

Figure S1. Box diagram of the gene expression distribution of each sample after feeding on mustard leaves by beet armyworm larvae. The X-axis represents sample name. The Y-axis represents $\log_2(\text{fpkm} + 1)$. Fpkm (expected number of Fragments Per Kilobase of transcript sequence per Millions base pairs sequenced) refers to the number of fragments per Kilobase length from a gene in per million fragments.

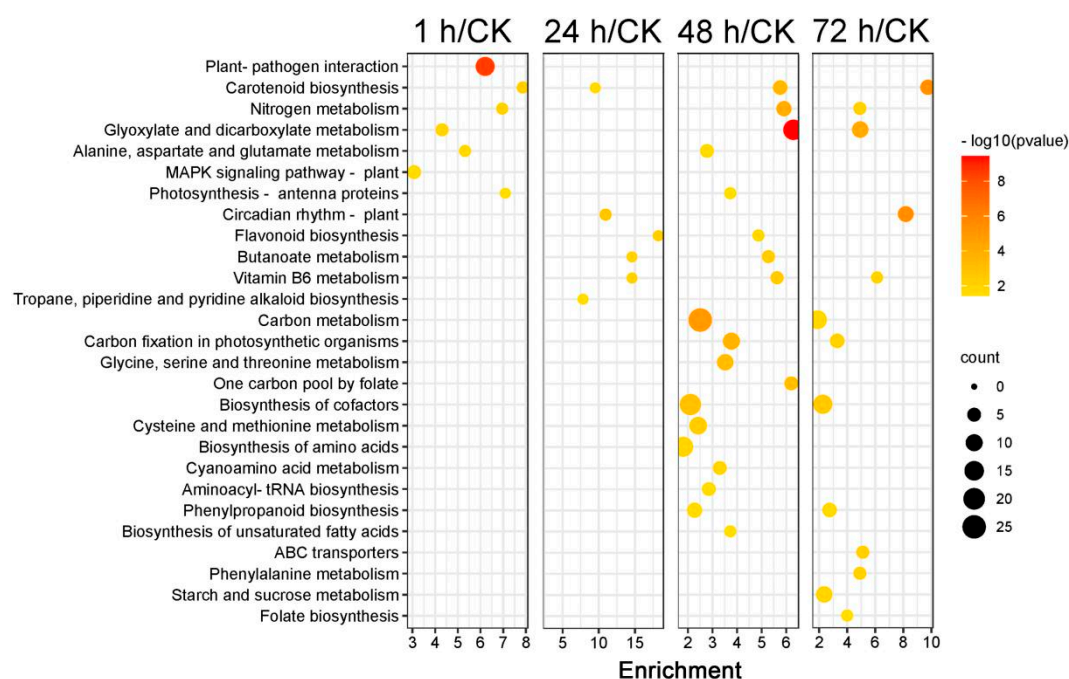


Figure S2. KEGG classification of the down-regulated DEGs. The X-axis represents the enrichment, which is the ratio of the number of differentially expressed genes to the total number of genes in a certain pathway. The color and size of the dots represent the range of the $-\log_{10}(\text{pvalue})$ and the number of DEGs mapped to the indicated pathways, respectively.

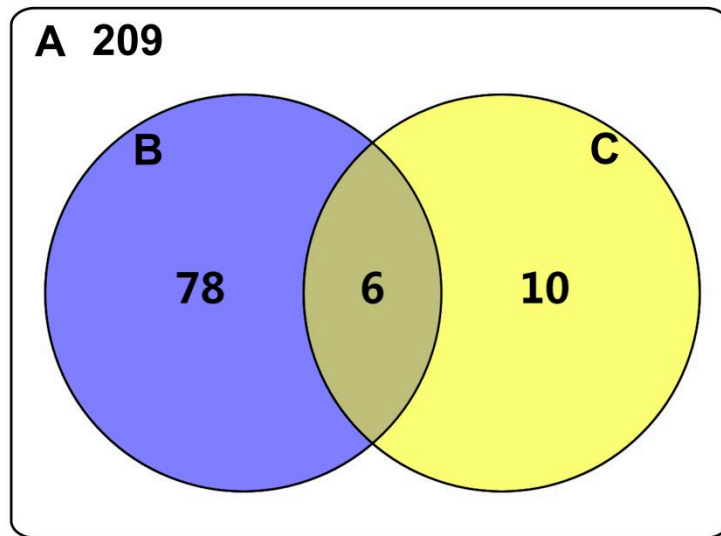


Figure S3. The number of DEGs involved in GSL biosynthesis and sulfur assimilation which have a different expression pattern after beet armyworm larvae chewing in *B. juncea*. **(A)** The total number of genes related to GSL biosynthesis and sulfur assimilation in *B. juncea*. **(B)** The DEGs which have been up-regulated at least at one time point after beet armyworm chewing in *B. juncea*. **(C)** The DEGs which have been down-regulated at least at one time point after beet armyworm chewing in *B. juncea*.