

Table S1. Mantel test of environmental factors against the relative importance of homogeneous selection and homogenizing dispersal in shaping soil bacterial and fungal community. HoS: homogeneous selection; HD: homogenizing dispersal. SWC: soil water content; ST: soil temperature; TC: total carbon; TN: total nitrogen; TP: total phosphorus; TK: total potassium; AP: available phosphorus; SLO: slope. The significant level is * $p < 0.05$, ** $p < 0.01$.

Environmental factors	Bacterial community		Fungal community	
	HoS	HD	HoS	HD
pH	0.200	0.015	0.141	0.249
SWC	0.153	0.421	-0.353	-0.070
ST	0.400 *	0.602 **	-0.055	0.228
TC	-0.032	0.008	0.390 *	0.082
TN	0.227	-0.120	-0.131	0.078
TP	0.338	0.642 **	0.066	0.535 *
TK	0.081	0.581 **	0.056	0.131
AP	0.382 *	0.497 *	0.471 *	0.499 *
SLO	-0.392	-0.063	-0.127	-0.359

Table S2. The relative abundance of each bin and contribution for all assembly processes in soil bacterial (a) and fungal (b) community. HeS: heterogeneous selection; HoS: homogeneous selection; DL: dispersal limitation; HD: homogenizing dispersal; DR: drift; RA: relative abundance.

(a)						
	HeS	HoS	DL	HD	DR	RA
bin1	Not Found	0.008	Not Found	0.005	0.001	1.84%
bin2	Not Found	0.002	0.009	0.003	0.009	0.88%
bin3	Not Found	0.018	0.007	0.002	0.005	0.98%
bin4	Not Found	0.030	Not Found	0.001	0.001	1.16%
bin5	Not Found	0.002	Not Found	0.003	0.003	1.83%
bin6	Not Found	0.011	Not Found	0.004	Not Found	1.96%
bin7	Not Found	0.019	Not Found	0.001	0.001	3.43%
bin8	Not Found	0.001	0.001	0.001	0.003	1.21%
bin9	Not Found	0.245	Not Found	0.016	0.050	3.12%
bin10	Not Found	0.293	Not Found	0.107	0.021	1.06%
bin11	Not Found	Not Found	Not Found	0.053	0.008	1.31%
bin12	Not Found	0.457	Not Found	0.350	Not Found	1.44%
bin13	Not Found	0.303	Not Found	Not Found	Not Found	1.84%
bin14	Not Found	0.207	Not Found	0.106	Not Found	1.35%
bin15	Not Found	0.015	Not Found	0.015	0.003	3.54%
bin16	Not Found	0.063	Not Found	Not Found	Not Found	1.76%
bin17	Not Found	0.023	Not Found	0.007	Not Found	1.24%
bin18	0.007	0.051	Not Found	Not Found	Not Found	1.96%
bin19	Not Found	0.082	Not Found	Not Found	Not Found	1.09%
bin20	Not Found	0.008	0.001	0.002	0.001	1.14%
bin21	Not Found	Not Found	Not Found	0.008	0.013	2.68%
bin22	Not Found	0.022	Not Found	Not Found	Not Found	1.06%
bin23	Not Found	0.003	Not Found	0.003	0.004	0.82%
bin24	Not Found	0.295	Not Found	Not Found	Not Found	2.94%
bin25	Not Found	Not Found	Not Found	0.192	Not Found	1.40%
bin26	Not Found	0.247	Not Found	0.151	0.024	1.80%
bin27	Not Found	0.035	Not Found	Not Found	Not Found	2.53%
bin28	Not Found	Not Found	Not Found	0.121	0.013	1.45%
bin29	Not Found	0.013	Not Found	0.021	0.002	2.48%
bin30	Not Found	0.104	Not Found	Not Found	Not Found	2.24%
bin31	Not Found	0.004	Not Found	0.033	0.002	2.22%
bin32	Not Found	0.003	Not Found	0.018	0.013	2.56%
bin33	Not Found	0.018	Not Found	0.028	0.018	1.49%
bin34	Not Found	0.104	Not Found	0.015	Not Found	2.14%
bin35	Not Found	0.012	0.008	Not Found	0.001	1.88%
bin36	Not Found	0.001	Not Found	0.001	0.005	0.83%
bin37	Not Found	Not Found	Not Found	Not Found	0.001	0.83%
bin38	0.002	0.012	Not Found	0.002	Not Found	1.76%
bin39	Not Found	0.034	Not Found	0.060	Not Found	2.46%
bin40	Not Found	0.020	Not Found	0.018	0.012	2.14%
bin41	Not Found	0.010	Not Found	0.068	0.020	5.24%
bin42	Not Found	0.162	Not Found	Not Found	Not Found	1.21%
bin43	Not Found	0.256	Not Found	0.152	0.050	1.35%
bin44	Not Found	Not Found	Not Found	0.114	0.037	1.67%
bin45	Not Found	Not Found	Not Found	0.128	0.034	2.11%

bin46	Not Found	0.120	Not Found	Not Found	Not Found	3.33%
bin47	Not Found	Not Found	Not Found	0.016	0.022	1.83%
bin48	Not Found	0.769	Not Found	Not Found	Not Found	1.86%
bin49	Not Found	0.156	Not Found	Not Found	Not Found	1.60%
bin50	Not Found	0.105	Not Found	Not Found	Not Found	2.55%
bin51	Not Found	0.071	Not Found	0.255	Not Found	3.56%
bin52	Not Found	0.013	Not Found	0.083	Not Found	1.84%

(b)						
	HeS	HoS	DL	HD	DR	RA
bin1	Not Found	Not Found	Not Found	0.028	0.053	2.61%
bin2	0.024	Not Found	Not Found	0.104	0.010	5.14%
bin3	Not Found	0.188	Not Found	0.004	Not Found	1.41%
bin4	Not Found	0.057	Not Found	0.064	Not Found	3.73%
bin5	Not Found	Not Found	Not Found	0.015	0.011	1.33%
bin6	Not Found	0.128	Not Found	0.098	Not Found	3.31%
bin7	Not Found	0.023	0.010	0.013	0.004	3.00%
bin8	Not Found	0.006	Not Found	0.010	0.007	1.80%
bin9	Not Found	0.106	Not Found	0.054	Not Found	3.23%
bin10	Not Found	0.365	Not Found	0.019	Not Found	1.62%
bin11	Not Found	0.109	Not Found	0.314	Not Found	4.90%
bin12	Not Found	0.098	Not Found	0.001	Not Found	2.58%
bin13	Not Found	0.115	Not Found	0.020	0.008	1.62%
bin14	Not Found	Not Found	Not Found	0.016	0.021	3.00%
bin15	Not Found	0.026	0.150	0.017	0.112	2.53%
bin16	0.003	Not Found	Not Found	0.001	0.023	1.82%
bin17	0.003	0.002	Not Found	0.003	0.005	1.49%
bin18	0.012	0.106	Not Found	0.022	0.027	1.43%
bin19	Not Found	Not Found	0.009	0.005	0.011	2.42%
bin20	Not Found	Not Found	Not Found	0.015	0.012	2.03%
bin21	Not Found	0.002	Not Found	0.004	0.003	1.54%
bin22	Not Found	0.005	Not Found	0.008	0.003	2.71%
bin23	Not Found	Not Found	Not Found	0.013	0.004	2.14%
bin24	Not Found	0.047	Not Found	0.021	0.051	1.88%
bin25	Not Found	0.004	Not Found	0.012	0.006	1.25%
bin26	Not Found	Not Found	Not Found	0.008	0.008	1.43%
bin27	Not Found	0.136	Not Found	0.010	Not Found	1.82%
bin28	Not Found	0.009	Not Found	0.006	0.001	1.56%
bin29	Not Found	0.021	Not Found	0.069	0.059	1.62%
bin30	Not Found	0.499	Not Found	0.024	Not Found	3.10%
bin31	Not Found	0.004	Not Found	0.017	0.015	1.72%
bin32	Not Found	0.316	Not Found	0.040	Not Found	1.96%
bin33	Not Found	0.332	Not Found	0.029	0.005	2.27%
bin34	Not Found	Not Found	Not Found	0.032	0.009	2.01%
bin35	Not Found	0.034	Not Found	0.082	0.079	1.69%
bin36	Not Found	0.001	Not Found	0.021	0.030	1.69%
bin37	Not Found	0.780	Not Found	0.141	0.164	2.50%
bin38	0.013	0.055	Not Found	0.045	0.008	4.51%
bin39	Not Found	0.425	Not Found	0.104	Not Found	3.44%
bin40	Not Found	0.240	Not Found	0.140	Not Found	3.02%

bin41	Not Found	0.066	Not Found	0.050	Not Found	3.26%
bin42	Not Found	0.014	Not Found	0.004	0.003	1.88%

Table S3. The number and relative abundance of dominant bacterial (a) and fungal (b) taxa among phylum.

(a)			
The dominant bacterial group	Abundant taxa	Moderate taxa	Rare taxa
Group 1B			
Acidobacteria	2 (0.125)	67 (0.154)	132 (0.023)
Verrucomicrobia	1 (0.063)	19 (0.044)	138 (0.024)
Proteobacteria	6 (0.375)	60 (0.138)	114 (0.020)
Total	9 (0.563)	146 (0.336)	384 (0.068)
Group 2B			
Proteobacteria	Not Found	23 (0.053)	194 (0.034)
Actinobacteria	1 (0.063)	25 (0.058)	203 (0.036)
Firmicutes	Not Found	4 (0.009)	35 (0.006)
Acidobacteria	Not Found	17 (0.039)	69 (0.012)
Total	1 (0.063)	69 (0.159)	501 (0.088)
(b)			
The dominant bacterial group	Abundant taxa	Moderate taxa	Rare taxa
Group 1F			
Basidiomycota	6 (0.188)	6 (0.462)	195 (0.053)
Ascomycota	1 (0.031)	Not Found	159 (0.043)
Zygomycota	7 (0.219)	1 (0.077)	84 (0.023)
Total	14 (0.438)	7 (0.539)	438 (0.118)
Group 2F			
Basidiomycota	1 (0.031)	1 (0.077)	60 (0.016)
Ascomycota	4 (0.125)	3 (0.231)	562 (0.151)
Total	5 (0.156)	4 (0.308)	622 (0.168)

Table S4. The richness of bacterial and fungal taxa in all elevation sample plots. AT: abundant taxa; RT: rare taxa; Overall: all taxa. DY9B1 indicates bacterial community at the elevation of 900 m in Daiyun mountain, and so on.

Sample plots	Richness			Sample plots	Richness		
	AT	Overall	RT		AT	Overall	RT
DY9B1	10116	69294	21553	DY9F1	28841	66780	22409
DY9B2	8969	67731	21796	DY9F2	30143	68114	21953
DY9B3	8955	67484	21581	DY9F3	29191	65599	20466
DY10B1	10017	69321	20080	DY10F1	35359	70522	21264
DY10B2	9536	70184	20686	DY10F2	30459	69637	23924
DY10B3	9722	69041	20344	DY10F3	46371	86973	25048
DY11B1	7924	67286	23591	DY11F1	33465	70801	9598
DY11B2	8136	68919	22548	DY11F2	35382	70725	9785
DY11B3	8251	69111	22576	DY11F3	33040	70406	9979
DY12B1	8520	69205	21350	DY12F1	17246	67223	26002
DY12B2	7909	66335	20278	DY12F2	17066	67993	25825
DY12B3	8473	69042	21086	DY12F3	16230	66578	25247
DY13B1	11184	69285	23264	DY13F1	30167	66266	27034
DY13B2	10304	68107	22832	DY13F2	28446	65619	28011
DY13B3	10593	70832	24084	DY13F3	31580	67903	27581
DY14B1	10606	68420	22778	DY14F1	39334	67691	14620
DY14B2	9947	70880	24341	DY14F2	39311	67270	14556
DY14B3	9706	68411	23623	DY14F3	37072	66497	15851
DY15B1	10265	69431	22893	DY15F1	26306	65344	22553
DY15B2	10068	70671	23445	DY15F2	27377	66537	22750
DY15B3	10201	70951	23643	DY15F3	29663	68889	21695

Figure captions for supplementary

Figure S1. The abundance of OTUs in the bacterial (a) and fungal (b) community. AAT: absolutely abundant taxa; ART: absolutely rare taxa; CAT: conditionally abundant taxa; CRAT: conditionally rare or abundant taxa; CRT: conditionally rare taxa; MT: moderate taxa.

Figure S2. The heatmap of the dominant bacterial (a) and fungal (b) community along the elevational gradient. DY9B indicates bacterial community at the elevation of 900 m in Daiyun mountain, and so on.

Figure S3. The relative importance of homogeneous selection and homogenizing dispersal on microbial community in different elevations.

Figure S4. The abundance of bacterial (a) and fungal (b) bins.

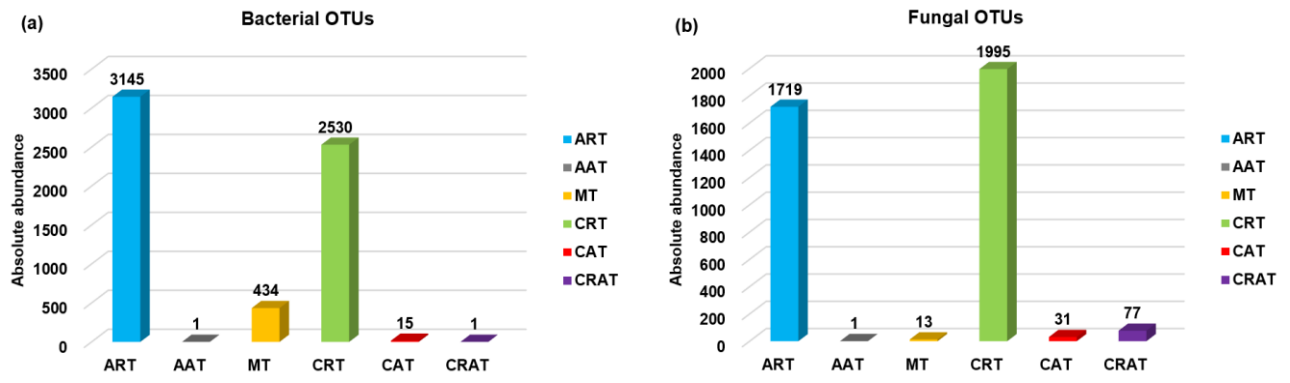


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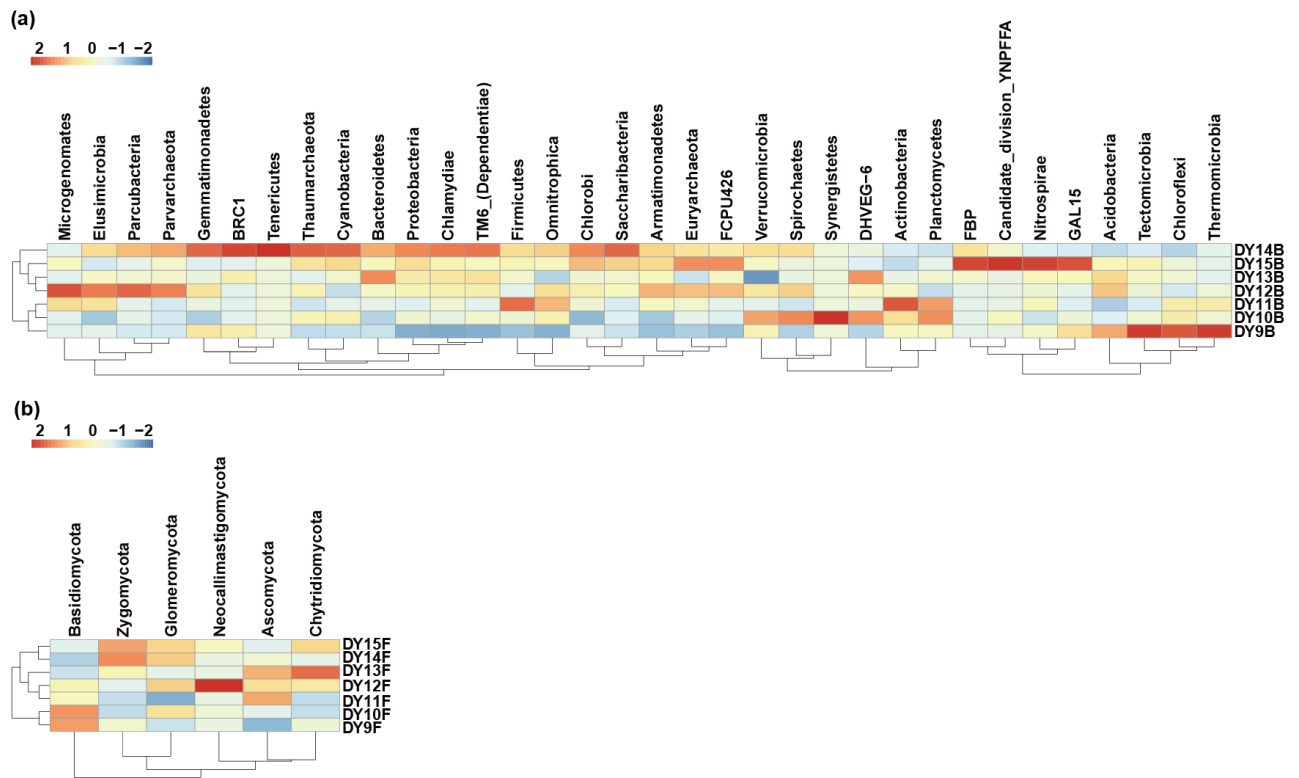


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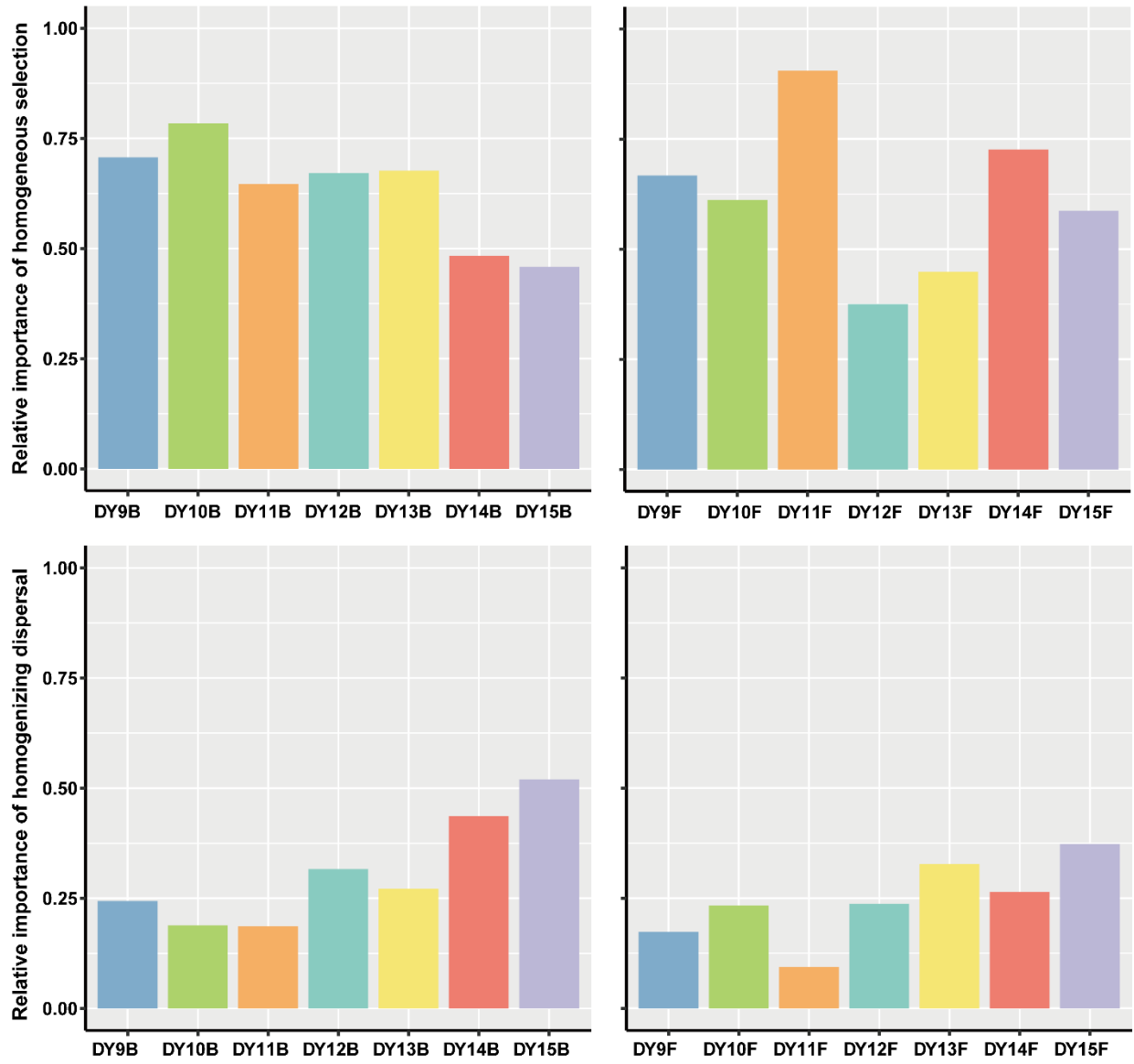


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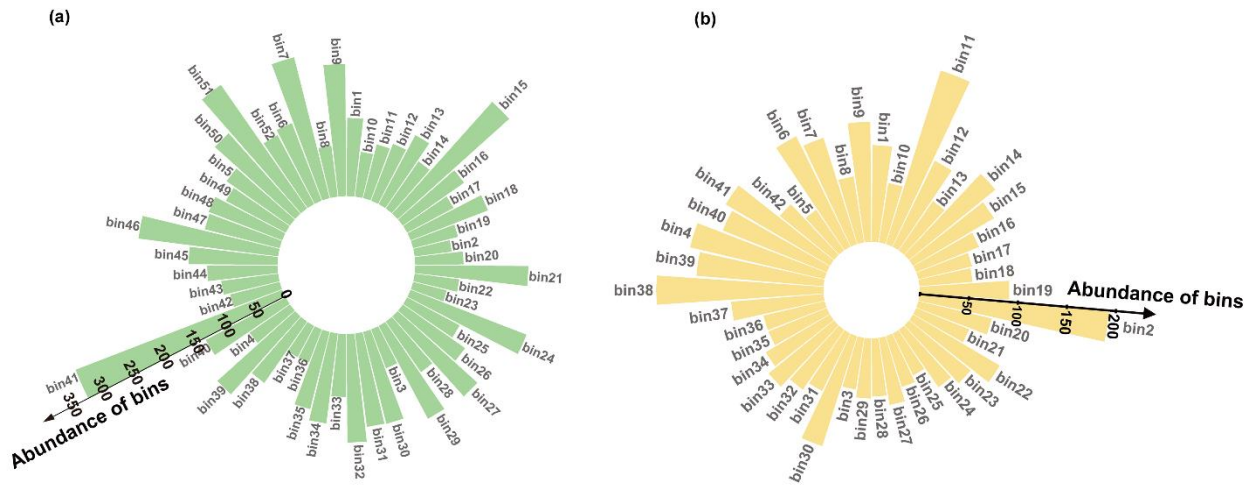


Figure S4. The abundance of bacterial (a) and fungal (b) bins.