



Technical Appendix Figure. A) Map with black dots indicating the 4 provinces where blood samples were collected for the study of the spread of vaccinia virus (VACV) to cattle herds, Argentina, 2011. B) Phylogenetic tree based on nucleotide sequences of orthopoxvirus hemagglutinin (HA) gene. The tree was constructed with HA sequences by using the neighbor-joining method with 1,000 bootstrap replicates and the Tamura 3-parameter model in MEGA4 (<http://megasoftware.net/>). Bootstrap values are represented on branches and only values >90% are shown. Nucleotide sequences were obtained from GenBank. Scale bar represents 0.02 substitutions per nucleotide position. C) Nucleotide sequence of the VACV Argentina A56R (HA) gene compared with homologous sequences from several other orthopoxviruses. The samples from Argentina showed 2 polymorphisms (C–A and C–G) in comparison with other VACV isolates. D) A56R (HA) gene nucleotide identity matrix. The analysis involved 17 nt sequences. Evolutionary analyses were conducted in MEGA4.