

Table S1: Physico-chemical properties of soil samples

SAMPLE	long	lat	alt	MAP	MAT	BD	clay	%	silt	sand	pH	CFC	Al ox	Fe ox	total C	total N	total P	soil_CN	CP_soil	available P	mic_P
	DD		m	mm ² ·m ⁻¹	°C·cm ⁻¹	g·cm ⁻³	%	%	%	%		cm ³ ·kg ⁻¹	mg·kg ⁻¹	mg·kg ⁻¹	mg·kg ⁻¹	mg·kg ⁻¹	mg·kg ⁻¹	mg·kg ⁻¹	mg·kg ⁻¹	mg·kg ⁻¹	mg·kg ⁻¹
RN4_1	46.187997	-10.587120	915	1504	21.9	1.52	29.04	4.42	66.54	4.72	3.92	1.57	0.91	15.10	1.00	0.2734	15.03	55.22	1.21	1.55	
RN4_2	46.082402	-10.598820	1031	1402	21.9	1.30	39.46	4.91	55.65	5.83	4.22	2.39	2.55	26.05	1.94	0.4491	14.44	62.44	0.46	2.83	
RN4_3	45.979408	-10.639120	813	1465	22.7	1.22	47.18	7.05	43.77	6.18	3.04	1.93	1.71	11.47	0.93	0.2313	12.32	49.60	0.14	1.06	
RN4_4	45.978117	-10.648419	680	1430	23.4	1.23	47.18	7.05	43.77	6.18	3.04	1.93	1.71	11.47	0.93	0.2313	12.32	49.60	0.17	1.41	
RN4_6	46.337189	-10.577919	945	1508	21.8	1.42	42.21	8.48	49.31	5.49	1.17	1.56	0.62	13.55	1.17	0.2539	15.57	17.20	0.49	4.26	
RN4_8	46.483831	-10.622050	1038	1512	20.9	1.42	61.62	0.98	37.39	5.39	3.40	1.94	1.98	16.14	1.26	0.5197	12.76	31.06	0.71	2.88	
RN4_10	46.617275	-10.721217	1128	1504	20.1	1.19	41.70	12.13	46.16	5.55	2.85	2.18	1.31	18.80	1.26	0.3917	14.92	48.01	0.51	2.46	
RN4_11	46.617275	-10.721217	1128	1504	20.1	1.19	41.70	12.13	46.16	5.55	2.85	2.18	1.31	18.80	1.26	0.3917	14.92	48.01	0.33	2.42	
RN4_12	46.617275	-10.721217	1128	1504	20.1	1.19	41.70	12.13	46.16	5.55	2.85	2.18	1.31	18.80	1.26	0.3917	14.92	48.01	0.26	2.20	
RN4_13	46.917856	-10.807017	1298	1479	18.6	1.13	55.48	5.64	38.18	5.29	2.15	3.96	1.78	24.68	1.70	0.6190	14.48	39.87	0.53	2.77	
RN4_36	46.917856	-10.807017	64	1608	26.8	1.52	16.00	11.84	72.15	6.31	8.29	1.02	1.29	3.74	0.32	0.2991	11.85	12.50	0.33	0.47	
RN4_37	46.806661	-17.116664	214	1694	26.7	1.32	38.36	15.62	46.02	6.44	3.45	0.61	2.24	7.66	0.48	0.2408	16.06	31.79	0.23	0.51	
RN4_38	46.806661	-17.116664	214	1694	26.7	1.32	38.36	15.62	46.02	6.44	3.45	0.61	2.24	7.66	0.48	0.2408	16.06	31.79	0.39	1.39	
RN4_39	46.806661	-17.116664	214	1694	26.7	1.32	38.36	15.62	46.02	6.44	3.45	0.61	2.24	7.66	0.48	0.2408	16.06	31.79	0.62	2.48	
RN4_40	46.930556	-17.359738	394	1759	25.7	1.34	56.92	2.67	40.41	5.86	3.44	0.91	1.59	13.52	0.89	0.3577	15.24	37.79	0.10	1.17	
RN4_41	46.987253	-17.486538	639	1776	24.0	1.35	47.37	3.13	49.50	5.61	2.52	1.64	1.29	23.87	1.29	0.3190	13.52	54.57	0.50	2.90	
RN4_42	46.954956	-17.622056	655	1817	24.0	1.15	46.05	3.64	50.31	5.75	3.07	2.46	1.29	23.87	1.22	0.4109	13.87	58.08	0.44	2.97	
RN4_43	46.954956	-17.622056	655	1817	24.0	1.15	46.05	3.64	50.31	5.75	3.07	2.46	1.29	23.87	1.22	0.4109	13.87	58.08	0.17	1.13	
RN4_44	46.954956	-17.622056	655	1817	24.0	1.15	46.05	3.64	50.31	5.75	3.07	2.46	1.29	23.87	1.22	0.4109	13.87	58.08	0.74	3.76	
RN4_46	47.100347	-17.908650	1477	1500	18.5	1.18	39.99	6.35	53.66	5.50	1.05	5.12	6.94	23.92	1.07	0.7240	22.42	33.03	0.08	0.91	
RN4_47	47.152844	-18.033647	1558	1468	18.1	1.13	47.55	3.32	49.13	5.37	1.75	6.71	1.51	36.58	2.08	0.3418	17.58	107.03	0.63	3.61	
RN4_48	47.152844	-18.033647	1558	1468	18.1	1.13	47.55	3.32	49.13	5.37	1.75	6.71	1.51	36.58	2.08	0.3418	17.58	107.03	1.07	6.34	
RN4_49	47.152844	-18.033647	1558	1468	18.1	1.13	47.55	3.32	49.13	5.37	1.75	6.71	1.51	36.58	2.08	0.3418	17.58	107.03	0.92	5.31	
RN4_50	47.215542	-18.131644	1556	1435	17.7	1.19	54.33	2.62	43.05	5.58	2.13	2.04	2.01	39.39	2.27	0.4752	17.56	82.89	0.59	5.66	
RN4_51	47.142747	-18.265542	1295	1466	19.1	1.36	38.41	3.07	58.52	5.36	3.09	3.23	0.53	22.59	1.08	0.3604	20.88	62.67	0.93	5.18	
RN4_52	47.142747	-18.265542	1295	1466	19.1	1.36	38.41	3.07	58.52	5.36	3.09	3.23	0.53	22.59	1.08	0.3604	20.88	62.67	0.54	3.71	
RN4_53	47.142747	-18.265542	1295	1466	19.1	1.36	38.41	3.07	58.52	5.36	3.09	3.23	0.53	22.59	1.08	0.3604	20.88	62.67	0.56	4.23	
RN4_54	47.137547	-18.395742	1308	1450	19.1	1.31	43.09	4.04	52.87	5.22	2.19	1.43	1.05	25.63	1.43	0.3743	17.94	68.48	0.99	6.91	
RN4_55	47.199544	-18.541639	1421	1402	18.5	1.22	42.22	5.23	52.55	5.17	3.59	1.43	3.19	36.82	1.86	0.6470	19.79	56.91	0.84	6.62	
RN4_56	47.293339	-18.686836	1308	1363	18.9	1.32	40.67	8.32	51.02	5.16	0.80	1.73	1.40	18.13	1.09	0.4561	16.67	39.75	0.53	1.92	
RN4_57	47.393133	-18.778133	1295	1327	18.8	1.21	41.78	2.42	55.80	5.62	1.34	1.68	1.26	28.08	1.60	0.7994	17.56	58.56	1.33	8.76	
RN4_75	45.477339	-22.537167	802	783	22.0	1.53	18.64	23.69	57.66	5.62	3.20	0.88	0.91	14.70	0.85	0.2590	17.24	50.70	2.80	3.63	
RN4_76	45.670431	-22.498169	955	790	21.2	1.46	21.84	5.93	72.23	5.27	0.99	1.18	0.42	13.85	0.85	0.2604	18.58	60.87	1.20	2.93	
RN4_77	45.854019	-22.429669	1031	798	20.7	1.50	23.82	3.91	72.27	4.75	1.99	0.62	0.72	17.10	0.86	0.2731	19.91	62.63	0.87	1.48	
RN4_78	45.854019	-22.429669	1031	798	20.7	1.52	33.55	2.7	63.75	4.75	1.95	0.62	0.72	12.35	0.69	0.1957	17.84	63.12	0.85	1.32	
RN4_79	45.854019	-22.429669	1031	798	20.7	1.49	21.39	15.33	63.28	4.75	2.85	0.62	0.72	10.73	0.68	0.2081	15.88	51.57	1.28	2.24	
RN4_80	46.027111	-22.400969	1123	819	20.2	1.20	27.78	4.38	67.84	4.86	3.04	0.58	0.50	19.95	1.16	0.5897	17.22	33.83	1.45	7.72	
RN4_81	46.297197	-22.298769	747	779	21.7	1.37	33.71	3.65	62.64	4.98	4.99	0.89	0.89	25.39	1.22	0.3281	20.75	77.39	3.53	3.02	
RN4_82	46.585951	-21.961678	774	926	21.1	1.49	32.54	6.70	60.96	5.75	3.98	1.57	0.65	18.00	1.08	0.5847	16.75	30.79	2.72	2.70	
RN4_83	46.738272	-21.931878	1014	990	19.6	1.12	42.80	12.91	44.29	5.94	2.20	1.96	1.34	16.22	1.37	0.4068	11.84	39.88	0.77	2.70	
RN4_84	46.738272	-21.931878	1014	990	19.6	1.31	52.00	11.55	36.45	5.94	3.09	1.96	1.34	15.57	1.09	0.4664	14.33	33.38	0.82	2.74	
RN4_85	46.738272	-21.931878	1014	990	19.6	1.23	46.10	6.89	47.00	5.94	2.98	1.96	1.34	17.45	1.13	0.4385	15.41	39.80	1.20	3.63	
RN4_87	46.952961	-21.774081	1098	1106	18.9	1.44	42.67	12.37	44.96	5.86	3.74	1.05	1.21	14.48	1.08	0.3992	13.47	46.83	0.54	2.05	
RN4_88	47.019431	-21.583611	1174	1171	18.6	1.26	56.40	3.48	40.12	4.93	2.52	1.56	1.31	24.58	1.36	0.3450	18.03	71.24	0.72	4.53	
RN4_89	47.123839	-21.445450	1135	1271	18.6	1.26	58.31	3.71	37.98	4.77	2.33	1.52	2.03	22.92	1.41	1.3371	16.29	17.14	0.31	5.25	
RN4_90	47.123839	-21.445450	1140	1327	18.6	1.16	39.67	5.49	54.84	5.53	1.49	3.88	1.73	28.58	1.64	0.4845	17.40	59.00	0.45	2.43	
RN4_91	47.174550	-21.338586	1140	1327	18.6	1.12	52.99	4.03	48.25	5.53	2.66	3.88	1.73	30.02	1.69	0.4040	17.71	74.31	0.62	3.93	
RN4_92	47.174550	-21.338586	1140	1327	18.6	1.13	47.33	4.42	48.25	5.53	3.14	3.88	1.73	21.59	1.21	0.3121	17.89	69.16	0.40	2.25	
RN4_93	47.244544	-21.130792	1238	1368	17.9	1.10	60.95	3.68	35.37	4.95	2.10	2.15	2.28	41.61	2.26	1.5117	18.38	27.53	1.13	10.19	
RN4_94	47.183330	-21.037592	1246	1333	17.8	1.29	45.17	5.03	35.30	5.89	2.13	1.97	0.78	22.82	1.31	0.2659	17.48	86.49	0.68	4.91	
RN4_95	47.137050	-20.893944	1443	1345	16.9	1.12	65.17	4.19	29.64	5.98	6.27	1.28	2.02	43.82	2.65	0.4822	16.55	90.88	1.43	20.98	
RN4_96	47.231631	-20.600300	1534	1418	16.4	1.30	46.01	3.68	50.31	5.73	2.41	2.12	0.77	35.42	1.84	0.2832	19.28	125.11	1.52	12.70	
RN4_97	47.231631	-20.461200	1343	1491	17.4	1.02	29.16	8.17	62.67	5.69	1.96	1.76	3.90	41.06	2.20	1.0145	18.68	40.47	0.60	7.96	
RN4_98	47.231631	-20.461200	1343	1491	17.4	1.15	67.04	5.61	27.35	5.69	2.93	1.76	3.90	39.93	2.25	0.9894	17.76	40.35	0.53	7.01	
RN4_99	47.231631	-20.461200	1343	1491	17.4	1.14	71.62	5.51	22.86	5.69	3.05	1.76	3.90	27.64	1.91	0.5560	14.47	49.71	0.47	11.29	
RN4_100	47.123950	-20.322406	1399	1441	17.4	1.28	58.73	4.5	36.77	6.29	3.17	2.33	1.08	27.84	1.62	0.3808	17.24	73.11	0.94	12.16	

Abbreviations: long: longitude; lat: latitude; alt: altitude ; MAP: Mean Annual Precipitation; MAT: Mean Annual Temperature; BD: Bulk density; Al ox: Aluminium oxidable; Fe ox: Iron oxidable, total C: total carbon; total N: total nitrogen; total P: total phosphorus; Soil_CN: total C on total N ratio; Soil_CN: totl C on total P ratio; available P: extractable

Table S2

Bacteria		Fungi	
Family	Phylum	Family	Phylum
Acetobacteraceae	α-Proteobacteria	Aqaricaceae	Basidiomycota
Acidimicrobinae incertae sedis	Actinobacteria	Agyriaceae	Ascomycota
Acidobacteria-Gp1	Acidobacteria	Ajellomycetaceae	Ascomycota
Acidobacteria-Gp13	Acidobacteria	Ambisporaceae	Glomeromycota
Acidobacteria-Gp2	Acidobacteria	Auriculariaceae	Basidiomycota
Acidobacteria-Gp3	Acidobacteria	Bionectriaceae	Ascomycota
Acidobacteria-Gp4	Acidobacteria	Boletaceae	Basidiomycota
Acidobacteria-Gp5	Acidobacteria	Bulgariaceae	Ascomycota
Acidobacteria-Gp6	Acidobacteria	Chaetomiaceae	Ascomycota
Acidobacteria-Gp7	Acidobacteria	Clavicipitaceae	Ascomycota
Actinospicaceae	Actinobacteria	Coniochaetaceae	Ascomycota
Armatimonadaceae	Armatimonadetes	Coniophoraceae	Basidiomycota
Bacillaceae	Firmicutes	Cordycipitaceae	Ascomycota
Bdellovibrionaceae	δ-Proteobacteria	Corticiaceae	Basidiomycota
Beijerinckiaceae	α-Proteobacteria	Davidiellaceae	Ascomycota
Bradyrhizobiaceae	α-Proteobacteria	Didymellaceae	Ascomycota
Burkholderiaceae	β-Proteobacteria	Endogonaceae	Mucoromycota
Catenulisporaceae	Actinobacteria	Entolomataceae	Basidiomycota
Caulobacteraceae	α-Proteobacteria	Environmental	-
Chitinophagaceae	Bacteroidetes	Glomeraceae	Glomeromycota
Chloroplast	Eucaryotes	Gomphaceae	Basidiomycota
Chthonomonadaceae	Armatimonadetes	Helotiaceae	Ascomycota
Comamonadaceae	β-Proteobacteria	Herpotrichiellaceae	Ascomycota
Conexibacteraceae	Actinobacteria	Hyaloscyphaceae	Ascomycota
Coxiellaceae	γ-Proteobacteria	Hypocreaceae	Ascomycota
Cyanobacteria.Chloroplast-F1	Cyanobacteria	Kickxellaceae	Kickxellomycotina
Cystobacteraceae	δ-Proteobacteria	Lycoperdaceae	Basidiomycota
Fervidicoccaceae	Crenarchaeota	Lyophyllaceae	Basidiomycota
Flavobacteriaceae	Bacteroidetes	Magnaporthaceae	Ascomycota
Gemmatimonadaceae	Gemmatimonadetes	Marasmiaceae	Basidiomycota
Geodermatophilaceae	Actinobacteria	Massariaceae	Ascomycota
Haliangiaceae	δ-Proteobacteria	Monoblepharidaceae	Chytridiomycota
Hyphomicrobiaceae	α-Proteobacteria	Montagnulaceae	Ascomycota
Ktedonobacteraceae	Chloroflexi	Mortierellaceae	Mortierellomycota
Methylobacteriaceae	α-Proteobacteria	Mycosphaerellaceae	Ascomycota
Methylocystaceae	α-Proteobacteria	Myxotrichaceae	Ascomycota
Microbacteriaceae	Actinobacteria	Nectriaceae	Ascomycota
Micromonosporaceae	Actinobacteria	Ophiocordycipitaceae	Ascomycota
Mycobacteriaceae	Actinobacteria	Ophiostomataceae	Ascomycota
Nitrospiraceae	Nitrospira	Orbiliaceae	Ascomycota
Nocardiodaceae	Actinobacteria	Pezizaceae	Ascomycota
Oxalobacteraceae	β-Proteobacteria	Phaeosphaeriaceae	Ascomycota
Paenibacillaceae	Firmicutes	Plectosphaerellaceae	Ascomycota
Pasteuriaceae	Firmicutes	Pleurosporeae	Ascomycota
Phyllobacteriaceae	α-Proteobacteria	Pleurotaceae	Basidiomycota
Planctomycetaceae	Planctomycetes	Pluteaceae	Basidiomycota
Planococcaceae	Firmicutes	Pyronemataceae	Ascomycota
Polyangiaceae	δ-Proteobacteria	Rhizophydiaceae	Chytridiomycota
Pseudonocardaceae	Actinobacteria	Sarcosomataceae	Ascomycota
Rhizobiales incertae sedis	Rhizobiales	Stereaceae	Basidiomycota
Rhodospirillaceae	α-Proteobacteria	Strophariaceae	Basidiomycota
Rubrobacteraceae	Actinobacteria	Teratosphaeriaceae	Ascomycota
Sinobacteraceae	γ-Proteobacteria	Trechisporaceae	Basidiomycota
Solirubrobacteraceae	Actinobacteria	Tremellaceae	Basidiomycota
Streptomycesaceae	Actinobacteria	Trichocomaceae	Ascomycota
Thermomonosporaceae	Actinobacteria	Tricholomataceae	Basidiomycota
Undefined	-	Tubeufiaceae	Ascomycota
Unknown	-	Unclassified	-
Xanthobacteraceae	α-Proteobacteria	Unknown	-
Xanthomonadaceae	γ-Proteobacteria	Ustilaginaceae	Basidiomycota

Table S3

Fobs.t7.summary

substrate	duration of incubation	statistical model	p-value
soil	7 days	lm	0.357
		fcust	0.675
	42 days	lm	0.933
		fcust	0.380
	7 days	lm	0.736
		fcust	0.720
bacteria	42 days	lm	0.049
		fcust	0.234
	7 days	lm	0.044
		fcust	0.360
	7 days	lm	0.118
		fcust	0.893
priming effect	42 days	lm	0.084
		fcust	0.483
	7 days	lm	0.118
		fcust	0.132
	7 days	lm	0.373
		fcust	0.174
fungi	42 days	lm	0.980
		fcust	0.331
	7 days	lm	0.919
		fcust	0.981
	42 days	lm	0.657
		fcust	0.215
bacteria and fungi	7 days	fcust	0.787
		fcust	0.186
	7 days	fcust	0.216
		fcust	0.386
	7 days	fcust	0.049
		fcust	0.832

Jaillard, B.; Razanamalala, K.; Violle, C.; Bernard, L. Nonlinear Effects Induced by Interactions among Functional Groups of Bacteria and Fungi Regulate the Priming Effect in Malagasy Soils. *Microorganisms*.

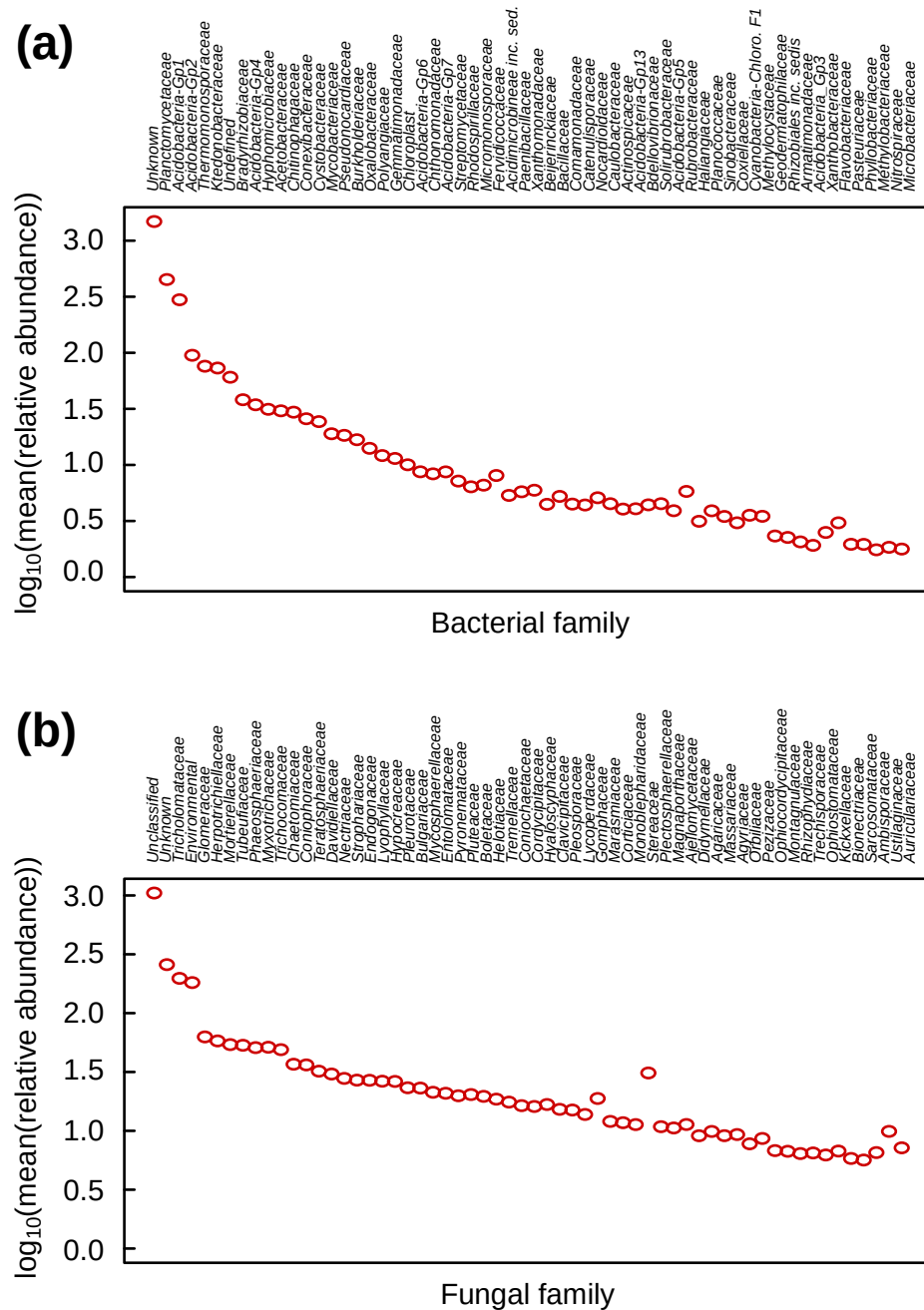


Figure S1. Relative abundance of bacterial and fungal families. (a) Bacteria. (b) Fungi. Families are sorted by decreasing sum of reads in the dataset.

Jaillard, B.; Razanamalala, K.; Violle, C.; Bernard, L. Nonlinear Effects Induced by Interactions among Functional Groups of Bacteria and Fungi Regulate the Priming Effect in Malagasy Soils. *Microorganisms*.

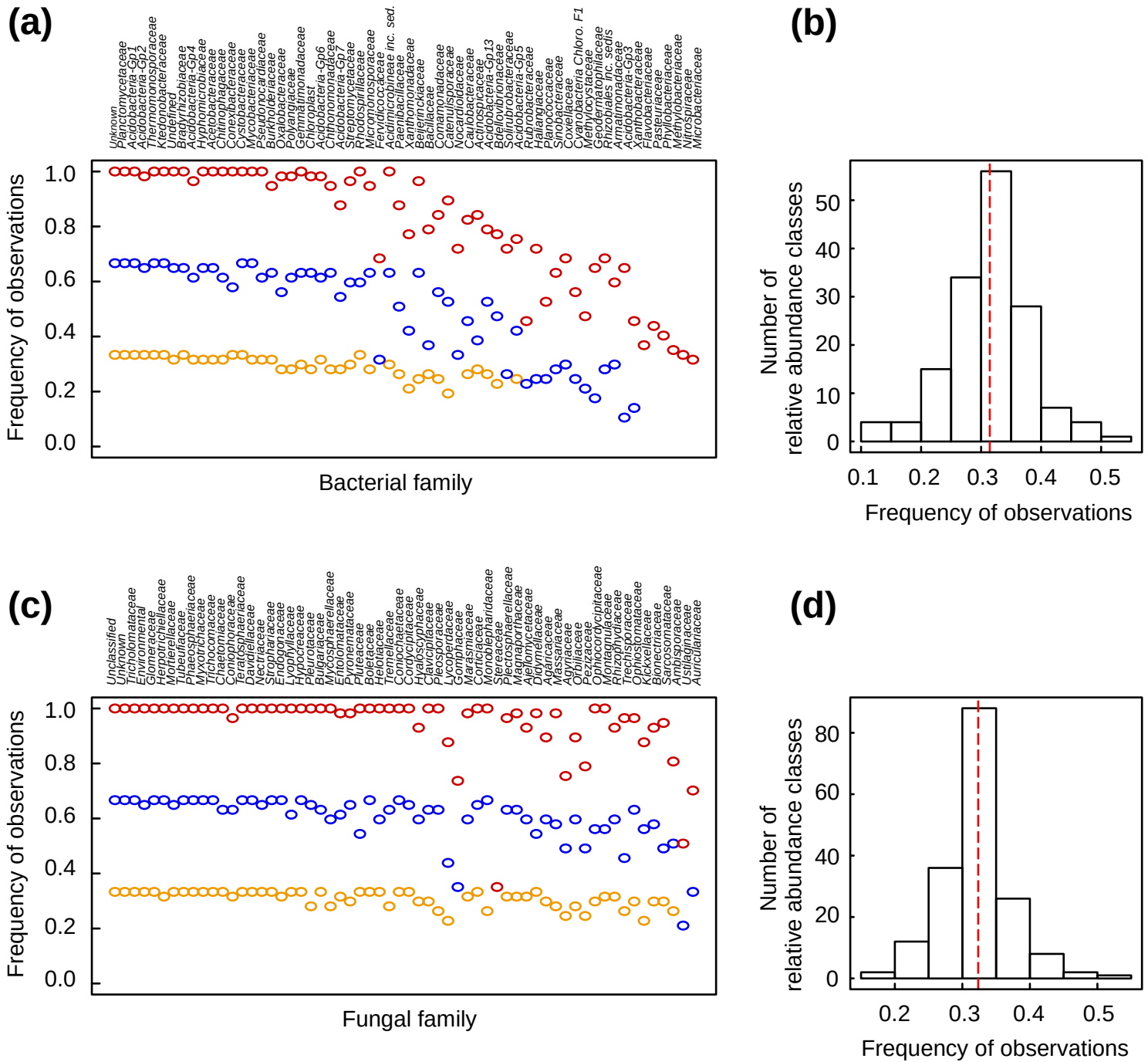


Figure S2. Conversion of abundances into classes of relative abundance for clustering analysis. (a) and (b) Bacteria. (c) and (d) Fungi. (a) and (c). Segmentation of the relative abundance distribution of each family into relative abundance classes. (b) and (d). Distribution of observation frequencies of the relative abundance classes obtained. The target frequency is 0.30. The median of the frequencies obtained is 0.322 and 0.333, for bacteria and fungus relative abundances, respectively. Families are sorted by decreasing sum of reads in the dataset, from left to right of the figure.

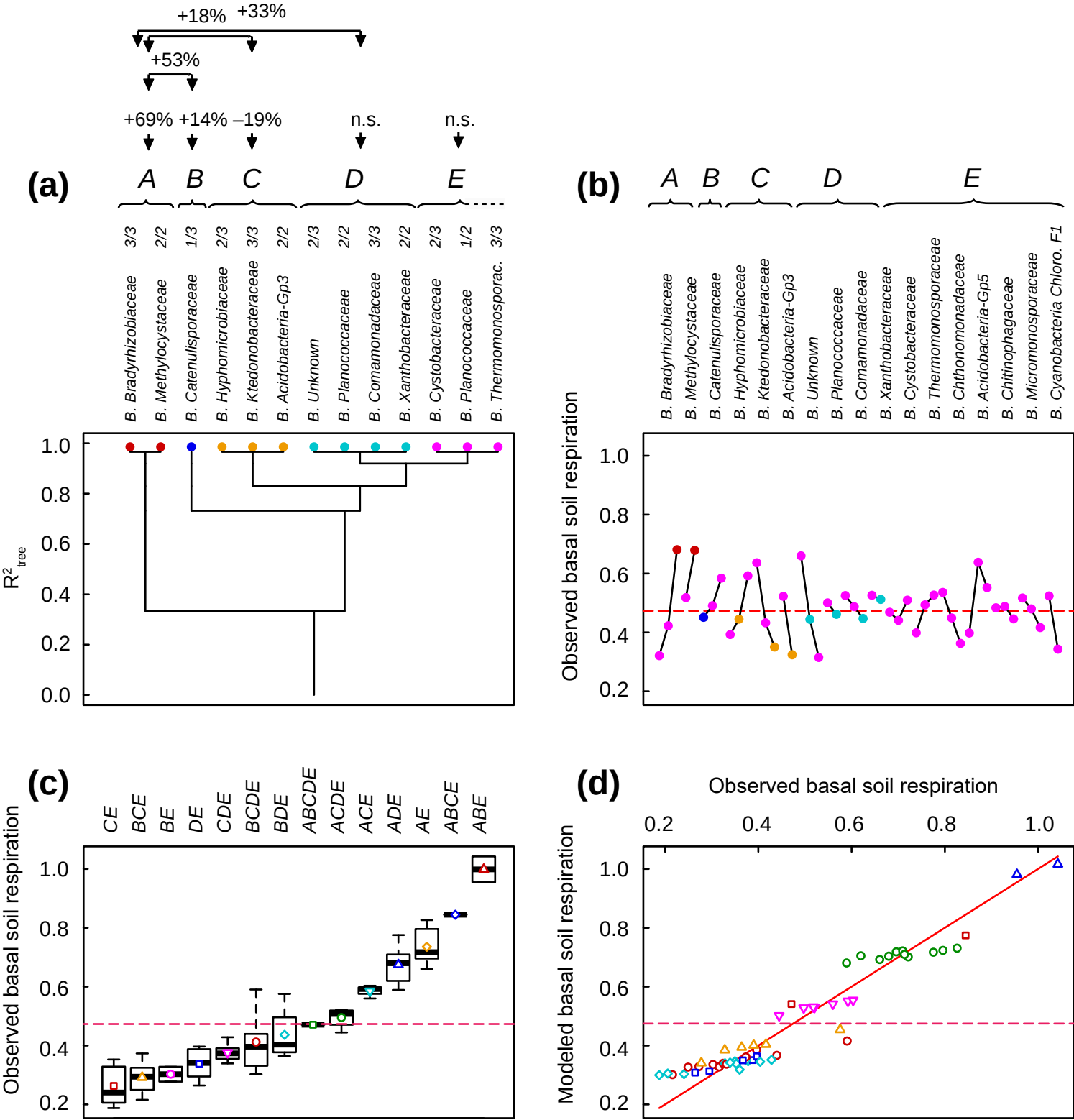


Figure S3. Clustering analysis of basal soil respiration after seven days of incubation, explained by the relative abundance classes of bacterial families in soil. **(a)** Clustering tree of classes of family relative abundance. The functional groups, and the classes of family relative abundance inside each functional group, are sorted from left to right by decreasing effect on the basal soil respiration. Each functional group has a color attributed: red for A, dark blue for B, yellow for C, light blue for D, and pink for E. The above box reports the significant effects (at $p < 0.001$) of the different functional groups and their interactions. **(b)** Mean observed basal soil respiration of soils containing a given class of family relative abundance. The linked points correspond to the different classes of increasing relative abundance (from left to right) for each family. The used symbols are the same as those used in **(a)**. **(c)** Boxplots of the observed basal soil respiration sorted by assembly motifs, i.e., combinations of functional groups. The used symbols are the same as those used in **(b)**. **(d)** Modeled versus observed soil property. Different symbols correspond to different assembly motifs, i.e., combinations of functional groups. The red line is the bisector. **(b)**, **(c)** and **(d)** The dotted line is the mean observed basal soil respiration.

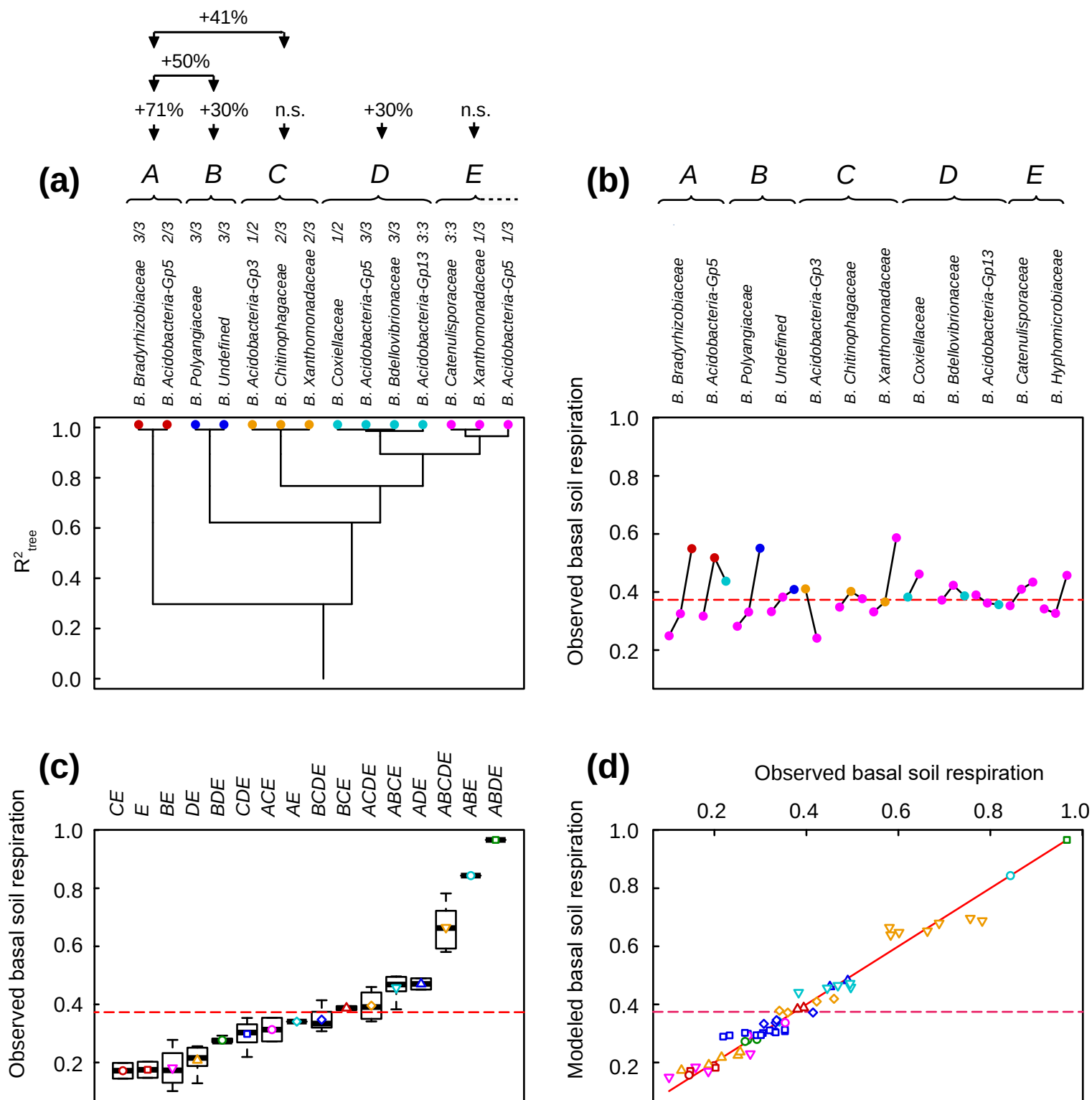


Figure S4. Clustering analysis of basal soil respiration after 42 days of incubation, explained by the relative abundance classes of bacterial families in soil. **(a)** Clustering tree of classes of family relative abundance. The functional groups, and the classes of family relative abundance inside each functional group, are sorted from left to right by decreasing effect on the basal soil respiration. Each functional group has a color attributed: red for A, dark blue for B, yellow for C, light blue for D, and pink for E. The above box reports the significant effects (at $p < 0.001$) of the different functional groups and their interactions. **(b)** Mean observed basal soil respiration of soils containing a given class of family relative abundance. The linked points correspond to the different classes of increasing relative abundance (from left to right) for each family. The used symbols are the same as those used in **(a)**. **(c)** Boxplots of the observed basal soil respiration sorted by assembly motifs, i.e., combinations of functional groups. The used symbols are the same as those used in **(b)**. **(d)** Modeled versus observed basal soil respiration. Different symbols correspond to different assembly motifs, i.e., combinations of functional groups. The red line is the bisector. **(b)**, **(c)** and **(d)** The dotted line is the mean observed basal soil respiration.

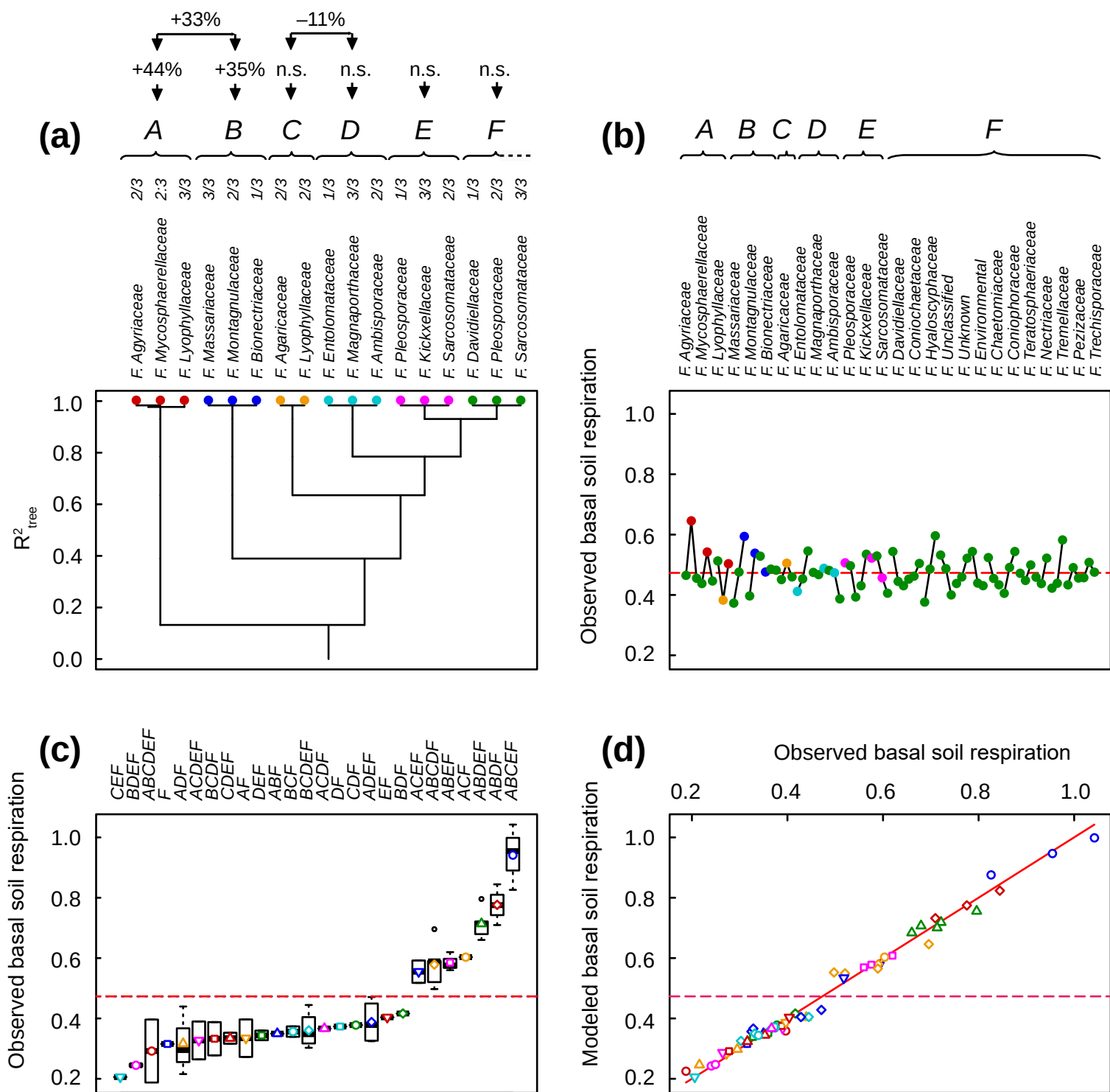


Figure S5. Clustering analysis of basal soil respiration after seven days of incubation, explained by the relative abundance classes of fungal families in soil. **(a)** Clustering tree of classes of family relative abundance. The functional groups, and the classes of family relative abundance inside each functional group, are sorted from left to right by decreasing effect on the basal soil respiration. Each functional group has a color attributed: red for A, dark blue for B, yellow for C, light blue for D, pink for E, and green for F. The above box reports the significant effects (at $p < 0.001$) of the different functional groups and their interactions. **(b)** Mean observed basal soil respiration of soils containing a given class of family relative abundance. The linked points correspond to the different classes of increasing relative abundance (from left to right) for each family. The used symbols are the same as those used in (a). **(c)** Boxplots of the observed basal soil respiration sorted by assembly motifs, i.e., combinations of functional groups. The used symbols are the same as those used in (b). **(d)** Modeled versus observed basal soil respiration. Different symbols correspond to different assembly motifs, i.e., combinations of functional groups. The red line is the bisector. (b), (c) and (d) The dotted line is the mean observed basal soil respiration.

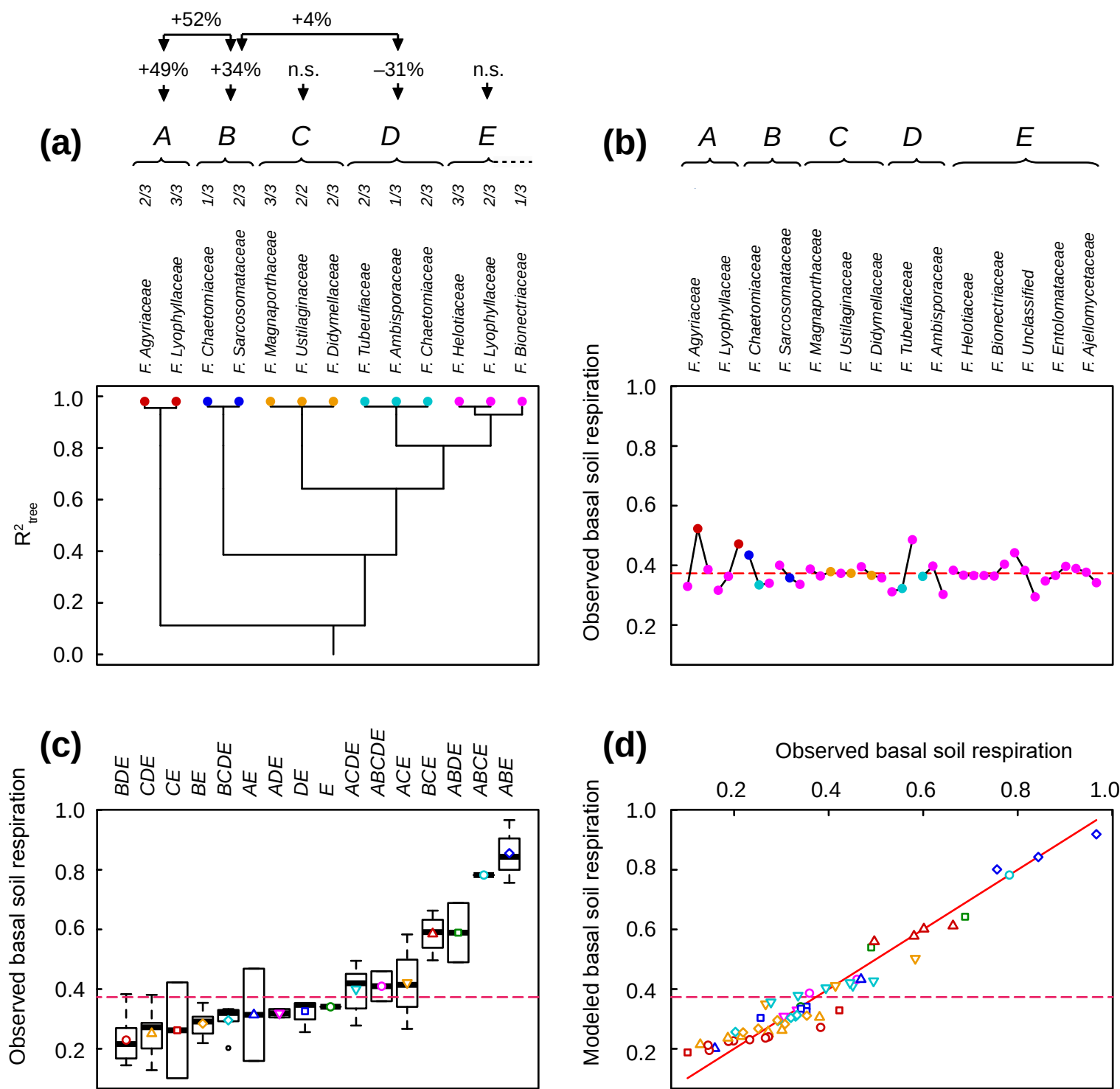


Figure S6. Clustering analysis of basal soil respiration after 42 days of incubation, explained by the relative abundance classes of fungal families in soil. **(a)** Clustering tree of classes of family relative abundance. The functional groups, and the classes of family relative abundance inside each functional group, are sorted from left to right by decreasing effect on the basal soil respiration. Each functional group has a color attributed: red for A, dark blue for B, yellow for C, light blue for D, and pink for E. The above box reports the significant effects (at $p < 0.001$) of the different functional groups and their interactions. **(b)** Mean observed basal soil respiration of soils containing a given class of family relative abundance. The linked points correspond to the different classes of increasing relative abundance (from left to right) for each family. The used symbols are the same as those used in (a). **(c)** Boxplots of the observed basal soil respiration sorted by assembly motifs, i.e., combinations of functional groups. The used symbols are the same as those used in (b). **(d)** Modeled versus observed soil property. Different symbols correspond to different assembly motifs, i.e., combinations of functional groups. The red line is the bisector. (b), (c) and (d) The dotted line is the mean observed basal soil respiration.

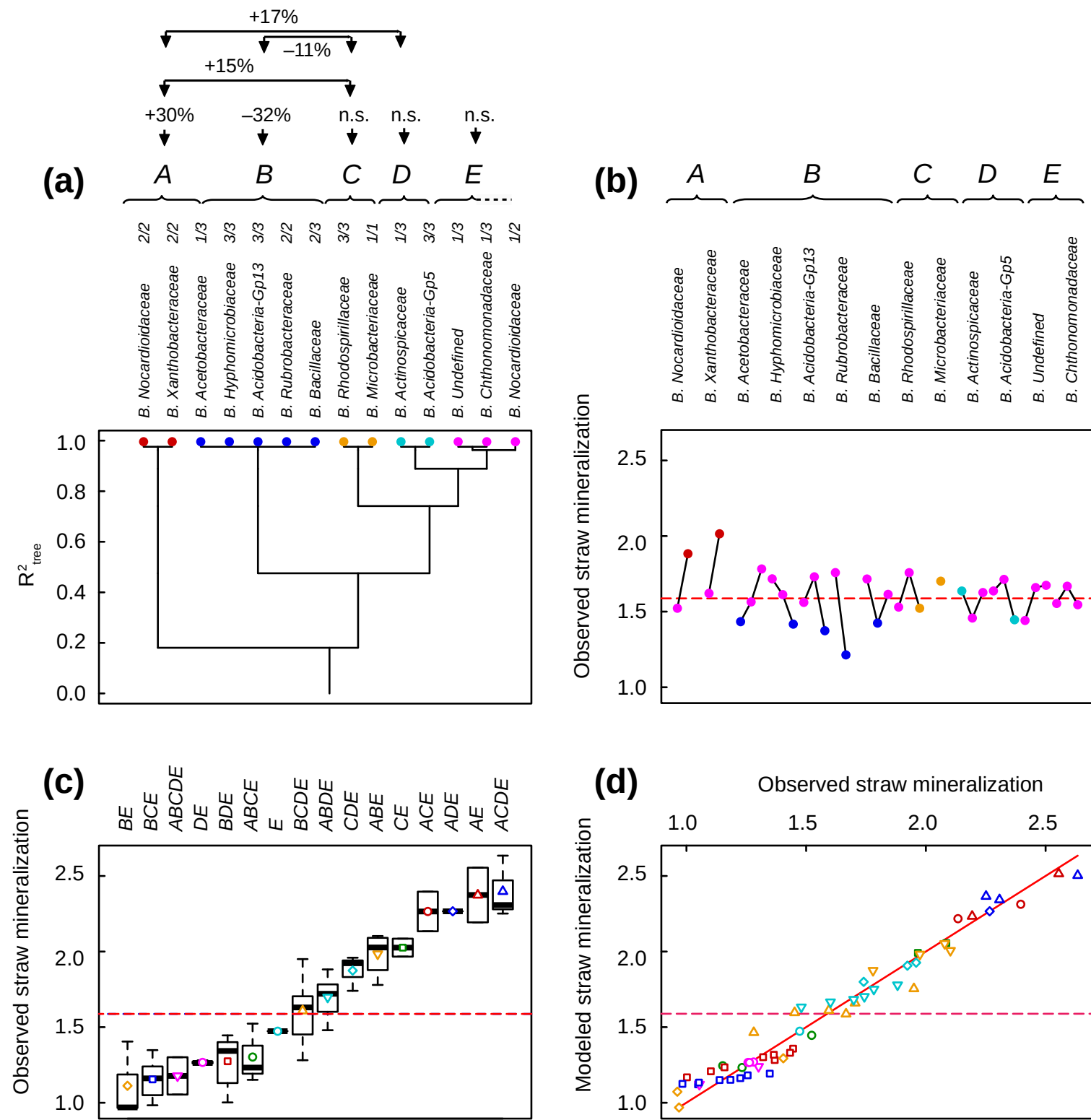


Figure S7. Clustering analysis of straw mineralization after seven days of incubation, explained by the relative abundance classes of bacterial families in soil. **(a)** Clustering tree of classes of family relative abundance. The functional groups, and the classes of family relative abundance inside each functional group, are sorted from left to right by decreasing effect on the straw mineralization. Each functional group has a color attributed: red for A, dark blue for B, yellow for C, light blue for D, and pink for E. The above box reports the significant effects (at $p < 0.001$) of the different functional groups and their interactions. **(b)** Mean observed straw mineralization of soils containing a given class of family relative abundance. The linked points correspond to the different classes of increasing relative abundance (from left to right) for each family. The used symbols are the same as those used in **(a)**. **(c)** Boxplots of the observed straw mineralization sorted by assembly motifs, i.e., combinations of functional groups. The used symbols are the same as those used in **(b)**. **(d)** Modeled versus observed straw mineralization. Different symbols correspond to different assembly motifs, i.e., combinations of functional groups. The red line is the bisector. **(b)**, **(c)** and **(d)** The dotted line is the mean observed straw mineralization.

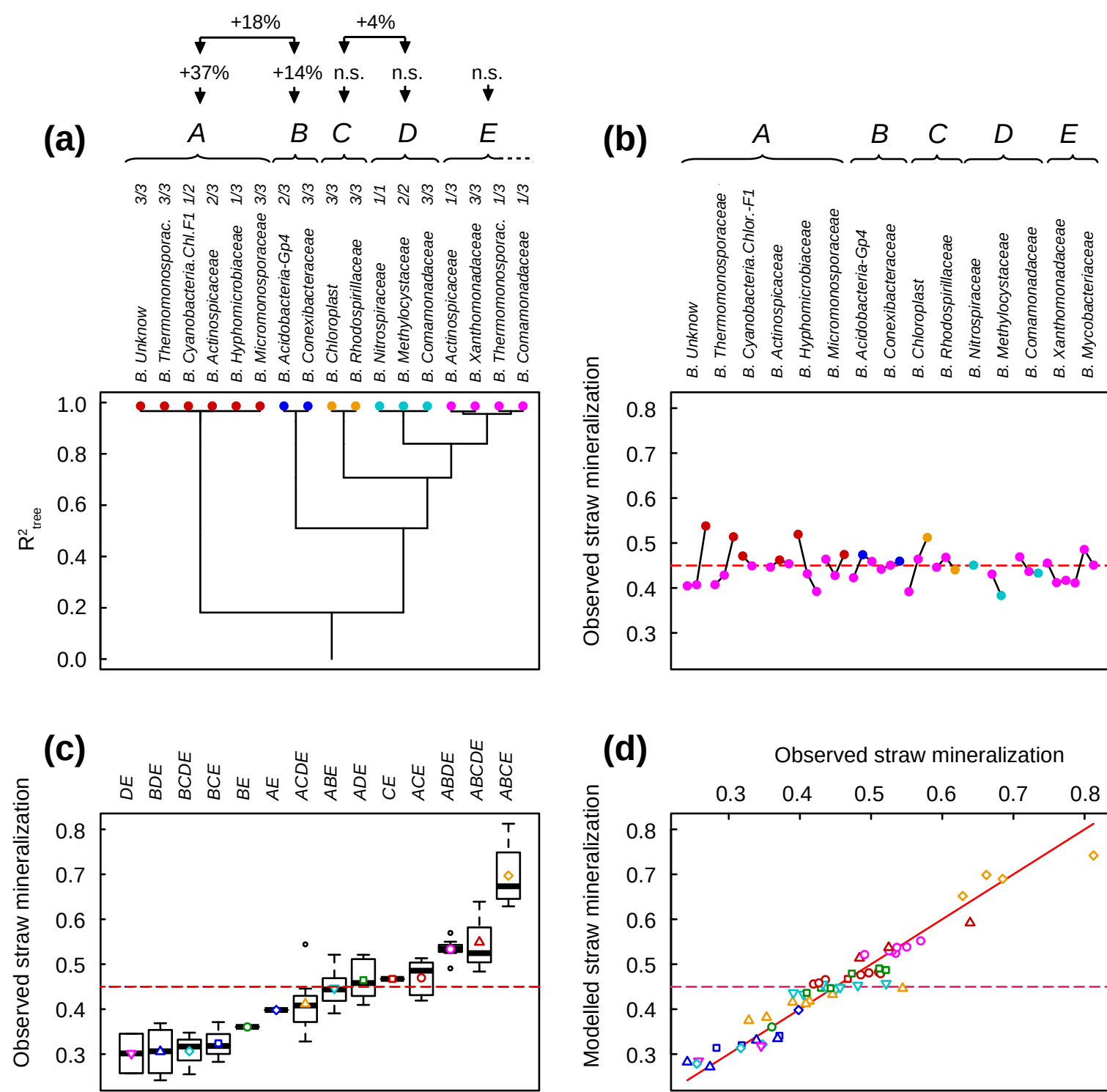


Figure S8. Clustering analysis of straw mineralization after 42 days of incubation, explained by the relative abundance classes of bacterial families in soil. **(a)** Clustering tree of classes of family relative abundance. The functional groups, and the classes of family relative abundance inside each functional group, are sorted from left to right by decreasing effect on the straw mineralization. Each functional group has a color attributed: red for A, dark blue for B, yellow for C, light blue for D, and pink for E. The above box reports the significant effects (at $p < 0.001$) of the different functional groups and their interactions. **(b)** Mean observed straw mineralization of soils containing a given class of family relative abundance. The linked points correspond to the different classes of increasing relative abundance (from left to right) for each family. The used symbols are the same as those used in **(a)**. **(c)** Boxplots of the observed straw mineralization sorted by assembly motifs, i.e., combinations of functional groups. The used symbols are the same as those used in **(b)**. **(d)** Modeled versus observed straw mineralization. Different symbols correspond to different assembly motifs, i.e., combinations of functional groups. The red line is the bisector. **(b)**, **(c)** and **(d)** The dotted line is the mean observed straw mineralization.

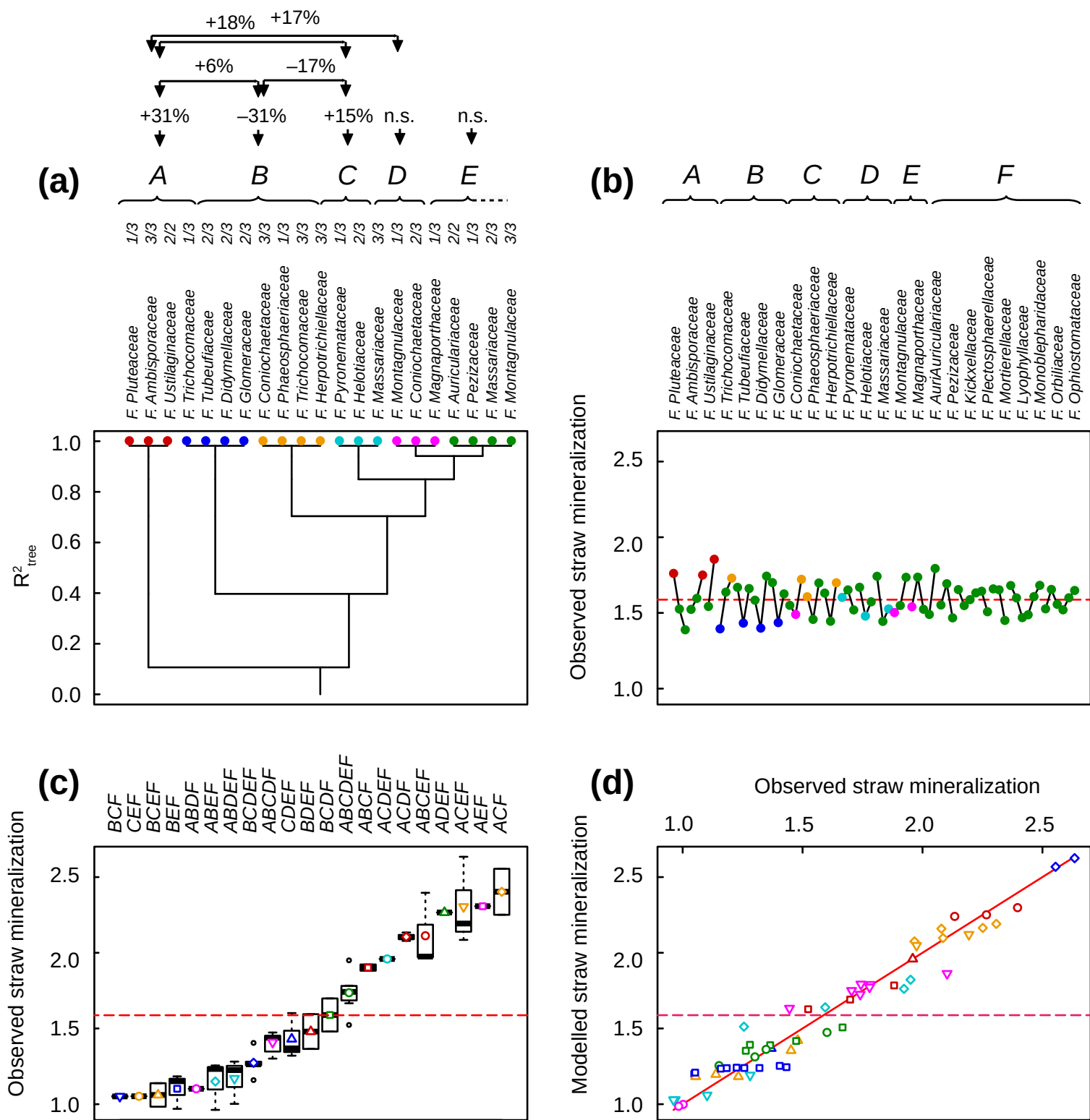


Figure S9. Clustering analysis of straw mineralization after seven days of incubation, explained by the relative abundance classes of fungal families in soil. **(a)** Clustering tree of classes of family relative abundance. The functional groups, and the classes of family relative abundance inside each functional group, are sorted from left to right by decreasing effect on the straw mineralization. Each functional group has a color attributed: red for A, dark blue for B, yellow for C, light blue for D, pink for E, and green for F. The above box reports the significant effects (at $p < 0.001$) of the different functional groups and their interactions. **(b)** Mean observed straw mineralization of soils containing a given class of family relative abundance. The linked points correspond to the different classes of increasing relative abundance (from left to right) for each family. The used symbols are the same as those used in **(a)**. **(c)** Boxplots of the observed straw mineralization sorted by assembly motifs, i.e., combinations of functional groups. The used symbols are the same as those used in **(b)**. **(d)** Modeled versus observed straw mineralization. Different symbols correspond to different assembly motifs, i.e., combinations of functional groups. The red line is the bisector. **(b)**, **(c)** and **(d)** The dotted line is the mean observed straw mineralization.

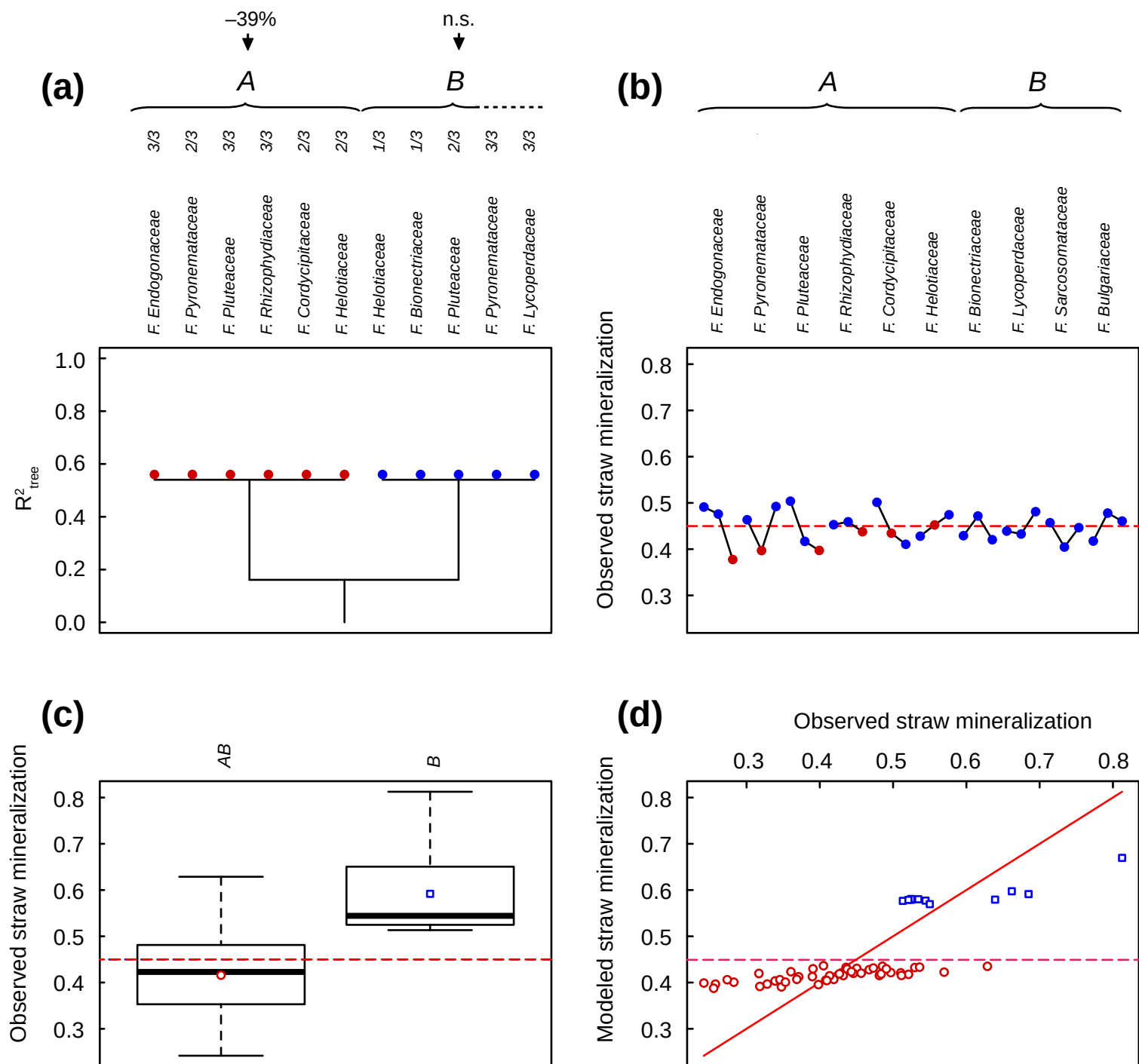


Figure S10. Clustering analysis of straw mineralization after 42 days of incubation, explained by the relative abundance classes of fungal families in soil. **(a)** Clustering tree of classes of family relative abundance. The functional groups, and the classes of family relative abundance inside each functional group, are sorted from left to right by decreasing effect on the straw mineralization. Each functional group has a color attributed: red for A, and dark blue for B. The above box reports the significant effects (at $p < 0.001$) of the different functional groups and their interactions. **(b)** Mean observed straw mineralization of soils containing a given class of family relative abundance. The linked points correspond to the different classes of increasing relative abundance (from left to right) for each family. The used symbols are the same as those used in **(a)**. **(c)** Boxplots of the observed straw mineralization sorted by assembly motifs, i.e., combinations of functional groups. The used symbols are the same as those used in **(b)**. **(d)** Modeled versus observed straw mineralization. Different symbols correspond to different assembly motifs, i.e., combinations of functional groups. The red line is the bisector. **(b)**, **(c)** and **(d)** The dotted line is the mean observed straw mineralization.

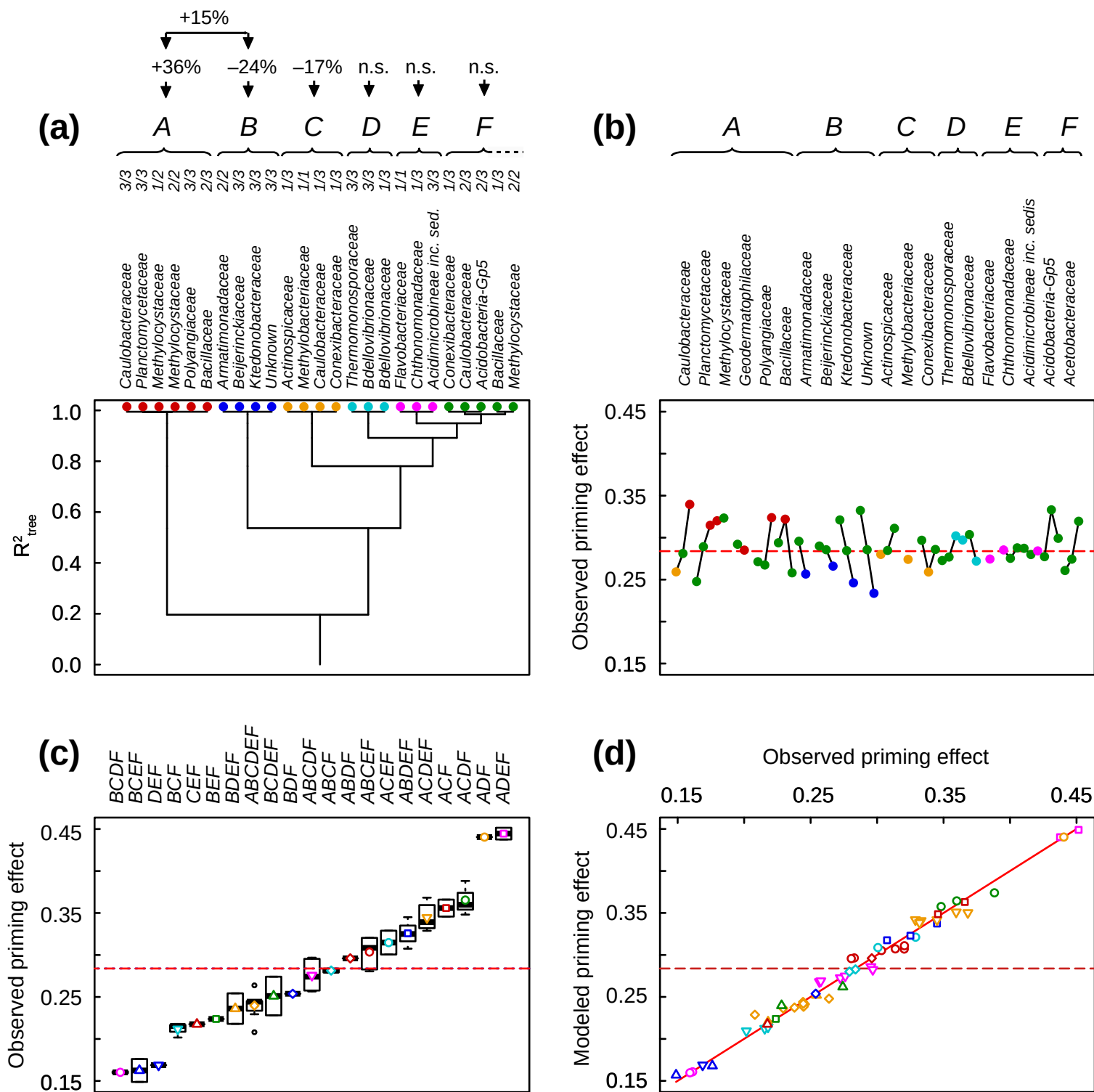


Figure S11. Clustering analysis of the priming effect after seven days of incubation, explained by the relative abundance classes of bacterial families in soil. **(a)** Clustering tree of classes of family relative abundance. The functional groups, and the classes of family relative abundance inside each functional group, are sorted from left to right by decreasing effect on the priming effect. Each functional group has a color attributed: red for A, dark blue for B, yellow for C, light blue for D, pink for E, and green for F. The above box reports the significant effects (at $p < 0.001$) of the different functional groups and their interactions. **(b)** Mean observed priming effect of soils containing a given class of family relative abundance. The linked points correspond to the different classes of increasing relative abundance (from left to right) for each family. The used symbols are the same as those used in **(a)**. **(c)** Boxplots of the observed priming effect sorted by assembly motifs, i.e., combinations of functional groups. The used symbols are the same as those used in **(b)**. **(d)** Modeled versus observed priming effect. Different symbols correspond to different assembly motifs, i.e., combinations of functional groups. The red line is the bisector. **(b)**, **(c)** and **(d)** The dotted line is the mean observed priming effect.

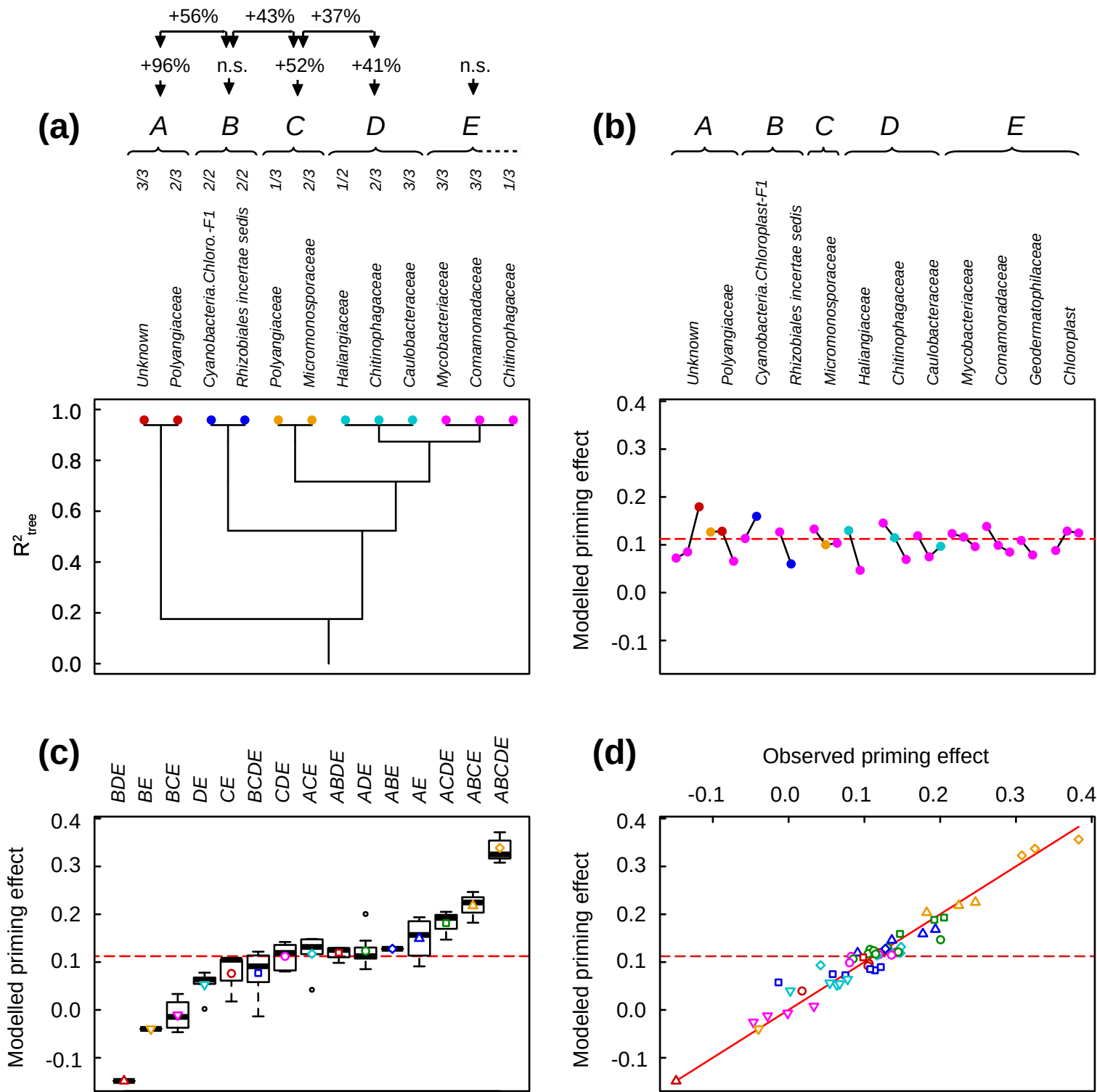


Figure S12. Clustering analysis of the priming effect after 42 days of incubation, explained by the relative abundance classes of bacterial families in soil. **(a)** Clustering tree of classes of family relative abundance. The functional groups, and the classes of family relative abundance inside each functional group, are sorted from left to right by decreasing effect on the priming effect. Each functional group has a color attributed: red for A, dark blue for B, yellow for C, light blue for D, and pink for E. The above box reports the significant effects (at $p < 0.001$) of the different functional groups and their interactions. **(b)** Mean observed priming effect of soils containing a given class of family relative abundance. The linked points correspond to the different classes of increasing relative abundance (from left to right) for each family. The used symbols are the same as those used in (a). **(c)** Boxplots of the observed priming effect sorted by assembly motifs, i.e., combinations of functional groups. The used symbols are the same as those used in (b). **(d)** Modeled versus observed priming effect. Different symbols correspond to different assembly motifs, i.e., combinations of functional groups. The red line is the bisector. **(b), (c)** and **(d)** The dotted line is the mean observed priming effect.

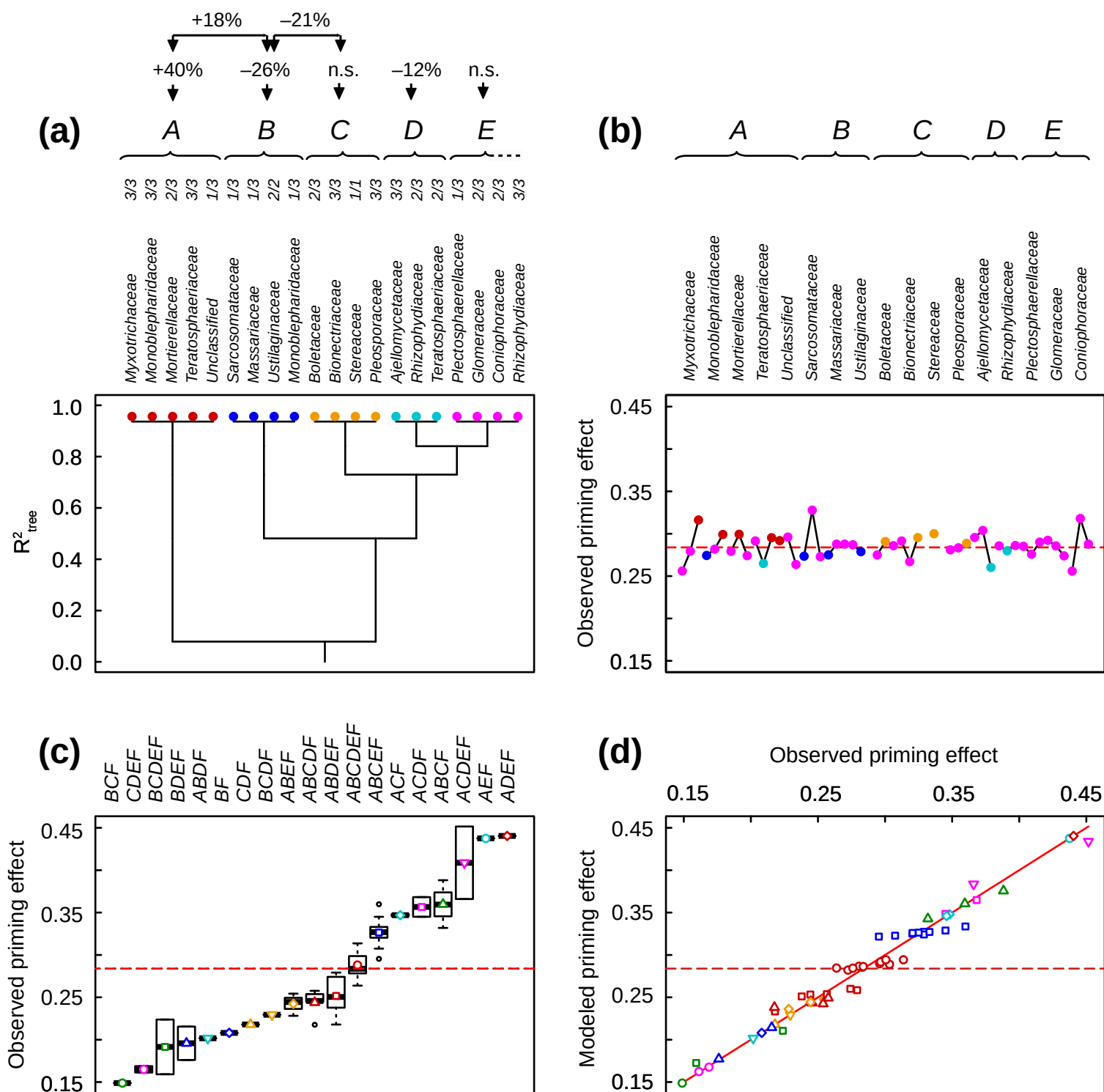


Figure S13. Clustering analysis of the priming effect after seven days of incubation, explained by the relative abundance classes of fungal families in soil. **(a)** Clustering tree of classes of family relative abundance. The functional groups, and the classes of family relative abundance inside each functional group, are sorted from left to right by decreasing effect on the priming effect. Each functional group has a color attributed: red for A, dark blue for B, yellow for C, light blue for D, and pink for E. The above box reports the significant effects (at $p < 0.001$) of the different functional groups and their interactions. **(b)** Mean observed priming effect of soils containing a given class of family relative abundance. The linked points correspond to the different classes of increasing relative abundance (from left to right) for each family. The used symbols are the same as those used in (a). **(c)** Boxplots of the observed priming effect sorted by assembly motifs, i.e., combinations of functional groups. The used symbols are the same as those used in (b). **(d)** Modeled versus observed priming effect. Different symbols correspond to different assembly motifs, i.e., combinations of functional groups. The red line is the bisector. **(b), (c)** and **(d)** The dotted line is the mean observed priming effect.

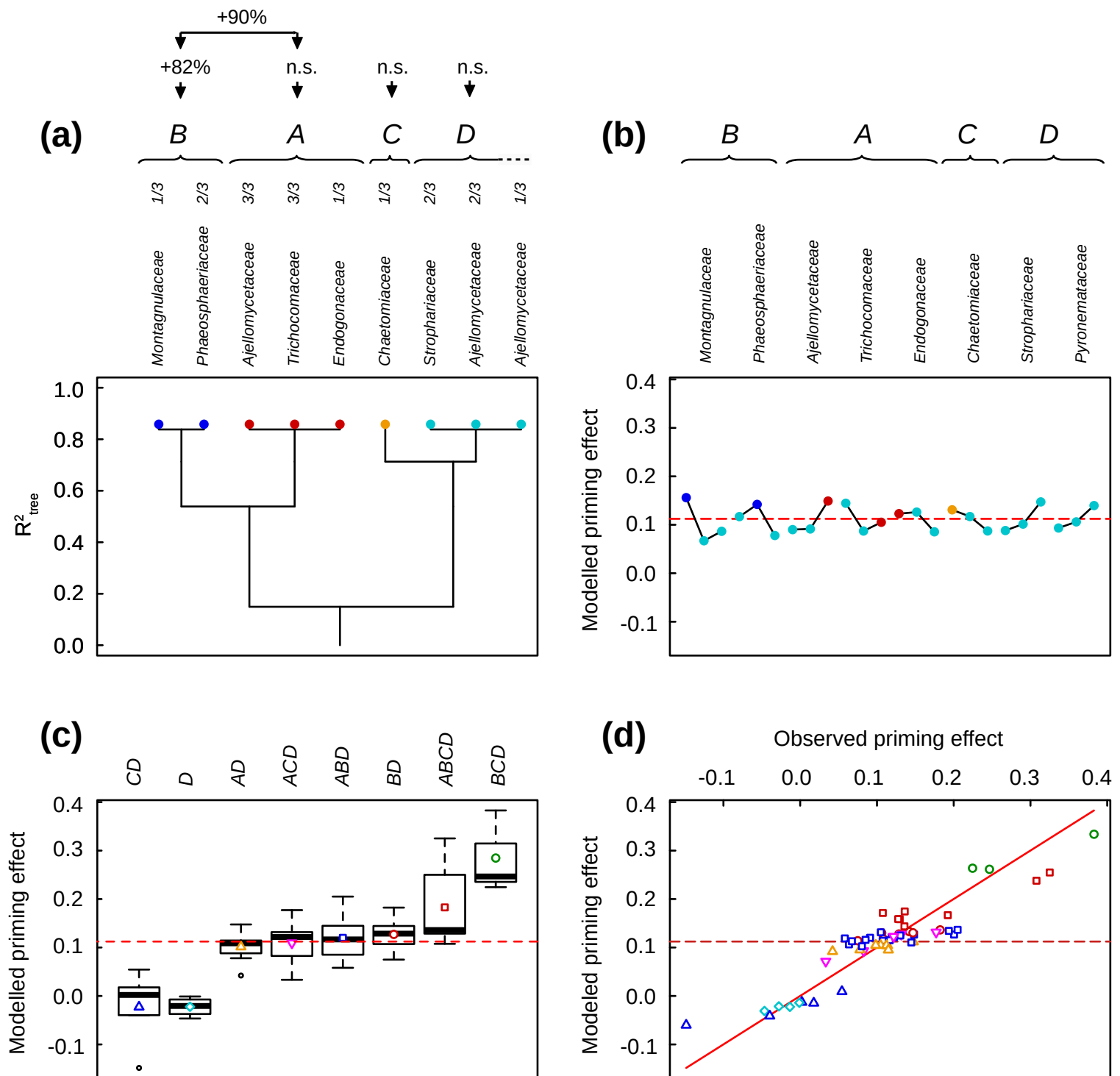


Figure S14. Clustering analysis of the priming effect after 42 days of incubation, explained by the relative abundance classes of fungal families in soil. **(a)** Clustering tree of classes of family relative abundance. The functional groups, and the classes of family relative abundance inside each functional group, are sorted from left to right by decreasing effect on the priming effect. Each functional group has a color attributed: red for A, dark blue for B, yellow for C, and light blue for D. The above box reports the significant effects (at $p < 0.001$) of the different functional groups and their interactions. **(b)** Mean observed priming effect of soils containing a given class of family relative abundance. The linked points correspond to the different classes of increasing relative abundance (from left to right) for each family. The used symbols are the same as those used in **(a)**. **(c)** Boxplots of the observed priming effect sorted by assembly motifs, i.e., combinations of functional groups. The used symbols are the same as those used in **(b)**. **(d)** Modeled versus observed priming effect. Different symbols correspond to different assembly motifs, i.e., combinations of functional groups. The red line is the bisector. **(b)**, **(c)** and **(d)** The dotted line is the mean observed priming effect.

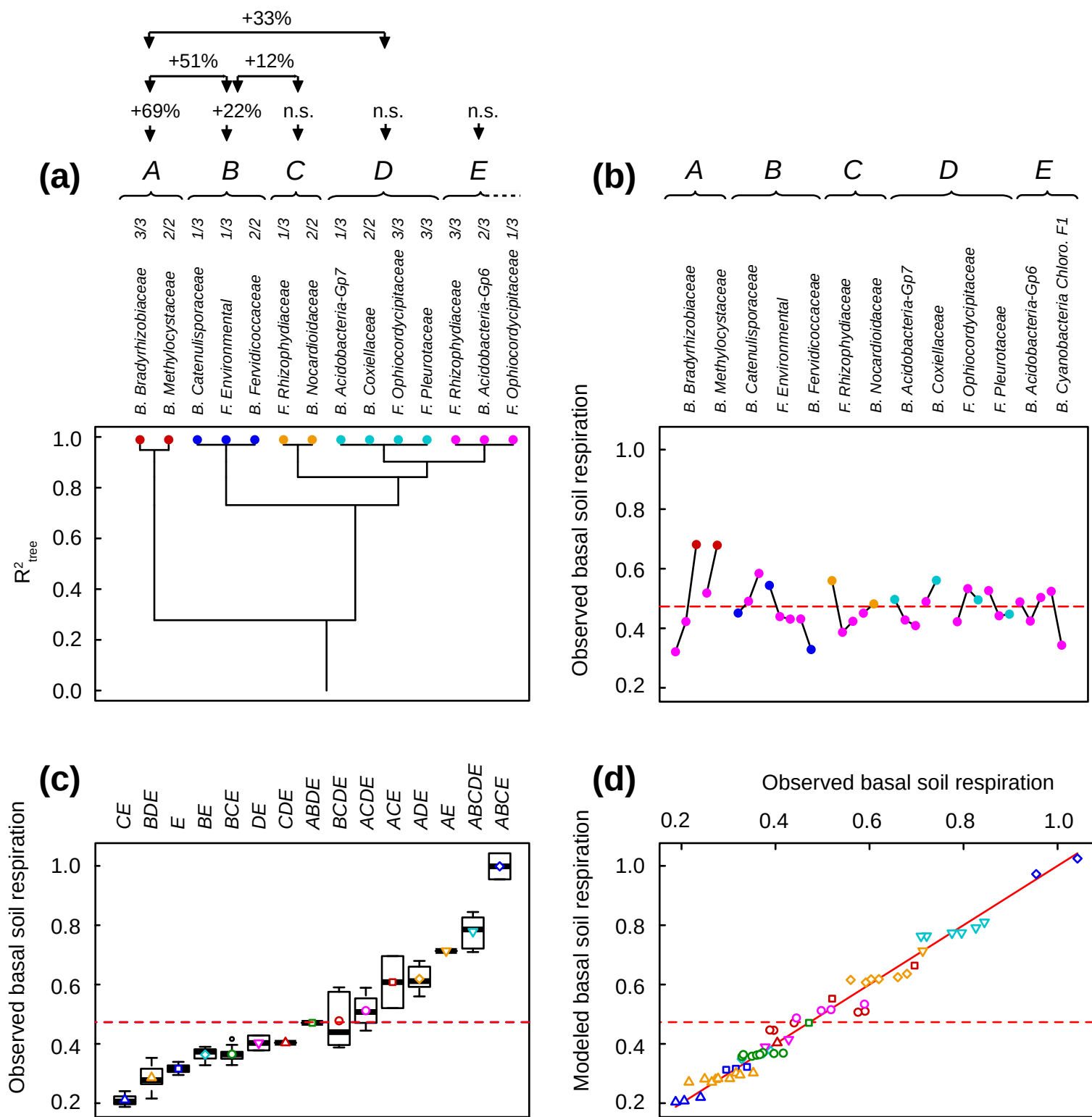


Figure S15. Clustering analysis of basal soil respiration after seven days of incubation, explained by the relative abundance classes of bacterial and fungal families together in soil. **(a)** Clustering tree of classes of family relative abundance. The functional groups, and the classes of family relative abundance inside each functional group, are sorted from left to right by decreasing effect on the basal soil respiration. Each functional group has a color attributed: red for A, dark blue for B, yellow for C, light blue for D, and pink for E. The above box reports the significant effects (at $p < 0.001$) of the different functional groups and their interactions. **(b)** Mean observed basal soil respiration of soils containing a given class of family relative abundance. The linked points correspond to the different classes of increasing relative abundance (from left to right) for each family. The used symbols are the same as those used in **(a)**. **(c)** Boxplots of the observed basal soil respiration sorted by assembly motifs, i.e., combinations of functional groups. The used symbols are the same as those used in **(b)**. **(d)** Modeled versus observed basal soil respiration. Different symbols correspond to different assembly motifs, i.e., combinations of functional groups. The red line is the bisector. **(b)**, **(c)** and **(d)** The dotted line is the mean observed basal soil respiration.

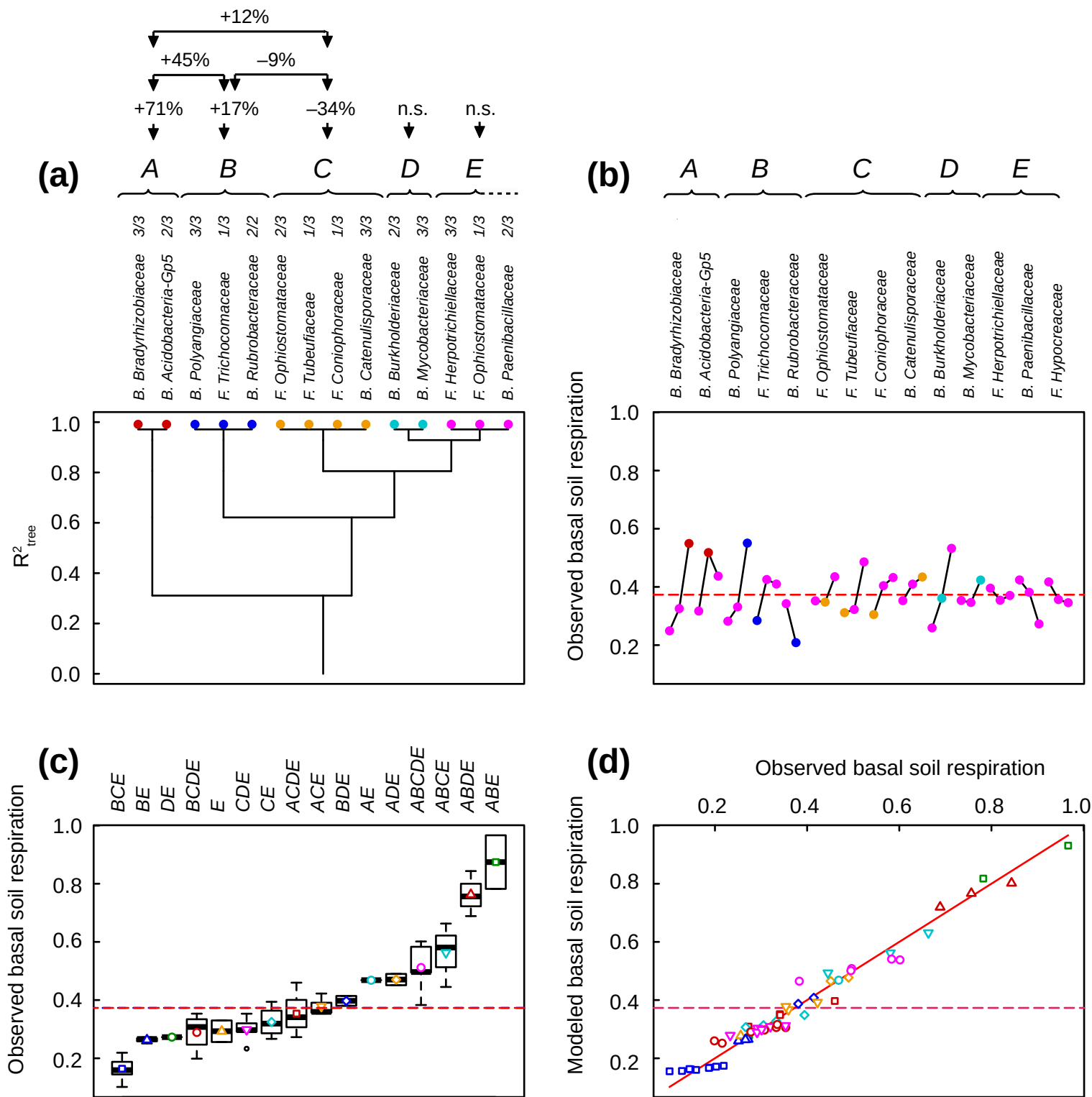


Figure S16. Clustering analysis of basal soil respiration after 42 days of incubation, explained by the relative abundance classes of bacterial and fungal families together in soil. **(a)** Clustering tree of classes of family relative abundance. The functional groups, and the classes of family relative abundance inside each functional group, are sorted from left to right by decreasing effect on the basal soil respiration. Each functional group has a color attributed: red for A, dark blue for B, yellow for C, light blue for D, and pink for E. The above box reports the significant effects (at $p < 0.001$) of the different functional groups and their interactions. **(b)** Mean observed property of soils containing a given class of family relative abundance. The linked points correspond to the different classes of increasing relative abundance (from left to right) for each family. The used symbols are the same as those used in (a). **(c)** Boxplots of the observed basal soil respiration sorted by assembly motifs, i.e., combinations of functional groups. The used symbols are the same as those used in (b). **(d)** Modeled versus observed basal soil respiration. Different symbols correspond to different assembly motifs, i.e., combinations of functional groups. The red line is the bisector. **(b)**, **(c)** and **(d)** The dotted line is the mean observed basal soil respiration.

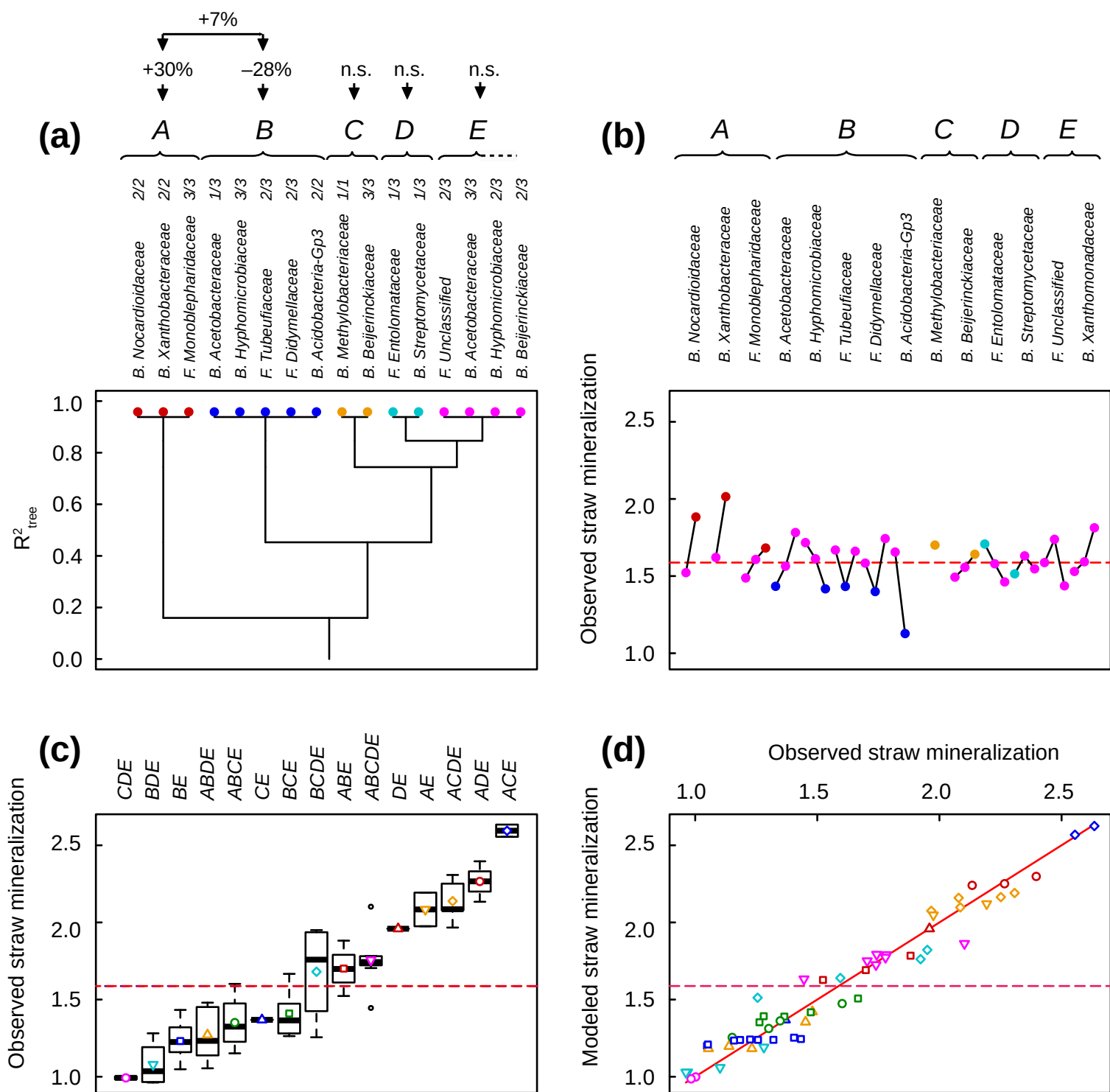


Figure S17. Clustering analysis of straw mineralization after seven days of incubation, explained by the relative abundance classes of bacterial and fungal families together in soil. **(a)** Clustering tree of classes of family relative abundance. The functional groups, and the classes of family relative abundance inside each functional group, are sorted from left to right by decreasing effect on the straw mineralization. Each functional group has a color attributed: red for A, dark blue for B, yellow for C, light blue for D, and pink for E. The above box reports the significant effects (at $p < 0.001$) of the different functional groups and their interactions. **(b)** Mean observed straw mineralization of soils containing a given class of family relative abundance. The linked points correspond to the different classes of increasing relative abundance (from left to right) for each family. The used symbols are the same as those used in **(a)**. **(c)** Boxplots of the observed straw mineralization sorted by assembly motifs, i.e., combinations of functional groups. The used symbols are the same as those used in **(b)**. **(d)** Modeled versus observed straw mineralization. Different symbols correspond to different assembly motifs, i.e., combinations of functional groups. The red line is the bisector. **(b)**, **(c)** and **(d)** The dotted line is the mean observed straw mineralization.

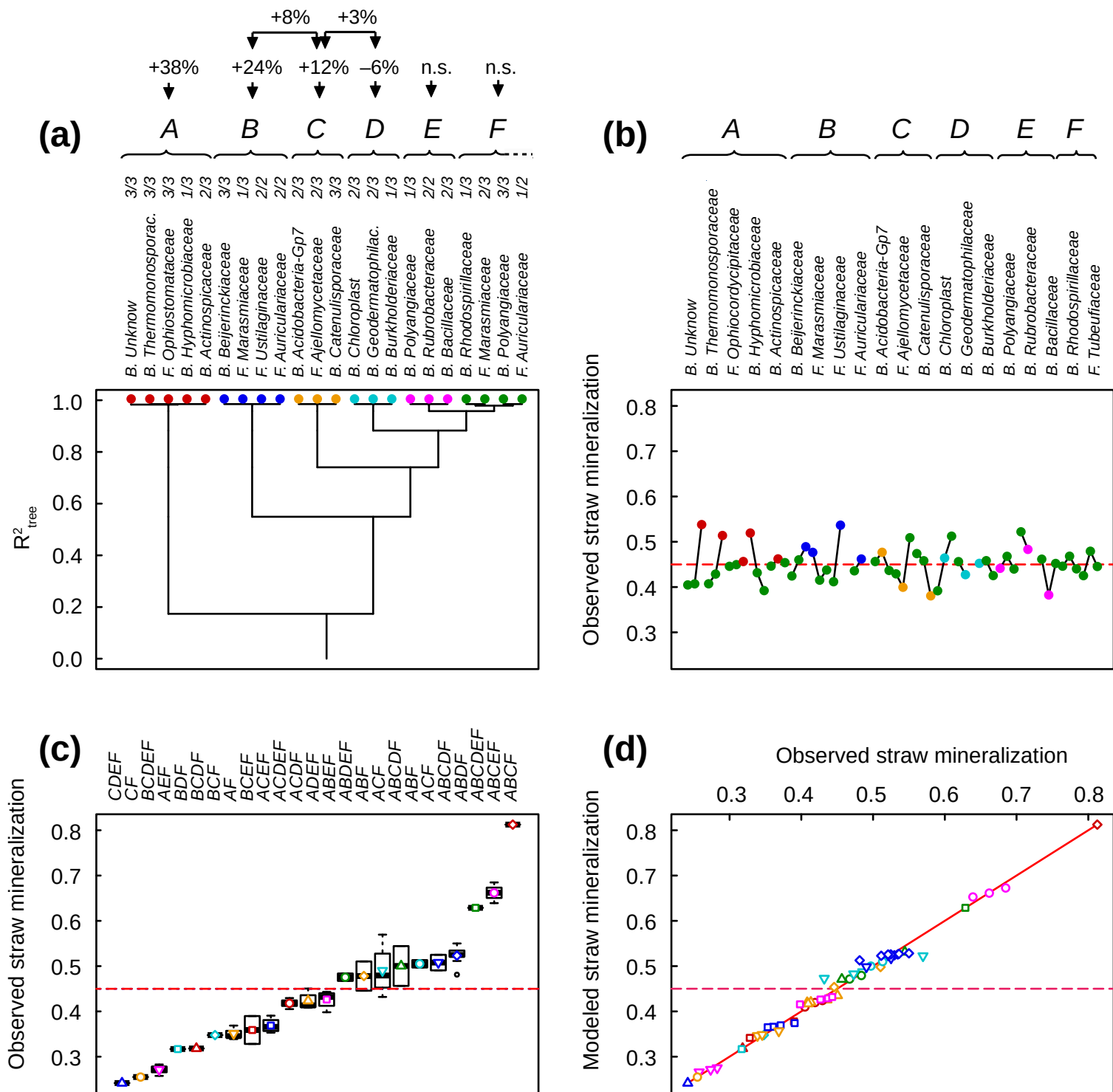


Figure S18. Clustering analysis of straw mineralization after 42 days of incubation, explained by the relative abundance classes of bacterial and fungal families together in soil. **(a)** Clustering tree of classes of family relative abundance. The functional groups, and the classes of family relative abundance inside each functional group, are sorted from left to right by decreasing effect on the straw mineralization. Each functional group has a color attributed: red for A, dark blue for B, yellow for C, light blue for D, pink for E, and green for F. The above box reports the significant effects (at $p < 0.001$) of the different functional groups and their interactions. **(b)** Mean observed straw mineralization of soils containing a given class of family relative abundance. The linked points correspond to the different classes of increasing relative abundance (from left to right) for each family. The used symbols are the same as those used in (a). **(c)** Boxplots of the observed straw mineralization sorted by assembly motifs, i.e., combinations of functional groups. The used symbols are the same as those used in (b). **(d)** Modeled versus observed straw mineralization. Different symbols correspond to different assembly motifs, i.e., combinations of functional groups. The red line is the bisector. **(b)**, **(c)** and **(d)** The dotted line is the mean observed straw mineralization.

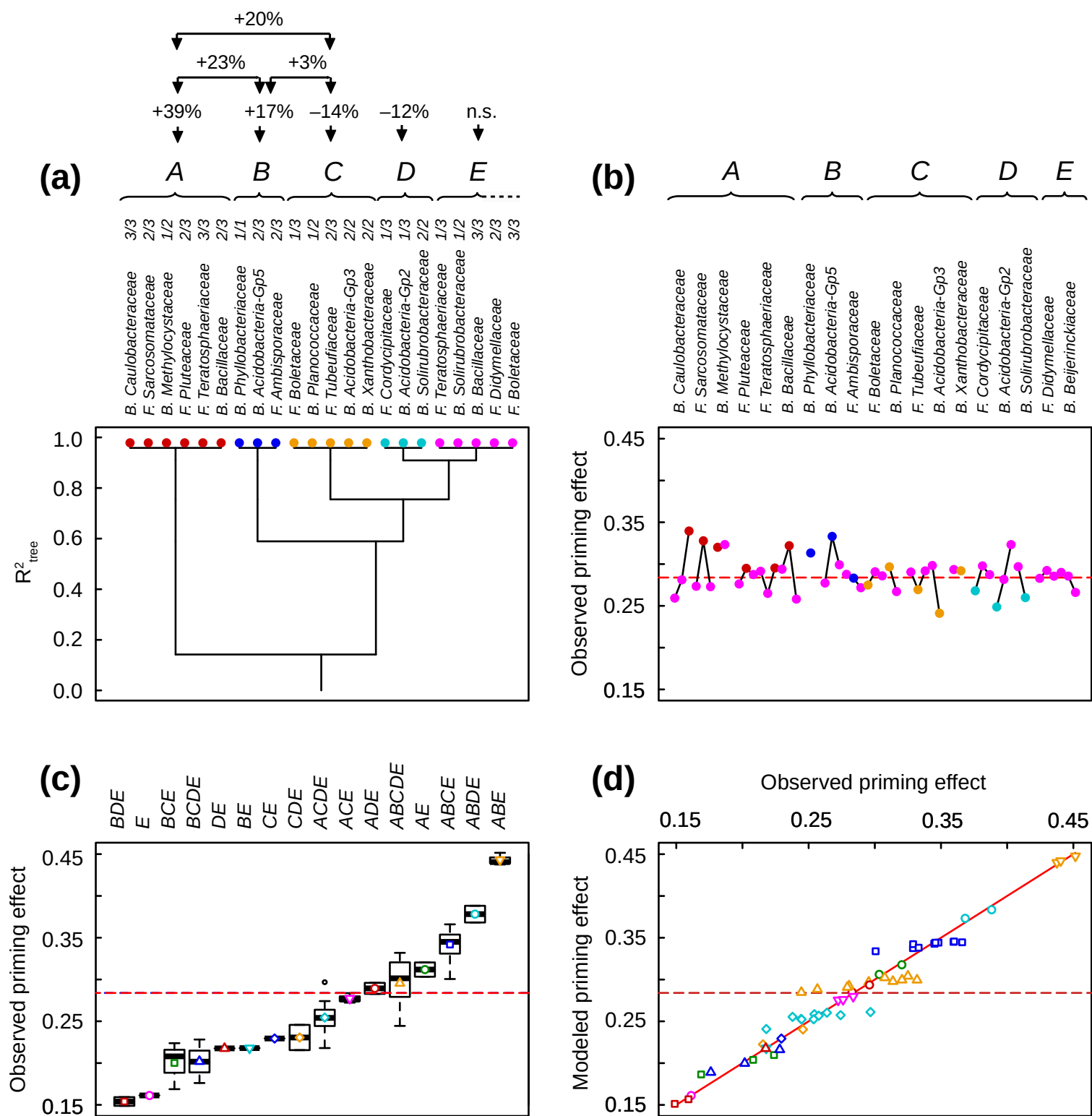


Figure S19. Clustering analysis of the priming effect after seven days of incubation, explained by the relative abundance classes of bacterial and fungal families together in soil. **(a)** Clustering tree of classes of family relative abundance. The functional groups, and the classes of family relative abundance inside each functional group, are sorted from left to right by decreasing effect on the priming effect. Each functional group has a color attributed: red for A, dark blue for B, yellow for C, light blue for D, and pink for E. The above box reports the significant effects (at $p < 0.001$) of the different functional groups and their interactions. **(b)** Mean observed priming effect of soils containing a given class of family relative abundance. The linked points correspond to the different classes of increasing relative abundance (from left to right) for each family. The used symbols are the same as those used in **(a)**. **(c)** Boxplots of the observed priming effect sorted by assembly motifs, i.e., combinations of functional groups. The used symbols are the same as those used in **(b)**. **(d)** Modeled versus observed priming effect. Different symbols correspond to different assembly motifs, i.e., combinations of functional groups. The red line is the bisector. **(b)**, **(c)** and **(d)** The dotted line is the mean observed priming effect.

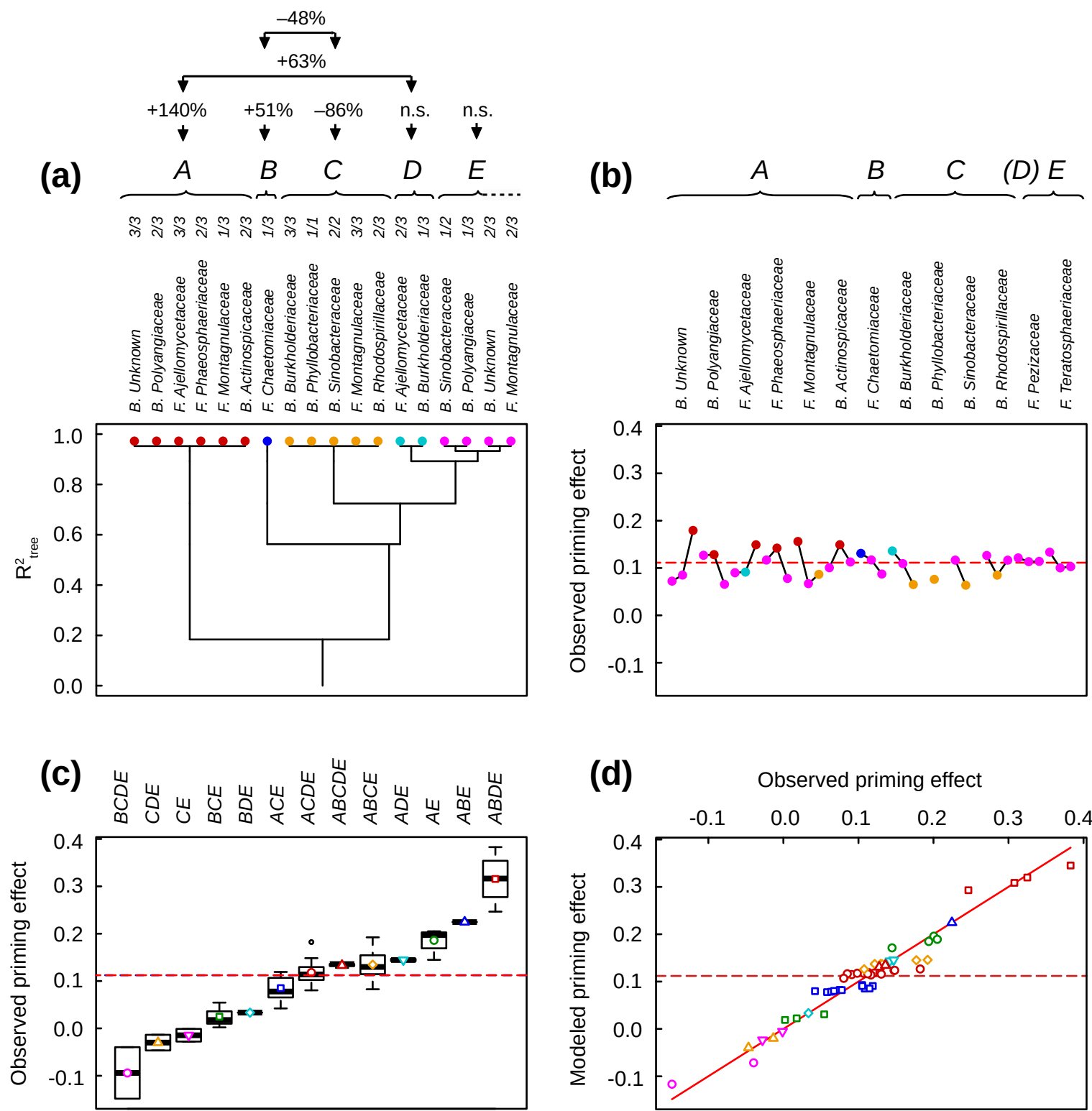


Figure S20. Clustering analysis of the priming effect after 42 days of incubation, explained by the relative abundance classes of bacterial and fungal families together in soil. **(a)** Clustering tree of classes of family relative abundance. The functional groups, and the classes of family relative abundance inside each functional group, are sorted from left to right by decreasing effect on the priming effect. Each functional group has a color attributed: red for A, dark blue for B, yellow for C, light blue for D, and pink for E. The above box reports the significant effects (at $p < 0.001$) of the different functional groups and their interactions. **(b)** Mean observed priming effect of soils containing a given class of family relative abundance. The linked points correspond to the different classes of increasing relative abundance (from left to right) for each family. The used symbols are the same as those used in (a). **(c)** Boxplots of the observed priming effect sorted by assembly motifs, i.e., combinations of functional groups. The used symbols are the same as those used in (b). **(d)** Modeled versus observed priming effect. Different symbols correspond to different assembly motifs, i.e., combinations of functional groups. The red line is the bisector. **(b)**, **(c)** and **(d)** The dotted line is the mean observed priming effect.