Response to Reviewer 1 Comments

Point 1: The authors should state the expected full length products from sheep in the Introduction and indicate the source of the data used to determine those expectations.

Response 1: Thank you very much for your comment and suggestion. We have added it, as presented in Lines 64-65 from revised version of this paper.

Point 2: It is unclear how many times assays were performed. The number of animals indicates there should be 8 replicates of the qRT-PCR, western blots, immunohistochemistry and immunofluorescence at each stage. However the figures do not indicate the number of replicates. Also, the methods text seem to indicate three biological replicates. This needs to be made more clear, as it is the basis of the reliability of the results presented.

Response 2: Thank you very much for your comment. We are very sorry for not clear description and our careless, regarding the number of replicates in the "Material and Methods" and figures. In this work, qRT-PCR was performed in 8 biological replicates with 3 technical replicates for each biological replicate, and western blots, immunohistochemistry and immunofluorescence were performed in 8 biological replicates with 2 technical replicates for each biological replicate. In the revised version of this manuscript, we have made modification and supplement where appropriate.

Point 3: Sequencing of three cloned products is not sufficient to determine SNP differences. Although, I recognize that the authors do not make conclusions from this data, otherwise I would consider this a major issue.

Response 3: Thank you very much for your comment. Admittedly, in this study, three independent positive clones is few, but it meets the minimum biological research requirement. In a relevant literature published recently, the number of cloned products used for sequencing is also n=3. **[**Sun, D.; Zang, X.; Guo, Y.; Xiao, D.; Cao, X.; Liu, Z.; Zhang, F.; Jin, Y.; Shi, J.; Wang, Z.; Li, R.; Yangzong, Z. Cloning of *pcB* and *pcA* Gene from *Gracilariopsis lemaneiformis* and Expression of a Fluorescent Phycocyanin in Heterologous Host. *Genes* **2019**, *10*, 322.**]**. Also, these positive cloned products were randomly selected and used for sequencing, and acquired sequences were same, proving that CDs sequence was correct.

Point 4: Line 327 Says "extremely significant" and I believe should read "significant".

Response 4: Thank you very much for your comment. We have made correction in revised version, as shown in Line 261.