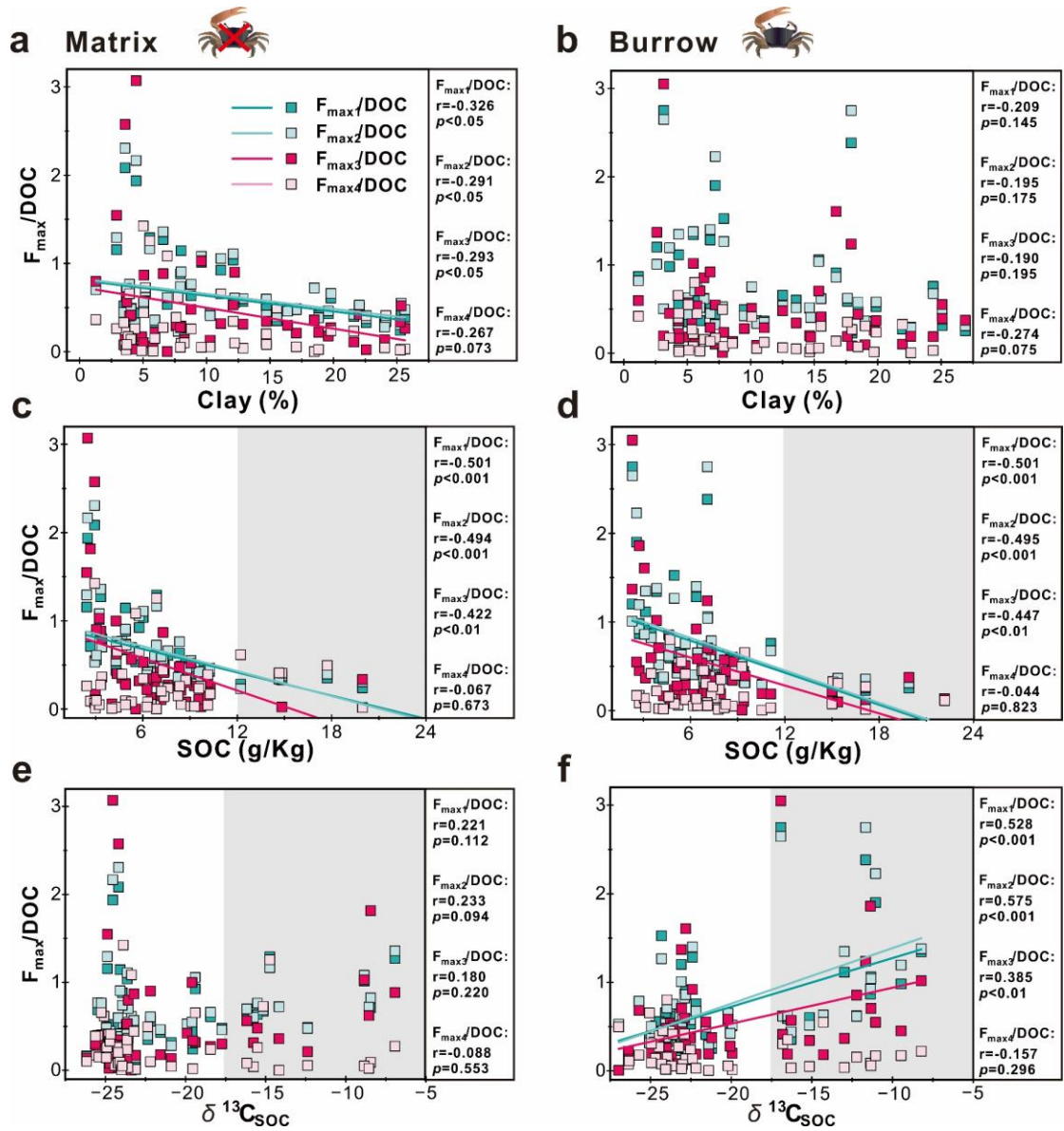
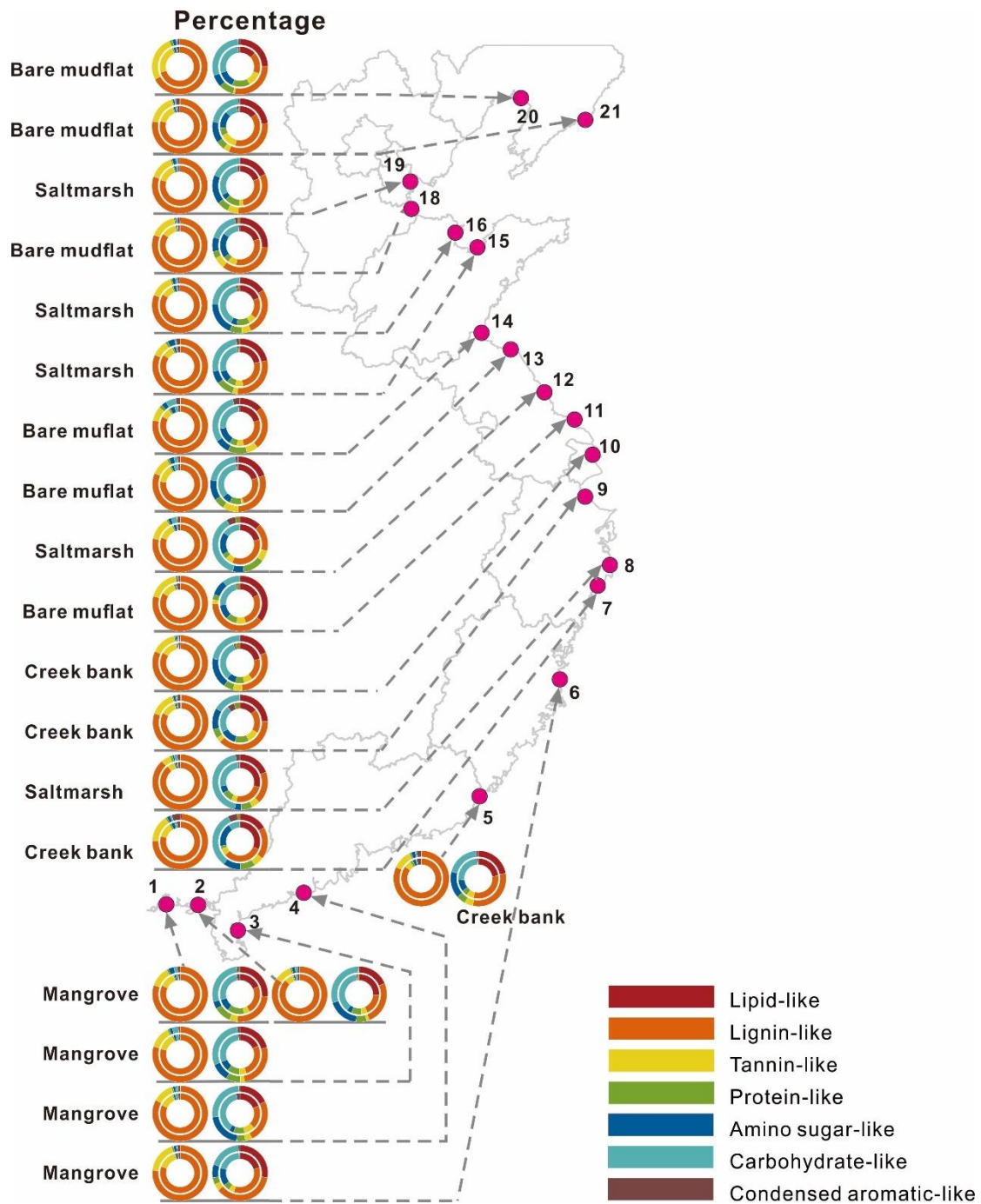


1  
 2 **Supplementary Figure 1 | Ratio of Fe and Mn minerals between crab burrows and sediment matrix**  
 3 **along the Chinese coast.** Color gradients indicate the ratio of mineral contents between crab burrows  
 4 and the sediment matrix.

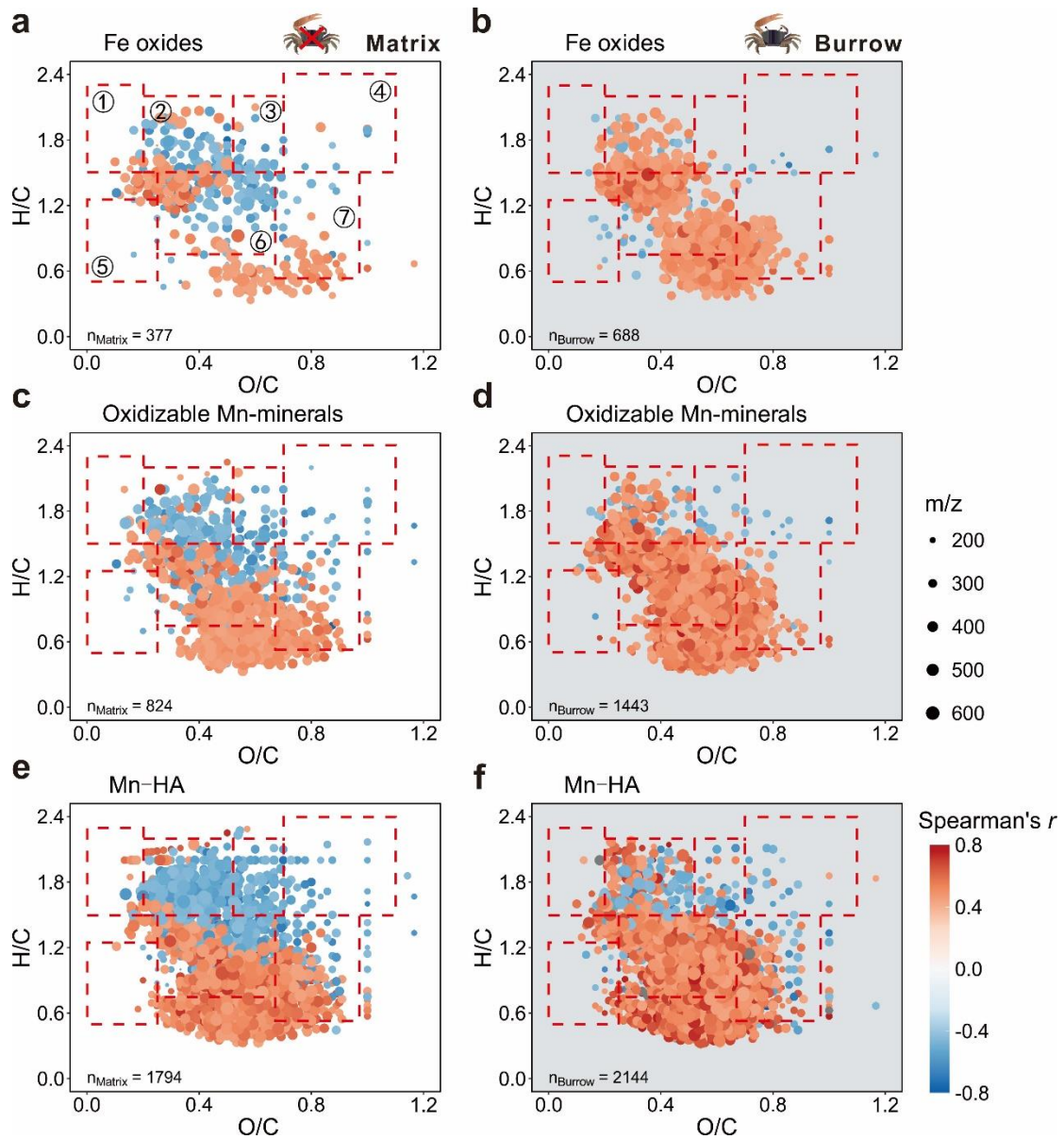


5

6 **Supplementary Figure 2 | Correlations of  $F_{max}/DOC$  with clay content (%), SOC, and  $\delta^{13}C_{SOC}$  in**  
 7 **the (a, c, e) sediment matrix and (b, d, f) crab burrows. The  $F_{max}/DOC$  ratio indicates the abundance**  
 8 **of various types of fluorescent component in the DOM[1].**

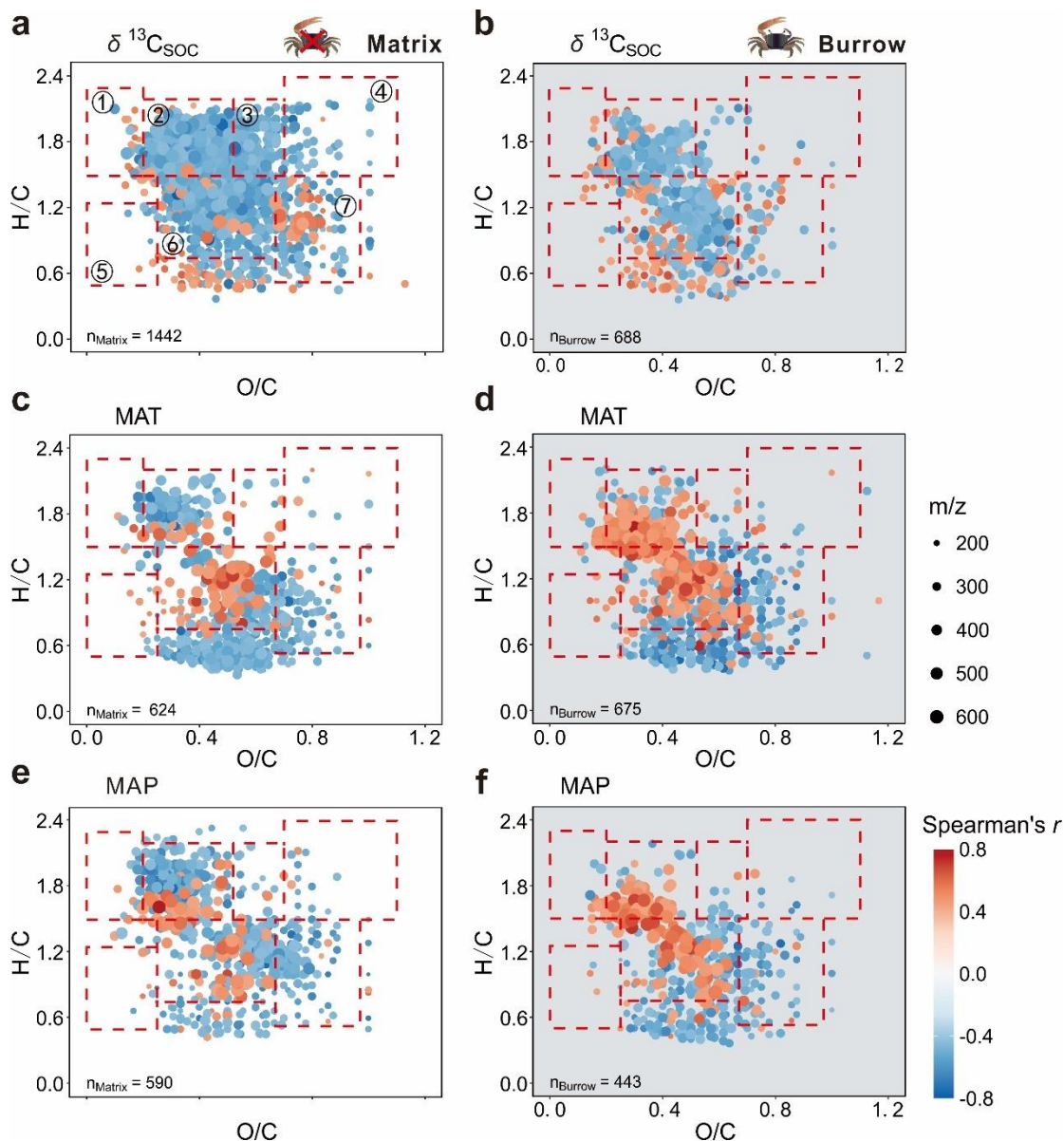


**Supplementary Figure 3 | Percentage of mass peak intensities in the biochemical groups.** The circles in the first column represent molecules in both the matrix and burrows, and the circles in the second column represent molecules unique to either the matrix or burrows. The outer and inner circles indicate the matrix and burrow, respectively.

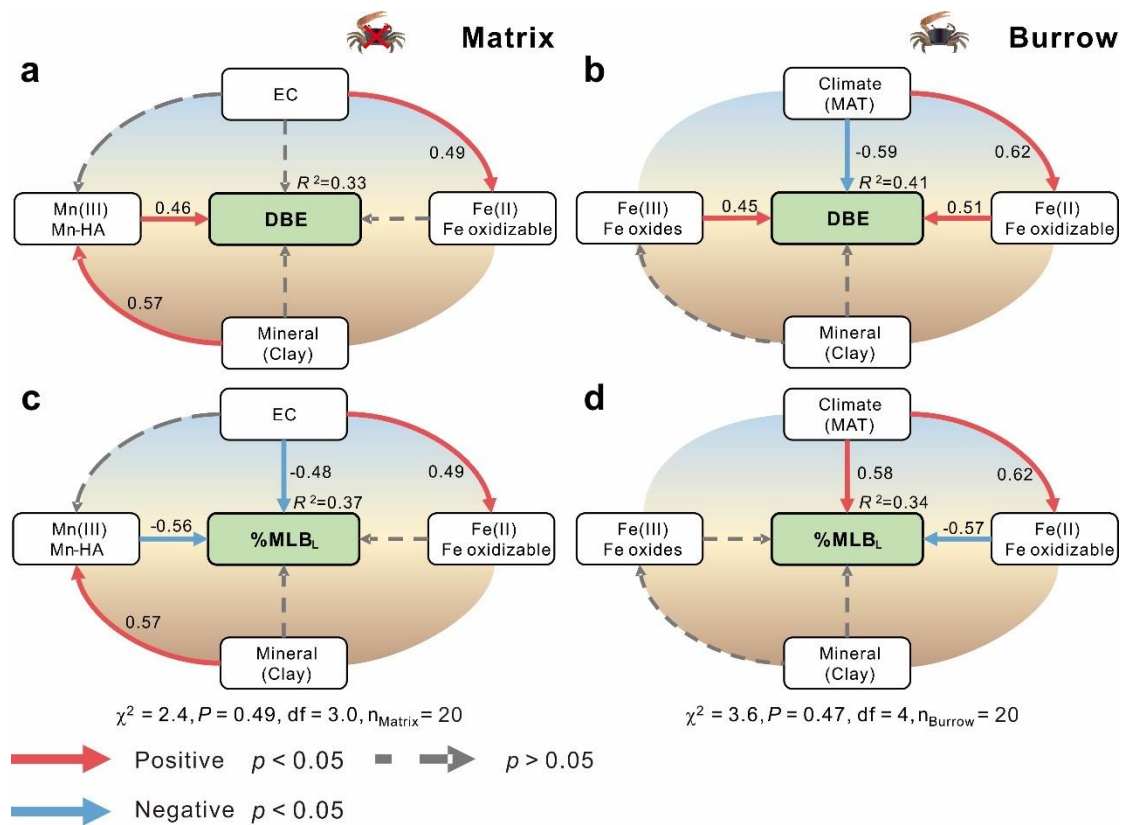


14

15 **Supplementary Figure 4. | Significant Spearman correlation coefficients ( $p < 0.05$ ) of individual**  
 16 **molecules with Fe oxides, oxidizable Mn minerals, and Mn-HA in (a, c, e) the sediment matrix and**  
 17 **(b, d, f) crab burrows.** The color scale indicates Spearman correlations between the intensity of  
 18 individual molecules and Fe oxides, oxidizable Mn minerals, and Mn-HA (red: positive; blue: negative).  
 19 Boxes overlain on the plots indicate major biomolecular compound classes, including: ① lipid-like, ②  
 20 protein-like, ③ amino sugar-like, ④ carbohydrate-like, ⑤ condensed aromatic-like, ⑥ lignin-like,  
 21 and ⑦ tannin-like.



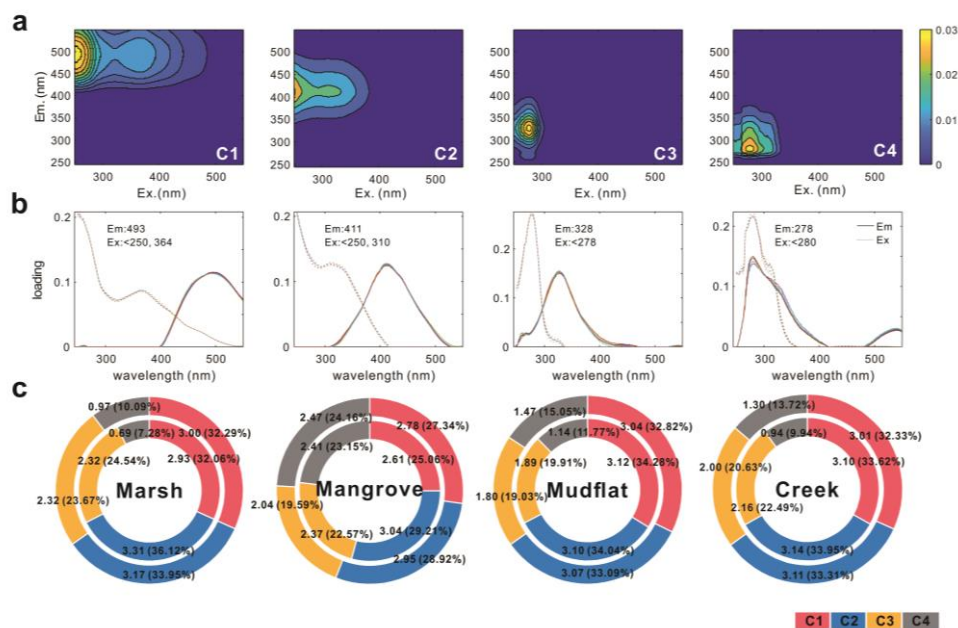
22  
 23 **Supplementary Figure 5. | Significant Spearman correlation coefficients ( $p < 0.05$ ) of individual**  
 24 **molecules with  $\delta^{13}\text{C}_{\text{SOC}}$ , manual mean annual temperature (MAT) and mean annual precipitation**  
 25 **(MAP) in (a, c, e) sediment matrix and (b, d, f) crab burrows.** The left column represents soil matrix  
 26 samples, and the right column represents burrow samples. The color scale indicates Spearman  
 27 correlations between the intensity of individual molecules and  $\delta^{13}\text{C}_{\text{SOC}}$ , MAT, and MAP (red, positive;  
 28 blue, negative). Boxes overlain on the plots indicate major biomolecular compound classes, including:  
 29 ① lipid-like, ② protein-like, ③ amino sugar-like, ④ carbohydrate-like, ⑤ condensed aromatic-like,  
 30 ⑥ lignin-like, and ⑦ tannin-like.



31

32 **Supplementary Figure 6. | Cascading relationships of DOM marks with environmental factors.**

33 Best-supported structural equation models showed major pathways of the influences of environmental  
 34 factors on (a, b) double-bond equivalent (DBE) ( $n = 20$ ) and (c, d) molecular lability boundary (%MLBL)  
 35 ( $n = 20$ ). Single-headed arrows indicate the hypothesized direction of causation. Numbers on the red (i.e.,  
 36 positive relationships) and blue (i.e., negative relationships) arrows indicate significant standardized path  
 37 coefficients at  $p < 0.05$ , whereas dotted arrows indicate insignificant pathways. The numbers adjacent to  
 38 the arrows are standardized path coefficients that reflect the relative effect size of the relationship. The  
 39 goodness-of-fit statistics for the model are presented below.



40

41 **Supplementary Figure 7 | Analysis of dissolved organic matter compositions using Parallel Factor**

42 **Analysis (PARAFAC) modeling.** (a) Contour maps of the four components (C1–C4). Colors represent

43 the relative intensities of the emissions. Dark blue and yellow correspond to the lowest and highest

44 intensities, respectively; (b) line plots for the half validation of excitation and emission loadings; and (c)

45 the average composition of the four components in the PARAFAC models at four crab habitats. The outer

46 and inner circles indicate the matrix and burrow sample, respectively.

47

48 **Supplementary Table 1 | Longitude, latitude, and habitat type of the sampling site.**

NO.	Sites	Habitat type	Longitude	latitude
1	Fangchenggang, Guangxi	Bare mudflat	108°31'09"E	21°35'49"N
1	Fangchenggang, Guangxi	Mangrove	108°31'10"E	21°35'50"N
2	Beihai, Guangxi	Bare mudflat	109°11'37"E	21°25'03"N
2	Beihai, Guangxi	Mangrove	109°11'39"E	21°25'04"N
3	Leizhou, Guangdong	Saltmarsh	110°10'23"E	20°54'04"N
3	Leizhou, Guangdong	Mangrove	110°10'20"E	20°54'04"N
3	Leizhou, Guangdong	Bare mudflat	110°10'24"E	20°54'03"N
3	Leizhou, Guangdong	Creek bank	110°10'34"E	20°53'43"N
4	Yangjiang, Guangdong	Bare mudflat	111°56'10"E	21°42'57"N
4	Yangjiang, Guangdong	Saltmarsh	111°56'11"E	21°42'55"N
4	Yangjiang, Guangdong	Mangrove	111°56'11"E	21°42'54"N
5	Dacheng, Guangdong	Creek bank	117°07'04"E	23°34'14"N
6	Fuzhou, Fujian	Bare mudflat	119°38'13"E	26°01'53"N
6	Fuzhou, Fujian	Saltmarsh	119°38'12"E	26°01'49"N
6	Fuzhou, Fujian	Mangrove	119°38'11"E	26°01'47"N

7	Wenzhou, Zhejiang	Bare mudflat	120°45'11"E	27°43'53"N
7	Wenzhou, Zhejiang	Saltmarsh	120°45'01"E	27°43'55"N
7	Wenzhou, Zhejiang	Creek bank	120°45'02"E	27°43'55"N
8	Taizhou, Zhejiang	Bare mudflat	121°37'17"E	28°20'49"N
8	Taizhou, Zhejiang	Saltmarsh	121°37'14"E	28°20'50"N
8	Taizhou, Zhejiang	Creek bank	121°37'16"E	28°20'53"N
9	Hangzhouwan, Zhejiang	Bare mudflat	121°24'45"E	30°18'59"N
9	Hangzhouwan, Zhejiang	Saltmarsh	121°24'05"E	30°19'14"N
9	Hangzhouwan, Zhejiang	Saltmarsh	121°24'26"E	30°19'06"N
9	Hangzhouwan, Zhejiang	Creek bank	121°24'48"E	30°18'43"N
10	Chongming, Shanghai	Saltmarsh	121°53'35"E	31°27'02"N
10	Chongming, Shanghai	Creek bank	121°53'34"E	31°27'02"N
11	Rudong, Jiangsu	Saltmarsh	121°06'53"E	32°32'29"N
11	Rudong, Jiangsu	Bare mudflat	121°07'15"E	32°32'27"N
12	Dongtai, Jiangsu	Saltmarsh	120°57'27"E	32°40'01"N
12	Dongtai, Jiangsu	Bare mudflat	120°57'41"E	32°39'55"N
13	Xingzhuanghe, Jiangsu	Bare mudflat	119°12'09"E	34°54'08"N
14	Mutaohu, Jiangsu	Bare mudflat	119°12'31"E	35°00'53"N
14	Mutaohu, Jiangsu	Saltmarsh	119°12'35"E	35°00'54"N
15	Weifang, Shandong	Bare mudflat	119°27'13"E	37°06'59"N
15	Weifang, Shandong	Saltmarsh	119°33'03"E	37°05'38"N
15	Weifang, Shandong	Creek bank	119°33'05"E	37°05'47"N
16	Nanhaipu, Shandong	Bare mudflat	118°55'47"E	37°27'42"N
16	Nanhaipu, Shandong	Saltmarsh	118°55'57"E	37°27'32"N
16	Nanhaipu, Shandong	Creek bank	118°56'05"E	37°27'38"N
17	Diaokou, Shandong	Bare mudflat	118°35'40"E	38°05'02"N
17	Diaokou, Shandong	Saltmarsh	118°35'29"E	38°05'12"N
17	Diaokou, Shandong	Creek bank	118°35'04"E	38°05'00"N
18	Cangzhou, Hebei	Bare mudflat	117°45'51"E	38°19'58"N
18	Cangzhou, Hebei	Saltmarsh	117°45'50"E	38°19'45"N
18	Cangzhou, Hebei	Creek bank	117°45'54"E	38°19'50"N
19	Binhaiyuchang, Tianjin	Saltmarsh	117°35'25"E	38°47'38"N
19	Binhaiyuchang, Tianjin	Bare mudflat	117°35'33"E	38°47'47"N
20	Panjin, Liaoning	Bare mudflat	121°40'18"E	40°50'05"N
20	Panjin, Liaoning	Creek bank	121°40'05"E	40°50'11"N
20	Panjin, Liaoning	Saltmarsh	121°40'11"E	40°50'05"N
21	Dandong, Liaoning	Bare mudflat	123°49'53"E	39°49'47"N
21	Dandong, Liaoning	Creek bank	123°49'49"E	39°49'46"N



49 **Supplementary Table 2 | Definitions of the fluorescence and molecular indices.**

Parameters	Description
Fluorescence index (FI)	High FI ~ 1.8, derived from extracellular release and leachate from bacteria and algae; low FI ~ 1.2, terrestrial plant and soil organic matter [2].
Slope ratio ( $S_R$ )	It usually has a negative correlation with the molecular weight (MW) of DOM [3].
Biological index (BIX)	An indicator of autotrophic productivity. High values correspond to recently produced DOM of autochthonous origin [4].
Humification index (HIX)	Indicator of humic substance content or extent of humification. The HIX is based on the idea that the emission spectra of fluorescing molecules will shift toward longer wavelengths (due to lower H:C ratios) as humification of DOM proceeds. Higher values indicate an increasing degree of humification [5].
Chromophoric dissolved organic matter (CDOM)	A fraction of the DOM pool, sometimes referred to as colored dissolved organic matter [6].
Specific ultraviolet absorbance at 254 nm ( $SUVA_{254}$ )	Absorbance per unit carbon. Typically, a higher number is associated with greater aromatic content [7].
Degradation index ( $I_{DEG}$ )	An indicator of degradation. of Higher $I_{DEG}$ values generally correspond to a higher degree of degradation[8].
Island of stability (IOS)	A set of marine dissolved organic compounds with the most stable combination of elements [9].
Double bond equivalent (DBE)	An indicator related with unsaturation of molecule. High values corresponding to high unsaturation [8].
Aromaticity index ( $AI_{mod}$ )	An indicator of aromaticity. High values indicate high aromaticity of DOM.
Molecular lability boundary (%MLB <sub>L</sub> )	An indicator to evaluate the lability of DOM. High values corresponding to high lability [10].
Nominal oxidation state of carbon (NOSC)	An indicator of biogeochemical reactivity and bioavailability, it reflects the thermodynamic stability of organic matter against microbial oxidation [11].
Carboxyl-rich alicyclic molecules (CRAM)	It is usually identified as the dominant oxygen-bearing functional group in marine DOM [12].

50

51

52 **Supplementary Note 1. Sediment physicochemical properties**

53 The sediment samples were lyophilized after being transported to the laboratory and stored in plastic  
54 boxes at room temperature. The samples were homogenized and passed through a 2 mm sieve before  
55 further analyses and DOM extraction experiments. The particle size distribution of the sieved  
56 sediments was measured using a laser diffraction particle size analyzer (LS I3 320, Beckman Coulter,

57 USA).

58 SOC was determined using the potassium dichromate external heating method. TN<sub>S</sub> was determined  
59 using the semi-micro Kjeldahl method, and the ratio of SOC to TN<sub>S</sub> (C/N ratio) was calculated. The  
60 oven-dried soil aggregates were finely ground (< 0.15 mm) before determining the isotopic  
61 composition ( $\delta^{13}\text{C}$ ). After removing the carbonates with hydrochloric acid (HCl), each fraction was  
62 washed with deionized water to remove excess chloride ions. Sediment samples were analyzed for  
63  $^{13}\text{C}$  isotopic composition using a GasBench II coupled to a 253 Plus mass spectrometer (Thermo  
64 Fischer Scientific) with a measurement error of  $\pm 0.2\%$  for  $\delta^{13}\text{C}_{\text{SOC}}$ .

65 The sequential extraction procedure for heavy metals in sediments follows the Geological Survey  
66 Technical Standards of the China Geological Survey (DD2005-03) [18, 19]. This scheme was  
67 modified from Tessier [20] to avoid the extraction of weakly bound and more reactive fractions from  
68 the organic-bound fraction of sediments, which could lead to the overestimation of certain element  
69 concentrations. Five morphological extractions were carried out: ion-exchangeable, carbonate-  
70 bound, humic acid-bound, iron-manganese oxide-bound, and strong organic-bound fractions. Each  
71 extraction step was followed by centrifugation at 3000 rpm for 20 min to separate the extract. The  
72 sediments were washed with ultrapure water between different extraction steps to avoid interference  
73 from residual reagents. The extracts were then appropriately diluted and analyzed for heavy metal  
74 content using inductively coupled plasma mass spectrometry (ICP-MS; PE NexiON 2000). This  
75 study used Chinese standard riverine sediment GBW07360 for method validation. The sum of all  
76 the extracted fractions was compared with the total element content to ensure data accuracy. The  
77 method recovery rates for Fe and Mn were 112.3% and 86.5%, respectively, and the RSDs for each  
78 fraction ranged from 4.3% to 23.6%.

79

## 80 **Supplementary Note 2. General water quality and DOM optical characterization**

81 Sediment DOM was extracted by shaking 3 g of soil in 60 mL of Milli-Q water at 200 rpm and  
82 20 °C for 24 h. The resulting supernatant was filtered through a polyethersulfone membrane with a  
83 pore size of 0.22  $\mu\text{m}$  (Millipore Express® Plus) to obtain the final DOM samples, which were stored  
84 at -20 °C prior to further analyses. General water quality was analyzed; specifically, pH was  
85 analyzed using a benchtop meter HQ440d and an Intellical™ PHC201 pH probe. The TC, DOC,  
86 and TN<sub>W</sub> concentrations were measured using a total organic carbon analyzer (TOC-L CSH/CSN  
87 analyzer, Shimadzu, Japan). Potassium hydrogen phthalate was used as the standard for calibration,  
88 with a linear regression coefficient  $R^2 > 0.999$ . Approximately 15 mL of the sample was acidified  
89 to pH 2.0 by adding at least 30  $\mu\text{L}$  of 6 M hydrochloric acid before DOC analysis. Then, DIC was  
90 calculated by subtracting the DOC from TC.

91           Ultraviolet-visible absorbance spectra were measured using a spectrophotometer (Horiba,  
92 Japan). The specific ultraviolet absorbance at 254 nm ( $SUVA_{254}$ ,  $L \cdot mg^{-1} \cdot C^{-1} \cdot m^{-1}$ ) was calculated by  
93 dividing the UV absorbance at 254 nm ( $A_{254}$ ) by the DOC concentration, indicating the aromaticity  
94 of DOM[7]. The absorption coefficient at 350 nm ( $a_{350}$ ) was selected as a proxy for chromophoric  
95 dissolved organic matter (CDOM) concentration[6]. The ratio of the spectral slope ( $S_R$ ) measured  
96 in the range 275–295 nm to the slope measured in the range 350–400 nm reflects the rate of  
97 absorbance change with wavelength, which is usually negatively correlated with the average  
98 molecular weight of DOM (R. G. M. Spencer et al., 2012). The groundwater samples were diluted  
99 using Milli-Q ultrapure water to an  $A_{254}$  less than 0.1, and then fluorescence excitation-emission  
100 matrices (EEMs) were measured using an Aqualog spectrofluorometer (Horiba, Japan) with  
101 excitation (Ex) and emission (Em) wavelengths ranging from 245 to 826 nm (1 nm intervals) and  
102 240–550 nm (2 nm intervals), respectively. The integration time was set to 3 s. Milli-Q ultrapure  
103 water was used as a blank sample to correct Rayleigh scattering and Raman scattering[21]. The  
104 biological index (BIX) represents the contribution of newly produced DOM and was calculated as  
105 the ratio of the fluorescence signal at an Em of 380 nm to the maximum signal observed in the range  
106 of 420–435 nm obtained at an Ex of 310 nm[4]. HIX, a proxy of the humic substance content or  
107 extent of humification, was calculated as the peak area at Em 435–480 nm divided by the peak area  
108 at Em300–345 nm and that at Em435–480 nm obtained at Ex 254 nm[5]. FI, a parameter for tracking  
109 DOM sources from aquatic (high FI of  $\sim 1.8$ , derived from microbial release and leachate) or  
110 terrestrial (low FI of  $\sim 1.2$ , terrestrial plant and soil organic matter) environments, was calculated as  
111 the ratio of Em at 470 nm to Em520 nm obtained at Ex 370 nm [22]. The fluorescent DOM  
112 components for the EEM data were determined by modelling of the parallel factor analysis  
113 (PARAFAC) using MATLAB (Vision, 2022a; MathWorks, USA) and validation of split-half  
114 analysis [23]. The components were compared to published models using the OpenFluor database  
115 (<http://www.openfluor.org>), with the Tucker congruence coefficient as a similarity criteria [24]. A  
116 four-component model explaining 99.5% of the fluorescence variability was selected. The  
117 maximum fluorescence intensity for each component was represented by  $F_{max}$  (in R.U.).

118           Four fluorescent components of DOM in groundwater were identified based on EEM-  
119 PARAFAC analysis, hereafter referred to as components one through four (C1-C4; Figure S2). The  
120 C1 (Ex/Em maxima: 250 (364)/493 nm) was identified as a UVC humic-like fluorophore mainly  
121 associated with fulvic-like matter, which common to a wide range of freshwater environments [7,  
122 24, 25]. C2 (Ex/Em maxima: 250 (310)/411 nm) was identified as a UVA humic-like fluorophore,  
123 which is attributed to peak M. Peak M is related to marine humic substances possibly of bacterial

124 origin [26-28]. The C3 (Ex/Em maxima: 278/328 nm) and C4 (Ex/Em maxima: 280/278 nm) were  
125 close to the traditionally defined tryptophan-like peak T and tyrosine-like peak B, respectively,  
126 which have been attributed to autochthonous sources [23, 29-31]. Tryptophan-like may indicate  
127 intact proteins or less degraded peptide material, whereas tyrosine-like may indicate more degraded  
128 peptide material [32].

129

### 130 **Supplementary Note 3. FT-ICR MS measurement**

131 SPE-DOM extracts were mixed with ultrapure water to yield a 1:1 water: methanol ratio (v/v) and  
132 DOC concentration of 5 mg C L<sup>-1</sup>. Samples were directly infused into the ESI unit at a flow rate of  
133 2 µL min<sup>-1</sup>, with the capillary voltage set to 4.5 kV in negative mode. Ions were accumulated for  
134 0.2 s in the quadrupole unit prior to transfer into the ICR cell, recording 1000 scans in broadband  
135 mode using 8 mega word data sets and a scan range of 94 to 2000 Da. Mass spectra were internally  
136 calibrated with a reference mass list covering the full detected mass range (mass accuracy < 0.1  
137 ppm) [33]. Molecular formulae above the method detection limit (MDL) were assigned using the  
138 ICBM-OCEAN. The MDL was 2.5, the sample junction was in fast join mode (0.5 ppm sample  
139 tolerance), and a recalibration tolerance of 0.5 ppm. The Minimum signal to MDL ratio as the  
140 backbone for recalibration was 5 using the mean recalibration mode. Molecular formulae were  
141 assigned with <sup>12</sup>C<sub>1-50</sub><sup>1</sup>H<sub>1-200</sub><sup>16</sup>O<sub>1-50</sub><sup>14</sup>N<sub>0-4</sub><sup>32</sup>S<sub>0-2</sub>P<sub>0-1</sub> with a tolerance of 0.5 ppm in the mass range  
142 from 100 to 1000 Da while excluding isotope ratio mismatches above signal to MDL ratios of  
143 isotope formulae >6. Isotope tolerance was set to 1000 ‰, and the homologous series network  
144 approach was applied (CH<sub>2</sub>, CO<sub>2</sub>, H<sub>2</sub>, H<sub>2</sub>O, and O). Molecular formulae containing nitrogen (N),  
145 sulphur (S), phosphorus (P), and singlet molecular formulae were excluded. All elemental formulae  
146 should meet basic chemical criteria: (1) the number of H atoms should be at least 1/3 of that of C  
147 atoms, and no more than 2C + N + 2; (2) the total number of N and H atoms should be even; (3) the  
148 H/C value < 3 and the O/C value < 1.5 [34, 35].

149

### 150 **Supplementary Note 4. Bioturbation on bulk and optical chemodiversity of dissolved** 151 **organic matter (DOM) among mangroves, saltmarshes, bare mudflat and creek bank**

152 The effects of fiddler crab bioturbation on the bulk and optical chemodiversity of DOM varied  
153 slightly among mangroves, salt marshes, bare mudflats, and creek banks. In mangroves, tryptophan-  
154 like compounds (C3) and DIC were 25.3% and 45.0% higher, respectively, in crab burrows than in  
155 the sediment matrix (Figure 2c; Supplementary Figure 7). This suggests that bioturbation increases  
156 tryptophan-like compounds in mangrove sediments, which can then be rapidly mineralized to  
157 dissolve in organic carbon (DIC) [13]. In salt marshes, total nitrogen in sediment (TN<sub>S</sub>), sediment

158 organic carbon (SOC), and dissolved organic carbon (DOC) were significantly higher in burrows  
159 than in the matrix ( $p < 0.05$ ), indicating that bioturbation and nitrate ( $\text{NO}_3^-$ ) enrichment promote  
160 the decomposition of more complex carbon forms into simpler ones, making organic matter more  
161 accessible to other microbial groups[14]. In bare mudflats and creek banks, unexpectedly lower  
162 levels of DOC were observed in crab burrows than in the sediment matrix, whereas other indicators  
163 varied by habitat (Figure 2c). In bare mudflats, water-extractable characteristics, such as electrical  
164 conductivity (EC), total carbon (TC), and total dissolved nitrogen of water extracts ( $\text{TN}_w$ ), were  
165 slightly lower in burrows than in the matrix, while the humification index (HIX) and fluorescence  
166 index (FI) were higher in burrows (Figure 2c). These results reflect the rapid microbial  
167 mineralization of bioavailable compounds due to crab burrowing activities [15]. The specific  
168 ultraviolet absorbance at 254 nm ( $\text{SUVA}_{254}$ ) exhibited flushing behavior with hydraulic exchange,  
169 and the DOM sources shifted from soluble intracellular materials to decayed plant byproducts [16].  
170 In creek bank, stronger hydraulic exchange and burrow flushing [17] resulted in two times larger  
171 aromatic humus ( $\text{SUVA}_{254}$ ) in crab burrows than in the matrix (Figure 2)

172

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