**Supporting Information**

**Biocontrol Endophytes *Bacillus subtilis* R31 Influence the Quality, Transcriptome and Metabolome of Sweet Corn**

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Figure S1. After assembling the clean reads, there are a alignment efficiency more than 84.0%.

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Figure S2. The proportion of read distribution located in exon regional is more than 86.0%.

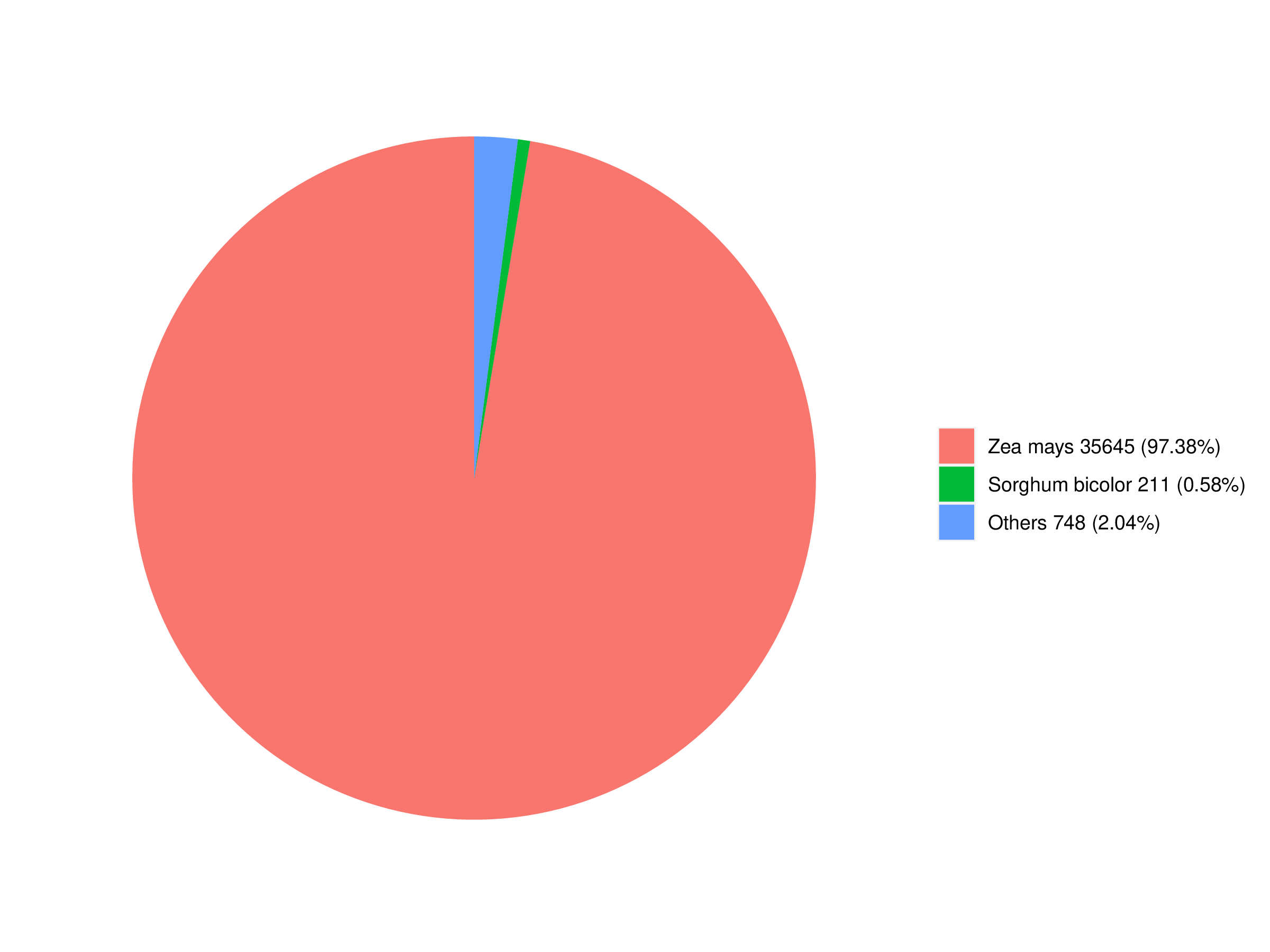


Figure S3. The unigenes of sweet corn after application of *B. subtilis* R31 annotated in NR (A) and eggNOG (B) databases.

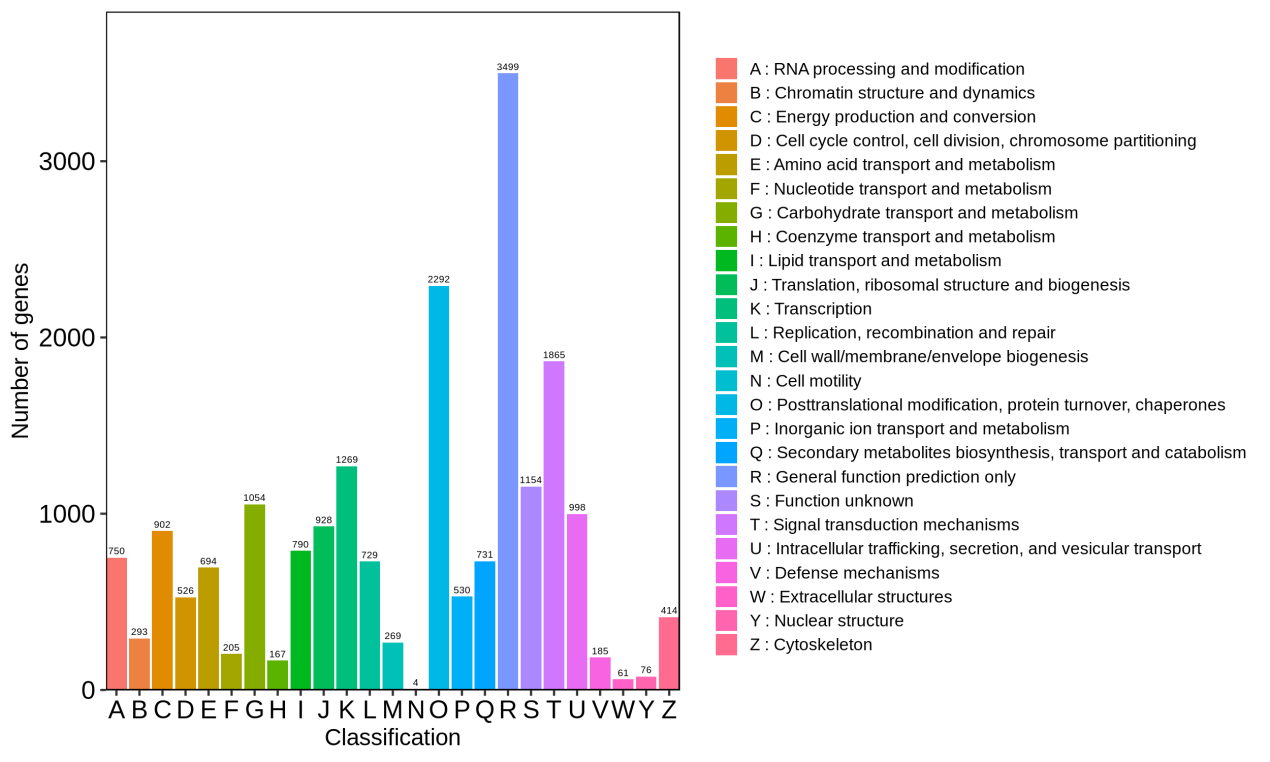
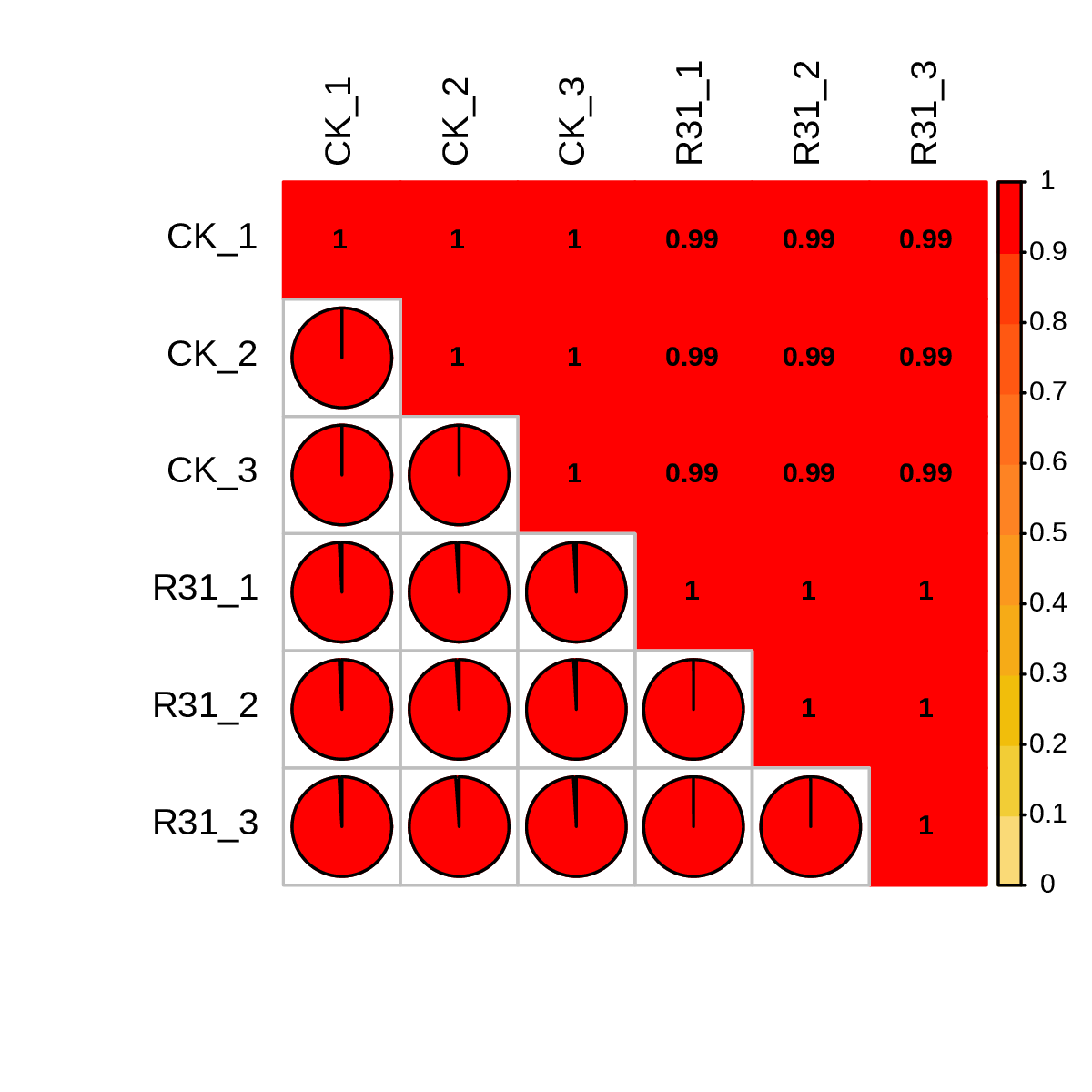
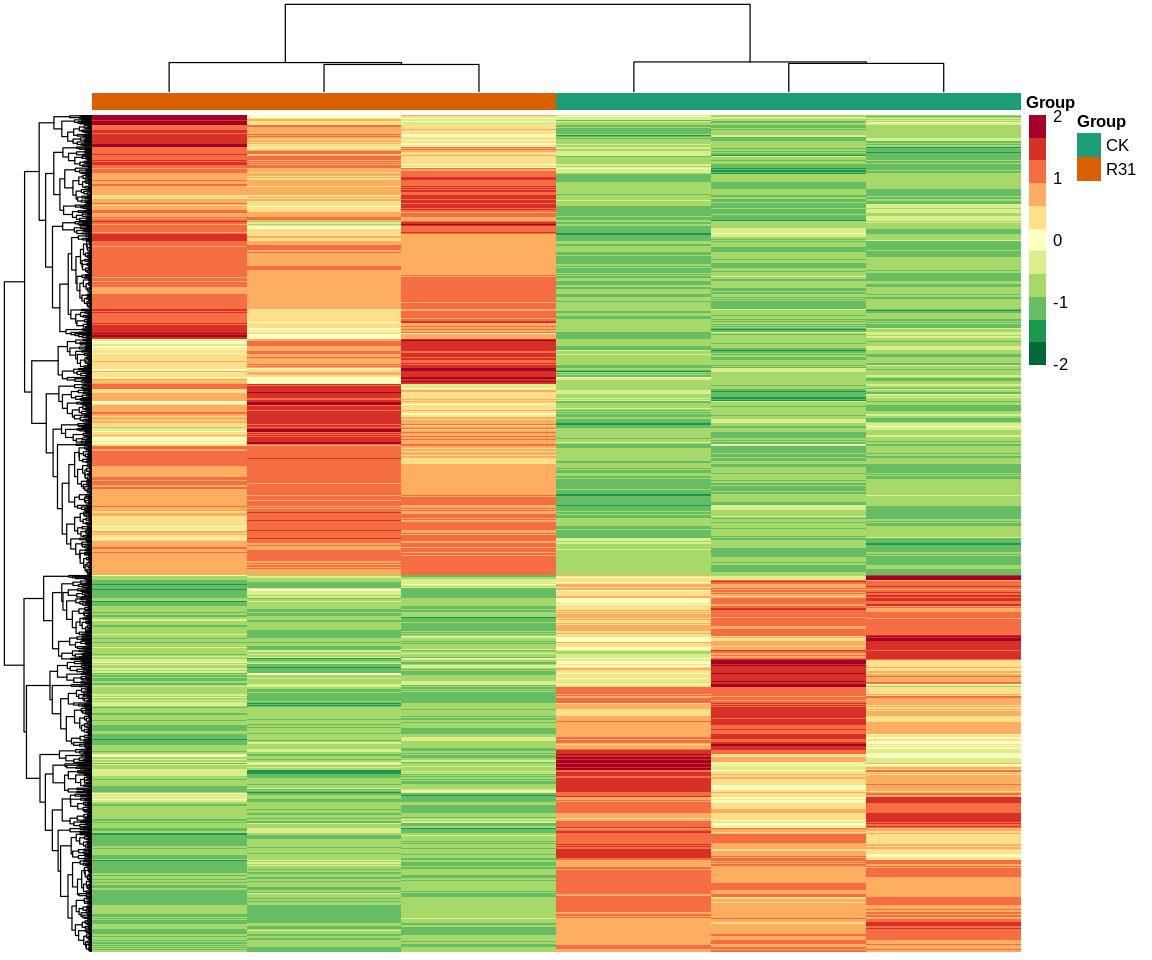


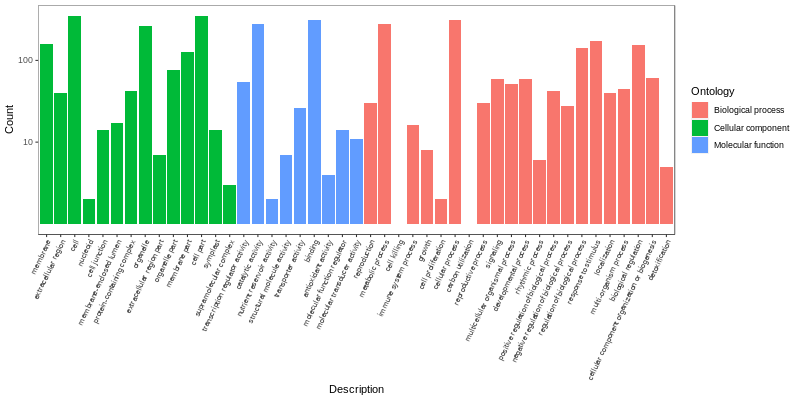
Figure S4. The unigenes annotated in the eggNOG database.



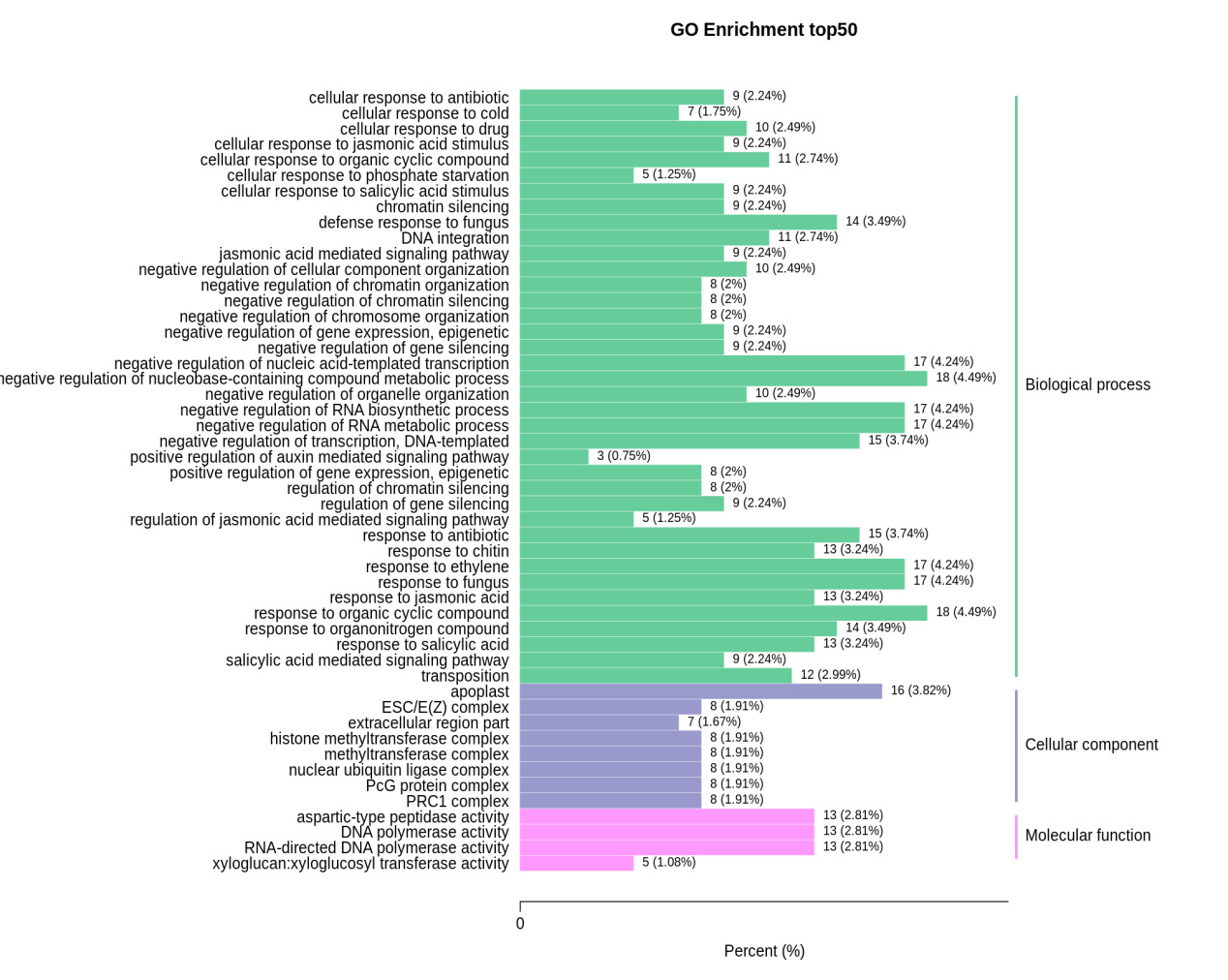
**Figure S5.** Correlation evaluation of biological repetition for transcriptome analyses of sweet corn after application of *B. subtilis* R31.



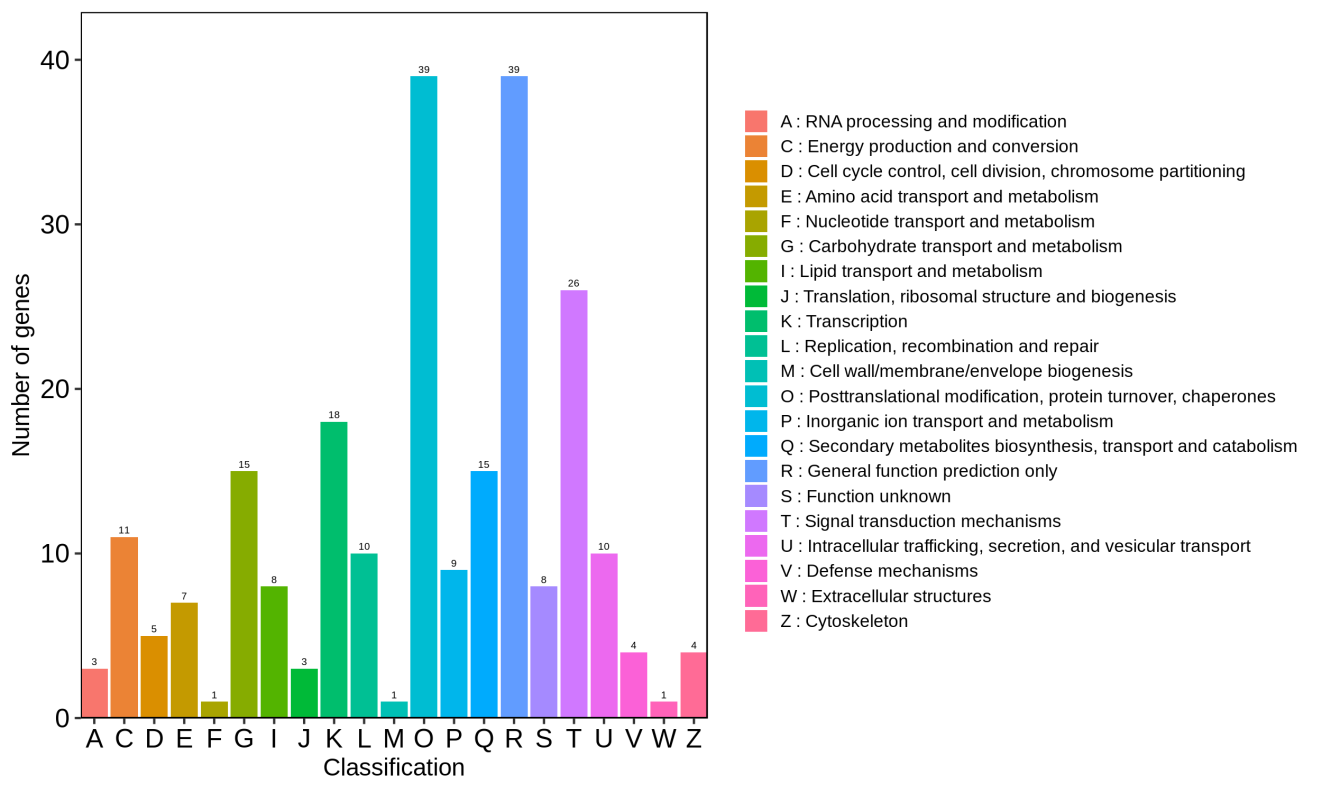
**Figure S6.** Heatmap of DEGs expression insweet corn after application of *B. subtilis* R31. Horizontal is sample name, vertical is metabolite information, group is grouping, class is substance classification, and different colors are values obtained after standardized treatment of relative content (red represents high content, green represents low content).



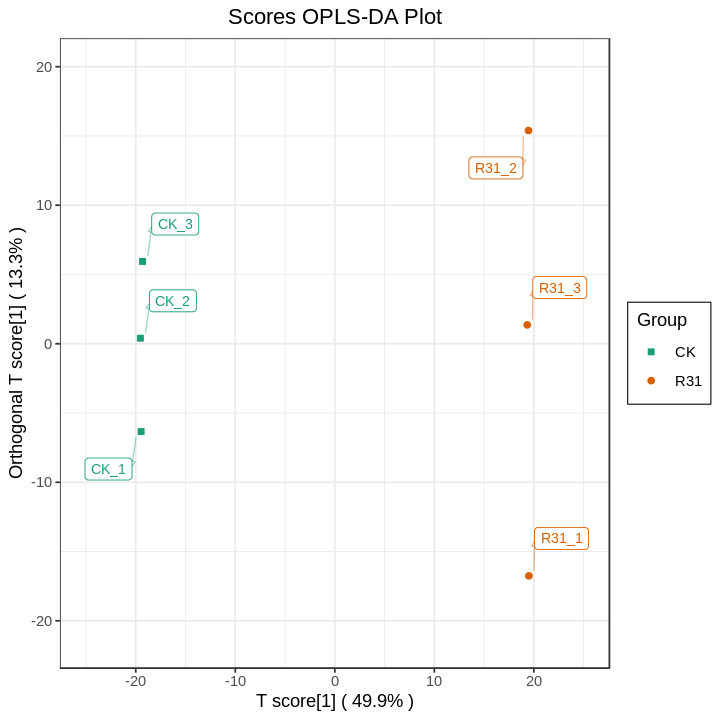
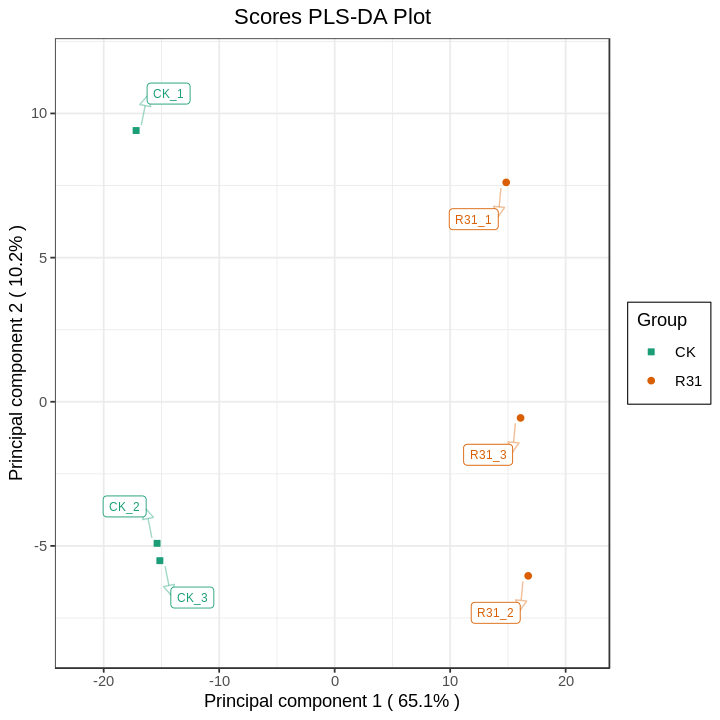
**Figure S7**. Classification map of secondary entries of DEGs expression insweet corn after application of *B. subtilis* R31.The horizontal coordinate represents the secondary GO entries, and the vertical coordinate represents the number of differential genes in the GO entries (Green column represents biological process, blue column represents cellular compound, and orange column represents molecular function).

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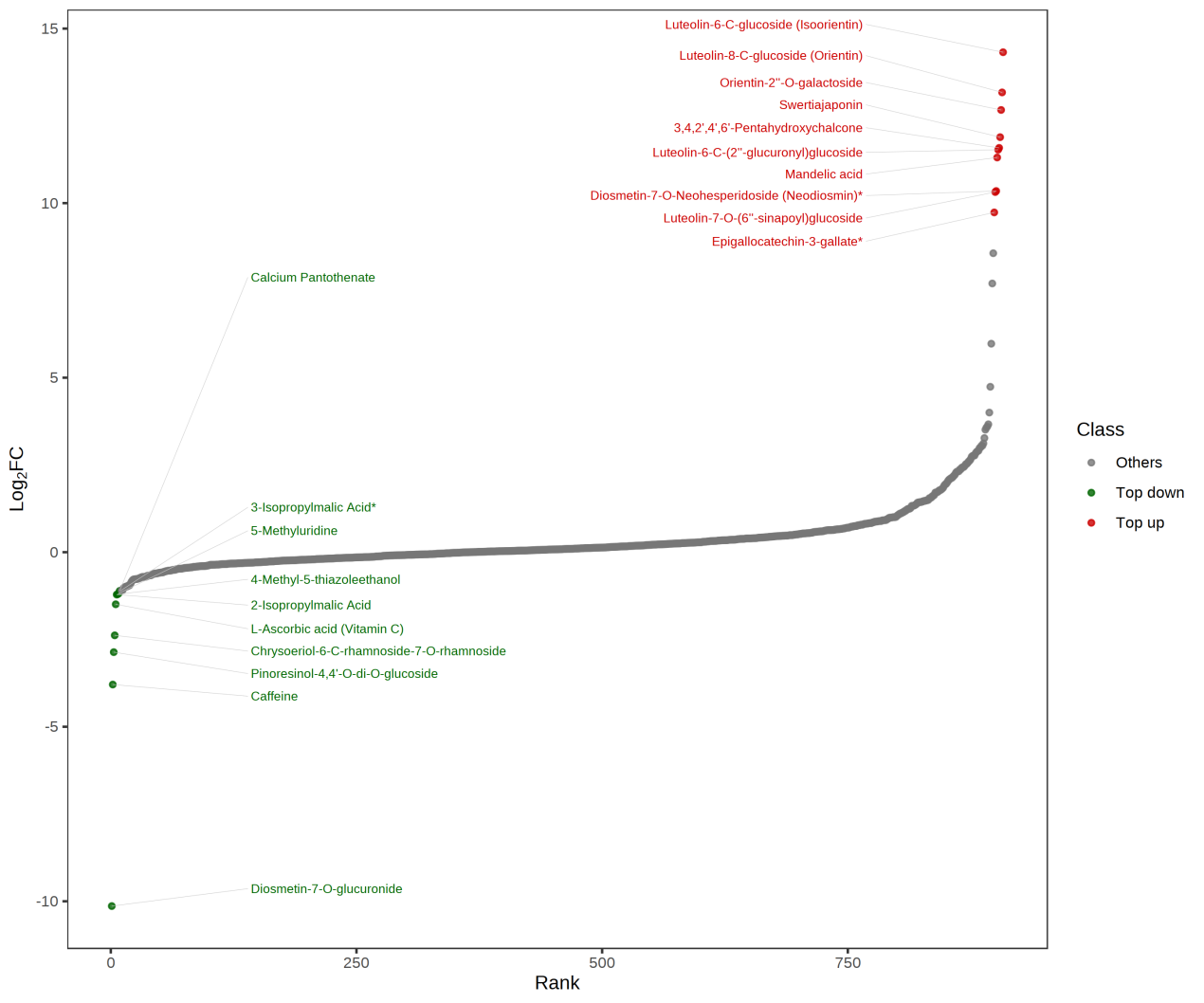
**Figure S8.** Histogram of GO enrichment for top50 DEGs expression insweet corn after application of *B. subtilis* R31. The horizontal coordinate represents the ratio of commented genes to the total number of annotated genes, and the vertical coordinate represents the name of the GO entry. The label to the right of the graph represents the category to which the GO entry belongs (Green column represents biological process, lilac column represents cellular compound, and pink column represents molecular function).



**Figure S9.** KOG classification bar chart of DEGs expression in sweet corn after application of *B. subtilis* R31.

**Figure S10.** OPLS-DA of DAMs identified among sweet corn after application of *B. subtilis* R31. (A) OPLS-DA score plot. (B) PLS-DA score plot.



**Figure S11** Top Fc distribution of DEGs expression in sweet corn after application of *B. subtilis* R31. The horizontal axis represents VIP value, and the vertical axis represents differential metabolites. The red dot represents up-regulated differential metabolites, and the green dot represents down-regulated differential metabolites.