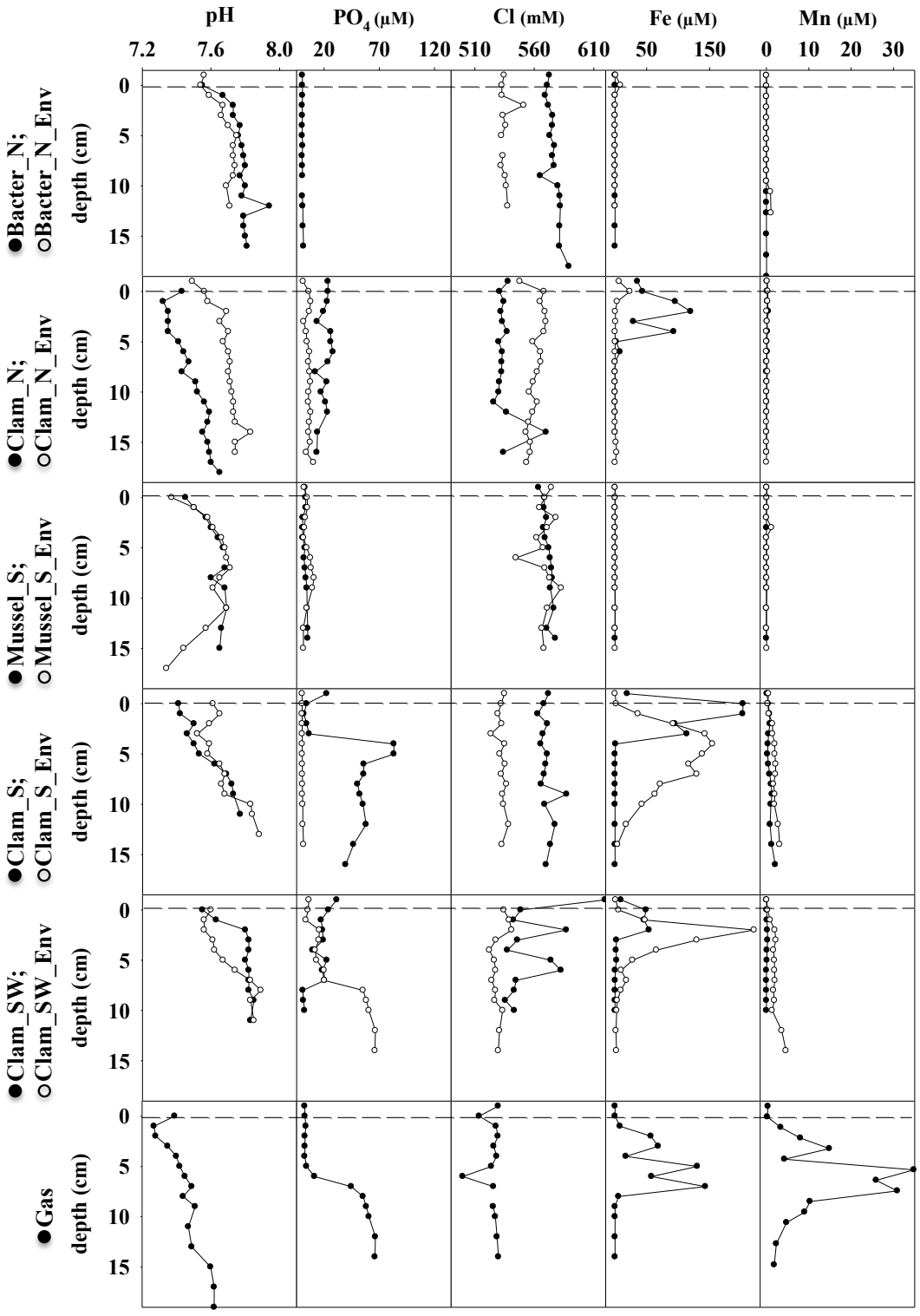
Supplement text 1:

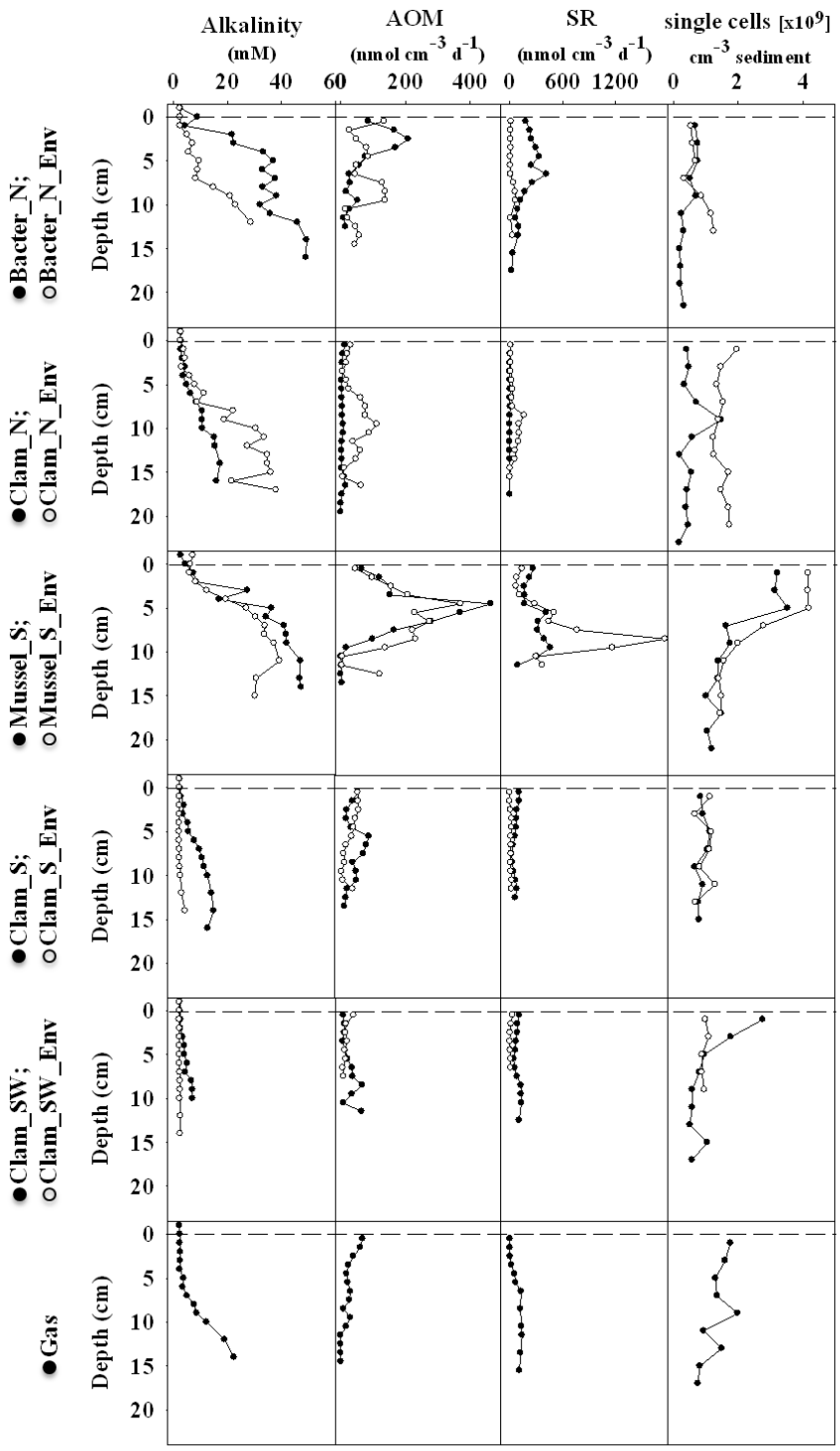
Porewater geochemistry

Immediately after recovery and transfer of the push cores to *in situ* temperature of 4 °C, pH of every centimetre sediment depth was determined with punch-in electrodes on undisturbed sediment cores. Porewater analyses of phosphate and iron (Fe^{2+}) were carried out on board. For the analyses of dissolved iron (Fe^{2+}) porewater subsamples of 1 ml were immediately complexed with 50 μl of "Ferrospectral" and determined photometrically. A photometric procedure was used to determine the concentration of phosphate in extracted porewater subsamples. Aliquots of the porewater were diluted 1:10 and acidified with $HNO_{3\ (suprapure)}$ for the determination of manganese concentration by Inductively Coupled Plasma - Atomic Emission Spectrometry (ICP-AES) and Atomic absorption Spectroscopy (AAS) in the home laboratory.

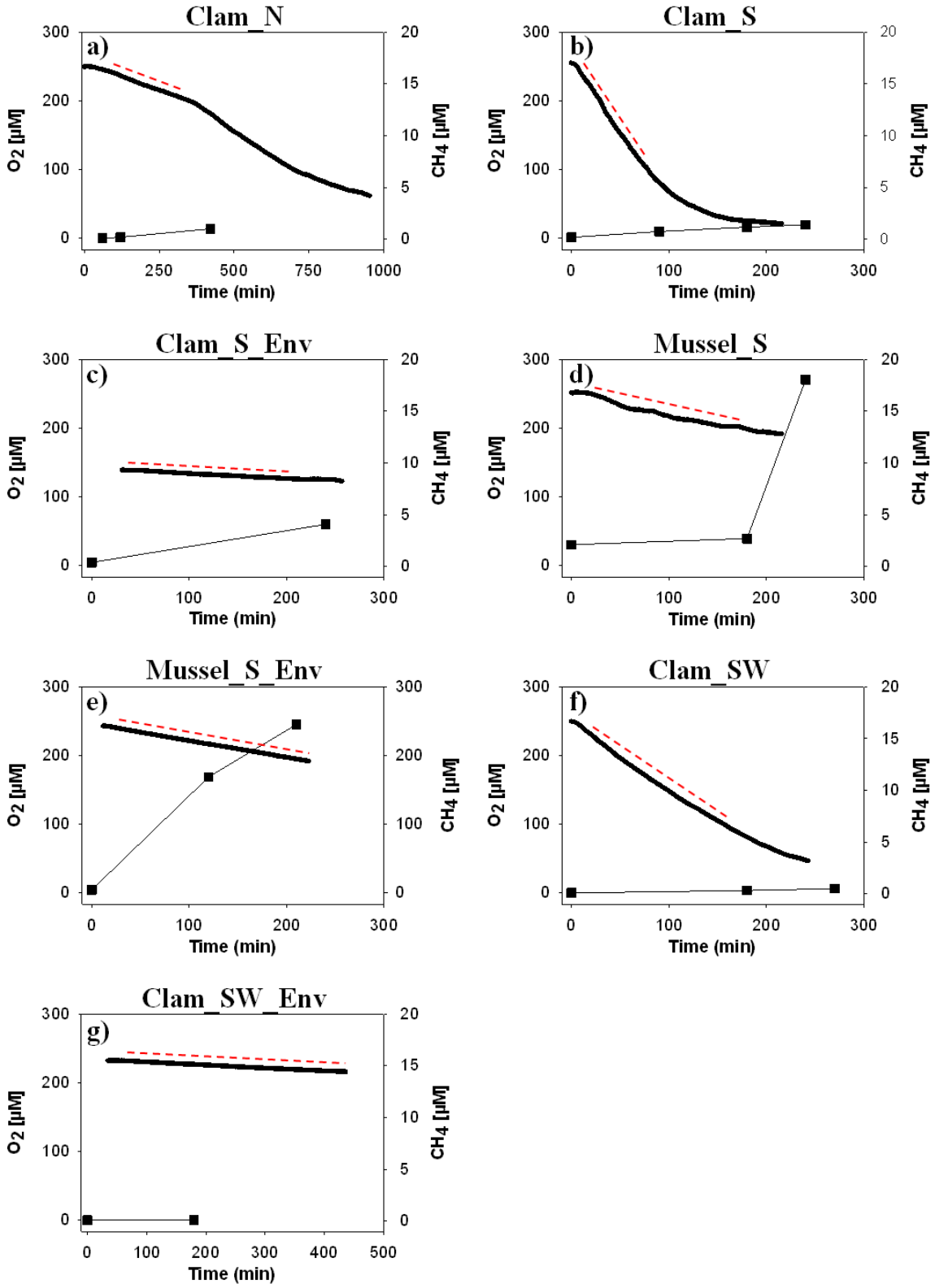
Elevated alkalinity values were detected at all sites where also enhanced AOM activity was measured, indicating potential variation in the seepage between sites (Fig. 3). At these sites alkalinity increased with depth to reach maximum values of 47 and 49 mM in the deepest investigated horizons at the Mussel_S and Bacter_N sites, respectively (Fig.3). Highest alkalinity flux of 0.4 mmol m^{-2} d^{-1} was detected at the Mussel_S and the Bacter_N sites. Near background (2.5 mM) values were detected at the Clam_S_Env, Clam_SW, Clam_SW_Env. The iron profiles matched well the sulphide depth pattern, with elevated concentrations detected at the clam habitats where free sulphide was absent from the topmost surface layers (Supplement Fig. 1).



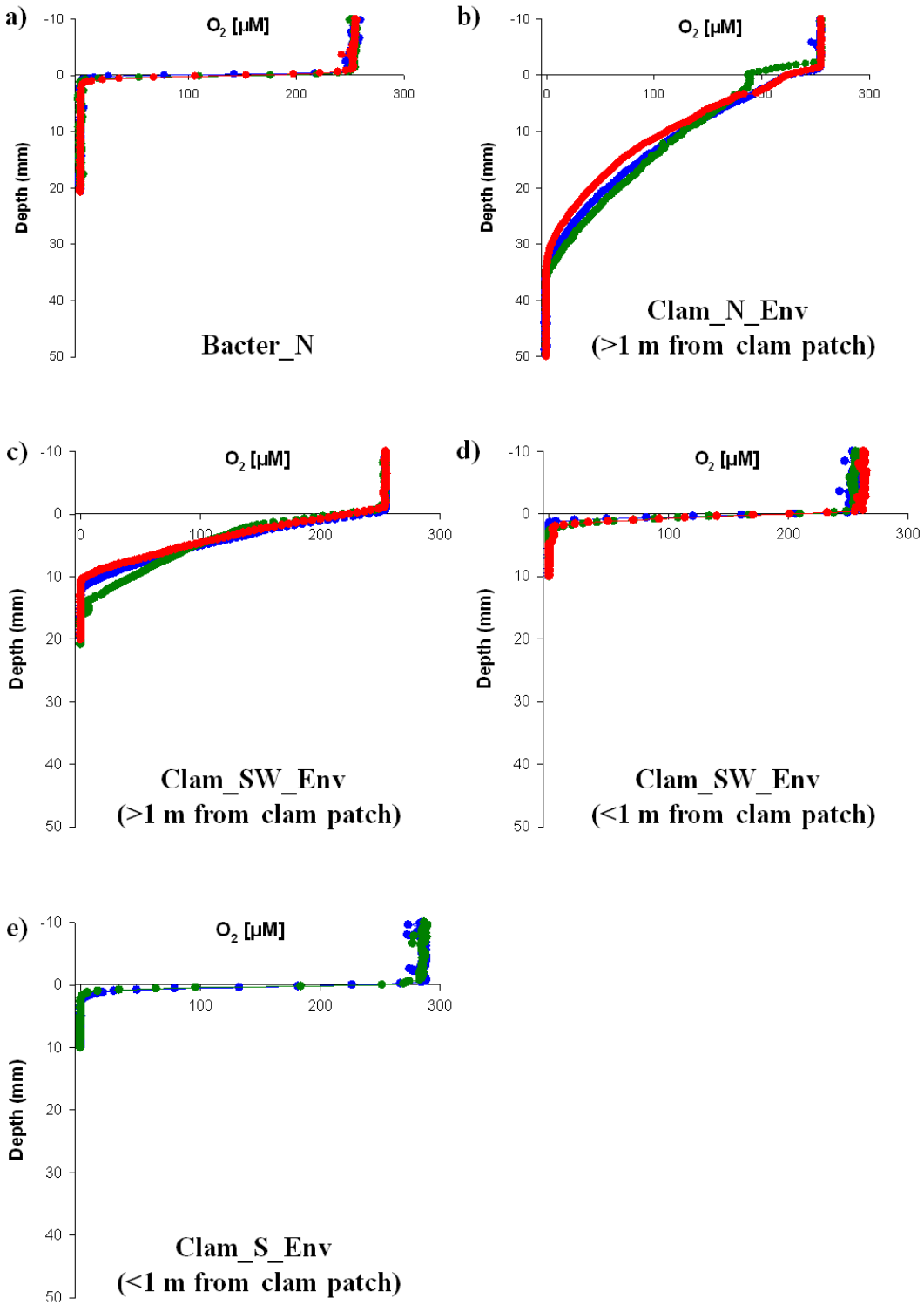
Supplement Fig. 1 Geochemical depth profiles of pH, PO_4, Cl, Fe and Mn at all investigated sites at REGAB. Closed symbols denote measurements taken within the patches/bacterial mat, and open symbols denote measurements taken at the respective bare sediments.



Supplement Fig. 2 Geochemical depth profiles of alkalinity, anaerobic oxidation of methane (AOM) and sulphate reduction (SR) rates, as well as single cell numbers measured at the different habitats at REGAB. Closed symbols denote measurements taken within the patches/bacterial mat, and open symbols denote measurements taken at the respective bare sediments.



Supplement Fig. 3 *In situ* benthic chamber incubations of oxygen (black line) and methane concentrations (squares) at the different habitats at REGAB. The concentration gradient from which the total oxygen uptake was calculated (see Table 2) is depicted with a red dashed line.



Supplement Fig. 4 *In situ* microsensor measurements of the sediment oxygen concentrations (µM) at different soft-bottom habitats at REGAB. At each measurement site, the microprofiler was equipped with 2 - 3 oxygen microsensors (here depicted with different colors) for simultaneous measurement of the oxygen concentration.

Supplement Table 1 Overview of the samples and measurements acquired at REGAB during M76/3b, with their PANGAEA reference numbers. All data has been deposited and is available online in the PANGAEA database (www.pangaea.de).

Location	Sampling site	Measurement; Sample	Pangaea Event Label
N REGAB	**Bacter_N** (Bacterial mat)	DNA	M76/3b_310_PUC13; M76/3b_310_PUC27
		Porewater	M76/3b_310_PUC28; M76/3b_310_PUC32
		pH	M76/3b_310_PUC8
		AOM; SR	M76/3b_310_PUC27; M76/3b_310_PUC13; M76/3b_310_PUC12
		MICP	M76/3b_312_MICP1
	Bacter_N_Env (Outside bacterial mat)	DNA	M76/3b_312_PUC7
		Porewater	M76/3b_312_PUC15
		pH	M76/3b_312_PUC34
		AOM; SR	M76/3b_312_PUC22; M76/3b_312_PUC23; M76/3b_312_PUC7;
	Clam_N (Clam patch)	DNA	M76/3b_323_PUC14
		Porewater	M76/3b_323_PUC15
		pH	M76/3b_323_PUC30
		AOM; SR	M76/3b_323_PUC28; M76/3b_323_PUC31; M76/3b_323_PUC14; M76/3b_323_PUC12
		CHAM	M76/3b_325_CHAM1
	Clam_N_Env (Outside clam patch)	DNA	M76/3b_332_PUC29
		Porewater	M76/3b_332_PUC31
		pH	M76/3b_332_PUC20
		AOM; SR	M76/3b_332_PUC23; M76/3b_332_PUC29; M76/3b_332_PUC34
		MICP	M76/3b_335_MICP1
S REGAB	**Mussel_S** (Mussel patch)	DNA	M76/3b_344_PUC23
		Porewater	M76/3b_344_PUC30
		pH	M76/3b_344_PUC29
		AOM; SR	M76/3b_344_PUC23; M76/3b_344_PUC28; M76/3b_344_PUC15
		CHAM	M76/3b_364_CHAM1
	Mussel_S_Env (Outside mussel patch)	DNA	M76/3b_361_PUC36
		Porewater	M76/3b_361_PUC14
		pH	M76/3b_361_PUC13
		AOM; SR	M76/3b_361_PUC36; M76/3b_361_PUC15
		CHAM	M76/3b_364_CHAM2
	Clam_S (Clam patch)	DNA	M76/3b_361_PUC24
		Porewater	M76/3b_361_PUC31
		pH	M76/3b_355_PUC9
		AOM; SR	M76/3b_361_PUC10; M76/3b_361_PUC21; M76/3b_361_PUC24
		CHAM	M76/3b_355_CHAM1
	Clam_S_Env (Outside clam patch)	DNA	M76/3b_355_PUC29
		Porewater	M76/3b_355_PUC35
		pH	M76/3b_355_PUC20
		AOM; SR	M76/3b_355_PUC11; M76/3b_355_PUC7; M76/3b_355_PUC29
		MICP	M76/3b_361_MICP1; M76/3b_361_MICP2
		CHAM	M76/3b_355_CHAM2
REGAB	**Gas** (Gas bubble)	DNA	M76/3b_364_PUC7
		Porewater	M76/3b_364_PUC21
		pH	M76/3b_364_PUC28
		AOM; SR	M76/3b_364_PUC7; M76/3b_364_PUC29; M76/3b_364_PUC9
SW REGAB	**Clam_SW** (Clam patch)	DNA	M76/3b_379_PUC28
		Porewater	M76/3b_379_PUC29
		pH	M76/3b_379_PUC34
		AOM; SR	M76/3b_379_PUC28; M76/3b_379_PUC14; M76/3b_379_PUC15
		CHAM	M76/3b_379_CHAM1
	Clam_SW_Env (Outside clam patch)	DNA	M76/3b_379_PUC10
		Porewater	M76/3b_379_PUC9
		pH	M76/3b_379_PUC5
		AOM; SR	M76/3b_379_PUC10; M76/3b_379_PUC13
		MICP	M76/3b_385_MICP1; M76/3b_385_MICP2
		CHAM	M76/3b_379_CHAM2

Supplement Table 2 Percentage of shared OTUs between all sites investigated at REGAB. Prior to this analysis, the depth samples within individual sites were merged.

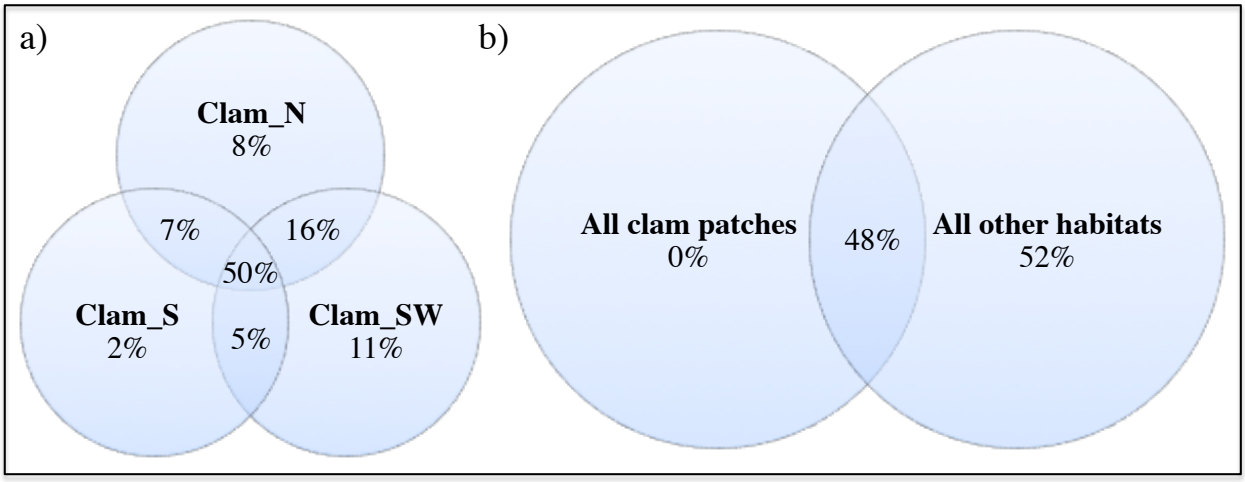
	Bacter_N	Bacter_N_Env	Clam_N	Clam_N_Env	Mussel_S	Mussel_S_Env	Clam_S_Env	Clam_S	Gas	Clam_SW
Bacter_N_Env	79									
Clam_N	83	73								
Clam_N_Env	84	77	82							
Mussel_S	69	65	67	71						
Mussel_S_Env	58	56	61	57	64					
Clam_S_Env	64	60	62	65	61	55				
Clam_S	68	64	69	68	66	57	67			
Gas	69	63	67	65	65	56	61	65		
Clam_SW	80	71	72	78	70	54	64	66	70	
Clam_SW_Env	73	65	69	72	68	53	60	63	65	79

Supplement Table 3 Comparison of the shared OTUs (given as percentage) among all depth samples, between bare sediment sites and clam populated sites. An OTU was regarded as shared only if it was present in all samples (0 – 10 cm or 0 – 5 cm). The percentage of shared OTUs was calculated as the fraction of the total OTUs at the individual habitat.

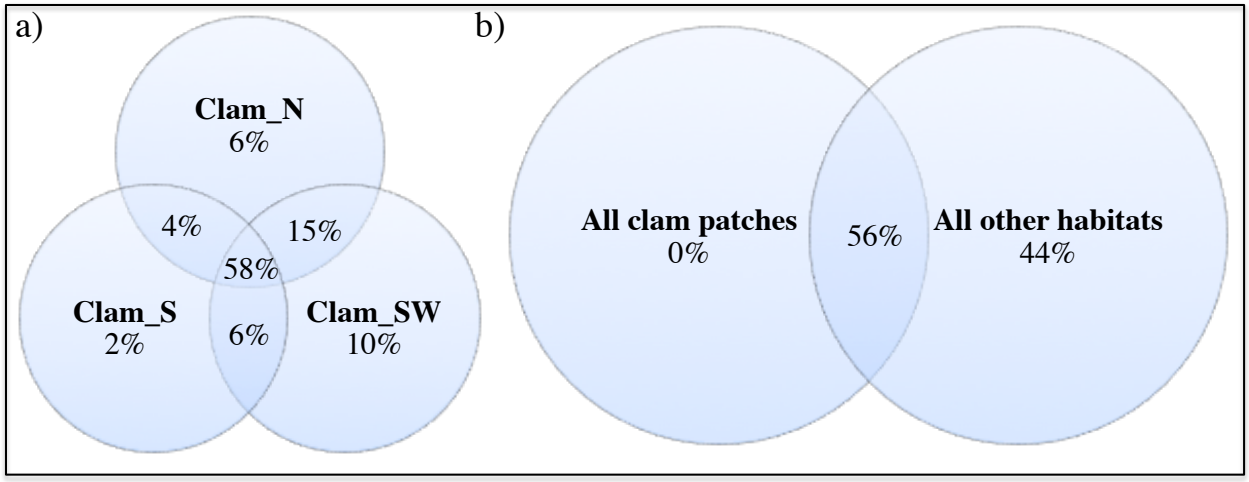
	Clam_N (0 - 10 cm)	**Clam_S** (0 - 10 cm)	**SW_Clam** (0 - 10 cm)	**Clam_N** (0 - 5 cm)	**Clam_S** (0 - 5 cm)	**SW_Clam** (0 - 5 cm)
Inside	36	30	22	47	40	47
Outside	34	30	36	42	44	44

Supplement Table 4 Distance-based test for homogeneity of multivariate dispersions. Table comprises average distances to the centroids, calculated based on Jaccard and Bray-Curtis dissimilarity indices. The higher the value of the average distance to the centroid, the higher the dispersion (variance) within the respective group. The test was performed incorporating only the surface samples (0 – 5 cm), or samples from all depths (0 – 10 cm).

	Clam_N	**Clam_N_Env**	**Clam_S**	**Clam_S_Env**	**Clam_SW**	**Clam_SW_Env**
0 - 5 cm (Jaccard)	0.3	0.3	0.4	0.3	0.3	0.3
0 - 5 cm (Bray-Curtis)	0.2	0.2	0.3	0.2	0.2	0.2
0 - 10 cm (Jaccard)	0.4	0.4	0.4	0.4	0.4	0.4
0 - 10 cm (Bray-Curtis)	0.2	0.2	0.3	0.3	0.3	0.3



Supplement Fig. 5 OTU partitioning analysis taking into account all sediment depth samples (0 – 10 cm). 50% of the total OTUs were found to be shared by all three clam patches (a). The clam patches had no unique OTUs relative to the other investigated habitats at REGAB (b).



Supplement Fig. 6 OTU partitioning analysis taking into account the topmost 5 cm sediment depth samples. 58% of the total OTUs were found to be shared by all three clam patches (a). The clam patches had no unique OTUs relative to the other investigated habitats at REGAB (b).