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Plant n-alkane production from litterfall altered the diversity and community structure of alkane degrading bacteria in litter layer in lowland subtropical rainforest in Taiwan

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Table S1. The taxonomy prediction of alkB lineage-like OTUs and the reference genes. Informatics prediction by UTAX algorithm gives the prediction up to genus level. An estimated probability that correct prediction was higher than 90% is showed on this table.

Phylum	**OTU**	**Taxonomy Prediction**	**Relative Abundance (%)**			**Reference of bacteria with alkB gene**	**Sequence ID**	**Identities**
			ravine	**windward**	**leeward**			
Proteobacteria	litter14	g: *Rhizobium* (97%)	4.5	1.0	0.2	*Agrobacterium fabrum*	NR074266.1	377/382(99%)
	litter44	f: *Rhizobiaceae* (91%)	2.2	0.2	0.1	*Rhizobium etli*	U28916.1	376/381(99%)
	litter50	o: *Rhizobiales* (98%)	2.1	0.9	0.6	*Ensifer adhaerens*	CP007236.1	375/382(98%)
	litter117	o: *Rhizobiales* (97%)	1.6	<0.1	<0.1	*Mesorhizobium amorphae*	NR024879.1	371/384(97%)
	litter6	f: *Bradyrhizobiaceae* (93%)	0.7	1.6	1.2	*Bradyrhizobium diazoefficiens*	AB909430.1	380/382(99%)
	litter159	f: *Pseudomonadaceae* (91%)	0.6	<0.1		*Stenotrophomonas maltophilia*	AM743169.1	390/406(96%)
	litter464	o: *Rhizobiales* (96%)	0.4	<0.1	<0.1	*Sinorhizobium meliloti*	CP003933.2	377/384(98%)
	litter189	c: *Gammaproteobacteria* (99%)	0.4	<0.1		*Stenotrophomonas maltophilia*	AM743169.1	394/408(97%)
	litter291	g: *Pseudorhodoferax* (97%)	0.3			*Delftia acidovorans*	CP000884.1	387/408(95%)
	litter199	g: *Caulobacter* (95%)	0.3	0.1	<0.1	*Caulobacter crescentus*	AE005673.1	384/384(100%)
	litter256	o: *Rhizobiales* (98%)	0.3	<0.1	0.1	*Bradyrhizobium diazoefficiens*	AB909430.1	376/387(97%)
	litter506	f: *Phyllobacteriaceae* (93%)	0.2	<0.1		*Mesorhizobium ciceri*	CP002447.1	375/382(98%)
	litter152	f: *Caulobacteraceae* (96%)	0.1	0.1	<0.1	*Caulobacter crescentus*	AE005673.1	370/384(96%)
	litter109	o: *Rhizobiales* (95%)	0.1	<0.1	0.7	*Ochrobactrum anthropi*	CP000758.1	374/382(98%)
	litter9	c: *Alphaproteobacteria* (99%)	0.1	1.6	0.4	*Ochrobactrum anthropi*	CP000758.1	369/382(97%)
	litter21	f: *Enterobacteriaceae* (98%)	0.1	0.7	<0.1	*Enterobacter lignolyticus*	CP002272.1	398/407(98%)
	litter505	g: *Pseudomonas* (95%)	<0.1	<0.1	<0.1	*Pseudomonas putida*	LT799039.1	396/408(97%)
	litter487	f: *Burkholderiaceae* (94%)	<0.1	0.2	0.2	*Burkholderia pseudomallei*	CP009163.1	401/413(97%)
	litter75	f: *Burkholderiaceae* (95%)	<0.1	0.2	1.4	*Burkholderia phenoliruptrix*	CP003863.1	402/409(98%)
	litter11	f: *Burkholderiaceae* (95%)	<0.1	1.2	0.4	*Burkholderia phenoliruptrix*	CP003863.1	399/409(98%)
	litter384	f: *Oxalobacteraceae* (96%)	<0.1		<0.1	*Herbaspirillum seropedicae*	CP002039.1	384/406(95%)
	litter209	f: *Burkholderiaceae* (96%)	<0.1	0.2	0.5	*Burkholderia phenoliruptrix*	CP003863.1	399/410(97%)
	litter208	g: *Ralstonia* (91%)		<0.1		*Ralstonia solanacearum*	AL646052.1	394/406(97%)
	litter220	f: *Burkholderiaceae* (95%)		0.1	0.2	*Burkholderia pseudomallei*	CP009163.1	389/407(96%)
Actinobacteria	litter32	f: *Pseudonocardiaceae* (97%)	4.0	<0.1		*Amycolatopsis orientalis*	NR 042104.1	375/389(96%)
	litter69	g: *Pseudonocardia* (98%)	1.6	<0.1		*Amycolatopsis orientalis*	NR 042104.1	373/391(95%)
	litter426	g: *Streptomyces* (91%)	0.5	<0.1	<0.1	*Streptomyces virginiae*	NR 115622.1	382/386(99%)
	litter147	g: *Pseudonocardia* (91%)	0.4	<0.1	<0.1	*Amycolatopsis orientalis*	NR 042104.1	366/387(95%)
	litter319	f: *Micromonosporaceae* (95%)	0.3			*Amycolatopsis vancoresmycina*	NR 025565.1	370/390(95%)
	litter89	g: *Mycobacterium* (97%)	0.1	0.2	0.3	*Mycobacterium smegmatis*	X52922.1	382/387(99%)
	litter228	g: *Mycobacterium* (91%)	0.1	0.1	0.1	*Mycobacterium kansasii*	FR822390.1	378/399(95%)
	litter352	f: *Mycobacteriaceae* (91%)	<0.1	<0.1	<0.1	*Mycobacterium abscessus*	LC149865.1	370/388(95%)
	litter465	g: *Mycobacterium* (97%)		<0.1	<0.1	*Mycobacterium kansasii*	FR822390.1	391/403(97%)

Table S2. Biodiversity index of plant vegetation, bacteria, and AlkB-lineage like OTUs.

Sample type	Habitat	Biodiversity Index		
		Shannon-Weiner	effective numbers of species	Evenness
Plant vegetation	Ravine	3.26	26	0.69
	Windward	3.64	38	0.78
	Leeward	3.78	44	0.78
Bacteria	Ravine	4.43	84	0.76
	Windward	4.22	68	0.70
	Leeward	4.12	62	0.72
OTUs of AlkB-lineage	Ravine	2.51	12	0.74
	Windward	2.39	11	0.70
	Leeward	2.46	12	0.76

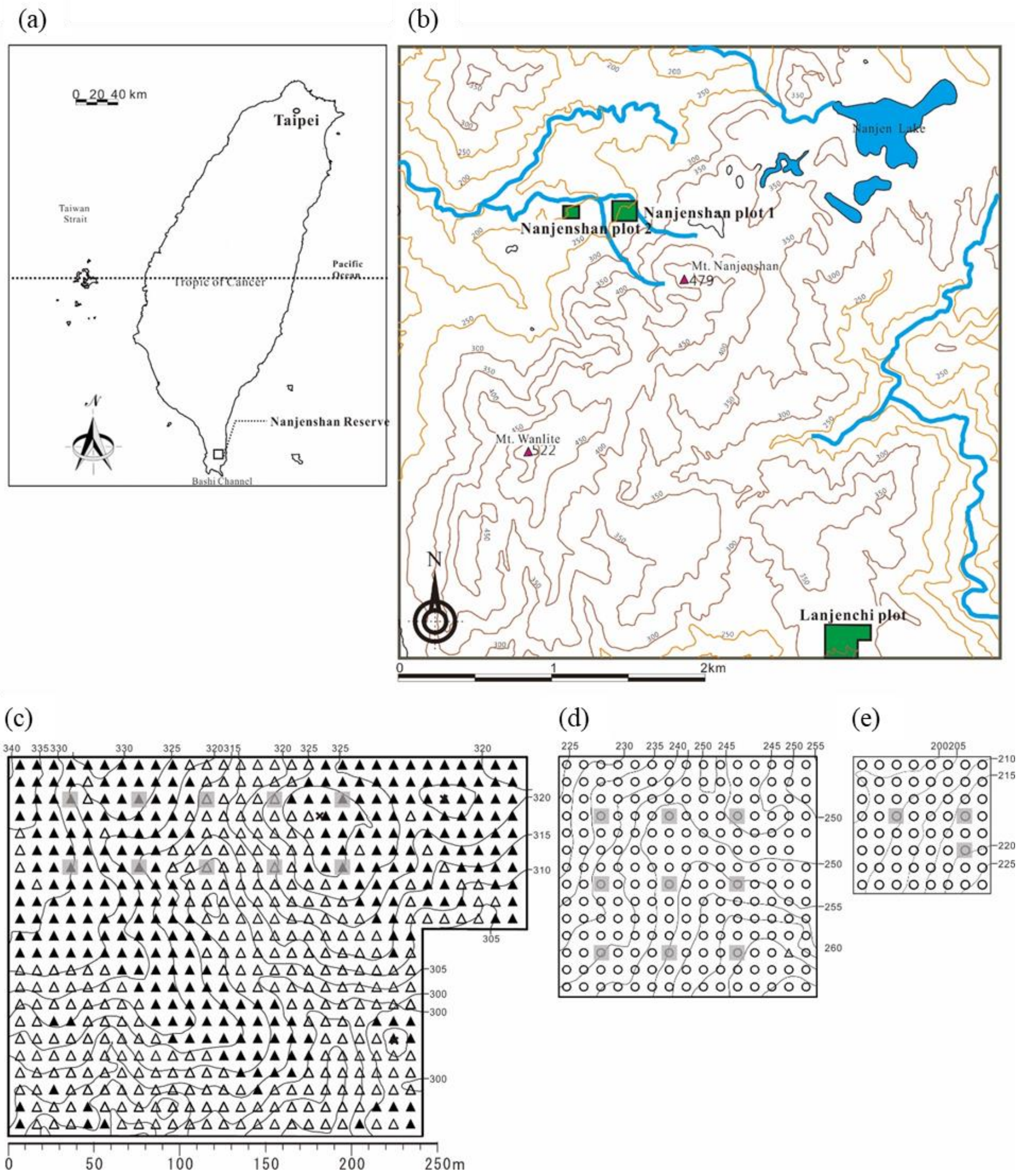

Figure S1. Location of the sampling site (from Chao et al, 2010). (a) Map of Taiwan. (b) Map of the Nanjenshan Reserve. (c) Stands set of windward habitat (▲) and Leewind habitat (△) in Lanjenchi plot. (d) Stands set of ravine habitat (○) in Nanjenshan plot I. (e) Stands set of ravine habitat (○) in Nanjenshan plot II.

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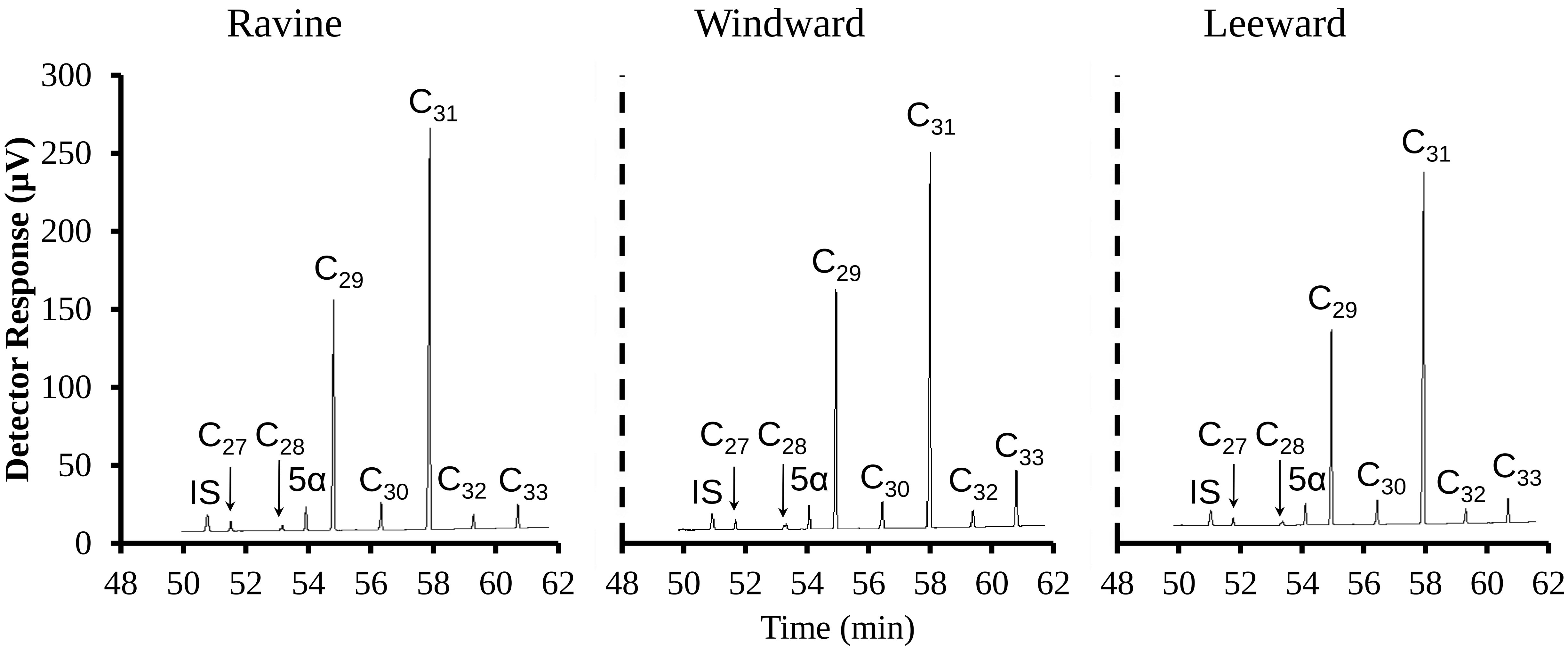

Figure S2. Representative GC-FID chromatograms of aliphatic hydrocarbons of *Iles rotunda* in each habitat.

Figure S3. Diversity of OTUs in phylum *Proteaobacter* and bacteria contained with AlkB in lowland rainfarest.

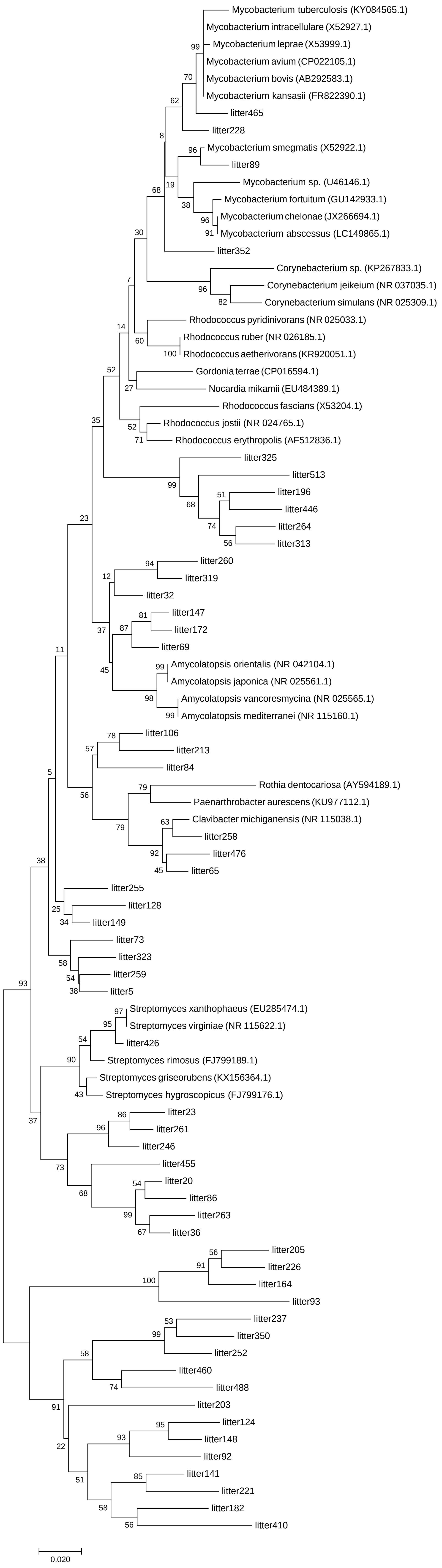

Figure S4. Diversity of OTUs in phylum *Actinobacteria* and bacteria contained with AlkB in lowland rainfarest.

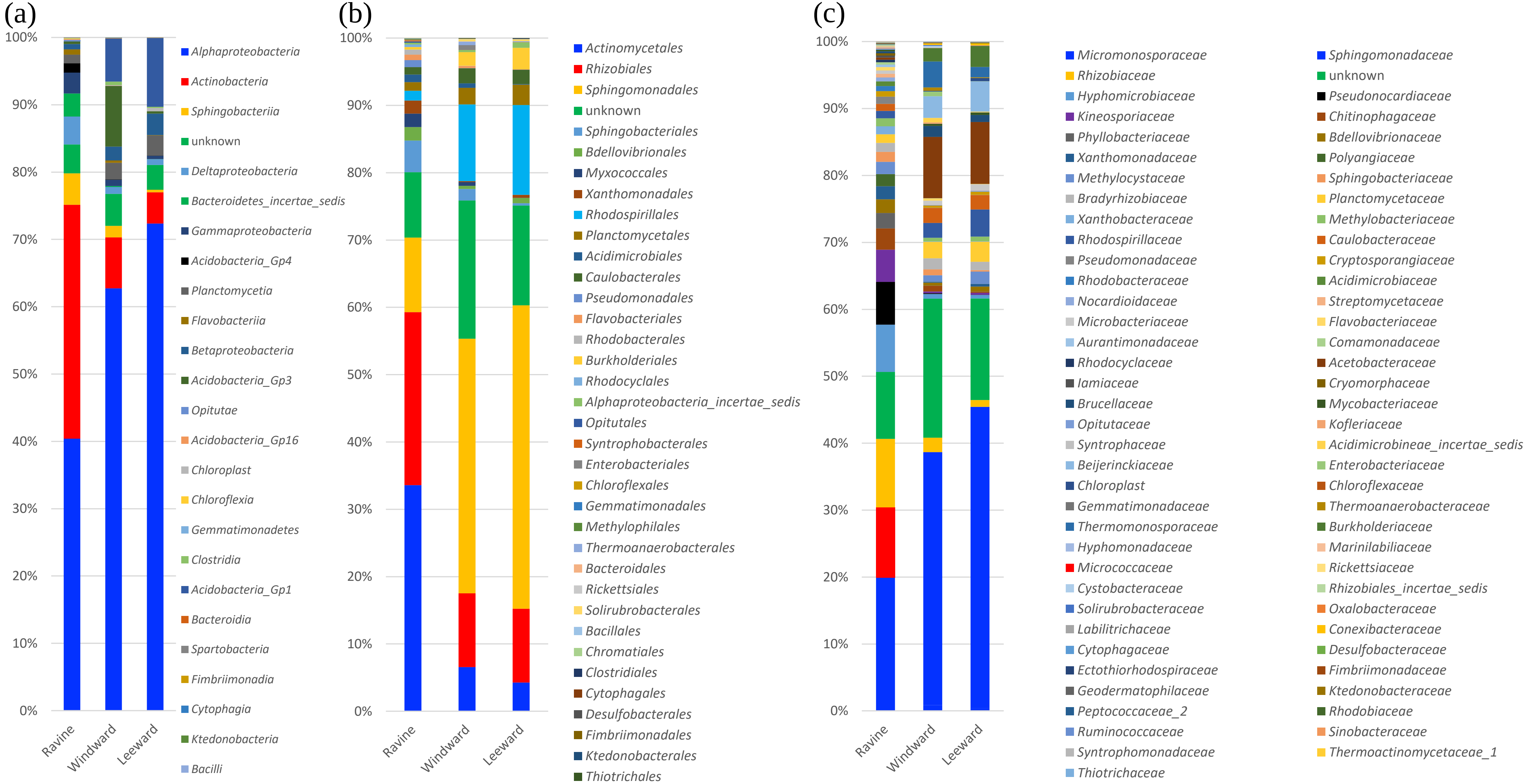

Figure S5. Microbial community structure in the three habitats of Nanjenshan Reserve. Bacterial lineages were indicated in (a) class, (b) order, and (c) family.

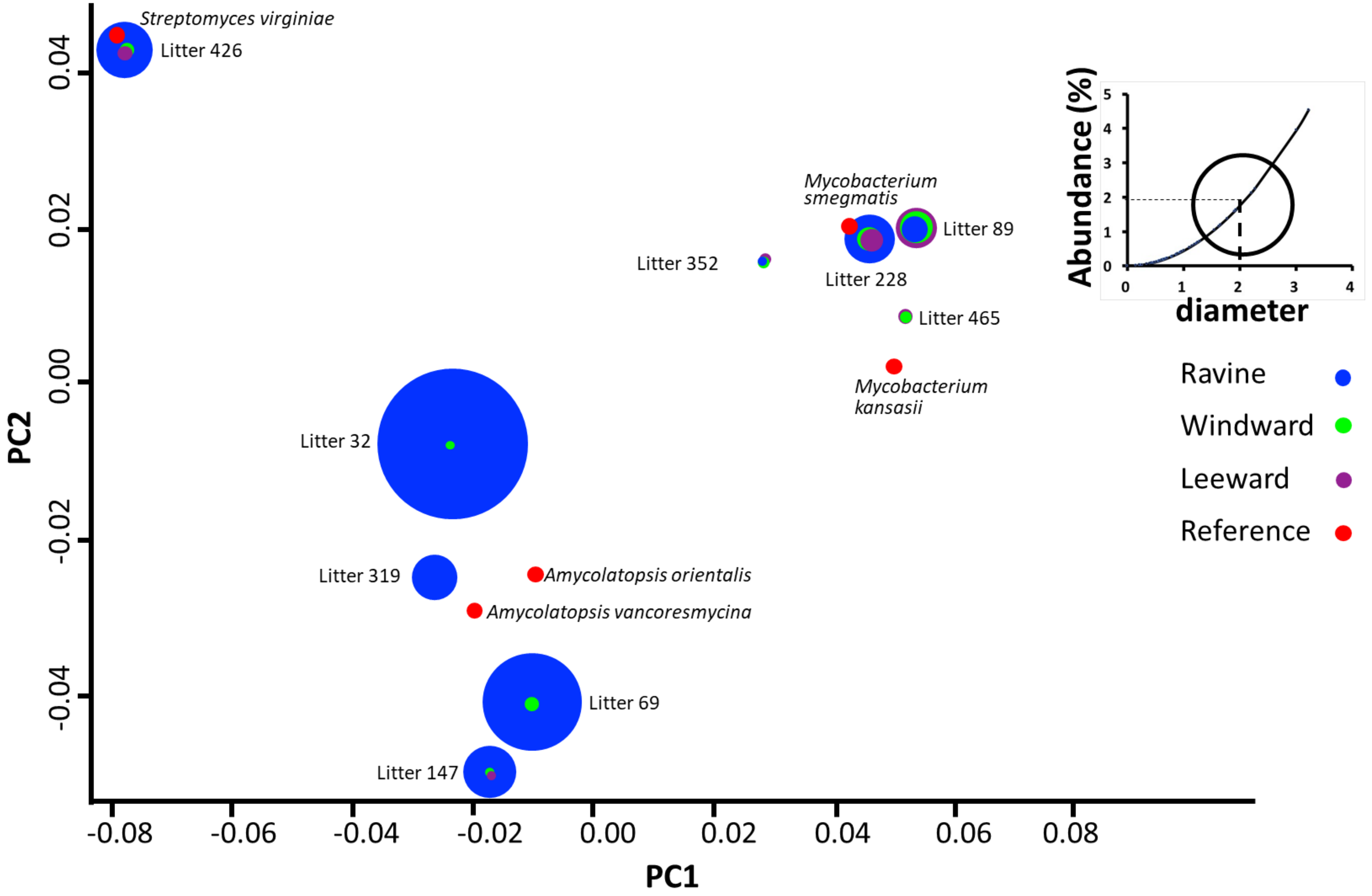

Figure S6. The distribution of OTUs and their relative abundance of microbial *Actinobacteria*. Size index of diameter vs relative abundance was showed at up-right panel.

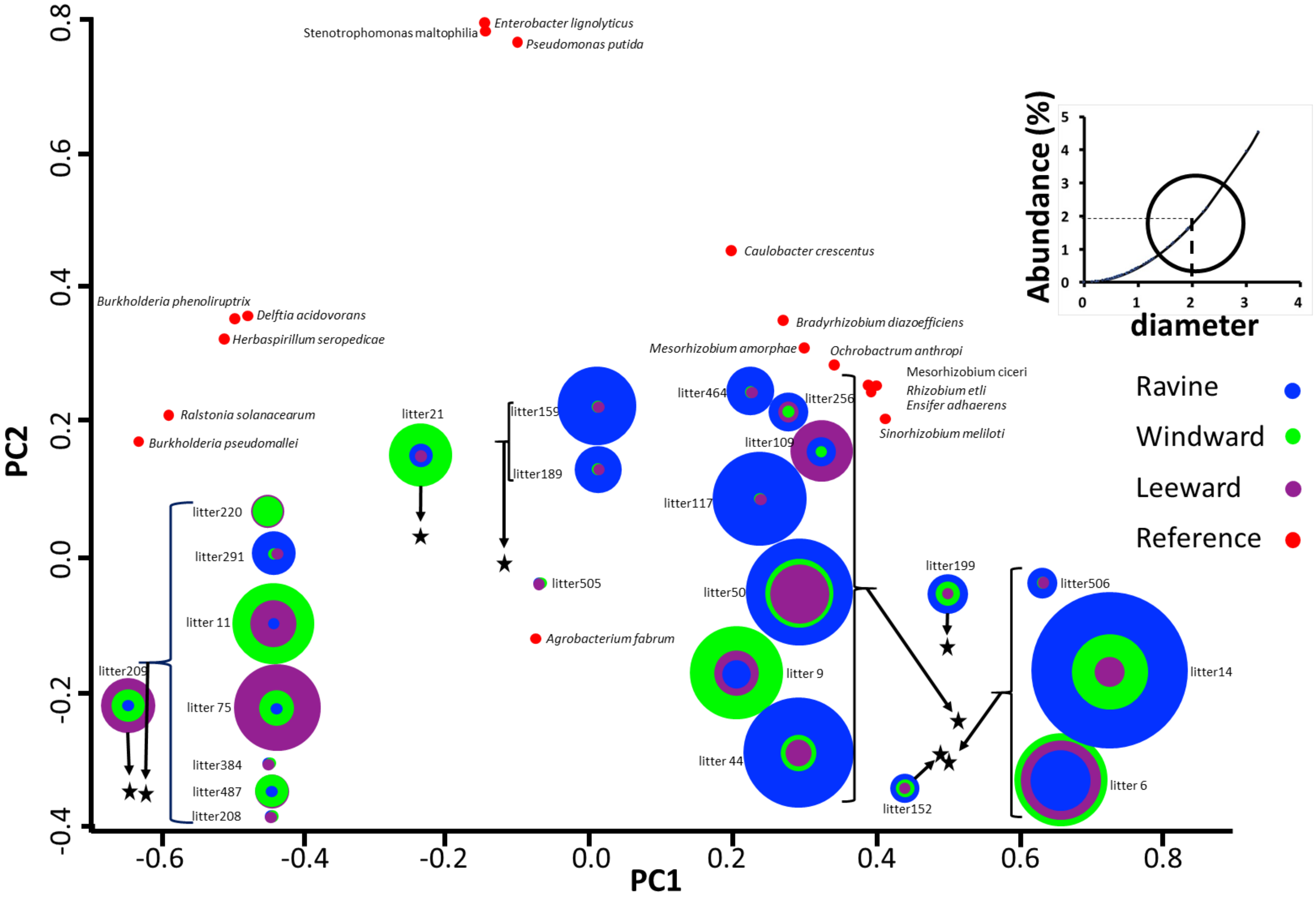

Figure S7. The distribution of OTUs and their relative abundance of microbial *Proteobacteria*. Star symbol (★) indicates the location with multiple OTUs. Size index of diameter vs relative abundance was showed at up-right panel.