

## Supplementary materials

**Table S1. Microbial contribution to genes encoding enzymes for the metabolism of biogenic amines during *Hongqu* rice wine brewing.**

Enzyme Function	Enzyme name	Enzyme No.	HBAs	LBAs
			Distribution of microbes (>1%)	Distribution of microbes (>1%)
Arginine degradation	arginine N-succinyltransferase	2.3.1.109	unclassified_g_ <i>Pantoea</i> (44.64%), unclassified_g_ <i>Klebsiella</i> (24.08%), <i>Klebsiella quasipneumoniae</i> (23.69%), unclassified_f_ <i>Enterobacteriaceae</i> (3.26%), <i>Klebsiella aerogenes</i> (1.53%), <i>Burkholderia gladioli</i> (1.42%)	unclassified_f_ <i>Enterobacteriaceae</i> (63.77%), <i>Cronobacter malonaticus</i> (12.32%), <i>Cronobacter sakazakii</i> (12.32%), <i>Leclercia adecarboxylata</i> (8.70%), <i>Klebsiella quasipneumoniae</i> (2.17%)
	arginine deiminase	3.5.3.6	unclassified_g_ <i>Pediococcus</i> (28.80%), <i>Lactococcus lactis</i> (28.53%), <i>Weissella confusa</i> (25.24%), unclassified_o_ <i>Enterobacterales</i> (10.45%), <i>Lactobacillus brevis</i> (2.58%), <i>Cronobacter sakazakii</i> (1.66%)	<i>Weissella confusa</i> (58.01%), <i>Pediococcus acidilactici</i> (26.67%), unclassified_g_ <i>Pediococcus</i> (6.38%), <i>Lactobacillus brevis</i> (3.62%), <i>Weissella cibaria</i> (2.74%), unclassified_o_ <i>Enterobacterales</i> (1.11%)
	arginine decarboxylase	4.1.1.19	unclassified_g_ <i>Pantoea</i> (52.72%), <i>Klebsiella pneumoniae</i> (44.07%), unclassified_f_ <i>Enterobacteriaceae</i> (1.10%)	unclassified_f_ <i>Enterobacteriaceae</i> (23.60%), unclassified_g_ <i>Pantoea</i> (12.36%), <i>Klebsiella pneumoniae</i> (15.73%), <i>Enterobacter kobei</i> (12.36%), unclassified_g_ <i>Enterobacter</i> (8.99%), unclassified_f_ <i>Erwiniaceae</i> (8.99%), <i>Cronobacter dublinensis</i> (5.62%), <i>Cronobacter universalis</i> (5.62%), <i>Metakosakonia</i> _sp._MRY16-398 (2.25%), <i>Enterobacter</i> _sp._kpr-6 (1.12%), <i>Enterobacter ludwigii</i> (2.25%), <i>Pantoea ananatis</i> (1.12%)

Cadaverine biosynthesis	lysine decarboxylase	4.1.1.18	<i>Pantoea dispersa</i> (39.31%), <i>Klebsiella quasipneumoniae</i> (29.17%), <i>Klebsiella</i> _sp._MS_92-3 (24.89%), unclassified_f_Enterobacteriaceae (4.31%)	unclassified_g_Kosakonia (40.88%), <i>Enterobacter</i> _sp._MGH_24 (15.33%), <i>Cronobacter malonaticus</i> (9.85%), <i>Enterobacter hormaechei</i> (8.76%), <i>Cronobacter turicensis</i> (4.38%), <i>Cronobacter sakazakii</i> (3.65%), <i>Enterobacter</i> _sp._kpr-6 (2.92%), unclassified_g_Enterobacter (2.92%), <i>Enterobacter cloacae</i> (2.55%), <i>Klebsiella</i> _sp._MS_92-3 (1.82%), <i>Siccibacter colletis</i> (1.82%), <i>Pantoea ananatis</i> (1.46%), <i>Cronobacter dublinensis</i> (1.09%), <i>Klebsiella quasipneumoniae</i> (1.09%)
Cadaverine degradation	primary-amine oxidase	1.4.3.21	<i>Klebsiella pneumoniae</i> (57.10%), unclassified_g_Klebsiella (31.12%), <i>Klebsiella aerogenes</i> (5.72%), <i>Enterobacter cloacae</i> (2.73%), <i>Monascus purpureus</i> (1.36%)	<i>Aspergillus awamori</i> (20.06%), <i>Aspergillus welwitschiae</i> (36.72%), <i>Aspergillus niger</i> (36.52%), <i>Monascus purpureus</i> (6.13%)
Glutamic biosynthesis	L-glutamate gamma-semialdehyde dehydrogenase	1.2.1.88	<i>Pantoea dispersa</i> (40.39%), <i>Klebsiella pneumoniae</i> (28.36%), <i>Klebsiella aerogenes</i> (7.90%), <i>Saccharomyces cerevisiae</i> (6.61%), <i>Klebsiella quasipneumoniae</i> (5.14%), unclassified_g_Klebsiella (3.92%), <i>Escherichia coli</i> (1.94%), unclassified_g_Enterobacter (1.62%), <i>Enterobacter cloacae</i> (1.17%)	<i>Aspergillus niger</i> (47.97%), <i>Saccharomyces cerevisiae</i> (39.65%), <i>Aspergillus vadensis</i> (4.25%), <i>Monascus purpureus</i> (3.70%), <i>Kosakonia cowanii</i> (1.58%)
	glutamate synthase (NADPH)	1.4.1.13	<i>Pantoea</i> _sp._R102 (29.32%), <i>Klebsiella pneumoniae</i> (17.19%), <i>Leuconostoc mesenteroides</i> (12.29%), <i>Klebsiella variicola</i> (10.46%), <i>Enterobacter cloacae</i> (5.03%), <i>Lactococcus lactis</i> (4.06%), <i>Escherichia albertii</i> (3.19%), unclassified_g_Enterobacter (2.94%), unclassified_g_Klebsiella (2.86%), <i>Kosakonia cowanii</i> (2.65%), <i>Salmonella enterica</i> (2.53%), <i>Cronobacter sakazakii</i> (1.90%)	<i>Enterobacter cloacae</i> (15.38%), <i>Kosakonia cowanii</i> (13.85%), <i>Leuconostoc mesenteroides</i> (12.31%), unclassified_g_Enterobacter (9.62%), <i>Cronobacter sakazakii</i> (9.10%), <i>Lactobacillus paracasei</i> (9.10%), <i>Klebsiella pneumoniae</i> (5.13%), <i>Salmonella enterica</i> (4.10%), <i>Enterobacter sichuanensis</i> (2.44%), <i>Lactococcus lactis</i> (2.44%), <i>Klebsiella variicola</i> (2.31%), <i>Escherichia albertii</i> (1.79%), <i>Franconibacter pulveris</i> (1.79%), <i>Enterobacter</i> _sp._ku-bf2 (1.67%), unclassified_g_Pantoea (1.15%), <i>Tatumella</i> _sp._TA1 (1.03%)

	glutamate synthase (NADH)	1.4.1.14	<i>Saccharomyces cerevisiae</i> (99.50%)	<i>Saccharomyces cerevisiae</i> (27.41%), <i>Monascus purpureus</i> (24.57%), <i>Aspergillus nomiae</i> (23.96%), <i>Cyberlindnera fabianii</i> (23.96%)
	glutamate dehydrogenase	1.4.1.2	<i>Saccharomyces cerevisiae</i> (98.72%), <i>Monascus purpureus</i> (1.28%),	<i>Saccharomyces cerevisiae</i> (65.57%), <i>Aspergillus flavus</i> (31.28%), <i>Monascus purpureus</i> (3.14%)
	glutamate dehydrogenase [NAD(P)+]	1.4.1.3	<i>Klebsiella pneumoniae</i> (86.29%), <i>Klebsiella quasipneumoniae</i> (5.86%), unclassified_g_ <i>Klebsiella</i> (3.25%), unclassified_g_ <i>Burkholderia</i> (1.64%), <i>Klebsiella variicola</i> (1.60%)	<i>Klebsiella pneumoniae</i> (33.33%), unclassified_f_ <i>Erwiniaceae</i> (33.33%), unclassified_g_ <i>Pantoea</i> (33.33%),
	glutamate dehydrogenase (NADP+)	1.4.1.4	<i>Klebsiella pneumoniae</i> (40.83%), <i>Saccharomyces cerevisiae</i> (23.37%), <i>Lactobacillus plantarum</i> (16.28%), <i>Klebsiella variicola</i> (12.36%), <i>Lactococcus lactis</i> (2.85%), unclassified_g_ <i>Enterobacter</i> (1.46%), <i>Acinetobacter johnsonii</i> (1.11%)	<i>Saccharomyces cerevisiae</i> (83.02%), <i>Aspergillus nomiae</i> (11.11%), <i>Lactobacillus plantarum</i> (2.08%), <i>Monascus purpureus</i> (2.39%)
	glutaminase	3.5.1.2	<i>Pantoea dispersa</i> (30.48%), unclassified_f_ <i>Enterobacteriaceae</i> (14.30%), <i>Leuconostoc mesenteroides</i> (13.50%), unclassified_g_ <i>Lactobacillus</i> (12.35%), <i>Leuconostoc pseudomesenteroides</i> (8.99%), <i>Weissella confusa</i> (3.85%), <i>Pediococcus pentosaceus</i> (2.95%), <i>Leuconostoc lactis</i> (3.63%), <i>Lactococcus lactis</i> (3.98%), <i>Lactobacillus curvatus</i> (2.53%), <i>Leuconostoc citreum</i> (1.00%)	<i>Weissella confusa</i> (70.53%), <i>Leuconostoc pseudomesenteroides</i> (6.76%), <i>Pediococcus pentosaceus</i> (7.96%), unclassified_g_ <i>Lactobacillus</i> (3.21%), <i>Leuconostoc lactis</i> (2.74%), <i>Weissella cibaria</i> (3.03%), <i>Kosakonia cowanii</i> (2.08%), <i>Leuconostoc mesenteroides</i> (1.17%)
	glutamin-(asparagin-)ase	3.5.1.38	<i>Acinetobacter johnsonii</i> (100.00%)	/
	N-formylglutamate deformylase	3.5.1.68	unclassified_g_ <i>Pantoea</i> (96.12%), <i>Burkholderia gladioli</i> (2.83%)	unclassified_d_ <i>Bacteria</i> (45.45%), <i>Kozakia baliensis</i> (36.36%), <i>Pantoea ananatis</i> (18.18%)
	succinylglutamate desuccinylase	3.5.1.96	<i>Klebsiella pneumoniae</i> (40.44%), unclassified_g_ <i>Pantoea</i> (37.14%), <i>Klebsiella quasipneumoniae</i> (16.64%), <i>Klebsiella aerogenes</i> (1.40%), <i>Enterobacter roggenkampii</i> (1.15%), <i>Enterobacter cloacae</i> (1.05%)	<i>Enterobacter kobei</i> (27.49%), <i>Kosakonia cowanii</i> (26.32%), <i>Cronobacter malonaticus</i> (14.04%), <i>Enterobacter roggenkampii</i> (12.87%), <i>Enterobacter hormaechei</i> (12.28%), <i>Leclercia adecarboxylata</i> (2.34%), <i>Enterobacter cloacae</i> (1.75%), <i>Pantoea ananatis</i> (1.75%)
	5-oxoprolinase (ATP-hydrolysing)	3.5.2.9	unclassified_f_ <i>Enterobacteriaceae</i> (41.66%), unclassified_g_ <i>Pantoea</i> (37.94%),	<i>Aspergillus niger</i> (57.86%), <i>Saccharomyces cerevisiae</i> (20.46%), <i>Aspergillus oryzae</i> (6.89%), <i>Monascus purpureus</i>

			<i>Leuconostoc_mesenteroides</i> (4.40%), <i>Saccharomyces_cerevisiae</i> (4.17%), unclassified_g_ <i>Lactobacillus</i> (3.53%), unclassified_g_ <i>Klebsiella</i> (2.72%), <i>Burkholderia_gladioli</i> (1.29%), <i>Leuconostoc_lactis</i> (1.21%)	(6.69%), <i>Aspergillus_phoenicis</i> (4.79%)
	formimidoylglutamase	3.5.3.8	unclassified_g_ <i>Klebsiella</i> (67.26%), <i>Klebsiell pneumoniae</i> (13.33%), <i>Enterobacter roggenkampii</i> (6.70%), <i>Klebsiella</i> <i>variicola</i> (5.44%), <i>Enterobacter cloacae</i> (4.95%), unclassified_g_ <i>Enterobacter</i> (1.23%)	<i>Kosakonia cowanii</i> (38.85%),unclassified_g_ <i>Enterobacter</i> (30.94%), <i>Enterobacter roggenkampii</i> (18.71%), <i>Enterobacter cloacae</i> (3.60%), <i>Leclercia adecarboxylata</i> (2.88%), <i>Enterobacter asburiae</i> (1.44%), <i>Enterobacter</i> sp._Tr-810 (2.88%)
Glutamic degradation	amino-acid N-acetyltransferase	2.3.1.1	<i>Leuconostoc_mesenteroides</i> (18.46%), <i>Saccharomyces_cerevisiae</i> (14.73%), <i>Klebsiella_variicola</i> (14.41%), <i>Leuconostoc_pseudomesenteroides</i> (11.65%), <i>Lactobacillus_plantarum</i> (11.61%), <i>Leuconostoc_lactis</i> (5.52%), unclassified_g_ <i>Pantoea</i> (4.66%), <i>Lactococcus_lactis</i> (4.25%), <i>Enterobacter roggenkampii</i> (2.62%), <i>Pantoea_sp._Seng</i> (2.15%), <i>Kosakonia_cowanii</i> (1.81%), unclassified_f_ <i>Enterobacteriaceae</i> (1.71%), <i>Acinetobacter_johnsonii</i> (1.20%), <i>Leuconostoc_citreum</i> (1.14%), <i>Acinetobacter_sp._BMW17</i> (1.10%)	<i>Saccharomyces_cerevisiae</i> (57.88%), <i>Monascus_purpureus</i> (18.00%), <i>Aspergillus_awamori</i> (12.25%), <i>Leuconostoc_pseudomesenteroides</i> (2.97%), <i>Leuconostoc_holzapfelii</i> (2.42%), <i>Lactobacillus_plantarum</i> (1.81%), unclassified_g_ <i>Weissella</i> (1.26%)
	carbamoyl-phosphate synthase (glutamine-hydrolysing)	6.3.5.5	unclassified_g_ <i>Lactobacillus</i> (15.37%), <i>Pectobacterium_carotovorum</i> (12.79%), <i>Leuconostoc_mesenteroides</i> (11.76%), <i>Saccharomyces_cerevisiae</i> (8.04%), <i>Leuconostoc_pseudomesenteroides</i> (7.92%), unclassified_g_ <i>Pantoea</i> (6.94%), <i>Weissella_confusa</i> (4.68%), <i>Lactobacillus_plantarum</i> (4.09%), <i>Lactococcus_lactis</i> (3.48%), <i>Klebsiella_pneumoniae</i> (3.17%), <i>Pediococcus_pentosaceus</i> (3.00%), <i>Leuconostoc_lactis</i> (2.66%), unclassified_g_ <i>Leuconostoc</i> (2.35%), <i>Klebsiella_aerogenes</i> (1.87%), unclassified_g_ <i>Enterobacter</i> (1.62%), <i>Cronobacter_sakazakii</i> (1.45%), <i>Raoultella_planticola</i>	<i>Saccharomyces_cerevisiae</i> (29.50%), <i>Weissella_confusa</i> (27.88%), <i>Pediococcus_acidilactici</i> (17.63%), <i>Aspergillus_niger</i> (9.23%), <i>Pediococcus_pentosaceus</i> (3.23%), <i>Monascus_purpureus</i> (2.26%), unclassified_g_ <i>Lactobacillus</i> (2.39%), <i>Leuconostoc_pseudomesenteroides</i> (1.75%), <i>Weissella_cibaria</i> (1.53%), <i>Leuconostoc_lactis</i> (1.03%)

			(1.43%), <i>Lactobacillus_curvatus</i> (1.35%)	
	glutamate 5-kinase	2.7.2.11	<i>unclassified_g_Pantoea</i> (31.52%), <i>Leuconostoc_mesenteroides</i> (13.34%), <i>Saccharomyces_cerevisiae</i> (12.41%), <i>Lactobacillus_plantarum</i> (11.42%), <i>Leuconostoc_pseudomesenteroides</i> (8.48%), <i>Lactococcus_lactis</i> (5.52%), <i>Klebsiella_pneumoniae</i> (3.89%), <i>Leuconostoc_lactis</i> (3.56%), <i>unclassified_f_Enterobacteriaceae</i> (3.53%), <i>Salmonella_enterica</i> (2.68%)	<i>Saccharomyces_cerevisiae</i> (70.02%), <i>Aspergillus_niger</i> (18.56%), <i>Leuconostoc_pseudomesenteroides</i> (3.15%), <i>Lactobacillus_plantarum</i> (2.11%), <i>Leuconostoc_lactis</i> (1.42%), <i>Aspergillus_oryzae</i> (1.01%)
Histamine biosynthesis	histidine decarboxylase	4.1.1.22	<i>unclassified_f_Enterobacteriaceae</i> (69.93%), <i>Tetragenococcus_halophilus</i> (30.07%)	/
Histidine biosynthesis	histidinol dehydrogenase	1.1.1.23	<i>unclassified_f_Enterobacteriaceae</i> (27.17%), <i>Pantoea_dispersa</i> (22.74%), <i>Leuconostoc_mesenteroides</i> (13.72%), <i>unclassified_g_Lactobacillus</i> (9.47%), <i>Leuconostocaceae_bacterium</i> (8.46%), <i>Saccharomyces_cerevisiae</i> (7.08%), <i>Lactococcus_lactis</i> (3.37%), <i>Klebsiella_quasipneumoniae</i> (1.74%), <i>Kalamiella_piersonii</i> (1.05%), <i>unclassified_g_Acinetobacter</i> (1.02%)	<i>Saccharomyces_cerevisiae</i> (49.02%), <i>Aspergillus_niger</i> (38.76%), <i>Monascus_purpureus</i> (3.20%), <i>Leuconostocaceae_bacterium</i> (3.08%), <i>unclassified_g_Lactobacillus</i> (2.06%)
Histidine degradation	L-histidine Nalpha-methyltransferase	2.1.1.44	<i>Monascus_purpureus</i> (37.50%), <i>Aspergillus_flavus</i> (33.33%), <i>Aspergillus_eucalypticola</i> (29.17%)	<i>Aspergillus_eucalypticola</i> (93.66%), <i>Monascus_purpureus</i> (4.09%), <i>Aspergillus_flavus</i> (2.24%)

	histidine ammonia-lyase	4.3.1.3	<i>Pantoea dispersa</i> (62.66%), unclassified_g_ <i>Pantoea</i> (14.06%), unclassified_g_ <i>Klebsiella</i> (8.70%), unclassified_f_ <i>Enterobacteriaceae</i> (3.88%), <i>Klebsiella pneumoniae</i> (3.50%), <i>Klebsiella quasipneumoniae</i> (2.79%), unclassified_g_ <i>Burkholderia</i> (2.33%)	<i>Enterobacter cloacae</i> (17.28%), unclassified_g_ <i>Enterobacter</i> (17.28%), <i>Kosakonia cowanii</i> (49.38%), <i>Escherichia coli</i> (4.94%), <i>Pantoea dispersa</i> (2.47%), unclassified_g_ <i>Pantoea</i> (2.47%), unclassified_g_ <i>Klebsiella</i> (1.23%), <i>Klebsiella pneumoniae</i> (1.23%), <i>Klebsiella quasipneumoniae</i> (1.23%), <i>Pantoea</i> _sp. (1.23%), unclassified_f_ <i>Erwiniaceae</i> (1.23%)
Lysine biosynthesis	diaminopimelate decarboxylase	4.1.1.20	<i>Pantoea dispersa</i> (32.36%), <i>Klebsiella pneumoniae</i> (22.58%), <i>Leuconostoc mesenteroides</i> (10.59%), <i>Leuconostocaceae bacterium</i> (8.14%), <i>Lactobacillus plantarum</i> (6.73%), <i>Lactococcus lactis</i> (5.17%), <i>Leuconostoc lactis</i> (3.90%), <i>Weissella confusa</i> (3.58%), <i>Klebsiella aerogenes</i> (2.41%)	<i>Weissella confusa</i> (69.65%), <i>Leuconostocaceae bacterium</i> (7.90%), <i>Pediococcus pentosaceus</i> (6.11%), <i>Kosakonia cowanii</i> (4.16%), <i>Lactobacillus plantarum</i> (3.24%), unclassified_g_ <i>Weissella</i> (2.27%), <i>Leuconostoc lactis</i> (1.83%), <i>Leuconostoc mesenteroides</i> (1.23%)
Lysine degradation	saccharopine dehydrogenase (NAD <sup>+</sup> , L-lysine-forming)	1.5.1.7	<i>Saccharomyces cerevisiae</i> (99.77%)	<i>Saccharomyces cerevisiae</i> (74.63%), <i>Aspergillus phoenicis</i> (24.88%)
Ornithine biosynthesis	glutamate N-acetyltransferase	2.3.1.35	<i>Leuconostoc mesenteroides</i> (29.74%), <i>Saccharomyces cerevisiae</i> (12.49%), <i>Leuconostoc pseudomesenteroides</i> (18.77%), <i>Lactobacillus plantarum</i> (18.70%), <i>Leuconostoc lactis</i> (8.89%), <i>Lactococcus lactis</i> (6.84%), <i>Leuconostoc citreum</i> (1.84%), <i>Acinetobacter</i> sp._BMW17 (1.77%)	<i>Saccharomyces cerevisiae</i> (54.65%), <i>Aspergillus niger</i> (23.15%), <i>Leuconostoc pseudomesenteroides</i> (5.62%), <i>Leuconostoc holzapfelii</i> (4.58%), <i>Lactobacillus plantarum</i> (3.41%), <i>Monascus purpureus</i> (3.00%), unclassified_g_ <i>Weissella</i> (2.37%), <i>Leuconostoc mesenteroides</i> (1.60%), <i>Leuconostoc lactis</i> (1.23%)
	acetylornithine deacetylase	3.5.1.16	<i>Pantoea dispersa</i> (28.17%), unclassified_g_ <i>Pantoea</i> (19.41%), <i>Pantoea</i> _sp._R102 (12.71%), unclassified_f_ <i>Enterobacteriaceae</i> (11.75%), <i>Klebsiella pneumoniae</i> (9.06%), <i>Klebsiella variicola</i> (6.07%), <i>Lactococcus lactis</i> (3.86%), <i>Kosakonia oryzae</i> (2.66%), <i>Izhakiella australiensis</i> (1.65%), unclassified_g_ <i>Klebsiella</i> (1.31%)	unclassified_f_ <i>Enterobacteriaceae</i> (1.73%), <i>Klebsiella pneumoniae</i> (1.19%)
Ornithine degradation	D-amino-acid oxidase	1.4.3.3	<i>Monascus purpureus</i> (60.00%), <i>Aspergillus steynii</i> (25.00%), <i>Sporisorium graminicola</i> (10.00%), <i>Aspergillus niger</i> (5.00%)	<i>Aspergillus niger</i> (81.89%), <i>Monascus purpureus</i> (11.26%), <i>Aspergillus steynii</i> (6.85%)
	ornithine aminotransferase	2.6.1.13	<i>Saccharomyces cerevisiae</i> (99.10%)	<i>Saccharomyces cerevisiae</i> (56.56%), <i>Aspergillus niger</i> (41.62%), <i>Monascus purpureus</i> (1.58%)

Phenethylamine biosynthesis	aromatic-L-amino-acid decarboxylase	4.1.1.28	<i>Monascus purpureus</i> (100%)	<i>Aspergillus niger</i> (92.31%), <i>Monascus purpureus</i> (7.57%)
Phenylalanine biosynthesis	aspartate transaminase	2.6.1.1	unclassified_g_ <i>Pantoea</i> (30.63%), Type-C_symbiont_of_ <i>Plautia stali</i> (25.82%), <i>Pantoea</i> sp._Cy-640 (11.40%), <i>Saccharomyces cerevisiae</i> (10.69%), <i>Klebsiella pneumoniae</i> (10.11%), <i>Klebsiella quasipneumoniae</i> (4.89%), unclassified_g_ <i>Klebsiella</i> (2.13%), unclassified_f_ <i>Enterobacteriaceae</i> (1.68%), <i>Enterobacter cloacae</i> (1.12%)	<i>Saccharomyces cerevisiae</i> (72.71%), <i>Aspergillus niger</i> (11.67%), <i>Aspergillus awamori</i> (8.62%), <i>Monascus purpureus</i> (3.84%), <i>Aspergillus neoniger</i> (1.65%)
	prephenate dehydratase	4.2.1.51	<i>Klebsiella pneumoniae</i> (27.16%), unclassified_g_ <i>Pantoea</i> (26.33%), <i>Pantoea</i> sp._R102 (19.25%), unclassified_f_ <i>Enterobacteriaceae</i> (12.48%), <i>Saccharomyces cerevisiae</i> (4.92%), <i>Lactococcus lactis</i> (5.13%), <i>Klebsiella variicola</i> (1.48%)	<i>Saccharomyces cerevisiae</i> (62.94%), <i>Aspergillus niger</i> (29.17%), <i>Enterobacter kobei</i> (1.48%), <i>Monascus purpureus</i> (2.39%), unclassified_f_ <i>Enterobacteriaceae</i> (1.70%),
	arogenate dehydratase	4.2.1.91	<i>Klebsiella pneumoniae</i> (50.96%), <i>Pantoea</i> sp._R102 (44.08%), <i>Klebsiella variicola</i> (2.63%), <i>Klebsiella aerogenes</i> (1.20%), <i>Burkholderia gladioli</i> (1.13%),	<i>Klebsiella pneumoniae</i> (50.00%), <i>Pantoea septica</i> (50.00%)
	phenylalanine ammonia-lyase	4.3.1.24	<i>Aspergillus niger</i> (100.00%)	<i>Aspergillus niger</i> (70.36%), <i>Aspergillus phoenicis</i> (28.56%), <i>Aspergillus awamori</i> (1.07%)
	chorismate mutase	5.4.99.5	<i>Pantoea</i> sp._BK028 (27.62%), unclassified_g_ <i>Pantoea</i> (23.90%), <i>Pantoea dispersa</i> (16.95%), unclassified_f_ <i>Enterobacteriaceae</i> (14.37%), <i>Klebsiella pneumoniae</i> (4.45%), <i>Saccharomyces cerevisiae</i> (4.17%), <i>Salmonella enterica</i> (2.73%), <i>Lactococcus lactis</i> (1.65%)	<i>Saccharomyces cerevisiae</i> (67.96%), <i>Aspergillus niger</i> (20.84%), unclassified_f_ <i>Enterobacteriaceae</i> (3.10%), <i>Enterobacter kobei</i> (1.71%), <i>Kosakonia cowanii</i> (1.17%)
	aromatic-amino-acid transaminase	2.6.1.57	<i>Plautia stali</i> symbiont (44.37%), <i>Klebsiella pneumoniae</i> (32.37%), unclassified_g_ <i>Klebsiella</i> (12.62%), <i>Saccharomyces cerevisiae</i> (5.51%), <i>Klebsiella quasipneumoniae</i> (1.73%)	<i>Saccharomyces cerevisiae</i> (41.87%), <i>Aspergillus piperis</i> (30.86%), <i>Aspergillus awamori</i> (23.75%)

	histidinol-phosphate transaminase	2.6.1.9	unclassified_g_Pantoea (30.42%), <i>Leuconostoc_mesenteroides</i> (13.35%), <i>Klebsiella_pneumoniae</i> (10.91%), <i>Leuconostoc_pseudomesenteroides</i> (9.78%), unclassified_g_Lactobacillus (9.28%), <i>Saccharomyces_cerevisiae</i> (6.70%), unclassified_g_Klebsiella (6.32%), <i>Lactococcu</i> <i>lactis</i> (4.17%), <i>Klebsiella_aerogenes</i> (2.02%), <i>Leuconostoc_lactis</i> (1.17%), <i>Burkholderia_gladioli</i> (1.11%)	<i>Saccharomyces_cerevisiae</i> (54.60%), <i>Monascus_purpureus</i> (29.98%), <i>Leuconostoc_pseudomesenteroides</i> (5.66%), <i>Leuconostoc_lactis</i> (2.90%), unclassified_g_Lactobacillus (2.65%), <i>Leuconostoc_mesenteroides</i> (1.38%)
	tyrosine transaminase	2.6.1.5	<i>Saccharomyces_cerevisiae</i> (97.96%), <i>Aspergillus_awamori</i> (1.36%)	<i>Saccharomyces_cerevisiae</i> (43.13%), <i>Aspergillus_piperis</i> (31.78%), <i>Aspergillus_awamori</i> (24.46%)
	phenylalanine(histidine) transaminase	2.6.1.58	<i>Saccharomyces_cerevisiae</i> (100.00%)	<i>Saccharomyces_cerevisiae</i> (100.00%)
Phenylalanine degradation	D-amino-acid N-acetyltransferase	2.3.1.36	<i>Saccharomyces_cerevisiae</i> (100.00%)	<i>Saccharomyces_cerevisiae</i> (100.00%)
Phenylethylamine degradation	primary-amine oxidase	1.4.3.21	<i>Klebsiella_pneumoniae</i> (57.10%), unclassified_g_Klebsiella (31.12%), <i>Klebsiella_aerogenes</i> (5.72%), <i>Enterobacter_cloacae</i> (2.73%), <i>Monascus_purpureus</i> (1.36%)	<i>Aspergillus_awamori</i> (20.06%), <i>Aspergillus_welwitschiae</i> (36.72%), <i>Aspergillus_niger</i> (36.52%), <i>Monascus_purpureus</i> (6.13%)
	monoamine oxidase	1.4.3.4	<i>Monascus_purpureus</i> (80.56%), <i>Aspergillus_flavus</i> (19.44%)	<i>Aspergillus_niger</i> (78.76%), <i>Monascus_purpureus</i> (20.76%)
Putrescine biosynthesis	agmatinase	3.5.3.11	unclassified_g_Pantoea (65.20%), <i>Klebsiella_pneumoniae</i> (15.95%), unclassified_f_Enterobacteriaceae (11.82%), <i>Franconibacter_pulveris</i> (2.88%), <i>Klebsiella_michiganensis</i> (2.24%)	<i>Aspergillus_phoenicis</i> (43.37%), <i>Aspergillus_niger</i> (27.82%), <i>Mucor_ambiguus</i> (9.27%), <i>Monascus_purpureus</i> (7.52%), <i>Aspergillus_luchuensis</i> (4.38%), <i>Aspergillus_udagawae</i> (3.14%), <i>Monascus_ruber</i> (2.46%), unclassified_f_Enterobacteriaceae (1.31%), <i>Monascus_ruber</i> (2.14%)
	ornithine decarboxylase	4.1.1.17	unclassified_g_Pantoea (46.21%), <i>Klebsiella_pneumoniae</i> (37.96%), <i>Saccharomyces_cerevisiae</i> (6.21%), <i>Lactobacillus_curvatus</i> (2.06%), unclassified_g_Enterobacter (1.58%), <i>Klebsiella_aerogenes</i> (1.49%)	<i>Saccharomyces_cerevisiae</i> (51.10%), <i>Aspergillus_niger</i> (36.33%), <i>Monascus_purpureus</i> (2.65%), <i>Aspergillus_flavus</i> (2.30%), <i>Kosakonia_cowanii</i> (1.53%), unclassified_g_Enterobacter (1.51%)



	N-carbamoylputrescine amidase	3.5.1.53	<i>Burkholderia gladioli</i> (67.24%), unclassified_f_Enterobacteriaceae (32.76%)	unclassified_f_Enterobacteriaceae (100.00%)
	D-ornithine/D-lysine decarboxylase	4.1.1.116	unclassified_f_Enterobacteriaceae (100.00%)	/
	arginine decarboxylase	4.1.1.19	unclassified_g_Pantoea (52.72%), <i>Klebsiella pneumoniae</i> (44.07%), unclassified_f_Enterobacteriaceae (1.10%)	unclassified_g_Pantoea (12.36%), <i>Klebsiella pneumoniae</i> (15.73%), unclassified_f_Enterobacteriaceae (23.60%), <i>Enterobacter kobei</i> (12.36%), unclassified_g_Enterobacter (8.99%), unclassified_f_Erwinaceae (8.99%), <i>Cronobacter dublinensis</i> (5.62%), <i>Cronobacter universalis</i> (5.62%), <i>Metakosakonia</i> _sp._MRY16-398 (2.25%), <i>Enterobacter</i> _sp._kpr-6 (1.12%), <i>Enterobacter ludwigii</i> (2.25%), <i>Pantoea ananatis</i> (1.12%)
	agmatine deiminase	3.5.3.12	<i>Lactococcus lactis</i> (59.10%), <i>Acinetobacter johnsonii</i> (14.41%), <i>Lactobacillus brevis</i> (9.55%), <i>Burkholderia gladioli</i> (8.11%), unclassified_g_Pediococcus (3.51%), <i>Pediococcus pentosaceus</i> (3.06%), <i>Kosakonia cowanii</i> (1.98%)	<i>Lactobacillus brevis</i> (61.66%), <i>Pediococcus pentosaceus</i> (12.33%), <i>Kosakonia cowanii</i> (12.11%), unclassified_g_Pediococcus (11.88%), <i>Lactococcus lactis</i> (1.79%)
	non-specific polyamine oxidase	1.5.3.17	<i>Cyberlindnera fabianii</i> (99.63%)	<i>Cyberlindnera fabianii</i> (100.00%)
Putrescine degradation	glutamate---putrescine ligase	6.3.1.11	unclassified_f_Enterobacteriaceae (62.63%), unclassified_g_Pantoea (21.41%), <i>Klebsiella variicola</i> (8.61%), <i>Klebsiella pneumoniae</i> (3.23%), unclassified_g_Enterobacter (1.08%)	<i>Kalamiella piersonii</i> (41.21%), <i>Enterobacter kobei</i> (13.42%), unclassified_f_Enterobacteriaceae (13.10%), <i>Cronobacter sakazakii</i> (8.63%), <i>Cronobacter malonaticus</i> (6.39%), <i>Enterobacter roggenkampii</i> (6.39%), unclassified_g_Enterobacter (5.43%), <i>Cronobacter dublinensis</i> (1.92%), unclassified_g_Pantoea (1.60%)

	diamine N-acetyltransferase	2.3.1.57	unclassified_g_Leuconostoc (20.55%), unclassified_f_Enterobacteriaceae (16.59%), <i>Pantoea</i> _sp._Cy-640 (15.61%), <i>Leuconostoc_lactis</i> (11.34%), <i>Weissella_confusa</i> (10.76%), unclassified_g_Lactobacillus (7.47%), <i>Lactococcus_lactis</i> (5.17%), <i>Lactobacillus_curvatus</i> (3.16%), <i>Pediococcus_pentosaceus</i> (2.34%), unclassified_g_Klebsiella (2.17%), <i>Leuconostoc_pseudomesenteroides</i> (1.73%), unclassified_g_Enterobacter (1.19%)	<i>Weissella_confusa</i> (81.92%), <i>Pediococcus_acidilactici</i> (9.76%), <i>Pediococcus_pentosaceus</i> (1.84%), unclassified_g_Lactobacillus (1.73%), unclassified_g_Leuconostoc (1.31%)
	putrescine---pyruvate transaminase	2.6.1.113	<i>Klebsiella pneumoniae</i> (100.00%)	<i>Klebsiella pneumoniae</i> (100.00%)
	putrescine---2-oxoglutarate transaminase	2.6.1.82	<i>Klebsiella_pneumoniae</i> (62.16%), unclassified_f_Enterobacteriaceae (14.87%), <i>Klebsiella_aerogenes</i> (6.25%), unclassified_g_Klebsiella (4.70%), <i>Klebsiella_quasipneumoniae</i> (3.90%), <i>Lactococcus_lactis</i> (3.10%), <i>Kosakonia_cowanii</i> (1.67%), <i>Cronobacter_sakazakii</i> (1.53%), <i>Cronobacter_dublinensis</i> (1.02%)	<i>Kosakonia_cowanii</i> (62.94%), <i>Cronobacter_sakazakii</i> (16.75%), unclassified_g_Enterobacter (7.11%), <i>Cronobacter_dublinensis</i> (6.60%), <i>Lactococcus_lactis</i> (3.55%), <i>Leclercia_adecarboxylata</i> (1.02%), unclassified_f_Enterobacteriaceae (1.02%)
Spermidine biosynthesis	spermidine synthase	2.5.1.16	<i>Pantoea dispersa</i> (60.95%), <i>Klebsiella variicola</i> (14.85%), <i>Klebsiella quasipneumoniae</i> (11.72%), <i>Saccharomyces cerevisiae</i> (9.02%), unclassified_g_Burkholderia (1.02%)	<i>Saccharomyces cerevisiae</i> (68.48%), <i>Aspergillus vadsensis</i> (28.46%), <i>Kosakonia cowanii</i> (1.06%)
	glutathionylspermidine amidase	3.5.1.78	unclassified_f_Enterobacteriaceae (93.00%), unclassified_g_Enterobacter (3.98%), <i>Enterobacter_cloacae</i> (1.94%), <i>Klebsiella pneumoniae</i> (1.01%)	unclassified_g_Enterobacter (86.00%), <i>Enterobacter_sp._WCHEn090032</i> (6.00%), <i>Enterobacter_cloacae</i> (4.00%), <i>Enterobacter_genomosp._O</i> (4.00%)
	non-specific polyamine oxidase	1.5.3.17	<i>Cyberlindnera fabianii</i> (49.91%), <i>Saccharomyces cerevisiae</i> (49.91%)	<i>Cyberlindnera fabianii</i> (50.00%), <i>Saccharomyces cerevisiae</i> (50.00%)
	spermine oxidase	1.5.3.16	/	<i>Aspergillus niger</i> (100.00%)
Spermidine degradation	spermidine dehydrogenase	1.5.99.6	<i>Cronobacter malonaticus</i> (96.88%), <i>Cronobacter sakazakii</i> (3.13%)	<i>Cronobacter malonaticus</i> (75.00%), <i>Cronobacter sakazakii</i> (25.00%)
	polyamine oxidase	1.5.3.14	/	<i>Aspergillus niger</i> (100.00%)

	(propane-1,3-diamine-forming)			
	glutathionylspermidine synthase	6.3.1.8	unclassified_f_Enterobacteriaceae (93.00%), unclassified_g_Enterobacter (3.98%), <i>Enterobacter_cloacae</i> (1.94%), <i>Klebsiella_pneumoniae</i> (1.01%)	unclassified_g_Enterobacter (86.00%), <i>Enterobacter_sp._WCHEn090032</i> (6.00%), <i>Enterobacter_cloacae</i> (4.00%), <i>Enterobacter_genomosp._O</i> (4.00%)
Spermine biosynthesis	spermine synthase	2.5.1.22	<i>Saccharomyces_cerevisiae</i> (100.00%)	<i>Saccharomyces_cerevisiae</i> (100.00%)
Tryptamine biosynthesis	L-tryptophan decarboxylase	4.1.1.105	<i>Monascus_purpureus</i> (100%)	<i>Aspergillus_niger</i> (92.31%), <i>Monascus_purpureus</i> (7.57%)
	aromatic-L-amino-acid decarboxylase	4.1.1.28	<i>Monascus_purpureus</i> (100%)	<i>Aspergillus_niger</i> (92.31%), <i>Monascus_purpureus</i> (7.57%)
Tryptophan biosynthesis	tryptophan synthase	4.2.1.20	unclassified_g_Pantoea (25.23%), <i>Leuconostoc_mesenteroides</i> (16.22%), <i>Pantoea_sp._R102</i> (12.59%), unclassified_g_Lactobacillus (11.19%), <i>Klebsiella_pneumoniae</i> (6.94%), <i>Lactococcus_lactis</i> (5.72%), <i>Saccharomyces_cerevisiae</i> (5.22%), <i>Pantoea_ananatis</i> (4.04%), unclassified_f_Enterobacteriaceae (3.90%), <i>Klebsiella_variicola</i> (3.36%), unclassified_g_Acinetobacte (1.20%)	<i>Saccharomyces_cerevisiae</i> (45.35%), <i>Aspergillus_niger</i> (22.25%), <i>Aspergillus_welwitschiae</i> (17.82%), <i>Leuconostoc_lactis</i> (6.18%), unclassified_g_Lactobacillus (3.23%), <i>Leuconostoc_mesenteroides</i> (1.58%), <i>Monascus_purpureus</i> (1.11%)
Tryptophan degradation	tryptophan 2,3-dioxygenase	1.13.11.1 1	<i>Burkholderia_gladioli</i> (100.00%)	/
	tryptophan transaminase	2.6.1.27	<i>Saccharomyces_cerevisiae</i> (97.96%), <i>Aspergillus_awamori</i> (1.36%)	<i>Saccharomyces_cerevisiae</i> (43.13%), <i>Aspergillus_piperis</i> (31.78%), <i>Aspergillus_awamori</i> (24.46%)
	tryptophanase	4.1.99.1	<i>Pantoea_ananatis</i> (36.36%), <i>Leclercia_adeboxylata</i> (27.27%), <i>Cronobacter_dublinensis</i> (27.27%), <i>Phytobacter_palmae</i> (9.09%)	<i>Pantoea_ananatis</i> (83.33%), <i>Leclercia_adeboxylata</i> (16.67%)
Tyramine biosynthesis	tyrosine decarboxylase	4.1.1.25	<i>Lactobacillus_curvatus</i> (92.15%), <i>Lactobacillus_brevis</i> (7.85%)	<i>Lactobacillus_brevis</i> (100.00%)
	aromatic-L-amino-acid decarboxylase	4.1.1.28	<i>Monascus_purpureus</i> (100%)	<i>Aspergillus_niger</i> (92.31%), <i>Monascus_purpureus</i> (7.57%)

Tyramine degradation	gamma-glutamylputrescine oxidase	1.4.3.-	<i>Klebsiella</i> _sp._MS_92-3 (38.05%), unclassified_g_ <i>Pantoea</i> (32.51%), unclassified_f_ <i>Enterobacteriaceae</i> (14.45%), <i>Klebsiella pneumoniae</i> (11.44%), <i>Klebsiella aerogenes</i> (2.00%)	<i>Cronobacter malonaticus</i> (78.57%), <i>Klebsiella</i> _sp._MS_92-3 (3.57%), unclassified_f_ <i>Enterobacteriaceae</i> (7.14%), <i>Pantoea ananatis</i> (7.14%), unclassified_f_ <i>Erwiniaceae</i> (3.57%)
	primary-amine oxidase	1.4.3.21	<i>Klebsiella pneumoniae</i> (57.10%), unclassified_g_ <i>Klebsiella</i> (31.12%), <i>Klebsiella aerogenes</i> (5.72%), <i>Enterobacter cloacae</i> (2.73%), <i>Monascus purpureus</i> (1.36%)	<i>Aspergillus awamori</i> (20.06%), <i>Aspergillus welwitschiae</i> (36.72%), <i>Aspergillus niger</i> (36.52%), <i>Monascus purpureus</i> (6.13%)
	monoamine oxidase	1.4.3.4	<i>Monascus purpureus</i> (80.56%), <i>Aspergillus flavus</i> (19.44%)	<i>Aspergillus niger</i> (78.76%), <i>Monascus purpureus</i> (20.76%)
Tyrosine biosynthesis	phenylalanine 4-monooxygenase	1.14.16.1	<i>Burkholderia gladioli</i> (100.00%)	/
	prephenate dehydrogenase (NADP+)	1.3.1.13	<i>Saccharomyces cerevisiae</i> (99.37%)	<i>Saccharomyces cerevisiae</i> (68.86%), <i>Aspergillus niger</i> (29.47%), <i>Monascus purpureus</i> (1.67%)
	arogenate dehydrogenase	1.3.1.43	unclassified_g_ <i>Acinetobacter</i> (100.00%)	unclassified_g_ <i>Acinetobacter</i> (100.00%)
Tyrosine degradation	tyrosinase	1.14.18.1	<i>Monascus purpureus</i> (87.50%), <i>Aspergillus violaceofuscus</i> (12.50%)	<i>Aspergillus niger</i> (43.67%), <i>Aspergillus violaceofuscus</i> (23.50%), <i>Aspergillus sclerotii carbonarius</i> (16.76%), <i>Aspergillus welwitschiae</i> (14.78%), <i>Monascus purpureus</i> (1.05%)

**Table S2. Microbial contribution to genes encoding enzymes for the metabolism of characteristic flavor components during *Hongqu* rice wine brewing.**

Enzyme Function	Enzyme name	Enzyme No.	HBA	LBA
			Distribution of microbes (>1%)	Distribution of microbes (>1%)
Lactic acid metabolism	D-lactate dehydrogenase (cytochrome)	1.1.2.4	<i>Saccharomyces cerevisiae</i> (86.23%), <i>Burkholderia gladioli</i> (9.94%), <i>Monascus purpureus</i> (3.73%)	<i>Saccharomyces cerevisiae</i> (30.99%), <i>Monascus purpureus</i> (27.46%), <i>Aspergillus welwitschiae</i> (24.72%), <i>Aspergillus niger</i> (16.70%)
	hydroxyacylglutathione hydrolase	3.1.2.6	unclassified_g_ <i>Pantoea</i> (33.96%), <i>Pantoea</i> _sp._BK028 (20.47%), <i>Saccharomyces cerevisiae</i> (11.57%), unclassified_f_ <i>Enterobacteriaceae</i> (12.39%), unclassified_g_ <i>Klebsiella</i> (10.07%), <i>Lactococcus lactis</i> (4.32%), unclassified_g_ <i>Acinetobacter</i> (1.24%), unclassified_g_ <i>Enterobacter</i> (1.55%), <i>Klebsiella aerogenes</i> (1.06%), <i>Klebsiella pneumoniae</i> (1.22%)	<i>Saccharomyces cerevisiae</i> (94.45%), unclassified_f_ <i>Enterobacteriaceae</i> (1.13%), unclassified_g_ <i>Enterobacter</i> (1.49%)
	D-lactate dehydrogenase	1.1.1.28	<i>Leuconostoc mesenteroides</i> (30.97%), <i>Leuconostoc lactis</i> (11.14%), unclassified_g_ <i>Lactobacillus</i> (11.84%), <i>synthetic construct</i> (10.10%), unclassified_g_ <i>Pantoea</i> (8.43%), <i>Leuconostoc pseudomesenteroides</i> (7.08%), unclassified_f_ <i>Enterobacteriaceae</i> (3.98%), <i>Leuconostocaceae bacterium</i> (3.67%), <i>Weissella confusa</i> (3.98%), <i>Klebsiella pneumoniae</i> (3.02%), <i>Lactobacillus curvatus</i> (1.43%), <i>Leuconostoc citreum</i> (1.42%), unclassified_g_ <i>Pediococcus</i> (1.51%)	<i>Weissella confusa</i> (44.91%), <i>Aspergillus niger</i> (13.88%), <i>Pediococcus acidilactici</i> (12.29%), <i>Leuconostoc lactis</i> (10.40%), <i>Leuconostoc pseudomesenteroides</i> (3.26%), <i>Leuconostocaceae bacterium</i> (1.61%), unclassified_g_ <i>Lactobacillus</i> (2.70%), unclassified_g_ <i>Pediococcus</i> (2.48%), <i>Lactobacillus brevis</i> (2.49%), <i>Leuconostoc mesenteroides</i> (2.29%)
	L-lactate dehydrogenase (cytochrome)	1.1.2.3	<i>Pantoea dispersa</i> (33.82%), unclassified_g_ <i>Klebsiella</i> (29.14%), <i>Klebsiella aerogenes</i> (10.66%), <i>Klebsiella quasipneumoniae</i> (3.35%), <i>Saccharomyces cerevisiae</i> (7.06%), unclassified_f_ <i>Enterobacteriaceae</i> (5.35%), <i>Klebsiella pneumoniae</i> (3.84%), unclassified_g_ <i>Cronobacter</i> (1.61%), <i>Enterobacter roggenkampii</i> (1.44%), <i>Cronobacter dublinensis</i> (1.02%)	<i>Saccharomyces cerevisiae</i> (38.05%), <i>Aspergillus luchuensis</i> (26.47%), <i>Aspergillus vadensis</i> (25.92%), <i>Aspergillus phoenicis</i> (4.95%), <i>Monascus purpureus</i> (2.15%)
	lactaldehyde dehydrogenase / glycolaldehyde dehydrogenase	1.2.1.22	<i>Klebsiella pneumoniae</i> (48.91%), <i>Kalamiella piersonii</i> (41.66%), unclassified_g_ <i>Pantoea</i> (7.45%)	<i>Kosakonia cowanii</i> (48.21%), unclassified_g_ <i>Enterobacter</i> (15.18%), <i>Cronobacter malonaticus</i> (12.50%), <i>Lactobacillus</i>

				<i>paracasei</i> (10.71%), <i>Cronobacter sakazakii</i> (8.04%), <i>Kalamiella piersonii</i> (5.36%)
	NADPH-dependent methylglyoxal reductase	1.1.1.283	<i>Saccharomyces cerevisiae</i> (80.71%), <i>Pediococcus pentosaceus</i> (8.34%), <i>Leuconostoc lactis</i> (7.20%), <i>Lactobacillus brevis</i> (3.66%)	<i>Saccharomyces cerevisiae</i> (81.52%), <i>Pediococcus acidilactici</i> (12.11%), <i>Lactobacillus brevis</i> (3.18%), <i>Pediococcus pentosaceus</i> (2.98%)
	L-lactate dehydrogenase	1.1.1.27	unclassified_g_ <i>Lactobacillus</i> (27.40%), <i>Lactobacillus plantarum</i> (15.60%), <i>Leuconostoc mesenteroides</i> (12.61%), unclassified_g_ <i>Klebsiella</i> (9.75%), <i>Lactococcus lactis</i> (8.13%), <i>Leuconostoc pseudomesenteroides</i> (8.24%), unclassified_g_ <i>Lactococcus</i> (3.59%), <i>Weissella confusa</i> (5.01%), <i>Lactobacillus curvatus</i> (1.99%), <i>Leuconostoc lactis</i> (3.71%), <i>Pediococcus pentosaceus</i> (2.14%)	<i>Weissella confusa</i> (40.77%), <i>Pediococcus acidilactici</i> (25.26%), <i>Aspergillus niger</i> (11.95%), unclassified_g_ <i>Lactobacillus</i> (5.04%), <i>Weissella cibaria</i> (3.42%), <i>Lactobacillus plantarum</i> (2.05%), <i>Leuconostoc lactis</i> (2.99%), <i>Leuconostoc pseudomesenteroides</i> (2.41%), <i>Pediococcus pentosaceus</i> (2.80%)
Acetic acid metabolism	acetyl-CoA synthetase	6.2.1.1	unclassified_g_ <i>Pantoea</i> (43.29%), <i>Klebsiella pneumoniae</i> (22.55%), <i>Saccharomyces cerevisiae</i> (14.26%), <i>Klebsiella variicola</i> (6.92%), <i>Acinetobacter johnsonii</i> (1.04%), <i>Burkholderia gladioli</i> (1.02%), <i>Enterobacter sichuanensis</i> (1.80%), <i>Klebsiella aerogenes</i> (3.80%), <i>Kosakonia cowanii</i> (1.05%)	<i>Saccharomyces cerevisiae</i> (72.72%), <i>Aspergillus niger</i> (22.08%), <i>Monascus purpureus</i> (1.76%)
	lactate 2-monooxygenase	1.13.12.4	<i>Monascus purpureus</i> (72.00%), <i>Aspergillus turcosus</i> (28.00%)	<i>Aspergillus niger</i> (41.93%), <i>Aspergillus luchuensis</i> (38.44%), <i>Aspergillus awamori</i> (13.75%), <i>Aspergillus turcosus</i> (1.21%), <i>Monascus purpureus</i> (4.65%)
	succinyl-CoA:acetate CoA-transferase	2.8.3.18	<i>Acinetobacter johnsonii</i> (69.90%), <i>Burkholderia gladioli</i> (24.76%), unclassified_g_ <i>Burkholderia</i> (5.34%)	<i>Acinetobacter johnsonii</i> (100.00%)
	acetyl-CoA hydrolase	3.1.2.1	<i>Saccharomyces cerevisiae</i> (98.13%), <i>Monascus purpureus</i> (1.21%)	<i>Saccharomyces cerevisiae</i> (58.71%), <i>Aspergillus brasiliensis</i> (38.52%), <i>Monascus purpureus</i> (2.44%)
	acylphosphatase	3.6.1.7	<i>Pantoea dispersa</i> (29.09%), <i>Klebsiella variicola</i> (14.90%), <i>Leuconostoc mesenteroides</i> (14.78%), unclassified_g_ <i>Leuconostoc</i> (8.69%), <i>Lactococcus lactis</i> (7.19%), unclassified_g_ <i>Lactobacillus</i> (7.22%), <i>Leuconostoc holzapfelii</i> (3.94%), unclassified_g_ <i>Pediococcus</i> (3.02%), <i>Weissella confusa</i> (3.77%), <i>Enterobacter cloacae</i> (1.23%), <i>Klebsiella</i>	<i>Weissella confusa</i> (48.98%), <i>Pediococcus acidilactici</i> (21.70%), unclassified_g_ <i>Pediococcus</i> (7.04%), <i>Leuconostoc holzapfelii</i> (6.46%), unclassified_g_ <i>Lactobacillus</i> (3.77%), unclassified_g_ <i>Leuconostoc</i> (3.85%), <i>Weissella cibaria</i> (3.34%), <i>Leuconostoc mesenteroides</i> (1.02%), unclassified_g_ <i>Enterobacter</i> (1.23%)

			<i>aerogenes</i> (1.13%), <i>Lactobacillus curvatus</i> (2.34%)	
acetate kinase	2.7.2.1	unclassified_g_ <i>Pantoea</i> (20.94%), unclassified_g_ <i>Lactobacillus</i> (14.72%), <i>Leuconostoc pseudomesenteroides</i> (11.26%), <i>Leuconostoc mesenteroides</i> (11.23%), <i>Lactococcus lactis</i> (11.25%), <i>Lactobacillus curvatus</i> (5.11%), <i>Lactobacillus plantarum</i> (7.94%), <i>Weissella confusa</i> (4.32%), <i>Leuconostoc lactis</i> (3.46%), <i>Pediococcus pentosaceus</i> (3.26%), unclassified_g_ <i>Enterobacter</i> (2.34%), <i>Franconibacter pulveris</i> (1.78%)	<i>Weissella confusa</i> (34.55%), <i>Pediococcus acidilactici</i> (32.34%), <i>Aspergillus niger</i> (12.70%), <i>Pediococcus pentosaceus</i> (4.70%), <i>Lactobacillus brevis</i> (1.64%), <i>Lactobacillus plantarum</i> (1.22%), <i>Leuconostoc lactis</i> (2.85%), <i>Leuconostoc pseudomesenteroides</i> (3.14%), unclassified_g_ <i>Lactobacillus</i> (2.74%), unclassified_g_ <i>Leuconostoc</i> (1.45%)	
phosphate acetyltransferase	2.3.1.8	<i>Pantoea dispersa</i> (34.29%), <i>Klebsiella aerogenes</i> (6.58%), <i>Lactococcus lactis</i> (4.54%), <i>Leuconostoc mesenteroides</i> (11.27%), unclassified_g_ <i>Lactobacillus</i> (9.82%), <i>Leuconostoc pseudomesenteroides</i> (7.12%), unclassified_g_ <i>Klebsiella</i> (5.23%), <i>Klebsiella quasipneumoniae</i> (2.97%), <i>Weissella confusa</i> (2.83%), <i>Pediococcus pentosaceus</i> (2.50%), <i>Kosakonia oryzae</i> (2.44%), <i>Lactobacillus curvatus</i> (1.99%)	<i>Weissella confusa</i> (46.12%), <i>Pediococcus acidilactici</i> (27.85%), <i>Pediococcus pentosaceus</i> (7.12%), <i>Leuconostoc lactis</i> (4.44%), <i>Leuconostoc pseudomesenteroides</i> (3.96%), <i>Lactobacillus brevis</i> (2.27%), unclassified_g_ <i>Lactobacillus</i> (2.62%)	
pyruvate oxidase	1.2.3.3	<i>Lactobacillus plantarum</i> (42.92%), unclassified_g_ <i>Lactobacillus</i> (19.08%), <i>Leuconostoc lactis</i> (8.19%), <i>Leuconostoc mesenteroides</i> (8.83%), <i>Leuconostoc pseudomesenteroides</i> (6.48%), <i>Pediococcus pentosaceus</i> (5.47%), <i>Lactobacillus curvatus</i> (4.03%), <i>Weissella cibaria</i> (1.42%), <i>Weissella confusa</i> (2.84%)	<i>Weissella confusa</i> (33.69%), <i>Weissella cibaria</i> (19.70%), <i>Pediococcus acidilactici</i> (17.53%), <i>Pediococcus pentosaceus</i> (8.88%), <i>Lactobacillus plantarum</i> (6.00%), unclassified_g_ <i>Lactobacillus</i> (5.92%), <i>Leuconostoc lactis</i> (3.14%), <i>Leuconostoc pseudomesenteroides</i> (2.26%), <i>Lactobacillus brevis</i> (1.72%)	
pyruvate dehydrogenase (quinone)	1.2.5.1	unclassified_g_ <i>Pantoea</i> (71.26%), <i>Klebsiella pneumoniae</i> (16.85%), unclassified_g_ <i>Klebsiella</i> (2.75%), <i>Burkholderia gladioli</i> (1.89%), <i>Cronobacter dublinensis</i> (1.00%), <i>Pantoea</i> _sp._ <i>BK028</i> (1.20%), unclassified_f_ <i>Enterobacteriaceae</i> (1.71%), unclassified_g_ <i>Kosakonia</i> (1.34%)	<i>Enterobacter cloacae</i> (28.77%), unclassified_f_ <i>Enterobacteriaceae</i> (23.58%), <i>Kosakonia cowanii</i> (20.75%), <i>Enterobacter asburiae</i> (7.08%), <i>Cronobacter dublinensis</i> (5.66%), <i>Cronobacter sakazakii</i> (5.66%), <i>Pantoea ananatis</i> (2.36%), <i>Acetobacter musti</i> (1.42%)	
aldehyde dehydrogenase (NAD+)	1.2.1.3	<i>Pantoea dispersa</i> (38.22%), <i>Saccharomyces cerevisiae</i> (38.54%), <i>Aspergillus piperis</i> (13.05%), <i>Burkholderia</i>	<i>Saccharomyces cerevisiae</i> (50.26%), <i>Aspergillus phoenicis</i> (19.18%), <i>Aspergillus piperis</i> (16.59%), <i>Aspergillus niger</i>	

			<i>gladioli</i> (2.06%), <i>Enterobacter ludwigii</i> (2.00%), <i>Klebsiella variicola</i> (1.15%), unclassified_g_ <i>Burkholderia</i> (1.45%), unclassified_g_ <i>Enterobacter</i> (1.40%)	(11.51%), <i>Aspergillus sergii</i> (1.09%)
	propionate CoA-transferase	2.8.3.1	unclassified_g_ <i>Klebsiella</i> (95.15%), <i>Burkholderia gladioli</i> (2.20%), unclassified_g_ <i>Burkholderia</i> (1.96%)	unclassified_g_ <i>Weissella</i> (83.57%), <i>Weissella confusa</i> (11.43%), <i>Bacillus ginsengihumi</i> (3.57%), unclassified_g_ <i>Klebsiella</i> (1.43%)
	aldehyde dehydrogenase [NAD(P)+]	1.2.1.5	<i>Saccharomyces cerevisiae</i> (99.51%)	<i>Saccharomyces cerevisiae</i> (70.44%), <i>Aspergillus niger</i> (15.59%), <i>Monascus purpureus</i> (13.92%)
Alcohol-Aldehyde-Carboxylate-Ester metabolism	alcohol dehydrogenase	1.1.1.1	<i>Lactobacillus plantarum</i> (69.00%), unclassified_g_ <i>Pantoea</i> (32.35%), <i>Lactobacillus curvatus</i> (19.68%), unclassified_g_ <i>Lactobacillus</i> (6.59%), <i>Saccharomyces cerevisiae</i> (10.84%), <i>Lactobacillus plantarum</i> (6.55%), <i>Lactococcus lactis</i> (6.16%), <i>Klebsiella pneumoniae</i> (5.80%), <i>Enterobacter asburiae</i> (1.40%), <i>Enterobacter huaxiensis</i> (2.20%), <i>Klebsiella variicola</i> (2.68%), <i>Lactobacillus curvatus</i> (2.43%), <i>Leuconostoc lactis</i> (3.31%), <i>Leuconostoc mesenteroides</i> (1.31%), <i>L euconostoc pseudomesenteroides</i> (2.17%), <i>Pantoea septica</i> (1.07%), unclassified_g_ <i>Klebsiella</i> (3.37%), unclassified_g_ <i>Leuconostoc</i> (3.12%), <i>Weissella confusa</i> (1.62%)	<i>Saccharomyces cerevisiae</i> (44.80%), <i>Aspergillus niger</i> (19.87%), <i>Weissella confusa</i> (9.11%), <i>Monascus purpureus</i> (8.57%), <i>Weissella cibaria</i> (1.00%), <i>Lactobacillus uvarum</i> (5.05%), <i>Pediococcus acidilactici</i> (4.21%), <i>Leuconostoc lactis</i> (1.51%)
	carboxylesterase	3.1.1.1	unclassified_g_ <i>Burkholderia</i> (4.38%), <i>Burkholderia gladioli</i> (4.27%), <i>Lactobacillus brevis</i> (2.67%)	<i>Aspergillus niger</i> (89.70%), <i>Lactobacillus plantarum</i> (6.09%), <i>Lactobacillus brevis</i> (4.21%)
	coniferyl-aldehyde dehydrogenase	1.2.1.68	<i>Lactobacillus plantarum</i> (83.69%), <i>Acinetobacter johnsonii</i> (7.34%), <i>Acinetobacter johnsonii</i> (4.84%), <i>Burkholderia gladioli</i> (3.67%)	<i>Lactobacillus plantarum</i> (99.49%)
	vanillin dehydrogenase	1.2.1.67	<i>Burkholderia gladioli</i> (100.00%)	/
	phospholipid:diacylglycerol acyltransferase	2.3.1.158	<i>Saccharomyces cerevisiae</i> (98.27%), <i>Monascus purpureus</i> (1.64%)	<i>Saccharomyces cerevisiae</i> (58.89%), <i>Aspergillus niger</i> (37.12%), <i>Monascus purpureus</i> (3.99%)
	diacylglycerol O-acyltransferase 2	2.3.1.20	<i>Acinetobacter johnsonii</i> (90.79%), <i>Monascus purpureus</i> (9.21%)	<i>Aspergillus niger</i> (93.38%), <i>Monascus purpureus</i> (6.55%)
	2-acylglycerol O-acyltransferase	2.3.1.22	<i>Saccharomyces cerevisiae</i> (99.02%)	<i>Saccharomyces cerevisiae</i> (61.93%), <i>Aspergillus awamori</i>



	3			(36.10%), <i>Monascus purpureus</i> (1.12%)
	diacylglycerol O-acyltransferase / wax synthase	2.3.1.75	<i>Acinetobacter johnsonii</i> (90.79%), <i>Monascus purpureus</i> (9.21%)	<i>Aspergillus niger</i> (93.38%), <i>Monascus purpureus</i> (5.61%)
	alcohol O-acetyltransferase	2.3.1.84	<i>Saccharomyces cerevisiae</i> (100.00%)	<i>Saccharomyces cerevisiae</i> (100.00%)
	acetyl esterase	3.1.1.-	unclassified_g_ <i>Pantoea</i> (19.96%), <i>Klebsiella pneumoniae</i> (15.36%), unclassified_f_ <i>Enterobacteriaceae</i> (11.80%), <i>Saccharomyces cerevisiae</i> (8.60%), <i>Leuconostoc mesenteroides</i> (8.51%), <i>Leuconostoc pseudomesenteroides</i> (5.67%), <i>Klebsiella variicola</i> (4.43%), <i>Lactococcus lactis</i> (4.14%), unclassified_g_ <i>Klebsiella</i> (4.11%), <i>Leuconostoc lactis</i> (2.56%), <i>Weissella confusa</i> (2.40%), <i>Klebsiella aerogenes</i> (2.32%), <i>Enterobacter cloacae</i> (1.91%), <i>Leuconostoc citreum</i> (1.49%), <i>Klebsiella michiganensis</i> (1.49%), unclassified_g_ <i>Lactobacillus</i> (1.23%)	<i>Saccharomyces cerevisiae</i> (53.77%), <i>Weissella confusa</i> (21.73%), <i>Aspergillus niger</i> (7.58%), <i>Pediococcus acidilactici</i> (5.90%), <i>Leuconostoc pseudomesenteroides</i> (2.11%), <i>Leuconostoc lactis</i> (1.72%), <i>Leuconostoc citreum</i> (1.32%), <i>Leuconostoc mesenteroides</i> (1.15%)
	triacylglycerol lipase	3.1.1.3	<i>Saccharomyces cerevisiae</i> (71.34%), unclassified_o_ <i>Enterobacterales</i> (22.30%), <i>Acinetobacter johnsonii</i> (2.31%), unclassified_g_ <i>Acinetobacter</i> (2.01%)	<i>Saccharomyces cerevisiae</i> (61.36%), <i>Aspergillus niger</i> (16.79%), <i>Aspergillus phoenicis</i> (10.36%), <i>Monascus purpureus</i> (8.00%), <i>Aspergillus oryzae</i> (2.26%)
	pyruvate decarboxylase	4.1.1.1	<i>Saccharomyces cerevisiae</i> (98.52%)	<i>Saccharomyces cerevisiae</i> (58.22%), <i>Aspergillus niger</i> (39.51%), <i>Monascus purpureus</i> (1.56%)
	tannase	3.1.1.20	<i>Aspergillus niger</i> (100.00%)	<i>Aspergillus niger</i> (71.03%), <i>Aspergillus awamori</i> (13.58%), <i>Aspergillus welwitschiae</i> (15.35%)
	phenylalanine ammonia-lyase	4.3.1.24	<i>Aspergillus niger</i> (100.00%)	<i>Aspergillus niger</i> (70.36%), <i>Aspergillus phoenicis</i> (28.56%), <i>Aspergillus awamori</i> (1.07%)
	aldehyde dehydrogenase [NAD(P)+]	1.2.1.5	<i>Saccharomyces cerevisiae</i> (99.51%)	<i>Saccharomyces cerevisiae</i> (70.44%), <i>Aspergillus niger</i> (15.59%), <i>Monascus purpureus</i> (13.92%)
	aldehyde dehydrogenase (NAD+)	1.2.1.3	<i>Pantoea dispersa</i> (38.22%), <i>Saccharomyces cerevisiae</i> (38.54%), <i>Aspergillus piperis</i> (13.05%), <i>Burkholderia gladioli</i> (2.06%), <i>Enterobacter ludwigii</i> (2.00%), <i>Klebsiella variicola</i> (1.15%), unclassified_g_ <i>Burkholderia</i> (1.45%),	<i>Saccharomyces cerevisiae</i> (50.26%), <i>Aspergillus phoenicis</i> (19.18%), <i>Aspergillus piperis</i> (16.59%), <i>Aspergillus niger</i> (11.51%), <i>Aspergillus sergii</i> (1.09%)

			unclassified_g_Enterobacter (1.40%)	
	acyl-CoA thioesterase I	3.1.1.2	<i>Pantoea dispersa</i> (74.12%), <i>Klebsiella pneumoniae</i> (20.62%), <i>Acinetobacter johnsonii</i> (1.18%), <i>Kalamiella piersonii</i> (1.83%)	<i>Kosakonia cowanii</i> (39.34%), <i>Franconibacter helveticus</i> (27.05%), <i>Kalamiella piersonii</i> (22.95%), unclassified_g_Lactobacillus (6.56%), <i>Cronobacter condimenti</i> (1.64%), unclassified_g_Pantoea (1.64%)
	alcohol dehydrogenase (NADP+)	1.1.1.2	unclassified_g_Pantoea (47.92%), <i>Klebsiella pneumoniae</i> (13.62%), <i>Pantoea dispersa</i> (12.89%), unclassified_f_Erwiniaceae (10.22%), unclassified_g_Klebsiella (7.37%), <i>Saccharomyces cerevisiae</i> (5.51%)	<i>accharomyces cerevisiae</i> (59.04%), <i>Aspergillus luchuensis</i> (29.16%), <i>Monascus purpureus</i> (3.99%), unclassified_g_Enterobacter (2.13%), unclassified_f_Enterobacteriaceae (1.99%), <i>Cronobacter malonaticus</i> (1.48%), <i>Kosakonia cowanii</i> (1.28%)
Phenolic metabolism	anthranilate 1,2-dioxygenase (deaminating, decarboxylating)	1.14.12.1	unclassified_g_Burkholderia (100.00%)	/
	1,6-dihydroxycyclohexa-2,4-diene-1-carboxylate dehydrogenase	1.3.1.25	<i>Klebsiella pneumoniae</i> (49.38%), <i>Klebsiella variicola</i> (44.88%), <i>Acinetobacter</i> _sp._BMW17 (4.14%), <i>Burkholderia gladioli</i> (1.59%)	/
	shikimate dehydrogenase	1.1.1.25	unclassified_f_Enterobacteriaceae (22.78%), unclassified_g_Pantoea (17.37%), unclassified_g_Lactobacillus (17.00%), unclassified_g_Klebsiella (9.31%), <i>Leuconostoc mesenteroides</i> (5.22%), <i>Saccharomyces cerevisiae</i> (5.17%), <i>Lactobacillus plantarum</i> (4.54%), unclassified_g_Leuconostoc (3.79%), <i>Klebsiella quasipneumoniae</i> (3.25%), <i>Lactococcus lactis</i> (2.50%), <i>Klebsiella aerogenes</i> (1.84%), <i>Leuconostoc lactis</i> (1.46%), <i>Burkholderia gladioli</i> (1.11%)	<i>Saccharomyces cerevisiae</i> (50.50%), <i>Aspergillus oryzae</i> (23.74%), <i>Weissella confusa</i> (11.48%), unclassified_g_Lactobacillus (5.71%), unclassified_g_Leuconostoc (2.36%), <i>Lactobacillus plantarum</i> (1.49%), <i>Weissella cibaria</i> (1.33%)

	salicylate 1-monooxygenase	1.14.13.1	<i>Monascus_purpureus</i> (45.61%), <i>Aspergillus_niger</i> (41.23%), <i>Aspergillus_flavus</i> (7.02%), <i>Aspergillus_oryzae</i> (2.63%), <i>Aspergillus_novoparasiticus</i> (1.75%), <i>Lachnellula_cervina</i> (1.75%)	<i>Aspergillus_niger</i> (88.38%), <i>Monascus_purpureus</i> (5.36%), <i>Aspergillus_welwitschiae</i> (3.66%), <i>Aspergillus_brasiliensis</i> (2.19%)
	phenacrylate decarboxylase	4.1.1.102	<i>Saccharomyces_cerevisiae</i> (98.69%)	<i>Saccharomyces_cerevisiae</i> (53.41%), <i>Aspergillus_niger</i> (44.98%), <i>Monascus_purpureus</i> (1.59%)
	6-methylsalicylate decarboxylase	4.1.1.52	unclassified_g_ <i>Lactobacillus</i> (99.61%)	<i>Aspergillus_niger</i> (89.53%), unclassified_g_ <i>Lactobacillus</i> (9.19%), <i>Kosakonia_cowanii</i> (1.24%)
	6-methylsalicylic-acid synthase	2.3.1.165	/	<i>Aspergillus_phoenicis</i> (99.95%)
	feruloyl esterase	3.1.1.73	<i>Monascus_purpureus</i> (71.43%), <i>Aspergillus_flavus</i> (28.57%)	<i>Aspergillus_niger</i> (55.09%), <i>Aspergillus_awamori</i> (39.97%), <i>Monascus_purpureus</i> (2.66%), <i>Aspergillus_flavus</i> (2.27%)
	isochorismate lyase	4.2.99.21	<i>Klebsiella_pneumoniae</i> (71.88%), <i>Klebsiella_oxytoca</i> (15.63%), <i>Escherichia_coli</i> (12.50%)	<i>Aspergillus_niger</i> (55.85%), <i>Aspergillus_welwitschiae</i> (44.00%)
	4-coumarate-CoA ligase	6.2.1.12	<i>Monascus_purpureus</i> (100.00%)	<i>Monascus_purpureus</i> (100.00%)
	aldehyde dehydrogenase [NAD(P)+]	1.2.1.5	<i>Saccharomyces_cerevisiae</i> (99.51%)	<i>Saccharomyces_cerevisiae</i> (70.44%), <i>Aspergillus_niger</i> (15.59%), <i>Monascus_purpureus</i> (13.92%)
	catechol O-methyltransferase	2.1.1.6	<i>Monascus_purpureus</i> (66.67%), <i>Aspergillus_niger</i> (33.33%)	<i>Aspergillus_niger</i> (97.56%), <i>Monascus_purpureus</i> (2.40%)
Butane-2,3-diolmetabolism	(R,R)-butanediol dehydrogenase / meso-butanediol dehydrogenase / diacetyl reductase	1.1.1.4	<i>Saccharomyces_cerevisiae</i> (52.66%), <i>Leuconostocaceae_bacterium</i> (27.85%), <i>Lactococcus_lactis</i> (12.40%), <i>Leuconostoc_citreum</i> (1.72%), <i>Leuconostoc_mesenteroides</i> (2.50%), unclassified_g_ <i>Acinetobacter</i> (2.27%)	<i>Saccharomyces_cerevisiae</i> (92.41%), <i>Leuconostocaceae_bacterium</i> (3.26%), <i>Leuconostoc_lactis</i> (2.91%), unclassified_g_ <i>Lactobacillus</i> (1.11%)
	meso-butanediol dehydrogenase / (S,S)-butanediol dehydrogenase / diacetyl reductase	1.1.1.76	<i>Pantoea_dispersa</i> (22.73%), <i>Leuconostoc_mesenteroides</i> (20.47%), <i>Klebsiella_pneumoniae</i> (17.67%), <i>Leuconostoc_suionicum</i> (16.93%), <i>Lactococcus_lactis</i> (3.23%), <i>Leuconostoc_citreum</i> (1.26%), <i>Leuconostoc_lactis</i> (3.47%), <i>Leuconostoc_pseudomesenteroides</i> (4.80%), <i>Pediococcus_pentosaceus</i> (1.52%), unclassified_g_ <i>Lactococcus</i> (2.26%), <i>Weissella_confusa</i> (1.83%)	<i>Leuconostoc_suionicum</i> (42.46%), <i>Weissella_confusa</i> (27.80%), <i>Pediococcus_acidilactici</i> (9.29%), <i>Weissella_cibaria</i> (6.72%), <i>Aspergillus_niger</i> (3.87%), <i>Lactobacillus_brevis</i> (1.74%), <i>Leuconostoc_pseudomesenteroides</i> (1.28%), <i>Pediococcus_pentosaceus</i> (1.90%), <i>Leuconostoc_lactis</i> (1.00%), <i>Leuconostoc_mesenteroides</i> (1.11%)
Fatty acid biosynthesis	medium-chain acyl-[acyl-carrier-protein] hydrolase	3.1.2.21	<i>Leuconostoc_mesenteroides</i> (28.74%), unclassified_g_ <i>Lactobacillus</i> (20.43%), <i>Leuconostoc_pseudomesenteroides</i> (17.29%), <i>Leuconostoc_lactis</i>	<i>Weissella_confusa</i> (44.53%), <i>Pediococcus_acidilactici</i> (28.87%), unclassified_g_ <i>Pediococcus</i> (6.27%), <i>Leuconostoc_pseudomesenteroides</i> (5.90%), unclassified_g_ <i>Lactobacillus</i>

			(8.25%), <i>Lactococcus lactis</i> (7.94%), unclassified_g_ <i>Pediococcus</i> (4.31%), <i>Lactobacillus curvatus</i> (4.82%), <i>Weissella confusa</i> (5.19%), <i>Leuconostoc citreum</i> (1.71%)	(3.57%), <i>Leuconostoc lactis</i> (3.15%), unclassified_g_ <i>Weissella</i> (2.81%), <i>Lactobacillus brevis</i> (2.67%), <i>Leuconostoc mesenteroides</i> (1.29%)
	acetyl-CoA carboxylase / biotin carboxylase 1	6.4.1.2	unclassified_g_ <i>Pantoea</i> (16.69%), <i>Leuconostoc mesenteroides</i> (14.48%), <i>Lactobacillus plantarum</i> (9.55%), unclassified_g_ <i>Klebsiella</i> (8.17%), unclassified_g_ <i>Lactobacillus</i> (6.44%), <i>Weissella confusa</i> (4.58%), <i>Cyberlindnera fabianii</i> (3.19%), unclassified_f_ <i>Enterobacteriaceae</i> (3.02%), <i>Saccharomyces cerevisiae</i> (3.00%), <i>Klebsiella pneumoniae</i> (2.21%), <i>Kluyvera cryocrescens</i> (1.30%), <i>Lactococcus lactis</i> (3.50%), <i>Leuconostoc lactis</i> (3.16%), <i>Leuconostoc pseudomesenteroides</i> (2.75%), <i>Leuconostocaceae bacterium</i> (2.19%), <i>Pantoea deleyi</i> (1.83%), <i>Pantoea</i> _sp._SM3 (1.62%), <i>Salmonella enterica</i> (1.15%), unclassified_g_ <i>Leuconostoc</i> (2.21%), unclassified_g_ <i>Pediococcus</i> (1.53%), <i>Enterobacter hormaechei</i> (1.00%)	<i>Weissella confusa</i> (35.71%), <i>Pediococcus acidilactici</i> (19.92%), <i>Cyberlindnera fabianii</i> (13.59%), <i>Saccharomyces cerevisiae</i> (12.98%), <i>Aspergillus welwitschiae</i> (6.80%), <i>Lactobacillus plantarum</i> (1.19%), unclassified_g_ <i>Pediococcus</i> (1.67%)
	fatty acid synthase subunit beta, fungi type	2.3.1.86	<i>Saccharomyces cerevisiae</i> (96.38%), <i>Monascus purpureus</i> (2.06%)	<i>Aspergillus niger</i> (47.45%), <i>Saccharomyces cerevisiae</i> (23.25%), <i>Aspergillus phoenicis</i> (8.95%), <i>Monascus purpureus</i> (7.22%), <i>Aspergillus welwitschiae</i> (6.44%), <i>Aspergillus awamori</i> (6.00%)
Fatty acid elongation	palmitoyl-protein thioesterase	3.1.2.22	<i>Monascus purpureus</i> (100.00%)	<i>Aspergillus niger</i> (98.09%), <i>Monascus purpureus</i> (1.00%)
	mitochondrial enoyl-[acyl-carrier protein] reductase / trans-2-enoyl-CoA reductase	1.3.1.38	<i>Saccharomyces cerevisiae</i> (98.20%), <i>Monascus purpureus</i> (1.70%)	<i>Saccharomyces cerevisiae</i> (63.02%), <i>Aspergillus welwitschiae</i> (34.62%), <i>Monascus purpureus</i> (2.37%)
	enoyl-CoA hydratase	4.2.1.17	<i>Pantoea cypripedii</i> (26.97%), unclassified_f_ <i>Enterobacteriaceae</i> (26.29%), <i>Pantoea dispersa</i> (22.94%), <i>Klebsiella aerogenes</i> (7.48%), <i>Klebsiella pneumoniae</i> (3.88%), <i>Klebsiella quasipneumoniae</i> (3.55%), <i>Klebsiella michiganensis</i>	<i>Trichomonascus ciferrii</i> (49.07%), <i>Aspergillus niger</i> (25.90%), <i>Klebsiella cf. planticola</i> _B43 (5.63%), <i>Enterobacter roggenkampii</i> (3.49%), <i>Monascus purpureus</i> (3.53%), <i>Cronobacter malonaticus</i> (2.10%), <i>Cronobacter sakazakii</i> (1.56%), unclassified_g_ <i>Enterobacter</i>

			(2.01%), <i>Acinetobacter johnsonii</i> (1.20%), <i>Enterobacter cloacae</i> (1.08%), <i>Enterobacter roggenkampii</i> (1.04%)	(2.40%), <i>Enterobacter hormaechei</i> (1.22%), unclassified_g_ <i>Citrobacter</i> (1.05%)
	3-hydroxyacyl-CoA dehydrogenase	1.1.1.35	<i>Pantoea cyripedii</i> (26.00%), <i>Pantoea dispersa</i> (22.10%), unclassified_f_ <i>Enterobacteriaceae</i> (19.10%), <i>Brochothrix thermosphacta</i> (12.59%), <i>Klebsiella aerogenes</i> (7.21%), <i>Klebsiella quasipneumoniae</i> (3.43%), <i>Acinetobacter johnsonii</i> (1.16%), <i>Burkholderia gladioli</i> (1.01%), <i>Enterobacter roggenkampii</i> (1.00%), <i>Klebsiella michiganensis</i> (1.94%)	<i>Brochothrix thermosphacta</i> (52.48%), <i>Aspergillus welwitschiae</i> (32.28%), <i>Klebsiella cf. planticola</i> _B43 (3.25%), <i>Monascus purpureus</i> (2.77%), <i>Enterobacter roggenkampii</i> (2.01%), <i>Cronobacter malonaticus</i> (1.21%), <i>Aspergillus niger</i> (1.00%)
	acetyl-CoA acyltransferase	2.3.1.16	unclassified_g_ <i>Pantoea</i> (71.05%), <i>Klebsiella quasipneumoniae</i> (9.60%), <i>Saccharomyces cerevisiae</i> (6.05%), <i>Klebsiella aerogenes</i> (4.91%), <i>Klebsiella pneumoniae</i> (1.56%), <i>Escherichia</i> _sp._E4208 (1.15%), unclassified_p_ <i>Proteobacteria</i> (1.07%)	<i>Aspergillus niger</i> (50.92%), <i>Saccharomyces cerevisiae</i> (42.98%), <i>Monascus purpureus</i> (2.17%), <i>Kosakonia cowanii</i> (1.09%)
Phenylacetaldehyde-Phenylethylalcohol metabolism	aryl-alcohol dehydrogenase	1.1.1.90	unclassified_g_ <i>Lactobacillus</i> (46.54%), <i>Klebsiella variicola</i> (27.96%), <i>Lactobacillus curvatus</i> (12.07%), <i>Pediococcus pentosaceus</i> (10.67%), <i>Lactobacillus vaccिनosterus</i> (1.08%)	<i>Pediococcus pentosaceus</i> (58.11%), unclassified_g_ <i>Lactobacillus</i> (21.31%), <i>Lactobacillus brevis</i> (16.94%), <i>Weissella bombi</i> (1.46%), <i>Weissella hellenica</i> (1.64%)
	primary-amine oxidase	1.4.3.21	<i>Klebsiella pneumoniae</i> (57.10%), unclassified_g_ <i>Klebsiella</i> (31.12%), <i>Klebsiella aerogenes</i> (5.72%), <i>Enterobacter cloacae</i> (2.73%), <i>Monascus purpureus</i> (1.36%)	<i>Aspergillus awamori</i> (20.06%), <i>Aspergillus welwitschiae</i> (36.72%), <i>Aspergillus niger</i> (36.52%), <i>Monascus purpureus</i> (6.13%)
	monoamine oxidase	1.4.3.4	<i>Monascus purpureus</i> (80.56%), <i>Aspergillus flavus</i> (19.44%)	<i>Aspergillus niger</i> (78.76%), <i>Monascus purpureus</i> (20.76%)
	aromatic-L-amino-acid decarboxylase	4.1.1.28	<i>Monascus purpureus</i> (100%)	<i>Aspergillus niger</i> (92.31%), <i>Monascus purpureus</i> (7.57%)

**Figure S1.** Analysis of microbial genera in HBAs and LBAs brewing. The relative abundance of the predominant bacterial (A) and fungal (B) genera. Principal component analysis (PCA) of bacterial (C) and fungal (D) communities. Visualization of the differences in the relative abundance of bacterial (E) and fungal (F) genera between HBAs and LBAs. Microbial genera with significant differences between HBAs and LBAs were determined using a Welch's t-test, and the Benjamini-Hochberg procedure was used to control the false-discovery rate due to multiple testing. Corrected P values are shown at right.

