

GeneMark

Version 2.5p (09.08.06)

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PROGRAM INFORMATION

Sequence : Streptomyces phage Gilson complete sequence, 128338 bp including 766 bp terminal repeat, Cl
Analysis Date : 2/24/18 at 2:59:56
Pages : 62
Sequence Length : 128338 bp
GC Content : 47.44%

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,

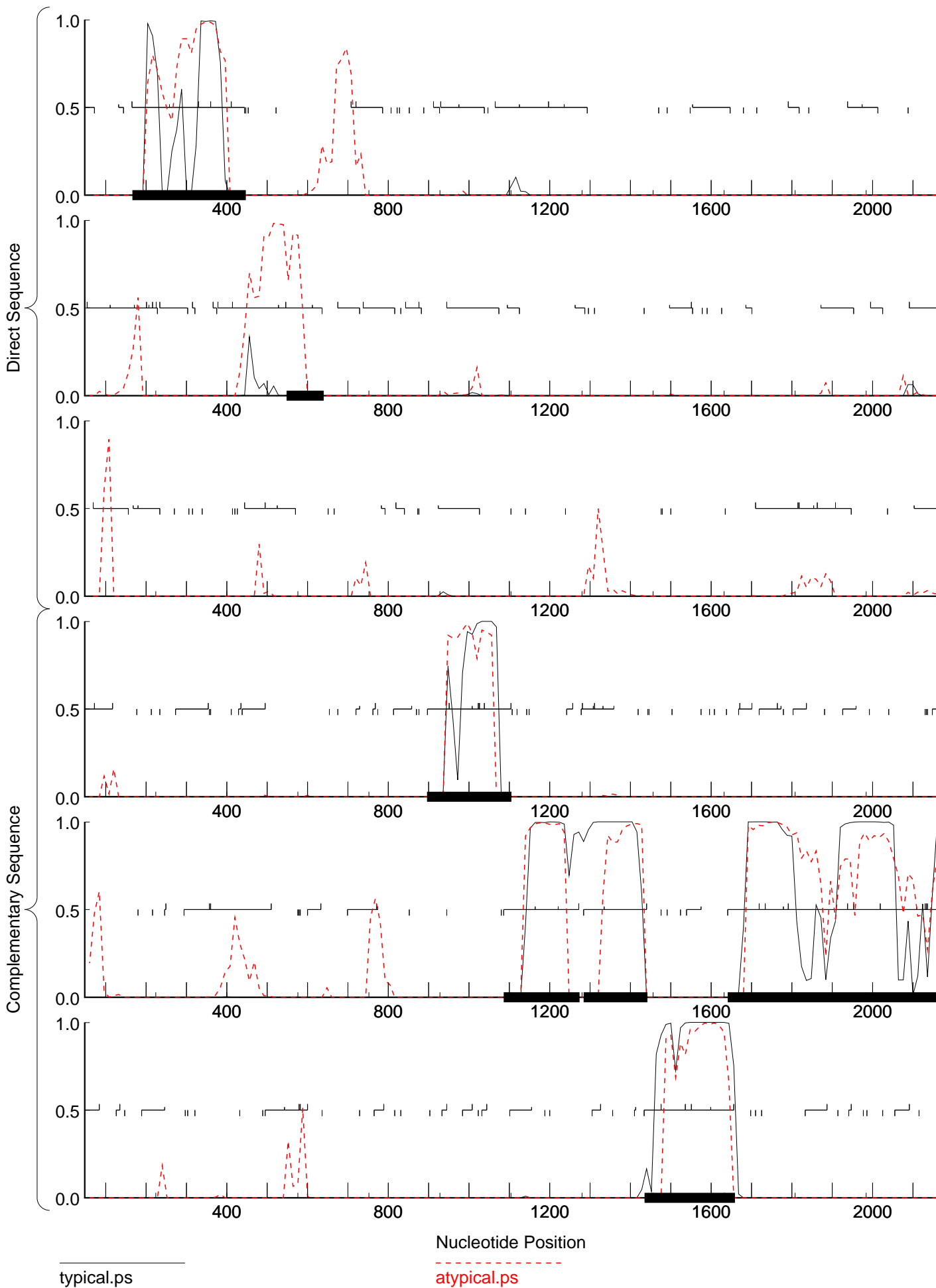
MATRIX INFORMATION

Matrix : -
Author : -
Order : 4

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

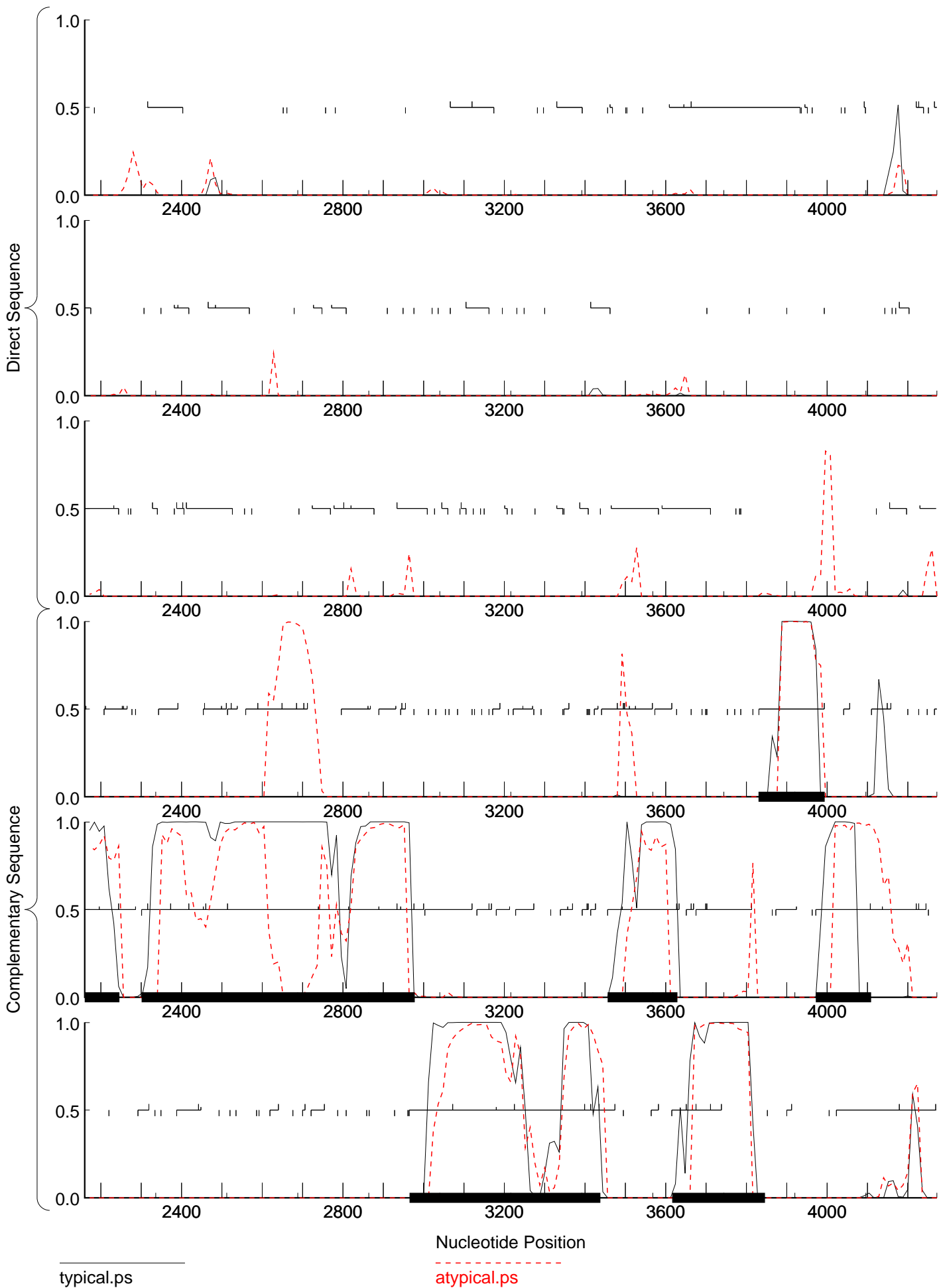
Matrix notes & comments

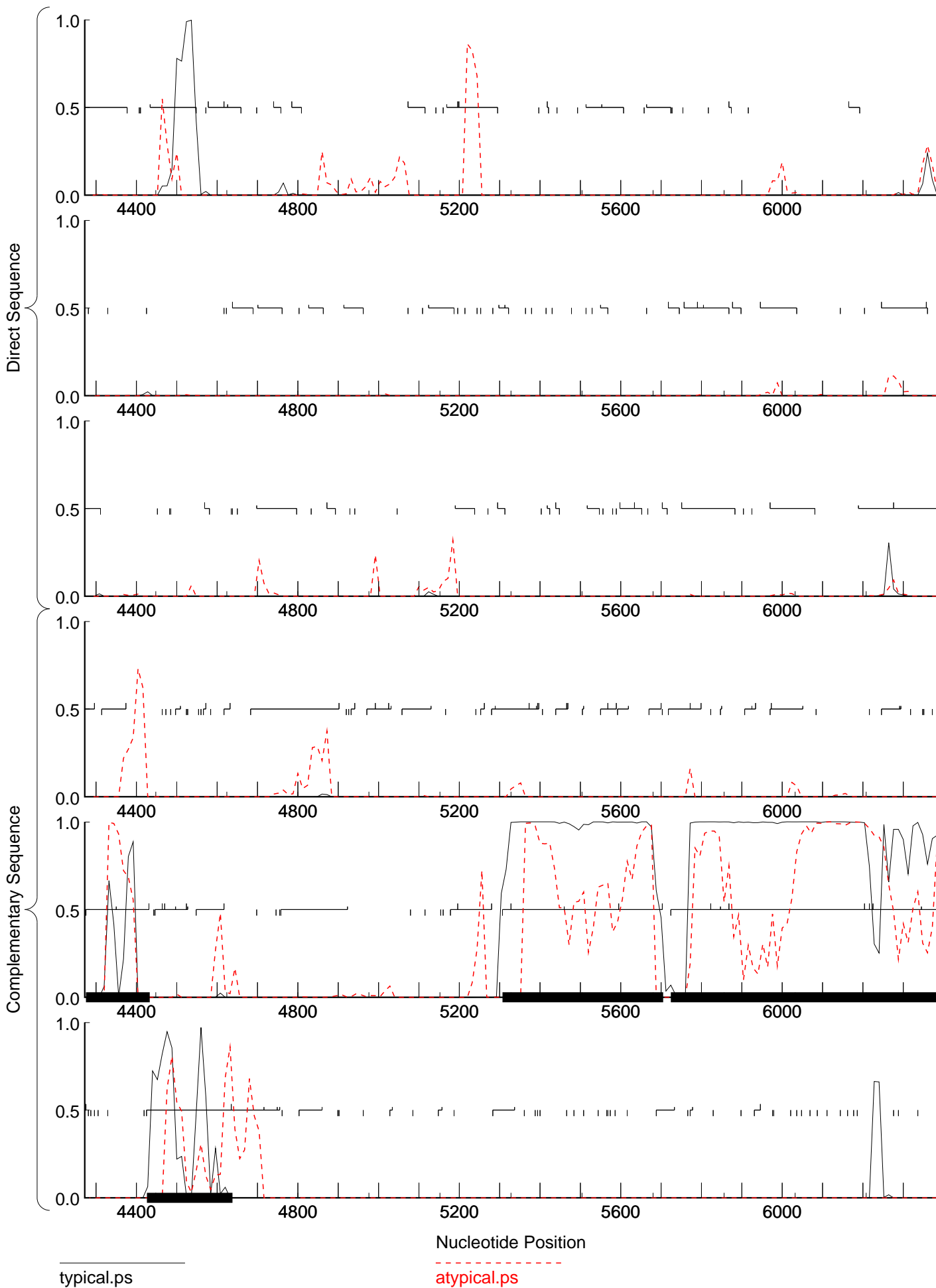
Training set derived by GeneMarkS, 4.30 October 2014
Sat Feb 24 02:59:56 2018



typical.ps

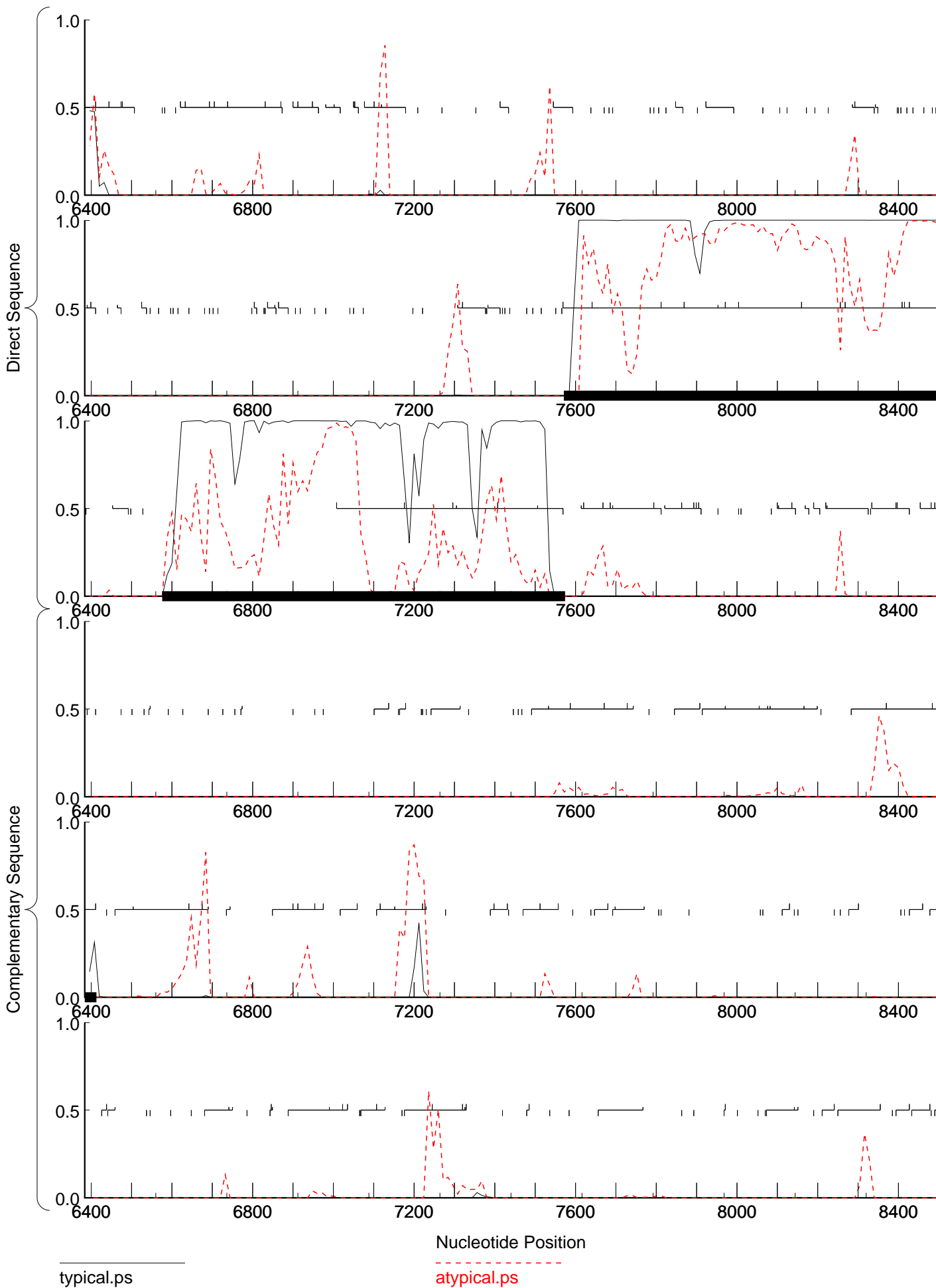
atypical.ps

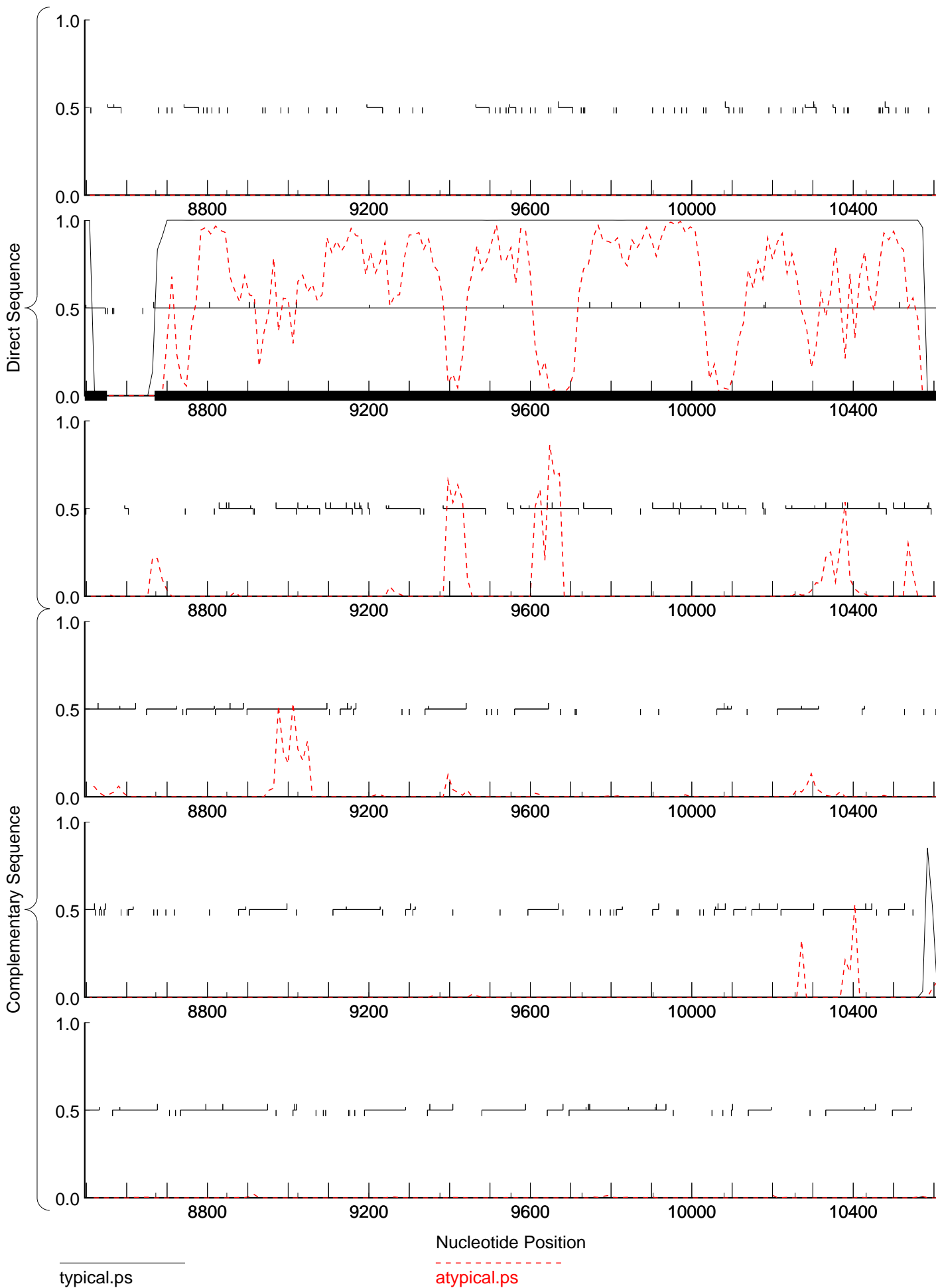




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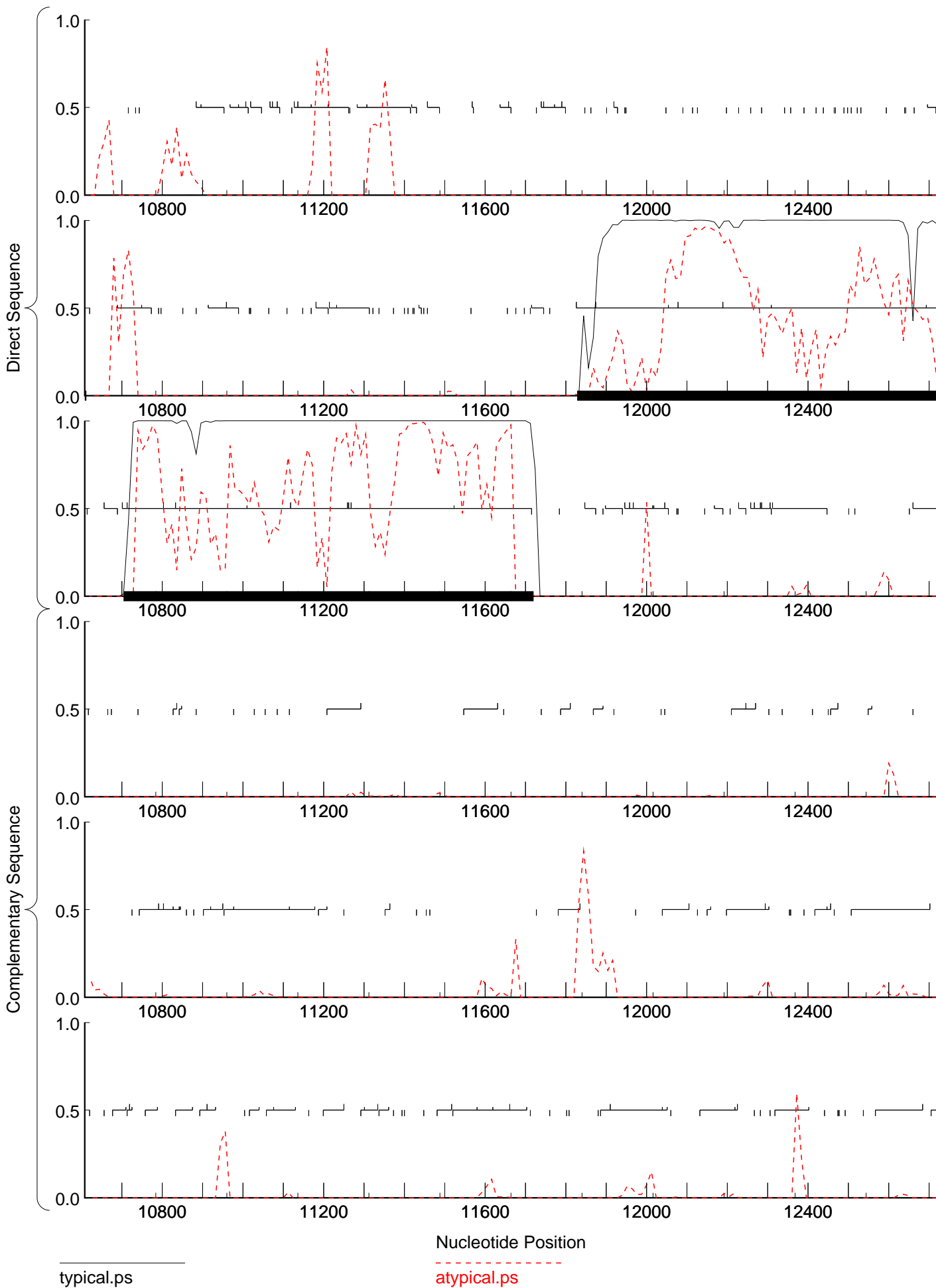
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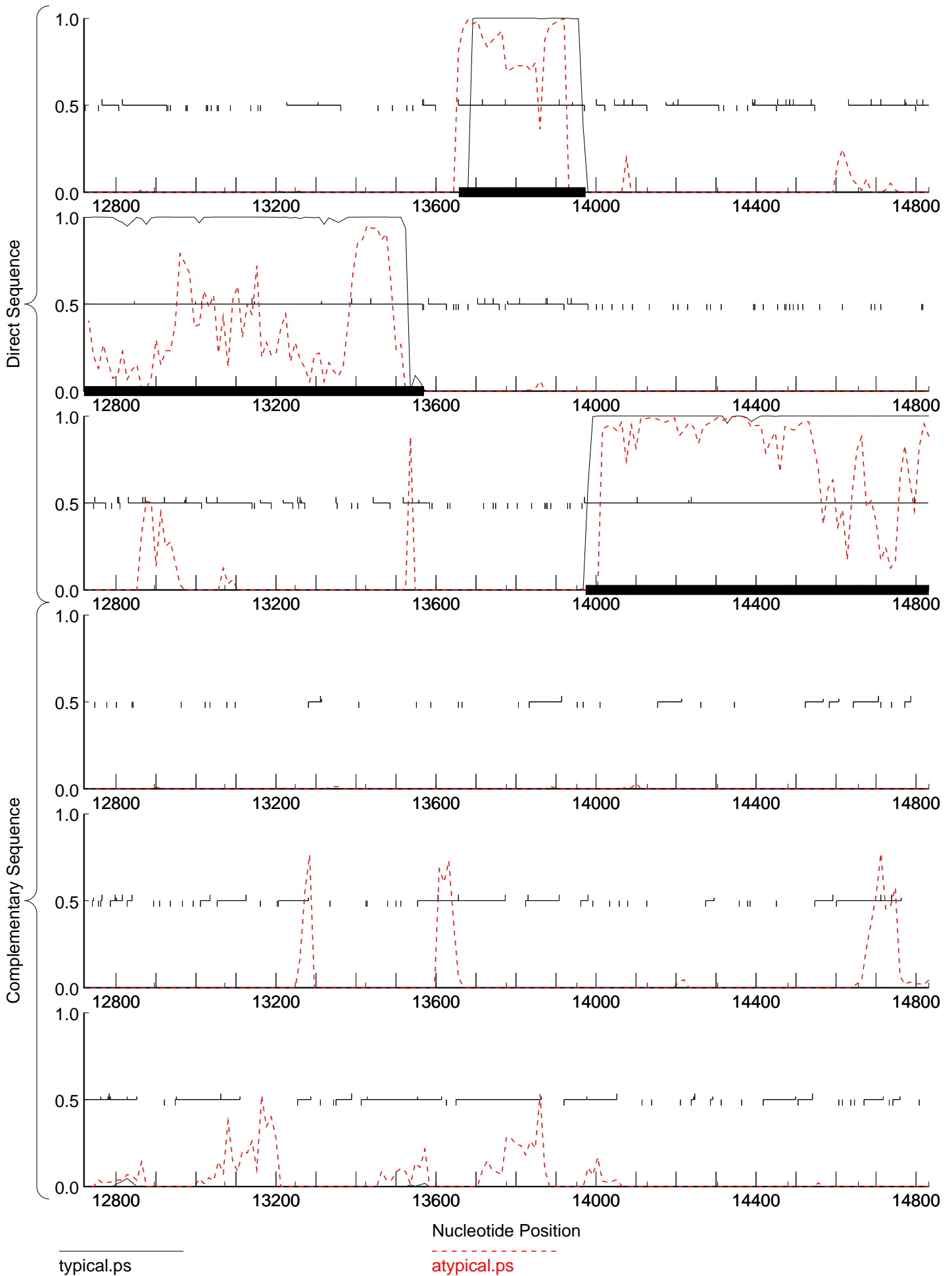


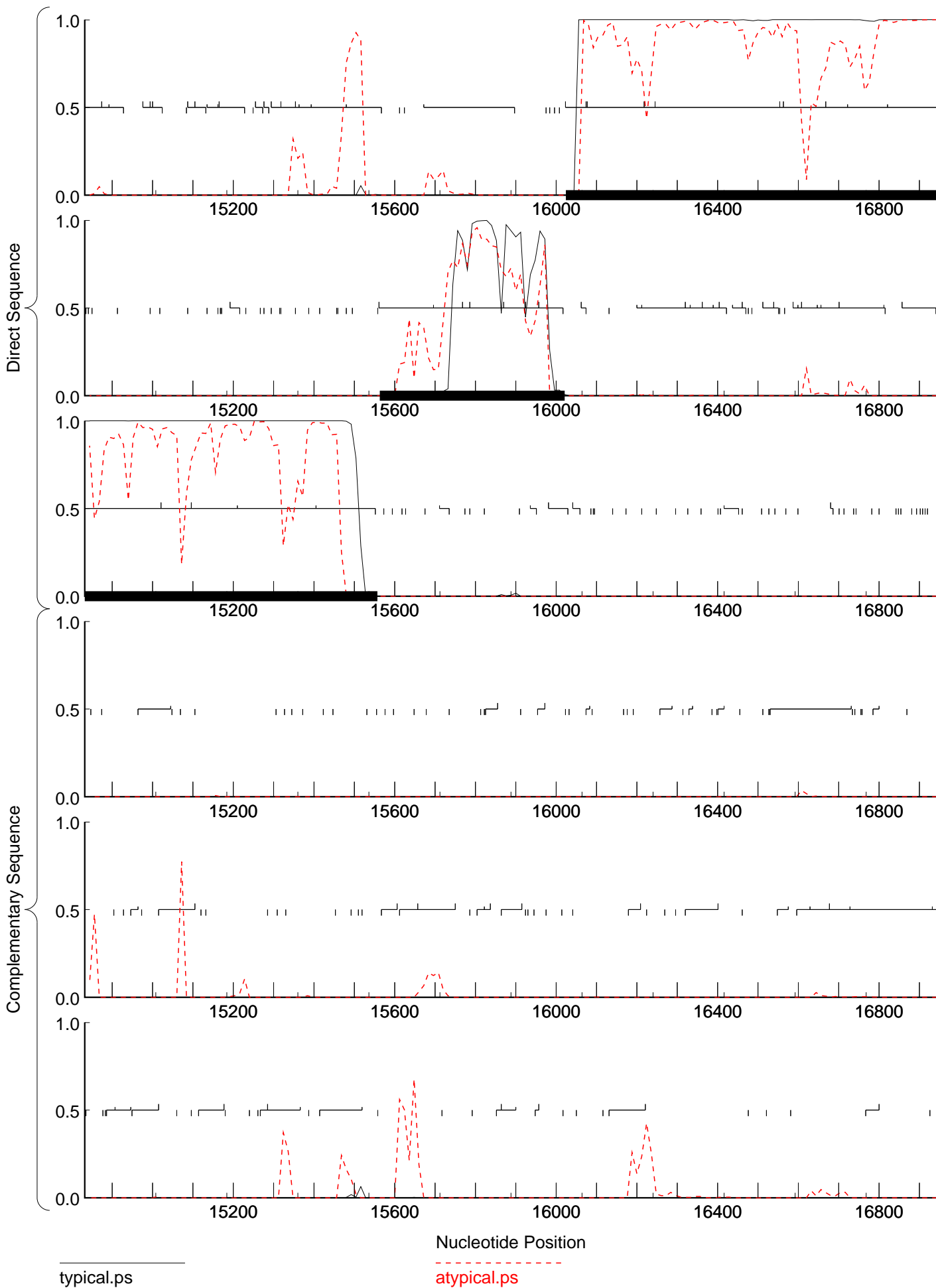


typical.ps

atypical.ps

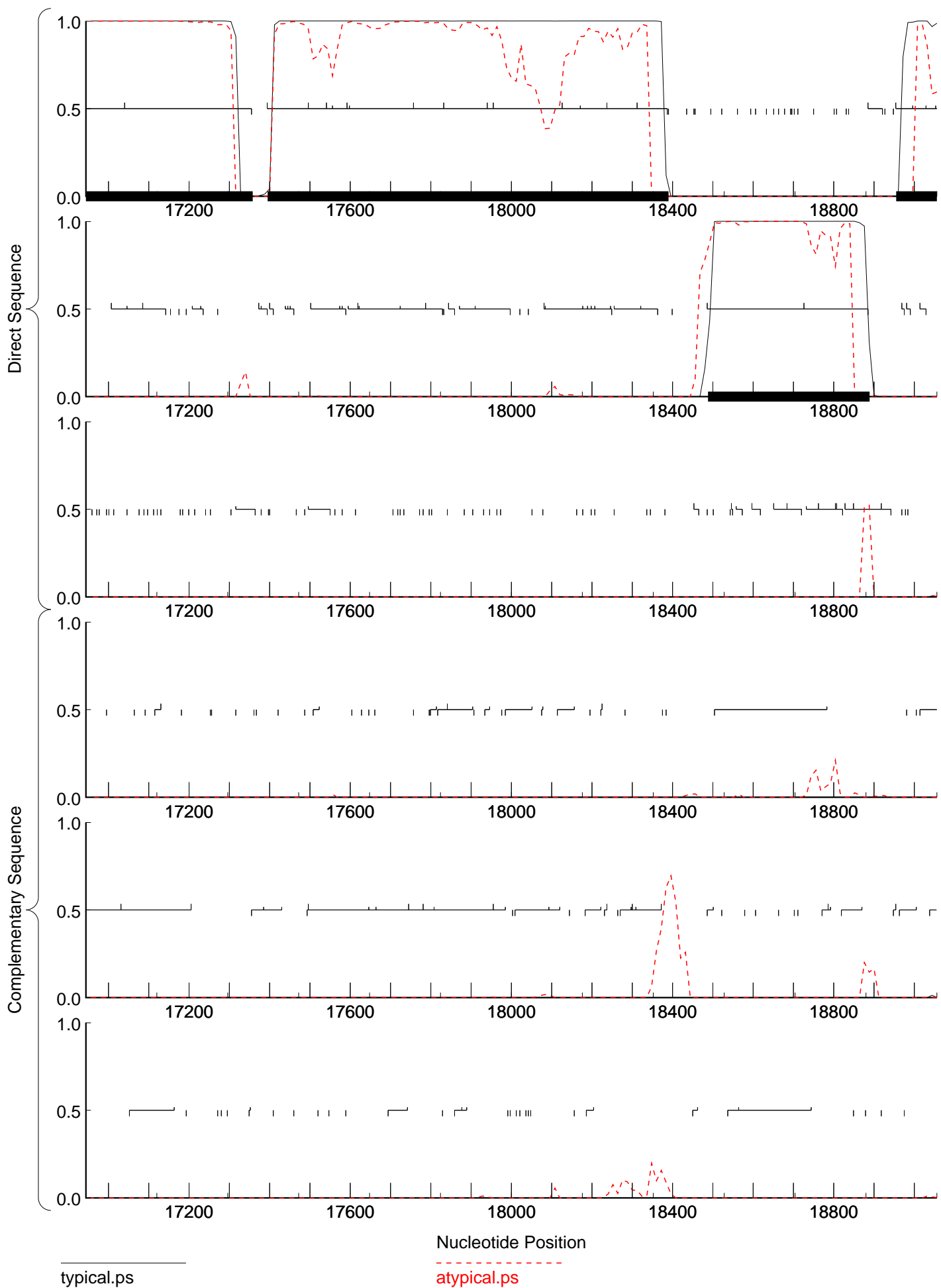


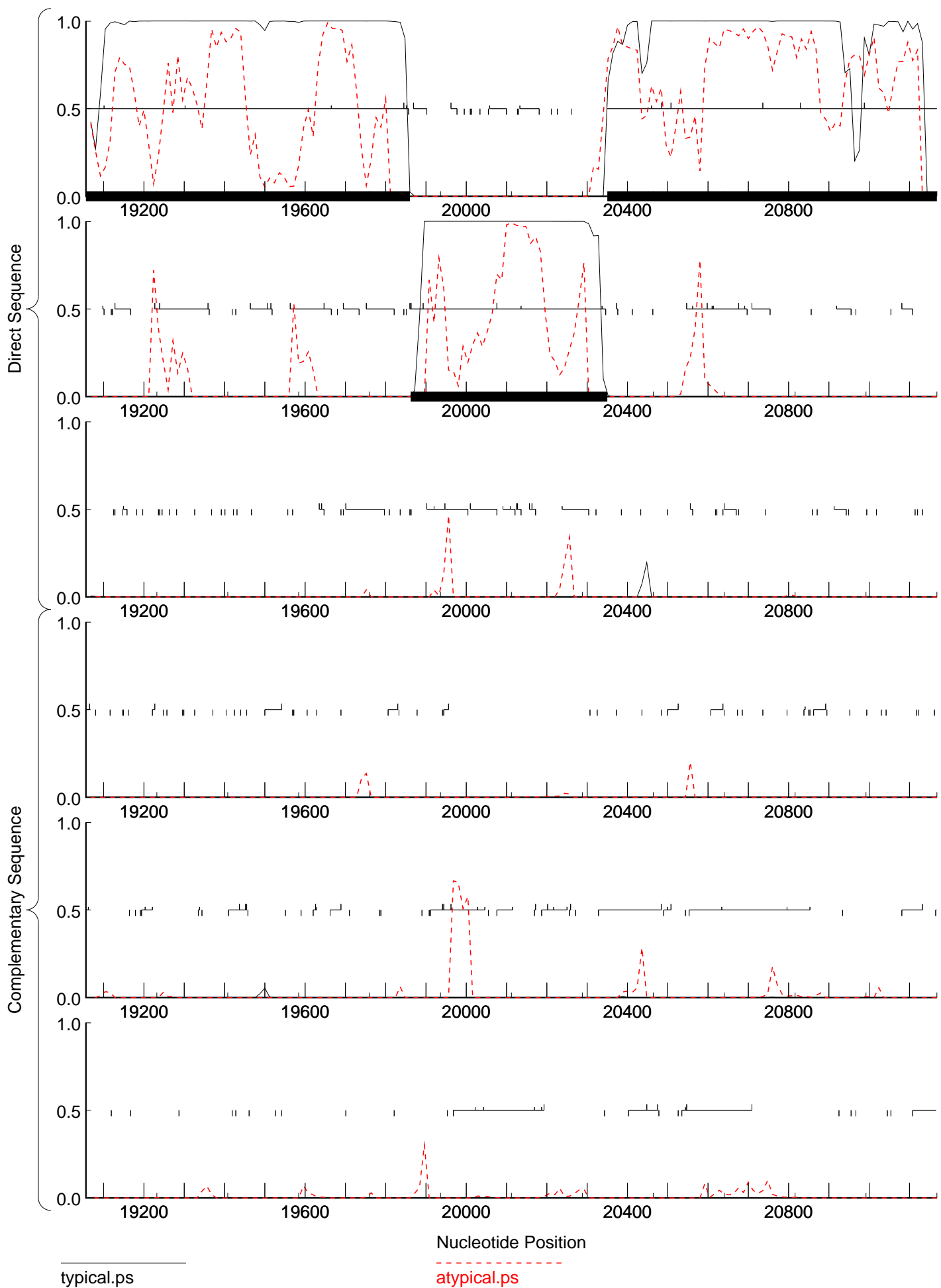


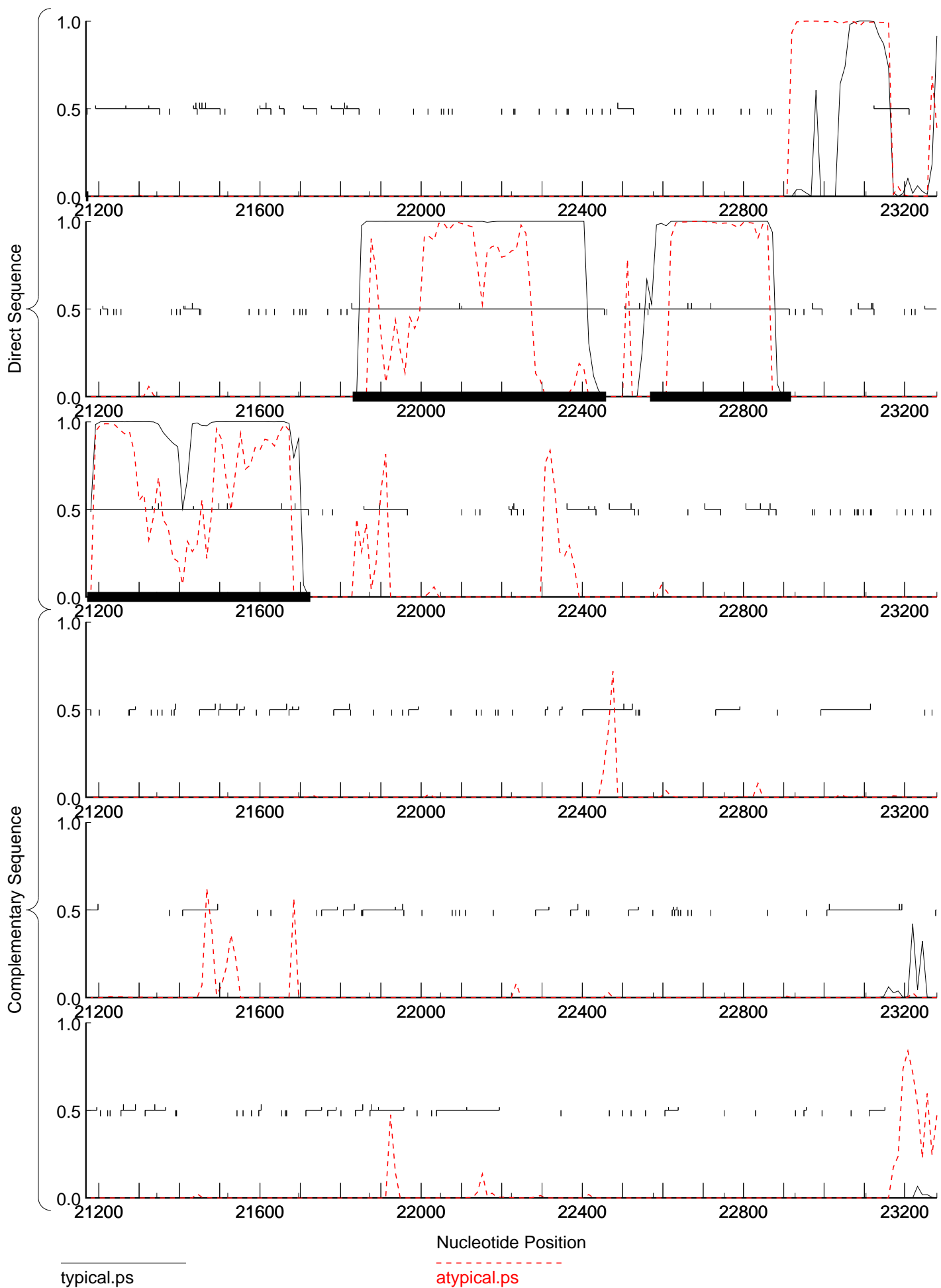


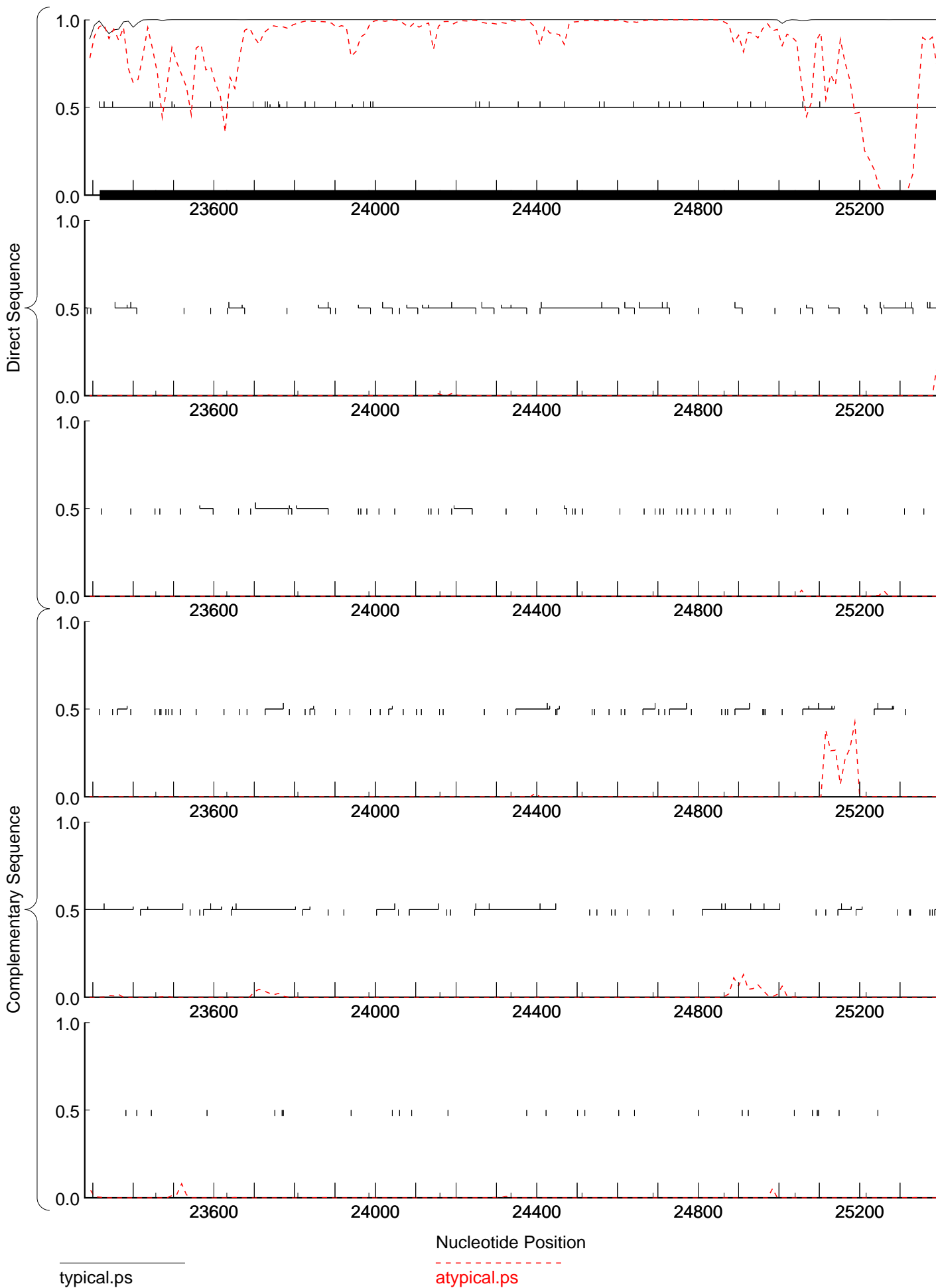
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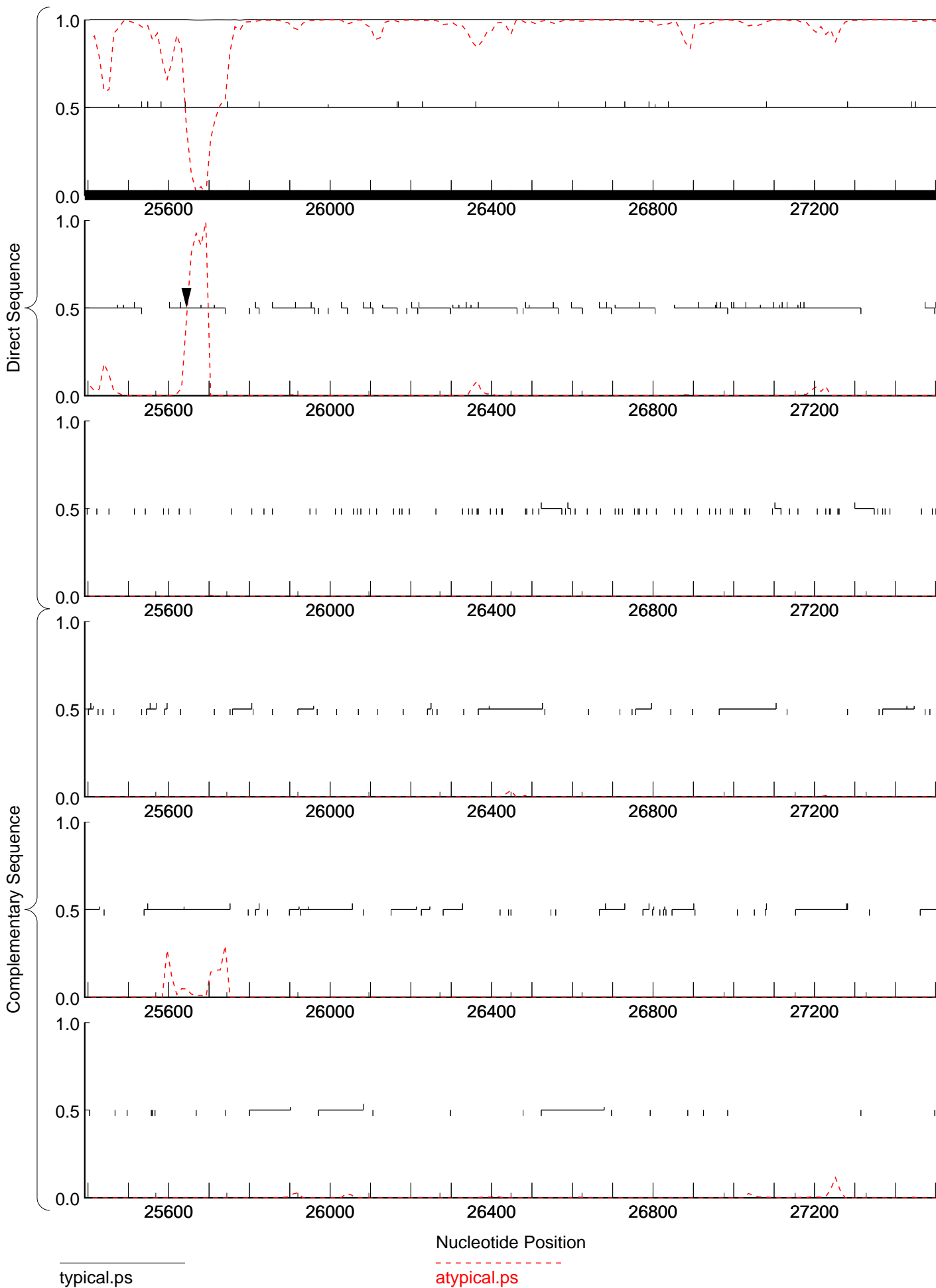
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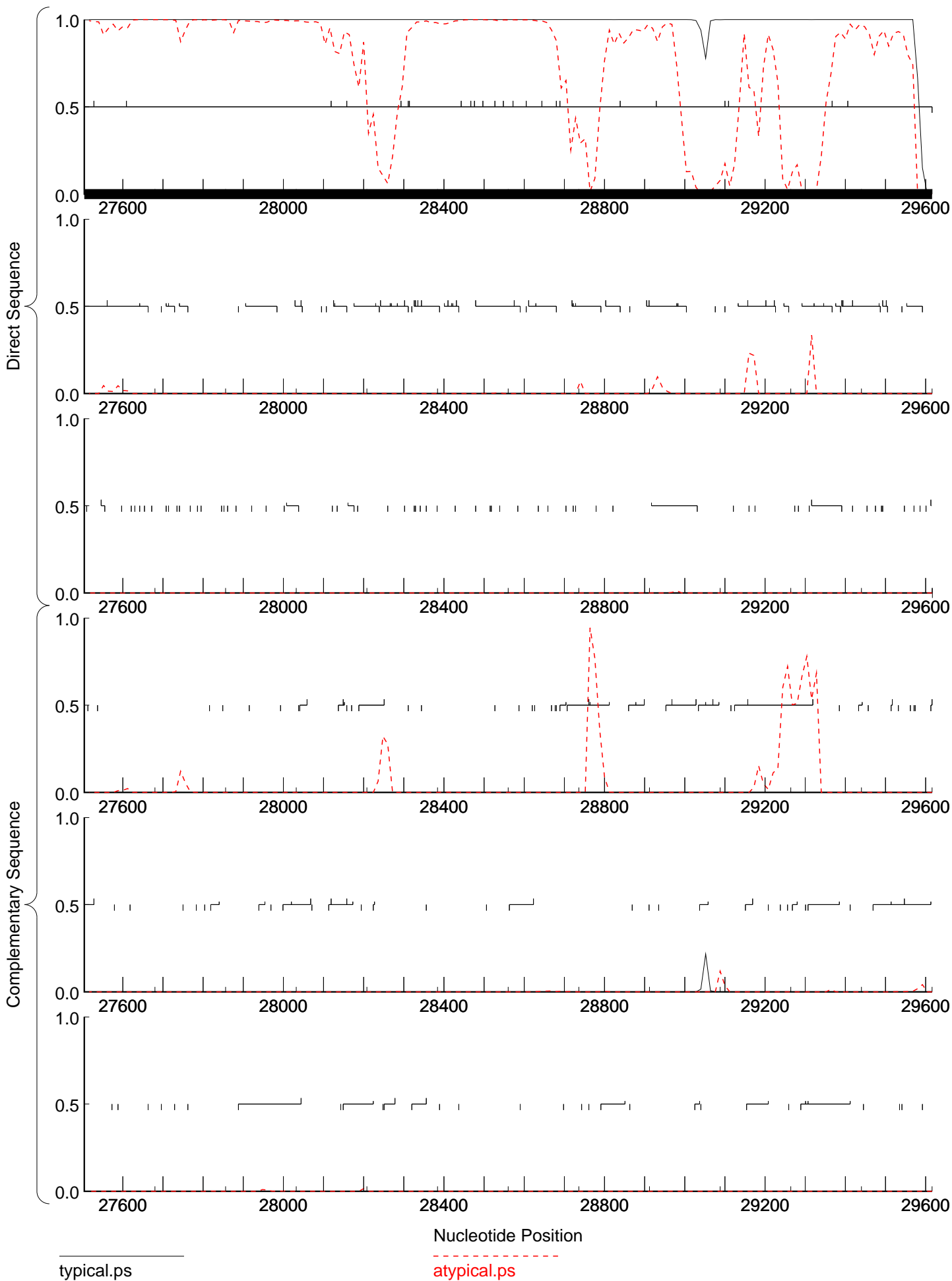






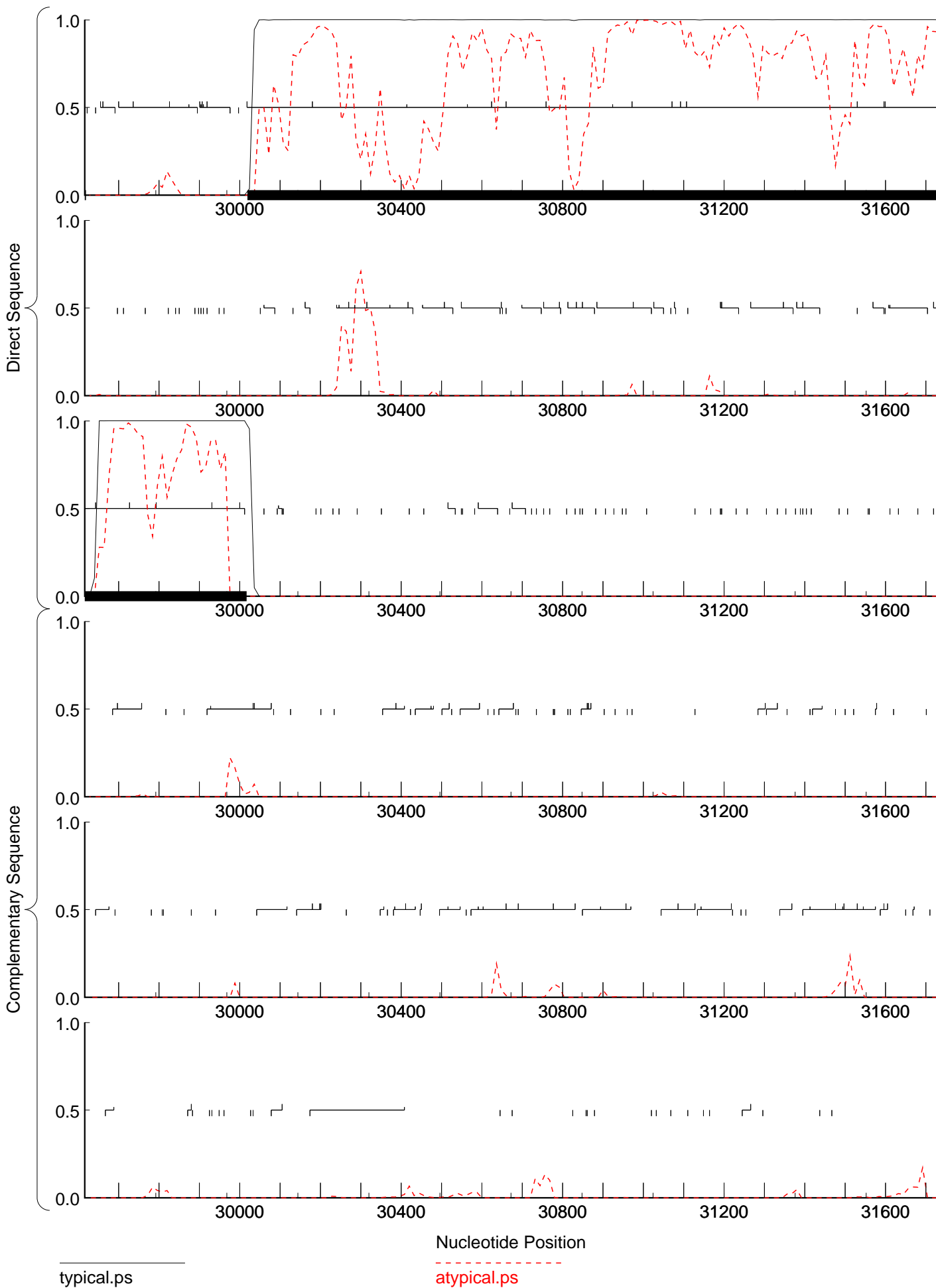


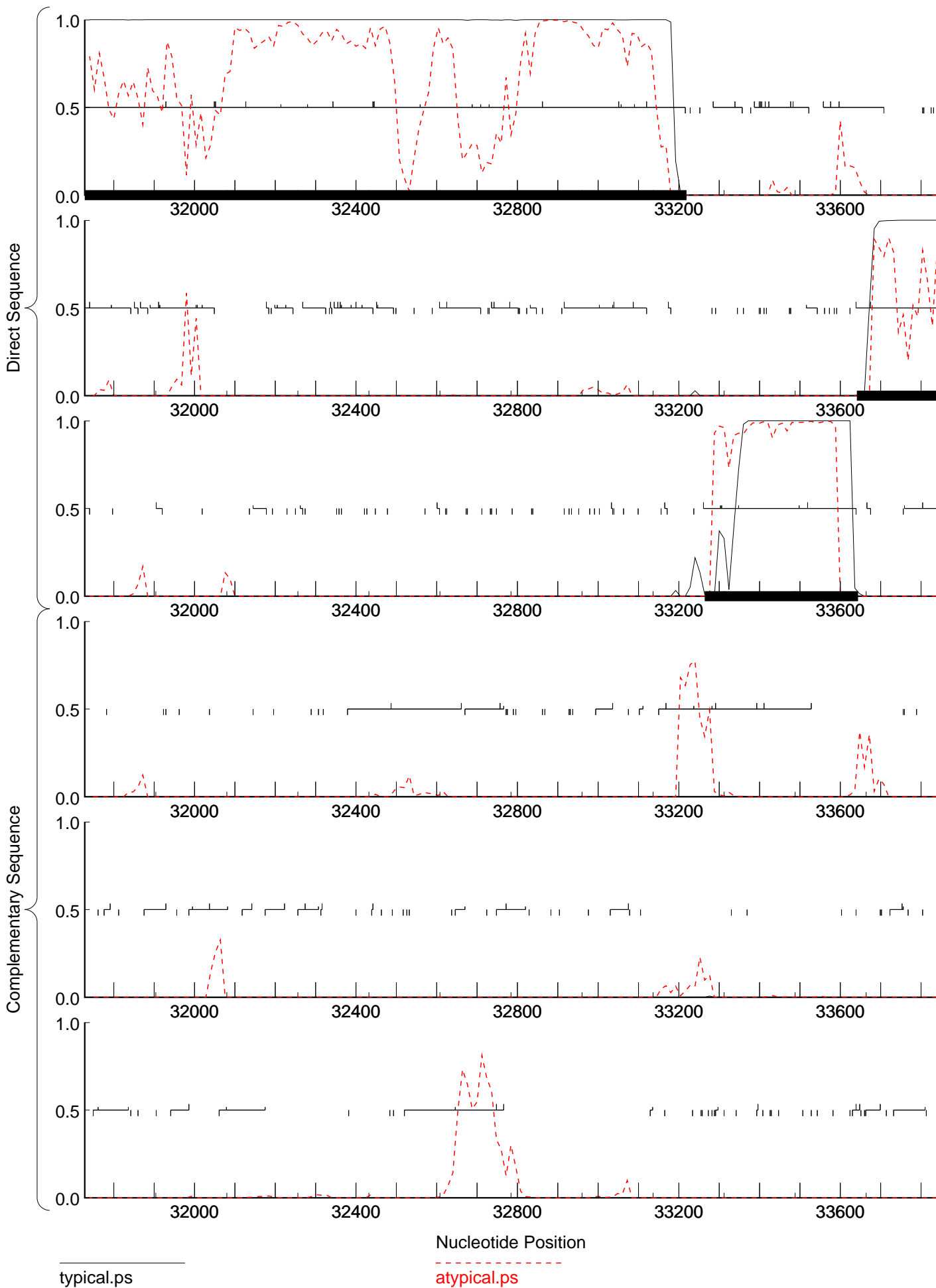


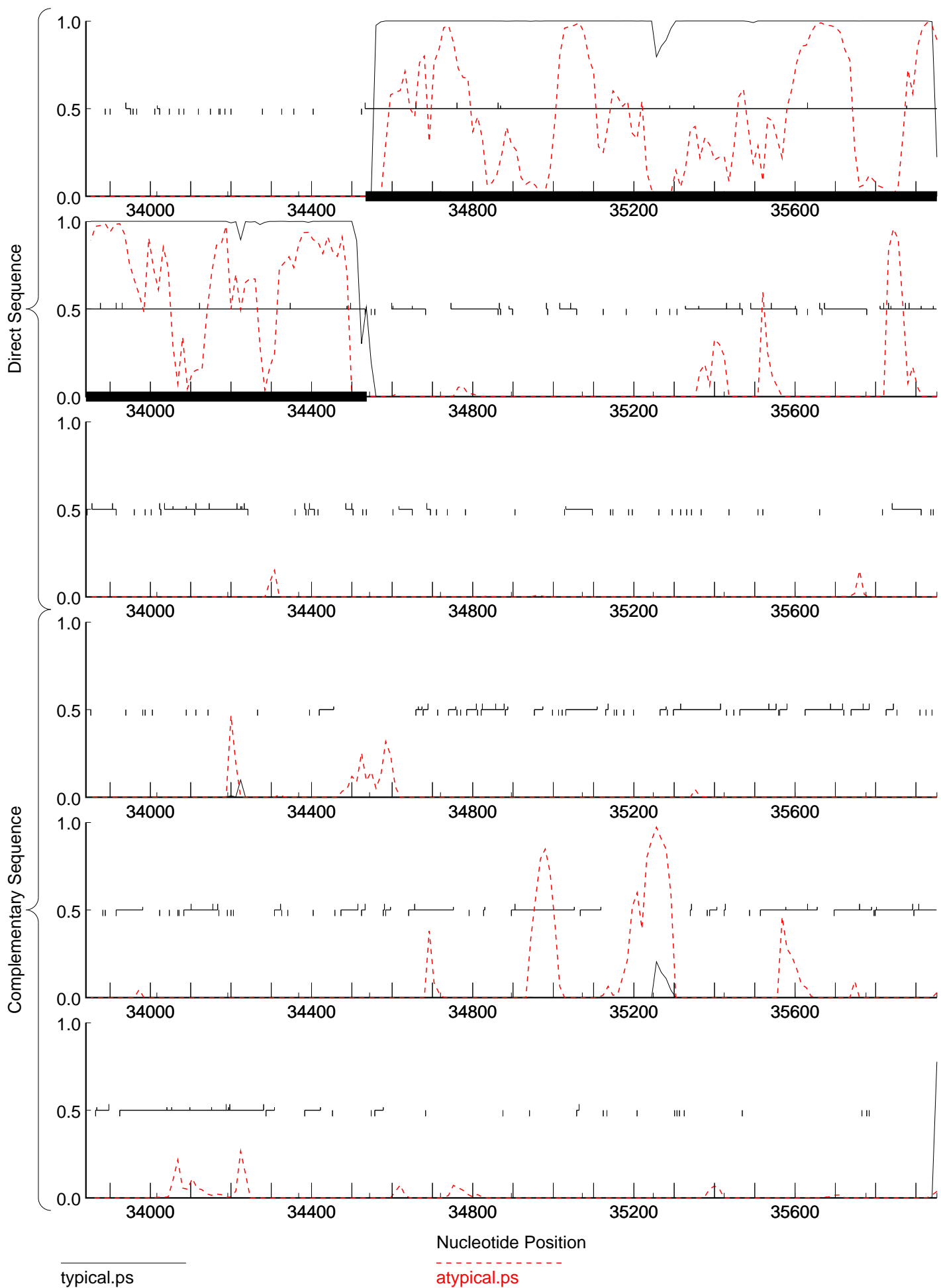


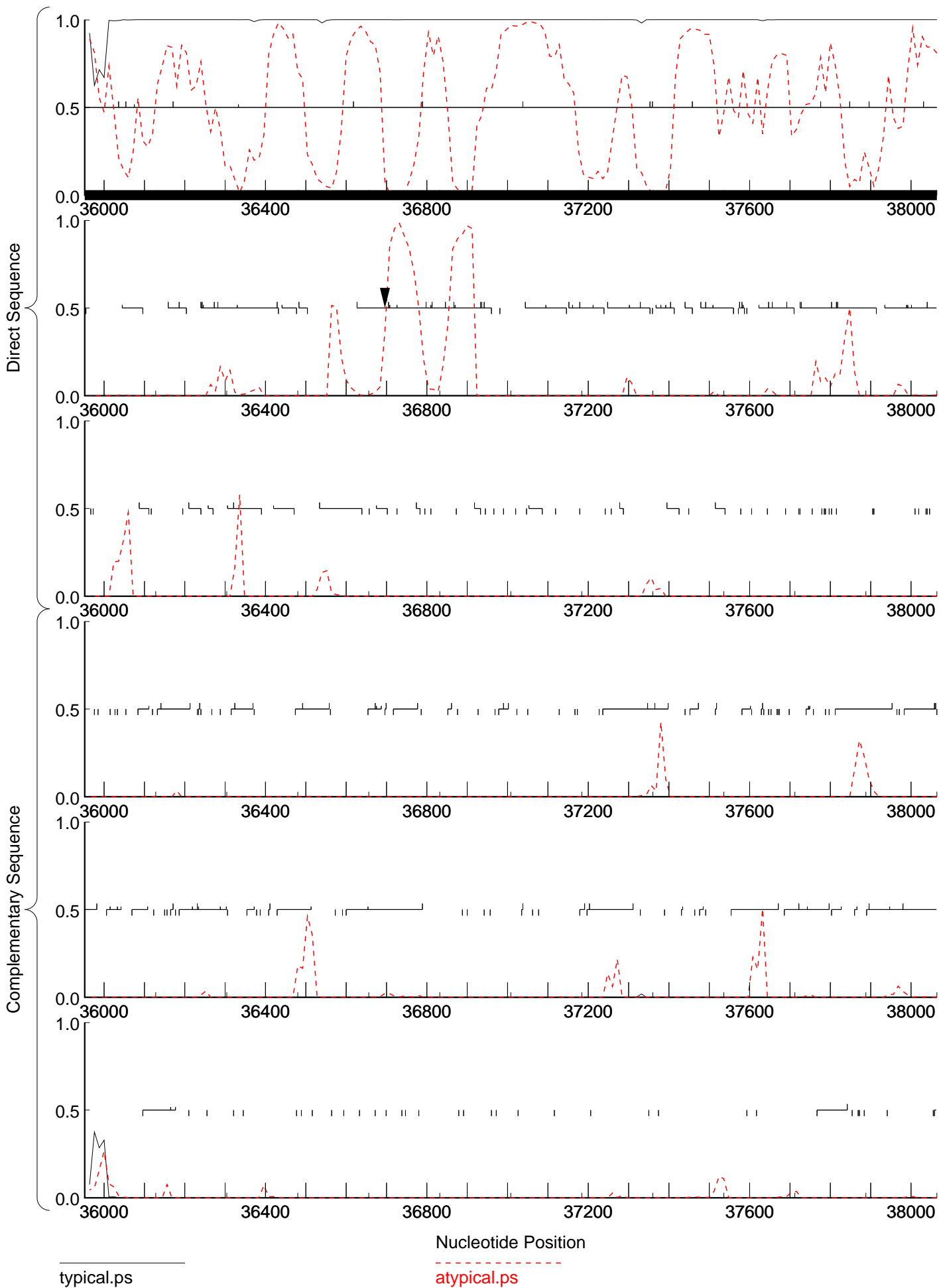
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atypical.ps



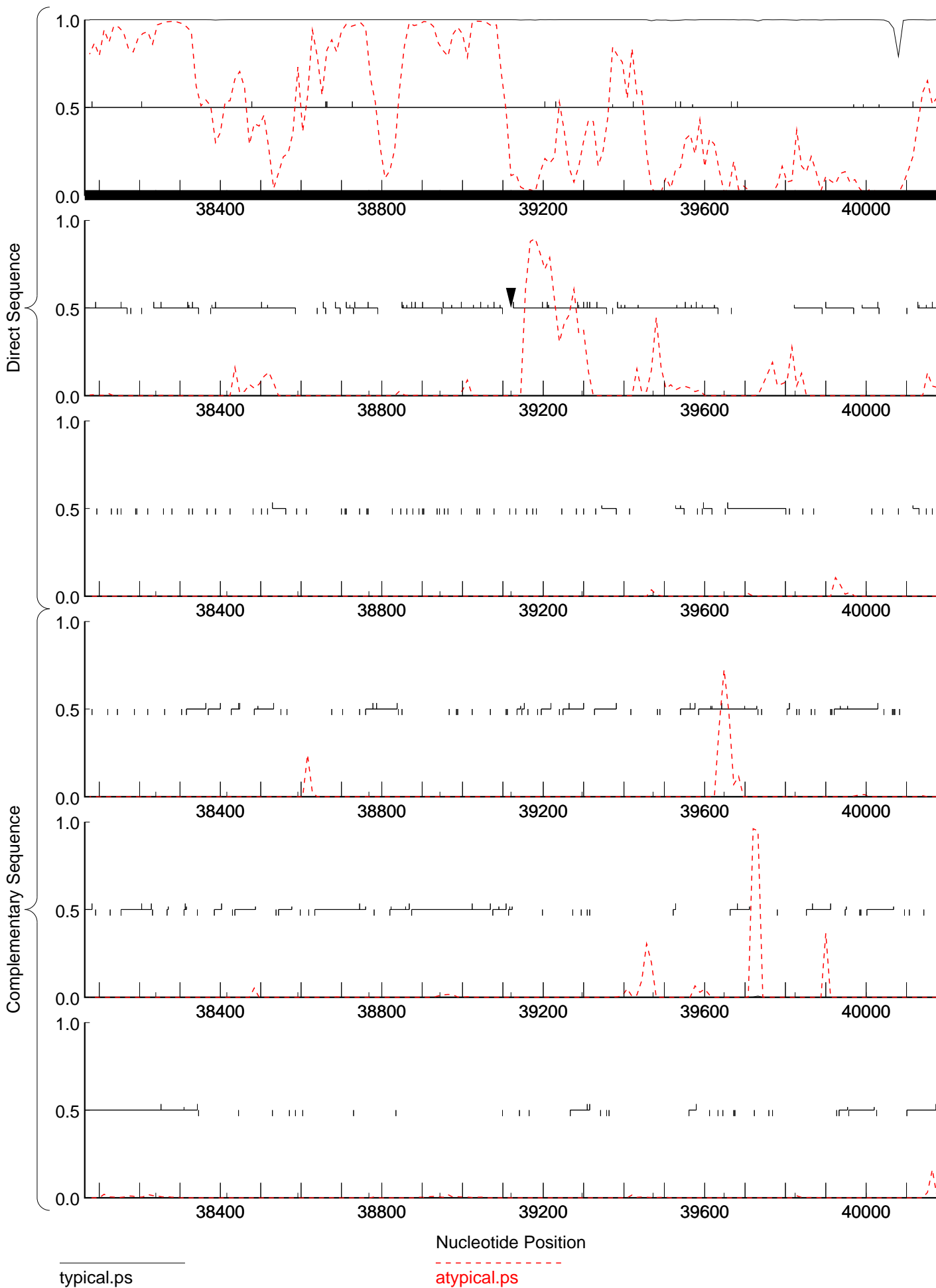






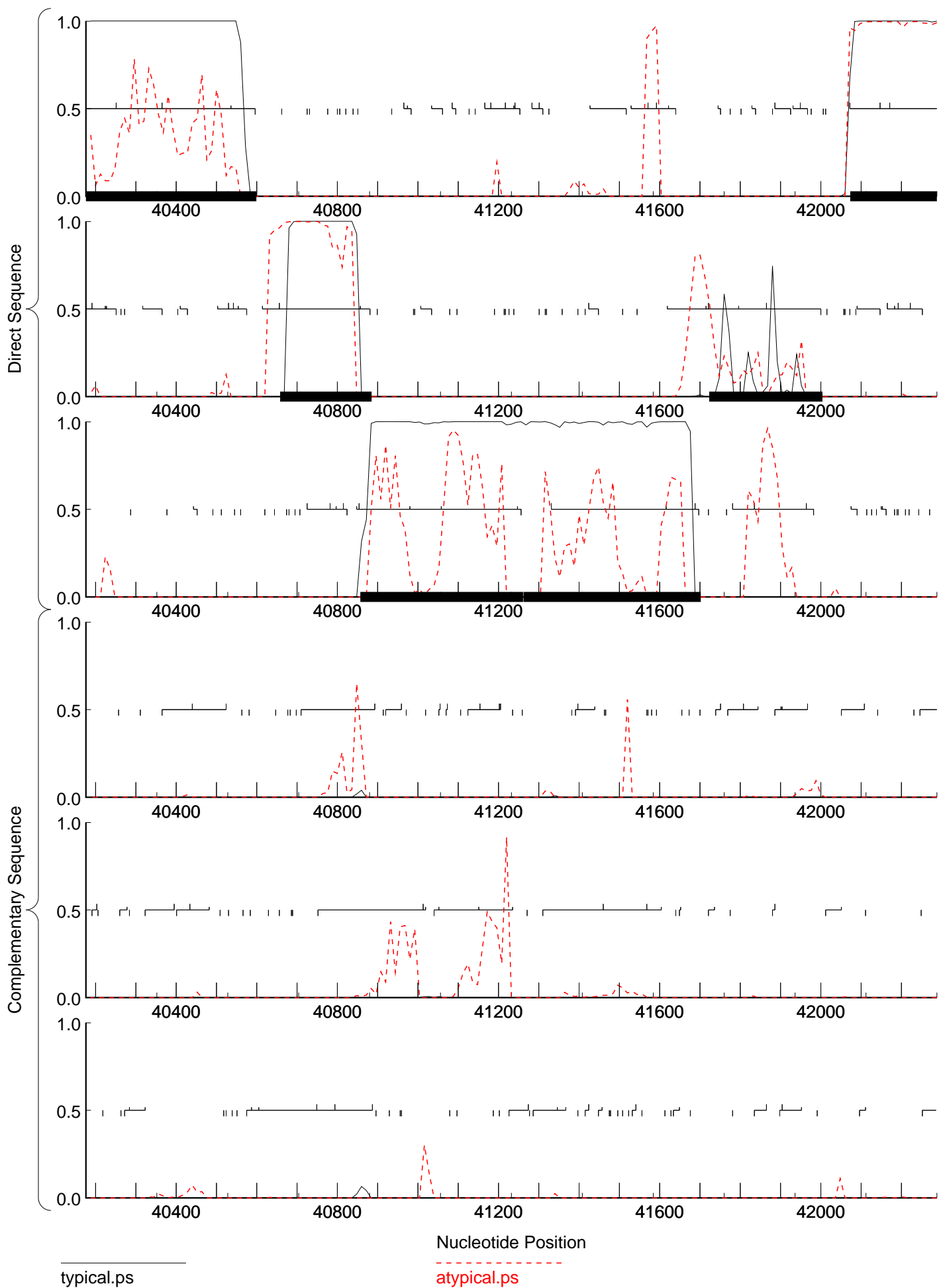
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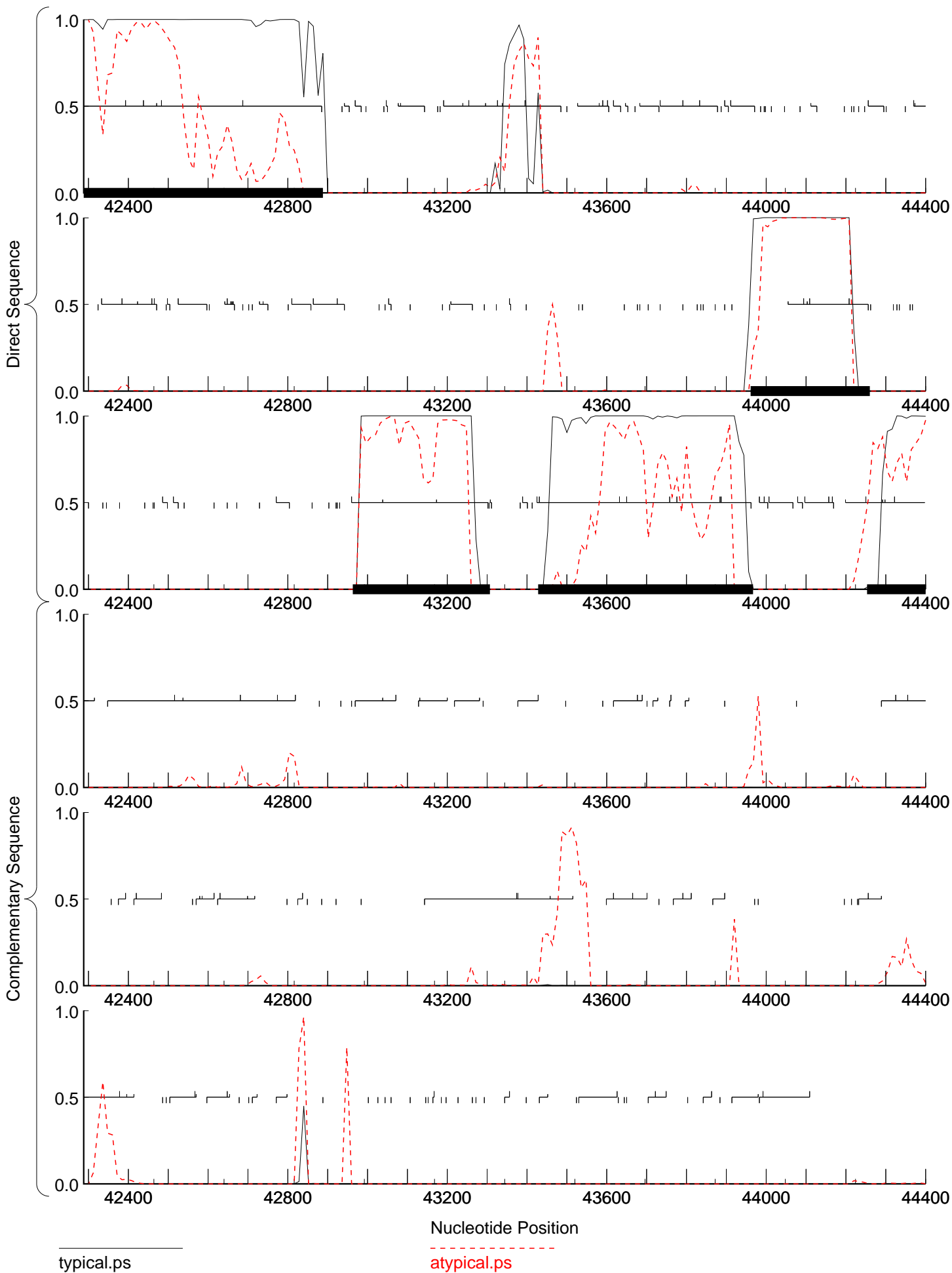
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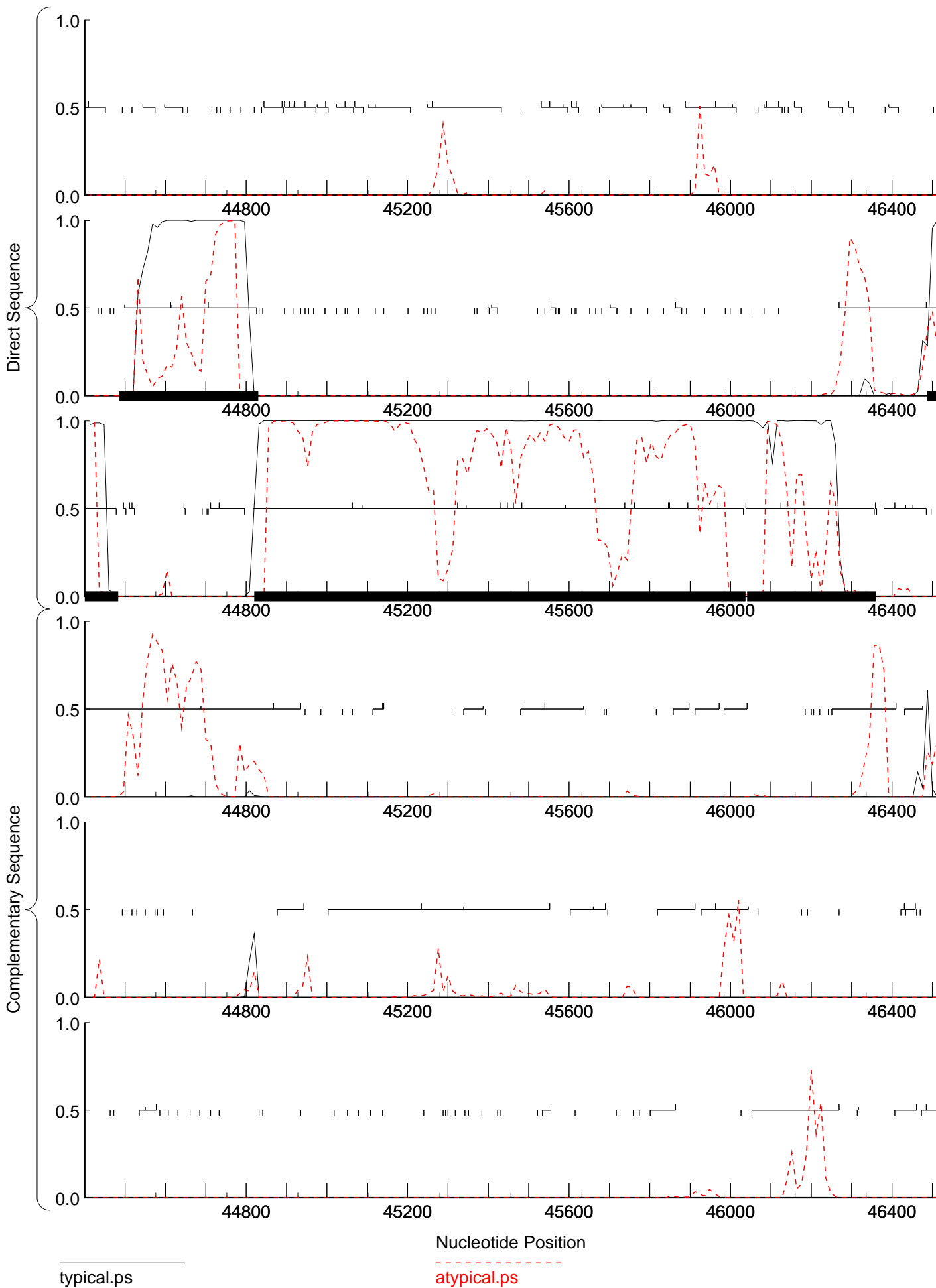


typical.ps

atypical.ps

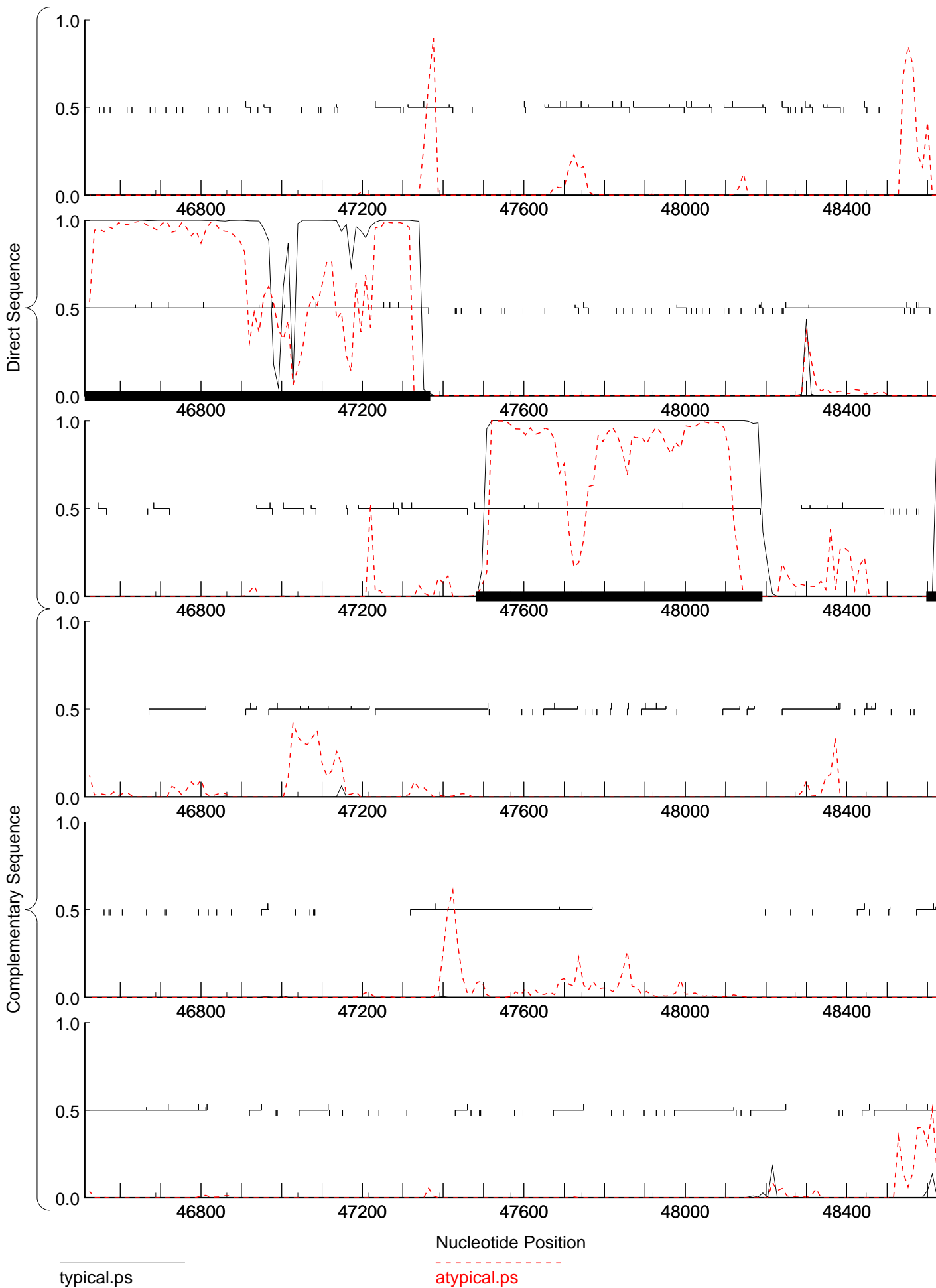


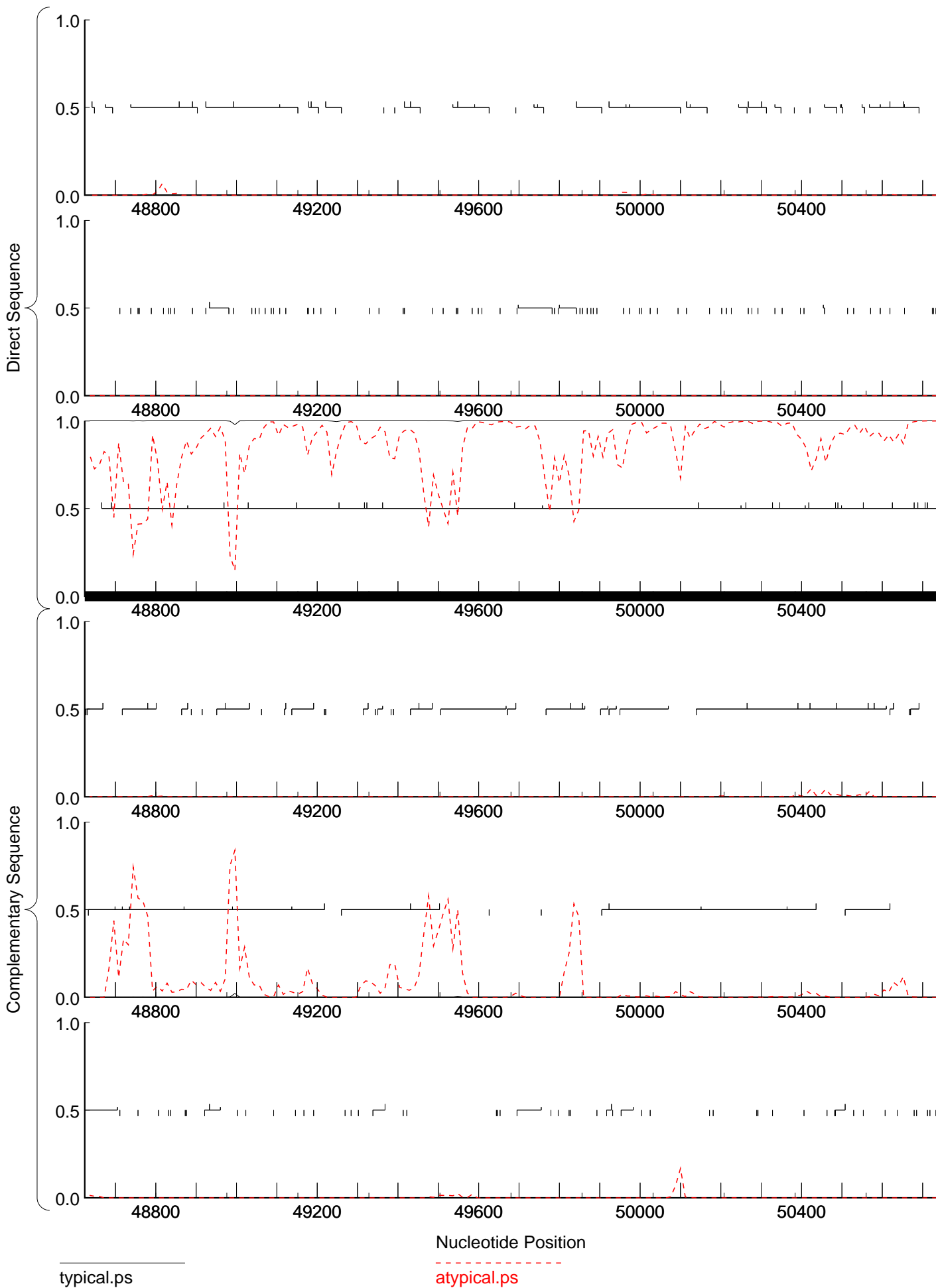


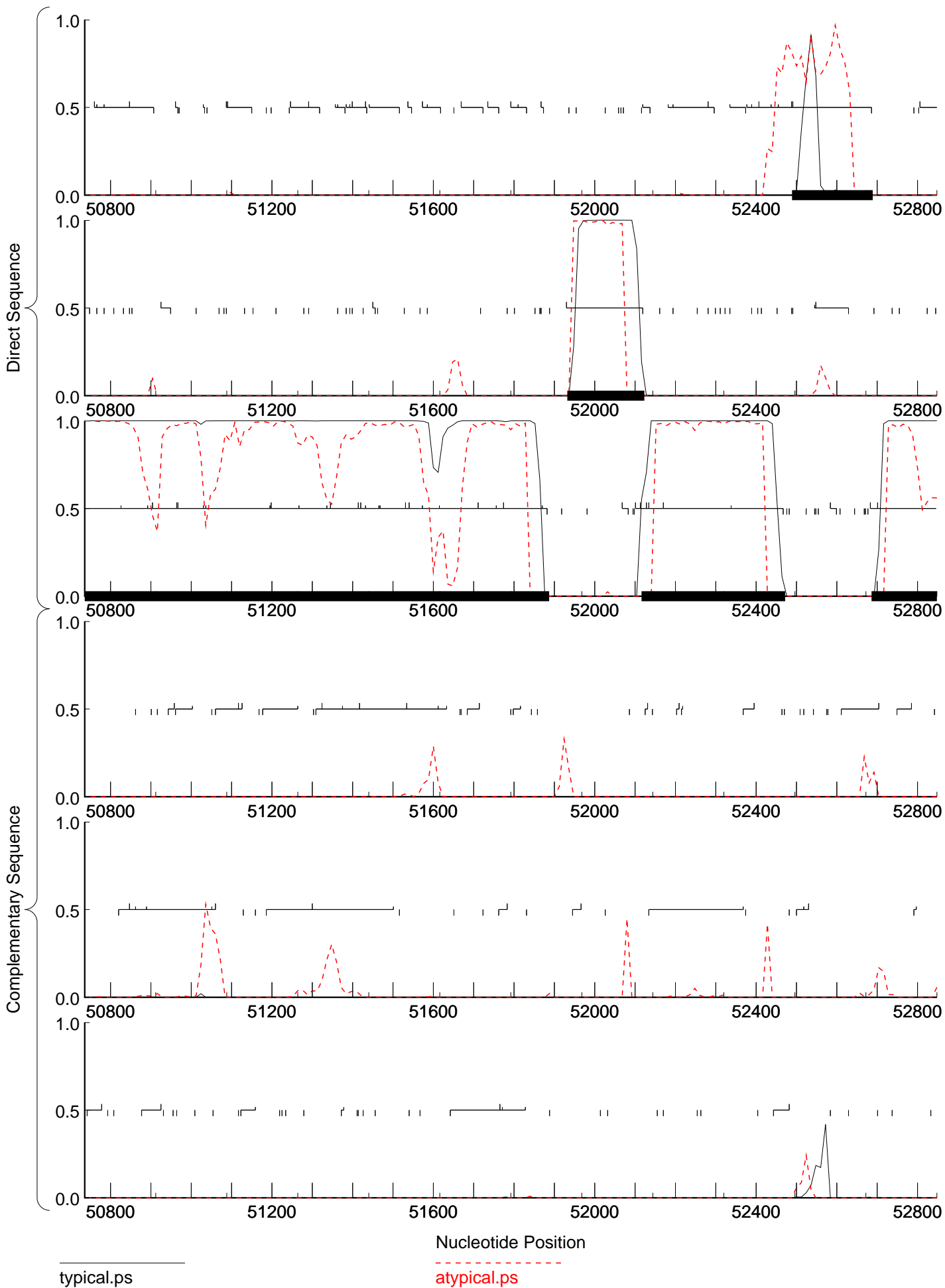


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atypical.ps

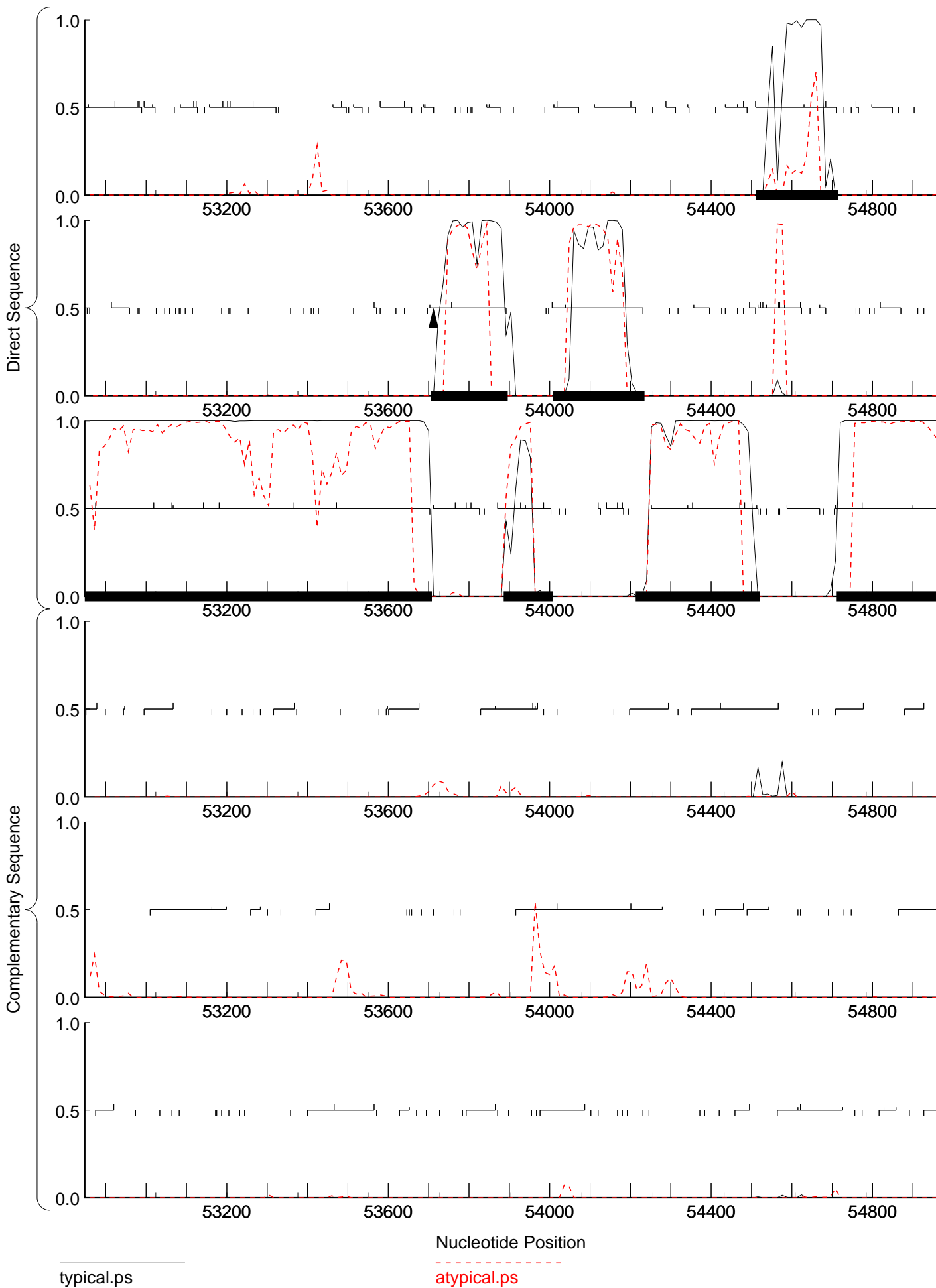


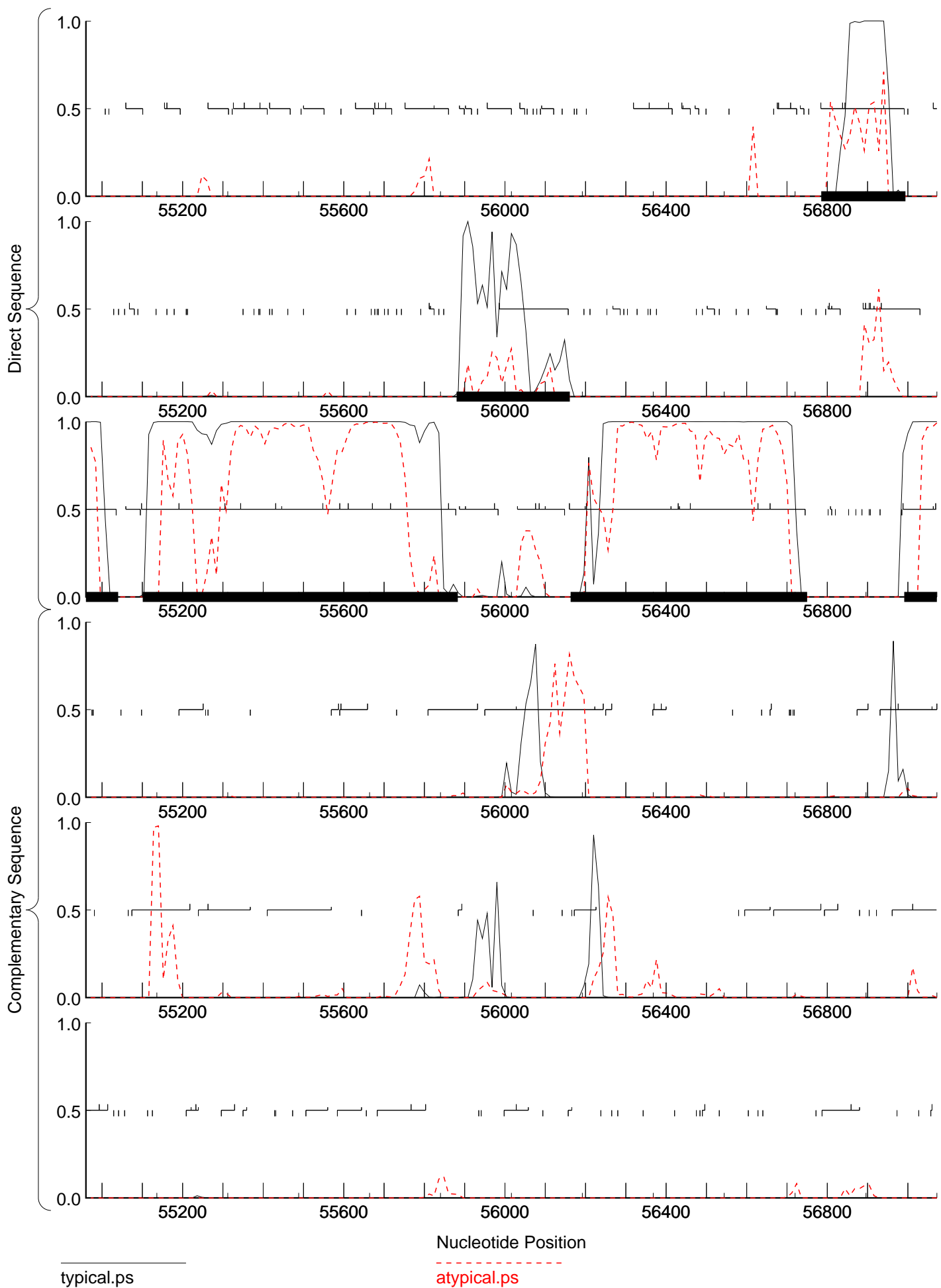


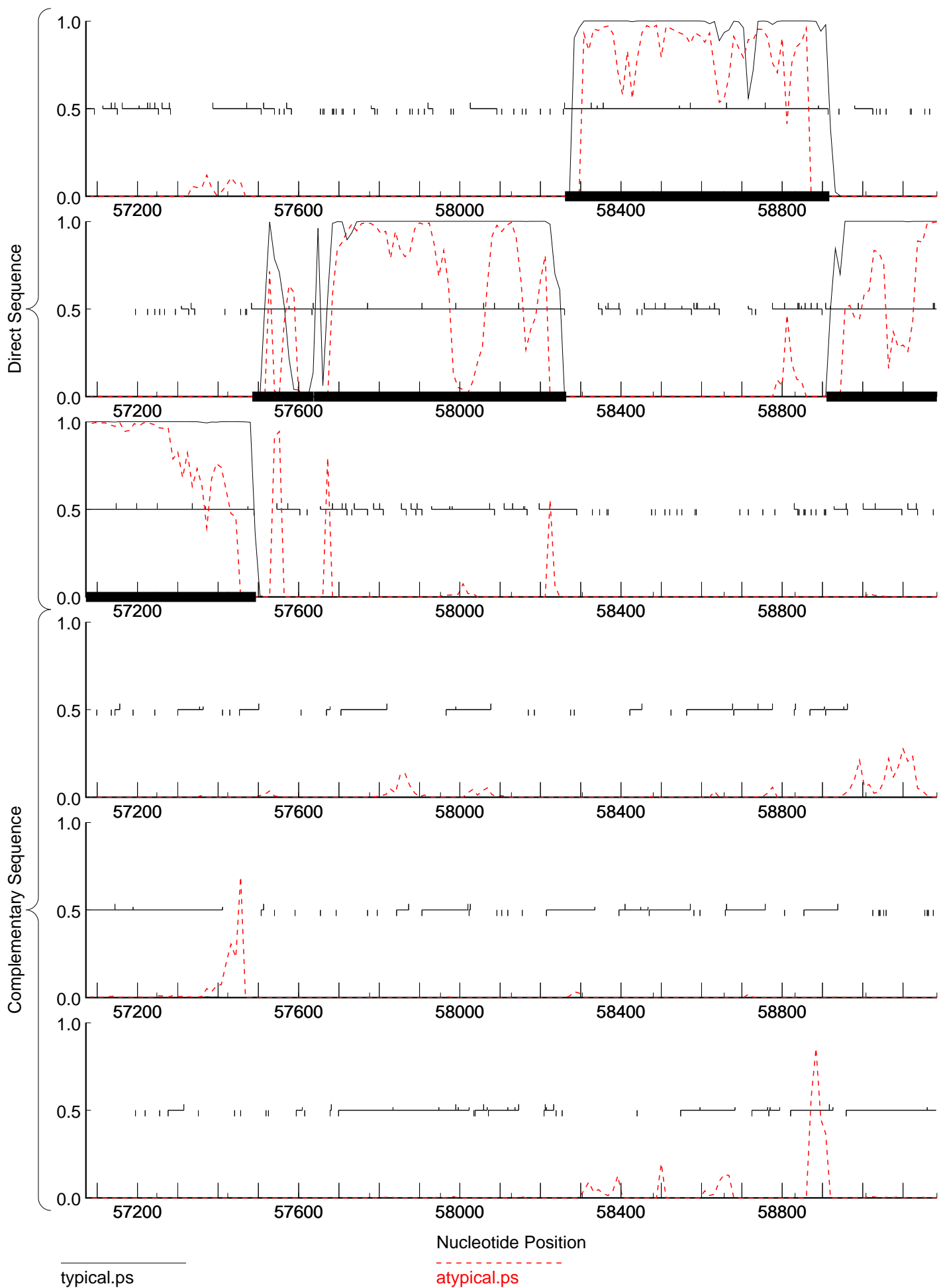


typical.ps

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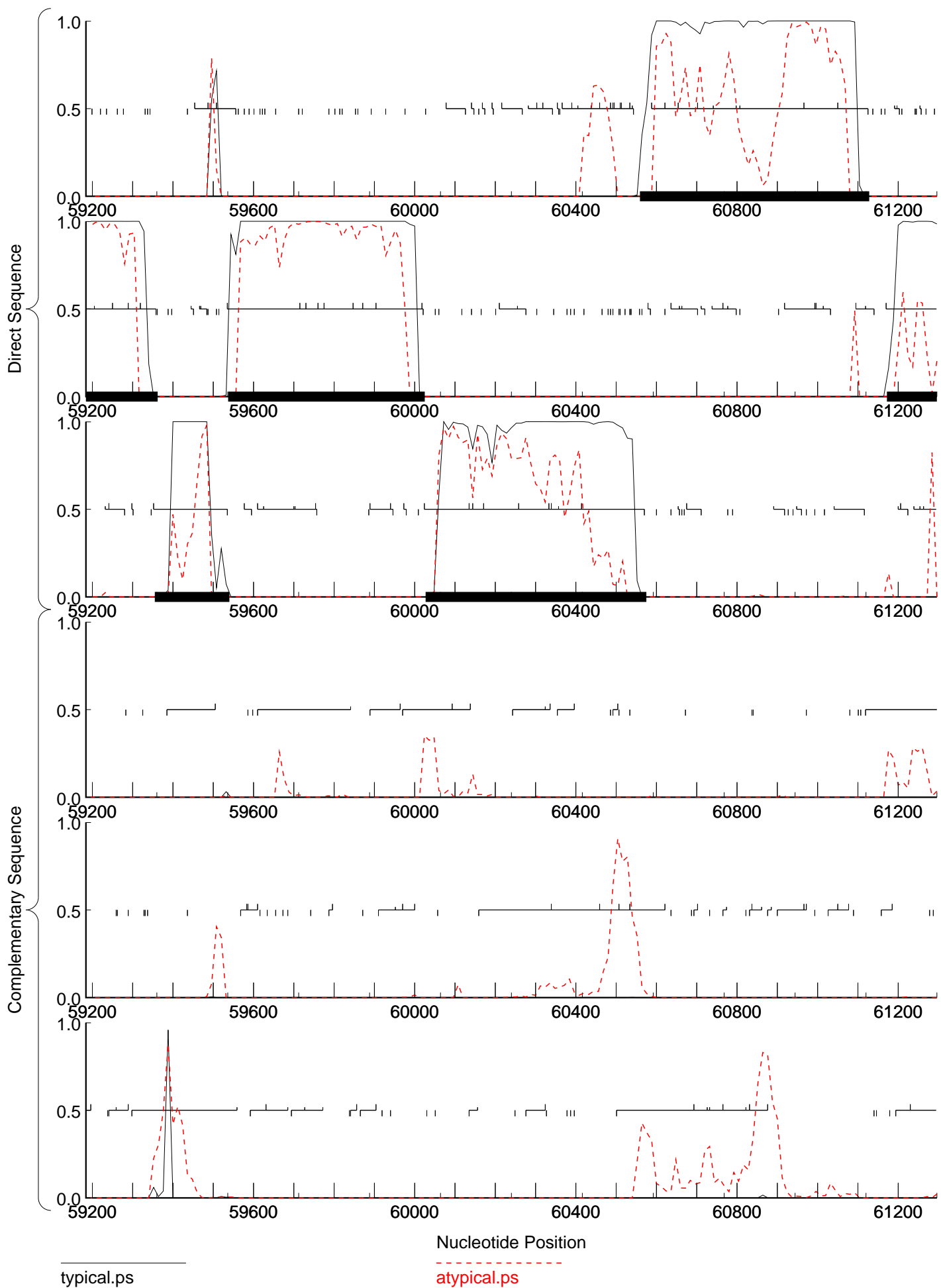


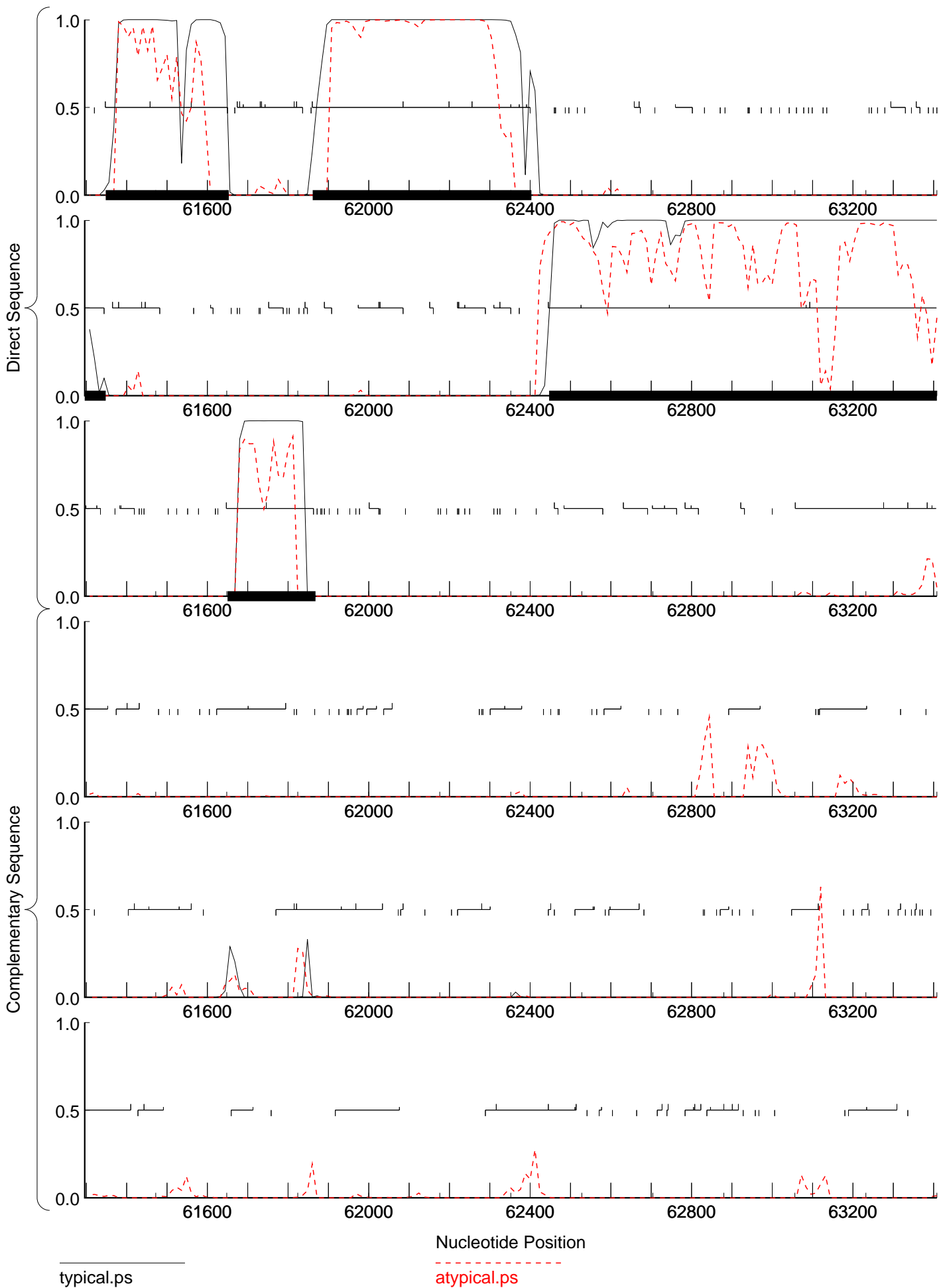


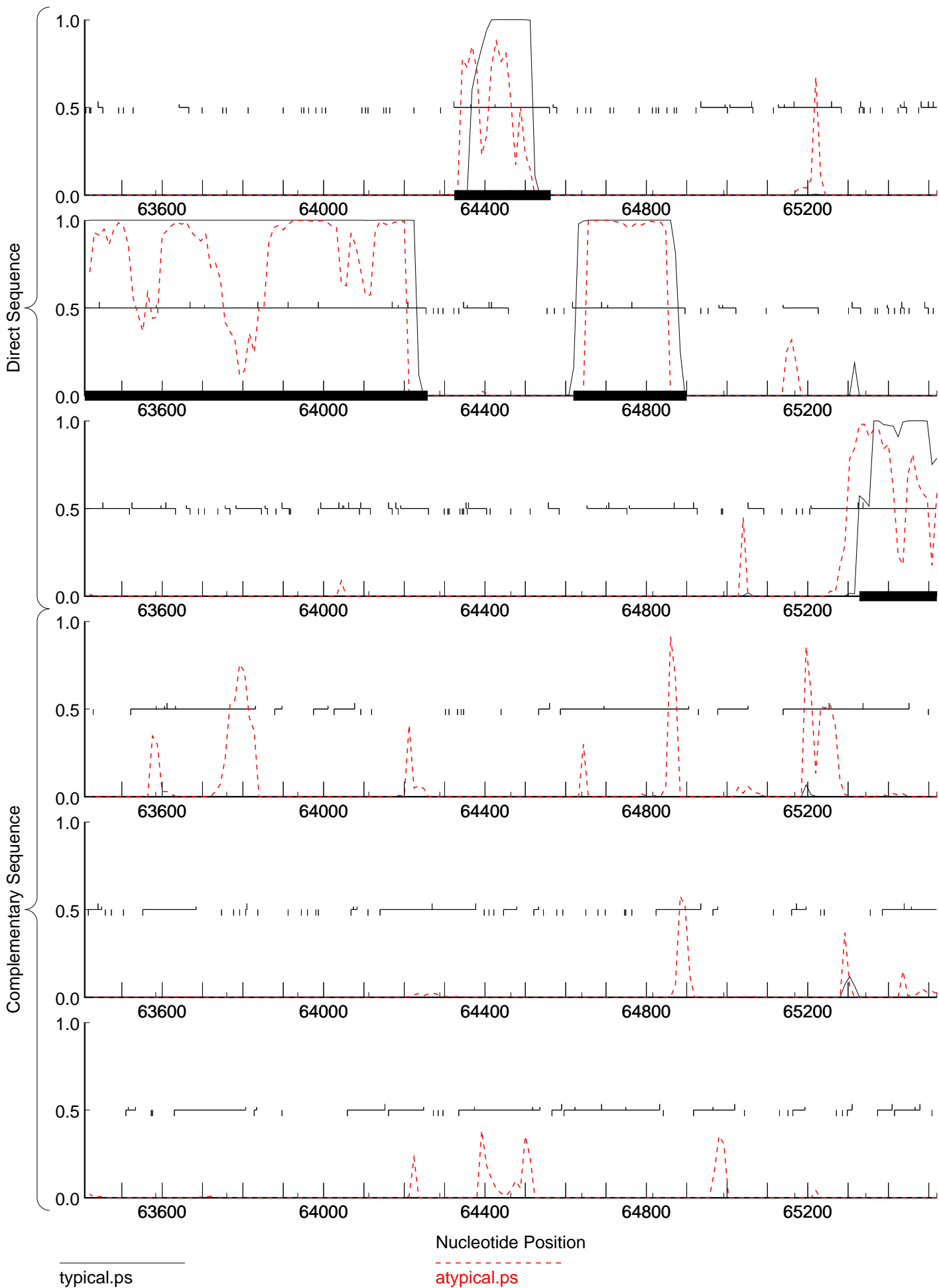


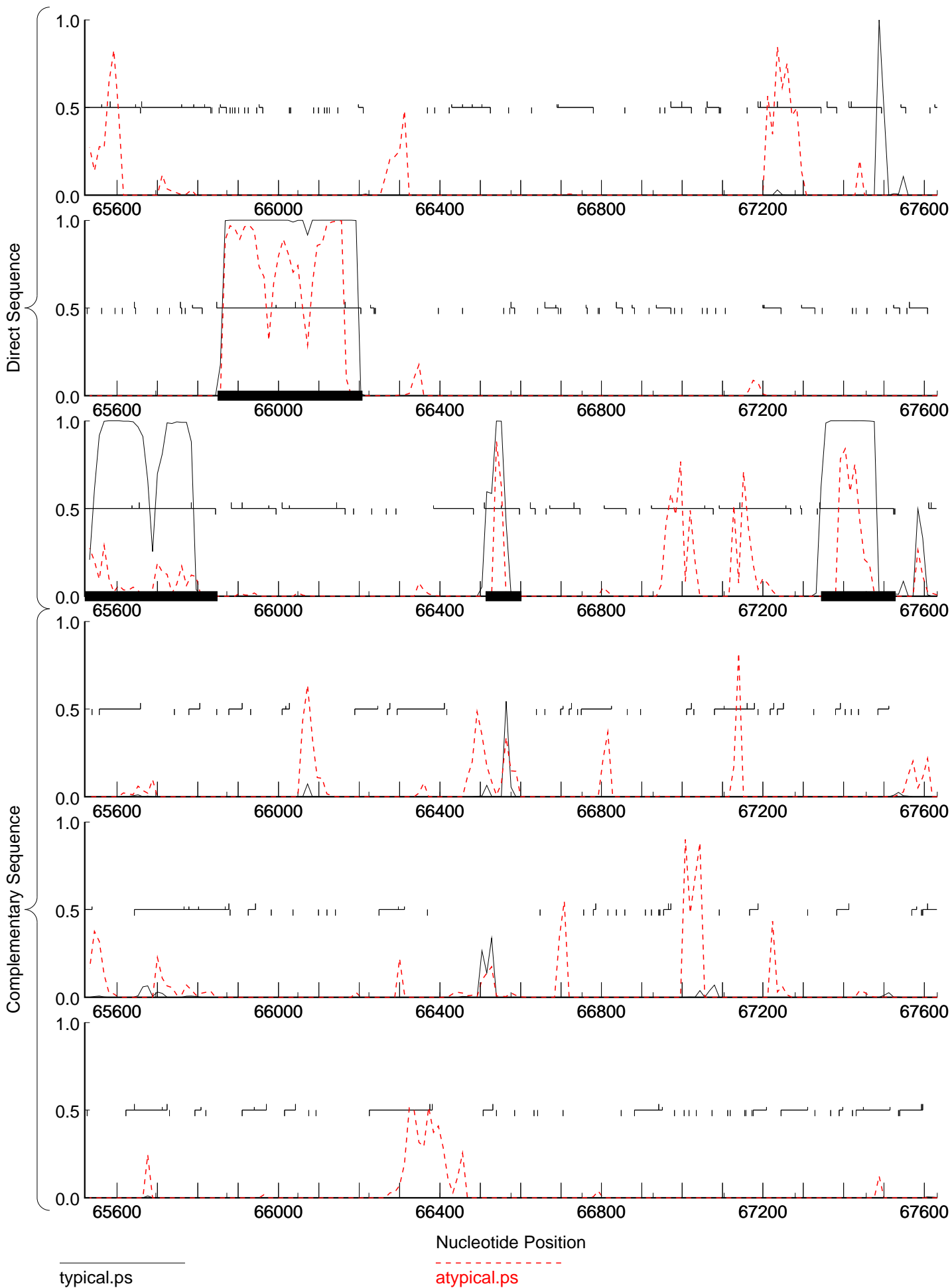
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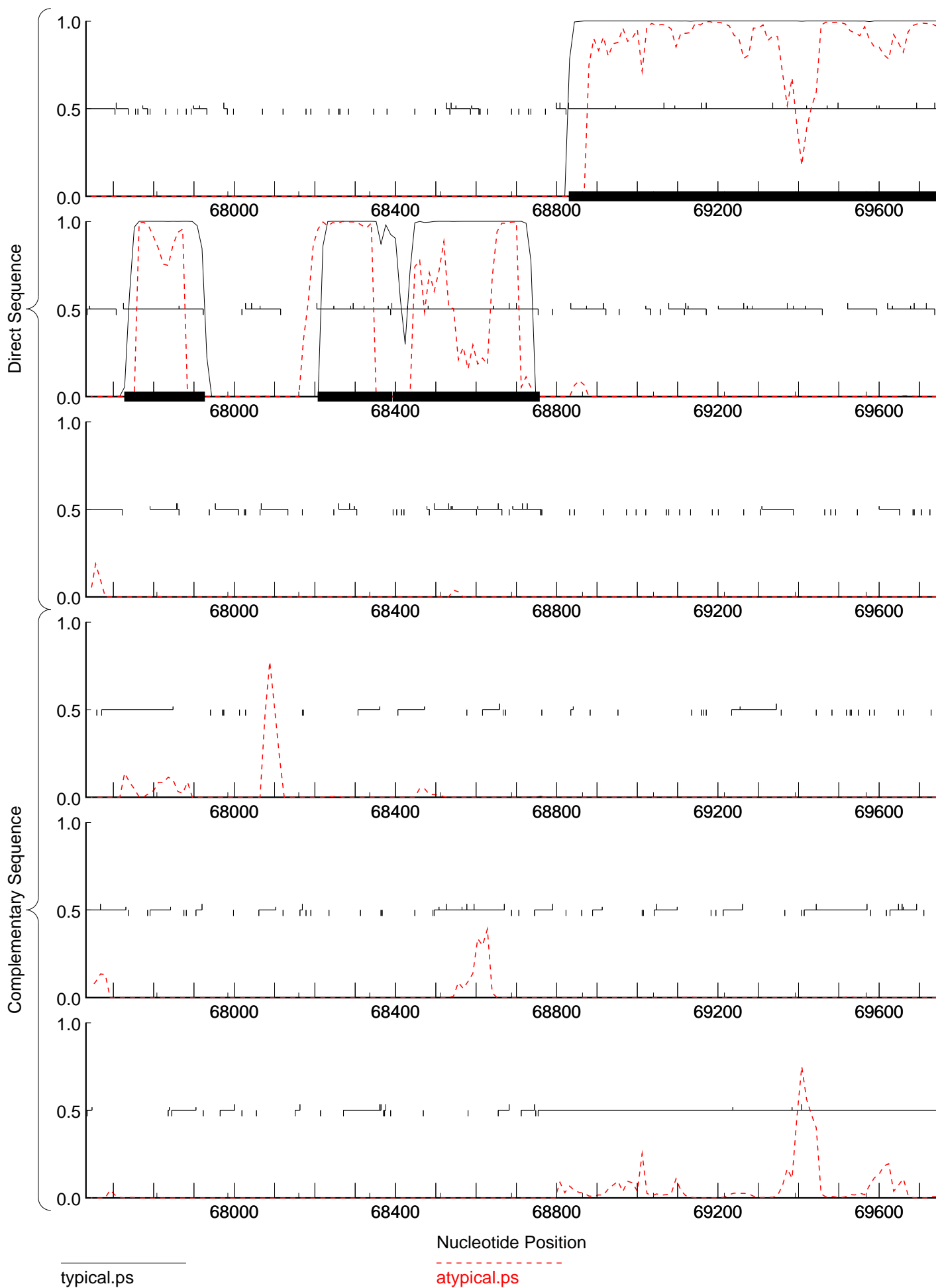
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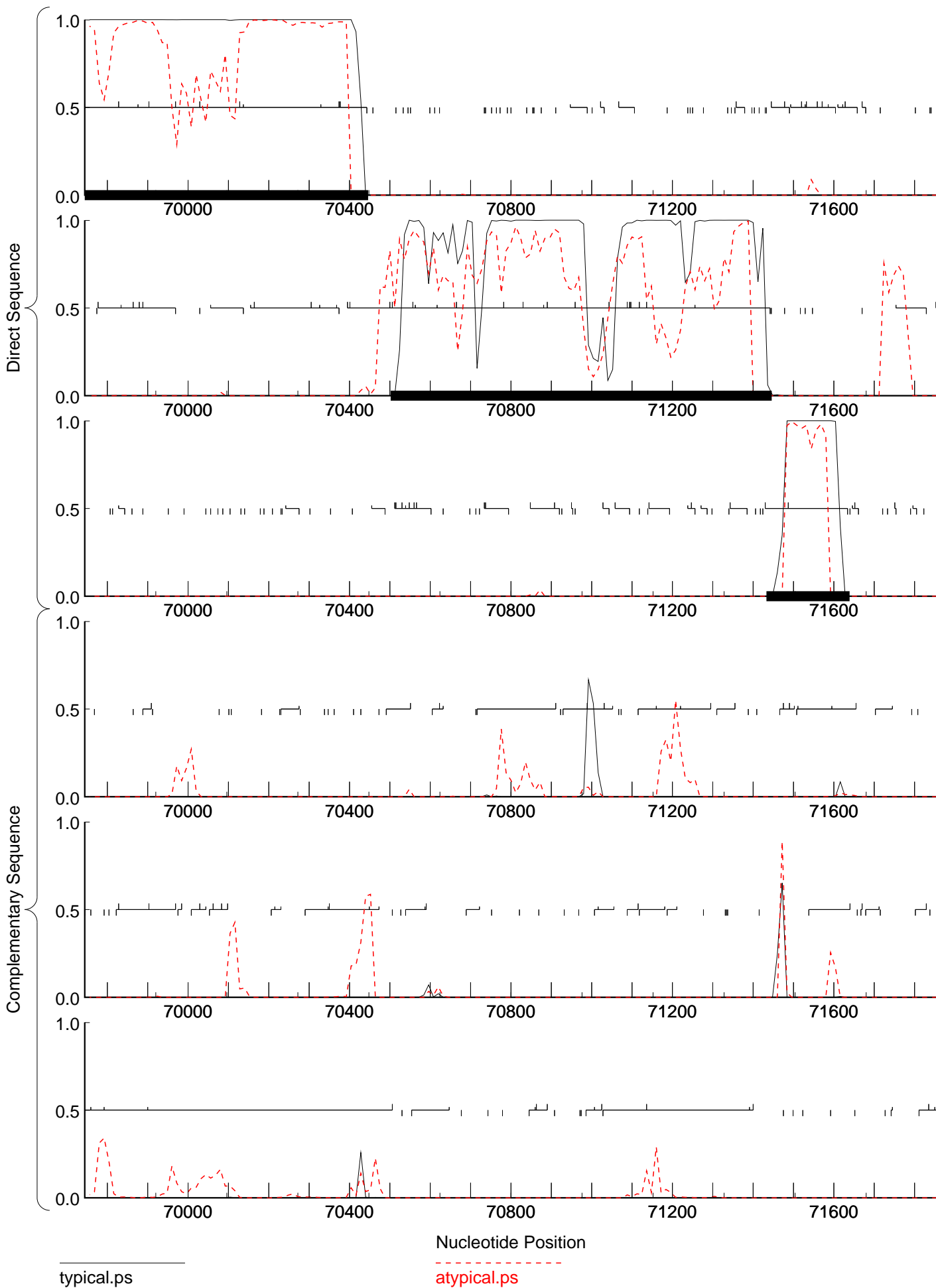


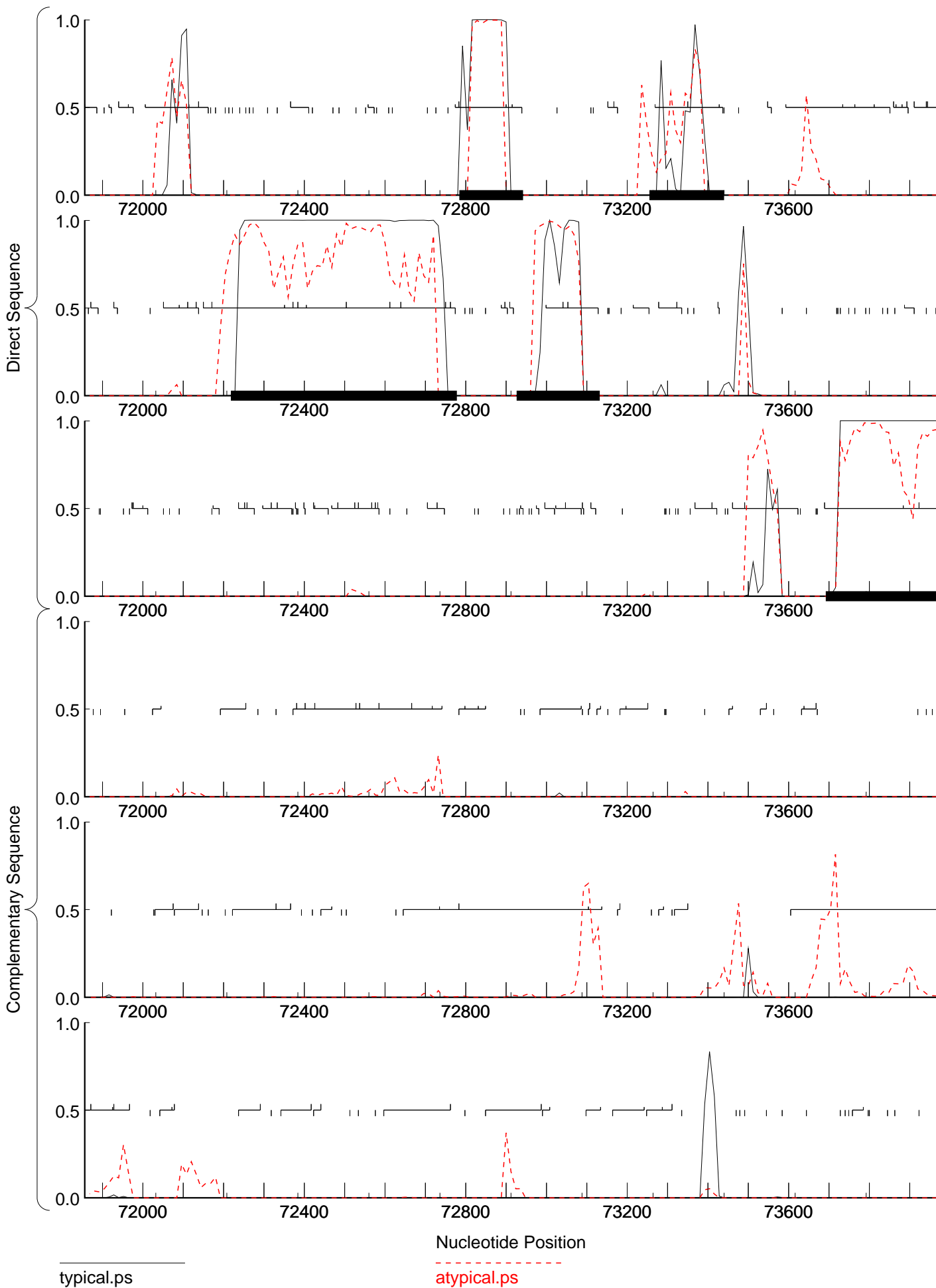


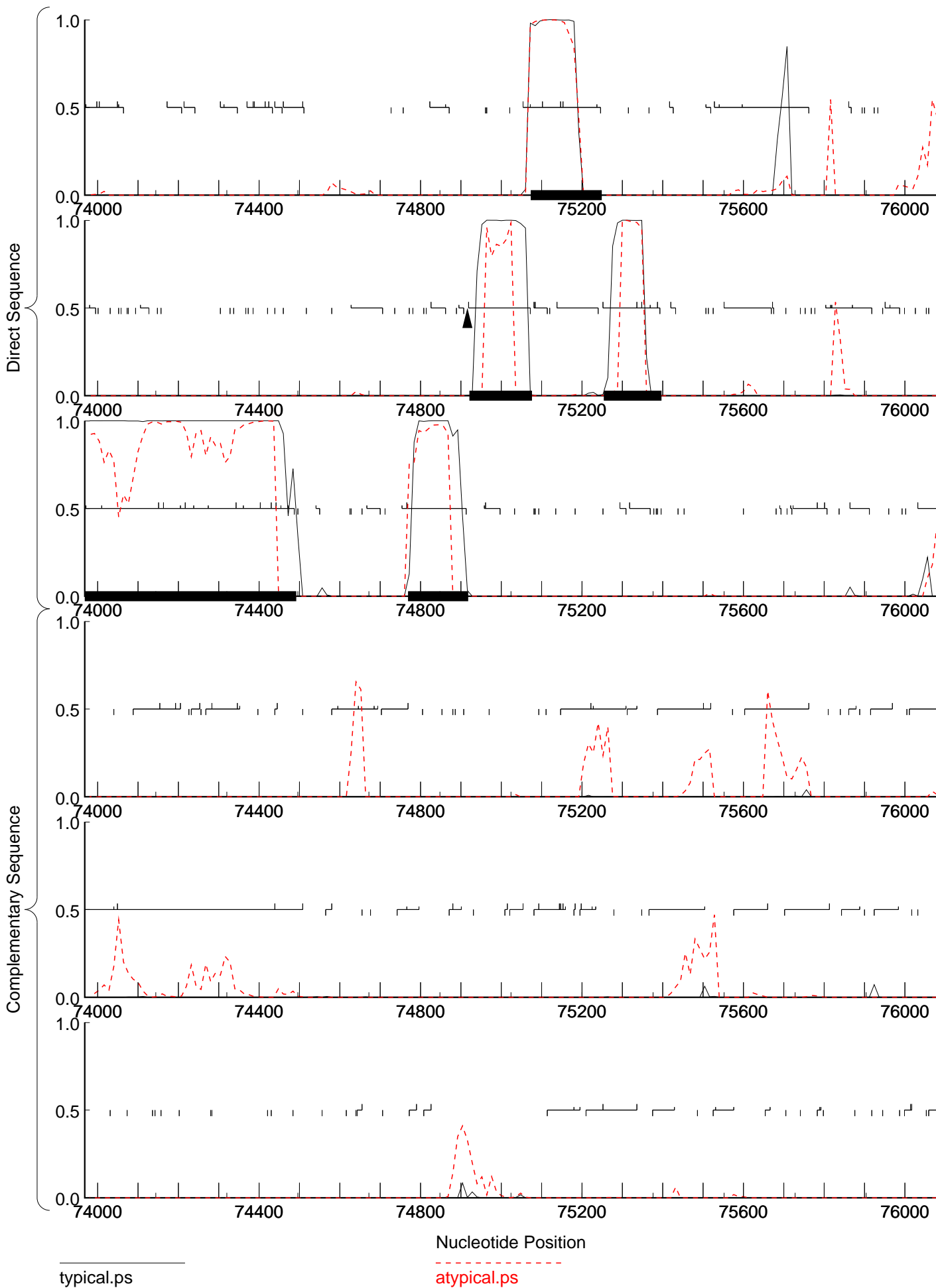


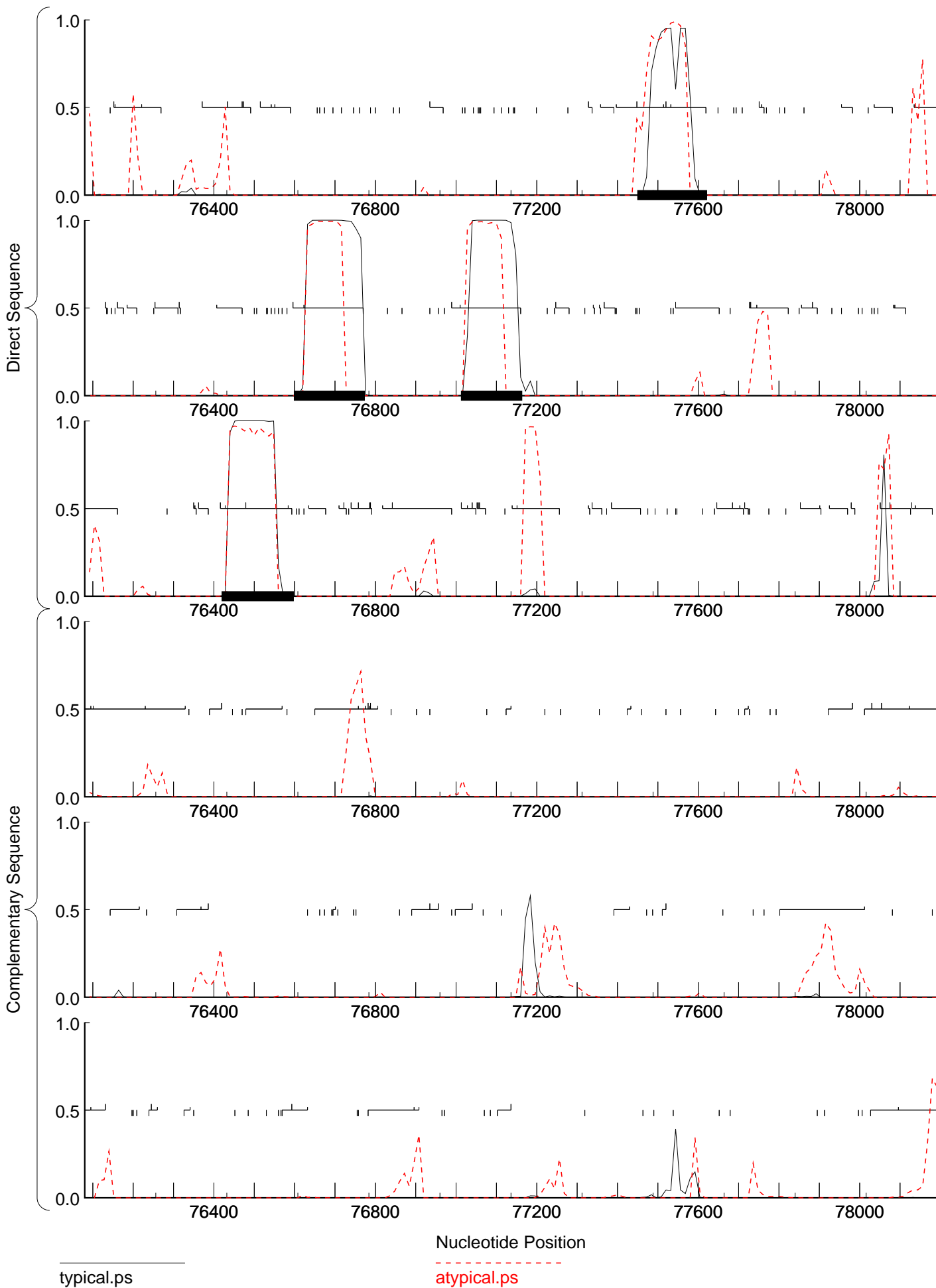






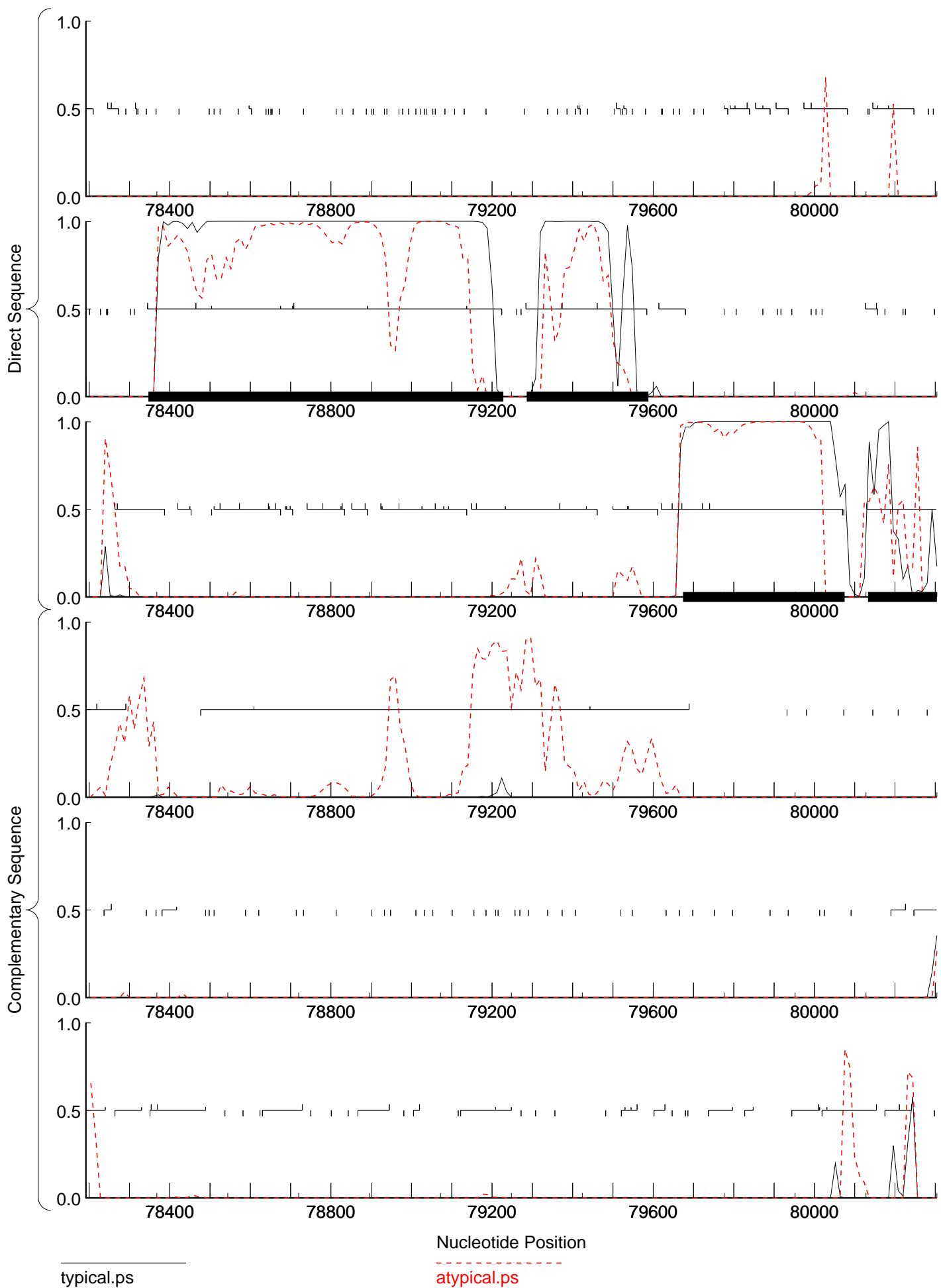




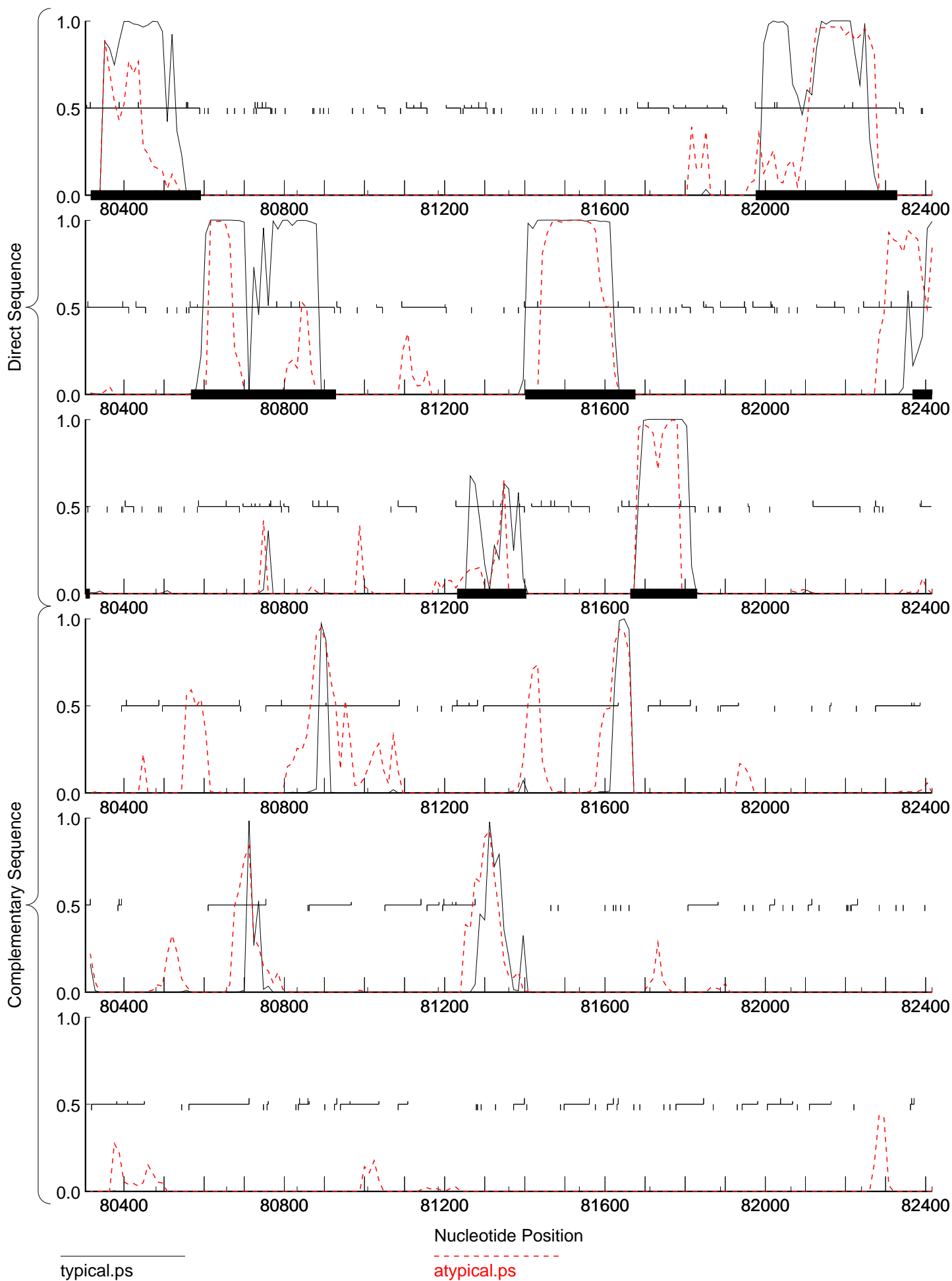


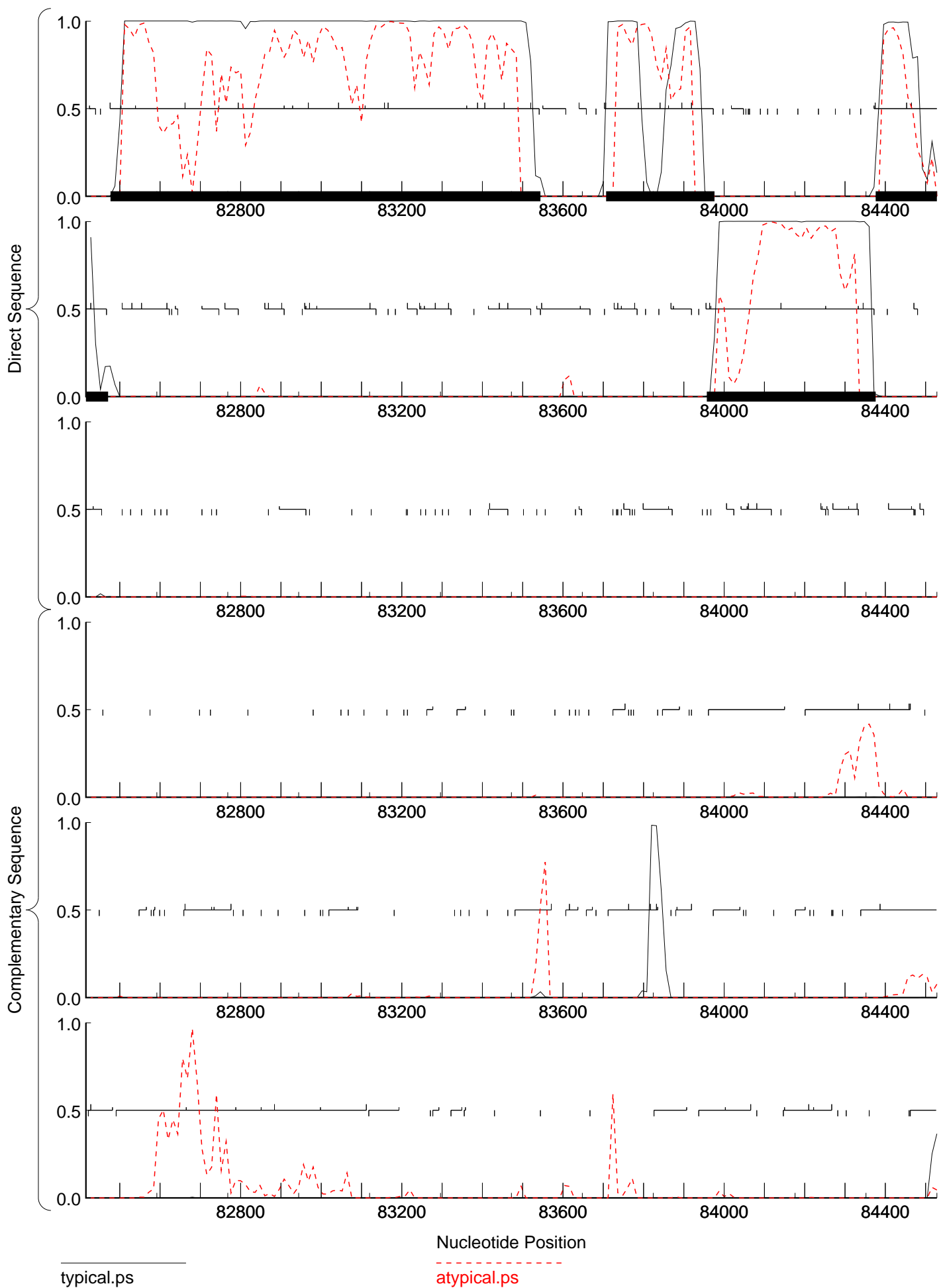
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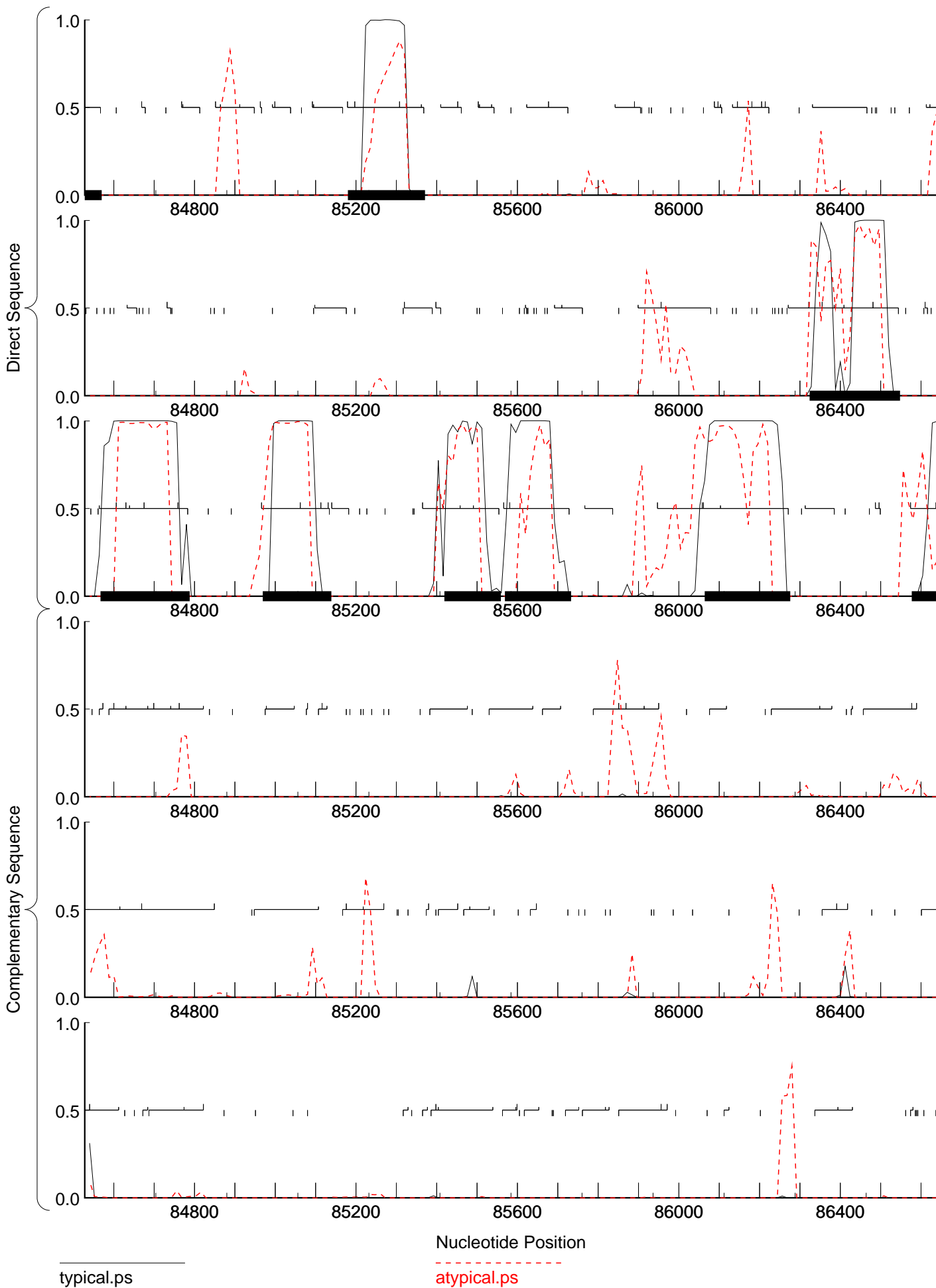
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GeneMark.hmm prediction

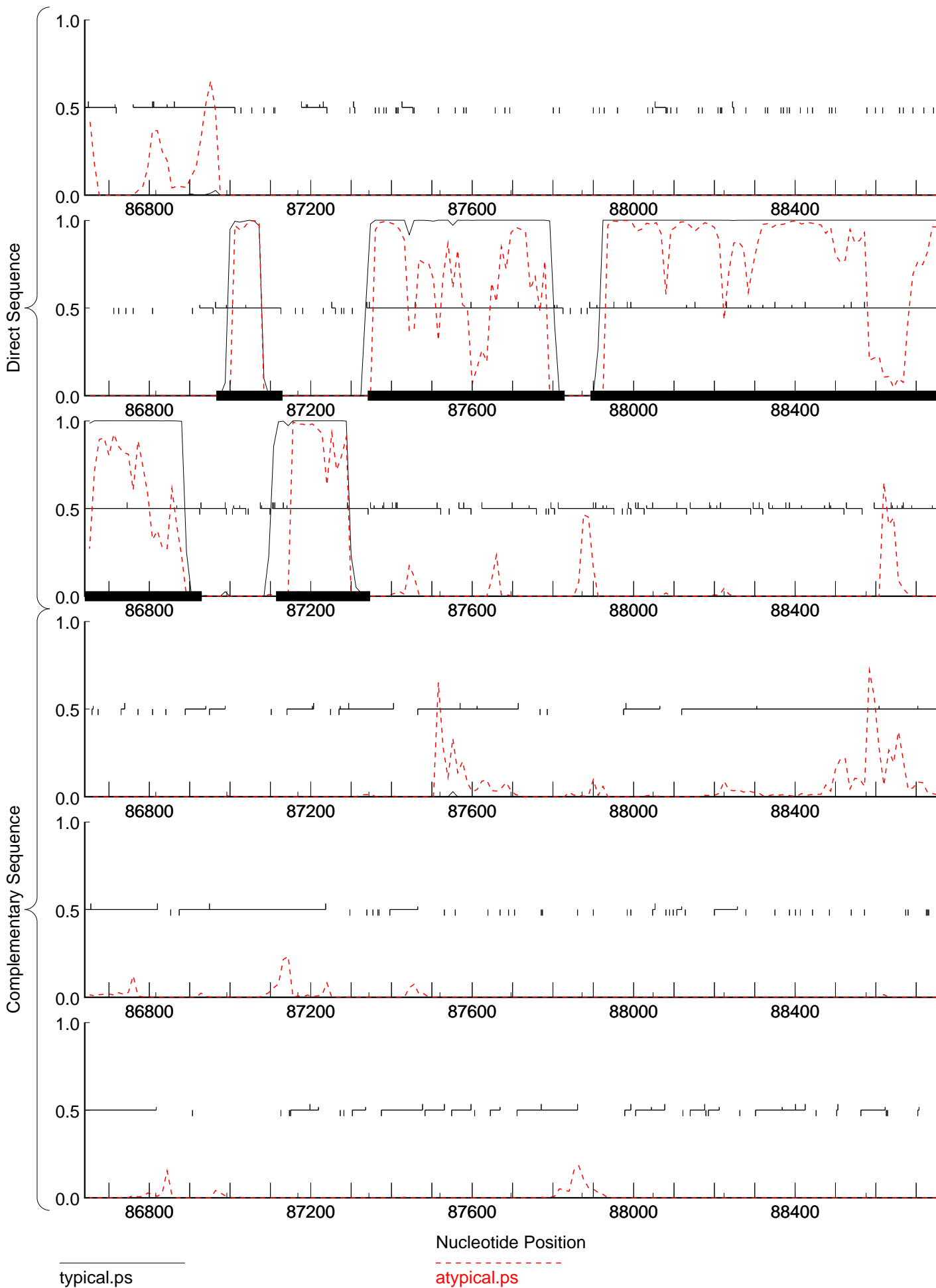


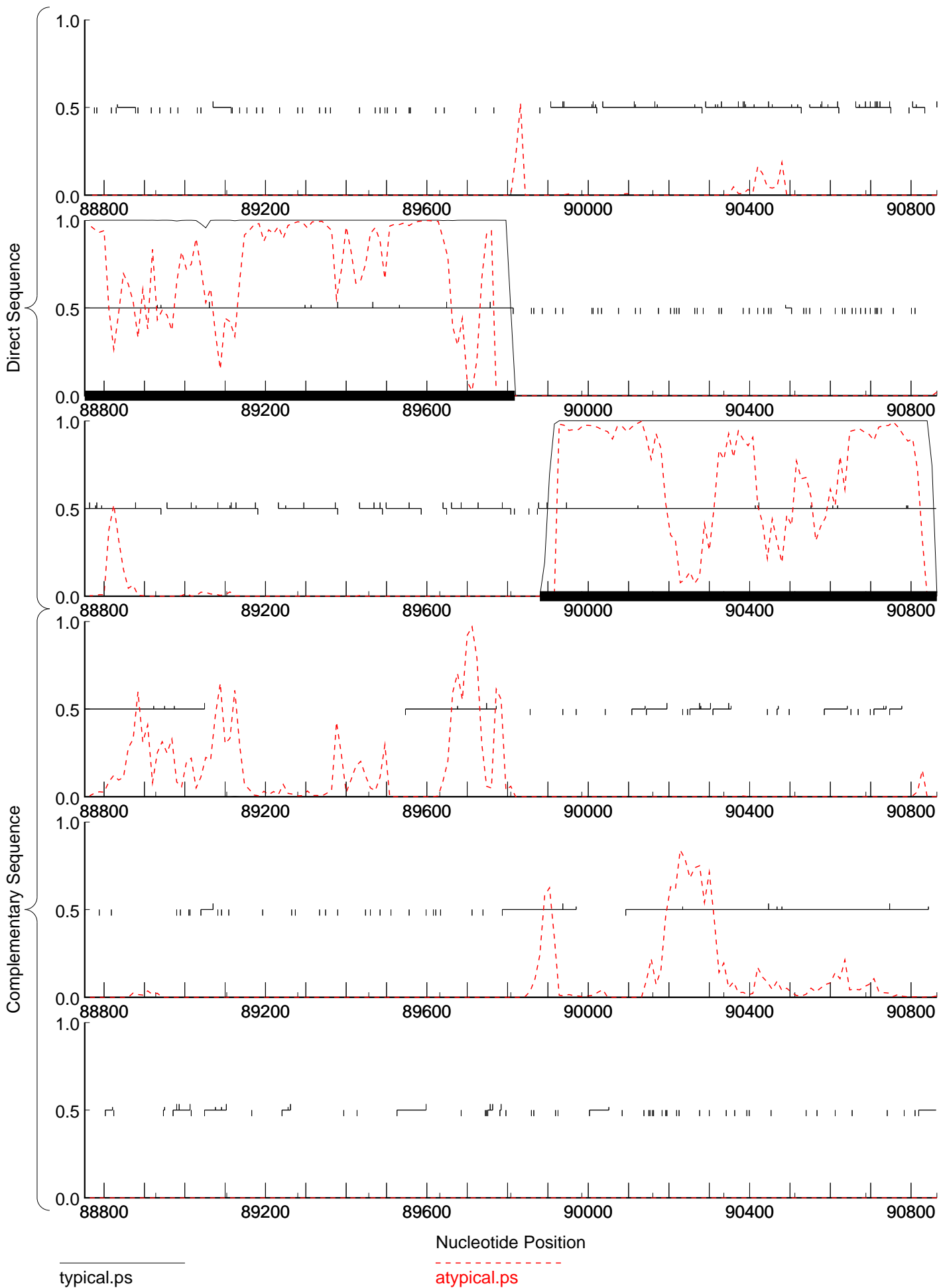


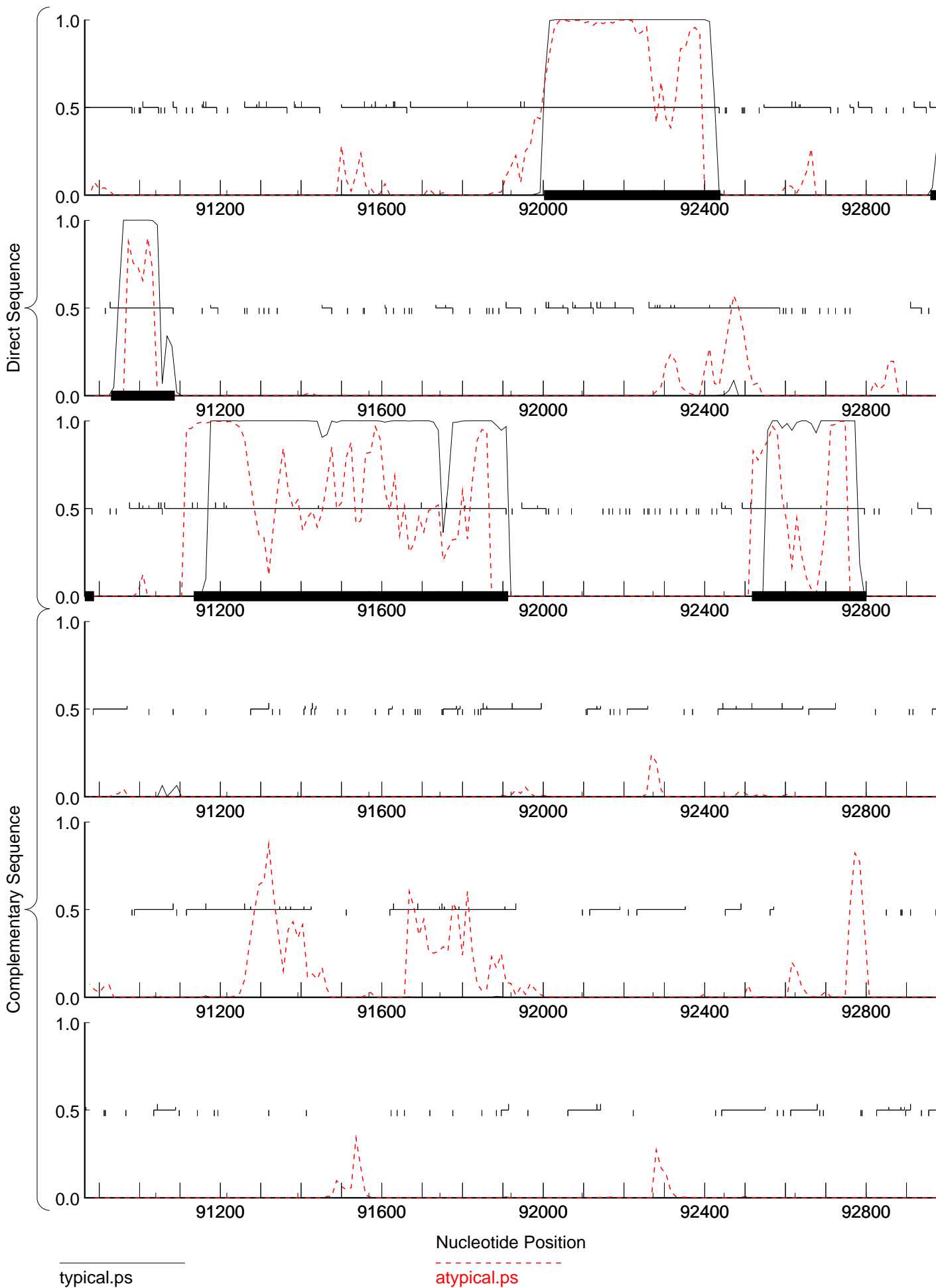


typical.ps

atypical.ps

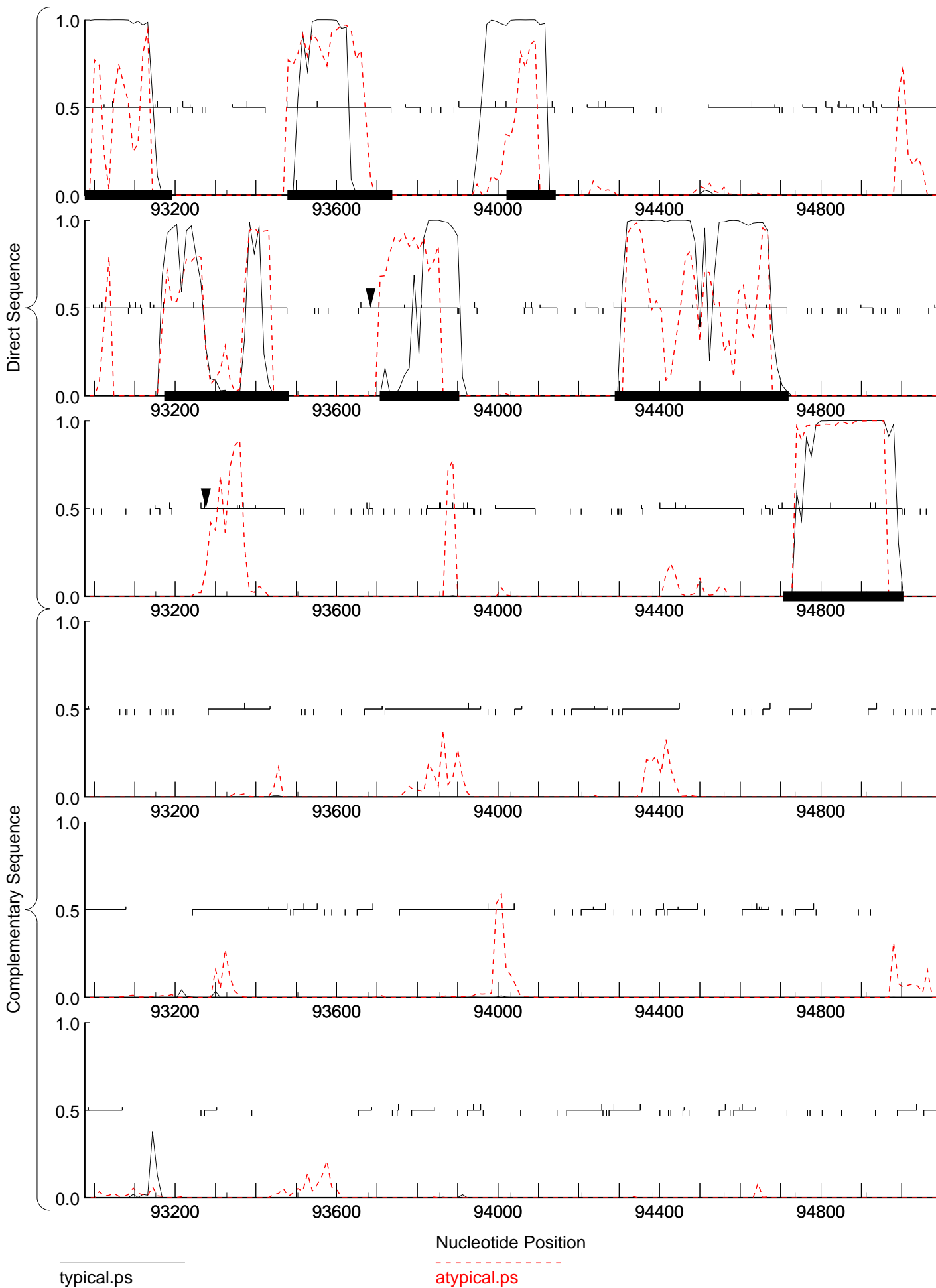


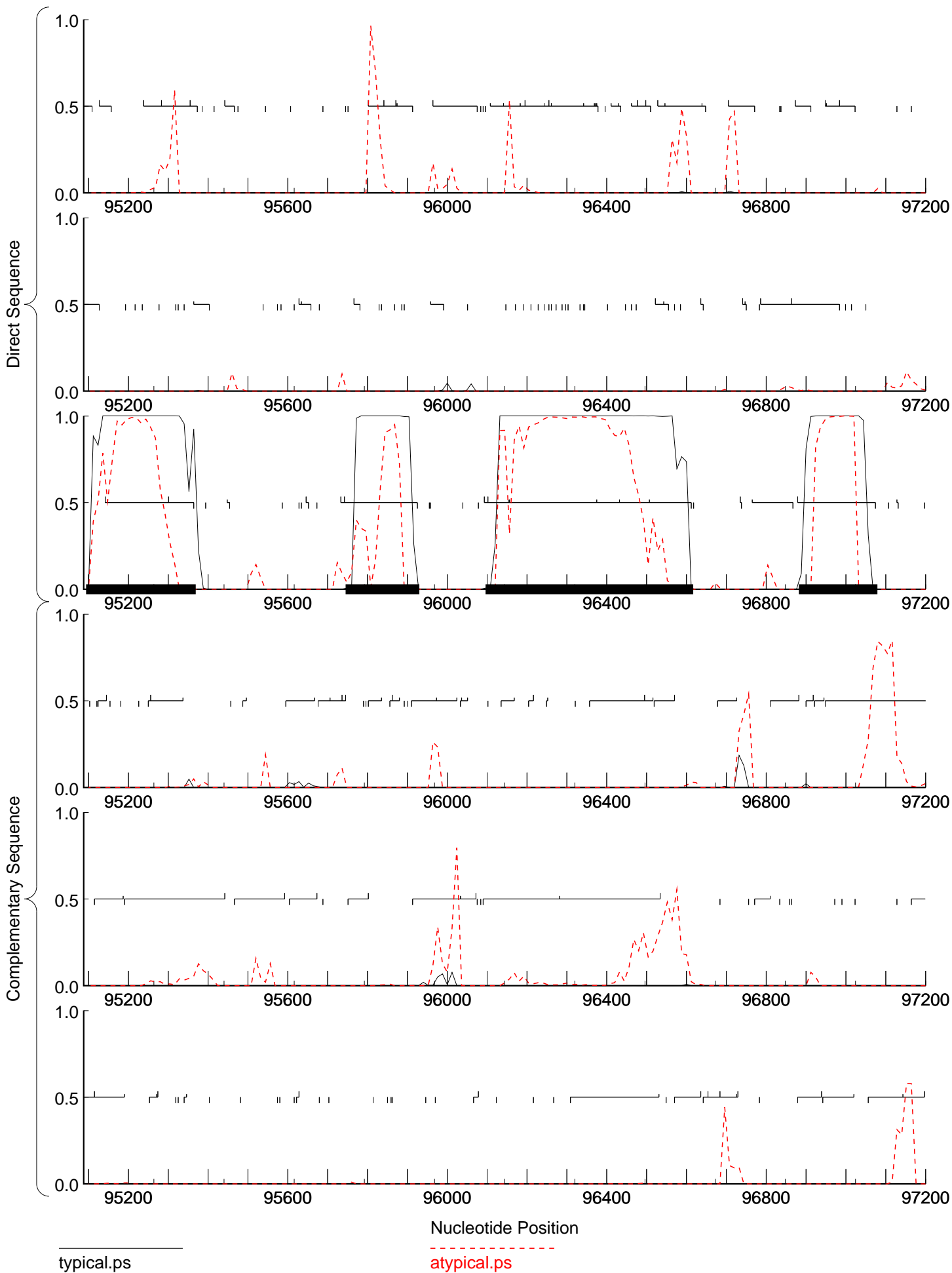


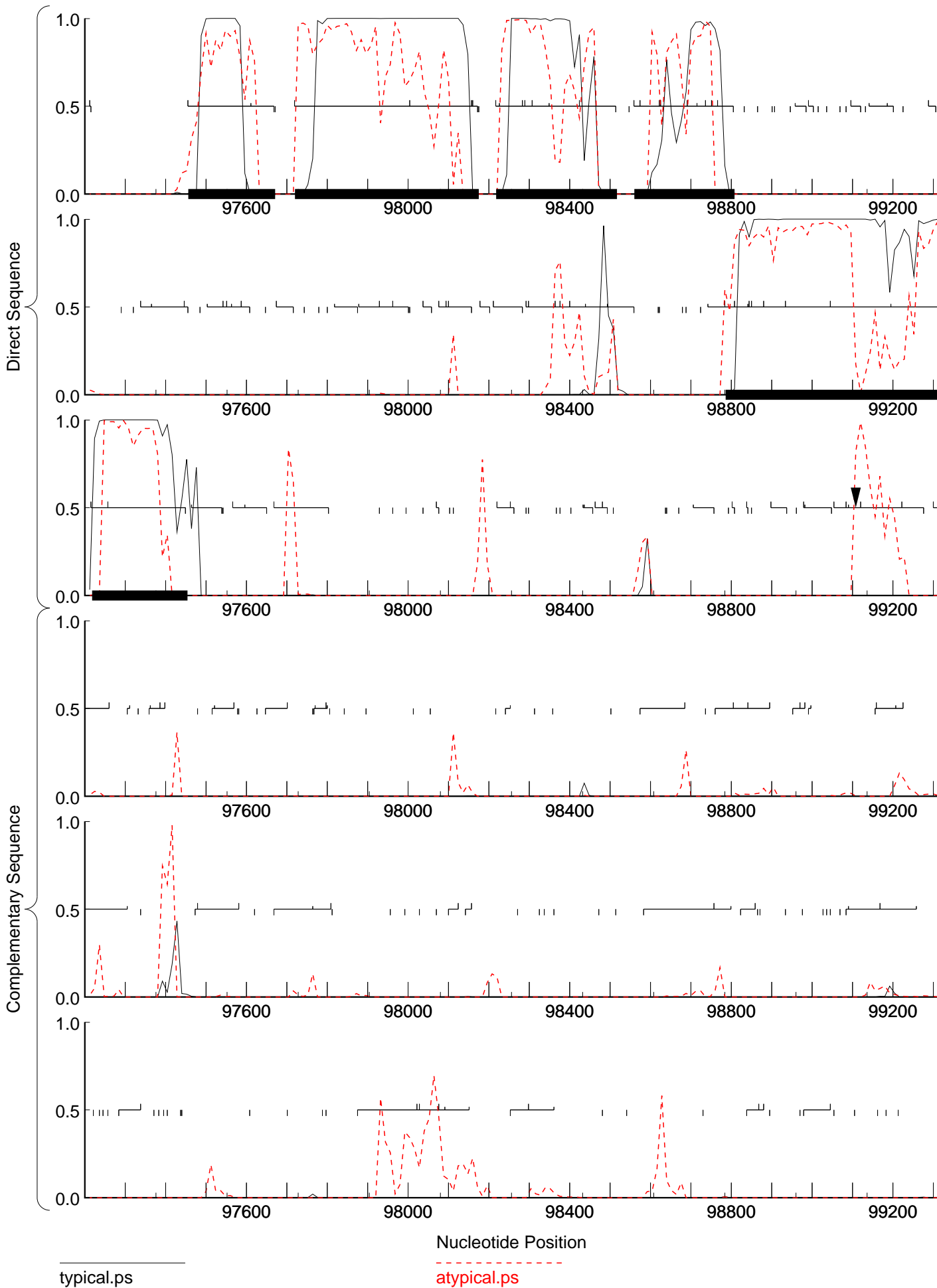


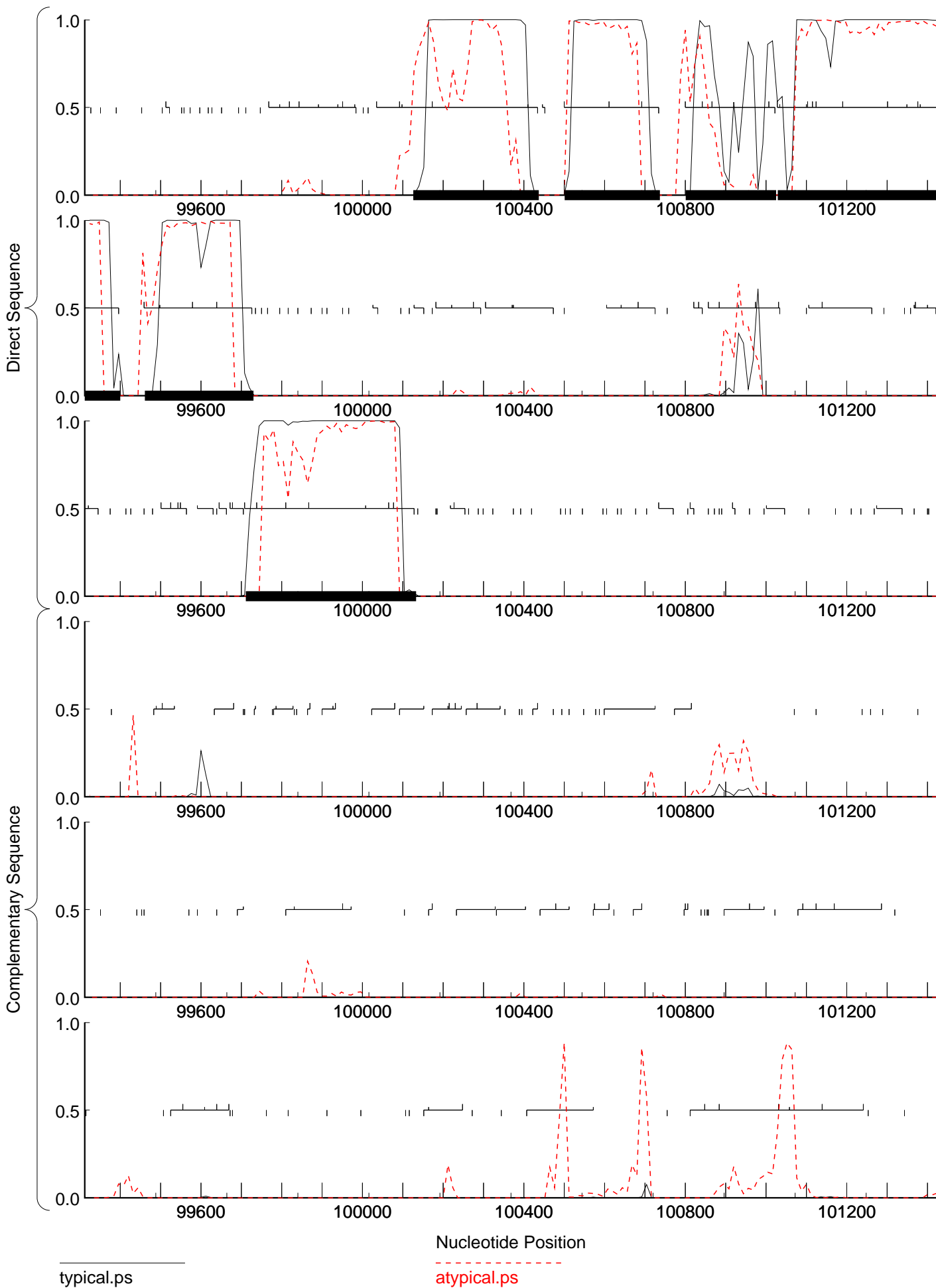
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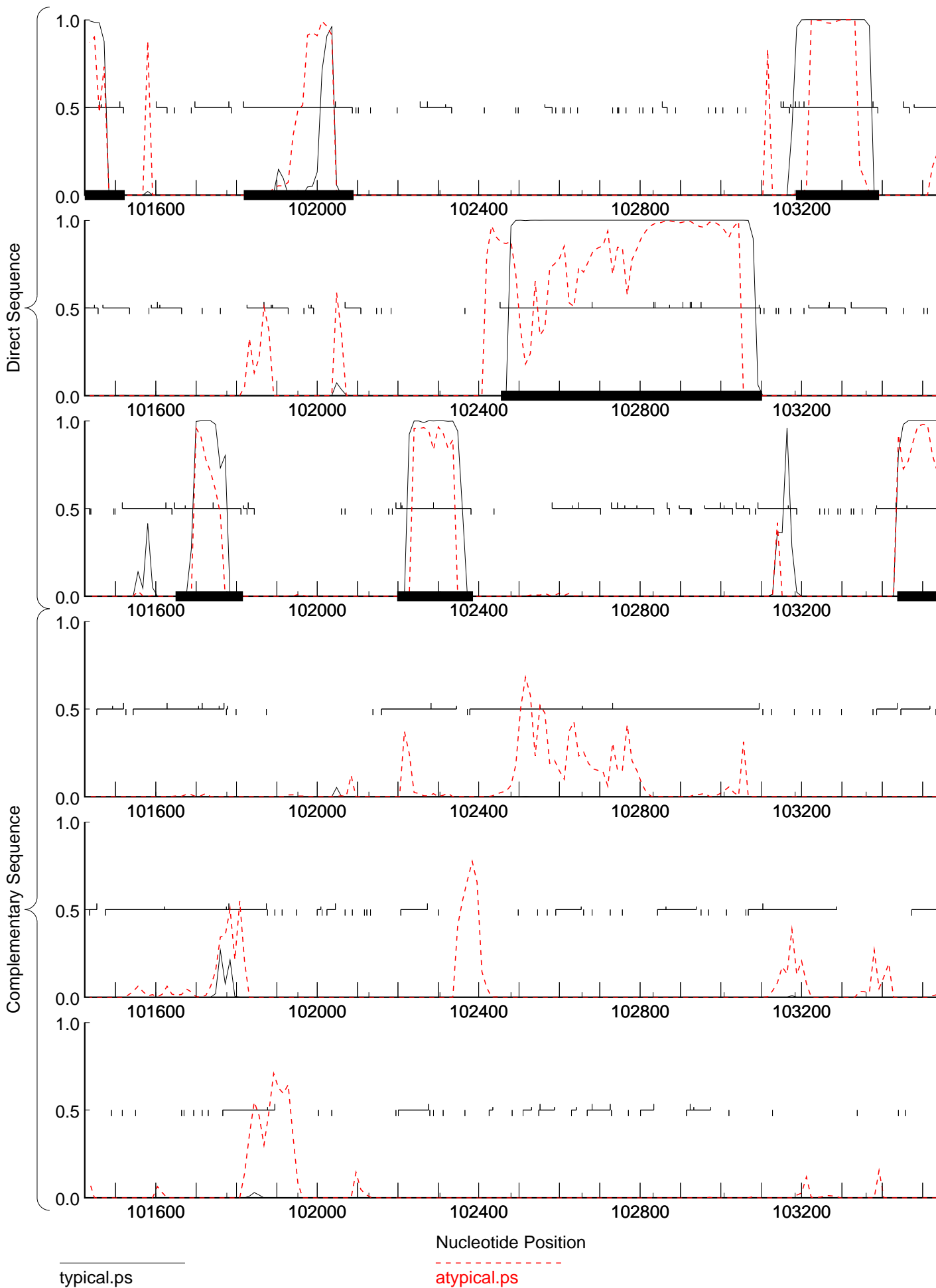
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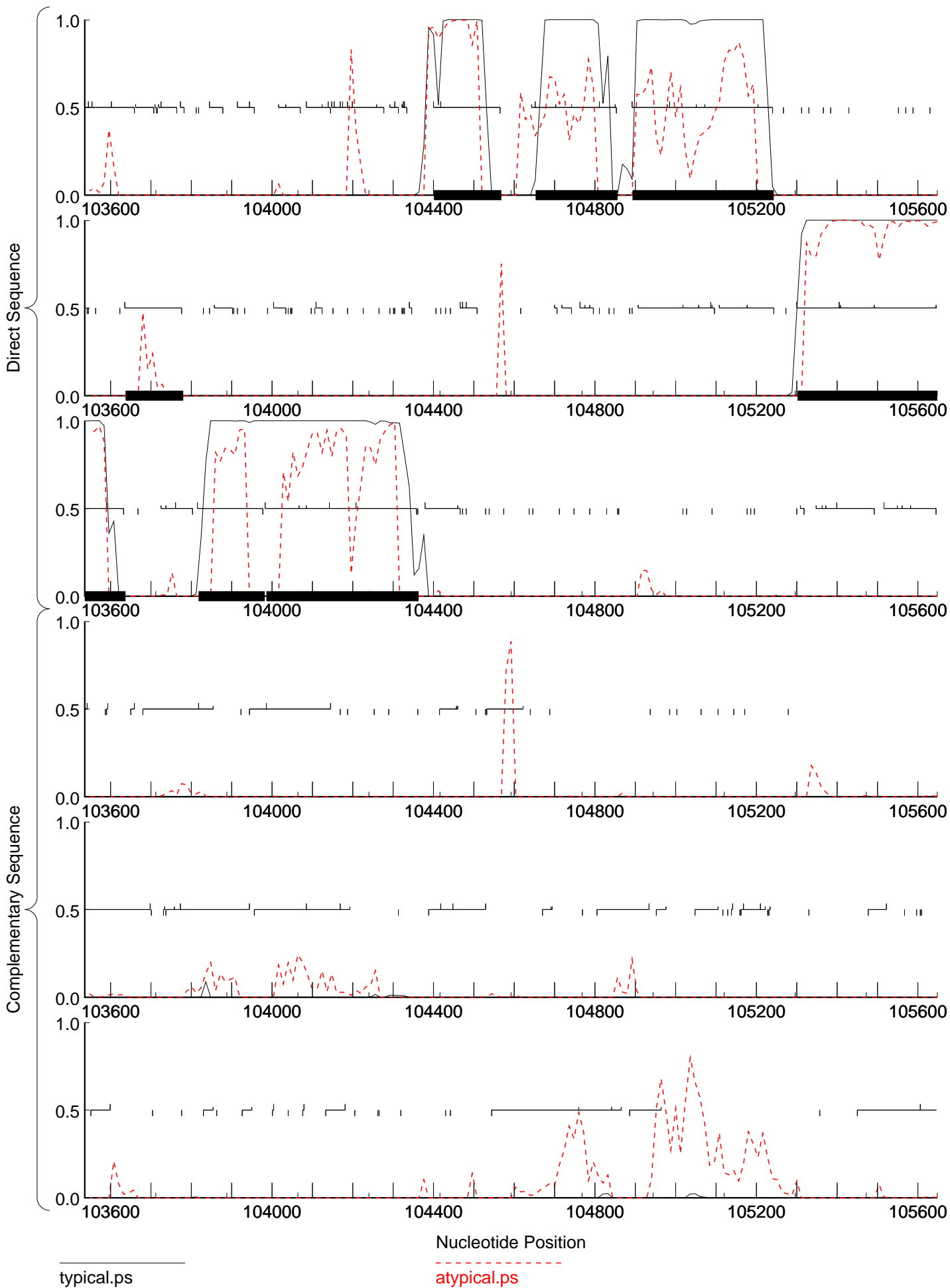


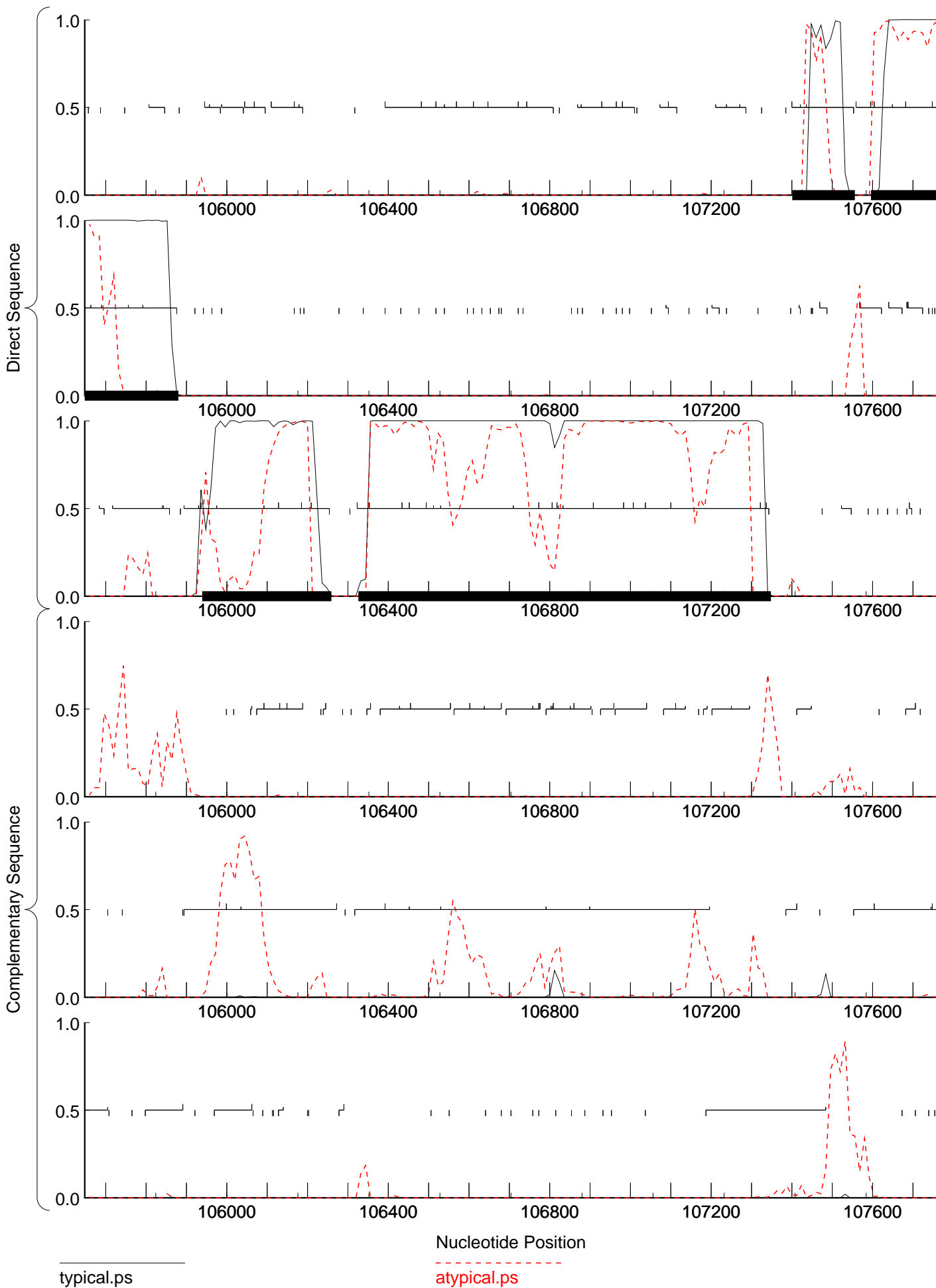


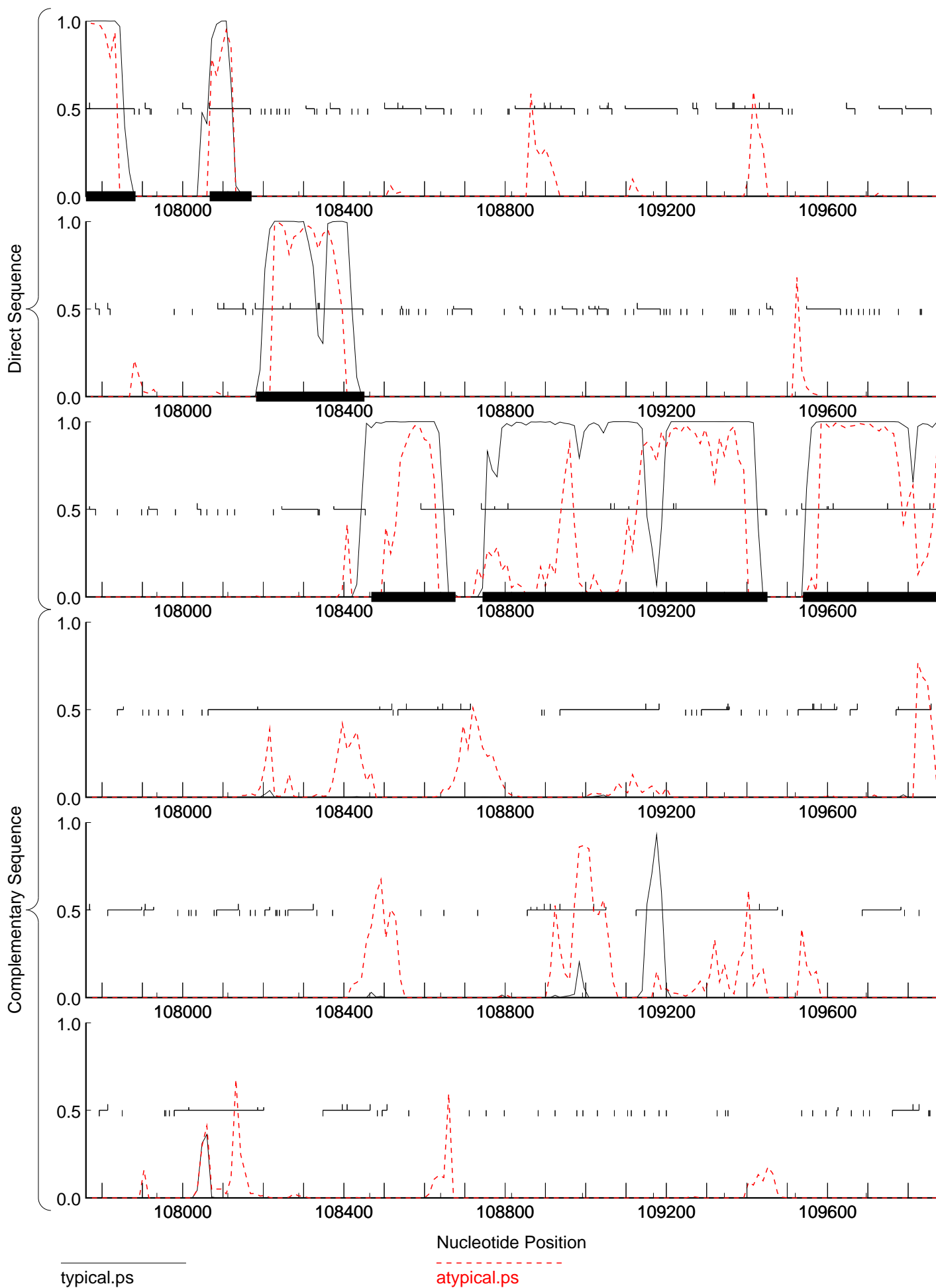






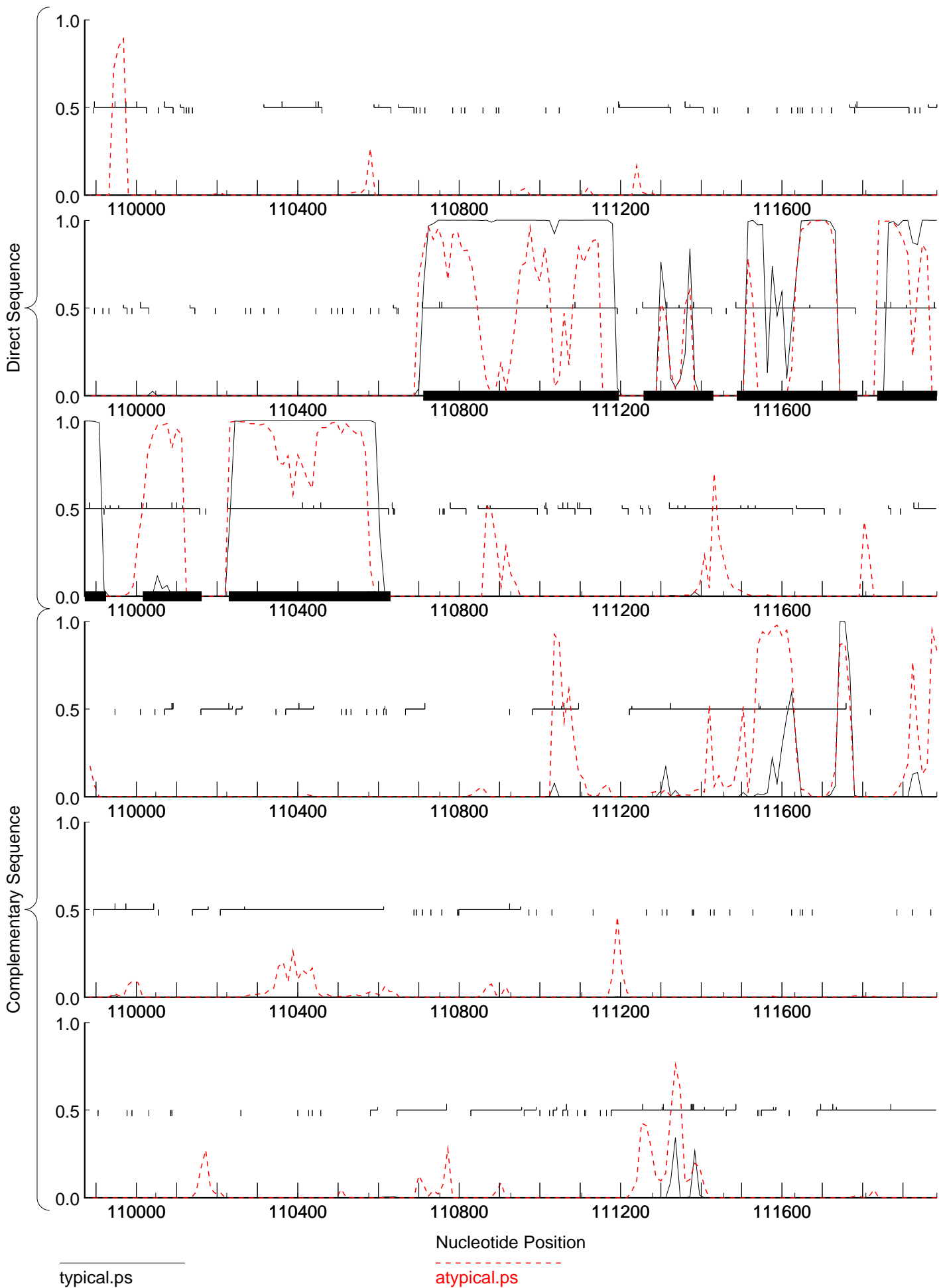


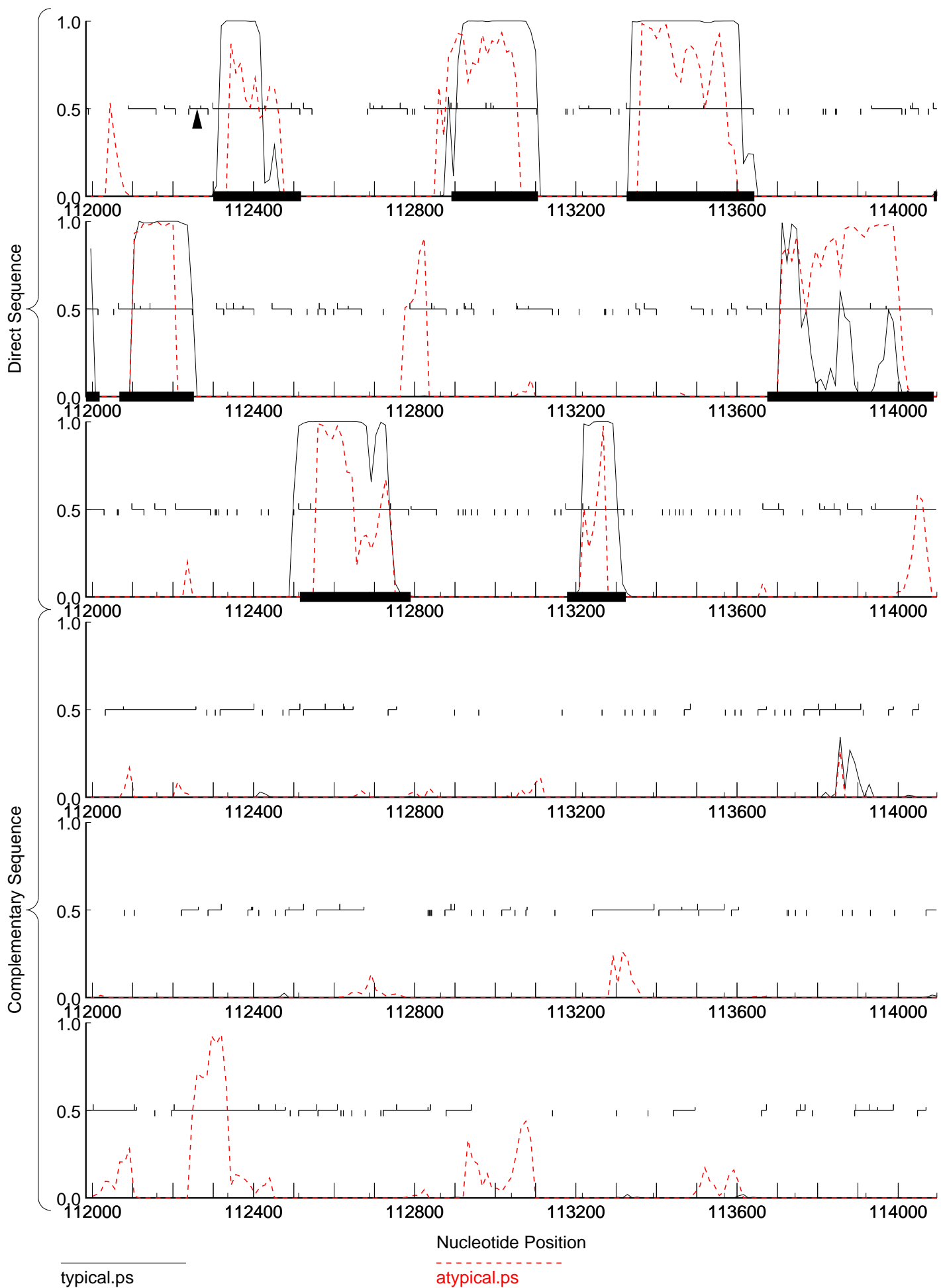




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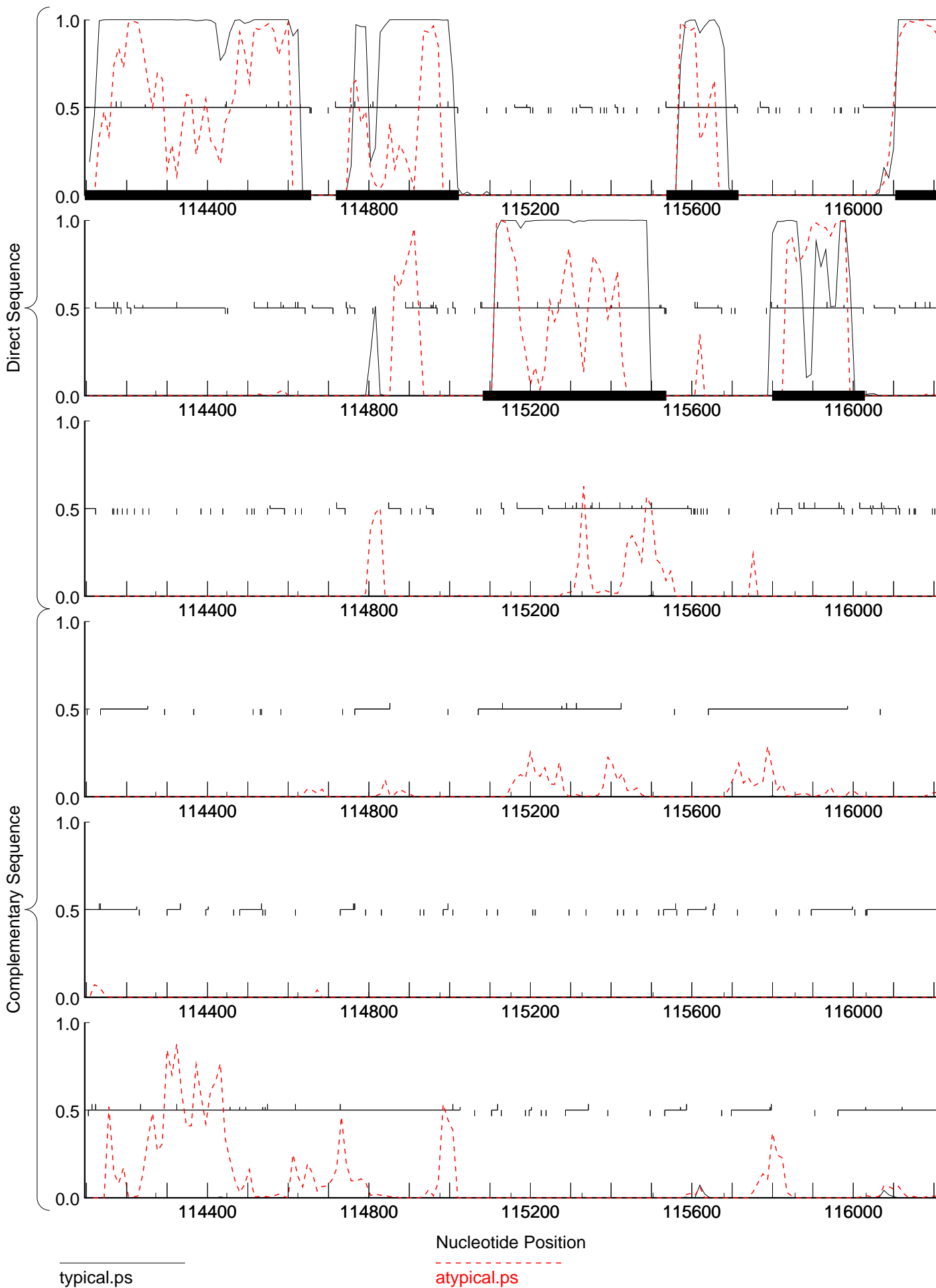
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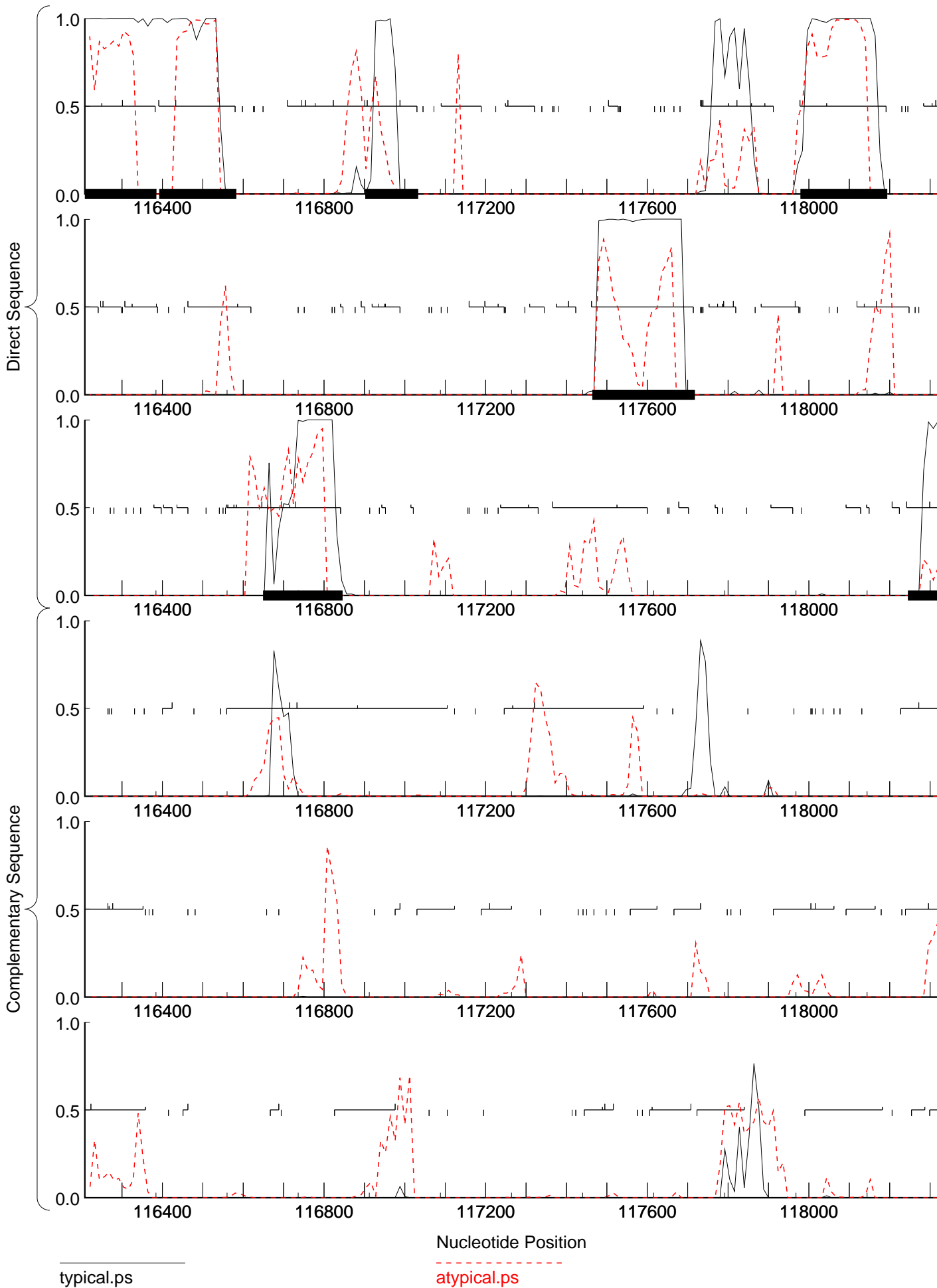
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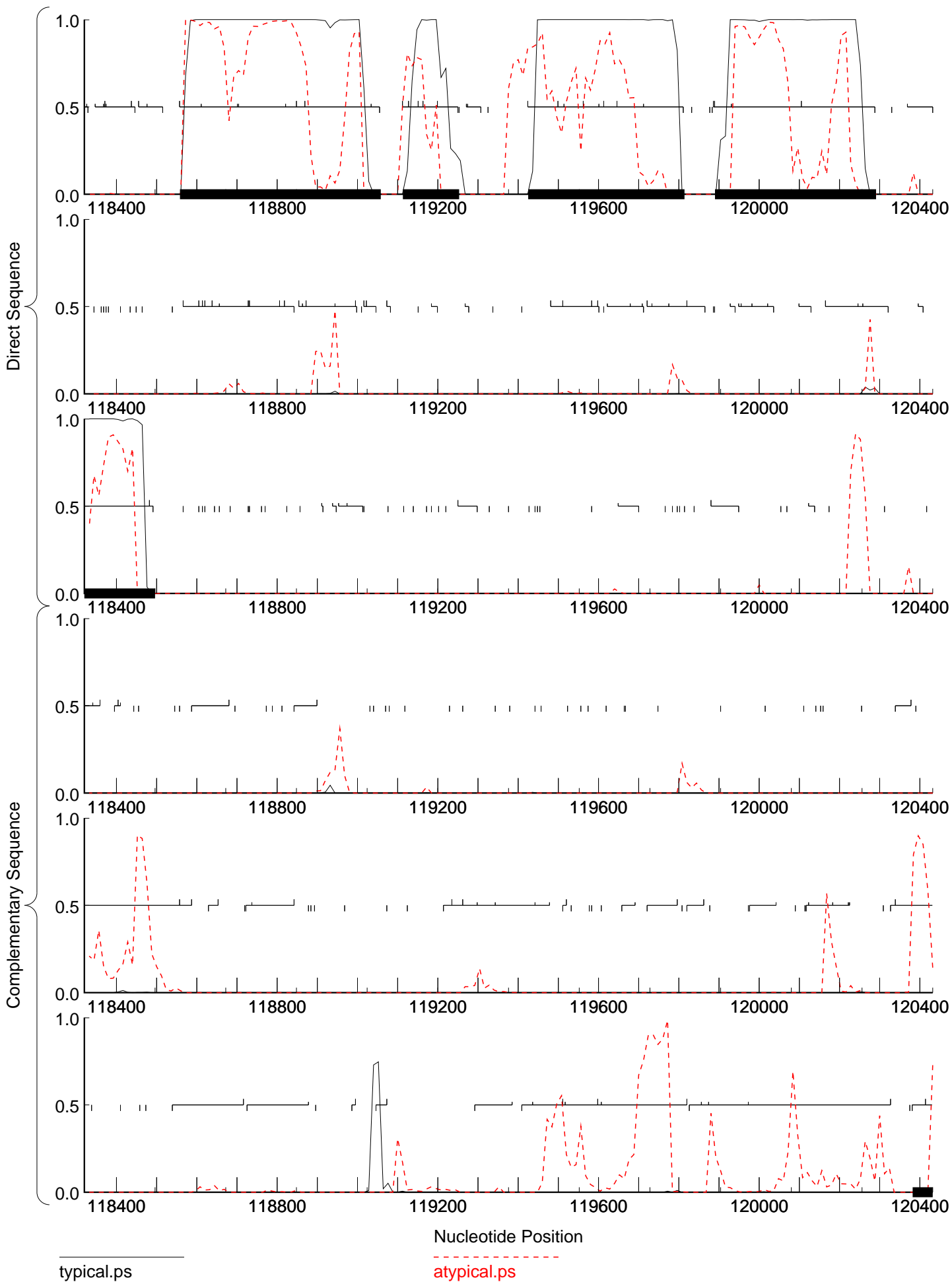
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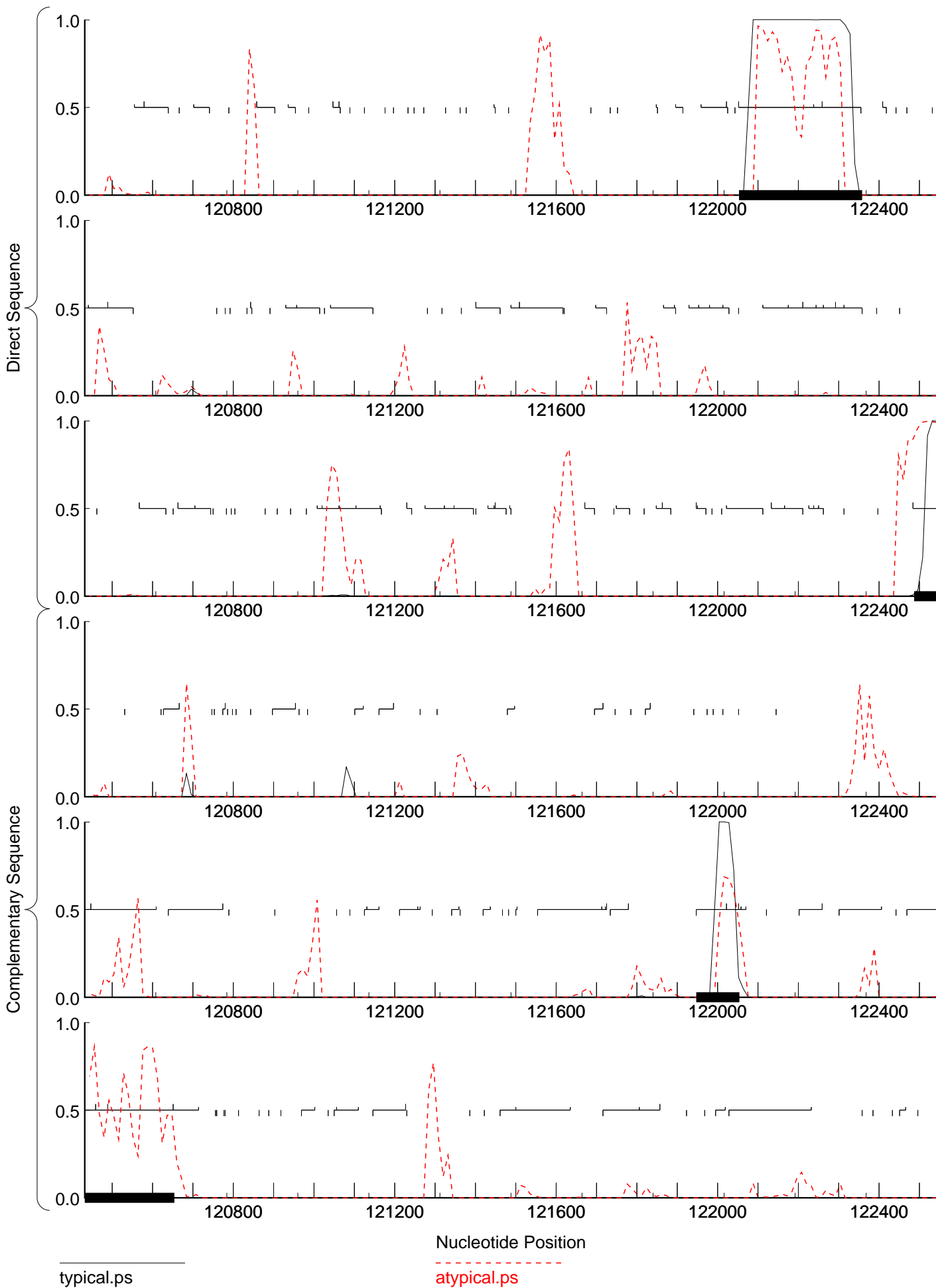
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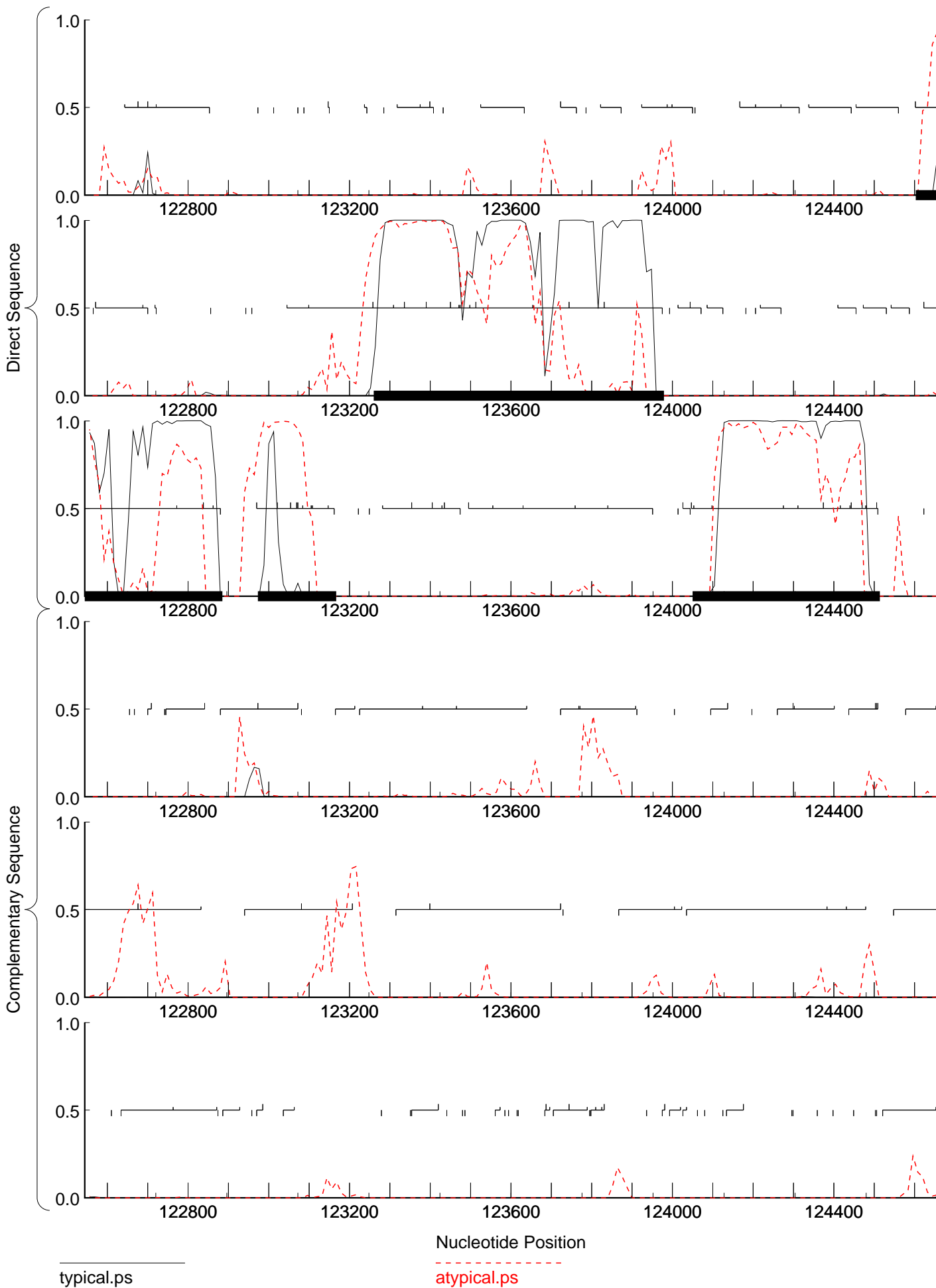


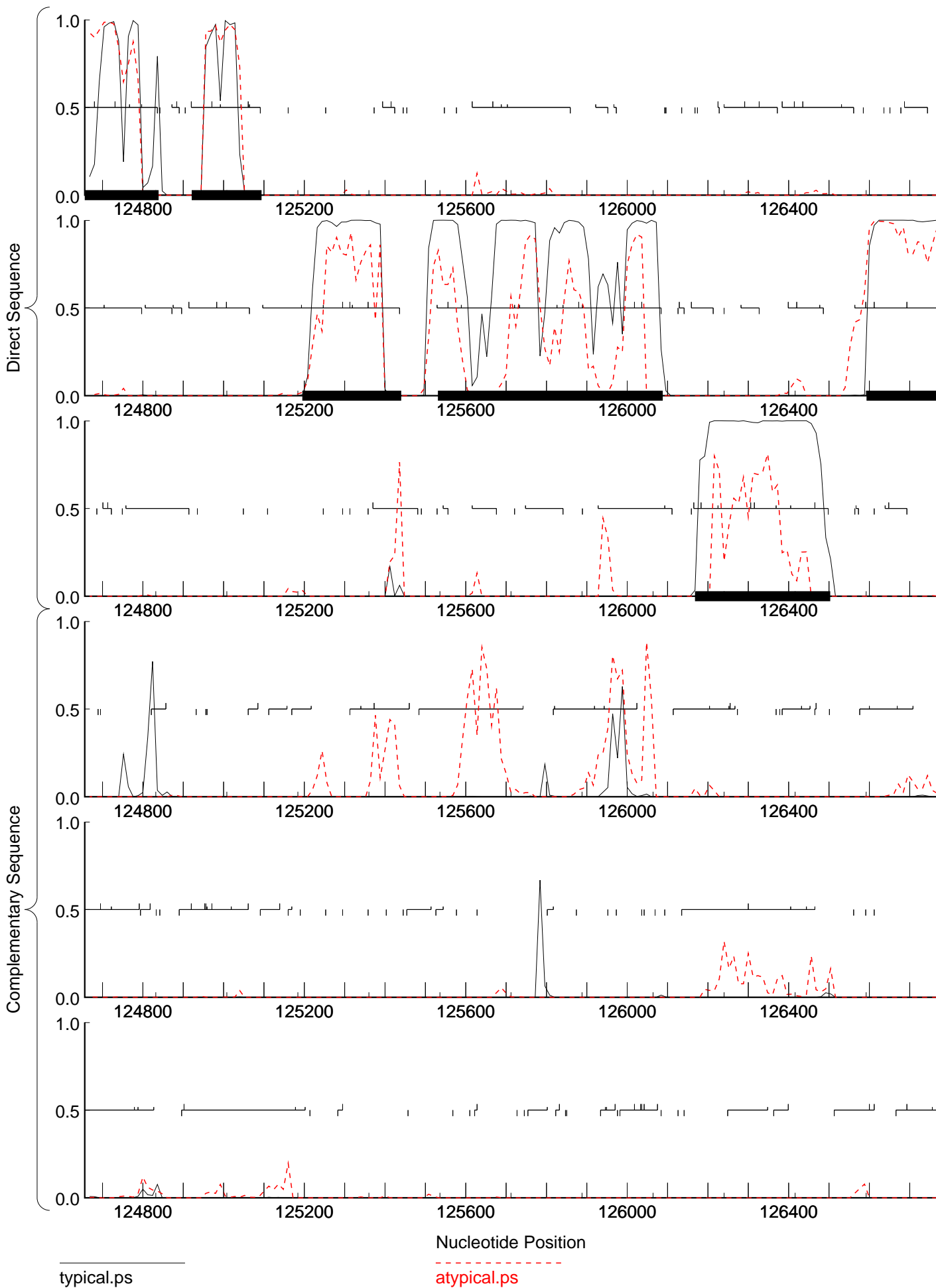


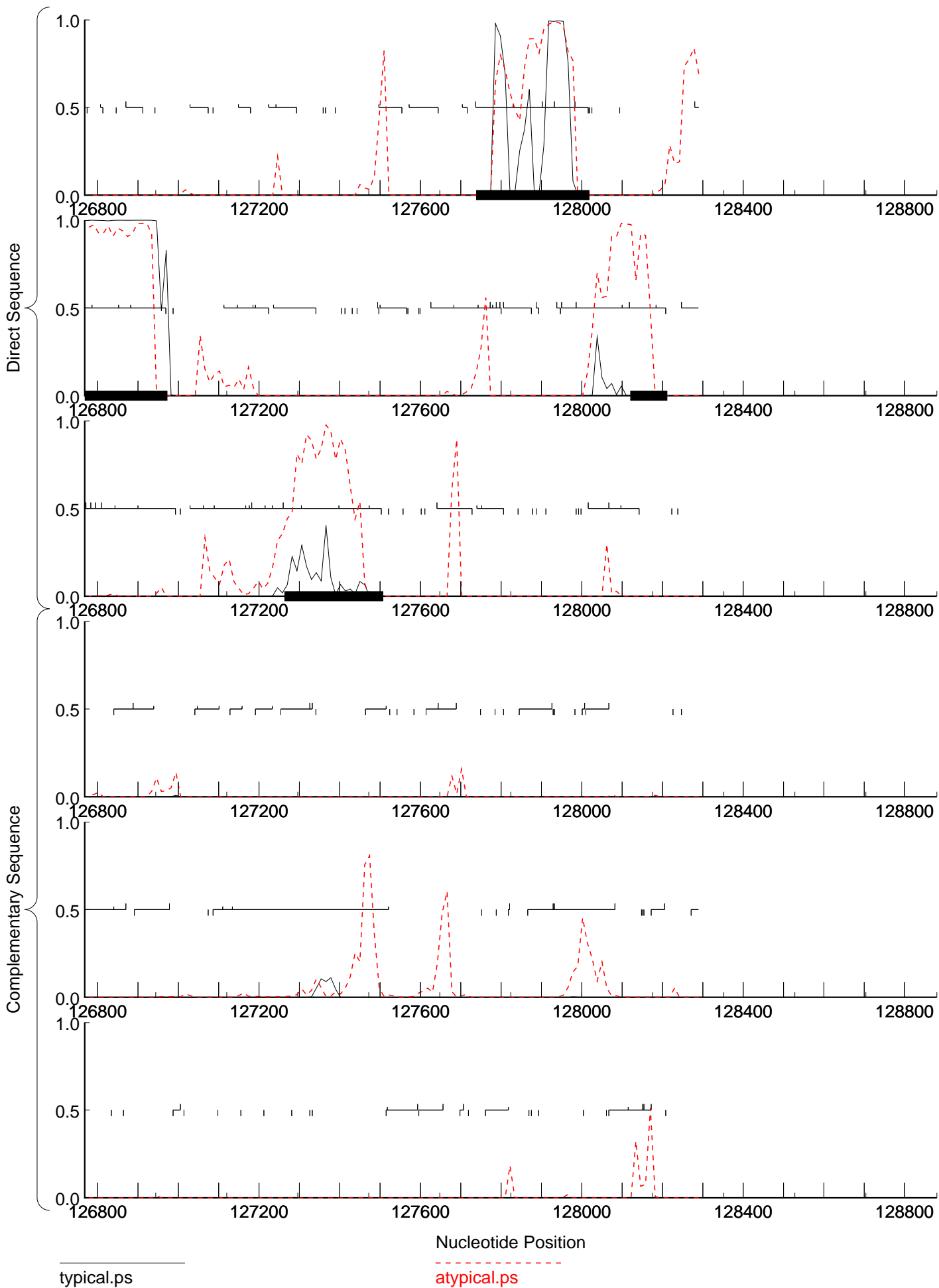
typical.ps

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