

GeneMark

Version 2.5p (09.08.06)

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PROGRAM INFORMATION

Sequence : Mycobacterium phage ChotaBhai complete sequence, 76145 bp including 9-base 3' overhang (CGC
Analysis Date : 4/22/18 at 4:11:11
Pages : 38
Sequence Length : 76145 bp
GC Content : 62.91%

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,

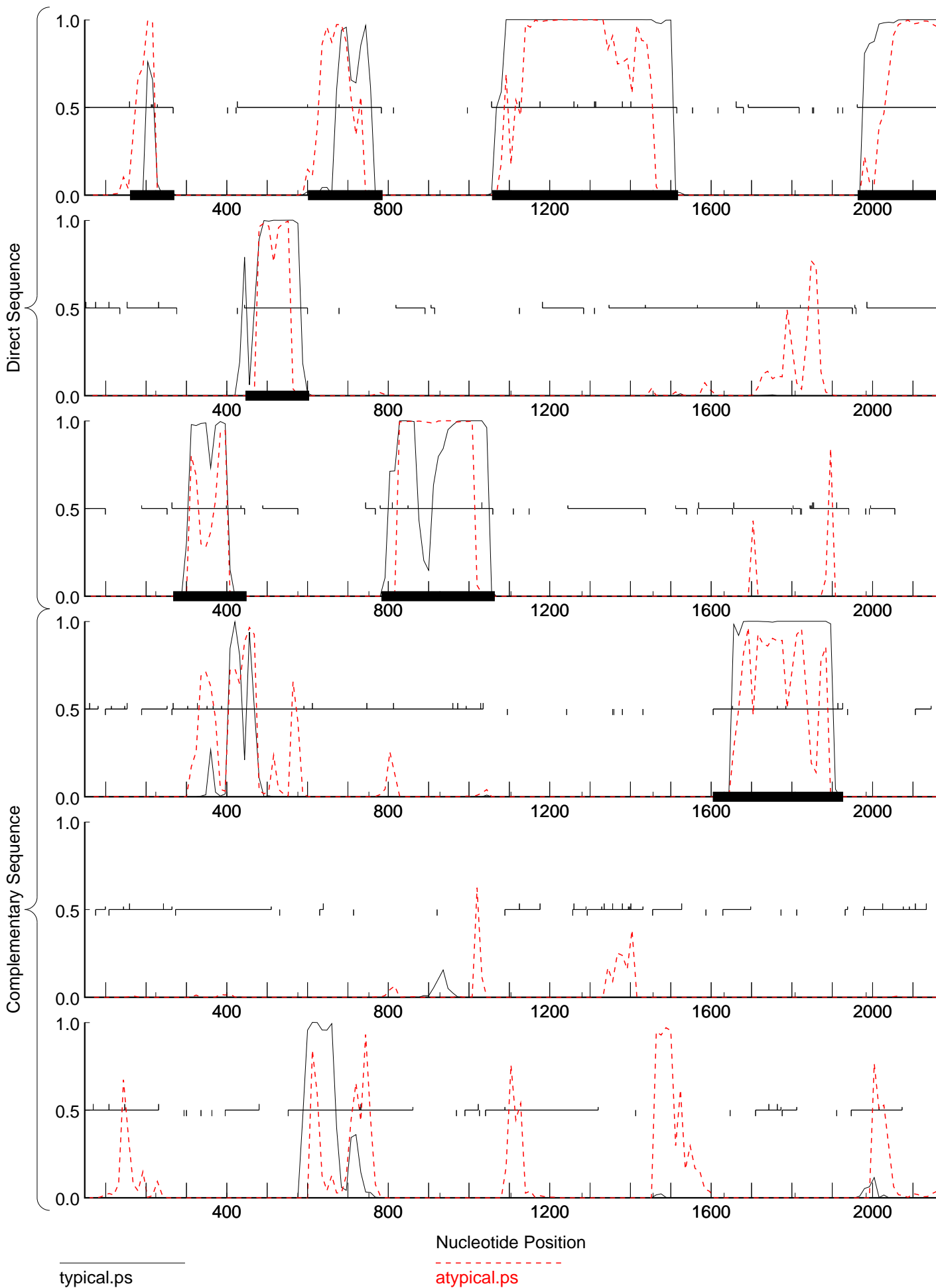
Matrix notes & comments

Training set derived by GeneMarkS, 4.30 October 2014
Sun Apr 22 04:11:11 2018

MATRIX INFORMATION

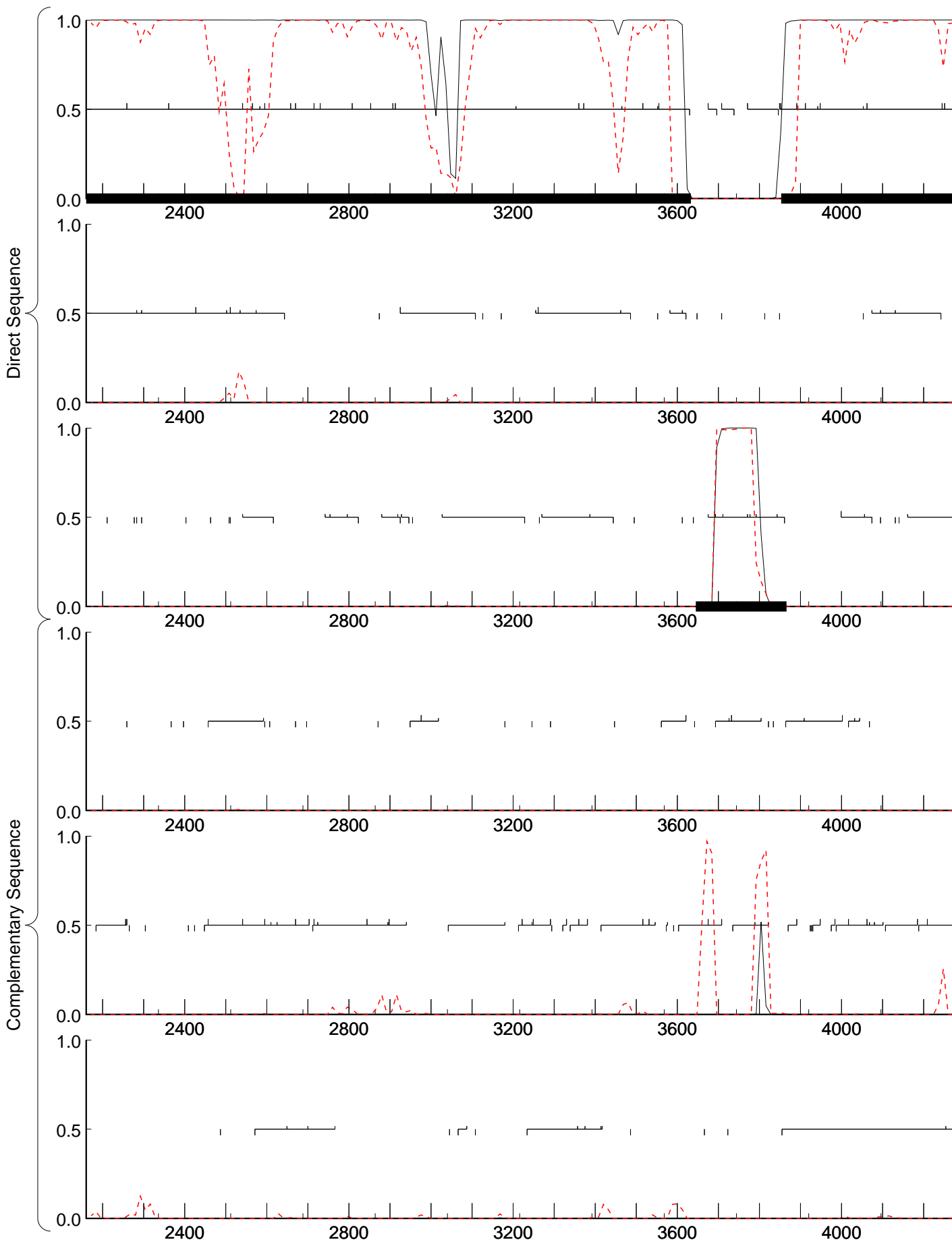
Matrix : -
Author : -
Order : 4

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



typical.ps

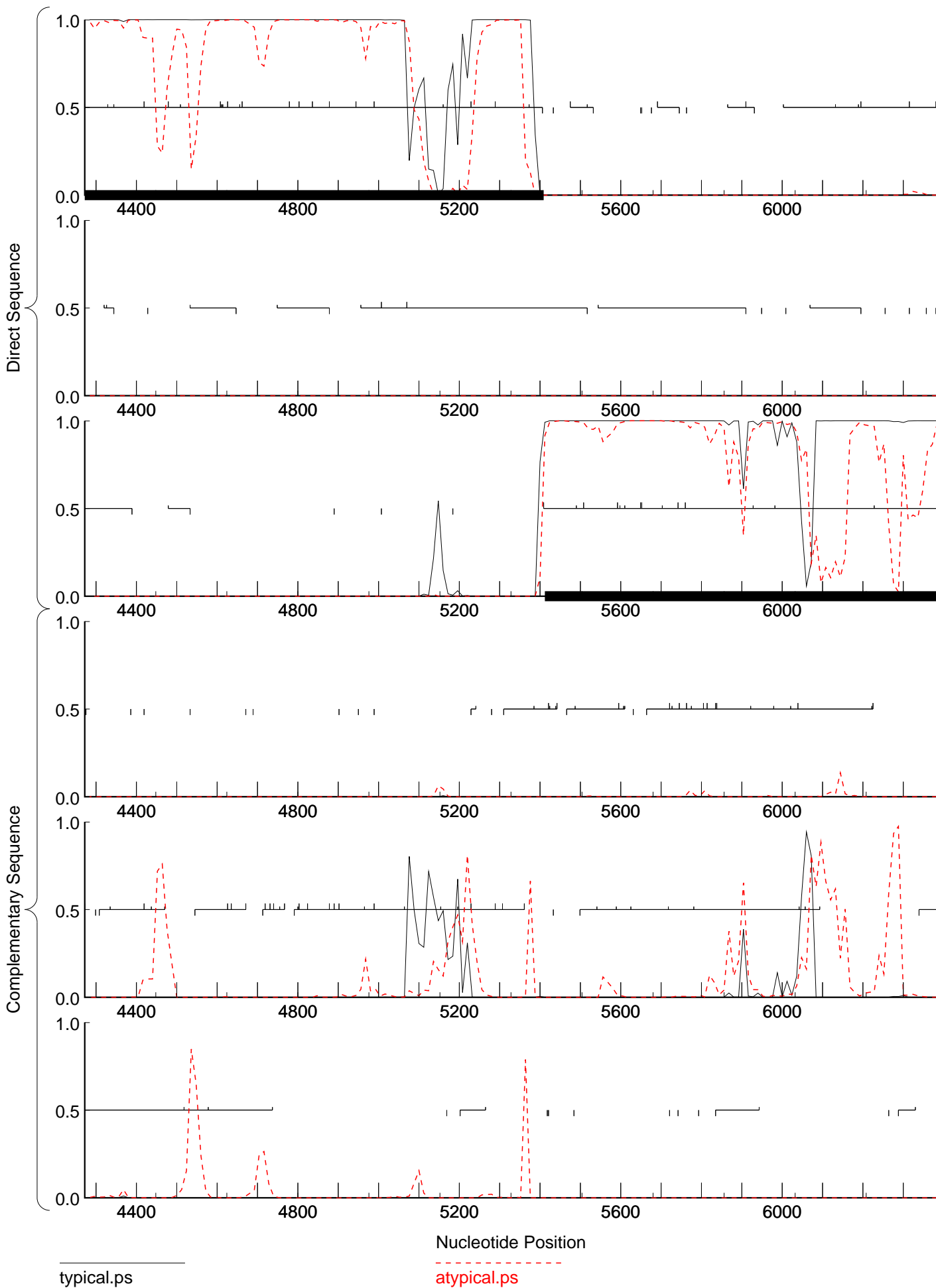
atypical.ps



Nucleotide Position

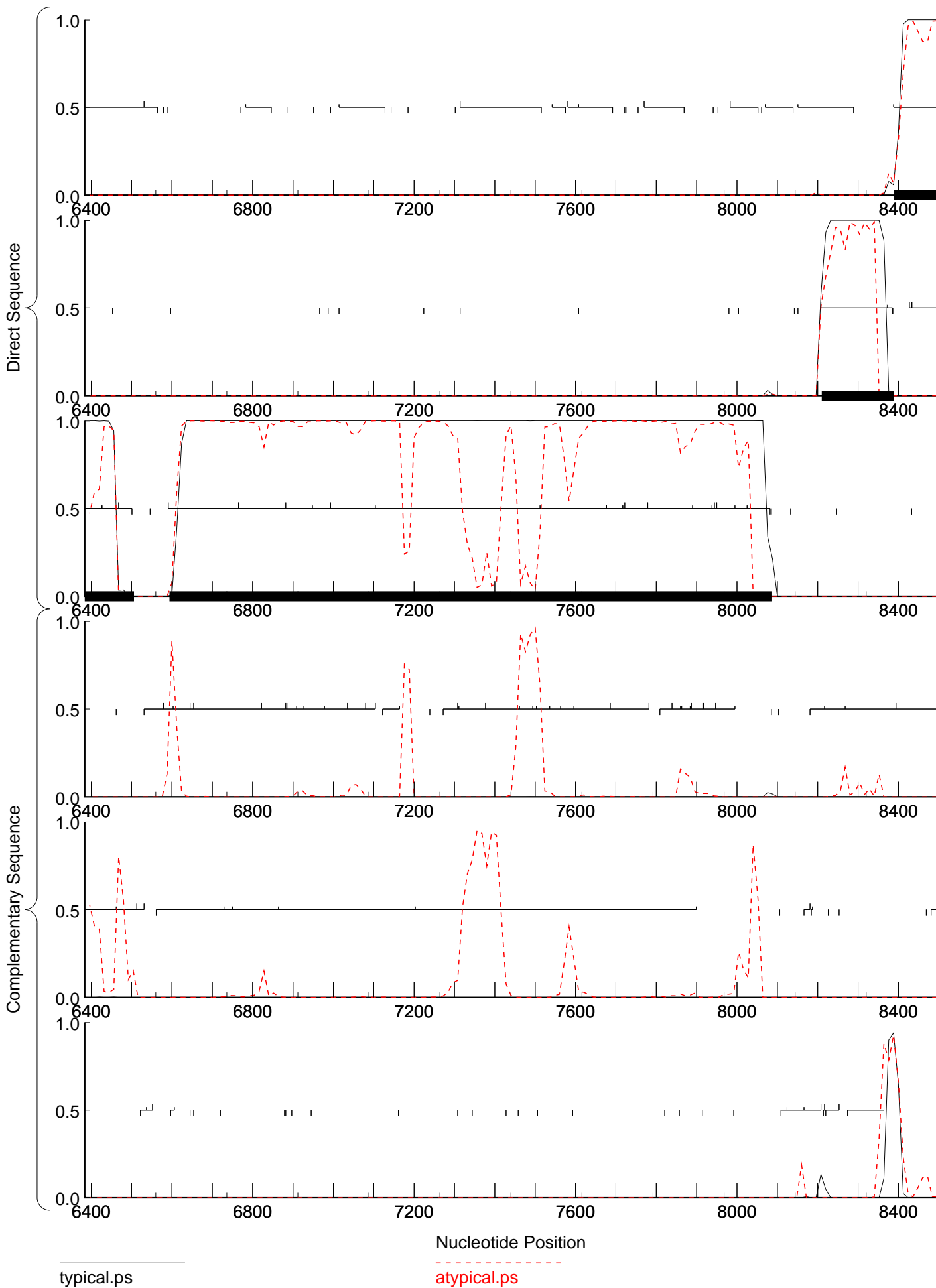
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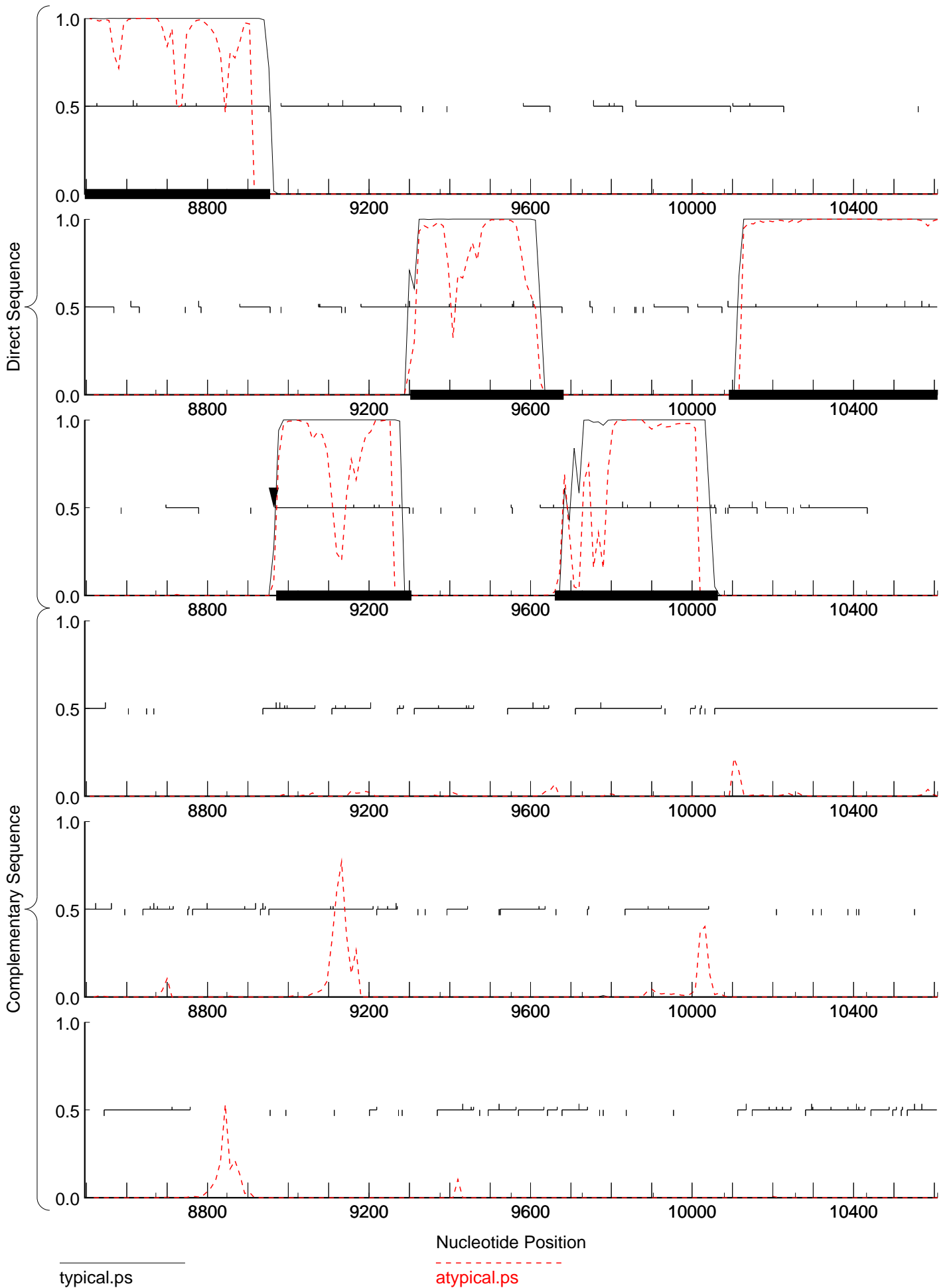
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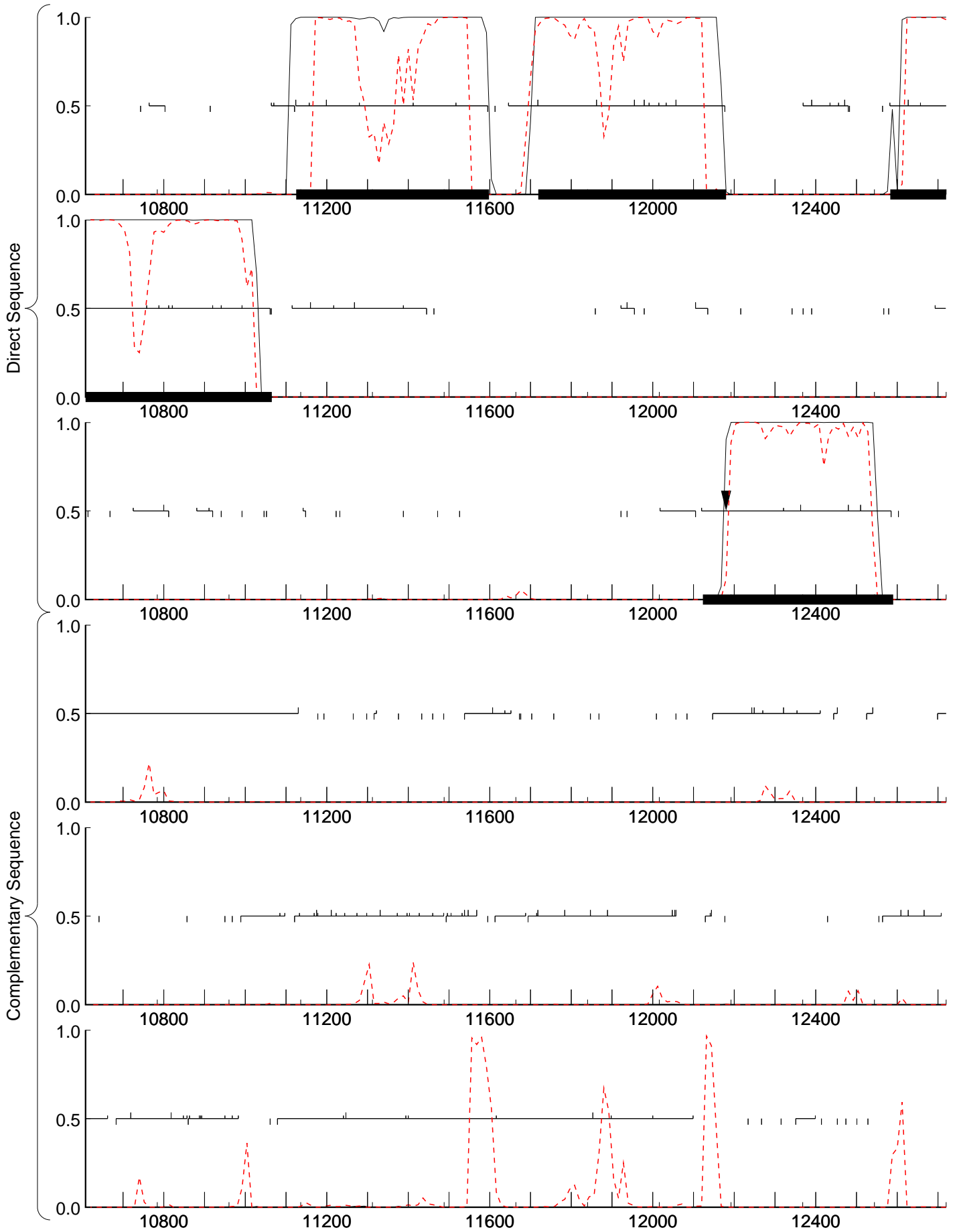


typical.ps

atypical.ps

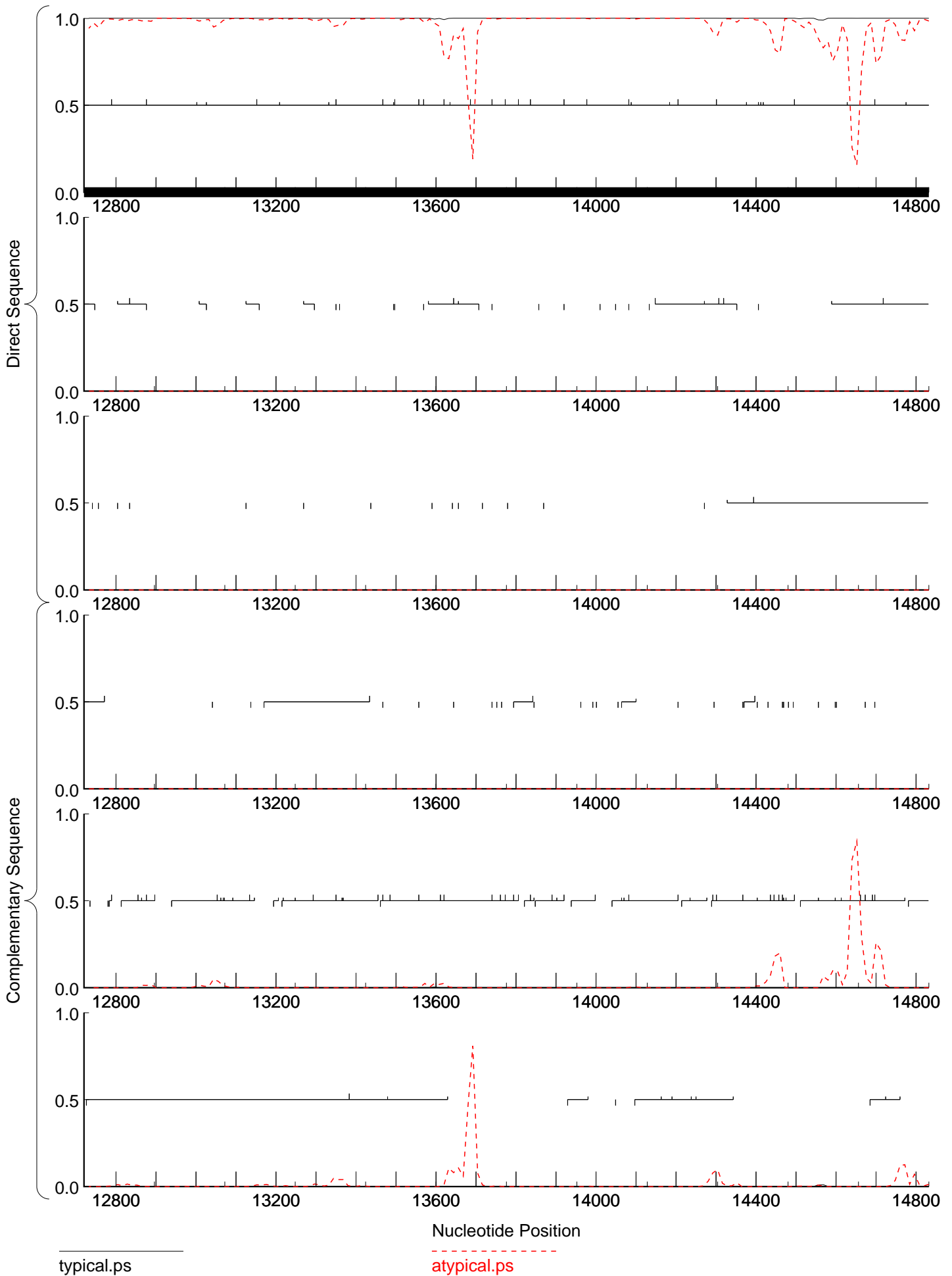


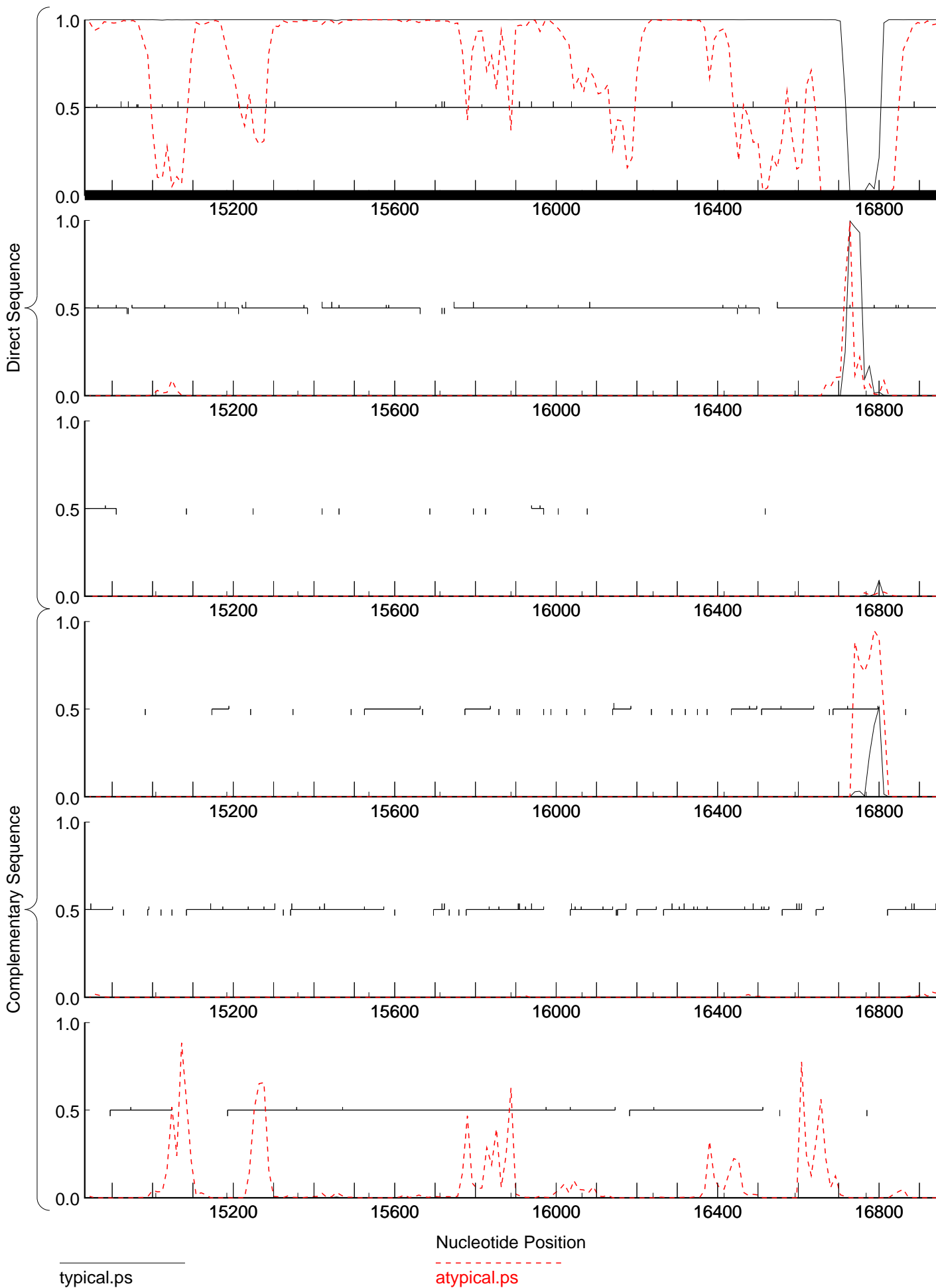




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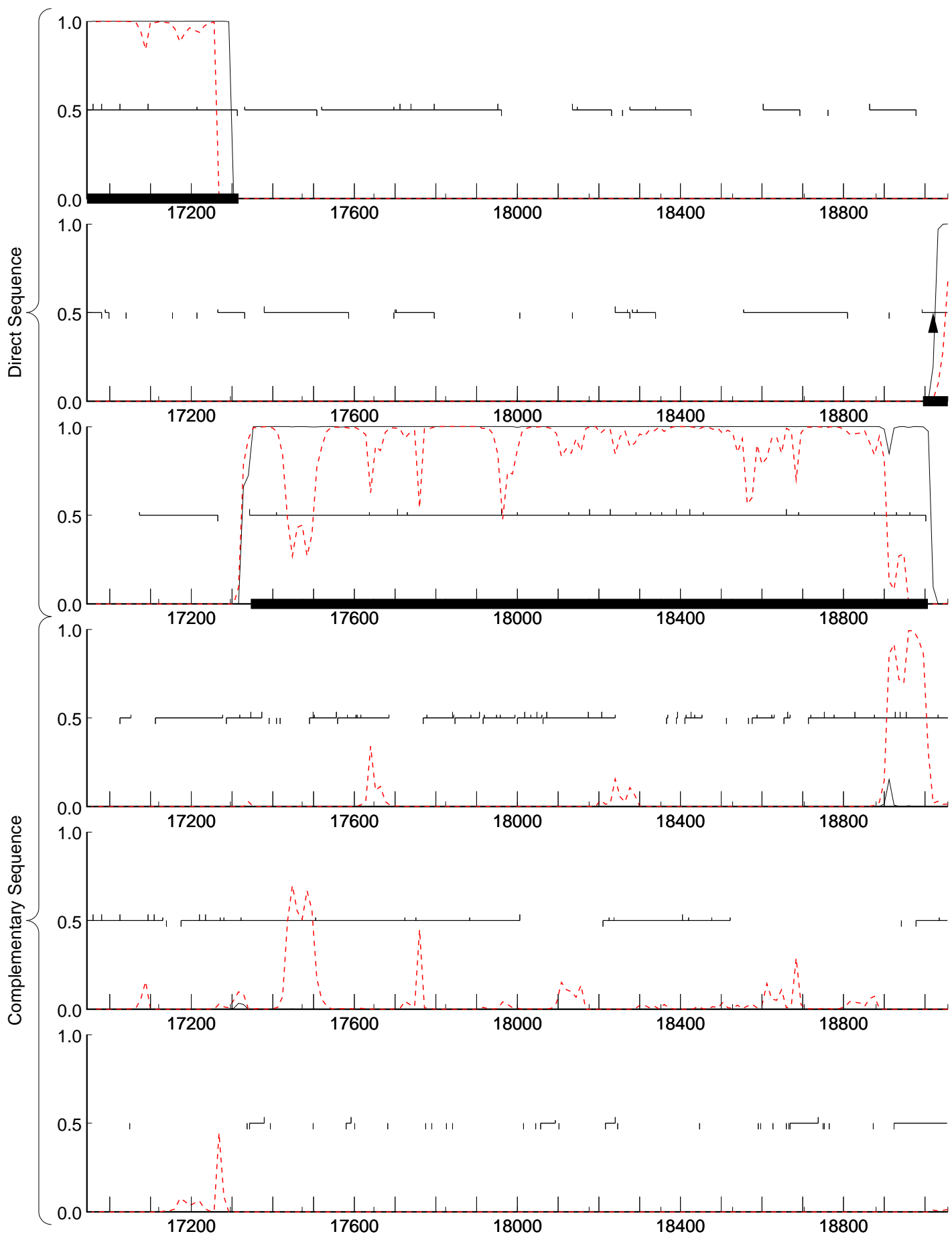
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typical.ps

atypical.ps

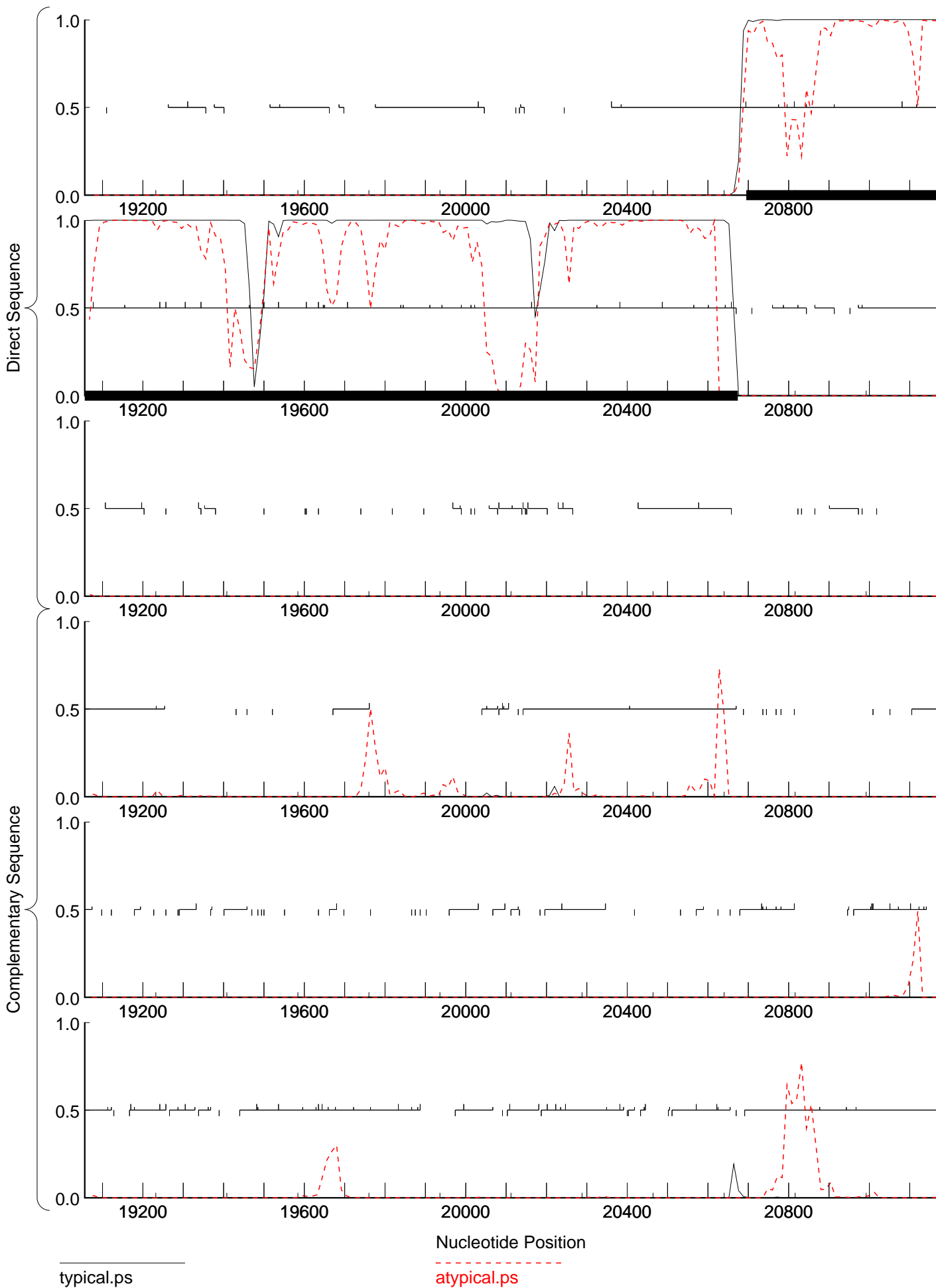


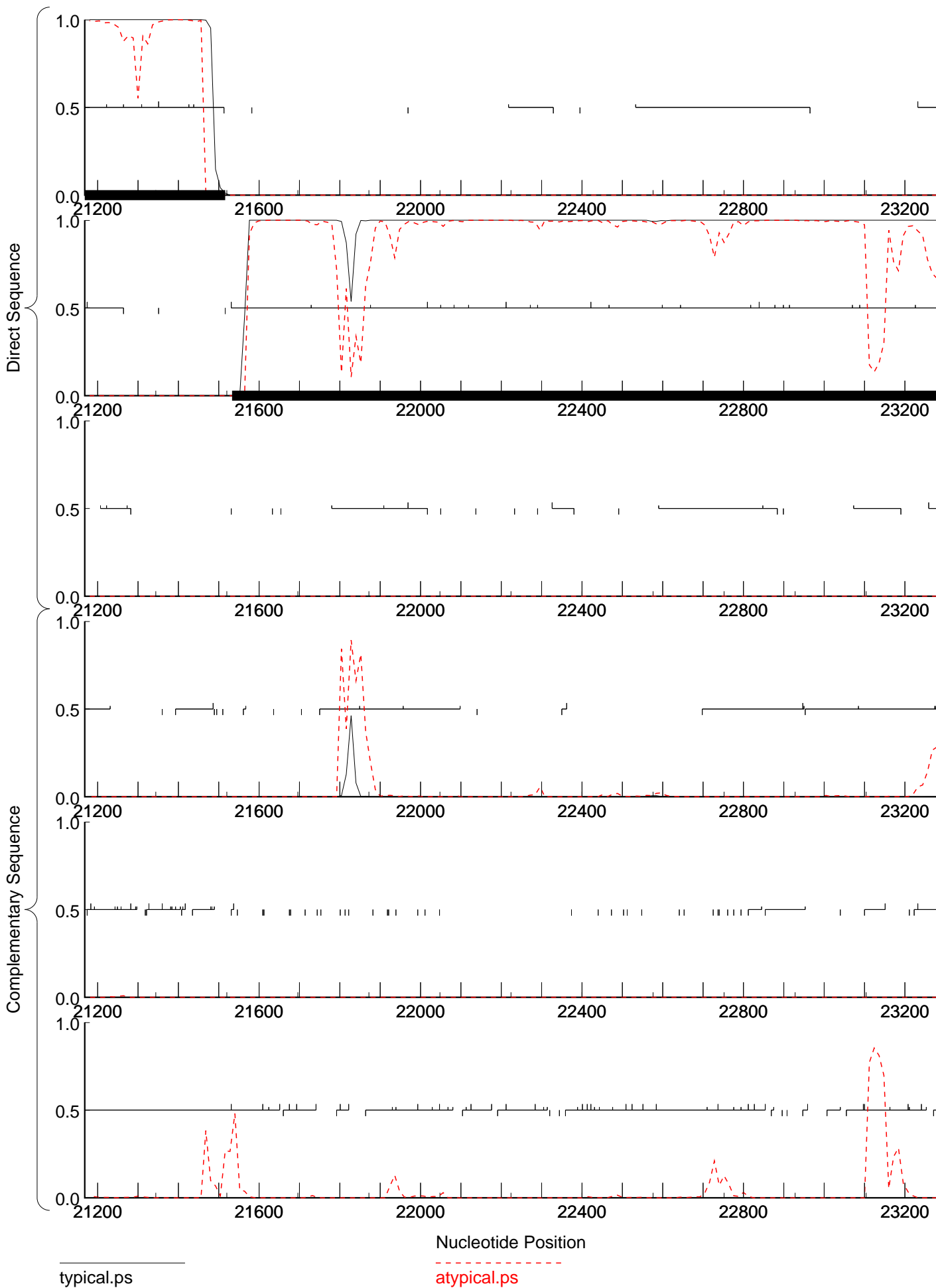
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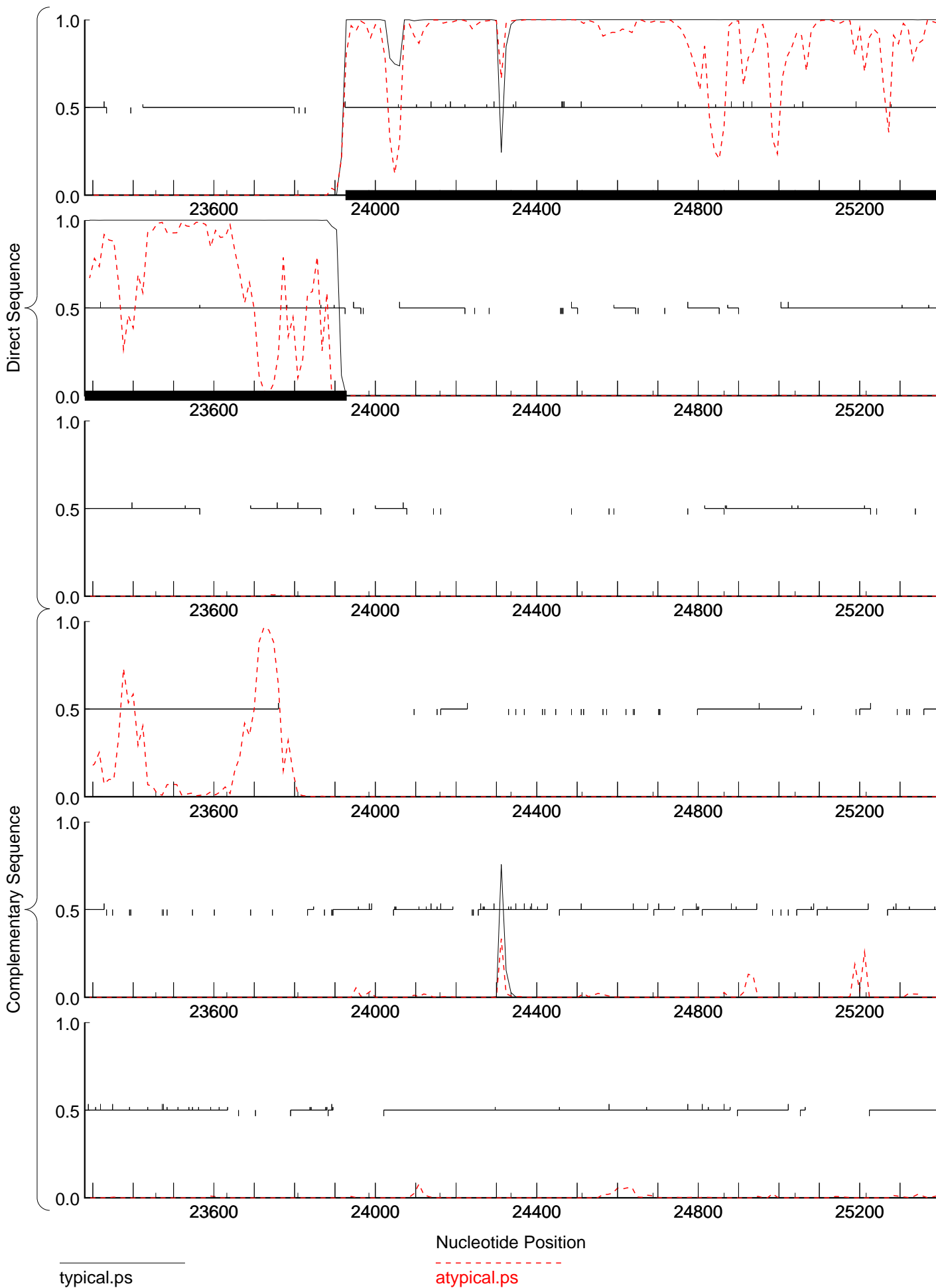
Nucleotide Position

atypical.ps

Bhai complete sequence, 76145 bp including 9-base 3' overhang (CGCTTGTC A), Cluster E, Order 4, Window 96, Step 12, 11/38
GeneMark.hmm prediction
Bhai complete sequence, 76145 bp including 9-base 3' overhang (CGCTTGTC A), Cluster E, Order 2, Window 96, Step 12, 11/38

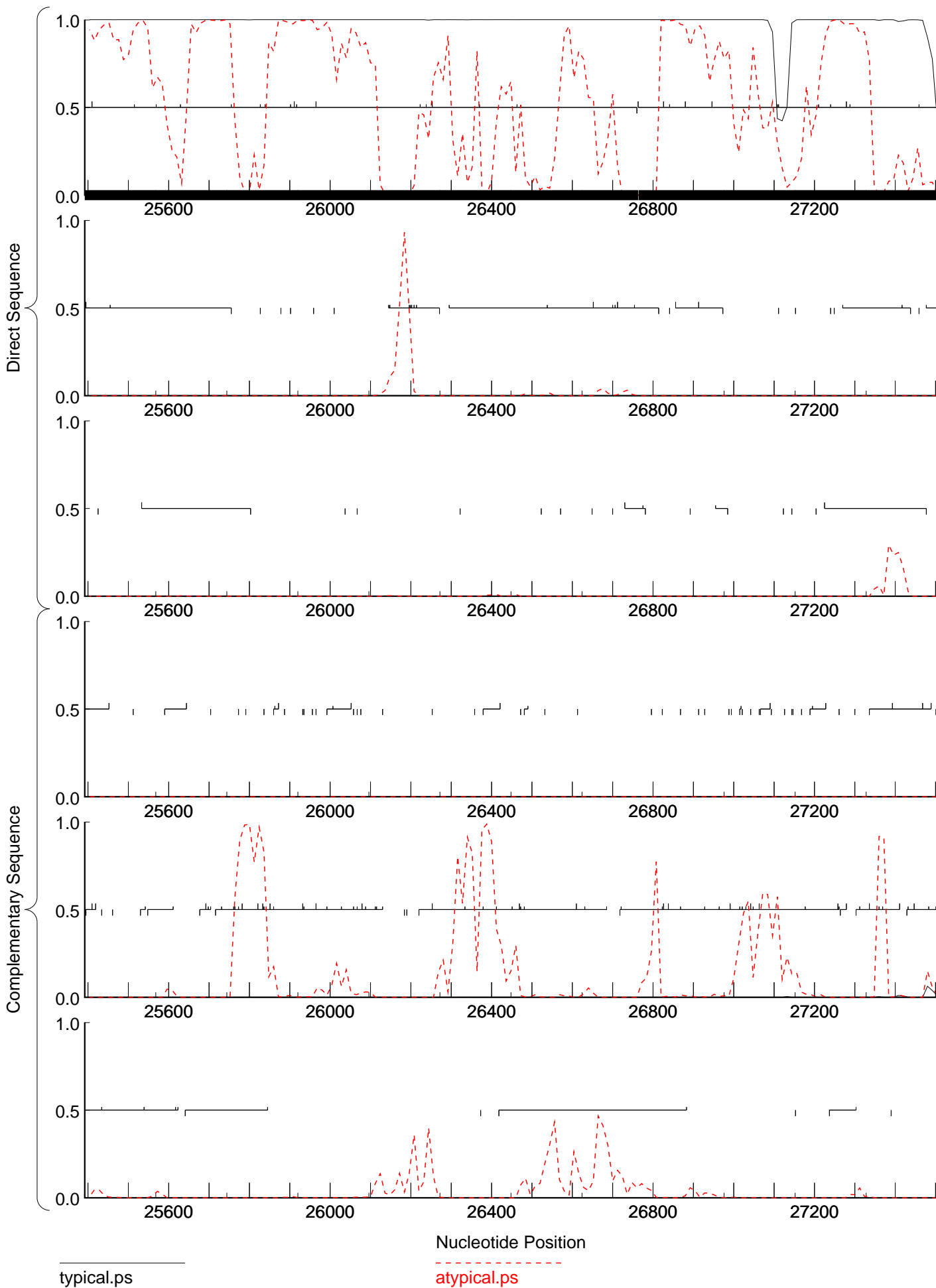






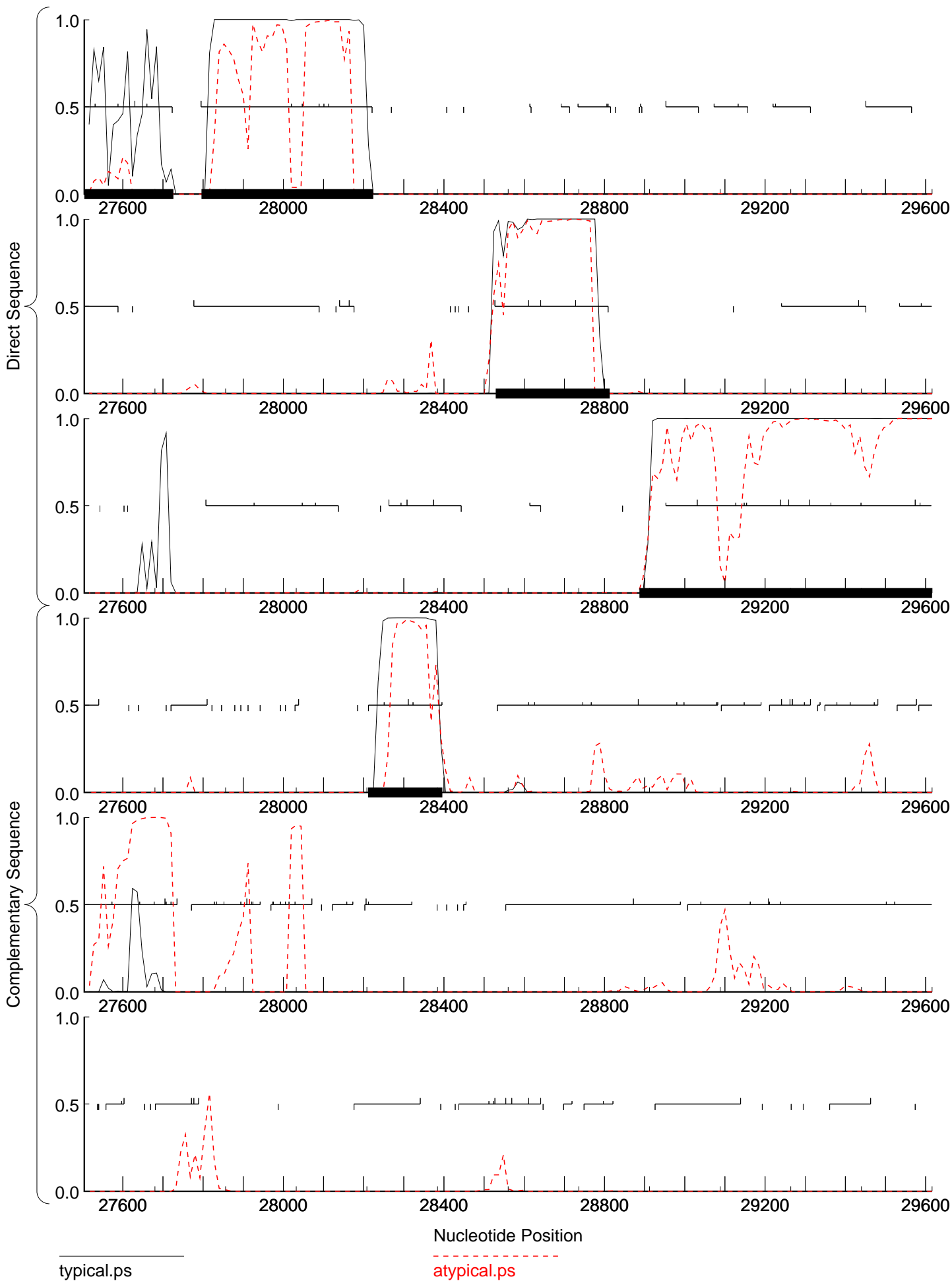
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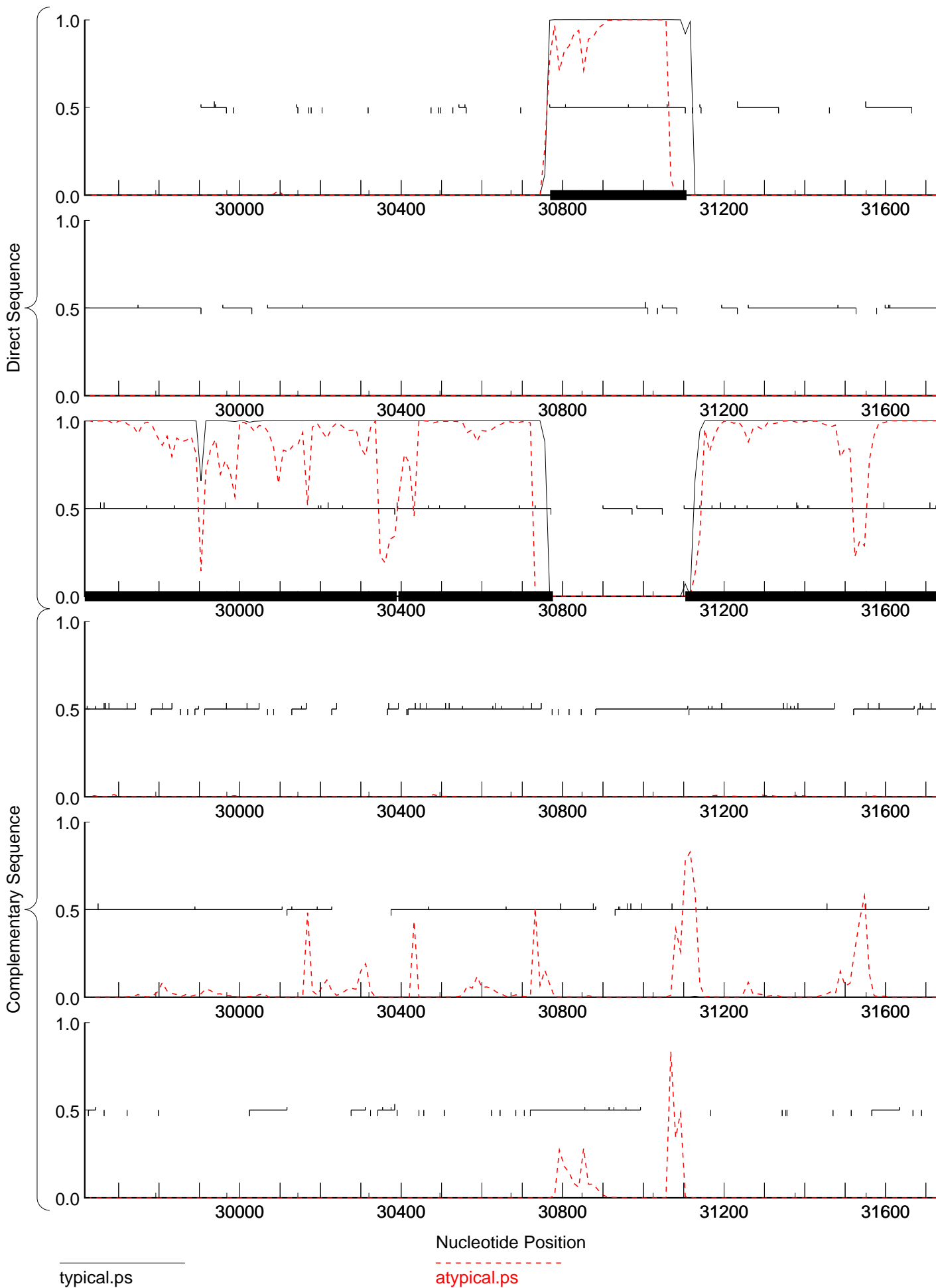
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typical.ps

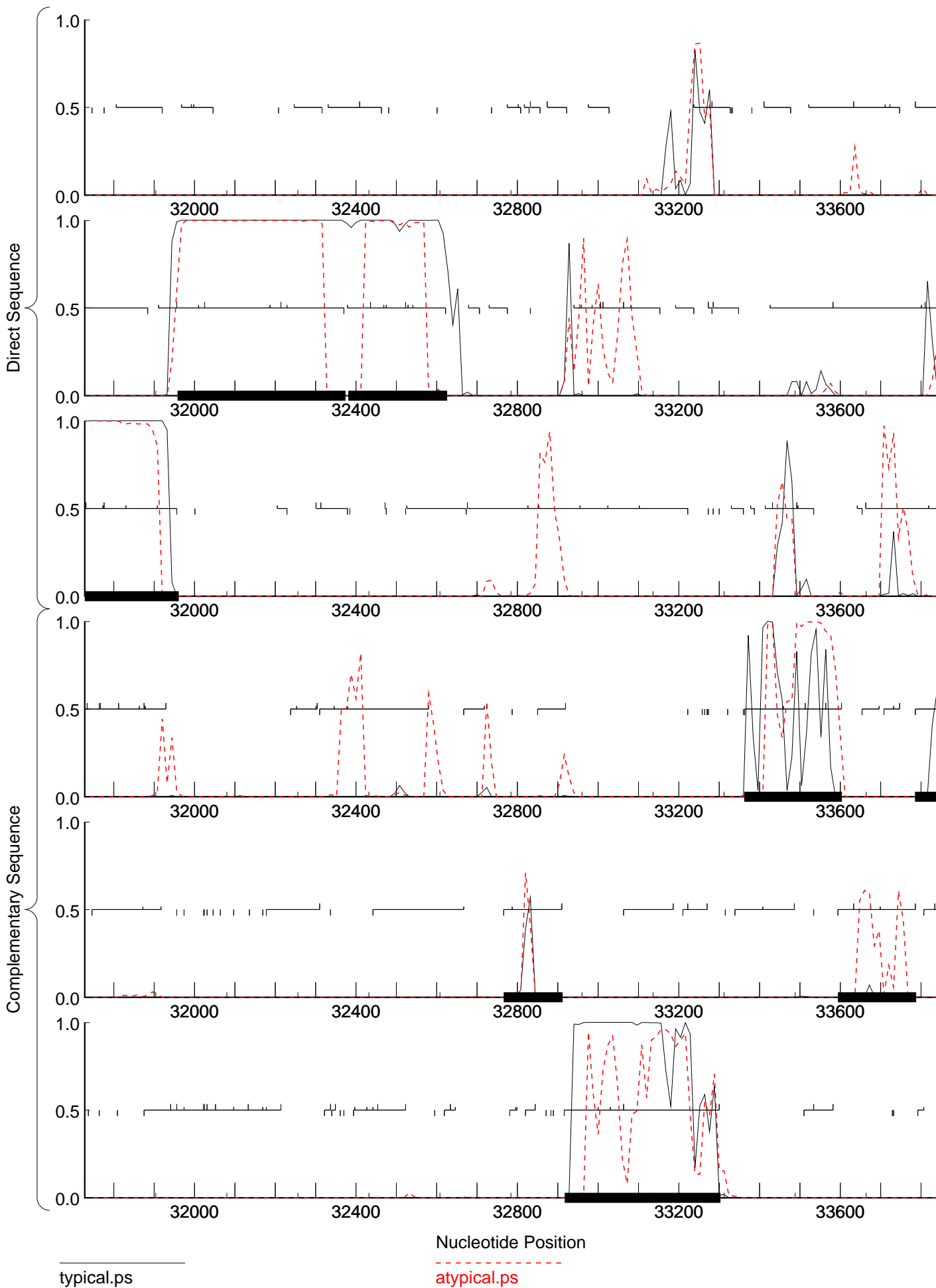
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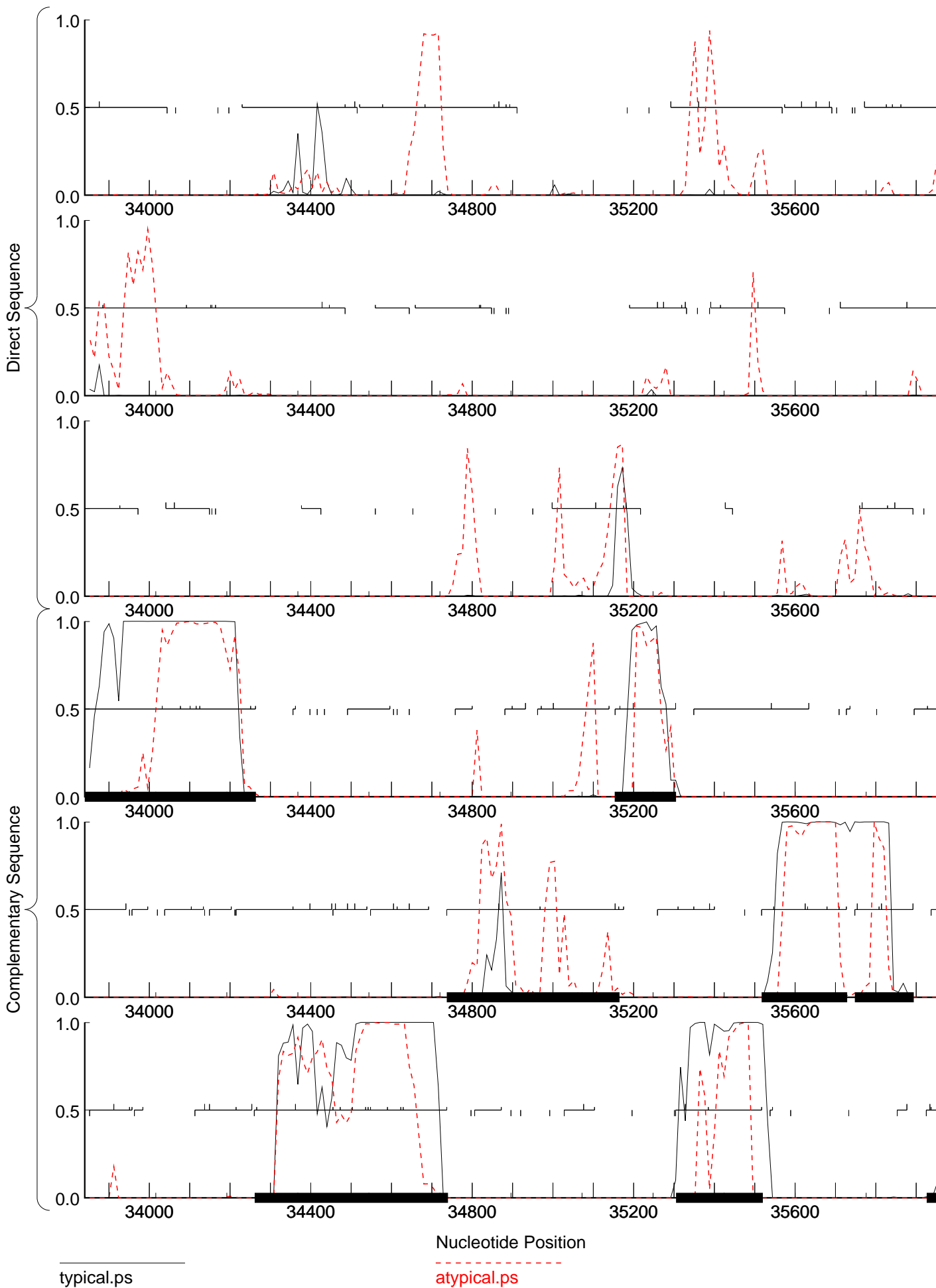


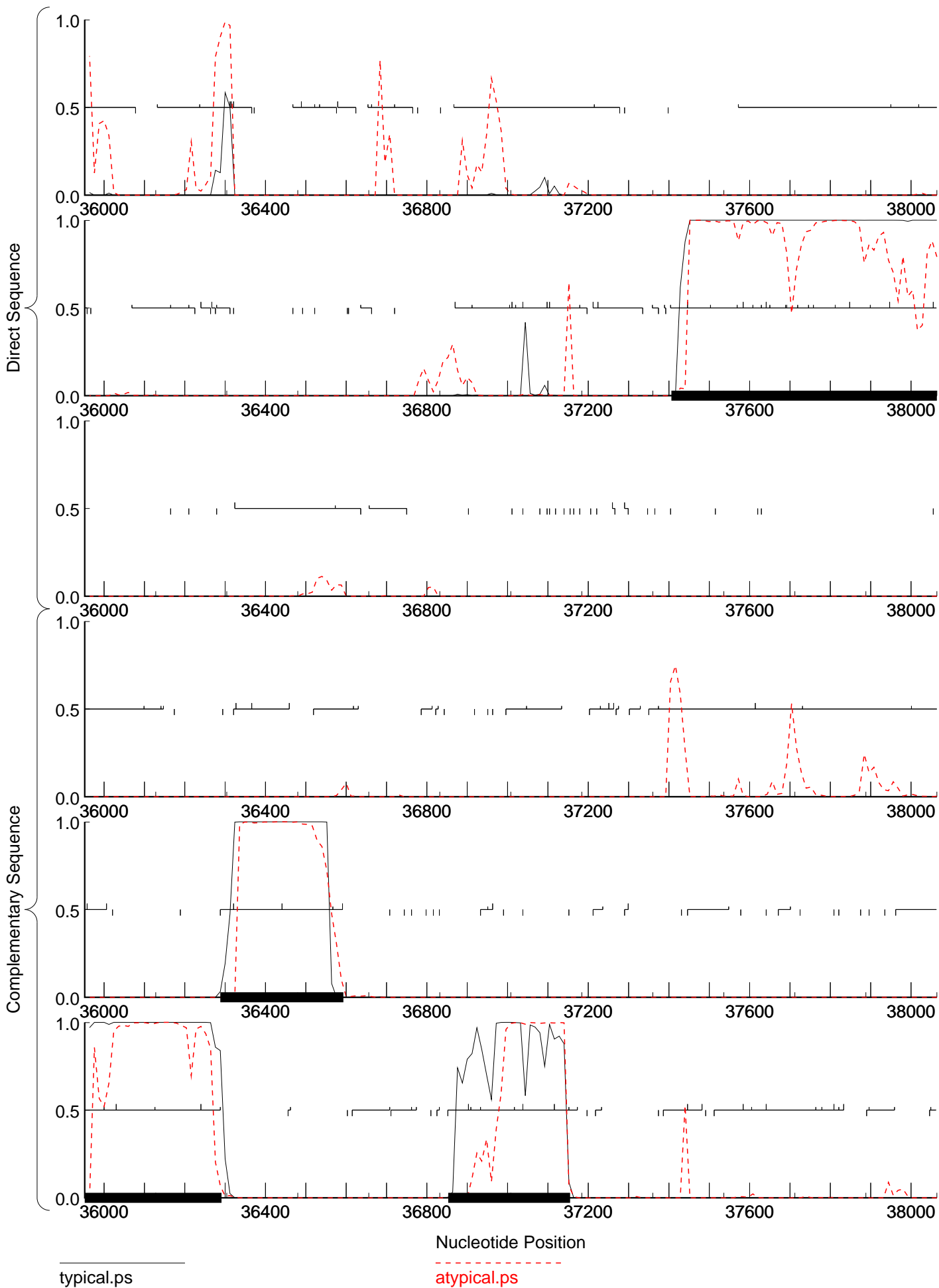


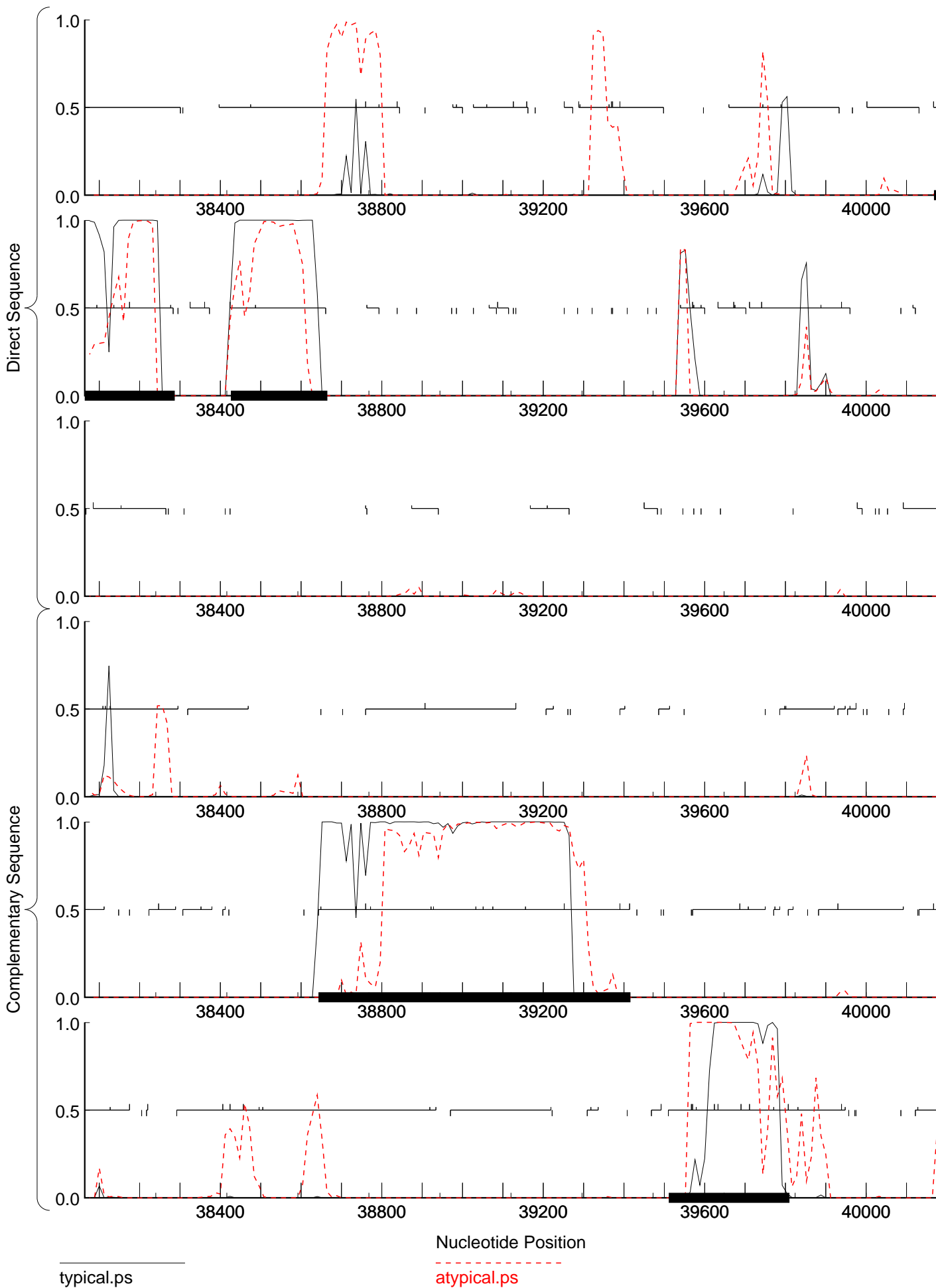
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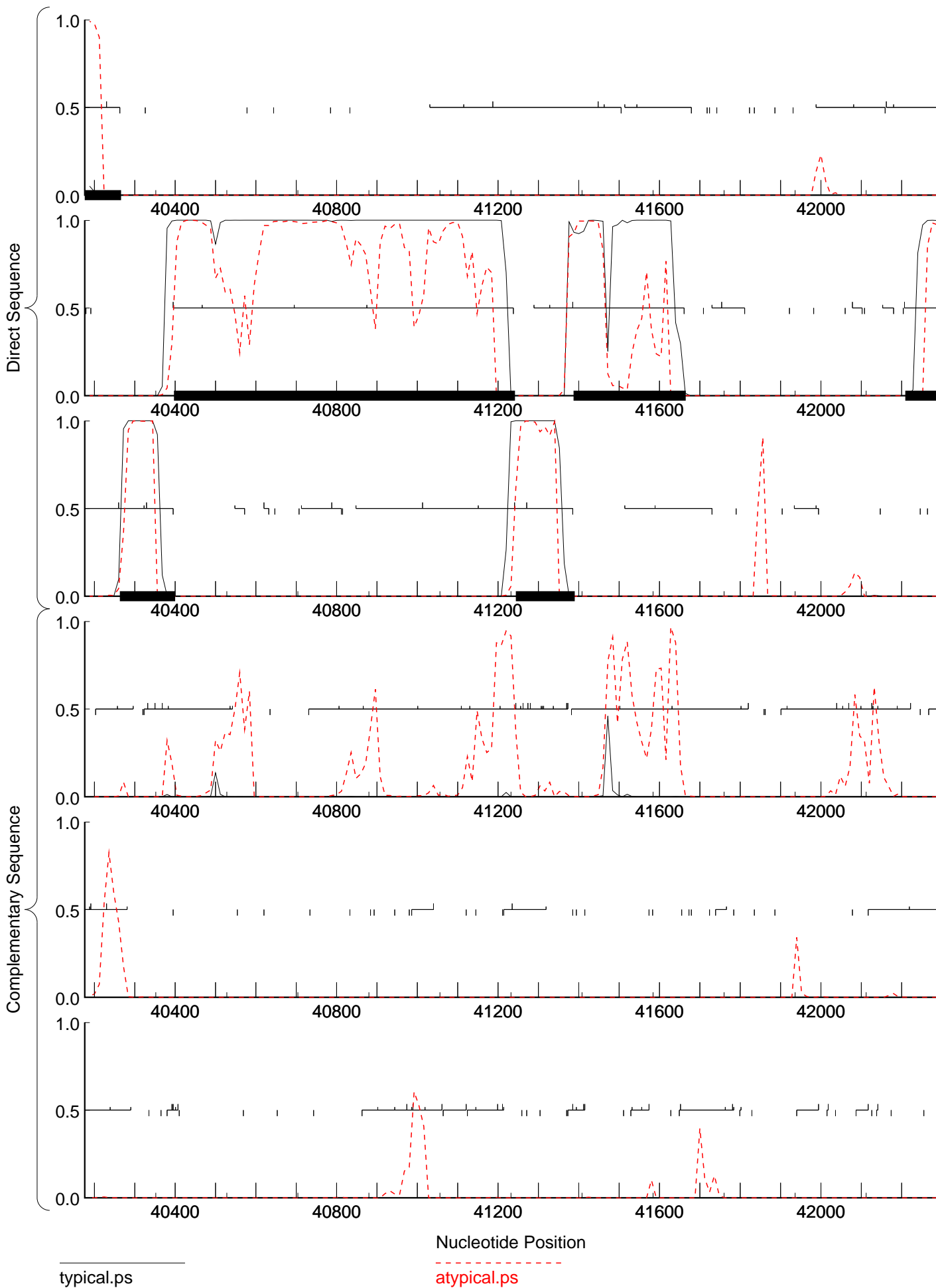
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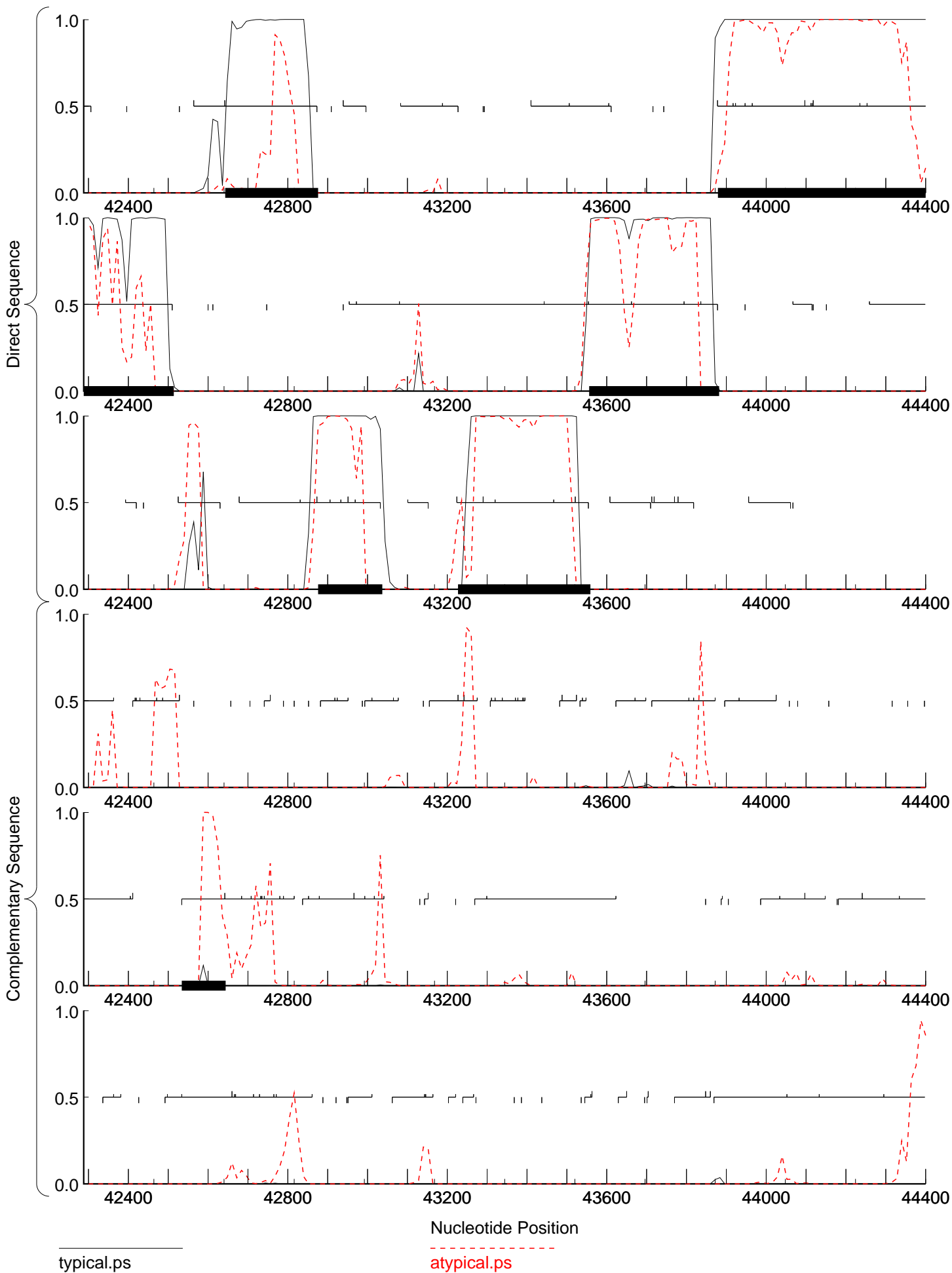






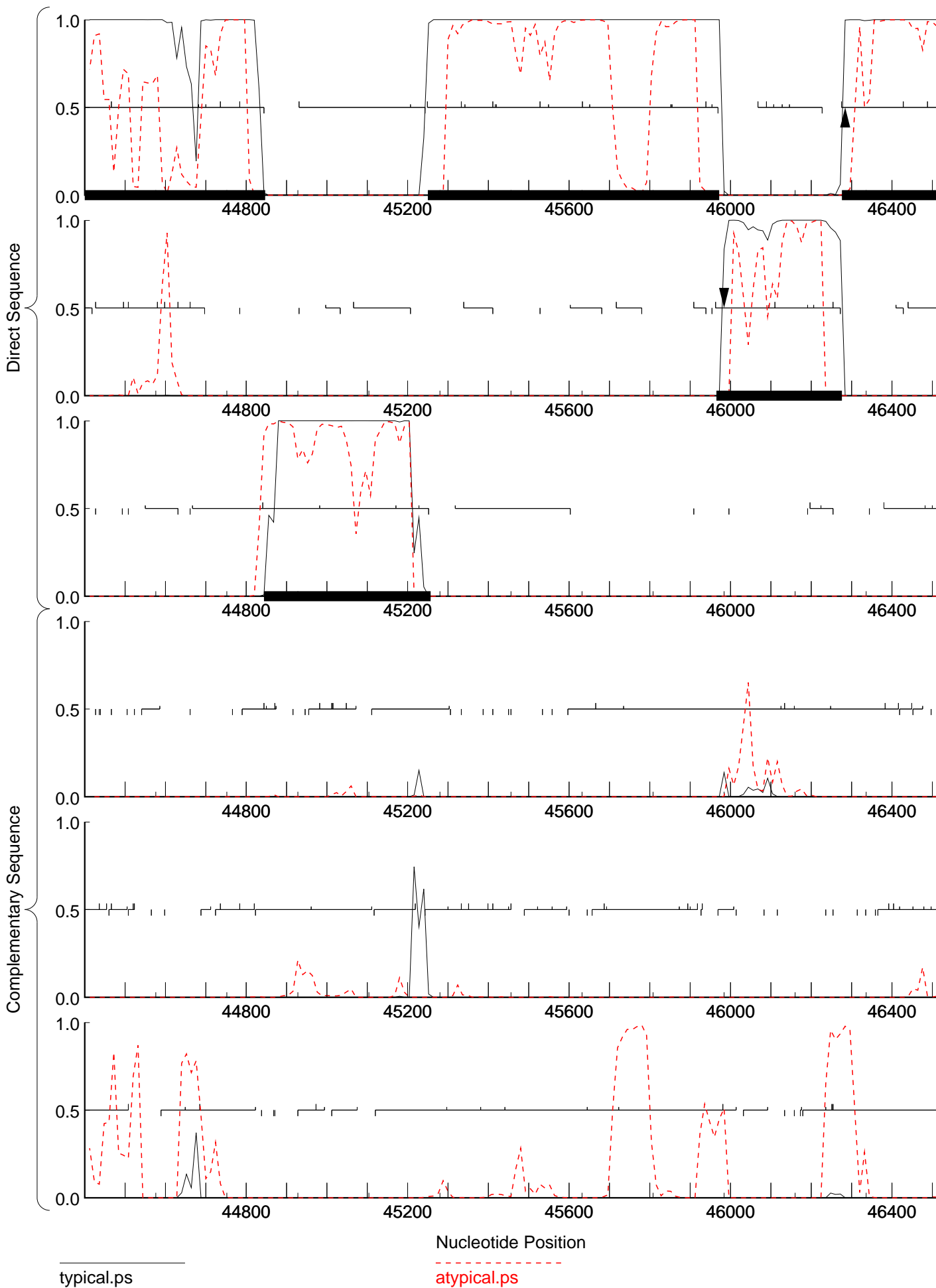






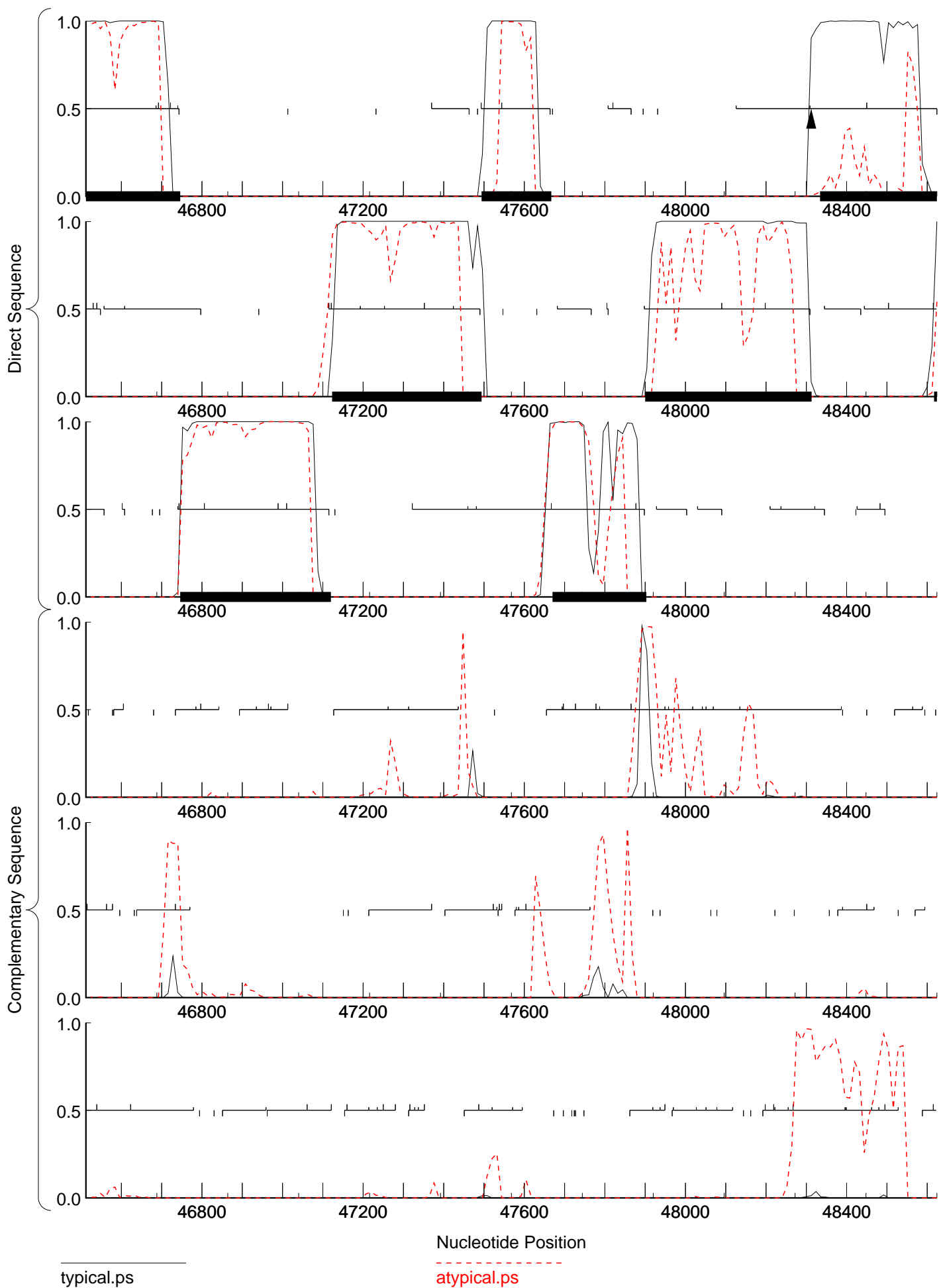
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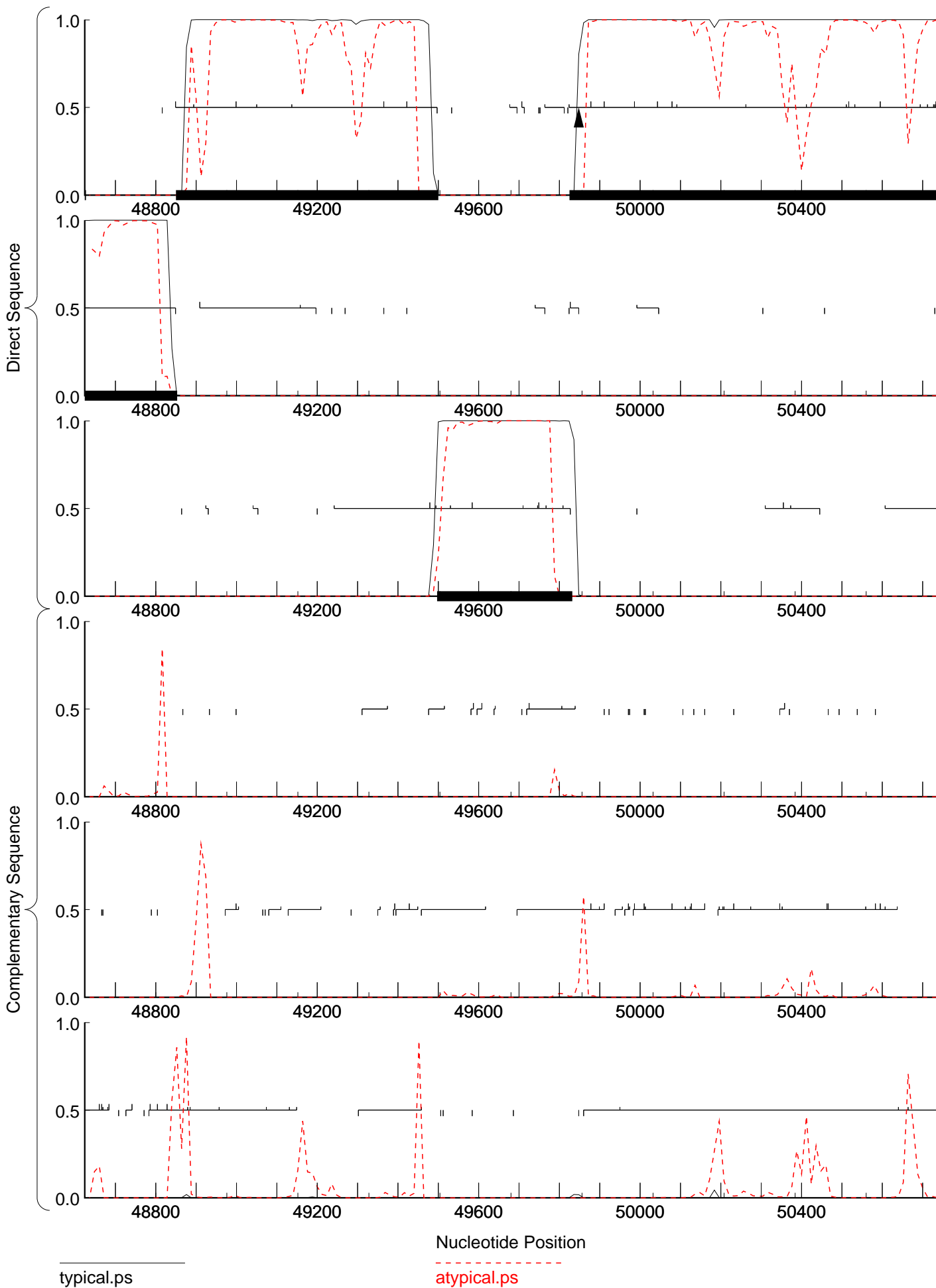
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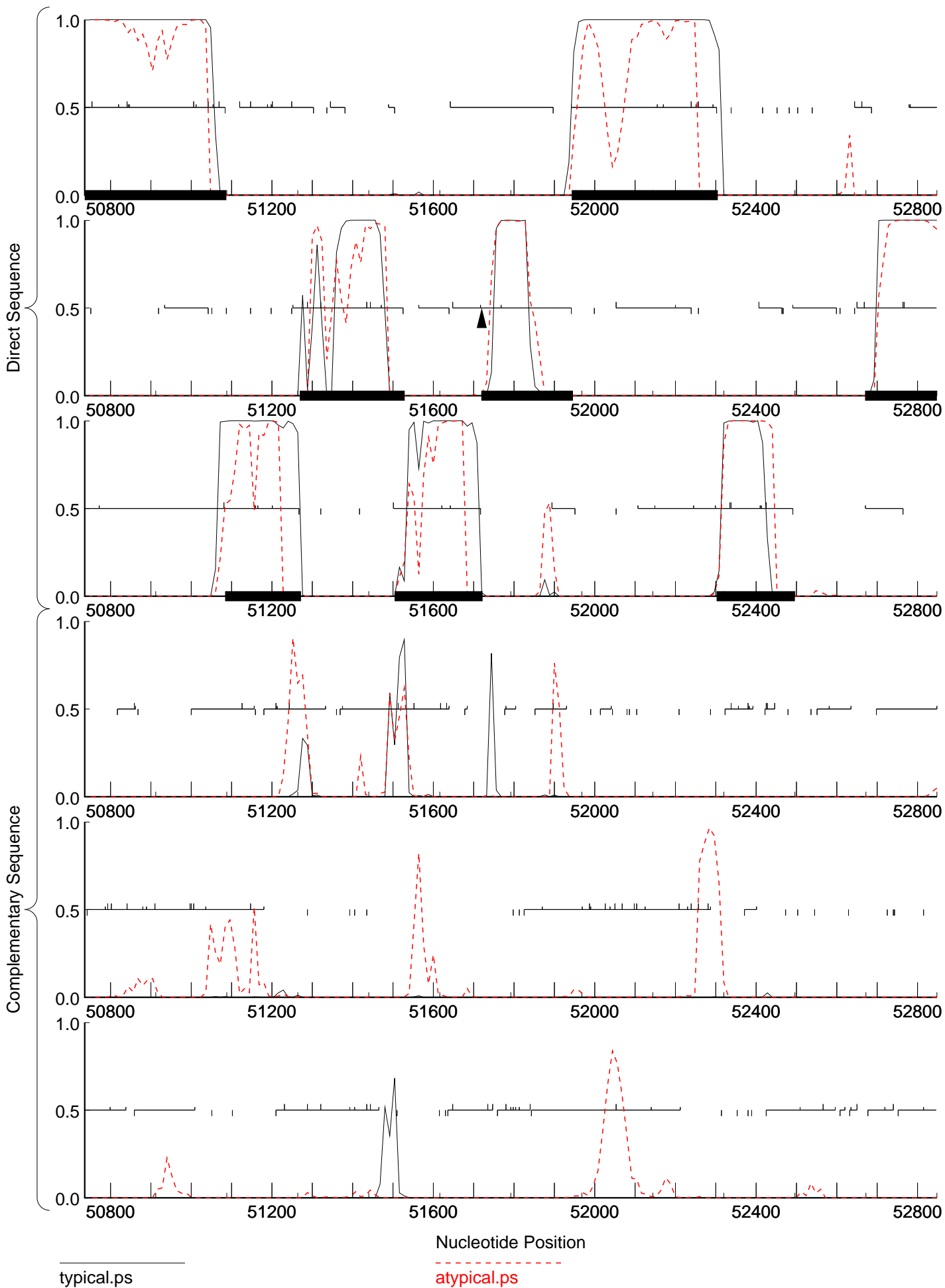


typical.ps

atypical.ps



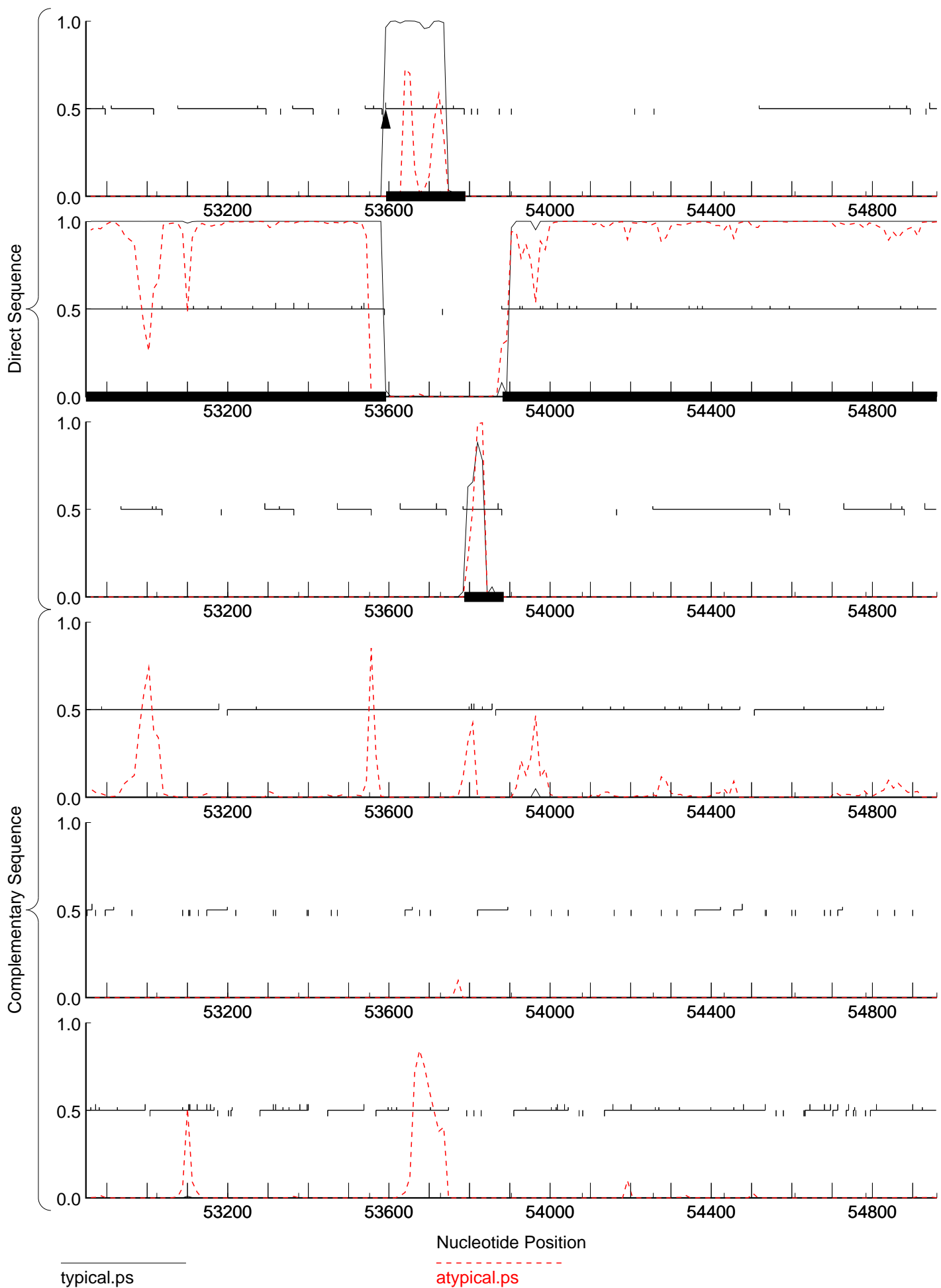




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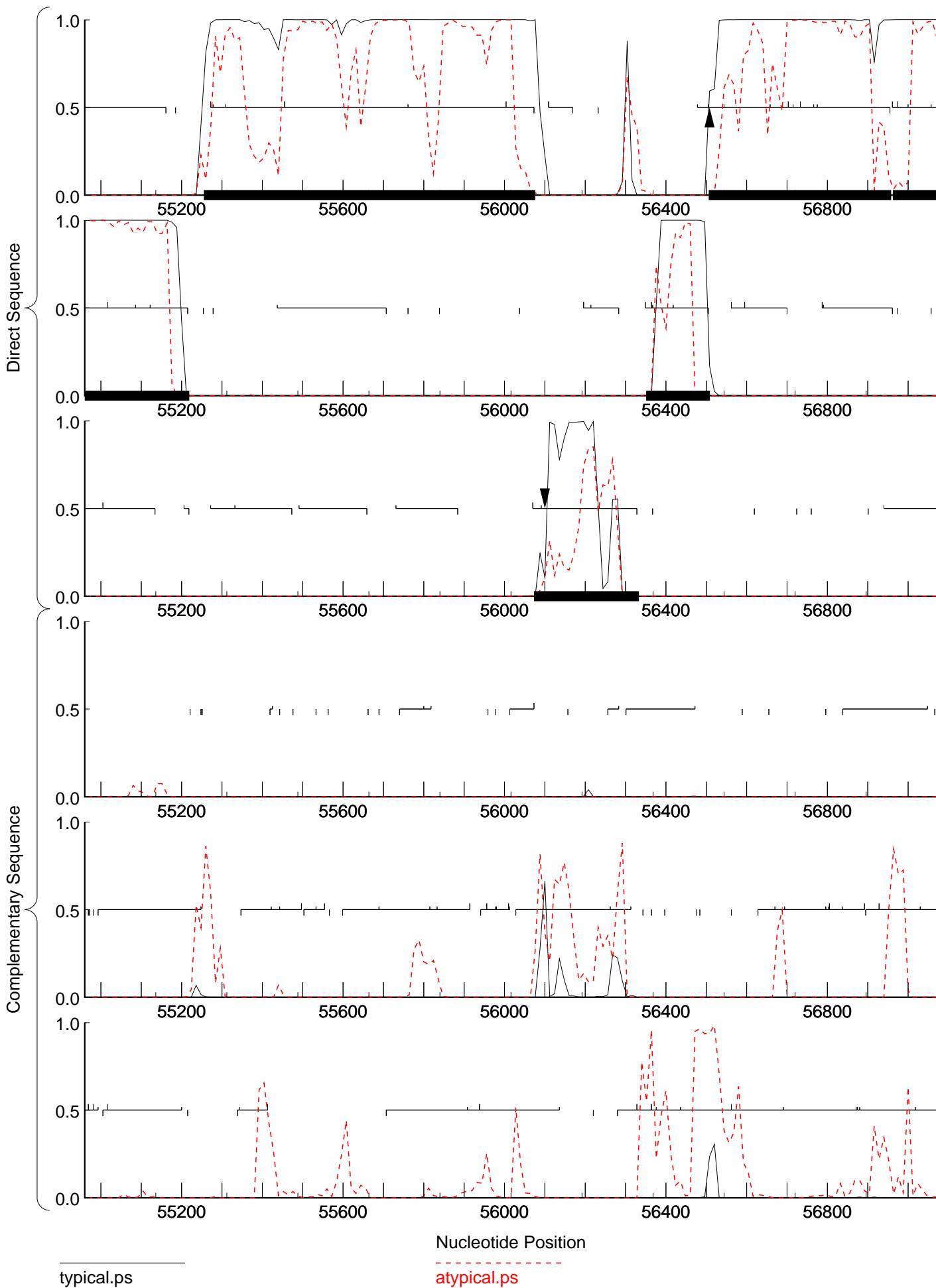
atypical.ps

Bhai complete sequence, 76145 bp including 9-base 3' overhang (CGCTTGTC A), Cluster E, Order 4, Window 96, Step 12, 27/38
GeneMark.hmm prediction
Bhai complete sequence, 76145 bp including 9-base 3' overhang (CGCTTGTC A), Cluster E, Order 2, Window 96, Step 12, 27/38



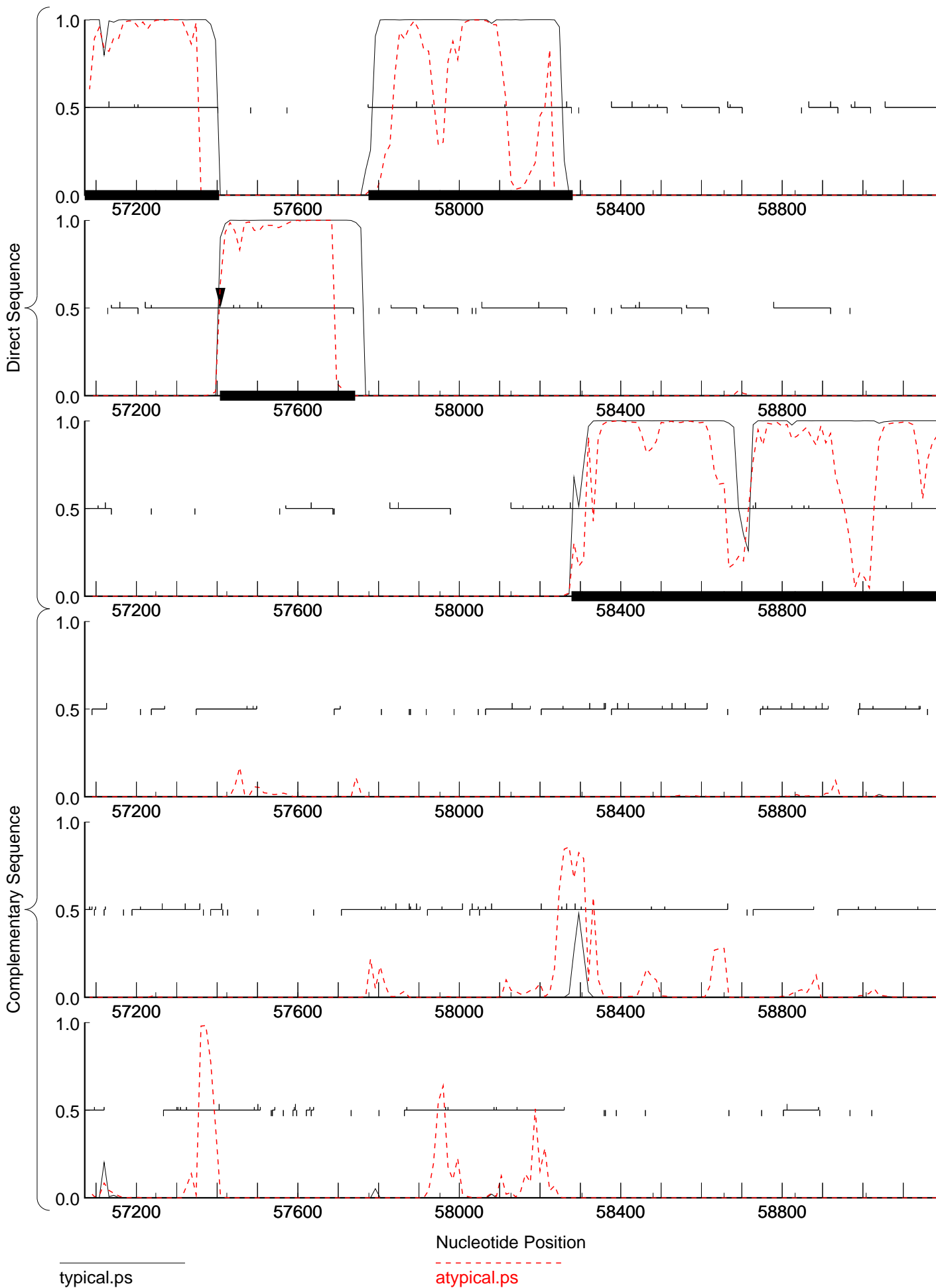
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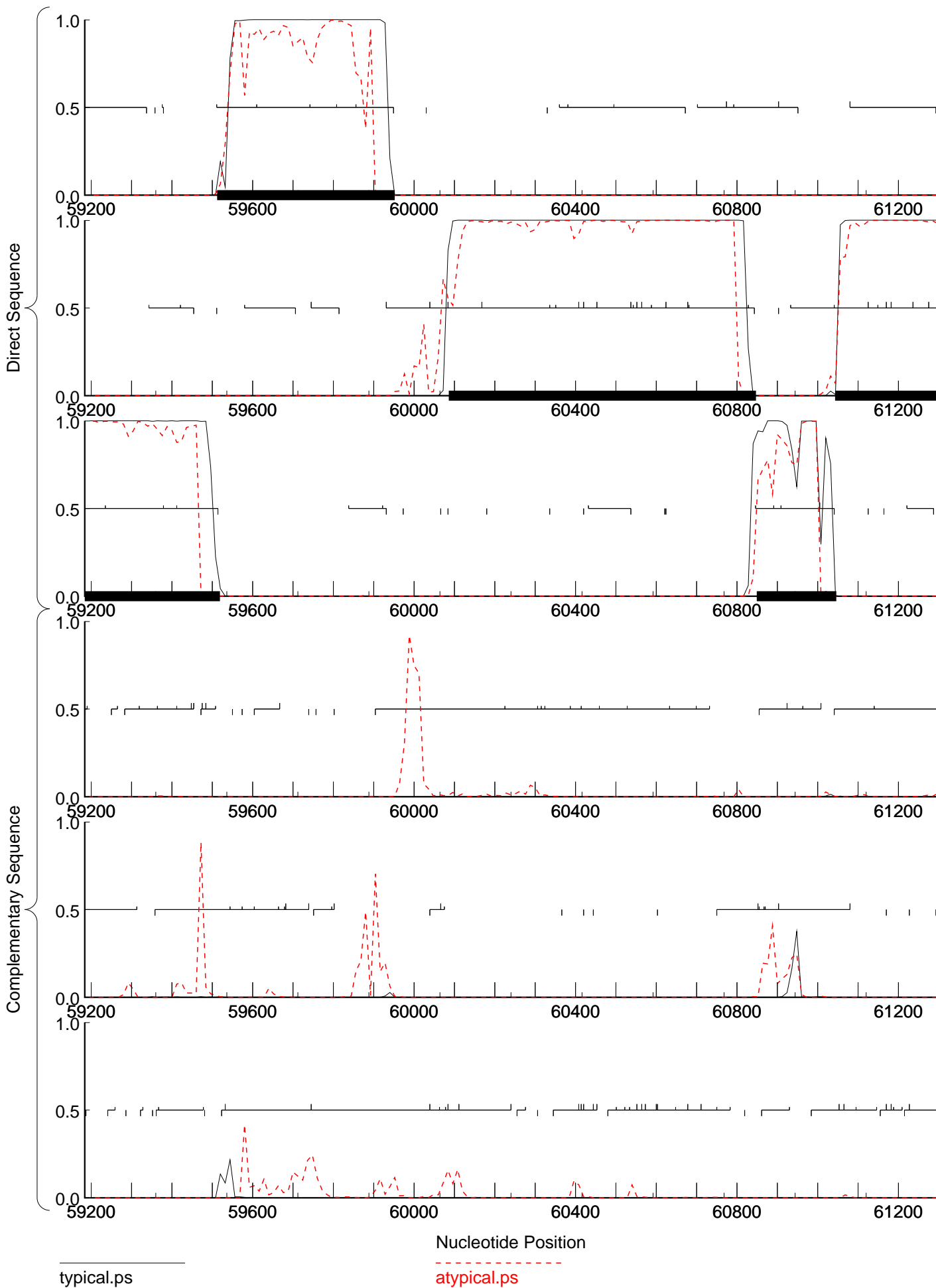
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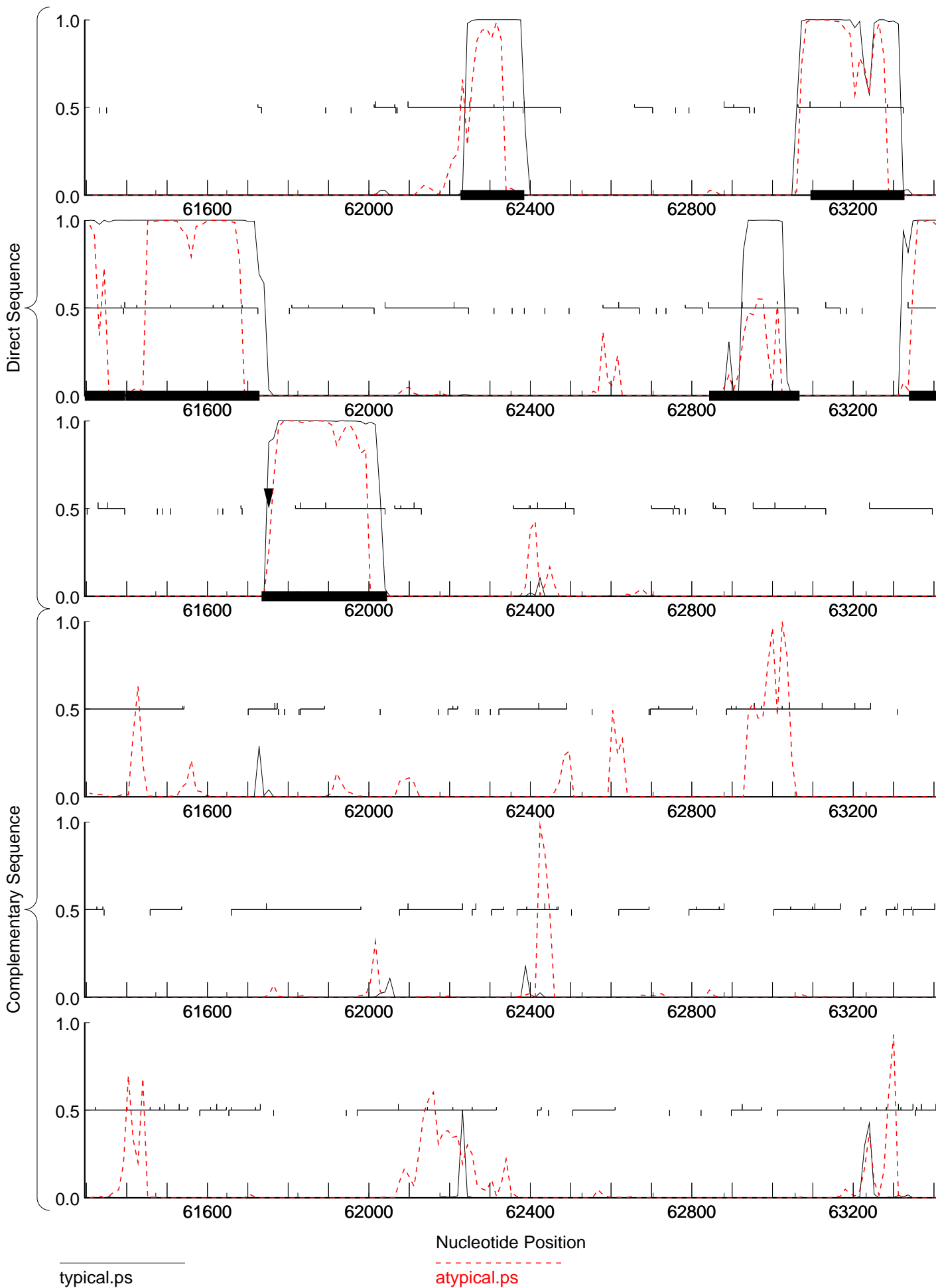


typical.ps

atypical.ps

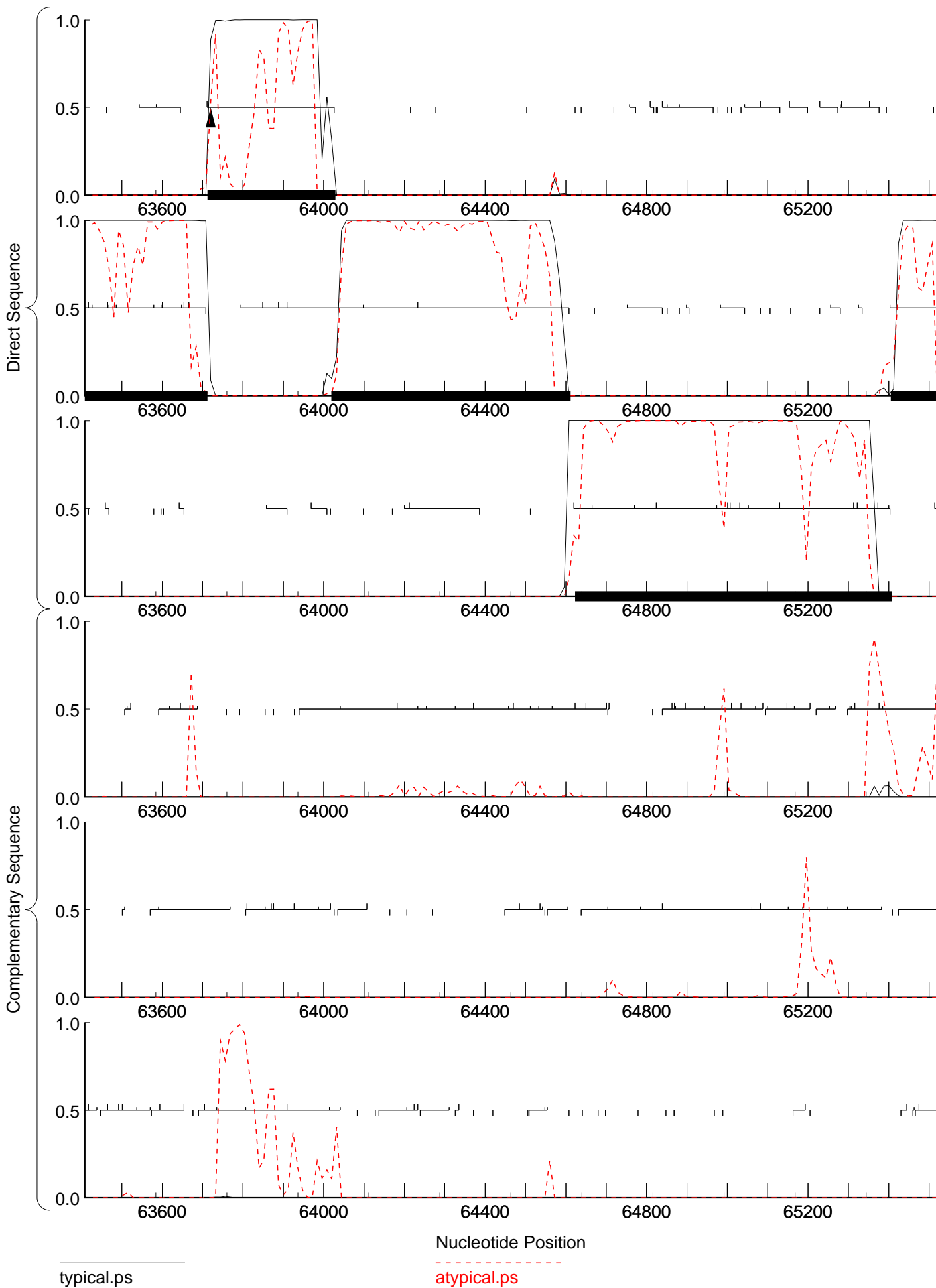


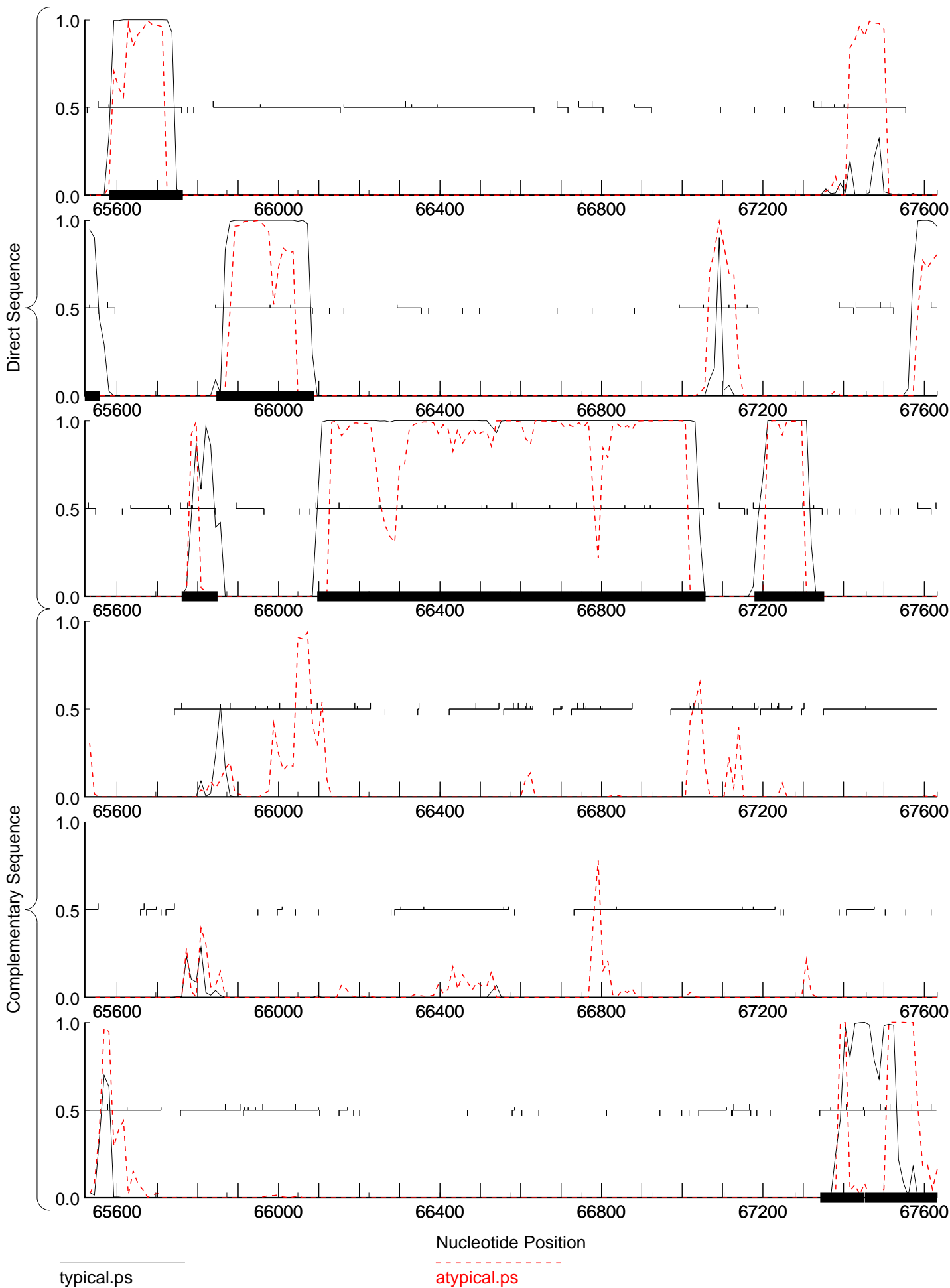


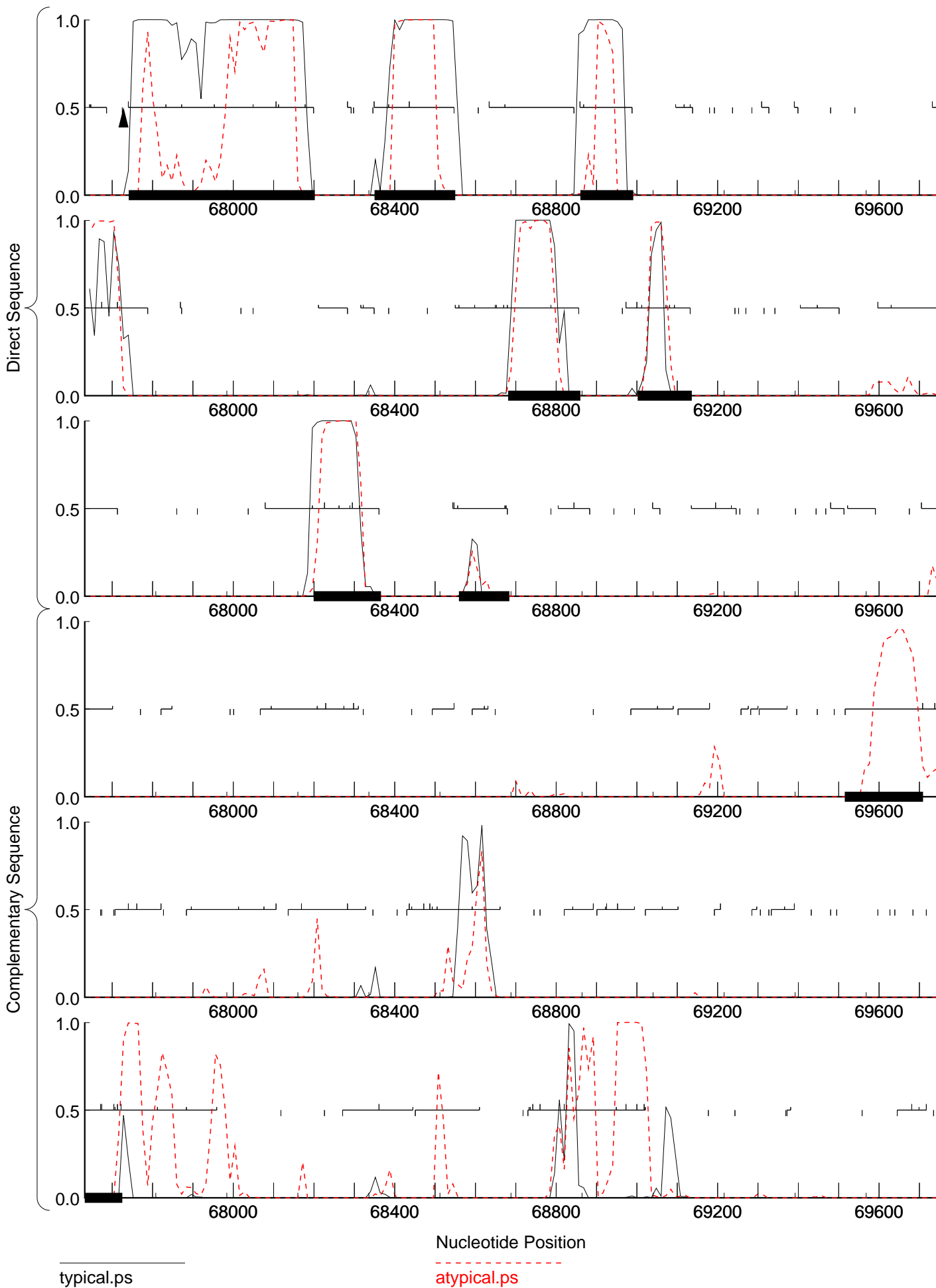


typical.ps

atypical.ps

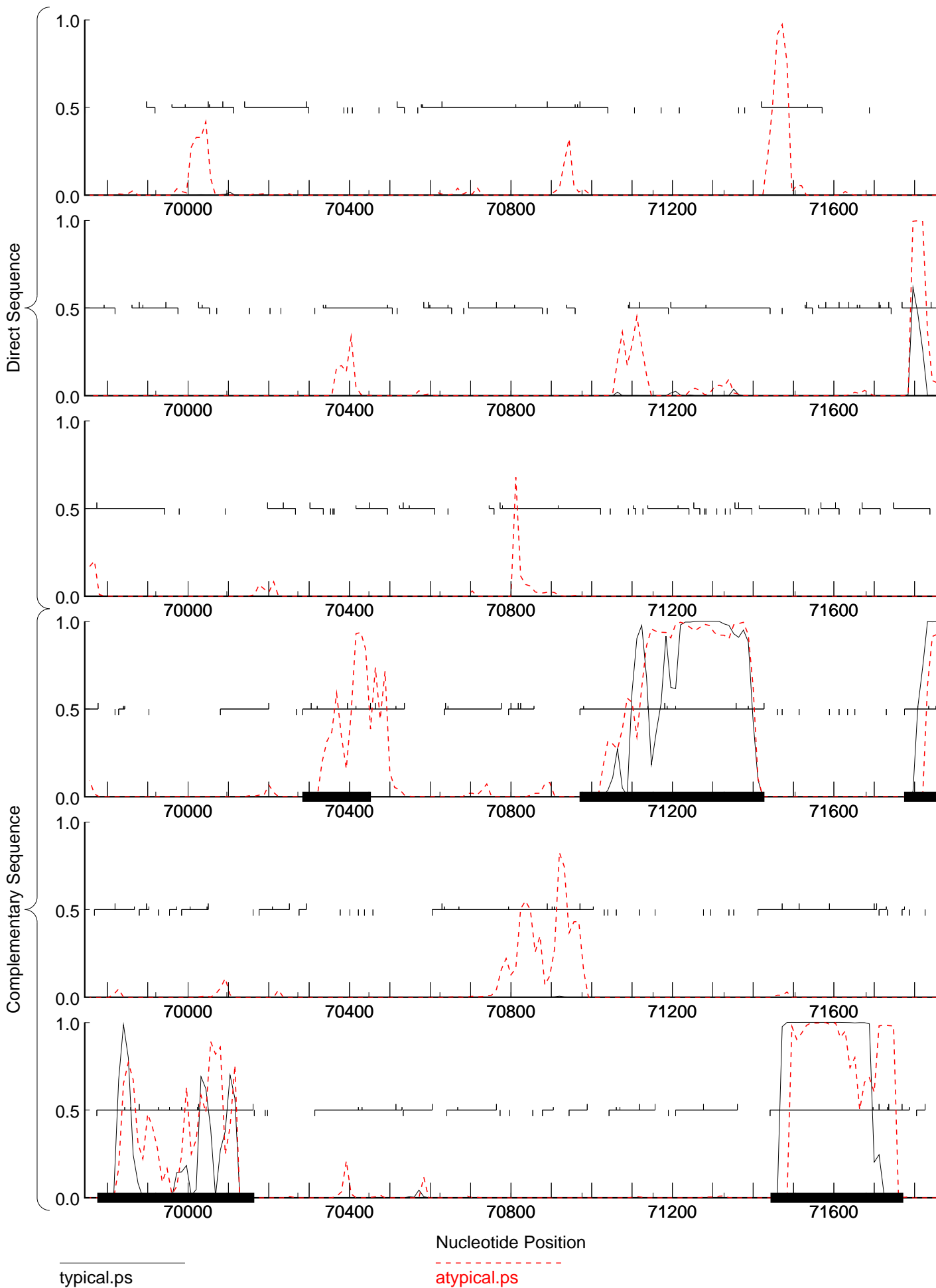






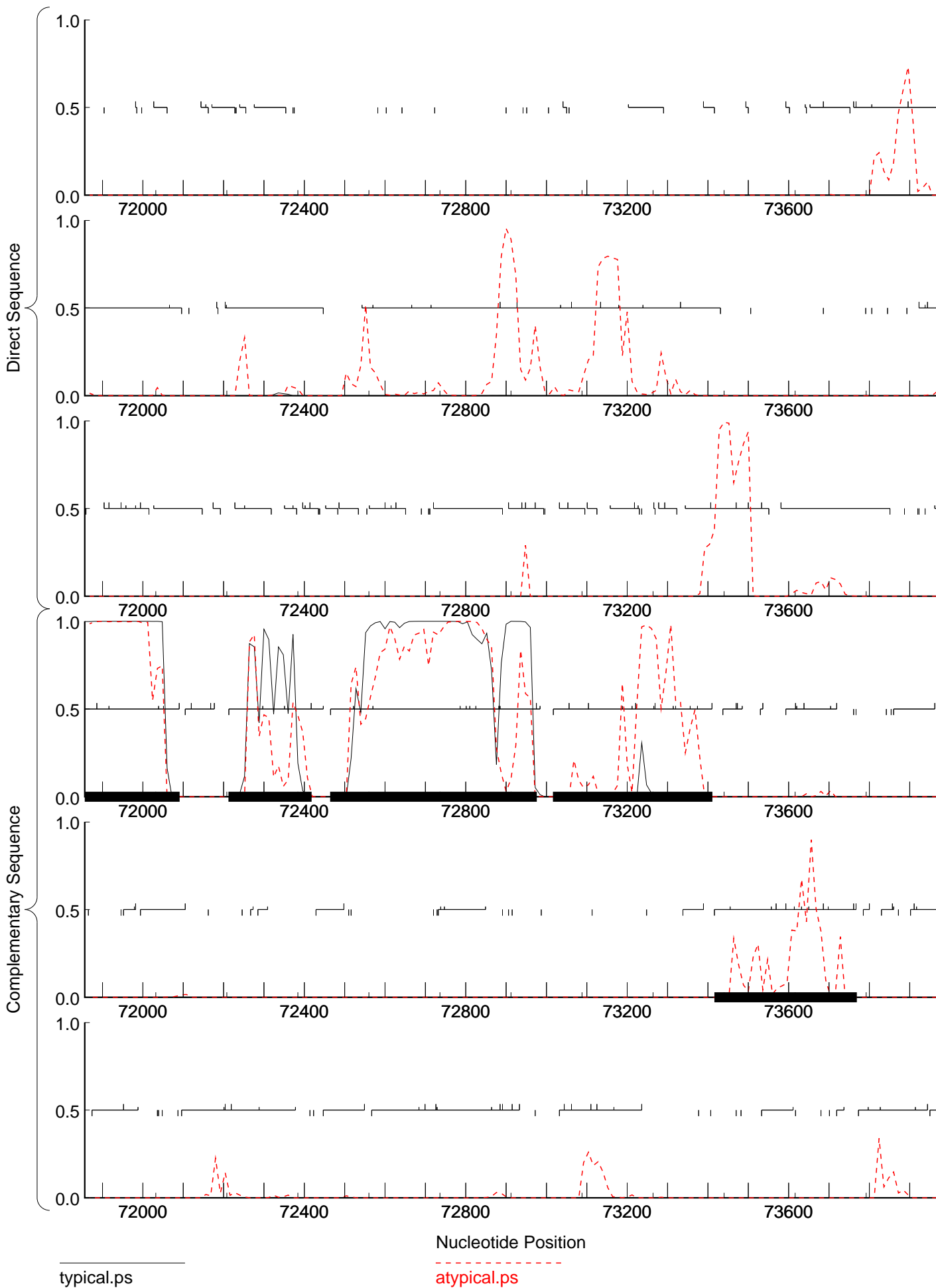
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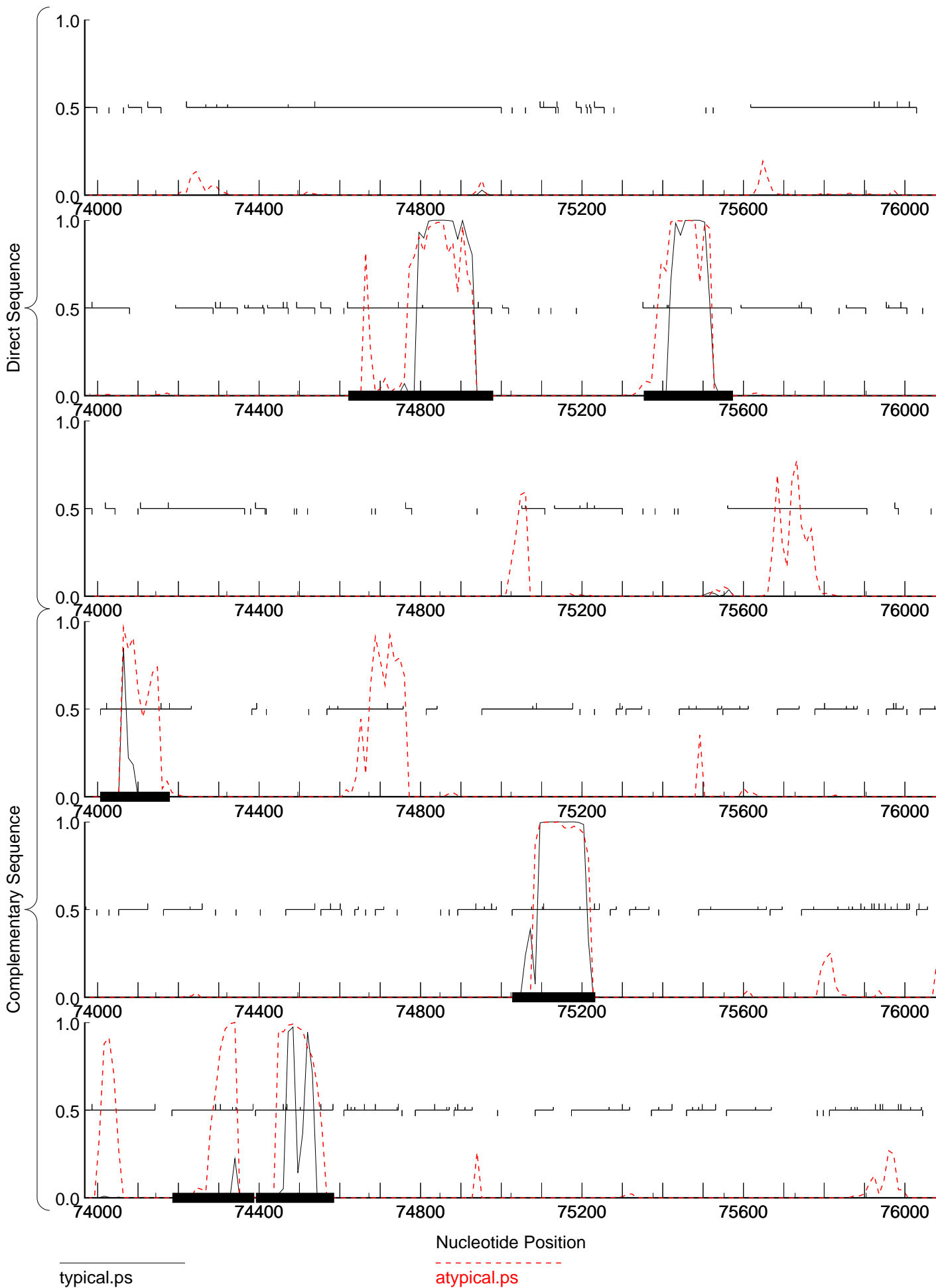
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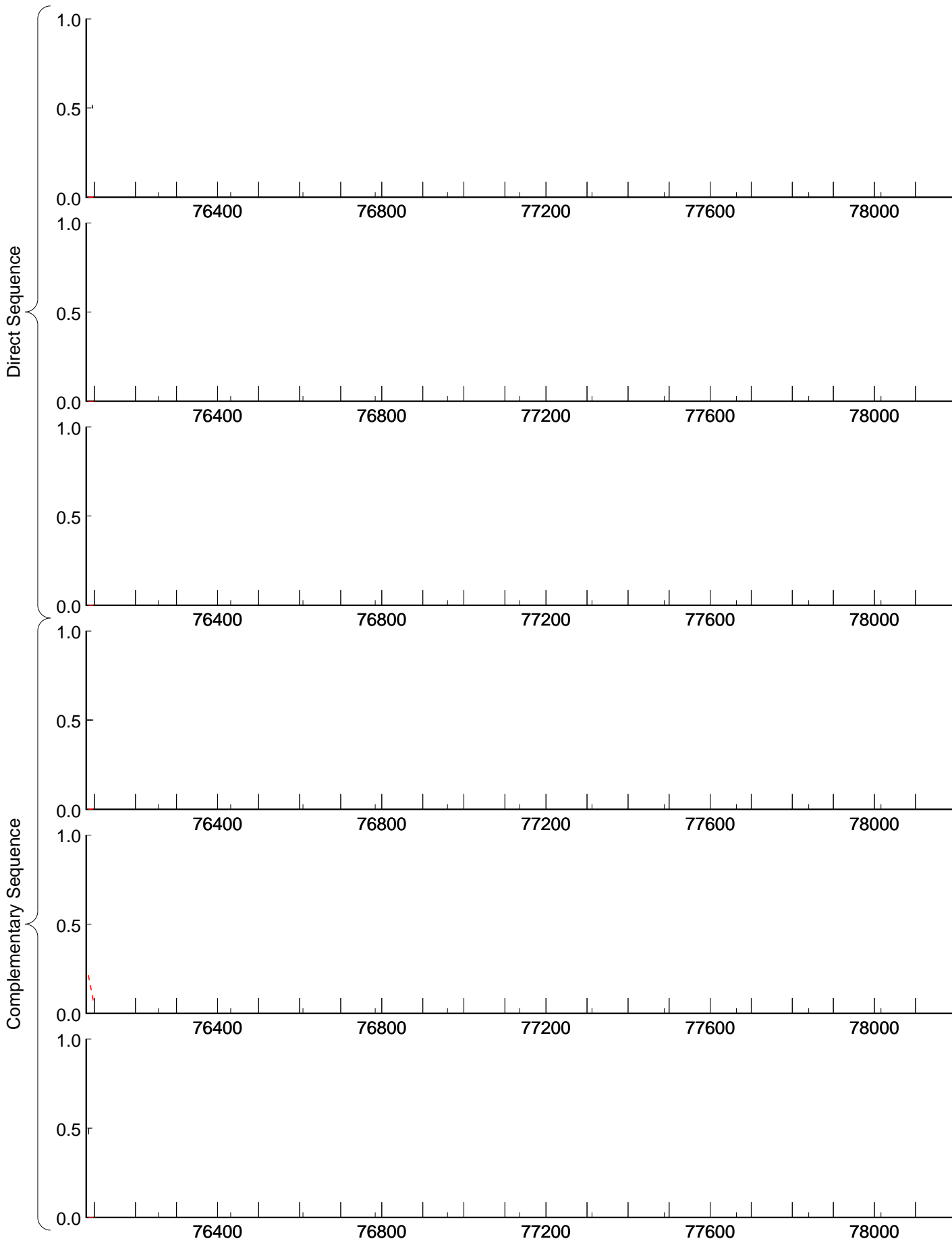


typical.ps

atypical.ps







typical.ps

Nucleotide Position

atypical.ps