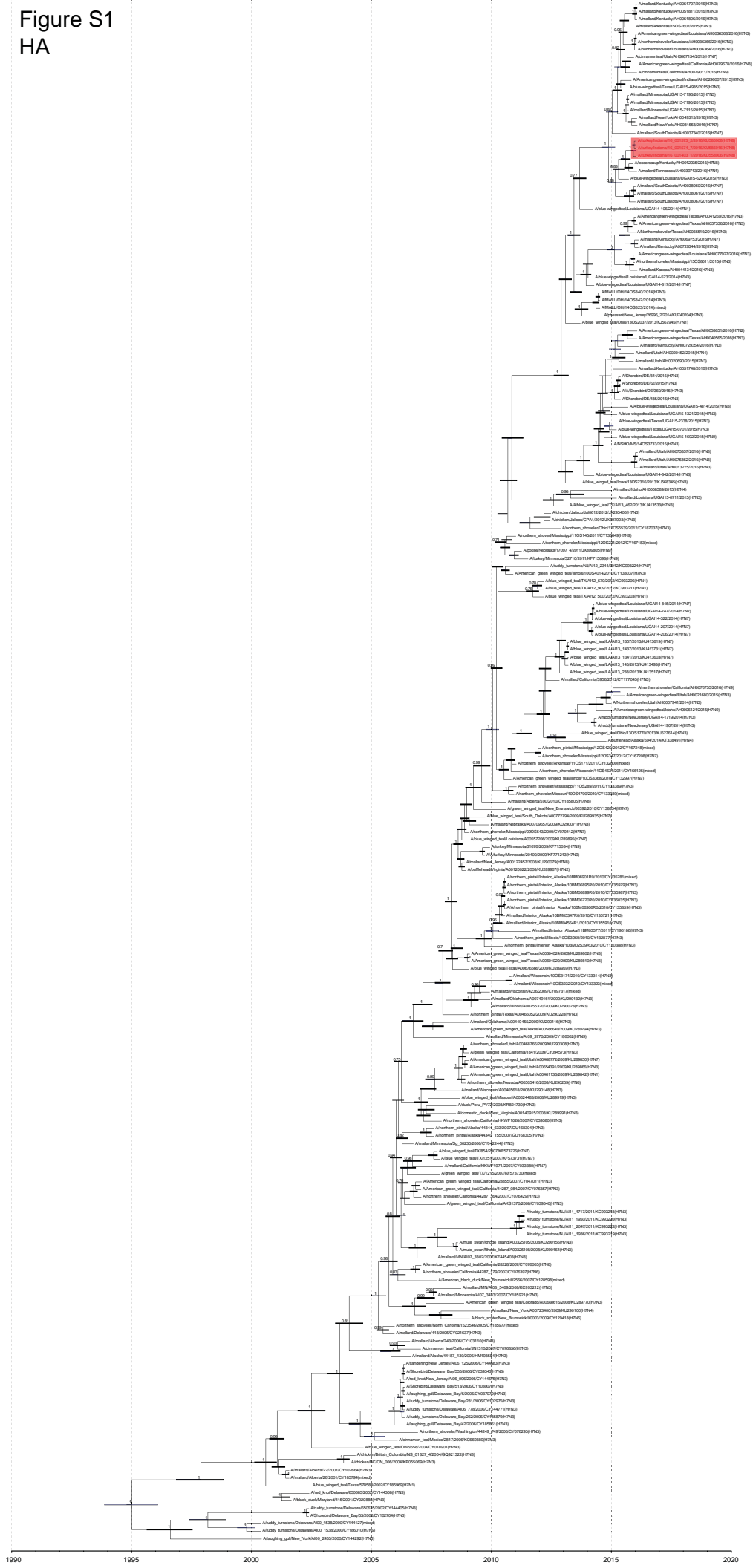


Supplemental materials

Figure S1. Maximum clade credibility phylogenetic trees for eight gene segments. H7N8 strains associated with the outbreak of disease in Indiana turkeys are highlighted by a red box. Clade posterior probabilities ≥ 0.7 are shown. Horizontal bars indicate 95% highest posterior density of age estimates of tree nodes.

Figure S2. Maximum clade credibility phylogenetic trees for eight gene segments. H7N8 strains associated with the outbreak of disease in Indiana turkeys are highlighted by a red box. Branches are colored according to the estimated ancestral state of host group from discrete trait reconstruction. Clade posterior probabilities ≥ 0.7 are shown. Horizontal bars indicate 95% highest posterior density of age estimates of tree nodes.

Figure S1
HA



1985 1990 1995 2000 2005 2010 2015 2020

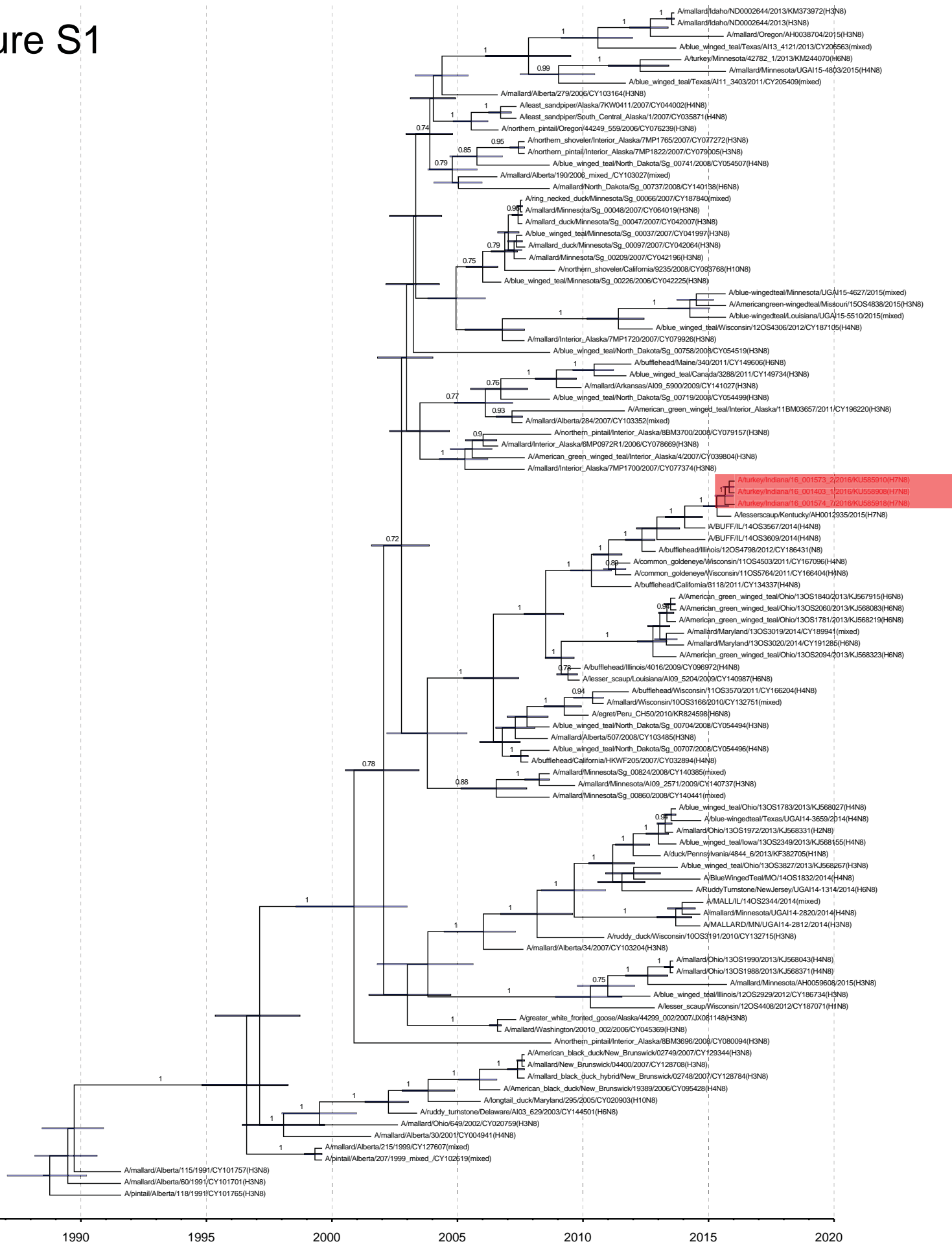


Figure S1
PB2

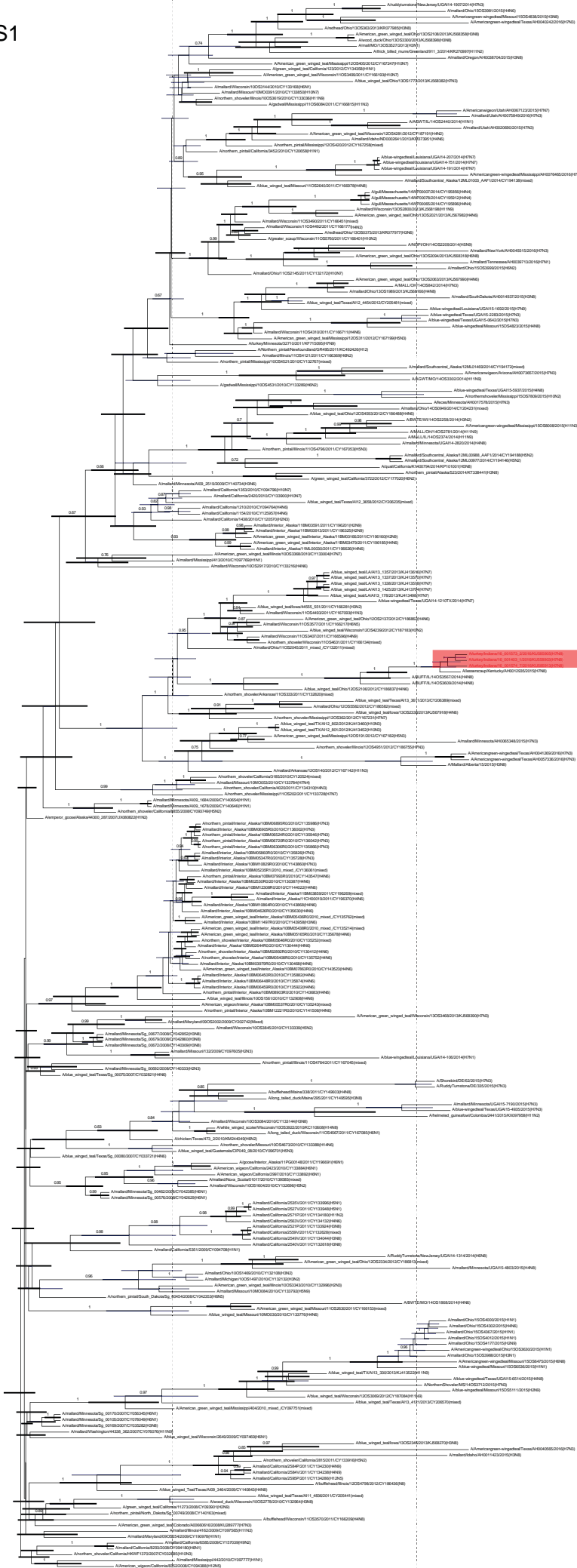


Figure PB1

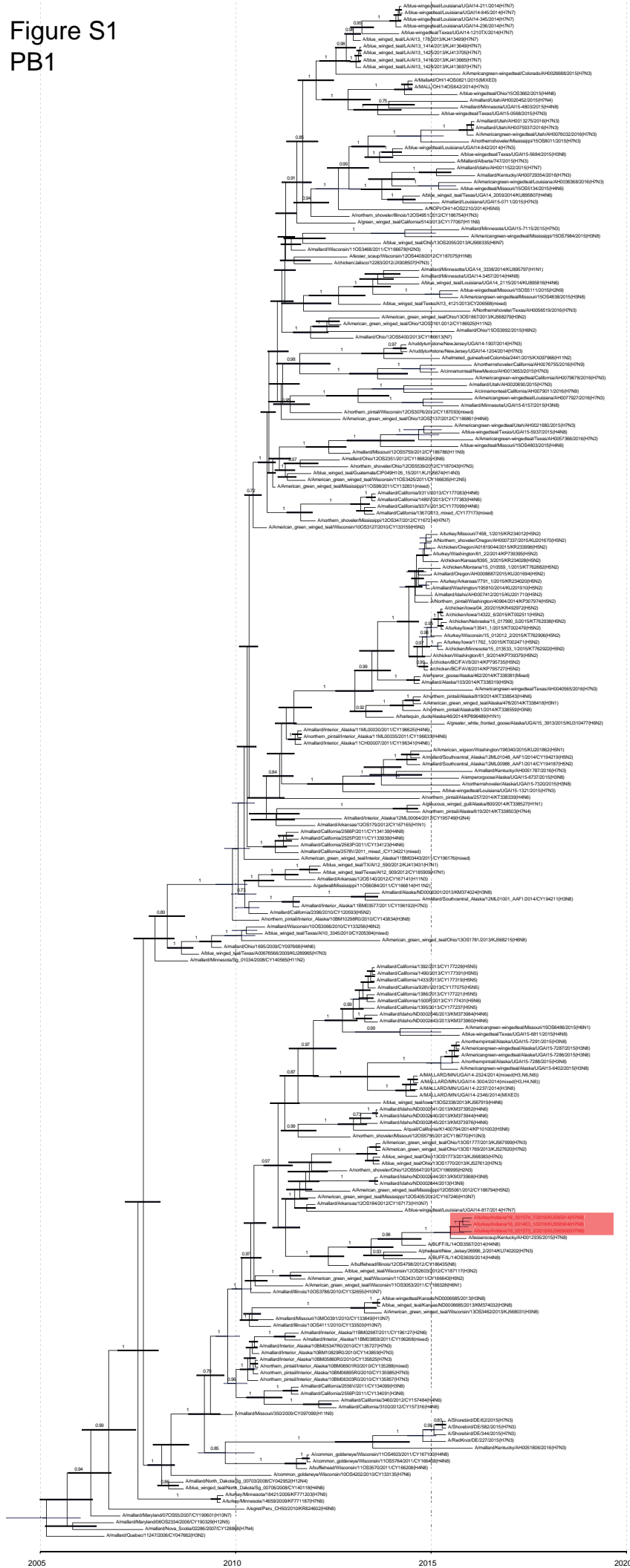


Figure S1
PA

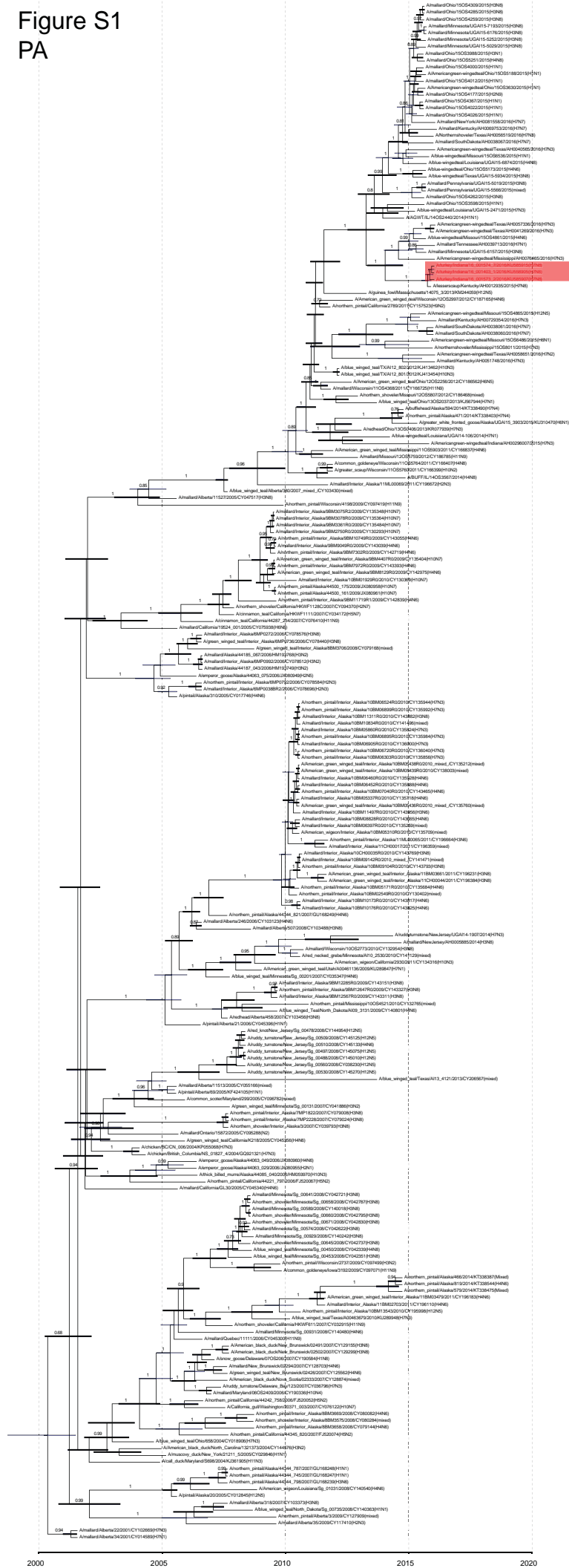


Figure S1
NP

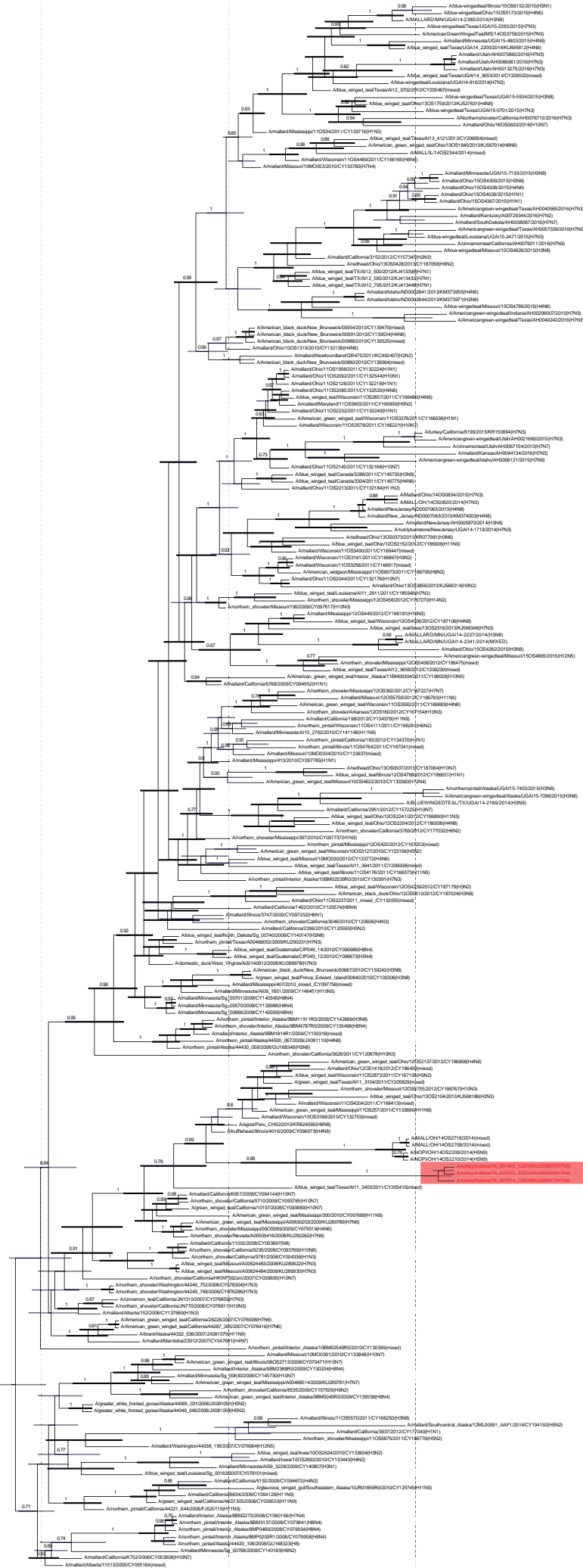


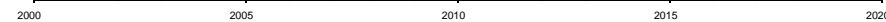
Fig
M

Figure S1
NS

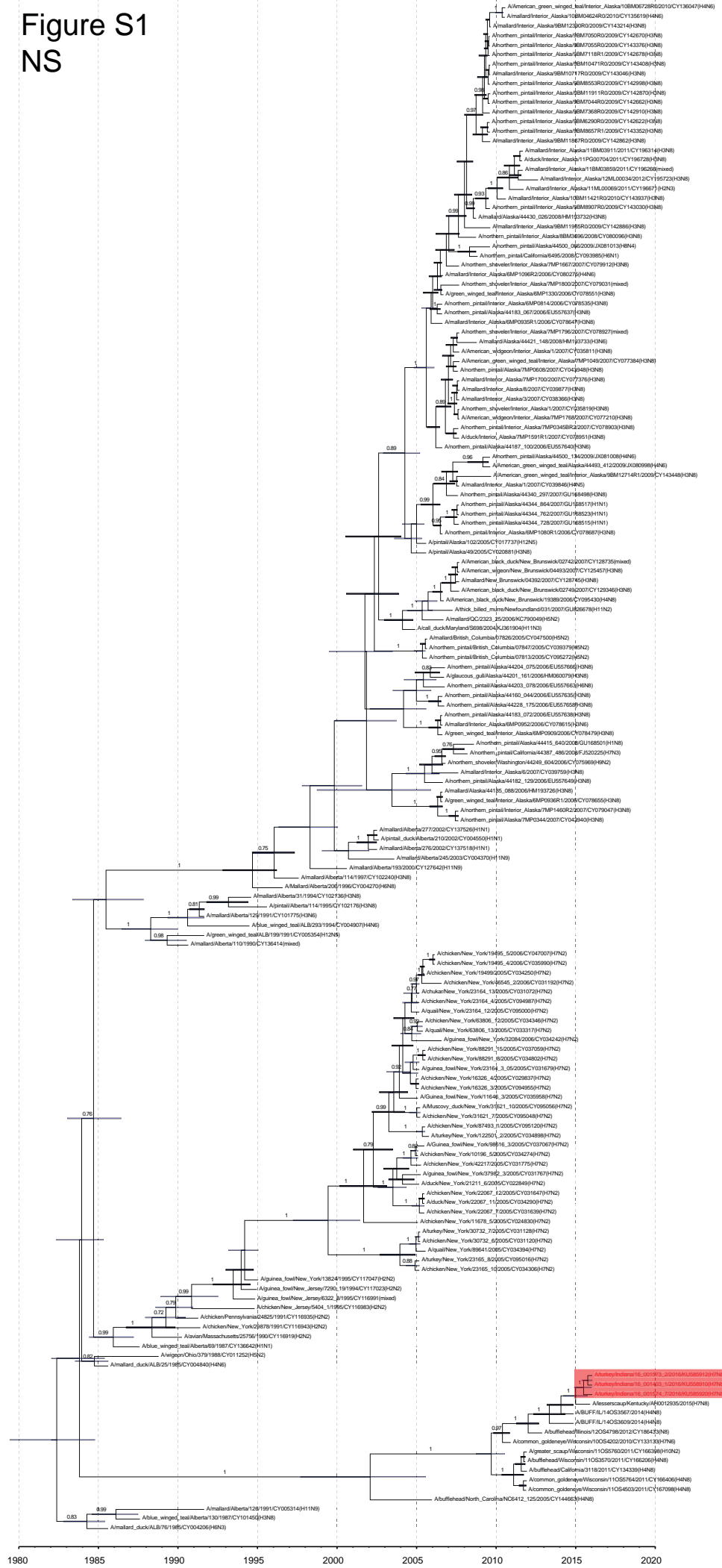
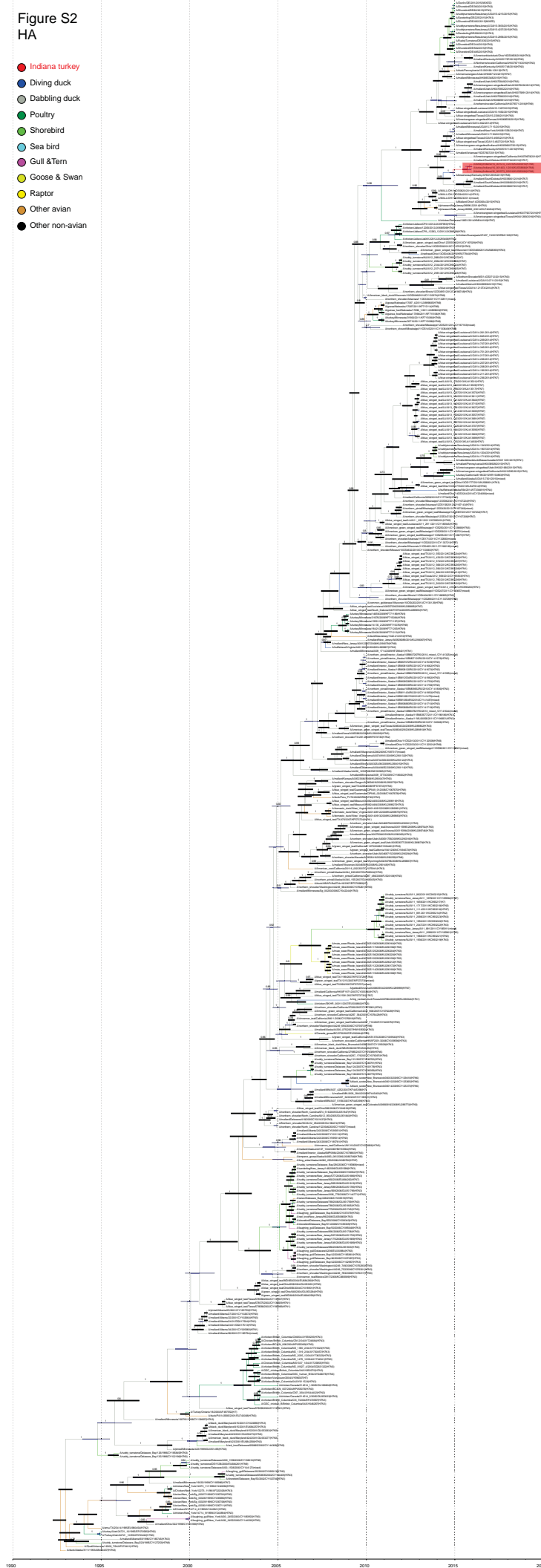


Figure S2
HA

- Indiana turkey
- Diving duck
- Dabbling duck
- Poultry
- Shorebird
- Sea bird
- Gull & Tern
- Goose & Swan
- Raptor
- Other avian
- Other non-avian



1985 1990 1995 2000 2005 2010 2015 2020

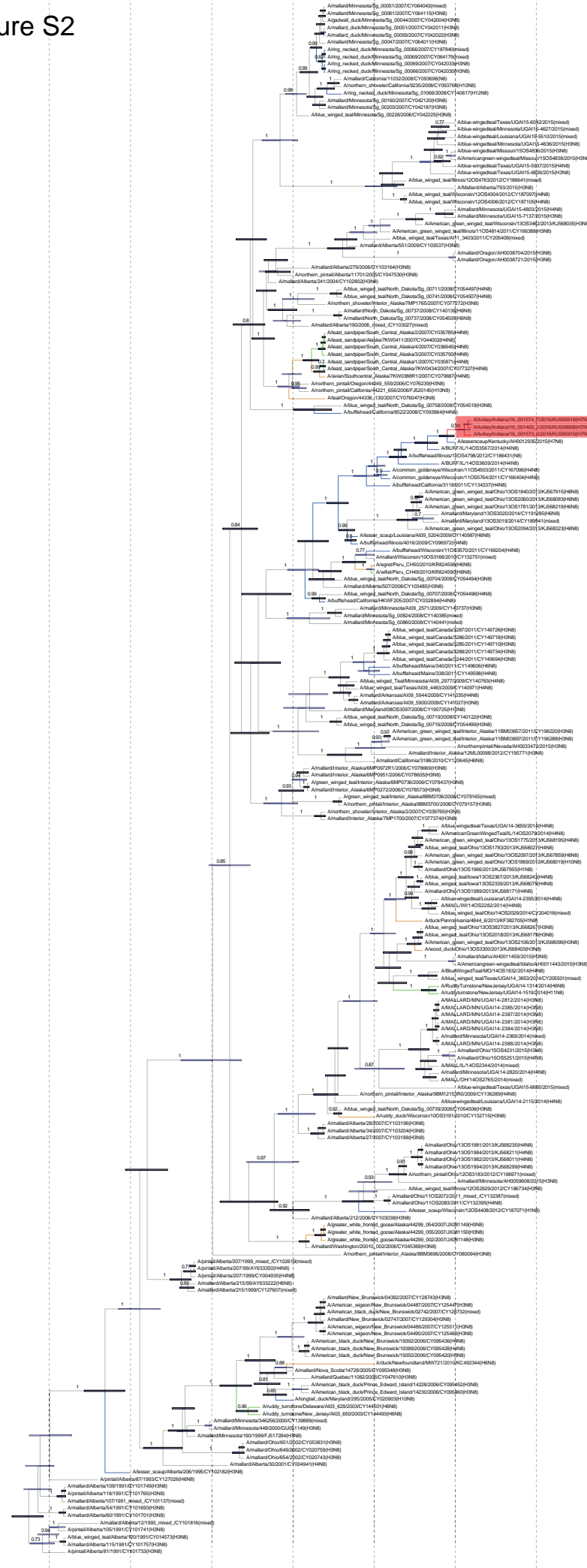
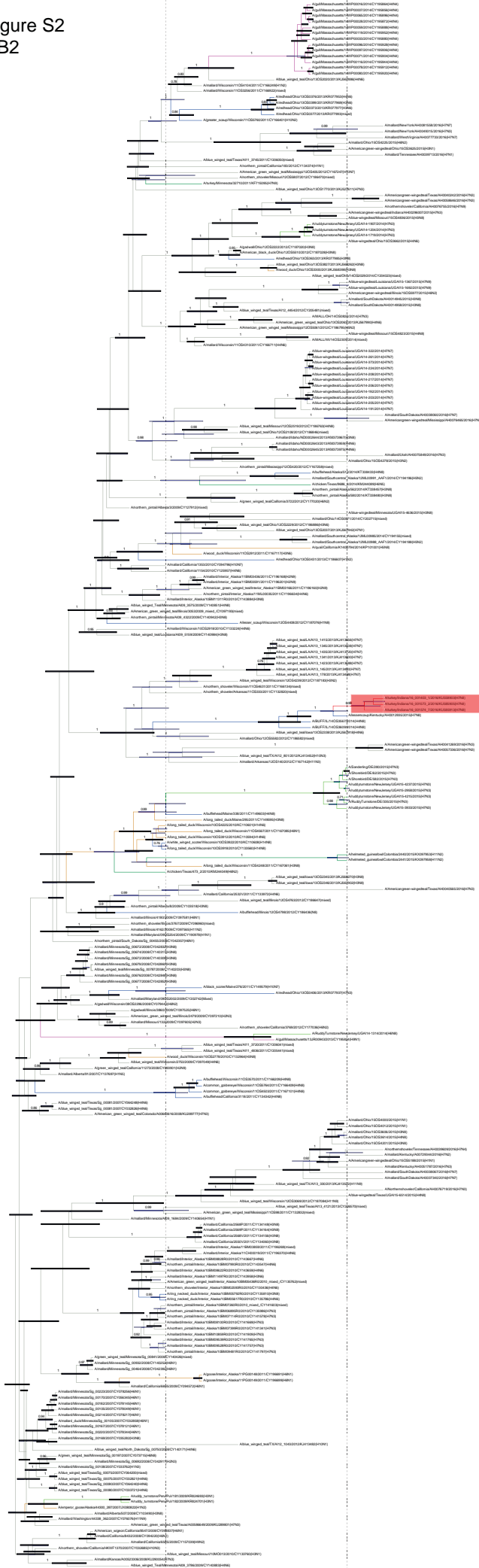
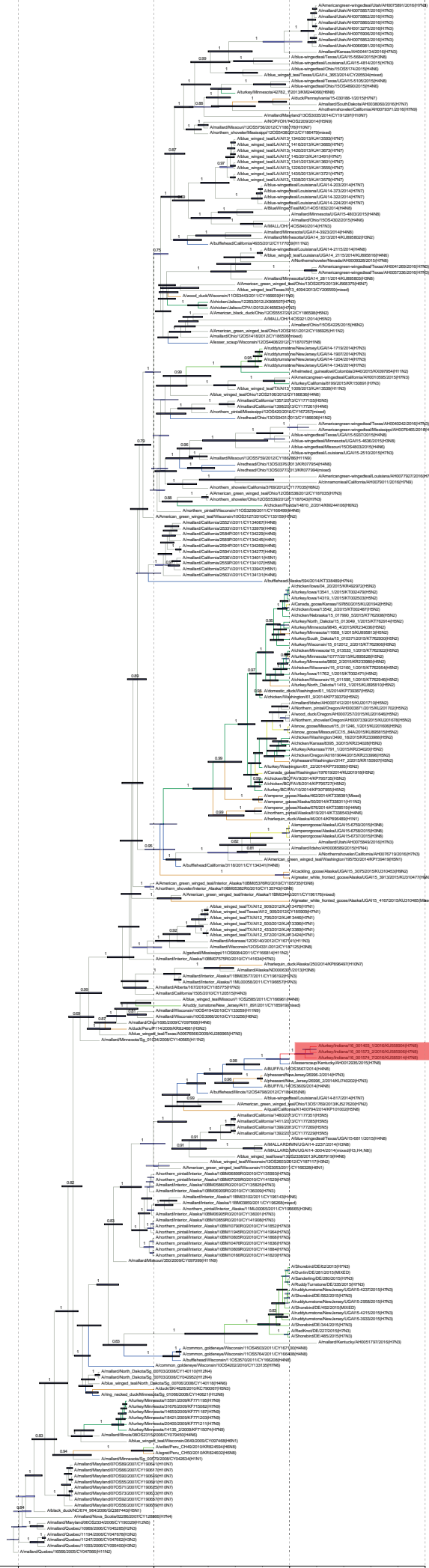


Figure S2
PB2



2000 2005 2010 2015 2020



1995



1995



M

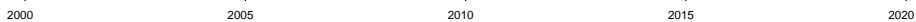


Figure S2
NS

