**Supplementary Figures**

Serum proteomic analysis for a new type of long-term persistent COVID-19 patients in Wuhan

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**Figure S1**

Figure S1 The identified protein numbers in each sample of LTPPs and HCs.
**Figure S2**

The proteomic profiling of serum from LTPPs and HCs. (A) Principal component analysis of the expressed proteins between the two groups. (B) Volcano plot showing the significantly upregulated (red dots) and downregulated (blue dots) proteins between the two groups (FC > 2). (C) Bar plot representing the number of differently expressed proteins (DEPs).
Figure S3 The bubble plot (A) and treemap (B) showing 34 clusters of GO biological processes for the 12 LTPPs.
Figure S4

The significantly enriched GO biological processes and the corresponding DEPs of the 12 LTPPs.
Figure S5 Bar plot showing 17 significantly enriched KEGG pathways for all the DEPs of LTPPs.
Figure S6 The bubble plot (A) and treemap (B) showing 28 clusters of GO biological processes for the seven LTPPs-NH.