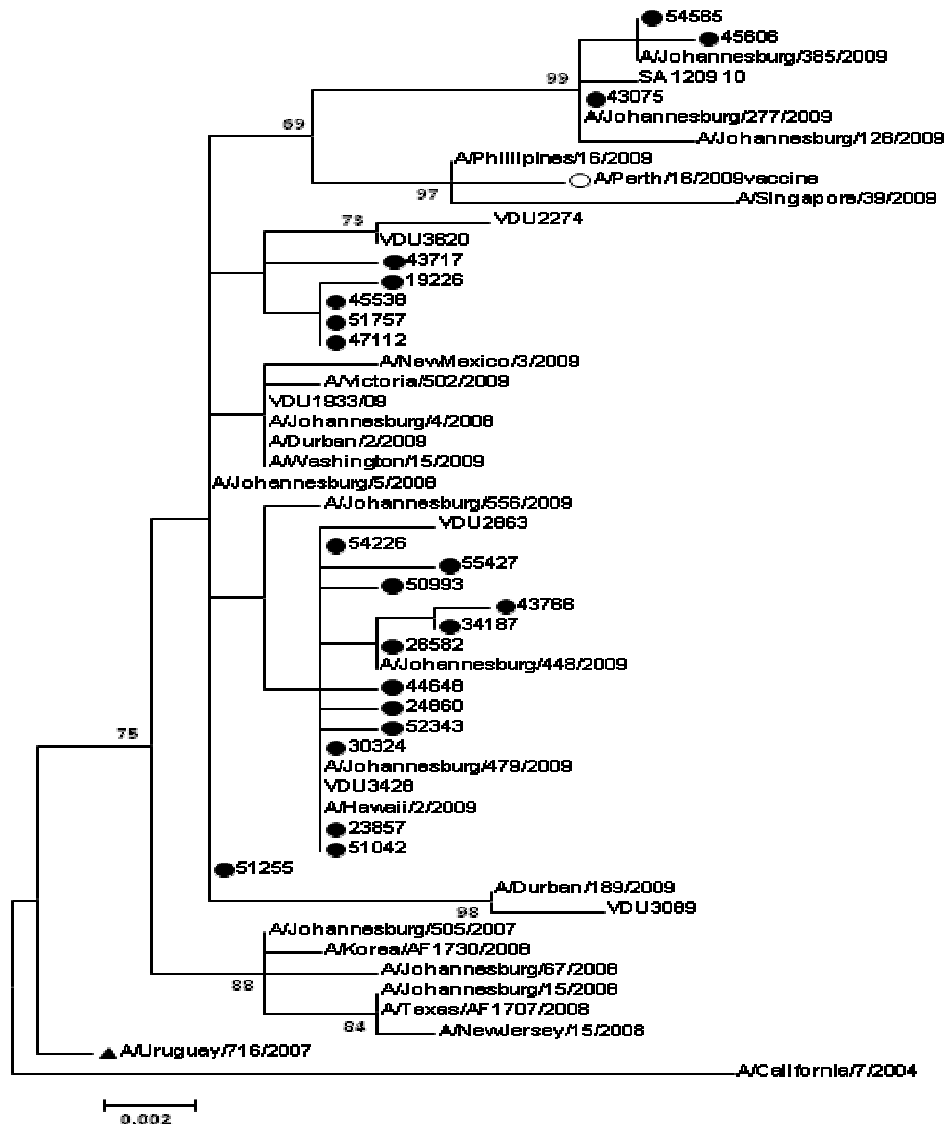


Supplementary digital material 1

Maximum likelihood tree of the HA1 nucleotide sequences (822 base pairs) showing the phylogenetic relatedness between A/H3N2 viruses from study participants and the H3N2 vaccine-strain.



Footnote: Strains from study participants are indicated by filled circles (●), the A/Uruguay/716/2007 vaccine-strain by a triangle (▲) and the A/Perth/16/2009 vaccine strain recommended for vaccination in 2010 by an open circle (○). A 2004 strain was included as outgroup, as well as South African isolates from 2007, 2008 and 2009 as references for the comparison.