## Additional file 3 Experimental methods and statistical analysis.

## RNA isolation, cDNA synthesis and qPCR

For the experiment on *ssc*-miR-15a and *ssc*-miR-15b RNA isolation, cDNA synthesis and qPCR were performed as described [18]. Briefly RNA was isolated from porcine lung tissue using miRNeasy Mini Kit (Qiagen, Germany) with DNAseI treatment according to manufacturer's recommendations.

Reverse transcription of 1 µg total RNA was performed according to Balcells et al. [9]. Briefly, 100 ng of total RNA were poly(A) tailed and reverse transcribed in a single tube reaction: 1 µl of 10x poly(A)polymerase buffer, 0.1 of ATP, 1 of **RT-primer** (5'mM μΜ CAGGTCCAGTTTTTTTTTTTTTTTTTTVN, V = A, C and G; N = A, C, G and T), 0.1 mM of dNTPs, 100 units of MuLV reverse transcriptase (New England Biolabs, USA) and 1 unit of poly(A) polymerase (New England Biolabs, USA) were mixed in a final volume of 10 µl and incubated at 42 °C during 1 hour followed by 5 minutes at 95 °C. The cDNA was diluted before the qPCR reaction.

All RT-qPCR experiments are MIQE guidelines compliant.

## **Statistical analysis**

The fraction of functional primers (see for example Table 4) is given with as a number with a margin (for example  $93 \pm 5$  % of the assays worked with the first primer pair selected). The number was calculated as the success rate: number of functional assays divided by the total number of assays. Next, I found the theoretical numbers of functional and failed assays that would give a P-value > 0.05 when compared to the observed numbers of functional and failed assays in a X<sup>2</sup>-test. Finally, margins were calculated as: observed success rate – theoretical success rate.

Comparison of primer success rate to the success rate for manually designed primers [9] was done by  $X^2$ -test.