Below we are responding to each of the comments of the two reviewers and also to one comment made by the editor.

Reviewer 1

1. The misspelling in Marten Koornneef's name in line 684 was corrected.
2. We added the y-axis labels in Fig. 1 and Fig. 2 as requested (also see other changes we did to Fig. 1 below).

Reviewer 2

1. With respect to Fig. 1 we agree with the reviewer that Fig. 1A was somewhat confusing. We considered replacing it with a standard Venn diagram but decided that a simple 2-section diagram really didn't add anything that wasn't already shown in Fig. 1B or described in the text. Furthermore, since later in the manuscript we describe genes that were specifically regulated by phyB1 or phyB2 (as defined in the second paragraph of the Results section) just showing two overlapping ovals with numbers wouldn't have illustrated well what was later compared and might also have been confusing to some. We therefore opted to simply delete Fig. 1A altogether and describe summary data of the RNA-seq analysis in the text and show it visually in Fig. 1B (now Fig. 1) only.

Regarding our DESeq analysis, and our choice for the 1.5-fold cut-off (versus for example 2.0) our rationale was as follows: Neither of the two is a default setting in DESeq since DESeq returns fold-changes and adjusted p-values for all genes. Any user can then choose what to call DE genes based on adjusted p-value, fold-change, or both. Here, and in a previously published paper (Carlson et al., 2019, Frontiers in Plant Biology), we called any gene DE that had an adjusted p-value less than 0.05. Because we wanted to compare the magnitude of change between WT in dark and light and *phyB* mutants in dark and light, we picked a fold-change cutoff of 1.5 because it seemed to us that changes in gene expression of even less than double could potentially have an effect at both the cellular and organismal levels. To further clarify (and also respond to the **editor**'s comment on the topic) we used an alpha level of 0.05 (which is, as pointed out, indeed not the default) for the multiple comparison adjustment. We corrected this important piece of information in the Methods in our revision. We also provide, as requested by the editor, a list of DE genes along with fold change values with standard error and adjusted p-values in Supplemental Table 1.

Regarding the double mutant, indeed we did not have the germplasm available for the inclusion of the *phyB1/phyB2* mutant. I am not sure if it is still available since Rob Alba sent to me what was described as the remnants of the seed collection from those early studies by Pratt and colleagues. Certainly, new double mutants can be made and we are in the process of doing just that.

2. We agree that the lack of available additional alleles limits the interpretation of our work to some degree. We note that to our knowledge this is the case for most (all?) published work on tomato *phyB1*. For *phyB2* a second allele has been described in the past with similar phenotypic properties to each other. We are in the process of creating more *phyB1* alleles but in tomato this process is slow and will take us a few years to complete. To account for the possibility of

background mutations in our material we have added some language towards the end of the discussion pointing out the possible limitations of the use of a single allele in this work.

With respect to the comment regarding R-induced randomization of gravitropism in Arabidopsis, we added another citation, which supports the reviewer's comment (Poppe et al., 1996) and added language to point out to the reader that this is an Arabidopsis-specific phenomenon - or at least not one seen in tomato - as has been shown e.g. in Behringer and Lomax, 1999.

In response to the reviewer's comment that our description of gravitropism in manuscript line 333 was too general and that from our data we could not extrapolate beyond a 24-h time period, we changed the language in the referenced section to be more specific. We now more clearly point out that this statement pertains to 5-d-old seedlings only.

With respect to root gravitropism, we did not make any observations and looking back at our raw data (photographs) we cannot determine any kind of response due to the random and haphazard orientation of the roots at the beginning of the experiment. Rather than speculating, we decided to simply not talk about root gravitropism and leave the discussion of this topic to another time when experimental data for this question exist.

Other comments:

1. Fig. 1A was removed as suggested. See more detailed response above under the main comment responses.
2. Citations were added or replaced as recommended.
3. We corrected that sentence. It should have said that phyB (not phyB1) in Arabidopsis represses phototropism.
4. Corrected as suggested.
5. Methods
   A) Light conditions:
   Green safelight: We added information about the handling of seedlings in safe light conditions (approximate exposure time, temperature, wavelength)
   Red light exposure: We clarified the exposure time by adding the information in the Methods (previously it had only been in the Results). The Methods section also contains information on the spectral properties and fluence.
   B: Photosynthesis: We added language that was omitted from the original methods that more clearly describes our efforts to use leaf material of developmentally comparable age. The leaves were inserted flat into the cuvette and kept flat in the clamp for the duration of the experiment.
   Normalization of assimilation rates: Thanks for catching that! We had gone back and forth about which way was best for showing the results and had not corrected the description in the methods to reflect our final choice for presentation in the figure. This was done in this revision. We did measure chlorophyll content but the data were not statistically significantly different between the genotypes. We decided in the revision to replace the reference to the supplemental figure (that we actually had not submitted) to "data not shown", since the data are fully, verbally described as insignificantly different from each other.

C: Seeds were germinated at slightly different times so that their developmental age was the same during the experiment, which we call “age-synchronized”. Since most experiments were performed with very young seedlings a difference of even 5 hours in germination time would have resulted in seedlings being about half the size of the isogenic mutant. We don’t know what the reason for the differences in germination time was. It is possible that seed quality differed but we normally use seeds from same-year harvests to prevent germination issues. Viability differences don’t seem to be the reason for the differences in germination time since seeds germinated well, just at slightly different times. It is possible that germination time is in fact influenced by phytochrome, but we don’t have good enough evidence to assert that. To better address the reviewer’s question, we added some clarifying language into the Methods section of the manuscript that hopefully will clear up questions a reader might have.
The differences in the direction of the R during the gravitropism experiment was not intentional but rather based on the fact that we had a large and heavy LED array versus smaller LED bulbs that were used in table top lamps. Since we only later considered that the difference in irradiation direction might be the reason for the difference in response we conducted the control experiments described in the manuscript to exclude this possibility.