Supplementary Information for

Shorebirds-driven trophic cascade helps restore coastal wetland multifunctionality

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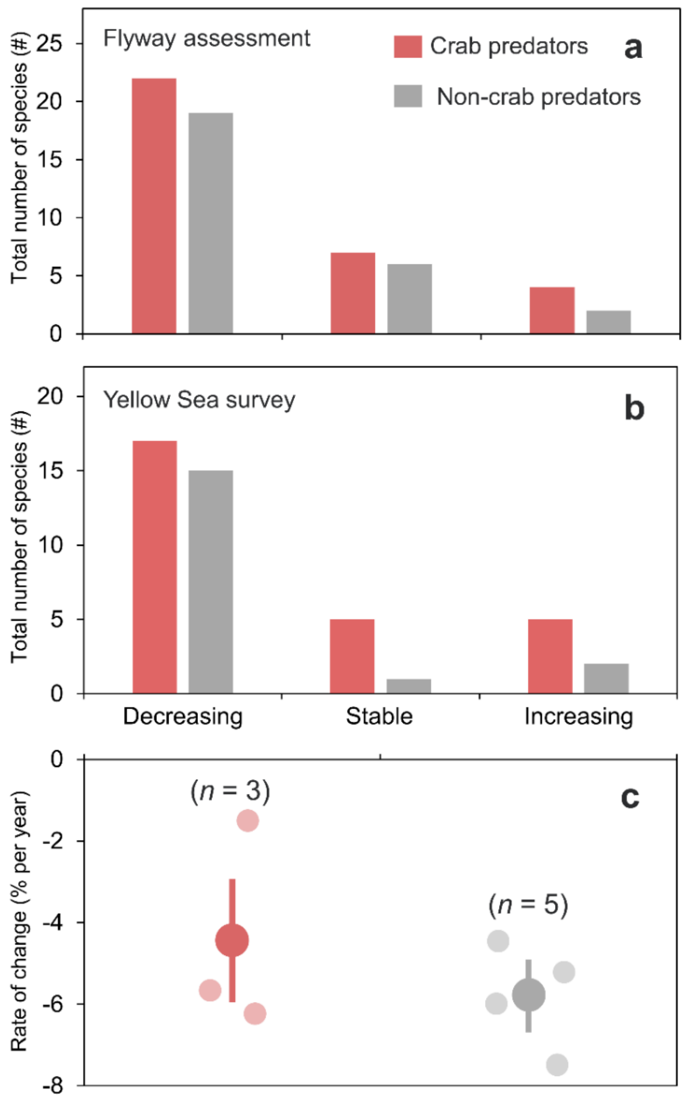
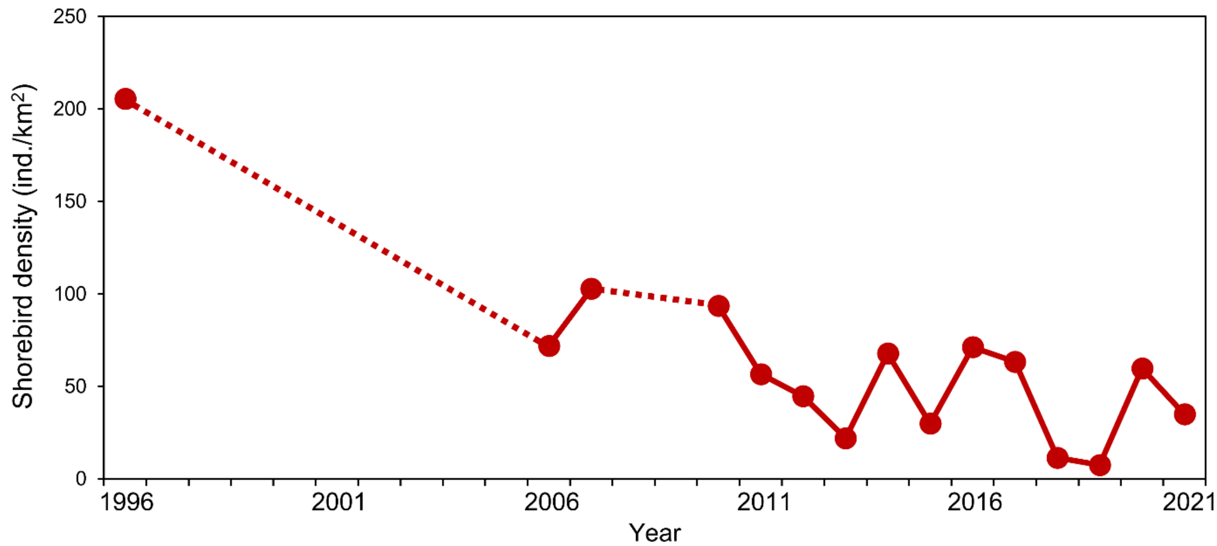
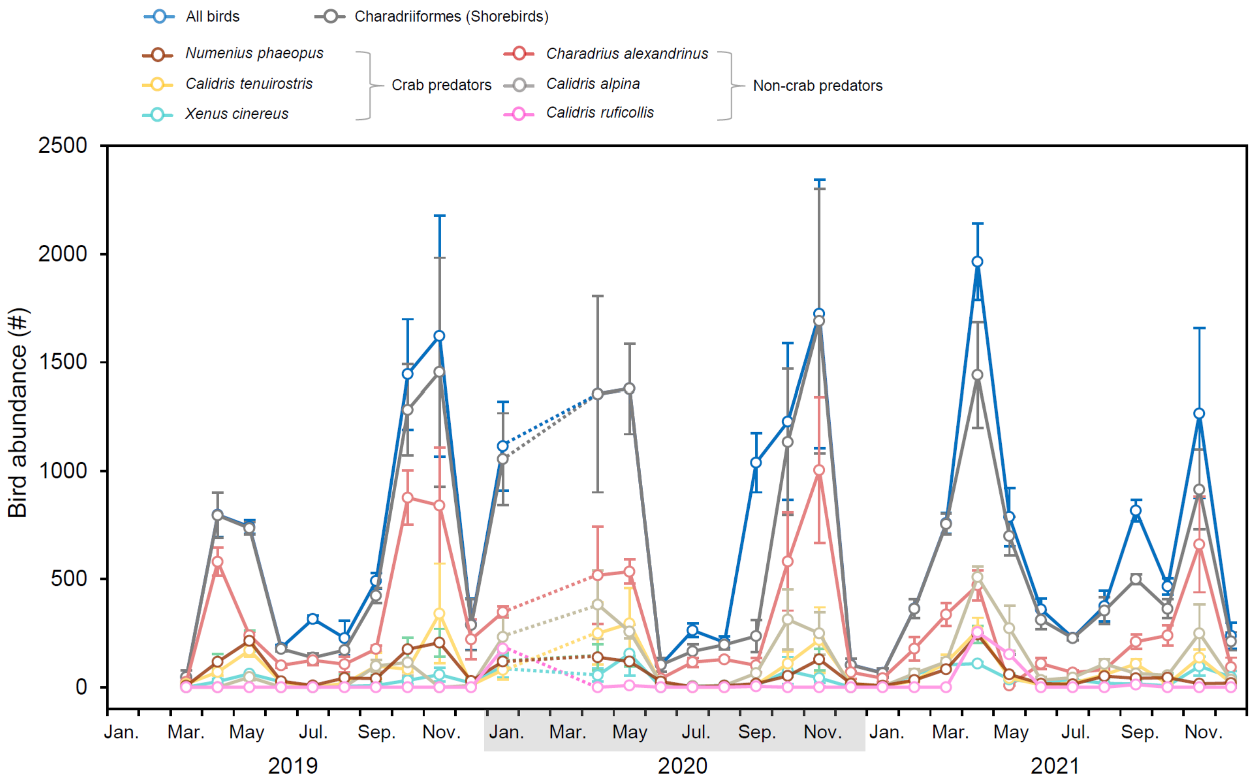


Supplementary Fig. 1: Population trends of shorebird species that consume and do not consume crabs. (**a**) Flyway assessment based on assessments of the global population of all shorebird species that utilize coastal habitats in the Yellow Sea. (**b**) Yellow Sea survey. Given in **a** and **b** are the numbers of shorebird species with a decreasing, stable, and increasing population. (**c**) Annual rate of change in the population size of shorebirds with a strong reliance on coastal habitats in the Yellow Sea (*n* indicates independent species; data from Studds *et al.* 2017).

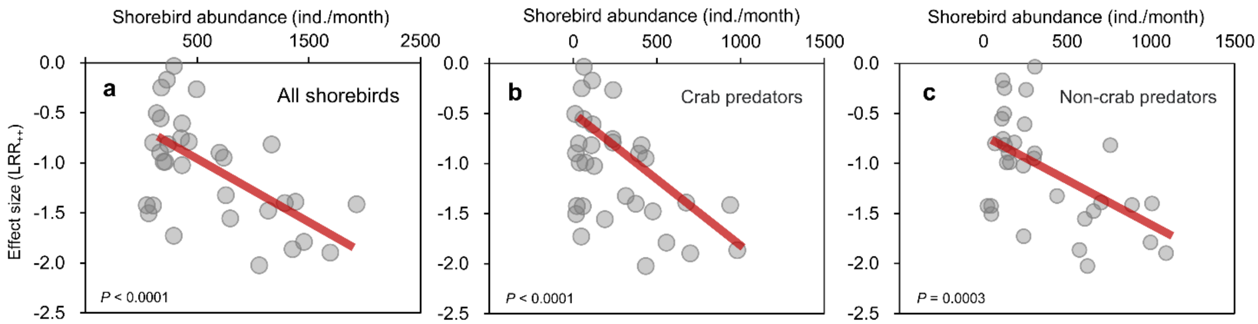


Supplementary Fig. 2: Long-term trend in shorebird density during northward migration. The shorebird surveys were conducted in the intertidal zones of Shanghai Chongming Dongtan National Nature Reserve.

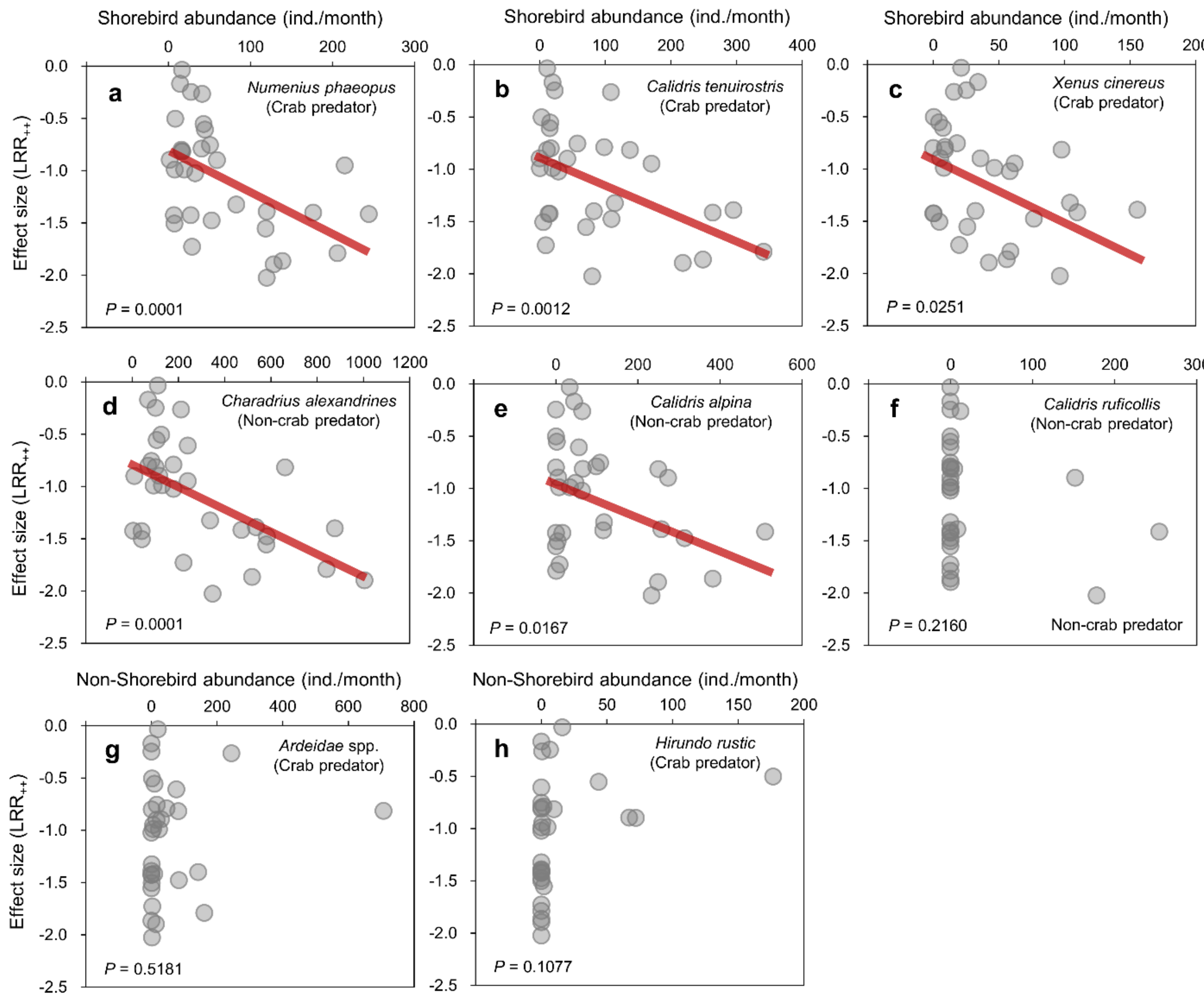
Supplementary Fig. 3: Photographs showing crab grazing on aboveground stems of planted *Scirpus*. Photo credit: Chunming Li. Also, see Supplementary Movie 1.



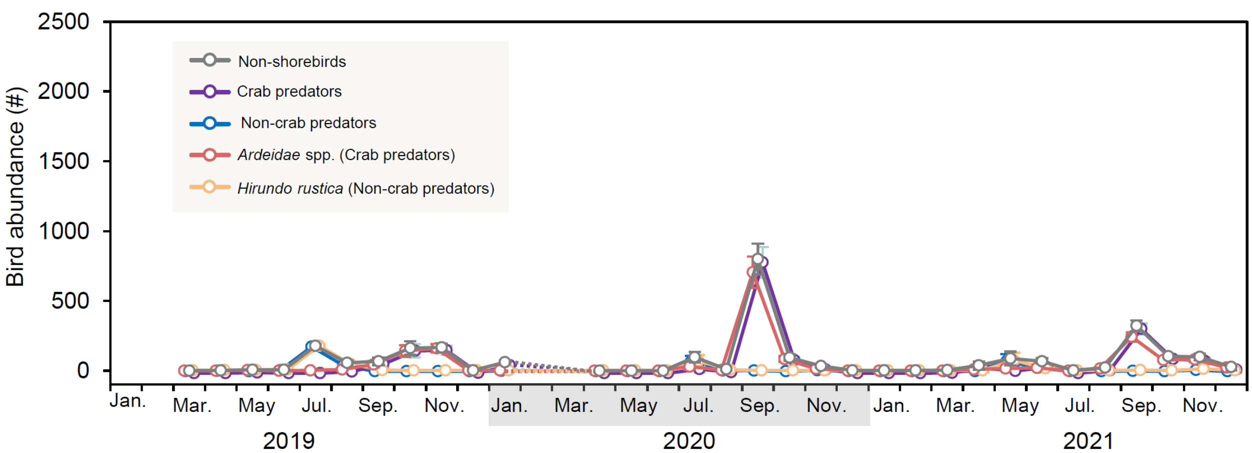
Supplementary Fig. 4: Monthly changes in shorebird abundance at the restoration site from 2019 to 2021. The total abundance of all birds, all shorebirds, as well as the abundance of six shorebird species with the highest total abundance, are shown. Data are shown as means ± SE (*n* = 3 independent camera traps).



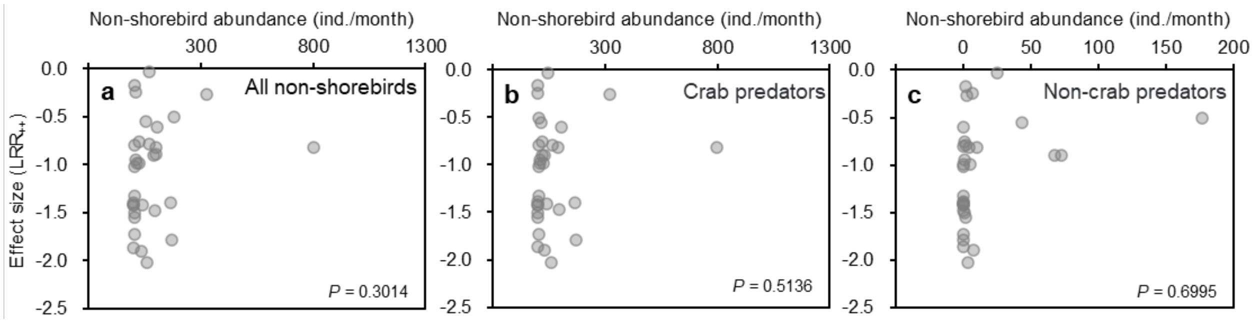
Supplementary Fig. 5: Variation in the effect size of shorebirds on crab abundance against shorebird abundance: (**a**) All shorebirds, (**b**) crab predators, and (**c**) non-crab predators. Red lines indicate a statistically significant meta-regression ($P < 0.05$; see Supplementary Table 3 for test statistics). For all panels, $n = 32$ repeated measurements (potential autocorrelation was accounted for by including plot ID as a random effect; see Methods).



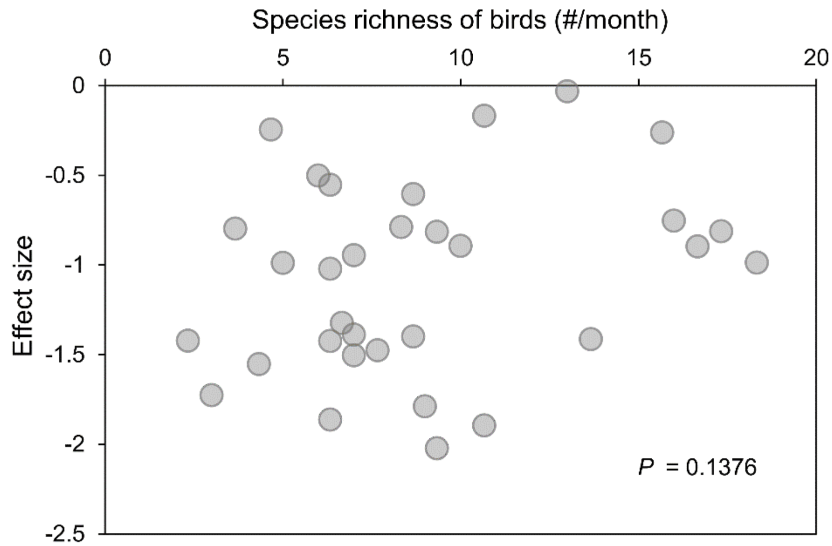
Supplementary Fig. 6: Variation in the effect size of birds on crab abundance against bird abundance. (**a**) *Numenius phaeopus*, (**b**) *Calidris tenuirostris*, (**c**) *Xenus cinereus*, (**d**) *Charadrius alexandrines*, (**e**) *Calidris alpina*, (**f**) *Calidris ruficollis*, (**g**) *Ardeidae spp.*, and (**h**) *Hirundo rustic*. Red lines indicate a statistically significant meta-regression ($P < 0.05$; see Supplementary Table 3 for test statistics). For all panels, $n = 32$ repeated measurements (potential autocorrelation was accounted for by including plot ID as a random effect; see Methods).



Supplementary Fig. 7: Trends in the abundances of non-shorebirds at the study site from 2019 to 2021. Non-shorebirds are further categorized into crab predators and non-crab predators. Two non-shorebird species with the highest total abundance are also shown. Data are shown as means with error bars for standard errors (n = 3 independent camera traps).

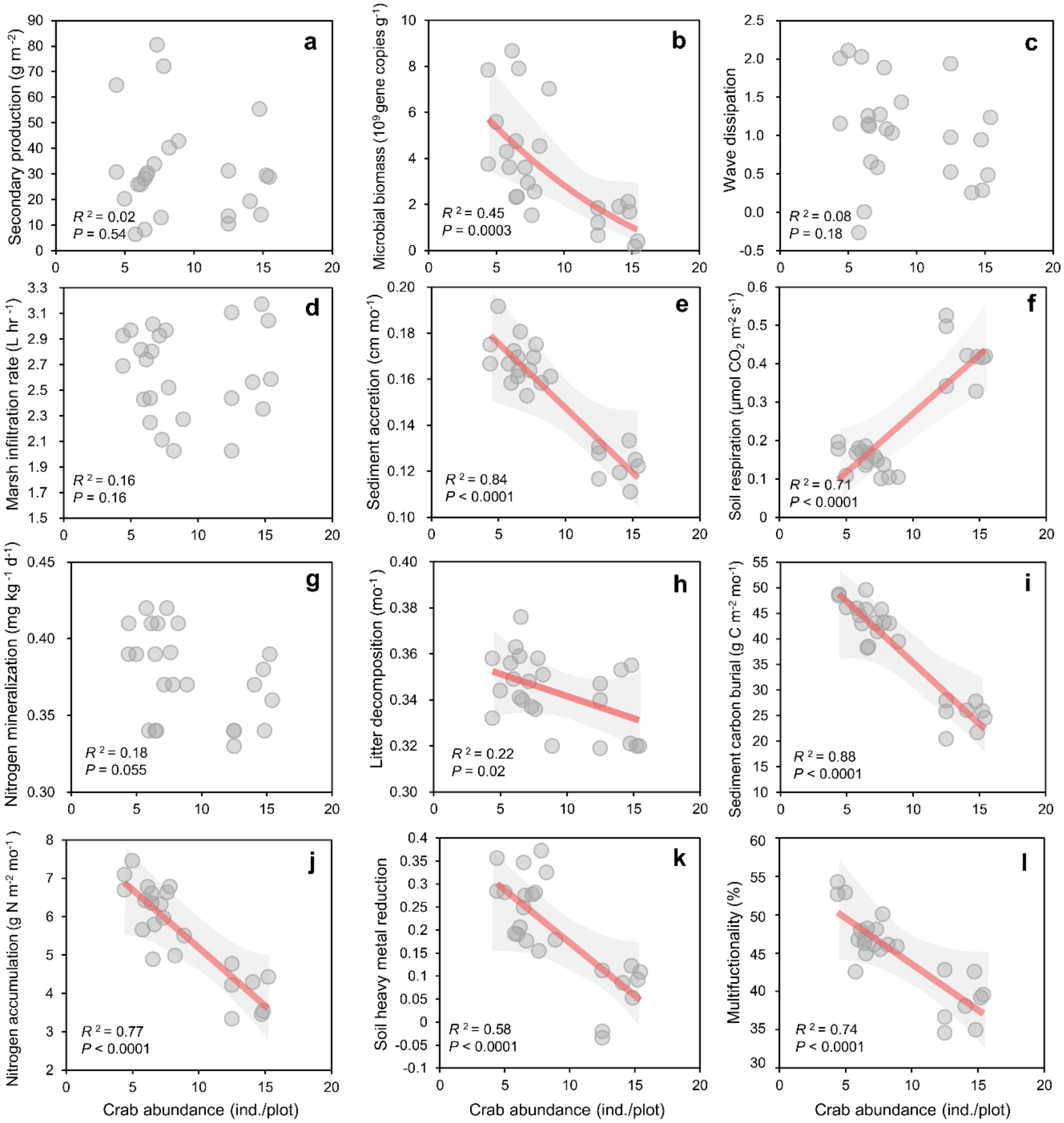


Supplementary Fig. 8: Variation in the effect size of birds on crab abundance against the abundance of non-shorebirds. (**a**) All non-shorebirds; (**b**) crab predators, and (**c**) non-crab predators. None of the meta-regression models were statistically significant (see Supplementary Table 3 for test statistics). For all panels, n = 32 repeated measurements (potential autocorrelation was accounted for by including plot ID as a random effect; see Methods).

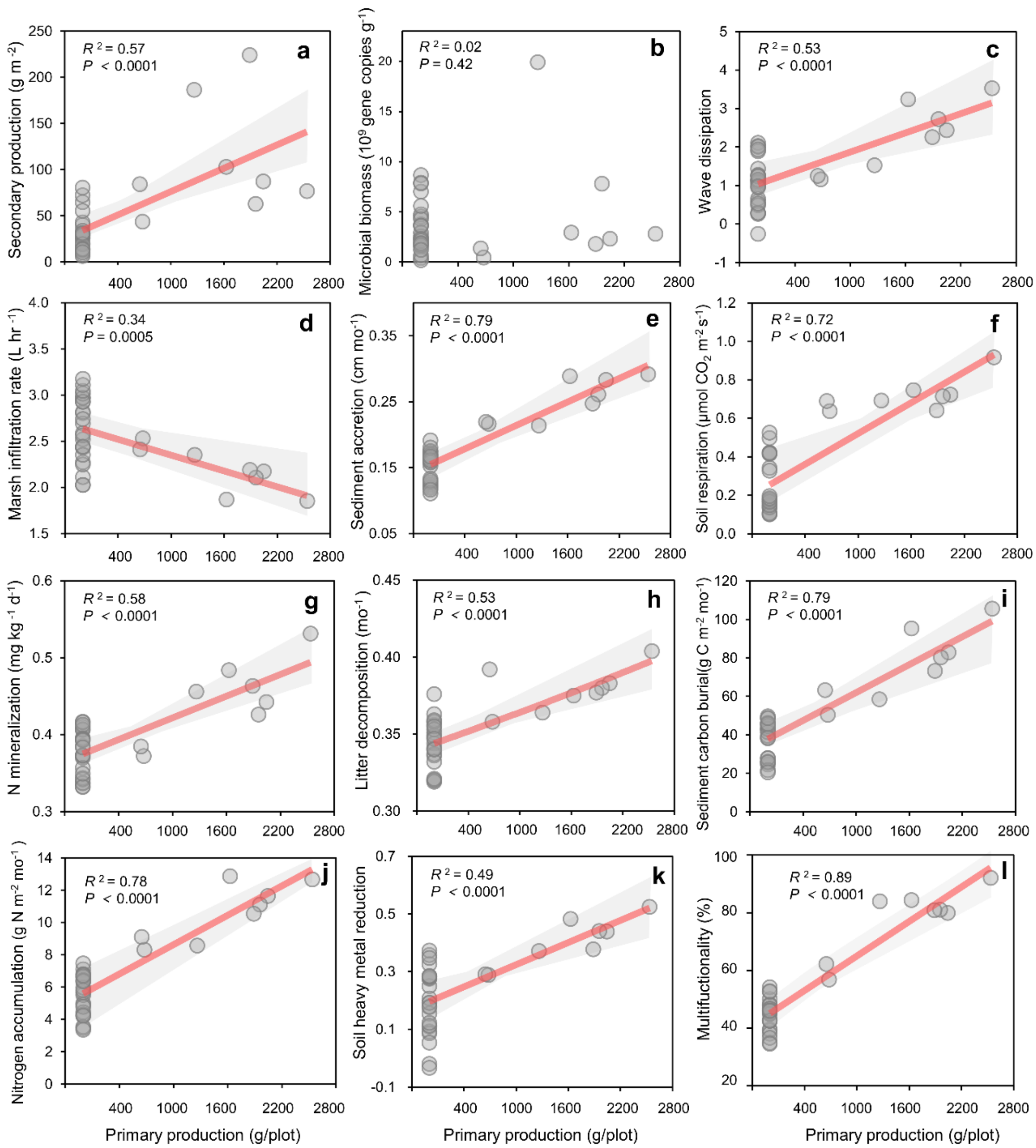


Supplementary Fig. 9: Variation in the effect size of birds on crab abundance against the species richness of birds. The meta-regression model was not statistically significant (n =32 repeated measurements; potential autocorrelation was accounted for by including plot ID as a random effect; see Supplementary Table 3 for test statistics).

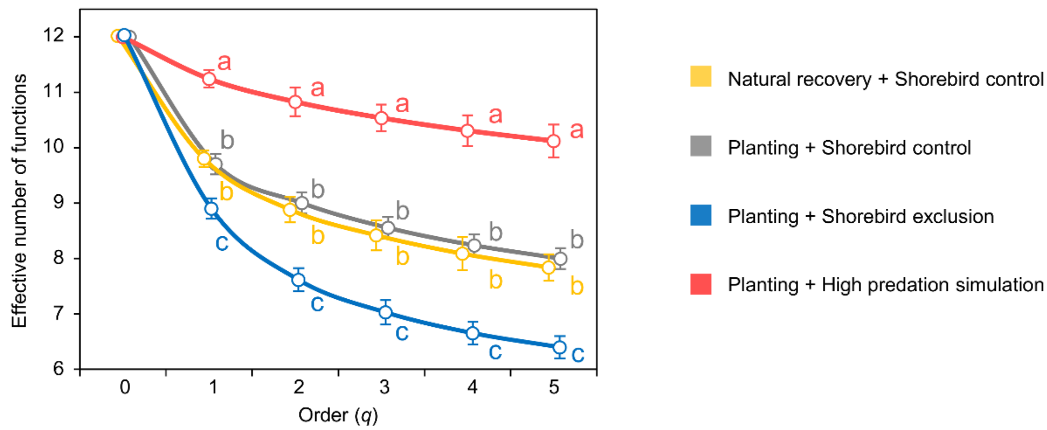
Supplementary Fig. 10: Non-consumptive effects of shorebirds on crab grazers. (**a**) Procedural control using a ball with similar size and color. (**b**) Simulation of the consumptive effects of shorebirds using a swinging shorebird (*Numenius phaeopus*) model. (**c**) Crab abundance in different treatments before and after the experimental set-up (one-way ANOVA; see Supplementary Table 4 for test statistics). Data are shown as means ± SE (n = 8 independent plots). Of a sampling date, points that do not share a letter differ significantly from one another based on Tukey's HSD multiple comparisons ($P < 0.05$; detailed statistical results are provided in Supplementary Table 5).



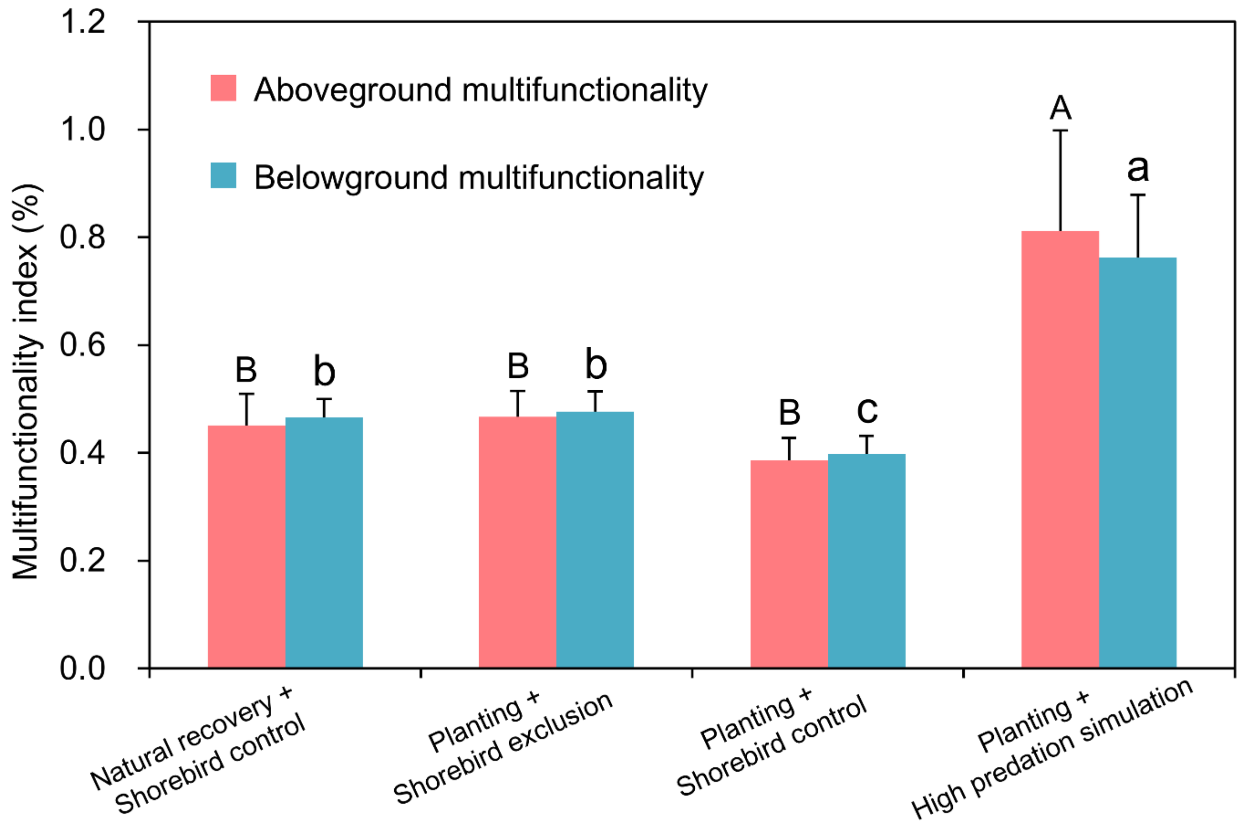
Supplementary Fig. 11: Individual ecosystem functions and average multifunctionality as a function of crab abundance. Red lines indicate a statistically significant linear or quadratic regression (P < 0.05; see Supplementary Table 9 for test statistics). Shaded areas are 95% confidence intervals (n = 24 independent plots).



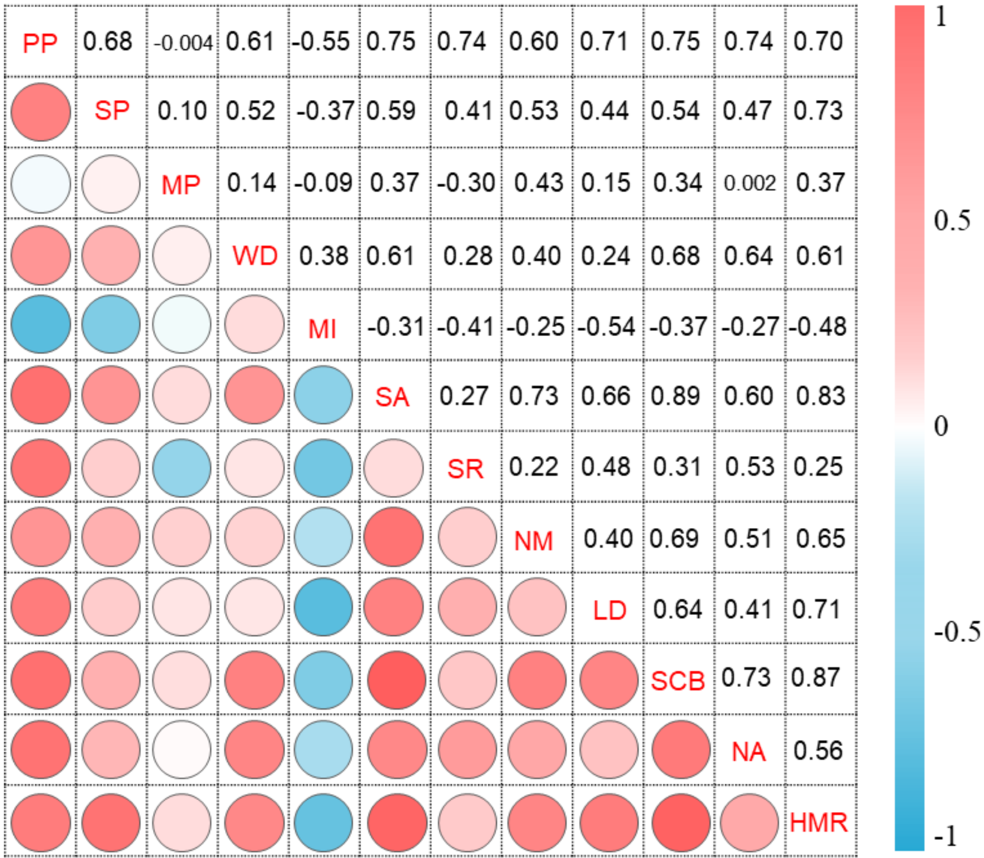
Supplementary Fig. 12: Individual ecosystem functions and average multifunctionality as a function of primary production. Red lines indicate a statistically significant linear or quadratic regression (P < 0.05; see Supplementary Table 10 for test statistics). Shaded areas are 95% confidence intervals (n = 32 independent plots).



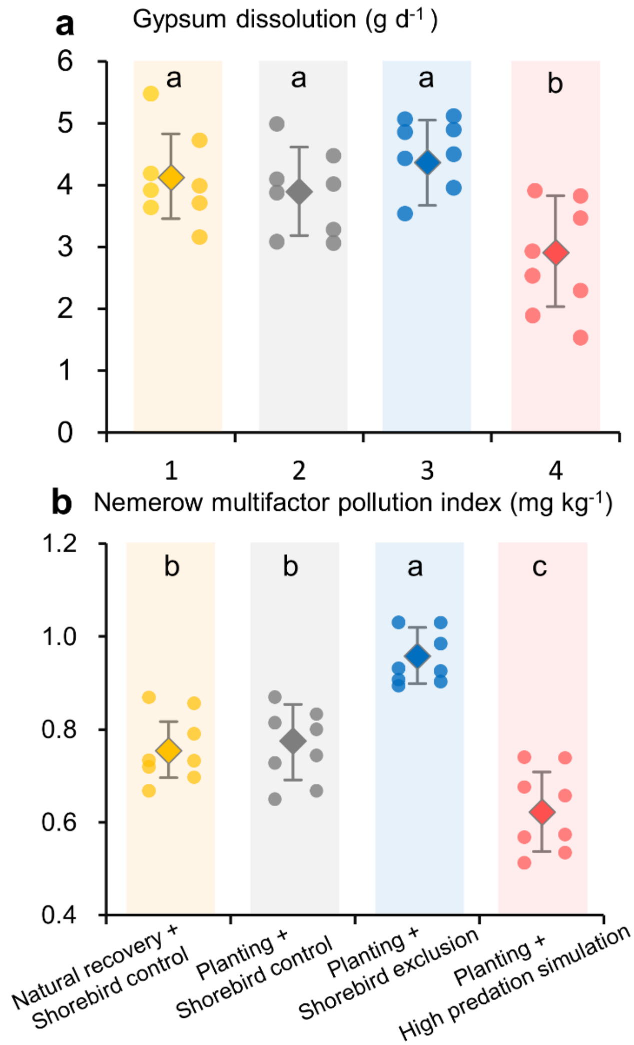
Supplementary Fig. 13: The effective number of functions in different restoration treatments. The effective number of functions is the equivalent number of functions were all functions provided at the same level (Byrnes *et al.* 2023). The effective number of functions is just the number of functions measured when order $q = 0$ and analogue to Shannon diversity for species when $q = 1$. When $q > 1$, functions performing at higher levels are given greater weight. Data are shown as means with error bars for standard errors ($n = 8$ independent plots, one-way ANOVA; see Supplementary Table 12 for test statistics). Treatments that do not share a letter differ significantly from one another based on Tukey HSD multiple comparisons ($P < 0.05$; detailed statistical results are provided in Supplementary Table 13).



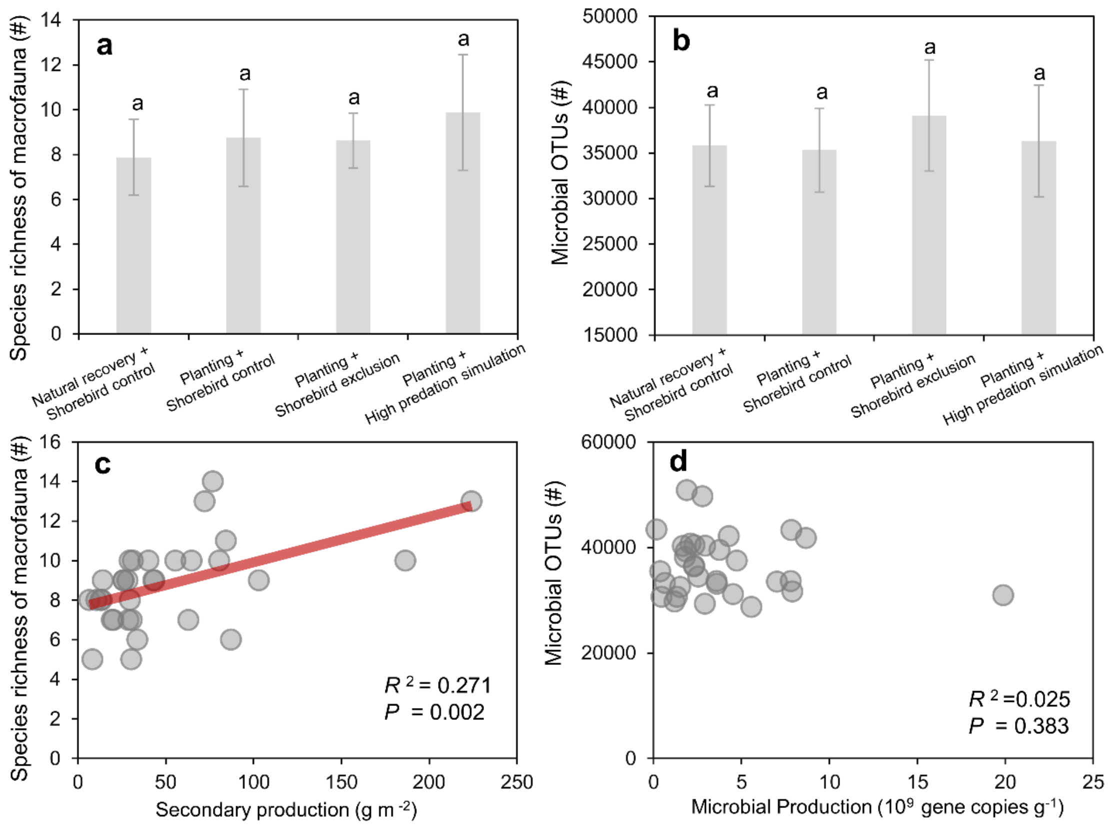
Supplementary Fig. 14: Below- and aboveground multifunctionality in different restoration treatments. Data are shown as means with error bars for standard errors (*n* = 8 independent plots). Within a group of belowground multifunctionality (one-way ANOVA, df = 3, 28, *F* = 27.76, *P* < 0.0001) and aboveground multifunctionality (one-way ANOVA, df = 3, 28, *F* = 55.5, *P* < 0.0001), bars sharing a letter are not significantly different from one another based on Tukey's HSD multiple comparisons (*P* < 0.05; detailed statistical results are provided in Supplementary Table 16).



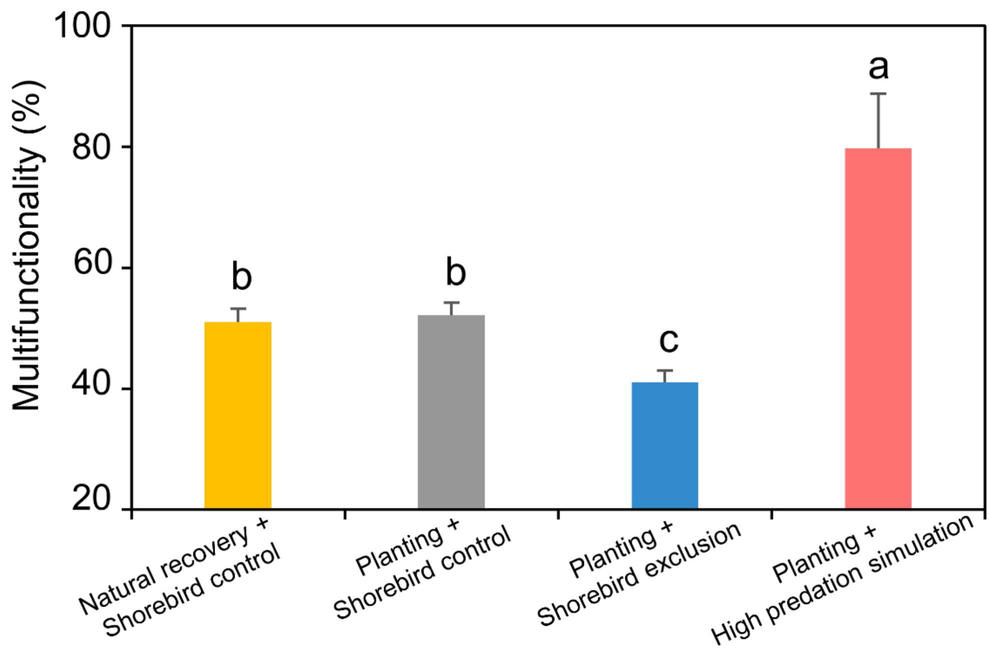
Supplementary Fig. 15: Correlation between the twelve ecosystem functions. PP: primary production of *Scirpus mariqueter*, SP: secondary production, MP: microbial production, WD: wave dissipation, MI: marsh infiltration, SA: sediment accretion, SR: soil respiration, NM: nitrogen mineralization, LD: litter decomposition, SCB: sediment carbon burial, NA: nitrogen accumulation, and HMR: soil heavy metal reduction.



Supplementary Fig. 16: Individual ecosystem functions in different restoration treatments. (**a**) gypsum dissolution (one-way ANOVA; df = 3, 28, F = 6.101, P = 0.0025), and (**b**) Nemerow multifactor pollution index (one-way ANOVA; df = 3, 28, F = 6.101, P < 0.0001). Data are shown as means with error bars for standard errors (n = 8 independent plots). Bars sharing a letter are not significantly different from one another based on Tukey's HSD multiple comparisons (P < 0.05; detailed statistical results are provided in Supplementary Table 19).



Supplementary Fig. 17: Treatment effects on macrofauna and microbial diversity. (**a**) Species richness of macrofauna (one-way ANOVA; df = 3, 28, F = 1.2191, P = 0.3211), (**b**) microbial operational taxonomic units (OTUs) (one-way ANOVA; df = 3, 28, F = 0.6984, P = 0.5609), (**c**) species richness of macrofauna as a function of macrofauna biomass, and (**d**) microbial OTUs as a function of microbial production. In **a** and **b**, data are shown as means with error bars for standard errors (n = 8 independent plots). Bars sharing a letter are not significantly different from one another based on Tukey's HSD multiple comparisons ($P < 0.05$; detailed statistical results are provided in Supplementary Table 20). In **c** and **d**, red lines indicate a statistically significant regression (n = 32 independent plots; $P < 0.05$).



Supplementary Fig. 18: Wetland multifunctionality in different restoration treatments. Here, species richness of macrofauna and microbial OTUs, instead of macrofaunal biomass and microbial production, were used to calculate the average standardized multifunctionality index. Data are shown as means with error bars for standard errors (n = 8 independent plots; one-way ANOVA; df = 3, 28, F = 45.78, $P < 0.0001$). Bars sharing a letter are not significantly different from one another based on Tukey's HSD multiple comparisons ($P < 0.05$; detailed statistical results are provided in Supplementary Table 21).

Supplementary Table 1: Shorebird and non-shorebird species observed at the restoration site from 2019 to 2021

Bird group	Foraging pattern	Species observed
Shorebird	Crab predators	*Numenius phaeopus, Calidris tenuirostris, Xenus cinereus, Tringa nebularia, Numenius arquata, Tringa stagnatilis, Tringa brevipes, Numenius minutus, Limosa limosa, Tringa erythropus, Calidris ferruginea, Limnodromus scolopaceus*
	Non-crab predators	*Charadrius alexandrinus, Calidris alpina, Calidris ruficollis, Eurynorhynchus pygmeus, Calidris acuminata, Calidris alba, Limicola falcinellus, Arenaria interpres, Actitis hypoleucos, Calidris minuta, Tringa tetanus, Charadrius dubius, Charadrius mongolus, Charadrius leschenaultii, Pluvialis fulva, Pluvialis squatarola, Charadrius placidus*
Non-shorebird	Crab predators	*Ardea cinerea, Ardeidae* spp., *Platalea leucorodia, Nycticorax nycticorax, Larus argentatus, Chlidonias leucopterus, Larus canus, Larus saundersi, Sterna hirundo, Chlidonias hybrida, Larus crassirostris, Larus ridibundus*
	Non-crab predators	*Hirundo rustica, Pica pica, Elanus caeruleus, Falco peregrinus, Pandion haliaetus, Anas platyrhynchos, Fringilla montifringilla*

Supplementary Table 2: The 12 ecosystem functions considered in this study and their corresponding ecosystem services and proxies measured in this study

Ecosystem function	**Ecosystem service**	**Proxy measured**	**References**
Primary production	Provisioning: fiber and biomass fuel	Plant biomass	Barbier *et al.* 2011, Michaletz *et al.* 2014, Ramus *et al.* 2017
Secondary production	Provisioning: food; Supporting: fisheries	Macrofaunal biomass	Barbier *et al.* 2011, Ramus *et al.* 2017
Microbial production	Supporting: nutrient cycling	Microbial biomass	Zhang et al. 2019, Garland *et al*. 2021
Wave dissipation	Regulating: storm protection	Rate of gypsum block dissolution	Barbier *et al.* 2011, Ramus *et al.* 2017
Marsh infiltration	Regulating: water runoff	Infiltration rate of water through marsh soils	Hemond *et al.* 1984, Hensel *et al.* 2013
Sediment accretion	Regulating: erosion	Sediment accretion rate	Barbier *et al.* 2011, Ramus *et al.* 2017, Thomsen *et al.* 2019
Soil respiration	Regulating: soil health	Rate of soil CO_2 release	Bastida *et al.* 2016, Lozano *et al.* 2021
Nitrogen mineralization	Regulating: soil fertility	Changes in soil inorganic nitrogen per day	Schimel J.P. and Bennett J. 2004, Risch *et al.* 2019
Litter decomposition	Supporting: nutrient cycling	Rate of plant litter biomass change	Barbier et al. 2011, Hensel *et al.* 2013, Ramus *et al.* 2017

Sediment carbon burial	Regulating: climate change	Increases in the organic carbon of surface accreted sediment per unit area per month	Schlesinger 1999, Rattan 2008, Christianen *et al.* 2022
Nitrogen accumulation	Supporting: waste treatment	Increases in sediment soil total nitrogen per unit area per month	Craft et al. 2009, Zhang *et al.* 2019, Geurts *et al.* 2020
Soil heavy metal reduction	Supporting: soil pollution mitigation	Changes in the Nemerow multifactor pollution index	Abdullah *et al.* 1972, Zhang *et al.* 2021, Yan *et al.* 2022

Supplementary Table 3: Estimated parameters of the meta-regression models for the effect size of birds on crab abundance against the abundances of different groups of birds, as well as bird species richness.

Bird taxa	Intercept			Slope		
	Estimate	SE	*P*-value	Estimate	SE	*P*-value
Shorebirds	-0.6649	0.1310	< 0.0001	-0.0006	0.0002	*P* < 0.0001
Crab predators	-0.7492	0.1235	< 0.0001	-0.0011	0.0003	*P* < 0.0001
Non-crab predators	-0.7721	0.1342	< 0.0001	-0.0012	0.0003	0.0003
Non-shorebirds	-1.1321	0.1153	< 0.0001	0.0007	0.0007	0.3014
Crab predators	-1.1050	0.1122	< 0.0001	0.0005	0.0007	0.5136
Non-crab predators	-1.1406	0.1063	< 0.0001	0.0047	0.0029	0.6995
Charadrius alexandrinus	-0.7180	0.1259	< 0.0001	-0.0012	0.0003	0.0001
Calidris alpina	-0.8846	0.1235	< 0.0001	-0.0017	0.0007	0.0167
Calidris tenuirostris	-0.8155	0.1195	< 0.0001	-0.0029	0.0009	0.0012
Numenius phaeopus	-0.7617	0.1242	< 0.0001	-0.0044	0.0013	0.0004
Ardeidae spp.	-1.1021	0.1107	< 0.0001	0.0005	0.0008	0.5181
Xenus cinereus	-0.8489	0.1392	< 0.0001	-0.0054	0.0024	0.0251
Calidris ruficollis	-1.0318	0.1065	< 0.0001	-0.0020	0.0017	0.2160
Hirundo rustica	-1.1344	0.1055	< 0.0001	0.0046	0.0029	0.1077
Species richness	-1.3932	0.2362	< 0.0001	0.0355	0.0239	0.1376

Supplementary Table 4: Summary statistics of one-way ANOVAs on the effects of different experimental treatments on crab abundance in the shorebirds' non-consumptive effects simulation experiment.

Sampling date	df	*F*-ratio	*P*-value
18-Jun-23	2, 21	0.263	0.7713
20-Jun-23	2, 21	0.156	0.8562
27-Jun-23	2, 21	25.14	< 0.0001
4-Jul-23	2, 21	49.921	< 0.0001
10-Jul-23	2, 21	63.964	< 0.0001

Supplementary Table 5: Summary statistics of multiple comparisons on the effects of different experimental treatments on crab abundance in the shorebirds' non-consumptive effects simulation experiment.

Sampling date	Pairwise comparison	Diff	Lwr	Upr	*P*-value
18-Jun-23	PC *vs.* C	0.625	-1.6739	2.9239	0.7745
	SM *vs.* C	0.125	-2.1739	2.4239	0.9897
	SM *vs.* PC	-0.500	-2.7989	1.7989	0.8484
20-Jun-23	PC *vs.* C	0.375	-1.970	2.7207	0.9147
	SM *vs.* C	-0.125	-2.470	2.2207	0.9901
	SM *vs.* PC	-0.500	-2.8457	1.8457	0.8539
27-Jun-23	PC *vs.* C	-1.250	-2.9508	0.4508	0.1774
	SM *vs.* C	-4.625	-6.3258	-2.9241	< 0.0001
	SM *vs.* PC	-3.375	-5.0758	-1.6741	0.0001
4-Jul-23	PC *vs.* C	-1.375	-2.9608	0.2108	0.0970
	SM *vs.* C	-6.000	-7.5858	-4.4141	< 0.0001
	SM *vs.* PC	-4.625	-6.2108	-3.0391	< 0.0001
10-Jul-23	PC *vs.* C	-1.000	-2.5281	0.5281	0.2478
	SM *vs.* C	-6.375	-7.9031	-4.8468	< 0.0001
	SM *vs.* PC	-5.375	-6.9031	-3.8468	< 0.0001

Note: C, PC, and SM refers to control, procedural control, and shorebird model treatments, respectively. Diff refers to the difference in mean value between two types of treatment. Lwr and Upr refer to the lower and upper bounds of 95% confidence interval, respectively.

Supplementary Table 6: Summary statistics of multiple comparisons on the effects of different restoration treatments on the rate of plant abundance change.

Pairwise comparison	Diff	Lwr	Upr	*P*-value
PL + BE *vs.* PL	-3.4406	-4.8689	-2.0123	< 0.0001
PL + HP *vs.* PL	2.7437	1.3154	4.1720	0.0002
PL + HP *vs.* PL +BE	6.1843	4.7560	7.6126	< 0.0001

Note: PL refers to planting + shorebird control treatments; NR refers to natural recovery + shorebird control treatments; PL + BE refers to planting + shorebird exclusion treatments; and PL + HP refers to planting + high predation simulation treatments. Diff refers to the difference in mean value between two types of treatment. Lwr and Upr refer to the lower and upper bounds of 95% confidence interval, respectively.

Supplementary Table 7: Summary statistics of one-way ANOVAs (or Wilcoxon tests) on the effects of different restoration treatments on wetland functions.

Wetland functions	**df**	***F*-ratio (V)**	***P*-value**
Primary production	-	36	0.01427
Secondary production	-	528	< 0.0001
Microbial production	3, 28	1.822	0.166
Wave dissipation	3, 28	6.111	0.0025
Marsh infiltration	3, 28	3.523	0.0277
Sediment accretion.	3, 28	68.46	< 0.0001
Soil respiration	3, 28	168.3	< 0.0001
Nitrogen mineralization	3, 28	9.651	0.000154
Litter decomposition	3, 28	13.23	< 0.0001
Sediment carbon burial	3, 28	37.67	< 0.0001
Nitrogen accumulation	3, 28	53.57	< 0.0001
Heavy metal reduction	3, 28	28.79	< 0.0001

Note: "V" stands for the Wilcoxon rank sum statistic (for primary production and secondary production).

Supplementary Table 8: Summary statistics of multiple comparisons on the effects of different restoration treatments on wetland functions.

Wetland function	Pairwise comparison	Diff	Lwr	Upr	*P*-value
Primary production	PL *vs.* NR	-	-	-	-
	PL + BE *vs.* NR	-	-	-	-
	PL + HP *vs.* NR	-	-	-	0.0012
	PL + BE *vs.* PL	-	-	-	-
	PL + HP *vs.* PL	-	-	-	0.0012
	PL + HP *vs.* PL + BE	-	-	-	0.0012
Secondary production	PL *vs.* NR	-	-	-	1.0000
	PL + BE *vs.* NR	-	-	-	1.0000
	PL + HP *vs.* NR	-	-	-	0.0037
	PL + BE *vs.* PL	-	-	-	1.0000
	PL + HP *vs.* PL	-	-	-	0.0321
	PL + HP *vs.* PL + BE	-	-	-	0.0019
Microbial production	PL *vs.* NR	0.1840	-4.7686	5.1366	0.9996
	PL + BE *vs.* NR	-3.2368	-8.1895	1.7157	0.3017
	PL + HP *vs.* NR	0.4376	0.2207	5.3902	0.9949
	PL + BE *vs.* PL	-3.4208	-4.5150	1.5317	0.2568
	PL + HP *vs.* PL	0.2536	-8.3735	5.2062	0.9990
	PL + HP *vs.* PL + BE	3.6745	-4.6990	8.6271	0.2028
Wave dissipation	PL *vs.* NR	0.2062	-0.7807	1.1932	0.9400
	PL + BE *vs.* NR	-0.2246	-1.2116	0.7620	0.9243
	PL + HP *vs.* NR	1.2077	0.2207	2.1947	0.0120
	PL + BE *vs.* PL	-0.4308	-1.4178	0.5561	0.6369
	PL + HP *vs.* PL	1.0015	0.0144	1.9885	0.0457

	PL + HP *vs.* PL + BE	1.4323	0.4453	2.4194	0.0024
Marsh infiltration	PL *vs.* NR	0.0018	-0.4610	0.4648	0.999
	PL + BE *vs.* NR	0.0438	-0.4190	0.5068	0.0731
	PL + HP *vs.* NR	-0.4330	-0.8959	0.0299	0.0731
	PL + BE *vs.* PL	0.0420	-0.4209	0.5049	0.9945
	PL + HP *vs.* PL	-0.4348	-0.8978	0.0280	0.0714
	PL + HP *vs.* PL + BE	-0.4768	-0.9398	-0.0139	0.0416
Sediment accretion	PL *vs.* NR	0.0011	-0.0241	0.0263	0.9993
	PL + BE *vs.* NR	-0.0440	-0.0692	-0.0187	0.0003
	PL + HP *vs.* NR	0.0855	0.0602	0.1107	< 0.0001
	PL + BE *vs.* PL	-0.0451	-0.0703	-0.0198	0.00021
	PL + HP *vs.* PL	0.0843	0.05910	0.1096	< 0.0001
	PL + HP *vs.* PL + BE	0.1295	0.1042	0.1547	< 0.0001
Soil respiration	PL *vs.* NR	0.0235	-0.0575	0.1045	0.8578
	PL + BE *vs.* NR	0.2837	0.2026	0.3648	< 0.0001
	PL + HP *vs.* NR	0.5828	0.5017	0.6639	< 0.0001
	PL + BE *vs.* PL	0.2602	0.1791	0.3413	< 0.0001
	PL + HP *vs.* PL	0.5593	0.4782	0.6404	< 0.0001
	PL + HP *vs.* PL + BE	0.2991	0.2180	0.3802	< 0.0001
Nitrogen mineralization	PL *vs.* NR	-0.0045	-0.0512	0.0420	0.9931
	PL + BE *vs.* NR	-0.0335	-0.0801	0.0131	0.2266
	PL + HP *vs.* NR	0.0562	0.0096	0.1028	0.0135
	PL + BE *vs.* PL	-0.0289	-0.0755	0.01770	0.3456
	PL + HP *vs.* PL	0.0608	0.0141	0.1074	0.0069
	PL + HP *vs.* PL + BE	0.0897	0.0431	0.1363	< 0.0001
Litter decomposition	PL *vs.* NR	-0.0025	-0.0226	0.0176	0.9863
	PL + BE *vs.* NR	-0.0148	-0.0350	0.0052	0.2065

	PL + HP *vs.* NR	0.0298	0.0097	0.0500	0.0019
	PL + BE *vs.* PL	-0.0123	-0.0325	0.0077	0.3540
	PL + HP *vs.* PL	0.0323	0.0122	0.0525	0.0008
	PL + HP *vs.* PL + BE	0.0447	0.0245	0.0649	< 0.0001
Sediment carbon burial	PL *vs.* NR	-0.3838	-13.732	12.9651	0.9998
	PL + BE *vs.* NR	-19.2300	-32.579	-5.8809	0.0026
	PL + HP *vs.* NR	31.9153	18.5663	45.2644	< 0.0001
	PL + BE *vs.* PL	-18.8461	-32.195	-5.4971	0.0032
	PL + HP *vs.* PL	32.2992	18.9502	45.6482	< 0.0001
	PL + HP *vs.* PL + BE	51.1453	37.7963	64.4944	< 0.0001
Nitrogen accumulation	PL *vs.* NR	0.3633	-1.0882	1.8149	0.9025
	PL + BE *vs.* NR	-2.0335	-3.4851	-0.5818	0.0035
	PL + HP *vs.* NR	4.5260	3.0743	5.9776	< 0.0001
	PL + BE *vs.* PL	-2.3968	-3.8484	-0.9452	0.0005
	PL + HP *vs.* PL	4.1626	2.7110	5.6142	< 0.0001
	PL + HP *vs.* PL + BE	6.5595	5.1078	8.0111	< 0.0001
Heavy metal reduction	PL *vs.* NR	-0.0153	-0.1148	0.0841	0.9742
	PL + BE *vs.* NR	-0.2021	-0.0350	-0.1026	< 0.0001
	PL + HP *vs.* NR	0.1342	-0.3016	0.2337	0.0050
	PL + BE *vs.* PL	-0.1867	0.0347	-0.0872	0.0001
	PL + HP *vs.* PL	0.1496	0.0501	0.2491	0.0017
	PL + HP *vs.* PL + BE	0.3363	0.2368	0.4358	< 0.0001

Note: PL refers to planting + shorebird control treatments; NR refers to natural recovery + shorebird control treatments; PL + BE refers to planting + shorebird exclusion treatments; and PL + HP refers to planting + high predation simulation treatments. Diff refers to the difference in mean value between two types of treatment. Lwr and Upr refer to the lower and upper bounds of

95% confidence interval, respectively. -, not available for multiple comparisons following a nonparametric Wilcoxon test (for Diff, Upr, and Lwr) and for *P* values when values in both groups of treatments are all zeros.

Supplementary Table 9: Summary statistics of the linear or quadratic regression models for ecosystem functions against crab abundance.

Ecosystem functions	df	*F*-statistic	*R*-squared	*P*-value
Secondary production	1, 22	0.3872	0.0173	0.5402
Microbial production	1, 22	17.75	0.4465	0.0003
Wave dissipation	1, 22	1.899	0.07946	0.182
Marsh infiltration	1, 22	1.976	0.1584	0.1636
Sediment accretion	1, 22	114.70	0.8391	< 0.0001
Soil respiration	1, 22	53.19	0.7074	< 0.0001
Nitrogen mineralization	1, 22	4.882	0.1816	0.05485
Litter decomposition	1, 22	6.169	0.219	0.0211
Sediment carbon burial	1, 22	157.90	0.8777	< 0.0001
Nitrogen accumulation	1, 22	73.80	0.7703	< 0.0001
Heavy metal reduction	1, 22	30.40	0.5802	< 0.0001
Multifunctionality	1, 22	29.58	0.738	< 0.0001

Supplementary Table 10: Summary statistics of the linear or quadratic regression models for ecosystem functions against primary production.

Ecosystem functions	**df**	***F*-statistic**	***R*-squared**	***P*-value**
Secondary production	1, 30	19.45	0.5729	< 0.0001
Microbial production	1, 30	0.669	0.02181	0.4199
Wave dissipation	1, 30	33.22	0.5255	< 0.0001
Marsh infiltration	1, 30	15.12	0.3351	0.0005
Sediment accretion	1, 30	119.7	0.7997	< 0.0001
Soil respiration	1, 30	36.89	0.7179	< 0.0001
Nitrogen mineralization	1, 30	42.25	0.5848	< 0.0001
Litter decomposition	1, 30	33.28	0.5259	< 0.0001
Sediment carbon burial	1, 30	109.9	0.7855	< 0.0001
Nitrogen accumulation	1, 30	108.2	0.7829	< 0.0001
Heavy metal reduction	1, 30	28.65	0.4885	< 0.0001
Multifunctionality	1, 30	122	0.8938	< 0.0001

Supplementary Table 11: Summary statistics of multiple comparisons on the effects of different restoration treatments on the averaged multifunctionality index.

Pairwise comparison	**Diff**	**Lwr**	**Upr**	***P*-value**
PL *vs*. NR	0.0113	-0.0781	0.1008	0.9853
PL + BE *vs*. NR	-0.0869	-0.1764	0.0025	0.0491
PL + HP *vs*. NR	0.3048	0.2153	0.3943	< 0.0001
PL + BE *vs*. PL	-0.0983	-0.1878	-0.0087	0.0272
PL + HP *vs*. PL	0.2934	0.2039	0.3830	0.0017
PL + HP *vs*. PL + BE	0.3917	0.3022	0.4813	< 0.0001

Note: Abbreviations follow Supplementary Table 8.

Supplementary Table 12: Summary statistics of one-way ANOVAs on the effects of different restoration treatments on the effective number of functions.

Order	**df**	***F*-ratio**	***P*-value**
$q = 1$	3, 28	42.46	< 0.0001
$q = 2$	3, 28	43.58	< 0.0001
$q = 3$	3, 28	49.80	< 0.0001
$q = 4$	3, 28	47.22	< 0.0001
$q = 5$	3, 28	47.90	< 0.0001

Supplementary Table 13: Summary statistics of multiple comparisons on the effects of different restoration treatments on the effective number of functions.

Order	Pairwise comparison	Diff	Lwr	Upr	*P*-value
$q = 1$	PL *vs.* NR	0.0645	-0.55458	0.6836	0.9917
	PL + BE *vs.* NR	-0.9082	-1.5273	-0.2891	0.0022
	PL + HP *vs.* NR	1.6101	0.9910	2.2293	< 0.0001
	PL + BE *vs.* PL	-0.9728	-1.59194	-0.3536	0.0010
	PL + HP *vs.* PL	1.5456	0.9264	2.1647	< 0.0001
	PL + HP *vs.* PL + BE	2.5184	1.8993	3.1375	< 0.0001
$q = 2$	PL *vs.* NR	0.1404	-0.636	0.9177	0.9598
	PL + BE *vs.* NR	-1.2574	-2.0346	-0.4802	0.0007
	PL + HP *vs.* NR	1.9693	1.1920	2.7465	< 0.0001
	PL + BE *vs.* PL	-1.3979	-2.1751	-0.6206	0.0002
	PL + HP *vs.* PL	1.8288	1.0516	2.6060	< 0.0001
	PL + HP *vs.* PL + BE	3.2267	2.4495	4.0039	< 0.0001
$q = 3$	PL *vs.* NR	0.1541	-0.6392	0.9474	0.9509
	PL + BE *vs.* NR	-1.3813	-2.1746	-0.5880	0.0003
	PL + HP *vs.* NR	2.1408	1.3475	2.9342	< 0.0001
	PL + BE *vs.* PL	-1.5354	-2.3288	-0.7421	< 0.0001
	PL + HP *vs.* PL	1.9867	1.1934	2.7800	< 0.0001
	PL + HP *vs.* PL + BE	3.5222	2.7289	4.3155	< 0.0001
$q = 4$	PL *vs.* NR	0.4603	-1.878	2.7989	0.9491
	PL + BE *vs.* NR	-3.6773	-6.0158	-1.3387	0.0010
	PL + HP *vs.* NR	6.3821	4.0436	8.7206	< 0.0001
	PL + BE *vs.* PL	-4.1377	-6.4762	-1.7991	0.0002
	PL + HP *vs.* PL	5.9217	3.5832	8.26029	< 0.0001

	PL + HP *vs.* PL + BE	10.0594	7.7209	12.3980	< 0.0001
q = 5	PL *vs.* NR	0.1766	-0.6820	1.0353	0.9425
	PL + BE *vs.* NR	-1.4301	-2.2888	-0.5714	0.0005
	PL + HP *vs.* NR	2.3033	1.4447	3.1620	< 0.0001
	PL + BE *vs.* PL	-1.6068	-2.4654	-0.7481	0.0001
	PL + HP *vs.* PL	2.1267	1.2680	2.9853	< 0.0001
	PL + HP *vs.* PL + BE	3.7335	2.8748	4.5921	< 0.0001

Note: Abbreviations follow Supplementary Table 8.

Supplementary Table 14: Summary statistics of one-way ANOVAs on the effects of different restoration treatments on the effective multifunctionality.

Order	**df**	***F*-ratio**	***P*-value**
$q = 0$	3, 28	54.25	< 0.0001
$q = 1$	3, 28	59.35	< 0.0001
$q = 2$	3, 28	59.12	< 0.0001
$q = 3$	3, 28	59.70	< 0.0001
$q = 4$	3, 28	55.22	< 0.0001
$q = 5$	3, 28	57.41	< 0.0001

Supplementary Table 15: Summary statistics of multiple comparisons on the effects of different restoration treatments on the effective multifunctionality.

Order	Pairwise comparison	Diff	Lwr	Upr	*P*-value
q = 0	PL *vs.* NR	0.0113	-0.0781	0.1008	0.9853
	PL + BE *vs.* NR	-0.0869	-0.1764	0.0025	0.0593
	PL + HP *vs.* NR	-0.0869	0.2153	0.3943	< 0.0001
	PL + BE *vs.* PL	0.3048	-0.1878	-0.0087	0.02725
	PL + HP *vs.* PL	-0.0983	0.2039	0.3830	< 0.0001
	PL + HP *vs.* PL + BE	0.3917	0.3022	0.4813	< 0.0001
q = 1	PL *vs.* NR	0.1370	-1.043	1.3175	< 0.0001
	PL + BE *vs.* NR	-1.1855	-2.366	-0.0049	0.9887
	PL + HP *vs.* NR	4.2090	3.028	5.3896	0.0487
	PL + BE *vs.* PL	-1.3225	-2.5030	-0.1420	< 0.0001
	PL + HP *vs.* PL	4.0720	2.8915	5.2525	0.0236
	PL + HP *vs.* PL + BE	5.3945	4.2140	6.5751	< 0.0001
q = 2	PL *vs.* NR	0.1623	-1.0406	1.3652	0.9825
	PL + BE *vs.* NR	-1.2554	-2.4583	-0.0525	0.0383
	PL + HP *vs.* NR	4.2557	3.0527	5.4586	< 0.0001
	PL + BE *vs.* PL	-1.4177	-2.6206	-0.2148	0.0161
	PL + HP *vs.* PL	4.0934	2.8904	5.2963	< 0.0001
	PL + HP *vs.* PL + BE	5.5111	4.3082	6.7141	< 0.0001
q = 3	PL *vs.* NR	0.1635	-1.0336	1.3608	0.9819
	PL + BE *vs.* NR	-1.2663	-2.4636	-0.0691	0.0351
	PL + HP *vs.* NR	4.2501	3.0529	5.4474	< 0.0001
	PL + BE *vs.* PL	-1.4299	-2.6271	-0.2326	0.0145
	PL + HP *vs.* PL	4.0866	2.8893	5.2838	< 0.0001

	PL + HP *vs.* PL + BE	5.5165	4.3193	6.7137	< 0.0001
q = 4	PL *vs.* NR	0.3817	-2.4642	3.2277	0.9828
	PL + BE *vs.* NR	-2.7916	-5.6376	0.0544	0.0560
	PL + HP *vs.* NR	-2.7916	6.9338	12.6258	< 0.0001
	PL + BE *vs.* PL	9.7798	-6.019	-0.3273	0.0244
	PL + HP *vs.* PL	-3.1733	6.5520	12.2440	< 0.0001
	PL + HP *vs.* PL + BE	12.5714	9.7254	15.4174	< 0.0001
q = 5	PL *vs.* NR	0.16742	-1.0371	1.3720	0.9810
	PL + BE *vs.* NR	-1.2392	-2.4438	-0.0346	0.0419
	PL + HP *vs.* NR	4.2007	2.9962	5.4053	< 0.0001
	PL + BE *vs.* PL	-1.4066	-2.6112	-0.2020	0.0173
	PL + HP *vs.* PL	4.0333	2.8287	5.2379	< 0.0001
	PL + HP *vs.* PL + BE	5.4400	4.2354	6.6446	< 0.0001

Note: Abbreviations follow Supplementary Table 8.

Supplementary Table 16: Summary statistics of multiple comparisons on the effects of different restoration treatments on above- and belowground multifunctionality.

Multifunctionality	Pairwise comparison	Diff	Lwr	Upr	*P*-value
Aboveground multifunctionality	PL *vs.* NR	0.0156	-0.1248	0.1562	0.9899
	PL + BE *vs.* NR	-0.0654	-0.2059	0.07511	0.5884
	PL + HP *vs.* NR	0.3604	0.21989	0.5009	< 0.0001
	PL + BE *vs.* PL	-0.0810	-0.2216	0.0594	0.4082
	PL + HP *vs.* PL	0.3447	0.20420	0.4852	< 0.0001
	PL + HP *vs.* PL + BE	0.4258	0.2853	0.5663	< 0.0001
Belowground multifunctionality	PL *vs.* NR	0.0081	-0.0842	0.1006	0.9949
	PL + BE *vs.* NR	-0.0868	-0.1792	0.0055	0.0471
	PL + HP *vs.* NR	0.3198	0.2274	0.4122	< 0.0001
	PL + BE *vs.* PL	-0.0950	-0.1874	-0.0026	0.0421
	PL + HP *vs.* PL	0.3116	0.2192	0.40411	< 0.0001
	PL + HP *vs.* PL + BE	0.4067	0.3143	0.4991	< 0.0001

Note: Abbreviations follow Supplementary Table 8.

Supplementary Table 17: List of the papers included in the meta-analysis on the effects of crab grazers on native plant biomass.

No.	Year	Title	Authors	Journal	Volume	Page/number
01	2021	Interactive effects of crab herbivory and spring drought on a *Phragmites australis*-dominated salt marsh in the Yellow River Delta	Zhang *et al.*	Science of the Total Environment	766	144254
02	2020	Hydrological connectivity and herbivores control the autochthonous producers of coastal salt marshes	Yin *et al.*	Marine Pollution Bulletin	160	111638
03	2019	Macrophytes and crabs affect nitrogen transformations in salt marshes of the Yangtze River Estuary	Zhang *et al.*	Estuarine, Coastal and Shelf Science	225	106242
04	2022	Native herbivores indirectly facilitate the growth of	Xu *et al.*	Ecology	103	e3610

		invasive Spartina in a eutrophic saltmarsh				
05	2019	Weather fluctuations affect the impact of consumers on vegetation recovery following a catastrophic die-off	He *et al.*	Ecology	100	e02559
06	2017	Natural enemies govern ecosystem resilience in the face of extreme droughts	He *et al.*	Ecology Letters	20	194-201
07	2015	Herbivory drives zonation of stress-tolerant marsh plants	He *et al.*	Ecology	96	1318-1328

Supplementary Table 18: Quantitative PCR primer information and reaction conditions*

Primer name	Primer sequence (5' - 3')		Thermal profile	Product fragment size
Eub338_Eub518	F1norA	ACTCCTACGGGAGGCAGCAG	95°C/5 min; 35 cycles of 95°C/30 s, 60°C/30 s, 72°C/1 min	191 bp
	R2norA	ATTACCGCGGCTGCTGG		

* All qPCR assays were run in triplicate. Total microbial genomic DNA was extracted using the FastDNA® Spin Kit for Soil (MP Biomedicals, Norcross, GA, USA) according to the manufacturer's instructions. The quality of extracted DNA was verified by 1.0 % agarose gel electrophoresis, and the DNA concentration was determined using a NanoDrop ND-2000 spectrophotometer (Thermo Fisher Scientific Inc., Waltham, MA, USA). The qPCR reaction system (a total of 20 μL) contained 10 μL of Master Mix (2 × ChamQ Universal SYBR qPCR Master Mix, Vazyme Biotech Co., Ltd., Nanjing, China), 0.8 μL of each primer (5 μmol L^{-1}), 1.0 μL of template DNA, and 7.4 μL of ddH_2O. Standard curves were constructed using 10-fold serially diluted standard plasmids amplified by qPCR in triplicate (R^2 = 0.996).

Supplementary Table 19: Summary statistics of multiple comparisons on the effects of different restoration treatments on gypsum dissolution and the Nemerow multifactor pollution index.

Multifunctionality	**Pairwise comparison**	**Diff**	**Lwr**	**Upr**	***P*-value**
Gypsum dissolution	PL *vs.* NR	-0.2062	-1.1935	0.7810	0.9401
	PL + BE *vs.* NR	0.2237	-0.7635	1.2110	0.9252
	PL + HP *vs.* NR	-1.2075	-2.1947	-0.2202	0.0120
	PL + BE *vs.* PL	0.4300	-0.5572	1.4172	0.6385
	PL + HP *vs.* PL	-1.001	-1.9885	-0.0139	0.0459
	PL + HP *vs.* PL + BE	-1.4312	-2.4185	-0.4439	0.0025
Nemerow multifactor pollution index	PL *vs.* NR	0.0154	-0.0841	0.1149	0.9741
	PL + BE *vs.* NR	0.2021	0.1026	0.3017	< 0.0001
	PL + HP *vs.* NR	-0.1341	-0.2337	-0.0346	0.0051
	PL + BE *vs.* PL	0.1867	0.0872	0.2863	0.0001
	PL + HP *vs.* PL	-0.14958	-0.2491	-0.0500	0.0017
	PL + HP *vs.* PL + BE	-0.3363	-0.4359	-0.2368	< 0.0001

Note: Abbreviations follow Supplementary Table 8.

Supplementary Table 20: Summary statistics of multiple comparisons on the effects of different restoration treatments on macrofaunal species richness and microbial OTUs.

Wetland functions	**Pairwise comparison**	**Diff**	**Lwr**	**Upr**	***P*-value**
Macrofaunal species richness	PL *vs.* NR	0.875	-2.0108	3.7608	0.8408
	PL + BE *vs.* NR	0.750	-2.1358	3.6358	0.8924
	PL + HP *vs.* NR	2.000	-0.8858	4.8858	0.2542
	PL + BE *vs.* PL	-0.125	-3.0108	2.7608	0.9993
	PL + HP *vs.* PL	1.125	-1.7608	4.0108	0.7135
	PL + HP *vs.* PL + BE	1.250	-1.6358	4.1358	0.6425
Microbe OTUs	PL *vs.* NR	-505.625	-8356.152	7344.902	0.9980
	PL + BE *vs.* NR	3295.875	-4554.652	11146.402	0.6646
	PL + HP *vs.* NR	501.500	-7349.027	8352.027	0.9980
	PL + BE *vs.* PL	3801.500	-4049.027	11652.027	0.5570
	PL + HP *vs.* PL	1007.125	-6843.402	8857.652	0.9849
	PL + HP *vs.* PL + BE	-2794.375	-10644.902	5056.152	0.7663

Note: Abbreviations follow Supplementary Table 8.

Supplementary Table 21: Summary statistics of multiple comparisons on the effects of different restoration treatments on the averaged wetland multifunctionality when calculated using species richness of macrofauna and microbial OTUs, instead of macrofaunal biomass and microbial production.

Pairwise comparison	**Diff**	**Lwr**	**Upr**	***P*-value**
PL *vs.* NR	0.0112	-0.0750	0.0973	0.9845
PL + BE *vs.* NR	-0.0592	-0.1454	0.0268	0.0459
PL + HP *vs.* NR	0.2795	0.1934	0.3657	< 0.0001
PL + BE *vs.* PL	-0.0704	-0.1566	0.0157	0.0413
PL + HP *vs.* PL	0.2684	0.1822	0.3545	< 0.0001
PL + HP *vs.* PL + BE	0.3388	0.2526	0.4249	< 0.0001

Note: Abbreviations follow Supplementary Table 8.

Appendix S1: Additional methods for quantifying microbial OTUs

DNA extraction and PCR amplification

Total microbial genomic DNA was extracted from 32 soil samples using the FastDNA® Spin Kit for Soil (MP Biomedicals, Norcross, GA, U.S.) according to the manufacturer's instructions. The quality and concentration of DNA were determined by 1.0% agarose gel electrophoresis and a NanoDrop® ND-2000 spectrophotometer (Thermo Scientific Inc., USA) and kept at -80 ℃ prior to further use. The hypervariable region V3-V4 of the bacterial 16S rRNA gene were amplified with primer pairs 338F (5'-ACTCCTACGGGAGGCAGCAG-3') and 806R (5'-GGACTACHVGGGTWTCTAAT-3') (Liu *et al.* 2016) by an ABI GeneAmp® 9700 PCR thermocycler (ABI, CA, USA). The PCR reaction mixture (20 μL in total) included 4 μL of 5 × Fast Pfu buffer, 2 μL of 2.5 mM dNTPs, 0.8 μL of each primer (5 μM), 0.4 μL of FastPfu polymerase, 10 ng of template DNA, and 12.6 μL of ddH_2O. PCR amplification cycling conditions were as follows: initial denaturation at 95 ℃ for 3 minutes, followed by 32 cycles of denaturing at 95 ℃ for 30 s, annealing at 55 ℃ for 30 s, and extension at 72 ℃ for 45 s, and single extension at 72 ℃ for 10 min, and end at 4 ℃. All samples were amplified in triplicate. The PCR product was extracted from 2% agarose gel and purified using the AxyPrep DNA Gel Extraction Kit (Axygen Biosciences, Union City, CA, USA) according to the manufacturer's instructions and quantified using Quantus™ Fluorometer (Promega, USA).

Sequencing and data processing

Purified amplicons were pooled in equimolar amounts and paired-end sequenced on an Illumina

MiSeq PE300 platform platform (Illumina, San Diego,USA) according to the standard protocols by Majorbio Bio-Pharm Technology Co. Ltd. (Shanghai, China). The raw 16S rRNA gene sequencing reads were demultiplexed, quality-filtered by fastp version 0.20.0, and merged by FLASH version 1.2.7 (Magoč *et al.* 2011) with the following criteria: (i) The reads (at any site receiving an average quality score of < 20) were truncated over a 50 bp sliding window (truncated reads shorter than 50 bp, as well as reads containing ambiguous characters, were discarded). (ii) Only overlapping sequences longer than 10 bp were assembled according to their overlapped sequence. The maximum mismatch ratio of the overlap region was 0.2. Reads that could not be assembled were discarded. (iii) Samples were distinguished according to the barcode and primers at the beginning and end of the sequences, with the sequence direction adjusted. The number of allowed mismatches per barcode and primer was 0 and 2, respectively.

Operational taxonomic units (OTUs) with 97% similarity cutoff (Stackebrandt *et al.* 1994, Edgar *et al.* 2013) were clustered using UPARSE version 7.1 (Edgar *et al.* 2013), and chimeric sequences were identified and removed. All optimized sequences were mapped to OTU representative sequences, and those with > 97% similarity to OTU representative sequences were selected to generate OTU table.

Appendix S2: Additional methods for calculating the Nemerow multifactor pollution index

To calculate the Nemerow multifactor pollution index, we first calculated a pollution index for each pollutant using the following equation:

$$P_i = \frac{C_i}{C_s}$$

where P_i is the index of pollutant i, C_i is the concentration of pollutant i, and C_s is the reference concentration value of pollutant i (0.2, 15, 35, 100, 90, 35 and 40 mg kg^{-1} for Cadmium, Arsenic, Lead, Zinc, Chromium, Copper, and Nickel, respectively, based on China National Soil Environmental Quality Standard). The Nemerow multifactor pollution index was then calculated as follows:

$$P = \sqrt{\frac{(P_i)^2_{max} - (\bar{P}_i)^2}{2}}$$

where P is the Nemerow multifactor pollution index, $(P_i)_{max}$ is the maximum of P_i, and $\bar{P}_i$ is the mean value of P_i. A greater value of the Nemerow multifactor pollution index denotes a higher risk of pollution (He *et al.* 1998, Kowalska *et al.* 2016, Martínez-Guijarro *et al.* 2019).

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