SUPPLEMENTARY FIGURE 1. Predictions of putative nuclear export sequences in EB1a/EB1b and EB1c proteins using the NetNES 1.1 server (La Cour, et al., 2004).
(**A**) Analysis of EB1a and EB1b proteins showed one putative NES at the position 193I in EB1a protein; however, the score is low over the treshold. Main domains are marked at the DOG protein model (http://dog.biocuckoo.org/). (**B**) Analysis of EB1c protein showed four putative NES at the positions 213L, 215I, 217S, 218L. Main domains, D-motif and putative NLS are marked at the DOG protein model of EB1c. NN - neural network algorithm; HMM: Hidden Markov Model algorithm; NES score: combination of NN and HMM algorithms; CH: calponin homology domain; EBH: end binding homology domain; D: D domain (serves as a platform for interaction with MAPK).