Supplementary material:

Figure S1: Amino acid substitutions (AASs) occurred in catalytic site, active site and positions related with resistance. The height of each amino acid represents its probability of occurrence, for each position in the pseudo-sequences analyzed. Perfectly conservation is showed in Africa, Central America and Oceania. New variants were found: E119K and Y406H (Asia, in CS), D198G and D198Y (Europe), G248R and G248E (Asia and Mexico).

LEGEND - Crystallographic Nomenclature								
Ps. Pos.	Prot. Pos.	Relevancy	Ps. Pos.	Prot. Pos.	Relevancy	Ps. Pos.	Prot. Pos.	Relevancy
1	118	CS	8	198	PRAS	15	274	RRAP
2	119	CS	9	222	AS+RRAP	16	276	CS
3	151	CS+PRAP	10	224	CS	17	277	AS+PRAP
4	152	CS	11	227	AS	18	292	CS
5	155	PRAP	12	246	PRAP	19	294	AS
6	156	AS	13	248	PRAP	20	371	CS
7	178	AS	14	261	PRAP	21	406	CS

Figure S2: Distribution of amino acid substitutions (AASs) from 2009 pandemic AH1N1 human influenza virus NA in Mexico and rest of the world. The NA sequence and its secondary structure are considered in regions (1-59). The trans-membrane and linker regions are represented together as number 0 (TM). Additionally, 2 alpha helices, and 27 beta sheets and 30 loops are shown in colors. The AASs located in regions involving the active site and the catalytic sites are indicated as triangle and circle, respectively.

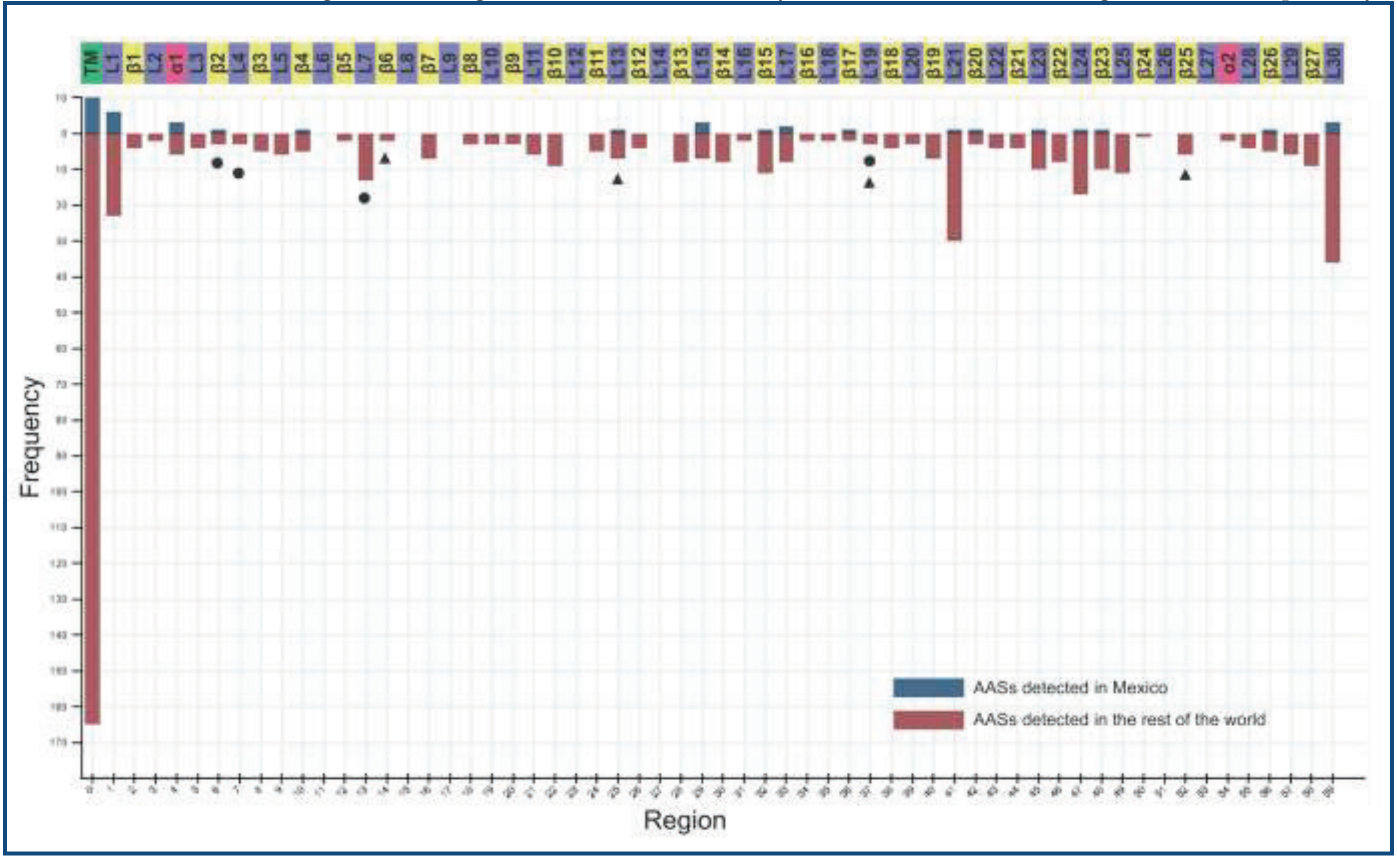

Figure S3: Distribution of amino acid substitutions (AASs) from 2009 pandemic AH1N1 human influenza virus NA in Africa, Asia, Oceania, Europe and America. The NA sequence and its secondary structure are considered as regions (1-59). The trans-membrane and linker regions are represented together as number 0 (TM). Additionally, 2 alpha helices, 27 beta sheets and 30 loops are shown in colors.