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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Published: 2011.12.01

Corrected article: Int J Biol Sci 2011; 7(7):947-959.

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) |
|---------|-----------------------------------------|-----------------|---------|
| ATP6V1B2| Forward: CAAGCCATGAAAGCCGTAAGTT         | 149             | 60      |
|         | Reverse: TGCCAGCCAATGTCCAAAGT           |                 |         |
| C3      | Forward: AAACTAAAGGGGGGGGACACT          | 133             | 60      |
|         | Reverse: CTIIGGAACATACATCCATACGG        |                 |         |
| CCL2    | Forward: AACTTGCCCTAAATACCCTCGA         | 179             | 61      |
|         | Reverse: GGAAAGCAATGIGGCCAAGTC          |                 |         |
| DDIT3   | Forward: ACGGCTCAACGAGAAATCT            | 173             | 58      |
|         | Reverse: CACTGGAAGAAAGTTGGG            |                 |         |
| GLRX2   | Forward: TACGGAAGCCAGTTCTCAAGAC         | 118             | 58      |
|         | Reverse: CTTGGTAGAAGCTCTAGGTGA          |                 |         |
| SLC39A14| Forward: TCTCTGCTGCTGCTGTACG            | 166             | 60      |
|         | Reverse: GCCCTTCCTTCCCTCTTCTC           |                 |         |
| TNF     | Forward: CATCGCCGTCTCTCTACCA            | 199             | 58      |
|         | Reverse: CCCACATCTGACCAAAGTCCA          |                 |         |
| RPL32\(a\) | Forward: CGGAAGTCTCTGTACAAATGTAA       | 94              | 58-61   |
|         | Reverse: TGGAAAGAGCTTTGGGAGCA           |                 |         |

\(a\)The annealing temperature represents the optimal temperature during quantitative PCR;

\(b\)RNA levels of RPL32 was assayed for normalization during quantitative PCR.