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TITLE
A PHENOTYPING METHOD TO IDENTIFY PRRSV-RESILIENT SOWS IN PRRSV-INFECTED FARMS UNDER EPIDEMIC AND ENDEMIC SCENARIOS

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CONTENT
Introduction
Porcine reproductive and respiratory syndrome (PRRSV) is a viral disease with negative impact on sow reproduction. A strategy to control this virus is to select animals more resilient to the infection. A key issue to deal with disease resistance is to set up a cost-efficient phenotyping strategy. The aim of this study was to develop a phenotyping criterion to discriminate susceptible from resilient sows in PRRSV-infected farms under epidemic and endemic scenarios.

Material & Methods
A total of 382 Landrace x Large White gilts were classified as resilient (R) or susceptible (S) to PRRSV virus following vaccination with MLV-PRRSV at 6-7 weeks of age. Gilts were phenotyped as R if serum was negative to PRRSV at 0, 7 and 21 days post-vaccination (DPV) or as S if any of the samples at 7 and/or 21 DPV was positive. The total number of piglets born, born alive, dead and mummified was recorded in each parity. Gilts were allocated in the same farm and followed up throughout 30 months. An animal mixed model with repeatability was used to assess the difference between R and S sows for number of dead and mummified piglets.

Results
The number of lost piglets (dead plus mummified) was lower in R versus S sows in the epidemic situation (2.43 ± 0.27 vs 3.36 ± 0.21 piglets, respectively, $P<0.05$). Remarkably, this was due to mummified piglets (associated to viral infection), which were two-fold higher in S as compared to R sows during the PRRSV outbreak (0.55 ± 0.09 vs 1.15 ± 0.07 piglets for R and S, respectively, $P<0.05$).

Discussion & Conclusion
The criterion used to identify resilient sows can effectively reduce the number of lost piglets at farrowing in PRRSV epidemic and endemic scenarios. There is also evidence that this trait could display enough genetic variation to respond to selection.