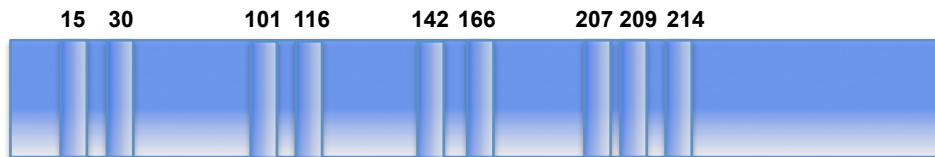
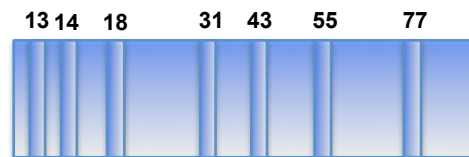


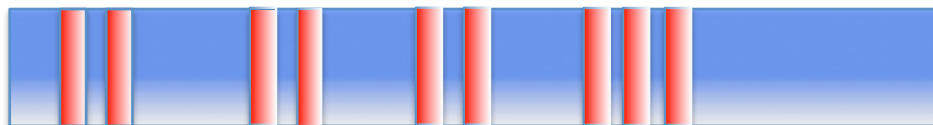
**A**

I S K S A A N T H

pH1N1 M1 and M2

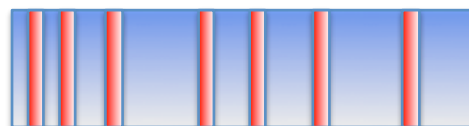


S E R N T F Q

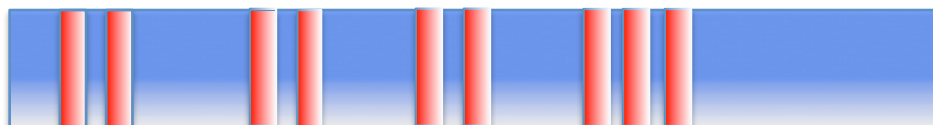
**B**

V D R A V V S A Q

Avian M1 and M2



N G K S L L R

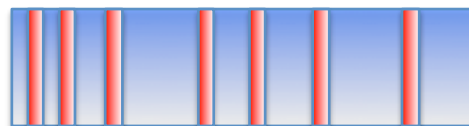
**C**

V D R A V V S A Q

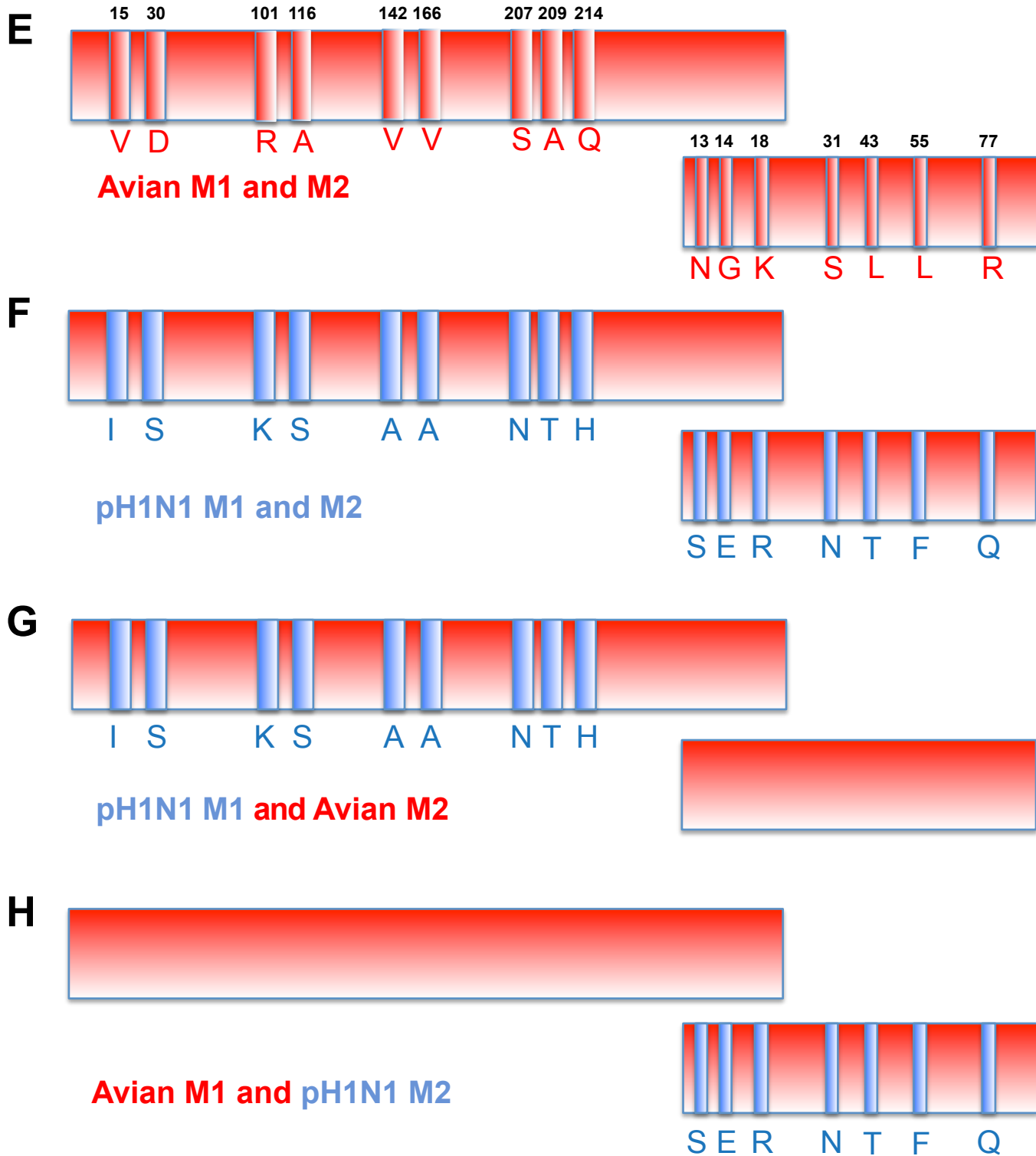
Avian M1 and pH1N1 M2

**D**

pH1N1 M1 and Avian M2



N G K S L L R



Supplementary Figure 9

**Supplementary Figure 9. Schematic depicting chimeric M Segment RNAs**

**(A)** Pandemic H1N1 influenza virus M1 and M2 proteins differ from the avian consensus sequences by 9 residues in M1 and 7 residues in M2. The pH1N1 amino acid identities are indicated in blue at their approximate positions within linear representations of M1 and M2 proteins. The pH1N1 M segment differs from the avian consensus by 8.3% at the nucleotide level. Here, pH1N1 RNA sequence is indicated by blue coloring. **(B-D)** Chimeric human-avian M segments were constructed in which only the non-synonymous changes in the avian consensus were introduced into the A/NL/602/09 (H1N1) M segment. **(E)** Avian consensus M1 and M2 proteins differ from the NL/09 sequences by 9 residues in M1 and 7 residues in M2. The avian amino acid identities are indicated in red and avian RNA sequence is indicated by red coloring. **(F-H)** A second set of chimeric M segments was constructed in which the NL/09 amino acid identities were introduced into the M segment of A/duck/Alberta/76 (H1N1) virus, yielding segments that encode avian consensus protein(s) but retain much of the nucleotide sequence of the NL/09 M segment.