

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 : 8/20/18 at 8:30:07
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,

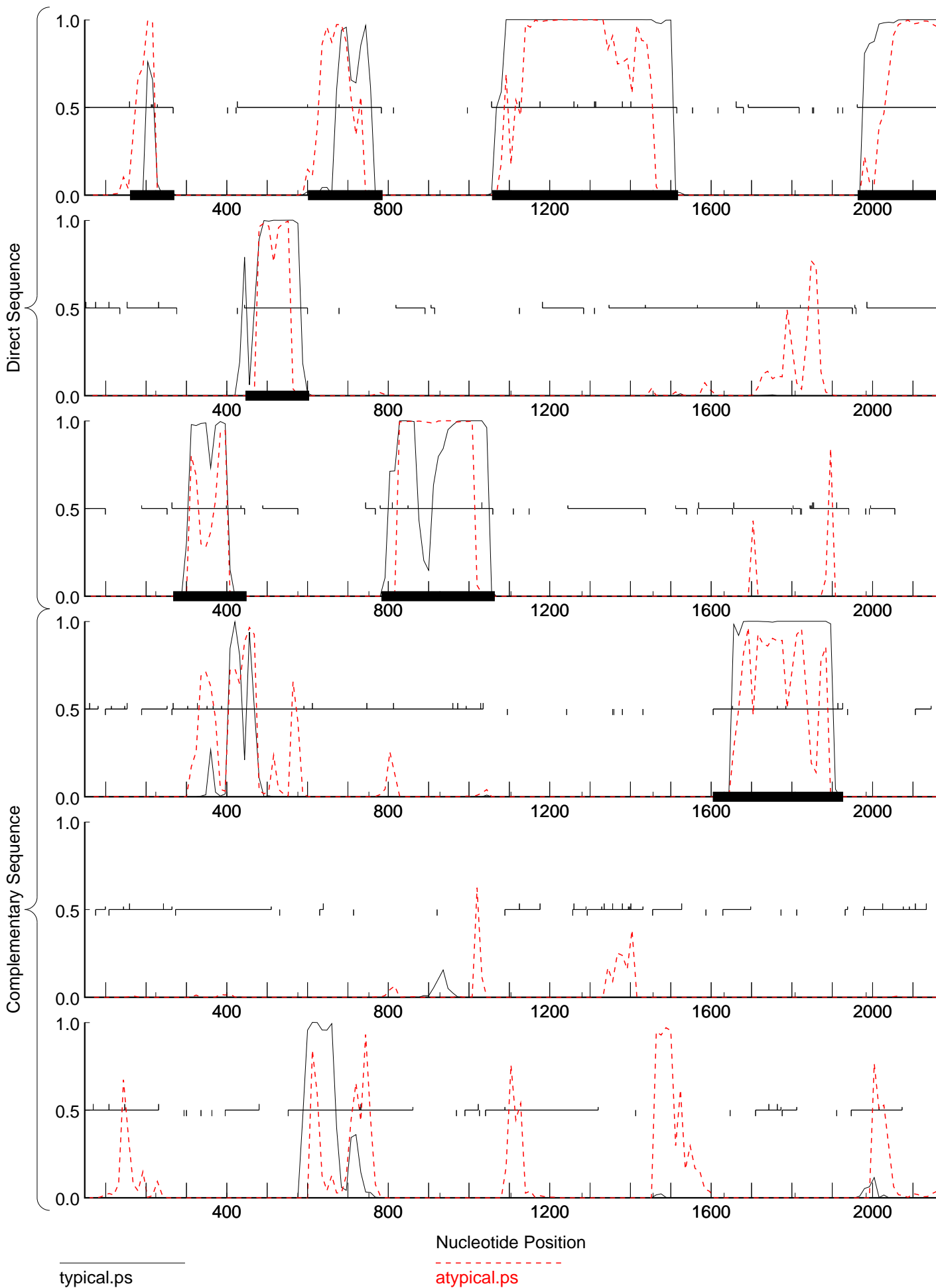
Matrix notes & comments

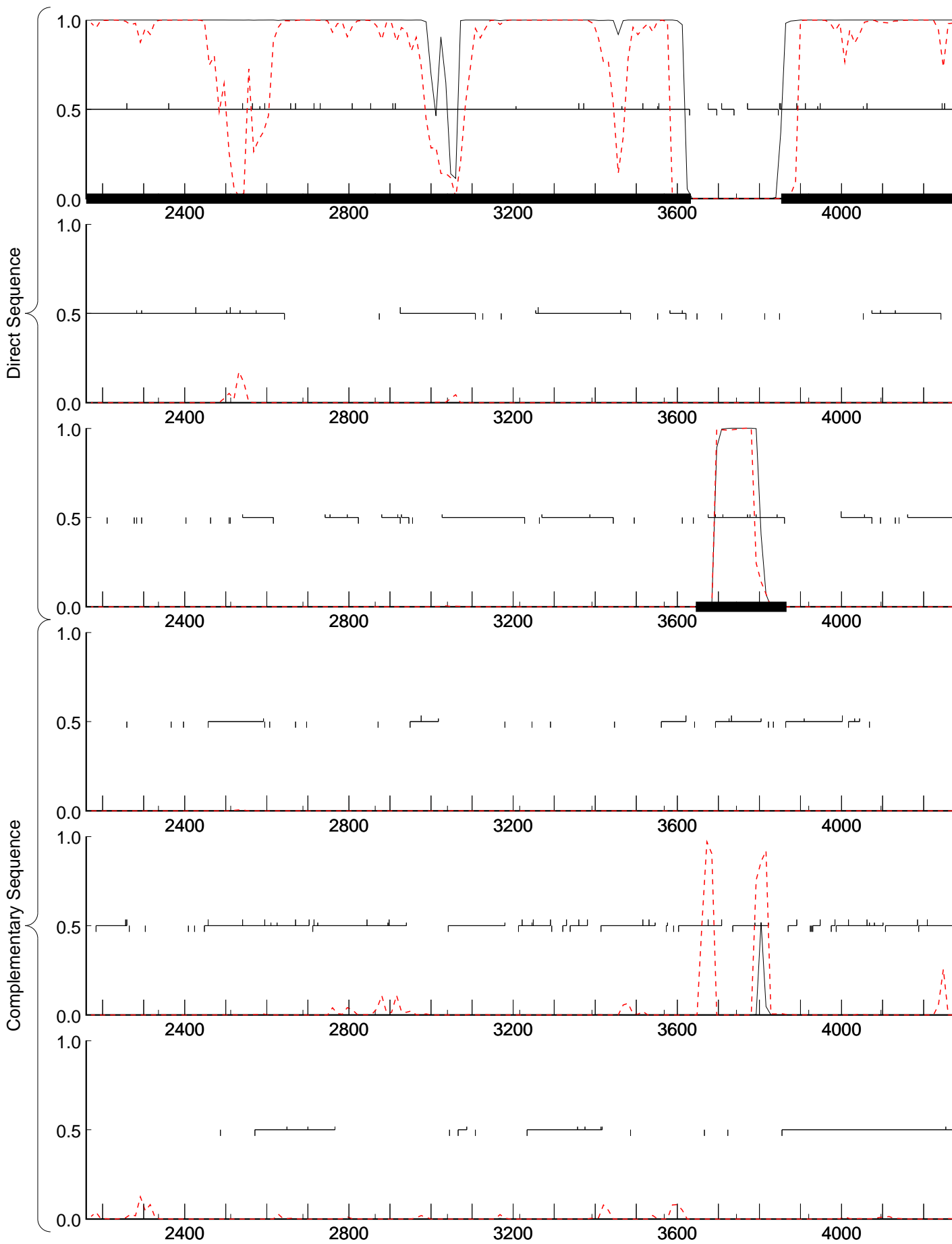
Training set derived by GeneMarkS, 4.30 October 2014
Mon Aug 20 08:30:07 2018

MATRIX INFORMATION

Matrix : -
Author : -
Order : 4

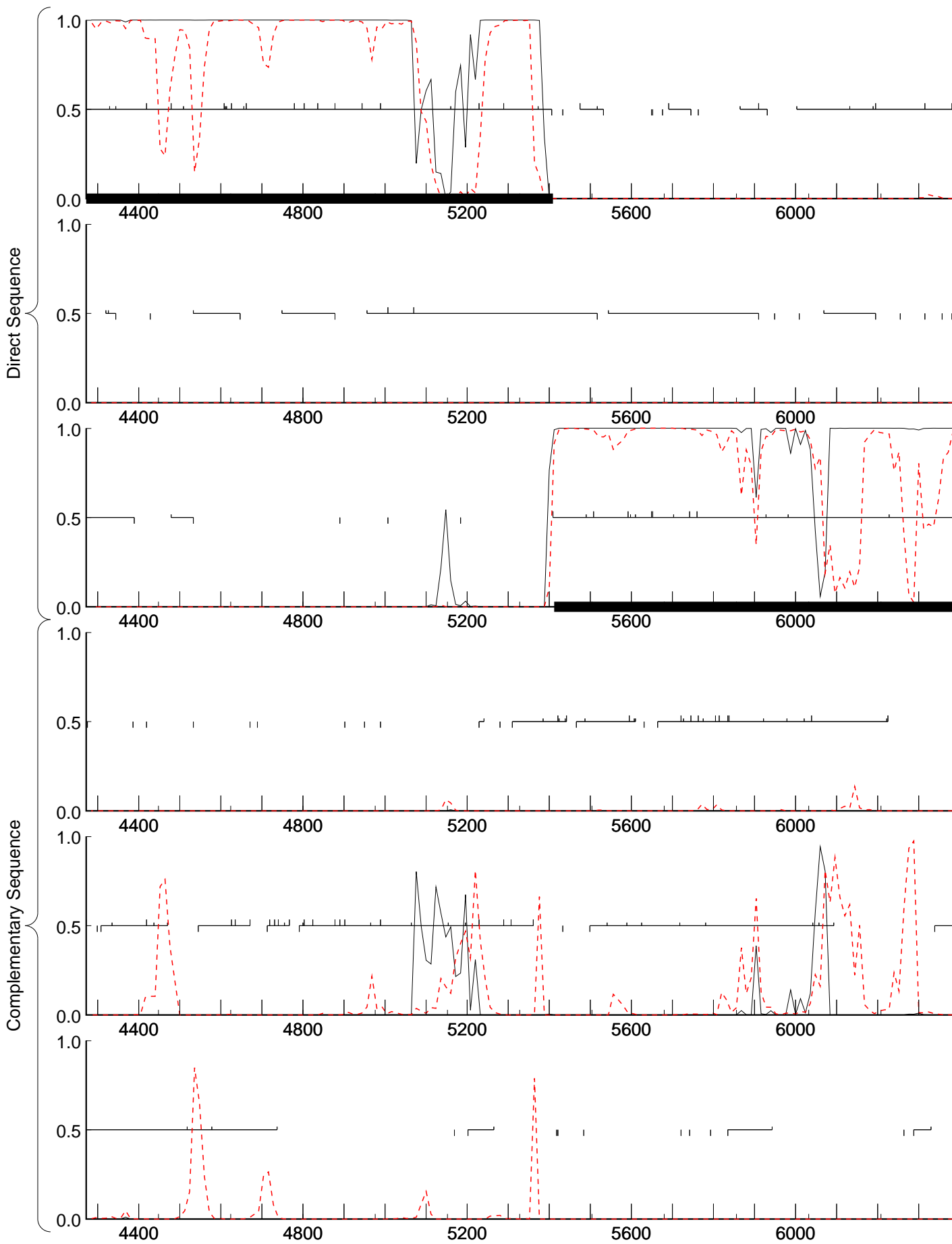
Send questions / comments to:
Dr. M. Borodovsky
Georgia Institute of Technology
School of Biology
Atlanta, GA 30332-0230





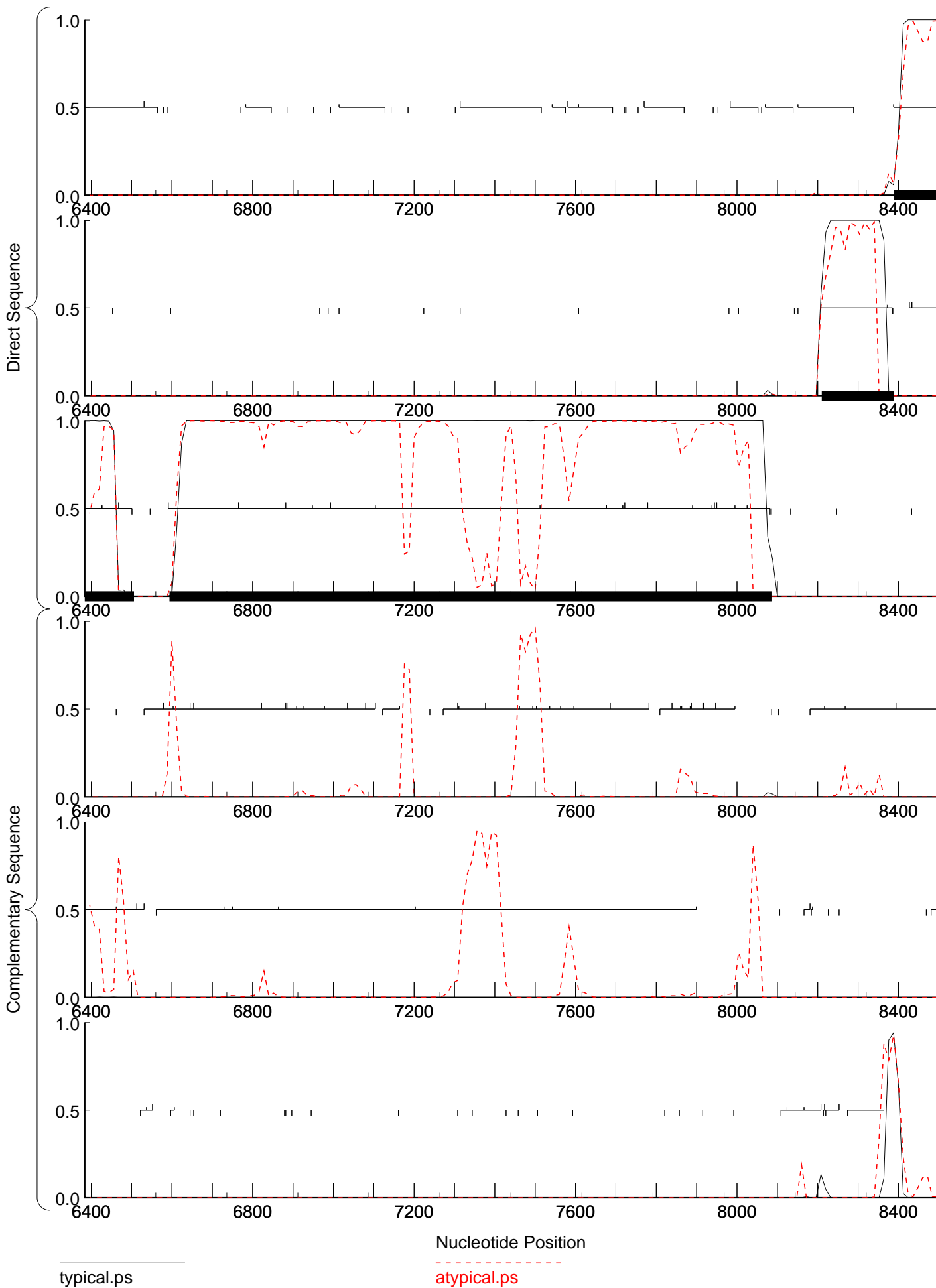
typical.ps

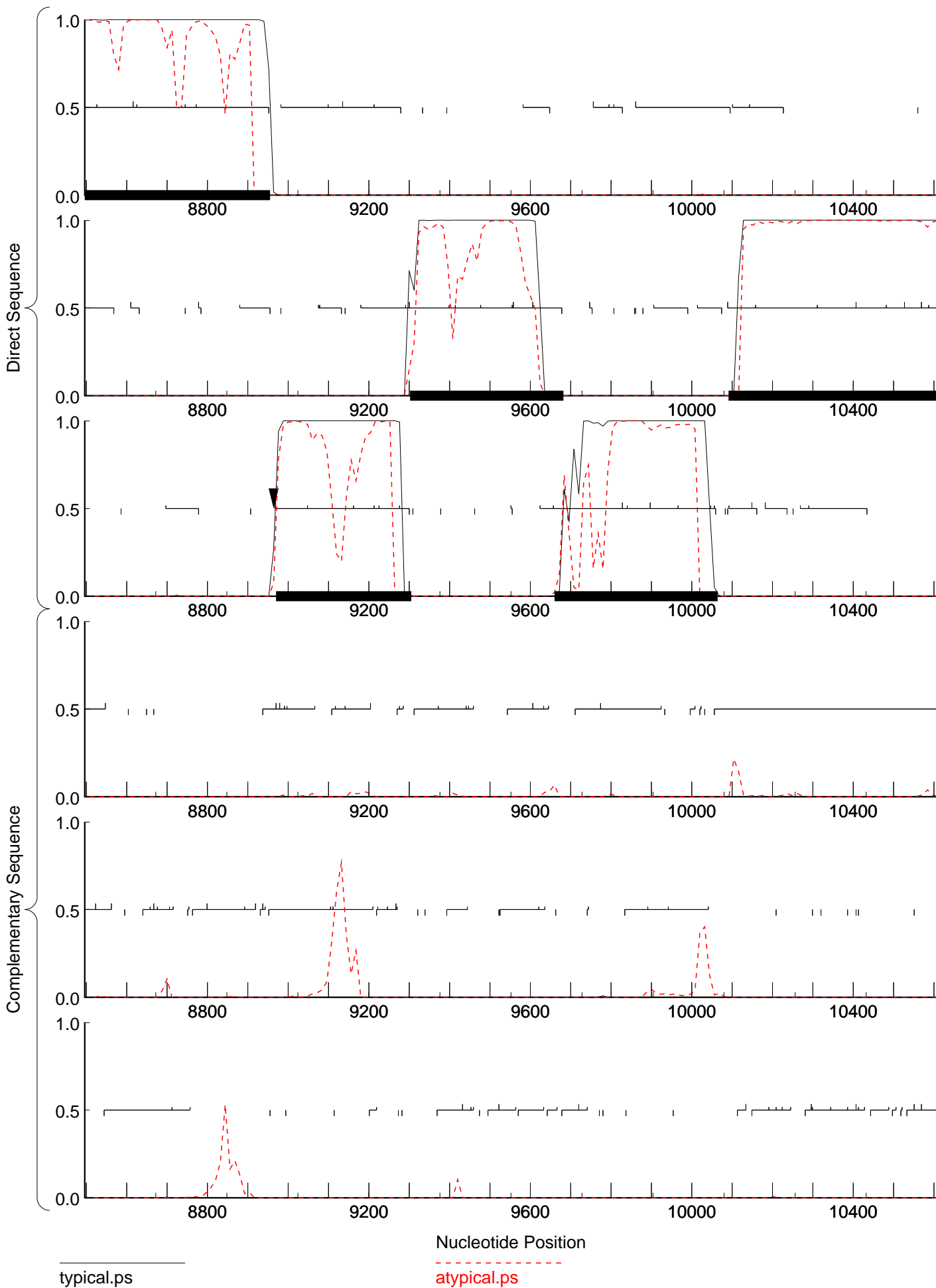
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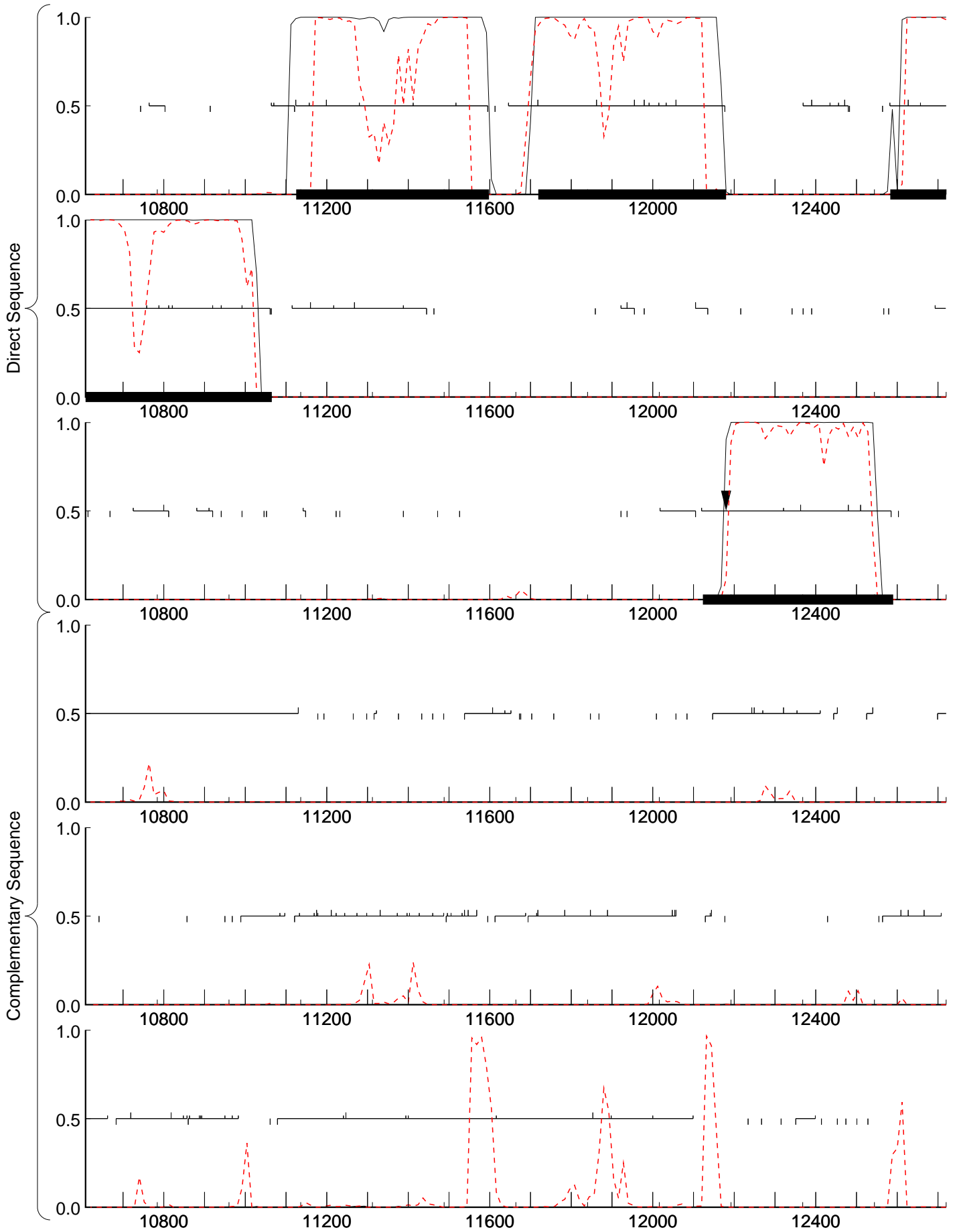


typical.ps

atypical.ps

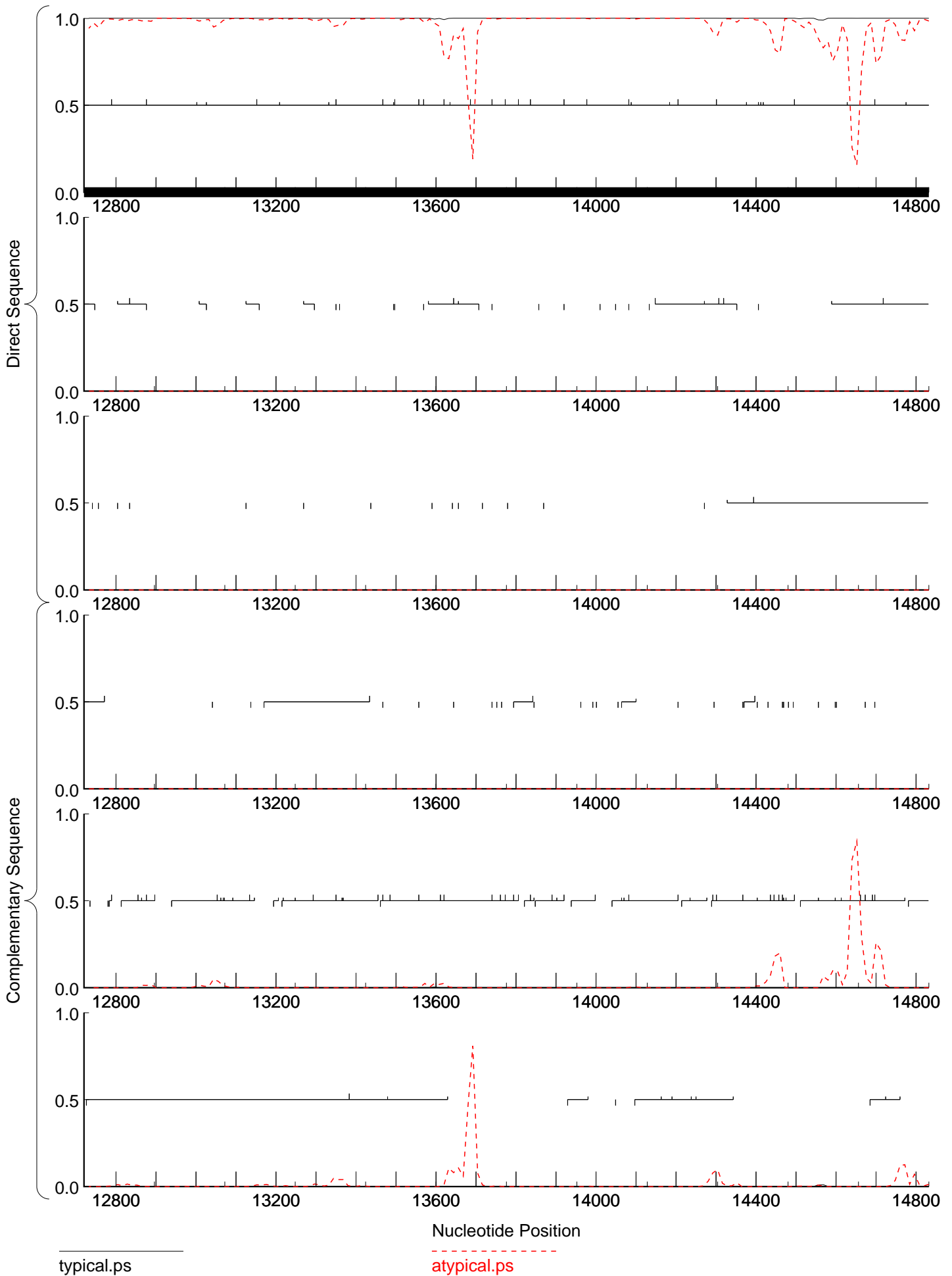


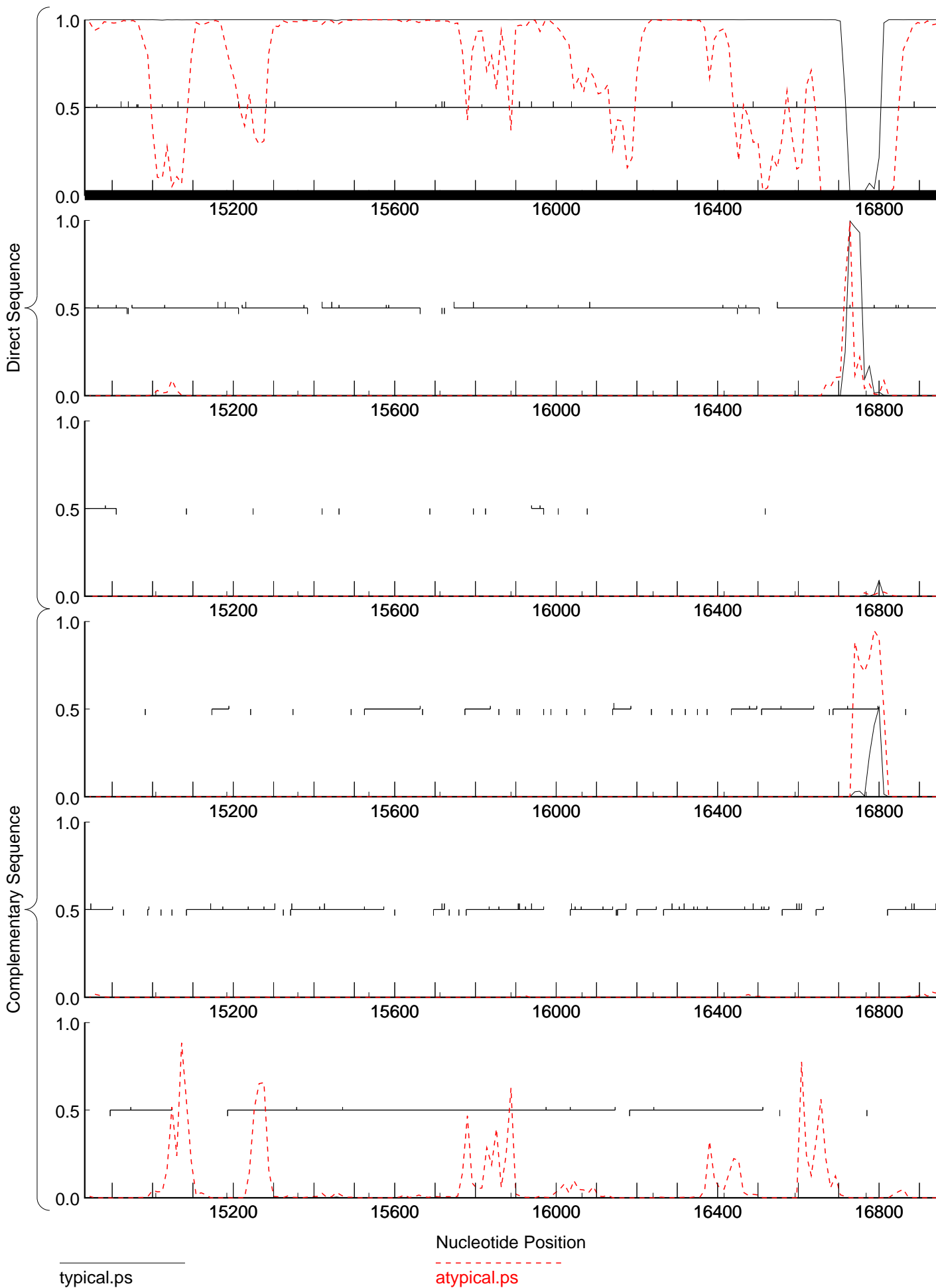


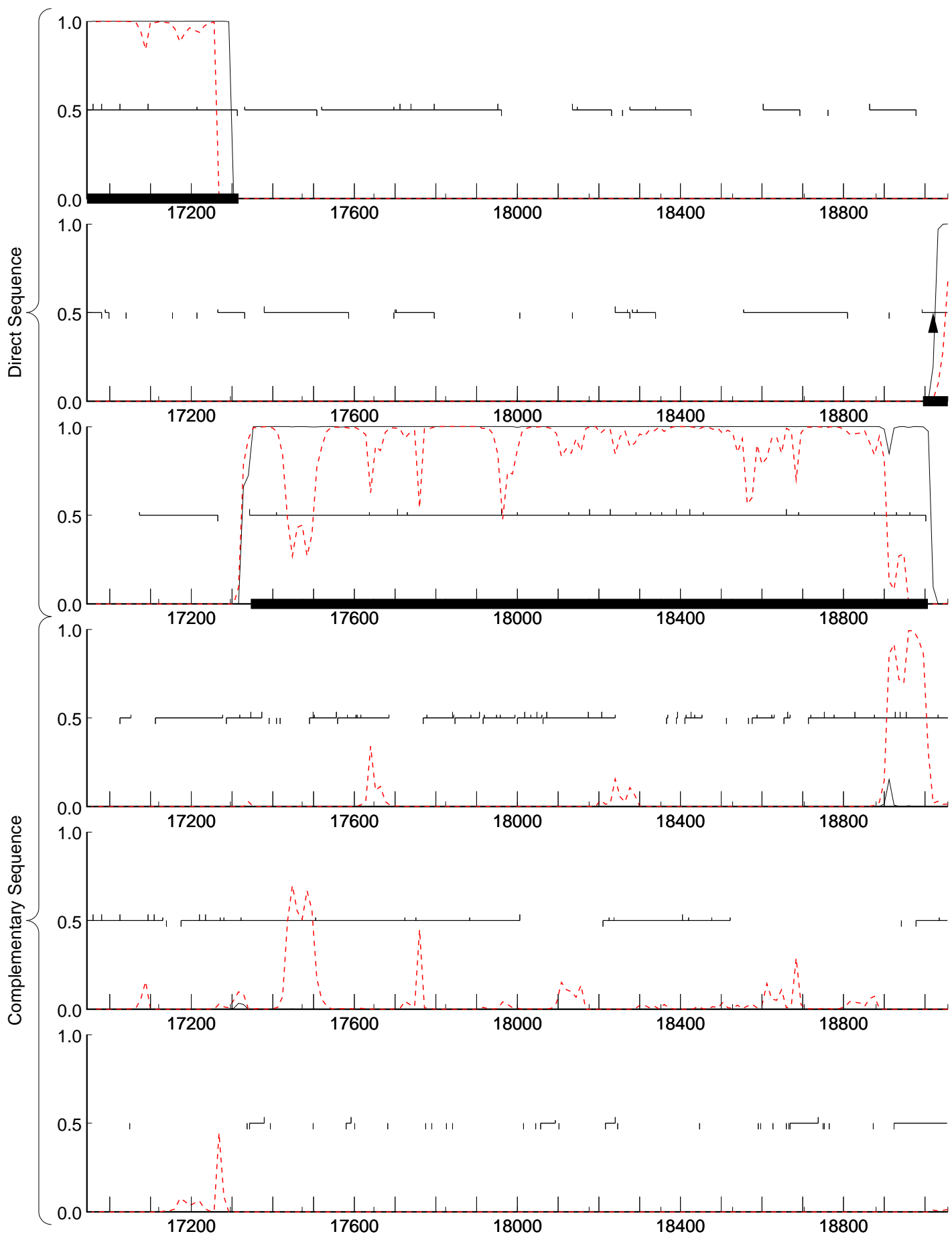


typical.ps

atypical.ps

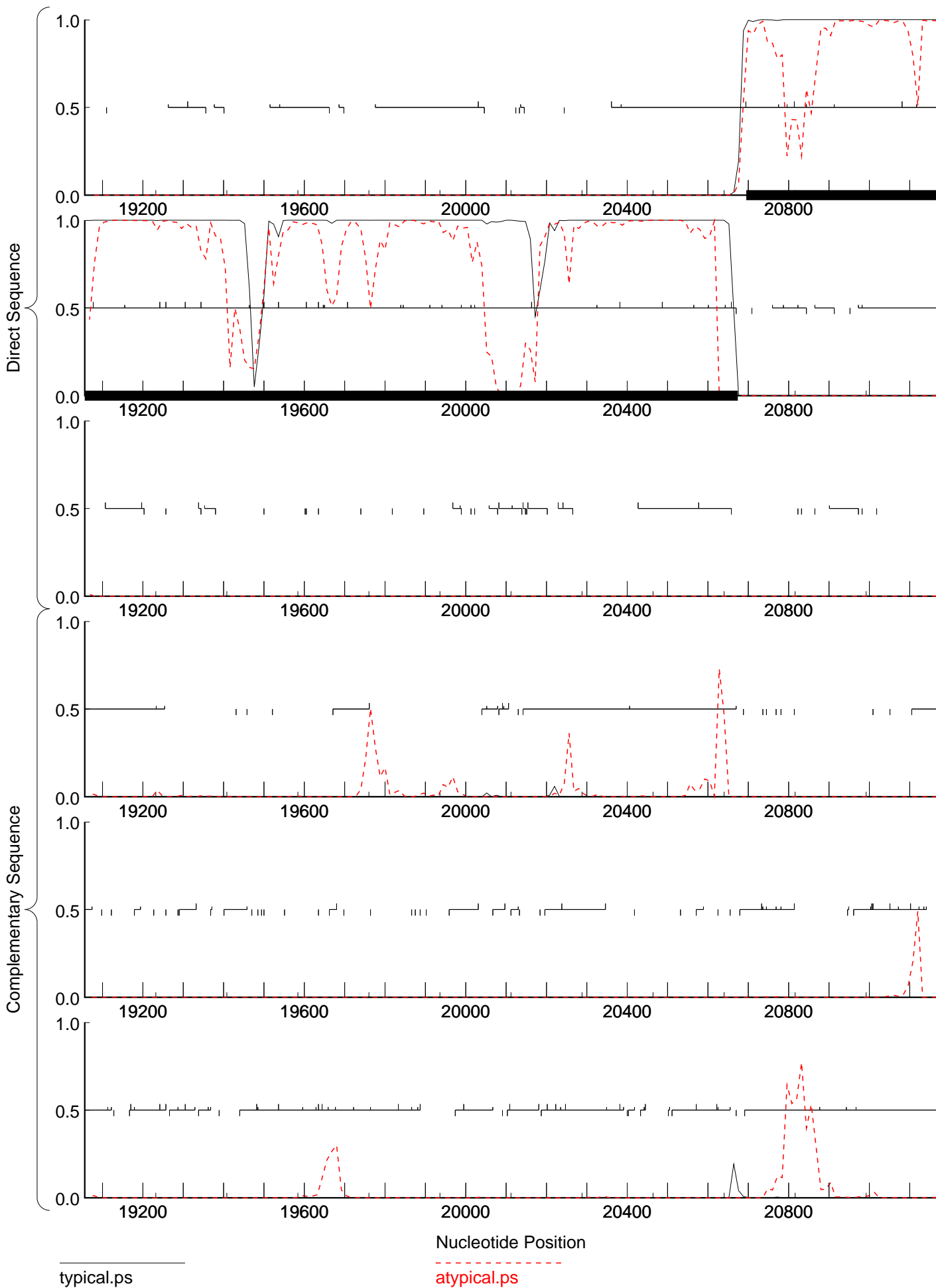




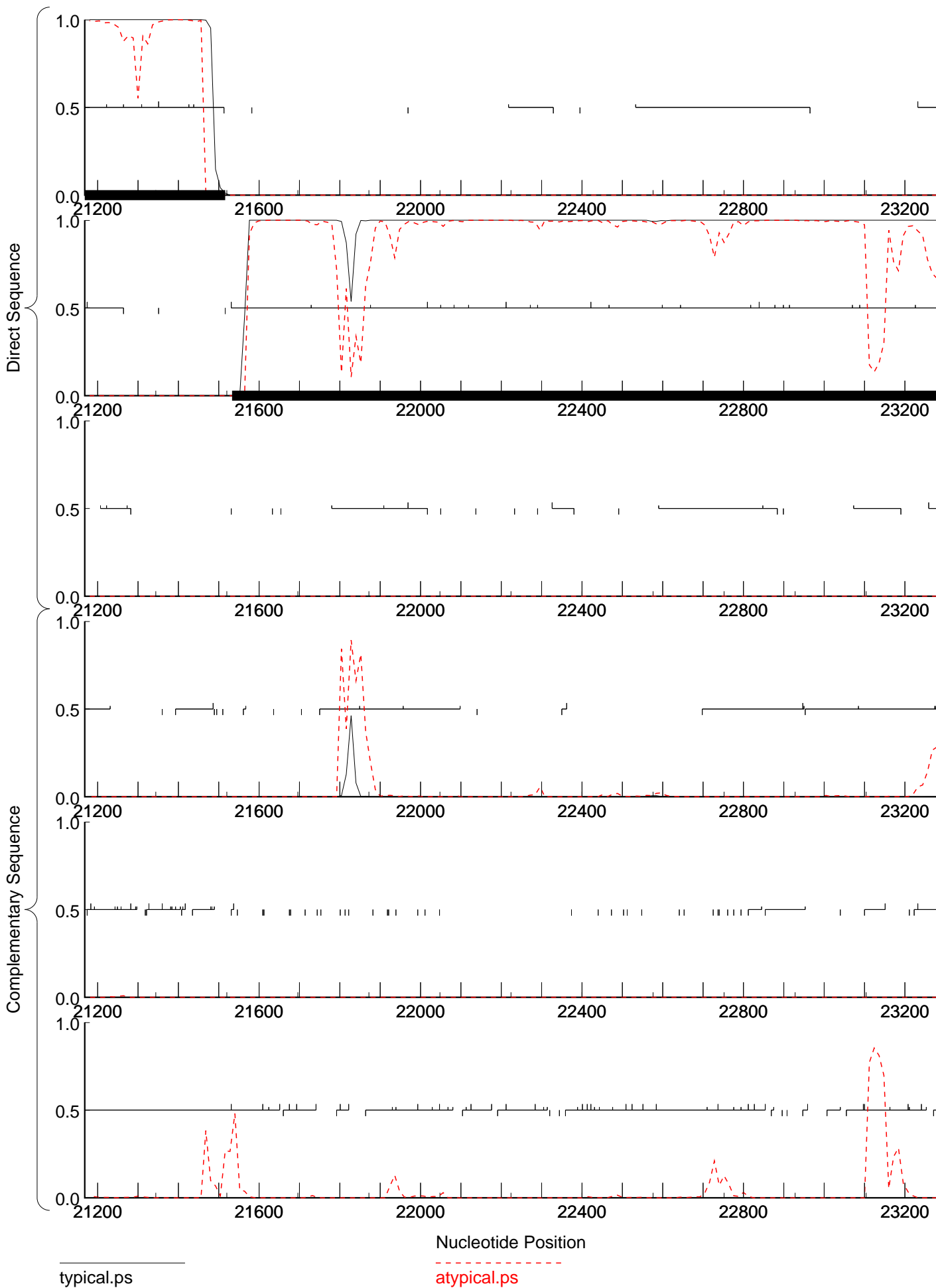


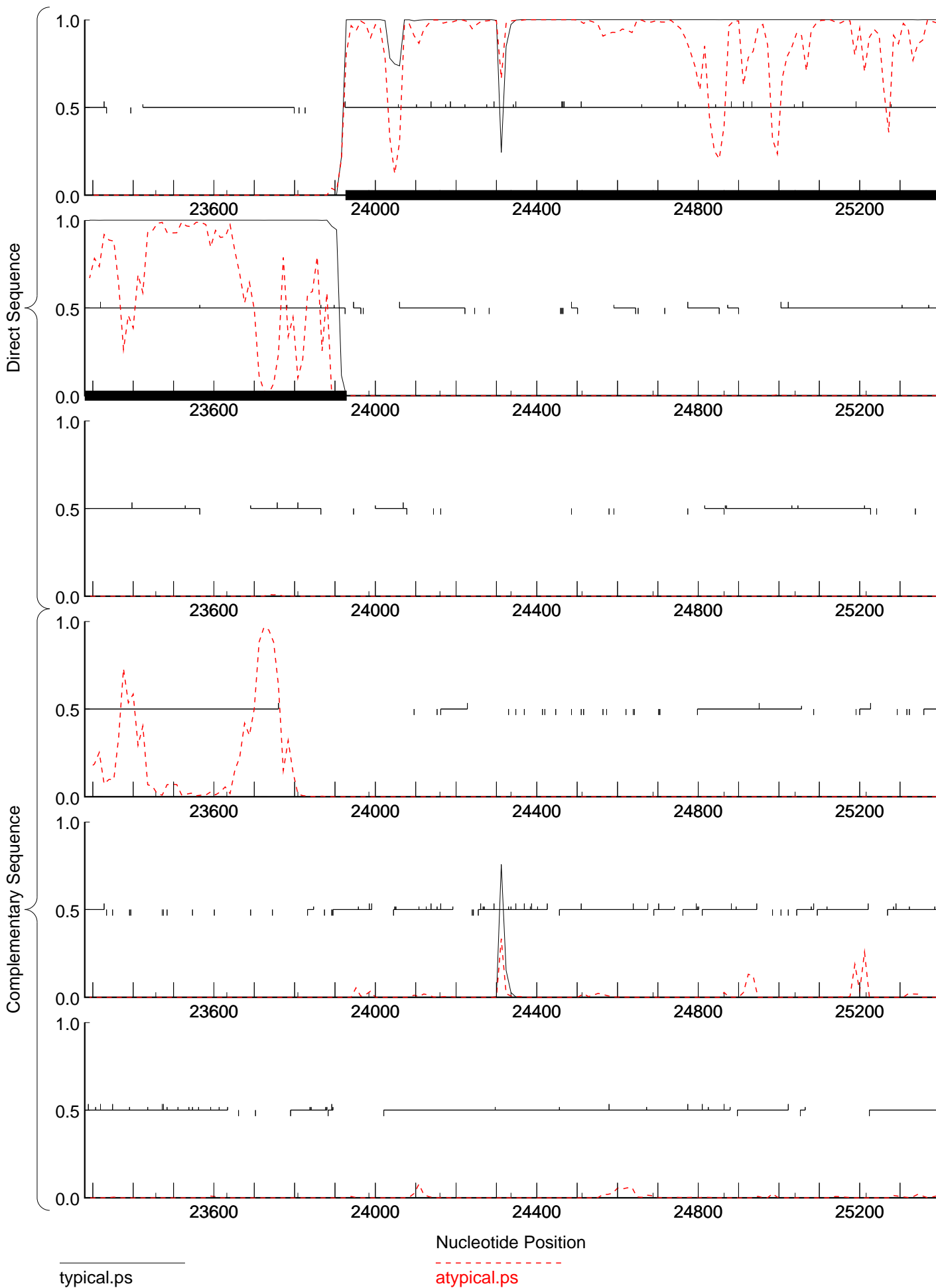
typical.ps

atypical.ps



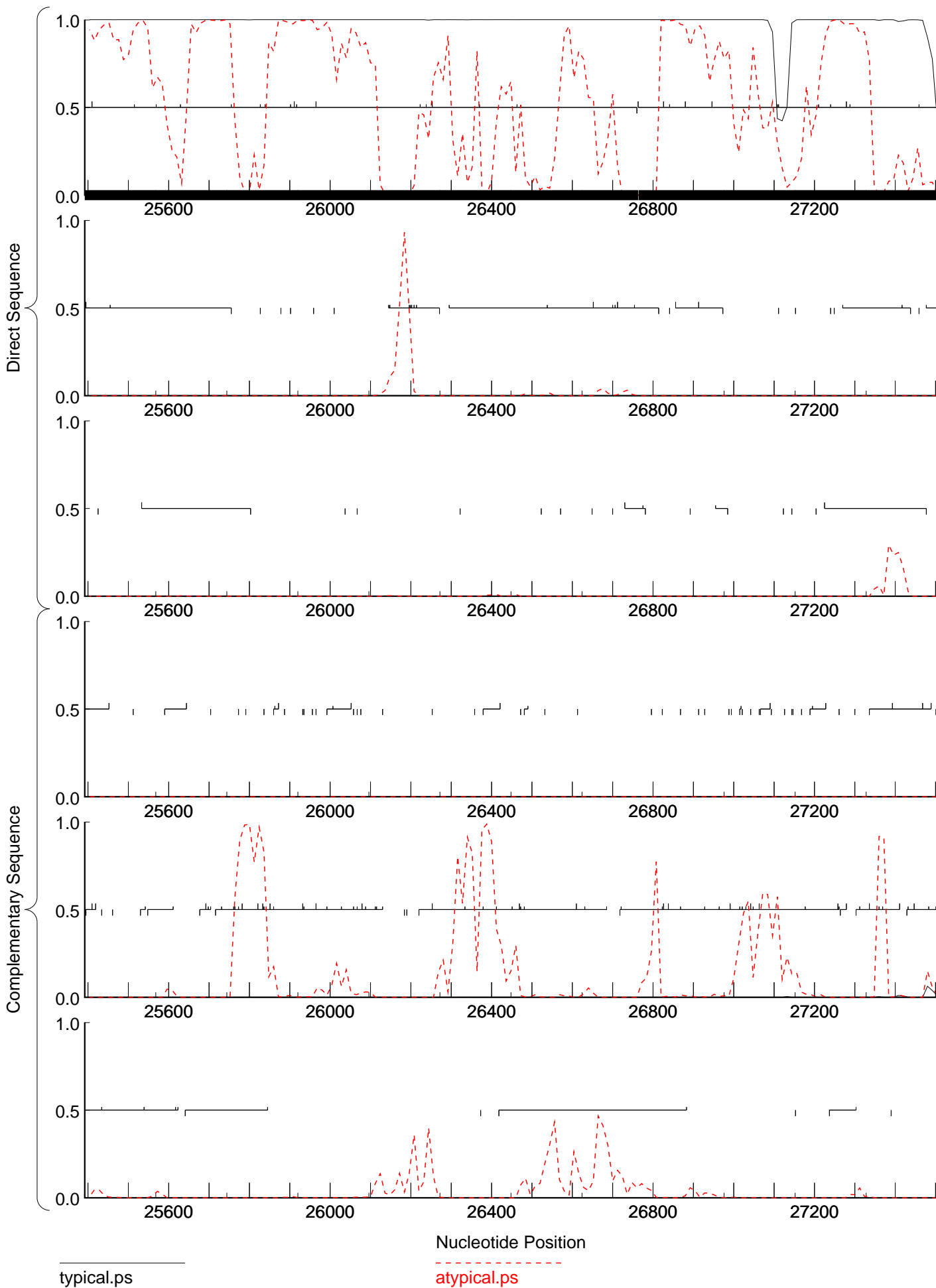
Bhai complete sequence, 76145 bp including 9-base 3' overhang (CGCTTGTC A), Cluster E, Order 4, Window 96, Step 12, 12/38
GeneMark.hmm prediction
Bhai complete sequence, 76145 bp including 9-base 3' overhang (CGCTTGTC A), Cluster E, Order 2, Window 96, Step 12, 12/38

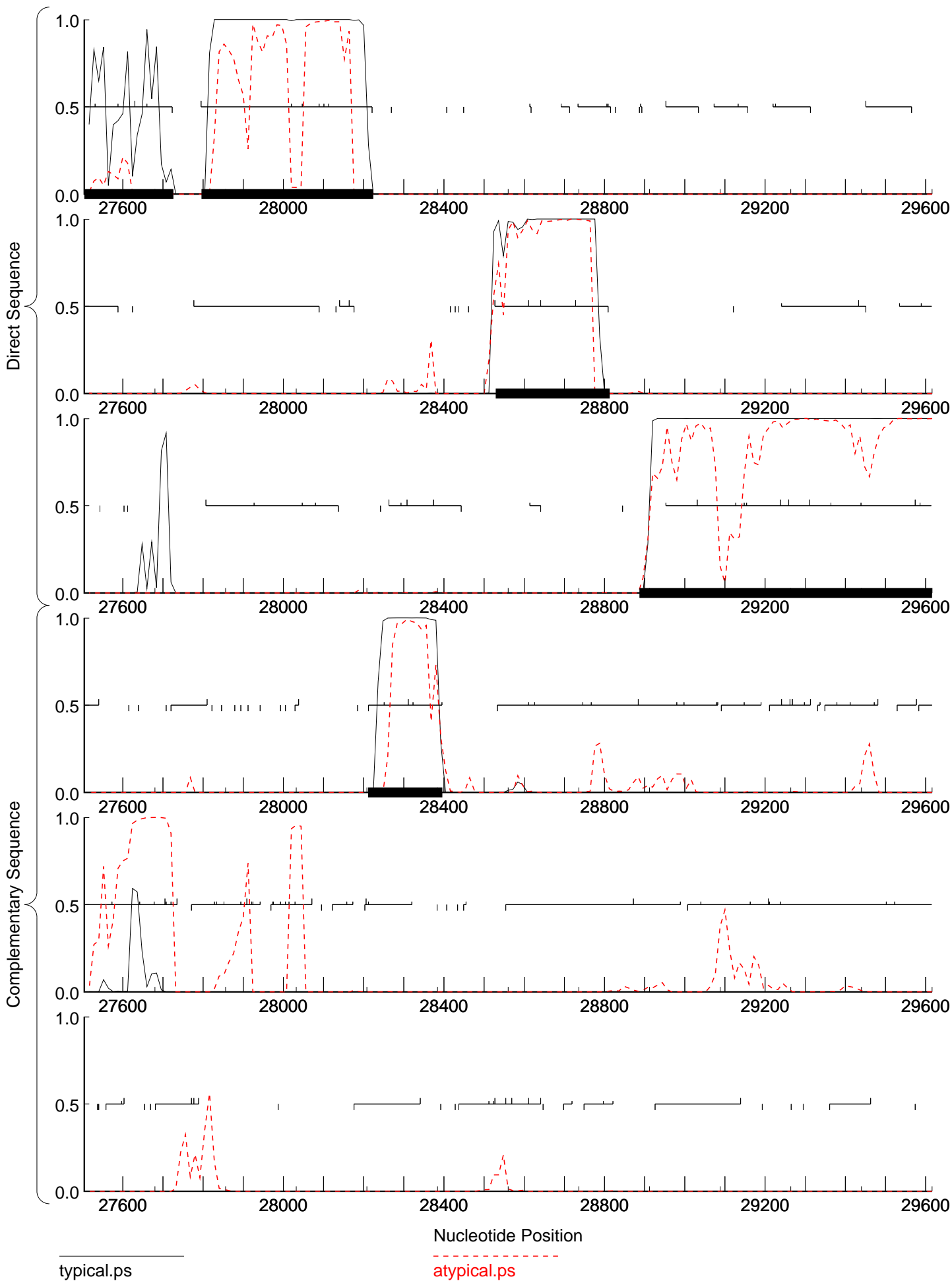


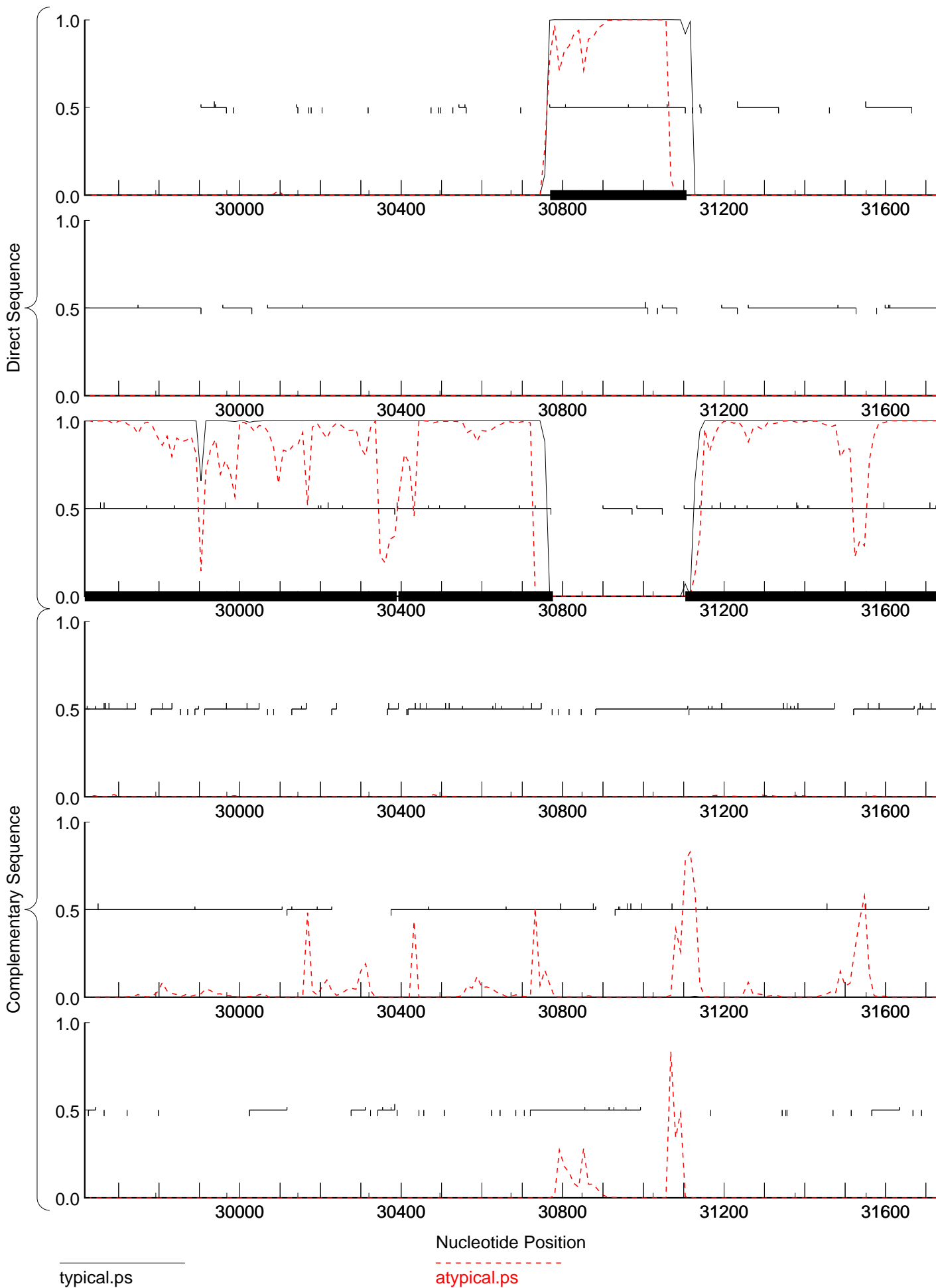


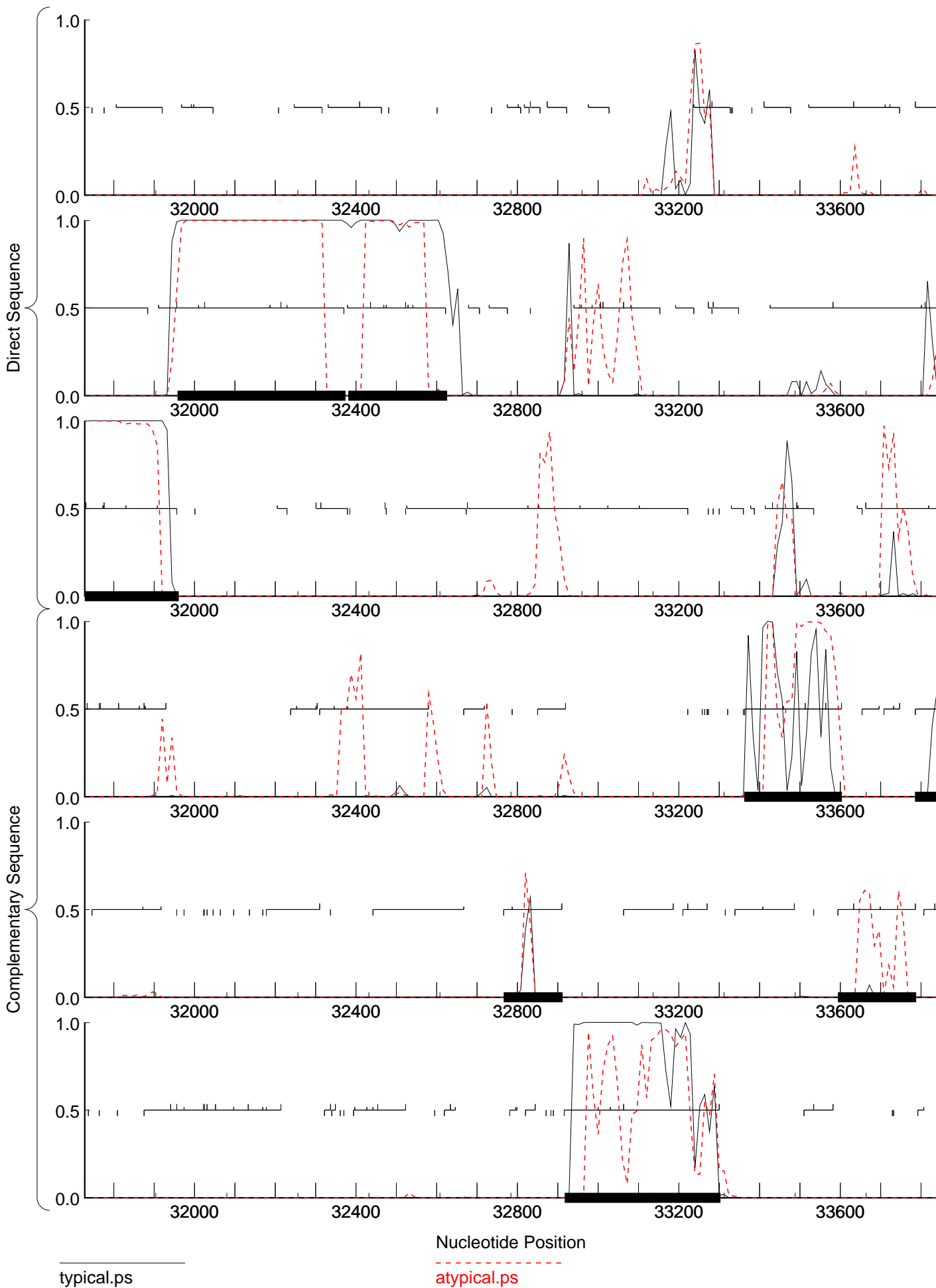
typical.ps

atypical.ps



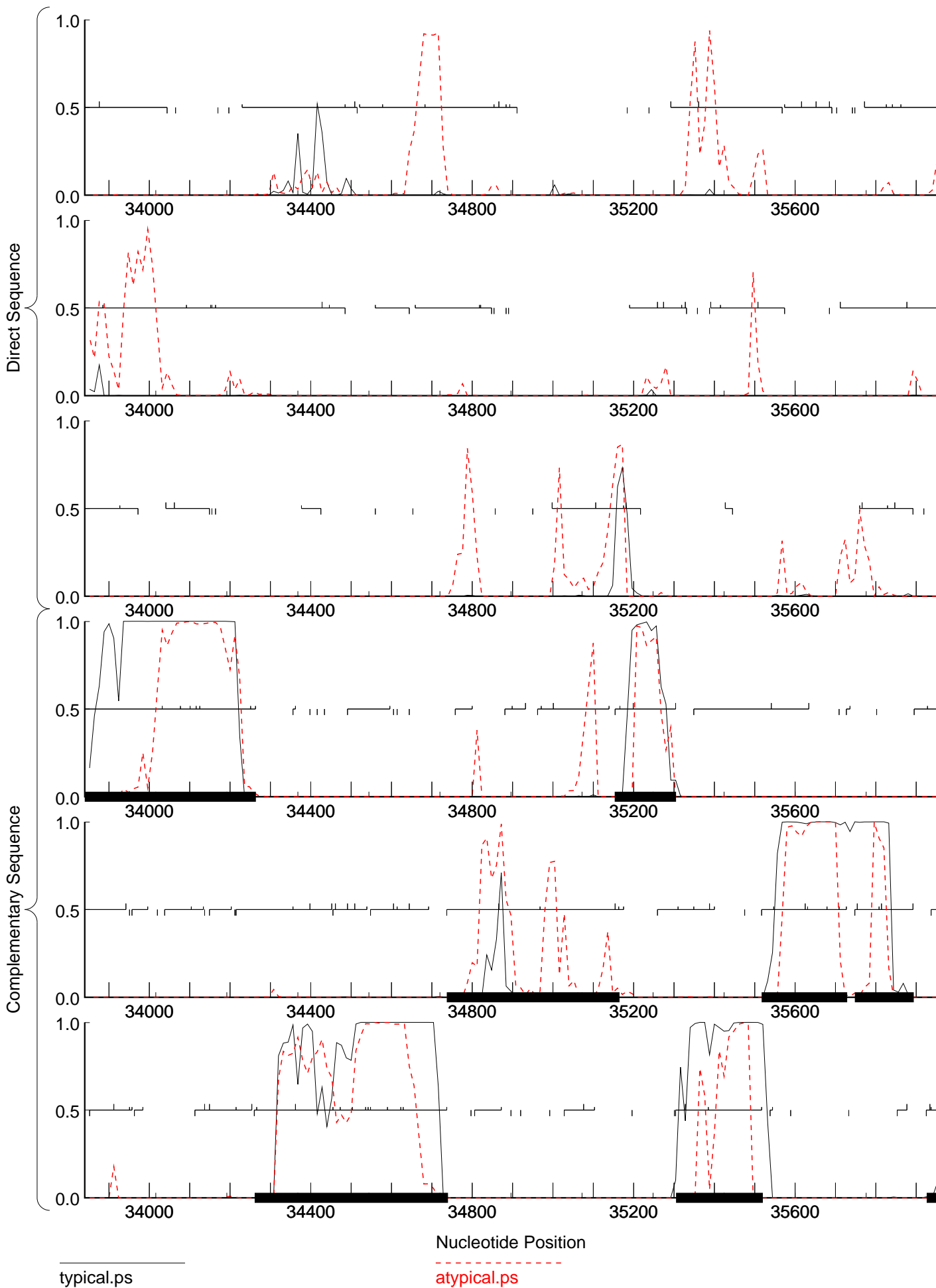


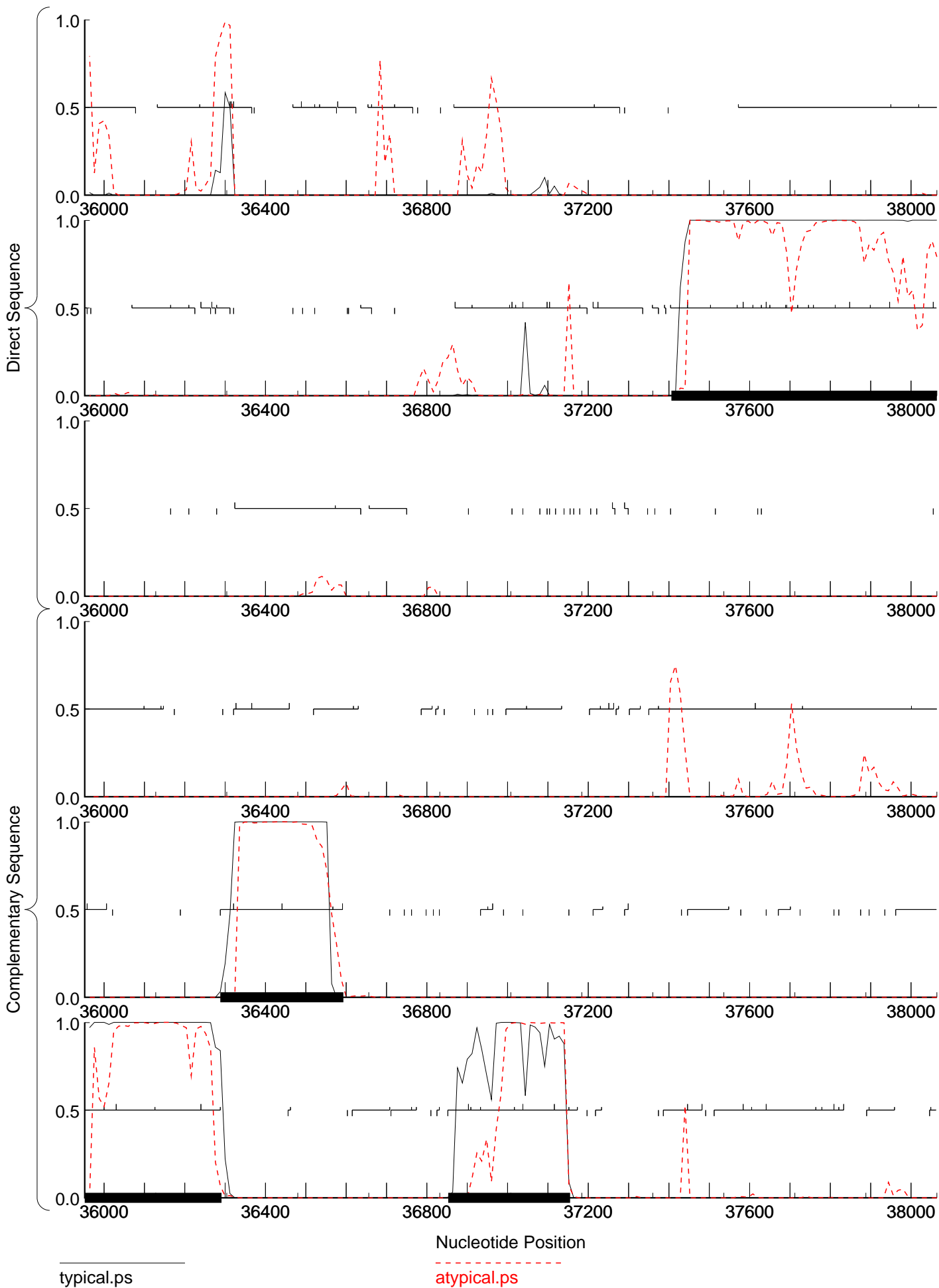


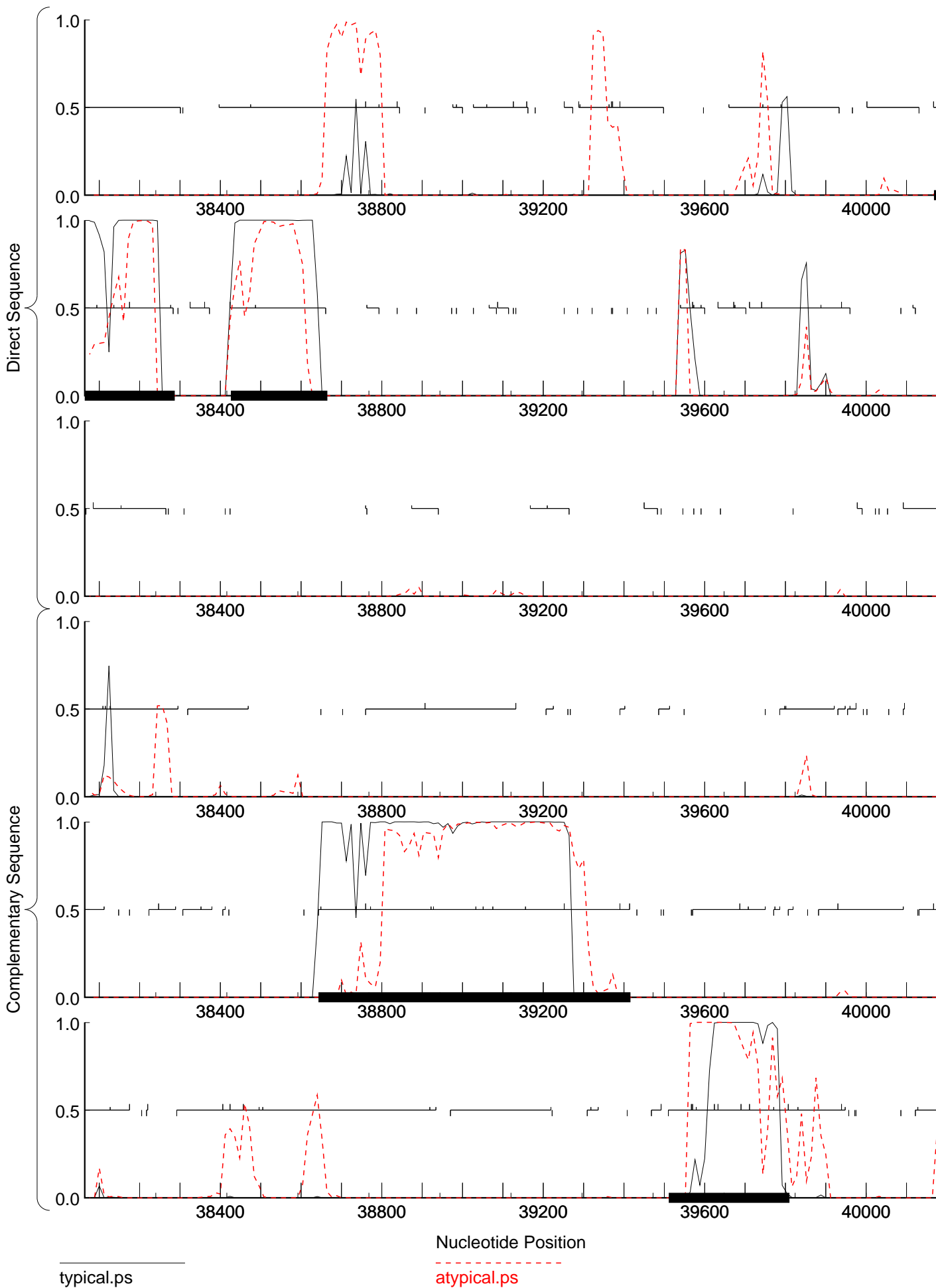


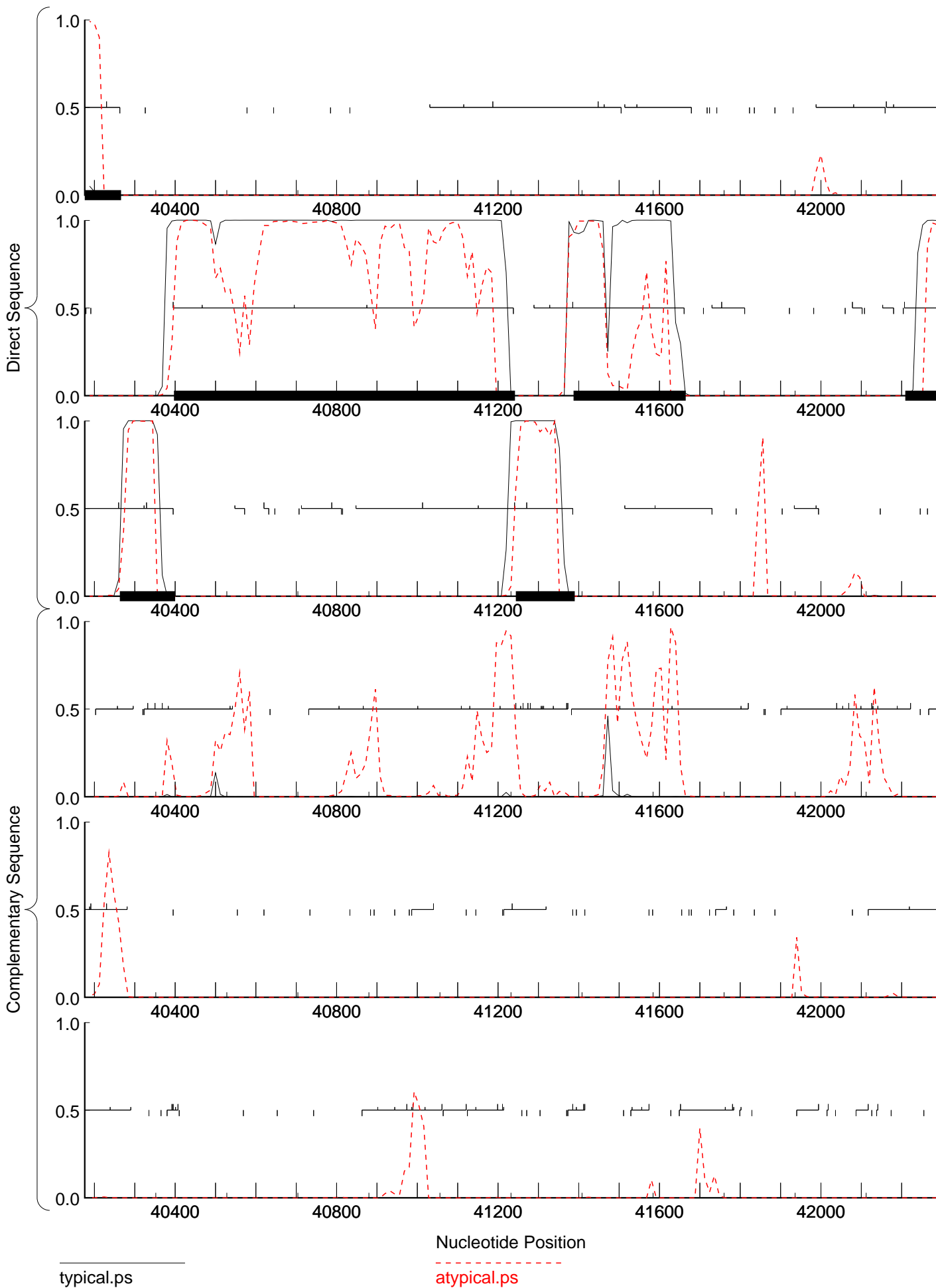
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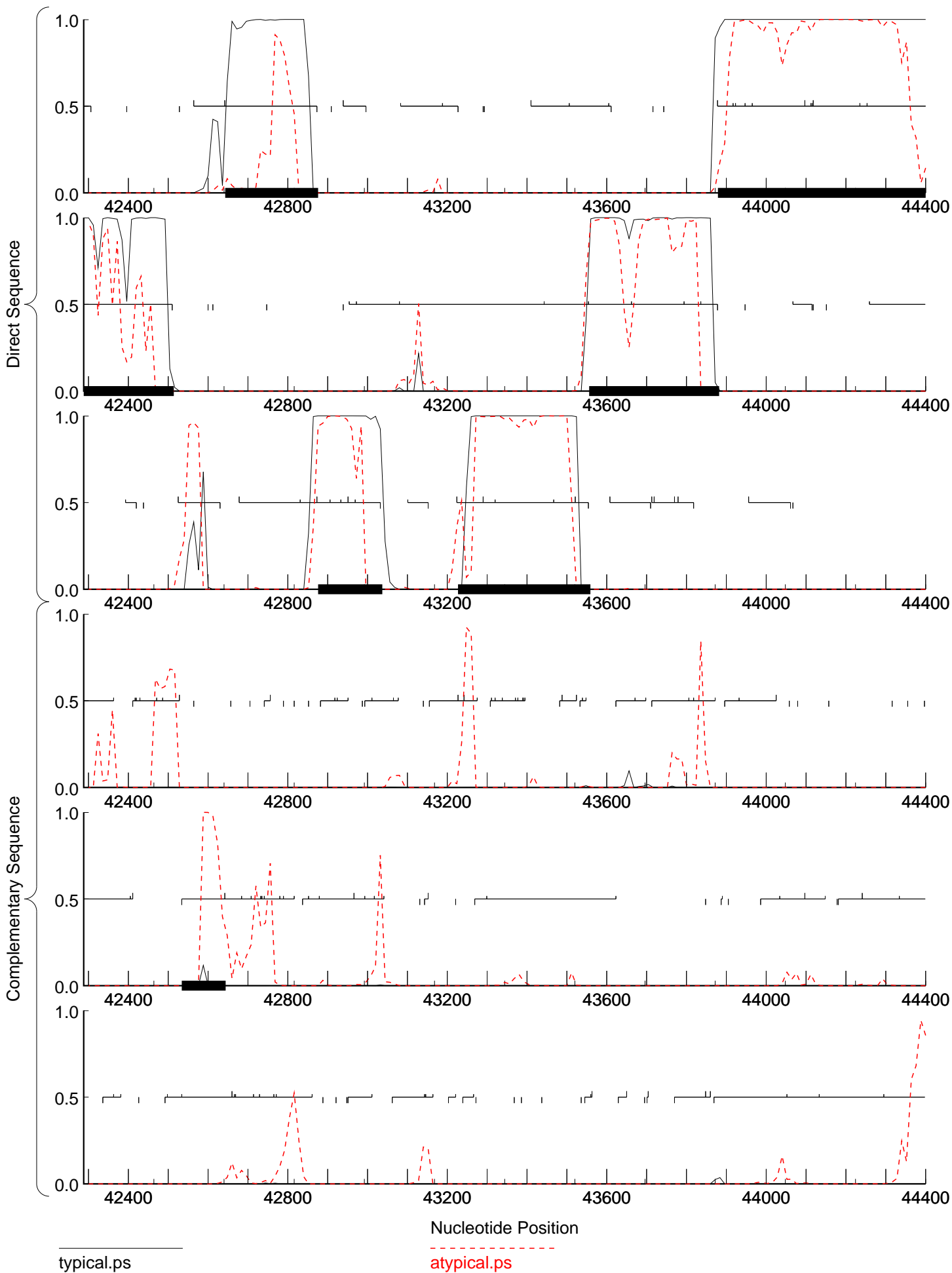
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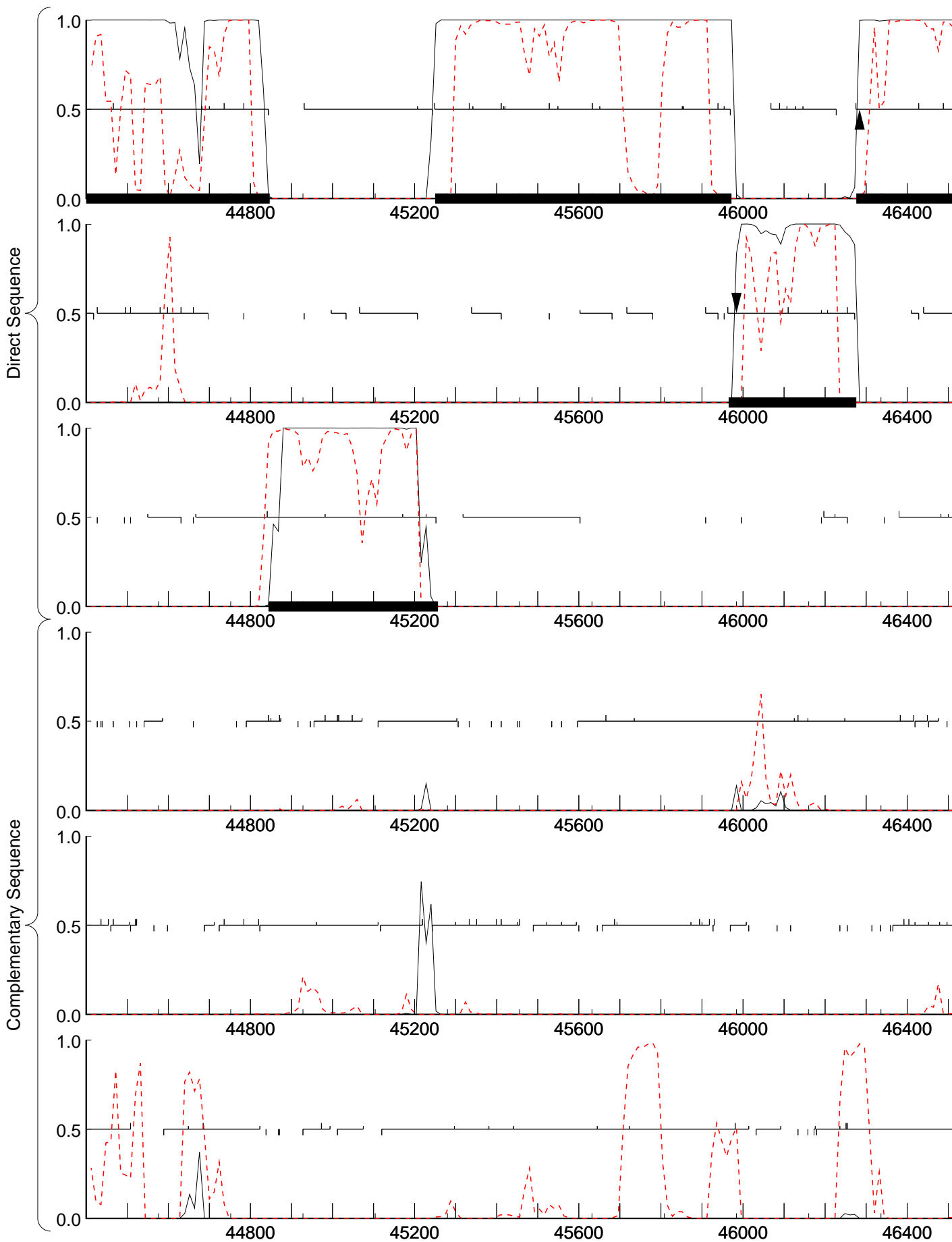


typical.ps

atypical.ps

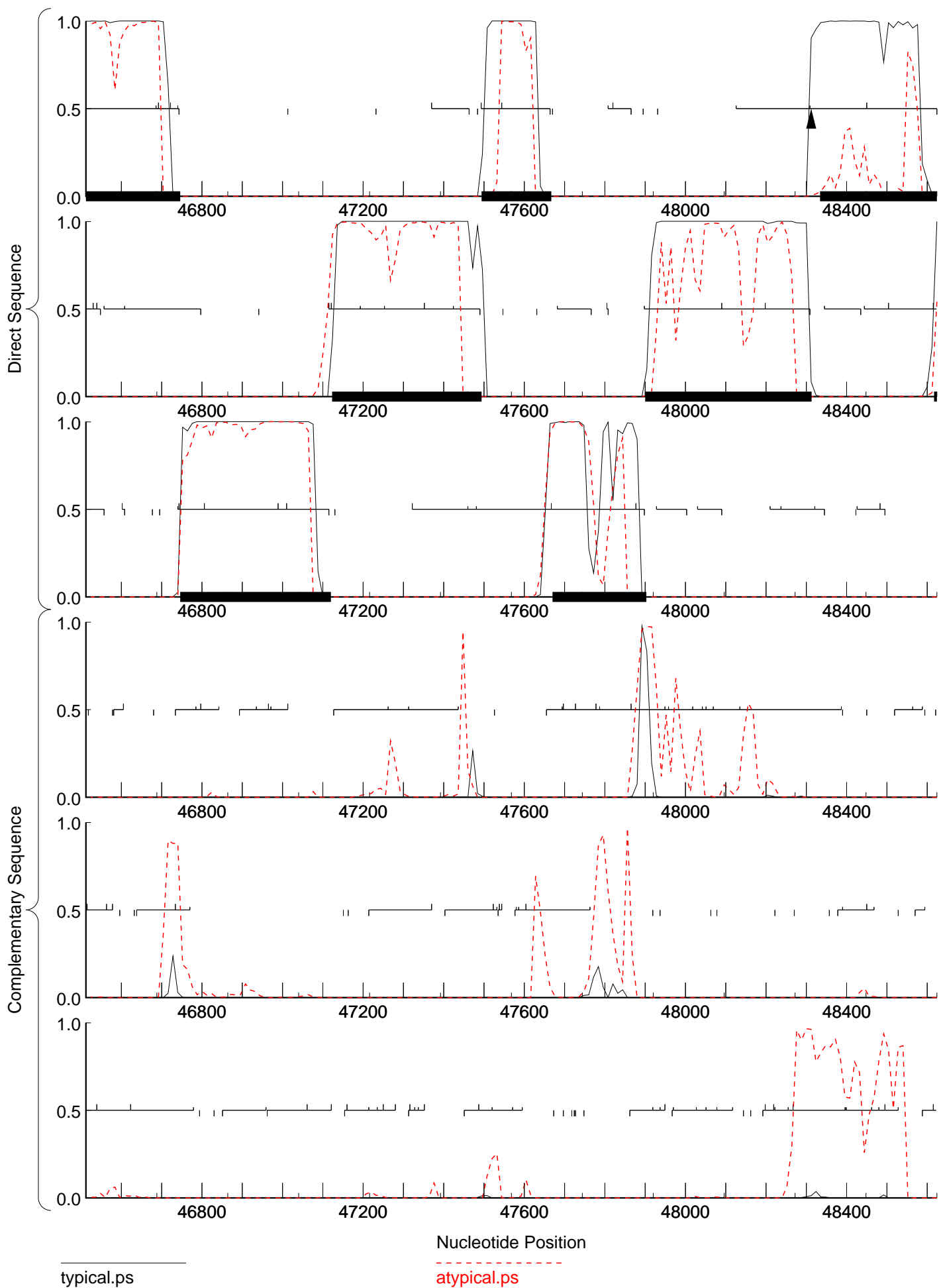
Bhai complete sequence, 76145 bp including 9-base 3' overhang (CGCTTGTC A), Cluster E, Order 4, Window 96, Step 12, 23/38
GeneMark.hmm prediction

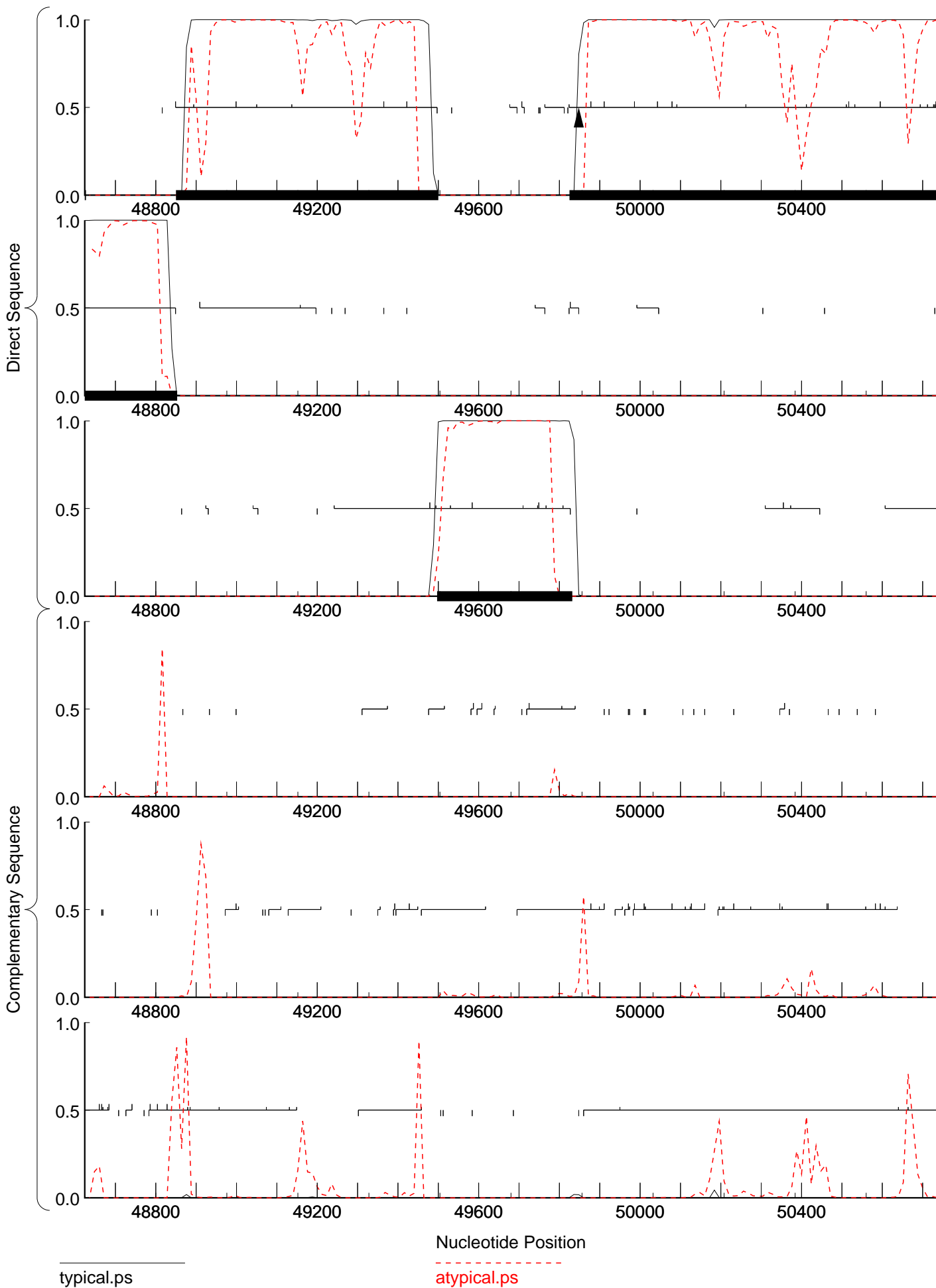
Bhai complete sequence, 76145 bp including 9-base 3' overhang (CGCTTGTC A), Cluster E, Order 2, Window 96, Step 12, 23/38

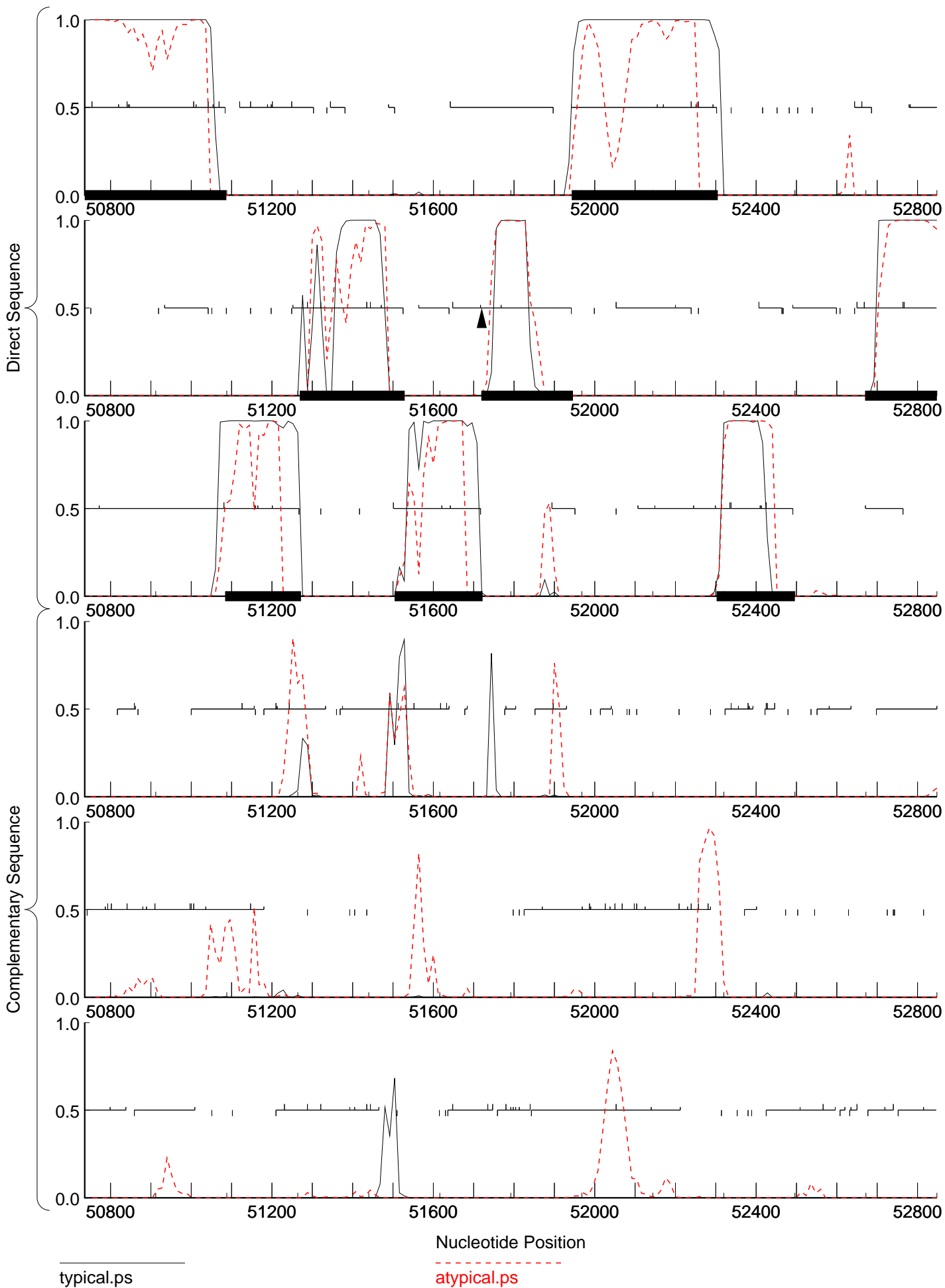


typical.ps

atypical.ps



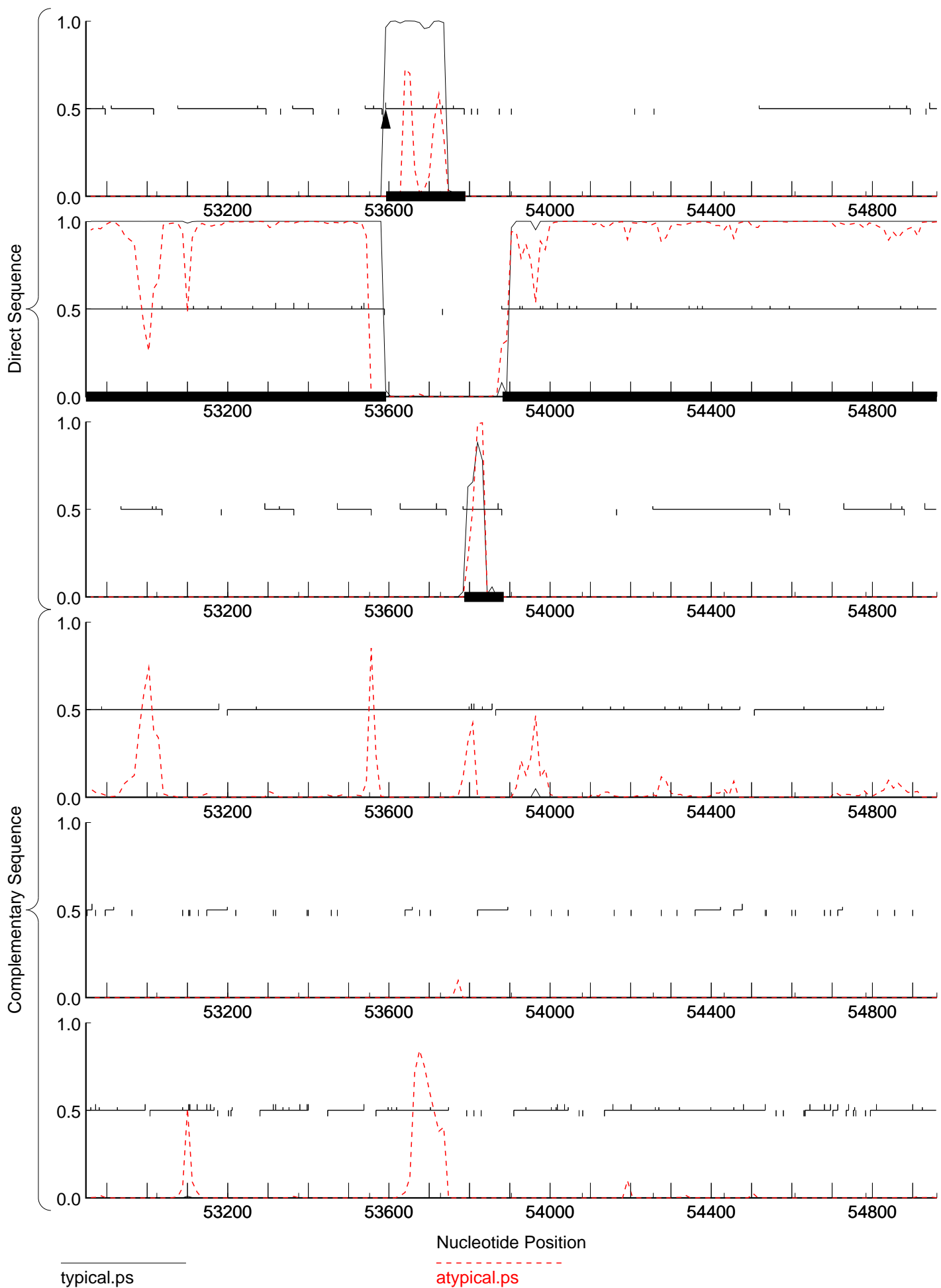


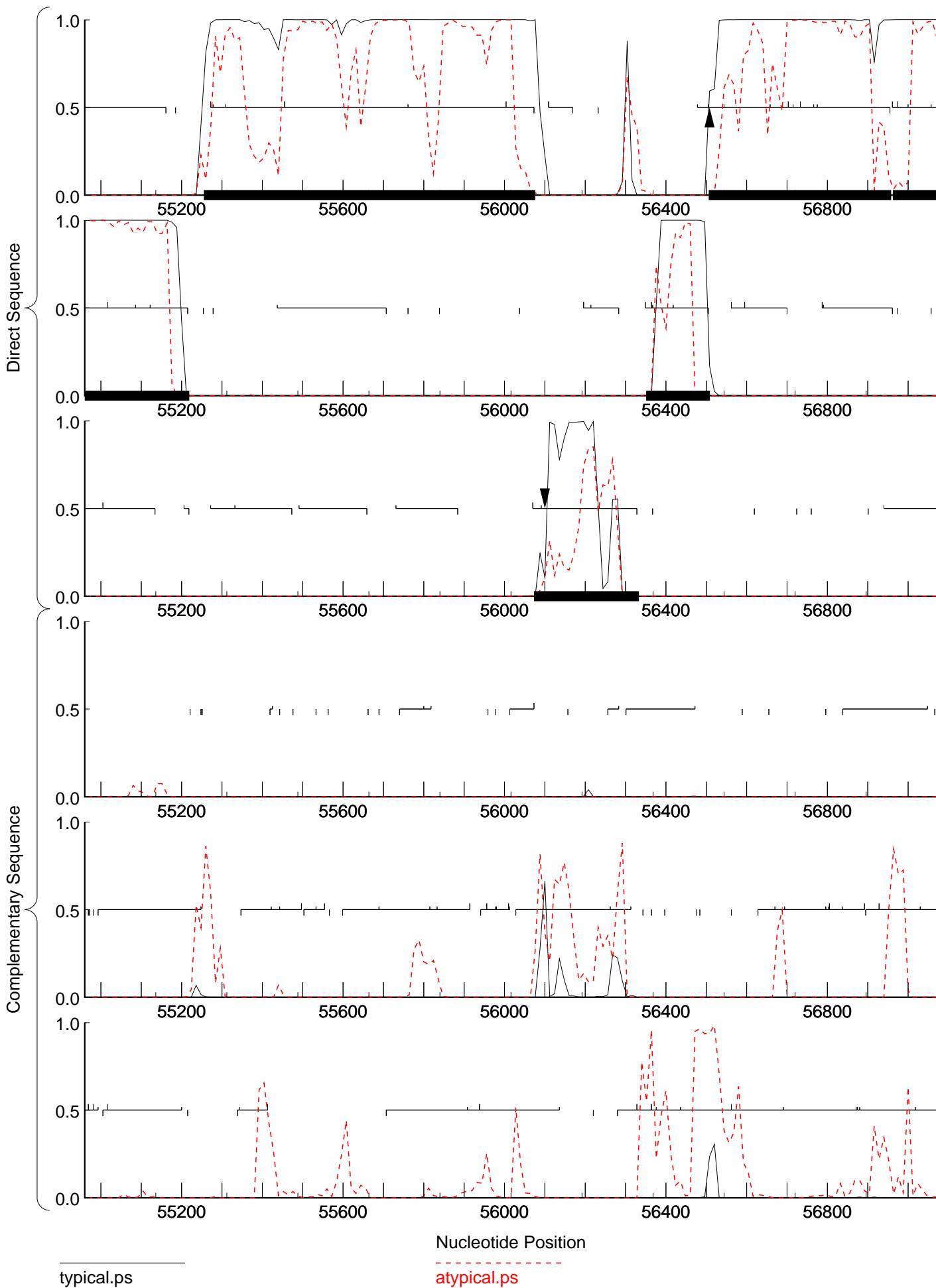


typical.ps

atypical.ps

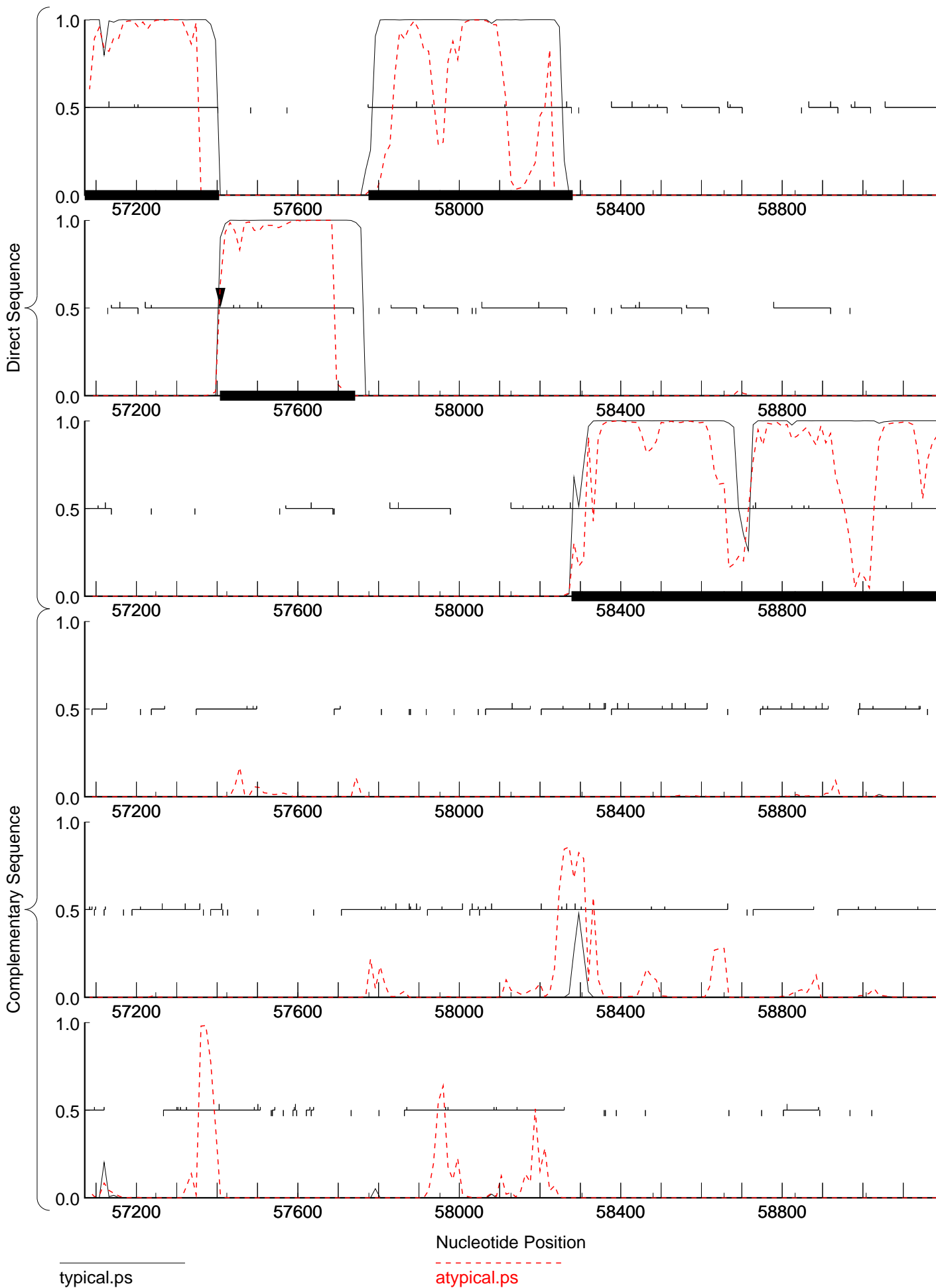
Bhai complete sequence, 76145 bp including 9-base 3' overhang (CGCTTGTC A), Cluster E, Order 4, Window 96, Step 12, 27/38
GeneMark.hmm prediction
Bhai complete sequence, 76145 bp including 9-base 3' overhang (CGCTTGTC A), Cluster E, Order 2, Window 96, Step 12, 27/38

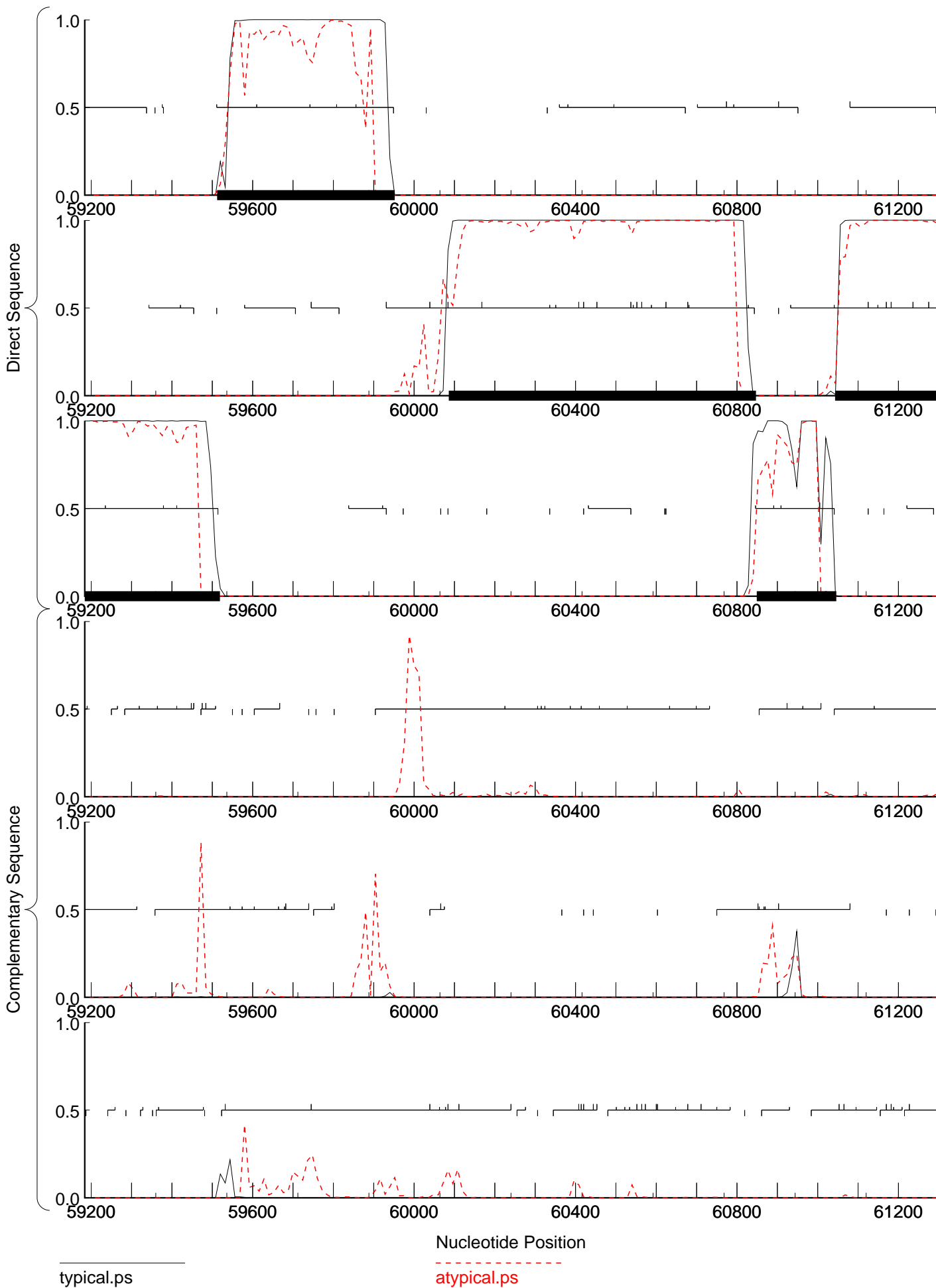


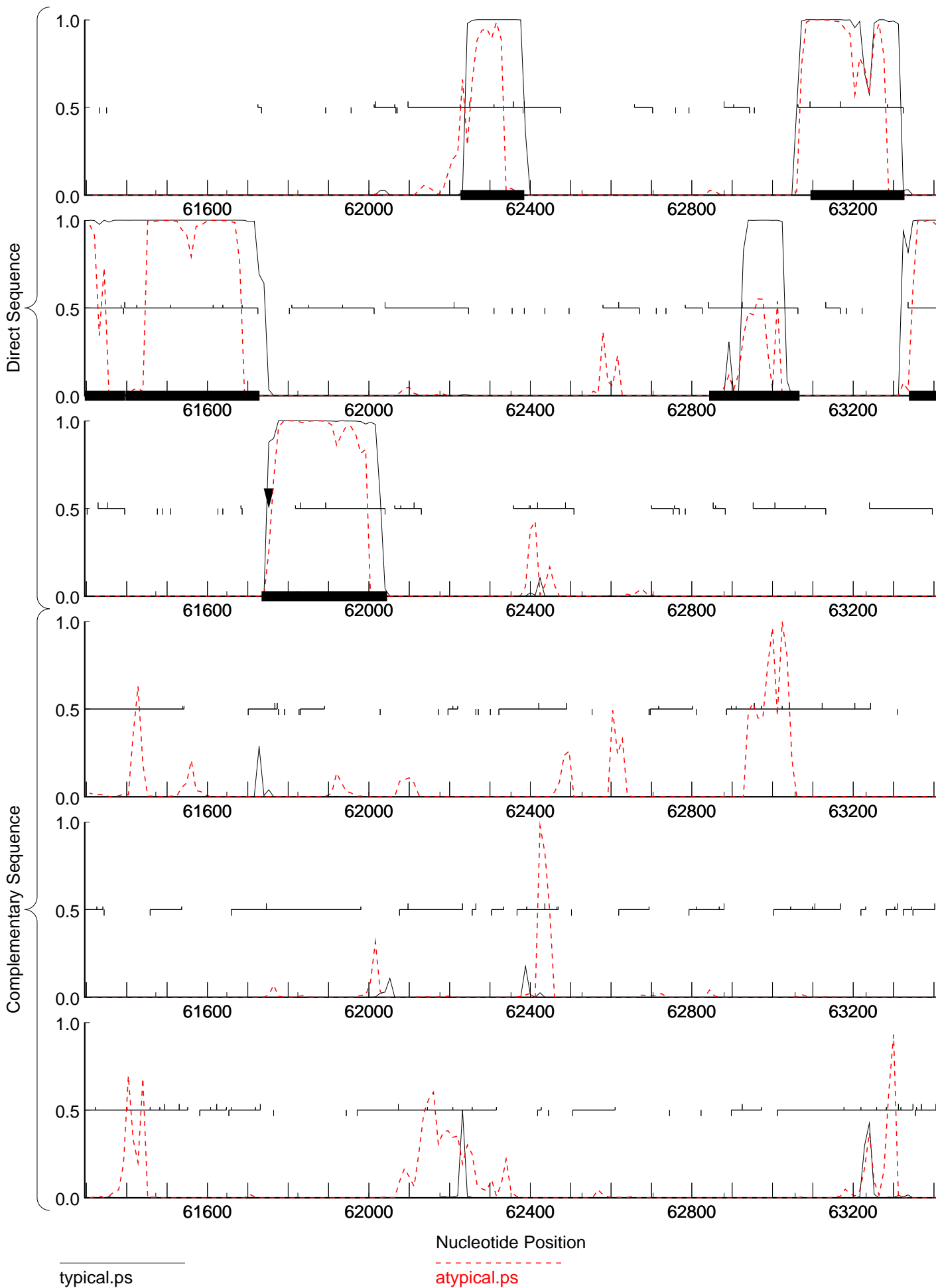


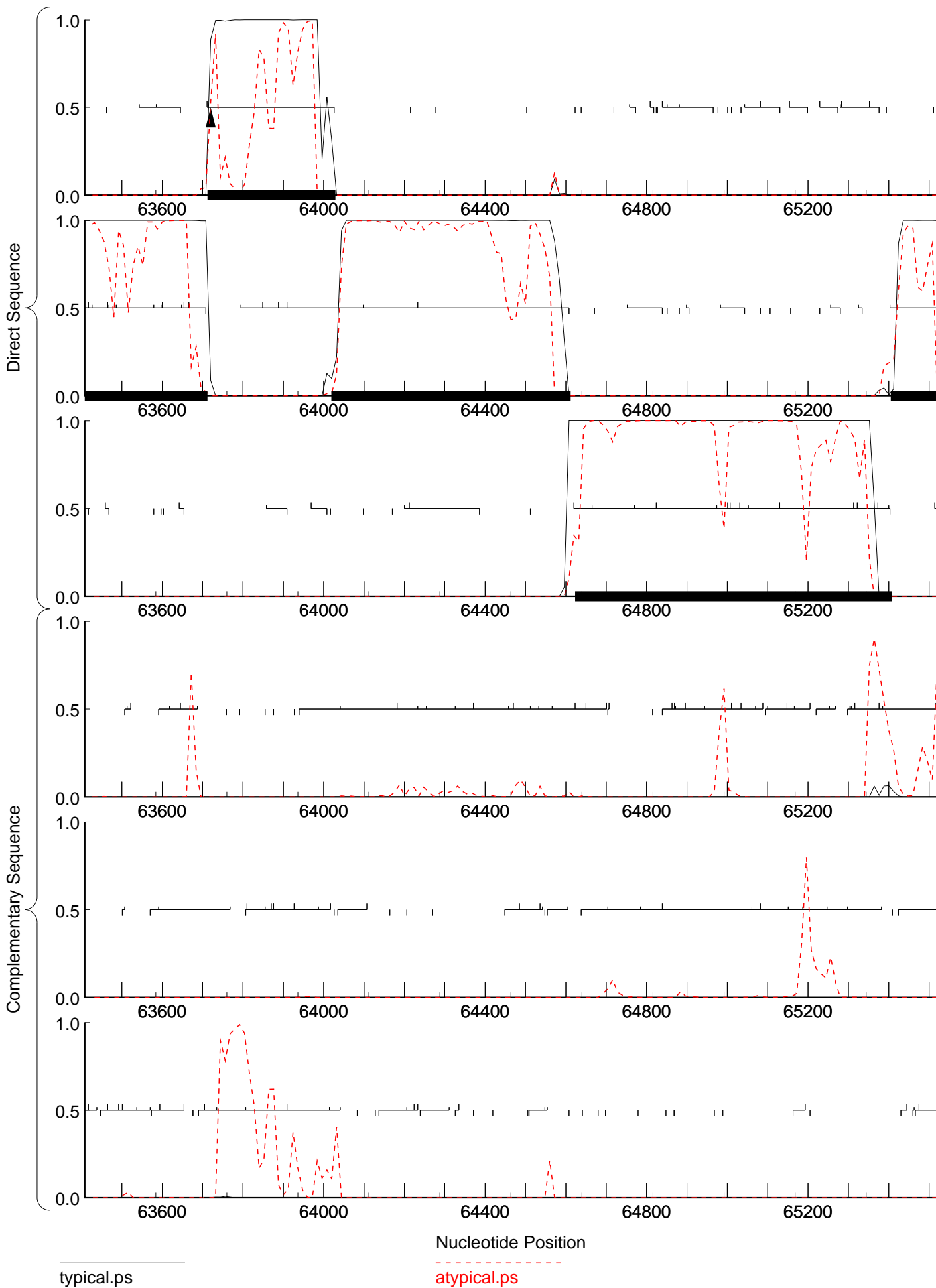
typical.ps

atypical.ps



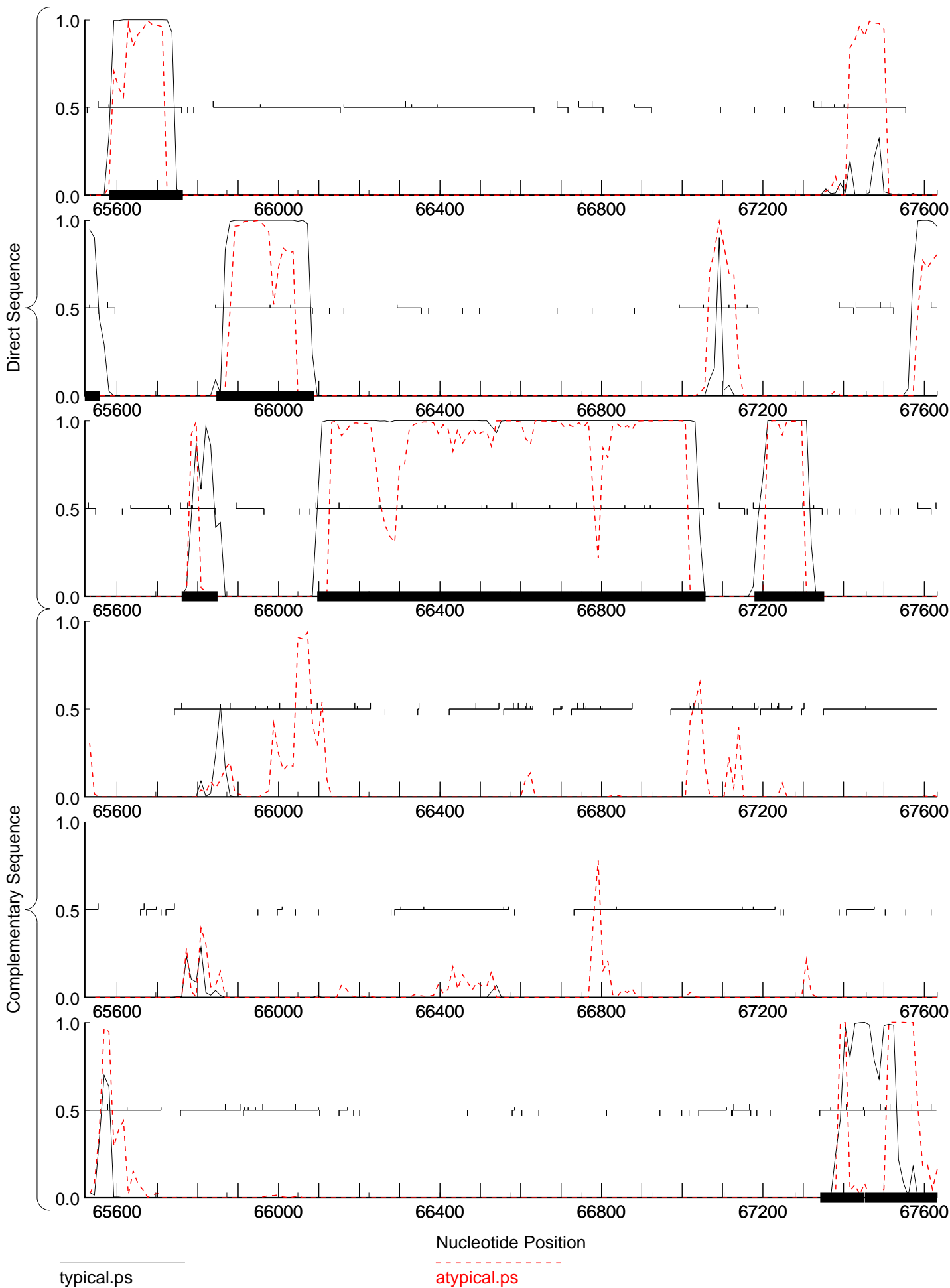


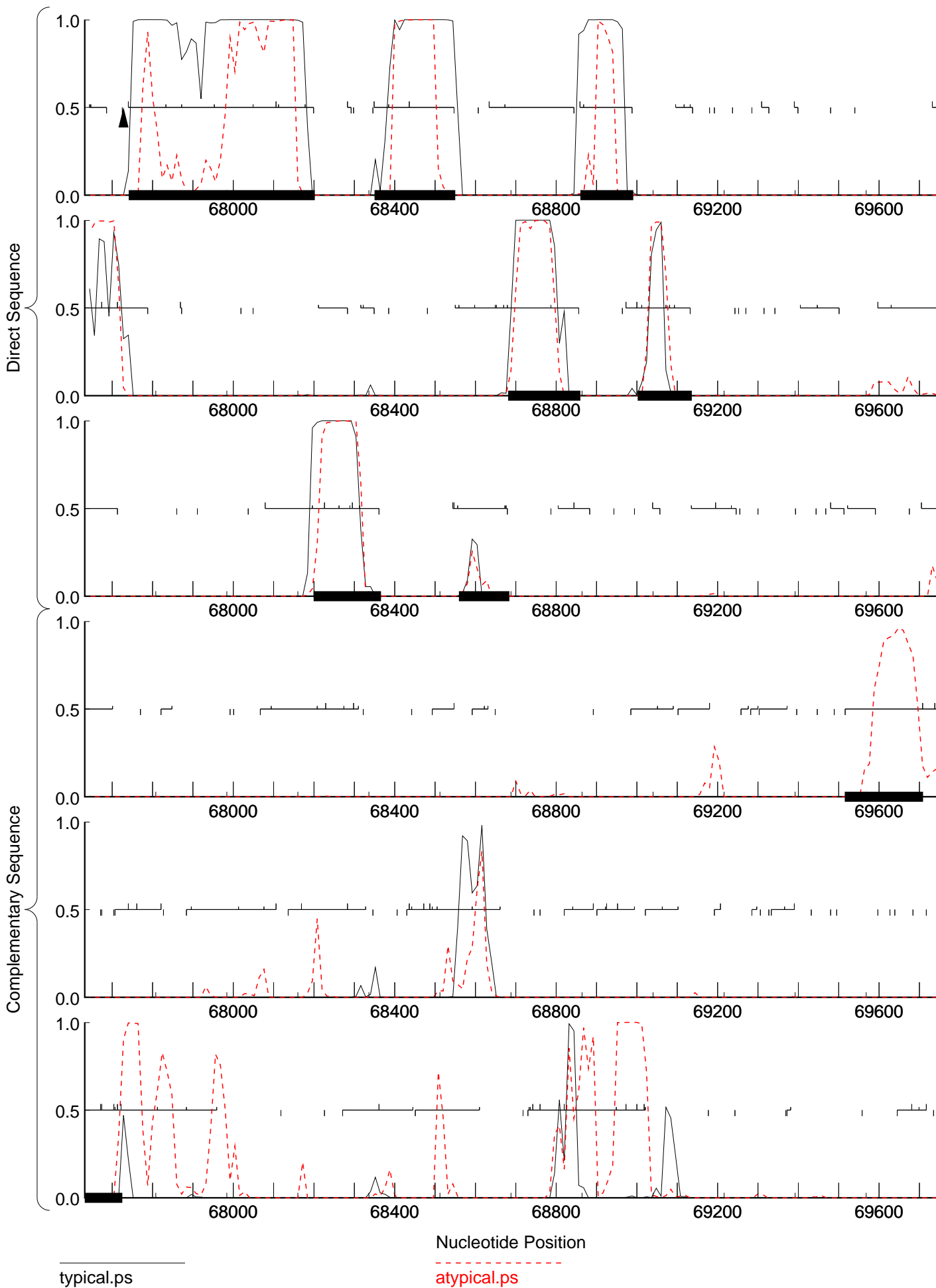


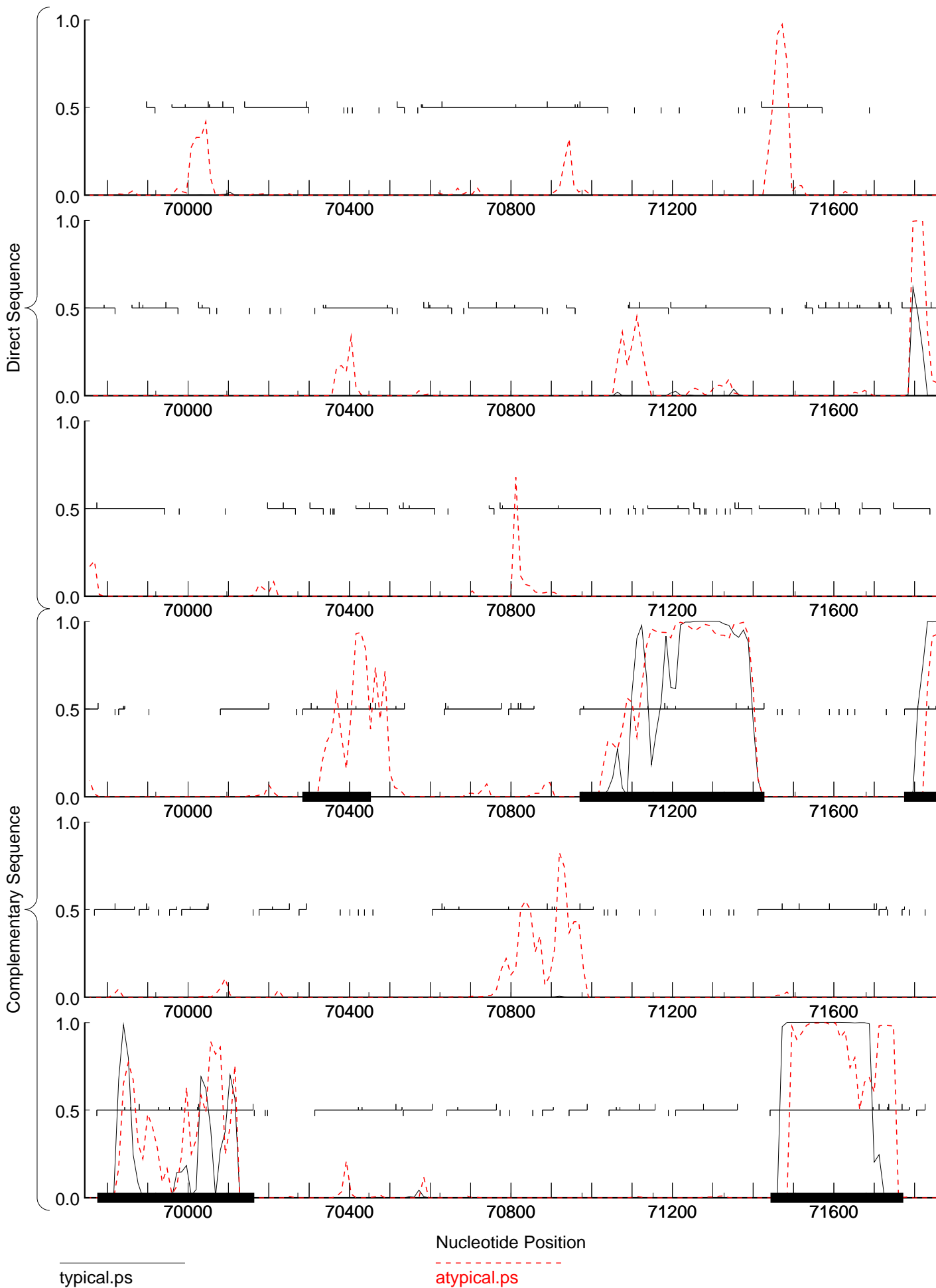


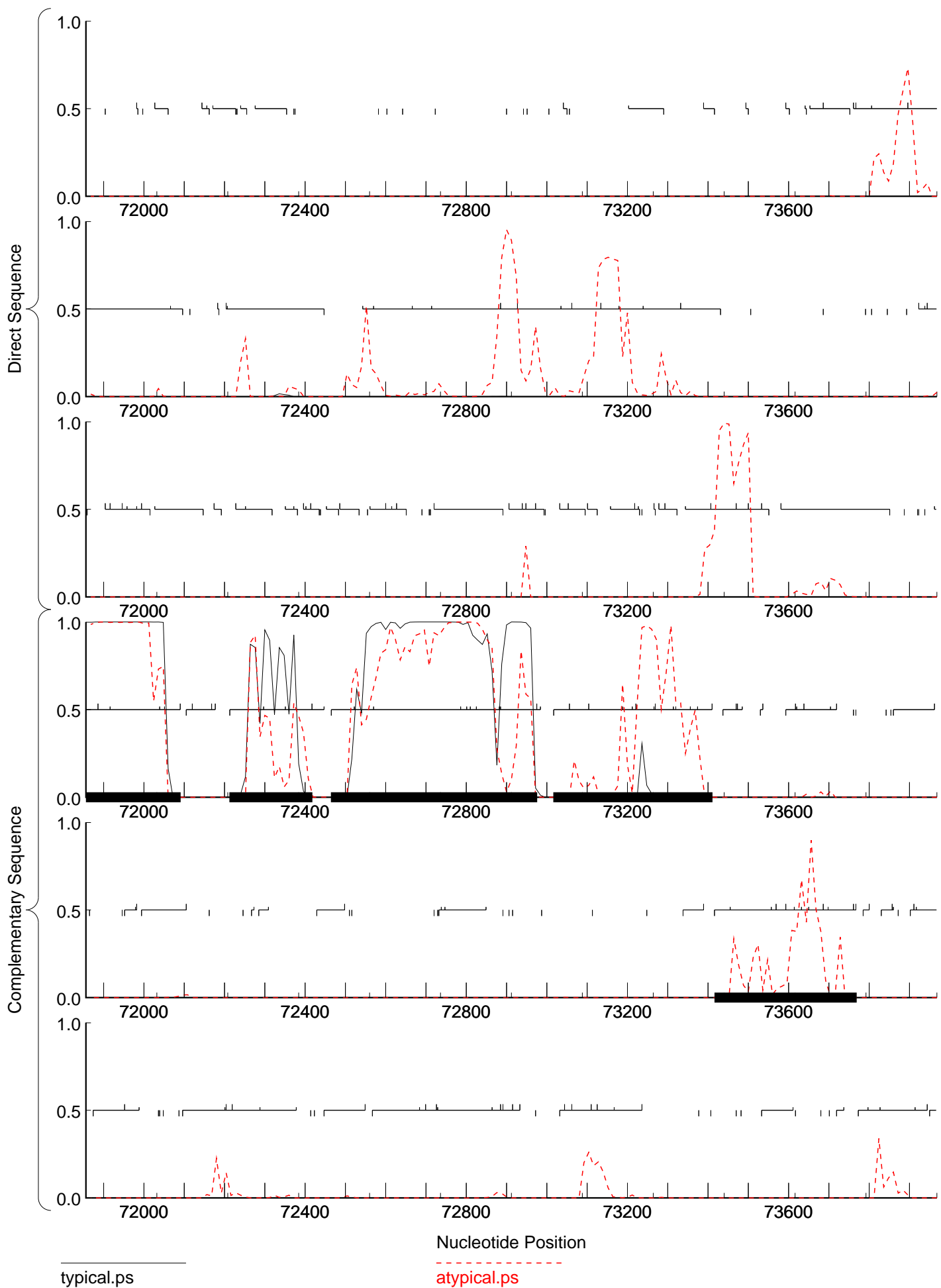
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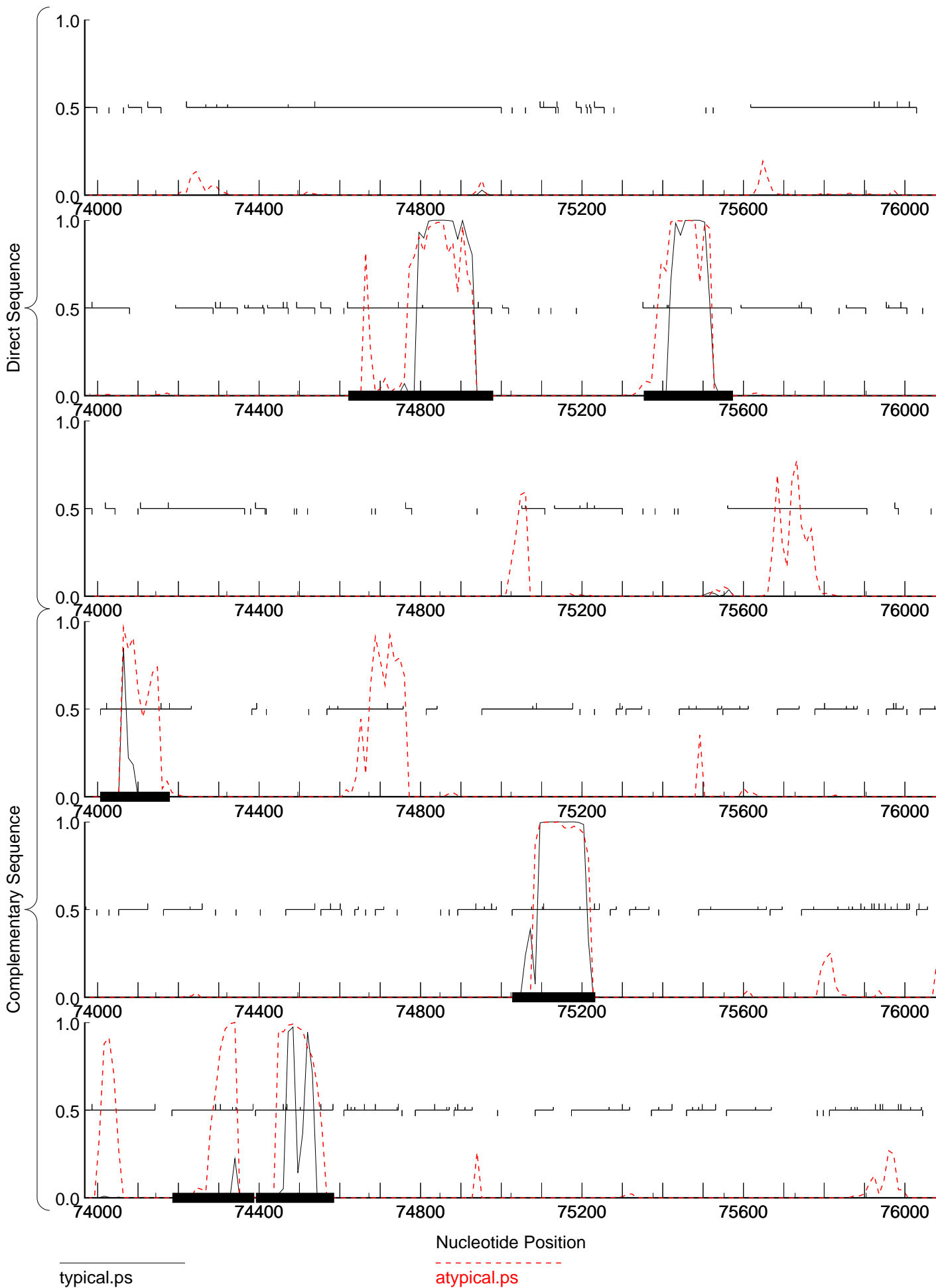
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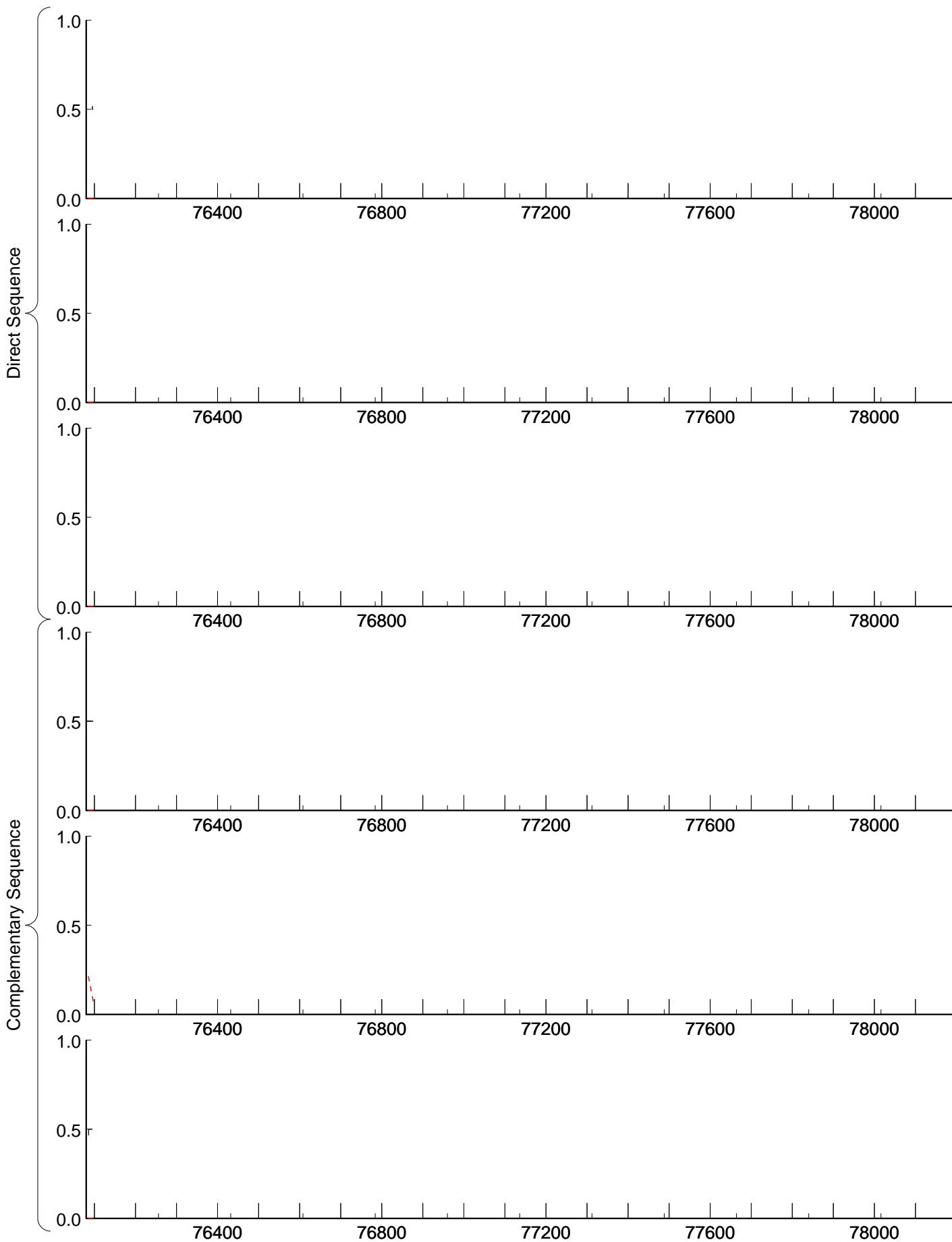






typical.ps

atypical.ps



typical.ps

Nucleotide Position

atypical.ps