

Supplementary Materials

Surviving winter on the Qinghai-Xizang Plateau: Extensive reversible protein phosphorylation plays a dominant role in regulating hypometabolism in hibernating *Nanorana parkeri*

Yong-Gang Niu^{1,*}, Deng-Bang Wei², Xue-Jing Zhang³, Ti-Sen Xu¹, Xiang-Yong Li¹, Hai-Ying Zhang¹, Zhi-Fang An², Kenneth B. Storey⁴, Qiang Chen³

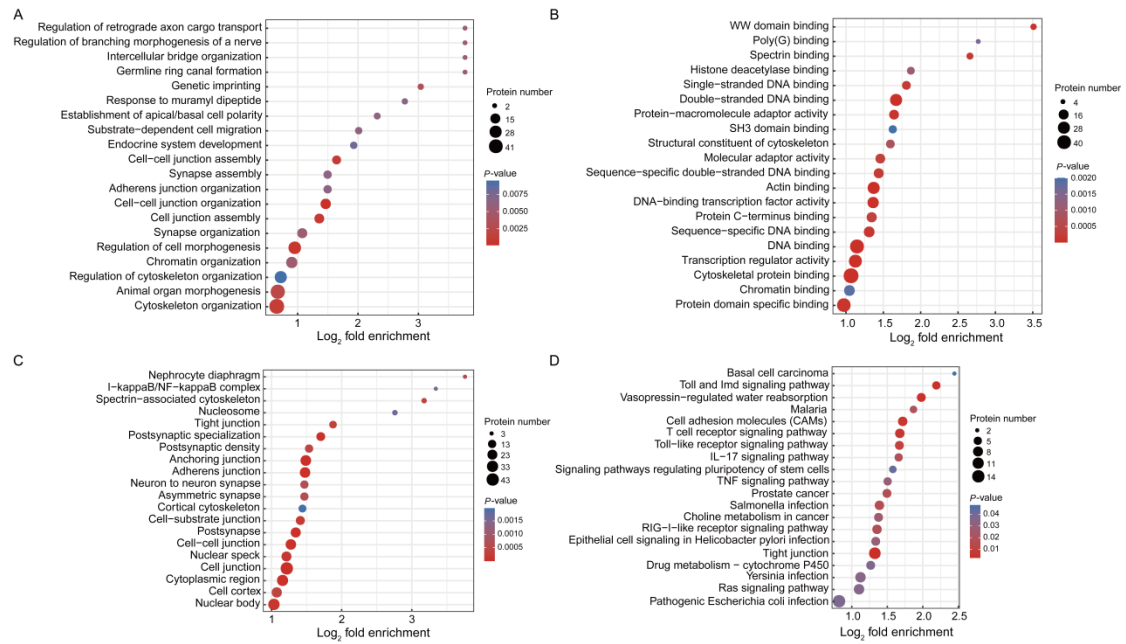
1 Department of Life Sciences, Dezhou University, Dezhou, Shandong 253023, China

2 State Key Laboratory of Plateau Ecology and Agriculture, Qinghai University, Xining, Qinghai 810016, China

3 School of Life Sciences, Lanzhou University, Lanzhou, Gansu 730000, China

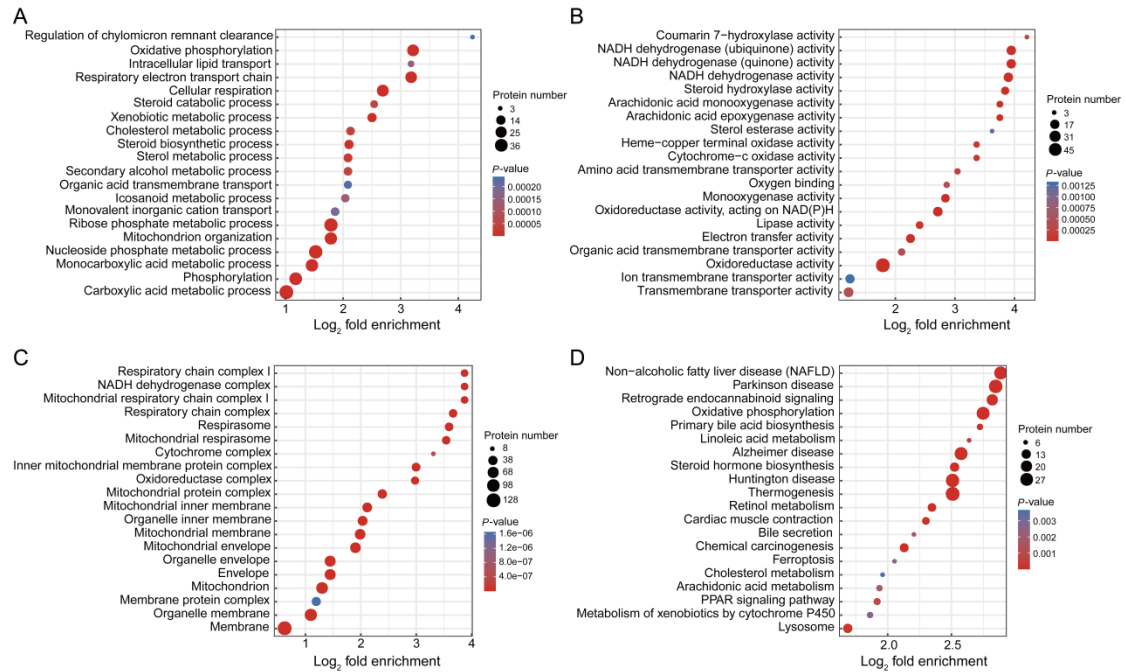
4 Department of Biology, Carleton University, Ottawa, ON K1S 5B6, Canada

*Corresponding author, E-mail: yonggangniu@126.com



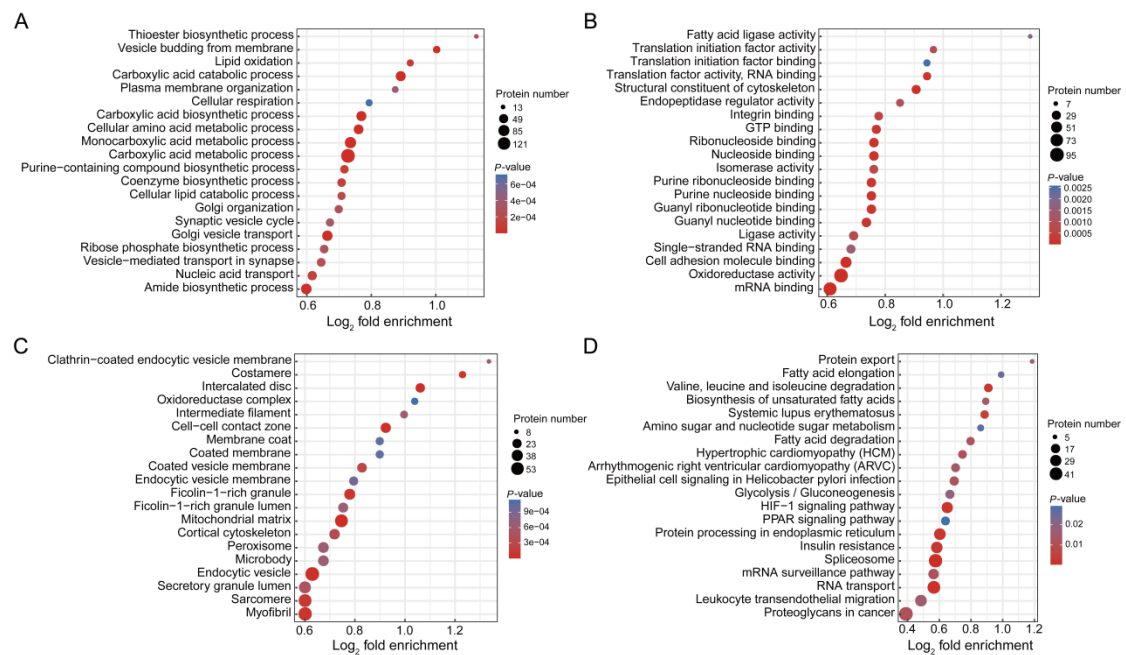
Supplementary Figure S1 Top 20 enriched GO terms and KEGG pathways in higher expressed proteins in the liver of hibernating *N. parkeri*

A: Biological process. B: Molecular function. C: Cellular component. D: KEGG pathway. Color shades and circle size represent different *P*-values and protein count, respectively.

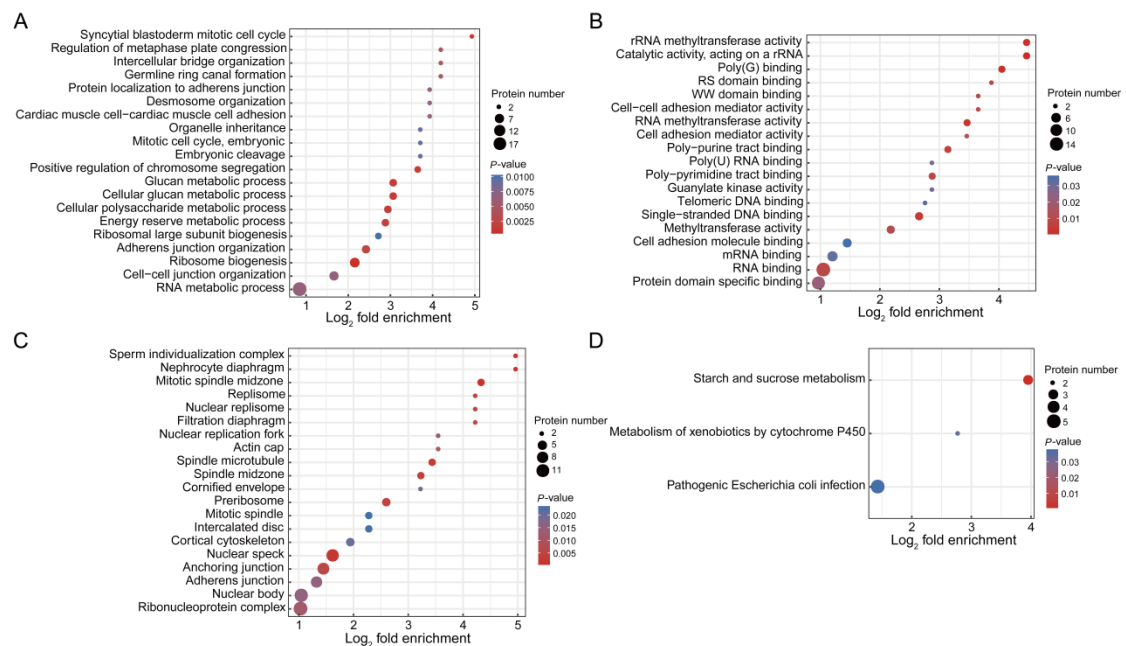


Supplementary Figure S2 Top 20 enriched GO terms and KEGG pathways in lower expressed proteins in the liver of hibernating *N. parkeri*

A: Biological process. B: Molecular function. C: Cellular component. D: KEGG pathway. Color shades and circle size represent different *P*-values and protein count, respectively.



Supplementary Figure S3 Top 20 enriched GO terms and KEGG pathways in higher expressed phosphorylated proteins in the liver of hibernating *N. parkeri*
A: Biological process. B: Molecular function. C: Cellular component. D: KEGG pathway. Color shades and circle size represent different *P*-values and protein count, respectively.



Supplementary Figure S4 Top 20 enriched GO terms and KEGG pathways in lower expressed phosphorylated proteins in the liver of hibernating *N. parkeri*
A: Biological process. B: Molecular function. C: Cellular component. D: KEGG pathway. Color shades and circle size represent different *P*-values and protein count, respectively.

Supplementary Table S1 Proteins identified and quantified in *N. parkeri* liver

Supplementary Table S2 Phosphopeptides identified and quantified in *N. parkeri* liver

Supplementary Table S3 Differentially expressed proteins in *N. parkeri* liver between summer and winter

Supplementary Table S4 Differential phosphorylation sites in *N. parkeri* liver between summer and winter

Supplementary Table S5 Motif analysis for differentially expressed phosphopeptide sequences

Supplementary Tables S1–S5 are listed as separate Excel files due to their large size.