Figure S3. Secondary structure prediction of the N-terminal region of Tip from Herpevirus saimiri strains and Tio from Herpesvirus ateles, performed using PSIPRED (http://bioinf.cs.ucl.ac.uk/psipred/psiform.html). The predicted amphipathic helix (red box) and the transmembrane domain (blue box) are indicated.

```
PSIPRED PREDICTION RESULTS
Кеу
Conf: Confidence (0=low, 9=high)
Pred: Predicted secondary structure (H=helix, E=strand, C=coil)
 AA: Target sequence
# PSIPRED HFORMAT (PSIPRED U2.5 by David Jones)
                          Amphipathic helix Transmembrane domain
Tip C488
Conf: 1103334333101111001040776321477899999998764358999999999999999999987310259
AA: ANLGERQASTURLHUKESNCKQPRERKANERNIUKDLKRLENKINUIICLUUUILAULLLUTULSILHIGMKS
                     210
                             220
Tip C484
Conf: 11033343321011110010317763214778999999998765689999999999999999999987310259
Pred: CCCCHHHHHHHHHHCCCCCHHHHHHCCH
 AA: ANLGERQASTURLHUKESNCKQPRERKANERNIUKDLKRLENKUNAIICLUUUILAULLLUTULSILHIGMKS
       200
               210
                      220
                             230
                                     240
                                            250
Tip C484-77
Conf: 22241024532105886454416764205778999999876556999999999999997051124777359
AA: ANLGASQASTURRHUREQNFKQLRERKANEGKIUKDLKRLEYKUNIILCLUUUILAIILLLTGLSILFIRIKS
                                             200
                       170
                              180
                                     190
        150
                160
Tio
AA: ANLGQKQSATSKNGPQIILREATEUESQQATDGQLNHRUEKUEKKLTCUICLLIGILULLILLFMLGFLFLLMK
     200
             210
                    220
                           230
                                   240
                                          250
```