

## **Supplementary Information**

Genome-wide transcriptional profiling for elucidating the effects of  
brassinosteroids on *Glycine max* during early vegetative development

Li Song<sup>1#\*</sup>, Wei Chen<sup>2#</sup>, Qiuming Yao<sup>3</sup>, Binhui Guo<sup>1</sup>, Babu Valliyodan<sup>2</sup>, Zhiyong Wang<sup>4</sup>, Henry T. Nguyen<sup>2\*</sup>

<sup>1</sup>Joint International Research Laboratory of Agriculture and Agri-Product Safety, Jiangsu Key Laboratory of Crop Genomics and Molecular Breeding, Yangzhou University, Yangzhou, 225009, China

<sup>2</sup>Division of Plant Sciences, University of Missouri, Columbia, MO 65211, USA

<sup>3</sup>Department of Computer Science, Christopher S. Bond Life Sciences Center, University of Missouri, Columbia, MO 65211, USA

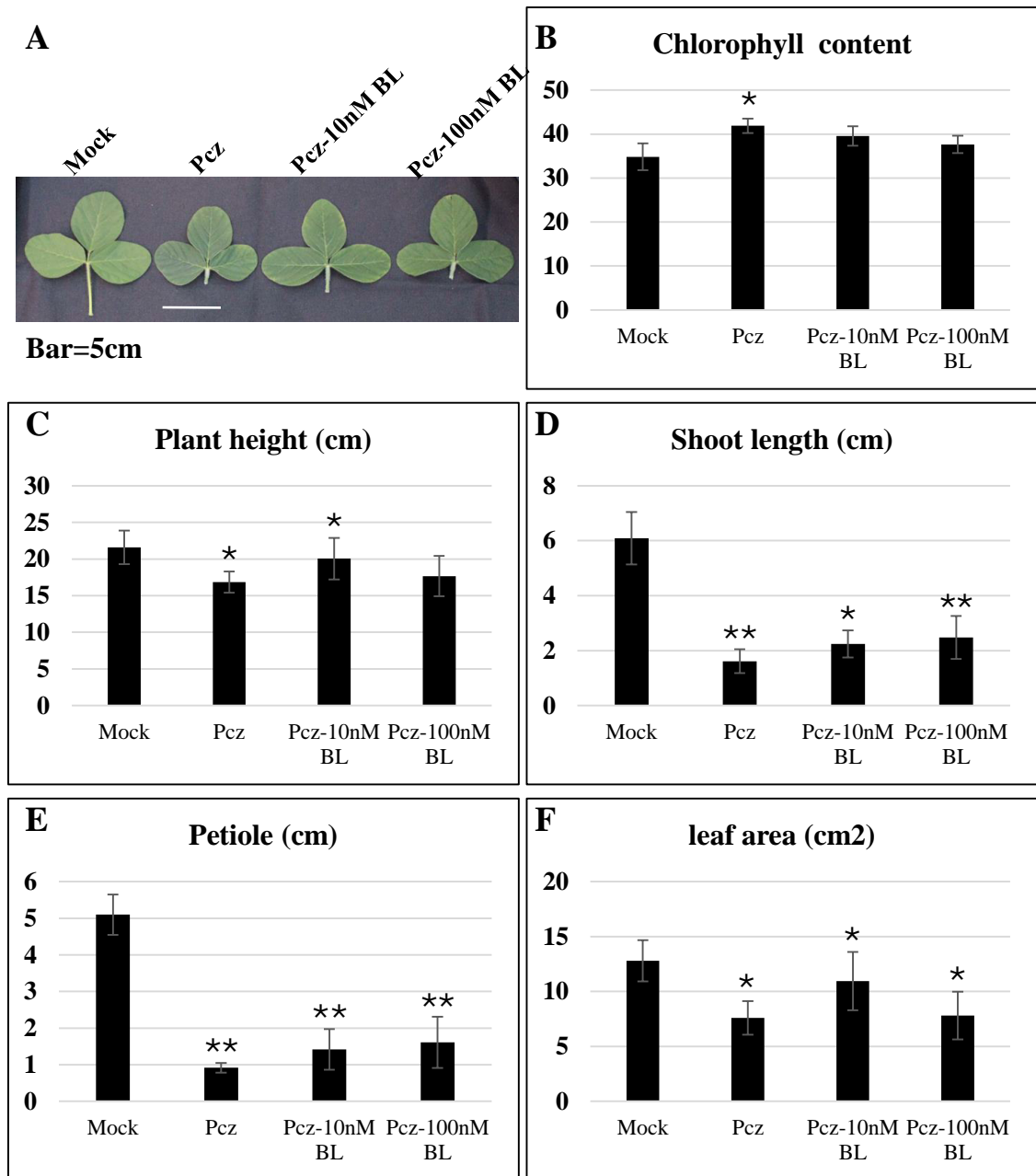
<sup>4</sup>Department of Plant Biology, Carnegie Institution for Science, Stanford, CA 94305, USA

# Equal contribution

Correspondence:

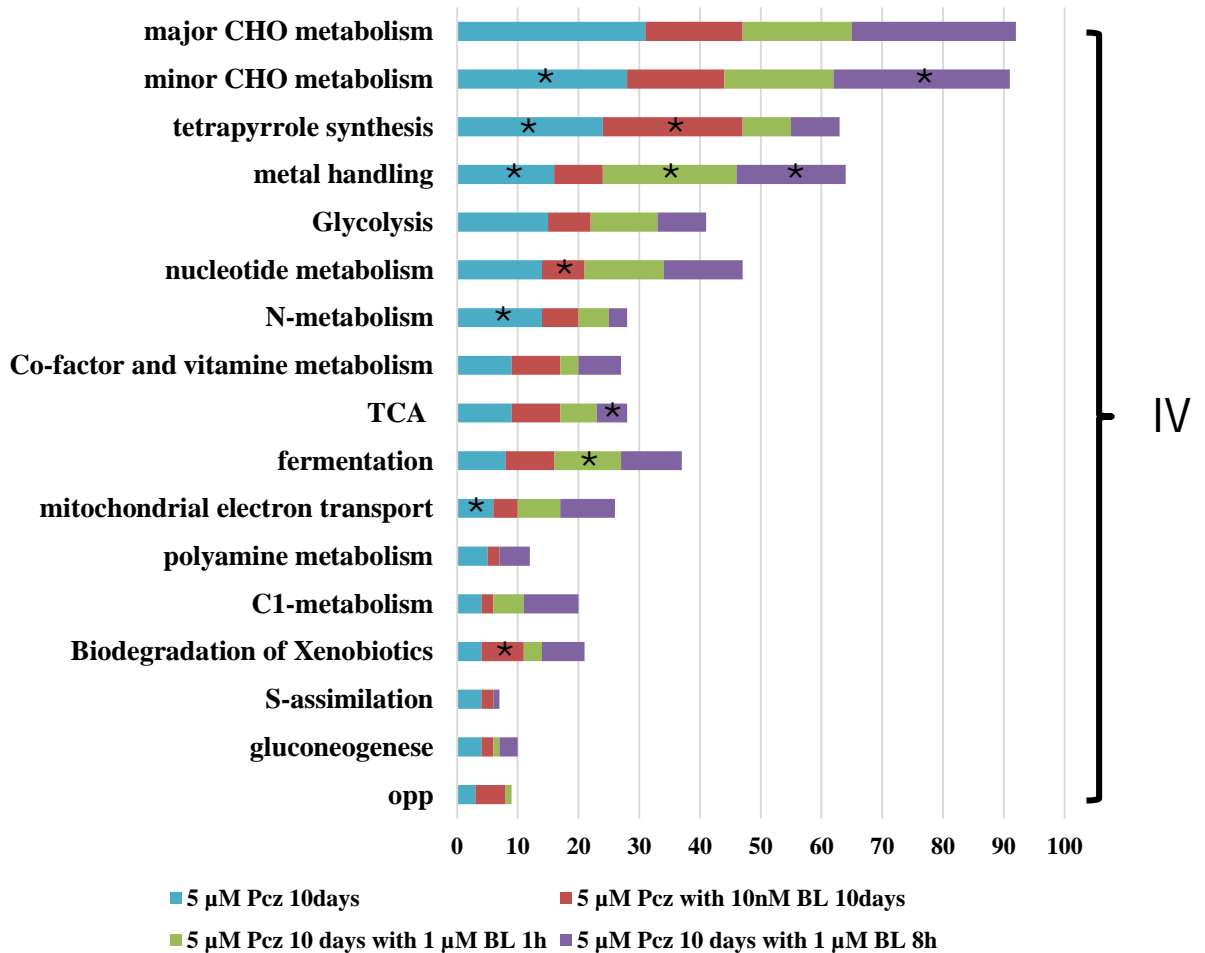
Dr. Li Song, Email: [songli@yzu.edu.cn](mailto:songli@yzu.edu.cn);

Dr. Henry T. Nguyen, Email: [nguyenhenry@missouri.edu](mailto:nguyenhenry@missouri.edu)

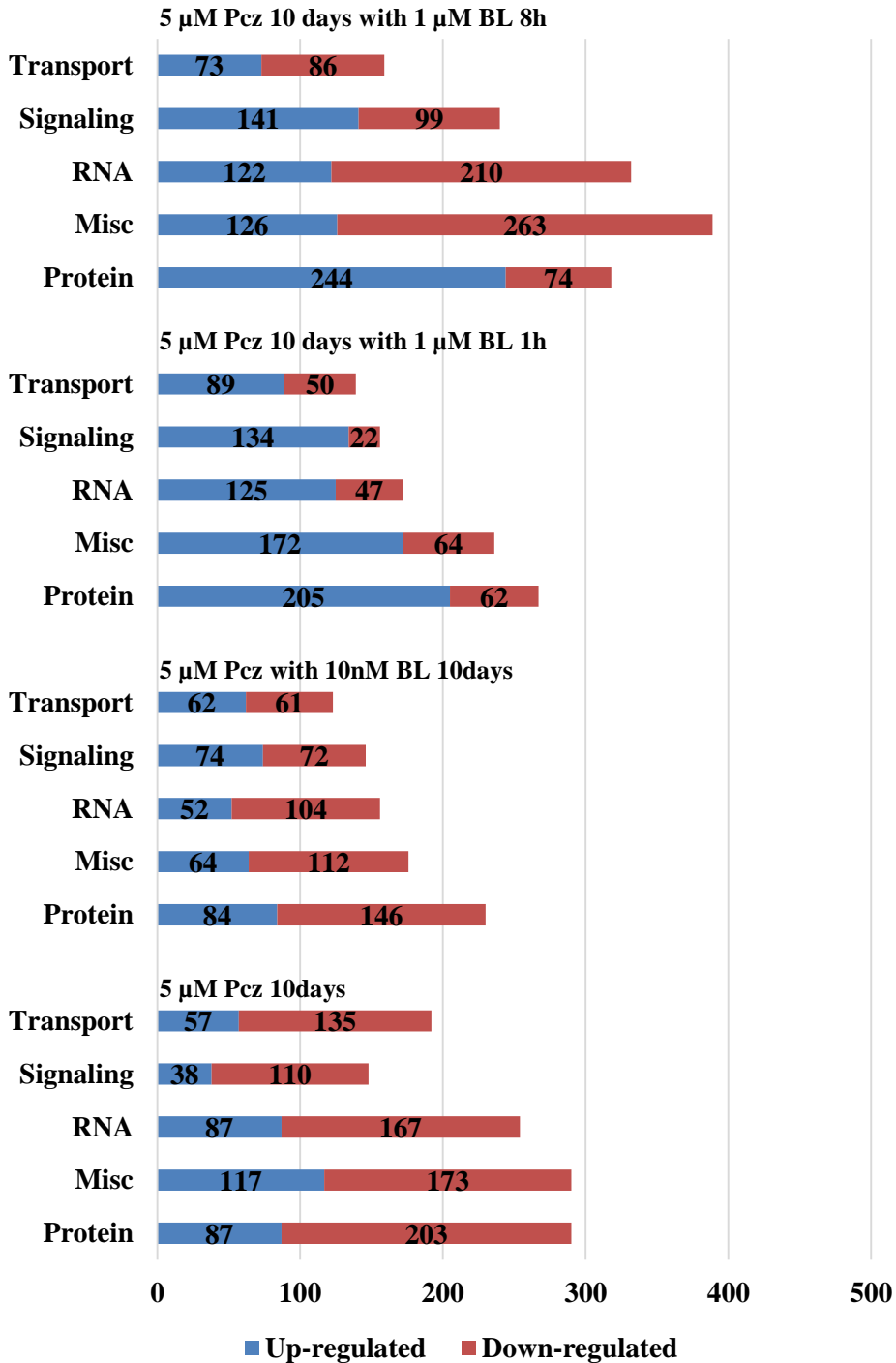


**Supplementary Figure S1. Responses of soybean seedlings to inhibitor treatments and BL complementation.** (A) Wm82 grows to V1 stage and then irrigated with 5 $\mu$ M Pcz or 5 $\mu$ M Pcz with 10nM BL or 100nM BL for 10 days. (B-F) Chlorophyll content, plant height, shoot length, petiole and leaf area were monitored after treatments. (n $\geq$ 30). Statistical differences are marked with \* (p  $\leq$ 0.05) or \*\* (p  $\leq$ 0.01) based on Student's *t*-test analysis.

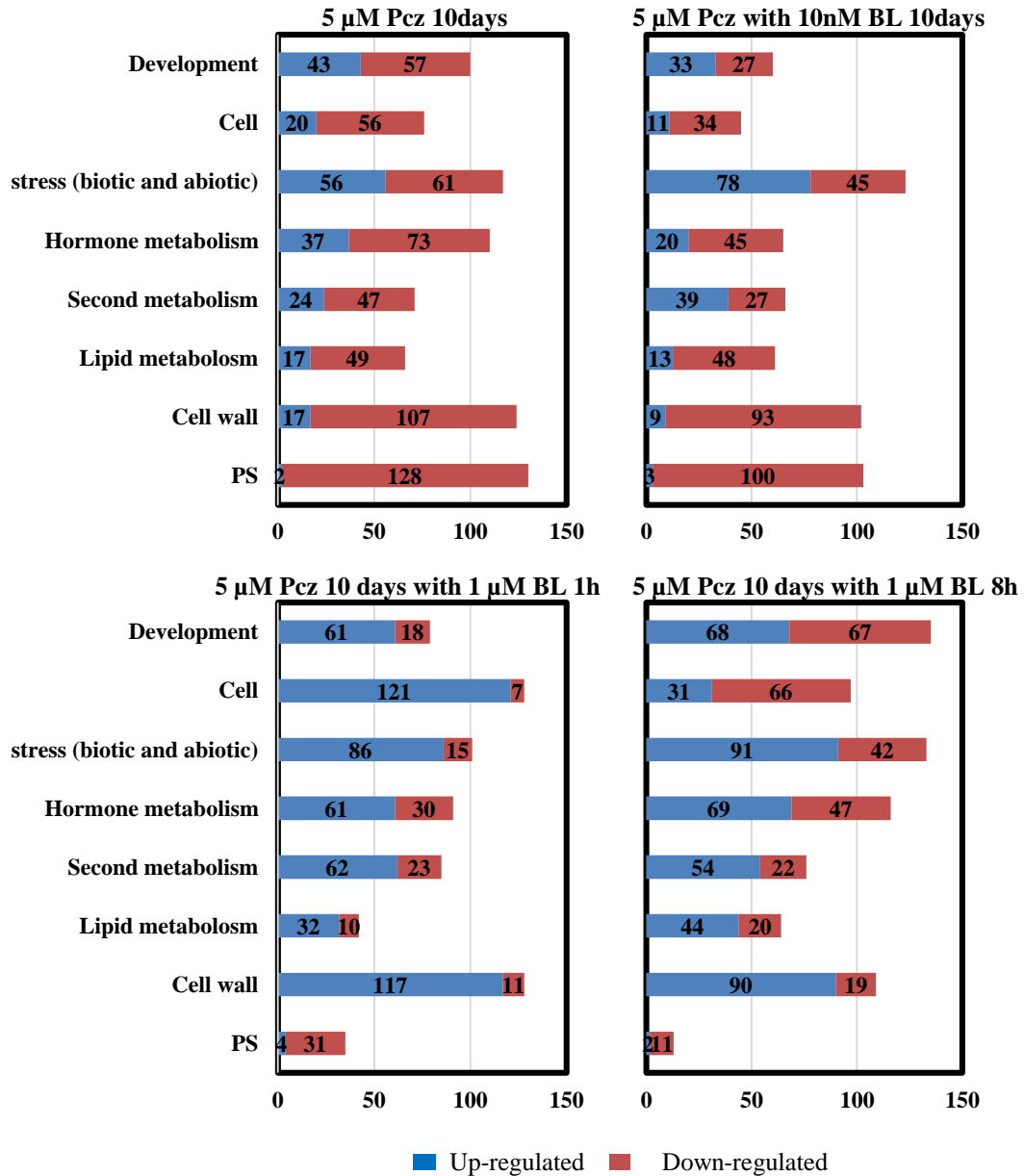
## Minor biological processes



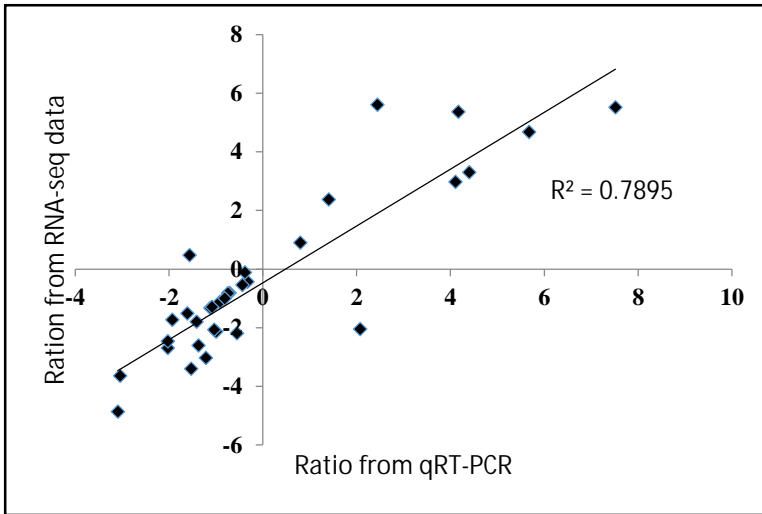
**Supplementary Figure S2. GO term assignment to the transcripts in different categories (group IV) of minor biological process.** Different color indicates number of genes involved in different conditions. Group IV < 100. Statistical significance of each process under all treatments were performed by Fisher's exact test. The overrepresented categories of biological process (P values  $\leq 0.05$ ) were labeled with star (\*).



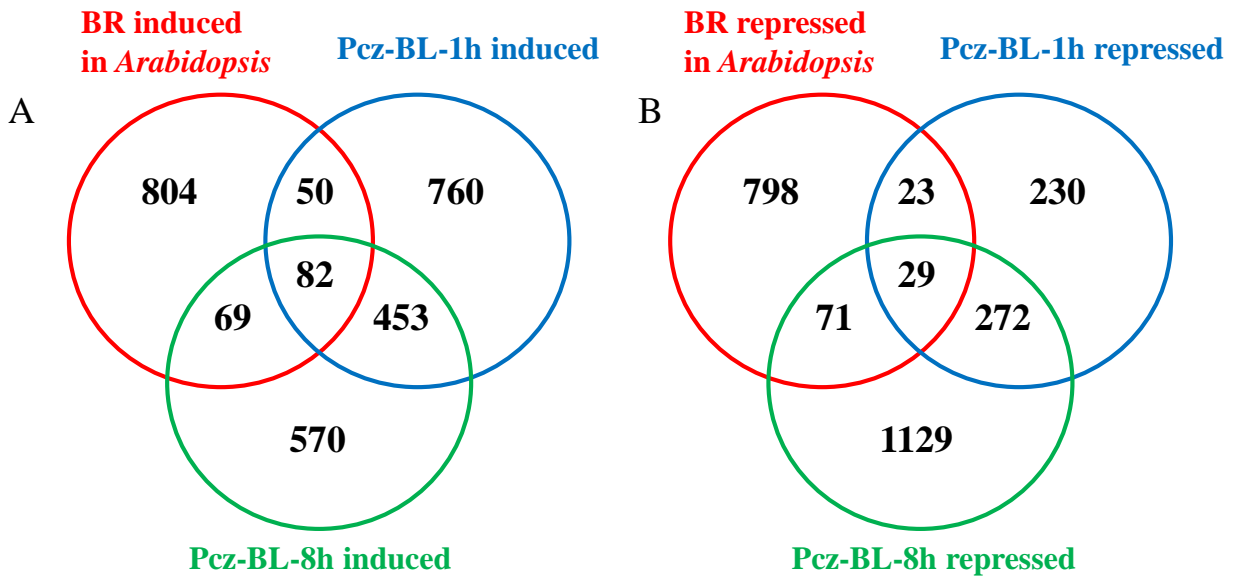
**Supplementary Figure S3. Response patterns of functional categories (transport, signaling, RNA, miscellaneous and protein) under different treatments.** Within each bin, the proportions of genes up- or downregulated are coded blue and red, respectively.



**Supplementary Figure S4. Functional categories (development, cell, stress, hormone metabolism, second metabolism, lipid metabolism, cell wall and PS) responding differently treatments. Within each bin, the proportions of genes up- or down-regulated are coded blue and red respectively.**



**Supplementary Figure S5. Coefficient analysis indicated RNA-Seq and qRT-PCR results had a high correlation using the log<sub>2</sub> values for different BRs levels. Each dot represents the average values for each gene from all the biological replicates.**



**Supplementary Figure S6. Venn diagram showing the overlap of BR induced or repressed genes in *Arabidopsis* and soybean.** (A) Comparison of BR induced genes in *Arabidopsis* and Pcz-BR-1h or Pcz-BR-8h treated soybean. (B) Comparison of BR repressed genes in *Arabidopsis* and Pcz-BR-1h or Pcz-BR-8h treated soybean. The response gene list comes from Sun et al., (2010).