No.	The name of the genus	OTU	Description of the genus
1	Pseudomonas	35253	g-, aerobic or facultative anaerobic bacteria
2	Chloroplast	18624	Cyanobacteria
3	Serratia	11878	g-, aerobic or facultative anaerobic bacteria
4	Massilia	10706	g-, aerobic bacteria
5	Mitochondria	775	g-, facultative anaerobic bacteria
6	Escherichia	250	g-, anaerobic or aerobic bacteria
7	Pediococcus	101	g+, facultative anaerobic bacteria
8	Sphingomonas	23	g-, aerobic or facultative anaerobic bacteria
9	Staphylococcus	22	g+, aerobic or facultative anaerobic bacteria
10	Paracoccus	16	g-, aerobic or facultative anaerobic bacteria

Table S1 The annotation of the original microbiome of plant inoculants.

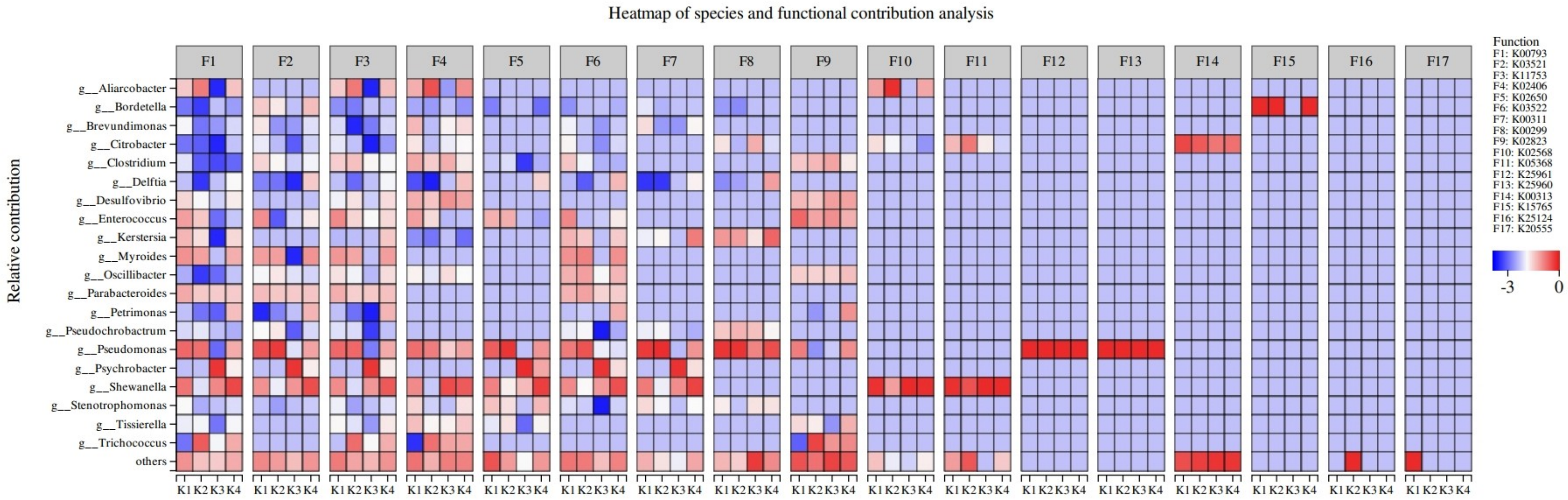
Heatmap of species and functional contribution analysis

Fig.S1 Relative analysis of functional contribution based on the top 20 species abundance.

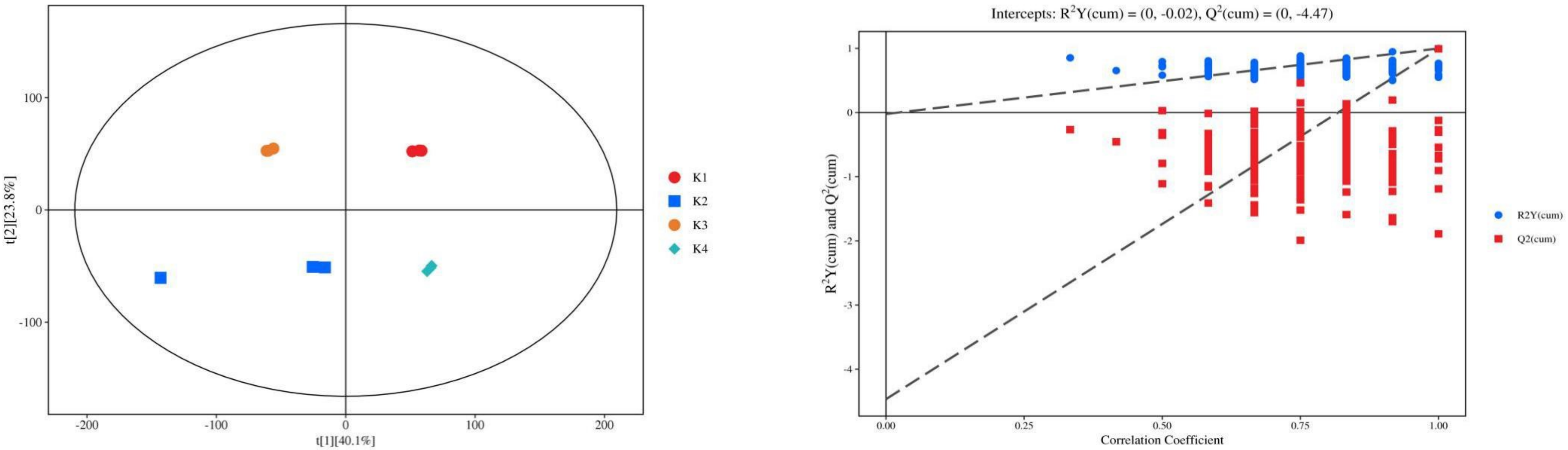

Fig.S2 Score scatter plot of OPLS-DA model (left), Permutation plot test of OPLS-DA model (right) for all test group.

In the FigureS2 (left), the abscissa t[1] represents the predicted principal component score of the first principal component, showing the differences between sample groups. The ordinate t[2] represents the orthogonal principal component score, showing the differences within sample groups. Each scatter point represents a sample, and the shape and color of the scatter points indicate different experimental groups. The greater the horizontal distance between samples, the larger the inter-group differences. The closer the vertical distance, the better the repeatability within groups.

As shown by FigureS2 (right), R'Y and Q'Y of the model are always substantially higher than the corresponding “pemuted" values, This indicates model validity with regard to treatment. However, there is a considerable spread among the permuted R'Y's and Q'Y's indicating that the PLS model obtained is weaker for this response. It would be desirable to somehow summarize the results of pemmutation testing in a quantitative manner. One way of doing this is to conduct conventional regression analysis in the two sets of points, i.e., oneregression line is fitted among the R`Y-points (blue circles) and another line among the Q'Y-points (red squares). The intercepts of the resulting regression lines are interpretableas measures of “background" R'Y and Q'Y obtained by fit to random data. Experience shows that the R`Y-intercept should not exceed 0 3-0.4 and that the Q'Y intercept should not exceed 0.05. Intercepts below these limits indicate valid models. Retuming to the valrdate plots of Figure S2, we may see that the OPLS model is valid and the results are also good according to the reference limits for intercepts.

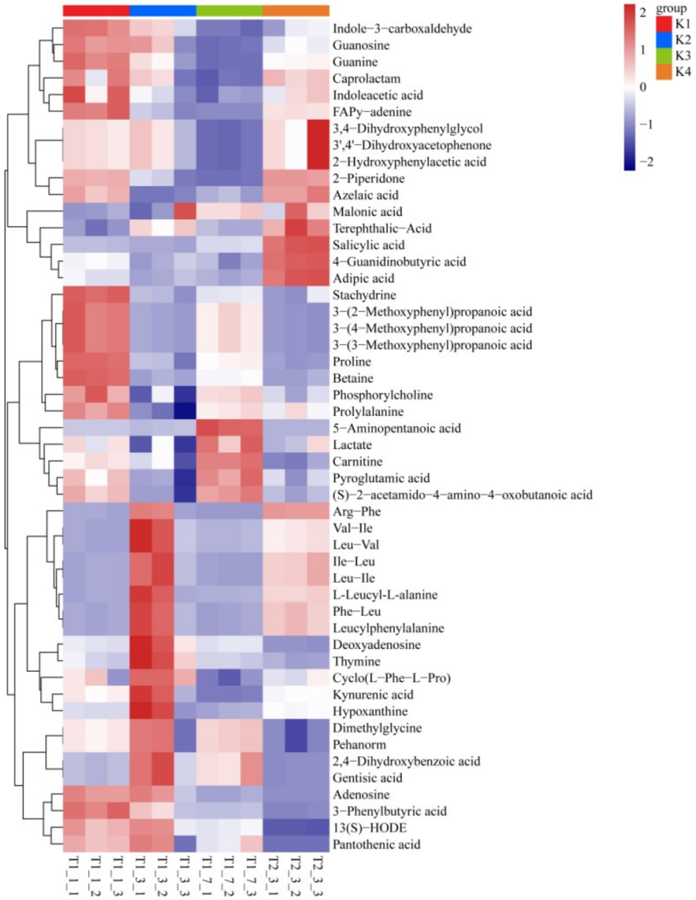

Fig.S3 Annotations of the top 50 metabolites in heat map analysis across all treatments.

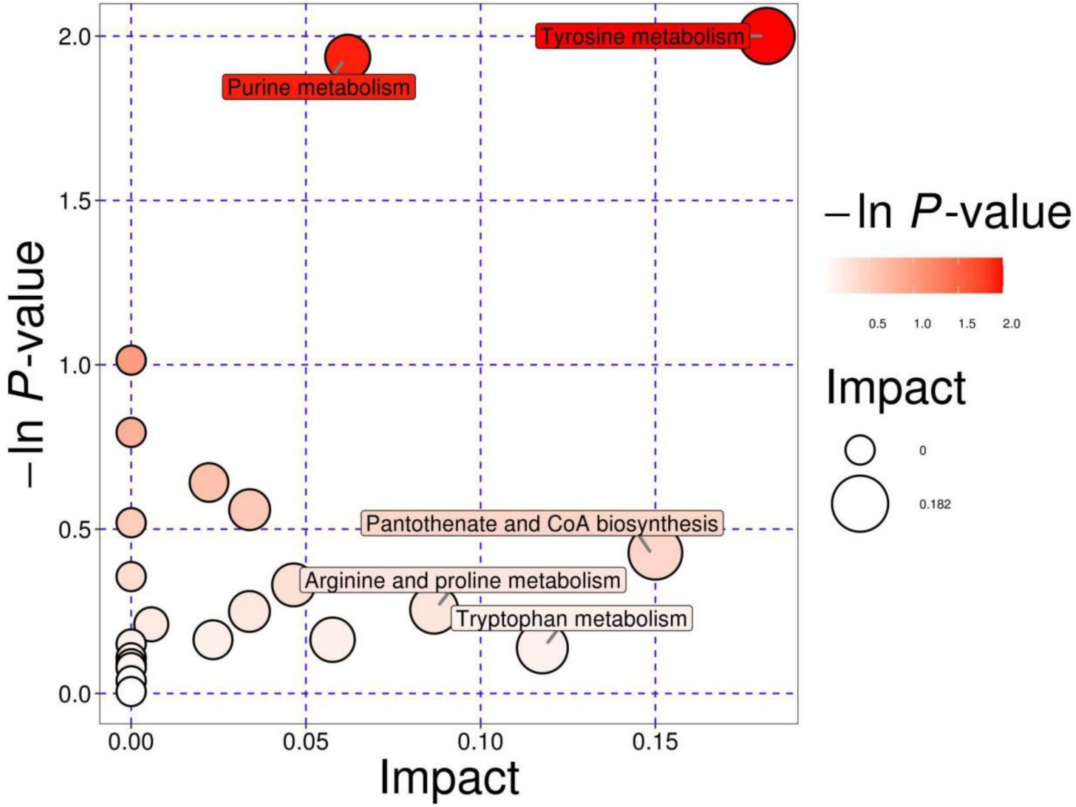

Fig.S4 Metabolic pathway prediction analysis conducted through the top 50 metabolites, in conjunction with other detectable substances.

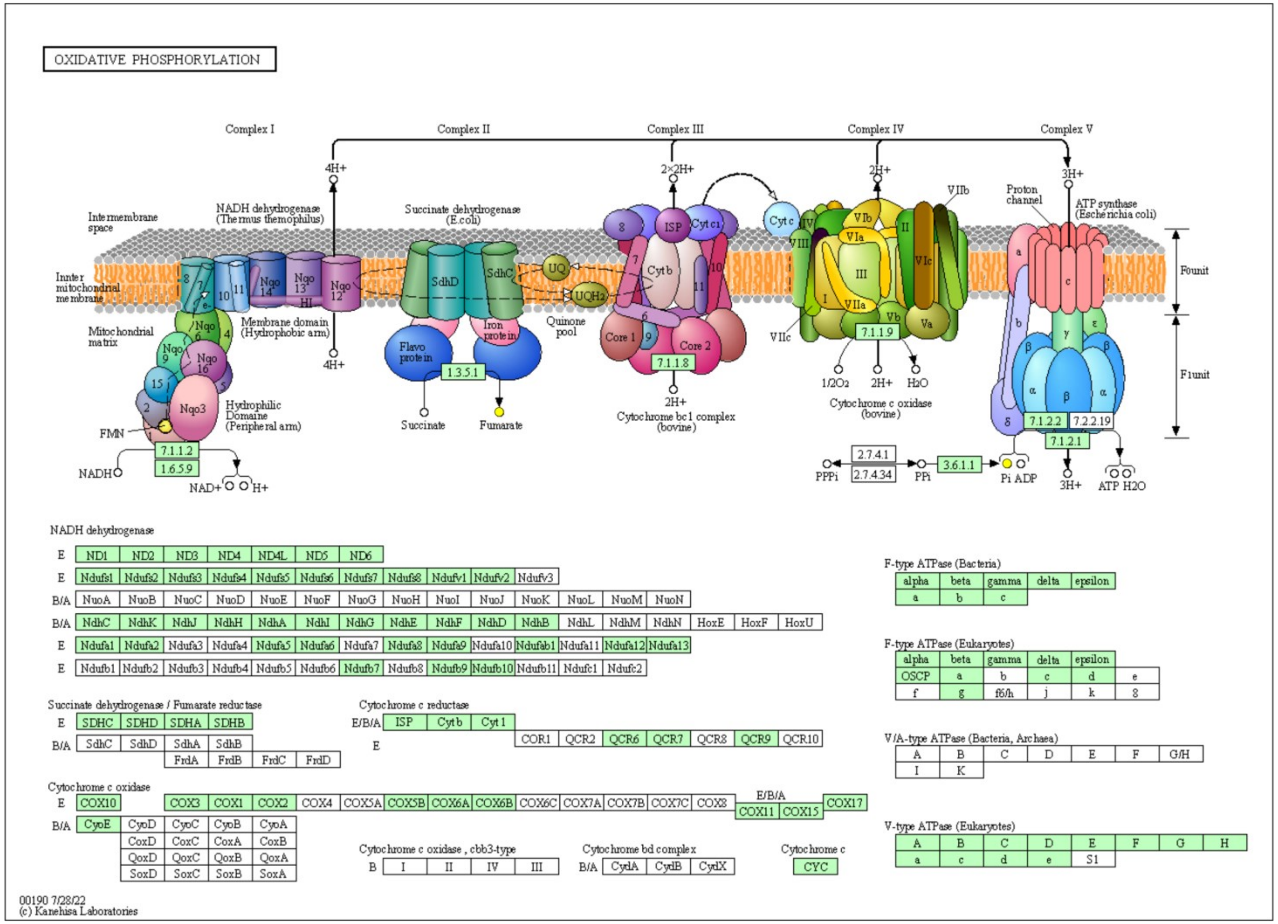

Fig.S5 The detected analysis related to the oxidative phosphorylation pathway in this study