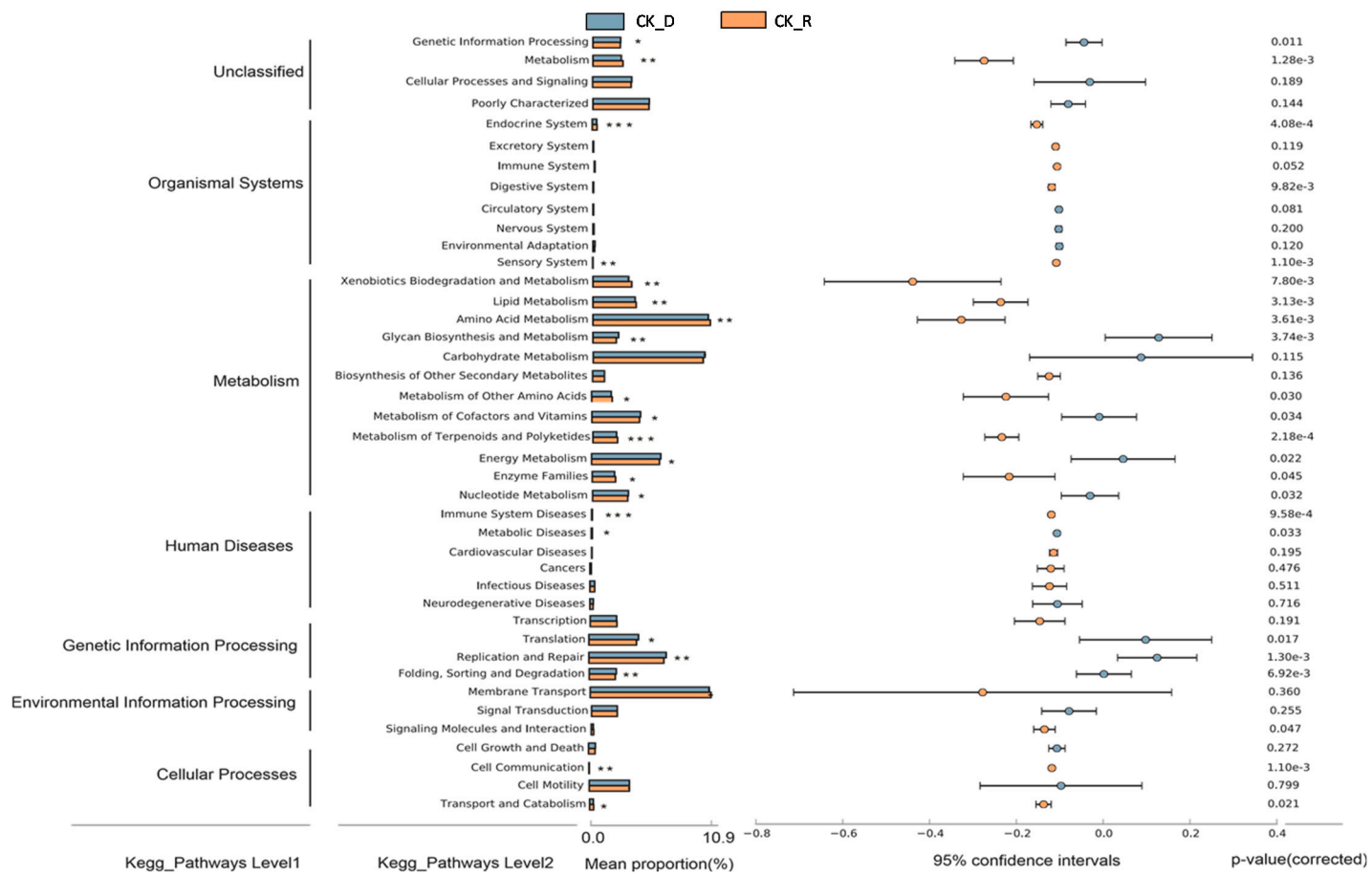
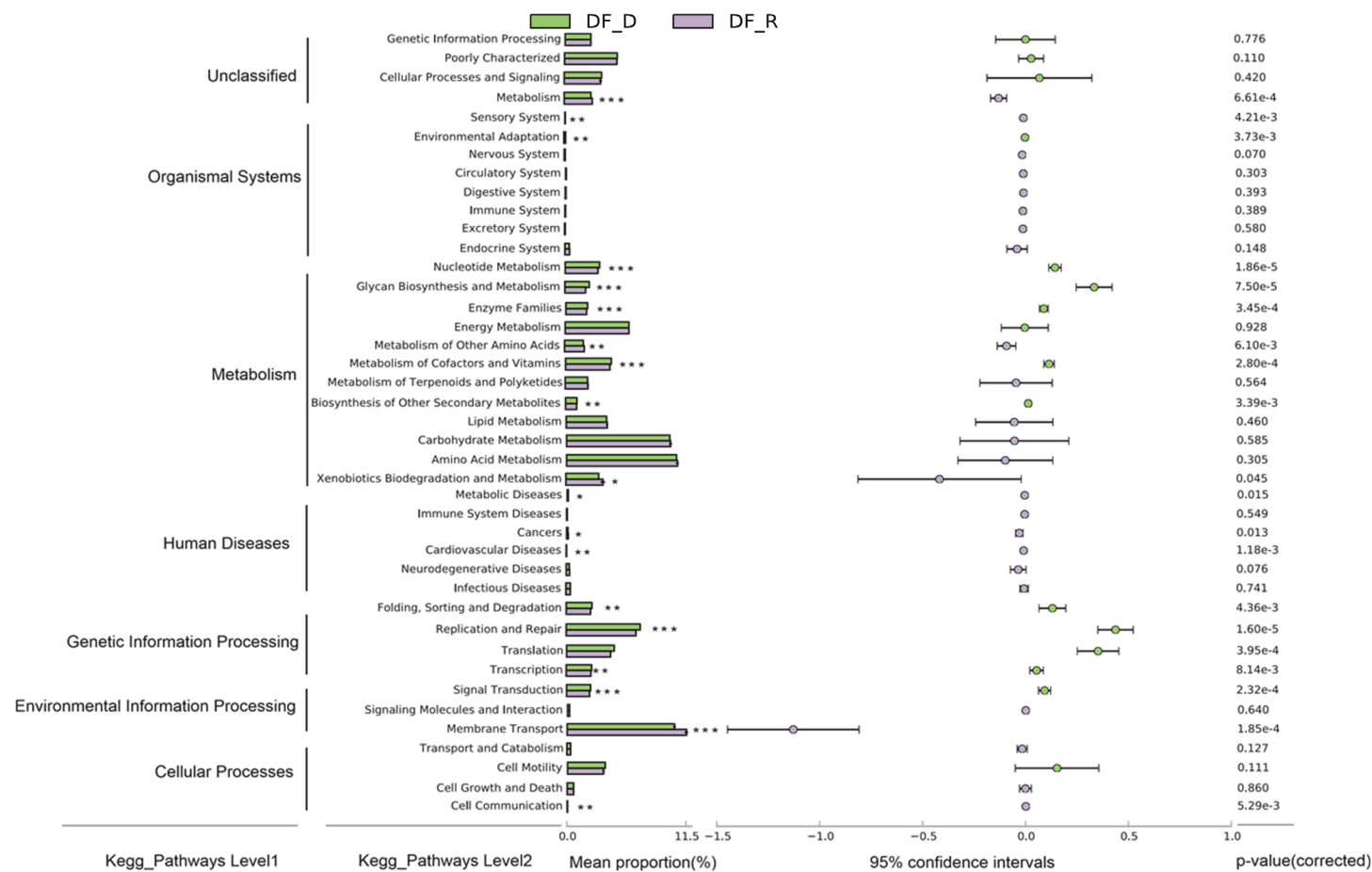
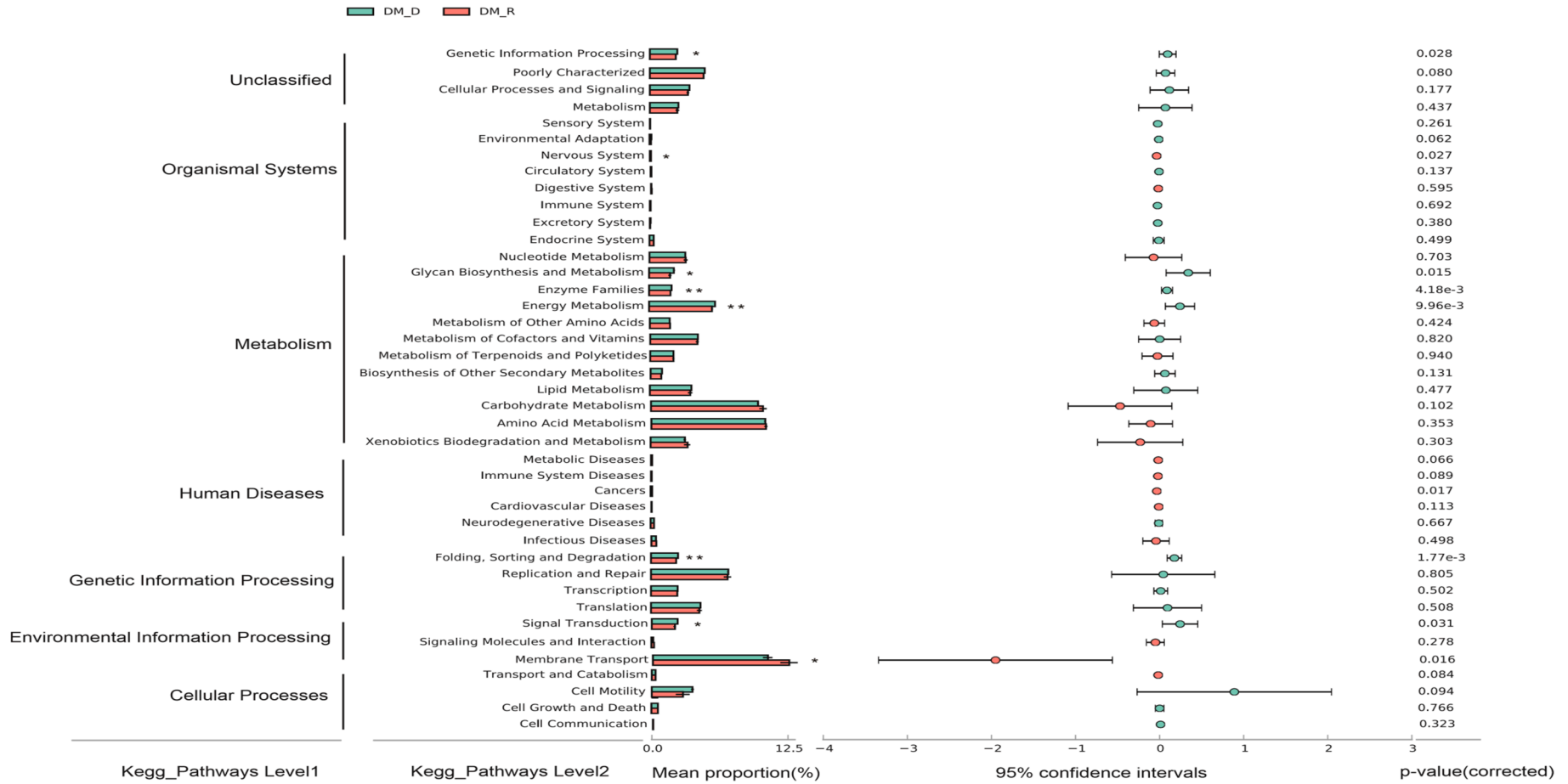
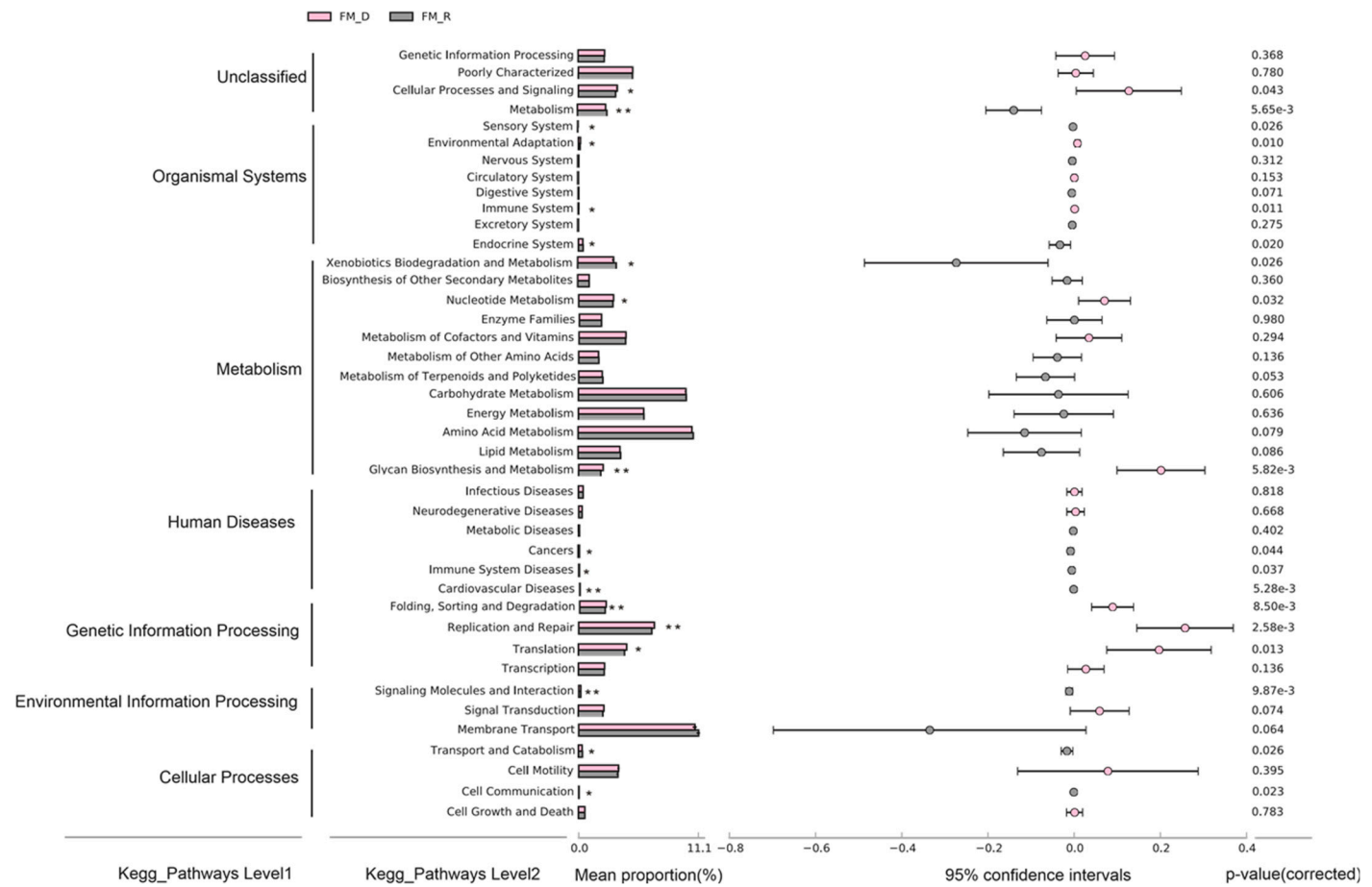


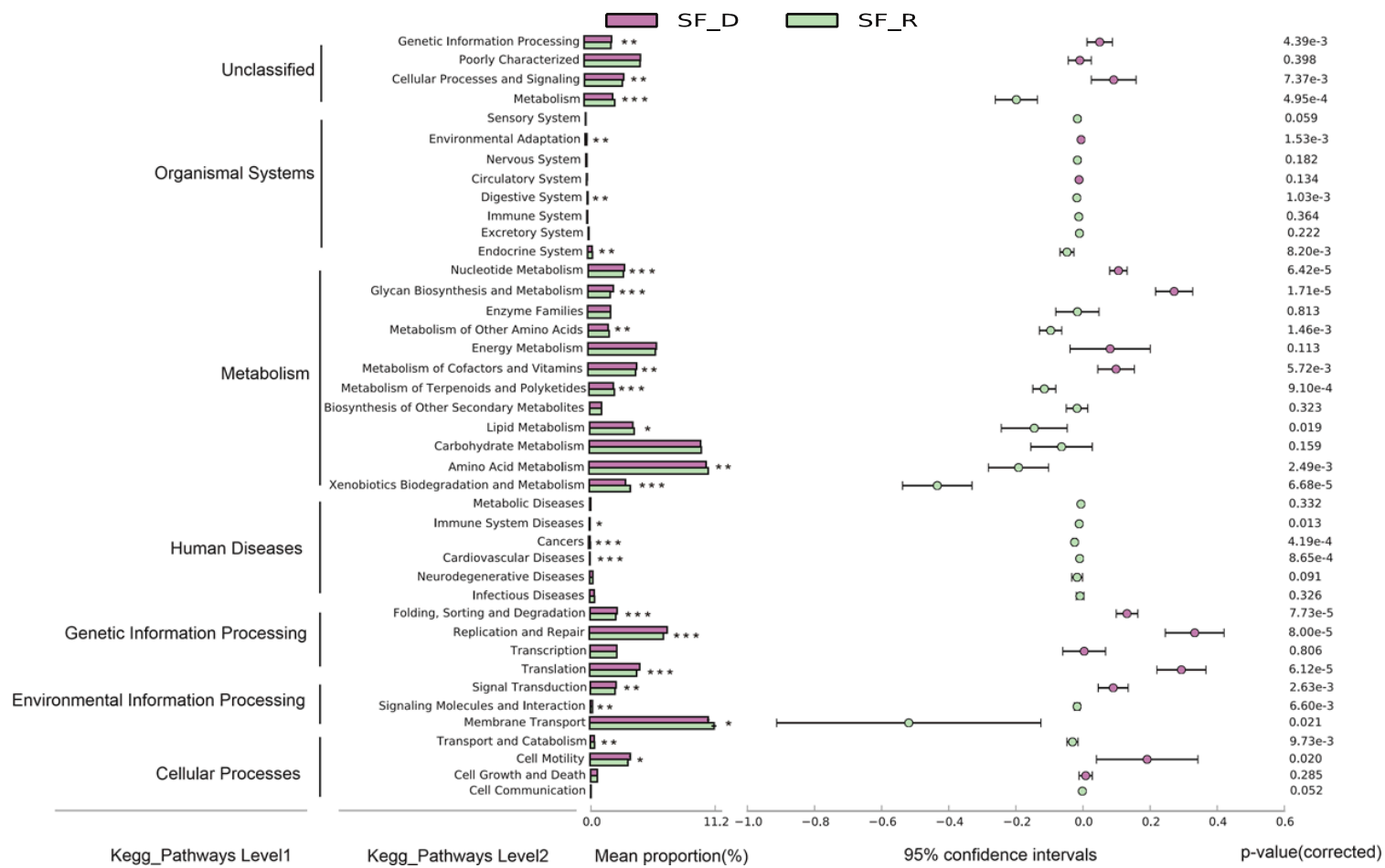
**Figure S1.** Heat map showing the relative abundance (Log2-transformed) of the top 30 classes from each treatment (a total of 71 classes). Color key is indicated at the bottom right corner. Vertical columns represent samples, and horizontal rows depict classes.

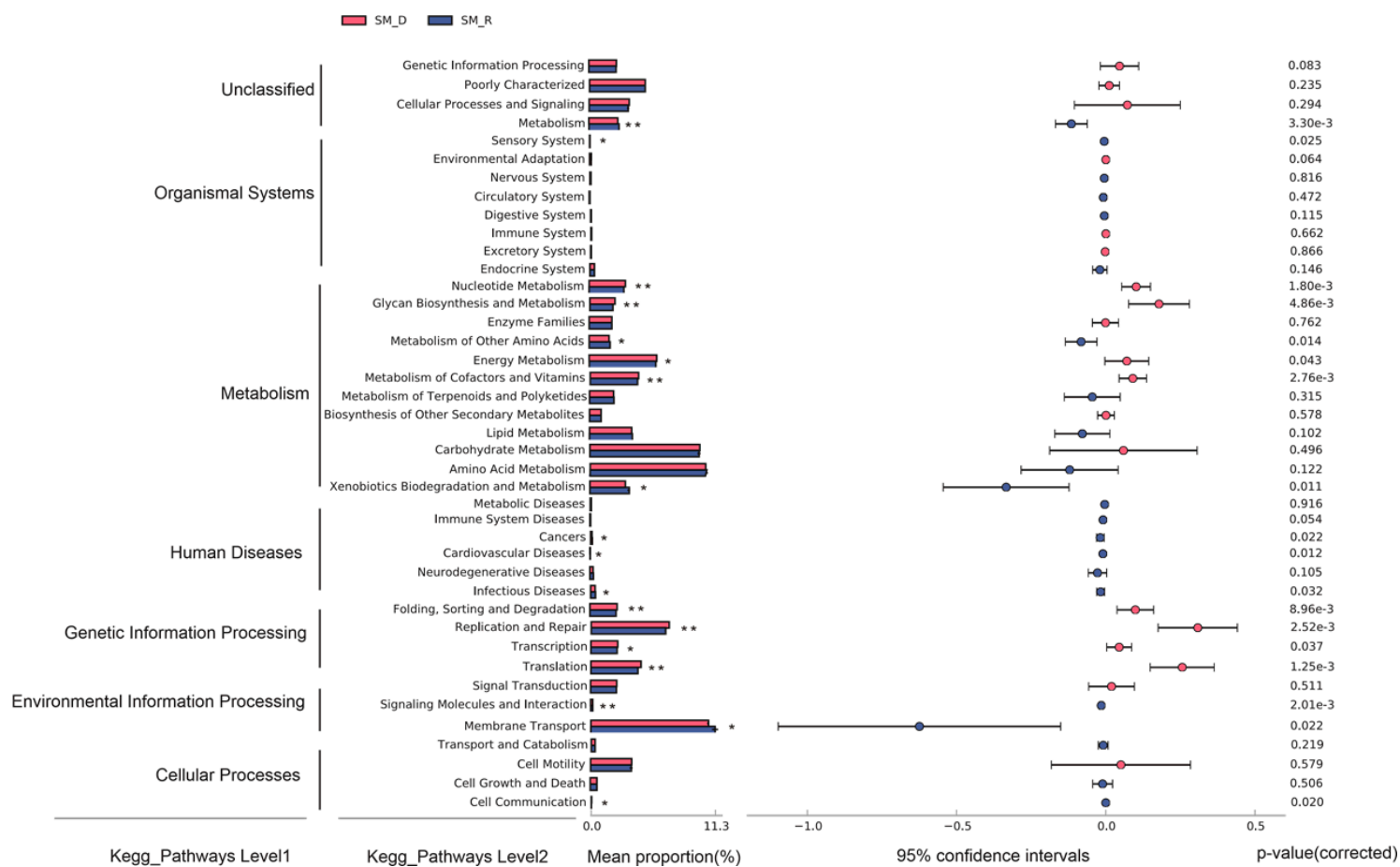




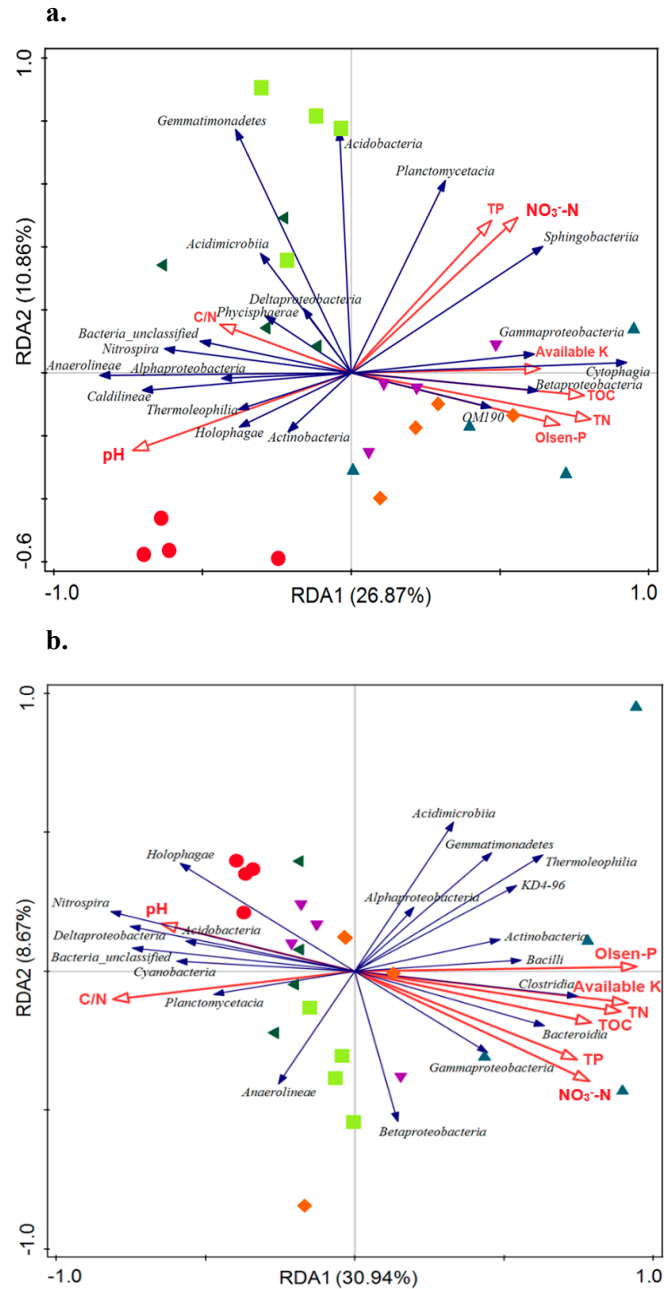








**Figure S2.** Relative abundance of predicted genes from the metagenome related to KEGG pathways at level 1 and 2; The terms given on the left are KEGG pathways annotation at level 1 and level 2 (from left to right). \*enriched in samples (LDA > 2, P < 0.05). \*\*Enriched in samples (LDA > 2, P < 0.01); \*\*\*Enriched in samples (LDA > 2, P < 0.001).



**Figure S3.** Redundancy analysis (RDA) diagram illustrating the relationship between the DNA-(a) and RNA-based (b) bacterial community structure at class level from different long-term fertility treatments and environmental variables (TOC, TN, TP, Olsen-P,  $\text{NO}_3^-$ -N, Available K, C/N, and pH). (● CK: no fertilizer; ▲ SF: mineral fertilizer input; ◆ SM: cattle manure input; ▼ FM: half mineral fertilizer input plus half manure applied; ■ DF: double amount mineral fertilizer input; ▲ DM: double amount cattle manure input).