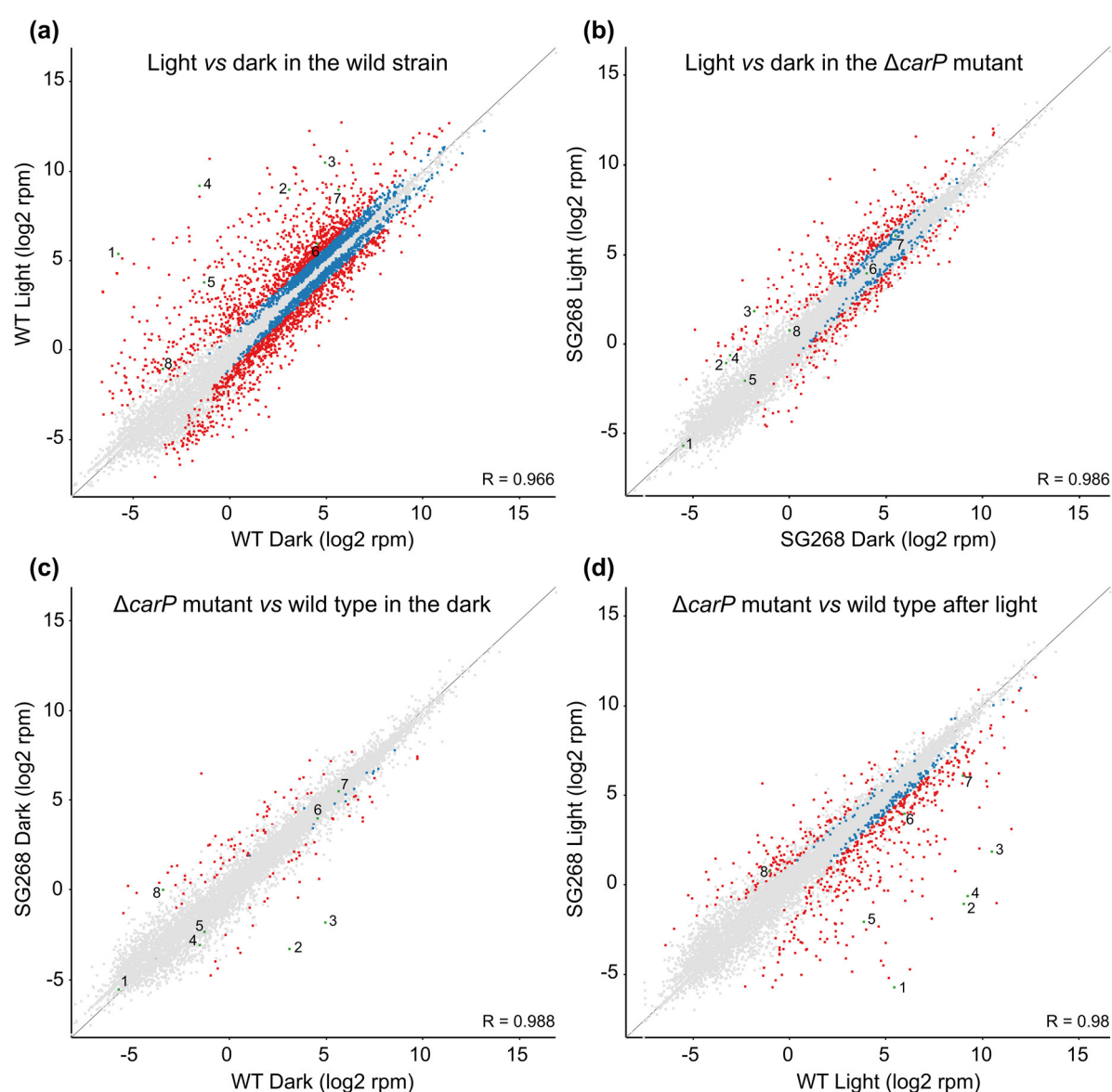


# The *carP* lncRNA Is a *carS*-Related Regulatory Element with Broad Effects on the *Fusarium fujikuroi* Transcriptome

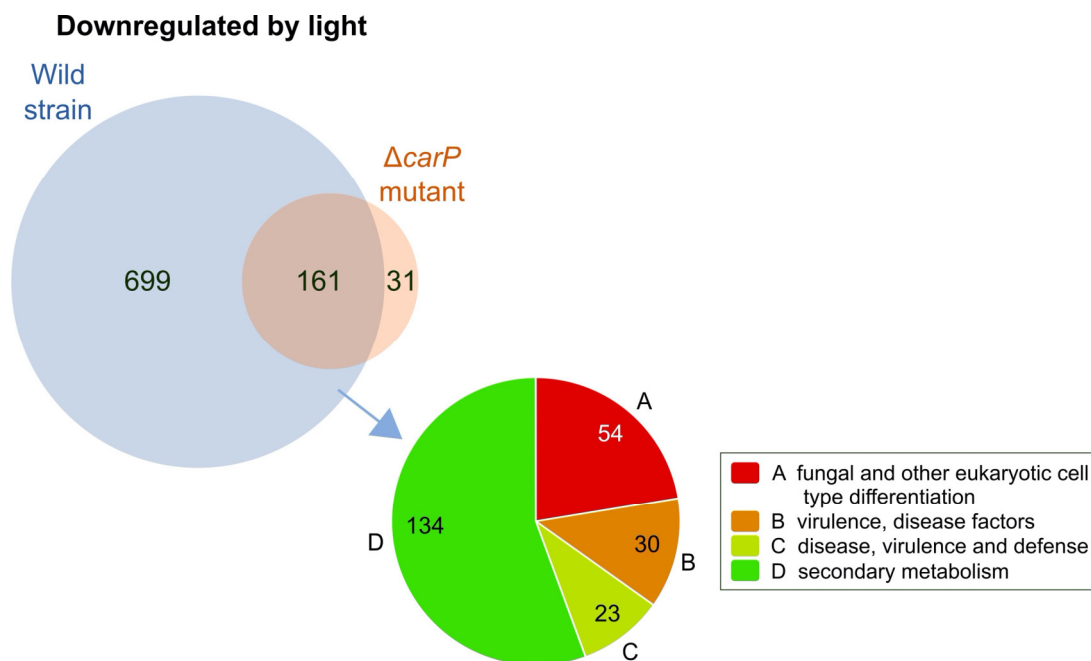
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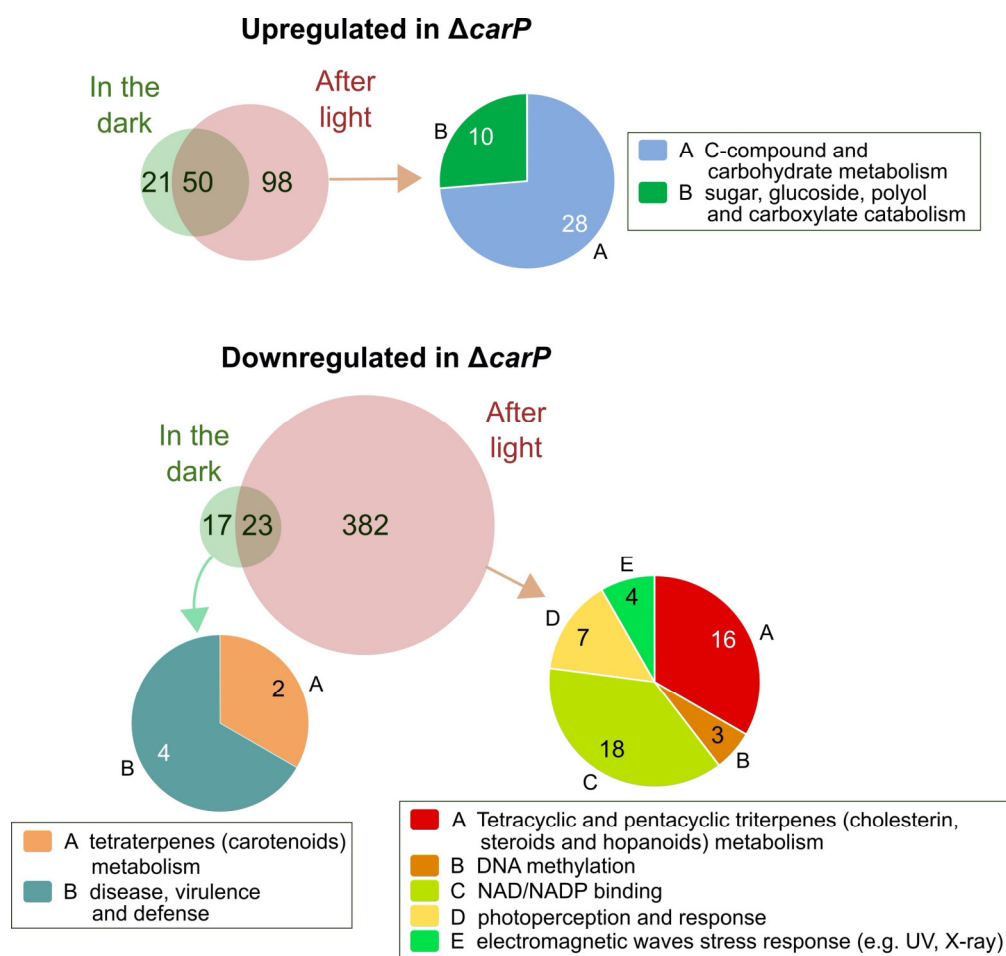
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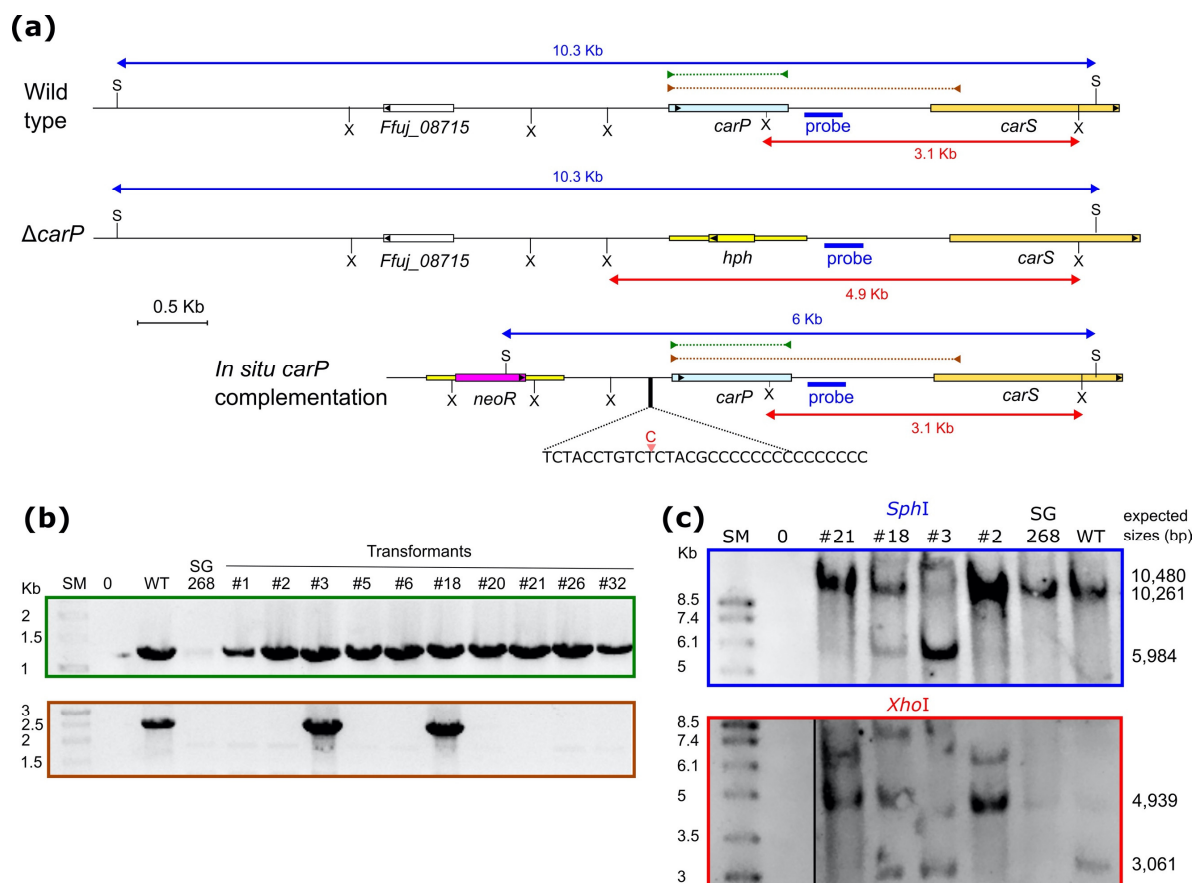
**Figure S1.** Scatter plot representations of the effect of light and *carP* deletion on the *F. fujikuroi* transcriptome. (a) Effect of light on the wild-type strain; (b) effect of light on the  $\Delta carP$  mutant; (c) effect of the  $\Delta carP$  mutation in the dark; (d) effect of the  $\Delta carP$  mutation in light. Genes differentially expressed according to the Deseq analysis are indicated in red. Genes exceeding the log2 values of +1 are indicated in red. Genes related to carotenoid metabolism are marked with green dots and a number. 1: *carX* (FFUJ\_11801); 2: *carRA* (FFUJ\_11802); 3: *carB* (FFUJ\_11803); 4: *carO* (FFUJ\_11804); 5: *carT* (FFUJ\_07962); 6: *carD* (FFUJ\_07503); 7: *ggs1* (FFUJ\_07352); 8: *carS* (FFUJ\_08714).



**Figure S2.** Funcat categories of the 680 genes downregulated by light in the wild strain. No significant Funcat categories were identified in the set of 192 transcripts from the  $\Delta carP$  mutant. This is an extension of data displayed in Figure 2.



**Figure S3.** Funcat categories of genes differentially expressed in  $\Delta carP$  mutant. Above, categories for the 148 genes upregulated after light. No significant categories were identified in the set of 71 genes upregulated in the dark. Below, categories for the 405 genes downregulated after light and the 40 genes downregulated in the dark. This is an extension of data displayed in Figure 3.



**Figure S4.** Molecular analysis of the reintegration of the *carP* sequence in SG268. (a) Genomic maps covering the area are shown for the wild strain, the  $\Delta carP$  mutant SG268 and the *carP* reintegrated strains. The hygromycin resistance cassette (*hph* gene) was replaced with a G418<sup>R</sup> cassette (*neoR* gene). Deleted cytosine is featured in red in the *carP* reintegration map. (b) Gel electrophoresis of PCRs of candidate transformants to check the insertion of the cassette. DNA from the wild strain (WT) and SG268  $\Delta carP$  mutant, or lack of DNA (0), were used as controls. PCR amplification products are indicated on the upper map with colored arrowheads and dotted lines. Expected PCR sizes are 1245 bp (green), and 2194 bp (brown). (c) Southern blot of the wild strain (WT), SG268, and four candidate transformants. SM: Size markers. 0: DNA-free control. *SphI* and *XhoI* restriction sites are indicated as S and X. The 412-bp hybridization probe (blue thick bar) and the expected hybridization fragments when DNA was digested with *SphI* (blue arrowed line) and *XhoI* (red arrowed line), are indicated on the upper map.

Supplementary Table S1. Genes affected by light and *carP* mutation.

Supplementary Table S2. Clusters Heat map.

Supplementary Table S3. Funct GO categories.

Supplementary Table S4. Data of RNAseq analysis.