Supplemental materials

1 supplemental material and method, 8 supplemental figures and 5 supplemental tables

Supplemental Figure 1. Salinity of irrigation water from north to the middle of the Tarim Desert Highway and the correlations with soil salinity.

Supplemental Figure 2. Co-occurrence networks of bacterial communities along the salinity gradient.

Supplemental Figure 3. Co-occurrence networks of fungal communities along the salinity gradient.

Supplemental Figure 4. Changes in the niche overlap of bacterial and fungal communities to soil salinity and modularity.

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Supplemental Table 1. The relative abundance of dominant soil bacterial phyla across study sites.

Supplemental Table 2. The relative abundance of dominant soil fungal phyla across study sites.

Supplemental table 3. Bivariate associations between soil properties and the stability indices of bacterial and fungal communities**.**

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Description of modularity, cohesion, and keystone species

Modularity provides insights into how compartmentalized the interactions of microbial communities are. High modularity indicates that interactions between taxa occur mainly within rather than between modules. Communities with high modularity tend to be stable, because the impacts of variation of a taxon are limited to its module (Dong et al., 2022). The modularity of networks was measured by the Clauset–Newman–Moore algorithm (Clauset et al., 2004).

The cohesion indictor provides insights into relationships across taxa caused by both positive and negative interactions and/or by both the similarity and differences in the niches of microbial taxa (Herren and McMahon, 2017). The cohesions (positive and negative) are the sum of positive or negative interactions between taxa and weighted by taxa abundances. Communities with higher absolute negative cohesion and low positive cohesion tend to be more stable, as facilitative interactions can trigger tandem responses of different taxa and negative interactions can decrease the co-oscillation in communities (Liu et al., 2021).

We used the negative:positive cohesion to determine whether the communities at high-salinity sites is characterized more by negative-interactions driven processes than those at low-salinity sites. We also evaluated total cohesion (i.e., the sum of positive cohesion and absolute negative cohesion) to characterize the network complexity.

We constructed bacterial and fungal global networks to determine keystone bacterial and fungal species. In the global network, the bacterial or fungal OTUs that have high within module connectivity ($Z_i > 2.6$) or/and among module connectivity ($P_i > 0.62$) were considered as keystone species (Dong et al., 2022). Then, we assessed changes in the relative abundance of modules and keystone species with increasing soil salinity by using Spearman's correlation test. The relative abundance of fungal keystone taxa (i.e., unknown fungi OTU1 and OTU4) rather than bacterial keystone taxa (i.e., Rhodospirillaceae OTU19 and OTU79, Halomonadaceae OTU26) increased along the salinity gradient (Supplemental Figure 9), which could promote the stability of fungal communities with increased stress.

Reference

Clauset, A., Newman, M.E.J., Moore, C., 2004. Finding community structure in very large networks. *Physical Review E* **70**. DOI:10.1103/PhysRevE.70.066111.

Dong, Y., Zhang, J., Chen, R., Zhong, L., Lin, X., Feng, Y., 2022. Microbial community composition and activity in saline soils of coastal agro-ecosystems. *Microorganisms* **10**. DOI:10.3390/microorganisms10040835.

Herren, C.M., McMahon, K.D., 2017. Cohesion: A method for quantifying the connectivity of microbial communities. *Isme Journal* **11**, 2426-2438. DOI:10.1038/ismej.2017.91.

Liu, L., Wang, S., Chen, J., 2021. Anthropogenic activities destabilized riverine bacterial communities by increasing synchrony between taxa. *Aquatic Sciences* **83**. DOI:10.1007/s00027-021-00818-3.

Supplemental Table 1. The relative abundance of dominant bacterial phyla across study sites. Values= Mean (standard deviation), *F* values, or correlation coefficients. Topsoils, 0–40 cm; subsoils 40–100 cm; correlation coefficient, Spearman's correlation coefficients between relative abundance and soil salinity. Different letters within columns for topsoils or subsoils denote significant difference at α = 0.05. Values in bold were the significant estimates. *, significant at α = 0.05; **, significant at α = 0.01; ***, significant at α = 0.001.

Layers	Sites	Proteobacteria	Firmicutes	Bacteroidetes	Actinobacteria	Chloroflexi	Planctomycetes	Others
Topsoils	s01	42.96(7.02) a	21.42(8.04) ab	19.35(9.82) abc	4.64(2.03) ab	2.75(2.18) ab	2.05(1.78) a	6.83(6.00) a
	s04	41.25(6.29) a	22.63(4.78) ab	25.56(10.64) ab	4.09(1.41) ab	1.70(2.70) ab	0.82(0.49) a	3.95(2.71) a
	s07	39.18(4.47) a	25.08(8.07) ab	28.3(10.65) a	3.37(1.62) ab	0.60(0.51) ab	0.80(0.42) a	2.68(1.92) a
	s10	38.33(2.12) a	25.69(5.29) ab	29.51(3.43) a	3.27(1.38) ab	0.19(0.16) b	0.63(0.54) a	2.39(2.06) a
	s13	45.47(7.86) a	27.27(6.47) ab	19.25(8.37) abc	2.95(2.53) b	0.77(0.87) ab	0.70(0.80) a	3.58(2.71) a
	s16	40.53(3.97) a	19.59(6.15) b	24.16(10.63) abc	6.39(3.98) ab	1.46(1.39) ab	2.11(2.08) a	5.74(4.59) a
	s19	39.41(8.89) a	32.97(7.02) a	15.17(9.28) abc	5.4(2.74) ab	1.47(1.04) ab	1.22(0.63) a	4.36(2.03) a
	s23	40.04(5.46) a	26.35(7.26) ab	18.02(9.56) ab	7.77(5.72) ab	2.80(3.14) ab	1.43(1.47) a	3.59(2.82) a
	s28	43.30(4.36) a	29.77(3.84) ab	13.34(9.20) bc	7.87(7.90) a	2.13(3.40) ab	0.88(1.12) a	2.72(2.98) a
	s34	38.73(3.36) a	32.08(10.22) ab	10.11(6.47) c	6.17(2.19) ab	3.77(4.55) a	2.80(2.06) a	6.33(5.59) a
Subsoils	s01	47.88(5.04) a	34.38(7.40) ab	10.67(1.86) ab	2.44(1.43) b	0.89(0.77) a	0.86(0.87) b	2.88(2.71) a
	s04	39.02(6.14) ab	34.49(5.66) ab	17.03(9.02) ab	3.03(1.05) b	1.25(0.64) a	0.86(0.35) b	4.31(1.81) a

	s07	43.76(4.92) ab	37.90(2.99) ab	12.07(5.07) ab	2.3(0.81) b	0.74(0.34) a	0.84(0.32) b	2.39(0.78) a
	s10	45.09(6.18) ab	30.49(8.98) ab	17.18(6.44) ab	2.73(0.97) b	0.72(0.34) a	0.87(0.36) b	2.93(0.77) a
	s13	41.18(5.61) ab	27.18(7.62) b	22.43(15.32) ab	2.13(1.32) b	1.48(1.38) a	0.86(0.63) b	4.72(4.35) a
	s16	39.17(6.73) ab	34.54(12.32) ab	8.91(5.79) ab	7.12(0.88) ab	2.13(0.69) a	2.34(0.74) ab	5.79(2.75) a
	s19	45.56(7.21) ab	31.92(3.60) ab	9.22(7.07) ab	4.61(2.09) ab	1.92(0.75) a	1.65(0.50) ab	5.12(1.85) a
	s23	37.22(6.76) b	31.74(7.07) ab	22.27(10.68) a	3.88(1.82) ab	1.04(0.42) a	1.09(0.62) ab	2.75(1.21) a
	s28	42.97(5.29) ab	33.76(5.63) ab	4.8(4.54) b	8.47(4.91) a	2.94(2.66) a	2.10(1.12) ab	4.96(3.39) a
	s34	38.98(7.33) ab	41.90(8.35) a	2.71(1.42) b	4.17(1.97) ab	3.60(1.59) a	2.34(0.89) a	6.31(2.32) a
ANOVA	Layer	1.70	**49.64*****	**25.88*****	**5.98***	0.11	0.06	0.00
Correlation coefficient		-0.06	**-0.26*****	**0.48*****	**-0.15***	**-0.29****	**-0.25****	-0.08

Supplemental Table 2. Spearman's correlation of bacteria and fungi genera with soil salinity

Bacteria genera	*Rho*	*P*	Fungi genera	*Rho*	*P*
Proteobacteria	-0.07	0.37	*Acremonium*	-0.15	0.04
Firmicutes	-0.37	0.00	*Chaetomium*	-0.25	0.00
Bacteroidetes	0.48	0.00	*Corollospora*	-0.02	0.76
Actinobacteria	-0.15	0.04	*Thielavia*	0.00	0.96
Chloroflexi	-0.30	0.00	Other genera	0.12	0.10
Planctomycetes	-0.25	0.00			
Other genera	-0.09	0.25			

Supplemental Table 3. The relative abundance of fungal phyla across study sites. Values= Mean (standard deviation) or *F* values. Topsoils, 0–40 cm; subsoils 40–100 cm; correlation coefficient, Pearson's correlation coefficients between relative abundance and soil salinity. Different letters within columns for topsoil or subsoil denote significant difference at α = 0.05. Values in bold were the significant estimates. *, significant at α = 0.05; **, significant at α = 0.01; ***, significant at α = 0.001.

Layers	Sites	Ascomycota	Basidiomycota	Rozellomycota	Chytridiomycota	Glomeromycota	Zygomycota	Others
Topsoils	s01	58.17(33.31) ab	1.11(0.41) a	0.10(0.23) b	0.03(0.03) a	0.08(0.10) a	0.20(0.29) b	40.32(33.33) ab
	s04	31.85(20.28) b	3.93(4.26) a	0.04(0.12) b	0.19(0.56) a	0.10(0.10) a	0.33(0.21) b	63.56(20.37) a
	s07	33.60(25.08) b	1.68(1.26) a	<0.01(0.00) b	0.02(0.02) a	0.10(0.09) a	1.53(2.98) ab	63.07(27.16) a
	s10	51.61(19.93) ab	2.75(2.77) a	0.01(0.01) b	0.09(0.11) a	0.20(0.20) a	2.27(3.63) a	43.07(14.93) ab
	s13	54.55(29.23) ab	7.33(7.84) a	0.03(0.06) b	0.04(0.09) a	0.06(0.07) a	0.35(0.48) ab	37.63(25.41) ab
	s16	43.38(14.51) ab	3.43(3.47) a	7.24(11.5) a	0.11(0.16) a	0.07(0.04) a	0.07(0.07) b	45.70(15.63) ab
	s19	52.98(26.8) ab	6.78(7.33) a	<0.01(0.01) b	0.06(0.08) a	0.04(0.04) a	0.07(0.07) b	40.06(24.12) ab
	s23	48.21(32.88) ab	6.78(10.9) a	0.08(0.23) b	0.37(0.49) a	0.12(0.11) a	0.12(0.15) b	44.32(34.35) ab
	s28	83.36(17.89) a	1.35(1.40) a	<0.01(0.00) b	0.14(0.30) a	0.15(0.18) a	0.06(0.08) b	14.94(16.80) b
	s34	55.5(25.99) ab	11.94(14.24) a	0.02(0.07) b	0.18(0.37) a	0.08(0.08) a	0.27(0.46) b	32.01(29.26) ab
Subsoils	s01	44.80(35.07) ab	9.24(19.49) a	<0.01(0.00) a	0.03(0.04) a	0.03(0.02) a	0.03(0.04) a	45.88(37.61) ab
	s04	36.79(16.08) b	6.96(11.34) a	0.36(0.91) a	0.01(0.01) a	0.06(0.05) a	0.26(0.27) a	55.56(14.28) ab
	s07	37.09(33.72) b	2.02(1.28) a	<0.01(0.01) a	<0.01(0.01) a	0.10(0.14) a	0.45(0.46) a	60.33(33.70) a
	s10	57.74(29.81) ab	2.41(2.65) a	<0.01(0.01) a	0.03(0.05) a	0.16(0.21) a	0.97(1.15) a	38.69(29.44) ab
	s13	39.13(33.04) ab	8.43(5.72) a	<0.01(0.00) a	0.14(0.32) a	0.04(0.05) a	0.18(0.41) a	52.09(27.92) ab
	s16	68.60(25.25) ab	1.49(1.79) a	2.58(4.86) a	0.13(0.16) a	0.06(0.05) a	0.11(0.11) a	27.03(22.17) ab
	s19	68.08(23.02) ab	5.64(4.74) a	<0.01(0.01) a	0.37(0.65) a	0.10(0.15) a	0.03(0.06) a	25.77(21.62) ab
	s23	64.43(19.73) ab	5.42(5.08) a	0.13(0.26) a	0.45(0.63) a	0.06(0.08) a	0.12(0.12) a	29.38(21.46) ab
	s28	81.75(13.34) a	2.27(2.91) a	0.07(0.11) a	0.40(0.67) a	0.08(0.13) a	0.02(0.02) a	15.41(11.04) b
	s34	81.21(13.94) ab	2.57(4.58) a	<0.01(0.01) a	0.29(0.29) a	0.17(0.15) a	0.01(0.01) a	15.75(10.66) b
ANOVA	Layer	3.06	0.00	1.10	1.46	0.57	3.52	2.52
Correlation coefficient		**-0.36*****	0.00	0.08	**-0.32****	0.06	**0.37****	**0.37*****

Supplemental table 4. Bivariate associations between soil properties and the stability properties of bacterial and fungal communities. Values denote the Spearman's rho. SOC, soil organic carbon (g kg^{-1}); STN, soil total nitrogen (g kg^{-1}); STP, soil total phosphorus (g kg^{-1}); C:N, SOC:STN ratio; C:P, SOC:STP ratio; N:P, STN:STP ratio; SM, soil moisture (g g^{-1}) ; Clay&Silt, soil clay and silt content (%). ***, P<0.001; **, P<0.01; *, P<0.05.

	Microbiome	Depth	SOC	STN	STP	C:N	C:P	N:P	pH	Clay&Silt	SM
Species richness (n=180)	bacteria	topsoils	**-0.34****	**0.22***	**-0.29****	**-0.51*****	**-0.29****	**0.29****	-0.02	**-0.32****	**0.27****
		subsoils	0.12	0.15	0.05	-0.15	0.04	0.13	-0.06	0.15	-0.20
		all	**-0.22****	**0.16***	**-0.17***	**-0.38*****	**-0.22****	**0.21***	0.02	**-0.17***	0.11
	fungi	topsoils	0.20	0.07	0.10	0.14	0.20	0.06	0.02	0.14	-0.09
		subsoils	0.13	**0.22***	**0.22***	**-0.24***	-0.03	**0.21***	**-0.24***	0.02	0.07
		all	0.12	**0.15***	**0.16***	-0.04	0.07	0.14	-0.09	0.08	-0.01
Modularity (n=20)	bacteria	topsoils	-0.50	-0.36	-0.02	0.09	-0.47	-0.25	-0.06	-0.49	-0.48
		subsoils	0.56	0.43	0.07	-0.39	0.38	0.58	0.13	0.14	0.24
		all	-0.15	0.17	-0.11	-0.28	-0.19	0.33	0.24	-0.22	0.11
	fungi	topsoils	0.37	0.33	**0.69***	0.30	0.22	0.21	-0.49	0.62	0.45
		subsoils	0.12	0.13	-0.02	-0.22	0.18	0.20	-0.32	-0.39	0.09
		all	0.02	0.22	0.22	-0.04	-0.01	0.17	-0.32	0.03	0.31
Negative:positive cohesion (n=60)	bacteria	topsoils	0.31	-0.31	0.28	**0.70*****	0.18	**-0.46***	-0.21	0.10	0.14
		subsoils	**-0.40***	-0.27	-0.21	0.22	-0.33	-0.29	-0.24	**-0.41***	-0.27
		all	**-0.53*****	**-0.31***	-0.12	-0.18	**-0.55*****	**-0.35****	0.14	**-0.51****	0.24
	fungi	topsoils	**0.38***	0.24	-0.23	0.03	**0.53****	0.33	0.14	0.18	0.18
		subsoils	-0.08	-0.17	0.20	0.13	-0.05	-0.22	-0.24	-0.24	0.06
		all	0.07	0.02	0.02	0.11	0.12	0.02	-0.07	-0.05	0.14
Total cohesion (n=60)	bacteria	topsoils	0.23	0.03	-0.23	0.13	0.30	0.06	**-0.42***	0.36	0.09
		subsoils	-0.06	-0.28	-0.13	0.22	0.04	-0.28	**-0.51****	0.14	-0.14
		all	0.11	-0.15	-0.08	0.17	0.15	-0.15	**-0.45*****	0.18	-0.03
	fungi	topsoils	0.15	0.16	-0.16	0.06	0.24	0.20	**-0.52****	0.27	0.17
		subsoils	-0.24	-0.21	-0.17	0.09	-0.05	-0.19	**-0.44***	-0.17	-0.06

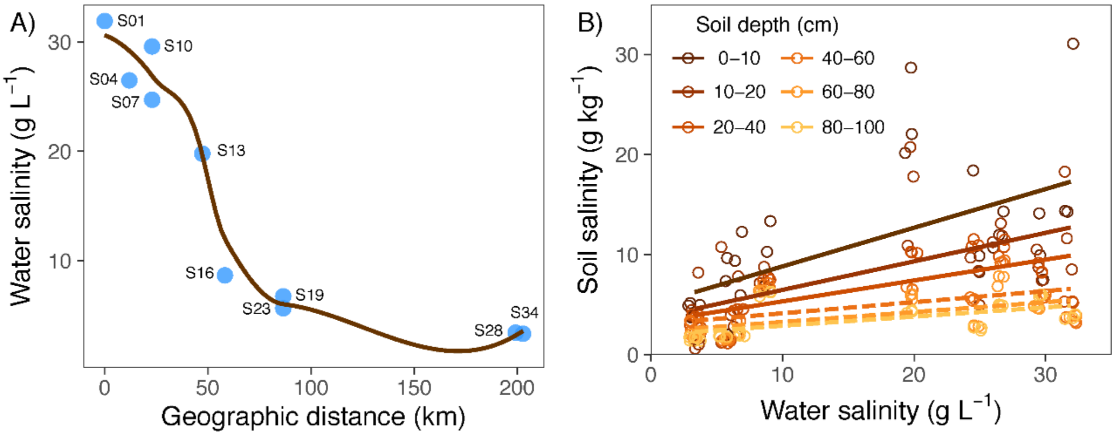
		all	-0.01	-0.01	-0.12	0.05	0.07	0.01	**-0.45*****	0.03	0.09
Positive cohesion (n=60)	bacteria	topsoils	0.21	0.26	-0.34	-0.18	0.32	0.36	-0.33	0.32	0.09
		subsoils	0.12	-0.07	-0.01	0.03	0.18	-0.06	**-0.36***	0.32	0.03
		all	**0.34****	0.05	0.05	0.20	**0.37****	0.07	**-0.42****	**0.39****	-0.07
	fungi	topsoils	-0.14	0.00	-0.15	-0.01	-0.09	0.01	**-0.62*****	0.13	0.01
		subsoils	-0.18	-0.01	-0.36	-0.07	0.06	0.05	-0.25	-0.03	-0.09
		all	-0.01	-0.01	-0.22	0.02	0.07	0.03	**-0.42****	0.09	-0.08
Negative cohesion (n=60)	bacteria	topsoils	-0.17	0.24	0.06	**-0.40***	-0.19	0.29	0.37	-0.27	-0.06
		subsoils	0.20	**0.40***	0.10	-0.31	0.10	**0.42***	**0.60*****	0.05	0.20
		all	0.19	**0.36****	0.12	-0.08	0.16	**0.38****	**0.34****	0.12	-0.07
	fungi	topsoils	-0.34	-0.27	0.17	-0.06	**-0.47****	-0.31	0.16	-0.31	-0.21
		subsoils	0.15	0.19	-0.08	-0.12	0.04	0.21	**0.36***	0.24	-0.04
		all	-0.04	-0.03	0.00	-0.08	-0.10	-0.03	**0.26***	0.00	-0.15

Supplemental Table 5. Effects of soil salinity and soil layer on the cohesions of bacterial and fungal communities. Estimate, the standard regression coefficient using general linear models; SE, standard error. Salinity, soil salinity; Layer, topsoil = 0 and subsoil = 1. Values in bold are significant at alpha level = 0.05. *F* tests were used to measure interactions between soil salinity and soil layer.

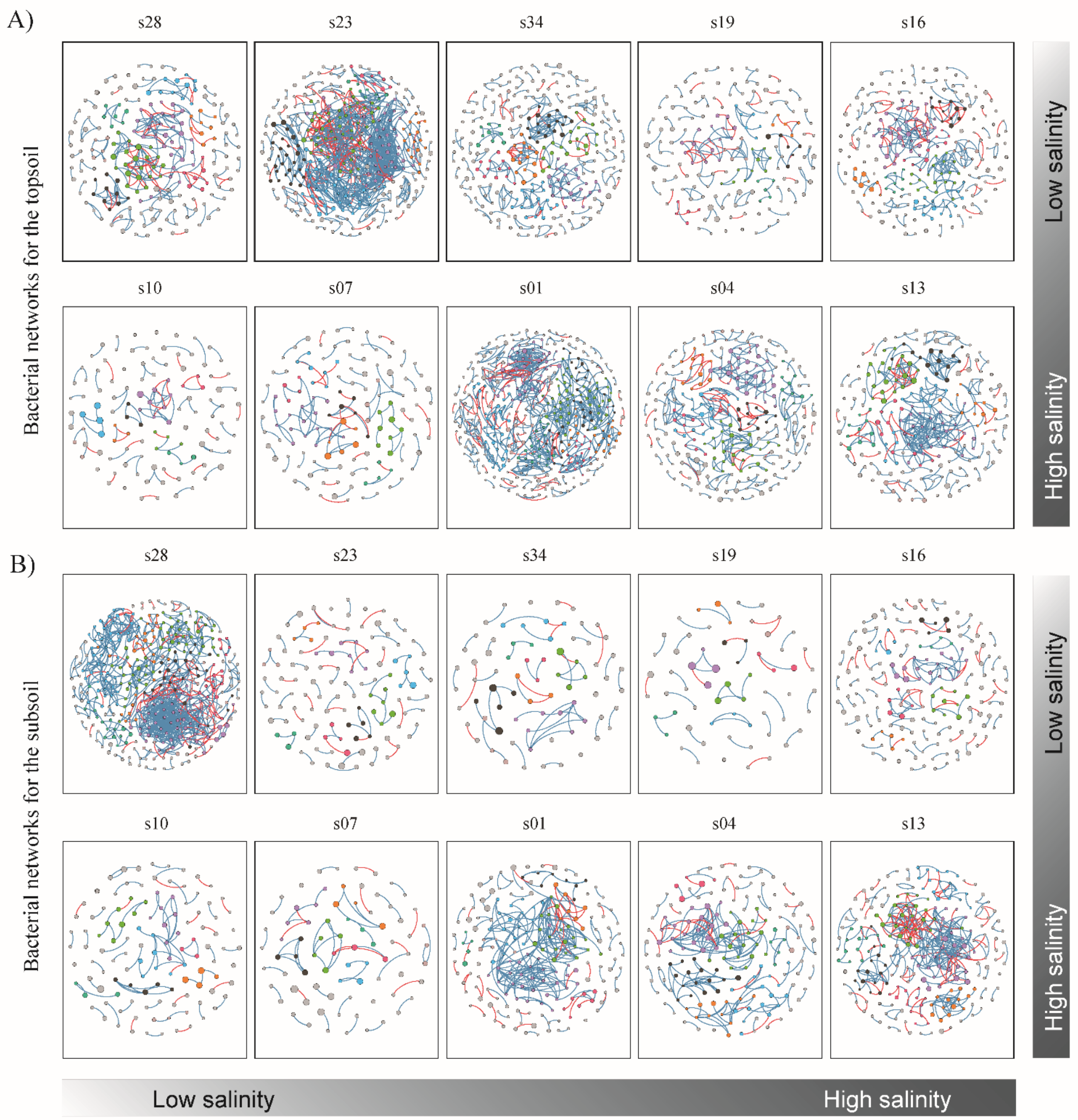
		Variable	*Estimate*	*SE*	*F*	*P* (>*F*)
Bacteria	Total cohesion	**Salinity**	**0.072**	**0.052**	**4.40**	**0.041**
		Layer	-0.014	0.036	0.57	0.455
		Salinity × Layer	0.155	0.124	1.56	0.217
						R^2= 0.052
	Positive cohesion	Salinity	0.009	0.036	0.78	0.382
		Layer	-0.047	0.025	1.73	0.194
		Salinity× Layer	0.114	0.086	1.73	0.194
						R^2= 0.070
	Negative cohesion	**Salinity**	**0.069**	**0.022**	**14.31**	**0.000**
		Layer	**0.036**	**0.015**	**17.62**	**0.000**
		Salinity× Layer	0.036	0.052	0.46	0.500
						R^2= 0.233
Fungi	Total cohesion	Salinity	0.170	0.084	3.61	0.063
		Layer	0.100	0.059	2.90	0.094
		Salinity× Layer	-0.148	0.202	0.54	0.467
						R^2= 0.028
	Positive cohesion	Salinity	0.064	0.044	0.82	0.369
		Layer	0.048	0.031	0.40	0.531
		Salinity× Layer	-0.164	0.106	2.39	0.128
						R^2= 0.004
	Negative cohesion	**Salinity**	**0.107**	**0.056**	**4.60**	**0.036**
		Layer	0.049	0.039	3.68	0.060
		Salinity× Layer	0.016	0.136	0.01	0.908
						R^2= 0.038

Supplemental Table 6. Sensitivities of the stability indices of bacterial and fungal communities against soil salinization. Topsoils, 0–40 cm; subsoils, 40–100 cm; All, 0–100 cm. rho, Spearman's rho. CI, the 0.95 confidence intervals. Z-test was used to compare the correlation coefficients of bacterial and fungal communities.

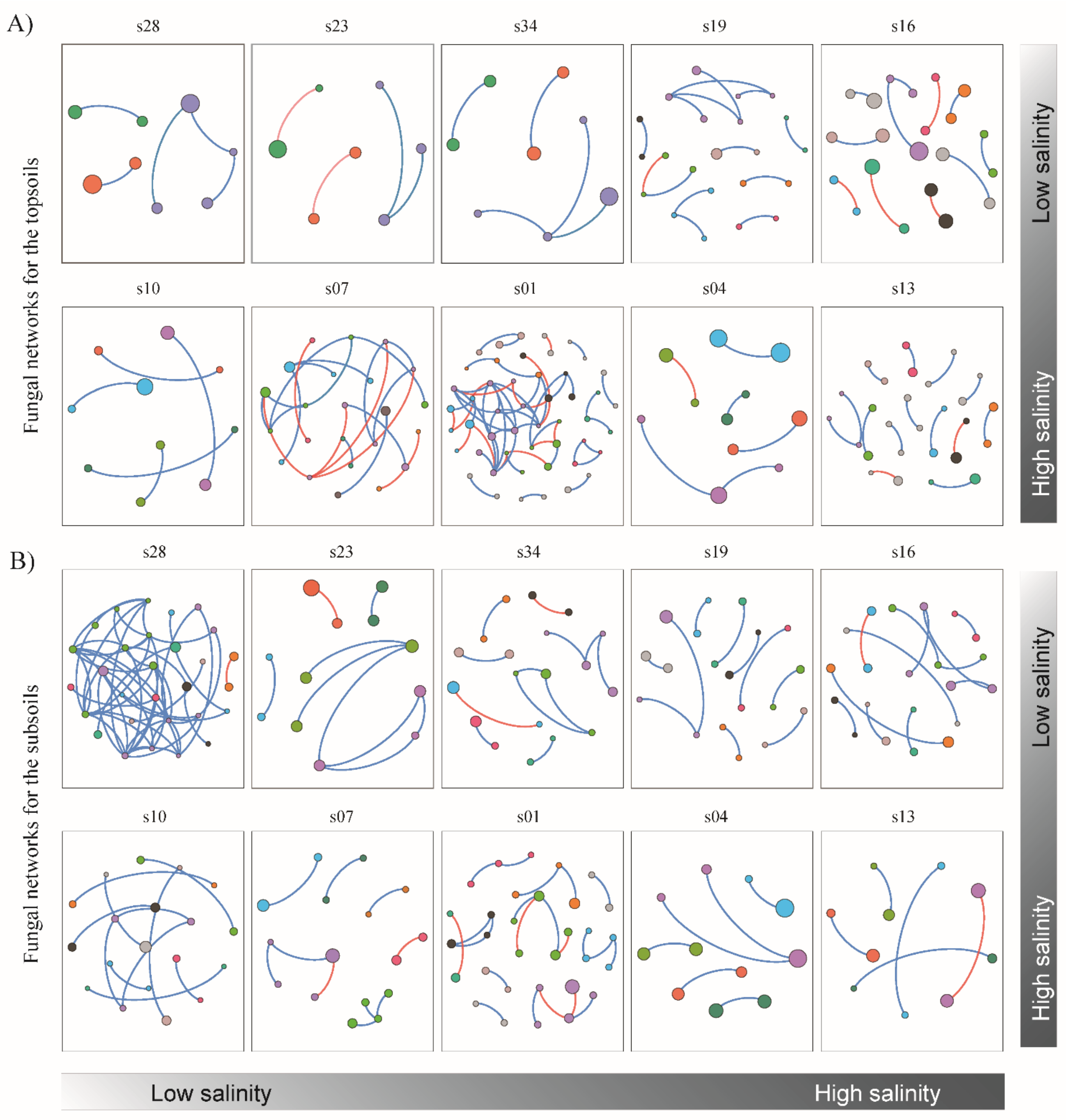
		Bacteria		Fungi		*Z-test*	*P*
		rho	95%CI	rho	95%CI		
Modularity	topsoils	-0.067	-0.870–0.725	0.565	-0.396–0.911	**2.06**	**0.039**
	subsoils	0.152	-0.585–0.812	0.285	-0.660–0.781	0.41	0.683
	all	-0.138	-0.604–0.372	0.311	-0.253–0.704	1.98	**0.047**
Negative: positive cohesion	topsoils	0.396	0.200–0.571	0.242	-0.004–0.484	1.61	0.105
	subsoils	0.003	-0.228–0.227	0.450	0.259–0.613	**5.53**	**0.000**
	all	-0.147	-0.275–-0.013	0.240	**0.087–0.379**	**3.70**	**0.000**
Total cohesion	topsoils	0.289	0.046–0.539	0.461	0.261–0.644	0.82	0.408
	subsoils	0.342	0.161–0.486	0.194	-0.015–0.369	1.50	0.132
	all	0.292	0.165–0.412	0.288	0.136–0.414	0.04	0.967
Positive cohesion	topsoils	0.091	0.203–0.619	0.270	0.15–0.573	1.34	0.178
	subsoils	0.281	0.228–0.541	-0.115	**0.241–0.611**	**3.80**	**0.000**
	all	0.317	0.190–0.434	0.124	-0.026–0.258	1.91	0.055
Negative cohesion	topsoils	0.418	0.187–0.623	0.367	0.133–0.562	0.57	0.570
	subsoils	0.398	0.236–0.557	0.445	0.245–0.609	0.54	0.591
	all	0.179	0.051–0.314	0.305	0.155–0.432	1.26	0.207



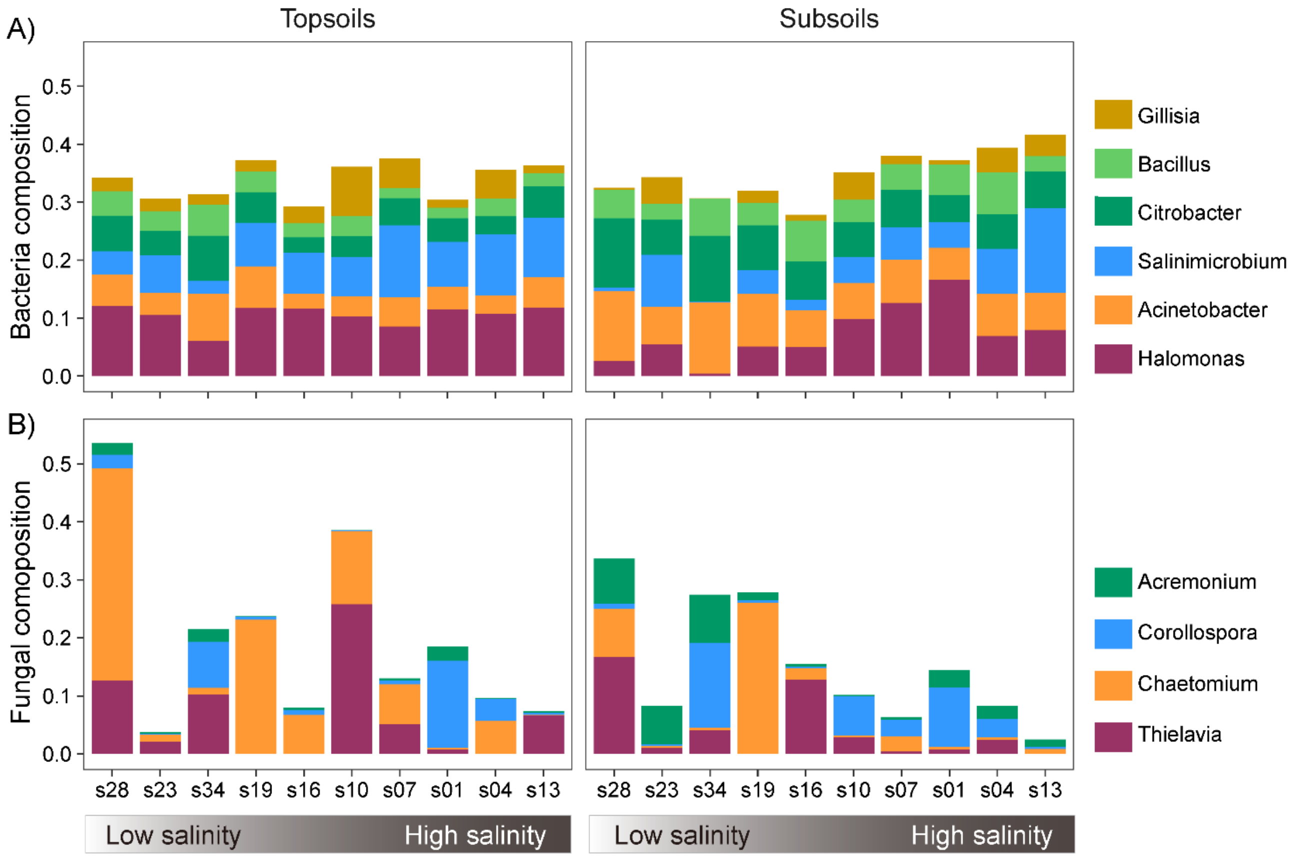
Supplemental Figure 1. Salinity of irrigation water from north to the middle of the Tarim Desert Highway and the correlations with soil salinity. A) The line denotes smooth estimates; B) solid and dashed line denote significant and insignificant regressions, respectively.



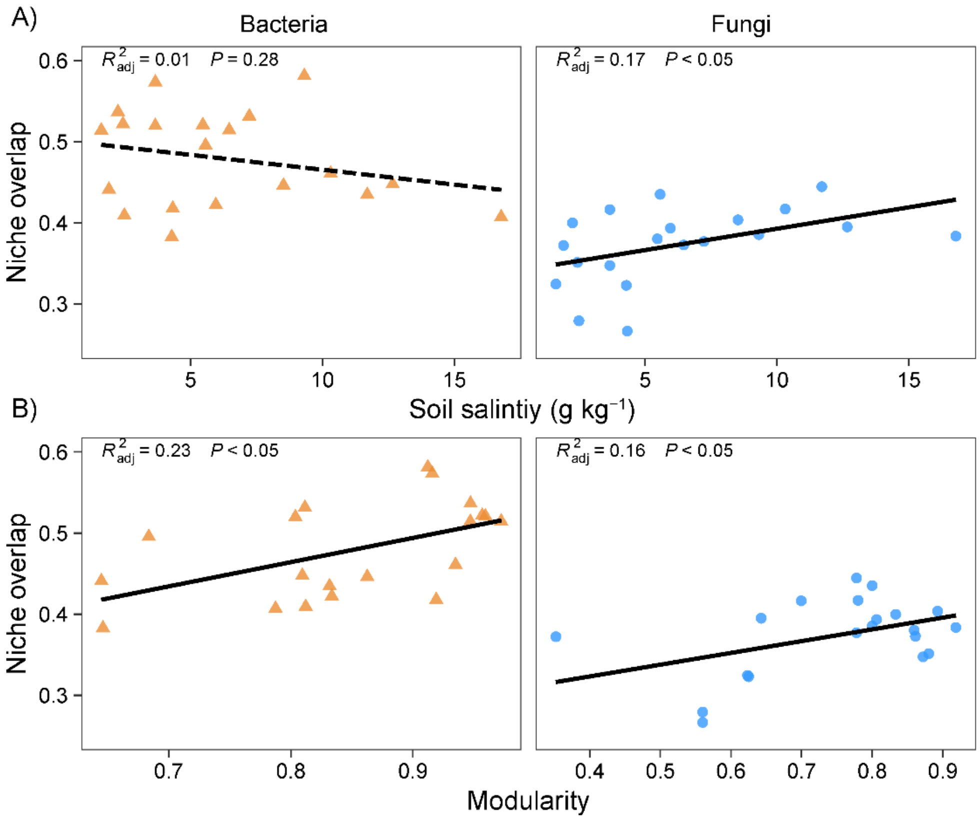
Supplemental Figure 2. Co-occurrence networks of soil bacteria along a salinity gradient. A, topsoil; B, subsoil. Nodes denote bacterial OTUs. Size of the nodes is proportional to the relative abundance of the OTUs Colors of the nodes denote different network modules and grey nodes denote the ⩾ 9th modules. Blue and red lines denote positive and negative interactions, respectively.



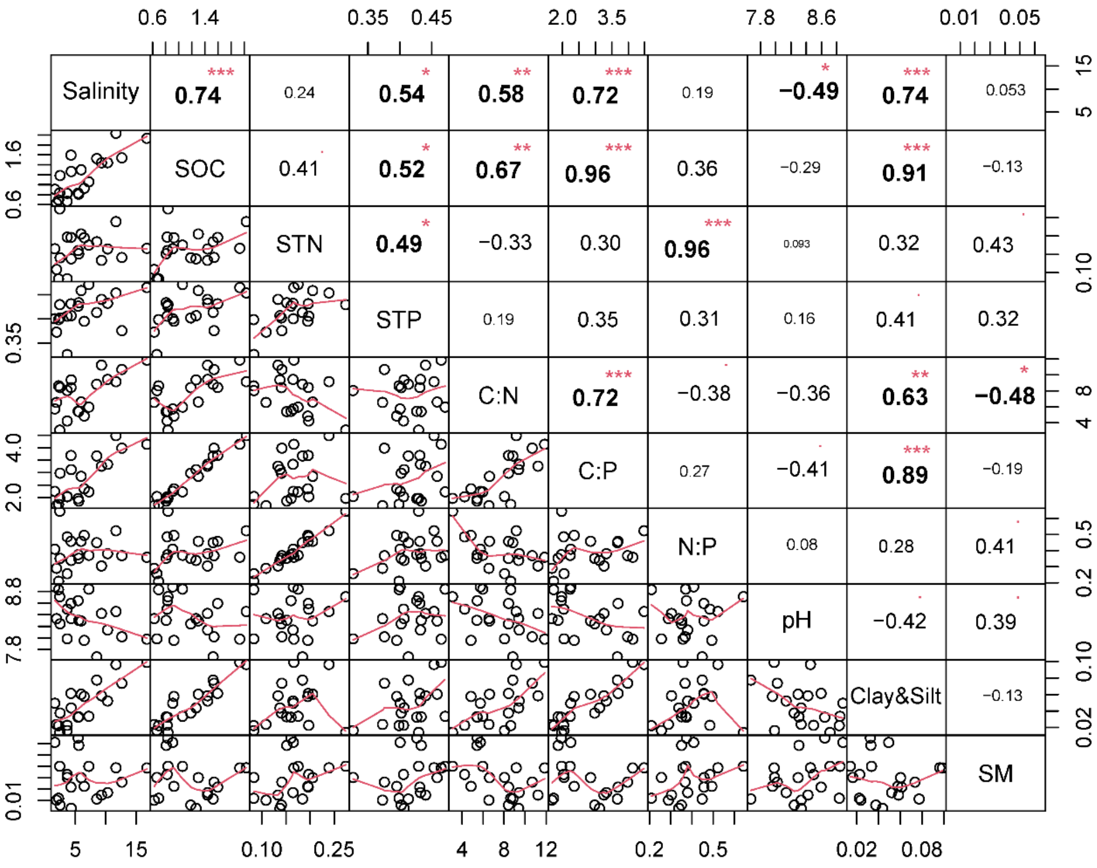
Supplemental Figure 3. Co-occurrence networks of soil fungi along a salinity gradient. A, topsoil; B, subsoil. Nodes denote fungal OTUs. Size of the nodes is proportional to the relative abundance of the OTUs Colors of the nodes denote different network modules and grey nodes denote the ⩾ 9th modules. Blue and red lines denote positive and negative interactions, respectively.



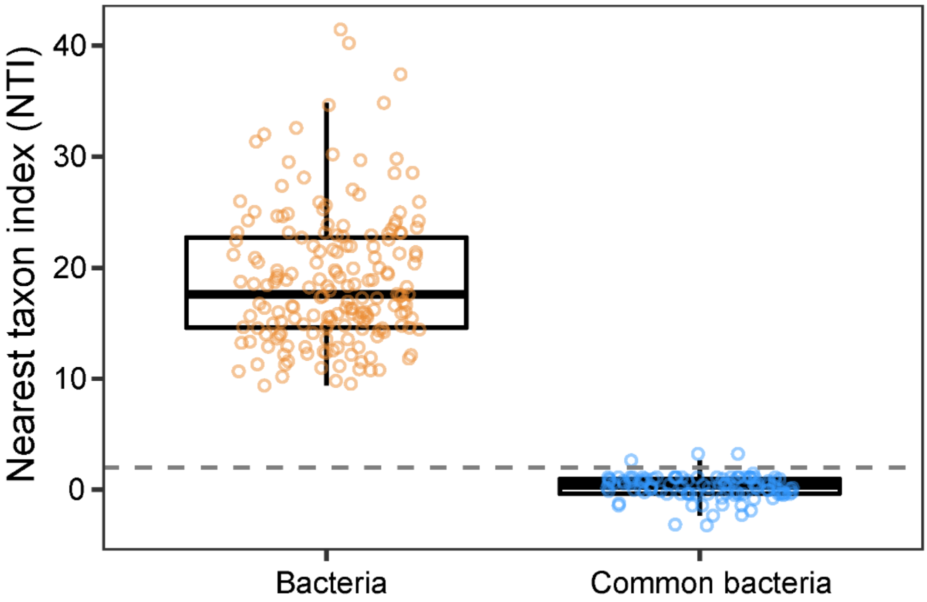
Supplemental Figure 4. The relative abundance of soil bacteria and fungi genera along the salinity gradient across ten sites. Topsoils, 0–40 cm (left); subsoils, 40–100 cm (right). (A) relative abundance of soil bacteria genera; (B) relative abundance of soil fungi genera.



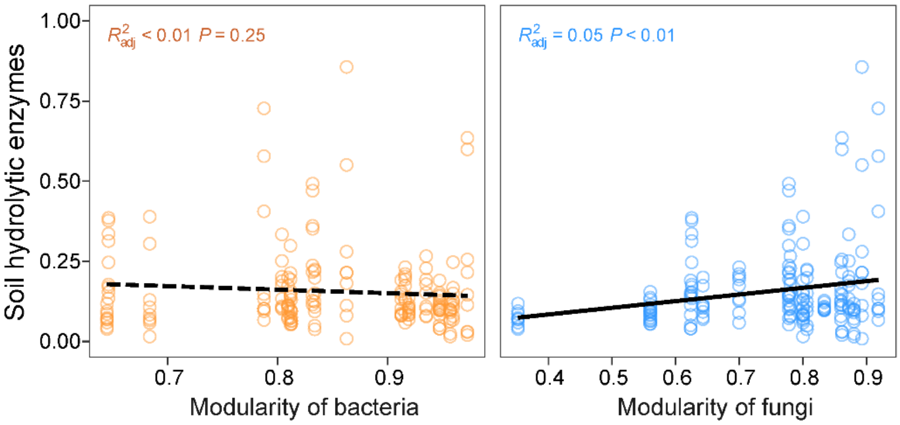
Supplemental Figure 5. Changes in the niche overlap of bacterial and fungal communities with soil salinity (A) and modularity (B). Solid and dash lines denote the significant and insignificant estimates.



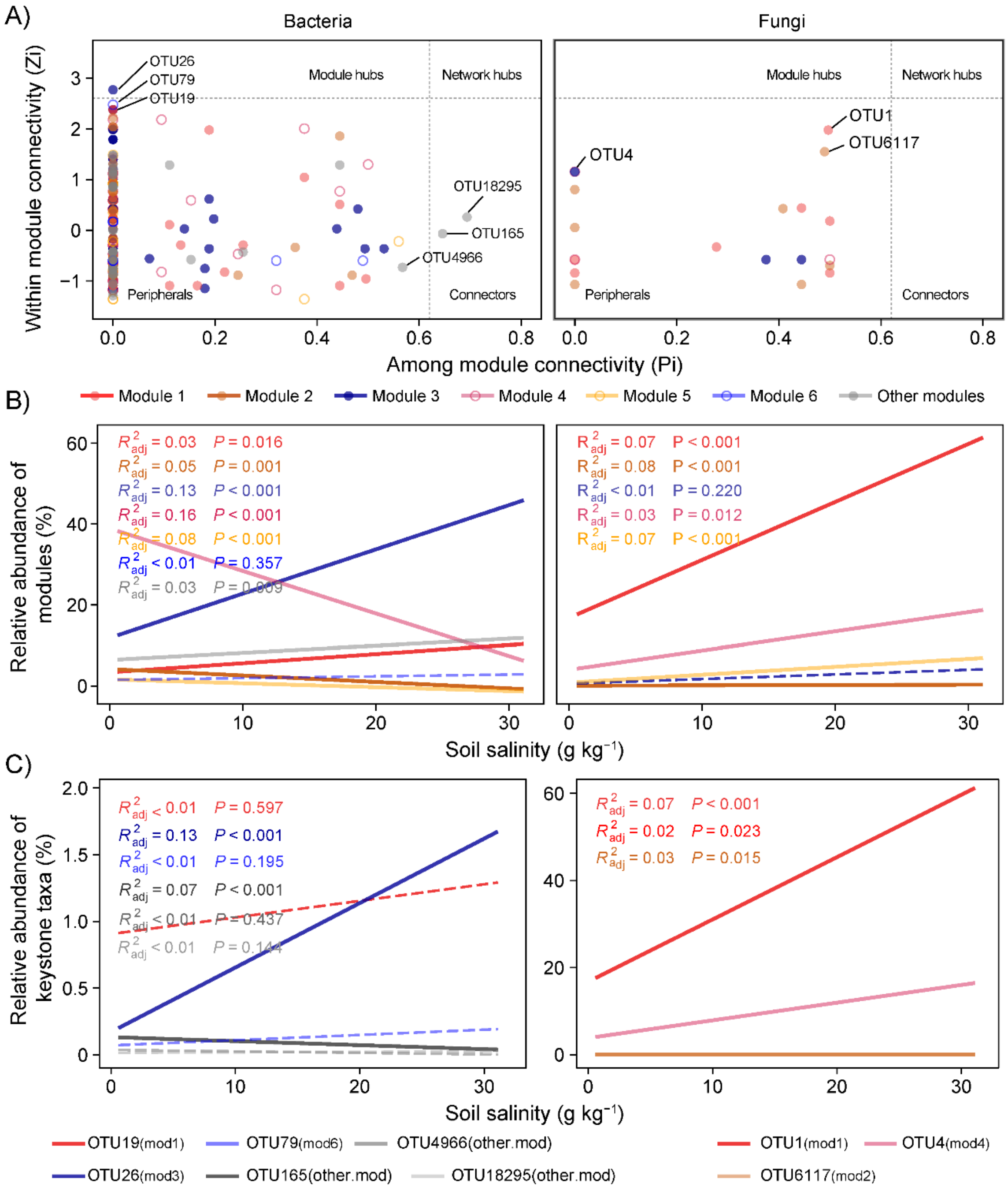
Supplemental Figure 6. Spearman correlations between soil properties in the Tarim desert. Values in box are the correlation coefficients. Salinity, soil salinity (g kg^{-1}); SOC, soil organic carbon (g kg^{-1}); STN, soil total nitrogen (g kg^{-1}); STP, soil total phosphorus (g kg^{-1}); C:N, SOC:STN ratio; C:P, SOC:STP ratio; N:P, STN:STP ratio; SM, soil moisture (g g^{-1}) ; Clay&Silt, soil clay and silt content (g g^{-1}). ***, P<0.001; **, P<0.01; *, P<0.05.



Supplemental Figure 7. Phylogenetical structure of bacterial and common bacterial communities in the Tarim desert. NTI ⩾ 2 and < 2, denote that communities are significantly phylogenetically clustered and overdispersed compared with null models, respectively.



Supplemental Figure 8. Changes in soil hydrolytic enzyme activities with the modularity of bacteria and fungi. Solid and dash lines denotes the significant and insignificant estimates, respectively.



Supplemental Figure 9. Identification of bacterial and fungal keystone taxa and the correlations with soil salinity. A) Identification of bacterial (left) and fungal (right) keystone taxa based on the topological roles; B) relative abundance of bacterial (left) and fungal (right) modules; C) relative abundance of bacterial (left) and fungal (right) keystone taxa. Different colors in A–-C denotes different modules. Solid and dashed lines in B–-C denote significant and insignificant estimates, respectively.