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Erratum

Correction: Molecular Characterization of Transcriptome-wide Interactions between Highly Pathogenic Porcine Reproductive and Respiratory Syndrome Virus and Porcine Alveolar Macrophages *in vivo*

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During the revision process several genes for Q-PCR validation were changed in the Figure 4 according to the suggestion from the reviewers, however, the Q-PCR primers information in the Table 1 has been ignored to be corrected accordingly. Here, the corrected version of the Table 1 is shown below. We apologize for this oversight and for any confusion that it has caused.

Table 1 Primers used for Q-PCR validation.

Gene	Primer sequence (5'-3')	Target size (bp)	Tm (°C)[a]
ATP6V1B2	Forward: CAAGCCATGAAAGCCGTAGTT Reverse: TGCCAGCCAATGTCCAAAGT	149	60
C3	Forward: AAACTAAAGGAGGGGGGACACT Reverse: CTTGGCATACATCACCATCAGG	133	60
CCL2	Forward: AACTTGCCCTAAATACCCTCAGA Reverse: GGAAAGCAATGTGCCCAAGTC	179	61
DDIT3	Forward: ACGGCTCAAGCAGGAAATC Reverse: CACTGGTAAGAAGGTGGTTGGT	173	58
GLRX2	Forward: TACGGAAGCCAGTTTCAAGAC Reverse: CTTGGTGAAGCCTATGAGTGTC	118	58
SLC39A14	Forward: TCTCTGCCTGCTGCTGTTACG Reverse: GCCTTCCTTTCATCCTCTTGG	166	60
TNF	Forward: CATCGCCGTCTCCTACCA Reverse: CCCAGATTCAGCAAAGTCCA	199	58
RPL32[b]	Forward: CGGAAGTTTCTGGTACACAATGTAA Reverse: TGGAAGAGACGTTGTGAGCAA	94	58-61

[a]The annealing temperature represents the optimal temperature during quantitative PCR;

[b]RNA levels of *RPL32* was assayed for normalization during quantitative PCR.