

Genesis of Influenza A(H5N8) Viruses

Technical Appendix

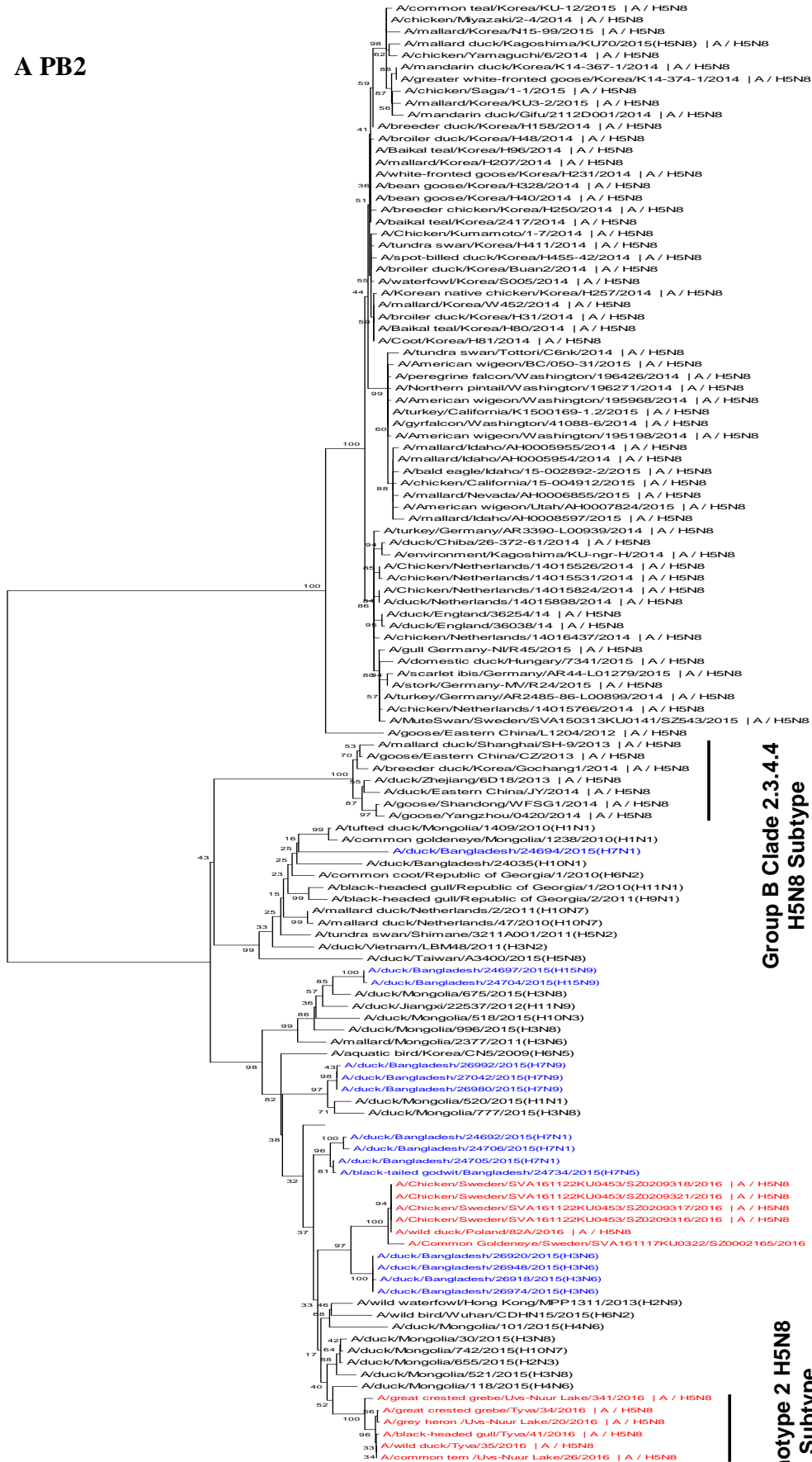
Technical Appendix Table. Summary of influenza viruses isolated from the Tanguar haor region of Bangladesh*

Isolates	Subtype	Host (Species)	GenBank Accession Numbers							
			PB2	PB1	PA	HA	NP	NA	M	NS
A/duck/Bangladesh/24692/2015	H7N1	domestic duck (<i>Anas sp.</i>)	KY635738	KY635673	KY635658	KY635574	KY635806	KY635787	KY635810	KY635768
A/duck/Bangladesh/24694/2015	H7N1	domestic duck (<i>Anas sp.</i>)	KY635469	KY635519	KY635624	KY635530	KY635523	KY635813	KY635603	KY635444
A/duck/Bangladesh/24697/2015	H15N9	domestic duck (<i>Anas sp.</i>)	KY635497	KY635750	KY635663	KY635719	KY635528	KY635723	KY635819	KY635715
A/duck/Bangladesh/24704/2015	H15N9	domestic duck (<i>Anas sp.</i>)	KY635570	KY635825	KY635563	KY635680	KY635694	KY635500	KY635683	KY635679
A/duck/Bangladesh/24705/2015	H7N1	domestic duck (<i>Anas sp.</i>)	KY635677	ND†	KY635807	KY635675	KY635484	KY635654	KY635804	KY635493
A/duck/Bangladesh/24706/2015	H7N1	domestic duck (<i>Anas sp.</i>)	KY635502	KY635462	KY635447	KY635584	KY635698	KY635443	KY635562	KY635446
A/black-tailed godwit/Bangladesh/24734/2015	H7N5	black-tailed godwit (<i>Limosa limosa</i>)	KY635643	KY635517	KY635496	KY635587	KY635709	KY635758	KY635591	KY635798
A/duck/Bangladesh/26918/2015	H3N6	domestic duck (<i>Anas sp.</i>)	KY635524	KY635797	KY635609	KY635482	KY635636	KY635579	KY635602	KY635490
A/duck/Bangladesh/26920/2015	H3N6	domestic duck (<i>Anas sp.</i>)	KY635499	KY635617	KY635731	KY635779	KY635705	KY635782	KY635634	KY635478
A/duck/Bangladesh/26948/2015	H3N6	domestic duck (<i>Anas sp.</i>)	KY635545	KY635604	KY635655	KY635661	KY635745	KY635653	KY635507	KY635792
A/duck/Bangladesh/26974/2015	H3N6	domestic duck (<i>Anas sp.</i>)	KY635593	KY635626	KY635597	KY635571	KY635639	KY635735	KY635720	KY635520
A/duck/Bangladesh/26980/2015	H7N9	domestic duck (<i>Anas sp.</i>)	KY635459	KY635811	KY635690	KY635734	KY635442	KY635689	KY635666	KY635659
A/duck/Bangladesh/26992/2015	H7N9	domestic duck (<i>Anas sp.</i>)	KY635525	KY635621	KY635802	KY635780	KY635633	KY635541	KY635753	KY635550
A/duck/Bangladesh/27042/2015	H7N9	domestic duck (<i>Anas sp.</i>)	KY635516	KY635641	KY635827	KY635561	KY635733	KY635739	KY635509	KY635772

*ND, not done.

Technical Appendix Figure (following pages). Phylogenetic trees for the (A) polymerase basic-2 (PB2), (B) polymerase basic-1 (PB1), (C) polymerase acidic (PA), (D) nucleoprotein (NP), (E) matrix (M), and (F) nonstructural (NS) genes of viruses isolated from the Tanguar haor area in Bangladesh (blue font) and HPAI A(H5N8) clade 2.3.4.4, 2016 viruses (red font). Phylogenetic analysis was performed with the neighbor-joining algorithm with the Kimura 2-parameter model. The reliability of the phylogenetic inference at each branch node was estimated by the bootstrap method with 1,000 replications. Evolutionary analyses were conducted with MEGA6 software.

A PB2



Group A Clade 2.3.4.4 H5N8 Subtype

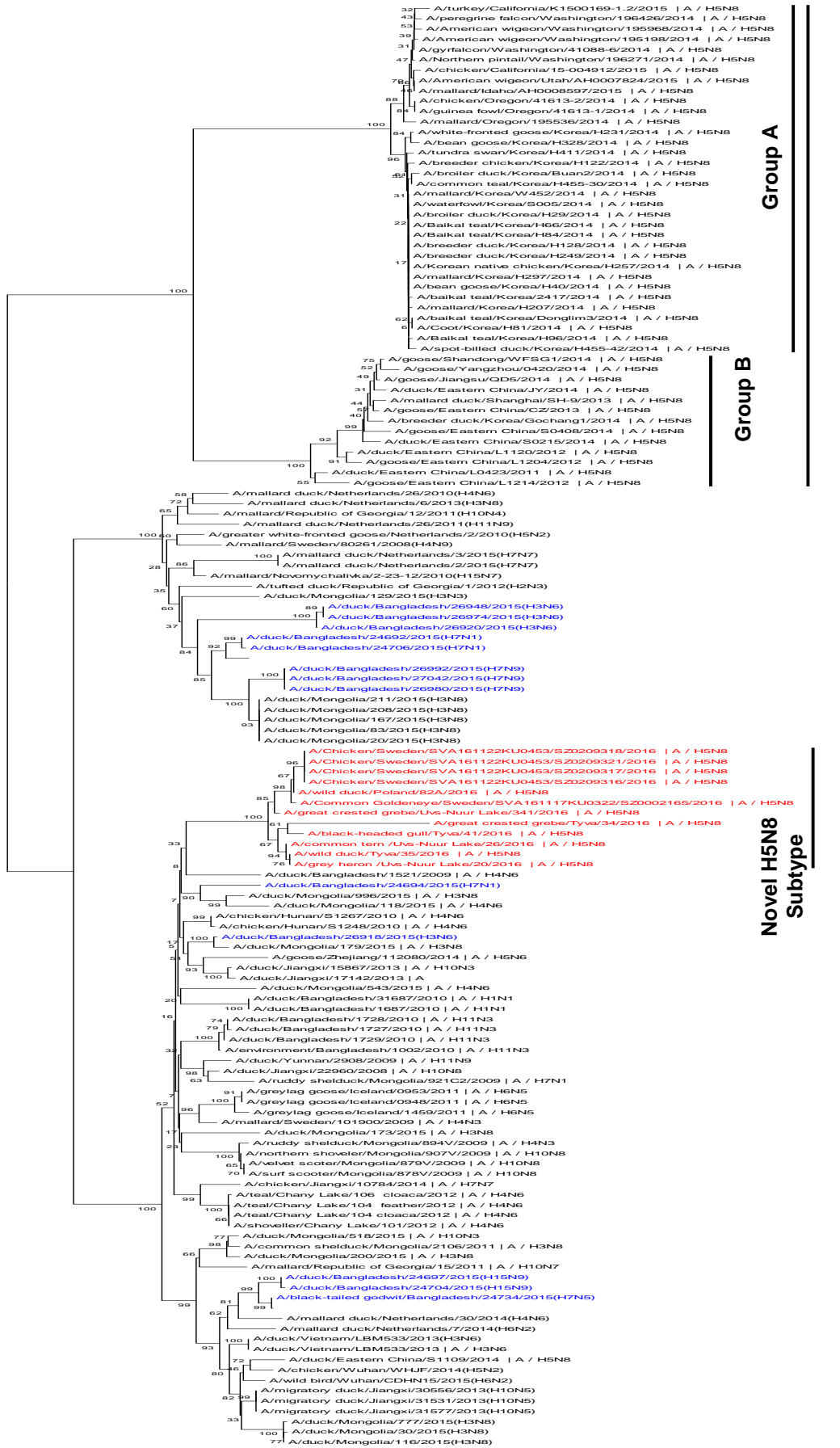
Group B Clade 2.3.4.4 H5N8 Subtype

Genotype 1 H5N8 Subtype

Genotype 2 H5N8 Subtype

Eurasian lineage

B PB1



Group A

Group B

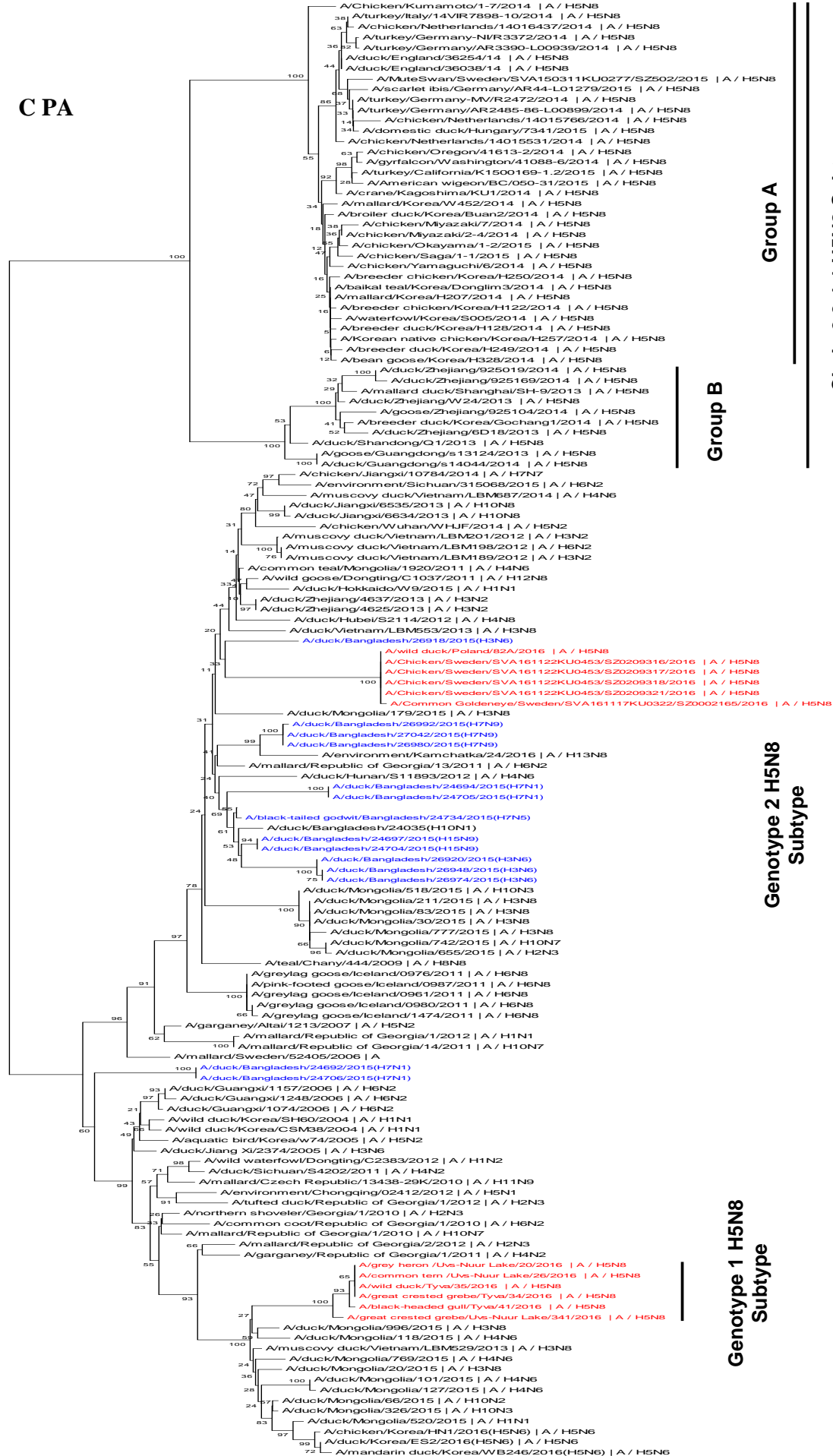
Novel H5N8 Subtype

Clade 2.3.4.4 H5N8 Subtype

Eurasian lineage

0.01

C PA



Clade 2.3.4.4 H5N8 Subtype

Eurasian lineage

D NP



Group A

Group B

Genotype 1 H5N8 Subtype

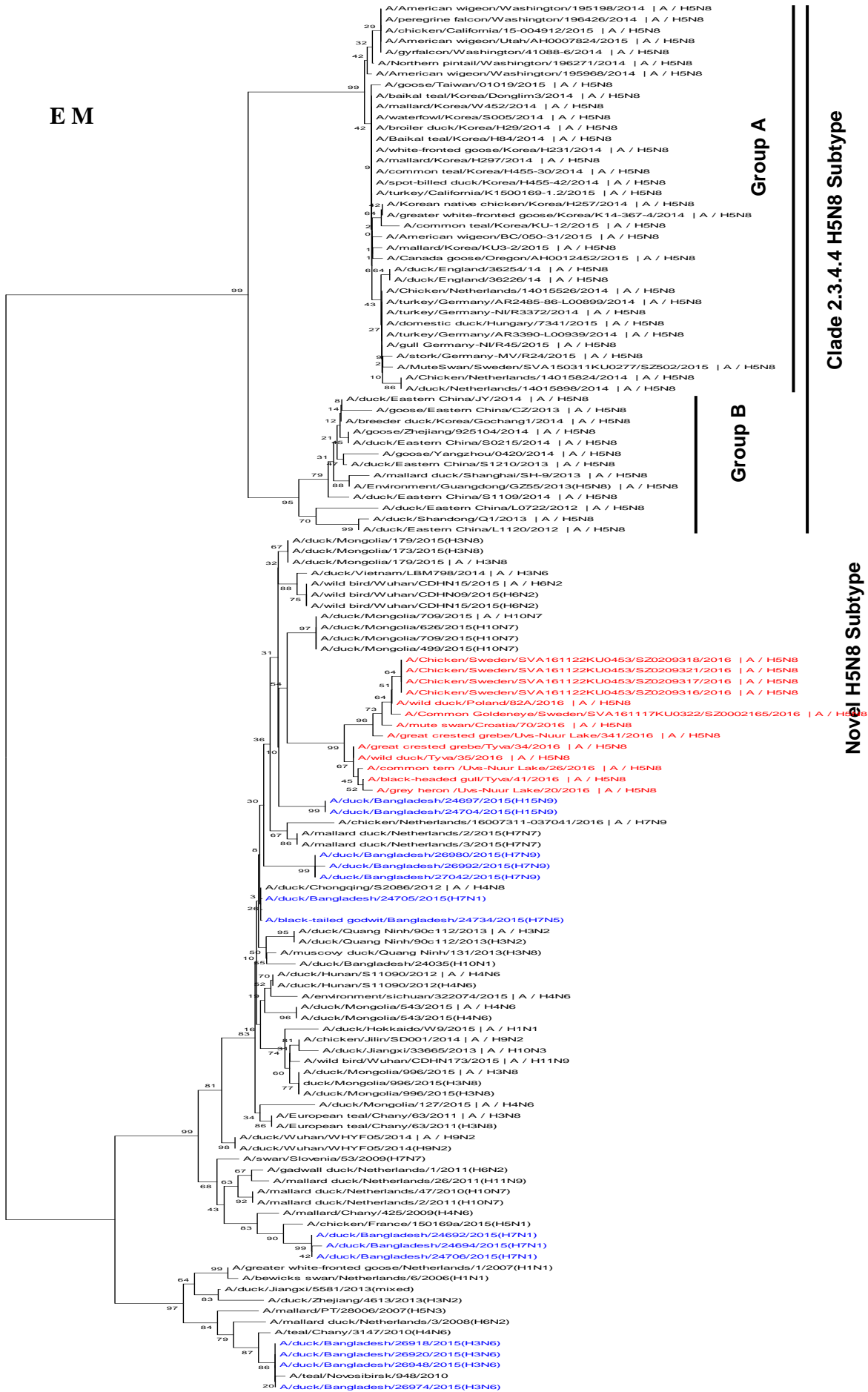
Genotype 2 H5N8 Subtype

Clade 2.3.4.4 H5N8 Subtype

Eurasian lineage

0.01

EM



Group A

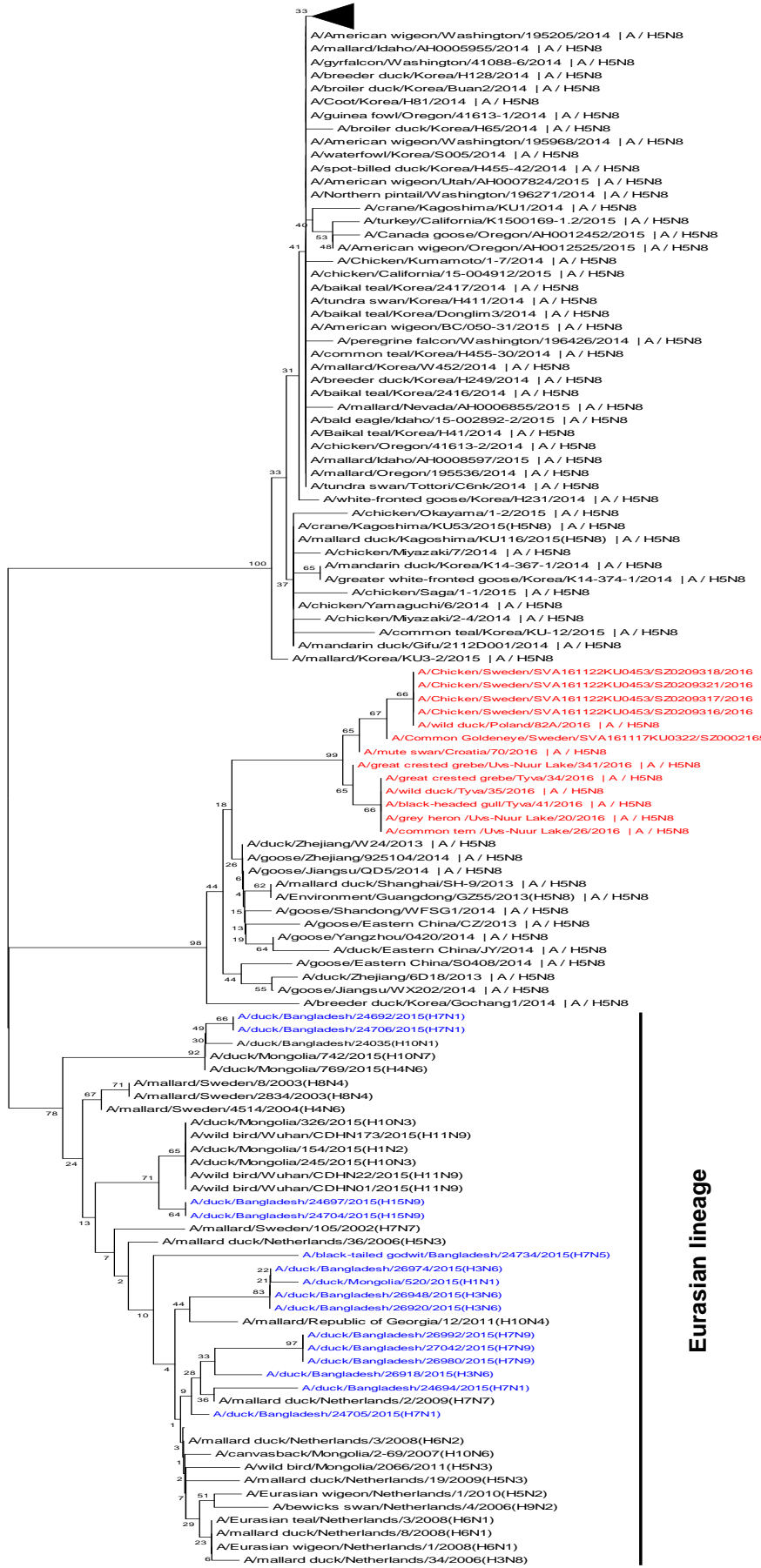
Clade 2.3.4.4 H5N8 Subtype

Group B

Novel H5N8 Subtype

Eurasian lineage

0.01



Group A Clade 2.3.4.4 H5N8 Subtype

Novel H5N8 Subtype

Group B Clade 2.3.4.4 H5N8 Subtype

Eurasian lineage

0.005