

Supplementary materials

Table S1. Characteristic volatile flavor components (VFCs) in GTW and WYW screened by SPME-GC/MS assay and OAV calculation.

No.	Compounds	CAS	RI	Concentration (ug/L)		Threshold (mg/L)#	OAV	
				WYW_D45	GTW_D45		WYW_D45	GTW_D45
Acid								
C37	γ-Hydroxybutyric acid	591-81-1	1623	14.21±1.73	6.78±0.5	-	-	-
C72	Octanoic acid	124-07-2	2065	1091±26.74	349.39±51.22	3	0.364	0.116
C82	n-Decanoic acid	334-48-5	2280	59785.04±146.6	11408.41±4078.87	10	5.979	1.141
C89	Dodecanoic acid	143-07-7	2495	28.34±1.81	13.67±5.51	10	0.003	0.001
Alcohol								
C3	Isobutanol	78-83-1	1095	64002.17±2374.71	21780.91±16540.6 7	6.5052	9.839	3.348
C7	1-Pentanol	71-41-0	1250	n.d.	258.04±51.16	0.1502	-	1.718
C21	1-Octen-3-ol	3391-86-4	1448	103.39±7.16	36.38±3.1	0.0015	68.927	24.255
C36	(2E)-2-Octen-1-ol	18409-17-1	1607	29.07±0.61	n.d.	0.04	0.727	-
C43	(3Z)-3-Nonen-1-ol	10340-23-5	1672	n.d.	3.08±0.32	-	-	-
C46	3-(Methylsulfanyl)-1-propanol	505-10-2	1709	2348.78±156.81	1152.95±171.92	0.12323	19.060	9.356
C50	1-Decanol	112-30-1	1751	n.d.	8.67±1.05	0.775	-	0.011
C51	Citronellol	106-22-9	1763	0.73±0.06	2.15±0.36	0.062	0.012	0.035
C58	Geraniol	106-24-1	1838	6.66±0.55	n.d.	0.0066	1.009	-
C73	2,4,7,9-Tetramethyl-5-decyn-4,7-diol	126-86-3	1976	96.69±13.45	3.56±0.57	-	-	-
C85	Farnesol	4602-84-0	2349	8.89±0.73	n.d.	1	0.009	-

Ester

C1	Ethyl acetate	141-78-6	906	196740.94±34968.17	88800.06±8597.6	7.5	26.232	11.840
C2	Ethyl butyrate	105-54-4	1039	707.6±354.38	237.5±175.61	0.0009	786.220	263.890
C4	Isoamyl acetate	123-92-2	1125	403.22±17.44	948.14±92.06	0.00015	2688.103	6320.952
C13	Ethyl heptanoate	106-30-9	1330	160.11±28.05	434.26±52.92	0.0019	84.266	228.556
C20	Ethyl octanoate	106-32-1	1429	9746.12±201.35	3056.34±235.04	0.0193	504.980	158.360
C28	Ethyl nonanoate	123-29-5	1528	n.d.	99.9±7.76	0.377	-	0.265
C38	Ethyl caprate	110-38-3	1632	18485.69±3276.89	5265.61±1139.65	0.005	3697.138	1053.122
C42	Diethyl succinate	123-25-1	1674	21411.91±922.29	1525.91±46.2	100	0.214	0.015
C52	Ethyl glutarate	818-38-2	1777	10.85±0.63	4.75±1.48	-	-	-
C53	Ethyl 2-phenylacetate	101-97-3	1780	875.43±42.22	139.08±5.58	0.15555	5.628	0.894
C54	Butyl ethyl succinate	67233-92-5	1759	139.68±8.01	16.08±1.37	-	-	-
C56	Phenethyl acetate	103-45-7	1808	231.64±9.3	560.37±22.91	0.24959	0.928	2.245
C57	Ethyl laurate	106-33-2	1837	47.78±4.34	13.21±2.66	5.9	0.008	0.002
C61	n-Butyl butanoate	109-21-7	1863	462.19±32.98	33.95±1.55	0.4	1.155	0.085
C62	Cyclopentyl butyrate	6290-13-7	1876	14.34±0.64	1.99±0.34	-	-	-
C63	Ethyl 3-phenylpropanoate	2021-28-5	1879	1.94±0.38	n.d.	0.0016	1.212	-
C65	Ethyl 3-methylbutyl succinate	28024-16-0	1897	400.52±19.41	29.84±4.03	-	-	-
C71	Ethyl myristate	124-06-1	2043	24.88±3.9	3.55±1.17	4	0.006	0.001
C74	Ethyl 3-hydroxytridecanoate	107141-15-1	1886	116.64±5.01	34.1±9.96	-	-	-
C81	Ethyl palmitate	628-97-7	2252	18291.63±3034.05	5502.63±3114.87	2	9.146	2.751
C84	Ethyl 9-hexadecenoate	54546-22-4	2327	22.8±3.6	n.d.	10	0.002	-
C87	Ethyl stearate	111-61-5	2462	132.84±22.96	29.85±6.88	0.51	0.260	0.059

C90	Ethyl linoleate	544-35-4	2533	13553.57±4656.02	n.d.	0.45	30.119	-
Ketone								
C8	3-Octanone	106-68-3	1255	23.24±15.27	n.d.	0.0214	1.086	-
C14	6-Methyl-5-hepten-2-one	110-93-0	1333	12.44±1.21	n.d.	0.068	0.183	-
C17	2-Nonanone	821-55-6	1379	55.38±1.02	5.96±0.24	0.2	0.277	0.030
C40	Acetophenone	98-86-2	1641	18.56±1.33	8.81±1.37	0.245	0.076	0.036
Phenol								
C49	4-(Methylsulfanyl)phenol	1073-72-9	1744	17.88±2.79	3.98±0.9	0.8	0.022	0.005
C69	Phenol	108-95-2	2006	n.d.	1.36±0.34	58.58525	-	-
C78	4-Ethylphenol	123-07-9	2180	182.81±8.26	n.d.	0.013	14.062	-
C80	2-Methoxy-4-vinylphenol	7786-61-0	2200	858.41±108.83	12.67±2.21	0.01202	71.415	1.054
Others								
C9	2-Methylpyrazine	109-08-0	1263	n.d.	191.91±62.35	30	-	0.006
C19	1,3-Di-tert-butylbenzene	1014-60-4	1419	12.08±5.56	n.d.	-	-	-
C86	2,3-Dihydro-1-benzofuran	496-16-2	2402	20.4±3.24	7.69±3.17	-	-	-

Threshold were from the literatures [Yu et al., 2019; Liu et al., 2022; Moreno et al., 2005; Salo et al., 2006], or from Compilations of Odour Threshold Values in Air, Water and Other media [Gemert, 2003] (Second Enlarged and Revised Edition), ISBN 978-7-03-058320-8

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Table S2. Microbial contributions to amino acids and biogenic amines metabolizing enzymes in GTW and WYW brewing.

Enzyme function	Enzyme name	Enzyme number	GTW	WYW
			Distribution of microbes (>1%)	Distribution of microbes (>1%)
Biogenic amines synthesis	aromatic-L-amino-acid decarboxylase	4.1.1.28	<i>Monascus purpureus</i> (100%)	<i>Aspergillus niger</i> (96.09%), <i>Monascus purpureus</i> (3.91%)
	ornithine decarboxylase	4.1.1.17	<i>Pantoea dispersa</i> (41.48%), <i>Kosakonia cowanii</i> (9.58%), <i>Klebsiella pneumoniae</i> (9.55%), <i>Enterobacter mori</i> (7.50%), <i>Enterobacter hormaechei</i> (6.66%), <i>Enterobacter roggenkampii</i> (5.95%), <i>Enterobacter cloacae</i> (4.37%), <i>Cronobacter malonaticus</i> (2.85%), <i>Enterobacter bugandensis</i> (2.08%), <i>Franconibacter pulveris</i> (1.86%), <i>unclassified_f_Enterobacteriaceae</i> (1.78%), <i>Enterobacter_sp._SES19</i> (1.36%)	<i>Aspergillus niger</i> (27.61%), <i>Saccharomyces cerevisiae</i> (16.65%), <i>Enterobacter cloacae</i> (14.08%), <i>Enterobacter mori</i> (10.86%), <i>Kosakonia cowanii</i> (10.80%), <i>Enterobacter asburiae</i> (4.70%), <i>Enterobacter bugandensis</i> (2.72%), <i>Enterobacter hormaechei</i> (2.58%), <i>Pantoea deleyi</i> (1.98%), <i>Monascus purpureus</i> (1.83%), <i>Enterobacter_sp._18A13</i> (1.74%), <i>Pantoea ananatis</i> (1.00%)
	agmatinase	3.5.3.11	<i>Burkholderia gladioli</i> (81.88%), <i>unclassified_c_Gammaproteobacteria</i> (6.45%), <i>Enterobacter chengduensis</i> (3.74%), <i>Leclercia adecarboxylata</i> (3.64%), <i>unclassified_g_Pantoea</i> (1.98%)	<i>Aspergillus niger</i> (31.82%), <i>Aspergillus phoenicis</i> (31.24%), <i>Enterobacter chengduensis</i> (7.80%), <i>Escherichia coli</i> (6.12%), <i>unclassified_c_Gammaproteobacteria</i> (5.43%), <i>Burkholderia gladioli</i> (4.82%), <i>Aspergillus udagawae</i> (2.95%), <i>Monascus purpureus</i> (2.12%), <i>Aspergillus awamori</i> (2.06%), <i>unclassified_g_Pantoea</i> (1.90%), <i>Monascus ruber</i> (1.51%), <i>Bacillus amyloliquefaciens</i> (1.50%)
	N-carbamoylputrescine amidase	3.5.1.53	<i>Burkholderia gladioli</i> (90.93%), <i>Klebsiella_cf._planticola_B43</i> (9.03%)	<i>unclassified_f_Enterobacteriaceae</i> (78.93%), <i>Burkholderia gladioli</i> (20.40%)

	non-specific polyamine oxidase	1.5.3.17	<i>Saccharomyces cerevisiae</i> (100%)	<i>Saccharomyces cerevisiae</i> (99.16%)
	agmatine deiminase	3.5.3.12	<i>Burkholderia gladioli</i> (92.43%), <i>Kosakonia cowanii</i> (4.85%), <i>Lactococcus lactis</i> (2.37%)	<i>Kosakonia cowanii</i> (54.10%), <i>Burkholderia gladioli</i> (30.79%), <i>Lactococcus lactis</i> (9.97%), <i>Burkholderia cepacia</i> (3.97%)
	arginine decarboxylase	4.1.1.19	<i>unclassified_g_Burkholderia</i> (59.21%), <i>Pantoea dispersa</i> (24.00%), <i>Klebsiella pneumoniae</i> (8.53%), <i>unclassified_g_Enterobacter</i> (2.71%), <i>Pantoea ananatis</i> (1.38%), <i>Cronobacter sakazakii</i> (1.06%)	<i>unclassified_g_Enterobacter</i> (22.48%), <i>unclassified_g_Burkholderia</i> (16.63%), <i>Klebsiella pneumoniae</i> (13.03%), <i>Pantoea deleyi</i> (11.64%), <i>Enterobacter hormaechei</i> (7.40%), <i>unclassified_f_Enterobacteriaceae</i> (5.23%), <i>Mixta calida</i> (4.56%), <i>Bacillus amyloliquefaciens</i> (4.36%), <i>Pantoea dispersa</i> (2.12%), <i>Cronobacter sakazakii</i> (2.11%), <i>Pantoea ananatis</i> (2.09%), <i>Kosakonia sacchari</i> (1.91%), <i>Bacillus ginsengihumi</i> (1.31%), <i>Variovorax_sp._SCN_67-85</i> (1.12%)
	spermine synthase	2.5.1.22	<i>Saccharomyces cerevisiae</i> (100.00%)	<i>Saccharomyces cerevisiae</i> (100.00%)
	L-tryptophan decarboxylase	4.1.1.105	<i>Monascus purpureus</i> (100.00%)	<i>Aspergillus niger</i> (96.09%), <i>Monascus purpureus</i> (3.91%)
	lysine decarboxylase	4.1.1.18	<i>Pantoea dispersa</i> (49.69%), <i>Klebsiella pneumoniae</i> (22.86%), <i>Enterobacter cloacae</i> (14.47%), <i>Kosakonia cowanii</i> (4.57%), <i>Cronobacter malonaticus</i> (1.82%), <i>unclassified_g_Kosakonia</i> (1.73%), <i>Pantoea deleyi</i> (1.65%)	<i>Enterobacter cloacae</i> (55.40%), <i>Kosakonia cowanii</i> (15.50%), <i>Pantoea deleyi</i> (6.99%), <i>unclassified_f_Enterobacteriaceae</i> (6.51%), <i>Klebsiella pneumoniae</i> (5.79%), <i>Pantoea ananatis</i> (2.78%), <i>Enterobacter kobei</i> (2.73%), <i>unclassified_g_Pantoea</i> (2.69%), <i>Enterobacter huaxiensis</i> (1.00%)
	spermidine synthase	2.5.1.16	<i>unclassified_g_Burkholderia</i> (39.27%), <i>Burkholderia gladioli</i> (35.08%), <i>Pantoea_sp._ICBG_985</i> (18.75%),	<i>Lichtheimia ramosa</i> (40.10%), <i>Saccharomyces cerevisiae</i> (28.91%), <i>Kosakonia cowanii</i> (9.63%), <i>Burkholderia gladioli</i> (6.16%), <i>unclassified_f_Enterobacteriaceae</i> (4.22%),

			<i>unclassified_f_Enterobacteriaceae</i> (3.09%), <i>Kosakonia cowanii</i> (1.46%)	<i>Enterobacter hormaechei</i> (2.94%), <i>unclassified_g_Bacillus_f_Bacillaceae</i> (1.96%), <i>Burkholderia pyrrocinia</i> (1.20%), <i>Burkholderia_sp._Bp8992</i> (1.10%)
	spermine oxidase	1.5.3.16	-	<i>Aspergillus niger</i> (52.16%), <i>Aspergillus welwitschiae</i> (47.84%)
	glutathionyl spermidine amidase	3.5.1.78	<i>Enterobacter cloacae</i> (36.07%), <i>unclassified_f_Enterobacteriaceae</i> (32.61%), <i>Enterobacter_sp._WCHEn090032</i> (13.14%), <i>Klebsiella pneumoniae</i> (8.32%), <i>Enterobacter_sp._50588862</i> (3.96%), <i>Salmonella enterica</i> (3.53%), [<i>Enterobacter</i>] <i>lignolyticus</i> (1.48%)	<i>Enterobacter cloacae</i> (26.26%), <i>Enterobacter_sp._WCHEn090032</i> (25.66%), <i>unclassified_g_Enterobacter</i> (24.51%), <i>Salmonella enterica</i> (9.95%), <i>Enterobacter_sp._50588862</i> (7.60%), [<i>Enterobacter</i>] <i>lignolyticus</i> (2.94%), <i>unclassified_f_Enterobacteriaceae</i> (2.29%)
	carboxynorspermidine decarboxylase	4.1.1.96	<i>Bacillus ginsengihumi</i> (100.00%)	<i>Bacillus ginsengihumi</i> (100.00%)
	tyrosine decarboxylase	4.1.1.25	-	-
Biogenic amines degradation	monoamine oxidase	1.4.3.4	<i>Monascus purpureus</i> (96.18%), <i>Aspergillus flavus</i> (3.82%)	<i>Aspergillus niger</i> (77.33%), <i>Monascus purpureus</i> (21.30%)
	primary-amine oxidase	1.4.3.21	<i>unclassified_g_Klebsiella</i> (33.00%), <i>Enterobacter asburiae</i> (16.48%), <i>Monascus purpureus</i> (13.98%), <i>Enterobacter cloacae</i> (13.72%), <i>Enterobacter ludwigii</i> (11.33%), <i>Enterobacter kobei</i> (6.26%), <i>Enterobacter hormaechei</i> (4.75%)	<i>Aspergillus niger</i> (55.08%), <i>Aspergillus awamori</i> (18.03%), <i>Aspergillus welwitschiae</i> (17.23%), <i>Monascus purpureus</i> (3.24%), <i>Enterobacter asburiae</i> (2.00%), <i>Enterobacter kobei</i> (1.28%), <i>Enterobacter ludwigii</i> (1.05%)
	spermidine synthase	2.5.1.16	<i>unclassified_g_Burkholderia</i> (39.27%), <i>Burkholderia gladioli</i> (35.08%), <i>Pantoea_sp._ICBG_985</i> (18.75%), <i>unclassified_f_Enterobacteriaceae</i> (3.09%), <i>Kosakonia cowanii</i> (1.46%)	<i>Lichtheimia ramosa</i> (40.10%), <i>Saccharomyces cerevisiae</i> (28.91%), <i>Kosakonia cowanii</i> (9.63%), <i>Burkholderia gladioli</i> (6.16%), <i>unclassified_f_Enterobacteriaceae</i> (4.22%), <i>Enterobacter hormaechei</i> (2.94%), <i>unclassified_g_Bacillus_f_Bacillaceae</i> (1.96%),

			<i>Burkholderia pyrrocinia</i> (1.20%), <i>Burkholderia_sp._Bp8992</i> (1.10%)
putrescine-2-oxoglutarate transaminase	2.6.1.82	<i>Klebsiella pneumoniae</i> (46.78%), <i>Klebsiella_cf._planticola_B43</i> (21.76%), <i>Lactococcus lactis</i> (6.77%), <i>Kosakonia cowanii</i> (6.71%), <i>Franconibacter pulveris</i> (4.99%), <i>Cronobacter dublinensis</i> (3.61%), <i>Enterobacter roggenkampii</i> (3.05%), <i>Citrobacter amalonaticus</i> (2.10%), <i>Digitaria exilis</i> (1.97%)	<i>Klebsiella_cf._planticola_B43</i> (43.29%), <i>Kosakonia cowanii</i> (14.29%), <i>Klebsiella pneumoniae</i> (13.81%), <i>Enterobacter roggenkampii</i> (6.41%), <i>Cronobacter dublinensis</i> (6.31%), <i>Digitaria exilis</i> (6.15%), <i>Citrobacter amalonaticus</i> (4.06%), <i>Lactococcus lactis</i> (2.12%), <i>Enterobacter kobei</i> (1.26%)
spermidine dehydrogenase	1.5.99.6	<i>Cronobacter sakazakii</i> (72.89%), <i>Cronobacter dublinensis</i> (27.11%)	-
polyamine oxidase (propane-1,3-diamine-forming)	1.5.3.14	-	<i>Aspergillus niger</i> (52.16%), <i>Aspergillus welwitschiae</i> (47.84%)
glutathionylspermidine synthase	6.3.1.8	<i>unclassified_f_Enterobacteriaceae</i> (32.61%), <i>Enterobacter cloacae</i> (22.99%), <i>unclassified_g_Enterobacter</i> (13.45%), <i>Enterobacter_sp._WCHEn090032</i> (13.14%), <i>Klebsiella pneumoniae</i> (8.32%), <i>Enterobacter_sp._50588862</i> (3.96%), <i>Salmonella enterica</i> (3.53%), <i>[Enterobacter] lignolyticus</i> (1.48%)	<i>Enterobacter cloacae</i> (26.26%), <i>Enterobacter_sp._WCHEn090032</i> (25.66%), <i>unclassified_g_Enterobacter</i> (24.51%), <i>Salmonella enterica</i> (9.95%), <i>Enterobacter_sp._50588862</i> (7.60%), <i>[Enterobacter] lignolyticus</i> (2.94%), <i>unclassified_f_Enterobacteriaceae</i> (2.29%)
non-specific polyamine oxidase	1.5.3.17	<i>Saccharomyces cerevisiae</i> (100.00%)	<i>Saccharomyces cerevisiae</i> (99.16%)
glutamate-putrescine ligase	6.3.1.11	<i>Pantoea dispersa</i> (42.27%), <i>Leclercia adcarboxylata</i> (30.48%), <i>unclassified_f_Enterobacteriaceae</i> (9.45%), <i>Cronobacter malonaticus</i> (4.05%), <i>Enterobacter cloacae</i> (3.71%), <i>Enterobacter</i>	<i>unclassified_g_Enterobacter</i> (32.72%), <i>unclassified_o_Enterobacterales</i> (31.49%), <i>Enterobacter roggenkampii</i> (9.21%), <i>Enterobacter_sp._M4-VN</i> (8.59%), <i>Pantoea deleyi</i> (3.89%), <i>Pantoea ananatis</i> (3.70%),

			<i>asburiae</i> (2.97%), <i>unclassified_g_Enterobacter</i> (2.71%), <i>Enterobacter roggenkampii</i> (1.15%), <i>Enterobacter kobei</i> (1.04%), <i>Franconibacter pulveris</i> (1.01%)	<i>Enterobacter cloacae</i> (2.96%), <i>unclassified_f_Enterobacteriaceae</i> (2.71%), <i>Enterobacter kobei</i> (2.34%), <i>unclassified_g_Pantoea</i> (1.86%)
	diamine N-acetyltransferase	2.3.1.57	<i>Weissella cibaria</i> (81.36%), <i>Leuconostoc citreum</i> (4.26%), <i>unclassified_g_Enterobacter</i> (3.69%), <i>unclassified_f_Enterobacteriaceae</i> (3.46%), <i>Pantoea_sp._Cy-640</i> (2.38%), <i>unclassified_g_Lactococcus</i> (1.75%)	<i>Weissella cibaria</i> (88.78%), <i>unclassified_g_Enterobacter</i> (3.25%), <i>unclassified_f_Enterobacteriaceae</i> (2.98%), <i>unclassified_g_Leuconostoc</i> (1.47%)
	putrescine-pyruvate transaminase	2.6.1.113	<i>Burkholderia gladioli</i> (100.00%)	<i>Burkholderia gladioli</i> (76.58%), <i>unclassified_g_Burkholderia</i> (23.42%)
	putrescine carbamoyltransferase	2.1.3.6	<i>Lactococcus lactis</i> (100.00%)	<i>Lactococcus lactis</i> (100.00%)
	spermine oxidase	1.5.3.16	-	<i>Aspergillus niger</i> (52.16%), <i>Aspergillus welwitschiae</i> (47.84%)
	aldehyde dehydrogenase (NAD ⁺)	1.2.1.3	<i>Burkholderia gladioli</i> (69.80%), <i>unclassified_g_Burkholderia</i> (22.66%), <i>Pantoea dispersa</i> (2.65%), <i>Enterobacter asburiae</i> (1.20%), <i>Saccharomyces cerevisiae</i> (1.05%)	<i>Saccharomyces cerevisiae</i> (35.33%), <i>Aspergillus niger</i> (31.72%), <i>Aspergillus phoenicis</i> (10.14%), <i>unclassified_g_Burkholderia</i> (5.82%), <i>Burkholderia gladioli</i> (4.47%), <i>Enterobacter asburiae</i> (3.94%), <i>Monascus purpureus</i> (2.20%), <i>Pantoea ananatis</i> (1.18%), <i>unclassified_g_Enterobacter</i> (1.02%), <i>Bacillus amyloliquefaciens</i> (1.01%)
Amino acid synthesis	histidinol dehydrogenase	1.1.1.23	<i>Burkholderia gladioli</i> (55.67%), <i>unclassified_g_Pantoea</i> (25.64%), <i>Klebsiella pneumoniae</i> (4.41%), <i>Leuconostoc lactis</i> (3.31%), <i>Kosakonia_sp._CCTCC_M2018092</i> (2.49%), <i>Enterobacter asburiae</i> (2.19%),	<i>Aspergillus niger</i> (41.27%), <i>Saccharomyces cerevisiae</i> (18.72%), <i>Leuconostoc lactis</i> (15.96%), <i>Kosakonia_sp._CCTCC_M2018092</i> (5.91%), <i>Enterobacter asburiae</i> (4.69%), <i>Burkholderia gladioli</i> (3.47%), <i>Monascus purpureus</i> (1.69%), <i>Enterobacter bugandensis</i>

			<i>Enterobacter cloacae</i> (1.59%), <i>Lactococcus lactis</i> (1.39%)	(1.65%), <i>Bacillus siamensis</i> (1.34%), <i>Enterobacter cloacae</i> (1.24%)
	peptidase A	3.4.13.18	-	-
	histidinol phosphate phosphatase	3.1.3.15	<i>unclassified_g_Pantoea</i> (42.97%), <i>Leuconostoc lactis</i> (18.64%), <i>unclassified_g_Klebsiella</i> (9.98%), <i>Leuconostoc citreum</i> (9.59%), <i>unclassified_f_Enterobacteriaceae</i> (6.32%), <i>unclassified_g_Enterobacter</i> (3.62%), <i>Lactococcus lactis</i> (2.78%), <i>Saccharomyces cerevisiae</i> (2.04%), <i>unclassified_g_Cronobacter</i> (1.16%)	<i>Leuconostoc lactis</i> (43.48%), <i>Saccharomyces cerevisiae</i> (21.90%), <i>Aspergillus niger</i> (14.80%), <i>unclassified_f_Enterobacteriaceae</i> (6.65%), <i>unclassified_g_Enterobacter</i> (4.23%), <i>Leuconostoc citreum</i> (2.59%), <i>unclassified_g_Pantoea</i> (1.29%), <i>Bacillus amyloliquefaciens</i> (1.13%), <i>Lactococcus lactis</i> (1.11%)
	prephenate dehydrogenase (NADP+)	1.3.1.13	<i>Saccharomyces cerevisiae</i> (83.33%), <i>Monascus purpureus</i> (16.67%)	<i>Aspergillus niger</i> (52.77%), <i>Saccharomyces cerevisiae</i> (45.41%), <i>Monascus purpureus</i> (1.77%)
	arogenate dehydrogenase	1.3.1.43	<i>Klebsiella pneumoniae</i> (100%)	<i>Klebsiella pneumoniae</i> (100.00%)
	lysine-2-oxoglutarate reductase	1.5.1.8	-	-
	phenylalaninase	1.14.16.1	<i>Burkholderia gladioli</i> (100%)	<i>Burkholderia gladioli</i> (99.50%)
	histidinol-phosphate transaminase	2.6.1.9	<i>Burkholderia gladioli</i> (71.25%), <i>unclassified_g_Pantoea</i> (15.54%), <i>unclassified_f_Enterobacteriaceae</i> (2.76%), <i>Leuconostoc citreum</i> (2.47%), <i>Leuconostoc lactis</i> (2.32%), <i>Escherichia coli</i> (1.47%)	<i>Aspergillus phoenicis</i> (22.37%), <i>Leuconostoc lactis</i> (20.80%), <i>Saccharomyces cerevisiae</i> (18.94%), <i>Burkholderia gladioli</i> (10.53%), <i>Escherichia coli</i> (5.23%), <i>unclassified_g_Burkholderia</i> (4.26%), <i>Enterobacter cloacae</i> (2.74%), <i>Leuconostoc</i>

			<i>citreum</i> (2.45%), <i>Enterobacter bugandensis</i> (2.08%), <i>unclassified_g_Enterobacter</i> (1.68%), <i>unclassified_g_Pantoea</i> (1.47%), <i>Bacillus amyloliquefaciens</i> (1.29%), <i>Enterobacter asburiae</i> (1.19%), <i>Burkholderia_sp._Bp8992</i> (1.08%), <i>Pantoea deleyi</i> (1.06%), <i>Monascus purpureus</i> (1.00%)
aromatic-amino-acid transaminase	2.6.1.57	<i>Burkholderia gladioli</i> (36.12%), <i>unclassified_g_Burkholderia</i> (34.04%), <i>Pantoea_sp._Ap-959</i> (17.60%), <i>Klebsiella pneumoniae</i> (2.80%), <i>Klebsiella quasipneumoniae</i> (2.36%), <i>unclassified_g_Enterobacter</i> (1.56%)	<i>Monascus purpureus</i> (33.55%), <i>Saccharomyces cerevisiae</i> (25.29%), <i>unclassified_g_Burkholderia</i> (12.94%), <i>Kosakonia cowanii</i> (4.98%), <i>unclassified_g_Enterobacter</i> (4.54%), <i>Enterobacteriaceae_bacterium_RIT693</i> (4.25%), <i>Enterobacter asburiae</i> (3.11%), <i>Pantoea ananatis</i> (2.32%), <i>Enterobacter cloacae</i> (2.13%), <i>Cedecea lapagei</i> (2.01%), <i>Pantoea_sp.</i> (1.66%)
tyrosine transaminase	2.6.1.5	<i>Saccharomyces cerevisiae</i> (82.63%), <i>Monascus purpureus</i> (11.80%), <i>Aspergillus awamori</i> (4.75%)	<i>Monascus purpureus</i> (56.04%), <i>Saccharomyces cerevisiae</i> (42.25%), <i>Aspergillus niger</i> (1.09%)
phenylalanine(histidine) transaminase	2.6.1.58	<i>Saccharomyces cerevisiae</i> (98.57%), <i>[Candida] glabrata</i> (1.43%), <i>Saccharomyces cerevisiae</i> (83.33%), <i>Monascus purpureus</i> (16.67%)	<i>Saccharomyces cerevisiae</i> (99.92%)
L-glutamate gamma-semialdehyde dehydrogenase	1.2.1.88	<i>Burkholderia gladioli</i> (52.24%), <i>Pantoea dispersa</i> (23.42%), <i>unclassified_g_Enterobacter</i> (7.49%), <i>Klebsiella pneumoniae</i> (4.63%), <i>Kosakonia cowanii</i> (3.94%), <i>Enterobacter kobei</i> (1.92%), <i>Enterobacter_sp._BWH52</i> (1.62%)	<i>Aspergillus niger</i> (31.47%), <i>Aspergillus welwitschiae</i> (23.90%), <i>unclassified_g_Enterobacter</i> (14.61%), <i>Saccharomyces cerevisiae</i> (6.57%), <i>Kosakonia cowanii</i> (6.01%), <i>Enterobacter kobei</i> (3.52%), <i>Burkholderia gladioli</i> (3.37%),

				<i>Enterobacter_sp._BWH52</i> (3.00%), <i>Monascus purpureus</i> (1.73%), <i>Bacillus amyloliquefaciens</i> (1.04%)
	glutamate synthase (NADPH)	1.4.1.13	<i>unclassified_g_Burkholderia</i> (49.75%), <i>Pantoea dispersa</i> (15.36%), <i>Burkholderia pseudomallei</i> (6.90%), <i>Klebsiella pneumoniae</i> (5.12%), <i>Enterobacter sichuanensis</i> (4.29%), <i>unclassified_g_Enterobacter</i> (3.62%), <i>Klebsiella_cf._planticola_B43</i> (2.99%), <i>Kosakonia cowanii</i> (2.45%), <i>Enterobacter roggenkampii</i> (1.85%), <i>Salmonella enterica</i> (1.62%), <i>Lactococcus lactis</i> (1.33%)	<i>unclassified_g_Enterobacter</i> (30.39%), <i>Klebsiella_cf._planticola_B43</i> (11.88%), <i>Kosakonia cowanii</i> (10.26%), <i>unclassified_g_Burkholderia</i> (7.59%), <i>Enterobacter roggenkampii</i> (6.22%), <i>Klebsiella oxytoca</i> (3.80%), <i>Klebsiella pneumoniae</i> (3.75%), <i>Bacillus amyloliquefaciens</i> (3.70%), <i>Pantoea deleyi</i> (3.08%), <i>Salmonella enterica</i> (2.58%), <i>Enterobacter_sp._MGH_22</i> (2.54%), <i>Lactococcus lactis</i> (2.01%), <i>unclassified_g_Pantoea</i> (1.82%), <i>Cronobacter dublinensis</i> (1.46%), <i>Pantoea stewartii</i> (1.38%), <i>Burkholderia pseudomallei</i> (1.01%)
	glutamate synthase (NADH)	1.4.1.14	<i>Saccharomyces cerevisiae</i> (68.77%), <i>Monascus purpureus</i> (30.79%)	<i>Aspergillus nomiae</i> (61.94%), <i>Saccharomyces cerevisiae</i> (34.01%), <i>Monascus purpureus</i> (3.11%)
	glutamate dehydrogenase	1.4.1.2	<i>Saccharomyces cerevisiae</i> (62.98%), <i>Monascus purpureus</i> (32.80%), <i>Rhodococcus erythropolis</i> (2.11%), <i>Rhodococcus_sp._ADH</i> (2.11%)	<i>Aspergillus eucalypticola</i> (54.98%), <i>Saccharomyces cerevisiae</i> (34.91%), <i>Monascus purpureus</i> (3.15%), <i>Bacillus amyloliquefaciens</i> (2.98%), <i>Burkholderia arboris</i> (2.03%)
	glutamate dehydrogenase [NAD(P)+]	1.4.1.3	<i>Burkholderia plantarii</i> (93.25%), <i>Klebsiella aerogenes</i> (5.42%)	<i>Burkholderia plantarii</i> (61.19%), <i>unclassified_g_Pantoea</i> (16.13%), <i>Pantoea_sp._ARC607</i> (8.73%), <i>unclassified_g_Burkholderia</i> (4.18%), <i>Klebsiella aerogenes</i> (2.13%),

			<i>Chitinophagaceae_bacterium_YG09</i> (2.06%), <i>Pantoea agglomerans</i> (1.93%), <i>Ferruginibacter_sp.</i> (1.70%), <i>Saccharopolyspora hirsuta</i> (1.68%)
glutamate dehydrogenase (NADP+)	1.4.1.4	<i>unclassified_f_Enterobacteriaceae</i> (28.80%), <i>Kosakonia cowanii</i> (20.28%), <i>Saccharomyces cerevisiae</i> (12.09%), <i>Enterobacter roggenkampii</i> (10.87%), <i>Enterobacter asburiae</i> (8.74%), <i>unclassified_g_Enterobacter</i> (6.72%), <i>Franconibacter pulveris</i> (6.08%), <i>Enterobacter cloacae</i> (3.60%), <i>Monascus purpureus</i> (1.95%)	<i>Saccharomyces cerevisiae</i> (41.44%), <i>Monascus purpureus</i> (37.45%), <i>Kosakonia cowanii</i> (6.86%), <i>Enterobacter roggenkampii</i> (4.90%), <i>Enterobacter asburiae</i> (4.19%), <i>unclassified_g_Enterobacter</i> (2.66%), <i>Enterobacter cloacae</i> (1.41%)
glutaminase	3.5.1.2	<i>unclassified_g_Burkholderia</i> (54.56%), <i>Pantoea dispersa</i> (22.52%), <i>Weissella cibaria</i> (10.07%), <i>Klebsiella pneumoniae</i> (3.82%), <i>Leuconostoc citreum</i> (2.85%), <i>unclassified_g_Enterobacter</i> (2.18%), <i>Kosakonia_sp._CCTCC_M2018092</i> (1.72%)	<i>Weissella cibaria</i> (51.68%), <i>unclassified_g_Burkholderia</i> (9.77%), <i>Kosakonia_sp._CCTCC_M2018092</i> (8.99%), <i>Bacillus amyloliquefaciens</i> (7.97%), <i>unclassified_g_Enterobacter</i> (7.78%), <i>Leuconostoc citreum</i> (3.92%), <i>unclassified_g_Pantoea</i> (2.59%), <i>Burkholderia_sp._Bp8992</i> (1.68%), <i>Leuconostoc holzapfelii</i> (1.42%), <i>Lactococcus lactis</i> (1.25%)
glutaminase-asparaginase	3.5.1.38	-	<i>Burkholderia gladioli</i> (97.81%), <i>Variovorax_sp._SCN_67-85</i> (2.19%)
N-formylglutamate deformylase	3.5.1.68	<i>Burkholderia gladioli</i> (82.90%), <i>unclassified_g_Pantoea</i> (16.44%)	<i>Burkholderia gladioli</i> (70.12%), <i>Pantoea ananatis</i> (12.10%), <i>Pantoea deleyi</i> (11.80%), <i>Burkholderia territorii</i> (5.26%)
succinylglutamate desuccinylase	3.5.1.96	<i>Burkholderia gladioli</i> (55.58%), <i>Pantoea dispersa</i> (27.94%), <i>Klebsiella pneumoniae</i> (5.14%), <i>unclassified_g_Klebsiella</i> (2.39%),	<i>Burkholderia gladioli</i> (23.42%), <i>Enterobacter asburiae</i> (14.10%), <i>Kosakonia_sp._CCTCC_M2018092</i> (12.23%),

			<i>unclassified_g_Enterobacter</i> (1.39%), <i>Enterobacter asburiae</i> (1.22%)	<i>Enterobacter kobei</i> (11.74%), <i>Enterobacter bugandensis</i> (9.39%), <i>Enterobacter cloacae</i> (6.78%), <i>Pantoea deleyi</i> (6.55%), <i>unclassified_g_Pantoea</i> (4.42%), <i>Burkholderia_sp._Bp8992</i> (3.56%), <i>Enterobacter ludwigii</i> (2.24%), <i>Enterobacter hormaechei</i> (2.15%), <i>Pantoea ananatis</i> (1.50%)
	5-oxoprolinase (ATP-hydrolysing)	3.5.2.9	<i>Burkholderia gladioli</i> (64.80%), <i>unclassified_g_Burkholderia</i> (12.15%), <i>unclassified_g_Pantoea</i> (5.78%), <i>Pantoea endophytica</i> (4.10%), <i>Enterobacteriaceae bacterium RIT692</i> (4.06%), <i>Enterobacter cloacae</i> (1.28%), <i>unclassified_g_Klebsiella</i> (1.18%), <i>unclassified_g_Enterobacter</i> (1.16%)	<i>Aspergillus niger</i> (31.33%), <i>Monascus purpureus</i> (17.07%), <i>Saccharomyces cerevisiae</i> (9.63%), <i>Aspergillus flavus</i> (9.04%), <i>Aspergillus awamori</i> (7.26%), <i>Burkholderia gladioli</i> (6.89%), <i>unclassified_g_Enterobacter</i> (3.96%), <i>Enterobacter cloacae</i> (3.56%), <i>Kosakonia cowanii</i> (1.59%), <i>unclassified_g_Burkholderia</i> (1.47%), <i>Enterobacter asburiae</i> (1.14%), <i>Pantoea ananatis</i> (1.13%)
	formimidoylglutamase	3.5.3.8	<i>Klebsiella pneumoniae</i> (36.79%), <i>Enterobacter asburiae</i> (35.96%), <i>Kosakonia cowanii</i> (12.39%), <i>Enterobacter cloacae</i> (8.20%), <i>Enterobacter_sp._18A13</i> (2.33%), <i>unclassified_g_Enterobacter</i> (2.06%), <i>Enterobacter kobei</i> (1.03%)	<i>unclassified_g_Enterobacter</i> (53.21%), <i>Kosakonia cowanii</i> (20.31%), <i>Enterobacter asburiae</i> (13.70%), <i>Bacillus amyloliquefaciens</i> (2.97%), <i>Enterobacter kobei</i> (2.76%), <i>Enterobacter_sp._18A13</i> (2.35%), <i>Enterobacter ludwigii</i> (1.77%), <i>Enterobacter_sp._NFIX59</i> (1.53%)
	acetylornithine deacetylase	3.5.1.16	<i>Burkholderia gladioli</i> (40.73%), <i>Pantoea dispersa</i> (19.98%), <i>unclassified_g_Burkholderia</i> (18.75%), <i>unclassified_g_Pantoea</i> (9.43%), <i>Klebsiella pneumoniae</i> (3.22%), <i>unclassified_f_Enterobacteriaceae</i> (1.79%),	<i>Aspergillus niger</i> (32.46%), <i>Leclercia adecarboxylata</i> (12.30%), <i>unclassified_f_Enterobacteriaceae</i> (12.08%), <i>Burkholderia gladioli</i> (11.11%), <i>Klebsiella pneumoniae</i> (7.04%), <i>unclassified_g_Burkholderia</i> (6.52%), <i>Pantoea_sp._JKS000250</i> (3.16%), <i>Pantoea</i>

			<i>Leclercia adecarboxylata</i> (1.32%), <i>unclassified_g_Enterobacter</i> (1.15%)	<i>ananatis</i> (2.79%), <i>Enterobacter cloacae</i> (2.73%), <i>Klebsiella oxytoca</i> (2.23%), <i>Pantoea_sp._OXWO6B1</i> (1.71%), <i>Monascus purpureus</i> (1.70%), <i>Lactococcus lactis</i> (1.57%)
	glutamate N- acetyltransferase	2.3.1.35	<i>Weissella cibaria</i> (60.91%), <i>Burkholderia gladioli</i> (32.81%), <i>Leuconostoc citreum</i> (2.53%), <i>Leuconostoc lactis</i> (2.21%)	<i>Weissella cibaria</i> (80.56%), <i>Leuconostoc lactis</i> (7.19%), <i>Saccharomyces cerevisiae</i> (5.42%), <i>Aspergillus niger</i> (3.06%), <i>Burkholderia gladioli</i> (1.47%)
	arginase	3.5.3.1	<i>Klebsiella pneumoniae</i> (57.01%), <i>Saccharomyces cerevisiae</i> (33.98%), <i>Aspergillus niger</i> (6.33%), <i>Escherichia coli</i> (1.19%)	<i>Monascus purpureus</i> (37.35%), <i>Aspergillus niger</i> (30.82%), <i>Saccharomyces cerevisiae</i> (29.06%), <i>Bacillus amyloliquefaciens</i> (2.09%)
	membrane alanyl aminopeptidase	3.4.11.2	<i>Weissella cibaria</i> (40.67%), <i>Burkholderia gladioli</i> (17.48%), <i>unclassified_g_Burkholderia</i> (13.56%), <i>Weissella confusa</i> (10.36%), <i>Pantoea dispersa</i> (8.37%), <i>Weissella cibaria</i> (1.70%), <i>unclassified_f_Enterobacteriaceae</i> (1.58%)	<i>Weissella cibaria</i> (78.71%), <i>Weissella confusa</i> (6.15%), <i>Leuconostoc lactis</i> (5.14%), <i>Kosakonia cowanii</i> (2.76%), <i>unclassified_g_Enterobacter</i> (1.27%), <i>Burkholderia gladioli</i> (1.14%)
	aspartate transaminase	2.6.1.1	<i>Burkholderia gladioli</i> (45.69%), <i>unclassified_g_Pantoea</i> (21.44%), <i>Type- C_symbiont_of_Plautia_stali</i> (16.00%), <i>Pantoea dispersa</i> (5.18%), <i>unclassified_g_Enterobacter</i> (3.55%), <i>unclassified_g_Kosakonia</i> (3.03%), <i>Saccharomyces cerevisiae</i> (1.19%), <i>Enterobacter cloacae</i> (1.05%)	<i>Saccharomyces cerevisiae</i> (28.08%), <i>Aspergillus luchuensis</i> (21.82%), <i>Aspergillus neoniger</i> (18.17%), <i>unclassified_g_Enterobacter</i> (7.57%), <i>unclassified_g_Kosakonia</i> (6.43%), <i>Monascus purpureus</i> (4.42%), <i>Burkholderia gladioli</i> (2.92%), <i>Bacillus amyloliquefaciens</i> (2.08%), <i>Aspergillus eucalypticola</i> (2.03%), <i>Shigella sonnei</i> (1.79%), <i>Enterobacter cloacae</i> (1.35%), <i>Enterobacter hormaechei</i> (1.31%)

	histidinol-phosphate transaminase	2.6.1.9	<i>Burkholderia gladioli</i> (71.25%), <i>unclassified_g_Pantoea</i> (15.54%), <i>unclassified_f_Enterobacteriaceae</i> (2.76%), <i>Leuconostoc citreum</i> (2.47%), <i>Leuconostoc lactis</i> (2.32%), <i>Escherichia coli</i> (1.47%)	<i>Aspergillus phoenicis</i> (22.37%), <i>Leuconostoc lactis</i> (20.80%), <i>Saccharomyces cerevisiae</i> (18.94%), <i>Burkholderia gladioli</i> (10.53%), <i>Escherichia coli</i> (5.23%), <i>unclassified_g_Burkholderia</i> (4.26%), <i>Enterobacter cloacae</i> (2.74%), <i>Leuconostoc citreum</i> (2.45%), <i>Enterobacter bugandensis</i> (2.08%), <i>unclassified_g_Enterobacter</i> (1.68%), <i>unclassified_g_Pantoea</i> (1.47%), <i>Bacillus amyloliquefaciens</i> (1.29%), <i>Enterobacter asburiae</i> (1.19%), <i>Burkholderia_sp._Bp8992</i> (1.08%), <i>Pantoea deleyi</i> (1.06%), <i>Monascus purpureus</i> (1.00%)
	tyrosine transaminase	2.6.1.5	<i>Saccharomyces cerevisiae</i> (82.63%), <i>Monascus purpureus</i> (11.80%), <i>Aspergillus awamori</i> (4.75%)	<i>Monascus purpureus</i> (56.04%), <i>Saccharomyces cerevisiae</i> (42.25%), <i>Aspergillus niger</i> (1.09%)
	tryptophan-phenylpyruvate transaminase	2.6.1.28	<i>Saccharomyces cerevisiae</i> (98.57%), [<i>Candida</i>] <i>glabrata</i> (1.43%) <i>Burkholderia gladioli</i> (59.83%),	<i>Saccharomyces cerevisiae</i> (99.92%)
	prephenate dehydratase	4.2.1.51	<i>Burkholderia gladioli</i> (59.83%), <i>Pantoea_sp._GL120224-02</i> (13.26%), <i>Pantoea dispersa</i> (13.02%), <i>unclassified_f_Enterobacteriaceae</i> (3.10%), <i>Klebsiella pneumoniae</i> (3.07%), <i>Kosakonia cowanii</i> (1.68%), <i>Enterobacter cloacae</i> (1.09%)	<i>Saccharomyces cerevisiae</i> (39.04%), <i>Burkholderia gladioli</i> (13.42%), <i>unclassified_f_Enterobacteriaceae</i> (9.99%), <i>Enterobacter cloacae</i> (7.95%), <i>Monascus purpureus</i> (7.54%), <i>unclassified_g_Enterobacter</i> (4.72%), <i>Pantoea ananatis</i> (3.84%), <i>Pantoea deleyi</i> (2.60%), <i>Pantoea agglomerans</i> (2.53%), <i>Enterobacter quasiormaechei</i> (2.07%), <i>Lactococcus lactis</i> (1.68%), <i>unclassified_g_Burkholderia</i> (1.26%), <i>Bacillus amyloliquefaciens</i> (1.17%)

	chorismate mutase	5.4.99.5	<i>Burkholderia gladioli</i> (50.24%), <i>unclassified_g_Pantoea</i> (13.65%), <i>Pantoea_sp._GL120224-02</i> (11.78%), <i>Pantoea dispersa</i> (8.34%), <i>Kosakonia cowanii</i> (2.86%), <i>unclassified_f_Enterobacteriaceae</i> (2.76%), <i>Klebsiella pneumoniae</i> (1.75%), <i>Enterobacter cloacae</i> (1.63%), <i>Enterobacter kobei</i> (1.16%), <i>Klebsiella variicola</i> (1.01%)	<i>Saccharomyces cerevisiae</i> (18.24%), <i>Kosakonia cowanii</i> (14%), <i>Aspergillus niger</i> (13.34%), <i>Burkholderia gladioli</i> (11.06%), <i>Enterobacter cloacae</i> (9.63%), <i>Enterobacter kobei</i> (7.73%), <i>unclassified_g_Enterobacter</i> (3.67%), <i>Pantoea ananatis</i> (3.05%), <i>Pantoea deleyi</i> (2.95%), <i>Bacillus amyloliquefaciens</i> (2.76%), <i>unclassified_g_Pantoea</i> (2.22%), <i>Enterobacter asburiae</i> (2.07%), <i>Enterobacter quasiormaechei</i> (1.61%), <i>Lactococcus lactis</i> (1.26%), <i>Enterobacter oligotrophica</i> (1.03%)
	arogenate dehydratase	4.2.1.91	<i>Burkholderia gladioli</i> (60.93%), <i>Pantoea dispersa</i> (30.17%), <i>Klebsiella pneumoniae</i> (7.12%), <i>Pantoea ananatis</i> (1.07%)	<i>Burkholderia gladioli</i> (52.11%), <i>Pantoea agglomerans</i> (24.16%), <i>Pantoea ananatis</i> (17.05%), <i>Burkholderia seminalis</i> (4.16%), <i>Klebsiella pneumoniae</i> (1.96%)
	phenylalanine ammonia-lyase	4.3.1.24	-	<i>Aspergillus niger</i> (71.89%), <i>Aspergillus phoenicis</i> (27.98%)
	saccharopine dehydrogenase (NAD ⁺ , L-lysine-forming)	1.5.1.7	<i>Saccharomyces cerevisiae</i> (97.39%), <i>Monascus purpureus</i> (2.61%)	<i>Aspergillus phoenicis</i> (52.31%), <i>Saccharomyces cerevisiae</i> (47.47%)
	diaminopimelate decarboxylase	4.1.1.20	<i>Weissella cibaria</i> (41.74%), <i>Burkholderia gladioli</i> (30.39%), <i>unclassified_g_Pantoea</i> (14.32%), <i>unclassified_f_Enterobacteriaceae</i> (3.25%), <i>Enterobacter cloacae</i> (2.65%), <i>Leuconostoc citreum</i> (1.88%), <i>Leuconostoc lactis</i> (1.59%)	<i>Weissella cibaria</i> (78.65%), <i>Leuconostoc lactis</i> (8.61%), <i>Enterobacter cloacae</i> (3.56%), <i>Enterobacter asburiae</i> (2.05%), <i>unclassified_g_Enterobacter</i> (2.00%), <i>Burkholderia gladioli</i> (1.64%)
	aromatic-amino-acid transaminase	2.6.1.57	<i>Burkholderia gladioli</i> (36.12%), <i>unclassified_g_Burkholderia</i> (34.04%), <i>Pantoea_sp._Ap-959</i> (17.60%), <i>Klebsiella pneumoniae</i> (2.80%), <i>Klebsiella</i>	<i>Monascus purpureus</i> (33.55%), <i>Saccharomyces cerevisiae</i> (25.29%), <i>unclassified_g_Burkholderia</i> (12.94%), <i>Kosakonia cowanii</i> (4.98%),

			<i>quasipneumoniae</i> (2.36%), <i>unclassified_g_Enterobacter</i> (1.56%)	<i>unclassified_g_Enterobacter</i> (4.54%), <i>Enterobacteriaceae_bacterium_RIT693</i> (4.25%), <i>Enterobacter asburiae</i> (3.11%), <i>Pantoea ananatis</i> (2.32%), <i>Enterobacter cloacae</i> (2.13%), <i>Cedecea lapagei</i> (2.01%), <i>Pantoea_sp.</i> (1.66%)
	phenylalanine(histidine) transaminase	2.6.1.58	<i>Saccharomyces cerevisiae</i> (98.57%), [<i>Candida</i>] <i>glabrata</i> (1.43%) <i>Saccharomyces cerevisiae</i> (83.33%), <i>Monascus purpureus</i> (16.67%)	<i>Saccharomyces cerevisiae</i> (99.92%)
	saccharopine dehydrogenase (NAD+, L-lysine-forming)	1.5.1.7	<i>Saccharomyces cerevisiae</i> (97.39%), <i>Monascus purpureus</i> (2.61%)	<i>Aspergillus phoenicis</i> (52.31%), <i>Saccharomyces cerevisiae</i> (47.47%)
	diaminopimelate decarboxylase	4.1.1.20	<i>Weissella cibaria</i> (41.74%), <i>Burkholderia gladioli</i> (30.39%), <i>unclassified_g_Pantoea</i> (14.32%), <i>unclassified_f_Enterobacteriaceae</i> (3.25%), <i>Enterobacter cloacae</i> (2.65%), <i>Leuconostoc citreum</i> (1.88%), <i>Leuconostoc lactis</i> (1.59%)	<i>Weissella cibaria</i> (78.65%), <i>Leuconostoc lactis</i> (8.61%), <i>Enterobacter cloacae</i> (3.56%), <i>Enterobacter asburiae</i> (2.05%), <i>unclassified_g_Enterobacter</i> (2.00%), <i>Burkholderia gladioli</i> (1.64%)
	tryptophan synthase	4.2.1.20	<i>unclassified_g_Burkholderia</i> (37.15%), <i>Burkholderia gladioli</i> (31.11%), <i>Pantoea dispersa</i> (12.55%), <i>unclassified_g_Pantoea</i> (5.86%), <i>Enterobacter ludwigii</i> (2.92%), <i>Klebsiella pneumoniae</i> (2.75%), <i>Leuconostoc lactis</i> (2.02%), <i>Kosakonia cowanii</i> (1.51%), <i>unclassified_g_Enterobacter</i> (1.07%), <i>unclassified_f_Enterobacteriaceae</i> (1.04%)	<i>Aspergillus welwitschiae</i> (27.51%), <i>Aspergillus niger</i> (26.57%), <i>Saccharomyces cerevisiae</i> (15.57%), <i>Enterobacter ludwigii</i> (5.01%), <i>Kosakonia cowanii</i> (4.11%), <i>unclassified_g_Burkholderia</i> (3.90%), <i>unclassified_g_Enterobacter</i> (3.61%), <i>Burkholderia gladioli</i> (2.94%), <i>unclassified_f_Enterobacteriaceae</i> (2.55%), <i>Bacillus amyloliquefaciens</i> (1.78%), <i>Monascus purpureus</i> (1.70%), <i>Leuconostoc lactis</i> (1.52%), <i>Enterobacter roggenkampii</i> (1.01%)

	alanine dehydrogenase	1.4.1.1	<i>Lactococcus garvieae</i> (59.60%), <i>Pantoea ananatis</i> (31.46%), <i>Burkholderia ubonensis</i> (8.94%)	<i>Lactococcus garvieae</i> (34.83%), <i>Pantoea allii</i> (27.27%), <i>Bacillus amyloliquefaciens</i> (14.57%), <i>unclassified_g_Bacillus_f_Bacillaceae</i> (12.10%), <i>Bacillus ginsengihumi</i> (8.90%), <i>Saccharopolyspora dendranthemae</i> (1.69%)
Amino acid degradation	histidine ammonia-lyase	4.3.1.3	<i>Pantoea dispersa</i> (30.85%), <i>unclassified_g_Burkholderia</i> (30.64%), <i>Burkholderia gladioli</i> (27.26%), <i>unclassified_g_Pantoea</i> (4.64%), <i>Klebsiella pneumoniae</i> (3.17%), <i>Klebsiella_cf._planticola_B43</i> (2.36%)	<i>unclassified_g_Enterobacter</i> (30.70%), <i>Klebsiella_cf._planticola_B43</i> (22.38%), <i>unclassified_g_Burkholderia</i> (13.60%), <i>Burkholderia gladioli</i> (11.43%), <i>unclassified_g_Pantoea</i> (7.25%), <i>Bacillus amyloliquefaciens</i> (5.34%), <i>Pantoea_sp._AG702</i> (2.04%), <i>Pantoea_sp._ARC607</i> (1.82%), <i>Lelliottia_sp._WB101</i> (1.13%), <i>Burkholderia_sp._Bp8992</i> (1.08%)
	L-histidine Nalpha-methyltransferase	2.1.1.44	<i>Monascus purpureus</i> (100%)	<i>Monascus purpureus</i> (99.86%)
	tyrosinase	1.14.18.1	<i>Aspergillus niger</i> (69.89%), <i>Monascus purpureus</i> (30.11%), <i>Saccharomyces cerevisiae</i> (82.51%),	<i>Aspergillus niger</i> (57.66%), <i>Monascus purpureus</i> (27.18%), <i>Aspergillus awamori</i> (14.82%)
	amino-acid N-acetyltransferase	2.3.1.1	<i>Burkholderia gladioli</i> (44.58%), <i>Weissella cibaria</i> (43.98%), <i>unclassified_g_Pantoea</i> (2.81%), <i>Leuconostoc citreum</i> (1.82%), <i>Leuconostoc lactis</i> (1.60%), <i>Cronobacter malonicus</i> (1.09%), <i>unclassified_g_Enterobacter</i> (1.08%)	<i>Weissella cibaria</i> (67.22%), <i>Saccharomyces cerevisiae</i> (11.49%), <i>Leuconostoc lactis</i> (6.00%), <i>Aspergillus phoenicis</i> (5.51%), <i>Aspergillus niger</i> (2.55%), <i>Burkholderia gladioli</i> (2.28%), <i>unclassified_g_Enterobacter</i> (1.17%)
	carbamyl phosphate synthetase (glutamine)	6.3.5.5	<i>Weissella cibaria</i> (64.37%), <i>unclassified_g>Weissella</i> (11.74%), <i>unclassified_g_Burkholderia</i> (10.46%), <i>unclassified_g_Pantoea</i> (2.64%), <i>Leuconostoc</i>	<i>Weissella cibaria</i> (71.44%), <i>unclassified_g>Weissella</i> (12.02%), <i>Aspergillus niger</i> (5.38%), <i>Saccharomyces cerevisiae</i>

		<i>citreum</i> (1.83%), <i>Leuconostoc lactis</i> (1.47%), <i>Kosakonia cowanii</i> (1.31%), <i>Klebsiella pneumoniae</i> (1.27%)	(3.45%), <i>Leuconostoc lactis</i> (3.41%), <i>Kosakonia cowanii</i> (1.03%)
glutamate 5-kinase	2.7.2.11	<i>unclassified_g_Burkholderia</i> (47.92%), <i>unclassified_g_Pantoea</i> (25.61%), <i>unclassified_f_Enterobacteriaceae</i> (4.37%), <i>Klebsiella quasipneumoniae</i> (4.11%), <i>Leuconostoc citreum</i> (3.93%), <i>Leuconostoc lactis</i> (3.83%), <i>Enterobacter roggenkampii</i> (3.50%), <i>Saccharomyces cerevisiae</i> (1.65%), <i>Lactococcus lactis</i> (1.65%), <i>Cronobacter sakazakii</i> (1.09%)	<i>Saccharomyces cerevisiae</i> (35.19%), <i>Leuconostoc lactis</i> (20.90%), <i>Aspergillus niger</i> (17.81%), <i>unclassified_f_Enterobacteriaceae</i> (7.80%), <i>Enterobacter roggenkampii</i> (6.74%), <i>unclassified_g_Burkholderia</i> (3.37%), <i>Leuconostoc citreum</i> (1.73%), <i>Bacillus amyloliquefaciens</i> (1.37%), <i>Pantoea deleyi</i> (1.06%)
D-amino-acid oxidase	1.4.3.3	<i>Monascus purpureus</i> (79.56%), <i>Aspergillus tanneri</i> (18.67%), <i>Saccharopolyspora spinosa</i> (1.78%)	<i>Aspergillus niger</i> (84.75%), <i>Monascus purpureus</i> (9.25%), <i>Aspergillus tanneri</i> (4.31%)
ornithine aminotransferase	2.6.1.13	<i>Saccharomyces cerevisiae</i> (82.51%), <i>Monascus purpureus</i> (16.67%)	<i>Aspergillus niger</i> (35.94%), <i>Aspergillus welwitschiae</i> (34.17%), <i>Saccharomyces cerevisiae</i> (26.89%), <i>Monascus purpureus</i> (1.34%), <i>Bacillus amyloliquefaciens</i> (1.24%)
D-amino-acid oxidase	1.4.3.3	<i>Monascus purpureus</i> (79.56%), <i>Aspergillus tanneri</i> (18.67%), <i>Saccharopolyspora spinosa</i> (1.78%)	<i>Aspergillus niger</i> (84.75%), <i>Monascus purpureus</i> (9.25%), <i>Aspergillus tanneri</i> (4.31%)
glycine oxidase	1.4.3.19	<i>Burkholderia gladioli</i> (69.86%), <i>unclassified_g_Pantoea</i> (29.45%)	<i>Burkholderia gladioli</i> (46.07%), <i>Pantoea_sp._Sc1</i> (17.22%), <i>Bacillus amyloliquefaciens</i> (15.68%), <i>unclassified_g_Pantoea</i> (15.01%), <i>Bacillus ginsengihumi</i> (2.46%), <i>Burkholderia seminalis</i> (2.06%)

glycine dehydrogenase (aminomethyl- transferring)	1.4.4.2	<i>Burkholderia gladioli</i> (46.20%), <i>Pantoea dispersa</i> (30.84%), <i>Klebsiella pneumoniae</i> (4.40%), <i>Kosakonia_sp._CCTCC_M2018092</i> (3.13%), <i>Enterobacter cloacae</i> (2.92%), <i>Enterobacter hormaechei</i> (2.90%), <i>Kosakonia cowanii</i> (2.16%), <i>unclassified_g_Enterobacter</i> (1.70%), <i>Cronobacter malonicus</i> (1.14%)	<i>Aspergillus niger</i> (29.31%), <i>Saccharomyces cerevisiae</i> (22.61%), <i>Kosakonia_sp._CCTCC_M2018092</i> (8.04%), <i>unclassified_g_Enterobacter</i> (7.29%), <i>Lupinus albus</i> (6.92%), <i>Kosakonia cowanii</i> (5.89%), <i>Burkholderia gladioli</i> (4.78%), <i>Pantoea deleyi</i> (2.96%), <i>Enterobacter cloacae</i> (2.29%), <i>Bacillus amyloliquefaciens</i> (2.05%), <i>unclassified_f_Enterobacteriaceae</i> (1.60%), <i>Monascus purpureus</i> (1.40%)
glycine C- acetyltransferase	2.3.1.29	<i>Burkholderia gladioli</i> (59.74%), <i>unclassified_g_Pantoea</i> (28.37%), <i>Kosakonia pseudosacchari</i> (3.16%), <i>unclassified_g_Enterobacter</i> (2.80%), <i>Klebsiella pneumoniae</i> (2.00%), <i>Enterobacter bugandensis</i> (1.85%), <i>Enterobacter roggenkampii</i> (1.33%)	<i>Kosakonia cowanii</i> (23.59%), <i>unclassified_g_Enterobacter</i> (21.96%), <i>Burkholderia gladioli</i> (14.96%), <i>Enterobacter bugandensis</i> (11.21%), <i>Enterobacter roggenkampii</i> (9.37%), <i>unclassified_g_Pantoea</i> (4.64%), <i>unclassified_g_Burkholderia</i> (3.55%), <i>Lactococcus garvieae</i> (3.10%), <i>Bacillus amyloliquefaciens</i> (2.79%), <i>Pantoea agglomerans</i> (2.05%)
5-aminolevulinate synthase	2.3.1.37	<i>Monascus purpureus</i> (54.33%), <i>Saccharomyces cerevisiae</i> (43.73%), <i>Pantoea ananatis</i> (1.94%)	<i>Aspergillus niger</i> (57.09%), <i>Saccharomyces cerevisiae</i> (31.17%), <i>Monascus purpureus</i> (10.93%)
D-amino-acid N- acetyltransferase	2.3.1.36	<i>Saccharomyces cerevisiae</i> (100%)	<i>Saccharomyces cerevisiae</i> (100.00%)
saccharopine dehydrogenase (NAD ⁺ , L-lysine-forming)	1.5.1.7	<i>Saccharomyces cerevisiae</i> (97.39%), <i>Monascus purpureus</i> (2.61%)	<i>Aspergillus phoenicis</i> (52.31%), <i>Saccharomyces cerevisiae</i> (47.47%)
lysine 2- monooxygenase	1.13.12.2	-	-

tryptophanase	1.13.11.11	<i>Burkholderia gladioli</i> (100%)	<i>Burkholderia gladioli</i> (81.76%), <i>Burkholderia_sp._Bp8992</i> (18.24%)
tryptophan transaminase	2.6.1.27	<i>Saccharomyces cerevisiae</i> (82.63%), <i>Monascus purpureus</i> (11.80%), <i>Aspergillus niger</i> (4.75%)	<i>Monascus purpureus</i> (56.04%), <i>Saccharomyces cerevisiae</i> (42.25%), <i>Aspergillus niger</i> (1.09%)
tryptophanase	4.1.99.1	<i>Pantoea ananatis</i> (94.30%), <i>Cronobacter dublinensis</i> (4.56%), <i>Klebsiella quasipneumoniae</i> (1.14%) <i>Weissella cibaria</i> (40.67%), <i>Burkholderia gladioli</i> (17.48%),	<i>Pantoea ananatis</i> (94.52%), <i>Klebsiella quasipneumoniae</i> (5.48%)
D-amino-acid oxidase	1.4.3.3	<i>Monascus purpureus</i> (79.56%), <i>Aspergillus tanneri</i> (18.67%), <i>Saccharopolyspora spinosa</i> (1.78%)	<i>Aspergillus niger</i> (84.75%), <i>Monascus purpureus</i> (9.25%), <i>Aspergillus tanneri</i> (4.31%)
glycine amidinotransferase	2.1.4.1	-	-
arginine N- succinyltransferase	2.3.1.109	<i>Burkholderia gladioli</i> (37.70%), <i>unclassified_g_Burkholderia</i> (35.81%), <i>Pantoea dispersa</i> (15.21%), <i>unclassified_g_Klebsiella</i> (3.23%), <i>Klebsiella pneumoniae</i> (2.80%), <i>unclassified_f_Enterobacteriaceae</i> (2.36%)	<i>unclassified_f_Enterobacteriaceae</i> (30.52%), <i>unclassified_g_Burkholderia</i> (22.36%), <i>Burkholderia gladioli</i> (19.23%), <i>Enterobacter huaxiensis</i> (9.32%), <i>unclassified_g_Enterobacter</i> (6.31%), <i>Pantoea deleyi</i> (3.94%), <i>unclassified_g_Pantoea</i> (3.81%), <i>Burkholderia cepacia</i> (2.22%)
arginine deiminase	3.5.3.6	<i>Weissella cibaria</i> (92.31%), <i>Enterobacter_sp._SES19</i> (4.59%), <i>unclassified_g_Lactococcus</i> (1.64%)	<i>Weissella cibaria</i> (94.98%), <i>Escherichia coli</i> (3.84%)
nitric-oxide synthase (flavodoxin)	1.14.14.47	<i>Bacillus ginsengihumi</i> (100.00%)	<i>Bacillus amyloliquefaciens</i> (87.44%), <i>Bacillus ginsengihumi</i> (9.06%), <i>Saccharopolyspora shandongensis</i> (2.44%), <i>unclassified_g_Staphylococcus</i> (1.07%)
D-arginine dehydrogenase	1.4.99.6	-	<i>Burkholderia gladioli</i> (86.67%), <i>Burkholderia cepacia</i> (13.33%)

Table S3. Microbial contributions to flavor metabolizing enzymes in GTW and WYW brewing.

Enzyme function	Enzyme name	Enzyme number	GTW	WYW
			Distribution of microbes (>1%)	Distribution of microbes (>1%)
Glycolysis	glycogen phosphorylase	2.4.1.1	<i>Weissella cibaria</i> (57.67%), <i>Pantoea dispersa</i> (13.96%), <i>Pantoea_sp._AG1095</i> (9.04%), <i>unclassified_o_Enterobacterales</i> (4.37%), <i>unclassified_f_Enterobacteriaceae</i> (2.61%), <i>Kosakonia cowanii</i> (2.60%), <i>Klebsiella pneumoniae</i> (2.16%)	<i>Weissella cibaria</i> (76.82%), <i>unclassified_o_Enterobacterales</i> (5.73%), <i>Saccharomyces cerevisiae</i> (3.94%), <i>Aspergillus niger</i> (3.32%), <i>Kosakonia cowanii</i> (2.55%), <i>Enterobacter cloacae</i> (1.08%)
	glucan 1,4-alpha-glucosidase	3.2.1.3	<i>Saccharomyces cerevisiae</i> (47.18%), <i>Monascus purpureus</i> (38.03%), <i>Pantoea ananatis</i> (35.21%), <i>Byssochlamys spectabilis</i> (9.15%), <i>Rhizopus oryzae</i> (9.15%), <i>Pantoea_sp._OXWO6B1</i> (8.45%)	<i>Aspergillus niger</i> (58.56%), <i>Saccharomyces cerevisiae</i> (30.21%), <i>Monascus purpureus</i> (3.86%), <i>Pantoea ananatis</i> (2.01%), <i>Caballeronia megalochromosomata</i> (1.54%), <i>Trinickia soli</i> (1.39%), <i>Byssochlamys spectabilis</i> (1.08%)
	amyl-alpha-1,6-glucosidase	3.2.1.33	<i>Saccharomyces cerevisiae</i> (84.96%), <i>Monascus purpureus</i> (15.04%),	<i>Monascus purpureus</i> (55.31%), <i>Saccharomyces cerevisiae</i> (44.35%)
	glucose-1-phosphatase	3.1.3.10	<i>unclassified_g_Pantoea</i> (66.36%), <i>Klebsiella pneumoniae</i> (8.14%), <i>Enterobacter cloacae</i> (4.36%), <i>Klebsiella_cf._planticola_B43</i> (3.67%), <i>Kosakonia cowanii</i> (3.40%), <i>unclassified_f_Enterobacteriaceae</i> (2.72%)	<i>Enterobacter cloacae</i> (20.86%), <i>Klebsiella_cf._planticola_B43</i> (15.28%), <i>Kosakonia cowanii</i> (14.42%), <i>Enterobacter kobei</i> (10.86%), <i>Enterobacter roggkampii</i> (6.26%), <i>Lactococcus lactis</i> (5.09%), <i>Klebsiella pneumoniae</i> (4.91%), <i>Type-F_symbiont_of_Plautia_stali</i> (4.42%), <i>Enterobacter bugandensis</i> (4.36%), <i>Pantoea ananatis</i> (3.93%), <i>Pantoea_sp._AMG_501</i> (3.50%)

	cyclomaltodextrinase	3.2.1.54	<i>Leuconostoc lactis</i> (88.21%), <i>Lactococcus garvieae</i> (9.63%)	<i>Leuconostoc lactis</i> (96.82%), <i>Lactococcus garvieae</i> (2.49%)
	isoamylase	3.2.1.68	<i>Burkholderia gladioli</i> (51.20%), <i>unclassified_g_Pantoea</i> (33.00%), <i>Enterobacter_sp._N18-03635</i> (8.22%), <i>Kosakonia cowanii</i> (3.28%)	<i>Enterobacter_sp._N18-03635</i> (51.92%), <i>Kosakonia cowanii</i> (17.89%), <i>Burkholderia gladioli</i> (11.76%), <i>Enterobacter kobei</i> (6.37%), <i>unclassified_g_Pantoea</i> (3.99%), <i>Enterobacter roggenkampii</i> (3.79%), <i>unclassified_g_Enterobacter</i> (1.22%)
	alpha-amylase	3.2.1.1	<i>Burkholderia gladioli</i> (54.91%), <i>Enterobacter asburiae</i> (7.36%), <i>Klebsiella pneumoniae</i> (6.14%), <i>unclassified_f_Enterobacteriaceae</i> (6.02%), <i>unclassified_g_Enterobacter</i> (4.58%), <i>Kosakonia cowanii</i> (4.53%), <i>Enterobacter bugandensis</i> (4.21%), <i>Lactococcus lactis</i> (2.26%)	<i>Aspergillus niger</i> (34.3%), <i>Enterobacter asburiae</i> (16.63%), <i>unclassified_g_Enterobacter</i> (9.06%), <i>Enterobacter bugandensis</i> (8.96%), <i>Kosakonia cowanii</i> (8.04%), <i>Enterobacter_sp._RIT_418</i> (3.06%), <i>Enterobacter roggenkampii</i> (2.54%), <i>Lactococcus lactis</i> (2.08%)
	glucan 1,4-alpha-maltohydrolase	3.2.1.133	<i>Leuconostoc lactis</i> (88.21%), <i>Lactococcus garvieae</i> (9.63%)	<i>Leuconostoc lactis</i> (96.82%), <i>Lactococcus garvieae</i> (2.49%)
	alpha-glucosidase	3.2.1.20	<i>Weissella cibaria</i> (64.93%), <i>Pantoea_sp._Ap-870</i> (11.26%), <i>Enterobacter asburiae</i> (5.93%), <i>unclassified_f_Enterobacteriaceae</i> (3.53%), <i>unclassified_g_Klebsiella</i> (3.24%), <i>Kosakonia_sp._CCTCC_M2018092</i> (2.26%)	<i>Weissella cibaria</i> (69.45%), <i>Aspergillus niger</i> (12.94%), <i>Enterobacter asburiae</i> (6.75%), <i>Leuconostoc lactis</i> (3.85%), <i>Kosakonia_sp._CCTCC_M2018092</i> (2.05%), <i>Kosakonia cowanii</i> (1.37%)
	4-alpha-glucanotransferase	2.4.1.25	<i>Pantoea dispersa</i> (33.99%), <i>Pantoea_sp._BK028</i> (23.42%), <i>unclassified_f_Enterobacteriaceae</i> (10.01%), <i>Kosakonia cowanii</i> (4.55%), <i>Saccharomyces cerevisiae</i> (4.49%), <i>Enterobacter hormaechei</i> (4.38%), <i>Enterobacter_sp._J49</i> (2.50%),	<i>Monascus purpureus</i> (33.99%), <i>Saccharomyces cerevisiae</i> (27.25%), <i>Enterobacter hormaechei</i> (6.99%), <i>Kosakonia cowanii</i> (5.75%), <i>Enterobacter_sp._J49</i> (4.41%), <i>Enterobacter cloacae</i> (3.88%), <i>Pantoea ananatis</i> (3.88%), <i>Enterobacter wuhouensis</i> (3.32%), <i>Enterobacter</i>

			<i>Pantoea ananatis</i> (2.26%), <i>Lactococcus lactis</i> (2.13%)	<i>asburiae</i> (2.62%), <i>Pantoea deleyi</i> (2.46%), <i>Lactococcus lactis</i> (1.41%)
maltose phosphorylase	2.4.1.8		<i>Weissella cibaria</i> (88.30%), <i>Leuconostoc mesenteroides</i> (6.49%), <i>Leuconostoc lactis</i> (4.61%)	<i>Weissella cibaria</i> (91.67%), <i>Leuconostoc lactis</i> (6.11%), <i>Leuconostoc mesenteroides</i> (1.80%)
oligo-1,6-glucosidase	3.2.1.10		<i>Leuconostoc citreum</i> (44.94%), <i>Saccharomyces cerevisiae</i> (28.18%), <i>Leuconostoc lactis</i> (13.97%), <i>Pediococcus damnosus</i> (3.56%), <i>Monascus purpureus</i> (2.70%), <i>Franconibacter pulveris</i> (2.55%), <i>unclassified_g_Cronobacter</i> (1.97%)	<i>Saccharomyces cerevisiae</i> (85.75%), <i>Leuconostoc lactis</i> (8.67%), <i>Leuconostoc citreum</i> (2.54%), <i>Monascus purpureus</i> (1.19%)
phosphoglucomutase (alpha-D-glucose-1,6-bisphosphate-dependent)	5.4.2.2		<i>unclassified_g_Weissella</i> (49.85%), <i>unclassified_g_Burkholderia</i> (25.62%), <i>unclassified_g_Pantoea</i> (12.59%), <i>Lelliottia nimipressuralis</i> (3.25%)	<i>unclassified_g_Weissella</i> (66.94%), <i>Saccharomyces cerevisiae</i> (11.78%), <i>Aspergillus niger</i> (8.31%), <i>Leuconostoc lactis</i> (4.89%),
hexokinase	2.7.1.1		<i>Saccharomyces cerevisiae</i> (79.56%), <i>Monascus purpureus</i> (20.24%)	<i>Saccharomyces cerevisiae</i> (54.9%), <i>Aspergillus niger</i> (26.02%), <i>Aspergillus welwitschiae</i> (9.82%), <i>Uncinocarpus reesii</i> (6.86%), <i>Monascus purpureus</i> (2.15%)
glucokinase	2.7.1.2		<i>unclassified_g_Weissella</i> (41.82%), <i>unclassified_g_Burkholderia</i> (25.92%), <i>Burkholderia gladioli</i> (16.40%), <i>unclassified_g_Pantoea</i> (10.39%), <i>unclassified_f_Enterobacteriaceae</i> (2.79%)	<i>unclassified_g_Weissella</i> (91.56%), <i>unclassified_g_Leuconostoc</i> (2.27%), <i>Enterobacter asburiae</i> (1.27%), <i>unclassified_f_Enterobacteriaceae</i> (1.12%)
polyphosphate---glucose phosphotransferase	2.7.1.63		<i>Burkholderia gladioli</i> (98.96%), <i>Pantoea ananatis</i> (1.04%)	<i>Burkholderia gladioli</i> (20.14%), <i>Pantoea ananatis</i> (9.20%)
glucose-6-phosphate isomerase	5.3.1.9		<i>Weissella cibaria</i> (51.22%), <i>Burkholderia gladioli</i> (24.13%), <i>unclassified_g_Pantoea</i> (11.06%), <i>Klebsiella pneumoniae</i> (4.13%),	<i>Weissella cibaria</i> (73.67%), <i>Leuconostoc lactis</i> (6.13%), <i>Saccharomyces cerevisiae</i> (5.27%), <i>Aspergillus welwitschiae</i> (4.85%), <i>Enterobacter</i>

			<i>Enterobacter hormaechei</i> (1.57%), <i>Leuconostoc citreum</i> (1.43%), <i>Leuconostoc lactis</i> (1.43%), <i>Klebsiella oxytoca</i> (1.17%)	<i>hormaechei</i> (2.03%), <i>Klebsiella oxytoca</i> (1.65%), <i>Klebsiella pneumoniae</i> (1.42%)
	fructose-6-phosphate kinase	2.7.1.11	<i>Klebsiella pneumoniae</i> (40.25%), <i>unclassified_f_Enterobacteriaceae</i> (22.94%), <i>Saccharomyces cerevisiae</i> (7.93%), <i>unclassified_g_Enterobacter</i> (7.41%), <i>Enterobacter_sp._UCD-UG_FMILLET</i> (5.78%), <i>unclassified_g_Pantoea</i> (2.52%), <i>Enterobacter cloacae</i> (2.22%), <i>Pantoea agglomerans</i> (2.08%), <i>Lactococcus lactis</i> (2.00%)	<i>Saccharomyces cerevisiae</i> (43.82%), <i>Aspergillus niger</i> (32.5%), <i>unclassified_f_Enterobacteriaceae</i> (7.77%), <i>unclassified_g_Enterobacter</i> (4.53%), <i>Enterobacter_sp._UCD-UG_FMILLET</i> (4.46%)
	diphosphate---fructose-6-phosphate 1-phosphotransferase	2.7.1.90	<i>Rhodococcus erythropolis</i> (50.00%), <i>unclassified_g_Variovorax</i> (50.00%)	<i>Rhodococcus erythropolis</i> (75.00%), <i>unclassified_g_Variovorax</i> (25.00%)
	fructose-bisphosphate aldolase	4.1.2.13	<i>unclassified_g_Pantoea</i> (50.82%), <i>unclassified_g_Burkholderia</i> (40.77%), <i>Pantoea dispersa</i> (18.17%), <i>unclassified_o_Enterobacterales</i> (12.18%), <i>unclassified_f_Enterobacteriaceae</i> (5.94%), <i>Klebsiella pneumoniae</i> (5.31%), <i>unclassified_g_Enterobacter</i> (4.22%), <i>Leuconostoc lactis</i> (2.14%), <i>Salmonella enterica</i> (2.06%)	<i>unclassified_o_Enterobacterales</i> (23.31%), <i>unclassified_f_Enterobacteriaceae</i> (15.81%), <i>Leuconostoc lactis</i> (15.53%), <i>Saccharomyces cerevisiae</i> (13.59%), <i>unclassified_g_Enterobacter</i> (11.85%), <i>Aspergillus welwitschiae</i> (9.39%), <i>Aspergillus niger</i> (8.83%), <i>Salmonella enterica</i> (5.22%), <i>Aspergillus sclerotium</i> (2.56%), <i>unclassified_g_Pantoea</i> (2.43%) <i>Klebsiella oxytoca</i> (2.32%)
	triose-phosphate isomerase	5.3.1.1	<i>Weissella cibaria</i> (69.56%), <i>Burkholderia gladioli</i> (19.76%), <i>unclassified_f_Enterobacteriaceae</i> (3.30%), <i>Klebsiella pneumoniae</i> (1.50%), <i>Leuconostoc</i>	<i>Weissella cibaria</i> (89.52%), <i>Monascus purpureus</i> (2.63%), <i>Saccharomyces cerevisiae</i> (2.58%), <i>Aspergillus neoniger</i> (1.40%)

			<i>citreum</i> (1.48%), <i>unclassified_g_Pantoea</i> (1.25%)	
	glyceraldehyde-3-phosphate dehydrogenase (phosphorylating)	1.2.1.12	<i>Weissella cibaria</i> (49.84%), <i>Burkholderia gladioli</i> (27.46%), <i>Pantoea_sp._BK028</i> (5.01%), <i>Leuconostoc citreum</i> (2.54%), <i>Enterobacter cloacae</i> (1.71%), <i>unclassified_o_Enterobacterales</i> (1.44%), <i>unclassified_f_Enterobacteriaceae</i> (1.39%), <i>Pantoea agglomerans</i> (1.33%), <i>unclassified_g_Enterobacter</i> (1.27%), <i>Enterobacter bugandensis</i> (1.24%), <i>unclassified_g_Lactococcus</i> (1.10%)	<i>Weissella cibaria</i> (69.92%), <i>Saccharomyces cerevisiae</i> (10.15%), <i>Aspergillus phoenicis</i> (2.40%), <i>Aspergillus niger</i> (2.13%), <i>Leuconostoc citreum</i> (2.04%), <i>unclassified_o_Enterobacterales</i> (2.03%), <i>Enterobacter cloacae</i> (1.54%), <i>unclassified_g_Enterobacter</i> (1.53%), <i>Enterobacter bugandensis</i> (1.38%)
	phosphoglycerate kinase	2.7.2.3	<i>Weissella cibaria</i> (52.15%), <i>unclassified_g_Burkholderia</i> (33.97%), <i>unclassified_g_Pantoea</i> (4.35%), <i>Leuconostoc lactis</i> (2.84%), <i>unclassified_g_Cronobacter</i> (1.76%), <i>unclassified_g_Lactococcus</i> (1.42%), <i>Leuconostoc citreum</i> (1.37%)	<i>Weissella cibaria</i> (77.95%), <i>Leuconostoc lactis</i> (8.03%), <i>Saccharomyces cerevisiae</i> (4.72%), <i>Monascus purpureus</i> (3.36%), <i>Enterobacter ludwigii</i> (1.30%), <i>unclassified_g_Cronobacter</i> (1.10%)
	phosphoglycerate mutase (2,3-diphosphoglycerate-independent)	5.4.2.12	<i>Kosakonia cowanii</i> (30.70%), <i>Klebsiella pneumoniae</i> (29.20%), <i>Kosakonia oryziphila</i> (6.23%), <i>Cronobacter malonaticus</i> (6.16%), <i>Enterobacter ludwigii</i> (6.04%), <i>unclassified_g_Enterobacter</i> (5.04%), <i>Franconibacter pulveris</i> (4.61%), <i>Enterobacter roggenkampii</i> (4.48%), <i>unclassified_g_Cronobacter</i> (2.99%), <i>Lelliottia nimipressuralis</i> (2.37%)	<i>Aspergillus niger</i> (50.29%), <i>Kosakonia cowanii</i> (24.48%), <i>Kosakonia oryziphila</i> (5.97%), <i>Enterobacter ludwigii</i> (4.15%), <i>Enterobacter roggenkampii</i> (2.94%), <i>unclassified_g_Bacillus_f_Bacillaceae</i> (2.67%), <i>Klebsiella pneumoniae</i> (2.10%),

	phosphoglycerate mutase (2,3-diphosphoglycerate-dependent)	5.4.2.11	<i>Burkholderia gladioli</i> (34.33%), <i>unclassified_g_Weissella</i> (34.04%), <i>unclassified_g_Pantoea</i> (7.95%), <i>Pantoea_sp._R102</i> (7.74%), <i>unclassified_f_Enterobacteriaceae</i> (5.98%), <i>Leuconostoc citreum</i> (2.72%)	<i>unclassified_g_Weissella</i> (65.21%), <i>Saccharomyces cerevisiae</i> (12.84%), <i>unclassified_g_Leuconostoc</i> (5.14%), <i>unclassified_f_Enterobacteriaceae</i> (4.93%), <i>Leuconostoc lactis</i> (3.23%)
	phosphopyruvate hydratase	4.2.1.11	<i>Weissella cibaria</i> (50.33%), <i>unclassified_g_Burkholderia</i> (29.82%), <i>unclassified_f_Enterobacteriaceae</i> (11.64%), <i>unclassified_g_Leuconostoc</i> (2.94%), <i>Lactococcus lactis</i> (1.44%), <i>Saccharomyces cerevisiae</i> (1.16%)	<i>Weissella cibaria</i> (69.14%), <i>Saccharomyces cerevisiae</i> (13.16%), <i>unclassified_g_Leuconostoc</i> (7.90%), <i>unclassified_f_Enterobacteriaceae</i> (5.15%)
	pyruvate kinase	2.7.1.40	<i>Burkholderia gladioli</i> (40.97%), <i>Weissella cibaria</i> (38.51%), <i>unclassified_g_Pantoea</i> (7.62%), <i>Klebsiella quasipneumoniae</i> (1.66%), <i>Enterobacter_sp._Crenshaw</i> (1.43%), <i>Leuconostoc citreum</i> (1.29%), <i>Pantoea wallisii</i> (1.03%)	<i>Weissella cibaria</i> (72.06%), <i>Saccharomyces cerevisiae</i> (8.51%), <i>unclassified_g_Leuconostoc</i> (4.48%), <i>Lichtheimia ramosa</i> (4.42%), <i>Enterobacter_sp._Crenshaw</i> (2.66%), <i>Burkholderia gladioli</i> (1.37%)
Fatty acids biosynthesis	acetyl-CoA carboxylase	6.4.1.2	<i>Weissella cibaria</i> (36.01%), <i>Burkholderia gladioli</i> (14.90%), <i>unclassified_g_Burkholderia</i> (13.34%), <i>Weissella_sp._DD23</i> (12.30%), <i>unclassified_g_Weissella</i> (10.79%), <i>unclassified_g_Pantoea</i> (3.99%), <i>Leuconostoc citreum</i> (1.40%)	<i>Weissella cibaria</i> (54.43%), <i>Weissella_sp._DD23</i> (16.53%), <i>unclassified_g_Weissella</i> (14.79%), <i>Saccharomyces cerevisiae</i> (4.23%), <i>Leuconostoc lactis</i> (2.18%), <i>Lichtheimia ramosa</i> (1.61%), <i>unclassified_g_Leuconostoc</i> (1.43%)
	Transferring groups other than aminoacyl groups	2.3.1.-	<i>Burkholderia gladioli</i> (50.21%), <i>unclassified_g_Burkholderia</i> (11.28%), <i>unclassified_g_Pantoea</i> (8.44%), <i>Pantoea dispersa</i> (6.24%), <i>unclassified_f_Enterobacteriaceae</i> (4.76%), <i>unclassified_g_Enterobacter</i> (3.36%),	<i>Saccharomyces cerevisiae</i> (35.67%), <i>Aspergillus niger</i> (15.54%), <i>Monascus purpureus</i> (8.27%), <i>unclassified_g_Enterobacter</i> (7.97%), <i>Kosakonia cowanii</i> (7.32%), <i>Aspergillus phoenicis</i> (3.85%), <i>Monascus ruber</i> (3.18%),

		<i>Pantoea_sp._BK028</i> (3.19%), <i>Kosakonia cowanii</i> (3.02%), <i>Klebsiella pneumoniae</i> (2.01%), <i>Saccharomyces cerevisiae</i> (1.09%)	<i>Burkholderia gladioli</i> (2.40%), <i>Enterobacter_sp._KINAN-G</i> (2.28%), <i>unclassified_f_Enterobacteriaceae</i> (1.90%)
fatty-acyl-CoA synthase system	2.3.1.86	<i>Monascus purpureus</i> (36.75%), <i>Lichtheimia ramosa</i> (19.45%), <i>Saccharomyces cerevisiae</i> (19.30%), <i>Monascus pilosus</i> (9.04%), <i>Monascus ruber</i> (9.04%), <i>Aspergillus oryzae</i> (3.06%), <i>Aspergillus niger</i> (1.99%), <i>Rhizopus delemar</i> (1.38%)	<i>Aspergillus niger</i> (66.20%), <i>Lichtheimia ramosa</i> (8.81%), <i>Saccharomyces cerevisiae</i> (8.65%), <i>Aspergillus welwitschiae</i> (7.13%), <i>Rhizopus delemar</i> (6.07%), <i>Monascus purpureus</i> (2.11%)
[acyl-carrier-protein] S-malonyltransferase	2.3.1.39	<i>Burkholderia gladioli</i> (43.54%), <i>unclassified_g_Burkholderia</i> (27.80%), <i>Salmonella enterica</i> (12.20%), <i>unclassified_f_Enterobacteriaceae</i> (2.87%), <i>Enterobacter cloacae</i> (2.78%), <i>Leuconostoc lactis</i> (2.15%), <i>Leuconostoc citreum</i> (2.09%), <i>Weissella confusa</i> (1.37%), <i>Klebsiella pneumoniae</i> (1.07%)	<i>Leuconostoc lactis</i> (27.31%), <i>Saccharomyces cerevisiae</i> (15.17%), <i>Enterobacter cloacae</i> (8.47%), <i>Aspergillus awamori</i> (7.27%), <i>Weissella confusa</i> (6.70%), <i>Kosakonia cowanii</i> (4.70%), <i>Burkholderia gladioli</i> (4.34%), <i>Salmonella enterica</i> (3.69%), <i>unclassified_g_Enterobacter</i> (3.65%), <i>Pantoea deleyi</i> (3.30%), <i>unclassified_g_Burkholderia</i> (2.91%), <i>unclassified_f_Enterobacteriaceae</i> (2.78%), <i>Leuconostoc citreum</i> (2.50%)
beta-ketoacyl-[acyl-carrier-protein] synthase III	2.3.1.180	<i>Weissella cibaria</i> (49.34%), <i>unclassified_g_Burkholderia</i> (28.02%), <i>Burkholderia gladioli</i> (8.97%), <i>Pantoea dispersa</i> (5.82%), <i>Leuconostoc citreum</i> (2.00%), <i>unclassified_g_Enterobacter</i> (1.31%), <i>Klebsiella pneumoniae</i> (1.07%)	<i>Weissella cibaria</i> (86.86%), <i>Leuconostoc lactis</i> (4.40%), <i>unclassified_g_Enterobacter</i> (1.97%), <i>unclassified_g_Leuconostoc</i> (1.86%), <i>Enterobacter_sp._UCD-UG_FMILLET</i> (1.29%)

	beta-ketoacyl-[acyl-carrier-protein] synthase I	2.3.1.41	<i>unclassified_g_Pantoea</i> (36.91%), <i>Pantoea dispersa</i> (35.21%), <i>unclassified_f_Enterobacteriaceae</i> (8.75%), <i>unclassified_g_Enterobacter</i> (8.22%), <i>Kosakonia cowanii</i> (3.93%), <i>Enterobacter cloacae</i> (1.91%), <i>Enterobacter roggenkampii</i> (1.46%)	<i>unclassified_g_Enterobacter</i> (44.48%), <i>Kosakonia cowanii</i> (16.86%), <i>unclassified_f_Enterobacteriaceae</i> (9.26%), <i>Enterobacter roggenkampii</i> (6.95%), <i>Enterobacter asburiae</i> (6.00%), <i>Pantoea deleyi</i> (4.81%), <i>Pantoea ananatis</i> (3.86%),
	beta-ketoacyl-[acyl-carrier-protein] synthase II	2.3.1.179	<i>Weissella cibaria</i> (42.24%), <i>unclassified_g_Burkholderia</i> (25.91%), <i>Type-C_symbiont_of_Plautia_stali</i> (9.07%), <i>unclassified_g_Pantoea</i> (6.99%), <i>unclassified_g_Enterobacter</i> (3.85%), <i>Kosakonia cowanii</i> (3.32%), <i>unclassified_f_Enterobacteriaceae</i> (2.22%), <i>Enterobacter cloacae</i> (1.84%), <i>Leuconostoc citreum</i> (1.43%)	<i>Weissella cibaria</i> (71.92%), <i>Saccharomyces cerevisiae</i> (5.01%), <i>Leuconostoc lactis</i> (4.96%), <i>Kosakonia cowanii</i> (4.77%), <i>unclassified_g_Enterobacter</i> (4.77%)
	3-oxoacyl-[acyl-carrier-protein] reductase	1.1.1.100	<i>Burkholderia gladioli</i> (36.08%), <i>unclassified_g_Burkholderia</i> (19.10%), <i>unclassified_g>Weissella</i> (10.75%), <i>Weissella cibaria</i> (7.78%), <i>Pantoea dispersa</i> (7.27%), <i>Pantoea_sp._BK028</i> (4.10%), <i>unclassified_g_Pantoea</i> (3.59%), <i>Pantoea rwandensis</i> (3.36%), <i>unclassified_f_Enterobacteriaceae</i> (1.59%), <i>Leuconostoc citreum</i> (1.58%)	<i>unclassified_g>Weissella</i> (36.32%), <i>Weissella cibaria</i> (33.36%), <i>Leuconostoc lactis</i> (5.03%), <i>Aspergillus phoenicis</i> (3.18%), <i>Saccharomyces cerevisiae</i> (2.98%), <i>Aspergillus niger</i> (2.53%), <i>Kosakonia cowanii</i> (2.35%), <i>Burkholderia gladioli</i> (2.33%), <i>unclassified_g_Burkholderia</i> (1.90%), <i>Aspergillus carbonarius</i> (1.72%), <i>unclassified_f_Enterobacteriaceae</i> (1.71%)

3-hydroxyacyl-[acyl-carrier-protein] dehydratase	4.2.1.59	<i>unclassified_g_Weissella</i> (33.79%), <i>Weissella cibaria</i> (28.90%), <i>unclassified_g_Burkholderia</i> (19.72%), <i>unclassified_g_Pantoea</i> (9.30%), <i>Enterobacter hormaechei</i> (2.76%), <i>unclassified_g_Leuconostoc</i> (1.44%), <i>Citrobacter koseri</i> (1.33%), <i>Leuconostoc lactis</i> (1.04%)	<i>unclassified_g_Weissella</i> (46.92%), <i>Weissella cibaria</i> (38.68%), <i>Leuconostoc lactis</i> (4.45%), <i>unclassified_g_Leuconostoc</i> (4.25%), <i>Enterobacter hormaechei</i> (2.93%)
enoyl-[acyl-carrier-protein] reductase (NADPH, Si-specific)	1.3.1.10	<i>Enterobacter hormaechei</i> (42.68%), <i>Klebsiella pneumoniae</i> (19.13%), <i>Leuconostoc citreum</i> (14.81%), <i>unclassified_g_Pantoea</i> (10.59%), <i>unclassified_g_Lactococcus</i> (7.32%), <i>Enterobacter_sp._FS01</i> (4.53%)	<i>Enterobacter hormaechei</i> (79.36%), <i>Leuconostoc citreum</i> (5.50%), <i>unclassified_g_Lactococcus</i> (4.94%), <i>unclassified_g_Bacillus_f_Bacillaceae</i> (3.27%), <i>unclassified_g_Pantoea</i> (2.23%), <i>Enterobacter_sp._FS01</i> (1.83%), <i>Lactococcus garvieae</i> (1.35%)
enoyl-[acyl-carrier-protein] reductase (NADH)	1.3.1.9	<i>unclassified_g_Burkholderia</i> (57.84%), <i>Enterobacter hormaechei</i> (8.20%), <i>Leuconostoc citreum</i> (6.81%), <i>Weissella confusa</i> (6.10%), <i>Enterobacter asburiae</i> (5.98%), <i>Klebsiella pneumoniae</i> (3.67%), <i>unclassified_f_Enterobacteriaceae</i> (3.17%), <i>unclassified_g_Pantoea</i> (2.03%), <i>unclassified_g_Leuconostoc</i> (1.89%), <i>Lactococcus lactis</i> (1.42%), <i>unclassified_g_Lactococcus</i> (1.41%)	<i>Enterobacter hormaechei</i> (26.82%), <i>Weissella confusa</i> (22.08%), <i>Enterobacter asburiae</i> (20.85%), <i>unclassified_g_Leuconostoc</i> (13.39%), <i>Leuconostoc citreum</i> (4.85%), <i>unclassified_g_Burkholderia</i> (3.31%), <i>Lactococcus lactis</i> (2.07%), <i>unclassified_g_Lactococcus</i> (1.67%), <i>unclassified_g_Bacillus_f_Bacillaceae</i> (1.10%)
enoyl-[acyl-carrier-protein] reductase (NADPH)	1.3.1.104	-	<i>Bacillus amyloliquefaciens</i> (50.00%), <i>Bacillus nakamurai</i> (50.00%)
trans-2-enoyl-CoA reductase (NAD+)	1.3.1.44	<i>unclassified_g_Burkholderia</i> (99.97%)	<i>unclassified_g_Burkholderia</i> (90.44%), <i>Burkholderia cepacia</i> (7.35%), <i>Variovorax_sp._SCN_67-85</i> (2.21%)

	dodecanoyl-[acyl-carrier-protein] hydrolase	3.1.2.21	<i>unclassified_g_Weissella</i> (91.57%), <i>Leuconostoc citreum</i> (3.74%), <i>Leuconostoc lactis</i> (3.46%)	<i>unclassified_g_Weissella</i> (91.48%), <i>Leuconostoc lactis</i> (7.32%)
Higher alcohols biosynthesis	aspartate transaminase	2.6.1.1	<i>Burkholderia gladioli</i> (45.69%), <i>unclassified_g_Pantoea</i> (21.44%), <i>Type-C_symbiont_of_Plautia_stali</i> (16.00%), <i>Pantoea dispersa</i> (5.18%), <i>unclassified_g_Enterobacter</i> (3.55%), <i>unclassified_g_Kosakonia</i> (3.03%), <i>Saccharomyces cerevisiae</i> (1.19%), <i>Enterobacter cloacae</i> (1.05%)	<i>Saccharomyces cerevisiae</i> (28.08%), <i>Aspergillus luchuensis</i> (21.82%), <i>Aspergillus neoniger</i> (18.17%), <i>unclassified_g_Enterobacter</i> (7.57%), <i>unclassified_g_Kosakonia</i> (6.43%), <i>Monascus purpureus</i> (4.42%), <i>Burkholderia gladioli</i> (2.92%), <i>Bacillus amyloliquefaciens</i> (2.08%), <i>Aspergillus eucalypticola</i> (2.03%), <i>Shigella sonnei</i> (1.79%), <i>Enterobacter cloacae</i> (1.35%), <i>Enterobacter hormaechei</i> (1.31%)
	histidinol-phosphate transaminase	2.6.1.9	<i>Burkholderia gladioli</i> (71.25%), <i>unclassified_g_Pantoea</i> (15.54%), <i>unclassified_f_Enterobacteriaceae</i> (2.76%), <i>Leuconostoc citreum</i> (2.47%), <i>Leuconostoc lactis</i> (2.32%), <i>Escherichia coli</i> (1.47%)	<i>Aspergillus phoenicis</i> (22.37%), <i>Leuconostoc lactis</i> (20.80%), <i>Saccharomyces cerevisiae</i> (18.94%), <i>Burkholderia gladioli</i> (10.53%), <i>Escherichia coli</i> (5.23%), <i>unclassified_g_Burkholderia</i> (4.26%), <i>Enterobacter cloacae</i> (2.74%), <i>Leuconostoc citreum</i> (2.45%), <i>Enterobacter bugandensis</i> (2.08%), <i>unclassified_g_Enterobacter</i> (1.68%), <i>unclassified_g_Pantoea</i> (1.47%), <i>Bacillus amyloliquefaciens</i> (1.29%), <i>Enterobacter asburiae</i> (1.19%), <i>Burkholderia_sp._Bp8992</i> (1.08%), <i>Pantoea deleyi</i> (1.06%), <i>Monascus purpureus</i> (1.00%)
	tyrosine transaminase	2.6.1.5	<i>Saccharomyces cerevisiae</i> (82.63%), <i>Monascus purpureus</i> (11.80%), <i>Aspergillus awamori</i> (4.75%)	<i>Monascus purpureus</i> (56.04%), <i>Saccharomyces cerevisiae</i> (42.25%), <i>Aspergillus niger</i> (1.09%)
	aromatic-amino-acid transaminase	2.6.1.57	<i>Burkholderia gladioli</i> (36.12%), <i>unclassified_g_Burkholderia</i> (34.04%),	<i>Monascus purpureus</i> (33.55%), <i>Saccharomyces cerevisiae</i> (25.29%),

		Pantoea_sp._Ap-959 (17.60%), Klebsiella pneumoniae (2.80%), Klebsiella quasipneumoniae (2.36%), unclassified_g_Enterobacter (1.56%)	unclassified_g_Burkholderia (12.94%), Kosakonia cowanii (4.98%), unclassified_g_Enterobacter (4.54%), Enterobacteriaceae_bacterium_RIT693 (4.25%), Enterobacter asburiae (3.11%), Pantoea ananatis (2.32%), Enterobacter cloacae (2.13%), Cedecea lapagei (2.01%), Pantoea_sp. (1.66%)
phenylalanine (histidine) transaminase	2.6.1.58	Saccharomyces cerevisiae (98.57%), [Candida] glabrata (1.43%) Saccharomyces cerevisiae (83.33%), Monascus purpureus (16.67%)	Saccharomyces cerevisiae (99.92%)
Carboxy-lyases	4.1.1.-	Pantoea_sp._BK028 (35.38%), unclassified_f_Enterobacteriaceae (16.61%), Enterobacter roggenkampii (12.32%), unclassified_g_Enterobacter (12.04%), unclassified_g_Cronobacter (5.18%), Enterobacter ludwigii (3.79%), Klebsiella pneumoniae (3.32%), Lactococcus lactis (2.74%), Saccharomyces cerevisiae (1.97%), Enterobacter asburiae (1.19%), Franconibacter pulveris (1.14%)	Saccharomyces cerevisiae (37.38%), unclassified_g_Enterobacter (17.61%), Enterobacter roggenkampii (15.53%), unclassified_f_Enterobacteriaceae (8.56%), Enterobacter ludwigii (4.43%), unclassified_g_Cronobacter (3.17%), unclassified_g_Bacillus_f_Bacillaceae (2.18%), Lactococcus lactis (2.02%), Pantoea deleyi (1.65%), Enterobacter asburiae (1.32%)
pyruvate decarboxylase	4.1.1.1	Saccharomyces cerevisiae (65.66%), Monascus purpureus (24.59%), Aspergillus piperis (6.26%), Penicillium coprophilum (1.86%), Rhizopus delemar (1.62%)	Saccharomyces cerevisiae (58.79%), Aspergillus niger (22.01%), Aspergillus piperis (16.20%), Monascus purpureus (2.23%)
phenylacetaldehyde dehydrogenase	1.2.1.39	Klebsiella pneumoniae (40.15%), unclassified_g_Klebsiella (27.22%), unclassified_g_Enterobacter (23.23%), unclassified_o_Enterobacterales (9.32%)	unclassified_g_Enterobacter (65.05%), unclassified_o_Enterobacterales (28.24%), Burkholderia cepacia (2.65%), Burkholderia ambifaria (1.72%)

aldehyde dehydrogenase [NAD (P)+]	1.2.1.5	<i>Saccharomyces cerevisiae</i> (78.82%), <i>Monascus purpureus</i> (20.00%), <i>Aspergillus phoenicis</i> (1.18%)	<i>Saccharomyces cerevisiae</i> (48.32%), <i>Aspergillus eucalypticola</i> (26.19%), <i>Aspergillus phoenicis</i> (22.68%), <i>Monascus purpureus</i> (2.77%)
aldehyde dehydrogenase (NAD+)	1.2.1.3	<i>Burkholderia gladioli</i> (52.73%), <i>unclassified_g_Burkholderia</i> (40.32%), <i>Pantoea dispersa</i> (2.45%), <i>Enterobacter asburiae</i> (1.09%)	<i>Saccharomyces cerevisiae</i> (45.01%), <i>Aspergillus niger</i> (24.84%), <i>Aspergillus phoenicis</i> (7.99%), <i>Enterobacter asburiae</i> (5.16%), <i>unclassified_g_Burkholderia</i> (4.22%), <i>Burkholderia gladioli</i> (3.29%)
With NAD+ or NADP+ as acceptor	1.2.1.-	<i>Burkholderia gladioli</i> (35.22%), <i>unclassified_g_Burkholderia</i> (30.03%), <i>Pantoea dispersa</i> (12.46%), <i>unclassified_g_Pantoea</i> (10.67%), <i>Pseudomonas aeruginosa</i> (5.67%), <i>unclassified_g_Klebsiella</i> (2.33%), <i>Enterobacter roggenkampii</i> (1.29%), <i>unclassified_g_Enterobacter</i> (1.03%)	<i>Burkholderia gladioli</i> (30.64%), <i>Enterobacter roggenkampii</i> (21.86%), <i>Kosakonia_sp._CCTCC_M2018092</i> (10.51%), <i>unclassified_g_Enterobacter</i> (10.21%), <i>unclassified_g_Burkholderia</i> (9.53%), <i>Pseudomonas aeruginosa</i> (4.31%), <i>Pantoea ananatis</i> (2.80%), <i>Burkholderia arboris</i> (1.66%), <i>Burkholderia cepacia</i> (1.66%), <i>unclassified_g_Pantoea</i> (1.59%), <i>Klebsiella pneumoniae</i> (1.13%)
aryl-alcohol dehydrogenase	1.1.1.90	<i>unclassified_f_Enterobacteriaceae</i> (99.19%)	<i>unclassified_g_Burkholderia</i> (47.50%), <i>Burkholderia cenocepacia</i> (15.00%), <i>unclassified_f_Enterobacteriaceae</i> (12.50%), <i>unclassified_g_Lactobacillus</i> (12.50%), <i>Rhodococcus_sp._YH3-3</i> (7.50%), <i>Pediococcus pentosaceus</i> (5.00%)

	alcohol dehydrogenase	1.1.1.1	<i>Weissella cibaria</i> (27.61%), <i>Pediococcus pentosaceus</i> (23.09%), <i>Burkholderia gladioli</i> (17.60%), <i>Weissella_sp._DD23</i> (11.46%), <i>Achromobacter xylosoxidans</i> (5.84%), <i>unclassified_g_Pantoea</i> (4.29%), <i>Klebsiella pneumoniae</i> (1.91%), <i>Weissella confusa</i> (1.02%), <i>Leuconostoc citreum</i> (1.00%)	<i>Weissella cibaria</i> (39.44%), <i>Pediococcus pentosaceus</i> (23.71%), <i>Weissella_sp._DD23</i> (15.40%), <i>Saccharomyces cerevisiae</i> (6.64%), <i>Aspergillus niger</i> (4.29%), <i>unclassified_g_Leuconostoc</i> (1.35%), <i>Kosakonia cowanii</i> (1.11%), <i>Enterobacter asburiae</i> (1.09%)
	alcohol dehydrogenase (NADP+)	1.1.1.2	<i>unclassified_g_Burkholderia</i> (39.88%), <i>Mixta calida</i> (19.51%), <i>Pantoea dispersa</i> (16.21%), <i>unclassified_f_Enterobacteriaceae</i> (10.71%), <i>Klebsiella pneumoniae</i> (3.51%), <i>unclassified_g_Enterobacter</i> (3.09%), <i>Klebsiella variicola</i> (1.23%)	<i>unclassified_f_Enterobacteriaceae</i> (22.81%), <i>Vanderwaltozyma polyspora</i> (20.97%), <i>Aspergillus piperis</i> (20.37%), <i>unclassified_g_Enterobacter</i> (12.49%), <i>Saccharomyces cerevisiae</i> (8.82%), <i>Enterobacter ludwigii</i> (2.83%), <i>unclassified_g_Pantoea</i> (2.42%)
	acetolactate synthase	2.2.1.6	<i>unclassified_g_Burkholderia</i> (24.53%), <i>Burkholderia gladioli</i> (21.18%), <i>Weissella cibaria</i> (20.32%), <i>unclassified_g_Pantoea</i> (15.16%), <i>unclassified_f_Enterobacteriaceae</i> (3.54%), <i>Kosakonia cowanii</i> (2.31%), <i>Klebsiella pneumoniae</i> (1.99%), <i>unclassified_g_Enterobacter</i> (1.61%), <i>Enterobacter cloacae</i> (1.47%), <i>unclassified_d_Bacteria</i> (1.34%)	<i>Weissella cibaria</i> (57.42%), <i>Saccharomyces cerevisiae</i> (5.32%), <i>Kosakonia cowanii</i> (5.29%), <i>Aspergillus niger</i> (4.81%), <i>Leuconostoc lactis</i> (4.60%), <i>unclassified_g_Enterobacter</i> (4.25%), <i>Enterobacter cloacae</i> (2.56%), <i>unclassified_f_Enterobacteriaceae</i> (2.19%), <i>unclassified_o_Enterobacterales</i> (1.82%)
	ketol-acid reductoisomerase (NADP+)	1.1.1.86	<i>unclassified_g_Burkholderia</i> (67.43%), <i>Kosakonia cowanii</i> (10.12%), <i>Enterobacter hormaechei</i> (5.52%), <i>Pantoea_sp._ARC607</i> (4.38%), <i>Pantoea ananatis</i> (3.18%), <i>Pantoea agglomerans</i> (1.77%), <i>Lactococcus lactis</i> (1.58%), <i>Klebsiella pneumoniae</i> (1.46%), <i>unclassified_g_Cronobacter</i> (1.12%)	<i>Saccharomyces cerevisiae</i> (29.46%), <i>Kosakonia cowanii</i> (21.28%), <i>Aspergillus awamori</i> (19.55%), <i>Enterobacter hormaechei</i> (5.75%), <i>Pantoea_sp._ARC607</i> (5.53%), <i>Pantoea agglomerans</i> (3.80%), <i>unclassified_g_Burkholderia</i> (3.66%), <i>Klebsiella pneumoniae</i> (2.48%), <i>Escherichia coli</i> (1.82%)

	dihydroxy-acid dehydratase	4.2.1.9	<i>Burkholderia gladioli</i> (52.92%), <i>Burkholderia_sp._SJZ089</i> (24.16%), <i>Pantoea_sp._R102</i> (8.87%), <i>unclassified_d_Bacteria</i> (3.92%), <i>Enterobacter cloacae</i> (2.59%), <i>Escherichia coli</i> (1.16%)	<i>Aspergillus niger</i> (43.07%), <i>Monascus purpureus</i> (20.12%), <i>Saccharomyces cerevisiae</i> (9.01%), <i>Enterobacter cloacae</i> (6.22%), <i>Aspergillus flavus</i> (4.16%), <i>Burkholderia gladioli</i> (3.50%), <i>Salmonella enterica</i> (3.04%)
	branched-chain-amino-acid transaminase	2.6.1.42	<i>Burkholderia gladioli</i> (47.63%), <i>Weissella cibaria</i> (43.33%), <i>unclassified_d_Bacteria</i> (3.03%), <i>unclassified_g_Pantoea</i> (1.40%), <i>Leuconostoc citreum</i> (1.17%),	<i>Weissella cibaria</i> (67.99%), <i>Aspergillus niger</i> (13.31%), <i>Saccharomyces cerevisiae</i> (8.74%), <i>Aspergillus awamori</i> (3.26%), <i>Burkholderia gladioli</i> (1.29%), <i>unclassified_o_Enterobacterales</i> (1.01%)
	valine dehydrogenase (NAD ⁺)	1.4.1.23	<i>Rhodococcus qingshengii</i> (100.00%)	<i>Rhodococcus qingshengii</i> (100.00%)
	valine---pyruvate transaminase	2.6.1.66	<i>Burkholderia gladioli</i> (33.38%), <i>Enterobacter ludwigii</i> (23.20%), <i>Pantoea dispersa</i> (16.76%), <i>unclassified_f_Enterobacteriaceae</i> (10.76%), <i>Burkholderia_sp._Tr-862</i> (7.35%), <i>Enterobacter asburiae</i> (1.66%), <i>Lactococcus lactis</i> (1.53%)	<i>unclassified_f_Enterobacteriaceae</i> (32.83%), <i>Enterobacter asburiae</i> (16.51%), <i>Enterobacter ludwigii</i> (16.40%), <i>Burkholderia gladioli</i> (4.13%), <i>Lactococcus lactis</i> (3.67%), <i>Pantoea_sp._ARC607</i> (3.36%), <i>Pantoea ananatis</i> (3.24%), <i>unclassified_f_Erwinia</i> (3.16%), <i>Kosakonia cowanii</i> (3.13%), <i>Enterobacter_sp._Acro-832</i> (2.55%)
	2-isopropylmalate synthase	2.3.3.13	<i>unclassified_g_Burkholderia</i> (57.23%), <i>Pantoea dispersa</i> (12.36%), <i>unclassified_g_Pantoea</i> (12.18%), <i>unclassified_f_Enterobacteriaceae</i> (5.65%), <i>Leuconostoc citreum</i> (1.97%), <i>Klebsiella pneumoniae</i> (1.91%), <i>Kosakonia cowanii</i> (1.62%), <i>Enterobacter cloacae</i> (1.38%)	<i>Saccharomyces cerevisiae</i> (37.18%), <i>Aspergillus niger</i> (14.61%), <i>unclassified_f_Enterobacteriaceae</i> (10.76%), <i>Kosakonia cowanii</i> (6.74%), <i>unclassified_g_Burkholderia</i> (5.34%), <i>Enterobacter roggenkampii</i> (2.98%), <i>Enterobacter cloacae</i> (2.87%), <i>Enterobacter hormaechei</i> (2.36%), <i>unclassified_g_Enterobacter</i> (2.01%)

	3-isopropylmalate dehydratase	4.2.1.33	<i>Burkholderia gladioli</i> (49.67%), <i>unclassified_g_Burkholderia</i> (15.36%), <i>unclassified_g_Pantoea</i> (13.52%), <i>Pantoea dispersa</i> (9.75%), <i>Leuconostoc citreum</i> (2.66%), <i>unclassified_f_Enterobacteriaceae</i> (2.59%), <i>unclassified_g_Enterobacter</i> (1.53%)	<i>Saccharomyces cerevisiae</i> (24.29%), <i>Aspergillus niger</i> (17.72%), <i>unclassified_f_Enterobacteriaceae</i> (15.08%), <i>unclassified_g_Enterobacter</i> (10.22%), <i>Burkholderia gladioli</i> (6.40%), <i>Leuconostoc citreum</i> (4.50%), <i>Escherichia coli</i> (3.90%), <i>unclassified_g_Pantoea</i> (3.15%), <i>unclassified_g_Burkholderia</i> (2.46%)
	3-isopropylmalate dehydrogenase	1.1.1.85	<i>Burkholderia gladioli</i> (53.17%), <i>unclassified_g_Pantoea</i> (26.64%), <i>Kosakonia_sp._CCTCC_M2018092</i> (5.43%), <i>Leuconostoc citreum</i> (4.40%), <i>unclassified_f_Enterobacteriaceae</i> (1.89%), <i>Enterobacter bugandensis</i> (1.54%), <i>Klebsiella pneumoniae</i> (1.25%), <i>Lactococcus lactis</i> (1.15%)	<i>Aspergillus niger</i> (21.18%), <i>Saccharomyces cerevisiae</i> (20.93%), <i>Kosakonia_sp._CCTCC_M2018092</i> (15.31%), <i>Monascus purpureus</i> (14.91%), <i>unclassified_f_Enterobacteriaceae</i> (5.41%), <i>Burkholderia gladioli</i> (3.88%), <i>Leuconostoc citreum</i> (3.48%), <i>Enterobacter bugandensis</i> (2.03%), <i>Klebsiella variicola</i> (2.03%), <i>unclassified_g_Enterobacter</i> (2.01%)
	leucine dehydrogenase	1.4.1.9	<i>unclassified_g_Rhodococcus_f_Nocardiaceae</i> (100.00%)	<i>Bacillus amyloliquefaciens</i> (93.88%), <i>unclassified_g_Rhodococcus_f_Nocardiaceae</i> (6.12%)
	methylglyoxal reductase (NADPH)	1.1.1.283	<i>Saccharomyces cerevisiae</i> (63.89%), <i>Lactococcus lactis</i> (35.61%)	<i>Saccharomyces cerevisiae</i> (96.32%), <i>Lactococcus lactis</i> (1.91%), <i>Bacillus amyloliquefaciens</i> (1.06%)
Valine and leucine biosynthesis	acetolactate synthase	2.2.1.6	<i>unclassified_g_Burkholderia</i> (24.53%), <i>Burkholderia gladioli</i> (21.18%), <i>Weissella cibaria</i> (20.32%), <i>unclassified_g_Pantoea</i> (15.16%), <i>unclassified_f_Enterobacteriaceae</i> (3.54%), <i>Kosakonia cowanii</i> (2.31%), <i>Klebsiella pneumoniae</i> (1.99%), <i>unclassified_g_Enterobacter</i> (1.61%),	<i>Weissella cibaria</i> (57.42%), <i>Saccharomyces cerevisiae</i> (5.32%), <i>Kosakonia cowanii</i> (5.29%), <i>Aspergillus niger</i> (4.81%), <i>Leuconostoc lactis</i> (4.60%), <i>unclassified_g_Enterobacter</i> (4.25%), <i>Enterobacter cloacae</i> (2.56%), <i>unclassified_f_Enterobacteriaceae</i> (2.19%), <i>unclassified_o_Enterobacterales</i> (1.82%)

			<i>Enterobacter cloacae</i> (1.47%), <i>unclassified_d_Bacteria</i> (1.34%)	
ketol-acid reductoisomerase (NADP+)	1.1.1.86	<i>unclassified_g_Burkholderia</i> (67.43%), <i>Kosakonia cowanii</i> (10.12%), <i>Enterobacter hormaechei</i> (5.52%), <i>Pantoea_sp._ARC607</i> (4.38%), <i>Pantoea ananatis</i> (3.18%), <i>Pantoea agglomerans</i> (1.77%), <i>Lactococcus lactis</i> (1.58%), <i>Klebsiella pneumoniae</i> (1.46%), <i>unclassified_g_Cronobacter</i> (1.12%)	<i>Saccharomyces cerevisiae</i> (29.46%), <i>Kosakonia cowanii</i> (21.28%), <i>Aspergillus awamori</i> (19.55%), <i>Enterobacter hormaechei</i> (5.75%), <i>Pantoea_sp._ARC607</i> (5.53%), <i>Pantoea agglomerans</i> (3.80%), <i>unclassified_g_Burkholderia</i> (3.66%), <i>Klebsiella pneumoniae</i> (2.48%), <i>Escherichia coli</i> (1.82%)	
dihydroxy-acid dehydratase	4.2.1.9	<i>Burkholderia gladioli</i> (52.92%), <i>Burkholderia_sp._SJZ089</i> (24.16%), <i>Pantoea_sp._R102</i> (8.87%), <i>unclassified_d_Bacteria</i> (3.92%), <i>Enterobacter cloacae</i> (2.59%), <i>Escherichia coli</i> (1.16%)	<i>Aspergillus niger</i> (43.07%), <i>Monascus purpureus</i> (20.12%), <i>Saccharomyces cerevisiae</i> (9.01%), <i>Enterobacter cloacae</i> (6.22%), <i>Aspergillus flavus</i> (4.16%), <i>Burkholderia gladioli</i> (3.50%), <i>Salmonella enterica</i> (3.04%)	
2-isopropylmalate synthase	2.3.3.13	<i>unclassified_g_Burkholderia</i> (57.23%), <i>Pantoea dispersa</i> (12.36%), <i>unclassified_g_Pantoea</i> (12.18%), <i>unclassified_f_Enterobacteriaceae</i> (5.65%), <i>Leuconostoc citreum</i> (1.97%), <i>Klebsiella pneumoniae</i> (1.91%), <i>Kosakonia cowanii</i> (1.62%), <i>Enterobacter cloacae</i> (1.38%)	<i>Saccharomyces cerevisiae</i> (37.18%), <i>Aspergillus niger</i> (14.61%), <i>unclassified_f_Enterobacteriaceae</i> (10.76%), <i>Kosakonia cowanii</i> (6.74%), <i>unclassified_g_Burkholderia</i> (5.34%), <i>Enterobacter roggenkampii</i> (2.98%), <i>Enterobacter cloacae</i> (2.87%), <i>Enterobacter hormaechei</i> (2.36%), <i>unclassified_g_Enterobacter</i> (2.01%)	

3-isopropylmalate dehydratase	4.2.1.33	<i>Burkholderia gladioli</i> (49.67%), <i>unclassified_g_Burkholderia</i> (15.36%), <i>unclassified_g_Pantoea</i> (13.52%), <i>Pantoea dispersa</i> (9.75%), <i>Leuconostoc citreum</i> (2.66%), <i>unclassified_f_Enterobacteriaceae</i> (2.59%), <i>unclassified_g_Enterobacter</i> (1.53%)	<i>Saccharomyces cerevisiae</i> (24.29%), <i>Aspergillus niger</i> (17.72%), <i>unclassified_f_Enterobacteriaceae</i> (15.08%), <i>unclassified_g_Enterobacter</i> (10.22%), <i>Burkholderia gladioli</i> (6.40%), <i>Leuconostoc citreum</i> (4.50%), <i>Escherichia coli</i> (3.90%), <i>unclassified_g_Pantoea</i> (3.15%), <i>unclassified_g_Burkholderia</i> (2.46%)
3-isopropylmalate dehydrogenase	1.1.1.85	<i>Burkholderia gladioli</i> (53.17%), <i>unclassified_g_Pantoea</i> (26.64%), <i>Kosakonia_sp._CCTCC_M2018092</i> (5.43%), <i>Leuconostoc citreum</i> (4.40%), <i>unclassified_f_Enterobacteriaceae</i> (1.89%), <i>Enterobacter bugandensis</i> (1.54%), <i>Klebsiella pneumoniae</i> (1.25%), <i>Lactococcus lactis</i> (1.15%)	<i>Aspergillus niger</i> (21.18%), <i>Saccharomyces cerevisiae</i> (20.93%), <i>Kosakonia_sp._CCTCC_M2018092</i> (15.31%), <i>Monascus purpureus</i> (14.91%), <i>unclassified_f_Enterobacteriaceae</i> (5.41%), <i>Burkholderia gladioli</i> (3.88%), <i>Leuconostoc citreum</i> (3.48%), <i>Enterobacter bugandensis</i> (2.03%), <i>Klebsiella variicola</i> (2.03%), <i>unclassified_g_Enterobacter</i> (2.01%)
branched-chain-amino-acid transaminase	2.6.1.42	<i>Burkholderia gladioli</i> (47.63%), <i>Weissella cibaria</i> (43.33%), <i>unclassified_d_Bacteria</i> (3.03%), <i>unclassified_g_Pantoea</i> (1.40%), <i>Leuconostoc citreum</i> (1.17%),	<i>Weissella cibaria</i> (67.99%), <i>Aspergillus niger</i> (13.31%), <i>Saccharomyces cerevisiae</i> (8.74%), <i>Aspergillus awamori</i> (3.26%), <i>Burkholderia gladioli</i> (1.29%), <i>unclassified_o_Enterobacterales</i> (1.01%)
valine---pyruvate transaminase	2.6.1.66	<i>Burkholderia gladioli</i> (33.38%), <i>Enterobacter ludwigii</i> (23.20%), <i>Pantoea dispersa</i> (16.76%), <i>unclassified_f_Enterobacteriaceae</i> (10.76%), <i>Burkholderia_sp._Tr-862</i> (7.35%), <i>Enterobacter asburiae</i> (1.66%), <i>Lactococcus lactis</i> (1.53%)	<i>unclassified_f_Enterobacteriaceae</i> (32.83%), <i>Enterobacter asburiae</i> (16.51%), <i>Enterobacter ludwigii</i> (16.40%), <i>Burkholderia gladioli</i> (4.13%), <i>Lactococcus lactis</i> (3.67%), <i>Pantoea_sp._ARC607</i> (3.36%), <i>Pantoea ananatis</i> (3.24%), <i>unclassified_f_Erwinaceae</i> (3.16%), <i>Kosakonia cowanii</i> (3.13%), <i>Enterobacter_sp._Acro-832</i> (2.55%)

	leucine dehydrogenase	1.4.1.9	<i>unclassified_g_Rhodococcus_f_Nocardiaceae</i> (100.00%)	<i>Bacillus amyloliquefaciens</i> (93.88%), <i>unclassified_g_Rhodococcus_f_Nocardiaceae</i> (6.12%)
Phenylalanine biosynthesis	chorismate mutase	5.4.99.5	<i>Burkholderia gladioli</i> (50.24%), <i>unclassified_g_Pantoea</i> (13.65%), <i>Pantoea_sp._GL120224-02</i> (11.78%), <i>Pantoea dispersa</i> (8.34%), <i>Kosakonia cowanii</i> (2.86%), <i>unclassified_f_Enterobacteriaceae</i> (2.76%), <i>Klebsiella pneumoniae</i> (1.75%), <i>Enterobacter cloacae</i> (1.63%), <i>Enterobacter</i> <i>kobei</i> (1.16%), <i>Klebsiella variicola</i> (1.01%)	<i>Saccharomyces cerevisiae</i> (18.24%), <i>Kosakonia cowanii</i> (14%), <i>Aspergillus niger</i> (13.34%), <i>Burkholderia gladioli</i> (11.06%), <i>Enterobacter cloacae</i> (9.63%), <i>Enterobacter</i> <i>kobei</i> (7.73%), <i>unclassified_g_Enterobacter</i> (3.67%), <i>Pantoea ananatis</i> (3.05%), <i>Pantoea</i> <i>deleyi</i> (2.95%), <i>Bacillus amyloliquefaciens</i> (2.76%), <i>unclassified_g_Pantoea</i> (2.22%), <i>Enterobacter asburiae</i> (2.07%), <i>Enterobacter</i> <i>quasihormaechei</i> (1.61%), <i>Lactococcus lactis</i> (1.26%), <i>Enterobacter oligotrophica</i> (1.03%)
	arogenate dehydratase	4.2.1.91	<i>Burkholderia gladioli</i> (60.93%), <i>Pantoea</i> <i>dispersa</i> (30.17%), <i>Klebsiella pneumoniae</i> (7.12%), <i>Pantoea ananatis</i> (1.07%)	<i>Burkholderia gladioli</i> (52.11%), <i>Pantoea</i> <i>agglomerans</i> (24.16%), <i>Pantoea ananatis</i> (17.05%), <i>Burkholderia seminalis</i> (4.16%), <i>Klebsiella pneumoniae</i> (1.96%)
	prephenate dehydratase	4.2.1.51	<i>Burkholderia gladioli</i> (59.83%), <i>Pantoea_sp._GL120224-02</i> (13.26%), <i>Pantoea dispersa</i> (13.02%), <i>unclassified_f_Enterobacteriaceae</i> (3.10%), <i>Klebsiella pneumoniae</i> (3.07%), <i>Kosakonia</i> <i>cowanii</i> (1.68%), <i>Enterobacter cloacae</i> (1.09%)	<i>Saccharomyces cerevisiae</i> (39.04%), <i>Burkholderia gladioli</i> (13.42%), <i>unclassified_f_Enterobacteriaceae</i> (9.99%), <i>Enterobacter cloacae</i> (7.95%), <i>Monascus</i> <i>purpureus</i> (7.54%), <i>unclassified_g_Enterobacter</i> (4.72%), <i>Pantoea</i> <i>ananatis</i> (3.84%), <i>Pantoea deleyi</i> (2.60%), <i>Pantoea agglomerans</i> (2.53%), <i>Enterobacter</i> <i>quasihormaechei</i> (2.07%), <i>Lactococcus lactis</i> (1.68%), <i>unclassified_g_Burkholderia</i> (1.26%), <i>Bacillus amyloliquefaciens</i> (1.17%)

aspartate transaminase	2.6.1.1	<i>Burkholderia gladioli</i> (45.69%), <i>unclassified_g_Pantoea</i> (21.44%), <i>Type-C_symbiont_of_Plautia_stali</i> (16.00%), <i>Pantoea dispersa</i> (5.18%), <i>unclassified_g_Enterobacter</i> (3.55%), <i>unclassified_g_Kosakonia</i> (3.03%), <i>Saccharomyces cerevisiae</i> (1.19%), <i>Enterobacter cloacae</i> (1.05%)	<i>Saccharomyces cerevisiae</i> (28.08%), <i>Aspergillus luchuensis</i> (21.82%), <i>Aspergillus neoniger</i> (18.17%), <i>unclassified_g_Enterobacter</i> (7.57%), <i>unclassified_g_Kosakonia</i> (6.43%), <i>Monascus purpureus</i> (4.42%), <i>Burkholderia gladioli</i> (2.92%), <i>Bacillus amyloliquefaciens</i> (2.08%), <i>Aspergillus eucalypticola</i> (2.03%), <i>Shigella sonnei</i> (1.79%), <i>Enterobacter cloacae</i> (1.35%), <i>Enterobacter hormaechei</i> (1.31%)
histidinol-phosphate transaminase	2.6.1.9	<i>Burkholderia gladioli</i> (71.25%), <i>unclassified_g_Pantoea</i> (15.54%), <i>unclassified_f_Enterobacteriaceae</i> (2.76%), <i>Leuconostoc citreum</i> (2.47%), <i>Leuconostoc lactis</i> (2.32%), <i>Escherichia coli</i> (1.47%)	<i>Aspergillus phoenicis</i> (22.37%), <i>Leuconostoc lactis</i> (20.80%), <i>Saccharomyces cerevisiae</i> (18.94%), <i>Burkholderia gladioli</i> (10.53%), <i>Escherichia coli</i> (5.23%), <i>unclassified_g_Burkholderia</i> (4.26%), <i>Enterobacter cloacae</i> (2.74%), <i>Leuconostoc citreum</i> (2.45%), <i>Enterobacter bugandensis</i> (2.08%), <i>unclassified_g_Enterobacter</i> (1.68%), <i>unclassified_g_Pantoea</i> (1.47%), <i>Bacillus amyloliquefaciens</i> (1.29%), <i>Enterobacter asburiae</i> (1.19%), <i>Burkholderia_sp._Bp8992</i> (1.08%), <i>Pantoea deleyi</i> (1.06%), <i>Monascus purpureus</i> (1.00%)
phenylalanine (histidine) transaminase	2.6.1.58	<i>Saccharomyces cerevisiae</i> (98.57%), <i>[Candida] glabrata</i> (1.43%) <i>Saccharomyces cerevisiae</i> (83.33%), <i>Monascus purpureus</i> (16.67%)	<i>Saccharomyces cerevisiae</i> (99.92%)
aromatic-amino-acid transaminase	2.6.1.57	<i>Burkholderia gladioli</i> (36.12%), <i>unclassified_g_Burkholderia</i> (34.04%), <i>Pantoea_sp._Ap-959</i> (17.60%), <i>Klebsiella pneumoniae</i> (2.80%), <i>Klebsiella</i>	<i>Monascus purpureus</i> (33.55%), <i>Saccharomyces cerevisiae</i> (25.29%), <i>unclassified_g_Burkholderia</i> (12.94%), <i>Kosakonia cowanii</i> (4.98%),

			<i>quasipneumoniae</i> (2.36%), <i>unclassified_g_Enterobacter</i> (1.56%)	<i>unclassified_g_Enterobacter</i> (4.54%), <i>Enterobacteriaceae_bacterium_RIT693</i> (4.25%), <i>Enterobacter asburiae</i> (3.11%), <i>Pantoea ananatis</i> (2.32%), <i>Enterobacter cloacae</i> (2.13%), <i>Cedecea lapagei</i> (2.01%), <i>Pantoea_sp.</i> (1.66%)
	tyrosine transaminase	2.6.1.5	<i>Saccharomyces cerevisiae</i> (82.63%), <i>Monascus purpureus</i> (11.80%), <i>Aspergillus awamori</i> (4.75%)	<i>Monascus purpureus</i> (56.04%), <i>Saccharomyces cerevisiae</i> (42.25%), <i>Aspergillus niger</i> (1.09%)
Esters biosynthesis	carboxylesterase	3.1.1.1	<i>unclassified_g_Burkholderia</i> (51.96%), <i>Burkholderia gladioli</i> (47.98%)	<i>Aspergillus niger</i> (83.26%), <i>Burkholderia gladioli</i> (6.01%), <i>unclassified_g_Burkholderia</i> (5.54%), <i>unclassified_g_Bacillus_f_Bacillaceae</i> (2.68%), <i>Bacillus ginsengihumi</i> (1.63%)
	triacylglycerol lipase	3.1.1.3	<i>Burkholderia gladioli</i> (81.08%), <i>unclassified_o_Enterobacterales</i> (8.19%), <i>Saccharomyces cerevisiae</i> (5.70%), <i>Enterobacter cloacae</i> (3.40%), <i>Monascus purpureus</i> (1.49%)	<i>Saccharomyces cerevisiae</i> (61.93%), <i>Aspergillus niger</i> (16.09%), <i>Aspergillus phoenicis</i> (12.99%), <i>Enterobacter cloacae</i> (4.65%), <i>Monascus purpureus</i> (1.75%), <i>Burkholderia gladioli</i> (1.49%)
	alcohol O-acetyltransferase	2.3.1.84	<i>Saccharomyces cerevisiae</i> (100.00%)	<i>Saccharomyces cerevisiae</i> (100.00%)
	alcohol dehydrogenase	1.1.1.1	<i>Weissella cibaria</i> (27.61%), <i>Pediococcus pentosaceus</i> (23.09%), <i>Burkholderia gladioli</i> (17.60%), <i>Weissella_sp._DD23</i> (11.46%), <i>Achromobacter xylosoxidans</i> (5.84%), <i>unclassified_g_Pantoea</i> (4.29%), <i>Klebsiella pneumoniae</i> (1.91%), <i>Weissella confusa</i> (1.02%), <i>Leuconostoc citreum</i> (1.00%)	<i>Weissella cibaria</i> (39.44%), <i>Pediococcus pentosaceus</i> (23.71%), <i>Weissella_sp._DD23</i> (15.40%), <i>Saccharomyces cerevisiae</i> (6.64%), <i>Aspergillus niger</i> (4.29%), <i>unclassified_g_Leuconostoc</i> (1.35%), <i>Kosakonia cowanii</i> (1.11%), <i>Enterobacter asburiae</i> (1.09%)
2-Methoxy-4-vinylphenol biosynthesis	ferulic acid decarboxylase	4.1.1.102	<i>Saccharomyces cerevisiae</i> (54.00%), <i>Monascus purpureus</i> (46.00%)	<i>Monascus purpureus</i> (58.62%), <i>Saccharomyces cerevisiae</i> (41.28%)