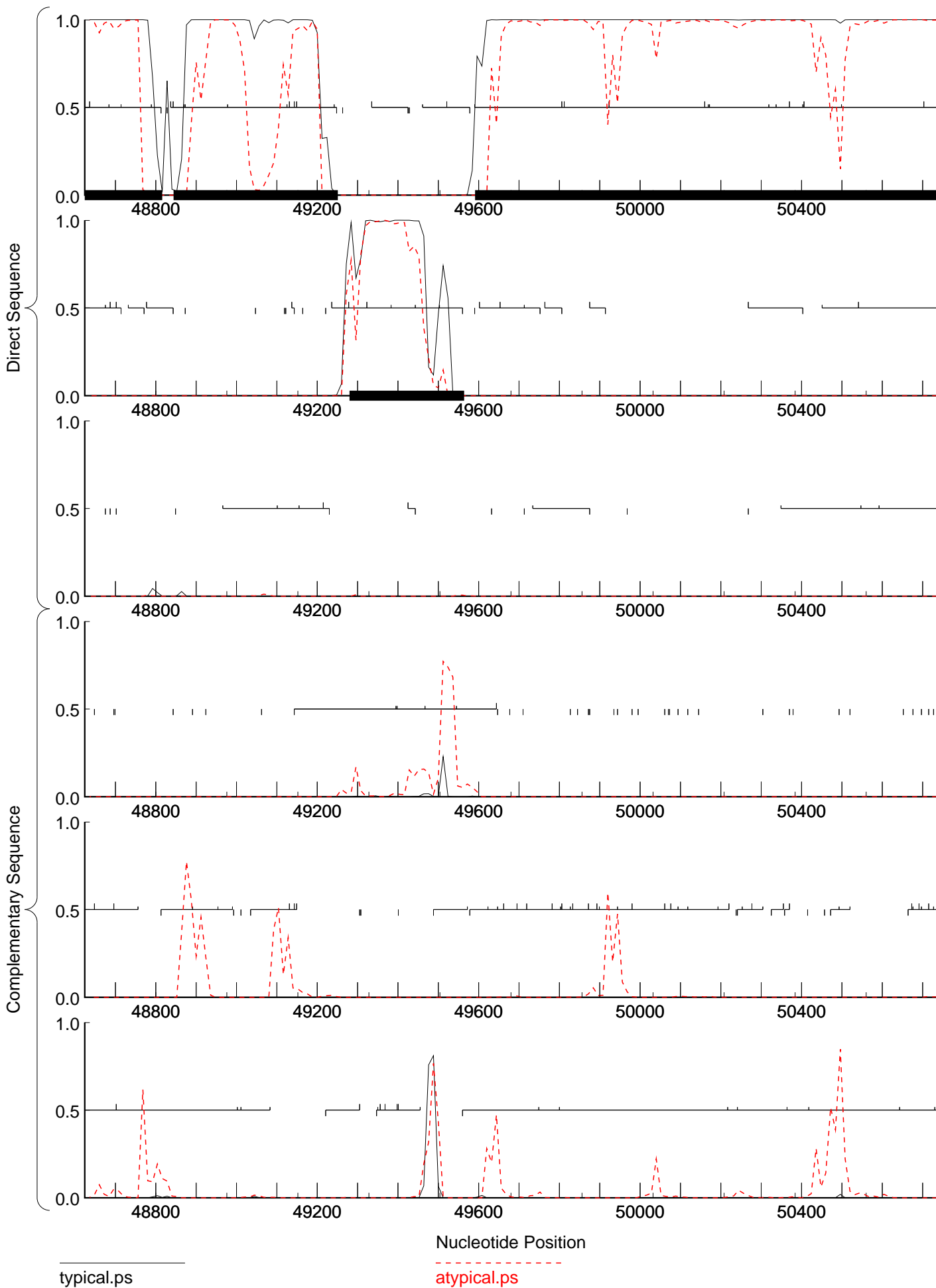
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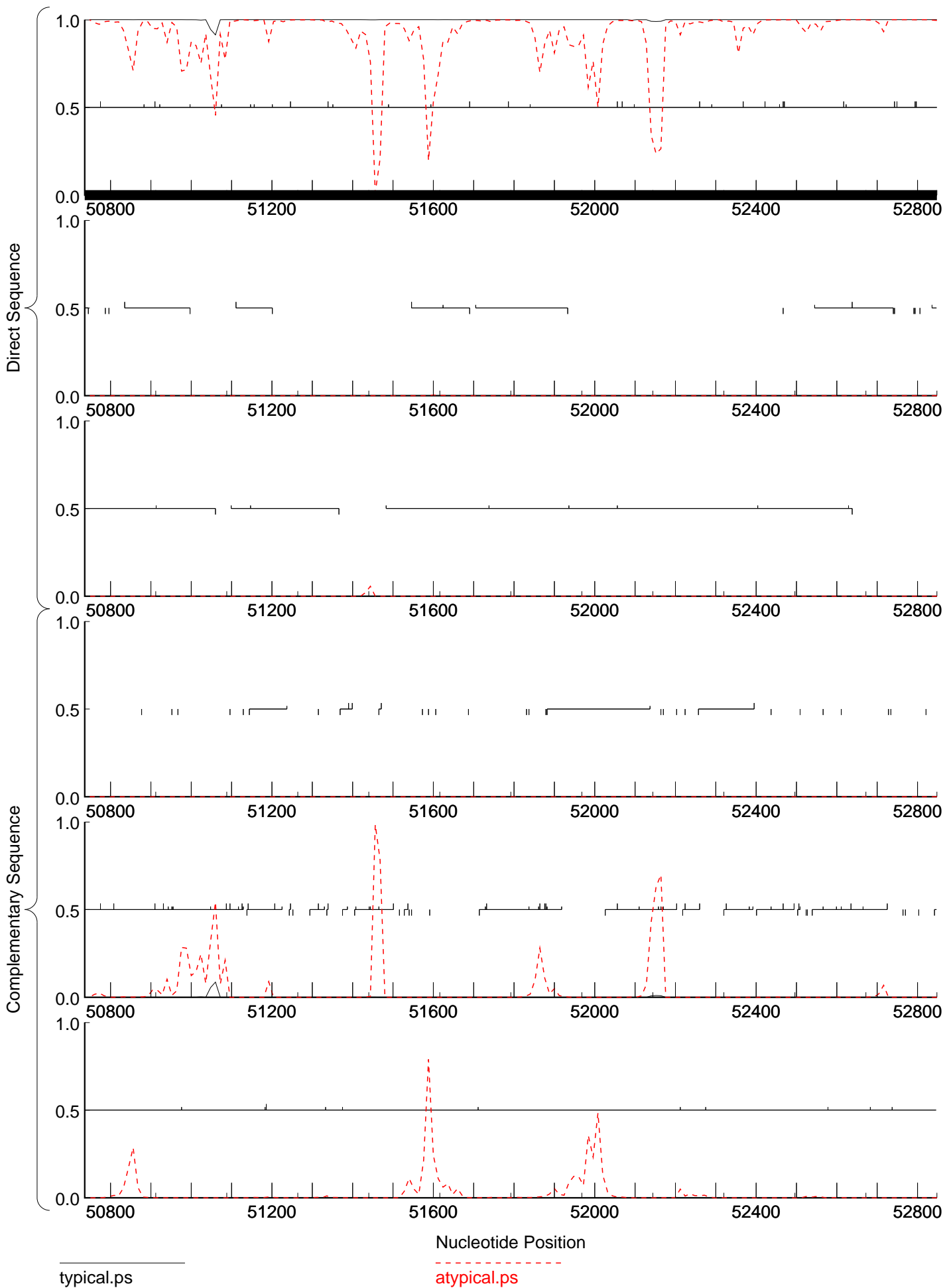


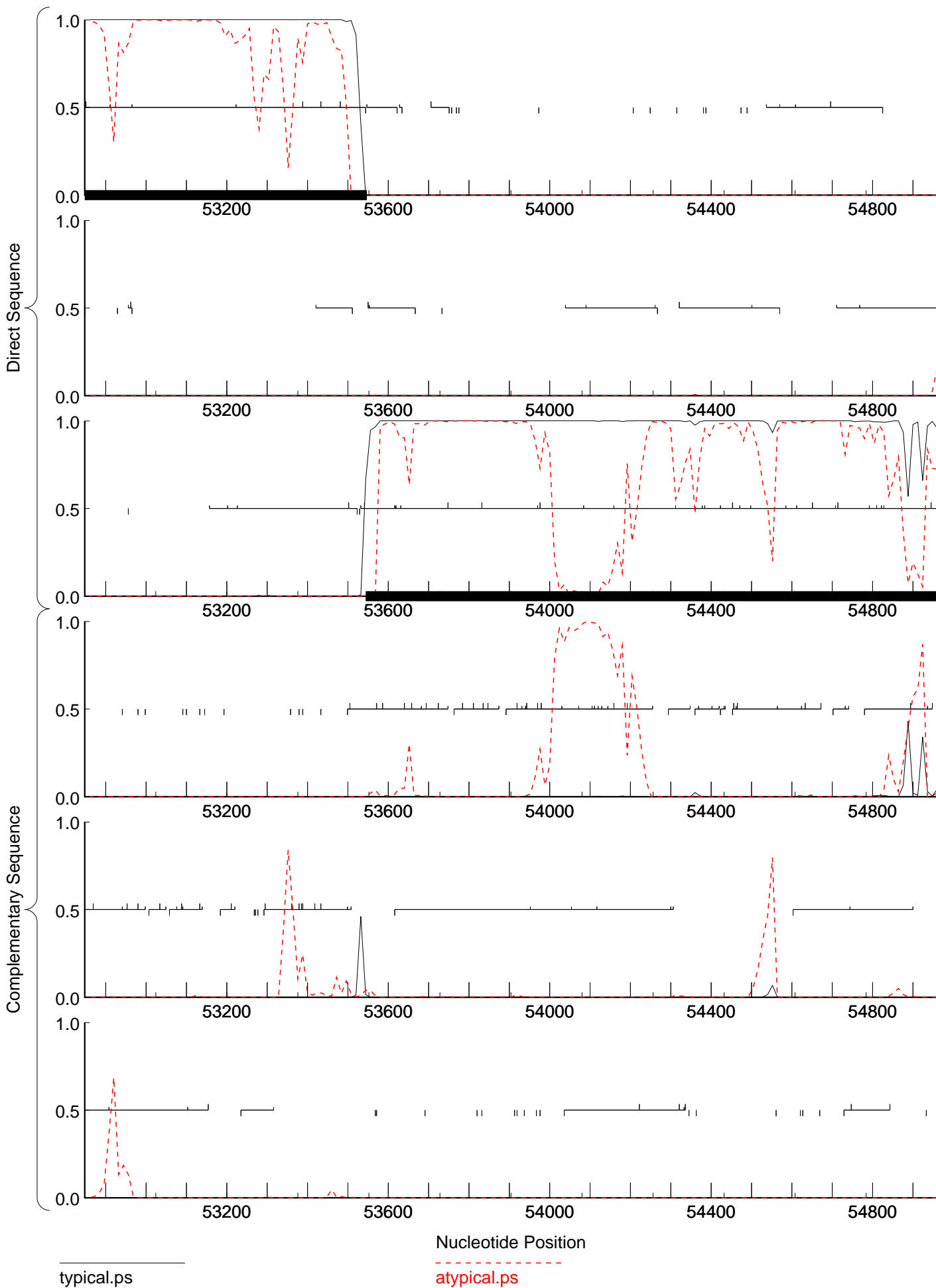


complete sequence, 65106 bp including 11-base 3' overhang (GCGCGCAGCGC), Cluster S, Order 4, Window 96, Step 12, 25/32  
GeneMark.hmm prediction  
complete sequence, 65106 bp including 11-base 3' overhang (GCGCGCAGCGC), Cluster S, Order 2, Window 96, Step 12, 25/32



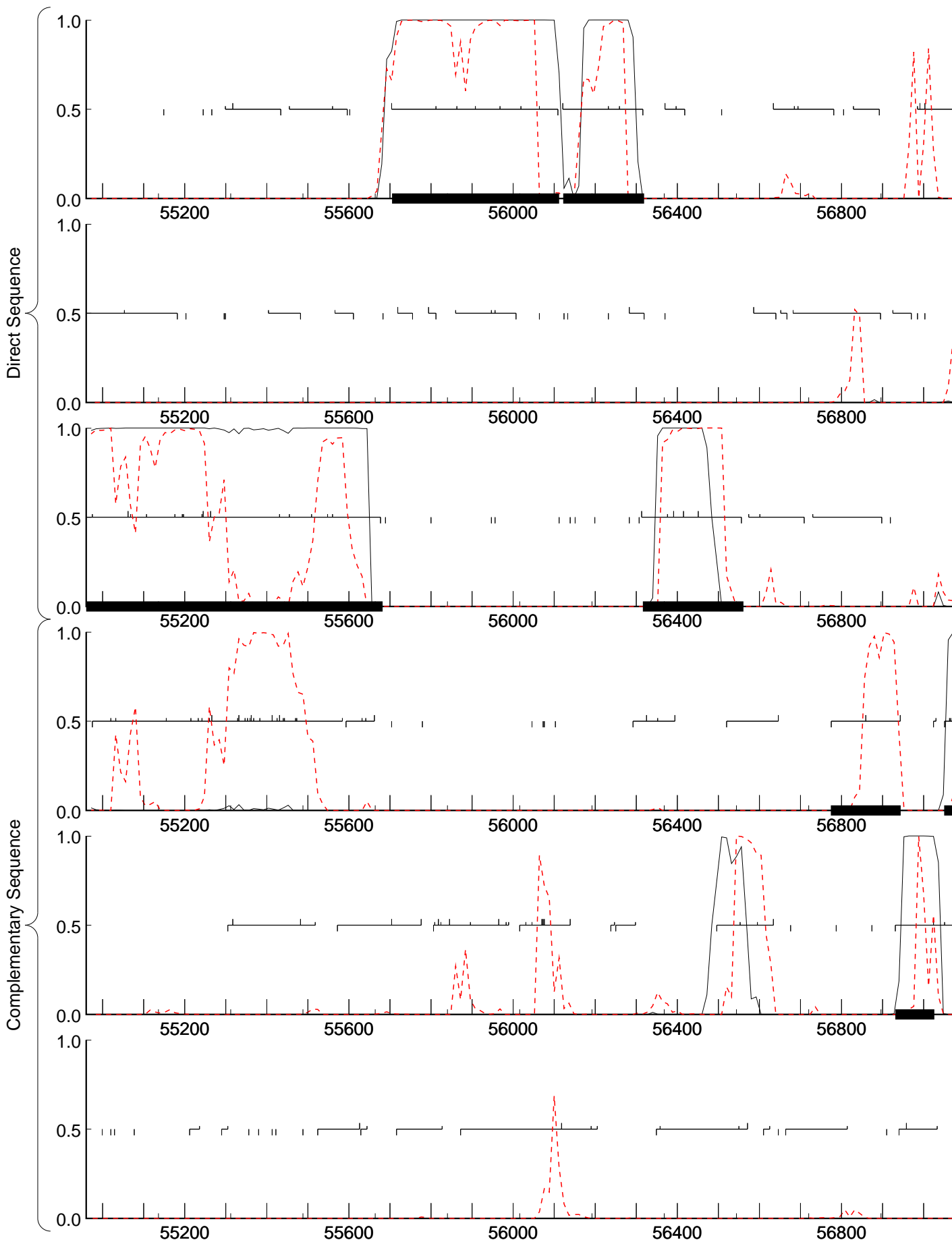
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complete sequence, 65106 bp including 11-base 3' overhang (GCGCGCAGCGC), Cluster S, Order 2, Window 96, Step 12, 26/32





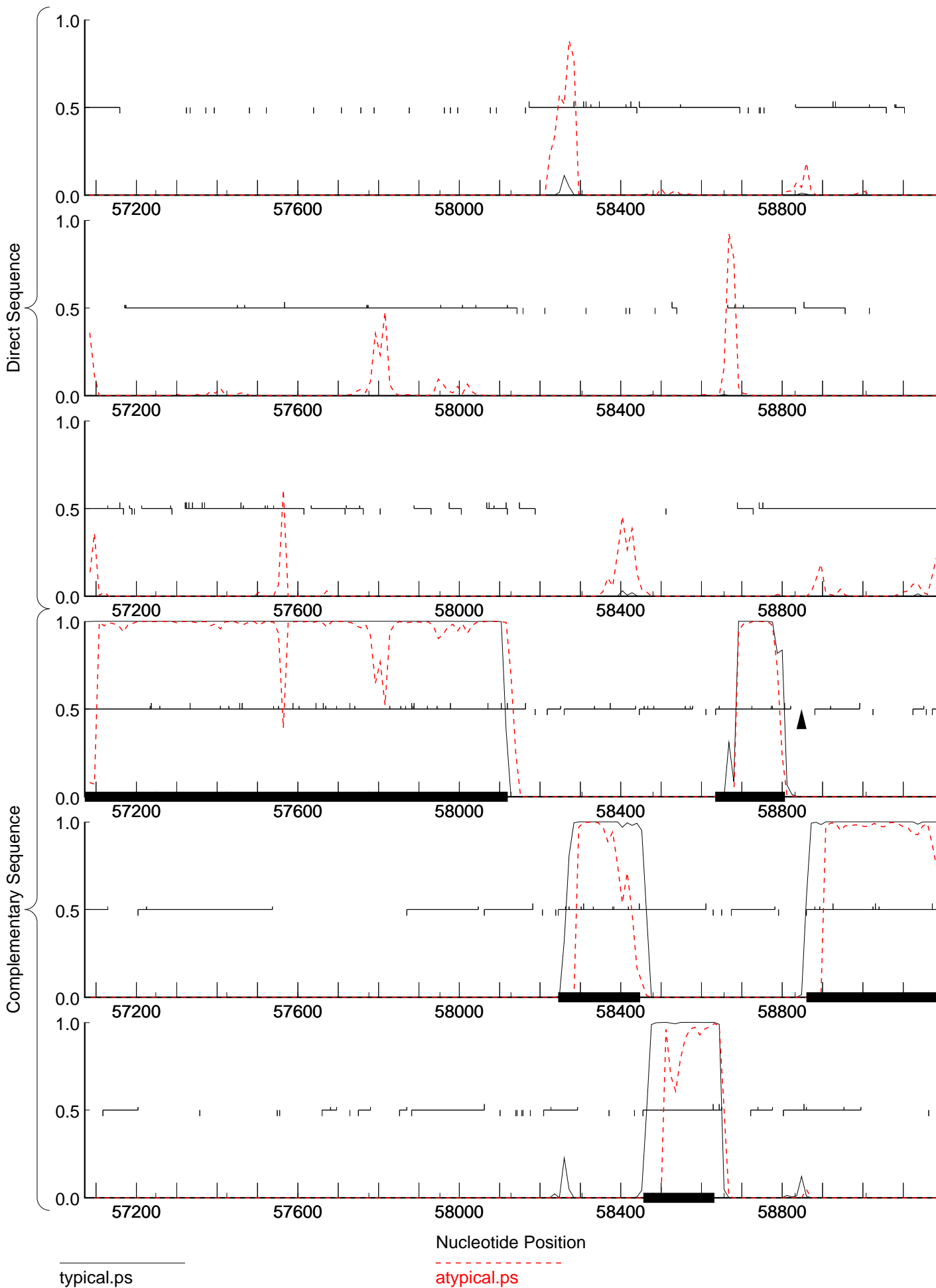
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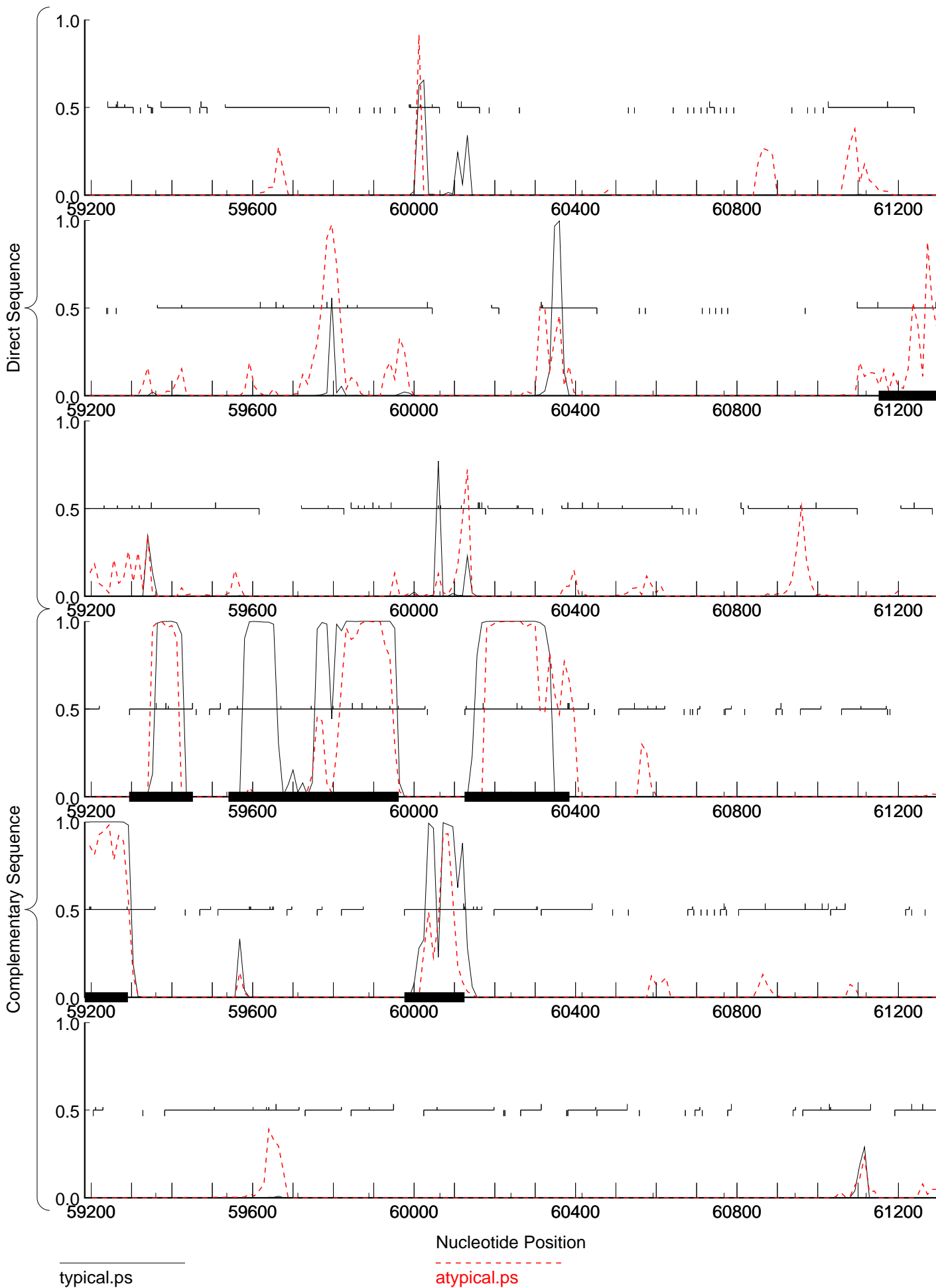
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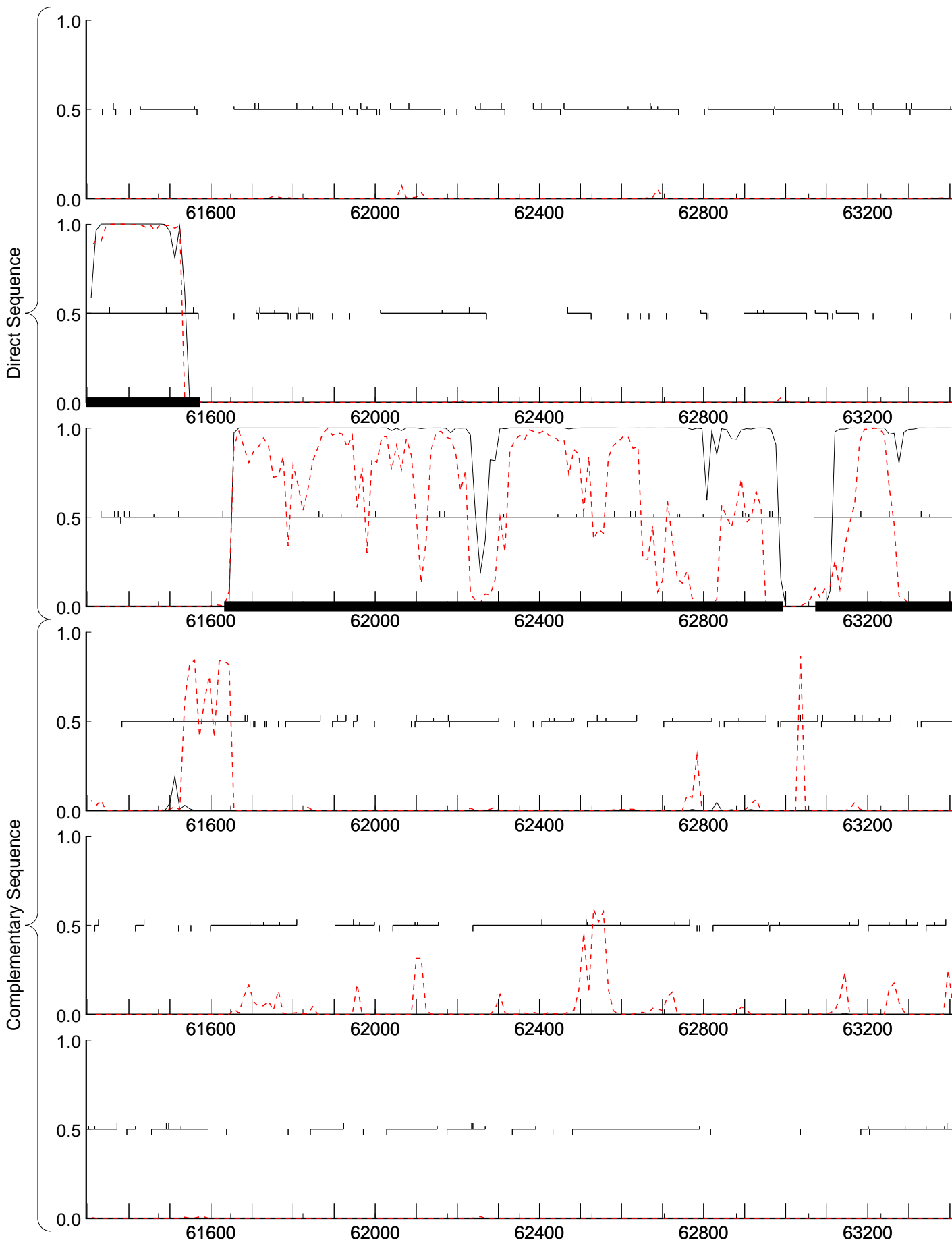


typical.ps

atypical.ps







typical.ps

Nucleotide Position

atypical.ps

