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Author Correction: Genome-wide analyses of long non-coding RNA expression profiles and functional network analysis in esophageal squamous cell carcinoma

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Correction to: *Scientific Reports* <https://doi.org/10.1038/s41598-019-45493-5>, published online 24 June 2019

This Article contains errors.

The numbers of the differentially expressed lncRNAs and microRNAs were inadvertently swapped in the description of the Results. The numbers reported in the Abstract are correct.

As such, in the Results, in the section ‘Expression profiles of lncRNAs in ESCC’,

“Based on the microarray data, 3,052 lncRNAs and 2,366 mRNAs were identified to be differentially expression (FC ≥ 2.0 or ≤ 0.5 , $p \leq 0.05$).”

should read:

“Based on the microarray data, 2,366 lncRNAs and 3,052 mRNAs were identified to be differentially expression (FC ≥ 2.0 or ≤ 0.5 , $p \leq 0.05$).”

These errors do not affect the conclusions of the Article.



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