Supplementary material

Table S1. Pearson correlation analysis between plant richness, chemical and physical parameters, enzymatic activities, microbial biomass, diversity and richness in litter samples.

	pH	**EC**	**N**	**C**	**TOC**	**WSC**	**WSN**	**GA**	**PA**	**UA**	**PheA**	**BB**	**FB**	**FD**	**BD**	**LM**	**DBH**	**PR**	**FR**
EC	0.01 ±0.98																		
N	0.70 ±0.03	-0.35 ±0.35																	
C	0.23 ±0.54	-0.69 ±0.04	0.77 ±0.01																
TOC	0.29 ±0.45	-0.71 ±0.03	0.78 ±0.01	0.10 ±0.00															
WSC	-0.62 ±0.07	-0.24 ±0.54	-0.29 ±0.45	0.25 ±0.51	0.22 ±0.57														
WSN	-0.00 ±0.99	0.39 ±0.29	0.19 ±0.62	0.06 ±0.88	-0.00 ±1.00	0.15 ±0.69													
GA	-0.08 ±0.83	-0.53 ±0.14	0.39 ±0.29	0.79 ±0.01	0.78 ±0.01	0.47 ±0.20	-0.04 ±0.92												
PA	0.30 ±0.44	-0.58 ±0.10	0.62 ±0.08	0.48 ±0.19	0.48 ±0.19	-0.37 ±0.33	0.14 ±0.72	0.11 ±0.78											
UA	0.31 ±0.41	-0.13 ±0.73	0.32 ±0.40	0.29 ±0.45	0.29 ±0.45	-0.44 ±0.23	0.09 ±0.82	0.32 ±0.40	0.40 ±0.28										
PheA	-0.07 ±0.85	-0.63 ±0.07	0.34 ±0.37	0.61 ±0.08	0.61 ±0.08	0.56 ±0.11	0.19 ±0.63	0.33 ±0.39	0.40 ±0.29	-0.28 ±0.42									
BB	-0.64 ±0.07	0.54 ±0.13	-0.69 ±0.04	-0.44 ±0.24	-0.47 ±0.20	0.43 ±0.25	0.05 ±0.90	-0.18 ±0.65	-0.80 ±0.01	-0.35 ±0.36	-0.25 ±0.52								
FB	-0.45 ±0.22	0.79 ±0.01	-0.59 ±0.09	-0.55 ±0.24	-0.58 ±0.10	0.17 ±0.66	0.26 ±0.49	-0.32 ±0.41	-0.74 ±0.02	-0.19 ±0.63	-0.47 ±0.20	0.92 ±0.00							
FD	0.44 ±0.24	-0.00 ±0.99	0.25 ±0.51	0.26 ±0.50	0.30 ±0.43	-0.17 ±0.67	-0.13 ±0.74	0.34 ±0.37	-0.08 ±0.83	0.60 ±0.09	-0.06 ±0.89	-0.03 ±0.94	-0.05 ±0.89						
BD	0.42 ±0.26	0.51 ±0.16	0.00 ±0.99	-0.46 ±0.21	-0.45 ±0.22	-0.30 ±0.43	0.48 ±0.19	-0.54 ±0.13	0.03 ±0.94	-0.11 ±0.77	-0.14 ±0.72	-0.24 ±0.54	0.83 ±0.01	0.02 ±0.96					
LM	-0.37 ±0.32	0.76 ±0.02	-0.55 ±0.12	-0.55 ±0.12	-0.59 ±0.09	0.35 ±0.36	0.57 ±0.11	-0.40 ±0.29	-0.64 ±0.06	-0.35 ±0.35	-0.14 ±0.72	0.74 ±0.02	0.83 ±0.01	-0.14 ±0.72	0.40 ±0.29				
DBH	-0.58 ±0.10	0.32 ±0.41	-0.41 ±0.27	-0.16 ±0.68	-0.22 ±0.58	0.13 ±0.73	0.13 ±0.74	0.11 ±0.78	-0.35 ±0.35	0.28 ±0.47	-0.47 ±0.20	0.66 ±0.05	0.71 ±0.03	-0.08 ±0.84	-0.51 ±0.16	0.35 ±0.35			
PR	-0.88 ±0.31	0.82 ±0.38	-0.93 ±0.23	-0.91 ±0.27	-0.92 ±0.26	-0.74 ±0.46	-0.45 ±0.70	-0.60 ±0.59	-0.72 ±0.49	0.16 ±0.90	-0.96 ±0.18	0.57 ±0.61	0.74 ±0.47	-0.76 ±0.45	-0.89 ±0.30	0.64 ±0.56	1.00 ±0.01		
FR	0.31 ±0.41	-0.01 ±98	0.07 ±0.85	0.22 ±0.57	0.25 ±0.51	0.16 ±0.68	0.05 ±0.90	0.34 ±0.36	-0.26 ±0.50	0.46 ±0.22	0.07 ±0.85	0.05 ±0.90	0.03 ±0.94	0.86 ±0.00	0.09 ±0.81	0.12 ±0.76	-0.05 ±0.90	-0.47 ±0.69	
BR	0.52 ±0.19	-0.93 ±0,00	0.64 ±0.09	0.73 ±0.04	0.75 ±0.03	-0.13 ±0.76	-0.06 ±0.88	0.44 ±0.27	0.79 ±0.02	0.36 ±0.39	0.54 ±0.16	-0.93 ±0.00	-0.95 ±0.00	0.17 ±0.68	0.95 ±0.00	-0.81 ±0.01	-0.72 ±0.04	-0.69 ±0.52	0.15 ±0.72

Values are means ± standard deviations of three replications. EC: electrical conductivity, N: total nitrogen, C: total carbon, TOC: total organic carbon, WSC: water soluble carbon, WSN: water soluble nitrogen, GA: glucosidase activity, PA: phosphatase activity, UA: urease activity, PheA: phenol-oxidase activity, BB: bacterial biomass, FB: fungal biomass, FD: fungal genomic diversity, BD: bacterial genomic diversity, LM: litter moisture, DBH: diameter at breast height, PR: plant richness, FR: fungal richness, BR: bacterial richness.

Table S2. Pearson correlation analysis between plant richness, chemical and physical parameters, enzymatic activities, microbial biomass, diversity and richness in soil samples.

	pH	**EC**	**N**	**C**	**TOC**	**WSC**	**WSN**	**GA**	**PA**	**UA**	**PheA**	**BB**	**FB**	**FD**	**BD**	**SM**	**DHB**	**PR**	**FR**
EC	-0,59 ±0,09																		
N	-0,93 ±0,00	0.59 ±0.09																	
C	-0,50 ±0.17	0.76 ±0.02	0.34 ±0.37																
TOC	-0.55 ±0.13	0.70 ±0.04	0.33 ±0.38	0.89 ±0.00															
WSC	-0.85 ±0.00	0.59 ±0.09	0.76 ±0.02	0.66 ±0.05	0.69 ±0.04														
WSN	-0.36 ±0.34	0.78 ±0.01	0.34 ±0.37	0.82 ±0.01	0.73 ±0.03	0.67 ±0.05													
GA	-0.63 ±0.07	0.57 ±0.11	0.43 ±0.24	0.75 ±0.02	0.92 ±0.00	0.83 ±0.00	0.73 ±0.03												
PA	-0.14 ±0.71	0.82 ±0.01	0.12 ±0.76	0.75 ±0.02	0.59 ±0.10	0.19 ±0.63	0.72 ±0.03	0.35 ±0.35											
UA	-0.79 ±0.01	0.73 ±0.02	0.89 ±0.00	0.56 ±0.11	0.49 ±0.18	0.81 ±0.01	0.63 ±0.07	0.52 ±0.15	0.35 ±0.35										
PheA	-0.37 ±0.33	0.69 ±0.04	0.41 ±0.27	0.39 ±0.30	0.53 ±0.15	0.20 ±0.61	0.31 ±0.42	0.33 ±0.39	0.52 ±0.15	0.46 ±0.22									
BB	-0.26 ±0.50	-0.45 ±0.22	0.26 ±0.50	-0.25 ±0.51	-0.14 ±0.71	0.35 ±0.36	-0.25 ±0.52	0.10 ±0.80	-0.80 ±0.01	0.15 ±0.70	-0.32 ±0.40								
FB	-0.79 ±0.01	0.48 ±0.19	0.84 ±0.00	0.38 ±0.31	0.33 ±0.38	0.83 ±0.01	0.41 ±0.28	0.43 ±0.25	-0.01 ±0.97	0.87 ±0.00	0.23 ±0.55	0.51 ±0.16							
FD	0.26 ±0.50	-0.08 ±0.83	-0.50 ±0.17	-0.06 ±0.87	0.21 ±0.58	-0.19 ±0.61	-0.07 ±0.85	0.21 ±0.59	0.06 ±0.89	-0.55 ±0.12	-0.08 ±0.84	-0.50 ±0.17	-0.57 ±0.11						
BD	0.45 ±0.22	-0.15 ±0.70	-0.63 ±0.07	-0.03 ±0.94	0.05 ±0.89	-0.49 ±0.18	-0.11 ±0.78	-0.02 ±0.95	0.26 ±0.50	-0.71 ±0.03	-0.09 ±0.82	-0.61 ±0.08	-0.86 ±0.00	0.73 ±0.02					
SM	-0.63 ±0.07	0.57 ±0.11	0.43 ±0.24	0.75 ±0.02	0.92 ±0.00	0.83 ±0.00	0.73 ±0.03	-0.46 ±0.21	0.62 ±0.07	-0.14 ±0.72	0.40 ±0.28	-0.80 ±0.01	-0.42 ±0.26	-0.10 ±0.80	0.30 ±0.43				
DHB	-0.40 ±0.29	0.26 ±0.49	0.37 ±0.33	0.45 ±0.22	0.17 ±0.67	0.54 ±0.13	0.39 ±0.30	0.19 ±0.63	0.09 ±0.82	0.46 ±0.21	-0.19 ±0.62	0.35 ±0.36	0.68 ±0.04	-0.54 ±0.13	-0.53 ±0.14	-0.21 ±0.58			
PR	-0.69 ±0.52	0.88 ±0.31	0.49 ±0.67	0.99 ±0.06	0.96 ±0.18	0.82 ±0.38	0.95 ±0.20	0.83 ±0.37	0.54 ±0.64	0.87 ±0.33	-0.97 ±0.14	-0.06 ±0.96	0.73 ±0.48	0.95 ±0.21	0.06 ±0.96	-0.36 ±0.76	1.00 ±0.01		
FR	0.33 ±0.39	-0.33 ±0.39	-0.47 ±0.20	0.05 ±0.89	0.17 ±0.67	0.09 ±0.81	0.17 ±0.66	0.29 ±0.45	-0.19 ±0.63	-0.25 ±0.52	-0.52 ±0.15	0.21 ±0.59	-0.18 ±0.64	0.45 ±0.22	0.13 ±0.75	-0.47 ±0.20	-0.09 ±0.82	0.95 ±0.20	
BR	0.51 ±0.16	-0.33 ±0.38	-0.68 ±0.04	-0.24 ±0.53	-0.10 ±0.79	-0.55 ±0.13	-0.27 ±0.48	-0.12 ±0.76	0.03 ±0.94	-0.81 ±0.01	-0.23 ±0.55	-0.47 ±0.20	-0.88 ±0.00	0.80 ±0.01	0.96 ±0.00	0.15 ±0.70	-0.60 ±0.09	-0.33 ±0.79	0.21 ±0.58

Values are means ± standard deviations of three replications. EC: electrical conductivity, N: total nitrogen, C: total carbon, TOC: total organic carbon, WSC: water soluble carbon, WSN: water soluble nitrogen, GA: glucosidase activity, PA: phosphatase activity, UA: urease activity, PheA: phenol-oxidase activity, BB: bacterial biomass, FB: fungal biomass, FD: fungal genomic diversity, BD: bacterial genomic diversity, SM: soil moisture, DBH: diameter at breast height, PR: plant richness, FR: fungal richness, BR: bacterial richness.

Table S3. The composition of the fungal communities at the genus level. Percentage of sequences with > 1% mean relative abundance.

Genus	LV1	LV2	LV3	SV1	SV2	SV3
Acrocalymma	0 ±0	1.12 ±1.93	0 ±0	0 ±0	0 ±0	0 ±0
Apiotrichum	0 ±0	0 ±0	0 ±0	1.95 ±3.38	0 ±0	0 ±0
Aspicilia	0 ±0	0 ±0	2.52 ±2.41	0 ±0	0 ±0	0 ±0
Banhegyia	0 ±0	0 ±0	1.68 ±1.53	0 ±0	0 ±0	0 ±0
Calonectria	0 ±0	10.26 ±15.37	0 ±0	0 ±0	0 ±0	0 ±0
Castanediella	0.81 ±1.4	13.15 ±18.13	0 ±0	0 ±0	0 ±0	0 ±0
Chaetomium	0 ±0	0 ±0	0 ±0	0.82 ±1.42	1.49 ±1.31	0.79 ±1.37
Cladosporium	0 ±0	0 ±0	0 ±0	0 ±0	2.41 ±4.18	0 ±0
Colletotrichum	0 ±0	1.52 ±1.32	0 ±0	0 ±0	0 ±0	0 ±0
Cordana	0 ±0	0 ±0	0 ±0	0 ±0	0 ±0	1.17 ±1.03
Corniculariella	5.45 ±0.74	2.67 ±4.63	0 ±0	0 ±0	0 ±0	0 ±0
Crinipellis	0 ±0	20.26 ±18.45	5.45 ±0.36	0 ±0	0.7 ±1.21	5.32 ±6.4
Delicatula	0 ±0	0 ±0	0 ±0	4.22 ±7.31	0 ±0	0 ±0
Dendrosporium	2.9 ±1.08	4.25 ±1.42	5.11 ±0.6	0 ±0	0 ±0	0 ±0
Diaporthe	0 ±0	0 ±0	0 ±0	12.06 ±10.13	5.99 ±5.27	7.87 ±4.82
Fusidium	4.12 ±2.97	4.99 ±1.63	2.82 ±1.34	0 ±0	0 ±0	0 ±0
Geastrum	0 ±0	0.72 ±1.24	0 ±0	0 ±0	0 ±0	0 ±0
Gymnopus	0 ±0	0.78 ±1.35	0 ±0	0 ±0	0 ±0	0 ±0
Hygrocybe	0.58 ±1.01	0 ±0	0 ±0	0.64 ±1.11	3.51 ±6.07	2.61 ±4.52
Leohumicola	0 ±0	0 ±0	0 ±0	0 ±0	0.7 ±1.22	0 ±0
Lepiota	0 ±0	0.99 ±1.71	0.96 ±1.66	0 ±0	0 ±0	0 ±0
Marasmius	7.41 ±6.86	0 ±0	0 ±0	0 ±0	0 ±0	0 ±0
Mycena	0 ±0	1.09 ±1.89	16.84 ±2.12	1.66 ±2.88	0 ±0	5.29 ±7.48
Ochroconis	6.47 ±4.79	0.66 ±1.15	0 ±0	0 ±0	0 ±0	0 ±0
Oliveonia	0.8 ±1.39	0 ±0	0 ±0	0 ±0	0 ±0	0 ±0
Parapleurotheciopsis	0 ±0	3.32 ±2.9	0 ±0	0 ±0	0 ±0	0 ±0
Penicillium	0 ±0	0 ±0	0 ±0	0.75 ±1.3	0 ±0	0 ±0
Rhinocladiella	3.34 ±3.49	0 ±0	0 ±0	2.06 ±2.05	0 ±0	0 ±0
Sarcodon	0 ±0	1.36 ±2.35	0 ±0	0 ±0	5.83 ±6.85	0 ±0
Trichoderma	0 ±0	0 ±0	0 ±0	1.72 ±1.49	1.43 ±2.48	0 ±0
Uncobasidium	6.91 ±6.87	0.79 ±1.37	0 ±0	0.73 ±1.26	0 ±0	0 ±0
Veronaeopsis	0 ±0	0 ±0	2.9 ±0.24	0 ±0	0 ±0	0 ±0
Xylaria	1.3 ±2.24	0 ±0	0 ±0	0 ±0	0 ±0	0 ±0
Unidentified	59.9 ±13.49	32.08 ±20.93	61.72 ±5.78	73.4 ±4.95	77.94 ±11.76	76.95 ±6.98

Values are means ± standard deviations of three replications. LV1, LV2 and LV3 are the litter samples corresponding to *V. pompona*, *V. odorata*, *V.* sp., respectively. SV1, SV2 and SV3 are the soil samples corresponding to each *Vanilla* sp., respectively.

Table S4. The composition of the bacterial communities at the genus level. Percentage of sequences with > 0.5% mean relative abundance.

Genus	LV1	LV2	LV3	SV1	SV2	SV3
Actinoallomurus	0 ±0	0 ±0	0 ±0	2.25 ±0.43	2.88 ±0.54	2.2 ±0.24
Anaeromyxobacter	0 ±0	0 ±0	0 ±0	1.88 ±1.63	1.16 ±1.01	1.18 ±1.14
Bacillus	0 ±0	0 ±0	0 ±0	1.32 ±1.15	1.24 ±1.08	1.89 ±0.12
Bradyrhizobium	23.71 ±4.31	24.75 ±6.45	25.94 ±2.99	5.08 ±0.61	4.21 ±0.98	5.28 ±1.43
Candidatus Koribacter	0 ±0	0 ±0	0 ±0	2.76 ±1.38	4.47 ±4.5	2.83 ±1.45
Candidatus Solibacter	0 ±0	0 ±0	3.64 ±0.09	5.77 ±0.87	5.43 ±1.16	4.68 ±0.62
Cystobacter	0 ±0	0 ±0	0 ±0	2.32 ±0.06	1.91 ±0.08	1.92 ±0.21
Denitratisoma	0 ±0	0 ±0	0 ±0	2.46 ±0.15	1.16 ±1.03	1.92 ±0.25
Devosia	1.34 ±2.32	5 ±0.16	0 ±0	0 ±0	0 ±0	0 ±0
Edaphobacter	0 ±0	0 ±0	0 ±0	0 ±0	0.95 ±0.82	0.42 ±0.73
Hyphomicrobium	2.71 ±4.69	0 ±0	0 ±0	0 ±0	0 ±0	0 ±0
Kineococcus	0 ±0	2.23 ±3.15	0 ±0	0 ±0	0 ±0	0 ±0
Lysinibacillus	0 ±0	0 ±0	0 ±0	0 ±0	0.53 ±0.92	1.65 ±0.1
Methyloligella	0 ±0	0 ±0	0 ±0	0 ±0	0 ±0	0.93 ±0.81
Niastella	1.37 ±2.37	0 ±0	0 ±0	0 ±0	0 ±0	0 ±0
Nitrospirillum	0 ±0	0 ±0	0 ±0	0 ±0	1.4 ±1.24	1.82 ±0.26
Novosphingobium	0 ±0	0 ±0	0.95 ±1.65	0 ±0	0 ±0	0 ±0
Pedomicrobium	3 ±5.2	0 ±0	0 ±0	0 ±0	0 ±0	0 ±0
Pseudolabrys	25.67 ±8.47	23.32 ±7.98	32.77 ±3.75	16.7 ±0.92	16.28 ±1.52	16.95 ±1.13
Ramlibacter	0 ±0	2.19 ±3.1	0 ±0	0 ±0	0 ±0	0 ±0
Rhodomicrobium	0 ±0	0 ±0	0 ±0	0 ±0	0 ±0	1.57 ±0.38
Rhodoplanes	3.95 ±3.43	2.87 ±4.06	4.73 ±1.97	2.22 ±0.08	1.18 ±1.03	2.04 ±0.68
Sinorhizobium	0 ±0	2.08 ±2.94	0 ±0	0 ±0	0 ±0	0 ±0
Skermanella	0 ±0	0 ±0	0 ±0	0.58 ±1.01	2.13 ±0.27	0.65 ±1.13
Stella	0 ±0	0 ±0	0 ±0	1.21 ±1.05	3.85 ±0.54	1.46 ±2.53
Streptomyces	0 ±0	0 ±0	0 ±0	0.72 ±1.25	0 ±0	0 ±0
Yokenella	0 ±0	0 ±0	1.27 ±2.2	0.68 ±1.17	0 ±0	0 ±0
Unidentified	38.24 ±12.15	37.57 ±6.81	30.69 ±2.12	54.05 ±1.1	51.22 ±2.73	50.62 ±2.33

Values are means ± standard deviations of three replications. LV1, LV2 and LV3 are the litter samples corresponding to *V. pompona*, *V. odorata*, *V.* sp., respectively. SV1, SV2 and SV3 are the soil samples corresponding to each *Vanilla* sp., respectively.

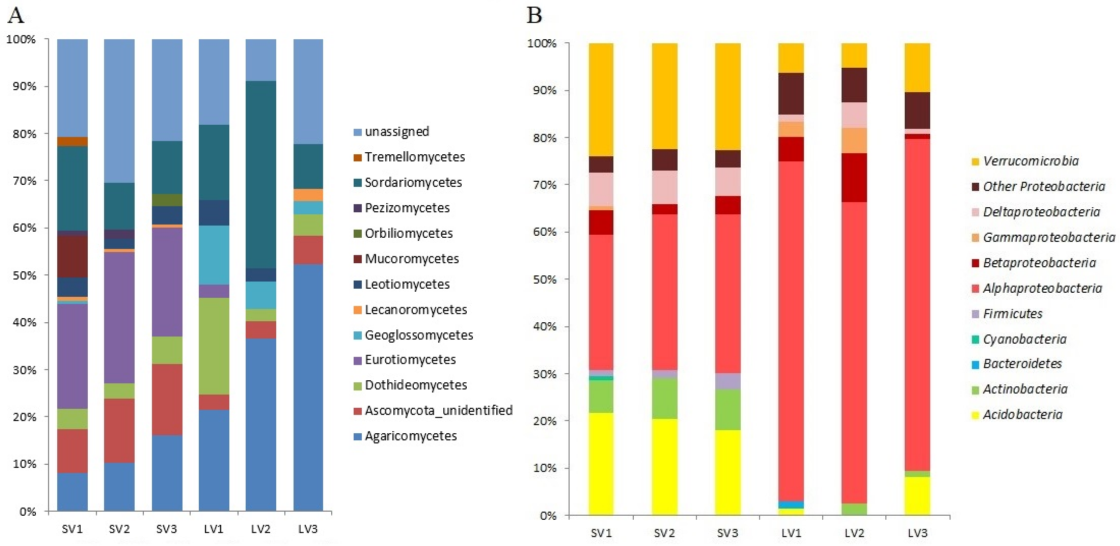

Fig. S1. Relative abundance of the fungal (A) and bacterial (B) communities at the class and phylum/class level, respectively, based on Illumina MiSeq sequencing of the fungal ITS2 region and the V4 region of the bacterial 16S rRNA gene. The figures include taxa with > 1% (for fungi) and > 0.5% (for bacteria) mean relative abundance. SV1, SV2 and SV3 are the soil samples corresponding to *V. pompona*, *V. odorata* and *V.* sp., respectively. LV1, LV2 and LV3 are the respective litter samples corresponding to these *Vanilla* species. Data represent the mean of 3 replicate samples.