

GeneMark

Version 2.5p (09.08.06)

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PROGRAM INFORMATION

Sequence : Mycobacterium phage Bartimeaus complete sequence, 51374 bp including 10-base 3' overhang (C
Analysis Date : 9/20/17 at 14:16:41
Pages : 26
Sequence Length : 51374 bp
GC Content : 63.87%

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,

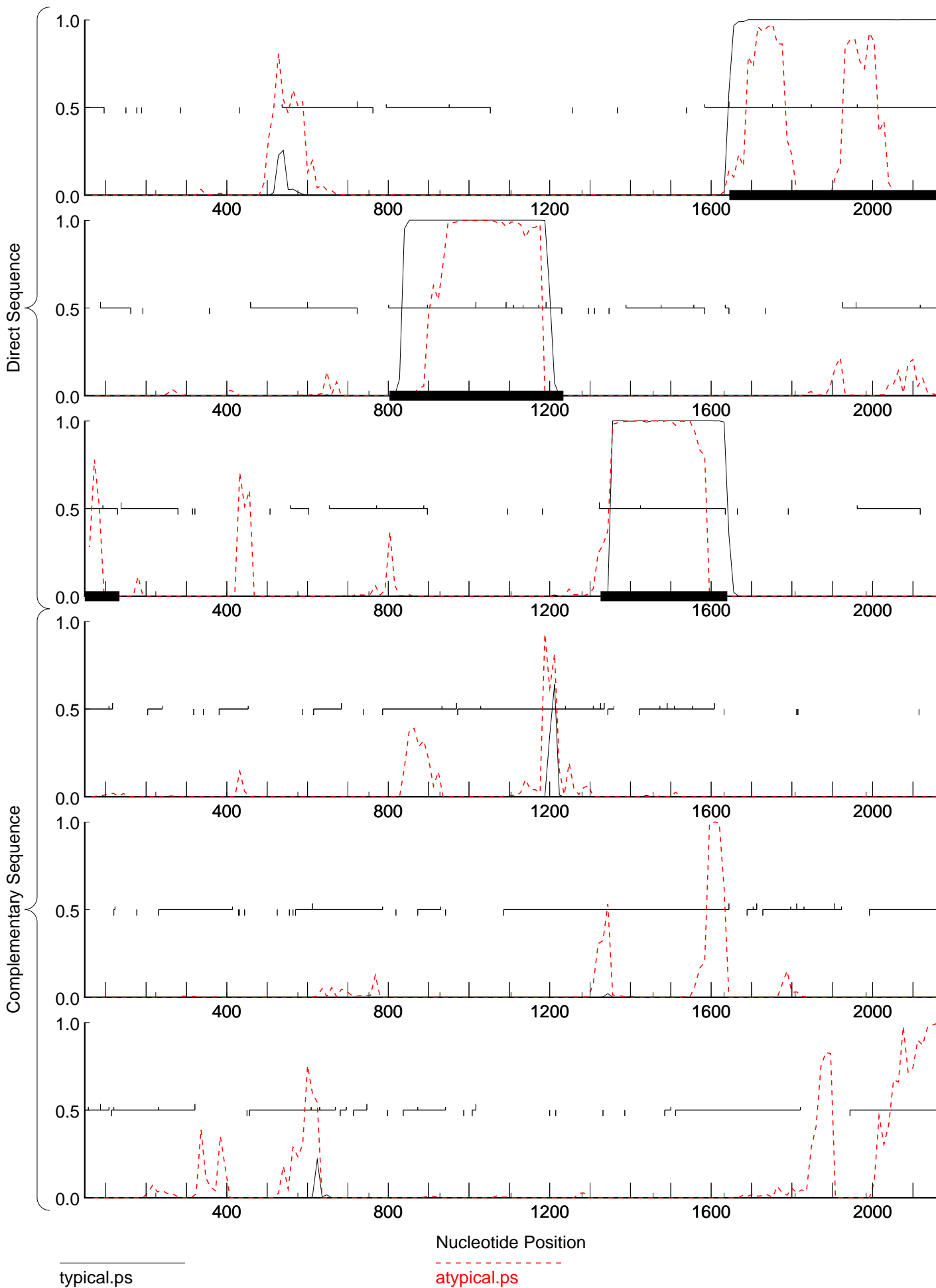
Matrix notes & comments

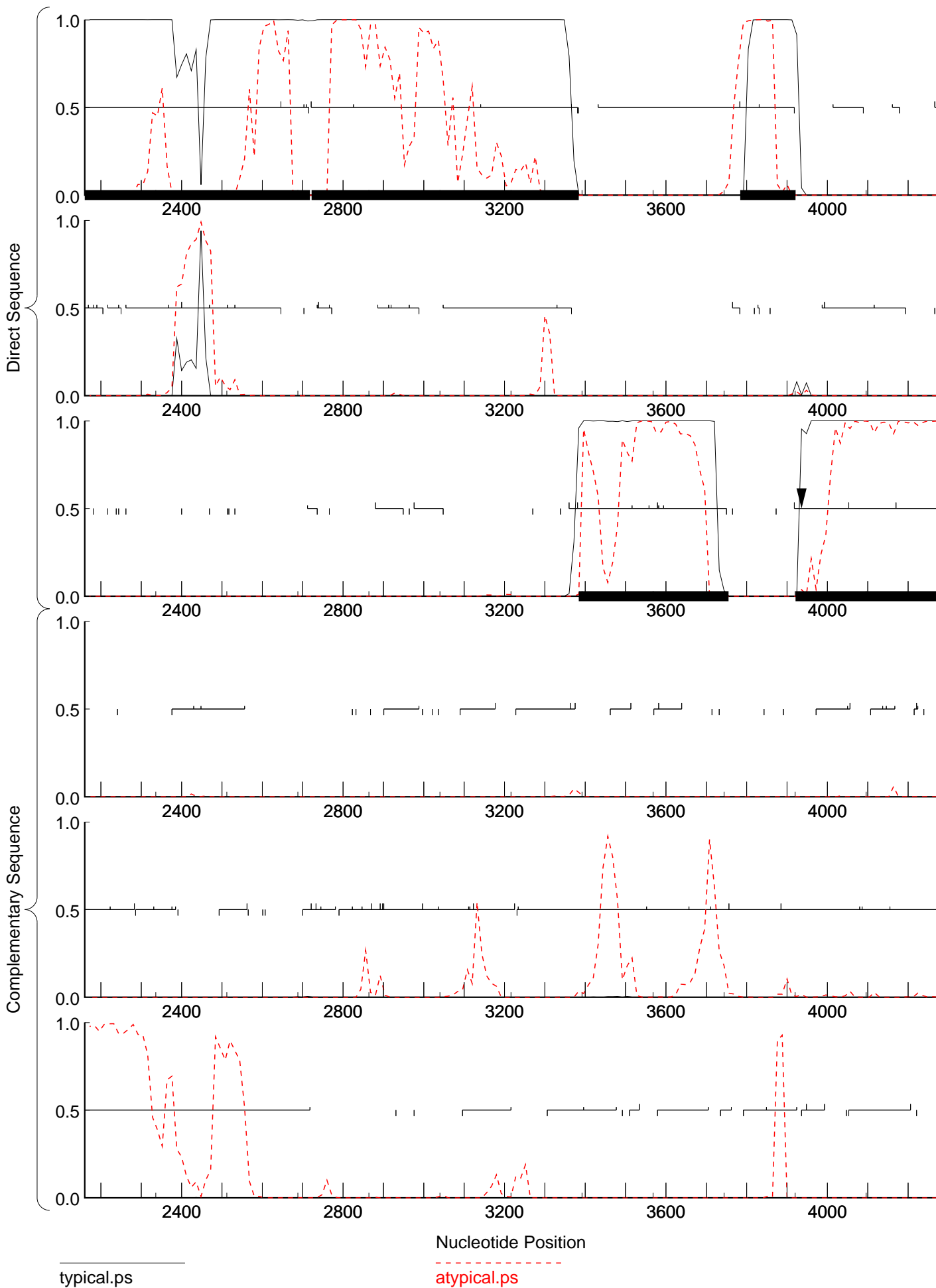
Training set derived by GeneMarkS, 4.30 October 2014
Wed Sep 20 14:16:41 2017

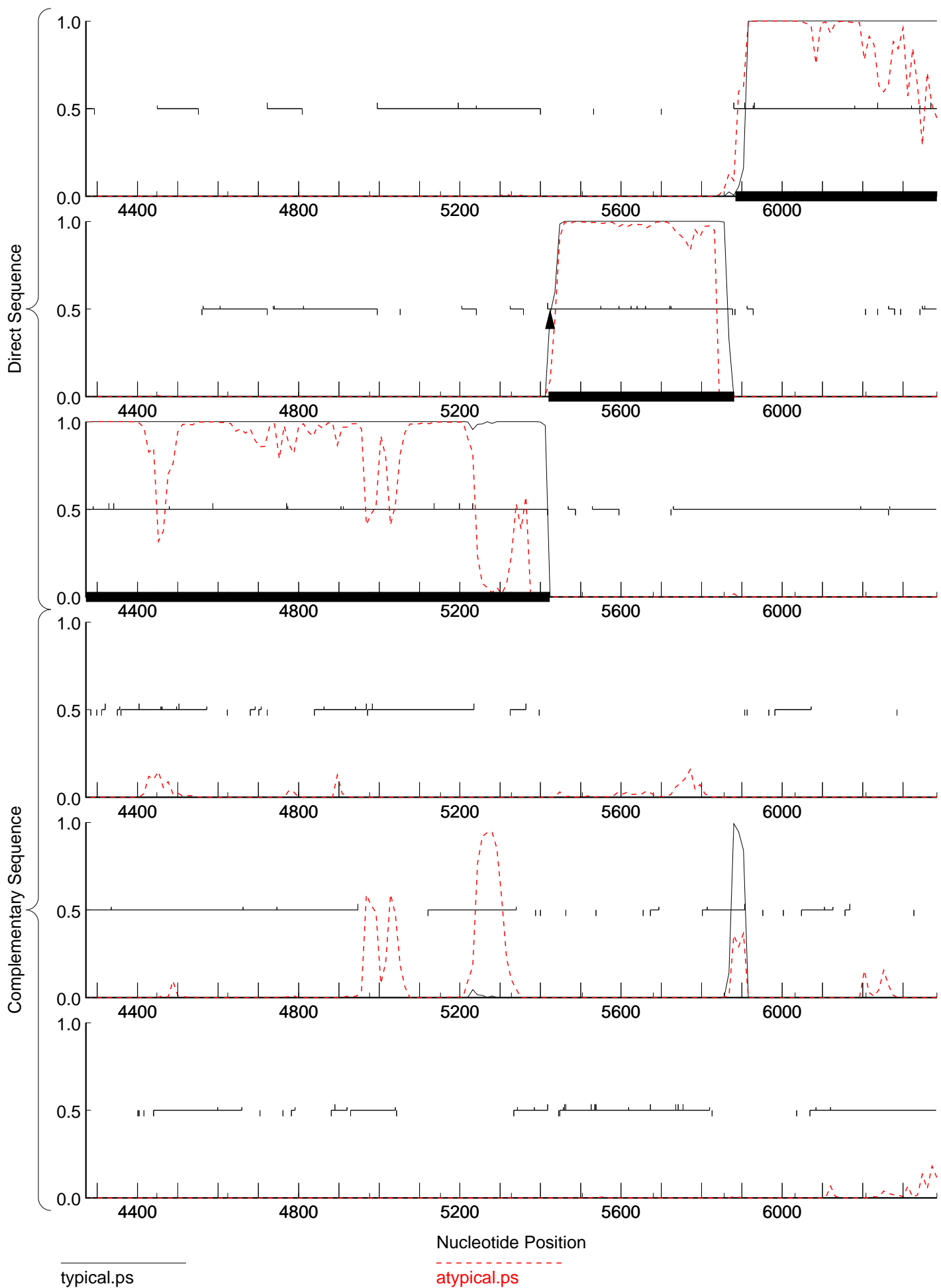
MATRIX INFORMATION

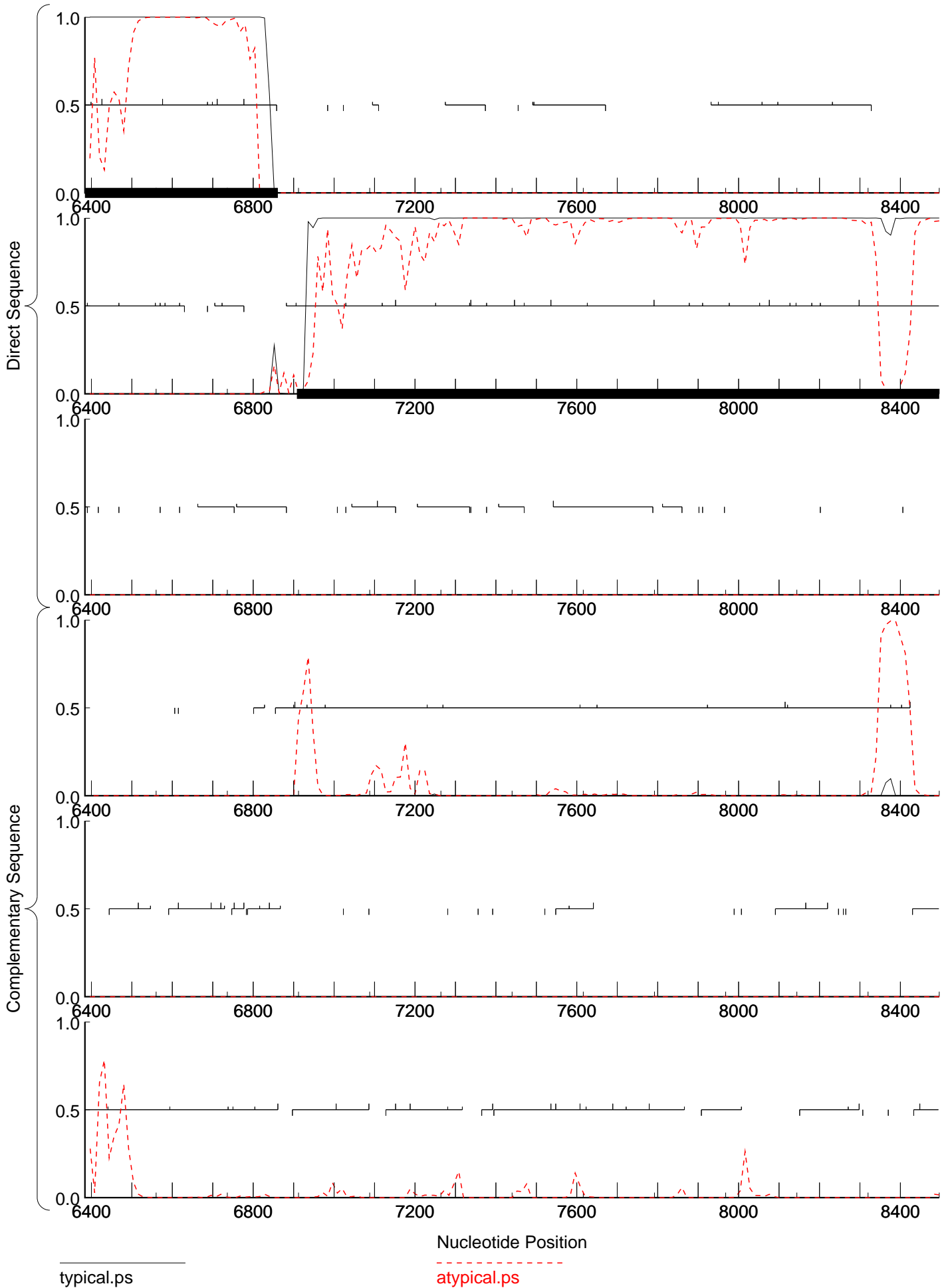
Matrix : -
Author : -
Order : 4

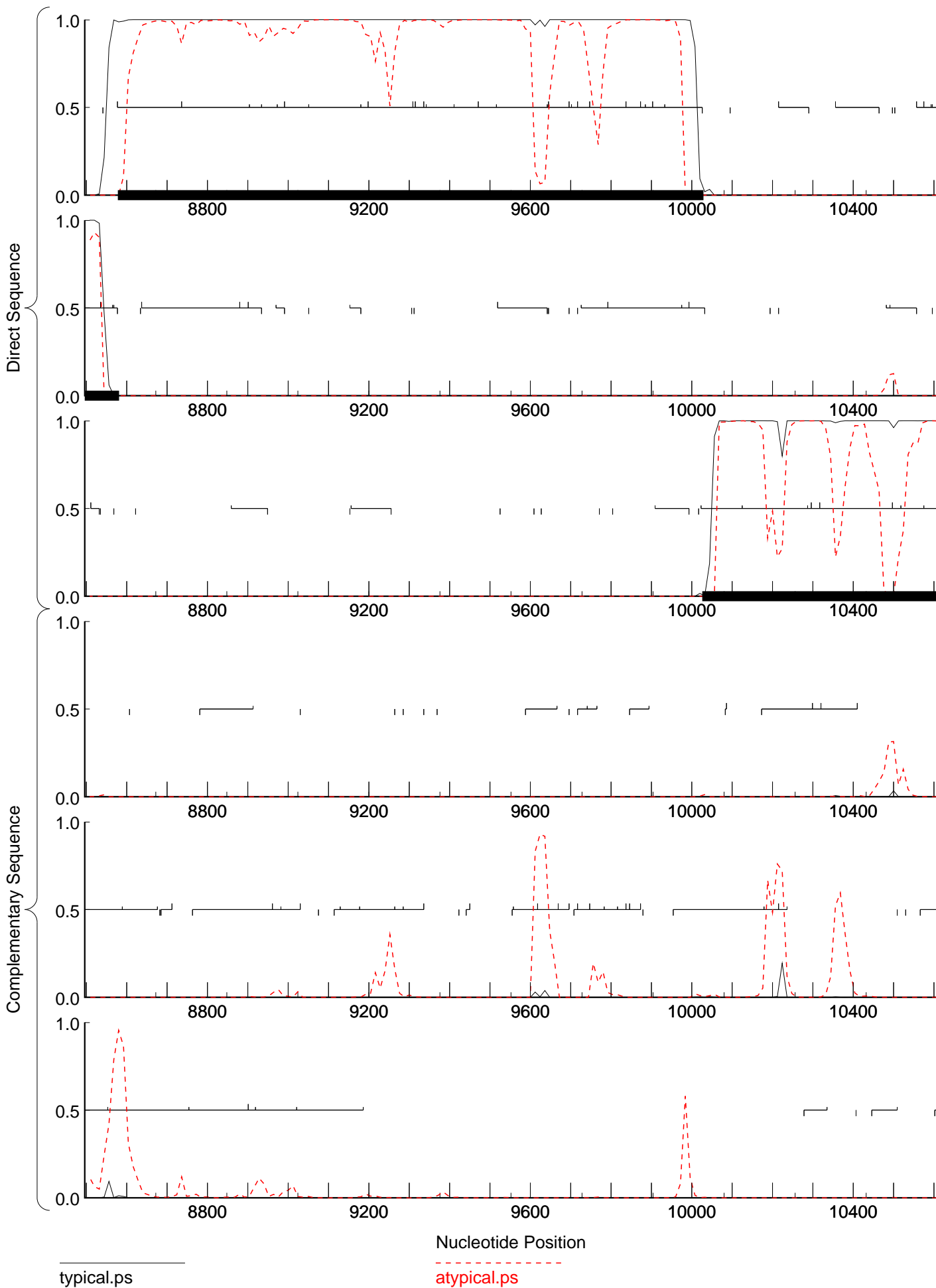
Send questions / comments to:
Dr. M. Borodovsky
Georgia Institute of Technology
School of Biology
Atlanta, GA 30332-0230



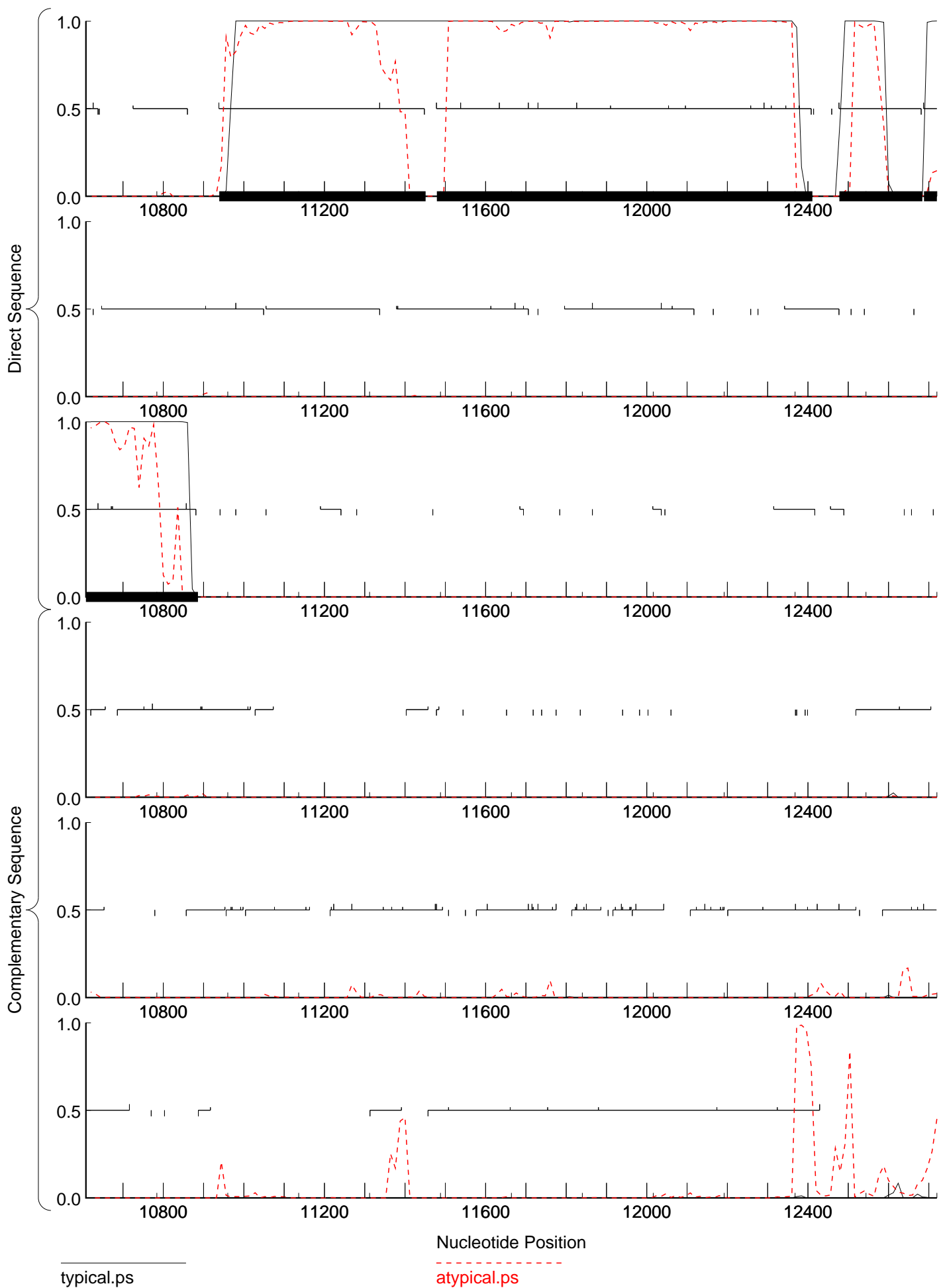




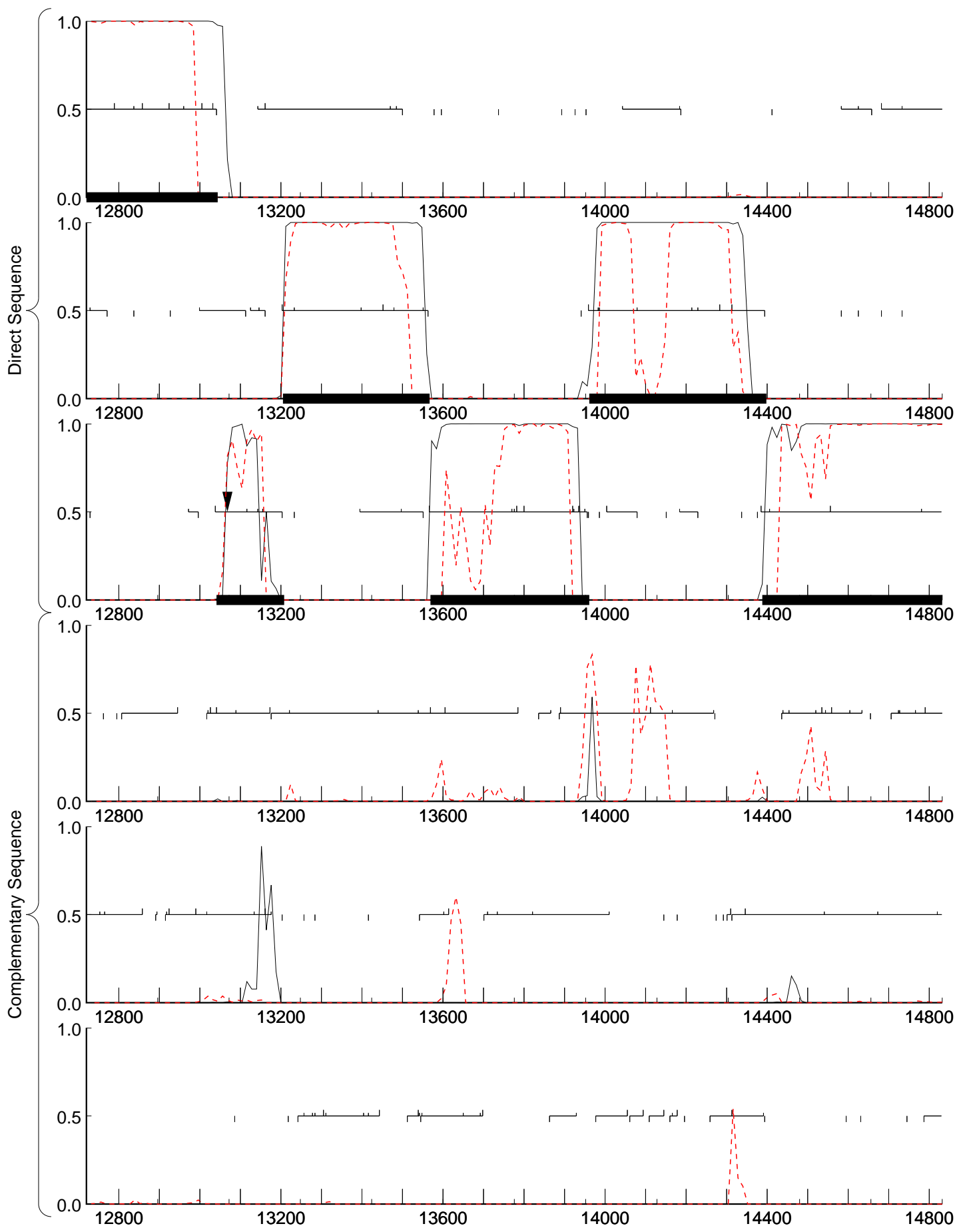




s complete sequence, 51374 bp including 10-base 3' overhang (CGGCCGGTAA), Cluster A4, Order 4, Window 96, Step 12, 7/26
s complete sequence, 51374 bp including 10-base 3' overhang (CGGCCGGTAA), Cluster A4, Order 2, Window 96, Step 12, 7/26

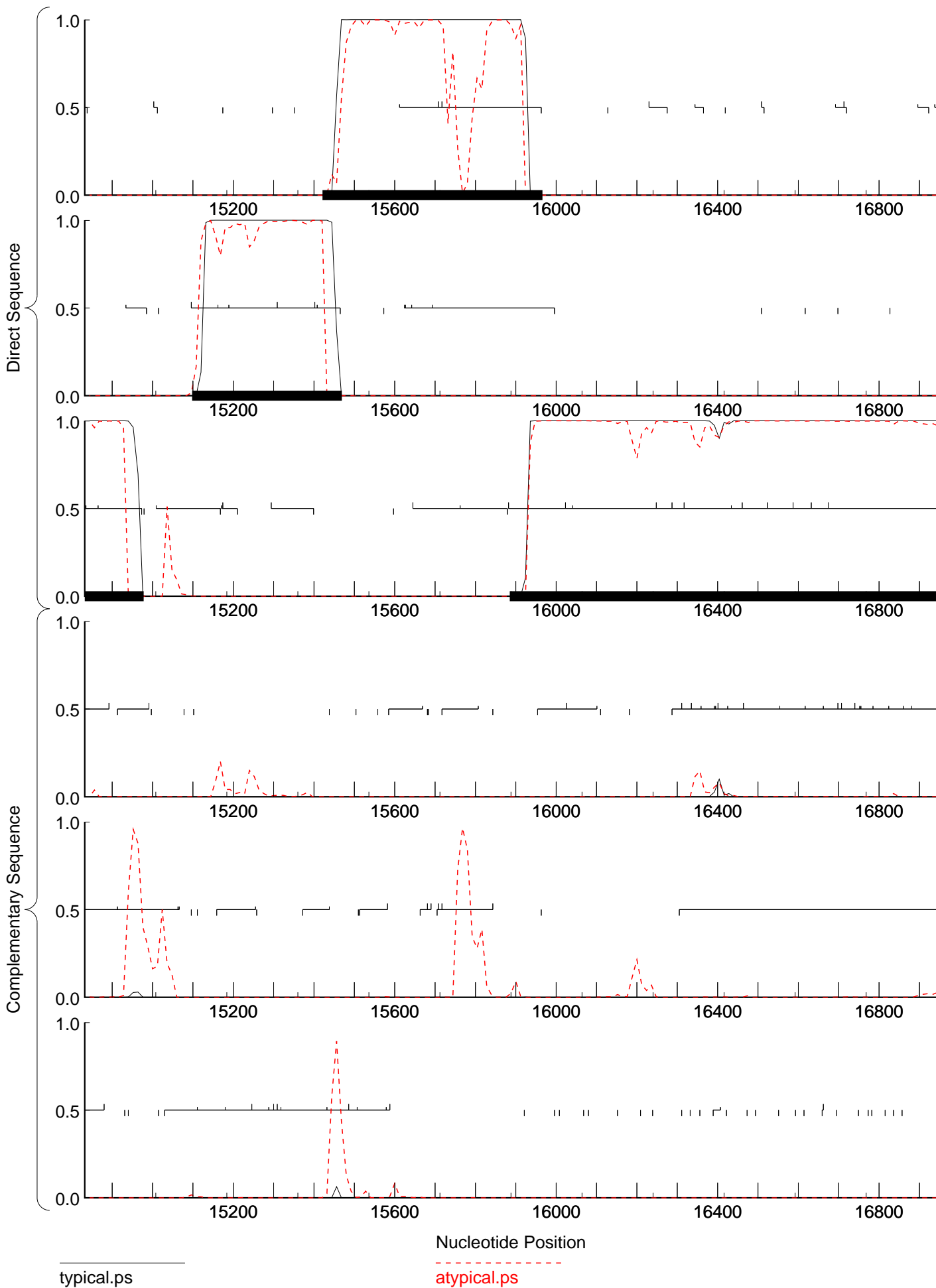


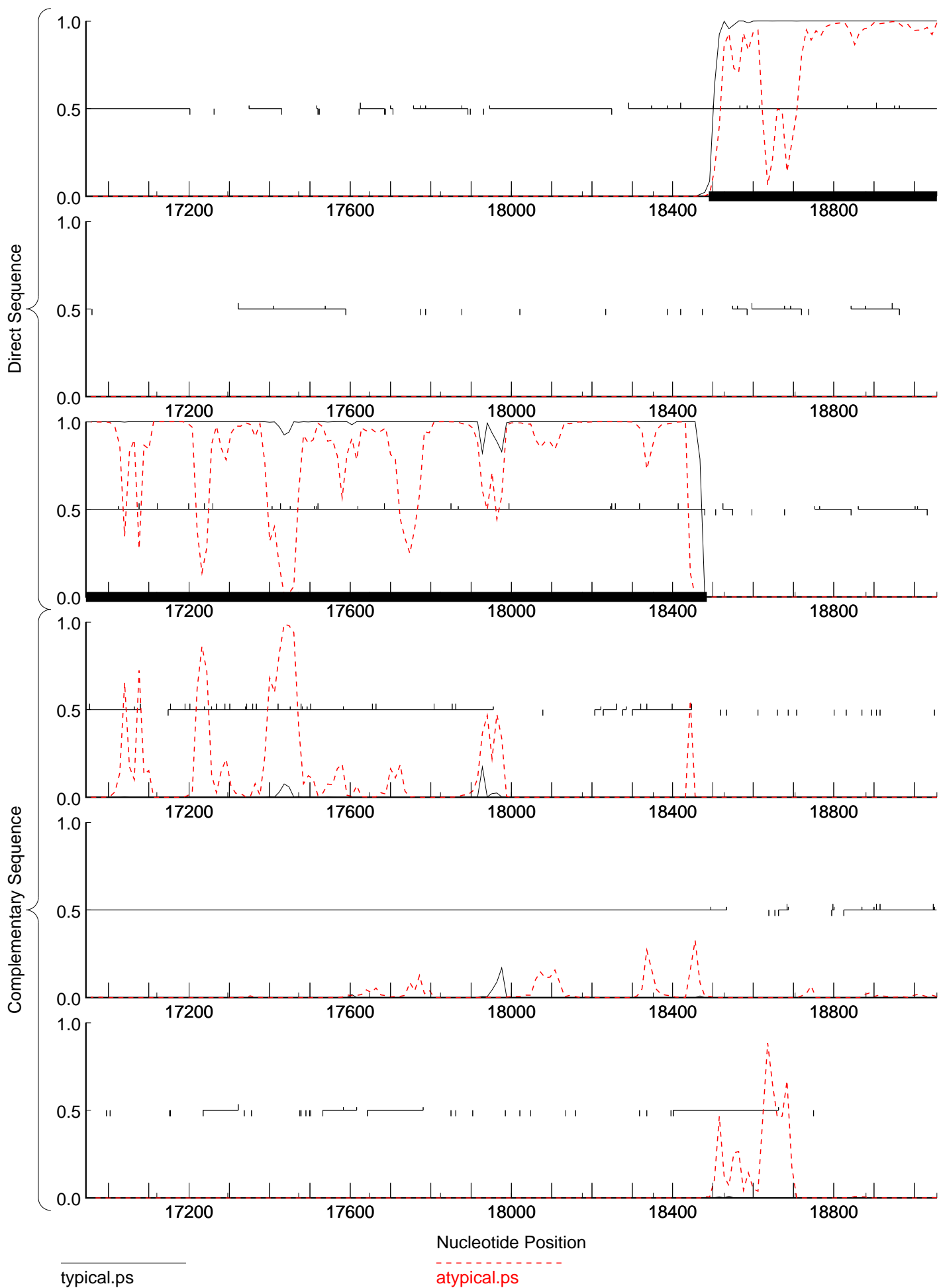
GeneMark.hmm prediction

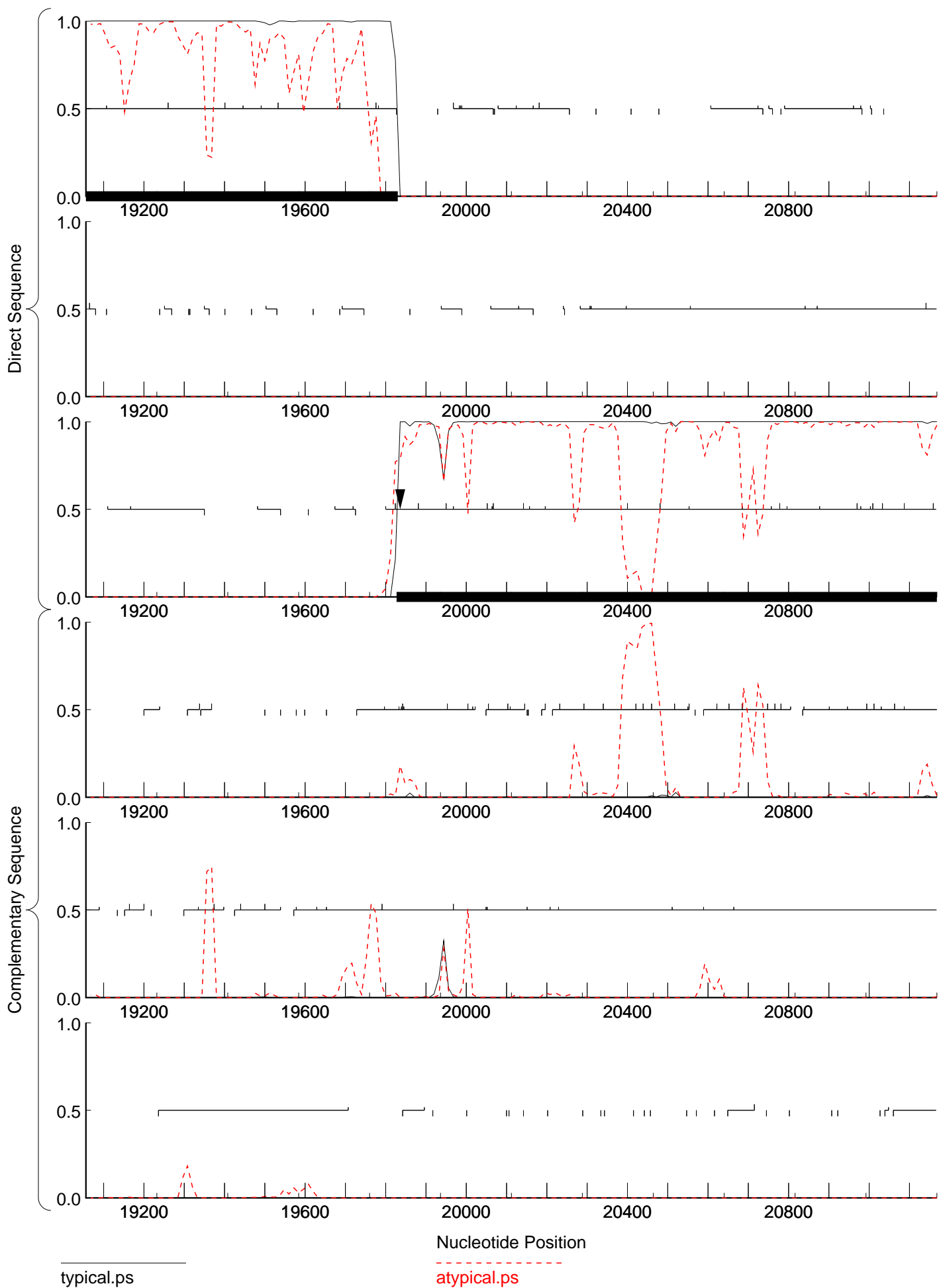


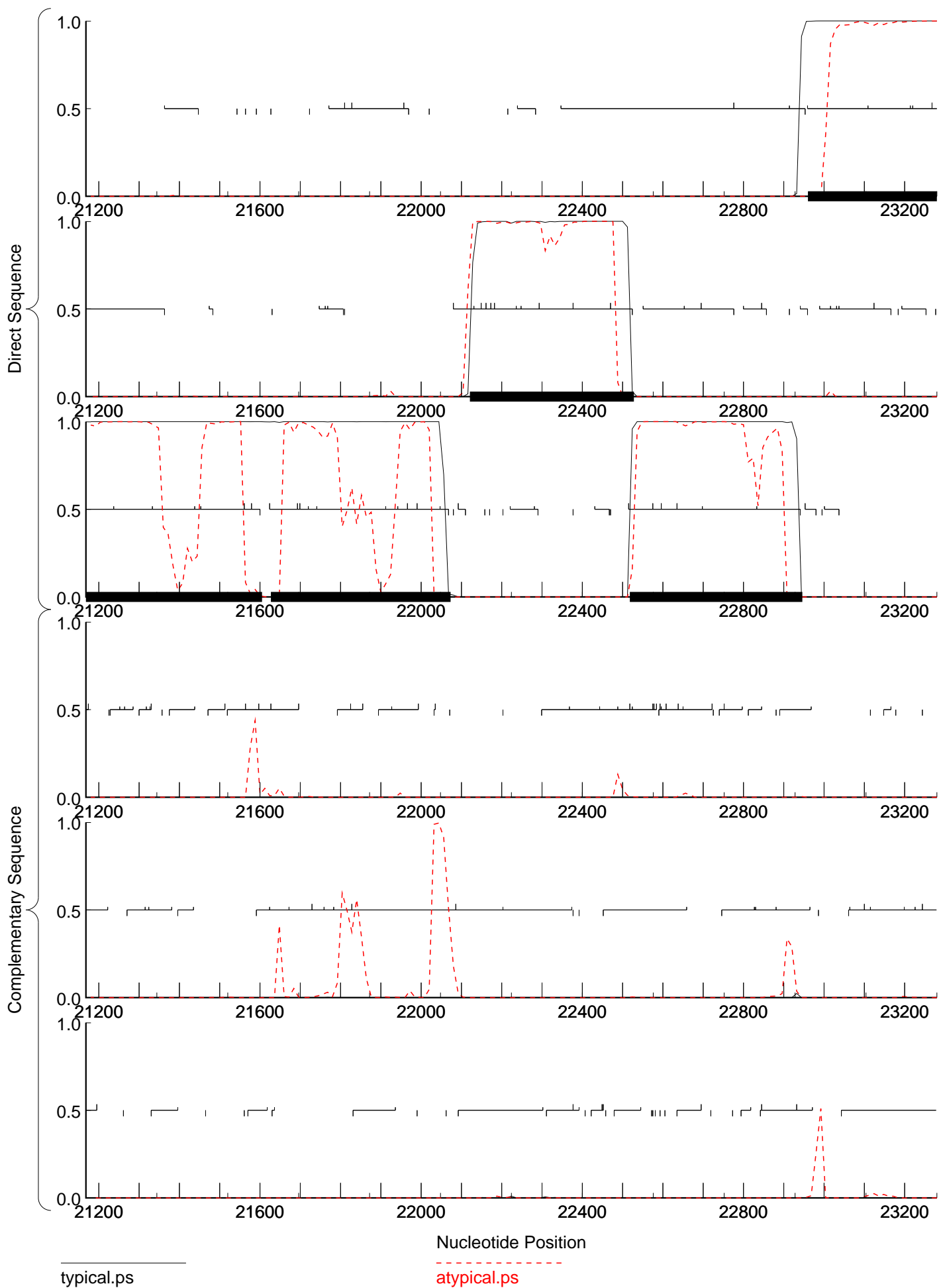
typical.ps

atypical.ps



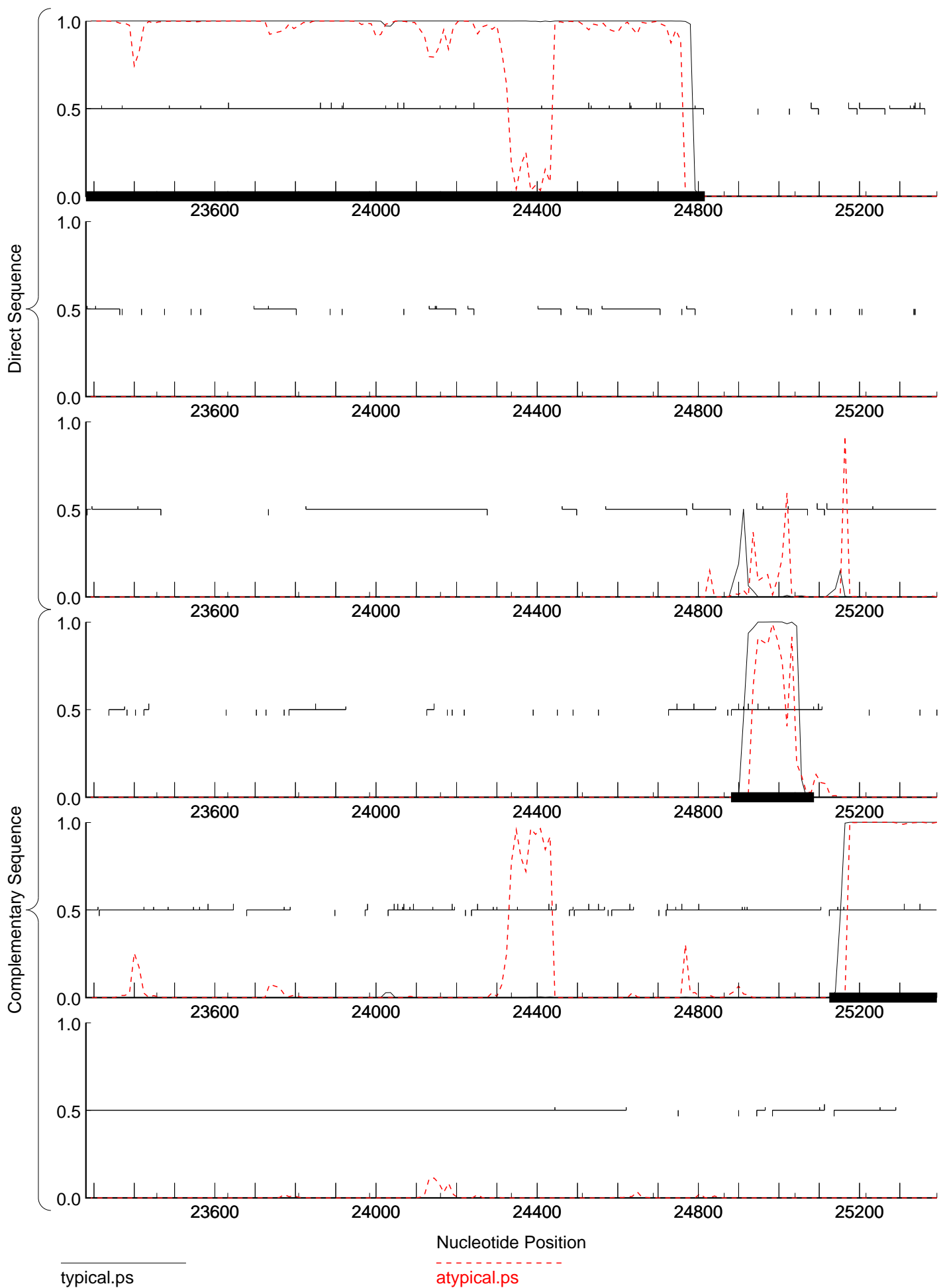


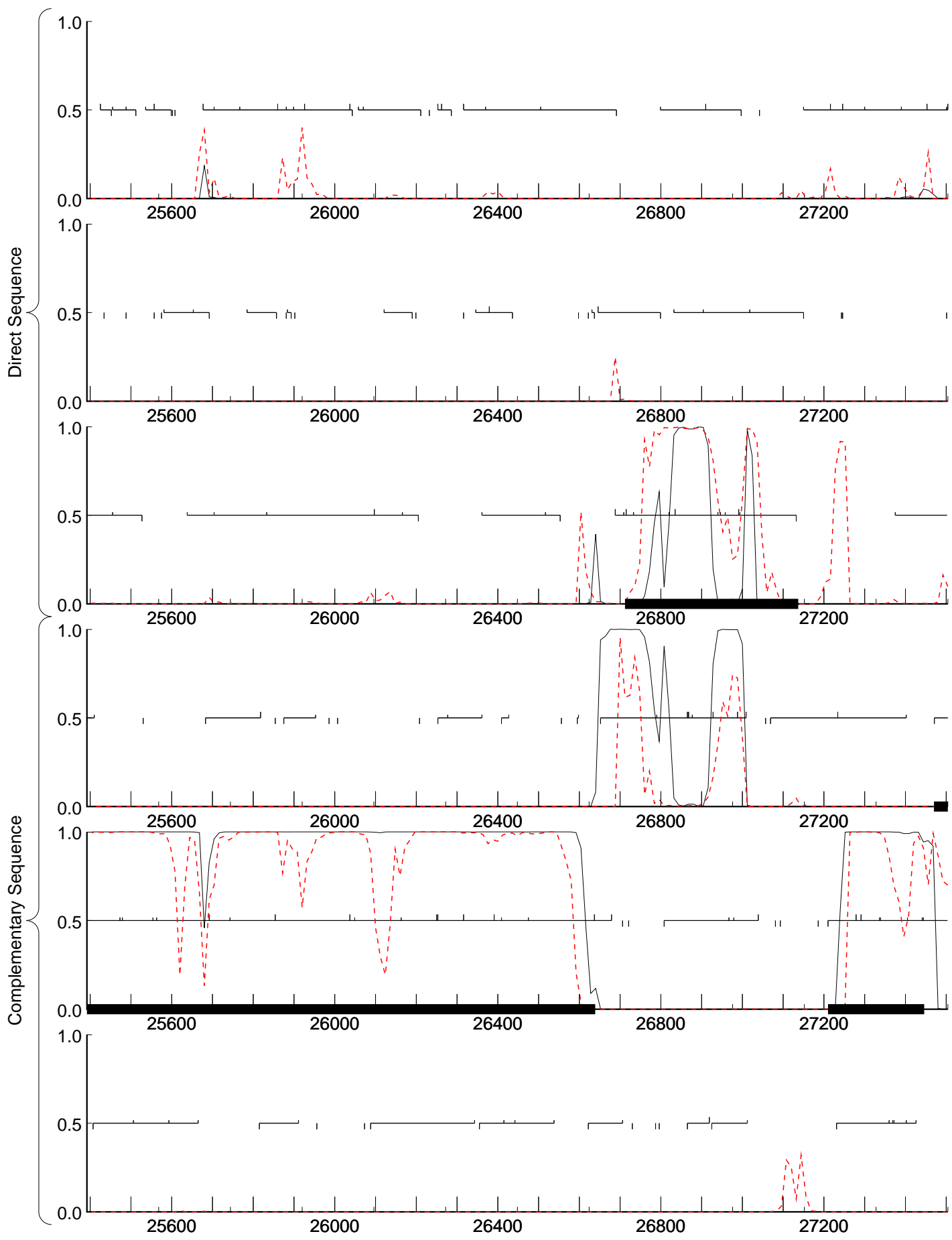




typical.ps

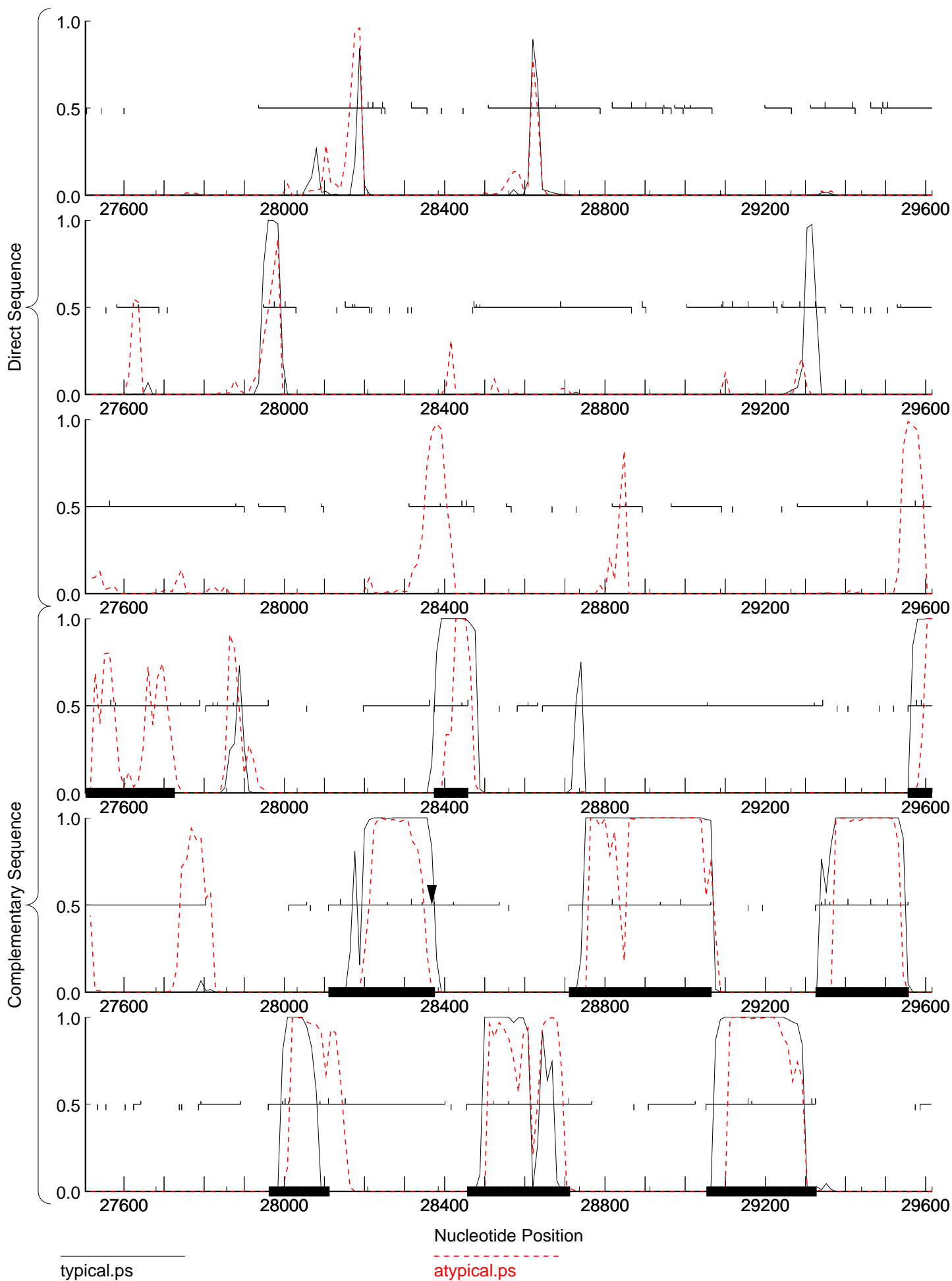
atypical.ps

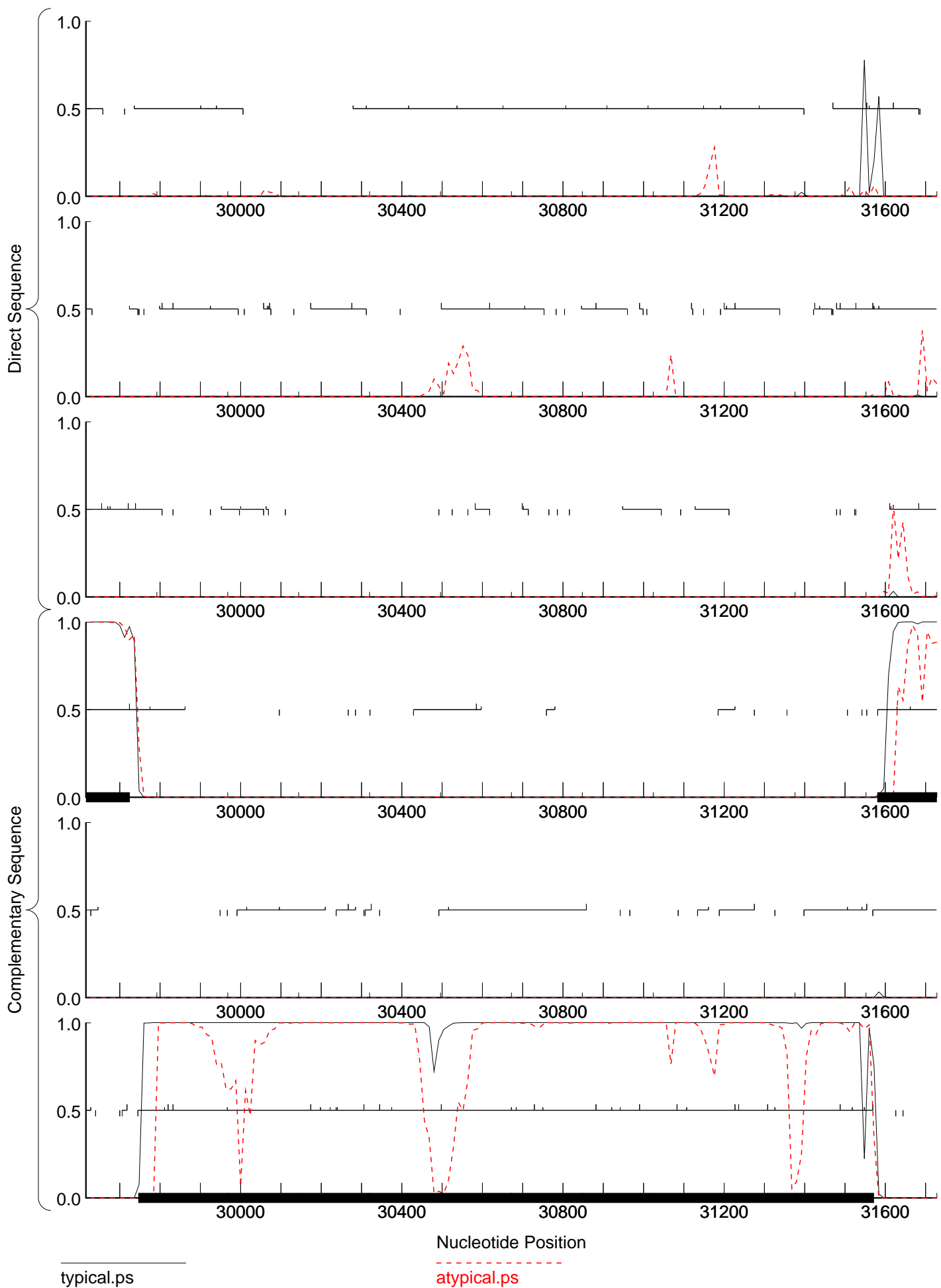




typical.ps

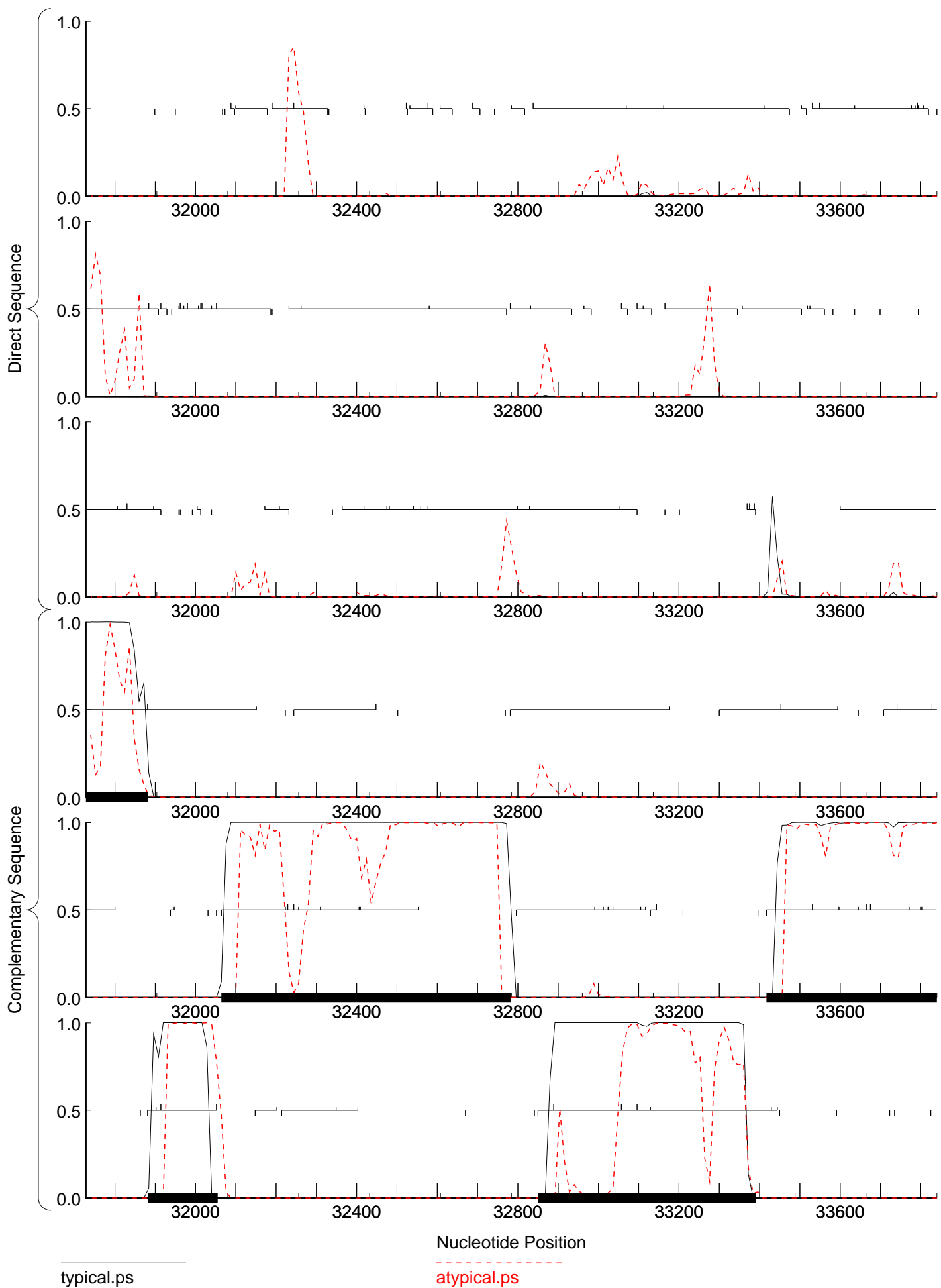
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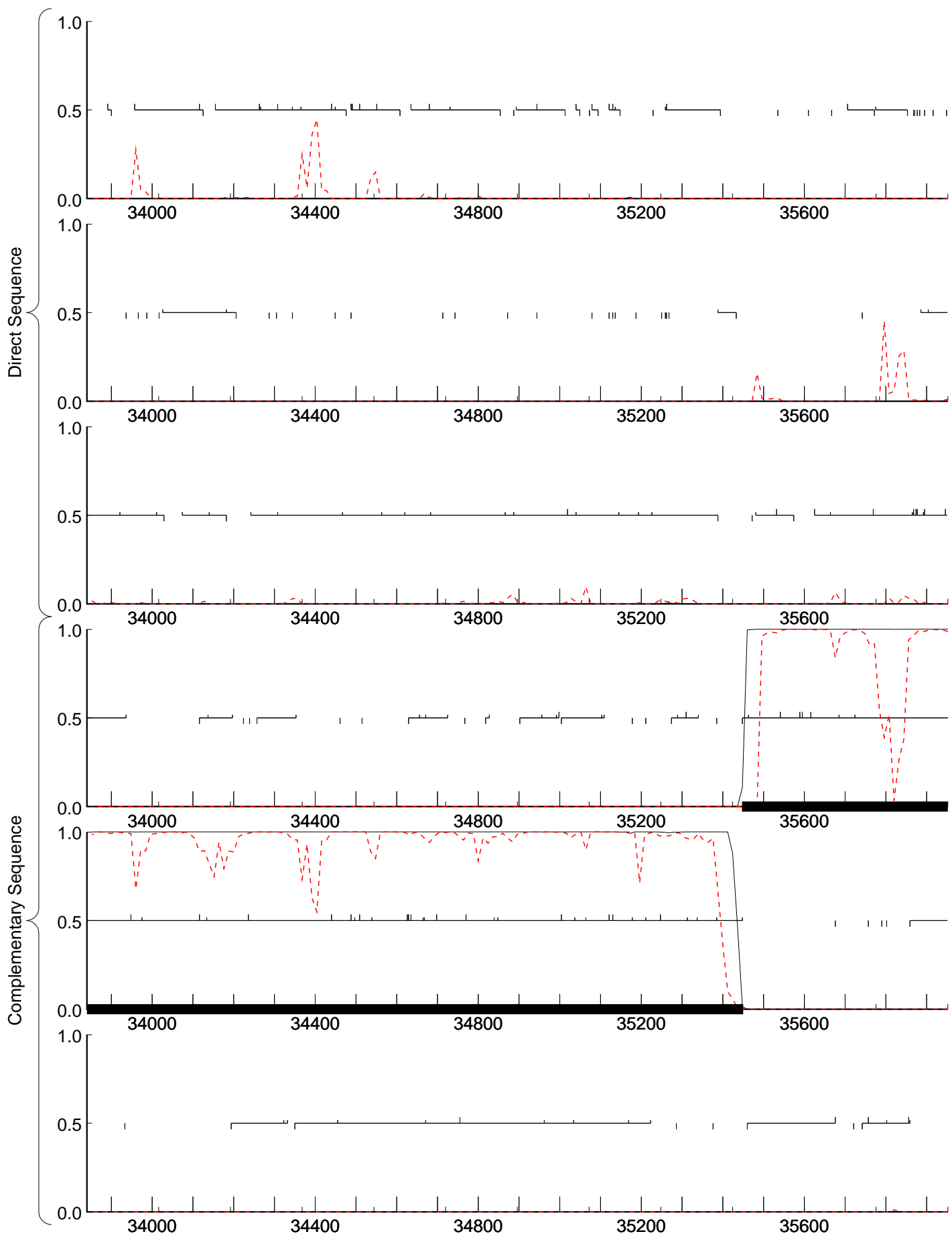




typical.ps

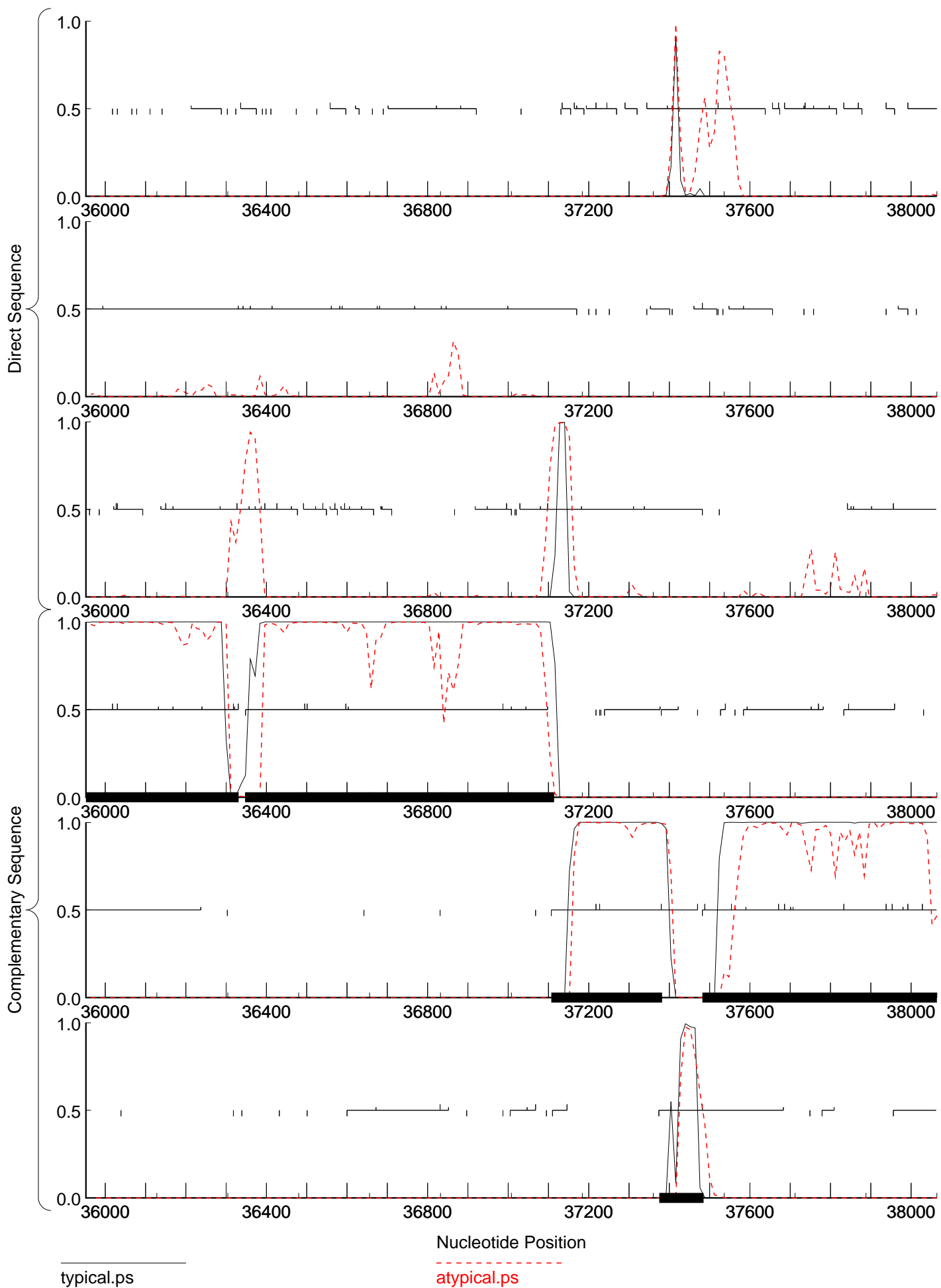
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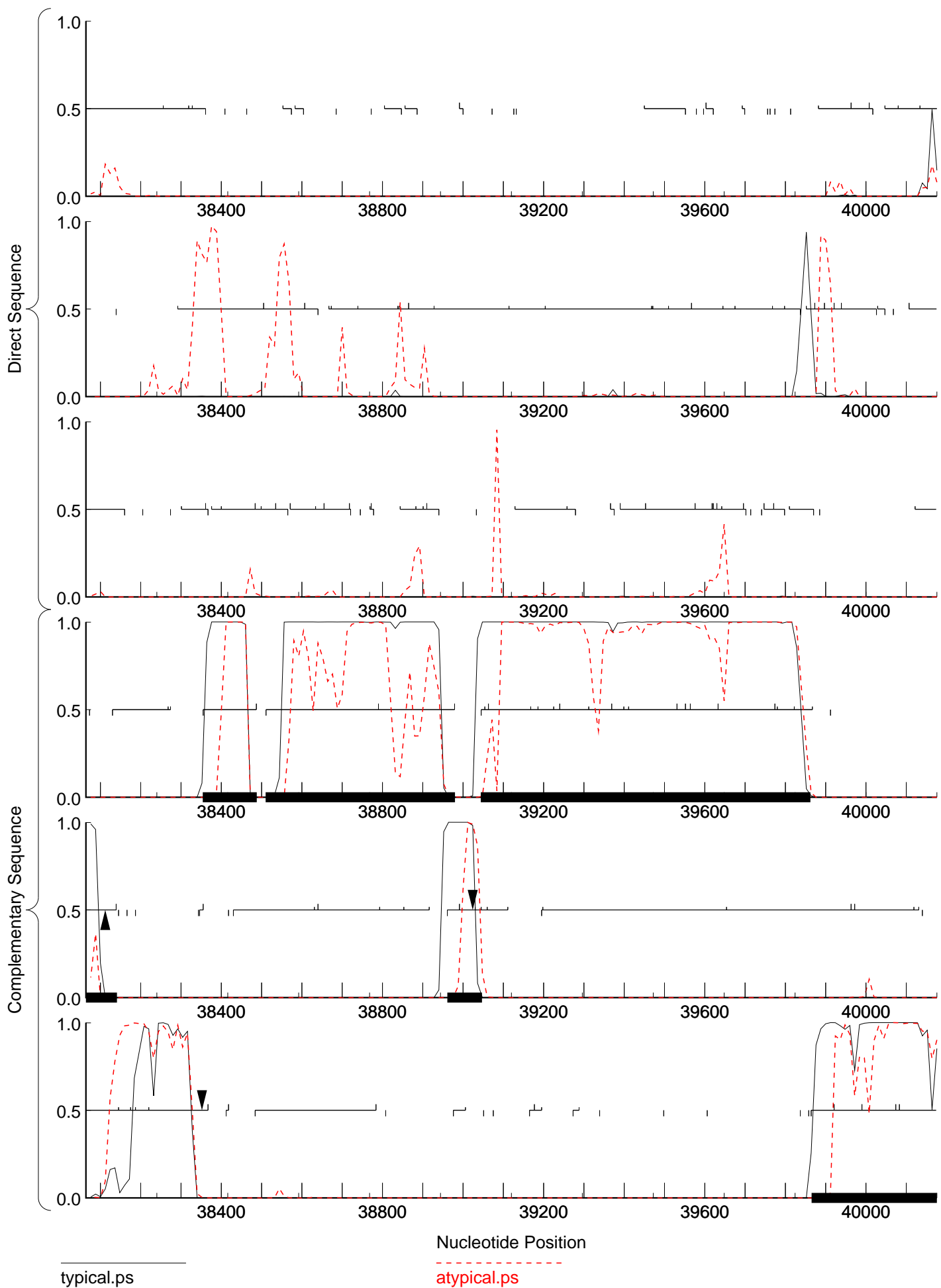


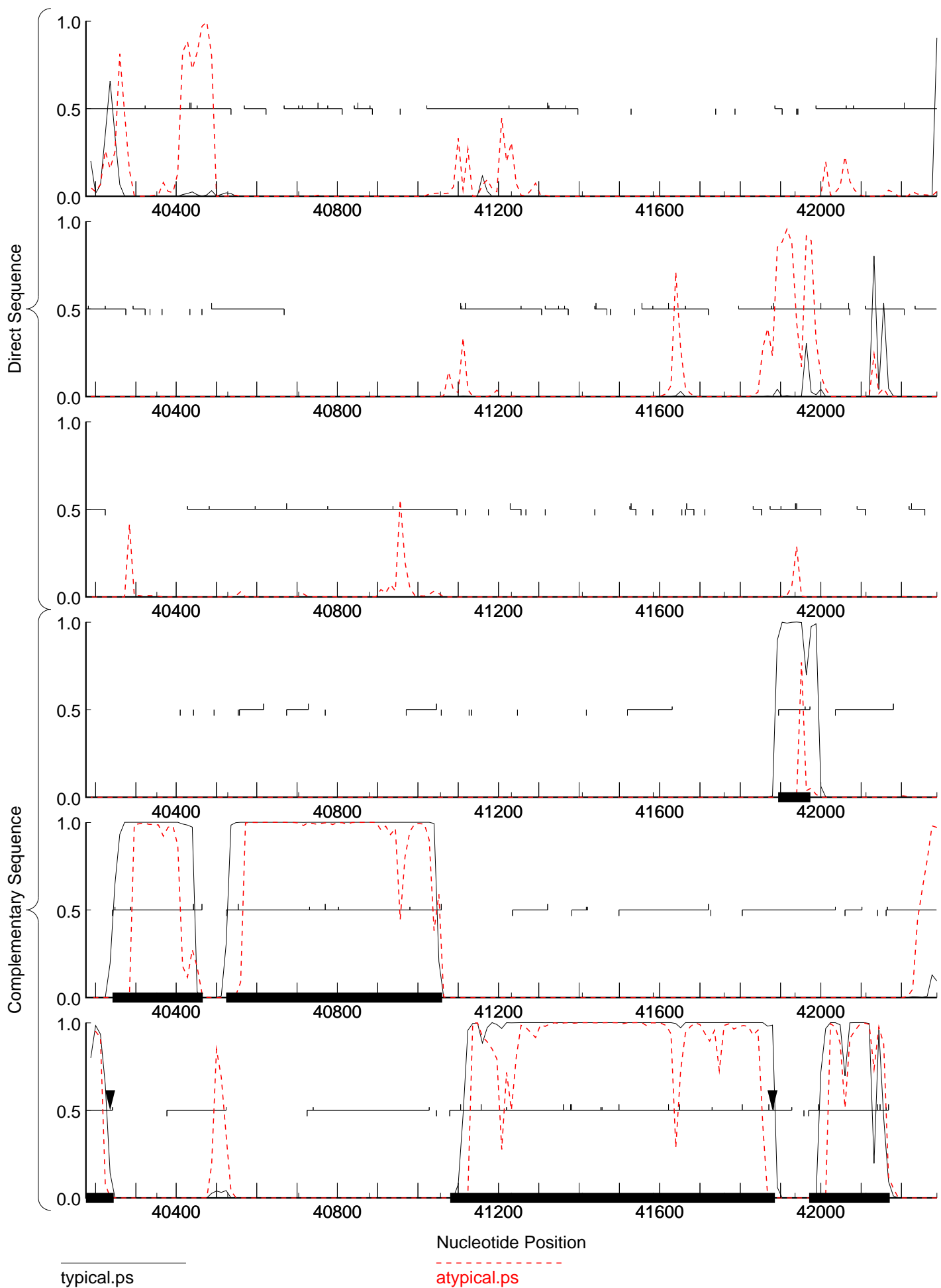


typical.ps

atypical.ps

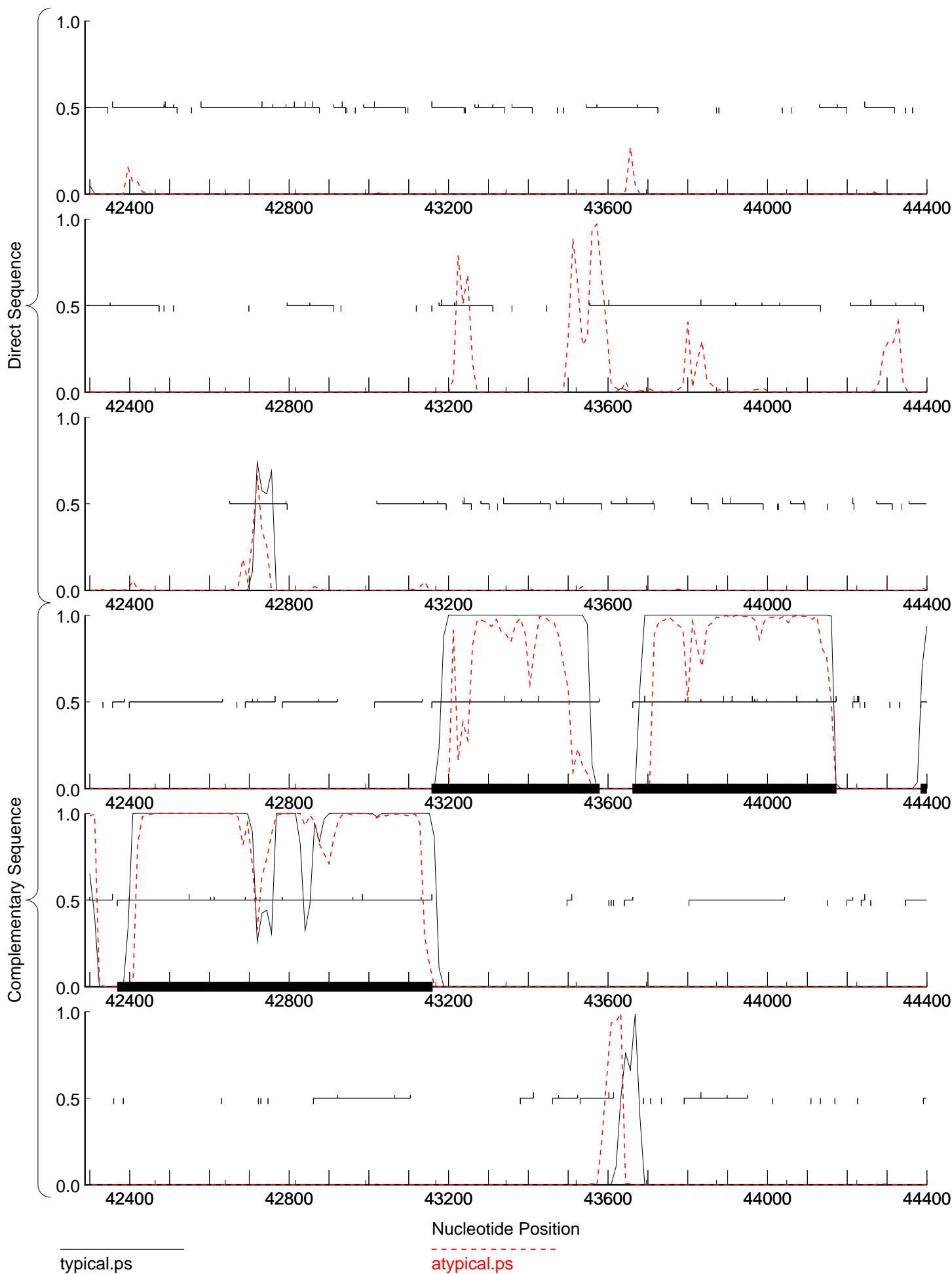


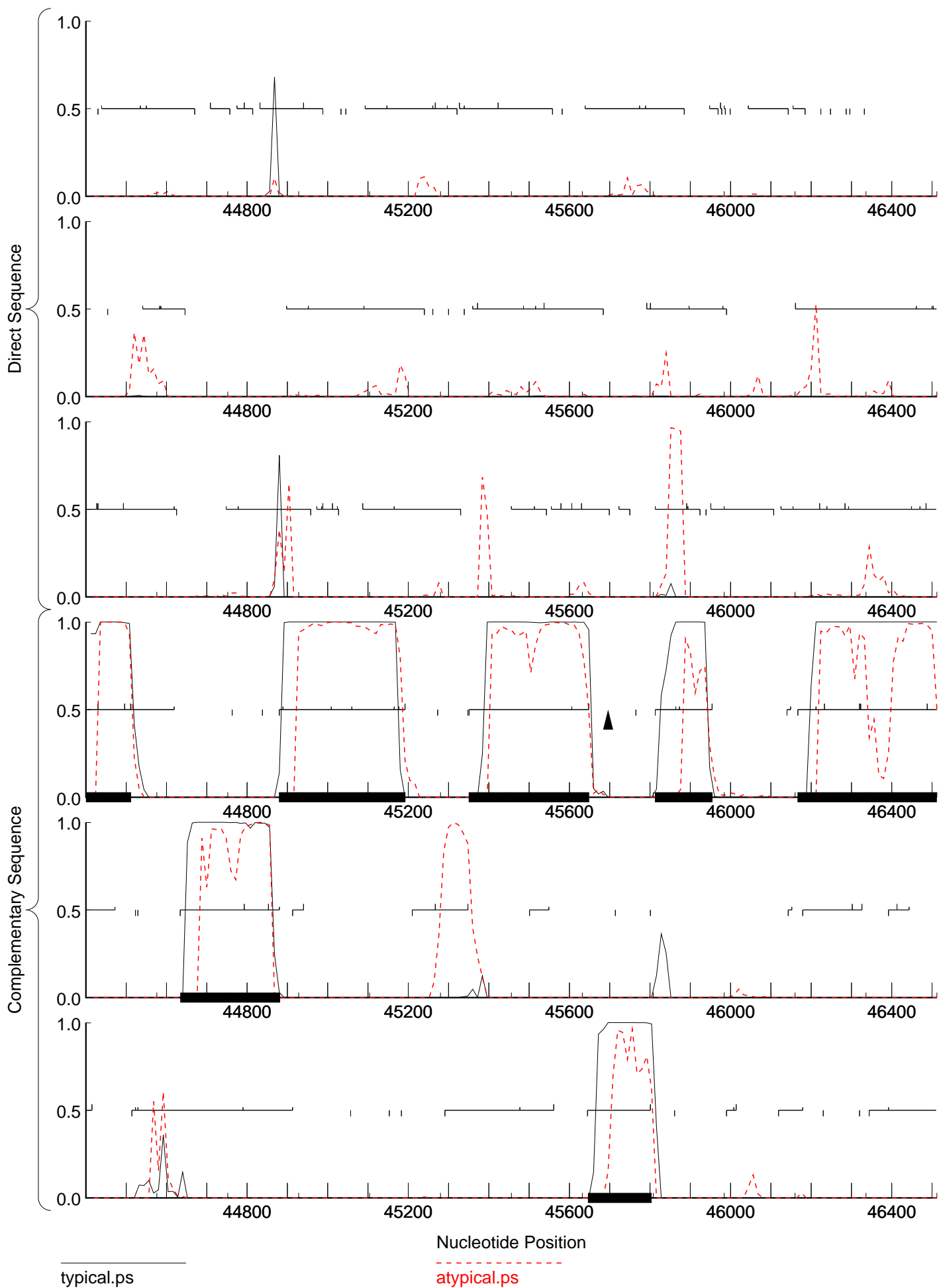


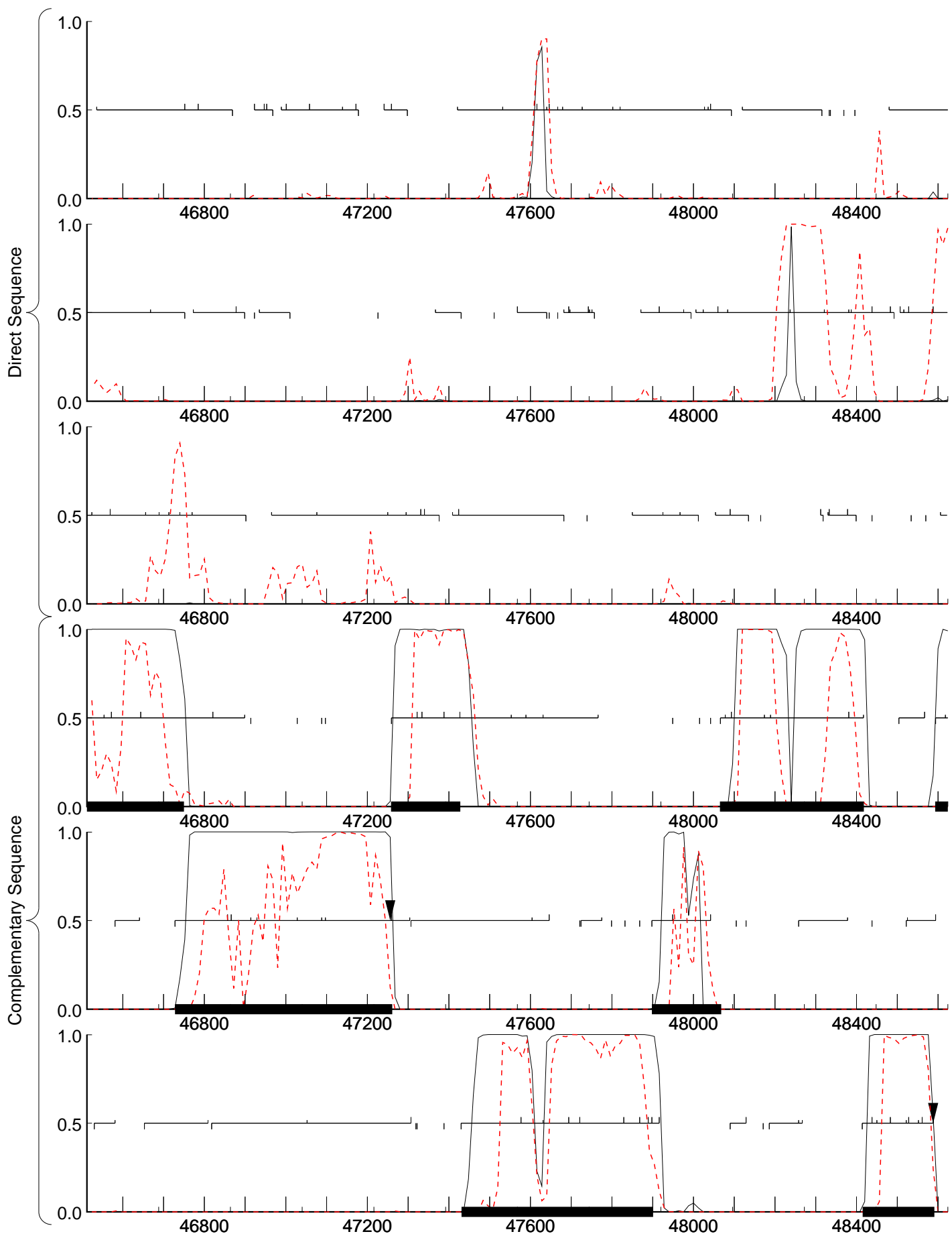


typical.ps

atypical.ps







typical.ps

atypical.ps

