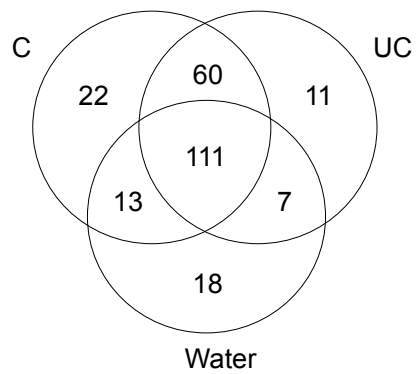
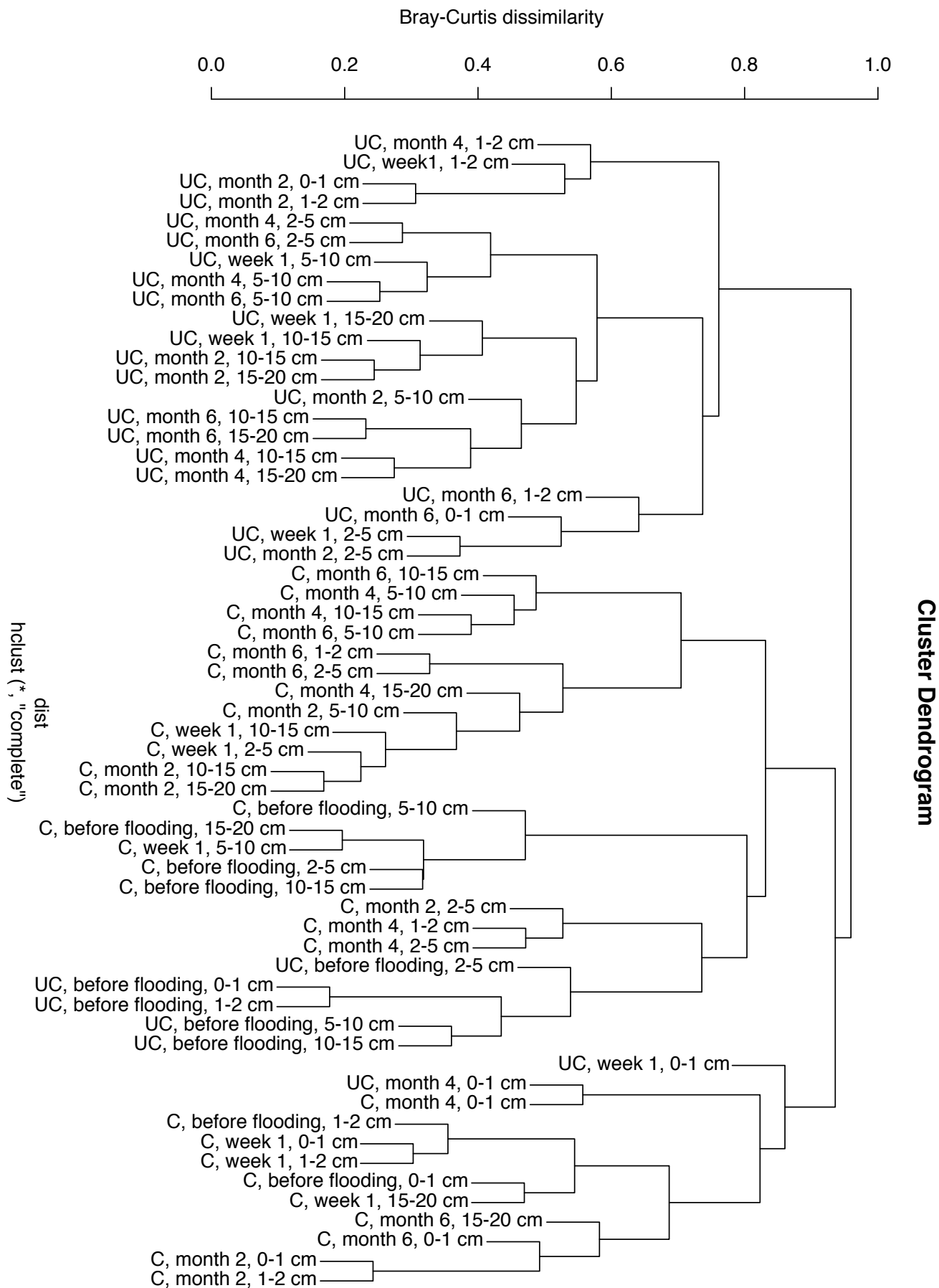


**Table S1** Description of primers used for T-RFLP and qPCR analysis.

Target organism	Gene	Primer	Sequence (5'-3')	Annealing temperature (°C)	Reference
Bacteria	16S rRNA	B27F	AGR GTT YGA TYM TGG CTC AG	54	Mason et al (2009)
		U519R	TTA CCG CGG CKG CTG		Ovreås et al (1997)
Bacterial nitrifiers	<i>amoA</i>	AOB-amoA-1F	GGG GTT TCT ACT GGT GGT	60	Rotthauwe et al (1997)
		AOB-amoA-2R	CCC CTC KGS AAA GCC TTC TTC		
Archaeal nitrifiers	<i>amoA</i>	AOA-amoA-f	CTG AYT GGG CYT GGA CAT C	59	Coolen et al (2007)
		AOA-amoA-r	TTC TTC TTT GTT GCC CAG TA		
Denitrifiers	<i>nirK</i>	F1aCu	ATC ATG GTS CTG CCG CG	58.3	Throback et al (2004)
		R3Cu	GCC TCG ATC AGR TTG TGG TT		
Denitrifiers	<i>nirS</i>	cd3aF	GTS AAC GTS AAG GAR ACS GG	58.3	Throback et al (2004)
		R3cd	GAS TTC GGR TGS GTC TTG A		



**Figure S1** Venn-diagram showing OTU distribution over all samples ( $n = 70$ ), including water samples from Gyldensteen, which the cores were flooded with, water samples of the tank at each core sectioning time point as well as the soil samples from before and after flooding. Total number of OTUs was 242.



**Figure S2** Hierarchical clustering dendrogram of all soil samples.

**Table S2** Adonis test results of experimental grouping factors: Time point (before flooding, week one, month two, four and six), station (uncultivated [UC] and cultivated [C]), depth categories (0-2 and 2-20 cm depth). Factors where tested as **(a)** crossed for the stations together and **(b)** separately.

**(a)**

Test variable	R <sup>2</sup>	p-value
Time point	0.19	0.001
Station	0.14	0.001
Depth	0.08	0.001
Time point : Station	0.08	0.001
Time point : Depth	0.09	0.001
Station : Depth	0.04	0.001
Time point : Station : Depth	0.05	ns

**(b)**

Test variable	Station UC		Station C	
	R <sup>2</sup>	p-value	R <sup>2</sup>	p-value
Time point	0.28	0.001	0.34	0.001
Depth	0.17	0.001	0.12	0.001
Time point : Depth	0.18	0.001	0.13	0.028

**Table S3** Adonis test results of environmental variables for time points after flooding. **(a)** The experimental factors depth (0-2 and 2-20 cm depth), time point (week one, month two, four and six) and soil characteristics were tested together. **(b)** Significance of total carbon dioxide (TCO<sub>2</sub>), dissolved organic carbon (DOC), ammonium (NH<sub>4</sub><sup>+</sup>) production rates, and reduction rates of sulfate (SO<sub>4</sub><sup>2-</sup>) were tested. Furthermore, **(c)** abundances of the bacterial 16S rRNA, *nirK*, *nirS*, bacterial and archaeal *amoA* genes were tested. Factors and variables were tested as crossed for the uncultivated (UC) and cultivated (C) stations separately. Only crossed factors that were significant are shown. Not significant R<sup>2</sup> values are indicated by p-value = ns.

(a)	Test variable	Station UC		Station C	
		R <sup>2</sup>	p-value	R <sup>2</sup>	p-value
	Depth	0.23	0.001	0.12	0.005
	Time point	0.06	0.005	0.09	0.006
	Water content (%)	0.07	0.005	0.07	0.025
	Chloride (mM)	0.05	0.010	0.05	ns
	Depth : Time point	0.07	0.004	0.02	ns
	Depth : Water content (%)	0.05	0.023	0.06	ns
	Depth : Chloride (mM)	0.08	0.001	0.03	ns
	Depth : Time point : Water content (%)	0.06	0.007	0.04	ns
	Depth : Water content (%) : Chloride (mM)	0.05	0.015	0.05	ns
(b)	Test variable	Station UC		Station C	
		R <sup>2</sup>	p-value	R <sup>2</sup>	p-value
	Anoxic TCO <sub>2</sub> production rate	0.20	0.001	0.10	0.001
	Anoxic DOC production rate	0.12	0.002	0.05	0.026
	Anoxic NH <sub>4</sub> <sup>+</sup> production rate	0.09	0.003	0.05	0.013
	Anoxic SO <sub>4</sub> <sup>2-</sup> reduction rate	0.03	ns	0.08	0.001
	Anoxic TCO <sub>2</sub> production rate : Anoxic DOC production rate	0.08	0.003	0.12	0.001
	Anoxic TCO <sub>2</sub> production rate : Anoxic NH <sub>4</sub> <sup>+</sup> production rate	0.04	ns	0.04	0.037
	Anoxic DOC production rate : Anoxic NH <sub>4</sub> <sup>+</sup> production rate	0.02	ns	0.05	0.011
	Anoxic TCO <sub>2</sub> production rate : Anoxic SO <sub>4</sub> <sup>2-</sup> reduction rate	0.02	ns	0.06	0.004
	Anoxic DOC production rate : Anoxic SO <sub>4</sub> <sup>2-</sup> reduction rate	0.04	ns	0.06	0.006
(c)	Test variable	Station UC		Station C	
		R <sup>2</sup>	p-value	R <sup>2</sup>	p-value
	Bacterial 16S rRNA gene	0.17	0.001	0.09	0.032
	<i>nirK</i> gene	0.16	0.001	0.11	0.002
	<i>nirS</i> gene	0.08	0.005	0.05	ns
	<i>amoA</i> gene (AOB)	0.11	0.001	0.10	0.004
	<i>amoA</i> gene (AOA)	0.05	ns	0.09	0.012
	<i>nirK</i> gene : <i>nirS</i> gene	0.08	0.008	0.02	ns
	<i>nirK</i> gene : <i>nirS</i> gene : <i>amoA</i> gene (AOA)	0.06	0.039	0.03	ns