S1 Additional supporting methods

S1.1 Dissolved methane sampling

To quantify dissolved methane in the porewater of the pioneer marsh and intertidal flat, the same push core liners were used as for the porewater and sediment sampling for general geochemistry (inner diameter 8.6 cm, 60 cm long). Before sampling the pre-drilled holes (5 cm depth intervales) of the push core liners were covered with gastight isolation tape. The core liners were pushed into the sediment and carefully removed. On site, immediately after removing the core liners from the sediment, the tape was cross-cut and a 5 mL cutoff gastight syringe was immediately inserted into the sediment of the cores. Wet sediment (2 cm^3) was immediately transferred into a 20 mL serum vial filled with 5 mL saturated NaCl solution. The serum vial was gastight sealed, shaken well, and stored upside down until 3 mL of the headspace was removed and transferred into a helium pre-flushed 12 mL Exetainer® vial. The samples were measured similar to the other gas samples (main manuscript section Gas sampling).

S1.2 Physical characteristics of the sediment

Bulk grain density: To determine the grain density, measurements were taken with a capillary pycnometer and calculated according to Equation S1. Grain density was determined from the bulk sediment from both zones. Degassed and deionized water was used for the measurement. Water temperature and salinity were taken into consideration for density measurement (~18 °C and <1 ‰).

Equation S1:

$$\rho_{sediment} = \frac{M_{sediment}}{V_{pycnometer} - \frac{M_{pycnometer\ filled} - M_{pycnometer\ empty} - M_{sediment}}{\rho_{H_2O}}}$$

$\rho_{sediment}$ = Density of the sediment [g cm^{-3}]

$M_{sediment}$ = Mass fraction of dry sediment [g]

$M_{pycnometer\ empty}$ = Mass of capillary pycnometer [g]

$M_{pycnometer\ filled}$ = Mass of capillary pycnometer with sample and filled with water [g]

$V_{pycnometer}$ = Volume of capillary pycnometer [cm^3]

ρ_{H2O} = Density of water at temperature and salinity [g cm^{-3}]

Bulk porosity: The bulk porosity of the sediment was determined with a metal cylinder. Samples were collected in 2022 from the upper 5 cm in both zones in areas not influenced by vegetation. The top centimetre was removed to get an even surface. The sediment filled metal cylinder was weighed before and after drying at 60 °C until stable weight was reached. To calculate the porosity, Equation S2 was used, assuming all pore spaces were filled with water. Temperature and salinity (20 °C and 25 ‰) were accounted for. The bulk porosity was 0.57 in the pioneer marsh and 0.54 in the intertidal flat.

Equation S2:

$$\phi = \frac{M_{H_2O}/\rho_{H_2O}}{(\frac{M_{H_2O}}{\rho_{H_2O}} + \frac{M_{sediment}}{\rho_{sediment}})} = \frac{V_{H_2O}}{V_{H_2O} + V_{sediment}}$$

Φ = Porosity

M_{H2O} = Mass fraction of H_2O [g]

$M_{sediment}$ = Mass fraction of dry sediment [g]

ρ_{H2O} = Density of water at temperature and salinity [g cm^{-3}]

$\rho_{sediment}$ = Density of the sediment [g cm^{-3}]

Moisture content: The moisture content (MC) was quantified in the field laboratory, with samples from both zones according to Equation S3. Hereby, the sediment was weighed right after sampling (wet sediment) and after air-drying (dry sediment). Dry sediment was defined after no weight difference occurred. MC of the pioneer marsh was 33.39 ± 2.86 % and for the intertidal flat 31.08 ± 1.52 %.

Equation S3:

$$MC\ [\%] = \frac{M_{sediment\ wet} - M_{sediment\ dry}}{M_{sediment\ wet}} * 100$$

$M_{sediment\ wet}$ = Mass of wet sediment [g]

$M_{sediment\ dry}$ = Mass of dry sediment [g]

Particle size analysis: For the particle size analysis, carbonates and salt were removed as recommended by International Organization for Standardization (ISO) 11277 (2002) and 17892-4 (2016). Specifications were further provided by the manufacturer of the used Pario Classic analyser (METER Group, Pario classic mode, USA). The fraction of sand was determined by wet sieving, while the silt and clay fractions were determined by an automated Pario Classic analyser with $Na_4P_2O_7$ as the dispersing agent. Texture classes following the German Classification (KA 5): coarse sand 630-2000 µm, middle sand 200-630 µm, find sand 63-200 µm, silt 2-63 µm, and clay < 2 µm.

S1.3 Preparation of injection solutions

For the acetate solution, sodium acetate was dissolved in double deionized water (Barnstead MQ system, Thermo Fisher Scientific, Germany). The pH was measured to confirm circumneutral conditions (pH 7.81) (Mettler Toledo SevenGo, Germany). Pahokee Peat humic acid, obtained from the International Humic Substances Society (IHSS) (Table S1), was used to prepare the humic acid solution and served as the carbon source. To prepare the solution, the Pahokee Peat humic acid powder was dissolved in double deionized water, and NaOH was gradually added until the Pahokee Peat humic acid fully dissolved, after which the pH was re-adjusted to 7.07 using HCl (no precipitation was observed). The two carbon solutions were adjusted to seawater salinity by adding NaCl to achieve a final concentration of 20 g L^{-1}. A control solution of the same NaCl concentration was prepared without carbon. Bromide (Br^-), as NaBr was added into the carbon and control solution (25 mM) as an inert tracer in the field. Finally, all solutions were purged with nitrogen to make them anoxic and aliquoted into sterile serum bottles in a nitrogen atmosphere, such that each bottle contained the volume needed for one injection.

S1.4 Calculation of increased (added), expected, and residual fraction of injected solution (DOC and Br^-)

The porewater volume within each cylinder was calculated based on the average porosity (see Section S1.2) and the volume of the experimental cylinder ($V = r^2 \cdot \pi \cdot h$). Using this information and the known injected volume (21 mL), the dilution factor of the added solution (1 g C L^{-1} or 25 mM Br^-) in each cylinder was calculated. This was used to estimate how much the carbon or Br^- in the porewater increased, assuming an equal distribution of the injection solution within the experimental cylinder.

To calculate the residual fraction, first the expected concentration of dissolved organic carbon (DOC) or Br^- was calculated by multiplying the native concentration (DOC or Br^-) by the porewater volume in the experimental cylinder and the added concentration (carbon or Br^-) multiplied by the added volume (21 mL). This sum was then divided by the total water volume, consisting of both porewater in an experimental cylinder and added solution (Equation S4). As native DOC concentration, the mean DOC concentration from the control plots of each cycle were used to account for temporal DOC differences between the injection cycles. Native Br^- concentrations were measured using the same sampling method (via porewater sampler) and depth as the porewater samples taken after each injection cycle, in the surrounding area of the experimental cylinders. These concentrations were assumed to remain constant throughout the experiment, with no temporal variation. For the residual fraction, the measured porewater concentration of Br^- or DOC (DOC in total and not individually for acetate and humic acid) at 48 h post injection was divided by the expected Br^- or DOC concentration and expressed as a percentage (Equation S5).

Equation S4:

$$\frac{([DOC_{native}] * V_1) + ([DOC_{added}] * V_2)}{V_1 + V_2} = \frac{m_{DOC\ native} + m_{DOC\ added}}{V_1 + V_2} = [DOC_{expected}]$$

or

$$\frac{([Br^-_{native}] * V_1) + ([Br^-_{added}] * V_2)}{V_1 + V_2} = \frac{m_{Br^-_{native}} + m_{Br^-_{added}}}{V_1 + V_2} = [Br^-_{expected}]$$

Equation S5:

$$\frac{[DOC_{measured}]}{[DOC_{expected}]} * 100 = residual\ fraction\ [\%]$$

or

$$\frac{[Br^-{}_{measured}]}{[Br^-{}_{expected}]} * 100 = residual\ fraction\ [\%]$$

DOC_{native} = Mean dissolve organic carbon (DOC) concentration measured in the porewater of the control plots after each cycle (48 h post injection). We assume this represents the current DOC concentration without any addition [mg L^{-1}].

Br^-_{native} = Mean porewater Br^- concentration taken in the surroundings of the experimental cylinder from the same depth as the porewater sample 48 h post injection without addition [mM].

DOC_{added} *or* Br^-_{added} = DOC, as acetate or humic acid or Br^- concentration (here, 1 g L^{-1} for DOC and 25 mM for Br^-) injected into the sediment within the experimental cylinder [mg L^{-1} for DOC] or [mM for Br^-].

$DOC_{measured}$ *or* $Br^-_{measured}$ = DOC or Br^- concentration measured in the porewater sample 48 h post injection [mg L^{-1} for DOC] or [mM for Br^-].

$DOC_{expected}$ *or* $Br^-_{expected}$ = The final concentration of DOC or Br^- in the experimental cylinders after the addition of the solution [mg L^{-1}].

V_1 = Volume of the porewater in the experimental cylinder (experimental cylinder volume * porosity) [L].

V_2 = Volume of injected solution (added solution was 21 mL) [L].

$m_{DOC\ native}$ = Mass of carbon present in the control plots without addition [mg].

$m_{DOC\ added}$ = Mass of added carbon, as acetate or humic acid into the sediment within the experimental cylinder [mg].

$m_{Br-\ native}$ = Mass of Br^- present in the surroundings of the experimental cylinder from the same depth as the porewater sample 48 h post injection without addition [mg].

$m_{Br-\ added}$ = Mass of added Br^- into the sediment within the experimental cylinder [mg].

Residual fraction = Representing the ratio of DOC or Br^- concentration measured in the porewater 48 h post injection (end of an injection cycle) to the expected total concentration in the experimental cylinder, which includes both native and added (expected).

S1.5 Calculation of CO_2 flux and cumulative CO_2 emission

CO_2 flux calculation: For calculating the gas fluxes, we used Equation S6 (similar to Minh et al. (2018)), where F is the flux of GHGs (µmol m^{-2} h^{-1}), Δc is the slope of measured gas concentrations (ppmv h^{-1}), p is the ambient pressure during measurement (101325 Pa), $V_{chamber}$ is the gas filled volume of the chamber (m^3), R is the ideal gas constant (8.31 J mol^{-1} K^{-1}), T the temperature during measurement in Kelvin [K], and $A_{sediment}$ is the area covered by the chamber during gas sampling (m^2).

Equation S6:

$$F = \Delta c \frac{p * V_{chamber}}{R * T * A_{sediment}}$$

Calculation of cumulative CO_2 emission: To calculate the cumulative CO_2 emission, a second order polynomial regression trendline was calculated using the individual CO_2 fluxes from 1.5, 24 and 48 h post injection [mmol m^{-2} h^{-1}] (Fig. S15). This was done in the software Microsoft Excel (Version 2505 Build 16.0.18827.20102). A second-order polynomial trendline, expressed as $ax^2 + bx + c = 0$, was used, with a as the coefficient of the second-order term, b the coefficient of the first-order term and c the constant term. For the example given in Fig. S15, a = 0.0008, b = 0.0347, and c = 3.042. The time intervals were 1.5, 26, and 49 h with the corresponding CO_2 flux of 2.99, 2.69, and 3.29 in mmol m^{-2} h^{-1}. Based on the coefficients, the polynomial equation was once integrated at x = 1.5 (beginning of an injection cycle) and again at x = 48 (or 49 in this example, end of the injection cycle). The value at x = 1.5 was subtracted from the value x = 48 to calculate the total CO_2 emission between 1.5 to 48 hours (one injection cycle) in mmol CO_2 m^{-2}. The calculation of the cumulative CO_2 emission was done for each individual plot within a treatment and for each injection cycle. Thus, to be able to calculate the cumulative emission all individual fluxes from each plot within one injection cycle were needed. We are aware that this approach is simplistic and does not capture all the variability in the CO_2 fluxes during this time frame. We attempted to decrease the effect of this variability by (a) measuring the CO_2 fluxes at the same times in the different treatments to minimize differences due to tides and temperature, and (b) emphasizing the differences in the treatments rather than the absolute calculated values. We acknowledge that we could not account for the effect of day/night changes in CO_2 fluxes.

S1.6 Microbial analysis: analytical method details

For qualitative and quantitative validation of the DNA and RNA extraction, NanoDrop (NanoDrop 1000, Spectrophotometer, Thermo Scientific, Waltham, MA, USA) and Qubit (Qubit® 2.0 Fluorometer, Invitrogen by Life Technologies, Carlsbad, CA, USA) were used. The TURBO DNA-freeTM kit was used for DNA digestion to purify RNA and qualitatively validated by gel electrophoresis, followed by reverse transcription using SuperScript™ III Reverse Transcriptase to obtain complementary DNA (cDNA) and again qualitatively validated by gel electrophoresis.

S1.7 Statistical analysis

To check normality of data within a group, Shapiro-Wilk test was used (if $p > 0.05$, normal distribution was assumed), followed by Levene test to analyse the homogeneity of variances (if $p > 0.05$, homogeneity was given). To test the correlation between parameters, Pearson's correlation test was applied for normally distributed data, while Spearman's rank correlation test was used when the normality assumption was not met. Statistical differences between two groups were analysed with a t-test. If normality was given and the variance between the two groups were equivalent, the Student's t-Test was applied; if variance was unequal, Welch's t-test. If neither normality nor homogeneity of variance was given, Wilcoxon rank test was used. To evaluate if there is a significant difference in the mean of more than two groups, a one-way Analysis of Variance (ANOVA) followed by a Tukey Honest Significant Difference (HSD)-Test was done, if data within a group were normally distributed and homogeneity of variances was given. If assumptions of ANOVA were not met, the Kruskal-Wallis rank sum test with Benjamini-Hochberg correction, followed with the Dunn's test as a post-hoc test was applied. To test the difference in CO_2 fluxes among treatments, a linear mixed model fitted by REML was used. The fit of the model was visually assessed by a quantile-quantile plot (Q-Q plot), residuals vs. fitted plot and a histogram of residuals. For the model, the response variable was CO_2 fluxes, the fixed effect was treatment and time (1.5, 24, and 48 h after injection), and the random effect was the treatment replicates. For a comparison among groups emmeans to evaluate marginal means was applied. To perform the listed statistical analysis following R packages were used: FSA, lme4, lmerTest, emmeans, dunn.test, and car.

S2 Additional supporting tables

Table S1. Humic acid used in this work: Physicochemical properties of Pahokee Peat humic acid (Standard HA) from the International Humic Substances Society (IHSS) – Cat. No. 1S103H. Given values are reported by the IHSS https://humic-substances.org/#products (accessed April 7th, 2025).

Product	Origin	Elemental composition in % (w/w) of a dry, ash-free sample						Acidic Functional Groups (meq/ g C)		Carbon distribution in %[1]	
		C	H	O	N	S	P	Carboxyl	Phenolic	Aromatic	Aliphatic
Pahokee Peat humic acid	Poorly drained soil, Florida, USA	56.37	3.82	37.34	3.69	0.71	0.03	9.01	1.91	47	19

[1] Carbon distribution was estimated by ^{13}C NMR.

Table S2. Targeted genes, standards, primer including sequence, and thermal programs of the 16S rRNA, *Geobacter* spp., and *dsr*A. The single prime symbol (‘) represents minutes and the double prime (’’) seconds.

Target gene	Standard	Primer	Primer sequence 5' to 3'	Primer concentration (µM)	Temperature profiles
Bacterial 16S rRNA	Thiomonas sp.	341F 797R	CCTACGGGAGG CAGCAG GGACTACCAGG GTATCTAATCCT GTT	5 5	1) 95 °C – 5’ 2) 95 °C – 10’’ 3) 60 °C – 15’’ 4) GOTO 2 – 39x 5) 95 °C – 30’’
Geobacteraceae 16S rRNA	*Geobacter* spp.	Geo577F Geo822R	GCGTGTAGGCG GTTTSTTAA TACCCGCRACAC CTAGTACT	10 10	1) 95 °C – 3’ 2) 95 °C – 30’’ 3) 55 °C – 20’’ 4) 72 °C – 30’’ 5) GOTO 2 – 39x 6) 95 °C – 2’
dsrA	*dsr_A*	DSR_1F+ DSR_1R	ACSCACTGGAAG CACGGCGG GTGGMRCCGTG CAKRTTGG	5 5	1) 95 °C – 10’ 2) 95 °C – 30’’ 3) 60 °C – 30’’ 4) 72 °C – 30’’ 5) GOTO 2 – 39x 6) 72 °C – 2’ 7) 94 °C – 2’

Table S3. Particle size distribution of sediment from the pioneer marsh and intertidal flat from the upper 10 cm. Soil classification after German Classification KA5 with the particle size classes: coarse sand 630-2000 µm, middle sand 200-630 µm, and fine sand 63-200 µm. The fraction of sand was determined by wet sieving, while the silt and clay fractions by an automated Pario Classic analyser (METER Group, Pario classic mode, USA) (details Section S1.2). Mean ± standard deviation of several samples is presented (pioneer marsh triplicate, intertidal flat duplicate).

Particle-size class	**Pioneer marsh distribution [%]**	**Intertidal flat distribution [%]**
Sand	41.7 ± 9.1	61.5 ± 0.5
Coarse sand	*0.1 ± 0.1*	*0.04 ± 0.01*
Middle sand	*0.1 ± 0.1*	*0.06 ± 0.03*
Fine sand	*41.4 ± 9.4*	*61.4 ± 0.46*
Silt	38.7 ± 2.5	29.0 ± 5.0
Clay	19.7 ± 8.1	9.5 ± 5.5

Table S4. T-Test of residual fraction from the pioneer marsh and the intertidal flat. Difference between residual fraction of Br^- vs. acetate, Br^- vs. humic acid, and acetate vs. humic acid. Depending on if assumption were met two sample t-test (reported p-value, df, t) or Wilcoxon rank sum test (reported p-value and W). Values are compared across all injection cycles as a group, not separated by cycles. Significant level $p < 0.05$ *, $p < 0.01$ **, and $p < 0.001$ ***. Difference of the residual fraction between acetate and humic acid are only reported for the pioneer marsh.

	Pioneer marsh				**Intertidal flat**			
	p-value	W	df	t	p-value	W	df	t
Br^- vs. acetate	< 0.001 ***	144			≤ 0.001 ***	61		
Br^- vs. humic acid	< 0.001 ***		13.185	4.995	< 0.001 ***		16	8.6714
Acetate vs. humic acid	< 0.002 **	17						

Table S5. Differences of CO_2 fluxes between treatments and the control for the pioneer marsh. Statistical parameters of linear mixed model (lmer) of the CO_2 fluxes. Significant level $p < 0.05$ *, $p < 0.01$ **, and $p < 0.001$ ***.

	p-value (tukey method)	estimate	SE	df (kenward-roger method)	t.ratio
Treatment contrast	**1st injection cycle**				
Acetate vs. control	0.0834	0.588	0.222	6.08	2.650
Acetate vs. humic acid	0.0143 *	0.914	0.222	6.08	4.119
Humic acid vs. control	0.3491	0.326	0.213	5.53	1.528
Treatment contrast	**2nd injection cycle**				
Acetate vs. control	0.5294	0.652	0.575	6	1.135
Acetate vs. humic acid	0.6884	0.488	0.575	6	0.850
Humic acid vs. control	0.9565	-0.164	0.575	6	-0.285
Treatment contrast	**3rd injection cycle**				
Acetate vs. control	0.7132	0.302	0.375	6.08	0.806
Acetate vs. humic acid	0.3298	0.586	0.375	6.08	1.562
Humic acid vs. control	0.7358	0.284	0.370	5.80	0.767
Treatment contrast	**4th injection cycle**				
Acetate vs. control	0.1742	0.921	0.443	6	2.081
Acetate vs. humic acid	0.0764	1.208	0.443	6	2.728
Humic acid vs. control	0.8008	0.287	0.443	6	0.647

Table S6. Spearman's rank correlation coefficient to test the strength of correlation between tidal condition and temperature on CO_2 flux for different treatments over the time of the experiment for the pioneer marsh. Interval to/past spring tide given in days. Temperature is air temperature measured at the beginning of each sampling time point.

Treatment		Spearman's correlation coefficient
Acetate	CO_2 flux vs. air temperature	0.30
	CO_2 flux vs. interval to/past spring tide	0.34
Humic acid	CO_2 flux vs. air temperature	0.51
	CO_2 flux vs. interval to/past spring tide	0.60
Control	CO_2 flux vs. air temperature	0.50
	CO_2 flux vs. interval to/past spring tide	0.48

Table S7. Output from Kruskal-Wallis-Test for the DOC concentration in the porewater followed by post hoc test in the pioneer marsh. Chi-quared = 6.0105 and df = 2. Significant level $p < 0.05$ *, $p < 0.01$ **, and $p < 0.001$ ***.

	p-value	Mean differences
Acetate vs. control	0.4614	0.0969
Acetate vs. humic acid	0.0191 *	-2.0731
Humic acid vs. control	0.0150 *	-2.170

Table S8. TOC content [%] of acetate, humic acid, and control treatment plots from the pioneer marsh and intertidal flat. Sediment sampling was performed at the end of the experiment, following four injection cycles. Sediment cores were divided into two depth intervals: 0-5 cm and 5-10 cm. Data are presented as mean ± standard error.

Pioneer marsh			
Depth [cm]	TOC [%]		
	Acetate	Humic acid	Control
0-5	1.2 ± 0.1	0.9 ± 0.1	0.9 ± 0.1
5-10	0.7 ± 0.1	0.7 ± 0.1	0.6 ± 0.1
Intertidal flat			
Depth [cm]	TOC [%]		
	Acetate	Humic acid	Control
0-5	0.4 ± 0.02	0.4 ± 0.04	0.5 ± 0.01
5-10	0.5 ± 0.1	0.4 ± 0.03	0.4 ± 0.002

Table S9. Output from Kruskal-Wallis-Test for the Fe(II) in the porewater followed by post hoc test in the pioneer marsh. Chi-quared = 9.7477 and df = 2. Significant level $p < 0.05$ *, $p < 0.01$ **, and $p < 0.001$ ***.

	p-value	Mean differences
Acetate vs. control	0.0018 **	2.9062
Acetate vs. humic acid	0.0073 **	2.4412
Humic acid vs. control	0.3210	-0.4650

Table S10. Output from ANOVA/ Kruskal-Wallis-Test followed by post hoc test for Fe(II) in solid phase in the pioneer marsh. Significant level $p < 0.05$ *, $p < 0.01$ **, and $p < 0.001$ ***. Further statistical values: 0.5 M HCl extraction: 0-5 cm depth (df = 2, F = 3.552), 5-10 cm depth (df = 2, chi-squared = 4.7937) and 6 M HCl extraction (df = 2, F = 6.045), 5-10 cm depth (df = 2, chi-squared = 8.7502).

	p-value			
	0.5 M HCl extraction		6 M HCl extraction	
	0-5 cm	5-10 cm	0-5 cm	5-10 cm
Acetate vs. control	0.1219	0.0202 *	0.0104 *	0.0264 *
Acetate vs. humic acid	0.0497 *	0.3608	0.0369 *	0.0017 **
Humic acid vs. control	0.8952	0.0453 *	0.7428	0.1546

Table S11. Results of t-test comparing statistical differences between treatment vs. control of absolute gene copy numbers (16S rRNA, *dsrA*, and *Geobacter* spp. 16S rRNA) in the pioneer marsh. W only reported for Wilcoxon rank test. Df and t only reported for two sample t.test (Welch's t-test and Student's t-test). Significant codes: p = 0.5 **.** , p ≤ 0.05 *, p ≤ 0.01 **, and p ≤ 0.001 ***.

Target gene	Depth [cm]	Comparison	**p-value**		**df**		**t**		**W**	
			DNA	RNA	DNA	RNA	DNA	RNA	DNA	RNA
Bacterial 16S rRNA	0-5	Acetate vs. control	0.0158 *	0.0244 *	15.003		2.7202			66
		Humic acid vs. control	0.1524	0.7304	13.985		-1.5134			45
	5-10	Acetate vs. control	0.0129*	< 0.001 ***	16	16	2.7995	6.2764		
		Humic acid vs. control	0.2224	0.9314					26	39
dsrA	0-5	Acetate vs. control	0.0055 **	0.4811		14.723		-0.7228	64	
		Humic acid vs. control	0.0148 *	0.0999		8.6947		-1.841	9	
	5-10	Acetate vs. control	0.4178	0.1893	16		0.8317			16
		Humic acid vs. control	0.867	0.2833	16	9.0557	0.1702	1.1405		

Geobacteraceae 16S rRNA	0-5	Acetate vs. control	0.135	0.0513 .	8.9013	16	1.644	2.1065		
		Humic acid vs. control	0.5988	0.0574 .	14.149	16	-0.5382	-2.0476		
	5-10	Acetate vs. control	0.0944	0.0079 **	9.2102	16	1.8647	3.0345		
		Humic acid vs. control	0.0697	0.2581	15.833		-1.9456			27

Table S12. Differences of CO_2 fluxes between treatments and the control for the intertidal flat. Statistical parameters of linear mixed model (lmer) of the CO_2 fluxes in the intertidal flat. Significant level $p < 0.05$ *, $p < 0.01$ **, and $p < 0.001$ ***.

	p-value (tukey method)	estimate	SE	df (kenward-roger method)	t.ratio
Treatment contrast	**1st injection cycle**				
Acetate vs. control	0.1531	0.1476	0.0662	5.33	2.230
Acetate vs. humic acid	0.5667	0.0619	0.0574	4.81	1.079
Humic acid vs. control	0.4534	-0.0857	0.0662	5.33	-1.295
Treatment contrast	**2nd injection cycle**				
Acetate vs. control	0.8281	0.0446	0.0748	5.06	0.596
Acetate vs. humic acid	0.0371 *	0.2407	0.0726	5.99	3.314
Humic acid vs. control	0.0994	0.1961	0.0811	7.44	2.418
Treatment contrast	**3rd injection cycle**				
Acetate vs. control	0.4826	0.2684	0.216	4.92	1.242
Acetate vs. humic acid	0.4130	0.2960	0.211	4.56	1.403
Humic acid vs. control	0.9890	0.0276	0.194	5.01	0.142

Table S13. Output from ANOVA/ Kruskal-Wallis-Test for the acid volatile sulfide (AVS) content in the intertidal flat. Significant level $p < 0.05$ *, $p < 0.01$ **, and $p < 0.001$ ***. Depth 0-5 cm: df = 2, F = 16.67; depth 5-10 cm: df = 2, chi-squared 1.2089.

	p-value	
	0-5 cm	5-10 cm
Acetate vs. control	0.0067 **	0.1376
Acetate vs. humic acid	< 0.0001 ***	0.3215
Humic acid vs. control	0.0579	0.2588

Table S14. Results of t-test comparing statistical differences between treatment vs. control of absolute gene copy numbers (16S rRNA, *dsrA*, and *Geobacter* spp. 16S rRNA) in the intertidal flat. W only reported for Wilcoxon rank test. Df and t only reported for two sample t.test (Welch's t-test and Student's t-test). Significant codes: $p \leq 0.05$ *, $p \leq 0.01$ **, and $p \leq 0.001$ ***.

Target gene	Depth [cm]	Comparison	**p-value**		**df**		**t**		**W**	
			DNA	RNA	DNA	RNA	DNA	RNA	DNA	RNA
Bacterial 16S rRNA	0-5	Acetate vs. control	0.0078 **	0.0115 *					70	55
		Humic acid vs. control	0.6084	0.0712	16		0.5226			14
	5-10	Acetate vs. control	0.2224	0.0083 **		8.1812		3.4626	26	
		Humic acid vs. control	0.0035 **	0.8574	16	13.122	3.4255	0.18324		
dsrA	0-5	Acetate vs. control	0.4894	0.1135					49	59
		Humic acid vs. control	0.0715	0.7304	15.168		1.9376			45
	5-10	Acetate vs. control	0.0011 **	0.2417	12.973	16	-4.1861	-1.2157		
		Humic acid vs. control	<0.001 ***	0.0939					78	60

Geobacteraceae 16S rRNA	0-5	Acetate vs. control	0.1615	<0.001m ***		16		4.4417	57	
		Humic acid vs. control	0.2581	0.7165		16		0.3697	27	
	5-10	Acetate vs. control	<0.001 ***	0.3784	16	16	4.1486	-0.9059		
		Humic acid vs. control	0.0142 *	0.3176		16		1.0317	13	

S3 Additional supporting figures

Experimental setup – pioneer marsh and intertidal flat (Figure S1)

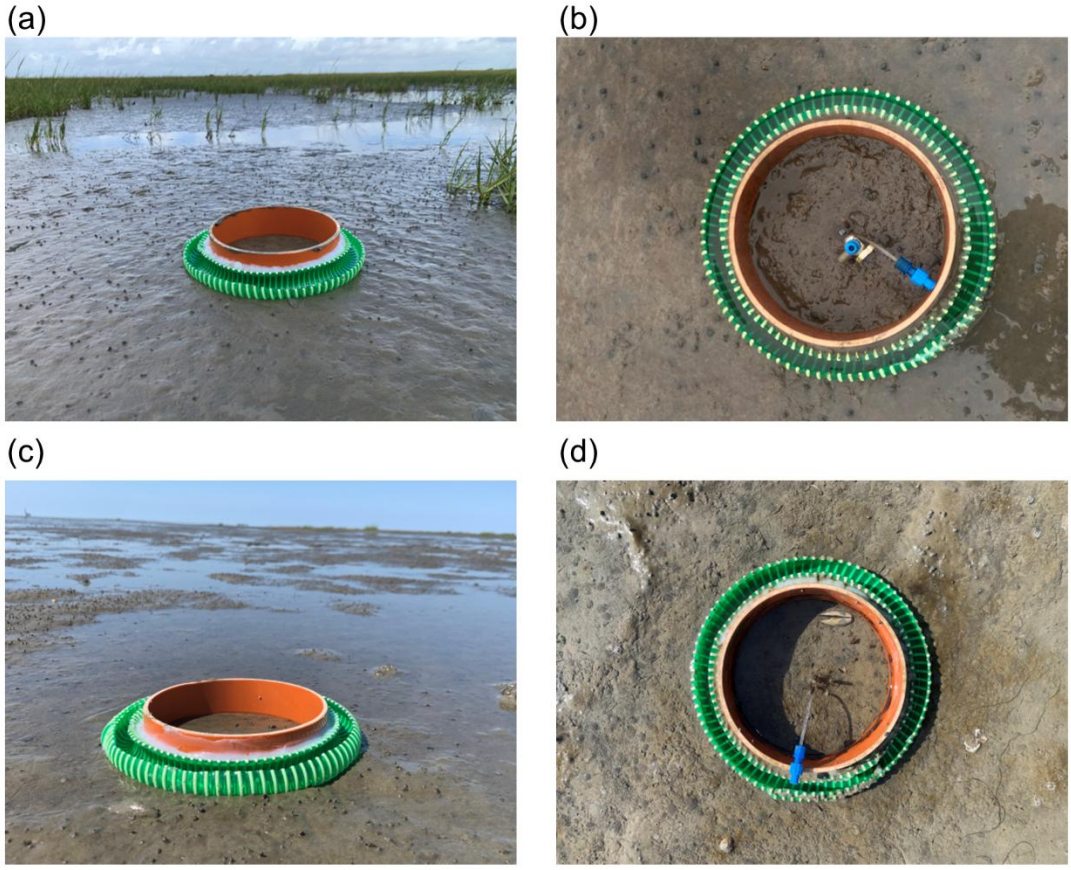

Figure S1. Pictures of the experimental setup. Picture (a) and (b) are from the pioneer marsh and (c) and (d) from the intertidal flat. Experimental setup was the same for both zones and each plot was identical across both treatments (acetate/ humic acid) and control. Plots in the pioneer marsh were placed outside of vegetated areas, i.e. the actual plot area of injection and sampling were free of vegetation although vegetation was present in the vicinity. In the intertidal flat, no vegetation was present, not in the surrounding area or in the plots. In both zones, plots within each treatment were spaced ~5 m apart, while the distance between treatment and control plots was ~10 m.

Sulfate and total organic carbon from push cores – pioneer marsh and intertidal flat (Figure S2)

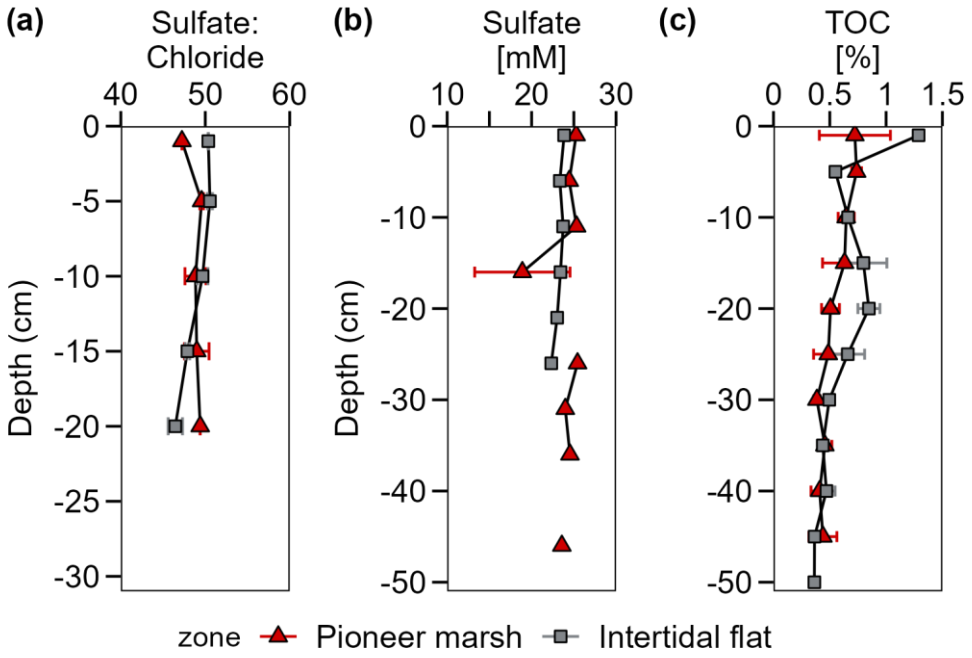

Figure S2. Porewater and sediment biogeochemistry in terms of electron acceptor (SO_4^{2-}) and donor (organic carbon) from in situ push cores in the pioneer marsh (red triangles) and intertidal flat (grey squares). Push cores were collected in (a) 2023 and in (b/c) 2022. (a) ratio of porewater sulfate [mM] and chloride [M] over 20 cm, (b) Sulfate (SO_4^{2-}) concentrations in the porewater and (c) total organic carbon (TOC) in the sediment over 50 cm. Markers denote mean ± standard deviation (due to limited sample mass, some depth values only show mean and the range of two samples, or only a single value).

Distribution of bromide in the sediment – pioneer marsh and intertidal flat (Figure S3)

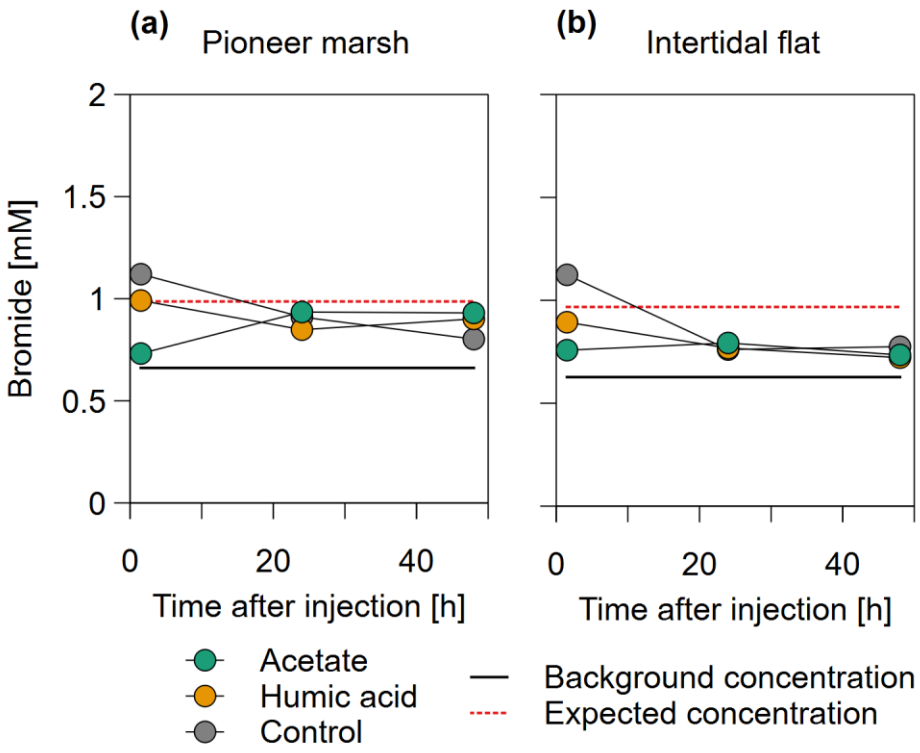

Figure S3. Distribution of inert tracer (Br^-) around the injection point over the course of one test injection for (a) the pioneer marsh and (b) the intertidal flat. Porewater samples (duplicates) were taken at the sampling times corresponding to those of gas sampling (1.5, 24, and 48 h after injection). Native Br^- concentration is indicated by the solid straight black line and expected Br^- (native concentration + added without dilution and constant over 48 h) is presented by a red dotted line. Bromide mass from the acetate plots in green, from the humic acid plots in orange, and from the control plots in grey. Markers represent the mean ± range of duplicates (too low to be visible).

DOC concentration in the porewater from the pioneer marsh (Figure S4)

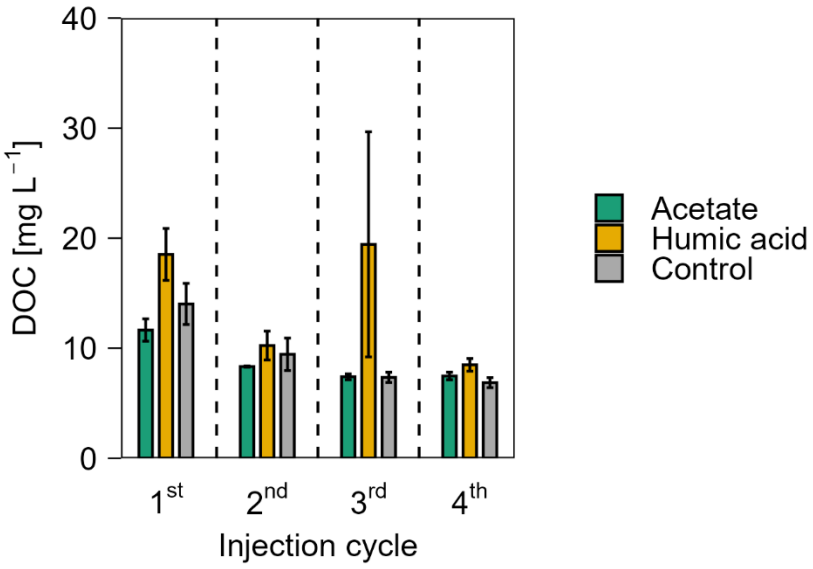

Figure S4. Dissolved organic carbon (DOC) of the porewater over four injection cycles for acetate (green) and humic acid (orange) treatments and control (grey) in the pioneer marsh. DOC [mg L^{-1}] in the porewater was sampled 48 h after injection. Data are shown as mean ± standard error of triplicates. Individual injection cycles are separated by a dashed line.

Dissolved inorganic carbon and pH in the porewater from the pioneer marsh (Figure S5)

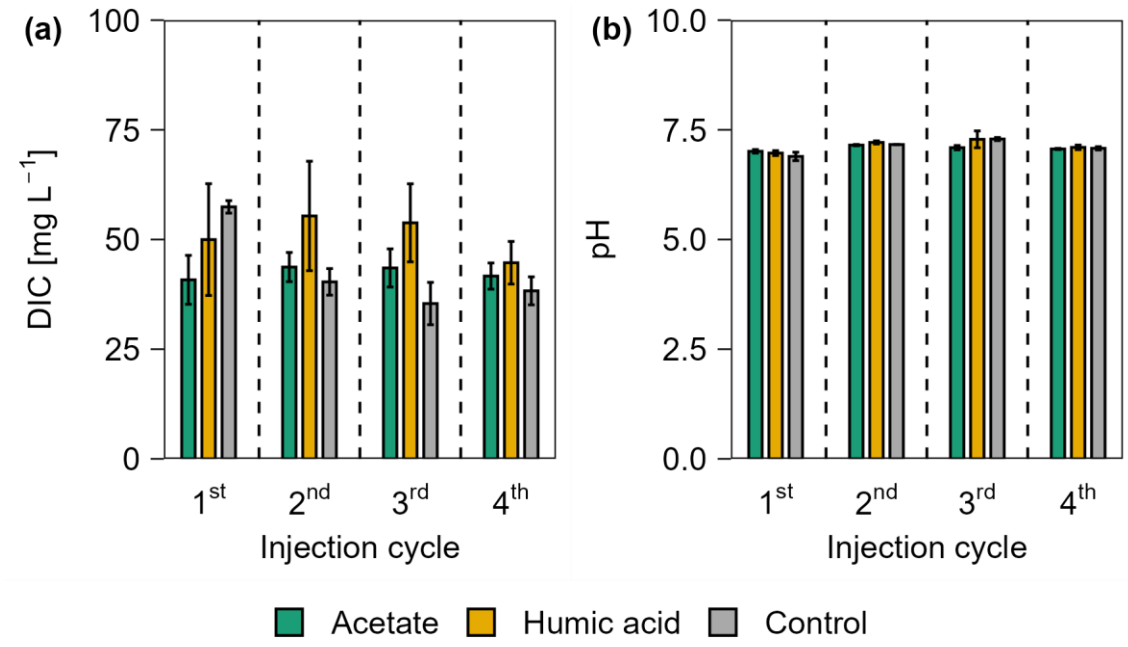

Figure S5. Dissolved inorganic carbon (DIC) and pH of the porewater samples 48 h post injection in the pioneer marsh. (a) shows the DIC concentrations [mg L^{-1}] and (b) pH of porewater samples over four injection cycles. Data are shown as mean ± standard error of triplicates. Individual injection cycles are separated by a dashed line.

Sulfide species in the porewater and sediment from the pioneer marsh (Figure S6)

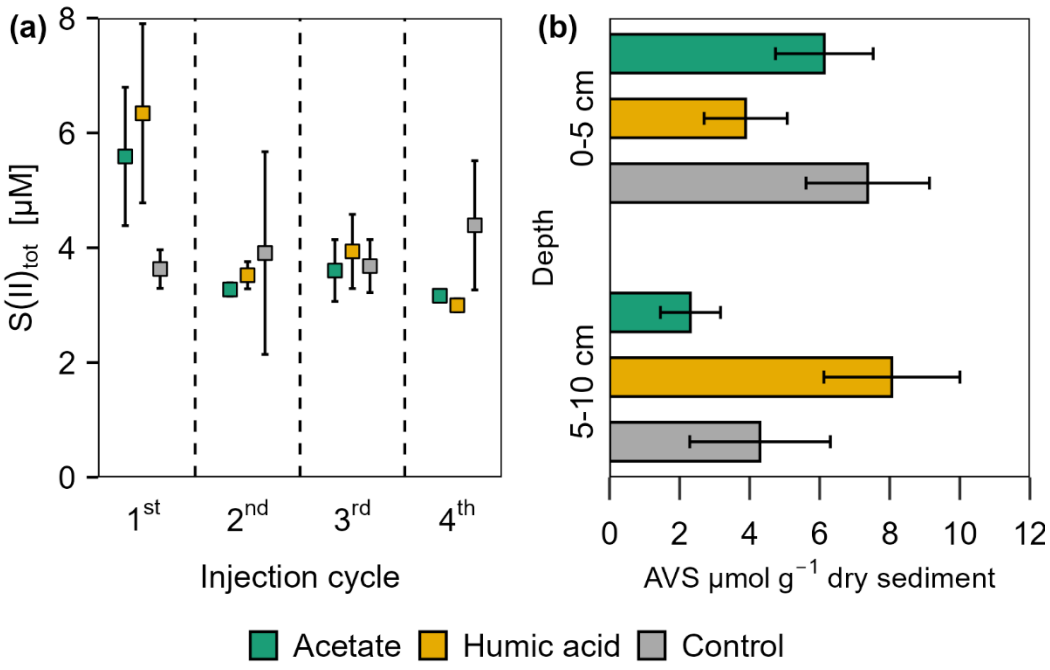

Figure S6. (a) Total sulfide ($S(II)_{tot}$) in the porewater over four injection cycles and (b) acid volatile sulfide (AVS) [µmol g^{-1} dry sediment] of the solid phase sampled at the end of the experiment for acetate (green) and humic acid (orange) treatments and control (grey) in the pioneer marsh. (a) $S(II)_{tot}$ [µM] in the porewater was sampled 48 h after injection. Data are shown as mean ± standard error of triplicates. Individual injection cycles are separated by a dashed line. (b) AVS content [µmol g^{-1} dry sediment] of the solid phase in the different treatments and control at the end of the experiment (after four injection cycles). Each spatial triplicate was analysed in duplicates; results are presented as mean ± standard error.

Effect of organic carbon input on microbial growth and metabolic activity in the pioneer marsh (Figure S7)

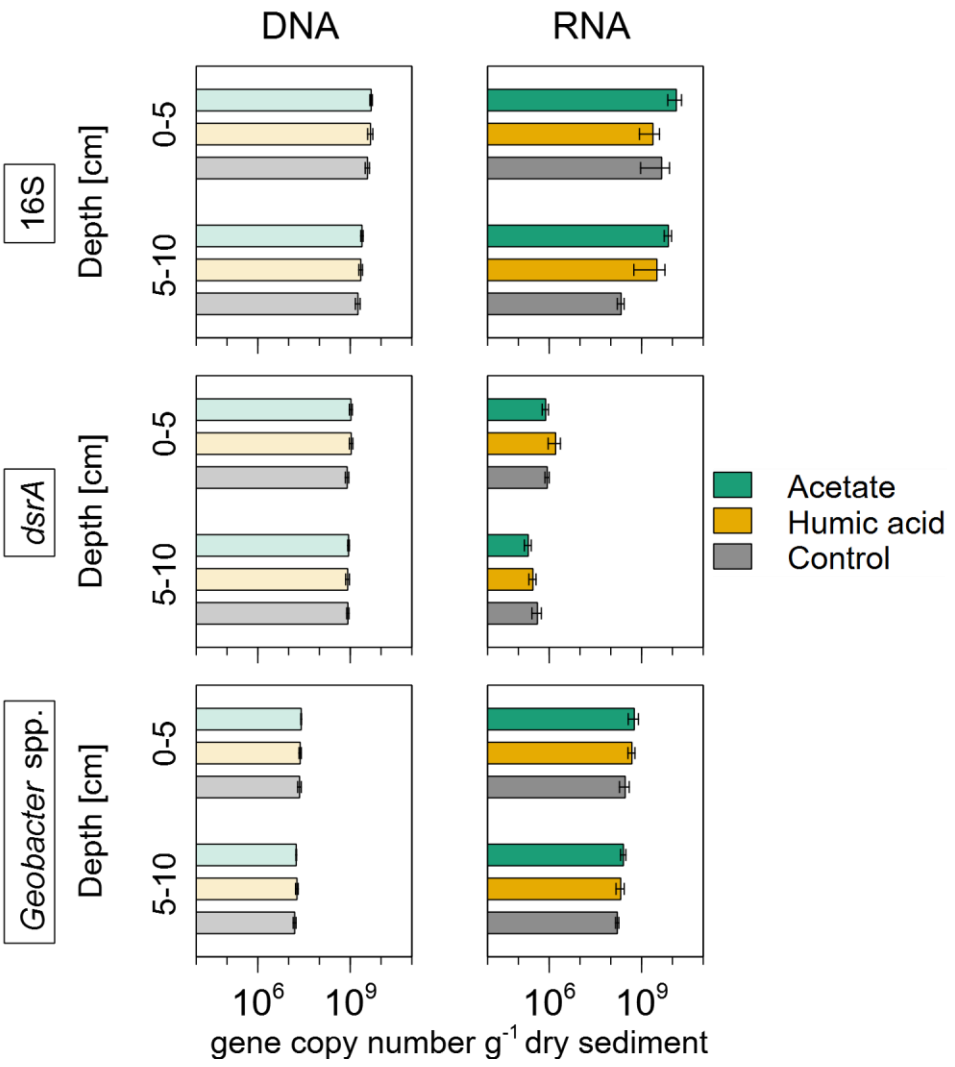

Figure S7. Total gene copy number of 16S, *dsrA*, and *Geobacter* spp. are shown separately for DNA and RNA for the pioneer marsh. DNA- (lighter colour) and RNA- based gene copies (darker colour) for acetate, humic acid treatment and the control in the pioneer marsh. Acetate treatment is shown in green, humic acid treatment in orange, and the control in grey. Two depths: upper layer (0-5 cm) and lower layer (5-10 cm). Samples size compress triplicates represented as mean ± standard error.

Dissolved inorganic carbon and pH in the porewater from the intertidal flat (Figure S8)

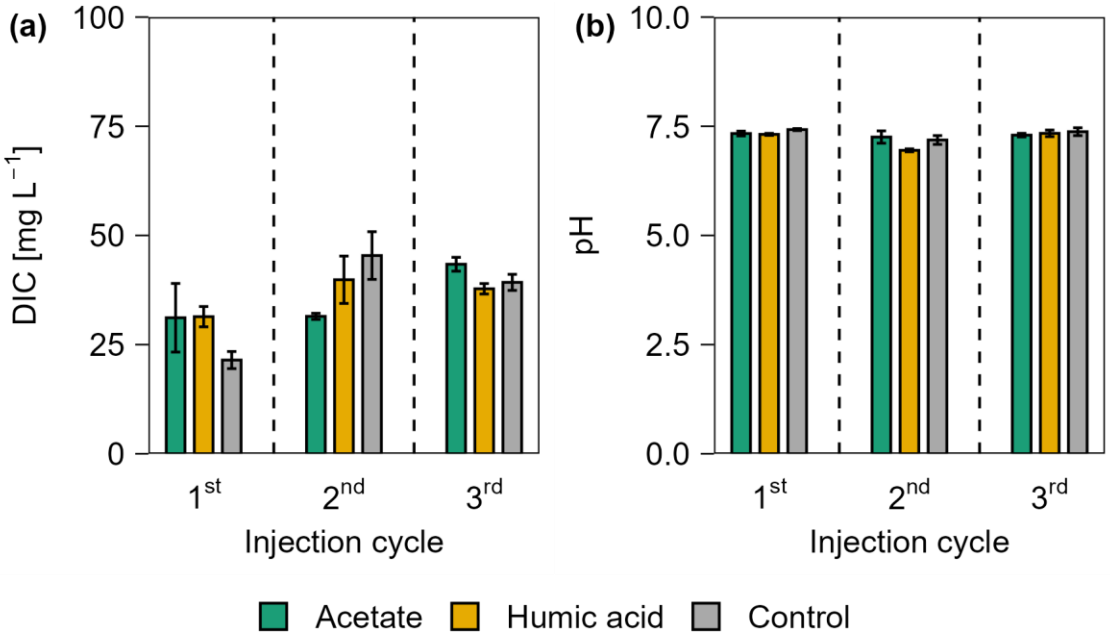

Figure S8. Dissolved inorganic carbon (DIC) and pH of the porewater samples 48 h post injection in the intertidal flat. (a) shows the DIC concentrations [mg L^{-1}] and (b) pH of porewater samples over three injection cycles. Data are shown as mean ± standard error of triplicates. Individual injection cycles are separated by a dashed line.

DOC concentration in the porewater from the intertidal flat (Figure S9)

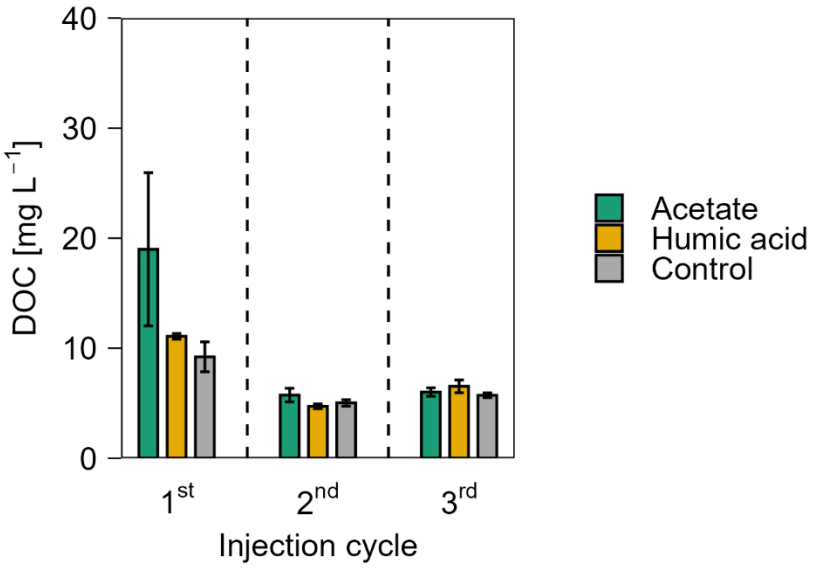

Figure S9. Dissolved organic carbon (DOC) of the porewater over three injection cycles for acetate (green) and humic acid (orange) treatments and control (grey) in the intertidal flat. DOC [mg L^{-1}] in the porewater was sampled 48 h after injection. Data are shown as mean ± standard error of triplicates. Individual injection cycles are separated by a dashed line.

Porewater and HCl extractable Fe(II) from the intertidal flat (Figure S10)

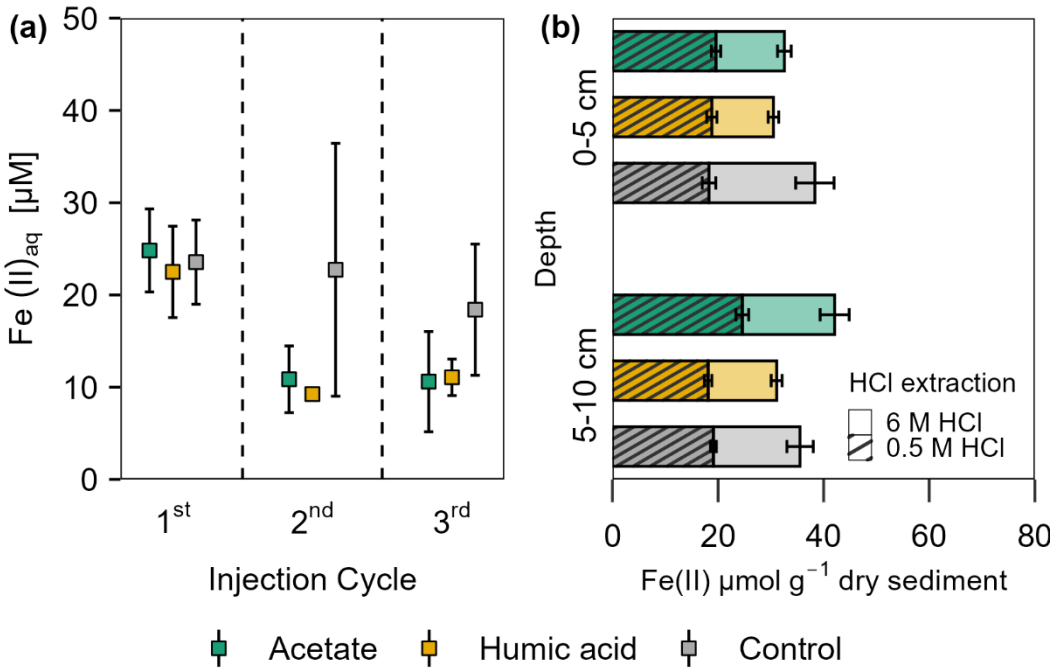

Figure S10. Ferrous iron in (a) porewater and (b) sediment from acetate and humic acid treated plots and the control plots in the intertidal flat. (a) Ferrous iron concentration in the porewater ($Fe(II)_{aq}$) sampled after each injection cycle (cycles are separated by the dashed line). Triplicates for each treatment and control were collected and mean ± standard error is shown. (b) HCl extractable Fe(II) content [µmol g^{-1} dry sediment] at two different depths (0-5 and 5-10 cm) sampled at the end of all four injection cycles. Different colour coding was used for contrasting treatments: acetate treatment (green), humic acid treatment (orange), and control (grey). Striped bars represent poorly crystalline Fe(II) (0.5 M HCl extraction) and solid bars higher crystalline Fe(II) (6 M HCl extraction). The 0.5 M HCl extract was subtracted from the 6 M HCl extracted fraction to separate poorly and higher crystalline Fe(II). Each spatial triplicate was analysed in triplicates; results are presented as mean ± standard error.

$S(II)_{tot}$ of porewater from the intertidal flat (Figure S11)

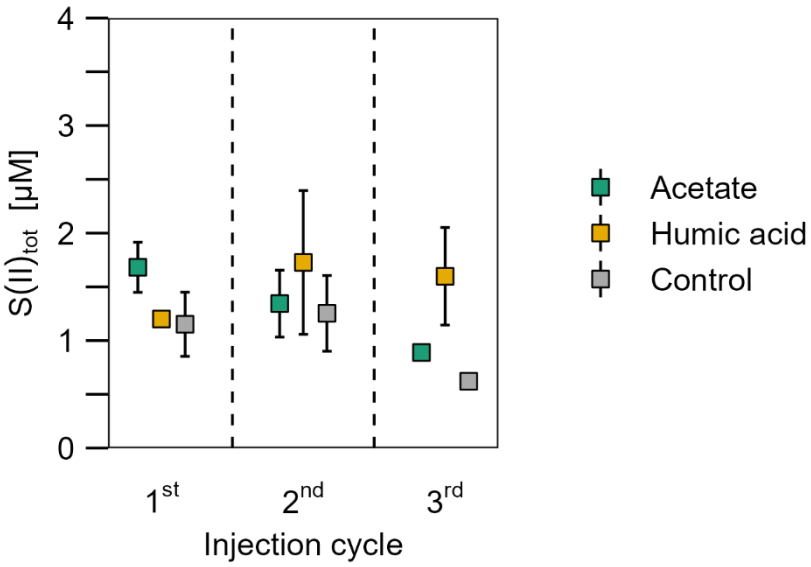

Figure S11. Total sulfide ($S(II)_{tot}$) in the porewater over three injection cycles for acetate (green), humic acid (orange), and control (grey) plots in the intertidal flat. Porewater was sampled after each injection cycle (injection cycles are separated by a dashed line). Markers show mean ± standard error of triplicates.

Effect of organic carbon input on microbial growth and metabolic activity in the intertidal flat (Figure S12 and S13)

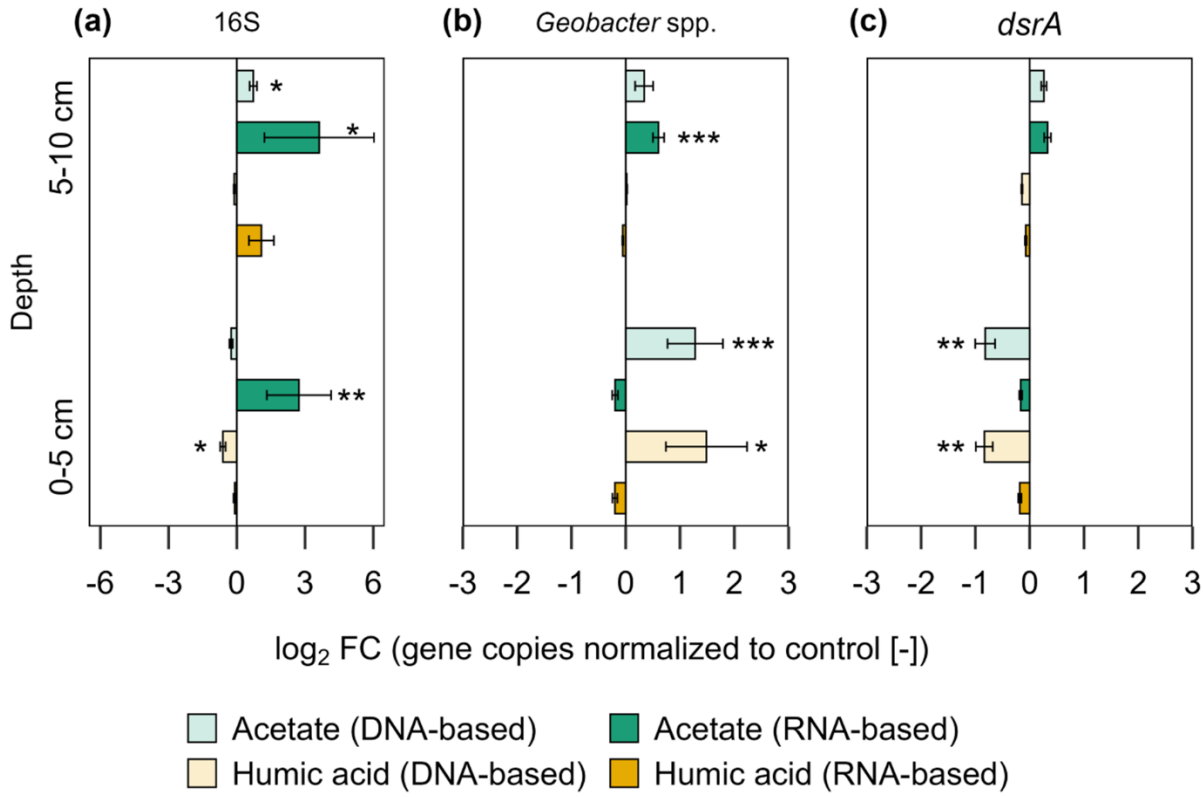

Figure S12. Bacterial gene copy numbers of (a) bacterial 16S rRNA (16S), (b) *Geobacter* spp., and (c) *dsrA* for acetate and humic acid treatment normalized to the control in the intertidal flat. The values are represented as $\log_2$ fold change (FC). Values > 0 indicate an upregulation while values < 0 indicate downregulation of the genes compared to the control (acetate in green, humic acid in orange). DNA-based numbers are given in lighter colors and RNA-based in darker colors. Statistical differences in the absolute gene copy numbers are indicated as stars in the figure: significant codes are $p \leq 0.05$ *, $p \leq 0.01$ **, and $p \leq 0.001$ ***. Absolute gene copy numbers and statistical details are given in Table S14 and Fig. S13. Sample sizes include triplicates, represented as mean ± standard error.

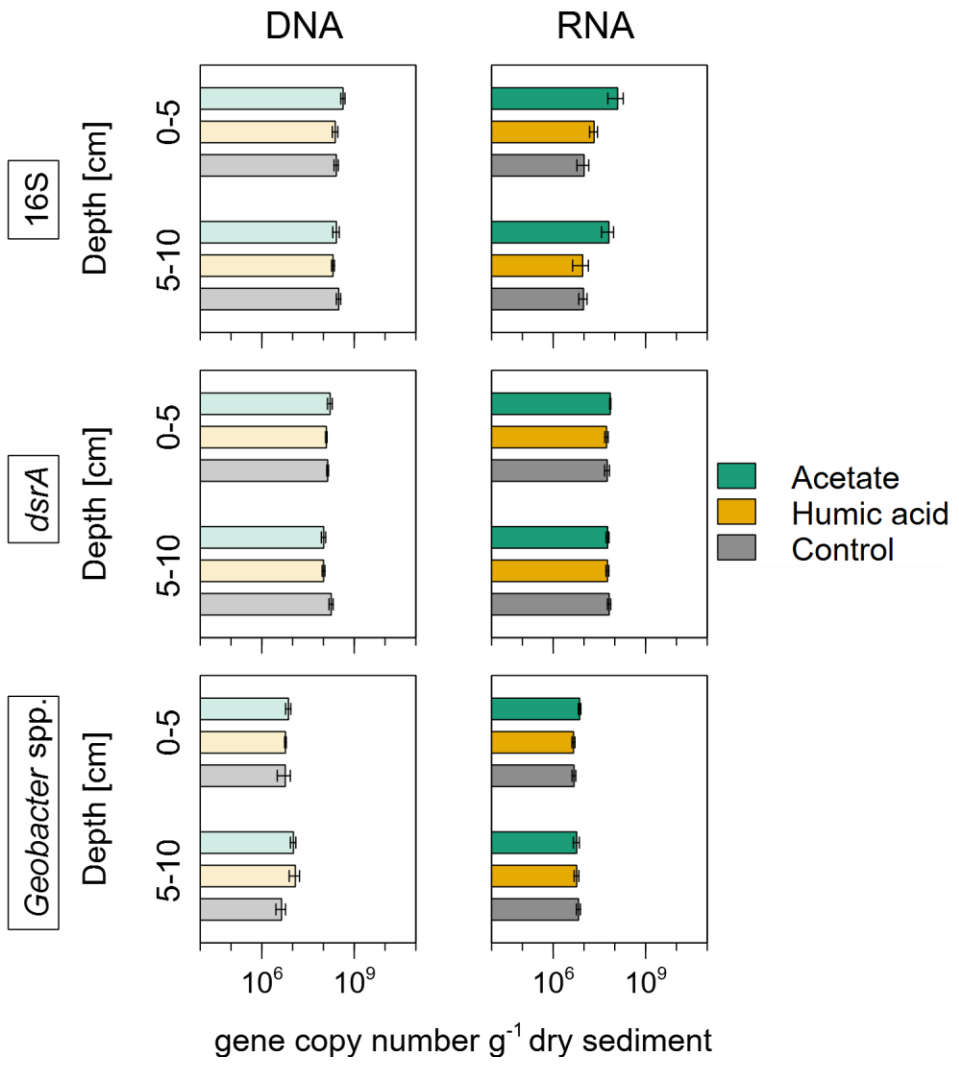

Figure S13. Total gene copy number of 16S, *dsrA*, and *Geobacter* spp. are shown separately for DNA and RNA for the intertidal flat. DNA- (lighter colour) and RNA- based gene copies (darker colour) for acetate, humic acid treatment, and the control in the intertidal flat. Acetate treatment is shown in green, humic acid treatment in orange, and the control in grey. Two depths: upper layer (0-5 cm) and lower layer (5-10 cm). Samples size compress triplicates, represented as mean ± standard error.

Benthic organisms at the study site – pioneer marsh and intertidal flat (Figure S14)

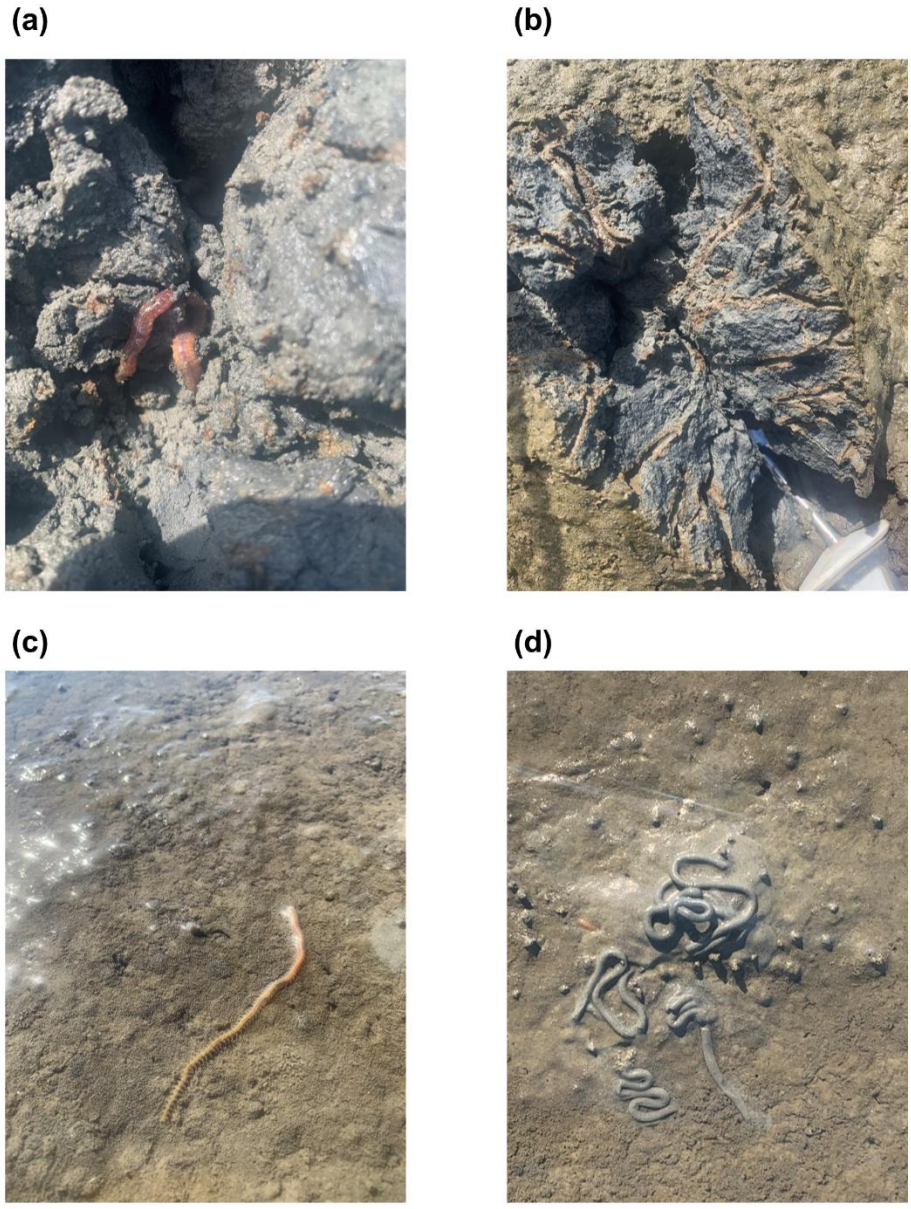

Figure S14. Visual observations of bioturbation and bioirrigation at the study site. (a) and (b) are from the pioneer marsh and (c) and (d) from the intertidal flat. (a) shows a worm burrowing into the sediment, (b) belowground channels evidence of oxygen infiltration, (c) worm on the sediment surface, (d) indication of burrowing organisms (lugworm).

Cumulative CO_2 emission calculation (Figure S15)

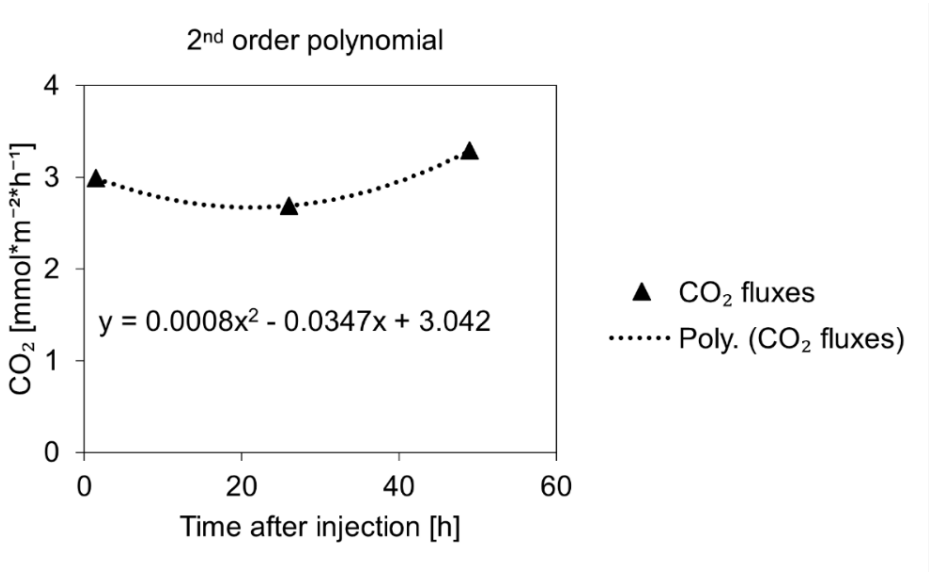

Figure S15. Example of cumulative CO_2 emission calculation with the 2nd order polynomial trendline. Calculation is explained in Section S1.5. The individual CO_2 emissions at 1.5, 24, and 48 h after injection are shown over time. A second order trendline, based on these values, is displayed in the plot. Given example is a replicate from the pioneer marsh, acetate treatment, and 4th injection cycle.

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ISO 17892-4 (2016), DIN EN ISO 17892-4:2017-04, EN ISO 17892-4:2016 (D). Geotechnical investigation and testing — Laboratory testing of soil — Part 4: Determination of particle size distribution (ISO 17892-4:2016).