

Microbial dynamics and metabolite changes in Chinese Rice Wine fermentation from sorghum with different tannin content

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Table. S1 Changes in acid, reducing sugar and alcohol found in JZ22(a) and JB3(b) Chinese Rice Wine brewed from Sorghum during fermentation. Every value is expressed as means \pm standard error (n=3).

a

JZ22 Compounds(g/L)	Fermentation time (days)							pvalue	Correl ation coeffic ient
	0 day	2 nd day	4 th day	6 th day	8 th day	10 th day	12 th day		
Acid	2.70 \pm 0.09	3.63 \pm 0.18	3.85 \pm 0.09	5.09 \pm 0.07	6.54 \pm 0.12	7.33 \pm 0.10	7.91 \pm 0.07	0.0039 83	-0.91
reducing sugar	18.29 \pm 0.19	19.85 \pm 0.24	17.54 \pm 0.34	17.03 \pm 0.19	16.68 \pm 0.35	15.14 \pm 0.15	14.73 \pm 0.27	2.556e -05	0.99
alcohol	2.9 \pm 0. 21	5.7 \pm 0. 22	8.9 \pm 0. 45	9.8 \pm 0. 14	10.5 \pm 0.21	10.9 \pm 0.22	11.1 \pm 0 .22	0.0042 41	0.91

b

JB3 Compounds(g/L)	Fermentation time (days)							pvalue	Correl ation coeffic ient
	0 day	2 nd day	4 th day	6 th day	8 th day	10 th day	12 th day		
Acid	1.8 \pm 0. 15	2.86 \pm 0.16	3.78 \pm 0.31	4.93 \pm 0.15	5.38 \pm 0.22	6.54 \pm 0.24	7.89 \pm 0.30	0.0001 436	-0.98
reducing sugar	20.64 \pm 0.23	19.25 \pm 0.16	17.61 \pm 0.14	17.23 \pm 0.19	16.67 \pm 0.21	15.72 \pm 0.25	15.15 \pm 0.12	2.259e -06	1.00
alcohol	3.1 \pm 0. 08	4.3 \pm 0. 14	6.5 \pm 0. 22	9.2 \pm 0. 17	9.6 \pm 0. 22	10.4 \pm 0.08	10.8 \pm 0.14	0.0005 339	0.96

Table.S2 Changes in organic acids found in JZ22(a) and JB3(b) Chinese Rice Wine during fermentation. Every value is expressed as means \pm standard error (n = 3).

a

JZ22	Fermentation time (days)
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Organic acid (mg/L)	0 day	2 nd day	4 th day	6 th day	8 th day	10 th day	12 th day
Oxalic acid	1.03±0	4.21±0.1 3	4.99±0.0 1	5.64±0.0 4	5.79±0.0 9	7.09±2.0 6	7.93±0.5 4
Tartaric acid	25.71±3. 68	30.65±2. 75	38.83±0. 14	38.98±0. 12	48.87±0. 19	51.55±0. 02	56.72±0. 31
Pyruvic acid	0.71±0.0 3	1.64±0.0 1	22.96±0. 41	22.25±0. 80	15.93±0. 34	15.23±0. 07	14.09±0. 01
Malic acid	22.06±0. 20	27.17±2. 09	36.85±0. 01	38.02±0. 28	48.70±0. 63	52.41±3. 06	58.86±5. 31
α-ketoglutaric acid	20.59±3. 12	18.44±0. 24	12.03±0. 29	8.60±0.1 3	8.27±0.0 8	11.72±0. 34	9.92±0.2 8
Lactic acid	156.44±3 3.79	999.67±4 .43	1350.52± 2.29	1366.41± 18.29	1449.45± 5.05	1640.75± 9.42	1646.58± 10.33
Citric acid	3.71±0.0 2	17.42±0. 12	18.19±0. 14	19.35±0. 12	19.77±0. 27	22.90±0. 09	26.14±0. 07
Succinic acid	70.26±8. 00	87.05±26 .40	859.81±4 .98	1236.97± 2.86	1458.78± 0.28	1771.71± 4.71	1954.38± 0.39

b

JB3	Fermentation time (days)						
Organic acid (mg/L)	0 day	2 nd day	4 th day	6 th day	8 th day	10 th day	12 th day
oxalic acid	1.03±0	3.32±0.0 1	4.52±0.1 2	7.79±0.0 6	8.52±0.0 2	9.37±0.1 6	10.68±0. 15
Tartaric Acid	4.67±0.7	48.22±0. 96	48.22±3. 21	53.59±1. 40	58.03±0. 73	59.58±1. 88	70.11±1. 37
pyruvic acid	0.50±0.0 1	1.38±0.0 2	1.72±0.0 4	1.59±0.0 1	1.28±0.0 6	1.29±0.0 8	1.17±0.0 2
malic acid	24.55±0. 74	32.59±1. 62	46.87±0. 23	48.10±0. 09	50.06±8. 95	58.72±0. 07	62.83±2. 04
α-ketoglutaric acid	1.05±0.3 1	8.35±0.6 8	6.83±0.3 3	5.50±0.5 7	4.16±0.1 4	5.56±0.1 5	5.24±0.5 6

lactic acid	86.69±0.	1048.63±	1351.92±	1536.10±	1768.18±	2233.19±	2084.23±
	89	18.14	36.80	6.06	2.971	47.18	7.39
citric acid	8.10±00.	15.89±0.	17.54±0.	17.99±0.	21.08±0.	21.96±0.	20.34±0.
	15	42	49	50	20	38	20
Succinic acid	150.19±1	182.35±0	634.74±5	687.69±0	863.81±1	1077.04±	942.43±7
	.55	.21	.09	.49	4.62	3.62	0.73

Table.S3 Changes in volatile compounds in JZ22(a) and JB3(b) Chinese Rice Wine during fermentation.

a

Relative content of volatile compounds in Jz22 fermentation stages(mg/l)								
No.	Compounds	Day 0	Day 2	Day 4	Day 6	Day 8	Day 10	Day12
alkane								
	Heneicosane	0.05		4.76	3.13	2.79		
	Pentacosane	1.50		49.86		12.68		
	Tetratriacontane	0.12		2.08	6.08			
	2,4,4-trimethyl-Hexane		0.11					
	2,6,10,15-tetramethyl-Heptadecane		0.31					
	3,7-dimethyl-Nonane	0.01	0.12	0.11	0.57		0.87	
	3,8-dimethyl-Decane	0.02						
	3-methyl-Undecane		0.18					0.50
	2,6,10-trimethyl-Dodecane	0.01						
	2,6,10,15-tetramethyl-Heptadecane				2.23			6.61
	2-ethoxy-Propane			0.58	1.69			
	Cyclodecane			0.16				
	2-Bromo dodecane					0.78		
	ethoxymethyl Oxirane				0.12			
	1,1'-Bicycloheptyl							0.08
	diethyl(decyloxy)-Borane							1.29
alcohol								
	1-Propanol		1.26	0.57	6.12	2.63	11.60	6.45
	1-Butanol		0.06		0.33	0.18	0.69	0.72

2-methyl-1-Propanol	0.04	4.44	2.42	22.11	10.96	40.98	25.77
1-Pentanol	0.01						
3-methyl-1-Butanol	0.07	25.51	17.12	113.19	73.88	198.80	172.43
1-Hexanol	0.04	0.14	0.14	0.62	0.61	1.40	1.58
1-Heptanol		1.04					
6-methyl-2-Heptanol							1.30
1-Octanol	0.01		0.04		0.20	0.36	0.46
1-Nonanol						1.05	1.54
1-Undecanol	0.01			0.59			
2-Furanmethanol	0.03						
2-ethyl-2-methyl-Tridecanol		0.29					
1-methoxy-2-Butanol						1.96	
3-ethoxy-1-Propanol		0.05				0.77	
2-(2-butoxyethoxy)-Ethanol		0.18					
1-(1-methylethoxy)-2-Propanol		0.65					
1,2-Propanediol						5.38	2.73
Glycerin	0.03	8.36	24.27	83.56	51.26	140.53	258.38
2,3-Butanediol	0.88	11.71	12.37	28.56	24.29	243.33	92.60
1-Octen-3-ol	0.01						
Phenylethyl Alcohol	0.03	0.18	7.05	14.69	40.39	105.83	93.27
3-(methylthio)-1-Propanol					0.49	1.07	0.74
2-Chloroethanol						4.52	
ester							
Formic acid ethyl ester						0.42	
Butanoic acid ethyl ester			0.10		0.25	0.30	0.36
Pentanoic acid ethyl ester			0.08		0.19	0.40	0.51
Hexanoic acid ethyl ester	0.01	0.19	1.74	0.91	5.73	11.32	14.17
Heptanoic acid ethyl ester			0.11		0.58	0.77	1.16
Octanoic acid ethyl ester		0.13	1.01	0.61	7.62	10.67	12.91
Nonanoic acid ethyl ester			0.25	0.17	2.37	2.80	3.48

Decanoic acid ethyl ester	0.47	1.52	2.01	15.84	17.66	23.04	
2-hydroxy-Propanoic acid ethyl ester	0.05	0.05	0.42	0.36	2.57	1.32	
Undecanoic acid ethyl ester			0.36				
Pentadecanoic acid ethyl ester				3.80			
Dodecanoic acid ethyl ester		0.48	1.07	5.18	5.30	6.13	
Tetradecanoic acid ethyl ester		0.19		2.13	2.01	1.96	
Hexadecanoic acid ethyl ester	0.17	3.99	14.96	48.57	50.78	81.02	
Ethyl 9-hexadecenoate				0.93		1.34	
Octadecanoic acid ethyl ester				1.29		5.30	
(E)-9-Octadecenoic acid ethyl ester	0.27	1.19	2.08	6.80	15.49	17.49	38.54
9,12-Octadecadienoic acid ethyl ester	0.04	0.67	1.79	6.76	10.95	12.60	29.47
Eicosanoic acid ethyl ester	0.01		0.08	0.34		1.03	
Benzoic acid ethyl ester		0.29	1.06	3.39	4.95	9.63	
Benzeneacetic acid ethyl ester					0.21		
Butanedioic acid diethyl ester			0.14	0.36	1.42	2.30	
Octanoic acid 3-methylbutyl ester				0.79			
3-methyl-1-Butanol acetate	0.02	0.21	0.59	0.19	0.91	2.07	2.23
Isopentyl hexanoate				0.38	0.52		
Amyl Nitrite		0.55	1.91			5.89	
Acetic acid phenylethyl ester	0.12	0.06		0.42	0.90	1.23	

acid								
Acetic acid	0.10		3.20	8.18			22.13	
Hexanoic acid	0.16				2.00		5.04	
2-methyl-Propanoic acid	0.07							
3-methyl-Butanoic acid	0.14	0.57						
hydroxy-Acetic acid							0.44	
phenol								
Phenol	0.02						1.74	
2-methoxy-Phenol	0.06	0.13	0.09		0.89	1.49	2.46	
4-ethyl-2-methoxy-Phenol	0.09	0.27	0.24	0.30	1.17	5.85	7.25	
2-Methoxy-4-vinylphenol	0.20	0.83	0.86	1.43	6.65	10.43	14.05	
other								
Benzothiazole	0.05	6.42	1.47	4.40	2.89	7.85	6.27	
2,3-dihydro-Benzofuran	0.01							
2-hydroxy-N,3,3-trimethyl								
-Butanamide		0.07						
2-Methoxyethyl ether		0.09						
Acetamide		0.07						
N-(2-methylpropyl)-Aceta								
mide,							0.70	0.27
Methylamine							0.13	
Vinylfuran								1.03

b								
Relative content of volatile compounds in JB3 fermentation stages(mg/l)								
No.	Compounds	Day 0	Day 2	Day 4	Day 6	Day 8	Day 10	Day12
alkane								
	Heneicosane	0.12		0.55				
	Pentacosane		2.09	0.97				
	2,4,4-trimethyl-Hexane							0.42
	3,7-dimethylnonane	0.02		0.04		0.40		0.79
	3,7-dimethyldecane							0.28

3-methylundecane	0.03						
3,8-dimethyundecane,	0.03						
6-methyl- Tridecane			0.17				
3,4,5,6-tetramethyloctane	0.05						
2,6,10,15-tetramethyl-Heptadecane	0.40	0.17					
cis-1-ethyl-3-methyl-Cyclopentane	0.01						
2,2'-oxybis-Pentane	0.01						
2-(1-hydroxy-2-propyl)-1,3-dimethyl-Cyclopentane				0.09			
ethoxymethyl-Oxirane				0.07			
1-(1-methylpropoxy)-Butane					0.29		
1-iodo-Decane					0.30		
alcohol							
1-Propanol	1.23	0.67	1.29	1.49	2.56	3.00	
1-Butanol	0.06	0.05	0.10	0.11	0.29	0.25	
2-methyl-1-Propanol	3.90	2.45	5.11	6.74	13.83	13.40	
1-Pentanol	0.01						
3-methyl-1-Butanol	0.21	21.76	16.56	35.04	50.89	107.59	96.68
1-Hexanol	0.05	0.15	0.13	0.24	0.44	1.06	0.81
Heptanol	0.02			0.07			
1-Octanol		0.13	0.08	0.19	0.49	0.28	
1-Nonanol				0.35			
1-Undecanol		0.09	0.17		0.72		
2-ethyl-1-Hexanol	0.02						
4-methyl-3-Hexanol		0.14			0.58	0.69	
2-butyl-1-Octanol					0.35		
6-methyl-1-Heptanol				0.17			
2,3-dimethyl-1-Pentanol		0.01					
3-ethoxy-1-Propanol	0.08						
1-(1-methylethoxy)-2-Prop			0.85				

ester							
Hexadecanoic acid ethyl ester	1.95	2.86	3.71	5.02	9.87	24.11	17.12
Octadecanoic acid ethyl ester	0.03						
(E)-9-Octadecenoic acid ethyl ester	0.76	1.38	1.65	2.34	2.95	10.12	7.38
9,12-Octadecadienoic acid ethyl ester		0.71		0.74	1.57	5.83	4.81
Eicosanoic acid, ethyl ester						0.53	
2-methyl-Butanoic acid ethyl ester				0.08	0.28	0.27	
3-methyl-Butanoic acid ethyl ester				0.10			
Butanedioic acid diethyl ester				0.08	0.29	1.22	1.21
3-methyl-1-Butanol acetate		0.34	0.38	0.59	0.90	2.00	
Acetic acid methylpropyl ester				0.07			
Acetic acid phenylethyl ester		0.09	0.09	0.06	0.39	0.98	0.60
Isopentyl hexanoate					0.24		
Amyl Nitrite					1.38	2.36	2.34
Formic acid heptyl ester							0.49
Sulfurous acid butyl decyl ester		0.12	0.14			1.00	
Sulfurous acid hexyl octyl ester	0.01						
Sulfurous acid ethylhexyl isohexyl ester				0.17			
Oxalic acid-6-ethyloct-3-yl heptyl ester				0.52			
Pentafluoropropionic acid		0.07					

undecenyl ester						
1,2-Benzenedicarboxylic acid bis(2-methylpropyl) ester	0.07			3.08		
aldehyde						
Nonanal	0.02	0.23		0.24	0.48	
2-methyl-Pentanal		0.06				
3-methyl-Hexanal		0.05			0.49	
Hydroxy Acetaldehyde	0.03					
Methoxy Acetaldehyde	0.03					
4-methyl-Benzaldehyde		0.07		0.28		0.54
ketone						
2-Octanone	1.14		1.18	12.42	29.78	6.56
3-hydroxy-2-Butanone	0.56	0.14	0.09	0.08		
5-hydroxy-2-Pentanone					0.48	
4-Hydroxy-3-hexanone	0.19					
1,3-dihydroxy-2-Propanone	0.04					
3,5-dimethyl-4H-Pyran-4-one	0.01					
5-ethylidihydro-2(3H)-Furanone	0.01	0.06				
5-hexyldihydro-2(3H)-Furanone					1.49	
dihydro-5-propyl-2(3H)-Furanone		0.09	0.08	0.61		1.29
acid						
Acetic acid		3.47	1.45	2.72		
Hexanoic acid	0.1		0.51			
2-methyl-Propanoic acid	0.08	0.64		0.37		
3-methyl- Butanoic acid		0.77				
phenol						
Phenol	0.04					

2-methoxy-Phenol	0.04					0.66	
4-ethyl-2-methoxy-Phenol	0.53	1.22	0.49	1.16	6.01	15.12	10.11
2-Methoxy-4-vinylphenol	1.11	2.36	1.87	2.26	10.20	27.61	22.35
other							
2,3-dihydro- Benzofuran	0.07					0.88	
methoxy-phenyl-Oxime	0.02						
Benzothiazole	0.17	4.96	0.97	7.40	1.74	7.36	3.75
2-(2-butoxyethoxy)-Ethanol		0.08					
Acetamide			0.04				
(E)-5-Decene				0.09			
N-(2-methylpropyl)-Acetamide					0.11	0.82	0.23
Phenanthrene					2.55		
1,3,5,7-Cyclooctatetraene						0.31	
9-methylene-9H-Fluorene							2.22

Table S4. Comparisons of alpha diversity indice among the two kinds of sorghum.

Estimators	shannon	simpson
Pvalue(JB3_D0-JB3_D10)	0.008879	0.104
Pvalue(JB3_D0-JB3_D12)	0.01504	0.009197
Pvalue(JB3_D0-JB3_D2)	0.1906	0.5166
Pvalue(JB3_D0-JB3_D4)	0.0008832	0.005293
Pvalue(JB3_D0-JB3_D6)	0.003188	0.001154
Pvalue(JB3_D0-JB3_D8)	0.001705	0.000384
Pvalue(JB3_D0-JZ22_D0)	0.1258	0.2563
Pvalue(JB3_D0-JZ22_D10)	0.04263	0.03221
Pvalue(JB3_D0-JZ22_D12)	0.01823	0.007066
Pvalue(JB3_D0-JZ22_D2)	0.9167	0.363
Pvalue(JB3_D0-JZ22_D4)	0.001686	0.001699
Pvalue(JB3_D0-JZ22_D6)	0.001731	0.002269
Pvalue(JB3_D0-JZ22_D8)	0.02023	0.001444
Pvalue(JB3_D10-JB3_D12)	0.8957	0.6109

Pvalue(JB3_D10-JB3_D2)	0.9931	0.8698
Pvalue(JB3_D10-JB3_D4)	0.01753	0.06244
Pvalue(JB3_D10-JB3_D6)	0.4479	0.2676
Pvalue(JB3_D10-JB3_D8)	0.04505	0.08367
Pvalue(JB3_D10-JZ22_D0)	0.2831	0.6782
Pvalue(JB3_D10-JZ22_D10)	0.106	0.3669
Pvalue(JB3_D10-JZ22_D12)	0.7653	0.6041
Pvalue(JB3_D10-JZ22_D2)	0.1218	0.1436
Pvalue(JB3_D10-JZ22_D4)	0.08265	0.1586
Pvalue(JB3_D10-JZ22_D6)	0.05594	0.1226
Pvalue(JB3_D10-JZ22_D8)	0.6279	0.5643
Pvalue(JB3_D12-JB3_D2)	0.9752	0.7219
Pvalue(JB3_D12-JB3_D4)	0.004092	0.06039
Pvalue(JB3_D12-JB3_D6)	0.1916	0.1352
Pvalue(JB3_D12-JB3_D8)	0.006498	0.02438
Pvalue(JB3_D12-JZ22_D0)	0.2942	0.4054
Pvalue(JB3_D12-JZ22_D10)	0.001308	0.002487
Pvalue(JB3_D12-JZ22_D12)	0.4448	0.8701
Pvalue(JB3_D12-JZ22_D2)	0.1403	0.1328
Pvalue(JB3_D12-JZ22_D4)	0.02186	0.08225
Pvalue(JB3_D12-JZ22_D6)	0.009841	0.07162
Pvalue(JB3_D12-JZ22_D8)	0.1458	0.7632
Pvalue(JB3_D2-JB3_D4)	0.2435	0.3012
Pvalue(JB3_D2-JB3_D6)	0.7859	0.5374
Pvalue(JB3_D2-JB3_D8)	0.3682	0.3329
Pvalue(JB3_D2-JZ22_D0)	0.5595	0.9541
Pvalue(JB3_D2-JZ22_D10)	0.5048	0.8416
Pvalue(JB3_D2-JZ22_D12)	0.9344	0.719
Pvalue(JB3_D2-JZ22_D2)	0.2252	0.244
Pvalue(JB3_D2-JZ22_D4)	0.4739	0.4411
Pvalue(JB3_D2-JZ22_D6)	0.4057	0.3989
Pvalue(JB3_D2-JZ22_D8)	0.8871	0.7006
Pvalue(JB3_D4-JB3_D6)	0.005878	0.1082

Pvalue(JB3_D4-JB3_D8)	0.08525	0.723
Pvalue(JB3_D4-JZ22_D0)	0.03221	0.0672
Pvalue(JB3_D4-JZ22_D10)	0.001032	0.0216
Pvalue(JB3_D4-JZ22_D12)	0.00591	0.05959
Pvalue(JB3_D4-JZ22_D2)	0.0397	0.06368
Pvalue(JB3_D4-JZ22_D4)	0.02977	0.2431
Pvalue(JB3_D4-JZ22_D6)	0.0524	0.3782
Pvalue(JB3_D4-JZ22_D8)	0.006079	0.049
Pvalue(JB3_D6-JB3_D8)	0.02472	0.05254
Pvalue(JB3_D6-JZ22_D0)	0.1591	0.2133
Pvalue(JB3_D6-JZ22_D10)	0.01594	0.01471
Pvalue(JB3_D6-JZ22_D12)	0.1536	0.1342
Pvalue(JB3_D6-JZ22_D2)	0.09773	0.103
Pvalue(JB3_D6-JZ22_D4)	0.0851	0.3765
Pvalue(JB3_D6-JZ22_D6)	0.03791	0.2368
Pvalue(JB3_D6-JZ22_D8)	0.1202	0.1629
Pvalue(JB3_D8-JZ22_D0)	0.05376	0.08993
Pvalue(JB3_D8-JZ22_D10)	0.00114	0.005739
Pvalue(JB3_D8-JZ22_D12)	0.009003	0.02177
Pvalue(JB3_D8-JZ22_D2)	0.05416	0.07402
Pvalue(JB3_D8-JZ22_D4)	0.2741	0.2267
Pvalue(JB3_D8-JZ22_D6)	0.625	0.4378
Pvalue(JB3_D8-JZ22_D8)	0.009011	0.01034
Pvalue(JZ22_D0-JZ22_D10)	0.8961	0.7635
Pvalue(JZ22_D0-JZ22_D12)	0.3261	0.4016
Pvalue(JZ22_D0-JZ22_D2)	0.3042	0.1825
Pvalue(JZ22_D0-JZ22_D4)	0.071	0.1432
Pvalue(JZ22_D0-JZ22_D6)	0.05979	0.1173
Pvalue(JZ22_D0-JZ22_D8)	0.3681	0.3785
Pvalue(JZ22_D10-JZ22_D12)	0.003283	0.0001959
Pvalue(JZ22_D10-JZ22_D2)	0.3104	0.2184
Pvalue(JZ22_D10-JZ22_D4)	0.00384	0.01625
Pvalue(JZ22_D10-JZ22_D6)	0.001708	0.01737

Pvalue(JZ22_D10-JZ22_D8)	0.005956	0.01487
Pvalue(JZ22_D12-JZ22_D2)	0.1484	0.1323
Pvalue(JZ22_D12-JZ22_D4)	0.02384	0.08049
Pvalue(JZ22_D12-JZ22_D6)	0.0125	0.07012
Pvalue(JZ22_D12-JZ22_D8)	0.2049	0.7963
Pvalue(JZ22_D2-JZ22_D4)	0.06363	0.08807
Pvalue(JZ22_D2-JZ22_D6)	0.05772	0.08119
Pvalue(JZ22_D2-JZ22_D8)	0.1582	0.1279
Pvalue(JZ22_D4-JZ22_D6)	0.489	0.6832
Pvalue(JZ22_D4-JZ22_D8)	0.02202	0.07227
Pvalue(JZ22_D6-JZ22_D8)	0.01215	0.05853

Table S5. Bacterial genera abundance during different fermentation stages of JZ22 and JB3.

OTU ID	JZ22 D0	JZ22 D2	JZ22 D4	JZ22 D6	JZ22 D8	JZ22 D10	JZ22 D12	JB3 D0	JB3 D2	JB3 D4	JB3 D6	JB3 D8	JB3 D10	JB3 D12
g__[Eubacterium]_coprostanoligenes_group	0	0	0	0	0	0	0	0	0	0	2	1	0	0
g__[Eubacterium]_eligens_group	0	0	0	0	0	1	0	0	0	1	0	0	0	1
g__[Eubacterium]_hallii_group	1	0	0	0	1	1	0	0	0	1	1	2	0	2
g__[Eubacterium]_rectale_group	0	0	2	1	1	5	6	0	0	5	1	3	4	9
g__[Eubacterium]_ruminantium_group	0	0	0	0	0	0	1	0	0	0	0	0	0	0
g__[Eubacterium]_ventriosum_group	0	0	0	0	0	0	0	0	0	0	0	2	0	0
g__[Ruminococcus]_torques_group	0	0	0	0	1	1	2	0	0	0	0	5	3	1
g__Acetobacter	16	4	11	10	5	1	5	2	15	3	4	8	3	3
g__Achromobacter	1	0	3	4	4	7	3	0	1	7	5	7	5	7
g__Acidibacter	0	0	0	0	0	0	0	0	0	1	0	0	0	0
g__Acinetobacter	4	1	17	6	6	10	68	5	4	11	7	15	9	9
g__Alistipes	0	0	0	0	0	0	0	0	0	0	1	0	1	0
g__Alloprevotella	0	0	0	0	0	0	0	0	0	1	0	0	0	0
g__Anaerococcus	0	0	0	0	0	0	0	0	0	1	0	0	0	1
g__Anaerostipes	0	0	0	0	1	1	3	1	0	3	1	2	1	3
g__Apibacter	15	19	49	91	14	11	4	7	42	64	31	37	10	7
g__Aquabacterium	3	1	7	4	5	7	7	1	2	10	5	8	8	7

g__Atopobium	0	0	0	0	0	0	22	0	0	0	0	0	0	0
g__Azospirillum	0	0	1	0	0	0	0	0	0	0	0	0	0	0
g__Bacillus	37925	36148	33308	34736	37303	37942	37252	38918	33378	32132	33412	31541	35042	35857
g__Bacteroides	3	1	1	3	4	4	5	1	5	3	2	3	3	4
g__Bdellovibrio	0	0	0	1	1	1	0	0	1	0	1	1	2	3
g__Bifidobacterium	0	2	1	3	3	8	11	0	3	15	5	13	10	17
g__Bilophila	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Blautia	1	1	2	2	3	8	11	1	2	9	4	16	8	14
g__Bradyrhizobium	0	0	1	1	1	1	2	1	1	2	1	2	1	1
g__Brevibacillus	1	0	1	88	32	7	1	38	78	972	3488	4400	1936	2080
g__Brevundimonas	1	1	3	1	0	0	0	0	1	2	0	1	0	0
g__Burkholderia-Paraburkholderia	1	1	13	18	12	15	9	2	4	7	10	17	9	12
g__Carnimonas	1	0	0	1	0	0	0	1	0	0	1	0	0	0
g__Catenibacterium	0	0	0	0	0	0	0	0	0	0	0	0	1	0
g__Cellulosimicrobium	0	0	0	0	0	0	0	0	0	0	0	0	0	1
g__Cetobacterium	0	0	0	0	0	0	0	0	0	1	0	0	1	0
g__Chroococcidiopsis	0	0	0	0	11	0	0	0	0	0	0	0	0	0
g__Chryseobacterium	0	0	0	0	0	1	9	0	0	0	0	0	0	0
g__Cloacibacterium	0	0	0	0	0	0	2	0	0	1	0	0	0	0
g__Clostridium_sensu_stricto_1	0	1	1	1	1	1	0	0	0	7	2	2	4	2
g__Clostridium_sensu_stricto_10	0	0	0	0	0	0	0	0	0	0	1	0	0	0
g__Clostridium_sensu_stricto_13	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Collinsella	0	1	1	0	1	5	6	0	1	2	2	7	2	5
g__Coprococcus_1	0	0	0	0	0	0	0	0	0	1	0	1	0	1
g__Coprococcus_3	1	0	0	0	1	1	1	0	0	0	0	1	0	1
g__Corynebacterium_1	1	2	7	4	4	3	5	1	1	4	6	4	2	5
g__Cupriavidus	0	0	0	0	0	1	0	0	0	2	0	2	1	1
g__Deinococcus	0	0	0	0	3	0	0	0	0	0	0	0	1	0
g__Desulfovibrio	1	1	0	0	0	0	0	0	0	1	0	0	0	0
g__Dialister	0	0	0	1	0	0	4	0	0	1	1	0	0	2
g__Dorea	0	1	0	1	1	2	1	0	0	2	1	3	1	0
g__Enhydrobacter	0	0	0	1	0	3	0	0	0	0	0	0	0	5
g__Enterococcus	1	1	3	1	0	0	3	0	1	0	1	0	1	1

g_norank_c_BD7-11	0	0	1	1	3	2	3	0	0	2	2	3	2	2
g_norank_c_Cyanobacteria	357	753	1042	924	674	344	272	132	2378	2728	1331	1173	1096	695
g_norank_c_Gemmatimonadetes	0	2	0	0	0	1	0	0	0	0	0	0	0	0
g_norank_f_0319-6G20	0	0	1	1	1	2	1	0	1	0	1	2	2	2
g_norank_f_Actinopolysporaceae	0	1	8	3	2	5	5	0	1	2	4	7	4	6
g_norank_f_Anaerolineaceae	0	0	0	0	0	0	0	0	0	0	1	0	0	0
g_norank_f_Bacteroidales_S24-7_group	2	0	2	0	0	0	0	0	1	2	1	0	0	1
g_norank_f_Cytophagaceae	0	0	0	0	0	0	1	0	0	0	0	0	0	0
g_norank_f_Elev-16S-1332	0	0	0	0	0	0	0	1	0	0	0	0	0	0
g_norank_f_env.OPS_17	0	0	0	0	0	0	0	0	0	0	0	0	1	0
g_norank_f_Holophagaceae	0	0	0	0	1	0	0	0	0	0	1	0	0	1
g_norank_f_Longimicrobiaceae	0	1	0	0	0	0	0	0	0	0	0	0	0	0
g_norank_f_Mitochondria	102	256	285	353	205	42	19	24	684	290	133	181	224	59
g_norank_f_Neisseriaceae	0	0	1	0	0	0	0	0	0	0	1	1	0	0
g_norank_f_Nitrosomonadaceae	0	0	0	0	1	0	0	0	0	0	0	0	0	0
g_norank_f_Porphyrimonadaceae	0	0	0	1	0	0	0	0	0	0	0	0	0	0
g_norank_f_Ruminococcaceae	0	0	0	0	0	0	0	0	0	0	1	1	1	1
g_norank_f_Synergistaceae	0	0	0	0	0	0	1	0	0	0	0	0	0	0
g_norank_f_Syntrophaceae	0	0	0	0	0	0	0	0	0	0	0	1	0	1
g_norank_f_Unknown_Family	0	0	1	1	0	0	0	0	0	0	0	0	0	0
g_norank_p_Saccharibacteria	0	0	0	0	0	0	0	0	0	0	0	1	0	0
g_norank_p_WWE3	1	0	3	0	0	0	0	0	16	1	0	0	0	0
g_Novosphingobium	0	0	1	0	0	1	0	1	1	1	0	1	1	1
g_Oceanobacillus	0	3	1	1	1	0	0	0	0	1	0	4	0	0
g_Paenibacillus	940	322	180	247	41	264	898	526	1111	553	189	635	349	162
g_Paeniclostridium	1	0	0	1	0	2	1	0	0	0	1	0	1	0
g_Pantoea	1	0	4	3	2	1	0	0	8	1	1	1	2	1
g_Parabacteroides	0	0	0	0	0	0	1	0	0	0	0	1	0	0
g_Paracoccus	1	0	2	1	0	1	0	0	0	0	0	1	0	1
g_Parasutterella	1	0	0	0	0	0	0	0	1	0	0	0	0	0
g_Pediococcus	38	58	92	182	20	18	21	20	31	22	2	8	7	6
g_Pelomonas	3	1	1	6	6	7	3	2	2	14	4	6	6	9
g_Perlucidibaca	0	0	0	0	0	1	0	0	0	1	0	0	0	0

g_Phascolarctobacterium	0	0	0	0	0	0	2	0	0	1	0	0	0	0
g_Porphyrromonas	0	0	0	0	0	0	2	0	0	0	0	0	0	0
g_Prevotella	0	0	0	0	0	0	70	0	0	2	0	0	0	0
g_Prevotella_1	0	0	2	0	0	0	0	0	0	0	0	0	0	0
g_Prevotella_6	0	0	0	0	0	0	5	0	0	0	0	0	0	0
g_Prevotella_9	0	3	1	3	5	18	16	2	1	2	0	3	1	2
g_Propionibacterium	0	1	2	4	2	1	3	0	0	2	1	1	1	4
g_Pseudomonas	2	4	17	7	2	4	3	0	3	7	2	4	7	2
g_Pseudorhodofera	0	0	0	1	0	0	0	0	0	0	0	0	0	0
g_Ralstonia	43	16	114	133	108	162	128	29	38	194	90	139	144	150
g_Rhizobium	0	0	0	0	0	0	1	0	0	0	0	0	1	0
g_Rhizomicrobium	0	0	0	0	0	1	0	0	0	0	0	0	0	1
g_Rhodococcus	38	13	93	128	81	123	127	35	29	199	78	140	81	163
g_Rikenellaceae_RC9_gut_group	0	0	0	0	1	0	0	0	0	1	0	0	0	0
g_Roseburia	0	0	1	0	0	1	4	0	1	0	0	1	1	1
g_Roseomonas	0	0	0	0	0	0	0	0	0	1	0	0	0	0
g_Rubellimicrobium	0	0	2	0	0	0	0	0	0	1	0	0	0	0
g_Ruminiclostridium	0	0	0	0	0	0	0	0	0	1	0	0	0	0
g_Ruminococcaceae_UCG-002	0	0	0	0	0	0	0	0	0	0	0	0	0	1
g_Ruminococcaceae_UCG-010	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g_Ruminococcus_1	0	0	1	0	0	4	1	0	0	1	0	4	2	2
g_Ruminococcus_2	2	0	0	0	0	0	1	1	0	5	0	3	1	1
g_Rummeliibacillus	6	28	5	6	2	6	5	8	44	65	31	75	25	10
g_Saccharopolyspora	7	26	82	76	47	46	41	4	34	43	58	86	47	72
g_Sediminibacterium	0	0	0	0	0	0	0	0	1	0	0	0	0	0
g_Shuttleworthia	1	1	0	0	0	0	232	0	0	1	0	0	0	0
g_Sneathia	0	0	0	0	0	0	11	0	0	0	0	0	0	0
g_Solibacillus	0	0	0	0	0	2	0	0	0	0	0	0	1	1
g_Sorangium	0	0	1	0	0	0	0	0	1	1	0	0	1	0
g_Sphingobacterium	0	2	3	3	0	0	0	0	0	1	0	1	0	0
g_Sphingomonas	0	0	0	0	1	1	6	0	0	1	0	1	1	0
g_Sporosarcina	0	0	0	0	0	0	0	0	0	1	0	0	0	0
g_Staphylococcus	8	38	86	123	22	16	11	6	76	15	7	8	5	5

g_Stenotrophomonas	0	0	1	0	1	0	6	0	0	1	0	1	3	3
g_Streptococcus	1	0	0	3	0	0	10	0	1	4	0	1	0	4
g_Streptomyces	13	79	186	206	88	119	68	3	147	102	115	132	122	144
g_Subdoligranulum	0	0	0	0	0	1	2	0	1	5	3	6	4	6
g_Sulfuritalea	0	0	0	0	0	0	0	0	0	0	0	0	0	0
g_Sva0081_sediment_group	0	0	0	0	0	0	0	1	0	0	0	0	0	0
g_Terrabacter	0	0	1	0	0	4	1	0	0	1	0	0	0	2
g_Terrisporobacter	0	0	0	0	0	0	0	0	0	1	0	0	0	0
g_Thermoactinomyces	0	0	1	0	0	1	0	0	0	1	2	2	1	0
g_Thermus	0	0	0	0	0	0	1	0	0	1	0	1	1	0
g_unclassified_c_Betaproteobacteria	0	0	0	0	0	1	0	0	0	0	0	0	1	0
g_unclassified_c_Gemmatimonadetes	0	0	1	0	0	0	0	0	0	0	0	0	0	0
g_unclassified_f_Comamonadaceae	0	0	0	0	3	0	0	0	0	0	0	0	0	0
g_unclassified_f_Corynebacteriaceae	0	0	1	1	0	0	1	0	0	1	0	0	1	0
g_unclassified_f_Enterobacteriaceae	1	1	4	6	4	0	0	0	0	4	8	3	4	0
g_unclassified_f_Erythrobacteraceae	0	0	0	0	0	0	0	0	0	0	0	1	0	0
g_unclassified_f_Lachnospiraceae	0	0	0	0	0	0	2	0	1	1	0	2	1	0
g_unclassified_f_Peptostreptococcaceae	0	0	0	1	1	1	1	0	1	2	1	1	3	2
g_unclassified_f_Prevotellaceae	0	0	0	1	0	0	1	0	0	0	0	0	0	0
g_unclassified_k_norank	0	2	4	0	0	0	1	1	4	5	2	1	9	1
g_unclassified_o_Bacillales	0	0	0	1	0	0	0	1	2	3	12	28	12	6
g_unclassified_o_Rhizobiales	0	0	0	0	1	0	0	0	0	0	0	1	0	0
g_unclassified_p_Firmicutes	0	0	0	0	0	0	0	0	0	0	0	0	0	1
g_unclassified_p_Proteobacteria	10	4	26	3	6	8	1	1	19	13	16	6	21	8
g_Undibacterium	0	0	0	0	0	1	0	0	0	1	1	2	1	1
g_Vibrio	0	0	0	0	1	0	0	0	0	1	0	0	0	0
g_Virgibacillus	0	0	0	0	0	0	0	0	0	1	0	0	0	0
g_Weissella	192	2134	4073	2294	1087	564	312	51	1702	2154	743	933	495	187

Table S6. Predicted gene functions related to KEGG pathways at levels 3

	JZ22	JZ22	JZ22	JZ22	JZ22	JZ22	JZ22	JZ22	JB3	JB3	JB3	JB3	JB3	JB3	JB3
	D0	D2	D4	D6	D8	D10	D12	D12	D0	D2	D4	D6	D8	D10	D12
1,1,1-Trichloro-2,2-bis(4-chlorophenyl)ethane	34	13	89	113	83	128	112	112	28	30	173	74	121	100	137

(DDT) degradation	67928	65210	67897	67926	68526	68130	71610	66753	72660	73077	71016	71265	70313	69745
ABC transporters	7	0	0	2	3	8	7	2	6	1	6	0	7	2
Adherens junction	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Adipocytokine signaling pathway	10320	9943	10688	10885	10831	10801	10901	10001	11204	11864	10842	10808	10882	11010
African trypanosomiasis	123	259	315	389	235	80	86	38	697	422	442	592	413	286
	17446	17041	17043	17314	17755	17829	18219	17613	18621	18497	18023	17685	18033	17993
Alanine, aspartate and glutamate metabolism	4	3	6	2	5	8	9	3	6	8	2	9	0	9
Aldosterone-regulated sodium reabsorption	0	0	0	0	0	0	0	0	0	0	0	1	1	0
Alzheimer's disease	10367	11059	11284	11665	10892	10256	10284	10001	13547	11672	10522	10517	10917	10184
Amino acid metabolism	56996	56797	57012	57168	59015	58794	57525	58572	62986	63327	62583	61926	61687	61042
	22329	22657	23151	23165	22986	22613	23204	22318	25696	24950	23225	22986	23359	22781
Amino acid related enzymes	1	9	7	0	9	4	2	0	2	3	7	3	4	4
	23958	23437	23731	23660	24194	24319	25015	24318	25857	25023	24284	23675	24363	24147
Amino sugar and nucleotide sugar metabolism	5	6	7	8	5	0	6	0	7	6	2	7	1	2
	15475	16435	17465	17109	16332	15644	16121	15139	19347	18844	16508	16558	16621	15847
Aminoacyl-tRNA biosynthesis	6	0	3	9	2	8	5	5	3	9	6	1	8	8
Aminobenzoate degradation	89724	85786	85733	87968	91638	93950	92263	93412	89300	91345	92258	92029	93290	95501
Amoebiasis	13290	12536	11807	12111	13347	13725	13333	14052	13125	12009	12818	12185	13249	13317
Amyotrophic lateral sclerosis (ALS)	22104	20794	18887	19800	22013	22862	22112	23853	21242	19119	20988	20552	22201	22382
Antigen processing and presentation	5080	5085	4868	5114	5009	4967	5216	4904	6113	5560	5140	4918	5081	4919
Apoptosis	170	697	1159	884	458	208	143	51	1040	778	302	415	366	148
Arachidonic acid metabolism	14484	14159	13441	14019	14751	14891	14497	14701	15180	14992	14810	14580	15102	15029
	24220	23627	24080	24239	24713	24582	25187	24156	26159	26150	24995	24635	25034	24834
Arginine and proline metabolism	4	4	7	3	1	0	8	8	7	0	2	3	1	0
Arrhythmogenic right ventricular cardiomyopathy (ARVC)	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ascorbate and aldarate metabolism	54560	50349	49574	50534	54361	56019	56159	56564	51955	47896	51468	49117	52765	53853
Atrazine degradation	2656	3115	4442	4407	2847	2130	2769	892	4641	6058	2911	2736	2365	2166
	12879	11986	11313	11739	12536	12881	13750	13107	11822	11350	12458	12307	12573	12806
Bacterial chemotaxis	0	1	6	6	7	7	6	2	0	1	1	9	1	3
Bacterial invasion of epithelial cells	181	366	512	448	341	170	145	134	1237	1534	750	678	609	408
Bacterial motility proteins	27587	26438	25472	26296	27546	27703	29198	27523	27900	27806	27943	27540	28019	28001

	2	1	0	6	3	1	2	1	5	2	8	1	6	1
Bacterial secretion system	73197	78532	82884	82780	77584	73420	75031	70416	95529	88801	76689	76368	78023	73334
Bacterial toxins	14623	14618	15354	14977	15118	14993	15081	15248	16160	17367	16550	16737	16146	15990
Basal transcription factors	116	57	115	149	75	116	162	66	176	253	389	553	288	305
Base excision repair	66617	67500	69144	69848	68625	67498	68996	65384	75688	75121	70358	71073	70534	69183
Benzoate degradation	71340	69913	73739	75200	73864	75500	74986	71770	70997	79454	76041	78338	75682	78382
Betalain biosynthesis	12	18	57	65	41	58	40	7	34	64	40	56	55	61
Bile secretion	7	29	77	81	36	47	39	2	55	42	46	58	51	59
Biosynthesis and biodegradation of secondary metabolites	9751	10161	10293	10542	10220	10436	10193	9977	11442	12167	11153	11047	10816	10928
Biosynthesis of 12-, 14- and 16-membered macrolides	15	85	217	231	107	136	83	2	156	116	133	164	139	170
Biosynthesis of ansamycins	13598	12706	12155	12498	13559	14072	14898	14301	13609	12650	13152	12802	13666	13786
Biosynthesis of siderophore group nonribosomal peptides	29198	28082	24021	25701	28763	30823	28755	33226	29093	27265	29330	27475	29834	30564
Biosynthesis of type II polyketide backbone	15	75	205	218	95	125	85	5	140	110	125	165	135	165
Biosynthesis of type II polyketide products	4	17	55	55	25	32	24	2	33	28	33	47	35	44
Biosynthesis of unsaturated fatty acids	56356	54543	52742	54638	57104	58528	57628	58258	58960	57366	57327	56294	58297	58706
Biosynthesis of vancomycin group antibiotics	885	1342	2587	1969	1353	863	1589	360	2999	3725	2023	2164	1668	1258
Biotin metabolism	28214	27191	26961	27491	28632	28798	29648	28894	31060	30171	29315	27939	29092	28905
Bisphenol degradation	39900	37674	36312	37550	40243	42326	41123	42836	38514	36669	38741	37664	40040	41446
Bladder cancer	23	23	94	107	68	94	86	16	49	113	66	99	80	108
	15754	15452	15817	16129	16178	16353	16377	15838	16038	16392	16223	16260	16245	16558
Butanoate metabolism	9	4	2	3	8	7	0	0	5	4	6	8	1	8
Butirosin and neomycin biosynthesis	5850	5956	7082	6645	6266	5813	6796	5262	7499	7864	6579	6869	6519	6157
C5-Branched dibasic acid metabolism	48767	46900	45519	47342	48462	49266	50428	49367	52528	51526	49544	48223	49552	49524
CAM ligands	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Caffeine metabolism	310	104	600	442	334	191	440	36	41	69	47	72	56	75
Calcium signaling pathway	177	365	504	442	334	168	133	65	1177	1340	662	581	538	342
Caprolactam degradation	16520	15213	18362	18810	17927	18155	18844	15261	15155	17902	16856	17907	17092	18550
Carbohydrate digestion and absorption	5075	4898	4841	4903	5196	5049	5310	5023	5532	5463	4918	4836	5197	5014
Carbohydrate metabolism	52518	49552	50084	50181	52433	52702	54131	52821	55200	52291	51515	49220	51866	51506
Carbon fixation in photosynthetic organisms	63864	67007	72598	71191	68337	64470	67857	60982	85703	86719	72013	71287	71254	67043

D-Alanine metabolism	26997	26505	25139	25593	26990	27856	27334	28958	27707	26876	27530	26491	27560	27773
D-Arginine and D-ornithine metabolism	4677	4455	4183	4357	4643	4733	4651	4886	4228	4214	4532	4391	4584	4705
D-Glutamine and D-glutamate metabolism	25084	25316	26617	26187	25899	25293	26049	24673	28394	27702	25701	25332	25790	25168
	38058	39620	41425	41049	39765	38469	39368	37234	45780	45244	40399	40333	40517	39057
DNA repair and recombination proteins	3	3	7	7	5	9	3	7	3	4	2	7	4	2
DNA replication	82750	87366	92177	90762	87056	83414	85560	80681	99647	96932	85934	86150	87244	83631
	14063	14839	15700	15464	14778	14149	14624	13639	17135	16779	14780	14793	14894	14257
DNA replication proteins	9	7	8	2	3	7	7	1	9	7	3	1	9	4
Dilated cardiomyopathy (DCM)	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dioxin degradation	18133	18677	18475	18428	18718	19364	18363	19656	20326	21136	20519	20357	20036	20228
Drug metabolism - cytochrome P450	16920	18374	20328	20115	18718	17716	17340	16163	24897	27706	21084	21149	20481	19393
Drug metabolism - other enzymes	47232	46920	46021	46421	47409	48616	48774	48868	47778	47042	47413	46572	47582	48205
ECM-receptor interaction	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Electron transfer carriers	8971	8650	7999	8349	8991	9307	8950	9491	9299	8821	9019	8579	9117	9207
Endocrine and other factor-regulated calcium reabsorption	0	0	0	0	0	0	0	0	0	0	0	1	1	0
Endocytosis	8	3	19	26	16	26	38	7	6	41	16	28	17	34
	11334	11122	11216	11439	11592	11634	11943	11343	12233	12186	11647	11553	11745	11719
Energy metabolism	5	6	4	9	5	8	2	7	4	9	7	2	5	5
Epithelial cell signaling in Helicobacter pylori infection	10392	10247	9622	10135	10049	10211	10711	10146	11300	11524	10480	10093	10239	10233
ErbB signaling pathway	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ether lipid metabolism	51	39	178	200	130	178	171	104	131	415	214	304	218	284
Ethylbenzene degradation	16578	16203	16179	16781	16333	16348	16473	16660	16405	19623	17277	17718	17068	17359
Fat digestion and absorption	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	11524	11282	11377	11608	11688	11621	11739	11405	12125	11964	11727	11679	11792	11729
Fatty acid biosynthesis	5	2	0	2	0	1	8	9	3	8	6	3	3	2
Fatty acid elongation in mitochondria	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	10150		10473	10671	10596	10677	10652	10022	10489	11237	10587	10707	10614	10894
Fatty acid metabolism	0	99174	4	6	9	3	9	1	2	3	5	9	8	7
Fc epsilon RI signaling pathway	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Fc gamma R-mediated phagocytosis	8	3	19	26	16	26	38	7	6	41	16	28	17	34
Flagellar assembly	15640	14588	13685	14236	15279	15686	16349	15981	13940	13305	14682	14416	15022	15364

sulfate														
Glycosaminoglycan degradation	128	122	240	271	124	186	529	70	280	278	445	620	356	387
Glycosphingolipid biosynthesis - ganglio series	25	66	160	175	84	115	144	9	121	100	96	124	110	135
Glycosphingolipid biosynthesis - globo series	5411	4816	5119	5219	5125	5233	6389	5022	4815	4381	4924	5133	5010	5141
Glycosphingolipid biosynthesis - lacto and neolacto series	0	0	0	0	0	0	1	0	0	0	0	0	0	0
Glycosylphosphatidylinositol(GPI)-anchor biosynthesis	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Glycosyltransferases	45483	51100	53840	52070	49124	47408	46947	45314	64906	67344	53286	51011	51608	48868
	12640	12200	12259	12563	12861	12951	13192	12623	13017	12798	12663	12364	12758	12852
Glyoxylate and dicarboxylate metabolism	0	8	6	2	9	5	9	1	2	0	6	8	6	7
GnRH signaling pathway	8	3	19	26	16	26	38	7	6	41	16	28	17	34
Hedgehog signaling pathway	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Hematopoietic cell lineage	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Hepatitis C	0	0	0	0	0	0	0	0	0	0	0	0	0	0
										10258				
Histidine metabolism	92833	90413	94870	94686	94691	93597	98312	90894	98168	6	95349	95359	95346	94989
		10755	11475	11241	10595	10070	10388		12674	12452	10670	10660	10713	10178
Homologous recombination	99688	1	8	1	4	9	3	96254	2	7	4	1	2	0
Huntington's disease	14726	14841	14394	15164	15353	14796	14404	14832	18429	16425	15642	15719	16175	15295
Hypertrophic cardiomyopathy (HCM)	1	0	1	0	1	1	3	0	0	2	0	3	3	4
Indole alkaloid biosynthesis	3	14	31	35	16	21	12	1	25	19	20	25	23	27
Influenza A	110	265	323	385	224	72	43	28	703	310	150	215	252	95
Inorganic ion transport and metabolism	24932	24470	25711	26016	25771	26157	26615	25544	28837	30280	28884	29881	28273	28241
Inositol phosphate metabolism	59653	55887	56091	56561	59868	61238	61212	61654	58673	53680	56654	54649	58291	58999
Insulin signaling pathway	6766	7396	8340	8136	7529	6539	7187	5715	11878	13252	8956	8690	8468	7459
Ion channels	5042	5735	6418	5977	5320	5164	5250	5044	6131	6502	5515	5265	5189	5106
Isoflavonoid biosynthesis	93	53	167	118	231	129	154	128	143	317	181	370	347	267
Isoquinoline alkaloid biosynthesis	5632	5344	6019	6059	5992	5658	6253	5248	6568	6674	6012	6392	6218	5985
Leishmaniasis	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Leukocyte transendothelial migration	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Limonene and pinene degradation	76251	71646	72386	74738	77399	79793	79098	78683	72518	74945	75768	75269	76937	79943
Linoleic acid metabolism	13932	13322	13058	13430	13926	14604	14467	14619	13048	13068	13433	13339	13743	14367

	14032	13888	14158	14439	14423	14385	14501	13892	15175	15213	14541	14494	14605	14580
Lipid biosynthesis proteins	7	9	7	7	5	5	1	8	3	5	3	3	0	6
Lipid metabolism	11831	12306	14788	14384	13412	12206	13218	10595	16970	17839	14259	14836	14339	13265
Lipoic acid metabolism	15302	15856	16064	16274	15866	15292	14995	14962	19277	18853	16545	16002	16326	15602
Lipopolysaccharide biosynthesis	1760	2802	4555	4144	3373	2364	2696	788	8773	10762	5362	5373	4947	3672
Lipopolysaccharide biosynthesis proteins	7160	9077	12090	10794	9283	7994	8841	6038	15666	18395	12136	12538	11265	9758
Long-term depression	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Long-term potentiation	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	10208	10219	10498	10573	10450	10259	10649	10007	11460	11310	10588	10589	10623	10408
Lysine biosynthesis	3	2	7	7	3	7	9	7	5	7	0	6	1	2
Lysine degradation	67351	63718	68140	69488	69321	69099	70714	64682	63683	66522	65311	65794	66393	68512
Lysosome	434	233	328	386	169	318	1118	238	628	446	246	530	351	345
MAPK signaling pathway	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MAPK signaling pathway - yeast	9709	9336	8682	9062	9839	9889	9627	10272	10108	10636	10148	10309	10540	10381
Measles	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Meiosis - yeast	4760	5295	5455	5448	5424	5140	4688	4869	8627	8867	6593	6049	6246	5688
Melanogenesis	9	4	26	30	25	37	28	6	9	45	20	31	32	34
Membrane and intracellular structural molecules	76070	75917	75437	76980	79219	78798	79219	78638	91254	89106	82867	81448	83611	81160
Metabolism of cofactors and vitamins	30382	29470	30113	30555	30444	30509	31224	30260	32728	34375	31979	31223	31157	31181
Metabolism of xenobiotics by cytochrome P450	16689	18296	20096	19892	18404	17456	16971	15915	24640	27068	20541	20231	19872	18811
	15729	15801	16201	16188	16220	16212	16705	15809	17892	18077	16551	16275	16533	16352
Methane metabolism	6	8	9	8	2	1	3	8	1	4	3	0	4	6
Mineral absorption	5428	5628	5805	5840	5721	5393	5314	5142	7966	8372	6829	6651	6453	5981
	10354	10940	11523	11351	10868	10432	10760	10061	12645	12354	10937	10931	10988	10527
Mismatch repair	7	2	1	3	5	5	8	7	3	4	9	7	3	4
N-Glycan biosynthesis	4656	4945	4853	4888	5014	4899	4575	4825	7527	7421	5881	5416	5660	5232
NOD-like receptor signaling pathway	5082	5085	4868	5129	5015	4969	5235	4978	6178	5913	5807	5744	5471	5328
Naphthalene degradation	58732	58501	58268	59503	59529	60827	59442	60688	60733	65089	60756	60063	60514	61827
Neuroactive ligand-receptor interaction	2	13	31	34	15	20	11	0	24	17	19	22	20	24
Neurotrophin signaling pathway	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Nicotinate and nicotinamide metabolism	57218	58304	62168	60990	59810	58156	60621	55668	65884	68901	61535	61543	61005	59659
	16335	15715	15216	15613	16411	16767	16868	16929	16882	16336	16443	15966	16614	16700
Nitrogen metabolism	0	4	8	0	5	3	9	9	6	8	5	1	9	4

Nitrotoluene degradation	956	745	2384	2065	1514	1250	2411	240	1640	2304	1251	1605	1274	1339
Non-homologous end-joining	13883	12960	12227	12824	13767	14378	14102	14438	12825	12102	13680	13755	14021	14416
Notch signaling pathway	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Novobiocin biosynthesis	15587	15080	15665	15969	16146	15779	16744	15145	17519	17751	16157	16237	16489	16156
Nucleotide excision repair	55653	57227	59739	59057	57750	56489	58320	54787	64242	62664	58124	58453	58523	56984
Nucleotide metabolism	9059	8768	9435	8913	9063	9318	9882	9565	8933	8674	9511	9499	9210	9356
Olfactory transduction	0	0	0	0	0	0	0	0	0	0	0	0	0	0
One carbon pool by folate	71123	73268	76391	75810	74010	72321	74721	69955	84060	83026	74896	74580	75225	73021
Oocyte meiosis	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Other glycan degradation	10733	9404	10316	10000	9713	10174	13152	10100	11315	9711	9405	9784	9777	9646
	41515	40935	38885	39654	41723	42762	41897	43706	41804	39741	40815	39285	41516	41861
Other ion-coupled transporters	0	9	9	6	3	7	2	8	3	5	0	5	2	7
Other transporters	30610	31238	32406	32138	31554	30809	32179	30043	37666	37806	33258	32661	32734	31580
Other types of O-glycan biosynthesis	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	27156	26629	26502	26677	27560	27724	27733	28038	29501	29401	28442	27847	28419	28156
Others	0	9	7	8	8	3	8	5	7	1	8	6	0	6
	17989	18628	19238	19541	19009	18207	18423	17595	23178	22581	20131	20087	20020	19064
Oxidative phosphorylation	6	2	4	4	9	9	1	4	0	4	1	4	0	1
PPAR signaling pathway	16658	16840	19240	19379	18117	17852	18167	15611	20183	22994	19216	19585	18686	18950
Pancreatic cancer	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pancreatic secretion	2	13	31	34	15	20	11	0	24	17	19	23	21	24
									10336	10451				
Pantothenate and CoA biosynthesis	90399	90196	92331	92770	92723	91705	94992	89823	7	5	96030	94693	95349	93582
Parkinson's disease	464	1022	1242	1506	931	328	249	129	2749	1316	597	862	1024	392
Pathogenic Escherichia coli infection	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pathways in cancer	10273	10466	10226	10755	10449	10061	10222	9938	12967	11654	10579	10321	10688	10129
Penicillin and cephalosporin biosynthesis	9573	8939	8982	9227	9519	9806	9798	9905	9933	9970	10126	10049	10004	10137
	15632	14748	14455	14550	15393	15857	16199	16104	14969	13613	14296	13577	14722	14941
Pentose and glucuronate interconversions	2	7	2	8	9	1	8	7	6	7	1	6	1	0
	13213	13410	13754	13552	13526	13482	13788	13325	15040	14971	13696	13371	13680	13445
Pentose phosphate pathway	3	4	5	2	3	8	8	5	1	5	9	9	4	7
	32921	33052	33215	33476	33855	33489	33985	33044	37498	37484	35259	34606	34945	34284
Peptidases	2	4	4	7	5	0	0	9	5	9	1	5	3	6

	10350	10995	11558	11338	10817	10442	10756	10109	12566	12506	11114	11118	11029	10623
Peptidoglycan biosynthesis	9	7	9	4	7	6	3	4	9	1	4	8	2	7
Peroxisome	52200	50810	49485	51131	53207	54013	53285	53767	55430	54319	53338	52484	54271	54414
Pertussis	236	396	671	611	470	351	383	100	1254	1574	785	761	704	528
Phagosome	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Phenylalanine metabolism	28940	27089	32137	32189	31444	30197	32425	26753	32327	36755	32725	35334	33107	33001
	10667	10309	10316	10577	10828	10757	11376	10523	11731	11928	11061	10958	11136	10989
Phenylalanine, tyrosine and tryptophan biosynthesis	8	7	2	4	3	2	7	3	8	0	2	5	7	0
Phenylpropanoid biosynthesis	23986	22021	22341	22440	23760	24144	27021	24185	25859	24085	23510	22983	24170	23833
Phosphatidylinositol signaling system	15708	16857	18050	17559	16662	15843	16103	15196	20260	20267	17632	17655	17306	16440
Phosphonate and phosphinate metabolism	9236	8485	7830	8340	8829	9413	9748	9895	8776	8686	9662	9762	9564	9801
	23201	21410	20700	21030	22832	23569	23503	24306	20795	18649	21025	19849	21716	22235
Phosphotransferase system (PTS)	4	0	0	6	6	3	3	0	5	2	8	3	9	0
									12174	12967				
Photosynthesis	51770	66060	76996	72345	63506	51796	52498	44042	7	3	82938	78113	75948	62257
Photosynthesis - antenna proteins	3013	6205	8568	7518	5670	2860	2261	1109	20013	22780	11250	9881	9146	5810
									14729	15807				
Photosynthesis proteins	59752	77121	90320	84742	74204	59654	59696	50162	0	9	99159	92749	90161	73028
Phototransduction	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Phototransduction - fly	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Plant-pathogen interaction	20186	20163	20655	20752	20335	20191	21705	19761	21653	21137	21008	20939	20552	20439
Polycyclic aromatic hydrocarbon degradation	33274	33621	35638	34931	34843	35209	35136	34434	36319	37264	34620	34188	34873	35192
Polyketide sugar unit biosynthesis	3807	5540	9964	7714	5105	3319	5608	1572	11140	13682	6926	7318	5758	4287
Pores ion channels	24254	27249	29303	29234	26798	24482	25339	21902	41461	46217	33133	31946	30810	27940
	11587	11890	13007	12938	12536	11614	12216	10750	17072	17618	14389	14277	13850	12815
Porphyrin and chlorophyll metabolism	6	6	2	9	6	3	3	0	6	6	5	1	2	0
Prenyltransferases	51903	54764	56741	56733	54691	52450	52558	50640	68463	68285	58440	57419	57535	54638
Primary bile acid biosynthesis	4169	4299	4353	4282	4355	4681	4805	4673	4288	4094	4155	4036	4258	4493
Primary immunodeficiency	5124	4997	5154	5344	5273	5339	5557	5055	5721	5886	5427	5415	5462	5482
Prion diseases	4286	3925	3596	3722	4429	4600	4416	4813	4165	3881	4415	4606	4788	4767
Progesterone-mediated oocyte maturation	5080	5085	4868	5114	5009	4967	5216	4904	6113	5560	5140	4918	5081	4919
	16347	15605	16004	16392	16698	16815	17036	16255	15946	16205	16345	16388	16530	16887
Propanoate metabolism	8	2	8	2	8	2	9	7	5	9	2	1	3	6

Prostate cancer	5080	5085	4868	5114	5009	4967	5216	4904	6113	5560	5140	4918	5081	4919
Proteasome	5127	5173	5155	5433	5181	5205	5414	4940	6289	5840	5334	5199	5285	5229
Protein digestion and absorption	10	36	91	102	49	68	98	7	69	139	347	446	226	254
		10354	10489	10538	10269	10061	10166		11758	11260	10289	10078	10329	10029
Protein export	99617	7	0	7	5	0	8	99118	4	8	9	1	4	3
Protein folding and associated processing	66562	69537	77524	76161	72812	67959	70439	62128	95083	98886	78502	78585	77731	72479
	15421	14886	14270	14597	15398	15671	15584	15933	16482	15691	15795	15312	15824	15721
Protein kinases	1	7	0	7	1	3	5	5	8	5	1	3	6	5
Protein processing in endoplasmic reticulum	14337	14460	13942	14432	14706	14644	14390	14474	17657	16872	15408	14543	15220	14783
Proximal tubule bicarbonate reclamation	9582	8845	9194	9224	9669	9708	9855	9543	9364	9053	9393	9074	9413	9524
	33181	34178	36073	35403	34390	33538	34455	32454	38190	38154	34437	34017	34343	33517
Purine metabolism	8	7	8	2	3	9	5	9	2	1	9	4	8	6
	24096	25034	26289	25840	25013	24305	25012	23603	27874	27681	25152	25138	25173	24463
Pyrimidine metabolism	8	5	7	9	8	0	0	8	6	6	0	3	2	4
	23515	23337	23646	23836	24112	24031	24173	23664	25272	25336	24333	24020	24370	24245
Pyruvate metabolism	7	2	6	0	1	5	4	6	7	9	8	4	8	1
RIG-I-like receptor signaling pathway	443	141	633	481	346	223	570	160	211	320	154	236	165	157
RNA degradation	62577	65642	69025	68380	65995	63051	65009	60606	80561	80907	69495	68530	68561	65194
RNA polymerase	25734	27573	29247	28527	27211	25981	26049	25104	31989	31197	27270	27122	27403	26103
RNA transport	20380	20920	22348	21428	20957	20455	21407	19940	22177	22529	20618	20377	20562	20154
Regulation of actin cytoskeleton	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Renal cell carcinoma	5085	5129	5066	5290	5231	5042	4974	5006	6175	5801	5308	5210	5375	5139
Renin-angiotensin system	7	1	2	1	4	2	4	1	1	5	1	7	5	8
	11254	10191	13682	12444	11494	10066	12110		12036	12447	10410	10325	10164	
Replication, recombination and repair proteins	9	7	7	0	3	4	0	89052	8	0	7	9	0	96166
Restriction enzyme	26584	26537	22910	24534	26480	27743	26911	28709	29203	27954	27699	26180	27852	27868
Retinol metabolism	15751	16520	17422	17386	16552	16320	15954	15546	19083	20913	17507	17320	17105	16965
Rheumatoid arthritis	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Riboflavin metabolism	40783	41185	42961	42884	42329	41237	42279	39909	48718	49170	44157	43483	43638	42353
	30275	32332	33743	33249	31669	30617	31084	29788	37537	36033	31893	31304	31820	30525
Ribosome	4	5	5	5	1	7	7	6	5	5	5	1	7	8
	18109	18864	19491	19275	18746	18351	18871	17971	21434	21056	19172	19061	19129	18549
Ribosome Biogenesis	4	5	5	4	7	2	8	4	8	8	1	2	2	5

Ribosome biogenesis in eukaryotes	5203	5598	6040	5921	5591	5350	5536	5051	6604	6472	5578	5619	5651	5404
Salivary secretion	0	0	0	0	0	0	0	0	0	0	0	1	1	0
Secondary bile acid biosynthesis	4096	4239	4080	3957	4163	4409	4534	4610	4170	3711	3957	3707	4048	4134
	23653	24359	24658	24853	24581	23976	24317	23396	27873	27269	24687	24309	24939	24122
Secretion system	1	8	1	3	6	5	1	1	5	9	7	5	9	1
Selenocompound metabolism	72047	71315	73367	73525	72978	71944	74921	70225	76412	77172	73643	73697	73334	72758
Sesquiterpenoid biosynthesis	4	26	62	69	30	40	23	0	48	34	38	44	40	48
Shigellosis	0	0	2	0	0	0	0	0	2	0	0	0	0	0
	11234	11144	11251	11283	11471	11417	11545	11288	12363	12261	11580	11301	11592	11443
Signal transduction mechanisms	2	8	8	0	5	7	6	7	9	7	8	3	6	9
Small cell lung cancer	108	252	292	351	209	52	32	28	679	293	131	193	232	71
Sphingolipid metabolism	10386	9707	10555	10382	10120	10336	12560	9985	10791	10299	10189	10527	10238	10316
Spliceosome	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	45398	42386	39115	40683	44399	46005	45956	47639	41073	38096	42537	40875	43604	44591
Sporulation	2	5	9	6	8	9	8	3	5	0	3	1	1	3
Staphylococcus aureus infection	29555	27840	24126	25677	28357	30411	28779	32810	27574	24417	27314	24872	27909	28798
	21104	20266	19714	19992	21075	21414	22128	21630	21877	20616	20288	19397	20812	20752
Starch and sucrose metabolism	0	8	2	9	5	2	7	2	3	9	7	1	3	7
Steroid biosynthesis	4685	4701	4673	4767	4991	5015	4755	4968	6663	6714	5811	5779	5765	5514
Steroid hormone biosynthesis	276	445	852	859	592	521	492	153	1331	1841	921	1023	816	806
Stilbenoid, diarylheptanoid and gingerol biosynthesis	17607	16903	16263	16814	18040	18742	17912	18901	18583	17553	18146	17404	18422	18729
Streptomycin biosynthesis	24805	26423	34152	30668	27385	24548	28420	21418	36151	38457	29167	29682	27959	25742
Styrene degradation	9977	9567	9978	10367	10534	10712	10629	10049	10225	11125	11014	11442	11061	11412
Sulfur metabolism	73119	69822	68025	70157	72488	73386	75146	73415	75418	74923	74769	72629	73691	74113
Sulfur relay system	63859	62436	61513	63473	64519	64555	65552	64121	71984	72028	66725	64246	66150	65334
Synthesis and degradation of ketone bodies	12487	13089	14380	14724	13268	13089	13137	11267	11257	14491	13423	14713	13121	13958
Systemic lupus erythematosus	0	1	3	1	2	1	1	0	1	1	0	1	2	0
TGF-beta signaling pathway	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Taurine and hypotaurine metabolism	28654	28285	27950	28329	29030	29372	29224	29209	29468	29025	28699	27906	28899	29090
Terpenoid backbone biosynthesis	77518	80956	85562	84108	81051	79218	80753	75713	91174	94009	83397	82988	82372	80670
Tetracycline biosynthesis	39215	38153	37285	38285	39413	39487	39210	39444	40341	40655	40295	39604	40090	40053
Thiamine metabolism	88076	86953	87985	88149	89095	89049	91893	88333	93537	92846	88845	86570	88858	88371

Vibrio cholerae infection	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Vibrio cholerae pathogenic cycle	15024	15192	15014	15326	15488	15123	15331	14785	18392	18770	16569	15690	16096	15570
Viral myocarditis	108	252	292	351	209	52	32	28	679	293	131	193	232	71
Vitamin B6 metabolism	32831	32272	30858	31836	32651	33668	33875	33794	35405	34583	33329	31504	32972	33213
Wnt signaling pathway	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Xylene degradation	9598	10092	10873	10626	10247	10403	10021	10165	11896	13268	12070	12333	11426	11513
Zeatin biosynthesis	5089	5520	5760	5680	5273	5112	5279	4972	6456	6208	5402	5219	5273	5066
alpha-Linolenic acid metabolism	5440	5489	5446	5774	5666	5654	5571	5214	5887	6509	5665	5753	5760	5837
beta-Alanine metabolism	60803	58006	61791	63022	63419	63756	65143	59598	61288	64904	62959	63882	63325	65056
beta-Lactam resistance	9043	8700	8146	8549	9066	9415	9069	9685	9510	9540	10105	9959	9821	9963
mRNA surveillance pathway	8	3	19	26	16	25	25	7	6	40	16	28	16	33
mTOR signaling pathway	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p53 signaling pathway	109	254	293	353	210	53	33	28	679	293	131	194	232	72

Table S7. Fungi genera abundance during different fermentation stages of JZ22 and JB3.

OTU ID	JZ22	JZ22	JZ22	JZ22	JZ22	JZ22	JZ22	JB3	JB3	JB3	JB3	JB3	JB3	JB3
	D0	D2	D4	D6	D8	D10	D12	D0	D2	D4	D6	D8	D10	D12
g__Cladosporium	28	0	0	0	0	0	1	185	0	0	0	0	0	0
g__Cochliobolus	11	0	0	0	0	0	0	100	0	0	0	0	0	0
g__Cryptosporidium	0	0	0	0	0	0	0	1	0	0	0	0	0	0
g__Galactomyces	0	0	0	0	0	0	0	2	0	0	0	0	0	0
g__norank_c__Agaricomycetes	10	0	0	0	0	0	0	21	0	0	0	0	0	0
g__norank_k__Fungi	1737	49	102	22	27	38	20	1917	24	38	97	53	62	71
g__norank_o__Malasseziales	4	0	0	0	0	0	0	11	0	0	0	0	0	0
g__norank_o__Tremellales	7	0	0	0	0	0	0	4	0	0	0	0	0	0
g__norank_p__Basidiomycota	3	0	0	0	0	0	0	0	0	0	0	0	0	0
g__norank_p__Chytridiomycota	2	0	0	0	0	0	0	0	0	0	0	0	0	0
g__norank_p__Glomeromycota	8	0	0	0	0	0	0	0	0	0	0	0	0	0
g__Oryza	30	0	0	1	0	0	0	48	0	2	0	1	1	1
g__Pichia	13410	89	60	54	39	80	90	19694	46	38	44	43	42	43
g__Saccharomycopsis	429	12	9	9	5	10	7	631	10	8	6	8	8	7
g__Symbiodinium	1	0	0	0	0	0	0	36	0	0	0	0	0	0
g__Trichosporon	2	0	0	0	0	0	0	11	0	0	0	0	0	0

g_unclassified_d_Eukaryota	4	0	0	0	0	0	0	0	0	0	0	0	0	0
g_unclassified_f_Colpodea	6	0	0	0	0	0	0	0	0	0	0	0	0	0
g_unclassified_f_Trichocomaceae	2158	45	22	18	11	35	26	1893	22	9	7	13	10	10
g_unclassified_o_Hypocreales	94	0	0	0	0	0	0	36	1	0	0	0	0	0
g_unclassified_o_Saccharomycetales	22659	40411	40415	40504	40526	40444	40463	16017	40505	40513	40453	40490	40486	40476
g_unclassified_p_Ascomycota	4	0	0	0	0	0	0	0	0	0	0	0	0	0

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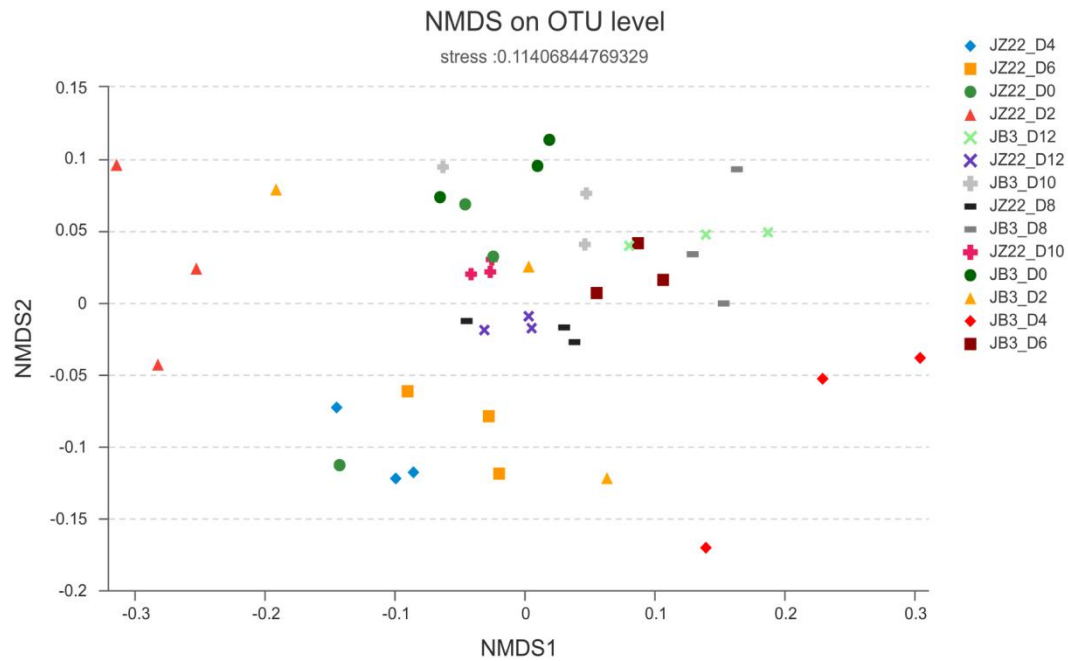


Figure S1. Non-metric Multidimensional Scaling (NMDS) distribution based on Weighted Unifrac distance.