**Whole transcriptome analysis resulted in the identification of Chinese sprangletop (*Leptochloa chinensis*) genes involved in cyhalofop-butyl resistance**

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**Supplementary material**

**Additional file 1:** Correlation pattern of each sample. Pearson correlation coefficients of samples within and between groups were calculated with the FPKM of all genes in each sample.

**Additional file 2: A)** The Volcano map of differentially expressed genes in B3vsB2. **B)** Gene ontology (GO) analysis of up-regulated-DEGs in B3vsB2. The DEGs were summarized in biological process, cellular component and molecular function. **C)** KEGG annotation of up-regulated-DEGs in B3vsB2.

**Additional file 3: A)** The Volcano map of differentially expressed genes in A3vsA2. **B)** Gene ontology (GO) analysis of up-regulated-DEGs in A3vsA2. The DEGs were summarized in biological process, cellular component and molecular function. **C)** KEGG annotation of up-regulated-DEGs in A3vsA2.

**Additional file 4: A)** The Volcano map of differentially expressed genes in B2vsB1. **B)** Gene ontology (GO) analysis of up-regulated-DEGs in B2vsB1. The DEGs were summarized in biological process, cellular component and molecular function.

**Additional file 5: A)** The Volcano map of differentially expressed genes in A2vsA1. **B)** Gene ontology (GO) analysis of up-regulated-DEGs in A2vsA1. The DEGs were summarized in biological process, cellular component and molecular function.

**Additional file 6:** FPKM distribution of each sample

**Additional file 7:** Sample number and their treatment information

**Additional file 8:** Primer information for qRT-PCR validation.