





Figure S10. Pairwise nucleotide distance comparison plots (PDCPs) showing phylogenetic incongruence between selected genetic regions of H7Nx influenza viruses. Each dot represents a pair of raw nucleotide distances between two sequences in two genomic regions (axis labeling). The count value indicates the number of virus pairs per bin by a color gradient. The region of subsequent analysis was highlighted with the black boxes. **(A)** PDCP constructed for the concatenated full genomic sequences of H7N1 viruses for which pairwise distances were calculated for even and odd sites (negative control); **(B)** PDCP constructed for NS and HA segments of H7N1 influenza viruses; **(C)** PDCP constructed for the concatenated full genomic sequences of H7N2 viruses for which pairwise distances were calculated for even and odd sites (negative control); **(D)** PDCP constructed for NS and HA segments of H7N2 influenza viruses; **(E)** PDCP constructed for the concatenated full genomic sequences of H7N3 viruses for which pairwise distances were calculated for even and odd sites (negative control); **(F)** PDCP constructed for NS and HA segments of H7N3 influenza viruses; **(G)** PDCP constructed for the concatenated full genomic sequences of H7N4 viruses for which pairwise distances were calculated for even and odd sites (negative control); **(H)** PDCP constructed for NS and HA segments of H7N4 influenza viruses; **(I)** PDCP constructed for the concatenated full genomic sequences of H7N6 viruses for which pairwise distances were calculated for even and odd sites (negative control); **(J)** PDCP constructed for NS and HA segments of H7N6 influenza viruses; **(K)** PDCP constructed for the concatenated full genomic sequences of H7N7 viruses for which pairwise distances were calculated for even and odd sites (negative control); **(L)** PDCP constructed for NS and HA segments of H7N7 influenza viruses; **(M)** PDCP constructed for the concatenated full genomic sequences of H7N8 viruses for which pairwise distances were calculated for even and odd sites (negative control); **(N)** PDCP constructed for NS and HA segments of H7N8 influenza viruses; **(O)** PDCP constructed for the concatenated full genomic sequences of H7N9 viruses for which pairwise distances were calculated for even and odd sites (negative control); **(P)** PDCP constructed for NS and HA segments of H7N9 influenza viruses.