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Proteomic analysis revealed the altered kidney protein profile of a *Cyld* knockout mouse model

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ABSTRACT. The aim of this study was to compare the proteomics pattern of the kidneys from *Cyld* knockout mice with that from normal mouse kidneys and establish a preliminary understanding of the role of *Cyld* in the kidney. Proteins from the kidneys of knockout *Cyld* mice and wild-type mice were extracted, isobaric tags for relative and absolute quantitation (iTRAQ) was performed, and the proteomics patterns of the two groups were compared. The genotypes of the mice were verified by polymerase chain reaction. A total of 1748 proteins with a local false discovery rate of ≤5% were identified, among which 1437 proteins were reliably recognized and quantified. The expression of two dysregulated proteins was confirmed by Western blotting. Gene

ontology and pathway analyses indicated that the proteins identified were involved in biological processes, cell components, and molecular functions, and participated in different pathways. Some of the proteins identified were relevant to renal function or kidney diseases. The difference between the proteomics profiles of kidneys from *Cyld* knockout mice and wild-type mice was prominent, which correlates to kidney dysfunction and the development of renal diseases.

Key words: iTRAQ; *Cyld* knockout; Kidney disease; Proteomics

