The paper by Silva et al. presents a comprehensive QTL study of resistance against Rice *hola blanca virus*. The use of digital images to evaluate the disease is innovative and convincing. In addition, this study, based on solid statistical analysis, led to the identification of interesting candidate genes, such as the STV11 gene.

The paper is clear, well-written and I have just few comments.
Several interesting candidate genes were identified; however, it is not clear which genome sequence was used for the candidate gene identification; is this genotype resistant or susceptible. In other words, do you have a resistant or a susceptible allele? This should be clarified. Similarly, the authors should mention that the sequence of the target region in the resistant genotypes should be obtained to identify the resistant allele(s) (or gene). Indeed, Copy Number Variation (CNV) have often been observed at resistance loci, and the resistance gene might not be present in the reference genome.

-L371-373: Can you clarify this sentence : "In addition, the little variation in nucleotides – less than 1% – in the region of *qHBV4.1*, between Badka and PTB 25 indicates a probable common local ancestry (Figure S2). "
Where did you get the sequence data of these two genotypes? What do you mean by "a probable common local ancestry".
I would suggest to reformulate this idea, thanks.

Figure S2: sorry, this Figure is not clear. Could you clarify it, thanks. What is in abscissa and ordinate. Is there a reference associated. What do you mean by "probable local ancestry"?

-L 319: can you explain/develop what is the "joint and meta-analyses approaches" and/or add a reference?

-Introduction L62-69: this paper is clearly not restricted to an audience working on rice, so could the authors develop/explain/put reference about indica/japonica;
Similarly, L62, "local ancestry analysis" is not obvious for non-expert audience.

Miscellaneous
-Abstract: L21, no "s" at "symptoms severity" and L29, no "s" at "candidate genes identification". In general, the MS could benefit from English revision.

-L230: what do you mean by "level of purity"?
-L362: I suggest to replace "immunity" with "complete resistance"
-L384-396 : please indicate the % of the phenotypic variation explained by the QTL.
L389: "putative gene" should be "putative candidate gene.

-L430: I suggest to use "gene" instead of "loci"

Table 1: precise the type of segregating population

Table 3, 4 and 5: problem in the presentation (for example "Dominance" written on 2 lines).