**A**

82 148

A/Puerto Rico/8/1934 (H1N1) GGTGATGCCCCATTCCTTGATCGGCTTCGCCGAGATCAGAAATCCCTAAGAGGAAGGGGCAGCACCC

A/Brevig Mission/1/1918(H1N1)GGTGATGCCCCATTCCTTGATCGGCTTCGCCGAGATCAGAAGTCCCTAAGAGGAAGAGGCAGCACTC

mutated sequence GGTGATGCCCCATTCCTTGATCGGCTTCGCCGAGATCAGAAATCCCTAAGGGGAAGAGGCAGCACTC

**B**

497 564

A/Puerto Rico/8/1934 (H1N1) TTCCAGGACATACTGCTGAGGATGTCAAAAATGCAGTTGGAGTCCTCATCGGGGGACTTGAATGGAAT

A/Vietnam/1194/2004 (H5N1) TTCCAGGACATACTGGTGAGGATGTCAAAAATGCAATTGGCGTCCTCATCGGAGGACTTGAATGGAAT

mutated sequence TTCCAGGACATACTAATGAGGATGTCAAAAATGCAATTGGGGTCCTCATCGGAGGACTTGAATGGAAT

**Fig. S1.** Nucleotide alignment of NS gene sequences at the 82-148 (a) and 497-564 (b) regions. All mismatching nucleotides in the PR8 strain were mutated to correspond to sequences of the aforementioned viruses.