

Supplementary Material

Title: Multi-Omics Analysis of the Co-Regulation of Wood Alcohol Accumulation in Baijiu Fermentation

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Figures

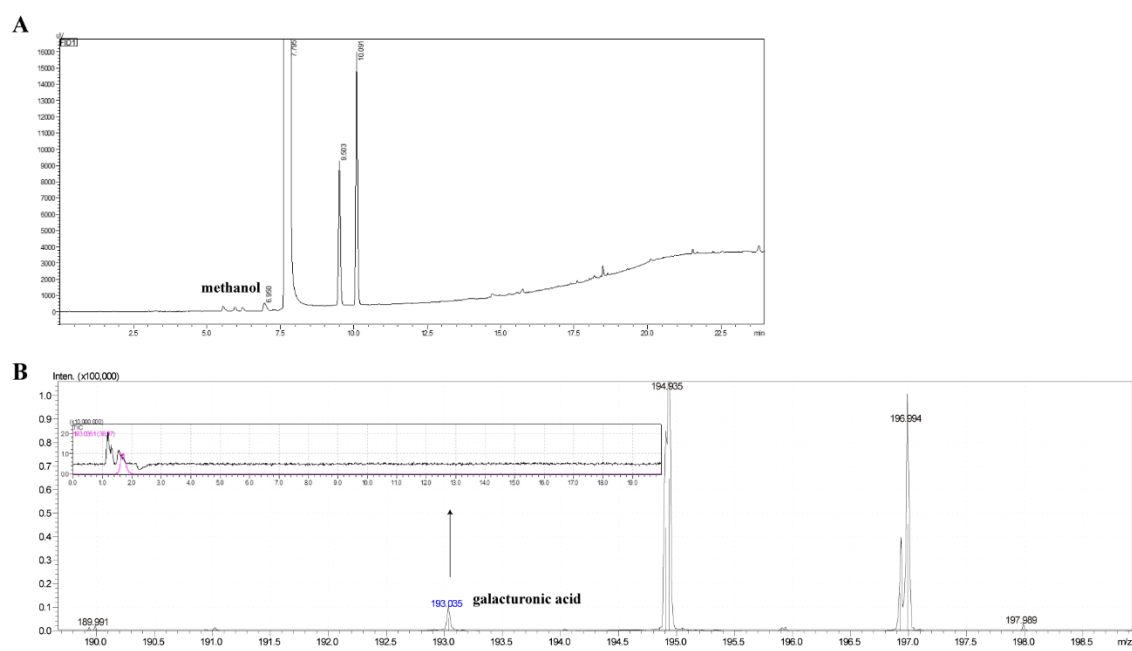


Figure S1. A: Characteristic peak of methanol retention time. B: Characteristic peak of galacturonic acid m/z ratio.

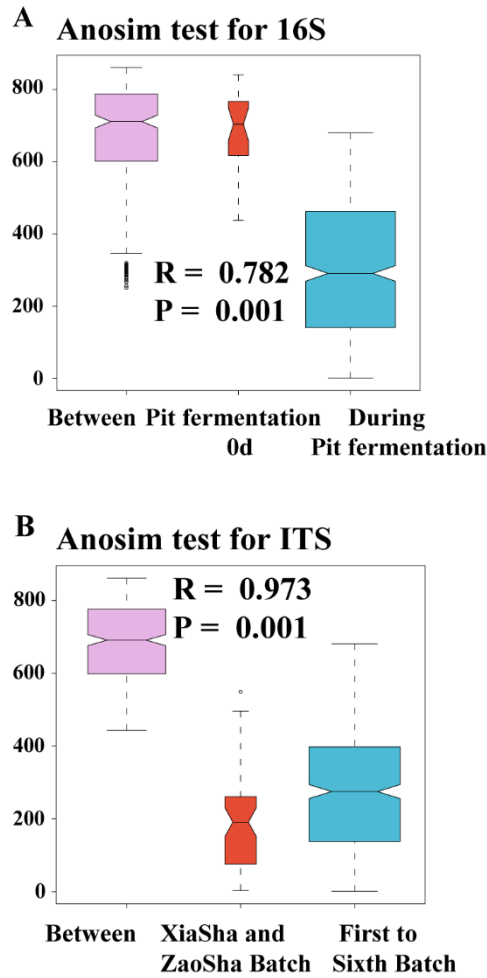


Figure S2. A: Anosim test for 16S grouping. B: Anosim test for ITS grouping (The “R” value is used to validate whether there are differences between different groups, the larger the R, the greater the differences between groups, while the “P” value is used to indicate the significance of the differences, with $P < 0.05$ indicating a significant correlation).

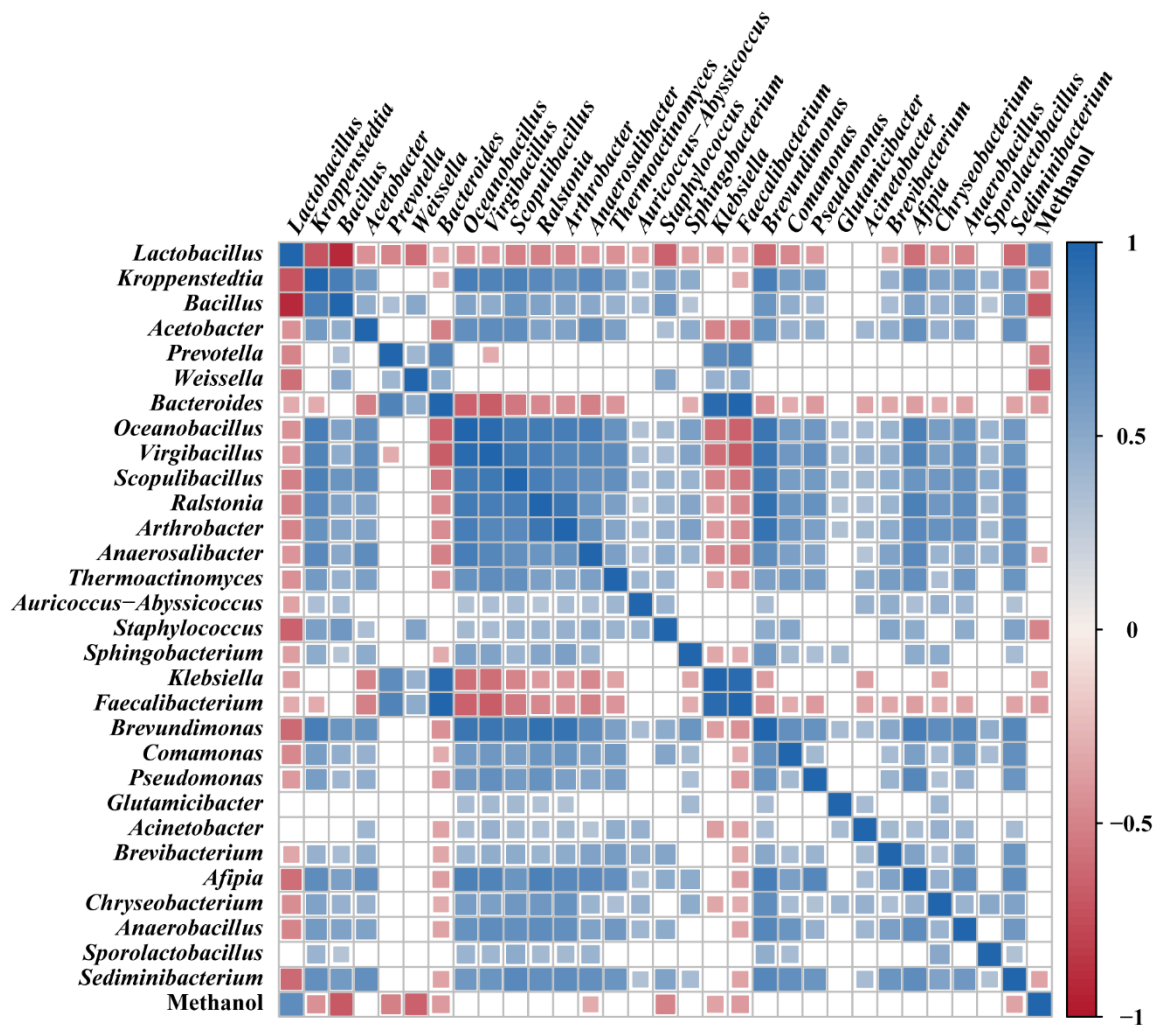


Figure S3. Spearman's correlation analysis of methanol and bacteria (with the sum of all sample's relative abundance greater than 0.5%). Correlation matrix (Spearman test, $p \leq 0.05$) showing the correlation coefficients between methanol content and bacteria genera. Positive correlations are displayed in blue and negative correlations in red. The color intensity and size of the square were proportional to the correlation coefficients. On the right side of the correlogram, the legend shows the correlation coefficients and the corresponding colors.

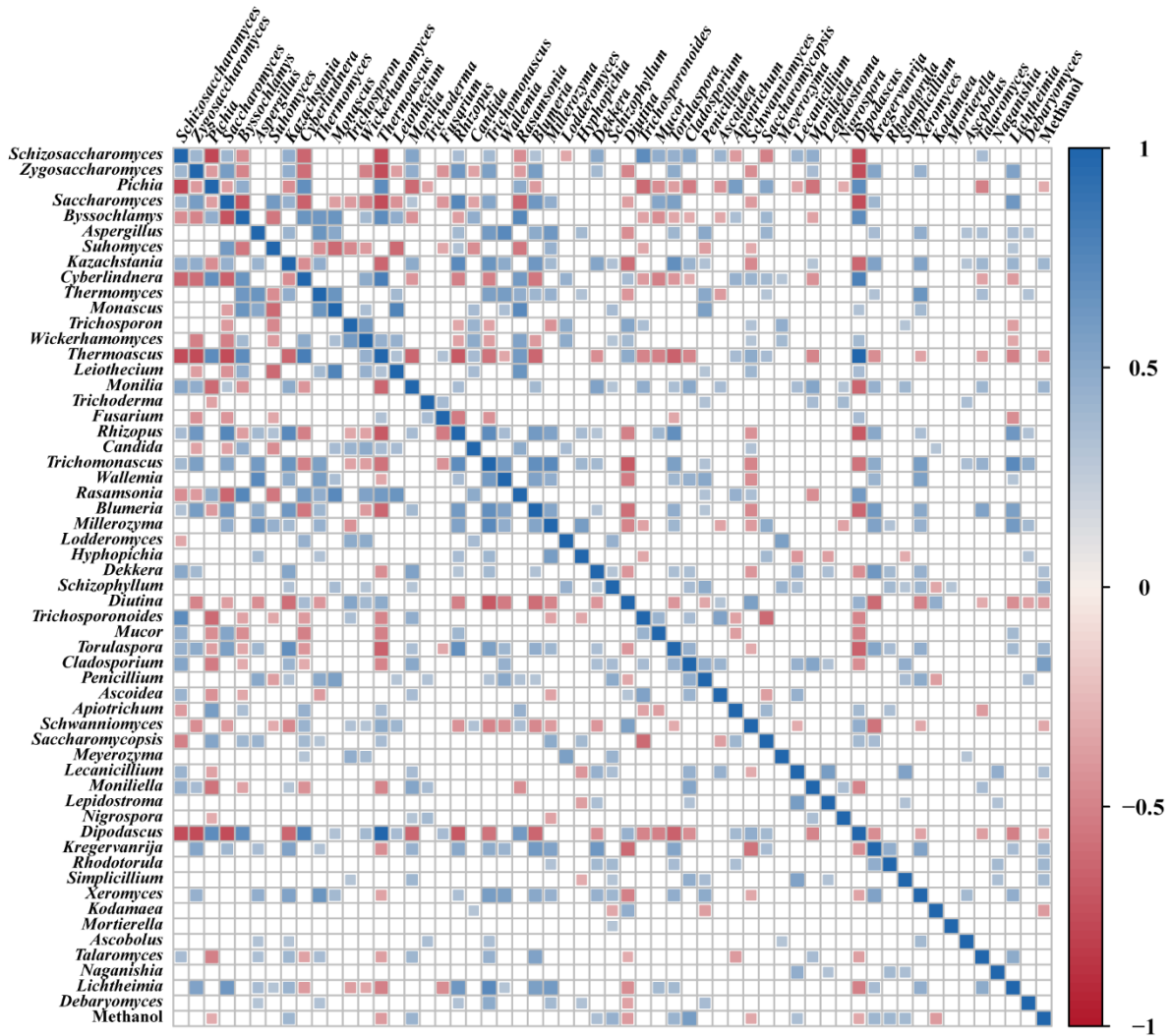


Figure S4. Spearman's correlation analysis of methanol and fungi (with the sum of all sample's relative abundance greater than 0.5%). Correlation matrix (Spearman test, $p \leq 0.05$) showing the correlation coefficients between the methanol content and fungal genera. Positive correlations are displayed in blue and negative correlations in red. The color intensity and the size of the square are proportional to the correlation coefficients. In the right side of the correlogram, the legend shows the correlation coefficients and the corresponding colors.

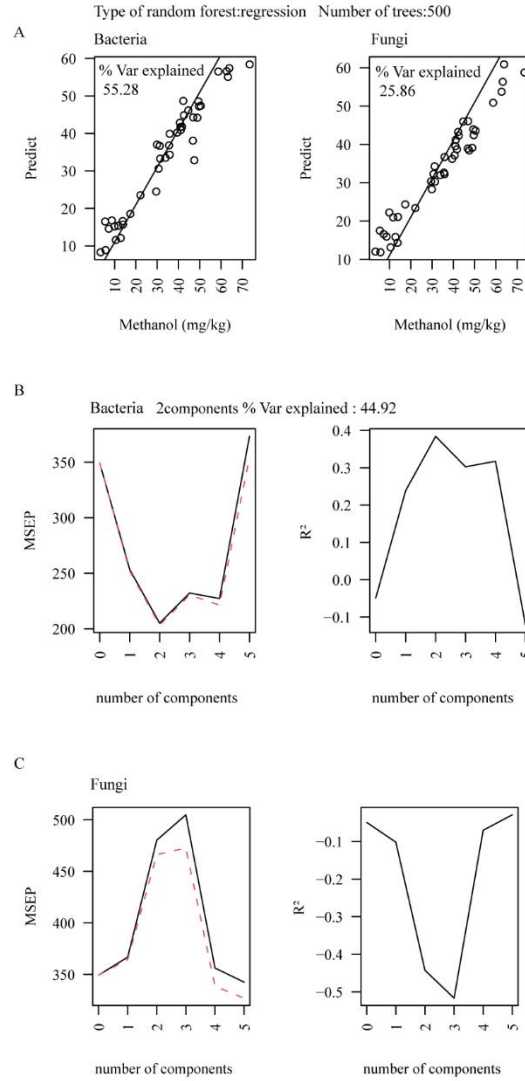


Figure S5. The major parameters of model establishment. A: The use of random forest to model the changes in microbial abundance and methanol content (% Var explained represents the degree of explanation of the changes in the abundance of microbial communities to the changes in methanol) B: The analysis of bacterial abundance and methanol content changes by PLS regression (the number of components represents the number of selected principal components, MSEP is the predicted mean square error of the regression model, the larger the MSEP, the greater the regression error, R^2 is used to evaluate the degree of regression fit, the larger the R^2 , the better the regression fit).

Tables

Table S1 The compound identification for methanol content detection

Name	retention time/min
methanol	6.95
ethanol	7.795
2-Methyl-2-butanol	10.091

Table S2 The corresponding enzyme names for KO related to methanol metabolism

KO	EC Number	Enzyme name
K00002	[EC:1.1.1.2]	alcohol dehydrogenase (NADP+)
K00012	[EC:1.1.1.22]	UDPglucose 6-dehydrogenase
K00122	[EC:1.17.1.9]	formate dehydrogenase
K00128	[EC:1.2.1.3]	aldehyde dehydrogenase (NAD+)
K00134	[EC:1.2.1.12]	glyceraldehyde 3-phosphate dehydrogenase
K00138	[EC:1.2.1.-]	aldehyde dehydrogenase
K00148	[EC:1.2.1.46]	glutathione-independent formaldehyde dehydrogenase
K00626	[EC:2.3.1.9]	acetyl-CoA C-acetyltransferase
K00627	[EC:2.3.1.12]	pyruvate dehydrogenase E2 component (dihydrolipoamide acetyltransferase)
K00656	[EC:2.3.1.54]	formate C-acetyltransferase
K00688	[EC:2.4.1.1]	glycogen phosphorylase
K00693	[EC:2.4.1.11]	glycogen synthase
K00700	[EC:2.4.1.18]	1,4-alpha-glucan branching enzyme
K00873	[EC:2.7.1.40]	pyruvate kinase
K00927	[EC:2.7.2.3]	phosphoglycerate kinase
K00963	[EC:2.7.7.9]	UTP--glucose-1-phosphate uridylyltransferase
K01027	[EC:2.8.3.5]	3-oxoacid CoA-transferase
K01034	[EC:2.8.3.8 2.8.3.9]	acetate CoA/acetoacetate CoA-transferase alpha subunit
K01067	[EC:3.1.2.1]	acetyl-CoA hydrolase
K01184	[EC:3.2.1.15]	polygalacturonase
K01196	[EC:2.4.1.25 3.2.1.33]	glycogen debranching enzyme
K01574	[EC:4.1.1.4]	acetoacetate decarboxylase
K01623	[EC:4.1.2.13]	fructose-bisphosphate aldolase, class I
K01640	[EC:4.1.3.4]	hydroxymethylglutaryl-CoA lyase
K01641	[EC:2.3.3.10]	hydroxymethylglutaryl-CoA synthase
K01689	[EC:4.2.1.11]	enolase
K01810	[EC:5.3.1.9]	glucose-6-phosphate isomerase
K01834	[EC:5.4.2.11]	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase
K01835	[EC:5.4.2.2]	phosphoglucomutase
K03841	[EC:3.1.3.11]	fructose-1,6-bisphosphatase I
K15633	[EC:5.4.2.12]	2,3-bisphosphoglycerate-independent phosphoglycerate mutase
K17066	[EC:1.1.3.13]	alcohol oxidase
K18372	[EC:3.1.1.114]	methyl acetate hydrolase
K00895	[EC:2.7.1.90]	diphosphate-dependent phosphofructokinase
K00163	[EC:1.2.4.1]	pyruvate dehydrogenase E1 component
K00132	[EC:1.2.1.10]	acetaldehyde dehydrogenase (acetylating)
K01051	[EC:3.1.1.11]	pectinesterase
K01213	[EC:3.2.1.67]	galacturan 1,4-alpha-galacturonidase

K01812	[EC:5.3.1.12]	glucuronate isomerase
K21619	[EC:5.1.2.7]	tagaturonate epimerase
K16258		mxkK protein
K17067	[EC:1.2.98.1 1.1.99.37]	formaldehyde dismutase / methanol dehydrogenase
K18371	[EC:1.14.13.226]	acetone monooxygenase (methyl acetate-forming)
