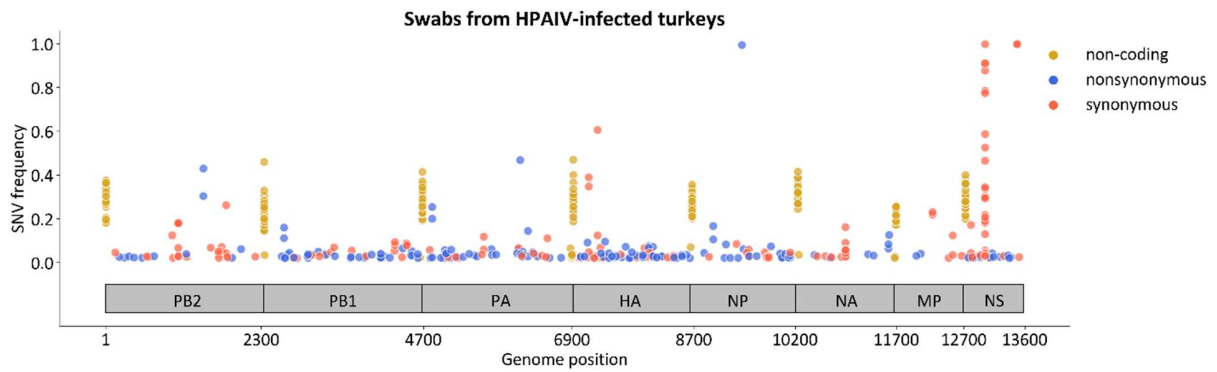
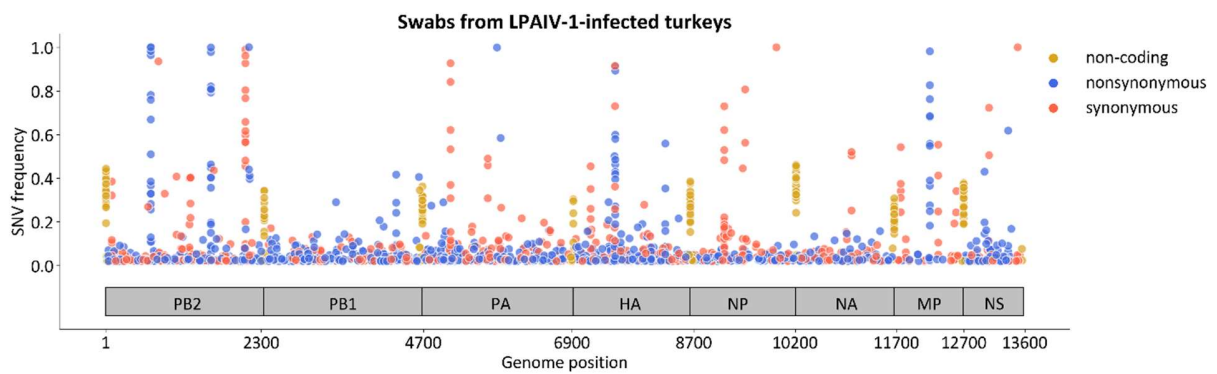


Figure S1. Distribution of iSNVs across the genome. Genome location of all iSNVs identified from turkeys (A-D) and chickens (E-H) experimentally infected with one of three H7N3 AIVs. All iSNVs from every sample in the indicated category were pooled and plotted along its position on the concatenated genome of the indicated H7N3 virus.

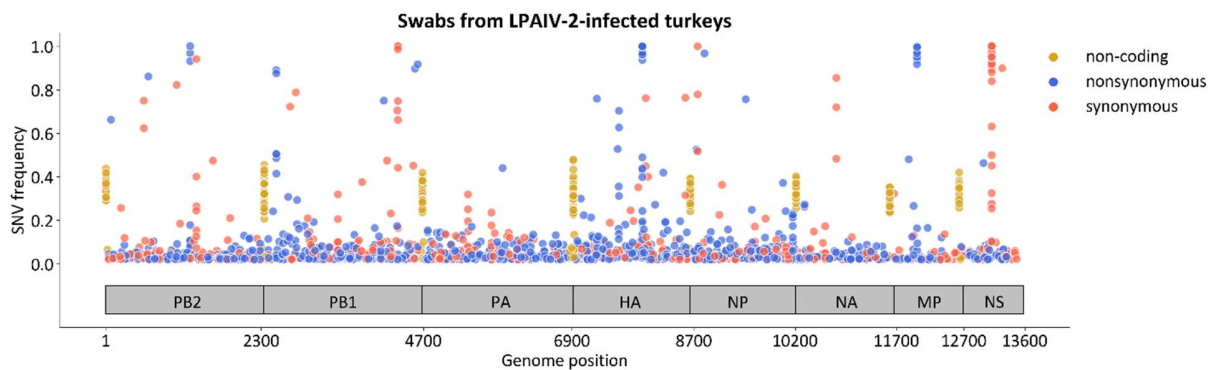
(A)



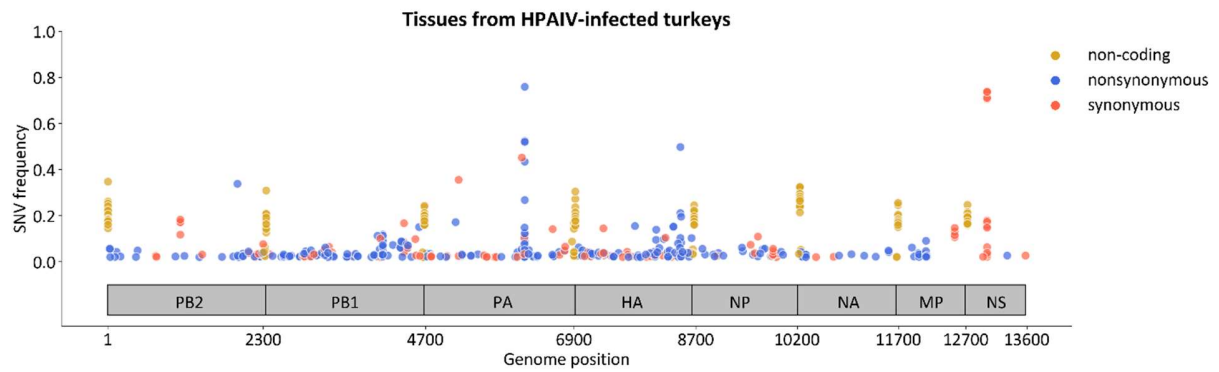
(B)



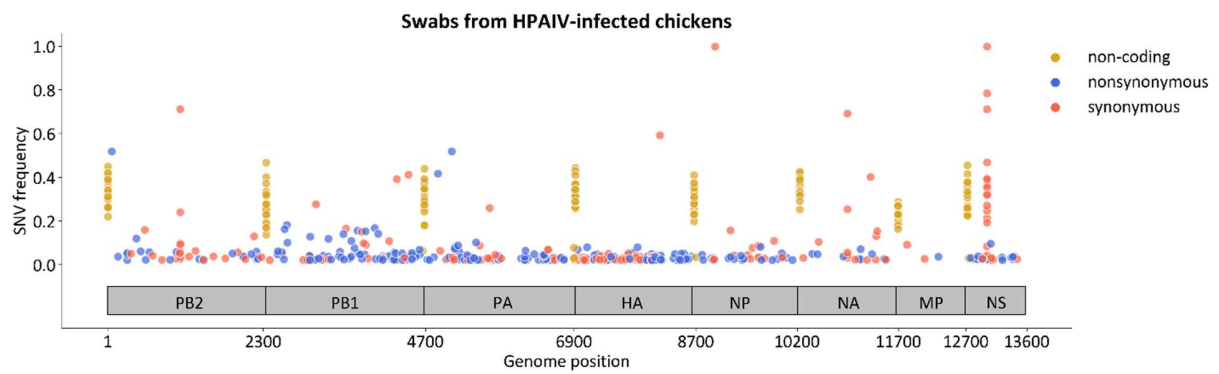
(C)



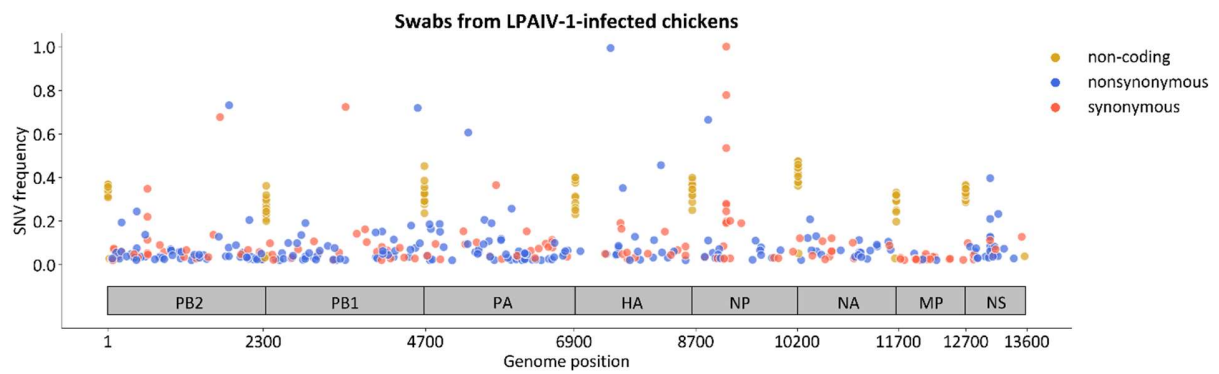
(D)



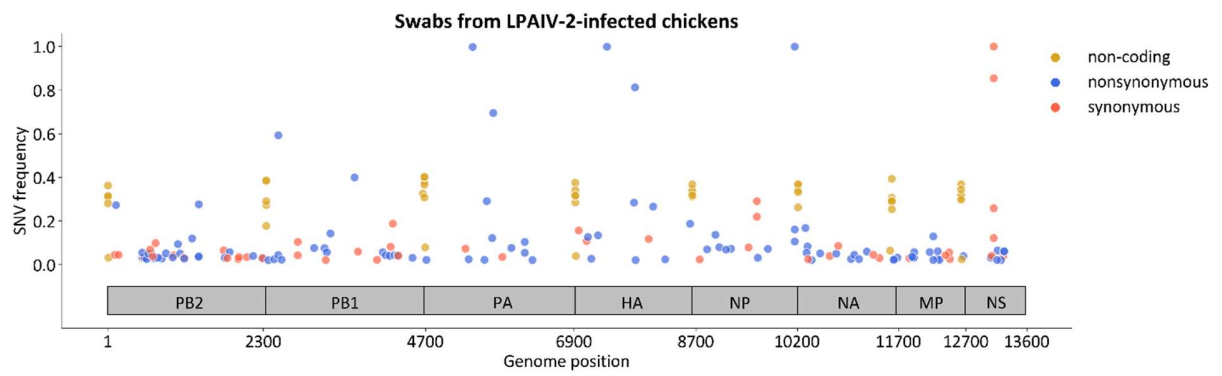
(E)



(F)



(G)



(H)

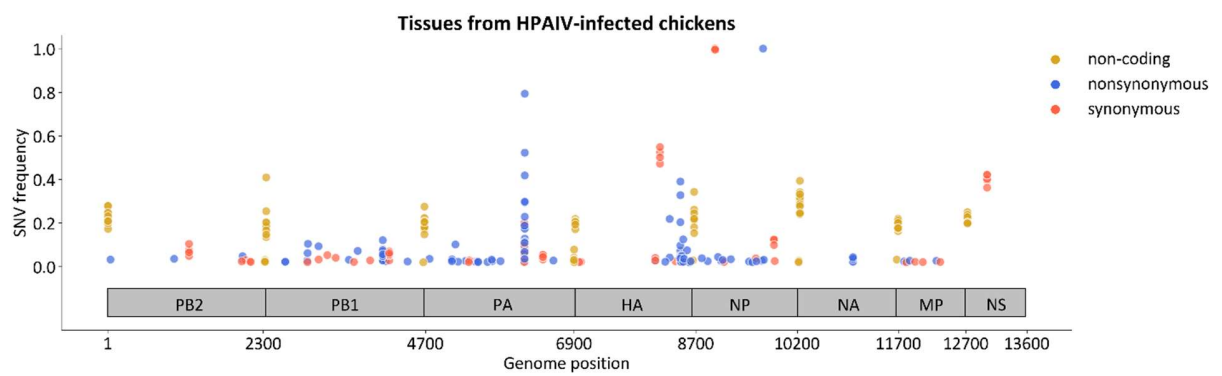


Figure S2. Mean iSNV frequency by virus gene segment. The mean frequency of iSNVs was calculated per segment for each sample. The dotted line indicates a frequency of 0.5 or 50%.

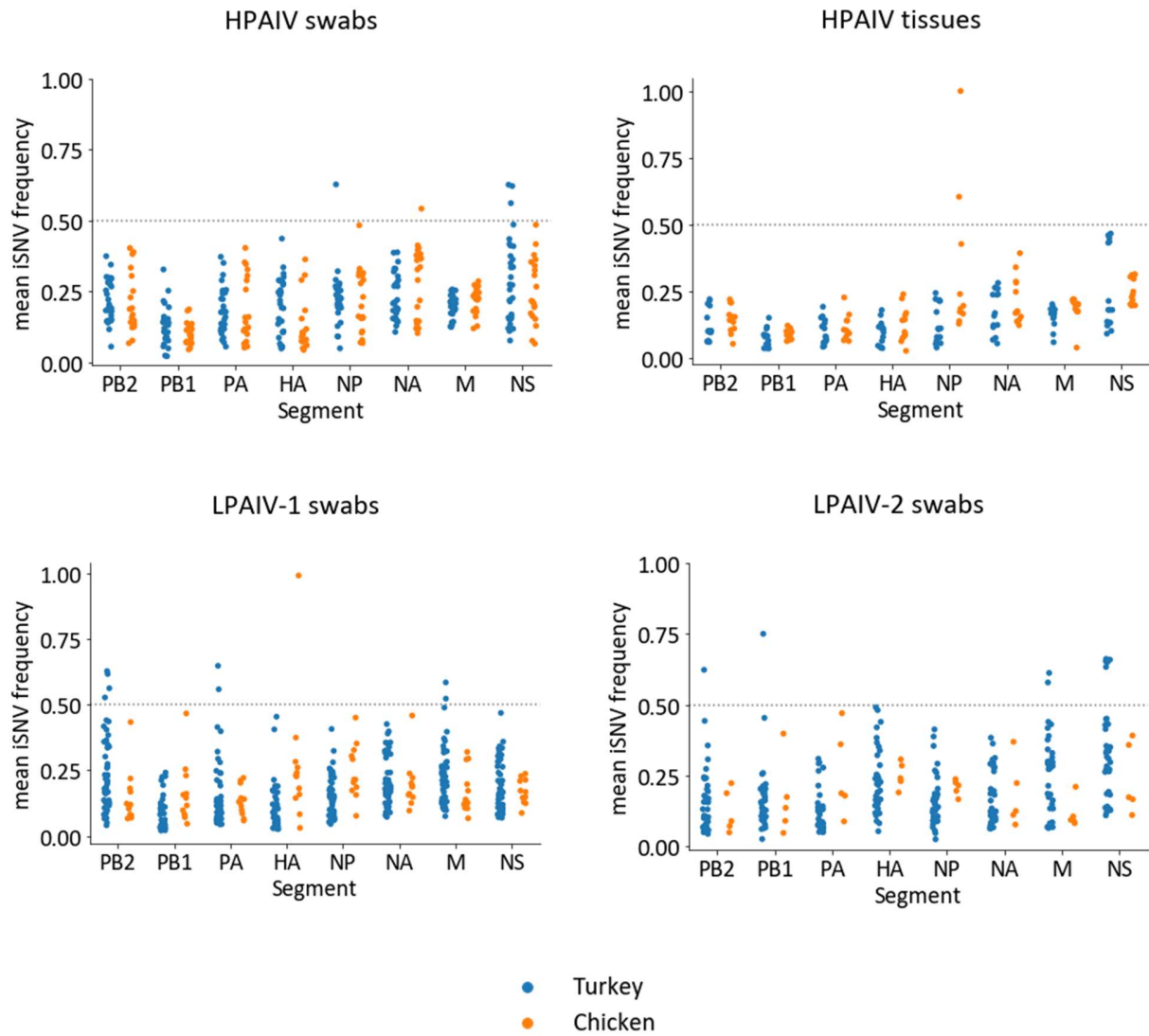


Figure S3. Common iSNVs types found in turkeys and chickens. The iSNVs from each sample were enumerated and pooled from samples in the same host species. The sets of unique iSNVs were then compared between samples from turkeys and chickens.

