

Corrigendum

Corrigendum to “Transcriptome Profiling across Five Tissues of Giant Panda”

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Following the publication of the article titled “Transcriptome Profiling across Five Tissues of Giant Panda” [1], the authors identified that the published Supplementary Material is not correct, and the correct Supplementary Materials are provided as follows.

Supplementary Materials

Supplementary 1. Table S1: individual information of the giant panda used in this study.

Supplementary 2. Table S2: quality summary of RNA-seq results in all samples of the giant panda.

Supplementary 3. Table S3: details of all genes mapped to the giant panda reference genome in the present study.

Supplementary 4. Table S4: list of tissue-specific differentially expressed genes of each tissue of giant panda.

Supplementary 5. Table S5: list of significantly enriched GO terms of tissue-specific differentially expressed genes of each tissue.

Supplementary 6. Table S6: list of significantly enriched KEGG pathways of tissue-specific differentially expressed genes of each tissue.

Supplementary 7. Figure S1: four-way Venn diagram of tissue-specific differentially expressed genes of each tissue (Supplementary Materials).

References

- [1] F. Li, C. Wang, Z. Xu et al., “Transcriptome Profiling across Five Tissues of Giant Panda,” *BioMed Research International*, vol. 2020, Article ID 3852586, 13 pages, 2020.