Response to Reviewer 2 Comments

**Point 1:** Pg 1 line 45: the wording "and so on" is awkward and imprecise. Please rephrase and indicate what other processes are being referred to.

**Response 1:** Thanks for your good suggestion. We removed “and so on” in our revised manuscript.

**Point 2:** Pg 2 line 67: don't assume that everyone reading the manuscript are aware of miRNA roles in plant stress physiology.

**Response 2:** Thanks for your reminding. We modified “As we all know” into “More and more research reveals that”.

**Point 3:** Pg 3 Plasmid and sweet potato genetic transformation section: Include relevant protocols instead of just referring to another manuscript. Citing the original source is required but so are details needed to reproduce and evaluate the soundness of the manuscript.

**Response 3:** It is really true as you mention that the details of methods is needed. But considering that this method is also expressed in thus way in our previous articles (Ren L, et al (2021) Genome-Wide Identification of TCP Transcription Factors Family in Sweet Potato Reveals Significant Roles of miR319-Targeted TCPs in Leaf Anatomical Morphology. Front. Plant Sci. 12: 686698. doi: 10.3389/fpls.2021.686698), we just cite the original source here.

**Point 4:** Pg 6 line 239: I don't understand the point being made here. "sequester the normal expression" is nonsensical. Please clarify and rephrase.

**Response 4:** Thanks for your question Target mimicry is a common method to study the function of miRNA. There is a non-coding protein gene IPS in *Arabidopsis*, and its transcription RNA can specifically bind to miRNA through sequence complementarity, but it forms incomplete complementary bubble structure at the cleavage site of miRNA, that is, miRNA cannot cleavage IPS RNA, thus inhibiting the degradation of miRNA to its target gene mRNA. IPS gene is equivalent to the target mimicry. (Franco-Zorrilla et al., 2007)