

GeneMark

Version 2.5p (09.08.06)

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PROGRAM INFORMATION

Sequence : Mycobacterium phage JangDynasty complete sequence, 70883 bp including 4-base 3' overhang (G
Analysis Date : 10/23/17 at 15:01:30
Pages : 35
Sequence Length : 70883 bp
GC Content : 65.43%

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,

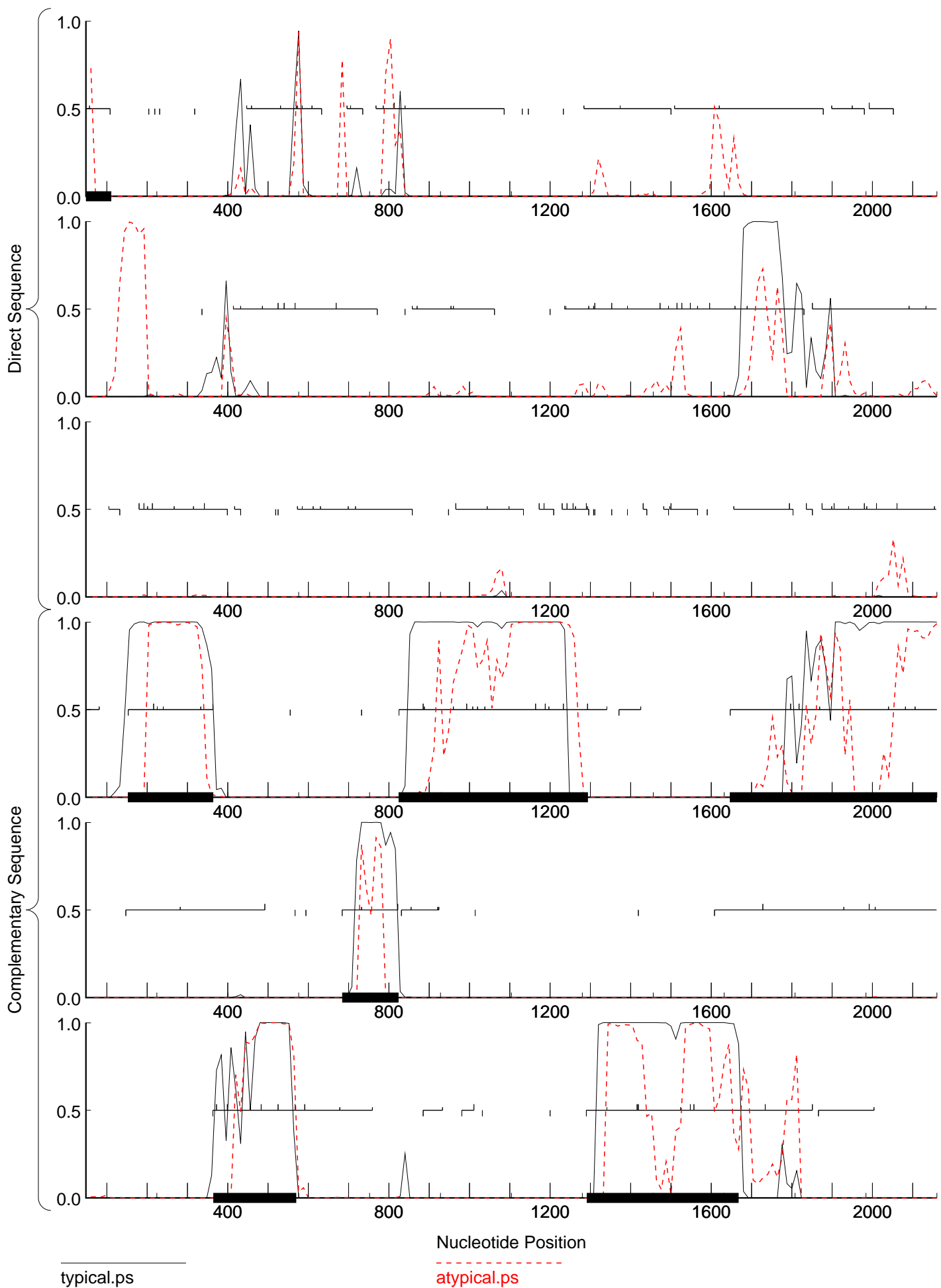
Matrix notes & comments

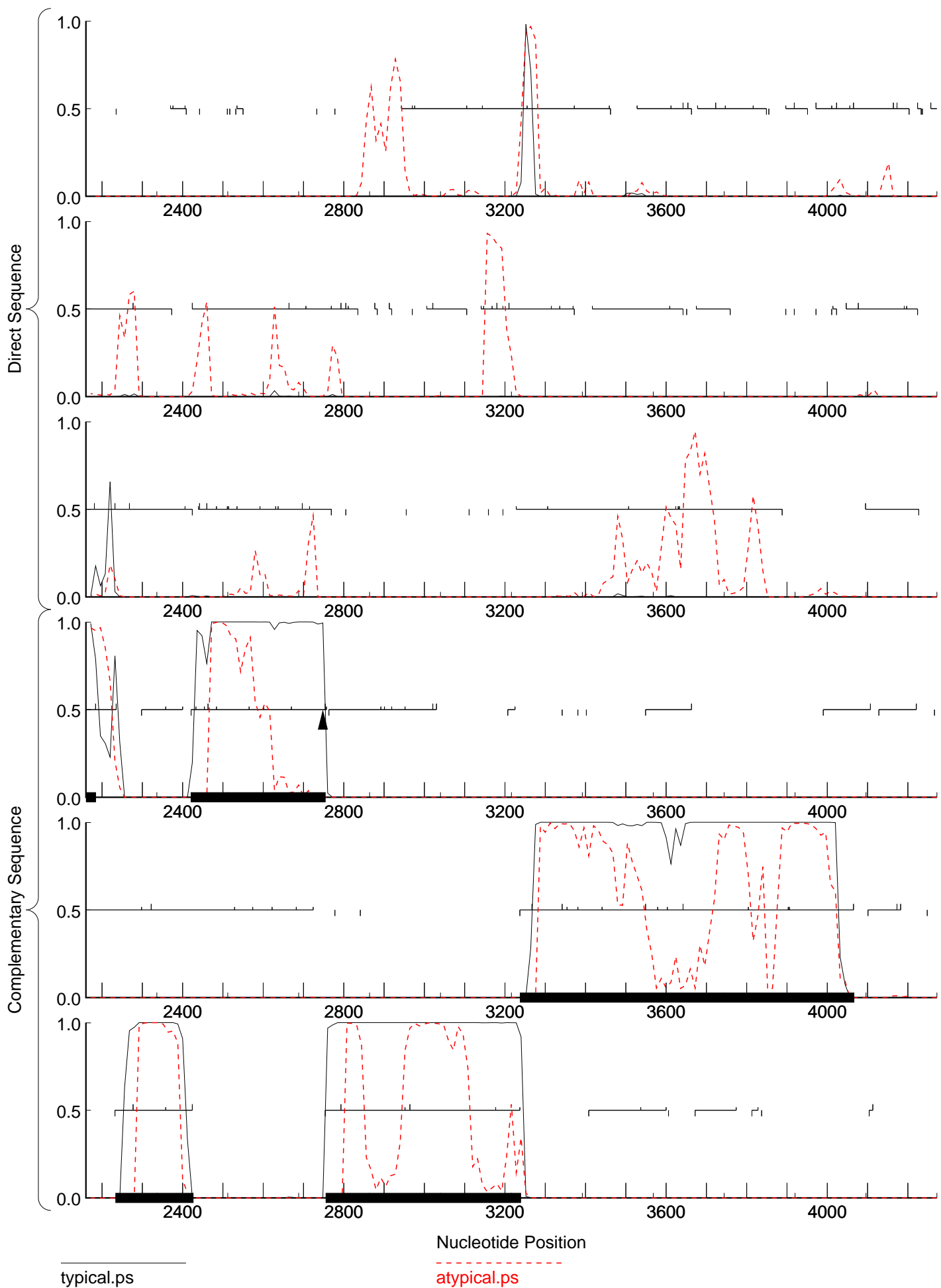
Training set derived by GeneMarkS, 4.30 October 2014
Mon Oct 23 15:01:30 2017

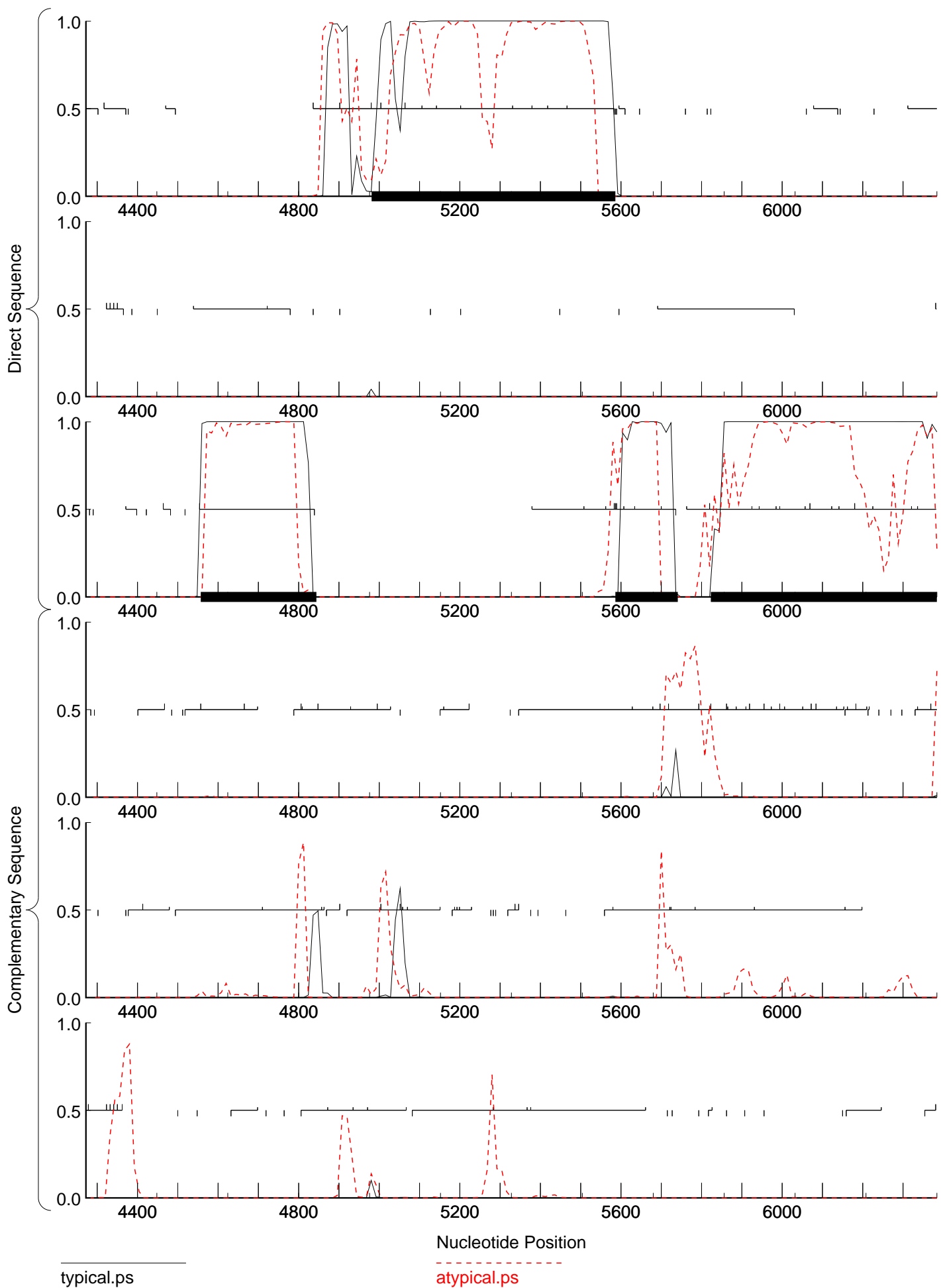
MATRIX INFORMATION

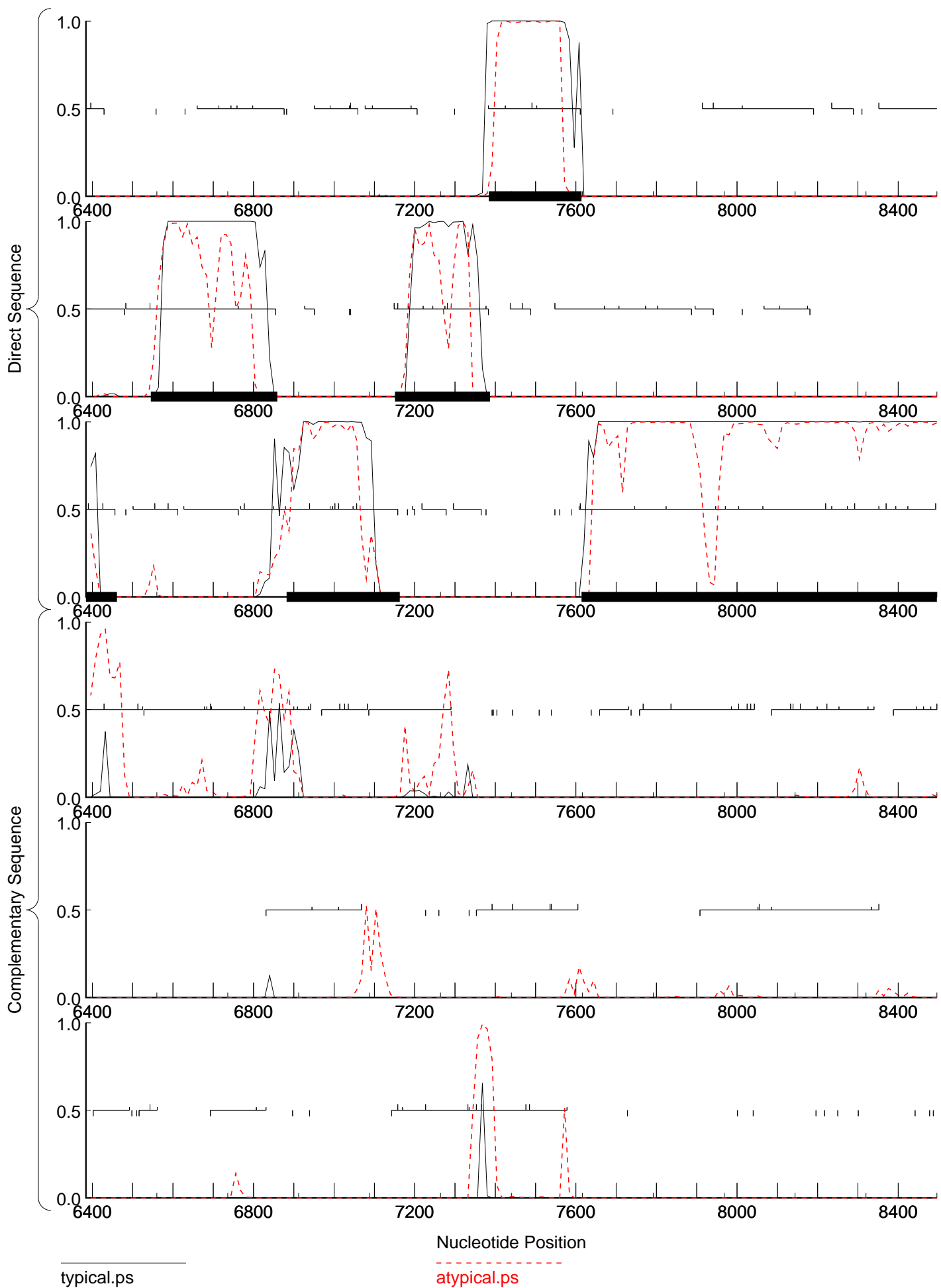
Matrix : -
Author : -
Order : 4

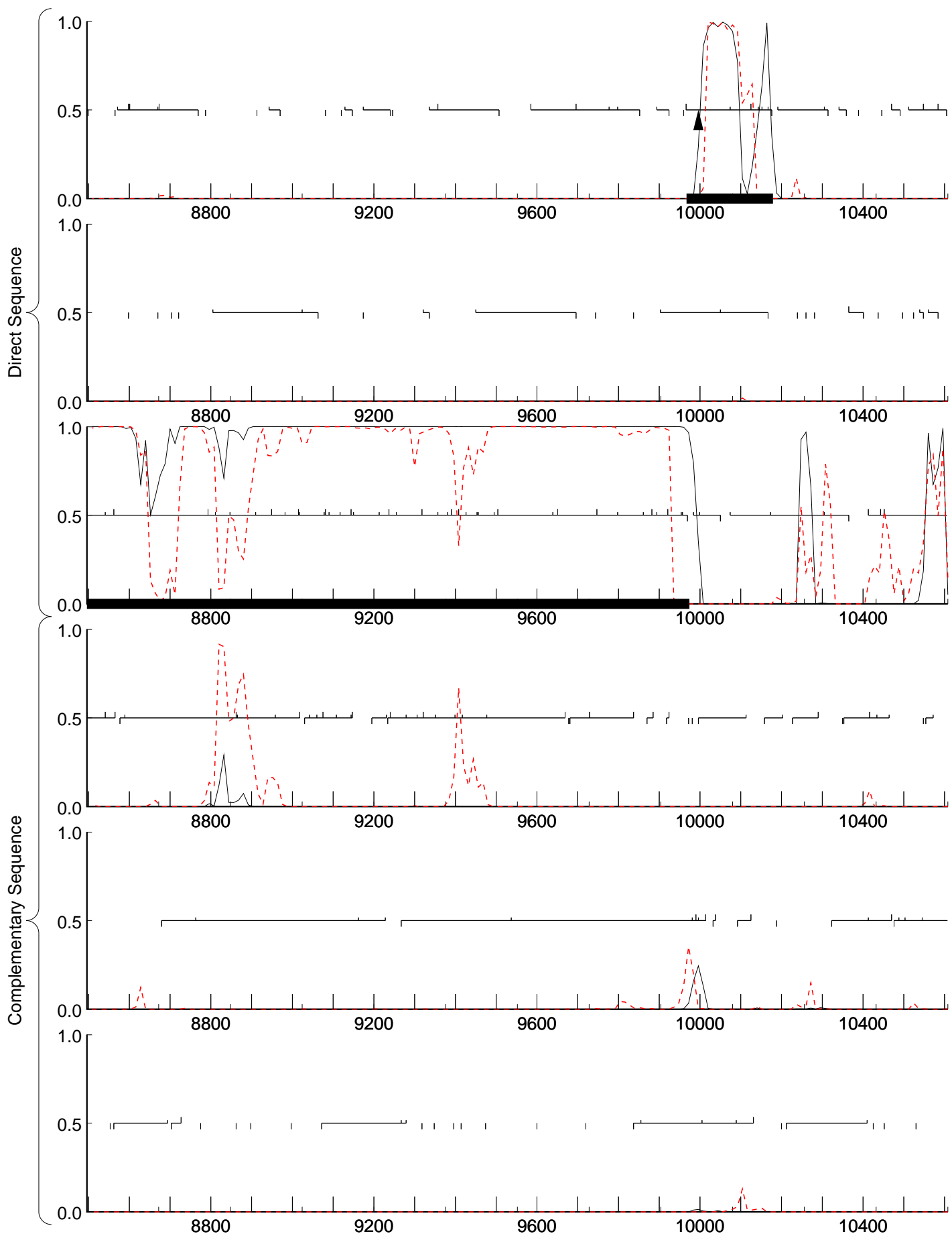
Send questions / comments to:
Dr. M. Borodovsky
Georgia Institute of Technology
School of Biology
Atlanta, GA 30332-0230







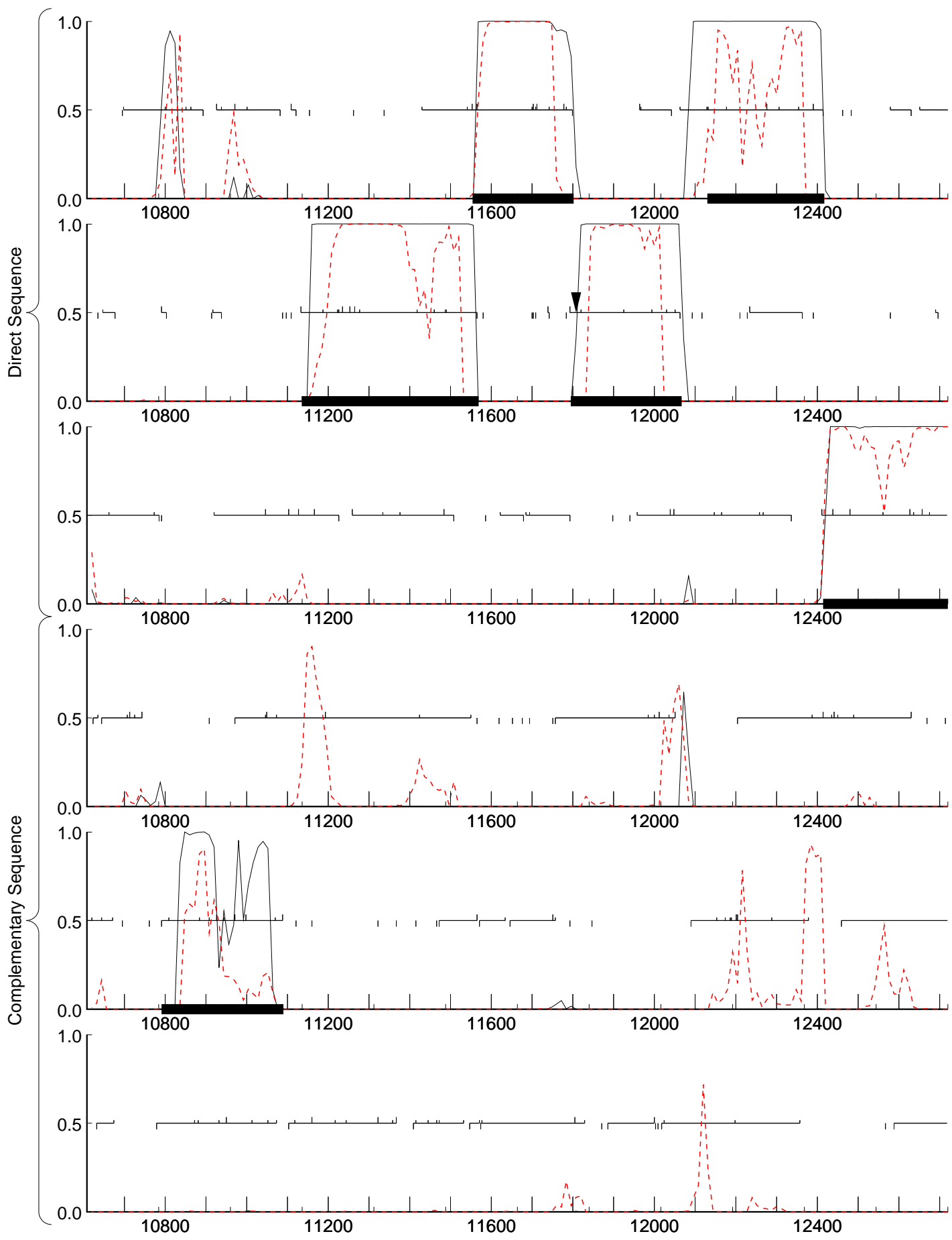




typical.ps

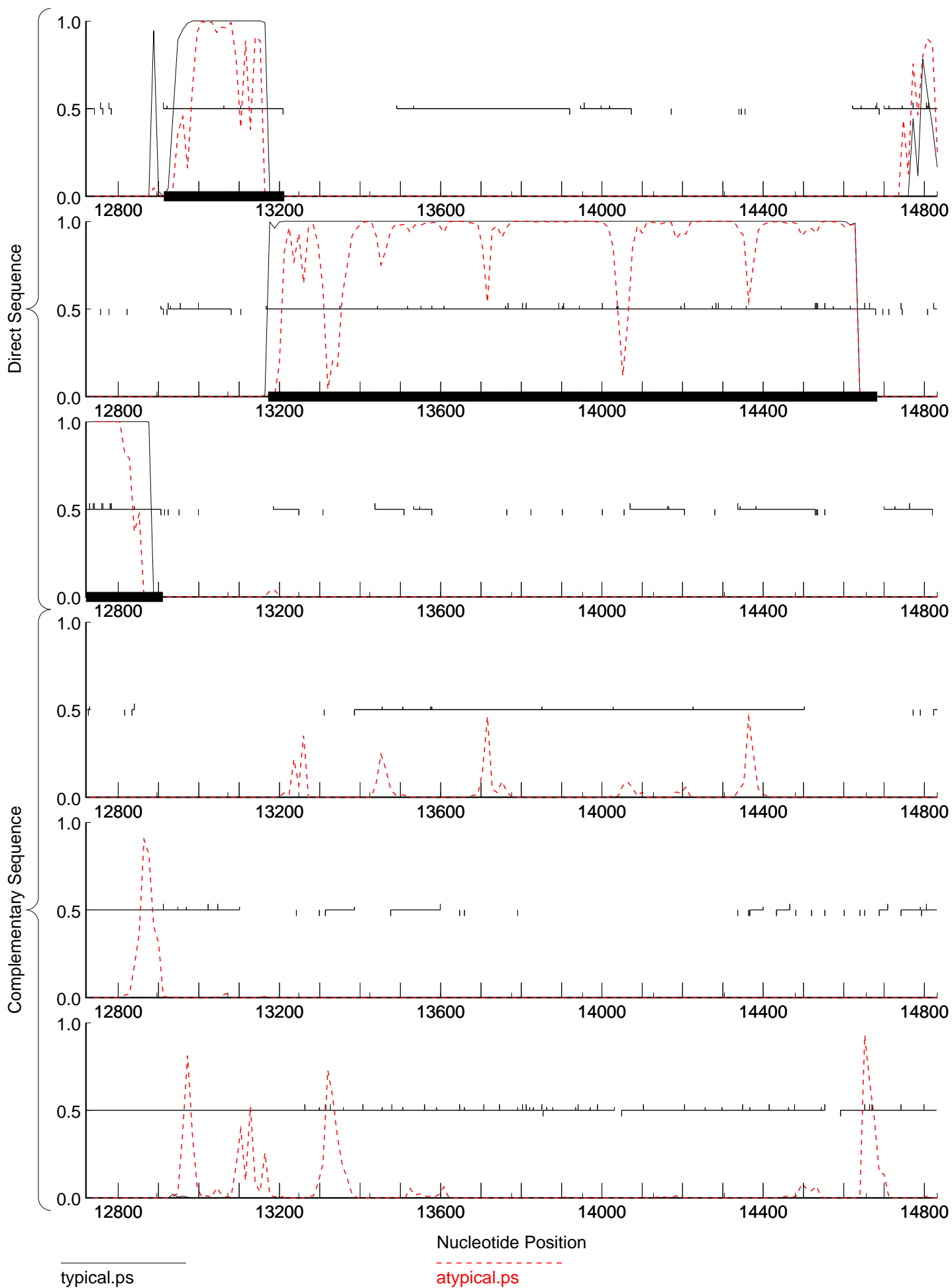
Nucleotide Position

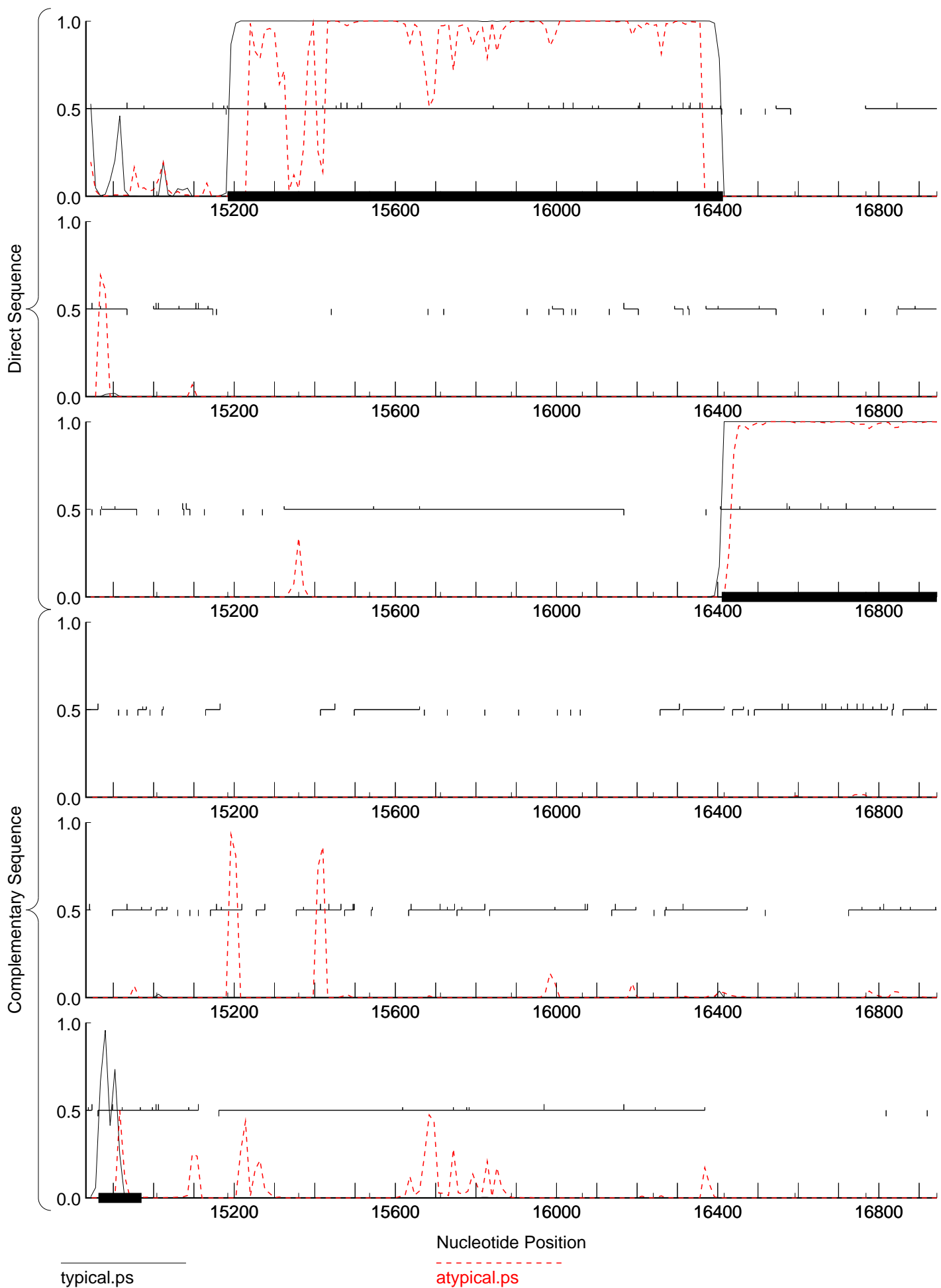
atypical.ps

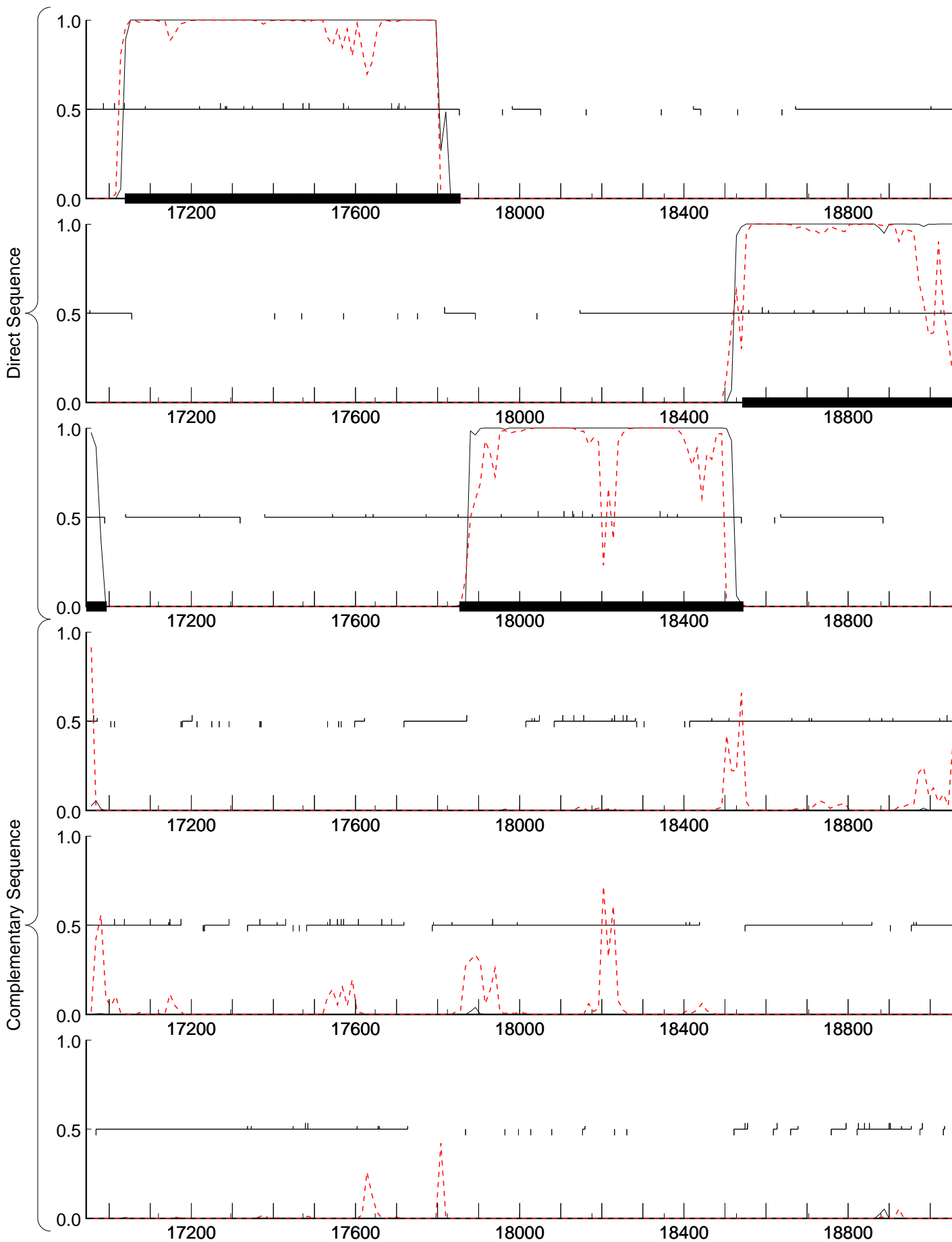


typical.ps

atypical.ps

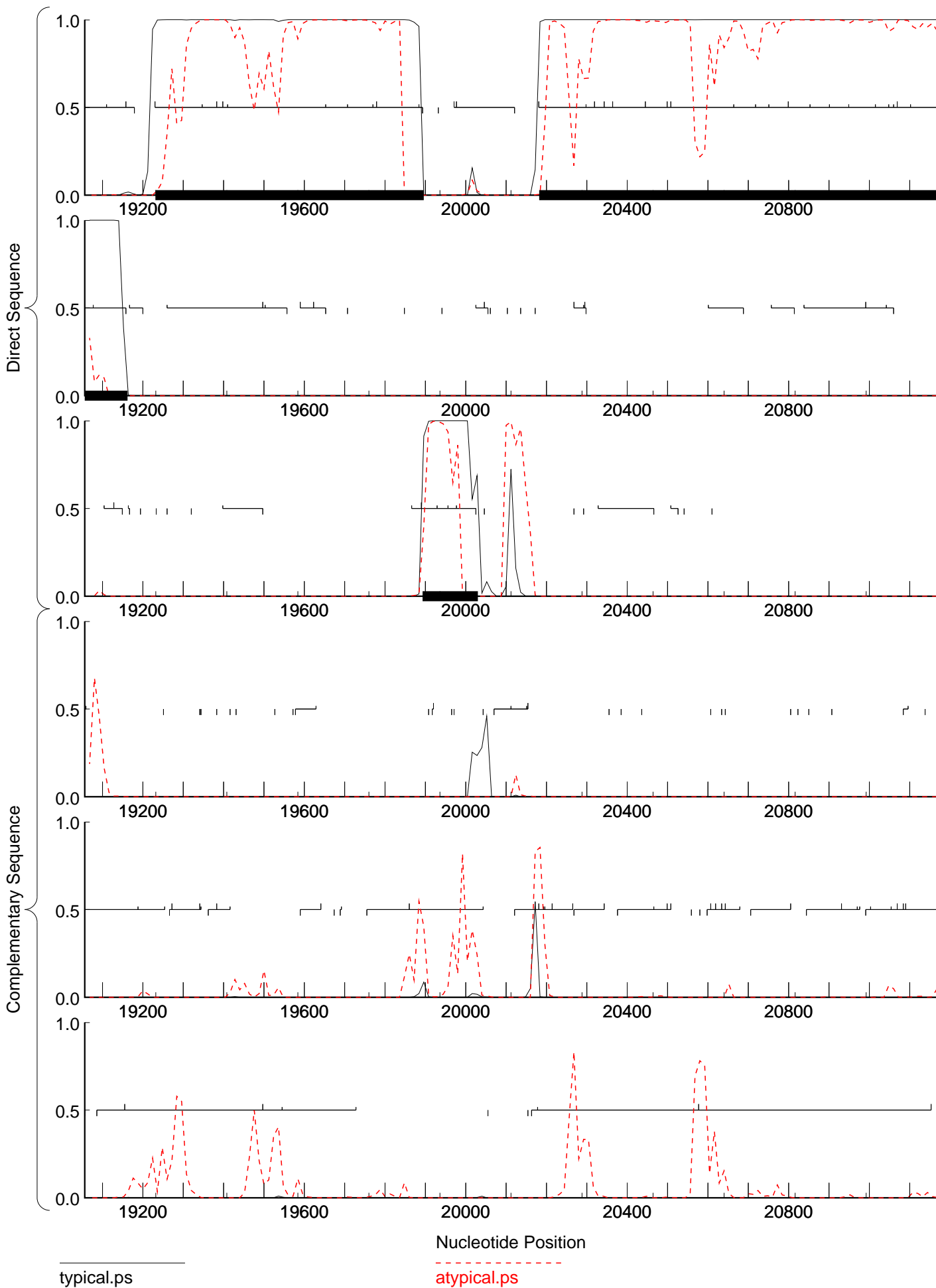


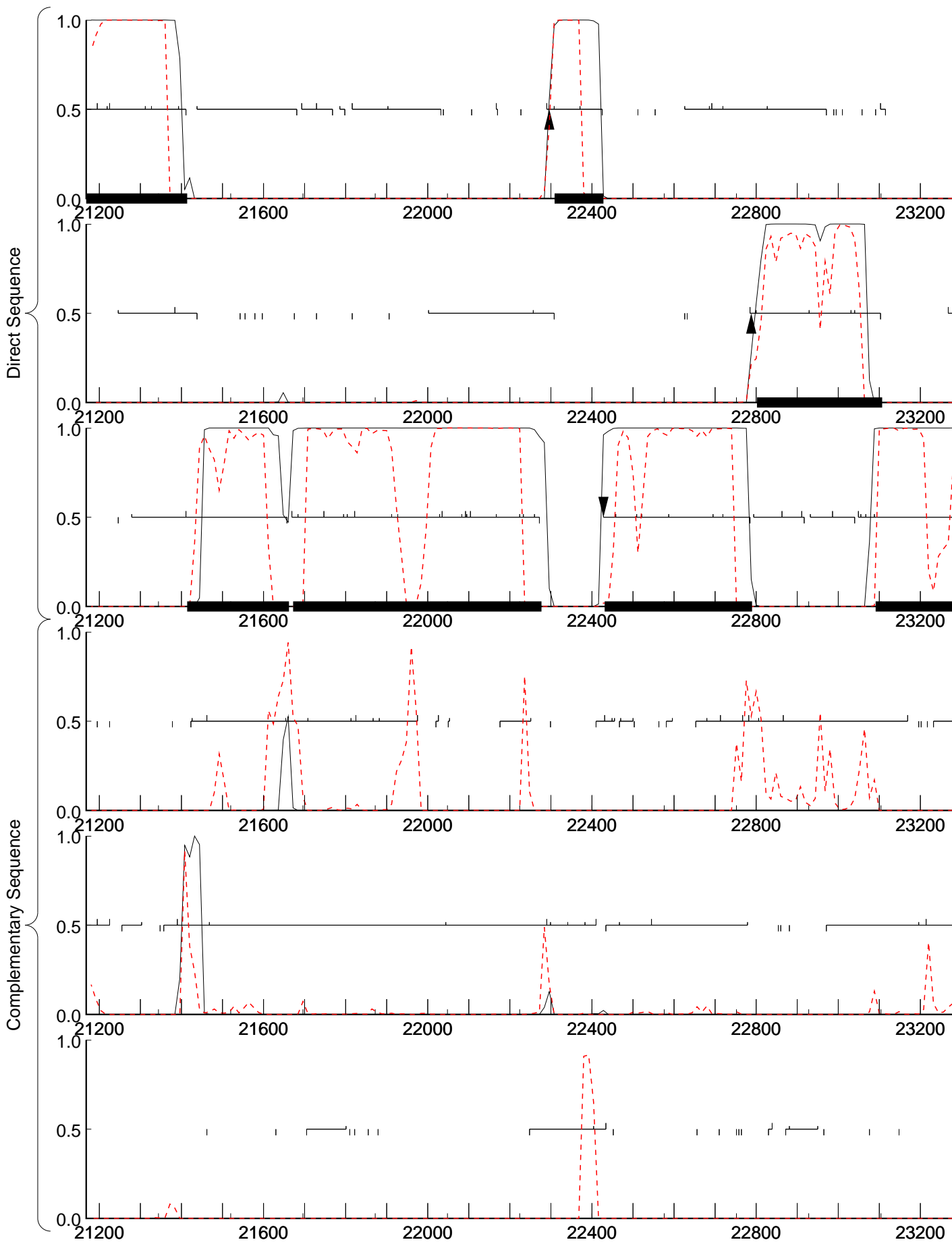




typical.ps

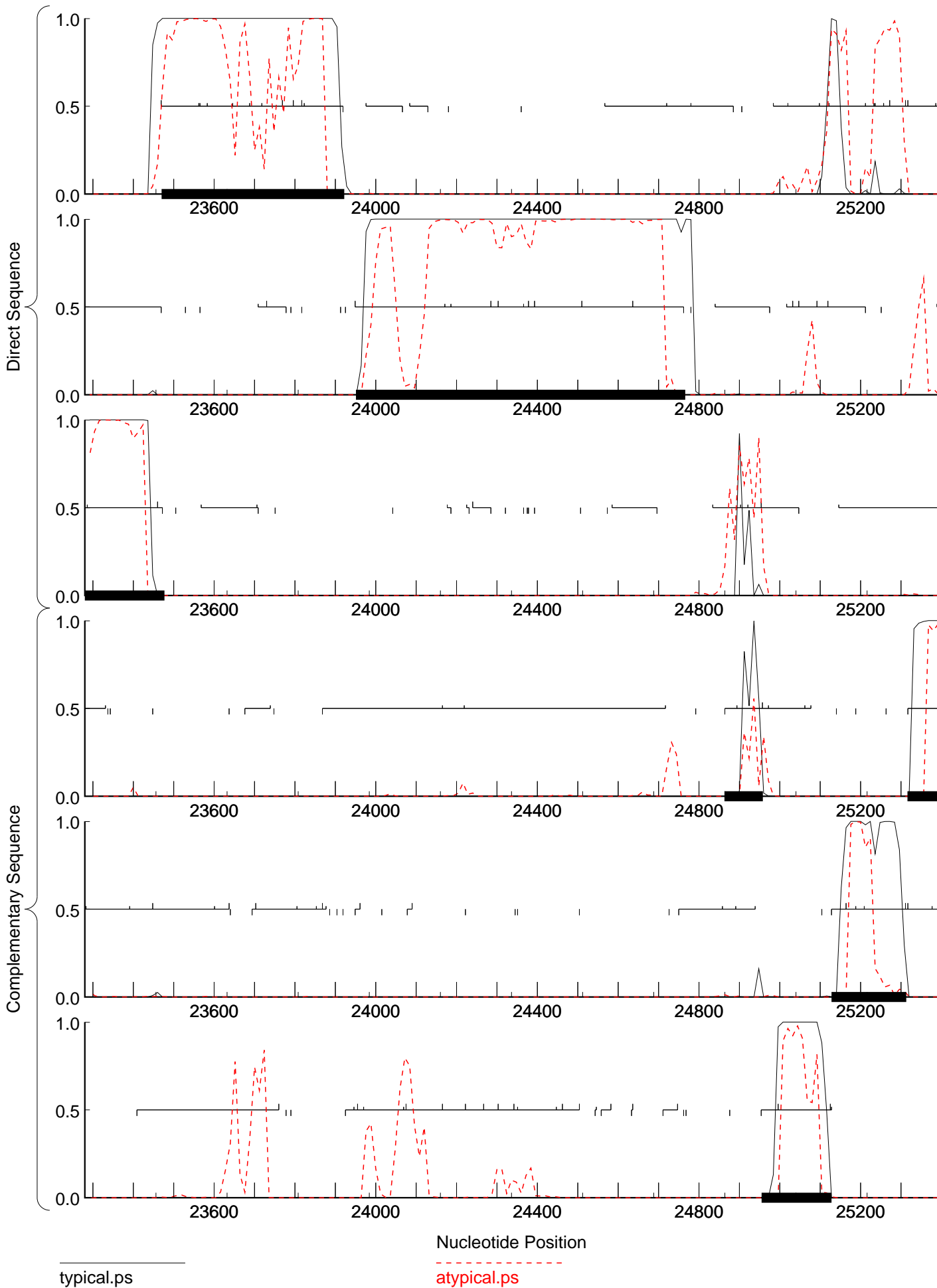
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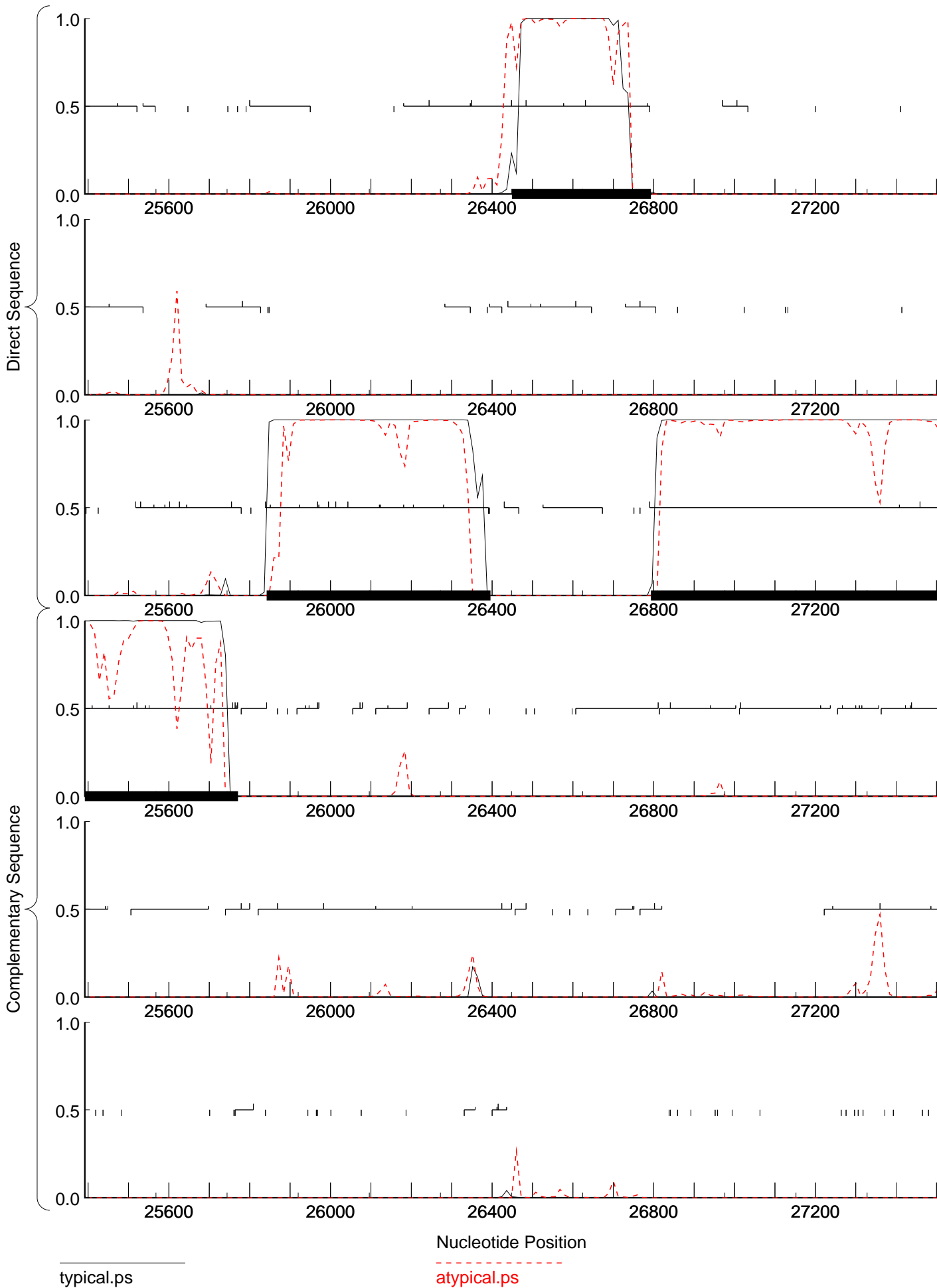
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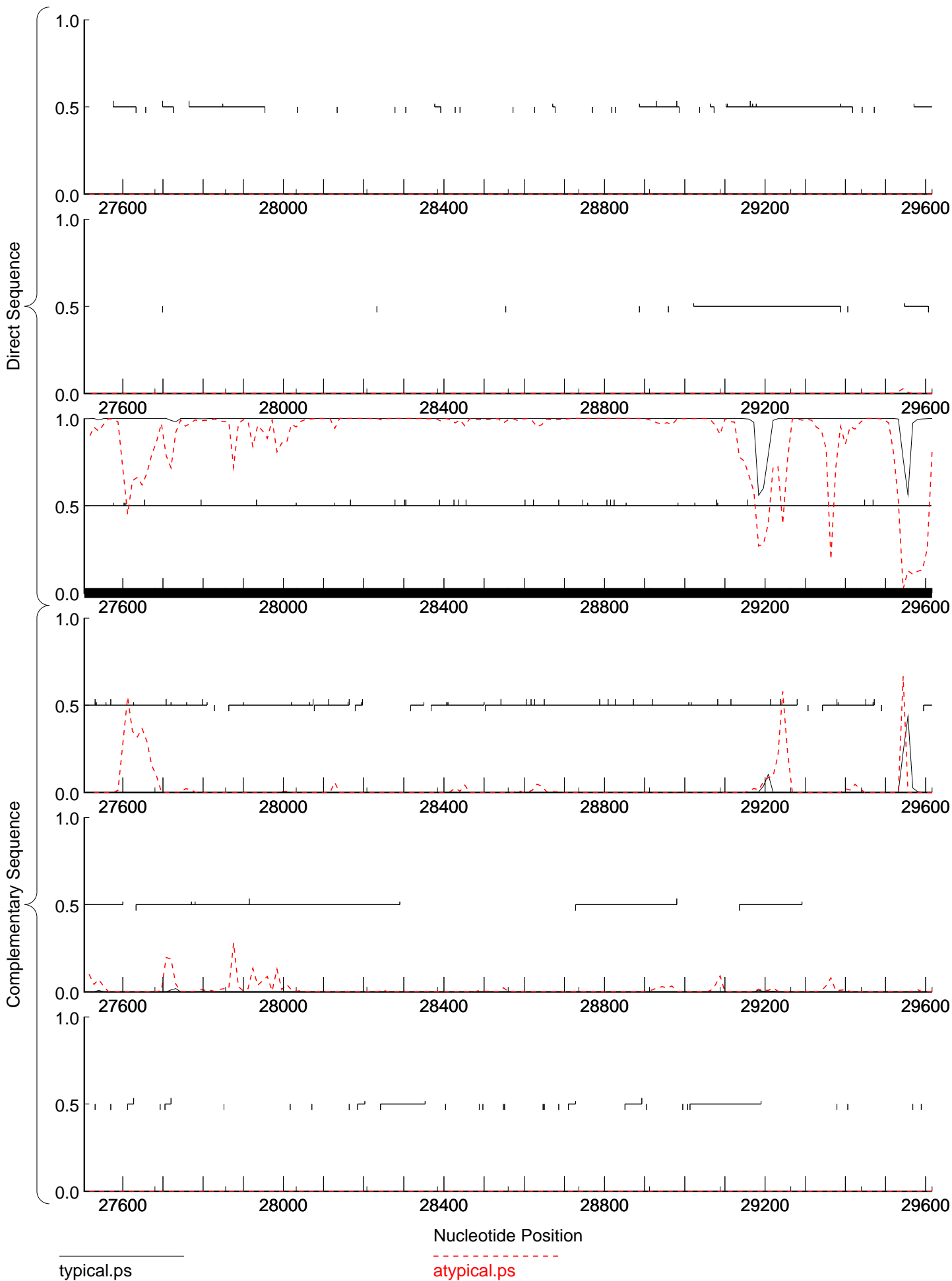
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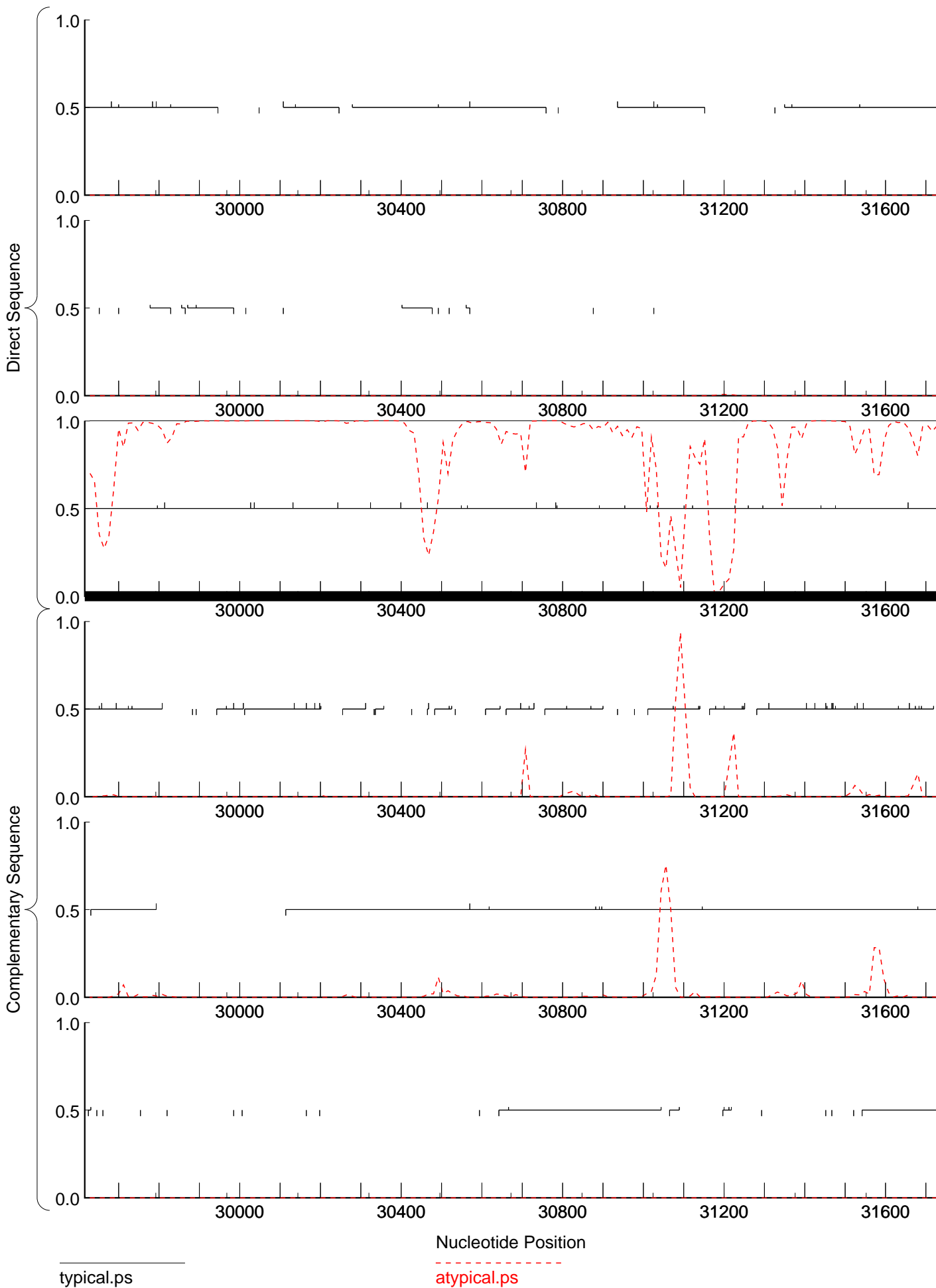


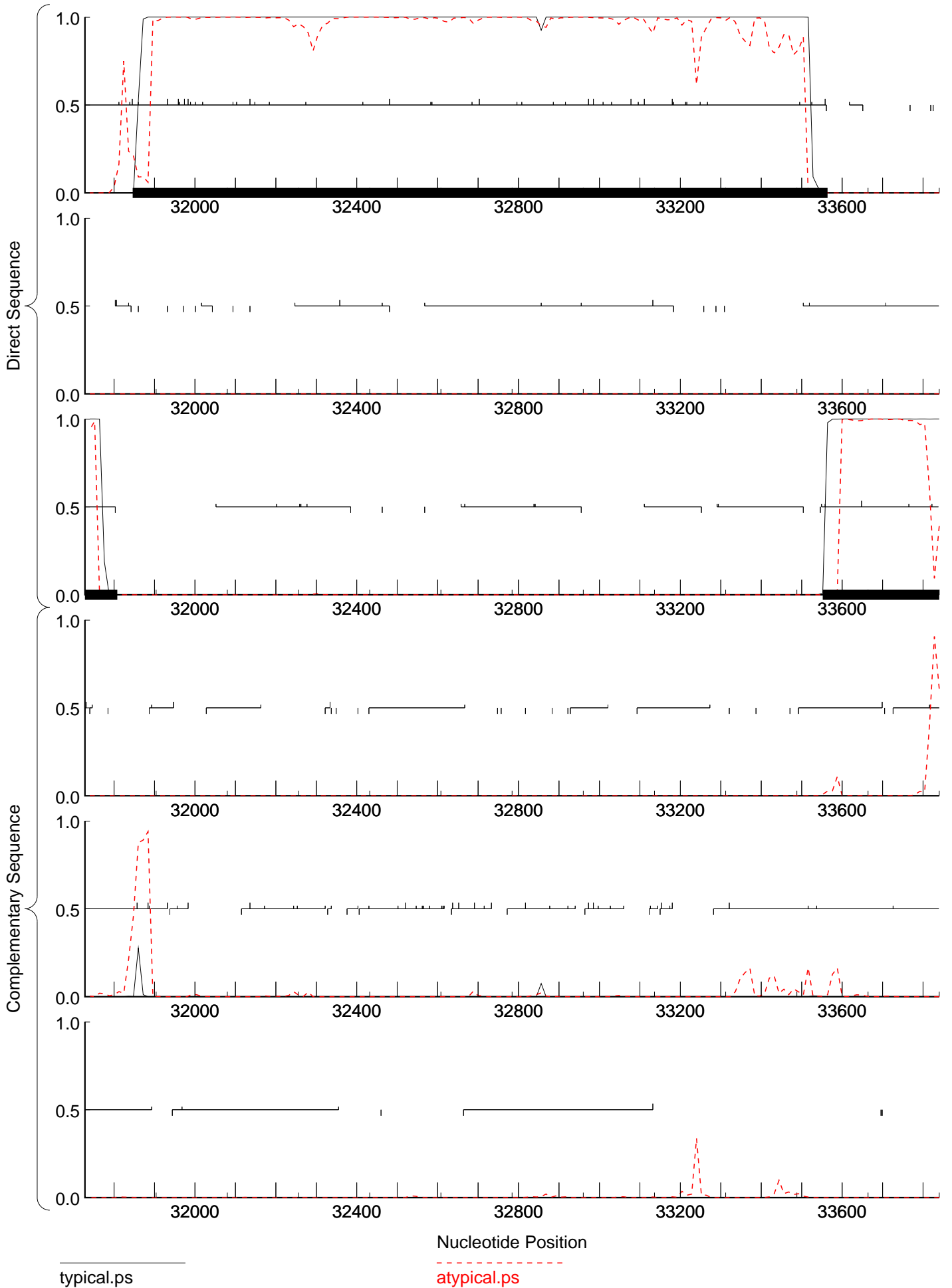
typical.ps

atypical.ps



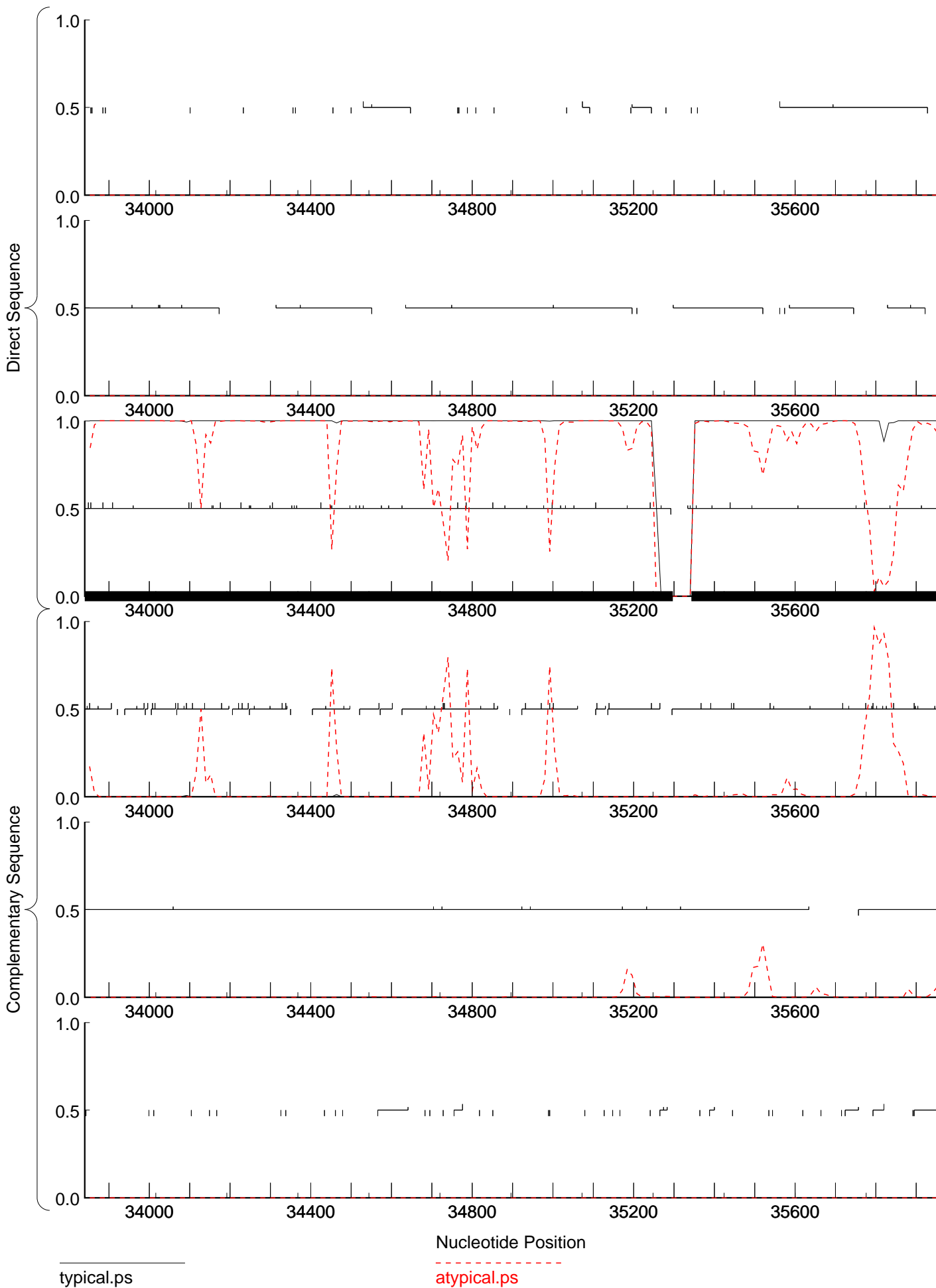


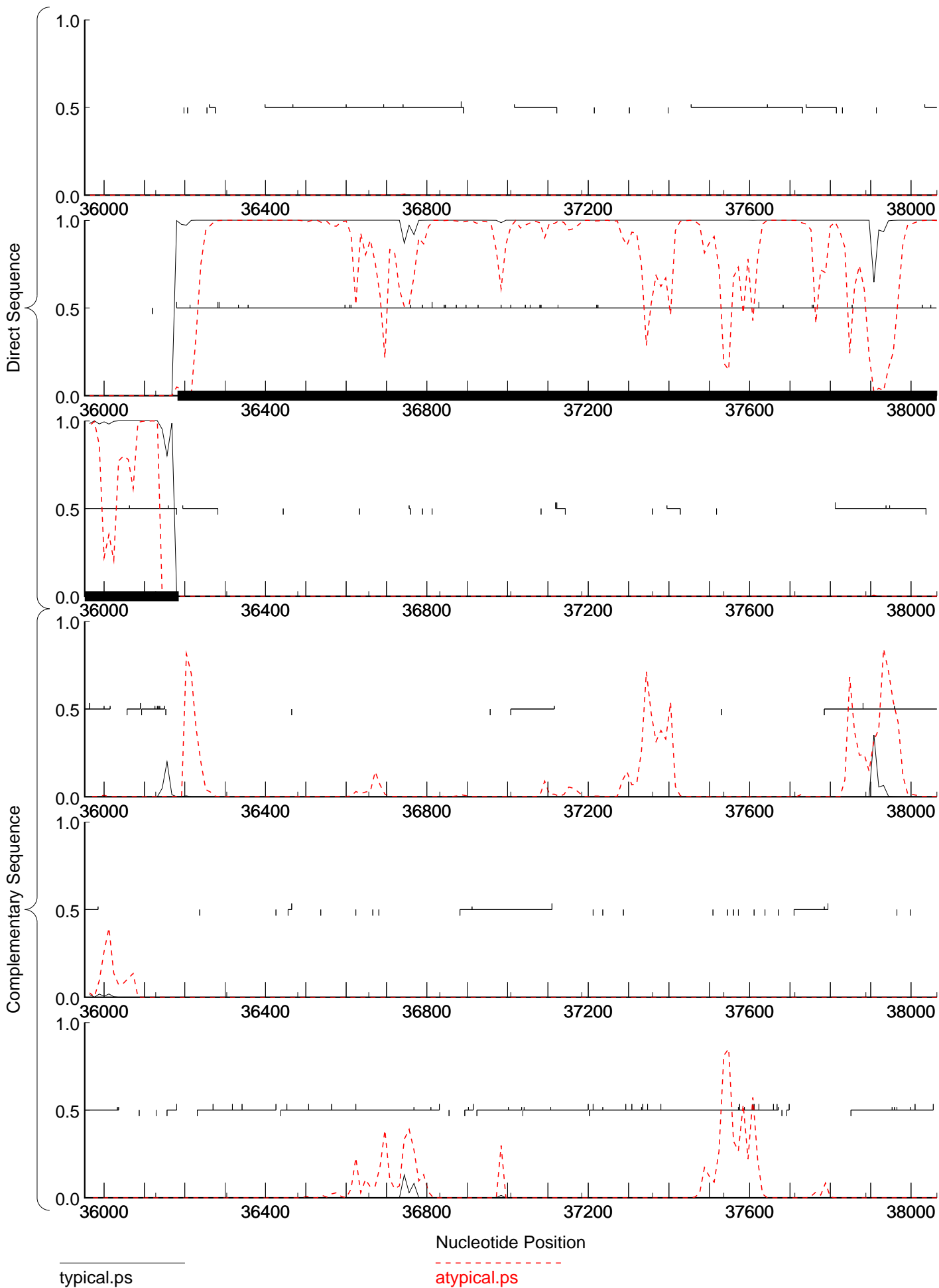


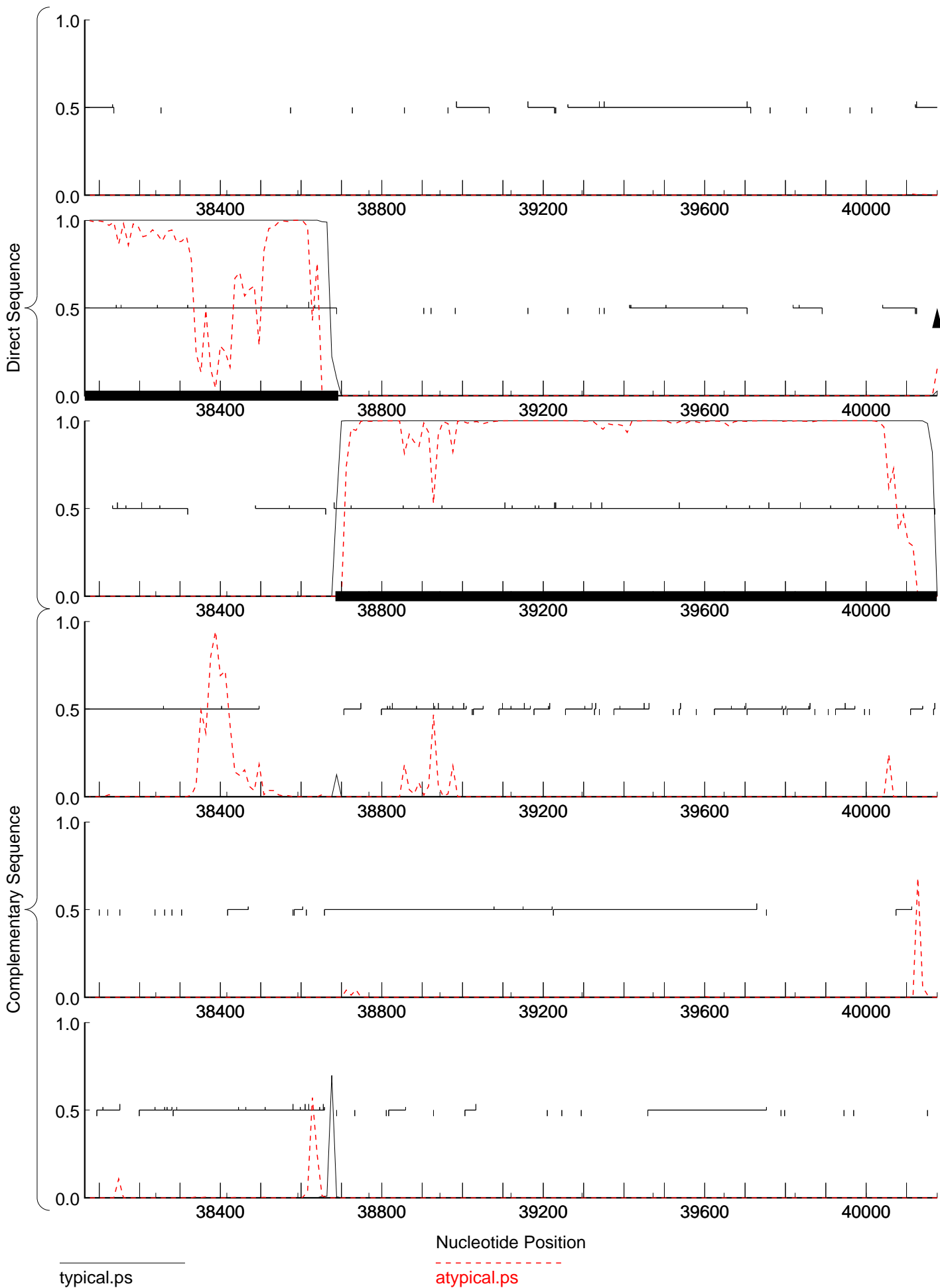


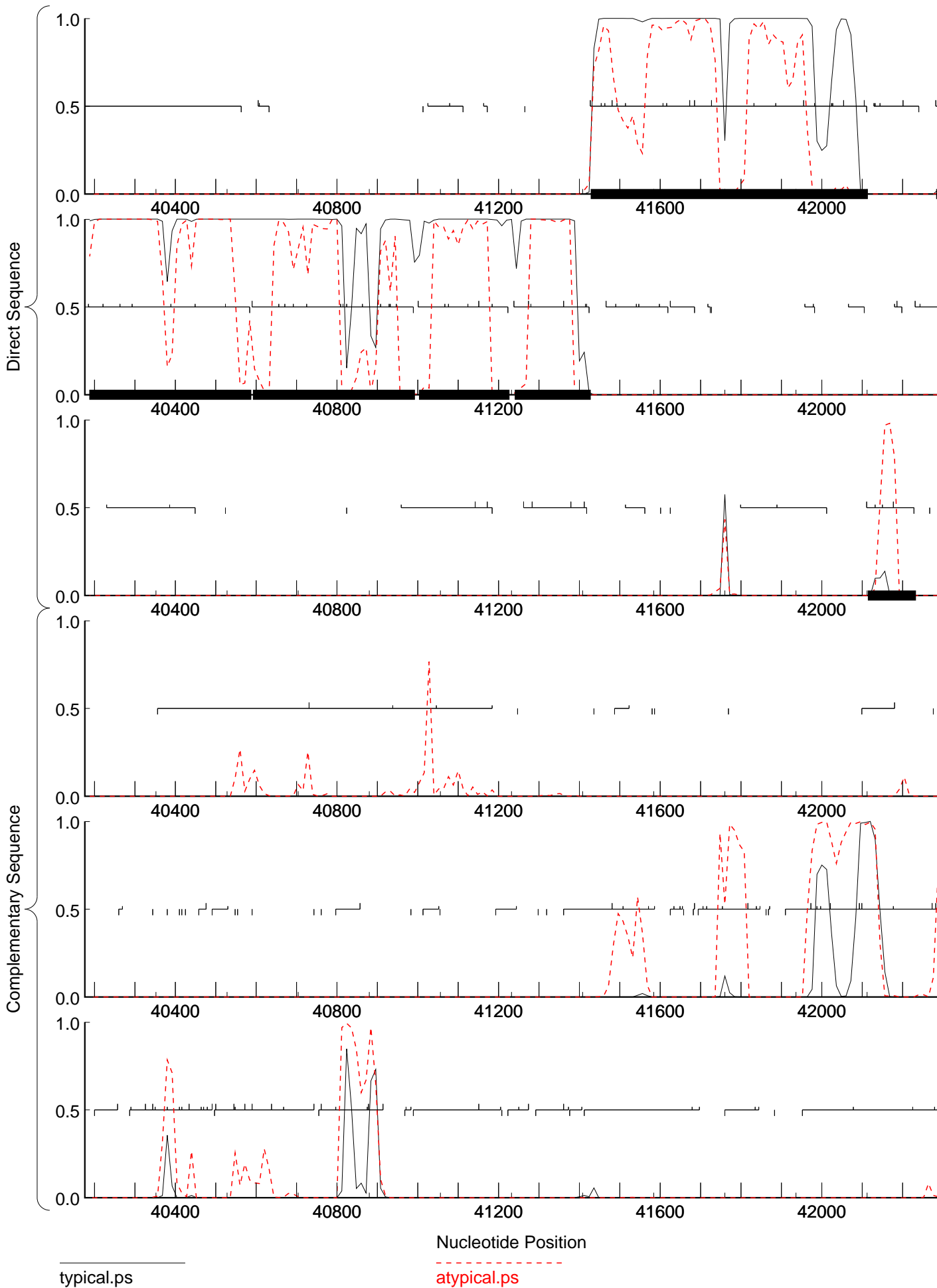
typical.ps

atypical.ps



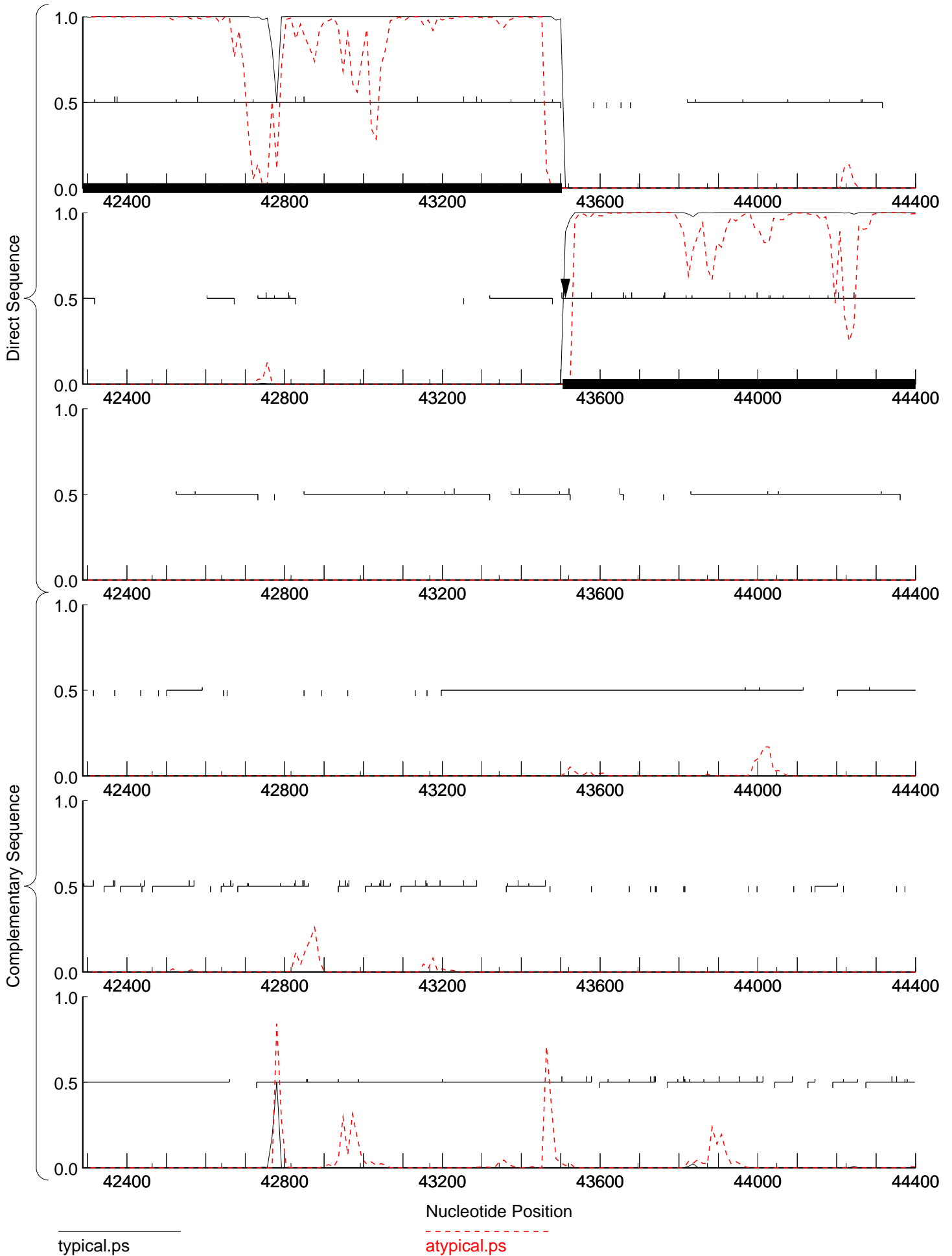


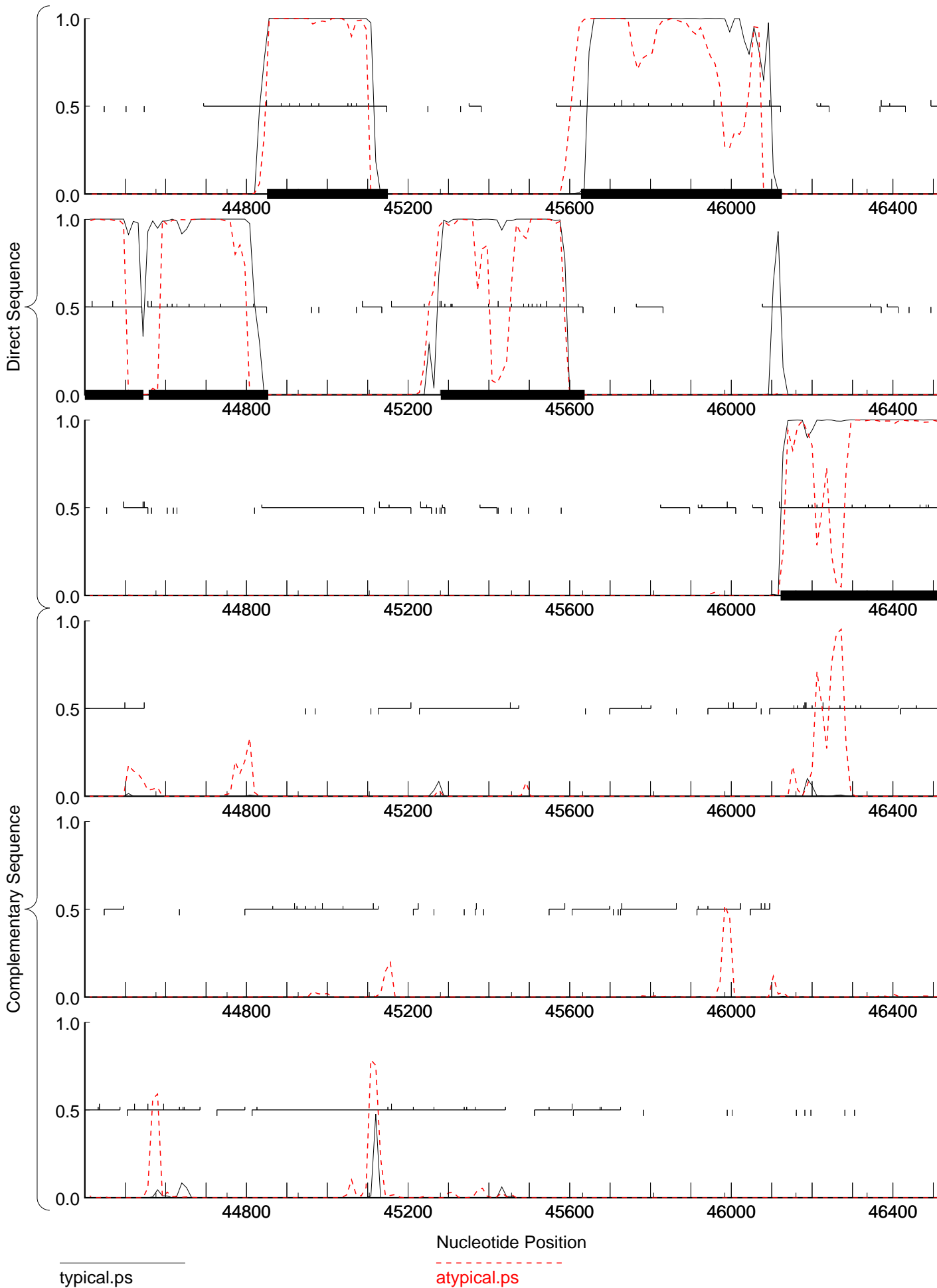


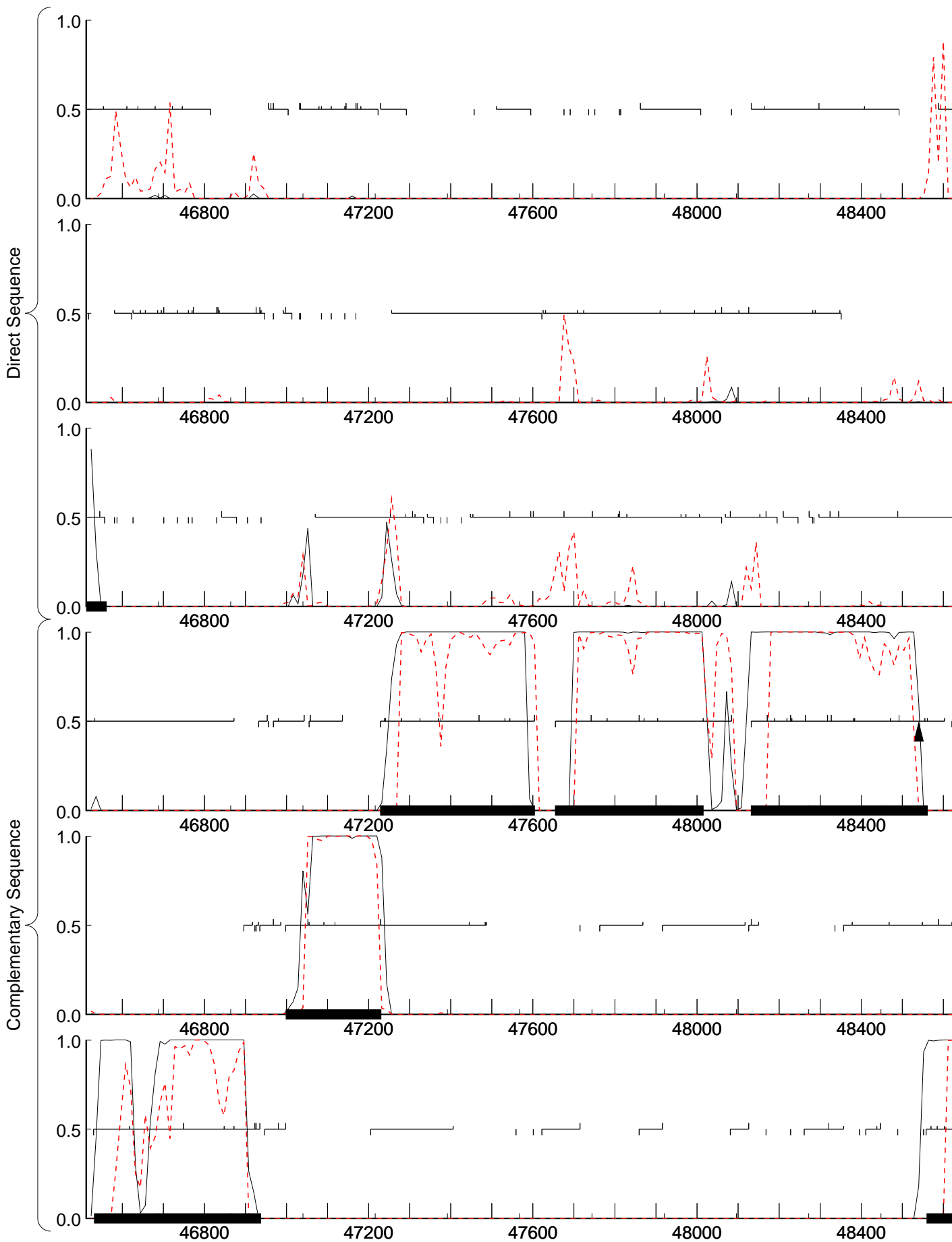


typical.ps

atypical.ps



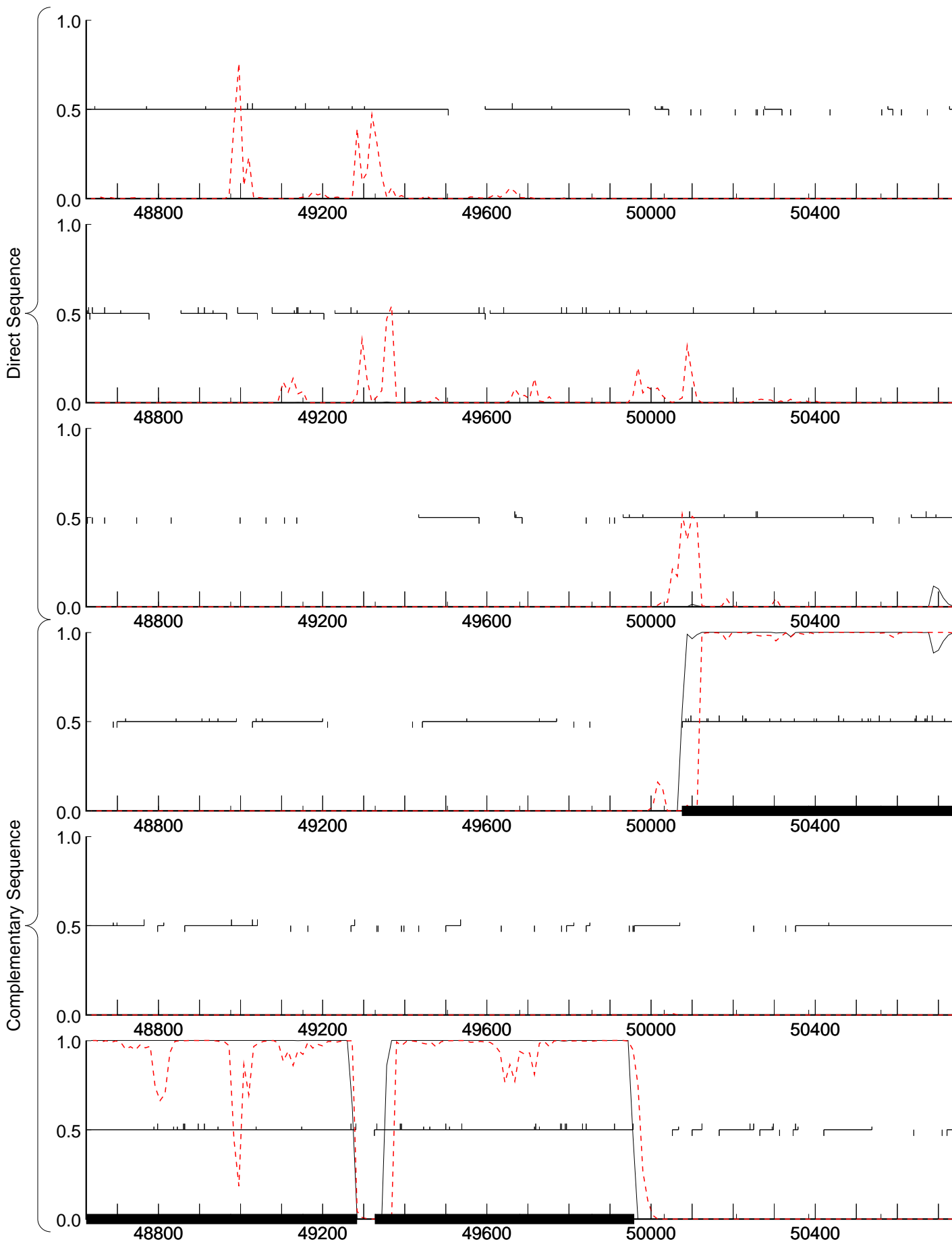




typical.ps

Nucleotide Position

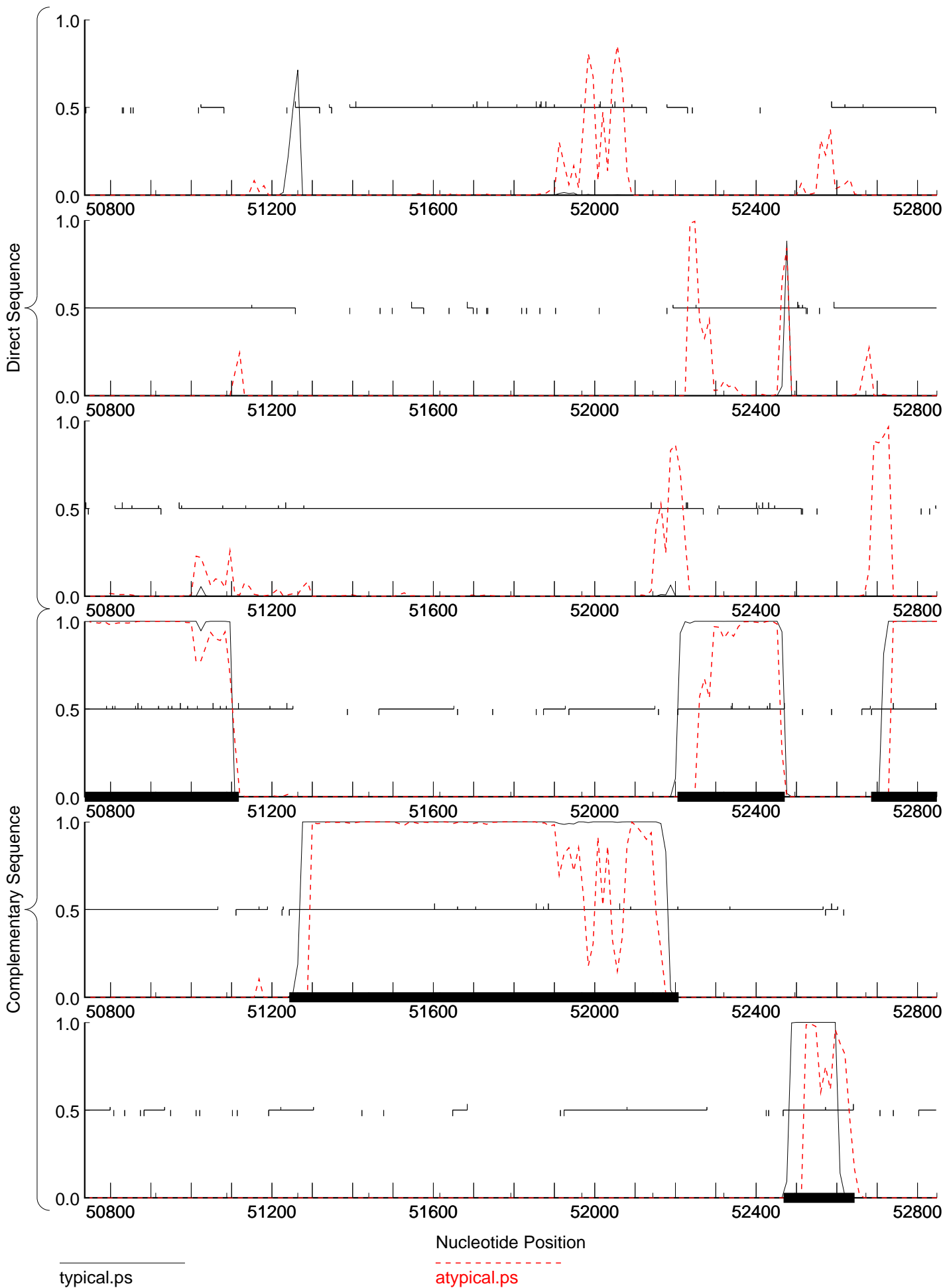
atypical.ps

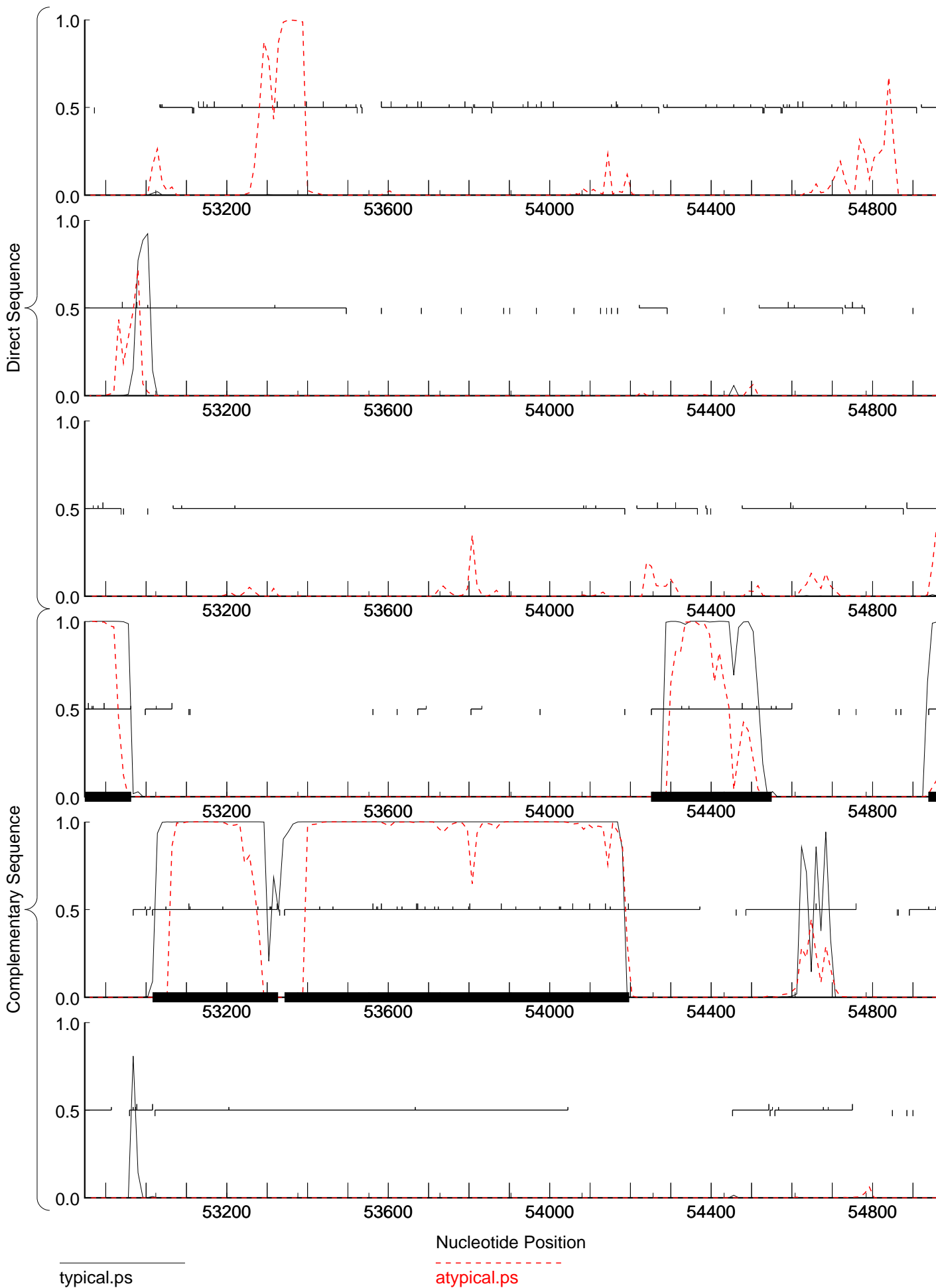


typical.ps

Nucleotide Position

atypical.ps

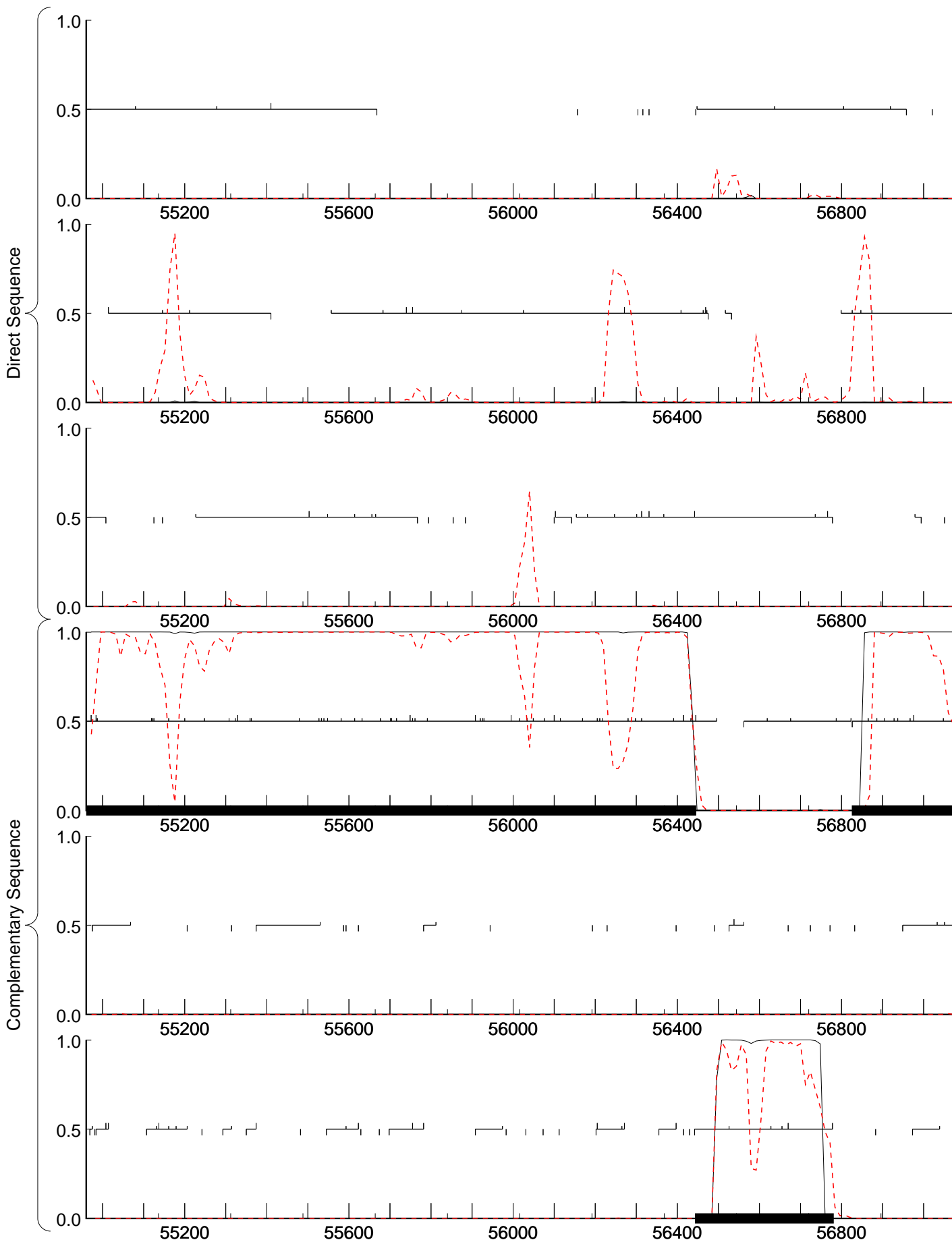




typical.ps

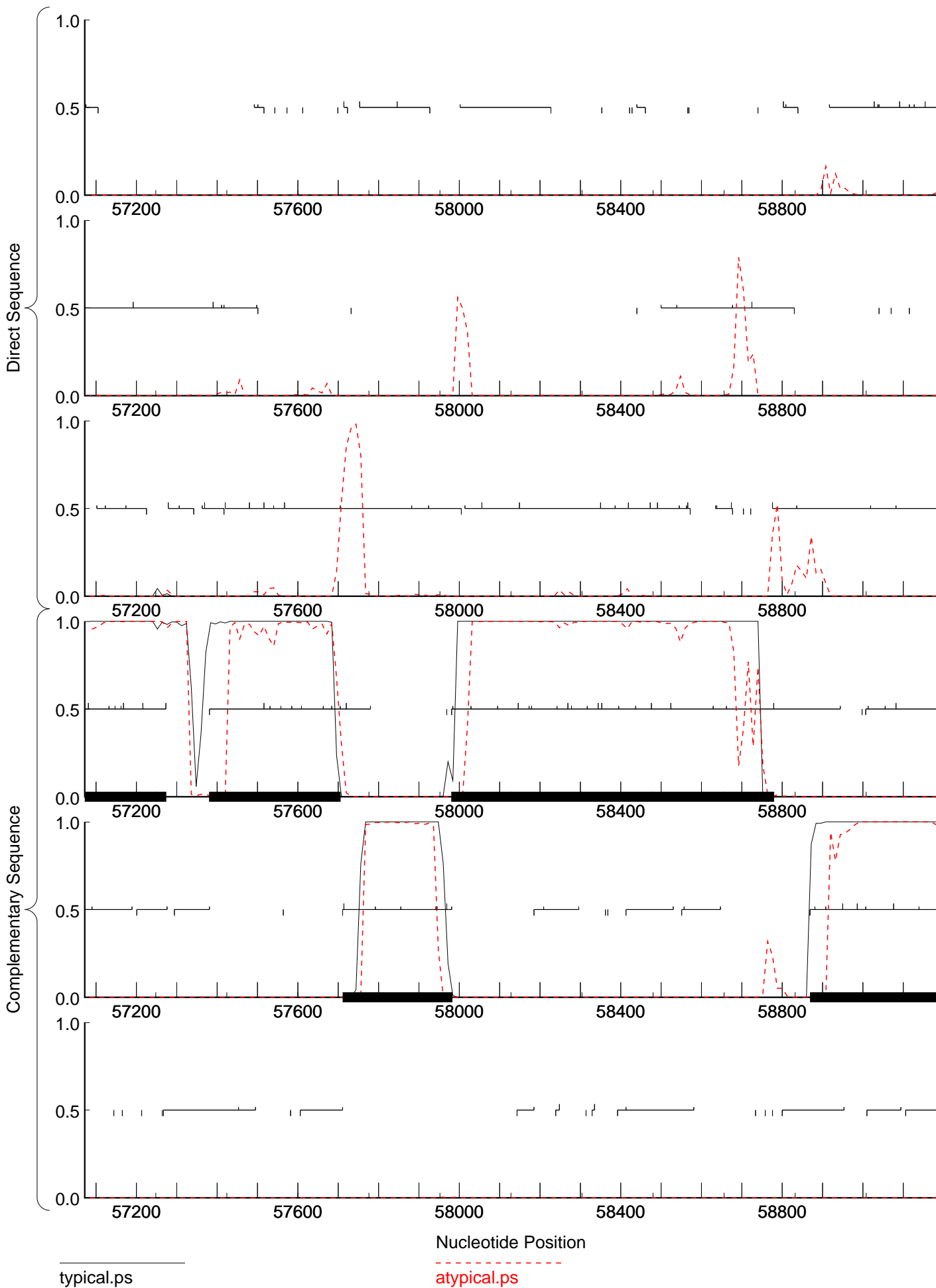
Nucleotide Position

atypical.ps



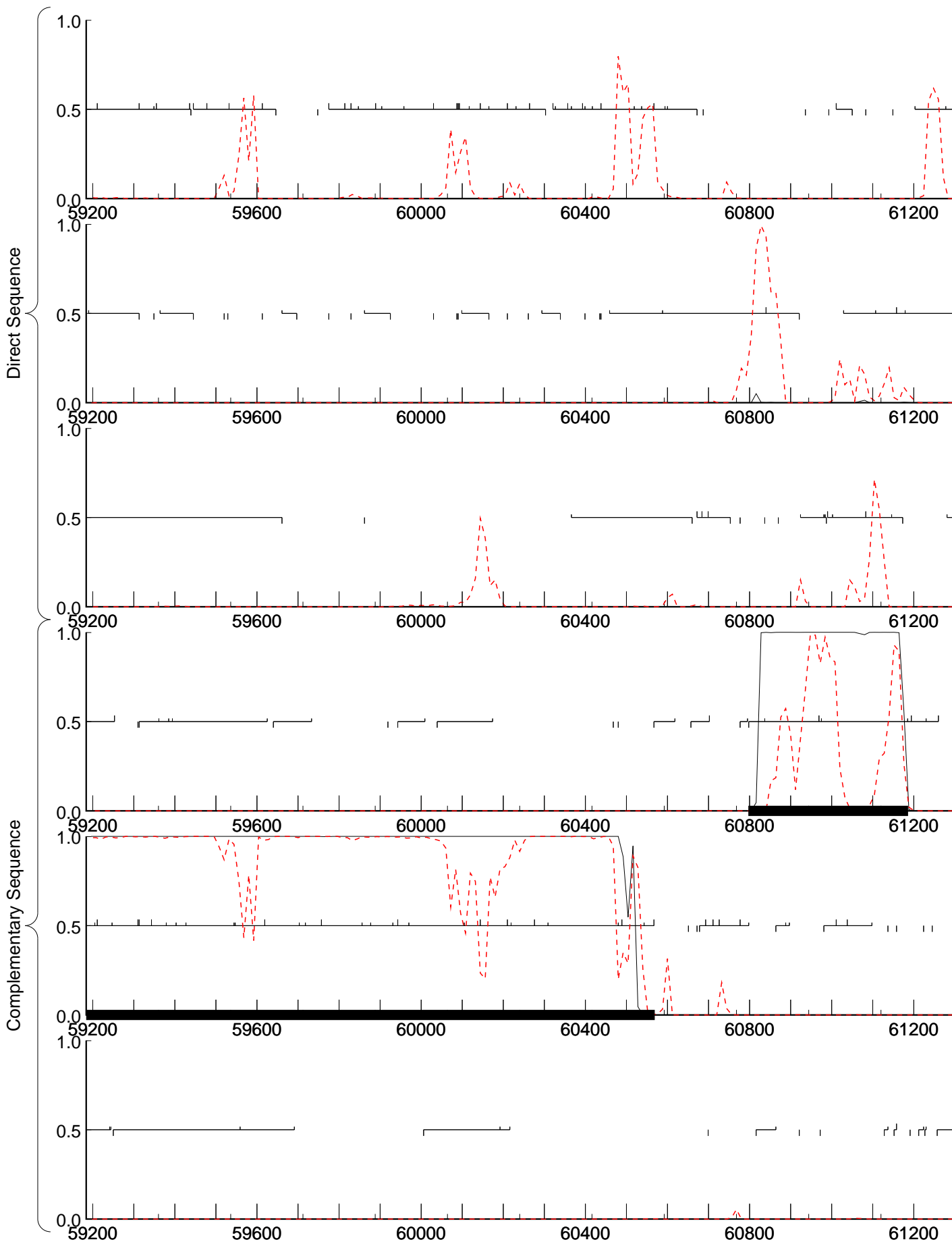
typical.ps

atypical.ps



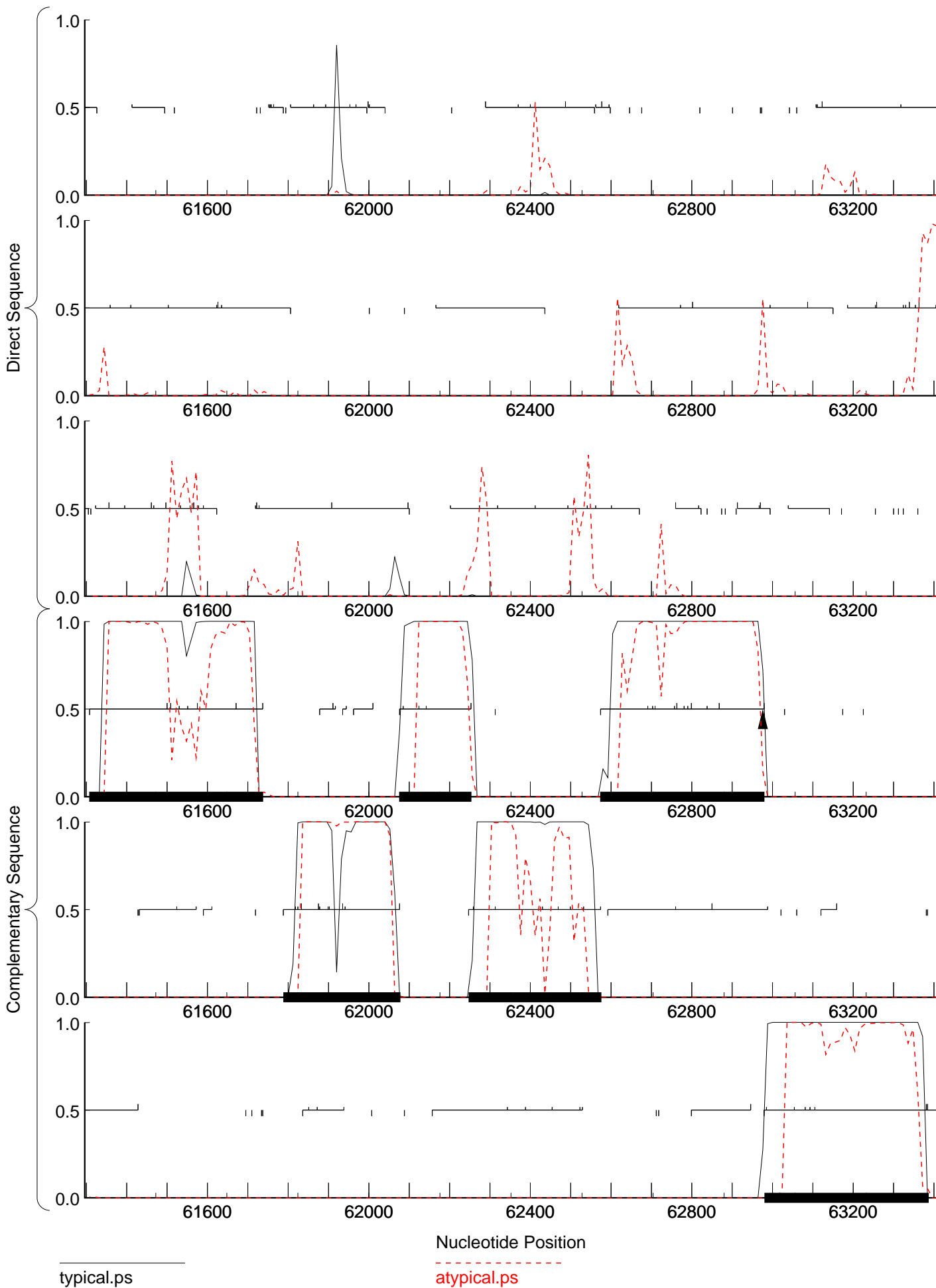
typical.ps

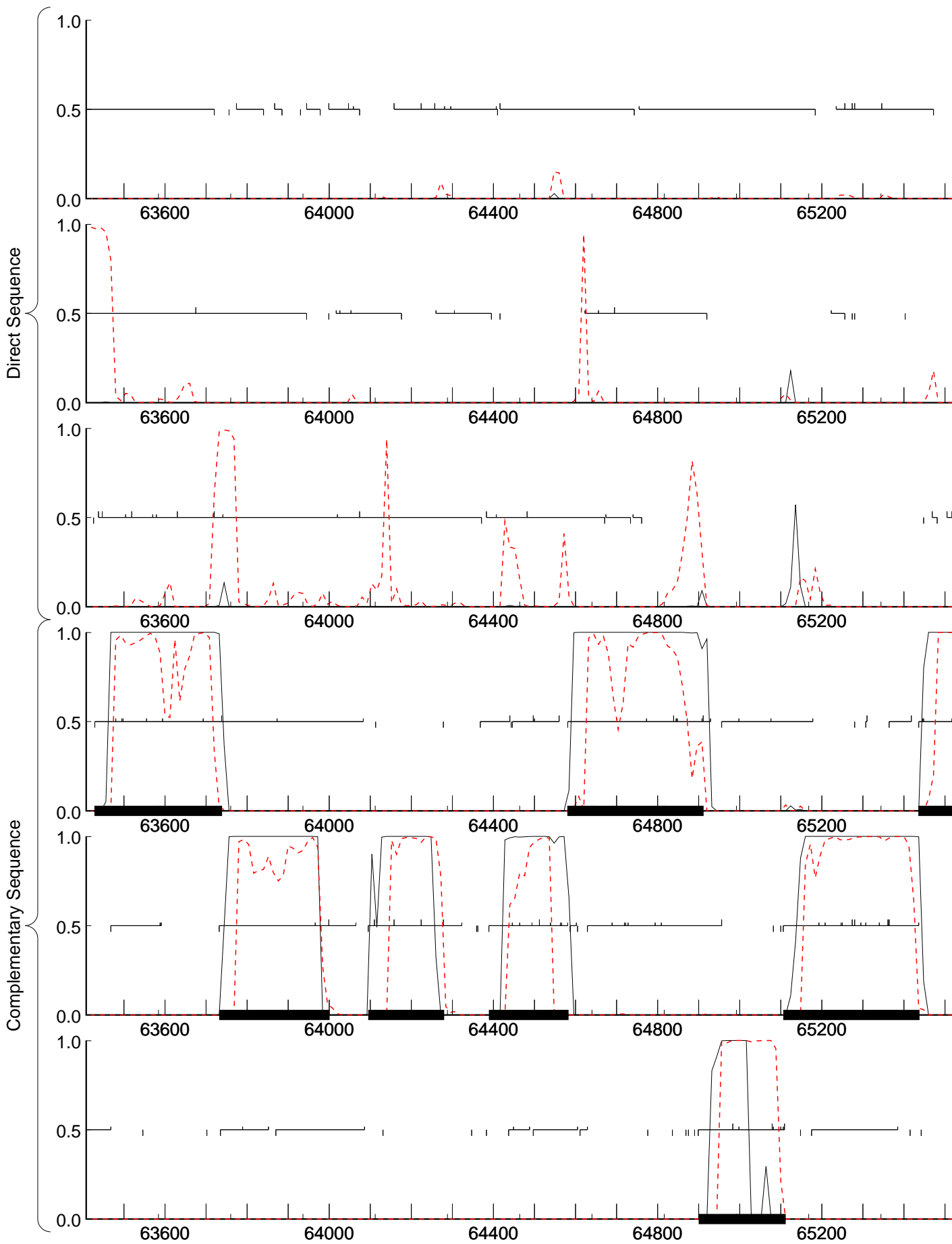
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typical.ps

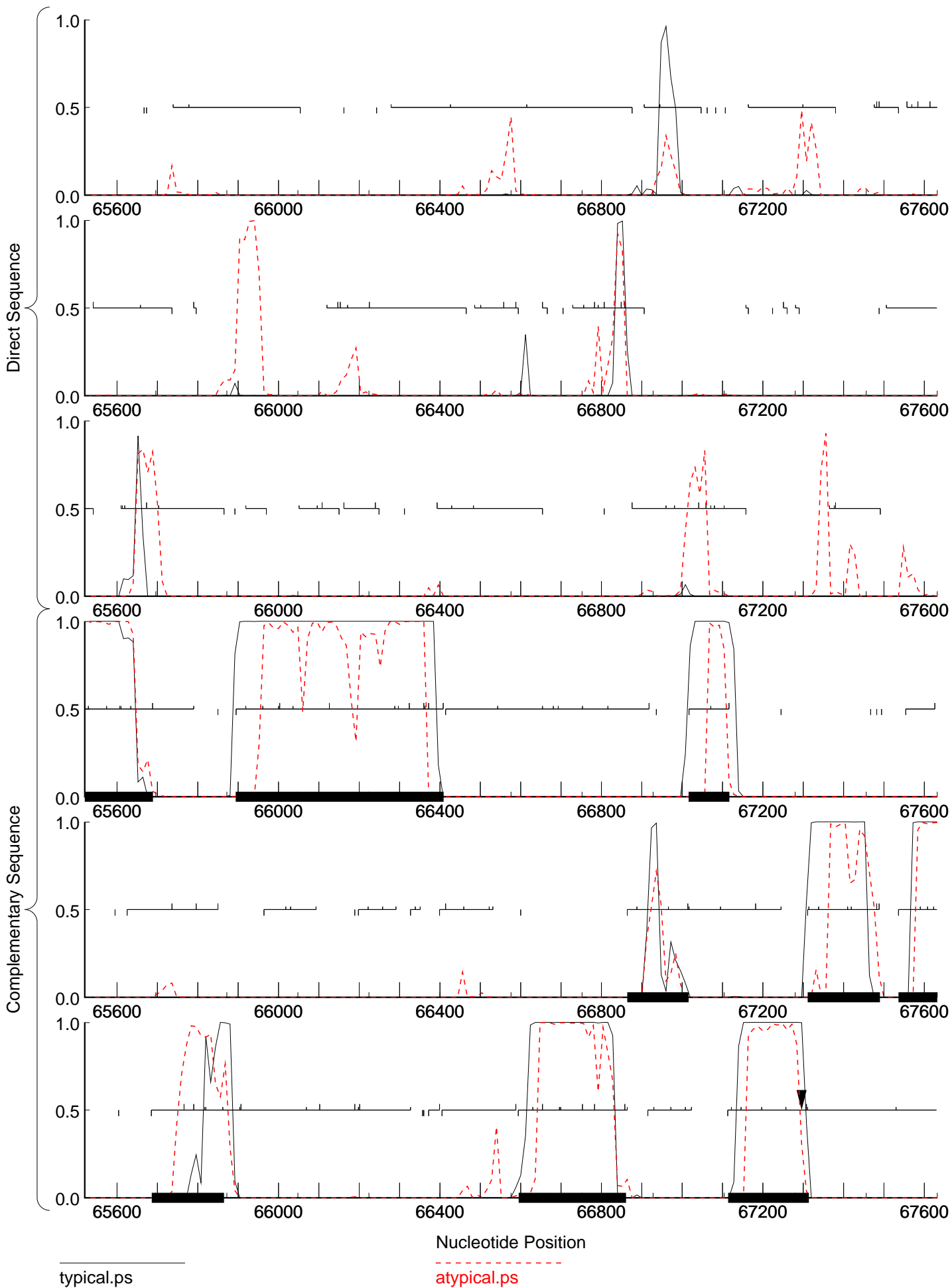
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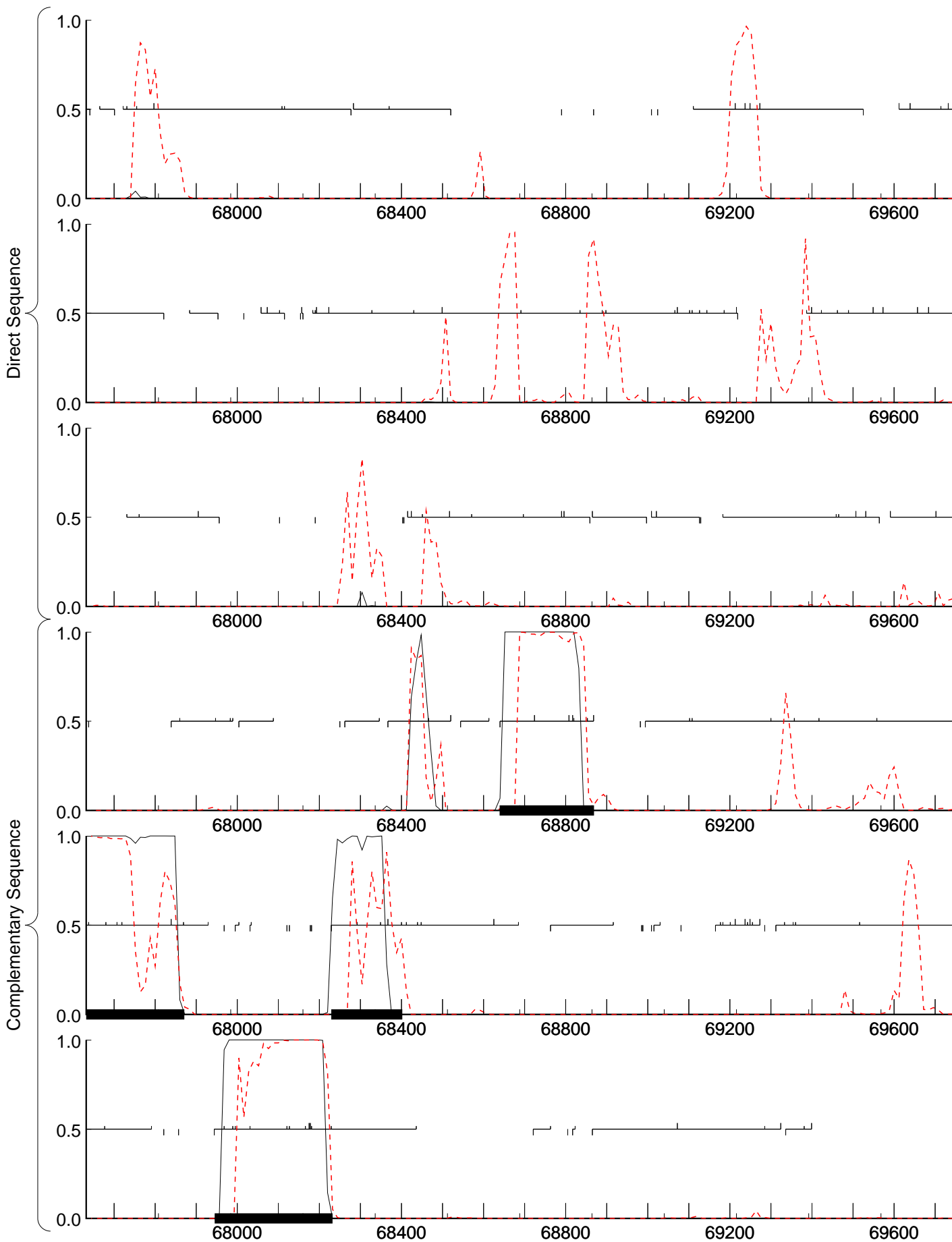




typical.ps

atypical.ps





typical.ps

Nucleotide Position

atypical.ps

