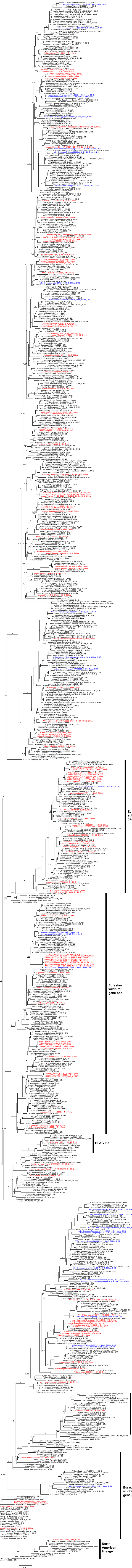


(b)PB1



1

5 polineage ne pool

1

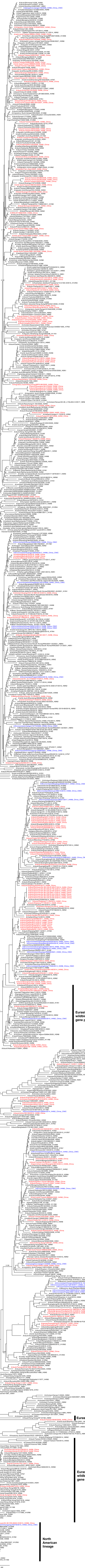
7_H5N6



(d)NP



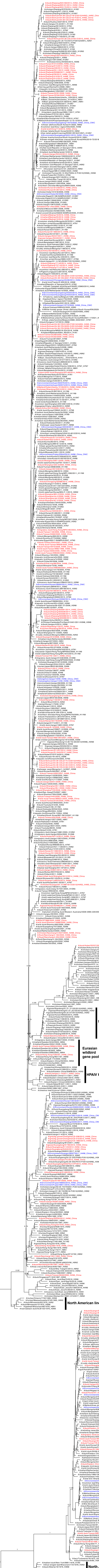
(e) M



Eurasian
wildbird
gene poo

1

sublineage
gene pool



2_China
_China
_China

A/duck/Jiangsu
A/velvet scot
A/common te
A/duck/Sichu
A/ruddy shield
A/duck/Mongc

ea/KNU2019-35/2019_H1N1
B_China_CNIC

52870/2006_H
1993_H5N2
402-6/1986_H5
andong/11708/2
nt/Chongqing/1
Shanghai/JDS1

= A/Gadwall/O
 k/Potsdam/221
 icken/Taiwan/G
 luck/Japan/9UC
 /duck/Hokkaido
 ck/Tsukuba/12

Figure S3. Maximum likelihood trees of internal-protein coding genes. (a) PB2 gene (n=937); (b) PB1 gene (n=929); (c) PA gene (n=890); (d) NP gene (n=914); (e) M gene (n=890); (f) NS gene (n=749). H4 strains sequenced in this study are in steel blue. Other H4 AIVs in China are in red. Branch lengths are scaled according to the number of substitutions per site. Branch support values of selected nodes are shown. Lineages, sublineages and subgroups are labeled with vertical lines on the right.