The manuscript by Yang R and colleagues delineates the molecular understanding of salt tolerance in Wheat (*Triticum aestivum*) utilizing both transcriptomic and proteomic analysis. The authors utilized salt-tolerant and salt-sensitive wheat to find differentially expressed genes and proteins to address the molecular pathways and processes important for the salt-tolerant phenotype in wheat. I found this study to be interesting, well-crafted, and insightful. I have some questions which need to addressed in a revised version:

Major concerns

1. qPCR validations were carried out using the same samples used for proteomic analysis. I would recommend using separate samples for the validation process to ensure the reproducibility of the findings.
2. The authors mentioned differentially expressed proteins in other species like barley, rice, sweet potatoes (in the introduction). It would be interesting to know the common DIPs among different species to single out the most prominent molecular pathways/processed involved in salt tolerance.
3. It would be helpful to dissect the role of some of the differentially expressed genes/proteins experimentally using genetic knockdown/knockout or overexpression experiments.

Minor concerns

1. I would suggest elaborating figure legends to ensure better readability.