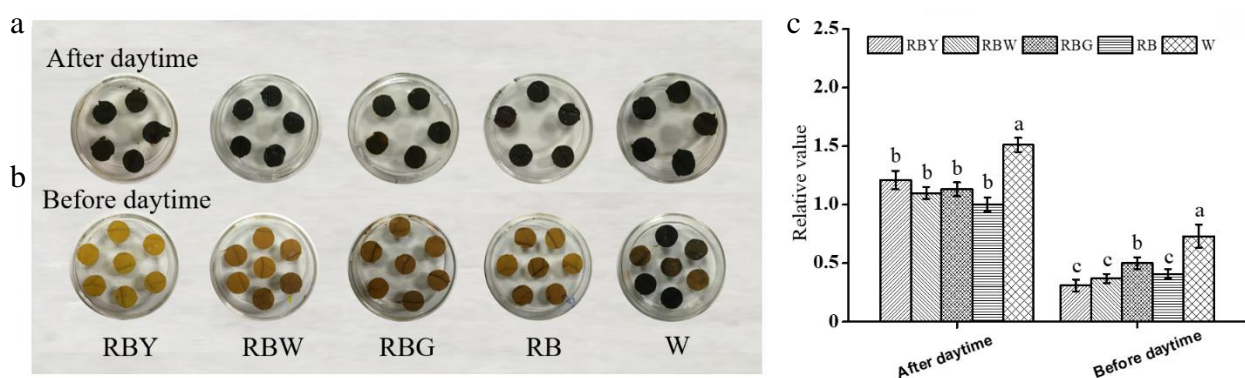
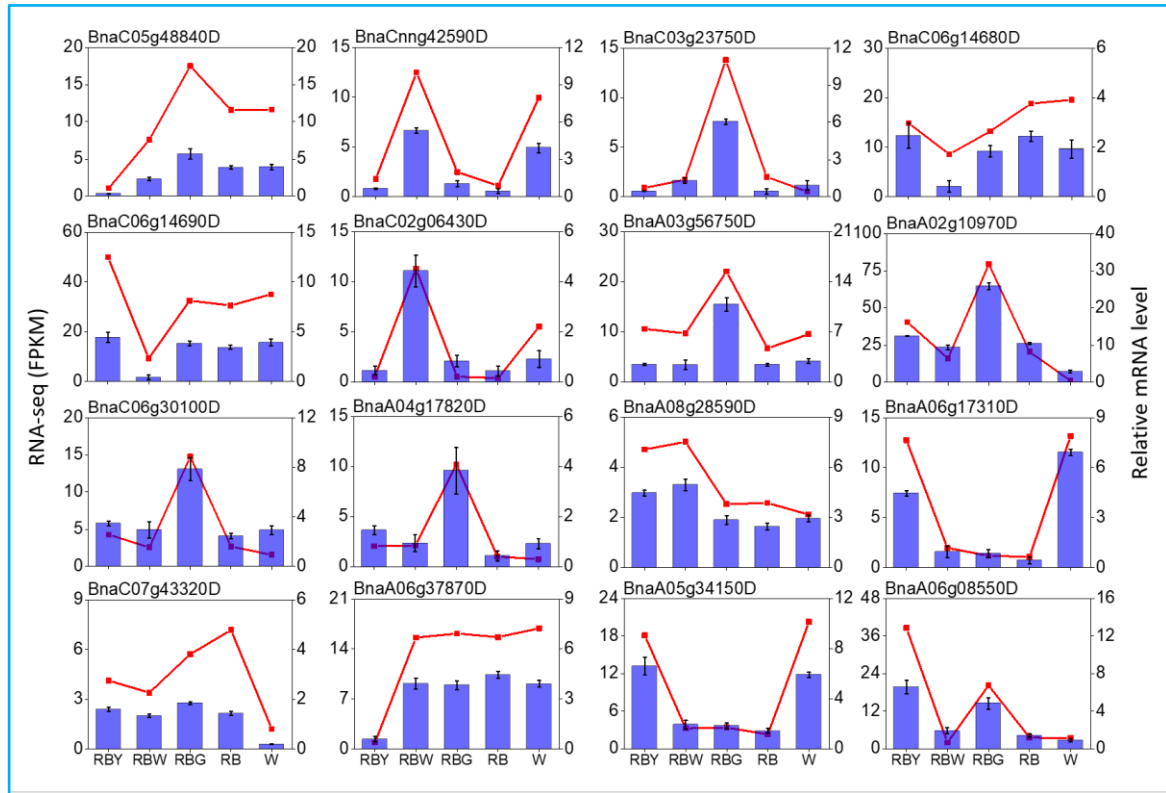


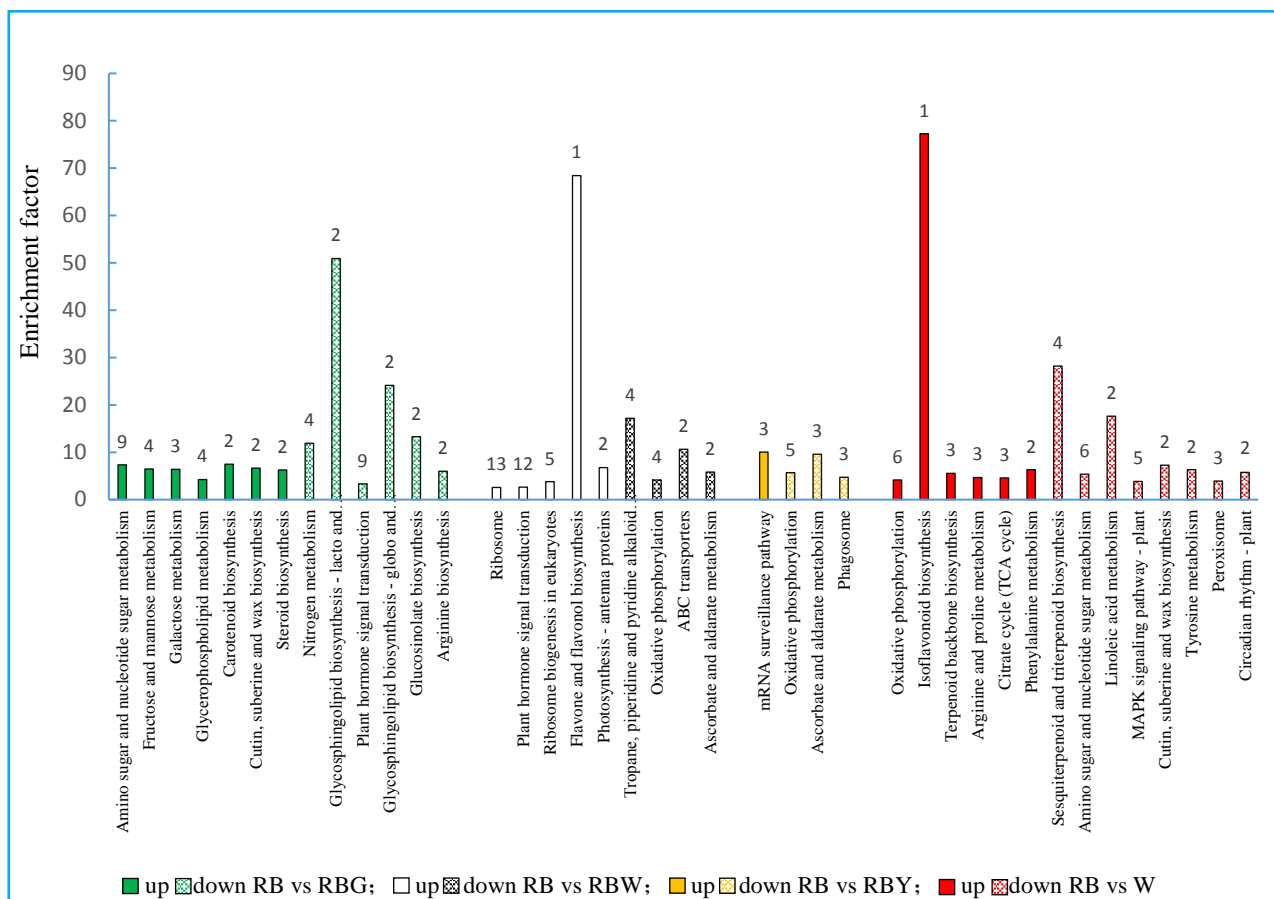
**Fig. S1 Chlorophyll fluorescence parameter including qN (a) and rETR (b) in the top third leaf of rape under different light treatments.** RB, red-blue light; RBG, red-blue-green light; RBW, red-blue-white light; RBY, red-blue-yellow light; W, white light. Vertical bars are means  $\pm$  SD (n=3). Bars labelled with lowercase letters are significantly different at  $P < 0.05$  level.



**Fig. S2 The leaf discs stained with iodine solution after daytime and before daytime respectively (a and b) and the relative content of starch (c) in different light treatments.** RB, red-blue light; RBG, red-blue-green light; RBW, red-blue-white light; RBY, red-blue-yellow light; W, white light. Vertical bars are means  $\pm$  SD (n=5). Bars labelled with lowercase letters are significantly different at  $P < 0.05$  level.

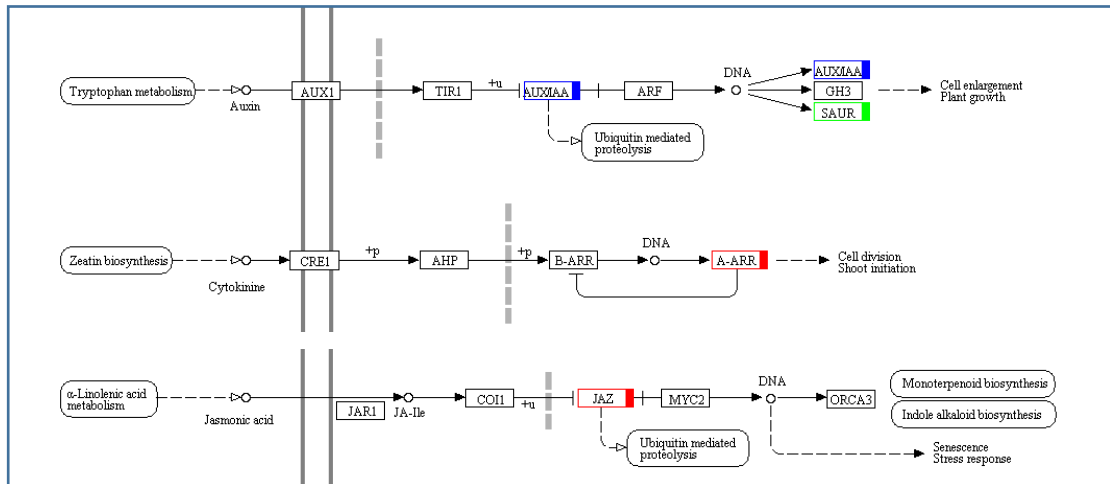


**Fig. S3 Validation of transcript abundance obtained from RNA-seq using qRT-PCR.** RB, red-blue light; RBG, red-blue-green light; RBW, red-blue-white light; RBY, red-blue-yellow light; W, white light. Sixteen randomly chosen genes were used for validation. Red line and blue column graph indicate relative expression by RNA-seq and qRT-PCR under different light treatments, respectively. Vertical bars are means ± SD (n=3). Bars labelled with lowercase letters are significantly different at  $P < 0.05$ .

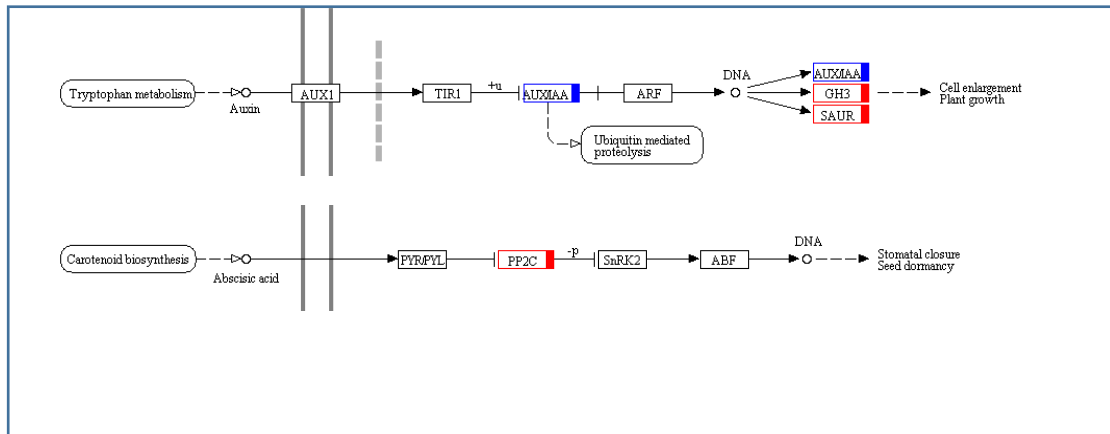


**Fig. S4 Functional categories of exclusive differentially expressed genes (DEGs) based on KEGG enrichment analyses.** Significantly enriched KEGG categories were analyzed in pairwise comparisons (RB vs RBG, RB vs RBW, RB vs RBY and RB vs W) at  $P < 0.05$  level. Enrichment factor represents the ratio of the proportion of genes annotated to the pathway among DEGs to the proportion of genes annotated to the pathway among all genes. The digit in the top of column graph represents the number of DEGs enriched in corresponding pathway. **RB, red-blue light; RBG, red-blue-green light; RBW, red-blue-white light; RBY, red-blue-yellow light; W, white light.**

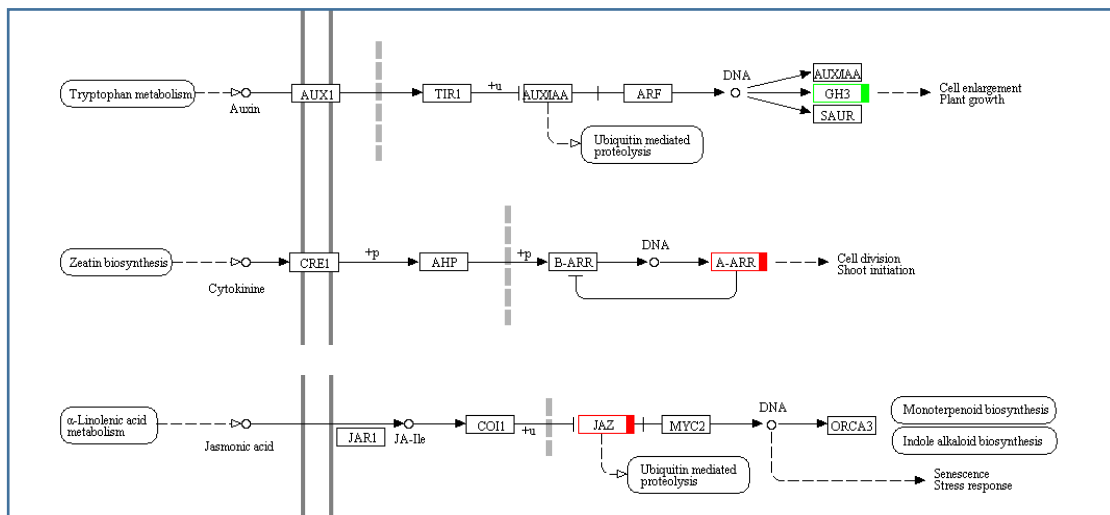
a

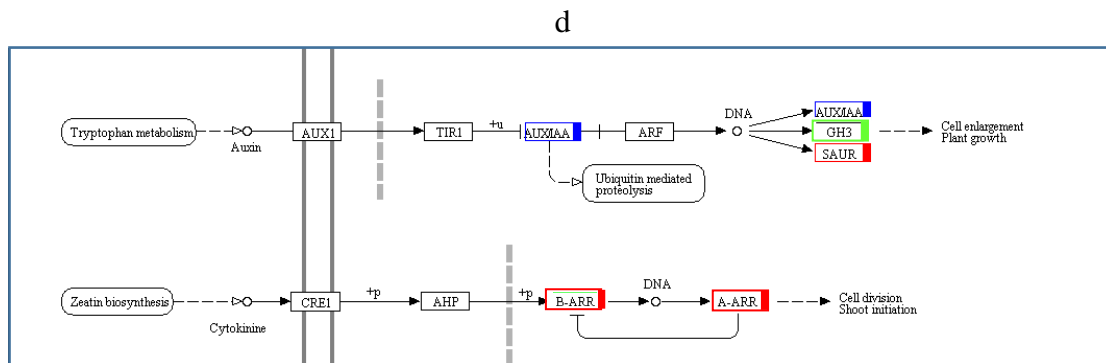


b

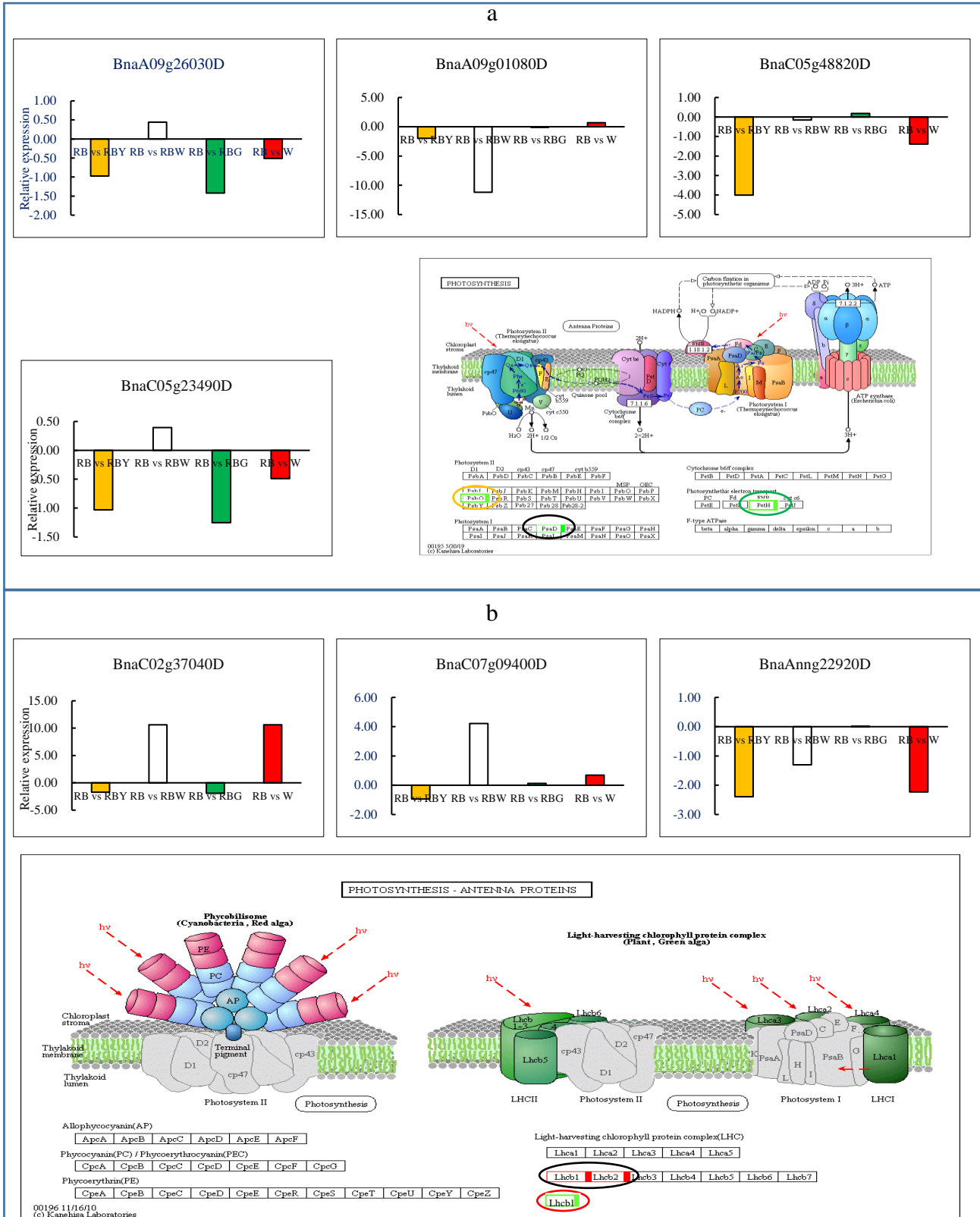


c





**Fig. S5 Differentially expressed transcripts involved in plant hormone signal transduction.** (a) RB vs RBG, (b) RB vs RBW, (c) RB vs RBY, (d) RB vs W. The red, green and blue separately represent up-regulation, down-regulation and up/down-regulation of the gene annotated to the enzyme. **RB**, red-blue light; **RBG**, red-blue-green light; **RBW**, red-blue-white light; **RBY**, red-blue-yellow light; **W**, white light.

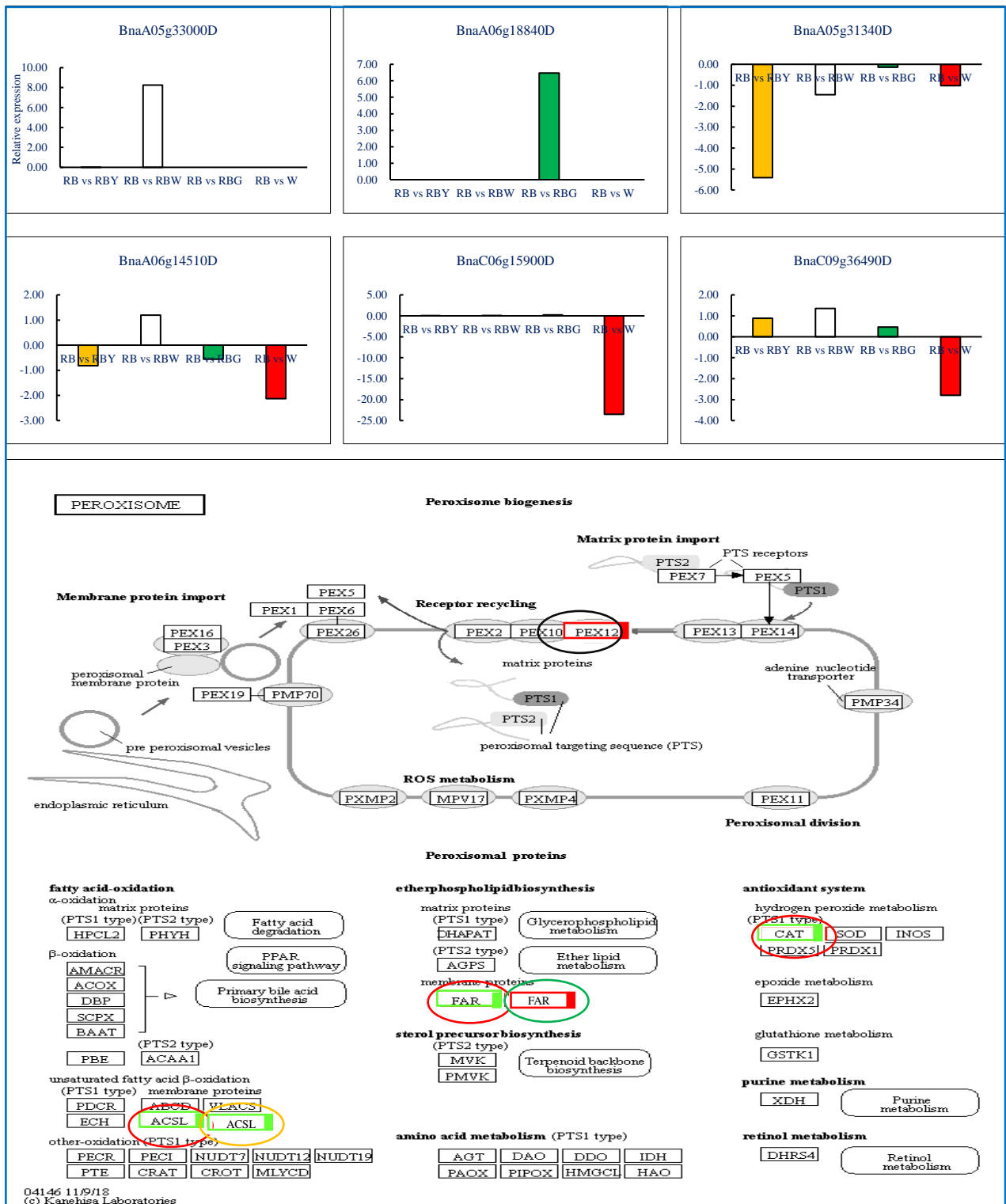


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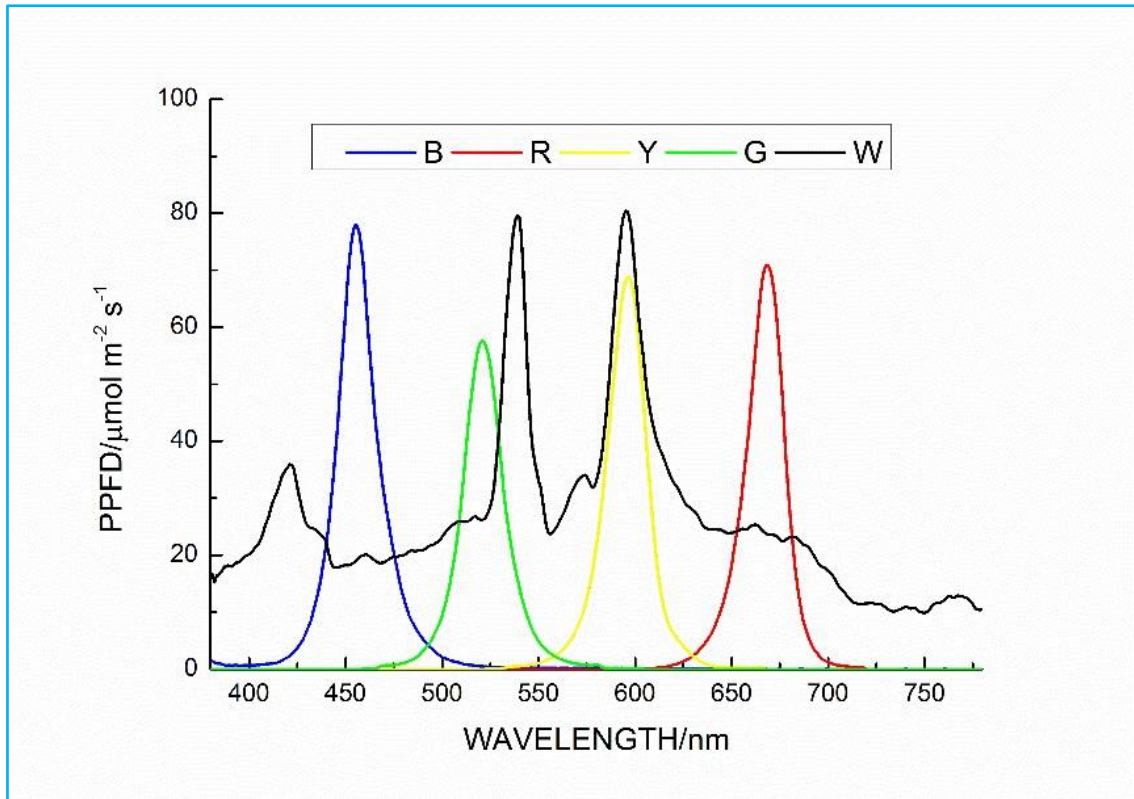
**BnaC07g09400D**

**BnaAnng22920D**

**Fig. S6 Differentially expressed transcripts involved in photosynthesis and photosynthesis-antenna proteins.** (a) photosynthesis, (b) photosynthesis-antenna proteins. The red, green and blue separately represent up-regulation, down-regulation and up/down-regulation of the gene annotated to the enzyme. The location circled by ○, ○, ○ and ○ represents responsive genes in the comparison of RB vs RBY, RB vs RBW, RB vs RBG and RB vs W, respectively. RB, red-blue light; RBG, red-blue-green light; RBW, red-blue-white light; RBY, red-blue-yellow light; W, white light.



**Fig. S7 Differentially expressed transcripts involved in peroxisome.** The red, green and blue separately represent up-regulation, down-regulation and up/down-regulation of the gene annotated to the enzyme. The location circled by ○, ○, ○ and ○ represent responsive genes in the comparison of RB vs RBY, RB vs RBW, RB vs RBG and RB vs W, respectively. RB, red-blue light; RBG, red-blue-green light; RBW, red-blue-white light; RBY, red-blue-yellow light; W, white light.



**Fig. S8** The spectral distribution of red, blue, yellow, green and white lights. PPFD, photosynthetic photon flux density; B, blue light; R, red light; Y, yellow light; G, green light; W, white light.