

GeneMark

Version 2.5p (09.08.06)

Copyright 1993 - M. Borodovsky, J. McIninch

PROGRAM INFORMATION

Sequence : Mycobacterium phage Lilizi complete sequence, 75360 bp including 9-base 3' overhang (CGCTTG
Analysis Date : 5/27/18 at 9:54:10
Pages : 37
Sequence Length : 75360 bp
GC Content : 63.01%

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,

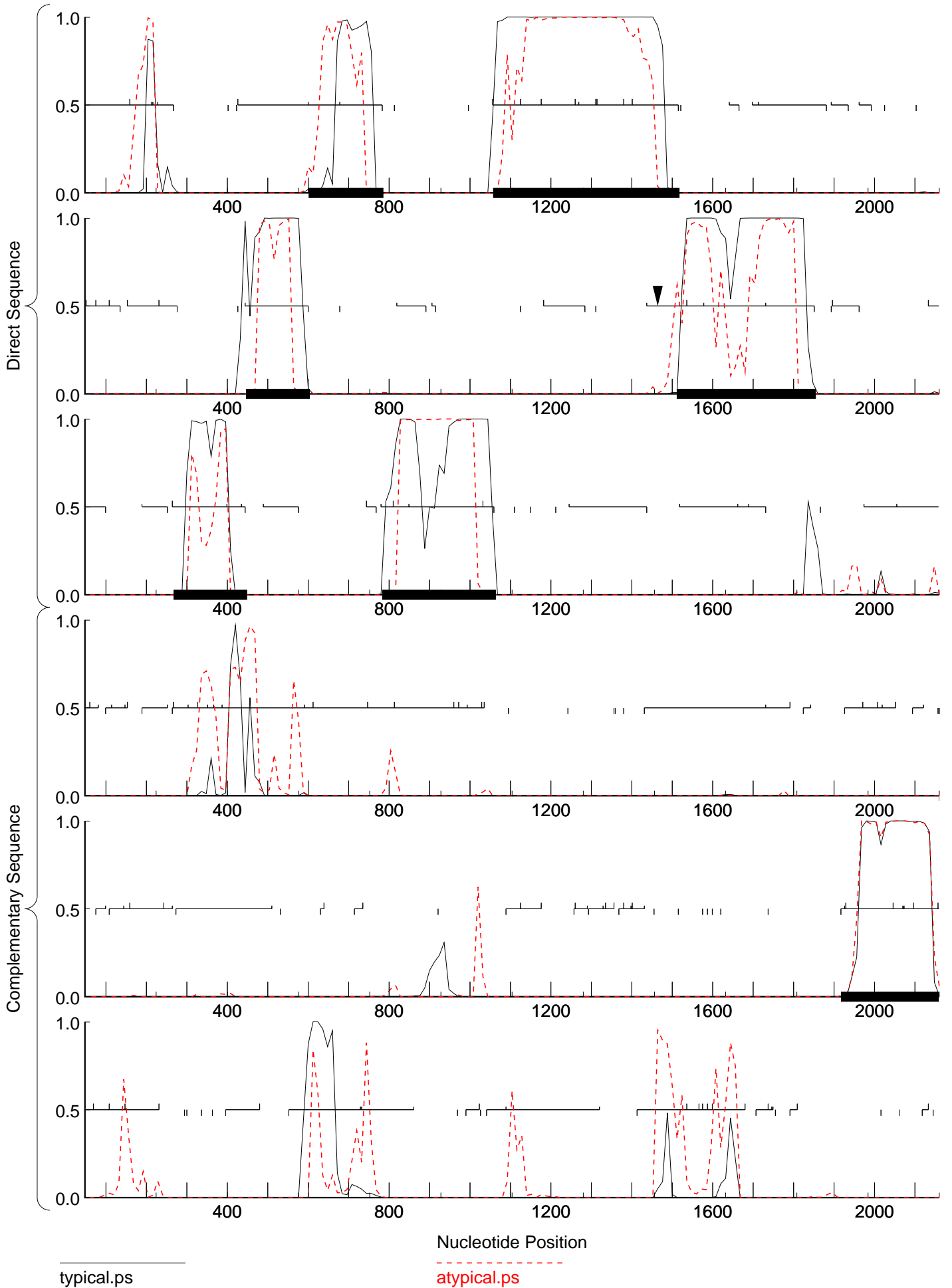
Matrix notes & comments

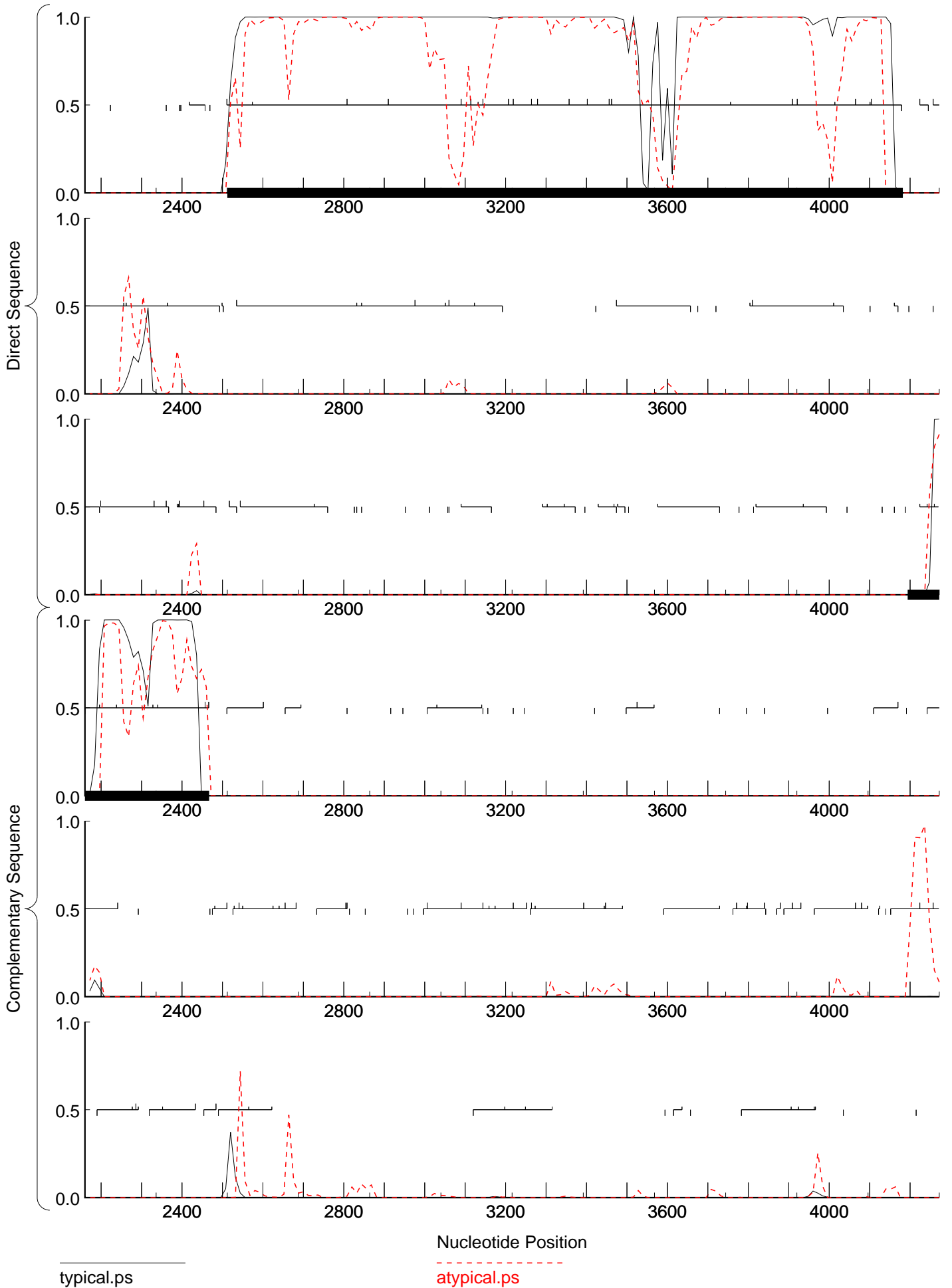
Training set derived by GeneMarkS, 4.30 October 2014
Sun May 27 09:54:10 2018

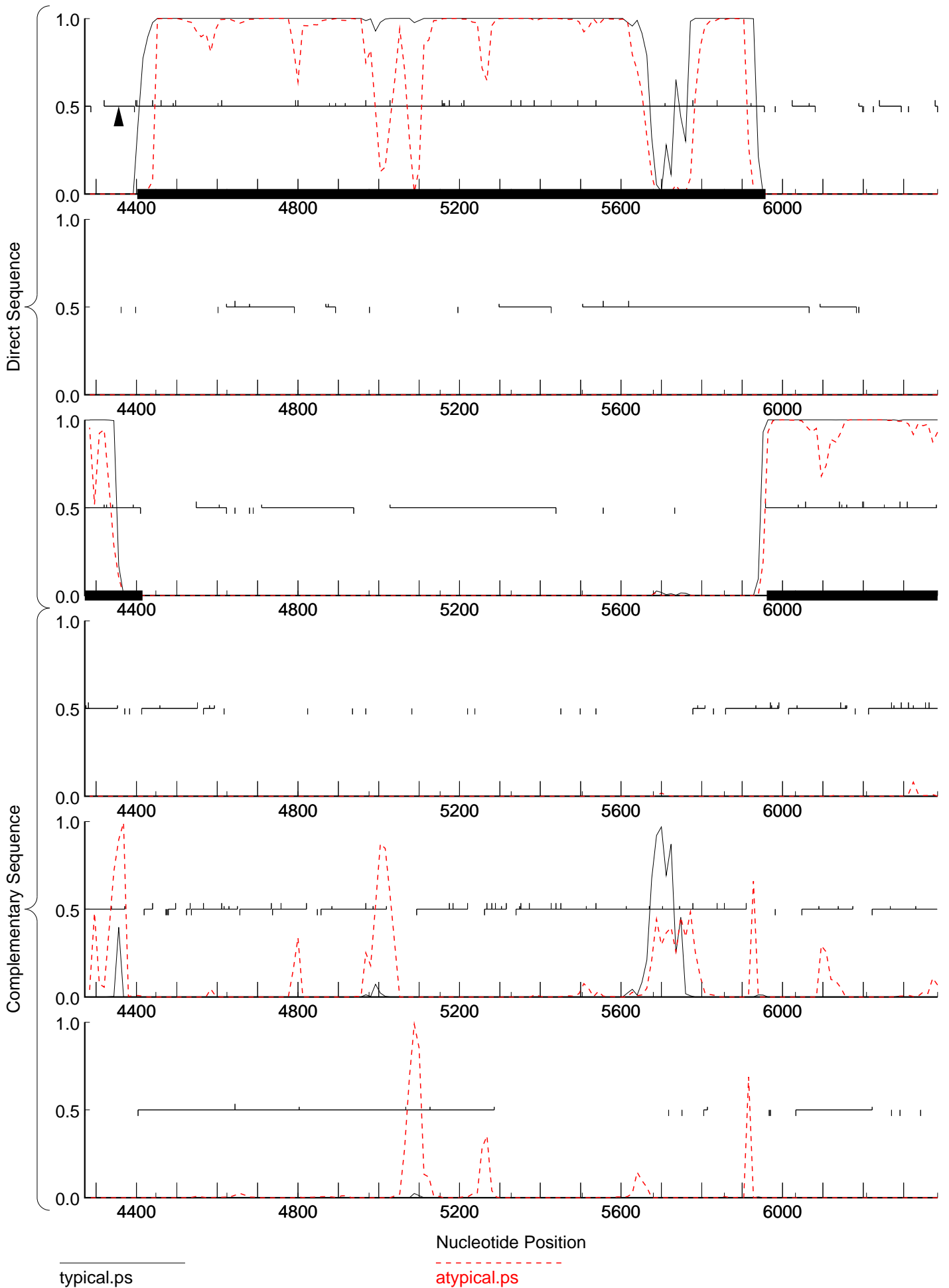
MATRIX INFORMATION

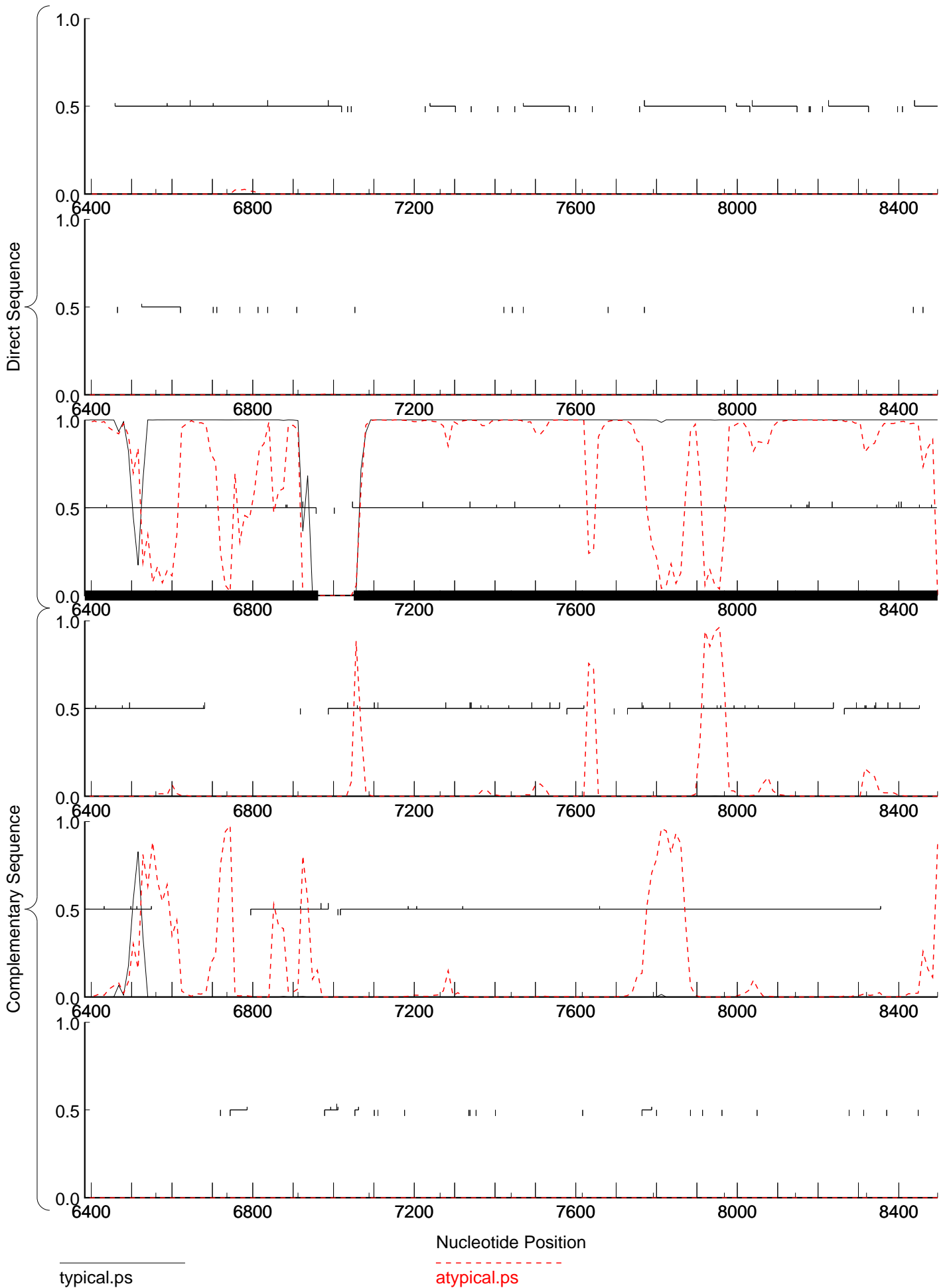
Matrix : -
Author : -
Order : 4

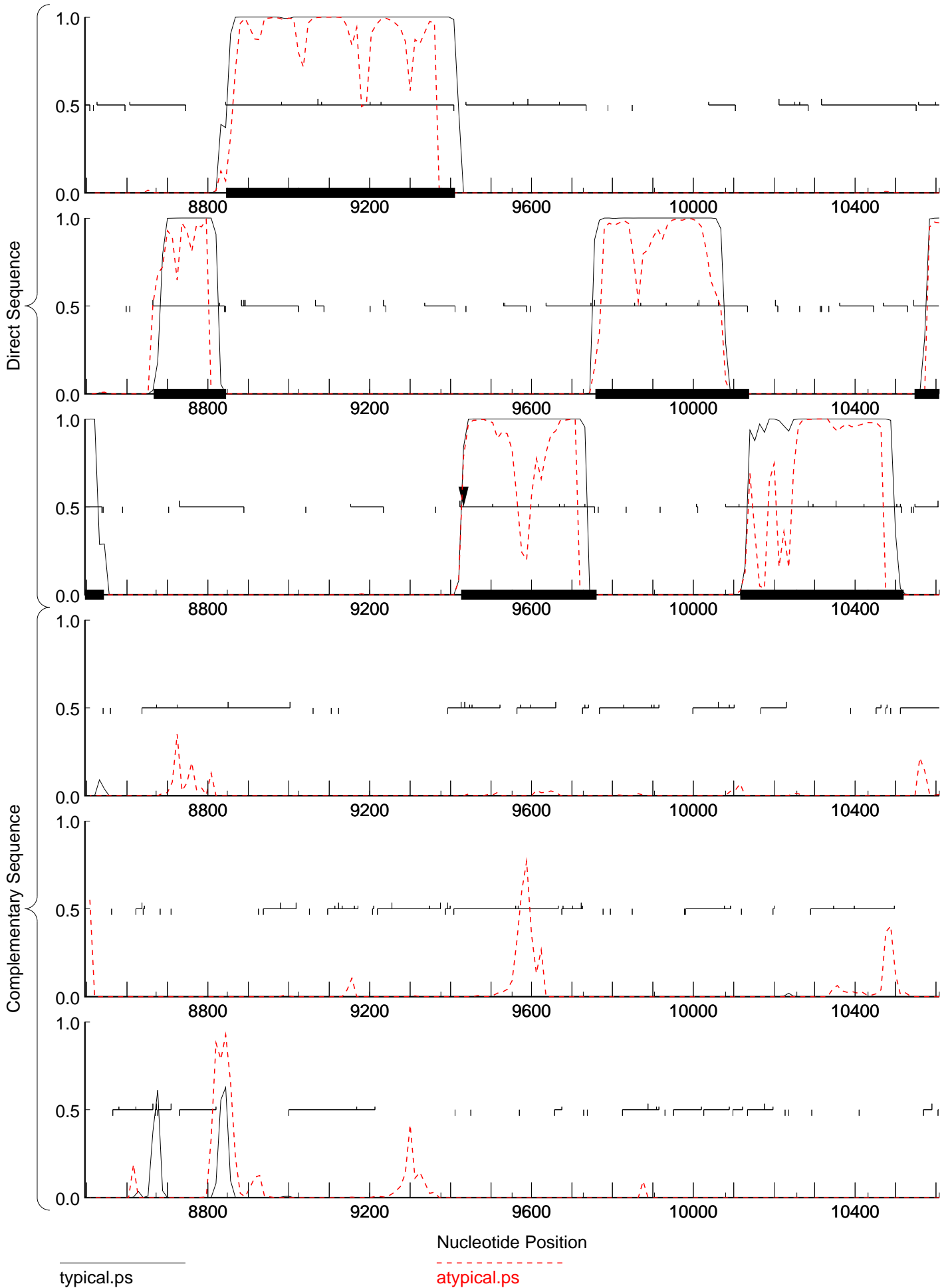
Send questions / comments to:
Dr. M. Borodovsky
Georgia Institute of Technology
School of Biology
Atlanta, GA 30332-0230

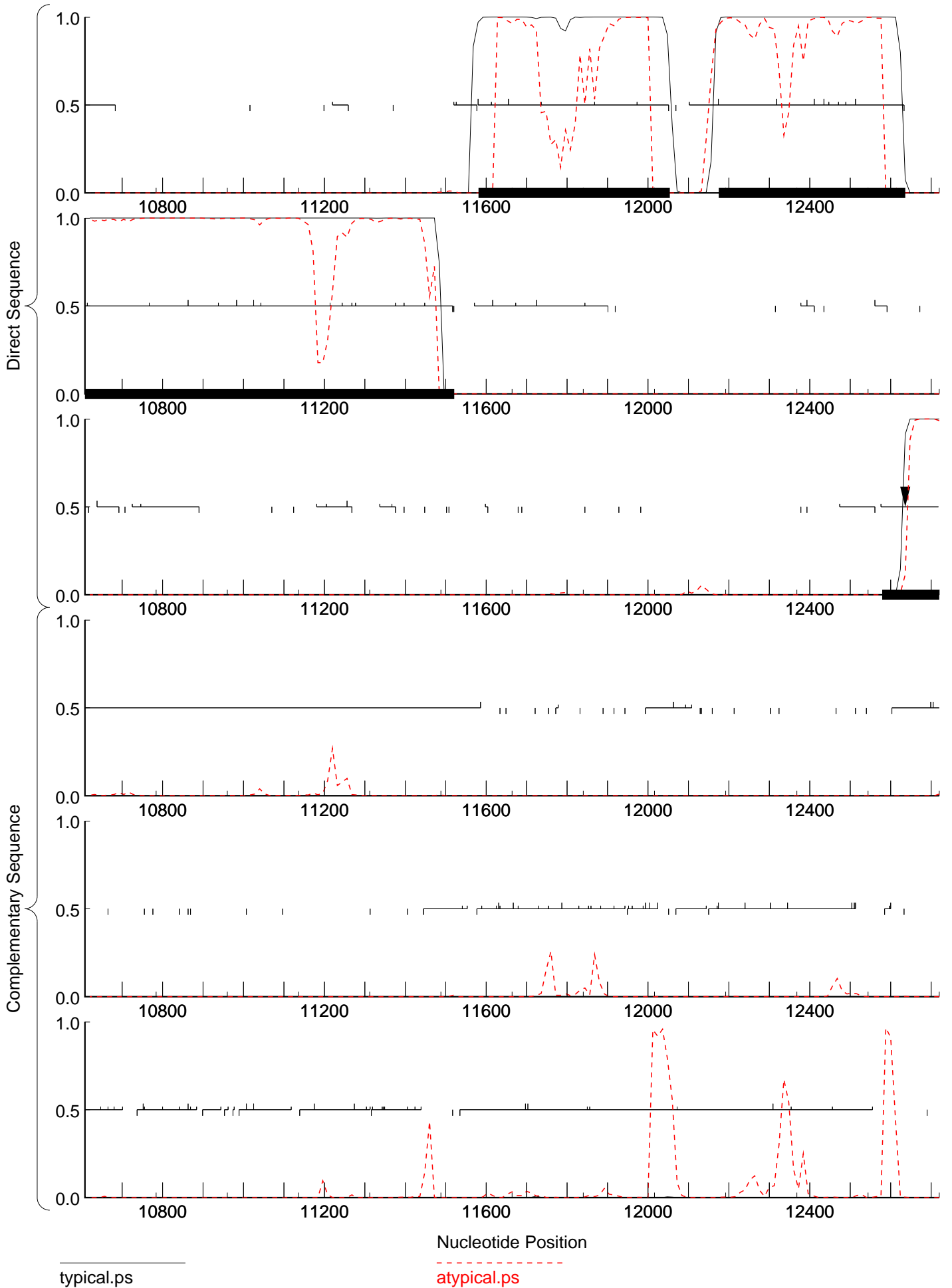


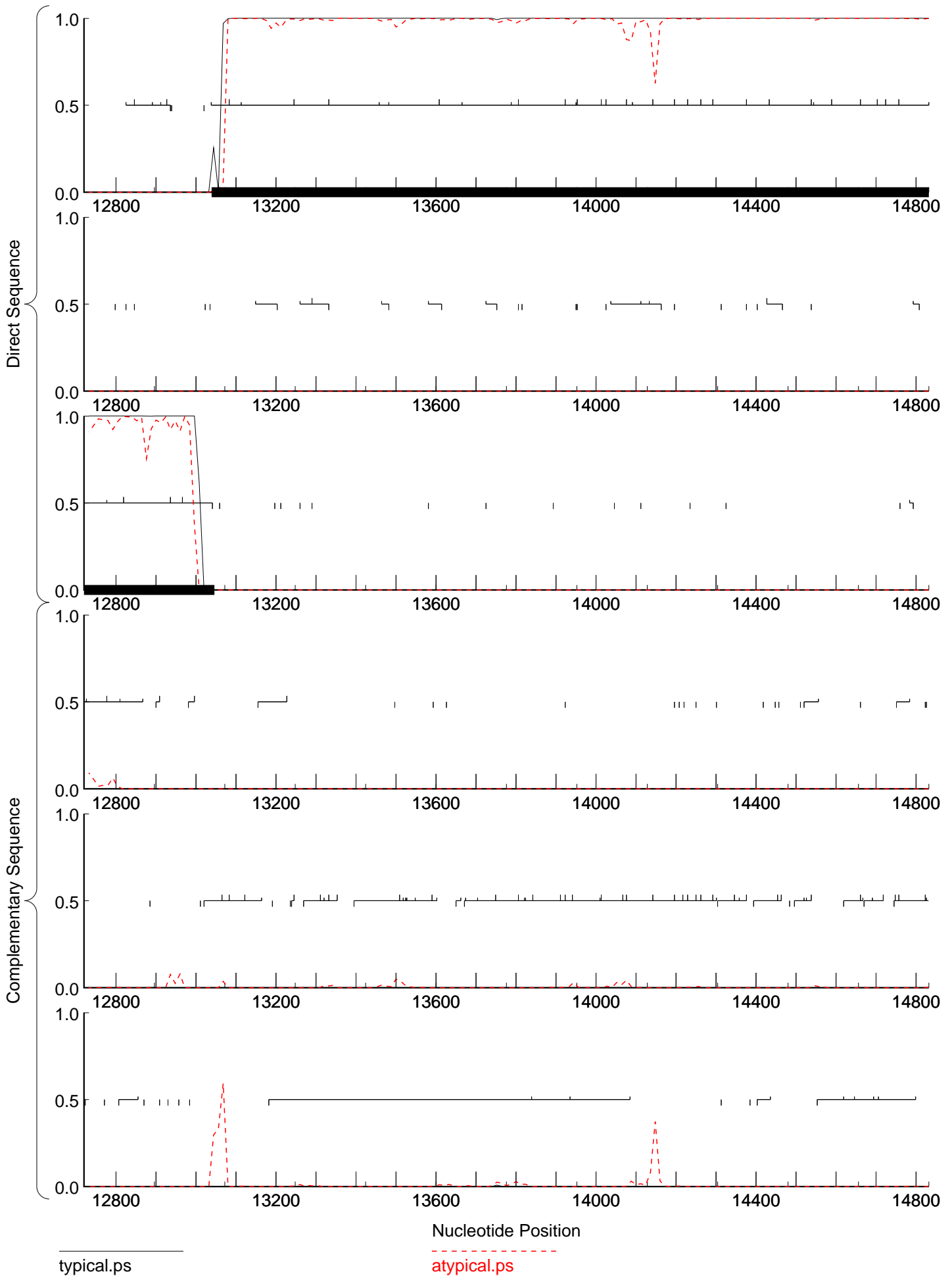






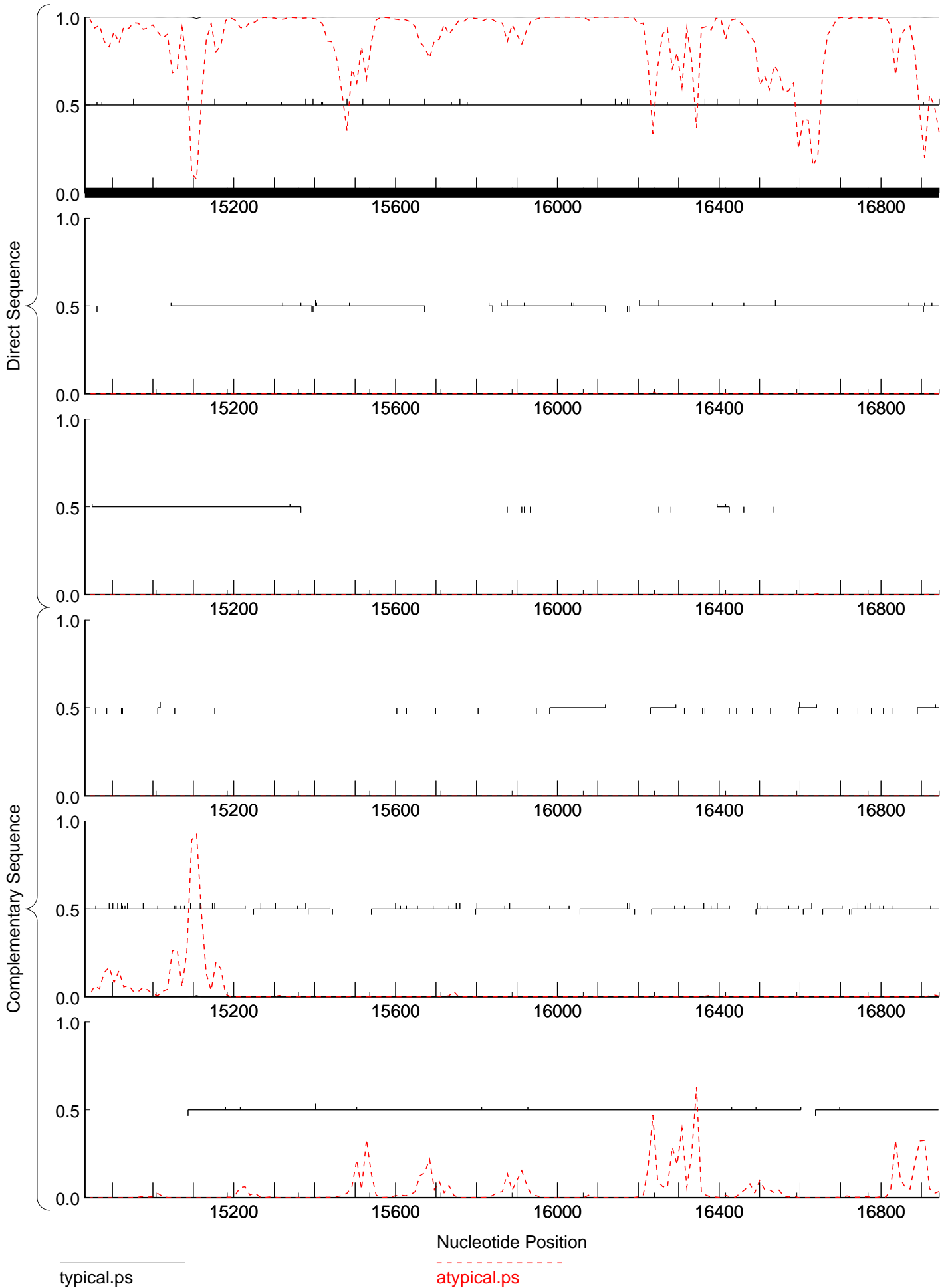


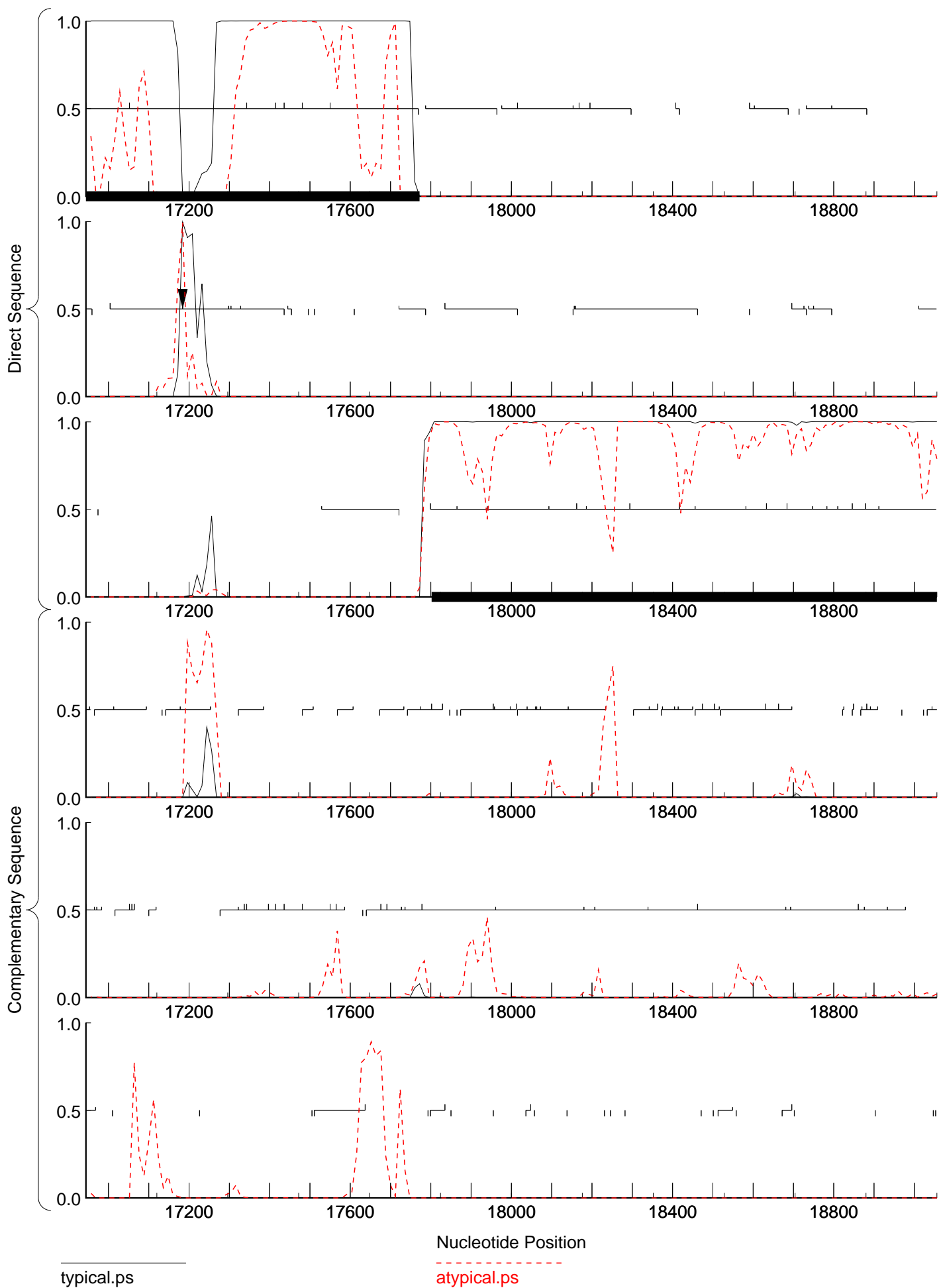


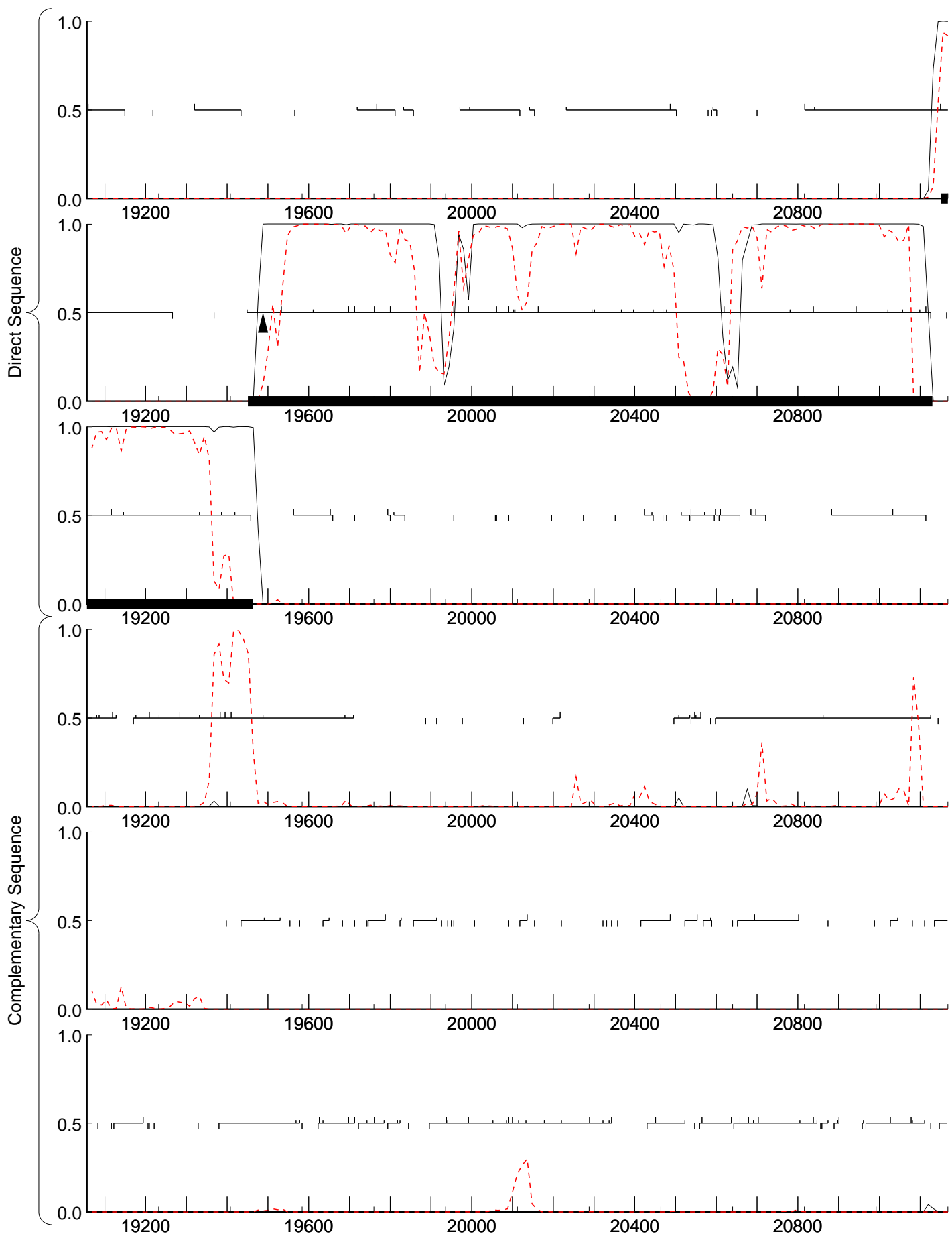


typical.ps

atypical.ps

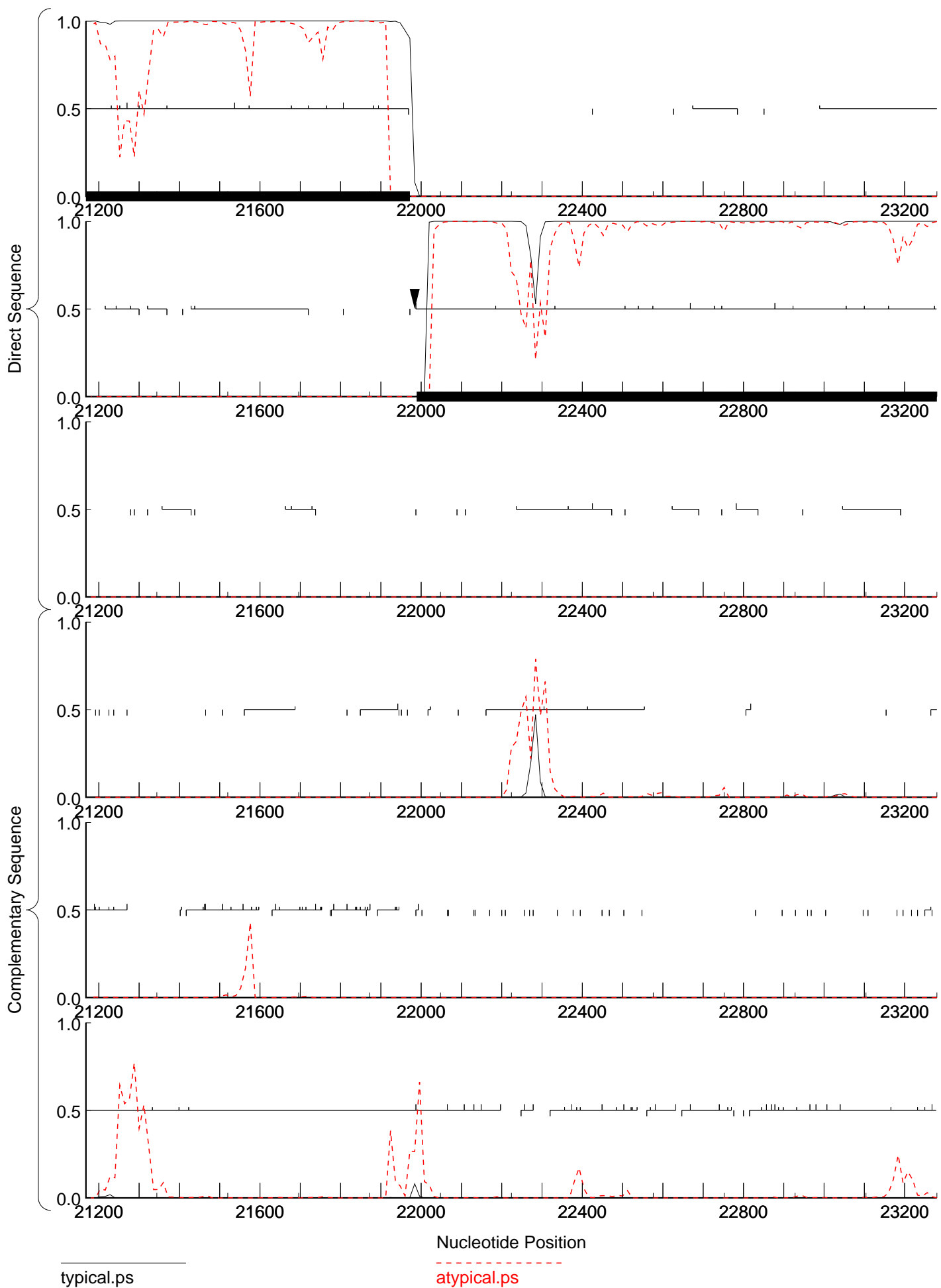






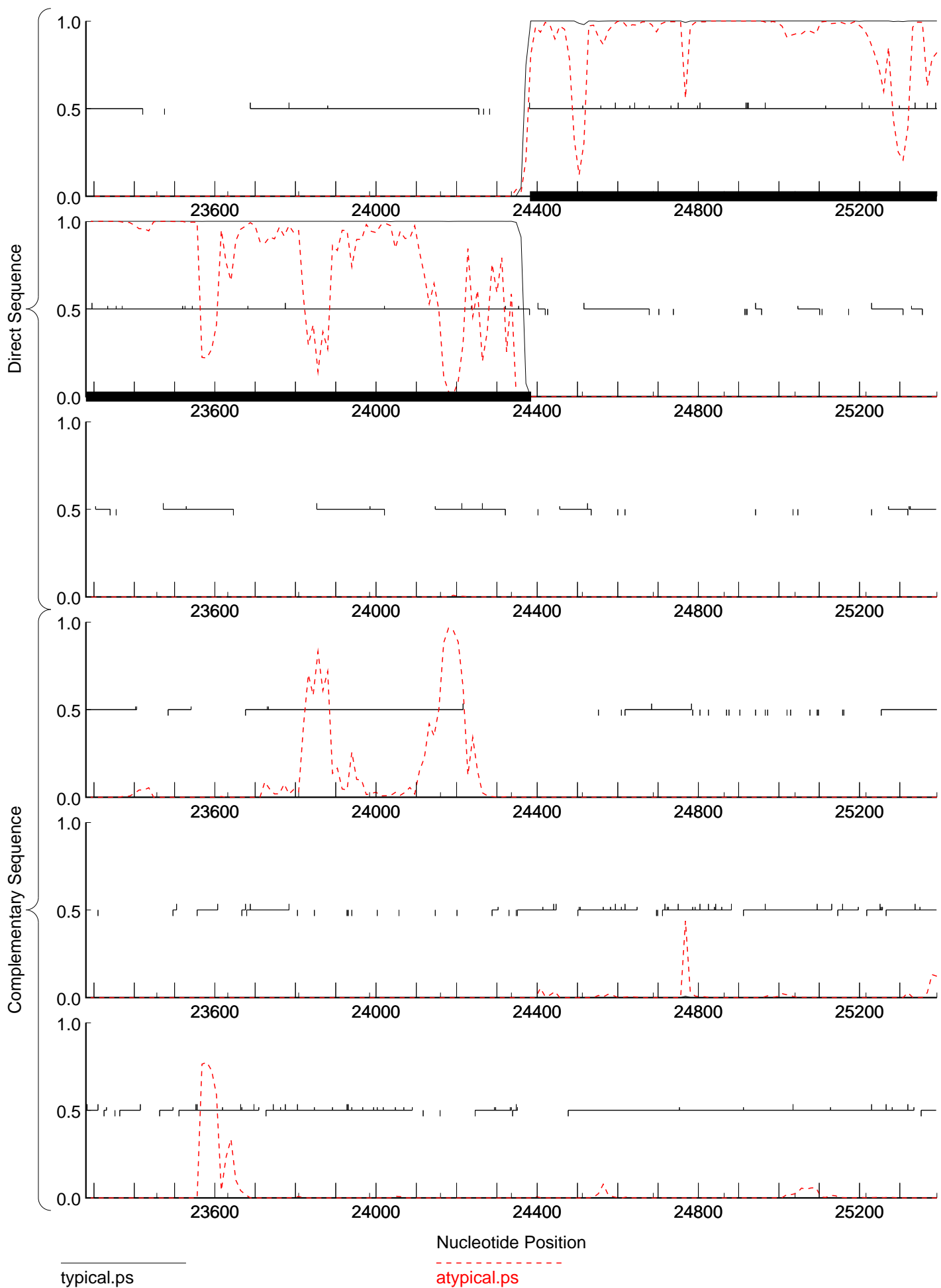
typical.ps

atypical.ps



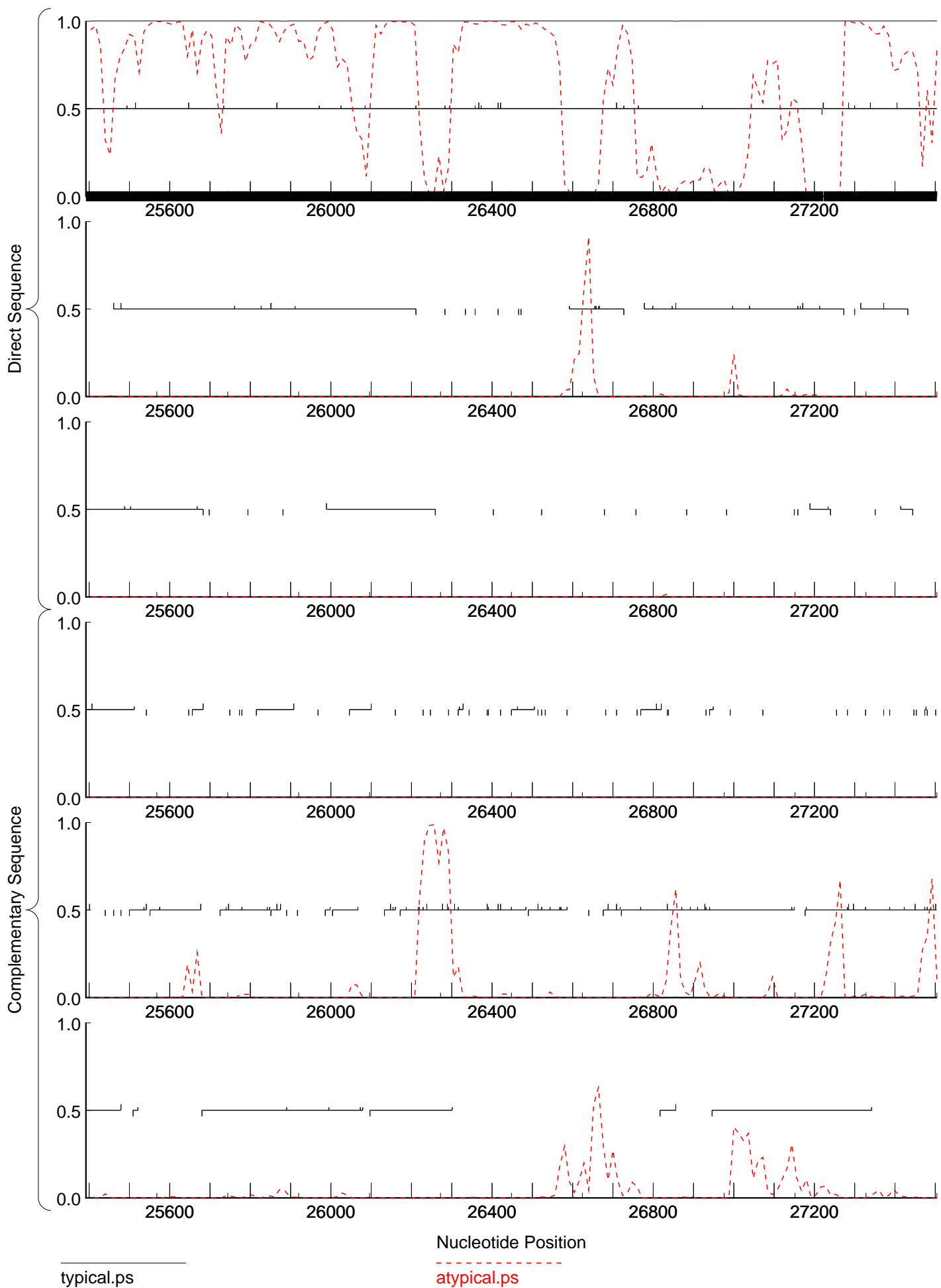
typical.ps

atypical.ps



typical.ps

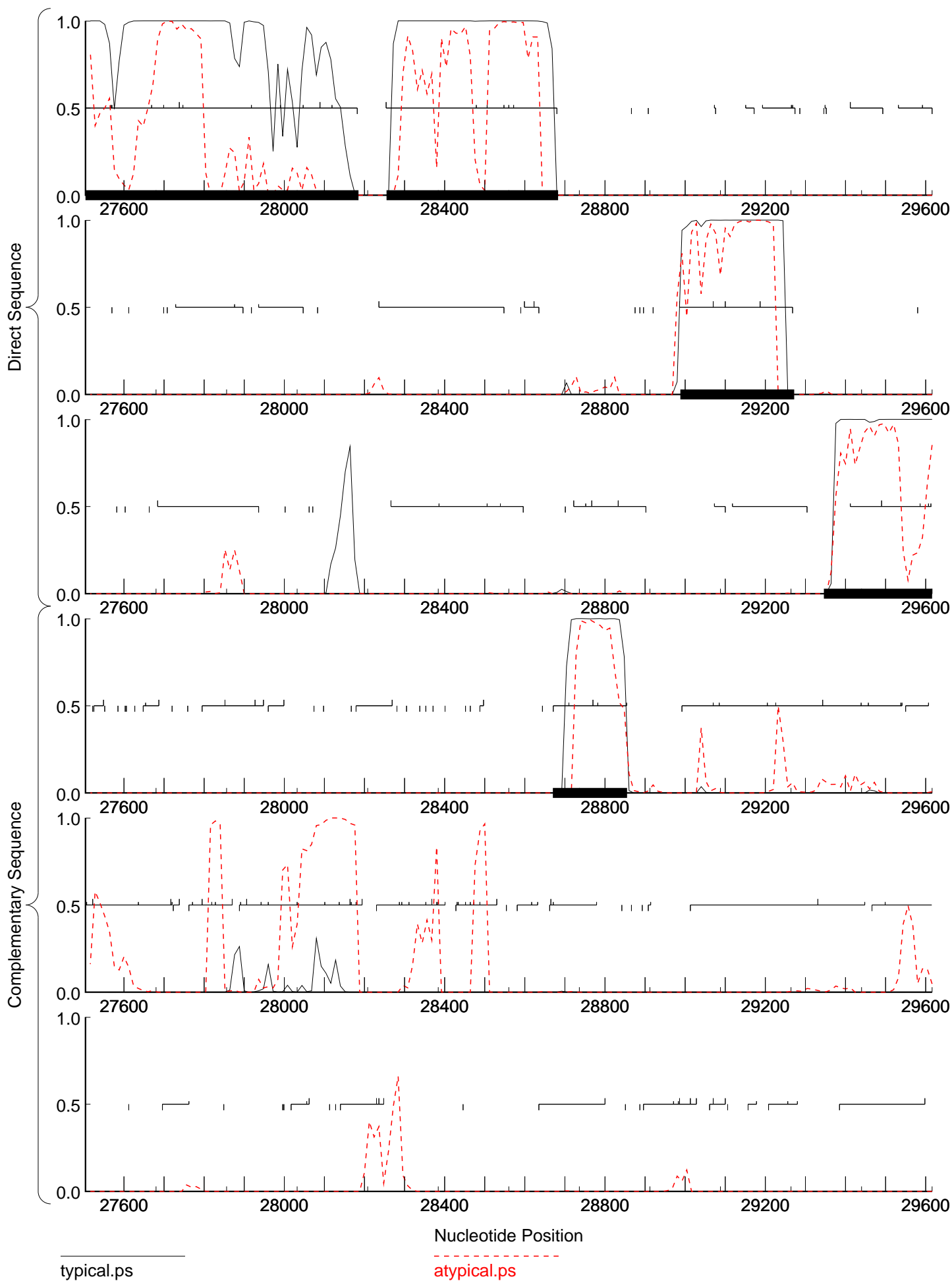
atypical.ps

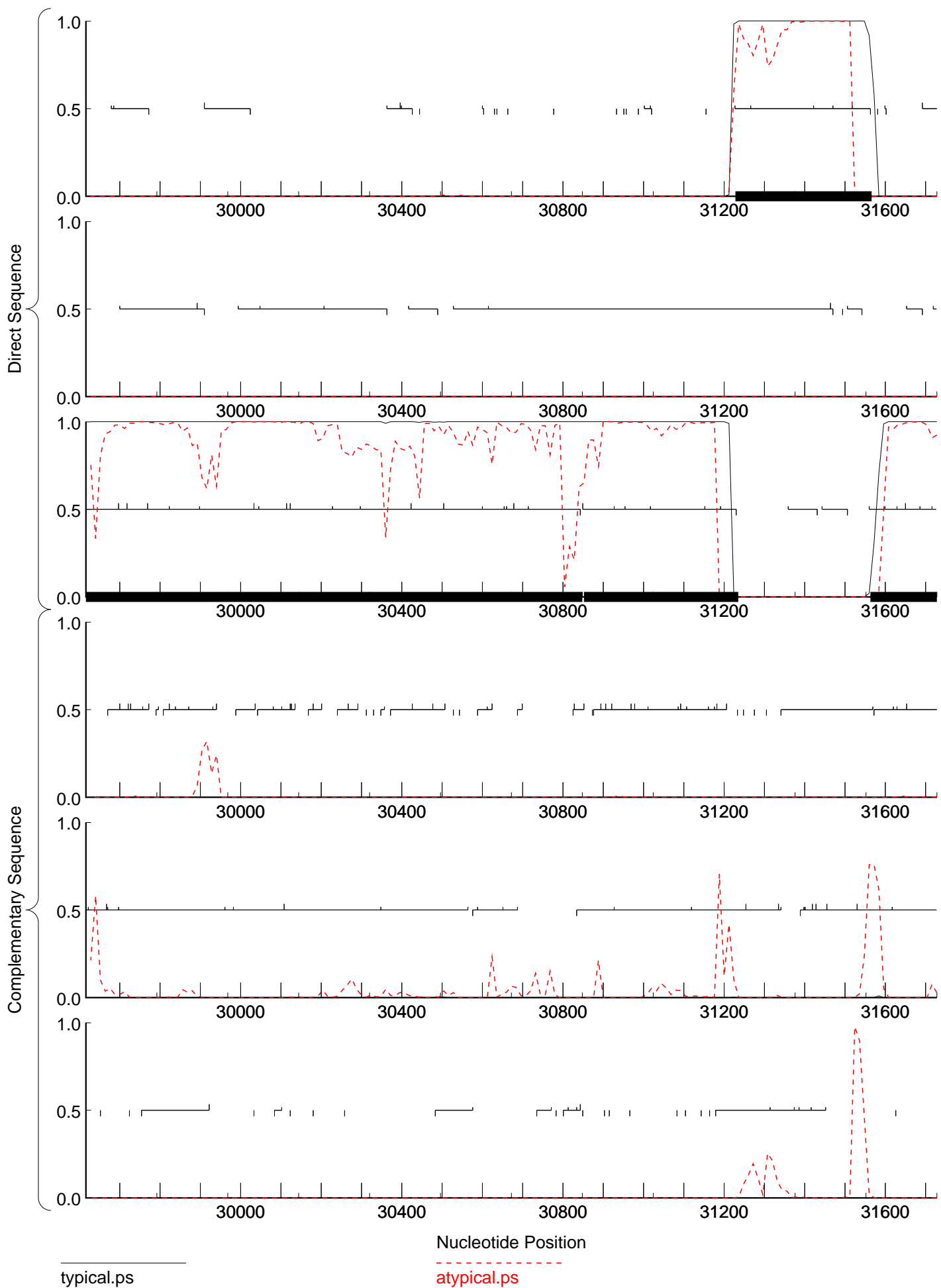


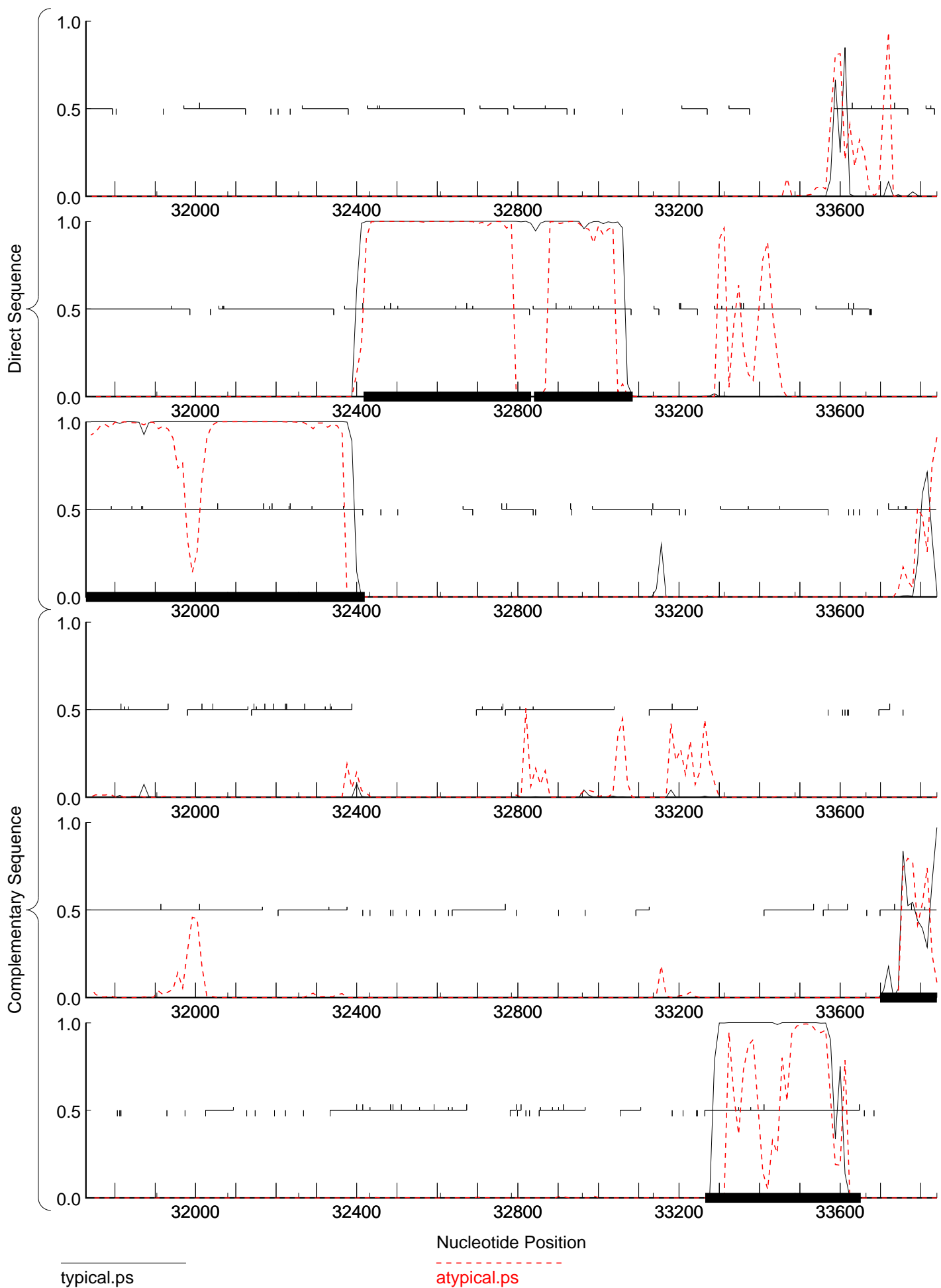
typical.ps

atypical.ps

Lilizi complete sequence, 75360 bp including 9-base 3' overhang (CGCTTGTC A), Cluster E, Order 4, Window 96, Step 12, 15/37
GeneMark.hmm prediction
Lilizi complete sequence, 75360 bp including 9-base 3' overhang (CGCTTGTC A), Cluster E, Order 2, Window 96, Step 12, 15/37

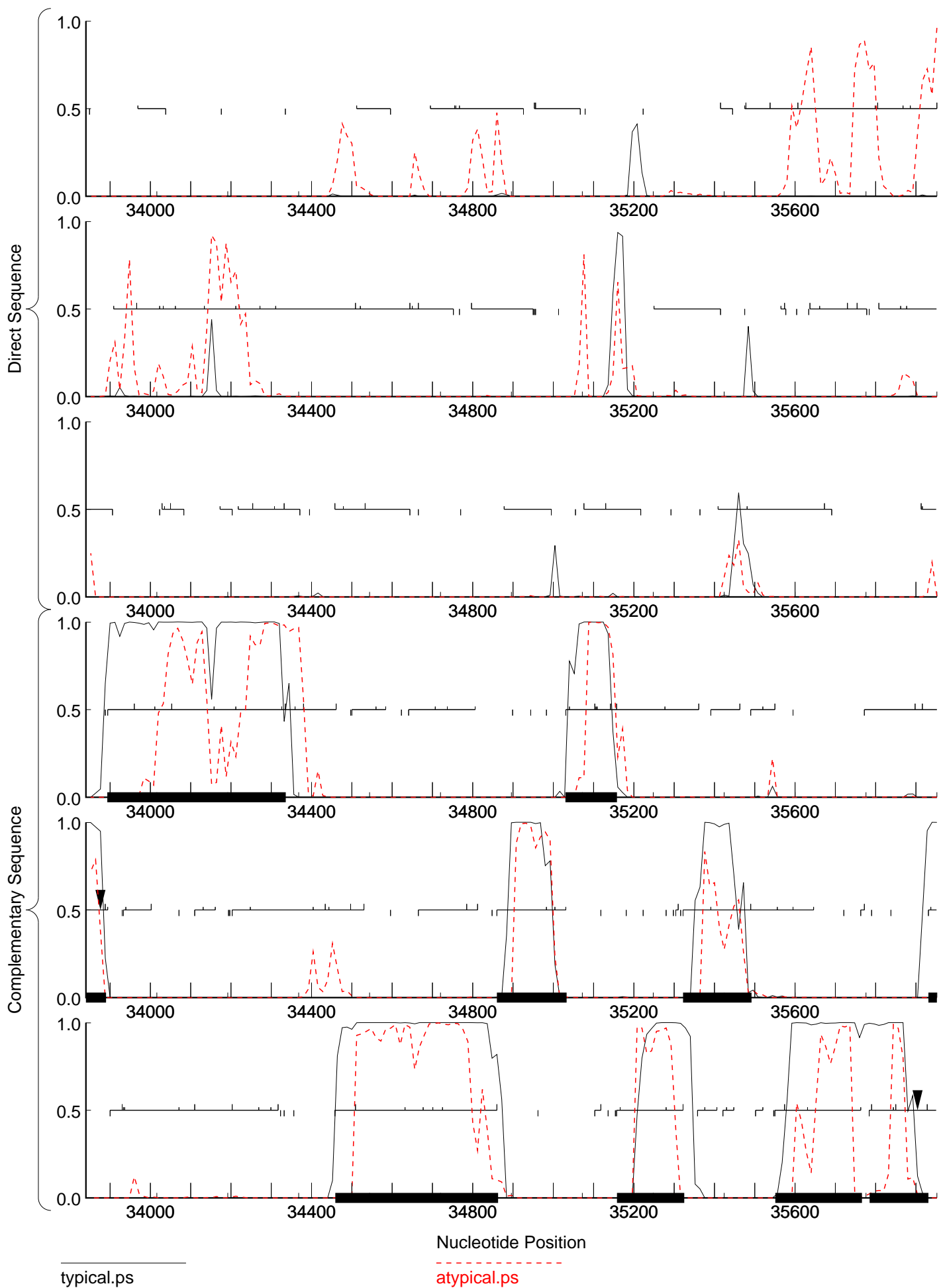


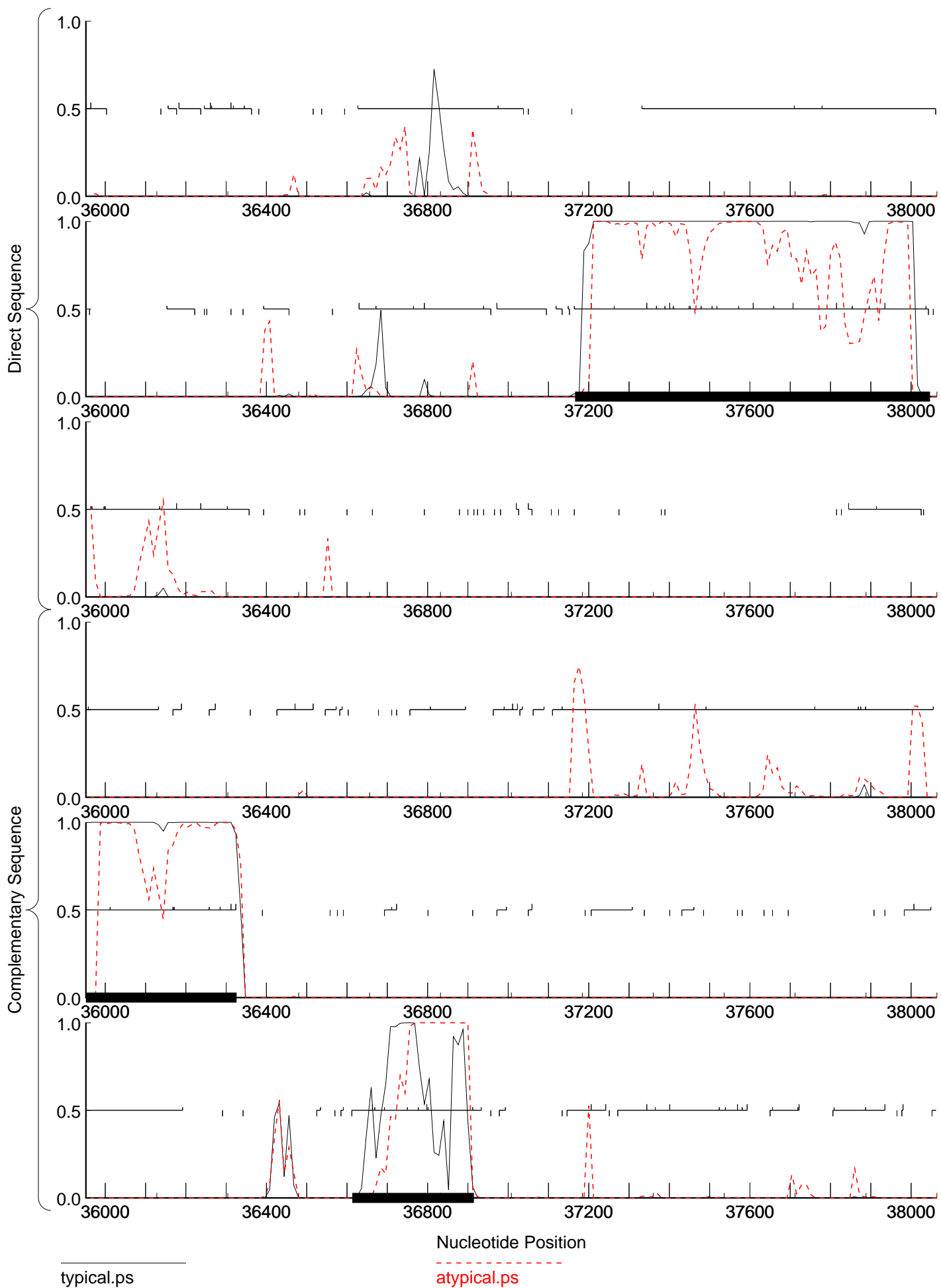


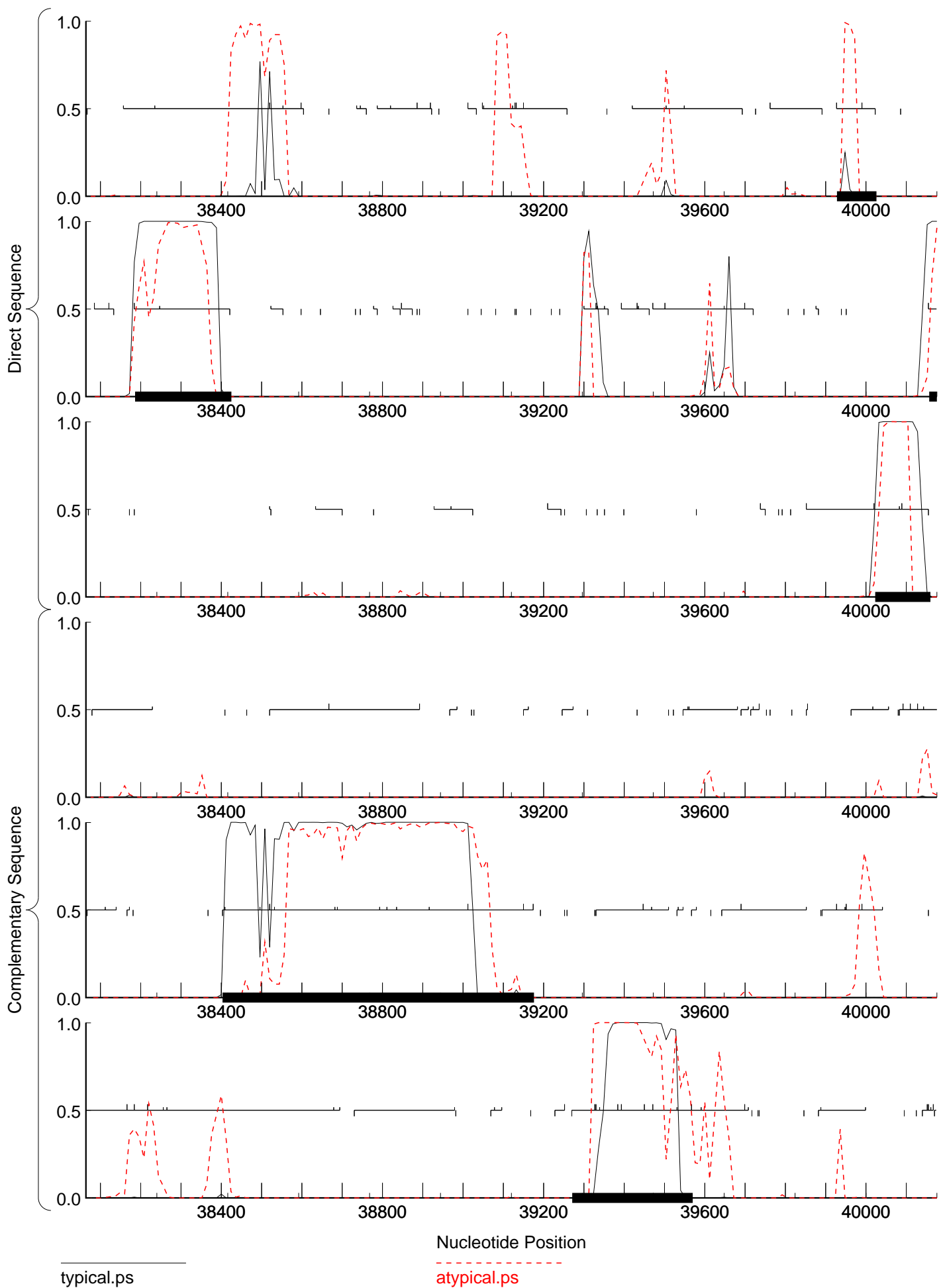


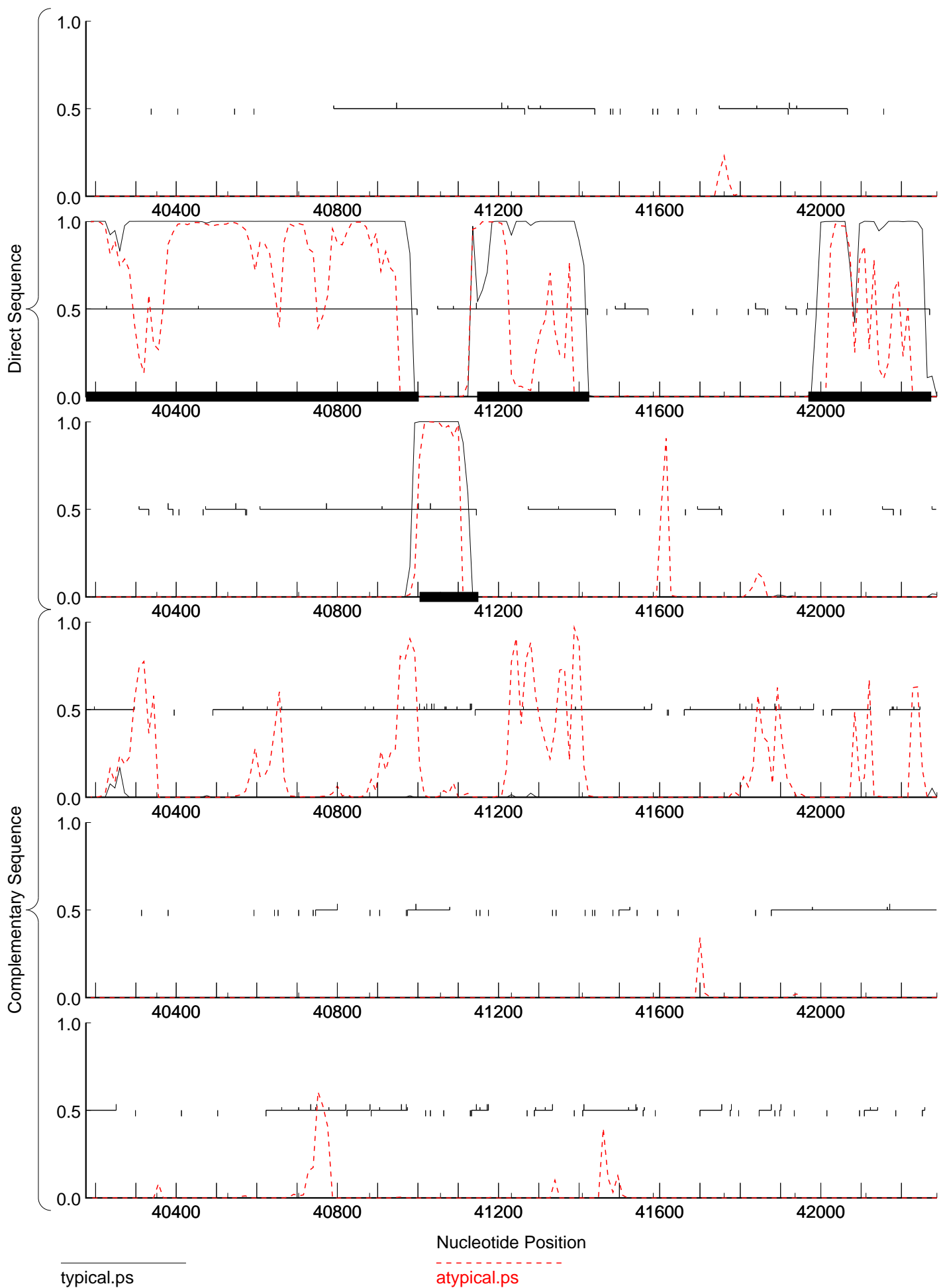
typical.ps

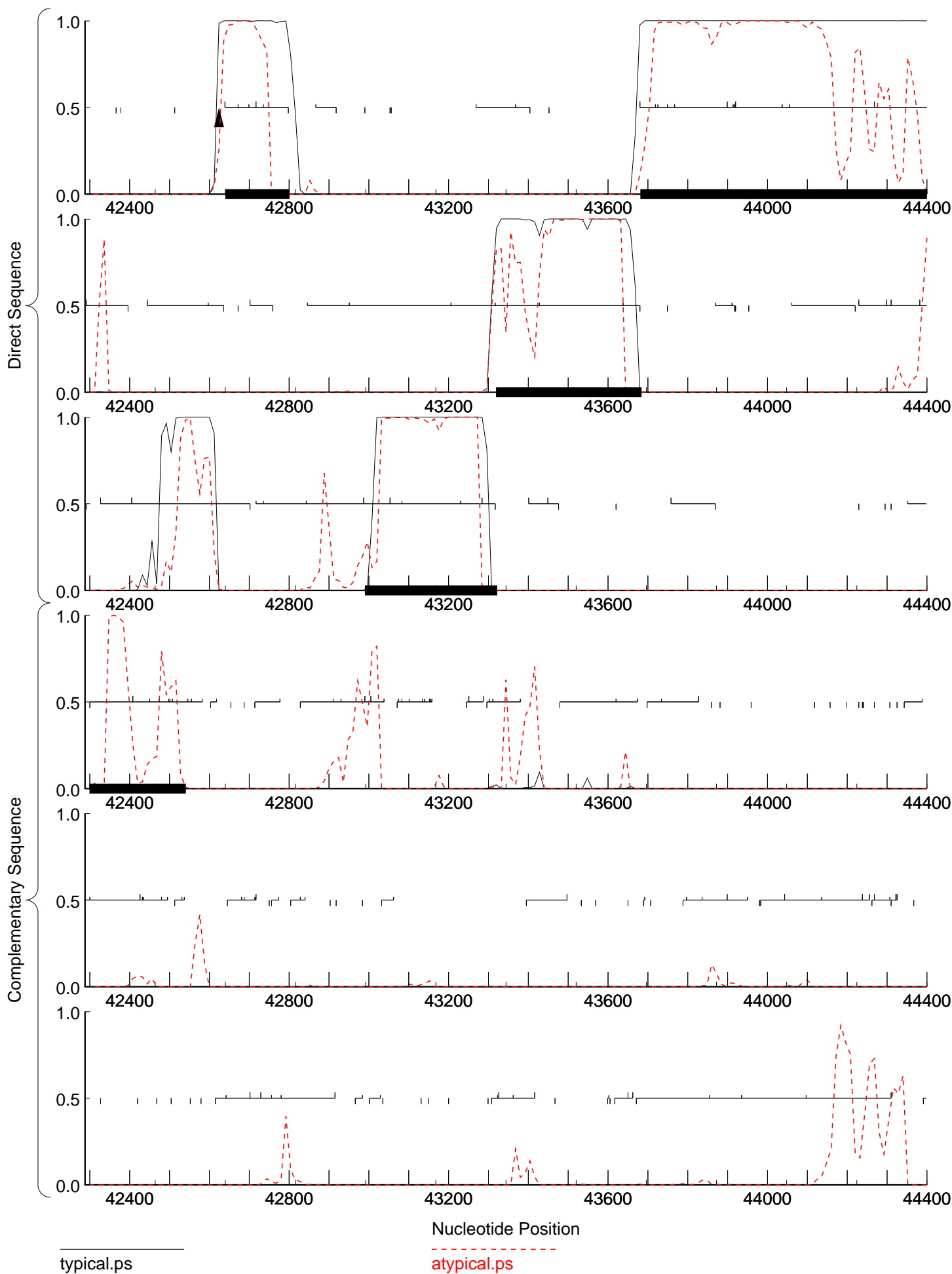
atypical.ps

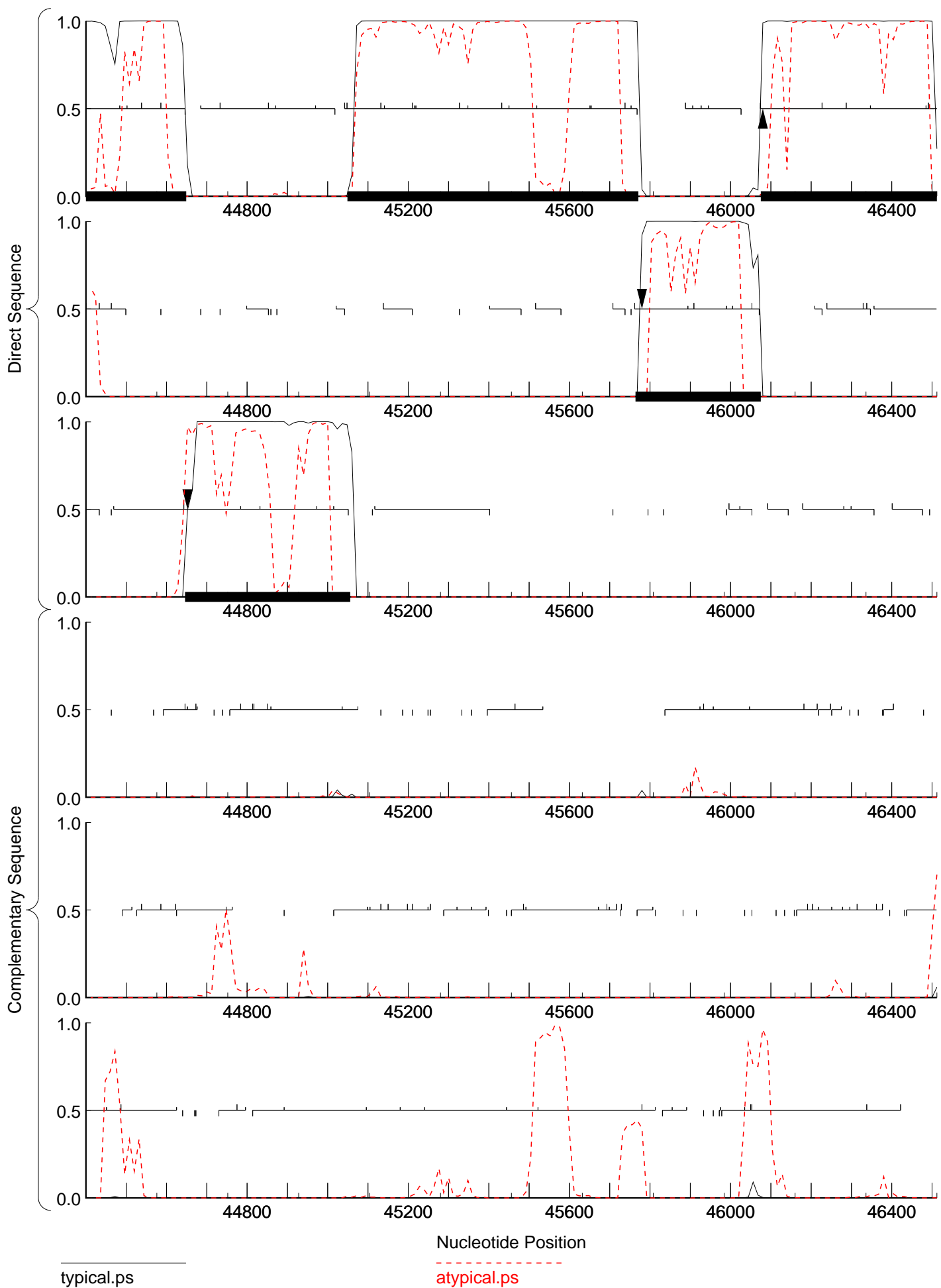


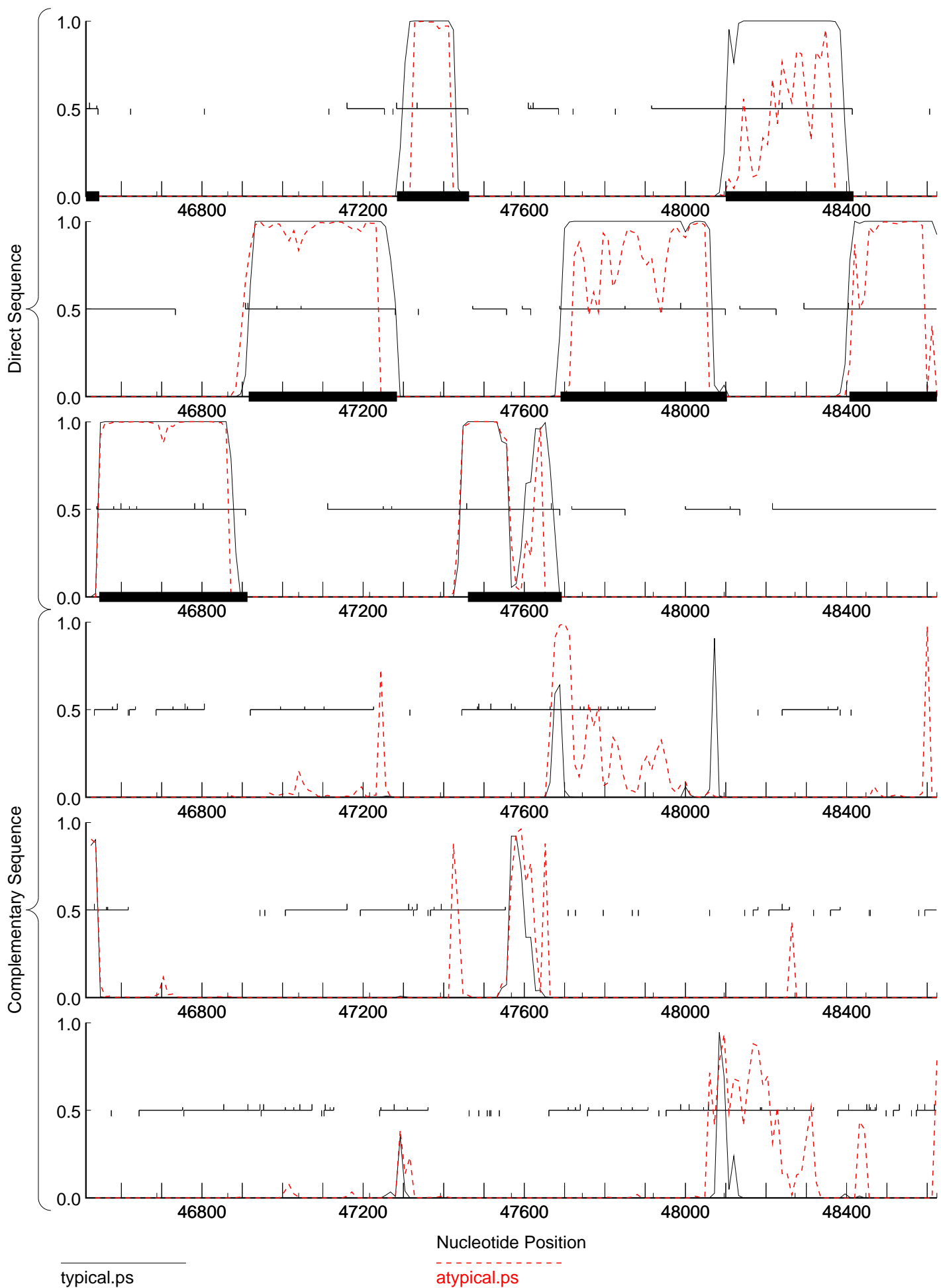


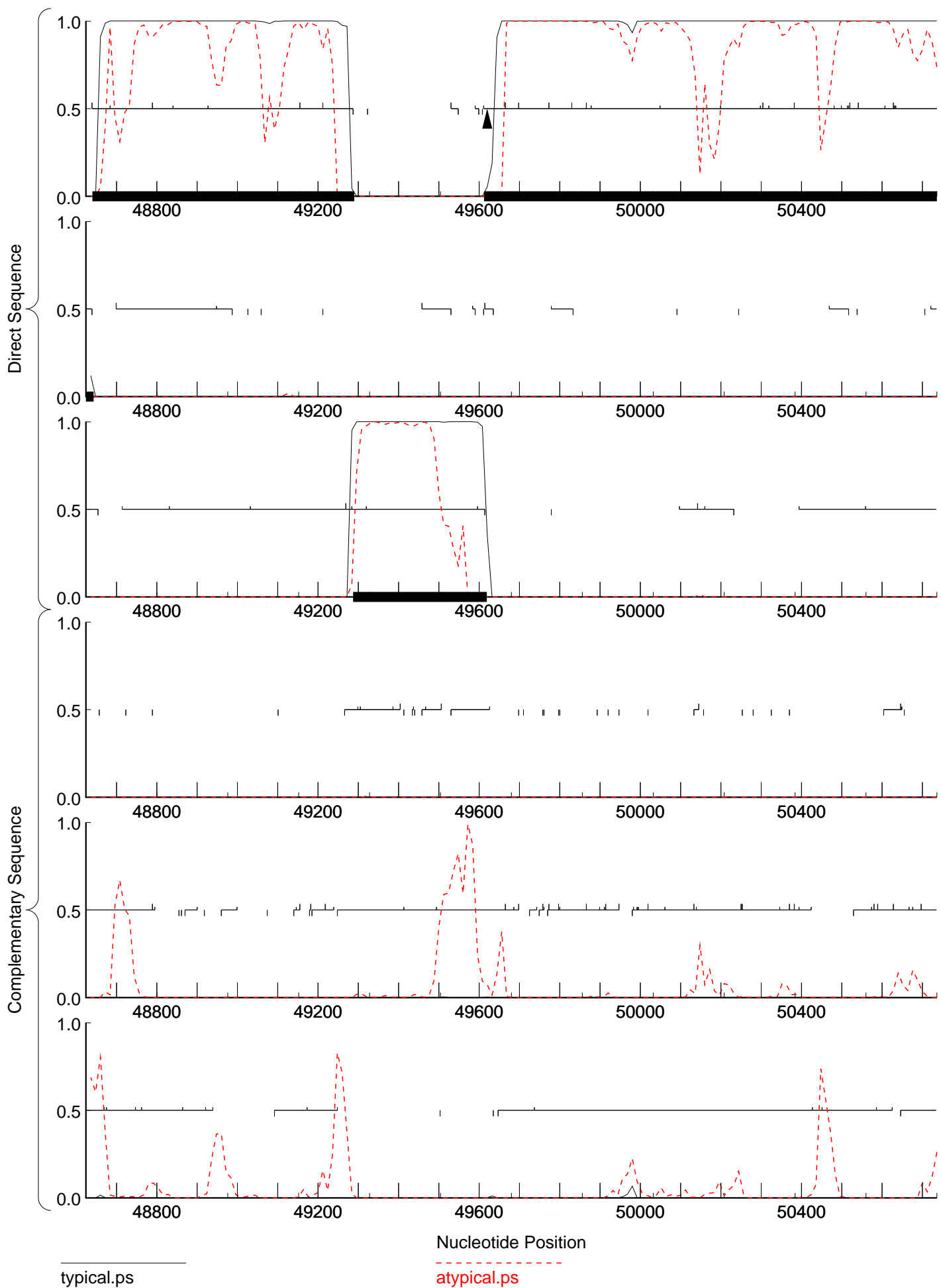


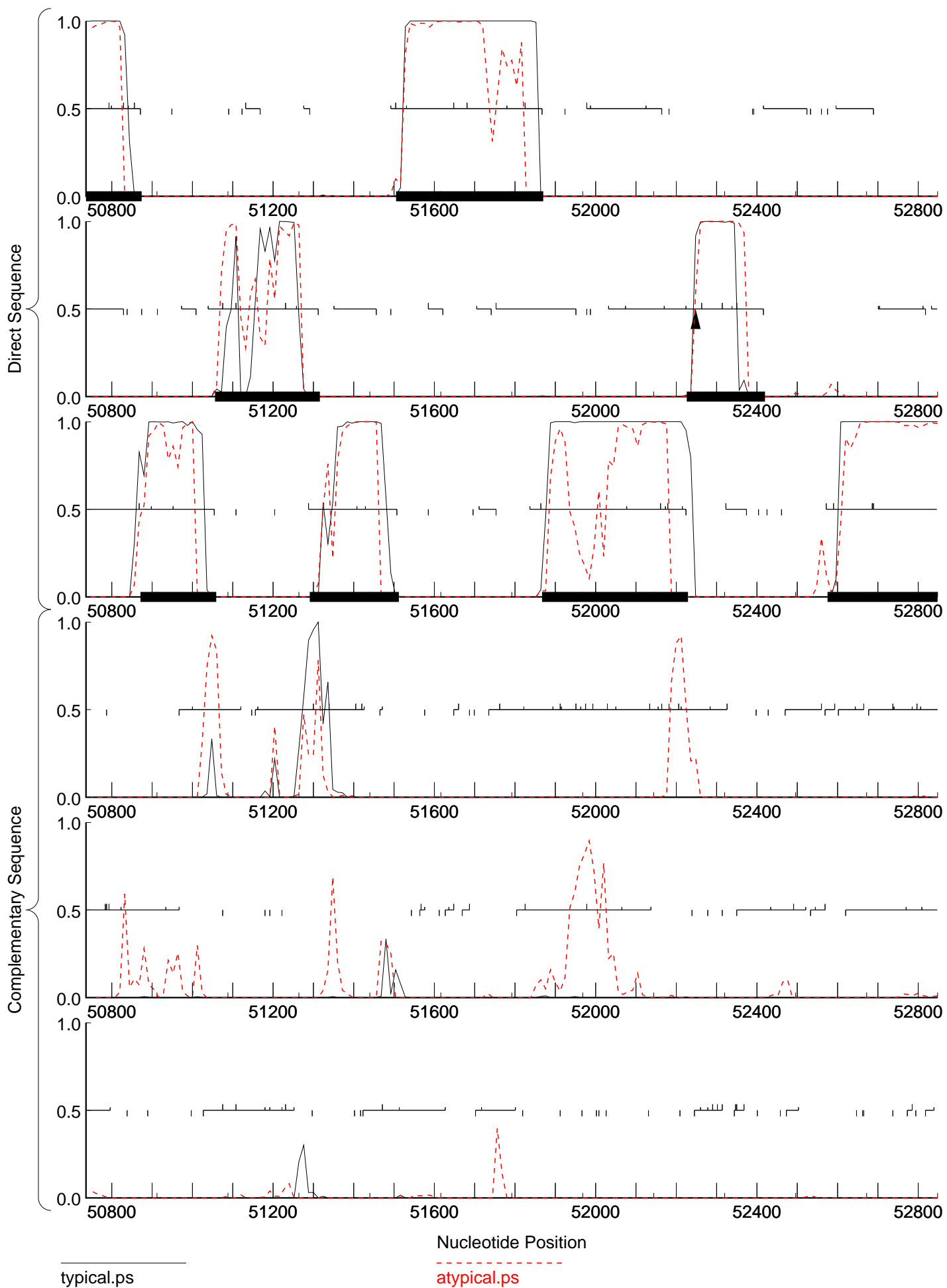






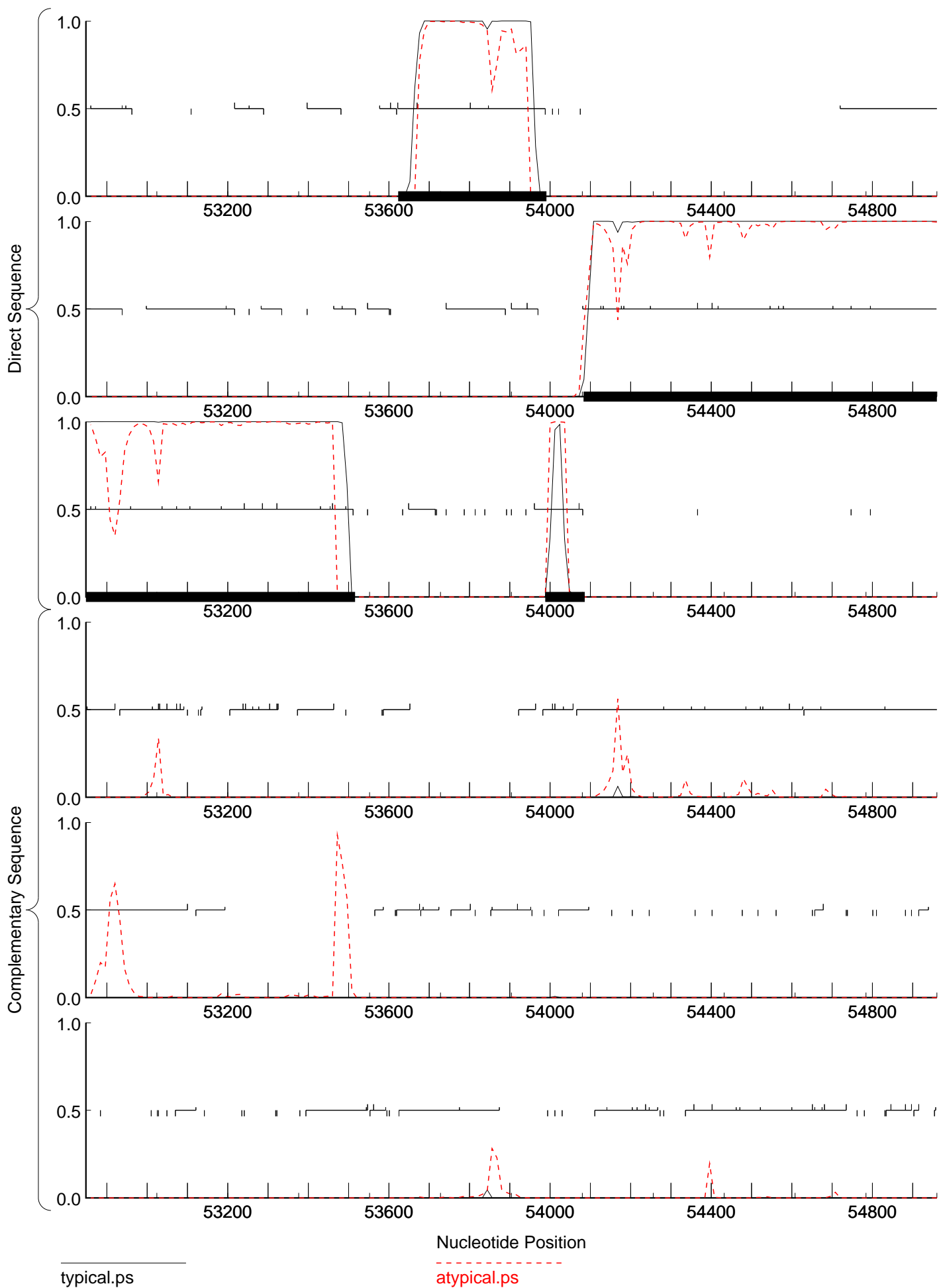


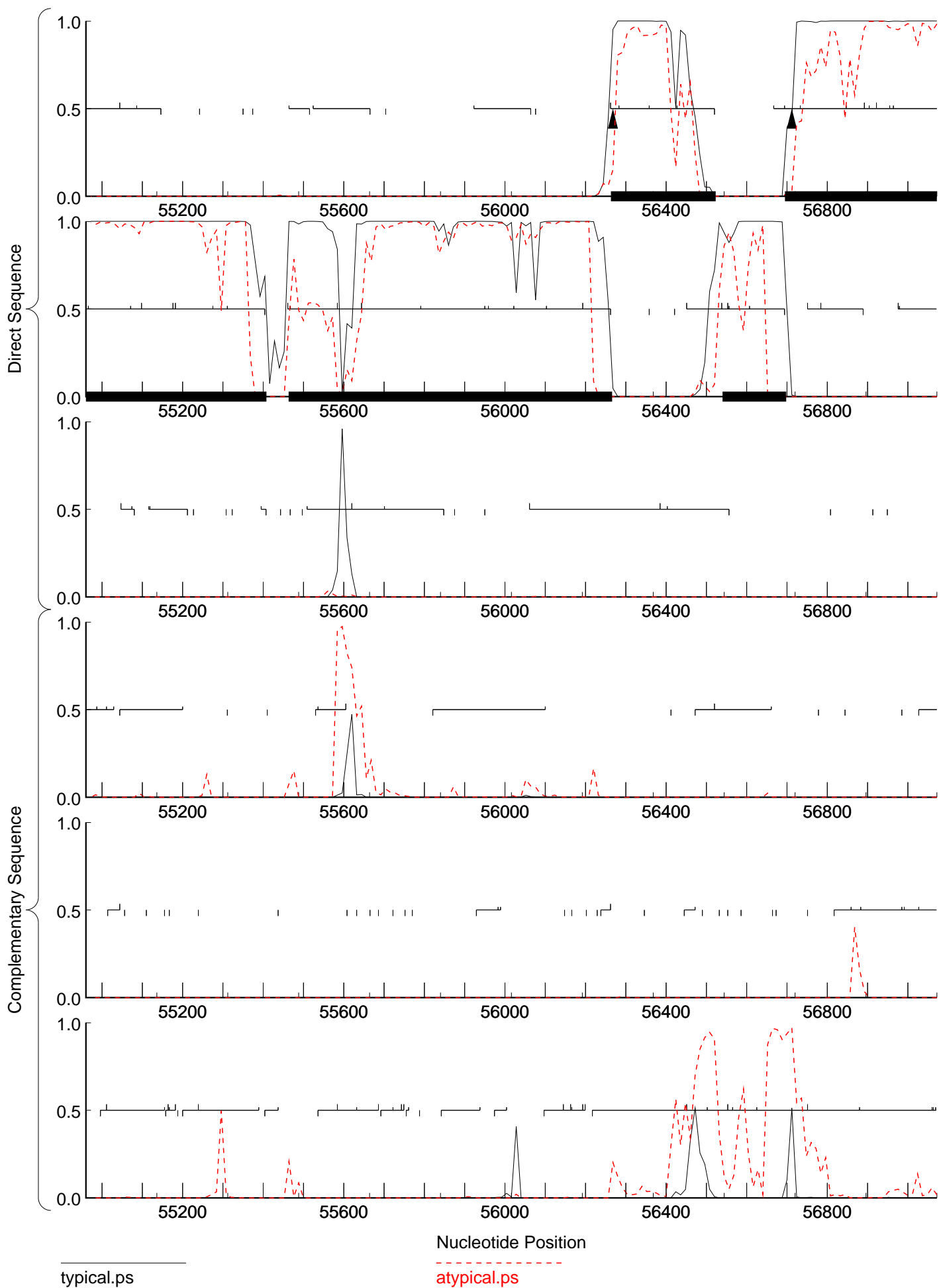




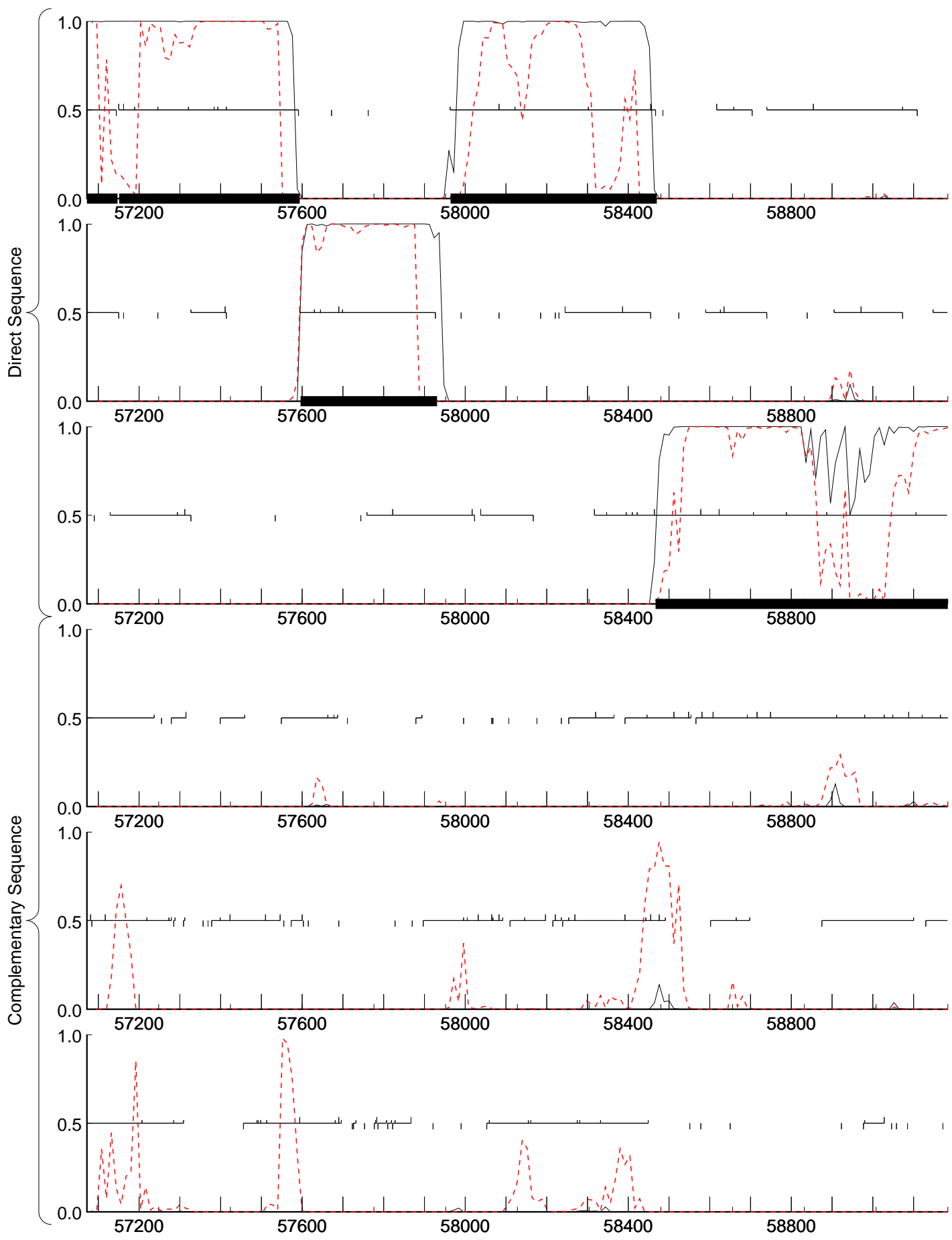
typical.ps

atypical.ps



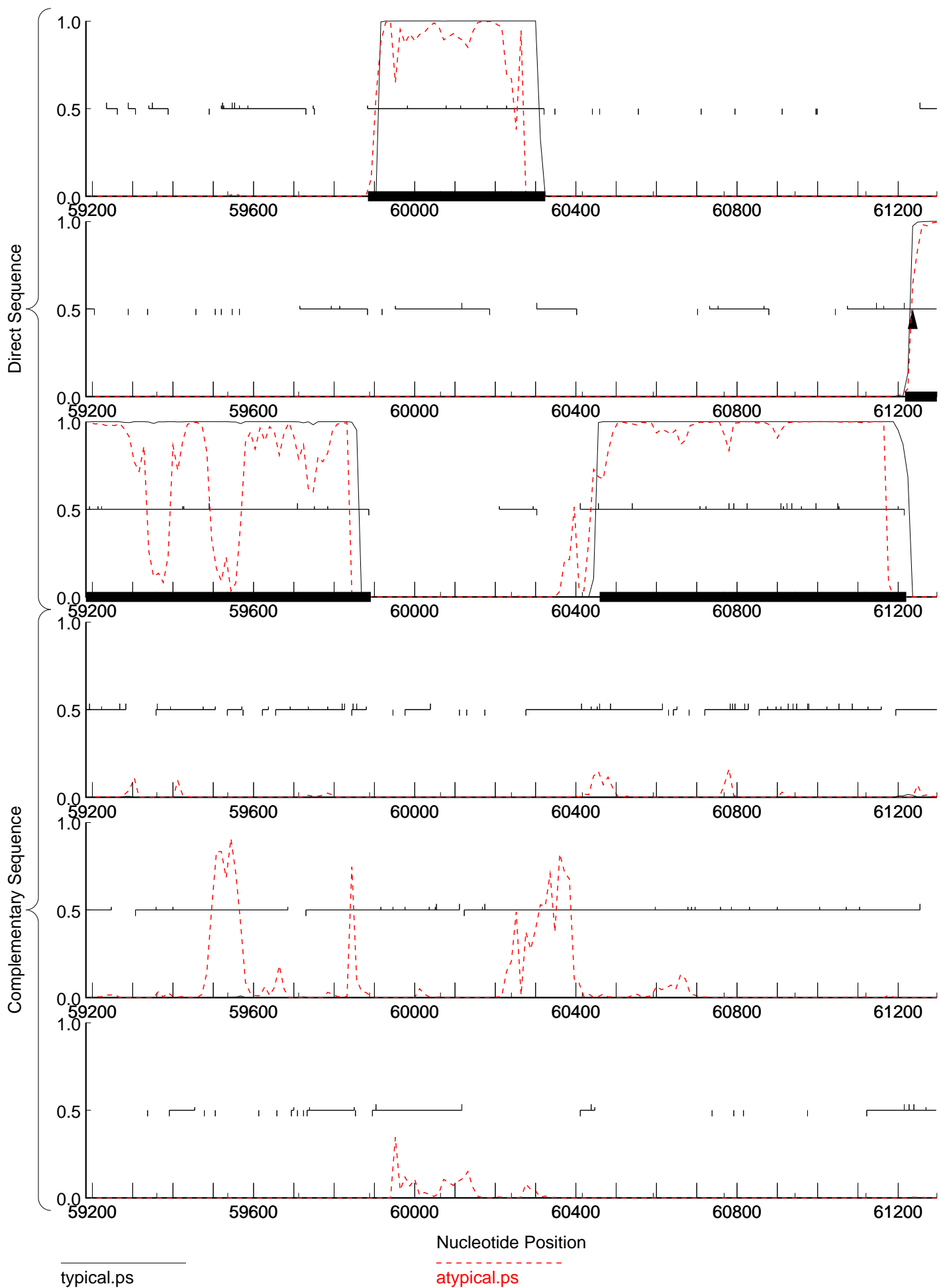


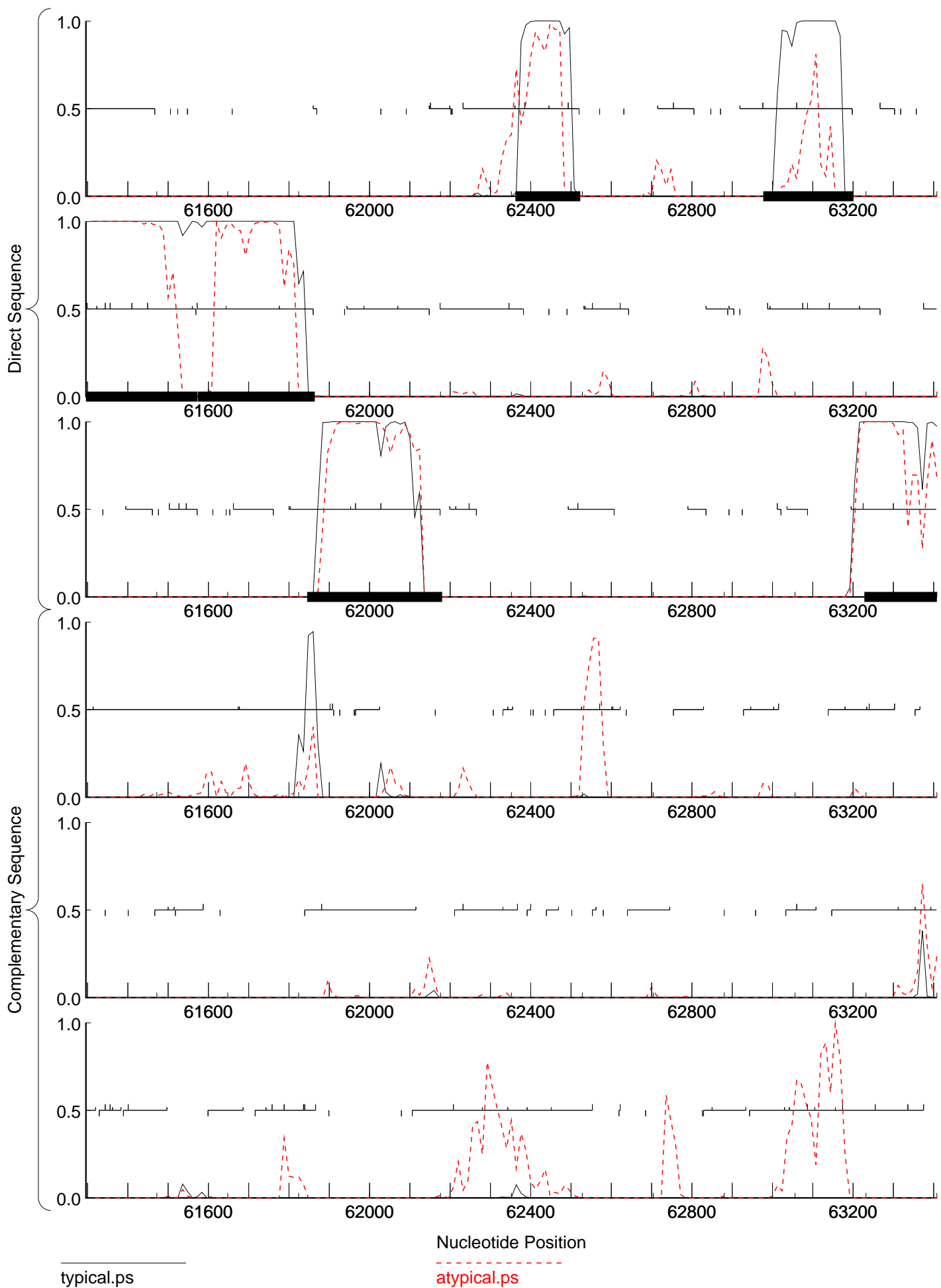
Lilizi complete sequence, 75360 bp including 9-base 3' overhang (CGCTTGTC A), Cluster E, Order 4, Window 96, Step 12, 29/37
GeneMark.hmm prediction
Lilizi complete sequence, 75360 bp including 9-base 3' overhang (CGCTTGTC A), Cluster E, Order 2, Window 96, Step 12, 29/37

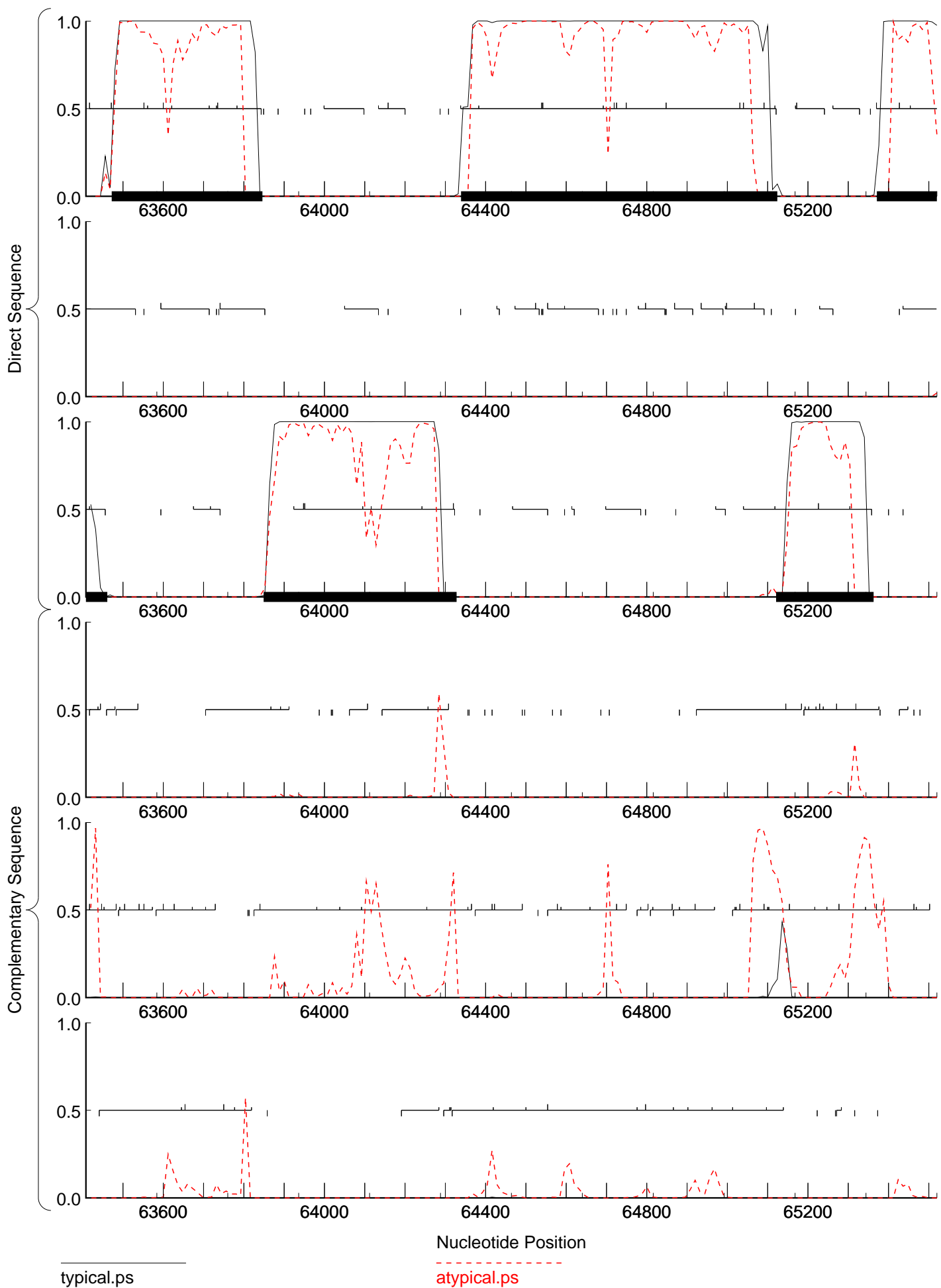


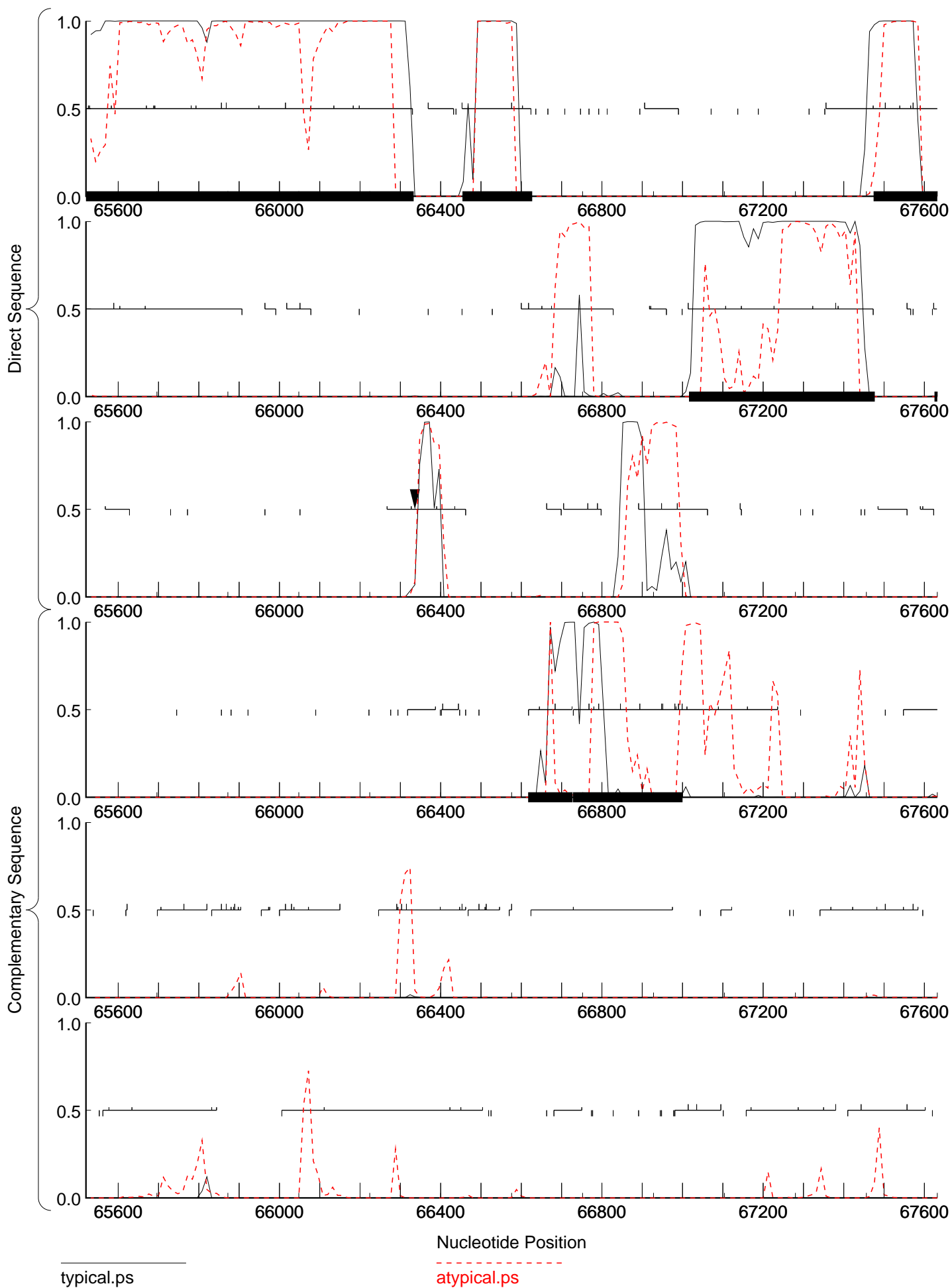
typical.ps

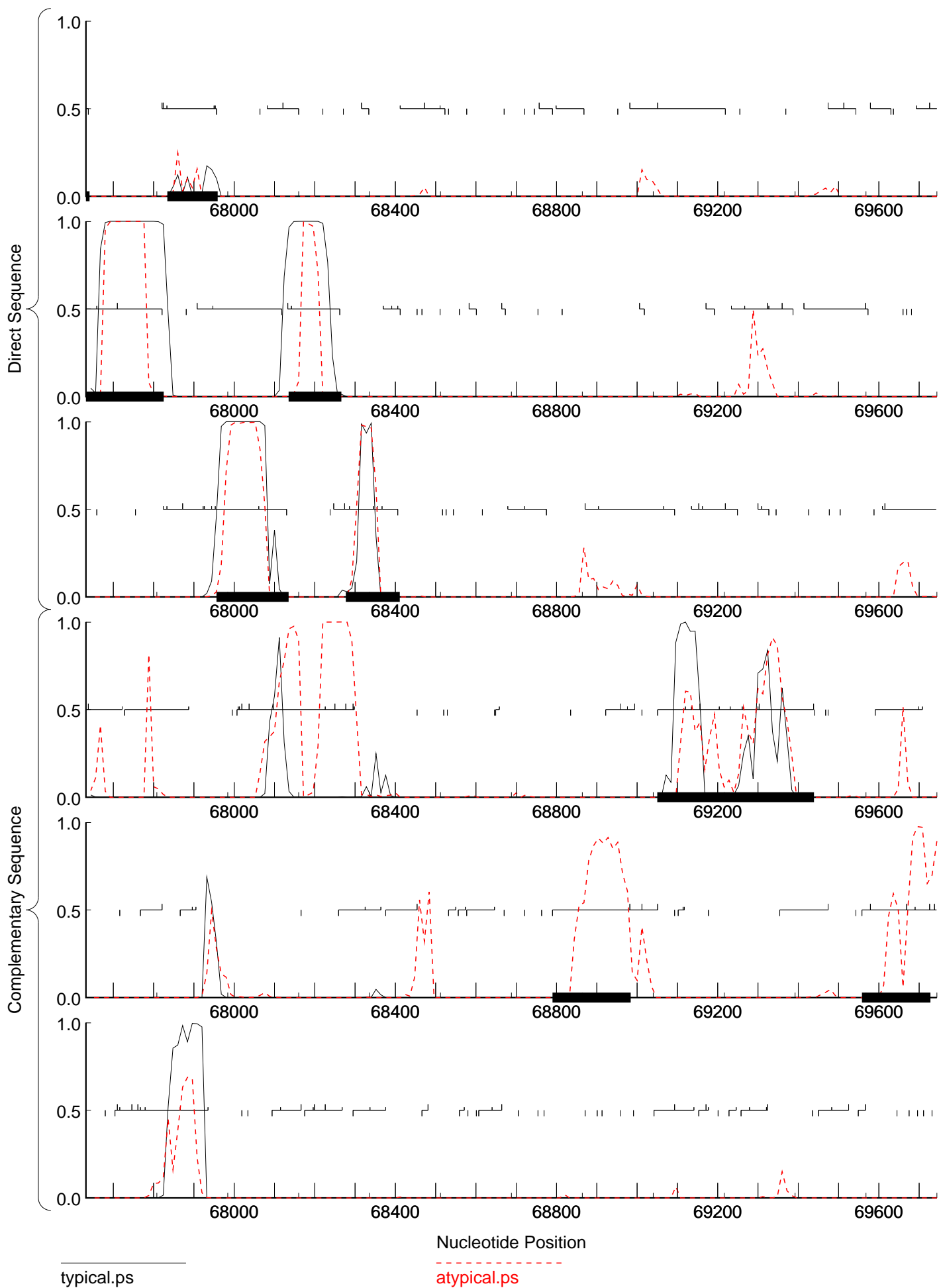
atypical.ps

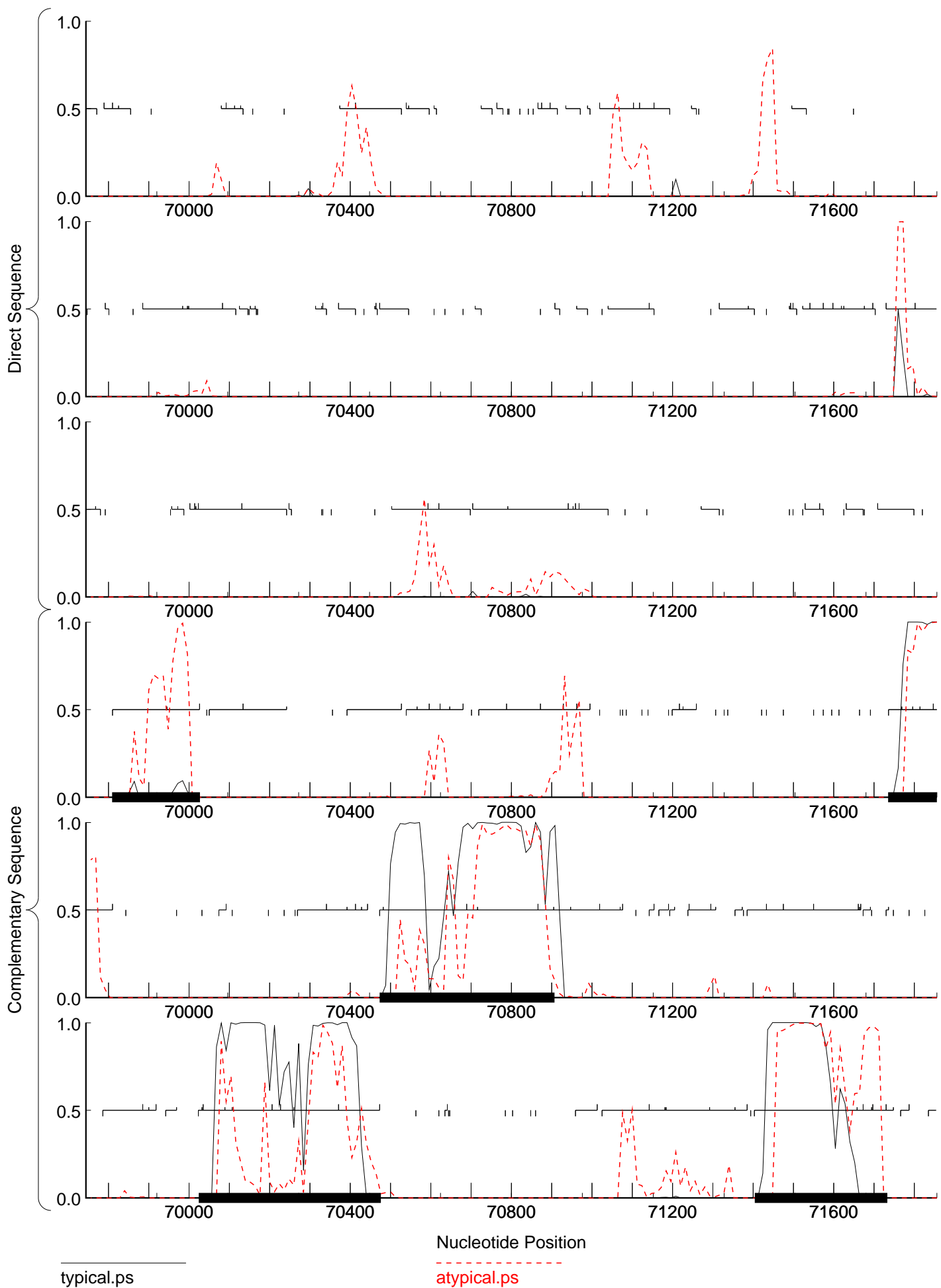






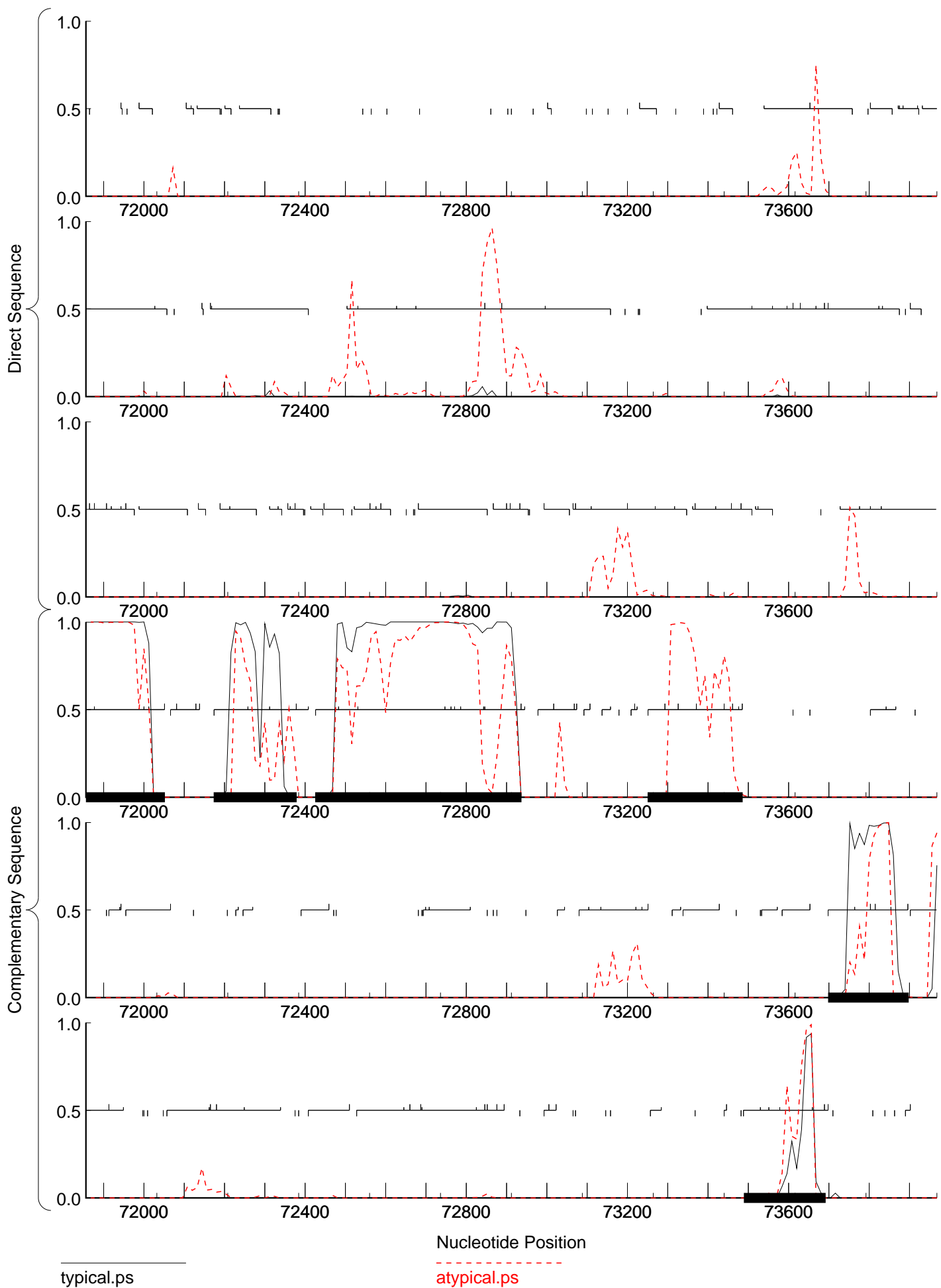






typical.ps

atypical.ps



typical.ps

atypical.ps

Lilizi complete sequence, 75360 bp including 9-base 3' overhang (CGCTTGTC A), Cluster E, Order 4, Window 96, Step 12, 37/37
GeneMark.hmm prediction
Lilizi complete sequence, 75360 bp including 9-base 3' overhang (CGCTTGTC A), Cluster E, Order 2, Window 96, Step 12, 37/37

