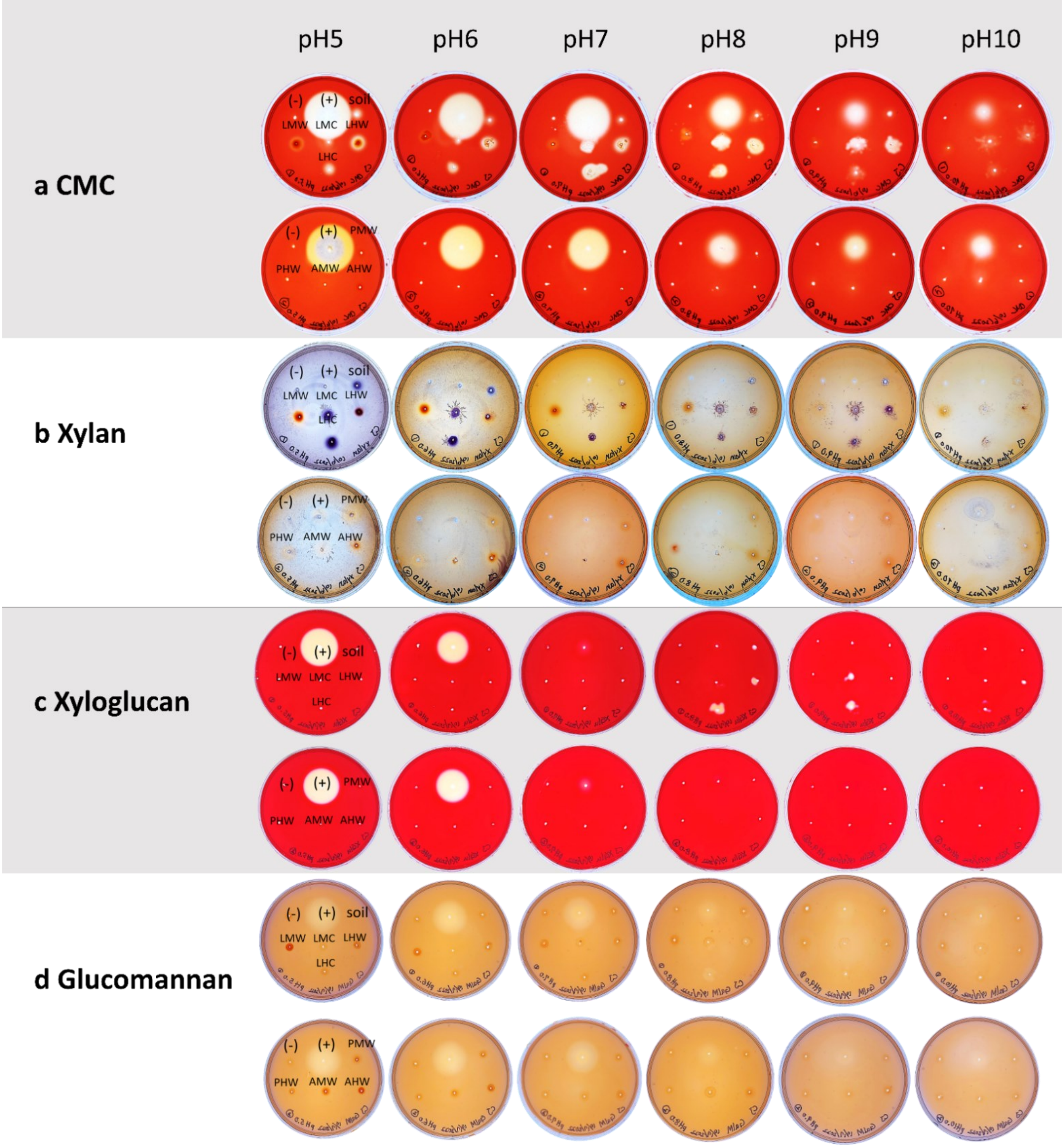
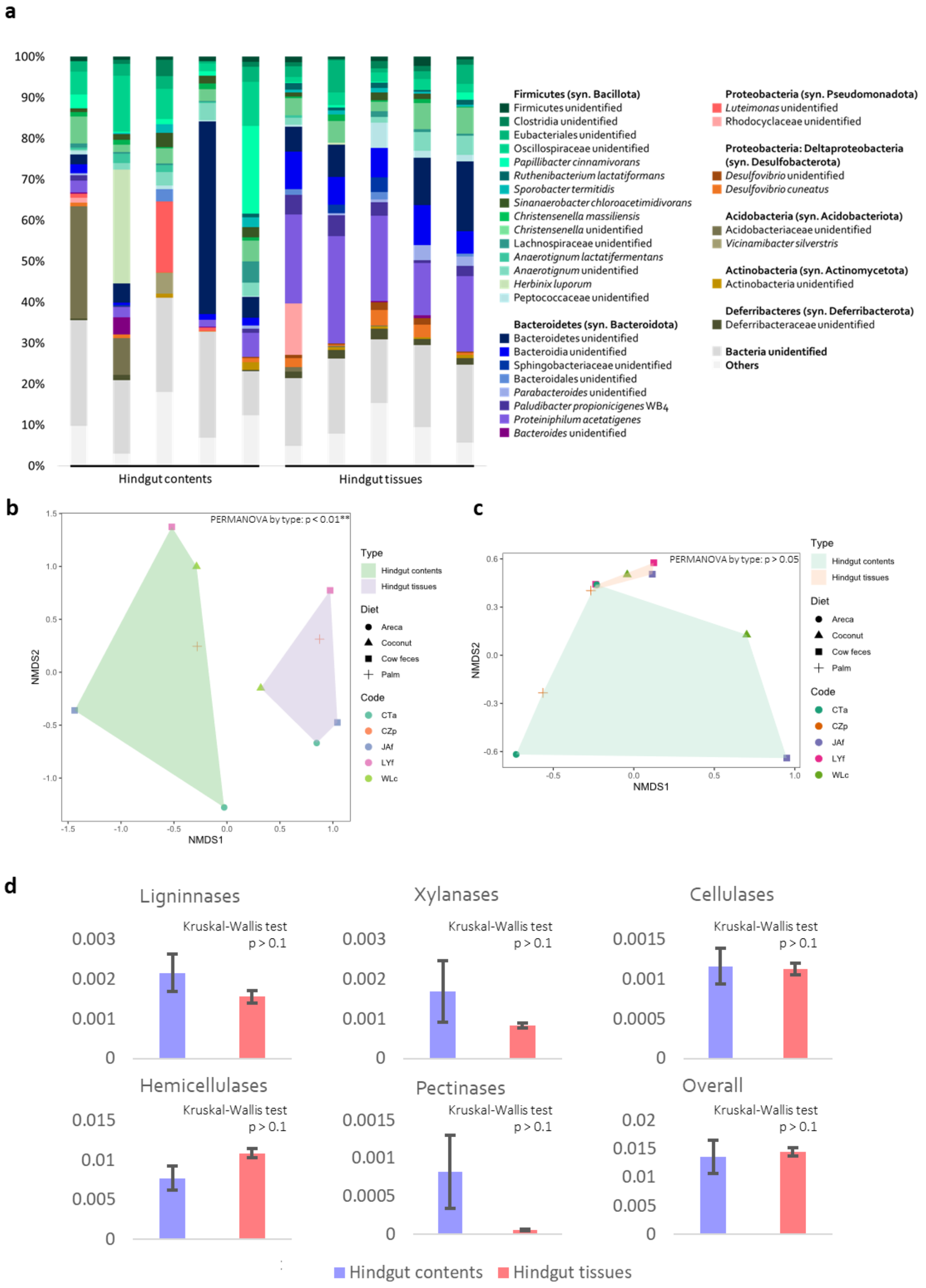
Supplementary Information



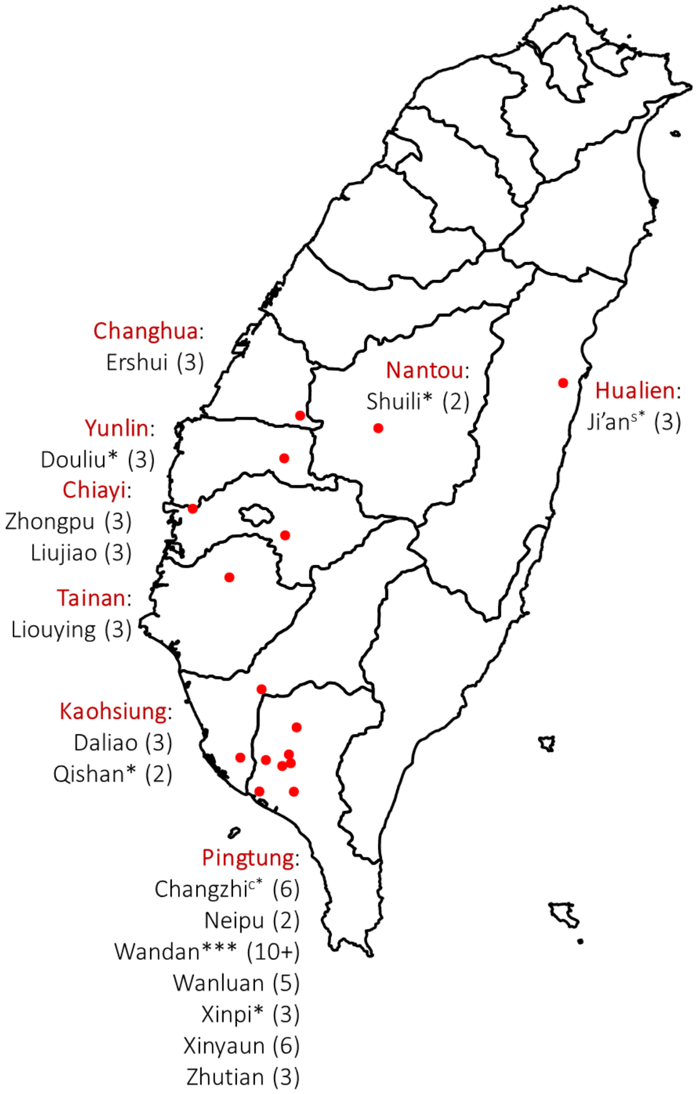
Supplementary Figure 1. Plate assays for testing the digestome activity of four substrates

If a clear halo surrounding the colony is formed, then digestive activity existed against that substrate. (-): buffer as negative control; (+): cellulase from *Aspergillus niger* as positive control; soil: the feeding substrate for the beetles; LMW: larval midgut wall; LMC: larval midgut contents; LHW: larval hindgut wall; LHC: larval hindgut contents; PMW: pupal midgut wall; PHW: pupal hindgut wall; AMW: adult midgut wall; AHW: adult hindgut wall.



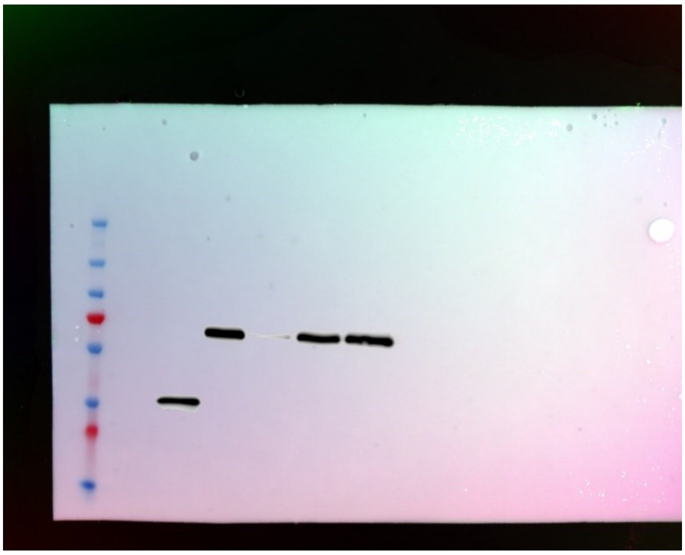
Supplementary Figure 2. The comparison of the microbiomes and functional profiles between 3rd instar larval hindgut contents and tissues.

(a) The relative abundance by taxonomic composition among hindgut contents and hindgut tissues from the late larval microbiomes. The details of samples used and the number of PacBio reads were displayed in Supplementary Table 2. (b) Non-metric multidimensional scaling (NMDS) plot of microbial structures between hindgut contents and tissues by Bray-Curtis distance (Stress = 0.065). A test of significance was conducted using PERMANOVA. Significant differences were found between hindgut contents and tissues ($p < 0.01$). (c) The NMDS plot of the predicted functional profile of the microbiome by Bray-Curtis distance (stress = 0.031). A test of significance was conducted using PERMANOVA. No significant differences were found between hindgut contents and tissues ($p > 0.05$). (d) The relative abundance of the five plant cell wall-degrading enzyme groups predicted according to the PICRUSt2 functional profile analysis. A test of significance was conducted using the Kruskal-Wallis test and pairwise Wilcox test by stadium. The Kruskal-Wallis test and Wilcox test of every group showed no significant differences between hindgut contents and tissues ($p > 0.1$). The error bar represents for the standard error (SE).

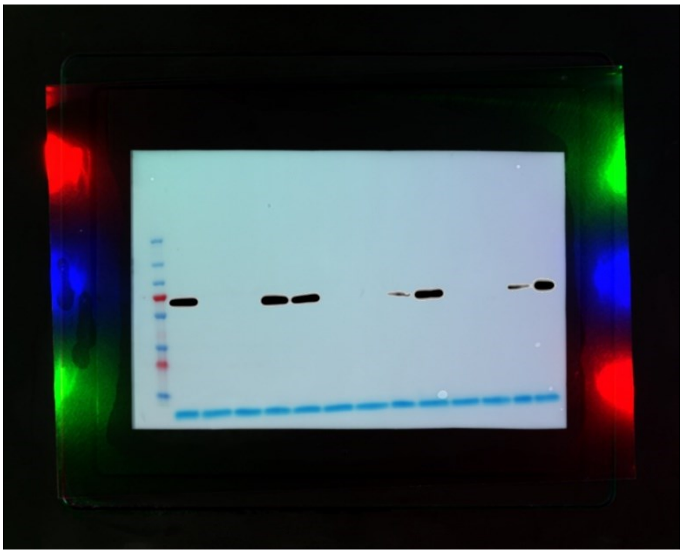


Supplementary Figure 3. CRB sample collection sites around Taiwan

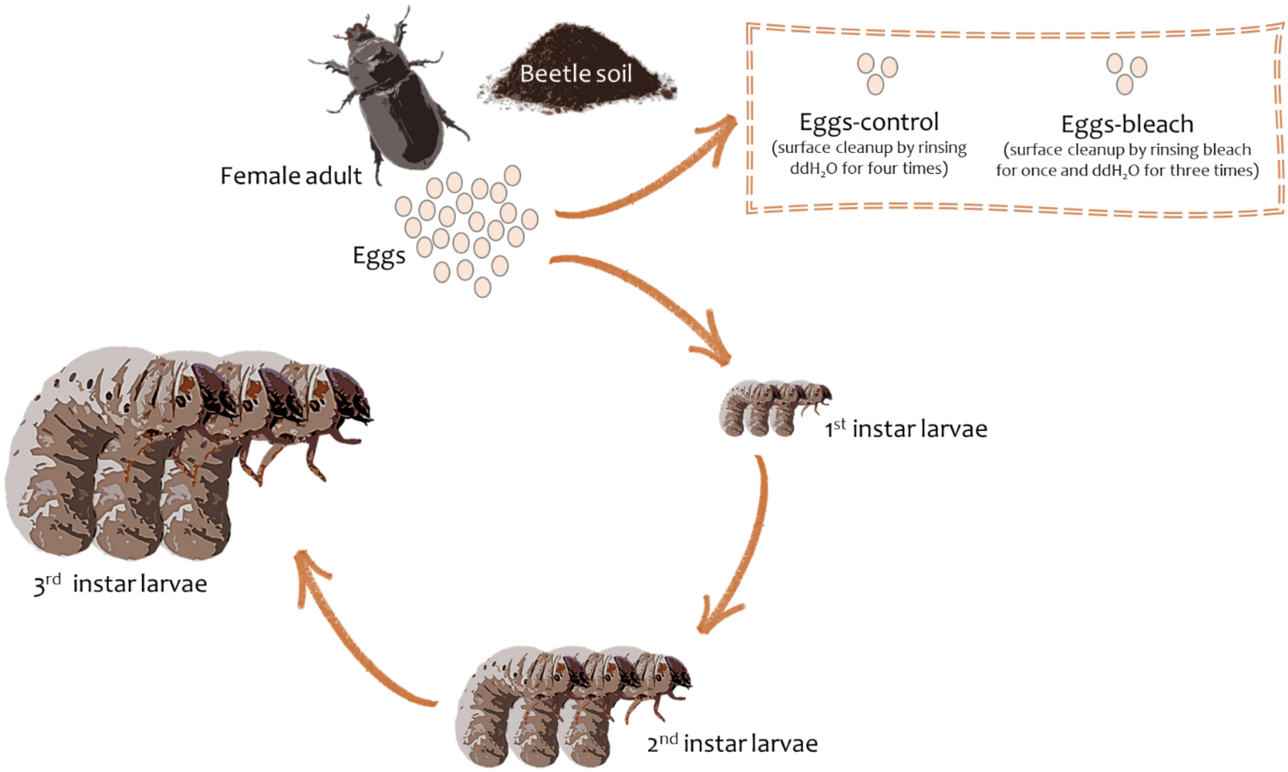
An asterisk in the top right of the code name indicates that these samples were only used for the culturing microbiome, double asterisks indicate that these samples were only used for the metagenomic microbiome, code names without asterisks are samples used for both metagenomic and culturing microbiome analyses, code names with triple asterisks indicates that these samples were reared in laboratory for the metagenomic microbiome of different developmental stages. For the Changzhi samples, only those from coconut were labeled with an asterisk. Similarly, for the Ji’an samples, only those from soil diets were labeled with an asterisk.



Supplementary Figure 4. The raw and unprocessed Western Blot of the cellulase from CRB expressed by *Sf9* cells as depicted in Figure 2 in the main article.



Supplementary Figure 5. The raw and unprocessed Western Blot of the enzyme after pull-down assays for thin layer chromatography (TLC) assays as depicted in Figure 3 in the main article.



Supplementary Figure 6. The experimental setup of how we sampled CRB in different developmental stages.

Female adults with fertile eggs were used for the experiment. For the adult, the midgut and hindgut were used for the microbiome analysis. To distinguish the possible route for vertical transmission of symbionts either on the surface of the egg shell or inside the egg (embryotic transmission), eggs from the same mother were first divided into two groups, one treated with ddH$_2$O as control group, while another was treated by 1% bleach for one minute, after rinsing using ddH$_2$O for one minute three times. The whole eggs were smashed to study the microbiome. For the first instar larvae, since the size of the hindgut was small, the whole intestinal tract was used for microbiome analysis; while for the second and third instar larvae, only the hindgut was used. Three individuals were used for each group or instar of larvae, with three biological replicates.

Supplementary Table 1. The PCWDE activity assays by isolated microbes

Isolates	Species	CMC	Xylanase	Pectinase
CTa1L2H2	*Leminorella grimontii*	-	+	-
CTa1L2M1	*Paraburkholderia caballeronis*	-	+	-
CZp1L1H1	*Klebsiella aerogenes*	+/-	+	-
CZp1L2M1	*Bacillus* sp.	+	+	-
CZp1L3M1	*Bacillus* sp.	+	-	-
DLs1L1M1	*Bacillus* sp.	+	+/-	-
LJf1L1M1	*Bacillus* sp. *Geobacillus stearothermophilus*	+	-	-
LJf1L1M2	*Acinetobacter baumannii*	+	+	-
LJf1L3M1	*Leminorella grimontii*	+	-	-
SLa1LM4	*Staphylococcus aureus*	-	+	-
SLa1LH2	*Bacillus* sp.	+	+	-
SLa1LH5	*Thauera* sp.	+	-	-
WLc1L3H1	*Bacillus* sp.	+	-	-
XPs1L3M2	*Serratia marcescens*	+	-	-
XYa1L3H2	*Edaphobacter* sp.	-	+	-
XYa1L5M2	*Priestia megaterium* *Bacillus* sp. *Priestia aryabhattai*	-	+	-
ZPa1L3H1	*Bacillus* sp.	+	+	-
ESs1L3H1	*Bacillus* sp.	+	-	-
ESs1L1H1	*Bacillus* sp.	+	-	-
ESs1L3H3	*Lysinibacillus macrolides* *Lysinibacillus xylanilyticus* *Bacillus* sp. *Lysinibacillus pakistanensis*	+/-	-	-
LYf1L3H1P	*Candida saraburiensis*	+	-	+
JAf1L3H1	*Bacillus* sp.	+	-	-
JAf1L2H3	*Serratia marcescens*	-	-	+
JAf1L2H1	*Bacillus* sp.	+	-	-
JAf1L3M1P2	*Pascua guehoae*	+	+	+
DOs1L1H1P	*Candida xylanilytica*	-	+	-

DOs1L1M1	*Paracoccus* sp.	-	+	-
DOs1L1M3	*Bacillus humi*	-	-	+
JAs1L1H2	*Bacillus* sp.	+	-	-
JAs1L1H1P	*Trichosporon siamense*	-	+	-
JAs1L2M2	*Lysinibacillus* sp.	+	-	-
JAs1L2M2P	*Trichosporon siamense*	-	+	+
JAs1L2M3P	*Candida tropicalis*	-	+	-
JAs1L2H1A	*Candida saraburiensis*	+	-	-

Supplementary Table 2. Details of samples and the number of reads for 16S rRNA gene metabarcoding sequencing.

Sample group	Code	Stage	Tissue types / treatment	Number of original reads			Number of filtered reads		
				replicate 1	replicate 2	replicate 3	replicate 1	replicate 2	replicate 3
Microbial profiling around Taiwan	ESs	3rd instar larvae	Hindgut contents	14724	14453	14704	1946	1940	1706
	ZPa			13329	14995	16697	2953	3166	4162
	LJf			13562	13220	14675	2681	2357	2728
	LYf			15061	14439	14406	2671	3606	4028
	DLs			12593	12935	14350	2969	4002	3110
	NPc			15634	14815	-	3515	3788	-
	WLa			14254	15425	-	3184	3681	-
	WLc			13399	14038	15732	1789	2195	2380
	XYa			13361	13225	15179	3697	4095	4393
	XYc			14508	14828	13003	3781	2081	1716
	CTa			13271	14857	14016	4295	5832	4430
	CZp			14114	12831	13921	5449	4123	1684
	CZc			17458	18284	18210	2624	3527	3071
	JAf			17614	18022	16892	3859	4657	3778
Microbiome comparison between hindgut contents and tissues	LYf	3rd instar larvae	Hindgut contents	14439	-	-	3089	-	-
	WLc			15732	-	-	2277	-	-
	CTa			13271	-	-	3744	-	-
	CZp			13921	-	-	1765	-	-
	JAf			16892	-	-	3547	-	-
	LYf		Hindgut tissues	10655	-	-	2159	-	-
	WLc			19738	-	-	3856	-	-
	CTa			10920	-	-	2642	-	-
	CZp			10074	-	-	2706	-	-
	JAf			12390	-	-	2532	-	-
Stages of development	WDc	Female adults	Midgut tissues	35014	24597	18776	24628	9888	10947
			Hindgut tissues	43773	24888	18422	13666	10254	6074
		eggs	Bleach treated	28338	20487	17790	20506	12755	2534
			ddH_2O treated	25018	25748	18681	14406	7415	3836
		1st instar larvae	Whole gut tissues	19591	20698	17383	4268	1989	2164
		2nd instar larvae	Hindgut tissues	25936	38736	22141	9876	20605	11514
		3rd instar larvae		20347	29297	22716	5478	13793	12652
	soil	soil	Environment control	14025	-	-	847	-	-

Abbreviations of code number as defined in the Supplementary Table 3.

Supplementary Table 3. CRB sample collection details for downstream experiments.

Administrative divisions	Locations	Habitat (host plant)	Stadium	Number of individuals	Code
Nantou	Shuili (SL)	*Areca catechu* (betel palm)	2nd instar	2 (pooled)	SLa*
Changhua	Ershui (ES)	*Areca catechu*	3rd instar	3	ESs
Yunlin	Douliu (DO)	Beetle soil (lab reared)	3rd instar	3	DOs*
Chiayi	Zhongpu (ZP)	*Areca catechu*	3rd instar	3	ZPa
Chiayi	Liujiao (LJ)	Cow feces	3rd instar	3	LJf
Tainan	Liuying (LY)	Soil + cow feces	3rd instar	3	LYf
Kaohsiung	Daliao (DL)	*Cocos nucifera* (coconut)	3rd instar	3	DLs
Kaohsiung	Qishan (QS)	*Cocos nucifera*	2nd instar	2	QSc*
Pingtung	Neipu (NP)	*Cocos nucifera*	3rd instar	3	NPc
Pingtung	Wandan (WD)	*Cocos nucifera*	Adults, eggs, and larvae	48	WDc***
Pingtung	Wanluan (WL)	*Areca catechu*	3rd instar	2	WLa
Pingtung	Wanluan (WL)	*Cocos nucifera*	3rd instar	3	WLc
Pingtung	Xinyuan (XY)	*Areca catechu*	3rd instar	3	XYa
Pingtung	Xinyuan (XY)	*Cocos nucifera*	3rd instar	3	XYc
Pingtung	Zhutian (CT)	*Areca catechu*	3rd instar	3	CTa
Pingtung	Changzhi (CZ)	*Phoenix loureiroi* (palm)	3rd instar	3	CZp
Pingtung	Changzhi (CZ)	*Cocos nucifera*	3rd instar	3	CZc**
Pingtung	Xinpi (XP)	Straw + beetle soil	2nd instar	3	XPs*
Hualien	Ji'an (JA)	Beetle soil (lab reared)	3rd instar	3	JAs*
Hualien	Ji'an (JA)	Soil + cow feces	3rd instar	3	JAf

An asterisk in the top right of the code name indicates that these samples were only used for the culturing microbiome, double asterisks indicates that these samples were only used for the 16S rRNA metabarcoding microbiome, code names without asterisks are samples used for both 16S rRNA metabarcoding and culturing microbiome analyses, code names with triple asterisks indicates that these samples were reared in lab for the 16S rRNA metabarcoding microbiome of different developmental stages.

Supplementary Table 4. Recipe of buffer used in plate assays for substrate activities

pH	0.1M Citric acid	0.2M Na_2HPO_4	0.1M Tris-HCl
5	4.85 mL	5.15 mL	0
6	3.685 mL	6.315 mL	0
7	1.765 mL	8.235 mL	0
8	0	0	10 mL (pH 8)
9	0	0	10 mL (pH 9)
10	0	0	10 mL (pH 10)

Supplementary Table 5. The recipe for thin layer chromatography assays

Plate 1: using Glu1-6, Xyl1-6 and Man1 as standards			Enzyme	substrate	CPB pH5.0	Merck water	Total volume
A	1	Carboxymethyl cellulose 4M (CMC4M)	14	4	2	0	20
	2	Regenerated amorphous cellulose (RAC)	14	4	2	0	20
	3	Cellohexaose (Glu6, 2.5 µg/µL)	14	4	2	0	20
	4	Cellopentaose (Glu5, 10 µg/µL)	14	1	2	3	20
	5	Cellotatraose (Glu4, 10 µg/µL)	14	1	2	3	20
	6	Cellotriose (Glu3, 10 µg/µL)	14	1	2	3	20
	7	Cellobiose (Glu2, 10 µg/µL)	14	1	2	3	20
	8	Xyloglucan (XGlu)	14	4	2	0	20
B	1	Glucomannan (GluM)	14	4	2	0	20
	2	Enzyme control	14	0	2	4	20
Plate 2: using Xyl1-6 and Man1-6, and Gal1 as standards			Enzyme	substrate	CPB pH5.0	Merck water	Total volume
C	1	Xylan beechwood (Xbee)	14	4	2	0	20
	2	Xylose hexamer (Xyl6)	14	1	2	3	20
	3	Xylose pentamer (Xyl5)	14	1	2	3	20
	4	Xylose tetramer (Xyl4)	14	1	2	3	20
	5	Xylose trimer (Xyl3)	14	1	2	3	20
	6	Xylose dimer (Xyl2)	14	1	2	3	20
	7	Galactomannan (GalM)	14	4	2	0	20
	8	Mannose hexamer (Man6)	14	1	2	3	20
D	1	Mannose pentamer (Man5)	14	1	2	3	20
	2	Mannose tetramer (Man4)	14	1	2	3	20
	3	Mannose trimer (Man3)	14	1	2	3	20
	4	Mannose dimer (Man2)	14	1	2	3	20
	5	Enzyme control	14	0	2	4	20

For negative controls (plates 3 and 4), the above plates were made using water instead of substrate.

Supplementary Table 6. Identified cultivable microbes from midgut and hindgut contents.

Isolates	Gene	Query length (bp)	Similarity	Bit-Score	BLAST Accession	Best match
CTa1L1H1	16S *rRNA*	1422	100	2627.06	JQ579628	*Bacillus thuringiensis*
CTa1L1M1	16S *rRNA*	1419	99.9	2617.82	KY653110	*Lysinibacillus fusiformis*
CTa1L2H2	16S *rRNA*	1412	99.6	2575.35	LC462165	*Leminorella grimontii*
CTa1L2M1	*rpoB*	797	95.6	1282.82	LT708255	*Paraburkholderia caballeronis*
CTa1L2M2	16S *rRNA*	1403	100	2591.97	MZ676064	*Bacillus albus*
CTa1L2M3	16S *rRNA*	1086	99.5	1982.58	MW802176	*Lysinibacillus fusiformis*
CTa1L3M1	16S *rRNA*	1406	92.4	2191.25	EU372963	*Bacillus* sp.
CZp1L1H1	16S *rRNA*	1390	99.5	2540.26	MT271951	*Klebsiella aerogenes*
CZp1L1H1	*rpoB*	1445	99.6	2638.14	CP024880	*Klebsiella aerogenes*
CZp1L2M1	16S *rRNA*	1332	99.2	2420.23	MZ676064	*Bacillus albus*
					MZ497322	*Bacillus cereus*
					MN746216	*Bacillus anthracis*
CZp1L2M2	16S *rRNA*	825	99.9	1519.07	OK083719	*Bacillus cereus*
					OK073274	*Bacillus paramycoides*
					OK056287	*Bacillus thuringiensis*
CZp1L2H3	16S *rRNA*	1456	99.5	2643.68	CP077291	*Citrobacter farmeri*
CZp1L3H1	16S *rRNA*	1094	99.5	1999.2	MZ914647	*Lysinibacillus fusiformis*
					KY407914	*Lysinibacillus sphaericus*
CZp1L3M1	16S *rRNA*	1151	99.7	2113.69	MZ934752	*Bacillus cereus*
					MW857094	*Bacillus pacificus*
					MW850424	*Bacillus nitratireducens*
CZp1L3H3	16S *rRNA*	1090	99.8	2001.04	GU125641	*Lysinibacillus fusiformis*
CZp1L4H2	*rpoB*	1447	99.5	2632.6	CP077291	*Citrobacter farmeri*
DLs1L1M1	16S *rRNA*	1419	99.9	2617.82	MZ497322	*Bacillus cereus*
					MZ310685	*Bacillus albus*
					MW931846	*Bacillus tropicus*
					MW380582	*Bacillus thringeniensis*
DLs1L1M2	16S *rRNA*	1405	99.8	2580.89	MG049778	*Lysinibacillus* sp.
DLs1L1M3	16S *rRNA*	1060	99.9	1951.18	MT355730	*Bacillus* sp.
DLs1L1H2	16S *rRNA*	1396	99.8	2558.73	KX357798	*Citrobacter koseri*
DLs1L2M1	16S *rRNA*	1419	99.9	2617.82	MZ497322	*Bacillus cereus*
					MZ310685	*Bacillus albus*
					MW931846	*Bacillus tropicus*
					MW380582	*Bacillus thuringiensis*

DLs1L2H1	16S *rRNA*	1406	99.7	2577.2	NR_112628	*Lysinibacillus fusiformis*
DLs1L2H2	16S *rRNA*	1405	99.4	2551.34	NR_112628	*Lysinibacillus fusiformis*
DLs1L2H3	16S *rRNA*	1367	98.5	2407.3	MF521962	*Lysinibacillus fusiformis*
DLs1L3M1	16S *rRNA*	1042	98.8	1862.54	MH532492	*Citrobacter koseri*
DLs1L3H2	16S *rRNA*	1409	99.8	2584.58	KY561619	*Bacillus* sp.
DLs1L3H3	16S *rRNA*	1027	99.6	1882.86	AB934966	*Bacillus aryabhattai*
LJf1L1M1	*rpoB*	1479	99.7	2710.16	CP038262	*Acinetobacter baumannii*
LJf1L1M1	16S *rRNA*	1411	99.9	2603.05	MT673788	*Bacillus subtilis*
					MK713704	*Bacillus tequilensis*
					MG651202	*Bacillus halotolerans*
					KT986166	*Bacillus amyloliquefaciens*
					KT986156	*Bacillus axarquiensis*
					KT986983	*Geobacillus stearothermophilus*
LJf1L1M2	*rpoB*	1481	99.7	2713.85	CP038262	*Acinetobacter baumannii*
LJf1L2H1	16S *rRNA*	694	99.1	1243.92	LC183868	*Lysinibacillus macroides*
LJf1L2H2	16S *rRNA*	1406	99.8	2580.89	MZ734317	*Bacillus safensis*
					MZ489518	*Bacillus australimaris*
					MZ328872	*Bacillus stratosphericus*
					MN750426	*Bacillus pumilus*
LJf1L3M1	16S *rRNA*	1413	99.7	2588.28	NR_025333	*Leminorella grimontii*
LJf1P1H2	16S *rRNA*	1437	90.7	1912.4	CP072199	*Serratia marcescens*
LJf1P3H1	16S *rRNA*	1436	99.4	2603	CP066089	*Citrobacter koseri*
QSc1L2H1P	ITS rDNA	476	95.6	776.713	MN904886	*Candida xylanilytica*
SLa1LH1	16S *rRNA*	1398	99.9	2579.04	KF484685	*Brevibacillus laterosporus*
SLa1LM2	16S *rRNA*	1397	99.9	2577.2	MZ923706	*Bacillus cereus*
SLa1LM3	16S *rRNA*	1351	97.9	2335.29	KC954751	*Telmatobacter* sp.
SLa1LM4	16S *rRNA*	1353	99.9	2492.25	MZ931308	*Staphylococcus aureus*
SLa1LM5	16S *rRNA*	1363	97.6	2338.98	KC954751	*Telmatobacter* sp.
SLa1LM7	16S *rRNA*	1417	99.4	2579.04	MG266284	*Bacillus* sp.
SLa1LM8	16S *rRNA*	1351	98.4	2375.91	MH686091	*Mesorhizobium* sp.
SLa1LM9	16S *rRNA*	1362	97.9	2351.91	KC954751	*Telmatobacter* sp.
SLa1LH2	16S *rRNA*	1418	100	2619.67	MW559318	*Bacillus cereus*
					MW405816	*Bacillus mobilis*
					MW205819	*Bacillus thuringiensis*
					KU898281	*Bacillus toyonensis*
					KU877666	*Bacillus oryzaecorticis*
SLa1LH5	16S *rRNA*	1399	99.8	2567.96	JQ724338	*Thauera* sp.

WLa1L1M2	16S *rRNA*	1019	99.1	1847.77	MZ312268	*Paracoccus* sp.
WLa1L1H2	16S *rRNA*	895	92.8	1297.47	KR706347	*Psedomonas flexibilis*
WLa1L2M3	*rpoB*	1503	90	1940.1	CP033934	*Chryseobacterium balustinum*
WLa1L2M3	16S *rRNA*	1505	86.8	1762.82	CP033934	*Chryseobacterium balustinum*
WLc1L3H1	16S *rRNA*	1400	99.2	2540.26	MN421133	*Bacillus xiamensis*
					MH396728	*Bacillus safensis*
					KT005170	*Bacillus altitudinis*
WLc1L2H1P	ITS rDNA	524	99.8	961.378	AB164370	*Trichosporon siamense*
XPs1L1M1	16S *rRNA*	1445	96.7	2409.15	CP066089	*Citrobacter koseri*
XPs1L1M2-2	16S *rRNA*	1447	93	2115.53	LS483470	*Leminorella richardii*
XPs1L1M3	16S *rRNA*	598	98.2	1051.86	KP997262	*Bacillus thuringiensis*
					FJ188319	*Bacillus cereus*
XPs1L3M2	16S *rRNA*	1417	98.6	2543.96	CP063354	*Serratia marcescens*
XYa1L1H3	16S *rRNA*	1353	99.4	2470.09	MZ947169	*Priestia megaterium*
					MZ923713	*Priestia aryabhattai*
					MZ923703	*Bacillus zanthoxyli*
XYa1L1M1	16S *rRNA*	1382	99.7	2534.72	MH532492	*Citrobacter koseri*
XYa1L3H2	16S *rRNA*	1111	95.2	1729.58	KY434003	*Edaphobacter* sp.
XYa1L3M1	16S *rRNA*	1086	99.8	1993.66	MZ569686	*Lysinibacillus macroides*
					MH385002	*Lysinibacillus sphaericus*
					MG991566	*Lysinibacillus boronitolerans*
					MF967404	*Lysinibacillus fusiformis*
XYa1L3M2	16S *rRNA*	1138	99.8	2091.53	MW830387	*Bacillus cereus*
					MW380523	*Bacillus subtilis*
					MW065486	*Bacillus paramycoides*
					MN882644	*Bacillus albus*
XYa1L5M2	16S *rRNA*	1350	99.8	2483.02	MZ712064	*Priestia aryabhattai*
					MZ569841	*Priestia megaterium*
					MZ496951	*Bacillus* sp.
XYa1L5H2	16S *rRNA*	1420	99.9	2619.67	MZ675431	*Bacillus cereus*
XYa1L5H3	16S *rRNA*	1363	97.3	2320.51	KY434001	*Edaphobacter* sp.
XYa1L5M3	16S *rRNA*	1403	100	2591.97	MZ676063	*Bacillus albus*
					MZ497322	*Bacillus cereus*
					MW931846	*Bacillus tropicus*
XYa1L6H2	16S *rRNA*	1403	99.8	2577.2	MZ722994	*Priestia megaterium*
					MZ026430	*Bacillus* sp.
					MW803060	*Priestia aryabhattai*

XYc1L1H1	16S *rRNA*	1403	99.8	2577.2	KX344022	*Bacillus altitudinis*
					KT986116	*Bacillus pumilus*
					KT380676	*Bacillus safensis*
XYc1L1H1P	ITS rDNA	516	98.3	909.672	MN904886	*Candida xylanilytica*
XYc1L1H2	16S *rRNA*	1238	99.5	2265	MZ723093	*Bacillus aerius*
					MZ713012	*Bacillus altitudinis*
					MZ675499	*Bacillus aerophilus*
XYc1L2M1	16S *rRNA*	1283	99.2	2327.9	KY652111	*Bacillus* sp.
XYc1L2M2	16S *rRNA*	1403	99.9	2588.28	MZ676063	*Bacillus albus*
					MZ497322	*Bacillus cereus*
					MW931846	*Bacillus tropicus*
XYc1L2M3	16S *rRNA*	1118	97.1	1941.95	MZ914647	*Lysinibacillus fusiformis*
XYc1L3H1P	ITS rDNA	516	98.1	905.979	MN904886	*Candida xylanilytica*
XYc1L4H1	16S *rRNA*	1372	99.9	2521.8	MN700259	*Bacillus* sp.
XYc1L4H1P	ITS rDNA	542	100	1002	MZ363142	*Candida tropicalis*
ZPa1L1H1	16S *rRNA*	1392	99.7	2551.34	KM016946	*Citrobacter koseri*
ZPa1L1H2	16S *rRNA*	1461	97.4	2486.71	CP034752	*Jinshanibacter zhutongyuii*
ZPa1L1H3	16S *rRNA*	1002	98.4	1753.59	MN057723	*Pragia* sp.
ZPa1L2M2	16S *rRNA*	921	98.4	1616.94	GQ423394	*Bacillus* sp.
ZPa1L2M3	16S *rRNA*	1416	99.1	2542.11	MN057723	*Pragia* sp.
ZPa1L2H1	16S *rRNA*	1393	98.1	2438.7	MN057723	*Pragia* sp.
ZPa1L2H2	16S *rRNA*	1410	99.1	2529.18	MN057723	*Pragia* sp.
ZPa1L2H3	16S *rRNA*	1396	98.1	2460.86	MN057723	*Pragia* sp.
ZPa1L3H1	16S *rRNA*	1406	99.7	2577.2	MW786727	*Bacillus toyonensis*
					MW559318	*Bacillus cereus*
					MW405816	*Bacillus mobilis*
					MW287205	*Bacillus thuringiensis*
ZPa1L3M1	16S *rRNA*	574	99.8	1053.71	MW175549	*Citrobacter koseri*
ZPa1L4H2	16S *rRNA*	1141	95.1	1751.74	FJ463782	*Citrobacter* sp.
ZPa1L4M1	16S *rRNA*	1384	99.6	2525.49	MT367744	*Citrobacter koseri*
					MN749522	*Citrobacter freundii*
ESs1L3H1P	ITS rDNA	532	99.8	979.845	FJ662410	*Candida tropicalis*
ESs1L3H1	16S *rRNA*	928	100	1714.81	MN073814	*Bacillus* sp.
ESs1L3H2	16S *rRNA*	1086	99.9	1999.2	MN428188	*Lysinibacillus macrolides*
					MK318259	*Lysinibacillus xylanilyticus*
					MF948384	*Bacillus* sp.
ESs1L1H1	16S *rRNA*	1063	100	1964.11	JQ661039	*Bacillus* sp.

ESs1L3H3	16S *rRNA*	1065	99.7	1947.49	MN428188	*Lysinibacillus macrolides*
					MK318259	*Lysinibacillus xylanilyticus*
					MF948384	*Bacillus* sp.
					KU983851	*Lysinibacillus pakistanensis*
NPc3L2	16S *rRNA*	975	99.8	1792.37	MN416232	*Bacillus toyonensis*
					KP813752	*Bacillus thuringiensis*
					KJ685393	*Bacillus cereus*
NPc3L1	16S *rRNA*	1408	99.6	2564.27	CP066089	*Citrobacter koseri*
LYf1L1M1	*rpoB*	1430	99.4	2604.9	CP081016	*Pseudomonas* sp.
LYf1L1M1	16S *rRNA*	825	99.3	1485.83	MH091341	*Pseudomonas mosselii*
LYf1L2M1	16S *rRNA*	942	99.9	1735.12	LR215149	*Bacillus cereus*
LYf1L3H1P	ITS rDNA	531	100	981.691	NR_151809	*Candida saraburiensis*
LYf1L3M2P	ITS rDNA	531	100	981.691	NR_151809	*Candida saraburiensis*
JAf1L3H1	16S *rRNA*	1085	99.6	1986.27	MW926960	*Bacillus tequilensis*
					MW888885	*Bacillus subtilis*
					MW776608	*Bacillus velezensis*
JAf1L2H2	16S *rRNA*	1383	99.1	2507.02	CP071070	*Citrobacter sedlakii*
JAf1L2H3	16S *rRNA*	1407	99.4	2547.65	MW365215	*Serratia marcescens*
JAf1L2H1	16S *rRNA*	1136	99.6	2084.14	MZ540090	*Bacillus proteolyticus*
					MZ485376	*Bacillus cereus*
					MZ443981	*Bacillus toyonensis*
					MZ411685	*Bacillus thuringiensis*
					MZ310685	*Bacillus albus*
JAf1L3M1P1	ITS rDNA	653	99.7	1195.9	MN268781	*Debaryomyces* sp.
JAf1L2M1P	ITS rDNA	656	99.7	1201.44	MN268781	*Debaryomyces* sp.
DOs1L1H2	16S *rRNA*	1055	99.8	1941.95	MW979588	*Fictibacillus phosphorivorans*
					MW363312	*Fictibacillus barbaricus*
					MT829784	*Bacillus* sp.
					MT704540	*Fictibacillus arsenicus*
					MG651557	*Fictibacillus halophilus*
					MG651493	*Fictibacillus nanhaiensis*
DOs1L1H1P	ITS rDNA	522	98.1	917.059	MN904886	*Candida xylanilytica*
DOs1L1H2P	ITS rDNA	548	95.9	909.672	MK394120	*Candida sojae*
DOs1L1M1	16S *rRNA*	1082	97.3	1820.07	MZ312268	*Paracoccus* sp.
DOs1L1M1A	16S *rRNA*	1074	99.8	1973.34	KY816740	*Brevibacillus parabrevis*
DOs1L1M2A	16S *rRNA*	1063	99.8	1951.18	KR077844	*Bacillus* sp.
DOs1L1M1P	ITS rDNA	522	98.1	918.905	MN904886	*Candida xylanilytica*

DOs1L1M3	16S *rRNA*	1084	98.6	1938.26	KC178941	*Bacillus humi*
DOs1L1M4	16S *rRNA*	1230	99.2	2230.03	MZ468617	*Brucella intermedia*
JAs1L1H2	16S *rRNA*	1068	99.9	1965.96	MZ712998	*Bacillus cereus*
					MZ675479	*Bacillus wiedmannii*
					MZ569844	*Bacillus mobilis*
					MZ234580	*Bacillus thuringiensis*
					MW786728	*Bacillus toyonensis*
JAs1L1H3	16S *rRNA*	1017	97.8	1770.21	MN410691	*Chryseobacterium* sp.
JAs1L1H4	16S *rRNA*	1061	99.5	1941.95	MK880382	*Pseudomonas guariconensis*
					KC634234	*Pseudomonas plecoglossicida*
JAs1L1H1P	ITS rDNA	470	100	869.046	AB164370	*Trichosporon siamense*
JAs1L1H1A	16S *rRNA*	1003	97.8	1762.82	NR_044932	*Microbacterium arabinogalactanolyticum*
					MF196241	*Microbacterium esteraromaticum*
					KM488483	*Microbacterium oxydans*
JAs1L1H2A	16S *rRNA*	1055	98.2	1879.16	MH894224	*Bacillus oceanisedimins*
					KT875347	*Bacillus firmus*
JAs1L2H1	*rpoB*	1457	93.7	2180.17	LS483470	*Leminorella richardii*
JAs1L2H1	16S *rRNA*	1226	95.9	2023.2	NR_025333	*Leminorella grimontii*
JAs1L2H2	16S *rRNA*	1063	100	1964.11	JN084129	*Bacillus asahii*
JAs1L2H3	16S *rRNA*	1171	99.6	2139.54	MZ047974	*Citrobacter amalonaticus*
JAs1L2M2	16S *rRNA*	1063	99.9	1958.57	JQ661039	*Bacillus* sp.
JAs1L2M1A	16S *rRNA*	1061	99.8	1949.34	JX847112	*Lysinibacillus* sp.
JAs1L2M2A	16S *rRNA*	911	98.1	1594.78	AB098571	*Arthrobacter* sp.
JAs1L2M1P	ITS rDNA	640	100	1182.98	MK394112	*Candida palmioleophila*
JAs1L2M2P	ITS rDNA	524	99.8	961.378	AB164370	*Trichosporon siamense*
JAs1L2M3P	ITS rDNA	537	100	992.771	MZ363142	*Candida tropicalis*
					KT715474	*Candida dubliniensis*
JAs1L2M4P	ITS rDNA	527	100	974.305	NR_151809	*Candida saraburiensis*
JAs1L2H1A	16S *rRNA*	1019	99.8	1875.47	MZ9347532	*Bacillus cereus*
					MZ569844	*Bacillus mobilis*
					MZ540090	*Bacillus proteolyticus*
					MZ520364	*Bacillus pacificus*
JAs1L2H2A	16S *rRNA*	1068	99.6	1954.88	KY816740	*Brevibacillus parabrevis*
JAs1L2H4A	16S *rRNA*	981	99.7	1796.06	MZ914416	*Bacillus mycoides*