

Table S1 Catabolic genes of aromatic compounds found in the draft genome of strain LLC-1.

ORF ^a	Gene	Length (bp) ^b	Function ^c	Affiliated catabolic pathway ^d
A0030_04025	<i>hmgR</i>	783	Transcriptional regulator, IclR family	PHE, TYR
A0030_04030	<i>hmgA</i>	1302	Homogentisate 1,2-dioxygenase (EC 1.13.11.5)	PHE, TYR
A0030_04035	<i>hmgB</i>	1293	Fumarylacetoacetase (EC 3.7.1.2)	PHE, TYR
A0030_04040	<i>hmgC</i>	633	Maleylacetoacetate isomerase (EC 5.2.1.2)	PHE, TYR
A0030_04880	<i>PcaR</i>	876	<i>Pca</i> regulon regulatory protein PcaR	4HBA,VA
A0030_04885	<i>pcaK</i>	1347	4-Hydroxybenzoate transporter	4HBA,VA
A0030_04890	<i>pcaF</i>	1203	β -ketoadipyl CoA thiolase (EC 2.3.1.-)	4HBA,VA
A0030_04895	<i>pcaT</i>	1290	Dicarboxylic acid transporter PcaT	4HBA,VA
A0030_04900	<i>pcaB</i>	1353	3-Carboxy-cis,cis-muconate cycloisomerase (EC 5.5.1.2)	4HBA,VA
A0030_04905	<i>pcaD</i>	792	β -ketoadipate enol-lactone hydrolase (EC 3.1.1.24)	4HBA,VA
A0030_04910	<i>pcaC</i>	393	4-Carboxymuconolactone decarboxylase (EC 4.1.1.44)	4HBA,VA
A0030_11560	<i>pcaJ</i>	642	3-Oxoadipate CoA-transferase subunit B (EC 2.8.3.6)	4HBA,VA
A0030_11565	<i>pcaI</i>	696	3-Oxoadipate CoA-transferase subunit A (EC 2.8.3.6)	4HBA,VA
A0030_12090	<i>hpaRI</i>	591	Transcriptional regulator, TetR family	4HPA
A0030_12095	<i>hpaB</i>	1170	<i>p</i> -Hydroxyphenylacetate hydroxylase C2:oxygenase component	4HPA
A0030_12100	<i>hpaC</i>	930	<i>p</i> -Hydroxyphenylacetate hydroxylase C1:reductase component	4HPA
A0030_12110	<i>hpaI</i>	804	2,4-Dihydroxyhept-2-ene-1,7-dioic acid aldolase (EC 4.1.2.n4)	4HPA
A0030_12115	<i>hpaH</i>	1308	4-Hydroxyphenylacetate symporter, major facilitator superfamily (MFS)	4HPA
A0030_12120	<i>hpaF</i>	405	5-Carboxymethyl-2-hydroxymuconate delta-isomerase (EC 5.3.3.10)	4HPA
A0030_12125	<i>hpaD</i>	924	3,4-Dihydroxyphenylacetate 2,3-dioxygenase (EC 1.13.11.15)	4HPA
A0030_12130	<i>hpaE</i>	1470	5-Carboxymethyl-2-hydroxymuconate semialdehyde dehydrogenase (EC 1.2.1.60)	4HPA
A0030_12135	<i>hpaG2</i>	765	5-Carboxymethyl-2-oxo-hex-3-ene-1,7-dioate decarboxylase (EC 4.1.1.68)/2-hydroxyhepta-2,4-diene-1,7-dioate isomerase (EC 5.3.3.-)	4HPA
A0030_12140	<i>hpaG1</i>	660	5-Carboxymethyl-2-oxo-hex-3-ene-1,7-dioate decarboxylase (EC 4.1.1.68)/2-hydroxyhepta-2,4-diene-1,7-dioate isomerase (EC 5.3.3.-)	4HPA
A0030_12145	<i>hpaR2</i>	906	Transcriptional activator of 4-hydroxyphenylacetate 3-monooxygenase operon, XylS/AraC family	4HPA

Table S1 *Cont.*

ORF ^a	Gene	Length (bp) ^b	Function ^c	Affiliated catabolic pathway ^d
A0O30_14370	<i>pcaG</i>	606	Protocatechuate 3,4-dioxygenase α chain (EC 1.13.11.3)	4HBA, VA
A0O30_14375	<i>pcaH</i>	720	Protocatechuate 3,4-dioxygenase β chain (EC 1.13.11.3)	4HBA, VA
A0O30_18255	<i>pobR</i>	879	Transcriptional regulator PobR, AraC family	4HBA
A0O30_18260	<i>pobA</i>	1188	4-Hydroxybenzoate 3-monooxygenase	4HBA
A0O30_19880	<i>antR</i>	972	Transcriptional regulator, AraC family	ANT
A0O30_19885	<i>antA</i>	1404	Anthranilate dioxygenase large subunit	ANT
A0O30_19890	<i>antB</i>	492	Anthranilate dioxygenase small subunit	ANT
A0O30_19895	<i>antC</i>	1032	Anthranilate dioxygenase reductase	ANT
A0O30_22000	<i>benR</i>	957	<i>BenABC</i> operon transcriptional activator BenR	BA, BFA
A0O30_22005		345	Hypothetical protein	
A0O30_22010	<i>benA</i>	1359	Benzoate 1,2-dioxygenase α subunit (EC 1.14.12.10)	BA, BFA
A0O30_22015	<i>benB</i>	486	Benzoate 1,2-dioxygenase β subunit (EC 1.14.12.10)	BA, BFA
A0O30_22020	<i>benC</i>	1011	Benzoate 1,2-dioxygenase, ferredoxin reductase component	BA, BFA
A0O30_22025	<i>benD</i>	762	1,2-Dihydroxycyclohexa-3,5-diene-1-carboxylate dehydrogenase (EC 1.3.1.25)	BA, BFA
A0O30_22030	<i>benK</i>	1329	Benzoate MFS transporter BenK	BA, BFA
A0O30_22035	<i>benL</i>	1200	Benzoate transport protein	BA, BFA
A0O30_22040	<i>benM</i>	1251	Benzoate-specific porin	BA, BFA
A0O30_22220	<i>paaN</i>	2055	Phenylacetic acid degradation protein PaaN, ring-opening aldehyde dehydrogenase (EC 1.2.1.3)	BA, BFA PAA
A0O30_22225	<i>paaM</i>	1233	Phenylacetic acid-specific porin PaaM	PAA
A0O30_22230		1563	Acetate permease ActP (cation/acetate symporter)	PAA
A0O30_22235	<i>paaL</i>	309	Putative membrane protein, clustering with ActP PaaL	PAA
A0O30_22240	<i>paaK</i>	1077	Phenylacetate-CoA oxygenase/reductase, PaaK subunit	PAA
A0O30_22245	<i>paaJ</i>	534	Phenylacetate-CoA oxygenase, PaaJ subunit	PAA
A0O30_22250	<i>paaI</i>	759	Phenylacetate-CoA oxygenase, PaaI subunit	PAA
A0O30_22255	<i>paaH</i>	282	Phenylacetate-CoA oxygenase, PaaH subunit	PAA
A0O30_22260	<i>paaG</i>	990	Phenylacetate-CoA oxygenase, PaaG subunit	PAA
A0O30_22265	<i>paaF</i>	1320	Phenylacetate-coenzyme A ligase (EC 6.2.1.30) PaaF	PAA
A0O30_22270	<i>paaE</i>	1221	Phenylacetic acid degradation protein PaaE, ketothiolase	PAA
A0O30_22275	<i>paaD</i>	441	Phenylacetic acid degradation protein PaaD, thioesterase	PAA
A0O30_22280	<i>paaC</i>	1518	3-Hydroxyacyl-CoA dehydrogenase PaaC (EC 1.1.1.-)	PAA

Table S1 *Cont.*

ORF ^a	Gene	Length (bp) ^b	Function ^c	Affiliated catabolic pathway ^d
A0O30_22285	<i>paaB</i>	792	Phenylacetate degradation enoyl-CoA hydratase PaaB (EC 4.2.1.17)	PAA
A0O30_22290	<i>paaA</i>	774	Phenylacetate degradation enoyl-CoA hydratase PaaA (EC 4.2.1.17)	PAA
A0O30_22295	<i>paaY</i>	600	Phenylacetic acid degradation protein PaaY	PAA
A0O30_22300	<i>paaX</i>	1005	Phenylacetic acid degradation operon negative regulatory protein PaaX	PAA
A0O30_24490	<i>vanK</i>	1332	Vanillate transporter VanK	VA
A0O30_24495	<i>bzfR</i>	897	LysR family transcriptional regulator	BFA
A0O30_24500	<i>bzfA</i>	1587	Benzoylformate carboxylase	BFA
A0O30_24505	<i>bzfB</i>	1341	BenK-like MFS transporter	BFA
A0O30_24510	<i>bzfC</i>	1476	Benzaldehyde dehydrogenase	BFA, VL
A0O30_24515	<i>bzfD</i>	1254	PhaK-like outer membrane porin	BFA
A0O30_24520	<i>vanR</i>	714	Transcriptional regulator	VA, VL
A0O30_24525	<i>vanA</i>	951	Vanillate O-demethylase oxidoreductase	VA, VL
A0O30_24535	<i>vanB</i>	1068	Vanillate O-demethylase oxygenase subunit	VA, VL
A0O30_24700	<i>catR</i>	873	Aromatic hydrocarbon utilization transcriptional regulator CatR (LysR family)	ANT, BA
A0O30_24705	<i>catC</i>	1122	Muconate cycloisomerase (EC 5.5.1.1)	ANT, BA
A0O30_24710	<i>catB</i>	291	Muconolactone isomerase (EC 5.3.3.4)	ANT, BA
A0O30_24715	<i>catA</i>	936	Catechol 1,2-dioxygenase (EC 1.13.11.1)	ANT, BA
A0O30_26225		1194	Putative <i>n</i> -hydroxybenzoate hydroxylase	4HBA
A0O30_26230	<i>hmgC</i>	642	Maleylacetoacetate isomerase (EC 5.2.1.2) @ Glutathione S-transferase, zeta (EC 2.5.1.18)	PHE, TYR
A0O30_26235		1353	4-Hydroxybenzoate transporter	4HBA
A0O30_26240	<i>hmgB</i>	699	Fumarylacetoacetase (EC 3.7.1.2)	PHE, TYR
A0O30_26245	<i>hmgA</i>	1056	Gentisate 1,2-dioxygenase (EC 1.13.11.4)	PHE, TYR
A0O30_26250	<i>hmgR</i>	944	Putative transcriptional regulator	PHE, TYR

^{a,b} Refers to GenBank/ENA/DDBJ Accession No. NZ_LUVY00000000; ^c annotated by RAST or NCBI-PAGP.

^d ANT, anthranilic acid catabolic pathway; BA, benzoic acid catabolic pathway; BFA, benzoylformic acid catabolic pathway; 4HBA, 4-hydroxybenzoic acid catabolic pathway; 4HPA, 4-hydroxyphenylacetic acid catabolic pathway; PHE, phenylalanine catabolic pathway; TYR, tyrosine catabolic pathway; VA, vanillic acid catabolic pathway; VL, vanillin catabolic pathway.

Table S2 List of data from GC/MS analysis

Peak	Retention time(min)	<i>m/z</i>	Products (trimethylsilylated)
1	6.2	77 105 135 179 194	Benzoic acid
2	8.4	73 105 135 178 207	Benzoylformic acid
3	5.3	65 135 165	Benzyl alcohol
4	6.2	77 105 135 179 194	Benzoic acid
5	9.7	59 73 179 209 253 268 298	Vanillyl alcohol
6	10.7	73 126 223 253 267 297 312	Vanillic acid
7	9.6	73 179 209 253 268 298	Isovanillyl alcohol
8	10.1	73 126 223 253 267 297 312	Isovanillic acid
9	10.8	59 78 209 239 298 313 328	Syringic alcohol
10	11.7	78 141 253 297 312 327 342	Syringic acid