**Tables**

**Table 1. TPM values of public transcriptome processed in Partek Flow software.**

**Table 2. Protein intensity of public proteome.**

**Table 3. All proteins identified in the mouse LV interactome.**

**Table 4. 14-3-3 interacting proteins obtained from three statistical methods.**

There are three sheets in the excel file: TTEST, QSPEC and countdata.

**Table 5. Overlap of two statistical methods countdata and QSPEC.**

**Table 6. Proteins identified in this study and recorded in the ANIA database.**

**Table 7. Clustering of the mouse LV protein-protein interaction network in STRING.**

There are four sheets in the excel file. The first sheet is the summary of all the proteins clustered in the kmeans method (n=3). The remaining three sheets are the features of the three clusters.

**Table 8. GO terms and KEGG pathways enriched from the mouse LV 14-3-3 interactome within clusterProfiler.**

There are four sheets in the excel file: BP (Biological Process), CC (Cellular Component), MF (Molecular Function), and KEGG pathway.

**Table 9. GO terms after redundancy reduction in REVIGO.**

There are three sheets in the excel file: BP (Biological Process), CC (Cellular Component), and MF (Molecular Function).

**Table 10. Canonical pathways enriched in IPA.**

There are four sheets in the excel file: (1) all canonical pathways, (2) metabolic pathways extracted from (1), (3) cardiovascular signaling pathways extracted from (1), and (4) description and ID numbers of input proteins recognized by IPA.

**Table 11. GO terms, KEGG pathways and IPA canonical pathways related to cellular metabolism when mapping to the cellular metabolism network.**

**Table 12. Summary of analysis methods and software.**