Report revision of "Transcriptome atlas of *Phalaenopsis equestris*" manuscript

1. Basic reporting

Orchids are one of the most beautiful and fascinating plant species. The high differences among orchids fascinated a large part of the scientific community during the centuries. Until now, the molecular pathways regarding orchid development are arduous to study for the absence of mutant of this species. The genome and transcriptome sequencing are two pivotal resources to understand which genes are involved in orchid differentiation. The data obtained with this study will be useful to all the scientific community that focus their analysis on orchids to understand which genes are involved in some unknown molecular pathways. The TraVa database will be helpful support for future orchid studies.

I suggest improving the introduction emphasizing the importance of this transcriptome data and why they will be important for the scientific community. It is necessary, in my opinion, to highlight why the transcriptome data is a relevant resource adding some work example where the use of transcriptome data was decisive to understand the role and evolution of some genes in orchid species.

The manuscript is clear and well written. I have listed some correction in the text in the attached file.

The figures are precise. I suggest, if it is possible, to change the interval colour to better highlight the differences of expression among genes, especially in Fig. 2.

2. Experimental design

No comment

3. Validity of the findings

I suggest adding to the conclusion the importance of this transcriptome sequencing, the TRaVa database and the orphan genes investigated. I recommend emphasizing on the importance of the data obtained and the use in future of these data.

General comments for the author

L.26: Remove “a” between “about” and “half”

L.47: Add “the” before “reliability

L. 79: Substitute “In order to” with “To”

L. 102: Add “an” between “showed” and “extremely”

L. 112: Add “the” before “analysis”

L. 112: Add “the” before “detailed”

L. 129-130: I believe that there is a problem in this part “when transcripts of 21 671 (74%) genes were found in at least one sample.” Probably “when” needs to be changed in “while”. If there isn’t a problem, I suggest changing this phrase because I believe it is unclear.

L. 138-140: “A number of samples where gene is expressed is the simplest method to characterize expression pattern width, as was shown for *Nicotiana tabacum* (Edwards et al., 2010) or *Vigna unguiculata* (Yao et al., 2016)” it should be reformulated in “Investigate some samples, where a gene is expressed, is the simplest methods to characterize expression pattern width, as was shown for *Nicotiana tabacum* (Edwards et al., 2010) or *Vigna unguiculata* (Yao et al., 2016)”.

L. 142: Replace “less” with “fewer”

L. 146: Add “the” between “on” and “clustering”

L. 147: Replace “less” with “fewer”

L. 155: Add “the” between “in” and “case”

L.156: Add a comma after “count”

L. 162: Replace “oxidation reduction” with “oxidation-reduction”

L. 178: Add “the” before “Graphical”

L. 180: Substitute “number of” with “several”

L. 183: Add “the” between “with” and “undifferentiated”

L. 210: Add commas before and after “however”

L. 214: Remove “an” between “is” and “evidence”

L. 216: Add a comma after “Notably”

L. 226: Remove “the” before “similar”

L. 227: Substitute “In order to” with “To”