

Porcine circovirus 2 (PCV-2) genetic variability under natural infection scenario reveals a complex network of viral quasispecies.

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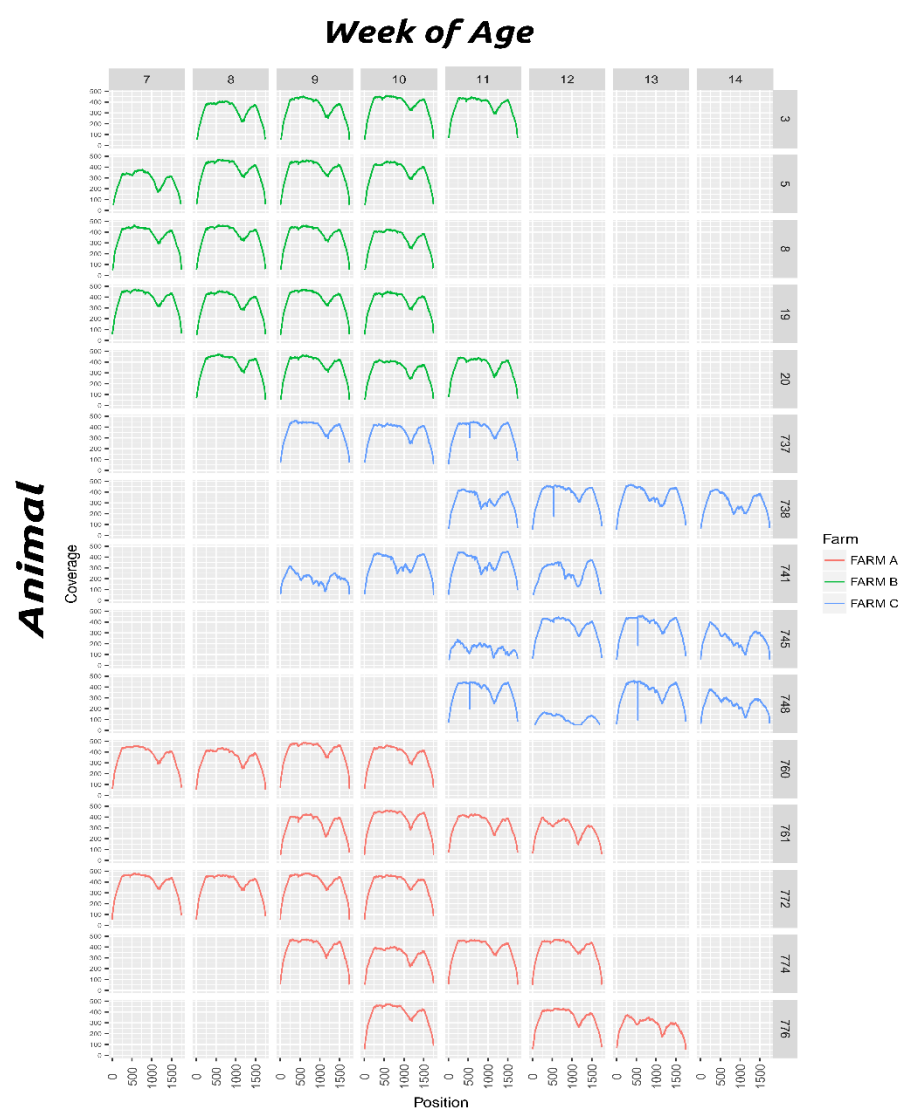
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Running Head: PCV-2 variability under natural infection scenario.

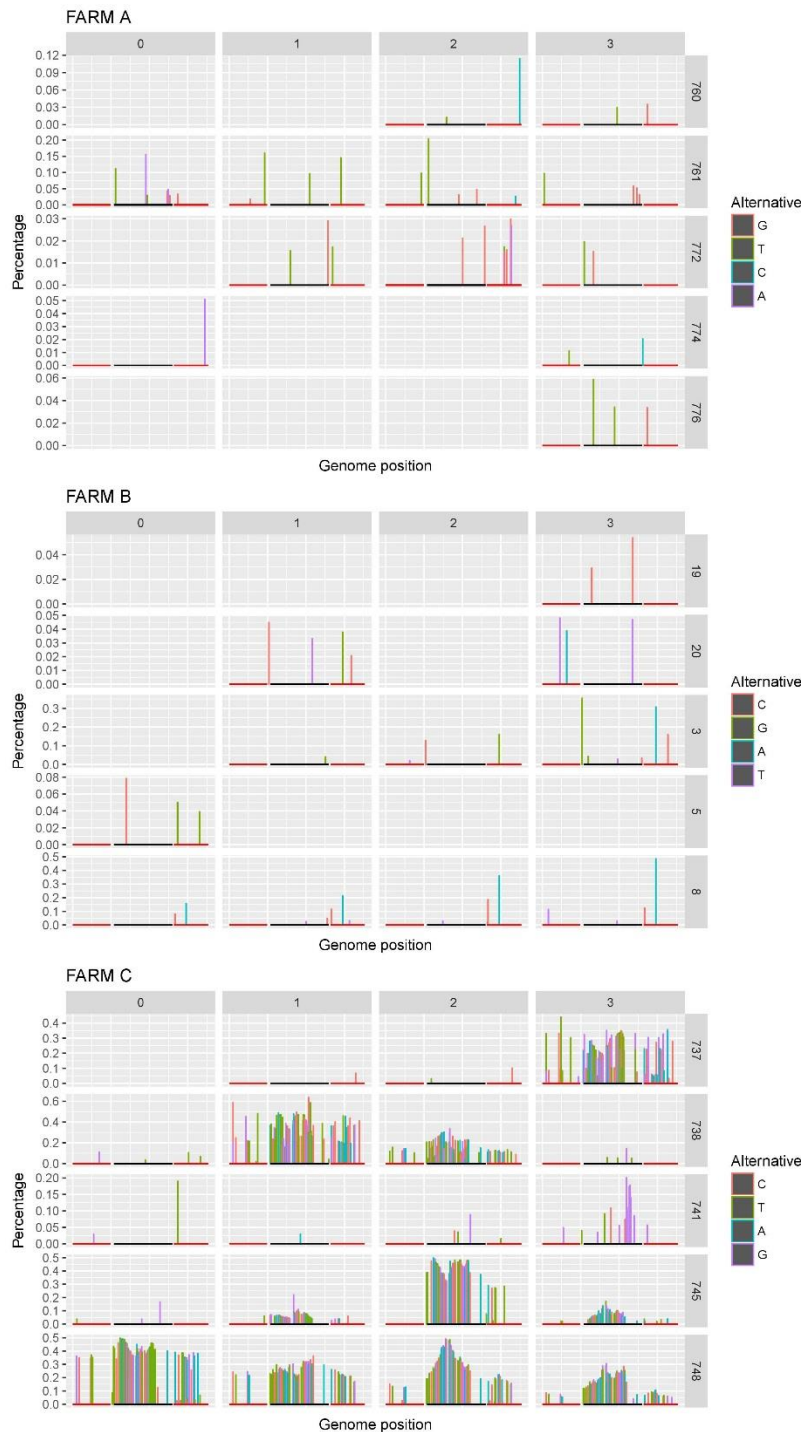
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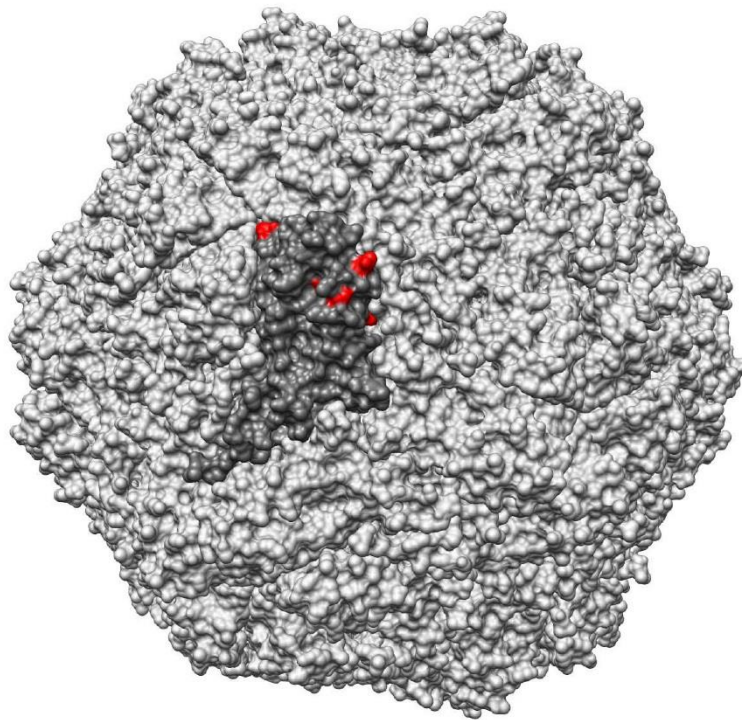
F.C.F. and G.F. contributed equally to this work.



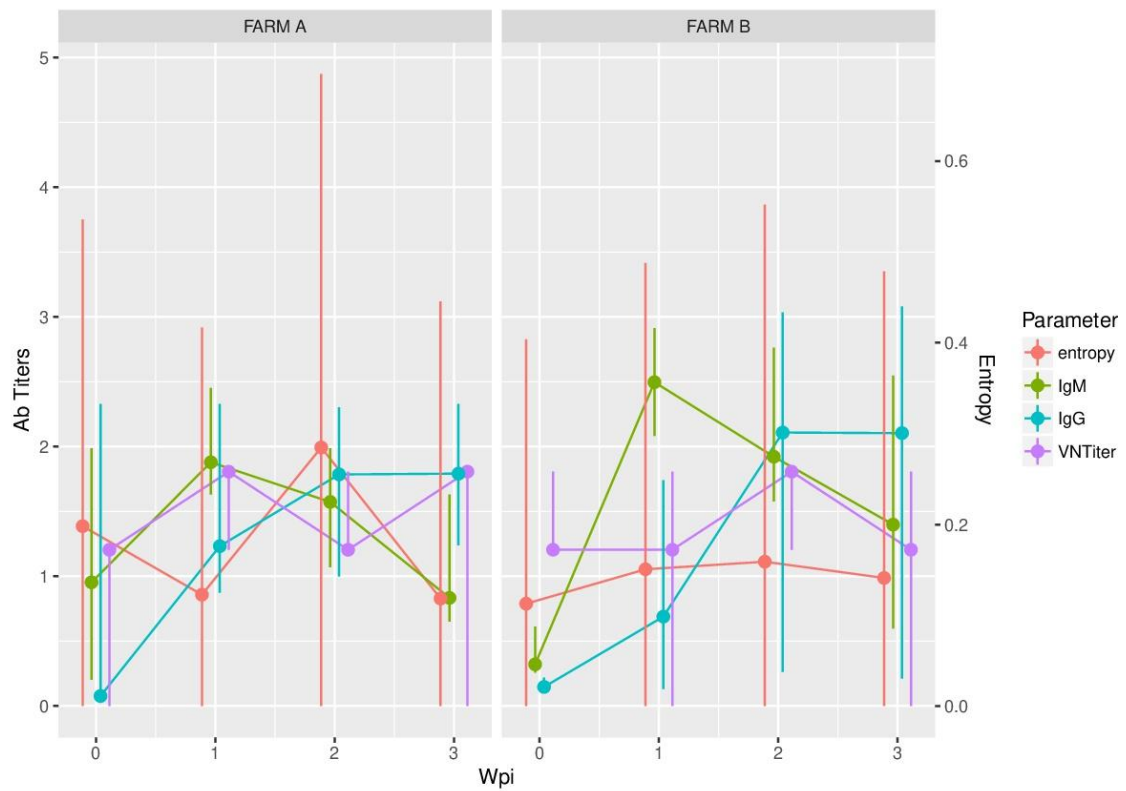
Supplementary Fig. S1. Sequencing depth at each sampling point associated to each genome position. Columns and rows code for animal age (in weeks) and ID, respectively. Different farms have been color-coded.



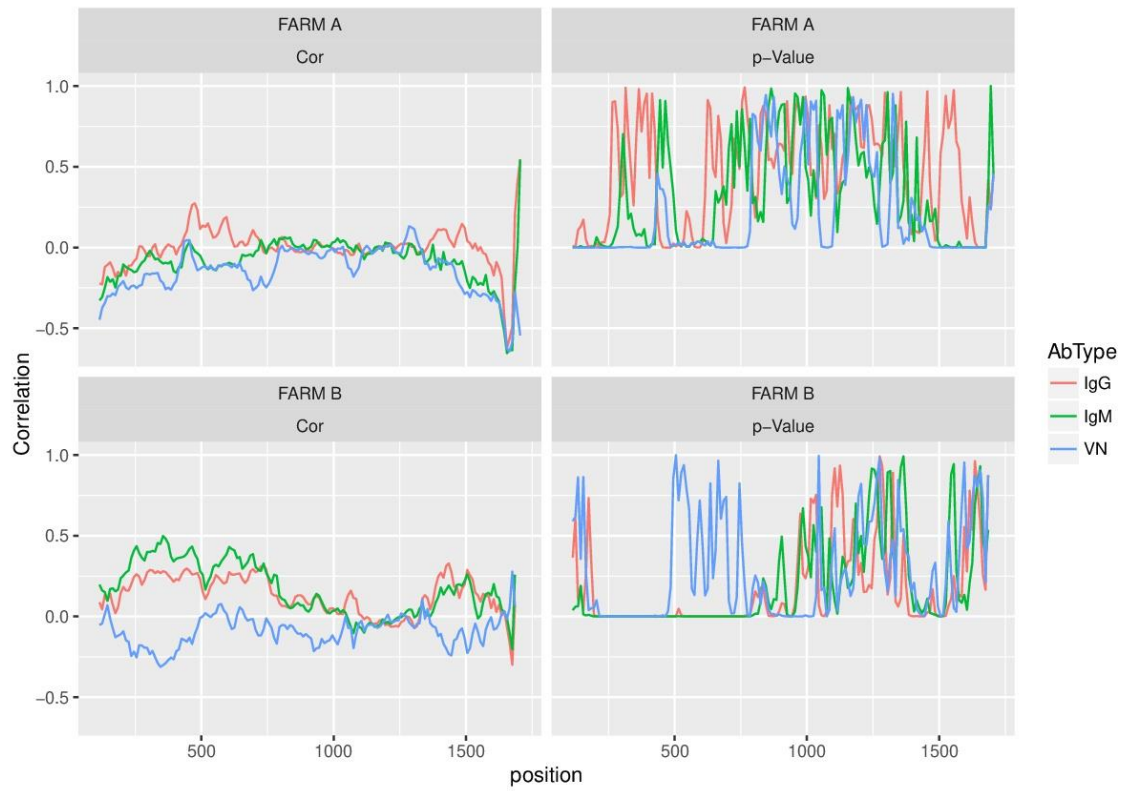
Supplementary Fig. S2. Minority variants nucleotide frequency (i.e. frequency lower than 50%) at each genome position are reported for farm A (top), B (middle) and C (bottom). Data for different animal and week post infection (wpi) have been reported separately. Different nucleotides have been color coded. The ORF1 and ORF2 have been respectively represented as red and black line in the lower part of each graph.



Supplementary Fig. S3. Quaternary structure reconstruction of the PCV-2 viral capsid. Sites detected to be under significant diversifying selection have been highlighted in red.



Supplementary Fig. S4. Median (point) and percentile range (error-bars) excluding the outer 25% values of IgM, IgG (expressed in OD 450nm), virus neutralization tiers (VN, expressed in log10 of antibody titre) and entropy (Sh) are reported for each week post infection (wpi). Although not comparable in absolute value, all the results have been provide to graphically show the relative trends.



Supplementary Fig. S5. Correlation calculated between entropy and IgM, IgG or virus neutralization (VN) titers for each considered genome window. The statistical significance of the detected correlation is also reported.