SUPPORTING INFORMATION (Mänz et al.)

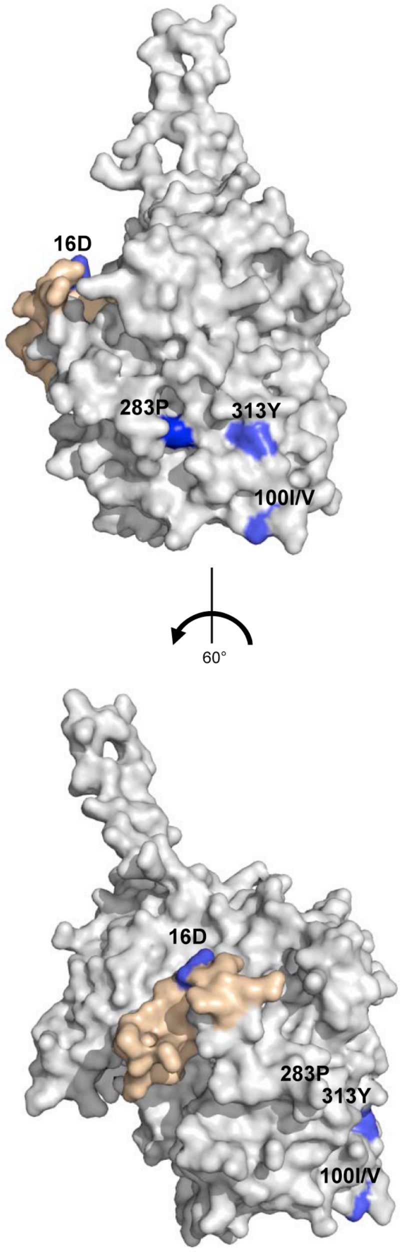

Fig. S4 Localization of the adaptive mutation 16D in NP.
The model for the full-length structure of H5N1 NP (A/Thailand/1(KAN-1)/04) harboring the mutations G16D, R100I, L283P and F313Y was generated utilizing I-TASSER. The N-terminus that was not resolved in the crystal structure (aa 1-20) is highlighted in light orange, whereas 1918-specific amino acids that confer Mx resistance are shown in blue (16D, 100I/V, 283P and 313Y).