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CORRECTION

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Correction to: Hepatitis, testicular degeneration, and ataxia in DIDO3-deficient mice with altered mRNA processing

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Correction to: Cell & Bioscience (2022) 12:84
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After publication of the original article [1], we realized that two files in the Supplementary Information, Additional files 4 and 7, were incorrect. The correct Additional files 4 and 7 are available on *Cell & Bioscience*'s website from the date of publication of this note.

In addition, a part of the Methods section was missing in the original article. Methods for Additional file 4 are as follows:

Burrows-Wheeler aligner BWA-MEM 0.7.15 (RRID: SCR_010910) was used to align paired-end reads to the UCSC mouse genome build mm10 with standard settings. Alignments were converted to BAM format and deduplicated with Picard tools 2.9.0 (RRID:SCR_006525). To quantify relative expression of transcripts, we ran StringTie 1.3.3 (RRID:SCR_016323) [2] and calculated the transcripts per million (TPM) reads. Sample scaling and statistical analyses were performed with the R package edgeR (RRID:SCR_012802) [3]. Transcripts with TPM > 0 in all samples were kept for downstream analysis. Differentially expressed genes with an absolute value of log2 fold change ≥ 1 and a false-discovery rate (FDR) < 0.05 were considered statistically significant.

Supplementary Information

The online version contains supplementary material available at https://doi.org/10.1186/s13578-022-00843-1.

Additional file 4. List of genes over- or underexpressed in E16 vs. WT livers.

Additional file 7. Analysis of compositional biases around splice sites in E16 vs. WT livers.

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References

1. Gutiérrez J, van Wely KHM, Martínez-A C. Hepatitis, testicular degeneration, and ataxia in DIDO3-deficient mice with altered mRNA processing. Cell Biosci. 2022;12:84.
2. Pertea M, Pertea GM, Antonescu CM, Chang TC, Mendell JT, Salzberg SL. StringTie enables improved reconstruction of a transcriptome from RNA-seq reads. Nat Biotechnol. 2015;33:290–5.
3. Robinson MD, McCarthy DJ, Smyth GK. edgeR: a Bioconductor package for differential expression analysis of digital gene expression data. Bioinformatics. 2010;26:139–40.

Publisher's Note

The original article can be found online at https://doi.org/10.1186/s13578-022-00804-8.

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