Porcine circovirus type 2 (PCV2) evolution before and after the vaccination introduction. A large scale epidemiological study.

Giovanni Franzo[*#1], Claudia Maria Tucciarone[#1], Mattia Cecchinato[1] and Michele Drigo[1].

[1]University of Padua, Legnaro (PD), Italy;

Supplementary figure 2. Maximum likelihood phylogenetic tree reconstructed using a collection of PCV2 ORF2 sequences sampled from wild and domestic pigs. On the left, the whole PCV2 topology is depicted while on the right genotypes specific sub-trees are reported. PCV2 genotypes have been colour-coded in red (PCV2a), blue (PCV2b) and green (PCV2d) while the sequence names of strains collected from wild boars are highlighted in red.