

**Table S2. Pairwise identity (%<sup>a</sup> (number of amino acid mutations)) in influenza A hemagglutinin 1 (HA1) peptide and antigenic sites across viruses used in antibody assays and A(H1N1)pdm09 challenge**

	HA1		Antigenic Sites*	
	A/Brisbane/10/2007 (reference)	A/Uruguay/716/2007 X-175C	Assay Brisbane/10/2007	A/Brisbane/10/2007 (reference)
<b>A/Brisbane/10/2007 (reference)</b>	–	–	–	–
<b>A/Uruguay/716/2007 X-175C</b>	99.0 (3)	–	97.7 (3)	–
<b>Assay Brisbane/10/2007</b>	99.4 (2)	99.0 (3)	98.5 (2)	97.7 (3)

	HA1					Antigenic Sites**					
	A/Brisbane/59/2007 (reference)	Brisbane/59/2007 IVR-148	Assay Brisbane/59/2007	A/California/07/2009 (reference)	Assay A/California/07/2009	Challenge A/California/07/2009	A/Brisbane/59/2007 (reference)	Brisbane/59/2007 IVR-148	Assay Brisbane/59/2007	A/California/07/2009 (reference)	Assay A/California/07/2009
<b>A/Brisbane/59/2007 (reference)</b>	–	–	–	–	–	–	–	–	–	–	–
<b>A/Brisbane/59/2007 IVR-148</b>	99.7 (1)	–	–	–	–	–	98 (1)	–	–	–	–
<b>Assay Brisbane/59/2007</b>	99.7 (1)	100 (0)	–	–	–	–	98 (1)	100 (0)	–	–	–
<b>A/California/07/2009 (reference)</b>	72.8 (89)	72.5 (90)	72.5 (90)	–	–	–	50 (25)	48 (26)	48 (26)	–	–
<b>Assay A/California/07/2009</b>	73.1 (88)	72.8 (89)	72.8 (89)	99.7 (1)	–	–	50 (25)	48 (26)	48 (26)	100 (0)	–
<b>Challenge A/California/07/2009<sup>‡</sup></b>	71.9 (92)	71.6 (93)	71.6 (93)	99.1 (3)	98.8 (4)	–	48 (26)	46 (27)	46 (27)	98 (1)	98 (1)

a. Percentage pairwise identity calculated as [1-(number of AA substitutions in HA1 or antigenic sites)/(total HA1 or antigenic site AA residues)]X100%

[1] Bush RM, Bender CA, Subbarao K, Cox NJ, Fitch WM. Predicting the evolution of human influenza A. *Science* 1999;286:1921-5.[2] Brownlee, G.G & Fodor E. 2001 The predicted antigenicity of the hemagglutinin of the 1918 Spanish influenza pandemic suggests an avian origin. *Phil. Trans. R. Soc. Lond.* 356, 1871-1876.<sup>‡</sup>A/Quebec/144147/2009(H1N1) [GenBank Accession Numbers FN434457-FN434464]