

Annex 10. Global results of the analysis of compositions with bias-correction (ANCOM-BC) for genotype between paddy soil and compartments. Taxa that are highlighted in orange are not differentially abundant at alpha = 0.01. *P* values were adjusted based on Bonferroni correction method.

Taxon	Italian paddy soil										Philippine paddy soil										W	P	P _{adjusted}	Differentially abundant?
	Loosely-associated compartment					Tightly-associated compartment					Loosely-associated compartment					Tightly-associated compartment								
	Bulk soil	IR64	Kasalath	Nipponbare	Rufi	IR64	Kasalath	Nipponbare	Rufi	Bulk soil	IR64	Kasalath	Nipponbare	Rufi	IR64	Kasalath	Nipponbare	Rufi						
Methylocystis (Methylocystis echinoides cluster)	8.13	8.95	8.09	7.97	8.07	9.23	8.42	8.52	8.45	7.7	7.04	6.77	6.45	7.12	6.54	5.62	6.16	6.76	1110.49	< .001	< .001	TRUE		
Methylocystis (Methylocystis cluster)	2.09	2.57	2.32	1.79	1.59	2.85	1.9	2.08	1.88	0.14	0.02	-0.02	-0.51	-0.19	-0.23	-0.95	-0.12	0.25	370.10	< .001	< .001	TRUE		
Methylocystis (Methylocystis rosea, hirsuta cluster)	4.38	4.93	4.53	4.63	4.81	4.62	4.32	3.59	4.23	7.06	6.23	5.82	5.1	6.32	6.27	5.46	5.9	6.12	567.71	< .001	< .001	TRUE		
Methylocystis (Methylocystis sp. cluster)	7.89	8.34	8.54	8.14	7.95	8.95	9.17	9.3	8.72	8.24	7.74	7.66	6.95	7.64	7.73	7.15	7.58	7.78	434.46	< .001	< .001	TRUE		
Methylosinus (Methylocystis, uncultured cluster)	3.99	5.12	4.6	4.27	4.34	5.27	4.93	5.69	4.39	1.94	0.63	1.02	0.99	0.67	0.16	-0.75	-0.17	0.95	1241.44	< .001	< .001	TRUE		
Methylosinus (Methylosinus sporium cluster)	0	0.46	0.49	0.4	0.28	0.54	0.59	0.46	0.22	0.46	0.3	-0.02	-1.11	0.44	0.62	0.08	0.22	1.04	43.41	< .001	< .001	TRUE		
Methylosinus (Methylosinus trichosporium cluster)	0	0.46	0.49	0.4	0.28	0.54	1.02	0.46	0.61	0.14	0.02	-0.22	-0.9	0.34	0.96	0.49	0.2	1.09	59.15	< .001	< .001	TRUE		
Methylocystis (Methylosinus, uncultured cluster)	1.51	0.92	0.99	0.87	0.85	0.54	0.64	0.63	0.38	1.54	0.53	0.99	-0.39	0.56	0.57	-0.72	0.15	0.31	77.90	< .001	< .001	TRUE		
Methylococcus (FWs 1a cluster)	0.8	1	0.49	1.1	0.94	0.54	1.09	0.6	0.8	3.8	3.61	3.52	2.32	2.99	3.36	2.57	3.01	3	896.95	< .001	< .001	TRUE		
Methylobacter (Methylobacter luteus cluster)	0.93	0.62	0.49	0.4	0.72	0.7	1.42	0.79	1.29	3.45	3.34	3.23	2.3	3.35	3.92	3.89	4.05	3.36	980.25	< .001	< .001	TRUE		
Methylobacter (Methylobacter luteus/whittenburyi/marinus, uncultured cluster)	2.74	1.32	1.8	2.28	1.47	2.9	2.64	2.21	1.49	4.17	3.46	3.6	2.71	3.34	4.24	3.84	4.09	4.26	156.46	< .001	< .001	TRUE		
Methylocaldum (Methylocaldum, uncultured cluster)	0.9	0.88	1.01	1.36	1.22	0.68	1.16	1.08	1.26	2.37	3.32	4.15	3.11	2.85	3.58	3.65	3.74	3.04	595.43	< .001	< .001	TRUE		
Methylococcus (Methyloparacoccus, uncultured cluster)	6.25	6.87	5.94	7.14	6.34	7.05	7.41	7.32	7.3	8.25	8.57	8.46	7.76	8.15	8.52	7.93	8.38	8.29	394.92	< .001	< .001	TRUE		
Methylococaceae 24a cluster	0	0.46	0.49	0.4	0.46	0.54	0.68	0.46	0.22	0.25	1.13	-0.22	-1.11	0.02	0.32	-0.35	-0.15	0.42	55.01	< .001	< .001	TRUE		
Methylococaceae	2.14	1.94	2.11	0.84	2.49	1.73	1.65	1.04	1.53	1.86	2.8	1.79	1.04	1.09	-0.34	-0.43	-0.46	0	164.22	< .001	< .001	TRUE		
Methylocystaceae 11 cluster	3.62	4.52	3.48	3.66	3.87	5.4	4.63	4.69	4.35	0.79	0.27	0.44	0.05	0.11	-0.05	-0.8	0.17	1.06	2128.81	< .001	< .001	TRUE		
Methylocystis parvus, pmoA2, uncultured cluster	0.55	0.46	1.32	1.1	0.88	1.02	2.27	1.7	1.6	0.91	0.02	0.15	-0.74	-0.02	0.2	-0.08	-0.23	0.28	114.65	< .001	< .001	TRUE		
Methylocystis, uncultured cluster	5.86	6.48	5.49	5.25	5.75	7.02	6.28	6.49	6.02	3.9	2.74	3.19	2.69	2.46	3.49	2.95	3.07	4.07	1394.85	< .001	< .001	TRUE		
Methylomicrobium	1.16	0.72	0.49	1.22	1.08	0.8	0.75	0.46	0.86	1.56	4.02	4.26	3.41	2.92	2.86	3.11	3.31	0.86	653.81	< .001	< .001	TRUE		
Methylomonas	0.47	0.46	0.49	0.4	0.28	0.54	0.26	0.46	0.4	0.78	0.24	0.38	-0.03	0.67	0.79	-0.24	0.92	0.59	13.97	< .001	< .001	TRUE		
Methylosarcina	3.85	4.39	3.88	4.01	4.18	3	3.89	3.24	2.45	4.97	4.36	4.22	3.82	4.84	4.27	3.89	4.21	4.02	42.09	< .001	.05	FALSE		
Methylosarcina, uncultured cluster	1.33	0.8	1.47	1.9	0.99	1.64	2.03	0.71	1.5	3.41	5.17	5.43	4.69	4.33	4.31	4.34	4.43	2.86	583.80	< .001	< .001	TRUE		
Methylosoma, uncultured cluster	1.91	1.33	2.38	2.42	1.72	2.25	1.98	2.02	2.48	2.73	2.85	2.94	2.7	1.93	2.71	2.94	2.45	1.72	19.41	.61	> .99	FALSE		
pmoA2 like 4 cluster	1.23	0.85	0.66	0.8	1.03	0.98	0.71	0.78	1.08	3.26	2.36	2.68	1.6	1.91	3.61	3.26	3.54	3.13	786.09	< .001	< .001	TRUE		
RPC 2a cluster	2.64	3.55	2.95	3.11	3.33	3.04	2.98	2.67	4.02	5.33	6.87	7.1	6	6.04	6.38	6.38	6.59	5.11	409.14	< .001	< .001	TRUE		
RPC 2d cluster	1.79	2.38	1.52	1.94	2.05	0.91	1.32	1.13	1.59	4.37	6	5.85	4.84	5.22	5.01	4.57	5	4.25	869.56	< .001	< .001	TRUE		
RPC1 3 like 10, RPC1 cluster	0.69	0.64	0.49	0.65	0.59	0.54	0.87	0.46	0.87	1.72	2.21	2.05	1.89	2.3	2.12	1.75	2.63	2.61	373.44	< .001	< .001	TRUE		
RPC1 3 like 19 cluster	0.45	0.46	0.49	0.4	0.28	0.54	0.44	0.46	0.49	0.14	0.48	0.85	0.86	0.16	0.23	0.63	0.98	-0.35	21.73	< .001	< .001	TRUE		
RPC1 3 like 22 cluster	0.23	0.46	0.49	0.4	0.28	0.54	0.78	0.46	0.4	0.14	0.24	0.07	0.37	0.07	-0.14	-0.1	0.36	0.18	24.47	< .001	< .001	TRUE		
Unclassified Methylococaceae cluster	0.53	0.46	0.66	0.4	0.28	0.54	0.26	0.46	0.22	0.57	1.37	1.88	0.32	0.54	0.01	-0.36	-0.02	-0.07	45.75	< .001	< .001	TRUE		
Unclassified Methylocystaceae cluster	7.73	8.43	7.64	7.58	7.66	8.69	8.04	8.27	8.05	7.26	6.45	6.19	5.83	6.58	6.04	5.31	5.69	6.43	1122.58	< .001	< .001	TRUE		
Unclassified Methylocystis echinoides cluster	5.99	6.74	6.15	5.64	5.88	7.02	6.56	6.62	6.35	3.42	3.38	3.68	2.72	3.31	2.67	1.7	2.57	3.51	955.53	< .001	< .001	TRUE		
Unclassified Methylocystis, uncultured cluster	1.49	2.3	1.99	1.99	2.13	1.99	2.43	3.68	2.74	3.43	3.66	2.91	2.34	3.35	3.12	2.28	3.15	2.85	82.14	< .001	< .001	TRUE		
Unclassified Methylosarcina, uncultured cluster	2.17	0.76	1.5	2.24	1.23	0.74	0.94	0.63	1.35	5.95	5.3	5.15	4.15	5.55	4.88	4.49	4.87	4.34	1460.48	< .001	< .001	TRUE		
Unclassified RCL a cluster	0.82	0.98	0.49	0.77	0.73	0.54	0.76	0.63	0.44	2.08	2.18	2.65	2.04	2.57	2.91	2.86	2.53	1.91	481.55	< .001	< .001	TRUE		

Annex 11. Global results of the analysis of compositions with bias-correction (ANCOM-BC) for nitrogen rate (kg ha⁻¹) between paddy soil and compartments. Taxa that are highlighted in orange are not differentially abundant at alpha = 0.01. *P* values were adjusted based on Bonferroni correction method.

Taxon	Italian paddy soil					Philippine paddy soil					W	P	P _{adjusted}	Differentially abundant?		
	Bulk soil		Loosely-associated		Tightly-associated	Bulk soil		Loosely-associated		Tightly-associated						
	0 kg ha ⁻¹	50 kg ha ⁻¹	0 kg ha ⁻¹	50 kg ha ⁻¹	0 kg ha ⁻¹	50 kg ha ⁻¹	0 kg ha ⁻¹	50 kg ha ⁻¹	0 kg ha ⁻¹	50 kg ha ⁻¹						
Methylocystis (Methylocystis echinoides cluster)	8.06	8.06	8.42	7.93	8.97	8.27	7.55	7.71	6.09	7.29	6.35	5.83	1045.80	< .001	< .001	TRUE
Methylocystis (Methylocystis cluster)	1.94	2.11	2.27	1.68	2.26	2.01	0.02	0.12	-0.86	0.18	-0.2	-0.69	671.17	< .001	< .001	TRUE
Methylocystis (Methylocystis rosea, hirsuta cluster)	4.35	4.29	4.68	4.54	4.11	4.13	6.93	7.05	5.31	6.12	5.95	5.58	571.21	< .001	< .001	TRUE
Methylocystis (Methylocystis sp. cluster)	7.83	7.81	8	8.23	8.81	9.13	8.23	8.12	6.86	7.81	7.62	7.16	184.55	< .001	< .001	TRUE
Methylosinus (Methylocystis, uncultured cluster)	4.19	3.66	4.6	4.34	5.18	4.9	2.45	1.29	-0.09	1.39	0.48	-0.78	114.79	< .001	< .001	TRUE
Methylosinus (Methylosinus sporium cluster)	0	-0.13	0.24	0.33	0.4	0.39	0.66	0.12	-0.61	0.09	0.27	0.36	462.07	< .001	< .001	TRUE
Methylosinus (Methylosinus trichosporium cluster)	0	-0.13	0.24	0.33	0.52	0.65	0.02	0.12	-0.85	0.15	0.77	0.27	454.99	< .001	< .001	TRUE
Methylocystis (Methylosinus, uncultured cluster)	1.02	1.88	1.08	0.54	0.48	0.5	1.65	1.29	-0.38	0.86	0.13	-0.33	610.99	< .001	< .001	TRUE
Methylococcus (FWs 1a cluster)	0.87	0.59	0.78	0.77	0.81	0.59	3.03	4.44	2.59	3.3	2.89	2.75	893.87	< .001	< .001	TRUE
Methylobacter (Methylobacter luteus cluster)	0.73	0.99	0.39	0.46	1.23	0.74	3.63	3.12	2.88	2.9	3.64	3.69	68.51	< .001	< .001	TRUE
Methylobacter (Methylobacter luteus/whittenburyi/marinus, uncultured cluster)	2.54	2.82	1.79	1.47	2.25	2.23	4.01	4.2	2.93	3.28	4.09	3.81	20.98	< .001	< .001	TRUE
Methylocaldum (Methylocaldum, uncultured cluster)	0.86	0.82	0.97	1.04	0.94	1.03	2.49	2.1	2.87	3.46	3.52	3.21	63.72	< .001	< .001	TRUE
Methylococcus (Methyloparacoccus, uncultured cluster)	6.2	6.18	6.42	6.56	7.01	7.39	8.11	8.25	7.6	8.55	8.23	8.01	64.17	< .001	< .001	TRUE
Methylococaceae 24a cluster	0	-0.13	0.33	0.33	0.4	0.42	0.24	0.12	-0.62	0.27	-0.06	-0.16	495.37	< .001	< .001	TRUE
Methylocococaceae	1.96	2.19	1.92	1.46	1.17	1.64	1.87	1.71	0.85	2.23	-0.49	-0.44	646.69	< .001	< .001	TRUE
Methylocystaceae 11 cluster	3.43	3.69	3.95	3.61	5.02	4.44	1.1	0.34	-0.7	0.79	0.53	-0.74	438.78	< .001	< .001	TRUE
Methylocystis parvus, pmoA2, uncultured cluster	0.55	0.41	0.45	1.13	1.18	1.94	0.88	0.8	-0.65	0.02	0	-0.23	685.46	< .001	< .001	TRUE
Methylocystis, uncultured cluster	5.73	5.85	5.84	5.43	6.57	6.25	3.34	4.32	1.76	3.41	3.61	2.82	136.94	< .001	< .001	TRUE
Methylomicrobium	1.1	1.1	0.79	0.75	0.61	0.69	1.73	1.25	3.16	3.79	2.35	2.52	294.12	< .001	< .001	TRUE
Methylomonas	0.66	0.15	0.24	0.33	0.49	0.25	0.76	0.66	-0.42	0.71	0.08	0.6	18.33	< .001	< .001	TRUE
Methylosarcina	3.72	3.84	4.07	3.94	3.47	2.71	4.24	5.57	3.88	4.41	4.03	3.86	159.07	< .001	< .001	TRUE
Methylosarcina, uncultured cluster	1.23	1.31	1.42	1	1.18	1.56	3.47	3.21	4.62	4.84	3.82	3.92	35.19	< .001	< .001	TRUE
Methylosoma, uncultured cluster	1.65	2.03	1.52	2.13	1.95	2.28	3.31	2.02	2.01	2.86	2.46	2.21	344.45	< .001	< .001	TRUE
pmoA2 like 4 cluster	1.03	1.29	0.8	0.64	0.9	0.77	3.11	3.28	1.65	2.27	3.47	3	210.09	< .001	< .001	TRUE
RPC 2d cluster	2.72	4.24	0.33	0.04	3.32	5.13	5.30	6.48	6.17	6.04	5.96	6.17	60.54	< .001	< .001	TRUE
RPC 2d cluster	1.39	2.06	2.02	1.73	1.28	1.12	4.25	4.35	5.07	5.56	4.75	4.37	269.76	< .001	< .001	TRUE
RPC 13 like 10, RPC1 cluster	0.63	0.63	0.5	0.46	0.57	0.66	1.77	1.53	1.42	2.5	2.16	2.04	792.50	< .001	< .001	TRUE
RPC1 3 like 19 cluster	0.42	0.35	0.24	0.33	0.4	0.45	0.02	0.12	0.39	0.43	0.31	0.18	24.15	0.02	0.85	FALSE
RPC1 3 like 22 cluster	0	0.33	0.24	0.33	0.49	0.47	0.02	0.12	-0.2	0.26	0.18	-0.35	260.66	< .001	< .001	TRUE
Unclassified Methylococaceae cluster	0.32	0.62	0.24	0.4	0.4	0.25	0.24	0.77	0.37	1.32	0.1	-0.63	234.11	< .001	< .001	TRUE
Unclassified Methylocystaceae cluster	7.66	7.67	7.94	7.53	8.54	7.92	7.04	7.35	5.56	6.65	5.93	5.45	441.28	< .001	< .001	TRUE
Unclassified Methylocystis echinoides cluster	5.95	5.91	6.11	5.86	6.79	6.39	3.72	2.99	2.23	3.96	2.7	2.12	159.59	< .001	< .001	TRUE
Unclassified Methylocystis, uncultured cluster	1.45	1.41	1.81	2.13	2.15	3.17	2.77	3.95	2.49	3.35	2.96	2.41	7.30	< .001	< .001	TRUE
Unclassified Methylosarcina, uncultured cluster	2.37	1.85	1.63	1.1	0.64	1.04	5.53	6.24	4.63	5.12	4.4	4.6	26.02	< .001	< .001	TRUE
Unclassified RCL a cluster	0.71	0.81	0.6	0.66	0.5	0.57	2.09	1.94	2.03	2.33	2.64	2.21	69.54	< .001	< .001	TRUE