CORRECTION

Correction: Deciphering Transcriptome and Complex Alternative Splicing Transcripts in Mammary Gland Tissues from Cows Naturally Infected with *Staphylococcus aureus* Mastitis

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The images for Figs 2 and 3 are incorrectly switched. The image that appears as Fig 2 should be Fig 3 and the image that appears as Fig 3 should be Fig 2. The figure captions appear in the correct order.

OPEN ACCESS

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Fig 2. Novel transcripts harboring QTLs associated with clinical mastitis in the two groups. BTA: Bovine autosome.

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Fig 3. Genes and their patterns of alternative splicing events in healthy and mastitic cow's mammary gland tissue. The red and green histograms show the numbers of genes and the corresponding numbers of alternative splicing events, respectively.

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Reference

1. Wang XG, Ju ZH, Hou MH, Jiang Q, Yang CH, Zhang Y, et al. (2016) Deciphering Transcriptome and Complex Alternative Splicing Transcripts in Mammary Gland Tissues from Cows Naturally Infected with *Staphylococcus aureus* Mastitis. PLoS ONE 11(7): e0159719. doi:10.1371/journal.pone.0159719 PMID: 27459697