



## Correction to: RNA as a Source of Biomarkers for Amyotrophic Lateral Sclerosis

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### Correction to: Metabolic Brain Disease

<https://doi.org/10.1007/s11011-021-00,738-z>

The original article contains error specifically Fig. 2. Please see correct figure below:

Fig. 2 legend should be:

The text describing Fig. 2 should be:

The changes in gene expression in Fig. 2 are from a pilot study. This pilot study was later expanded and the updated results are presented in Fig. 3 (Barham et al., 2018).

**Fig. 2** Heat map of differentially expressed transcripts in the spinal cords from Non-TG, hPFN1<sup>WT</sup> (TG WT) and hPFN1<sup>G118V</sup> (TG MUT) animals at the late stage of ALS (n=2 per group). Each row of the heat map represents the differentially expressed genes (blue, low expression; red, high expression). Black arrows point to proinflammatory genes. Red arrows point to novel genes with highest values of upregulation or downregulation. Green arrow points to the gene of prion, serving as internal control for RNA-Seq data



The original article can be found online at <https://doi.org/10.1007/s11011-021-00738-z>.

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### Reference:

Barham C, Fil D, Byrum SD, Rahmatallah Y, Glazko G, Kiaei M (2018) RNA-Seq analysis of spinal cord tissues from hPFN1(G118V) transgenic mouse model of ALS at pre-symptomatic and end-stages of disease. *Sci Rep* 8:13737. <https://doi.org/10.1038/s41598-018-31132-y>

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