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Corrigendum: Proteomic profiling reveals the potential mechanisms and regulatory targets of sirtuin 4 in 1-methyl-4-phenyl-1,2,3,6tetrahydropyridine-induced Parkinson's mouse model

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A corrigendum on

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In the published article, an error occurred in the representative immunoblot plot of TH in Figure 2B and Figure 8. The corrected Figure 2 and Figure 8 appear below.

The authors apologize for this error and state that this does not change the scientific conclusions of the article in any way. The original article has been updated.

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FIGURE 2

SIRT4 plays a role in a PD model. (A) Flow chart of stereotactic injection of SIRT4-AAV virus and the establishment of a mouse model of PD induced by MPTP. (B) Representative western blots and densitometric analysis for TH protein between groups. TH protein extracts from substantia nigra after mice were intraperitoneally injected with saline and MPTP for 5 days. GAPDH was used as a loading control (n = 4 mice per group). (C) Representative western blots and densitometric analysis for SIRT4 protein between groups. SIRT4 protein extracts from substantia nigra after mice were intraperitoneally injected with saline or MPTP for 5 days. GAPDH was used as a loading control (n = 4 mice per group). (C) Representative western blots and densitometric analysis for SIRT4 protein between groups. SIRT4 protein extracts from substantia nigra after mice were intraperitoneally injected with saline or MPTP for 5 days. Tubulin was used as a loading control (n = 4 mice per group). (D, E) Representative western blots and densitometric analysis for SIRT4 protein between groups, respectively. DJ-1 or SIRT4 protein extracts from substantia nigra of WT rats or DJ-1 KO rats. Tubulin was used as a loading control (n = 4 mice per group). All results are depicted as means \pm SEM. The comparison across groups was analyzed by t-test. **P < 0.01, ***P < 0.0001 compared with the control group. TH, tyrosine hydroxylase; SIRT4, NAD-dependent protein lipoamidase sirtuin-4, mitochondrial.



FIGURE 8

Data visualizations of the results from the KEGG enrichment analysis of differentially expressed genes and proteins in SH-SY5Y cells after SIRT4 overexpression with ClueGO. A KEGG enrichment analysis of differentially expressed proteins in SH-SY5Y cells after SIRT4 overexpression was performed using ClueGO. The figure clearly shows the main proteins in the enriched pathways and the connection between A protein and different pathways. The size of the circle represents the number of different proteins.