

Mechanisms of overwintering frost tolerance in alfalfa roots based on 4D-Label-free quantitative proteomics

YAJUN MA¹, YU ZHANG³, QIAOXIAN ZHANG², GUO SUN⁴, YAJUN YAN⁵,
CHUAN WANG¹, WENBIN MIAN¹, TIANHUI YANG¹, TING GAO¹

¹*Institute of Animal Science (Grass Livestock Engineering and Technology Research Center),
Ningxia Academy of Agriculture and Forestry, Yinchuan, Ningxia, P.R. China*

²*Ningxia Autonomous Region Animal Husbandry Workstation, Yinchuan, Ningxia, P.R. China*

³*Ningxia Grassland Workstation, Ningxia Autonomous Region Forestry and Grassland Bureau,
Yinchuan, Ningxia, P.R. China*

⁴*Yan Chi County Forestry and Grassland Bureau, Yan Chi, Ningxia, P.R. China*

⁵*College of Life Sciences, Sichuan University, Chengdu, Sichuan, P.R. China*

Electronic Supplementary Material (ESM)

The authors are fully responsible for both the content and the formal aspects of the electronic supplementary material. No editorial adjustments were made.

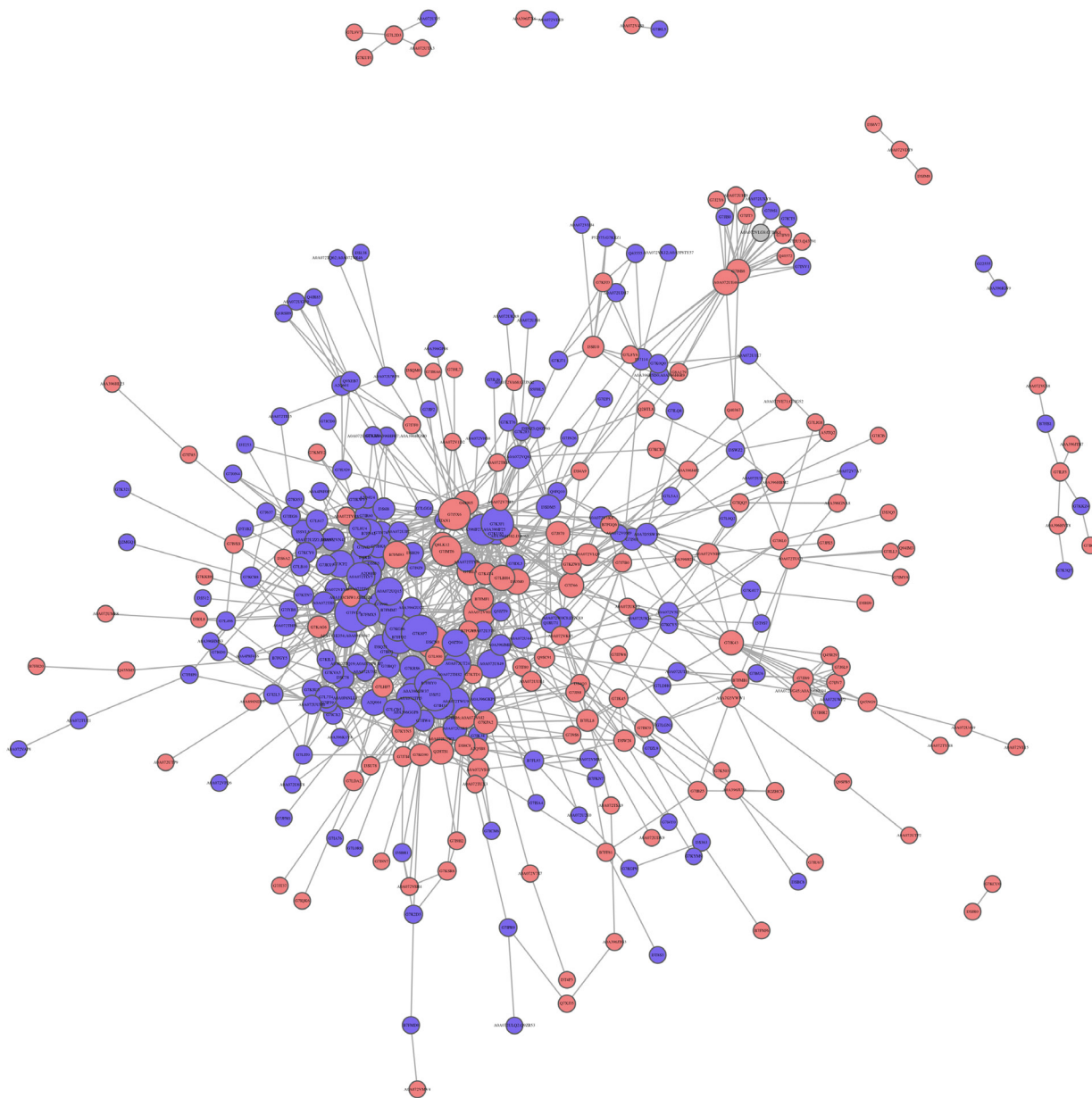


Figure S1. Network diagram of differentially expressed protein interactions in QD2_vs_QD1 group

The circle nodes in the figure indicate differentially expressed proteins, and the lines indicate protein-protein interactions; the colour of the circle indicates the difference in protein expression (down-regulation is marked in blue, up-regulation in red), and the size of the circle indicates the degree of connectivity of the protein (i.e., the number of proteins that directly interact with a protein); QD1 – the Qingda No.1 samples before overwintering; QD2 – the Qingda No.1 samples after overwintering

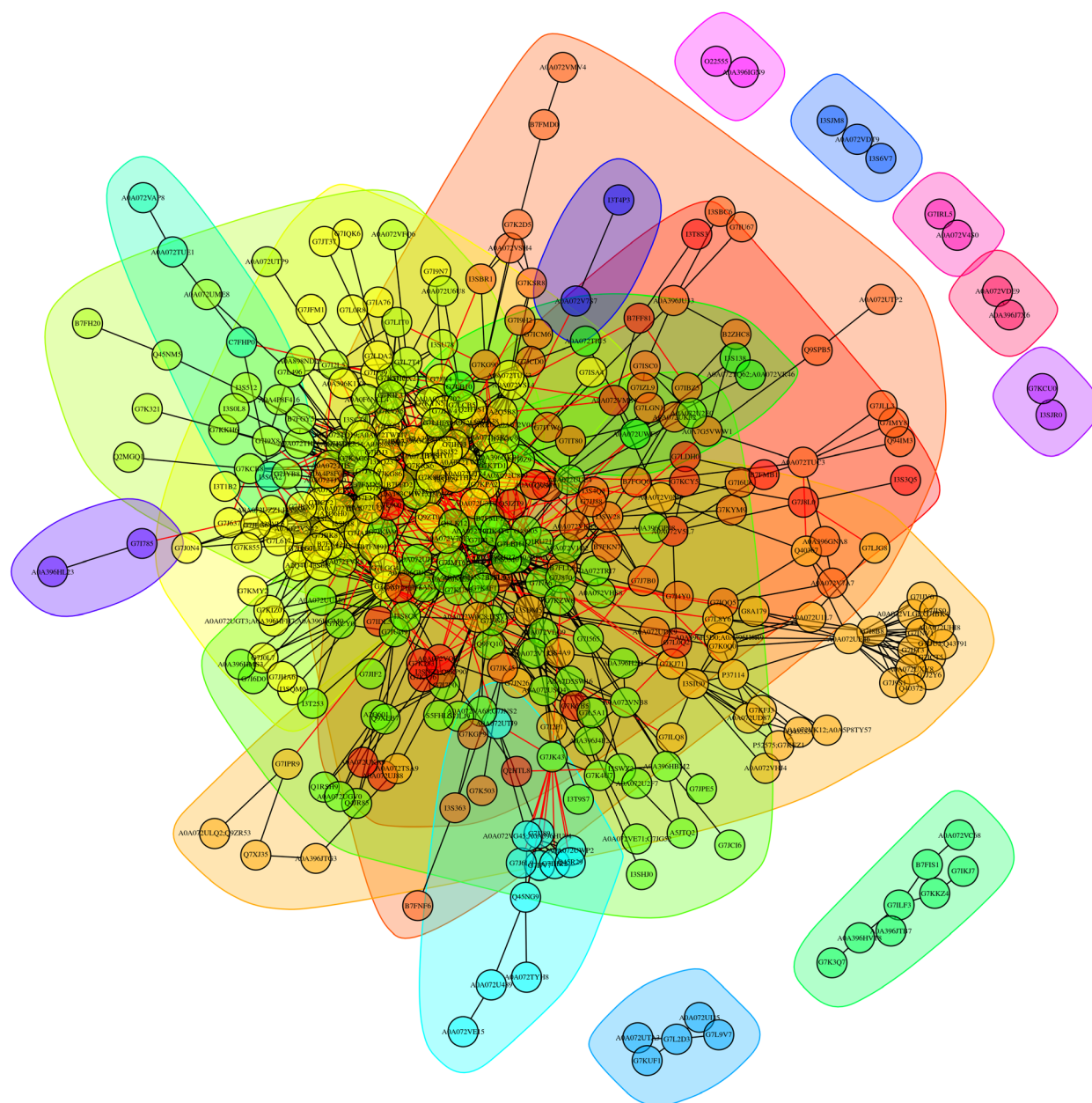


Figure S2. QD2_vs_QD1 group interaction network diagram for functional categorization

Proteins within the same network module often have similar biological functions; QD1 – the Qingda No.1 samples before overwintering; QD2 – the Qingda No.1 samples after overwintering